

Ecol_Zea_mays -----
 Ecol_Oryza_sativa -----NGGEFIITVWLLVHHRMYIARYNKFINMLNGRSEMAMQPKISAFFKRQAPGPKSSG---GDTHRGSSDATEAK-RPKSCADGKVLNKKRNYA QFHLELGOPDFLL-HMCSVC 108
 Ecol_Sorghum_bicolor -----HEADCRRLLRISPRRQQRQIGEGRGEHVGRSEAMQPKISAFFKRQEADPDNSGDGEGNGHGS DIAATEAKRKAKGCRRLDELVSKKRNYA QFHLELGOPDFLL-HTCSVC 110
 Ecol_Hordeum_vulgare -----SVMVL-----G--SEATEAK-RPKSCGDGKVLNKKRNYGQFHLELGOPDFLLPHVAVC 52
 Ecol_At_new -----MOAKINSFFKPSSSSSIAASVTITDDGLAVWENNRNAIVNTYQRRSAITERS-----EVLKGCIEKTLKGS SSVPKNHKKRNYTQFHLELGOSDFLL-RHCAEC 101
 Ecola_Mm HEVQNEERLRONPSGAVVSSKGSDDLKDHDFPSNSLDENKTISPESVY--PIFNVS SVNTRK--PEEQSSVGS TACTNFKQTNVPKNINSRDTNKGKDKLVIDAGQKHFGI-TVCKSC 115
 Ecola_Hs -----ASSVNSKRSLGEEQFSVGS-----VNFMKQTNIQLYTNTRDTSKTKDQLIIDAGQKHFGA-TVCKSC 62
 Ecol_Danio_rerio -----LR-----REMKQTDNQLIIDAGQKQFGA-TTCASC 30
 Ecolb_Mm --APDONFSICSAEVEINPLENTAAASILLSSAKIDE-DRTFPGSAPNQHSVLSDEASINRKNRDPVPPNHSQLKHDSHLEITIPKSLKLDSEKVDKQLVIDAGHKRFGA-VSCNIC 116
 Ecolb_Hs --ASNKNFSQCLESKLENSPVENVTAASILLSSAKIDTGENKFPGSAP-QQHSILSNQTSKSSDNRETPRNHS LKPCNSHLEITIPKDLKLEAEKTDKQLIIDAGQKRFGA-VSCNVC 116
 Ecol_Xl -----
 Ecol_Strongylocentrotus_purpur -----
 Ecol_Ciona_intestinalis -----MGSINSQ-----KPQKIQSILALPS-----NFKKITCSTCDMTYNPHISQDKLLHNKYHTNFINGIPWN----- 59
 Ecol_Saccharomyces_kluyveri -----MKARKSQRKAGSKPNLIQSKLQVNNGS-----K-SNKIVKCDKCEMSYSSTSIEDRAIHEKYHTLQLHGRKWSF-----NWG 71
 Ecol_Sc -----PLSDETNKRAFLDNFLG-----NGGNLTPNWKKQTPKAISNSDNMTQLHLDLANSTVT-----CSEC 59
 Ecol_Sp -----VQPKLFFPIFTQRLQP-----VVQKSLRRRPDTSMRLLTAAGGSNOYQIDAGQKAFG-ARQCCQC 58
 Ecol_Dm -----MKDPGLPKNSLKKSKLDDYFKKVERNTEENLQEQS--SADVQKSLRCPKRK--VLDDDATDDNI LAKKRAVRRKSSGHSMKLAQSMLVDCGOSVIGS-TKCKDC 104
 Ecol_Ce -----MKTYRAKRKYLSSEDDVFSSSPQSPETSPLOPPNESRLN-----IKAAQAVSPCQKRAKVVKPAKTKAPVMTLSLGGTTSTI--CKTC 85
 Ecol_Yarrowia_lipolytica -----RVC SRPLFTVFDTASP-----ARRRCFECRHMSSTWTQTHARYLRRGAALQISRNTCKGA 57
 Ecol_Leishmania -----MHNSVPASNLCSPFREETS-----KRKRSRGTGGDDKITRGTCSQPFSSVITLPPGKLEWLVCSPC 63
 Ecol_Trypanosoma_brucei
 ruler 1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120

 Ecol_Zea_mays -----LMS-----KSKVKEVITVVEKELGFEGE-----KLLHKLCKVYLYI-SAQR---IVGCLVTEPI 50
 Ecol_Oryza_sativa GMMYARGNDDDEKAHKAVKHSYFEGVP--FKGWRNETVVARSS--EGGD--RIILVADENSCAR-NSKVQEVIKVQKELGFEGE-----QLLHKLCKVYLFY-SSQR---IVGCLVVEPI 212
 Ecol_Sorghum_bicolor GMMYARG-----NDEDEKVRAYHKNYSXG-----VPFKGWKN-----ETV 146
 Ecol_Hordeum_vulgare GMMYAPX-----GN-DDDEERFTGAVHKEAYFR-G-----PSRSKQXGR-----RRLN-----RGL 96
 Ecol_At_new GAKYAPGDELDEKNHQSFKDYMYGLP--FKGWQNEKAFISP--LFIKNIIVMSENDS PAH-RNKVQEVVKMMEVELGED-----WILHQHCKVYLFY-SSQR---ISGCLVAEPI 204
 Ecola_Mm GMIYTASNPEDEIQHLQHHRFLEGIK--FVGWKRERVVAEF--W--DGKIVLVLPRDPSVA-IKKVEDVQELVDLELGFQQTIV--PVC PDKTKTFLFI-DEKR---VVGCLIAEPI 219
 Ecola_Hs GMIYTASNPEDEMCHVQHHRFLEGIK--YVGWKKERVVAEF--W--DGKIVLVLPHDP SFA-IKKVEDVQELVDNLELGFQOVV--PKCPNKIKTFLFISDEKR---VVGCLIAEPI 167
 Ecol_Danio_rerio GMLYSTDSPEDNFQHTQFHQRFLDTIK--FVGWKKERVVAEF--W--DGKIILVLPDDPKYA-TRKAEDVRIADSELGFQOQIT--LSSPSSAKTYLFIINTDKX---VVGCLVAENI 135
 Ecolb_Mm GMLYTASNPEDETQHLLFHNQFISAVK--YVGWKKERILA EY--P--DGRIIMVLPEDPKYA-LKKVDEIREMVDNDLGFQOQAP--LMCYSRTKTLLFISNDKK---VVGCLIAEHI 221
 Ecolb_Hs GMLYTASNPEDETQHLLFHNQFISAVK--YVGWKKERILA EY--P--DGRIIMVLPEDPKYA-LKKVDEIREMVDNDLGFQOQAP--LMCYSRTKTLLFISNDKK---VVGCLIAEHI 221
 Ecol_Xl -----LGFQOQVP-----LRLHSRTKTLVFTISDCK--VAGCLIAEHI 35
 Ecol_Strongylocentrotus_purpur -----
 Ecol_Ciona_intestinalis -----HDHQHKLHQRFNVILR--FPSWKNERTVASY--V--DGRIVKILPTDPKFA-QKQVEDILELIDSELGFSN-----ISTTRVSYLYVSDQQE--VVGCLIAEQI 93
 Ecol_Ca --YKTDND--VLIITENFELVEIP--KLNSTGKSLKSTK--TRQTFKGSIIICINKSNKRHIQKVELLLNMVNQELNASQDS--GQWKKPEFDRSKAFVII-IDSK--ATGLCTIDTI 162
 Ecol_Saccharomyces_kluyveri -----RKKRX----- 5
 Ecol_Sc SIVYTERNHS--RIVHLRSRTGITIP--LNSSPLKSSPSI--HQE EKIVYVRFDKSNCE-VRAMTEIMTLVNNELNAPHDENVIWNS TEEKGAFVYI-RNDR---AVGIIIIENL 179
 Ecol_Sp SMEYNSTSEEDILLHSRFRSRVLGGVT--VSFQCSPIYRVN--YGLSSDCIYINSNESSLIDQRKAEALSFVNNLSSEP-----IETIGVDKYTTFLFIS-DKK---CVGLLLAERI 165
 Ecol_Dm GLVYTVHEPEEELLHREYHN-SIHVLR--FKGWIDEDIVSVYPEWASDGRIRIRINERAP TAR-LDRLRDLIGVVDKELGYSS-----YIVPKIFVAFIAVR-KQ---IVGFCLVQPL 163
 Ecol_Ce RMMYSVDSAEDVAHEKFNARFRFE--ISRIFVFNFLNFHN-RDHGNFKVYYLATFADGPFKFLFNEHMKKINEELGYCDEK---NDLWSPKRIFLVLSVREERMLIGGILVIEKI 217
 Ecol_Yarrowia_lipolytica GMIYQVAYGPDISAHKSFSHTALNGPK--WKP SVAVVVD-----KSKTYTVYKSRLLSHPCVSQFLKLVNSELNAP E P-----ILSSQAAYVYVVDQR---AVGCVLVDRI 183
 Ecol_Leishmania PAACAGCDDSADSAPGRHQKRSKVRPS--CCS-ATLR-----SAVLAVLHAAHESIGSP EAVSHGGCVVIVHVKAARDG---VRCASAKTAS---RAFPVWFVDGVCVAEDI 154
 Ecol_Trypanosoma_brucei R-VYDVNLPRSRNNDNNISSLQCAVLPNFVEYVGRS VSCVAKVCKPQLKRVLLRALAAVRQEMGSVDDIPHDLSLLVAVS PIN---AFSSECIHDASRTAMP RAREGCKIVGLCVAREL 179
 ruler130.....140.....150.....160.....170.....180.....190.....200.....210.....220.....230.....240

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Ecol_Zea_mays KTGHRVIPSSSTEGSPNDLFPVSSTERGKNCHTLEFGSISFKREIIRRSRVKNKEECQDPGAILCETEAVPALCGFRAIIVVAPSCRRKRIASKLMDVARKTFCEG-RTLGISQFAFSPPT 169
Ecol_Oryza_sativa KTAHKVIPGSTE-----ENGN-----KNKEEYRDPGAIICEKEGVPACGFRAIWVPSRRKRIGSOLMDAARKSFLEG-ETLCISQCAFSPPT 296
Ecol_Sorghum_bicolor MXXXXXXXXXX-----RRHNS-----IKNKEECQDPGAIICEETEAVPALCGFRAIIVVPSRRKRIASKLMDVARKPFCEG-RTLGISQFAFSPPT 233
Ecol_Hordeum_vulgare XXXXXXXXXXXXX-----XXXXX-----XXXXXXXXXXXXXXXXXAVAAALCGFRAIIVVPSCTIKGIASQLVDAARKSFCEG-GALGISQCAFSPPT 182
Ecol_At_new KEAFKLIASPDD-----ERQLDNQVIVCEEEAKPAVCGIRAIWVSPSNRRKGIATWLLDTTRESFCNNGCMLEKSQLAFSQPS 282
Ecola_Mm KQAFRVLSEFS-----ASK-----ECSRAWRCSDVPEPAICGISRIWVFRKRRKRIARRLVDIVRNCFMFG-CFLSTNEIAFSDPT 295
Ecola_Hs KQAFRVLSEPIG-----P-ES-----PSST---ECPRAWQCSVPEPAVCGISRIWVFRKRRKRIARRLVDIVRNCFMFG-CFLSTNEIAFSDPT 248
Ecol_Danio_rerio RQAYRVLEQQEK-----Q-KD-----MSKKNFMQHRTWXCVPEKAICGVSRIWVFSLMRRKSVATRLLDIARNTFMYG-SHLTKEEIAFSDPT 219
Ecolb_Mm QWGYRVIEEKL-----VIRS-----EEEKVRFERQKAWCCSTLPEPAICGISRIWVFSMMRRKKIASRMIECLRSNFIYG-SYLSKEEIAFSDPT 306
Ecolb_Hs QWGYRVIEEKL-----VIRS-----EEEKVRFERQKAWCCSTLPEPAICGISRIWVFSMMRRKKIASRMIECLRSNFIYG-SYLSKEEIAFSDPT 306
Ecol_Xl QWGYRVIDDLIP-----EGTS-----QKEKALSERVKAWCCSTSEPAICGVSRIWVFSMMRRKKIASRMIECLRSNFIYG-SFLNKDEIAFSDPT 120
Ecol_Strongylocentrotus_purpur -QGYRVIVD-----EQKAEGNDSQKAWCCETESAPALCGISRIWVPRSTX--QIASRMVDCLR----- 55
Ecol_Ciona_intestinalis KRGFPLET-----MTSSGMMSCSLQSTPVTTCGVSRIWCHAPHRKRGVATRLMDALRCSFVLG-ERLNMNQVAFSDPT 165
Ecol_Ca Q-----PD-----QGRWMIHKTSIVPNQINKNVIGISRIWISRKWRQYGLGKLLNVVLKNSIYS-VQLLKNQVAFSQPS 233
Ecol_Saccharomyces_kluyveri -----WMILGTDIVP-QVSPIVKLGISRIWVCKNHRGEGIALRLLLETARKYSIYG-TEVAKWELAWSQPS 69
Ecol_Sc YGNGKSS-----RGRWMVYDSRRLVQ-NVYPDFKIGISRIWVCRARKLGIATKLLIDVARENIVYG-EVIPRYQVAWSQPT 255
Ecol_Sp SSAIVVDELELN-----NNNSISSAVYIKNENLRKGFVLGISRIWVSASRRKQGIASLLLDNALKKFIYG-YVISPAEVAFSQPS 244
Ecol_Dm SQAHR-----FIQVDGTDYFS-EESYPASCQVSRIVVSPLORRSGIASKLLRVVCHIVLQ-QEIARCEIAFSTPT 232
Ecol_Ce SRAWTN-----VQKMEVTDNNDINDWIVGVDRIVVSDHCRMKGVANSLDDAATTQDRQMEFRSRRRLRIAFCDPT 286
Ecol_Yarrowia_lipolytica TKCR-----FVDIQTGTLGLKEYPAVMGVSRMVVSQLFRRTGIVTKLLDLAKSDFIYG---IGA----- 239
Ecol_Leishmania PRAYRALR-----AQVTRVGD SWCTGTPLCGVRLMWVSPASRGRGVAYLMIERARHVCYGFVVP AEHVAFSEPT 224
Ecol_Trypanosoma_brucei SAPHRMHCESNWSHEKSEASGVGAAVQEG-----LGDCWEEDATRVGTTNNVRKAFCGVQLVWVADCYRRHGVAKVLVDIARRHISYGF- FEVVPVERVAFSEPT 276
ruler .....250.....260.....270.....280.....290.....300.....310.....320.....330.....340.....350.....360

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Ecol_Zea_mays SSGKGLACRYCKTSAFLVYKDGVP----- 193
Ecol_Oryza_sativa SSGKXLARSYCKTSAFLVYKEQDA----- 320
Ecol_Sorghum_bicolor SFGKGLACRYCKTSSFLVYKDGVP----- 257
Ecol_Hordeum_vulgare SDGKELASSCYKTSFAFLVYRNGDV----- 206
Ecol_At_new SIGRSFGSKYFGTCSFLLYKAQLIDTHFS 311
Ecola_Mm PDGKLFATKYCNPFLVYNFHN----- 318
Ecola_Hs PDGKLFATKYCNPFLVYNFNS----- 271
Ecol_Danio_rerio PQGKLFATKYCQPTFLVYNFIS----- 242
Ecolb_Mm PDGKLFATQYCGTQFLVYNFINGQNTT- 334
Ecolb_Hs PDGKLFATQYCGTQFLVYNFINGQNST- 334
Ecol_Xl PDGKLFATRYCGTQFLVYN----- 140
Ecol_Strongylocentrotus_purpur ----- 55
Ecol_Ciona_intestinalis ISGKSFAIKYFKPHFLTYNCST----- 188
Ecol_Ca FSGGMLAKSFNGVKH-KSGEMLLPVYIE- 260
Ecol_Saccharomyces_kluyveri ESGGELAKKYNVVFHEKSGKLLIPCYI-- 96
Ecol_Sc DSGGKLASKYNGIMH-KSGKLLPVYI-- 281
Ecol_Sp ESGKQFIISWHRERNNGSSKSLRYAVYE 273
Ecol_Dm DDGRALARFTGLDNFLTYDQ----- 253
Ecol_Ce DDGIKLARRFIEIRYQKEDQYNGEILTY- 314
Ecol_Yarrowia_lipolytica ----- 239
Ecol_Leishmania AMGSAFARRYQARQDFLVYHY----- 245
Ecol_Trypanosoma_brucei SLGKLFAKSYSGRPDFLIF----- 295
ruler .....370.....380.....

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