**Supplementary Table 1. DNA polymerase-relevant Gene Ontology (GO) annotations for the DNA polymerases of *D. melanogaster***

Aspect abbreviations: BP = biological process; MF = molecular function; CC = cellular component. ‘Relevant annotations’ are defined as manual (i.e. not computational) annotations using BP terms mapping under ‘DNA biosynthetic process’ (GO:007189) and/or ‘DNA replication’ (GO:0006260); MF terms ‘DNA-directed DNA polymerase activity’ (GO:0003887), ‘DNA primase activity’ (GO:0003896), ‘3'-5'-exodeoxyribonuclease activity’ (GO:0008296), DNA polymerase processivity factor activity (GO:0030337) or ‘deoxycytidyl transferase activity’ (GO:0017125) (for Rev1); and CC terms mapping under ‘DNA polymerase complex’ (GO:0042575). Evidence abbreviations: IDA = inferred from direct assay; IPI = inferred from physical interaction; IMP = inferred from mutant phenotype; ISS = inferred from sequence similarity. IDA, IPI and IMP indicate there is experimental evidence for the given GO term (shown in blue); ISS means that the GO annotation is based on sequence similarity to another gene, and is only shown here where experimental data are lacking. Data were obtained from the Gene Ontology Annotation database (1), accessed 29th November 2019.

|  |  |
| --- | --- |
| **Symbol** | **GO annotations** |
| **Aspect** | **GO term (ID)** | **Evidence** | **Reference(s)** |
| PolA1 | BP | DNA-dependent DNA replication (GO:0006261)DNA replication proofreading (GO:0045004) | IDAIDA | (2-8)(6,9) |
| MF | DNA-directed DNA polymerase activity (GO:0003887)3'-5'-exodeoxyribonuclease activity (GO:0008296) | IDAIDA | (2-5,7,8,10)(6,9) |
| CC | alpha DNA polymerase:primase complex (GO:0005658) | IDA | (2-5,7,8) |
| PolA2 | BP | DNA-dependent DNA replication (GO:0006261) | IDA | (4,7) |
| MF |  |  |  |
| CC | alpha DNA polymerase:primase complex (GO:0005658) | IDA | (3,4,7) |
| Prim1 | BP | DNA-dependent DNA replication (GO:0006261)DNA replication, synthesis of RNA primer (GO:0006269) | IDAIDA | (2,4,7)(3,7,11,12) |
| MF | DNA primase activity (GO:0003896) | IDA | (12) |
| CC | alpha DNA polymerase:primase complex (GO:0005658) | IDA | (2-4,7,11,12) |
| Prim2 | BP | DNA-dependent DNA replication (GO:0006261)DNA replication, synthesis of RNA primer (GO:0006269) | IDAIDA | (2,4,7)(3,7,11) |
| MF |  |  |  |
| CC | alpha DNA polymerase:primase complex (GO:0005658) | IDA | (2-4,7,11) |
| PolD1 | BP | DNA-dependent DNA replication (GO:0006261)DNA replication proofreading (GO:0045004) | IDAIDA | (8,13,14)(14) |
| MF | DNA-directed DNA polymerase activity (GO:0003887)3'-5'-exodeoxyribonuclease activity (GO:0008296) | IDAIDA | (8,13,14)(8,13,14) |
| CC | delta DNA polymerase complex (GO:0043625) | IDA | (8,15) |
| PolD2 | BP | mitotic DNA-dependent DNA replication (GO:1990506) | IMP | (15) |
| MF |  |  |  |
| CC | delta DNA polymerase complex (GO:0043625)zeta DNA polymerase complex (GO:0016035) | IDAISS | (15)n/a |
| PolD3 | BP | DNA synthesis involved in double-strand break repair via homologous recombination (GO:0043150)mitotic DNA replication (GO:1902969)positive regulation of DNA-directed DNA polymerase activity (GO:1900264) | IMPIMPIMP | (16)(17)(16) |
| MF | DNA polymerase processivity factor activity (GO:0030337) | IMP | (16) |
| CC | delta DNA polymerase complex (GO:0043625)zeta DNA polymerase complex (GO:0016035) | IDAISS | (15)n/a |
| PolE1 | BP | DNA-dependent DNA replication (GO:0006261)DNA replication proofreading (GO:0045004)DNA synthesis involved in DNA replication (GO:0090592) | IDAIDAIDA | (18)(19)(19) |
| MF | DNA-directed DNA polymerase activity (GO:0003887)3'-5'-exodeoxyribonuclease activity (GO:0008296) | IDAIDA | (18,19)(18,19) |
| CC | epsilon DNA polymerase complex (GO:0008622) | IPI | (19) |
| PolE2 | BP | DNA replication proofreading (GO:0045004)mitotic DNA replication (GO:1902969) | IDAIMP | (19)(20) |
| MF |  |  |  |
| CC | epsilon DNA polymerase complex (GO:0008622) | IPI | (19) |
| PolE3 | BP | DNA-dependent DNA replication (GO:0006261) | ISS | n/a |
| MF |  |  |  |
| CC | epsilon DNA polymerase complex (GO:0008622) | ISS | n/a |
| PolE4 | BP | DNA-dependent DNA replication (GO:0006261) | ISS | n/a |
| MF |  |  |  |
| CC | epsilon DNA polymerase complex (GO:0008622) | ISS | n/a |
| PolZ1 | BP | DNA synthesis involved in double-strand break repair via homologous recombination (GO:0043150)DNA biosynthetic process (GO:0071897)DNA synthesis involved in DNA repair (GO:0000731) | IMPIDAIDA | (16)(21)(22) |
| MF | DNA-directed DNA polymerase activity (GO:0003887) | IDA | (21) |
| CC | zeta DNA polymerase complex (GO:0016035)  | IPI | (21) |
| PolZ2 | BP |  |  |  |
| MF |  |  |  |
| CC | zeta DNA polymerase complex (GO:0016035)  | IPI | (21) |
| PolH | BP | translesion synthesis (GO:0019985) | IDA | (23) |
| MF | DNA-directed DNA polymerase activity (GO:0003887) | IDA, IMP | (23) |
| CC | n/a |  |  |
| PolI | BP | translesion synthesis (GO:0019985) | IDA | (23) |
| MF | DNA-directed DNA polymerase activity (GO:0003887) | IDA, IMP | (23) |
| CC | n/a |  |  |
| Rev1 | BP | DNA synthesis involved in double-strand break repair via homologous recombination (GO:0043150)translesion synthesis (GO:0019985) | IMPISS | (16)n/a |
| MF | deoxycytidyl transferase activity (GO:0017125) | ISS | n/a |
| CC | n/a |  |  |
| PolQ | BP | DNA synthesis involved in DNA repair (GO:0000731)DNA synthesis involved in DNA repair (GO:0000731)DNA biosynthetic process (GO:0071897)  | IDAIMPIDA | (24)(25)(26) |
| MF | DNA-directed DNA polymerase activity (GO:0003887) | IDA | (24,26,27) |
| CC | n/a |  |  |
| PolG1 | BP | DNA-dependent DNA replication (GO:0006261)mitochondrial DNA replication (GO:0006264)DNA replication proofreading (GO:0045004)DNA replication proofreading (GO:0045004) | IDAIMPIDAIMP | (28-41)(42-44)(33,35)(43) |
| MF | DNA-directed DNA polymerase activity (GO:0003887)DNA-directed DNA polymerase activity (GO:0003887)3'-5'-exodeoxyribonuclease activity (GO:0008296)3'-5'-exodeoxyribonuclease activity (GO:0008296) | IDAIMPIDAIMP | (28,33,35,37,38,40,41)(43)(33,35,37,40)(43) |
| CC | gamma DNA polymerase complex (GO:0005760) | IDA | (28,33,37,38,40,41) |
| PolG2 | BP | DNA-dependent DNA replication (GO:0006261)DNA-dependent DNA replication (GO:0006261)mitochondrial DNA replication (GO:0006264)positive regulation of DNA-directed DNA polymerase activity (GO:1900264) | IDAIPIIMPISS | (28-34,36-41)(45)(42)(46) |
| MF | DNA polymerase processivity factor activity (GO:0030337) | ISS | (46) |
| CC | gamma DNA polymerase complex (GO:0005760)gamma DNA polymerase complex (GO:0005760) | IPIIDA | (45)(28,33,37,38,40,41) |

**Supplementary Table 2. Proposed and previous FlyBase symbols/names for the DNA polymerases of *D. melanogaster***

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Proposed symbol** | **Proposed name** | **Previous symbol** | **Previous name** | **FBgn ID** | **CG number** |
| PolA1 | DNA polymerase alpha subunit 1 | DNApol-ɑ180 | DNA polymerase ɑ 180kD | FBgn0259113 | CG6349 |
| PolA2 | DNA polymerase alpha subunit 2 | DNApol-ɑ73 | DNA polymerase ɑ 73kD | FBgn0005696 | CG5923 |
| Prim1 | DNA primase subunit 1 | DNApol-ɑ50 | DNA polymerase ɑ 50kD | FBgn0011762 | CG7108 |
| Prim2 | DNA primase subunit 2 | DNApol-ɑ60 | DNA polymerase ɑ 60kD | FBgn0259676 | CG5553 |
| PolD1 | DNA polymerase delta subunit 1 | DNApol-δ | DNA-polymerase-delta | FBgn0263600 | CG5949 |
| PolD2 | DNA polymerase delta subunit 2 | Pol31 | Pol31 polymerase delta subunit | FBgn0027903 | CG12018 |
| PolD3 | DNA polymerase delta subunit 3 | Pol32 | Pol32 polymerase delta subunit | FBgn0283467 | CG3975 |
| PolE1 | DNA polymerase epsilon subunit 1 | DNApol-ε255 | DNA polymerase ε 255kD subunit | FBgn0264326 | CG6768 |
| PolE2 | DNA polymerase epsilon subunit 2 | DNApol-ε58 | DNA polymerase ε 58kD subunit | FBgn0035644 | CG10489 |
| PolE3 | DNA polymerase epsilon subunit 3 | Chrac-14 | Chromatin accessibility complex 14kD protein | FBgn0043002 | CG13399 |
| PolE4 | DNA polymerase epsilon subunit 4 | Mes4 | Mesoderm-expressed 4 | FBgn0034726 | CG11301 |
| PolZ1 | DNA polymerase zeta subunit 1 | mus205 | mutagen-sensitive 205 | FBgn0002891 | CG1925 |
| PolZ2 | DNA polymerase zeta subunit 2 | rev7 | rev7 | FBgn0037345 | CG2948 |
| PolH | DNA polymerase eta | DNApol-η | DNApol-η | FBgn0037141 | CG7143 |
| PolI | DNA polymerase iota | DNApol-ɩ | DNApol-ɩ | FBgn0037554 | CG7602 |
| Rev1 | DNA polymerase Rev1 | Rev1 | Rev1 | FBgn0035150 | CG12189 |
| PolQ | DNA polymerase theta | mus308 | mutagen-sensitive 308 | FBgn0002905 | CG6019 |
| PolG1 | DNA polymerase gamma subunit 1 | tam | tamas | FBgn0004406 | CG8987 |
| PolG2 | DNA polymerase gamma subunit 2 | DNApol-ɣ35 | DNA polymerase gamma 35kD | FBgn0004407 | CG33650 |

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