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Supplementary appendix

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Appendix 1: supplementary methods and results to "Global burden of bacterial antimicrobial resistance in 2019"

This appendix provides further methodological details and supplementary results for "Global burden of bacterial antimicrobial resistance in 2019".

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Section 1: List of abbreviations

Abbreviation Full phrase

AGAR Australian Group on Antimicrobial Resistance

AHC Angkor Hospital for Children

AMASS AutoMated tool for Antimicrobial resistance Surveillance System

AMR antimicrobial resistance

APUA Alliance for the Prudent Use of Antibiotics

ARSP Antimicrobial Resistance Surveillance Program

ATLAS Antimicrobial Testing Leadership and Surveillance

AURA Antimicrobial Use and Resistance in Australia

AWARE Assessing Worldwide Antimicrobial Resistance Evaluation

BARNARDS Burden of Antibiotic Resistance in Neonates from Developing Societies

BD Becton, Dickinson, and Company

BSI bloodstream infections

CAESAR Central Asian and European Surveillance of Antimicrobial Resistance

CAI community-acquired infection

CDC Centers for Disease Control and Prevention

CFR case fatality ratio

CHAIN Childhood Acute Illness and Nutrition

CHAMPS Child Health and Mortality Prevention Surveillance

cIAI complicated intra-abdominal infection

COMRU Cambodia Oxford Medical Research Unit

CTMRF CHILDS Trust Medical Research Foundation

cUTI complicated urinary tract infection

DALYs Disability-adjusted life-years

DHS Demographic Health Surveys

EARS-Net European Antimicrobial Resistance Surveillance Network

ECDC European Centre for Disease Prevention and Control

GAM generalised additive models

GBD Global Burden of Diseases, Injuries, and Risk Factors Study

GBS group B Streptococcus

GLASS Global Antimicrobial Resistance Surveillance System

GLM generalised linear model

GPR Gaussian process regression

HAI hospital-acquired infection

HAQ Index Healthcare Access and Quality Index

HHS U.S. Department of Health and Human Services

ICD International Classification of Diseases

ICU intensive care unit

INFORM International Network for Optimal Resistance Monitoring

INICC International Nosocomial Infection Control Consortium

iNTS invasive non-typhoidal Salmonella

IORD Infections in Oxfordshire Research Database

IQVIA IMS Health and Quintiles

JANIS Japan Nosocomial Infections Surveillance

KEMRI Kenya Medical Research Institute

LRI lower respiratory infection

MCoD multiple causes of death data

MEPCO multinomial estimation of partial and composite observations

MICS Multiple Indicators Cluster Surveys

MITS minimally invasive tissue sampling

MR-BRT meta-regression—Bayesian, regularised, trimmed

MRC Medical Research Council

NARMS National Antimicrobial Resistance Monitoring System for Enteric Bacteria

NICD National Institute for Communicable Diseases

OUCRU Oxford University Clinical Research Unit

PPS HAI Point Prevalence Survey on Nosocomial Infections and Antibiotic Use

PRISMA Preferred Reporting Items for Systematic Reviews and Meta-Analyses

SDI Socio-demographic Index

SEV summary exposure value

SGUL-GARPEC St. George's Hospital, University of London - Global Antimicrobial Resistance,

Prescribing and Efficacy Among Neonates and Children

SOAR Survey on Antibiotic Resistance

ST-GPR spatiotemporal Gaussian process regression

TB tuberculosis

TESSy The European Surveillance System

TEST Tigecycline Evaluation Surveillance Trial

TSAP Typhoid Fever Surveillance in Africa Program

UI uncertainty interval

UPCH Cayetano Heredia University

USDA U.S. Department of Agriculture

UTI urinary tract infection

VR vital registration

WHO World Health Organization

WRP Walter Reed Project

YLDs years lived with disability

YLLs years of life lost

Section 2: Data sources

The data used for this study can be categorised into the following types: multiple causes of death (MCoD), hospital discharge, linkage, mortality surveillance, literature reviews, , microbial, single drug-resistance profiles, pharmaceutical sales, and antibiotic use data; as well as estimates from the Global Burden of Diseases, Injuries, and Risk Factors Study (GBD) 2019. More detailed information on data inputs are available at http://ghdx.healthdata.org/record/ihme-data/global-bacterial-antimicrobial-resistance-burden-estimates-2019.

Section 2.1: Multiple causes of death and vital registration (MCoD-VR)

Multiple cause of death (MCoD) data is a type of vital registration obtained from death certificates that contain the underlying cause of death, intermediate and immediate causes of death, and contributing conditions. MCoD data differ from other vital registration (VR) sources, because many countries have VR systems that only document the underlying cause of death. MCoD data were used in the sepsis, infectious syndrome, and pathogen distribution component models and data processing, and modelling methods can be found in sections 4 and 6. MCoD-VR data came from the following sources.

- United States National Vital Statistics System
- Brazil Mortality Information System
- National Institute of Statistics (Italy)
- Statistics South Africa
- National Institute of Statistics and Geography (Mexico)
- National Administrative Department of Statistics (Colombia)
- Taiwan Ministry of Health and Welfare

Section 2.2: Hospital discharge

Hospital admissions and discharge data are data sources collected from inpatient hospital and other clinical settings. These data include information on the primary and secondary diagnosis for each patient, as applicable, and were obtained from the sources listed below. Hospital data were used in the sepsis, infectious syndrome, pathogen

distribution, and case fatality ratio component models and data processing, and modelling methods can be found in sections 4–6.

- USA National Hospital Discharge Survey
- USA State Inpatient Databases
- Brazil Hospital Information System
- Italy Hospital Inpatient Discharges
- Sistema Automatizado de Egresos Hospitalarios (Mexico)
- Austria Hospital Inpatient Discharges
- New Zealand National Minimum Dataset
- Canada Discharge Abstract Database

Section 2.3: Microbial data with outcome

Microbial data are data sources from hospital and lab networks that collect pathogen cultures from patients. The cultures are tested for both pathogen and the pathogen's resistance to antibiotics. The culture results are linked to patient outcome, diagnoses, or both. Microbial data without these outcomes or diagnoses are listed in section 2.4. These data also include the specimen from which the pathogen was isolated and whether the infection was community- or hospital-acquired, if available. When hospital versus community acquisition was not specified, we used the difference between admission or diagnosis date and the specimen collection date, and if 48 hours or fewer had passed between those two dates, then the infection was assumed to be community-acquired. We assumed the infection was hospital-acquired when more than 48 hours had passed, consistent with CDC/National Healthcare Safety Network guidelines.² Microbial data with outcome were used in the case fatality ratio, pathogen distribution, prevalence of resistance, and relative risk component models and data processing, and modelling methods can be found in sections 5–8. Microbiology data types, with outcome and diagnoses were obtained from the sources below.

- USA Becton, Dickinson, and Co. (BD) Insights, Research and Analytics Database microbiology test and in-patient hospital data: data procured by BD via MedMined. Covers a range of regions in the United States from 2011 to 2017.
- UK Infections in Oxfordshire Research Database (IORD): patient microbiology and episodes data from Oxford University Hospitals NHS Foundation Trust.
- International Nosocomial Infection Control Consortium (INICC) surveillance online system: data from the INICC data collection software. ICU patient microbiology and hospital data from 50 countries across Latin America, Asia, the Middle East, eastern Europe, and Africa from 2009 to 2020.
- Bulgaria antimicrobial resistance data: Medical University of Varna in Varna, Bulgaria. Covers 2014–2020.
- St. George's Hospital, University of London Global Antimicrobial Resistance, Prescribing and Efficacy Among Neonates and Children (SGUL-GARPEC) Project bloodstream infection data: Penta-sponsored global surveillance network focusing on neonatal and paediatric antimicrobial resistance and the organisms causing blood stream infections.
- Burden of Antibiotic Resistance in Neonates from Developing Societies (BARNARDS): BARNARDS includes locations in Nigeria, South Africa, Pakistan, Rwanda, Bangladesh, Ethiopia and India from 2015 to 2018
- Lao-Oxford-Mahosot Hospital-Wellcome Trust Research Unit (LOMWRU). Children and adults with fever, inpatient admissions: information from children and adults with fever who were admitted as inpatients between 1996 and 2019 to Mahosot Hospital, Vientiane, Laos. Microbial analysis was carried out by the Microbiology Laboratory at Mahosot Hospital.
- Kumasi Centre for Collaborative Research in Tropical Medicine (KCCR), Kumasi, Ghana together with the Bernhard Nocht Institute for Tropical Medicine. Data on children and adults admitted in hospital with fever: information from children and adults with fever admitted as inpatients at the Bernhard Nocht Institute for Tropical Medicine in Ghana between 2007 and 2015.
- Vietnam Hospital for Tropical Diseases, Ho Chi Minh City. Hospital-acquired infections in ICU patients: prospective observational study at the Oxford University Clinical Research Unit (OUCRU) in the

- Ho Chi Minh City Hospital for Tropical Diseases, Vietnam from November 2014 to January 2016 to assess the ICU-acquired colonisation and infections among adult patients with more than 48 hours of ICU stay.
- Medical Research Council (MRC) Unit The Gambia. Diagnostic antimicrobial susceptibility testing: information on hospital admission and discharge, pathogens cultured, resistance susceptibility test and antibiotics prescribed between 2005 and 2015 from the MCR Unit The Gambia, now part of the London School of Hygiene and Tropical Medicine.
- Cambodia Oxford Medical Research Unit (COMRU) and Angkor Hospital for Children (AHC). Suspected invasive bacterial infection hospitalisations: reports children aged 0–21 years who were hospitalised with suspected invasive bacterial infection between 2015 and 2018.
- Taiwan hospital-acquired infections and outcomes: infectious disease surveillance linked to vital registration from Taiwan (province of China).
- Childhood Acute Illness and Nutrition (CHAIN) Network antimicrobial resistance data: CHAIN Network study informs on hospitalised children under 2 years old with acute illness in Bangladesh, Burkina Faso, Pakistan, Kenya, Malawi, and Uganda.
- Lima, Peru Cayetano Heredia University (UPCH) antimicrobial resistance data: data from UPCH hospital sites across Lima, Peru with discharge disposition for infectious pulmonary disease
- **Jordan King Abdulla University Hospital culture and sensitivity tests:** information on inpatients at the King Abdulla University Hospital in 2020 part of the Jordan University of Science and Technology.
- Iran antimicrobial resistance in burn patients and identified in blood, cerebrospinal fluid, and urine cultures: data from inpatients across different hospital sites in Iran between 2016 and 2020.
- Dhaka, Bangladesh Bangabandhu Sheik Mujib Medical University hospital inpatient data: data from 201 inpatients in 2017 at the Bangabandhu Sheikh Mujib Medical University, Dhaka, Bangladesh.
- Chiangrai Prachanukroh Hospital, Chiangrai Clinical Research Unit and Mahidol Oxford Tropical Medicine Research Unit: data from inpatients with positive cultures at the Chiangrai Prachanukroh Hospital from 2017 to 2019.
- KEMRI/US Army Medical Research Directorate
- Chennai, India Kanchi Kamakoti CHILDS Trust Medical Research Foundation (CTMRF) hospital inpatient data

Section 2.4: Microbial data without outcome

Microbial data were also obtained from laboratories, which do not necessarily link to patients' hospital records nor information on their discharge disposition. These sources report specimen or site of infection, pathogens isolated, antimicrobial susceptibility tests, age and gender and other demographic characteristics. This information proved useful to inform pathogen distribution and prevalence of resistance component models and data processing, and modelling methods can be found in sections 6 and 7. Microbial data without outcome and diagnoses were obtained from the sources below.

- **SENTRY:** SENTRY Antimicrobial Surveillance Program established by JMI Labs in 1997. Sites are in the USA, Europe, Latin America, parts of Asia, and the Western Pacific
- Germany National Point Prevalence Survey on Nosocomial Infections and Antibiotic Use (PPS HAI): Point Prevalence Survey for 2016 data reporting the pathogen distribution for hospital-acquired infections.
- Madagascar Fondation Merieux: data collected from inpatients with positive culture admitted in three hospital sites in Madagascar, funded by Fondation Merieux.
- AMASS: data collected in an automated tool by Oxford Tropical Network Research Units.
- **The European Surveillance System (TESSy):** managed by the European Centre for Disease Prevention and Control (ECDC), provided data from the following surveillance systems:
 - European Antimicrobial Resistance Surveillance Network (EARS-Net)
 - Food-and Waterborne Diseases and Zoonoses Surveillance Network.
 - Invasive Pneumococcal Disease Surveillance Network, including discharge disposition.
 - Gonococcal Antimicrobial Surveillance Programme.

- Healthcare Associated Infections Surveillance Network (ICU protocol), including discharge disposition.
- European Tuberculosis Surveillance Network
- European Surveillance of Antimicrobial Consumption Network

For the European Union/European Economic Area (EU/EEA), data were obtained from the European Surveillance System (TESSy) as provided by Austria, Belgium, Croatia, Cyprus, Czechia, Denmark, Estonia, Finland, France, Germany, Greece, Hungary, Iceland, Ireland, Italy, Latvia, Luxembourg, Malta, Netherlands, Norway, Poland, Portugal, Romania, Slovakia, Slovenia, Spain, Sweden, and the United Kingdom, and released by the European Centre for Disease Prevention and Control (ECDC).

- Pfizer ATLAS Programme: the Antimicrobial Testing Leadership and Surveillance (ATLAS) database
 includes the Tigecycline Evaluation Surveillance Trial (TEST), the Assessing Worldwide Antimicrobial
 Resistance Evaluation (AWARE) and the International Network for Optimal Resistance Monitoring
 (INFORM) programs. The study spans in coverage across more than 70 countries between 2004 and 2017.
- Malawi Queen Elizabeth Hospital microbiology tests of blood specimens: microbiology tests of blood specimens from inpatients at the Queen Elizabeth Hospital in Malawi from 1998 to 2016, part of the Institute of Infection and Global Health, University of Liverpool in collaboration with the Malawi-Liverpool-Wellcome Trust and the Wellcome Trust Sanger Institute.
- Central African Republic National Laboratory of Clinical Biology and Public Health: data collected by the Laboratoire National de Biologie Clinique et de Sante Publique in Central African Republic between 2017 and 2020.
- The Ethiopian AMR surveillance: conducted from July 2018 to July 2020 across sentinel surveillance sites and the National AMR Surveillance Coordinating Centre for the Ethiopian Public Health Institute.
- Lancet Labs: data obtained from Lancet Laboratories, a network of private laboratories across different sites in Africa.
- The Typhoid Fever Surveillance in Africa Program (TSAP): was established by the International Vaccine Institute to obtain comparable incidence data on typhoid fever and invasive non-typhoidal Salmonella disease in Ghana, Burkina Faso, Ethiopia, Guinea Bissau, Kenya, Madagascar, Senegal, South Africa, Sudan, and Tanzania.
- Invasive *Salmonella* infections at multiple surveillance sites in the Democratic Republic of the Congo study: data published as part of the study on invasive *Salmonella* infections at multiple surveillance sites in the Democratic Republic of the Congo between 2011 and 2014.
- Suva, Fiji Colonial War Memorial Hospital: Information on sequential *S. aureus* and Enterobacterial bloodstream infections at the Colonial War Memorial Hospital (analysis by Monash University) in Suva, Fiji, between 21 July 2020 and 29 October 2020.
- World Health Organization (WHO) Global Tuberculosis Programme
- Germany EARS-Net surveillance data 2017–2018
- WHO Meningitis surveillance: sentinel hospital surveillance of suspected meningitis cases among
 children under 5 years old and positive cultures, provided by the World Health Organization (WHO)
 Global Rotavirus, Invasive Bacterial Vaccine Preventable Diseases Surveillance Network Collaboration
 from 2008 to 2020.
- United States Active Bacterial Core Surveillance (ABCs) Reports: case reports on healthcare-associated Infections and community interface infections from the Emerging Infections Program Network coordinated by the Center for Disease Control and Prevention (CDC).

Section 2.5: Literature studies

We conducted literature searches to obtain input data for the following components in the analysis: maternal and neonatal sepsis aetiology, lower respiratory infections (LRIs) aetiology, urinary tract infections (UTIs) aetiology, skin infections aetiology, meningitis aetiology and case fatality, intra-abdominal infection aetiology, bone and joint infections aetiology, prevalence of resistance, relative risk and length of stay. Literature searches were performed on

PubMed using the following search strings, and extracted studies covered the time range 1980–2020. The search string for these searches can be found below. Literature was used in the case fatality ratio, pathogen distribution, prevalence of resistance and relative risk component models and data processing, and modelling methods can be found in sections 5–8. Literature studies were also used as input into the modelling of the antibiotic usage covariate.³

Section 2.5.1: Maternal sepsis, neonatal sepsis, and LRI aetiology

Aetiology terms, combined with OR:

- Infection (Infect*)
- Microbiology (Microbiolog*
- Aetiology (Aetiolog*)
- Etiology (Etiolog*)
- Virology (Virolog*)
- Bacteriology (Bacteriolog*)
- Fungus (fung*)

AND

Syndrome terms, combined with OR:

Maternal Sepsis

- puerperal sepsis (puerper* sepsis)
- maternal sepsis (matern* sepsis)
- puerperal septicaemia (puerper* septicaemia, American spelling too septicemia)
- maternal septicaemia (matern* septicaemia, American spelling too septicemia)
- puerperal infection (puerper* infection)
- maternal infection (matern* infection)
- puerperal bacteraemia (puerper* bacteraemia, American spelling too bacteremia)
- maternal bacteraemia (matern* bacteraemia, American spelling too bacteremia)

Neonatal Sepsis

- Neonatal sepsis (Neonat* sepsis within 3 or 5 words of each other)
- Neonatal septicaemia (Neonat* septicaemia within 3 or 5 words of each other, American spelling too-septicemia)
- Infant sepsis (Infant* sepsis)
- Infant septicaemia (Infant* septicaemia, American spelling too septicemia)
- Neonatal bacteraemia (Neonat* bacteraemia, American spelling too bacteremia)
- Infant bacteraemia (Infant* bacteraemia, American spelling too bacteremia)

Lower respiratory infections

- LRI
- Lower respiratory infection
- LRTI
- Lower respiratory tract infection
- Pneumonia

Section 2.5.2: Urinary tract infections aetiology

("complicated"[Title/Abstract] OR "uncomplicated"[Title/Abstract]) AND (("Cystitis/etiology"[majr:noexp] OR "Cystitis/microbiology"[majr:noexp]) OR ("Pyelonephritis/etiology"[marj:noexp] OR

"Pyelonephritis/microbiology"[majr:noexp]) OR ("Urinary Tract Infections/etiology"[majr:noexp] OR "Urinary Tract Infections/microbiology"[majr:noexp])) OR ("Urinary tract infections"[tiab] AND ("etiology"[tiab] OR "microbiology"[tiab]))

Section 2.5.3: Skin infections aetiology

(("Cellulitis/epidemiology"[majr:noexp] OR "Cellulitis/etiology"[majr:noexp] OR

"Cellulitis/microbiology"[majr:noexp]) OR ("Pyoderma/epidemiology"[majr:noexp] OR

"Pyoderma/etiology"[marj:noexp] OR "Pyoderma/microbiology"[majr:noexp]) OR

"Pressure Ulcer/microbiology"[majr:noexp])

Section 2.5.4: Intra-abdominal infection aetiology

(("Peritonitis/epidemiology"[majr:noexp] OR "Peritonitis /etiology"[majr:noexp] OR "Peritonitis /microbiology"[majr:noexp]) OR ("Intraabdominal infections/epidemiology"[majr:noexp] OR "Intraabdominal infections /etiology"[majr:noexp] OR "Intraabdominal infections /microbiology"[majr:noexp]) OR ("abdominal abscess/epidemiology"[majr:noexp] OR " abdominal abscess /etiology"[majr:noexp] OR "abdominal abscess/microbiology"[majr:noexp]))

Section 2.5.5: Bone and joint infections aetiology

("Osteomyelitis/etiology"[majr:noexp] OR "Osteomyelitis/microbiology"[majr:noexp] NOT 'chronic') OR ("Arthritis, infectious/etiology"[majr:noexp] OR "Arthritis, infectious/microbiology"[majr:noexp] NOT 'lyme')

Section 2.5.6: Meningitis infection aetiology

((meningitis[title]) AND (1990/05/01[PDat] : 2018/12/31[PDat]) AND ((etiolog*[title/abstract]) AND Humans[MeSH Terms])

Section 2.5.7: Relative risk studies for specific drug-bug combinations

("Acinetobacter baumannii" [MeSH Terms] AND "carbapenem resistance" [All Fields]) OR ("Acinetobacter baumannii" [MeSH Terms] AND "carbapenem resistant" [All Fields])

('Escherichia coli'[MeSH Terms] AND 'carbapenem resistance'[All Fields]) OR ('Escherichia coli'[MeSH Terms] AND 'carbapenem resistant'[All Fields])

('Escherichia coli'[MeSH Terms] AND 'fluoroquinolone resistance'[All Fields]) OR ('Escherichia coli'[MeSH Terms] AND 'fluoroquinolone resistant'[All Fields])

('Escherichia coli'[MeSH Terms] AND 'third generation cephalosporin'[All Fields]) OR ('Escherichia coli'[MeSH Terms] AND ESBL OR extended-spectrum beta lactamase'[All Fields])

('Klebsiella pneumoniae'[MeSH Terms] AND 'third generation cephalosporin'[All Fields]) OR ('Klebsiella pneumoniae'[MeSH Terms] AND 'ESBL OR extended-spectrum beta lactamase'[All Fields])

('Klebsiella pneumoniae'[MeSH Terms] AND 'carbapenem resistance'[All Fields]) OR ('Klebsiella pneumoniae'[MeSH Terms] AND 'carbapenem resistant'[All Fields])

('Streptococcus pneumoniae'[MeSH Terms] AND 'penicillin resistance'[All Fields]) OR ('Streptococcus pneumoniae'[MeSH Terms] AND 'penicillin resistant'[All Fields])

('Pseudomonas aeruginosa'[MeSH Terms] AND 'carbapenem resistant'[All Fields] AND 'mortality' [MeSH Terms]) OR ('Pseudomonas aeruginosa'[MeSH Terms] AND 'carbapenem resistant' AND 'mortality' [All Fields])

('Enterococcus faec*'[MeSH Terms] AND 'vancomycin-resistant'[All Fields])

("haemophilus influenzae" [MeSH Terms] AND ("penicillin resistance" [MeSH Terms] OR ("penicillin" [All Fields] AND "resistance" [All Fields]) OR "penicillin resistance" [All Fields])) AND ("mortality" [Subheading] OR "mortality" [MeSH Terms])

("streptococcus agalactiae" [MeSH Terms] AND ("azithromycin resistance" [MeSH Terms] OR ("azithromycin" [All Fields] AND "resistance" [All Fields]) OR "azithromycin resistance" [All Fields] OR "penicillin resistance" [MeSH Terms] OR ("penicillin" [All Fields] AND "resistance" [All Fields]) OR "penicillin resistance" [All Fields] OR "clindamycin resistance" [MeSH Terms] OR ("clindamycin" [All Fields] AND "resistance" [All Fields]) OR "erythromycin resistance" [MeSH Terms] OR ("erythromycin" [All Fields]) AND "resistance" [All Fields]) OR "clindamycin resistance" [All Fields]) AND ("mortality" [Subheading]) OR "mortality" [MeSH Terms])

Section 2.5.8: Prevalence of resistance for specific organisms

Medical Subject Heading (MeSH) terms with free text terms in the title and abstract fields for Escherichia coli, Klebsiella pneumoniae, Streptococcus pneumoniae and Staphylococcus aureus with the terms for antimicrobial drug resistance (resistan*, suscept*, surveil*, etc), limited from 1990 up to the search date. The search was undertaken on MEDLINE, Ovid Embase, Global Health, Cochrane Library.

Medical Subject Headings (MeSH) and free text terms for the pathogens of interest (e.g. S. Typhi, S. Paratyphi A, enteric fever) with terms for antimicrobial resistance (e.g. resistan*, suscept*, surveil*). The search was undertaken on MEDLINE, Ovid Embase, Global Health, Cochrane Library, Scopus, Web of Science-Core Collection and LILACS regional WHO database.

Medical Subject Heading (MeSH) terms with free text terms in the title and abstract fields for non-typhoidal Salmonella or Salmonellosis (non-typhi or non-typh or non-typh Salmonel...) with the terms for antimicrobial drug resistance (resistan*, suscept*, surveil*, etc) and invasive (blood stream infection, septicaemia etc), limited from 1990 up to the search date. The search was undertaken on MEDLINE, Ovid Embase, Global Health, Cochrane Library, Scopus, Web of Science-Core Collection and LILACS regional WHO.

Medical Subject Heading (MeSH) terms with free text terms in the title and abstract fields for Shigella or Shigellosis with the terms for antimicrobial drug resistance (resistan*, suscept*, surveil*, etc), limited from 1990 up to the search date. The search was undertaken on MEDLINE, Ovid Embase, Global Health, Cochrane Library, Scopus, Web of Science-Core Collection and LILACS regional WHO database.

Medical Subject Heading (MeSH) terms with free text terms in the title and abstract fields for Neisseria gonorrhoeae, with the terms for antimicrobial drug resistance (resistan*, suscept*, surveil*, etc), MDR, XDR, limited from 1990 up to the search date. The search was undertaken on MEDLINE, Ovid Embase, Global Health, Cochrane Library, Scopus, Web of Science-Core Collection and LILACS regional WHO database.

Section 2.6: Single drug-resistance profiles

Data sources used to inform single drug resistance profiles were obtained from surveillance networks and aggregated reports where the full antibiogram of a pathogen for all drugs tested is not reported. Data from these sources generally do not include any individual records linked to a patient outcome. They are used to inform current and past resistance trends for specific pathogen—drug combinations. Single drug resistance data were used in the prevalence of resistance component model and data processing, and modelling methods can be found in section 7. The data sources for single drug resistance profiles were obtained from the sources below.

- GLASS: Global Antimicrobial Resistance Surveillance System by WHO
- CAESAR: Central Asian and European Surveillance of Antimicrobial Resistance (CAESAR) is a network of national AMR surveillance systems and includes 19 countries in the WHO European Region that are not part of EARS-Net.
- Japan Nosocomial Infections Surveillance (JANIS): is a national surveillance program designed to provide basic information on the incidence and prevalence of nosocomial infections and antimicrobial-resistant bacteria in Japanese medical settings. Data available from 2013.
- NARMS: The National Antimicrobial Resistance Monitoring System for Enteric Bacteria (NARMS) is a collaboration of agencies within The U.S. Department of Health and Human Services (HHS) (FDA and CDC) and the U.S. Department of Agriculture (USDA). It tracks enteric bacteria and selected animal pathogens and their resistance to antimicrobials, and data is available from 1997 onwards.
- **SOAR:** Survey on Antibiotic Resistance (SOAR) sponsored by GSK.
- ReLAVRA and SIREVA: The Latin American Network for Antimicrobial Resistance Surveillance (ReLAVRA by its Spanish acronym) and the Serotype and Antimicrobial Resistance Surveillance Program (SIREVA by its English acronym) which are coordinated by the Pan-American Health Organization (WHO/PAHO)
- SMART: Study for Monitoring Antimicrobial Resistance Trends which monitors complicated intraabdominal infections (cIAIs), complicated urinary tract infections (cUTIs) and respiratory infections worldwide, funded by Merck & Co.

- **South Africa National Institute for Communicable Diseases (NICD):** Aggregated data from South Africa's AMR surveillance in public healthcare centres which is submitted to the GLASS.
- Surveillance on Invasive Pulmonary Disease by the New Zealand Public Health Action.
- Surveillance of Antimicrobial Resistance in Hospital Acquired Infection by Kendokteran Laboratorium, Indonesia
- Alliance for the Prudent Use of Antibiotics (APUA), Nepal
- Hospital Civil de Guadalajara Fray Antonio Alcalde, Mexico
- Australian Group on Antimicrobial Resistance (AGAR)
- Antimicrobial Resistance Surveillance Program (ARSP)
- Antimicrobial Use and Resistance in Australia (AURA)
- Australian Government Department of Health
- Canadian Antimicrobial Resistance Surveillance System
- The China Antimicrobial Surveillance Network
- National Surveillance of Antimicrobial Resistance, Malaysia
- Pakistan Antimicrobial Resistant Network

Section 2.7: Pharmaceutical sales and antibiotic use

These data were used to model the antibiotic use covariate, which was used as an input in the prevalence of resistance models; full details on this model can be found in section 7. Pharmaceutical sales and antibiotic use data were obtained from the following sources.

- IMS Health and Quintiles (IQVIA): antibiotic sales data for 77 countries between 2000 and 2018...
- Demographic Health Surveys (DH): households health surveys carried out across more than 90 countries, they include questions on antibiotic usage among those who had cough or diarrhoea in a period of two weeks before the survey.
- Multiple Indicators Cluster Surveys (MICS): households health surveys carried out across more than 90 countries, they include questions on antibiotic usage among those who had cough or diarrhoea in a period of two weeks before the survey.
- European Surveillance of Antimicrobial Consumption Network (ESAC-NET): antibiotic consumption data for 5 countries over 101 country-years
- WHO report on surveillance of antibiotic consumption: 2016-2018 early implementation: report on antibiotic consumption for 21 countries over 21 country-years

Section 2.8: Mortality surveillance

Mortality surveillance data were used in the sepsis, syndrome, and pathogen distribution models; full details on these models can be found in sections 4 and 6. Mortality surveillance data came from the source listed below.

• Child Health and Mortality Prevention Surveillance (CHAMPS): Under-5 mortality surveillance sites in South Africa, Mali, Bangladesh, Kenya, Ethiopia, and Mozambique. Researchers use minimally invasive tissue sampling (MITS) to gather information about pathogens involved and are able to discern a more accurate cause of death.

Section 2.9: Linkage (mortality only)

Linkage data were used in sepsis and infectious syndrome models; full details on these models can be found in section 4. Mortality-only linkage data include:

- Italy Friuli-Venezia Giulia MCoD data
- New Zealand linked national minimum dataset to mortality collection data

Section 3: Summary of GBD 2019 estimation process

A comprehensive description of data sources, data quality, statistical modelling and analyses for GBD 2019 have been reported elsewhere.¹ A brief summary of the fatal and non-fatal estimation processes are briefly summarised below.

Section 3.1: GBD 2019 cause of death estimation process

The overarching steps for the fatal estimation process for each age, sex, location, and year are to first estimate allcause mortality rates, then calculate cause-specific mortality rates, and finally scale the cause-specific mortality rates to the all-cause mortality rates for internal consistency. First, all-cause mortality is estimated using 7417 sources as data inputs for under-5 mortality estimation and 7355 sources as data inputs for adult mortality estimation. ST-GPR was used to produce estimates of HIV-free mortality rate for every location-year after adjusting for completeness and other known biases in the input data. Added to this HIV-free mortality rate are the HIV-specific mortality rate and deaths from fatal discontinuities, or shocks, which are events that are stochastic in nature and cannot be modelled, such as natural disasters and conflicts. GBD then estimated the cause-specific mortality rates of 301 diseases and injuries. This cause of death analysis utilizes 19 354 sources covering 2525 country years in the cause of death (CoD) database. There are eight types of data sources in the CoD database: vital registration, verbal autopsy, a cancer registry, police records, sibling history, surveillance, survey/census, and minimally invasive tissue sampling (MITS) diagnoses. VR is considered the most comprehensive source of cause of death data, but less than half the world's population has deaths captured in a VR system (appendix figure S6), so causes of death statistics are supplemented with other data types. These various data sources are largely ICD coded causes of death and use heterogenous ICD versions so are standardised to GBD causes of death. Once standardised and adjusted for known biases due to ICD classification changes,⁵ garbage coding,^{5–7} HIV correction,⁸ stochastic noise,¹ and completeness,⁹ causes of death are modelled using CODEm¹⁰ to determine the cause fraction for each underlying cause of death by age, sex, year, and location. CODEm provides an ensemble prediction based on a combination of candidate models that vary across outcome and covariate combinations chosen for out-of-sample predictive performance. Because each cause is modelled independently, it is possible the sum of these models will not equal the all-cause mortality estimates, so cause-specific results are run through the CoDCorrect process to make cause-specific and all-cause mortality estimates internally consistent. This process rescales cause-specific estimates to the all-cause mortality envelope.

Section 3.2: GBD 2019 non-fatal estimation process

Non-fatal health outcomes are estimated using DisMod-MR 2.1, a Bayesian-regression analytical tool that synthesises various data inputs to produce estimates of disease incidence and prevalence. The data used for this analysis include systematic reviews done at the Institute of Health Metrics and Evaluation (IHME), data from household surveys including the demographic and health surveys, multiple indicator cluster surveys, living standards measurement surveys, reproductive health surveys, administrative claims data, inpatient hospital discharge records, outpatient hospital data, disease registries, programme-level data on disease burden from government agencies, surveillance system data on disease burden, and sources suggested to us by in-country collaborators and surveys identified in major multinational survey data catalogues such as the WHO Central data catalog. 51 272 sources were used for this analysis, 31 499 reporting incidence and 19 773 reporting prevalence. Data from these sources are extracted. Pre-modelling bias adjustments are made using crosswalking to account for various sources of bias, such as heterogeneous case definitions and methods of measurement. The pre-modelling bias adjustments are made using the MR-BRT environment, a meta-regression tool that allows for Bayesian priors, regularization, and trimming and has been described in greater detail previously.¹¹ Using these bias-adjusted data an estimate of prevalence and incidence for each cause is produced using the DisMod-MR 2.1 modelling framework. DisMod-MR 2.1 accepts all available data on mortality, incidence, prevalence, and remission and uses a compartmental model to enforce consistency between all quantities.

Section 4: Deaths where infection plays a role and infectious syndrome estimation

Section 4.1: Input data

Section 4.1.1: Multiple causes of death

MCoD data are individual-based records that provide underlying causes of death and two or more intermediate causes in the chain of death. Additionally, each record includes age, sex, residence, and the date of death.

Section 4.1.2: Hospital record with multiple diagnoses and discharge status of death

This type of data is an individual-based hospital record of a patient that provides the main diagnosis and two or more additional diagnoses. Additionally, each record includes age, sex, residence, date of admission, date of discharge, and outcome (dead or alive). Only hospital discharges with discharge status of death were used in this component model, since we aimed to estimate the fraction of deaths that involve infection and the infectious syndrome distribution of those deaths.

Section 4.1.3: Linkage data

Linkage data are generated using probabilistic methods in a defined population that link individual-based hospital data to individual-based MCoD data. Linkage data offer a wider dataset that includes main diagnosis, other diagnoses, underlying cause of death, and intermediate causes of death in the chain.

Section 4.1.4: Mortality surveillance (Child Health and Mortality Prevention Surveillance [CHAMPS])

The CHAMPS network tracks the causes of under-5 mortality and stillbirths at sites in sub-Saharan Africa and south Asia through epidemiological surveillance of under-5 deaths and stillbirths utilising minimally invasive tissue sampling (MITS), laboratory diagnostics including conventional and advanced histopathology and molecular screening of various pathogens, verbal autopsy, and available clinical and demographic data.

Table 4.1.5: Input different data point for calculation of fraction of death by sepsis in different underlying causes

Location	Data type	Years	Year range	Deaths
United States	MCoD	38	1980–2017	82,453,798
	Hospital data with fatal outcome	31	1980–2010	2,028,371
	Linkage data			
Brazil	MCoD	19	1999–2017	16,930,050
	Hospital data with fatal outcome	2	2015–2016	294,461
	Linkage data			
Italy	MCoD	13	2003–2015	7,640,383
	Hospital data with fatal outcome	12	2005–2016	2,385,430
	Linkage data	16	2003–2018	112,555
South Africa	MCoD	20	1997–2016	4,696,348
	Hospital data with fatal outcome			
	Linkage data			
Mexico	MCoD	8	2009–2016	4,336,713
	Hospital data with fatal outcome	7	2003–2009	168,582
	Linkage data			
Colombia	MCoD	20	1998–2017	3,624,771
	Hospital data with fatal outcome			
	Linkage data			
Taiwan (province of China)	MCoD	10	2007–2016	1,189,309
	Hospital data with fatal outcome			
	Linkage data			
Austria	MCoD			

	Hospital data with fatal outcome	14	2001–2014	461,538
	Linkage data			
New Zealand	MCoD			
	Hospital data with fatal outcome	18	2000–2017	169,454
	Linkage data	11	2000–2010	151455
Canada	MCoD			
	Hospital data with fatal outcome	16	1994–2009	38,405
	Linkage data			
CHAMPS Surveillance Sites	MITS	3	2017–2019	870
Total	MCoD	128	1980–2017	120,871,372
	Hospital data with fatal outcome	100	1980–2017	5,546,241
	Linkage data	27	2000–2018	264,010
	MITS	3	2017–2019	870

Section 4.2: Data processing

Data for the USA, Brazil, Italy, South Africa, and Mexico were extracted at the subnational level by GBD 2019 age groups, sex, year, and causes of death and/or diagnoses, while data for the remaining countries and territories were analysed at the national level. This allowed us to expand the location-years of data that we had for each Sociodemographic Index (SDI)¹² value.

Section 4.3: Mapping the data

Prepared data were mapped to GBD causes. The GBD cause list is a mutually exclusive and collectively exhaustive list of diseases and injuries. The GBD cause list is organised hierarchically to accommodate different purposes and needs of various users. The first two levels aggregate causes into general groupings. At Level 1, there are three cause groups: communicable, maternal, neonatal, and nutritional diseases (Group 1 diseases); non-communicable diseases (Group 2); and injuries (Group 3). These Level 1 aggregates are subdivided at Level 2 of the hierarchy into 22 cause groupings (eg, neonatal disorders, neurological disorders, and transport injuries). The disaggregation into Levels 3 and 4 contains the finest level of detail for causes captured in GBD 2019. See section 14, table S1 for the full GBD cause hierarchy by level.

The underlying cause of death or main diagnosis for each record in the data was mapped to a GBD cause. After the mapping of underlying cause, we used the GBD 2019 garbage code redistribution algorithm (see appendix 1, section 2.4 in Vos et al.¹) to ensure that all deaths had a plausible and specific underlying cause of death. The redistribution of garbage codes for underlying causes of death followed the same age and sex restrictions as GBD 2019. We did not redistribute garbage codes in the chain causes because the concept of a garbage code applies only to plausible underlying cause of death (see Rudd et al.¹³ and appendix 1, section 2.5 in Vos et al.¹).

Section 4.4: Intermediate cause and infectious syndrome mapping hierarchy

Section 4.4.1: Intermediate cause mapping

Within our modelling framework, an infectious syndrome is the infection directly responsible for sepsis and serves as the bridge between the underlying cause of death and sepsis. Infectious syndromes can be both underlying causes of death and intermediate causes of death.

For mapping underlying and intermediate causes of death and hospital diagnoses to sepsis and infectious syndromes, we designed a new map, called "AMR, sepsis, and infectious syndrome map". This map is a list of mutually exclusive and collectively exhaustive infectious syndromes that we divided into four levels to form the infectious syndrome hierarchy.

Each level of infectious syndrome is mutually exclusive and collectively exhaustive. Furthermore, the infectious syndrome hierarchy is internally consistent across any metric (eg, number, cause fraction)—aggregating across

Level 3 syndromes gives us Level 2 syndromes, aggregating the Level 2 syndromes gives us Level 1 syndromes, and the total of Level 1 syndromes is equal to the value of sepsis (figure 4.4.2.1).

Level 0: All International Classification of Diseases 9th (ICD-9) or 10th revision (ICD-10) coded deaths divided into three groups:

- Explicit sepsis (A40, R65.2 in ICD-10 and 039 in ICD-9): Any death has specific ICD code for sepsis in the MCoD chain or hospital diagnoses was considered explicit sepsis¹³
- Implicit sepsis: Any death that has an infectious disease code in the underlying cause or cause chain and a specific organ dysfunction code was considered implicit sepsis
- Non-sepsis: Any death that does not meet either of the two above criteria (section 14, tables S2, S3)

Of the estimated infection-related deaths with explicit sepsis or implicit sepsis and infectious diseases, 59.4% occur with communicable, maternal, neonatal, and nutritional underlying causes of death. 38.9% infection related deaths occur with non-communicable disease as the underlying cause of death, and 1.7% occur with injuries as the underlying cause of death.

Level 1: All implicit and explicit sepsis deaths were divided into 12 Level 1 infectious syndromes and an "other" category (table 4.4.1.1).

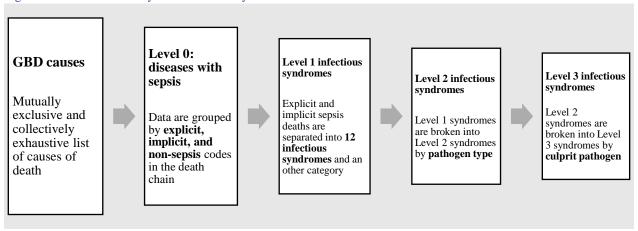
Table 4.4.1.1: Level 1 of infectious syndromes

	Infectious syndrome
1	Bacterial infections of the skin and subcutaneous systems
2	Bloodstream infections
3	Gonorrhoea and chlamydia
4	Diarrhoea
5	Endocarditis and other cardiac infections
6	Infections of bones, joints, and related organs
7	Lower respiratory infections and all related infections in the thorax
8	Meningitis and other bacterial central nervous system infections
9	Peritoneal and intra-abdominal infections
10	Tuberculosis
11	Typhoid, paratyphoid, and invasive non-typhoidal Salmonella
12	Urinary tract infections and pyelonephritis
13	Other infections

Level 2: Each Level 1 infectious syndrome was divided into Level 2 infectious syndromes based on the pathogen type (eg, bacterial, fungal, viral) causing the infection. Examples include specified bacterial, fungal, viral, and unspecified pathogen.

Level 3: Each specified bacterial infectious syndrome in Level 2 was divided to Level 3 infectious syndromes by the bacterium causing infection. Table S3 (section 14) shows this list and bacterial hierarchy.

Figure 4.4.2.1. Infectious syndrome hierarchy



Section 4.4.3: Informative ranking

Due to our data often having multiple diagnoses associated with each record, a single case of sepsis could potentially map to multiple candidate infectious syndromes. Because multiple infectious syndrome assignments pose a risk of double counting, we employed an informative ranking hierarchy. The informative ranking allowed us to determine the infectious syndrome that provided the most information on the culprit pathogen. The goal of this hierarchy was to produce the most accurate pathogen burden estimate such that when there were multiple infectious syndromes, we prioritised the syndrome with the most distinctive distribution. For example, bloodstream infections (BSIs) are common infections in sepsis but there is often an earlier source of the infection such as a UTI, cellulitis, or LRI, and each has a unique pathogen distribution that provides more information than the distribution of BSI. In the event that a patient record reflected both BSI and LRI, we would assign the infectious syndrome based on the pathogen distribution that would be the most proximal aetiologic syndrome, LRI (see table 4.4.3.1).

Table 4.4.3.1. Level 1 Infectious syndrome informative ranking hierarchy Organised from most informative (top) to least (bottom).

Level 1 infectious syndrome informative ranking hierarchy
Meningitis and other bacterial central nervous system infections
Endocarditis and other cardiac infections
Peritoneal and intra-abdominal infections
Lower respiratory infections and all related infections in the thorax
Bacterial infections of the skin and subcutaneous systems
Infections of bone, joints, and related organs
Diarrhoea
Urinary tract infections and pyelonephritis
Other infections
Bloodstream infections

Section 4.4.4: Two modelling pathways

After mapping the underlying and chain causes of death, our database went through two separate modelling pathways. The first model estimated the fraction of deaths that are sepsis-related in each GBD cause; these sepsis-related deaths for non-infectious GBD causes were combined with GBD deaths for infectious causes to create the total envelope of all deaths where infection plays a role. The second pathway estimated each infectious syndrome as a fraction of sepsis-related mortality in each GBD cause. In the last step of infectious syndrome estimation, the fractions of sepsis by Level 1 infectious syndromes were squeezed to sum to one so as to not exceed the sepsis mortality envelope and multiplied by the sepsis estimate in each GBD cause by country and territory, age, and sex in

Section 4.5: First pathway: deaths where infection plays a role

Section 4.5.1: Sepsis model

We used a mixed-effects binomial logistic regression to model the logit of the fraction of sepsis-related deaths by GBD cause-age-sex-location, consistent with the modelling approach used by Rudd et al.¹³ Sex and Healthcare Access and Quality Index (HAQ Index)¹⁴ were included as covariates and a nested random effect on underlying cause of death was included. A separate model was run for each GBD 2019 age group (0–6, 7–27, 28-364 [days], 1–4, 5–9, 10–14, 15–19, 20–24, 25–29, 30–34, 35–39, 40–44, 45–49, 50–54, 55–59, 60–64, 65–69, 70–74, 75–79, 80–84, 85–89, 90–94, 95+ [years]):

sepsis related deaths ~
$$B(\text{total deaths, sepsis fraction})$$
 (4.5.1.1)
 $logit(\text{sepsis fraction}) = \beta_0 + \beta_1 * HAQ Index + \beta_2 * sex + \pi_{level 1, level 2}$

Where $\pi_{level\ 1,level\ 2}$ is a nested random effect on underlying cause of death. The nested random-effect's structure in the model on underlying cause of death allowed the prediction of sepsis fractions where data were limited by borrowing information from diseases within the same group. There were 22 groups of underlying causes of death, each categorised by physiological relatedness. We produced our predictions and uncertainty intervals (UIs) by generating 1000 draws from the normal distribution of the fixed coefficients, separately for each GBD location, age group, sex, and cause in 2019. The means of our results were used for the point estimates and the 95% UIs were delineated using the 2.5^{th} and 97.5^{th} percentiles of the draws. Uncertainty is attributable to sample size variability between data sources, data availability, and model specifications.

All underlying causes of death that are infectious diseases were included in the model; however, for these causes we used the GBD death estimates rather than the modelled sepsis estimate, since infection inherently plays a role in these deaths even if the pathway doesn't include sepsis. These causes and their associated infectious syndromes are listed in table 4.5.1.1.

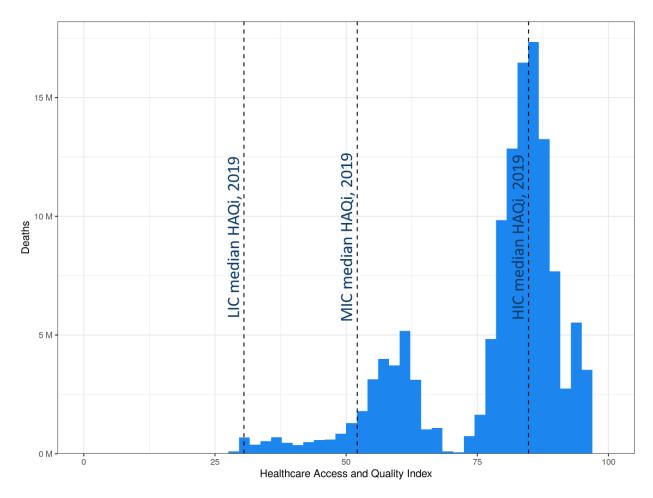
Cause name Infectious syndrome	
Appendicitis	Peritoneal and intra-abdominal infections
Bacterial skin diseases	Bacterial infections of the skin and subcutaneous systems
Chlamydial infection	Gonorrhoea and chlamydia
Diarrhoeal diseases	Diarrhoea
Endocarditis	Endocarditis and other cardiac infections
Gonococcal infection	Gonorrhoea and chlamydia
Invasive non-typhoidal Salmonella	Typhoid, paratyphoid, and invasive non-typhoidal Salmonella
Lower respiratory infections	Lower respiratory infections and all related infections in the thorax
Maternal sepsis and other maternal infections	Bloodstream infections
Meningitis	Meningitis and other bacterial central nervous system infections
Neonatal sepsis and other neonatal infections	Bloodstream infections
Paratyphoid fever	Typhoid, paratyphoid, and invasive non-typhoidal Salmonella
Tuberculosis	Tuberculosis
Typhoid fever	Typhoid, paratyphoid, and invasive non-typhoidal Salmonella
Upper respiratory infections	Lower respiratory infections and all related infections in the thorax
Urinary tract infections and interstitial nephritis	Urinary tract infections and pyelonephritis

For all other causes, we calculated the number of sepsis-related deaths in 2019 by multiplying our predictions of cause-, age group-, sex-, year-, and location-specific sepsis fractions by GBD 2019 death estimates. Finally, we aggregated our results to arrive at regional and global sepsis-related mortality in non-infectious underlying causes of death, which we combined with the GBD infectious disease deaths estimates to create the mortality envelope of all deaths related to infection.

For transparency, histograms of the available input data by HAQ Index are shown below. MCoD input data is used to estimate the proportion of non-infectious disease that involves sepsis, while the GBD mortality data for Group 1

causes (communicable, maternal, neonatal, and nutritional diseases) is inclusive and representative of the input data used to estimate mortality associated with primary infection underlying cause.

Figure 4.5.1.1. MCoD input data by HAQ Index



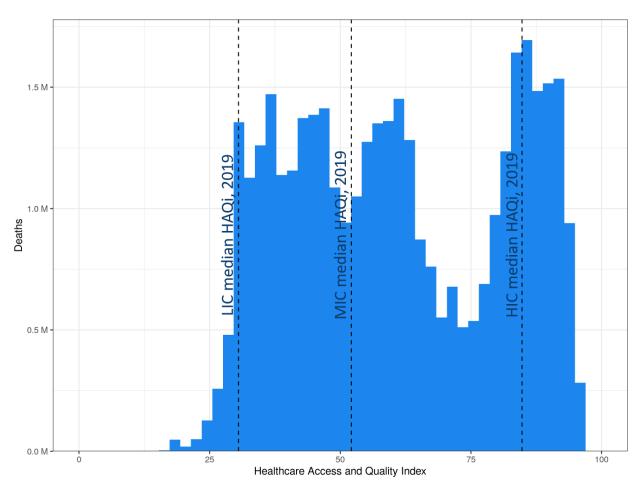


Figure 4.5.1.2. GBD mortality input data for Group 1 (communicable, maternal, neonatal, and nutritional diseases) by HAQ Index

HIC = high-income country, LIC = low-income country, MIC = middle-income country

Section 4.6: Second pathway: fraction of deaths where infection plays a role by infectious syndrome in each GBD cause

We used a mixed-effects binomial logistic regression to model the logit of the infectious syndrome fraction of sepsis-related mortality by GBD cause. The model covariates varied by infectious syndrome (table 4.6.1). All models included HAQ Index as a covariate and most included a summary exposure value (SEV) scalar calculated for GBD 2019.

The pathogen distribution for hospital-acquired infections (HAIs) and community-acquired infections (CAIs) differs markedly for some infectious syndromes. ^{15–20} To more accurately estimate the burden of pathogens responsible for infection, we separated infectious syndromes into hospital-acquired and community-acquired for LRI+ and UTI. For all ICD-coded administrative datasets (hospital discharge, MCoD, and linkage), we assumed that an infection was community-acquired if it was the primary diagnosis or underlying cause of death. Similarly, an infection was considered hospital-acquired if it was not the primary diagnosis or underlying cause of death. We recognise that this is a strong assumption that will not always be correct; however, there is no established method for determining HAI versus CAI in administrative data. ^{21,22} We considered it to be more important to estimate hospital- and community-acquired separately to account for their distinct pathogen distributions despite the strong assumptions involved. We present the fraction of all infectious syndrome deaths in 2019 that our model predicted to be hospital-acquired for LRI+ and UTI in table 4.6.2 for transparency.

Table 4.6.1: Infectious syndrome model covariates and age groups

Infectious syndrome	Covariates	Age groups modelled
Bloodstream infections	HAQ Index ¹⁴ Sex SEV scalar of maternal sepsis ²³ SEV scalar of neonatal sepsis ²³	GBD 2019 age groups
Infections of bone, joints, and related organs	HAQ Index Sex	0-9, 10-14, 15-19, 20-24, 25-39, 40-44, 45-49, 50-54, 55-59, 60-64. 65-69, 70-74, 75-79, 80-84, 85-89, 90-94, 95+
Endocarditis and other cardiac infections	HAQ Index Sex SEV scalar of age-standardised endocarditis ²³	GBD 2019 age groups
Meningitis and other bacterial central nervous system infections	HAQ Index Sex SEV scalar of age-standardised meningitis ²³	GBD 2019 age groups
Diarrhoea	HAQ Index Sex SEV scalar of age-standardised diarrhoea ²³	GBD 2019 age groups
Other infections	HAQ Index Sex	GBD 2019 age groups
Peritoneal and intra-abdominal infections	HAQ Index Sex	GBD 2019 age groups
CAI lower respiratory infections and all related infections in the thorax	HAQ Index Sex SEV scalar of age-standardised LRIs ²³	Neonatal, Post neonatal–5, 5–69, 70+
HAI lower respiratory infections and all related infections in the thorax	HAQ Index Sex SEV scalar of age-standardised LRIs	Neonatal, Post neonatal–5, 5–69, 70+
Bacterial infections of the skin and subcutaneous systems	HAQ Index Sex SEV scalar of age-standardised no access to handwashing facility ²³	GBD 2019 age groups
CAI urinary tract infections and pyelonephritis	HAQ Index Sex SEV scalar of age-standardised no access to handwashing facility	0–39, 40+
HAI urinary tract infections and pyelonephritis	HAQ Index Sex SEV scalar of age-standardised no access to handwashing facility	0–39, 40+

CAI=community-acquired infection. HAI=hospital-acquired infection. HAQ Index=Healthcare Access and Quality Index. LRI=lower respiratory infection. SEV=summary exposure value. SEVs are a risk-weighted prevalence calculated based on exposure, from 0, where the entire population (among the age groups where exposure is possible) is exposed at the minimum risk level, to 100, where the entire population is exposed at the maximum risk exposure level.

Table 4.6.2: Model predictions for proportion of deaths in 2019 that were hospital-acquired by GBD super-region and infectious syndrome

and injections syndronic				
Infectious syndrome	Super-region	Proportion (95% UI)		
Lower respiratory infections and all related infections in the thorax	Global	17.4% (13.1 - 22.4)		
	Southeast Asia, east Asia, and Oceania	23.3% (18.0 - 28.9)		

	Central Europe, eastern Europe, and central Asia	27.9% (20.5 - 35.8)
	High-income	17.8% (12.5 - 24.8)
	Latin America and Caribbean	24.8% (19.1 - 30.7)
	North Africa and Middle East	22.2% (17.7 - 26.8)
	South Asia	16.4% (13.0 - 20.1)
	Sub-Saharan Africa	9.3% (6.9 - 12.8)
Urinary tract infections and pyelonephritis	Global	39.1% (32.4 - 61.5)
	Southeast Asia, east Asia, and Oceania	64.5% (48.4 - 74.7)
	Central Europe, eastern Europe, and central Asia	48.4% (32.4 - 61.5)
	High-income	27.2% (15.8 - 40.7)
	Latin America and Caribbean	28.5% (20.2 - 40.6)
	North Africa and Middle East	73.0% (58.2 - 80.0)
	South Asia	29.9% (20.2 - 40.7)
	Sub-Saharan Africa	24.9% (18.0 - 31.1)

The infectious syndrome models were specified as mixed-effects binomial logistic regressions, one for each infectious syndrome and age group:

$$syndrome\ related\ deaths \sim B(total\ sepsis\ deaths, syndrome\ fraction)$$
 (4.6.2.1)

$$logit(syndrome\ fraction) = \beta_0 + \beta * X + \pi_{level\ 1,level\ 2}$$

where β and X are vectors of length n+1 for n covariates and $\pi_{level\ 1,level\ 2}$ is a nested random effect on underlying cause of death. The granularity of the age groups estimated for each infectious syndrome was chosen based on the age pattern of the infectious syndrome and the limitations of data sparsity.

As in the first pathway, we derived our predictions and UIs by generating 1000 draws from the normal distribution of the fixed coefficients separately for each GBD location, age group, sex, and cause in 2019. We used the means of our results for the point estimates and the 95% UIs were delineated using the 2.5th and 97.5th percentiles of the draws.

Section 4.6.3: Aggregation to the sepsis mortality envelope

We calculated the number of deaths attributable to each infectious syndrome in 2019 by multiplying our predictions of cause-, age group-, sex-, year-, and location-specific infectious syndrome fractions by our sepsis-mortality estimates from the first pathway. All infectious syndrome fractions were squeezed to sum to one prior to multiplication in order to ensure that we did not exceed the sepsis mortality envelope.

Finally, we aggregated our results to arrive at regional and global sepsis-related mortality by infectious syndrome.

Section 4.6.4: Infectious syndromes using GBD 2019 results

Out of the 12 explicit Level 1 infectious syndromes included in our hierarchy, we excluded (i) tuberculosis (TB), (ii) typhoid, paratyphoid, and invasive non-typhoidal Salmonella, and (iii) gonorrhoea and chlamydia from our binomial mixed-effects linear regression model. Instead, we used the published results from GBD 2019¹ for these causes of death, as we believe the GBD 2019 estimates fully represent these infectious syndromes because they are usually not intermediate causes of death.

Section 4.7: Model validation

Infectious syndrome modelling aims to predict which cases of infection belong to a specific infectious syndrome, which is a multi-class classification problem. We therefore use the Area Under the Receiver Operating Characteristics (ROC) Curve (AUC) to evaluate model performance. The ROC Curve is determined by the sensitivity (or true positive rate) and the specificity (or false positive rate) of the model, and a higher AUC score

indicates that the model is capable of discerning between the different categories. Accuracy is a related measure which considers the proportion of true positives and true negatives predicted by the model with respect to the total number of predictions.

The out-of-sample strategy for this validation excluded 20% of the sample on each iteration. Table 4.7.1 reports the Accuracy and AUC score²⁴ for each of the age groups within the infectious syndrome models and table 4.7.2 reports the same metrics for the sepsis models. 99% of the models have an AUC score between 0.7 and 1, indicating an overall excellent performance of this modelling framework.

Table 4.7.1: Accuracy and AUC score for out-of-sample validation of infectious syndromes models

Model	Age group name	Accuracy	AUC score
Bacterial infections of the skin and subcutaneous systems	1 to 4	1.00	0.87
Bacterial infections of the skin and subcutaneous systems	10 to 14	0.99	0.87
Bacterial infections of the skin and subcutaneous systems	15 to 19	0.98	0.90
Bacterial infections of the skin and subcutaneous systems	20 to 24	0.99	0.93
Bacterial infections of the skin and subcutaneous systems	25 to 29	0.99	0.94
Bacterial infections of the skin and subcutaneous systems	30 to 34	0.99	0.95
Bacterial infections of the skin and subcutaneous systems	35 to 39	0.99	0.94
Bacterial infections of the skin and subcutaneous systems	40 to 44	0.98	0.94
Bacterial infections of the skin and subcutaneous systems	45 to 49	0.98	0.93
Bacterial infections of the skin and subcutaneous systems	5 to 9	0.99	0.87
Bacterial infections of the skin and subcutaneous systems	50 to 54	0.98	0.92
Bacterial infections of the skin and subcutaneous systems	55 to 59	0.97	0.92
Bacterial infections of the skin and subcutaneous systems	60 to 64	0.97	0.92
Bacterial infections of the skin and subcutaneous systems	65 to 69	0.97	0.92
Bacterial infections of the skin and subcutaneous systems	70 to 74	0.98	0.92
Bacterial infections of the skin and subcutaneous systems	75 to 79	0.98	0.93
Bacterial infections of the skin and subcutaneous systems	80 to 84	0.98	0.94
Bacterial infections of the skin and subcutaneous systems	85 to 89	0.98	0.95
Bacterial infections of the skin and subcutaneous systems	90 to 94	0.98	0.96
Bacterial infections of the skin and subcutaneous systems	95 plus	0.98	0.97
Bacterial infections of the skin and subcutaneous systems	Early Neonatal	0.99	0.94
Bacterial infections of the skin and subcutaneous systems	Late Neonatal	0.99	0.98
Bacterial infections of the skin and subcutaneous systems	Post Neonatal	1.00	0.89
Bloodstream infections	1 to 4	0.91	0.95
Bloodstream infections	10 to 14	0.85	0.92
Bloodstream infections	15 to 19	0.84	0.91
Bloodstream infections	20 to 24	0.89	0.94
Bloodstream infections	25 to 29	0.92	0.94
Bloodstream infections	30 to 34	0.93	0.94
Bloodstream infections	35 to 39	0.92	0.93
Bloodstream infections	40 to 44	0.90	0.92
Bloodstream infections	45 to 49	0.89	0.90
Bloodstream infections	5 to 9	0.87	0.94

Bloodstream infections	50 to 54	0.88	0.89
Bloodstream infections	55 to 59	0.88	0.87
Bloodstream infections	60 to 64	0.88	0.87
Bloodstream infections	65 to 69	0.89	0.87
Bloodstream infections	70 to 74	0.90	0.88
Bloodstream infections	75 to 79	0.91	0.89
Bloodstream infections	80 to 84	0.92	0.91
Bloodstream infections	85 to 89	0.93	0.92
Bloodstream infections	90 to 94	0.94	0.93
Bloodstream infections	95 plus	0.94	0.95
Bloodstream infections	Early Neonatal	0.94	0.96
Bloodstream infections	Late Neonatal	0.95	0.96
Bloodstream infections	Post Neonatal	0.93	0.96
CAI lower respiratory infections and all related infections in the thorax	5 to 69	0.99	0.99
CAI lower respiratory infections and all related infections in the thorax	70+ years	0.99	1.00
CAI lower respiratory infections and all related infections in the thorax	Neonatal	0.95	0.96
CAI lower respiratory infections and all related infections in the thorax	Post Neonatal to 5	0.99	1.00
CAI urinary tract infections and pyelonephritis	0 to 39	1.00	1.00
CAI urinary tract infections and pyelonephritis	40 plus	1.00	1.00
Diarrhoea	1 to 4	0.99	1.00
Diarrhoea	10 to 14	0.99	0.99
Diarrhoea	15 to 19	0.99	0.99
Diarrhoea	20 to 24	0.99	1.00
Diarrhoea	25 to 29	0.99	1.00
Diarrhoea	30 to 34	0.99	1.00
Diarrhoea	35 to 39	0.99	1.00
Diarrhoea	40 to 44	0.99	0.99
Diarrhoea	45 to 49	0.99	0.99
Diarrhoea	5 to 9	0.99	0.99
Diarrhoea	50 to 54	0.99	0.98
Diarrhoea	55 to 59	0.99	0.97
Diarrhoea	60 to 64	0.99	0.97
Diarrhoea	65 to 69	0.99	0.96
Diarrhoea	70 to 74	0.99	0.96
Diarrhoea	75 to 79	0.99	0.97
Diarrhoea	80 to 84	0.99	0.97
Diarrhoea	85 to 89	0.99	0.98
Diarrhoea	90 to 94	0.99	0.98
Diarrhoea	95 plus	0.99	0.99
Diarrhoea	Early Neonatal	1.00	1.00
Diarrhoea	Late Neonatal	1.00	1.00
		1	

Diarrhoea	Post Neonatal	0.98	0.99
Endocarditis and other cardiac infections	1 to 4	0.99	0.94
Endocarditis and other cardiac infections	10 to 14	0.99	0.97
Endocarditis and other cardiac infections	15 to 19	0.99	0.96
Endocarditis and other cardiac infections	20 to 24	0.99	0.96
Endocarditis and other cardiac infections	25 to 29	0.99	0.97
Endocarditis and other cardiac infections	30 to 34	0.99	0.97
Endocarditis and other cardiac infections	35 to 39	0.99	0.97
Endocarditis and other cardiac infections	40 to 44	0.99	0.97
Endocarditis and other cardiac infections	45 to 49	0.99	0.96
Endocarditis and other cardiac infections	5 to 9	0.99	0.95
Endocarditis and other cardiac infections	50 to 54	0.99	0.96
Endocarditis and other cardiac infections	55 to 59	0.99	0.95
Endocarditis and other cardiac infections	60 to 64	0.99	0.95
Endocarditis and other cardiac infections	65 to 69	0.99	0.95
Endocarditis and other cardiac infections	70 to 74	0.99	0.96
Endocarditis and other cardiac infections	75 to 79	0.99	0.96
Endocarditis and other cardiac infections	80 to 84	0.99	0.97
Endocarditis and other cardiac infections	85 to 89	0.99	0.98
Endocarditis and other cardiac infections	90 to 94	0.99	0.98
Endocarditis and other cardiac infections	95 plus	0.99	0.98
Endocarditis and other cardiac infections	Early Neonatal	0.99	0.98
Endocarditis and other cardiac infections	Late Neonatal	0.99	0.98
Endocarditis and other cardiac infections	Post Neonatal	0.99	0.89
HAI lower respiratory infections and all related infections in the thorax	5 to 69	0.96	0.89
HAI lower respiratory infections and all related infections in the thorax	70+ years	0.96	0.89
HAI lower respiratory infections and all related infections in the thorax	Neonatal	0.99	0.50
HAI lower respiratory infections and all related infections in the thorax	Post Neonatal to 5	0.97	0.94
HAI urinary tract infections and pyelonephritis	0 to 39	0.99	0.77
HAI urinary tract infections and pyelonephritis	40 plus	0.99	0.86
Infections of bone, joints, and related organs	0 to 9	0.99	0.94
Infections of bone, joints, and related organs	10 to 14	0.99	0.95
Infections of bone, joints, and related organs	15 to 19	0.99	0.88
Infections of bone, joints, and related organs	20 to 24	0.99	0.82
Infections of bone, joints, and related organs	25 to 29	0.99	0.85
Infections of bone, joints, and related organs	30 to 34	0.99	0.83
Infections of bone, joints, and related organs	35 to 39	0.99	0.85
Infections of bone, joints, and related organs	40 to 44	0.99	0.84
Infections of bone, joints, and related organs	45 to 49	0.99	0.84
Infections of bone, joints, and related organs	50 to 54	0.99	0.88
Infections of bone, joints, and related organs	55 to 59	0.99	0.89

Infections of bone, joints, and related organs	60 to 64	0.99	0.90
Infections of bone, joints, and related organs	65 to 69	0.99	0.90
Infections of bone, joints, and related organs	70 to 74	0.99	0.91
Infections of bone, joints, and related organs	75 to 79	0.99	0.92
Infections of bone, joints, and related organs	80 to 84	0.99	0.93
Infections of bone, joints, and related organs	85 to 89	0.99	0.94
Infections of bone, joints, and related organs	90 to 94	0.99	0.94
Infections of bone, joints, and related organs	95 plus	0.99	0.95
Meningitis and other bacterial central nervous system infections	1 to 4	0.98	0.98
Meningitis and other bacterial central nervous system infections	10 to 14	0.97	0.98
Meningitis and other bacterial central nervous system infections	15 to 19	0.98	0.97
Meningitis and other bacterial central nervous system infections	20 to 24	0.99	0.97
Meningitis and other bacterial central nervous system infections	25 to 29	0.99	0.98
Meningitis and other bacterial central nervous system infections	30 to 34	0.99	0.98
Meningitis and other bacterial central nervous system infections	35 to 39	0.99	0.97
Meningitis and other bacterial central nervous system infections	40 to 44	0.99	0.96
Meningitis and other bacterial central nervous system infections	45 to 49	0.99	0.96
Meningitis and other bacterial central nervous system infections	5 to 9	0.97	0.97
Meningitis and other bacterial central nervous system infections	50 to 54	0.99	0.94
Meningitis and other bacterial central nervous system infections	55 to 59	0.99	0.93
Meningitis and other bacterial central nervous system infections	60 to 64	0.99	0.93
Meningitis and other bacterial central nervous system infections	65 to 69	0.99	0.92
Meningitis and other bacterial central nervous system infections	70 to 74	0.99	0.92
Meningitis and other bacterial central nervous system infections	75 to 79	0.99	0.91
Meningitis and other bacterial central nervous system infections	80 to 84	0.99	0.92
Meningitis and other bacterial central nervous system infections	85 to 89	0.99	0.92
Meningitis and other bacterial central nervous system infections	90 to 94	0.99	0.93
Meningitis and other bacterial central nervous system infections	95 plus	0.99	0.92
Meningitis and other bacterial central nervous system infections	Early Neonatal	0.99	0.99
Meningitis and other bacterial central nervous system infections	Late Neonatal	1.00	0.99
Meningitis and other bacterial central nervous system infections	Post Neonatal	0.99	0.98
Peritoneal and intra-abdominal infections	1 to 4	0.99	0.97
Peritoneal and intra-abdominal infections	10 to 14	0.97	0.96
Peritoneal and intra-abdominal infections	15 to 19	0.96	0.96
Peritoneal and intra-abdominal infections	20 to 24	0.97	0.97
Peritoneal and intra-abdominal infections	25 to 29	0.98	0.98
Peritoneal and intra-abdominal infections	30 to 34	0.98	0.98
Peritoneal and intra-abdominal infections	35 to 39	0.98	0.98
Peritoneal and intra-abdominal infections	40 to 44	0.97	0.97
Peritoneal and intra-abdominal infections	45 to 49	0.97	0.96
Peritoneal and intra-abdominal infections	5 to 9	0.98	0.97

Peritoneal and intra-abdominal infections	50 to 54	0.96	0.95
Peritoneal and intra-abdominal infections	55 to 59	0.96	0.95
Peritoneal and intra-abdominal infections	60 to 64	0.96	0.95
Peritoneal and intra-abdominal infections	65 to 69	0.96	0.95
Peritoneal and intra-abdominal infections	70 to 74	0.97	0.96
Peritoneal and intra-abdominal infections	75 to 79	0.97	0.97
Peritoneal and intra-abdominal infections	80 to 84	0.98	0.98
Peritoneal and intra-abdominal infections	85 to 89	0.98	0.98
Peritoneal and intra-abdominal infections	90 to 94	0.98	0.98
Peritoneal and intra-abdominal infections	95 plus	0.99	0.98
Peritoneal and intra-abdominal infections	Early Neonatal	0.99	0.97
Peritoneal and intra-abdominal infections	Late Neonatal	0.99	0.97
Peritoneal and intra-abdominal infections	Post Neonatal	0.98	0.94

Table 4.7.2: Accuracy and AUC score for out-of-sample validation of sepsis models

Model	Age group name	Accuracy	AUC
			score
Sepsis	1 to 4	0.89	0.93
Sepsis	10 to 14	0.90	0.92
Sepsis	15 to 19	0.95	0.94
Sepsis	20 to 24	0.95	0.94
Sepsis	25 to 29	0.94	0.95
Sepsis	30 to 34	0.93	0.94
Sepsis	35 to 39	0.93	0.93
Sepsis	40 to 44	0.93	0.91
Sepsis	45 to 49	0.93	0.88
Sepsis	5 to 9	0.89	0.92
Sepsis	50 to 54	0.93	0.86
Sepsis	55 to 59	0.94	0.84
Sepsis	60 to 64	0.94	0.83
Sepsis	65 to 69	0.94	0.83
Sepsis	70 to 74	0.95	0.84
Sepsis	75 to 79	0.95	0.85
Sepsis	80 to 84	0.96	0.87
Sepsis	85 to 89	0.96	0.88
Sepsis	90 to 94	0.96	0.90
Sepsis	95 plus	0.96	0.92
Sepsis	Early Neonatal	0.91	0.87
Sepsis	Late Neonatal	0.87	0.88
Sepsis	Post Neonatal	0.88	0.89

Section 5: Case fatality ratios

Section 5.1: Input data

Case fatality ratios (CFRs) were modelled for the pathogens and infectious syndromes of interest using all available data detailing the organism responsible for infection, the infectious syndrome, and patient outcome. This included hospital and microbial data, totaling 19.7 million isolates and cases, as shown in table S4 (section 14). We additionally included 52 907 cases from literature sources for CNS infections, which had been previously extracted for a systematic review in GBD.

Section 5.2: Data processing

All input data sources were processed as described in sections 6.2.1–6.2.4 and section 6.2.7 and pathogens of interest were chosen as described in section 6.2.5. Input data for the CFR models were aggregated based on data source, year, GBD location, and age group (as well as hospital/community acquired status, in the case of the lower respiratory and urogenital infectious models). For lower respiratory and blood stream infections, for which CFRs could be vastly different in neonates, we modelled the following age groups: neonatal, post-neonatal–5 years, 5–50 years, 50–70 years, and 70 years and older. For all other infectious syndromes, we modelled the following age groups: neonatal–5 years, 5–50 years, 50–70 years, and 70 years and older. We excluded from the analysis any source-location-year-age with fewer than five cases and zero deaths.

To allow us to implement linear models, CFRs were logit-transformed. We used the delta method to compute the standard error of CFRs in logit space. To incorporate data with zero deaths, or with an equal number of deaths and cases, we applied a 1% offset, such that the CFRs for data with zero deaths was represented as 1% and the CFR for data with an equal number of deaths and cases was represented as 99%.

Section 5.3: Modelling overview

Pathogen-specific CFRs were modelled separately by infectious syndrome and were calculated as a function of HAQ Index and age. We used the HAQ Index to extrapolate CFRs determined from the input data, which often had a broad but not comprehensive geographic scope, to all 204 GBD countries and territories. To account for heterogeneity across the sources of input data, we implemented a mixed-effects meta-regression framework, modelling data source as a random effect. We further incorporated a binary fixed-effect denoting whether the data source only included intensive care unit (ICU) patients, for which CFRs were expected to be higher.

The pathogens of interest for each infectious syndrome were determined by prevalence in the data and expert opinion, with the goal of modelling approximately 90% of specified-pathogens associated with each infectious syndrome (see section 6.2.5). Because each data source generally reported only a set of the pathogens we evaluated in our research, the input data for the pathogens varied in geographic coverage; nearly all pathogens were well reported in high-income areas, but some pathogens were not well represented in the smaller subset of data we collected from low- and middle-income locations.

For those pathogens with 'rich' data, defined by our method as having at least ten high-quality data points below a moderate HAQ Index (0.7), we modelled a unique effect of HAQ Index, achieved by interacting the HAQ Index fixed-effect with the pathogen-specific fixed-effect. This process, referred to from here on as the 'interaction model,' allowed the relative deadliness of pathogens to vary depending on a location's HAQ Index. For those pathogens with fewer than 10 high quality data points below 0.7 HAQ Index, or those whose results in the interaction models indicated an unrealistically large influence of HAQ Index (eg, 70% CFR in low HAQ Index countries, 1% CFR in high HAQ Index countries), we modelled a pathogen-specific intercept with an HAQ Index fixed-effect shared across the pathogens. As a consequence of the single fixed-effect on HAQ Index, a pathogen that was predicted to be the deadliest in low HAQ Index countries would also be predicted to be the deadliest in high HAQ Index countries in these 'intercept models.' To estimate the CFRs for other known bacteria, which either were not selected as a pathogen of interest or lacked sufficient data for inclusion in the intercept models, we pooled all bacterial data together and estimated a single CFR curve from age, HAQ Index, and the data source heterogeneity covariates. Thus, up to three models were run for each infectious syndrome:

- an interaction model including data for all data rich pathogens and 'other specified bacteria' (which
 was included to inform the overall influence of HAQ Index on CFR, predictions were only generated
 for the data rich pathogens),
- 2) an intercept model including data for data rich and data sparse pathogens, as well as 'other specified bacteria' (predictions were only generated for the data sparse pathogens), and
- 3) an 'other bacteria' model that included data for all bacterial pathogens (predictions were generated by HAQ Index and age, without any pathogen specific term).

Table S5 (section 14) details which CFR model framework was used to assess the pathogens for each infectious syndrome. Whenever needed, the CFR for any bacterial pathogen "not explicitly modelled" was estimated using the 'other bacteria' model for subsequent steps of our modelling processes.

For some infectious syndromes, the relative deadliness of a pathogen may be strongly determined by either the age of the patient or whether the infection was community- or hospital-acquired. For bloodstream infections, we ran two distinct sets of CFR models, one for neonates (0-27 days) and another for post neonates, to capture the differing dynamics of pathogen deadliness in these two populations. As is done for our other modelling processes, we also separate community-acquired and hospital-acquired cases in our CFR models for lower respiratory and urogenital infections. Because some data sources did not provide enough information to infer whether an infection was community- or hospital-acquired, but still included important information on the relative pathogenesis and the difference in CFRs across varying HAQ indices, infections of unknown origin were included in both the community-acquired and hospital-acquired models for these two syndromes. Any bias in these 'unknown origin' infections was adjusted for using a binary fixed-effect representing an 'unknown origin' infection, and predictions were generated for the community- and hospital-acquired infections only.

Section 5.4 Modelling framework

The data were analysed using a meta-analytic mixed effects structure. The main model can be specified as follows:

$$logit(y_i) = X_i \beta + u_i 1 + \epsilon_i, \qquad \epsilon_i \sim N(0, \Sigma_i), \qquad u_i \sim N(0, \gamma)$$
 (5.4.1)

where

- y_i contains CFRs for data source i
- Design matrix X_i contains as columns the following covariates
 - o in all models:
 - HAO Index
 - dummy-coded indicator for age group
 - dummy-coded ICU indicator for data source (1 if data source only compiles information on ICU patients, 0 if a mix between ICU/non-ICU patients)
 - o in 'interaction' and 'intercept' models:
 - dummy-coded indicator for pathogen
 - o in 'interaction' models only:
 - interaction between pathogen and HAQ Index (product of dummy-coded pathogen columns and HAQ Index)
 - o in models evaluating community/hospital acquired infection (LRI+, UTI):
 - dummy-coded variable indicating source of infection (1 if unknown source, 0 if community OR hospital acquired, depending on whether the model is evaluating community or hospital infections)
- β are fixed effect multipliers
- ϵ_i are observation error terms with known variances
- u_i are data source-specific random intercepts with unknown covariance γ

The underlying program used to fit the model (meta-regression, Bayesian, regularized, trimmed [MR-BRT]) is described elsewhere. ¹¹ The program allows specification of priors on γ and β .

- Prior on γ, data source random effect: Many input data-sources cover only a single country, leading to low variability in HAQ Index within each data-source. Such collinearity adversely influenced the accuracy of the estimated effect of HAQ Index, which was instrumental in extrapolating trends from the input data to global results. To emphasise the contribution of HAQ Index over data-source in the modelled estimates, we implemented a strong Gaussian prior (mean 0, standard error 0.001) on γ.
- Prior on β for HAQ Index: There were a handful of cases in which the estimated effect of HAQ Index on CFRs given our data was clinically implausible. For skin and neonatal bloodstream infections, we had very limited data from low HAQ Index locations, with available data indicating a very intense influence of HAQ Index. Initial model results for these syndromes indicated more than 10-fold higher CFRs in low HAQ Index countries relative to high HAQ Index countries. To attenuate the effect of HAQ Index in these models we implemented a Gaussian prior on the HAQ Index β with mean 0 and standard error 0.2.

Similarly, the peritoneal and intra-abdominal infection CFR models did not have enough input data from low HAQ Index countries to estimate a sensible HAQ Index-CFR trend; initial models indicated very strong positive associations between CFR and HAQ Index such that the CFR in low HAQ Index countries were nearly zero. To amend this, we implemented a Gaussian prior on the HAQ Index β with mean equal to the coefficient estimate for HAQ Index in the adult BSI models. The standard error for this prior was 0.2.

For the urogenital infection models (which were ran separately for community- and hospital-acquired infections) and those for hospital-acquired lower respiratory infections, there was substantial collinearity between HAQ Index and the indicator variable for infections of unknown origin; data that did not indicate the origin of infection were generally sourced from countries with much lower HAQ Indices and much higher baseline CFRs. To emphasize the attribution of this effect to HAQ Index, rather than 'unknown infection origin,' we implemented a Gaussian prior on the HAQ Index β . The mean of this prior was centered at a value estimated for the coefficient of HAQ Index on CFR from weighted simple linear regression, with the weights equal to the inverse of the standard error of the CFRs. The standard error for this prior was 0.2.

Table 5.4.1: Number of data points and parameters estimated in each case fatality ratio model

Infectious syndrome	Sub-model	CFR model type	Data points (source-location- years)	Estimated parameters
CNS	-	Interaction	2094	13
CNS	-	Intercept	2756	15
CNS	-	Other	2756	7
Intra-abdominal	-	Intercept	639	12
Intra-abdominal	-	Other	639	6
LRI+	Community-acquired	Intercept	10485	23
LRI+	Community-acquired	Other	10485	8
LRI+	Hospital-acquired	Intercept	10122	23
LRI+	Hospital-acquired	Other	10122	8
Skin	-	Intercept	1866	15
Skin	-	Other	1897	6
Bone+	-	Intercept	432	12
Bone+	-	Other	432	5
UTI	Community-acquired	Intercept	1596	20
UTI	Community-acquired	Other	1596	7
UTI	Hospital-acquired	Intercept	1844	20
UTI	Hospital-acquired	Other	1844	7
BSI	Neonatal	Intercept	1413	18

BSI	Neonatal	Other	1271	3
BSI	Non-neonatal	Interaction	7468	24
BSI	Non-neonatal	Intercept	10842	25
BSI	Non-neonatal	Other	10842	6
Diarrhoea	-	Intercept	4041	14
Diarrhoea	-	Other	3525	6

BSI = Bloodstream infections. CNS = Meningitis and other bacterial central nervous system infections. LRI+ = Lower respiratory infections and all related infections in the thorax. Intra-abdominal = Peritoneal and intra-abdominal infections. Skin = Bacterial infections of the skin and subcutaneous systems. UTI = Urinary tract infections and pyelonephritis. Bone+ = Infections of bones, joints, and related organs.

Section 5.5 Predictions and uncertainty

Predictions for 2019 CFRs were generated for each country, age group, and pathogen as a function of each country's HAQ Index, assuming mixed ICU/non-ICU patients and, in the case of models for UTI and LRI+, that the infection was community- or hospital-acquired (in contrast to infections of unknown origin). For pathogens with insufficient data to estimate a syndrome-specific CFR, we predicted out using the 'other bacteria' CFR associated with the infectious syndrome. Importantly, all of the CFRs we calculate by infectious syndrome are independent of that syndrome's underlying cause.

Uncertainty estimates were generated using asymptotic uncertainty intervals. Specifically, for the model, the posterior uncertainty for the coefficients β is Gaussian, with mean and variance given below:

$$\hat{\beta} = (\sum_{i} X_{i}^{T} V_{i}^{-1} X_{i})^{-1} (\sum_{i} X_{i}^{T} V_{i}^{-1} y_{i})$$
(5.5.1)

$$Var(\hat{\beta}) = (\sum_{i} X_{i}^{T} V_{i}^{-1} X_{i})^{-1}$$
(5.5.2)

where

$$V_i = 11^T + \hat{\gamma}I \tag{5.5.2}$$

The variance-covariance matrix was used to obtain 1000 draws for the coefficients, which are then used to get intervals for the predictions.

Section 6: Pathogen distribution

Section 6.1: Input data

With this model, we aimed to estimate the distribution of pathogens causing each infectious syndrome. To get input data for this model, we gathered all available data sources described in section 2 that meet the following criteria:

- Sufficient diagnosis (for patient- or admission-level datasets) or sample specimen type (for isolate- or culture-level datasets) information for us to determine the infectious syndrome
- Information on which pathogen(s) caused the infection or which pathogen(s) were detected in an infectious sample, as determined through culture or genomic-based methods
- Did not have a strongly biased sampling framework across pathogens (for example, did not deliberately sample until 100 cases of every pathogen of interest had been obtained)

The input data source types that met these criteria were:

- Multiple causes of death data
- Hospital discharge
- Linkage data
- Microbial data with and without outcome information
- Literature studies from the aetiology literature reviews
- Mortality surveillance (Child Health and Mortality Prevention Surveillance [CHAMPS])

From these sources combined, there was a total of 30.4 million isolates and cases. Table S6 (section 14) provides a detailed breakdown of this total by pathogen.

Section 6.2: Data processing

Section 6.2.1: Extraction and standardisation

We extracted and standardised the location, year, age, sex, diagnoses, specimen type, pathogens, and hospital- and community-acquired (HAI and CAI) status of each record in every dataset. HAI or CAI status in microbial data was determined as described in section 2.3, while in MCoD, hospital discharge, and linkage data, a record was considered CAI if the infectious syndrome was the primary or underlying diagnosis and HAI otherwise, as described in section 4. These datasets report a variety of metrics, including deaths, admissions, cases, cultures, and isolates. While these metrics are not completely comparable (for example, a single patient may often have multiple cultures taken during a single hospital admission), we chose to standardise them into two categories: "deaths," for any unit associated with an outcome of death, and "cases," for any unit regardless of outcome. We assigned a unique identifier, sample ID, to track each unique unit of analysis whenever a dataset included enough line-level data to make this possible. We did not track the relationship between sample ID and patient or admission, in many cases because this was not possible; an improvement to future analyses may be to track this information and account for multiple isolates or cultures from a single admission. The majority of the data informing culprit pathogen were from microbiological analysis of various isolates, but we also considered antigen testing, such as the urinary strep antigen, and polymerase chain reaction (PCR)-based testing when assigning the pathogen responsible for infection.

Section 6.2.2: Assigning infectious syndrome

After standardising the data, we mapped every sample ID or tabulated figure in the data to infectious syndrome based on its diagnoses and specimen type. Infectious syndrome was assigned first based on any diagnosis associated with a given sample ID or tabulated figure. For samples IDs or tabulated figures with multiple diagnoses and/or an underlying diagnosis, we followed the rules laid out in section 4 for assigning infectious syndrome based on multiple causes. If a dataset contained no diagnoses or the diagnoses provided no information on infectious syndrome, we assigned infectious syndrome based on specimen type (table 6.2.2.1). This is an imprecise method because a patient may have a sample taken from an organ system that is not the site of their primary infection, most commonly from the blood. Finally, if neither diagnosis nor specimen information provided information on infectious syndrome, we assigned infectious syndrome based on pathogen for a select number of pathogens (table 6.2.2.2).

Table.6.2.2.1: Syndrome assignment based on standardised specimen types

Standard specimen	Assigned to syndrome
Blood	Bloodstream infections
Bone & joint	Infections of bones, joints, and related organs
Catheter	Bacterial infections of the skin and subcutaneous systems
Cerebrospinal fluid	Meningitis and other bacterial central nervous system infections
Gastrointestinal tract & bowel	Diarrhoea
Urinary tract infection	Urinary tract infections and pyelonephritis
Intra-abdominal	Peritoneal and intra-abdominal infections
Rectal/stool	Diarrhoea
Lower respiratory	Lower respiratory infections and all related infections in the thorax
Skin	Bacterial infections of the skin and subcutaneous systems
Upper respiratory	Other infections
Urogenital	Other infections
Other and unspecified specimens	No infectious syndrome

Table 6.2.2.2: Syndrome assignment based on pathogen for entries lacking diagnostic and specimen information

Pathogen	Assigned to syndrome
Salmonella Typhi	Typhoid, paratyphoid, and invasive non-typhoidal Salmonella
Salmonella Paratyphi	Typhoid, paratyphoid, and invasive non-typhoidal Salmonella
Salmonella Typhi or Paratyphi	Typhoid, paratyphoid, and invasive non-typhoidal Salmonella
Non-typhoidal Salmonella species	Typhoid, paratyphoid, and invasive non-typhoidal Salmonella
Mycobacterium tuberculosis	Tuberculosis
Neisseria meningitidis	Central nervous system infections
Neisseria gonorrhoeae	Gonorrhoea and chlamydia

Section 6.2.3: Contaminants and no aetiology detected

Some pathogens cause disease so rarely or are so commonly contaminants that we considered them to be contaminants, unlikely to be the true cause of disease. Examples include many *Corynebacterium* species and *Staphylococcus epidermidis*. We dropped all such contaminants from the analysis, as well as any record listed by treating clinicians in the data as a contaminant. Contaminants are identified at the most-detailed species or serotype level reported in the data; thus, in the broad pathogen categories that are eventually modelled, like fungi in LRI+, specific contaminant species have already been removed.

We also dropped from the analysis all records where no pathogen was detected, or the patient diagnosis indicated an unspecified bacterium. This assumes that the distribution of pathogens among cases with known aetiology are the same as those with unknown aetiology; in other words, that the probability of detection is the same for every pathogen. This assumption may break down if certain pathogens are more difficult to detect than others, or in cases where a pathogen is irregularly tested for within a laboratory.

Section 6.2.4: Polymicrobial infections

A single infection may be caused by multiple bacteria, and the co-occurrence of several bacteria can have significant effects on the treatment and outcome of disease. Some of our line-level data sources report multiple pathogens per individual record, allowing us to quantify the extent of polymicrobial infection. Other data sources tabulate over pathogen with no linking clinical information, thereby masking this information, or do not report the co-occurrence of additional bacteria.

For data sources where multiple pathogens were listed per sample ID, we classified these cases according to the following criteria. First, if a case contained more than one of "unspecified bacteria," "virus," "fungus," and another pathogen(s), we chose to drop all these pathogens except the one(s) most likely to be responsible for disease, with the following ranking from most to least likely:

- 1. Another pathogen(s)
- 2. Unspecified bacteria
- 3. Virus
- 4. Fungus

This was to drop co-occurrence profiles that we consider to be uninformative, like a viral infection co-occurring with a fungal infection. For example, for a sample ID with pathogens *Escherichia coli*, *Acinetobacter baumannii*, and a virus, we would drop the virus and retain both the *E. coli* and *A. baumannii*. After applying this drop, we considered any sample ID that contained more than one pathogen to be polymicrobial. Polymicrobial was treated as a distinct pathogen category in all further analysis. We did not estimate the exact composition of the pathogens comprising the polymicrobial category for a given infectious syndrome. Furthermore, it can be difficult to determine the clinical meaning of a polymicrobial result, as it is unclear which pathogen or if any pathogen is ultimately responsible for the infection. For these reasons, we were unable to include any AMR burden from polymicrobial infections in our final results. This possibly underestimates the burden of AMR by hiding infections caused by resistant pathogens of interest in the polymicrobial category.

By standardising all datasets that report polymicrobial infections into distinct mono-pathogen and poly-pathogen categories, we created an inconsistency between these datasets and datasets that do not report the co-occurrence of pathogens. For example, a dataset that reports the co-occurrence of *E. coli* and *A. baumannii* would be standardised into three groups, mono-*E.coli*, mono-*A. baumannii*, and co-occuring *E. coli* and *A. baumannii*, while a dataset that reports *E. coli* and *A. baumannii* separately would have two categories that both have some unknown overlap. In order to allow us to use both data types, we chose to assume that the relative prevalences of pathogens in datasets that do not report co-occurrence would be comparable to their mono-pathogenic counterparts in datasets that do report co-occurrence. This assumes that the co-occurrence of pathogens is random and is not correlated for certain pathogens. We did not have sufficient data to fully test the validity of this assumption, given that few datasets report the full universe of pathogens which may co-occur.

Section 6.2.5: Selecting pathogens for estimation

For each infectious syndrome, we selected roughly 10–20 pathogens to estimate explicitly in the pathogen distribution based on the following criteria:

- The prevalence of each pathogen in the raw data
- Clinical knowledge about the primary etiologies of each infectious syndrome
- The amount of available data, which limits the number of pathogens that can be estimated successfully

In addition to the n pathogens for a given syndrome that we estimate explicitly, we also included an "other specified pathogens" category for every infectious syndrome, to which we mapped all other aetiologies identified in the data. Thus, the set of estimated pathogens for each infectious syndrome is mutually exclusive and collectively exhaustive of all possible aetiologies. Polymicrobial infections were either estimated explicitly or included in the "other" category, making all explicitly estimated individual pathogens mono-pathogenic. In addition to these criteria, we also considered the following factors:

- Since we were ultimately interested in estimating the burden of AMR in bacteria, we erred on the side of
 estimating bacteria with strong evidence of AMR, rather than bacteria with low evidence of AMR or nonbacterial aetiologies.
- Clinically relevant aetiologies differ from syndrome to syndrome, and we were unable to estimate all pathogens explicitly in every syndrome due to a lack of data. Therefore, the "other" pathogen category is composed of slightly different pathogens for every infectious syndrome, and can occasionally contain pathogens that are explicitly estimated for another infectious syndrome. We attempted to mitigate this by including bacteria with strong evidence of AMR in the estimation of all infectious syndromes whenever possible.
- We included enough explicitly estimated pathogens to ensure that the "other" category remained below 10% for all infectious syndromes.

For a list of pathogens covered in each infectious syndrome model, please refer to table 6.3.2.

Section 6.2.6: Estimating unbiased other and polymicrobial categories

One of the central challenges of estimating pathogen distributions was that not every data source tested for or reported every possible aetiology of a given infectious syndrome. For example, many literature studies on the aetiologies of meningitis only report on bacterial aetiologies. Some surveillance systems, like the US Centers for Disease Control and Prevention (CDC) Active Bacterial Core surveillance (ABCs), only collect data on certain pathogens of interest. Only certain pathogens are referenced explicitly in the International Classification of Diseases (ICD), limiting which pathogens can be identified from ICD-based data types like MCoD and hospital discharge. Finally, some datasets reported only a subset of the pathogens that we are interested in for a given infectious syndrome, reporting the remaining aetiologies in an aggregate "other" category. These practices have led to inconsistencies in the "other" and "polymicrobial" categories across data sources. Datasets can either over or underreport "other," and datasets that report fewer specific pathogens will automatically report fewer polymicrobial infections.

To address this problem, we maintained a list of data sources that we believe have sufficient testing and reporting to give unbiased estimates of other and polymicrobial for all syndromes. We dropped any data on polymicrobial or other that did not come from these data sources. These data sources all had a complete sampling framework (eg, they do not limit the scope of aetologies that they test for) and reported their results without any deliberate aggregation. While we believe this list provided an accurate starting place for the estimation of other and polymicrobial, future work to improve this method would involve a more detailed analysis of sampling framework and reporting categories in each dataset, specific to each infectious syndrome.

There were two major exceptions to this method for handling "other specified pathogens." First, determining the pathogenic aetiology of LRI with microbiology represents challenges that have been well described previously. ^{25,26} In order to account for this limitation, we utilised a vaccine probe design to inform the *Streptococcus pneumoniae* cause fraction of LRI, consistent with the approach used in the GBD aetiology estimation process. ^{27,28} In brief, we

extracted the vaccine efficacy of the pneumococcal vaccine against all pneumonia from 18 vaccine probe studies with randomised-control trial, before-after, and cohort designs among children and adults. We then calculated the PAF of pneumonia due to *S. pneumoniae* in each study ($Strep\ Base\ PAF$) based on these vaccine efficacies ($VE_{all\ pnuemonia}$), the vaccine efficacy of pneumococcal vaccine against vaccine-type pneumococcal pneumonia as pooled from three studies (two in children and one in adults) (VE_{vtpp}), the percentage of the population covered by the pneumococcal vaccine as modelled in GBD (100% for RCTs) (Cov_{PCV3}),²⁹ and the percent of serotypes covered by the vaccine³⁰ ($Cov_{serotype}$) (equation 6.2.6.1). We modelled a global age-specific PAF for *S. pneumoniae* based on these data in the MR-BRT environment and finally adjusted this PAF based on the vaccine coverage in children in every GBD location in 2019 and optimal vaccine efficacy in children ($Strep\ Final\ PAF$) (equation 6.2.6.2). In adults (age 5+), we assumed the effects of vaccination on adults would be primarily indirect from vaccination in children, and included an adjustment factor on the vaccine efficacy to account for this, derived from Grijalva et al.³¹

$$Strep\ Base\ PAF = \frac{VE_{all\ pneumonia}}{VE_{vtpp}Cov_{PCV3}Cov_{serotype}} \tag{6.2.6.1}$$

$$Strep\ Final\ PAF = \frac{Strep\ Base\ PAF \left(1 - Cov_{PCV3}Cov_{serotype}VE_{PCV3\ Optimal}\right)}{1 - (Strep\ Base\ PAF)Cov_{PCV3}Cov_{serotype}VE_{PCV3\ Optimal}} \tag{6.2.6.2}$$

In this vaccine probe analysis, $(1 - Strep\ Final\ PAF)$ is not consistent with the "other" category in our model, since it includes all non-S. pneumoniae aetiologies. We retained all of the data from the vaccine probe analysis as two categories, S. pneumoniae and "not S. pneumoniae" and addressed the inconsistencies between them and our other data using our modelling framework.

The second major exception involves several literature studies on the proportion of neonatal bacterial meningitis caused by *Streptococcus agalactiae* (Group B *Streptococcus*; GBS). We found that these literature studies were important to our estimation of the pathogen distribution of neonatal meningitis, which is distinct from other age groups because of its high proportion of GBS. However, these studies either only reported or were only extracted with two categories, GBS and "other bacterial, not GBS." We retained both these categories and addressed the inconsistencies between them and our other data using our modelling framework.

Section 6.2.7: Age-sex splitting

We standardised age and sex across all datasets to the following most-detailed groups using the GBD causes of death age-sex splitting algorithm for age: 1 0–6, 7–27, and 28–364 days, and 1–4, 5–9, 10–14, 15–19, 20–24, 25–29, 30–34, 35–39, 40–44, 45–49, 50–54, 55–59, 60–64, 65–69, 70–74, 75–79, 80–84, 85–89, 90–94, 95+ years; and sex: male and female. This algorithm is based on the assumption that age-sex pattern of the death or case rate for a given infectious syndrome or pathogen is inherent to the pathology of the disease and is therefore constant across location and year.

To apply the algorithm, we first calculated distinct age-sex weights for every infectious syndrome and pathogen, separately for deaths and cases. These weights are the aggregate death and case rates across all datasets that report every detailed age-sex group. If we were to use a dataset that only reported some of the detailed age-sex groups, then the unreported age-sex groups would be biased downwards in the weight distribution. Calculating rates based on raw data counts could lead to extremely low rates, since we are typically comparing the entire population of a given location-year to deaths or cases captured within a single study, hospital, or surveillance system. Since the age-sex splitting algorithm only relies on the relative distribution of the weights, however, rather than their absolute level, this bias ultimately had no effect. For any infectious syndrome or pathogen combination for which we did not have enough data to create plausible age-sex weights, we used a set of all-pathogen weights for that infectious syndrome instead.

Since we split cases and deaths independently, it is possible for a detailed age-sex group produced by the splitting algorithm to contain fewer cases than deaths. When this occurred, we capped the deaths to match the cases. For

future improvement, a possible solution to this problem may be to split deaths, survivors, and cases without indication of outcome separately.

Section 6.2.8: Standardising measures

The input data sources reported a variety of combinations of measures, including some that reported deaths only, some that reported cases only, and some that reported both cases and deaths. In order to standardise these measures to cases, we estimated infectious syndrome- and pathogen-specific CFRs (see section 5) and used these CFRs to convert all deaths-only datasets to cases. For any infectious syndrome or pathogen combination for which we did not have enough data to estimate plausible CFRs, we used a set of all-bacteria CFRs for that infectious syndrome instead. All modelling was done in case space.

Several of our microbial databases came exclusively from ICUs and were therefore heavily biased towards severe illness. In order to mitigate this bias, we dropped all information on cases in ICU-only datasets and recalculated implied cases based on reported deaths and our CFRs. No similar adjustment was made to attempt to account for biases between hospitalised and un-hospitalised populations, although we did account for HAI versus CAI for two infectious syndromes—LRI and thorax infections and UTI—within our modelling framework. The use of hospital-based data to calculate both pathogen-specific case fatality ratios and pathogen distributions biases our estimate of the distribution of pathogens in incident cases towards more severe disease, particularly for less-severe infectious syndromes like lower respiratory infections; adjusting for this bias would improve the accuracy of our non-fatal estimates

Section 6.2.9: Year adjustments

Over the course of this study, we received a total of approximately 57 000 individual records from 2020 from seven microbial and mortality surveillance data sources. Additionally, we found a total of eight literature studies on pathogen distributions from 1975–1979 that were appropriate for inclusion. We included these 2020 and 1975–1979 data as inputs into our case fatality ratio and pathogen distribution models with the nearest year of covariate estimates available (2019 and 1980 respectively) in order to maximise data availability. While the COVID-19 pandemic had a significant impact on LRI disease burden in 2020, we found a total of only seven viral LRI and thorax infections reported in 2020 in our input data, and so we believe that the inclusion of these data did not significantly skew our estimates of the pathogen distribution of LRI in 2019.

Section 6.3: Modelling framework

Section 6.3.1: Overview

To model the distribution of pathogens for each infectious syndrome, we developed a method for the multinomial estimation of partial and compositional observations (MEPCO). We assumed that the aetiologies of a given infectious syndrome followed a multinomial distribution. Due to inconsistencies in which pathogens are tested for and reported by different data sources, each data source contained partial observations of the possible outcomes of the underlying multinomial distribution. Certain data sources like the vaccine probe estimates and the GBS neonatal meningitis studies represent compositional observations, where pathogens like "not *S. pneumoniae*" and "other bacterial, not GBS" represent aggregates of more detailed pathogens.

In order to use both partial and compositional data, we constructed a network model with the dependent variable as the log ratio of cases between different pathogens and estimated over a flexible parameterisation of multinomial parameters using a maximum likelihood approach. Consider a given infectious syndrome with a multinomial distribution of n mutually exclusive, collectively exhaustive aetiologies with probabilities $p=(p_1,\ldots,p_n)$, so that each $p_j\in(0,1)$ and $\sum_j p_j=1$. The likelihood of an observation of $c=(c_1,\ldots,c_n)$, where $c_j=$ number of cases of pathogen j in a total sample of N infections ($\sum_j c_j=N$), is:

$$P(c|p) = N! \prod_{j=1}^{n} \frac{p_j^{c_j}}{c_j!}$$
 (6.3.1.1)

We modelled the probabilities using a composition of a link function with a linear predictor:

$$p_{i,j} = \exp\left(x_{i,j}^T \beta_j\right) \tag{6.3.1.2}$$

for observations i, a vector of covariates $x_{i,j}$, and a vector of coefficients β_j for each pathogen j. Table 6.3.2 shows the covariates used for infectious syndrome model; a typical specification included an intercept term, HAQ Index, a categorical age group dummy for large age bins, and any relevant vaccine coverage proportions by country. However, we did not observe these probabilities directly. Rather, we observed ratios between sums of these probabilities, which reduce to ratios between sums of cases within each study. These observations therefore take the form:

$$y_i = \frac{cases\ of\ pathogen\ A}{cases\ of\ pathogen\ B} = \frac{\sum_{j=1}^n w_{i,j}^a \exp\left(x_{i,j}^T \beta_j\right)}{\sum_{j=1}^n w_{i,j}^b \exp\left(x_{i,j}^T \beta_j\right)} \tag{6.3.1.3}$$

where $w_{i,j}^a$ is a weight of 0 or 1 that selects the mutually exclusive, collectively exhaustive most-detailed pathogens that make up observed pathogen A, which may be a composite observation. For example, for the "other bacterial, non-GBS" pathogen, $w_{i,j}$ would be 1 for Staphyloccocus aureus, S. pneumoniae, Haemophilus influenzae, Neisseria meningitidis, Listeria monocytogenes, K. pneumoniae, E. Coli, and other pathogens and 0 for GBS and virus. We dropped all observations where either the numerator or denominator had 0 observed cases in order to make this calculation and a forthcoming log transform possible. This may bias the model towards overestimating less common pathogens.

It is not possible to infer all coefficients β_j from the observations, since they are all relative. However, if we fix all of the coefficients for one pathogen to 0 as a reference group, then we obtain a well-posed inverse problem, as long as there is enough data to estimate the remaining coefficients. Without loss of generality, we assumed $\beta_1 = 0$ for all elements and obtain estimates of the remaining β_2, \dots, β_n by minimising the sum of the residuals between log-transformed observations y and corresponding log-transformed predictions from equation 6.3.1.3:

$$\min_{\beta_{2},\dots,\beta_{n}} f(\beta) := \sum_{i} \frac{1}{\sigma_{i}^{2}} \left[\ln(y_{i}) - \ln\left(\sum_{j=1}^{n} w_{i,j}^{a} \exp(x_{i,j}^{T} \beta_{j})\right) + \ln\left(\sum_{j=1}^{n} w_{i,j}^{b} \exp(x_{i,j}^{T} \beta_{j})\right) \right]^{2}$$
(6.3.1.4)

where σ_i^2 are variances corresponding to the data points. Equation 6.3.4 is a nonlinear likelihood minimisation problem that that we optimised using a standard implementation of the Gauss-Newton method.³² We then renormalised the optimal coefficients to obtain final predictions of the probabilities of each pathogen:

$$p_{i,j} = \frac{\exp(x_{i,j}^T \beta_j)}{\sum_{\hat{i}} \exp(x_{i,\hat{j}}^T \beta_{\hat{i}})}$$
(6.3.1.5)

To quantify the uncertainty of this estimate, we used asymptotic statistics to obtain the posterior distribution of $(\beta_2, ..., \beta_n)$. Specifically, using the Gauss-Newton Hessian approximation gave us the asymptotic information matrix for all β_j except for the reference pathogen, allowing us to sample draws of $\beta = (\beta_1 = 0, \beta_2, ..., \beta_n)$. For each β draw and given feature x, we obtained a corresponding draw of p using equation 6.3.1.5.

Finally, to convert $p_{i,j}$ for a given demographic group i from case space to deaths space, we transformed using our CFR estimate for demographic i:

$$p_{i,j}^{deaths} = \frac{p_{i,j} \times CFR_i}{\sum_{\hat{j}} p_{i,\hat{j}} \times CFR_i}$$
(6.3.1.6)

This network regression with covariates framework allowed us to use partial and composite data that reported on one or only a few pathogens, or that reported multiple pathogens aggregated together. Networks, however, can be unstable with sparse data and stable estimates have in some cases required the use of Bayesian priors in these models. In particular, we imposed Gaussian priors with mean 0 and non-zero variance on all coefficients except

intercepts, to bias the model away from spurious effects driven by data sparsity. These priors were based on expert opinion and can improved with further empirical validation in the future. Table 6.3.4 provides a list of these priors.

Table 6.3.2: Pathogens assessed, covariates, and age groups for each infectious syndrome

Infectious syndrome	Pathogens assessed	Model covariates	Age groups
Bloodstream infections	Acinetobacter baumannii, Citrobacter spp., Enterobacter spp., Enterococcus faecalis, Enterococcus faecium, other enterococci, Escherichia coli, fungus, group A Streptococcus, group B Streptococcus, Klebsiella pneumoniae, Neisseria meningitidis, non-typhoidal Salmonella, polymicrobial, Proteus spp., Pseudomonas aeruginosa, Salmonella Typhi, Serratia spp., Staphylococcus aureus, Streptococcus pneumoniae	HAQ Index, ¹⁴ age group, age- standardised proportion of intravenous drug use, ²³ proportion coverage by PCV3 vaccine, ³³ indicator variable for Europe	Neonatal, Post-neonatal–5, 5–50, 50–70, 70+
Infections of bones, joints, and related organs	Enterococcus faecalis, Enterococcus faecium, other enterococci, Escherichia coli, group A Streptococcus, group B Streptococcus, Klebsiella pneumoniae, Pseudomonas aeruginosa, Staphylococcus aureus	HAQ Index, age group	Under 5, 5–50, 50–70, 70+
Endocarditis and other cardiac infections	See bloodstream infection pathogens	Not explicitly modelled. Pathogen distribution for bloodstream infections is used.	Neonatal, Post-neonatal–5, 5–50, 50–70, 70+
Diarrhoea	Adenovirus, Aeromonas spp., Amebiasis, Campylobacter spp., Clostridium difficile, cryptosporidium, enteropathogenic Escherichia coli, enterotoxigenic Escherichia coli, non- typhoidal Salmonella, norovirus, rotavirus, Shigella spp., Vibrio cholerae	Not modelled here. GBD diarrhoea aetiology estimates are used.	GBD most detailed age groups
Lower respiratory infections and all related infections in the thorax	Acinetobacter baumannii, Chlamydia spp., Enterobacter spp., Escherichia coli, fungus, group B Streptococcus, Haemophilus influenzae, Klebsiella pneumoniae, Legionella spp., Mycoplasma spp., polymicrobial, Pseudomonas aeruginosa, Staphylococcus aureus, Streptococcus pneumoniae, virus	HAQ Index, proportion coverage by PCV3 vaccine, proportion coverage by Hib3 vaccine, ³³ age group, HAI/CAI	Neonatal, Post-neonatal–5, 5–50, 50–70, 70+
Meningitis and other bacterial central nervous system infections	Escherichia coli, group B Streptococcus, Haemophilus influenzae, Klebsiella pneumoniae, Listeria monocytogenes, Neisseria meningitidis, Staphylococcus aureus, Streptococcus pneumoniae, virus	HAQ Index, proportion coverage by PCV3 vaccine, proportion coverage by Hib3 vaccine, age group, proportion of population covered by '10-'15 MenAfriVac rollout ^{1,34}	Neonatal, Post-neonatal–5, 5-50, 50-70, 70+
Peritoneal and intra- abdominal infections	Citrobacter spp., Enterobacter spp., Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Klebsiella pneumoniae, other Klebsiella species, Proteus spp., Pseudomonas aeruginosa, Serratia spp., Staphylococcus aureus	HAQ Index, age group	Under 5, 5–50, 50–70, 70+
Bacterial infections of the skin and subcutaneous systems	Acinetobacter baumannii, Enterobacter spp., Enterococcus faecalis, other enterococci, Escherichia coli, group A Streptococcus, group B Streptococcus, Klebsiella pneumoniae, Proteus spp., Pseudomonas aeruginosa, Staphylococcus aureus	HAQ Index, age group	Under 5, 5–50, 50–70, 70+
Urinary tract infections and pyelonephritis	Acinetobacter baumannii, Citrobacter spp., Enterobacter spp., Enterococcus faecalis, Enterococcus faecium, other enterococci, Escherichia coli, group B Streptococcus, Klebsiella pneumoniae, Morganella spp., Proteus spp., Providencia spp., Pseudomonas aeruginosa, Serratia spp., Staphylococcus aureus	HAQ Index, age group, HAI/CAI	Under 5, 5–50, 50–70, 70+

Group A Streptococcus = Streptococcus pyogenes. Group B Streptococcus = Streptococcus agalactiae. HAQ Index = Healthcare Access and Quality Index. HAI/CAI = hospital-acquired infection/community-acquired infection.

Table 6.3.3: Number of data points and parameters in each pathogen distribution model

Infectious syndrome	Subtype	Number of data points	Number of parameters
LRI+		158967	135
BSI		126417	180
Skin		1105	55
CNS	Neonatal	25615	81
CNS	Post neonatal	25579	81
UTI		23662	96
Bone+		1870	45
Intra-abdominal		2458	55

BSI = Bloodstream infections. CNS = Meningitis and other bacterial central nervous system infections. LRI+ = Lower respiratory infections and all related infections in the thorax. Intra-abdominal = Peritoneal and intra-abdominal infections. Skin = Bacterial infections of the skin and subcutaneous systems. UTI = Urinary tract infections and pyelonephritis. Bone+ = Infections of bones, joints, and related organs.

Table 6.3.4. Gaussian prior standard deviations for non-intercept coefficients for each pathogen distribution model

Infectious syndrome	Sub-type	Gaussian prior standard deviation
BSI		0.1
CNS	Neonatal	0.1
CNS	Non-neonatal	0.1
LRI+		0.1
Intra-abdominal		0.3
Skin		0.3
UTI		0.02 for A. baumannii/HAQ Index coefficient
		0.1 for all others
Bone+		0.5

BSI = Bloodstream infections. CNS = Meningitis and other bacterial central nervous system infections. LRI+ = Lower respiratory infections and all related infections in the thorax. Intra-abdominal = Peritoneal and intra-abdominal infections. Skin = Bacterial infections of the skin and subcutaneous systems. UTI = Urinary tract infections and pyelonephritis. Bone+ = Infections of bones, joints, and related organs.

Section 6.4: Exceptions and special handling

There were several notable exceptions and special handling decisions made for each individual pathogen distribution model. We hope to address many of these exceptions with more sustainable methods in our future work.

Section 6.4.1: Cardiac infections

For cardiac infections, we used the pathogen distribution for bloodstream infections rather than estimating specific distributions for these syndromes, due to a lack of complete literature reviews on the aetiologies and case-fatality rates of these syndromes. We consider this to be a serious limitation of our methodology, but do not anticipate that is seriously impactful on our final estimates, since cardiac infections are the third-lowest syndrome by deaths and years lived with disability (YLDs), comprising just 1.33% (95% UI 1.02–1.67) of all deaths associated with AMR.

Section 6.4.2: Diarrhoea

In diarrhoea patients, cultures of specimens taken from the gastrointestinal tract, bowels, rectum, or stool are almost always affected by contaminants or pathogens that are not the cause of diarrhoea. For this reason, we believe that our input data and modelling framework are not able to accurately capture the aetiologies of diarrhoea. We chose to use GBD estimates of the aetiologies of diarrhoea in deaths instead of running our own model.³⁵ These estimates are based on the odds ratio of having diarrhea given the detection of a pathogen, obtained from the Global Enteric Multicenter Study, therefore removing the influence of any pathogen that does not increase the risk of diarrhea.

A major limitation of using this study is that the GBD diarrhoea aetiology estimates are population attributable fractions (PAFs) for each pathogen. These PAFs may add to greater than 1 and the authors made no attempt to quantify the extent of co-occurrence of pathogens. This is inconsistent with the pathogen distribution estimation method used in our study, which quantifies polymicrobial infections and estimates all pathogens as mono-infections. In order to avoid duplication of cases in our framework, we had to make some assumptions about the co-occurrence of pathogens in diarrhoea. We chose to normalise the PAFs to 1 for any demographic where the sum of GBD diarrhoea aetiology PAFs was greater than 1. This assumed that co-occurrence of pathogens was random and that

the "other" pathogens category was negligible in these demographics. We made no adjustment to demographics where the PAFs added to less than 1. To convert the fatal PAFs to a distribution of aetologies in incidence, we rescaled the distribution according to our estimates of the pathogen-specific case fatality ratios of diarrhea, calculated as described in section 5.

Section 6.4.3: Bacterial infections of the skin and subcutaneous systems

Certain skin and subcutaneous samples are easily affect by contaminants, colonization, and other pathogens that are not the cause of infection. For this reason, we considered microbial data and mortality surveillance to be too difficult to extract meaningful aetiology information from, and instead used only ICD-coded databases (multiple cause of death, hospital discharge, and linkage data) and literature studies as inputs into our model of the pathogen distribution of skin infections.

Section 6.4.4: Lower respiratory infections and all related infections in the thorax

We dropped all data on *S. pneumoniae* for community-acquired LRI and thorax infections in non-neonatal age groups except our estimates from the vaccine probe analysis. Our model also predicted a high fraction of polymicrobial in neonates for community-acquired infections for this infectious syndrome based off of only 1 study, CHAMPS. We found this to be implausible and so dropped polymicrobial from the estimates for this age group in community-acquired infections and renormalized the proportions for all other pathogens to 1.

Section 6.4.5: Peritoneal and intra-abdominal infections

Because dedicated anaerobic cultures were not routinely performed for peritoneal samples, we dropped all anaerobes observed in the data for and excluded anaerobes as an etiology of intra-abdominal infections.

Section 6.4.6: Meningitis and other bacterial central nervous system infections

Due to the unique pattern of meningitis in neonates, particularly the high prevalence of GBS, we modeled neonatal and adult central nervous syndrome infections separately.

Section 6.4.7: Infectious syndromes not modelled

For three infectious syndromes, we did not run a pathogen distribution model. These syndromes are all caused by distinct pathogens whose individual burdens are already estimated in GBD as separate causes of death. For these syndromes, we simply used GBD estimates (table 6.4.6.1)

Table 6.4.6.1: Infectious syndromes	for which we used GBD estimates to	obtain the pathogen distribution
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Infectious syndrome	Pathogens	GBD causes
Typhoid, paratyphoid, and invasive non-	Salmonella Typhi	Typhoid fever
typhoidal Salmonella	Salmonella Paratyphi	Paratyphoid fever
	Non-typhoidal Salmonella	Invasive non-typhoidal Salmonella
Tuberculosis	Mycobacterium tuberculosis	Tuberculosis
Gonorrhoea and chlamydia	Neisseria gonorrhoeae	Gonococcal infection
	Chlamydia trachomatis	Chlamydial infection

Section 6.5: Model validation

To assess model validity, we calculated the root mean square error (RMSE) and coefficient of determination (R²) for each pathogen distribution model in proportion space for both in-sample and out-of-sample predictions (Table 6.5.1). Proportions were predicted for each observation using the specific denominator observed from that study. For example, if a given study reported on only *E. coli* and *S. pneumoniae*, the predictions for model validation for this study were calculated as proportions of the total for *E. coli* and *S. pneumoniae*. In order to calculate out-of-sample fit, we perform non-exhaustive cross-validation, with each round of the validation holding out 1 country of data at a time. This leave-one-country-out approach simulates the prediction task of estimating the pathogen distribution of a country for which we have no data.

R² ranges from 0.784 to 0.867 in-sample and from 0.755 to 0.837 out of sample, indicating good model fit with only modest losses when data are moved out of sample. RMSE ranges from 0.129 to 0.149 in-sample and from 0.141 to

0.159 out of sample. Given that the data are expected to vary from the model predictions according to the observation-level variance, and the fact that the RMSEs are relatively consistent between in-sample and out-of-sample, these RMSEs are reasonable. Overall, these metrics show that these models have good fit and good out-of-sample predictive ability.

Table 6.5.1 In-sample and out-of-sample validation metrics for pathogen distribution models

Infectious syndrome	Model type	R ²		RMSE	
		In sample	Out of sample	In sample	Out of sample
Bacterial infections of the skin and subcutaneous systems		0.808	0.771	0.129	0.141
Bloodstream infections		0.822	0.785	0.128	0.141
Infections of bones, joints, and related organs		0.858	0.837	0.141	0.151
Lower respiratory infections and all related infections in the thorax		0.810	0.780	0.142	0.153
Meningitis and other bacterial central nervous system infections	Neonatal	0.858	0.803	0.134	0.158
nervous system infections	Non-neonatal	0.867	0.822	0.129	0.150
Peritoneal and intra-abdominal infections		0.815	0.812	0.147	0.148
Urinary tract infections and pyelonephritis		0.784	0.755	0.149	0.159

Out of sample metrics calculated using leave-one-country-out cross validation

Section 7: Prevalence of resistance

Section 7.1: Input data

We identified line level and aggregate data on the prevalence of resistance in bacterial pathogens, which were linked to the country and year in which the infection was acquired, from datasets obtained from pharmaceutical companies, surveillance networks, academic institutions, and individual hospitals (see section 2). In total, we gathered over 52.8 million test results for the 88 pathogen—drug combinations we assessed. Table S7 provides a detailed breakdown of this total by pathogen—drug combination.

We supplemented microbiological data with systematic reviews following the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) guidelines,³⁶ to collect resistance data published from countries and territories where surveillance systems do not routinely collect data to ensure extensive coverage of the pathogen–drug combinations thought to contribute the greatest burden of drug resistant infections, which we termed core pathogen–drug combinations (table 7.2.1). Data on the prevalence of AMR in these pathogen–drug combinations were extracted from published literature and compiled into comprehensive datasets. The systematic reviews followed similar methodologies; a detailed description can be found either in published literature (*S.* Typhi and *S.* Paratyphi³⁷) or in the corresponding PROSPERO records (*E.* coli, *K. pneumoniae*, *S. aureus* and *S. pneumoniae* PROSPERO registration CRD42019145148; *Shigella* species PROSPERO registration CRD42019127603; iNTS PROSPERO registration CRD42020189935; *N. gonorrhoeae* SPF unique identifier osf.io/4vy5n). The *S.* Typhi and *S.* Paratyphi A systematic review was expanded to include non-blood culture isolates for the current analysis.

Forms were created, and screening and data extraction were completed using web-based systematic review software (DistillerSR, Evidence Partners, Ottawa, Canada) for all pathogens except *Salmonella*, for which a smaller number of manuscripts were identified.

To more comprehensively account for the burden of AMR in bacteria, we also estimated the prevalence of resistance for 71 supplementary pathogen—drug combinations for which we did not conduct a systematic literature review. Data for these supplementary combinations were extracted from the datasets obtained from pharmaceutical companies, academic institutes, and individual hospitals using the same processing procedure as was used for the core pathogen—drug combinations. The list of supplementary combinations is presented in table 7.2.2.

For the prevalence of drug resistance in *Mycobacterium tuberculosis* for multi-drug resistance (MDR, characterised by isoniazid and rifampicin co-resistance) excluding extensive drug resistance (XDR, characterised by resistance to isoniazid, rifampicin, and fluoroquinolone, as well as either aminoglycosides or capreomycin) and XDR, we used previously published GBD results. Notably, GBD MDR excluding XDR TB estimates and the MDR/rifampin mono-resistant TB estimate from WHO differ, primarily because HIV/TB cases are included as part of WHO TB estimates. GBD adjusts the miscoding of deaths cause by HIV and TB in locations with high prevalence of both diseases, such as South Africa, assigning more deaths to HIV/TB (which are attributed to HIV) and these methodological differences lead to lower MDR TB mortality across GBD burden estimates. An additional difference in estimates for MDR is that WHO includes rifampicin mono-resistance as part of their MDR TB figures.

Section 7.2: Data processing

The prevalence of resistance for each pathogen—drug combination was calculated for each data source, by country and year. Whenever possible, we classified resistance using the most recent CLSI guidelines based on the MICs provided in the data. When MICs were unavailable, we deferred to lab interpretation to classify the isolates. All isolates determined to have intermediate resistance were classified as resistant. To determine the prevalence of resistance to a class of antibiotics (eg, fluoroquinolones), resistance to any one of the antibiotics in the class was sufficient to classify an isolate as resistant for line level data (ie, susceptibility data for individual isolates). For aggregate data (ie, the proportion of isolates resistant to various antibiotics), the highest prevalence of resistance to any antibiotic in the class was selected. Multidrug resistance in *Salmonella* species was defined as concurrent resistance to ampicillin/amoxicillin, chloramphenicol, and trimethoprim-sulfamethoxazole; and fluoroquinolone resistance was defined as ciprofloxacin minimum inhibitory concentration of 0.125µg/ml or higher, or nalidixic acid resistance (CLSI breakpoint for *Salmonella* spp. were updated in 2012 to include 0.125 µg/ml as isolates with 'decreased ciprofloxacin susceptibility', and we have considered these as resistant). Nalidixic acid resistance was also used as a proxy for fluoroquinolone non-susceptibility for *Shigella* species.

Table 7.2.1: Core pathogen–drug combinations

Pathogen	Antimicrobial
Escherichia coli	Third-generation cephalosporins
	Fluoroquinolones
Klebsiella pneumoniae	Third-generation cephalosporins
	Carbapenems
Staphylococcus aureus	Methicillin
Streptococcus pneumoniae	Penicillin
Salmonella Typhi & Paratyphi A	Multidrug resistance
	Fluoroquinolones
Invasive non-typhoidal Salmonella	Fluoroquinolones
Shigella species	Fluoroquinolones
Neisseria gonorrhoeae	Third-generation cephalosporins
Mycobacterium tuberculosis	Isoniazid mono-resistance, Rifampicin mono-
	resistance

Table 7.2.2: Supplementary pathogen-drug combinations

Pathogen	Antimicrobial
Acinetobacter baumannii	Aminoglycosides, Anti-pseudomonal penicillin/Beta-lactamase inhibitors, Beta-lactam/Beta-lactamase inhibitors, Carbapenems, Third-generation cephalosporins, Fourth-generation cephalosporins, Fluoroquinolones
Citrobacter species	Aminoglycosides, Anti-pseudomonal penicillin/Beta-lactamase inhibitors, Carbapenems, Third-generation cephalosporins, Fourth-generation cephalosporins, Fluoroquinolones
Enterobacter species	Aminoglycosides, Anti-pseudomonal penicillin/Beta-lactamase inhibitors, Carbapenems, Fourthgeneration cephalosporins, Fluoroquinolones, Trimethoprim-Sulfamethoxazole
Enterococcus faecalis	Fluoroquinolones, Vancomycin
Enterococcus faecium	Fluoroquinolones, Vancomycin
Enterococcus species	Fluoroquinolones, Vancomycin

Escherichia coli	Aminoglycosides, Aminopenicillin, Beta-lactam/Beta-lactamase inhibitors, Carbapenems, Trimethoprim-Sulfamethoxazole
Group A Streptococcus	Macrolide
Group B Streptococcus	Fluoroquinolones, Macrolide, Penicillin
Haemophilus influenzae	Aminopenicillin, Third-generation cephalosporins
Klebsiella pneumoniae	Aminoglycosides, Beta-lactam/Beta-lactamase inhibitors, Fluoroquinolones, Trimethoprim-Sulfamethoxazole
Morganella species	Third-generation cephalosporins, Fourth-generation cephalosporins, Fluoroquinolones
Neisseria gonorrhoeae	Fluoroquinolones
Proteus species	Aminoglycosides, Aminopenicillins, Third-generation cephalosporins, Fluoroquinolones, Trimethoprim-Sulfamethoxazole
Pseudomonas aeruginosa	Aminoglycosides, Anti-pseudomonal penicillin/Beta-lactamase inhibitors, Carbapenems, Third-generation cephalosporins, Fourth-generation cephalosporins, Fluoroquinolones
Serratia species	Aminoglycosides, Anti-pseudomonal penicillin/Beta-lactamase inhibitors, Carbapenems, Third-generation cephalosporins, Fourth-generation cephalosporins, Fluoroquinolones
Staphylococcus aureus	Fluoroquinolones, Macrolide, Trimethoprim-Sulfamethoxazole, Vancomycin
Streptococcus pneumoniae	Beta-lactam/Beta-lactamase inhibitors, Carbapenems, Third-generation cephalosporins, Fluoroquinolones, Macrolide, Trimethoprim-Sulfamethoxazole

Group A Streptococcus = Streptococcus pyogenes. Group B Streptococcus = Streptococcus agalactiae

To account for biased level of resistance found in tertiary care settings, we reviewed all input data used for the prevalence of resistance estimation and classified each data source as either tertiary, non-tertiary, or unknown/mixed designation, which was a commonly used classification for large resistance surveillance networks which don't report on the hospitals they collect data from. We located datasets that either provided facility information at the line-level or reported samples from exclusively tertiary or non-tertiary facilities. Where possible, we used tertiary/non-tertiary assignments from the data providers. When no assignments were available, we classified sites as tertiary, primary, and secondary by following the definitions provided by Jamison et al.³⁸ in table 7.2.3. We first considered hospital name when classifying. If the name did not include any of the terms listed in table 7.2.3, we searched the facility website for self-designations of tertiary/non-tertiary (most preferred), number of specialties, and bed-size. We classified facilities with vague names and with no websites or websites with insufficient information as "mixed/unknown"; data from these facilities could contain both tertiary and non-tertiary samples. Finally, we grouped primary and secondary facilities together in the non-tertiary category.

Table 7.2.3: Definitions and terms for different levels of hospital

Disease Control Priorities Project: terminology and definitions	Alternative terms commonly found in the literature
Primary-level hospital: few specialties—mainly internal medicine, obstetrics and gynecology, pediatrics, and general surgery, or just general practice; limited laboratory services available for general but not specialized pathological analysis	District hospital Rural hospital Community hospital General hospital
Secondary-level hospital: highly differentiated by function with 5 to 10 clinical specialties; size ranges from 200 to 800 beds; often referred to as a provincial hospital	Regional hospital Provincial hospital (or equivalent administrative area such as county) General hospital
Tertiary-level hospital: highly specialized staff and technical equipment— for example, cardiology, intensive care unit, and specialized imaging units; clinical services highly differentiated by function; could have teaching activities; size ranges from 300 to 1,500 beds	National hospital Central hospital Academic or teaching or university hospital

For systematic review data collected from sub-Saharan Africa, we referred to Maina et al.³⁹ who identified and defined health facilities at each service delivery level (primary to tertiary) in sub-Saharan Africa using both information from health sector policies and strategic plans for each country in the region. They also undertook further comparative/validation analyses to cross reference the completeness/robustness of their classifications against the corresponding number of facilities reported at each level in the most current country-level health sector strategic plans and other health sector reports. Using this hierarchy by country (please see online table 2 in Maina et al.) we classified facilities in sub-Saharan Africa from the systematic review data as tertiary versus non-tertiary.

The proportion of data classified as originating from a tertiary facility differed substantially by super region, ranging from 0.3% of cases in the high-income super-region to 25.0% of cases in sub-Saharan Africa; this stark difference reaffirmed the importance of adjusting the data. To create robust inputs for the crosswalk, data were aggregated by source, year, tertiary/non-tertiary status, and super-region. Because there was no reliable way to determine the mix of hospital types in mixed/unknown data, this data was grouped with non-tertiary. We chose to cluster this data with non-tertiary rather than omit it, as, for some super-regions, the proportion of definitively non-tertiary data was very low (e.g., 0.05% for high-income). After aggregating the data in this way, we created a set of matched pairs, matching every tertiary data point to non-tertiary data for the same pathogen—drug combination from the same super-region collected within 5 years from one another.

Because the degree of bias in resistance between tertiary and non-tertiary data could vary across different parts of the world, we ran a separate crosswalk for each super region and pathogen—drug *super group* combination. Certain bacteria and antimicrobials were clustered into super groups to provide the models with more robust input data, though, crucially, while a given model would contain several pathogen—drug combinations in its inputs, every matched pair was made comparing tertiary and non-tertiary values for the same combination. Bacteria were classified as follows:

Table 7.2.4: Pathogens in each pathogen super group

Pathogen super group	Incorporated pathogens	
Gram-negatives	Enterococcus faecalis, Enterococcus faecium, Enterococcus spp.,	
Group A Streptococcus, Group B Streptococcus, Staphyla		
	aureus, Streptococcus pneumoniae	
Enterobacterales Citrobacter spp., Enterobacter spp., Escherichia coli, Ha		
	influenzae, Klebsiella pneumoniae, Proteus spp., Serratia spp.	
Pseudomonadales	Acinetobacter baumannii, Pseudomonas aeruginosa	

Notably, some pathogens were excluded from the tertiary crosswalk procedure because it was believed that infections with such pathogens would be robust to tertiary care bias. These pathogens were: *Mycobacterium tuberculosis*, *Neisseria gonorrhoeae*, non-typhoidal *Salmonella*, *Salmonella paratyphi*, *Salmonella typhi*, and *Shigella* spp. Data for *Morganella* spp. was not crosswalked as there was no input data for that pathogen from tertiary facilities.

Only one group of antimicrobials was clustered to create an antimicrobial super group, the β -lactam group, which was comprised of: aminopenicillin, anti-pseudomonal penicillin, β -lactamase inhibitors, carbapenems, third and fourth generation cephalosporins, methicillin, and penicillin. All other antibiotic classes (aminoglycosides, fluoroquinolones, macrolides, sulfanoamides, and vancomycin) each individually comprised their own antimicrobial super group.

To allow us to implement linear models, resistance values were logit-transformed. We used the delta method to compute the standard error of the prevalence of resistance in logit space. To incorporate data with zero resistance, or with complete resistance, we applied a 0.1% offset, such that the prevalence of resistance for data with zero resistance was represented as 0.1% and the prevalence of resistance for data with total resistance was represented as 99.9%. We then used the MR-BRT modelling framework to estimate the logit difference of tertiary and non-tertiary data for each super region-pathogen/antimicrobial 'super combination,' including a random effect for each pathogen—drug combination within the super combination and employing a positivity prior to enforce the constraint that the tertiary data exceed or be equal to the non-tertiary data. For the super region-pathogen/antimicrobial super combinations with sparse input data (fewer than 250 matched pairs) we instead used global estimated logit

differences between tertiary and non-tertiary data for that pathogen/antimicrobial super combination, employing the same positivity prior.

After modelling the difference between tertiary and non-tertiary data, we implemented the models to adjust all the country-level tertiary input data that was indicated as biased. We then used the adjusted prevalence of resistance estimates from tertiary care facilities and unadjusted prevalence of resistance from non-tertiary/mixed care facilities as data inputs for the prevalence of resistance models. As was done before, resistance values were offset prior to logit-transformation to allow the use of linear models; data with zero resistance or complete resistance was offset by 2%. Exceptions to this offset were made for two combinations, *Staphylococcus aureus*/vancomycin and Group B *Streptococcus*/penicillin, which were anticipated to often have values beneath 2% resistance. For these combinations, we applied a 0.5% offset instead.

Section 7.3: Modelling framework

The prevalence of AMR in each pathogen—drug combination was modelled separately. For the core combinations, excluding *N. gonorrhoeae*/3GC, we selected a range of spatially- and temporally-explicit health and sociodemographic-related covariates with biologically plausible associations to the prevalence of AMR in each pathogen from the Global Health Data Exchange (http://ghdx.healthdata.org/), and from published literature. This list was narrowed down by fitting a lasso penalised regression model between the data and the covariates for each dataset (using the 'glmnet' package version 3.0.2 in R version 3.6.1) and selecting the most influential covariates in each of the pathogen—drug models to be taken forward. For the supplementary pathogen—drug combinations and *N. gonorrhoeae*/3GC, we utilised a standard set of covariates for all models: HAQ Index, pigs per capita (as a proxy for antibiotic use in animal husbandry), mean temperature, and antibiotic consumption of the antibiotic class relevant to each pathogen—drug combination. Determining more individualised sets of covariates for each of these supplementary pathogen—drug combinations is an ongoing focus for future extensions of this research.

Due to the high heterogeneity of the input datasets, we outliered data points found to have the most extreme values for the prevalence of resistance. An initial generalised linear model (GLM) was fit to the data and covariates and input data points that lay outside of two times the median absolute deviation from the modelled estimate for each location were determined to be outliers and removed. The GLM was fit with nested random effects based on the GBD super-region, region, and country or territory to capture spatial effects, and was fit using the 'lme4' package version 1.1-21 in R version 3.6.1.

After the removal of extreme values, the datasets were used to fit spatiotemporal statistical models of the prevalence of AMR. Firstly, we used a stacked ensemble model to fit the associations between selected covariates and data. For each of the pathogen–drug combinations, we considered the following child models for inclusion: generalised additive models (GAM), penalised regression models (elastic-net, ridge, lasso), random forest, cubist, and neural-networks. Models were fit in R version 3.6.1, using the packages 'CARET' version 6.085, 'mgcv' version 1.8.31, and 'glmnet' version 3.0.2. We fit the child models using five-fold cross validation for each combination and selected the best performing, non-correlated child models based on the out-of-sample predictive performance (final covariates for each pathogen–drug combination are shown in table S8). We then calculated the R²-weighted mean of the estimates of the child models, constraining the coefficients to sum to one, and used these ensemble estimates to fit a spatiotemporal Gaussian process regression (ST-GPR) model for each pathogen–drug combination.

ST-GPR is described in detail elsewhere.¹ In brief, spatial and temporal weights were applied to the residuals of the stacked ensemble model; these were then added to the modelled estimates to smooth them in time and space. A Gaussian process regression (GPR) was then fit, and the mean prevalence of AMR was calculated from 1000 draws of the GPR for each location and year with endemic disease. The 1000 draws of the model were taken through to the next stage of calculations to propagate uncertainty throughout.

Section 7.4: Covariates

Appendix table S8 shows all of the covariates used to model the core pathogen—drug combinations and provides citations detailing the methods used to estimate these covariates. For certain covariates, we provide a brief summary of the estimation method below.

Mean temperature: Temperature data are obtained from Climatic Research Unit, University of East Anglia. ⁴⁰ For each GBD geography, the temperature and population datasets (rasters) are cropped to just cover said geography. The population weighted mean temperature is calculated for each pixel of data in that geography, and then those values are aggregated to produce a single value for the geography. This is repeated for each country-year.

Pigs per capita: Data on the global distribution of pigs were obtained from the Food and Agriculture Organization of the United Nations. 41,42 The raw pig count raster is cropped to GBD geography. Total number of pigs is calculated by summing all pixels in that geography, the result is then divided by the total population of that geography to calculate pigs per capita. This is repeated for each country-year.

Population density: First, population density per pixel was calculated by dividing the population count per pixel by the land area per pixel. The result raster is then thresholded for those pixels where there are more than 1000 people per sq km. The result is multiplied by population, and then the area summed to get a total population in a geography in that bin. Finally this value is divided by total population in the geography to get the final proportion result.

Oral rehydration: Data on oral rehydration, defined as the proportion of children under 5 who had diarrhea in the last 2 weeks who received oral rehydration (ORS) treatment, were collected from multi-country population health surveys such as the Demographic and Health Surveys (DHS), Multiple Indicator Cluster Surveys (MICS), Reproductive Health Surveys (RHS), and Living Standards Measure Study (LSMS) survey, as well some country-specific surveys (see http://ghdx.healthdata.org/gbd-2019/data-input-sources). Only nationally representative datasets are included, and the most extreme 10% of the data is removed from each quintile of Socio-demographic Index (SDI) or HAQ Index. A forward stepwise method is used to select covariates, resulting in SDI and antenatal care (1 visit) coverage being selected. Finally, ST-GPR is run using a mixed effects stage 1 regression with fixed effects on SDI and antenatal care coverage and random effects for super-regions, regions, and countries. Predictions are made for all GBD geographies.

Section 7.5: Resistance profiles

To accurately assess the burden associated with resistance to each antibiotic, we needed to first understand the landscape of multidrug-resistant bacteria, for which the burden would be shared across several antibiotics. We therefore estimated, for each bacteria studied, a set of 'resistance profiles' characterized as the probabilities for each possible combination of resistance/susceptibility for all of the antibiotics analyzed. For example, for a bacterium for which we assessed three antibiotics, we would estimate eight probabilities: SSS, SSR, SRS, RSS, RRS, RRS, and RRR (S – susceptible, R – resistant). These probabilities encompass the entire set of possibilities of resistance for the bacterium, and sum to 1.

For a pathogen for which we assessed n antibiotics, resistance profiles were estimated by optimising over a 2^n - 1-dimensional probability simplex with $\frac{n(n+1)}{2}$ linear constraints. Every such set of resistance profiles corresponds to a full specification of a multivariate binomial distribution. The target set of constraints were as follows:

- The inferred marginal probability of resistance for each antibiotic (the prevalence of resistance to an antibiotic irrespective of all others analyzed) exactly matches the estimates from our prevalence of resistance models. Since there are *n* antibiotics, this set comprises *n* constraints.
- The inferred pairwise likelihood of co-resistance for each pair of antibiotics exactly matches the likelihood inferred from the marginal probability of each antibiotic in the pair, and the Pearson correlation of resistance between the two antibiotics observed across all of the laboratory data we compiled. These represent $\frac{n^2-n}{2}$ additional constraints.

The input format for these constraints for an example case with n = 3 is shown in figure 7.5.1.

Figure 7.5.1: Example input matrix for calculating resistance profiles for a pathogen with 3 antibiotic classes (A,B,C)

Prev(A)	Prev(A&B)	Prev(A&C)	
-	Prev(B)	Prev(B&C)	
-	-	Prev(C)	

Prev(X): prevalence of resistance of antibiotic X from ST-GPR model, by location and draw

Prev(X&Y): prevalence of resistance in both X and Y, back calculated from Prev(X), Prev(Y) and the Pearson correlation of X&Y in the lab data with multiple resistance screens

In the n=2 case, the number of constraints in our framework (3) is equal to the number of unknowns in the probability simplex $(2^n - 1 = 3)$, and therefore at most one set of resistance profiles is possible. For all larger values of n, however, the number of unknowns exceeds the number of constraints, and there are infinite potential resistance profiles. Thus, our resistance profiles are generated by solving for a single sample from the probability simplex formed under the established constraints of marginal resistance and co-resistance.

There is no a priori guarantee that the observables generate a feasible solution. To prevent the constraints from delineating an infeasible probability simplex (for example, an input suggesting the individual resistances to antibiotics A and B are both above 90% but the probability of co-resistance to A and B is below 10%), we solved an optimization problem that identified, for each input matrix, the closest feasible set of input constraints and a corresponding set of resistance profiles that fits these constraints. The 1-simplex in any dimension is specified by

$$\Delta \coloneqq \{p: \quad 0 \le p_i \le 1, \ \sum p_i = 1\} \tag{7.5.1.1}$$

Each marginal observation and each pairwise co-resistance corresponds to a linear constraint, where a sum over a subset of the p in the simplex should be a given value v_i :

$$\mathbf{m}_{i}^{\mathrm{T}} p = v_{i} \tag{7.5.1.2}$$

where m_i is a 'mask vector' of zeros and ones, used to pick out the appropriate summands. Overall, there are $\frac{n(n+1)}{2}$ such affine constraints. The optimisation problem we solve is to find the nearest feasible simplex given these constraints:

$$\min_{p \in \Delta} f(p) := \sum_{i=1}^{n(n+1)/2} \frac{1}{\sigma_i^2} (m_i^T p - v_i)^2$$
 (7.5.1.3)

Where $\frac{1}{\sigma_i^2}$ can be used to provide importance weights for the data. This is a least squares problem with linear equality and inequality constraints (corresponding to the simplex), and can be solved very efficiently even for relatively large n (such as 10 co-occurring antibiotic classes). The result is guaranteed to return the probability simplex closest to the specified constraint, even if the original set of constraints is infeasible, and corresponding set of resistance profiles that fits this nearest simplex.

To propagate uncertainty, we repeat this procedure for each of the 1,000 draws we estimate for prevalence of antibiotic resistance. To generate the *i*-th draw of our resistance profiles, we input the *i*-th draw of the marginal probability of resistance for each antibiotic analyzed for a given pathogen into the probability simplex optimization algorithm. Updating the marginal probabilities of resistance in turn influences the probabilities of co-resistance, and each element of the input we feed the algorithm is unique to the *i*-th draw. The optimization is also initialized randomly for every draw. This process is implemented for each GBD country, resulting in 1000 resistance profiles for each country for each pathogen in our analysis.

It is important to note that while we produce resistance profiles unique to each country, the Pearson correlations of co-resistance that we derive from the input data are assumed to be constant across location, sex, and infectious syndrome. Due to data sparsity, we cannot currently identify co-resistance patterns in several locations (particularly LMICs) with insufficient or non-existent line-level data; indeed, the data sources providing multiple resistance tests for a single isolate are among the most detailed of those we collected for this research and require exceptional data quality standards that are not easily achieved throughout the world. Identifying differences in patterns of co-resistance by location or infectious syndrome is of considerable interest in the future.

Section 7.6: Model validation

Validation of prevalence of resistance modelling occurs in two instances. For the ensemble estimates, machine-learning candidate models are validated using five random holdout sets, and we select models correlated below a Pearson correlation coefficient threshold of 0.8 which showed the best performance based on the R^2 predictive validity for the out-of-sample predictions. These intermediary results are not reported in this paper because they do not pertain to the final prevalence of resistance estimate.

We then validate the entire ensemble ST-GPR process by calculating in-sample and out-of-sample accuracy metrics. Accuracy is measured as the proportion of correctly classified resistant/susceptible isolates based on the modelled estimate and the raw data's prevalence of resistance. As a written example, if there were 10 isolates with 50% resistance in the raw data and the model predicted 60% resistance for that location, we would have 5 correctly classified resistant samples (true positives), 1 incorrectly classified resistant sample (false positive), and 4 correctly classified susceptible samples (true negatives), for 90% accuracy. For out-of-sample cross-validation, we withheld, at the outset of the ensemble modelling process, a set of countries with data as a holdout group: for the corecombinations we withheld 20% of countries each iteration, for 5 total holdout sets, while for the supplementary-combinations we withheld 10% of countries each iteration, for 10 holdout sets. By holding out all of the data for a set of countries, our out-of-sample accuracy metrics reflect the potential model fit we have for countries that have no input data in the entire prevalence of resistance process. Table 7.6.1 reports the accuracy metric for each pathogen—drug combination. Our in-sample accuracy values range from 77.2% to 99.8%, while our out-of-sample accuracy values range from 57.1% to 99.7%.

Table 7.6.1: In-sample and out-of-sample accuracy estimates for prevalence of resistance models

Pathogen	Antibiotic class	IS accuracy	OOS accuracy
Acinetobacter baumannii	3GC	0.98	0.892
Acinetobacter baumannii	4GC	0.964	0.88
Acinetobacter baumannii	AG	0.772	0.645
Acinetobacter baumannii	Anti-pseudomonal	0.96	0.816
Acinetobacter baumannii	BL-BLI	0.969	0.636
Acinetobacter baumannii	CP	0.901	0.768
Acinetobacter baumannii	FQ	0.964	0.821
Citrobacter spp.	3GC	0.987	0.922
Citrobacter spp.	4GC	0.991	0.974
Citrobacter spp.	AG	0.993	0.959
Citrobacter spp.	Anti-pseudomonal	0.984	0.912
Citrobacter spp.	CP	0.995	0.973
Citrobacter spp.	FQ	0.989	0.967
Enterobacter spp.	4GC	0.982	0.941
Enterobacter spp.	AG	0.989	0.976
Enterobacter spp.	Anti-pseudomonal	0.984	0.939
Enterobacter spp.	СР	0.988	0.973
Enterobacter spp.	FQ	0.991	0.98
Enterobacter spp.	TMP-SMX	0.996	0.883
Enterococcus faecalis	FQ	0.982	0.856
Enterococcus faecalis	Vanco	0.993	0.987
Enterococcus faecium	FQ	0.992	0.985
Enterococcus faecium	Vanco	0.976	0.703
Escherichia coli	3GC	0.977	0.973
Escherichia coli	AG	0.979	0.96
Escherichia coli	Aminopenicillin	0.959	0.915
Escherichia coli	BL-BLI	0.932	0.909
Escherichia coli	СР	0.988	0.972
Escherichia coli	FQ	0.983	0.98
Escherichia coli	TMP-SMX	0.907	0.903
Group A Streptococcus	Macrolide	0.987	0.863
Group B Streptococcus	FQ	0.993	0.731
Group B Streptococcus	Macrolide	0.986	0.907
Group B Streptococcus	PCN	0.997	0.992
Haemophilus influenzae	3GC	0.995	0.981
Haemophilus influenzae	Aminopenicillin	0.958	0.849
Klebsiella pneumoniae	3GC	0.981	0.985
Klebsiella pneumoniae	AG	0.983	0.901
Klebsiella pneumoniae	BL-BLI	0.979	0.832
Klebsiella pneumoniae	СР	0.987	0.992
Klebsiella pneumoniae	FQ	0.935	0.755
Klebsiella pneumoniae	TMP-SMX	0.973	0.816
Morganella spp.	3GC	0.922	0.834
Morganella spp.	4GC	0.974	0.917
Morganella spp.	FQ	0.928	0.839
Mycobacterium tuberculosis (new)	Mono INH	0.993	0.966
Mycobacterium tuberculosis (new)	Mono RIF	0.996	0.987
Mycobacterium tuberculosis (retreated)		0.982	0.968

Mycobacterium tuberculosis (retreated)	Mono RIF	0.994	0.966
Neisseria gonorrhoeae	3GC	0.987	0.982
Neisseria gonorrhoeae	FQ	0.972	0.841
Non-typhoidal Salmonella	FQ	0.911	0.967
Other enterococci	FQ	0.928	0.829
Other enterococci	Vanco	0.966	0.924
Proteus spp.	3GC	0.993	0.981
Proteus spp.	AG	0.989	0.906
Proteus spp.	Aminopenicillin	0.991	0.571
Proteus spp.	FQ	0.966	0.842
Proteus spp.	TMP-SMX	0.997	0.986
Pseudomonas aeruginosa	3GC	0.949	0.908
Pseudomonas aeruginosa	4GC	0.988	0.96
Pseudomonas aeruginosa	AG	0.977	0.95
Pseudomonas aeruginosa	Anti-pseudomonal	0.975	0.895
Pseudomonas aeruginosa	СР	0.977	0.912
Pseudomonas aeruginosa	FQ	0.986	0.95
Salmonella Paratyphi	FQ	0.839	0.74
Salmonella Paratyphi	MDR	0.962	0.96
Salmonella Typhi	FQ	0.83	0.8
Salmonella Typhi	MDR	0.87	0.77
Serratia spp.	3GC	0.984	0.946
Serratia spp.	4GC	0.992	0.951
Serratia spp.	AG	0.987	0.965
Serratia spp.	Anti-pseudomonal	0.958	0.894
Serratia spp.	СР	0.991	0.986
Serratia spp.	FQ	0.987	0.953
Shigella spp.	FQ	0.934	0.86
Staphylococcus aureus	FQ	0.984	0.924
Staphylococcus aureus	Macrolide	0.945	0.934
Staphylococcus aureus	Methicillin	0.975	0.883
Staphylococcus aureus	TMP-SMX	0.995	0.992
Staphylococcus aureus	Vanco	0.998	0.997
Streptococcus pneumoniae	3GC	0.98	0.953
Streptococcus pneumoniae	BL-BLI	0.982	0.956
Streptococcus pneumoniae	СР	0.981	0.966
Streptococcus pneumoniae	FQ	0.949	0.925
Streptococcus pneumoniae	Macrolide	0.984	0.884
Streptococcus pneumoniae	PCN	0.945	0.901
Streptococcus pneumoniae	TMP-SMX	0.97	0.884

3GC = Third-generation cephalosporins. 4GC = Fourth-generation cephalosporins. AG = Aminoglycosides. Anti-pseudomonal = Anti-pseudomonal penicillin/Beta-Lactamase inhibitors. BL-BLI = Beta Lactam/Beta-lactamase inhibitors. CP = Carbapenems. FQ = Fluoroquinolones. MDR excluding XDR in TB = Multi-drug resistance excluding extensive drug resistance in TB. MDR in S. Typhi and Paratyphi = Multi-drug resistance in Salmonella Typhi and Paratyphi. Mono INH = Isoniazid mono-resistance. Mono RIF = Rifampicin mono-resistance. PCN = Penicillin. TMP-SMX = Trimethoprim-Sulfamethoxazole. Vanco = Vancomycin. XDR in TB = Extensive drug resistance in TB.

Section 8: Relative risk

Section 8.1 Input data

The input data for the relative risk estimation step included literature data that provided relative risk of death for resistant and susceptible organisms and hospital-based microbiology surveillance data linked to outcomes, as well as other clinical parameters (eg, demographics, diagnoses). Published studies were identified from a recent meta-analysis performed by Cassini and colleagues.⁴³

The data inputs for the excess duration estimates were literature data that reported on length of stay for resistant and susceptible organisms and hospital-based microbiology surveillance data that were linked to outcomes as well as various other clinical parameters (eg, demographics, diagnoses). The number of days between a positive specimen date and discharge date was used to obtain the mean duration of infection. We considered days elapsed between admission and discharge as mean duration of stay if this was the only piece of information provided in the study. We also considered median duration of infection or median duration of stay if the study only provided this piece of information.

Section 8.2: Data processing

There were 9.4 million possible samples from 73 countries to inform our relative risk of death estimates. Many of the 9.4 million potential samples were further de-duplicated as part of the modeling process (modelling details in 7.3). A detailed breakdown of this 9.4 million by pathogen—drug is in table S9 (section 14). Relative risk estimates were extracted from primary literature as were study characteristics that described the adjustments made by the study. When no adjustments were made, or an adjusted odds ratio was presented, we extracted the crude relative risk. For hospital data that contained admission diagnoses, diagnoses were mapped to GBD Level 2 causes. Admission diagnoses were mapped to GBD causes using ICD codes when provided; when admission diagnoses were free-text entries, they were mapped using two expert reviews.

Section 8.3 Modelling overview

The measure of excess risk used to estimate the fatal burden of AMR was the relative risk of death from an infection with a pathogen resistant to the antibiotic of interest as compared to an infection of the same site with the same organism that was susceptible to the antibiotic of interest. The relative risk estimate was produced after adjusting for various potential confounders including age, admission diagnosis (mapped to GBD causes), site of culture, and hospital versus community onset. Because of data sparsity, a single measure of relative risk was estimated for each pathogen—drug combination, representing a global estimate for all sites of infection and all underlying causes.

When data availability allowed it, relative risk from hospital-based microbiology surveillance data was estimated after adjusting for age, admission diagnosis, site of culture, and hospital- versus community-acquired infection, otherwise a crude relative risk was used. The adjusted estimates of relative risks were then included with the crude relative risks in a two-stage nested mixed effects meta-regression model using MR-BRT. The stage one model was a meta-regression for each antibiotic class, which was used to produce a prior for the stage two model. We considered study-specific adjustments such as age of patients, admission diagnosis, site of culture and hospital-versus community acquired infection as potential covariates to be included in the second stage. Covariate selection was based on a set of log-linear models with a range of Lasso penalty parameters, and only statistically significant covariates were selected. The stage two model was run for each antibiotic class with a random effect for pathogen and fixed effects for study level characteristics that described whether the relative risk estimate from a study or dataset adjusted for each parameter using the prior from the stage one model for the antibiotic class.

Relative Risk_{pathogen_ndrug_d} =
$$\beta_0 + \beta_d \cdot x + u_{pathogen_n} + \epsilon_d$$
 (8.3.1)

Where x is a bias covariate, $u_{pathogen_n}$ is a random effect for pathogen n within an antibiotic class, ϵ_K is the measurement error, d is antibiotic class and β and X are vectors of length i+1 for i covariates. From this stage two model, we produced 1000 draws to estimate the relative risk of death and uncertainty attributable to resistance for each pathogen–drug combination.

For non-fatal burden estimation, we estimated the excess duration attributable to resistance—comparing the length of hospital stay for an infection with a pathogen resistant to the antibiotic of interest to an infection of the same site with the same organism that was susceptible to the antibiotic of interest. For community-acquired infections the entire duration of length of stay was attributed to the infection, for hospital-acquired infections we used the time from first positive culture to time of discharge to estimate length of stay. To address the potential confounding effect of longer admissions resulting in higher probability of acquiring resistant infections, we adjusted the relative length of stay obtained from patient level data for the number of hospital days prior to culture positivity. We observed a generally lower relative length of stay when we applied this adjustment, which was expected. We then used the same two-stage nested mixed effects meta-regression modelling framework described for fatal estimation to produce a relative length of stay attributable to resistance for each pathogen—drug combination. One exception to this estimation process was *Neisseria gonorrhoeae*, which had too little data to produce an estimate on the impact of resistance on duration of illness. As a result, we produced a YLD estimate based on the excess duration of illness for a given antibiotic class. This was a 1.29 fold increase in duration for fluoroquinolones-resistant bacteria and a 1.43 fold increase in duration for third-generation cephalosporin-resistant bacteria.

The analysis of relative risk followed the definitions of the prevalence of resistance step (section 7) as closely as possible. Both analyses identified resistance to a given antibiotics class if the isolate had an intermediate or resistant interpretation to any one of the antibiotics in that given class. But the analysis of relative risk diverged from the analysis of prevalence of resistance in the following circumstances. First, the relative risk step included molecular resistance testing if this was the only data provided by a study, eg, β-lactamase or MecA positive pathogens; this could potentially misclassify some resistant organisms as sensitive if they had an alternate mechanism for resistance, such as a porin alteration leading to carbapenem resistance. Second, the relative risk estimate produced was for sterile sites of infection, as there was limited data from non-sterile sites. Third, it was not possible to assess relative risk of multidrug-resistant pathogens because of limited data availability and because it did not fit in the modelling strategy at the antibiotic class level. Instead, the relative risk of each of the components of multidrug-resistant pathogens was calculated and the antibiotic class with the highest relative risk was used; for Salmonella Typhi this was relative risk to Trimethoprim-Suflamethoxazole. Fourth, we had limited availability of data on fatalities attributable to Salmonella Paratyphi and Shigella species; as a result, we used fatal relative risk estimates from Salmonella Typhi as a proxy. Fifth, there were limited data on fatalities attributable to resistant N. gonorrhoeae, so we excluded the fatal estimate for this pathogen. Finally, the relative risk of Mycobacterium tuberculosis was assessed for multidrug and extensively drug-resistant infections as reported previously in GBD. Estimates of relative risk of death for sterile sources of specimen across 88 pathogen-drug combinations are given in table S10.

Section 8.4 Model validation

We report three summary metrics to evaluate the relative risk of death models: the root-mean squared error (RMSE), the Mean Average Error (MAE) and the percent coverage of observed data within the full variance of the model. These three metrics were calculated using the real relative risk ratio in the whole sample of data and also by holding out 25% of the sample within antibiotic class in 4 iterations. Table 8.4.1 provides details for each of the antibiotic class model evaluated. Large MAE and RMSE values indicate that observed data deviates from the mean model estimate. We also see a large proportion of the data (82% and more) falls within the total variance of each model estimates. This indicates that large deviations from the mean estimate coincide with large variances of the data observed.

Table 8.4.1: In-sample and out-of-sample performance metrics for relative risk of death models

	MAE		RMSE		Coverage	
Antibiotic class	in-sample	out-of- sample	in- sample	out-of- sample	in- sample	out-of- sample
Vancomycin	0.71	0.65	1.33	0.94	82%	82%
Fluoroquinolones	0.73	0.75	1.61	1.52	88%	90%
Third-generation cephalosporins	0.75	0.76	1.63	1.49	93%	93%
Macrolide	0.71	0.73	1.25	1.24	95%	94%
Methicillin	0.65	0.67	1.3	1.13	96%	94%
Penicillin	0.48	0.69	0.83	0.97	96%	98%
Carbapenem	0.64	0.64	1.54	1.29	98%	97%
Aminoglycosides	0.37	0.41	0.61	0.58	100%	100%
Aminopenicillin	0.9	0.86	1.82	1.68	100%	100%
Anti-pseudomonal penicillin/Beta-Lactamase inhibitors	0.76	0.8	1.76	1.64	100%	100%
Beta Lactam/Beta-lactamase inhibitors	0.36	0.3	0.61	0.37	100%	100%
Fourth-generation cephalosporins	1.22	1.54	3.21	3.46	100%	100%
Trimethoprim-Sulfamethoxazole	0.64	0.6	1.17	0.97	100%	100%

This approach for relative risk estimation had a number of limitations; most were attributable to data sparsity. First, it is likely that the impact of resistance on mortality is different across locations. In locations where overall health-care access and quality are very poor, the impact of resistance may be smaller because the management of susceptible infections is sub-optimal. On the other hand, in locations where broad, second- and third-line antimicrobials are not available, one would expect the impact of resistance to be greater. Second, it is possible that the relative risk of death attributable to resistance is different across anatomical sites of infection because of variable penetrance of antibiotics to different anatomical locations. As we continue efforts to expand data collection and reporting, we hope to be able to address these limitations in future iterations.

Section 9: Counterfactuals and AMR estimation

Section 9.1: Estimating AMR burden with counterfactual of no infection

We computed two counterfactuals to estimate the drug-resistant burden. First, we estimated the burden of AMR using the counterfactual of no infection. We estimated the fatal burden of individual pathogen—drug combinations by taking the product of the deaths for each underlying cause, fraction of deaths related to infection, infectious syndrome fraction, fatal pathogen fraction, and fatal prevalence of resistance and then summed across all infectious syndromes and underlying causes:

Deaths with Resistance_{Kd} =
$$\sum_{I} \sum_{L} D_{J} \times S_{J} \times M_{LJ} \times P_{LK} \times R_{Kd}$$
 (9.1.1)

where D = deaths, S = fraction related to infection, M = infectious syndrome fraction, P = fatal pathogen fraction, R = fatal prevalence of resistance, L = syndrome, L = syndro

$$R_{Kd} = \frac{R'_{Kd}RR_{Kd}}{(1 - R'_{kd}) + R'_{Kd}RR_{Kd}}$$
(9.1.2)

We calculated the fatal prevalence of resistance to any antibiotic estimated based on the non-fatal prevalences of each resistance profile, incorporating all resistance profiles δ that are resistant to at least 1 drug with corresponding relative risks RR_{Kd^*} , determined by the method described below (section 9.2):

$$R_{K,all\ drugs} = \frac{\sum_{\delta} R'_{K\delta} R R_{Kd^*}}{\left(1 - \sum_{\delta} R'_{K\delta}\right) + \sum_{\delta} R'_{K\delta} R R_{Kd^*}}$$
(9.1.3)

We then estimated YLLs using standard GBD methods to convert age-sex specific deaths into YLLs.¹

For the non-fatal estimate, we first estimated the incidence of each infectious syndrome in each underlying cause. For infectious underlying causes (table 9.1.1), we simply used the incidence estimated in GBD. For non-infectious underlying causes, we divided the infectious syndrome deaths $(D_j \times S_J \times M_{LJ})$ by the syndrome- and pathogen-specific CFRs calculated in section 5, aggregated across pathogen using the nonfatal pathogen distribution P' calculated above.

$$Incidence_{JL} = \frac{D_J S_J M_{LJ}}{\sum_K CF R_{LK} P'_{LK}}$$
(9.1.4)

Table 9.1.1: Infectious GBD causes for which we used GBD YLD and incidence estimates

Infectious syndrome	GBD cause
Meningitis and other bacterial central nervous system infections	Meningitis
Lower respiratory infections and other related infections in the thorax	Lower respiratory infections
Bacterial infections of the skin and subcutaneous systems	Pyoderma
·	Cellulitis
	Decubitis ulcer
Urinary tract infections and pyelonephritis	Urinary tract infections
Bloodstream infections	Maternal sepsis
	Neonatal sepsis
Diarrhoea	Diarrhea
Tuberculosis	Tuberculosis
Typhoid, paratyphoid, and invasive non-typhoidal Salmonella	Typhoid fever
	Paratyphoid fever
	Invasive non-typhoidal Salmonella
Gonorrhoea and chlamydia	Chlamydia
	Gonococcal infection

We then took the product of the infectious syndrome incidence, the non-fatal pathogen fraction, and the non-fatal prevalence of resistance and summed across all infectious syndromes and underlying causes to get incidence with resistance for every pathogen and drug. As with the fatal estimate, to produce an estimate of incident infections with resistance to any antibiotic, we used the same formula and used the non-fatal prevalence of resistance to any antibiotic estimated from the resistance profiles.

We then calculated YLDs for each pathogen. For some GBD causes, we simply used the GBD YLD estimates and multiplied them by the corresponding nonfatal pathogen distribution (table 8.1.2) For all other causes, we multiplied together the infectious syndrome incidence, the non-fatal pathogen fraction, and a syndrome-specific YLDs per incident case rate, calculated using a proxy cause from GBD. To estimate the YLDs per incident case rate, we extracted GBD incidence and YLD estimates for the proxy causes and divided the YLDs by the incidence for each age, sex, and location. Three infectious syndromes are not estimated in the GBD, and therefore have no standard sequelae or disability weights: bloodstream infections, intra-abdominal infections, and bone and joint infections. For the proxy causes for these three syndromes, we used the closest approximate disease as determined by a group of experts in infectious diseases and epidemiology (table 9.1.2). This approach is a significant limitation of the study and should be improved in future work.

Table 9.1.2. Proxy	v causes used to calculate YI	LDs per	incidence case rate	for each in	fectious syndrome

Infectious syndrome	Proxy cause
Meningitis and other bacterial central nervous system infections	Meningitis
Endocarditis and other cardiac infections	Endocarditis
Peritoneal and intra-abdominal infections	Paralytic ileus and intestinal obstruction
Lower respiratory infections and all related infections in the thorax	Lower respiratory infections
Bacterial infections of the skin and subcutaneous systems	Bacterial skin diseases
Infections of bones, joints, and related organs	Bacterial skin diseases
Diarrhoea	Diarrhoea
Bloodstream infections	Maternal sepsis – Extrapolated to males
Urinary tract infections and pyelonephritis	Urinary tract infections

To get the YLDs associated with resistance for each pathogen, we used the non-fatal prevalences of resistance for each drug and resistance profile and relative length of stay (LOS) for each pathogen—drug combination to calculate the fraction of YLDs associated with resistance for each pathogen, using equations analogous to equations 9.1.2 and 9.1.3. We multiplied this fraction by the YLDs for each pathogen to get YLDs associated with resistance to each pathogen—drug combination and YLDs associated with resistance any antibiotics estimated. We then added YLLs and YLDs to produce the DALY estimate for burden associated with resistance.

Section 9.2: Estimating AMR burden with counterfactual of infection with susceptible organism

For the second counterfactual—comparing resistant to susceptible infections—we calculated mutually exclusive pathogen—drug estimates. To do this, we first estimated the population attributable fraction of deaths (Mortality PAF) for each resistance profile with resistance to at least 1 drug, δ . The inputs for the PAF were the non-fatal prevalence of the given resistance profile, $R'_{K\delta}$, and the relative risk of death for resistant infection compared to susceptible infection for each drug, RR_{kd} . Because of data sparsity, we were unable to calculate the relative risk for every possible resistance profile, and so instead used the highest relative risk of all of the drugs in the resistance profile. For example, if for a resistance profile of resistant to penicillin and fluoroquinolones, the relative risk was 1.1 for penicillin and 1.4 for fluoroquinolones, we would use a relative risk of 1.4 for this profile. The mortality PAF is calculated as a multi-category exposure:

Mortality
$$PAF_{K\delta} = \frac{R'_{K\delta}(RR_{Kd^*} - 1)}{1 + \sum_{\delta} R'_{K\delta}(RR_{Kd^*} - 1)}$$
 (9.2.1)

where d^* is the drug in the resistance profile δ with the highest relative risk.

We then took the product of the deaths for each underlying cause, fraction of deaths related to infection, infectious syndrome fraction, fatal pathogen fraction, and the mortality PAF for each resistance profile to get the deaths attributable to resistance for every resistance profile:

Deaths due to Resistance_{Kδ} =
$$\sum_{I} \sum_{L} D_{J} \times S_{J} \times M_{LJ} \times P_{LK} \times Mortality PAF_{K\delta}$$
(9.2.2)

When the resistance profile described resistance to more than one antibiotic, the deaths were then distributed to the component pathogen–drug combinations based on the excess risk of the pathogen–drug combination divided by the sum of the excess risk of all pathogen–drug combinations in the resistance profile. For a resistance profile δ with resistance to drugs i = 1, ..., n:

$$Redistribution\ Weight_{Kd_i} = \frac{RR_{Kd_i} - 1}{\sum_{\hat{i}} (RR_{Kd_i} - 1)} \tag{9.2.3}$$

For co-resistance amongst beta-lactam antibiotics (i.e. carbapenems, 4GC, 3GC, antipseudomonal, BL/BLI, aminopenicillins, and penicillin), we used a different approach to redistributing burden. Similar to Cassini et al., we applied a hierarchy such that the burden was categorically attributed to the broadest beta-lactam antibiotic, rather than split the burden between multiple beta-lactam antibiotics. We used the hierarchy in table 9.2.1 to assign burden in the presence of co-occurring beta-lactam resistance. When a pathogen was resistant to multiple beta-

lactams and a non-beta-lactam antibiotic, we first applied the hierarchy to determine the 'highest' beta-lactam resistance and then generated redistribution weights using only the 'highest' beta-lactam and the non-beta-lactams. We then used these attributable death estimates to estimate YLLs using standard GBD methods to convert age-sex specific deaths to YLLs.

A similar approach was taken to estimate non-fatal burden for the counterfactual of antibiotic-susceptible infection. We first assumed that antibiotic resistance has no effect on the attack rate of pathogens; therefore, there are 0 incident cases attributable to resistance and all non-fatal burden comes from increased length of illness. To quantify the extent of this increased length of illness, we first produced a length of stay (LOS) PAF for each resistance profile using the non-fatal prevalence of resistance and relative LOS for resistant infections as compared to susceptible infections in a method analogous to equation 9.2.1. Because of data sparsity, we were unable to calculate the relative LOS for every resistance profile, and so instead used the relative LOS for the drug with the highest relative LOS in the profile. We then took the product of the YLDs for each infectious syndrome, the non-fatal pathogen distribution, and the LOS PAF to produce attributable YLD estimates. This assumes that the attributable LOS PAF is equally applicable to all sequelae, which is an assumption made because of a lack of data on the impact of resistance on the likelihood of different sequelae and the duration of specific sequelae. We then added YLLs and YLDs to produce an estimate of DALYs attributable to resistance.

Table 9.2.1 Beta-lactam hierarchy

Rank	Antibiotic class
1	Carbapenem
2	Antipseudomonal Penicillin/Beta-lactamase Inhibitor
3	Fourth Generation Cephalosporin
4	Third Generation Cephalosporin
5	Beta-lactam/Beta-lactamase Inhibitor
6	Aminopenicillin
7	Penicillin

Because of the optimisation approach used to derive each resistance profile, the prevalence of resistance to for a given pathogen–drug as modelled using ensemble ST-GPR (section 7.3), R'_{Kd} , will not necessarily be exactly equal to the sum of all resistance profiles $R'_{K\delta}$ that include resistance to drug d. Due to this inconsistency, in extremely rare cases, an estimate of AMR burden in the susceptible counterfactual may slightly exceed the corresponding estimate of AMR burden in the no infection counterfactual for a specific pathogen–drug. We consider the ensemble ST-GPR estimate to be more accurate than the resistance profiles, since the latter are based on Pearson correlations of multidrug resistance that are calculated from limited microdata and generalized to all locations. For this reason, we cap all individual pathogen–drug estimates of burden for the susceptible counterfactual, which are based on the resistance profiles, to the burden for the no infection counterfactual, which are based on the ensemble ST-GPR estimates.

Section 9.3: Excluded combinations

Although our approach attempted to be exhaustive and include all clinically-relevant pathogen—drug combinations, there are two combinations included in the WHO priority list for which we could not produce an estimate. The first is clarithromycin resistance in *Helicobacter pylori* and the second is fluoroquinolone resistance in *Campylobacter* species. These were excluded due to limited data availability as highlighted by a recent study in the European Union that found that, as of 2019, no member countries had implemented publicly accessible, mandatory reporting surveillance programmes for these two pathogen—drug combinations. ⁴⁴ *H. pylori* and *Campylobacter* spp are commonly diagnosed without culture so resistance profiles are uncommon in passive surveillance systems. The burden of *H. pylori* is not currently estimated in GBD, though some of the consequent diseases are, like peptic ulcer disease and gastric cancer. Producing a burden estimate of *H. pylori was* outside the scope of this work, and without a pathogen burden estimate, we could not produce an estimate of the burden attributable to clarithromycin-resistant

H. pylori. In contrast, GBD does produce an estimate on the burden of Campylobacter spp. There were, however, too few data to produce an estimate on the excess risk of death or duration associated with fluoroquinolone resistance and limited data to inform a global prevalence of resistance estimate. Given these limitations, we did not produce burden estimates for clarithromycin-resistant *H. pylori* or fluoroquinolone-resistant *Campylobacter* spp. Because of the lack of data on risk of death associated with drug-resistant Neisseria gonorrhoeae, we were unable to produce an estimate of the fatal burden of resistance so produce only a non-fatal estimate. Many potential pathogen drug combinations were excluded due to the spectrum of antimicrobial activity (ie, Vancomycin and E. coli), intrinsic resistance (eg, BL/BLI resistance in Pseudomonas aeruginosa) or resistance that is exceedingly common (eg, penicillin resistance in S. aureus); these combinations were decided by a group of experts in infectious diseases, microbiology, epidemiology, and population health. There was insufficient data to produce a global estimate for many pathogen-drug combinations of interest, such as aminopenicillin resistance in *Enterococcus* spp, fluoroquinolone resistance in Acinetobacter baumannii, or colistin resistance in any pathogen estimated. This is largely due to either a lack of regional data to inform the prevalence of resistance component or a lack of microbial data linked to outcomes to inform the measure of excess risk component. A final constraint was the computational burden of estimating more than seven antibiotic classes for a single pathogen. Because of the approach to coresistance described in section 7.4, each antibiotic class added led to an exponential increase in the computation needs and anything above seven antibiotic classes was not tenable. As additional data are made available, we plan to add clinically relevant combinations and iterate on the computational approach so that we can describe the burden of bacterial AMR more comprehensively.

Section 10. Analysis of total AMR burden decomposed by infection and resistance

Appendix table S11 shows our estimates of the fatal burden of AMR by GBD region, decomposed into several key components: all-cause mortality, the fraction of all deaths that involve infection (infection fraction), the fraction of deaths involving infection that are associated with resistance (prevalence of resistance), and the fraction of deaths involving infection that are attributable to resistance (PAF). The number of deaths associated with resistance is the product of all-cause deaths, infection fraction, and resistance-associated fraction, while the number of deaths attributable to resistance is the product of all-cause deaths, infection fraction, and resistance-attributable fraction. Decomposing our results into these components shows how the burden of AMR is variously influenced by overall regional death rates, the prevalence of infectious disease, and the prevalence of resistance in different regions of the world.

While the regions of sub-Saharan Africa have among the highest death rates per 100,000 person-years associated with and attributable to AMR in the world, the majority of this burden is driven by the high rates of infectious disease in these regions, rather than the prevalence of resistance itself. The GBD regions of central, eastern, southern, and western sub-Saharan Africa have the four leading infectious fractions, at 48.0% (95% UI 40.2 - 56.1), 50.7% (43.1 - 58.8), 45.6% (38.4 - 52.7), and 53.5% (45.4 - 62.0) respectively, but also have the bottom 4 fraction of infectious deaths that are associated with AMR, 27.0% (24.3 - 30.1), 27.9% (25.6 - 30.1), 18.6% (16.6 - 20.9), and 28.3% (25.4 - 30.8) respectively. In contrast, the three regions with the lowest death rate associated with AMR, Australasia, north Africa and the Middle East, and east Asia, have significantly higher fractions of infectious deaths that are associated with AMR than sub-Saharan Africa (31.0% (29.2 - 32.8), 45.3% (42.6 - 47.7), and 47.1% (44.6 - 49.2)), but relatively low infectious fractions (12.7% (8.9 - 17.6), 18.1% (13.2 - 24.2), and 12.2% (8.2 - 17.5)). The burden of AMR can also be analysed through the lens of death counts, in which case the large populations of east Asia and south Asia combined with relatively high infection fraction in south Asia (31.8% [26.0 - 39.2]) and relatively high fraction of infectious deaths that are associated with AMR (36.4% [30.8 - 41.4] in south Asia, 47.1% [44.6 - 49.2] in east Asia), result in these regions having the most deaths associated with and attributable to AMR in 2019.

Analysing infection and AMR as distinct the drivers of AMR burden has critical consequences for any policy intervention. Investments in infection control and prevention (IPC), water, sanitation, and hygiene, and vaccination can be made in areas with high infection fraction, while efforts in antibiotic stewardship can be enhanced in areas with high prevalence of resistance. Notably, our estimates show that rates of infectious disease are ultimately a

stronger driver of the burden of AMR than the prevalence of resistance itself, and should therefore be addressed first and foremost in any effort to reduce the burden of AMR.

Section 11. GATHER compliance

This study complies with GATHER recommendations.⁴⁵ We have documented the steps in our analytical procedures and detailed the data sources used. See table S12 for the GATHER checklist. The GATHER recommendations can be found on the GATHER website.

Section 12: References

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Section 14: Appendix tables and figures

Table S1. GBD cause hierarchy with levels	
Cause	level
All causes	0
Communicable, maternal, neonatal, and nutritional diseases	1
HIV/AIDS and sexually transmitted infections	2
HIV/AIDS	3
HIV/AIDS-drug-susceptible tuberculosis	4
HIV/AIDS-multidrug-resistant TB without extensive drug resistance	4
HIV/AIDS-extensively drug-resistant tuberculosis	4
HIV/AIDS resulting in other diseases	4
Sexually transmitted infections excluding HIV	3
Syphilis	4
Chlamydial infection	4
Gonococcal infection	4
Trichomoniasis	4
Genital herpes	4
Other sexually transmitted infections	4
Respiratory infections and tuberculosis	2
Tuberculosis	3
Latent tuberculosis infection	4
Drug-susceptible tuberculosis	4
Multidrug-resistant TB without extensive drug resistance	4
Extensively drug-resistant tuberculosis	4
Lower respiratory infections	3
Upper respiratory infections	3
Otitis media	3
Enteric infections	2
Diarrhoeal diseases	3
Typhoid and paratyphoid	3
Typhoid fever	4
Paratyphoid fever	4
Invasive non-typhoidal Salmonella (iNTS)	3
Other intestinal infectious diseases	3
Neglected tropical diseases and malaria	2
Malaria	3
Chagas disease	3
Leishmaniasis	3
Visceral leishmaniasis	4
Cutaneous and mucocutaneous leishmaniasis	4
African trypanosomiasis	3
Schistosomiasis	3
Cysticercosis	3
Cystic echinococcosis	3
Lymphatic filariasis	3
Onchocerciasis	3

Trachoma	3
Dengue	3
Yellow fever	3
Rabies	3
Intestinal nematode infections	3
Ascariasis	4
Trichuriasis	4
Hookworm disease	4
Food-borne trematodiases	3
Leprosy	3
Ebola virus disease	3
Zika virus disease	3
Guinea worm disease	3
Other neglected tropical diseases	3
Other infectious diseases	2
Meningitis	3
Encephalitis	3
Diphtheria	3
Whooping cough	3
Tetanus	3
Measles	3
Varicella and herpes zoster	3
Acute hepatitis	3
Acute hepatitis A	4
Acute hepatitis B	4
Acute hepatitis C	4
Acute hepatitis E	4
Other unspecified infectious diseases	3
Maternal and neonatal disorders	2
Maternal disorders	3
Maternal haemorrhage	4
Maternal sepsis and other maternal infections	4
Maternal hypertensive disorders	4
Maternal obstructed labor and uterine rupture	4
Maternal abortion and miscarriage	4
Ectopic pregnancy	4
Indirect maternal deaths	4
Late maternal deaths	4
Maternal deaths aggravated by HIV/AIDS	4
Other maternal disorders	4
Neonatal disorders	3
Neonatal preterm birth	4
•	4
Neonatal encephalopathy due to birth asphyxia and trauma	
Neonatal encephalopathy due to birth asphyxia and trauma Neonatal sepsis and other neonatal infections	4

Other neonatal disorders	4
Nutritional deficiencies	2
Protein-energy malnutrition	3
Iodine deficiency	3
Vitamin A deficiency	3
Dietary iron deficiency	3
Other nutritional deficiencies	3
Non-communicable diseases	1
Neoplasms	2
Lip and oral cavity cancer	3
Nasopharynx cancer	3
Other pharynx cancer	3
Oesophageal cancer	3
Stomach cancer	3
Colon and rectum cancer	3
Liver cancer	3
Liver cancer due to hepatitis B	4
Liver cancer due to hepatitis C	4
Liver cancer due to alcohol use	4
Liver cancer due to NASH	4
Liver cancer due to other causes	4
Gallbladder and biliary tract cancer	3
Pancreatic cancer	3
Larynx cancer	3
Tracheal, bronchus, and lung cancer	3
Malignant skin melanoma	3
Non-melanoma skin cancer	3
Non-melanoma skin cancer (squamous-cell carcinoma)	4
Non-melanoma skin cancer (basal-cell carcinoma)	4
Breast cancer	3
Cervical cancer	3
Uterine cancer	3
Ovarian cancer	3
Prostate cancer	3
Testicular cancer	3
Kidney cancer	3
Bladder cancer	3
Brain and central nervous system cancer	3
Thyroid cancer	3
Mesothelioma	3
Hodgkin lymphoma	3
Non-Hodgkin lymphoma	3
Multiple myeloma	3
Leukaemia	3
Acute lymphoid leukaemia	4
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Chronic lymphoid leukaemia	4
Acute myeloid leukaemia	4
Chronic myeloid leukaemia	4
Other leukaemia	4
Other malignant neoplasms	3
Other neoplasms	3
Myelodyspastic, myeloproliferative, and other haematopoietic	4
neoplasms	
Benign and in situ intestinal neoplasms	4
Benign and in situ cervical and uterine neoplasms	4
Other benign and in situ neoplasms	4
Cardiovascular diseases	2
Rheumatic heart disease	3
Ischaemic heart disease	3
Stroke	3
Ischaemic stroke	4
Intracerebral haemorrhage	4
Subarachnoid haemorrhage	4
Hypertensive heart disease	3
Non-rheumatic valvular heart disease	3
Non-rheumatic calcific aortic valve disease	4
Non-rheumatic degenerative mitral valve disease	4
Other non-rheumatic valve diseases	4
Cardiomyopathy and myocarditis	3
Myocarditis	4
Alcoholic cardiomyopathy	4
Other cardiomyopathy	4
Atrial fibrillation and flutter	3
Aortic aneurysm	3
Peripheral artery disease	3
Endocarditis	3
Other cardiovascular and circulatory diseases	3
Chronic respiratory diseases	2
Chronic obstructive pulmonary disease	3
Pneumoconiosis	3
Silicosis	4
Asbestosis	4
Coal workers pneumoconiosis	4
Other pneumoconiosis	4
Asthma	3
Interstitial lung disease and pulmonary sarcoidosis	3
Other chronic respiratory diseases	3
Digestive diseases	2
Cirrhosis and other chronic liver diseases	3
Cirrhosis and other chronic liver diseases due to hepatitis B	4
Cirrhosis and other chronic liver diseases due to hepatitis C	4

Cirrhosis and other chronic liver diseases due to alcohol use	4
Cirrhosis and other chronic liver diseases due to NAFLD	4
Cirrhosis and other chronic liver diseases due to other causes	4
Upper digestive system diseases	3
Peptic ulcer disease	4
Gastritis and duodenitis	4
Gastro-oesophageal reflux disease	4
Appendicitis	3
Paralytic ileus and intestinal obstruction	3
Inguinal, femoral, and abdominal hernia	3
Inflammatory bowel disease	3
Vascular intestinal disorders	3
Gallbladder and biliary diseases	3
Pancreatitis	3
Other digestive diseases	3
Neurological disorders	2
Alzheimer's disease and other dementias	3
Parkinson's disease	3
Idiopathic epilepsy	3
Multiple sclerosis	3
Motor neuron disease	3
Headache disorders	3
Migraine	4
Tension-type headache	4
Other neurological disorders	3
Mental disorders	2
Schizophrenia	3
Depressive disorders	3
Major depressive disorder	4
Dysthymia	4
Bipolar disorder	3
Anxiety disorders	3
Eating disorders	3
Anorexia nervosa	4
Bulimia nervosa	4
Autism spectrum disorders	3
Attention-deficit/hyperactivity disorder	3
Conduct disorder	3
Idiopathic developmental intellectual disability	3
Other mental disorders	3
Substance use disorders	2
Alcohol use disorders	3
Drug use disorders	3
Opioid use disorders	4
Cocaine use disorders	4

Amphetamine use disorders	4
Cannabis use disorders	4
Other drug use disorders	4
Diabetes and kidney diseases	2
Diabetes mellitus	3
Diabetes mellitus type 1	4
Diabetes mellitus type 2	4
Chronic kidney disease	3
Chronic kidney disease due to diabetes mellitus type 1	4
Chronic kidney disease due to diabetes mellitus type 2	4
Chronic kidney disease due to hypertension	4
Chronic kidney disease due to glomerulonephritis	4
Chronic kidney disease due to other and unspecified causes	4
Acute glomerulonephritis	3
Skin and subcutaneous diseases	2
Dermatitis	3
Atopic dermatitis	4
Contact dermatitis	4
Seborrhoeic dermatitis	4
Psoriasis	3
Bacterial skin diseases	3
Cellulitis	4
Pyoderma	4
Scabies	3
Fungal skin diseases	3
Viral skin diseases	3
Acne vulgaris	3
Alopecia areata	3
Pruritus	3
Urticaria	3
Decubitus ulcer	3
Other skin and subcutaneous diseases	3
Sense organ diseases	2
Blindness and vision loss	3
Glaucoma	4
Cataract	4
Age-related macular degeneration	4
Refraction disorders	4
Near vision loss	4
Other vision loss	4
Age-related and other hearing loss	3
Other sense organ diseases	3
Musculoskeletal disorders	2
Rheumatoid arthritis	3
	3

Osteoarthritis hip	4
Osteoarthritis knee	4
Osteoarthritis hand	4
Osteoarthritis other	4
Low back pain	3
Neck pain	3
Gout	3
Other musculoskeletal disorders	3
Other non-communicable diseases	2
Congenital birth defects	3
Neural tube defects	4
Congenital heart anomalies	4
Orofacial clefts	4
Down syndrome	4
Turner syndrome	4
Klinefelter syndrome	4
Other chromosomal abnormalities	4
Congenital musculoskeletal and limb anomalies	4
Urogenital congenital anomalies	4
Digestive congenital anomalies	4
Other congenital birth defects	4
Urinary diseases and male infertility	3
Urinary tract infections	4
Urolithiasis	4
Benign prostatic hyperplasia	4
Male infertility	4
Other urinary diseases	4
Gynaecological diseases	3
Uterine fibroids	4
Polycystic ovarian syndrome	4
Female infertility	4
Endometriosis	4
Genital prolapse	4
Premenstrual syndrome	4
Other gynaecological diseases	4
Haemoglobinopathies and haemolytic anemias	3
Thalassaemias	4
Thalassaemias trait	4
Sickle cell disorders	4
Sickle cell trait	4
G6PD deficiency	4
G6PD trait	4
Other haemoglobinopathies and haemolytic anaemias	4
Endocrine, metabolic, blood, and immune disorders	3
Oral disorders	3

Caries of deciduous teeth	4
Caries of permanent teeth	4
Periodontal diseases	4
Edentulism and severe tooth loss	4
Other oral disorders	4
Sudden infant death syndrome	3
Injuries	1
Transport injuries	2
Road injuries	3
Pedestrian road injuries	4
Cyclist road injuries	4
Motorcyclist road injuries	4
Motor vehicle road injuries	4
Other road injuries	4
Other transport injuries	3
Unintentional injuries	2
Falls	3
Drowning	3
Fire, heat, and hot substances	3
Poisonings	3
Poisoning by carbon monoxide	4
Poisoning by other means	4
Exposure to mechanical forces	3
Unintentional firearm injuries	4
Other exposure to mechanical forces	4
Adverse effects of medical treatment	3
Animal contact	3
Venomous animal contact	4
Non-venomous animal contact	4
Foreign body	3
Pulmonary aspiration and foreign body in airway	4
Foreign body in eyes	4
Foreign body in other body part	4
Environmental heat and cold exposure	3
Exposure to forces of nature	3
Other unintentional injuries	3
Self-harm and interpersonal violence	2
Self-harm	3
Self-harm by firearm	4
Self-harm by other specified means	4
Interpersonal violence	3
Physical violence by firearm	4
Physical violence by sharp object	4
Sexual violence	4
Physical violence by other means	4

Conflict and terrorism	3
Executions and police conflict	3

Table S2: List of International Classification of D	biseases (ICD) codes mapped to the Global Burden of Disease cause	list for causes of death
Cause	ICD10	ICD9
Communicable, maternal, neonatal, and nutritional diseases	A00-A00.9, A01.0-A14, A15-A28.9, A32-A39.9, A48.1-A48.2, A48.4-A48.5, A50-A58, A60-A60.9, A63-A63.8, A65-A65.0, A68-A70, A74, A74.8-A75.9, A77-A96.9, A98-A98.8, B00-B06.9, B10-B10.8, B15-B16.2, B17.0, B17.2, B19.1, B20-B27.9, B29.4, B33-B33.1, B33.3-B33.8, B47-B48.8, B50-B54.0, B55.0, B56-B57.5, B60-B60.8, B63, B65-B67.9, B69-B72.0, B74.3-B75, B77-B77.9, B83-B83.8, B90-B91, B94.1, B95-B95.5, B97.4-B97.6, C58-C58.0, D50.1-D50.8, D51-D52.0, D52.8-D53.9, D70.3, D89.3, E00-E02, E40-E46.9, E51-E61.9, E63-E64.0, E64.2-E64.9, F02.1, F02.4, F07.1, G00.0-G00.8, G03-G03.8, G04-G05.8, G14-G14.6, G21.3, H70-H70.9, 100, 102, 102.9, 198.0-198.1, J00-J02.8, J03-J03.8, J04-J04.2, J05-J05.1, J06.0-J06.8, J09-J15.8, J16-J16.9, J20-J21.9, J36-J36.0, J91.0, K52.1, K67.0-K67.8, K75.3, K76.3, K77.0, K93.0-K93.1, M03.1, M12.1, M49.0-M49.1, M73.0-M73.1, M89.6, N74.1, N96, N98-N98.9, O00-O07.9, O09-O16.9, O20-O26.9, O28-O36.9, O40-O48.1, O60-O77.9, O80-O92.7, O96-O98.6, O98.8-P04.2, P04.5-P05.9, P07-P15.9, P19-P22.9, P23.0-P23.4, P24-P29.9, P35-P37.2, P37.5-P39.9, P50-P61.9, P70-P70.1, P70.3-P72.9, P74-P78.9, P80-P81.9, P83-P84, P90-P94.9, P96, P96.3-P96.4, P96.8, R19.7, U04-U04.9, U06-U06.9, U82-U89, Z16-Z16.3	001-001.9, 002.0-029, 032-034.9, 036-036.3, 036.5-037.9, 040, 040.1-041.0, 042-066.9, 070.0-070.2, 071-075.9, 078.3-078.7, 079-079.7, 080-083.9, 084.0-084.5, 084.7-084.9, 085.0, 086-088, 088.8-088.9, 090-101.6, 104-104.9, 120-124.9, 125.4-125.9, 127-127.1, 128-129.0, 136-136.2, 137-139.0, 181-181.9, 244.2, 260-263.9, 265-269.9, 281.0-281.9, 320.0-320.8, 321-323.9, 381-383.9, 390-390.9, 392, 392.9, 425.6, 460-464.4, 464.8-464.9, 465.0-465.8, 466-469, 470.0, 475-475.9, 476.9, 480-482.8, 483.0-483.9, 484.0-484.7, 487-489, 630-636.9, 638-638.9, 640-679.1, 716.0, 730.4-730.6, 760-760.6, 760.8-768, 768.2-770, 770.1-775.0, 775.4-779.3, 779.6-779.8, V09-V09.9
HIV/AIDS and sexually transmitted infections	A50-A58, A60-A60.9, A63-A63.8, B20-B24.9, B63, F02.4, I98.0, K67.0-K67.2, M03.1, M73.0-M73.1	042-044.9, 054.1, 090-099.9
HIV/AIDS	B20-B24.9, F02.4	042-044.9
HIV/AIDS-drug-susceptible tuberculosis	B20.0	
HIV/AIDS-multidrug-resistant tuberculosis without extensive drug resistance		
HIV/AIDS–extensively drug-resistant tuberculosis		
HIV/AIDS resulting in other diseases	B20, B20.1-B24.9, F02.4	042-044.9
Sexually transmitted infections excluding HIV	A50-A58, A60-A60.9, A63-A63.8, B63, I98.0, K67.0-K67.2, M03.1, M73.0-M73.1	054.1, 090-099.9
Syphilis	A50-A53.9, I98.0, K67.2, M03.1, M73.1	090-097.9
Chlamydial infection	A55-A56.8, K67.0	
Gonococcal infection	A54-A54.9, K67.1, M73.0	098-098.9
Other sexually transmitted infections	A57-A58, A63-A63.8, B63	099-099.9
Respiratory infections and tuberculosis	A10-A14, A15-A19.9, A48.1, A70, B90-B90.9, B97.4-B97.6, H70-H70.9, J00-J02.8, J03-J03.8, J04-J04.2, J05-J05.1, J06.0-J06.8, J09-J15.8, J16-J16.9, J20-J21.9, J36-J36.0, J91.0, K67.3, K93.0, M49.0, N74.1, P23.0-P23.4, P37.0, U04-U04.9, U84.3	010-019.9, 034.0, 079.6, 137-137.9, 138.0-138.9, 381-383.9, 460-464.4, 464.8-464.9, 465.0-465.8, 466-469, 470.0, 475-475.9, 476.9, 480-482.8, 483.0-483.9, 484.1-484.2, 484.6-484.7, 487-489, 730.4-730.6
Tuberculosis	A10-A14, A15-A19.9, B90-B90.9, K67.3, K93.0, M49.0, N74.1, P37.0, U84.3	010-019.9, 137-137.9, 138.0-138.9, 730.4-730.6
Drug-susceptible tuberculosis	A10-A14, A15-A19.9, B90-B90.9, K67.3, K93.0, M49.0, N74.1, P37.0	010-019.9, 137-137.9, 138.0-138.9, 730.4-730.6
Multidrug-resistant tuberculosis without extensive drug resistance	U84.3	
Extensively drug-resistant tuberculosis		
Lower respiratory infections	A48.1, A70, B97.4-B97.6, J09-J15.8, J16-J16.9, J20-J21.9, J91.0, P23.0-P23.4, U04- U04.9	079.6, 466-469, 470.0, 480-482.8, 483.0-483.9, 484.1-484.2, 484.6-484.7, 487-489
Upper respiratory infections	J00-J02.8, J03-J03.8, J04-J04.2, J05-J05.1, J06.0-J06.8, J36-J36.0	034.0, 460-464.4, 464.8-464.9, 465.0-465.8, 475-475.9, 476.9
Otitis media	H70-H70.9	381-383.9
Enteric infections	A00-A00.9, A01.0-A09.9, A80-A80.9, K52.1, R19.7	001-001.9, 002.0-009.9, 045-045.9, 138
Diarrheal diseases	A00-A00.9, A02-A02.0, A02.8-A07, A07.2-A07.4, A08-A09.9, K52.1, R19.7	001-001.9, 003.8-006.9, 007.4-007.8, 008.2-009.9
Typhoid and paratyphoid	A01.0-A01.4	002.0-002.9
Typhoid fever	A01.0	002.0
Paratyphoid fever	A01.1-A01.4	002.1-002.9
Invasive non-typhoidal Salmonella (iNTS)	A02.1-A02.2	003-003.7
Other intestinal infectious diseases	A07.0-A07.1, A07.8-A07.9, A80-A80.9	007-007.3, 007.9-008.1, 045-045.9, 138
Neglected tropical diseases and malaria	A68-A68.9, A69.2-A69.9, A75-A75.9, A77-A79.9, A82-A82.9, A90-A96.9, A98-A98.8, B33.0-B33.1, B50-B54.0, B55.0, B56-B57.5, B60-B60.8, B65-B67.9, B69-B72.0, B74.3-B75, B77-B77.9, B83-B83.8, K93.1, P37.1, U06-U06.9	060-061.8, 065-066.9, 071-071.9, 080-083.9, 084.0-084.5, 084.7-084.9, 085.0, 086-088, 088.8-088.9, 120-124.9, 125.4-125.9, 127-127.1, 128-129.0, 425.6
Malaria	B50-B54.0	084.0-084.5, 084.7-084.9
Leprosy	A30-A30.9	030-030.9
Chagas disease	B57-B57.5, K93.1	086-086.2, 086.9, 425.6
Leishmaniasis	B55.0	085.0
Visceral leishmaniasis African trypanosomiasis	B55.0 B56-B56.9	085.0 086.3-086.5
Schistosomiasis	B65-B65.9	120-120.9
Cysticercosis	B69-B69.9	123.1
Cystic echinococcosis	B67-B67.4, B67.8-B67.9	122-122.4, 122.8-122.9
Dengue	A90-A91.9	061-061.8
Yellow fever	A95-A95.9	060-060.9
Rabies	A82-A82.9	071-071.9
Intestinal nematode infections	B77-B77.9	127.0
Ascariasis	B77-B77.9	127.0
Ebola virus disease	A98.4	
Zika virus disease	U06-U06.9	
Other neglected tropical diseases	A68-A68.9, A69.2-A69.9, A75-A75.9, A77-A79.9, A92-A94.0, A96-A96.9, A98-A98.3, A98.5-A98.8, B33.0-B33.1, B60-B60.8, B67.5-B67.7, B70-B71.9, B74.3-B75, B83-B83.8, P37.1	065-066.9, 080-083.9, 087-088, 088.8-088.9, 122.5-122.7, 123-123.0, 123.2-124.9, 125.4-125.6, 125.9, 127, 127.1, 128-129.0

Table S2: List of International Classification of D	viseases (ICD) codes mapped to the Global Burden of Disease cause	list for causes of death
Cause	ICD10	ICD9
Other infectious diseases	A20-A28.9, A32-A39.9, A48.2, A48.4-A48.5, A65-A65.0, A69-A69.1, A74, A74.8-A74.9, A81-A81.9, A83-A89.9, B00-B06.9, B10-B10.8, B15-B16.2, B17.0, B17.2, B19.1, B25-B27.9, B29.4, B33, B33.3-B33.8, B47-B48.8, B91, B94.1, B95-B95.5, D70.3, D89.3, F02.1, F07.1, G00.0-G00.8, G03-G03.8, G04-G05.8, G14-G14.6, G21.3, I00, I02, I02.9, I98.1, K67.8, K75.3, K76.3, K77.0, M49.1, M89.6, P35-P35.9, P37, P37.2, P37.5-P37.9, U82-U84, U85-U89, Z16-Z16.3	020-029, 032-034, 034.1-034.9, 036-036.3, 036.5-037.9, 040, 040.1-041.0, 046-054.0, 054.2-059.9, 062-064.9, 070.0-070.2, 072-075.9, 078.3-078.7, 079-079.5, 079.7, 100-101.6, 104-104.9, 136-136.2, 139-139.0, 320.0-320.8, 321-323.9, 390-390.9, 392, 392.9, 484.0, 484.3-484.5, 771.0-771.3, V09-V09.9
Meningitis	A39-A39.9, A87-A87.9, G00.0-G00.8, G03-G03.8	036-036.3, 036.5-036.9, 047-049.9, 320.0-320.8, 321-322.9
Encephalitis	A83-A86.4, B94.1, F07.1, G04-G05.8, G21.3	062-064.9, 139.0, 323, 323.4-323.9
Diphtheria	A36-A36.9	032-032.9
Whooping cough	A37-A37.9	033-033.9, 484.3
Tetanus	A33-A35.0	037-037.9, 771.3
Measles	B05-B05.9	055-055.9, 484.0
Varicella and herpes zoster	B01-B02.9, P35.8	052-053.9
Acute hepatitis	B15-B16.2, B17.0, B17.2, B19.1, P35.3	070.0-070.2
Acute hepatitis A	B15-B15.9	070.0-070.1
Acute hepatitis B	B16-B16.2, B17.0, B19.1, P35.3	070.2
Acute hepatitis C		
Acute hepatitis E	B17.2	
Other unspecified infectious diseases	A20-A28.9, A32-A32.9, A38-A38.9, A48.2, A48.4-A48.5, A65-A65.0, A69-A69.1, A74, A74.8-A74.9, A81-A81.9, A88-A89.9, B00-B00.9, B03-B04, B06-B06.9, B10-B10.8, B25-B27.9, B29.4, B33, B33.3-B33.8, B47-B48.8, B91, B95-B95.5, D70.3, D89.3, F02.1, G14-G14.6, I00, I02, I02.9, I98.1, K67.8, K75.3, K76.3, K77.0, M49.1, M89.6, P35-P35.2, P35.9, P37, P37.2, P37.5-P37.9, U82-U84, U85-U89, Z16-Z16.3	020-029, 034, 034.1-034.9, 040, 040.1-041.0, 046-046.9, 050-051.9, 054-054.0, 054.2 054.9, 056-059.9, 072-075.9, 078.3-078.7, 079-079.5, 079.7, 100-101.6, 104-104.9, 136-136.2, 139, 323.0-323.3, 390-390.9, 392. 392.9, 484.4-484.5, 771.0-771.2, V09-V09.9
Maternal and neonatal disorders	C58-C58.0, N96, N98-N98.9, O00-O07.9, O09-O16.9, O20-O26.9, O28-O36.9, O40-O48.1, O60-O77.9, O80-O92.7, O96-O98.6, O98.8-P04.2, P04.5-P05.9, P07-P15.9, P19-P22.9, P24-P29.9, P36-P36.9, P38-P39.9, P50-P61.9, P70-P70.1, P70.3-P72.9, P74-P78.9, P80-P81.9, P83-P84, P90-P94.9, P96, P96.3-P96.4, P96.8	181-181.9, 630-636.9, 638-638.9, 640-679.1, 760-760.6, 760.8-768, 768.2-770, 770.1-771, 771.4-775.0, 775.4-779.3, 779.6-779.8
Maternal disorders	C58-C58.0, N96, N98-N98.9, O00-O07.9, O09-O16.9, O20-O26.9, O28-O36.9, O40-O48.1, O60-O77.9, O80-O92.7, O96-O98.6, O98.8-O99.9	181-181.9, 630-636.9, 638-638.9, 640-679.1
Maternal haemorrhage	020-020.9, 043.2, 044-046.9, 062-062.9, 067-067.9, 070, 072-072.3	640-641.9, 661-661.9, 665, 666-666.9
Maternal sepsis and other maternal infections	O23-O23.9, O85-O86.8, O91-O91.2	659.3, 670-670.9
Maternal hypertensive disorders	O10-O16.9	642-642.9
Maternal obstructed labor and uterine rupture	O32-O33.9, O64-O66.9, O71-O71.9	652-653.9, 660-660.9, 665.0-665.3
Maternal abortion and miscarriage	N96, O01-O07.9	630-632.9, 634-636.9, 638-638.9, 646.3
Ectopic pregnancy	O00-O00.9	633-633.9
Indirect maternal deaths	O24-O25.3, O98-O98.6, O98.8-O99.9	646-646.2, 646.4-649.9
Late maternal deaths	O96-O97.9	
Maternal deaths aggravated by HIV/AIDS		
Other maternal disorders	C58-C58.0, N98-N98.9, O09-O09.9, O21-O22.9, O26-O26.9, O28-O31.8, O34-O36.9, O40-O43.1, O43.8-O43.9, O47-O48.1, O60-O61.9, O63-O63.9, O68-O69.9, O70.0-O70.9, O73-O77.9, O80-O84.9, O87-O90.9, O92-O92.7	181-181.9, 643-645.2, 650-651.9, 654-659.2, 659.4-659.9, 662-664.9, 665.4-665.9, 667-669.9, 671-679.1
Neonatal disorders	P00-P04.2, P04.5-P05.9, P07-P15.9, P19-P22.9, P24-P29.9, P36-P36.9, P38-P39.9, P50-P61.9, P70-P70.1, P70.3-P72.9, P74-P78.9, P80-P81.9, P83-P84, P90-P94.9, P96, P96.3-P96.4, P96.8	760-760.6, 760.8-768, 768.2-770, 770.1-771, 771.4-775.0, 775.4-779.3, 779.6-779.8
Neonatal preterm birth	P01.0-P01.1, P07-P07.3, P22-P22.9, P25-P28.9, P61.2, P77-P77.9	761.0-761.1, 765-765.9, 769-769.9, 770.2-770.9, 776.6, 777.5-777.6
Neonatal encephalopathy due to birth asphyxia and trauma	P01.7, P02-P03.9, P10-P15.9, P20-P21.9, P24-P24.9, P90-P91.9	761.7-763.9, 767-768, 768.2-768.9, 770.1, 772.1-772.9, 779.0-779.2
Neonatal sepsis and other neonatal infections	P36-P36.9, P38-P39.9	771.4-771.9
Hemolytic disease and other neonatal jaundice	P55-P59.9	773-774.9
Other neonatal disorders	P00-P01, P01.2-P01.6, P01.8-P01.9, P04-P04.2, P04.5-P05.9, P08-P09, P19-P19.9, P29-P29.9, P50-P54.9, P60-P61.1, P61.3-P61.9, P70-P70.1, P70.3-P72.9, P74-P76.9, P78-P78.9, P80-P81.9, P83-P84, P92-P94.9, P96, P96.3-P96.4, P96.8	760-760.6, 760.8-761, 761.2-761.6, 764-764.9, 766-766.9, 770, 771, 772-772.0, 775-775.0, 775.4-776.5, 776.7-777.4, 777.7-779, 779.3, 779.6-779.8
Nutritional deficiencies	D50.1-D50.8, D51-D52.0, D52.8-D53.9, E00-E02, E40-E46.9, E51-E61.9, E63- E64.0, E64.2-E64.9, M12.1	244.2, 260-263.9, 265-269.9, 281.0-281.9, 716.0
Protein-energy malnutrition	E40-E46.9, E64.0	260-263.9
Other nutritional deficiencies	D51-D52.0, D52.8-D53.9, E00-E02, E51-E61.9, E63-E64, E64.2-E64.9, M12.1	244.2, 265-269.9, 281.0-281.9, 716.0

Table S2: List of International Classification of D	biseases (ICD) codes mapped to the Global Burden of Disease cause	list for causes of death
Cause	ICD10	ICD9
Non-communicable diseases	A46-A46.0, A66-A67.9, B18-B18.9, B33.2, B86, C00-C13.9, C15-C22.8, C23-C25.9, C30-C34.9, C37-C38.8, C40-C41.9, C43-C45.9, C47-C54.9, C56-C57.8, C60-C63.8, C64-C67.9, C68.0-C68.8, C69.0-C69.8, C70-C73.9, C75-C75.8, C81-C86.6, C88-C91.0, C91.2-C91.3, C91.6, C92-C92.6, C93-C93.1, C93.3, C93.8, C94-C96.9, D00.1 D00.2, D01.0-D01.3, D02.0-D02.3, D03-D06.9, D07.0-D07.2, D07.4-D07.5, D09.0, D09.2-D09.3, D09.8, D10.0-D10.7, D11-D12.9, D13.0-D13.7, D14.0-D14.3, D15-D16.9, D22-D27.9, D28.0-D28.7, D29.0-D29.8, D30.0-D30.8, D31-D36, D36.1-D36.7, D37.1-D37.5, D38.0-D38.5, D39.1-D39.2, D39.8, D40.0-D40.8, D41.0-D41.8, D42-D43.9, D44.0-D44.8, D45-D47.9, D48.0-D48.6, D49.2-D49.4, D49.6, D52.1, D55-D58.9, D59.0-D59.3, D59.5-D59.6, D60-D61.9, D63.1, D64.0, D66-D67, D68.0-D69.8, D70-D70.2, D70.4-D75.8, D76-D78.8, D86-D86.9, D89-D89.2, E03-E07.1, E09-E11.9, E15.0, E16.0-E16.9, E20-E34, E34.1-E34.8, E36-E36.8, E65-E68, E70-E85.2, E88-E89.9, F00-F02.0, F02.2-F02.3, F02.8-F03.9, F10-F16.9, F18-F18.9, F24, F50.0-F50.5, G10-G13.8, G20-G20.9, G21.0-G21.1, G23-G26.0, G30-G31.9, G35-G37.9, G40-G41.9, G45-G46.8, G47.3, G61-G61.9, G62.1, G70-G73.7, G90-G90.9, G93.7, G95-G95.9, G97-G97.9, H05.0-H05.1, 101-101.9, 102.0, 105-109.9, 111-113.9, 120-125.9, 127.0-127.2, 128-128.9, 130-131.1, 131.8-137.8, 138-141.9, 142.1-142.8, 143-143.9, 147-148.9, 151.0-151.4, 160-163.9, 165-166.9, 167.0-167.3, 167.5-167.7, 168.0-168.2, 169.0-169.3, 170.2-170.8, 171-173.9, 177-189.9, 195.2-195.3, 197-198, 198.2, 198.9, 130-135.9, 137-139.9, J41-J46.9, J60-J63.8, J65-J68.9, J70-J70.9, J82, J84-J84.9, J91, J91.8-J92.9, J95-J95.9, K20-K20.9, K22-K22.6, K22-8-K29.9, K31-K31.8, K35-K38.9, K40-K46.9, K50-K52.0, K52.2-K52.9, K55-K62.9, K63.5, K64-K64.9, K66.8, K67, K68, K70-K70.3, K71.7, K73-K75, K75.1-K75.2, K75.4-K76.2, K76.4-K77, K77.8, K80-K83.9, K85-K86.9, K90-K91.9, K92.8, K93.8-K95.8, L00-L05.9, L08-L08.9, L10-L14.0, L51-L51.9, L88-L89.9, L93-L93.2, L97-L98.4, M00-M03.0, M03.2-M03.6, M05-M09.8, M30-M36.8, M40-M43.1, M65-M65.0, M71.0-M71.1, M72.5-M72.6, M80-M82.8,	
Neoplasms	C00-C13.9, C15-C22.8, C23-C25.9, C30-C34.9, C37-C38.8, C40-C41.9, C43-C45.9, C47-C54.9, C56-C57.8, C60-C63.8, C64-C67.9, C68.0-C68.8, C69.0-C69.8, C70-C73.9, C75-C75.8, C81-C86.6, C88-C91.0, C91.2-C91.3, C91.6, C92-C92.6, C93-C93.1, C93.3, C93.8, C94-C96.9, D00.1-D00.2, D01.0-D01.3, D02.0-D02.3, D03-D06.9, D07.0-D07.2, D07.4-D07.5, D09.0, D09.2-D09.3, D09.8, D10.0-D10.7, D11-D12.9, D13.0-D13.7, D14.0-D14.3, D15-D16.9, D22-D24.9, D26.0-D27.9, D28.0-D28.1, D28.7, D29.0-D29.8, D30.0-D30.8, D31-D36, D36.1-D36.7, D37.1-D37.5, D38.0-D38.5, D39.1-D39.2, D39.8, D40.0-D40.8, D41.0-D41.8, D42-D43.9, D44.0-D44.8, D45-D47.9, D48.0-D48.6, D49.2-D49.4, D49.6, K62.0-K62.1, K63.5, N60-N60.9, N84.0-N84.1, N87-N87.9	140-148.9, 150-155.1, 155.3-158.9, 160-164.9, 170-175.9, 180-180.9, 182-183.8, 184.0-184.4, 184.8, 185-186.9, 187.1-187.8, 188-188.9, 189.0-189.8, 190-190.8, 191-193.9, 194.1-194.8, 200-204.0, 204.2, 205-205.3, 206-206.1, 207-208.9, 209.0-209.1, 209.4-209.5, 210.0-210.9, 211.0-211.8, 212.0-212.8, 213-213.9, 217-217.8, 219.0, 220-220.9, 221.0-221.8, 222.0-222.8, 223.0-223.8, 224-228.9, 229.0, 229.8, 230.1-230.8, 231.0-231.2, 232-232.9, 233.0-233.2, 233.4-233.5, 233.7, 234.0-234.8, 235.0, 235.4, 235.6-235.8, 236.1-236.2, 236.4-236.5, 236.7, 237-237.3, 237.5-237.9, 238.0-238.9, 239.2-239.4, 239.6, 569.0, 610-610.9, 622.1-622.2, 622.7
Lip and oral cavity cancer	C00-C08.9, D10.0-D10.5, D11-D11.9	140-145.9, 210.0-210.6, 235.0
Nasopharynx cancer	C11-C11.9, D10.6	147-147.9, 210.7-210.9
Other pharynx cancer	C09-C10.9, C12-C13.9, D10.7	146-146.9, 148-148.9
Oesophageal cancer	C15-C15.9, D00.1, D13.0	150-150.9, 211.0, 230.1
Stomach cancer	C16-C16.9, D00.2, D13.1, D37.1	151-151.9, 211.1, 230.2
Colon and rectum cancer	C18-C21.9, D01.0-D01.3, D12-D12.9, D37.3-D37.5	153-154.9, 209.1, 209.5, 211.3-211.4, 230.3-230.6, 569.0
Liver cancer	C22-C22.8, D13.4	155-155.1, 155.3-155.9, 211.5
Liver cancer due to hepatitis B		
Liver cancer due to hepatitis C		
Liver cancer due to alcohol use		
Liver cancer due to NASH	G22.2	
Hepatoblastoma Liver cancer due to other causes (internal)	C22.2	
Gallbladder and biliary tract cancer	C23-C24.9, D13.5	156-156.9
Pancreatic cancer	C25-C25.9, D13.6-D13.7	157-157.9, 211.6-211.7
Larynx cancer	C32-C32.9, D02.0, D14.1, D38.0	161-161.9, 212.1, 231.0, 235.6
Tracheal, bronchus, and lung cancer	C33-C34.9, D02.1-D02.3, D14.2-D14.3, D38.1	162-162.9, 212.2-212.3, 231.1-231.2, 235.7
Malignant skin melanoma	C43-C43.9, D03-D03.9, D22-D23.9, D48.5	172-172.9
Non-melanoma skin cancer	C44-C44.9, D04-D04.9, D49.2	173-173.9, 222.4, 232-232.9, 238.2
Non-melanoma skin cancer (squamous-cell carcinoma)	C44-C44.9, D04-D04.9, D49.2	173-173.9, 222.4, 232-232.9, 238.2
Soft tissue and other extraosseous sarcomas	C49-C49.9	171-171.9
Malignant neoplasm of bone and articular cartilage	C40-C41.9	170-170.9
Breast cancer	C50-C50.9, D05-D05.9, D24-D24.9, D48.6, D49.3	174-175.9, 217-217.8, 233.0, 238.3, 239.3, 610-610.9
Cervical cancer	C53-C53.9, D06-D06.9, D26.0	180-180.9, 219.0, 233.1, 622.1-622.2, 622.7
Uterine cancer	C54-C54.9, D07.0-D07.2, D26.1-D26.9	182-182.9, 233.2
Ovarian cancer	C56-C56.9, D27-D27.9, D39.1	183-183.0, 220-220.9, 236.2
Prostate cancer	C61-C61.9, D07.5, D29.1, D40.0	185-185.9, 222.2, 236.5
Testicular cancer	C62-C62.9, D29.2-D29.8, D40.1-D40.8	186-186.9, 222.0, 222.3, 236.4
Kidney cancer	C64-C65.9, D30.0-D30.1, D41.0-D41.1	189.0-189.1, 189.5-189.6, 223.0-223.1
Bladder cancer	C67-C67.9, D09.0, D30.3, D41.4-D41.8, D49.4	188-188.9, 223.3, 233.7, 236.7, 239.4
Brain and central nervous system cancer	C70-C72.9	191-192.9
Eye cancer Retinoblastoma	C69.0-C69.8 C69.2	190-190.8 190.5
Other eye cancers	C69.2 C69.0-C69.1, C69.3-C69.8	190.5 190-190.4, 190.6-190.8
Other eye cancers	Cu7.0-Cu7.1, Cu7.3-C07.8	170-170.4, 170.0-170.8

Table S2: List of International Classification of D	biseases (ICD) codes mapped to the Global Burden of Disease cause	list for causes of death
Cause	ICD10	ICD9
Neuroblastoma and other peripheral nervous cell tumors	C47-C47.9	
Thyroid cancer	C73-C73.9, D09.3, D09.8, D34-D34.9, D44.0	193-193.9, 226-226.9
Mesothelioma	C45-C45.9	
Hodgkin lymphoma	C81-C81.9	201-201.9
Non-Hodgkin lymphoma	C82-C86.6, C96-C96.9	200-200.9, 202-202.9
Burkitt lymphoma	C83.7-C83.8	200.2
Other non-Hodgkin lymphoma	C82-C83.6, C83.9-C86.6, C96-C96.9	200-200.1, 200.3-200.9, 202-202.9
Multiple myeloma	C88-C90.9	203-203.9
Leukaemia	C91-C91.0, C91.2-C91.3, C91.6, C92-C92.6, C93-C93.1, C93.3, C93.8, C94-C95.9	204-204.0, 204.2, 205-205.3, 206-206.1, 207-208.9
Acute lymphoid leukaemia	C91.0, C91.2-C91.3, C91.6	204.0, 204.2
Chronic lymphoid leukaemia		
Acute myeloid leukaemia	C92.0, C92.3-C92.6, C93.0, C94.0, C94.2, C94.4-C94.5	205.0, 205.2-205.3, 206.0, 207.0, 207.2-207.8 205.1
Chronic myeloid leukaemia Other leukaemia	C93.1, C93.3, C93.8, C94.1, C94.3, C94.6-C95.9	203.1
Other leukachila		
Other malignant neoplasms (internal)	C17-C17.9, C30-C31.9, C37-C38.8, C48-C48.9, C4A, C51-C52.9, C57-C57.8, C60-C60.9, C63-C63.8, C66-C66.9, C68.0-C68.8, C75-C75.8, D07.4, D09.2, D13.2-D13.3, D14.0, D15-D16.9, D28.0-D28.1, D28.7, D29.0, D30.2, D30.4-D30.8, D31-D31.9, D35-D35.2, D35.5-D36, D36.1-D36.7, D37.2, D38.2-D38.5, D39.2, D39.8, D41.2-D41.3, D44.1-D44.8, D48.0-D48.4	152-152.9, 158-158.9, 160-160.9, 163-164.9, 183.2-183.8, 184.0-184.4, 184.8, 187.1-187.8, 189.2-189.4, 189.8, 194.1-194.8, 209.0, 209.4, 211.2, 211.8, 212.0, 212.4-212.8, 213-213.9, 221.0-221.8, 222.1, 222.8, 223.2, 223.8, 224-224.9, 227-228.9, 229.0, 229.8, 230.7-230.8, 233.4-233.5, 234.0-234.8, 235.4, 235.8, 236.1, 238.0-238.1, 239.2
Other neoplasms	D32-D33.9, D35.3-D35.4, D42-D43.9, D45-D47.9, D49.6, K62.0-K62.1, K63.5, N60-N60.9, N84.0-N84.1, N87-N87.9	225-225.9, 237-237.3, 237.5-237.9, 238.4-238.9, 239.6
Myelodysplastic, myeloproliferative, and other haematopoietic neoplasms	D45-D47.9	238.4-238.9
Cardiovascular diseases	B33.2, G45-G46.8, I01-I01.9, I02.0, I05-I09.9, I11-I11.9, I20-I25.9, I27.0, I27.2, I28-I28.9, I30-I31.1, I31.8-I37.8, I38-I41.9, I42.1-I42.8, I43-I43.9, I47-I48.9, I51.0-I51.4, I60-I63.9, I65-I66.9, I67.0-I67.3, I67.5-I67.6, I68.0-I68.2, I69.0-I69.3, I70.2-I70.8, I71-I73.9, I77-I83.9, I86-I89.0, I89.9, I98, K75.1	036.4, 391-391.9, 392.0, 393-398.9, 402-402.9, 410-414.9, 416.0, 417-417.9, 420-423, 423.1-423.9, 424.0-424.3, 424.8, 425.0-425.3, 425.5, 425.7-425.8, 427.0-427.3, 427.6-427.8, 429.0, 430-435.9, 437.0-437.2, 437.5-437.8, 440.2, 440.4, 441-443.9, 447-454.9, 456, 456.3-457, 457.1, 457.8-457.9, 459, 459.1-459.3
Rheumatic heart disease	I01-I01.9, I02.0, I05-I09.9	391-391.9, 392.0, 393-398.9
Ischaemic heart disease	I20-I25.9	410-414.9
Stroke	G45-G46.8, I60-I63.9, I65-I66.9, I67.0-I67.3, I67.5-I67.6, I68.1-I68.2, I69.0-I69.3	430-435.9, 437.0-437.2, 437.5-437.8
Ischaemic stroke	G45-G46.8, 163-163.9, 165-166.9, 167.2-167.3, 167.5-167.6, 169.3	433-435.9, 437.0-437.1, 437.5-437.8
Intracerebral haemorrhage	I61-I62, I62.1-I62.9, I68.1-I68.2, I69.1-I69.2	431-432.9, 437.2
Subarachnoid hemorrhage	I60-I60.9, I62.0, I67.0-I67.1, I69.0	430-430.9
Hypertensive heart disease	II1-II1.9	402-402.9
Non-rheumatic valvular heart disease	134-137.8	424.0-424.3, 424.8
Non-rheumatic calcific aortic valvular heart disease	135-135.9	424.1
Non-rheumatic degenerative mitral valvular heart disease	I34-I34.9	424.0
Other non-rheumatic valvular heart diseases	I36-I37.8	424.2-424.3, 424.8
Cardiomyopathy and myocarditis	B33.2, I40-I41.9, I42.1-I42.8, I43-I43.9, I51.4	422-422.9, 425.0-425.3, 425.5, 425.7-425.8, 429.0
Myocarditis Alcoholic cardiomyopathy	B33.2, I40-I41.9, I51.4 I42.6	422-422.9 425.5
Other cardiomyopathy	142.1-142.5, 142.7-142.8, 143-143.9	425.0-425.3, 425.7-425.8, 429.0
Pulmonary arterial hypertension	127.0, 127.2	416.0
Atrial fibrillation and flutter	148-148.9	427.3
Aortic aneurysm	I71-I71.9	441-441.9
Peripheral artery disease	170.2-170.8, 173-173.9	440.2, 440.4, 443.0-443.9
Endocarditis	133-133.9, 138-139.9	421-421.9
Other cardiovascular and circulatory diseases (internal)	I28-I28.9, I30-I31.1, I31.8-I32.8, I47-I47.9, I51.0-I51.3, I68.0, I72-I72.9, I77-I83.9, I86-I89.0, I89.9, I98, K75.1	036.4, 417-417.9, 420-420.9, 423, 423.1-423.9, 427.0-427.2, 427.6-427.8, 442-443, 447-454.9, 456, 456.3-457, 457.1, 457.8-457.9, 459, 459.1-459.3
Chronic respiratory diseases	D86-D86.2, D86.9, G47.3, J30-J35.9, J37-J39.9, J41-J46.9, J60-J63.8, J65-J68.9, J70, J70.8-J70.9, J82, J84-J84.9, J91, J91.8-J92.9	135-135.9, 327.2-327.8, 470, 470.9-474.9, 476-476.1, 477-479, 491-493.9, 495- 504.9, 506-506.9, 508-509, 515, 516-517.8, 518.6, 518.9, 519.1-519.4
Chronic obstructive pulmonary disease	J41-J44.9	491-492.9, 496-499
Pneumoconiosis	J60-J63.8, J65-J65.0, J92.0	500-504.9
Silicosis	J62-J62.9	502-502.9, 503.0, 503.9
Asbestosis	J61-J61.0, J92.0	501
Coal workers pneumoconiosis	J60-J60.0	500-500.9, 501.0-501.9
Other pneumoconiosis	J63-J63.8, J65-J65.0	503, 503.1, 504-504.9
Asthma Interctitial lung disease and pulmonary sarcoidesis	J45-J46.9	493-493.9
Interstitial lung disease and pulmonary sarcoidosis	D86-D86.2, D86.9, J84-J84.9	135-135.9, 515, 516-516.9 327.2-327.8, 470, 470.9-474.9, 476-476.1, 477-479, 495-495.9, 506-506.9, 508-509,
Other chronic respiratory diseases Digestive diseases	G47.3, J30-J35.9, J37-J39.9, J66-J68.9, J70, J70.8-J70.9, J82, J91, J91.8-J92, J92.9 B18-B18.9, I84-I85.9, I98.2, K20-K20.9, K22-K22.6, K22.8-K29.9, K31-K31.8, K35-K38.9, K40-K42.9, K44-K46.9, K50-K52, K52.2-K52.9, K55-K62, K62.2-K62.6, K62.8-K62.9, K64-K64.9, K66.8, K67, K68, K70-K70.3, K71.7, K73-K75, K75.2, K75.4-K76.2, K76.4-K77, K77.8, K80-K83.9, K85-K86.9, K90-K90.9, K92.8, K93.8, M09.1	517-517.8, 518.6, 518.9, 519.1-519.4 455-455.9, 456.0-456.2, 530-530.0, 530.2-530.6, 531-536.1, 537-537.6, 537.8, 538, 540-543.9, 550-551.1, 551.3-552.1, 552.3-553.6, 555-558.9, 560-560.3, 560.8-560.9, 562-562.1, 564-564.1, 564.5-564.7, 565-566.9, 569.1-569.5, 569.7, 571-571.9, 572.2-573.0, 573.4-577.9, 579-579.2, 579.4-579.9
Cirrhosis and other chronic liver diseases	B18-B18.9, I85-I85.9, I98.2, K70-K70.3, K71.7, K73-K75, K75.2, K75.4-K76.2, K76.4-K76.9, K77.8	456.0-456.2, 571-571.9, 572.2-573.0, 573.4-573.9
Cirrhosis and other chronic liver diseases due to hepatitis B		
Cirrhosis and other chronic liver diseases due to hepatitis C		
Cirrhosis and other chronic liver diseases due to alcohol use		

Table S2: List of International Classification of D	iseases (ICD) codes mapped to the Global Burden of Disease cause	list for causes of death
Cause	ICD10	ICD9
Cirrhosis and other chronic liver diseases due to NAFLD		
Cirrhosis and other chronic liver diseases due to other causes		
Upper digestive system diseases	K25-K29.9	531-535.9
Peptic ulcer disease	K25-K28.9	531-534.9
Gastritis and duodenitis	K29-K29.9	535-535.9
Appendicitis	K35-K37.9, K38.3-K38.9	540-542.9
Paralytic ileus and intestinal obstruction	K56-K56.9	560-560.3, 560.8-560.9
Inguinal, femoral, and abdominal hernia	K40-K42.9, K44-K46.9	550-551.1, 551.3-552.1, 552.3-553.0, 553.6
Inflammatory bowel disease	K50-K52, K52.8-K52.9, M09.1	555-556.9, 558-558.9, 569.5
Vascular intestinal disorders	K55-K55.9	557-557.9
Gallbladder and biliary diseases	K80-K83.9	574-576.9
Pancreatitis	K85-K86.9	577-577.9, 579.4
Other digestive diseases	I84-I84.9, K20-K20.9, K22-K22.6, K22.8-K24, K31-K31.8, K38-K38.2, K52.2-K52.3, K57-K62, K62.2-K62.6, K62.8-K62.9, K64-K64.9, K66.8, K67, K68, K77, K90-K90.9, K92.8, K93.8 F00-F02.0, F02.2-F02.3, F02.8-F03.9, G10-G13.8, G20-G20.9, G23-G24, G24.1-	455-455.9, 530-530.0, 530.2-530.6, 536-536.1, 537-537.6, 537.8, 538, 543-543.9, 553.1-553.3, 562-562.1, 564-564.1, 564.5-564.7, 565-566.9, 569.1-569.4, 569.7, 579-579.2, 579.8-579.9
Neurological disorders	G25.0, G25.2-G25.3, G25.5, G25.8-G26.0, G30-G31.1, G31.8-G31.9, G35-G37.9, G40-G41.9, G61-G61.9, G70-G71.1, G71.3-G72, G72.2-G73.7, G90-G90.9, G95-G95.9, M33-M33.9	290-290.9, 294.1-294.9, 330-331.2, 331.5-332.0, 333-337.9, 340-341.9, 345-345.9, 349, 349.2-349.8, 353.8-353.9, 356-356.9, 357.0-357.1, 357.3-357.4, 357.7, 358-359.9, 775.2
Alzheimer's disease and other dementias	F00-F02.0, F02.8-F03.9, G30-G31.1, G31.8-G31.9	290-290.9, 294.1-294.9, 331-331.2
Parkinson's disease	F02.3, G20-G20.9	332-332.0
Idiopathic epilepsy	G40-G41.9	345-345.9
Multiple sclerosis	G35-G35.9	340-340.9
Motor neuron disease	G12.2-G12.9	335-335.2, 335.8-335.9
Other neurological disorders	F02.2, G10-G12.1, G13-G13.8, G23-G24, G24.1-G25.0, G25.2-G25.3, G25.5, G25.8-G26.0, G36-G37.9, G61-G61.9, G70-G71.1, G71.3-G72, G72.2-G73.7, G90-G90.9, G95-G95.9, M33-M33.9	330-330.9, 331.5-331.9, 333-334.9, 335.3, 336-337.9, 341-341.9, 349, 349.2-349.8, 353.8-353.9, 356-356.9, 357.0-357.1, 357.3-357.4, 357.7, 358-359.9, 775.2
Mental disorders	F24, F50.0-F50.5	307.1
Eating disorders	F50.0-F50.5	307.1
Anorexia nervosa	F50.0-F50.1	307.1
Bulimia nervosa	F50.2-F50.5	
Substance use disorders	E24.4, F10-F16.9, F18-F18.9, G31.2, G62.1, G72.1, P04.3-P04.4, P96.1, Q86.0, R78.0-R78.5, X45-X45.9, X65-X65.9, Y15-Y15.9 E24.4, F10-F10.9, G31.2, G62.1, G72.1, P04.3, Q86.0, R78.0, X45-X45.9, X65-	291-292.9, 303-303.9, 304.0-304.8, 305.0, 305.2-305.8, 357.5, 760.7, 790.3, E850, E860
Alcohol use disorders	X65.9, Y15-Y15.9	291-291.9, 303-303.9, 305.0, 357.5, 790.3, E860
Drug use disorders	F11-F16.9, F18-F18.9, P04.4, P96.1, R78.1-R78.5	292-292.9, 304.0-304.8, 305.2-305.8, 760.7, E850
Opioid use disorders	F11-F11.9, P96.1, R78.1	304.0, 305.5
Cocaine use disorders	F14-F14.9, R78.2	304.2, 305.6
Amphetamine use disorders	F15-F15.9	304.4, 305.7
Other drug use disorders	F13-F13.9, F16-F16.9, F18-F18.9, P04.4, R78.3-R78.5	292-292.9, 304.1, 304.5-304.8, 305.3-305.4, 305.8, 760.7
Diabetes and kidney diseases	D63.1, E10-E11.9, I12-I13.9, N00-N08.8, N15.0, N18-N18.9, P70.2, Q61-Q62.8	403-404.9, 580-583.9, 585-585.9, 589-589.9, 753-753.3, 775.1
Diabetes mellitus	E10-E10.1, E10.3-E11.1, E11.3-E11.9, P70.2	775.1
Diabetes mellitus type 1	E10-E10.1, E10.3-E10.9, P70.2	775.1
Diabetes mellitus type 2	E11-E11.1, E11.3-E11.9	7,01
***	,	402 404 0 501 502 0 505 505 0 500 500 0 752 752 2
Chronic kidney disease	D63.1, E10.2, E11.2, I12-I13.9, N02-N08.8, N15.0, N18-N18.9, Q61-Q62.8	403-404.9, 581-583.9, 585-585.9, 589-589.9, 753-753.3
Chronic kidney disease due to diabetes mellitus type 1	E10.2	
Chronic kidney disease due to diabetes mellitus type 2	E11.2	
Chronic kidney disease due to hypertension	I12-I13.9	403-404.9
Chronic kidney disease due to glomerulonephritis	N03-N06.9	581-583.9
Chronic kidney disease due to other and unspecified causes	N02-N02.9, N07-N08.8, N15.0, Q61-Q62.8	589-589.9, 753-753.3
Acute glomerulonephritis	N00-N01.9	580-580.9
Skin and subcutaneous diseases	A46-A46.0, A66-A67.9, B86, D86.3, I89.1-I89.8, L00-L05.9, L08-L08.9, L10-L14.0, L51-L51.9, L88-L89.9, L97-L98.4, M72.5-M72.6	035-035.9, 102-103.9, 133-133.6, 457.2-457.3, 680-689, 694-695.3, 707-707.9
Bacterial skin diseases	A46-A46.0, A66-A67.9, I89.1-I89.8, L00-L05.9, L08-L08.9, L88, L97-L98.4, M72.5-M72.6	035-035.9, 102-103.9, 457.2-457.3, 680-689
Cellulitis	L03-L03.9, M72.5-M72.6	681-682.9
Pyoderma	A46-A46.0, A66-A67.9, I89.1-I89.8, L00-L02.9, L04-L05.9, L08-L08.9, L88, L97- L98.4	035-035.9, 102-103.9, 457.2-457.3, 680-680.9, 683-689
Decubitus ulcer	L89-L89.9	707-707.9
Other skin and subcutaneous diseases	D86.3, L10-L14.0, L51-L51.9	694-695.3
Musculoskeletal disorders	I27.1, I67.7, L93-L93.2, M00-M03.0, M03.2-M03.6, M05-M09.0, M09.2-M09.8, M30-M32.9, M34-M36.8, M40-M43.1, M65-M65.0, M71.0-M71.1, M80-M82.8, M86.3-M86.4, M87-M87.0, M88-M89.0, M89.5, M89.7-M89.9	416.1, 437.4, 446-446.9, 695.4-695.5, 710-711.9, 714-714.3, 714.8-714.9, 730.1, 732 732.9, 733.0-733.1
Rheumatoid arthritis	M05-M06.9, M08.0-M08.8	714-714.3, 714.8-714.9
Other musculoskeletal disorders	I27.1, I67.7, L93-L93.2, M00-M03.0, M03.2-M03.6, M07-M08, M08.9-M09.0, M09.2-M09.8, M30-M32.9, M34-M36.8, M40-M43.1, M65-M65.0, M71.0-M71.1, M80-M82.8, M86.3-M86.4, M87-M87.0, M88-M89.0, M89.5, M89.7-M89.9	416.1, 437.4, 446-446.9, 695.4-695.5, 710-711.9, 730.1, 732-732.9, 733.0-733.1

Table S2: List of International Classification of D	iseases (ICD) codes mapped to the Global Burden of Disease cause	list for causes of death
Cause	ICD10	ICD9
Other non-communicable diseases	D25-D26, D28.2, D52.1, D55-D58.9, D59.0-D59.3, D59.5-D59.6, D60-D61.9, D64.0, D66-D67, D68.0-D69.8, D70-D70.2, D70.4-D75.8, D76-D78.8, D86.8, D89-D89.2, E03-E07.1, E09-E09.9, E15.0, E16.0-E16.9, E20-E24.3, E24.8-E34, E34.1-E34.8, E36-E36.8, E65-E68, E70-E85.2, E88-E89.9, G21.0-G21.1, G24.0, G25.1, G25.4, G25.6-G25.7, G71.2, G72.0, G93.7, G97-G97.9, 195.2-195.3, 197-197.9, 198.9, J70.0-J70.5, J95-J95.9, K43-K43.9, K52.0, K62.7, K91-K91.9, K94-K95.8, M87.1, N10-N12.9, N13.6, N14-N15, N15.1-N16.8, N20-N23.0, N25-N28.1, N29-N30.3, N30.8-N32.0, N32.3-N32.4, N34-N34.3, N36-N36.9, N39-N39.2, N41-N41.9, N44-N44.0, N45-N45.9, N49-N49.9, N65-N65.1, N72-N72.0, N75-N77.8, N80-N81.9, N83-N83.9, N99-N99.9, P96.0, P96.2, P96.5, Q00-Q07.9, Q10.4-Q18.9, Q20-Q28.9, Q30-Q36, Q37-Q45.9, Q50-Q60.6, Q63-Q86, Q86.1-Q87.8, Q89-Q89.8, Q90-Q93.9, Q95-Q99.8, R50.2, R95-R95.9	218-219, 219.1-219.9, 236.0, 240-243.9, 244.0-244.1, 244.3-244.8, 245-246.9, 251-259.1, 259.3-259.9, 270-273.9, 275-276, 277-277.2, 277.4-277.9, 278.0-278.8, 282-284.9, 286-286.5, 286.7-289.0, 289.4-289.7, 357.6, 518.7, 519.0, 536.4, 539-539.9, 551.2, 552.2, 564.2-564.4, 569.6, 579.3, 588-588.9, 590-590.9, 592-593.8, 594-599.6, 599.8, 601-602.9, 604-604.9, 608.2, 617-618.9, 620-620.9, 621.4-621.9, 622.3-622.6, 629-629.8, 740-749.0, 749.2-752.9, 753.4-758.9, 759.0-759.8, 775.3, 779.4-779.5, 788.0, 798-798.0
Congenital birth defects	G71.2, P96.0, Q00-Q07.9, Q10.4-Q18.9, Q20-Q28.9, Q30-Q36, Q37-Q45.9, Q50-Q60.6, Q63-Q86, Q86.1-Q87.8, Q89-Q89.8, Q90-Q93.9, Q95-Q99.8	740-749.0, 749.2-752.9, 753.4-758.9, 759.0-759.8
Neural tube defects	Q00-Q01.9, Q05-Q05.9	740-741.9, 742.0
Congenital heart anomalies	Q20-Q28.9	745-747.9
Orofacial clefts	Q35-Q36, Q37-Q37.9	749-749.0, 749.2-749.9
Down syndrome	Q90-Q90.9	758.0
Other chromosomal abnormalities	Q87-Q87.8, Q91-Q93.9, Q95-Q95.9, Q97-Q97.9, Q99-Q99.8	758, 758.1-758.6, 758.8-758.9
Congenital musculoskeletal and limb anomalies	Q65-Q79, Q79.6-Q79.9	742.5, 754-756.5, 756.8-756.9
Urogenital congenital anomalies	P96.0, Q50-Q60.6, Q63-Q64.9	752-752.9, 753.4-753.9
Digestive congenital anomalies	Q38-Q45.9, Q79.0-Q79.5	750-751.9, 756.6-756.7
Other congenital birth defects	G71.2, Q02-Q04.9, Q06-Q07.9, Q10.4-Q18.9, Q30-Q34.9, Q80-Q86, Q86.1-Q86.8, Q89-Q89.8	742, 742.1-742.4, 742.8-744.9, 748-748.9, 757-757.9, 759.0-759.8
Urinary diseases and male infertility	N10-N12.9, N13.6, N15, N15.1-N16.8, N20-N23.0, N25-N28.1, N29-N30.3, N30.8-N32.0, N32.3-N32.4, N34-N34.3, N36-N36.9, N39-N39.2, N41-N41.9, N44-N44.0, N45-N45.9, N49-N49.9	588-588.9, 590-590.9, 592-593.8, 594-598.1, 598.8-599.6, 599.8, 601-602.9, 604-604.9, 608.2, 788.0
Urinary tract infection and interstitial nephritis	N10-N12.9, N13.6, N15, N15.1-N16.8, N30-N30.3, N30.8-N30.9, N34-N34.3, N39.0-	590-590.9, 595-595.9, 597-597.9, 599.0
	N39.2	
Urolithiasis Other urinary diseases	N20-N23.0 N25-N28.1, N29-N29.8, N31-N32.0, N32.3-N32.4, N36-N36.9, N39, N41-N41.9, N44-N44.0, N45-N45.9, N49-N49.9	592-592.9, 594-594.9, 788.0 588-588.9, 593-593.8, 596-596.9, 598-598.1, 598.8-599, 599.1-599.6, 599.8, 601-602.9, 604-604.9, 608.2
Gynaecological diseases	D25-D26, D28.2, E28.2, N72-N72.0, N75-N77.8, N80-N81.9, N83-N83.9	218-219, 219.1-219.9, 236.0, 256.4, 617-618.9, 620-620.9, 621.4-621.9, 622.3-622.6, 629-629.8
Uterine fibroids	D25-D26, D28.2	218-219, 219.1-219.9, 236.0
Endometriosis	N80-N80.9	617-617.9
Genital prolapse	N81-N81.9	618-618.9
Other gynaecological diseases	N72-N72.0, N75-N77.8, N83-N83.9	620-620.9, 621.4-621.9, 622.3-622.6, 629-629.8
Haemoglobinopathies and haemolytic anaemias	D55-D58.9, D59.1, D59.3, D59.5, D60-D61.9, D64.0	282-284.9
Thalassaemias	D56-D56.9	282.4-282.5
Sickle cell disorders	D57-D57.8	282.6
G6PD deficiency	D55-D55.2	282.2-282.3
Other haemoglobinopathies and haemolytic anaemias	D55.3-D55.9, D58-D58.9, D59.1, D59.3, D59.5, D60-D61.9, D64.0	282-282.1, 282.7-284.9
Endocrine, metabolic, blood, and immune disorders	D52.1, D59.0, D59.2, D59.6, D66-D67, D68.0-D69.8, D70-D70.2, D70.4-D75.8, D76-D78.8, D86.8, D89-D89.2, E03-E07.1, E09-E09.9, E15.0, E16.0-E16.9, E20-E24.3, E24.8-E28.1, E28.3-E34, E34.1-E34.8, E36-E36.8, E65-E68, E70-E85.2, E88-E89.9, G21.0-G21.1, G24.0, G25.1, G25.4, G25.6-G25.7, G72.0, G93.7, G97-G97.9, I95.2-I95.3, I97-I97.9, I98.9, J70.0-J70.5, J95-J95.9, K43-K43.9, K52.0, K62.7, K91-K91.9, K94-K95.8, M87.1, N14-N14.4, N65-N65.1, N99-N99.9, P96.2, P96.5, R50.2	240-243.9, 244.0-244.1, 244.3-244.8, 245-246.9, 251-256.3, 256.8-259.1, 259.3-259.9, 270-273.9, 275-276, 277-277.2, 277.4-277.9, 278.0-278.8, 286-286.5, 286.7-289.0, 289.4-289.7, 357.6, 518.7, 519.0, 536.4, 539-539.9, 551.2, 552.2, 564.2-564.4, 569.6, 579.3, 598.2, 775.3, 779.4-779.5
Sudden infant death syndrome	R95-R95.9	798-798.0
Injuries	L55-L55.9, L56.3, L56.8-L56.9, L58-L58.9, N30.4, U00-U03, V00-V86.9, V87.2-V87.3, V88.2-V88.3, V90-V98.8, W00-W46.2, W49-W62.9, W64-W70.9, W73-W75.9, W77-W81.9, W83-W94.9, W97.9, W99-X06.9, X08-X39.9, X47-X48.9, X50-X54.9, X57-X58.9, X60-X64.9, X66-X83.9, X85-Y08.9, Y35-Y84.9, Y87.0-Y87.1, Y88-Y88.3, Y89.0-Y89.1	349.0-349.1, 457.0, E800-E807, E830-E838, E840-E849, E856-E857, E861-E865, E867-E869, E870-E876, E878-E879, E880-E886, E888-E928, E930-E979, E990-E999
Transport injuries	V00-V86.9, V87.2-V87.3, V88.2-V88.3, V90-V98.8	E800-E807, E830-E838, E840-E849
Road injuries	V01-V04.9, V06-V80.9, V82-V82.9, V87.2-V87.3	
Pedestrian road injuries	V01-V04.9, V06-V09.9	
Cyclist road injuries	V10-V19.9	
Motorcyclist road injuries	V20-V29.9	
Motor vehicle road injuries	V30-V79.9, V87.2-V87.3	
Other road injuries	V80-V80.9, V82-V82.9	
Other transport injuries	V00-V00.8, V05-V05.9, V81-V81.9, V83-V86.9, V88.2-V88.3, V90-V98.8	E800-E807, E830-E838, E840-E849
Unintentional injuries	L55-L55.9, L56.3, L56.8-L56.9, L58-L58.9, N30.4, W00-W46.2, W49-W62.9, W64-W70.9, W73-W75.9, W77-W81.9, W83-W94.9, W97.9, W99-X06.9, X08-X39.9, X47-X48.9, X50-X54.9, X57-X58.9, Y40-Y84.9, Y88-Y88.3	349.0-349.1, 457.0, E856-E857, E861-E865, E867-E869, E870-E876, E878-E879, E880-E886, E888-E928, E930-E949
Falls	W00-W19.9	E880-E886, E888
Drowning	W65-W70.9, W73-W74.9	E910
Fire, heat, and hot substances	X00-X06.9, X08-X19.9	E890-E899, E924
Poisonings	X47-X48.9	E856-E857, E861-E865, E867-E869
Poisoning by carbon monoxide	X47-X47.9	E862, E868-E869
Poisoning by other means	X48-X48.9	E856-E857, E861, E863-E865, E867
Exposure to mechanical forces	W20-W38.9, W40-W43.9, W45.0-W45.2, W46-W46.2, W49-W52	E916-E922
Unintentional firearm injuries	W32-W34.9	E922

Table S2: List of International Classification of I	Diseases (ICD) codes mapped to the Global Burden of Disease cause	list for causes of death
Cause	ICD10	ICD9
Other exposure to mechanical forces	W20-W31.9, W35-W38.9, W40-W43.9, W45.0-W45.2, W46-W46.2, W49-W52	E916-E921
Adverse effects of medical treatment	N30.4, Y40-Y84.9, Y88-Y88.3	349.0-349.1, 457.0, E870-E876, E878-E879, E930-E949
Animal contact	W52.0-W62.9, W64-W64.9, X20-X29.9	E905-E906
Venomous animal contact	X20-X29.9	E905
Non-venomous animal contact	W52.0-W62.9, W64-W64.9	E906
Foreign body	W44-W45, W45.3-W45.9, W75-W75.9, W78-W80.9, W83-W84.9	E911-E915
Pulmonary aspiration and foreign body in airway	W75-W75.9, W78-W80.9, W83-W84.9	E911-E913
Foreign body in other body part	W44-W45, W45.3-W45.9	E914-E915
Environmental heat and cold exposure	L55-L55.9, L56.3, L56.8-L56.9, L58-L58.9, W88-W94.9, W97.9, W99-W99.9, X30-X32.9, X39-X39.9	E900-E902, E926
Exposure to forces of nature	X33-X38.9	E907-E909
Still Born	P95-P95.9	768.0-768.1
Other unintentional injuries	W39-W39.9, W77-W77.9, W81-W81.9, W85-W87.9, X50-X54.9, X57-X58.9	E903-E904, E923, E925, E927-E928
Self-harm and interpersonal violence	U00-U03, X60-X64.9, X66-X83.9, X85-Y08.9, Y35-Y38.9, Y87.0-Y87.1, Y89.0-Y89.1	E950-E979, E990-E999
Self-harm	X60-X64.9, X66-X83.9, Y87.0	E950-E959
Self-harm by firearm	X72-X74.9	E955
Self-harm by other specified means	X60-X64.9, X66-X71.9, X75-X83.9, Y87.0	E950-E954, E956-E959
Interpersonal violence	X85-Y08.9, Y87.1	E960-E969
Physical violence by firearm	X93-X95.9	E965
Physical violence by sharp object	X99-X99.9	E966
Physical violence by other means Conflict and terrorism	X85-X92.9, X96-X98.9, Y00-Y04.9, Y06-Y08.9, Y87.1	E961-E964, E967-E969
Police conflict and executions	U00-U03, Y36-Y38.9, Y89.1 Y35-Y35.9, Y89.0	E979, E990-E999 E970-E978
Garbage Code (GBD Level 1)	A40-A41.9, A48.0, A48.3, A49.0-A49.1, A59-A59.9, A71-A71.9, A74.0, B07-B07.9, B30-B30.9, B35-B36.9, B85-B85.4, B87-B88.9, B94.0, D50-D50.0, D50.9, D62-D63.0, D63.8-D64, D64.1-D65.9, D68, D69.9, E15, E16, E50-E50.9, E64.1, E85.3-E87.6, E87.8-E87.9, F06.2-F06.4, F07.2, F09-F09.9, F19-F23.9, F25-F49, F51-F99.0, G06-G08.0, G32-G32.8, G43-G44.2, G44.4-G44.8, G47-G47.2, G47.4-G47.9, G50-G60.9, G62-G62.0, G62.2-G65.2, G80-G83.9, G89-G89.4, G91-G91.2, G91.4-G93, G93.1-G93.2, G93.4-G93.6, G94.0-G94.8, G99-H05, H05.2-H69.9, H71-H99, I26-I26.9, I31.2-I31.4, I46-I46.9, I50.0-I50.4, I76, I95-I95.1, I95.8-I95.9, J69-J69.9, J80-J80.9, J81.0, J85-J85.3, J86-J86.9, J93-J93.1, J93.8-J93.9, J94.2, J96-J96.9, J98.1-J98.3, K00-K19, K30, K65-K66.1, K66.9, K68.1-K68.9, K71-K71.6, K71.8-K72.9, K75.0, L20-L30.9, L40-L50.9, L52-L54.8, L56-L56.2, L56.4-L56.5, L57-L57.9, L59-L68.9, L70-L76.8, L80-L87.9, L90-L92.9, L94-L96, L98.5-L99.8, M04, M10-M12.0, M12.2-M29, M37-M39, M43.2-M49, M49.2-M64, M65.1-M71, M71.2-M72.4, M72.8, M73, M73.8-M79.9, M83-M86.2, M86.5-M86.9, M87.2-M87.9, M89.1-M89.4, M90-M99.9, N17-N17.9, N19-N19.9, N32.1-N32.2, N32.8-N33.8, N35-N35.9, N37-N37.8, N39.3-N39.8, N42-N43.4, N44.1-N44.8, N46-N48.9, N50-N53.9, N61-N64.9, N82-N82.9, N91-N91.5, N95, N95.1-N95.9, N97-N97.9, R02-R02.9, R03.1, R07.0, R08-R09, R09.3, R11-R12.0, R14-R19.6, R19.8-R23, R23.1-R30.9, R32-R50.1, R50.8-R57.9, R58.0-R72.9, R74-R78, R78.6-R94.8, R96-R99.9, U05, U07-U81, U89.9-U99, X40-X44.9, X46-X46.9, X49-X49.9, Y10-Y14.9, Y16-Y19.9, Z00-Z15.8, Z17-unsp.	038-038.9, 040.0, 041.1, 076-078.2, 110-111.9, 125-125.3, 126-126.9, 127.2-127.9, 131-132.9, 133.8-134.9, 136.6, 139.1, 139.9, 247-248, 264-264.9, 274-274.9, 276.0-276.5, 276.7-276.9, 277.3, 280-281, 285-285.9, 286.6, 289.1-289.3, 293, 294-294.0, 295-302.9, 305, 305.9-307.0, 307.2-307.4, 307.6-319.9, 324-327.1, 328-329, 338-339.1, 339.3-339.8, 342-344.9, 346-346.9, 350-353.6, 354-355.9, 360-362, 362.1-376, 376.2-380.9, 384-389.9, 415-415.9, 423.0, 424, 424.4-424.5, 424.9, 427.5, 427.9-428.9, 437.3, 458-458.9, 459.0, 507-507.9, 510-510.9, 512-513.9, 518.1-518.2, 520-529.9, 536.3, 536.8-536.9, 537.7, 537.9, 564.8-564.9, 567-568.9, 570-570.9, 572-572.1, 573.1-573.3, 584-584.9, 586-587.9, 603-603.9, 605-608.1, 608.3-609, 611-612.1, 615-616.9, 619-619.9, 621-621.3, 622-622.0, 622.8-623.6, 623.8-624.5, 624.8-628.9, 629.9, 690-693.9, 695.8-706.9, 708-709.9, 712-713.8, 715-716, 716.2-721.6, 721.8-730.0, 730.2-730.3, 730.7-731.9, 733, 733.2-734.2, 737-738, 738.2-739.9, 780-782.4, 782.6-784.6, 784.9, 785.4-786, 786.6, 786.8, 787, 787.3-788, 788.3-789, 789.1-789.2, 789.5, 790-790.1, 790.4-796.1, 796.3-797.9, 798.1-799, 799.2-799.9, 999.0-999.9, E851-E855, E858, E866, E980-E982, V01-V08, V10-uns
Garbage Code (GBD Level 2)	A14.9, A29-A30.9, A45-A45.9, A47-A48, A48.8-A49, A49.3-A49.9, A61-A62, A72-A73, A76, A97, B08-B09, B11-B14, B28-B29, B31-B32.4, B34-B34.9, B61-B62, B68-B68.9, B73-B74.2, B76-B76.9, B78-B81.8, B84, B92-B94, B94.8-B94.9, B95.6-B97.3, B97.7-B99.9, D59, D59.4, D59.8-D59.9, F17-F17.9, G44.3, G91.3, G93.0, G93.3, I10-I10.9, I15-I15.9, I27, I27.8-I27.9, I50, I50.8-I50.9, I67.4, I70-I70.1, I70.9, I74-I75.8, J81, J81.1, J90-J90.0, J94-J94.1, J94.8-J94.9, K92.0-K92.2, N70-N71.9, N73-N74.0, N74.2-N74.8, R03-R03.0, R04-R06.9, R09.0-R09.2, R09.8-R10.9, R13-R13.9, R23.0, R58, S00-T98.3, W47-W48, W63, W71-W72, W76-W76.9, W82, W95-W97, W98, X07, X55-X56, X59-X59.9, Y20-Y34.9, Y86-Y87, Y87.2, Y89, Y89.9-Y99.9	000-000.9, 030-030.9, 041.2-041.9, 067-069, 078.8-078.9, 079.8-079.9, 089-089.9, 105-109.9, 119, 136.8-136.9, 139.8, 304, 304.9, 305.1, 339.2, 401-401.9, 405-405.9, 416, 416.2-416.9, 440-440.1, 440.3, 440.8-440.9, 444-445.8, 490-490.9, 494-494.9, 511-511.9, 514-514.9, 515.0-515.9, 518-518.0, 518.3-518.5, 518.8, 536.2, 578-578.9, 599.7, 613-614.9, 714.4, 716.1, 721.7, 735-736.9, 738.0-738.1, 784.7-784.8, 786.3, 787.0-787.2, 789.0, 789.3-789.4, 789.6-789.9, 796.2, 799.0-799.1, 800-999, E000-E80, E83, E839, E85, E859, E87, E877, E88, E887, E929, E983-E985, E988-E989

	Table S2: List of International Classification of Diseases (ICD) codes mapped to the Global Burden of Disease cause list for causes of death	
Cause Garbage Code (GBD Level 3)		1CD9 002, 031-031.9, 039-039.9, 070, 070.4-070.9, 085, 085.1-085.9, 088.0-088.7, 112-118.9, 130-130.9, 136.3-136.5, 149-149.9, 155.2, 159-159.9, 165-169, 176-179.9, 183.9-184, 184.5, 184.9, 187, 187.9, 189, 189.9, 190.9, 195-199.9, 209, 209.2-209.3, 209.6-210, 211, 211.9-212, 212.9, 214-216.9, 221, 221.9-222, 222.9-223, 223., 223, 223.1, 229.9-230.0, 230.9-231, 231.8-231.9, 233, 233.3, 233.6, 233.9-234, 234.9-235, 235.1-235.3, 235.5, 235.9-236, 236.3, 236.6, 236.9, 237.4, 239-239.1, 239.5, 239.7-239.9, 249-249.9, 259.2, 276.6, 278, 279-279.9, 293.0-293.9, 331.3-331.4, 332.1-332.9, 347-348.9, 349.9, 357, 357.8-357.9, 399-400.0, 406-409.4, 418-419.9, 426-427, 427.4, 429, 429.2-429.9, 459.5-459.9, 464.5, 465, 465.9, 505-505.9, 519, 519.8-519.9, 530.1, 530.7-530.9, 544-549, 553.8-553.9, 559-559.0, 560.4-560.7, 561, 562.2-563, 569, 569.8-569.9, 591-591.9, 593.9, 599.9-600.9, 623.7, 624.6, 637-637.9, 639-639.9, 749.1, 759, 759.9, 779.9, 782.5, 785-785.3, 786.0-786.2, 786.4-786.5, 786.7, 786.9, 788.1-788.2, E986-E987
Garbage Code (GBD Level 4)	B16.9, B64, B82-B82.9, B83.9, C69, C69.9, C91.1, C91.4-C91.5, C91.7-C91.9, C92.7-C92.9, C93.2, C93.5-C93.7, C93.9, E12-E14.9, G00, G00.9-G02.8, G03.9, I37.9, I42-I42.0, I42.9, I51.5, I64-I64.9, I67, I67.8-I68, I68.8-I69, I69.4-I69.9, J07-J08, J15.9, J17-J19.6, J22-J29, J64-J64.9, P23, P23.5-P23.9, P37.3-P37.4, R73-R73.9, V87-V87.1, V87.4-V88.1, V88.4-V89.9, V99-V99.0, X84-X84.9, Y09-Y09.9, Y85-Y85.9	070.3, 084, 084.6, 194-194.0, 194.9, 204.1, 204.5-204.9, 205.8-205.9, 206.2-206.9, 238, 244, 244.9, 250-250.9, 289.8-289.9, 307.5, 320, 320.9, 357.2, 362.0, 425.4, 425.9, 429.1, 436-437, 437.9-439.6, 482.9-483, 484, 484.8-486.9, 770.0, 790.2, E808 E829

Infectious syndromes mapped to International Classification of Diseases (ICD) code Infectious syndrome name and level Level L0 L1 L2 L3	Infectious syndrome name and ICD code ICD Codes for all level L0	Infectious Syndrome to ICD C Infectious syndrome name and level L1 L2 L3	Infectious syndrome name and ICD code ICD Codes for all level
0 explicit sepsis	A02.1, A20.7, A21.7, A22.7, A26.7, A28.2, A32.7, A40-A41.9, A42.7, A48.8, A50-A50.0, B37.7, I76, O03.0, O03.5, O04.5, O08.0, O23-O23.9, O41.1, O75.3, O85-O86.8, O88.3, O91-O91.2, O98, P36-P37, R65.2	licit sepsis	038-038.9, 670-670.9, 771.4-771.9, 995.9
	A00-A02.0, A02.2-A20.3, A20.8-A21.3, A21.8-A22.2, A22.8-A26.0, A26.8-A28.1, A28.8-A32.1, A32.8-A39.9, A42-A42.2, A42.8-A48.5, A49-A49.9, A50.1-B37.6, B37.8-B99.9, D65-D65.9, D69.5, D70.3, D89.3, E87.2-E87.9, F02.1, F02.4, F07.1, G00-G08.0, G14-G14.6, G21.3, G93.4, H05.0-H05.1, H60.2, H62-H62.3, H65-H68.0, H70-H70.9, H73.0, H75-H75.0, I00, I01-I02.9, I30, I30.1, I33-I33.9, I38-I41.9, I46-I46.9, I80-I80.9, I87.0, I89.1, I00-I06.9, I00-I22.9, I31.132.9, I35-I37.1, I30.0-I39.1, I40.142.6, I80-I80.9, I85-I85.3		001-018.9, 020-037.9, 039-104.9, 110-139.9, 275.8-276.9, 286.6, 293-294, 320-326.9, 347-347.9, 376.0-376.1, 38
0 implicit sepsis	M46.2-M46.5, M49.0-M49.1, M65.0-M65.1, M71.0-M71.1, M72.5-M72.6, M73.0-M73.8, M86-M86.9, M89.6,	olicit sepsis	383.9, 390-392.9, 420-424.9, 425.6, 427.5, 451-453.9, 457-458.9, 460-469, 470.0, 472-476.9, 480-491.9, 510-511.9, 513-513.9, 519.1-519.9, 522-523.9, 540-542.9, 550-551.1, 551.3-552.1, 552.3-553.1, 553.3-558.0, 558.2-558.9, 560-560.3, 560.8-560.9, 562-562.1, 567-567.9, 569.5, 572.0-572.1, 574-576.9, 584-584.9, 590-590.9, 595-595.9, 597-597.9, 599.0, 601-601.9, 604-604.9, 614-616.9, 634.0, 635-635.0, 635.5, 636.0, 636.5, 637-637.0, 637.5, 638.0, 639.0, 647-647.9, 658.4, 659.3, 669.1, 671.2-671.5, 672-672.0, 675-675.9, 680-689, 707-707.9, 711-
	N00-N01.9, N10-N12.9, N13.6, N15, N15.1-N17.9, N30-N30.9, N34-N34.3, N39.0-N39.2, N41-N41.9, N45-N45.9, N49-N49.9, N70-N77.8, N98.0, O04.0, O05.0, O05.5, O06.0, O06.5, O07.0, O07.5, O98.0-O98.9, P00.2, P22-P23.9, P35-P35.9, P37.0-P39.9, R02-R02.9, R09.2, R19.7, R40.0-R40.4, R55-R55.0, R57-R57.9, R65.0, R83.5, R84.5, R85.5, R86.5, R87.5, T80.2, T81.4, T82.6-T82.7, T83.5-T83.6, T84.5-T84.7, T85.7, T87.4, T88.0, U04.9, U06-U07.2, U82-U89.9, Y62-Y62.9, Y95, Z03.0, Z11.1, Z16-Z16.3, Z21-Z22.9		637.5, 638.0, 639.0, 647-647.9, 638.4, 639.3, 669.1, 671.2-671.5, 672-672.0, 673-673.9, 680-689, 707-707.9, 711-711.9, 730-730.9, 768.9-769, 770.0, 771-771.3, 780-780.3, 785.4-785.5, 790.7, 798-799.2, 996.6
 Diarrhoea Diarrhoea due to specific bacteria 	A00-A00.9, A02-A02.0, A02.8-A09.9, K52.1-K52.3, R19.7 A00-A00.9, A02-A02.0, A02.8-A03.9, A04.0-A04.7	Diarrhoea Diarrhoea due to specific bacteria	001-001.9, 003.8-009.9, 558.2-558.9 001-001.9, 003.8-004.9, 007.4-007.7, 008.0-008.3
 Diarrhoea due to vibrio cholerae Diarrhoea due to salmonella enterica 	A00-A00.9 A02-A02.0, A02.8-A02.9	Diarrhoea due to vibrio cholerae Diarrhoea due to salmonella enterica	001-001.9 003.8-003.9
 Diarrhoea due to shigella spp Diarrhoea due to enteropathogenic escherichia coli 	A03-A03.9 A04.0	Diarrhoea due to shigella spp Diarrhoea due to enteropathogenic escherichia coli	004-004.9 008.0
 Diarrhoea due to Enterotoxigenic escherichia coli Diarrhoea due to campylobacter Diarrhoea due to yersinia enterocolitica 	A04.1-A04.4 A04.5 A04.6		
3 Diarrhoea due to clostridium difficile 3 3	A04.7	Diarrhoea due to proteus spp Diarrhoea due to paracolon bacilli	008.3 008.1
32 Diarrhoea due to unspecified bacteria	A04, A04.8-A05, A05.8-A05.9, K52.1-K52.3, R19.7	Diarrhoea due to aerobacter aerogenes	008.2
 Diarrhoea due to food borne pathogen or intoxication Diarrhoea due to food borne illness staphylococcus aureus Diarrhoea due to food borne illness clostridium botulinum 	A05.0-A05.5 A05.0 A05.1	Diarrhoea due to food borne pathogen or intoxication Diarrhoea due to food borne illness staphylococcus aureus Diarrhoea due to food borne illness clostridium botulinum	005.0-005.9 005.0, 005.8-005.9 005.1
 Diarrhoea due to food borne illness clostridium perfringens Diarrhoea due to food borne illness parahaemolyticus Diarrhoea due to food borne illness bacillus cereus 	A05.2 A05.3 A05.4	Diarrhoea due to food borne illness clostridium perfringens Diarrhoea due to food borne illness parahaemolyticus	005.2-005.3 005.4
 Diarrhoea due to food borne illness vibrio vulnificus Diarrhoea due to protozoal 	A05.5 A06-A07.9 A06-A06.9	Diarrhoea due to protozoal	006-006.9, 007.1 006-006.9
 Diarrhoea due to amebiasis Diarrhoea due to cryptosporidiosis 	A06-A06.9 A07.2	Diarrhoea due to amebiasis Diarrhoea due to giardiasis Diarrhoea due to cryptosporidiosis	006-006.9 007.1 007.4, 007.7
 Diarrhoea due to isosporiasis Diarrhoea due to cyclosporiasis Diarrhoea due to various 	A07.3 A07.4 A08-A08.9	Diarrhoea due to cyclosporiasis	007.5
Diarrhoea due to rotavirus Diarrhoea due to norovirus Diarrhoea due to adenovirus	A08.0 A08.1 A08.2		
 Diarrhoea due to viral other Diarrhoea to unspecified Pathogen 	A08.3-A08.9 A09-A09.9	Diarrhoea to unspecified Pathogen	005, 007-007.0, 007.2-007.3, 007.8-008, 008.4-009.9, 558.2-558.9
 Typhoid, paratyphoid and Invasive Non-typhoidal Salmonella (iNTS) Typhoid or paratyphoid unspecified Typhoid fever 	A01-A01.4, A02.2, A02.1 A01 A01.0	Typhoid, paratyphoid and Invasive Non-typhoidal Salmonella (iNTS) Typhoid or paratyphoid unspecified Typhoid fever	002-003.7 002, 002.9 002.0
 3 typhoid fever salmonella typhi 2 Paratyphoid fever 3 paratyphoid fever salmonella paratyphi 	A01.0 A01.1-A01.4 A01.1-A01.4	typhoid fever salmonella typhi Paratyphoid fever paratyphoid fever salmonella paratyphi	002.0 002.1-002.4 002.1-002.4
 Invasive Non-typhoidal Salmonella (iNTS) Invasive Non-typhoidal Salmonella (iNTS) 	A02.2, A02.1 A02.2, A02.1	Invasive Non-typhoidal Salmonella (iNTS) Invasive Non-typhoidal Salmonella (iNTS)	003-003.7 003.2-003.7
 Tuberculosis Respiratory tuberculosis Tuberculosis of nervous system 	A10-A19.9, K67.3, K93.0, M49.0, N74.1-N74.2, O98.0, P37.0, U84.3 A10-A16.9 A17-A17.9	Tuberculosis Respiratory tuberculosis Tuberculosis of nervous system	010-018.9, 320.4, 647.3, 730.4-730.6 010-013 013.0-013.9, 320.4
 Tuberculosis of intestines, peritoneum and mesenteric glands Tuberculosis of other organs 	K67.3, K93.0 A18-A18.9, M49.0, P37.0, U84.3	Tuberculosis of intestines, peritoneum and mesenteric glands Tuberculosis of other organs	014-014.9 015-015.9, 017-017.9, 647.3, 730.4-730.6
 Tuberculosis of genitourinary system Milliary Tuberculosis 	N74.1-N74.2, O98.0 A19-A19.9 A20-A20.3, A20.8-A21.3, A21.8-A22.2, A22.8-A26.0, A26.8-A28.1, A28.8-A28.9, A30-A32.0, A32.8-A35.0,	Tuberculosis of genitourinary system Milliary Tuberculosis	016-016.9 018-018.9
1 Bloodstream infections	A38-A38.9, A39.1-A39.9, A20.7, A21.7, A22.7, A26.7, A28.2, A32.7, A40-A41.9, A48.8, A50-A50.0, I76, O03.5, O04.5, O08.0, O23, O23.9, O85-O86.8, O88.3, O91-O91.2, P36-P36.9, R65.2, A44-A45.9, A47-A48, A48.3-A48.5, A49-A49.9, A50.1-A53.9, A65-A65.0, A68-A69.9, A72-A79.9, B20.1, B94.9-B96.8, B98-B99.9, I98.0-I98.1, K04-K05.5, M49.1, O04.0, O05.0, O05.5, O06.0, O06.5, O07.0, O07.5, O98.1, P37.2, P37.8-P39.9, T80.2, T83.5-T83.6, T85.7, T87.4, T88.0, U82-U84, U85-U89.9, Y62-Y62.9, Y95, Z03.0, Z11.1, Z16-Z16.3, Z22-Z22.4, Z22.8-Z22.9	Bloodstream infections	020-031.9, 034, 034.1-034.9, 038-038.9, 670-670.9, 771.4-771.9, 995.9, 036.2-037.9, 040-041.9, 076.0-076.9, 078.3, 080-083.9, 087-088.8, 090-097.9, 100-101.6, 634.0, 635-635.0, 636.0, 637-637.0, 638.0, 639.0, 647, 647.8-647.9, 658.4, 659.3, 671.2-671.5, 672-672.0, 675-675.9, 771-771.3, 790.7, 996.6, E872-E872.9
 Bloodstream infections due to specified bacteria Bloodstream infections due to specified bacteria 	A20.7, A21.7, A22.7, A26.7, A32.7, A40-A40.9, A41.0-A41.5, A50-A50.0 A20-A20.3, A20.8-A21.3, A21.8-A22.2, A22.8-A25, A26-A26.0, A26.8-A27.9, A30-A32.0, A32.8-A35.0, A38-A38.9, A39.1-A39.9, A44-A44.9, A48.5, A49.0-A49.3, A50.1-A53.9, A65-A65.0, A68-A69.9, A72-A79.9, B95.0-B95.8, B96.0-B96.7, 198.0, M49.1, O98.1	Bloodstream infections due to specified bacteria Bloodstream infections due to specified bacteria	038.0-038.4 020-031.9, 034, 034.1-034.9, 036.2-037.9, 041-041.2, 041.4-041.8, 076.0-076.9, 080-083.9, 087-088.8, 090-097.9 100-101.6
 Bloodstream infections due to bacillus-anthracis Bloodstream infections due to yersinia pestis Bloodstream infections due to francisella tularensis 	A22.7 A20-A20.3, A20.8-A20.9, A20.7 A21-A21.3, A21.8, A21.7	Bloodstream infections due to yersinia pestis Bloodstream infections due to francisella tularensis	020-020.8 020.9-022
 Bloodstream infections due to erysipelothrix rhusiopathiae Bloodstream infections due to anthracis 	A26.7 A21.9-A22.2, A22.8-A22.9	Bloodstream infections due to anthracis	022.0-022.6
Bloodstream infections due to brucella Bloodstream infections due to burkholderia pseudomallei Bloodstream infections due to erysipelothrix rhusiopathiae	A23-A23.9, M49.1 A24-A25 A26-A26.0, A26.8-A26.9	Bloodstream infections due to brucella Bloodstream infections due to burkholderia pseudomallei Bloodstream infections due to erysipelothrix rhusiopathiae	022.8-023.9 024-025.9 027.1
 Bloodstream infections due to listeria Bloodstream infections due to anaerobes Bloodstream infections due to non tuberculous mycobacteria 	A27-A27.9, A32-A32.0, A32.8-A32.9, A32.7 A41.4 A30-A31.9	Bloodstream infections due to listeria Bloodstream infections due to anaerobes Bloodstream infections due to non tuberculous mycobacteria	027.0 038.3 031.0-031.2
 Bloodstream infections due to clostridium tetani Bloodstream infections due to group a strep 	A33-A35.0 A38-A38.9, B95.0, A40-A40.0	Bloodstream infections due to clostridium tetani Bloodstream infections due to group a strep	037-037.9 034, 034.1-034.9
Bloodstream infections due to neisseria meningitidis Bloodstream infections due to bartonella Bloodstream infections due to clostridium botulinum	A39.1-A39.9 A44-A44.9 A48.5	Bloodstream infections due to neisseria meningitidis	036.2-036.9
 Bloodstream infections due to staphylococcus aureus Bloodstream infections due to group b strep Bloodstream infections due to haemophilus influenzae 	A49.0, B95.6-B95.8, A41.0-A41.2 A49.1, B95.1, A40.1-A40.3 A49.2, B96.3, A41.3	Bloodstream infections due to staphylococcus aureus Bloodstream infections due to haemophilus influenzae	041.1, 038.1 041.5
Bloodstream infections due to mycoplasma Bloodstream infections due to treponema pallidum	A49.3, B96.0-B96.1 A50.1-A53.9, A65-A65.0, I98.0, O98.1, A50-A50.0	Bloodstream infections due to treponema pallidum	090-097.9, 100
Bloodstream infections due to rickettsias spp Bloodstream infections due to chlamydia spp Bloodstream infections due to enterococcus spp	A68-A69.9, A75-A79.9 A72-A74.9 B95.2	Bloodstream infections due to chlamydia spp	076.0-076.9
Bloodstream infections due to streptococcus pneumoniae Bloodstream infections due to unspecified streptococcus Bloodstream infections due to due to klebsiella spp	B95.3 B95.4-B95.5, A40.8-A40.9 B96.2	Bloodstream infections due to streptococcus pneumoniae Bloodstream infections due to unspecified streptococcus	041.2, 038.2 041.0
 Bloodstream infections due to proteus spp Bloodstream infections due to Pseudomonas aeruginosa 	B96.4 B96.5 B96.6	Bloodstream infections due to proteus spp Bloodstream infections due to escherichia coli	041.6 041.4
Bloodstream infections due to bacteroides fragilis Bloodstream infections due to clostridium perfringens	B96.6 B96.7	Bloodstream infections due to pseudomonas spp	041.7
3 3 Bloodstream infections due to gram negative other	A41.5	Bloodstream infections due to borrelia recurrentis Bloodstream infections due to non typhoidal salmonellae Bloodstream infections due to gram negative other	080-083.9, 087-088, 088.8, 100.0-101.6 003.1 038.4
2 Bloodstream infections due to other specified bacteria	A25.0-A25.9, A28-A28.1, A28.8-A28.9, A28.2 A45-A45.9, A47-A48, A49, A49.8-A49.9, B20.1, B94.9-B95, B96, B96.8, B98-B99.9, I98.1, K04-K05.5, O04.0,	Bloodstream infections due to other specified bacteria	078.3
 Bloodstream infections due to unspecified bacteria Bloodstream infections unspecified pathogen 	O05.0, O05.5, O06.0, O06.5, O07.0, O07.5, T80.2, T83.5-T83.6, T85.7, T87.4, T88.0, U82-U84, U85-U89.9, Y62-Y62.9, Y95, Z03.0, Z11.1, Z16-Z16.3, Z22-Z22.4, Z22.8-Z22.9, A41.6-A41.9, A48.8, I76, O03.5, O04.5, O08.0, O23, O23.9, O85-O86.8, O88.3, O91-O91.2, R65.2 A41	Bloodstream infections due to unspecified bacteria Bloodstream infections unspecified pathogen	634.0, 635-635.0, 636.0, 637-637.0, 638.0, 639.0, 647, 647.8-647.9, 658.4, 659.3, 671.2-671.5, 672-672.0, 675-675.9, 670-670.9, E872-E872.9 040-040.8, 041.3, 041.9, 790.7, 996.6, 038, 038.5-038.9
3		Bloodstream infections due to staph aureus with toxin production	040.9
2 Bloodstream infections due to group a strep with toxin production	A48.3-A48.4		
Bloodstream infections due to group a strep with toxin production Bloodstream infections due to unspecified bacteria with toxin production Neonatal bloodstream infections due to specified bacteria	A48.3-A48.4 A48.3-A48.4 P36-P36.9, P37.2, P37.8-P39.9	Neonatal bloodstream infections due to specified bacteria	771.3

Level	ist of infectious syndromes mapped to International Classification of Diseases (ICD) codes Infectious syndrome name and level L0 L1 L2 L3	Infectious syndrome name and ICD code	Infectious Syndrome to ICD Co Infectious syndrome name and level L1 L2 L3	Infectious syndrome name and ICD code ICD Codes for all level
01 3 02 3 03 3	Neonatal bloodstream infections due to anaerobes Neonatal bloodstream infections due to listeria Neonatal bloodstream infections due to unspecified bacteria	P36.5 P37.2 P36	Neonatal bloodstream infections due to unspecified bacteria	771-771.2, 771.4-771.9
04 1	Other and non bacterial infectious	A29, A36-A36.9, A42-A42.2, A42.8-A43.9, A42.7, B37.7, P37, A54.3, A54.5-A54.6, A59-A63.8, A71-A71.9, A80-A86.4, A88-B20.0, B20.2-B34.1, B34.3-B37.6, B37.8-B94.8, B97-B97.1, B97.3, B97.7-B97.8, F07.1, G04-G05.8, G14-G14.6, G21.3, H05.1, H60.2, H62-H62.3, H65-H68.0, H70-H70.9, H73.0, H75-H75.0, I02.9, J00-J06.9, J31-J32.9, J35-J37.1, J39.0-J39.1, J85-J85.3, J86-J86.9, J91.0, K93.1, M89.6, N72-N72.0, N75-N77.8, O98.4-O98.7, P35-P35.9, P37.1, P37.3-P37.5, T81.4, T82.6-T82.7, T84.5-T84.7, U06-U06.9, Z21-Z21.0, Z22.5-	Upper respiratory infections and otitis due to corynebacterium diphtheriae	032-032.9, 034.0, 042-046.9, 050-072.9, 074-076, 077-078.2, 078.4-079.5, 079.8-079.9, 084-086.9, 088.9-089.9 098.4, 098.6-098.7, 099, 099.4-099.9, 110-134.9, 136-139.9, 323-323.9, 381-383.9, 425.6, 460-465.9, 472-476.9 522-523.9, 616-616.9, 647.4-647.6
os 2	Non bacterial protozoal infections	Z22.6 A59-A59.9, B50-B64, P37.1, P37.3-P37.4	Non bacterial protozoal infections	084-086.9, 089-089.9, 647.4
6 2 7 2	Non bacterial protozoal infections Non bacterial fungal infections	P37 B65-B94, B94.2-B94.8, H05.1, K93.1, U06-U06.9	Non bacterial fungal infections	088.9, 120-134.9, 136-137.9, 138.0-139, 139.1-139.9, 425.6
2 2	non bacterial fungal infections non bacterial viral infections	B35-B36.9, P37.5 A60-A63.8, B01-B20.0, B20.2-B34.1, B34.3-B34.9, B94.1, B97-B97.1, B97.3, B97.7-B97.8, J91.0, M89.6,	non bacterial fungal infections non bacterial viral infections	110-119 042-046.9, 050-061.8, 070-072.9, 138, 647.5-647.6
2	Other opportunistic infatious	O98.4-O98.7, P35-P35.9, Z21-Z21.0, Z22.5-Z22.6 A29, A42-A42.2, A42.8-A43.9, B37-B37.6, B37.8-B49.9, T81.4, T82.6-T82.7, T84.5-T84.7, A42.7, B37.7		
2 2	Viral encephalitis Other locl infectious	A80-A86.4, A88-B00.9, F07.1, G04-G05.8, G14-G14.6, G21.3 A54.3, A54.5-A54.6, A71-A71.9, B94.0, N72-N72.0, N75-N77.8	Viral encephalitis Other locl infectious	062-069, 139.0, 323-323.9 076, 098.4, 098.6-098.7, 099, 099.4-099.9, 522-523.9, 616-616.9
2	Upper respiratory infections and otitis due to specified bacteria Upper respiratory infections and otitis due to corynebacterium	A36-A36.9, I02.9, J02.0, J03.0	Upper respiratory infections and otitis due to specified bacteria	034.0
3	diphtheriae Upper respiratory infections and otitis due to group a strep	A36-A36.9 I02.9, J02.0, J03.0	Upper respiratory infections and otitis due to corynebacterium diphtheriae	032-032.9
2	Upper respiratory infections and otitis due to unspecified bacteria	H60.2, H62-H62.3, H65-H68.0, H70-H70.9, H73.0, H75-H75.0	Upper respiratory infections and otitis due to unspecified bacteria	381-383.9
2	Upper respiratory infections and otitis due to unspecified bacteria	J36-J36.0, J39.0-J39.1, J85-J85.3, J86-J86.9	Upper respiratory infections and otitis due to unspecified bacteria Upper respiratory infections and otitis due to Virus	464.5, 465, 465.9, 472-474.9, 476-476.1 074-075.9, 077-077.9, 078.8, 079.8-079.9
2	Upper respiratory infections and otitis due to unspecified pathogen	J00-J02, J02.8-J03, J03.8-J06.9, J31-J32.9, J35-J35.9, J37-J37.1	Upper respiratory infections and otitis due to unspecified pathogen	460-464.4, 464.8-464.9, 465.0-465.8, 475-475.9, 476.9
2	Meningitis and other bacterial central nervous system abases	A32.1, A39-A39.0, A87-A87.9, G00-G03.9, G06-G08.0, R83.5	Urogenital infections due to virus Meningitis and other bacterial central nervous system abases	078-078.2, 078.4-078.7, 078.9-079.5 036-036.1, 047-049.9, 320-320.3, 320.5-322.9, 324-326.9
2	Meningitis due to specific bacteria	A32.1, A39-A39.0, G00.0-G00.3	Meningitis due to specific bacteria	036-036.1, 320.0-320.3, 320.5-320.8
3	Meningitis due to listeria Meningitis due to neisseria meningitidis	A32.1 A39-A39.0	Meningitis due to neisseria meningitidis	036-036.1, 320.5-320.8
3	Meningitis due to haemophilus Meningitis due to streptococcus pneumoniae	G00.0 G00.1	Meningitis due to haemophilus Meningitis due to streptococcus pneumoniae	320.0 320.1
3	Meningitis due to group b strep Meningitis due to staphylococcus aureus	G00.2 G00.3	Meningitis due to group b strep Meningitis due to staphylococcus aureus	320.2 320.3
2 2	Meningitis due to virus Meningitis due to unspecified pathogen	A87-A87.9, G03.0 G00, G00.8, G01-G02.8, G03.1-G03.9, G06-G08.0, R83.5	Meningitis due to virus Meningitis due to unspecified pathogen	047-049.9 320, 320.9-321.8, 322.0-322.9, 324-326.9
2 1	Meningitis due to unspecific bacteria Respiratory infectious	G00.9, G03 A37-A37.9, A48.1-A48.2, A70, B34.2, B97.2, B97.4-B97.6, J09-J22.9, J40-J42.6, P00.2, P22-P23.9, R84.5, U04.9, U07-U07.2	Meningitis due to unspecific bacteria Respiratory infectious	322 033-033.9, 039.1, 073-073.9, 079.6-079.7, 466-469, 470.0, 480-491.9, 510-511.9, 513-513.9, 519.2, 519.8-519.770.0
2	Lower respiratory infections due to specific bacteria	A37-A37.9, A48.1-A48.2, A70, J13-J14.0, J15.0-J15.7, J16.0, J20.0-J20.2, P23.1-P23.5	Lower respiratory infections due to specific bacteria	033-033.9, 039.1, 073-073.9, 466-469, 470.0, 481-481.9, 482.0-482.4, 483.0-483.1, 484.2-484.5
3	Lower respiratory infections due to bordetella pertussis Lower respiratory infections due to legionella spp	A37-A37.9 A48.1-A48.2	Lower respiratory infections due to bordetella pertussis	033-033.9, 484.3
3	Lower respiratory infections due to chlamydia spp	A70, J16.0, P23.1	Lower respiratory infections due to actinomyces Lower respiratory infections due to chlamydia spp	039.1 073-073.9, 483.1, 484.2
3	Lower respiratory infections due to streptococcus pneumoniae Lower respiratory infections due to haemophilus influenzae	J13-J13.9, J15.4, J20.2 J14-J14.0, J20.1	Lower respiratory infections due to streptococcus pneumoniae Lower respiratory infections due to haemophilus influenzae	481-481.9, 482.3 482.2
3	Lower respiratory infections due to klebsiella pneumoniae	J15.0	Lower respiratory infections due to klebsiella pneumoniae Lower respiratory infections due to pseudomonas spp	482.0 482.1
3	Lower respiratory infections due to Pseudomonas aeruginosa Lower respiratory infections due to staphylococcus aureus	J15.1, P23.5 J15.2, P23.2	Lower respiratory infections due to staphylococcus aureus	482.4
3	Lower respiratory infections due to group b strep Lower respiratory infections due to escherichia coli	J15.3, P23.3 J15.5, P23.4		
3	Lower respiratory infections due to mycoplasma	J15.7, J20.0	Lower respiratory infections due to mycoplasma Lower respiratory infections due to francisella-tularensis	483.0 484.4
3			Lower respiratory infections due to bacillus-anthracis	484.5
2 3	Lower respiratory infections due to unspecified Bacteria Lower respiratory infections due to other gram negative bacteria	J15, J15.8-J16, J16.8-J17, J17.1, J18-J20, J20.9-J21, J21.8-J22.9, J40-J42.6, P23.6-P23.9, R84.5 J15.6	Lower respiratory infections due to unspecified Bacteria	482, 482.8-483, 483.8-484, 484.8-486.9, 490-491.9
2 3	Lower respiratory infections due to virus Lower respiratory infections due to coronaviruses	B34.2, B97.2, B97.4-B97.6, J09-J12.9, J17.0, J17.2-J17.8, J20.3-J20.8, J21.0-J21.1, P23.0, U04.9, U07-U07.2 B34.2, B97.2, J12.8	Lower respiratory infections due to virus	079.6-079.7, 480-480.9, 484.0-484.1, 487-489
3	Lower respiratory infections due to syncytial virus (rsv) Lower respiratory infections due to influenza viruses	B97.4, J12.1, J20.5, J21.0 J09-J11.8		
3	Lower respiratory infections due to other virus Lower respiratory infections due to adenoviruses	J12, J12.3, J12.9, J17.0, J17.2-J17.8, J20.3, J20.7-J20.8, J21.1 J12.0		
3	Lower respiratory infections due to parainfluenza viruses Lower respiratory infections due to rhinoviruses	J12.2, J20.4 J20.6		
3			Lower respiratory infections due to fungi Lung abscess and pyothorax due to unspecified pathogen	484.6-484.7 510-511.9, 513-513.9
2	Lower respiratory infections due to unspecified pathogen	P00.2, P22-P23	Lower respiratory infections due to unspecified pathogen	519.2, 519.8-519.9, 770.0
1	Skin Bacterial Infectious Bacterial infections of skin and subcutaneous system due to specific	A46-A46.0, A48.0, A66-A67.9, H05.0, I89.1, I96-I96.9, K61-K61.4, L00-L08.9, L30.3, L88-L89.9, L97-L98.1, L98.4, M72.5-M72.6, R02-R02.9 A46-A46.0, A48.0, A66-A67.9, L00	Skin Bacterial Infectious Resterial infections of skin and subsutaneous system due to specific heatering	035-035.9, 039-039.0, 039.3-039.9, 102-104.9, 376.0-376.1, 457.1-457.9, 680-689, 707-707.9, 785.4
2	bacteria Bacterial infections of skin and subcutaneous system due to group a	A46-A46.0	Bacterial infections of skin and subcutaneous system due to specific bacteria Bacterial infections of skin and subcutaneous system due to group a strep	035-035.9
3	strep Bacterial infections of skin and subcutaneous system due to clostridium perfringens	A48.0		
3	Bacterial infections of skin and subcutaneous system due to treponent pallidum		Bacterial infections of skin and subcutaneous system due to treponema pallidum	102-102.9, 104-104.9
3	Bacterial infections of skin and subcutaneous system due to treponen carateum Bacterial infections of skin and subcutaneous system due to			
3	staphylococcus aureus	L00	Bacterial infections of skin and subcutaneous system due to yersinia pestis	103-103.9
3 2	Bacterial infections of skin and subcutaneous system due to unspecified	H05.0, I89.1, I96-I96.9, K61-K61.4, L01-L08.9, L30.3, L88-L89.9, L97-L98.1, L98.4, M72.5-M72.6, R02-R02.9	Bacterial infections of skin and subcutaneous system due to other specific bacteria Bacterial infections of skin and subcutaneous system due to unspecified bacteria	039.0 376.0-376.1, 457.1-457.9, 680-689, 707-707.9, 785.4
1	bacteria chlamydia and gonorrheae	A54-A54.2, A54.8-A56.8	chlamydia and gonorrheae	098-098.3, 098.8-098.9, 099.1, 099.3
1 2	infections of bone, joints and related part due to specific bacteria	A54.4, M00-M01.8, M46.2-M46.5, M65.0-M65.1, M71.0-M71.1, M73.0-M73.8, M86-M86.9 A54.4, M00-M00.2	infections of bone, joints and related part due to specific bacteria	098.5, 711-711.9, 730-730.3, 730.7-730.9 098.5
3	infections of bone, joints and related part due to neisseria gonorrheae	A54.4	infections of bone, joints and related part due to neisseria gonorrheae	098.5
3	infections of bone, joints and related part due to staphylococcus aureus	M00-M00.0		
3	infections of bone, joints and related part due to streptococcus pneumoniae	M00.1		
3 2	infections of bone, joints and related part due to group a strep infections of bone, joints and related part due to unspecified bacteria	M00.2 M00.8-M01.8, M46.2-M46.5, M65.0-M65.1, M71.0-M71.1, M73.0-M73.8, M86-M86.9	infections of bone, joints and related part due to unspecified bacteria	711-711.9, 730-730.3, 730.7-730.9
1	Urinary tract infections and nephritis	A57-A58, A64-A64.0, N10-N12.9, N13.6, N15, N15.1-N16.8, N30-N30.9, N34-N34.3, N39.0-N39.2, N41-N41.9, N45-N45.9, N49-N49.9, O23.0-O23.5	Urinary tract infections and nephritis	099.0, 099.2, 590-590.9, 595-595.9, 597-597.9, 599.0, 601-601.9, 604-604.9, 647.2
2	Urinary tract infections and nephritis due to specific bacteria Urinary tract infections and nephritis due to haemophilus ducreyi	A57-A58 A57-A57.0	Urinary tract infections and nephritis due to specific bacteria Urinary tract infections and nephritis due to haemophilus ducreyi	099.0, 099.2 099.0
3	Urinary tract infections and nephritis due to klebsiella granulomatis		Urinary tract infections and nephritis due to klebsiella granulomatis	099.2
2	Urinary tract infections and nephritis due to unspecified bacteria Endocarditis and other cardiac infections	A64-A64.0, N10-N12.9, N13.6, N15, N15.1-N16.8, N30-N30.9, N34-N34.3, N39.0-N39.2, N41-N41.9, N45-N45.9, N49-N49.9, O23.0-O23.5 I00, I01-I02.0, I30, I30.1, I33-I33.9, I38-I41.9	Urinary tract infections and nephritis due to unspecified bacteria Endocarditis and other cardiac infections	590-590.9, 595-595.9, 597-597.9, 599.0, 601-601.9, 604-604.9, 647.2 390-392.9, 420-424.9, 457
1 2 3	Endocarditis due to specific bacteria	100, 101-102.0	Endocarditis due to specific bacteria	390-392.9, 421-421.9
3 2	Endocarditis due to group a strep Endocarditis due to unspecific bacteria	100, 101-102.0 130, 130.1, 133-133.9, 138-141.9	Endocarditis due to group a strep Endocarditis due to unspecific bacteria	390-392.9 420-420.9, 422-424.9, 457
1	Peritoneal and intra abdomen infections	K35-K37.9, K38.3-K38.9, K40-K42.9, K44-K46.9, K50-K52, K52.8-K52.9, K55-K57.9, K63.0-K63.1, K65-K65.9, K67-K67.2, K67.8-K69, K75.0-K75.1, K75.3, K76.3, K77.0, K80-K83.9, M09.1, N70-N71.9, N73-N74.0, N74.3-N74.8, N98.0, O98.2-O98.3, O98.8-O98.9, R65.0, R85.5, R86.5, R87.5; O03.0, O41.1, O75.3, O98	Peritoneal and intra abdomen infections	039.2, 540-542.9, 550-551.1, 551.3-552.1, 552.3-553.1, 553.3-558.0, 560-560.3, 560.8-560.9, 562-562.1, 567.9, 569.5, 572.0-572.1, 574-576.9, 614-615.9, 647.0-647.1
2	Peritoneal and intra abdomen infections due to specific bacteria	K67.0-K67.2	Peritoneal and intra abdomen infections due to specific bacteria	039.2
3	Peritoneal and intra abdomen infections due to chlamydia spp Peritoneal and intra abdomen infections due to neisseria gonorrheae	K67.0 K67.1	Peritoneal and intra abdomen infections due to neisseria gonorrheae	647.1
3	and the incisoria goliofficate		Peritoneal and intra abdomen infections due to actinomyces	039.2
3	· · · · · · · · · · · · · · · · · · ·	K67.2		
2	Peritoneal and intra abdomen infections due to due to specific bacteria	N74.3-N74.4, O98.2	Peritoneal and intra abdomen infections due to due to specific bacteria	647.1

Table S3. List of infectious syndromes mapped to International Classification of Diseases (ICD) code	es	Infectious Syndrome to ICD	O Codes (ICD9)
Infectious syndrome name and level	Infectious syndrome name and ICD code	Infectious syndrome name and level	Infectious syndrome name and ICD code
Level L0 L1 L2 L3	ICD Codes for all level	L0 L1 L2 L3	ICD Codes for all level
Peritoneal and intra abdomen infections due to unspecified Bacteria	K35-K37.9, K38.3-K38.9, K40-K42.9, K44-K46.9, K50-K52, K52.8-K52.9, K55-K57.9, K63.0-K63.1, K65-K65.9, K67, K67.8-K69, K75.0-K75.1, K75.3, K76.3, K77.0, K80-K83.9, M09.1, N70-N71.9, N73-N74.0, N74.8, N98.0, O98.3, O98.8-O98.9, R65.0, R85.5, R86.5, R87.5, O03.0, O41.1, O75.3, O98	Peritoneal and intra abdomen infections due to unspecified Bacteria	540-542.9, 550-551.1, 551.3-552.1, 552.3-553.1, 553.3-558.0, 560-560.3, 560.8-560.9, 562-562.1, 567-567.9, 569.5, 572.0-572.1, 574-576.9, 614-615.9, 647.0
199 () No Sepsis, No infectious diseases and unspecified	C00-D64.9, D66-D69.4, D69.6-D70.2, D70.4-D89.2, D89.8-E87.1, E88-F02.0, F02.2-F02.3, F02.8-F07.0, F07.2-F99.0, G09-G13.8, G15-G21.2, G21.4-G93.3, G93.5-H05, H05.2-H60.1, H60.3-H61.9, H62.4-H62.8, H68.1-H69.9, H71-H73.1-H74.9, H75.8-H99, I00.0, I03-I29.9, I30.0, I30.8-I32.8, I34-I37.9, I42-I45.9, I47-I75.8, I77-I79.8, I83-I87, I87.1-I89.0, I89.8-I95.0, I97-I98, I98.2-ID5.9, J07-J08, J23-J30.9, J33-J34.9, J38-J39, J39.2-J39.9, J42.9-J79, J81-J84.9, J85.9, J87-J91, J91.8-J95.1, J95.4-J95.9, J97-K03.9, K05.6-K34, K38-K38.2, K39, K43-K43.9, K47-K49, K52.0, K53-K54, K58-K60.5, K62-K63, K63.2-K64.9, K66-K66.9, K70-K71.9, K73-K75, K75.2, K75.4-K76.2, K76.4-K77, K77.8-K79, K84-K93, K93.8-K99, L09-L30.2, L30.4-L87.9, L90-L96, L98.5-L99.8, M02-M09.0, M09.2-M46.1, M46.8-M49, M49.2-M65, M65.2-M71, M71.2-M72.4, M72.8-M73, M74-M85.9, M87-M89.5, M89.7-M99.9, N02-N09, N13-N13.5, N13.7-N14.4, N15.0, N18-N29.8, N31-N33.8, N35-N39, N39.3-N40.9, N42-N44.8, N46-N48.9, N50-N69, N78-N98, N98.1-O03, O03.1-O03.4, O03.6-O04, O04.1-O04.4, O04.6-O05, O05.1-O05.4, O05.6-O06, O06.1-O06.4, O06.6-O07, O07.1-O07.4, O07.6-O08, O08.1-O22.9, O24-O41.0, O41.8-O75.2, O75.4-O84.9, O87-O88.2, O88.8-O90.9, O92-O97.9, O99-P00.1, P00.3-P21.9, P24-P34.2, P40-R01.2, R03-R09.1, R09.3-R19.6, R19.8-R40, R41-R54.9, R56-R56.9, R58-R65, R65.1, R66-R83.4, R83.6-R84.4, R84.6-R85.4, R85.6-R86.4, R86.6-R87.4, R87.6-T80.1, T80.3-T81.3, T81.5-T82.5, T82.8-T83.4, T83.7-T84.4, T84.8-T85.6, T85.8-T87.3, T87.5-T88, T88.1-U03, U05, U08-U81, U90-Y61.9, Y63-Y94, Y96-Z03, Z03.1-Z11.0, Z11.2-Z15.8, Z17-Z20.9, Z33-ZB0, D65-D65.9, D69.5, D70.3, D89.3, E87.2-E87.9, F02.1, F02.4, G93.4, I46-I46.9, I80-I82.9, I87.0, I95.1-I95.9, J80-J80.9, J95.2-J95.3, J96-J96.9, K72-K72.9, L98.2-L98.3, N00-N01.9, N17-N17.9, R09.2, R40.0-R40.4, R55-R55.0, R57-R57.9, T78-T80.1, T80.3-T81.3, T81.5-T82.5, T82.8-T83.4, T83.7-T84.4, T84.8-T85.6, T85.8-T87.3, T87.5-T88, T88.1-T98.3, Y40-Y61.9, Y63-Y84.9, Y88-Y88.3, S00-T76.9	No Sepsis, No infectious diseases and unspecified	000-000.9, 019-019.9, 105-109.9, 140-275.5, 277-286.5, 286.7-292.9, 294.0-319.9, 327-346.9, 348-376, 376.2-380.9, 384-389.9, 393-419.9, 425-425.5, 425.7-427.4, 427.6-450, 454-456.9, 459-459.9, 470, 470.9-471.9, 477-479, 492-509, 512-512.9, 514-519.0, 520-521.9, 524-539.9, 543-549, 551.2, 552.2, 553.2, 558.1, 559-559.0, 560.4 560.7, 561, 562.2-566.9, 568-569.4, 569.6-572, 572.2-573.9, 577-583.9, 585-589.9, 591-594.9, 596-596.9, 598-599, 599.1-600.9, 602-603.9, 605-613, 617-634, 634.1-634.9, 635.1-635.4, 635.6-636, 636.1-636.4, 636.6-636.9, 637.1-637.4, 637.6-638, 638.1-639, 639.1-646.9, 648-658.3, 658.8-659.2, 659.4-669.0, 669.2-669.9, 671-671.1, 671.8-671.9, 673-674.9, 676-679.1, 690-706.9, 708-710.9, 712-729.9, 731-768.7, 769.0-770, 770.1-770.9, 772-779.9, 780.4-785.3, 785.6-790.6, 790.8-797.9, 799.3-995.8, 996-996.5, 996.7-E871.9, E873-E999.1, 800-995.8, E000-E871.9, E873-E930, E950-E999.1, 996-996.5, 996.7-999.9, E930.0-E949.9, 135-135.9, 275.8-276.9, 286.6, 293-294, 347-347.9, 427.5, 451-453.9, 457.0, 458-458.9, 519.1, 519.3-519.4, 584-584.9, 635.5, 636.5, 637.5, 669.1, 768.9-769, 780-780.3, 785.5, 798-799.2, 135-135.9, 275.8-276.9, 286.6, 293-294, 347-347.9, 427.5, 451-453.9, 457.0, 458-458.9, 519.1, 519.3-519.4, 584-584.9, 635.5, 636.5, 637.5, 798-799.2

Pathogen	Hospital	Literature	Microbiology	Total
Acinetobacter baumannii		•	287390	28739
Adenovirus	3904			3904
Aeromonas spp.			280	280
Campylobacter spp.	24330		62	24392
Chlamydia spp.	14362			14362
Citrobacter spp.			156376	156376
Clostridium difficile	415011		7171	422182
Cryptosporidium	2010			2010
Entamoeba histolytica	9438			9438
Enterobacter spp.			730786	730786
Enterococcus faecalis			177234	177234
Enterococcus faecium			242584	242584
Other enterococci	6771		15062	21833
Escherichia coli	430064		2393259	2823323
Fungi	702794		6052	708846
Group A Streptococcus	280314		80761	361075
Group B Streptococcus	165579	2726	172333	340638
Haemophilus influenzae	56781	2134	197294	256209
Klebsiella pneumoniae	52983		1212459	1265442
Other Klebsiella species	39855		140357	180212
Legionella spp.	1396		54	1450
Listeria monocytogenes	5502		41	5543
Morganella spp.			87403	87403
Mycobacterium tuberculosis	102402		3032	105434
Mycoplasma spp.	53762			53762
Neisseria gonorrhoeae	11483		5540	17023
Neisseria meningitidis	9505	20952	110	30567
Non-typhoidal Salmonella	6194		172130	178324
Norovirus	8266			8266
Other pathogens	920212		357838	1278050
Polybacterial			92	92
Proteus spp.	41032		405684	446716
Providencia spp.			47268	47268
Pseudomonas aeruginosa	21773		1010873	1032646
Rotavirus	22818			22818
Salmonella Paratyphi	818		364	1182
Salmonella Typhi	5010		5088	10098
Serratia spp.	6497		260684	26718
Shigella spp.	4273		11361	15634
Staphylococcus aureus	932990		2545845	3478835
Streptococcus pneumoniae	214761	27095	441302	68315
Vibrio cholerae	740		6	74
Viruses	3903630		2	3903632
TOTAL	8477260	52907	11174177	1970434

Table S5. Case fatality ratio modelling framework by pathogen and syndrome

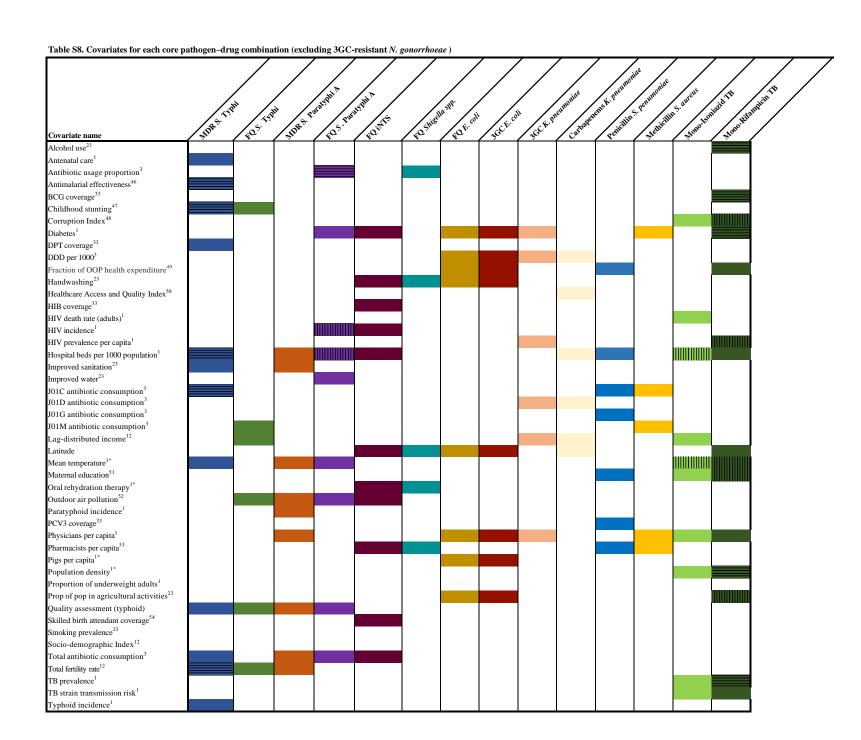
BSI = bloodstream infections. CNS = meningitis and other bacterial central nervous system infections. LRI+ = lower respiratory infections and all related infections in the thorax. Intra-abdominal = peritoneal and intra-abdominal infections. Skin = bacterial infections of the skin and subcutaneous systems. UTI = urinary tract infections and pyelonephritis.

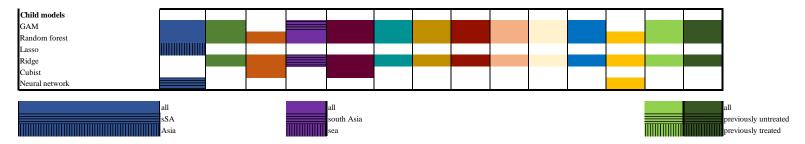
Active Agreement of Composition was all and Composition was all and Composition was all and Composition was and equitaly modeled as equitaly modeled		BSI (neonatal)	BSI (post-neonatal and older	r) CNS	Diarrhoea	LRI+ (community- acquired)	LRI+ (hospital-acquired)	Intra-abdominal	Skin	UTI (community-acquired)	UTI (hospital-acquired)
	Acinetobacter baumannii	intercept	interaction	not explicitly modelled	not explicitly modelled	intercept	intercept	not explicitly modelled	intercept	intercept	intercept
	Campylobacter spp.	not explicitly modelled	not explicitly modelled	not explicitly modelled	intercept	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled
Process of particular process of process o	Chlamydia spp.	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled	intercept	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled
Commondation of explainty modelled one ex	Citrobacter spp.	not explicitly modelled	intercept	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled	intercept	intercept
Second Instruction Second	Clostridium difficile	not explicitly modelled	not explicitly modelled	not explicitly modelled	intercept	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled
Intervalue Int	Cryptosporidium	not explicitly modelled	not explicitly modelled	not explicitly modelled	intercept	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled
Patrice content Patrice co	Entamoeba histolytica	not explicitly modelled	not explicitly modelled	not explicitly modelled	intercept	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled
Interconce of configuration of the explicitly modelled Intercopt Interco	Enterobacter spp.	intercept	interaction	not explicitly modelled	not explicitly modelled	intercept	intercept	intercept	intercept	intercept	intercept
Oble Emercoci on explicitly modelled intercept interce	Enterococcus faecalis	not explicitly modelled	intercept	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled
Intercept Inte	Enterococcus faecium	not explicitly modelled	intercept	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled	intercept	not explicitly modelled	intercept	intercept
Figures intercept on explicitly modelled on e	Other Enterococci	not explicitly modelled	intercept	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled	intercept	not explicitly modelled	not explicitly modelled
Intercept Inte	Escherichia coli	intercept	interaction	intercept	intercept	intercept	intercept	intercept	intercept	intercept	intercept
Providence of the Providence	Fungus	intercept	interaction	not explicitly modelled	not explicitly modelled	intercept	intercept	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled
Production of the splicity modelled mercept mercep	Group A Streptococcus	intercept	not explicitly modelled	not explicitly modelled	not explicitly modelled	intercept	not explicitly modelled	not explicitly modelled	intercept	not explicitly modelled	not explicitly modelled
Retabile paramoniae Intercept Interc	Group B Streptococcus	intercept	interaction	intercept	not explicitly modelled	intercept	intercept	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled
Legionella spp. not explicitly modelled on explicitly modelled intercept not explicitly modelled not	Haemophilus influenzae	not explicitly modelled	not explicitly modelled	interaction	not explicitly modelled	intercept	intercept	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled
Listeria monocytogenes not explicitly modelled not exp	Klebsiella pneumoniae	intercept	interaction	intercept	not explicitly modelled	intercept	intercept	intercept	intercept	intercept	intercept
Morasella sp. not explicitly modelled not explicitly m	Legionella spp.	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled	intercept	intercept	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled
Mycopanum spp. not explicitly modelled not explicitly	Listeria monocytogenes	not explicitly modelled	not explicitly modelled	intercept	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled
Nexuserial meningitidis intercept intercept intercept not explicitly modelled	Moraxella spp.	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled	intercept	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled
Neisseria memingitidis intercept intercept intercept not explicitly modelled n	Morganella spp.	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled	intercept	intercept
Polybacterial intercept interaction not explicitly modelled not explicitly mod	Mycoplasma spp.	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled	intercept	intercept	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled
Proteus spp. not explicitly modelled not explicitly mo	Neisseria meningitidis	intercept	intercept	intercept	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled
Providencia spp. not explicitly modelled not explicitl	Polybacterial	intercept	interaction	not explicitly modelled	not explicitly modelled	intercept	intercept	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled
Pseudomonas aeruginosa not explicitly modelled not exp	Proteus spp.	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled	intercept	intercept	intercept
Salmonella Typhi not explicitly modelled not explicitl	Providencia spp.	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled	intercept	intercept
Non-typhoidal Salmonella not explicitly modelled intercept not explicitly modelled not explicitly mode	Pseudomonas aeruginosa	not explicitly modelled	interaction	not explicitly modelled	not explicitly modelled	intercept	intercept	intercept	intercept	intercept	intercept
Servatia spp. Servatia spp. Servatia spp. Intercept	Salmonella Typhi	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled
Singella spp. not explicitly modelled not explicitly m	Non-typhoidal Salmonella	not explicitly modelled	intercept	not explicitly modelled	intercept	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled
Suphylooccus aureus intercept interc	Serratia spp.	intercept	intercept	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled	intercept	intercept
Streptococcus pneumoniae intercept intercept intercept intercept on texplicitly modelled intercept intercept intercept on texplicitly modelled on texp	Shigella spp.	not explicitly modelled	not explicitly modelled	not explicitly modelled	intercept	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled
Vibrio cholerae not explicitly modelled not explicitly	Staphylococcus aureus	intercept	interaction	intercept	intercept	intercept	intercept	intercept	intercept	intercept	intercept
	Streptococcus pneumoniae	intercept	intercept	interaction	not explicitly modelled	intercept	intercept	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled
Virus not explicitly modelled	Vibrio cholerae	not explicitly modelled	not explicitly modelled	not explicitly modelled	intercept	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled
	Virus	not explicitly modelled	not explicitly modelled	interaction	intercept	intercept	intercept	not explicitly modelled	not explicitly modelled	not explicitly modelled	not explicitly modelled

Pathogen	distribution data CHAMPS	Hospital	Linkage	Literature	MCOD	Microbiology	Total
Acinetobacter baumannii	162			2449		95614	98225
Chlamydia spp.		14362	7	481	730	1	15581
Citrobacter spp.				3330		64006	67336
Enterobacter spp.	9			9357		263748	273114
Enterococcus faecalis	13			13858		338708	352579
Enterococcus faecium	11			1464		411508	412983
Other enterococci	2	6771	44	12749	1	7351	26918
Escherichia coli	79	430064	482	205847	4628	4964020	5605120
Fungi	41	702794	334	8276	92562	6405	810412
Group A Streptococcus	9	280314	258	1947	48148	34637	365313
Group B Streptococcus	16	165579	203	8656	31183	8898	214535
Haemophilus influenzae	42	56781	310	5900	7831	25840	96704
Klebsiella pneumoniae	259	52983	144	22780	19126	1369389	1464681
Other Klebsiella species		39855	116	17240	28	13800	71039
Legionella spp.		1396	35	112	3726	54	5323
Listeria monocytogenes	5	5502	38	221	10416	41	16223
Morganella spp.				1480		63705	65185
Mycobacterium tuberculosis	6	102402	126	945	661806	3063	768348
Mycoplasma spp.		53762	56	1061	2722		57601
Neisseria gonorrhoeae		11483	1	115	220	5162	16981
Neisseria meningitidis	3	9505	107	10921	14304	5719	40559
Non-typhoidal Salmonella	9	6194	17	472	2002	34478	43172
Other bacteria	130	920212	1202	49723	299761	143107	1414135
Polybacterial	1			4565		115	4681
Proteus spp.	2	41032	52	19493	180	328345	389104
Providencia spp.				592		35144	35736
Pseudomonas aeruginosa	26	21773	541	17358	25725	819446	884869
Salmonella Paratyphi	1	818			29	365	1213
Salmonella Typhi		5010	1	4	573	10892	16480
Serratia spp.		6497	3	1360		96314	104174
Staphylococcus aureus	57	932990	1936	19521	227064	3109956	4291524
Streptococcus pneumoniae	100	214761	909	11044	130684	623928	981426
Viruses	164	3903630	2779	46049	2064708	4	6017334
TOTAL	1147	7986470	9701	499370	3648157	12883763	25028608

Table S7. Summary of p	revalence of resistance data Antibiotic Class	Literature	Microbiology	Surveillance report	Total
Acinetobacter baumannii	Aminoglycosides	Littrature	52393	Sur vemance report	52393
Acinetobacter baumannii	Anti-pseudomonal penicillin/Beta-lactamase inhibitors		15723		15723
Acinetobacter baumannii	Beta-lactam/Beta-lactamase inhibitors		20205		20205
Acinetobacter baumannii	Carbapenem		43437		43437
Acinetobacter baumannii	Fluoroquinolones		38766		38766
Acinetobacter baumannii	Fourth-generation cephalosporins		26953		26953
Acinetobacter baumannii	Third-generation cephalosporins		49034		49034
Citrobacter spp.	Aminoglycosides		194936	4996	199932
Citrobacter spp.	Anti-pseudomonal penicillin/Beta-lactamase inhibitors		229701	2931	232632
Citrobacter spp.	Carbapenem		273016	6907	279923
Citrobacter spp.	Fluoroquinolones		240317	5862	246179
Citrobacter spp.	Fourth-generation cephalosporins		126201	2931	129132
Citrobacter spp.	Third-generation cephalosporins		353349	8793	362142
Enterobacter spp.	Aminoglycosides		1050287	6737	1057024
Enterobacter spp.	Anti-pseudomonal penicillin/Beta-lactamase inhibitors		766210	6072	772282
Enterobacter spp.	Carbapenem		891579	14916	906495
Enterobacter spp.	Fluoroquinolones		785309	12809	798118
Enterobacter spp.	Fourth-generation cephalosporins		417357		417357
Enterobacter spp.	Trimethoprim-Sulfamethoxazole		437597		437597
Enterococcus faecalis	Fluoroquinolones		637781		637781
Enterococcus faecalis	Vancomycin		846045		846045
Enterococcus faecium	Fluoroquinolones		193447		193447
Enterococcus faecium	Vancomycin		353515		353515
Other Enterococci	Fluoroquinolones		801		801
Other Enterococci	Vancomycin		3287		3287
Escherichia coli	Aminoglycosides		10524486	13012	10537498
Escherichia coli	Aminopenicillin		5162728	3582	5166310
Escherichia coli	Beta-lactam/Beta-lactamase inhibitors		4547346	3582	4550928
Escherichia coli	Carbapenem		8443688	224	8443912
Escherichia coli	Fluoroquinolones	946267	6505222	2398783	9850272
Escherichia coli	Third-generation cephalosporins	433884	2043110	2900403	5377397
Escherichia coli	Trimethoprim-Sulfamethoxazole		3459423	7164	3466587
Group A Streptococcus	Macrolide		10915	7933	18848
Group B Streptococcus	Fluoroquinolones		20050		20050
Group B Streptococcus	Macrolide		34507		34507
Group B Streptococcus	Penicillin		20424		20424
Haemophilus influenzae	Aminopenicillin		297932	3128	301060
Haemophilus influenzae	Third-generation cephalosporins		476427	2900	479327
Klebsiella pneumoniae	Aminoglycosides		3453036		3453036
Klebsiella pneumoniae	Beta-lactam/Beta-lactamase inhibitors		1556408		1556408
Klebsiella pneumoniae	Carbapenem	268169	873691	1182391	2324251
Klebsiella pneumoniae	Fluoroquinolones		2551051		2551051
Klebsiella pneumoniae	Third-generation cephalosporins	245676	851217	1059474	2156367
Klebsiella pneumoniae	Trimethoprim-Sulfamethoxazole		1225771		1225771
Morganella spp.	Fluoroquinolones		48697	3054	51751
Morganella spp.	Fourth-generation cephalosporins		23231	1527	24758
Morganella spp.	Third-generation cephalosporins		49780	4581	54361
Mycobacterium tuberculosis	Extensive drug resistance		15210		15210
Mycobacterium tuberculosis	Isoniazid mono-resistance		1980958	81360	2062318
Mycobacterium tuberculosis	Multi-drug resistance		14028		14028
Mycobacterium tuberculosis	Rifampicin mono-resistance		2846360	54169	2900529
Neisseria gonorrhoeae	Fluoroquinolones		27356		27356
Neisseria gonorrhoeae	Third-generation cephalosporins		49779		49779
Non-typhoidal Salmonella	Fluoroquinolones	6660	14		6674
Proteus spp.	Aminoglycosides		553876	3816	557692
Proteus spp.	Aminopenicillin		334346		334346
Proteus spp.	Fluoroquinolones		538122	7632	545754
Proteus spp.	Third-generation cephalosporins		656754	11448	668202
Proteus spp.	Trimethoprim-Sulfamethoxazole		171233		171233
Pseudomonas aeruginosa	Aminoglycosides		2801891		2801891
Pseudomonas aeruginosa	Anti-pseudomonal penicillin/Beta-lactamase inhibitors		2029407		2029407
Pseudomonas aeruginosa	Carbapenem		2311724		2311724
Pseudomonas aeruginosa	Fluoroquinolones		2331732		2331732
Pseudomonas aeruginosa	Fourth-generation cephalosporins		1138828		1138828
Pseudomonas aeruginosa	Third-generation cephalosporins		1315517		1315517
Salmonella Paratyphi	Fluoroquinolones	11123	6		11129
Salmonella Paratyphi	Multi-drug resistance	31383	12	237	31632
Salmonella Typhi	Fluoroquinolones	41718	162	1528	43408
Salmonella Typhi	Multi-drug resistance	113258	3608	6593	123459
Serratia spp.	Aminoglycosides		261873	1652	263525
Serratia spp.	Anti-pseudomonal penicillin/Beta-lactamase inhibitors		302571	1652	304223
Serratia spp.	Carbapenem		355742	3986	359728
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Serratia spp.	Fluoroquinolones		322402	3304	325706
Serratia spp.	Fourth-generation cephalosporins		167538	1652	169190
Serratia spp.	Third-generation cephalosporins		419093	4956	424049
Shigella spp.	Fluoroquinolones	72148	13911	53514	139573
Staphylococcus aureus	Fluoroquinolones		4009367		4009367
Staphylococcus aureus	Macrolide		5963254		5963254
Staphylococcus aureus	Methicillin	178620	1893838	2471297	4543755
Staphylococcus aureus	Trimethoprim-Sulfamethoxazole		2645319		2645319
Staphylococcus aureus	Vancomycin		2859122		2859122
Streptococcus pneumoniae	Beta-lactam/Beta-lactamase inhibitors		5968		5968
Streptococcus pneumoniae	Carbapenem		298257		298257
Streptococcus pneumoniae	Fluoroquinolones		527610		527610
Streptococcus pneumoniae	Macrolide		760157	2687	762844
Streptococcus pneumoniae	Penicillin	60129	259584	314432	634145
Streptococcus pneumoniae	Third-generation cephalosporins		787948	2669	790617
Streptococcus pneumoniae	Trimethoprim-Sulfamethoxazole		31189	2684	33873
TOTAL		2409035	101202814	10695960	114307809





^{*}See Appendix Section 7.4 for more details

Pathogen	ve risk data Antibiotic class	Literature	Microbiology	Total
Acinetobacter baumannii	Antibiotic class Aminoglycosides	Luerature	Microbiology 26547	26547
Acinetobacter baumannii Acinetobacter baumannii	Aminogrycosides Anti-pseudomonal penicillin/Beta-lactamase inhibitors		8594	26547 8594
Acinetobacter baumannii	Beta-lactam/Beta-lactamase inhibitors		10107	10107
Acinetobacter baumannii	Carbapenem		33071	33071
Acinetobacter baumannii	Fluoroquinolones		21091	21091
Acinetobacter baumannii	Fourth-generation cephalosporins		17670	17670
Acinetobacter baumannii	Third-generation cephalosporins Third-generation cephalosporins		31653	31653
Citrobacter spp.	Aminoglycosides		27196	27196
Citrobacter spp.	Anti-pseudomonal penicillin/Beta-lactamase inhibitors		9695	9695
Citrobacter spp.	Carbapenem		18268	18268
Citrobacter spp.	Fluoroquinolones		21393	21393
Citrobacter spp.	Fourth-generation cephalosporins		9533	9533
Citrobacter spp.	Third-generation cephalosporins		22418	22418
Enterobacter spp.	Aminoglycosides		99118	99118
Enterobacter spp.	Anti-pseudomonal penicillin/Beta-lactamase inhibitors		40914	40914
Enterobacter spp.	Carbapenem		69258	69258
Enterobacter spp.	Fluoroquinolones		76075	76075
Enterobacter spp.	Fourth-generation cephalosporins		38593	38593
Enterobacter spp.	Trimethoprim-Sulfamethoxazole		44611	44611
Enterococcus faecalis	Fluoroquinolones		1948	1948
Enterococcus faecalis	Vancomycin		2832	2832
Enterococcus faecium	Fluoroquinolones		20642	20642
Enterococcus faecium	Vancomycin		37044	37044
Other Enterococci	Fluoroquinolones		670	670
Other Enterococci	Vancomycin	5948	8827	14775
Escherichia coli	Aminoglycosides	3740	843033	843033
Escherichia coli	Aminopenicillin		372390	372390
Escherichia coli	Beta-lactam/Beta-lactamase inhibitors		439472	439472
Escherichia coli	Carbapenem	220	545090	545310
Escherichia coli	Fluoroquinolones	5734	646667	652401
Escherichia coli	Third-generation cephalosporins	15176	634823	649999
Escherichia coli	Trimet-generation cephatosporms Trimethoprim-Sulfamethoxazole	13176	394397	394397
Group A Streptococcus	Macrolide		413	413
Group B Streptococcus	Fluoroquinolones		135	135
Group B Streptococcus	Macrolide	432	208	640
Group B Streptococcus	Penicillin	432	128	128
Haemophilus influenzae	Aminopenicillin	1403	1577	2980
Haemophilus influenzae	Third-generation cephalosporins	1403	553	553
Klebsiella pneumoniae	Aminoglycosides		293876	293876
Klebsiella pneumoniae	Beta-lactam/Beta-lactamase inhibitors		157604	157604
Klebsiella pneumoniae	Carbapenem	5019	204322	209341
Klebsiella pneumoniae	Fluoroquinolones	3019	222853	222853
		1507	226729	228236
Klebsiella pneumoniae	Third-generation cephalosporins	1307	135376	135376
Klebsiella pneumoniae Morganella spp.	Trimethoprim-Sulfamethoxazole		22376	22376
Morganella spp.	Fluoroquinolones		10417	10417
Morganella spp.	Fourth-generation cephalosporins		23186	23186
	Third-generation cephalosporins			
Mycobacterium tuberculosis	Extensive drug resistance		15210	15210
Mycobacterium tuberculosis	Multi-drug resistance		14028	14028
Neisseria gonorrhoeae	Fluoroquinolones		6	6
Neisseria gonorrhoeae	Third-generation cephalosporins		10	2050
Non-typhoidal Salmonella	Fluoroquinolones		3059	3059
Proteus spp.	Aminoglycosides		171236	171236
Proteus spp.	Aminopenicillin		74260	74260
Proteus spp.	Fluoroquinolones		127450	127450
Proteus spp.	Third-generation cephalosporins		118679	118679
Proteus spp.	Trimethoprim-Sulfamethoxazole		77075	77075
Pseudomonas aeruginosa	Aminoglycosides		332015	332015
Pseudomonas aeruginosa	Anti-pseudomonal penicillin/Beta-lactamase inhibitors	21.11	138518	138518
Pseudomonas aeruginosa	Carbapenem	6141	180048	186189
Pseudomonas aeruginosa	Fluoroquinolones		218513	218513
Pseudomonas aeruginosa	Fourth-generation cephalosporins		129631	129631
Pseudomonas aeruginosa	Third-generation cephalosporins		132327	132327
Salmonella Paratyphi	Fluoroquinolones		66	66
Salmonella Typhi	Fluoroquinolones		795	795
Serratia spp.	Aminoglycosides		37402	37402
Serratia spp.	Anti-pseudomonal penicillin/Beta-lactamase inhibitors		11760	11760
Serratia spp.	Carbapenem		25054	25054
Serratia spp.	Fluoroquinolones		29148	29148

Serratia spp.	Fourth-generation cephalosporins		14622	14622
Serratia spp.	Third-generation cephalosporins		32521	32521
Shigella spp.	Fluoroquinolones		471	471
Staphylococcus aureus	Fluoroquinolones		292371	292371
Staphylococcus aureus	Macrolide		504053	504053
Staphylococcus aureus	Methicillin	25051	385688	410739
Staphylococcus aureus	Trimethoprim-Sulfamethoxazole		278366	278366
Staphylococcus aureus	Vancomycin		277781	277781
Streptococcus pneumoniae	Beta-lactam/Beta-lactamase inhibitors		2318	2318
Streptococcus pneumoniae	Carbapenem		4600	4600
Streptococcus pneumoniae	Fluoroquinolones	233	12940	13173
Streptococcus pneumoniae	Macrolide	871	20166	21037
Streptococcus pneumoniae	Penicillin	9172	44986	54158
Streptococcus pneumoniae	Third-generation cephalosporins	5100	37484	42584
Streptococcus pneumoniae	Trimethoprim-Sulfamethoxazole		9386	9386
TOTAL		82007	9627436	9709443

Pathogen	mates for sterile sources of specimen across 88 pathogen-drug	Sample size Mean relative risk	Lower be	ound Upper b	ound
Acinetobacter baumannii	Anti-pseudomonal penicillin/Beta-lactamase inhibitors	948	1.31	1.12	1.5
Acinetobacter baumannii	Beta-lactam/Beta-lactamase inhibitors	1555	1.27	1.11	1.4
Acinetobacter baumannii	Carbapenem	3232	1.42	1.27	1.5
Acinetobacter baumannii	Fourth-generation cephalosporins	1439	1.31	1.14	1.5
Acinetobacter baumannii	Third-generation cephalosporins	2055	1.35	1.13	1.6
Acinetobacter baumannii	Aminoglycosides	2066	1.1	0.97	1.2
Acinetobacter baumannii	Fluoroquinolones	3020	1.38	1.21	1.5
Citrobacter spp.	Aminoglycosides	4069	1.09	0.94	1.2
Citrobacter spp.	Anti-pseudomonal penicillin/Beta-lactamase inhibitors	3127	1.32	1.14	1.5
Citrobacter spp.	Carbapenem	3097	1.48	1.25	1.7
Citrobacter spp.	Fluoroquinolones	4387	1.36	1.18	1.5
Citrobacter spp.	Fourth-generation cephalosporins	2718	1.31	1.1	1.5
Citrobacter spp.	Third-generation cephalosporins	3984	1.38	1.16	1.6
Enterobacter spp.	Aminoglycosides	15211	1.19	1.06	1.3
Enterobacter spp.	Anti-pseudomonal penicillin/Beta-lactamase inhibitors	11857	1.23	1.13	1.3
Enterobacter spp.	Carbapenem	13299	1.53	1.4	1.6
Enterobacter spp.	Fluoroquinolones	17552	1.28	1.17	1.
Enterobacter spp.	Fourth-generation cephalosporins	11482	1.31	1.18	1.4
Enterobacter spp.		14798	1.09		1.4
**	Trimethoprim-Sulfamethoxazole			0.98	
Enterococcus faecalis	Fluoroquinolones	1126	1.43	1.24	1.6
Enterococcus faecalis	Vancomycin	36	1.7	1.39	2.0
Enterococcus faecium	Fluoroquinolones	4082	1.37	1.14	1.6
Enterococcus faecium	Vancomycin	9242	1.54	1.39	1.
Other Enterococci	Fluoroquinolones	107	1.28	1.07	1.5
Other Enterococci	Vancomycin	7730	1.37	1.29	1.4
Escherichia coli	Aminoglycosides	164196	1.2	1.16	1.2
Escherichia coli	Aminopenicillin	157276	1.21	1.17	1.2
Escherichia coli	Beta-lactam/Beta-lactamase inhibitors	143458	1.15	1.11	1.1
Escherichia coli	Carbapenem	131382	1.7	1.5	1.9
Escherichia coli	Trimethoprim-Sulfamethoxazole	164240	1.14	1.11	1.1
Group A Streptococcus	Macrolide	130	1.07	0.89	1.2
Group B Streptococcus	Fluoroquinolones	44	1.26	1.04	1.5
Group B Streptococcus	Macrolide	465	1.18	0.99	1.4
Group B Streptococcus	Penicillin	15	1.29	1.06	1.5
Haemophilus influenzae	Aminopenicillin	1438	1.27	1.06	1.5
		308	1.48		
Haemophilus influenzae	Third-generation cephalosporins			1.23	1.7
Klebsiella pneumoniae	Aminoglycosides	51811	1.24	1.17	1.3
Klebsiella pneumoniae	Beta-lactam/Beta-lactamase inhibitors	46753	1.19	1.13	1.2:
Klebsiella pneumoniae	Fluoroquinolones	53414	1.19	1.12	1.2
Klebsiella pneumoniae	Trimethoprim-Sulfamethoxazole	51737	1.12	1.06	1.19
Morganella spp.	Fluoroquinolones	3290	1.26	1.1	1.4
Morganella spp.	Fourth-generation cephalosporins	2352	1.23	1.02	1.4
Morganella spp.	Third-generation cephalosporins	3407	1.33	1.12	1.5
Proteus spp.	Aminoglycosides	21844	1.1	1.01	1.3
Proteus spp.	Aminopenicillin	20638	1.01	0.94	1.0
Proteus spp.	Fluoroquinolones	22141	1.13	1.05	1.2
Proteus spp.	Trimethoprim-Sulfamethoxazole	21838	1.06	0.98	1.1
Proteus spp.	Third-generation cephalosporins	18775	1.27	1.08	1.:
Pseudomonas aeruginosa	Aminoglycosides	39341	1.03	0.98	1.09
		36016	1.3	1.22	1.3
Pseudomonas aeruginosa	Anti-pseudomonal penicillin/Beta-lactamase inhibitors				
Pseudomonas aeruginosa	Carbapenem	41177	1.27	1.22	1.32
Pseudomonas aeruginosa	Fluoroquinolones	47417	1.19	1.15	1.2
Pseudomonas aeruginosa	Fourth-generation cephalosporins	34020	1.24	1.17	1.3
Pseudomonas aeruginosa	Third-generation cephalosporins	31041	1.35	1.15	1.59
Serratia spp.	Aminoglycosides	5250	1.05	0.93	1.15
Serratia spp.	Anti-pseudomonal penicillin/Beta-lactamase inhibitors	3003	1.17	1.01	1.3
Serratia spp.	Carbapenem	3639	1.39	1.2	1.6
Serratia spp.	Fluoroquinolones	5252	1.09	0.94	1.2
Serratia spp.	Fourth-generation cephalosporins	3928	1.17	0.99	1.3
Serratia spp.	Third-generation cephalosporins	5960	1.29	1.09	1.5
Staphylococcus aureus	Fluoroquinolones	37963	1.07	1.02	1.1
Staphylococcus aureus	Macrolide	53005	1.06	1.02	1.0
Staphylococcus aureus	Trimethoprim-Sulfamethoxazole	59632	1.17	1.09	1.2
Streptococcus pneumoniae	Beta-lactam/Beta-lactamase inhibitors	1419	1.14	0.95	1.3
Streptococcus pneumoniae	Carbapenem		1.37		
• •	*****	1947		1.16	1.6
Streptococcus pneumoniae	Fluoroquinolones	6499	1.23	1.05	1.4
Streptococcus pneumoniae	Macrolide	7348	1.05	0.94	1.1
Streptococcus pneumoniae	Trimethoprim-Sulfamethoxazole	5413	1.14	1.01	1.2
Streptococcus pneumoniae	Third-generation cephalosporins	10457	1.33	1.13	1.5
Escherichia coli	Fluoroquinolones	171311	1.31	1.27	1.3
Escherichia coli	Third-generation cephalosporins	163801	1.37	1.17	1.6
Klebsiella pneumoniae	Carbapenem	41943	1.68	1.56	1.8
Klebsiella pneumoniae	Third-generation cephalosporins	52090	1.36	1.16	1.
Aycobacterium tuberculosis	Extensive drug resistance	428524	2.59	2.46	2.7
Aycobacterium tuberculosis	Isoniazid mono-resistance	14537	1.19	0.84	1.6
Aycobacterium tuberculosis	Multidrug resistance	427342	2.5	1.17	4.7
Mycobacterium tuberculosis	Rifampicin mono-resistance	7161	1.39	1.06	1.7
Non-typhoidal Salmonella	Fluoroquinolones	42	1.23	1.01	1.
Calmonella Paratyphi	Fluoroquinolones	24	1.24	1.02	1.5
Salmonella Paratyphi	Multidrug resistance	25	1.24	1.03	1.
Salmonella Typhi	Fluoroquinolones	24	1.24	1.02	1.5
Salmonella Typhi	Multidrug resistance	25	1.24	1.03	1.
Shigella spp.	Fluoroquinolones	24	1.24	1.02	1.52
Staphylococcus aureus	Methicillin	95696	1.43	1.2	1.1
Streptococcus pneumoniae	Penicillin	30849	1.27	1.18	1.3
	Vancomycin	53623	1.52	1.28	1.8
Staphylococcus aureus					

GBD region	All-cause death counts	All-cause death rate per 100 I	raction of all deaths that	Death counts involving infection	Death rate per 100 000	Fraction of deaths	Death counts associated with	Death rate per 100 000	Fraction of deaths	Death counts attributable to	Death rate per 100 000
322.1.		000	involve infection	•	involving infection	involving infection that are associated with resistance	resistance	associated with resistance	involving infection that are attributable to resistance	resistance	attributable to resistance
Central Asia	637,000 (587,000-697,000)	681.5 (628.0-744.7)	16.1% (11.9%-21.5%)	102,000 (74,200-140,000)	109.5 (79.3-150.1)	48.6% (46.7%-50.2%)	49,800 (35,300-69,500)	53.3 (37.7-74.3)	12.6% (11.1%-14.3%)	12,900 (8,870-18,200)	13.8 (9.5-19.5)
Central Europe	1,370,000 (1,230,000-1,520,000)	1201.3 (1074.6-1329.3)	11.5% (7.9%-16.1%)	157,000 (106,000-227,000)	137.8 (92.5-198.7)	49.1% (46.6%-51.5%)	77,600 (49,400-115,000)	68.0 (43.2-100.9)	12.0% (10.7%-13.4%)	19,000 (12,000-28,500)	16.6 (10.5-25.0)
Eastern Europe	2,730,000 (2,520,000-2,970,000)	1300.9 (1202.0-1415.4)	11.5% (8.1%-16.0%)	315,000 (217,000-434,000)	150.0 (103.5-206.6)	49.2% (46.7%-51.6%)	155,000 (103,000-222,000)	74.0 (48.8-105.6)	13.3% (11.7%-15.0%)	41,800 (27,600-59,900)	19.9 (13.1-28.5)
Australasia	205,000 (202,000-209,000)	706.6 (695.7-717.7)	12.7% (8.9%-17.6%)	26,200 (18,400-36,100)	90.0 (63.2-124.4)	31.0% (29.2%-32.8%)	8,140 (5,460-11,600)	28.0 (18.8-39.9)	7.2% (6.2%-8.2%)	1,880 (1,250-2,730)	6.5 (4.3-9.4)
High-income Asia Pacific	1,740,000 (1,730,000-1,760,000)	931.0 (921.9-940.3)	18.3% (14.2%-23.1%)	319,000 (248,000-405,000)	170.2 (132.5-216.0)	41.5% (39.6%-43.4%)	132,000 (99,700-173,000)	70.7 (53.2-92.3)	9.7% (7.9%-11.5%)	30,900 (21,700-43,300)	16.5 (11.6-23.1)
High-income North America	3,240,000 (3,210,000-3,260,000)	887.4 (881.1-893.8)	13.8% (10.0%-18.9%)	448,000 (323,000-612,000)	122.8 (88.7-167.9)	41.4% (39.5%-43.2%)	186,000 (129,000-261,000)	51.0 (35.4-71.5)	10.0% (8.6%-11.5%)	44,800 (30,300-63,900)	12.3 (8.3-17.5)
Southern Latin America	496,000 (485,000-507,000)	742.7 (726.9-760.0)	22.7% (18.1%-28.4%)	112,000 (89,800-141,000)	168.3 (134.5-210.8)	42.8% (40.9%-44.9%)	48,200 (36,800-62,300)	72.3 (55.1-93.4)	11.0% (9.5%-12.6%)	12,400 (9,280-16,500)	18.6 (13.9-24.7)
Western Europe	4,280,000 (4,240,000-4,320,000)	979.9 (970.7-989.4)	14.3% (10.7%-19.1%)	613,000 (457,000-816,000)	140.5 (104.7-186.9)	37.2% (34.9%-39.6%)	229,000 (162,000-318,000)	52.5 (37.0-73.0)	8.3% (7.3%-9.4%)	51,100 (35,100-72,400)	11.7 (8.0-16.6)
Andean Latin America	321,000 (270,000-381,000)	504.6 (423.9-599.2)	27.3% (22.0%-33.7%)	87,500 (64,700-116,000)	137.6 (101.7-182.1)	45.9% (43.3%-48.0%)	40,200 (28,900-54,300)	63.2 (45.4-85.4)	11.5% (10.1%-13.2%)	10,100 (7,050-13,900)	15.9 (11.1-21.9)
Caribbean	379,000 (335,000-427,000)	804.0 (709.5-905.2)	22.5% (17.5%-28.6%)	85,200 (63,900-112,000)	180.6 (135.5-237.8)	35.9% (32.9%-38.8%)	30,700 (21,500-42,700)	65.1 (45.5-90.5)	8.9% (7.7%-10.2%)	7,630 (5,200-10,900)	16.2 (11.0-23.2)
Central Latin America	1,430,000 (1,260,000-1,630,000)	573.2 (503.8-651.2)	19.9% (14.7%-26.5%)	285,000 (204,000-391,000)	113.9 (81.4-156.2)	44.3% (42.0%-46.3%)	127,000 (86,700-177,000)	50.6 (34.7-70.9)	11.4% (10.0%-13.0%)	32,600 (22,000-46,200)	13.0 (8.8-18.5)
Tropical Latin America	1,450,000 (1,410,000-1,490,000)	646.3 (629.1-664.3)	22.0% (17.2%-27.9%)	318,000 (249,000-404,000)	142.2 (111.5-180.6)	44.2% (42.3%-46.1%)	141,000 (105,000-186,000)	63.0 (47.1-83.1)	10.7% (9.6%-11.9%)	34,000 (24,800-46,000)	15.2 (11.1-20.6)
North Africa and Middle East	3,100,000 (2,820,000-3,420,000)	509.7 (462.6-561.1)	18.1% (13.2%-24.2%)	563,000 (402,000-774,000)	92.5 (66.0-127.1)	45.3% (42.6%-47.7%)	256,000 (174,000-362,000)	42.0 (28.7-59.5)	12.1% (10.7%-13.5%)	68,300 (45,600-99,000)	11.2 (7.5-16.3)
South Asia	11,900,000 (10,900,000-13,000,000)	661.3 (604.0-721.0)	31.8% (26.0%-39.2%)	3,800,000 (3,040,000-4,730,000)	210.6 (168.3-262.2)	36.4% (30.8%-41.4%)	1,390,000 (1,030,000-1,830,000)	76.8 (57.2-101.2)	10.2% (8.1%-12.7%)	389,000 (273,000-538,000)	21.5 (15.1-29.8)
East Asia	11,100,000 (9,730,000-12,500,000)	752.3 (661.0-848.3)	12.2% (8.2%-17.5%)	1,350,000 (900,000-2,000,000)	91.6 (61.2-135.8)	47.1% (44.6%-49.2%)	638,000 (404,000-973,000)	43.3 (27.4-66.1)	11.4% (9.9%-13.0%)	154,000 (96,000-235,000)	10.5 (6.5-16.0)
Oceania	97,200 (80,000-118,000)	732.4 (602.3-891.7)	33.1% (27.0%-40.4%)	32,200 (23,300-42,900)	242.6 (175.7-323.3)	29.5% (24.9%-33.0%)	9,500 (6,820-13,000)	71.6 (51.4-98.0)	7.0% (5.7%-8.3%)	2,260 (1,610-3,080)	17.0 (12.1-23.2)
Southeast Asia	4,390,000 (4,010,000-4,750,000)	651.3 (595.7-704.9)	25.8% (20.8%-32.0%)	1,130,000 (899,000-1,440,000)	168.2 (133.4-213.7)	32.4% (28.8%-35.7%)	369,000 (262,000-505,000)	54.8 (38.9-74.9)	8.5% (7.3%-9.9%)	97,000 (67,500-135,000)	14.4 (10.0-20.0)
Central Sub-Saharan Africa	872,000 (748,000-1,010,000)	662.8 (568.6-769.2)	48.0% (40.2%-56.1%)	418,000 (335,000-520,000)	317.7 (254.9-395.6)	27.0% (24.3%-30.1%)	113,000 (86,600-144,000)	86.0 (65.9-109.8)	6.5% (5.3%-8.1%)	27,200 (19,600-36,400)	20.7 (14.9-27.7)
Eastern Sub-Saharan Africa	2,590,000 (2,340,000-2,900,000)	628.3 (568.1-703.1)	50.7% (43.1%-58.8%)	1,310,000 (1,080,000-1,610,000)	318.9 (261.3-390.1)	27.9% (25.6%-30.1%)	366,000 (290,000-464,000)	89.0 (70.5-112.6)	6.7% (5.7%-7.9%)	88,200 (67,000-116,000)	21.4 (16.3-28.1)
Southern Sub-Saharan Africa	732,000 (688,000-787,000)	932.2 (875.3-1002.1)	45.6% (38.4%-52.7%)	334,000 (276,000-399,000)	425.4 (351.5-507.4)	18.6% (16.6%-20.9%)	62,400 (48,400-79,800)	79.4 (61.7-101.6)	4.6% (3.7%-5.7%)	15,300 (11,300-20,400)	19.4 (14.3-25.9)
Western Sub-Saharan Africa	3,460,000 (3,070,000-3,940,000)	757.8 (672.5-864.4)	53.5% (45.4%-62.0%)	1,850,000 (1,510,000-2,270,000)	405.5 (331.6-497.6)	28.3% (25.4%-30.8%)	524,000 (412,000-663,000)	114.8 (90.4-145.3)	6.7% (5.7%-7.7%)	125,000 (95,400-161,000)	27.3 (20.9-35.3)

Table S12. GATHER checklist

Item #	Checklist item	Reporting location:
	ves and funding	
1	Define the indicator(s), populations (including age, sex, and geographic entities), and time period(s) for which estimates were made.	Main text methods section (overview)
2	List the funding sources for the work.	Main text funding statement and acknowledgements
Data In	puts	
	l data inputs from multiple sources that are synthesized as part of the study:	
3	Describe how the data were identified and how the data were accessed.	Main text methods section + supplementary appendix (sections 2, 4.1, 5.1, 6.1, 7.1, 8.1)
4	Specify the inclusion and exclusion criteria. Identify all ad-hoc exclusions.	Supplementary appendix (section 2)
5	Provide information on all included data sources and their main characteristics. For each data source used, report reference information or contact name/institution, population represented, data collection method, year(s) of data collection, sex and age range, diagnostic criteria or measurement method, and sample size, as relevant.	Some data source information in supplementary appendix (section 2); main characteristics of data, metadata, and/or NIDs available at http://ghdx.healthdata.org/record/ihme-data/global-bacterial-antimicrobial-resistance-burden-estimates-2019
6	Identify and describe any categories of input data that have potentially important biases (e.g., based on characteristics listed in item 5).	Main text limitations section + supplementary appendix (biases for input data in each modelling step identified in each section)
For do	ata inputs that contribute to the analysis but were not synthesized as part of the study:	
	Describe and give sources for any other data inputs.	GBD 2019 estimates (http://ghdx.healthda ta.org/gbd-results- tool)
For al	ll data inputs:	
8	Provide all data inputs in a file format from which data can be efficiently extracted (e.g., a spreadsheet rather than a PDF), including all relevant meta-data listed in item 5. For any data inputs that cannot be shared because of ethical or legal reasons, such as third-party ownership, provide a contact name or the name of the institution that retains the right to the data.	Data inputs and/or contact information available at http://ghdx.healthdata.org/record/ihme-data/global-bacterial-antimicrobial-resistance-burden-estimates-2019
Data an		
9	Provide a conceptual overview of the data analysis method. A diagram may be helpful.	Main text methods section + main text figure 1 (flowchart of methods)
10	Provide a detailed description of all steps of the analysis, including mathematical formulae. This description should cover, as relevant, data cleaning, data pre-processing, data adjustments and weighting of data sources, and mathematical or statistical model(s).	Supplementary appendix (sections 4–9)

11	Describe how candidate models were evaluated and how the final model(s) were selected.	Supplementary appendix (sections 4–8)
12	Provide the results of an evaluation of model performance, if done, as well as the results of any relevant sensitivity analysis.	Supplementary appendix (sections 4.7, 6.5, 7.6, 8.4)
13	Describe methods for calculating uncertainty of the estimates. State which sources of uncertainty were, and were not, accounted for in the uncertainty analysis.	Main text methods section (uncertainty analysis) + limitations section (scarcity of data) + supplementary appendix (sections 4–8)
14	State how analytic or statistical source code used to generate estimates can be accessed.	GitHub code found at: http://ghdx.healthdata.org/record/hme-data/global-bacterial-antimicrobial-resistance-burden-estimates-2019
Results	and Discussion	
15	Provide published estimates in a file format from which data can be efficiently extracted.	CSVs of tabulated estimates are available at: http://ghdx.healthdata.org/record/ihme-data/global-bacterial-antimicrobial-resistance-burden-estimates-2019
16	Report a quantitative measure of the uncertainty of the estimates (e.g. uncertainty intervals).	UIs provided for all estimates throughout the main text (summary, results, and discussion sections)
17	Interpret results in light of existing evidence. If updating a previous set of estimates, describe the reasons for changes in estimates.	Main text introduction and discussion sections
18	Discuss limitations of the estimates. Include a discussion of any modelling assumptions or data limitations that affect interpretation of the estimates.	Main text limitations section + supplementary appendix (sections 4–8; table S21)

Table S13. GBD location hierarchy with levels	
Location	level
Global	0
Central Europe, eastern Europe, and central Asia	1
Central Asia	2
Armenia	3
Azerbaijan	3
Georgia	3
Kazakhstan	3
Kyrgyzstan	3
Mongolia	3
Tajikistan	3
Turkmenistan	3
Uzbekistan	3
Central Europe	2
Albania	3
Bosnia and Herzegovina	3
Bulgaria	3
Croatia	3
Czechia	3
Hungary	3
Montenegro	3
North Macedonia	3
Poland	3
Romania	3
Serbia	3
Slovakia	3
Slovenia	3
Eastern Europe	2
Belarus	3
Estonia	3
Latvia	3
Lithuania	3
Moldova	3
Russia	3
Ukraine	3
High income	1
Australasia	2
Australia	3
New Zealand	3

High-income Asia Pacific	2
Brunei	3
Japan	3
Singapore	3
South Korea	3
High-income North America	2
Canada	3
Greenland	3
USA	3
Southern Latin America	2
Argentina	3
Chile	3
Uruguay	3
Western Europe	2
Andorra	3
Austria	3
Belgium	3
Cyprus	3
Denmark	3
Finland	3
France	3
Germany	3
Greece	3
Iceland	3
Ireland	3
Israel	3
Italy	3
Luxembourg	3
Malta	3
Monaco	3
Netherlands	3
Norway	3
Portugal	3
San Marino	3
Spain	3
Sweden	3
Switzerland	3
UK	3
Latin America and Caribbean	1
Andean Latin America	2
Bolivia	3
Ecuador	3
Peru Caribbean	3 2
Caribbean Antigua and Barbuda	3
Anugua and Barbuda The Bahamas	3
The Banamas Barbados	3
ม _ิ สเขสนบร	3

Belize	
	3
Bermuda	3
Cuba	3
Dominica	3
Dominican Republic	3
Grenada	3
Guyana	3
Haiti	3
Jamaica	3
Puerto Rico	3
Saint Kitts and Nevis	3
Saint Lucia	3
Saint Vincent and the Grenadines	3
Suriname	3
Trinidad and Tobago	3
Virgin Islands	3
Central Latin America	
Colombia	2
	3
Costa Rica	3
El Salvador	3
Guatemala	3
Honduras	3
Mexico	3
Nicaragua	3
Panama	3
Venezuela	3
Tropical Latin America	2
Brazil	3
Paraguay	3
North Africa and Middle East	1
North Africa and Middle East	2
Afghanistan	3
-	
Algeria	3
	3
Algeria	
Algeria Bahrain	3
Algeria Bahrain Egypt	3
Algeria Bahrain Egypt Iran	3 3 3
Algeria Bahrain Egypt Iran Iraq	3 3 3 3
Algeria Bahrain Egypt Iran Iraq Jordan	3 3 3 3
Algeria Bahrain Egypt Iran Iraq Jordan Kuwait	3 3 3 3 3
Algeria Bahrain Egypt Iran Iraq Jordan Kuwait Lebanon	3 3 3 3 3 3
Algeria Bahrain Egypt Iran Iraq Jordan Kuwait Lebanon	3 3 3 3 3 3
Algeria Bahrain Egypt Iran Iraq Jordan Kuwait Lebanon Libya Morocco	3 3 3 3 3 3 3
Algeria Bahrain Egypt Iran Iraq Jordan Kuwait Lebanon Libya Morocco Oman	3 3 3 3 3 3 3 3
Algeria Bahrain Egypt Iran Iraq Jordan Kuwait Lebanon Libya Morocco Oman Palestine	3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3
Algeria Bahrain Egypt Iran Iraq Jordan Kuwait Lebanon Libya Morocco Oman Palestine Qatar	3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3

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Tunisia	3
Turkey	3
United Arab Emirates	3
Yemen	3
South Asia	1
South Asia	2
Bangladesh	3
Bhutan	3
India	3
Nepal	3
Pakistan	3
Southeast Asia, east Asia, and Oceania	1
East Asia	2
China	3
North Korea	3
Taiwan (province of China)	3
Oceania	2
American Samoa	3
Cook Islands	3
Fiji	3
Guam	3
Kiribati	3
Marshall Islands	3
Federated States of Micronesia	
Nauru	3
Niue Northern Mariana Islands	3
	3
Palau	3
Papua New Guinea	3
Samoa	3
Solomon Islands	3
Tokelau	3
Tonga	3
Tuvalu	3
Vanuatu	3
Southeast Asia	2
Cambodia	3
Indonesia	3
Laos	3
Malaysia	3
Maldives	3
Mauritius	3
Myanmar	3
Philippines	3
Seychelles	3
Sri Lanka	3
Thailand	3
Timor-Leste	3

Vietnam	3
Sub-Saharan Africa	1
Central sub-Saharan Africa	2
Angola	3
Central African Republic	3
Congo (Brazzaville)	3
DR Congo	3
Equatorial Guinea	3
Gabon	3
Burundi	3
Comoros	3
Djibouti	3
Eritrea	3
Ethiopia	3
Kenya	3
Madagascar	3
Malawi	3
Mozambique	3
Rwanda	3
Somalia	3
South Sudan	3
Uganda	3
Tanzania	3
Zambia	3
Southern sub-Saharan Africa	2
Botswana	3
Botswana Eswatini	3
Eswatini	3
Eswatini Lesotho	3
Eswatini Lesotho Namibia	3 3 3
Eswatini Lesotho Namibia South Africa	3 3 3
Eswatini Lesotho Namibia South Africa Zimbabwe	3 3 3 3 3
Eswatini Lesotho Namibia South Africa Zimbabwe Western sub-Saharan Africa	3 3 3 3 2
Eswatini Lesotho Namibia South Africa Zimbabwe Western sub-Saharan Africa Benin	3 3 3 3 2 2
Eswatini Lesotho Namibia South Africa Zimbabwe Western sub-Saharan Africa Benin Burkina Faso	3 3 3 3 2 2 3
Eswatini Lesotho Namibia South Africa Zimbabwe Western sub-Saharan Africa Benin Burkina Faso Cape Verde	3 3 3 3 2 3 3 3
Eswatini Lesotho Namibia South Africa Zimbabwe Western sub-Saharan Africa Benin Burkina Faso Cape Verde Cameroon	3 3 3 3 2 3 3 3 3
Eswatini Lesotho Namibia South Africa Zimbabwe Western sub-Saharan Africa Benin Burkina Faso Cape Verde Cameroon Chad	3 3 3 3 2 2 3 3 3 3 3
Eswatini Lesotho Namibia South Africa Zimbabwe Western sub-Saharan Africa Benin Burkina Faso Cape Verde Cameroon Chad Côte d'Ivoire	3 3 3 3 3 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3
Eswatini Lesotho Namibia South Africa Zimbabwe Western sub-Saharan Africa Benin Burkina Faso Cape Verde Cameroon Chad Côte d'Ivoire The Gambia	3 3 3 3 3 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3
Eswatini Lesotho Namibia South Africa Zimbabwe Western sub-Saharan Africa Benin Burkina Faso Cape Verde Cameroon Chad Côte d'Ivoire The Gambia Ghana	3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3
Eswatini Lesotho Namibia South Africa Zimbabwe Western sub-Saharan Africa Benin Burkina Faso Cape Verde Cameroon Chad Côte d'Ivoire The Gambia Ghana Guinea	3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3
Eswatini Lesotho Namibia South Africa Zimbabwe Western sub-Saharan Africa Benin Burkina Faso Cape Verde Cameroon Chad Côte d'Ivoire The Gambia Ghana Guinea Guinea-Bissau	3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3
Eswatini Lesotho Namibia South Africa Zimbabwe Western sub-Saharan Africa Benin Burkina Faso Cape Verde Cameroon Chad Côte d'Ivoire The Gambia Ghana Guinea Guinea-Bissau Liberia	3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3
Eswatini Lesotho Namibia South Africa Zimbabwe Western sub-Saharan Africa Benin Burkina Faso Cape Verde Cameroon Chad Côte d'Ivoire The Gambia Ghana Guinea Guinea Guinea-Bissau Liberia Mali	3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3
Eswatini Lesotho Namibia South Africa Zimbabwe Western sub-Saharan Africa Benin Burkina Faso Cape Verde Cameroon Chad Côte d'Ivoire The Gambia Ghana Guinea Guinea Guinea-Bissau Liberia Mali Mauritania	3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3

Senegal	3
Sierra Leone	3
Togo	3

Table S14. Deat	hs and DALYs (in counts and	age-specific ra	tes) associated w	rith and attribut	table to bacterial	antimicrobial :	resistance by patl	hogen-drug com	bination; by age	group; 2019; co	entral Europe, ca	stern Europe, an	d central Asia super	region							1-1								
Pathogen	Antibiotic Class			with resistance	MLYx		Attributabli Deaths	le to resistance Di	MAY	п	Associated kuths	with resistance DA	LYs	And Duds	outside to resistance	DALYs		Associates Deaths			1504	Attributali Deaths	de to resistance	DALYs	Associated Deaths	with resistance	M.Ys	Deaths	antibutable to resistance DALYs
	Resistance to one or more	Counts	Rate per 100 000 1142.5 (816.3-		Rate per 100 000 301677.2 (72609.5-		Rate per 100 000 277.2 (194.4-385.8)				Rate per 100 000			Counts Rate per 1000 (809-1400) 22.0 (16.7-28.	000 Counts	Rate per 100 000	Counts	Rate per 100 000	Counts 162000 (130000-			Rate per 100 000	Counts	Rate per 100 000	Counts Rate per 100 000	Counts	Rate per 100 000	Counts Rate per	00 000 Count Rate per 100 000 -26.3) 1740000 (1180000 -26.3) 451.2 (303.4-643.2)
Advantagent	authorics Authorites	4540 (3240-6320)	1591.5) 40.3 (24.8-60.8)		141632.7) 3581.9 (2207.5- 3) 5407.9)				34326.8) 149.9 (0.3-372.2)				10400.6) 107.3 (88.6-204.2) 3 (0			2559.7) 5.7 (0.0-13.7)	77 (16 47)		204000) 2340 (1400-3690)			00 00 00 00	49900) 98 (1-241)	94(99-1.1)	39000) 57.7 (46.3-97.8) 11900 (6300-20000) 3.0 (1.6-5.1)		2414.3) 303 67.1 (36.3-114.7) 494		
hannennii Acinetobacter	Annioglycostacs Anti-pseudomoral penicillis Beta-	100 (99-241)	40.5 (24.8-00.8) 51.8 (32.1-78.1)	18300 (11300-	4906.3 (2853.8-			647 (316-1140)	162.9 (79.6-288.1)				178.3 (114.6-262.4) 3 (2			6.4 (3.1-11.0)	27 (16-43)	02 (01-02)	2990 (1820-4700)			00 (0.00.0)	105 (50-182)	0.5 (0.2-0.8)	14400 (7860-24000) 3.7 (2.0-6.1)	449000)	82.2 (44.8-137.2) 415		
hannennii Acinetobacter	Lactamuse inhibitors Beta Lactam/Beta-lactamuse	206 (127-310)	51.8 (32.1-78.1) 46.4 (28.7-69.6)	27000) 16400 (10100-	GP43.1)	7 (4-13)			162.9 (79.6-288.1) 2.3 (0.6-4.9)				178.3 (114.6-262.4) 3 (2 159.3 (101.5-231.9) 0 (0			6.4 (3.1-11.0)	38 (21-84)	02 (01-02)		13.4 (8.2-21.1)			2 (0-4)	0.5 (0.2-0.0)	14400 (7860-24000) 3.7 (2.0-6.1) 13000 (7100-21700) 3.3 (1.8-5.6)	333440)	73.9 (40.2-123.6) 40:		
haumannii Acinetobacter	inhibitors Carbanenem	184 (114-277) 171 (106-257)	46.4 (28.7-69.6) 43.1 (26.6-64.8)	24600) 15200 (9380-2290)	6294.4)	28 (14-48)		9 (3-20) 2450 (1280-4260)	2.3 (0.6-4.9) 617.9 (321.5- 1077.4)				199.3 (101.5-231.9) 0 (0 147.8 (93.7-218.1) 13 (23.8 (12.9-39.8)	31 (19-48) 29 (18-46)	01 (01-02)		12.0 (7.3-18.6)		00 (0.00.0)	2 (0-4) 405 (215-698)	1.8 (1.0-3.1)	13000 (7100-21700) 3.3 (1.8-5.6) 12500 (6860-20800) 3.2 (1.8-5.3)			(11-84) 0.0 (0.0+ 20 (980-3700) 0.5 (0.3+	
Acinetobacter Isasmennii	Phoroquinolone	193 (119-290)	48.7 (29.9-73.1)	17200 (10600- 25000)	4330.3 (2000.5- 6505.7)	25 (12-44)		2180 (1080-3920)					167.7 (106.7-247.0) 12 (21.3 (11.1-35.5)	33 (20-52)		2830 (1730-4470)			00 (0.00.0)		1.6 (0.8-2.7)	13900 (7530-23100) 3.6 (1.9-5.9)	307000 (167000- 515000)	78.7 (42.8-131.9) 174	90 (789-3180) 0.4 (0.2-4	82100) 38500 (17400- 9.9 (4.4-18.1)
Acinetobacter Isasmennii	Fourth-generation caphalosporius	198 (123-299)	49.9 (31.0-75.3)	17600 (10900- 26600 17900 (11100-	4435.8 (2755.3- 6695.4)	0 (0-0)	0.0 (0.0-0.1)		4.0 (1.5-8.4)				171.8 (110.1-252.9) 0 (0			0.2 (0.1-0.3)	33 (20-52)	0.1 (0.1-0.2)	2880 (1790-4520)			00 (0.00.0)	3 (1-6)	0.0-0.0)	14100 (7670-23600) 3.6 (2.0-6.1)	313000 (170000- 534000)	80.3 (43.5-134.4) 37	(15-74) 0.0 (0.0+	0) 751 (302-1500) 0.2 (0.1-0.4)
Activitobacter beamennii	Third-generation caphalospories	202 (125-304)	50.8 (31.4-76.6) 52.9 (32.8-79.6)	17900 (11100- 27000) 18700 (11600-	4513.5 (2767.3- 6807.9) 4703.8 (2913.5-	1 (0-1)	02 (0.1-0.5)		15.6 (5.7-30.9)				174.6 (111.7-258.3) 0 (0 181.9 (116.5-267.4) 32 (.,,,		0.6 (0.2-1.2)	34 (21-53)	02 (01-02)	2940 (1790-4610)			00 (0.00.0)	11 (4-22) 975 (570-1560)	0.0 (0.0-0.1)	14400 (7850-24000) 3.7 (2.0-6.2)			(31-179) 0.0 (0.0+	
Annensii Cindontara	Resistance to one or more antibiotics	210 (130-316)	52.9 (32.8-79.6)	28100)	7081.6) 92.1 (48.6-162.6)		0.1 (0.0-0.2)	5960 (3500-9400) 20 (0-55)	2366.9) 5.1 (0.0-13.9)	99 (64-146)			6.1 (3.0-90.8) 0 (0		2830 (1730-4420 16 (0-46)	0 58.0 (35.7-91.4)	35 (22-56)	02 (01-02)	3060 (1870-4810)	0.4 (0.2-0.7)	11 (7-18)	01 (0.00.1)	975 (570-1560) 5 (0-13)	44(2.67.0)	15300 (K360-25400) 3.9 (2.1-6.5) 138 (76-232) 0.0 (0.0-0.1)	561000)	0.9 (0.5-1.5) 8 (i		186000)
Citrobucter app.	Anti-pseudomoral penicillis Beta-	8 (4-15)	20 (1.0-3.8)	700 (107-000)	178.3 (86.8-334.9)		0.4 (0.1-0.8)		33.5 (13.0-73.9)	7 (3-13)			124 (5.9-23.3) 1 (0			24 (0.9-5.1)	7/10	00 (00-0.0)			0 (0-1)			02 (0.1-0.5)	565 (306-1040) 0.1 (0.1-0.3)		3.5 (1.9-6.4) 12		
Caronicus app.	Luctamuse inhibitors	8 (+13)	19 (1.0-3.3)		1/8.3 (86.8-334.9)		0.5 (0.2-0.9)		41.3 (18.5-83.5)				11.2 (5.7-19.8) 2 (1			28 (12-55)	2(1-5)	an (an-an)			0 (0-1)		42 (1+10) 37 (1480)	02 (0.1-0.4)	277 (190-494) 0.1 (0.1-0.5)		15(0.926) 61		
Citobacter see.	Photographology	11 (6-18)	27 (1.44.7)		296 (1253-414.3)		04(0208)		37.6 (14.9-75.4)				156(7,927.7) 1(1			24 (09-50)	3 (1-5)	00 (0000)	224 (100-437)		0.0-1)	00 00000	36 (12-77)	02 (0.1-0.5)	437 (254-250) 0.1 (0.1-0.2)	10900 (5890-18600)			.,
Citrobucter app.	Fourth-generation caphalosporius	5 (3-10)	1.4 (0.7-2.4)	487 (252-851)	122.5 (63.5-214.3)	0 (0-1)	0.1 (0.0-0.2)	26 (10-54)	6.5 (2.5-13.7)	5 (2-9)	0.1 (0.0-0.2)	411 (197-760)	8.5 (4.1-15.7) 0 (0	1) 0.0 (0.0-0.0)	22 (6-47)	0.5 (0.2-1.0)	1 (1-3)	0.0 (0.0-0.0)	117 (49-233)	0.5 (0.2-1.0)	0 (0-0)	00 (0.0-0.0)	7 (2-15)	0.0 (0.0-0.1)	228 (119-399) 0.1 (0.0-0.1)	5660 (2990-9820)	1.5 (0.8-2.5) 13	(5-27) 0.0 (0.0+	0) 330 (132-671) 0.1 (0.0-0.2)
Citrobucter app.	Third-generation cephalospories	18 (9-31)	4.4 (2.3-7.8)		395.3 (204.7-492.4)		0.5 (0.2-1.0)		41.5 (15.2-91.2)	15 (7-28)			27.2 (13.3-51.1) 2 (1			2.9 (1.0-6.3)	5 (2-10)	0.0 (0.0-0.0)	413 (169-846)	1.8 (0.8-3.8)	0 (0-1)		43 (13-102)	0.2 (0.1-0.5)	NS (465-1610) 0.2 (0.1-0.4)	38900)	5.6 (2.9-10.0) 85		
Citrobucter app.	Resistance to one or more authiotics	25 (13-43)	63 (3.3-10.8)		564.1 (292.4-963.0) 966.4 (200.3-				165.5 (79.7-302.4)	21 (11-38)			38.3 (19.3-69.2) 6 (3			11.3 (5.4-21.2)	7 (3-13)	0.0 (0.0-0.1)	578 (248-1160)		2 (1-4)			0.8 (0.3-1.6)	1260 (671-2210) 0.3 (0.2-0.6) 1370 (873-2090) 0.4 (0.2-0.5)	54000)		(177-679) 0.1 (0.0-	
Enterobacter app.	Aminophycosides	43 (26-69)	10.9 (6.6-17.4)		966.4 (590.3- 1546.1)				62.3 (16.1-129.1)	15 (10-22)			28.1 (18.9-41.1) 1 (0			1.8 (0.5-3.5)	6 (4-9)	0.0 (0.0-0.0)	520 (353-753)		0 (0-1)	00 (0.0-0.0)	34 (9-66)	0.2 (0.0-0.3)		41500)	8.3 (5.2-12.7) 89		0) 2130 (623-4240) 0.5 (0.2-1.1) 4) 21500 (11600- 5.5 (3.0-8.9)
Enterobacter app.	Lactarase inhibitors	140 (91-214)	35.4 (23.0-53.9)	12500 (8120-1900)	3145.7 (2044.1- 3) 4792.3)			1670 (904-2690)		51 (36-71)			93.8 (66.6-131.0) 7 (4			12.6 (7.3-19.5)	21 (14-29)	0.1 (0.1-0.1)	1790 (1250-2550)		3 (2-4)		243 (136-379)		6270 (4020-9170) 1.6 (1.0-2.3)	222000)		(484-1440) 0.2 (0.1+	34100)
Enterobacter app.	Carbapenens	37 (23-57) 48 (30-75)	93 (5.9-14.4)	3290 (2080-5070) 4240 (2670-6690)	829.5 (524.2- 1277.7) 9966.5 (671.8- 1682.5)	9 (5-15)	23 (1.3-3.8)	817 (459-1350)	205.7 (115.6-338.7) 109.3 (53.5-198.7)	14 (10-20)	0.3 (0.2-0.4)		25.0 (17.7-36.3) 3 (2 31.8 (21.0-45.5) 2 (1		301 (185-460) 159 (81-277)	62 (38-95) 33 (17-57)	5 (4-8)	00 (000.0)	475 (328-678) 610 (398-897)	2.1 (1.5-3.0)	1 (1-2)	00 (0000)	118 (72-181) 63 (31-180)	05(0303)	1410 (891-2120) 0.4 (0.2-0.5) 1830 (1140-2790) 0.5 (0.3-0.7)	500001		(211-579) 0.1 (0.1- (100-345) 0.1 (0.0-	1) 8790 (9030-14100) 2.2 (1.3-3.6) 1) 4630 (2310-8180) 1.2 (0.6-2.1)
Enterobacter app.	Fourth-generation caphalosporius	123 (80-184)	31.0 (20.0-46.4)	10900 (7080-1640)	2754.1 (1783.1-	7 (3-12)	1.6 (0.8-3.0)	434 (212-789) 579 (269-1060)	145.7 (67.6-266.4)	45 (32-64)			82.6 (58.3-116.5) 2 (1		211 (106-367)	44 (22-7.6)	18 (13-26)	0.1 (0.1-0.1)	1590 (1110-2240)		1 (0-1)	00 (0.000)	85 (43-149)	0.4 (0.2-0.7)	1500 (140-270) 0.5 (0.5-0.1) 5500 (5420-8220) 1.4 (0.9-2.1)	66(900)	33.9 (20.5-50.8) 274		1) 4630 (2310-8180) 1.2 (0.6-2.1) 1) 6690 (3030-12100) 1.7 (0.8-3.1)
Enterobacter app.	Trimethopeim-Sulfamethosaasik	130 (83-202)	32.7 (20.9-50.8)	11600 (7360-1790)	2908.4 (1854.3-	8 (0-17)		704 (0-1500)	177.2 (0.0-378.2)	46 (32-66)			84.7 (58.6-120.4) 3 (0			5.1 (0.0-11.1)	18 (13-26)	0.1 (0.1-0.1)	1580 (1110-2240)		1 (0-2)	00 (0.0-0.0)	96 (0-206)	0.4 (0.0-0.9)	4300 (2690-6300) 1.1 (0.7-1.6)	299000) 204000 (62900- 155000)	26.7 (16.4-39.8) 254	(0-545) 0.1 (0.0-	1) 6270 (0-13400) 1.6 (0.0-3.4)
Enterobacter app.	Resistance to one or more antibiotics	230 (152-349)	57.8 (38.2-87.8)	20400 (13500- 31000)	5043.9 (5400.5-	50 (31-76)		4450 (2750-6740)	1120.6 (693.5- 1698.2)	84 (60-115)	1.7 (1.2-2.4)	7400 (5300-10200)	153.0 (109.6-210.4) 18 (3-26) 0.4 (0.3-0.5)	1620 (1116-2330	33.5 (23.0-48.1)	33 (23-47)	0.1 (0.1-0.2)	2900 (2050-4050)	13.0 (9.2-18.3)	7 (5-11)	00 (0.0-0.0)	638 (428-924)	2.9 (1.9-4.1)	9290 (5810-13300) 2.4 (1.5-3.4)	324000)		10 (1240-3100) 0.5 (0.3-4	75500)
Enterococcus faeculis	Planroquinolones	93 (61-141)	23.3 (15.4-35.5)	8250 (5450-12600)	2078.3 (1371.0- 3165.4)		5.8 (2.6-10.2)	2060 (924-3610)	518.6 (232.8-907.9)	21 (12-33)	0.4 (0.3-0.7)		38.2 (22.8-61.8) 5 (2		455 (202-843)	9.4 (4.2-17.4)	10 (6-17)	0.0 (0.0-0.1)	992 (591-1610)		3 (1-5)	0.0-0.0)	231 (104-426)	1.0 (0.5-1.9)	10200 (5880-15900) 2.6 (1.5-4.1)	400000)		10 (1140-4620) 0.7 (0.3-	114000)
Enterococcus faeculis	Vancomycin Resistance to one or more	N (5-13)	2.0 (1.3-3.2)		180.4 (111.6-285.4) 2143.5 (1415.6-		0.6 (0.3-1.2) 6.4 (3.2-11.0)		54.0 (22.9-103.9)				3.2 (1.9-5.4) 1 (0			0.9 (0.4-1.9)	1 (0-2)	0.000.0)	83 (48-142)		0 (0-1)	0.00000		0.1 (0.0-0.2)	739 (417-1200) 0.2 (0.1-0.3)			(86-420) 0.1 (0.0-	
Enterococcus fascalis Enterococcus fasciam	Resistance to one or more ambiotics	96 (63-145)	24.1 (15.9-36.6)	8510 (5620-12900)	3259.0) 2244.9 (1454.9- 3564.7)	26 (13-44)		2270 (1140-3880) 1740 (529-3340)			0.4 (0.3-0.7)		39.3 (23.5-63.4) 6 (3 77.7 (45.7-127.2) 8 (2			10.4 (5.1-18.6) 15.2 (4.5-31.8)	11 (6-18)	0.0 (0.0-0.1)	1020 (607-1640) 1660 (842-2930)		3 (1-5) 4 (1-8)	00/0000		1.1 (0.5-2.1)	1990 (8010-16200) 2.7 (1.5-4.2) 19900 (11500- 28700) 4.8 (2.9-7.3)	409000) 469000 (280000-	68.0 (39.7-104.8) 275	10 (1320-4940) 0.7 (0.3- 10 (3060-7080) 0.9 (0.3-	3) 123000) 18.0 (8.7-31.2) 8) 99900 (26500- 178000) 23.3 (6.8-45.6)
Enterococcus faeciam		22 (13-37)	5.5 (3.4-9.2)	1960 (1200-3250)	3564.7) 494.1 (301.9-818.8)	5 (2-10)			115.0 (53.7-217.7)				17.7 (9.8-30.0) 2 (1			41 (19-81)	4 (2-8)	00 (00-0.0)	377 (188-688)		1 (0-2)	00 (0.00.0)	88 (35-190)	04 (0.2-0.8)	29700) 4620 (2790-7160) 1.2 (0.7-1.8)			10 (492-1920) 0.3 (0.1-	
Enterococcus faeciam	Resistance to one or more	100 (65-159)	25.3 (16.4-40.0)	8950 (5800-14200)	2253.6 (1460.2-	25 (12-44)	62 (3.0-11.2)	2200 (1080-3950)	554.0 (271.1-994.4)	43 (25-69)			78.0 (45.9-127.4) 11 (932 (413-1810)	19.3 (8.5-37.4)	19 (10-34)	0.1 (0.0-0.2)		7.4 (3.8-13.1)	5 (2-10)	00(0.00.0)	411 (169-864)	1.8 (0.8-3.9)	19900 (11600- 19700) 4.9 (3.0-7.4)	170000)		0 (2290-8180) 1.2 (0.6-	
Other enterococci	Planroquinolones	86 (49-143)	21.7 (12.3-35.9)	7680 (4340-12700)	3571.3) 2933.1 (1091.8- 3190.4)	17 (2-33)	4.2 (0.6-8.4)	1470 (211-2990)	369.7 (53.0-749.2)	24 (12-43)	0.5 (0.3-0.9)	2140 (1100-3780)	44.3 (22.7-78.2) 5 (1	10) 0.1 (0.0-0.2)	408 (60-877)	8.4 (1.2-18.1)	9 (4-18)	0.0 (0.0-0.1)	839 (432-1990)	3.8 (1.9-7.1)	2 (0-4)	00 (0.0-0.0)	155 (25-346)	0.7 (0.1-1.5)	4670 (2730-7330) 1.2 (0.7-1.9)	98400 (57700- 156000)	25.2 (14.8-40.0) 883	(123-1760) 0.2 (0.0-	5) 18500 (2650-37200) 4.8 (0.7-9.5)
Other enterococci	Vancomycin		2.2 (1.3-3.7)		197.5 (111.2-327.8)				34.1 (16.2-67.3)				4.9 (2.5-8.8) 0 (0		41 (17-85)	0.8 (0.4-1.8)	1 (0-2)	0.0 (0.0-0.0)	102 (50-199)		0 (0-0)	0.0-0.0)		0.1 (0.0-0.2)	708 (405-1160) 0.2 (0.1-0.3)			(59-240) 0.0 (0.0-	
Other enterococci	authorics	87 (49-143) 220 (156-313)	21.8 (12.3-36.0) 55.4 (39.2-78.8)		2939.4 (1093.0- 3198.8) 4937.8 (3494.0- 3013.4)	18 (5-35) 13 (8-19)		1600 (413-3130) 1150 (744-1680)					44.4 (22.8-78.5) 5 (1 199.4 (152.3-261.2) 6 (4			9.3 (2.2-19.1) 11.6 (8.1-16.2)	9 (4-18) 48 (36-64)	0.0 (0.0-0.1)	843 (435-1600) 4530 (3460-5980)			0.000000	173 (47-372) 260 (180-360)	0.8 (0.2-1.7)	4700 (2740-7430) 1.2 (0.7-1.9) 17900 (11000- 4.6 (2.8-6.8)	1560001 409000 (253000-	25.4 (14.9-40.1) 301	00 (311-1890) 0.3 (0.1- 00 (999-1690) 0.3 (0.2-	5) 21100 (8500-39900) 5.4 (1.7-10.2) 4) 24100 (13700- 6.2 (3.5-9.7)
Escherichia coli	Aminophycosides	735 (527-1030)		27900)				1150 (744-1680)	288.6 (187.3-423.6)				199.4 (152.3-261.2) 6 (4 663.3 (511.9-864.5) 5 (3					02 (02-03)	4530 (3460-5980) 15900 (11600-						26500) 4.6 (2.8-6.8) 63100 (40100)			(563-1500) 0.2 (0.1+	
Escherichia coli	Aminopenicillin	735 (527-1030)			16484.2 (11807.6- 29036.9)		2.4 (1.5-3.5)	836 (542-1240)	210.5 (136.4-312.6)	355 (275-464)		418M)				8.5 (5.9-12.2)	160 (122-211)	0.7 (0.5-0.9)	19600)			00(0.00.0)		0.9 (0.6-1.2)	94000) 16.2 (10.3-24.1)	2204440)			J.Cato)
Eucherichia coli	Beta Lactum/Beta-lactumuse inhibitors	578 (413-811)	145.6 (104.0-204.2)	51500 (36800- 72300)			5.8 (3.8-8.3)	2040 (1350-2950)	514.4 (540.2-742.0)	277 (214-363)	5.7 (4.4-7.5)	25000 (19400- 32700)	517.4 (400.6-675.6) 11 (972 (702-1330)	20.1 (14.5-27.6)	125 (96-164)	0.6 (0.4-0.7)	11800 (8980-15400	52.9 (40.2-49.0)	5 (3-7)	00 (0.00.0)	458 (325-626)	2.1 (1.5-2.8)	48900 (30900- 72900) 12.5 (7.9-18.7)	1540000)		10 (1260-3210) 0.5 (0.3+	70900)
Escherichia coli	Carbapenens	75 (49-111)		6670 (4360-9840)		16 (8-27)	4.0 (2.1-6.7)	1430 (756-2360)		39 (26-54)	0.8 (0.5-1.1)		72.3 (49.4-101.1) 8 (5			15.3 (8.4-24.6)	18 (12-24)	0.1 (0.1-0.1)	1650 (1140-2270)			0.0-0.0)	343 (199-542)		5660 (3290-9200) 1.5 (0.8-2.4) 40000 (25200-			10 (629-2150) 0.3 (0.2-4	
Eucherichia coli	Phoroquinolones	475 (337-671) 471 (335-668)	119.6 (\$4.8-169.0) 118.7 (\$4.3-168.1)	59800)	90654.7 (7556.7- 15058.9) 90574.6 (7508.5- 14994.6)	49 (33-69)	12.2 (8.3-17.4) 16.2 (7.1-29.5)	4320 (2940-6140)		235 (183-311) 230 (172-304)	4.9 (3.8-6.4) 4.8 (3.6-6.3)	28000)	437.3 (341.3-578.6) 24 (428.9 (320.3-569.6) 31 (() 44.7 (32.8-40.6) () 57.7 (26.0-98.7)	106 (81-138) 104 (78-136)	0.5 (0.4-0.6) 0.5 (0.3-0.6)	9930 (7630-12900) 9800 (7360-12900)	44.4 (34.1-57.9)		0.0 (0.0-0.1)	1000 (736-1350) 1320 (627-2260)		40000 (25200- 59400) 10.2 (6.5-15.2) 40000 (25300- 10.3 (6.5-15.5)	1340000)		10 (2500-6430) 1.1 (0.6- 10 (2600-10800) 1.5 (0.6-	143000)
Escherichia coli	Third-generation cephalosporius		118.7 (84.3-168.1)	590000	14994.60 12238.1 (8763.0- 17247.0)		78 (5.1-11.6)	5740 (2520-10400) 2770 (1820-4090)			4.8 (3.6-6.3) 5.5 (4.2-7.2)	21.7601	428.9 (320.3-569.6) 31 (492.9 (380.9-649.8) 15 (27.7 (26.0-98.7)	104 (78-136)		9800 (7360-12900) 11200 (8590-14700						603001 10.3 (6.5-15.5) 44700 (28500- 11.5 (7.3-17.1)	13600000		10 (2400-10800) 1.5 (0.6- 10 (1530-3990) 0.7 (0.4-	243000
Escherichia coli	Trimethoprim-Sulfamethoxazole			68500)					DOM: N			31400)			1340 (921-1870)	27.7 (19.0-38.7)	120 (92-158)	0.5 (0.4-0.7)				00 (0.0-0.0)		2.7 (1.8-3.9)	66700) 11.5 (7.3-17.1)	Princes.			0) 90000) 15.0 (KB-23.1)
Eucherichia coli	Resistance to one or more ambiotics						51.7 (34.4-75.6)					40800)	725.7 (563.8-946.1) 100			0) 185.6 (130.7-254.9	176 (136-232)	0.8 (0.6-1.0)	16600 (12900- 21700)			02 (0.1-0.3)	4290 (3000-5780)		70400 (44800- 109000) 18.0 (11.5-26.8)	2540000)	407.4 (259.3-598.5) 252	300)	629000)
Group A Streptococci			3.5 (2.1-5.7) 3.5 (2.1-5.7)		311.3 (187.7-907.1) 311.3 (187.7-907.1)		03(0.0-1.1)	118 (0-384)	29.8 (0.0-96.8) 29.8 (0.0-96.8)				22.2 (13.8-34.8) 1 (0		103 (0-335)	2.1 (0.0-6.9)	4 (2-8)	00 (00-0.0)	428 (223-751)	19 (1.03.4)	0 (0-1)	00 (0.00.0)	41 (0-134)	02 (0.00.6)	809 (368-1620) 0.2 (0.1-0.4) 809 (368-1620) 0.2 (0.1-0.4)	388001	5.4 (2.7-9.9) 78 5.4 (2.7-9.9) 78	(0-308) 0.0 (0.0+	
Group & Steptococci	Resistance to one or more authiotics				311.3 (187.7-907.1) 2109.4 (1370.1- 3096.4)		0.3 (0.0-1.1) 4.1 (0.7-9.2)		29.8 (0.0-96.8) 361.5 (63.8-817.2)				22.2 (13.8-34.8) 1 (0 50.3 (36.6-69.5) 5 (1			2.1 (0.0-6.9) 8.6 (1.4-79.2)	4 (2-8)	0.1 (0.0-0.1)		1.9 (1.0-3.4)		00/0000		0.2 (0.0-0.6)	809 (368-1620) 0.2 (0.1-0.4) 699 (432-1100) 0.2 (0.1-0.3)		5.4 (2.7-9.9) 78 4.8 (3.1-7.4) 114		.,
Group B Streptococci			62.6 (42.6-90.5)			24 (0-67)	61 (0.0-167)		545.5 (0.0-1498.7)		1.7 (1.2-2.2)		150.5 (109.3-199.0) 8 (0			14.9 (0.0-39.1)	35 (25-47)	02 (01-02)		13.6 (9.9-18.2)		00 (0.00.0)		13(0.0-3.6)	4750 (3000-7210) 1.2 (0.8-1.8)	28700) 121000 (78700-	30.9 (20.2-45.1) 485	(0-1380) 0.1 (0.0)	4) 12300 (0-34000) 3.1 (0.0-8.7)
Group II Straptococci	s Penicilin	19 (13-29)	4.9 (3.2-7.4)	1730 (1130-2600)	436.1 (283.3-454.8)	4 (1-8)	0.9 (0.2-1.9)		79.3 (15.3-171.8)				10.4 (7.2-14.6) 1 (0			1.9 (0.4-4.1)	2 (2-3)	0.0 (0.0-0.0)		09 (0.6-1.3)		00 (0.00.0)	37 (8-81)	02 (0.0-0.4)	152 (95-236) 0.0 (0.0-0.1)		1.1 (0.7-1.6) 32		0) 847 (164-1890) 0.2 (0.0-0.5)
Group II Streptococci	Resistance to one or more antibiotics	297 (205-420)	74.9 (51.5-205.8)	26500 (18200- 37400)	6661.9 (4582.0- 9418.2)	44 (7-92)	11.1 (1.8-23.2)	3920 (641-8290)	986.3 (161.3- 2062.5)	96 (72-126)	2.0 (1.5-2.6)	8510 (6410-11200)	176.0 (132.5-231.1) 14 (-26) 0.3 (0.0-0.6)	1230 (176-2490)	25.4 (3.6-51.4)	40 (30-54)	0.2 (0.1-0.2)	3540 (2630-4720)	15.9 (11.8-21.2)	6 (1-12)	0.0 (0.0-0.1)	505 (75-9020)	2.3 (0.3-4.6)	5000 (3210-7580) 1.3 (0.8-1.9)	128000 (84100- 187000)	32.8 (21.5-47.9) 630	0.2 (0.0-	4) 16200 (0-39300) 4.1 (0.0-10.1)
Harmophilar influençae	Aminopenic film	23 (15-36)	5.9 (3.7-9.0)	2080 (1320-3190)	523.2 (332.5-802.4)		0.8 (0.1-1.8)	299 (25-643)	75.4 (6.4-161.9)	42 (30-58)			76.7 (54.9-106.2) 6 (0		533 (40-1120)	11.0 (0.8-23.2)	18 (13-24)	0.1 (0.1-0.1)		68 (5.0-9.4)		0.0-0.0)		1.0 (0.1-2.1)	213 (153-294) 0.1 (0.0-0.1)		1.5 (1.1-2.0) 32		
influençae Haemonkilar	Third-generation cephalospories Resistance to one or more		4.1 (2.6-6.0) 8.6 (5.7-12.9)	1440 (924-2130) 3040 (2010-4550)	363.8 (232.6-535.7) 765.0 (505.1-				106.5 (42.5-192.9) 181.9 (77.3-313.8)	31 (22-41)			56.0 (40.9-74.6) 9 (4 114.4 (87.3-150.5) 15 (793 (335-1370) 1330 (629-2160)		12 (9-16) 26 (20-34)	0.1 (0.0-0.1) 0.1 (0.1-0.2)	1070 (791-1410) 2240 (1720-2930)			00 (0.00.0)	312 (134-533) 533 (250-864)	1.4 (0.6-2.4) 2.4 (1.1-3.9)	148 (107-200) 0.0 (0.0-0.1) 319 (240-420) 0.1 (0.1-0.1)		1.0 (0.8-1.3) 44	(18-75) 0.0 (0.0+ (36-128) 0.0 (0.0+	
influençae Elebricila resemente	Resistance to one or more antibiotics or Aminophycosides		8.6 (5.7-12.9) 104.0 (73.1-147.5)		765.0 (505.1- 1145.5) 9250.5 (6500.0- 13119.5)	N (3-14)		722 (507-1250) 2790 (1660-4260)		63 (46-82) 797 (775-380)	13(10-17) 60(47-80)		534.1 (412.1-705.9) 22 (27.4 (13.0-44.8) 0 40.6 (26.4-58.6)	26 (20-34)	01 (01-02)	2240 (1720-2930) 10500 (7970-14000			00 (0.00.0)	533 (250-864) 795 (506-1170)		23100 (15100- 23100 (15100-			(36-128) 0.0 (0.0-1 10 (989-2860) 0.4 (0.3-1	
	Beta Lactum/Beta-lactumase	707 (866 1130)	199.5 (139.8-278.2)		13119.5) 17741.1 (12431.8- 24748.4)		26(0.9-5.2)		229.8 (79.4-463.4)	647 (FTD 775)	11.7 (9.1-14.9)		1051.0 (804.2- 1319.2) 7 (2			13.3 (4.4-26.6)	232 (180-303)	10 (08-14)		89.9 (70.0-117.4)		00(0.00.0)		1.2 (0.4-2.3)	35900 (23400- 9.7 (6.0.13.4)		212.2 (138.6-308.8) 430		2) 9890 (4870-17200) 2.5 (1.2-4.4)
Elebricila encumenta		204 (126-329)	51.5 (31.7-83.0)	98300) 18200 (11200- 29300)	34748.4) 4577.0 (2816.5- 7375.6)	07/7770	11.8 (6.7-19.1)	4170 (2380-6740)		142 (89-229)			280.3 (163.2-419.0) 33 (n 59.7 (35.2-96.6)	58 (56.05)	03/02040	26200) 5050 (3150-8090)			01(0001)	1150 (682-1880)		52100) 5.2 (337-334) 16800 (30700- 4.3 (2.7-6.3)	1200000)		10 (2210-5740) 1.0 (0.6-	
Klebriella pneumonia		558 (294-782)	140.4 (99.1-196.8)		7375.6) 12491.4 (8817.7- 17504.9)	47 (27-76) 38 (23-56)	95 (5.7-14.7)	3360 (2010-5190)	1698.0) 845.7 (506.0-		8.2 (6.4-30.5)		722.3 (505.5-930.1) 27 (0 48.9 (30.7-71.2)	163 (126-215)	0.7 (0.6-1.0)		63.1 (49.2-83.5)		00(0.00.1)	999 (600-1410)		24600) 4.3 (27-6.3) 29500 (79300- 7.6 (4.9-11.1)	555000) 679000 (442000-	174.0 (113.4-253.9) 195	10 (2210-5740) 1.0 (0.5- 10 (1130-3150) 0.5 (0.3-	5) 132000) 21.8 (13.0-33.8) 8) 49900 (26400- 8) 72300) 11.8 (6.8-18.6)
Elebricilla manamania	Third according conhabatoring	778 (574-1170)	195.9 (131.9-282.6)		17420.7 (11728.5- 25142.7)		24.2 (8.8-44.9)	8540 (3120-15900)	2149.9 (785.7-	595 (413.730)	115 (85) 152)	49100 (36400-	1015.9 (753.6- 69.0	7.175 14006760		0) 126.7 (49.4-232.8)	227 (167-299)	10/07-13		88.2 (65.0-116.1)		01/00/02)	2440 (936-4490)		33600 (22200- 8.6 (5.7-12.6)			10 (957-5570) 0.7 (0.2-	
		,,		(9900) (9900)	25142.2) 17466.7 (12256.7- 34736.1)							65100) 40300 (36500)	1345.9) 1018.5 (796.4 1311.7)			0 51.8 (25.1-82.2)		10 (08-1.3)		88.2 (69.4-114.9)			993 (502-1590)		49000) 31800 (20900- 8.2 (5.3-11.9)	11,54440)	190.2 (124.9-274.5) 146		7) 34200 (16200- 8.8 (4.1-15.6)
Klebxiella pneumonia	e Trimethoprim-Sultamethosazole	780 (547-1100)	196.4 (137.8-278.0)	98200)			10.0 (4.8-16.9)	3520 (1680-5980)		557 (435-717)	11.5 (9.0-14.3)	63400)		4-45) 0.6 (0.3-0.9)	2530 (1210-3980		227 (179-297)		25,000)			0.1 (0.0-0.1)			46400)	1070000)			60900)
Klebsiella pneumonia	Resistance to one or more authiotics	923 (647-1290)	232.3 (162.9-325.4)	N2100 (57600- 115000)	20663.4 (14490.8- 289.79.6)	262 (164-385)	65.9 (41.2-97.0)	23300 (14600- 34300)	5864.3 (3664.3- 8625.1)	658 (518-845)	13.6 (10.7-17.5)	58300 (45900- 74800)	1546.1)	127-268) 3.9 (2.6-5.5)	16500 (11200- 25700)	341.2 (232.5-489.9	9) 269 (212-351)	1.2 (0.9-1.6)	30400)	104.4 (82.5-136.0)	76 (52-110)	0.3 (0.2-0.5)		29.6 (20.1-42.5)	31000 (25600- 57100) 10.0 (6.6-14.6)	1320000)		00 (7670-18300) 3.1 (2.0-	419000)
Morgandia spp.	Plaoroquinolones	0 (0-0)	0.000.00	3 (1-9)	08 (0.2-2.3)	0 (0-0)	00(0.0-0.0)	1 (0-2)	0.1 (0.0-0.4)	0 (0-0)	0.0(0.0.0)		0.2 (0.1-0.5) 0 (0 0.0 (0.0 -0.1) 0 (0	0.00000	1 (9-3)	00 (00-01)	0 (0-0)	00 (00-0.0)	9 (5-16)	00 (0.0-0.1)	0 (0-0)	00 (0.00.0)	1 (1-3)	00 (0.00.0)	72 (42-115) 0.0 (0.0-0.0) 18 (10-20) 0.0 (0.0-0.0)	1460 (886-2280)	0.4(0.2-0.6) 11 0.1(0.1-0.1) 46		0) 231 (90-441) 0.1 (0.0-0.1) 00 83 (39-160) 0.0 (0.0-0.0)
Morganella spp. Morganella spp.	Fourth-generation cephalosporius Third-generation cephalosporius	0 (0-0)	0.0 (0.0-0.0)	1 (0-2) 2 (1-7)	0.2 (0.1-0.6)	0 (0-0)	0.0(0.0-0.0)	0 (0-1)	0.1 (0.0-0.3)	0 (0-0)	0.0 (0.0-0.0)		0.1(0.1-0.3) 0(0		1 (0-3)	00 (00-00)	0 (0-0)	00 (00-0.0)	2 (1-4) 8 (4-15)	00 (0.00.0)	0 (0-0)	00 (0.00.0)	0 (0-1) 2 (1-3)	00 (0.00.0)	18 (10-29) 0.0 (0.0-0.0) 112 (67-182) 0.0 (0.0-0.0)	365 (224-576) 2140 (1330-3370)		(9-47) 0.0 (0.0+	0) 83 (39-160) 0.0 (0.0-0.0) 0) 445 (180-881) 0.1 (0.0-0.2)
Morgandia upp.	Resistance to one or more ambiotics	0 (0-0)	0.00.00	4 (1-13)	1.1 (0.3-3.3)	0 (0-0)	0.0 (0.0-0.0)	1 (0-3)	0.1 (0.0-0.5)	0 (0-0)	0.0(0.0.00)		0.2(0.1-0.5) 0(0		3 (1-7)	0.1 (0.0-0.1)	0 (0-0)	00 (00-0.0)	14 (7-25)	0.1 (0.0-0.1)	0 (0-0)	00 (0.000)	3 (2-7)	00 (0.00.0)	147 (88-232) 0.0 (0.0-0.1)	2880 (1820-4500)		(19-71) 0.0 (0.0+	
Mycobacterium tuberculosis	anthiotics Extensive drag resistance in TB	-	_	0 (0-0)	0.0 (0.0-0.0)	-	-	0 (0-0)	0.0(0.0-0.0)	26 (14-43)	0.5 (0.3-0.9)		48.4 (25.3-79.6) 16 (1430 (747-2360)	29.6 (15.5-46.8)	14 (8-24)	0.1 (0.0-0.1)	1270 (683-2090)			0.0 (0.0-0.1)	740 (400-1210)		2990 (1470-3920) 0.7 (0.4-1.0)			10 (1916-2400) 0.4 (0.24	6) 62200 (549000- 92300) 15.7 (8.9-23.7)
Mycobacterium tuberculosis	Isoniarid mono-resistance	ŀ	-	0 (0-0)	0.0 (0.0-0.0)	-	-	0 (0-0)	0.0(0.0-0.0)	21 (12-33)	0.4 (0.3-0.7)	1850 (1090-2910)	38.3 (22.4-60.2) 3 (0	0.1 (0.0-0.2)	288 (0-1010)	6.0 (0.0-20.9)	11 (7-17)	0.1 (0.0-0.1)	1090 (665-1610)	49 (3.0-7.2)	2 (0-6)	00 (0.0-0.0)	156 (0-518)	0.7 (0.0-2.3)	1900 (1230-2750) 0.5 (0.3-0.7)	85500 (55000- 125000)	21.9 (14.1-31.5) 297	(0-987) 0.1 (0.0+	3) 12000 (9-39200) 3.1 (0.0-10.0)
Mycobacterium tuberculosis	Multi-drug resistance excluding extensive drug resistance in TB	-	-	0 (0-0)	0.0 (0.0-0.0)	-	-	0 (0-0)	0.0 (0.0-0.0)	58 (31-92)	1.2 (0.6-1.9)	5120 (2770-8190)	105.8 (57.4-169.1) 33 (1-70) 0.7 (0.1-1.4)	2930 (455-6140)	60.7 (9.4-127.0)	31 (18-49)	0.1 (0.1-0.2)	2880 (1660-4520)	12.9 (7.4-20.2)	18 (3-38)	0.1 (0.0-0.2)	1510 (219-3200)	6.8 (1.0-14.3)	5670 (3330-8210) 1.5 (0.9-2.1)	240000 (141000- 354000)	61.5 (36.1-90.7) 325	10 (487-6350) 0.8 (0.1-	6) 125000 (17700- 340000) 32.0 (4.5-63.0)
Mycobacterium nabercalonis	Rifampicia mono-resistance	-	_	0 (0-0)	0.0 (0.0-0.0)	-	-	0 (0-0)	0.0 (0.0-0.0)	13 (8-20)	0.3 (0.2-0.4)	1160 (695-1800)	23.9 (14.4-37.2) 4 (1	8) 0.1 (0.0-0.2)	322 (50-701)	6.7 (1.0-14.5)	7 (4-10)	00 (00-0.0)	658 (398-956)	2.9 (1.8-4.3)	2 (0-4)	00 (0.00.0)	173 (36-355)	0.8 (0.2-1.6)	1040 (665-1450) 0.3 (0.2-0.4)	46200 (29900- 64200)	11.8 (7.6-16.5) 281	P (45-584) 0.1 (0.0+	
Mycobacterium tuberculosis	Resistance to one or more authiotics	ŀ	-	0 (0-0)	0.0-0.0)	-	-	0 (0-0)	0.0(0.0-0.0)	118 (82-166)	2.4 (1.7-3.4)	10500 (7310-14700)	216.4 (151.2-304.3) 56 (1.2 (0.4-2.1)	4980 (1870-8900	0 102.9 (38.7-184.0)	63 (45-88)	03 (02-0.4)	5900 (4220-8080)	26.4 (18.9-36.2)	30 (12-53)	0.1 (0.1-0.2)	2580 (991-4560)	11.6 (4.4-20.4)	11200 (8670-14100) 2.9 (2.2-3.6)	597(000)		20 (2120-9040) 1.4 (0.5-	348000)
Neisseria gonorrhosa	r Phoroquinolones	-	-	-	-	-	-	-	-	-	-	-		-	-	-	-	-	-	-	-	-	-	-			0.4 (0.2-0.7) -	-	166 (40-355) 0.0 (0.0-0.1)
Neisseria gonorrhosa	Third-generation cephalosporius Resistance to one or more authorics	ľ	-	-	-	-	-	-	-	-	-	-		-	-	-	-	-	-	-	-	-	-	-	-	(10)	0.0(0.000)	-	7 (2-16) 0.0 (0.0-0.0) 173 (47-367) 0.0 (0.0-0.1)
Protess see	ambiotics Aminophysoides	8 (5-12)	19 (1.2-7 %	681 (429-1049)	71.4 (JOS 1-261 **	0.60-1)	01/0007	35 (4-78)	8.8(1.0-19.7)	4(2-9)	0.1/00/010	343 (206-540)	7.1(4.3-11.3)	n nnaner	18 (7-40)	04 (00.00)	2 (1-3)	 gp:gnam	189 (116-790)	08/05/176	0.00-01	99,8500	19 (2-21)	00 (0.0-0.1)	1980 (1280-2870) 0.5 (0.3-0.7)		11.0 (7.0-16.2) 95		1/3 (4/-30/) 0.0 (0.0-0.1) 1) 2320 (262-5180) 0.6 (0.1-1 %
Protest upp.	Aminoponic illin	23 (14-36)	58 (3.6-9.2)	2070 (1270-3250)	520.3 (319.6-818.1)	0 (0-2)	0.1 (0.0-0.4)	43 (0-134)	10.7 (0.0-33.7)	12 (7-18)	0.2 (0.1-0.4)	1050 (633-1660)	21.6 (13.1-34.4) 0 (0	1) 0.0 (0.0-0.0)	22 (0-70)	0.4 (0.0-1.4)	6 (4-10)	00 (00-0.0)	567 (349-902)	2.5 (1.6-4.0)	0 (0-0)	00 (0.00.0)	12 (0-36)	01 (0.002)	5780 (5730-8380) 1.5 (1.0-2.1)	630001	31.7 (20.2-46.1) 133	(0-420) 0.0 (0.0-	1) 2830 (0-8800) 0.7 (0.0-2.5)
Protess upp.	Phoroquinolous	S (5-13)	2.1 (1.2-3.3)	731 (437-1180)	184.2 (110.0-296.5)	1 (0-1)	0.1 (0.1-0.3)	48 (18-98)	12.2 (4.6-24.8)	4 (2-7)	0.1 (0.1-0.1)	371 (220-592)	7.7 (4.6-12.2) 0 (0	1) 0.0 (0.0-0.0)	24 (9-51)	0.5 (0.2-1.1)	2 (1-3)	00 (00-0.0)	199 (123-314)	0.9 (0.5-1.4)	0 (0-0)	00 (0.0-0.0)	12 (5-27)	0.1 (0.0-0.1)	1910 (1210-2640) 0.5 (0.3-0.7)	40500 (25500- 60000)	10.4 (6.5-15.4) 131	(51-256) 0.0 (0.0-	1) 2750 (3070-5440) 0.7 (0.3-1.4)
Protest upp.	Third-generation cephalosporius	7 (4-11)	1.7 (1.0-2.9)	611 (344-1090)	153.8 (86.7-255.2)	1 (0-3)	0.4 (0.1-0.8)	132 (40-274)	33.1 (10.2-69.1)	3 (2-5)	0.1 (0.0-0.1)	302 (178-486)	6.2 (3.7-30.0) 1 (0	0.0 (0.0-0.0)	65 (21-129)	1.3 (0.4-2.7)	2 (1-3)	00 (00-0.0)	161 (98-252)	0.7 (0.4-1.1)	0 (0-1)	00 (0.0-0.0)	35 (11-69)	02 (0.1-0.3)	1270 (773-1910) 0.3 (0.2-0.5)	27100 (16600- 42000)		(93-563) 0.1 (0.0-	1) 6000 (2010-12100) 1.6 (0.5-3.1)
Proteur spp.	Trimethoprim-Sulfamethosazole	14 (8-22)	3.4 (2.1-5.5)	1220 (733-1950)	307.4 (184.5-490.2)	0 (0-1)	0.1 (0.0-0.3)	43 (0-102)	10.9 (0.0-25.6)	7 (4-11)	0.1 (0.1-0.2)	608 (365-971)	12.6 (7.6-20.1) 0 (0	1) 0.0 (0.0-0.0)	22 (0-49)	0.4 (0.0-1.0)	3 (2-6)	0.0 (0.0-0.0)	329 (203-520)	1.5 (0.9-2.3)	0 (0-0)	0.0 (0.0-0.0)	12 (1-27)	0.1 (0.0-0.1)	2990 (1900-4560) 0.8 (0.5-1.1)	54700 (40000- 54900)	16.6 (10.5-24.3) 105	(0-244) 0.0 (0.0-	1) 2280 (6-5240) 0.6 (0.0-1.3)

emplosa 2226 555.)	20-02) 6570 (23-16600) 1.7 (0.0-4.3) 211-0.3) 29300 (11100- 4.9 (2.8-8.0)
Productional Auto-productional position Res 2000 (1700 C170 (1705 S) 2000 (1700 S) 200	11-0.3) 29300 (11100- 4.9 (2.8-8.0)
Final control Final contro	31300)
Parison Pari	3.5-1.2) 69400 (42100- 17.8 (10.8-27.6)
Table Tabl	1.3-0.7) 40600 (24200- 64300) 10.4 (6.2-16.5)
Section Control Cont	3.0-0.1) 4930 (2750-7910) 1.3 (0.7-2.0)
Table Section Table Ta	3.0-0.2) 9930 (4100-18200) 2.5 (1.1-4.7)
Angular 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1.0-2.6) 151000 (91100- 38.6 (23.4-60.3)
- PRO 080000 PPO 08000 PPO 08000 PPO 08000 PPO 080000 PPO 080000 PPO 08000 PPO 080000 PPO 080000 PPO 08000 PPO 08000 PPO 08000 PPO 0	2000) 28 (2-63) 0.0 (0.0-0.0)
Manual Purple Manual Purpl	10-00) 0 (0-0) 0.0 (0.0-0.0)
Salamonda Paraggal	10-00) 28 (2-63) 0.0 (0.0-00)
The control	0.0-0.1) 2430 (295-6840) 0.6 (0.1-1.8)
Annual Type Hall Sign colors 5 Annual Hall S	10-00) 506 (0-1830) 0.1 (0.0-0.5)
Tables and great area (2017) \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$	3.0-0.1) 2940 (534-7670) 0.8 (0.1-2.0)
National Perspections (1/2) 0.18/2-06 [11/57/30] S.48/4-04 [0-D] 0.18/0-04 [14/50] S.58/5-14 [14/50] S	10-00) 265 (43-678) 0.1 (0.0-0.2)
Non-pikel Annies on ear state 1/2 0.5/2-66 11/107-200 2.6/10-64-06 0.10 0.00 0.	3.0-0.0) 265 (43-678) 0.1 (0.0-0.2)
	1.0-0.0) 1490 (0-2940) 0.4 (0.0-1.0)
Angular addition. 1975 1875	10-0.1) 3470 (1670-6310) 0.9 (0.4-1.6)
Servici App. Codeposes 11(6-57) 27(6-6-1) 27(6	33-0.1) 33-40 (1540-5620) 0.8 (0.4-1.4)
	3.0-0.0) 554 (104-1240) 0.1 (0.0-0.3)
Terminal upon Poor Poor Poor Poor Poor Poor Poor Po	30-0.1) 3970 (3640-7750) 1.0 (0.4-2.0)
Take garmatine copinal departures (19.50) \$1.05 (11.50) \$1	3.0-0.0) 1470 (502-3000) 0.4 (0.1-0.8)
Table Tabl	11-02) 14100 (7610-27900) 3.6 (2.0-6.1)
Signifut opp. Therapteristance 21.5 61.5 61.5 11.5 17/95-40 45.013-17/103 0.6-1 45.013-17/103 0.6-1 45.013-17/103 14.5 0.016-103 14.5 0	30-00) 285 (0-892) 0.1 (0.0-0.2)
Supera trans to see cases: \$2.65\$ \$5.61.43\$ \$179.05-09\$ \$6.033374390\$ \$6.99\$ \$1.00-05\$ \$7.00-05\$ \$1.00-05\$ \$7.00-05\$ \$1.00-05\$ \$7.00-05\$ \$1.00-05\$	3.0-0.0) 285 (0-892) 0.1 (0.0-0.2)
Supplementariant Hampingham Supplement Hampingham Supplement Hampingham Supplement Hampingham Supplement Hampingham Supplement	11-0.4) 19900 (7860-33700) 4.8 (2.0-8.6)
Supplementarian Marchide Supplementarian Supplem	11-0.4) 29500 (7460-36800) 5.0 (1.9-9.4)
Supplementaries Market M	3.6-2.4) 130000 (55800- 227000) 33.4 (14.3-58.2)
Supplementarium Timediprin-Salimentumania Timediprin-S	3.0-0.1) 5660 (2710-9360) 1.4 (0.7-2.4)
Supplementariant Vacampon 9:612 21:05:10) 77(09)180 897 (036-273, 9 10-9) 0:6(0.512, 22'015-40) 0:5(0.512, 22'	3.0-0.1) 4420 (2170-8220) 1.1 (0.6-2.1)
Spinish and contract of the	1.0-3.2) 179000 (94800- 298000) 45.9 (24.3-76.4)
	3.0-0.0) 841 (52-2000) 0.2 (0.0-0.5)
September 19/12/20 41/03-19/40 19/12/20 41/03-19/40 19/12/20 41/03-19/40 19/12/20 41/03-19/40 19/12/20 41/03-19/40 19/12/20 41/03-19/40 19/12/20 41/03-19/40 19/12/20	32200 (15300- 3400) 8.3 (3.9-13.9)
	330 (819-6930) 0.9 (0.2-1.8)
Topposition	3.0-0.2) 6400 (0-16600) 1.6 (0.0-4.3)
September Parkin Mill September	11-0.2) 12000 (5980-20900) 3.1 (1.5-5.4)
	0.0-0.2) 9680 (3840-18600) 2.5 (1.0-4.8)
5075-0003 5075	11-0.8) 45900 (6630-92700) 11.7 (1.7-23.8)
September Sept	3.6-1.5) 110000 (68500- 150000) 28.2 (17.6-40.8)

Table NS. Drade	and DALTs (in counts an	dagrapnille nie) executed with and	ativituishir in hasir	relat antimisrabile o	reddamer by pathog	or drag combination	to age group, 2021	. high-income super-r	rgion			Post	Neonated								164							3 and ove	w		
Pathogra	Anthreis stern	Comp	Arresciated Deaths Exir per 100 000	with eminimum Electric Committee		Contr	Airbeidi Dealle Kair per 100-000	E in renbiamer E	MANA	Comp.	Accessisted	f with renistance (Darwin	E.V.	Comp	Aindraide Dealte Exir per 130 000	to resistance	DALY.	Contr	Associated Deaths Eater per 200 000	with reministers .	DALW.	Comb	Attributed Drafts Extr per 133 000	De la malalance	DALYA		Annesiain Irailin	DALS). Counts Este	10000 Co	Druk	Allesbariable is	DALY)
All palogram	Eminiature in one or more antibiotics	1910 (1200-2990		170000 (397000- 297000) e620 (4060-30300)			H3(H3H24)	20700 (20000- 40000)	2563.7 (2963.1- 7562.8)	1300-(890-1890)	12.8 (8.7 (8.0)	1 18000 (80000 147900)	11.09.8 (798.4- 1627.9)	301 (201-421)	3.0(2.04.3)	27,800 (18400) 21000()	268.7 (278.3- 386.6)	367 (173 629)	12 (0.0 1.0)	32700 (33600 79700)	115.1 (77.8-046.3	n) 130 (sh 190)	63 (82 64)	11700 (7610- 17900)	28.6 (17.0-38.2)	11100-0210 93-0000 100000-1112000	NA (424-79.7)	9120000 (4610000 944.0 17900000 1334.	(MR.4 12 2) 29	2000 (1930) NOO) I	14(14212)	Creek Sir per 200 000 2230000 (1900000 224.9 (184.0 22.0 1100 (190.0000) 12.7 (1
Animalia	Antingly-make. Anti-paradismonal posts film Bets.	79 (26-334)	X7(83134) 133(81200)		1286.7) 1183.7 (722.3- 1821.2)		0.1 (0.0 0.9)	20 (0.490)	31.1 (0.0 81.1) 31.9 (0.2 40.4)	33 (18-84)	0.3 (0.2-0.3) 0.3 (0.3-0.8)	2103 (3639-4730) 4800 (2009-6920)			60(1.060)	126 (9-317) 129 (99-220)	12(0011)	12 (9-22)	40 (00 40) 40 (00 41)	3079 (524-0940)	23 (11-42)	1 (9.1)	60 (5.0-60)	48 (1-124)	0.1(0.00.3)	2180) 2280 (1800	12(1313)			MO (MOD 1980) 6: 12 (0: 3660) 6:		1180 (29-200) 1.1 (00-10) 1700 (270- 2720) 1.8 (09-12)
Antoniolista Antoniolista Instrumenti	Datamar inhibitors Data Lacian/Data Incianare inhibitors	96 (39-231)		25600) 8550-15200-155001		1(24)	0.1 (0.2 0.7)	298 (143 MZ) 78 (20-191)	\$1 (2.1 (2.7)	80 (28 79) 88 (28 79)	0.1 (0.3 0.3)	1800 (2000-01/20) 2890 (2210-0210)			60(0.060)		0.4 (0.1 0.2)	28 (9.52)	00(0001)	388 (796-2970) 3783 (778-2820)	34(1743)	0 (0 1)	1012-101	40 (29 013) 22 (9 00)	41(0142)	21200 (12000- 21200 (12000- 21000 (11000-	22(1333) 23(1448)			HO (NO. 1480) G		7900-2230-14000 -0.8-02-1-61
Animateluster Instrumenti Animateluster Instrumenti	Categorea Electrosistem	227 (48-244) 227 (48-242)	12.6(7.6-09.0)	1120-(1700-12800)		12 (9-31) 13 (7-23)	11 (11 12)	1670 (R24 2790) 1160 (791 200)	290.9 (96.0 (20.1) 126.2 (89.1-237.7)	47 (26-79) 68 (26-72)		4190 (2330-0420) 4090 (2270-0420)			61(8061)	712 (810-1230) 808 (279-800)		DE (9.31)	00(0001) 00(0001)	1929 (743-2790) 1869 (712-2600)		3 (2-4) 2 (2-8)	10204102	287 (114-912) DEI (20-300)	0.0(0.21.1)	21100) 21100) 21200 (20700- 21200)	18(1138)	577000) 35.2		30 (170 4130) 6 30 (1120 3770) 6		67200 (12000) 113000) 4.2 (1.2-11.0) 67200 (21000) 150001 4.2 (2.0-7.2)
Antoniological	Facility pression ophilopein	112 (48-174)	13.1 (7.9-204)	9960 (HOSD 18700)	11649 (706.4 1891.0)	1(02)	01 (00 02)	79 (28-144)	K2 (5.3-07.0)	29 (29 79)	03 (03 03)	£120 (2120-0190)	42.0 (23.8 47.4)	0 (0.1)	60(0.060)	NI (12-41)	0.1 (0.1 0.4)	20 (9.32)	00(0001)	3629 (79th 2990)	33 (17-63)	0 (0 0)	00/00-00	11 (9-29)	40(0041)	21800 (12900- 32800)	21(1234)		222424 26	7 (99-824) 6	00001	400(179-900) 0.1(0.201)
Americani Americani	Contraction contraction contraction contraction Emissioner to come or	142 (93-22%	16.4789-2830 18.2 (18.9-28.1)		2290.0 1814.0 (988.3	E0100	09/02/10	721 (790 1790)	84.1 (21.0 112.0) 294.3 (212.4: 809.4)	62 (35-9%)	04-03-145	1440 (1840 8770)	811 (28.7 88.2)	7 (3-40	60/8061) 62/8163)	MACHEMIN	10(110.8)	29 (12-44)	01/00/01	2179 (1040-1040)	47/23/840	20-8	60/8060	180 (91-202)	0.100.000	3150-(1600- 3150-(1600-	18/2849		21.0 (T.) (10.0 (T.) (T.) (T.) (T.) (T.) (T.) (T.) (T.)	120 (1000-2000) G		2780 (7900 7000 41 (1778) 1000 (8400 3400 54 (21100)
Assessed Citebater upp.	Aminophomian	110 (45 240)	0.1 (0.1-0.2)		2299.2) 25.9 (5.9 183)	8 (27:76) 0 (0:0)	84 (82/91) 88 (88/88)	4 (9 19)	67 (80-17)	1 (1-2)	0.7 (0.0 l.1) 0.0 (0.0 d.0)	990 (33 (82)	14(0314)	21 (11 (1) 0 (0:0)	62(8.163)	1840 (965 3680) 6 (9 17)	0.1 (0.0 0.2)	28 (10 Mb) 0 (0 I)	0.00000	2630 (1190-6390) 26 (17-72)	01 (00 02)	0 (0 O)	60 (3.0 6.0)	737 (NO 1505) 2 (9-4)	1.0(0.72.9)	992 (126-292)	3.9(2.0.8.7) 0.0(0.00.0)	100000) 62.4: 3699 (2340-3470) 0.4 ((36.3-969) 17 (2-6.9) 12	(0.29) 0	0 (0.0-0.7) 0 (0.0-0.0)	20 (0.00) 18.6 (0.0.0.1) 20 (0.00) 0.0 (0.0.0.1)
Citebater up.	Anti-provincemal posts film lister Lactamere inhibitore	8 (84)	0.6(0.3 (.1)	487 (244-82%)	85.5 (26.5 45.7)	1 (0-2)	0.1 (0.1 0.3)	103 (43-207)	12.1 (0.1-24.2)	n(3-11)	0.1 (0.0 0.1)	NAK (290-NAZ)	8.3 (2.2-9.2)	1 (0.0)	60(5.060)	124 (94-247)	1.2 (0.3-2.4)	2(18)	0.0 (0.0 0.0)	213 (90-397)	0.5 (0.2-0.9)	1 (9.1)	60 (8.0-6.0)	49 (19-100)	0.1 (0.0-0.2)	1230 (808-1830)	0.1 (0.1-0.2)	22300 (18000 33000) 2.1 (1	43.0 29	0(130.299) 0	10.00.00	H10(2009-9980) 0.3 (0.3-0.9)
Citebater upp. Citebater upp.	Categorea Florospinstenn	1 (3-2) 4 (2-7)		117 (83 205) 391 (194 382)			03 (80 01) 01 (80 01)	30 (23-99) 30 (23-12)	3.8 (2.6-69) 6.8 (2.6-13.1)	2 (1-7) 3 (2-9)	40 (00 40) 40 (00 41)	137 (99-236) 808 (217-706)		0 (0.1) 1 (0.2)	60 (5.060)	29 (29-49) 68 (20-22)	0.7 (0.3 0.7) 0.7 (0.3 0.7)	1 (0-1) 2 (1-9)	0.0 (0.0 d.0) 0.0 (0.0 d.0)	27 (20:40) 138 (42:298)	01 (00 02) 03 (01 04)	0 (0 t) 0 (0 t)	pa-aayoa	12 (9-20) 23 (8-27)	4.0(0.04.1) 4.0(0.04.1)		0.0(0.00.0) 0.1(0.00.1)	4439 (2730-4839) 0.4 (1 12409 (8629 18409) 1.2 (1				1170 (413-2020)
Citebater upp.	Poseds preceding cophalosparies Third granuline cophalosparies	2 (3-3) 8 (2-14)		176 (99-009) 729 (378-1280)			03 (80-03) 03 (80-02)	12 (9:24) 46 (28:140)	1.4 (8.6-2.9) 8.0 (2.9-36.8)	2 (1-4)	0.0 (0.0 0.2) 0.1 (0.0 0.2)	207 (99-542) 847 (430-1479)		0 (0:0) 1 (0:2)	60(3.060)	13 (9-24) 79 (29-344)	0.1 (0.0 0.3)	1 (0-1) 4 (2-7)	0.0 (0.0 d.0) 0.0 (0.0 d.0)	67 (29-126) 214 (178-896)	01 (01 03) 07 (03 13)	0 (0 t) 0 (0 t)	pa-aay oa	4 (1-9) 29 (9-40)	4.0 (0.04.0)		0.0(0.00.0)	3750 (3500-3670) 0-4 (5 33000 (35300 36600) 3-0 (3			02000	299 (192-627) 0.0 (0.0-0.1) 2020 (1140-9380) 0.3 (0.1-0.3)
Citedaster app.	Entitioner to one or more artifestics	11 (0-1%)	1.5(0.5.2.2)	962 (529-3670) 1210 (727-1989)			0.1 (0.2 0.7)	277 (139-908)	32.4 (33.839.8)	11 (7-22)	0.1 (0.1-0.2)	1110 (903-0100) 328 (196-520)	11.0(0.7-10.0)	4 (2.7)	60(8061)	329 (334-999) 33 (334-999)	32(1363)	8 (24) 1 (3.7)	00(0000)	404 (362 779)	07 (04 17)	10.0	po anj os	119 (48-23%	41(0.14.5)		02(0103)		1889 6E	(1 (772 H00) 6	1 (0.0-0.1)	11800 (AMID: 1.1 (Dat 1.8)
200020-00	Anti-provincemal provide Sets Lacismos inhibitors	11(622)	10(1023)		799.8 (201.4)		12/8028	W1.179.1949	863 (Ma 1764)		92/92/93	177 (199 209)			52/5050	200/100400	2311342	1(14)		NT (179-179)	18/10/20		50/3050	100,000,000	920399		10/0714	199000 (129000		70.ND 2200 S		2700 (1200 2000 23 (1230
Entendanter type	Categorea	33 (20-31)	3.8(2.44.0)	2920 (1790-2040)	301.7 (20% 2- 333.8) 294.6 (182.8-	1(14)	10 (86 17)	201 (233 1320)		9 (6 11)		R35 (NO. 1279)	X1 (4.9 12.4)		60(1060) 60(1060)		2.2 (3.2 (5.4)	4(24)	00/0000)	327 (299-834)		1(1-2)	60 (3.0-60) 60 (3.0-60)		0.2(0.10.3)	4040 (2820 F710)	04(0304)	7300 (8300- 16000) 7.0 (1		20 (400 1480) 6	1 (0.1 0.2)	23 (1.5.19) 19700 (11800 3000) 1.9 (1.2.29)
Entendarior app.	Florespinstern Fourth prevailes cephalogories Trimologories	28 (10-29)	5.5(2.5.8.8) 5.7(5.5.8.8)	2120 (1840-2005) 4100 (2840-6700)		2(2.0)	02 (01 04)	29 (112 89)	31.5 (8.8.96.5) 31.1 (8.8.96.5)	14 (8-21)	0.1 (0.1-0.2)	1210 (727-1890)	11.8 (7.1-18.9)	1 (0.1)	6.0 (5.0 6.0)	47 (21-90)	0.8 (0.2 0.8)	3 (2.8) 3 (3.8)	0.00000	DEC (245-241)	11 (86 17)	0 (0 c)	100-0.0)	18 (8-70)	0.0 (0.0 0.1)	NAM (1870 TESS)	0.9 (0.4 0.8)	100000 (MAZIO- 144000) 9.8 (I	14:14:0) 29	W (200-200) B		MMD(1790-6790) 0.1 (0.2-0.4)
Entenhator app.	Sallamethonards Entitioner in one or more arithmics	37 (22-90) 112 (70-170)	4.5 (2.6-6.9) 13.2 (8.2-20-4)	3260 (1980-5230) 10080 (4210- 13500)	608/9 1169/3 (726-3- 1812-3)	2 (0-8) 27 (36-42)	03 (00 04) 32 (19 50)	194 (0-426) 2400 (1470-7779)	22.7 (0.0 NO.0) 280.6 (171.4 480.9)	32 (19-29)		121 (141-1421) 2671 (1730-4770)		1 (0-1) 8 (0-12)	61 (8.0 6.1)	33 (0.129) 684 (200.1368)	0.8 (0.0 LZ) 0.7 (0.9 LD.3)	6 (2-7) 14 (8-22)	00 (00 00) 00 (00 00)	394 (222-611) 1290 (700-2920)	0.8 (0.9-1.3) 2.4 (1.9-4.2)	3 (2 5)	60 (8.0 60)	21 (9.80) 281 (189-861)	0.1 (0.0 0.1) 0.0 (0.3 1.0)	2440 (3290 4830) 13300 (30900- 23800)	03(0304) 13(1020)			14 (0.790) 0 14 (0.790,7080) 0		NOR(0-2000) 0.9 (0.0 LE) 62900 (20000 92700) 6.1 (3.9 LE) 82300 (20000 93900) 5.1 (2.4 LE)
famile Entrement famile	Florespieden Vancespois	41 (26-42) 6 (3-9)	4.7 (3.0.7.2) 0.0 (0.4.1.1)	3620 (2390 5500) 292 (296 828)	52.5 (32.6-55.6)	20 (8-28) 2 (2-4)	12 (63-21) 62 (61-64)	898 (212 1430) 163 (70-314)		14 (9.28) 2 (1-4)		1429 (770-3470) 208 (109-346)				308 (349-674) 68 (28-344)		n(4:11) 1 (0:2)		609 (313 1020) 87 (30 130)		2(1-3)	60 (0.0-60)		0.1(0.00.1)	1380 (794-2220)	13(1028) 11(0218) 01(0102)			NO (1340-3230) 6 (1 (200-909) 6		WINCOM COMPANY
familie Entercore facility	Entitioner to one or more arithmics. Plantopinstone.	41 (28:47) 97 (82:391)	8.1 (8.2/2.8) 18.4 (7.8-17.7)	3870 (2490 8920) 8640 (3390 13900)	492.9 (296.5- 692.9) 1930.6 (646.3- 1931.1)	12 (0-21) 36 (0-21)	14 (87-23)		124.3 (45.5-218.3) 164.9 (80.9-318.2)	17 (9.80) 68 (39.100)		1120 (823-2490) 2770 (8390-9790)			61(8.062)	424 (299 789) 109 (244 200)	4.0 (1.0.7.7) 9.1 (2.0.49.8)	7 (4-12) 26 (17-00)	0.0 (0.0 0.0) 0.1 (0.0 0.1)	696 (372 6100) 2220 (1090 3900)		2 (3-7) 4 (3-7)	(02-03) 02	172 (80-307) 278 (100-819)	0.0(0.20.7)	21100 (2K700)	12(0713)			00(10'0.000) 0 00(200.0000) 0	19264 89215	41100-(30700) 104000 4.0-(3.0-10.3) 124000 (27300) 264000 16.3 (6.2-27.4)
Entercaccus function Entercaccus	Vancompoin Emissioner in one or	34 (33-90) 38 (43-90)		9010 (7190-7940) 8790 (9420-17700)	200.2 (200.2 911.2) 1020.2 (403.2 1402.7)	27 (0-22)	14 (88-28) 34 (20-87)	1190 (173 2110)	179.4 (67.1-247.2) 36.3 (176.1-	28 (21-64) 66 (26-617)	0.1 (0.2 0.4) 0.6 (0.3 1.1)	3370 (3620-8720) 3670 (3170-9760)			61(8.062) 62(8.163)	807 (360 1700) 1740 (800 700)		14 (7.24)	0.000.000	2280 (1991-2090) 2280 (1990-2980)		3(2-4)	10 (5.0-60)	282 (139-812) 482 (111-1298)	0.6(0.31.2) 1.4(0.72.7)	19200 (12100- 2800) 2800 (29000-	17(1228)	79 0000 (24 0000 59 0000) 78.1 (86 0000 (54 4000 17 00000) 81.5 (23.0 No.61 4N 120 (82.0 129.4) 20	NO (2700-7660) 6 000 (8560 000) 1	19267)	95200 (27000 150000) 9.1 (4.7-19.3) 242000 (170000 293000) 26.8 (17.2-28.4)
Other reterminant	Pleasopinston	29 (17-26)		2830 (1279-4230) 1460 (829-2390)	491.1)	F(1-11)	04 (01-12) 04 (02-07)		819 (7.4-119.3) N.R (17.0-62.1)	10 (9-10)	0.1 (0.1-0.2)	911 (347 0400) 824 (279-933)	K#(4.8 18.8)	2 (0-0)	60(8.060)	194 (24-327) 197 (91-200)		4(27)	0.000.00	332 (138-616)		1 (9.1)	10 (2.0-40)	39 (9-120)	0.1(0.00.3)	acco (2710 ANTO)	0.2(0.30.3)	6060 (2060) 88200) 6.0 (2		1 (100 1700) 0	1 (0.0-0.1)	2010 (1720- 2010) 1.0 (0.2-2.6) 2010 (2023-1730) 0.8 (0.3-1.7)
Other microscosi	Vancompole Exciting to our or more artificials	33 (34-95)		2970 (1710-2620) 2970 (2700-2620) 4790 (2000-7200)			10(03-17)	267 (148-831) 724 (350-1335)		12 (9.21)		1079 (872-1879)	19.4 (9.0-19.2)	3 (3-4)		261 (117-255)		4(24)	an-(00-an)	204 (218 799)		1 (9.2)	60 (5.0-60)		0.1(0.00.2)		0.2(0.20.3) 0.3(0.30.7) 2.4(1.73.4)			(2 (105 797) 6 (00 (444 1890) 6		14790-(12700-
Endertelia sell	Animply-mile	88 (88-80)					0.1 (0.2-0.7)		36.2 (21.0 58.1)	29 (18-64)	0.1 (0.2-0.4)	2360 (1779-4140) 12900-19830			60 (5.060)		1.7 (1.1-0.7)	23 (9-29)	0.0 (0.0 0.0)	1330 (902 2960)	10 (10 41)	1 (9.1)	60 (5.0-60)	Ni (55-126)	0.2(0.10.5)				27.0 (MA) 171	100 (1000-2010) G	2 (0.1 0.2)	2008) 18 (10.24) 27100 (1000) 2008) 24 (10.24)
Enderskie od	Anticoposicille Data Laciano Beta- Incianaca infeligera	200 (100-100)	34.9 (24.9-35.0) 26.1 (26.3-40.1)	2010E) 1990E (1290E- 2040E)			28 (12-11)	687 (796 2270) 1940 (972 248)		199 (180-299) 117 (78-177)	13 (10 23)	1200 (1000 2200) 11200 (1220 1000)			61(8.161)	373 (232.840) 854 (548.1261)		60 (20 100) 52 (30 ***	02 (01 02) 01 (01 02)		9 Mar (10.7.23.1) 9 Mar (10.7.23.1)	2(1-7)	50/30-50	181 (118-279) 417 (271-409)			124 (K7-177) 92 (6.0 128)	1330000 (1000000 128.8 71400000 7111.0	(80.5		70310	NAME (1880) 80'00) 13 (1.0-7.6) 13 (1.0-7.6) 14 (1.0-7.6) 14 (1.0-7.6)
Enderthis sell	Categorea	8 (9 12)	0.9 (0.9 1.4)	471 (229-2090)	76.5 (29.1-122.3)		03(0104)	PH (800-331)	22.7 (11.8.78.7)	4(24)		279 (242-MP)				109 (98-179)		2(10)			0.1(0.104)		00/0000		01(0103)	3290 (2200 4420)	0.3 (0.2 0.3)	52600 (52900- 79900) 5.1 (7	147.0 99	H (120 110) 6	1 (0.1-0.1)	10.00 (KTO- 24.00) 1.9 (KR-2.4)
Endertelia seli Endertelia seli	Plansquindown Third governion cophalosparios	147 (91 225) 102 (63 199)	17.2 (10.7-26.1) 12.0 (7.3-1840	13100-(NE70- 19900) 9120-(NE20-12200)	1333.9 (983.4 2330.8) 1069.2 (686.9- 1459.8)	27 (80-27) 28 (0-31)	28 (12:31) 18 (87:34)	1800 (894 2770) 1780 (840 2780)	277.7) 277.3) 298.4 (88.1-322.0)	80 (30-122) 80 (30-82)	0.8 (0.8 1.2) 0.3 (0.3 0.8)	7649 (8179 11300) 3299 (8779 7640)			81(8181) 81(8882)	871 (549-1330) 762 (339-1460)		36 (20-83) 26 (10-83)	41 (69 41) 41 (69 41)	3779 (2130-5490) 2540 (1700-3770)		4(3-4)	(0.0.0)	628 (275-668) 286 (347-668)	0.9(0.61.5)	71200 (21200) 109003) 41000 (11100- 67200)	45(4893)	113000 (74000 140000) 110.1 72000 (24000 100000) 71.0	(TERONA) XX	100 (2000-12300) 6	8 (0.8-1.2) 16 (0.8-1.2)	17,000 (8900). 19900) 12,8 (K.4.09.0) 199000 (2730). 199000) 10,2 (K.4.09.1)
Endertolia soli	Trimologoise Sallamelonamie	148 (106-290)	19.6 (12.4-29.9)	1908 (9680 2298)		11 (0-17)	13 (68-20)	961 (872-1820)	112.4 (66.9 177.6)	88 (55 120)		K290 (NASO 12400)	83.4 (12.8 (20.3)	8 (8 %)	61(8061)	NOS (NOS 77%)		20 (20-10)	0.1 (0.1-0.1)	£129 (2760-6010)		2 (2-4)	60 (8.0-60)	28 (189-377)			7.2 (4.9 (0.1)	118000 (70000 167000) 114.5	(77.1-162.3) 470	100 (1020 4800) 0.	3 (0.3 67)	79300 (27200 113000) 7.2 (4.6-10.7)
Endertable and Group A	Entitioner in our or more architects	329 (207-290) 18 (11-29)	38.4 (24.5-38.2) 2.1 (1.5-5.4)	29000 (18900- 41600)	30344 (2041.8- 5217.4) 183.1 (103.0- 391.4)	79 (46-119) 2 (9-4)	84 (8.2-19.4) 62 (60-67)	4940 (1970-1000)	767.7 (244.2) (1798.3) (7.7 (8.0.78.0)		1.7 (1.1-2.8)	1460 (1000 2460) 190 (1149-250)			0.1(0.20.4)	3400 (2340-3990) 179 (0-380)		77 (30 114)	02 (0.1-0.2) 0.0-000 0.00	8180 (5480 11800 2000 (813-1780)	n 17.9 (12.0-29.8)	17 (11-27)	60 (88-61)	1760-(1170-2600) 99 (2-307)	3.8(2.6.8.7) 0.2(0.0.0.7)	206000) 126000 (193000	113 (99-200) 0.1 (0.2-0.7)		(185.6 32) 47 (0.15.0) 38		2(23-44)	721000 (1010000 750000) 80.9 (10.2-73.8) 7000-0-24200 0.7 (0.0-2.4)
Crosp A Steptomorae Cross B	Macrolide Emissioner in one or more anishinian	18 (11-29)	2.1 (1.3-3.4)	1160 (966-2500) 1160 (966-2500)	301.6) 183.1 (113.0- 301.6) 281.4 (138.7-	2 (0:4)	62 (66 67)	127 (0.2%)	17.5 (8.0.78.0)	21 (12-11)	0.2 (0.1-0.3)	1900 (1140-2970)	18.5 (11.1-28.9)	2 (0-4)	60(8.061)	179 (0.380)	1.7 (0.0-5.4)	9 (8-27)	40-(00-40)	1060 (613-1760)	23 (13.58)	10.0	60 (3.0-60)	99 (0.303)	0.2 (0.0 0.7)	2710 (1890 AND)	0.4(0.2-0.7)	7380 (4070) 13800) 7.2 (10.13.0) 391	(0-1300) G	0 (0.0-0.1)	7010 (0-24400) 0.7 (0.0-2.4)
Stephenous Group B Stephenous	Hampinian Mankir	27 (19-42) 113 (68-175)	3.2 (1.8.6.2) 13.2 (7.8-207)	2220 (1360 3960) 10000 (4090 19700)	11704 (NT 2- 16112)	F(1-11) 11 (0-33)	04 (0.1-1.7) 1.7 (0.0-3.9)	1020 (0.2940)	90.7 (7.4-119.7) 129.1 (8-0.343.8)	13 (N-19) Na (No-83)	03 (04 03)	1123 (T23-0480) 2993 (T230 T330)	44 (11.2-71.1)	4 (9 14)	61 (8.062)	NIT (0-1430)	20 (0.344) 49 (0.013.5)	28 (18-48)	61 (09 61)	321 (321 813) 2230 (1340 3340)	49 (80.77)	1(9.0)	60 (8.0-60)	227 (0:404)	0.2(0.00.4)	17900-(4260- 20000)	14(0320)	94400) 6.2 (I 267000 (171000 398000) 26.01	264-263) IP	#(11812%) 6 #0(0.7940) 6	1 (0.0-0.1)	2000 (0.7200) 2.6 (0.0.7.5)
Stoptoscow Group B Stoptoscow	Penindia Excisioner in our or more architects	2 (3-3) 129 (78-205)	0.2 (0.1 0.4) 18.0 (8.1 28.0)	178 (109-284) 11400-(8900- 18100)	28.9 (12.3-33.4) 1338.4 (807.4 2136.0)	0 (0.1) 17 (0.79)	01 (00:01) 20 (00:44)	22 (8 100) 1290 (0.3900)	49 (1.0-11.7) 174.8 (0.0-499.7)	1 (1-2) 63 (22-93)	0.00000) 0.00000)	90 (15 £19) 5620 (5680 8290)			61 (5.062)	21 (0-67) 729 (0-1700)	0.2 (0.0 0.8) 7.1 (0.0 0.4)	0 (0.1) 28 (17-49)	0.0 (0.0 0.0) 0.1 (0.0 0.1)	27 (29-64) 2920 (1990-1960)	01 (01 01) 3 18 (14 84)	4 (9 H)	60 (88-60)	19 (2-22) 32k (0-772)	0.0 (0.0 0.0) 0.7 (0.0 1.7)		0.0(0.00.0) 1.9(1.0.2.2)	3290 (3390-3000) 0.3 (5 299000 (294000) 438000) 29.1 ((12-124) 6 20 (190-2740) 6		1790 (278-2620) 0.1 (0.0-0.3) 29000 (827-8800) 3.8 (0.1-8.4)
Managhtin influence Managhtin influence	Animposistin Third generation cophalosperies	2 (3-7)		1480 (668-2790) 149 (86-279)			0.3 (0.0 0.8) 0.1 (0.0 0.1)	200 (04-900) 44 (14-99)	26.2 (3.7647.8) 5.1 (3.743.8)	20 (14 27)		1760 (1280-2790) 171 (120-230)			60(3.063)	301 (29:420) 31 (24:89)	20(0383)	10(7.10)	00 (00 00) 00 (00 00)	930 (651 123) 87 (65 123)		2 (9.1)	pacayoa	197 (22-305) 28 (13-49)	0.1(0.00.1) 0.1(0.00.1)		0.0(0.00.0)	1200 (2300-4000) 0.1 (i 1200 (2300-4000) 0.1 (i 120000) 20.1 (H(F7-1210) 0 1(M-199) 0	0.0000	9920 (823 17000) - 0.9 (0.1-1.7) 1390 (688 2270) - 0.1 (0.1-0.2)
Manuphila inflamor Klahada manusiar	Emissioner in one or more artifestics	17 (8-30) 97 (80-090)	2.0(0.9.3.7)	1900 (708-2000) 8600 (7480-1730)	1005.6 (471.4: 1560.7)	E(440)	0.1 (0.1 0.0)	203 (94-645) 203 (799-1200)	36.7 (6.3-79.4) 86.2 (86.3-1887)	20 (19-27) 84 (20-79)		1920 (1730-2470) 2770 (1220-7940)			69(5061)	392 (82-666) 393 (233-624)	34 (9.84.3) 3.8 (3.34.0)	20 (8 12)	00 (00 00) 00 (00 01)	988 (717 6270) 1880 (1280-2790)		2(9.4)	pa-aay oa		0.010.10.7	14800 (11400- 17800)	0.4(0.30.3) 1.6(0.12.2)	20000 (18200) 124001 24.1		2 (188 1930) 6 90 (89 230) 6		20100 (2020) 20100) 1.0 (0.2 1.8) 22100 (13100) 23100 (13100) 22 (1.3 5.8)
Eleberatio procumentar Eleberatio	Aminophysicales Bris Lavium Bris- lavium are inhibitors.	292 (126-396)	23.7(147.39.8) 5.8(5.49.5)	18080-(11200- 27200)	2108-6 (1719-0- 3191.2) 317.3 (301.9-	7 (8 12)	14(8823)	464 (139 1139)	72.0 (78.0 120.7) 121.4 (88.2 202.7)	116 (78-049)	1.1 (0.0 1.4) 0.1 (0.2 0.4)	10000 (4990 14600)	1000 (07.2 142.1)	4 (27)	61(5061)	362 (209.877) 791 (353.998)	3.8 (3.8-8.4)	47 (70-71)	01(0102)	4140 (2790-4080) 879 (884-1390)	98 (89-183)	2 (3-7)	60 (3.0-60) 60 (3.0-60)	160 (87-266)	0.01020.0	38900-(27900- 83600)	38(2.752)	472000 (£78000 309000) 61.6:	(427-86.9) 17	20 (1000-2000) 0 (00 (1120-2070) 0	20165	27(15:15) 27(15:15) 42:00) 27(15:15) 27(15:15) 27(18:16) 27(18:16)
Eleberation processories Eleberation	Categorea Florespiedens Third granuline	101(10:30)	17.1 (10.8-26.0)	1220 (2883 7070) 17000 (8270) 17600 (8770)	2013) 1518.7 (197.4 2018.5) 1827.7 (1148.7	12 (7-19)	13 (67-21)	970 (128 1400)	131.4 (41.7 196.7)	28 (18-27) 82 (10-117)	0.8 (0.8 1.1)	7290 (8940 10400)	79.9 (26.0-200.7)	4 (4 10)	61(8061)	847 (318-869)	5.5 (5.2 8.4)	32 (21-29)	0.1 (0.0 0.1)	2010 (1000-4220)	61 (40.92)	2(1-4)	100 (3.0-0.0)	217 (126-386)	0.1 (0.3 0.3)	7120 (2770-10700 24700 (17600- 34000) 29600 (21100-	24(1733)	201000 (20200) 572000) 29.3 (27.0 (9.7) 180	BO (1120-2900) 6	20165	3000-(1600- 4600) 30-(18-67)
Gamp A. Josephonous Gamp A. Josephonous Gamp A. Josephonous Gamp G. Josephonous G. Josephono	Florospinsions Third premision cephalospeins Trimelospeins Sallamelospeins	176 (110-267) 139 (47-234)	20:0 (12.8-31.2) 18.1 (11.4-27.4)	27700) 17800 (MAD 22000)	2774.7) 1411.4 (2003.9- 2494.4)	21 (8-47) 9 (4-17)	28 (89-8.1) 18 (89-18)	764 (146 E770)	221.7(79.1-492.1) 99.3 (89.4 149.2)	88 (80 127)	18 (07 14) 69 (08 12)		76.2 (81.8-009.3)	8 (2.9)	61 (8.062) 60 (8.061)		4.1 (2.0-7.7)	39 (20.5%) 36 (20.5%)	61 (01-61) 61 (01-61)	3000 (2230-3540) 3170 (2090-2490)	0.7 (4.0-20.7)	8 (2-88) 2 (1-8)	60 (5.0-60)	429 (156-879) 161 (86-339)	0.0(0.3.03)	78900 (70000)	18(2035)	494000 (122000 494000) 49-3 (21.4-63.0 170	NO (1210-7280) 6 NO (830-2920) 6	20165	12000 40 (22 11.4) 2700 (1500 27 (1.5 44) 2700 (2700)
Mergandia upp	Parapinian	276 (240 780) 0 (2-0)		1 (1-7)		68 (40 187) 0 (0-0)	19 (\$7-124) 03 (\$0.03)	4000 (This HIS)	11142) 60 (80-61)	0.00.00	1.4 (1.0-2.0) 0.0-(0.0-0.0)	4 (2.8)	126.8 (No. 9 (NO. 1) 0.0 (0.0 O.1)	0 (0:0)	69 (5.060)		0.0 (0.0 0.0)	0 (04)			03 (60 03)	0 (0 d)	00/0000	1 (0.1)	10(1848)		48/34475 00(0000)	2140 (1900-1110) 0-2 ((11.91) 0		200000 19.5 (12.6-29.2) 294 (144-662) 4.0 (0.0-6.1)
Mercandir om Mercandir opp	Participantine containments Third generation cophalosperies	0 (2-0)		0:00:11 2:(1-4)		0 (0-0)	03 (50 03)	0 (0.0)	60 (50 65)	0.00	02:00:00 02:00:00			0 (0-0) 0 (0-0)		1 (9.7)	400040	0.000		1(0:0)	02 (0.0 02)	0100	60/88-63 60/88-63	1 (0.2)	40/0840		0.01(0.00.03) 0.01(0.00.03)	397 (273.995 6.0 d) 2678 (1870.3836) 6.7 d				97 (27 172) 9.0 (0.0 (0.0) NZ (229 1090) 9.1 (0.0 (0.1)
Monandia um Monhadorias subsociosis	Entitioner in one or more antibiotics Enteroiser desg resistance in TE	0 19-01	400040	2 (2 6) 0 (0 0)	010107	0.000	00/00/00	110.0	61/80-621	0.00	42-02-42) 42-02-42)	7 (3-03) 6 (2-03)	01(0003)	0.000	60(3.060)	2(34)	40 (00 4.0)	0.000	0.0 (0.0 d.E)	6(1-20) E(1-20)	02 (50 02)	0120	60/88-68 60/88-68	2 (3-4) 4 (2-11)	40,004.0		0.0(0.00.0)	388 (230 NRS 0.1 d		(22-136 6 (22-136) 6	0120-001	999 (830-1790) - 0.1 (0.1-0.2) ECDI (800-2130) - 0.1 (0.0-0.2)
Mysolautoise informinis	Inminist remove	-		0.000	0.000.00			0.00	60/88-60	0.00.11	42-02-421	36 (28 82)	04/020/0	0.000	0010000	619.00	0.1 (0.0 0.2)	100.01	0.000.00	N 477-708	01/01/02	0.00	60/30-6/3	749.28	0.00.00.0		0.1/0.10.11	1400 (mass 2000) 1.4 (.01m IN	0.0-401 0	00000	2130-0-300 02-00-07:
Mysobasisriam informalisis Mysobasisriam informalisis Mysobasisriam informalisis Natuuria suurorbasuu Natuuria guurorbasuu Natuuria guurorbasuu Natuuria	Makis drug centriames excluding extensive drug emistance in TR Edinspic in more emissioner	-		0 (0.0) 0 (0.0)	0.00000			012-01	02-03) 02	0 (0.1)	0.00 (0.00 (0.0) 0.00 (0.0)	22 (7:Ne) 8 (4:8)	02(0103)	0 (0:0)	60(5.060)	12 (0.0%)	0.1 (0.0 0.2)	0 (0.1)	40-(00-40) 40-(00-40)	31 (11-75) 7 (8-9)	01 (80 02)	0 (0 1)	00 (0.0 c) 00 (0.0 c)	14 (2.82)	0.0000.0		0.0(0.00.1)	4940 (2000 11400) 0.7 (31.0 20	H (21-400) 6	0 (2.0-0.1)	2730(M24990) 0.1(0.0.1.0)
Mysorbackerium indicernalisate Nationeria	more analysis in	-		0 (04)	0.00000			0100	1012010	1 (0.1)	0.000.00			0 (0.1)		23 (9-8%)	0.2 (0.1 0.3)	1(12)		96 (47 199)	02 (0.1-0.3)	0 (0 1)	001000	39 (7-79)	0.1 (0.00.2)		01(0102)	1479 (1290-2180) 0.2 of 29200 (20000- 34700) 2.3 (1		H(112499) 6		T100(2900 18700) 0.7 (0.2 LH)
Notaeria generalment Notaeria	Plearmaindean Third gravation cephalogories Emissace in one or	-								-								-								-		209 (123-141) 0-0 (1060) -			41 (19.82) 0.0 (0.0 0.0)
Protess upp.	Aminophysiales	2 (3-3)	0.2(0.1-0.4)	178 (109-287)	 28.8 (12.8-354)	0(00)	00 (00 00)	9 (1-20)	10(81-23)	2(1-9)	40 (00 40)	197 (79-224)	13(8822)	0 (0:0)	60(8.060)	7 (3-19)	0.1 (0.0 (0.1)	1 (0-1)	0.0 (0.0 0.0)	36 (37-60)	01(0102)	0 (0.0)	00 (0.0-0.0)	3 (3-4)		1.128 (We 2100)	01(0102) 18/0714		30.0 10	(8.199) 6	0 (0.0-0.0)	DN (71-NI) 00-00-00 HN (177-22%) 0.1 (00-0.2)
Protess san. Protess app.	Antonomistin Planopinskom	11 (8-20) 7 (8-11)	1.810.9.2.01 0.810.9.1.71	1140-756-1620 623 (391-988)	1982 (824-212.) 72.9 (844-118.9)		01 (00-01)	20 (0.02) 30 (20-50)	3.1 (0.0-5.0) 3.8 (2.3-01.4)	9 (3-9) 3 (3-9)	61 (03 62) 61 (08 61)	827 (290-1400) 484 (279-790)		0 (0.1)	60 (5.0 6.0)	29 (29 (42) 28 (29 (42)	0.2 (0.0 0.0)	2(14)	0.0 (0.0 d.0)	265 (212-621) 267 (119-528)	03 (03-02)	0100	60/88-63 60/88-63	9 40 28 19 (9 52)	4.0(0.04.1)		18/8714 03/8304)	227000 11.81	109 22.11 22 (109.0 26			2700 (0 11700) 0.4 (0.0 L1) 6200 (2600 11700) 0.6 (0.0 L1)
Protess upp. Protess um. Protess upp.	Third presents containments Trimologoise Sallamelenande	8 (9 12)	0.9 (0.6 1.7)	719 (187-914) 709 (827-1110)	82.4 (98.0-130.2)		01 (00 02) 03 (00 01)	48 (23-149) 27 (0-43)	19 (2.6 (1.0) 3.2 (8.0 (1.4)	3 (2-D) 6 (3-R)	0.000 0.0 0.1 (0.0 0.1)	228 (139-201) 338 (308-887)		0 (0.1)	60(0.060)	82 (0.40) 20 (0.40)	0.5 (0.2 0.1)	1 (1 d) 3 (1 d)	00:00:00 00:00:00	312 (643 (947)	02 (03 03) 03 (03 09)	0100	60 (3.0 6.0) (0.0 6.0) 0.0	21 (8-26) 10 (9-25)	41/0841		03/0204i 07(0303)	104000 (72000-	79142) 27	2/21912W) 6 2(0:407) 6		9770-(2280-12800) 1.0-(0.3-1.2) 4110-(3-5280) 0.4 (0.0-0.5) 2280-(17700- 42000) 2.4 (1.3-0.5)
Frances Familianes sempleme	Eministra in our or more antibiotics Antirophysmides	14 (10-29) 49 (29-20)	1.8(1.0.29) 5.7(3.489)	1200 (807-2200)	143.6 (100.2: 236.9) 308.1 (100.7: 794.0)	2(14)	02(010A) 01(000A)	179 (H 326) 109 (H 281)	21.0 (00 to 28.4) 12.8 (0.0 32.7)	12 (7-19)		2092 (MER 2720) 2092 (1230-2000)			60(3.060)	134 (44-249) 48 (9-121)	1.1 (0.4-2.4) 9.1 (0.0-1.2)	9 (849) 9 (843)		80 (00 NH)		1 (9.1)	10204102	61 (29-111) 21 (1-91)	41(0.14.5)	17600 (9000 1760) 9710 (7000 1780	12(0913)			200 (RNS 2990) 6		22800 (1700) 2000) 2.4 (1.5.5%) 2790 (21.00200) 0.4 (0.0.10)
	Anti-paradisessed post-file Beta Laciannes inhibitors	BE 178 ATT	TRAIN C 70 TO	MOTO CHINA ETHINA	964.2 (975.9-	7/8/75	05/05/15	40.000.000	20.000.000	et ettern	21,0120	340 (777) 1700		1/10	60/000 D	100×170×100	200200	F (1) - Th	20.002.01	THE CHI THE	Marian	7/2-9	50/3550	117.734.739	annian	22100-(14100-	11//418	397000 (228000	20.00	20/199-5500 6	20102	23 NOS (23 000)
Faralismon arregiona Faralismona	Categorea	111 (47-170)	13.0 (7.8-20.4)	1830 (PIDS 13300) 30000 (4230	1192.1 (200.8- 1192.1 (200.8-	19 (11.12)	23 (13-37)	1730 (983 2880)	201.9(115.5 201.4)	49 (13-72)	0.3 (0.3 0.7)	£90 (379-6£8)	42.5 (27.8-42.5)	9 (9 14)	61(8161)	777 (479 1200)	7.8 (2.6-12.7)	21 (19-92)	0.00000	1820 (1190-2760)	44 (2.8-6.1)	4(24)	60 (5.0-60)	322 (196-317)	0.7(0.4 l.1) 0.8(0.3 0.7)	24300-(17900- 33200) 24300-(17900-	24(1732)			70 (2870 4480) 0 70 (2870 7880) 0	4 (0.3-04)	70000 33 (20 AB) 7100 (4700 70 (43 933) 20000 70 (43 933) 4300 (4900 43 (29 47)
Frediment arterions Frediment arterions Frediment arterions Frediment arterions Frediment arterions Frediment	Forth premine ophshaparin Third granuline	89 (91-132)		780(479 (170)	1873 0 1371 0 1911 9 (613.8-	2(10)	02(0104) 02(0104)	172 (89-200) 274 (149-770)	20.1 (20.0 32.0)	28 (29.56)	0.1 (0.2 0.3)	2100 (2000 4040) 3380 (2200 4040) 2000 (2330 5050)			69 (5.060)	77 (43-127)	0.8 (0.4 LZ) 1.7 (0.7 0.3)	26 (20 22)	48-(09-41) 48-(09-41)	1879 (1990-2020) 1899 (890-2110)		9(9.1)	00 020 00	22 (18-84) 72 (18-84)	01(0801)	2100 (1100 2100 (1100 2100 (1100	18(1328) 18(1328) 22(1318)	318000 (214000) 411000) 30.4 (210-429 42	DE (240-648) 0	(1844)	THE (230 1100) 07 (0.0 1.1) 1400 (270) 14107-271
Paradimenta arregiment	Entitioner in our or more arithmics	192 (116-299)	22.4 (13.6-38.9)	17100-(10000- 26600)	19964 (1210.4- 2000.1)	47 (27:7%)	88 (81/92)	290 (2790 700)	86.7 (27.5.40.2) 89.7 (279.2) 89.6)	88 (37 627)	0.2 (0.0 1.2)				62(8163)	179/71 3390 1890 (1340-2990)		36 (20-55)		3230 (2040-0490)		9 (3-10)	102050	79 (470-147)	17(1023)	90000) 91300-(31800- 31300)	43(3153)	733000 (103000 1020000) 71.3	262 NI NI NI 263 NI NI NI	12 (7927-1790) 6 1900 (75-20- 1900) 1	19714	30000 (11900) 16000 (11900) 271000 (17.5 (11.3-36.3)
Salmondia Paratyp	ti Plescopinskom. Multi-drug croisianur in Kalmonda Tvols ar **			0 (0.0)	0.0 (0.0 0.0)			0 (0.0)	80 (38-80)	olod	4.0 (0.0 4.0)	3 (3-4)	0.0(0.0.0.0)	0 (0-0)	60(5060)	1 (9.2)	0.0 (0.0-0.0)	0 (04)	0.00000	K(8-00)	03 (60-03)	0 (0 0)	60 (8.0-6.0)	1 (0.7)	0.010.00.03	1 (24)	0.0(0.00.0)	X2 (41 /W) 6.0 (1000) 10	(9.2) 6	100-00)	34 (3.29) GE-(GE-GE)
Administra Paratra	Entitioner in one or in more antibiotics	_		0.000	0.000000			010.0	0.010.00	0.000	0.00 (0.00 (0.00)	100	0.00000		60(3.060)		0.00000	0.000		na m	02 (50 02)	0100	60/88-68		40,004.0			1 (0-1) 0.0 (32 (41/9) 0.0 (1060) 0/		0.03-0.01	0 (0 0) 0 (0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
Salmondia Typis	Pleasupinsisse. Makirahag renisiasur in	6 (2-11)	0.7(0.21.8)	919 (180-1190)	48.8 (21.1-131.8)	1 (0.0)	01 (00 0.0)	107 (12-292)	12.8 (5.4.94.2)	3 (1-7)	48 (08 4.1)	212 (94 505)	24(093.7)	1 (0-2)	60(5.060)	88 (7-180)	0.5 (0.1 0.3)	1 (0-2)	0.0 (0.0 0.0)	11 (11-200)	02(0103)	0 (0.1)	60 (8.0-6.0)	19 (3.80)	0.0(0.00.1)	265 (96.332)	0.0(0.00.0)	488 (1770-1620) 0.2 (1269) N	(9.82) 6	10 (0.0-0.0)	W2 (129.22W) 0.1 (0.0-0.2)
Salmandir Typis Admindir Typis	Malir drug centriance in Subscrapfu Typhi and Faratyphi Eminiance in one or more aniibinia.	1 (9.2)		90 (St. 292) 997 (231-1280)			02 (00 02) 02 (00 02)		13 (2.5 Ma)	1(0.1)		29 (29 229) 234 (317 494)			60 (5.060)		0.1 (0.0 0.2)	0(01)	40 (00 40) 40 (00 40)		02 (0.0 0.1) 02 (0.1 0.3)	a ia si		2 (0-8) 21 (0-80)	40(0844)		0.0(0.00.0)	1010 (201-2000) 0.1 (5320 (2220 10700) 0.8 (0 (20-60)	EN (0-40) 00 (00-00)
Xalmendir Typhi New typholdd Xalmendir New typholdd Xalmendir	Plantonindon Entition is one or more arithmics	213-71	0.210.10.21	368 (YG 280)	HA(HA-327)	010.01	08 (80 01)	20 (0.40)	33 (83 80) 33 (83 80)		0.0-10.0 O.D.	827 (180 (200) 827 (180 (200)	A14A115	0.0013	60(5.060)	81 (2 120)	0.000121	1000		628 (28-2130)	14 (0.1-44)	01000	60/8068	44 (9.20)	0.1 (0.0 0.0) 0.1 (0.0 0.0)	172 (83.330)	0.010.00	4750 (1470 14700) 0.4 ((9.86) 0	0 /2.0-0.01	MM (222320 01 (00 02)
Servatio see.	Aminoshovatiles	X (2-12)		671 (798-0090)			01(0001)		41/00/20			229 (120-300)			60/3.060)		0.1 (0.0 0.0)	100	00:00:00					4013	400000			9600 (7000 12000) 6.9 (MAG 1800 01 (00 0.1)
Zerostie upp	Anti-paradimental presi din Belo Las inmos inhibitors		1.1(0.82.2)				63 (61 63)		25.9 (11.3-49.3)			396 (203-994)			60(5.060)		0.7 (0.3 0.3)	1 (1-2)			63 (61 63)			29 (10-47)	0.1 (0.0-0.1)	962 (369-1920)	01(0101)	19200 (11400- 20400) 1.9 (1	.100 10	o (43.336) - 6	o pa-eoj	2010 (2000 7520) 0.4 (0.2-0.7)
Zernatia app. Zernatia app.	Catopeen Floropinion	7 (9 12)	0.9 (0.9 1.8)	666 (200-1110)	77.9 (44.7 (29.8)	1 (0.2)	01 (01 02) 01 (00 02)	76 (13-047)	11.1 (8.6-20.3) R6 (1.3-28.6)	3 (1-4)	0.0 (0.0 0.0)	135 (73-216) 236 (133-387)	23(133.8)	0 (0.1)	60 (5.0 60)	28 (9-61)	0.1 (0.2 0.4) 0.1 (0.1 0.4)	1 (0.2)	40 (99 40)	79 (79 130)	01 (00 02) 02 (01 03)	0 (0 c) 0 (0 c)	60 (5.0-6.0)	11 (9-20) 9 (2-22)	20/0243 20/0243	660 (793-0050)	0.0(0.00.1)	21800 (8000 21800) 1.3 (0				2689 (1280 4899) 0.2 (0.1 0.4) 1990 (200 3989) 0.2 (0.0 0.3)
Zeronie spp. Zeronie spp. Zeronie spp. Zeronie spp. Zeronie spp. Zeronie son. Ziejelle spp. Zielenle son.	Catoperen Florespinsten Foreir prevaies exploiteparies Titel prevaies exploiteparies Entitioner in our or more attibities	9 (5 15) 19 (11-20)	1.1 (0.6-1.7) 2.2 (1.3-5.4)	819 (273-1290) 1670 (1089-2620)	99.3 (193.3 (191.3) 199.2 (197.9- 396.0)	1 (0-2)	01 (00 02) 01 (01 03)	112 (99-226)	82 (53-060) 151 (64-267)	7 (4-11)	0.1 (0.0-0.1)	267 (148-491) 392 (146-997)	3.8(3.49.3)	0 (0.1)	60 (5.060) 60 (5.060)	42 (14 W)	0.2 (0.1 0.4)	1 (0·2) 2 (1·2)		291 (99-300)	04 (02 08)	0 (2-0) 0 (2-0)	102-02) 02	14 (9-70)	0.000000	427 (297 476) 2649 (986-2890)	0.0(0.00.1) 0.2(0.10.2)	3830 (3230 14388) 6.9 (32300 (39390 30900) 3.2 (1	(1-1.0) N (1-1.0) 12	(12.00) 0 (10.200) 0	02240	70 (29 130) 0.1 (0.0 0.1) 2021 (200 130) 0.3 (0.1 0.4)
Zerostie son. Zbigotle spp.	Entitioner in our or more arithmics Plannapinshops	28 (16-80) O (9.1)	2.2(1.5.54) 3.1(1.647) 0.0(0.00.1)	2120-1140-1990 27 (9-42)	275.4 (148.9- 419.7) 3.2 (6.0.7.8)	7 (8 62) 0 (8 0)		M4 (125-1545) 5 (1-15)				K21 (475-0120) 178 (42-709)			60(5.060)			3 (2 8) 0 (0 1)	40-100-481 40-100-481		08 (0.7 L0)		10 (5.0 4.0)		02:010.h 01:000.h	2340 (1430 3890) 113 (43 282)	02/01031	880 (320 1100) 69 (3200 (3700 3000) 3.2 (4700 (2000 7000	1870 60	(7-726-1970) G ((3-67) G		12 (0.0 2 2 1 1 2 (0.0 2 2 1 1 2 (0.0 2 2 1 1 2 (0.0 2 2 1 1 2 1 1 2 (0.0 3 2 1 1 1 2 1 1 1 2 1 1 1 2 1 1 1 2 1 1 1 2 1 1 1 2 1 1 1 2 1
Shinda see	Plearupinshum Eminimur in our or more anibiotics	0 (0 1)	0.010.00.11	27 (9-62)	120.173	01000	03/00/02	810-00	66/83-57	100.20	0.000.00	190 (42,000)	13/043/0	0.00	60/8.060)	21 (0.9%)	0.2 (0.0 0.4)	0.0031	0.000.00	228 (102-109)	0.0011.0	0100	60/88-68	30 (0.90)	010000	111 (43 292)	0.010.00	340-1390-1090 0.1-0	11679 28	chan e	0 /5.0-0.01	N7 (K2 (3ME) 0.1 (0.0 0.1)
Suphylanovan annua Suphylanovan annua	Florespinstern Marriale		17.9 (16.7-28.1) 26.9 (16.1-41.8)					411 (288 1298) 813 (288 1278)		1.00 (97-230)		1900 (1990 1990 (1200 2000)				768 (278 1090) 747 (279 1390)		68 (22.7%)	01(0102) 02(0103)				60 (5.0-60)	287 (114-479) 327 (428-407)				13,0000 (9,0000 18,0000) 130,3 179,000 (12,0000 171,5 2,00000) 241,4				62900 (27000 20000) 4.0 (27-10.5) 71700 (27000 13000) 4.9 (27-12.7)
Stephylanous seeses				20MR-(12MR-	2005.1 (1627.9)		13 (80 II.e)			210 (179-299)		2690) 1820 (1290- 2690)					7.2 (2.7 (3.1)	90 (36 132) 97 (36 132)	02(0103)				01 (80·01) 00 (80·00)	221 (123-60°) 2000-010-3170)				1440000 (1180000 141.3	(113.0 27)	200 (12100)		477000 (190000-
Suphylarorus seenes Suphylarorus seenes Suphylarorus seenes	Melandia Trimelopias Sullamelomanie Vancospois	14 (10-24)	210(143-223) 1.9(1.030) 0.0(0.244)	1240 (878-2700)	170.8 (100.3- 269.1)	1 (1 2)		124 (97-332)				286 (849-2820) 286 (149-277)			60 (5.060)		1.1 (0.5 1.0)	6(44)	40 (00 40) 40 (00 40)		12(8818)		60 (8.0-60)	47 (23.81)		6990 (9090-9030) 1390 (900-2930)	0.7(0.80.8)	114000 (80000- 164000) 11.3 (22400 (8200- 22400) 2.2 (1				70000 (0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.
Suphylanous	Eminimum in one or more architics	TTI (1900-1900)	namen.	2860 (1700	3340.7 (2021.1-	N (80 180)	93 (47-363)	7190 (3600-1200)	NI.0(2357- 1) 12953)	292 (296-418)	28(1843)	28900 (17800- 37100)	292.0 (149.2) 360.9)	73 (18 120)	67 (8.61.2)	400 (190 100)	0 42.8(528-105.5)	129 (80-189)	0.1 (0.2-0.4)	11200 (7360- 16400)	26.9 (26.3 (29.8)	31 (34-83)	61 (88-61)	2790 (1420-1420)	4.0(3.010.1)	182000 (113000 203000)	14.8 (11.0-18.7)	2480000 (1700000 - 278.7 37900000) - 330.1	(109.2) 36	(700 (20400) 1400) 3.	4(20.54)	NAMES (127000- 10800) NT.4 (11.742.3)
Закради бисковна автома Закрановичения закрановичения Закрановичения зак	Site Lectors Site: Sectors adultions Carbonomic	23 (13-37) 49 (29-81)	24(1343) 58(5493)			0 (0.1) 12 (9.22)	09 (60-01) 13 (60-24)	38 (3-184)	44 (8.1-11.8) 109.8 (81.5-238.8)			3799 (2649-5290) 8280 (6129-11200)	80.3 (90.3-000.3)	22 (10-39)	62(8.060) 62(8.164)			ET (12-24)	41 (91-91)	1949 (1110-2140)	34 (24-47)	0 (9.1)		28 (1-67) 8N (426-1489)			0.8 (0.4 0.7) 1.4 (1.1-1.8)	93800 (90000- 128000) 9-0 (0 238000 (180000- 300000) 22.49 98800 (72300-	18123) 11 175362) 31	(5.212) 6 (0.(1710.9900) 6		1270 (66-3280) 6.1 (0.0-6.3) MARIO (27200 96200) 5.3 (27-6.3)
Etropiconomi procumentar Etropiconomi programma	Florespinstern Marriel	17 (10-27) 87 (10-041)	1.9(1.0.52)	1480 (MM-2420) 7710 (4890 12900)	172.8 (101.2- 283.1) 988.3 (828.7- 1284.8)	2(18)	07(0104)	208 (84-887)	28.4 (8.4 (8.5)	28 (20-00)	0.3 (0.2-0.4) 1.7 (1.3-2.2)	2909 (2709-3910) 15500 (11200- 20000)			0.0 (0.0 0.1)	362 (80.799)		11 (10-21) 80 (80-100	40 (99 40)	1280 (904-1800)	28 (20 40) 18 (18 209)	2 (9.8)	60 (3.0-60) 60 (3.0-60)	Em (42.789)			04(0308) 33(2340) 17(1320	13200) 9-4 (1 504000 (200000 433000 43.10	(0.11.0) 98	H(ZZ3 1930) 6 (00)0-4230) 6	1 (0.0-0.2)	1200 (1300 23 (03.24) 24 (03.24) 25 (03.00) 2.3 (03.54) 25 (03.00) 2.3 (03.54) 25 (03.00
Etropiconomi procumentar Etropiconomi	Free die Third prevention cophalmparies Trimelopoine Sulfamelomanie	62 (TR-307)	7.5(4.512.6)	3120 (3000 HENG)	623.1 (260.7h 1970.2) 183.7 (188.1-	1(24) 1(24)	03 (02 10)	ATT (250-760) ATT (24-760)	41.1 (21.7 89.8)	112 (83-190)	11 (0813)	9960 (7770 13300)	96.6 (71.6-129.4)	X (4-13)	61(8061)		49 (57 (1.2)	30 (31-40) 19 (11-21)	0.1 (0.1-0.1)	4149 (1240-4009)	97 (5.1-15.2)	4 (2-4)	60 (3.0-60) 60 (3.0-60)		0.7 (0.4 1.2)	17100-(13200- 22100)	17(1320)	284000 (214000 379000) 27.81			1 (0.1 0.2)	
Emplementar Emplementar Emplementar	representation Transferance Sulfamelianance Emissace in our or	79 (42-109)	21(1254) 83(45135)	6240 (7720 2010) 12100 (7720 2010)	need) 793.4 (235.6- 1233.1) 1306.9 (877.3-	6(0.0)	01 (80 01) 07 (81-17)		47 (1.7 (0.3) 68.8 (8.8 (48.3) 387.7 (46.3)		13 (10 13)	2000 (2190-2000) 12100 (9000) 16200) 24200 (18200)	287.0 (178.4)	12 (2-24)	61(5.062) 61(5.062) 63(5.368)				0.1 (0.1-0.2)	1120 (1000-0770) 1120 (1000-0770)	11.2 (8.5.14.8)	9 (2-20)	100 (3.0-0.0)		1.0(0.11.75)	2000 (4130 THK) 2000 (1420 2000) 9000 (1130	04(0407) 19(1424) 49(4039)	12000 (22000) 312000 (22000) 202000) 30.41 742000 (400000)	263-961) 170	20(20:380) 6 2(86:280) 6 20(20:380) 6	2 (0.0-0.7)	220(1090-0070) 0.2 (0.1-0.9) 2688(-)8200 2598() 2.6 (0.2-0.2) 116800 (96600
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| Table S16, Dea | ths and DALYs (in c | sents and age-so | pecific rates) ass | ociated with and
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| Antoniological
Instrumenti | Bris Laciano Briso
laciamente inhibitore | 887 (989 1249) | 109-4 (79.7-167.9) | 78700-(12200
111000)
 | 20627.1 (7089.3-
12978.9) 2 (| 0.2(010 | 0 184 (86 | n.386) 20.8 (3.1-26.8) | 398 (236-680)
 | 43(2349) | 35200-(20900-
53800) | 397.3 (203.5
606.0) | 1 (0.2) 6.0 (0.0 6) | 76 (27 (29) 6.9 (8.2 (.9)
 | 208 (W-082) | 0.1 (0.2-0.1) | 9100 (HEDS 19700) | 26.7 (11.1-40.7)
 | 0 (0.1) | 0.00000 | 14 (0-29) | 0.0(0.00.1) | 11800-(12800-
12800)
 | 41 (2.5 6.5) | 40000-(270000-
753000) | M-3 (NO.3 LEG.7) | as (10-40)
 | 60 (3.0-60) | 92" (218-2190) 0.2 (0.0-0.4) |
| Antoniological
Insurancei | Carbayessess | 919 (411-1290) | 121.4 (92.4 174.7 | 2 115000)
2 82300-(82200)
 | 20997.3 (TSUK-5:
15299.7) IX | (89-290) 28-6 (11.8 | 13.40 (22300) | (7940 3001.1 (1009.9-
3001.1) | 412 (242-426)
 | 44(237.1) | 36800-(21800-
33300) | 416.8 (241.5
626.7) | 68 (SE 117) 6.8 (S. & S. | 4040 (1100-10400) 48.1 (19.0 11
 | 7) 806 (17-00) | 0.3 (0.1-0.3) | 1900 (2100 11900) | 26.2 (12.8-00-0)
 | 18 (8-35) | 0.0(0.00.1) | 1990 (729-2000) | 4.0(1.97.4) | 25100-(15300-
M200)
 | 43 (23 63) | 30000 (2000)
7000) | 96.7 (83.3 (46.8) | 3000 (1930-0000)
 | 67 (84 1.7) | 8400 (11400
15000) 15.7 (7.7-26.8) | | |
| Antestalante
Insuranti | Pleanquistines | | 127.4 (83.0 00.3 |
 | 11367.6 (7961.1)
16683.6) | | | (NEZD: 1417.9 (799.7:
2314.9) |
 | | | 422.X (290.%
641.X) | | 880 (210 860) 11.7 (24.2 90
 | | | 9779 (KZ40 1420K) | |
 | | 0.0000000000000000000000000000000000000 | 1220 (NEI-2000) | |
 | | | |
 | | 1120005 |
| Animaleholar
Instrumenti | Possib generation
exploitogenies | | |
 | 1190£4 (7898.8- 3 c) | | | H-HU 99.7 (20.9-126.7 |
 | | | 418.9 (218.0
668.9) | | 28 (42-47) 2.1 (8.7-4.7)
 | | | 1000 (1710
1700) | |
 | | | 28 (24-240) | |
 | | 327800 (249880)
833800) | |
 | | |
| Animaliante | Third premation
regulatorymies | | |
 | | | | 192.3 (NE.3 (NE.3 277) |
 | | | 681.6 (265.7)
681.6) | | 89 (97 NO) 87 (22 W.7)
 | | | 10000 (NIZS-
17790) | |
 | | | 130 (49-271) | |
 | | | |
 | | 7020 (2350 13900) 1.3 (0.3-2.4) |
| Assessed | anibatics | | |
 | | | | (1940) 419.6 (3621.7)
619.0) |
 | | | | | 2300) 21.6 (M/h 2
 | | | 1100 (4180
1100 (4180 | |
 | | | 3420 (1000-4100) | |
 | | | |
 | 18 (88 23) | 161000 (97500
300000) 34.1 (34.2-55.9) |
| Citebatir spp. | Animply mides Anti-paradominal penisillin little Lacianese | | |
 | 222.9 (126.1-
368.9) 1 (
368.4 (208.0-
461.0) 4 (| | | 291) 13.9 (80-38.9)
(7-1980) 76.7 (76.0 143.0 |
 | | | 11.6(6.2.262)
19.8(18.8.813) | | 42 (0.176) 0.7 (0.0.20)
278 (040-721) 4.3 (1.0.6.1)
 | | | 329 (353-604) 1
575 (260-3040) 1 | |
 | | | 20 (0.5%)
119 (27-24%) | |
 | | 2830 (2200-8390) | |
 | 60 (3.0-60) | 222 (0.001) 0.0 (0.0.0.0.1) |
| Contractor | address. | | |
 | MTR(MTR27M2) 30 | | | B-905 41.9 (B-170.0) |
 | | | H3(84177) | | 20 (00 40) 24 (1.1 5.2)
 | | | 29 (123-25) | |
 | | | 68 (26-134) | |
 | | | |
 | | 180 (17 180) 0.1 (0.1 0.5) |
| Citebasir spp. | Pleasupointines. | | |
 | | | | 10-900) 6EX (26.3-122.4 |
 | | | | | 32 (18 70) 19 (14 80)
 | | 40 (00 40) | 425 (309-1100) | 14(883.0)
 | | | 98 (96-207) | |
 | | | |
 | | 120 (422 2990) 0.7 (0.1-0.7) |
| Citebasir spp. | Provide generation
cophologosius | | |
 | 200.0 (271.9-
703.0) | | | (7-8K) 27.6 (IK-645.5) |
 | | | 23.4(11.9-40.4) | | 212 (79-490) 24 (89-49)
 | | | 70 (927-6280) |
 | | 60(8.060) | 79 (23-192) | 0.2(0.10.4) | 177 (208 FLQ
 | 41 (69 41) | 800 (270 1200) | 1.8 (8.9-2.8) | 34 (43-42)
 | 60 (3.0-60) | NO (81-100) 0.2 (0.1-0.3) |
| Citebaser app. | Third gramation
cophologosius | 79 (88-121) | III.1 (4.0-16.3) | M20 (7930 10700
 | 896.4 (591.3-
1497.7) E) | 3.00) 1.1 (0.4-2 | 744 (20 | 10 1270) 100 A (79 3 19K | 2) 87 (30-98)
 | 0.6(0.3 1.1) | NO20 (2679 8630) | MA(M1954) | 7 (3 19) 0.1 (8.0 0. | 403 (327-1396) 7.4 (2.8-05.0)
 | 26 (8-29) | 48 (99 4.1) | 1779 (472-2290) | 3.6(2.7-6.8)
 | 2 (0-4) | 00/0000 | 192 (92 929) | 0.0 (0.1 0.8) | 100 (373-1340)
 | 0.2 (0.1-0.3) | 21200 (17100-
32700) | 49 (24-61) | 121 (89-329)
 | 60 (88-60) | 289 (190-829) 0.8 (0.2 1.8) |
| Citebaser app. | Environment to some or most
antibiotics | 202 (80-047) | 13.7 (8.1-22.0) | 9000 (3330 1400)
 | 1216.2 (732.0 20
1009.7) 20 | (1949) 39 (20-6 | 5 2890 (3 | 200-470) 345.0 (275.3-
200.3) | 79 (41-128)
 | 0.8(0.51.4) | 6620 (1990-11300) | 1 76.6(83.628.0) | 21 (11 79) 0.2 (8.1 0. | DBD (979-5290) 21.2 (10.5-79
 | 21 (10:39) | 0.1 (0.0 (0.1) | 1842 (879-3380) | 4.8(2.5.8.8)
 | 4 (5 12) | 60(8060) | 824 (229-1008) | 1.0(0.02.4) | (180 (50 150)
 | 02(0103) | 27800 (27200
42000) | 82 (82.78) | 338 (210-330)
 | 61 (88-61) | 790 (480-1300) 13 (03-24) |
| Entercharter app. | Animplyomides | 192 (129-284) | 26.0 (16.7-38.4) | 17180-(11000
29280)
 | 2003 (1882.5: 12
3012.9) | (924) 14 (69-3 |) 1890 (I | 798 2300) 146 E (40.4 284) | (i) Na (19-80)
 | 0.0(0.00) | 4790 (8060 7090) | 33.7 (34.5 80.0) | 4 (9.7) B.O (0.0 B. | 30 (83-66) 3.8 (1.0-6.9)
 | P (12:30) | 48 (99 4.1) | 1969 (1049 2960) | 43(2743)
 | 1 (0.2) | 60(5060) | 109 (30-207) | 0.1(0.1-0.1) | 1000 (1790-3090)
 | 0.1 (0.3 0.4) | 46780 (71400-
73800) | 9.1 (8.9-18.7) | 161 (42-270)
 | 60 (88-61) | 3260 (972 4560) | | |
| Entercharter app. | Anti-paradorenal
post-film Bris Lavianus
adultion | | |
 | 7018.0) ET | | | 2000-0000) NR.1 (117.2-
200-2) |
 | | | 1261 (76.2-177.8) | | 1190 (428 1990) 13.8 (7.1 22.6
 | | | 3700 (2340 5540) | |
 | | | 894 (212-642) | |
 | | | |
 | | 1960 (196-
2260) 2.6 (1.0-6.2) |
| Enterohester app. | Carbonom | | |
 | | | | DESO TORE) 668 N (TREE.) |
 | | | | | 1870 (796-2220) 18.8 (8.8-28.0
 | | | 2093 (1269-3940) | |
 | | | 893 (266-792) | |
 | | | |
 | | 1860 (KSN) 2.7 (1.8-6.7) |
| | Pleasupindone. | | | 22.700)
 | 6017 (2016) at
60178) at | | | 1840-6000) 477.2 (248.9-
812.4) |
 | | | 79.8(91.2-109.4) | | 80 (EF-170) 51 (E7-017)
 | | | 3120 (3120-1770) | |
 | | | 399 (278-484) | |
 | | | |
 | | TIME (M20-12800) 1.3 (0.7-2.3) |
| Entercharter app. | | | |
 | 6987.2 (\$699.2)
10094.2) 29 | | | 1470-4280) 852-0)
1420-4280) 762-1 (0.0-877.8) |
 | | | 195.1 (385.4:
296.2)
196.4 (385.1:
296.4) | | 80 (20 (40) 10 (47 (47 (47 (47 (47 (47 (47 (47 (47 (47
 | | | 9110 (1260 T700) | |
 | | | 339 (344-990) | |
 | | | |
 | | X90 (200 (200) 1.6 (0.7 (2)) |
| | Trimelopine
Sellenethroanie
Erobinser in me or ma | | |
 | | | | (1290 2713.9(1711.7-
2003.0) |
 | | | | | NAT (0.1003) 4.7 (0.0-30.7)
NATO (1000-0090) 40.7 (70.0-92)
 | | | 4110 (2010 7030)
8410 (8410 1200) | |
 | | | 262 (0-N62)
1960 (1210-2000) | |
 | | | |
 | | X780-(0-18900) 1.6 (0.0-3.3)
MICOO (31200) 10.5 (6.4-25.4) |
| Entercorrectional | Pleasupinelines | | |
 | | | | 2001.0
030-11200; 500.7 (200.0- |
 | | | | | 1710 (773.5130) 91.3 (8.8.31.)
 | | | 2700 (1990 4100) | |
 | | | 67 (29-129) | |
 | | | |
 | | 2000 (1470) 47 (3.1-12.4) |
| Enteron conformati | Vancompoin | | |
 | | | | 102.0230 202.7 (194.6-
202.7) 202.7) |
 | | | | | 462 (800 1289) 7.4 (5.4 64.0)
 | | | 300 (329-943) | |
 | | | 179 (83-284) | |
 | | | |
 | | 1200 (No. |
| Enteronous formals | Environment or one or more and more | | |
 | | | | 107.6 (SEC.6) |
 | | | | | 290 (120-890) 264 (14.2-49
 | | | 300 (1780-0180) | |
 | | | 897 (421-1900) | |
 | | | |
 | | 2000 (2000
8200) 9.2 (4.7-19.2) |
| Enteron complexion | | | |
 | | | | 781.6 (201.0)
1605.10 |
 | | | | | 2620 (779.6270) 26.8 (6.7.69.2
 | | | |
 | | 0.0000000000000000000000000000000000000 | 984 (271-2180) | 24(0787) | 12100)
12100 (1810)
 | 28 (1742) | N4800 (221000)
N48000) | er 3 (41.3 (42.1) | 2000 (727-0770)
 | 64 (83 69) | NEISO (17900.
11200) 16.9 (1.3-26.9) |
| Enteronous formin | Vancompoin | 276 (162-378) | 31.9 (21.8-49.7) | 21000 (14000
2000)
 | 2013 (2015) 19
2013) 19 | (23.96) 8.0 (4.5.1 | a) 1300 (3 | (197.6) TELT (197.6) | 134 (80-213)
 | 1.1(0.9-2.4) | 11800 (7090)
18900) | 133.8 (78.9-213.6) | 11 (18-80) 0.2 (0.2 0) | 3020 (1980-3900) 34.0 (17.9.59
 | 38 (17.8%) | 0.1 (0.0 0.2) | 2800 (1299.5130) | 7.4 (3.9-13.3)
 | X (2-17) | 00/2000 | 712 (829-1939) | |
 | | | |
 | | 54000 (29400 16.8 (5.8 (7.4) |
| | | | |
 | | | | (APR) 1298.2 (191.4:
2209.4) |
 | | | | | NOTO (1040-9420) 47.5 (17.7-10
 | | | | |
 | | | 1700 (604 5040) | |
 | | | |
 | | 119000 (64000 21.4 (12.5-35.0) |
| Other entermouses | | | |
 | | | | 1110-13100) 990.3 (120.0-
2001.4) |
 | | | | | 2020 (112-2920) 27.5 (1.7-95.2
 | | | | |
 | | | ME(94-1380) | |
 | | | |
 | | 2000 (200
4000) |
| Other microscovi | | | |
 | 1002.001.5- 10
1007.1) 10 | | | 173.2448 184.3 (NO.3-333. |
 | | | | | #7 (219-1009) No (2.8-10.4)
 | | | 667 (760-1200) | | |
 | | | 117 (90-244) | |
 | | | |
 | | NAME (2000-10000) 1.0 (0.4 1.0) |
| Other microscosi | and the control of th | | | |
 | | | 130 1680) 181 X (423.7)
130 1680) 288 A) | |
 | | | | 2010 (923 5000) 32.9 (10.242
929 (426 1400) 11.0 (7.2 13.7 |
 | | 7120 (1600 NOTE) | |
 | | 674 (239-1369)
277 (239-680) | | |
 | | | |
 | 3000 (11900 3.6 (22.9.7)
3200) 3.6 (22.9.7)
11000 (7230 2.1 (13.5.1) |
| Enderthin sell | Animply-miles
Animprojetic | | |
 | | | | 190 (280) 281 (1811
180 (180) 281 (1811
180 (180) 281 (1811 |
 | | | | | 1900(1920-2280) 17.9 (11.0-28
 | | | | |
 | | | 477 (140-690)
398 (394-827) | |
 | | 297800)
207800)
200800 (82800-
266800) | |
 | | |
| Endership of | Anterpretelle | | |
 | | | | 1490-1220) 348-3)
1170-1870) 1781-1) |
 | | | | | 1980 (1980-2280) 17.9 (11.5-29
3290 (1990-2000) 76.0 (27.0-34
 | | | | |
 | | | 1320 (969 1830) | |
 | | | |
 | | 2800) 3.7 (2.5.6.4)
4800 (31300 8.5 (5.8.12.0)
62000 |
| Enderthia sell | Carbonness | | |
 | | | | 199.4000) 329.3 (174.8-
1290.4000) 329.3 |
 | | | | | 1190 (480-1970) 13.4 (7.3-22.)
 | | | 2770 (1790-2070) | |
 | | | 297 (TIL-198) | |
 | | | |
 | | 1200 (4920 23 (1.3-3.8)
2000) |
| Enderskie od | Phoropoleciones | | |
 | | | | (7780 1678.6 (1886.6 1
2016.1) |
 | | | | | Nec (1930-1930) - 66.0 (14.3.10)
 | | | 2000 (1820)
1200) | |
 | | | | |
 | | | |
 | | 79000 (82000.
110000) 14.7 (8.7-21.1) |
| Enderskie od | Third generation
caphalogenies | | |
 | | | | (500) 1833.8 (793.0-
3498.7) |
 | | | | | 600(260-000) TL2(TL01)
 | | | | |
 | | | | |
 | | | |
 | | 80'00 (9000)
14000) 16.5 (7.5-30.2) |
| Endertelia sell | Trianthopies
Self-methopies | 1560 (1090-2260) | 210.8(142.1
308.7) | Scenaci
Taxeno (azenzo
 | 18779.7 (12600.8-
27221.4) 12 | (99.121) 12.6 (6.0) | 1.0) X300 (7 | 1240-12700) 1121-8 (708-1-
1080-0) | 791 (842-1980)
 | K9 (6.3 (2.2) | 70200 (100000-
11000) | 794.0 (NIX.5:
1090.5) | 27 (12-00) 0.3 (0.4-0) | 2110 (2840-4879) - BL4 (32.3-48
 | 201 (241 415) | 0.9 (0.6 1.2) | 29800 (21800-
40090) | 77.5 (88.9 186.4)
 | 20 (13-28) | 0.1 (0.00.1) | 1730-(1130-2448) | |
 | | 923000-juli2000-
1270000) | |
 | | M200 (34/80) 16.5 (6.9-25.0) |
| Endertella soli | Resistance to one or mos
authorize | 2210 (1270-3180) | 286.2(196.2
490.3) | 294800 (271000)
 | 207840-(17797.5- xp
36724.4) | (102 802) T2.9 (24.3 | 1993) 28000 (
72800) | (7060) 687.7 (4176.7)
1794.8) | 1110 (792 1910)
 | 12.8 (8.9-170) | 99000 (70800-
132000) | 1116/9 (79ER-
1912.7) | 247 (161-785) 3.0 (2.0-4 | 2980 (1600) 266.1 (161.2
1680) 361.0
 | 477 (341 642) | 12 (99.17) | 4230 (1020)
1730) | 185.X (79.0-145.0)
 | 117 (80 170) | 0.3 (9.2 0.4) | 19490 (7130-
1900) | 27.0 (18.3-38.9) | IOME (ZNEE
COM)
 | 11.5 (8.3-19.5) | 1112000 (123000-
1812000) | 365.9 (172.0-
397.0) | 12100 (1990)
20100]
 | 27 (1.9-3.9) | 313000 (213000) NL4 (31.448.7) | | |
| Group A
Stoptomous | Marriale | | |
 | | | | 248) 98.1 (8.0.323.9) |
 | | | | | 80 (0-2770) 9.3 (8.0-31.2)
 | | | 1800 (1820 2940) | |
 | | | 171 (0-300) | |
 | | | |
 | | 30'0 (0.1398) 0.7 (0.0.23) |
| Group A.
Ziropianovan | Environment or one or more
antibiotics | | |
 | 2032.6 (MILE: E) | | | 2400) 98.1 (0.0.323.9) |
 | | | | | NES (0-2770) 9.5 (0.0-31.2)
 | | | 1800 (1820-2940) | |
 | | | 171 (0-398) | |
 | | 40600 (27000-
72700) | |
 | | 300 (0.1330) 0.7 (0.0.2.8) |
| Group II
Stephenous | Pleomysissiones | | |
 | | | | 100.0 100.0 |
 | | | | | 990 (191-2289) 11.2 (1.7-24.9
 | | | 2890 (1890-1990) | |
 | | | 29K (K1-1110) | |
 | | | |
 | | 380 (90 818) 0.7 (0.1-1.5) |
| Group II
Xinginomous
Group II | Marrisin | | |
 | 11108.2) 73
314.1(208.0 4c) | | | 0 1180) |
 | | | 74(4949.5) | | 200 (0.040) 22 8 (0.041)
 | | | | |
 | | | 672 (B-3838)
Na (EE-327) | |
 | | 294200) | |
 | | 19800 (0.30800) 2.0 (0.0 6.7)
689 (129-1920) 0.1 (0.0 6.7) |
| Simplements
Group II | Preis Ein
Ensistence to one or one | | |
 | | | | (1180) 690 (33.8.193.8
(1180 1892.8 (197.6
1288.8) |
 | | | | | 100 (11-200) 1.6 (83-3.4)
3500 (200-6800) 28.8 (2.4-77.6
 | | | | |
 | | | NE (EE-017) | |
 | | | |
 | | 689 (129-1920) 0.1 (0.0-0.5)
19000 (0.32800) 2.8 (0.0-0.5) |
| Namphine
Manaphiles
inflamor | Antiques die | | |
 | | | | 1283)
1023070 1073 (138414 |
 | | | | | 200(171490) 224(1847)
 | | | | |
 | | | | |
 | | | |
 | | 200 (200 FME) 0.6 (0.2 (.2) |
| | | | |
 | 1802.1) | | | |
 | | | | |
 | | | |
 | | | | |
 | | | |
 | | |
| | Third presenting
contributions in a | 29 (17-80) | 39 (2.3 6.2) | 2990 (1930-2080)
 | 390.2 (204.5- E) | 11 (65.2 | 0 799 (10 | 10.1910) 102.0 (41.9.201 |
 | | | | |
 | 20 (14-29) | | 1760 (1220-2160) | 44(124.4)
 | 4 (3-10) | | 110 (230-901) | | PP (132-265)
 | | | | |
 | 100 (2.0-00) | |
| Namphia
iglampe
Namphia
iglampe | Third generation
explodreposites
Environce to one or one
authorize | | |
 | | 3-07) 11 (63-2
(6-04) 33 (10-4 | | 10 1000 102.0 (11.0 201.
100-1070 201.0 (12.7 hav | R) 29 (27 89)
 | 0.4 (0.3 0.4) | 3430 (2779-4830) | | 11 (9-21) 0.1 (9.1 0. | 997 (236-1810) 11.2 (9.2-30.)
2000 (2220-2020) 23.9 (21.6-42
 | | 0.1 (0.0 0.1) | 1760 (1229-2040) - 6560 (2729-8070) - |
 | | 00/2000 | | 1.1(0.6-2.1) |
 | 40 (64 44) | 2110 (1240-4010) | 68 (66 L1) | NI (27-000)
 | | 1300 (440 2270) 0.2 (0.1 0.4)
4300 (1900 7000) 0.8 (0.3 1.4) |
| | Third generation
exploit operation. Environment to one or one
analysis in. Analogy consider. | 113 (49-179) | 18.2 (8.3-28.0) | 20000-(41200-
17100)
 | 1996.7 (829.3 34
2006.3) | (846) 33 (10-6 | 2180 (4 | | (i) 39 (27 69)
(i) 340 (112-219)
 | 0.4(0.30.4)
1.8(1.32.8) | 3230 (2779 4870)
14230 (9910
19480) | 38.6 (28.8 SL7)
199.6 (111.7
218.7) | 11 (0-23) 0.1 (0.1 0)
31 (12-05) 0.2 (0.1 0) | 97 (286 2810) 11.2 (9.2-20.1
 | 79 (59-162) | 61 (69 61)
62 (61 63) | | 17.1 (12.3-23.0)
 | 16 (6-30) | 60/2063 | 110 (230-901) | 1.3(0.6.2.3)
3.7(1.3.6.7) | H (709-1170)
 | 02 (0102) | 2193 (1240-4070)
2000 (19900
21700) | 0.8 (0.0-1.1)
3.9 (3.0-3.0) | NI (27-000)
NI (27-000)
 | 60 (80-61) | 100(44)229) 02(0104) |
| | Third generation
explodespation. Broblemer in one or not
antibiate. Animagly-smiller Bris Lavium Brise lavium authorises | 113 (49-179)
1100 (100-200) | 35.2 (5.5.25.6)
262.4 (196.8)
260.9) | 20000-(4120-
213000 (41300-
213000)
 | 1394.7 (829.3 24
2844.3) 24
17998.8 (12342.3 21 | (844) 33 (104
1 (8617) 154 (82 | 1) 2140 pt
1.7) 16200 p
1.7) 18000) | Me 2019 2013 (12.152) | (0) 29 (27 69)
(1) 140 (112-239)
(8)2 (601-1239)
 | 0.1(0.30.0)
1.8(1.32.8)
9.7(6.813.8) | 3430 (2770-4630)
14200 (9910-
19480)
34000 (87200-
194800) | 28.6 (28.8-94.7)
199.6 (111.7:
218.7)
280.4 (399.6:
1194.7) | 11 (9-21) 0.1 (9.1 0.1
31 (12-01) 0.1 (9.1 0.1
47 (11-00) 0.8 (9.8 1.1 | 997 (236-1830) 11.2 (5.2-30.)
2000 (220-2000) 23.9 (21.6-40
 | 39 (39 (82)
389 (399-409) | 0.1 (0.0 0.1)
0.2 (0.1 0.3)
0.8 (0.9 1.1) | 4940 (2740-9070) | 17.1 (12.3-23.0)
68.0-(12.7-90.0)
 | 28 (6-30)
22 (13-33) | es izoes)
es izoes) | 110 (230-900)
1210 (100-200) | 1.5(0.6-2.5)
3.7(1.3-6.7)
5.0(1.0-7.4) | 918 (709-1170)
19180
(11800-
17180) | 68 (69 68)
62 (61 62)
34 (23 88) | 2000 (3240-4000)
20000 (20000
20000 (200000
90000) | 08 (00 L1)
28 (20 A0)
263 (823 188 1) | N (27 000)
192 (47 300)
1810 (923 2300)
 | 63 (32-64) | 1990 (449-2270) - 0.2 (0.3-0.4)
4790 (1990-7700) - 0.8 (0.3-0.4) |
| Manuphila
olf-tenpe
Edulate
promoter
Edulate
promoter
Edulate
promoter | Animply-miles | 112 (49-170)
1500 (100-200)
2770 (1600-3000)
764 (477-1000) | 15.2 (5.5.25.6)
26.2 (136.6
20.0)
25.2 (236.6
313.5)
45.2 (250.16.4) | 20000-(4530-
15100)
151000-(95300-
151000)
227000-(309000-
350000)
95300-(50000-
95300)
 | 1967 (09.5 21
204.3) 17963 (1912.3 21
2068.3) 11
2068.3 (1912.3 21
2068.3 21
2068.3 21
2068.3 21
2068.3 21 | (6.04) 3.3 (1.0 6
8 (86.139) 13.6 (6.2
(17.119) 9.3 (5.0 1
8 (86.289) 22.3 (13.6 | 1) 2140 pt
1.7) 18000
1.000
4) 6240 (1
10.1) 28000 | (800) 280.5 (82.5.529)
(800) 198.4 (823.6
2206.0)
(825.1028) 825.2 (421.8
(825.1028) 199.4)
(835.1028) 2978.5 (1186.1 | 8) 29 (27.69)
9) 140 (112.29)
862 (601.126)
1420 (1140.236)
862 (328.712)
 | 0.4 (0.3 0.4)
1.8 (1.3 2.5)
9.7 (0.8 12.5)
1.8 (1.3 1.2 0.3)
3.8 (1.3 4.6) | 3430 (2779-4630)
14200-(9900-
17900)
34300 (92200-
109000)
143000 (133000-
199000)
41300 (20000- | 28.6 (28.8.51.7)
199.6 (121.7:
218.7)
200.1 (299.6:
1194.7)
1432.6 (1398.3:
2229.3)
490.7 (321.5:
710.4) | 11 (9-21) 0.1 (9.1 0.1
31 (12-01) 0.2 (9.1 0.1
67 (12-01) 0.3 (9.3 1.1
12 (22-01) 0.3 (9.3 1.1
11 (9-174) 1.3 (9.3 2.1 | 987 (486 6430) 11.2 (8.2-26.) 3000 (1370-3980) 33.9 (31.4-63 3000 (1370-3980) 43.7 (22.3-66 3000 (1470-3980) 41.8 (22.3-66 3000 (1430-3980) 41.8 (22.3-66 3000 (1430-3980) 41.8 (22.3-66
 | 3 78 (39-162)
3 289 (399-209)
3 262 (393-700)
3 223 (79-394) | 0.1 (0.0 0.1)
0.2 (0.1 0.3)
0.8 (0.3 1.1)
1.8 (1.0 2.0)
0.3 (0.2 0.8) | 2800 (2720-3070)
28000 (27200-
38000)
28000 (33200-
67790)
2800 (6070-
16000) | 17.1 (12.3-23.0)
68.0-(42.7-90.7)
126.3 (68.4-175.7)
28.2 (17.8-43.4)
 | 22 (33-32)
22 (33-32)
34 (31-32)
36 (33-34) | esitoesi
esitoesi
esitoesi
esitoesi | 110 (230-901) 1200 (110-2000) 1700 (1110-2000) 1200 (420-2000) 2500 (1120-4110) | 1.5(0.62.5)
3.7(1.56.7)
5.0(1.07.4)
3.1(1.65.2)
4.6(1.010.7) | 114 (709-1170)
19100
(11800-
17100)
19100 (21800-
19700)
11900 (8280-
17100) | 02 (0 0 02)
02 (0 1 0.2)
3.6 (2.5 4.0)
0.8 (4.8 9.2)
2.2 (4.5 4.2) | 2000 (1240-0200)
2000 (1990-
2070)
20700 (22100-
20300)
27700 (12400-
20300)
20300 (17200-
30300) | 0.8 (0.0 1.1)
2.9 (1.0-3.0)
26.3 (32.3-108.1)
166.8 (300.8-
206.2)
47.1 (32.1-68.6) | 36 (27-008)
362 (67-339)
1800 (923-2338)
922 (881-1398)
2790 (1788-4138)
 | 60 (83-61)
63 (83-64)
63 (83-68) | 1100 (445 1275) 0.2 (0.1 0.4) 4100 (1990 7500) 0.8 (0.5 1.4) 73200 (1980) 0.8 (0.6 1.4) 73200 (1980) 0.7 (19 0.7) 73200 (1980) 0.7 (19 0.7) 73200 (1980) 0.7 (19 0.7) |
| Manusphilas
influence
Ethnicila
promoniae
Ethnicila
promoniae | Animply-mides Bris Lavium Bris- laviumes inhibitors | 2770 (1990-2000)
2770 (1990-3000)
2880 (1990-3000)
2880 (1990-2070) | 25.2 (5.5.23.8)
26.2 (5.8.8.
26.5)
25.5 (25.8.
25.2 (25.8.8.
25.2 (25.0.12.4)
25.2 (25.0.12.4)
25.2 (27.8. 25.2) | 20000-04220-
191000-191000-
191000-191000-
227000-1910000-
228000-191000-
91100-
228000-1110000-
228000-1110000-
 | 1394.7 (129.3.) 24
2394.3) 22
17998.8 (1294.3.) 22
2398.8) 21
2398.8) 22
2498.8) 26
2498.8) 26
2298.3.) 26
2298.3.) 26
2298.3.) 26
2298.3.) 26
2298.3.) 26
2298.3.) 26 | (0.44) 33 (10.6
(0.439) 154 (6.2)
(0.119) 93 (6.1)
(0.29) 223 (114
(0.29) 154 (0.2) | (1) 2180 (1) 10000 (1) 100 | 280.3 (92.3 520.3 (92.3 520.3 (92.3 520.3 620.3 520.4 62.3 520.4 62.3 520.4 62.3 520.4 62.3 520.4 62.3 520.4 62.3 520.4 62.3 520.4 62.3 520.3 62.3 520.3 62.3 520.3 62.3 520.3 62.3 520.3 | (i) 29 (27.09)
(i) 140 (112.239)
(iii) (140.1289)
(iii) (140.238)
(iii) (120.712)
(iii) (iii) (iii) (iii)
 | 0.4(0.30.4)
1.8(1.32.5)
9.7(0.813.5)
1.88(13.1.08.3)
3.8(1.34.0)
12.6(89.17.2) | 3.200 (2279-6898)
14.200 (9910-
19420)
36.000 (93200-
36.000)
14.000 (33000-
199000)
4.000 (20000-
6.000)
99000 (70100-
13000) | 28.6 (28.84.7) 195.6 (111.7) 218.7) 218.7) 218.7 (195.6) 195.2 (196.3) 229.7 (101.6) 716.6 (196.3) 1117.6 (196.5) 1117.6 (196.5) | 11 (9.21) 0.1 (9.10) 11 (9.21) 0.1 (9.10) 11 (9.10) 0.1 (9.10) 12 (9.10) 0.3 (9.30) 113 (90.174) 1.3 (9.32) 70 (80.111) 0.9 (9.31) | 907 (488 1610) 11.2 (3.2.36) 2000 (1310-3000) 23.9 (13.4.43) 2000 (1310-3000) 46.7 (36.7 (36.7 4)) 2000 (1310-3000) 41.2 (22.3.44) 2000 (1310-3000) 41.2 (20.3.1 1) 2000 (1310-3000) 70.0 (16.5.1 2)
 | 17 (30.00)
28 (39.00)
38 (39.00)
38 (39.00)
40 (27.00)
41 (28.00)
41 (28.00) | 0.1 (0.0 0.1)
0.2 (0.1 0.3)
0.8 (0.0 1.1)
1.8 (1.0 2.0)
0.3 (0.2 0.3)
1.0 (0.7 1.4) | 4500 (2730-3030) :
25000 (27200-
35000) :
45000 (32500-
47730) :
25000 (32500-
25000) :
32300 (22500-
45000) : | 17.1 (12.3-23.0)
66.0-(12.7-90.0)
126.3 (98.0-176.0)
28.2 (17.8-63.0)
86.3 (98.0-176.0)
 | 16 (6-30)
22 (18-33)
14 (7-20)
30 (18-40) | #1 (20#1) #1 (20#1) #1 (20#1) #1 (20#1) #1 (20#1) #1 (20#1) | 110 (230-903)
1200 (330-2003)
1900 (1140-2003)
1200 (420-2113)
2500 (1150-2113) | 1.7(0.62.7)
3.7(1.56.7)
8.6(1.67.4)
3.1(1.68.2)
4.6(1.61.2)
3.9(1.69.6) | HE (709-1170) PERSON (TENSO
PERSON (TENSO PERSON (TENSO LENSO (TENSO | 02 (0.10.2)
0.2 (0.10.2)
1.6 (2.5.45)
0.8 (2.6.42)
2.2 (2.5.4.2)
4.6 (2.5.6.4) | 2000 (1340-0000)
2000 (1990-
20700)
41000 (23100-
30300)
72700 (33400-
120000)
223000 (17200-
30400)
33300 (34600-
77900) | 0.8 (0.0.1.1)
2.9 (1.0.3.0)
20.3 (32.5.109.1)
114.8 (302.8
209.2)
47.1 (32.1.48.4)
49.3 (68.6.137.8) | M (27-000)
M2 (47-330)
M30-(423-2300)
922 (343-1300)
2790 (1790-4230)
 | 61/62/61/
61/62/61/
61/62/61/ | 1700 (1240 2270) 0.2 (0.1 d.0)
1200 (1200 7200) 0.8 (0.3 1.4)
2200 (1200 0.00 (1.6 d.0)
2200 (1300 0.00 0.00 0.00 (1.6 d.0)
2200 (1300 0.00 0.00 0.00 0.00 0.00 0.00 0.00 |
| Managelilas
influenças
Eleksirlis
procumentas
Eleksirlis
procumentas
Eleksirlis
procumentas
Eleksirlis
procumentas
Eleksirlis
procumentas | Animply-mides Bris Lavium Bris- laviumes inhibitors | 113 (89-179)
1500 (100-200)
2770 (100-300)
704 (477-100)
1670 (129-279)
2730 (130-320) | 18.2 (8.5.28.0) 28.24 (18.8. 28.08) 28.24 (28.8. 28.3.5) 48.2 (28.0.12.4) 28.26 (28.8. 28.3.5) 28.2 (28.0.12.4) 28.26 (28.8. 28.3.5) 28.26 (28.8. 28.3.5) 28.26 (28.8. 28.3.5) 28.3.6 (28.8. 28.3.5) 28.3.6 (28.8. 28.3.5) 28.3.6 (28.8. 28.3.5) 28.3.6 (28.8. 28.3.5) 28.3.6 (28.8. 28.3.5) 28.3.6 (28.8. 28.3.5) 28.3.6 (28.8. 28.3.5) 28.3.6 (28.8. 28.3.5) 28.3.6 (28.8. 28.3.5) 28.3.6 (28.8.) 28.3.6 (28.8.) 28.3.6 (28.8.) 28.3.7 (28.8.) 28.3 (28.8.) 28.3 (28.8.) 28.3 (28.8.) 28.3 (28.8.) 28.3 (28.8.) 28. | 20000-04220-
15100) ETRIBO (NE NOO-
ERNIBO) 247000-(159000-
758000) 42400-(150000-
91100) 247000-(112000-
279000) 266000-(1790000-
760000)
 | 2004.7 (2015.) 24 2004.7 (2014.) 21 2006.8 (2014.) 22 2006.8 (2014.) 20 2006.1 (2015.) 20 2006.2 (2016.) 20 2006.2 (2016.) 20 2006.2 (2016.) 20 2006.2 (2016.) 20 2006.2 (2016.) 20 2006.2 (2016.) 20 2006.2 (2016.) 20 | (844) 33 (104
(8139) 184 (82
(2513) 93 (80
(2513) 93 (80
(2523) 223 (138
(2623) 174 (80
(2633) 372 (138 | (i) 2140 (i) 1500 (i) | 086-0750 286.5 (92.5 520
(8870) 1384.2 (32.6 5
1206.6) 2306.0 (22.5 50.0 0) (22.5 5.0 0) (22.5 | (i) 29 (27.09)
(ii) 140 (112.29)
(iii) 140 (110.23)
(iii) (110.23)
(iii) (110.23)
(iii) (100.103)
(iii) (100.103) | 0.1(0.30.4)
1.8(1.32.5)
9.7(0.813.4)
11.8(1.31.30.3)
3.8(1.34.6)
12.6(0.9.17.2)
13.1(0.2.17.7)
 | 3230 (2779-0690) 12300-(9910-19930) 26300-(93200-199300) 123000-(23000-199000) 413000-(25000-133000) 123000-(25000-133000) | 38.6 (28.94.7) 199.6 (1817. 200.1 (199.6 1194.7) 104.2 (100.3 200.7 (101.6 101.6 (190.6 101.6 | 11 (9.21) 0.1 (0.14) 0.2 (0.14) 0 | 987 (188 1810) 31.2 (0.3.30) 3800 (1830 3880) 31.9 (11.4 e/d. 5880) 3800 (1830 3870) 46.7 (10.5 e/d. 5880) 3800 (1830 3870) 46.7 (10.5 e/d. 5880) 3800 (1830 3870) 31.1 (2.3.6 e/d. 5880) 3800 (1830 3880) 381.1 (2.3.6 e/d. 5880) 3800 (1830 3880) 381.1 (2.3.6 e/d. 5880) 3800 (1830 3880) 381.1 (2.3.6 e/d. 5880) | 19 78 (99-102)
20 209 (99-209)
3 82 (98-200)
5 82 (98-200)
5 129 (98-320)
5 279 (88-320)
5 279 (81-677)
 | 0.1 (0.0 0.1)
0.2 (0.1 0.1)
0.8 (0.5 1.1)
1.8 (1.0 2.0)
0.3 (0.2 0.3)
1.0 (0.7 1.4)
1.2 (0.6 1.8) | 680 (2720-8270) : 28000 (2720-
38000 (27200-
38000 (33200-
67700) : 5000 (6030-
36000) : 52000 (22300-
32300) : 52000 (22300-
34300) : 52000 (33200-
34300) : 52000 (33200-
34000) : 52000 (33200-
34000) : 52000 (33200-
34000) : 52 | 17.1 (12.3 (23.0)
46.0 (42.7 (00.0)
126.1 (00.6 (77.0)
26.2 (17.8 (23.0)
86.3 (30.3 (20.6)
266.7 (72.3 (23.0) | 14 (9-39)
22 (18-39)
14 (7-29)
39 (18-49)
24 (18-49)
59 (22-113) | 62(8163)
61(8061)
61(8061)
61(8061)
60(8061)
 | 200 (230-900) 1200 (120-2200) 1200 (120-2200) 2200 (1200-2210) 2200 (1200-2210) 2200 (1200-2210) | 1.7(0.62.5)
2.7(1.56.7)
2.0(1.07.4)
3.1(1.63.2)
4.6(1.010.7)
3.9(1.04.6)
11.2(1.62.3) | 114 (709-1170) PHORO (11700- 11700) MAGIO (21600- 17000) 11700 (21600- 11700) 11700 (21600- 11700) 11700 (21600- 11700) | 02(0102)
02(0102)
34(1302)
03(1302)
04(1302)
34(1302) | 2000
(3.400-0000) 2000 (2000- 2000 (2000- 20000 (3.4000- 30000) 20000 (3.4000- 30000) 333300 (3.4000- 30000) 333300 (3.4000- 30000) | 0.8 (0.6-1.1)
X.9 (1.0-3.0)
76.3 (32.3-108.1)
164.8 (102.8-
203.2)
47.1 (32.1-68.4)
49.3 (68.6-127.8)
154.9 (83.2-60.4) | M (27-000)
H2 (47-339)
H30 (423-230)
H32 (443-1300)
2790 (1708-4120)
H300 (1270-4000) | 60 (82-61)
63 (82-64)
62 (81-63)
63 (83-63)
63 (82-63) | 100 (45.1278) 8.2 (91.14.6) 400 (1900 700) 8.8 (93.14.6) 7200 (1940 700) 8.0 (16.4.9) 7000 (1940 700) 8.7 (16.4.9) 7000 (1940 700) 10.7 (16.4.9) 7000 (1940 700) 7000 7000 7000 (1940 700) 7000 7000 7000 (1940 700) 8.1 (16.1.21.6)
 |
| Manuphila
olf-tenpe
Edulate
promoter
Edulate
promoter
Edulate
promoter | Animply-mides Bris Lavium Bris- laviumes inhibitors | 113 (49-179)
1100 (100-200)
2730 (100-200)
704 (477-100)
1030 (100-200)
2130 (100-200) | 10.2 (0.5.25.0) 20.2 (10.8.2 20.0) 20.14 (20.8.2 10.1.5) 20.14 (20.8.2 10.1.5) 20.16 (20.8.2 20.17 (20.8.2 20.8.2 20.17 (20.8.2 20.17 (20.8.2 20.8.2 20.8.2 20.17 (20.8.2 20.8.2 20.8.2 20.17 (20.8.2 20.8.2 20.8.2 20.17 (20.8.2 20.8.2 20.8.2 20.17 (20.8.2 20.8.2 20.8.2 20.17 (20.8.2 | 20080-(14200-
123000 (76300-
123000 (76300-
323000 (129000-
320000 (129000-
229000) (129000-
229000) (129000-
200000 (129000-
200000 (123000-
200000 (123000-
200000) (123000-
 | 1984.7 (1993.5 24 2984.9) 12994.1 (1934.5 22 29894.9) 2984.1 (1934.5 22 29894.9 (1934.6 23 29894.1 (1934.6 23 29894.1 (1934.6 23 29894.1 (1934.6 23 29894.1 (1934.6 23 29894.1 (1934.6 3) 29894.1 (1934.6 3) 29894.1 (1934.6 3) 29894.1 (1934.6 3) 29894.1 (1934.6 3) 29894.1 (1934.6 3) 29894.1 (1934.6 3) 29894.1 (1934.6 3) | (6.44) 3.3 (10.64) (6.413) 18.6 (6.2) (75.113) 93 (80.61) (75.113) 93 (80.61) (76.200) 22.3 (31.61) (76.200) 17.6 (90.20) 17.6 (90.20) 17.2 (31.81) (76.200) 18.3 (30.610) 18.3 (30.610) | (i) 2140 (ii) 18200 (ii) 18200 (ii) 18200 (ii) 18200 (ii) 18200 (iii) 18200 (iiii) 18200 (iiii) 18200 (iiiii) 18200 (iiiiii) 18200 (iiiiiii) 18200 (iiiiiiii) 18200 (iiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiii | 280.5 (VLT.5.296.6) 180.6 (180.5) 180.4 (VLT.5.296.6) 180.5 (180.5) 180.5 (VLT.5.296.6) | (0) 200 (27.00)
(0) 140 (117.20)
202 (100.120)
1440 (110.220)
202 (127.712)
1120 (702.1020)
1320 (703.1020)
 | 0.1(0.30.6)
13(1.32.8)
9.7(0.813.8)
113(131.08.3)
3.8(2.38.6)
12.6(2.912.2)
13.3(10.2.12.7)
14.9(10.8.20.6) | 3280 (2279-4890) 14280 (9910- 79100) (32280- 201000) 143000 (23280- 43300 (23880- 43300) (23880- 133000) 123000 (23880- 133000) 143000 (23800- 133000) 143000 (23800- 143000) | NEA(28.8317) INA(ISI2.7 2883 2884 (NNA 1194.7) 1843.4 (1083.7 288.7 (NLA 1194.8) 1843.4 (1083.7 1843.4 (1083.8 | 11 (9-21) | 907 (284 1839) 31.2 (0.3.30) 3000 (1830 1830) 32.6 (11.4 n/s 10.4 | 9 79 (30 102) 9 20 (30 102) 9 32 (30 102) 9 32 (30 102) 14 12 (30 320) 15 12 (30 320) 16 12 (30 402) 16 12 (30 402)
 | 0.1 (00.0.1)
0.2 (01.0.2)
0.8 (05.1.1)
1.8 (10.20)
0.3 (02.0.3)
1.0 (02.1.4)
1.2 (08.1.8)
1.2 (08.1.7) | 6800 (2730-8870) 28000 (27200- 38000) 28000 (23200- 37000) 28000 (23200- 2320 (23200- 2320 (23200- 23200 (23200- 2 | 17.1 (12.3 (2.0)
46.0 (42.7 (0.0)
126.1 (08.4 (75.4)
26.2 (17.8 (2.4)
86.3 (38.8 (18.4)
166.7 (72.3 (18.8)) | 22 (13-32)
14 (3-22)
30 (18-42)
24 (13-42)
39 (22-413)
23 (12-42)
 | e1(toe1)
e1(toe1)
e1(toe1)
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Shipshe upp.	Pleanspiedown	8 (1-12)	00 (0.2 1.4)	£72 (129-1090)	M.4 (17.4-141.7)	1 (0-3)	01 (60 0.0)	89 (30-279)	120 (14-77.8)	44 (19-94)	0.8 (0.2 1.1)	4010 (1790 XXXX)	48.8 (19.7-99.2)	9 (0.00)	01 (0.003)	NT (109.22%)	9.4 (1.2-29.4)	21 (7-44)	0.1 (0.0 0.1)	2210 (798-4490)	3.8 (2.0 12.2)	4 (9 12)	00/1000	427 (49-1170)	1.1 (0.2 0.0)	No (20-119)	0.0 (0.0 0.0)	2679 (1040-5590)	69 (62-14)	12 (1-90)	60 (3.0-60)	429 (78-0940)	0.1 (0.0-0.2)
Shipshe upp.	Emissioner in one or more analysis o	8 (3-12)	00 (0.2-1.4)	272 (129-1090)	96.4 (17.4-141.7)	1 (0.3)	01 (00 04)	NY (30-279)	120 (14-773)	44 (19 94)	0.8 (0.2 1.1)	4040 (1790 XXXX)	49.8 (19.7-99.2)	9 (0.00)	01 (0.0 0.3)	N17 (100 2270)	94 (12-29.6)	28 (7-44)	0.1 (0.0 0.1)	2210 (798-2490)	18(20122)	4 (9 12)	00/1000	427 (49-1170)	1.1 (0.2 8.0)	No (20-118)	0.0 (0.0 0.0)	2(79 (1040-5990)	63 (62-14)	12 (1-70)	00 (3.0-00)	429 (78-0900)	0.1 (0.0-0.2)
Suphylanasas	Phonopsindows	766 (906 1990)	205.6 (46.6 147.5)	66200 (27000 97100)	92178 (6005.1- 15125.8)	39 (14-61)	47 (20 83)	3000 (1290 5170)	417.4 (176.0: 739.1)	642 (442-899)	7.2 (8.0-100)	NAME (1920) TRANS	METAL CHIEF IN	29 (12 NI)	0.7 (0.1 0.4)	2990 (1100-4420)	26.2 (12.8-26.8)	284 (179-348)	0.7 (0.9-0.9)	22200 (19700- 30500)	27.7 (40.7 CW.H)	11 (9-20)	00(0.00.1)	996 (416-1700)	2.6(1.0-0.4)	20000-(12H00- 27100)	18 (28 5.1)	412000 (713000 613000)	N2.4 (NK.4 113.7)	101 (201 (170)	62 (9.1-63)	20200 (89%) 32900)	38 (17-63)
Suphylanasas	Marriale	1940 (1020-2180)	207.7 (139.4 209.1)	177000 (10000- 210000)	18283.2 (12307.6 26229.8)	42 (25 112)	X3 (3.1-13.1)	5.270 (2070 9980)	799.9 (280.1- 1309.2)	1310 (962 1790)	14.8 (10.0-20.2)	114000 (X3400 116000)	1313.8 (MILL- 1780.9)	83 (21 48)	04 (8.2 t.0)	£700 (1630-8240)	N1 (20 4-92 N)	ant (335-432)	12 (09 14)	4750 (2960) 31200)	100.7 (76.9-143.4	0 18(7.02)	00(0.00.1)	1400 (477-2790)	42 (13 7.2)	41400 (19700- 19000)	X 2 (6.2 10.3)	2240000 (411000)	178.5 (128.7: 288.7)	1830 (TUR. S180)	63 (83 64)	71000 (11000 61000)	7.8 (2.9 (2.9)
Suphylanasas	Methodis	1290 (980-2130)	202.0 (132.6- 203.4)	113000 (87300-	17979.9 (11798.4 29696.0)	209 (123-488)	359 (25.4 95.1)	39900 (19400- 41200)	2795.9 (2082.0 8272.2)	1200 (827-1665)	134 (93-187)	107000 (TURO) 147000)	1203.0 (M23.5- 1660.0)	321 (143.546)	3.6 (3.6-6.2)	26400 (12700- 26300)	320.3 (145.3- 541.3)	489 (324-471)	1.2 (0.8 1.6)	7900 (2820) 3120)	105.5 (75.7 645)	2) 120 (10 207)	03(8103)	10000 (2700) 18000)	27.7 (12.2-46.8)	ADMIN (29700- SAMIN)	74 (8.5 (8.2)	80000-js29000 1220005	366.1 (117.2) 227.6)	201000 (2000)	20 (89-34)	29600 (10900) 39900)	440 (91774.4)
Stephylorocous serves	Trimelopies Salismelosande	233 (189.321)	31.6 (21.5-43.4)	2000 (1200 2000)	2008.4 (2919.9- 2008.1)	22 (11-39)	28 (1.8-47)	1920 (999 5110)	299.6 (129.1 439.4)	141 (110-219)	1.8(1.3.2.9)	1486 (1008)	161.0 (113.6 219.3)	19 (7-24)	62 (8.1 6.3)	1330 (629-2300)	14.8 (7.3-23.4)	90 (43-127)	0.2 (0.2 0.3)	7923 (5443 1390)	28.7 (14.1 (28.1)	X (0.17)	eagroes	792 (No. 1189)	1.9(0.9(0.0)	3210 (2779-4735)	0.6(0.203)	72900 (120000 007000)	15.9 (9.8-19.2)	201 (149-441)	61 (88-61)	6490 (1340-1000)	0) 12 (0.0 LN)
Suphylanosan	Vancompoin	31 (20-24)	43 (2.7 6.2)	2770 (1790-4110)	374.4 (242.4: 383.7)	E(4-00)	11 (66-21)	792 (No. 1230)	208.7 (29.5 1904)	26 (18:07)	0.1(0.20.4)	2290 (2000-1200)	28.9 (17.8-36.8)	7 (8 12)	01 (0.001)	421 (909 1089)	7.0 (3.4-12.2)	10 (7-14)	0.0 (0.0 0.0)	NH (NH-1200)	22(183.0)	3 (0-8)	00/1000	291 (114-407)	0.0(0.3 0.1)	Bar (618-1220)	02 (01 02)	38793 (13000) 26630)	38 (24-80)	217 (129-627)	60 (88-61)	1000 (Z160-9210)	1 10 (0.5 1.0)
Suphylanosan	Environment to some or some antibiotics	2070 (1370-2900)	201 (185.9- 201.0)	28000 (12200) 28000)	20121.2 (14837.4 30877.6)	323 (276-846)	71.0 (87.4 114.4)	00700 (20400- 79000)	675 L G (3724 R- 100 94 F)	1730 (1210-2310)	194 (133-263)	192000 (194000- 204000)	1714.9 (1224.2- 2329.1)	428 (259-481)	48 (2.7-2.7)	37400 (21100 40200)	231.6 (278.4 679.4)	483 (843 977)	17 (12-23)	N600 (4080- N600)	125.5 (205.0- 196.4)	161 (92.294)	0.1(9.20.7)	1200 (8330) 22400)	36.9 (20.9-36.3)	97980-(42700- 79200)	18.6 (8.0 14.0)	1230000 (894000) 3680000)	229.6 (147.1: 312.9)	11200 (7920) 22000)	24 (1.8-4.1)	307000 (149000- 489000)	85.8 (96.846.2)
Simplements procured as	Bris Laviano Bris: Inciamano infolhènes	314 (298-474)	£1.1 (26.7 66.8)	27900 (17600 42200)	3778.4 (2879.2: 5698.2)	7 (0-38)	09 (60 Lt)	621 (30-1970)	83.9 (2.2-212.5)	719 (106-1000)	X.1 (8.0-11.7)	6360 (1130) 8830)	717.9 (201.7) 997.4)	16 (0-41)	0.2 (0.00.8)	1290 (79.3690)	36.7 (5.4-41.1)	299 (208-209)	0.8 (0.9 1.1)	2800 (2800- 2800)	66.7 (26.8 %) 0)	7 (0.13)	00/1000	609 (14-1530)	14(0040)	NAME (8080 TORS)	1.0 (0.0 1.3)	233000-(97300- 276000)	26.8 (18.2-19.1)	111 (8-290)	60 (88-61)	280 (15-660)	0.8 (0.0 1.2)
Streptoneous procuration	Carboponess	NOT (\$29 THZ)	68.4 (23.1-200.3)	27100 (26200 66800)	6003 (NNA7- 90360)	111 (26-262)	19.0 (6.9 27.4)	1870 (1280 1888)	1394.4 (979.4) 2499.7)	1140 (800 1400)	13.0 (9.1-18.1)	102000 (71100- 142000)	1193.9 (ME.2- 1606.7)	294 (114-449)	29 (5.3 8.0)	22400 (10200) 39200)	293.1 (114.4: 447.1)	471 (NO.979)	1.1 (0.8 1.9)	77200 (26200- 90800)	97.1 (6K.6-130.1)	97 (41 044)	02(810.0	X100-(3020-14300	21.1 (9.4-97.1)	1860 (7270 12900)	18 (1.02.4)	212000 (1000000 312000)	D-1 (34.1-660)	2190 (1040-3710)	64 (93 67)	33600 (26200 12600)	160 (49-17.7)
Streptoneous procuration	Phonopsindows	148 (109-219)	23.7 (14.8-33.2)	19000-(9720- 21800)	2021.1 (1014.1- 2091.2)	20 (1-24)	28 (67 62)	1800 (222-0070)	225.0 (60.1 525.0)	373 (246-926)	42(2848)	3300 (2190) 4470)	272.2 (267.1) 227.0)	29 (30 49)	0.8 (0.1 0.1)	200 (877 8300)	811(101/964)	PH (132-279)	0.8 (0.3 0.7)	17500 (11400- 24100)	41.1 (29.6-62.7)	24 (6 82)	0.1 (0.0 0.1)	2010 (203-2270)	84(13117)	1790 (1280-2280)	0.3 (0.2 0.4)	42300 (12900) 60200)	X3 (6.1-11.2)	297 (24-200)	00 (10-01)	3190 (1220 1080)	0) 1.0(0.2.2.0)
Streptomores presentar	Marriale	1830 June 1300j	179.0 (88.0 201.5)	15300-(27900- 133000)	12364.4 (7823.2 18296.3)	41 (0.115)	3.8 (0.0 (3.8)	3630 (0 10000)	240.8 (0.0 1376/0)	2120 (1740 3190)	27.2 (24.9.38.9)	21,000 (15000 28200)	2004 (1797A- 3177.4)	97 (0-247)	11 (8.02.8)	2000 (O 21800)	96.9 (9.0-249.9)	No. (422-1149)	2.5 (1.6.58)	79200 (94200- 98700)	199.2 (148/9- 296.8)	34 (0.00)	0.1 (0.0 0.2)	2930 (0.1880)	7.6(0.019.2)	22000 (17600- 27000)	41 (8.9 8.1)	32200 (41300 66300)	97.3 (76.9 123.7)	RM (0.2330)	62 (9.0-64)	20100 (0.51200)	39 (00 101)
Streptomores presentar	Presiden	787 (900-1146)	206.4 (47.8 296.3)	7000 (1200 20100)	10017 (MTLR- 179022)	33 (29/90)	71 (83-198)	awa (2200 8920)	633.2 (308.7: 1392.5)	1800 (1290-2440)	20.3 (14.8-27.8)	199000 (114000- 214000)	1798.2 (1282.5- 2480.7)	121 (40-200)	14 (872.9)	10700 (3130- 17700)	121.1 (62.0 199.0)	47% (BEE 942%)	1.7 (1.2-2.2)	3300 (4000 7300)	143.3 (204.0- 290.1)	40 (21 48)	0.1(0.10.2)	3270 (3830-5880)	10(4813.3)	1880 (1280 2000)	29 (23 53)	36400 (21600 91500)	71.9 (31.6-93.8)	1110 (847 1870)	62 (81 63)	27000 (14000 40000)	50 (24 84)
Simplements presentate	Third generation cophalesparies	238 (149.397)	32.1 (20.1-48.3)	21100-(15200 31800)	2699.1 (2788.0- 4297.6)	E(3-07)	11 (84.23)	729 (268-1090)	980 (N.2-2003)	383 (362-770)	42(43.87)	2000 (1300- 6020)	993.1 (190.9- 771.3)	19 (7.03)	02(0.104)	1700 (483 3290)	19.1 (7.4-37.1)	229 (183-304)	0.6 (0.2 0.8)	2400 (1100- 2400)	49.7 (36.7-49.7)	X (5.10)	eastroest	681 (261-1360)	18(07)3.0	4490 (XMO MOS)	0.8 (0.0 L.1)	20000 (7990) 11200)	20.1 (14.9-26.9)	194 (43-299)	60 (58-61)	3600 (1420-6800)	9 97 (93 63)
Simplements presentate	Trimelopies Salismelosande	1200 (787-1790)	362.6 (396.4 256.1)	207080 (70300) 214800)	16367.9 (96700- 20878.4)	III (II-212)	13.7 (2.0-26.7)	9020 (1700-1890)	1219.7 (176.1- 2892.8)	2820 (2090-1730)	31.8 (23.1-41.8)	229000 (163000 328000)	2812.9 (2849.4 3699.3)	280 (10-899)	27 (8.6 8.6)	21.300 (2470) 2000)	299.8 (33.8-293.7)	1150 (850 1480)	30 (22 33)	99900 (72000- 12000)	296.2 (292.8- 330.7)	99 (14 (90)	0.3 (0.00.3)	8900-(1210-14800	22.1 (3.1-454)	21100-(17000- 24000)	39 (3248)	304000 (207000 483000)	96.2 (76.0 (21.8)	1760 (292.1900)	63 (88-67)	22700 (4330- 37200)	80 (12 189)
Stoptomous prosentiae	Emiliance to one or more antibiotics	1470 (1890-2800)	228.8 (147.8- 224.4)	123000) 213000)	20065 9 (27120:0 2007:3)	NI (204-925)	49.2 (27.6 70.4)	30800 (18200- 66000)	4309.0 (2007.8- 6282.9)	3900 (2870-9120)	44.2 (12.3-17.8)	344000 (234000 433000)	2906.9 (2829.3- 2111.7)	761 (921 1190)	K 9 (8.9-12.8)	70300 (24200- 200000)	790.7 (839.3- 1139.7)	1910-(1130-1900)	39 (29 84)	131000 (97900- 147000)	335.0 (234.6 436.0)	38 (196-220)	0.8 (0.5-1.1)	26400 (17300- 37000)	48.4 (28.0-96.7)	31700-(28400- 21700)	3.9 (4.8.7.3)	50000 (412000 50000)	143.2 (114.2- 180.8)	4120 (1120 8780)	12 (9.8-14)	156000 (106000- 217000)	26.0 (28.8-29.3)

Table NC Deaths a	nd EVLVs jie counts and agrospositi	nder)assariated raid	and all of the last of the last	ativid selected to	resistante by pullenges	deg continuins, by	age group, 2013, north	Witnessel the White I	ine.																					
Palanges	Ambiericulum	Count	Acceptated	with recisionary	DALY. Eate per 100:000	Create I	Antibusah Davida Bate per 18:000	Oners	ALVo Kair per XX-000			Create		Death County E		No investment Date Create.				d with revisionar Dis. Counts		Courts	Antibush Deales Bair per 100:000			Accordan Eleabs Creats Rate per 3X-000	d with emissioner DAI Crossis	Namico Sair per 28 000 C	Araba Draka mata Este per 20-00	DALYs. Cleanis Eatr pre 100 000
All pelogras	Environments one or more until biology					7230-2770-3000)								2700,000,000 4						62000 (27000 80000)										170000 (999000) 2024 (160 0.77.4)
Arismolamer Instrumenti Arismolamer	Antispychian Antiponismusi posisilaria				9762.2 (99623. 1986.8) 12966.8 (7425.2. 1966.6)		44(9411.5)	2780 (4.5140) 4140 (2340-7000)						20(0.70) 6 21(12.40) 6						1000 (400-2000)				600 (MICE)		2200 (200 3900) 41(2344)				1900(1002900) 3.5(6.6.6)
Arismeni Arismeteror Arismeni	initiation Eric Lavierellinis Incomer initiation		2019(82,32647)		19647(7385- 19867(7385-	190			64(1419)			1986/1200 N/100				3(4.2)				1000 (9101.7500)			00,0000		00(0000)	2000 (2200 10700) 19(2241)		MINERAL I		30,0000 01,0000
Arismbuner Isameni	Cathopranse		1188/7241817)	1 Second	IONZ KINEMA. INTERO			1980 (890 300)						M(M.PT) 0						1200 (7000 2000)				2300 (1099) 4900)		1900 (1900 2970) X1(20A4)	2000 (2000) 3200)	847 (P.S. 1912) N	MI(190.52%) 64(63.14)	7090(N386 (N4)442NB) 17980)
Arismbane Instanti	Pleasupainelesses Francis promotion cephalosposies				12863/7776. 1876.7) 1291.7/5690.3. 1798.23		172 (88.76.1) 92 (91.94)	1200 (890 2000) 130 (8132)	25623) 26623)			1986-(1986-8280) 1998-(2786-8680)		TO(NLISS) 4	(63.12) (68.66)	40(315) 40(315)				1700 (1700 2000)			01(0001)	210(10)300		2000 (2000 NAME) 40(2343) 2000 (2000 NAME) 40(2343)	0000-2500 0000-2500 0200-2500		101201200 6192400 11143 6898600	(2000) 123(17214)
Animanni Animana Instrumenti	replainqueies Third gramation controller				15814(1518 15814)		97/9199		388(52.073)		A7(3.387)	1998-(2200-8200)			18460	MICHAEL MICHAE	100000		40,000	Cherken Seed	MADISMA	1(0.1)	00/0000		01(0003)	2000 (2000 5000) 40(2245)	8000) 8000-2500 8000		(FLIS) 60 (666)	72(00.00) 63(0.00)
Actorolocus Insumerni	Environments and common auditories	179 (82-200)	105.6/16.622019	121000/10000 100000	11096.1 (M231.1- 2000.4)	431,011.463)								212,022,095 1		2750 (2000-2750)				16200 (PF10) (1000)	361(367464)	46(0.116)	01(0102)	Nevo (Neso 16000)	12(63.24)	2000 (1000 3000) 42(2444)	962000-752000 952000)	987 (CANN) T	(B)(1980-12980) 1.3 (67.52)	18000/1080 X2.5(272.647) 30000
Citabater app.	Antesphonian Antesphonia					160						1070(707.2000)				80.35			60,00.60		090410	0(0.1)		23 (6.64)		10 (C34) 60(600)				28(070) 66(666)
Citabaser app.	Anti-paradirented proteille little Lectures inhibition				901(0L1981				88.1(M.3.868)			200(2170.000)			(8862)	70 (89 190) 60 (29 120)		91(6.00)	00,000.0	196 (NL2NE) 78 (126 193)		2(1.0)	020222	231(96.80)	010100	275 (256.40% 01/0003) 275 (256.40% 00/0003)	690/3031130) 8700/3001130)		(0.10) 140140	180(89.970) 63(6267) 180(70.280) 63(6267)
Citabaser app.	Phonepinion					5 11 (4.2%)						7090 (9600 17000)				1340-(817-2620)			61 (80 6.1)	200 (01-200)			00,0000	313 (112.NP)		MD (40.198) 0.1(0.102)			19,14,249 64,06449	200(2704276) 64(621.1)
Citabater app.	Franti-gramation orpholograms				4/03/(//DAII)44				81 (17 T M II)			amo(2270-1020)				399 (234.899)		17 (7.8%)		180 (47.30%)				(21 (91.30)		PR(273.80) 01(0001)	2000 (400 2000)	24(1339) #	(A.M) 60 (66.60)	1180 (28.290) 62 (6.16.4)
Citabaser upp.		111 (N. 291) 168 (M. 290)			100.0 (MO.1 100.0 (MO.1 100.0 (MO.1							800,000,000				#8(281100) 3720(2790700)		30-(27-8%)	61 (80 6.1)	200 (210 500) 270 (340 700)		2(1.6)	00/0000	211 (49.2%)		96/GE368 62/6163)	2000 (1200 2000) 3100 (2000 8700)		(77.70) 66/6666	290(81,800) 64(6265)
Citabanir qq. Zaundanir qq.	Environment on our or more antiferior.				2007) 2000(2003)		53(2495) 21(9445)	410 (279.790) 170 (48.390)				12900 (4790 20900) 7720 (4940 11200)			(6247)	200 (276 700) 200 (276 700)		32 (36.8%)	11 (00.83)	2780 (2460-2730) 2780 (2490-2730)		2(1.0)	00(0003)	174(47.7%)		120 (KC 200) 63 (62 64)			1(2970) 61(666) 8(1.25) 66(666)	200(020100) 15(1515) 200(0100) 45(111)
	Anti-predictional possible lists factorises addition				7627 (M61) 11760)				KNA (\$723.1461.5)							200-000-1130		77 (27.120)	42,6143	000 (200, 200)	119(84224)	9(2.25)	00,0000	Na/861/88		NBO (\$00.700) 69 (04.14)	2000 (7600 2000)	218 (218 274) #	M/MG.1009 61 (61.62)	1000(5002000) 28(1449)
Emmharier spp.	Cathopranse													20(13.9) 6					61 (80 6.1)	N20 (360-2740)		9(8.28)	00/00003	10 (811.00)						1990(79002290) 2.0(1.04.1)
Zamenharan app.	Pleasaguiseinen Proofingemeine				01 400.1) 01 400.1) 01 470.1(2000.				264 (264 264 3) 264 (264 267 3)			10780-(M000-14000) 14880-(11200-20900)			(6.1.62)	1140 (NA. 2000) 807 (NR. 1940)		20(2126)	61/61/63	796 (201-04) 666 (301-070)		8(2.0)	00/0000	29(30.7%)		260 (270 N20) 01(0.100)			F(12.70) 61(666) F(12.70) 68(666)	700(8801888) 1.5(672.6) 360(8967888) 67(631.3)
	rephalopeies Teachopeies Sellenthopeies					34,070						1400 (890 2000)				MO(0.1790)				AND (\$240.4070)				28(1.68)		400 (200 400) 07(0 4 L2)			NAME -	420(01700) 11(0023)
Emmission opp.	Environments and common authorists					314 (915 470)						3900 (2000-0200)			(8.8.L1)	Tele-(8000 1 8000)	majanen	112 (81.300)	61/62/64	TABLE (TOTAL SHIPE)	218/42/20	N (29.80)	0.1(0.00.1)	2700 (1000 4300)	84(549.0)	K201,879.2009 17(0+27)	3.300().2000 3.200)	387(22.584) 19	90(139299) 63(6269)	PRECINETING ENGLISED
	in Phompinion								428/9(2724-1772.7)							2010-(200-2020)			60 (60.6.3)	PHI (GR. 190)		8(3.11)		ans (173.423)		280 (280-230) 0.0 (0.3 0.0)				1200(21012200) 3.1(1.345)
Emmanar anjana Emmanar anjana	ile Vaccespois de Brokesporte par comme antièries				2004/2007-0044 01 27084/2002		TERRATE SECTION		112.8(MA.287.8) 762.4(MKZ.1962)			704 (189 - 1270) 4750 (188 - 2790)			(6162)	264 (HD 490) 1540-(AN 2590)		4(27) 26(11.69)	00,0000	221 (147.847) 2000 (8231.8730)		160	00,0000	100 (EL 201) 174 (241 1100)			1200(000.2120) 2000(2200		P(79.29) 04(0040)	200(02029) 68(53.5) 2300(02082900) 38(187.2)
	or Phospinion													20,044 6						601 (DW-1036)		11 (1.72)		1100(110.2700)						ZNR(DNRAGNO) RA(DAZZ)
Entereconomicania														20(19.40) 6						359 (309-6730)	74(15141)	1(13)	00/0000	KIO (TO) 1770)	17(97.54)	NGO (290-900) 13 (04.17)				1900(1998-0900) 63(2A1L4)
Emmonourfact	Ensistence in one or more antibiotics					126 (69.212)		11200 (4100 18900)	12949 (CLL) 2006() 7867 (1133 14844)			14700 (870-2000)				270 (200 200) 2120 (200 200)		81 (91.1%) 40 (91.7%)		2000 (2000-2000)			00(0002)	500 (MC 400)		1200 (PM 1800) 21(1237)			(B)(250,880) 64(63.14)	8800(42700. 143(7.828.5) 14900)
Other reterminosi	Pleonquissione Vancoquis					19 (13.176)			761.7(113.16618) 167.8(148.7503)							2130/310-2000) Mil-(277-1130)				788 (265.093)				(31/9130)		120 (26.180) 02(0103) 120 (26.180) 04(0110)	2000 (1000 2200)		0(0.23) 61(660) 0(0.23) 61(660)	230(230200) 24(644)
									171.2 (MAT. 186.8)							200,000,020				380 (ACS 300)				76(23.238)		200 (200 KM) 04(0110)			COMMENT REPORT	1900(T30,1280) 33(1440)
Endertship only	Assimply-malm				7884 (N291. 11852)		12(1079)		4910(2763.76E4)			309 (386 (386			6143)	280 (130.1126)			61(6245)	1000 (1000 2000)			00/0000	Karloviani		500 (840.020) 1.6(0.20)	30000 (112000 30000)			1800(6EN-1980) 18(L128)
	Animproisille Bits Latinelles Interner idélies													21(14.70) 6 21(21.70) 6						THE (CAN LLINE) NAME (THE ACTO)				701/201/200 270/201/200		2800 (1800 2700)				NAC(NAC1380) 1.5(0.9.2.4)
Endertida cali						27 (2.17)								76(21.05) 6 76(21.05) 6						1489 (1790-2210)										THRESTON SALES
Endertship only	Phompsindom					30 (90 40)						129800/92800 129800)				17300 (9020-10900)				1240 (1130-790)			01(0102)						W(100.100) 64(62.64)	1200(12007000) 15(17344)
Endonistia cell	Third grammine explosio-posics					48 (70.80)								212(94.075) 1						POSE (PCNLAUZO)						2800 (4700-1700) 42(2744)			W(100700) 67(526%)	6766(2896. 12.5 (1.3.22.5) 12660)
Endertida sell Endertida sell	Trinerlaysin Sallawritenanis Environanis nar sessen antitiria					100 (10.2%) 12% (11.2%)						142000-(20000). 199000) 199000-(19900).		MONEY A	ISSAU	7640 (1000 11000) 5540 (1000 7900)				NUM (NUM ARRA)				200 (700.075)		2800 (1800 3900) 43 (29 47) 2800 (2800 4900) 42 (40 94)			10(00200) 02(0200)	22000(1988) #4(1983) 22000(1988) #44787473
Group A Streptonous	andrinies Marchin				475E14)		07/0015		277(00.0076)			20200)			(886)		SAMPLE S			101(03.300)			000000		02/00/08		12700(4170.2480)		P122 0000000	120(9.620) 62(666)
Group A Emphasicos	Environments one or more analysistics	12 (11 85)	MILLAR	280 (27% 764b)	296.1 (106.0 x00.0)	162)	07(9013)	49(6.203)	277(60.MER)			200(2130-000)			(886)	275 (0.1220)	34(6611)	ET-(N-27)	00 (00.00)	101(03.300)	28(6245)	160	00/0000	112 (6.50)	02/00/00	40 (36.8% 0.1(0.0.2)	2790 (42 % 2400)	23(1148) 4	(6173) 66(6666)	120(9.629) 63(6668)
George E.Stroptocou	or Phonquiscions					199 (\$1.700)						14400-(14000-25400)				240-(20-900)				869 (906-909)			00(0003)	964 (173.2179)		29(29138) 01(0102)			1(939) 66(666)	390(92,870) 62(6114)
Group E. Deceptores	our Manufair					32 (8.90)						40 to 100 med		e(0.00) 0	(8817)		20(0444)			22800 (1480) 27800) 289 (262, 827)			03/0303/ 01/0301)	276 (A.160) EL (A.160)		250 (860.720) 69(66.12) 26(26.76) 69(66.03)			(r), (r), (r), (r), (r), (r), (r), (r),	1800(0.000) 24(0.03)
Group B.Stroptocou	Entition to one or more authorized					AH (21.490)								m(120) 0		X20-308-0400		219(178-800)		2700 (1/200.3200)				330/0.579		400 (\$70.500) 69(04.14)	2000/000 2000			1800(0.0700) 3.5(0.000)
Numeral des influences	Antequalitie													27 (2.88) B						100 (400.1700)				1470 (124 700)		49 (10.6% 01,0101)	(2900)/090-12900)			200 (24.900) 64(6667)
Managhiles inflames	Third gramation explaint/posites					(C) (M, (24)								26(12.8% 6		420-(200-2008) 200-(200-2008)				389 (250-890) 1110 (250-190)				2010/01-010		(21)(MPNM) 01(0101) (MP)(10722) 00(0000)				120(01200) 63(6160)
Managhiles inflamour Klabalela	Environments over consume antiferation. Assisting Systemation.					67 (34 134) 189 (188 294)		1000 (920 3000)	693.4(2563.12863) 1926.4(19868)					71(27,03) 6 20(16,03) 6		400-5200 T3000 430-5200 30000			109415	THE CONTRACTOR			01(0001)	220(90.200)		1000 (000 1000) 19(1229)			N/MERRS 62/6162)	200(1200700) 64(6311) 2000(12003000) 14(2343)
Elebelela promotion	Reta Lacture Brita Incommer inhibition								STREET, STREET,					20(7.60) 6						7600 (CHIII. 12500)	1657 (1804-281.5)	1(120)	00(0003)	K4(29-209)		2000 (1000 (1000) 44(2044)				emo(2201300) 13(6424)
Allebrada promonio	Cathoprone					30 (31.47)								196(61.27%) 1.						29400 (11700-70000)						1000 (1001 1440) 20(17.50)			W(190.00) 67(0.00)	emplements supplies
Elebrida promotion Elebrida	Plantopoleolosos Tital gramation corboleorosis		100.0(007.149.7) 80.4(1928.778.5)			204 (114.221) 687 (248.2231)					164 (888-994) 284 (888-827)			200(06.200) 1. 300(226.400) 3.	(0.248)	900 (100 1200) 300 (1100 5400)			12 (66 LB) 20 (13 3 B)	NORM (1349-7360) K249 (1399- 12490)				380(300.80)		2200 (1900 2900) 3.1 (20.44)			(0) (0) (0) (0) (0) (0) (0) (0) (0) (0)	2000(2700-2000) 8.6(3.6.1) 4200(2700- 31.6(4.3.14)
Eleberia Management	rephalopeies Telephopies Sellenthopeie		#93(NST4#7)	E-Commit	6012) 6914(7164 7010		200(00.00)	1000) 1000 (000 570)			PHE (144-268)	7080(1208) 2080(1208)			183.14)	990(000100)			17(1128)	0000 (2000 2000)				THE CHE HES		2000 (1000 2000) 17(24.64)	8000/1000 2000/1000		B(25.00) 62(6165)	2000(1200-2000) 4.9(2.18.1)
Kindonista processorius	Environments one nemore antibiotics	NAME (TIME THREE)	684(864.87.2)	20000 (2000) 70000	NAME OF THE PARTY NAME OF THE	1620 (424-2280)	1764 (605.1.2004)			2000 (3.10.7648)	362 (993.569)	201000-(20100) 201000	2023/sem2 887.5	MILITARIS 7	(4.6.11.2)	76700 (27700). 201000)	снацинальнал	2000 (70% 2 Mall)	22(18.13)	1000 pictor. 15000)			07(0410)	2000 (1900-2720	h M1(31463)	2500 (8000-2000) 14(3.524)	C1000-1210000 2010000)	DIONAL B	W(XXX1200) 14(18.24)	28600 (13600. 32600) 36.6 (213.99.2)
Moquentle upp.	Phonepissions	1 (9.7)	0.00000	18 (90.285)	128(12275)	0 (0.1)	00(0003)		11(04.00)	1(6.2)	00/0000)		67 (62.17)	0,000	(64.60)	12 (5.86)	61/6663)	0.(9.1)	60,00.60			0,000	00/0000		00/00/03	46(21.273) 60(6600)	1470/962,000	616266 17	(4.25) 64(6846)	32(9678) 61(6661)
Moqueella spp.	Frank premise ophilopein This granules orbitomic	1 (9.2)	61/00/63	81 (31.82) 88 (34.132)	433.843	100	00/00000	4(1.0)	01(0111)	0(0.0)	00/0000)	27 (844) 20 (440)	63,6167)		(8460) (8460)	10.00	61(6662)	0.000	00,000.00		0000001	0000	00/0000	3 (1.8) 2 (0.8)	00,0000	27 (CAR) 60(6000) 27 (CAR) 60(6000)	20 (28 40)	01(0102) 0	L10;	10(2620) 60(6660) X0(2629) 60(6660)
Moqueotte opp.	Encirios en como or more antiferior.	2(9.0)	62/80.64	18 (91.70)	16.1 (6.1.75.0)	0 (0.1)	00(0003)	24 (8.80)	10(00.02)	1 (0.7)		88 (98.224)	68,6224)	4,61) 6	(8.66)	24 (6.8%)	62(6867)	1 (0.1)	00,000.00	47(34.00)	0.1 (0.0 6.2)	0,049	00/0000	11 (0.2%)	00(000.0)	12 (52.7%) 60(60.0%)	270(103.790)	04(0307) 20	(0.13 0.0000)	120(201.000) 61(6662)
Mysobacterian referentiate	December along environments Till	-		0/04)	00/0000			0,000	00/0000)	2(84)	00(0003)		11(03.14)		(0.00)		44(8324)	164	00,000.00	131 (29.300)		160	00/0000	74 (17.220)	62(900.5)	N(SLIK) SO(SSSS)	210,001729		12.50 60,0000	120(98.580 63(6.64)
Mysohummian nelsenskesis Mysohummian	Serviced mean emissioner Michigan emissioner	-		000	000000			100	00,0000	4(1.15) 70.44 70.	62(0167)			100 0	9460	#(0.70)	101000	F-(1-20)	00,000.0		119420	100	000000	77.0.260	92(9994) 20(924)	10(20/00 01(0001) 10(00200 02(0100)	1900/sub-2000) 3000 (1900-7600)		D.C.200 010000	190(0470) 63(6412)
Mysoluminis Mysoluminis referencies	mintere is TE Education measurables			ejesj	00/0000			100	00/0000	1(0.1)	00/0000	12 (26.90)	69,63446		p.e.co	H(2.8)	61/6663)	1 (0.1)	60,0040	44 (34/8)	01(0102)	000	00/0000	10,000	00(000.0)	42 pts.125 00 pts.005	ami(200.42%)	67(6514) 26	p. 10 000000	WI (28-289) 62(6664)
Mysobarovian referenciasi	Environments one or more analysistics	-		0,000	00/0000			100	00(0000)	N (12.80)	03(0100)	2990 (2070 7640)	21.2 (9.7 (91.7)	17(2.8%) 6	9440	1930 (107 AMI)	107 (1342.5)	201/201409	61 (80.63)	200 (91.990)	1100.04	23 (2.3%)	00(0003)	100/06/00	21(814%	180 (66 300) 63 (61 65)	96900/31900. 200905	167 (57.164) 49	0,091749 61,6663)	2900(40007900) 43(04304)
Returnia generalment	Photopoleoloon	-							-																		770(290403)			39(90739 61(6661)
generalment Animania generalment	Third grammine explosionposies Environments are sessor antitionies								-																	-				20(2220) 64(6640) 20(2220) 61(6661)
Proteon age					262 (269 764)				214(28/86)											478 (486 278)			00/0000			180(120300) 03(0200)				\$80(\$1.686) \$3(6666)
Proteon aggs	Antoqualitie					2,615						1600,7000.1085				R(0.20)				248 (278-228)			************			200 (200 (20) 07 (0 t L)				100(6370) 62(6664)
Proteon upp.					667 (36.1 ST)			265 (267.765) 1686 (266.2765)	417(16681% 1114(106293)			2000,2750,8000 2790,3480,4000				99 (75.62) N7 (85.690)				170 (421.230) 170 (771.200)			93/9393	81 (28.88) 221 (48.875)		260 (920.800) 61(63.62) 280 (920.800) 61(63.66)				900(200400) 64(6312) 900(2002000) 1266336
Protest typ.									313(08383) 313(08383)							107 (313 300) 318 (8302)				280 (90.230)			00/0000			380/800/289 04/03/09 380/800/289 02/03/09				200(100) 64(644)
Protest typ.	Resistance to one or more authorize.	125(07.2%)	141/02/84	1000/1000/2000	1021-000A 2007-0	24 (12.44)	26(8.547)	200 (400 300)	2932(1131-483.1)	3 (943)	00(0410)	420,710,975	81.018.905	12(6.2) 6						268 (278-849)			00/0000			489 (710-679) 01(03-12)				1000(6003160) 33(1443)
Paradomena arraginasa	Antiophysioles Antiporalismad													10/0.24 6						Date (FOR LICE)				30 (6.82)		600 (800 N30) 13 (0.7 L7)				200(0.2000) 0.7(0.0.11)
Paralamena arraginasa Paralamena	Anti-paradiomenal postedio listo Lactomare addition Carbapturan					202 (101 307)								30(31.05) A 90(01.09) A						1900 (1000 2000)			00/00000							1700(2002200) 2.6(1.64.1) 1700(20064700) 7.6(4.12.3)
Paradomena arregiona	Phompsinion					131 (% 300)								N(0.76 &						1680 (CHRS.2380)										2000(1390.0000) 43(2344)
Paradomena arraginasa	Franti-gramation orpholograms											23 NE (2900 NASO)				1800 (719) 2620)				1000 (1000 2700)			00/00003			209 (480-1889) 13 (59-19)				200 (240 830) 64 (63 1.5)
	Third grammine explainequates Environments are some antibiotics					117 (H-28) 694 (M-800)						6278 (2000 8700) 8000 (4200		20(34) 0 20(34)76 2		ETC.(100:000)				2800 (1700-3200) 3200 (2700-400)			92(9193)			1800 (790 1790) 22(14.12) 1800 (1800 2800) 31(20.45)				1960(K251390) 3.5 (1.54.2) 1860(K251390)
	antitions to Phonepinstone	268 (109.500)			99(994)			### (\$200 H) X				3 (42)				200(1700.0000)				1288 (2788-4680) 28 (26-28)				27 (L115)		20(1.8) 60(66.00)				17000) H3 (11.512) 26.0170 61.0161
	Multi-degreciment in Schwerfe Typhi and Featureli	-		0,000	00/0000			100			00/0000)		00/00/00	.,	(8.66)	0(0.0)		0.000		4(3.17)		0,000		192)		1 (6.2) 60(60.00)	4000	68/6660 O		49.13 66(666)
Salmonalla Panity	de Entitioner to our comme antitionies				00/0000			100				3 (42)				1(0.2)				10" (26.290)			00/0000			20(7.40) 60(6000)				26(670) 61(660)
	Pleasupainelesses Made drug resistance in Administra Typic and								1000(900.2011.3) 211.000.000.00							260,780,870				100 (NO. 200)			000000			100 (N2.180) 02(0103)				1200(1002988) 23(6384) 230(6298) 68(6414)
Xelmontle Typis Xelmontle Typis						22 (671)						1600 (760 7600)				70 (92245) 360(703.896)				200 (100 700) 1200 (100 200)			01(0001)			20(21.764 01(001) 180(70.276 02(0104)				1930(1901290) 2a(4744)
Non-typhosidal Xelmonalla	Phonepiteleses	9(817)	10/6419	78 (50.180)	\$5.00(TEA.248.2)	166	02(0000)	164(25.449)	(18)(23.47%)	10 (4.36)	01/0003)	1200/0062999	89 (37.264)	2(67) 6	(886)	ZT (EAR)	21(6387)	7(247)	60 (60.64)	H4 (H1.202)	109453	1904	00/0000	141 (17.49)	07/00/10	43(23.75) 60(66.00)	2700/00/4079	68/6217) 9.	12) 68/6666)	20 (4.190) 61 (66.2)
	Environments and services and basis.															27 (0.40)				86(20.203)				141 (17.49)		£2(227) 60(6696)				20 (4129) 61 (6662)
Zerostie upp.	Animplyonide Anipproximand provide Set Lectures iddition													2(80) 6		32 (34.40)		K(130)		TR(SE270)				44 (6.1%) 101 (43.37)	02/0003	48(3270) 01(0001) 42(3270) 01(0001)				76(0.000) 61(0.004)
Zeronia upp.									1662(TK3.864)							40(95.60)		40.00		att (dansta)			000000			Sections of local				200(220,099) 6.6 (6.24.9)
	Photopoleoloon	48 (96.136)	74(09.034)	460 (270.000)	4967 (189 1 11214	B) 7 (\$.27)	08/01179	401/28/1009	7011(110.1668)	06 (18 No)	02(0103)	1600/00027903	84(17.254)	2(67) 6			14(63.57)	6(511)	60 (60.64)	NE(28.66)	10(85.20)	160	00/00004			STREET, GLEGGE	800(279.1986)	14(0923) 3	(A.E.) 64 (66.66)	90(2720) 03(664)
									121.7(464.2949)											19(40.09)			***************************************			30 (Dh.138) 01 (01 02)				280 (89-220) 64 (624.8)
Zernatia upp. Zernatia upp.	Third grammine explosiosperies Environmento non common antibiotics								#15(331.130.3)							291(SA10) 160(913.500)				196 (NA.224) 266 (NA.224)			00/0000	79 (23.180) 803 (222.860)		486 (HE 188) 62(6163) 1800 (HE 188) 63(6268)				100(523,000) 63(6162) 1000(526,000) 15(1633)
Abigotla upp.	antitionies Planniquincinnos											1460(400,750)				200 (201.024)				190 (290 2140)				DESIGNATES		Ne(SLIM) co(code)			C. 00 000000	(200(96.300) 62(6864)
Abigothe upp.	Resistance to one necessor antifestion								Neph 28.0							200-201-0105				190 (290.2)40)			00(0001)			Mc(SLIRE) EN(ENGE)				126 (6.595) 62 (6644)
Emphylanacous aurosa	Pleasupriseissen	961 (611 1770)	100.0 (40.0.100.0)	12000 (1200.	1016.0 (190%). 17099.4)	42 (17.74)	44(3.880)	2790 (1290.4990)	4000(1423.791.0)	605 (407.87%)	19(1279)	1748 (AROS 7710)	823 (F2.676LI)	20(11-8) 6	9144	2280 (9120-2290)	224 (53.750)	267(177.369)	04/0403	2800 (2000.0200)	8002347.0	11 (5.20)	00/0000	993/429-1290	21(99.33)	18790 (120 1998) 20(13 28)	27000 (27000	209 (EATER) 20	P(29647) 61 (6662)	1000(20002070) 23(6544)

Suphylamous	Marekir	1121 (2011 4740)	mezzante	29000 (100000	30387(2969).3.	101020	127/106/2009	1040 (710,0000	11343 (887.3.	P79 (200 200)	DEPOSE ZNO	179000 (17000).	1963/2084	70/10/09	978312	440-2780 LEWIN	MA GALLEDO	291 (529 1129)	17/11/24	ORIO (2750-4750)	1600/997.205.61	2010	91/99931	279 (1831-290)	MGIAN	2000/790/790) 48(3340)	C200-14000	(ELIGIALTIA	96/26/200	92/61/07	2010/1420-01800	411792
200000				Transaction (2200				3041.0)			210000)	2015														esaxs					
Emphylacocour aurons	Medicilla	200 (200-200)	391(261480)	20000 (10000). 36000)	2760.1 (1765.1. 3661.1)	741 (031.034)	MIT (TLA 141.5)	6760 (2600 11600)	73429 (738K3. 1362L3)	279-1296-2179	161 (123.21.6)	17780(12908) 21980)	MANAGEMENT.	499(212799)	42(5540)	2000 (1000 cTox	384 (797497)	736 (908.2020)	18(11.23)	1200 (2200 7000)	1311 (934.1864)	211 (96.529)	94(9297)	1000 (100.2000)	367(857,894)	2000-2000-2000) 7.7(7.7.5)	2000/0000	131.3 (67.8191.4)	776 (160 (100)	14(0424)	79000/0480. 20000	343 (1944)
Emphylacuscus aucres	Trine lasprin. Sullame lasprancie	2010 (707.2478)	190(568160)	1500 p240. 13000	1098 T (403 A. 1278 T)	99 (27.199)	107 (11.160)	\$20 (\$100 LT00)	100.7(252.1203.0)	ac (sava)	62(\$783)	4000-(2000-0000)	893 (642 2390)	M(30.45)	416340	посрежда	278 (244 744)	219 (348,392)	00/04/08	2700 (HIII) 2700)	JA475375-0	28 (11.56)	00(0003)	2020 (1994-1290)	42(214%)	780 (000 0000) 14(0.9.20)	2000(13000 2000)	M4 (SLA ALI)	401/111109	61 (61.62)	1000 (120 2000)	3.0(4.8.0)
Emphylacocom assess	Vanconquin	86 (EL 120)	9.0 (18.103)	THE (CHICAN)	X064 (505 A 1206 A	21 (81.79)	22(1.142)	1840 (889 549)	299.7(964.275.2)	JF (71.44)	04(0304)	200(270.500)	367 (364 (54)	11 (4.20)	61 (61.62)	977 (894.1790)	89(63.00)	20(13.2%	00 (00 8.3)	(38 (100.200)	140453	1(21)	00/0000	49(80.50)	01/01/10	FT(NEAP) 01(0102)	1800(900.2000)	27 (1842)	100(70.30)	68(5860)	360 (870.733)	42(6313)
Emphylacocoms aurona	Environments and someon antibiotics	NW (SWI AND)	ENR/2757-MER)	20000 (23000) 20000)	7786.8(2478.1- 5766.7)	2020 (100.000)	1004/617.0000	1000) 1000)	96232 (NESS.). 14896-1)	200 (000.720)	22.3 (36.8.2%)	21780(36408) 2000()	972.1/1487.A. 267.9	472 (300 900)	17(1480)	8900 (1270) 8700	M2(874762)	ARCTHOUGH 200	21(1429)	2000 (0200 12000)	(812 (384 3814)	20 (10.40)	0.00300	2340 (200,700)	#3.0693EK)	NEED CHEEN FAMILY & 44(LT-9.7)	90200 (100000 (100000)	1667 (1705.2410)	998(586.1688)	18(1838)	28000 (17800) 48000)	41.1(239.747)
Emphasica promission	line Lancerline incomer address	660(EZZ-976)	37(8888.0	50'00 (1790.8000)	608.1 (879.3. 908.0)	4 (0.30)	04(9317)	N11 (G.14%)	M4(13.049)	H20-(870-3103)	129(9417.5)	12480/9460	1101.6/KIDA 2003.5	17(9.75)	61 (68-62)	1130 (23.380)	167 (62 264)	KN0(3N0/3M)	11(67.14)	APRIL (TOTAL ACTO)	960(6541987)	4(0.15)	00/0000	200 (10.0149)	01/0024	360 (250 (59) 67 (63 L6)	2000-07900 2000)	22.1 (20.9-30.4)	27(6.4%)	44 (54.66)	XTX (42.2045)	63(6864)
Emphasica prostruction	Cathoprane	198 (100.250)	172 h (1884 291 2)	12000 (4080) 20000)	18767 (WZ20. 2279 I)	329 (239.800)	387 (8.1467)	2180 (240.1108	32764 (SMLA. 27863)	2000 (2000-2720)	No(224.993)	210000 (20000) 30000)	2073 (2003) 32% (470/021170)	61 (55 817)	M700(2880. 20400)	107 (Ph.1103)	1280(896.17%)	27(48.33)	12000/7000. 20000	202(683.994)	30 (03.2%)	04(8310)	2500 (10700-2000)	#1 (22.5 HF-4)	1800 (1801 1900) 18(1428)	3200-2000 4900)	MA (E.B.76.2)	2170 (1000-3000)	64 (62.67)	47000 (12700) 117000)	12.3 (4.9.3%)
Emphasica prostruction	Plempinion	490(212.200)	760 (811105)	4210 (2000 NORO	600 F (200 F)	78 (28.170)	88(59385)	6420 (1980 1980)	792.1(171.6.1607.6)	2790 (22027HIS)	197 (11.1.21.8)	113000 (20000) 21200)	1395.3/9864. 2395.3/9864.	290(28.890)	18 (64.57)	(1900-1200-1900)	1879 (MASSLE)	HTT (338.62T)	12(67.18)	2900 (7000.0000)	1017 (604.147.7)	er (13.144)	41(9343)	900 (100 1000)	11.8(2.3.28.9)	PRO (290-200) 0.2(0.707)	4000 (FRE 900)	124(91.174)	201(21)-275	44(6840)	7300 (2770-29400)	13(6328)
Emphasica prostruction	Maredale	PHR (1301-260)	2010/024380	176000 (117000) 267000)	18967.7(1230.3. 27909.3)	er (0.330)	77 (9329)	en poem	681(661752)	2000 (2002-0000)	354 (368-458)	34000 (2000). 42000)	333.7(386) 885.3	136(9.30)	12(6831)	(2000/0.3000)	101 (0.2754)	1130 (100.300)	32(23.44)	COMM-(NZYM). DOMES	294 (980.794)	N (0.170)	41(9343)	ACTO (0. 27900)	97 (99.250)	1800 (900 1798) 14(18.52)	4000-(1000 (1000)	751 (91.1-96.8)	270(0.120)	61 (6662)	1200 (0.7700)	24(6848)
Emphasica prostruction	Probable	2098 (1320-3080)	227 J (\$460.596.2)	28000 (17800) 28000)	20217.8(12989.0: 2028.0)	112 (% 24%)	122 (60:214)	ma (200.1700)	10022 (NTA 19054)	200 (E00,NAN)	393 (293.814)	3000 (2000) 2000)	307.1 (296.2) (863.5)	227(118.98)	21 (1839)	200(100.170	H24(E3.867)	M70(1180.2570)	38(28.88)	12000 (10200) 20000)	301 (334-291)	89 (26.11G)	42(8187)	2000/9701/0009	160(3.274)	1800-p0000-18000) 2.0(1-0.33)	44000-(14000 (62000)	753 (87.2 (88.8)	700/961299	61 (61.62)	2200(1798.5000)	+ 41(2344)
Emphasica prostruction	Third gramation cophaloqueiro	20K(3£17H6)	#3 (MANAS)	3880 (2798-5280)	900.1 (200.3 9700.7)	3 (14)	03/0104	228 (74.634)	24.8 (8.0.17.1)	201-1106-2000)	72(8187)	4992-(2000-1990)	693 (423 8942)	4 (1.00)	44(646)	T1 (26.80)	34(1379)	313(213.441)	47,644.55	2500 (2000.3000)	MA/K7800	2(1.0)	00/0000	140 (10.704)	03/01/07)	NO (200-EN) 04(0-EN)	9000 (8000 (2000)	112 (12.4.28.4)	36 (45.75)	44 (54.66)	(20) (23-200)	62(6167)
Emphasica prosession	Triantequin Sallambranch	2760 (2760,3920)	XC1(P64-2X4)	22500 (1980). 3800)	2685.2(1758-5. 376846)	219 (12.40)	208(54491)	2100 (200.400)	21148(312.4: 4368.2)	No. (200700)	ELE (913-664)	50000/92000. 60000)	anna nann Millin	478 (42.623)	48(64.73)	3000 (1120-72700)	354 (62-61.7)	2130(1886-2940)	41(1143)	28000 (1900) 28000)	389 (75 6 85 9)	101 (23.547)	43(9447)	1410 (190.200)	201(4242.4)	1000-1210-2000) 14(22-37)	20000-772000 62700)	893 (88.2.1039)	128 (19.208)	62 (66.64)	(960(6601460)	69(18134)
Enquision on procure	Encirios en un sensor antiférico	3180 (2800-2000)	30.1 (2000.107)	714000 (20000). 447000)	31614(11983 47812)	R14 (BM, ECR)	86F (G.R.(10.7)	7380 (2700 1000)	70759 (2701.1- 11775.6)	2010 (800) 0000)	48 (514 854)	62000-(00000. 51200)	MICHIGANA THE R	1490 (1390-2590)	114/101214	121000 (302000. 201000)	138.6 (CTA 188.5)	2780 (3496-2780)	88(41.78)	25000 (7000) 12000)	2864 (786.2 479.4)	461 (804 409)	17(6817)	H780 (1030-8030)	1944(73.3.9638)	2000 paxis 2700) 18(2+44)	67500-(275000 (E4000)	1014/0183101.0	200 (270 470)	69(6612)	110000 (312000) 212000)	27.8 (184.365)

Table N.E. Drude and D.M. Voj	in company and agreeper	to rates) ensulated with	and attributable to	harbytal antimieral	hid ordane by pa	dager dag ambie	nation, by age group,	2009, week Ania				Peak	Nematal															3 and over		
Pallege Asibatic	Class	Associated Deaths Eater per 200 000	with renintance E	ALN: Rate per 100 000	Counts	Attributels Studies Kaie per 100 000	Grants	UE.Ys. Eate per 200 000	Create	Associated allo Rate per 100-200	with resistance Di	ALSIs Eate per 100 000	Create	Aprelhende Deudes Kaier per 100 000	le in resistance El Cinasio	MLYs. Rain per 200 000	Counts	Associated teaths Nate per 100-000	with retitionar Di Counts	ALTA Este per 130 000	Cineto	Attributed Smaller Easie per 100 000	de los emilitianos e ESAE. Coussin.	No. Rate per 100 000	Counts	Associated allo. Rate per 100 000	EMLS). Create East p	er 200 000 Create	Administration Direction Easier prev 200 000	ENEXY. Counts Kale per 100-000
All pulsagess or more and	107000 (1270) Berlin 207000	8211.0 (9838.0- 11296.4)	28300000 (13200000- 294000000		719200 (788000 716700)									38.5 (23.6 78.4)			21200 (12000- 91200)	36.6 (20.4 66.7)	7940000 (1000000 5130000)	2009.7 (2009.8- 2009.7)			130000 130000 (47000				530000 247. (230000 247. (230000 247.	(1422.7: 304000 (2000 () 476000)	980 (8.0 (12.7 de.7)	848080 (174800 - 727.4 (101.6 1290800) - 747.4)
Antoniolocae Instrumenti Aminoglycos	Miles (1780 (1780 17	00 NA I)	Name (25400) 115000)	3008.1 (3886.5 3777.6)	394 (0.878)	144 (60 NLB)	75400 (121-79200)	1292.5(4.8 3887.0)	1200 (409-2020)	47(1047)	124000 (80000- 178000)	413.4 (208.2) 999.0)	27 (0 LM)	62 (9.0-64)	NORE (9-11000)	17.0 (0.0 79.3)	NA (309-809)	0.1 (0.3-0.7)	28600 (10600 74100)	36.8 (28.2-56.1)	29 (9-89)	0.010.01.03	2000 (7-4740)	1.8 (0.0.3.4)	84000 (2K700- 13N000)	3.1 (5.0-8.2)	200000 (202000 120.3 200000)	(43.3 179.4) 3240 (0.4890)	02 (00 0.0)	7900 (M2 (100 11.8)
Anti-possion Anti-possion presidentisi Instrumenti Lanisman inhibitory	10000 (0000 11000)	201.2 (241.7: 424.7)	1110000) 411000-(800000	77129 7 (23124.7 31620 7)	170 (% 317)	68 (58-124)	15200 (4800- 26200)	60L6 (209.7- 1117.0)	1740 (1130-2990)	3.8(3.8.8.9)	194000 (100000) 228000)	912.6 (198.8- 792.8)	28 (13-92)	61 (9.0-62)	2090 (1130-0900)	8.7 (5.8-19.2)	750 (162 0000)	03 (03 03)	41200 (78300 93900)	864 (28.9.79.9)	12 (9-22)	40/004/9	2000 (201-2000)	0.8(0.3.1.4)	162000-(99000- 162000)	62 (5.65%)	2200000 (1240000 2040000)	(76.6-217.2) 1600 (670.72	III) 0.1 (0.0 0.2)	3800 (1700) 2.1 (0.8-4.3) 7000)
Antendente Bris Lation Assessmil Internet id	elleta Melani Massicinno sa	NA 2 (212.3- NA 2)	840000 (122000 1240000)	22713.7 (2048.3 2073.0)	8 (2-17)	0.3 (0.1-0.7)	499 (387-1480)	27.6 (7.4 (8.4)	1890 (1800-2270)	32(3.074)	1,0000 (P9000- 20000)	499.0 (297.1- 671.6)	1 (0.0)	60 (0.0-60)	124 (10-271)	0.1 (0.1-0.9)	627 (200-987)	03 (03-02)	51900 (11900- 81200)	42.3 (26.3 64.4)	1 (0.2)	anjananj	20 (29-109)	0.1 (0.0 0.1)	141800) SENSE (10000-	5.4 (5.1 8.4)	193800 (118800 12800) 116.9	(47.0 (48.0) 35 (4.71)	0.0 (0.0 0.0)	820 (218-1800) 0.0 (0.0-0.1)
Arisatelanter Carlagonese Instrumenti	9820 (4230 12	90.7 (24L) 90.7)	874000 (128000 1712000)	NETER (217%).2- 10983.1)	1400 (821-2710)	65.7 (25.3-105.4)	142000 (74900- 201000)	NATA 7 (2948.7: 9383.7)	0400 (MRO-2370)	3.4 (3.5 7.8)	142000 (42000- 204000)	275.6 (309.7: 689.7)	261 (142-476)	69 (0.3-1.3)	29100 (12900 30300)	77.2 (41.8 (28.7)	47 (29 MI)	0.5 (0.5 0.0)	Nacco (19700- 87400)	419 (26.7 64.8)	104 (87-17%)	0.1 (0.0-0.1)	100 (2100 1100)	7.0(3.7-11.7)	94790 (34800- 132000)	3.8 (3.3-9.3)	200000 (1140000 124.7 313000)	(71.0-201.1) 15400 (7400-	0.9 (0.8 1.7)	312000 (140000) 20.2 (9.8 (0.3)
Antestature Pleasupinsi	2040 (400 1990)	49.1 (242.9 429.5)	941000-(990000-	27327.7 (223%.3- M042.9)	1330 (668-2280)	32.8 (26.5-90.5)	10000 (9900) 202000	2893.7 (2397.8- 8622.2)	1790 (1139-2820)	18(1884)	183000-(100000- 223000)	311.6 (394.2- 743.8)	218 (114-382)	07 (0.4-1.7)	2000 (1000 2000)	46.5 (56.5 112.8)	700 (329-3080)	0.8 (0.3-0.8)	61200 (78200- 92900)	86.1 (29.1-79.4)	99 (26-199)	0.1 (0.0-0.1)	7720 (8990 13300)	N. P. (N. O. 40. E)	100300-(99000- 142300)	62 (5.64.8)	230000 (120000 313000) 131.2	(76/9-214.6) 12400-(4000-	0.8 (0.4 1.8)	275000 (129000) 475000) 14.6 (7.9-26.8)
Animalista Possile green hosesanni ophilogoni		634.2 (206.8- 634.0)					4940 (1990-9320)				194000 (102000- 227000)			60 (0.0-61)					42900 (29900 92900)				288 (100-998)				2230000 (1200000 3600000) 136.2			
Arisatelector Third general humannii orphilosporii		211.7 (200.9 600.2) 600.2 (270.4 600.7)					7070 (2720 14400) 770000 (180000)				23000) 23000)			60 (0.0-6.1)					4000 (7920)				NAN (209-2000) 1							1000 (120) 0.9 (0.5 1.9) 1000) 0.9 (0.5 1.9) 11000 (11000 45.2 (26.5 76.9) 120000)
Assessed or more and Citaduster upp. Assimply on		883.15 37.1 (28.3 48.7)					72000 (14000 2000) 720 (0-2000)							20(1231)					98300) 7620 (7740 13400)				3080 (1260 3280)		107000 (42700- 149000) 3700 (2280-9940)					120000) 252 (25.3 (5.6) 4390 (6 1000) 0.3 (6.0 (6.7)
Anti-possion Climbuster upp. Landanae		3 at a (22.4-70.8)												61 (9.0-62)									979 (780-2003)							10000 (2000 OA (0.3-1.2)
Addition Climbuster upp. Carbaponess	973 (323-0439	36.6 (20.7 46.7)	MINOD (24800)	NS1.2 (1822.8-	198 (No. 200)	78 (14-012)	17600 (7670- 34200)	696.5 (106.1- 1394.7)	219 (109-389)		2000 (4690)	48.5 (31.9 131.9)	44 (17.90)	61 (0.1-63)	2000 (1740-7940)	12.9 (5.1-26.5)			7070 (7240 12400)			anjananj	1420 (100-2070)	1.1 (0.0.2.2)	8479 (2990 T218)		11 NGGO (MENGO) 7.0 (A			2500 (1100- 4200 14 (67 24)
Citebatir up. Plempini		9.4(38.111.4) 9.462(39.2.008.4)					1990 (X10) 1990 700 (2X20 1X20)	789.8 (921.8- 1899.%			72800 (36900- 96000) 72800 (27800- 56900)		89 (20-102)	62 (0.1-6.7)	4420 (1790 8990) 1670 (1999 3410)	14.7 (9.8 (0.0)			13300 (6200) 23200) 12200 (8730) 22300)				2022 (497-2720)		6490 (1800-1018) 6490 (2000-11188)		174000 (W790- 263000 (B7000-			2300 (980 14 (66 2.7) 4000 14 (66 2.7)
Citabater up. Frank green caphilingues Citabater up. reshibitates		9 86.2 (19.2 (198.4) 8) 79.1 (198.4 (122.8)			N1(20-110)		4960 (2780-9790)		339 (238-442) 430 (288-730)			121.1 (44.4-213.3)			100 (99 22%)			01(8102)		114 (84-193)			400 (200-1320) 417 (140-891)		7649 (4490-12100)			1.1 (14.0) 201 (16.00) 1.1 (14.0) 201 (16.01)		410 (020 1880) 0.4 (0.2 0.8)
Citeductor upp. Erektower to or more and		0 911(0221961)	201000 (117000) 204000)	8297.4 (2641.3- 14093.1)	719 (569 1230)	28.7 (18.0-48.0)				17(0933)	04700 (27200- XURO)	1943 (77.3-279.1)	199 (78-293)	63 (63 L0)	12100-jamin- 29900)	at 7 (23.1 MLI)		02 (01 03)				0.0(0.0-0.1)	1979 (3620-1940N)	42(2078)	9830 (3730-1998)		20000 (127000- 21000) 23.4 (7960 (2200 13200) 47 (24 K.I)
Established up. Antegly on	4120 (2000 en	01 279.2)	201000 (201000 60000)	1996K7 (1009K7 2496K9)	274 (71-840)	109 (28-21.5)	2000 (470) 2000)	970.0 (290.7- 1908.7)	429 (200-429)	1.4(1.0.2.1)	37400 (21200- 54600)	129.4 (96.2 (92.8)	28 (7-48)	61 (9.0-62)	2270 (643-4260)	7.6 (2.1-16.2)	301 (132-299)	02 (01 02)	17900 (11400 29800)	13.1 (8.7-19.3)	12 (9-20)	aninnan	1040 (815-2010)	0.8(0.2.1.8)	14190 (8979- 22790)	0.9(0.0.1.0)	367000 (218000) 22.4 (990000)	13.3.36.4) 967 (242-172	m) 0.1 (0.0 0.1)	2300 (62%) 4500) 1.4 (6.4-2.8)
Antiquesian presidente Entendante app. Lacisman intérior.	7390 (4779-11	00 2014 (1891) 00 407 N	494000 (224000) 20000000)	29/28/2 (36/07.4- 29/28/2)	830 (362-897)	204 (11.2.51.0)	44700 (27000 74700)	1877.2 (996.6- 3624.3)	719 (272-0000)	24(1833)	6360 (4790) 9760)	212.4 (188.0 306.9)	11 (29-87)	62 (0.1 6.3)	4870 (2870 7700)	19.1 (9.9-24.4)	327 (211-294)	0.1 (0.2 (0.2)	3000 (1990) 62700)	227 (01.1-12.4)	24 (14-79)	0.010.0-0.03	2080 (1179-1170)	14(0923)	22790 (13800- 34300)	14 (8821)	501000 (324000) 23.9 (21.1.94.9) 1679 (879-27	78) 0.1 (0.1-0.2)	21000 (22200 72700) 2.4 (1.6-6.6)
Entenhalor upp. Carbapowee		273.9 (279.3- 27.9)					180000 (82900- 229000)				59300 (39400- 82000)			63 (0.3 63)	14200-(KIDD- 20900)	47.4 (27.8 73.2)						0.1 (0.0-0.1)	6670 (7920-10300)	1.0(1.07.8)	21200 (12900- 32000)	11(8820)	M1000 (123000 31-4 (19.7.51.7) 8200 (2790.8	(80) 0.1 (0.2-0.1)	139000 (71200 X.2 (4.6-13.4)
Enterchaster upp. Pleasupinel							NSURO (24/200- 87700)				47900 (31900- 70400)			62 (0.1 6.3)					27900 (14800 32900)				2180 (1179-3630)							27000 (27000 29 (13-3-1) 87000)
Enterhalier upp replaitsperi		00 NO.7 (287.7)					29700 (12000 33000)				11700 (19700- 117000)			61 (68-62)					37900 (29900 39000)				1229 (994-2229)							2000 (1200 17 (68.54) 2000)
Enterhalis up Sullimeles		01 100.3 (76.0-206.3 007.2 (767.8- 765.6					11000 (0.27900) 717000 (200000 479000)				2000 (3000 4200) 10400 (7000			11 (0.7 1.4)					2000) 2000) 2700 (3200				371 (0-1190) 17700 (0090-							20700 (14-21700) 0.7 (0.0.1.8) 207000 (140000) 17.8 (10.2.27.1)
Antonios Phonopini		793.6 206.9 (127.4 323.6								12(071%)				63 (63 63)					1900 (1700 1900 (1700				2720 (2130 K130)							29000 (119000 143 (70-20.1)
Entercore Vancouprie	200 (344-913)	23.5 (13.6-37.8)	32300 (30600 82800	2072.6 (1213.3- 2061.8)	139 (10-290)	88 (2.1-11.8)	12000 (4750) 256000	291.9 (187.h- 1621.%)	42 (29-68)		3730 (2170-4070)	12.4 (7.9.20.1)	19 (4-21)	12-0.00	383 (113-2840)	29 (12-62)			2290 (1240 3890)				N24 (206-1109)		£190 (2£80-£790)	03(0.10.0)	123000 (70700) 7.4 (E	3-11.8) 991 (983-202	R) 0.1 (0.0 0.1)	2890 (1180: 18 (67:33) F200:
Entercore Enteror in some self Entercore Planspirel		01 28.1 (128.0 53.2) 01 92.9 (86.8 186.7)	THE R. P. LEWIS CO., LANSING, MICH.	9776 T (2006 A	1410 (728 2420) 494 (128 873)		129000 (42700- 219000) 40900 (11400-	2010.3 (2566.1 8021.4) 1999.8 (485.7)						63 (0.2 64) 62 (0.1 64)					19700 (12000- 32000) 19200 (7930- 27900)				3230 (2630-8700) : 2940 (782-6670) :		34000 (20000- 53400) 33300 (29400- 83200)	200232		16.249.3) 4080(2690.1 11.849.3) 4270(1790.1		367900 (196000) 16.2 (K.9-27.4) 479000 (479000) 19.4 (2.9-21.7)
Facilities Endowners Facilities Facilities Endowners Endowners Endowners		22.4(13.1-36.8)		2923 (1968) 327231	131 (99-240)	82 (24-97)	11400 (1290- 21700)	1999 X (2013 7- 3076 4) 466 4 (2019 8- 366 7-	74 (42-124)	02(010.4)	4990 (3600-11100)	22.0(120.072)	17 (5.00)	61 (0.0-6.1)	1550 (645-3070)	8.1 (2.2-98.2)	44 (21-89)	08 (60-01)	7000 (1810 7110)	29(149.0)	19 (0-22)	40/0848	889 (334-2988)	0.7(0.3-1.4)	15100 (Note:	04 (83 1.1)		10.29.5) 2980 (1000-4		6200 (2600) 12200) 12200)
Entercore Entition in faction or more still Other entercores Plantage in the	2330 (1423.57 Seen. 3280 (2983.57	0) 93.5(97.1-146.7) 0) 178.0(77.6-284.4		8294.3 (9874.8: 13947.4) 12368.3 (9874.8:	505 (26a 2025) 475 (95 1410)	25.2 (31.548.4) 26.8 (3.856.8)	52000 (25400 10000) 60000 (8290- 176000	2001.2 (1007.4 3611.2) 2758.3 (136.6 2758.0		11(0.01.0)		96.8 (867-1807) 96.4 (852-1624)		62 (0.0 64)	4000 (2000 1200) MOD (555 11700)			01 (61 02)		11.6 (8.9-20.9) 10.2 (8.9-17.0)		0.0(0.0-0.1)	7828 (8429-7939) : 2888 (429-8230) :		3380 (3790 3380) 1820 (1160 2670)	28 (8.2-3.3) 1.1 (8.7-1.4)	1290000) 21.4 (20000 (249000 23.4 ((2.1-90.7) MOD (228) 1 (4.1-37.6) MOD (338-7)	3200) 0.3 (0.3 0.8) 30) 0.2 (0.0 0.4)	29000 (11000 19000) 113 (70-20.8) 70000 (1200 18000) 44 (0.8-9.4)
Other reterescont Vancouspoin	209 (112 334)	81 (63-153)	3130 (YW) 29900	TEAK (TINGO: ITEM 71	37 (16-78)	13 (84-31)	3270 (1490-6930)	129.8 (97.6-274.4)	29 (20.33)	0.1 (0.0 0.1)	1490 (900-2000)	14(1013)	3 (3-7)	60 (0.0-60)	306 (132-628)	1.0 (0.0 2.1)	1 (3-20)	03 (60.03)	781 (478-1770)	04(831.0)	2 (1-7)	40,004.03	141 (49 295)	0.1 (0.0 0.2)	1060 (MR-0600)	01 (8.0 01)	27900 (17000) 368001 1.5 (0	9-2.2) 89 (92-372)	48 (94 48)	499 (200 830) 0.1 (0.1 0.3)
Other entermonent or more and		0 1981(77.8-298.7 301.7(298.0-												62 (0.1 6.9)					13900 (7790- 22900) 139000 (80000-				2730 (629-3580) : 6420 (8279-9520) :							1200 (1900 14200) 11 (12-9.8) 7300 (2700 142000) 44 (2-9.44)
Enterthined Assimption		001 301.7 (239.0- 002.1) 1003.5 (709.0- 1000.7)							2820 (1740-7670) 8000 (8280-11700)			2277.9 (3424-4- 3468.0)		63 (9.3-67)	2000 (1420-2700)		2779 (1140-4090)	18 (87 Li) 33 (24 44)	10000-(00000 140000) 700000-(276000- 140000				1230 (764 1880)		(3000 (34700- 70400) 129000 (200000- 201000)		2790000 (2710000 229.4 N190000) 211.0			1200(2700 1200(700 1200(700 03(0312)
Andreadia and Bris Larian							22900 (11900 22900)				104000) 91500(40400 81600)			619264					12000 (221000- 12000)				200 (200-2720)							24 (13.14)
Enderthis cell Carbon							22000 (122000 127000							24 (1.4.5%)									31790-(17600- 31800)				20000) 291.4 187000 (170000 20000) 111.8			
Endorship cell - Photosphed	22300 (24900) 22300)	962.8 (MR.A- 1960.2)					32'000) 2'0000 (134000 32'000)							28 (2.7-87)									31000) 36000 (28000- 31900)		13300 (4500- 13300 (4500-		3190000 (240000 26.0 410000) 20.0			312000 (242000) 21.4 (14.9 30.4) 50000)
Endertable cell Third greens explainment	alon 2000 (1600) in 3000)	907.1 (MIT.2) 1909.1)	2180000 (180000 3080000)	36/78 I (996/2.6- 122386.8)	2120 (1090-4200)	91.9 (41.7-146.9)	207000 (94400 274000)	X204.3 (7718.3) 14872.8)						23 (1.0-4.3)			3920 (2790-3560)	18 (2.1-6.2)	32000 (22000) 20000)	268.4 (DRS.8- 369.7)	386(477-710)	0.3 (0.1 0.3)	32300-(19700- 62900)			K1 (8.7-11.0)	114000-276000 20.1 260000 20.1	(148.9- 11400-(9190- 22000)	0.7 (0.3 1.3)	29000 (19000 17.7 (K2-N-N) 52000)
Endertebis sell Trimologia Sellameles		965.8 (\$197.3) 968.5]					79900 (19300) 107000)							68 (9.3-1.2)					279000 (170000- 370000)				11200 (7190- 16200)		1 PRAIS		22,2000 (140000) 314000)			10000 (4700 4.7 (4.1 9.5)
Enteroble of a more and Group A Marchin		1134.7 (804.0- 1634.7) 14.0 (8.3.22.9)						1982.1 (29/129- 1979.3) 198.9 (8.0.798.7)						0 88 (8.8-01.2) 60 (8.8-61)									12000 (8200 18200) 799 (9-1240)				212000 (210000 224.1 513000) 234.8 4120 (31700			130000 (84000) 76.6 (92.8 109.4) 6070 (9.29900) 0.4 (8.0 1.3)
Comp A Brokinson in Stephenson or man and		14.0 (8.3 22.9)																					719 (0 1245)							600 (0.2000) 0.1 (0.0 1.5)
Group II Pleasupinel		803.7 (240.5- 807.0)	40000 (10000 133000)	3609 1 (2180°.2 31331.0)	1730 (263-1970)	68.1 (11.2-197.4)	191000 (29700- 394000)	6007.8 (2009.9- 14021.7)															6960 (1260 13600)							2000 (89%) 3.0 (0.3-6.3) (0700)
Group II Macrolide Group II Proxidin		691.3 (201.6 877.3)		NAMES (NOTE 7: TRIBLE)	1200 (D.3000) 67 (12-127)		129000 (9.729000)				142000 (98800- 198000) 2920 (1690-3610)			63 (0.0-1.3)	12900 (0.33900) 683 (126-1370)				72900 (92900- 99900) 1300 (891 1830)				66(0 (0 17300)							7500 (0.9000) 2.1 (0.040) 1001 (011 7700) 0.1 (0.042)
Zionicercus Penkilin Cirup II Erskinser in Ziopicercus ur mass anil		25.5 (6.7 13.4) 777.8 (523.8)		1796.00 69796.1 (20006.3- 98325.2)			3990 (1210-13300) 260000 (62700- 360000)							11 (0.2.20)									721 (47-470) 17600 (2890 2620)							1000 (211.0790) 0.1 (0.0.0.2) 10000 (22100- 100000) 3.4 (1.3-10.3)
Manuphiles Assimpaniel influence Namphiles Third general	dia 413 (229-425) dia 929 (314-726)	16.6 (9.9 29.4)	37300 (23200 37900 24200 (23200	1277.7 (890.0- 2294.8) 1826.7 (1120.3- 2664.8)	87 (4-122)	22 (92-43) 60 (23-009)	3000 (230 11000) 13600 (3210- 22700)	2014 (07.0439.2)	268 (266-417) 328 (225-487)	0.9 (0.0 1.4)	23400 (14790- 34900) 26000 (20000-	78.2 (29.2 123.3) 96.0 (87.0 134.9)	36 (3-79)	61 (0.0-63)	3220 (249 7938) 8490 (3390 14900)	10.7 (0.8 (2.0)		01 (01 02)	12700 (8290 18000 14200 (10900	9.6 (8.6 04.0) 30.9 (7.9 14.9)	39 (2-01) 89 (21-86)	0.0(0.0-0.1)	1790 (144-3748) 4230 (1790-7480)		471 (112-490) 481 (280-921)		1500 (930) 6.8 (9 1930) (1230) 1.2 (9 2030) 1.2 (9	4-1.2) 44 (3-134)	0.0 (0.0 0.0)	1820 (230-3830) 0.1 (0.0-0.2)
Acomphiles Entitioner in influence or more and	-	32.1 (20.4-26.9)	67200 77200 (44600 307000)	2900.4 (1806.6- 2256.3)	207 (96-362)		22700 18700 (8290- 32600)				49700 (12700- 64900)				11700 (1100 2000)		272 (280-347)		2500 (17400 31700)				9180 (2033-9130)		1620 (733-1390)				0.00000	160 (179 HWG 0.5 (0.2 0.7)
Eleberia promoniar Aminglyon	27100 (28900 38700)	1996.7 (708.2- 1838.7)					100000 (114000- 200000)	7273.1 (4909.1- 11297.9)	6930 (NI30-9230)	23.1 (17.1-90.9)	617000 (414000 816000)	2006.2 (1914.7- 2792.2)	X10 (X28 763)	18 (1.1-2.8)	2000 (2000 6700)	196.7 (96.9-229.1)	3480 (2430-4500)	24 (20 54)	38000 (23000) 342000)	227.7 (171.1- 296.8)	269 (170-379)	0.2(0.1-0.5)	22800 (14700) 32400)	17.5 (11.1-28.4)	89100 (N/700- 124000)	3.2 (3.8-7.4)	21,20000 (14,20000 31,00000) 129,1	(864-189.7) 6770 (7620-1	000) 0.4 (0.2-0.4)	147000 (97100 287000) 18.0 (8.9 18.7)
Alleborie Bris Laviene provenier lecterary in	Meta 2500 (2500 Meta 2500)	1000 A (909.3- 2927.9)	3130000 (213000 4340000)	129092.9 (84963.1 171996.2)	2 398 (200-409)	18.7 (8.1-28.3)	35000 (1600) 54000)	1997.0 (724.3) 2294.3)	1000 (0990 L1000)	29.4 (22.0-39.4)	794000 (1900000- 1040000)	2606.0 (2926.7: 3283.7)	99 (83-067)	63 (92 64)	2000 (2400 1.2000)	29.4 (19.4-29.3)	4282 (3770-3790)	14 (2+44)	786000 (216300- 500000)				4K20 (2740 TURS)	3.7(2.1-8.7)	108000 (72000- 133000)	6.6 (2.4.9.3)	200000 (200000 St.3 300000) 254.8	92 (80.00	0) 0.1 (0.0 0.1)	2800 (1700 2800) 14 (67-24)
Alleholis Carlegowen promonius	27900 (DANO 2000)							23628.8 (14704.5- 33607.8)		29.1 (17.9-30.4)				14 (8.7.7.8)				28 (18.53)	284000 (240000- 378000)				62700 (27700- 91300)	28.0 (33.1 48.4)	94000 (48000- 141000)	3.7 (3.8.8.4)	2120000 (1700000 3270000) 141.3	(94.5 210.2) 22400 (1900)	14 (08 2.1)	52000 (19000 313 (20.7 62.4) 86200)
Klahada Planopind promotor	South (2000) 42100)	1206.3 (827.3- 1670.1)					260000 (167000- 260000)							17 (1.0-24)					33000-(25000- 45000)				22,000 (1,7700) 373,000)							187000 (10000 9.5 (8.5-18.2) 289000)
Educido Tidal passa promentar esphilospori Elebado Trimebano	ation 31000-(22700- in 24000)	1004 (004 1074)					120000 (20000) 200000 100000 (20000) 170000							11 (0.4-2.7) 69 (0.4-2.7)	2000 (1960 6000) 2000 (1900			31 (23-41)	314000 (24000) 240000) 242000 (222000)			0.1 (0.0-0.1)	11200-(1110- 20000) 12200-(1110- 11100)				203000 (170000 100.6 303000) 211.4 203000 (170000			99000(31200- 190000) 8.7 (1.9-11.9) 89000-(20000-
Eristic Entires in	17100) is one 2000 (2000)	1980.2 (1989.A-					170000 (817000- 1400000 (817000-							0.012(8203.4)					27500) 20000(734000 52000)				142000 (194000				20000) 20000 BL4 67000 2000			20000 (2000) 5.2 (2.3-9.2) 200000 (75900) 65.3 (21.8-97.1)
Marganella ago Pleanapinel	1 (2-12)	02(0103)	ATT (340 1130)	H0(6444.0)	1 (9-2)	60 (8.0-6.1)	71 (20-182)	2.8(0.87.2)	11 (9-29)	0.0(0.00.1)	929 (263 1720)	3.2 (5.8-8.7)	2 (1-4)	60 (0.0-60)	190 (92 (03)	0.5 (0.2 1.1)	E (4-09)	03 (00.03)	733 (379-1270)	04(0.31.0)	1 (1-2)	0.010.00.03	114 (44 291)		1930 (942-2240)	01 (0.1 0.1)	31200 (23600 30000 2.1 (1	3-3.0) 249 (102-449	0.00000	1800 (2290-1948) 0.3 (0.1 0.4)
Mergandia upp — Possib press explainment Mercandia usa — Third press	to 2 (14)	61 (69 62) 61 (69 62)	221 (77-80%)	88 (80-28.8) 98 (81-28.9)	0 (0.1)	103-03 03	29 (8-90)	12(023.0)			275 (229 829)				60 (15 146) 21 (9.72)			03 (80 03)	764 (289-672) 767 (287-674)				28 (12-119) 21 (8-81)		672 (206 1090) 798 (282 1090)		22400) 6.9 (9 20400) 6.9 (9	e-14) W(25-189)		190 (SEATER) 0.1 (SOO.2)
Marquada up Entitus in se marquada	in one Destan	42(6143)	are (343 1120)	18.2 (6.5 48.5)			119 (28-289)	4.0(1.011.0)			962 (468 1730)				289 (110-497)				741 (186-1280)			anjananj	284 (89-240)				21000			NAME (TAND TANK) 0.3 (0.3 0.9)
Mysobototam Enterder de fabrositato estátano la Mysobototam Inspiral mo	- ·		0 (0.0)	03 (50-03)			0 (0.0)	40/004/9		0.1(0.00.3) 1.7(1.0.2.3)		11.0 (8.1-28.2) 148.6 (92.0-238.7)		61 (0.0-62)	200 (N2 449)			03 (60-03)	2920 (799-8940) 37800 (2890)			0.0(0.00.0)	1290 (428-3300)		3290 (770-7600) 47900 (80000- 61400)			7 (6.7) 2020 (279 48 (70.6 144.6) 7220 (0-2000		66700 (19900: 4.1 (1.0-9.7)
Automotivate revisioner Medicaleng revisioner	ľ		1(1-3)	63 (60-61)			0,000	40,024.0								21.4 (0.0 49.1)		03 (02-03)	17000 (24000- 10000)				M10 (0-14200)				25.0000)			22500-(0.83500) 18.0-(0.0-80.0)
Mymboletian mobiling or informities drug resisten TR	alemaker .		1 (0-2)	03 (60 01)			0 (0.0)	40,004.0	722 (210-1MH)	24(0782)	179000)	213.6 (42.3-242.4)	424 (42-1130)	14 (0.1-33)	37500 (3720-	128.0 (12.8-394.4)	994 (176-1199)	0.1 (0.1-0.9)	109000)	38.1 (12.0 82.4)	324 (33-995)	0.2 (0.0-0.7)	27800 (2990 26800)		6380 (2000 19100)	19 (1942)	224000 (12300 523000) 177.8	(25.0 (25.0) (25.00)	23 (92-63)	1220000 (1110000 TH.4 (T-0-209 I) 3430000)
Mysolutoise Elimpia e niteno li Mysolutoise Entimo i			2(0.0)	01 (50 03)			000	10,0010	80 (24 42) 1338 (728 2220)	62(8163)	4400 (2190 8200) 114000 (44700-	14.7 (7.2-27.4) 387.9 (214.1-	14 (2-99) NO (100-1200)	18 (0.447)	2710 (197 2900) 1270 (1970 2900)	41 (07:93)	47 (29.87) 1029 (393-0460)	02 (00 01)	9200 (9200 9200 (9200	3.3 (3.4448) 71.8 (81.0 (1057)	17 (2-70) 427 (83-0020)	0.000000	1140 (200-2790) 34000 (7300	0.9 (0.2-2.1) 27.3 (3.6-63.8)	2280 (1430.3970) 119000 (42800-	01 (8.1 02) 10 (8.8 12 fb	21000 (31000 3.1 (3 210000 (212000 211.5	4 8.4) 679 (800 139 (141.4) 47300 (8000	29(03.7.1)	2500 (2500 14 (0.5.5.0) 175000 (35000 95.5 (35.5.25.5)
Animaria processiali Animaria Photophol	den -							-		-							-		-		-	-		-			1790 (1800 2000 11 (1	6-17) —		130 (427-3280) 0.1 (0.0-0.2)
Notauria Phenoquini noncritorar Thirligment Notauria Estátuno i genericar or none anii	terms																i.							-			17700 (10000 1.1 (0 20700)	esq - est) -		29 (11 139) 0.0 (0.0 0.0) 1790 (002 3340) 0.1 (0.0 0.2)
Protest typ. Antingly-re	798 (233-427)	18.8 (9.3-28.7)	29400 (20900 27400 2200-111-1	1016.7 (KSK.0- 2262.7) 2006.0-1	17 (2-99)	0.7 (0.1-1.9)	1520 (176 5400)	46.2 (7.1-139.0)	80 (80 123)	03(0204)	7130 (1440-1098)	25.8(14.8-36.4)	3 (9.7)	60 (0.0-60)					2800 (2770-4920)				294 (22-415)		8180 (9280 12880) 1780 (1180	03 (0.3-07)	20000 (12000- 20000 (12000- 20000)	7.6-17.9) 327 (33-780)		X262 (890-17785) 0.3 (6.1-1.1) 6993 (6-21200) 0.4 (6.0-1.3)
Protess up. Assimpated	= \$79 (392-132) dam 479 (397-112)	18.8 (9.3.28.7) 52.5 (19.2.850) 28.9 (18.8.44.2)	179080 60100 (31000 91000	2791-01 2792-9 (1404.5- 2902-7)	17 (0-01) 28 (29-88)	10 (29:39) 03 (20:14)	1190 (0-3620) 4190 (1720-8480)	27.1 (9.0-144.7) 171.4 (98.2-736.8)	141 (89-217)	03(0303)	22900 12900 (1980 14900)	41.8 (26.2-61.7)	3 (9-8) 18 (4-20)	12-0.00	909 (341 (369)	30 (11-60)	88 (89 130)	01 (00 01)	9320 (9820-1100) 7730 (1890-1190)	89(8393)	6 (5-12)	0.010.00.03	180 (0-409) NAR (214-1080)	04(0203)	17900 (11300- 26000) 18200 (1890- 22200)	0.9 (0.0-1.0)	36000 (227000- 21.9 (13.8.32.4) 1120(407.2)	M) 0.1 (0.0-0.1)	26200 (10700) LA (0.7-3.0)
France up. Third power confidence France up. Trimeloguia	287 (169-479)	11.4 (6.9 183) 28.8 (12.1 560)	29400 (12790) 42290)	1003.8 (980.2- 1674.1)	33 (14-114)	21 (9.6-43)	4700 (1270 1000) 1400 (0.3200)	186.4 (90.3-401.9)	97 (35-89)	02(0103)	900 (900 700) 930 (970 1440)	16.9 (10.3-26.7)	10 (3-22)		993 (244-2948) 263 (2-412)				3390 (3990-2903) 3920 (3600-9023)				787 (148 1290) 178 (2-780)		8779 (1620-8870) 11288 (7179- 16600)	01(0.103)	20000 (82000 K4 (7 20000 (70000 M3)			2000 (7100 1.0 (0.5.1.0) 2000 (0.07200) 0.5 (0.0.1.0)
Protess up. Sullandon Protess up. Britisher in or more said		20.8 (12.1-32.0) 27.2 (21.9-40.4)									17200 (3970-12400) 17200 (39800- 24300)				2670 (1790-2790)			01(8101)		ER(ER-123)		2010020	100 (821-200)		20400 (23300- 20000)					1000 (61 (1200) 6.5 (66 (.1)) 1000 (4120) 4.5 (2.5 7.5)
Faradonnes Assimply or arregions		200 and 200 a					25000 (141-0800)				147000 (109000) 142000)				7720 (0-8670)				4900 (11100 8000)			anjananj	2560 (6-2770)		3288 (21480 47980)					12000) 1990(NC1000) 12(0033)
Faradonomo posidiniliri arregione Lacionae		m 26.1 (281-1 26.7)	MIDSHE-(NLIMO- 1120MR)	71820-4 (21479.4- 41740-0)	267 (119-612)	10.4 (8.3:17.8)	25000 (12000 39600)	128.4 (278.8- 1870.4)			183000-(113000- 204000)			62 (0.1 6.7)	490 (229) 730)	15.0 (7.0 (5.1)	762 (963-998)	04 (0.4 03)	6200 (2700 8600)	4K3 (7K44K4)	24 (13-79)	0.010.00.03	2080 (1190-1170)	14(0924)	23400 (21400- 51100)	21 (5.8.8.1)	803000 (102000 - 20.9 (11.279.4) 797 (82-177	10 0.0 (0.0 0.1)	3000 (KSB) 13 (B3-2.0)
Fredman Categoria		65.0 (236.9- 82.0)					219000 (140000- 360000)							18 (1.2-27)			1299 (942 1799-	10(0713)	111000-01100-	842 (H. 8 110**	217 (196.100	02/010.h	20900 (13700- 30000)	18.8 (18.4-22.7)						235000 (150000 15.5 (9.4-24.9)
Antiques Calapses Finalment Plempini							19000 (4700) 18000 (4700)																7000) 700 (1240 (1800)							99000) 153 (9.2-22.9) 94200 (52000 3.8 (53.9-3) 189000) 3.8 (53.9-3)
Paradirana Postis gran araginas replatogran		752.5 (761.2- 766.4)					47000 (25400 71400 (25400				234000 (187000 244000 (187000 318000)			61 (0.2 63)									2780 (2230-2630)							MARC (2000) 6120) 22 (12-17)
Faradomona Third general arraginase cophalospori		402.8 (425.7) 863.0)	3440000) 2730000 (AP2000	MR31.2 (R148.1 388912)	431 (263-1090)	280 (31.848.4)	NATIO (25400 97500)	2212.0 (1008.4: 3879.4)	3040 (2240-409E)	19.2 (7.8-13.4)	273000 (279000) 364000)	900.0 (MIT.O 1203.9)	119 (97-200)	64 (9.2 67)	EONE (NEED- DAME)	30.1 (34.741.9)							NAME (2079-00103)				1240000 (813000 TES)	PA 1150) 100 (415 27	THY 0.1 (0.0 0.2)	M790 (1960) 22 (69-4-2)
Paradirense Bristone in ampiene mass and	to one 23900 (11200 destan 2000)		2990000 (110000 2990000)	75290-8 (95298-6- 802713-8)	5550 (1988-8445)		249000 (112000- 196000)							3.8 (2.4-8.2)									41 800 (27900- 60600)		7380 (2K200- 107900)					848000 (272000) 26.1 (36.6-43.2) 522000)
Johnson Photospini Paraypia Photospini Malicing	-		0 (0-0)	03 (60 03)			0 (0.0)	0.010.00.03			RHK (299-2420)				179 (23-968)								38300 (\$200- 209000)		17400 (7540- 33800)					29000 (1600) 163 (22-963) 60000)
Admindia matematic Peretyphi Admindia T and Peretyph	Typhi in		0 (0-0)	03 (80 03)			0 (0.0)	0.010.00.03	0-(0-1)	0.0(0.00.0)	42 (11-117)	61 (606.0)	0 (9.0)	60 (0.0-60)	3 (0.12)	40 (00 40)	41 (29.224)	01 (00 02)	7860 (2270-29800)	6.0 (1.9.16.8)	7 (9.23)	0.010.0-0.01	627 (9-1860)	0.5 (0.0 1.4)	6% (260-1300)	02 (0.0-01)	4000 (1000 2.7 (1	3.5.5) 25 (9.153)	0.0 (0.0 0.0)	360 (0.1800) 0.2 (0.0 0.4)
Zolmondo Brakismo in Paratyphi or more and				03 (0.0 03)				4.0(0.04.0)			907 (240 248)				DK2 (24-971)								28800 (NASO							222000 (70000 600000) 16.7 (2.6-27.1)
Schemic Typic Plempini Making		00 208.1 (127.8- 007.0)	1040000) 1040000)	29838-6 (22248-9- 21998-2)	1200 (211 2010)	31.0 (9.2-114.3)	112000 (20000- 242000)	4994.1 (914.2- 16931.7)	909 (20s. 1439)	27(1.047)	71200 (19900- 129000)	237.7 (119.9: 417.8)	133 (31-360)	68 (6.1-1.2)	13500 (2750- 21600)	(8.1 (9.3 (06.2)	4129 (1740-17700)	69 (28 134)	78000 (723000- 1330000)	997.8 (348.0- 1362.9)	1740 (279-4939)	1.1(0.2.1.1)	182000 (23600 371000)	114.9 (17.9-281.4)	5000 (27700 81000)	31 (5.69.4)	323000 (1430000 4610000) 208.7	(99.2.372.7) 9890 (1879.2	(2000) (0.4-(0.1-1.4)	69900 (20000 48.2 (6.5 91.2) 180000)
Multi-drog Subsecutio Typis Subsecutio T and Paratypi	Typisi Digital	0) 18.2 (28.0 (76.8)	230000 (110000 200000)	8713.9 (2394.9- 19730.8)	278 (0.483)	9.3 (9.0-27.1)	20100 (0.40700)	K2K 9 (0.0 2406.4)	294 (140-945)	1.0(0.0-1.0)	26000 (12400- 08300)	86.8 (41.5 (60.4)	28 (9:7%)	61 (6.0-6.7)	2600 (0.7040)	8.1 (0.0-21.4)	2879 (1290 MINS)	22 (69-4.8)	24000 (10000) 20000)	187.9 (TTA-171.8)	277 (0-798)	0.2(0.0-0.4)	23900 (0-68700)	18.1 (0.0-82.1)	21900 (7940- 26900)	0.9 (0.9-0.4)	1040000 (F11000) ell-4 (91.1-110.2) 1920-(0-4980	0.1 (0.0 0.3)	102000 (0.20000) 6.2 (0.0 17.6)
Administra Typis - Brakismar in or more and	14 Mars - 742 (1000) 12	00 NH I)					139000 (34200- 269000)		906 (249-1990)	3.0 (3.0-3.3)	80200 (41100- 141000)	267.6 (197.3- 269.1)	180 (48.78%)			M.2 (14.1-1143)						1.5(0.4.5.0)	179000 42400 419000	133.0 (32.3-314.0)						762000 (189000) 26.2 (11.3 (01.6)
Non-typhoidd Pleasupánd Zalmandia Pleasupánd Non-typhoidd Braininne in	2090 (2003-00 in new 2007-00	0) 1004(7573057 0) 1004(7573057	30000 (17900) 60000 (17900)	14280-8 (7083.9- 28981 W 14280-8 (7083.9-	XN (114 1935)	33.2 (8.3-36.7)	72000 (11900) 172000 72000 (11900)	2988.5 (272.9- 6806.0 2988.5 (272.9-	1389 (N.I2790)	43(1398)	122000 (90200-	407.4 (168.4)	279 (40-687)	69(0.123)	22800 (3480- 40400) 22800 (3480-	80.7 (12.5 200.2)	796 (272 0683)	04(0213)	48000 (23400- 142000- 48000 (23400-	91.7 (07.7-123.1) 91.7 (07.7-123.1)	111 (20-416)	0.1(0.00.5)	1100 (2000 2000) 1100 (2000 2000)	10.2 (1.0.30.2)	14790 (MENO- 29600) 14790 (MENO-	07(0.010)	274000 (197000- 993000- 274000 (197000-	12.0-00.9) 2090 (414-77	NO 02 (00 0.5)	9000(13800 229000 9000(13800 22900) 3.5 (0.9.13.7)
Non-typholid Erationer in Automobile or more and Armetic app. Anticophysic	design 2000/2009-00	0 100.0(70.7-200.7 0 10.1(29.8-86.8)	117000 (MADE) 217000 (MADE)	29981.9) 8629.8 (2620.1- 1092.5)	8% (150 19%) 78 (0-21%)	312 (8.0-87)	172000) 6830 (0-29800)	6004) 230 (60713)	1-80 (NE 2700) 97 (82-148)	0.7(0.204)	24 800) 8420 (2400 1440)	817.6) 28.8(13.0-48.8)	279 (20-007) 6 (9-00)	60(0.061)	60400) 312 (0 1400)	41.7 (12.5 2012) 1.7 (0.0 5.4)			162000) 2000 (2170-6000)				201(0.700)							22000) 3.3 (6.9-11.7) 2000 (6.1200) 0.3 (6.0-0.9)
Anti-ponder penidis typ Lavinner		0.1(29.249.8)												60(0.061)					2840 (1440-9020)				429 (179-908)							1900 (4140 0.9 (0.4 1.7) 2000)
Armeis up. Carbonese		31.8 (18.4-91.4) 29.8 (16.8-48.7)									5230 (2890-8710)			61 (0.0-61)					2140 (1120,7780)				NO (245-1120)			02 (0.1 0.3)	MIND (2300) 49 (2	3.83) 89 (84-11)	m) 0.1 (0.0 0.1)	21900 (1979) 117 (1941 2.4)
Zerosia spp. Plantopini Zerosia spp. Pouris prae cephaloperi		28.8 (14.8-28.7) N.2 (30.0-83.4)	66200 (77700 209000 119000 (47200	3623.8 (1.077.0- 2330.01 2833.7 (2664.0-	76 (12-172)	10(1348)	4200 (1110-13300)	281 (131 AUL)						124402					2120 (3880-3710) 3270 (3810-4120)				214 (39.600) (262 (89.607) (#99 (229 1980) 0.1(0.1 0.9)
Zeronia upp urphalospori Zeronia upp urphalospori	ation 1200 (710-207	08.2 (28.1 82.3)	130000-(47100- 194000)	4712 (2800) 7014 (1	29 (7 (9)	1.1 (9.3-3.0)	2500 (429-6440)	100.7 (23.0 243.2)	95 (30-136)	0.3 (0.2 0.3)	X270 (1290 1780)	27.6 (15.0-06.0)	2 (9.8)		88 (22-1370) 88 (42-847)				780 (1810-8120)				91 (21-200)			02 (8.1 0.0)	19400 (9100 6.3 (3	e-10.7) 60 (1e-14c)	0.000.00	149 (817-800) 0.1 (60-0.2)
Zeronia upp Brokinsor in se more and	2790 (1690 at	0) 110.3 (48.6 177.2)							209 (313-332)	0.7 (0.0 1.0)	19300 (20000- 29300)	60.7 (33.6 98.6)	48 (29-89)		4280 (2180 7570) 4000 (4710)				7670 (£360 £3200) £3000 (£3600				1920 (PN-3190) : 2620 (1790		8900 (9110 11200) 13100 (2010	01(0.10%)	20000 (13000 14.3 (36000) 14.3 (5000 (1100 24 (1944) 2000)
Shipile up. Pleasupind Shipile up. Brainne is		28.8 (7.3.68.8) 28.8 (7.3.68.8)									199000 (43900- 199000 (43900- 479000)			18 (0.2-42)	20000-(2700- 11 Years 20000-(2700- 112000)		1410 (272-3280) 1410 (272-3280)		18000-(11800- 18000-(11800-				26200 (3390) *1.6900 26200 (3390) 71400)		13400 (4000- 13400 (4000- 13400)	0 X (0.2.2.0)	27-1000 (118000- 22-4 (27-1000 (118000- 22-4 (90-1000) 22-4 (7.2 04.0) 2790 (279 TK 7.2 04.0) 2790 (279 TK	MI) 0.2 (0.0 0.3) MI) 0.2 (0.0 0.3)	70000 (20000) 4.3 (Ed-11.7) 70000 (20000) 4.3 (Ed-11.7) 70000()
Suphylanous Planopini		796.4 (599.8- 1165.6)												10 (0.4 14)									71400) 12400 (870- 21200)							20000 (2000 2000) 63 (29 113)
Suphylamous Manufale	17100-(12100- 21300)	676.6 (276.0 923.3)	283000 (227000 208000)	60977.4 (42897.4 82438.7)	530 (200 HON)	21.0 (8.0-36.7)	27200 (18000 82900)	1872.1 (714.9- 3270.9)	6720 (2730 KEID)	21.1 (15.8-28.1)	599000-(418000- 748000)	2881.0 (1796/9- 2686.6)	PN (79-324)	67 (9.3-1.2)	17100 (7520- 3060)	M.1 (21.4-102.1)	3230 (2430-4300)	24 (1931)	20000 (21400) 307000)	212.7 (162.5- 279.2)	99 (23 142)	0.1 (0.0-0.1)	BANG (NASS 14200)	6.6 (2.8 19.8)						6000 (2700 41 (17.7.4) 12000)
	L	403.0 (ESS 2- 802.2)	1110000 (112000	22729.4 (27420.9)			TT000 (17100)	1700 X (1701 A						44 (1.9-7.6)			i .						97400 (29200- 98200)				MANAGE CELEBOOR	N100 (340)		28.4 (12.2 MLI) 82208)

Staphylaroccus annua	Trimeloprim Sellimerkovansk	20MR (75MP 14MR)	622.4 (249.9- 822.9)	129000 (MJ000 129000)	77611.0 (36726.2- 72069.9)	XX (413-1345)	332 (36.5.53.0)	119000 (1990)	297 X (1041.9: 4712.0)	7900 (2000-0230)	13.0 (9.8-17.9)	34800 (29200) action)	1191.7 (NEZ-2- 19060)	308 (131-497)	10 (9.3-17)	27200-(13000- 47900)	90.9 (20.7:140.4)	2020 (1930-2960)	1.8 (1.2-20)	176000 (132000- 232000)	135.1 (100.3- 149.4)	199 (82-244)	0.1 (0.1-0.2)	11790-(7090- 21290)	10.4 (0.4 (0.1)	24793 (32990- 70793)	3.0 (2.1-4.7)	189000 (411000-	76.2 (55.8 113.7)	2000 (2022-4200)	0.2 (0.1-0.4)	100000 (10700 171000)	63 (3.1-19.4)
Stephylanome	Vancompoin	284 (173-362)	10.1 (6.8 14.4)	22400 (13400 32200	207.4-(409.3) 1279.91	74 (35-138)	29 (14 83)	4890 (3170-11900)	260 (123 h 473 7)	91 (66 129)	0.1(0.2-0.4)	X270 (MIRO 11700)	5 27.6 (200-37.8)	27 (13-27)	61 (9.0-62)	2990 (1180-4360)	80 (59 (59)	an (10 40)	03 (60.03)	3980 (2940-5320)	10(2240)	13 (7-20)	0.010.00.03	1190 (980-2000)	0.9 (0.4 1.9)	1330 (913-0970)	01 (0.1 0.1)	30800 (23400 10400)	2.1 (1.4-5.1)	290 (383-730)	0.0 (0.0 0.0)	20030 (2K%) 24500	04 (03-12)
Stephylanome	Erokianor in one or more antibiotics	22000 (14900) 32900)	900.8 (875.4- 1308.4)	2140000 (1500000 2650000)	5 NETSKY (PREST.O. 114346-8)	1840 (1240-1010)	231.7 (136.7 236.9)	32000 (307000- 306000)	2881.8 (121918- 33984.7)	8830 (seat) 11400)	29.9 (22.2-38.4)	792000 (1000000 1020000)	2008.8 (2968.9- 3419.7)	2190 (1290-3260)	7.2 (8.3-00.9)	20000 (113000- 20000)	601.0 (TML0 961.0)	4400 (TMO MGE)	33 (23-43)	30000-(219000- 28000)	290.8 (222.8 396.7)	1000 (6070 1620)	0.8 (0.8 1.2)	19700-(54700- 140000)	71.0 (22.7 (86.8)	122000-93500- 172000y	7.4 (9.2-09.9)	3140000 (2210000 2010000)	251.6)	29/200 (14700) 442/00)	18 (10 28)	754000-(470000- 1290000)	86.0 (36.3 72.4)
Steptomore promortor	Bris Laviano Bris In tamore inhibitors	2960 (1860-6090)	117.6 (72.9-176.9)	200000 (100000 200000)	10911.4 (0077.0- 19629.1)	30 (149)	12 (88-39)	2700 (14-8680)	107.2 (1.7.544.5)	3430 (2330 4940)	11.4 (7.8-16.8)	70 0000 (20 0000 £77000)	100KO (MR.1	28 (8 111)	61 (0.0-64)	300 (102 164)	10.2 (0.3 (2.5)	1219 (962-2093)	1.1 (0.7-1.9)	122000-(83000- 179000)	924 (62.9 (32.7)	13 (9-40)	0.010.0103	1149 (43-3499)	0.9(0.02.4)	11400 (7779- 14000)	0.7 (0.4-1.0)	317000 (212000- at2000)	19.5 (12.9.28.1)	127 (4-707)	0.0 (0.0 0.0)	X120 (140-10900)	0.1(0.0.0)
Employees procuredor																												80 1000 (102000- 11 10000)					
Etropiosocous mountanios	Floropinism	3120 (7980-2700)	123.8 (78.7-186.8)	20000 (17600) 421000	11165.2 (7642.1- 1667X.1)	208 (No. 800)	162 (3.4-36.3)	36000 (7700- 77900)	1441.9 (209.4 2074.0)	3979 (2279-9040)	11.9 (82-169)	314000 (214000- 444000)	1099.2 (728.4: 1494.4)	487 (209-103)	14(9431)	22 100 (9400) 92 2001	197.4 (31.4-279.9)	1239 (962-2020)	11 (67-13)	123000 (XX000 179000	95.9 (62.9 £32.4)	109 (41-371)	0.1 (0.0 0.3)	31900 (3560 31900)	12.1 (2.7 (4.2)	12490 (K260- 17900)	0.8 (0.3-1.1)	313000 (233000- 204000)	20.9 (14.5.29.4)	1620 (No. 3289)	0.1 (0.0-0.2)	\$2500 \$2000	27 (04-14)
Etropiosecous procursorior	Macrobile	23600-(1000- 21000)	317.8 (364.0- 361.8)	1220000 (K21000- 1720000)	60232 9 (123466.3- 66286.2)	578 (0.1560)	22.9 (6.0-44.8)	ataso lo taxosi	2015.5 (0.0 526.0)	21100)	12.2 (16.0·30.2)	1,58000 (100000 187000)	6223.X)	667 (0-3800)	22 (0.0-60)	Motte-fo-Taketed	296.9 (0.0.330.0)	4990 (9000-9290)	8.8 (8.9.7.0)	400000 (\$22000- 797000)	495.0 (334.0- 606.1)	298 (0.793)	0.2 (0.0 0.4)	21400 (0-47500)	PLE (0.0-91.2)	27900 (32400- 64000)	29 (2140)	1370000-(2010000 DESCRIPT)	N3.4 (N1.4 113.0)	2010 (0-3430)	0.1 (0.0 0.1)	MATER (II- 21000E)	3.4 (80.9.1)
Simplement procure pro	Proteille	7970 (2980-12200	304.4 (197.5- 307.1)	720000 (444000- 2200000)	20275.0 (27680.0- 27508.5)	399 (127-799)	142 (80.81.7)	32100 (11300- 71200)	1272.1 (494.4 2823.8)	1170 (1840-1770)	38.6 (19.3-49.7)	X12000-(914000- 1220000)	2798.5 (1723.7- 4962.4)	414 (191-879)	14 (9.3-29)	36600 (13000- 77400)	123.2 (44.7-296.2)	4120 (2730-X890)	3.1 (2.1-4.8)	335000 (236000- 530000)	201.4 (178.8- 286.5)	182 (70-387)	0.1 (0.1-0.3)	17700-(4080- 30700)	11.9 (4.6-23.5)	27900 (27300- 62600)	1.7 (5.1-2.4)	794000 (107000- 1170000)	48.8 (30.8 72.4)	1290 (42a 2880)	0.1 (0.0-0.2)	36200 (12700- 79900)	22 (88-4.%)
Simplemone	Third generation	3990 (2830 4000)	198.1 (188.5- 901.0	397900 (227000) 81.5000	14178.9 (WELL)	100 (21-290)	10 (18.69)	8960 (1860-22400)	398.4 (73.7-889.4)	44N9 (1229-4590)	19.9 (19.7-22.0)	412000 (280000) 1870000	1373.6 (990.3-	118 (27-299)	64 (9.1-1.0)	20100 (2010) Notes	38.0 (7.8 87.3)	2999 (1400-2860)	1.8 (1.1-2.2)	172000 (121000- 1.00000	130.4 (91.0 1879)	48 (10 414)	0.0 (0.0 0.1)	3990 (927-20000)	3.0(0.7.7.4)	19390 (30200) *********	69 (844.13)	271000 (241000) 4010000	26.1 (18.0 36.9)	411 (99-3080)	0.0 (0.0 0.1)	13000 (2779)	07 (02-13)
Etropiosescom processorios	Trimeloprim Sellimerkovansk	11780-(7910- 14780)	983.0 (313.4- 962.2)	2010000 (701000 1210000)	11947 (2013).6 2021.7)	971 (178-2003)	28.6 (3.5-92.4)	37900 (11800 180000)	3429.2 (927.6- 7364.6)	1100 (900 1700)	48.0 (32.7 (96.7)	1740000 (MATOON 1760000)	7983.0 (2894.0 9282.9)	1120 (140-2330)	38 (0.3-28)	WHEE (1220) 201000)	352.0 (28.0-685.5)	9760 (2180-7670)	44 (3.1-53)	247000 (338000- 662000)	376.9 (271.7: NO.0)	478 (48 988)	0.4 (0.1-0.7)	11200-(1010-	75.2 (6.4-66.6)	43900 (10400- 40900)	27 (8.9-3.7)	1270000 (000000 1700000)	31.8 (93.7-193.4)	3600 (830 7000)	0.2 (0.0 0.3)	100 ME (1 MIN) 2079 ME)	62 (1.0 124)
Etropiosecom processorior	Erokianor in one or more antibistics	2008 (11100 2798)	891.4 (NRC 7- 1106.1)	383080 (124000 280080)	A T259919 (M000LX) W022KH)	£130 (2440-4360)	175.7 (1004a- 252.2)	367000 (236000- 366000)	18347.8 (1979.7 22811.8)	23300-(28000- 30000)	78.6 (60.2 (62.8)	2080000 (1990000 2720000)	- 4992.6 (5323.8- 9094.7)	NOO (1300-7130)	16.7 (11.2-23.8)	421000 (2N000) 471000)	1877.4 (987.0- 2004.9)	20100 (7823- 23300)	TR (89-10.1)	892000 (477900- 1290000)	675.9 (813.8- 872.9)	2220 (1470-3140)	1.7 (1.1-2.4)	290000 (127000- 272000)	121.0 (%.1-201.2)	73480 (19300- 97780)	43 (544.0)	299000 (142000 272000)	127.9 (98.6 148.9)	19300 (10000- 22900)	0.9 (0.0 1.7)	43600 (21600) 60900)	26.6 (17.7 (17.1)

Table S19. Deaths and DALYs	i (la counts and age-specific rates) associated with and attributable to bacterial antinierablal resistance by pathogen-drug combinati Nomali	nation; by age group; 2015; seatheast Asia, east Asia, and Oceania Per Newsoni	784	Santon
Paloges Asibidis Clor	Anti-marked with recitioner EAATh Break. Death. Someth. Eate per 100 000 Create. Eate per 200 000 Create. Eate per 100 000 Create. Eate per 200 000 Create.	Decides Decide	Acceptated with enablance	Access kind with enablance Association of Deadle Deadle Deadle Committee Deadle
All pulsagess. Emblance in our survey authorizes	- 2000 (2300 1343.8 (1123-5 20000 (20000 1757) 2 (00003.1 2000 (207) 1757) 2 (00003.1 2000 (207) 1757) 2 (00000 1231) 2 (00000 13420 (2100.7 1200) 2010 (27) 1757 (27)			90000 (42000 10 10 (10.8 (8.7) (140000 1996.7 (711.7 25000 (18000 11.8 (7.6 17.2) Na0000 (19000 270.3 (713.6 19000) 11.8 (7.6 17.2) Na0000 (19000 270.3 (713.6 19000) 190.1) Na0000 (190.0) Na000 (190.0)
Animaliania Animalyaniahn Animalianiah	1270 (762 1730) 97.8 (75.94.5) 138000 8736.0 NLL 8 (7612) 2.7 (60.6.2) 200 (96.1200) 258.1 (1.8.07.4)			38000 (38000 2.8 (1.5 4.6) 128000 (480000 46.3 (35.1 302.9) 2600 (5 4600) 6.1 (5.0 6.2) 78320 (320 29 (6-2.5) 92000)
Arizotaluster punis din Brita La tamara siddin Arizotaluster Brita La tam Brita Instrumenti Instrumenti Britana siddiner	200 (100 500) 061 (95 2147) 19900 (1200 500) 5204 (8400) 1910 (95 20) 64 (5.4 15.) 1539 (623) 85.5 (501 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1			198000 (1880) 2139000 (1830) (182)
Animanii Interner Militer Animanii Calopeen	222000 1004.5 (1004.5			120000 120000 1270000 1270000 120000 120000 120000 120
Arisatelanter Phonopiedoses				91200 (NIXBO 4.8 (2.8 7.2) 2018000 (1110800 180.4 (N.1 042.0) 1380 (1110 0.4 (8.5 1.0) 29000 (10.800 13.800) 12.8 (8.7 32.4) 139000 (1.8 (8.7 32.4)
Arisotoluster Pearlic generalites Instrumenti exploite peries				$\frac{136000}{(72000)} - 6.2 (1.6+8.9) - \frac{260000}{430000} - 118.9 (77.421840) - 210 (791.4380) - 6.1 (8.0-6.2) - \frac{46300 (10900)}{100000} - 2.4 (9.8.60) - 100000$
Ariestohete Tiled generales humanni ophidoperies	2000 (1350 2000) 980 (64.7-62.4) 17000 (10000 12700.7) 20 (13.71) 1.7 (5.7.8.) 330 (230-630) 131-0 (100-631.2) 1270 (1.71) 1.7 (5.7.8.) 200 (230-630) 131-0 (100-631.2) 1270 (1.71) 1.7 (5.7.8.) 1270 (1.71) 1.7 (5.7.8.) 1270 (1.71) 1.7 (5.7.8.) 1270 (1.71) 1.7 (5.7.8.) 1270 (1.71) 1.7 (5.7.8.) 1270 (1.71) 1.7 (5.7.8.)			12000 (1900)
Assessed more addition. Citedwater upp. Assimply-cooler.	280 (1420-140) 1226 (16.5 177.) 22300 (14200 1600 27.7 193.) 1000 27.7 193.0 1820 (1720 160) 27.5 (17.5 17.) 4230 (1720 160) 27.5 (1720 160) 2		211 (225-645) 0.4 (3-2-6.4) 7.3800 (7030) 21.2 (14.9-61.7) 227 (67.25) 0.1 (61.02) 1200 (7530) 0.4 (51.5-6.5) 1000 (7530) 0.2 (14.9-61.7) 1200 (7530) 0.2 (14.9-61.7) 1200 (7530) 0.2 (14.9-61.7) 1200 (7530) 0.2 (14.9-61.7) 1200 (7530)	120000 (12000) 120000 (1200000) 1611 (PL.12016) 120000 (120000) 1611 (PL.12016) 120000 (120000) 17000000 17000000 17000000 17000000000 1700000000 17000000000 170000000000
Anti-producend Citabator upp. past-file first				2000(1070-010) 0.1 (0.1-0.2) 7200(40200 3.4 (2.0-0.0) 333 (238-985) 6.0 (0.0-0.0) 2000 6.0 (0.3-0.2) 2000 6.0 (0.3-0.2)
La tamer idebin Citebater up. Calopsen	70(42-118) 3.8 (2.0.8.7) 4286 (1720-18380) 3884 (32.5) 17 (8.30) 0.8 (0.0.1.8) 1888 (720-2830) 72.7 (38.6.131.1)		24 (11-44) 0.0 (0.0-0.0) 286 (420-7770) 1.8 (0.0-0.1) 0.2 (2-0.2) 0.0 (0.0-0.0) NET (20-0.00) 0.4 (2.0-0.0) 2	2290 (1360 7738) 0.1 (0.1-0.7) MARC (8700) 2.7 (1.5-1.7) MAR (245 1690) 0.0 (0.0-0.1) 25308 0.7 (0.5-1.7)
Citabatic up. Plessquindens				2000 (1710-2940) 0.2 (0.1-0.2) 75800 (11100) 2.7 (2.1-0.0) 200 (193-0.0) 0.0 (0.0-0.0) 11200 (2730 0.3 (0.2-0.0) 2000) 0.3 (0.2-0.0)
Citabatic up. Parth prevales ephdoperies		9) \$14.600.999\$ 6.0 (52.648) \$1800.(520) 41.0 (22.771.2) \$11.(4.22) \$0.01(0.0.1) \$944.(966.990) \$1.9 (1.7.7.8)\$		2900 (1600-1730) 0.1 (0.1-0.2) 73800 (11700) X.4 (2.0-3.5) 212 (192-642) 6.0 (6.0-6.0) 4020 (200-11500) 0.2 (3.1-6.4)
Circlaster up. epidesperies Circlaster up. Rekisser in our a	271 (16-140) 13.4 (78.214) 2000 (1800) 1993 (1904) 21 (19-14) 1.1 (6-12.2) 200 (181-200) 12.1 (19-19) (19-14)			ORDE (1200 120
Antoniario app. Antoniposida				313003 12300000 1230000 1230000 1230000 1230000 123000 123000 123000 123000 1230000 12300000 1230000 1230000 1230000 1230000 1230000000 123000
Anti-producend Entendante upp. pent disclinic La tensor infolio	4 1230 (023-0770) 39-7 (78-9-07.1 180000) (723000 3178-6 (3585.7) 123 (08-009) 6-1 (1-0-10.1) 11300 (0000 306.1) 1100000 7736.4) 123 (08-009) 6-1 (1-0-10.1) 11300 (0000 306.1) 100000 306.1)	289 (198-612) 1.2 (3.8-6.7) 28000 (1980 165.5 (7.1.2-147.6) 31 (17.80) 0.1 (6.1-0.2) 2720 (1880-6120) 11.6 (6.1-17.0)	\$144(71-079) 0.1 (0.1-0.2) \$120(4000-10000) X.6 (0.0-0.2) 12 (0-20) 0.0 (0.0-0.0) 1200 (020-0.730) 0.0 (0.7-0.2)	27000 (14800 1.2 (0.5 1.5) 72000 (15000 26.2 (14.4 44.9) 2600 (1200-2444) 0.1 (6.1 6.2) 45000 (15000 5.1 (1.5 6.5)
Entendarior app. Carbaponess	766 (989-1120) 27.6 (21.0 (9.1.2) 60200 (18300 3147.8 (2124.0) 760 (156-200) 9.3 (0.7.14.8) 10020 (10100 321.6 (198.0) 1113.3)			1000 (NAD: 0.7 (0.44.7) 37000 (20000 17.8 (18.7.28.8) 3700 (200-668) 0.2 (61.0.3) 9000 (NAD) 4.7 (2.8.8.1) 2000(
Entendario spp. Plearopiedean				1400 (1900 0.3 (0.5 5.1.5) 20000 (23000 19.5 (1.1.4.52.5) 1930 (93.0525) 6.1 (0.0.6.2) 20000 (23000 2.3 (1.1.4.5) 20000 (23000 0.3 (0.5 5.1.5) 1930 (1.1.4.5) 1930 (1.1.6.6.2) 20000 (23000 0.3 (0.5 5.1.5) 1930 (23000 0.3 (0.5 5.1.5) 1930 (23
Entendarior app. cophalogories Entendarior see. Trimologories	** X50 (Fe-748) 441 (ELS 91.2) 11600 (7000) 5757 (5000.5) 44 (D-11) 3.2 (LB.7.) 713 (2750 200.5) 203 (ULS 5.) 713 (2750 200.5) 203 (ULS 5.) 713 (ULS 5.0.) 7			1800 (1800 8 (1800 (12300) 214 (110-112) 497 (271 178) 6-9 (10-11) 1128 (550) 6-8 (0.5.17) (2000) 1100 (1900) 1100 (1900) 1100 (1900) 1100 (1900) 1100 (1900) 1100 (1900) 1100 (1900) 1100 (100-12) 11
Entercharter upp Sections in our a				40700 (21400 2.3 (1.3 3.3) 111000 (407000 35.2 (12.2 48.8) 1000 (4770 0.3 (8.3 4.6.8) 24000 (33300 13.1 (7.6.214) 70000 0.3 (8.3 4.6.8) 423000 13.1 (7.6.214)
Entercarrant facults Pleasupinisms	$ \begin{array}{llllllllllllllllllllllllllllllllllll$			TMODE (11800 1.0 (0.3 1.7) 294000 (254000 214 (11.1 29.7) 2540 (2500 9140) 0.2 (5.1 0.3) 22300 (35900 6.1 (2.7 0.3 3) 23300)
Entercore Vanconycia faculto	$11 (34.77) \qquad 2.9 (1.73.8) \qquad 4370 (3000 6030) \\ 233.5) \qquad 13 (7.20) \qquad 0.7 (6.34.4) \qquad 2343 (90.2000) \qquad 64.1 (20.34222) \\ 335.5) \qquad 10 (7.20) \qquad 0.7 (6.34.4) \qquad 2343 (90.2000) \qquad 64.1 (20.34222) \\ 335.5) \qquad 10 (7.20) \qquad 10 (20.200) \qquad $			1700-(972-3035) 0.1 (0.0-0.1) 4700-(21500) 2.2 (1.3.3.7) 379-(223-1040) 0.0 (0.0-0.1) 1700-(1730 0.7 (0.3.3.3) 0.7 (0.3.3.3)
faculty may addition	*** WE (188 80) 291 (18.8.17) 2000 (1980) 291 (18.8.17) (1990) 391 (1914 10) 110 (14.01) 7.8 (4.1.11) 110 (14.01) 611 (14.01)			2000 (1400 b) (1500 (2000) 25.4 (14.5 4.1) 100 (2000 t) 6.3 (4.1 6.5) 1000 (2000) 25.4 (1.5 3.2) 2000
Salaman Vancanyon				702000 1902000 190200 19020 19
Entercorum Enteracrim our s faccion more addition	200 X20 (150-722) 26-0 (17.6-30.6) 47.00 (20000 2122.7 (1752.6- 124 (175-254) 6.1 (2.6-19.4) 1120 (2000 MLS (200.0- 120-4) (176-254) 6.1 (2.6-19.4) 1120 (200.0- MLS (200.0- 120-4) (176-254) 1120 (175-254) 6.1 (2.6-19.4) 1120 (200.0- 120-254) 1120 (175-254) 1120	283 (465-488) 1.2 (5.3-5.49) 2800 (1280) 108-4 (98-8 173.6) 47 (26-137) 0.2 (6.1-6.4) 9940 (290-12108) 24.2 (4.3-64.6)		$ \begin{array}{llllllllllllllllllllllllllllllllllll$
Other enteressori - Photospinstone	$821 \ (889.980) \qquad 30.5 \ (81.4.2.4) \\ 83.200 \ \qquad 2731.4 \ (7795.9 \ \ 117 \ (19.239) \\ \qquad 3.7 \ (69.11.5) \qquad 3080 \ (279. \ \ 303.1) \\ \qquad 3080 \ \qquad 303.1 \ \ 303.1 \ \ \ 303.1 \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \$			$ \begin{array}{cccccccccccccccccccccccccccccccccccc$
Oher entercover Vancoury in				2806 (2110-8008) 0.2 (0.1-0.5) 122000
Color reterenced more artifeties Enderthis self Assingly-relate	- 227 (312 942) 303 (31 24.1) 27800 4802.) 131 (1.2 20) 4.4 (2.1 1.17) 22900 1134 (1.1 20) 113 (1.2 20) 4.4 (2.1 1.17) 22900 1134 (1.1 20) 113 (1.1			2000 (1900 0.7(0.21.0) 0.4000 (1.1000 11.6 (0.8.22.0) 10.0 (1.200 Marc) 0.2 (3.1.0.1) 12000 (1.2000 1.2000 (1.2000 (1.2000 1.2000 (1.2000 (1.2000 1.2000 (1.2000 (1.2000 (1.2000 (1.2000 (1.2000 (1.2000 (1.2000 (1
Enterthional Antoposidis	2000 (Timo 4730) 227.2 (185.5: 413000 (20000 6 2009.5) 32 (10.70) 2.8 (1.6.5.7) 4620 (2000 6600) 325.0)			18000 (PRIN) 4.7 (L4-9.8) A00000 (PRIND) 191.8 (PC.8-223.2) 2120 (120-3230) 6.1 (8.1-6.2) 75300 2.8 (1.3-5.4) 190000 4.7 (14-9.8) 4.100000 191.8 (PC.8-223.2) 2120 (120-3230) 6.1 (8.1-6.2) 75300
Endertebis sell Bris Lacture Bris. Inclument Milities	2 380 (290 2900) 251.5 (17.5 15000 (25000 1320.4 (1357.5 10 (47.10) 3.0 (47.11) 401 (970 1300) 422 (170.5 1300) 401 (970 1300) 407.5	\$840(150-240) 7.4(53-9) \$1800(2000) \$40.5(200.5 \$15(50.5) \$2.0(0.20.5) \$2.00(200-640) \$1.5(55.20.5) \$2.0(0.20	NID(790-1998) 0.7 (5.3-LO) 72380 (42300 41.4(46.83.N) 29 (17.34) 03 (60-03) 299 (130-3000) 19 (1.4.2.7)	$ \begin{array}{llllllllllllllllllllllllllllllllllll$
Endershie sell Carbopross	791 (180 ACC) 292 (18.7-42.9) 2980 (1990) 2981 (1004L) 117 (99 491) 3.8 (2.9-9.3) 8680 (299) 312.6 (28.7-7.700) 3181.1) 117 (99 491) 3.8 (2.9-9.3) 11280) 314.1)			$\frac{19800 (7908.}{6.5 (63.63.6)} - \frac{218800 (19800.}{277800)} - \frac{12.3 (78 (87)}{213 (78 (87)} - \frac{2380 (120.3930)}{230 (120.3930)} - 6.1 (61.6.2) \\ - \frac{38900}{38900} - \frac{2.6 (1.4.44)}{2.000} - \frac{10.000}{2.000} - \frac{10.000}$
Enteristic sell Photopindone Enteristic sell Third promotion and determine	THE CHIEF NUMBER OF THE CHIEF NUMBER CHIEFS AND THE CHIEF NUMBER CHIEFS AND THE CHIEF NUMBER CHI			9800 (1880) 4 (12.5.1) 23000 (12000 1110 (73.545.1) 1980 (700 6.3 (13.56.6) 2000 (1880) 114 (73.545.1) 1980 (70 6.3 (13.56.6) 2000 (1880) 114 (73.547.0) 1980 (70 6.3 (13.56.6) 2000 (18.5
Enterthical aphilopain Enterthical Trianspain	\$100 (1700-1840) 210.4 (1 £1000) 21204.5 \$444 (154.877) 21.0 (15.811) 24800 \$889.2] \$100 (1700-1840) 583 (134.4 \$2000) (10000) \$1207.4 (168.8) \$170 (168.27) \$1.4 (15.17) \$1200 (1700-1840) 583 (134.4) \$10000 (1707-187) \$170 (168.27) \$1.4 (15.12.7) \$120 (1700-187) \$120			12000
Endership and Statement in our a more addition	200 (100 e00) 255 (40.2 4000) 29900 2512.5 (107.6 100) 46.8 (27.4 46.1) 1280 (100 e00) 255 (100 e00)			. 18000 (1900) 12000 (18000) 120000 141.1 (181.5 1830) (2480 18 (1.3.2.5) 18000 (18000 4.3.5 (18.5.4.5) 110000 (18.5.4.5) (18.
Group A Macrobile Steptonerous	$200 \; (126.520) \qquad 1000 \; (6.5 \; 13.7) \qquad 10230 \; (11000 \qquad 2014.0 \; 04.5) \qquad 20 \; g_0 \; a_0 \qquad 0.9 \; (6.0 \; 5.0) \qquad 2000 \; (9.0 \; 23.7) \\ 1400.0) \qquad 1400.00 \qquad 1$			2000 (9420 1.2 (3.5.2.5) MARKO (231000 24.0 (12.4.5.5) 299 (54230) 0.1 (3.0.6.4) 5100 (6.19300) 2.4 (6.0.4.7) MARKO
Group A Herbitanov in our a Supplemental more artificials	287 (126-235) 200 (6.5-18.7) ECRO (1300) SFLE (166.2) 19 (5-40) 0.9 (6-5.8) 2640 (9-839) 36.7 (6-5-24.3)			2800(NAB) 1.2 (0.3 2.5) MARRO (28000 28.0 (12.4 M.3) 299 (9.8740) 6.1 (0.0 6.2) MARRO (3.19300) Z.6 (0.0 6.7) MARRO (28000) Z.6 (0.0 6.7)
Comp II Pleasupindon Comp II Marchite	TH (Max Max) 25.2 (Max Max) 25.2 (Max Max) 25.2 (L1 (MAX Max) 47 (14.2 Max) 4.8 (0.7 14.6 Max) (1300 1300) 42.2 (Max Max) 25.2 (Max) 25.2		80 (23 N) 0.1 (0.0 A1) 3220 (300 5220) 4.6 (3.2 A.4) 30 (3.2 3) 0.0 (0.0 G)) 886 (164 1900) 6.8 (3.1 A7) 3	3000 (170-0-1400) 0.2 (0.1-0.5) \$1200 (1700-0-1) \$1200 (1
Ziopianous Comp II Ziopianous	387000 1984.5 2004.6 20			ACCOS 1180000 1180000 118000 11800 11800 11800 1180
Cleany B Entitioner in our o Emphasizes more authorities	2000 (1010 2020) 111.7 (91.6 197.9) 210000 (143000 1775.0 (7051.1 369 (20404) 15.7 (1.4 40.1) 2200) 2041.1)			20000 [19000 LA (LA 2.4) 25200 [190000 27.3 (22.7 08.7) 2020 (A 970) 0.2 (8.0 6.5) 90200 (9.220000) 4.8 (6.0 18.5)
Namephiles Antespecialles influence	$ \begin{array}{llllllllllllllllllllllllllllllllllll$			600-(430-833) 0.3 (9.2-0.) 12900-(9800 6.2 (Lb.K4) 990 (P.1970) 0.0 (Lb.0.1) 2090 (2070 10 (b.1.2-0)
Namephilas Tital generates influence explain quarter Namephilas Radionarios and				78 (NA 1896) 0.0 (NA 0.1 27786) 0.5 (NA 1.2) 216 (NA 1.2) 0.6 (NA 6.0) 200 (NA 6.0)
Namophila Enkiance is our o inflampe mer militation Elebricia Animplyonida	■ MR (75 Me) 2 A3 (M.3 Me 2) 1000 (7330 2 Me) 1244 (46006 129 (75 27) 3 × (1.8 14.1) 2070 (733) 18.1 (1.6 14.1) 2070 (733) 18.1 (1.6 14.1) 2070 (733) 18.1 (1.6 14.1) 2070 (733) 18.1 (1.6 14.1) 2070 (733) 18.1 (1.6 14.1) 2070 (734) 18			4406(1480420) 43(0.24.4) 176000 4.1(4.84.8) 1230(124.220) 6.1(4.0.6.1) 4480(1.16.0.1) 13(0.4.2.1) 1160(1600. 4.1(4.6.4.1) 13000(12000 13.1(16.0.2.1) 1300(12000 13.1(16.0.2.1) 1300(12000 13.1(16.0.2.1) 1300(12000 13.1(16.0.2.1) 1300(120.0.1) 1300(120.0.1) 1300(120.0.1) 1300(120.0.1)
Alichada Bria Laciana Bria provinciar Indianano Militar	2000 (2700-8286) 2932 (1842) 38888 (22306) 23314 (1842.5) 14.60-82.6) 2490 (1820-8780) 122.6(83-282.5) 100 (2700-8286) 2333) 478880) 23314.6 28 (18-20) 14.60-82.6) 2490 (1820-8780) 122.6(83-282.5)			2000 (1900 2.9 (1.9.4.2) (19000) (19000) 68.2 (425.96.7) 874 (197.1430) 6.0 (8.0.6.1) 1730 (435.0 6.0 (9.2.1.9) 18000)
Alchielie Carlopeens promonier Carlopeens	1860 (1270-2480) 90.1 (42.2 127.8) 14800 (11800 8864.5 (883.5) 486 (201-905) 22.4 (14.3-34.0) 4880 (3800 994.4 (128.5- 21.0) 11871.4) 11874.4 (128.5-405) 4880 (3800 994.4 (128.5-405) 4880 (3			27600 (14200 1.4 (0.7 2.7) 418000 (12400 20.4 (0.4 0.9 2.7) 7220 (1800 14000 0.4 (0.2 0.7) 122000) 8.0 (4.0 0.4 1) 122000 (1200 0.4 (0.2 0.7) 122000)
Alchielle Plerreguindenn promonier Plerreguindenn	NGO (2003-0998) 218-0 22800 (20000 1981.1-4 (1982.4 262 (168-134) 13.9 (6.3-21.4) 2028 (19800 128-6 (222.8) 2020 (1980.4) 1981.5)			HILDO(13800 2.5 (1.5.0.0) 118000 (780000 NA.8 (72.2.00.0) 4000 (2300-6470) 0.2 (6.1.0.1) 10000 (2300-6470) 118000 4.5 (2.6.5.2)
promonier ophilopoles Elekside Trimbipole	\$\text{PMO}\$ (\$\text{\$100}\$ \$\text{\$6400}\$ \$\text{\$252.5}\$ \$\text{\$100}\$			THOMODISMOD ALIZA AND THOMODO THOMODO ALIZA ALIZA AND AND ALIZA ALIZA AND ALIZA ALIZA AND ALIZA
Elebriche Rekrause in our o promonier mare militaire.				9800 (4100 1210000 12100000 1210000 1210000 1210000 1210000 1210000 1210000 1210000 1210000 1210000 1210000 12100000 1210000 12100000 12100000 12100000 12100000 12100000 12100000 12100000 12100000 12100000 12100000
Mequalic up. Pleropinion	0.01) 60(0.06) 22(546) 1.1(0.325) 6(0.0) 60(0.00) 4(1.11) 62(60.03)	1(84) 60(8066) A4(799) 02(6104) 6(64) 02(6003) X(219) 60(6061)	0 (8 I) 0.0 (8 0.0 0.1) 27 (27 KB) 0.0 (80 0.0) 0.0 (60 0.0) 7 (2 M) 0.0 (80 0.0) 1	38 (19-30) 40 (40-4) 600 (820 1980) 6.7 (6.1-6.5) 37 (77-114) 60 (6.0-6) 3340 (19-220) 6.1 (60-6.1)
Mongandie upp. Pearle generalien asphalosperies	* 0,000 0.0,00.000 II (3.2% 0.3,03.1.4) 0,000 0.0,00.00 2,000 0.1 (0.0.03)	0 (9-1) 60 (10-60) 22 (9-44) 0.1 (00-0.2) 0.(9-0) 0.0 (00-0.0) 4 (1-11) 60 (10-60)	e (sel de predict 16 (2,12) de (de de) e (de de) de (de de) 3 (1-14) de (de de de	91 (28-141) 0.0 (10-0.0) 1829 (20-3210) 0.1 (0.0 0.2) 18 (7-39) 0.0 (0.0 0.0) 361 (120-772) 0.0 (10-0.0)
Margandia app. aphabapania Margandia app. Rebitator in our s	9 (44) 69 (8.06.04) 19 (4.40) 0.7 (0.2.24) 0.000 0.0 (8.00.05) 2 (0.7) 0.1 (8.00.1) *** *** *** *** *** *** ***	9(9.1) 60(80-64) 30(12-61) 6.1(60-6.3) 6(6-6) 68(60-60) 2(0.11) 60(80-60) 1(0.2) 60(80-64) 64(28.17) 6.1(60-6.3) 6(6-6) 68(60-60) 16(6-30) 61(60-6)	0(81) 0.0 (8.0 (8.0 (8.0 (8.0 (8.0 (8.0 (8.0	98 (% 1.14) 0.0 (0.0 0.0) 2790 (7890 6890) 0.2 (0.1 0.2) 30 (10 64) 0.0 (0.0 0.0) 780 (200 1180) 0.0 (0.0 0.1) 127 (200 720) 0.0 (0.0 0.0) 8 122 (200 1.238) 0.1 (0.2 0.7) 181 (12 202) 0.0 (0.0 0.0) 1990 (22 7890) 0.1 (0.0 0.7)
Mysobactorian Estimates drug adversalant emissions in TR	0 (34) 4.0 (30-84) 0 (60) 03 (50-60)	M(3-M) 01(88-02) 1400(403323) 4.6(23-143) 11(6-21) 0.0(0.0-1) 977(276-230) 4.0(1.8-K)	II (6.25)	1700/094-3870 0.1 (0.0-0.2) N3880-(21100- 2.4 (1.0-3.3) 1000 (273-2200) 0.1 (0.0-0.1) 27000 (131000 1.3 (0.4-3.1) 12000 (131000 1.3 (0.4-3.1)
Mysobacterium bominal mone adversalente emissioner	0 (9 I) 0.0 (0.0 4.0) 0 (64) 03 (0.0 60)	MI (27-130) 6-1 (62-6-7) 7900 (620-10400) 32.0 (28.7-47-7) 14-(0-40) 6.1 (60-6-2) 1240 (0-6200) 3-0 (60-617-6)	25 (25-87) 0.0 (6.0-0.1) 4690 (4110-8600) 5.4 (5.0-2.7) 9 (0.90) 0.0 (6.0-0.0) MEI (0.2990) 0.7 (6.0-2.7)	980-(880-1750) 0.1-(0.1-0.7) 37800-(17800 14.1-(11.8-22.7) 1800-(8-180) 0.1-(0.0-0.7) 47500-(9-17300) 22-(0.0-2.8)
Mysoluniseium Militideg enistan nabarulinis dine enistance in l	THE THE STREET S			9800 (9700 18800) $0.4 (0.2 0.5)$ $\frac{207000 (121000)}{384000}$ $11.2 (40.0 287)$ $8330 (970.41350)$ $0.3 (0.0 6.7)$ $\frac{139000 (12400)}{386000}$ $1.4 (0.2 37.2)$
Mymbolorium Kilangia in mon- indonulius emisiane Mandonulius Kalangia in mon-	0 (244) 4.0 (250.44) 6 (44) 0.2 (450.45)			300 (286-286) 0.2 (0.1-0.2) 12800 (9180
Mysokolovian Rekisancia om s advendenia mere additeles Notarria amerikanci		200 (127-300) 1.0 (3.6.1) 21000 (1000	187(0-225) 0.1 (0.1 0.21 1.000 (1020) 17.6 (0.0 20 q) No. (14.125) 0.0 (0.0 0.1) 0.000 (1.0 0.000) 0.1 (1.3.9.q)	2800 (1400 L 2 (0.5 L C) 111000 274 (14.0 L C) 11100 (17.0 L C) 11100 (
Arisonia Thedgenesian generalasar sephalopasian				24000) - 1110 (89-3220) 0.1 (80-0.1) 170-(89-301) 0.0 (80-0.0)
Notaceir Embianorie our s generalment more midiation				- 13500 (550) 0.3 (6.9 l.3) - 1 1430 (500 5120) 0.1 (6.9 0.2)
Froise up. Animply-mides		$9 (5.15) \\ \hline 60 (50.64) \\ \hline 79 (201.1200) \\ 3.1 (1.8.49) \\ \hline 6 (0.1) \\ \hline 0.0 (0.004) \\ \hline 39 (4.89) \\ \hline 6.2 (5.004) \\ \hline$		1770 (1300-2028) 0.1 (0.1-0.1) 77800 (23000 1.0 (1.1-2.3) 28 (10-199) 6-0 (0.0-0.0) 1890 (220-4200) 6.1 (0.0-0.2) 1890 (720-7200 1.1) 1890 (720-7200 1.1) 1890 (720-7200 1.1)
Froise up. Antequalille Froise up. Plessquindens		\$\frac{1}{2}\left(\frac{1}{4}\left(\frac{1}{2}\left(\frac{1}2\left(\frac{1}{2}\left(\frac{1}{2}\left(\frac{1}{2}\left(\frac{1}{2}\left(\frac{1}{2}\left(\frac{1}2\left(\fr	10 (20-80) 0.0 (6.0 6.0) 11 3186 (710 (100) 2.2 (1.6.44) 1 (6.2) 0.0 (6.0 6.0) 19 (0.0 6.0) 10 (1.6.62) 1 14 (6.20) 0.0 (6.0 6.0) 1270 (710 (100) 1.1 (6.6.15) 1 (6.2) 0.0 (6.0 6.0) 19 (10.0 77) 6.1 (6.6.42) 1	1800 (120) 1800 (120) 1800 (1700) 181 (0.2.14) 200 (0.00) 0.0 (1.0.00) 1800 (1700) 0.3 (0.0.00) 1200 (1700) 1200 (
Protess up. The granulus optical species			14 (8.24) 8.0 (8.04.0) 1280 (88.2180) 1.1 (98.18) 3 (1.4) 03 (8.0.03) 271 (88.86) 02 (8.1.63)	26809 21338
Protess upp. Trimelogein: Sallamelomande	$m_{(29.13)} = 4.2(3.74.4) = 779(390011720) \begin{array}{ccccccccccccccccccccccccccccccccccc$	\$2 (26-47) \$2 (61-63) 2000 (2320-600) 18.6 (63-26.3) 2 (6-4) 0.0 (60-0.0) 186 (6-36) 0.0 (6-6)	28 (33.90) 0.0 (0.0-0.0) 2000 (1330 3320) 1.8 (1.0-2.9) 1 (0-2) 0.0 (0.0-0.0) 79 (0-187) 0.1 (0.0-0.2) 0	X20((13012300) 0.4(0.34.6) 17300()180000 X.E(X-811.5) 354(0-605) 60 (0.0-63) 4940(0.1890) 6.3 (0.0-67)
Protess upp. Knishmar in our a more addition				1800(1820) 0.8(0.5.1.2) 35000(1800) 17.5(28.2.44) 200(18004456) 0.1(0.16.2) 5500(2720) 2.7(1.4.4.7) 2000(
Fundament Antophysoides semplement Antophysoides				990: (1796-1880) 0.4;0.3.6.3; 20000 (12000 18.2;0.3.13.4) 244;0.420, 6.0;0.6.0) 4070;0.1889; 6.1;0.6.61 32000 (1270) 44800 (12700 44800 (12700 1800)
Faralismus pais die lites arregione La tamor inhibite Faralismus Cathapum	\$25 (80.5 120) \$444 (\$1.5 44.9) \$12800 \$252.1 \$2.0 \$4.1 (\$2.5 4.4 \$2.5 \$2.5 \$2.5 \$2.5 \$2.5 \$2.5 \$2.5 \$2.5			2000(1780 0.0(14.17) 42000(17800 228(15.512) 160(17.310) 0.1(10.01) 4200(17800 1.0(15.51) 160(17.310) 0.1(10.01) 4200(17.01) 170(17.01)
Faralismus Plensquindoss areginas				AMONG 12000 1.0 (SA 8.1.5) 4270000 21.0 (LA 3.1.2) 22.0 (1270.3390) 0.1 (S.1.6.2) 427000 24.(3.3.49) 22.0 (1270.3390) 0.1 (S.1.6.2) 427000 24.(3.3.49)
Paralimente Paralis praevalen arregione regisalo paries	90 (MA-125) 900 (ZT-0-36.2) 7000 (EROSO META-2399.1 IX (D-31) 0.0 (ES-1.3) 1000 (ET-2720) 78.7 (A1.3-131.0)	9) N7 (275-189) 1.4 (1.0-1.8) 28000 (2200 120.8 (92.3-184.1) N (4-12) 0.0 (0.0-0.0) 687 (90.1000) 2.7 (1.0-1.3)	\$10(45.03) 0.1 (61.0.2) 11280 (600) 49 (5.0 (5.7) 2 (2.9) 0.0 (60.00) 281 (104.03) 0.2 (61.0.4)	17000 (1800) 0.8 (0.5 l.7) 272000 (21200) 18.3 (11.4 (28.4) 391 (196739) 0.0 (8.0 6.0) 8620 (120 1990) 0.4 (0.2 6.0)
Faralment Titel generates amplement explainments				2500-2500 Le(1.0.2.5) 50000(12500 Me(28+M.9) 278 (130-800) 6.1 (6.1.0.2) MSE (250-80) 29 (1.3.6.7) 2700 (130-800) 6.1 (6.1.0.2) MSE (250-800) 29 (1.3.6.7)
Favalance Relation is one of arrapines more addition. Lideratic Parietti Permainten	*** Z00 (170 2000) 0.04 (71.3 141.1) 10000 (173.00) 173.00 174.1 (183.00) 173.00 174.1 (183.00) 173.00 174.1 (183.00) 173.00 174.1 (183.00) 173.00 174.1 (183.00) 173.00 174.1 (183.00) 174.1 (183.00		MYC(254-85) 0.3 (0.2 0.4) 2006(21200 22.2 (M3.575)) MY(M18) 0.1 (0.0 0.1) 729 (878-1138) A7 (1.4 0.4) 2 (1.4 0	\$1000 (2000) 24(15.5.0) 175000 72300 752 (15.3.0) 1500 (773) 6.7(5.4.4.1) 20300 (3330) 143(15.2.7.4) 200(15.2.7.4)
Zainendie Ferstydei Phrosopiedosen Malit drug sreinie Zainendie Ferstydei Salemedie Tydei e				286 (265-325)
Family de Salatan de sur a Salatan de Salatan de sur a Salatan de				275 (207-345) 0.0(20-0.0) 27200) 0.0 (0.0.1.2) 10.0 (0.0.1.2) 0.0 (0.0.0) 3660 (10.0.0) 27200 0.2 (0.0.0.1)
Salmondio Typhi – Phrosquindoss	$ \begin{array}{cccccccccccccccccccccccccccccccccccc$	18) 20 (18-120) 0.3 (18-64) 4600 (2000 12300) 240 (12-645.5) 14-(2.54) 0.1 (0.0-64) 1220 (190-2000) 1.0 (18-11)	209(2006499) 0.3 (0.1-0.4) 2000(9020) 21.7 (7.6-0.5) 99 (7.6-0.6) 0.1 (6.0-0.1) 5120 (908-14500) 4.3 (5.3-12.7) 2	2010 (1200-1800) 0.1 (0.1-0.2) 133000 (40000 7.3 (3.5 14.6) 506 (75 1270) 0.0 (6.0-0.1) 29000 (8200 1.3 (6.2-3.0)
Melit deg erstem Kalmendir Typki — Kalmendir Typki a Paniroki				777 (786-1389) 0.0 (8.0-0.1) 42796 (79980) 2.2 (1.0-4.2) 81 (9-277) 61 (8.0-610) N20 (0.1498) 6.1 (8.0-0.7) 82390)
Zelmende Typis Resistance in our or more arbitries Non-typicalid Photographics		10 80 (C-141) 6.1 (62.544) 7886 (MTS-12780) 28.7 (14.950.5) 5.6 (2.34) 6.1 (63.64.5) 1280 (E7.2500) 8.7 (1.8.14.5) 2.2006 (1180) 81.0 (1.8.17.3.3.5) 8.0 (1.8.1.5.3.3.5) 81.0 (1.8.1.5.3.3.5) 81.0 (1.8.1.5.3.3.5) 81.0 (1.8.1.5.3.3.5.5) 81.0 (1.8.1.5.3.3.5.5) 81.0 (1.8.1.5.3.3.5.5) 81.0 (1.8.1.5.3.3.5.5) 81.0 (1.8.1.5.3.3.5.5) 81.0 (1.8.1.5.3.3.5.5) 81.0 (1.8.1.5.3.3.5.5) 81.0 (1.8.1.5.3.3.5.5) 81.0 (1.8.1.5.3.3.5.5) 81.0 (1.8.1.5.3.3.5.5) 81.0 (1.8.1.5.3.3.5.5) 81.0 (1.8.1.5.3.3.5.5) 81.0 (1.8.1.5.3.3.5.5) 81.0 (1.8.1.5.3.3.5.5) 81.0 (1.8.1.5.3.3.5.5) 81.0 (1.8.1.5.3.5.5) 81.0 (1.8.1.5.3.5.5) 81.0 (1.8.1.5.3.5.5) 81.0 (1.8.1.5.3.5.5) 81.0 (1.8.1.5.3.5.5) 81.0 (1.8.1.5.3.5.5) 81.0 (1.8.1.5.3.5.5.5) 81.0 (1.8.1.5.3.5.5.5) 81.0 (1.8.1.5.3.5.5.5) 81.0 (1.8.1.5.3.5.5.5) 81.0 (1.8.1.5.3.5.5.5) 81.0 (1.8.1.5.3.5.5.5.5) 81.0 (1.8.1.5.3.5.5.5.5) 81.0 (1.8.1.5.3.5.5.5.5) 81.0 (1.8.1.5.3.5.5.5.5) 81.0 (1.8.1.5.3.5.5.5.5) 81.0 (1.8.1.5.3.5.5.5.5.5) 81.0 (1.8.1.5.3.5.5.5.5.5) 81.0 (1.8.1.5.3.5.5.5.5.5) 81.0 (1.8.1.5.3.5.5.5.5.5.5) 81.0 (1.8.1.5.3.5.5.5.5.5.5.5) 81.0 (1.8.1.5.3.5.5.5.5.5.5.5) 81.0 (1.8.1.5.3.5.5.5.5.5.5.5) 81.0 (1.8.1.5.3.5.5.5.5.5.5.5.5) 81.0 (1.8.1.5.5.5.5.5.5.5.5.5) 81.0 (1.8.1.5.5.5.5.5.5.5.5.5.5.5) 81.0 (1.8.1.5.5.5.5.5.5.5.5.5.5.5) 81.0 (1.8.1.5.5.5.5.5.5.5.5.5.5.5.5.5) 81.0 (1.8.1.5.5.5.5.5.5.5.5.5.5.5.5.5.5.5) 81.0 (1.8.1.5.5.5.5.5.5.5.5.5.5.5.5.5.5.5) 81.0 (1.8.1.5.5.5.5.5.5.5.5.5.5.5.5.5.5) 81.0 (1.8.1.5.5.5.5.5.5.5.5.5.5.5.5.5.5.5) 81.0 (1.8.1.5.5.5.5.5.5.5.5.5.5.5.5.5.5.5) 81.0 (1.8.1.5.5.5.5.5.5.5.5.5.5.5.5.5.5.5.5.5.		2000/100-0800 0.1 (0.1-0.3) \$10000/1000 \$0.0(1.1-0.0) \$11 (13-1300 0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.
Noriogistid Hermanian Educatio Plenoquindam Noriogistid Rekissorio ou s Educatio our attituto		L5 24 (100-274)		230(1200-0320) 2.7(0.1-0.5) 4300(00000 430(1.0.2.5) 827(121.1996) 63 (0.0-1) 7280(1000) 14 (0.3.52) 100(1200-0320) 12(0.1-0.5) 1200(00000 100(1200-0320) 12(0.1-0.5) 1200(00000 100(1200-0320) 12(0.1-0.5) 1200(00000 100(1200-0320) 12(0.1-0.5) 1200(00000 100(1200-0320) 12(0.1-0.5) 12(0.0-1.5) 12(
Armeis sp. Aningly-reidn		22 (12 34) 61 (36 61) 15% (366 330) 7.6 (4.6 12.7) 1 (6.4) 0.1 (6.0 6.0) 130 (6.319) 0.4 (8.0 1.7)		1880(10.520) 0.1 (0.0-0.1) 3220(-)(10.0-0.1) 1.7 (0.9-2.9) 1.3 (0.202) 0.3 (0.0-0.0) 299(0.000) 0.1 (0.0-0.1)
Anti-paradomenal Javania app. periodic Bris. La taman inhibito	$ \frac{d}{dt} = \frac{100 (40 147)}{311 (31 8.2)} - 3.1 (31 8.2) - 9000 (3000 14000) - \frac{4011 (278.2)}{228.0)} - 311 (9.2) - 0.0 (9.2) (9.2) - 0.0 (9.2) (9.2) - 0.0 (9.2) (9.2) - 0.0 (9.2) (9.2) - 0.0 (9.2)$	2) 27 (19-44) 0.1 (8.1-6.2) 220 (1770-1989) 9.8 (5.6-13.8) 9.(2-05) 0.0 (6.0-0.0) 429 (220-896) 1.8 (5.8-3.5)	20 (F-10) 0.0 (S-0.04) 200 (200-1500) 0.0 (S-0.04) 2 (1-4) 0.0 (0-0.04) 144 (20-20) 0.1 (0.1-0.7)	2000 (1390-2079) 0.1 (0.1-0.2) 99000 (11000 3.0 (1.0-1.7) 279 (218-910) 6-0 (0.0-6.0) 11000 (1900 6-0 (0.3-1.1) 99000)
Sensite upp. Carboproses		20, 28 (16-42) 6.1 (3.1-62) 2270 (3480 9900) 16.0 (3.8-53.0) 8 (4-52) 6.2 (59-6-1) 682 (329-1230) 2.8 (3.3-6.0)		1470 (500 2000) 0.1 (0.0-0.1) 42300 (2000) 2.1 (1.2-3.3) 462 (220-879) 6-0 (0.0-0.0) 1370 (899) 6-6 (0.3-0.1) 2000 (2200)
Zernis spp. Pleospiedom Zernis spp. Purck prevalen		1 26 (14-26) 0-1 (21-0-2) 2100 (2200-2020) 8.7 (10-14-1) 1 (0-14) 0-2 (0-2-0-1) 222 (10-3-2) 1-2 (10-2-2) 1 26 (10-14-2) 2100 (2200-2020) 3.7 (10-14-1) 2 (1-4) 0-2 (10-2-0) 122 (20-2-2) 0-2 (10-2-2)		1000 008 2700 0.1 (0.0-0.1) 20000 (2.1000 0.2 (0.1.1.3.5) 104 (204.20) 0.0 (0.0-0.0) 4440 (710.10000) 0.2 (0.0-0.1) 1000 (120.0-0.2) 4540 (120
- spennelsone		T	ı	

Zerostia upp.	The grantes	182 (187-297)	10(32140)	14300 (9900)	797.8 (466.9-	12 (0.29)	04(0214)	1070 (TW 2270)	NA (16.6 (21.1)	ar (27:73)	62(81-63)	2600 (2360-6400)	16.1 (9.6-28.9)	2 (2 4)	0.000.000	291 (89-870)	10(8322)	14 (8-2%)	0.000.00	M10 (726 2800)	12 (0 t 22)	1 (0-2)	03 (00-03)	XT (26-295)	0.1 (0.0-0.2)	3660 (2000-6130)	0.2(0.10.5)	1130 (2100)	4.8(2.87.8)	236 (71-814)	60 (8.060)	NEO (1620-1300)	0 03/83/04
	- comment																											172000					
Servatio upp.	mer adhesis	373 (240-569)	18.0 (11.8-28.0)	NOMBO)	24(7.3)	48 (88-182)	47 (2.7.7.9)	9210 (2400 E1100)	60.0	MI (NZ-132)	63 (92-63)	700 (840 11700)	36.5 (36.7-27.4)	22 (12.89)	0.1 (0.0.0.1)	1920 (3070-3130)	7.8 (8.3-12.7)	31 (12:04)	4.0 (0.04.0)	2790 (1429-avat)	24 (13-41)	K(4-14)	03 (60-03)	487 (339-1230)	0.6 (0.3-1.1)	4210 (1940-1000)	0.1(0.2-0.1)	210000 (00000 210000)	7.7 (4.0 12.4)	1400 (832-2800)	61 (8.061)	enam)	20 (1.0-3.4)
Shipshe app.	Pleasupinstone	11 (4-32)	0.9(0.21.2)	1000 (No. 2000)	81.4 (17.9-112.9)	2 (0.4)	0.1 (0.0 0.7)	230 (26 599)	10.3 (1.3-27.9)	W (14-200)	64 (83 63)	100 (330 (170)	38.3 (33.3-79.7)	20 (2:N)	0.1 (0.0.0.2)	1890 (291-9090)	7.8 (1.0-20.4)	28 (13-82)	0.0 (0.0 0.1)	4280 (2180 12900)	84 (12 (8.1)	E(0-20)	03 (00.03)	1620 (187 0940)	09(82-23)	207 (83-995)	0.010.00.03	24800 (7710- 41400)	1.2 (0.0.3.8)	82 (8-142)	60 (6.060)	3280 (127-9730)	62 (86-63)
Shipshe spp.	Emission in one or more authorize	11 (4-28)	0.9(9.21.2)	1090 (364-2000)	81.4 (17.9-112.9)	2 (0.4)	0.1 (0.0 0.3)	230 (29-599)	10.5 (1.3-27.5)	W (14-200)	64 (83 63)	100 (1110 1170)	38.3 (33.8-79.7)	20 (2:84)	0.1 (0.0 0.2)	1880 (201-9090)	7.8 (1.0-20.4)	28 (23-82)	0.0 (0.0 0.1)	4780 (2780 12900)	84 (12 (8.1)	E(0-20)	03 (60-03)	1020 (187 0940)	09(8223)	207 (80-990)	0.010.00.03	24800 (7710- 41490)	1.2(0.03.0)	82 (8-142)	60 (8.060)	3280 (127-9730)	62 (80-63)
Stephylorocous serves	Pleropinion	1220 (806-1730)	60.0 (EL-0-89.0)	194000 (79300- 154000)	5385.4 (1798.0- 7980.1)	N (22-97)	27 (1248)	2960 (2130-8670)	203.0 (190.8) 423.9)	1020 (TK3 1330)	41 (12/84)	10000) 10000 (4820)	396.3 (281.0- 478.8)	46 (29 7%)	02(0103)	4130 (1820-4930)	16.6 (7.6-26.6)	402 (209.50%)	0.4 (0.3 0.3)	39100-(28900 49000)	38.8 (22.4-42.7)	18 (8-32)	03 (00.03)	1600 (724 2790)	14 (9.6-24)	1800 (1720) 20700)	2.9 (1.8 4.4)	119000 (K22000- 2090000)	68.9 (49.7 (69.4)	2630 (1120-2710)	0.1(0.10.2)	99400 (29300 109000)	29 (1.2-54)
Stephylarocens owner	Marriale	1800 (1270-2910)	88.2 (62.0 123.1)	140000 (113000- 224000)	7973.1 (RNAS.1- 13008.9)	72 (28-129)	33 (1464)	6990 (2400 11300)	314.1 (120.4c 367.1)	DENO (1440-2360)	24 (88/93)	147000 (127000- 201000)	6/8.1 (906/0- 821.8)	71 (39 129)	0.7(0.1-0.3)	4990 (2700-11300)	26.7 (20.9-20.9)	487 (482-994)	0.0 (0.4 0.3)	97900-(422000 787000)	88.4 (87.1 4910)	26 (10-17)	03 (00.03)	2310 (921 4090)	20 (88-34)	121000 (79900- 181000)	6.1 (5.9/9.1)	272000 (1490000- 4170000)	134.5 (87.6-206.5)	2990 (1770/9770)	62(8163)	110000 (19200- 217000)	8.8 (8.8-30.8)
Suphylanosan	Methodia	2970 (1830-3688)	1264 (88.7 177.2)	224000 (144000 324000)	11366.2 (7911.0- 19783.0)	704 (140-1290)	36.7 (16.7 (60.3)	62900 (30300- 109000)	3091.2 (1097.6- 3366.7)	2110 (1490-2480)	83 (67 (63)	187000 (144000- 277000)	797.1 (391.4- 940.0)	976 (272-499)	23(1138)	50000 (24000- 82700)	2014 (97.3.0310)	877 (642-1180)	0.8 (0.0 1.0)	76200 (M/000 207000)	47.0 (28.3-90.1)	262 (119-662)	02 (01 02)	20900 (10000- 34700)	18.4 (8.8-30.4)	15000 (MR00- 15000)	8.1 (8.8.7.8)	2290000 (1440000 3440000)	113.6 (72.8 171.4)	27000 (11400- 28000)	13(842.0)	607000 (299000- 1090000)	30.1 (12.8 56.0)
Stephylorocous serves	Trimelopine Sallamelomande	430 (229-844)	300 (20 9-42.8)	5£800 (37900) 79300)	2689.1 (1878.2) 3780.4)	97 (29-90)	28 (1.044)	1000 (2110-X2MI)	290.8 (129.2) 409.0)	224 (339 A34)	17 (13-22)	77600 (21000 27000)	192.1 (118.0- 192.1)	39 (21 44)	02(0102)	3470 (3890-3370)	14.1 (7.9-21.7)	179 (139-247)	0.2 (0.1 0.2)	18900-(11300 21400)	13.6 (18.0-18.8)	17 (8:26)	03 (00.03)	1410 (728 2280)	13 (84-20)	17000 (11400- 29000)	0.9 (0.6 1.2)	400000 (294000 992000)	19.8 (12.8-29.3)	1940 (774-2940)	0.1 (0.0 0.1)	38300 (17900 38600)	17 (0.9-29)
Stephylorocous serves	Yanconysis	N4 (27:70)	24(1837)	2800 (1000-4800)	235.7 (361.8- 335.8)	16 (8-28)	0.8 (0.0 1.4)	1200 (917-2300)	66.9 (34.2 (22.8)	at (34.9%)	62 (81 62)	7900 (2980 5270)	18.9 (12.1-21.3)	13 (7-22)	0.1 (0.0 0.1)	1190 (464-0900)	47 (2.8 80)	DE (E3-29)	0.0 (0.0 0.0)	DMD (1100-2100)	14 (10 19)	3 (3.4)	03 (00.03)	490 (207-791)	04 (9.2-07)	2470 (1710-2000)	0.1 (0.1 0.2)	41300 (99000- 93300)	3.0(2.9.4.4)	797 (783 146)	60(5061)	33000) 18300 (8690-	69 (0.4-1.7)
Stephylorocous serves	Emission in one or more authorize	1800 (2120-4720)	167.1 (118.7: 231.8)	303000 (213000- 423000)	1489.1 (1997).5 2066.1)	907 (909-1460)	44.8 (24.8-71.8)	80780 (20100- 130880)	7966.3 (2213.8- 6766.2)	2940 (2330-3300)	11.9 (9.4-19.0)	240000 (201000- 320000)	1003.9 (837.0- 1328.9)	729 (429-1149)	38(1744)	66400 (19000) 100000)	268.7 (183.9- 206.8)	1170-077-1940)	1.0 (0.8 1.4)	12080) 10080 (2830)	WA (478-1179)	308 (170-292)	63 (61 64)	24700 (1.8900- 42900)	233 (33.1-87.4)	1 Nation (182000- 229000)	7.7 (8.0-11.3)	3280000 (2220000- 3220000)	173.1 (110.8- 289.9)	37000 (29700- 61800)	18(1030)	X70000 (271000- 1790000)	41.1 (21.4-68.9)
Simplements presentate	Bris Laviere Bris Incomer Middison	732 (296-1090)	36.0 (24.5-55.1)	44200 (11200)	3306.1 (2177.9- 4790.9)	17 (9-45)	0.9 (0.0 2.3)	1949 (27-4149)	75.6 (1.3-203.6)	2070 (1430-2440)	84 (63-007)	28000) 16000 (14000	743.2 (977.8- 993.0)	48 (1-120)	02(0003)	4230 (66 10900)	17.1 (0.3-44.3)	712 (839-942)	0.0 (0.3 0.3)	61700 (20000 87200)	NL2 (89.4-79.2)	38 (0.49)	03 (00.03)	1920 (29-3686)	13 (88-34)	22700 (11400 3200)	1.1 (0.8 1.4)	219000 (172000 718000)	28.5 (16.4-35.5)	339 (4-983)	60 (5.060)	7920 (127-21900)	0.000011)
Simplements presentate	Carlopeness	1000 (702 1920)	91.9 (NLS-7LT)	13900) 13900)	0679.3 (3071.6: 6672.3)	231 (389-412)	11.4 (8.1-20.2)	20400 (12000- 36700)	201.6 (201.8) 201.6)	2990 (2390-3720)	12.1 (9.8 (9.1)	249000 (200000- 330000)	1871.7 (842.0- 1394.1)	629 (309-2300)	24(1244)	57800 (27800- 97000)	212.6 (119.7) 312.7)	979 (727-1289)	0.9 (0.6-0.1)	87000-(47700 112000)	76.7 (89.4-98.0)	218 (992-979)	62 (61 63)	12700 (8900- 32700)	164 (7.8-28.4)	39700 (28700 34700)	2.0 (1.4-2.9)	8542000 (4000000 12200005)	42.5 (39.1 40.4)	X100 (7920-1908)	0.1(0.207)	189000 (04200- 329000)	92 (83 (61)
Simplements presentate	Pleropinion	287 (180-017)	13.9 (6.0-20.3)	29300 (14300) 36800)	12% 9 (802.6- 1806.0)	28 (8-79)	17 (04.57)	3080 (992-6690)	191.8 (34.0-327.0)	499 (132-904)	28 (22-37)	42900 27000 30000)	290.4 (190.2- 323.8)	82 (19.174)	0.5(0.1-0.7)	7430 (1680-1538)	30.0 (6.8 42.4)	292 (189 349)	0.2 (0.2 0.3)	21800 (11800 29000)	19.2 (13.9-28.9)	31 (7:64)	03 (00.01)	2670 (636-5342)	23 (84-49)	1560 (2760-K100)	0.1(0.2-0.4)	128000 (87000 183000)	63(4393)	401 (140 1730)	60 (5061)	14990 (1040- 30300)	67 (0.2-1.3)
Steptomore processories	Marriale	2190 (1490-3090)	1083 (71.3 1469)	193000 (130000- 270000)	9201.2 (6786-0- 17267-0)	81 (0.210)	40/00/04	7240 (9-19100)	38.8 (0.8-97.3)	4290 (1230-1199)	29.3 (21.1-39.3)	357000 (242000- 666000)	2220.9 (1369.8) 2696.4)	270 (9.892)	10(0024)	21 800 (0-82200)	89.9 (800-211.9)	2020 (1990-2990)	1.8 (1.4-2.3)	176000 (170000- 225000)	194.4 (121.5- 297.4)	27 (0.297)	61 (60-62)	6600 (O 17000)	3.8 (8.0-14.9)	82900 (40800 114000)	4.1 (5.0-5.7)	1770000 (1270000- 2440000)	87.7 (62.7 (21.7)	370 (3.860)	62(8.06.0)	67000 (9.18)0000)) 33(00-51)
Steptomore processories	Periodia	1470 (909-2140)	72.0 (86.6 207.1)	11000 (8400- 11000)	6113.1 (1133.5- 9367.9)	K2 (89 109)	40(2073)	7910 (TNO 11200)	391 (179.0- 627.1)	3970 (3080-2970)	16.1 (12.9-29.1)	35000 (27000- 44000)	1423.7 (1809.2) 1779.8)	219 (111-399)	0.9 (0.0 1.9)	31,200) 14000 (4830	77.0 (79.8 129.5)	1140 (990-1770)	1.2 (0.9 1.4)	114000 (M000)	101.8 (79.6-119.2	79 (17-120)	01 (00 01)	4390 (3190 10000)	34(28/94)	4700 (30300 47000)	2.2(1.8.9.1)	497000 (MAXIOO 1790000)	47.4 (12.7 (8.8)	1410 (817 3360)	0.1 (0.0 0.2)	41300 (19600 79300)	21 (1.0-39)
Simplements presentate	Third premation explosion position	Net (379-841)	288 (38.4-0.3)	90700 (13400- TUND)	2289.0 (3400.9 3678.3)	27 (11-87)	13 (03 28)	2239 (992-9980)	129.1 (44.9-248.4)	1290 (1130-2900)	59 (84:57)	12000 (10000- 14000)	529.5 (206.6- 680.7)	61 (29-119)	02(0103)	8970 (2090-1020E)	21.7(89-41.1)	F14 (TR2-711)	0.3 (0.3 0.4)	41700 (19100 61400)	39.3 (29.1-940)	29 (30-30)	03 (00.03)	2170 (879-4290)	19 (8.8-3.8)	1900 (11200 2200)	0.8 (0.6-1.1)	315000 (204000 307000)	17.6 (12.2-28.1)	ate (197.836)	60 (5.060)	20100) 20100)	63 (0.2 L0)
Stephanous promiser	Trimelopies Salismelonanie	3280 (2230-4360)	368.0-(308.7- 228.2)	293000 (197000- 404000)	14199.4 (9682.0 19967.9)	299 (82-612)	14.8 (2.0.901)	34289 (1900- 14489)	SHELD) ESHED (SHE'S)	EEO (MAD 1979)	32.8 (27.0-49.8)	717000 (109000- X71000)	2901.9 (2390.0 3351.9)	704 (100-1410)	2.8(0.0.8.7)	62200 (0000 128000)	292.0 (39.8/664.1)	2890 (2200-3900)	2.8 (3.9 (3.3)	227000 (193000- 32000)	207.4 (168.0- 201.4)	282 (56-504)	02 (00 03)	21800 (1800- 64800)	191 (27-39.8)	7800 (7700 10000)	3.9 (2.9.5.4)	174000 (120000- 247000)	87.1 (69.2 (20.2)	4330 (924-13200)	0.3 (0.0 0.7)	143000 (21200- 290000)	7.0 (1.0-14.4)
Stoptomous prosentiae	Resistance in one or more artificials	7900 (2660 5430)	1923 (1388- 2669)	329000 (277000- 464000)	17139.4 (11694.4 23798.9)	269 (266-1190)	37.8 (22.9 (64.0)	68200 (21900) 312000)	2962.1 (2036.2- 2026.9)	MAIO (KTIR: 13000)	40.1 (01.0-18.4)	394000 (744000- 1940000)	3978.2 (3083.6 4299.3)	2000 (1419-2700)	X1(X7100)	177000 (127000 279000)	714.0 (NOL9: 966.9)	3180 (2710-4290)	31(2439)	300000 (234000-	261 (2812- 361.5)	et (345-977)	04 (04-09)	31800 (20800-	32.5 (38.5-74.0)	100000 (79400- 140000)	8.1 (8.57.6)	2270000 (1690000- 3120000)	113.2 (82.0-184.7)	21400 (17900- 30700)	1.1 (8.7-1.9)	44900 (10900- 67400)	28.2 (18.1-18.4)

Table S20. Deaths	and DALYs (in counts a	nd ago-specific rates) associ	red with and arteri	tetable to bacterial	antimicrobial re-	sistance by patho	gra-drug combi	nation, by ago grow	p. 2019, sub-Sub	aran Africa															
Pologra	Ambiesis Class	Accer Directo Creasis Bair per 100	risted with emissioner	DALW		Android Drafts	No to entirioner	DADA		Accessisted males Eater per 100-000		Pant N Balay per 180-200	Created D	Andreal Inde	ENLY: Create Bale per 1001000	Counts	Associated builts Bair per 18-00	I with strike and Table Strike	Desir Desir	Antibushi la Lair per 200000	DACN. Counts Note per 201-000	Deales Count. Entryre 100 000	d with evaluation (DALN). Cleanin Eater per (10000)	Andrew Drudes Create: Retryper 200 %	EMAYs DIALYs Consein Extr per 100 000
All palesgran	Resistance to one or more architectus	27980 (2608) 9831 (1295 3680) 18817)	240000 (1840 (200000)	1000 MARINE DISCORDE	- companies	2523 (1665) 2663)	798000 (21,0000 798000)	20/763-(10/012) 25/28/9	140000(124000. 200000)	PR3 (TRLK-077.1)	1420000 (100000 1420000)	8 4009/32509 8407)	NAME (27100-2010)	1134(963.04.1)	(2800) (2800) 109(14/24).4	12480 (4100 1410)	967(9534278)	1980000 (8800000. X7933 (6177-0. 1480000) 12074-0.	2000 (2020 3890)	ISB (354.268)	209000(178000 9923(1783 37900) 27946		1670000 (1700000 1870.2) (270.4) 280000 280.4)		12 mm (24000). 250+(26.5-66.2)
Arismotore Isomonii Arismotore Isomonii	Anteposite Antepositement residu Seu Latanae	296(200.00) 179(013 826(00.120) 869(203.										20.0 (MA. (12.7)			NIM (L160) 109 (0.33L2) SUM (0.000.5200) 999 (52.1754)			7960 (2700 17900) 601 (344975) 17600 (3000 2000) 1849 (768.222.5)					2008 (22000 417 (317 491) 8000) 417 (317 491) 8100 (3200) 918 (311 512 4)		2000 (1000 120(0.1202)
de inemitiente Française	Sets Lanton Sets Sets Lanton Sets Setsman Military	NPR(1785.789) 3616(121.7)				62,6163)	40,124,199					#10 (M.2484)			27(0.62) 07(0.217)			HERRINGS TOLINGS			19029 61660	2800(2398.1980) 23(6.430)	9200 (1900) 664 (N2419) 9700)		NR(28.180) 01(00.02)
de inervitue nor Incommenti	Carlogressen	3436(2340-9996) 0343(91.417										200(000400) 201(002400)			Mater (MCTH.2000) 151 (247-001)							1890(969022380) 14:69-24)	9398 (2986 419 (293.642) 9698)		6A60 (3300. 72(33.04) 1990)
Arismolarne Instanti Arismolarne Instanti	Florespierieses Frontis praemine contributorosies	acto(000.490) 1667(160.5 800(100.500) 1664(100.5				222 (ELA M2) 62 (6664)		167 (5 8 54.7)				#6.1 (P0.2 4864) #8.7 (P0.8 4865)			THE (THE DOES)			\$200,0700 204(H1110) 10000,0700 764(H1110)			40(0.28) 61(0.02) 1200(120.280) 41(14.14)	2000(1700-2700) 21(13.33) 2000(1800-3100) 22(13.34)	N2000 (20000) NA4 (228 A23) NA000 (20000) NA3 (348 A04) A23000 (20000) NA3 (348 A04)		17500) 7.6(17.024) 88(38.380) 01(00.02)
Actionalisation Parameters	Third generation orphologosius	eare (2000 NOTE) 2000 (2004)	a.1, /7900/9000 84000	2006.5 (2006.5 30626.2)	46 (36.136)	1469440	NEW (22% 11286)	211.1(42.6487.1)	200-(230-)270)	68(6289)	28000 (27000. 28000)	874(997854)	28(11.89)		200(000.000) 77(1181)			10000/3000 HELI (NEL 1003) 20000)			199(90209) 11(6423)	2000-04200-0430-04-04-0-0	7600 (2700) 765 (275 (204)		1000(EDE)200(11(65.21)
Actionalise con Incompanie	Resistance in one or more analysis in	200(000.000) 10-2(220. 200(00.000) 20-01246													THE (LEEK 2001) (TAXABLE) (1998)			2000(2000) 100(010202) 2000(1000(1000) 114(0220)					12300 (1600 MILO (655 MIL) 2000 (1600 600) 3.1 (165 MI		279000 (47500) 3040 (773-474) 48000)
Citabaser app.	Antophonian Antopondomenal postalin Bria Latanace	50(010128) 364(0124 50(011108) 364(0124													200(2000) 14(6200) 200(2000) 14(6200)			2980 (82831798) 114 (4.224.8) 2990 (8890-11286) 147 (7.731.8)					2000(1000-0000) 3.1(1.8.5.1) 2000(2200-0000) 4.5(1.4.5.2)		120(0300) 02(0340) 620(2001230) 02(0312)
Citalwar spp.	Carlogoraera	413 (216473) HO(64244		100.0 (NA.0 2170.0)	B-(41.00)	32(5489)	7070-7070-14000	26.3(294.69.3)	146/70.2909	64(6288)	1268 (170-2800)	97(9832)	31 (13.40)	0.1 (0.0.02)	ZWGCNING KIGAZA	122 (68.286)	01(0002)	1000 (250 250) X0 (A.IX.I)	26 (1879)		279(98479) 17(67.54)	KP-(NEW) 61 (6861)	MANAGEMENT (A)1624)	111(11.20) 00(00.00)	329(9096249) 0.0(9.247)
Citebaser upp.	Florespieriese														200 (200 420) 112 (12 52 50) 200 (200 420) 124 (12 52 5)			2280(00002000) 204(112413)			2000,0000-000) 22,000.00 2700,0300.7000 28,000.00		2900(2000/2000) 47(2333) 6200(2000) 26(24314)	189(81.90) 60 (80.80)	MMCGERIUM, GASSIES
Citabaser up.	replainquein This gravation replainquein	melinima avinori													SERVICION TRUSTER			ACRE (DESIGNATION) TO A (ALL ALL A)			100/71/00 13/6125		2000) AUGUSTAN 27000) KAJARIAN	111(8122) 00(9000)	200 (200 at 0) 0.02.07)
Citabaser app.	Resistance to one or more artification	200(270.700) 764(63.22					F100-(\$200-100)					200 (062 (701)			2000 (1500 2000) 627 (293 123 0)			MBD (2700-1000) 36.7(17.870.0)			1200(0002900) 114(15.234)	280(736-835) 63 (62-65)	1000) 48(44143) 820(1000 48(44143)	KLITMETAND - 61-(61-6-2)	2689 (2889-2680) 29(3.8.82)
Entroheser up.	Antiposites Antipositement position for a Lantaneo	NING (1980-1980) 20-7 (1980-1 NING (1980-1980) 20-8 (1284-1													(NE)(2962)NE) 212(6363)			9980 (COS 76.7)(CA1136) 19880 (COS 76.0) 7380 (COS 76.0)					2008 (15100 265 (173.965) 2008 (15100 220 (143.726)		1880 (500-2000) 1.0 (4.24)
Enteroheror app.	inhibition Codeposess	2001/12/2003 767/51800													KINGINGAN, DEGLESIA			2200-2000-2000) 247-(31477-4)					MANUFACTURE STREET, ST		(1800/96802000) 19(11-11)
Enterobacter app.	Pleanquiscian	200/00.000 200/H.S.													1200(70003000) 278(221773)			17500/7500 917(N.3.1%4) 17600)				1000/97811780 11:67.140	2700 (Fellin 124 (312-677) (1900)		2900 (1400-1400) 31(14A)
Emmhaner opp. Emmhaner opp.	Frank promise orphilospoie. Trianthopsis Salisanthopsis	2000 (700 2000) 307 (2754) 2000 (700 2200) 307 (244)						2987-(1074 2887-(1074							1886(1752986) 841(233793) 526(63986) 287(63405)			20000 (10000 1264 (197.1862) 20000 (19000 1262 (198.1762) 214400 1262 (198.1762)				1800/90022000) 14(1123) 1800/97202000) 14(1123)	2000 (2000) 400 (800.00.2) 2200 (27000 4700) 477 (813.663)		2010 (1480 N 201) 3.5(4.64) 2010 (1420) 22(0.47)
Entrohester app.	Resistance to one or more artificials	2790/909-2790) #24/3004				IRI (SARORA)	209000-(242000) 209000)	97917 (49612) 142912)							438(978.980) 192(IZ1426.3			29600 (2000) 26000)				1800-(1200-2000) 2.6-(1.129)	(2000 (1000) No. (364.834)	CROMINI MINIST	(2400)(NON. 134(K3214)
Enterconcus facults	Photopinsinos	PROCESSORS 2012(1423)				11.01.01.01.00						B 1841 (858227.5)			1790(419.2000) 362(449.623)			3990 (3000 6900) 268 (314 NO.);			4200(360010000) 21(20110)	1860-927617080) 1.2-pl.7.14)	9900 (2000) NA (223-62)		2000 (0000) 94(42.074)
Emmourou jasulis Emmourou jasulis		TRO(TERM) DES (64.20.)						2010 (2010) 2010 (2010)							82(M170) 24(1144) 290(621200) 391(9040)			200 (200 400) 14 (44.0) 2000 (2000 4000) 362 (14.0)			65(25150) 65(6312) 1000(250100) 75(5110)		2900(1390.0000) 2.0(1.0.1.2) 2000(27900 200(27.01.2)		620 (290 (200) 07 (0.3 LQ 1000 (200) 10.3 (2.3 LQ 1000)
Emmouverjacium		DESCRIPTION INTERNAL	Lin 20000 (14000 2000)	1081.4 (NTSA. 1138.41)	67 (86 186)	228 (45.423)			420-(192.2000)	18(1.1.2)	ANDREAST COMPANY	0.1107.23636	130(34.287)	0.0 (0.00)	BH0(NH2750) 314(N4755)	NU CREATING	04/02/03	400 (370 H0) N1(117 H)	201/202004				2008 (2008) 278 (347.814)		
Entracaccas faction Entracaccas faction	Vancospole Residence to one or more	200 (1381-270) 261 (187)(1881						9 413/9151024 24251783				#4(817.525) 1523/9612863			270 (180418) 191 (18208) 1980 (280200) 272 (198814)			1380(801208) 12(8107) 4800(82001000) 172(81083)			2600,0000,0000 22,600,400 12200,0000,20000 93,(33,194)	1800/7902000 64:62.000 1800/77022000 14:62.27)	2008 (7908 11.0 (43.314) 2008) 11.0 (43.314) 2008 (2008 2008 21.0 (44.17)		2000 (1000 AND) 27 (3.143) 18000 (4000 120 (4.223)
Other minmussi	ambinion Pleanquisciano	2000/2003/000 ET2(TE2													NACOSAN DIGADA			2780 (2780 (1880) 214 (1823) (18					Taken March 124 (17.04)		2000(730-000) 24(4.55)
Other mineracci	Yancospin	PR(117.80) 71(63.118)													40 (81.48) 13(6424)						260,017460) 62,61465		#80(23011W) 68(6512)		190 (90 290) 02(0107)
Other reterminal Endersida cell	Resistance to one or more antibiotics	2000/2000/000 274/7723 1400/900/2000 5007/9124					6200 (2700 12900) 7200 (2700	23300 (2013) 2014) 2013 (2013)				9 ISLA (67.739A) IMC7(1967. 217A)			200 (200 (200) 25 (5 4 5 5) 200 (200 (200) 1127 (25 4 4 5 5)			2780(2780/280) 214(912/9) 51200(2780) 342(2812/9)			NON-1980-1280) 43-584-10 2940-12800-1280) 22-514-128)	200(200790) 67 (63.68) 2000(3006.000) 27 (63.33)	11200 (7000) 123 (77.000) 11200) 123 (77.000) 10000 (70000) 75.4 (67.000)		ZHANGKARANIN ZAGAAZI
Endertida cell		27780-(24900-24986) 10722-(479-4													MINI (2002-2004) 301 (92-967)			73000) 2023 (PL) 170000 (90000 2023 (PL) 190000 10004				MRK-(178-1688) 7.1 (1.417)			2000 (2000 2000) 11(2142)
Endertida cell	Bris Lastano Bris. Instantoro infektione	2000 (2000-1148) 2001 (731-4		m. YEAR (MIRE)											ATTROCHMENTON TOTAL (N. L. PALE)						писсиния этрына		273000 (240000) 176 0 (274 276 2		NRM (PORE-7000) 42(LSA7)
Endertida sell Endertida sell	Catagorea	200(290.620) M18(80X)		3067.6) 66. 1903.6(100.6.			7900 (2000 17000) 19000 (2900)					MARCON I			2010 (2010 6400) 1210 (410 2010) 9000 (4200 2010 (410 427.0) 17500)			2000) U12(T1.00.0) 2000) U12(T1.00.0)			TOROGRAMMO MATCHARDO TOROGRAMMO MATCHARDO	700(00000) 68(641) 2000(2000/180) 41(124)	2900 (2000) 2000) 2000 (2000) 2000 (2000) 2000 (2000)		2880 (2880 7380) 49 (27.78) 12880 (7880 122)(4340)
Endertable will	Third gramming orghologonies	2000/000020003 877/943	January .				27880) 20800-00880 27880)		11400-(9070-1440)	314(210.00)	200800 (TUNO. 143800)	388.8(228.1 489.0	150 (73.290)	43 (1842)	22000 (1200. 25000) 56.2 (199.3713.6)	120 (27) 1200)		2000,5000 400 (00.400.00.2 2000)				DESCRIPTION AZGLAS	17980 (RAME) 17980 (RAME) 17980)		12000 (270). 16 ((4.24)) 20000
Endertakia seli	Triantingsins Sullinerkonande	508-(2000-2008) 1754-1762-8 308-3)										800,0766.3 607.3			1000 (000 DECK (000 6.224.0)			1270000 (MUNION) 90K4 (MUNION 1420)			7100(0400 NJ (81462)	6000-UT38-8080) 18 (4.2.4.2)	213 (274262) 27366)		124(64174) 10380)
Endershie ook	Resistance to one or more architects. Manufale	2000 (2000 ANNE) 2017) 2000 (2000 ANNE) 2017 (2000 ANNE)				TELEGRAPHICS TRIPOLITY		STARROTTAN				1000 (100 (100 (100 (100 (100 (100 (100			ACMINI (1900) 1760 / 518 7 (1900) 1780) 170 (1903)			20000/00000 2014/0143. 200000 2004/000 201/00/313)			200(0200) 2018(201422) 200(020) 19(0843)	7200(27004000) 74(54304) 290(200870) 67(6160)	20000 (2000) 29.1 (29.1374) 2000(200) 85(44385)		7000 (7000 H3(0040) 7000 (7000 H3(0040)
George A. Empressa van							100 (0.2000)	XTR/RESTAN	496 (776 770)	14(6923)	ATTRICUMENTS	017/758499.0	41(0.170)	0.0 (0.0 (0.0)	366 p. 1280) 120 (94.9K)			2001/2002/000 201/00375				290(340.975) 63 (61.64)	7600 (2000 8.7) (4.6) (7.7)	327(6-927) 60(60-8.1)	760(62780) 66(6630)
Group Edingstoneous		2280 (1880-2628) 467 (1873) 2280 (1880-2688) 851 (1860-													###(###1###) 1741(#41700)								3000 (79000 367 (31.575) 3000 (7000 417 (31.644)		standowness nelsonal
George E.Droptococcus	Probilin	2200/0000000 011/0000 20/001090 212/00179													300(0.000) 104(0.000) 201(01.00) 80(1.174)			180 (81.01) 180 (80.100) To(A.01)				70-20-100 12-0-10 70-20-100 10-0-10	DECOMPTED LABOUR	71(3139) 60(6044)	200(00A20) 0.1(0.144)
George E. Drogeton consum	Resistance to one or more antibiotics	2000/2000/2000/ 1006/07/4							100-100-2303	19.2 (139.264)	A2380 (NYSSE 18980)	296.0/238.3 296.0	209 (29.298)	33 (69.44)	1000/2750 2017(N+1014) 21000								MANN (1868) HA (CA 723)	200(90.00) 67(61.65)	2000 (2300 X1(24364)
Manuphile inflame.		2000/2004 101/2401					2900-(2300-5200 2900-(2200-5200	9 1801 (182 2839 1802 (889				ATT-CON-LINETO			2000(2000/000) 1224(20.203) 3220(2000/000) 1022(81.002)						2000(10004200) 201(0.5.0.1)		17500 (1750) 11200) 2000(7200-2000) 440(345.1)	201(26/MZ) 62 (60.63)	(760 (760.3760) 17(0.2.17)
Austraphile inflame		300(290.000) 124(51.01)					67800 (31800) 128000)					HOLOUGH HOLO			740(100 200(83.00)			29000 (10000 29000 (10000 29000)			PERCONSTRUCT (\$1,07374)	360(370-660) 6163-60	1000(1000 141(14174)		2900 (1200-2000) 10(12.00)
Elebriolis procumento		2300 (1800,000) 16267 (187. 229.0)										D88(7942 8953			CHINE CLEAN TOUR CHILANAL OF						1000/0000 (6.5 (E.3.105.5)	XTXX0-(00400-70400) X.R.(E.A.730)	343000 (234000. 273000) 276.8 (28.9 2)7.7		12000(7300. 120(63165)
Elebricke presentation		5240 (7600 7340) 2941 S) 600 (340 1300) 204 S (237)					61.800/2000/9870 17800/97200								2900 (200-4800) 800 (200-100) 2000 (2000) 1700 (84-2040) 1480)								23000 (20000) 2414 (94.5.223) 24000 (12000 244 (95.4.42)		NUMERON AND ADDRESS
Kirbirla promonio	Florespiecies	EVEN (1000-1100) 2000)					20600 (17600 32600)		PR00(1230-2400	Majasa Naj	108800 (17500) 218800)	ESPRIMEN ETES	1340 (489,1780)	34(21.88)	SCHOOL TANK TANK TOWN			120000/900000 9773/908.4.103.			7600(1890) 864(513414)	2000-posts 7000) 1.8 (LAT?)			20000 (4750) 15 (475144)
Elebriolis procumento		2000 (1000.000) 20127 (1027.										ESTAGETO EST.)			20100 (CDED 7004 (STALING			200000 (200000 12122 (001A 200000) 12722)			17900-(8000 3000) 1944 (817.2004)	M200 (R200 M200) 7.2 (F.F.R.T)	20000 (20000 287 (87 8 24 3 26000)		2000 (WKA 274 (WKA 2)
Elebriola provenenio	Trianshopsin Salkinnshonande	NAME (4800 7000) 2014 (1815 PORE (4800 7000) 2014 (1815		200400 200400 00. 200423/200400				(2004) (2004) (2004) (2004)				6687/0367. 8903) 7907/6963. 9909			9000 (2300 3067 (427.4494) 17300 3067 (427.4494) 44000 (2300 3067 (3311.4			100000 (100000 17012) 170000 (100000 10074 (901.1. 170000) 100000 10074 (901.1.			71000 (1000) N.3 (MANAS) 12000 (1000) 2714 (2021 2009) 72000 (2008 (8880 267 (864 552 2008) 2008 (8880 264 552 562 562 568 2008)		(7000) 11.2(6.100) 67000(47000 72.0(67.1001)
Morganilla spp.	Pleanquiscians	193) 00(0003)	18 (44.30)	47(14.803)	***	00/0000)	19 (4.00)	67 (63.14)			294 (429-701)	00/00/14	1 (9.1)		#(K80) 02(6163)		00/00/03	28(19.86) 02(01.04)	0(0.0)	10/0000)	20(2.00) 00(00.00)	197(121) 66(666)	DR(180/180) 64/6264)	27 (6.47) 00 (00.60)	EN (201.000) 01(0001)
Moquentle upp	Frank-promise orphilospoise Third-promise	192) 00(0001)	49 (14.217)	34(1376)	49.0	00/0000)	2(64)	61,0863)				67(6413) 63(6163)		00 (00 80)	N(1091) 02(0002)			75(5.8%) 616163)	49.0	10/0000)	11 (AM) 00 (MAG)	90(C.00) 60(6560) 41(C.40) 60(6560)	240(130300) 63(6164)	14 (4.76) 00 (00.60)	49(17.90) 00(004)
Moqueola sp.	orgholospories Erololospories in one or more arotholospories	2(14) 01(0003)	10 (8.7%)	87(22488)	***	00/0000)	27,5349	13 (68.13)	42.6			12(6423)		00,0000	William animan			29(2342) 62(6165)	100	10/0000)	Name of Street		28(38679) 61(363)	11 (9175) 80 (9084)	W(CLTR) 01(0142)
Mysotherinian referenciasis	Dates along strict sour in TR		160	00(0000)			0,000	60 (06.00)	17(7.84)			47 (1853)		00(00.62)	911(NO.180) 28(1167)			100(98.300) 12(68.24)	10 (4.22)		901(796388) 67(63.14)	78(12.40) 66(660)	(900)(628-2900) 1.6 (642.6)	207 (07.40) 00 (00.00)	779 (2001/00) 08(0117)
Mysolumeniae rationalistis Mysolumeniae	Statistical mean emissioner Makisleng emissioner		1910	00,0000				******	612 (175 mag)	19(1229)	74300 (33400.84000 120000 (244000.	277.000.000.00	47(0.10) 78(0) (780)	27,0220	#89 (6.2948) 247 (6.694.4) #89 (7.994.1988) 2627 (2.1.481.1)	709 (423 1130)	010105	11400/2000 R11(T11402)		11/0003)	980 (0.3900) Ta (0.0201)	1200/820/1200 136414)	42000 (2000) 120 (30 7.24) 42000 (2000) 120 (30 7.24)	HE(049) 42(045)	7800 (0.2000) X1 (0.0300)
Mysoluminia Mysoluminia referencias	Elimpia man- minar		160	60(5000)				44 (64 64)	PR(123.30)	*****	23000) 1780 (3000-2750	1000000	11(0.120)	02/00840	are post soon 152 (2.5.11%)	210 (120.00)	92(9143)	22000) 2000-)2000-2000; 147(9-122-9)	m (miles)	10(0001)	520(96.1386) 40(67.84)	200(200700) 67,63.000	25000 (10000 (10000 (1000) (100) (100)	179(94290) 61(6063	See Carrier volumes
Mysodostorium radiovalistis	Resistance to one or more architects		163	00(0003)			0 (0.0)	44,0440)	2070-1230-3330)						7600 (1000) 2072 (10.3.091.2) 27500)			20000(17900) 2000()			MMEC/1800. GLE/CLAIPING	AND DIRECTOR AND AND AND	36000 (87000 30.4 (87.62%)		(2000) (1900) 76.7 (94.5 (95.2)
Reineria generilana	Florespiecies This generates																						279(4982799) 12(6717) 27(832) 60(6669)		2010(2012(20) 0.1(0.002)
Notaeria pararriana	Resistance to one or more analysis in								-							-							8700(600.0380) 1.2(63.10)		200 (29-200) 01(00.02)
Protour upp.															27(8/90) 13(6131)			778-(480-2000) 51-(51-01) 2780-(2200-2000) 57-(51-01-20-0)					9000(7988 7.5(4.511.5) 20000(15088 21.6(427.517)		201(12.401) 63(6867)
Proteon upp.	Antopolisille Pleanquisclass														MIGHAM INDAM			2200/02002000 47/49740			MEGRISS 049214		21.6 (27.317) 2700) 21.6 (27.317) 2700 (7000 11.3 (47.178) 2700)		margaren) 0.0(0.12) margarens 0.0(0.14)
Protess upp.	Third gramming orginal reporter	38(3858) IZ/SARZ	3800 (1000-2	700) 2004-2013. 270-2)	46 (20.14)	28 (67.8.1)	400 (160 1200)	288(67,492)	KT-(46.470)	63(6264)	7500 (4500-11400)	20(0434)	17(8.09)	02 (00.02)	100(231330) 44(1393)	72 (17.126)	01 (00 0.1)	cap(thouses) ascala)	10 (4.70)	10(0000)	1290/3002790 14/653.14)	1970 (1840 NYN) 62 (61 67)	630(2000.0000) 13(1340)	391(127.827) 60-(60.6.1)	1988 (1982) 489 12(0.423)
Proteon upp.	Trianshopsin Relianshopsin Resistance in one or more architects														98 (0.223) 30 (0.045) 479 (239.734) 154 (4.7.225)			2000/2000/2000; 161/67274) 2000/2000/2000; 161/683240;					2000 (2000) 262 (118.317) 2000 (1000) 266 (148.70)		680 (0.1880) 0.8 (0.0.17)
Paradomena armpinas	Antophonia														600 p.1000 212 pasts to			29000 127000 1444 (NY.3 PM.6					2000 (2000 12+(23+44)		NAME (6.20700) 0.0(0.0.2.1)
Paradomena arregiment	Anti-provinces of presidin Teta Lasteners tableton																				2600(22003730) (64(64343)		3600 (2000) 200 (361.064)		
Paradionenas arregimens Paradionenas arregimens	Catagorana														THE CHARGE STATES						2990(48903290) H4(23-244)		2908 (2008) 324 (212.02) 2208) 325 (2018.02) 2308 (2008.03) 427 (212.042)		5280 (3680-7360) 57(37.65) 6880 (3680-6880) 67(27.67)
Paralonese	Frantis praesains orphilospoins														THE (475-176) 242 (19-77)			25,000 18800 (2000 13,007 10,01 2,000)					1500 (2000 120 (200 (00))		ORIGINATING LOCALIS
Paradomena arregimen															2000 (CHRISTON TRACKLES)						1000/2002000 25/(5.27)		NAME (1938) 129 (183-774) 76600)		2000 (2000 A200) 21(12A0)
Paradomenae acregimus Zalmoniila Pantyylei	Resistance to come or more antibletion Floresquiencleurs		(H.4) 22000) 0(64)	60,00000 60,00000	aux,300.090) -		12000) 12000)			189(161-264) 60(1686)		276.0 276.0			Triang angular and Carrows at						1000) 713 (F1.1004) 1000) 713 (F1.1004)		7000 (42000 K24 (441.12) 200(401.000) 64 (411.1)		204(20-717) 2010) 20(4278) 21(0007)
Zalmonila Pantyphi	Multi-drug emissioner in Kalenmella Typiki and Panatrolia		160	00/00/00			***	44 (64.64)	0(0.0)	******	40.9	00 (0.00.0)	0.003	00/00/00	0(0.2) 00(0000)	1(215)	00/0000	AC(1911A) 016109)	183	10(0000)	mp34 69663	12(7.70) 60(60.00)	M20(777.29%) 61(666.3)	204 60,0004	(8(6421) 00(0300)
Zalmonila Pantyphi	Resistance to one or more antibiotics			00(0000) 21737(1900			0 (0.0) 9980 (7200					61 (6662)			7(112) 00(0003)								200(1901190) 65(6212)		88 (18:25%) 0.1 (0.0.6.7) 7988 (288)
Xelmentle Typhi Xelmentle Typhi	Florespierieum Multi-dreg emisteur in Kalemelle Typki and Restorie	000(300,000) 202(024: 1700(000,210) 87+(275													2009/2009 NATIONAL						2000 (2000 TANK) 25 (3.5 MA) (3.5 MA) (3.5 MA)		2008 (2008) 8/2 (04.1.762) 2008 (2008) 9/3 (642.00.0) 12008)		2000 (1.000) (1.000)
Asimonila Typis	Resistance to one or more architectus	1000 (00002000) 421(300)	(4.4) 25000)	6 ALMAT (12718-L NESS 2)	ZWIJICAN	200.0 (77.520%.0)	212000-12000- 712000)	MANUFACTOR W	1520-3890-7290)	18(13.062)	27600 (12600 27600)	MET (MEA 129-2)	N06(87.1120)	14(65.55)	470(NBND) 192(DADA)	NGS (303 MW)	41(2274)	2704 (1813-1813) 19000)	n me (100.2000)	17(0113)	77300 (12700) Mili (67.11524) 17900()	1500-0000-2000) 14-(-2.2%)	20000 (2000) 1010 (510.003) 2000)	200(96720 616164	19600/8000 (63/(63/2) 50000
Non-typhosidal Estimanulla Non-typhosidal															NAME OF TAXABLE						AND PARTIES AT \$1.07.117		2000(2000-2000) 24(1313) 2000(2000-2000) 24(1313)		CONCORNO MANTE
Non-typhesidd Xalmenella Xernetia syp.	ambients Ambreghonides														200 (MARIN) 119 (AND AND AND AND AND AND AND AND AND AND			2500 (2500 2000) 214 (25.35%)			600(00.000) 12(03.12) 170(0.00) 12(00.0)		2000(2000-2000) 2.6(12.63) 2000(4000) 11.6(72.178) 34000) 11.6(72.178)		400(01900) 07(0117) 000(01900) 07(0017)
Xerontia upp.		000(KIT-200) NE+(31784	() (SMR)(CMR)	2071.2(2096.6 1207.1)	20 (48 50)	209 (54 248)	20700-01200-2820	m estatestation of	DEC (104.70E)	64(6318)	1688 (1981 ZTHE)	81(8588)	27 (24-70)	0.1 (0.1 (0.2)	200000000000000000000000000000000000000	120 (40 27)	01(0003)	2000/030.0000) TH(50.023)	20(00.00)	10/0000	20%(62,02%) 14 (64.1.3)	120 (09.220) 82 (61.62)	###(\$P\$6.77%) \$1(1.17%)	30(19699) 60(604.0)	100(400040) 10(03.10)
Zerostie 1939. Zerostie 1939.															230(C0.200) 58(3.024) C00(C0.000) 58(3.024)								1990(758-2000) 1.6(64.23) 6990(7286-8000) 8.7(1.6.84)		
Zerostie upp.															THE (DELETE) 242 (AAPL)								2000 (1200-2000) 17 (144.0) 2000 (1000) 17.0 (144.27.6)		
Zerostie 1939.	Third grammation cophalinguoise	ana (200 400) 167 (3044)	27.1) 48000;21400 68000;	1278.1 (4741.2. 2309.8)	m/s 2%	82 (1 9 30 2)	1260 (840-200	9 4663 (1655 8877)	ATT (MIK MAI)	13(1828)	2798 (270m 80m)	1000,000,000.00	17(6.09)	02 (00.02)	200(03.876) 47(1497)	EN (31370)	07/02040	3070 (8090-8000) 3K1 (340-92.1)	10 (42%)	10/0000)	1100/212900 09/03.110		23000 (8700). 144 (42.232) 22000)		
Zeronie 1939. Zbigotke 1939.															2500 (875 2000) ALE(279 No.) 4000 (885 16000) 2127 (274 AAA)						0300(000,2700) 10.2 (4.7 Ma) 0300(000,2700) 10.8 (4.7 Ma)		2000 (1000 227 (442.92) 12000 (2000 121 (44.20)		2000 (2000 2000) 3.5 (2.14.5) 2000 (2010 2000) 2.6 (3.44)
Shipsle upp		01(0780) PERIOD	3800 pares 2	2786.0	90 (10 200)	33,0484)	NO (N. 2000)	2024(3157014)	1700-(1700-7240)	11.9(4.122.4)	12680 (13680 64680)	2000 0 (1660) 2000 0	TTI (M-30M)	24/6744)	#300 (#800 (#800) 2127 (27 ± N/LO)	279-120-790)	29(50.53)	27500()17000 2904 (9X1.902.2) 67500(36/8300	14(0117)	6780 (REG. 27800) R.B.(A.LULI)		2000 (2000). 121 (44-20)		2800 (SUB-PRIN) 24(6344)
Esquiples occur arrow	Pleanquiscians	120/08/88 (98) 297/HDA	(C.5) 98880 (C200	28817 (7140.1 3750.4)	80 (08.65)	114 (47, 847)	2000-1100-000	m; 477.3(479.106.2)	200-200-070)	SERVING PRO	AZDERO (MARRIO MARRIO)	296.0 296.0	PHT (81.325)	04/67.09	PHIR/PROMPS 112 (\$2.500)	2000-2200-24005	26(38.55)	2123 (28.6.86.4 2123 (28.6.86.4	0.00(6.09	1 (000.2)	1000(000,000) 10(18.15)	21700-(14600-27900) 2.3 (1.8.34)	1000 (2000) Tel (160 YES)	MICTELES 61 (60.63)	3600 (1100-1700) 24(12-17)

English communication	Marchie	1969 (19902)	M6.1 (817 to 742.9)	(7000-) (2000) (C000)	MML1 (7710.1. 4788.2)	NO (34-94)	H7(78364)	DCEC-21700-N230	1791 (78.4 3609)	HR0 (7640 E308)	314(235.484)	20000 yaasan. 110000)	2071/2004 2071/2004	327 (380-000)	11(68.19)	N700 (1700-1700)	907(03.1003)	7730 (1940 1090)	******	6/800 (2030) 1000)	H12(M73493)	201 (201-274)	62(6164)	21280/930-11300	E7(64NA)	2600-(120-2000) 43 (1432)	174000 (Charles 184000)	1800 (86.8 (709)	148 (99.258)	62(61.63)	4240 (1000 Y000)	440078
Expliple some accord	Mekicille	1210 (1000 2100)	NL1(MAR-687.5)	(2000) (PHOSE (7000)	47%1.8 (CDF% 2 623(F,0)	290(1393499)	1911/09/02/05/9	210001-(12000- 50700)	19097 (2019 a 19092)	HORE (M30.130M)	28.5(21.21.21)	NOTES (METERS)	200.0 (MTA)	2180 (802.7780)	44(27.03)	2000/NAN 2000	NL2 (27 X 2011))	7010 (200.470)	14(1875)	67800 (27800 84800)	4664 (TB.2-6818)	2000 part 2000	13(0.8.2.2)	142000 (FN000 201000)	BB(*(44.1.093.2)	закражаты этрлан	20000 (2000) 27000)	124/64/809	768 (320-1700)	09/04/15	28000 (16200) 20000)	26.1 (11.1 494)
Empliylar scores arrows	Trianshopsins Relianselscounde	20200 (14000 27200)	753.3 (1564-046.0)	18008-(15008- 32008)	68493.7 (27496.3. 38287.9)	200 (090 (270)	363 (84-191)	24000 (HHID) 24000)	ENGA (ROKA	11000/1990 17390)	467(866.634)	134800 (CY00) 173800)	366.2(272.9 276.9	1390 (711-2000)	42 (22 44)	(2000) (2000 (8400)	TER(MARTIN)	900(718-1700)	78 (88 882)	#0000,927000. 2200003	491.9 (271.8 981.4)	200 712 790)	08(0412)	2790 (M00) 13600)	62(03)004	2000/900044000) 14/4370)	(12000 (11000) 20000)	1662 (0762992)	1240 (2400-1240)	00/03/09	19000/01400 20000)	17493274
Suphylanacus across	Yancospole	am(UTAIT)	16.7 (51.923.2)	2000 (PHOD NOTE)	109.7 (1091.3 2061.9)	(0.00.31)	48 (2.537)	1380-(830-3000)	396 (300 ARL)	NW (227-427)	18(6713)	27400 (2000) 3000)	W1003-010	X7(42.196)	43 (61 64)	7500 (7700-12200)	228(114.966)	28 (199.38)	92(9193)	2180 (see 240)	16.7(11.2.22%)	46 (0.115)	60(6663)	NO(200170)	43 (33.74)	1100(000.000) 0.1 (0.1 0.2)	3290(2980-8000)	18(2813)	312(345.634)	00/00/03	100 (200.000)	100510
Suphylacocon arrow	Resistance to come or more ambients	2000 (2.200.7000)	10484 (773.4 1407.5)	20'000-(18'000) 34000()	1007.8 (MTBIO. 12868.7)	670,703100)	28.0 (42.3 3435)	50000-72900. 50000	38933 (DIFON 38629)	18900 (17900-24100)	174(413.793)	114800 (23000. 21300)	500.7(509.7 600.9	200 (200 MIII)	127(78-964)	30000 (2200) (2000)	1128.6 (689.7) 1667.9)	1400 (1000 000)	W7(77464)	(2000)/200 (6400)	1000/08/5 (2017)	230,000,030	24(1434)	279000 (340000) 400000)	363 (031 802)	TOTO (MARKACHIO) AL (ALAIA)	23000 (15000) 26000)	288 (999.524)	1980 (9200-2300)	17(1128)	27600 (1000) 7000)	621(031773)
Etroptococcus procumentas	Seta Lautano Seta. Santamano infolizione	100(216)790)	2114(1911.296.0)	12000/7900. 72000	2001.9 (32%) 2005.0)	10 (6.05)	19/00214	1480 (8.7780)	(043)131090)	11700 (00700 10700)	364(366487)	204000 (Thomas LTTMIN)	2010/2904 2010	323 (1.621)	10/8024	2600 (47.7500)	MF(8.2.2340)	\$140 (PRE-1100)	61(21.00)	7,3800/10980. 10980)	RNL3 (TMLR 79L1)	20 (67%)	62(6668)	2000 (23.5000)	1136630	1900-powerton; 13 (13.14)	(2400 (2000) (4200)	874 (463.707)	380(1.69)	00/00/03	1200 (11.3000)	14(93.49)
Etropriscoccus procumentar	Catagorana	ente parte many	280.2 (349.8.102.1)	15000 18000/12400	21483 (HIZIO 2601.9)	100(413200)	807 (23.3 96.0)	12800-(4298- 22000)	2012 (1993). MDLQ	1700(1000 1700)	414(514.605)	179000 (PC000. 179000)	750.6(279.3. #12.5)	269 (120 890)	X8(40.187)	2000 (1000 4000)	7769 (923.1964)	4240-1400-13004	78 (83.483)	\$2000,99580. 236000)	6429 (296.3 888.9)	200 (44.300)	14(6723)	17600 (7600 3000)	1962 (46.42474)	1000 (1380-2000) 1.8 (1.8.23)	42308 (27500 30300)	483 (941.893)	3120 (2490-9190)	60/6264	15000 p2000. 22000)	16.0(8.26.0)
Etropriscoccus procumentar	Pleampionisson	(82) (82) (20)	284(176.10.4)	69000 (MIRRO) 12000)	221814 (1996) N. 3001.2)	800 (915 MHH)	302 (18464)	7980 (2730) 17300)	3893 (CLP. 1892)	1200 (3000 1000)	44.5 (333.784)	127000 (12000) 147000)	3064/2064 5863	(180 (488, 5930)	A4(13.00)	21400 (7500 3/200)	297 (1812/01.1)	Moto yalko 1700)	74 (83 890)	27,000,79500. 27,0000	6962 (2017-9013)	179 (NE 200)	69(6313)	20000 (2000 2000)	TIGALINA	1000 (1300-2000) 1.8 (1.8.23)	47300 (17400 82300)	71.0 (94.9 (94.9)	209 (27.402)	62(61.64)	7800 (7700). 1900)	84(21.03)
Etroptococcus procumentos	Marrish	4730 (2000 NOV)	264.6 (7167.199.7)	59000 (2000) 67000	217034 (1875.2. 29(23.6)	20,640	XF (0021.2)	2000 (0.7000)	796.0 (68.000.0)	1360 (304B-1CB)	413 (134.968)	125000 (CMID. 312000)	307 N (2004 A MCLT)	484 (0.1220)	17/00/30	23600 (n. 206000)	1112 (90.1963)	1000 (790 1000)	79 (87 899)	250000 (12700) 122000)	603 (2014/012)	30 (640)	63(6667)	11200 (0.79900)	25.8 (0.0 (0.1)	1900(290.2900) 17(L421)	7900 (2700) 7900)	(82 (GAME)	NO(0.190)	61/0083	2000 (0.00700)	23(99.84)
Etropriscoccus procumentar	Probilin	9520 yakin 13200)	3010(2013-2013)	20000 (40000) 220000)	3969.4 (2366.5 4191.4)	NO (75 NO)	294 (99.313)	2000 (3200 N.100	2002) 1789-979-6	1900 (1900-2800)	M3(412.7KB)	100000 (23000. 223000)	2014/3074 2016	208 (124.240)	34(14.89)	9750 (ACTO) ACTOR)	2012 (588.8324.6)	1400 (140 2700)	IO7(73.148)	138000 (U 700) 167000)	1002 (626.7 6273.4	KD (94.180)	04(03.1.1)	7960 (1790) 12700)	NAGRAMO	2000(0700.2000) 24(1820)	8000 (12700) 9100)	M1 (No.1864)	1170 (475, 1990)	41/61/63	ATTHE CTURE (MICH)	48(2838)
Etropriscoccus procumentar	Third generation orphologories	ECOLOMBIADO	HT0(80K8.238.3)	38000,217000. 112000)	1992.8 (CU12. 2009.0)	26(9.48)	74(29383)	2860 (Total 3000)	CK1(2661204)	MRD (0300 T3080)	27.8(288.27.4)	7000 (Nam. 2000)	2014)798A 2013)	424(199.887)	1.0(6.0.27)	2900 (4200 7900)	1164 (27.8.29.8)	etan intaramen	49(8478)	19600/3000 3000)	4284 (241.5 MKS)	32 (24.4%)	62(6168)	27000 (9990 8000)	367 (7.4-42.8)	960(790.0300) 1.1 (6.8.1.4)	27000 (2000) a(700)	466 (51.8.512)	414(348.788)	00/00/03	1000-9420-2000)	17(97.52)
Etroposocous procumentias	Trimelopsin Solimelo-sandr	27100-(2000-31400)	9827(7387.1094)	22000-170000- 23000)	STREE SOUTH	379(91.60%	MIR (D.R. ML4)	22800-/1180- 27800)	7908 (1801) 16807)	MNOC(ZZNIK TOROS)	1700 (1518-2014)	20000 (T200) (2000)	90109 (1969.2 90109 (1969.2	Note (TSL 2000)	187(23.93)	same order water	1983 (96A 2653)	2000 (7000.0700)	10(2840)	710000,277000 ACR003	30349 (2944.3 30349)	270 (44.749)	29(0489)	102000 (27000 66600)	2014 (314 9007)	480(9200300) 78(5584)	22000 (2000) 2000)	264 (294 (296)	NNO (NSL 1149)	00(0113)	20000 (1000) 45000)	2010/03/47/40
Enophosocom procumentar	Resistance to come or more architectus	21000-21000-21000	10078 (7%.4. 12700)	3030E-71000E- 7030E)	12361.4 12361.4 14301.4 14301.4	840,005499)	2014 (1771 4 7172)	12880-/2486 74880)	27964)	HT00-(\$1000-74000)	1899 (1824-2947)	(2000) (2000) (2000)	2002.0(2019.3 2003.5)	1760 (760-1730)	271(255454)	posses juctors. PCHING	IDEX (INTA- INTER)	4360 (1200 F700)	35.7 (26.6 (6.2)	778000,778000 248000	2007 (2024.1 2020)	8700 (7000 L2000)	67(2193)	79000-(#700) 112000)	#3.1 (1842.8812)	4000 (MMERZEN) 74 (4.5 to)	34000 (2000) 5400)	286.0 (200.9 (0.00))	1700 (170 2000)	18 (18 2.1)	12100 (1400) 7400)	F00073.778)

Table S21. Lin	nitations of each primary mod	elling component			
Type of limitation	1. Fraction of sepsis and infectious syndromes	2. Case fatality ratio	3. Pathogen distribution	4. Fraction of resistance	5. Relative risk
	Limited geographic coverage in the data. Analysis of the fraction of sepsis included multiple cause of death (MCoD), hospital discharge, linkage, and CHAMPS surveillance data which represented 16 countries	Almost all of the input data relies on hospital-based sampling, excluding all community infections and deaths from the analysis.	Many data sources like microbial databases and hospital discharges rely on hospital-based sampling, excluding community-based infections.	There is heterogeneity in the interpretation guidelines used for antimicrobial susceptibility test and in most cases it was not possible to harmonise this interpretation to the most recent CLSI guidelines.	There was limited data on the fatalities due to resistant Neisseria gonorrhoeae so we did not produce a fatal estimate for this pathogen.
		Literature review of case fatality ratios available for central nervous system infections only.	We excluded from analysis all records of infection where no pathogen was detected. This assumes that all pathogens are equally like to be detected, which may be untrue to due issues like variable diagnostic methods (PCR, culture, etc) and irregular testing.	There is heterogineity in the breath of data gathered for the 17 core pathogen-drug combinations, for which we implemented a systematic review, and the remaining 69 combinations for which no systematic review was implemented.	There was limited data on fatalities due to resistant Shigella and Salmonella Parathyphi, for which we based our results on estimates for Salmonella Typhi.
Input data		Because each data source generally reported only a set of the pathogens we evaluated in our research, the input data for the pathogens varied in geographic coverage; nearly all pathogens were well reported in high-income areas, but some pathogens were not well represented in the smaller subset of data we collected from low- and middle-income locations.	Lack of diagnostic data linked with microbiology lab results for some data sources forces us to rely only on specimen type to assign infectious syndrome, obscuring the primary site of infection for samples such as blood.	Were unable to collect data on resistance prevalence more recently than 2018; we estimated resistance for 2018 and assumed no change in prevalence of resistance for 2019.	There was limited availability of outcomes dissagregated by age and gender groups and different anatomical sites of infection.
		For some pathogen-syndrome combinations, we had no data available with outcomes that could be used to model CFRs; for these, we defaulted to a general bacteria model of CFR.		Some facilities could not be classified as tertiary/non-tertiary due to vague facilities names and/or lack of sufficient website information (see appendix section 7.2).	
				When data providers did not describe a facility as tertiary or non-tertiary and the name of the facility was not descriptive, we used self-assignments of tertiary/non-tertiary from facility websites. This form of classification is vulnerable to differences in tertiary/non-tertiary definitions (such as describing a facility as tertiary when only a select ward offers tertiary care).	

	Tuberculosis, Gonorrhoea and chlamydia, and Typhoid, paratyphoid, and invasive non-typhoidal Salmonella were not included as infectious syndrome models. We used GBD 2019 results by setting the fraction of sepsis to 100% for all deaths in these causes prior to multiplying onto the sepsis-related mortality envelope	Pathogen-syndrome-specific case fatality ratios assumed to be constant across underlying cause of illness.	causing a given infectious syndrome is assumed to be	0 0	We assumed the same relative risk for different age and gender groups, different anatomical sites of infection, and different locations.
Modelling	We assumed that infections were community acquired if they were listed as primary diagnoses or underlying causes of death. Otherwise, the infection was assumed to be hospital acquired.	Geographic distribution of CFR based solely on Healthcare Access and Quality Index.	Co-infection of pathogens is assumed to be random and not correlated for certain pathogens.	We assumed that the correlation structure of coresistance of multiple drugs	We assumed that the relative risk of a co-resistant infection is the same as the highest mono-resistant relative risk among the antibiotics considered, which is likely an underestimation of the true co-resistant relative risk.
	Data stochasticity. At the most granular age-, sex-, location-, year-, cause-specific level, the dataset for each individual model is stochastic and there are few clusters to guide the model fit.		Use of expert-opinion Gaussian priors with mean 0 and non-zero variance on model coefficients to bias the models away from spurious effects driven by data sparsity.	We included designations of "mixed/unknown" in the crosswalk to attenuate the effect of tertiary samples in our results. This was due to the low proportion of definitively non-tertiary samples in several super regions for which we produce estimates.	We assumed that the relative length of stay has the same impact duration for all sequelae, which impacts specifically bloodstream infections and intraabdominal infections
			Pathogen distribution of cardiac infections is assumed to the same as bloodstream infections.		

Pathogen	Antibiotic Class	Г	eaths	Associated with resistance	DALYs	Г	Deaths	ttributable to resistance DALYs	
1	A muddete Causs	Counts (thousands)	Rate per 100 000	Counts (thousands)	Rate per 100 000	Counts (thousands)	Rate per 100 000	Counts (thousands)	Rate per 100 000
ns	Resistance to one or more antibiotics	4,950 (3,620-6,570)	64.0 (46.8-84.9)	192,000 (146,000-248,000)	2,477.7 (1,889.9-3,199.1)	1,270 (911-1,710)	16.4 (11.8-22.0)	47,900 (35,300-63,700)	618.7 (455.7-823.2)
cter baumannii	Aminoglycosides	239 (140-374)	3.1 (1.8-4.8)	6,730 (4,120-10,300)	86.9 (53.3-133.5)	10.4 (0-26.7)	0.1 (0.0-0.3)	296 (1.84-737)	3.8 (0.0-9.5)
er baumannii	Anti-pseudomonal penicillin/Beta-Lactamase inhibitors	359 (213-551)	4.6 (2.8-7.1)	10,300 (6,400-15,600)	132.7 (82.7-202.2)	13.3 (6.88-22.6)	0.2 (0.1-0.3)	463 (243-753)	6.0 (3.1-9.7)
er baumannii	Beta Lactam/Beta-lactamase inhibitors	306 (182-469)	3.9 (2.4-6.1)	8,490 (5,260-13,000)	109.8 (68.0-167.5)	0.811 (0.219-1.65)	0.0 (0.0-0.0)	17.3 (4.64-35.1)	0.2 (0.1-0.5)
er baumannii	Carbapenem	326 (192-504)	4.2 (2.5-6.5)	8,790 (5,380-13,400)	113.6 (69.5-173.5)	57.7 (30.3-102)	0.7 (0.4-1.3)	1,540 (817-2,630)	19.9 (10.6-34.0)
ter baumannii	Fluoroquinolones	316 (186-488)	4.1 (2.4-6.3)	8,800 (5,390-13,300)	113.7 (69.7-172.0)	40 (19.8-66.6)	0.5 (0.3-0.9)	1,120 (557-1,880)	14.4 (7.2-24.3)
er baumannii	Fourth-generation cephalosporins	360 (212-554)	4.7 (2.7-7.2)	9,880 (6,090-15,000)	127.7 (78.7-194.4)	3.28 (1.36-6.27)	0.0 (0.0-0.1)	79.1 (33.7-150)	1.0 (0.4-1.9)
r baumannii	Third-generation cephalosporins	377 (222-575)	4.9 (2.9-7.4)	10,400 (6,430-15,800)	134.3 (83.1-204.6)	6.86 (2.66-12.9)	0.1 (0.0-0.2)	163 (64.7-306)	2.1 (0.8-4.0)
r baumannii	Resistance to one or more antibiotics	423 (252-647)	5.5 (3.3-8.4)	11,800 (7,290-17,800)	152.3 (94.2-229.8)	132 (75.7-213)	1.7 (1.0-2.8)	3,670 (2,150-5,760)	47.5 (27.8-74.5)
· spp.	Aminoglycosides	8.48 (5.23-12.8)	0.1 (0.1-0.2)	384 (234-584)	5.0 (3.0-7.5)	0.411 (0-1)	0.0 (0.0-0.0)	18.6 (0-45.2)	0.2 (0.0-0.6)
spp.	Anti-pseudomonal penicillin/Beta-Lactamase inhibitors	14.1 (8.65-21.7)	0.2 (0.1-0.3)	568 (348-867)	7.3 (4.5-11.2)	2.17 (1-3.78)	0.0 (0.0-0.0)	83.9 (41.8-147)	1.1 (0.5-1.9)
spp.	Carbapenem	10.4 (6.18-16.1)	0.1 (0.1-0.2)	404 (242-621)	5.2 (3.1-8.0)	2.3 (1.15-4)	0.0 (0.0-0.1)	87.5 (44.1-151)	1.1 (0.6-1.9)
spp.	Fluoroquinolones	17.9 (10.9-27.3)	0.2 (0.1-0.4)	734 (451-1,110)	9.5 (5.8-14.4)	2.51 (1.12-4.58)	0.0 (0.0-0.1)	102 (46.4-191)	1.3 (0.6-2.5)
spp.	Fourth-generation cephalosporins	18.7 (11.4-28.4)	0.2 (0.1-0.4)	821 (498-1,260)	10.6 (6.4-16.2)	1.34 (0.577-2.53)	0.0 (0.0-0.0)	60.7 (27-109)	0.8 (0.3-1.4)
spp.	Third-generation cephalosporins	28.1 (17.3-43)	0.4 (0.2-0.6)	1,120 (689-1,700)	14.5 (8.9-21.9)	1.84 (0.762-3.38)	0.0 (0.0-0.0)	63.4 (26-115)	0.8 (0.3-1.5)
spp.	Resistance to one or more antibiotics	35.5 (21.7-52.9)	0.5 (0.3-0.7)	1,400 (861-2,110)	18.1 (11.1-27.2)	10.6 (5.93-17.3)	0.1 (0.1-0.2)	416 (237-668)	5.4 (3.1-8.6)
spp.	Aminoglycosides	51.6 (34.9-73.6)	0.7 (0.5-1.0)	2,310 (1,600-3,280)	29.9 (20.7-42.3)	3 (0.879-5.87)	0.0 (0.0-0.1)	135 (40.2-253)	1.7 (0.5-3.3)
spp.	Anti-pseudomonal penicillin/Beta-Lactamase inhibitors	99.2 (65.3-142)	1.3 (0.8-1.8)	3,640 (2,460-5,230)	47.0 (31.8-67.6)	9.95 (5.61-15.9)	0.1 (0.1-0.2)	337 (190-532)	4.4 (2.5-6.9)
spp.	Carbapenem	61.6 (40-90.1)	0.8 (0.5-1.2)	2,340 (1,550-3,350)	30.2 (20.1-43.3)	15.3 (8.87-24.2)	0.2 (0.1-0.3)	568 (334-884)	7.3 (4.3-11.4)
r spp. r spp.	Fluoroquinolones		, ,		40.6 (27.9-59.0)	7.8 (4.15-13.2)	0.2 (0.1-0.3)	, ,	4.1 (2.3-7.0)
* *	1	74.7 (49.2-107)	1.0 (0.6-1.4)	3,150 (2,160-4,560)				319 (176-544)	
spp.	Fourth-generation cephalosporins	112 (74.5-159)	1.4 (1.0-2.1)	4,730 (3,270-6,720)	61.1 (42.2-86.9)	5.32 (2.66-9.29)	0.1 (0.0-0.1)	238 (119-412)	3.1 (1.5-5.3)
spp.	Trimethoprim-Sulfamethoxazole	87.5 (57.6-125)	1.1 (0.7-1.6)	3,580 (2,470-4,960)	46.3 (31.9-64.1)	4.65 (0-9.8)	0.1 (0.0-0.1)	180 (0-377)	2.3 (0.0-4.9)
spp.	Resistance to one or more antibiotics	185 (122-264)	2.4 (1.6-3.4)	7,070 (4,830-10,000)	91.4 (62.4-129.8)	46.1 (29.6-67.1)	0.6 (0.4-0.9)	1,780 (1,160-2,580)	23.0 (15.1-33.4)
faecalis	Fluoroquinolones	109 (66.6-162)	1.4 (0.9-2.1)	3,780 (2,460-5,450)	48.9 (31.8-70.5)	26.8 (12.4-47.3)	0.3 (0.2-0.6)	930 (455-1,560)	12.0 (5.9-20.2)
faecalis	Vancomycin	12.1 (7.25-19.6)	0.2 (0.1-0.3)	403 (253-611)	5.2 (3.3-7.9)	3.42 (1.46-6.48)	0.0 (0.0-0.1)	111 (48.2-209)	1.4 (0.6-2.7)
faecalis	Resistance to one or more antibiotics	112 (69.2-167)	1.4 (0.9-2.2)	3,880 (2,540-5,610)	50.2 (32.8-72.5)	30.2 (15.5-51.2)	0.4 (0.2-0.7)	1,040 (545-1,700)	13.4 (7.0-22.0)
faecium	Fluoroquinolones	198 (122-300)	2.6 (1.6-3.9)	5,390 (3,290-8,340)	69.6 (42.5-107.8)	37.2 (11-70.7)	0.5 (0.1-0.9)	1,020 (303-1,930)	13.1 (3.9-25.0)
aecium	Vancomycin	59.9 (37.3-92.1)	0.8 (0.5-1.2)	1,610 (990-2,490)	20.8 (12.8-32.2)	14.3 (7.19-24.7)	0.2 (0.1-0.3)	384 (192-667)	5.0 (2.5-8.6)
necium	Resistance to one or more antibiotics	200 (123-303)	2.6 (1.6-3.9)	5,440 (3,320-8,420)	70.3 (42.9-108.8)	51.5 (27.1-87.7)	0.7 (0.4-1.1)	1,400 (734-2,400)	18.1 (9.5-31.1)
eci	Fluoroquinolones	65.2 (42.8-96)	0.8 (0.6-1.2)	2,110 (1,380-3,120)	27.2 (17.9-40.3)	12.2 (1.87-24)	0.2 (0.0-0.3)	398 (63.9-782)	5.1 (0.8-10.1)
eci	Vancomycin	11.8 (7.62-17.1)	0.2 (0.1-0.2)	301 (196-444)	3.9 (2.5-5.7)	2.22 (1.19-3.94)	0.0 (0.0-0.1)	56.5 (30.3-100)	0.7 (0.4-1.3)
cci	Resistance to one or more antibiotics	67.1 (44-98.4)	0.9 (0.6-1.3)	2,150 (1,410-3,170)	27.7 (18.3-41.0)	14.5 (4.9-26.5)	0.2 (0.1-0.3)	454 (144-841)	5.9 (1.9-10.9)
li	Aminoglycosides	200 (146-266)	2.6 (1.9-3.4)	7,560 (5,700-9,860)	97.7 (73.7-127.4)	11.7 (7.65-16.5)	0.2 (0.1-0.2)	437 (291-612)	5.6 (3.8-7.9)
li	Aminopenicillin	764 (554-1,030)	9.9 (7.2-13.3)	26,000 (19,600-34,200)	336.6 (253.3-442.0)	10.5 (6.94-15.1)	0.1 (0.1-0.2)	298 (201-416)	3.9 (2.6-5.4)
oli	Beta Lactam/Beta-lactamase inhibitors	586 (425-788)	7.6 (5.5-10.2)	20,400 (15,400-26,800)	263.2 (198.6-346.1)	21.3 (14.7-30)	0.3 (0.2-0.4)	634 (452-873)	8.2 (5.8-11.3)
li	Carbapenem	140 (102-188)	1.8 (1.3-2.4)	5,270 (3,930-6,980)	68.1 (50.8-90.1)	29.5 (17.1-45)	0.4 (0.2-0.6)	1,090 (640-1,670)	14.1 (8.3-21.5)
li	Fluoroquinolones	532 (384-708)	6.9 (5.0-9.1)	18,400 (13,900-24,100)	238.0 (179.1-311.4)	56 (38.5-78.7)	0.7 (0.5-1.0)	1,890 (1,310-2,580)	24.4 (16.9-33.3)
li	Third-generation cephalosporins	499 (362-673)	6.5 (4.7-8.7)	17,900 (13,400-23,800)	231.2 (173.4-307.2)	59.9 (26.3-109)	0.8 (0.3-1.4)	2,080 (947-3,660)	26.9 (12.2-47.2)
oli	Trimethoprim-Sulfamethoxazole	536 (390-713)	6.9 (5.0-9.2)	19,500 (14,700-25,500)	251.8 (190.2-329.9)	30.2 (20.2-42.8)	0.4 (0.3-0.6)	1,080 (718-1,520)	14.0 (9.3-19.6)
li	Resistance to one or more antibiotics	829 (601-1,120)	10.7 (7.8-14.4)	28,000 (21,000-36,900)	362.2 (272.0-476.8)	219 (152-316)	2.8 (2.0-4.1)	7,520 (5,270-10,500)	97.1 (68.2-136.2)
ococcus	Macrolide	39 (18.3-77.1)	0.5 (0.2-1.0)	1,170 (653-2,090)	15.1 (8.4-27.0)	3.63 (0-13.9)	0.0 (0.0-0.2)	108 (0-376)	1.4 (0.0-4.9)
ococcus	Resistance to one or more antibiotics	39 (18.3-77.1)	0.5 (0.2-1.0)	1,170 (653-2,090)	15.1 (8.4-27.0)	3.63 (0-13.9)	0.0 (0.0-0.2)	108 (0-376)	1.4 (0.0-4.9)
ococcus	Fluoroquinolones	67.5 (49-91)	0.9 (0.6-1.2)	4,240 (3,070-5,750)	54.8 (39.6-74.4)	11.5 (1.92-24.9)	0.1 (0.0-0.3)	723 (125-1,580)	9.3 (1.6-20.4)
ococcus	Macrolide	142 (102-193)	1.8 (1.3-2.5)	7,230 (5,230-9,740)	93.4 (67.6-125.9)	13.5 (0-36.3)	0.2 (0.0-0.5)	672 (0-1,780)	8.7 (0.0-23.0)
cococcus	Penicillin	3.74 (2.59-5.25)	0.0 (0.0-0.1)	203 (141-281)	2.6 (1.8-3.6)	0.799 (0.165-1.7)	0.0 (0.0-0.0)	42.9 (8.52-91.5)	0.6 (0.1-1.2)
tococcus	Resistance to one or more antibiotics	173 (125-232)	2.2 (1.6-3.0)	9,190 (6,770-12,300)	118.8 (87.5-158.4)	25.8 (3.92-51.8)	0.3 (0.1-0.7)	1,440 (281-2,780)	18.6 (3.6-36.0)
ıfluenzae	Aminopenicillin	27.4 (21.8-34.2)	0.4 (0.3-0.4)	1,450 (1,120-1,840)	18.7 (14.4-23.8)	4.29 (0.393-8.3)	0.1 (0.0-0.1)	218 (21.5-431)	2.8 (0.3-5.6)
ıfluenzae	Third-generation cephalosporins	8.57 (6.41-11.1)	0.1 (0.1-0.1)	560 (413-738)	7.2 (5.3-9.5)	2.47 (1.14-4.16)	0.0 (0.0-0.1)	161 (71.7-272)	2.1 (0.9-3.5)
yluenzae yfluenzae	Resistance to one or more antibiotics	31.5 (25.5-39)	0.4 (0.3-0.5)	1,720 (1,340-2,180)	22.3 (17.4-28.2)	6.76 (2.63-11.3)	0.1 (0.0-0.1)	379 (156-619)	4.9 (2.0-8.0)
moniae	Aminoglycosides	345 (254-463)	4.5 (3.3-6.0)	16,500 (12,400-21,600)	213.5 (160.2-279.4)	26.3 (16.2-38.9)	0.3 (0.2-0.5)	1,230 (773-1,780)	16.0 (10.0-23.0)
moniae	Beta Lactam/Beta-lactamase inhibitors	545 (396-725)	7.0 (5.1-9.4)	24,100 (17,900-31,700)	311.4 (232.0-409.8)	7.93 (4.59-12.1)	0.1 (0.1-0.2)	316 (182-478)	4.1 (2.3-6.2)
umoniae	Carbapenem	234 (164-332)	3.0 (2.1-4.3)	9,280 (6,640-12,800)	119.9 (85.9-165.6)	55.7 (36.3-81.3)	0.7 (0.5-1.1)	2,170 (1,430-3,120)	28.0 (18.5-40.3)
rumoniae	Fluoroquinolones	426 (312-576)	5.5 (4.0-7.4)	18,900 (14,100-24,900)	244.3 (181.8-322.1)	29 (17.4-44.1)	0.4 (0.2-0.6)	1,260 (761-1,880)	16.2 (9.8-24.3)
rumoniae	Third-generation cephalosporins	526 (384-717)	6.8 (5.0-9.3)	22,900 (17,100-30,100)	296.4 (221.4-388.9)	50.1 (19-94.4)	0.6 (0.2-1.2)	2,210 (836-4,070)	28.6 (10.8-52.6)
гитопиае гитопіае	Trimethoprim-Sulfamethoxazole	488 (356-653)	6.3 (4.6-8.4)	21,900 (16,300-28,800)	282.4 (211.3-372.3)	23.5 (11.5-39.7)	0.3 (0.1-0.5)	1,010 (494-1,660)	13.1 (6.4-21.5)
rumoniae rumoniae	Resistance to one or more antibiotics	642 (465-863)	8.3 (6.0-11.2)	27,400 (20,300-28,800)	282.4 (211.3-372.3) 354.5 (261.8-466.0)	23.5 (11.5-39.7) 193 (130-272)	2.5 (1.7-3.5)	8,200 (5,550-11,400)	13.1 (6.4-21.5) 106.0 (71.8-147.5)
pp.	Fluoroquinolones	2.59 (1.64-3.94)	, ,	27,400 (20,300-36,100) 56.7 (36.4-85.8)	0.7 (0.5-1.1)	0.427 (0.174-0.78)		8,200 (5,550-11,400) 9.21 (3.76-16.8)	
pp. pp.	Fluoroquinolones Fourth-generation cephalosporins	2.59 (1.64-3.94) 1 (0.621-1.55)	0.0 (0.0-0.1) 0.0 (0.0-0.0)	56.7 (36.4-85.8) 23.7 (14.7-36.2)	0.7 (0.5-1.1) 0.3 (0.2-0.5)	0.427 (0.174-0.78) 0.154 (0-0.321)	0.0 (0.0-0.0) 0.0 (0.0-0.0)	9.21 (3.76-16.8) 3.5 (1.14-7.23)	0.1 (0.0-0.2) 0.0 (0.0-0.1)
•	Third-generation cephalosporins Third-generation cephalosporins	1.45 (0.907-2.19)	0.0 (0.0-0.0)	30.2 (19-45.6)	0.3 (0.2-0.5) 0.4 (0.2-0.6)	0.154 (0-0.321)	0.0 (0.0-0.0)	3.5 (1.14-7.25) 3.2 (1.28-6.52)	0.0 (0.0-0.1)
op.			, ,			, ,			
pp.	Resistance to one or more antibiotics	3 (1.93-4.59)	0.0 (0.0-0.1)	64.7 (41.5-98)	0.8 (0.5-1.3)	0.749 (0.394-1.27)	0.0 (0.0-0.0)	15.9 (8.56-27)	0.2 (0.1-0.3)
tuberculosis	Extensive drug resistance in TB	8.5 (4-15.2)	0.1 (0.1-0.2)	311 (151-553)	4.0 (1.9-7.1)	5.21 (2.48-9.31)	0.1 (0.0-0.1)	181 (88.4-319)	2.3 (1.1-4.1)
n tuberculosis	Isoniazid mono-resistance	73.8 (50.7-103)	1.0 (0.7-1.3)	2,880 (2,040-3,930)	37.2 (26.4-50.7) 54.5 (22.5.103.3)	11.6 (0-40.2)	0.2 (0.0-0.5)	419 (0-1,410)	5.4 (0.0-18.3)
n tuberculosis	Multi-drug resistance excluding extensive drug resistance in TB	110 (43.6-210)	1.4 (0.6-2.7)	4,210 (1,740-7,990)	54.5 (22.5-103.3)	64.6 (6.6-160)	0.8 (0.1-2.1)	2,320 (225-5,660)	30.0 (2.9-73.2)
tuberculosis	Rifampicin mono-resistance	12 (8.85-15.6)	0.2 (0.1-0.2)	494 (368-644)	6.4 (4.8-8.3)	3.35 (0.569-6.54)	0.0 (0.0-0.1)	130 (26.6-249)	1.7 (0.3-3.2)
tuberculosis	Resistance to one or more antibiotics	204 (134-303)	2.6 (1.7-3.9)	7,900 (5,260-11,600)	102.0 (68.0-149.9)	84.8 (18.3-182)	1.1 (0.2-2.4)	3,050 (693-6,550)	39.4 (9.0-84.7)
rrhoeae	Fluoroquinolones			53.7 (32.6-84.1)	0.7 (0.4-1.1)			5.14 (1.46-10.3)	0.1 (0.0-0.1)
rrhoeae	Third-generation cephalosporins			1.95 (1-3.49)	0.0 (0.0-0.0)			0.374 (0.119-0.797)	0.0 (0.0-0.0)
rhoeae	Resistance to one or more antibiotics	-		53.9 (32.7-84.4)	0.7 (0.4-1.1)			5.51 (1.77-11)	0.1 (0.0-0.1)
	Aminoglycosides	19.4 (12.6-28.1)	0.3 (0.2-0.4)	533 (345-774)	6.9 (4.5-10.0)	0.887 (0-1.91)	0.0 (0.0-0.0)	24.1 (2.79-51.4)	0.3 (0.0-0.7)
	Aminopenicillin	70 (46.2-101)	0.9 (0.6-1.3)	1,750 (1,140-2,540)	22.6 (14.7-32.9)	1.33 (0-3.96)	0.0 (0.0-0.1)	32.4 (0-95.9)	0.4 (0.0-1.2)
	Fluoroquinolones	40.7 (26.7-59)	0.5 (0.3-0.8)	1,040 (680-1,530)	13.5 (8.8-19.7)	2.97 (1.24-5.64)	0.0 (0.0-0.1)	74.7 (30.7-142)	1.0 (0.4-1.8)
	Third-generation cephalosporins	23.4 (15-34.2)	0.3 (0.2-0.4)	582 (365-859)	7.5 (4.7-11.1)	4.73 (1.56-9.45)	0.1 (0.0-0.1)	116 (37.6-233)	1.5 (0.5-3.0)
	Trimethoprim-Sulfamethoxazole	45.6 (30.3-66.2)	0.6 (0.4-0.9)	1,190 (780-1,750)	15.4 (10.1-22.6)	1.62 (0-3.57)	0.0 (0.0-0.0)	41.9 (0-90.6)	0.5 (0.0-1.2)
	Resistance to one or more antibiotics	80 (52.7-115)	1.0 (0.7-1.5)	2,000 (1,310-2,900)	25.8 (16.9-37.5)	11.5 (6.33-18.6)	0.1 (0.1-0.2)	290 (159-466)	3.7 (2.1-6.0)
ieruginosa	Aminoglycosides	115 (81.3-160)	1.5 (1.1-2.1)	4,530 (3,290-6,080)	58.5 (42.6-78.6)	3 (0-7.61)	0.0 (0.0-0.1)	120 (0-294)	1.6 (0.0-3.8)
aeruginosa	Anti-pseudomonal penicillin/Beta-Lactamase inhibitors	156 (109-216)	2.0 (1.4-2.8)	5,540 (3,960-7,520)	71.7 (51.2-97.2)	10.3 (6.47-16)	0.1 (0.1-0.2)	378 (239-587)	4.9 (3.1-7.6)
aeruginosa	Carbapenem	210 (146-292)	2.7 (1.9-3.8)	7,250 (5,140-9,840)	93.6 (66.4-127.1)	38.1 (24.3-57.2)	0.5 (0.3-0.7)	1,310 (848-1,940)	16.9 (11.0-25.0)
aeruginosa	Fluoroquinolones	172 (120-236)	2.2 (1.6-3.1)	6,130 (4,380-8,210)	79.2 (56.6-106.1)	18.3 (11.7-27.8)	0.2 (0.2-0.4)	652 (422-967)	8.4 (5.5-12.5)
aeruginosa	Fourth-generation cephalosporins	169 (118-231)	2.2 (1.5-3.1)	6,260 (4,550-8,420)	80.9 (58.8-108.9)	4.37 (2.62-6.9)	0.1 (0.0-0.1)	178 (108-279)	2.3 (1.4-3.6)
aeruginosa aeruginosa	Third-generation cephalosporins Third-generation cephalosporins	213 (146-297)	2.7 (1.9-3.8)	7,970 (5,660-10,900)	103.0 (73.2-141.0)	10.4 (4.61-18)	0.1 (0.1-0.2)	407 (186-689)	5.3 (2.4-8.9)
aeruginosa aeruginosa	Resistance to one or more antibiotics	334 (234-457)	4.3 (3.0-5.9)	12,000 (8,630-16,100)	155.0 (111.5-208.5)	84.6 (53-127)	1.1 (0.7-1.6)	3,050 (1,980-4,530)	3.3 (2.4-8.9) 39.4 (25.5-58.5)
aeruginosa iratyphi						, ,			, ,
	Fluoroquinolones Multi-drug resistance in Salmonella Typhi and Paratyphi	20.1 (8.5-38.9) 0.779 (0.322-1.54)	0.3 (0.1-0.5) 0.0 (0.0-0.0)	1,410 (584-2,750) 55 (22.6-110)	18.2 (7.5-35.5) 0.7 (0.3-1.4)	4 (0.622-10.2) 0.066 (0-0.197)	0.1 (0.0-0.1)	283 (42-711)	3.7 (0.5-9.2) 0.1 (0.0-0.2)
atyphi	DVIDID-OTTO TESISTANCE IN NAIMONEILA L'VONT AND PARAIVONT	10.779 (0.322-1.54)	v.u (v.u-v.u)	11 L/./. D-1 LUI	U. / UU.3-1.41	IU.UOD (U-U.197)	0.0 (0.0-0.0)	4.53 (0-13.3)	U.1 (U.U-U.Z)

Salmonella Paratyphi	Resistance to one or more antibiotics	20.2 (8.54-39.1)	0.3 (0.1-0.5)	1,420 (588-2,760)	18.3 (7.6-35.7)	4.11 (0.677-10.3)	0.1 (0.0-0.1)	287 (47.2-718)	3.7 (0.6-9.3)
Salmonella Typhi	Fluoroquinolones	90.6 (54.1-143)	1.2 (0.7-1.9)	6,570 (3,880-10,600)	84.9 (50.2-136.7)	17.2 (2.96-39.1)	0.2 (0.0-0.5)	1,240 (213-2,810)	16.0 (2.8-36.3)
Salmonella Typhi	Multi-drug resistance in Salmonella Typhi and Paratyphi	58.3 (38.2-84.2)	0.8 (0.5-1.1)	4,400 (2,860-6,410)	56.9 (37.0-82.8)	6.46 (0-16.5)	0.1 (0.0-0.2)	488 (0-1,240)	6.3 (0.0-16.0)
Salmonella Typhi	Resistance to one or more antibiotics	127 (80.9-193)	1.6 (1.0-2.5)	9,350 (5,890-14,200)	120.8 (76.1-183.9)	23.7 (7.55-47.2)	0.3 (0.1-0.6)	1,720 (536-3,400)	22.3 (6.9-43.9)
Non-typhoidal Salmonella	Fluoroquinolones	27.1 (14-46.8)	0.4 (0.2-0.6)	1,390 (717-2,450)	18.0 (9.3-31.7)	5.62 (0.809-13.1)	0.1 (0.0-0.2)	264 (46.3-597)	3.4 (0.6-7.7)
Non-typhoidal Salmonella	Resistance to one or more antibiotics	27.1 (14-46.8)	0.4 (0.2-0.6)	1,390 (717-2,450)	18.0 (9.3-31.7)	5.62 (0.809-13.1)	0.1 (0.0-0.2)	264 (46.3-597)	3.4 (0.6-7.7)
Serratia spp.	Aminoglycosides	16.5 (10.4-25)	0.2 (0.1-0.3)	830 (531-1,260)	10.7 (6.9-16.2)	0.953 (0-2.52)	0.0 (0.0-0.0)	48.1 (0-128)	0.6 (0.0-1.6)
Serratia spp.	Anti-pseudomonal penicillin/Beta-Lactamase inhibitors	13.7 (8.41-21.3)	0.2 (0.1-0.3)	567 (357-871)	7.3 (4.6-11.3)	2.48 (1.21-4.34)	0.0 (0.0-0.1)	103 (51.3-181)	1.3 (0.7-2.3)
Serratia spp.	Carbapenem	8.99 (5.35-14.3)	0.1 (0.1-0.2)	342 (211-524)	4.4 (2.7-6.8)	2.45 (1.23-4.35)	0.0 (0.0-0.1)	93.1 (47.9-164)	1.2 (0.6-2.1)
Serratia spp.	Fluoroquinolones	10.4 (6.55-16.1)	0.1 (0.1-0.2)	477 (308-736)	6.2 (4.0-9.5)	1 (0.224-2.31)	0.0 (0.0-0.0)	49.1 (9.48-109)	0.6 (0.1-1.4)
Serratia spp.	Fourth-generation cephalosporins	23.8 (14.9-36.6)	0.3 (0.2-0.5)	1,180 (764-1,820)	15.3 (9.9-23.5)	2.61 (1.12-4.9)	0.0 (0.0-0.1)	140 (59.8-254)	1.8 (0.8-3.3)
Serratia spp.	Third-generation cephalosporins	25.1 (16-38.1)	0.3 (0.2-0.5)	1,150 (736-1,710)	14.8 (9.5-22.1)	1.1 (0.403-2.13)	0.0 (0.0-0.0)	44.6 (16.9-85)	0.6 (0.2-1.1)
Serratia spp.	Resistance to one or more antibiotics	42.7 (27-65.3)	0.6 (0.3-0.8)	1,930 (1,260-2,900)	24.9 (16.3-37.5)	10.7 (6.11-17.5)	0.1 (0.1-0.2)	478 (274-760)	6.2 (3.5-9.8)
Shigella spp.	Fluoroquinolones	29.1 (11.8-57.7)	0.4 (0.2-0.7)	1,650 (705-3,070)	21.3 (9.1-39.7)	5.99 (0.689-15.4)	0.1 (0.0-0.2)	330 (48-803)	4.3 (0.6-10.4)
Shigella spp.	Resistance to one or more antibiotics	29.1 (11.8-57.7)	0.4 (0.2-0.7)	1,650 (705-3,070)	21.3 (9.1-39.7)	5.99 (0.689-15.4)	0.1 (0.0-0.2)	330 (48-803)	4.3 (0.6-10.4)
Staphylococcus aureus	Fluoroquinolones	366 (266-494)	4.7 (3.4-6.4)	11,800 (8,680-15,800)	152.8 (112.2-203.6)	15.9 (7-27.5)	0.2 (0.1-0.4)	501 (226-853)	6.5 (2.9-11.0)
Staphylococcus aureus	Macrolide	522 (380-704)	6.7 (4.9-9.1)	16,600 (12,300-22,000)	214.5 (158.9-284.3)	19.6 (7.78-35)	0.3 (0.1-0.5)	603 (245-1,050)	7.8 (3.2-13.5)
Staphylococcus aureus	Methicillin	473 (344-642)	6.1 (4.5-8.3)	15,200 (11,100-20,500)	195.9 (143.8-264.6)	121 (53.2-207)	1.6 (0.7-2.7)	3,790 (1,650-6,390)	48.9 (21.3-82.5)
Staphylococcus aureus	Trimethoprim-Sulfamethoxazole	201 (154-262)	2.6 (2.0-3.4)	9,310 (7,190-11,900)	120.3 (92.9-154.1)	18.7 (9.75-28.7)	0.2 (0.1-0.4)	878 (463-1,340)	11.3 (6.0-17.3)
Staphylococcus aureus	Vancomycin	10.3 (7.35-14.6)	0.1 (0.1-0.2)	358 (258-500)	4.6 (3.3-6.5)	3.12 (1.61-5.65)	0.0 (0.0-0.1)	103 (53.9-181)	1.3 (0.7-2.3)
Staphylococcus aureus	Resistance to one or more antibiotics	748 (554-1,000)	9.7 (7.2-13.0)	24,900 (18,600-32,700)	321.3 (240.4-423.2)	178 (104-280)	2.3 (1.3-3.6)	5,870 (3,550-9,220)	75.9 (45.9-119.2)
Streptococcus pneumoniae	Beta Lactam/Beta-lactamase inhibitors	107 (82-138)	1.4 (1.1-1.8)	5,430 (4,150-6,960)	70.2 (53.6-89.9)	2.65 (0.054-6.62)	0.0 (0.0-0.1)	114 (1.44-284)	1.5 (0.0-3.7)
Streptococcus pneumoniae	Carbapenem	191 (148-242)	2.5 (1.9-3.1)	9,100 (7,070-11,500)	117.6 (91.3-148.7)	41.9 (20.5-70)	0.5 (0.3-0.9)	1,990 (957-3,310)	25.7 (12.4-42.8)
Streptococcus pneumoniae	Fluoroquinolones	89.8 (70.8-113)	1.2 (0.9-1.5)	5,240 (4,100-6,680)	67.7 (53.0-86.3)	11.2 (2.64-22.3)	0.1 (0.0-0.3)	643 (153-1,280)	8.3 (2.0-16.5)
Streptococcus pneumoniae	Macrolide	313 (252-391)	4.0 (3.3-5.1)	13,300 (10,700-16,700)	172.2 (138.6-216.0)	12.5 (0-32.6)	0.2 (0.0-0.4)	517 (0-1,330)	6.7 (0.0-17.2)
Streptococcus pneumoniae	Penicillin	230 (184-290)	3.0 (2.4-3.8)	11,200 (8,910-14,000)	144.4 (115.1-181.2)	12.4 (6.69-20.3)	0.2 (0.1-0.3)	597 (327-980)	7.7 (4.2-12.7)
Streptococcus pneumoniae	Third-generation cephalosporins	94.2 (72.5-123)	1.2 (0.9-1.6)	4,720 (3,690-6,140)	61.0 (47.6-79.3)	3.33 (1.39-6.21)	0.0 (0.0-0.1)	177 (73.2-336)	2.3 (0.9-4.3)
Streptococcus pneumoniae	Trimethoprim-Sulfamethoxazole	446 (364-548)	5.8 (4.7-7.1)	23,600 (19,100-29,300)	305.3 (247.3-379.2)	38.7 (5.73-77.2)	0.5 (0.1-1.0)	2,070 (298-4,160)	26.8 (3.9-53.8)
Streptococcus pneumoniae	Resistance to one or more antibiotics	596 (490-727)	7.7 (6.3-9.4)	29,800 (24,400-36,700)	385.8 (314.7-473.8)	122 (82.4-166)	1.6 (1.1-2.1)	6,110 (4,050-8,330)	78.9 (52.4-107.7)

Figure S1 Flowchart of antimicrobial resistance fatal and non-fatal estimation steps

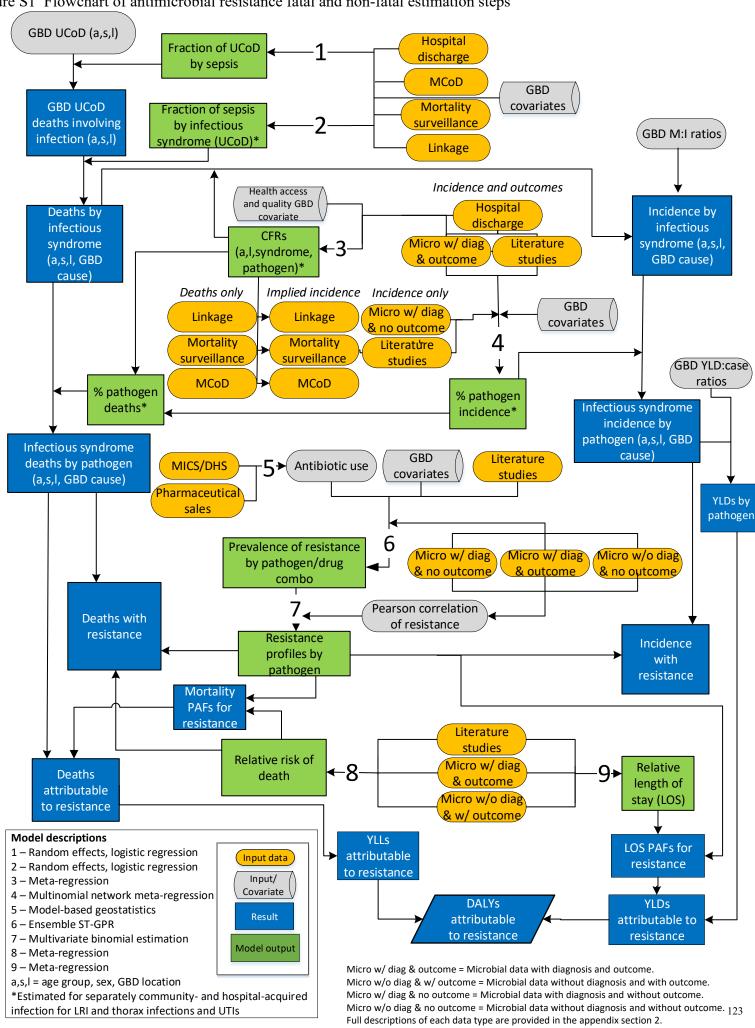


Figure S2 All-age rate of DALYs attributable to and associated with bacterial antimicrobial resistance by GBD region, 2019 10,000 7,500 DALYs (rate per 100 000 population) GBD super-region Central Europe, Eastern Europe, and Central Asia High-income Latin America and Caribbean 5,000 North Africa and Middle East South Asia Southeast Asia, East Asia, and Oceania Sub-Saharan Africa Resistance 2,500 Associated with resistance Attributable to resistance Estimates were aggregated across drugs, taking into account the co-occurrence of resistance to multiple drugs. Error bars show 95% uncertainty intervals. DALYs = disability-Eastern Sub-Saharan Africa Central Sub-Sahatan Artica Southern Sub-Sahatan Africa Worth Africa and Middle East High income Asia Pacific High-income Moth America Andean Latin America Tropical Jain America Central Latin America Southern Latin America Catibbean Central Asia Western Europe Eastern Europe CentralEurope SOUTH ASIR adjusted life-years. GBD = Global Burden of Diseases, Injuries, and Risk Factors Study. 124 **GBD** Region

Figure S3 Global DALYs (in counts) attributable to and associated with bacterial antimicrobial resistance by infectious syndrome, 2019 100,000,000 Estimates were aggregated across drugs, taking into account the co-occurrence of resistance to multiple drugs. Error bars show 95% uncertainty intervals. The DALYs shown are all caused by Neisseria gonorrhoeae; we do not estimate antimicrobial resistance in Chlamydia spp. DALYs = disability-adjusted life-years. LRI+ = lower respiratory infections and all related infections in the thorax. BSI = bloodstream infections. Intra-abdominal = peritoneal and intra-abdominal infections. UTI = urinary tract infections and pyelonephritis. Skin = bacterial infections of the skin and subcutaneous systems. CNS = meningitis and other bacterial central nervous system infections. TB = tuberculosis. TF/PF/iNTS= typhoid fever, paratyphoid fever, and invasive non-typhoidal Salmonella. Cardiac = endocarditis and other cardiac infections. Bone+ = Infections of bones, joints, and related organs. GC/CT = gonorrhoea and chlamydia. 75,000,000 -Resistance Associated with resistance DALYs (count) Attributable to resistance 50,000,000 25,000,000 125 LRI+ BSI ТB CNS TF/PF/iNTS UTI Intra-abdominal Diarrhoea Skin GC/CT Cardiac Bone+ Infectious syndrome

Figure S4 Global DALYs (in counts) attributable to and associated with bacterial antimicrobial resistance by pathogen, 2019 Estimates were aggregated across drugs, taking into account the co-occurrence of resistance to multiple drugs. Error bars show 95% uncertainty intervals. AMR = antimicrobial resistance. DALYs = disability-adjusted life-years. 30,000,000 DALYs (count) Resistance Associated with resistance Attributable to resistance 10,000,000 -Color of Street of the Color of the Color of Street of the Color of Salmonella typhi niae Lecheichia coli preumoniae cue auteus aeruginosa terumamii Lecheichia cella preumonococous auteus aeruginosa terumamii per periodocote la proportiona de la proportiona del la proportiona de la proportiona del la proportiona de la proportiona Pathogen

Figure S5A Pathogen-attributable fraction of DALYs attributable to bacterial antimicrobial resistance for the six leading pathogens by GBD super-region, 2019 0.30 Pathogen-attributable fraction of AMR DALYs attributable to resistance Pathogen Acinetobacter baumannii Escherichia coli Klebsiella pneumoniae Pseudomonas aeruginosa Staphylococcus aureus Streptococcus pneumoniae 127 C. Europe, E. Europe, and C. Asia Latin America and Caribbean N. Africa and Middle East S. Asia SE. Asia, E. Asia, and Oceania Sub-Saharan Africa High-income Super-region

Figure S5B Pathogen-attributable fraction of DALYs associated with bacterial antimicrobial resistance for the six leading pathogens by GBD super-region, 2019 Pathogen-attributable fraction of AMR DALYs associated with resistance Pathogen Acinetobacter baumanii Escherichia coli Klebsiella pneumoniae Pseudomonas aeruginosa Staphylococcus aureus Streptococcus pneumoniae

S. Asia

SE. Asia, E. Asia, and Oceania

Sub-Saharan Africa

Latin America and Caribbean N. Africa and Middle East

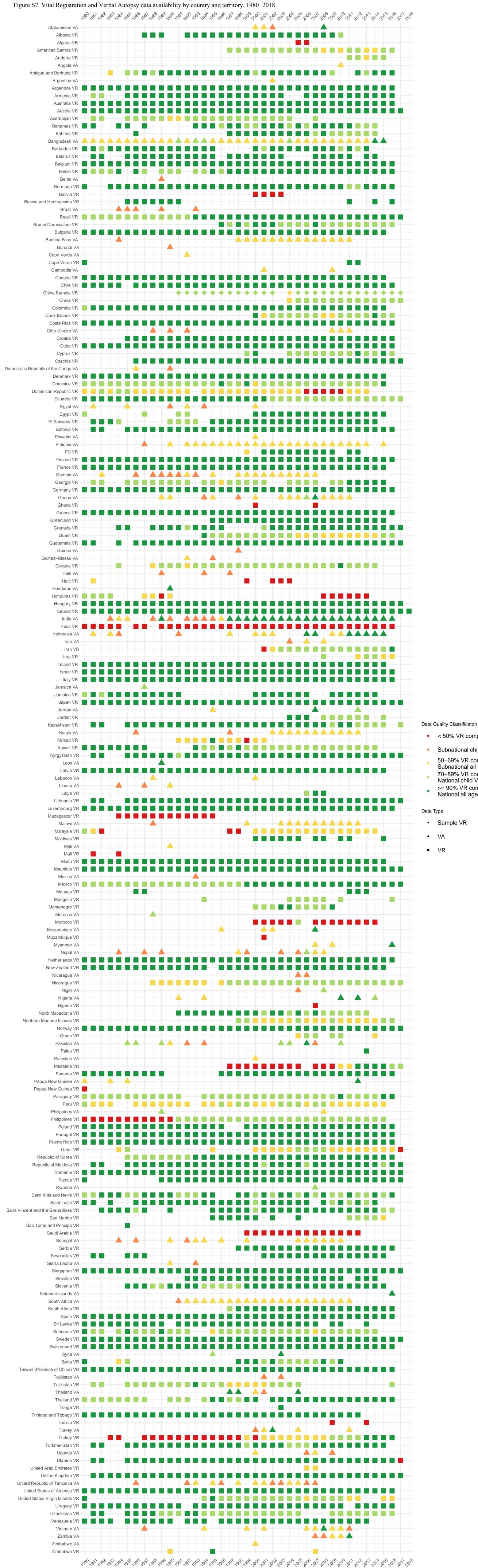
Super-region

C. Europe, E. Europe, and C. Asia

High-income

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Figure S6 Global DALYs (in counts) attributable to bacterial antimicrobial resistance by pathogen-drug combination, 2019 17,300 3,670,000 163,000 79,100 296,000 463,000 1,540,000 1,120,000 Acinetobacter baumannii Citrobacter spp. 416,000 63,400 60,700 18,600 83,900 87,500 102,000 568,000 180,000 Enterobacter spp. ,780,000 238,000 135,000 337,000 319,000 930,000 Enterococcus faecalis 111,000 384,000 Enterococcus faecium Other enterococci 454,000 398,000 56,500 298,000 ,090,000 1,890,000 Escherichia coli 7,520,000 2,080,000 437,000 634,000 Group A Streptococcus 108,000 108,000 Group B Streptococcus 723,000 672,000 42,900 Haemophilus influenzae 379,000 161,000 218,000 Counts 316,000 2,170,000 Klebsiella pneumoniae 8,200,000 | 2,210,000 ≥ 2M 1.5M- <2M 3,200 9,210 Morganella spp. 15,900 3,500 1M - <1.5M 500k - <1M 3,050,000 2,320,000 130,000 181,000 Mycobacterium tuberculosis 419,000 100k - <500k <100k 5,510 374 5,140 Neisseria gonorrhoeae NA 74,700 41,900 290,000 116,000 24,100 32,400 Proteus spp. 3,050,000 407,000 178,000 120,000 378,000 652,000 Pseudomonas aeruginosa Salmonella Paratyphi 287,000 283,000 4,530 488,000 Salmonella Typhi Non-typhoidal Salmonella 264,000 264,000 478,000 44,600 140,000 48,100 103,000 93,100 Serratia spp. 49,100 Shigella spp. 330,000 330,000 5,870,000 501,000 603,000 3,790,000 878,000 103,000 Staphylococcus aureus 177,000 114,000 ,990,000 643,000 517,000 597,000 2,070,000 Streptococcus pneumoniae All pathogens 47,900,000 5,430,000 699,000 2,310,000 549,000 8,840,000 11,800,000 1,900,000 2,320,000 492,000 3,790,000 419,000 130,000 640,000 655,000 GBD = Global Burden of Diseases, Injuries, and Risk Factors Study. Error bars show 95% uncertainty intervals. 129



< 50% VR completeness

- - Subnational child VA study 50-69% VR completeness or
- Subnational all age VA study 70-89% VR completeness or National child VA study >= 90% VR completeness or
- National all age VA study

Sample VR

- VA VR