

cenH3_updated_aligned.fasta

Drosophila 22024004 cenH3MPRHSRA*RAPRPSANNSKSPN.....DDDTAFRSPEFEDGTDYGLEF*TSQLTLQDNNRRSSTLRRDAGRRQPAARDSST.....S*EEDQENRYPTTRSPQT*RMTVQQESKTRAAG	110
Perkinsus 294874934 cenH3MART*HRVTRSQ.....P*RNQTDAAGASSSQAAGPTTTPTRRG.....E*GDNTQQTNP*TS*PATGTRGAK*SRQAMPRGS	27
Arabidopsis 18378832 cenH3MART*HRVTRSQ.....P*RNQTDAAGASSSQAAGPTTTPTRRG.....E*GDNTQQTNP*TS*PATGTRGAK*SRQAMPRGS	73
Tetrahymena 118356028 cenH3MART*HRVTRSQ.....P*RNQTDAAGASSSQAAGPTTTPTRRG.....E*GDNTQQTNP*TS*PATGTRGAK*SRQAMPRGS	70
Plasmodium 124513424 cenH3MART*HRVTRSQ.....P*RNQTDAAGASSSQAAGPTTTPTRRG.....E*GDNTQQTNP*TS*PATGTRGAK*SRQAMPRGS	70
Cyanidioschyzon 544210412 cenH3	MVRVFGNPVGGAHQYRQTQALNRDESL*EQLQRTTVAEQDENIEPEPERSSPDEAQSRLKSLLGSVAR*SSLLGRRVAGPPGSSLSNLAETRLLT*EEAANRPTGAGRSERVS*Q*RAEPLPPGP*TTATTNADANTVQRGLSVASAF	145
Guillardia 13794280 cenH3MART*HRVTRSQ.....P*RNQTDAAGASSSQAAGPTTTPTRRG.....E*GDNTQQTNP*TS*PATGTRGAK*SRQAMPRGS	6
Thalassiosira 223995905 cenH3MARA*P.....P*GSSSSSARRRNDPLGRARERESS.....A*CGGGRLSAGS*AAAGGG.....*ERPRGPTSA	61
Phytophthora 695416328 cenH3MASP*PPALPASDASSSSVTDSGTDDSTPPNSPQ*QRSPSPFFAA*RGPAARAPPAAPSSVSSASTPSPPNLPARRPSVA.....P*V*QRQAIIHATP*APRRKR*ATPP*RRPSSPASA	116
consensus*.....*.....**.....*	

Drosophila 22024004 cenH3	PVAA.....QNQT*RR*KA*ANP*SRAKRMD*E*IRRL*QHHPGT*LI*KL*P*SR*LVRE*FI*VKYS.DDEPL*RVTEG*AL*LA*MQ*ES*CE*MY*TI*QRL*AD*SY*LT*KA*RN*RV*TI*EV*RD*MA*IM*AY*TI*CDRGRQF.....	225
Perkinsus 294874934 cenH3R*Y*RP*GT*VAL.....E*IRRH*QE*ITD*PL*IE*KR*CF*Q*AL*AR*SL*SR*EV*E.AS..M*W*QP*Q*SL*VA*LQE*AS*ES*TI*VG*ML*EA*SQ*LL*AV*H*GR*RI*TL*ME*KD*VK*NT*TR*CA*IM*FG*ST*TF*MD*QE*KQ*VG*G	136
Arabidopsis 18378832 cenH3Y*Y*RP*GT*VAL.....E*IRRH*QE*ITD*PL*IE*KR*CF*Q*AL*AR*SL*SR*EV*E.AS..M*W*QP*Q*SL*VA*LQE*AS*ES*TI*VG*ML*EA*SQ*LL*AV*H*GR*RI*TL*ME*KD*VK*NT*TR*CA*IM*FG*ST*TF*MD*QE*KQ*VG*G	178
Tetrahymena 118356028 cenH3Y*Y*RP*GT*VAL.....E*IRRH*QE*ITD*PL*IE*KR*CF*Q*AL*AR*SL*SR*EV*E.AS..M*W*QP*Q*SL*VA*LQE*AS*ES*TI*VG*ML*EA*SQ*LL*AV*H*GR*RI*TL*ME*KD*VK*NT*TR*CA*IM*FG*ST*TF*MD*QE*KQ*VG*G	187
Plasmodium 124513424 cenH3Y*Y*RP*GT*VAL.....E*IRRH*QE*ITD*PL*IE*KR*CF*Q*AL*AR*SL*SR*EV*E.AS..M*W*QP*Q*SL*VA*LQE*AS*ES*TI*VG*ML*EA*SQ*LL*AV*H*GR*RI*TL*ME*KD*VK*NT*TR*CA*IM*FG*ST*TF*MD*QE*KQ*VG*G	170
Cyanidioschyzon 544210412 cenH3	PPRAPLQAAGFTVARRTTRSGVQRK*RR*RP*GSRA*.....E*IRK*F*QR*ST*ELL*IR*LP*PAR*LV*RE*IC*ER*F.GSSAF*RW*Q*AS*AL*EAL*QT*AA*ED*YL*HL*F*ED*SN*LCAI*HARR*VT*IM*PD*IAL*AR*IR*CY*HS*DP*HG*YL.....	275
Guillardia 13794280 cenH3L*K*RP*EK*SS*NSL.....E*IRK*F*QR*ST*ELL*IR*LP*PAR*LV*RE*IC*ER*F.GSSAF*RW*Q*AS*AL*EAL*QT*AA*ED*YL*HL*F*ED*SN*LCAI*HARR*VT*IM*PD*IAL*AR*IR*CY*HS*DP*HG*YL.....	103
Thalassiosira 223995905 cenH3	QPTV.....RRKR*MR*P*EKAL.....E*IR*Q*Y*QS*ST*SL*IR*LP*PAR*LV*RE*IQ*Y*GM*F.RQ.PY*RW*Q*AS*AL*LA*LQE*AA*AH*LV*GL*F*ED*SN*LCAI*H*GR*VT*IM*PK*DM*Q*LA*RI*RC*W*V*RE.....	166
Phytophthora 695416328 cenH3	TQTV.....KK*RR*P*GEA*AL.....E*IR*RL*LR*ST*KL*LL*KL*LP*PAR*VV*RE*I*Q*TE*FT.GV.GY*RW*Q*AE*AL*LA*LQE*AA*ET*VL*V*RT*F*ED*NL*CAI*H*GR*VT*LV*Q*V*KI*QL*SL*RI*RC*IR*PT*AS.....	222
consensus	R**** ** **IR *Q ** *L* ***F R***** * R** A**ALQ** E *** **D*****H**RV* **D* L*****	

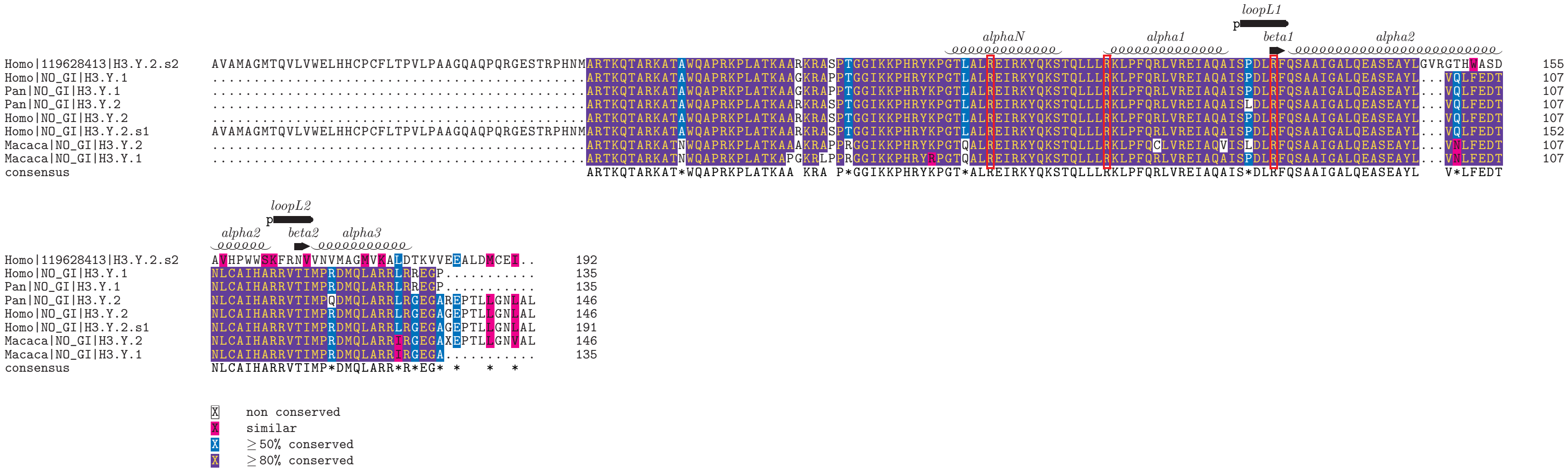
Drosophila 22024004 cenH3	.	225
Perkinsus 294874934 cenH3	T	137
Arabidopsis 18378832 cenH3	.	178
Tetrahymena 118356028 cenH3	.	187
Plasmodium 124513424 cenH3	.	170
Cyanidioschyzon 544210412 cenH3	.	275
Guillardia 13794280 cenH3	.	103
Thalassiosira 223995905 cenH3	.	166
Phytophthora 695416328 cenH3	.	222
consensus		

- ⬜ non conserved
- ⬜ similar
- ⬜ ≥ 50% conserved
- ⬜ ≥ 80% conserved

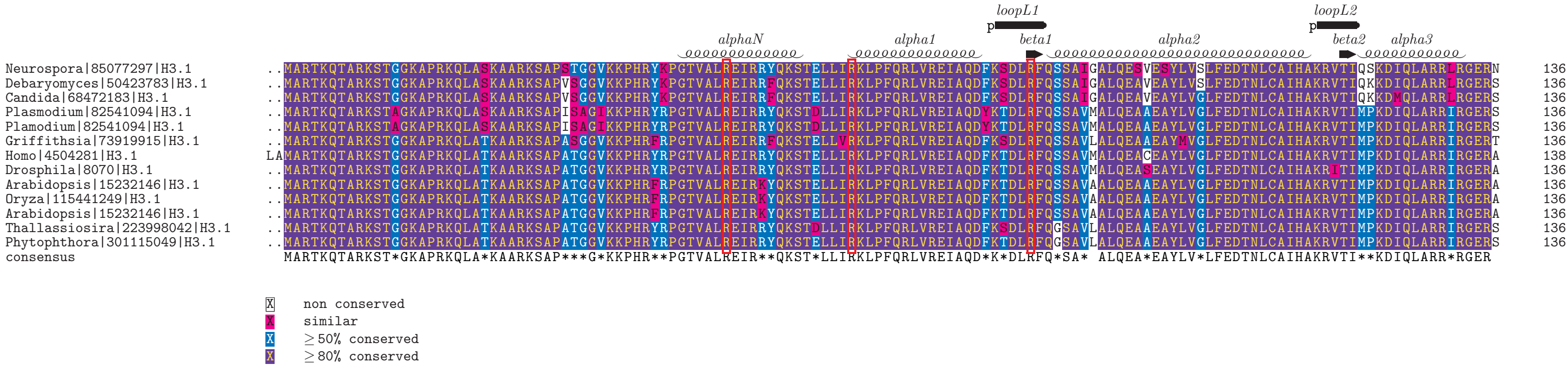
H3.3_aligned.fasta

Sequence logo for the P-loop region of the P-loop NTPase domain. The logo shows conservation across 136 species. The x-axis represents the amino acid position (1-100). The y-axis represents the conservation score (0-100). The logo is color-coded by conservation level: red for non-conserved, yellow for similar, green for ≥ 50% conserved, and blue for ≥ 80% conserved. The logo shows a high degree of conservation in the P-loop region (positions 1-10) and the NTPase domain (positions 100-136).

H3.Y_updated_aligned.fasta



H3.1_updated_aligned.fasta



H3.2_updated_aligned.fasta

