

File S1

Phosphatase sequences used for the phylogenetic analysis

>AfPphA

MSDLDRAlAQLRACRLIPESEVRELCYKAREILIEEGNVVSDAPVTICGDIHGQFHDLMElFRVGGDVPDTN
YLFMGDFVDRGFYSLESFLLLLCLKVRYPDRI TLIRGNHESRQITTVYGFYDECIRKYGSANVWRYCCEVFDYL
ALGALVLGASSELEPTGSTMNDTTQSTMPIDGAELETEVLNSRGEVTMSTYRRRQRSSSDASTDSRNLSPPR
DISAVPGQAPARSGAPGTGASNGAGSNTSRTGAVLCVHGGLSPLIDTVDKIRLIDRKQEVPEHGAMCDLL
WSDPDEIEGWGLSPRGAGFLFGGDIVKQFNyKNDLSLVARAHQLVMEGYKEMFDGGIVTVWSAPNYCYR
CGNVAAILELGEDTSNGGTVARSNyGRSNyVSGVDSGGSRVSPGRRYRVFEAAAQDTRGMPAKKPV
ADYFL

>PPH3

MMDLDKIIASLRDGKHIPEETVFRlCLNSQELLMNEGNVTQVDTPVTICGDIHGQLHDLLTFEKSGGVEKT
RYIFLGDVDRGFYSLESFLLLLCYKLRYPDRI TLIRGNHETRQITKVYGFYDEVVRKYGNSNVWRYCCEVFDYL
SLGAIINNSIFCVHGGLSPDMTTVDEIR TIDRKQEVPEHGAMCDLLWSDPEDVDTWLSLPRGAGFLFGKREV
DQFLEKNNVELIARAHQLVMEGYKEMFDGGLVTVWSAPNYCYRCGNVA AVLKIDDDL NREY TIFEAVQAQ
NEVGNAIIPTKKSQMDYFL

>PPG1

MELDECLERLYKAQLLPEVTVRALCFKLEMLVKESNVIHIQTPVTVVGD MHGQFHDMLEIFQIGGPVPDT
NYLFLGDYVDRGLYSVETIMLLIVLKLRYPSRIHLLRGNHESRQITQSYGFYTECLNKYGGNSRVWQYLTDIFD
YLVLCIIIDDEIFCVHGGLSPNVQTIDQIKIIDRFREIPHDGAMADLVWSDPEENNNPTLDHPD NSGQHFQV
SPRGAGYTFGRSVVEKFLRMNDMNRIYRAHQLCNEGYQIYFDGLVTTVWSAPNYCYRCGNKASILELYSKD
QFYFNVFEEAPENKLLKENS MNDALEDSISNPVANRKL IADYFEDDSASADGSTDPEMYIFSDVYQARSAS
NRHVDYFL

>AfGlcA

MADQEVLDLNIIDRLLEVRGSRPGKQVQLLEA IRYLCTKAREIFISQPILLELEAPIKICGDIHGQYYDLLRLFY
GGFPPEANYLFLGDYVDRGKQSLETICLLAYKIKYPENFFVLRGNHECASINRIYGFYDECKRRYNIKLWKTFT
DCFNCLPIAAIIDEKIFTMHGGLSPDLNSMEQIRRV MRPTDIPDCGLLCDLLWSDPKDITG WSENRGVSF
TFGPDVVSRLQKHDMDLICRAHQVVEDGYEFFSKRQLVTLFSAPNYCGEFDNAGAMMSVDESLLCSFQIL
KPAEKKQKYVYGGMSSGAPTPPRKPKKK

>GLC7

MDSQPVDVDNIIDRLLEVRGSKPGQVQV DLEENEIRYLCSKARSIFIKQPILLELEAPIKICGDIHGQYYDLLRLFY
YGGFPPESNYLFLGDYVDRGKQSLETICLLAYKIKYPENFFILRGNHECASINRIYGFYDECKRRYNIKLWKTFT
DCFNCLPIAAIIDEKIFCMHGGLSPDLNSMEQIRRV MRPTDIPDVGLLCDLLWSDPKDIVG WSENRGVSF
TFGPDVVNRFLQKQDMELICRAHQVVEDGYEFFSKRQLVTLFSAPNYCGEFDNAGAMMSVDESLLCSFQIL
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>AfSitA

MVDNKIPEPGPAKLKRNAGPDEWLEAAKDCKYLSEQHMKQLCEIVKEYMMEESNIQPVSTPVTICGDIHG
QFYDLLELFRVSGGMPDGSEAEAPKTQSAVITSDDIEPPSTISDPKLRKKLRNTFAPEDGSEDSSASQRDRSS
SGSRDVELKRNRFVFLGDYVDRGYFSLETTLTLLCLKAKYPDRVTLVRGNHESRQITQVYGFYEFCFQKYGNAS
VWKACCQVDFMTLGAIIDGRVLCVHGGLSPEIRTLDQVRVVARAQEIPHEGAFCDLVWSDPDDVETWAV
SPRGAGWLFGDKVADEFCHVNDLTLIARAHQLVNEGYKYHFANQNVVTVWSAPNYCYRCGNLASVCEIG
DDLKPTFKLFSAVSDDQRHVPVSRPGRSEYFL

>SIT4

MVSRGPDEWLETIKKQALTENEMKQLCEMVKELLMEESNIQPVQTPVTVCGDIHGQFHDLLELFRTAGG
FPDDINYIFLGDYVDRGYYSLETFTLLMCLKVYPAKITLVRGNHESRQITQVYGFYEECLNKYGSTTVWKYCC
QVFDFTLAAIIDGKILCVHGGLSPEIRMLDQIRVLSRAQEVPHGEGFSDLLWSDPDNVEAWQVSPRGAGW
LFGSKVAREFNHVNGLNLIARAHQLVMGEGFKYHFPEKDVVTVWSAPNYCYRCGNVASVMKVDEDEDLEPTFK
IFSAVPDDYIRESTANHNNQRAGYFL

>AfPpzA

MGQSHSKGNSGPGDSLQSYPSFSRSDTKESLRSRSGSIRSKIRSSDSPRGSTAGLSDDKSDAASVKSTTSRRSS
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ILIKRENQLNPILDFIMNAPLETSGSPGMGMGALKSIDLDDMISRLLDAGYSTKVTKTVCLKNAEIMAICSA
RELFLSQPALLELSAPVKIVGDVHGQYTDLIRLFEMCGFPPASNYLFLGDYVDRGKQSLETILLLLCYKLKYPEN
FFLLRGNHECANVTRVYGFYDECKRRCNIKIWKTFIDTFNCLPIAATVAGKIFCVHGGLSPLSHMDDIRGIAR
PTDVPDYGLLNDLLWSDPADMEEDWEPNERGVSYCFGKKVIMNFLQRHDFDLVCRAHMVVEDGYEFYQ
DRILVTVFSAPNYCGEFDNWGAIMSVSGELLCSFELLKPLDSTALKNHKGRKERNMMLSSPVPPLLRV
AKEDHNLVQHRRDACGLFLAYPSLVTSWGISR

>PPZ1

MGNSSSKSSKKDSHSNSSSRNRPQVSRTESSHVKSASKNKSSRSRSLPSSSTTNTNSNVPDPSTPSKPNL
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TNNSTHVSKHKSSYSSTYYENALTDNDDNDKNDISHTKRFSRSSNSRPSSIRSGSVSRKSDVTHEEPNNG
SYSSNNQENYLVQALTRSNSHASSLSRKSFGSDGNTAYSTPLNSPGLSKLTDHSGEYFTSNSTSSLNHSS
RDIYPSKHISNDDDIENSSQLSNIHASMENVNDKNNITDSKDPNEEFNDIMQSSGNKNAPKKFKPIDID
ETIQKLLDAGYAAKRTKNVCLKNNEILQICIKAREIFLSQPSLLELSPVKIVGDVHGQYGDLLRFLTKCGFPPSS
NYLFLGDYVDRGKQSLETILLFCYKIKYPENFFLLRGNHECANVTRVYGFYDECKRRCNIKIWKTFIDTFNTP
LAAIVAGKIFCVHGGLSPVLNSMDEIRHVVRPTDVPDFGLINDLLWSDPTDSPNEWEDNERGVSYCYNKVAI
NKFLNKFGFDLVCRAHMVVEDGYEFFNDRSLVTVFSAPNYCGEFDNWGAVMSVSEGLLCSFELLPLDSAA
LKQVMKKGRQERKLANQQQMMETSITNDNESQQ

>AfPphB

MENNMEIDPARSPEPHHLSPTTDPGSIPTLDGWIEINLMACKQLAEDDVRRLCDRAREVLQEESNVQPVKC
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TQVYGFYDECLRKYGNANVWKYFTDLFDYLPLTALIENQIFCLHGGLSPSIDTLDNIRSLDRIQEVPHGPMC
DLLWSDPDDRCGWGISPRGAGYTFGQDISEAFNHNNGLTLVARAHQLVMEGYNWSQDRNVVTIFSAPNY
CYRCGNQAAIMEIDEHLKYTFLQFDPCPRAGEPMVSRRTPDYFL

>PPH21

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DQWIEHLSKCEPLSEDDVARLCKMAVDVLQFEENVKPINVPVTICGDVHGQFHDLELFKIGGPCPDTNYLF
MGDYVDRGYYSVETVSYLVAMKVRYPHRITILRGNHESRQITQVYGFYDECLRKYGSANVWKMFTDLFDYF
PITALVDNKIFCLHGGLSPMIETIDQVRELNRIQEVPHGPMCDLLWSDPDDRGGWGISPRGAGFTFGQDV
SEQFNHTNDLSLIARAHQLVMEGYAWSHQQNVVTIFSAPNYCYRCGNQAAIMEVDENHNRQFLQYDPSV
RPGEPSVSRKTPDYFL

>AfPptA

MAASDLEAATALKVQGNKAFAHEWPTAVEFYTQAIDKYDREPSFFSNRAQAYIKLEAYGFAIADATKALEL
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DIDAIAVDSSYDGVRLKEMTQEFIDDMIERFKNGKKIHRKYAFQIIKAVKDIVYAeptMVEIGVEEGTKLTVc
GDTHGQFFDLLNIFNINGYPSETHAYLFGDFVDRGSWSTEIALLLYAYKWLRPNRIFLNRGNHETDDMNK
VYGFEGECKAKYNERLFKVFSESFSALPLATLIGSKYLVLHGGLFSDDKVTLDDIRKLNHRNQRPQGQGLM
MEMLWTDQPTEPGRGPKRGVGLQFGPDVTKRCEKNGLEAIIRSHEVRMEGYEVEHDGRCITVFSAPKY
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>PPT1

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CQTLNLSSFDANADLANYESGPKLEFEQLYDDKNAFKGAKIKNMSQEFISKMVNDLFLKGKYLPKKYVAAIISH
ADTLFRQEPSMVELENNSTPDVKISVCGDTHGQFYDVLNLFKFKGKVGPKHTYLFNGDFVDRGSWSCEVAL
LFYCLKILHPNFFLNRRGNHESDNMNKIYGFEDCEKYKYSQRIFNMFAQSFESLPLATLINNDYLVMHGGLPS
DPSATLSDFKNIDRFAQPPRDGAFMELLWADPQEANGMGPSQRGLGHAFGPDITDRFLRNNKLRKIFRSH
ELRMGGVQFEQKGLMTVFSAPNYCDSQGNLGGVIHVVPGHGILQAGRNDQNLIIETFEAVEHPDIKPM
AYSNGGFGL

>AfCaIA

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DRGYFSIECVLYLWALKIWYPNSLWLLRGNHECRHLTDYFTFKLECKHKYSERIYEACIESFCALPLAAVMNK
QFLCIHGGLSPELHTLEDIKSIDRFREPPTHGLMCDILWADPLEEFQEKTDGYFVHNSVRGCSYFFSYAAC
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PHPYWLPNFMDVFTWVSLPFVGEKITDMLIAILNNTCSKEELEDPTSVSPSAPSPLPMDVESSEFKRRAIKN
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RSEEERRAALERAQQEADNDTGLATVARRISMSAGSGRSRRQRDAARETREA

>CMP2

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FDLLKLFVGGDPATTSYLFLGDYVDRGSFSFECLIIYLSLKNFNDFHWLLRGNHECKHLTSYFTFKNEMLHK
YNLDIYEKCCESFNNLPLAALMNGQYLCVHGGISPELNSLQDINNLRNFREIPSHGLMCDLLWADPIEEYDEV
LDKDLTEEDIVNSKTMVPHHGKMAPSRDMFV PNSVRGCSYAFTYRAACHFLQETGLLSIIRAHEAQDAGYR
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KVTEMLVAILNICTEDELNDTPVIEELVGTDKKLPQAGKSEATPQPATSASPKNHASILDDEHRRKALRNKILA
VAKVSRMYSVLREETNKVQFLKDHNSGVLPRGALSNGVKGLDEALSTFERARKHDLINELKPPSLDELKNEN
KYYYEKVWQKVHEHDAKNDK

>AfPtcA

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LVPDIPNYQTEGRTRIAQIIAKAQALSVDMLLTPLEYVHYFPESDDVFDPIEMVNMMDPTNDRSPGELRRLWF
RIKLAYTPVTYIRANFEESNTELVRSEVLLMPENTFVALPKRHQNTNSAVSANSRVPKRPEFHDFVFTLLPS
SSLHPDPRGLSSSYHKFPRSASVPHTGAISHPPTSFAQALVDRETTVRIPLRRAKHHFGAATSRGTRVSNEDT
HQAGVLDIPAFAKRPPASVTIKRTTAPLENRGADSASGDPQVYFVGFVFDGHGGSECSTFLKDTLHEYIQDTA
AESEFQSSLSKDRGHFSKNESEICRGDLPIIQRGNHHRMAEMEKTLVQNWRRLVGGYFKRFVPAHFSYRG
NSAQNGSATGNGDDHTGGVTIEEILEYAFRADLDFVSAQAAKEDDELATAHKPQYQDDILYGPKHTQQ
MKLGGYRRFKGGSTASVALISTPSPFPWHPSAPSSLLVSHVGDTRILLCSTATGAAIPLTSNHHPSPIEANR
LRRYAATFVTDSFGSEERMSGLANTRAFGDVQSKRIGVSAEPEIRRIEMGPAEYSFLVLMTDGISGTLTDQEV
VDIIEAKTPDEGARNVNFATEVTKEGDNATCLVVRLGGWERRLEGGLSLGTESREWRRQEATDPRSS
RR

>PTC6

MRLGNAYAYCKPSQNVGLKLDLLRGLPGYVGHATSINRLENQDNYSIKMMRSPNAYGSALNCSVFDG
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DPNAPIDEGKDDDSWIISHSGLLKLIVTQVGDSKIILCDQDIAHALTTTHHINSRERHRLSIDPSRLDPDAFG
ETRFLNNFANTRSFVDVAGKPYGISSEPDIFFLVGNTLHLPRSESKLPFNGDECFLALVTDGITNKLADQEV
VDLITSTVNSWGLKKATPQFVAEETIKFIQAIATKHSNATCVVRLSNWGNWPNVDRTGPQRETKLMNA
QSNETKLN

>AfPtcB

MRTCSTSEGGQDECCLYGLSAMQGWRISEMEDAHAVALDLQAKSTGGSEKPTDPDKRLAFFGVYDGHGG
DKVALFAGENVHKIVAKQEAFAKGDIEQALKDGFATDRAILEDPKYEEVSGCTAAVSVISKNKIWVANAG
DSRSVLGVKGRAKPLSFDHKPQNEGEKARISAAGGFVDFGRVNGNLALSRAIGDFEFKKSPELSPEQQIVTA
YPDVTVHEVTDDDEFVLIACDGIWDCQSSQSVVEFVRRGIAAKQELYRICENMMDNCLASNSETGGVGC
NMTMIIIGLLNGKTKEEWYNQISERVANGDGPCAPPEYKSEFRGPGIRNQFEETPDNYDLENDRSRGSV

RSGRIILLGDGTELIPEQNDEELFDQREENRDVTNHLQHDKAEETSTAANLSESPSSANKNSSGSGTEATEKS
ASS

>PTC2

MGQILSNPVIDKESHSGADSLTAFGLCAMQGW RMSMEDSHILEPNVLT KSDKDHIAFYGIFDGHGGAKVA
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TVLATDGNAKALS YDHKPTLASEKSRIVAADGFVEMDRVNGNLALSRAIGDFEFKSNPKLGPEEQIVTCVPDI
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ALLKEGEDVAQWSDRMKSKAHR TSVRSFADKRRRVFSYDFSKCNDEQVFAITTKK PQDKFTRDHEAAVAS
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AQLLQTMGHDPASSHPENDSNTD HKAGRSHLQ

>AfPpmA

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VGLEDGQVELANLGD SGSM LRLAAVHHYSVPQTHGFNTPYQLSIIPRMRAQASIFGGSFLEDSPRDAVV
TNLHMQHGDVLM LATDGVYDNLNNQDILKLITSRMILTGAWTATDLGIKVSDNLGALTGPDGLASLLPW
PSPSPKPSAADPSTSGNVAPSSRINQHHTLQSLLASTVAGEAKRASMDSRRDGPFAKEAQRYYPGDWYRG
GKVDDICVLIIVAVEEGRGHESC

>PTC7

MFANVGFRTL RVSRGPLY GSCSQIISFSKR TFYSSAKSGYQSNNSHGDAYSSGSQSGPFTYKTAVAFQPKDR
DDL IYQKLKDSIRSPTGEDNYFVTSNNVHDIFAGVADGVGGWAEHGYDSSAISRELCKMDEISTALAENSS
KETLLTPKKIIGAAYAKIRDEKVVKVGTTAIVAHFPSNGKLEVANLGD SWCGVFRDSKLVFQTKFQTVGFNA
PYQLSIPEEMLKEAERRGSKYILNTPRDADEYSFQLKKKDIILATDGVTDNIATDDIELFLKD NAARTNDELQL
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>AfPtcD

MGPLSSSASGD KLALKDAGGNSALGSRPSQQDQYTILLPAQIPFKTEKTLFLGVYDGHVTS DVSLSHAKQHF
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EHYPNGWEVQRITKAHKPGSDTEKERIKEAGGVNRELGSPRIAAGALNMSRALGDLQYKAPLINADEPFSL
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TTEATGGPMSDNATCICAFIYGRQAA

>AfPtcE

MFRNTILSTSDALLLFDAGAGQVQGARPFEQEDRCTFVLPDQFPSQTNDKLT YFAVYDGHGSELVSDHASRN
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AERDNRDHP SHIRRLSKSHKPDTPDEKSRIEDAGGAVNTRRG TARLGLSNMSRALGDLQYKNPINNAGDE

YSSSKTRRASASTSAPETRGNFLSVEPHMTRMTLSPDRRYLVVVTSDGVSDNIDDATLIHHVMRLSMRGMR
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>PTC3

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LSTGGNSKAMSFDPKPTLLSEKSRIVAADGFVEMDRVNGNLALSRAIGDFEFKSNTKLGPHQVVTCPDII
CHNLNYDEDEFVILACDGIWDCLTSQECVDLVHYGISQGNMTLSDISSRIVDVCCSPTTEGSGIGCDNMSISI
VALLKENESESQWFERMRSKNYNIQTSFVQRRKSIFDFHDFSDDDNEVFAITTKKLQDRLNRSKDNDDMEI
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>AfPtcF

MRRALQTFRTARRVPVWVKVGARRPSVVSFSHNHQPLGLRLSSRGRHPSFIPATLQSSMHLRNFLAVISTV
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DSDRRILEMLTPEQATQKLRNEQSFMVNRGKGVVRYDVVQVPSNSPIEDDHAEKIVEPSSVAAAANDGG
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HSSVDKVLKSNRRAAAELLAPALSGSCALLAFYDSQSKDLKACAGDSRAVLGRRGPTGKWTATPLSEDT
GGTPSEMKRLEEHGEPNVVRNGRILGQLEPSRSGDAFYKWSKETQEIKKQFFGRTPHLLKTPPYVTA
EPVITTTKIEPSKGFVVMATDGLWEMLSNEEVVGLVGQWIDQQRAGNNGTSKAWLQSWFGLDDKHL
VEAPKETTTEGQRRPIRQQYDISGVASRFVVEDKNAATHLVRNAMGGKDRDMVCALLTLPSPYSRRYRD
DITVEVIFFGDGPDRNRTITVNQEASASEENQKAKL

>PTC5

MSPLTRTVAIKKTVKVLKQCSGREYTKFLQRAYSTSHANSTYYSRTKLFISHSKALNIALLSGSLLLTYSYYS
PKKILSLDTINGIKDYSTNTSGNINMPSPNPKGTETQKSQRSQNDQSVLILNDSKIEAKLHDREESHVNRGT
GIFRYDVAQLPSNHPIEDDHVEQIITIPIESEDGKSIEKDLYFFGIFDGHGGPFTSEKLSKDLVRYVAYQLGQVY
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KNMNLAPVKAEPGKLPKVIDVSEDKEAQRPAFRYKDNSSSPSGSNPEYLIEDKNVATHLIRNALSAGGRKE
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>AfPtcG

MFGSSSPPKDKLETIPHSEAITPSLTVKTDATVSQKKFSPPSGFFGRRASDEPSPGGEKKRRSSTVTKAATL
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RCRRTMEDTHAYLYNFGTAPSGRADVNGRRQSGDVSPSAAEETS SVVETDNGYFAIFDGHAGTFAAECW
GKKLHLILEEVMRKNPNTVPPELLDQFTSVDQQLKPLKNSGCTAVIALLRWEDRVPCSHSVTGSAALAP
AAVAAAAEPNSEADNTPTQSAPVSVLPTLQEKASRQRVLYTANVGDARIILCRNGKALRLSYDHKGSDENE

GKRIANAGGLILNRRVNGVLAVTRALGDAYLKDLVTGHPYTTETVIQPDQDEFIILACDGLWDVCSQAEAV
DLIRNIQDAQEASKMLVDHALARFSTDNLSCMVIRFDNNRVKEVVNRAVDPIGVDGDPVTHVGYGVSEAD
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>PTC1

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KHLHTIIEQNILADETRDVRDVLNDSFLAIDEEINTKLVGNSGCTAAVCVLRWELPDSVSDDSMDLAQHQRK
LYTANVGDSRIVLFRNGSIRLTYDHKASDTLEMQRVEQAGGLIMKSRVNGMLAVTRSLGDKFFDSLTVGS
PFTTSVEITSEDKFLILACDGLWDVIDDQDACELIKDITEPNEAAKVLVRYALENGTTDNVTVMVVFL

>AfPtcH

MRVSGSRKVAQHAKRHISELLFEGDALQAGRFEAIRQAIQKEETLLEECQEGEDKFAISGSTVSVVIVNLN
NGVMVHRLTQDHPENPKEKERIEDAGGVVNYASETARIGALNMSRALGDLQYKNPLNNDTMGPSTAGQ
EIAAMTPSIEQGSFVSSEPSIIRVDLRQDRRYILALTTDGVTVLKDVIINEIKTRHEGGLGVQQVADELVRG
VTQGERRDNATCIAVFLDGCLS

>PTC4

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RSFNTLEGLVSQIFKDAFILQDEELRHFANSSCGSTAVVACIINEESLYVANCGDSRCILSSKSNGIKTMSFDH
KPQHIGELIRINDNGGTVSLGRVGGVLALSRAFSDQFKRGVTPHRRKLTNITQNLTYGTPPQEAQVTVPE
DVLMLKIDYSKDEFLVLACDGIWDIYNNKQLIHFIKYHLVSGTKLDTIITKLLDHGIAQANSNTGVGFDNMTA
IIVVLNRKGETLQDWFNKMKTRLERERGLV

>AfNemA

MNSLNILSSRVIGQTSNSNRLRQRSRSQGEIGPVAPPEDRSKLSYSHDNLHSPDVLEKSHNNAPGISSADID
YSEHTLTKSPLIQSIQRDGPLATRSTLGLIAERFFDAIAETIKFILSTLAAPGVFLAQCFRDDDQYSPMAPVR
KLRRSMASVSASRRSTS AKKEPKPTGARRRSGSTRKLRSHVSRDSIASSTSESEGDRRSTQCLTSTRARPVSKS
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>NEM1

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>AfFcpA

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>FCP1

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>AfPsrA

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>PSR1

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>AfPpsA

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>PPS1

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MKYT

>AfDspC

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>YVH1

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NR

>AfDspD

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>MSG5

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>AfCdcA

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>CDC14

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>AfDspA

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>AfPtpB

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>PTP1

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EKCYQYWPRGGVDDTVRIASKWESPGGANDMTQFP SDLKIEFVNVHKVKDYTVTDIKLTPDPLVGPVKT
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>AfPypA

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>PTP3

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>AfLtpA)

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>LTP1

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>AfSsuA

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WTLAWL

>SSU72

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>AfCdcA

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>MIH1

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>AfYphA

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>AfPtyA

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>PTP2

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