

Phage virion proteins

>VIR|P82889|CAPSD_BP

MDFNPSEVASQVTNYIQAIAAAGVGVLALAIGLSAAWKYAKRFLKG

>VIR|P03619|CAPSD_BP

MKKSVVAKIAGSTLVIGSSAFAADDATSQAKAAFDSLTAQATEMSGYAWALVVLVVGATV
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>VIR|P03620|CAPSD_BP

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>VIR|P03621|CAPSD_BP

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>VIR|P03623|CAPSD_BP

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>VIR|P15794|CAPSD_BP

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AAAGPKLSAIAQKSVGTAAPSWLTMRRNFFKQLNNGTTEIADLPRVGYRIAAIHIKAAGV
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>VIR|P22535|CAPSD_BP

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VNTAKQGAPFLSSMVTDSPIKYGDVMNVIDAPATIAAGATGELTMYYWVPLAYSETDLTG
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>VIR|P85987|CAPSD_BP

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KRDNEGIFLLKDRAGDAGSATKPRLTASFGSLIDASMKKTADLDEATLFEMTAKLYTEGA
DPTLIMYHPSNANFFASLQEKSGTRMRIFENDKRFVKQVEYIVDPLGQELKCIPNRWCPED
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GGGESVKS

>VIR|P85989|CAPSD_BP

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FIRTMNFTAVRFKKFGTNGVVDVAADVSGRWALEKWYLVFMLEVEANGVVDTRRGK
ANRVL CSPNVASALAMAGMLDYSPALNVQAQLAVDPTGQTFAGVLSNGMRVYIDPYAVA
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>VIR|P03622|CAPSD_BP

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>VIR|P03614|COAT_BPF

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>VIR|P49861|COAT_BPH

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>VIR|Q04754|COAT_BPL

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>VIR|P85500|COAT_BPP

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PLTKDFFERKTLEPLKVANIAVATMEVIRDSSPSADVIIRDQLAAALRERLDIDFIDPAKAAV
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>VIR|P03630|COAT_BPP

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VPLGR

>VIR|P03616|COAT_BPP

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>VIR|P04535|COAT_BPT

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TDNPWNEMGFRIDKQVIEAKSRQLKAAYSIELAQDLRAVHGMDADAELS GILATEIMLEI
NREVVDWINYSAQVGKSGMTLTPGSKAGVDFDQDPIDIRGARWAGESFKALLFQIDKEAV
EIARQTGRGEGNFIIASRN VVNLASVDTGISYAAQGLATGFSTDTTKSVFAGVLGGKYRV
YIDQYAKQDYFTVGYKGNEMDAGIYYAPYVALTPLRGS DPKNFQPVMGFKTRYGIGINP
FAESAAQAPASRIQSGMPSILNSLGKNAYFRRVYVKGI

>VIR|P11128|FUS_BPPH

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>VIR|P19192|F_BPCHP

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>VIR|P03661|G3P_BPFD

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SGGGSGGGSEG GGGSEG GGGSEG GGGSGGGSGGDFDY EKMANANKGAMTENADE
NALQSDAKGKLD SVATDYGA AIDGFIGDV SGLANGNGATGDFAGS NSQMAQVGDGDN SP
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ANILRNKES

>VIR|O80297|G3P_BPIF

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SIPANVVKSDSIGSQFSLYTNASCTMCSGYLSN NADSIAIANITETVKADYNQPD MWFEQ
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>VIR|P03663|G3P_BPIK

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SSSAWKPTGYVPESGEPSSSPLKDGDGTGGTGEGGSDTGGDTGGGDTGGGSGTGGDTGGSS
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>VIR|P69532|G6P_BPM1

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>VIR|P69535|G7P_BPM1

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>VIR|P69538|G9P_BPM1

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>VIR|P31281|G_BPAL3

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LK

>VIR|P03644|G_BPG4 M

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>VIR|Q9T1S4|HEAD_BPA

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LAHFMMNNGALSLSGSPNTAIKKWADVAQTASFIDIGIKTGENYAIMDPWSAQRLADAQS
GLHAADQLVRTAWENAQISGNFGGIRALMSNGLASRKQGDFDGAITVKTAPNVLYLSVK
DSYQFTVALTGATPSKTGFLKAGDQLKFTSTHWLNQQSKQTLYNGSTAMSFTATVLEETN
STASGDVTVKLSGVPIYDEKNSQYNAVDKVKAGDAVSIIGTAKQMKPNLFYNKFFCGL
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P

>VIR|P19193|H_BPCHP

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GSASTPQGAFYSPVNPMEGLNSAISVADKVFYDQRLAHADFGRLNSAMSVVQLASAV
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>VIR|P03646|H_BPPHX

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RDYLAAPPELNAWERAGADASSAGMVDAGFENQKELTKMQLDNQKEIAEMQNETQKE
IAGIQSATSQRNTKDQVYAQNEMLAYQQKESTARVASIMENTNLSKQQQVSEIMRQMLTQ
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>VIR|P85991|IGLVP_BP

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VEWSSSDEAKAKSLGNGVFDLKAAGTGIIVSATSIDGGVIGEAELETTAAVVAVTGVTLSPK
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>VIR|P69592|J_BPPHX

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>VIR|P07582|LYS_BPPH

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>VIR|P26596|MCP_BPF4

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GRRDKVVTGEFVDGYRVVYPNLTPTAEATKESETDSVDGVDPIQWTLAVQATESDIYLN
G GKKVPAIEYEWGEQAKDFVKKMESGLFIMQPDTVLGAILVAVVIPNVTTATKGNNDGT
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HS

>VIR|D6RRG7|ORF10_BP

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>VIR|D6RRG1|ORF4_BPK

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EKSELVYAHMQDEAYTGGVVDVIAICSPFFSKLISHPTVVEAYKYYASQPQILRERLRA
RGFDARYREFYFGNVLYIEYRGGFQGRPGGEKRRYVPAGEAVFIPGSGTEDLTKTFFAPAS
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>VIR|P11130|P13_BPPH

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ATTLAARGL

>VIR|P11126|P1_BPPH6

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AVGKVPPTAILEQLRTLAPSEHELFFHITDFVCHVLSPLGFILPDAAYVYRVGRTATYPNFY
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NSNGAEMTLGFPSVVERDYALDRDPMVAIAALRTGIVDESLEARASNDLKRSMFNYYAAV
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NKPIQPSEVLQAKVLDLANHTTSIHIWPWHEASTEFAYEDAYSVTIRNKRYTAEVKEFELL

GLGQRRERVRILKPTVAHAIQMWYSWFVEDDRTLAAARRTSRDDAEKLAIDGRRMQNA
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>VIR|P27378|P2_BPPRD

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>VIR|P11129|P3_BPPH6

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>VIR|Q9XJR6|P3_BPPM2

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>VIR|P11125|P4_BPPH6

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ALMGATGSGKSITLNEKLRPDVLRWGEVAEAYDELDTAVHISTLDEMLIVCIGLGALGFN
VAVDSVRPLLFRKGAASAGGIVAVFYSLTDISNFTQYDCSVVMVNVNPMVDAEKIEYVF
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>VIR|Q37958|P4_BPPM2

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>VIR|Q9XJR2|P5_BPPM2

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>VIR|P22536|P5_BPPRD

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>VIR|Q9XJR1|P6_BPPM2

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AASGVEL

>VIR|P11123|P7_BPPH6

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>VIR|Q9XJR8|P7_BPPM2

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>VIR|P07579|P8_BPPH6

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>VIR|Q9XJR5|P8_BPPM2

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IVGAVVIGLFLVIKRR

>VIR|Q9XJR9|P9_BPPM2

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KASPHWGQLSRKGRKYGVQLYVATQSPQEIDKTIVRQC�FKFCGALNSASAWRSMADNL
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>VIR|P11124|RDRP_BP

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SERDNLFRAAVRLMFSLEPVPLKIRKGSSTCIPYFSNDMGTKIEIAERALEKAEEAGNL
MLQGKFDDAYQLHQMGGAYYVVYRAQSTDAITLDPKTGKFVSKDRMVADFEYAVTGGE
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YTFHHTTRLNKEEKVKEWSLCVATDVSDHDTFWPGWLRDLICDELLNMGYAPWWWKLF
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TAPHLNSRIKDMPSACRFLDSYWGHEEIRQISKSDDAILGWTKGRALVGGHRLFEMLKE
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RSKRKRPFPLAWASMKDYGACPIYSVLEAIERCWWNAFGESYRAYREDMLKRDITLE
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FLRSVMPR

>VIR|Q9XJR3|SPIKE_BP

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VDIWIGGENMTALNGIVDGGKFEAGQEFQINTFGSVNYWVSDEEIRVFKEYSARAKYQA

NEGRTALEANNVPPFDIDVPELDGVPFSLKARVRHKS KGVDGLGDYTSISVKPAFYITEG
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>VIR|P85501|STRU1_BP

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EQAKITKSNQDRVDASREW EKENEKYLSSRVKMEKEISAARELGRKAGLNEIEIEDRIAQI
RKS YE EKPSRSRSGSLDAGQRMLDSL RQQYASMQAQLEATEKLG TQAQALVKWEQQLAD
LKSRGSL SADQKALLANADLITAQLKRNA ALEDELNTRKEIQKTLDDYKRLNESLR TDAE
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IGSSFGMRRSGT

>VIR|P85502|STRU2_BP

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SSSVFSLGDGVIFRPTIPEGDFQCEDCEVSGCTFSNIERQCITVESGFNIRILSNGFYNSTYAA
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KLSTLKITGTSTSPITVQSTSGLRIEEVDVLINTGAGVVIQNCASPIIRNLKMVGAVT LSVPA
VSFIGTTTNPVGGLDIAGFTVGVSVTTSATTTIHSLSNNVFAGVATPWSVNP GNYIKGQFS
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>VIR|P85503|STRU3_BP

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>VIR|P85992|TAILF_BP

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>VIR|P09009|TERM_BPP

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YRKTTPGKPVYITQRELPIKFENMEQWLTELKAAGFQLQPGEQIYFTFNGNYSRRTYTSF
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>VIR|P12528|TSPE_BPP

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YSVKLSDYPTLQDAASAAMDGLLIDRDYNFYGGGETVDFGGKVLTIIECKAKFIGDGNLIFTK
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>VIR|Q9XJP3|TSPE_BPS

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ADADGTEQFTGIYFRTPSTQSHKIVSGVHINTANKNTAANNQSAIEQSAIFVFSGCTLT
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>VIR|P09677|VA1_BPSP

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>VIR|P19726|VC10A_BP

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>VIR|P03714|VCF2_LAM

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>VIR|P26747|VG05_BPP

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VGLPGQTA

>VIR|P19060|VG06_BPT

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DFVGADGGGDPEDIERIRELGTIKRETQQRVCVTATDYDTFVSRFSGSIIQAVQTFDSTKPG
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>VIR|P19062|VG08_BPT

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>VIR|P10927|VG09_BPT

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QAIDSIKGVSGNLVVTSPYSKVTLCISSDNSTSVWNYSIESMFGQKESPAEGTWNISTSGS
VDIPLFHRTEYNMAKLLVTCQSV DGRKIKTAEINILVDTVNSEVISSEYAVMRVGNETEED
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>VIR|P10928|VG10_BPT

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PNSLEVRFNGLQELAGTVGMPLFHCVGADSDDEVECSVLGGTWEQSHTDYSVETDENG
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>VIR|P10929|VG11_BPT

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>VIR|P15132|VG13_BPP

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SVRYITWVNVHESPLPFDVGKKLKKGDLMGHTGIGGNVTGDHWHFNVIDGKEYQGWTK
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>VIR|P13332|VG18_BPT

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DVQLFIAGSCAGESLETA STVQKHVVSIGDARQDCLVLCSPPRETVVGIPVTRAVDNLVN
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>VIR|P13333|VG19_BPT

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>VIR|Q05229|VG23_BPM

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VKTGQTNEKAVLVVIEDGDMRLGHHAHKAGVRRDDAIELPIDDLAALPVRFTYLDHEDE
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>VIR|P19896|VG24_BPT

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LALQIAIVLLKVRLFS DAASTSKFESSDSEIADARFQINKWQTAVKSRK LKTGITVELAQDL
EANGFDAPNFLEDLLATEMADEINKDILQSLITVSKRYKVTGITDSGFIDLSYASAPEAGRS
LYRMVCEMVSHIQESTYTATFCVASARAAA ILAASGWLKHKPEDDKYLSQNAYGFLAN
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>VIR|P35837|VG26_BPP

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LDGRVTTAENNISALQADYVSKTATTSQSLASPLNVTTSSYSVGGKKVLGARQTGWTAATG
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>VIR|P17172|VG27_BPT

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KRDPMKNATIYAHSFLDSSIPMITTGKGENSIVVSRSGAYSEM TYRNGYEEAIRLQTMAQY
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>VIR|P13339|VG48_BPT

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>VIR|P08767|VGF_BPAL

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PKFLHQSYLNIYNNYFRAPWMPERTEANPSNLNEDDARYRFRCCHLKNIWSAPLPPETKL
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>VIR|P13559|VLYS_BPP

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>VIR|P03733|VMTV_LAM

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>VIR|P27379|VP06_BPP

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>VIR|P27380|VP07_BPP

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>VIR|P27381|VP09_BPP

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TQGRSKKIPMILSQRPVWLTRFAISESDFQIFQLGDQRDRQTVQGFVPVDLEKLMQAPV
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>VIR|P27382|VP11_BPP

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MAQVDLSKYLGDQSTTSTALAGMQSDTAKYQSNLQQAENIRANTSLAEIDAQKYIVGK
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>VIR|P27392|VP16_BPP

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>VIR|P27388|VP22_BPP

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>VIR|P27391|VP30_BPP

MALINPQFPYAGPVPPIGPAPTETMPLLNYRVEGRIAGIQQARQFMPFLQGPHRAVAEQTY
HAIGTGIQMGQTFNQPLINTQEG

>VIR|P27384|VP31_BPP

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TIAQGVW

>VIR|P27390|VP34_BPP

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>VIR|P85225|VPN1_BPP

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QVLRSGDLLDAIELAWNASDVNTASAGDILAVRVEDAKNATLTKGGLTFASTIYGVANEI
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LTLNVGSEPESTTEVMKYELGQGVYSETNVLVSAINSLPDWEAKFFPIGDKNLPTDALEAV
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NKFPLLANEGGYLVPLTDKQAVHSEALAFVKDRTDNGDPMRIIVGGGTNETVEESITRAT
NLRDPRASLVGFSGTRKMDDGRLKLPGYMMASQIAGIASGLEVGEAITFKHFNVTSVDR
VFESSQLDMLNESGVISIEFVRNRTLTAFRVVQDVTTYNDKSDPVKNEMSVGEANDFLVSE
LKIELDNNFIGTKVIDTSASLIKNFIQSFLDNKKRAREIQDYTPPEEVQVVLEGDVASISMTV
MPIRSLNKITVQLVYKQQLTA

>VIR|P85226|VPN2_BPP

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KFRDEDLTIDTEYKVVVVSSDDAESAPSDVASVVIDDKKKQVKLEITINMYQARPQYVAI
YRKGLETGLFYQIARVPASKAVEGVITFIDVNDIEPETADVFGELTPSVVHLFELPMML
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>VIR|P85227|VPN3_BPP

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GIHTDLVSKASSEKALLPTDVTDAGILQFFENRQQNRTSDVILKEKFIITMENKKSVKQ

>VIR|P85228|VPN4_BPP

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RFKLGVYVFLADEPFVYGDKTE

>VIR|P85229|VPN5_BPP

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VTSESTQFTYLTSAKVK

>VIR|P85230|VPN6_BPP

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>VIR|A8E283|VPN7_BPP

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SKQLSRTQFSNSDPKDELIGDMHQKFSLYPSLTYSVDGEGGRVVTFSGKSFIADFDTKEV
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DQWMEYSIEGWAVMANGSTDLTVWRRFTKFTIGTSGYLDILPKTIVESWTHRSFWREL
KIEEGSQATTWVPNKEDGAFTGGIVETTQTEELANLGFSGFVSSKRPSSSLTQSVELPEIG
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WAFVPSFE

>VIR|P25477|VPN_BPP2

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YQDFQLRIRNAIIKRQSLDFIMAGFNGVKRAETSDRSSNPMLQDVAVGWLQKYRNEAPAR
VMSKVTDDEGRTTSEVIRVGKGGDYASLDALVMDATNNLIEPWYQEDPDLVVIVGRQLLA
DKYFPVFNKEQDNSEMLAADVIISQKRIGNLPAVRVPYFPADAMLITKLENLSIYYMDDSH
RRVIEENPKLDRVENYESMNIDYVVEDYAAGCLVEKIKVGDFSTPAKATAEPGA

>VIR|P36275|VSHP_BPP

MVTKTITEQRAEVRIAGNDPAHTATGSSGISSPTPALTPLMLDEATGKLVVWDGQKAGSA
VGILVPLEGTETALTYKSGTFATEAIHWPEVDEHKKANAFAGSALSHAALP

>VIR|P03715|VSOC_BPT

MASTRGYVNIKTFEQKLDGNKKIEGKEISVAFPLYSDVHKISGAHYQTFPSEKAAYSTVYE
ENQRTEWIAANEDLWKVTVG

Phage non-virion proteins

>NON|Q37976|AEPE_BPA

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NPHLQFNKYKGYGTDTFGKGASTSNSSKPSADTNTNSLGLVDYMNLNKLDSSFANRKKLA
TSYGIKNYSGTATQNTLLAKLKAGKPHTPASKNTYYTENPRKVKTLYQCDLYKSVDFTT
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>NON|Q37979|AEPE_BPA

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GFKWGGDWKSFKDYPHFELCDAVSGEKIPAAATQNTNTNSNRYEGKVIDSAPLLPKMDFKS
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>NON|Q38653|ALYS_BPA

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>NON|O03979|ALYS_BPD

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MHAWLIENGYELISENAPWDAKRGDIFIWGRKGASAGAGGHTGMFIDSDNIIHCNYAYDG
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EYIEENKSWFYFDDQGYMLAEKWLKHDTGNWYWFDRDGYMATSWKRIGESWYFNR
DGSMVTGWIKYYDNWYYCDATNGDMKSNAFIRYNDGWYLLLPDGRRLADKPQFTVEPD
GLITAKV

>NON|P32762|ALYS_BPH

MDIDRNRLRTGLPQVGVQPYRQVHAHSTGNRNSTVQNEADYHWRKDPELGGFFSHVVG
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LPKTLDTDDLGIKTHEYCTNNQPNHSDHVPYPYLASWGISREQFKQDIENGLSAATG
WQKNGTGYWYVHSDGSYSKDKFEKINGTWYYFDGSGYMLSDRWKKHTDGNWYYFDQ
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TGWYYLKPDTLADKPEFTVEPDGLITVK

>NON|P15879|ARC3_CBD

MKGLRKSILCLVLSAGVIAPVTSGMIQSPQKCYAYSINQKAYSNTYQEFNIDQAKAWGN
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PENIMLFRGDDPAYLGTQNTLLNSNGTINKTAFEKAKAKFLNKDRLEYGYISTSLMNV
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MGTAINPK

>NON|P32267|ASIA_BPT

MNKNIDTVREIITVASILIKFSREDIVENRANFIAFLNEIGVTHEGRKLNQNSFRKIVSELTQE
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>NON|O64174|BNRDF_BP

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QINEVFEWVKNNRFLQKKARTIVSVYKTIKKNDEISLFGKGMVASVFLESFLFYSGFYPLY
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>NON|P22499|BOF_BPP1

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>NON|P26814|BOR_LAMB

MKKMLLATALALLITGCAQQTFTVQNKPAAVAPKETITHHFFVSGIGQKKTVDAAKICGG
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>NON|P19194|B_BPCHP

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EKVQIRKSKLQKDQKEEVSSEEK

>NON|P03633|B_BPPHX

MEQLTKNQAVATSQEAVQNQNEPQLRDENAHNDKSVHGVNLNPTYQAGLRRDAVQPDIEA
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>NON|P08773|DCHM_BPT

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>NON|P16006|DCTD_BPT

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>NON|P32270|DDA_BPT4

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LFKILLSTIPPWCTIIGIGDNKQIRPVEPGENTAYISPFTHKDFYQCELTEVKRSNAPIIDVAT
DVRNGKWNVDKVVVDGHGVRGFTGDTALRDFMVNYFSIVKSLDDLLENRVMAFTNKS
DKLNSIIRKKIFETDKDFIVGEIIVMQEPLFKTYKIDGKPVSEIIFNNGQLVRIIEAEY
TSTFVKARGVPGEYLIRHWDLTVETYGDDEYYREKIKIISSEELYKFNFLAKTAETYKN
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>NON|P04392|DMA_BPT4

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NFTTTPFGKRTINKNSEKQYNHFKQNCDKIIFSSLHFKDVKILDGDFVYVDPPLYLITV
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>NON|P39232|DMD_BPT4

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>NON|P03015|DNIV_BPM

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STLYKKHPA KRAHIENDDRIN

>NON|P00969|DNLI_BPT

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>NON|P04531|DNMK_BPT

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>NON|Q06259|DOC_BPP1

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>NON|P04526|DPA44_BP

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>NON|O80164|DPA5_BPR

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>NON|P04527|DPA62_BP

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>NON|P03680|DPOL_BPP

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IYDSLKLPFPVKKIAKDFKLTVLKGDIDYHKERPVGKITPEEYAYIKNDIQIIAEALLIQF
KQGLDRMTAGSDSLKGFKDITTKFKKVFPPTLSLGLDKEVRYAYRGGFTWLNDRFKEKE
IGEGMVFDVNSLYPAQMYSRLLPYGEPVFEKGYVWDEDYPLHIQHIRCEFELKEGYIPTIQ
IKRSRFYKGNLYLSSSGEIALWLSNVLELMKEHYDLYNVEYISGLKFKATTGLFKDFI
DKWTYIKTTSEGAIKQLAKLMLNSLYGKFASNPVDTGKVPYLKENGALGFRLGEEETKDP
VYTPMGVFITAWARYTTITAAQACYDRIICYDTSIHLTGTEIPDVIKDIVDPKKGWYWAHE
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>NON|Q38087|DPOL_BPR

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GGFPGPKCPFHIRGILTYNRAIKGNIDAPQVVEGEKVYVLPPLREGNPFQDKCIAWPSGTEIT
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>NON|P00581|DPOL_BPT

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>NON|P13320|DSBA_BPT

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>NON|P31654|DUHM_BPS

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YGVNLETDEAPVVEDFEELDPNPRMSYTMNELNQFLNEYFGIVDSLMRDDETYMHDG
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>NON|P04382|DYR_BPT4

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>NON|P69486|D_BPPHX

MSQVTEQSVRFQTALASIKLIQASAVLDLTEDDFDLTNSKVVWIATDRSRARRCVEACVYG
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>NON|Q04830|ENAN_BPK

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>NON|P07059|END2_BPT

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>NON|P04418|END5_BPT

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>NON|P13340|END7_BPT

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>NON|P00641|ENRN_BPT

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>NON|P06229|EXO5_BPT

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>NON|P03697|EXO_LAMB

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>NON|P03639|E_BPPHX

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>NON|P03657|G1P_BPF1

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>NON|P03666|G4P_BPF1

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FGIFNGDVLGLSVRALKTNSHKSILSVPRILTSGQKGSISVGQNVPFITGRVTGESANVNN
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>NON|O80294|G5P_BPIF

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>NON|P03670|G5P_BPIK

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>NON|P03671|G5P_BPPF

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>NON|P03672|G5P_BPPF

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>NON|P68676|G5P_BPPH

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>NON|P00276|GLRX_BPT

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>NON|P04519|GSTA_BPT

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KEKGIPYEEYGNREIDKMNLAPNQAQILDCYINSEMLERMSSGFGYQLSKLNQKYLQR
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>NON|P04547|GSTB_BPT

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>NON|Q37993|HEAD_BPC

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>NON|A9CRA7|HEAD_BPM

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NDVLEALMGAKLTVNADITKLNLQSAIDKFNDEDLEPMVLFINPLDAGKLRGDASTNFT
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>NON|B2ZYY5|HEAD_BPM

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>NON|P34081|HMUI_BPS

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>NON|P03718|IPI1_BPT

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>NON|P03719|IPI2_BPT

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>NON|P13302|IPI3_BPT

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>NON|P06855|KIPN_BPT

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VASGDF

>NON|Q38162|LLP_BPT5

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>NON|P15057|LYS_BPCP

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FDKNIVLLDDEEDDKPKTAGTWKQDSKGGWFRNRNNGSFPYNKWEKIGGVWYYFDSKG
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>NON|P33486|LYS_BPMV

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>NON|Q37875|LYS_BPP1

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CNSLRTYYSKARGMRVETSIHKWAQKGEWVNMCNHLPDFVNSNGVPLRGLKIRREKER
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>NON|P27359|LYS_BPP2

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>NON|P09963|LYS_BPP2

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LWKKAGKDPDILLPRRRRERALFLS

>NON|Q6QGP7|LYS_BPT5

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>NON|P03706|LYS_LAMB

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>NON|P39423|MODA_BPT

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>NON|P39421|MODB_BPT

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KCSTYTIYTLDFEGFNL

>NON|P22915|MOTA_BPT

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>NON|P00806|NAAA_BPT

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>NON|P06020|NER_BPMU

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>NON|P03765|NINB_LAM

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>NON|P07071|NRDD_BPT

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>NON|Q58MU6|PEBS_BPP

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>NON|Q06253|PHD_BPP1

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>NON|P26744|PORTL_BP

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>NON|P54309|PORTL_BP

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>NON|P03772|PP_LAMBD

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>NON|P10277|PRIM_BPP

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QSQQNSDEALNIKRDADPTDFIGYLETLPTSGMYMGNASIIPRNYRKYLYHAYLAYME
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>NON|P03692|PRIM_BPT

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SGLGCDVILDHISIVVSASGESDERKMIDNLMTKLKGFAKSTGVVLVICHKLNPKGKA
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>NON|P03037|RANT_BPP

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>NON|P03050|RARC_BPP

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>NON|P09964|RCRO_BPP

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>NON|P03040|RCRO_LAM

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KTTA

>NON|P15965|RDRP_BPF

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FSTMGNFTFELES MIFWAIVRATQIHFRNTGTIGIYGDDIICPTEIAPRVLEALS FYGFKPNL
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VWEKLSRLVPRYLFGGTDLQADYYVVSPPILKGIYSKMNGRREYAEARTTGFKLARIARW
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>NON|P14647|RDRP_BPQ

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GRLPDG SVVTYEKISSMGNGYTFELES LIFASLARSVCEILDLSSEVTYVGDDIILPSCAVP
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WATIDGVWD PRAHSVYLK YRKLLPKQLQRNTIPDGYGDGALVGSVLINPFAKNRGWIRY
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>NON|P06956|RECR_BPP

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RRIRKENVDAGERAKQALAFERTDFDQVRSLMENS DRCQDIRNLAFLGIAYNTLLRIA EIA
RIRVKDISRTDGG RMLIHIGRTKTLVSTAGVEKALSLGVTKLVERWISVSGVADDPNNYLF
CRVRKNGVAAPSATSQLSTRALEGIFEATHRLIYGAKDDSGQRYLAWSGHSARVGAARDM

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>NON|P35926|REF_BPP1

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GCHKKQLPLCRWHHQHAAPAEVREKYPWLVPVHADGVVGGKKEFTLLNKSEMELLADA
YEMANIMH

>NON|P69628|REGA_BPR

MIEITLKKPEDFLKVKETLTRMGIANNKDKVLYQSCHILQKKGLYIVHFKEMLRMDGRQ
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N

>NON|P13312|REGB_BPT

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>NON|P04891|REGN_BPP

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>NON|P07243|REGN_BPP

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>NON|P03045|REGN_LAM

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>NON|P03631|REPA_BPP

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ANDSHADCYQYFCVPEYGTANGRLHFHAVHFMRTLPTGSVDPNFGRRVRNRRQLNSLQN
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>NON|P03759|REXB_LAM

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CILVFQLYNLTREQE

>NON|P32277|RLIG2_BP

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>NON|P00971|RLIG_BPT

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RENETGEYISYDDIYKDATLRPYLVERYEIDSPKWIEEAKNAENIEGYVAVMKDGSHFKIKS
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>NON|P03049|RMNT_BPP

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>NON|P13319|RNH_BPT4

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PYIVMDIDKYEADDHIAVLVKKFSLEGHKILISSDGDFTQLHKYPNVKQWSPMHKKWVK
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NEF

>NON|P07879|RPBA_BPT

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YYE AIDREVS NKWIELMRKHTTESL NAGAKFIMTSCGERLEDDYCGNADERLIVAAQIVA
ETIAADFNR

>NON|P08707|RPC1_BP1

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>NON|P06019|RPC1_BPM

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>NON|P13121|RPC1_BPP

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IQKSAGINEHSAKYIENLEATKELMKQYPEDEKFRMRVHGFSETMLRVHYISSSPNYNDG
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>NON|P14819|RPC1_BPP

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>NON|P03034|RPC1_LAM

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>NON|P69202|RPC2_BPP

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CSEDSFWLDVQGDSTAPAGLSIPEGMIILVDPEVEPRNGKLVVAKLEGENEATFKKLVMD
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>NON|P03042|RPC2_LAM

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>NON|P18681|RPC3_BPH

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>NON|P03044|RPC3_LAM

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>NON|P15238|RPC_BP16

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TNMEPRKKKLLPVLGEAVGGEDGEYIFNGSVLDYVDCPPSLENVPNAYAVYIDGESMVPR
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>NON|P06153|RPC_BPPH

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>NON|P06221|RPOL_BPS

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WQQFINWKGEARLYTAETKRGSKSAVVVMVVGQARKYSAFESIYFVYAMDSRSRVYV
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AVAEGRTANKVHPFEDDRQDYLTPGAAYNYMTALIWPSISEVVKAPIVAMK MIRQLARFA
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>NON|P00573|RPOL_BPT

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>NON|Q37935|RZ1_LAMB

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>NON|P39230|SPAC_BPT

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>NON|Q38504|SSB_BPPH

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>NON|P09385|STXA_BP9

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>NON|P09386|STXB_BP9

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>NON|P08763|T3MO_BPP

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FPVFINS ENKVYVTD DDKPLNEDDYVLYPV SPTGEELSWSWGKKKINDEFYNLIVIDIKDG
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>NON|A9CRB8|TAIL_BPM

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SSDLSM

>NON|B2ZYZ1|TAIL_BPM

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>NON|P26745|TERL_BPP

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>NON|P54308|TERL_BPS

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>NON|P17312|TERL_BPT

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GMSMV

>NON|P04893|TERM_BPP

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>NON|P03681|TERM_BPP

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>NON|P54307|TERS_BPS

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PWR

>NON|P03707|TERS_LAM

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>NON|P13299|TEV1_BPT

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LGPDGRKALYSKPGSKNGRWNPECHKFCCKGVRIQTSAYTCSKCRNRSGENNSFFNHKHS
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>NON|P04445|TF1_BPSP

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>NON|P03739|TFA_BPT4

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>NON|P03740|TFA_LAMB

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>NON|P09176|TOPL_BPT

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>NON|P23992|TOPS_BPT

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>NON|P07636|TRA_BPMU

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>NON|P41063|TUM_BP18

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>NON|P00471|TYSY_BPT

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>NON|P20703|UVSW_BPT

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>NON|P04529|UVSX_BPT

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>NON|P03775|V03_BPT7

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>NON|P23541|VA2_BPT5

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>NON|P15966|VASS_BPF

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>NON|P07394|VASS_BPG

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>NON|P09676|VASS_BPS

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>NON|P21680|VDHR_BP1

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VFGYS

>NON|P10310|VDMB_BPT

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>NON|P15236|VFIL_BP1

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>NON|P26746|VG04_BPP

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>NON|P16009|VG05_BPT

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>NON|Q05278|VG06_BPM

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>NON|Q01074|VG07_BPP

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>NON|P26748|VG08_BPP

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>NON|P04332|VG10_BPP

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>NON|O64205|VG12_BPM

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>NON|P20345|VG12_BPP

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>NON|P10930|VG12_BPT

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>NON|P16517|VG167_BP

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>NON|Q05222|VG16_BPM

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>NON|Q01146|VG16_BPP

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>NON|Q05223|VG17_BPM

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>NON|P03686|VG17_BPP

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>NON|P03679|VG1_BPPH

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>NON|P04534|VG22_BPT

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>NON|Q05233|VG26_BPM

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>NON|Q05234|VG27_BPM

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>NON|Q05235|VG28_BPM

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KSSEFSY YEATDTSFLAGGQSAPGINEGIALVNIIGDLLTSFINSQLAALGAVGGAILDPLL
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>NON|P17313|VG31_BPT

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>NON|P13338|VG33_BPT

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>NON|P03744|VG37_BPT

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>NON|P17171|VG40_BPT
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>NON|P04530|VG41_BPT
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>NON|P03682|VG4_BPPH
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RRKSMV

>NON|P04532|VG57_BPT
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>NON|P13342|VG59_BPT
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>NON|P13848|VG7_BPPH
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>NON|P20344|VG85_BPP
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>NON|P03702|VGAM_LAM
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>NON|P03654|VGK_BPG4
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>NON|P03695|VHED_BPT

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>NON|P03696|VHED_BPT

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>NON|P21442|VINT_BPH

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>NON|P03700|VINT_LAM

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>NON|P03701|VLOM_LAM

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>NON|P09962|VLY1_BPP

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>NON|Q38008|VLYS_BPC

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>NON|P23848|VMOR_BPM

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>NON|P03732|VMTU_LAM

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>NON|P18683|VNUN_BPH

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>NON|P03763|VPB_BPMU

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>NON|P07696|VPB_BPP2

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>NON|P22501|VPF1_BPP

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>NON|P03709|VPF1_LAM

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>NON|P22502|VPF2_BPP

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>NON|P25475|VPL_BPP2

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>NON|P08558|VPP_BPMU

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>NON|P05460|VPSU_BPP

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>NON|P31340|VPV_BPP2

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>NON|P17309|VR3_BPT4

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>NON|P03704|VRPI_BPT

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>NON|P13310|VS_BPT4

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>NON|P03748|VTFP_BPT

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>NON|P68927|VXIS_BPH

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>NON|P10104|WAC_BPT4

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>NON|Q9ZX29|WHIB_BPM

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