

Supplementary Figure S1 Kosmaczewski et al.

E.coli|NP_417879.1 1 -----MNY-----EL--LTTENAPVKMWTKGVPEADARQOLINTAKMPFIFKHIAVMPDVHLGKGS
P.horikoshii|pdb1UC2|A 1 -----MNVFIRKRIDKIRWEIP-KFDKMRVVEGRVYADEVLEKMKND-----RTLEOATNVAMLPGIYKYSTVMPDGHQGYGF
C.elegans|NP_492498.1 1 -MPRTFEEECDFIDRLTDTKFRIKKGFVPMNVEGRFVYVNSLEQLMFDLKFSCDGOIGGGFLPAVROIANVASLPGIVGHSIGLVDIHSYGYF
C.reinhardtii|XP_001699521.1 1 -----MHVPGTFYVNDALKGLMFEELQOAVVRGDHGGFLPAVKQLANVAALPGIVKRSIALPDVHSGYGF
H.sapiens|AAH00151.1 1 -MSRSYNDLEQLFKINKNCWRIKKGFPNMOVGVFYVNDALKGLMFEELRNA CRGGVGGFLPAMKQIGNVAALPGIVHRSIGLVDVHSGYGF
M.musculus|NP_663397.1 1 -MSRNYNDEQLFKINKNCWRIKKGFPNMOVGVFYVNDALKGLMFEELRNA CRGGVGGFLPAMKQIGNVAALPGIVHRSIGLVDVHSGYGF
D.melanogaster|NP_609965.1 1 MVVVRPYNDELRLYLEKVS DHCWRIKKGFPNMOVGVFYVNSRLERLMLTEELKNSCRPGA VGGFLPQVQI ANVAALPGIVHRSIGLVDIHSYGYF

E.coli|NP_417879.1 56 TIGSVIP-----TKGAIIPAAVGVDIGCGMNA LRTALTAEDLPENLAELROAIETAVPHGRRTTGCRCKRDKGAWENPPVNVDAKWAEL EAGYOWLT
P.horikoshii|pdb1UC2|A 73 PIGGVAADFVK--EGVISPPGGIGVDINCGVRLIRTNLTEKEVVRPRIKQLVDTLFFKNVPSGVGSGRITKLHWTQIDDLVDCAKWA--VDNGYGWER
C.elegans|NP_492498.1 95 SIGNIAAFDVGNPESVLSPPGGVGF D INCGVRLRLTNLFEENVKPLKEQLTQSLFDHIPVGVGSRGATPMLASDLVECELEMGMDWT--LREGYSWAE
C.reinhardtii|XP_001699521.1 66 AIGNVAADFMDNPEAVVSPGGVGF D INCGVRLRLTNLFEAEVGPVREQLAQLFDHIPVGVGSGTIPTAKDMESALEMGMDWS--LREGYAWAE
H.sapiens|AAH00151.1 95 AIGNMAADFMDNPEAVVSPGGVGF D INCGVRLRLTNLDES DVOPVKEQLAQLAAMFDHIPVGVGSKGVIIPMNAKDLEEALEMGV DWS--LREGYAWAE
M.musculus|NP_663397.1 95 AIGNMAADFMDNPEAVVSPGGVGF D INCGVRLRLTNLDES DVOPVKEQLAQLAAMFDHIPVGVGSKGVIIPMNAKDLEEALEMGV DWS--LREGYAWAE
D.melanogaster|NP_609965.1 96 AIGNMAADFMDNPELSVVSPPGGVGF D INCGVRLRLTNLYEKDVO PVKEQLAQLS LFDHIPVGVGSKGITIPMNAKDLEEALEMGV DWS--LREGYVWAE

E.coli|NP_417879.1 146 OK-----YPRFLNT-----NYYKHLGLTGTGNHFIEIC-----LDES DVWIMLHSGSRGIGNAIGTYFIDLAKEMOE
P.horikoshii|pdb1UC2|A 165 DLERLEEGGRMEGADPEAVSORAKORGAPOLGSLGSGNHFELEVQVVDKTFDPEVAKAYGLF--EGQVVMVHTGSRGLGHQVATDYLIRIMERAIRK
C.elegans|NP_492498.1 189 DKEHCEEYGRMLQADASKVSLRAKKRGLPQLGTLGAGNHYAEVQVDEIYDKHAASTMGIDE EGQVVMVHTGSRGLGHQVATD SLVEMEKAMAR
C.reinhardtii|XP_001699521.1 160 DKEHCEEYGRMLNADPRYVSSRAKKRGLPQMGTLGAGNHYAEVQVDEIYDVAARRMGIDTPGOVVMVHTGSRGLGHQVATDALVAMEKAMAR
H.sapiens|AAH00151.1 189 DKEHCEEYGRMLQADPNKVSARAKRGLPQLGTLGAGNHYAEIQVDEIFNEYAAKKMGIDHKGOVVMVHTGSRGLGHQVATDALVAMEKAMKR
M.musculus|NP_663397.1 189 DKEHCEEYGRMLQADPNKVSARAKRGLPQLGTLGAGNHYAEIQVDEIFNEYAAKKMGIDHKGOVVMVHTGSRGLGHQVATDALVAMEKAMKR
D.melanogaster|NP_609965.1 190 DKEHCEEYGRMLNADPAKVSARAKRGLPQLGTLGAGNHYAEIQVDEIYDKWSASKMGIEEKGOVVMVHTGSRGLGHQVATDALVAMEKAMKR

E.coli|NP_417879.1 210 TLETLPSPRDLAYFMEGTEYFDDYLKAVAWAQLFASLNRDAMMENVVTLQOSITOKTVROPOTLAMEE--INCHHNYVQKEQHFQ----EEIYVTRK
P.horikoshii|pdb1UC2|A 259 YRIPWPDRLELVSPFQSEEGORYFSAMKAAANFAWANROMITHWVRESFOEVFKODPEG--DLGMDIYDVVAHNIGKVEEHEVDGKRVKVI VHRK
C.elegans|NP_492498.1 284 DGIVVNDKQLACARINSVEGKNYFSGMAAANFAWVNRSCITFCVRNFAQKTFGMSAD---DMDMOVIYDVSHNVAKMEEHVVDGRPRQLCVHRK
C.reinhardtii|XP_001699521.1 255 DGIITNDRQLACARINSEEGQAYLKAMSCAANFAWVNRSSMTFLRQAFAKIFKSTPD---DLDMHVYDVSHNIKVEQHCVDGQHRRLLVHRK
H.sapiens|AAH00151.1 284 DKIIIVNDRQLACARIASPEGODYLKMAAAAGNYAWVNRSSMTFLRQAFAKVFNTTPD---DFDHHVYDVSHNIKVEQHCVDGKERTLLVHRK
M.musculus|NP_663397.1 284 DKIIIVNDRQLACARIASPEGODYLKMAAAAGNYAWVNRSSMTFLRQAFAKVFNTTPD---DLDLHHVYDVSHNIKVEQHCVDGKERTLLVHRK
D.melanogaster|NP_609965.1 285 DKIIETNDRQLACARINSVEGODYLKMAAANFAWVNRSSMTFLRQAFAKVFNTTPD---DLDMHVYDVSHNIKVENHMDVDGKERKLLVHRK

E.coli|NP_417879.1 300 GAVSA-----RAGQYGIIPGSMGAKSFIVRGL--GNESESFCSCSHGAGRVMRSRTKAKKLF SVE DQIRATA----HVECRKDAEVIDE
P.horikoshii|pdb1UC2|A 352 GATRAFPPGHEAVPRLVYRDVGOPVLIIPGSMGTASYILAGTEGAMKETF GSTCHGAGRVLRSKAATRQYRGDRIRQELLNRTIYVRAASMRVVAEE
C.elegans|NP_492498.1 376 GATRAFPPHPLIPVDYQLTGQPVLIIGSMGTCSYVLTGTEOGLVETFGTCHGAGRALSRAKSRRTITWDSVIDDLKKKEITSRIASPKLIMEE
C.reinhardtii|XP_001699521.1 347 GSTRAFPPHPLIPVDYQLTGQPVLIIGSMGTCSYVLTGTEOGLVETFGTCHGAGRALSRAKSRRNNSRNKLDYQDVLNKLKAGIARVASPKLVMEE
H.sapiens|AAH00151.1 376 GSTRAFPPHPLIPVDYQLTGQPVLIIGSMGTCSYVLTGTEOGLVETFGTCHGAGRALSRAKSRRNLDYQDVLNKLADMGAIARVASPKLVMEE
M.musculus|NP_663397.1 376 GSTRAFPPHPLIPVDYQLTGQPVLIIGSMGTCSYVLTGTEOGLVETFGTCHGAGRALSRAKSRRNLDYQDVLNKLADMGAIARVASPKLVMEE
D.melanogaster|NP_609965.1 377 GSTRAFPPHPLIPVDYQLTGQPVLIIGSMGTCSYVLTGTEOGLVETFGTCHGAGRALSRAKSRRNLDYKDVLDKLDQLGAIARVASPKLVMEE

E.coli|NP_417879.1 376 IPMAYKDIDAVMAAQS--DLVEVIYTLRQVVCVKG
P.horikoshii|pdb1UC2|A 447 APGAYKNVDNVVQVSEAGIAKLVARMRPIGVAKG
C.elegans|NP_492498.1 471 APESYKNVTDVVDTCDAAGISKKAIVKLRPIAVIKG
C.reinhardtii|XP_001699521.1 442 APESYKDVSEVVDTCDAQISKKAIVKLRPIAVIKG
H.sapiens|AAH00151.1 471 APESYKNVTDVVDTCHDAGISKKAIVKLRPIAVIKG
M.musculus|NP_663397.1 471 APESYKNVTDVVDTCHDAGISKKAIVKLRPIAVIKG
D.melanogaster|NP_609965.1 472 APESYKDVTDVVDTCDAAGISKKCIKMRPIAVIKG

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