

144 phage proteins located in host cell (PH proteins)

>hostc|P51769|ANTIH_

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>hostc|P13304|ANTIH_

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>hostc|P68572|BDBB_B

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>hostc|O64038|BHLB_B

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>hostc|P82889|CAPSD_

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>hostc|P15416|CAPSD_

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>hostc|P03621|CAPSD_

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>hostc|P68674|CAPSD_

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>hostc|P03639|E_BPPH

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>hostc|P15418|G1P_BP

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EG

>hostc|O55247|G1P_BP

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>hostc|Q37972|G3P_BP
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>hostc|Q9XJJ6|SPAN1_

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>hostc|P03668|VG430_

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>hostc|P03701|VLOM_L

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>hostc|Q38008|VLYS_B

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>hostc|Q9ZXD8|VLYS_B

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>hostcc|Q9T1W1|CAPSD

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>hostcc|P03708|TERL_

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VEPTIRDIPSLLALAPWYGKKHRDNTLTMKRFTNGRGFWCLGGKAAKNYREKSVDVAGY
DELAADFDDIEQEGSPTFLGDKRIEGSVWPKSIRGSTPKVVRGTCQIERAASESPHFMRFHV
ACPHCGEEQYLKFGDKETPFGLKWTDPDPSSVFYLCEHNACVIRQQELDFTDARYICEKT
GIWTRDGILWFSSSGEEIEPPDSVTFHIWTAYSPFTTWVQIVKDWMTKGDGTGKRKTFVN
TTLGETWEAKIGERPDAEVMAERKEHYSAPVPDRVAYLTAGIDSQLDRYEMRVWGWGPG
EESWLIDRQIIMGRHDEQTLRLVDEAINKTYTRRNGAEMSISRICWDTGGIDPTIVYERSK
KHGLFRVIPIKGASVYGKPVASMPKRKNKNGVYLTEIGTDTAKEQIYNRFTLTPEGDEPLP
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>hostcc|Q9T1W6|TERL_

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TPARDIPVLRFEAPDDFESLTPQMRHGIVQDWCEQELLPLLDALSPLNKHVLGEDFARRGD
LTVFVPLAITPDLRKRECFRVELRNVTYDQQRQILLFILSRLPRFTGAAF DATNGGYLAE
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HQFERGGW

>hostcc|P03732|TERP_
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DLTYVITYEM

>hostcc|Q9T1W7|TERS_
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>hostcc|P03707|TERS_
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>hostcc|P03749|TIPJ_
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LYVIGQYCDQSVDPDGFGGTEPRITCNAYLTTQRKA WDLVLSDFCSAMRCMPVWNGQTLTF
VQDRPSDKTWTYNRSNVMPDDGAPFRYSFSALKDRHNAVEVNWIDPNNGWETATELV
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DVIEICDDDYAGISTGGRVLAVNSQTRTLTLDREITLPSSGTALISLVDGSGNPVSVEVQSVT
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DNGAHFDGEQSGTVNGVTPPAVQHLTA EVTADS GEYQVLARWDT PKVVKGV SFLLR LTV
TADDGSERLVSTARTTETTYRFTQLALGN YRLTVRAVNAWGQQGDPASVSFRIAAPAAPSR
IELTPGYFQITATPHLAVYDPTVQFEFWFSEKQIADIRQVETSTRYLGTALYWIAASINIKPG
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SRLEEF SKWKDASDKWNAMWAVKIEQTKDGKHYVAGIGLSMEDTEEGKLSQFLVAANR
IAFIDPANGNETPMFVAQGNQIFMNDVFLKRLTAPTITSGGNPPAFSLTPDGKLTAKNADISG
SVNANSGLT LSNVTIAENCTINGTLRAEKIVGDIVKAASAAFP RQRESSVDWPSGTRT VTVT
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>hostcc|P03729|TIPK_
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>hostcc|Q9T1V6|TMP_B
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LSEQSKGAQASAMNSWDGMFAQMEANLLEFRIKVANS GPFEEIKNEMRRVLNWHDMAD

KSGELDALAENIGQKFLTTFRTVKISAQELWRWLKPGKDALAWVDQNIVSLKKLA AVLVS
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LLQGIGIQRVFVINWPRGFGDYGSGGRRVRSGGRMAPLLPRQPLLLSGPQPLALPAPRPV
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NKLAGSAIGRVVTKGAGALGWMGKGAGRALSRLGGPVMGALQLAPVLMDEQASTHEK
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>hostcc|P03736|TMP_L

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ITLPMVGATSLAVATGALAYAWYQGNSTLSDFNKTLLVLSGNQAGLTADRMLVLSRAGQAA
GLTFNQTSESLSALVKAGVSGEAQIASISQSVARFSSASGVEVDKVAEAFGKLTDPDTSGLT
AMARQFHNVS AEQIAYVAQLQRS GDEAGALQA ANEAATKGFDDQTRRLKENMGTL ETW
ADRTARAFKSMWDAVLDIGRPDTAQEMLIKAEAA YKKADDIWNLRKDDYFVNDEARAR
YWDREKARLAL EAARKKAEQQTQQDKNAQQQSDTEASRLKYTEEAQKAYERLQTPLE
KYTARQEELNKAL KDGKILQADYNTLMAAAKDY EATLKKPKQSSVKVSAGDRQEDSA
HAALLTLQAE LRTLEKHAGANEKISQRRDLWKAESQFAVLEEAAQRRQLSAQEKSLLAH
KDETLEYKRQLAALGDKVTYQERLNALAQQADKFAQQQRAKRAAIDAKSRGLTDRQAE
REATEQRLKEQY GDNPLALNNVMSEQKKTWAAEDQLRGNWMAGL KSGWSEWEESATD
SMSQVKSAAATQTFD GIAQNMAAMLTGSEQNWR SFTRSVLSMMTEILLKQAMVGIVGSIG
SAIGGAVGGGASASGGT AIQAAA AKFH FATGGFTGTGGKYEPAGIVHRGEFVFTKEATSRI
GVGNLYRLMRGYATGGYVGT PGMADSR SQASGTFEQNNHV VINNDGTNGQIGPAALKA
VYDMARKGARDEIQTQMRDGGGLFSGGGR

>hostcc|P07636|TNPA_

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DEMLNQGISTKTAFATVAGHYQVSASTLRDKYYQVQKFAKPDWAAALVDGRGASRRNV
HKSEFDED AWQFLIADYLRPEKPAFRKCYERLELAAREHGW SIPS RATAFRRIQQLDEAM
VVACREGEHALMHLIPAQQRTVEHLDAMQWINGDGYLHN VFVRWFNGDVIRPKTWFQ
DVKTRKILGWRC DVSENIDSIRLSFMDVVTRYGIPEDFHITIDNTRGAANKWLTGGAPNRY
RFKVKEDDPKGLFLLMGAKMHWTSV VAGKGWGQAKPVERAFGVGGLEEYVDKHPALA
GAYTGPNPQAKPDNYGDRAVDAELFLKTLAEGVAMFNARTGRETEMCGGKLSFDDVFER
EYARTIVRKPTTEE QKRMLLLPAEAVNVSRKGEFTLKVGGSLKGAKNVYYNMALMNAGV
KKVVVRFDPQQLHSTVYCYTLDGRFICEAECLAPVAFNDAAAGREYRRRQKQLKSATKA
AIKAQKQMDALEVAELLPQIAEPAAPESRIVGIFRPSGNTERVKNQERDDEYETERDEYLN
HSLDILEQNRKKAI

>hostcc|Q9T1V8|TRP_B

MLEETE AALLARVRELF GATLRQVEPLTGTWTNEDVHRLFLAPPSVFLAWMGCGEGRTR
REVESRWAFFVVAELLNGEPVNRPGIYQIVERLIAGVNGQTFGPTTGMRLTQVRNLCDDN
RINAGVVLYGVLFSGTTP LPSVVDLDSLDDYERHWQTWKFPDETPEFAAHINVNQEKDH
DAEN

>hostcc|P79678|TSP_B

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YIAGQRLAVSVAAGATGAALADLLVARIKQPDLPVTAEVRADSGDDDDTHADVLSAKFT
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YAATLCAVASQALSIDPARPLQTLPLGRMPPAVGDRFTWSERNALLFDGISTFNVNDGGE
MQIERMITMYRTNKYGSDPSYLVNVTIATLSYLRYSLRTRITQKFPNYKLASDGTRFATG
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>hostcc|P79679|TUBE_

MAGNQRQGVAFIRVNGMELESMEGASFTPSGITREEVTGSRVYGWKGKPRAAKVECKIP
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>hostcc|P03733|TUBE_

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VDVFRGWVSSIGKAVTAKEVITRTVKVTNVGRPSMAEDRSTVTAATGMTVTPASTSVVKG
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VAEITVTAS

>hostcc|P0DJY5|U2_BP

MMHLKNITAGNPKTKEQYQLTKQFNKWLTYEDGKNWYEEQKNFQPDTLKMVYDHNG
VIICIEKDVSAINPEGANVVEVPDITANRRADISGKWMFKDGVVIKRTYTEEEQRQQAENE
KQSLQLVRDKTQLWDSQLRLGIISDENKQKLEWMLYAQKVESTDTSSLPVTFPEQPE

>hostcc|P17313|VG31_

MSEVQQLPIRAVGEYVILVSEPAQAGDEEVTESGLIIGKRVQGEVPELVCVHVSVPDVPEG
FCEVGDLTSLPVGQIRNVPHPFVALGLKQPKEIKQKFVTCHYKAIPCLYK

>hostcc|Q9ZX29|WHIB_

MHMHMGGDPSAICAQTDPELWFPDKGQSTRDAKRMCMRCPLLDECALALRDPHLVGV
WGGLSAQERRRIRKGASA

134 phage proteins not located in host cell (non-PH proteins)

>n|P16009|VG05_BPT4

MEMISNNLNWFVGVVEDRMDPLKLGRVVRVVGHLHPPQRAQGDVMGIPTEKLPWMSVI
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GQYPRRLGNDTNVLNQGGEVGYDSSSNVIQDSNLDTAINPDDRPLSEIPTDDNPNMSMAE
MLRRDEGLRLKVYWDTEGYPTIGIHLIMKQPVRDMAQINKVLSKQVGREITGNPGSITM
EEATTLFERDLADMQRDIKSHSKVGPVWQAVNRSRQMALENMAFQMGVGGVAKFNTML
TAMLAGDWEKAYKAGRDSLWYQQTGKRASRVTMILTGNLESYGVEVKTPARSLSAMAA
TVAKSSDPADPPIPNDSRILFKEPVSSYKGEYPYVHTMETESGHIQEFDDTPGQERYRLVHP
TGTYEEVSPSGRRTRKTVDNLYDITNADGNFLVAGDKKTNVGGSEIYYNMDNRLHQIDGS
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>n|P15879|ARC3_CBDP

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PENIMLFRGDDPAYLGTEFQNTLLNSNGTINKTAFEKAKAKFLNKDRLEYGYISTSLMNVS
QFAGRPIITKFKVAKGSKAGYIDPISAFAGQLEMLLPRHSTYHIDDMRLSSDGKQIITATM
MGTAINPK

>n|P09386|STXB_BP933

MKKMFMAVLFALASVNAMAADCAKKGIEFSKYNEDDTFTVKVDGKEYWTSRWNLQPL
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>n|P22535|CAPSD_BPPR

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VNTAKQGAPFLSSMVTDSPIKYGDVMNVIDAPATIAAGATGELTMYWVPLAYSETDLTG
AVLANVPQSKQRLKLEFANNNTAFAAVGANPLEAIYQGAGAADCEFEEISYTVYQSYLDQ
LPVGQNGYILPLIDLSTLYNLENSAQAGLTPNVDFVQYANLYRYLSTIAVFDNGGSFNAG
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VVNPKTVNQARLLMGYEYFTSRTELVNAGTISTT

>n|P11124|RDRP_BPPH6

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SERDNLFRAAVRLMFSDELPEVPLKIRKGSSTCIPYFSNDMGTKIEIAERALEKAEEAGNL
MLQGKFDDAYQLHQMGGAYYVVYRAQSTDAITLDPKTGKFVSKDRMVADFEYAVTGGE
QGSFAASKDASRLKEQYGIDVPDGFCCERRRTAMGGPFALNAPIMAVAQPVRNKIYSKYA
YTFHHTTRLNKEEKVKEWSLCVATDVSDHDTFWPGWLRDLICDELLNMGYAPWWWKLF
ETSLKLPVYVGAPEQGHLLGDPSNPDLVGLSSGQATDLMGTLLMSITYLVMQLDH
TAPHLNSRIKDMPSACRFLDSYWQGHEEIRQISKSDDAILGWTKGRALVGGHRLFEMLKE
GKVNPSPYMKISYEHGGAFLGDILLYDSRREPGSAIFVGNINSMLNNQFSPEYGVQSGVRD
RSKRKRPFPGLAWASMKDITYGACPIYSDVLEAIERCWWNAFGESYRAYREDMLKRDITLE
LSRYVASMARQAGLAELTPIDLEVLADPNKLYKWTEADV SANIHEVLMHGVSVKTER
FLRSVMPR

>n|P04535|CAPSH_BPT4

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VFALRAVYKDPVAAGAKEAFHPMYGPDAMFSGQGAACKFPALAASTQTTVGDYIYTHFF
QETGTVYLQASVQVTIDAGATDAAKLDAEIKKQMEAGALVEIAEGMATSIAELQEGFNFS
TDNPWNEMGFRIDKQVIEAKSRQLKAAYSIELAQDLRAVHGMDADAELSGILATEIMLEI
NREVVWDWINYSAQVGKSGMTLTPGSKAGVDFDQDPIDIRGARWAGESFKALLFQIDKEAV
EIARQTGRGEGNFIIASRNVVNLASVDTGISYAAQGLATGFSTDTTKSVFAGVLGGKYRV
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>n|P10929|BP11_BPT4

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FVAKVRVALQEAIASFTAINSYKDHPDGSKLEVITYLDNQKHVLSYSTYGITISQEIISESK
PGYGTWNLGAQTVTLDNQQTPTVYHFERTA

>n|P17172|BP27_BPT4

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IHTKMDGNEIIQISVANANDINNVKTRIYGCKHFSVSVDSKGDNIIAIELGTIHSIENLKFR
PFFPDAGESIKEMLGVIYQDRLLTPAINAINAYVPDIPWTSTFENYLSYVREVALAVGSDK
FVFWQDIMGVNMMDYDMMINQEPYPMIVGEP SLIGQFIQELKYPLAYDFVWLT KSNPH
KRDP MNATIYAHSFLDSSIPMITTGKGENSIVVSRSGAYSEM TYRNGYEEAIRLQTMAQY
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TIDPVKVKNEFKSDTTTEESSSSNKQ

>n|P10930|FIB12_BPT4

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LNNAFETR VSTESSNGVIKISSLPQALAGADDTTAMT PLKTQQLAIK LIAQIAPSETTATESD
QGVVQLATVAQVRQGT LREGY AISP YTFMNSSSTEEYKGVIKLGTQSEVNSNNASVAVTG
ATLN GRGSTTSMRGVVKLT TTAGS QSGDASSALAWNADVIQQRGGQIYGTLRIEDTFTI
ANGGANITGTVRMTGGYIQGNRIVTQNEIDRTIPVGA IMMWAADSLPSDAWRFC HGGTVS
ASDCPLYASRIGTRYGGNPSNPGLPDMRGLFVRGSGRGS HLTNPNVNGNDQFGK PRLGVG
CTGGYVGEVQIQMSYHKHAGGFGEHDDLGA FGNTRRSNFV GTRKGLDWDNRSYFTN
DGYEIDPESQRNSKYTLNRPELIGNETRPWNISLNYI IKVKE

>n|P09385|STXA_BP933

MKCILFKWVLC LLLGFSSVSY SREFTIDFSTQSSYVSSLNSIRTEISTPLEHISQGTTSVSVIN
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TVSMTT DSSYTTLQRVAALERSGMQISRHSLVSSYLALMEFSGNTMTRDASRAVLR FVTV
TAEALRFRQIQREFRQALSETAPVYTMTPGDVDLTLNWGRISNVLPEYRGEDGVRVGRISF
NNISAILGT VAVILNCHHQGARSVRAVNEESQPECQITGDRPVIKINNTLWESNTAA AFLNR
KSQFLYTTGK

>n|P13332|TSP_BPT4 T

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VSDDIETEGKITEVDADGKIKKINIPTGKNYAKAKEVGEYPTLGSNWTAEISSSSSGLAAVI
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DVQLFIAGSCAGESLETASTVQKHVVSIGDARQDCLVLCSPPRETVVGIPVTRAVDNLVN
WRTAAGSYTDN NFNISSTYAAIDGNHKYQYDKYNDVNRWVPLAADIAGLCARTDNVSQT
WMSPAGYNRGQILNVIKLA IETRQAQRDRLYQEAINPVTGTGGDGYVLYGDKTATSVPSP
FDRINVRRLFNMLKTNIGRSSKYRLFELNNAFTRSSFR TETAQYLQGNKALGGIYEYRVVC
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>n|P10104|WAC_BPT4 F

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DSILADIGPFNAEANSVYRTIRNDLLWIKRELGYTGQDINGLPVVG NPSSGMK HRIINNT
DVITSQ GIRLSELETKFIESDVGSLTIEVGNLREELGPKPPSFSQNVYSRLNEIDTKQTTVES
DISAIKTSIGYPGNNSIITSVNTNTDN IASINLELNQSGGIKQRLTVIETSIGSDDIPSSIKGQIK
DNTTSIESLNGIVGENTSSGLRANVSWLNQIVGTDSSGGQPSPPG SLLNRVSTIETSVSGLN
NAVQNLQVEIGNNSAGIKGQVVALNTLVNGTNPNGSTVEERGLTNSIKANETNIASVTQEV
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>n|P11125|P4_BPPH6 P

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ALMGATGSGKSITLNEKLRPDVLRWGEVAEAYDELDTAVHISTLDEMLIVCIGLGALGFN
VAVDSVRPLLFRKGAASAGGIVAVFYSLTLDISNLTQYDCSVVMVVNPMVDAEKIEYVF
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>n|P22536|P5_BPPRD S

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GIKGDKGDGPAGPAGGTVVVEDSGASFGESLLDTTSEPGKILVKRISGGSGITVTDYGDQ
VEIEASGGGGGGGGVTDALSLMYSTSTGGPASIAANALDFDLGALTVNSVGTGLTKSA
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>n|P49861|COAT_BPHK7

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IPGIIMPGLRRLTIRDLLAQGRTSSNALEYVREEVFTNNADVVAEKALKPESDITFSKQTAN
VKTIAHWVQASRQVMDDAPMLQSYINNRLMYGLALKEEGQLLNGDGTGDNLEGLNKVA
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>n|P03612|COAT_BPMS2

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>n|P27378|P2_BPPRD A

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ADPETCPAQPTTDKVIIRTTDLNPEGSPCAYEAGIILVRQTSNPMNAVAGRLVPYVEDIAVDI
FLTGKFFTLNPLRITNNYFADDEVKENTVTIGNYTTTLSSAYYAVYKTDGYGGATCFIASG
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RQLEAINPQDGPQYDLFILDDSGAYASFSSFIGYPEAAYVAGAATFMDVENPDEIIFILRN
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>n|P12528|TSPE_BPP22

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YSVKLSDYPTLQDAASAAMDGLLIDRDYNFYGGGETVDFGGKVLTIIECKAKFIGDGNLIFTK
LGKGSRIAGVFMESTTTPWVIKWTDDNQLWLDAAAVVATLKQSKTDGYQPTVSDYVKF
PGIETLLPNAKQNTSTLEIRECIGVEVHRASGLMAGFLFRGCHFCKMVDANNPSGGKD
GIITFENLSGDWGGKGNVIGGRTSYGSVSSAQFLRNNGGFERDGGVIGFTSYRAGESGVK

TWQGTVGSTTSRNYNLQFRDSVVIYPVWDGFDLGADTDMNPELDRPGDYPTQYPLHQL
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GNIRANSFGYDSAAIKLRIHKLSKTLDSGALYSHINGGAGSGSAYTQLTAISGSTPDAVSLK
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>n|P35837|VG26_BPP2

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LDGRVTTAENNISALQADYVSKTATTSQSLASPLNVTTSSVGGKKVLGARQTGWTAATG
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>n|P03681|TERM_BPPH2

MARSPRIRIKDNDKAEYARLVKNTKAKIARTKKKYGVDLTAEIDIPDLDSFETRAQFNKW
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GGKPGQTIEQRIAMTSPAHTGINRPHDFDFSKVRSYRLRTLEESMEMRTDPQYYEKKMI
QLQLNFIKSVESFN SFDAADELIEELKKIPPDDFYELFLRISEISFEEDSEGN TVENVEGN
VYKILSYLEQYRRGDFDLSLKG F

>n|P15132|VG13_BPPH2

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YIKSTKTPRELAMIFLASYERPANPNQPERGDQAEYWYKNLSGGGGGGLQLAQFPMDIINI
SQGENGSFSHKGTLCIDFVGKTEKYPYAPCDCTCVWRGDASAYLAWTSDKEVMCADG
SVRYITWVNVHESPLPFDVGKKLKKGDLMGHTGIGGNVTGDHWHFNVIDGKEYQGWTK
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>n|P31281|G_BPAL3 Ma

MYQNFVTKHDTAIQTSRFSVTGNVIPAAPTGNIPVINGGSITAERAVVNLNANMNVSTSSD
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LK

>n|P08767|VGF_BPAL3

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PKFLHQSYLNIYNNYFRAPWMPERTEANPSNLNEDDARYRFRCCHLKNIWSAPLPPETKL
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TDFWASGYDVDGTDQSSLGQFSGRVQQTFKHSVPRFFVPEHGVMMLLALIRFPPISPLEHH
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PTVRDSIMTS

>n|P19060|BP06_BPT4

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IIYDKNIDRNQVKLYVDGAEWINWTRKSMVHAGSTSTIYYMRETIDGNTEFYFGEGEISV
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DFVGADGGGDPEDIERIRELGTIKRETQQRCVTATDYDTFVSERFGSIIQAVQTFTDSTKPG
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PEAGIKYNNQIKDRSMESNTFSFNSSGRKVVNPDTGLEEDVLYDVRIVSTDRDSKIGKVII
GPFASGDVTENENIQPYTGNDFNKLANSDGRDKYYVIGEINYPADVYWNIAKINLTSEKF
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>n|P19062|BP08_BPT4

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ATESGAGWLVRCLDVPDTGMCSIASLTDKDECLKLGKWTSPARSMTPEGRGDAEGTI
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>n|P13331|VG03_BPT4

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>n|P10927|VG09_BPT4

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QAIDSIKGVSGNLVVTSPYSKVTLCISSDNSTSVWNYSIESMFGQKESPAEGTWNISTSGS
VDIPLFHRTEYNMAKLLVTCQSV DGRKIKTAEINILVDTVNSEVISSEYAVMRVGNETEED
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>n|P11112|VG15_BPT4

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RYEDDMFQIVEQILPYFQPHFNTTMYEQFGNDIPFKRDIKIVLMSAAIDEAIDGDNLSRRI
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>n|P27380|VP07_BPPRD

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>n|P13559|VLYS_BPPRD

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>n|P19896|CAPSP_BPT4

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LYRMVCEMVSHIQKESTYTATFCVASARAAAAILAASGWLKHKPEDDKYLSQNAYGFLAN
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>n|P18056|HOC_BPT4 H

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>n|P36275|VSHP_BPP21

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>n|P03715|VSOC_BPT4

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>n|P68660|W_LAMBD He

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RRGPAGFYV

>n|P10928|BP10_BPT4

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AVPVEINVRFSDELVYCAPGRWEYVKNKQIDKITSSDISNVARKEFLVEVQGGTDFLDVF
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PNSLEVRFNGLQELAGTVGMPLFHCVGADSDDEVECSVLGGTWEQSHTDYSVETDENG
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>n|P13336|BP28_BPT4

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>n|P04538|GP68_BPT4

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AQRKRKKALKRRKALGLS

>n|P06807|PCPP_BPT4

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>n|P13333|VG19_BPT4

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>n|P04534|VG22_BPT4

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ELFVEHNVVVPEESVDVVAEMEEELQEHKEESPRLFEELNMRDAYINYVQREVALSESTK
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>n|P03744|VG37_BPT4

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QLGQSAYIDAECTDAVRPAGAGSFASQNNEDVRAPFYMNIIDRTDASAYVPILKQRYVQGN
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GNITGGSGNFANLNSTIESLKTDMSSYPIGAPIWPSPDSVPAGFALMEGQTFDKSAYPKLA
VAYPSGVIPDMRGQTIKKGPSGRAVLSAEADGVKAHSHSASASSTDLGTTSSFDYGTK
GTNSTGGHTHSGSGSTSTNGEHSHYIEAWNGTGVGGNKMSSYAISYRAGGSNTNAAGNH
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>n|P11126|P1_BPPH6 M

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GLGQRRERVRILKPTVAHAIIQMWYSWFVEDDRTLAAARRTSRDDAEKLAIDGRRMQNA
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>n|Q9XJR6|P3_BPPM2 P

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>n|P27392|VP16_BPPRD

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>n|P15794|CAPSD_BPPM

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AAAGPKLSAIAQKSVGTAPSWLTMRRNFFKQLNNGTTEIADLPRVGYRIAAIHIKAAGV
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>n|P19061|BP07_BPT4

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FIQEKFTLNNSDYVNFNNDTIMAALMNESFQFSPSYVDVSSISNFIIGENEYHEIQGSIQQV
CKDINRVYLMESGILYLFERYQPVVKVSNDKGQTKAVKLFNDRVGYPLSKTVYYQSA
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QPGYANMSTDGKLVSLSSNFKFLSDNVNDPETAACYQLIGAVKYEFPREWLADKHYH
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IDYINRSRSYYVMKIKSNLPSRWKSDVIRFVHPVGFVGFIAITLLTMFINVGLTLKHTETIIN
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>n|Q9XJR1|P6_BPPM2 P

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AASGVEL

>n|P54309|PORTL_BPSP

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>n|P27391|VP30_BPPRD

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>n|P03726|GP16_BPT7

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>n|P03710|PORTL_LAMB

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PVEDGQTRGANVFYSVMEQMMLDTLQNTQLQSAIVKAMYAATIESELDTQSAMDFILG
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SLLRYIAAGLGVSYEQLSRNYAQMSYSTARASANESWAYFMGRRKFVASRQASQMFLCW
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>n|P26747|VG05_BPP22

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>n|P04332|VG10_BPPH2

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>n|Q37979|AEPE_BPA50

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>n|P32762|ALYS_BPHB3

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>n|P03748|FIBER_BPT7

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SATASANSAHLAEQQADRAEREADKLENYNGLAGAIDKVDGTNVYWKGNIHANGRLYM
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>n|P03728|GP8_BPT7 H

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>n|Q9XJR3|SPIKE_BPPM

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>n|P09009|TERM_BPPRD

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>n|Q9XJP3|TSPE_BPSFV

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>n|P03610|VASS_BPMS2

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>n|P03725|GP15_BPT7

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>n|P68570|BDBA_BPSPB

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>n|P11128|FUS_BPPH6

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>n|Q37958|P4_BPPM2 P

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>n|P27382|VP11_BPPRD

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>n|P27388|VP22_BPPRD

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>n|P07579|P8_BPPH6 M

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>n|P11129|P3_BPPH6 S

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>n|P13339|BP48_BPT4

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>n|P13302|PI3_BPT4

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>n|P11111|NECK2_BPT4

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SINP
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VVNNRG
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>n|P11110|NECK1_BPT4

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>n|P13341|VG54_BPT4

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>n|Q38646|GP19_BPMU

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>n|P27381|VP09_BPPRD

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>n|P85500|COAT_BPPAJ

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WGAA

>n|P19193|H_BPCHP Mi

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GGLASGLLSYRAAKKQNKVMQDIANRQMAFQERMSSTAVRRHVEDLKKAGLNPL
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>n|P07582|LYS_BPPH6

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>n|P11123|P7_BPPH6 A

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>n|P15240|SAK_BPP42

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>n|P0DJY8|SPEA_BPT12

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>n|P85502|STRU2_BPPA

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>n|P27390|VP34_BPPRD

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>n|P27379|VP06_BPPRD

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>n|P03630|COAT_BPPP7

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>n|P03616|COAT_BPPRR

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>n|P20344|VG85_BPPH2

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>n|P25477|VPN_BPP2 C

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YQDFQLRIRNAIIKRQSLDFIMAGFNGVKRAETS DRSSNPMLQDVAVGWLQKYRNEAPAR
VMSKV TDEEGRTTSEVIRV GKGGDYASLDALVMDATNNLIEPWYQEDPDLV VIVGRQLLA
DKYFPIVNKEQDNSEMLAADVIISQKRIGNLPAVRVPYFPADAMLITKLENLSIYYMDDSH
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>n|Q04765|VSP1_BPLLH

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DNNVNQ SLLSTNAGKNPALRVYQDIINKSTLAVTTGLKTPQE AIFDNIDDWVKTGLPTTLI
DKGGHKWSLEGYTRTVITTTTLRTYNDVRMQSLKDYSQTLAIMTSHPAARHACAPIQ GK
VVNTVDHGDPRFNPKYPTIYDYGYGTPAGTLGINCMHQLYPYVEGVTINRQKH YDEQEAI
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>n|Q37976|AEPE_BPA18

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NPHLQFN YKGYGTDTFGKGASTSNSSKPSADTNTNSLGLVDYMNLNKLDSSFANRKKLA
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>n|Q38653|ALYS_BPA51

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>n|P03746|TUBE1_BPT7

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>n|P03751|GP73_BPT7

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>n|P51772|VPX_BPP2 T

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>n|P09677|VA1_BPSP R

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>n|P68578|SUNA_BPSPB

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>n|P09676|VASS_BPSP

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>n|Q9XJR2|P5_BPPM2 P

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>n|Q9XJR8|P7_BPPM2 P

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>n|Q9XJR5|P8_BPPM2 P

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>n|Q38623|VG20_BPMU

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>n|Q9XJR9|P9_BPPM2 P

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>n|P68650|HEAD_BPP21

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>n|P26596|MCP_BPF41

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GKKVPAIEYEIWGEQAKDFVKKMESGLFIMQPDTVLAGAITLVAPVIPNVTTATKGNNDGT
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HS

>n|P51720|VPN_BPHC1

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>n|P03647|VGH_BPG4 M

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>n|P85501|STRU1_BPPA

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>n|P85503|STRU3_BPPA

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>n|Q04764|VG20_BPMV4

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>n|P42548|YO13_BPL2

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>n|Q38362|VG23_BPMD2

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>n|P03724|GP14_BPT7

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>n|O48449|GP171_BPSP

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>n|Q9T1S4|HEAD_BPAPS

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>n|P85991|IGLVP_BPSK

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>n|D6RRG1|ORF4_BPKPP

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EKSELVYAHMQDEAYTGGVVGDVIAICSPEFFSKLISHPTVVEAYKYASQPQILRERLRA
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>n|P85988|TAILC_BPSK

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>n|P03747|TUBE2_BPT7

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>n|P85225|VPN1_BPPHE

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>n|P85227|VPN3_BPPHE

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>n|P85229|VPN5_BPPHE

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>n|P85228|VPN4_BPPHE

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RFKLG VY NVFLADEPFVYGDKTE

>n|P85230|VPN6_BPPHE

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>n|A8E283|VPN7_BPPHE

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>n|P19728|VC10B_BPT3

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>n|P85993|TAILA_BPSK

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EQKVGYPRLGVPVMTDQEVTAQLRVIAKQLRAFSYSYCDGCETIAEAKTYREQFAERE
GMLIWPNFIAYNVSVGENEFPVAYALGLRAKIDNEQGWKSLSNVAVSNVLGITKDVFW
ALQAEDSDANELNANEVTTLIKRDGFRFWGNRTTDKDEYIFEVYTRTAQILADTIAEAQFT
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VPPLDLTMIQTFDQYYEAAFASLGGA

>n|P11130|P13_BPPH6

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>n|Q04755|COAT_BPMV4

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RDKVAVQKLFDSAAKKATDSITKDNALDAYDTAEAYMFDNEVPGGFVMFVSSAYYTALK
QSAAVTRTFSTDGTMAINGIDRRVAQLDGGVPIVRVSSDRLKGLGITDHVNFILTPLSAIAPI
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>n|Q9G055|H_BPPHM Mi

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NLREEKKPNQMPLKNGKLN

>n|D6RRG7|ORF10_BPKP

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>n|P85987|CAPSD_BPSK

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KRDNEGIFLLKDRAGDAGSATKPRLTASFGSLIDASMKKTADLDEATLFEMTAKLYTEGA
DPTLIMYHPSNANFFASLQEKSGTRMRIFENDKRFVKQVEYIVDPLGQELKCIPNRWCPED
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GGGESVKS

>n|P85992|TAILF_BPSK

MATVNEFRGAMSRGGGVQRQHRWRVTISFPSFAASADQTRDVCLLAVTTNTPTGQLGEIL

VPWGGRELFPFGDRRFEALPITFINVVNNGPYNSMEVWQQYINGSESNRASANPDEYFRD
VVLELLDANDNVTKTWTLQGAWPQNLGQLELDMSAMDSYTQFTCDLRYFQAVSDRSR