

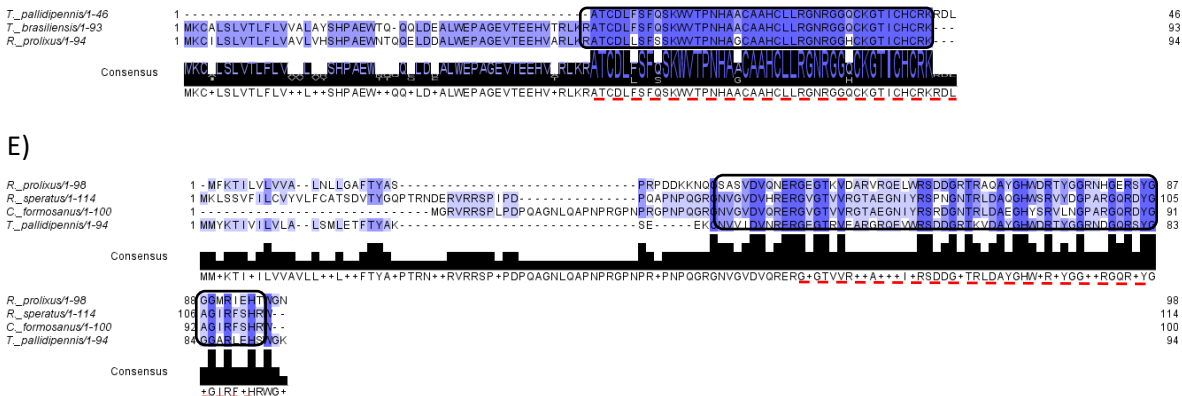
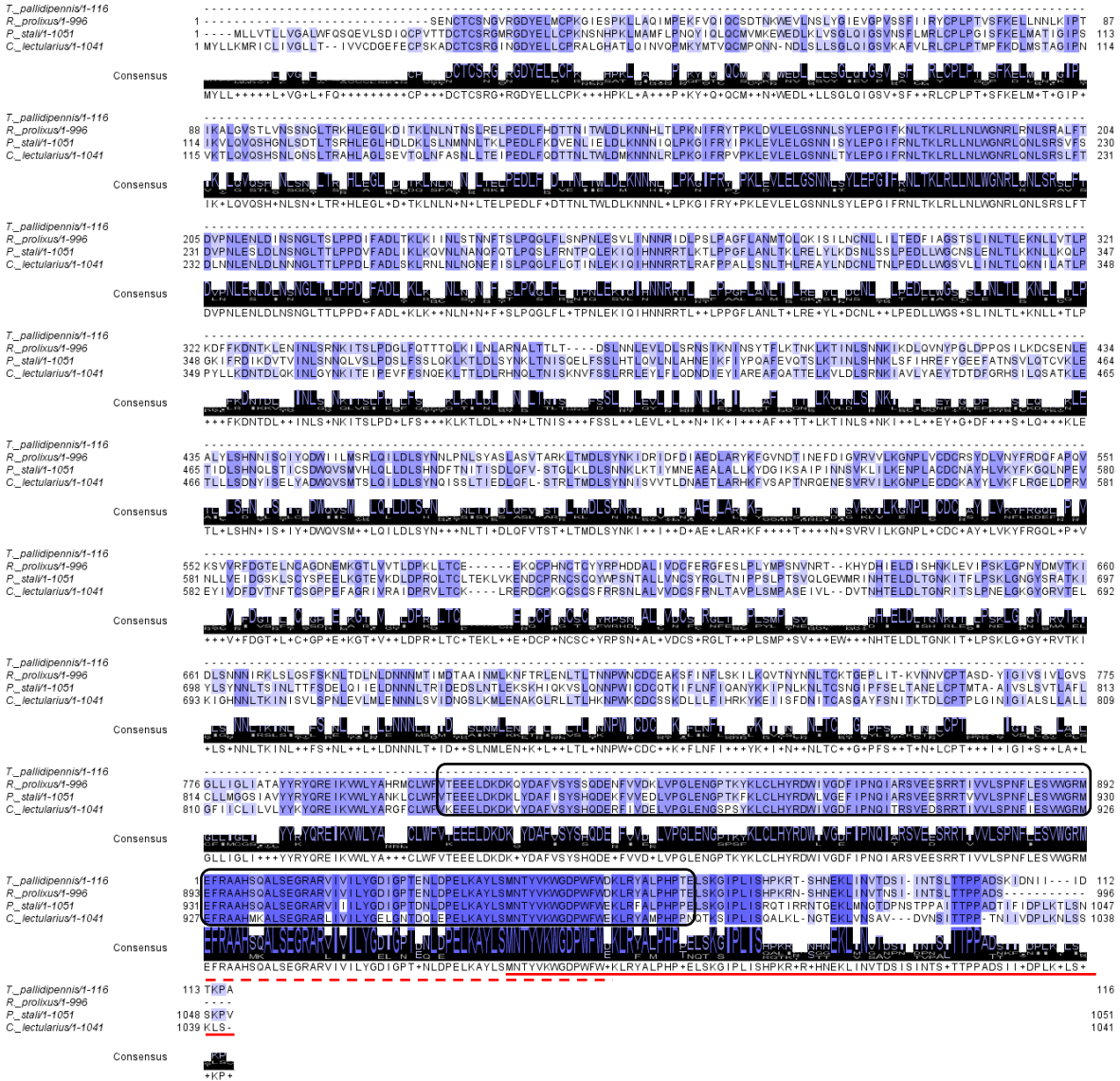
T. pallidipennis?f-329 1 MEGL VLAE NIETDNWIDSKIE ILL PKDL ELGNCSEDDA 41
T. prolixus?f-359 1 MSTSEFRVE QEVKSAMVWCSRAQC PEE IQLKSLNATDIFS 41
D. melanogaster?f-500 1 MPFSNIETEMSCSNAKRRVNDLP LTPKNCSTSS TSDSGV I LNDNVAAFRPEKET D KDRGTGGGFGSKSEETKSKRIISVEHTNIITNKVGKTSPPAVS IIRSTT I SVSVIDNA IDS S ISDSDEAE 126
Consensus TSHRLK.....CEQMA BK IQRHRS..... IETM.....CSGQVETELPS.....
MPFSNIETEMSCSNAKRRVNDLP LTPKNCSTSS TSDSGV I LNDNVAAFRPEKET D KDRGTGGGFGSKSEETKSKRIISVEHTNIITNVWSS.....STTISVSPSDA.....ELSN.....S.....AE

T. pallidipennis?f-329 42 DTKTS SITDN EEI S P HOLENNILNITSCSGV IHWYDITQYLWKSQA VH 101
T. prolixus?f-359 42 TNIISVVKY IEDTVYKLSBKETFI TKDMQ IEG NNDIKTEVKKLRKELE IAINAGPKQLD RRVNSQERRRLKLTLD 101
D. melanogaster?f-500 127 AEDYTVQKLGHQVITYPPNSSHLRD LNOGLTVISIRHVAVGEAAVPPNP L EAG I VAKQL LNLNLAVATPTSPAGGATQGIS IALTNSTDITFGDKHFVEPTIOTGL I DNRQKWP BEGPAGGOD 252
Consensus ETTL.....RSTVYKLTTHRY.....TAMAKL.....NDG.....HPRV.....RRLNN.....G.....G.....
AEDYTVQKLGHQVITYPPN+SV+V.....SIS.....EAAVPPNP L E A.....I.....GNLAVATPTSPN+.....IG+L+T.....V+G+Q+Y+G+VTIO+V+S+D+.....GGOD

T. pallidipennis?f-329 102 ALPDCDVGQITTF I ESD KEENKNLKS ILS SVK GRHWY I I LVLVLGAVAL ILLLTONEED DWLSK DRLITRGVYLALERTGVKFKL RVH IWHATSGSMBLSLTAAT 217
T. prolixus?f-359 102 IIS IQLNLTQFDPAYNE KEENKNLKS ILS SVKR RRHLLF I I V I LVL IGAVAL ILLLTONEEDSEEMANN I LTLWDAERSPKVELD LKVPV IWHATAGNSGTST 238
D. melanogaster?f-500 253 NPANFGNSPTNGSARGSKHEDPAQTPT I C P F I PNTGRKAVYTVTVFVLTFLGL I V I LATTN I LFGKLTNODLVDV I NDTLVL I LKVAEGGRFAKRLMDAQL I P I NRV I SH I AEGGDSREVE 377
Consensus HNVG.....G.....EENKRLKS ILS SVK GRHWY I I LVLVLGAVAL ILLLT EN D NSTL I L+R+W+V+A+P+G+V+.....KLN+H+V+I+HTA+S+C+S+.....C
NPAA+G+G+TN+...+P+A+...E+ENKRLKS ILS+NSV+RK+RHL+...I F+I+LVL IGAVAL ILLLT+...EN+D+...NSTL I L+R+W+V+A+P+G+V+.....KLN+H+V+I+HTA+S+C+S+.....C

T. pallidipennis?f-329 219 SLKRTV I AD A F SROVSD IGVN I LVGGDGN I REGRMD I AHT I LQVNI I LVA I I Q IARDP LKPKS I FAL I SEVKG I LQ I LQVNI I LK I LQVNI I KTS P A I S I 329
T. prolixus?f-359 219 KQVRD I Q I D L SROVSD IGVN I LVGGDGN I REGRMD I AHT I LQVNI I LVA I I Q IARDP LKPKS I FAL I SEVKG I LQ I LQVNI I KTS P A I S I 329
D. melanogaster?f-500 378 SARNVIVSGFHMDVGVGH I GYN I LVGGDGRV I EGRMD I GAHT I GYN I S I G I I GTF I LPP I ROL A I L L EGVKGL I L I N Y L I H K V A I T E S P 500
Consensus S.....R.....SROVSD IGVN I LVGGDGN I EGRMD I GAHT I GYN I S I G I I GTF I LPP I ROL A I L L EGVKGL I L I N Y L I H K V A I T E S P
S+VR I Q I D I SROVSD IGVN I LVGGDGN I EGRMD I GAHT I GYN I S I G I I GTF I LPP I ROL A I L L EGVKGL I L I N Y L I H K V A I T E S P

[illegible]



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