TITLE: Eukaryotic Translesion DNA Synthesis on the Leading and Lagging Strands: Unique Detours Around the Same Obstacle

AUTHORS: Mark Hedglin[†] and Stephen J. Benkovic[†,*]

[†] *Department of Chemistry, The Pennsylvania State University, University Park, PA 16802, U.S.A.*

[*] Author to whom correspondence should be addressed

Email:sjb1@psu.edu

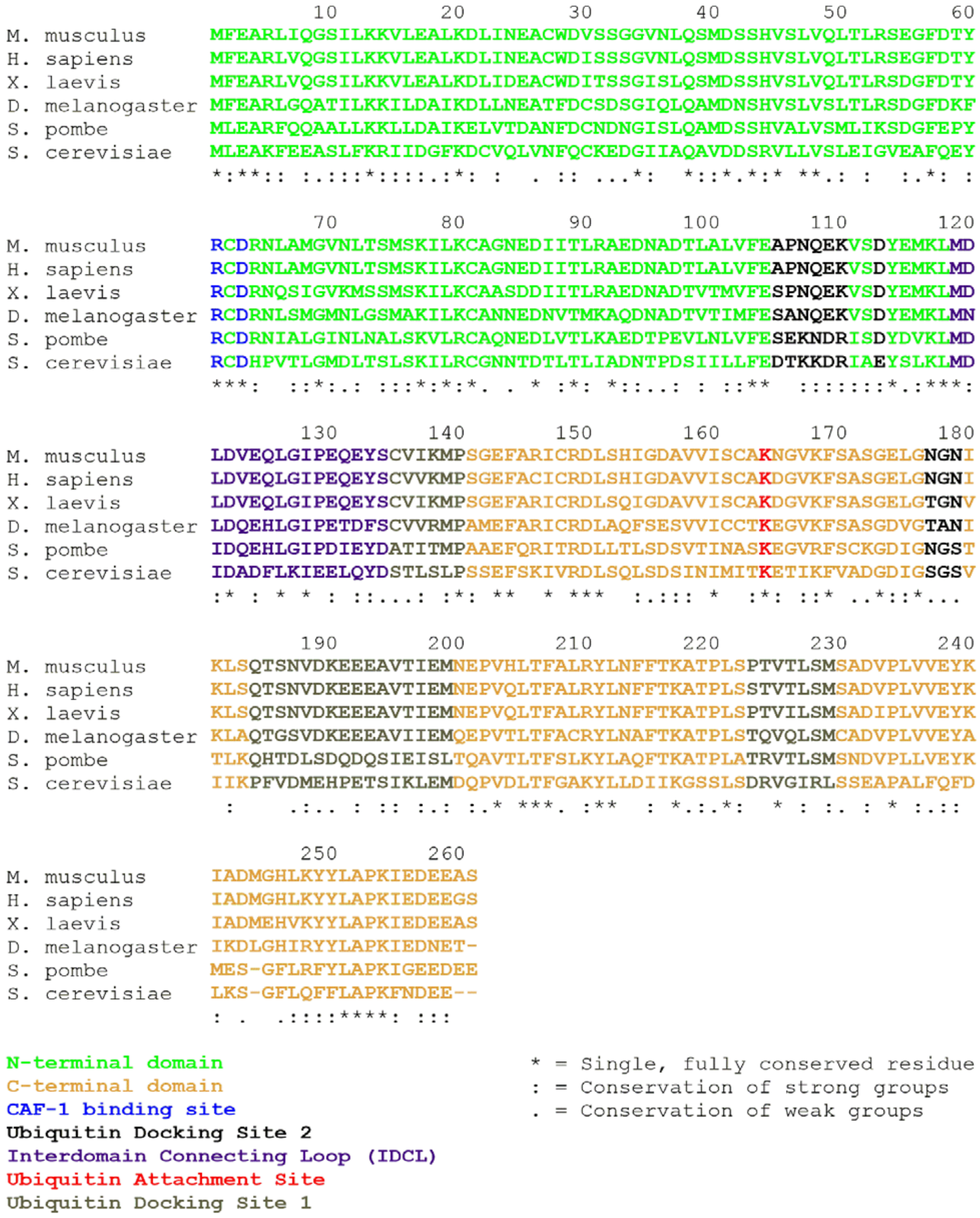
Phone: 814-865-2882

Supporting Information

Supporting Information Figure Legend

Figure S1 Conservation of PCNA. Amino acid sequences of PCNA from *M. musculus* (mouse), *H. sapiens* (human), *X. laevis* (frog), *D. melanogaster* (fruit fly), *S. pombe* (fission yeast), and *S. cerevisiae* (budding yeast) were aligned using SDSC Biology workbench. Color scheme of highlighted residues (indicated) is identical to **Figure 11B** in the main text. Fully, strongly, and weakly conserved residues are indicated.

Supporting Information Figure



```
                         10        20        30        40        50        60
M. musculus      MFEARLIQGSILKKVLEALKDLINEACWDVSSGGVNLQSMDSSHVSLVQLTLRSEGFDTY
H. sapiens       MFEARLVQGSILKKVLEALKDLINEACWDISSSGVNLQSMDSSHVSLVQLTLRSEGFDTY
X. laevis        MFEARLVQGSILKKVLEALKDLIDEACWDITSSGISLQSMDSSHVSLVQLTLRSDGFDTY
D. melanogaster  MFEARLGQATILKKILDAIKDLLNEATFDCSDSGIQLQAMDNSHVSLVSLTLRSDGFDKF
S. pombe         MLEARFQQAALLKKLLDAIKELVTDANFDCNDNGISLQAMDSSHVALVSMLIKSDGFEPY
S. cerevisiae    MLEAKFEEASLFKRIIDGFKDCVQLVNFQCKEDGIIAQAVDDSRVLLVSLEIGVEAFQEY
                 *:**:: :.:::*::::.:*: :  . :: ...*:  *::*.*:* **.: :  :.*: :

                         70        80        90       100       110       120
M. musculus      RCDRNLAMGVNLTSMSKILKCAGNEDIITLRAEDNADTLALVFEAPNQEKVSDYEMKLMD
H. sapiens       RCDRNLAMGVNLTSMSKILKCAGNEDIITLRAEDNADTLALVFEAPNQEKVSDYEMKLMD
X. laevis        RCDRNQSIGVKMSSMSKILKCAASDDIITLRAEDNADTVTMVFESPNQEKVSDYEMKLMD
D. melanogaster  RCDRNLSMGMNLGSMAKILKCANNEDNVTMKAQDNADTVTIMFESANQEKVSDYEMKLMN
S. pombe         RCDRNIALGINLNALSKVLRCAQNEDLVTLKAEDTPEVLNLVFESEKNDRISDYDVKLMD
S. cerevisiae    RCDHPVTLGMDLTSLSKILRCGNNTDTLTLIADNTPDSIILLFEDTKKDRIAEYSLKLMD
                 ***:  ::*:.: :::*:*:*. . * :*: *::..: : ::**  :::::::*.:***:

                        130       140       150       160       170       180
M. musculus      LDVEQLGIPEQEYSCVIKMPSGEFARICRDLSHIGDAVVISCAKNGVKFSASGELGNGNI
H. sapiens       LDVEQLGIPEQEYSCVVKMPSGEFACICRDLSHIGDAVVISCAKDGVKFSASGELGNGNI
X. laevis        LDVEQLGIPEQEYSCVIKMPSGEFARICRDLSQIGDAVVISCAKDGVKFSASGELGTGNV
D. melanogaster  LDQEHLGIPETDFSCVVRMPAMEFARICRDLAQFSESVVICCTKEGVKFSASGDVGTANI
S. pombe         IDQEHLGIPDIEYDATITMPAAEFQRITRDLLTLSDSVTINASKEGVRFSCKGDIGNGST
S. cerevisiae    IDADFLKIEELQYDSTLSLPSSEFSKIVRDLSQLSDSINIMITKETIKFVADGDIGSGSV
                 :* : * * : ::...: :*: **  * ***  :.::: *  :*: ::* ..*::*...

                        190       200       210       220       230       240
M. musculus      KLSQTSNVDKEEEAVTIEMNEPVHLTFALRYLNFFTKATPLSPTVTLSMSADVPLVVEYK
H. sapiens       KLSQTSNVDKEEEAVTIEMNEPVQLTFALRYLNFFTKATPLSSTVTLSMSADVPLVVEYK
X. laevis        KLSQTSNVDKEEEAVTIEMNEPVQLTFALRYLNFFTKATPLSPTVILSMSADIPLVVEYK
D. melanogaster  KLAQTGSVDKEEEAVIIEMQEPVTLTFACRYLNAFTKATPLSTQVQLSMCADVPLVVEYA
S. pombe         TLKQHTDLSDQDQSIEISLTQAVTLTFSLKYLAQFTKATPLATRVTLSMSNDVPLLVEYK
S. cerevisiae    IIKPFVDMEHPETSIKLEMDQPVDLTFGAKYLLDIIKGSSLSDRVGIRLSSEAPALFQFD
                  :    .:.. : :: :.: :.* ***. :**  : *.:.*:  * : :. : * :.::

                        250       260
M. musculus      IADMGHLKYYLAPKIEDEEAS
H. sapiens       IADMGHLKYYLAPKIEDEEGS
X. laevis        IADMEHVKYYLAPKIEDEEAS
D. melanogaster  IKDLGHIRYYLAPKIEDNET-
S. pombe         MES-GFLRFYLAPKIGEEDEE
S. cerevisiae    LKS-GFLQFFLAPKFNDEE--
                 : .  .::::****: :::
```

N-terminal domain
C-terminal domain
CAF-1 binding site
Ubiquitin Docking Site 2
Interdomain Connecting Loop (IDCL)
Ubiquitin Attachment Site
Ubiquitin Docking Site 1

* = Single, fully conserved residue
: = Conservation of strong groups
. = Conservation of weak groups

Figure S1