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                                                                                    ▼                               ▼
Spn      1 MSKKRRNR-HKKEAQEPQFDFDEAKELTVGQAIRKNEEVEAGVLPEDSILDKYVKQHRDEIEADKFATRQYKKEEFV---------ETQSLDDLIQEMREAV-----------------
Sppn     1 MSKKRRNR-HKKEGQEPQFDFDEAKELTVGQAIRKNEEVEAGVLPEDSILDKYVKQHKDEIEADKFATRQYKKEELV---------ETHSLDDLIQEMREAV-----------------
Smi      1 MSKKRHDR-HITEHQEAQFDFDDAKELTVGEAMLKNEEVEAGVLPGDSILDKYVKQHKDEIEADKFETRQFSKDDLVEKEGIEEIEETQTLDNLLQELREET-----------------
Sor      1 MSKKRRDR-HKKGHQEPQFDFDEAKDLTVGQVIRKNEEVEAGVLPEDSILDKYIKQHREEIEADKFETRQFKKEELA---------STQNLEEMIQEVRE-------------------
Ssu      1 MGEKNSH--HLPLDEEKVLDFEVAKDLTIEEAVKKHKEIEAGVTEDDGLLDRYIKQHRAEIESQKFETKI---------------NHLPLVEVADEEKNQGHE---------------
Sint     1 MSKDEK---HLPEQEESILDFETAKEMTIGQAARKSEELEAGVTEEDNVLDKYIKQHRQEIEAGKFSAQSAEEWAKI--EDQEQL-SQSDLAELIQEVHDDIQREEALESTDV-------
Sang     1 MSKDEKHL-PEQEEKESILDFETAKEMTIGQAARKSEELEAGVTEEDNVLDKYIKQHRQEIEAGKFSAQSAEEMSEA--EDQEQL-SQLDLAEFIQEMHDEVQEEAPLEPAEV-------
Scon     1 MSKDEKY---LSEQEESILDFETAKEMTIGQAARKSEELEAGVTEEDNVLDKYIKQHRQEIEAGKFSAQSAEKASEV--EGQEQL-SQLDLAEFIREMHEGVQ-EEVLEAADV-------
Ssan     1 MTKEENYS-PEEEKKESVLDFEEAKEMTVGQATRKKEELEAGVNESDNVLDKYIKQHRQEIEAGKFETQKIRKLQEQEAAQAEQ--ASSDLTDFIKERRQEVE----------------
Sgo      1 MSKENTK--PESQEQESILDFEEAKEMTIGQAARKSEELEAGVKEDDSVLDKYIKQHRQEIEAGKYTATVQ---------------AQKKQDEKAEEAKKETVLTDE-------------
Ssal     1 MSEDKTQ---NGYEGSQELDFQDAKEMTVGEAVRKEAEINAGVTETDSILDKYIKQHREEVASQKFSKKIEADG------------DTSPLDAFIQKQRQEFADSGLISQSMANESINST
Sthe     1 MSEDKTQ---NGYEESQELDFQDAKEMTVGEAVRKEAEINAGVTETDSILDKYIKQHREEVTSQKFSKKIEADG------------DTSPLDAFIQKQRQEFADSGLIGQTLANESTNST
Smu      1 MSEKEKNP-IENSESKDSLDFQDAKEMTIGEAVRKDSEIKAGVTEEDSVLDRYIKQHRDEVTARKFDTSSDDFESI----------DTSTLDNFIKQQRQELVDTGLIDPIEEQEEEIPS
Sinf     1 MSEKKDM---PSSEEKDGLNFEDVKNLTIEEAVRKGSEMKAGITESDGVLDKYIKQHRDEVTSQKFETKLSDFEDL----------DTKALDNFIKKQREELVNSGIVSKDVFEETVEPK
Sgal     1 MSDKKEL---PSSEEQEGLNLEDVKNMTIGEAVRKDSELKAGVTESDGVLDKYIKQHRDEVTSQKFEAKLSDFDDL----------DTKALDNFIKKQREELVNNGIV-----------
Spas     1 MSDKKEL---PSSEEQEGLNLEDVKNMTIGEAVRKDSELKAGVTESDGVLDKYIKQHRDEVTSQKFEAKLSDFDNL----------DTKALDNFIKKQRAELVNSGLV-----------
Sag      1 MSEDQKHPFFEPKKETDGLEFKDAKEMTVEEAVRKDSEIKAGITEEDSILDKYIKQHRDEVASQKFETKSSDFANL----------DTASLDDFIKKQREELSAMLAAEELSK-------
Spub     1 MSEENKD--FEINQEGQSLDIDQAKNMTVGEAVRKDSEIKAGVTENDNILDKYIKQHREEVASQKFDTKYSDLETL----------DTETLDNFIKKQREELSKS--------------
Seqe     1 MSEKSKA--FESEAESQNLELHEAKKMTIGEAVRKDSELKAGITEDDSVLDKYIKRHRNEVSSQKFDAKYMEL-------------DTASLDNFIKKQREELSKAGLVDV----------
Seqz     1 MSEKSKA--VESEAESQNLELHEAKKMTIGEAVRKDSELKAGITEDDSVLDKYIKRHRNEVSSQKFDAKYMEL-------------DTASLDNFIKKQREELSKAGLVDV----------
Spy      1 MSEESKE--VEVTKESQTLGLNEAKSMTIGEAVRKQSEIKAGVTKDDSILDKYIKQHRDEVSSQKFDAKYTEL-------------DTASLDNFIKKQREALSKAGLVDDEPV-------
Sdy      1 MSEESKE--VEVTKESQTLGLNEAKSMTVGEAVRKESEIKAGVTEDDSILDKYIKQHRDEVSSQKFDAKYTEL-------------DTASLDNFIKKQREELSKAGLVDDDFV-------
Sini     1 MSEKKD---FEINKDGQTLDIDQAKNMTVGEAVRKDSELKAGITDQDSVLDKYIKQHREEVASKKFETKLSELETL----------DTASLDKFIQKQRQELAKAGLIKKESS-------
Sub      1 MSEENKD--FELQNEEQGISIDKAKQMTVGEAVRKDTELKAGITEDDSVLDKYIKQHRQEVASQKFETKVSEVESL----------DTASLDNFIKKQREELAKTGFFNQ---------
           *  ..                    :  :   .*.:*: :.   *   *::**:    *.:**.*:*.*.  *: : *:                                :  .
Spn     93 -----------------------------------------------------------------------------------------------EKSEASSEEVPSSEDILLPLPLDD
Sppn    93 -----------------------------------------------------------------------------------------------EESEASSEEVPSSEDILPPLPLDD
Smi    102 -----------------------------------------------------------------------------------------------GVTSPASEDELSQFDDLELTRVSE
Sor     91 -----------------------------------------------------------------------------------------------SSESSEQVDDSDVVAEESIEEIEN
Ssu     86 -----------------------------------------------------------------------------------------------SAEEVEANESSLTEVSEEIAPIVE
Sint   108 -----------------------------------------------------------------------------------------------TSEESDFDETVGTLSTSDVEPQDI
Sang   110 -----------------------------------------------------------------------------------------------ASEESAFDETVAALAASEAEPQET
Scon   107 -----------------------------------------------------------------------------------------------ASEESAFDETVAALAASEAEPQET
Ssan   101 -----------------------------------------------------------------------------------------------SEQEIPTARLTAAETASEPEAAPN
Sgo     91 -----------------------------------------------------------------------------------------------TKEEVIASPKSPGLEAEVSQAFSD
Ssal   106 TATEEVTPVTFGFGATDNKADETQSHIDKQLPNAPVEPEVIAEPESQSSEVIITSTNADRFITSETEKFDLGDALADSSTLTNHPAYNDALVDNIDDNNPLIANIDDPEPQNPVVANIDD
Sthe   106 TADETVTPITSGFGTTETKADDTQ---------APVDSEITVKPESESSETIITSTNADRFITSEAEKFDLGEALTATTTSTNQQV----------DNTAMVDNVDDPEPESTLPADDKS
Smu    110 ASAISAD----------------------------------------------------------------------------------------TAKEQSLEDTIVAPAINPNQEIWK
Sinf   108 SEDVVEPVV--------------------------------------------------------------------------------------EVAEVKEVEAEPEQAETVDAEKEA
Sgal    96 -----------------------------------------------------------------------------------------------GESALKENEATPRAVDFEAEKIED
Spas    96 -----------------------------------------------------------------------------------------------GESALKENEATPKAVDFEAEKVED
Sag    104 -----------------------------------------------------------------------------------------------KLDNSVSQEQDTEANAVSPKEESS
Spub    94 -----------------------------------------------------------------------------------------------EQEEIISEEPNQTEEDSGAAGAAI
Seqe    96 -----------------------------------------------------------------------------------------------EPVDEASTEEKPAGETSFIEPLAA
Seqz    96 -----------------------------------------------------------------------------------------------EPVDEASTEEKPADETSLIEPAAA
Spy     99 -----------------------------------------------------------------------------------------------SAESAEQDSTLVEEVAEDLAPMET
Sdy     99 -----------------------------------------------------------------------------------------------ENEPAATELSEPSSEGVPDELASV
Sini   101 -----------------------------------------------------------------------------------------------ANETLYNEETSSVKTEEVPVPDTL
Sub     99 -----------------------------------------------------------------------------------------------TSEEQKLETEAEEDLALSSKRNDH

Spn    117 EEQGLDPLLLDDE---------------NPTEMTEEVEEEQNLSRL--------DQEDSEK----------------KSKKGFILTVLALVSVIICVSAYYVYRQVARSTKEIETSQSTT
Sppn   117 EEQGLDPLLLEDE---------------TPTEMTEEVEEEQNLSRL--------DQEDSEK----------------KSKKGFVLTALALVSVIICVSAYYVYRQVNRSTKEIETSQSTT
Smi    126 ----------------------------TPLVEASETEDIPTLYRV--------TDSEDGK----------------SKKKWVLYGILAALVVLILGTGYYIYRQVARSTKEIQTSQSTT
Sor    115 EETTQFVPPLQDEESTEIEPLVLTETEPKQINEEQEEETYTPLSRS--------AQTEPET---------------GSKKKGVIIIASVVAAILVLAGTYYVYRQVSRSNQEIQSSQAAS
Ssu    111 ELSVTPMETLEETVIASTVAMEGLSSVADDSSLELEEDETEDLDHS--------EGADRDQ-----------------KKKFYFWSAVGLSMIGVMATALVWMNSVNKSNTATSSSSTST
Sint   131 LDGNHTQPLEEPEAETKVVEVIQPKIDVIPVYSANPTEENSTVIAS--------NEEMGTE------------TVPVYKNKKVLYSVVSVALLALIGWTVYLSLNRKQAKPTTNSTSQTS
Sang   133 SEENSTQTPEELEAETKIMEPIQPEMDDIPVSSTESTESYPTFTAL--------DEEMETE------------KVPFYKNKKVLYSAASVALLALIGGTVYLSLNRKQAKPATNSTSQTS
Scon   131 LEKNSTQISEESEAETKVMEAIQPEMDNIPVSSTETMESYSTFTVS--------DEEMETG------------NVPFYKNKKVLYSAASVALLALIGGTVYLSLNRKQAKPVTNSTSQTS
Ssan   125 PLGSRSQRSEQED--------------AVPVAPVQKTSYGPIPEPL--------DEKELQV-----------PKTPFYKKKAFLYPVLGLLGIAVAGTGLYFALGHNWGHKTVTSSSSST
Sgo    115 EPEDKTQVDLEPV---------------APVSTPVTEDSYE-------------EDDEKTG----------------SGSKKVIYALVALLAVAGIAATAYFAMNRNQAGKTVTSSSSQA
Ssal   226 TEPQASNPLLDDVTISDTIDLAAIASTVAGVTGVKADEEKTTPKVSMAVNHPSAEDRISSESISPSHKSAFDGDIPVYRRKGVVIGALAVLALAIIGGSYALYKGTHSQSAKTTSTASSA
Sthe   207 SEPQASKPLLEDVGVSETIDSDAIATTVAGVTGVKADEAKATPKVSMTVSRPSAEDKISSGSISPSHKGVFDGDIPVYRRKGVVIGALTVLALAIIGGSYALYKVTHSQSAKTTSTASSA
Smu    141 KDEFDDVPLSDTQETAKLDTEEKSSFLTAPTSDLDKDDVGNSEDFD--------EDDETKP--------------PFYKRKKVIMASFIVLLLLAAGATYSVYQLSHHTAKTKRTTKSTS
Sinf   141 AKEVKATTPKVEEAVAAVEEPKEAPVAIPAEEVKEAEKEATSIALS--------ADDNKPT----------------SKKKRVIIGGLAVLVVAIFGAGYALHYTKDSTTTVASSSTSSS
Sgal   120 TQETSQEVPVSENGASENDSTIQQENVSIEIPNANSAVSEPTPEAASAVVA---DDKNSEA-----IALETADEQPTYKNKRVIIGGLAALVVAIFGVAYGLNYTRESSTSVASSSTSTT
Spas   120 TQETSQEVPVSEDVASENDSTIQQENVSIEIPNADSAVSEPTPEAASAVVA---DDKNSEA-----IALETADEQPTYKNKRVIIGGLAVLVVAIFAVAYGLNYTKEPSTSVASSSTSTT
Sag    128 QEQENSVTPVPPL---------------NTEAEPTATEPDSTIADS--------EEYKSSS-----------------KKRGGIVGTLIALILLLIVAIFGYNYFKNNNSTNSQTATSQS
Spub   118 AGAGAGIGASTLA---------SDPVVAEDKNEAVSESTESRQSIL--------ADNEKPR--------------KSSGKMKKILASLLALILLILAIFFGMDYLKGSSTSTKTDPSTKQ
Seqe   120 RADTSAAATDSAS-----------DFTGQLADDAVSERPAEVESIL--------SDSYASR----------------RSKKKKPLFAILLATLTLVASAFALNHIYQLSKHKPQSKATVS
Seqz   120 KAGTPALATDSAS-----------DFTGQLADDAVSERPAEVESIL--------SDSYASR----------------RSKKKKPLFAILLATLTLVASAFALNHIYQLSKHKPQSKATVS
Spy    123 TAVVTGIPVEATVPVLDLDPSERV----IPEPQMTKEEPKRDQFLS--------EDSHHPA---------------KQNTKKGWLIALFLLLLAILAVVFGWNHFLRQDSGKTTQTASKQ
Sdy    123 EAAAVTTGIPVEA----MVPVTDPVEKTIPEPQVTQEQPVREQFFT--------DTDASNP-----------------RQKRGWLIALLLLLLAILATVFGWNYLKQDNTKTNKAASSPT
Sini   125 GTADTDFPK-------------------ETLYDKIDYPEGQTFGTV--------SRGQANS-----------------RKKKKVIPILLAILFLALVVFLGVNFASQSNSPKAREEVAKQ
Sub    123 VSHGITDEIKEDQKPV-------FDQVEPVVPIVDSSREDDQVAFL--------DSERSGN----------------KKSKKKFLLALLSLLLLLVGGAFGLNVLKQNDSGTTNTKVSSQ

Spn    198 AN--------------QSDVDDFNTLYDAFYTNSNKTALKNSQFDKLSQLKTLLDKL-EGSREHTLAKSKYDSLATQIKAIQDVNAQFEKPAIVDGVLDTNAKAKSDAKFTDI-----KT
Sppn   198 AN--------------QSDVDDFNTLYDAFYTDSNKTALKNSQFDKLSQLKTLLDKL-EGSREHTLAKSKYDSLATQIKAIQDVNAQFEKPAIVDGVLDTNAKAKSDAKFTDI-----KT
Smi    194 NT--------------QSDVEEFNNLYDAFYTDSNKTALKNSQFDKLSQLKTLLDKL-EGSREYTLAKSKYDSLAIQIKAIQDVNAQFEKPAIVDGVLDTNAKAKSDAKFTDI-----KT
Sor    212 SD----------DQGTQTALKDFNDLYDTFYTDANKTALKNSQFDKLSQLKTLLDKL-EGSREYTLAKSRYDSLATQIKAIQDVNALFESPAITDGVLDTNAKAKADAKFTEI-----KT
Ssu    206 SQ-----TSSTASSSTDANVTAFEQLYNSFFTDSSLTKLKNSEFGKLAELKVLLEKLDKNSDSYTKAKEQYDHLEKAIAAIQAINGQFDKEVVVNGEIDTTATVKSGESLSAT-----TT
Sint   232 KY-------STASSSENKDLKAFNSLYDSFFTDANKLALKNSSFGNLDKLKAALEKL-KNTNEYNVAKAKYDSLVKQVEAVKNVNAQFTSVAITDGVLDTKAKIKSDAKFTDI-----TT
Sang   233 KS-------STTSSSENKNLKAFNSLYDSFFTDANKLALKNSSFGNLNKLKAALEKL-KNTNEYNVAKAKYDSLVKQVEAVQNVNAQFTSAAITDGVLDTKAKIKSDAKFTDV-----TT
Scon   231 KS-------STTSSSENKDLKAFNSLYDSFFTDANKLALKNSSFGNVDKLKAALEKL-KNTKEYNVAKEKYDSLLKQVEAVKTVNAQFTSVAITDGVLDTKAKIKNDAKFTDI-----TT
Ssan   212 SQSSKKSSSSSSSDNTAKNLKAFNDEYAAFFTDSNQTAVKNSKFGDLEKLKTLLEKL-KGSKDYDAAKSKYDSLVKQISAIQSVNSQFDGGAITDGVLNKEAKANTNATFSDV-----SS
Sgo    191 SK----KTSSSSSSSENKALKKFNDLYDSFFTDKNKLALKNSSFANLDQLKAALEAL-KNDKEYTVAKAKYDSLVKQISAIQAVNSQFETAAIKDGVLDTNAKVKGDATFTET-----KT
Ssal   346 VT------SSSSKDTAAADNKAFEEMYKNFFTDDEQTKLANDQFGKLSDLEKLLKKL-EKTKYYDAAKKKYDNLKKQIEAVQKINSQFESDALVDGSYNASIAVKSDANFNNLPESVTTT
Sthe   327 VI------SSSSKGASASDNKAFEDMYKNFFTDDEQTKLANDQFGKLSDLEKLLKKL-EKTKYYDAAKTKYDNLKKQIEAIEKVNSKYESDALVDGSYNASISVKSDANFNDLSERVTNT
Smu    239 TK---------KSTDFTAASKRFEKSYTAFFADAKRTKLKNNQFANLPKLEKHLKKL-KDSKYYDEAKKKYESLKRQISAINAVNGKFKTTAILNGDKKAA-AVKDNANFDDISEKSLNT
Sinf   237 QK-----KTISSSSAAKKAKKVFDDAYAALFTDDTKTKLKNSEFDKISVLKEKLDDL-KGTDFYDAAKKQYDTVAAHITAIKAINALFEKDVIVDGKKVSG-TVKADAKFDSLSSDVLNT
Sgal   232 KK----STSSSSSAAAKKAKTAFDDAYAAFFTDDTKTKLKNSEFDNISSLKEKLDDL-KDTDYYDDAKKEYDTLAAQITAIQTINALFESNVIVNGEKASA-TVKSDANFDNLSSDLLNT
Spas   232 KK----STSSSSSAVAKKAKRAFDDAYAAFFTDDTKTKLKNSEFDNISSLKEKLDDL-KDTDYYDDAKKEYDTLAAQITAIQTINALYESNVIVNGEKASA-TVKSDANFDNLSSDLLNT
Sag    208 SSSKATTTSSEEDKKASQNLDNFNKSYANFFVDDKKTQLKNSEFDKLSELEKKVDAL-KGTKYYGKVKVKFDSLKRQIDAVKAVNDKFKSPAVVDGKKSEKLEVKDGANFDSLDSKTLNT
Spub   207 TT--SKKEKSSSAAIAKKKNKAFTDVYAGFFTDEKKDKLKNESFAKLGDLETALKDL-KGTAYYDKAKEKFDALKKQVTAIEAVNGKFSTEAIKDGKKISA-TVKSNAKFDDLKDDLVNT
Seqe   205 KKARSKASTANQTNKTKANAKAFEDLYKTFFTDNDKTTLKNSAFDQLPNLETALKRL-EGTAYYDKAKEKVTGLKKQVTAIQAVNGKFTTAAIVNGEKIAA-EVKADANFDDLASDTLTT
Seqz   205 KKARSKASTANQTSKTKADAKAFEDLYKTFFTDNDKTTLKNSAFDQLPNLETALKRL-EGTAYYDKAKEKVTGLKKQVTAIQAVNGKFITAAIVNGEKIAA-EVKADANFDDLASDTLTT
Spy    216 TKTSLQTDSAKKATRLKAAAKAFEKLYGTFYTDATKSKLKNSAFATLPDLEAALKAL-EGSAYYDKAKAKVDSLKKAIAAITAVNGKFVSDVVVDGEKVSA-EVKADANFDDLSSATLTI
Sdy    213 TQ-TSKTAASKKAQQLKADVKAFEKKYSAFYTDATKSNLKNSAFTNLPELEKALKSL-EGSSYYDKAKEKVDALKKAITAITAVNGKFVSDTIVDGNKVAA-EVKPDANFDDLSSATLTT
Sini   201 VA--EQEKENEQAKKAKANAKAFNSELKAFYSDDKQTKLKNDHFDKLTDLEKILSKL-KKTAYYDNAKEKFDLLSKQIVAIKAVNGKFATEVIKDGEKIAA-TVKSGVHFDDLQADILKT
Sub    212 QS----SSKDSKASLAKKAYKAFDKGLKAFYLDDEMTKLKNSEMTHLDDLTKKLDAL-KNTNYYDKAKEKWESLKKQITAIQTVNGKFSTEAIKDGQKTAA-TIKSDANFDDFTADSLKT
                                  *      :: :     : *. :  :  *   :. * :    :  .*      :    : *:  :*  :    .: :*        :  .  :         .
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Spn     298 GNTELDKVLDKAISLGKSQQTSTSSSSSSQTSSSSSSQASSNTTSEPKPSSSNETRSSRSEV---------------------------------------NMG----LSSAGVA----
Sppn    298 GNTELDKVLDKAISLGKSQQTSTSSSSSSETSSSSTSQTSSNTTSETSPSSSNAASNETRSS-----------------------------------RSKVNMG----VSSAGVA----
Smi     294 GNTELDKVLDKAISLGKSQQTSTSSSSSSETSSSSSSQASSNTTSETSPSSSNAASNETRSS-----------------------------------RSEVNMG----LSSAGVA----
Sor     316 GNTELDKLLDKAISLGKSQQTSASSSSSSSSTSQ----ASSSSATESNASSTTPSTSNTAPA-----------------------------------RDTNGG----LSGDGVN----
Ssu     316 GISAVDSLLASVVNFGRSQQEVASATVASEAAVTRNQGADETVSTGVPATTEVASTTVSGST---------------------------------------TDFG---IAVPAGVV----
Sint    339 GNTDLDKVLKAAISLGKSQQGTT---------------KTGSAATAPSQSPAQAPAAASGPT-----------------------------------------------------
Sang    341 GNTDLDKVLKSAISLGKSQQTSAPQSEAAAAP------SQSSAQAPVAEQPASVPAQTTAPV-----------------------------------------------APASGAN----
Scon    338 GNTDLDKVLKAAISLGKSQQSAISAPKSET--------ATTPSQSPAQTQTPKTEAPAATPA-----------------------------------------------TQASGPT----
Ssan    326 GNAKLDEVLKAAIAQGRGQQIPTPAP------------ATDQGGTGAGTSGGSSASGSGASS-----------------------------------SYSGYG----LPSNGVN----
Sgo     301 GNDNLDKLISSAISQGKGQQTVSQSAGGQGT-------ASNTTPAPAETTPTAPTTNNTDQS-----------------------------VITGGSTGYG-GLSSTGVA----
Ssal    459 GNASLDSTIQEAIKGGKTQLEEKAKAASATSAAT----AADSANTASPAAPSGDNTSGAASTGGGAAASNTSGAQNGSANSGAAGSTGATGGTTGGSAAASTVVTRG-ITNYNPSI----
Sthe    440 GNASLDSIIQEVIKGGKTQLEEKDKAASTTSAATAS--ESVNTATPSGDNTSGAANSGVTGAAGGVS---------------------------SGTAATSTVVTRGIMNYNPSI----
Smu     348 GNATLDAILKSVIADGRKQLEANNKKSGSSAASSNANSGTSSNTEGSNQNAQAPAADSNTPANGSPGSNNTSGSTSPSTPAAPNNGTS-----------NAGASGYG-ISSYDVSK----
Sinf    350 GDANLDNLLQSVITDGKNQLAAKAQSSSQAQ-------AAANSASQTESNDKAAEAKPAAPA-----------------------------------------------SDNSN----
Sgal    346 GNANLDTLLQSAITDGKNQLATLASSSSQEAS------ASTSSQTESASSSDTSTTQTVSGA-----------------------------------SGYG---ITSYDAST----
Spas    346 GNANLDTLLQSAITDGKNQLAALASSSSQE--------ASASISSQTESATQSSSDTSTTPT-----------------------------------VSGASGYG-ITSYDAST----
Sag     327 GNASLDSLLHSIVSTGRNQVKQSEEQASSNKVSDTQITEQPNVTNGQSSSSAATINNQAAGT-----------------------------------ASGN-----------------
Spub    323 GNPSLDLLIQSAIKDGRDQLSKKAEAEKAAASKKAEEDKKAADAAEQQGQANAAASANQAAG-----------------------------------STTNNGSSANTNNAAPSTQIP
Seqe    323 GNAKLDSLLQSSIKAGREQLASRSATQA----------ASTPAASALPASPAAPQVPAVPAP-----------------------------------VAPMYG---ITGYDPSI----
Seqz    323 GNAKLDSLLQSSIKAGREQLASRSATQA----------ASTPAASALPASPAAPQVPAVPAP-----------------------------------VAPMYG---ITGYDPSI----
Spy     334 GNANLDAVLQASITEGRQQLASKAEA------------AKAANEQAVQDQAAQGQSTSVAPS-----------------------------------GYG---LTSYDPAS----
Sdy     331 GNANLDAVLQASITEGRQQLATKAEAAKA---------ASDQAAAQSQQATEVPAAQTSSAT-----------------------------------VTSSGYG-ITAYNPAS----
Sini    317 GNASLDSMLQSAISDGRKQLSDKEKSEKEAAAKA----AEEKQAAESAAANQASAATSSPLA-----------------------------GQSPANPGVA-LSQYAG------
Sub     326 GNATLDKLLQEVVSDGRKQVDDKNKAEKEKADAQAKADAEQKAAQDAATAEQANAAQSATTTSGATT-------------------------------GAQAPATGGTYGTAASG----
            *   :*  :   :  *. *

Spn     370 ------VQRSASRVAYNQSAIDDSNNSAWDFADGVLEQILATSRSRGYITGDQYILERVNIVNGNGYYNLYKPDGTYLFTLNCKTGYFVGNGACHADDLDY
Sppn    374 ------VQRSASRVAYNQSAIDDSNNSAWDFADGVLEQILATSRSRGYITGDQYILERVNIVNGNGYYNLYKPDGTYLFTLNCKTGYFVGNGACHADDLDY
Smi     370 ------VQRSASRVAYNQSAIDDSNNSAWDFADGVLEQILATSRSRGYITGNQYILERVNIVNGNGYYNLYKPDGTYLFTLNCKTGYFVGNGACHADDLDY
Sor     387 ------LQRSASRVPYNQSAVDDSNNPAWTFADGVLEQVLATSRARGYITGNQYILERVNIVNGNGYYNLYKPDGTYLFTLNCKTGYFVGNGSCHADDLDY
Ssu     390 ------LQRDRSRVPYNQAMIDDVNNPAWNFNDGILENIVTISQQRGYITGNQYILEKVNIINGNGYYNMFKPDGTYLFSINCKTGYFVGNGACHSDALDY
Sint    386 ------LQRHLSRVPYDQAKINDASNPSWNFNDGVLEKILATSRERGYFAGDDYILEKVNIIKGNGYYNLFRKDGTYLFSINCKTGYFVGNGACYADALDY
Sang    406 ------LQRHLSRVPYDQTKINDSNNPAWNFNDGVLEKILATSRERGYFTGDNYILERVNIINGNGYYNLFRTDGTYLFSINCKTGYFVGNGACYADALDY
Scon    399 ------LQRHLSRVPYDQAKINDASNPSWNFNDGVLEKILATSRERGYFTGDNYILERVNIINGNGYYNLFRTDGTYLFSINCKTGYFVGNGACYADALDY
Ssan    389 ------LQRDLSRVPYNQAAIDDVNNPAWIFNDGVLEKILQTSRERGYISGDNYILERVNIIKGNGYYNLFKPDGTYLFSINCKTGYFVGNGPCHADSLDT
Sgo     374 ------LQRNLSRVPYNQAVIDDVNNPAWVFNDGILEKILKISRERGYITGDQYIIERVNIIKGNGYYNLFKPDGTYLFSINCKTGYFVGNGPCYADSLDY
Ssal    570 ------LQRDRSRVPYNANVVADTSNPAWTWADGVLDKIINESHSRGYFSGDNFILEPVNIINGNGYYNLYLPDGTYLFSINCKTGYYVGNGSCHSDKLDY
Sthe    526 ------LQRDRSRVPYNANVVADTSNPAWTWADGVLDKIIATSHSRGYFSGDNFILEPVNIINGNGYYNMYLPDGTYLFSINCKTGYYVGNGSCHSDKLDY
Smu     452 ------LQRDRSRVPYDQSKIADSNNSAWVFNAGILEKIVAISQQRGYITGNDYILEKVNIINGNGYYNMFKPDGTYLFSINCKTGYFVGNAACHSDKLDY
Sinf    410 ------LQRDKSRVPYNDSAIADSNNPAWTFSDGVLEKIVSTSQARGYFSGNDYILEKVNIINGNGYYNMFRKDGTYLFSINCKTGYFVGNGSCHSDALDY
Sgal    414 ------LQRSLSRVPYSDSAIADSSNSAWTFADGVLDKIVATSQSRGYFSGNDYILEKVNIINGNGYYNMFKADGTYLFSINCKTGYFVGNASCNSDALDY
Spas    416 ------LQRSLSRVPYSDSAIADSSNSAWTFADGVLDKIVATSQSRGYFSGNDYILEKVNIINGNGYYNMFKADGTYLFSINCKTGYFVGNASCNSDALDY
Sag     393 ------LERNRSRVPYNNAAIADTGNPAWIFNDGVLEKIVATSQARGYFSGNNYILEPVNIINGNGYYNMFKLDGTYLFSINAKTGYFVGNAPCRADSLDY
Spub    406 SGNYSGLQRDLSRVPYNSAVIADTTNPAWLFSDGILEKVVATAQARGYISGNNYILEPVNIVNGNGYYNMFKADGTYLFSINCKTGFFVGNAKCHSDGLDY
Seqe    389 ------LQRDLSRVPYNQAMIADTGNPAWAFNDGVLERIVATSQARGYISGNDYILEPVNIINGNGYYNMFKPDGTYLFSINCKTGYFVGNGKCHAEDLDY
Seqz    389 ------LQRDLSRVPYNQAMIADTGNPAWAFNDGVLERIVATSQARGYISGNDYILEPVNIINGNGYYNMFRPDGTYLFSINCKTGYFVGNGKCHAEDLDY
Spy     395 ------LQRHLSRVPYNQDVIADRANPSWAFNDGVLEKIVATSQARGYISGNQYILEPVNIINGNGYYNMFKPDGTYLFSINCKTGYFVGNGKCYADALDY
Sdy     399 ------LQRQLSRVPYNDSLIADSGNPAWAFNDGILEKIVATSQARGYISGNQYILEPVNIINGNGYYNMFKPDGTYLFSINCKTGYFVGNAKCYSDALDY
Sini    391 ------LQRDLSRVPYNNVAIADSGNPAWLINDGVLERIIATSQARGYFTGSNYIIEPVNIINGNGYYNMFKTDGTYLFSINGKTGYFVGNAKCNADALDY
Sub     410 ------IQRNLSRVPYNNAAIADSTNPAWLFNDGVLEKIIATSQARGYFTGNNYYLEPVNIINGNGYYNMFKSDGTYLFSINCKTGYFVGNASCYADGLDY
                 ::*  ***.*.   : *  * :*    *:*.::  :. ***::*.:: :* ***::******::  ******::* ***::***. * :: **:
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