

CLUSTAL O(1.2.4) multiple sequence alignment

RRX₈W

```

AGW18155.1  -----MARSTIGYTPGVWGNQFLSVASGPLMKNKKEE IHQHLQNLKQQL    44
AGW18154.1  -----MGRPTANFSSVWGNQFLSIASGPLLKNKEAE IHQHLQNLKEQV    44
SgSTPS1     -----MGRPTANFSPSVWGNQFLSIASGPLLKNKEAE IHQHLNLKEQV    44
AGW18156.1  MATEVSEHVALSSIQNADRPLVKYVPSIWGDFFLQYASEFMEVD--DNMKQKVGVLKEEV  58
APO20772.1  MSAQVLATVSSS-TEQTVRPIAGFHPNLWGDYFLTASDCKTND--TTHQEEYEALKQEV  57
AIO10965.1  MSPVVSATISQNAKPKVIRKTANFQPSIWGDDQFVTYTSDDAITH--AHKEKQVEELKEEV  58
AGW18157.1  MSVAALAIATSTPSSDVPRRSANYHPSVWGDHFLKYASQPLEVD--EKMEDRIGTLKETV  58
SgSTPS2     MSVAALAIPTSTPSSDVPRRSANYHPSVWGDHFLKYASQPLEVD--ERMEDHIGTLKETV  58
          *      :  .:***: *:  :*      .      ...      **::
    
```

```

AGW18155.1  GRQLK-SVKEP-CEKLNLDITMQLRGLVSYHFQSEIEESLKHHLKHNPPSSWNAKDINSHLL  102
AGW18154.1  RKQLKNGVEEP-SEKLNLDITMQLRGLVSYHFETEIVESLQQLHKNPPSSWDAEDVDAHLL  103
SgSTPS1     RKQLKNGVEEP-SEKLNLDITMQLRGLVSHHFEREIEESLKHHLKHNPPSSWNAEDIDAHLL  103
AGW18156.1  RRMLVSSVNHNFNRKLDIFDISIQLRGLVSYHFQHEIDEALKQIHDSFTNNAIITPSDHDLDH  118
APO20772.1  RSMITATADTP-AQKLQLVDAVQRLGVGYHFEQEIEDALENIFHNSFDNN----DDVDLH  112
AIO10965.1  RRELMTDVDQP-SKQLKFIDAIQLRGVAYHFDREIEEALQHIYDRLDNG----DEDLY  112
AGW18157.1  RKMLVPATDKP-LTKVRLIDS IQLRGVDYHFESEIDEVLCQIQNNYVKDGIIT-LNEDLH  116
SgSTPS2     KKMLVPATDKP-LTKVKLIDS IQLRGVYHFESEIDEVLCQIQNNYVKNGIIT-LDEDLH  116
          :  ..      :: :*:*** **:: ** : * : : ..      : .*
    
```

EDXXD

```

AGW18155.1  GTALWFRLLRQQGYVSCDIFNFKDKDKGDFKTI LIDDVEGMLALYEAHLGIRGEEILD  162
AGW18154.1  SISLWFRLLRQQGYVSCDVFNFKDKDKGVFKTALIDDVEGMLALYEAAYLIRGEEILD  163
SgSTPS1     SISLWFRLLRQQGYVSCDVFDFKDKDKGMFKTTLIDDVEGMLALYEATYLGIRGEEILD  163
AGW18156.1  SIALLFRLLRQQGYHVSSGIFIQYKQNGNFNEKLRNDVRGMLSLEYAAQLRIDGDDILA  178
APO20772.1  TVSLRFRLLRQQGFKVSCDVFDFKDKDEGKFKASLVKEVQGILSLYEAGHLAIRGEDILD  172
AIO10965.1  NVSLWFRLLRQEGYNVSSDILYKFNDEGNFKESLIGDVQGMLGLYEATHLRIHGEDVLD  172
AGW18157.1  SLALLFRLLRQQGYHVSPDVFNFKDEQGKISETIANDVEGMLSLYEAHLRIHGEDILD  176
SgSTPS2     SMSLLFRLLRQQGYHVSPGVFNFKDEQGKISETIANDIEGMLSLEYEAHLRIQGEDILD  176
          :* *****:*: ** ..: :*:***: . . : :*.**.* ** * * : : *
    
```

```

AGW18155.1  QMLEFTMSYLKSRLE-GMT-PYLQERANRALHCP IHKGLRIETRYIPIYSKKDSRNDL  220
AGW18154.1  QVLEFTVFHLKSRLE-GMT-PYLQERVDRALYCPINKGLPRIETRYFISTYSKKDSRNDL  221
SgSTPS1     QVLEFTMFHLKSRLE-GMT-PYLRERADRALYCPINKGLPRIETRYFISMYSKKDSRNDL  221
AGW18156.1  EALDFTSTQLKLLSS-QLG-PSLVTEVEHSLRPLHKTQLRIEARHYMSFYQDDPSHNEI  236
APO20772.1  EAIAFTRTHLQSMVSHDVRPNNLAEQINHALDCPLRRALPRVETRFVSVYPRDDKDKDKT  232
AIO10965.1  EALAFTTIHLESMATSRAS-DPLMAQV IHALKQPIRKGLPRLEAGRFISIQEDGSHNEA  231
AGW18157.1  EALDFTSTHLKFLTT-QLS-DSHAGN VIRSLKRPLRMLPRLEARHYFFTYQEDPSHIET  234
SgSTPS2     EALDFTSTHLKSLTT-QLS-GSLAGEVIRSLKRPLHRRALPRLEAWNYFSTYQEDPSHDKT  234
          : : **  *:      . :*: *:. : *:*: : : * . . : .
    
```

```

AGW18155.1  LLEFAILDFNILQQYQKELSYITKWKYKLDVFSKVPYTRDRIVEGYFWPLATYFEKQCS  280
    
```


AI010965.1	ECYMKQYGASKQEVFDEFNKQVVNAWKDINEEFLRPTD-VPFPLLLRALNFARVMDVLYK	529
AGW18157.1	ECYMKQHGATEEETIVEFRRRVENAWKDINEACLQPFV-VAKPLLMRSLNLSRVISLLYT	532
SgSTPS2	ECYMKQNGATEEETIVEFCRRVENAWKDINEDCLQPFV-VPKPLLMRSLNLSRVIYLLYM	532
	** ::* :*: : : :*: :** :: . : : * *. .	
AGW18155.1	RFVDNYT-IGEGMKDDVAAVFLDPIDIDHNK	548
AGW18154.1	HFVDKYT-NAEMLKDQIASLFDVPIAIELNK	549
SgSTPS1	HFVDKYT-NAEMLKDHIASLFDVPIAIDVNK	549
AGW18156.1	KYQDGYT-KGEFLKKYVDAVIVNPIP-----	560
APO20772.1	KG-DWYTHSH-AIKDQIAAVLRDPVTI-----	555
AI010965.1	DK-DGYTHVGKTKDRIASLLIDPVAI-----	555
AGW18157.1	DD-DCYTRSAGNTKKNIEALLINPVA-----	557
SgSTPS2	DD-DSYTHSSGNTKKNIEALLINPVA-----	557
	* ** * . : : : :*:	

CLUSTAL O(1.2.4) multiple sequence alignment

AGW18158.1	-----	0
SgDTPS1	MSSANFFTLCSNNAIGSLPSSMHPILFSSPLSFSNCYPTSksfngvslfksraipvnssf	60
XP_010277558.1	MPNTTAF--LRLLP--PVP-----VSRTYPSSDPG-AVLSGVCSFATENKRSGFGL	46
OMP05060.1	-----M-TSFFGNWPLRGKDKGENFDI	21
EOX94746.1	-MSSHSIHHPFLS-SSPIPY-----SSISFSNKHPP-IPSAGNRLRWGKDKGENFDI	49
XP_021281194.1	-MSSHSIHQPFLTGFSPIPY-----SSISFSDKHPP-IPFAGNRLRWGKDKGENFDI	50
XP_002302110.1	-----MA-SFSIGVWLYGARGKQDNFHA	22
XP_002520733.1	-MSSQSLHFLST-----A-----SSFSTPNSRPL-LSSGG-GLFGVKDTRITFDV	42
XP_021612241.1	MSTAQSFHLFSTVPATTRSS-----SSFSAIRHRPL-LFS-GVWLHGAKDKRGNVDI	50
XP_012092234.1	-MSSQPFHLLSS--SSSS-----SSFSPIRLRPT-LFSGGVWLYGAKDKQVNFDF	48
AGW18158.1	-----MNYEIQ	6
SgDTPS1	-RIKSATSR--LSAPPSPDISGDKSGLPPFARIEILPSRKV---GEASKVSVINYEQ	113
XP_010277558.1	LRSRRNA--IPRISAHVYTEILQ--NGLPTAEWLETI-KNDRE--GEAPKVS-ISKEIV	97
OMP05060.1	-RPLCSAISKPR--TQEYAGVFQ--NGLPVIKWK-EIVDDDIEQGEEELKVF-EWNTIK	74
EOX94746.1	-RPLCSAISKPR--TQEYAGVFQ--NGLPVIKWK-EIVDDDIEQG--EALKVF-ESNKIK	100
XP_021281194.1	-RPLCSAISKPR--TQEYAGVLQ--NGLPVIKWK-EIVDDDIEEV--EALKVF-ESNKIK	101
XP_002302110.1	-HSRCSAISKPR--TQGYADLFHQQLNGLPLINWPHDVVEDDTEE--DAAKVS-VAKEID	75
XP_002520733.1	-RPRCSALSNPP--TQEYDPVFQRN-GVAVIKRR-EVVEDAIEE--QVTKIS-VSNEIL	93
XP_021612241.1	-RPRCSAISNSR--TQEYPEVFQKN-GAPVIKWH-EIVEDDIEQ--KVSKVS-ISTEII	101
XP_012092234.1	-RPRCAAVSQSQTHTQEYDIVFQKNGGVPVIKWH-EIVEDDIEE--QVPKVK-ISKEIT	102

*

QXXDGGWG

AGW18158.1 MRVDAVKAMWESIEDGWLNISAYDTAWVALVEDINGSGSPQFPSCLOWIVENQLPDGSWG 66
SgDTPS1 MRVDAVKAMWESIEDGWLNISAYDTAWVALVEDINGNSSPQFPSCLOWIVDNQLPDGSWG 173
XP_010277558.1 ERVDSIKAMLSSMEDGEISISAYDTAWVSLVQDILGGGAPQFPSSLWIVDNQLPDGSWG 157
OMP05060.1 ERIDTIKAMLGSMEDGEISSAYDTAWVALIEDVNGSGTPQFPISLEWIANNQLPDGSWG 134
EOX94746.1 ERVGTIKSMLGSMEDGEISSAYDTAWVALVEDVNGGGTPQFPSSLEWIANNQLPDGSWG 160
XP_021281194.1 ERVDTIKSMLGSMEDGEISSAYDTAWAALVEDVNRGGTPQFPSSLEWIANNQLPDGSWG 161
XP_002302110.1 EHVKTIKAMLEMMEDGEISISAYDTAWVALVEDINGSGLPQFPSSLQWIANNQLPDGSWG 135
XP_002520733.1 KRVQNVKSMDSMEDGEISISAYDTAWVALVEDINGSGAPQFPSSLQWIANNQLSDGSWG 153
XP_021612241.1 KRIQSIKSMDSMEDGEISISAYDTAWVALVEDVNGSGAPQFPSSLEWIANNQLSDGSWG 161
XP_012092234.1 ERVDSIKMLESMEDGEITISAYDTAWVALVEDVNGSGAPQFPSSLQWIANNQLPDGSWG 162

:: :* * :*** :. *****.!:!: :. . . ***** . * ** :*** *****

AGW18158.1 DRAVFLSYDRLLSTLACVVALRHWNVHPEKSKRGIEFFKENLERLAKEDPANMSVGFEMI 126
SgDTPS1 DRAVFLSYDRLLSTLACVIALRYWNVHPEKSKRGIEFFKENLERLAEEDPANMPASFEMI 233
XP_010277558.1 DHRIFSAHDRIISTLACVIALKSWNICPRKCDKGVVFIENMSRLESENPEHMSIGFEVA 217
OMP05060.1 DRRIFMAHDRLNLTALCVIALKWDVHPDKCQKGVCFNENISKLEKENAEHMPIGFEVA 194
EOX94746.1 DRQIFMAHDRLINTLACVIALKTWDIHPDKCEKGVFFKENISKLENENAEHMPIGFEVA 220
XP_021281194.1 DRQIFMAHDRLINTLACVVALKTWDVHPDKCEKGVFFKENISKLENENAEHMPIGFEVA 221
XP_002302110.1 DAEIFLAHDRLINTLACVVALKSWNLHQEKCEKGMFFRDNLCKLEDENAEHMPIGFEVA 195
XP_002520733.1 DGDIFTAHDRIINTLACVVALKSWNIHPDKCERGMKYFKENLCKLEDENAEHMPIGFEVA 213
XP_021612241.1 DAEIFTAHDRIINTLACVIALKTWNIHPDKCEKGMKYFKENLCKLEDENAEHMPIGFEVA 221
XP_012092234.1 DADIFTAHDRIINTLACVIALKSWNLHPDKAAKGMKYFKDNLCKLEDENAEHMPIGFEVA 222

* :* :***: :. *****: * : : * : * : : : * : * : * : * : *

AGW18158.1 FPSLIEMARDLNIEVDPNTHPILKQIYAMKNEKLRIPMEVHVHKMPTSLLSLEAMPGL 186
SgDTPS1 FPSLIEMARNFDIEVDPDPSTHPIFKQIYAMKNEKLRIPMEVMHKMPTSLLSLEAMPGL 293
XP_010277558.1 FPSLIEIARKLHLQVPV--DSTMQMISAKRNKLRIPKEMMHIVPTLLHSLEGMPGL 275
OMP05060.1 FPSLLQLARSLNIEVAY--DSPVFQDIYERRSLKLRIPKEIMHKVPTLLHSLEGMPGL 252
EOX94746.1 FPSLLEIARSLNIEVPY--DSPVFQDIYAKRSLKLRIPKEIMYVPTLLHSLEGMPGL 278
XP_021281194.1 FPSLLEIARSLNIEAPY--DSRVFQDIYAKRSLKLRIPKEIMQNVPTLLHSLEGMPGL 279
XP_002302110.1 FPSLLEIAKKL DIEVPY--DSPVLQEIYASRNKLRIPKDIMHNVPTLLHSLEGMPGL 253
XP_002520733.1 FPSLLELAKNLDIEVPE--DSPVLKEIYASRNKLRIPKDIMHKVPTLLHSLEGMPGL 271
XP_021612241.1 FPSLIELARKLDIEVPE--DSPVLQEIYASRNKLRIPKDIMHKVPTLLHSLEGMLGL 279
XP_012092234.1 FPSLIELASKLDIEVPE--DSPVLQQIYASRNKLRIPKDIMHKVPTLLHSLEGMPDL 280

***: : * . . . : . : : * . : . * . : * : : : * : * : * . *

AGW18158.1 QWDKLLKQSENGSFLSPPASTAFALMQTKDKNCLRYLNDVVQKFGAVPNFYIEFFEQ 246
SgDTPS1 QWDKLLKQSENGAFLSPPASTAFVAVMQTKDKNCLRYLNDVVQKFGAVPAFYIDFFEQ 353
XP_010277558.1 DWEKLLKQSPDGSFLSPPASTAFALMQTKDENCLRYLKRVERFNGGVPNVYPVDLFEH 335
OMP05060.1 DWEKLLKQCKDGSFLSPPASTAFALMQTKDENCLSYLNKTVQRFNGGVPNVYPVDMFEH 312
EOX94746.1 DWEKLLKQCQDGSFLSPPASTAFALMQTKDENCLRYLNRTVQRFNGGVPNVYPVDLFEH 338
XP_021281194.1 DWEKLLKQCQDGSFLSPPASTAFALMQTKDENCLRYLNKTVQRFNGGVPNVYPVDLFEH 339
XP_002302110.1 EWKRLKQSQDGSFLSPPASTAFALSQTKDKNCMEYLNKAVQRFEGGVPNVYPVDLFEH 313

XP_002520733.1 EWEKLLKLQCPDGSFLFSPSSTAFALMQTKNENCLAYLNKIVQRFNGGVPNVYPVDLFEH 331
XP_021612241.1 DWEKLLKLQSQDGSFLFSPSSTAYALMQTKDENCLSYLNKIVQRFKGGVPNVYPVDLFEH 339
XP_012092234.1 EWDKLLKLQSQDGSFLFSPSSTAYALMQTKDDNCLAYLNKIVQRFKGGVPNVYPVDLFEH 340

:*.:*****. :*:** **:*:**:*: ***.:.** **: *.:*.**.* * :.:**:

DXDDTAM

AGW18158.1 SWAIDRLTRLGISRYFGGEIKESMNFYKNWKNKTGLGWNRYTCDVPLDDT¹IMAFRLRL 306
SgDTPS1 GWAVDRLTRLGISRYFGGEIKESMDFYHKNWKSTGLSWSRYTCEVPLDDT¹IMALRLRL 413
XP_010277558.1 IWAVDRLERLGISRYFQSEIKECLDYVYRYWTEDEGICWARN-STVHDIDD¹TAMAFRLRL 394
OMP05060.1 IWSVDRLQRLGISRYFQPEIKECLDYIYRYWTEDEGICWARN-TRVHDIDD¹TAMGFRILRL 371
EOX94746.1 IWTVDRLQRLGISRYFQPEIKECLDYVYRYWTEDEAISWARN-TRVQDIDD¹TAMGFRLLRL 397
XP_021281194.1 IWTVDRLQRLGISRYFQPEIKECLDYVYRYWTEDEGISWARN-TRVQDIDD¹TAMGFRLLRL 398
XP_002302110.1 IWAVDRLQRLGISRYFESQIDECVNYIHRYWTEDEGICWARN-SEVHDIDD¹TAMGFRVLRL 372
XP_002520733.1 IWAVDRLQRLGISRYFRKELKECIDYVARYWEEDGICWARN-SAVHDIDD¹TAMGFRLLRL 390
XP_021612241.1 IWAVDRLQRLGISRYFKEELKESINYVARYWREDEGICWARN-SEVHDIDD¹TAMGFRMLRL 398
XP_012092234.1 IWAVDRLQRLGISRFQEELKECIDYVARYWREDEGICWARN-SEVHDIDD¹TAMGFRMLRL 399

*.:**:*: *****:.* :.:*.:.: : * . . : * * * *:*** *.:***

AGW18158.1 HGYPDISCDVLKHFETDGEFFCMVQSSSEAVTAMFNLFRRASQVSPGGEKIMEDAKRFSCEF 366
SgDTPS1 HGYPDISPDVLKHFEDGKFFCFAGQSSSEAVTVMFNLFRRASQVSPGGEKIMEDAKRFSRDF 473
XP_010277558.1 HGHDVSPDAFRHFKEKGGFFCFAGQSNQAITGMFNLYRASQVLPGEKILEEAKTFSRRF 454
OMP05060.1 HGYEVSADVFRHFKEKGGFFCFVQSNQAITGIFNLFRRASQVMFPGDKILEEAKRFSNNF 431
EOX94746.1 HGYEVSADVFRHFKEKGGFFCFVQSNQAVTGIFNLFRRASQVLPFGDKILEEAKRFSKSF 457
XP_021281194.1 HGYEVSADVFRHFKEKGGFFCFVQSNQAVTGIFNLFRRASQVMFPGDKILEEAKRFSKSF 458
XP_002302110.1 NGHHSADVFKHFKEKGGFFCFAGQSTAAVTGMFNLYRASQLLFPGEKILEEAKRFSKSF 432
XP_002520733.1 YGHEVSSDVFKHFKEKGGTFFCFAGQSTQAVTGMFNLYRASQVLPGEKIVLEEAKEYSSSF 450
XP_021612241.1 YGHEVSADVFKHFKEKGGTFFCFAGQSTQAVTGMFNLYRASQVMFPGGEKILEEAKRFSKSF 458
XP_012092234.1 FGHDVSPDVFKHFKEKGGTFFCFAGQSTQAVTGMFNLYRASQVLPGENILEEAKRFSSTF 459

*.:** *.:**:. . ***.:.***. *: * :.:**:*: ***: :.:**.* * : * *

AGW18158.1 LTEKRAANQLGDKWVIAKDIAGEIGFSLDLPWYGILPRIETRFYLDQYGGANDVWIAKVL 426
SgDTPS1 LTEKRAANQLGDKWVMAKDIAGEVGFALDFPWWYGILPRIETRFYLDQYGGANDVWISKGL 533
XP_010277558.1 LSEKQASNQLLDKWIITKDLPEVRYALDIPWYASLPRLEARYYLEQYGGEDDVWIGKTL 514
OMP05060.1 LTEKQASGELFDKWIITKDLPEVGFALKIPWYASLPRVETRFYIEQYGGEDDVWIGKTL 491
EOX94746.1 LTEKQAADELLEDKWIITKDLPEVGFALKIPWYASLPRVETRFYIEQYGGEDDVWIGKTL 517
XP_021281194.1 LTEKQAADELLEDKWIITKDLPEVGFALKIPWYASLPRVETRFYIEQYGGEDDVWIGKTL 518
XP_002302110.1 LREKQAANELLEDKWLITKDLPEVGFALDIPWYASLPRVESRFYIEQYGGEDDVWIGKTL 492
XP_002520733.1 LKEKQANEVLDKWIITKDLPEVKYALDIPWYASLPRVESRFYIEQYGGEDDVWIGKTL 510
XP_021612241.1 LKEKQANEVLDKWIITKDLPEVEYSLDVPWYANLPRVESRFYIEQYGGEDDVWIGKTL 518
XP_012092234.1 LREKQANEVLDKWIITKDLPEVEYALDMPWFANLPRVEARFYIEQYGGEDDVWIGKTL 519

* ***: .: .: *****:***: ***: :.:**.*. ***:**:*:***: :****.* *

AGW18158.1 YRLLRVNNEIYLELGLDYNNCQALHRTEWAALQEWYSEGLDQFGLDRDLLVLFFLAS 486
SgDTPS1 YRVPRVNNIEYVELAKLDYNNCQALHRTEWAALQEWYSEGLDQFGLDTRDLLVLFVFSGI 593
XP_010277558.1 YRMPLVNNVYLELAKLDYNNCQALHQHEWVNLQWYTDNCLGEGVNRGTLQAYVVA 574

OMP05060.1 YRMENVNNNVYLELAKLDYNNCQALHQKEWDSIQKWYSEMNLGDFGVTRRSLLLTYFIAA 551
 EOX94746.1 YRMRYVNNNVYLELAKLDYNNCQALHQMEWNSIQKWYSEMNLGDFGVSRRSLLLYTFMAA 577
 XP_021281194.1 YRMRYVNNNVYLELAKLDYNNCQALHQMEWNSIQKWYSEMNLGDFGVSRRSLLLYTFMAA 578
 XP_002302110.1 YRMPYVNNNEYLQLARLDYNNCQALHRIEWANFQKWYEECNLDFGISRKTLLYSYFLAA 552
 XP_002520733.1 YRMPYVNNNEYLDLAKLDYNNCQALHRKEWDFQKWYEECELGNFVSRRELLLAYFVAA 570
 XP_021612241.1 YRMPYVNNNEYLQLARLDYNSCQALHRIEWDNFQKWYEECSLDFGVSRELLFCYFLAA 578
 XP_012092234.1 YRMPFVNNNEYLELAKIDYNSCQALHRVEWDFQKWYEECNLGAFGVSKRELLYAYMAA 579

: ***: *:*.*:.*:*.**: ** .*:** : * **: ** :. .

AGW18158.1 SSVFEPERARERLAWVKTALMEAITSTYNHQ-----RLRSFVHEFTNATATS----- 535
 SgDTPS1 LKYF----- 597
 XP_010277558.1 ASIFEPERWTERLAWARTAVLVEAVSLEYEKE----DPQRGAFVHDFFSNIGGSSIFSSD 630
 OMP05060.1 ASIFEPERSQERLAWAKTAFLVETIASAFENEMKPTDEQRKAFVQVFRSVIDAR----- 605
 EOX94746.1 ASIFEPERSQERLAWAKTAFLVEAIACSFDNEMRPS-EQRKAFVQVFRSVVDAR----- 630
 XP_021281194.1 ASIFEPERSQERLAWAKTAFLVEAIASSFDNEMRPS-EQRKAFVQVFRSVVDAR----- 631
 XP_002302110.1 ASVFEPERSNERLAWAKTTILLEMIHSYFHEDDDNSGAQRRTFVHEFSTGISIN----- 606
 XP_002520733.1 ASIFEPERSKERLAWAKTTLLHTIESYFDAS-NSTYEQRTAFVHEFKNGVAS----- 622
 XP_021612241.1 ASIFEPERSKERLAWAKTIVLLETIDSYFDEN-NSSIEQRRAFVQEFKNGAEA----- 630
 XP_012092234.1 ASIFEPERSKERVAKTTILLRTIDAYFNDNSNNSVEERKDFVQQFKHGVGAP----- 633

. *

AGW18158.1 -----LRSSKVNERSPGLVNTLMKTLHDISLSTSTAHY----GTLQKMWKKWLLRWESE 585
 SgDTPS1 ----- 597
 XP_010277558.1 NKNKLDKRRWGSKRTAERLVEALLGTLNRLSLDLSLAHQDVLHLRRAWATWLLISLDE 690
 OMP05060.1 -FSHISGRKLNANRTIQKLDILLRNLNHLSDALVAHGRDISSIRRAWEKWMMMWVEE 664
 EOX94746.1 -FSHINGRKLDSNRRVQKLDITLLRNLNHLSDALVAHGRDISCSIRRAWEKWMLMWLEE 689
 XP_021281194.1 -FSHINGRKLDSNRRVQKLDITLLRNLNHLSDALVAHGRDISCSIRRAWEKWMLMWLEE 690
 XP_002302110.1 -----GRRSGTK-TRKELVKMLGTLNQLSFGALEVHGRDISHSLRHAWERWLISWELE 660
 XP_002520733.1 -IPHLNARKLEVK-TNEELVRIAIGILNDVSLDTLLAHGKDI SHDLRHAWEKWLLKWAEG 680
 XP_021612241.1 -RGPVNGRTMEAK-TRQELVRIVLGTLDVSLDALVAHGRDISHSLRHAWQNLLKWEEE 688
 XP_012092234.1 -AGLVNGRKLETK-TRQELVGIVLGTLDVSLDALVAHGTDI SHSLRHAWEKWLTNWEKE 691

AGW18158.1 GD-----DCEGGAELLANMININAGYFLSRKIQ-LNPEYQRLVQLTNQLCHRLQSL 635
 SgDTPS1 ----- 597
 XP_010277558.1 AEEEEEEEDKQQTGREAE LLVRTINLCAGRPLSEELL-CHPHYRRLVQLTNRVCHHLRRF 749
 OMP05060.1 GD-----RQQGVAELVVQTNLSCGRCSLEELL-SHPKYQRLSNLTNSVCHQLSHY 714
 EOX94746.1 GD-----RHQGVAELVVQTNLSSGRWSLEELL-SHPQYERLSSLTNTVCHQLCHY 739
 XP_021281194.1 GD-----RHHGVAELVVQTNLSSGRWSLEELL-SHPQYERLSSLTNTVCHQLCHY 740
 XP_002302110.1 GD-----RRRGEAELVQTIHLTAGYKVSEELLVYHPQYEQADLTNRICYQLGHY 711
 XP_002520733.1 GE-----IHQGTGELLVKTITLTAGGSTP-----DHHKYAQLFQLTDKLCYQLAHY 726
 XP_021612241.1 GD-----RHQGEAELIVKTINLAAGRWISEELLSCHSQYEKLFQLTNRICYQLGHY 739
 XP_012092234.1 GD-----RHQGEAELIVKTINLTGRWVSEELLNYSKYERFFQLTNRICHQLGHH 742

AGW18158.1	QNSKEPASSNNSNK----TGLSDPEIESKMQELVQLVLLN--SSNGIDSNIKKTFLALTK	689
SgDTPS1	-----	597
XP_010277558.1	REWKVNERSSDDPNT---SSITTCEIESDMQELVQCVLR---SSDGIDPAIKQTFLAVAK	803
OMP05060.1	QKQKVQENGHCYNADTD---NIRTQKIDSMDKQLVQLVLASSSSDDGINSINQTFLTVAR	771
EOX94746.1	QKQKVHDNGCYNTDTD---NSRSQKIESDMQQLVQSVLQH--CSDGINPDIKHTFLTVAR	794
XP_021281194.1	QKQKVHDNGCYNTDTG---NSRSQKIESDMQQLVQSVLQH--CSDGINPDIKHTFLTVAR	795
XP_002302110.1	QKNKVHDNGSYSTITGSTRITTPQIESDMQELMQLVIQK--TSDGIDPKIKQTFLQVAK	769
XP_002520733.1	RKNKVQGN-----KKSTTPEIESDMQQLVQLAIQN--SSDEIDSEIKQTFMVAK	774
XP_021612241.1	RKNKVNDN-----KRSTTEIETEMQELMQQVIQN--SSDGMSNIKETFFTVAK	787
XP_012092234.1	SKNKVYDR-----ERSTTPEIESDMQELTQLVLQN--SSDGMSNIKQTFFTVVK	790

AGW18158.1	TFYYAAAYCDSKTIDTHIAKVLFEVFN	715
SgDTPS1	-----	597
XP_010277558.1	SYYYTAHCPPAMINLHIAKVLFEVFN	829
OMP05060.1	SFYAAHCDLDTITFHIKVLFEKVR	797
EOX94746.1	SYYYAAHCDLETMTFHIKVLFEKVR	820
XP_021281194.1	SYYYAAHCDLETITFHIKVLFEKVR	821
XP_002302110.1	SFYTAFCDPGTINYHIKVLFEVFN	795
XP_002520733.1	SFYQAISDPGTLNYHIARVLFERY	800
XP_021612241.1	SFYTAICDPGTINYHISKVLFERY	813
XP_012092234.1	SFYTAVCDPGTINYHISKVLFERY	816

CLUSTAL O(1.2.4) multiple sequence alignment

SgDTPS2	-----MSISRPFILQN-SISPTR	17
SgDTPS3	-----	0
SgDTPS4	-----	0
XP_004488548.1	-----MSLSRFITPLSCISSTSD	18
XP_007149183.1	QNKAPHTTHALHFVRELYIYLPLP--WCLQQHHSFHS--DAMSLRITPLFCSSSTSA	57
KHN21375.1	-----MI-SFLT	6
XP_006585394.1	-----MHFTL-LHTYTCPHFGVCNSSNTIFFHSLDDAMSLSHLTTPLCCT-SSTS	48

SgDTPS2	ASLKPLNVRMKSNTATLLIEESKEKFQKMFKKVELSVSSYDTAWLALIPSPSPDAPFF	77
SgDTPS3	-----MKSNTATLLIEESKEKFQKMFKKVELSVSSYDTAWLALIPSPSPDAPFF	50
SgDTPS4	-----	0
XP_004488548.1	SSMIT-STEKKNKNTTLCFEDTKERVKNMFKVELSISYDTAFVAMIPSSSTSHAPLF	77
XP_007149183.1	DSLVAASYVKEKMESTSWCLADSKERIRKLFNKVELSISYDTAWVAMITSPASPHNPLF	117
KHN21375.1	DSLLTASCVKKMNSTALCHEASKERIRKLFNKVELSVSSYDTAWVAMIPSPASPHNPLF	66
XP_006585394.1	DSLLTASCVKKMNSTALCHEASKERIRKLFNKVELSVSSYDTAWVAMIPSPASPHNPLF	108

QXXDGGWG

SgDTPS2	PECLKWLLKNQLCDGSWGLPDRHPLLMKDTLLSTLACVLALKQWNVGEEHINRGLQFIES	137
SgDTPS3	PECLKWLLKNQLCDGSWGLPDRHPLLMKDTLLSTLACVLALKQWNVGEEHINRGLQFIES	110
SgDTPS4	-----MKDTLLSTLACVLALKQWNVGEEHINRGLQFIES	34
XP_004488548.1	PQCLNWLLDNQLLDGSWGLPGRHPLLTNDALLSTLACILALKQWVGEDKMNKGLFIES	137
XP_007149183.1	PQCVNWLLANQLLDGSWGLPDRHPLLMNDALLSTLACILALKQWVGEDQINRGLFIES	177
KHN21375.1	PQCLNWLLYNQLLDGSWGLPDRHPLLMNDALLSTLASILALKQWVGEDQINRGLRFIQS	126
XP_006585394.1	PQCLNWLLYNQLLDGSWGLPDRHPLLMNDALLSTLASILALKQWVGEDQINRGLRFIQS	168

:*:*****. :*****. **:::*:*. **:*

SgDTPS2	NFASANDEKLQSPIGFDIIFPSLIENAQNLGIILPLQAKILEAVNQKRELELKRCYQSNS	197
SgDTPS3	NFASANDEKLQSPIGFDIIFPSLIENAQNLGIILPLQAKILEAVNQKRELELKRCYQSNS	170
SgDTPS4	NFASANDEKLQSPIGFDIIFPSLIENAQNLGIILPLQAKILEAVNQKRELELKRCYQSNS	94
XP_004488548.1	NFTSINDDKQHHPIGFHILFPSLIEYAQTLGISLPIRSTSLIAMIQRDNELQRGFQSNS	197
XP_007149183.1	NITSIKDEKQHLPIGFGINFPSLIEYAQNLGINLPIGATLLDTMVQNREIELQRGTESNS	237
KHN21375.1	NITSINDENQHPPIGFGLFPSMIEYAQNLGINLPIGATSLEAMIQKREIELHRGSQSNS	186
XP_006585394.1	NITSINDENQHPPIGFGLFPSMIEYAQNLGINLPIGATSLEAMIQKREIELHRGSQSNS	228

: * :*: : **** * **:* ** **.* ** :. *::: *. * : **:* :***

SgDTPS2	EGSRAYLAYISEGIGKSQDWQVMKYQRKNGSLFNSTTAAAFTRLQNADCLKYLQMLL	257
SgDTPS3	EGSRAYLAYISEGIGKSQDWQVMKYQRKNGSLFNSTTAAAFTRLQNADCLKYLQMLL	230
SgDTPS4	EGSRAYLAYISEGIGKSQDWQVMKYQRKNGSLFNSTTAAAFTRLQNADCLKYLQMLL	154
XP_004488548.1	EGWREYLAYLSEGMLKSLDSNTIMKYQRKNGSLFNSTTAAAFQHLKNADCLSYLQSVL	257
XP_007149183.1	EGWRAYQAYVSEGMLDSQDWKTIKIKYQRKNGSLFNSTTAAAFQRLKNAECLGYLQSVL	297
KHN21375.1	DGRRAYLAYVSEGMLDSQDWKSIKIKYQRKNGSLFNSTTAAAFQCHKNAECLGYLQSVL	246
XP_006585394.1	DGRRAYLAYVSEGMLDSQDWKSIKIKYQRKNGSLFNSTTAAAFQCHKNAECLGYLQSVL	288

:* * * **:* : * * : :*****:*****. * :**:* ** * :

SgDTPS2	EKFGNAVPTIYPLDTYARLCMIDSLQRLGIDYHFRKEIQSVLDDTYRHWLHGEEIDFLDP	317
SgDTPS3	EKFGNAVPTIYPLDTYARLCMIDSLQRLGIDYHFRKEIQSVLDDTYRHWLHGEEIDFLDP	290
SgDTPS4	EKFGNAVPTIYPLDTYARLCMIDSLQRLGIDYHFRKEIQSVLDDTYRHWLHGEEIDFLDP	214
XP_004488548.1	EKFGNAVPTVYPLDIYARLYMIDSLERLGINHHFKKEIRSVLDETYRYWLQGEENIFLDP	317
XP_007149183.1	EKFGNAVPTTHPLDIYARLCMIDSLERLGINHHFKKEIRSVLDDTYRFVWQGVEDIFLDP	357
KHN21375.1	EKFENAVPTTYPLDIYARLCMIDSLERLGINHHFKKEIRSVLDEIFRYWMQGVEDIFLDP	306
XP_006585394.1	EKFENAVPTTYPLDIYARLCMIDSLERLGINHHFKKEIRSVLDEIFRYWMQGVEDIFLDP	348

*** ***** :*** ***** *****:*****:*****: **.*:* * :*****

SgDTPS2	TTCAIAFRLRLNGYDVSSEIFDQYTEDKFSNSLKGYLKDVGAILEIYRASQIVTSADES	377
SgDTPS3	TTCAIAFRLRLNGYDVSSEIFDQYTEDKFSNSLKGYLKDVGAILEIYRASQIVTSADES	350
SgDTPS4	TTCAIAFRLRLNGYDVSSEIFDQYTEDKFSNSLKGYLKDVGAILEIYRASQIVTSADES	274
XP_004488548.1	TTCAMAFRLRLNGYDVSSDPFYQYSEDKFSNSLKGYLKDVSAVLELYRASQFI IHPDES	377
XP_007149183.1	TTCAMAFRILRLNGYDVSSDPFYQYSEDKFGDSLKGYLKDVGAILELYRASQTI IHPDES	417
KHN21375.1	TTCAMAFRMLRLNGYDVSSDPFYQYSEDKFAESLKGYLKDVGAILELYRASQAI IHPDES	366
XP_006585394.1	TTCAMAFRMLRLNGYDVSSDPFYQYSEDKFAESLKGYLKDVGAILELYRASQAI IHPDES	408

*****:*****:*****: * **:******. *****:*****: **.*:* * :*****

SgDTPS2 ILVKQNDWTGHLKQDT-TYPGYVDRFRNYIEHEVKDALKFPSYANLERLLNRRSIDHYN 436
 SgDTPS3 ILVKQNDWTGHLKQDT-TYPGYVDRFRNYIEHEVKDALKFPSYANLERLLNRRSIDHYN 409
 SgDTPS4 ILVKQNDWTGHLKQDT-TYPGYVDRFRNYIEHEVKDALKFPSYANLERLLNRRSIDHYN 333
 XP_004488548.1 ILVKQSWTRRLKQDSSPYQLYADKLRIYVDNEVNDILNFPHANLERLLNRRSVEHYN 437
 XP_007149183.1 ILVRQSLWTKQLLKQESSPYRLYADKLRSYVDQEVKDVLSFPHANLERLLNRRSMEYYN 477
 KHN21375.1 ILVRQSLWTKHLLKQESSPYRLYADKLRSYVDLEIKDVLNFPYHANLERLLNRRSMEHYN 426
 XP_006585394.1 ILVRQSLWTKHLLKQESSPYRLYADKLRSYVDLEIKDVLNFPYHANLERLLNRRSMEHYN 468

:* ** :*: * *.*: * *: * : * * .** :*****:***

SgDTPS2 VDNRILKTSYRSYNLGNQEILNLAVEDFNQCQSIHREELKILGRWVVESRLDKLKFARQ 496
 SgDTPS3 VDNRILKTSYRSYNLGNQEILNLAVEDFNQCQSIHREELKILGRWVVESRLDKLKFARQ 469
 SgDTPS4 VDNRILKTSYRSYNLGNQEILNLAVEDFNQCQSIHREELKILGRWVVESRLDKLKFARQ 393
 XP_004488548.1 ADETRILKTSYRSCNLANQEILKLAVEDFNLCQSIHNKELKQLARWIVTSRLDKLEFARQ 497
 XP_007149183.1 VEETRILKSSYRSCNLANQEILKLAADFNICQSIHIEELKQLSRWVVESRLDKLTFARQ 537
 KHN21375.1 TVETRILKASYRSCNLANQEILKLAVEDFNICQAIHIEELKQLSRWVVERRLDTLKFARQ 486
 XP_006585394.1 TVETRILKASYRSCNLANQEILKLAVEDFNICQAIHIEELKQLSRWVVERRLDTLKFARQ 528

. :*****:**** *.*****:*.***** **:** :*** *.**:* ***. * ****

DDXXD

SgDTPS2 KLAYCYFSSSATLYLPELSDARISWAKNGVLTTVVDDFYDVGSEELANLIELFEKWDV 556
 SgDTPS3 KLAYCYFSSSATLYLPELSDARISWAKNGVLTTVVDDFYDVGSEELANLIELFEKWDV 529
 SgDTPS4 KLAYCYFSSSATLYLPELSDARISWAKNGVLTTVVDDFYDVGSEELANLIELFEKWDV 453
 XP_004488548.1 KLAYCYFSSAATLFSPELSDARISWAKNGVLTTVVDDFFDVGSEEEQVNLIQLEKWDV 557
 XP_007149183.1 KLAYCYFSGAATLFSPELSDARISWAKNGVLTTVVDDFYDVGSEKELVDLIQLEKWDV 597
 KHN21375.1 KLAYCYFSCAATIFSPELSDARISWAKSGVLTTVVDDFFDVGSEEEHVNLIQLEKWDV 546
 XP_006585394.1 KLAYCYFSCAATIFSPELSDARISWAKSGVLTTVVDDFFDVGSEEEHVNLIQLEKWDV 588

***** :*:* :*****:*****.*****:***.***.* :*:*.* *****

SgDTPS2 DVNTECCSEQVAIFSAIRSTICEIEEKAFKWQGRSVKNHVINIWLDLIQSMKAEQWLK 616
 SgDTPS3 DVNTECCSEQVAIFSAIRSTICEIEEKAFKWQGRSVKNHVINIWLDLIQSMKAEQWLK 589
 SgDTPS4 DVNTECCSEQVAIFSAIRSTICEIEEKAFKWQGRSVKNHVINIWLDLIQSMKAEQWLK 513
 XP_004488548.1 DVDTVCCSEAVKIFSAVRSTICEIGEKSVERQGRNVKDNVIKIWLNLKSMYTEAEWLR 617
 XP_007149183.1 DINTVCCSETVKIIFSAIHSTVCEIGERSVKRQGRNVKNNVIKIWLDLIQSMYKAEWLR 657
 KHN21375.1 DINTVCCSETVKIIFSAIHSTVCEIGEKSVKQGRNVKNNVIKIWLNLVQSMFREAWEWR 606
 XP_006585394.1 DINTVCCSETVKIIFSAIHSTVCEIGEKSVKQGRNVKNNVIKIWLNLVQSMFREAWEWR 648

: .*** * *****:***:*** *:. : ***.***:***:***:*** **:**

SgDTPS2 SKSVPTIDEYMANAYISFALGPIVLPALYLVGPKLPTTLAENPEFNCLYELMSTGGRLN 676
 SgDTPS3 SKSVPTIDEYMANAYISFALGPIVLPALYLVGPKLPTTLAENPEFNCLYELMSTGGRLN 649
 SgDTPS4 SKSVPTIDEYMANAYISFALGPIVLPALYLVGPKLPTTLAENPEFNCLYELMSTGGRLN 573
 XP_004488548.1 TKT IPTIDDYMQNAYVSFALGPIVLPALYLVGPKLSDDVAENQELDCLFKMTSTCGRLN 677
 XP_007149183.1 TKT VPTIDEYMANAYVSFALGPIVLPALYLVGPKLSDEDAESHELNLHYKLMSTCGRVLN 717
 KHN21375.1 TKT VPTIGDYMANAYISFALGPIVLPALYLVGPKLSDEV TENHELNLHYKLMSTCGRLN 666
 XP_006585394.1 TKT VPTIGDYMANAYISFALGPIVLPALYLVGPKLSDEV TENHELNLHYKLMSTCGRLN 708

:*::***. :** ***:*****:**** *** :*. *:: *:: *** **:**

NSE/DTE

SgDTPS2	DIHSFKRESEEGKLNAGLRLVHGNGAIAAEDVIKEMKGAEDKRRELLRLVLQ-KGSSI	735
SgDTPS3	DIHSFKRESEEGKLNAGLRLVHGNGAIAAEDVIKEMKGAEDKRRELLRLVLQ-KGSSI	708
SgDTPS4	DIHSFKRESEEGKLNAGLRLVHGNGAIAAEDVIKEMKGAEDKRRELLRLVLQ-KGSSI	632
XP_004488548.1	DIHSFKRESEEGKLNAGLRLVHGNGAIAAEDVIKEMKGAEDKRRELLRLVLQ-KGSSI	737
XP_007149183.1	DIHSFKRESEEGKLNAGLRLVHGNGAIAAEDVIKEMKGAEDKRRELLRLVLQ-KGSSI	777
KHN21375.1	DIHSFKRESEEGKLNAGLRLVHGNGAIAAEDVIKEMKGAEDKRRELLRLVLQ-KGSSI	726
XP_006585394.1	DIHSFKRESEEGKLNAGLRLVHGNGAIAAEDVIKEMKGAEDKRRELLRLVLQ-KGSSI	768

*****. :. * :. ****. :***. :::** *:* *****: * :*** :

SgDTPS2	PRACKDLFWKMARVLNLFYIKDDGFTSNEMISIVKALLEEPVVLDDRGAVADVQ-----	789
SgDTPS3	PRACKDLFWKMARVLNLFYIKDDGFTSNEMISIVKALLEEPVVLDDRGAVADVQ-----	762
SgDTPS4	PRACKDLFWKMARVLNLFYIKDDGFTSNEMISIVKALLEEPVVLDDRGAVADVQ-----	686
XP_004488548.1	PRACKDLFWKMARVLNLFYIKDDGFTSNEMISIVKALLEEPVVLDDRGAVADVQ-----	791
XP_007149183.1	PRACKDLFWKMARVLNLFYIKDDGFTSNEMISIVKALLEEPVVLDDRGAVADVQ-----	836
KHN21375.1	PRACKDLFWKMARVLNLFYIKDDGFTSNEMISIVKALLEEPVVLDDRGAVADVQ-----	786
XP_006585394.1	PRACKDLFWKMARVLNLFYIKDDGFTSNEMISIVKALLEEPVVLDDRGAVADVQ-----	828

** ***** :*:***:*****:*** * *:*::..*::: . . :

SgDTPS2	-----	789
SgDTPS3	-----	762
SgDTPS4	-----	686
XP_004488548.1	-----	791
XP_007149183.1	SNVMPQSS	844
KHN21375.1	TNDLML--	792
XP_006585394.1	TNDLML--	834