





H1.0.fasta

Thalassiosira|220970504|H1.0
Salmo|223672729|H1.0
Esox|742177175|H1.0
Salmo|197632441|H1.0
Salmo|221219746|H1.0
Salmo|221221998|H1.0
Taenopygia|449481975|H1.0
Gallus|113206128|H1.0
Carina|122111|H1.0
Xenopus|47498062|H1.0
Homo|4885371|H1.0
Pongo|197098626|H1.0
Bos|115496898|H1.0
Rattus|6981004|H1.0
Mus|31560697|H1.0
consensus

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.....MSYKAGTAKTITELDRTCSSSIATKKHMQNLPADKKWMATFLKALKDMVASGEIVKTK.....ASYKLSAVAKQMASSAG....PKMAPKKAPKKTAPKKAA.....PT....102
.MAETAAAPAP..KAKKAKAPKKPASHPKYSDMIKAAVHADKSRGCASRQSVQKYIKSHYKVGDN.ADSQIKLSLKKRMVSEGVLRRHTKGTGASGSPKLAKAEDTTKAPKVKAUVMAKMSPVKSAKPKKVAKPKVVGQITKKSQESKSGSE146
.MAETVAAPAP..KAKKAKAPKKPASHPKYSDMIKAAVQADKSRGCASRQSVQKYIKSHYKVGDN.ADSQIKLSLKKRMVSGGLRRHTKGTGASGSPKLAKAEDTTKAPKPKPVVMAKMSPVKAAKPKKVAKPKVVKSPAKAKKAAVAVK146
.MAETAAAPAP..KAKKAKAPKKPASHPKYSDMIKAAVHADKSRGCASRQSVQKYIKSHYKVGDN.ADSQIKLSLKKRMVSEGVLRRHTKGTGASGSPKLAKAEDTTKAPKVKAUVMAKMSPVKSAKPKKVAKPKVVKSPAKAKKAAVAVK146
.....MIKAAVHADKSRGCASRQSVQKYIKSHYKVGDN.ADSQIKLSLKKRMVSEGVLRRHTKGTGASGSPKLAKAEDTTKAPKVKAUVMAKMSPVKSAKPKKVAKPKVVKSPAKAKKAAVAVK117
.....MIKAAVHADKSRGCASRQSVQKYIKSHYKVGDN.ADSQIKLSLKKRMVSEGVLRRHTKGTGASGSPKLAKAEDTTKAPKVKAUVMAKMSPVKSAKPKKVAKPKVVKSPAKAKKAAVAVK117
.....MVTAAVRADKSRGCASRQSIQKYIKSNYKVGQN.ADVQIRLAIIRLLAAGVLKQTKGVGASGSPRLAKAGKAKRSPSR....ARKHAARRSTSPKTAARSRM...ARSPAKKPASA..108
MTESLVLSFAP.AKPKRVKASRRSASHPTTYSEMIAAATRAEKSRGSSSRQSIQKYIKSHYKVGHN.ADLQIKLSIRRLAAGVLKQTKGVGASGSPRLAKAGKAKRSPG....KKKHAARRSTSPKTAARSRM...ARSPAKKPAT..138
MTDSPIPAPAPAAKPKRAKAPKKPASHPSYSEMIAAATRAEKSRGSSSRQSIQKYIKSHYKVGQH.ADLQIKLSIRRLAAGVLKQTKGVGASGSPRLAKAGKAKRSPAGKK....KKKHAARRSTSPKTAARSRM...ARSPAKKPAA..142
MTENSAAAPAG..KPKRSKASKKATDHPKYSDMILAAVQAEKSRSGSSSRQSIQKYIKSHYKVGDN.ADSQIKLSIKRLVITGVLKQTKGVGASGSPRLAKADEGKKPAK....PKKKEIKKAAKSPKKAAPKKAAPKSPAKAKKPVVAEK142
MTENSTSAFAP..KPKRAKASKKSTDHPKYSDMIVAAIQAEKNRAGSSSRQSIQKYIKSHYKVGDN.ADSQIKLSIKRLVITGVLKQTKGVGASGSPRLAKSDEPKKSVAFK....TKKKEIKKVATPKKASPKKMAA.SKAPTKKPAT..141
MTENSTSAFAP..KPKRAKASKKSTDHPKYSDMIVAAIQAEKNRAGSSSRQSIQKYIKSHYKVGDN.ADSQIKLSIKRLVITGVLKQTKGVGASGSPRLAKSDEPKKSVAFK....TKKKEIKKVATPKKASPKKMAA.SKAPTKKPAT..141
MTENSTSTPAA..KPKRAKASKKSTDHPKYSDMIVAAIQAEKNRAGSSSRQSIQKYIKSHYKVGDN.ADSQIKLSIKRLVITGVLKQTKGVGASGSPRLAKSDEPKKSVAFK....TKKKEIKKVATPKKAAKPKMAA.SKAPSKKPAT..141
MTENSTSTPAA..KPKRAKASKKSTDHPKYSDMIVAAIQAEKNRAGSSSRQSIQKYIKSHYKVGDN.ADSQIKLSIKRLVITGVLKQTKGVGASGSPRLAKGDEPKKSVAFK....TKKKEIKKVATPKKAAKPKMAA.SKAPSKKPAT..141
MTENSTSAFAP..KPKRAKASKKSTDHPKYSDMIVAAIQAEKNRAGSSSRQSIQKYIKSHYKVGDN.ADSQIKLSIKRLVITGVLKQTKGVGASGSPRLAKGDEPKKSVAFK....TKKKEIKKVATPKKAAKPKMAA.SKAPSKKPAT..141
*      **      *      *****      *      *****M*      AA*      A*K*R*G*SRQS*K*Y*K**YKVG**      AD*QI*L***R***      G*L**TKG*GASGS**LAK***      K**      *      K      KK      **      **P*K      ****K      *      *      ***K
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Thalassiosira|220970504|H1.0
Salmo|223672729|H1.0
Esox|742177175|H1.0
Salmo|197632441|H1.0
Salmo|221219746|H1.0
Salmo|221221998|H1.0
Taenopygia|449481975|H1.0
Gallus|113206128|H1.0
Carina|122111|H1.0
Xenopus|47498062|H1.0
Homo|4885371|H1.0
Pongo|197098626|H1.0
Bos|115496898|H1.0
Rattus|6981004|H1.0
Mus|31560697|H1.0
consensus

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.KKT.ATKK...AATAKKPAAKKATTAK.....KSTTKTAKK.....135
ESEK.VPEESCTKAQESSK.ENQGGQASQNETQEQCSETQTQGRSQESRMEEVNGHFRETTYNKSHCKYFEMFFVYVILFLYGLMRTYTFPLPIVFHSSIDAVKEGLELKFWCVTALIVGLLCLRLFLCDL276
KVKK.SPKRVAPKPKKVVK.KVKAAPKAVKPKKAAAKKPKPKAAAKKAAKKK.....198
KVKK.SPKMAAPKPKKVAK.KTKVAKPAKAKPKPKKAAAKKPKPKAAAKMAAKKK.....198
KVKK.SPKMAAPKPKKVVK.KTKVAKPAKAKPKPKKAAAKKPKPKAAAKMAAKKK.....169
KVKK.SPKMAAPKPKKVAK.KTKVAKPAKAKPKPKKAAAKKPKPKAAAKMAAKKK.....169
.AKKLARKMSRS.PKKAKKPKTVKAKSLKASKPKKARRSKRASKGARKSPKKK.....159
.AKKLARKMSRASPKKAKKPKTVKAKSRKASKAKKVRRSKPRASKGARKSPKKK.....190
.AKKLARKMSRASPKKAKKPKTVKAKSLKTSKVKKARRSKPRASKGARKSPKKK.....194
KVKKPAKKKPAAPSPKKAKKTKTVKAKPVKASVKKAKPSKPKAKASPKKSGRKK.....196
PVKK.AKKHLAATPKKAKKPKTVKAKPVKASKPKKAPVKPKAKSSAKKAGKKK.....194
PVKK.AKKHLAATPKKAKKPKTVKAKPVKASKPKKAPVKPKAKSSAKKAGKKK.....194
PVKK.AKKHPAATPKKTKKKPKTVKAKPVKASKPKKTKPVKPKAKSSAKKAGKKK.....194
PVKK.AKKHPAATPKKAKKPKTVKVPVKASKPKKAPVKPKAKSSAKKAGKKK.....194
PVKK.AKKHPAATPKKAKKPVVVKPVKASKPKKAKTVKPKAKSSAKKAGKKK.....194
**K      ***K      *      *****K*****      *****      ***K*      ***      **K*
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-  non conserved
-  similar
-  ≥ 50% conserved
-  ≥ 80% conserved

H1.6.fasta

Rattus|6981006|H1.6
Mus|112807207|H1.6
Homo|20544168|H1.6
Macaca|124053434|H1.6
Canis|545554579|H1.6
Equus|379643033|H1.6
Salmo|221221722|H1.6
Xenopus|147901299|H1.6
consensus

MSETAPAASSTLWPAPV.EKPAIKRRGKKPG..MATARKPRGFVSVKLIPEALSSSQERACMSLAALKKALAAAGYDVEKNNSRIKLALKRLVNMKGVLVQTKGTGASGSFKLSKKA.ASGNDKCKGCKKSASAKAKK..LGLSRASRSPKSKTKV149
MSETAPAASSTLWPAPVEEKPSKKRRGKKPG..LAPARKPRGFVSVKLIPEALSSSQERACMSLAALKKALAAAGYDVEKNNSRIKLALKRLVNMKGVLVQTKGTGASGSFKLSKKA.ASGNDKCKGCKKSASAKAKK..YGLPRASRSPKSKTKA150
MSETVPAASASAGVAAM.EKLPKKRGKKPAGLISASRRVPNLSVSKLITEALSVSQERVMSLVALKKALAAAGYDVEKNNSRIKLSKSLVNMKGILVQTRGTGASGSFKLSKKV.IPKSTSKAKKSVSAKTKK..LVLSRDSKSPKTAKTNK151
MSETVPAASAGAPAVM.EKPLKKRGKKPAGLTSASRRAPNLSVSKLITEALSVSQERVMSLAALKKALAAAGYDVEKNNSRIKLSKSLVNMKGILVQTRGTGASGSFKLSKKV.LPKSTSRKANKSASAKTKK..LVLSRDSKSPKTAKTNK151
MSETVPAVAAGTALASM.ENPSAKKRGRKPGCIPEAAPMAPCLSVSKLIMEALSVSQERACMSLAALKKALAAAGYDVEKNNSRIKLCLKSLVSKGTLVQTKGTGASGSFKLNKKALLPTPAKSVVKKPPSTMTKR..LVLSRDSKSPKAAKTNK152
MSETAPAAPAEPLSSM.EKPPAKKRGRKPVCLTGGSRRVPCLSVSKLITEALSVSQERACMSLAALKKALAAAGYDVEKNNRRIKLCLKSLVSKGTLVQTRGTGASGSFKLSKKA.TPEPAKCHVKKGASANAKK..LVLPKGSKSPKSAKTNK151
.....MSGVLAIPATPATPKRRSKP.....KKTKPTVSDRLKVVVASSGRSSGVSLAALKKSLAASGYDVVKNNARLKLAVRRLVAKGYLLQPKGTGASGSFKLNKK.....AVAKKRPTKNKVKK..VGAKKVRNAS..PKKAA130
MAATTEFAPVAPPAEPAAAQKTKKQQPKKAVAG.GAKAKKPSGPSASELIVKAVSASKERSGVSLAALKKALAAAGYDVKNNSRKLALKLALVTGTLTVKGSASGSFKLNKKQ.PETKDQAKKKPAAPKAPKAPKPAAGAKKAPKSPKKPKKVS153
M**T *** * * * *** *K****KP** *K * SVS*LI *A*S*S*ER G*SLAALKKALAAAGYDV*KNN*R*KL*LK LV KG L*Q**GTGASGSFKL*KK *** K* ***K KK * * * **SPK* K*





Rattus|6981006|H1.6
Mus|112807207|H1.6
Homo|20544168|H1.6
Macaca|124053434|H1.6
Canis|545554579|H1.6
Equus|379643033|H1.6
Salmo|221221722|H1.6
Xenopus|147901299|H1.6
consensus

.VKKP..KAT.PTTCSG.SRRITKGAKGLQQRKS.....PAKARATNSNSCKSKMVMQITDLRKAAGTK208
.VKKP..KAT.PTKASG.SGRATKGAKGVQQRKS.....PAKARAANFNSCKAKMVMQITDLRKAAGTK209
RAKKP..RATTP.KTVF.SGRRAKGAKGKQQQKS.....FVKARASKSKLTQ....HHEVNVRRKATSKK207
RAKKP..RATAPKKAVF.SGRRAKGAKGKQQQKS.....FVKARATKPKLTQ....HHANIRKATSKK208
.AKKP..GAGAQAAC.SGRRAKGAKDKQPRKS.....PGKAPTCKPKAAKPRLNQQKVNPRKAVSKK212
RTSIA..RTPAAQPSAF.GGRKSKGAKGKQQQKS.....PGKCRTGKPKTGKPKLTQQRTNPRKTASKK212
GAKKS.....PKTKTKSPKAKRPAAAKPKS.....PRTKRRVAKSTK.....AKTAPKKK179
AAATSPKVKKPAKAAK.SPKPKKVKAKKVAKSPAKKATKPKTAKSPAKKVAKPKAAK.....AKAPAPKK220
K* ** * K* * SK K**K**** KS P*K** *** ** * *K* *K

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

H1.7.fasta

Mus 257196238 H1.7MAEAVQPSGESQCAELTIQIQCPAERAIRTAKRCTQSVLRVSQLEIRAIAGTQHLLDALKKEICNAGYEVRR	EISSHHEC	KSTRLEKCTLLRVSGSDAAGYFRVWKISKPREKAGQSRLTLGSHSGKTVLK	134
Homo 32401437 H1.7	MEQALTGEAQSFWPRRGSGAMAEAPGPSGESRCHSAT...LPAEKTVGGHSRGCSSEVLRVSQLVQAISTKGLTLAALKKEIRNAGYEVRR	KSGRHEAP	GGQ...AKATLLRVSGSDAAGYFRVWVKPKPRKPCRARQEECTRAPWRTP.A	149
consensus	*****MAEA* PSGES G* T**Q PAE* * P * ** SVLRVSQLE AI H *LTL ALKKEI NAGYEVRR	H* ** **	K*TLRVSGSDAAGYFRVWK**KPR K*G R G** * *T**	
Mus 257196238 H1.7	SPPPLRPISR..RKAAKKAREVWRRKARALKARSRRVTRSTSGARSRTSRASSRATSRTSRARSRA	RSRAQSSARSSARSSAKSSAKSSTRSSAKSWARSKARSRARSR	AKDLVRSKAREQAQARECARARAREQAHARARTQDWVRAKAQE	287
Homo 32401437 H1.7	APRSSRRRQPLRKAAKKAREVWRRNARA.....KAKANARAR.....RTR.....RAPRAKEPPCAR.....			203
consensus	PR* R*R **RKAA*KAREVWRR ARA*****A* AR R*****R*R***** AR*RA*E** AR*****			
Mus 257196238 H1.7	FVSAKEQQYVRAKEQERAKAREQVRIGARDEARIKAKDYNRVRPTKEDTSPNPAEKSSNSKLREEKGQEPERFVKQ	TIQKPALDNAPSIQGGKACTKSFTKSGQPGDTESP		398
Homo 32401437 H1.7AKEEAGATADEGRGQIVKEDTTPRSGKDKRRSSMPREEKQEEKKFAQR	TIQ.....		255
consensus	*****A**EA A D R * KEDT*PR** *K SKREEK*QEP *P TIQ*****			

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

H1.9.fasta

Homo|38372285|H1.9
Mus|9055232|H1.9
Peromyscus|207081162|H1.9
Rattus|157818369|H1.9
consensus

MLHASTIWHLRSTPPRRKQWGHCDPHRILVASEVTETSPTPAPRQVCGGTPWVTIVLDELSGHTGREAEERHFATVSISAVELKYCHGWRPAGQRVPSKATCQRTCAKPCQKPSISKVILRAVADKGTCKYVSLATLKKAVSTGYDM150
.....MAQMVAGDDACTLWVP.....SQSESQTESDISTQSLRKPTMSYVILKTLADKRVHNCVSLATLKKAVSTGYNM71
.....MQRDTLLVSPSAAPNSAVAVDDASTSDDP.....SKSETCGPYTCTPTVRKPSMSKVILRAVTDKGLHRRVSLAALKKAVSTGYNM82
.....MSLVSPSPDSNAVMAAGDDASTSQVP.....SQSESKITCPNVATQTLRKPTMSKVILRTVADKGVHSRVSLAALKKAVSTGYNM80
* *****Q***T* P **S * ** *****KP**S*VIL* **DK****VSLA LKKAVS TGY*M

Homo|38372285|H1.9
Mus|9055232|H1.9
Peromyscus|207081162|H1.9
Rattus|157818369|H1.9
consensus

ARNAYHFKRVLKGLVDKQSA.....GSFTLGKKQASKSKLKVKR.....QRQQRWISGQRPFGQIRSLIGSKQGHKRLIKGVRRVAKCHCN...231
THNTWRFKRVLQNLIDKGMIMHVTCKKGASGSLCLCKERALKSNHRAKRCQDRQSCKPQKPGQRESEPCQLLSKKKKNDQLFKGVRRVAKGNRHCHY170
AHNSWRFKRVLKGLVDKQSA.....GSFTLGKKQASKSKLKVKR.....QRQQRWISGQRPFGQIRSLIGSKQGHKRLIKGVRRVAKCHCN...162
AQNTWRFKRVLQNLIDKGMIMHVTCKKGASGSLCLCKERALKSNHRAKRCQDRQSCKPQKPGQRESEPCQLLSKKKKNDQLFKGVRRVAKGNRHCHY169
N*FKRV* *L* KG***** **GS**L*K**A*KS* ***R ***Q*****QR***** *LL*S*****L***** **

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

H1.10.fasta

Homo|5174449|H1.10 .VSVLEEEAIPVTTLEGMAKKVTKAGG.....SAA[SSKKRKNSKKKNQPGKYSQLVVE[TRRLGERNGSSLAKIYTEAKKVPWFDDQNGRTYLKYSIKALVQNDTLQVKCTGANGSFRLNRKLEGGGERGAP...AAATA 136
Xenopus|147898445|H1.10 .VAFLEENLHTEEEEEEEEEEGDEMRSRSTRNKGAASSSGNKKKKKKNQPGKYSQLVVD[TRKLGERNGSSLAKIYSEAKKVSWFDDQNGRTYLKYSIKALVQNDTLQVKCTGANGSFRLNKKLEGLPYDKPP...PAKPS 146
Osmerus|225708114|H1.10 .VASTDEVVPAAEAPVAAKSKKRTATKPKPKA...KPATVATSSAKKKRKGKCPGKYSVLVD[TRQLGERNGSSLAKIYNEAKKBAIWFDDQHGRTYLRYSSIRALVLNNTLIQVKCTGANGSFRLNKKFETKAPKKAPPVKAVTK 145
Salmo|221221588|H1.10 MVKSEVEVTINAEAPV.....ASSLKPAKKKKNKKKKNKPGKYSVLVD[AVKKLNERSGSSLVKIYNEAKKASWFDEQNGRTYLRYSSIRALVLNNTLIQVKCMGANGSFRLNEDFAKGVPKKTQS...KPAKNT 128
Caligus|225709312|H1.10 MVKSEVEVTINAEAPV.....ASSLKPAKKKKNKKKKNKPGKYSVLVD[AVKKLNERSGSSLVKIYNEAKKASWFDEQNGRTYLRYSSIRALVLNNTLIQVKCMGANGSFRLNEDFAKGVPKKTQS...KPAKNT 128
Uncorhynchus|225703540|H1.10 MVKSEVDVTINAEAPV.....ASGPKPAKKKKNKKKKNKPGKYSVLVD[AVKKLNERSGSSLVKIYNEAKKASWFDEQNGRTYLRYSSIRALVLNNTLIQVKCMGANGSFRLNEDFAKEVPKKTQS...KPAKNT 128
consensus * *E*E* * * EAA* * * * **KK KKKKN PGKYS*LV*D****L ER GSSL KIY*EAKK**WFD QNGRTYL*YSI*ALV*N TL*QVKG*GANGSF*LN K* **K * **AK *

Homo|5174449|H1.10 PAPTAHKAKKA[PGAAGSRRADKKPARQK[EQ[SHKKGAGAKDKGGKA[KTAAGG[VKKAAKFSVPKVPKGK. 213
Xenopus|147898445|H1.10 SSSSNKKQQQQ[PSSSPKSHKKAKPKAAAEKE[PTSSA[KA.....KSPKKSAKCHKMKKGAKPSVKA[KSKKA 218
Osmerus|225708114|H1.10 APAKKAAAI[TKAKPKASPKK[STPKKKFAAMPKKLA[K.....KATPVKSKMPKPKKASKPAAKS.PRKK.. 211
Salmo|221221588|H1.10 TKAKASTTKKATV.VKAKSSPKKAPDAKMFAAKLKKLGVK.....KVSAAQKN[KPKKASKPPAKS.PRKK.. 193
Caligus|225709312|H1.10 TKAKASTTKKATV.VKAKSSPKKAPDAKMFAAKLKKLGVK.....KVSAAQKN[KPKKASKPPAKS.PRKK.. 193
Uncorhynchus|225703540|H1.10 TKAKASTTKKATVKPKAKSSPKKAPDAKMFAAKMKKLGVK.....KVIAAQKN[KPKKASKPPAKS.PRKK.. 194
consensus * * * * * K* P *K P**K KK** K K **A * K K*KKAKP *** P**K

[] non conserved
[X] similar
[X] ≥ 50% conserved
[X] ≥ 80% conserved