Table S1: datasets used					
Species	common name[1]	Kingdom	Phylum/class	Dataset number	Reference
Amphimedon queenslandica	sponge	Metazoa	Porifera	SRR1511621	(1)
Nematostella vectensis	starlet sea anemone	Metazoa	Cnidaria	SRR836055	(2)
Danio rerio	zebrafish	Metazoa	Chordata/Actinopteri	SRR2733359	-
Xenopus tropicalis	tropical clawed frog	Metzoa	Chordata/Amphibia	SRR2105090, SRR1795664	(3, 4)
Sarcophilus harrisii	Tasmanian devil	Metazoa	Chordata/Mammalia	SRR1793358	-
Homo sapiens	human	Metazoa	Chordata/Mammalia	ERR789216	-
Anopheles gambiae	African malaria mosquito	Metazoa	Arthropoda/Insecta	ERX502992	-
Coboldia fuscipes		Metazoa	Arthropoda/Insecta	SRR5559333, SRR5559334	-
Proctacanthus coquilletti		Metazoa	Arthropoda/Insecta	SRR4346725	-
Drosophila melanogaster	Fruit fly	Metazoa	Arthropoda/Insecta	SRR070395, SRR1197414	-
Caenorhabditis elegans	nematode	Metazoa	Nematoda	SRX1130124	-
Trichuris muris		Metazoa	Nematoda	ERR279681	-
Crassostrea gigas	pacific oyster	Metazoa	Mollusca	SRR334212, SRR497890	(5, 6)
Capsaspora owczarzaki		N.A.[2]		SRR515464, SRR515465	-
Spizellomyces punctatus		Fungi	Chytridiomycota	SRX096917	-
Lichtheimia corymbifera		Fungi	Zygomycota	ERX300995	-
Rhizopus delemar		Fungi	Mucoromycota	SRR1013688	-
Ustilago maydis		Fungi	Basidiomycota	ERX159409, ERR184023, SRR3038908, SRR5002417	(7)
Cryptococcus neoformans		Fungi	Basidiomycota	SRR1796376, SRR1796479, SRR1797881, SRR1797885	(8)
Lachancea kluyveri		Fungi	Ascomycota	SRP129038	This study
Neurospora crassa		Fungi	Ascomycota	SRR100067, SRR1043827, SRR1055985, SRR1562549, SRR1588284, SRX042065	(9-11)
Fusarium graminearum		Fungi	Ascomycota	SRR1185280, SRR1596060, SRR1772865, SRR3168567, SRR3203806, SRR4372406	(12-14)
Aspergillus fumigatus		Fungi	Ascomycota	SRR1171330	-
Dictyostelium discoideum	slime mold	N.A.[2]	Amoebozoa	SRX256341, SRX256342, SRX757000, SRR867011, SRR867006, SRR1593424, SRR1593442, SRR1593443, SRR5099646, SRR5099649, SRR5099652, SRR5099655,	(15-19)
Arabidopsis thaliana	thale cress	Viridiplantae	Streptophyta	ERR754085, ERX546050, SRR1773578, SRX1166222	-
Oryza sativa	rice	Viridiplantae	Streptophyta	SRR1952788, SRR1952808, SRR1976517	(20, 21)
Pinus lambertiana	sugar pine	Viridiplantae	Streptophyta	SRR3723921	-
Physcomitrella patens	spreading earthmoss	Viridiplantae	Bryophyta	SRR1798064, SRR1798065, SRR1798066, SRR1798067, SRR2225590	(22)
Chlamydomonas reinhardtii	green alga	Viridiplantae	Chlorophyta	ERR1000644, ERR1000645	-
Phytophthora infestans		SAR[3]	Oomycetes	SRR5208985, SRR5208986, SRR5208987, SRR5208988, SRR5209018	-
Tetrahymena thermophila		SAR[3]	Ciliophora	SRR5077779, SRR3470619 SRR3145125	(23-25)
Leishmania donovani		Excavata[3]	Euglenozoa	SRR5272531, SRR5272535	(26)

Trichomonas vaginalis		Excavata[3]	Metamonada	SRR5004966, SRR5004967, SRR1156251	(27)
Giardia intestinalis		Excavata[3]	Sarcomastigophora	SRR445165, SRR445166	(28)

[1] If available

[2] N.A: Not applicable. Dictyostelium and Capsaspora fall between kingdoms.

[3] Although not officially a kingdom, SAR and Excavata are unranked clades equivalent to one.

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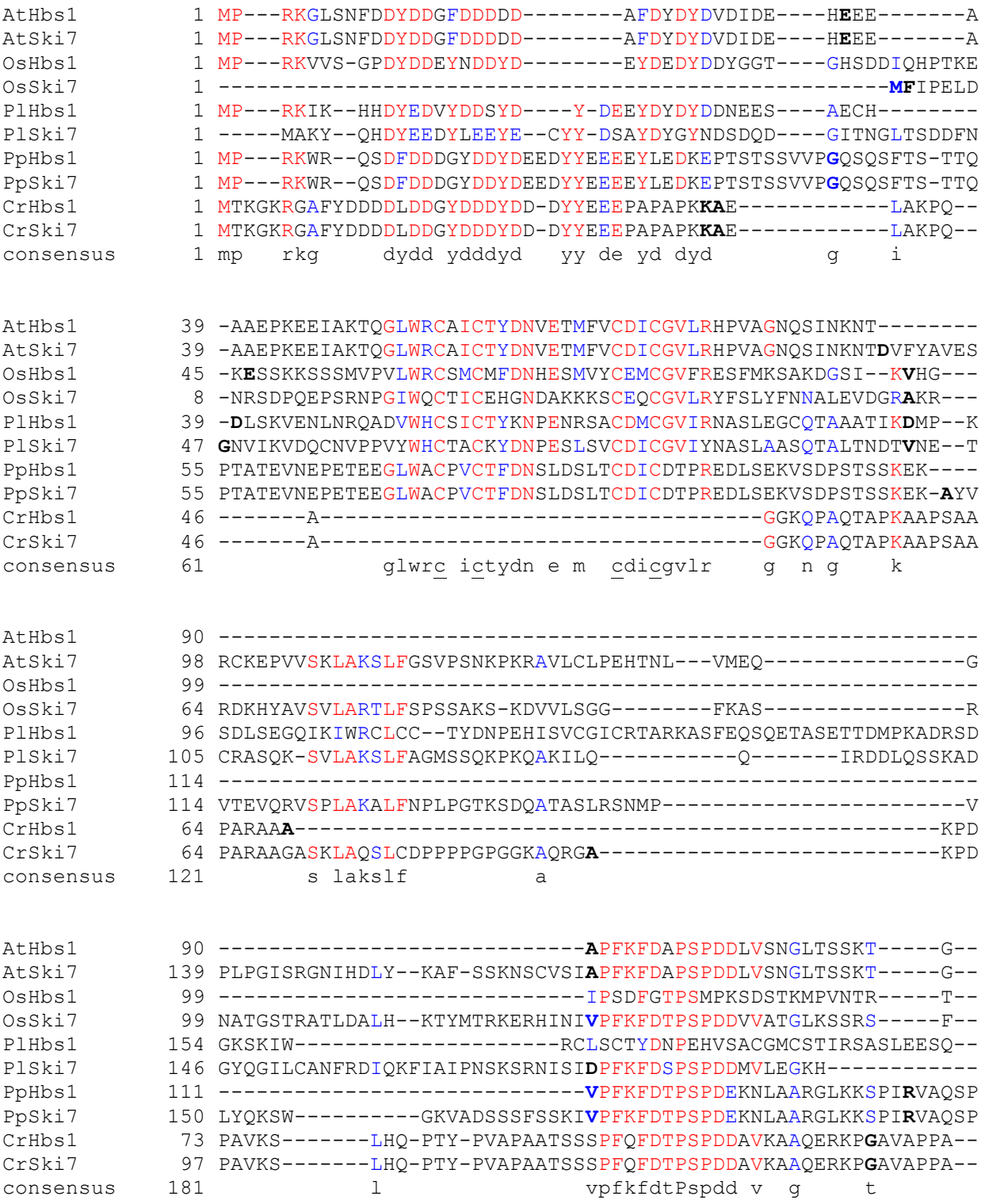
Figure S1. Protein sequence alignment that include protein sequences from five diverse plant species including: two splice isoforms of *Arabidopsis thaliana* (At), the moss *Physcomitrella patens* (Pp), and the alga *Chlamydomonas reinhardtii* (Cr) as well as duplicated genes from *Oryza sativa* (Os; rice) and *Pinus lambertiana* (Pl; pine). Sequences were aligned using Clustal Omega. The sequences from the land plants (all but Cr) share a Zn finger that is not in the algal sequence or in animals and fungi (CxxCxxxxxxxxxCxxC; conserved cysteines underlined in the consensus sequence). Letters in bold span an exon junction.



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AtHbs1      114 -PKGSGDASMRQKEK---------QDSVEQKPLKKGGD----SSETSSRGRHDKLDDKGG
AtSki7      189 -PKGSGDASMRQKEK---------QDSVEQKPLKKGGD----SSETSSRGRHDKLDDKGG
OsHbs1      123 -TDFGGDPEIKN-------------ASISHEKV---GS-----------TQYASVGSSSG
OsSki7      150 -RKVDTDAPHVTE-----------------KRVMDNDS----STPEK-----D-------
PlHbs1      191 -ASASGTAAMSNPASTTKKASLDITAKVEAEIVEDNAK----S----SK----E---PAP
PlSki7      194 -ATGKTAAAKSNSSSATPTSSL--SNNVEGEVEAQETR----SVVQKQK----ALTSTAL
PpHbs1      142 DDILNGARSSMAKAGTS--------KSISSAV--------------------SKLNVPGL
PpSki7      200 DDILNGARSSMAKAGTS--------KSISSAV--------------------SKLNVPGL
CrHbs1      122 -AAAAPTAPSLP----QNKNFLRPSPMLQQQKQQQGGPANGEGADEAARGV-AALGLTSA
CrSki7      146 -AAAAPTAPSLP----QNKNFLRPSPMLQQQKQQQGGPANGEGADEAARGV-AALGLTSA
consensus   241  a g g a   q             sv    l   g     s     r     l   gg

AtHbs1      160 A-----GGIKSGKSLPKAKADMSNETS-SSSKYMETSESLTGTMNKMS-LIGETE-----
AtSki7      235 A-----GGIKSGKSLPKAKADMSNETS-SSSKYMETSESLTGTMNKMS-LIGETE-----
OsHbs1      155 A-----G-----KKL---KEDQSSRAT-SSAQNEDVAQKLSSDIQKLG-L----------
OsSki7      176 --------TTADSNLPVKSNEFGESSESVSVGSQNETLCLDHELQHLS-LE-RKS-----
PlHbs1      235 S-----SLSKADKHEKRENG-VLREDKSSSNG------LVSEELQKLSFSTGYNF-----
PlSki7      243 P-----IVNRTDKKQKEAGCRFLGQQEAL----------SDR--TSEGTAGDHE-----
PpHbs1      174 S--QSSGASTSESH-------VGNGSSSAPEG------ELADALKQMN-VGGDYMESKSR
PpSki7      232 S--QSSGASTSESH-------VGNGSSSAPEG------ELADALKQMN-VGGDYMESKSR
CrHbs1      176 ASGGSEGGTTPGGGTRQHH---------PHLGHPE----APNALSHPGGLHGLHT-----
CrSki7      200 ASGGSEGGTTPGGGTRQHH---------PHLGHPE----APNALSHPGGLHGLHT-----
consensus   301 a     ggt   k     k          s g  e    lt  lnkm  l g

AtHbs1      208 -NSSDIKIRGPKSQSKHKPEEW----------------MLLDKESDALSQLNLAIVGHV
AtSki7      283 -NSSDIKIRGPKSQSKHKPEEW----------------MLLDKESDALSQLNLAIVGHV
OsHbs1      190 -EKNEVDTAKPYLPEEYKPEKW----------------MFANEESGVLSQLNLAIVGHV
OsSki7      221 -QKSKANIKKPVSSSLYKPEPW----------------MLQHEDEGIPRQLNLAIVGHV
PlHbs1      278 -HNSNKVLKNAVPLEEYKAEPW----------------MLHEQSDEGKNLLHLAIVGHV
PlSki7      280 -QRNPSNLKKVLPLEEYKPESW----------------MLVEEKEPYKSLLHLAIVGHV
PpHbs1      218 ENADASTSTYGLSLESYEPEPW----------------MLKDANKDSRQLLHLIVVGHV
PpSki7      276 ENADASTSTYGLSLESYEPEPW----------------MLKDANKDSRQLLHLIVVGHV
CrHbs1      218 ----------RRPVTEYVMEADLARDVAAATASESSSTSTSGSSSGSSKPPLHLVVLGHV
CrSki7      242 ----------RRPVTEYVMEADLARDVAAATASESSSTSTSGSSSGSSKPPLHLVVLGHV
consensus   361  n     ir  vpleeykpE w                ml d     k  LhLaivGHV

AtHbs1      250 DSGKSTLSGRLLHLLGRISQKQMHKYEKEAKLQGKGSFAYAWALDESAEERERGITMTVA
AtSki7      325 DSGKSTLSGRLLHLLGRISQKQMHKYEKEAKLQGKGSFAYAWALDESAEERERGITMTVA
OsHbs1      232 DSGKSTLSGRLLHLLGRISKKDMHKNEKEAKEKGKGSFAYAWAMDESSEERERGVTMTVA
OsSki7      263 DSGKSTLCGRLLHALGRISKKQMHKYEKEAKEKGKGSFAYAWAMDESADERERGITMTVG
PlHbs1      320 DAGKSTLTGRLLHLMGRVSQKEMHKYQREAKQKGKESFAYAWVLDESTEERERGVTMTVA
PlSki7      322 DAGKSTMMGRLLHLMGQVSEKEMRKYEREAKQKGKGSFAYAWVLDESAEERERGLTMTVA
PpHbs1      261 DAGKSTLMGRILHLLGRVSQKEMHKNEKESKQQGKGSFAYAFVLDEGAEERARGVTMTVA
PpSki7      319 DAGKSTLMGRILHLLGRVSQKEMHKNEKESKQQGKGSFAYAFVLDEGAEERARGVTMTVA
CrHbs1      268 DAGKSSLMGRLLHDLGLVSAKEAHKFQRDAAAAGKGSFAWAWVLDERPEERERGVTMDVA
CrSki7      292 DAGKSSLMGRLLHDLGLVSAKEAHKFQRDAAAAGKGSFAWAWVLDERPEERERGVTMDVA
consensus   421 DaGKStlmGRlLHllGrisqKemhKyekeak  GKgSFAyAw lDEsaeEReRGvTmtVa

AtHbs1      310 VAYFNSKRHHVVLLDSPGHKDFVPNMIAGATQADAAILVIDASVGAFEAGFDNL------
AtSki7      385 VAYFNSKRHHVVLLDSPGHKDFVPNMIAGATQADAAILVIDASVGAFEAGFDNL------
OsHbs1      292 VAYLETNKYRVVLLDSPGHKDFVPNMISGATQADAAILVVDACTGSFEAGMDGE-----G
OsSki7      323 VAYFDTKNYHVVLLDSPGHKDFVPNMISGATQSDAAILVIDASIGSFEAGMGIN------
PlHbs1      380 VAHFDTVKFHVVLLDSPGHKDFVPNLIVGASQADAAVLVVDASTGAFEAGMDGQ------
PlSki7      382 VAHFELRNFKVVLLDSPGHKDFVPNMISGASQADAAVLVIDASIGAFEAGMYGQ------
PpHbs1      321 VAHFETPKLRVVLLDAPGHRDFVPNMISGASQADAAILVVDASIGAFEAGLEGE-----G
PpSki7      379 VAHFETPKLRVVLLDAPGHRDFVPNMISGASQADAAILVVDASIGAFEAGLEGE-----G
CrHbs1      328 MTRFATNRFAVTLLDAPGHRDFVPNMIAGAAQADAALLLVDGSPGGFEAGFSEGSGGLHG
CrSki7      352 MTRFATNRFAVTLLDAPGHRDFVPNMIAGAAQADAALLLVDGSPGGFEAGFSEGSGGLHG
consensus   481 vahfet ryhVvLLDsPGHkDFVPNmIsGAtQaDAAiLvvDasvGafEAGmdg
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AtHbs1       364 --KGQTREHARVLRGFGVEQVIVAINKMDIVGYSKERFDLIKQHVGSFLQSCRFKDSSLT
AtSki7       439 --KGQTREHARVLRGFGVEQVIVAINKMDIVGYSKERFDLIKQHVGSFLQSCRFKDSSLT
OsHbs1       348 KSVGQTKEHAQLIRSFGVEQLIVAVNKMDAIGYSKERFEFIKVQLGSFLRACNFKDSSVT
OsSki7       377 GGIGQTKEHSQLVRSFGVDNLIVVVNKMDSVEYSKERFNFIKSQLGAFLRSCGYKDSAVA
PlHbs1       436 GTGGQTKEHAQLIRSFGVEQLIIAINKMDVVDYSKERFDFIKSQLGLFLRRCGFKESSLM
PlSki7       438 -GEGQTKEHAQLIRSFGIEQLIIAVNKMDTVDKTEGRFCFIKSQLGPFLRRCGFKESSTI
PpHbs1       377 QGRGQTREHAQLVRSLGVEQLIVAVNKLDAVDFSKERFDFIRGTLQPFLKQCGFKDGSLQ
PpSki7       435 QGRGQTREHAQLVRSLGVEQLIVAVNKLDAVDFSKERFDFIRGTLQPFLKQCGFKDGSLQ
CrHbs1       388 APGGQTREHAALARSLGIEQMAVVVSKLDTCGYDQSRFESIRAALLPYLKSVGFKESGLQ
CrSki7       412 APGGQTREHAALARSLGIEQMAVVVSKLDTCGYDQSRFESIRAALLPYLKSVGFKESGLQ
consensus    541    GQTrEHaqllRsfGveqlivavnKmDsvgyskeRFdfIk qlgpfLrscgfkdssl

AtHbs1       422 WIPLSAMENQNLVAAPS-DNRLSSWYQ--GPCLLDAVDSVKSPDRDVSKPLLMPICDAVR
AtSki7       497 WIPLSAMENQNLVAAPS-DNRLSSWYQ--GPCLLDAVDSVKSPDRDVSKPLLMPICDAVR
OsHbs1       408 WIPLSAVENQNLIKIPS-DVRLTSWYQ--GFCLLDAIDSLQLPSRDVSKPLILPICDVIK
OsSki7       436 WVPISAMENENLMTTAS-DTRLSSWYD--GNCLLKAIDTLPPPSRDVSKPLRLPICDVFS
PlHbs1       494 WIPMSVIENQNLVTSTS-DGRLMSWYT--GPHFLESIDLFKPPTRDISRPLRIPISEVIQ
PlSki7       495 WIPLSALDNQNLTSATS-DTRLNSWYS--GPYLLEAIDNLQPPKRDISRPLRLPISEVSK
PpHbs1       436 WVPVSASEGQNLTMA-STESALKAWYN--GPCLIELVDSLKPPPRLVARPLRLTIAEVMK
PpSki7       494 WVPVSASEGQNLTMA-STESALKAWYN--GPCLIELVDSLKPPPRLVARPLRLTIAEVMK
CrHbs1       448 WLPAAGPLGENLVGPPQ-DPALKAWWGPGRPCVTDAIDAFAPRERAVSRPLRLPVSDVFK
CrSki7       472 WLPAAGPLGENLVGPPQ-DPALKAWWGPGRPCVTDAIDAFAPRERAVSRPLRLPVSDVFK
consensus    601 WiPlsamenqNLv  ps d rLssWy   gpclldaiDsl pp RdvskPlrlpi dvvk

AtHbs1       479 STSQGQVSACGKLEAGAVRPGSKVMVMPSGD-QGTIRSLERDSQACTIARAGDNVALALQ
AtSki7       554 STSQGQVSACGKLEAGAVRPGSKVMVMPSGD-QGTIRSLERDSQACTIARAGDNVALALQ
OsHbs1       465 SQSTGQLAAFGKLETGAIRIGSKVLISPCGE-VATVKSIERDSNSCDIARAGDNVAVSLQ
OsSki7       493 SHKLGQVAIGGKVEVGATRSGSKILVMPFGE-LAVVKTIERNSSSCNLARAGDNVAIGLQ
PlHbs1       551 SRTLGQVAASGKLDAGAIKVGTKLLVMPAGQ-GAIVKAIEQDGNELNIAKAGDSVDIGLQ
PlSki7       552 SRSLGQVAISGKLEGGALKIGTKVLVMPAGV-VATVKAIEQDTQVCAVARAGDNVDIALQ
PpHbs1       493 TRTLGPSAFGGKLESGAIHSGTKVRVMPSGE-IATVKSIELQGQQLKTARAGEGVDVGLN
PpSki7       551 TRTLGPSAFGGKLESGAIHSGTKVRVMPSGE-IATVKSIELQGQQLKTARAGEGVDVGLN
CrHbs1       507 SK-TGAVVLGGKLEGGAMRPGSRVVLVPGPAQPFAVRSLEVGGGAANLARAGDSCEVALV
CrSki7       531 SK-TGAVVLGGKLEGGAMRPGSRVVLVPGPAQPFAVRSLEVGGGAANLARAGDSCEVALV
consensus    661 shslGqvaigGKleaGAvr Gskvmvmp gd vatvkslErdgqacniArAGdnvdlaLq

AtHbs1       538 ----------GIDANQVMAGDVLCHPDFPVSVATHLELMVLVLEGATPILLGSQLEFHVH
AtSki7       613 ----------GIDANQVMAGDVLCHPDFPVSVATHLELMVLVLEGATPILLGSQLEFHVH
OsHbs1       524 ----------GIDGSKLIAGGILCNPGFPVPVSNFLELRVLVLDVTIPILIGYQVEFHIH
OsSki7       552 ----------GIDPSHIMPGGVICHPDYPVSVASCLELKILVLDITVPILVGLQFELHIH
PlHbs1       610 ----------GIDSSILMTGGVLCHPDFPVPVARRIELKVAVLDIKQPILFGAEVELHAH
PlSki7       611 ----------GIDISFLMIGGVLCHPDYPVPIAIRIELRVVILDITMPILVGSQVELYIH
PpHbs1       552 ----------GIDPGMLAPGGVVCHPDYPVPVATRFEVQLLTLDIRTPILKGSQVILHVH
PpSki7       610 ----------GIDPGMLAPGGVVCHPDYPVPVATRFEVQLLTLDIRTPILKGSQVILHVH
CrHbs1       566 AHGGGGGGGGAIDPSLVAPGAVLCHADFPAVLVTKFQLRLVVLDVPVPLLRGQAVTLHAH
CrSki7       590 AHGGGGGGGGAIDPSLVAPGAVLCHADFPAVLVTKFQLRLVVLDVPVPLLRGQAVTLHAH
consensus    721           giD s lmpGgvlChpdfpvpvathlelrvlvldv iPiLlGsqvelhvH

AtHbs1       588 HAKEAATVVKLVAMLDPKTGQPTKKSPRCLTAKQSAMLEVSLQNPVCVETFSESRALGRV
AtSki7       663 HAKEAATVVKLVAMLDPKTGQPTKKSPRCLTAKQSAMLEVSLQNPVCVETFSESRALGRV
OsHbs1       574 HVKEAARVTKIVALLD-KAGKPSKTAPRFLKSKQNAVVQVTLDAPVCVEEFSKCRALGRA
OsSki7       602 HAKVSASMVKILSLLEQKTGKASKKIPRFLTSRQTAVIEVKLEKEVCVEEFSNLKALGRV
PlHbs1       660 HSKEAAKIVQILAILDPKTGLVRKKAPRLLTANQSALIEVLPHRGICIEEYCNYKPLGRV
PlSki7       661 HVREAAKVVQLLSILDPKTGLVRKKAPRCLTANQNALMEVVPDRGACIEEYNNYKALGRV
PpHbs1       602 HARQPARVDQLVSLLDPKKGTVLRQRPRHLTANQSAIVVIVPDEGVCIEKYSDFRALGRI
PpSki7       660 HARQPARVDQLVSLLDPKKGTVLRQRPRHLTANQSAIVVIVPDEGVCIEKYSDFRALGRI
CrHbs1       626 VAREEGHLSALVALLDPRTGEEVKARPRCLTRGQSALVEVTSSRGLVLEEYAHYRALGRV
CrSki7       650 VAREEGHLSALVALLDPRTGEEVKARPRCLTRGQSALVEVTSSRGLVLEEYAHYRALGRV
consensus    781 hakeaarvv lvalLdpktG   kk PRcLta QsAmvevs drgvcvEeys yraLGRv
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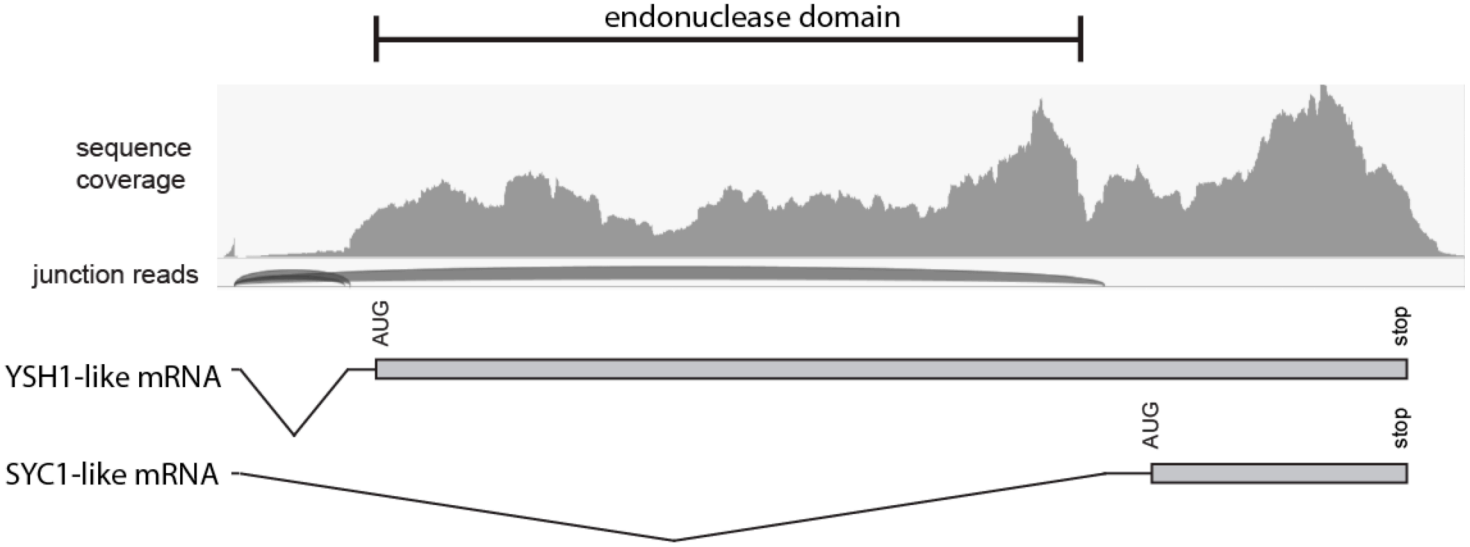
AtHbs1       648 FLRSSGRTVAMGKVTRIIQDS*--
AtSki7       723 FLRSSGRTVAMGKVTRIIQDS*--
OsHbs1       633 FLRSGGSTIAVGVVTRVLGQDQN*
OsSki7       662 FLRSQGNTIAVGIVSRVREQA*--
PlHbs1       720 TLRATGKTIAVGIVTRIIEQQ*--
PlSki7       721 TLRATGKTIAVGIVTRIIEQQ*--
PpHbs1       662 ALREGGKTIAVGIVTDILERK*--
PpSki7       720 ALREGGKTIAVGIVTDILERK*--
CrHbs1       686 ALREGGRTLAVGVVTQLLE*----
CrSki7       710 ALREGGRTLAVGVVTQLLE*----
consensus    841  LRsgGrTiAvGiVtriieq
```

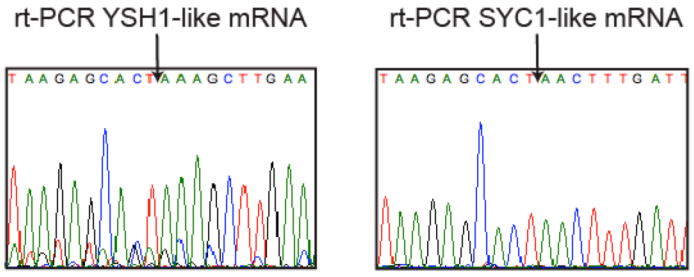
Figure S2. Duplication of *YSH/SYC1* in the *Saccharomyces* lineage was also followed by loss of alternative splicing. A. RNA sequencing analysis identifies a novel intron in the 5' UTR of a single YSH1/SYC1 gene (SAKL0A08096) in *Lachancea kluyveri.* Expression of the annotated Ysh1-like protein is mediated by 3' splice sites at -90 and -72 relative to the AUG start codon. Expression of an alternative Syc1-like protein is mediated by a 3' splice site at +1592. **B.** Depiction of the YSH1 and SYC1 genes from *Saccharomyces cerevisiae* aligned with panel A. SYC1 is named because it is "Similar to Ysh1 C-terminal". **C.** rtPCR conformation of the *Lachancea kluyveri* alternative splicing. A primers to the shared first exon was combined with primers downstream of the 3' splice sites for rt-PCR. The rt-PCR products were directly sequenced. Arrow indicated the exon junction. **D.** Clustal Omega alignment that of the *Lachancea kluyveri* splice isoforms and S. cerevisiae proteins

A. *Lachancea kluyveri YSH1/SYC1 RNAseq*



B. *Saccharomyces cerevisiae YSH1 and SYC1 genes*

C. *Lachancea kluyveri* rtPCR conformation



D. Sequence alignment

```
LkYsh1            1 MVQEQTSNTSFKFFSLGGSNEVGRSCHILQYKGKTVMLDAGVHPAHQGLASLPFYDEFDL
LkSyc1            1 ------------------------------------------------------------
ScYsh1            1 --MERTNTTTFKFFSLGGSNEVGRSCHILQYKGKTVMLDAGIHPAYQGLASLPFYDEFDL
ScSyc1            1 ------------------------------------------------------------
consensus         1    e t  tsfkffslggsnevgrschilqykgktvmldagvhpa qglaslpfydefdl

LkYsh1           61 ETIDVLLISHFHLDHAASLPYVMQRTNFQGRVFMTHPTKAIYRWLLSDFVKVTNIGSSST
LkSyc1            1 ------------------------------------------------------------
ScYsh1           59 SKVDILLISHFHLDHAASLPYVMQRTNFQGRVFMTHPTKAIYRWLLRDFVRVTSIGSSSS
ScSyc1            1 ------------------------------------------------------------
consensus        61   idvllishfhldhaaslpyvmqrtnfqgrvfmthptkaiyrwll dfvkvt igssst

LkYsh1          121 ---SKDDNLYTDEDLAESFDRIETIDYHSTMDVNGIKFTAFHAGHVLGAAMFQVEIAGLR
LkSyc1            1 ------------------------------------------------------------
ScYsh1          119 SMGTKDEGLFSDEDLVDSFDKIETVDYHSTVDVNGIKFTAFHAGHVLGAAMFQIEIAGLR
ScSyc1            1 ------------------------------------------------------------
consensus       121    skdd lytdedl esfdrietidyhstmdvngikftafhaghvlgaamfqveiaglr
```

```
LkYsh1          178 VLFTGDYSREMDRHLNSAEIPPLPSDVLVVESTFGTATHEPRVNREKKLTSLIHSTVSKG
LkSyc1            1 ------------------------------------------------------------
ScYsh1          179 VLFTGDYSREVDRHLNSAEVPPLSSNVLIVESTFGTATHEPRLNRERKLTQLIHSTVMRG
ScSyc1            1 ------------------------------------------------------------
consensus       181 vlftgdysremdrhlnsaeippl s vlvvestfgtatheprvnrekklt lihstv kg

LkYsh1          238 GRVLLPVFALGRAQEIMLILDEYWSQHADDLGGGQVPVFYASNLARRCMSVFQTYVNMMN
LkSyc1            1 ------------------------------------------------------------
ScYsh1          239 GRVLLPVFALGRAQEIMLILDEYWSQHADELGGGQVPIFYASNLAKKCMSVFQTYVNMMN
ScSyc1            1 ------------------------------------------------------------
consensus       241 grvllpvfalgraqeimlildeywsqhaddlgggqvpvfyasnlarrcmsvfqtyvnmmn

LkYsh1          298 DDIRKKFRDSQTNPFIFKNISYLKNLDEFQDFGPSVMLASPGMLQNGLSRDLLEKWCPDE
LkSyc1            1 ------------------------------------------------------------
ScYsh1          299 DDIRKKFRDSQTNPFIFKNISYLRNLEDFQDFGPSVMLASPGMLQSGLSRDLLERWCPED
ScSyc1            1 ------------------------------------------------------------
consensus       301 ddirkkfrdsqtnpfifknisylknldefqdfgpsvmlaspgmlq glsrdllekwcpde

LkYsh1          358 KNLVLITGYSVEGTMAKFLMLEPDTLPSINNPDLTIPRRCQVEEISFAAHVDFQENLDFI
LkSyc1            1 ------------------------------------------------------------
ScYsh1          359 KNLVLITGYSIEGTMAKFIMLEPDTIPSINNPEITIPRRCQVEEISFAAHVDFQENLEFI
ScSyc1            1 ------------------------------------------------------------
consensus       361 knlvlitgysvegtmakflmlepdtlpsinnpdltiprrcqveeisfaahvdfqenldfi

LkYsh1          418 EKISAANIILVHGESNPMGRLKSALLSNFASLKGTENEVRVFNPRNCVCVDLEFKGIKIA
LkSyc1            1 ------------------------------------------------------------
ScYsh1          419 EKISAPNIILVHGEANPMGRLKSALLSNFASLKGTDNEVHVFNPRNCVEVDLEFQGVKVA
ScSyc1            1 ------------------------------------------------------------
consensus       421 ekisa niilvhge npmgrlksallsnfaslkgtenevrvfnprncv vdlef gikia

LkYsh1          478 KAVGNIVDEASNILKT----EGEKKVSEIKEETEEEAA-------GKLKIDGETVVSGIL
LkSyc1            1 ------------------------------------------------------------
ScYsh1          479 KAVGNIVNEIYKEENVEIKEEIAAKIEPIKEENEDNLDSQAEKGLVDEEEHKDIVVSGIL
ScSyc1            1 ------------------------------------------------------------
consensus       481 kavgniv e           e   kv  ikee ee                 e vvsgil

LkYsh1          527 VSDEKNFDLNLVSLSDLREHHTDLSTTVLKERQTIHVDCKKELIYWHLCQMFGDIEVLLD
LkSyc1            1 MSKSTNFDLNLVSLSDLREHHTDLSTTVLKERQTIHVDCKKELIYWHLCQMFGDIEVLLD
ScYsh1          539 VSDDKNFELDFLSLSDLREHHPDLSTTILRERQSVRVNCKKELIYWHILQMFGEAEVLQD
ScSyc1            1 --------------MDLPKDKSDRTHQ--RINLNNSGTDRTNDLYLHIVQTFGCIETTAT
consensus       541 vsdeknfdlnlvslsDLrehhtDlsttvlkerqtihvdckkeliYwHlcQmFGdiEvlld

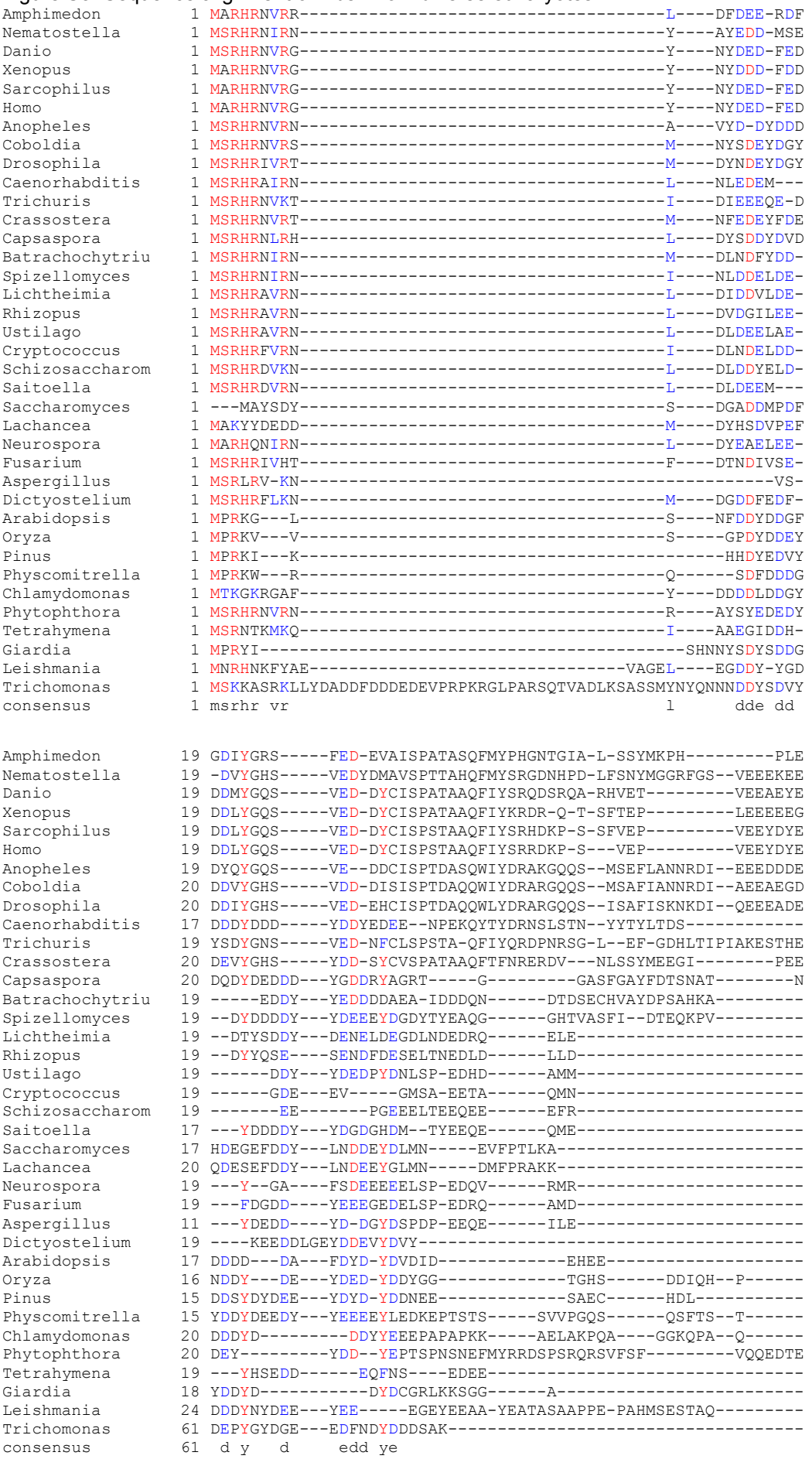
LkYsh1          587 DEGVTLLNNLQDKNPKTSDVKSGELELRVMGDIKVSIVRDVATLEWTQGII-NDTVADSI
LkSyc1           61 DEGVTLLNNLQDKNPKTSDVKSGELELRVMGDIKVSIVRDVATLEWTQGII-NDTVADSI
ScYsh1          599 DDRVTNQEPKVKEESKDNLTNTGKLILQIMGDIKLTIVNTLAVVEWTQDLM-NDTVADSI
ScSyc1           45 EN----------------------ATKLLMLGDVEVEISASSVSIEWTQKSMISQTIADSI
consensus       601 degvtllnnlqdknpktsdvksgeleLrvmGDikvsIvrdvatlEWTQgii ndTvADSI

LkYsh1          646 LAILLSIDSSPASVKLSSRSCNHDHHDCG----DKLHDDVWKIKEISRLFTEQFGDCFTL
LkSyc1          120 LAILLSIDSSPASVKLSSRSCNHDHHDCG----DKLHDDVWKIKEISRLFTEQFGDCFTL
ScYsh1          658 IAILMNVDSAPASVKLSSHSCDDHDHNNVQSNAQGKIDEVERVKQISRLFKEQFGDCFTL
ScSyc1           84 VIMIIGLC-------------ASDKNVLSESELKERNHNVWKIQELQNLFREQFGDSFSI
consensus       661 laillsidsspasvklssrscnhdhhdcg s  dklhddVwkikeisrLFtEQFGDcFtl

LkYsh1          702 LLDKNET--DHKEDIKGAITIGKSTARINFSNMSVEECNSNPLKGRIESLLGIGTDLVAP
LkSyc1          176 LLDKNET--DHKEDIKGAITIGKSTARINFSNMSVEECNSNPLKGRIESLLGIGTDLVAP
ScYsh1          718 FLNKDEYASNKEETITGVVTIGKSTAKIDFNNMKILECNSNPLKGRVESLLNIGGNLVTP
ScSyc1          131 D----EGIGKKENVKNGSVTIGKSKATIDFSTMKLIDCNSNPLKGRVESILSIGQKLTTP
consensus       721 lldknEt  dh edikGaiTIGKStArI FsnM veeCNSNPLKGRiESlLgIGtdLv P

LkYsh1          760 LC*
LkSyc1          234 LC*
ScYsh1          778 LC*
ScSyc1          187 LC*
consensus       781 LC
```

Figure S3. Sequence alignment of Hbs1 from diverse eukaryotes.



```
Amphimedon          62 TQSEK---------LPSS--------------------------AGAS---G-------
Nematostella        70 EEEEE------NSLTSSQDYKRPQLDALSEAKLSSCLD-QLNSI-LGDD---C-HEPTAV
Danio               63 EEEEE---------MPTSPTMTSTLDSLQQGRLYSCLD-QMRTV-LGDS---I-PDSTLT
Xenopus             61 E-YEE---------LDKLKATDSSLSAVDQARLYSCLD-HMREV-LGES---V-MEQVMI
Sarcophilus         62 D-TKE----------PTNSISNHQLSGIDQARLYSCLD-HMREV-LGDD---V-PDQTMI
Homo                60 D-LKE----------SSNSVSNHQLSGFDQARLYSCLD-HMREV-LGDA---V-PDEILI
Anopheles           68 LAAETGREGPAHKRRDSECFQMPELNDEDRARLMSCMD-EIRDI-VGET---C-SDRQMV
Coboldia            70 DDDD-----LGKPRRDSDNFQMPTLSKENQVLLDSCMD-AIRDV-VGDA---F-SEKKIV
Drosophila          70 DEDE--DAAFAKARRDSESFQMPQLDEIEQAKLSSCVD-EVRSV-VGDA---V-SERRIV
Caenorhabditis      56 ------------------GRNSPALPAPHPAPTTS----------------------LS
Trichuris           68 ------------------DYDLPED-----ETTVTC------------------SPIVVM
Crassostera         63 EDESD------PEPLSDSGRDNLKLDDVEQAKLNSCKE-EIVNV-IGDT---I-PEHIVS
Capsaspora          55 A-------------TADDLPDLSTLTLKEKDLLREARA-KIEPV-VGNT---V-TNAEIV
Batrachochytriu     55 ---------------------------SVNANIQKEIS-IVSQF-VGPSYS----EAYIK
Spizellomyces       57 ---------------------------TETRGAINLVE-EVRNI-VGDDFP----TEQIS
Lichtheimia         45 ------------------------------------NGLS-HVRNI-VGEDIGIS--DTEIK
Rhizopus            44 ------------------------------------EGLE-YIESV-IGENNGIL-SSRQIK
Ustilago            40 ------------------------------------EAYAQTLEVI-GPTVSNGF-TEREIK
Cryptococcus        35 ------------------------------------RAVS-VARNL-LKDVTPPI-SDNEIA
Schizosaccharom     36 ------------------------------------SAVATVRETL-LGV---PI-SEKEIA
Saitoella           40 ------------------------------------AGVA-AVHDA-LNGV-PGI-TLKEIR
Saccharomyces       44 ----------------------------------------QLQD------YQGW-DNLSLK
Lachancea           47 ----------------------------------------EMAD------YQGW-NNLAVK
Neurospora          40 ------------------------------------EGTAQVLEALGVEA--HKV-PKTQIE
Fusarium            42 ------------------------------------QGTAEVRAALGTEA--NKV-TTTQIE
Aspergillus         33 ------------------------------------QCTAEVLAQLLSGEPSVTA-TRDEVQ
Dictyostelium       36 ----------------------------------------DV-VVEKFPDI-TYPEIE
Arabidopsis         37 ------------------EAAAEP------------------------------K-EEIAKT
Oryza               42 ----------------TKEKESS-----------------------------K-KSSSMV
Pinus               41 ----------------------SK-----------------------------V-ENLNRQ
Physcomitrella      53 ----------------TQPTATE-----------------------------V-NEPETE
Chlamydomonas       54 ----------------TAPKAAP-----------------------------S-AAPARA
Phytophthora        60 K-----------------ETQEPTNDPGDVEILEAMIP-QVQQA-VGSR---F-SAHQIT
Tetrahymena         34 ----------------------------------------IIEDI-IFHYKNQF-TKKEVV
Giardia             36 ------------------------------------------------------V-----EG
Leishmania          65 ----------------ATASAAPAV----RVNPYTTIS----PQ-VDDDYELLDMLLPQL
Trichomonas         82 ---------------------------------------IDEL--------I----AKL
consensus          121                                          l  i l      i     l

Amphimedon          76 ---------------------------------------------APTQPN---------
Nematostella       118 DAILKHD--------------------FNVEKALDYIFNRETKQDKSCESNKG---TG--
Danio              108 QAALKYD--------------------CDPHRALDFILSENTNTQAPSARTNP---QL--
Xenopus            105 DAVLKCQ--------------------FDVAKALDLVFKQDCNKNIKPAN----------
Sarcophilus        105 EAVLQSK--------------------FDVEKALAMVLEQDKKQT---KSE---------
Homo               103 EAVLKNK--------------------FDVQKALSGVLEQDRVQSLKDKNE---------
Anopheles          122 EAIMKHD--------------------YECSKALDEILNSNKTPPAALGAKSGSKLTA--
Coboldia           119 ETIIKFD--------------------YDFTKSLDAILNPEKVDPPQGLKVT-LPPAT--
Drosophila         122 ETSMKFD--------------------YDMQKILDEILNEETNKSAKPAVNK---M----
Caenorhabditis      75 STIVR---------------------------NMTAPLLHQNQKPPKNLNSRPS-------
Trichuris           87 QSVTRPT-----------------------SKLVSGNFYDPRSPKAEPLQR---------
Crassostera        111 QAVVKHQ--------------------YNIQAALNELLNQSEAPKPQRQPRPDRRANR--
Capsaspora          96 DAILHYN--------------------FDVEKAIVWLLEGYDPDEDADNDQDDVVLAKRK
Batrachochytriu     82 TILASNG--------------------NNPEQSINYILNHQK------------------
Spizellomyces       84 DVLQDSG--------------------NDIERAVNLLYDQGPRIAPPPGFPV--------
Lichtheimia         67 EALWYYY--------------------FDREETVNWVFDKVAKIKAEEEKQ---------
Rhizopus            67 EALWYYY--------------------LNKEETLEWALDEISKAKALEEKK---------
Ustilago            64 DVLWDAY--------------------FDVDSAVTQLVEEKSRREAKAEKDRQKQ-----
Cryptococcus        58 DSVWHYW--------------------FDGEKAAAWLRQDREKKAAKAKAAQ--------
Schizosaccharom     57 DTVWYYY--------------------FDVEKSVNYLLQKASSKAGAKEKQNTDSQKEKK
Saitoella           62 ETLYYYY--------------------FDLEKSIAWLLEQHSVKKPAAKPKA--------
Saccharomyces       58 LALFDNN--------------------FDLESTLAELKKTLKKKKTPKKPIA-----AAN
Lachancea           61 LAIFDQN--------------------FDFNQAMIELKRIYRKKQFAQPKQE-----AKK
Neurospora          63 ESLWHYY--------------------WDVDKTITYLISKYIDPPKKPAKTA--------
Fusarium            65 EALWHYY--------------------YDVDKSVTYLIKTFIAPAPKPAKKT--------
Aspergillus         58 EALWHYY--------------------NDVEKSVNYLRGKKTKEMKKKQNPA--------
Dictyostelium       52 KVLMDFD--------------------YNVDDAIDFILNGGLNNKGKKKNNK--------
Arabidopsis         50 QGLWRCAICTYDN--------VETMFVCDICGVLRHPVAGN---QSINKNT---------
Oryza               56 PVLWRCSMCMFDN--------HESMVYCEMCGVFRESFMKSAKDGSIKVHG---------
Pinus               50 ADVWHCSICTYKN--------PENRSACDMCGVIRNASLEGCQTAAATIKD---------
Physcomitrella      67 EGLWACPVCTFDN--------SLDSLTCDICDTPREDLSEKVSDPSTSSKE---------
Chlamydomonas       68 AA-------------------------------------KPDPAVKSLH----------
Phytophthora        97 QELRSAN--------------------YDLDKTVVALLERGKAPAAAGGVLPL-------
Tetrahymena         53 RILDKHN--------------------WVEDDVYDALDDLKKKREQKQNKV----TEEKK
Giardia             39 RPAWQS--------------------------------------------------------
Leishmania         100 HALWKASAPTMLPLSEGEAVTALRASDYDVEPAFLQLKEKRDEERS---------------
Trichomonas         90 KKTYDISKCDMDEI-----FLAFRNLDYDYSVVSRNLEKGDYG-KAIKK-------------
consensus          181 d i k                     fdve  l  il
```

```
Amphimedon        82 Q---PSQPALPSQYLRSEPSI---KKPDK-------AT-------A-PV------ETVTI
Nematostella     153 H---PLSVHPPQPSLLSAPAK---IKPTP-------APIFVGLPKA-KAESVVASAVAAN
Danio            143 E---PNTTAAPQKAKV-----------------------REAPES-RVESEVVPKVARM
Xenopus          135 Q---ELISGKPTKGLA-----------------------RGLQAP-EHEHEIVPKMAKM
Sarcophilus      133 E---AISMGKATKGKS-----------------------VDHQSS-RSESEIVPKVTKM
Homo             134 A---TVSTGKIAKGKP-----------------------VDSQTS-RSESEIVPKVAKM
Anopheles        160 G---AAMEKGIGERLLERSEKKLQAAGRN-------VPIIVATPSA-DVRPSNDAASTVI
Coboldia         156 T---VTSDKGEANKLK-----------------------EKPPA-PLVQKEKPVTITV
Drosophila       155 ---------------------------------------KAPAA-PVLPKTVSKTVPT
Caenorhabditis   102 ------TPQ-TSSNL---------------------------NTPK---------------
Trichuris        115 --------P-MSQNLL-----------------------------NANN-----QRETIEL
Crassostera      149 Q---EFAPVQPTVQLK-TPVK---KNTT------------SDLAQATSATSQIKLETSNQ
Capsaspora       136 QAFGSSATQPTAKSGSANSAASGKAAGKNVSSTASKANSAKSTPAAASPA--------KG
Batrachochytriu  104 ------------------PEPSASSVITNK------PTFTFNKPSPDDIV--------KQ
Spizellomyces    116 -------APPPGFALKSDSRQPASRIADDV------APFAFDAPSPDDVV--------NQ
Lichtheimia       98 -------------KKKAAKKAAA--AAAS------------KGPTATQSK----------
Rhizopus          98 -------------KLKEKAKKEKKEVKSN------------NNPAAKSAV----------
Ustilago          99 --------------------AAKKAAAANA-----------SAPASGTSTPLHRKAAVSQ
Cryptococcus      90 --------------------TAKSASLP-------------GKPRVQQVANQKSKLAVSQ
Schizosaccharom   97 Q-------------------NKSK-EALADA-----------K-DPLDESSNGIKNLSLNK
Saitoella         94 -------AP-T---------ASK-ASAAPE------VAKVFSGPSPDDVV--------IA
Saccharomyces     93 G-----------------------S-A----------N---------------------
Lachancea         96 Q-------------------------AIS----------NFNKPSPDDVVLTAQKKAFTD
Neurospora        95 --------PPKT--------------------------------APKQDVATAGKK-----
Fusarium          97 --------PEAG--------------------------------KQPA--PKAAKK-----
Aspergillus       90 --------PPVAAKG-----------------------------KGPSPDDVVLNAQS-----
Dictyostelium     84 -------KPPQAVNIINNNNNNKKSEPVNT-----------NKSTSKDVTNSLKTLSIGG
Arabidopsis       90 APF-----------------------------------KFDAPSPDDLVSNGLTSSKTG
Oryza             99 IPS-----------------------------------DFGTPSMPKSDSTKMPV----
Pinus             93 MPKSDLSEGQ--------------------IKIWRCLCCTYDNPEHIS--VCGIC--RTA
Physcomitrella   110 KAYVVTEVQR------------------------VSPLAKALFNPLPGT---------K--
Chlamydomonas     80 QPTYPVAP-----------------------AATSSSPFQFDTPSPDDAVKAAQER-KPG
Phytophthora     130 Q---IQIPRLDAVALA---------------------------IGNEEKQELKPKKEIV
Tetrahymena       89 Q-----------------------------------------PTGGNVLV---KKQQNQ
Giardia           45 ---------------------------------------------------------
Leishmania       146 ---------------------------------------------------------
Trichomonas      133 ---------------------------------------------------------
consensus        241                                         p

Amphimedon       115 K---------------------------------------------QS---Q--------
Nematostella     199 K---------------------------------------------VS-------------
Danio            175 T---------------------------------------------VS---G--------
Xenopus          167 I---------------------------------------------VT---G--------
Sarcophilus      165 T---------------------------------------------VS---G--------
Homo             166 T---------------------------------------------VS---G--------
Anopheles        209 I-----------------------------------------------TPSASV-------
Coboldia         187 S-----------------------------------------------AATSDK-------
Drosophila       173 P-----------------------------------------------PPKISL-------
Caenorhabditis   114 ---------------------------------------------------------
Trichuris        133 T---------------------------------------------DS-ASC--------
Crassostera      190 T---------------------------------------------VKSANN--------
Capsaspora       188 -----------------------------GS--------------GSGSAG---------
Batrachochytriu  132 A-----------------------------RS--------------KKSVKV--------
Spizellomyces    155 A-----------------------------RS--------------KIGPSG--------
Lichtheimia      121 -------------------------------------------------KT---------
Rhizopus         123 ---------------------------------------------KPAA---------
Ustilago         128 A-----------------------------A-----------------------------
Cryptococcus     117 P-----------------------------NS--------------PSTSAS--------
Schizosaccharom  126 N---------------------------------------------------------
Saitoella        122 A-----------------------------RE--------------EGPKSG--------
Saccharomyces     97 -----------------------------------------------VTQ---------
Lachancea        121 V-------------------------------E-----------------KVAN-------
Neurospora       111 -----------------------------------------------SAN---------
Fusarium         111 ---------------------------------------------------------
Aspergillus      111 -------------------------------------------------SAKG-------
Dictyostelium    126 N-----------------------------N-------------------NN--------
Arabidopsis      114 PKGS---------GDASMRQKE--------KQDSV--EQKPLKK-GGDSS---ETS--SR
Oryza            119 -----------------------------------NTRTTDF-GGDPE---IKN--AS
Pinus            129 RKASFEQSQETASETTDMPKAD--------RSDGKSKIWRCLSCTYDNPE---HVS--AC
Physcomitrella   136 ------SDQATASLRSNMPVLYQKSWGKVADSSSFSSKIVPFKFDTPSPD---EKNLAAR
Chlamydomonas    116 A--VAPPAAAAAPTAPSLPQNK--NFL---RPSPM---LQQQKQQQGGPANGEGADEAAR
Phytophthora     159 M---------------------------------------------PAPARG--------
Tetrahymena      104 N-----------------------------Q---------------QGKSNN--------
Giardia           45 ---------------------------------------------------------
Leishmania       146 -------------------------------------------------KRG-------G
Trichomonas      133 ---------------------------------------------------------
consensus        301
```

```
Amphimedon       119 ------------------SNTKM--------------------GFITHH--------RSN
Nematostella     202 ------------------SNVVL--------------------GFTTSR-----------
Danio            179 ------------------KKQTM--------------------GFDVRS--------A--
Xenopus          171 ------------------KKQTM--------------------GFDVPS--------AAS
Sarcophilus      169 ------------------KKQTM--------------------GFEIPG--------VTA
Homo             170 ------------------KKQTM--------------------GFEVPG--------VSS
Anopheles        216 ------------------AKKTL--------------------AFEVTSSPRMQ------
Coboldia         194 ------------------GIIKK--------------------GFEIAS-PLIQ------
Drosophila       180 ------------------KEPRR--------------------GFEIPSPKVPS------
Caenorhabditis   114 ------------------------------------------------------------
Trichuris        139 ------------------AEERL--------------------ADVV-------------
Crassostera      197 ------------------SETVF--------------------GTEKNTVKDLR--TKAG
Capsaspora       196 ------------------KGTAASASKPGATNLKPLV--MPSSQPKQQQPQQPTDTHREP
Batrachochytriu  141 ------------------DKLSTADSGSTSDDVNVVVSDMEALGFKQV--KTPL--APQM
Spizellomyces    164 ------------------KSAKLPSSKPTP-------------QIRKK--QEPI--PEPM
Lichtheimia      123 --------------------KSTEP-----------------SSASNQS--EDQL--SQ--
Rhizopus         127 ------------------KPATKPTAKPTVKK-----STGDEVEFLSD--EEEL--DR--
Ustilago         130 ----------------------KAAGGKPVGTTVSQ-------------------------
Cryptococcus     126 ----------KST-----SKSGSASSTPRTLGKSN-------------------------
Schizosaccharom  127 ---------------------DE-----------------------------PA------
Saitoella        131 ------------------KKAKTA----------------------KK--DQAI--AAPT
Saccharomyces    100 ------------------KLANI--------------------SISQQRPNDR-------
Lachancea        127 ------------------EVSKL--------------------SVNG-----G-------
Neurospora       114 ------------------VHNKK-------GSS--------------------------SA
Fusarium         111 --------------------PQKE-------KVK-------------------------DA
Aspergillus      115 ------------------FKSKQPASKSAGDKK-------------------------NQ
Dictyostelium    130 ----------KVP-----VESKTPYNTPIGTPIND-----------KNLPHSPK------
Arabidopsis      149 ------GRHDKLDD-----KGGAGG-------------------------I---------
Oryza            136 ------ISHEKVGSTQYASVGSSSG---------------------------------------
Pinus            176 GMCS-TIRSASLEESQASASGTAAMSNPASTTKKA-------------SLDITA--KVEA
Physcomitrella   187 GLKKSPIRVAQSPDDI--LNGARSSMAKAGTSK-----------------SISS--AVSK
Chlamydomonas    166 GVA-------ALGLTSAASGGSEGGTTPGGGTRQH-------------HPHLGH--P---
Phytophthora     166 ------------------KALAI--------------------GALPSTPKEE-------
Tetrahymena      112 --------------------DQA-----------------------------------------
Giardia           45 ------------------KKSSTGSTPSNTGSTT--CSTPKTTFETVSTPTPI------
Leishmania       150 GVLK-------VT--AAAGPANRASTFPA-----------------VKSPEPGG------
Trichomonas      133 ------------------KSQK-------------------------HIQIPA------
consensus        361

Amphimedon       133 -----IDSSPARSPSPS----------------------VLPGRS-----------TP--
Nematostella     213 --------------------------------E--EKRSSATSSPD-----------QQ--
Danio            191 EENGGVAPSLRRGPSPEATAV----PTT-----------ETPS-K-----------QS--
Xenopus          185 EINGQIVKGQTTDEAMEET------------D--NGQESANPVPS-----------FQ--
Sarcophilus      183 EENGDSVHTPHKGPPSEDASI----VSSGILE--TVSKSTLPSHT-----------IQ--
Homo             184 EENGHSFHTPQKGPPIEDA-I----ASSDVLE--TASKSANPPHT-----------IQ--
Anopheles        232 ------------SPSVS------------------GR--NTPEIT------------E--
Coboldia         209 ------------SPALS------------------GR--NTPESS------------E--
Drosophila       196 ------------SPVVS------------------GR--NTPVDI------------S--
Caenorhabditis   114 -----------RTPQVKNL----------------QAESTTPTVSRP---------SS--
Trichuris        148 -------KGMREGEM------------------------NSEEGS-----------LQ--
Crassostera      217 NLNANNEVDVTDSAVLNDSKLQAVNSEIDLVGDLVGRDLDTPSKS-----------SS--
Capsaspora       236 SLATKDVVAMGFSPAVSANASLV---SS-AT---ASPLSLSPSLASSGDKSKGKLPSSKG
Batrachochytriu  179 GARNKALLTSTETPVIPGKSVPP---SK-MVR-VQS------SDNGP-------------
Spizellomyces    189 DQLQMDLSGLNLAPPKSATLAPP---PA-MAR-TVSASSSNSSLAPP-------------
Lichtheimia      141 -----DMLGMGLEDVAKKAA------QA-RLK-VSSA-TSTPAGTPP-------------
Rhizopus         158 -----DMNAMGLS---------------------------------E-------------
Ustilago         144 --LRNEIESLEIHGGSSSKA------------------------A-S-------------
Cryptococcus     146 --LSTDLEGLHLNEEMDEAE-------------------------R-E-------------
Schizosaccharom  131 -FQTNGEVKMKNS--------------------------SESDNQP-------------
Saitoella        147 NQLEVDMQAMNMGSSATGGA---------------------PAPAPP-------------
Saccharomyces    115 --LPDWLDEEE-SEGERN-----------------G---EEAN-----------------
Lachancea        137 --SDQDID-IE-SEESDD-----------------D---RKPK-----------------
Neurospora       124 DGVTNQVSQLK-------------------------------------------------
Fusarium         120 SEAEKDVAGLK-------------------------------------------------
Aspergillus      132 GDLAGGMNNLS-------------------------------------------------
Dictyostelium    158 ESLIDSINATT-------------------------------------------------
Arabidopsis      164 ------------KSGKSLPKA-----KADMSNETSSSSKYM---ETS-----ESLTGT--
Oryza            155 -------------AGKKL--------KEDQSSRATSSAQNE---DVA-----QKLSSD--
Pinus            220 EIVEDNAKSSKEPAPSSLSKA-------DKHEKRENGVLREDKSSSN-----GLVSEE--
Physcomitrella   226 ----LNVPGLSQSSGAST---------------SESHVGNGSSSAPE-----GELADA--
Chlamydomonas    201 ------------EAPNAL--------------------------SHP-----GGLHGL--
Phytophthora     181 -----------KKPRISAAD----------------AASAAPTISRA---------QT--
Tetrahymena      115 -------AQLTKQASSSVTAA-------------STSGATTAPSDKSK----AGEY-I---
Giardia           78 ---------------------------------------TPSTSLS-------------
Leishmania       178 -------------EEASD----------------NEGNSASPSASS-------------
Trichomonas      143 ---------------------------------------SQTPSKLIP----------PKG
consensus        421                                          p
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Amphimedon        153 ----------TTTPIRQ-PQLTRSS--LKGKQLHLIDVLSEYKKRQESEKPTINLVVIG
Nematostella      227 ----------NMSPATEASRSPELK--QKSKAKDRLDAKAELEKRH-QGKELLNLVIIG
Danio             222 ----------TVT--EDSAAPTPTR--PSGKSKQQLNIRAELEKRQ-GGKPLLNLVVIG
Xenopus           218 ----------NTE--EPNSTMTPGK--SSNKAKQKINVKEELEKRQ-GGKQLLNLVVIG
Sarcophilus       224 ----------ALE--EQNTTPTPVK--KSNKLKQQIDVKAELEKRQ-GGKQLLNLVVIG
Homo              224 ----------ASE--EQSSTPAPVK--KSGKLRQQIDVKAELEKRQ-GGKQLLNLVVIG
Anopheles         246 ----------EA--ARQQ--QQQSF--KSTPKEPSRNAKELFGKERGDRKDHIHMVVIG
Coboldia          223 ----------LRNQ------------GIKAKDISRNIEEIYNKERANEKPHIHMVVIG
Drosophila        210 ----------AGDDISRS--SATVF--KVSKEQAVRNARQLYEKERADQKSHIHMIVIG
Caenorhabditis    136 ----------EVDLTS--FRRNQL----QNIA-KAPSVARKTPKPRVADKDLINLIVVG
Trichuris         164 ----------KLSLTDQSYPNEPSE--ISTSEKLKTETRQ-TTAQQQDGKPILNLVVVG
Crassostera       264 ----------SSVPAT------PKS--TSKVKQDKAKLKEEYERRK-TGKDLLNLVVIG
Capsaspora        289 VDAALAYEDNFAGGSGPSSGTSSPRP--GGGHRAPRMDILEEYKK-RGAGKAHLNMVVVG
Batrachochytriu   215 --------GMVRVQ-SNSSVK--------SSPKFKRVNIKEELAK-RSAQKDHLNLIVVG
Spizellomyces     231 --------AMARTGSSSSTGR--------SSPKLKRINVAEEYKK-RNAEKESLNLVVVG
Lichtheimia       174 ----------DTPRSASPLA--------KIPASKRVNVMEEYAK-RSGEKPKLNLVVIG
Rhizopus          167 ----------KKKEAPEPLA--------KIPNSKRINIMEEYQK-RSGEKSKLNVIFIG
Ustilago          164 --------------SAGSAAPSAVST--PMGIAHER--IIEEYRKREREGKAELSLVVVG
Cryptococcus      166 ----------------REKEKFKERQ--VLSMKQEEL-IAKAKEEEEKSGKKNVSLIVVG
Schizosaccharom   150 ----------------EKKK--IK----KQNPTDLVSVPEIFE--QSNPKPVVHLVVTG
Saitoella         173 ----------------------------IKIARKKVNVVEEYAK-VD-VKESANFVIIG
Saccharomyces     135 ------------DEKTVQRYY--KTT--VPTKPKKPHDI-SAFV---KSALPHLSFVVLG
Lachancea         156 ------------AEPVTKTYK--KIT--TPTKPRNPVDI-QSYV---SSRKPHLNFVVLG
Neurospora        135 ------------------------IDD--TPLPKSRNLNVLSEFEK--QKGKKTASFVVVG
Fusarium          131 ------------------------IVD--APPPKSKGLDVLKEYEN--SSNKRSISFVVVG
Aspergillus       143 ----------------------VQE--KVAVKSKNLDVLSEYHK--SQRKRAMNFAVIG
Dictyostelium     169 ------------------VNKNLNVKQ--HSINRKKELEEMVHVAFSSSDNKPHLNMVVIG
Arabidopsis       197 -MNKMSLIGETE-NSS-----DIKIRGPKSQSKHKP--EEWMLLDKESDALSQLNLAIVG
Oryza             184 -IQKLGL------EKN-----EVDTAKPYLPEEYKP--EKWMFANEESGVLSQLNLAIVG
Pinus             266 -LQKLSFSTGYNFHNS-----NKVLKNAVPLEEYKA--EPWMLHEQSDEGKNLLHLAIVG
Physcomitrella    260 -LKQMNVGGDYMESKSRENADASTSTYGLSLESYEP--EPWMLKDANKDSRQLLHLIVVG
Chlamydomonas     216 --HTRRPVTEYVMEADLA----RDVAAATAS--ESS--STSTSGSSSGSSKPPLHLVVLG
Phytophthora      203 ----------QFTPAEKK----ALE--RAELKTQEQAVK-LEEEARTGGKTKISMVVIG
Tetrahymena       148 ----------KIE--RDV----VK----FNQAYPSVEYDIEADK-KEENVKNMNLVIVG
Giardia            85 ---SVANIGTMKATPSQQ-----HIA--KFIADVERSEEVIKGAAGLIKSRNTINVLVVG
Leishmania        195 --------------------GRTTTTL--RGSKGTSQRRTKQMLEMEPDKEKPDCTFVIAG
Trichomonas       155 IASTFS------CASI------KDI----EQHLTTKV-TKDQVYKQISTGKKHVNLVIVG
consensus         481                                    i v     k     k  lnlvviG


Amphimedon        199 HVDAGKSTLMGHLLFLLGHVSKRTMHKYETDSQKLGKASFLYAWILDETGEERNRGITMD
Nematostella      273 HVDAGKSTLMGHLLFLLGDVSKKAMHKYETESKKAGKASFAYAWVLDETGEERERGITMD
Danio             266 HVDAGKSTLMGHLLYLLGNVNKRTMHKYEQEAKKAGKASFAYAWVLDETGEERDRGVTMD
Xenopus           262 HVDAGKSTLMGHLLYLLGHVNKRTMHKYEQESKKAGKASFAYAWVLDETGEERQRGVTMD
Sarcophilus       268 HVDAGKSTLMGHLLYLLGNVNKRTMHKYEQESKKAGKASFAYAWVLDETGEERERGVTMD
Homo              268 HVDAGKSTLMGHMLYLLGNINKRTMHKYEQESKKAGKASFAYAWVLDETGEERERGVTMD
Anopheles         289 HVDAGKSTLMGHLLYDTGNVSQRIMHKHEQESKKLGKSSFMYAWVLDETGEERERGITMD
Coboldia          259 HVDAGKSTLMGHLLLDLGNVTQRVMHKYEQESKKVGKQSFMYAWVLDETGEERTRGITMD
Drosophila        255 HVDAGKSTLMGHLLYDTGNVSQRVMHKHEQESKKLGKQSFMYAWVLDETGEERARGITMD
Caenorhabditis    178 HVDAGKSTLMGHLLHDLEVVDSRTIDKFKHEAARNGKASFAYAWVLDETEEERERGVTMD
Trichuris         210 HVDAGKSTLMGHLLYIMGNVEQKTMHKYKQESQRLGKSSFAYAWVLDESVEERERGITMD
Crassostera       304 HVDAGKSTLMGHLLYQMGVVNKRSMHKYEQESKKRGKGSFAFAWVLDETEEERTRGVTMD
Capsaspora        346 HVDAGKSTLMGHILFQLGHVSRRTLHKYETESQKLGKASFAFAWVLDETDAERARGVTID
Batrachochytriu   257 HVDAGKSTMMGHLLVLLGEVSERTIKKYERERAEKIRKKSFAFAWVLDETEDERSRGVTID
Spizellomyces     274 HVDAGKSTLMGHVLYLLGEVNERTMKKYERDAEKMKKSSFAYAWVLDETEEERTRGVTID
Lichtheimia       214 HVDAGKSTLMGHLLYEIGHVNDRTMKKYERDSQKIGKGSFAYAWVLDETGEERDRGITMD
Rhizopus          207 HVDSGKSTTIGHLSFRLGHVDERKMHKLERDSQKIGKGSFAYAWLLDETEEERNRGITMD
Ustilago          206 HVDAGKSTLMGRMLLELGSLSQREYSTNERASQKIGKGSFAYAWALDSSEEERERGVTID
Cryptococcus      207 HVDAGKSTLMGRVLYDIGELSEKEKIANERGSKKLGKGSFAFAWGLDALGDERDRGVTID
Schizosaccharom   185 HVDSGKSTMLGRIMFELGEINSRSMQKLHNEAANSGKGSFSYAWLLDTTEEERARGVTMD
Saitoella         202 HVDAGKSTMMGRLLYDIGAVDERTIQKFRKESEKMGKGSFALAWVMDSTDEERARGVTVD
Saccharomyces     175 HVDAGKSTLMGRLLYDLNIVNQSQLRKLQRESETMGKSSFKFAWIMDQTNEERERGVTVS
Lachancea         196 HVDAGKSTLMGRLLYDVGAVNYKLIRKLKKESEQAGKGSFHLAWVMDQTSEERDRGVTVD
Neurospora        168 HVDAGKSTMMGRLLLDLNVVDQRTVDKLRKEAEKIGKTSFALAWVLDQRHEERSRGVTID
Fusarium          164 HVDAGKSTLMGRLLLELKFVEKHTIDRYRKQAEKSGKQSFALAWVMDQRSEERERGVTID
Aspergillus       176 HVDAGKSTLMGRLLADLKAVDQRTLERYQREAEKIGKGSFALAWVLDQGTEERARGVTID
Dictyostelium     210 HVDAGKSTTMGHILFKLGYVDKRTMSKFENESNRMGKSSFHFAWVLDEQEEERERGVTMD
Arabidopsis       248 HVDSGKSTLSGRLLHLLGRISQKQMHKYEKEAKLQGKGSFAYAWALDESAEERERGITMT
Oryza             230 HVDSGKSTLSGRLLHLLGRISKKDMHKNEKEAKEKGKGSFAYAWAMDESSEERERGVTMT
Pinus             318 HVDAGKSTLTGRLLHLMGRVSQKEMHKYQREAKQKGKESFAYAWVLDESTEERERGVTMT
Physcomitrella    317 HVDAGKSTLMGRILHLLGRVSQKEMHKNEKESKQQGKGSFAYAFVLDEGAEERARGVTMT
Chlamydomonas     266 HVDAGKSSLMGRLLHDLGLVSAKEAHKFQRDAAAAGKGSFAWAWVLDERPEERERGVTMD
Phytophthora      245 HVDAGKSTITGHLLYRLGYVSKRLMHKYEKESREAGKSSFAYAWVMDADEEERSRGVTMD
Tetrahymena       186 HVDSGKSTLVGHLCHLKKVIDQKLAHKNEKESKNIGKESFKFAWVNDEFEAERQRGITID
Giardia           135 HVDAGKSTIFGHLAVLSGSVSMRERTRTQALADTYNKSTFSYAFLLDTNDEERQRGVTMD
Leishmania        234 HVDAGKSTTLGHLLLLLGRVSIQDVERNEKADRTHRKDSFKYAWLLDQCEEERRRGVTID
Trichomonas       198 HVDAGKSTLIGHVLLLSNFVEKQRMDKIMEDSKATGHGQDYLAWIMAEDESERSHGVTID
consensus         541 HVDaGKStlmGhllf lg v  r mhkyehes k gkasfayAwvldet eER rGvTmd
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Amphimedon       259 IAQQQFET----------EHLKIHLLDAPGHRDFIPNMITGAAQADVAVLVVDATIGSFE
Nematostella     333 VGLTRFQT----------KNKVITLMDAPGHKDFIPNMITGAAQADVAILVVDAITGEFE
Danio            326 VGMTKFET----------DSKVVTLMDAPGHKDFIPNMITGAAQADVAVLVVDASRGEFE
Xenopus          322 VGMTKFET----------KSKVITLMDAPGHKDFIPNMITGAAQADVAVLAVDASRGEFE
Sarcophilus      328 VGMTKFET----------KTKVITLMDAPGHKDFIPNMITGAAQADVAVLVVDASRGEFE
Homo             328 VGMTKFET----------TTKVITLMDAPGHKDFIPNMITGAAQADVAVLVVDASRGEFE
Anopheles        349 VGSTRFET----------AKKEITLLDAPGHKDFIPNMISGANQADVALLVVDATRGEFE
Coboldia         319 IGESRFET----------DTKQITLLDAPGHRDFIPNMISGVTQADVALLVVDATTGEFE
Drosophila       315 VGQSRIET----------KTKIVTLLDAPGHKDFIPNMISGATQADVALLVVDATRGEFE
Caenorhabditis   238 IGRTSFET----------SHRRIVLLDAPGHKDFISNMITGTSQADAAILVVNATTGEFE
Trichuris        270 IAQTRFET----------EKFSFILLDAPGHKDFIPNMITGASQADVALLVINATRGEFE
Crassostera      364 IAQTAFET----------PHKQITLLDAPGHKDFIPNMITGAAQADVAILVVNATRGEFE
Capsaspora       406 VAMTSFET----------KTKRITLLDAPGHRDFIPNMISGAAQADVAVLVVNAGVGEFE
Batrachochytriu  317 VAVSKFET----------PNHSFTLLDAPGHKDFIPNMISGASQADVALLVVDSIQGEFE
Spizellomyces    334 VAITKFHT----------PHRKFTLLDAPGHRDFIPNMMSGAAQADVAILVVDATPGEFE
Lichtheimia      274 IATNNFET----------DHRSFTLLDAPGHRDFIPNMISGTAQADAAVLVVDASTGGFE
Rhizopus         267 IGTNYFET----------RHRHITILDAPGHRDFIPNMISGTAQADAAILVA--PASGFE
Ustilago         266 IAQDHFST----------QHRTFTLLDAPGHRDFIPNMISGAAQADSALLVVDSIQGAFE
Cryptococcus     267 IATTHFVT----------PHRNFTLLDAPGHRDFIPAMISGAAQADVALLVIDGSPGEFE
Schizosaccharom  245 VASTTFES----------DKKIYEIGDAPGHRDFISGMIAGASSADFAVLVVDSSQNNFE
Saitoella        262 IATNQFET----------PKRKFTILDAPGHADFVPNMIAGAAQADFAVLVIDASTGGFE
Saccharomyces    235 ICTSHFST----------HRANFTIVDAPGHRDFVPNAIMGISQADMAILCVDCSTNAFE
Lachancea        256 ICTSDFET----------DRATFTIIDAPGHRDFVPNAITGISQADAAVLTIDCCVDAFE
Neurospora       228 IATNRFET----------ETTSFTILDAPGHRDFIPNMIAGASQADFAILVIDASTGAFE
Fusarium         224 IATNHFET----------EKTSFTILDAPGHRDFVPNMIAGASQADFAILVIDANTGAYE
Aspergillus      236 IAMNKFET----------ENTVFTIVDAPGHRDFVPNMIAGASQADFAVLVIDSGTGNFE
Dictyostelium    270 VCVRYFET----------EHRRITLLDAPGHRDFIPNMISGTTQADVAILLINA--SEFE
Arabidopsis      308 VAVAYFNS----------KRHHVVLLDSPGHKDFVPNMIAGATQADAAILVIDASVGAFE
Oryza            290 VAVAYLET----------NKYRVVLLDSPGHKDFVPNMISGATQADAAILVVDACTGSFE
Pinus            378 VAVAHFDT----------VKFHVVLLDSPGHKDFVPNLIVGASQADAAVLVVDASTGAFE
Physcomitrella   377 VAVAHFET----------PKLRVVLLDAPGHRDFVPNMISGASQADAAILVVDASIGAFE
Chlamydomonas    326 VAMTRFAT----------NRFAVTLLDAPGHRDFVPNMIAGAAQADAALLLVDGSPGGFE
Phytophthora     305 VGTSHFET----------ETKHVTLLDAPGHRDFIPKMIAGAAQADVAVLVVPAVTGEFE
Tetrahymena      246 IGYKVIQT----------KNKNITFLDAPGHKDFVPNMIQGVTQADYALLVIEGSLQAFE
Giardia          195 VCNHTLTLAFPELGDNYSVPHTVFLQDCPGHRDFVPSLIRAVSQPDAAVLVLDASPKEFE
Leishmania       294 SGSFCFET----------EHRRVHILDAPGHKDFVLSMISSATQADAALLVVTAATSEFE
Trichomonas      258 VALNNFET----------EDRKITVLDAPGHRDFVPNMIAGASQADSAILVVDVSNPNIE
consensus        601 va trfet           hk itllDaPGHrDFipnmitgatqaD AvLvvdat gefE

Amphimedon       309 SGFES---------GGQTREHALLVRSLGVTQLVVAINKMDTVSWSRERFDEIVTKLKSF
Nematostella     383 AGFES---------GGQTREHAILVRSLGVTQLIVAINKLDMMSWSEERYLHIVSKLKHF
Danio            376 AGFEA---------GGQTREHALLVRSLGVTQLAVAVNKMDQVNWQQERFQEIISKLGHF
Xenopus          372 AGFEA---------GGQTREHALLVRSLGVTQLAVAVNKMDQVNWQQERFNEVISKLRHF
Sarcophilus      378 AGFET---------GGQTREHGLLVRSLGVTQLAVAVNKMDQVNWQQERFQEITGKLGHF
Homo             378 AGFET---------GGQTREHGLLVRSLGVTQLAVAVNKMDQVNWQQERFQEITGKLGHF
Anopheles        399 TGFEQ---------GGQTREHALLVRSLGVSQLGVVVNKLDTVGWSKERFDEIVNKLKVF
Coboldia         369 SGFEQ---------GGQTREHALLVRSLGVSQLGVVINKLDTVEWSKERFDEIVGKLRLF
Drosophila       365 SGFEL---------GGQTREHAILVRSLGVNQLGVVINKLDTVGWSQDRFTEIVTKLKSF
Caenorhabditis   288 TGFEN---------GGQTKEHALLLRSLGVTQLIVAVNKLDTVDWSQDRFDEIKNNLSVF
Trichuris        320 SGFDL---------GGQTREHTVLVRSLGVVQLLIAVNKMDTVEWSEERFVEVKNRVGNF
Crassostera      414 TGFES---------GGQTREHALLARSLGVSQLLVAVNKMDTVDWSQSRYDDIVKKLGLF
Capsaspora       456 AGFEG---------GGQTREHALLVRSLGVNQLIVAVNKLDACDWSKARFDELVARLSLF
Batrachochytriu  367 AGFDN---------GGQTREHAILIRSLGVSQIIVAINKLDAIDWSMVRFEQIQAQLQTF
Spizellomyces    384 TGFDS---------GGQTREHAVLLRSLGVTQLIVAVNKLDVVDWSKTRFDEISEKLSHF
Lichtheimia      324 SGFEA---------NGQTKEHALLARSLGVQQMIIAVNKLDTLNWDQGRFDTIVEKLNLF
Rhizopus         315 AGFEA---------GGQTKEHAILARSLGVQQVIVAVNKLDLVGWSQERFMEIKDKLSTY
Ustilago         316 AGFGP---------NGQTREHALLVRSLGVQQLVVVVNKLDAVGYSQERYDEIVGKVKPF
Cryptococcus     317 AGFER---------GGQTREHAWLVRSLGVKEIIVGVNKMDLVSWSQDRYEEIVESLKPF
Schizosaccharom  295 RGFLE---------NGQTREHAYLLRALGISEIVVSVNKLDLMSWSEDRFQEIKNIVSDF
Saitoella        312 SGFNV---------RGQTKEHALLVRSLGVQNLIVAVNKLDSVDWNHERFEEIEMQVSQF
Saccharomyces    285 SGFDL---------DGQTKEHMLLASSLGIHNLIIAMNKMDNVDWSQQRFEEIKSKLLPY
Lachancea        306 SGFSL---------DGQTKEHTLLARSLGARHIVVAMNKMDHEGWYPTRFFDIKWELESF
Neurospora       278 SGL-----------KGQTREHSLLIRSMGVSRIIVAVNKLDTVNWSQERFDEITHQVSGF
Fusarium         274 KGL-----------KGQTREHVLLLRSLGVQRLVIAVNKLDMVGWSQERYDEIAQQVSGF
Aspergillus      286 SGL-----------RGQTKEHALLVRSMGVQRIIIAVNKMDAVEWSRDRYEEIEQQISSF
Dictyostelium    318 AGFSA---------EGQTKEHALLAKSLGIMELIVAVNKMDSIEWDQSRYDYIVETIKTF
Arabidopsis      358 AGFDN----L----KGQTREHARVLRGFGVEQVIVAINKMDIVGYSKERFDLIKQHVGSF
Oryza            340 AGMDG----EGGKSVGQTKEHAQLIRSFGVEQLIVAVNKMDAIGYSKERFEFIKVQLGSF
Pinus            428 AGMDG----QGT--GGQTKEHAQLIRSFGVEQLIIAINKMDVVDYSKERFDFIKSQLGLF
Physcomitrella   427 AGLEG----EGQ-GRGQTREHAQLVRSLGVEQLIVAVNKLDAVDFSKERFDFIRGTLQPF
Chlamydomonas    376 AGFSEGSGGLHGAPGGQTREHAALARSLGIEQMAVVVSKLDTCGYDQSRFESIRAALLPY
Phytophthora     355 AAFEN---------SGQTKEHTLLVRSLGVAQMVVAVNKMDMVNWDKERFDSIVTSLSMF
Tetrahymena      296 RGFEF---------GGQTKEHAFLVKQLGVQRLIVLINKMDTVNWDRNRFEYIKLELTRF
Giardia          255 KGLSD---------DGQTREHLQLLMIFGVKHIMVAVNKLDRTDWNEGRFVEIVTVLTKV
Leishmania       344 TGLHH----------GTKSHLLVLKTLGVGSIVVAVNKMDAVAYSQERYDYVVRELQLL
Trichomonas      308 R--------------GQAGEHILLCRSLGVKHLIVAINKMDSLEYMQSAYEDVCNTLTEH
consensus        661  gfe          ggqtreHallvrslGv qlivavnKmD v ws erfdei   l  f
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Amphimedon        360 LK-QGGYKEGDITYVPCSGMTGDNLT--STL-----TDSWY-K-GPSLAQSIDRFRPP--
Nematostella      434 LK-QVGFKDSDVVYVPVSGLSGENLV--KPCTE-EKLKKWY-Q-GQCLVDRIDEFKSP--
Danio             427 LK-QAGFKDSDVFYVPTSGLSGENLT--TKSKV-ADLTAWY-T-GPCLVEQIDAFKPP--
Xenopus           423 LK-QAGFKESDVYYIPTSGLSGENLV--KRSQI-SELVGWY-K-GPCLLEQIDSFKAP--
Sarcophilus       429 LK-QAGFKESDVAFIPTSGLSGENLI--TKSQS-SELTKWY-K-GQCLLEQIDSFKPP--
Homo              429 LK-QAGFKESDVGFIPTSGLSGENLI--TRSQS-SELTKWY-K-GLCLLEQIDSFKPP--
Anopheles         450 LK-QAGFRDADVTYVPCSGLTGENLV--KDPTD-PALTAWY-S-GPTLLKVIDSFKTP--
Coboldia          420 LK-QAGFKDSDVTYVPCSGLTGENLV--KPATD-PILLSWY-K-GPTLLAVIDSFTVP--
Drosophila        416 LK-LAGFKDSDVSFTPCSGLTGENLT--KKAQE-PALTNWY-S-GRHLLDVIENFKIP--
Caenorhabditis    339 LTRQAGFS--KPKFVPVSGFTGENLI--KRME-----LDWY-D-GPCLLELIDSFVAP--
Trichuris         371 LK-QVGFGA-KCLFVPCSGLTGENLK--TVPDDSCPLTRWY-S-GPTLVQALDSMEPI--
Crassostera       465 LK-QAGYKDIDLSYIPCSGLGGENLT--KAVSE-PKLASWY-K-GSTLVEQIDKFKAV--
Capsaspora        507 LK-TSGYRLDNVTFVPVSGLIGENLI--ERK-E-PKLTQWY-S-GPTLVEQIDQFQPP--
Batrachochytriu   418 LV-QVGFKKQRIVFIPCSGFSGENLK--ERQ-V-DGLCRWY-S-GPTLIEALDALEAP--
Spizellomyces     435 LS-QVGFRKQKVAFIPTSGYTGENLV--KRE-S-DKLNAWY-S-GSTLVEQIDAFEAP--
Lichtheimia       375 LV-QAGYRKSNLTYIPVSGLTGENLI--KKSD----LVNWY-S-GPSLLELIDAFEPP--
Rhizopus          366 LL-QIGFKKSNLFFVPISGLTGENLV--EKSAI-PELTSWYQA-GPSLIEQIDQLEPP--
Ustilago          367 LM-SCGFDAAKLRFVPCGGSVGENLA--VRERG-GALSAWY-S-GPTLVELLDELEPP--
Cryptococcus      368 LL-SAGFNSTKTTFLPLAAMEGINIL--D-NDQ-PELKKWY-S-GPALIDALDDVEVP--
Schizosaccharom   346 LIKMVGFKTSNVHFVPISAISGTNLI--QKD-S-SDLYKWY-K-GPTLLSALDQLVPP--
Saitoella         363 LT-NAGFDPQNVQYIPCSGLTGENLV--KRSAE-P-ALTWF-N-GPTVLGALESIAPT--
Saccharomyces     336 LV-DIGFFEDNINWVPISGFSGEGVY--KIEYT-DEVRQWY-N-GPNLMSTLENAAFKIS
Lachancea         357 FK-DIGIKKEQVSWVTCSGLSGEGVY--NIKRP-LG-IDWY-N-DPSLVDCLEDVAKKLN
Neurospora        327 LT-ATGFQPKNIAFVPVSGLHGDNLV--RKSTD-P-AASWY-T-GKTLVEELEASEPS--
Fusarium          323 LA-GLGFVSKNIDFVPISGLNGDNLA--RRTED-P-AASWY-T-GPTLIEALENSEPT--
Aspergillus       335 LT-TAGFQAKNIAFVPCSGFRGDNVT--RRSDD-P-NASWY-T-GRTLVEELEATEPY--
Dictyostelium     369 LV-HAKFNEKNIRFIPISGFTGENLI--DRQ-E-SKLLKWYDSKQPTLIECIDSFSVG--
Arabidopsis       410 LQ-SCRFKDSSLTWIPLSAMENQNLV--AAPSD-NRLSSWYQ--GPCLLDAVDSVKSP--
Oryza             396 LR-ACNFKDSSVTWIPLSAVENQNLI--KIPSD-VRLTSWYQ--GFCLLDAIDSLQLP--
Pinus             482 LR-RCGFKESSLMWIPMSVIENQNLV--TSTSD-GRLMSWYT--GPHFLESIDLFKPP--
Physcomitrella    482 LK-QCGFKDGSLQWVPVSASEGQNLT--MASTE-SALKAWYN--GPCLIELVDSLKPP--
Chlamydomonas     436 LK-SVGFKESGLQWLPAAGPLGENLV--GPPQD-PALKAWWGPGRPCVTDAIDAFAPR--
Phytophthora      406 LQ-GAGFRPKNLRFVPLSGITGANLE--KTGGV--DECSWY-S-GPSLVEAIDTFAPP--
Tetrahymena       347 LT-SIGYSEDNLIFVPISAFYAENIV--EKSKL--PEAGWY-E-GKCLMELLDTLPVP--
Giardia           306 LRKDIQFG-GEVTFIPVSGIGEDGSHNLTPGNA-GCLPDWVRK-HTSLGEEIYKTQSIRS
Leishmania        393 LKQTRIPEEAIIGFCPISGMAGVNIT--QRGAK---ETPWYH--DLSLIEMIDKCPLE--
Trichomonas       354 LK-RISW--SAVHFIPTVATDKSVLL--NPKE----KMPWY-K-GPTILQAINQIPPY--
consensus         721 lk   gfke  i fvpvsgmtgenlv   k      l  Wy   gpslve id   pp


Amphimedon        408 ----PRPVEKPFRC---CIADIFKGQ-G----AGICVAGKIESGYVQSGETVLVVPAN-E
Nematostella      486 ----KRDMDKPWRF---CVSDVYKGL-G----TGINLAGKMEAGHIQTGDKALAMPAG-E
Danio             479 ----QRSVEKPFRL---CVSDVFKDQ-G----SGFCVTGKIEAGYIQTGDKVLAMPPN-E
Xenopus           475 ----QRSIDKPFRL---CVSDVFKDQ-G----SGFCVTGKIEAGFVQTGDRLLAMPPN-E
Sarcophilus       481 ----QRSIEKPFRL---CVSDVFKDQ-G----SGFCVTGKIEAGYIQTGDRLLAMPPN-E
Homo              481 ----QRSIDKPFRL---CVSDVFKDQ-G----SGFCITGKIEAGYIQTGDRLLAMPPN-E
Anopheles         502 ----DRAIDKPFRL---SVADIFKGT-G----SGFCLCGRIESGMVCVNDKVLVCPSK-E
Coboldia          472 ----VRSISKPFRM---SINDIFKGT-G----SGYCLSGRLETGMISVNDKILIMPCR-E
Drosophila        468 ----ERAIDRPLRM---SVSDIYKGT-G----SGFCISGRVETGVLCLNDKVLVGASR-E
Caenorhabditis    386 ----QPPSDGPLRI---GISDVLKVA-S----NQLVVSGKIESGEVEKDDKVYIMSSV-T
Trichuris         423 ----KRLVERPLRF---TVSNVFKAQRG----SNFYVAGKVATGSVSNGDKLVVVPSG-Q
Crassostera       517 ----ERPMDKPFRL---IISDVFKGL-G----SGFSVVGRVSSGSVQAGDRVLVQPAG-D
Capsaspora        558 ----ERPIDKPLRF---SVNDIFSRP-----NSGVSLGGKVISGSVQIGDKVLIAPINQE
Batrachochytriu   469 ----PRSIERPFRI---SVQDLFKGAMAAGTSGDVTVSGRIESGSVQLGDTMMAMPIF-E
Spizellomyces     486 ----QRAVDKPFRL---SIADYFKGGIGAGGGGAVSVSGRIEAGGIQVGEVVLVMPIN-E
Lichtheimia       424 ----VRALDKPLRM---GVTDFFKGGIGS--SGGVSVGGSIDAGHVQVGEQVMVVPGG-E
Rhizopus          419 ----TRLLDKPLRM---RVADFFKGGIGS--SGGVSVAGHIESGSVQVGEQVMVVPGN-E
Ustilago          419 ----ARQLDSPLRL---PVTNVFKGQTAI--ASGVAVSGRVVSGIVQIGDRVRPVPGD-E
Cryptococcus      419 ----TRPYDSPLRI---PLSNVFKGQTAI--ASGVAVSGRLCSGVVQVGDRLRAVPGD-E
Schizosaccharom   398 ----EKPYRKPLRL---SIDDVYRSP------RSVTVTGRVEAGNVQVNQVLYDVSSQ-E
Saitoella         414 ----ARAIEKSLRI---SVQDVYKAGVT---GGSVTISGRVDAGNVQVGETVHAAPSG-E
Saccharomyces     390 KENEGINKDDPFLF---SVLEIIPSKKT--SNDLALVSGKLESGSIQPGESLTIYPSE-Q
Lachancea         410 KDESSEAIEANFLF---SILDVSPTSK----NNEVIVSGKVEAGSIQPGETITIYPSE-Q
Neurospora        378 ----ARALAKPLRM---TISEVMRTP-Q----SSISITGRIDAGSLQMGDALLVQPSG-E
Fusarium          374 ---TARALKSPFRM---AISEVFRSQ-L----GTTTIAGRVDAGSFQIGDALLVQPSG-E
Aspergillus       386 ----SYALDKPLRM---TISDVFRGGVQ----NPLSISGRIDAGSLQVGDQILTMPSG-E
Dictyostelium     422 ----ERLLNKPFRM---NISDVYKSSSK----GYVAVGGKIEAGLLGNGDKILISPGN-D
Arabidopsis       462 ----DRDVSKPLLM---PICDAVRSTSQ----GQVSACGKLEAGAVRPGSKVMVMPSG-D
Oryza             448 ----SRDVSKPLIL---PICDVIKSQST----GQLAAFGKLETGAIRIGSKVLISPCG-E
Pinus             534 ----TRDISRPLRI---PISEVIQSRTL----GQVAASGKLDAGAIKVGTKLLVMPAG-Q
Physcomitrella    534 ----PRLVARPLRL---TIAEVMKTRTL----GPSAFGGKLESGAIHSGTKVRVMPSG-E
Chlamydomonas     490 ----ERAVSRPLRL---PVSDVFKSKT-----GAVVLGGKLEGGAMRPGSRVVLVPGPAQ
Phytophthora      457 ----QRQISKPFRM---TVSDVSKSM-S----LGQTISGRVYAGAAAVGDSFLLMPIG-L
Tetrahymena       398 ----TRPVNTPLRL---NIYNSFYQK-----NKGLIIQGKVEGGVIFEKSKALIMPQG-L
Giardia           363 TSQIKGEKTSPTIILFDVTPDTYEGK------KVFAANCVVESGILQLSDSIVHLPSM-Y
Leishmania        444 ----SRLLNRPLRL---SLQDVQGT----------TLYAKVESGRLFTGDTVHFVPSE-V
Trichomonas       401 ----EYDINDSFLM---CISEAVETSR-----NSITVSGRVESGYVAIGDNVKVLPGE-Q
consensus         781      r vekplrl    isdvfk         gi vtgkieaG vqvgdkvlvvp   e
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Amphimedon        455 LTSVKTIFGGDD-------I-SAWAVAGDQVVLTLI----------GID-----------
Nematostella      533 KGLLKALNIHDE-------P-TQWACAGDHVTLTLS----------GID-----------
Danio             526 TCTVKGISLHDE-------A-LDWAAAGDHVSLTVT----------GMD-----------
Xenopus           522 TCTVKGITLHQE-------A-VDWAAAGDHVSLTLT----------GMD-----------
Sarcophilus       528 TCTAKGIMLHDE-------P-VDWAAAGDHVSLTLV----------GMD-----------
Homo              528 TCTVKGITLHDE-------P-VDWAAAGDHVSLTLV----------GMD-----------
Anopheles         549 QAVVKNITIDEL-------P-QQTAFAGDQVSLTLA----------NID-----------
Coboldia          519 QTQIKSITIDEG-------S-RTKAFAGDQIVVTLS---------SAVD-----------
Drosophila        515 QAQVKSLTMNEF-------P-QTCVFAGDQVSVTLP----------ALD-----------
Caenorhabditis    433 AATVKECANNDG-------S--RHCFAGDYILLTLQ---------GTFE-----------
Trichuris         471 TGVVKSILIGED-------EERREAKTGEQCNILLT----------GLD-----------
Crassostera       564 LAVVKAVTMDDS-------D-NTCGFAGDHVTVVLT----------GMD-----------
Capsaspora        606 IGTVKAIEIH-E-------EGVTWAAAGDAASILLD----------KVD-----------
Batrachochytriu   521 TGQVRAIEIG-G-------EGVSWAVAGDQVSMSLG----------GLD-----------
Spizellomyces     538 YGTVRALEVS-E-------EAVKWAAAGDSVLMSLT----------GVE-----------
Lichtheimia       474 IGIVKAMQVN-D-------ETSTWAAAGDSVLMTLS----------GLD-----------
Rhizopus          469 MGYIKSMQVN-D-------ESTNWAVAGDSVLMTLA----------NFD-----------
Ustilago          469 SGIVRAIEVD-T-------ESVPWAVAGANATVYLS----------GID-----------
Cryptococcus      469 VANVRTIEVD-D-------DSAPYAVAGQNVTLYLS----------NID-----------
Schizosaccharom   444 DAYVKNVIRNSD-------PSSTWAVAGDTVTLQLA----------DIE-----------
Saitoella         463 PATVKSMQVN-D-------DIADWAVAGSNVVLNLN----------DID-----------
Saccharomyces     444 SCIVDKIQVGSQQGQSTNHEETDVAIKGDFVTLKLR----------KAY-----------
Lachancea         462 SVLVDSILSGNDR------ASVKIGVAGDFVMLKLR----------EAY-----------
Neurospora        425 KAYVKSLQVDDG-------EPADWAVAGQNVVLHLS----------NID-----------
Fusarium          422 EAYVKSIMVD-S-------DMQDWAVAGQNVSVALT----------NID-----------
Aspergillus       434 TATIRSLEVD-G-------EPNDWAVAGQNVVLNLA----------NID-----------
Dictyostelium     470 ICTIKSIRRN-N-------LESEWAVGGDNVDLSLV----------VEN-----------
Arabidopsis       510 QGTIRSLERDSQ--------ACTIARAGDNVALALQ----------GID-----------
Oryza             496 VATVKSIERDSN--------SCDIARAGDNVAVSLQ----------GID-----------
Pinus             582 GAIVKAIEQDGN--------ELNIAKAGDSVDIGLQ----------GID-----------
Physcomitrella    582 IATVKSIELQGQ--------QLKTARAGEGVDVGLN----------GID-----------
Chlamydomonas     538 PFAVRSLEVGGG--------AANLARAGDSCEVALVAHGGGGGGGGAID-----------
Phytophthora      504 TLTVKGMEQDGK-------A-CSLARAGDTIEMGVT----------GID-----------
Tetrahymena       445 VVTVKEINRE-N-------VKVKYAKVGENIDVHIV----------HKE-----------
Giardia           416 LFQIVSIMVDAV--------EADKAVAYDTVTLYLAPDKRATKLCNNCDKLDSSVVVKEM
Leishmania        486 RVAVKSIQKPTVA------GPVLVAFAGEMVEISTN-----------SS-----------
Trichomonas       448 IVRVCDVQLNGE--------PVDFAAAGYIADITLT---------TSMN-----------
consensus         841  g vk i i              wa agd v l l           gid

Amphimedon        486 ---------QTKLALGSVLCSPEA-PVSITSLVRARIIIF-NIELPITAGYPVIFHYQSV
Nematostella      564 ---------MMHVGVGTVLCDPAS-PIRGTCRIKARIIVF-NIEVPITNGFMVLFHYQNL
Danio             557 ---------IIKINVGCVFCDPKE-PIRACTRFRARILLF-NIELPITQGFPVLLHYQTV
Xenopus           553 ---------IIKINVGCVFCSPNE-PIKGCTRFRARVLIF-NFEVPITQGFPVLIHYQTV
Sarcophilus       559 ---------IIKINVGCIFCGPKE-PIKACTRFKARILIF-NIEIPITKGFPVLLHYQTV
Homo              559 ---------IIKINVGCIFCGPKV-PIKACTRFRARILIF-NIEIPITKGFPVLLHYQTV
Anopheles         580 ---------INNISVGYILSDIFH-PVPLATRILARIVVF-NIKVPITRGYPVLLHHQSL
Coboldia          551 ---------VSSISVGYFLCDLIN-PIPVATRFQVRIITF-NVKVPITIGCPVILHHQAL
Drosophila        546 ---------INNVTVGCIISDPQT-PIPVTTRFQARIIVF-NVKVPITMGFPVLLHHQSL
Caenorhabditis    464 ---------PESIQTGSVVVRAGPDTLIPSKKFEVRLVAF-EIAMPIIKGAKAELYAHSL
Trichuris         503 ---------MSAVGSGDVLCPVGS-PVTAVSRFQAKIVTF-DPNMPLVKGMQVIVHGNGS
Crassostera       595 ---------MAHVNVGSVLCDPQN-PIKSAMRIRARIVIF-NLELPITRGFTVVFHYQSI
Capsaspora        637 ---------PIHFAVGCMLTEVDR-PVPVHSSFRAKIIVF-DVKVPITHGFHVVLHYLTF
Batrachochytriu   552 ---------IQQLSTGSILCDPSA-PVSITSHFRAQIVTF-DINIPLTIGIPIVVHHLGR
Spizellomyces     569 ---------IAHINVGSILCDPSA-PVAVTSHFRAQIVTF-DIQIPLTIGVPVVLHHQSL
Lichtheimia       505 ---------IMNLSNGCVICNPQF-PVPVTSTFTAQIVVF-DIKIPITAGFPVVLHQQSL
Rhizopus          500 ---------IINLSNGCVICTGSN-PVPVTSIFEAQIVVF-DVRIPLTLGYQVVLHHGSL
Ustilago          500 ---------QIQISVGAVLCSPSA-PIALCSSFLAQILVF-EPTYPLVAGTSIELFHHSA
Cryptococcus      500 ---------PINLSIGTVLCPTSI-PVPLVTKFTAQILVF-DLQSPIIAGTPVELFHHSM
Schizosaccharom   476 ---------VNQLRPGDILSNYEN-PVRRVRSFVAEIQTF-DIHGPILSGSTLVLHLGRT
Saitoella         494 ---------PMHLKAGDILCDPLN-PVPTVRAFRARIITF-DLARPITNGATIVLHRGRI
Saccharomyces     483 ---------PEDIQNGDLAASVDYSSIHSAQCFVLELTTF-DMNRPLLPGTPFILFIGVK
Lachancea         495 ---------YEDIQSGDLATTVGN-DIPTAQEFTAQLLTF-KLDRPLLPGTSFMLFRGGC
Neurospora        457 ---------PIHVRVGDIVCDPAK-PIQCVDTFTLKALAF-DILMPM----QVDVHRGRL
Fusarium          453 ---------PIHIRVGDMLCPTKN-PINCSDNFVMKAMAF-EHLMPM----PVDLHRGRL
Aspergillus       465 ---------PIHLRSGDVICRPSA-PIANITSFTAKVLAF-DHLMPS----MVDIHRGRL
Dictyostelium     501 ---------PSILRVGCILSDPEK-PIPLSKRFIAQIVTF-TLPIPMTNGYQVVFHAHSM
Arabidopsis       541 ---------ANQVMAGDVLCHPDF-PVSVATHLELMVLVL-EGATPILLGSQLEFHVHHA
Oryza             527 ---------GSKLIAGGILCNPGF-PVPVSNFLELRVLVL-DVTIPILIGYQVEFHIHHV
Pinus             613 ---------SSILMTGGVLCHPDF-PVPVARRIELKVAVL-DIKQPILFGAEVELHAHHS
Physcomitrella    613 ---------PGMLAPGGVVCHPDY-PVPVATRFEVQLLTL-DIRTPILKGSQVILHVHHA
Chlamydomonas     579 ---------PSLVAPGAVLCHADF-PAVLVTKFQLRLVVL-DVPVPLLRGQAVTLHAHVA
Phytophthora      535 ---------PSALTTGSILCSIAS-PVQLAKKFEAKIMTMPAVEVPLVKGTYMTIHMHNV
Tetrahymena       476 ---------DCEIRSGDVLCSIEH-PIPISRIFEVELSAF-ELSYPILKGAQIVMYINTA
Giardia           468 PQGSCFVLTGILLQQGPVSKGVWINNMILATTVKALVLVL-NTPRGISVGDVYDCYVGSS
Leishmania        518 ---------VTGLYPGCVGCEPNL-LIHSSTDFEAHIQTFRTLTKSILPGASFTIIVHAL
Trichomonas       480 ---------VEQFAIGSAIFDPKK-KLQLSNRFTAHLRTF-DIKKPILQGTPLVFHRHAV
consensus         901            l  G vlc p   pv i srf ariiif ei lpi  g  vilh   v
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Amphimedon        535 SEPAVIKKLLSQVSKTSG-DVIRKKPRCLTKNSSAIVEIEISR--------PLSLELYSD
Nematostella      613 SEPATIKKLHALLNKSTG-EVIQRKPRCLPKNSNAEVELQTSR--------PVCVELYKD
Danio             606 SEPATIRKLVSVLHKSSG-EVLKKKPKCLSKGQNAVVEIQTQR--------PVAMELYKD
Xenopus           602 IEPATIRKLVSVLHKSTG-EVMKKKPKCLTKGMNAVIELQTQR--------PIAVELYKD
Sarcophilus       608 SEPATIRRLISILHKSTG-EVTKKKPKLLTKGQNALVELQTQR--------PIALELYKD
Homo              608 SEPAVIKRLISVLNKSTG-EVTKKKPKFLTKGQNALVELQTQR--------PIALELYKD
Anopheles         629 IEPATIRKLKAQLHKGTG-EVIKKNPRCLGNNSCALVEIEFQR--------PIGMERYAD
Coboldia          600 VEPATIVKIKAQLHKGTG-EVIKKNPRFLGNNSCALVEIETTK--------AICIEKYAD
Drosophila        595 IEPAVVCKLTASIHKSTG-EVVKKKPRCLGNNSCALVELETSR--------PICIERYAD
Caenorhabditis    514 CVPCTFTNLLYTINKSNG-EILKKGPRFIAKGASAVVEIETEY--------DIAIETFTS
Trichuris         552 QQPGYLSKLIAEVSKSTG-KVTKSKPRCLARNSSGVVEVTTEK--------PMCFETSHV
Crassostera       644 TEPAIIKRLNCQLNKNTG-EVVKNKPKCLVKNSSAVVEIEFER--------PVCLEMYKD
Capsaspora        686 NEPAVITRLETLLDRSTG-EIVKKHPRALPKNSSAIVTITL-Q-------RPVCLELYEN
Batrachochytriu   601 SEAGYIERLVSLLNKSTG-AVVKKNPRALGQSVTAVVEIRT-Q-------RPMCLETFQT
Spizellomyces     618 TEQSTITKLSALLNKSTG-ETIKKNPRALPKNVTAVVEIKT-S-------RPICLETFKD
Lichtheimia       554 DEPASIIKLLCTLDKSTG-EVTKRNPRHLGKGMTAKVKIQLSN-------RAIPLETFKQ
Rhizopus          549 DEPASIIKLVEILDKSTG-QVVKKNPRCLTKGMTAKIQVKLSQ-------RAIPLETFKD
Ustilago          549 NIAATLTELVSILDKTTG-SVTKAKPRVLTKGCTAMVKVTVKAGGQAGQSSGIPLEDAKT
Cryptococcus      549 NLPATISKLVSILEK--G-QVVKERPRVLQKGTTAMVELSLRPS-SSGKISSIPLETATD
Schizosaccharom   525 VTSVSL-KI--------V-TVNNKRSRHIASRKRALVRISFLD-------GLFPLCLAEE
Saitoella         543 NEAARIQALVATIDRADG-QIIKKKPRHLASGQSAVVEIAFLG-------NGIPMETFKD
Saccharomyces     533 EQPARIKRLISFIDKGN--TASKKKIRHLGSKQRAFVEIELIE-----VKRWIPLLTAHE
Lachancea         544 EQPARIKKLVSIVCKDPKKILKKKVKHLGSDQAAIVEIELIE-----KKRRIPILTIEK
Neurospora        502 HAAGKIEAIDAILDKVTG-KVTKKKPMIVKPGTVSRVRVTLHS--------KVPLEAG--
Fusarium          498 HSAGQIVSIAATLDKVTG-AVVKKKARVVQPGGVARVSVKLAA--------KVPLEAG--
Aspergillus       510 HVPGRISRLVATLDKGSG-SVIKKKPKIVPPGSVARIVVEMDQ--------AVPLEAP--
Dictyostelium     550 EEPATITRLISLLDS-NG-AVSKKNPRCISDTCTALVEITLGR--------LSCLELYSS
Arabidopsis       590 KEAATVVKLVAMLDPKTG-QPTKKSPRCLTAKQSAMLEVSLQN--------PVCVETFSE
Oryza             576 KEAARVTKIVALLD-KAG-KPSKTAPRFLKSKQNAVVQVTLDA--------PVCVEEFSK
Pinus             662 KEAAKIVQILAILDPKTG-LVRKKAPRLLTANQSALIEVLPHR--------GICIEEYCN
Physcomitrella    662 RQPARVDQLVSLLDPKKG-TVLRQRPRHLTANQSAIVVIVPDE--------GVCIEKYSD
Chlamydomonas     628 REEGHLSALVALLDPRTG-EEVKARPRCLTRGQSALVEVTSSR--------GLVLEEYAH
Phytophthora      585 DEPVNITRLVSMLSK-TG-EVEKKKPRCITRERSAVVQITCHR--------KICLEEFAN
Tetrahymena       525 KCPGYIKKITAILDKANG-QITKKNPKCIRNNECAIVEVCIEK--------ENCMELFSN
Giardia           527 RVEARVHKINAQINPSTQ-EVIRKNPPLVGKSAYVRMTLIFNV--------AVIVKEFSK
Leishmania        568 TVRVHVVALISKMDGKTG-NWSKGMVKCVPPAAQAMMLFRAES--------PVALEPATE
Trichomonas       529 DLPLKIESFTAQLDPKTK-KTIKKGIKFCLARQFIEATFSIES--------PIPIDTAES
consensus         961  epa i kll lldk tg  vikkkpr l     aivei             l le y d


Amphimedon        586 CKDLGRFMLRYAGNTVAAGLIIKIL*----------------------
Nematostella      664 YKDLGRFMLRYGGNTIAAGVITQV*----------------------
Danio             657 YKELGRFMLRYVGSTIAAGVVTEIKE*----------------------
Xenopus           653 FKELGRFMLRYSGSSIAAGVVTEIKE*----------------------
Sarcophilus       659 FKELGRFMLRYSGSTIAAGVVTEIKE*----------------------
Homo              659 FKELGRFMLRYGGSTIAAGVVTEIKE*----------------------
Anopheles         680 FKDLGRIMLRVEGVTIAAGLVTEIVK*----------------------
Coboldia          651 IKELGRVTLRVAGVTIAAGLVTKILK*----------------------
Drosophila        646 FKELGRVMLRVAGVTIAAGMVTKIR*----------------------
Caenorhabditis    565 CRALGRVTFRAGGNTIAAGIVEKVITPQ*----------------------
Trichuris         603 SKELSRVTLRFKGSTIAAGVVTELK*----------------------
Crassostera       695 YKDLGRFMLRQGGHTIAAGLVEEVLKTKSKTEENSTE*-----------
Capsaspora        737 IKDMGRITLRSSGATIGAGIITELIPLAPASSSTPGLLV*---------
Batrachochytriu   652 TKELGRFMLRNGSTTVAAGIVTDILSFE*--------------------
Spizellomyces     669 SKELGRFMLRAGPVTVAAGIVLEILSFERGLPVERT*------------
Lichtheimia       606 NKQLGRIMLRRGGETIAAGVVDEILTFGS*-------------------
Rhizopus          601 NKQLGRIMLRKGGETIAAGVVTEILSFES*-------------------
Ustilago          608 NKEMARVLMRMNGETVAAGIVVEAQNC*----------------------
Cryptococcus      605 NKEMGRVLIRRNGETIAAGMVMELLG*----------------------
Schizosaccharom   568 CPALGRFILRRSGDTVAAGIVKELC*----------------------
Saitoella         595 SKDLGRVILRTGGDTIAAGIVDELF*----------------------
Saccharomyces     586 NDRLGRVVLRKDGRTIAAGKISEITQ*----------------------
Lachancea         599 SKHLGRIVLRKEGRTVAAGVVESLDF*----------------------
Neurospora        551 ----QRVVLRSGGQTVAAGLLE*--------------------------
Fusarium          547 ----QRVVIRSGGETVAAGLLE*--------------------------
Aspergillus       559 ----TRIVLRSGGDTVAAGLLE*--------------------------
Dictyostelium     600 YRQLGRFTLRNGGVTIAAGLITEFYDNPPKKSSSSPLTTTTTTTSNKK*
Arabidopsis       641 SRALGRVFLRSSGRTVAMGKVTRIIQDS*--------------------
Oryza             626 CRALGRAFLRSGGSTIAVGVVTRVLGQDQN*------------------
Pinus             713 YKPLGRVTLRATGKTIAVGIVTRIIEQQ*--------------------
Physcomitrella    713 FRALGRIALREGGKTIAVGIVTDILERK*--------------------
Chlamydomonas     679 YRALGRVALREGGRTLAVGVVTQLLE*----------------------
Phytophthora      635 YRQLGRFTLRDRGKTLAAGIITQIIA*----------------------
Tetrahymena       576 FKSFGRVVLREKMNTIGVGSITKIL*----------------------
Giardia           578 SKLMGRMILRSDNRSVGLGKIERISEK*---------------------
Leishmania        619 CRALGRFVLQQDGETVAGGLVTRVVDKP*--------------------
Trichomonas       580 SRSFGTFIVRTGGETVGFGGIISVLQAK*---------------------
consensus        1021  k lgrimlr ag tiaaGlvteil
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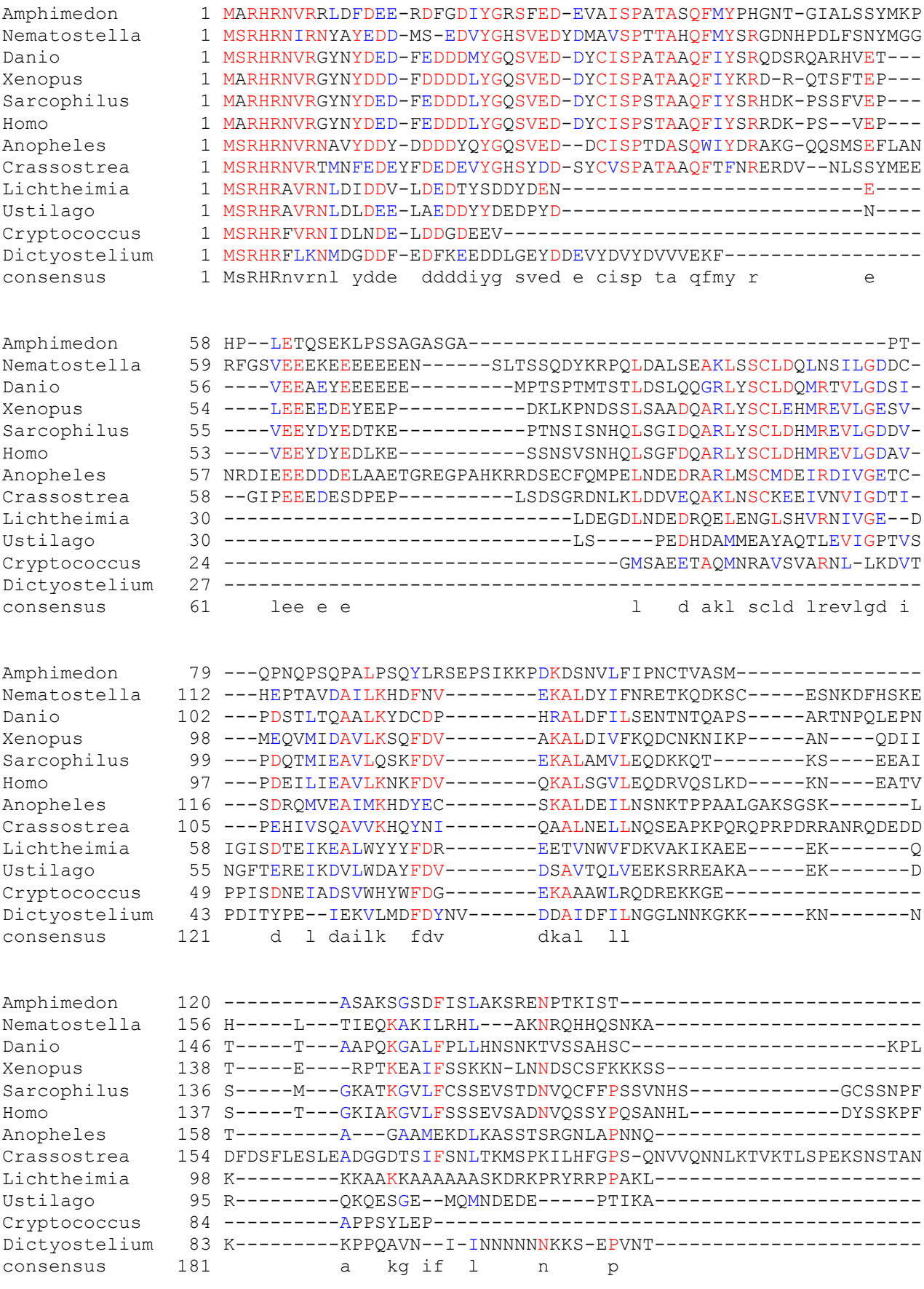
Figure S4. Sequence alignment of Ski7L1s from diverse eukaryotes.



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Amphimedon      144 --CPPSLGELMKTPSSGPPSLGELMKTPSTGPPSLGELMKTPSTGPPSLGELMKTPSSGP
Nematostella    182 --------TQLADAT---------------------------------------------
Danio           176 KQ---NPSYNLSD--------LLAVPEPNMTK-------PKAQNPPPGFGSLAKDHLKGV
Xenopus         166 -VCSTVSSM--SKN-----------------------------E---------------
Sarcophilus     175 EFCDSVPKDGLSCNSSNILSHRLLHKKKKLDR-------PHSDKK---------------
Homo            176 DFASSVGKYGLSHNS-SVPTHCLLHRKKKLDT-------RKSEKK---------------
Anopheles       183 --PAALGSA------------RFALPK--------------------VQFGAVGG------
Crassostrea     213 DFCEPARTS-------------------------------------------SQLAKKHEGAP
Lichtheimia     126 --------Y--ADVQ-QSP-------S--------------------SSSSPMGS-SSLQ
Ustilago        116 --------F--KQLS-LQRDRRAEIRA--------------------GRGMPQGKAQGLR
Cryptococcus     92 ------------TPL-QQPRHRPKILV--------------------PPSQPTQAQEDIQ
Dictyostelium   107 --------N--KSTS-K-----------------------------GQRRPRKSTSENN
consensus       241              s

Amphimedon      202 PSLGELMKTSS----SGPTSLGELMKTSSS-----------------GPTSLGELM--KT
Nematostella    189 --------VNK----SKYIILGSKIKDGEN-KPLPN--RIDPHQLLCTPLYVLGLV--DI
Danio           218 SSHNLGNGQST----TGQSSLAHLIAQHEH-KHSTVP-PLVPSTGLST--DYTIPL--TT
Xenopus         178 -----SFAFDI----TPNLSLSTLISASPN-QTYNIT-EP---GSLSN-INLLDLI--TD
Sarcophilus     213 -----LESCKS----SKELSLADLINDMPH-DSFYESLNSQPKVKFSSRSDLENMI--SD
Homo            213 -----LESCKL----TKELSLANLIHDMSR-DS----CESQPSVRLSSTDSLESLL--SK
Anopheles       204 --------GGSGGGGSG--NLNDLVKQRMKQNSLSDP-PV------------------DK
Crassostrea     233 QTHKGLFQGESTGENKSRLSLAQLAAKRKP-SSLAQL-ALAKKGG-----SLAQIT--SE
Lichtheimia     147 S-----LA------------------QRAS----T---NNKPT-----------QKASSL
Ustilago        145 G-----LAT--GG--------RAGMAKRNL----A---GLAPN-------FVQDSQSSSL
Cryptococcus    119 P---------------------------PL----T---ALQRL-------TLSRRQGSPA
Dictyostelium   126 NSNNNSNNNDDDDDNNKN--KNNNNNNKNN----N---GYKPS-------SLAQ----DL
consensus       301               s   slg lm  h          i p         l  lm  t

Amphimedon      239 SSSGPPSLGE-------LMKTSSAGPPSLGE------LMKTSSSGPPSLGELMKTSSSGP
Nematostella    232 T------------PGQ---------PIP--------SLGTNKFKAGNA-NELLTT-SLSS
Danio           268 SP-----LGSFNGPSGPL-----------------------STLQGPNVPPLSVG-SAAT
Xenopus         221 SK-----VGSDTGKGSDMLDAKL-SEIA--------SLETKCLHKAPNLQPLLTG-NNSS
Sarcophilus     261 S------------VDGKLLGADS-SVSP--------SLDISEYKGGPDLKALMQT--KRS
Homo            257 N------------LDADLLRPHA-SECI--------SKDDSAFKEIPDLKTIIIK-GTTP
Anopheles       235 NT----ITGCAEGGG-------------------------KENNEPKKASLDSPKQATT
Crassostrea     284 QQ--TPSVAQPAGQKVSVLDSGV-KVLPLAQLATKHKVGTSVEEKKPSLALLAAK-QKET
Lichtheimia     166 QSLAQKAAG---------------------------------QRGMSALQTLASRQQQRT
Ustilago        176 PSSNAPPAP---------------------------------SKAVSKLSALAARSSAKR
Cryptococcus    138 SPAPSSSVG---------------------------------EKPMSKLALLAQKRREAA
Dictyostelium   166 SAI-------------------------------------TNTISNIKIINDKEFSFQ
consensus       361 s       g       l                        k  p l  l  k    s

Amphimedon      286 ---PS--------LGELMKTSSAGPPSLGELMKTSSAGPPSLGELMKTSST-------GP
Nematostella    261 LGT-----------------NTFRAGN-AKELLTT-----PLSSLALPQ-SG------QA
Danio           299 ---LSL---------GSSVPAGLGATP-SSCLLTC-----SLSNLALQD-SQRS--APLP
Xenopus         266 MDVLQYKQEN---MENSG--CSLKDIQ-DDWFPT---------KMSQDD-KVF---HKEG
Sarcophilus     298 DSSLSIENNLLPIVENIPVQNNMES-I-NSFYLTN-----TLENMTLDN-NVSHLQNKKA
Homo            295 NNSLYIQNNSLSDFQNIPVQDSLGSSN-NPLYLTS-----SLENMTVDN-LNA----SKE
Anopheles       265 ----------LAQFAALSIGASAPV----PMKSFT-----NLSDLAKHH---------LE
Crassostrea     340 S-------------EGTMISKSSGV---------------SLADLAAKETKNQSI---LG
Lichtheimia     193 AT-------------------------------------TTSSTTT------------
Ustilago        203 SAD---------NV---PLHAG-----TRER---------PLSPASTS------------
Cryptococcus    165 AAA---------TTTSETIQSGIVSPQTSRQ---------PSASGTQP------------
Dictyostelium   187 S-------------------------------------LYKNNKD------------
consensus       421                 v  s          t       l  ls
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Amphimedon      328 PSLGELMKTPST-GPP-SLGELMKTSSTGPPSLGELMKTS---STGPP-----------
Nematostella    291 PITGSL------------------------SLSSLATNTSRTVNVNDLL---------T
Danio           338 VSIGSLSSVMRGSGPL---GVPVQGKSSASLSLAELIQE---HQDSSPKL---------Y
Xenopus         307 DLFGSLSSVLQNT------ESDQSVSKYGSPSLADLIHE---HYEMNPLQ---------D
Sarcophilus     350 ELSGTVLSAQQCSKKHNLEKDRVQFSKCESPSLTELFQE---HKENNPSQ---------Y
Homo            344 TEVGNVSLVEQSAKNHTFKNDNLQFSQCESPSLTELFQE---HKENNISQ---------C
Anopheles       297 SK-GTPPSFP-------------ATATSPRFAVPQLFKQ---------------------
Crassostrea     369 KKGASLTQLLNTSKEL-------HLEKSPKTSLAQLAQK---HKQTSNITATVNEKLSKE
Lichtheimia     202 TNTTA---------------TPS--SSPKPSSLAALAQKSSASKGRTS------------
Ustilago        225 SPSGH---------------SPS--ATPAPVS------ASTASSGRTS------------
Cryptococcus    195 SSGTQ---------------SPS-------------------------------------
Dictyostelium   195 -----------------------------------------------------------
consensus       481    gsl                         sl  l

Amphimedon      371 -SLGEL---------------MKTSSSGPTSLGELMKTSSAGPPSLGELMKTSSGPPSL
Nematostella    317 TSLSSL--------AL------SGTSKGPDNLQRAS--AGRYASST-DQLLTTSLSSLAL
Danio           383 DSLPGL--------NISTN-SFHVTGTQNNAHS-Q-------KPAL--------------
Xenopus         349 ISFISP--------QQ--NPHSKGKLATDSVLS-QL--SGQSIAALDMPSLSLSLSSLSV
Sarcophilus     398 FSLSDL--------CNQSSASFTDKSLGSTPLS-QI--T-QYQSSTGIPELTGSLSSLAF
Homo            392 FTLSDL--------CNQSSASFTDLSLGSFPLS-QL--ANRCQSSPGISELTGSLSSLAF
Anopheles       322 -----------PFACASPPTAVAGGGGTAAPPS-QS--TD--QQVLGQTGWILDLKSA--
Crassostrea     419 KSLAQLALKHKNESCTETDVEQKGKGISLA----QL--ASKHKTPL--SQSGISLMQVAK
Lichtheimia     233 -L-AHLA------------TRSRPSETSARPTS-----SNQGLSGL-----AKLASKS--
Ustilago        250 -KLAALA------------AARTGTGVSAANVI-----VPP---AL-----QTSGSSI--
Cryptococcus    203 -----------------------------------------------------------
Dictyostelium   195 -----------------------------------------------------------
consensus       541  sl  l                         ls q          l       slssl

Amphimedon      415 GELMKTPSTGPPSLGELVKENIGLAKERDKGQ----------------------------
Nematostella    360 ADSS----LSKPSLAQGISQHNPQA---------TSE---DT-------F--S--LPLSS
Danio           412 --NIPPRLSEAPSLSDLMSQHQASLGPQLLALKNENG---SI-------T--A--LRKPA
Xenopus         396 SNTLNT-KATPVSLSDLFAQSNKHVKNNHHN-----------------------LLSHT
Sarcophilus     446 SKASPTRDLENLSLSDLIAESINEVDKSQIKK--------DP-------S--M--LDLPE
Homo            441 HKASPTRDLENLSLSELIAETID-VDNSQIKK--------ES-------F--E--VSLSE
Anopheles       364 ----------------LIK------------KKPDAT---TV-------A--T--GSGKS
Crassostrea     471 QKEERETETKNVSLSDLVKQNKEKSSDSDNPQSKDGQ---QV-------T--T--VSQPS
Lichtheimia     267 ----NVSDKPSLS-----PSLE---KQRQQQQQPVKETMKDV--TPKKAFHITNDQPANP
Ustilago        282 ----GASDAPAKPLSKLQQRML---ANKQQRQAATPEA-KEA--AATQAAE-EEARSRPQ
Cryptococcus    203 -------QLEKKPLSKLAQKMA---AARAAREEAAAAAKSSKLEKNSVGDQMEGDEPLPS
Dictyostelium   195 -----------------------------------------------------------
consensus       601             slselv                                    l

Amphimedon      447 ----------GFVDLSVLLRKAPQS-----------------DT---KKSAL--------
Nematostella    393 LSIRATSQPK-------KQLSPSFKPVNIVDQCQ--HTYTQRKIYG---------------
Danio           456 VPKPHPLSLNRSIDLSTLMSKTSPV----------------------SRSPALLNFT----
Xenopus         431 VPL---TEPDKVIDLSALINSPEKNENGLVLNE---------KSLSTEKSKPENYLKKTS
Sarcophilus     487 IKS---SAVDSNIDLSVLIKTPEIFPKPIENQSN--ILISGAKVPSSKLVKNSSFSKENK
Homo            481 VRS---PGIDSNIDLSVLIKNPDFVPKPVVDPSI--APSSRTKVLSSKLGKNSNFAKDNK
Anopheles       382 LKQTGTASVD-HIQ------------YGFIDCD----------ITETVKPTIDEFCTID-
Crassostrea     517 A-----Q----GLSLRDLVKESSGN--VLKDKSKKIKQLKGNDTQTVDSTEDSDVFHEGK
Lichtheimia     313 LCAK--PSAAANFLFMHMYPQ--QA-----------------------------------
Ustilago        331 TCFG--S----DLPISSLFPAPDHA-----------------------------------
Cryptococcus    253 LSS-------PADPMLSLFSPPATS-----------------------------------
Dictyostelium   195 -----------------------------------------------------------
consensus       661 l           v ls ll  p
```

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Amphimedon      469 --E---SSHLSSPSLSLVNPPSAKPMSGVGVVICRQG---NRSSLQ--------------
Nematostella    430 ----SPSKQRHPKRKSFSSAIK-SRPTMFALTLCHKS---MMSSHG--------------
Danio           491 -----------EETASLKKRVF-AKPSIFALAMCVPV---RCSKSR-RGR--VT------
Xenopus         479 SSKQMHVSKGSKKCTYRARILK-ARPSAFALTLCFTY---IPKTCKKNIL--MI------
Sarcophilus     542 KSKKGYITRKPAFSLSWTKALA-ARPSAFASTLCLRY---PPKTCKRHTF--DL------
Homo            536 KNNKGSLTRKPPFSLSWTKALA-ARPSAFASTLCLRY---PLKSCKRRTL--DL------
Anopheles       418 ------ASAVLERDLSSHRTLT-SS--PMGVVVGIRY-----------------------
Crassostrea     566 TAE-DLVIEKLSLDFDALVNIT-KGPSCFGKVICGRF---GAFKNKLKNNDSPS------
Lichtheimia     334 ----------------NT--TTTPSPIPAFS--SI------------------------
Ustilago        350 ----------------QE--SKTPSAIGLVSVSAI----AGSSKDAVDQLVAPLSLLRRV
Cryptococcus    271 ----------------PKPKLKPTHPSPFFSIITSTSSQGGAPGPAKDHLP-PE------
Dictyostelium   195 ------------------------------------------------------------
consensus       721                s    i   rps fg  icv

Amphimedon      507 -GI--TDKVM-----SRLKEQYFLEPRF-NFSTPSPDELILTEQSKIFHK*---------
Nematostella    468 ---FATKRKRLGCPAPSLVQAYSLIKPF-DFSTLSPDDIVKQQQKKRFGNKI*-------
Danio           527 HSAFLYSRQMERVKERVQCAPLHHIEPF-SFNTPSPDDIVKANQRKAFTRD*--------
Xenopus         527 HQY-PHN-DLVELTR---ENHNPTLVPF-DFQTPSPDDIVKENQKKAFAR*---------
Sarcophilus     590 YKTFLYSRQVQEVKDK-EIGPLKVITPF-DFKSASPDDIVKANQKKAFTRE*--------
Homo            584 YKTFLYSRQVQDVKDK-EISPLVAITPF-DFKSASPDDIVKANQKKAFTRE*--------
Anopheles       446 ------RKRKLPVHISHYFPKYTTVVPF-RFDVPSPDDVVLGHIKKYRP*----------
Crassostrea     615 QGPFSYAKQKQITCH-HSPEHRVKLVPF-DFSTPSPDDIIKEKQKRAFTRPKERNDSK*-
Lichtheimia     349 -GRAFYEA-VKTS--------DDTIKAF-SFDVPSPDDIVMEAQSQRSGGQLRKS-----
Ustilago        388 PGRSPFTLYVQGAD--EGSGLEIETVKK-AFAGPSPDDIVMQAREGTRLGAK*-------
Cryptococcus    308 PTSANLHAPL-------ITDVDVLVKQFEQAFAESPDEIVLRKRQGRAGTADMVTAVKKQ
Dictyostelium   195 --------------------SDGTIIPF-DFKTPSPDDTILNKQKQAFKPKHNSTDNDDT
consensus       781      y k m              i pf df tpSPDdivk  qkkaf k

Amphimedon          -------------
Nematostella        -------------
Danio               -------------
Xenopus             -------------
Sarcophilus         -------------
Homo                -------------
Anopheles           -------------
Crassostrea         -------------
Lichtheimia         -------------
Ustilago            -------------
Cryptococcus    361 ATGTGIKPKVK*-
Dictyostelium   234 NDKDKNNKINKK*
consensus       841
```
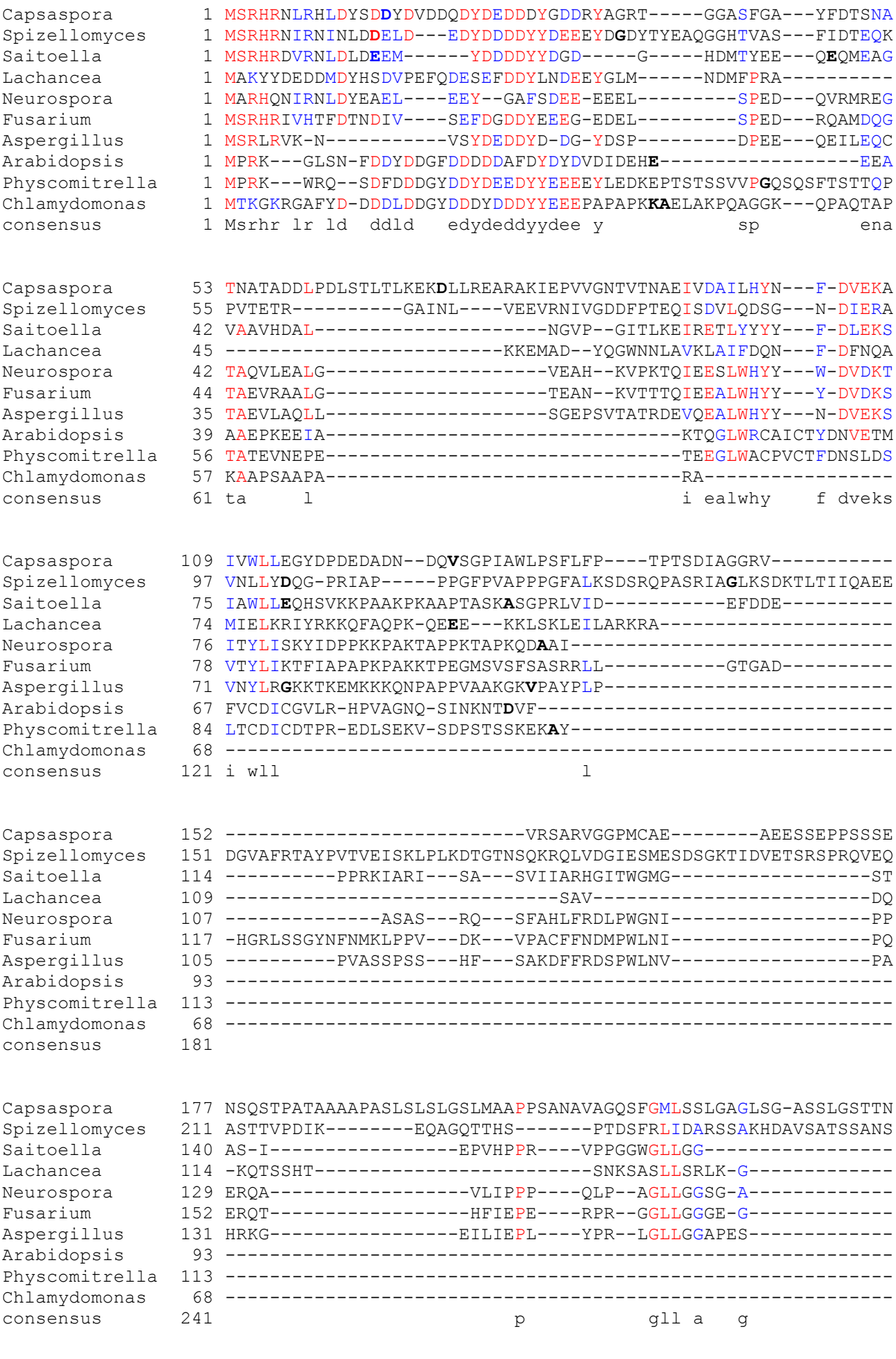

Figure S5. Sequence alignment of Ski7L2s from diverse eukaryotes.



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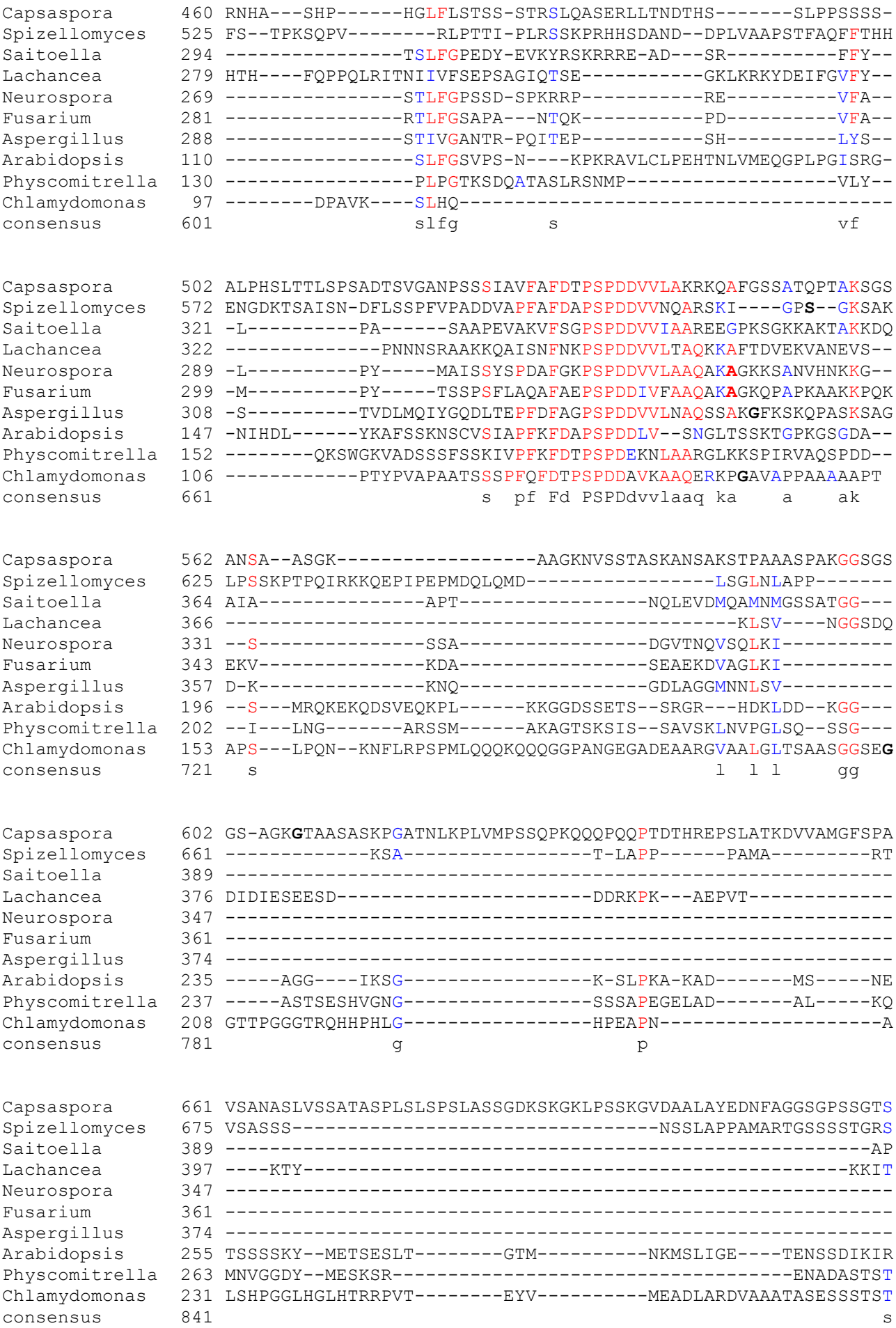
Capsaspora      236 AFGSLASLSTF-----SSLSSLGTGPS------SLIAPNPSSS----SGGVAPTSIASLS
Spizellomyces   256 MYGSLPAPSSLGSSLLSSLPASGQSLAPFAFPQGLAGAPPSEQ----R--AKETAVSSLS
Saitoella       161 ------------SGKMSKLAA-------------LAKARKEAQAASKAEKGAAPGLASV-
Lachancea       134 ----KTTPSRLGSFHDSTLSS----------------HRSSEV----ESDAAKPSLA---
Neurospora      151 ------------PPKMSKLQQ-------------LAAARKKKAEEKSASGEVEQTQVKMT
Fusarium        174 ------------APKMSKLQA-------------LAAARKKKTEEKKEQEKLEKGVSKLS
Aspergillus     155 ------------GGKVSKLAA-------------LAAARKKKETDKAASGAPTTPGE---
Arabidopsis      93 ----YAVESRCKEPVVSKLAK-----------------------------------------
Physcomitrella  113 --------VVTEVQRVSPLAKALFN-----------------------------------------
Chlamydomonas    68 ------------AGAASKLAQSLCDPPPPGPGGKAQRGAKP-------------------
consensus       301               klskl               laaar                i  l

Capsaspora      281 SLTAPLSLLSSSSP-------SSLTPAPPTMSLLSG-----------------APGLLS
Spizellomyces   310 Q-AQPLSSLLLQSPSSNLSQTNSLFPLQPQGTLLSSLHQS-----TSSLTKSGDAIGVLG
Saitoella       195 ----------------------------S----LLSK------------LT---------A
Lachancea       167 --------LLMRSKQ-----RRVHTSLEPTQSLPESRTETSPRSSSLAFLLAGR-----R
Neurospora      186 ELTVN---------DNQASKENR----P----LAGV------------FG---------K
Fusarium        209 VAGSE--------------KE-----------NQSP------------FN---------Q
Aspergillus     187 -PGTP---------DRTPTVESKLASLS----LRER------------LA---------G
Arabidopsis     110 -----------------------------------------------------------
Physcomitrella  130 -----------------------------------------------------------
Chlamydomonas    97 -----------------------------------------------------------
consensus       361                                 l

Capsaspora      316 ASSIPAMSTSLASLSLNAPSPNPPSLSALS--------TAPIPAETSALSLASLSLASLS
Spizellomyces   364 NSLAPENA----VKSVPFPVPAVPQSQSLS----SLLSNTRSP--SGALPLSSLA--SVS
Saitoella       203 AKTAPKAAAAP-DTPTEPPAPQAPAEPAVSEPESSQPSSIPPPQSPSPPP-------VVA
Lachancea       209 RTVSPQNS-------------------------------------LASKLMALK-----
Neurospora      208 RVKISETTAQG-RI------PLTMAEPTRPEIPQAQ--AP----E---------------
Fusarium        223 RQQIPTP--------------ASQAQPTQYDMDIDHEENEY---K---------------
Aspergillus     212 NGKAQKPSESG-QL------PRTLRRGTPSESPLAQKKLSPEPSK---------------
Arabidopsis     110 -----------------------------------------------------------
Physcomitrella  130 -----------------------------------------------------------
Chlamydomonas    97 -----------------------------------------------------------
consensus       421     p               p

Capsaspora      368 LMTPAASEPPQQSTAPKATLS-TSSVVGAQTAAPITGTAPSVNVAIAKPKV---------
Spizellomyces   412 LGNTMAATPL--SLSNLSSLSGTSGLLGATQK-SSINDAPGLSQL-ASNSANIMSGTDAI
Saitoella       255 DDVDMSEAPLLVSPT---PSP----S---SPEHPTFEP----------------------
Lachancea       226 -------TERKVANGSKAELH-T------TPA-DEREEKPVI---VHE------------
Neurospora      240 -----A------------TPS----Q---HQEEDPIDPEPAV------------------
Fusarium        251 -----K------------PTP----A---HKDEFTLDSFPGV------------------
Aspergillus     250 -----AKSPEMIPGEPTTRKP----C---AGEEETERPK----------------------
Arabidopsis     110 -----------------------------------------------------------
Physcomitrella  130 -----------------------------------------------------------
Chlamydomonas    97 -----------------------------------------------------------
consensus       481                                       p v

Capsaspora      418 --------------SAEVAWGSLQLA----MPSQLAQSICAKPSSTDHTRVSSVALRNVL
Spizellomyces   468 RSALAAFSLQSAGNASEGSLGTVPAASTKEPLSVFPTPFKTLPNSGIGKPDAE---TSIP
Saitoella       283 -------------------------ALVEATPSVFA-----------------------
Lachancea       256 --------------EKTDPWSSFQKLR----ES-----------QG-QGNTS-------L
Neurospora      258 ------------------------A-PPKAQPSAFA-----------------------
Fusarium        269 ------------------------EIVTGPTPSALS-----------------------
Aspergillus     277 -------------------------ASIRAPPSTFA-----------------------
Arabidopsis     110 -----------------------------------------------------------
Physcomitrella  130 -----------------------------------------------------------
Chlamydomonas    97 -----------------------------------------------------------
consensus       541                                 ps  a
```


Capsaspora 460 RNHA---SHP------HGLFLSTSS-STRSLQASERLLTNDTHS-------SLPPSSSS-
Spizellomyces 525 FS--TPKSQPV--------RLPTTI-PLRSSKPRHHSDAND--DPLVAAPSTFAQFFTHH
Saitoella 294 ----------------TSLFGPEDY-EVKYRSKRRRE-AD---SR----------FFY--
Lachancea 279 HTH----FQPPQLRITNIIVFSEPSAGIQTSE----------GKLKRKYDEIFGVFY--
Neurospora 269 ----------------STLFGPSSD-SPKRRP----------RE----------VFA--
Fusarium 281 ----------------RTLFGSAPA---NTQK----------PD----------VFA--
Aspergillus 288 ----------------STIVGANTR-PQITEP----------SH----------LYS--
Arabidopsis 110 ----------------SLFGSVPS-N----KPKRAVLCLPEHTNLVMEQGPLPGISRG-
Physcomitrella 130 ----------------PLPGTKSDQATASLRSNMP----------VLY--
Chlamydomonas 97 --------DPAVK----SLHQ----------
consensus 601 slfg s vf
Capsaspora 502 ALPHSLTTLSPSADTSVGANPSSSIAVFAFDTPSPDDVVLAKRKQAFGSSATQPTAKSGS
Spizellomyces 572 ENGDKTSAISN-DFLSSPFVPADDVAPFAFDAPSPDDVVNQARSKI----GPS--GKSAK
Saitoella 321 -L----------PA------SAAPEVAKVFSGPSPDDVVIAAREEGPKSGKKAKTAKKDQ
Lachancea 322 --------------PNNNSRAAKKQAISNFNKPSPDDVVLTAQKKAFTDVEKVANEVS--
Neurospora 289 -L----------PY-----MAISSYSPDAFGKPSPDDVVLAAQAKAGKKSANVHNKKG--
Fusarium 299 -M----------PY-----TSSPSFLAQAFAEPSPDDIVFAAQAKAGKQPAPKAAKKPQK
Aspergillus 308 -S----------TVDLMQIYGQDLTEPFDFAGPSPDDVVLNAQSSAKGFKSKQPASKSAG
Arabidopsis 147 -NIHDL------YKAFSSKNSCVSIAPFKFDAPSPDDLV--SNGLTSSKTGPKGSGDA--
Physcomitrella 152 --------QKSWGKVADSSSFSSKIVPFKFDTPSPDEKNLAARGLKKSPIRVAQSPDD--
Chlamydomonas 106 ------------PTYPVAPAATSSSPFQFDTPSPDDAVKAAQERKPGAVAPPAAAAAPT
consensus 661 s pf Fd PSPDdvvlaaq ka a ak
Capsaspora 562 ANSA--ASGK----------AAGKNVSSTASKANSAKSTPAAASPAKGGSGS
Spizellomyces 625 LPSSKPTPQIRKKQEPIPEPMDQLQMD----------LSGLNLAPP-------
Saitoella 364 AIA----------APT----------NQLEVDMQAMNMGSSATGG---
Lachancea 366 ----------KLSV----NGGSDQ
Neurospora 331 --S----------SSA----------DGVTNQVSQLKI----------
Fusarium 343 EKV----------KDA----------SEAEKDVAGLKI----------
Aspergillus 357 D-K----------KNQ----------GDLAGGMNNLSV----------
Arabidopsis 196 --S---MRQKEKQDSVEQKPL------KKGGDSSETS--SRGR---HDKLDD--KGG---
Physcomitrella 202 --I---LNG-------ARSSM------AKAGTSKSIS--SAVSKLNVPGLSQ--SSG---
Chlamydomonas 153 APS---LPQN--KNFLRPSPMLQQQKQQQGGPANGEGADEAARGVAALGLTSAASGGSEG
consensus 721 s l l l gg
Capsaspora 602 GS-AGKGTAASASKPGATNLKPLVMPSSQPKQQQPQQPTDTHREPSLATKDVVAMGFSPA
Spizellomyces 661 ----------KSA----------T-LAPP------PAMA---------RT
Saitoella 389 ----------
Lachancea 376 DIDIESEESD----------DDRKPK---AEPVT----------
Neurospora 347 ----------
Fusarium 361 ----------
Aspergillus 374 ----------
Arabidopsis 235 -----AGG----IKSG----------K-SLPKA-KAD-------MS-----NE
Physcomitrella 237 -----ASTSESHVGNG----------SSSAPEGELAD-------AL-----KQ
Chlamydomonas 208 GTTPGGGTRQHHPHLG----------HPEAPN----------A
consensus 781 g p
Capsaspora 661 VSANASLVSSATASPLSLSPSLASSGDKSKGKLPSSKGVDAALAYEDNFAGGSGPSSGTS
Spizellomyces 675 VSASSS----------NSSLAPPAMARTGSSSSTGRS
Saitoella 389 ----------AP
Lachancea 397 ----KTY----------KKIT
Neurospora 347 ----------
Fusarium 361 ----------
Aspergillus 374 ----------
Arabidopsis 255 TSSSSKY--METSESLT--------GTM----------NKMSLIGE----TENSSDIKIR
Physcomitrella 263 MNVGGDY--MESKSR----------ENADASTST
Chlamydomonas 231 LSHPGGLHGLHTRRPVT--------EYV----------MEADLARDVAAATASESSSTST
consensus 841 s

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Capsaspora        721 SPRPGGGHRAPRMDILEEYKKRGAGKAHLNMVVVGHVDAGKSTLMGHILFQLGHVSRRTL
Spizellomyces     702 S------PKLKRINVAEEYKKRNAEKESLNLVVVGHVDAGKSTLMGHVLYLLGEVNERTM
Saitoella         391 APAPPIKIARKKVNVVEEYAKV-DVKESANFVIIGHVDAGKSTMMGRLLYDIGAVDERTI
Lachancea         404 TP---T----KPRNPVDIQSYVSSRKPHLNFVVLGHVDAGKSTLMGRLLYDVGAVNYKLI
Neurospora        347 DDT--PLPKSRNLNVLSEFEKQ-KGKKTASFVVVGHVDAGKSTMMGRLLLDLNVVDQRTV
Fusarium          361 VDA--PPPKSKGLDVLKEYENS-SNKRSISFVVVGHVDAGKSTLMGRLLLELKFVEKHTI
Aspergillus       374 QEK--VAVKSKNLDVLSEYHKS-QRKRAMNFAVIGHVDAGKSTLMGRLLADLKAVDQRTL
Arabidopsis       291 GPKSQSKHK-P--EEWMLLDKESDALSQLNLAIVGHVDSGKSTLSGRLLHLLGRISQKQM
Physcomitrella    285 YGLSLESYE-P--EPWMLKDANKDSRQLLHLIVVGHVDAGKSTLMGRILHLLGRVSQKEM
Chlamydomonas     273 S-----------------GSSSGSSKPPLHLVVLGHVDAGKSSLMGRLLHDLGLVSAKEA
consensus         901         k k mdvl ey k    k  lnfvvvGHVDaGKStlmGrlL dlg v  rtl

Capsaspora        781 HKYETESQKLGKASFAFAWVLDETDAERARGVTIDVAMTSFETKTKRITLLDAPGHRDFI
Spizellomyces     756 KKYERDAEKMKKSSFAYAWVLDETEEERTRGVTIDVAITKFHTPHRKFTLLDAPGHRDFI
Saitoella         450 QKFRKESEKMGKGSFALAWVMDSTDEERARGVTVDIATNQFETPKRKFTILDAPGHADFV
Lachancea         457 RKLKKESEQAGKGSFHLAWVMDQTSEERDRGVTVDICTSDFETDRATFTIIDAPGHRDFV
Neurospora        404 DKLRKEAEKIGKTSFALAWVLDQRHEERSRGVTIDIATNRFETETTSFTILDAPGHRDFI
Fusarium          418 DRYRKQAEKSGKQSFALAWVMDQRSEERERGVTIDIATNHFETEKTSFTILDAPGHRDFV
Aspergillus       431 ERYQREAEKIGKGSFALAWVLDQGTEERARGVTIDIAMNKFETENTVFTIVDAPGHRDFV
Arabidopsis       348 HKYEKEAKLQGKGSFAYAWALDESAEERERGITMTVAVAYFNSKRHHVVLLDSPGHKDFV
Physcomitrella    342 HKNEKESKQQGKGSFAYAFVLDEGAEERARGVTMTVAVAHFETPKLRVVLLDAPGHRDFV
Chlamydomonas     316 HKFQRDAAAAGKGSFAWAWVLDERPEERERGVTMDVAMTRFATNRFAVTLLDAPGHRDFV
consensus         961 hky keaeklgKgSFalAwvlDet eER RGvTidvam kFet h rftllDaPGHrDFv

Capsaspora        841 PNMISGAAQADVAVLVVNAGVGEFEAGFEG---------GGQTREHALLVRSLGVNQLIV
Spizellomyces     816 PNMMSGAAQADVAILVVDATPGEFETGFDS---------GGQTREHAVLLRSLGVTQLIV
Saitoella         510 PNMIAGAAQADFAVLVIDASTGGFESGFNV---------RGQTKEHALLVRSLGVQNLIV
Lachancea         517 PNAITGISQADAAVLTIDCCVDAFESGFSL---------DGQTKEHTLLARSLGARHIVV
Neurospora        464 PNMIAGASQADFAILVIDASTGAFESGL-----------KGQTREHSLLIRSMGVSRIIV
Fusarium          478 PNMIAGASQADFAILVIDANTGAYEKGL-----------KGQTREHVLLLRSLGVQRLVI
Aspergillus       491 PNMIAGASQADFAVLVIDSGTGNFESGL-----------RGQTKEHALLVRSMGVQRIII
Arabidopsis       408 PNMIAGATQADAAILVIDASVGAFEAGFDN--------LKGQTREHARVLRGFGVEQVIV
Physcomitrella    402 PNMISGASQADAAILVVDASIGAFEAGLEGE-----GQGRGQTREHAQLVRSLGVEQLIV
Chlamydomonas     376 PNMIAGAAQADAALLLVDGSPGGFEAGFSEGSGGLHGAPGGQTREHAALARSLGIEQMAV
consensus        1021 PNmiaGasQAD AiLvidas gafEtGf           rGQTrEHallvRslGv qliv

Capsaspora        892 AVNKLDACDWSKARFDELVARLSLFLKTSGYRLDNVTFVPVSGLIGENLIE-RKEPKLTQ
Spizellomyces     867 AVNKLDVVDWSKTRFDEISEKLSHFLSQVGFRKQKVAFIPTSGYTGENLVK-RESDKLNA
Saitoella         561 AVNKLDSVDWNHERFEEIEMQVSQFLTNAGFDPQNVQYIPCSGLTGENLVK-RSAEPALT
Lachancea         568 AMNKMDHEGWYPTRFFDIKWELESFFKDIGIKKEQVSWVTCSGLSGEGVYN-IKRPLGID
Neurospora        513 AVNKLDTVNWSQERFDEITHQVSGFLTATGFQPKNIAFVPVSGLHGDNLVR-KSTDPAAS
Fusarium          527 AVNKLDMVGWSQERYDEIAQQVSGFLAGLGFVSKNIDFVPISGLNGDNLAR-RTEDPAAS
Aspergillus       540 AVNKMDAVEWSRDRYEEIEQQISSFLTTAGFQAKNIAFVPCSGFRGDNVTR-RSDDPNAS
Arabidopsis       460 AINKMDIVGYSKERFDLIKQHVGSFLQSCRFKDSSLTWIPLSAMENQNLVAAPSDNRLSS
Physcomitrella    457 AVNKLDAVDFSKERFDFIRGTLQPFLKQCGFKDGSLQWVPVSASEGQNLTMASTESALKA
Chlamydomonas     436 VVSKLDTCGYDQSRFESIRAALLPYLKSVGFKESGLQWLPAAGPLGENLVGPPQDPALKA
consensus        1081 avnKlD vdwskeRfdei   ls fl   gfr  nv fvpvsgl genlvk rsed l t

Capsaspora        951 WYS--GPTLVEQIDQFQPP------ERPIDKPLRFSVNDIFSRP-----NSGVSLGGKVI
Spizellomyces     926 WYS--GSTLVEQIDAFEAP------QRAVDKPFRLSIADYFKGGIGAGGGGAVSVSGRIE
Saitoella         620 WFN--GPTVLGALESIAPT------ARAIEKSLRISVQDVYKAGVT---GGSVTISGRVD
Lachancea         627 WYN--DPSLVDCLEDVAKKLNKDESSEAIEANFLFSILDVSPTS----KNNEVIVSGKVE
Neurospora        572 WYT--GKTLVEELEASEPS------ARALAKPLRMTISEVMRTP-Q----SSISITGRID
Fusarium          586 WYT--GPTLIEALENSEPT-----TARALKSPFRMAISEVFRSQ-L----GTTTIAGRVD
Aspergillus       599 WYT--GRTLVEELEATEPY------SYALDKPLRMTISDVFRGGVQ----NPLSISGRID
Arabidopsis       520 WYQ--GPCLLDAVDSVKSP------DRDVSKPLLMPICDAVRST----SQGQVSACGKLE
Physcomitrella    517 WYN--GPCLIELVDSLKPP------PRLVARPLRLTIAEVMKTR----TLGPSAFGGKLE
Chlamydomonas     496 WWGPGRPCVTDAIDAFAPR------ERAVSRPLRLPVSDVFKSK-----TGAVVLGGKLE
consensus        1141 Wys  gptlve ld   p        raidkplrlsi dvfkt       g vslsGkve
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```
Capsaspora        998 SGSVQIGDKVLIAPINQEIGTVKAIEIHE-EGVTWAAAGDAASILL----------DKVD
Spizellomyces     978 AGGIQVGEVVLVMPINEY-GTVRALEVSE-EAVKWAAAGDSVLMSL----------TGVE
Saitoella         669 AGNVQVGETVHAAPSGEP-ATVKSMQVND-DIADWAVAGSNVVLNL----------NDID
Lachancea         681 AGSIQPGETITIYPSEQSVLVDSILSGNDRASVKIGVAGDFVMLKL----------REAY
Neurospora        619 AGSLQMGDALLVQPSGEK-AYVKSLQVDDGEPADWAVAGQNVVLHL----------SNID
Fusarium          634 AGSFQIGDALLVQPSGEE-AYVKSIMVDS-DMQDWAVAGQNVSVAL----------TNID
Aspergillus       647 AGSLQVGDQILTMPSGET-ATIRSLEVD-GEPNDWAVAGQNVVLNL----------ANID
Arabidopsis       568 AGAVRPGSKVMVMPSGDQ-GTIRSLERDS-QACTIARAGDNVALAL----------QGID
Physcomitrella    565 SGAIHSGTKVRVMPSGEI-ATVKSIELQG-QQLKTARAGEGVDVGL----------NGID
Chlamydomonas     545 GGAMRPGSRVVLVPGPAQPFAVRSLEVGG-GAANLARAGDSCEVALVAHGGGGGGGGAID
consensus        1201 aGsvqiGd vlvmPsge  atvkslev e e   wavAGdnvll L           id

Capsaspora       1047 PIHFAVGCMLTEVDRPVPVHSSFRAKIIVFDVKVPITHGFHVVLHYLTFNEPAVITRLET
Spizellomyces    1026 IAHINVGSILCDPSAPVAVTSHFRAQIVTFDIQIPLTIGVPVVLHHQSLTEQSTITKLSA
Saitoella         717 PMHLKAGDILCDPLNPVPTVRAFRARIITFDLARPITNGATIVLHRGRINEAARIQALVA
Lachancea         731 YEDIQSGDLATTVGNDIPTAQEFTAQLLTFKLDRPLLPGTSFMLFRGGCEQPARIKKLVS
Neurospora        668 PIHVRVGDIVCDPAKPIQCVDTFTLKALAFDILMPM----QVDVHRGRLHAAGKIEAIDA
Fusarium          682 PIHIRVGDMLCPTKNPINCSDNFVMKAMAFEHLMPM----PVDLHRGRLHSAGQIVSIAA
Aspergillus       695 PIHLRSGDVICRPSAPIANITSFTAKVLAFDHLMPS----MVDIHRGRLHVPGRISRLVA
Arabidopsis       616 ANQVMAGDVLCHPDFPVSVATHLELMVLVLEGATPILLGSQLEFHVHHAKEAATVVKLVA
Physcomitrella    613 PGMLAPGGVVCHPDYPVPVATRFEVQLLTLDIRTPILKGSQVILHVHHARQPARVDQLVS
Chlamydomonas     604 PSLVAPGAVLCHADFPAVLVTKFQLRLVVLDVPVPLLRGQAVTLHAHVAREEGHLSALVA
consensus        1261 pihi  Gdmlc p  pv v s f akil fdv vPi  g  vvlhrgrlhe ari rlva

Capsaspora       1107 LLDRST-GEIVKKHPRALPKNSSAIVTITL-Q--RPVCLELYENIKDMGRITLRSSGATI
Spizellomyces    1086 LLNKST-GETIKKNPRALPKNVTAVVEIKT-S--RPICLETFKDSKELGRFMLRAGPVTV
Saitoella         777 TIDRAD-GQIIKKKPRHLASGQSAVVEIAFLG--NGIPMETFKDSKDLGRVILRTGGDTI
Lachancea         791 IVCKKDPKKILKKKVKHLGSDQAAIVEIELIEKKRRIPILTIEKSKHLGRIVLRKEGRTV
Neurospora        724 ILDKVT-GKVTKKKPMIVKPGTVSRVRVTL-H--SKVPLE------AGQRVVLRSGGQTV
Fusarium          738 TLDKVT-GAVVKKKARVVQPGGVARVSVKL-A--AKVPLE------AGQRVVIRSGGETV
Aspergillus       751 TLDKGS-GSVIKKKPKIVPPGSVARIVVEM-D--QAVPLE------APTRIVLRSGGDTV
Arabidopsis       676 MLDPKT-GQPTKKSPRCLTAKQSAMLEVSL-Q--NPVCVETFSESRALGRVFLRSSGRTV
Physcomitrella    675 LLDPKK-GTVLRQRPRHLTANQSAIVVIVP-D--EGVCIEKYSDFRALGRIALREGGKTI
Chlamydomonas     664 LLDPRT-GEEVKARPRCLTRGQSALVEVTS-S--RGLVLEEYAHYRALGRVALREGGRTL
consensus        1321 lldk t g ivkkkpr l  gqsaivei l      vple y   kalgRvmlRsgg Tv

Capsaspora       1163 GAGIITELIPLAPASSSTPGLLV*
Spizellomyces    1142 AAGIVLEILSFERGLPVERT*---
Saitoella         834 AAGIVDELF*--------------
Lachancea         851 AAGVVESLDF*-------------
Neurospora        774 AAGLLE*----------------
Fusarium          788 AAGLLE*----------------
Aspergillus       801 AAGLLE*----------------
Arabidopsis       732 AMGKVTRIIQDS*-----------
Physcomitrella    729 AVGIVTDILERK*-----------
Chlamydomonas     720 AVGVVTQLLE*-------------
consensus        1381 aaGivd li
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