

# Bacterial Cell Wall Lyase

>sp|P10773|LYB\_BACIU B-enzyme OS=Bacillus subtilis GN=lyzB PE=1 SV=1

ISPLGSVTKKNQDSTAYNWTGNKTANGNWPVLGICAVHRKKDIGGSGNSPVIPFGTTLKT  
DKDIWLPDGVGYKSSFNVDDTGSgpKkTDYWIDIYYSKDTKAAINYGVVKLSYTYST

>sp|P34020|LYS\_CLOAB Autolytic lysozyme OS=Clostridium acetobutylicum (strain ATCC 824 / DSM 792 / JCM 1419 / LMG 5710 / VKM B-1787) GN=lyc PE=1 SV=1

MKGIDIYSGQGSVDFNAVKESGVEVVYIKATEGLTYTDSTYKDFYDGAKNAGLKIGFYHY  
LRANDPTSEAEHFFNTISGLSLDCKCAIDVEVTLGQSIDQISSNVRKFADYLINKGLDVCVY  
TYTNFYKDNLNSTVKDLPLWIAEYGVSKPNIDASYVGFQYSDSGSVNGISGSADLDEFSE  
GILVGGTVVIDPGQGDDNIKAIQQDLNILLKRGLEVDGIEGPETEAAIKDFQSIMGLTVDG  
IWGTNTSGAAQQIFSRPLDGVAYPHYEYATRYIQYRVGASVDGTFGSGTKAKVAAWQSNQ  
GLMADGVVGSATWSKLLDEN

>sp|P0C960|EMTA\_ECOLI Endo-type membrane-bound lytic murein transglycosylase A OS=Escherichia coli (strain K12) GN=emtA PE=1 SV=1

MKLRWFAFLIVLLAGCSSKHDTNPPWNAKVPVQRAMQWMPISQKAGAAWGVDPQLIT  
AIIAESGGNPNAVSKSNAIGLMQLKASTSGRDVYRRMGWSGEPTTSELKNPERNISMGAA  
YLNILETGPLAGIEDPKVLQYALVVSANGAGALLRTFSSDRKKAISKINDLDADEFLEHV  
ARNHPAPQAPRYIYKLEQALDAM

>sp|O33599|LYTM\_STAA8 Glycyl-glycine endopeptidase LytM OS=Staphylococcus aureus (strain NCTC 8325) GN=lytM PE=1 SV=3

MKKLTAATAIATMGFATFTMAHQADAAETTNTQQAHTQMSTQSQDVSYGTYTIDSNGD  
YHHTPDGNWNQAMFDNKEYSYTFVDAQGHYFYNCYPKNANANGSGQTYVNPATAG  
DNNDYTASQSQQHINQYGYQSNVGPDASYSHSNNNQAYNSHDGNGKVNYPNGTSNQ  
GGSASKATASGHAKDASWLTSRKQLQPYGQYHGGGAHYGVDYAMPENSPVYSLTDGTV  
VQAGWSNYGGGNQVTIKEANSNNYQWYMHNNRLTVSAGDKVKAGDQIAYSSTGNST  
APHVHFQRMMSGGIGNQYAVDPTSYLQSR

>sp|P33673|CHIS\_BACCI Chitosanase OS=Bacillus circulans GN=csn PE=1 SV=2

MHMSNARPSKSRKFLLAFLCFTLMASLFGATALFGPSKAAAASPDDNFSPELQFLRNNT  
GLDGEQWNNIMKLINKPEQDDLNWIKYYGYCEDIEDERGYTIGLFGATTGGSRDTHPDGP  
DLFKAYDAAKGASNPSADGALKRLGINGKMKGSILEIKDSEKVFCEGKIKKLQNDAAWRK  
AMWETFYNVYIRYSVEQARQRGFTSAVTIGSFVDALNQGATGGSDDLQGLLARGSSSN  
EKTFMKNFHAKRTLVDNKNYKPPNGKNRVKQWDTLVDMGKMNLKNVDSEIAQVTD  
WEMK

>sp|O33635|ATL\_STAEP Bifunctional autolysin OS=Staphylococcus epidermidis GN=atl PE=1 SV=1

MAKKFNYKLPSMVALTLFGTAFTAHAQANAAEQPQNQSNHKNVLDLDDQTALKQAEKAKSE  
VTQSTTNVSGTQTYQDPTQVQPKQDTQSTTYDASLDEMSTYNEISSNQKQSLSTDDAN  
QNQTNSVTKNQEETNDLTQEDKTSSTDNQLQETQSVAKENEKDLGANANNEQQDKM  
TASQPSENQAIETQASNDNESQKQSQVTSEQNETATPKVSNTNASGYNFDYDDEDDDS  
STDHLEPISLNNVNATSKQTTSYKYKEPAQRVTNTVKKETASNQATIDTKQFTPFSAQAQ  
RTVYSVSSQKTSPLKYPKVNSSINNYIRKKNMKAPRIEEDYTSYFPKYGYRNGVGRPEG  
IVVHDTANDNSTIDGEIAFMKRNNTNAFVHAFVDGNRIIETAPTDYLSWGAGPYGNQRFI

NVEIVHTHDYDSFARSMNNYADYAAATQLQYYNLKPDSAENDGRGTVWTHAAISNFLGGT  
DHADPHQYLRSNYSYAELYDLIYEKYLKTKQVAPWGTTSTKPSQPSKPSGGTNNKLTV  
SANRGVAQIKPTNNGLYTTVYDSKGHKTDQVQKTL SVTKTATLGNNKFYLVEDYNSGKK  
YGWVKQGDVVYNTAKAPVKVNQTYNVKAGSTLYTPWGT PKQVASKVSGTGNQTFKA  
TKQQQIDKATYLYGTVNGKSGWISKY YLTTASKPSNPTKPSTNNQLTVTNNSGVAQINAK  
NSGLYTTVYDTKGKTTNQIQR TLSVTKAATLGDKKFYLVGDYNTGTNYGWWVKQDEVIYN  
TAKSPVKINQTYNVKPGVKLHTVPWGTYNQVAGTVSGKGDQTFKATKQQQIDKATYLYG  
TVNGKSGWISKY YLTAPSKVQALSTQSTPAPKQVKPSTQTVNQIAQVKANNSGIRASVYD  
KTAKSGTKYANRTFLINKQRTQGNNTYVLLQDGTSNTPLGWVNINDVTTQNIGKQTQSIG  
KYSVKPTNNGLYSIAWGTKNQQLLAPNTLANQAFNASKAVYVVKDLYLYGTVNNTGWI  
AAKDLIQNSTDAQSTPYN YTFVINNSKSYFYMDPTKANRYS LKPYEQTFTVIKQKNING  
VKWYYGQLLDGKYVWIKSTDLVKEKIKYAYTGMTLNNAINIQSRLKYKPQVQNEPLKWS  
NANYSQIKNAMDTKRLANDSSLKYQFLRLDQPQYLSAQALNKLKKGKGVLENQGA AFS  
QAARKYGLNEIYLISHALVETGNGTSQLAKGGDVSKGKFTTKTGHKYHNVFGIGAFDNN  
ALVDGIKYAKNAGWTSVSKAIIGGAKFIGNSYVKAGQNTLYKMRWNPANPGTHQYATDI  
NWANVNAQVLKQFYDKIGE V GK YFEIPT YK

>sp|O07532|LYTF\_BACSU Peptidoglycan endopeptidase LytF OS=Bacillus subtilis (strain 168)  
GN=lytF PE=1 SV=2

MKKKLAAGLTASAIVGTTLVVTPAEAAIKVKSGDSLWKL AQT YNTSVAALTSANHLSTT  
VLSIGQTLTIPGSKSSTSSSTSSSTTKKSGSSVYTVKSGDSLWLIANEFKMTVQELKKLNL  
SSDLIRAGQKLKVS GTVSSSSSSSKSNSNKSSSSSSKSSSNKSSSSSSSTGTYKVQLGDSL  
WKIANKVNMSIAELKVLN NLKSDTIYVNQVLKTKSSGSDTSSKDNSSKSNQTSATTKYTV  
KSGDSLWKIANNYNLTVQQIRNINNLKSDVLYVGQVLKLTGKASSGSSSSSSSSSNASSGT  
TTTTYTVKSGDSLWVIAQKFN VTAQQIREKNLKT DVLQVGQKLVISGKASSSSSSSSSNTT  
SSTSAKINTMISA AKAQLGVPYRWGGTTPSGFDCSGFIYYVLNKVTSVSR LTAAGYWNTM  
KSVSQPAVGDFVFFSTYKAGPSHVGIYLGNGEFINANDSGVVISNMNNSYWKQRYLGAKR  
YF

>sp|P0AGC3|SLT\_ECOLI Soluble lytic murein transglycosylase OS=Escherichia coli (strain K12)  
GN=slt PE=1 SV=1

MEKAKQVTWRLLAAGVCLLTVSSVARADSLDEQRSRYA QIKQAWDNRQMDVVEQMMP  
GLKDYPLY PYLEYRQITDDL MNQPAVTVTNFVRANPTLPPARTLQSRFVNELARREDWRG  
LLAFSPEKPGTTEAQCNY YAKWNTGQSEEAWQ GAKELWLTGKSQPNACDKLFSVWRA  
SGKQDPLAYLERIRLAMKAGNTGLVTVL AGQMPADYQTIASAIISLANNPNTVLT FARTTG  
ATDFTRQMAAVAFASVARQDAENARLMIPSLAQAQQLNEDQIQELRDIVAWRLMGNDVT  
DEQAKWRDDAIMRSQSTSLIERRVRMALGTGDRRGLNTWLARLPMEAKEKDEWRYWQ  
ADLLERGREAEAKEILHQLMQQRGFYPMVAAQRIGEEYELKIDKAPQNVDSALTQGPE  
MARVRELMYWNLDNTARSEWANLVKSKSKTEQAQLARYAFNNQWWDLSVQATIAGKL  
WDHLEERFP LAYNDL FKRYTSGKEIPQSYAMAIARQESAWNPKVKSPVGASGLMQIMP GT  
ATHTVKMFSIPGYSSPGQLDPETNINIGTSYLQYVYQQFGNNRIFSSAAYNAGPGRVRTW  
LGNSAGRIDA VAFVESIPFSETRGYVKNV LAYDAYRYFMGDKPTLMSATEWGRRY

>sp|Q5HEA4|SCED\_STAAC Probable transglycosylase SceD OS=Staphylococcus aureus (strain COL)  
GN=sceD PE=1 SV=1

MKKTLLASSLAVGLGIVAGNAGHEAHASEADLNKASLAQMAQSNDQTLNQP I EAGAYN  
YTFDYEGFTYHFESDGT HFAWNYHATGTNGADMSAQAPT TNNVAPS AVQANQVQSQEV

EAPQNAQTQQPQASTSNNSQVTATPTESKSSEGSVNVNAHLKQIAQRESGGNIHAVNPTS  
GAAGKYQFLQSTWDSVAPAKYKGVSPANAPESVQDAAAVKLYNTGGAGHWVTA

>sp|P41052|MLTB\_ECOLI Membrane-bound lytic murein transglycosylase B OS=Escherichia coli (strain K12) GN=mltB PE=1 SV=1

MFKRRYVTLPLFVLLAACSSKPKPTETDTTTGTPSGGFLEPQHNVMQMGDFANNPN  
AQQFIDKVMNKHGFDQRQLQEILSQAKRLDSVLRMLMDNQAPTTSVKPPSGPNGAWLRYS  
KKFITPDNVQNGVFWNQYEDALNRWQVYGVPEIIVGIIGVETRWGRVMGKTRILDA  
LATLSFNYPRAEYFSGELETFLMARDEQDDPLNLKGSFAGAMGYGQFMPSSYKQYAV  
DFSGDGHINLWDPVDAIGSVANYFKAHGWWKGDQVAVMANGQAPGLPNGFKTKYSISQL  
AAAGLTPQQPLGNHQQASLLRLDVGTYQYWYGLPNFYTITRYNHSTHYAMAVWQLGQ  
AVALARVQ

>sp|P39800|XLYA\_BACSU N-acetylmuramoyl-L-alanine amidase XlyA OS=Bacillus subtilis (strain 168) GN=xlyA PE=1 SV=1

MVNIQDFIPVGANNRPGYAMTPLYITVHNTANTAVGADAAAHARYLKNPDTTTSWHFTV  
DDTEIYQHLPLNENGWHAGDNGSGNRASIGIEICENADGDFAKATANAQWLIKTLMAE  
HNISLANVVPKHYWSGKECPRKLLDTWDSFKAGIGGGGSQTYVVKQGDTLTSIARAFGV  
TVAQLQEWNNIEDPNLIRVGQVLIVSAPSAAEKPELYPLPDGIIQLTTPYTSGEHVFQVQRA  
LAALFYFPDKGAVNNGIDGVYGPKTADAVARFQSVNGLTADGIYGPATKEKIAAQLS

>sp|P0AGC5|MLTF\_ECOLI Membrane-bound lytic murein transglycosylase F OS=Escherichia coli (strain K12) GN=mltF PE=1 SV=2

MKKLKINYLFIGILALLAVALWPSIPWFGKADNRIAAIQARGELRVSTIHTPLTYNEINGKP  
FGLDYELAKQFADYLGVKLVTVRQNISQLFDDLDNGNADLLAAGLVYNSERVKNYQPG  
PTYYSVSQQLVYKVGQYRPTLGNLTAEQLTVAPGHVVVNDLQTLKETKPELSWKVDD  
KKGSAELMEDVIEGKLDYTIADSV AISLFQRVHPELAVALDITDEQPVTWFSPLDGDNTLS  
AALLDFFNEMNEDGTLARIEEKYLGHGDDFDYVDTRTFLRAVDVLPQLKPLFEKYAEEI  
DWRLAAIAYQESHWDAQATSPTGVRGMMMLTKNTAQLGITDRDQAEQSISGGVRYLQ  
DMMSKVPESVPENERIWFALAAYNMGYAHMLDARALTAKTGNPDSWADVQRLPLLS  
QKPYYSKLTGYARGHEAYAYVENIRKYQISLVGYLQEKEKQATEAAMQLAQDYPAVSPT  
ELGKEKFPFLSFLSQSSSNYLTHSPSLLFSRKGSEEKQN

>sp|P25310|LYSM1\_STRGL Lysozyme M1 OS=Streptomyces globisporus GN=acm PE=1 SV=1

MPAYSSLARRRRPAVVLLGGLVSASLALTLAPTAAPLAPPPGKDVGPGEAYMGVGR  
IEQGLGAGPDERTIGPADTSGVQGIDVSHWQGSINWSSVKSAGMSFAYIKATEGTNYKDD  
RFSANYTNAYNAGIIRGAYHFARNASSGTAQADYFASNGGGWSRDNRTLPGVLDIEHNP  
SGAMCYGLSTTQMRTWINDFHARYKARTTRDVVIYTTASWWNTCTGSWNGMAAKSPF  
WVAHWGVSAPTVPSPGFTWTFWQYSATGRVGGVSGDVDRNKFNGSAARLLALANNTA

>sp|O07921|CHIS\_BACSU Chitosanase OS=Bacillus subtilis (strain 168) GN=csn PE=1 SV=1

MKISMQKADFWKKA AISLLVFTMFFTLMMSETVFAAGLNKDQKRAEQLSIFENGTTTEI  
QYGYVERLDDGRGYTCGRAGFTTATGDALEVVEVYTKAVPNNKLLKYLPELRLAKEES  
DDTSNLKGFASAWKSLANDKEFRAAQDKVNDHLYYQPAMKRSNAGLKTALARAVMY  
DTVIQHGDGDDPDSFYALIKRTNKKAGGSPKDGIDEKKWLNKFLDVRYDDLMPANHDT  
RDEWRESVARVDVLRSAKENNYNLNGPIHVSNEYGNFVIK

>sp|P39848|LYTD\_BACSU Beta-N-acetylglucosaminidase OS=Bacillus subtilis (strain 168) GN=lytD PE=1 SV=1

MKKRLIAPMLLSAASLAFFAMSGSAQAAAYTDYSLYKVEPSNTFSTESQASQAVAKLEKD

TGWDASYQASGTTTTTYQISASGIHSESEAKAILSLAKQTSITGTSSPVGSKQPYVTISSGAI  
SGEKQANTILAKLKQETGVAGAVKAYGAAQPYMNVMTSDIADETKVKALIQSLAKQTGI  
KSSYQPITHTVSVTTIQSGTIVGDSRAAQIKNAFQKESGLQASLKETVKGQAYYFTTAAIS  
GEANAKTLLQQLKQSTGITGSYKSINQKTTVESYNVQSAYFKGLSTVKDAISQIKKNTGVS  
GSYQQVVGKSTSYTVNMKGITKQQLQKIDTFFKKKKWHYTSSSVKKTTTSAAYQITTAKIL  
GEQQANKAAFFAQKKVKAATAAGSTAENQYQLISEETSDQAKVTKGLNILKKNQLSA  
SAKSVKKQIADTFKITTESLLDQTKVNQALTTFFKSNHISVASQKTGQTAASSYQITTEAIISSQ  
EIDRVLTTFFKQNHIAVTTSTKTGQTAYTQYKIVTTQLSSKTALNNGLTYLKSKSVTPSYTTK  
SNTLYKISVNEQFTGNDTAAAASTKLKQLYGWTSSIVKIKNGPQIMKTNYNLSLRDMVQK  
QMTVSPQTDGAAYVSLTYINTATSTVTADVLNIRSTPEVSPTNVIGQFKKGDVKVIGQIN  
GWAKINLGWRNASSDEVVQYVDPNNFSRDSKYFYFQLKLSQTAGLSVTEVNQKVLGK  
GILTGRAKAFIDAANQYSINELYLISHALLETGNGTSSALANGLTYNGKTVYNMYGIGAYDS  
NPNYYGAKYAYEQGWFTPEAAIIGGAKFIGSSYIHNTAYNQDTLYKMRWSATATHQYATDI  
GWAYKQVNRMYSLYSLLDGYTLYFDVPEYR

>sp|P59206|LYTB\_STRR6 Putative endo-beta-N-acetylglucosaminidase OS=Streptococcus pneumoniae (strain ATCC BAA-255 / R6) GN=lytB PE=1 SV=1

MKKVRFIFLALLFFLASPEGAMASDGTWQGKQYLKEDGSQAANEWVFDTHYQSWFYIK  
ADANYAENEWLKQGDDYFYLKSGGYMAKSEWVEDKGAFYYLDQDGKMKRNAWVGTS  
YVGATGAKVIEDWVYDSQYDAWFYIKADGQHAKEWLQIKGKDYFYKSGGYLLTSQWI  
NQAYVNASGAKVQQGWLFDKQYQSWFYIKENGNADKEWIFENGHYYYLKSGGYMAA  
NEWIWDKESWFYLFKFDGKIAEKEWVYDSHSQAWYYFKSGGYMAANEWIWDKESWFYL  
KFDGKMAEKEWVYDSHSQAWYYFKSGGYMTANEWIWDKESWFYLFKSDGKIAEKEWV  
YDSHSQAWYYFKSGGYMTANEWIWDKESWFYLFKSDGKMAEKEWVYDSHSQAWYYFK  
SGGYMAKNETVDGYQLGSDGKWLGGKATNKNAAYYQVVPVTANVYDSGGEKLSYISQ  
GSVVWLDKDRKSDDKRLAITISGLSGYMKTEDLQALDASKDFIPYYESDGHFRFYHYVAQ  
NASIPVASHLSMEVGGKYYASADGLHFDGFKLENPFLFKDLTEATNYSAEELDKVFSLLNI  
NNSLLENKGATFKEAEHYHINALYLLAHSALSNWGRSKIAKDKNFFGITAYDTTPYLS  
AKTFDDVDKILGATKWIKENYIDRGRTFLGNKASGMNVEYASDPYWGEKIASVMMKIN  
EKLGGKD

>sp|P13656|CHIA\_ECOLI Probable bifunctional chitinase/lysozyme OS=Escherichia coli (strain K12) GN=chiA PE=1 SV=2

MKLNIFTKSMIGMGLVCSALPALAMEAWNNQQGGNKYQVIFDGKIYENAWVVSSTNCP  
GKAKANDATNPWRLKRTATAAEISQFGNTLSCEKSGSSSSNSNTPASNTPANGGSATPAQ  
GTVPSNSSVVAWNKQQGGQTYVVFNGAVYKNAWWVASSNCPGDAKSNDASNPWRYV  
RAATATEISETSNPQSCTSAQPSPDVKPAPDVQAPADKSNNDYAVVAWKGQEG  
SSTWYVIYNGGIYKNAWWVGAANCPGDAKENDASNPWRYVRAATATEISQYGNPGSCS  
VKPDNNGGAVTPVDPTPETPVTPTPDNSEPSTPADSVNDYSLQAWSGQEGSEIYHVFNGN  
VYKNAWWVGSKDCPRGTSSENSNPWRLERTATAAELSQYGNPTTCEIDNGGIVADGF  
QASKAYSADSIVDYNDAAHYKTSVDQDAWGFVPGGDNPWKKYEPAKAWSASTVYVKGD  
RVVVDGQAYEALFWTQSDNPALVANQNATGSNSRPWKPLGKAQSYSNEELNNAQFNPE  
TLYASDTLIRFNGVNYISQSKVQKSPSDSNPWRVFDWTGKERVGTPKAWPKHVYAP  
YVDFTLNTIPDLAALAKNHNVNHFTLAFVVSKDANTCLPTWGTAYGMQNYAQYSKIKAL  
REAGGDVMLSIGGANPLAASCKNVDDLQHYDYDIVDNLNLKVLDFDIEGTWVADQA  
SIERNLAVKKVQDKWKSEGKDIAIWYTLPIPTGLTPEGMNVLSDAKAGVELAGVNV

MTMDYGNAICQSANTEGQNIHGKCATSAIANLHSQLKGLHPNKSDAEIDAMMGTTMPV  
GVNDVQGEVIFYLSARLVMQDAQKRNLGMVGIWSIARDLPGGTNLSPEFHGLTKEQAPK  
YAFSEIFAPFTKQ

>sp|P0C066|MLTC\_ECOLI Membrane-bound lytic murein transglycosylase C OS=Escherichia coli (strain K12) GN=mltC PE=1 SV=1

MKKYLALALIAPLLISCSTTKKGDYNEAWVKDTNGFDILMGQFAHNIENIWGFKEVVIA  
GPKDYVKYTDQYQTRSHINFDDGTITIEIAGTEPA AHLRRAI IKTLLMGDDPSSVDLYSDV  
DDITISKEPFLYGQVVDNTGQPIRWEGRASN FADYLLKNRLKSRNGLRIIYSVTINMVPNH  
LDKRAHKYLG MVRQASRKYGVDESLILAIMQTESSFNPYAVSRSDALGLMQVVQHTAGK  
DVFRSQGKSGTPSR SFLFDPASNIDGTAYLAMLNNVYLGIDNPTSRRYAVITAYNGGAG  
SVLRVFSNDKIQAANIINTMTPGDVYQTLTRHPSAESRRYLYKVNTAQKSYRRR

>tr|Q8ZLC6|Q8ZLC6\_SALTY Putative phage endolysin OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) GN=STM3605 PE=1 SV=1

MPHISSRFSSACIAFIKQWQGLSLEKYRDRQGNWVIGYGHMLTPDETTLTFITPDQAEAFLL  
DDLNSCDILLQNCLPELNDRFQRETLIALMFSIGHQRFLSLINTGDISQPEISGLRI

>sp|P06653|ALYS\_STRPN Autolysin OS=Streptococcus pneumoniae serotype 4 (strain ATCC BAA-334 / TIGR4) GN=lytA PE=1 SV=2

MEINVS KLRTDLPQVGVQPYRQVHAHSTGNPHSTVQNEADYHWRKDP ELGFFSHIVGNG  
CIMQVGPVDNGAWDVG GGWNAETYAAVELIESHSTKEEFMTDYRLYIELLRNLADEAGL  
PKTLDTGSLAGIKTHEYCTNNQPNHSDHVD PYPYLA KWGISREQFKHDIENGLTIETGW  
QKNDTGYWYVHSDGSYPKDKFEKINGTWY YFDSSGYMLADRWRKHTDGNWYWF DNS  
GEMATGWKKIADKWYFNEEGAMKTGWV KYKDTWY YLDAKEGAMVSNAFIQSADGT  
GWYYLKP DGT LADKPEFTVEPDGLITVK

>sp|I6XEI5|LYS25\_MYCTU Putative peptidoglycan hydrolase Rv2525c OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=Rv2525c PE=1 SV=1

MSVSRRDV LKFAAATPGVLGLGVVASSLRAAPASAGSLG TLLDYAAGVIPASQIRAAGAV  
GAIRYVSDRRPGGAWMLGKPIQLSEARDLSGNL KIVSCYQY GKGSTADWLGGASAGVQ  
HARRGSELHAAAGGPTSAPIYASIDNPSYEQYKNQIVPYLRSWESVIGHQRTGVYANSKT  
IDWAVNDGLGSYFWQHNW GSPKGYTHPAAHLHQVEIDKRKVGGVGV DNVNQLKPFQFQ  
WA

>sp|I6Y4D2|PEPAM\_MYCTU N-acetylmuramoyl-L-alanine amidase Rv3717  
OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=Rv3717 PE=1 SV=1

MIVGVLVAAATPIISSASATPANIAGMVVFIDPGHNGANDASIGRQVPTGRGGTKNCQASG  
TSTNSGYPEHTFTWETGLRLRAALNALGVRTALS RGN DNALGPCVDERANMANALRPNA  
IVSLHADGGPASGRGFHVNYSAPPLNAIQAGPSVQFARIMRDQLQASGIPKANYIGQDGLY  
GRSDLAGLNLAQYPSILVELGNMKNPADSALMESA EGRQKYANALVRGVAGFLATQGQA  
R

>sp|P33665|CHIS\_STRSN Chitosanase OS=Streptomyces sp. (strain N174) GN=csn PE=1 SV=1

MHSQHRTARIALAVVLT AIPASLATAGVGYASTQASTAVKAGAGLDDPHKKEIAMELVSSA  
ENSSLDWKAQYKYIEDIGDGRGYTGGIIGFCSGTGDMLELVQHYTDLEPGNILAKYLPAL  
KKVNGSASHSLGTPFTKDWATAAKDTVFQQA QNDERDRVYFDP AVSQA KADGLRALG  
QFAYYDAIVMHGPGNDPTSFGGIRKTAMKKARTPAQGGDETTYLNAFLDARKAAMLTEA  
AHDDTSRVDTEQRVFLKAGNLDLNPPLKWKTYGDPYVINS

>sp|P37710|ALYS\_ENTFA Autolysin OS=Enterococcus faecalis (strain ATCC 700802 / V583)

GN=EF\_0799 PE=1 SV=2

MKKESMSRIERRKAQQRKKTTPVQWKKSTTLFSSALIVSSVGTVPVALLPVTAEEATEEQPTNA  
EVAQAPTTETGLVETPTTETTPGTTEQPTTDSSTTTTESTTESKETPTTPSTEQPTADSTTPVE  
SGTTDSSVAEITPVAPSATESEAAPAVTPDDEVKVPPEARVASAQTFSALSPTQSPSEFIAELA  
RCAQPIAQANDLYASVMMAQAIVESGWGASTLSKAPNYNLFGIKGSYNGQSVYMDTWE  
YLNKWLKKEPFRKYPSYMEFQDNAHVLTTSFQAGVYYYAGAWKSNTSSYRDATA  
WLTGRYATDPSYNAKLNNVITAYNLTQYDTPSSGGNTGGGTVNPVTGGSSNNQSGTNTYY  
TVKSGDTLNKIAAQYGVSVANLRSWNGISGDLIFVGQKLIVKKGASGNTGGSGSGGSNNN  
QSGTNTYYTVKSGDTLNKIAAQYGVSVANLRSWNGISGDLIFVGQKLIVKKGASGNTGGS  
NNGGSNNNQSGTNTYYTIKSGDTLNKIAAQYGVSVANLRSWNGISGDLIFAGQKIIVKKG  
TSGNTGGSSNNGGSNNNQSGTNTYYTIKSGDTLNKISAQFGVSVANLQAWNNISGLIFAGQ  
KIIVKKGANSGSTNTNKPTNNGGATTSYTIKSGDTLNKISAQFGVSVANLRSWNGIKGDL  
IFAGQTIIVKKGASAGGNASSTNSASGRHTVKSGDSLWGLSMQYGISIQKIKQLNGLSGD  
TIYIGQTLKVG

>sp|A7IY64|ISAA\_STAXY Probable transglycosylase IsaA OS=Staphylococcus xylosus  
GN=isaA PE=1 SV=1

MKKTILASSLAVALGVTGYATTADHNQAHASEENIDKAHLADLAQNNPEELNPKPLHAG  
AYNYNFVLGGNEYTFTSNGQSWSWNYTAAGAQSATSNSVQDVTTQATTNTNETSASEVS  
AQKQSSNTPVAAVEAPKASSNTQTSAASTRYKVAQTSAASTGGSVKAQFLAAGGTEAMW  
NSIVMPESGPNPNAVNPAgyRGLGQTKESWGSGSVASQTKGMINYGESRYGSMEAAMTF  
RASHGWW

>sp|P39046|MUR2\_ENTHA Muramidase-2 OS=Enterococcus hirae (strain ATCC 9790 / DSM  
20160 / JCM 8729 / LMG 6399 / NBRC 3181 / NCIMB 6459 / NCDO 1258) GN=EHR\_05900  
PE=1 SV=1

MENIARKERRRLNETKRFRKVKRSAALVGTAMVGCSSVAAPLIQPVQVDADQTPTQFGARI  
NTAAFIAEIATYAQPIAQANDLYASVMIAQAVVESGWGSSALSQAPYYNLFGIKGSYQGQT  
VYMDTLEYLNNKWVSKKEPFRQYPSFAESFNDNAYVLRNTSFGNGYYYAGTWKSNTKS  
YTDATACTGRYATDPGYAGKLNIIITTYGLTKYDTPASGNAGGGVTIGNGGNTGNTSNG  
STSGNSGGSATTTGTTYTVKSGDSVWGISHSFGITMAQLIEWNNIKNNFIYPGQKLTIKGG  
QSAGSSTTNTGNNASSGNTSGTNTSGSTGQATGAKYTVKSGDSVWKIANDHGISMNQLI  
EWNNIKNNFVYPGQQLVSKGSSASGSTSNTSTGNTSSNTANTGSTTSGSTYTVKAGES  
VWSVSNKFGISMNQLIQWNNIKNNFIYPGQKLIVKGGSSSNASTSTANNKNTASSNTSST  
ATGQATYTVKAGESVWGVANKNGISMNQLIEWNNIKNNFIYPGQKLIVKGGSSKASATATI  
KPTASTPASTPTASSTGDTKYTVKAGESVWGVANKHHITMDQLIEWNNIKNNFIYPGQE  
VIVKKGTAQSTPAKSDEKTYTVKAGESVWGVADSHGITMNQLIEWNNIKNNFIYPGQQLI  
VKK

>tr|Q183J9|Q183J9\_PEPD6 Putative N-acetylmuramoyl-L-alanine amidase OS=Peptoclostridium  
difficile (strain 630) GN=CD630\_27610 PE=1 SV=1

MKKKLLDGGKITLICKSVKIYTKKDEEMSKGNNNNNSRNKSKKTSHLNRKKRKLNKKKL  
AVLICFTVLFLFIATKATQGVVALVKSMDKSNKTSQQQNVNSEQFDLGNEEENKKKKYTV  
FIDPGHGGNDKGTESKTSNRYEKDLNLQIAKLANKLSKQKDIQVVVSRDDTYISLKDR  
AILANNSSADVLVSIHLNAEKNGNTATGIETWYRNKATDGSKELAQTVQSTIVSYVKVRD  
RGIVENNFEVLRESNMPAILIECGFLTTPSEEQKIINEKYQDQLAEGIVQGVLSYLDKGNK

>sp|P63883|AMIC\_ECOLI N-acetylmuramoyl-L-alanine amidase AmiC OS=Escherichia coli

(strain K12) GN=amiC PE=1 SV=1

MSGSNTAISRRLQAGAMWLLSVSQVSLAAVSQVVAVRVWPASSYTRVTVESNRQLK  
YKQFALSNERVVVDIEDVNLNSVLKGMAAQIRADDPFIKSARVGQFDPQTVRVMVFELKQ  
NVKPQLFALAPVAGFKERLVMDLYPANAQDMQDPLLALLEDYNKGDLEKQVPPAQSGPQ  
PGKAGRDRPIVIMLDPGHGGEDSGAVGKYKTREKDVVLQIARRLRSLIEKEGNMKVYMT  
RNEDIFIPLQVRVAKAQKQRADLFVSIHADAFTSRQPSGSSVFALSTKGATSTAAKYLAQT  
QNASDLIGGVSKSGDRYVDHTMFDMVQSLTIADSLKFGKAVLNKLGKINKLHKNQVEQA  
GFAVLKAPDIPSILVETAFISNVEEERKLTATFQQEAESILAGIKAYFADGATLARRG

>sp|P24808|CWLA\_BACSU N-acetylmuramoyl-L-alanine amidase CwlA OS=Bacillus subtilis  
(strain 168) GN=cwlA PE=1 SV=1

MAIKVVKNLVSKSKYGLKCPNPMKAEYITIHNTANDASAANEISYMKNNSSTSFHFAVD  
DKQVIQGIPTNRNAWHTGDGTNGTGNRKSIGVEICYSKSGGVRYKAAEKLAIKFVAQLLK  
ERGWGIDRVRKHQDWNQKYCPHRILSEGRWIQVKTAEAEELKKLGGKTNSSKASVAKKK  
TTNTSSKTSYALPSGIFKVKSPMMRGEKVTQIQKALAAALYFYPDKGAKNNGIDGVYGP  
TADAIRRFQSMYGLTQDGIYGPCKAKLEALLK

>sp|L7N653|CWLM\_MYCTU N-acetylmuramoyl-L-alanine amidase CwlM OS=Mycobacterium  
tuberculosis (strain ATCC 25618 / H37Rv) GN=cwlM PE=1 SV=1

MPSPRREDGDALRCGDRSAVTEIRAALTAALGMLDHQEEDLTTGRNVALELFDAQLDQAV  
RAFQQHRGLLDGIVGEATYRALKEASYRLGARTLYHQFGAPLYGDDVATLQARLQDLGF  
YTGLVDGHFGLQTHNALMSYQREYGLAADGICGPETLRSYFLSSRVSGGSPHAIREELV  
RSSGPKLSGKRIIDPGRGGVDHGLIAQGPAGPISEADLLWDLASRLEGRMAAIGMETHLS  
RPTNRSPSDAERAATANAVGADLMISLRCETQTSLAANGVASFHFGNSHGSVSTIGRNLAD  
FIQREVVARTGLRDCRVHGRTWDLRLTRMPTVQVDIGYITNPHDRGMLVSTQTRDAIAE  
GILAAVKRLLYLLGKNDRPTGTFTFAELLAHELVERAGRLLGS

>tr|Q81YZ2|Q81YZ2\_BACAN Endolysin OS=Bacillus anthracis GN=yegX PE=1 SV=1

MGHIIDISKWNGDINWSIAKQHIDFIIARVQDGSNYVDPLYKGYVQAMKQHGIPFGNYAFC  
RFVSIADAKKEAQDFWNRGDKSATVWVADVEVKTMNDMRAGTQAFIDELYRLGAKKV  
GLYVGHMYPFGMANVKSDFVWIPRYGGNKPAYPCDIWQYTETGNVPGIGKCDLNSLI  
GNKSLSWFTESATQESVQAPTQNIQSGAFSPYETPDVTGALTSLKMTAKFILKPDGLTYFIS  
DPTSDAQLNAMKEYLDRKGGWYEVK

>sp|P50864|CWLD\_BACSU Germination-specific N-acetylmuramoyl-L-alanine amidase  
OS=Bacillus subtilis (strain 168) GN=cwlD PE=1 SV=1

MRKKLKWLSFLLGFILLFLFKYQFSNNDSWKPWSLPLSGKIIYLDPGHGGPDGGAVGGK  
LLEKDVTLVAFRVRDYLQEQALVIMTRESDTDLAPEGTKGYSSRKAEDLRQVRKLNH  
SEAELYISIHNAIPSQKWSGAQSFYYGKYAENEKVAKYIQDELRRNLENTTRKAKRIHGI  
YLMQNVTKPGALIEVGFLSNPSEATLLGKPKYQDKVASSIYKILRYFTEKGDPE

>sp|P82974|AMPD\_CITFR 1,6-anhydro-N-acetylmuramoyl-L-alanine amidase AmpD  
OS=Citrobacter freundii GN=ampD PE=1 SV=1

MLLDEGWLAEARRVSPHYDCRPDDENPSLLVHNISLPPGEFGGPWIDALFTGTIDPNAH  
PYFAGIAHLRVSACHLIRRDGEIVQYVPFDKRAWHAGVSSYQGRERCNDFSIGIELEGTDT  
LAYTDAQYQLAAVTNALITRYPAIANNMGTGHCNIAPERKTDPGPSFDWARFRALVTPSSH  
KEMT

>sp|Q02114|LYTC\_BACSU N-acetylmuramoyl-L-alanine amidase LytC OS=Bacillus subtilis  
(strain 168) GN=lytC PE=1 SV=1

MRSYIKVLTMCFLGLILFVPTALADNSVKRVGGSNRYGTAVQISKQMYSTASTAVIVGGSS  
YADAISAAPLAYQKNAPLLYTNSDKLSYETKTRLKEMQTKNVIIVGGTPAVSSNTANQIKS  
LGISIKRIAGSNRYDTAARVAKAMGATSKAVILNGFLYADAPAVIPYAAKNGYPILFTNKTSI  
NSATTSVIKDKGISSTVVVGGTGSISNTVYNKLPSPTRISGSNRYELAAANIVQKLNLSSTSV  
YVSNNGFSYPDSIAGATLAAKKKQSLILTNGENLSTGARKIIGSKNMSNFMIIIGNTPAVSTKV  
ANQLKNPVVGETIFIDPGHGDQDSGAIGNLLEKEVNLDAKRVNTKLNASGALPVLRS  
NDTFYSLQERVNKAASAQADLFLSIHANANDSSSPNGSETYYDTTYQAANSKRLAEQIQP  
KLAANLGRDRGVKTAIFYVIKYSKMPSVLVETAFITNASDASKLKQAVYKDKAAQAIH  
DGTVSYYR

>sp|P78285|LYSD\_ECOLI Lysozyme RrrD OS=Escherichia coli (strain K12) GN=rrrD PE=1  
SV=1

MPPSLRKAVAAAIGGGAIASVLTGPGSGNDGLEGVSYIPYKDIVGVWTVCHGHTGKDIM  
LGKTYTKAECKALLNKDLATVARQINPYIKVDIPETTRGALYSFVYNVVGAGNFRTSTLLRK  
INQGDIKGACDQLRRWYAGGKQWKGLMTRREIEREVCLWGQQ

>sp|P15931|FLGJ\_SALTY Peptidoglycan hydrolase FlgJ OS=Salmonella typhimurium (strain  
LT2 / SGSC1412 / ATCC 700720) GN=flgJ PE=1 SV=1

MIGDGKLLASAAWDAQSLNELKAKAGQDPAANIRPVARQVEGMFVQMMLKSMREALPK  
DGLFSSDQTRLYTSMYDQQIAQQMTAGKGLGLADMMVKQMTSGQTMPADDAPQVPLK  
FSLETVNSYQNQALTQLVRKAIPKTPDSSDAPLSGDSKDFLARLSLPARLASEQSGVPHHLI  
LAQAALSGWGQRQILRENGEPSYNVFGVKATASWKGVPVTEITTEYENGEAKKVKAKF  
RVYSSYLEALSDYVALLTRNPRYAAVTTAATAEQGAVALQNAGYATDPNYARKLTSMIQQL  
KAMSEKVSPTYSANLDNLF

>sp|P0AEZ7|MLTD\_ECOLI Membrane-bound lytic murein transglycosylase D OS=Escherichia  
coli (strain K12) GN=mltD PE=1 SV=1

MKAKAILLASVLLVGCQSTGNVQQHAQSLSAAGQGEAAKFTSQARWMDDGTSIAPDGD  
LWAFIGDELKMGIPENDRIREQKQKYLNRKSYLHDVTLRAEPYMYWIAGQVKKRNMPM  
ELVLLPIVESAFDPHATSGANAAGIWQIIPSTGRNYGLKQTRNYDARRDVVASTTAALNM  
MQRLNKMFDGDWLLTVAAYNSGEGRMKAIKTNKARGKSTDFWSLPLPQETKQYVPKM  
LALSDILKNSKRYGVRLPTTDESRLARVHLSSPVEMAKVADMAGISVSKLKTFFNAGVKG  
STLGASGPQYVMVPKKHADQLRESLASGEIAAVQSTLVADNTPLNSRVYTVRSGLTSSIA  
SRLGVSTKDLQQWNKLRGSKLPGQSLTIGAGSSAQLRANNSDSITYRVRKGDSSLSSIAKR  
HGVNIKDVMRWNSDTANLQPGDKLTLFVKNNNMPDS

>sp|P26365|AMIB\_ECOLI N-acetylmuramoyl-L-alanine amidase AmiB OS=Escherichia coli  
(strain K12) GN=amiB PE=1 SV=2

MMYRIRNWLVAATLLLLCTPVGAATLSDIQVSNGNQQARITLSFIGDPDYAFSHQSKRTVAL  
DIKQTGVIQGLPLLFSGNNLVKAIRSGTPKDAQTLRLVVDLTENGKTEAVKRQNGSNYTV  
VFTINADVPPPPPPVVAKRVPVAVPRVSEPARNPFKTESNRTTGVISSNTVTRPAARA  
TANTGDKIIAIDAGHGGQDPGAIGPGGTREKNVTIAIARKLRTLLNDPMPFKGVLTRDGD  
YFISVMGRSDVARKQANFLVSIHADAAPNRSATGASVWVLSNRRANSEMASWLEQHEK  
QSELLGGAGDVLANSQSDPYLSQAVLDLQFGHSQRVGYDVATSMISQLQRIGEIHKRPEH  
ASLGVLRSPDIPSVLVETGFISNNSEERLLASDDYQQQLAEAIYKGLRNYFLAHPMQSAPQ  
GATAQTASTVTPDRTLPN

>sp|Q9HXN1|MLTF\_PSEAE Membrane-bound lytic murein transglycosylase F  
OS=Pseudomonas aeruginosa (strain ATCC 15692 / PAO1 / 1C / PRS 101 / LMG 12228)



GN=mltF PE=1 SV=2

MFALTAYRLRCAAULLATGIFLLLAGCSEAKAPTALERVQKEGVLRVITRNSPATYFQDRN  
GETGFYEYELAKRFAERLGVELKIETADNLDDLYAQLSREGGPALAAAGLTPGREDDASVR  
YSHTYLDVTPQIIYRNGQQRPTRPEDLVGKRIMVLKGSSHAEQLAELKKQYPELKYEESD  
AVEVVDLLRMVDVGDIDLTLVDSNELAMNQVYFPNVRVAFDFGEARGLAWALPGGDDDS  
LMNEVNAFLDQAKKEGLLQRLKDRYYGHVDVLGYVGAYTFAQHLQQLPRYESHFKQS  
GKQLD TDWRLLAAIGYQESLWQPGATSKTGVRGLMMLTNRTAQAMGVS NRLDPKQSIQ  
GGSKYFVQIRSELPESIKEPDRSWFALAAYNIGGAHLEDARKMAEKEGLNPNKWL DVKK  
MLPRLAQKQWYAKTRYGYARGGETVHFVQNVRRYYDILT WVTQPQMEGSQIAESGLHL  
PGV NKTRPEEDSGDEKL

>sp|P36548|AMIA\_ECOLI N-acetylmuramoyl-L-alanine amidase AmiA OS=Escherichia coli  
(strain K12) GN=amiA PE=1 SV=1

MSTFKPLKTLTSRRQVLKAGLAAL TSLGMSQAI AKDELKTSNGHSPKAKKSGGKR VV  
VLDPGHGGIDTGAIGRNGSKEKHVVLAI AKNVR SILRNHGIDARLTRSGDTFIPLYDRVEIA  
HKHGADLFMSIHADGFTNPKAAGASV FALSNRGASSAMAKYLSERENRADEVAGKKATD  
KDHL LQQV LFDLVQTDTIKNSLTLGSHILKKIKPVHKLHSRNTEQA AFVVLKSPSVPSVLV  
ETSFITNPEEERLLGTAAFRQKIATAIAEGVISYFHWFDNQKAHSKKR

>sp|Q06320|CWLC\_BACSU Sporulation-specific N-acetylmuramoyl-L-alanine amidase  
OS=Bacillus subtilis (strain 168) GN=cwlC PE=1 SV=1

MVKIFIDPGHGGSDPGATGNGLQEKTTLQIALALRTILTNEYEGVSLLSRTSDQYVSLND  
RTNAANNWGADFFLSIHVNSGGGTGFESYIYPDVGAPTTTTYQSTIHSEVIQAVDFADRGKK  
TANFHVLRRESAMPALLTENGFIDTVSDANKLKTSSFIQSLARGHANGLEQAFNLKKTSSSG  
LYKVQIGAFKVKANADSLASNAEAKGFDSIVLLKDGLYKVQIGAFSSKDNADTLAARAK  
NAGFDAIVILES

>sp|Q8SCY1|EXLYS\_BPDPK Peptidoglycan hydrolase gp181 OS=Pseudomonas phage phiKZ  
PE=1 SV=1

MAKKVTL PKGQTGATGTTLGQAGNILDLSVDVDDIFGDTPKAKKGSPVTEFFNGIKQGLFD  
SVKPQQALKA FMRSAAPDGF SRMFGVYEDTMSTIRDVKDSVERTSASDLLFLTREAQDLA  
VKLKDKVPASVFDRLNNRLESQIENYKYAEDSNRNYKEIRRRMEAEDEDELKSAIDQVT  
LVQRDLAIAEQQGEVKRFAIGQAERGIRDKVSADRFDWMAKAMGQTV DNL SKLASYNE  
QVNYSIQKKGLEIQFRSMLHLRKIAQQTEATMELLNNGFAALVRNTGIPDHKSSMKDLV  
GFNAAQRVSSSFVDNAIQTLPNFLGNFGSAVTN NATRFANENIRNFADAVRAGNMFGADA  
WENRYNIAGQFAGSYLGDWTRNSVIPVLGRMARPGIERFSNNYLGGRHNQASYLLDNFP  
AWTQEYMNNYQNTY GARGILRDIMAPFIPQFTLQDRLKTGSYQTIGQDSGFNQLTQRTIV  
EAIPGYLSRLLQETRMIRTGRDDITREVF DLSTG SFMSVEDSAANTERRLVSRSTVRGVSG  
ALTDVLEAFDPNKELSIDARKALTERLIRDANMNRFDPEAYARAGGYDRSKVSGETIKEL  
TEYIKRQYNIGADGRMASTNENFARRQEISTLFLDVRNFSRDPIKEIERLTNAGKTDQLRE  
MGIITEQGIDRINYPRIWELMSSEVKYEGWGNDNPFDRYSDTPPSDNGGPEQLSPLGDQN  
NPHFIGPMYQSQTERKMRQAQEQVIRASKLAQEQANKGYDYAQQKVS LATDYVRDNVP  
NQFSELRRNVNIPASMNFGDLRDQLYGQAGDMYSRAVNYSNQLNGYSDIINQSIADLYTK  
ANTFTPVIKGMDFLNGNLIDINTGMIVEKISDITGEIKNQAGITVVTAQEVATGLYNQRGDL  
LTKATDIASQLRDKAAQIAGDARERLTQGLDNVSDMAKD WYIPGREEAVILGRDLLAGEY  
IDTATNQIITNLKDAKGTIINRAGDVVVTAQELAKGLIRSDGFNLRRNIADTSNWIQRNVLG  
GGSTTQKIFNAMGTVANKAKDFTIGLGDILSNRDAYLPGMLKPV LQKVKLKAGEYYTT

AGNLLKSFDEINGPVLDRDGNIVVDEEQISELINS DGSKHTAAKSKGLFRTGLGNLARGYA  
NMSMRYWKWL GKKSVD TAKGMAGLGYKLLGSPFKKRFS AFTGKVETQIDKKALD TTTD  
QLLAGIWEELRNQKPDANKPRRGSWQDLTSRVSDTLNGKNNGDEETTESKGLFGKLGDT  
LKNIFGKKKGDEEDEGLLEDLGLGGKKGKWAARQILGRGALAIGGGALSTAAAYASF  
GGTGASTNDKLAGAAIVTSPIMWALKDFLIKPVLGWRGSQKFKDDLISYRMMQYGATT  
TDQMNVTELEQLVSSVATRGGDASFDV RALNARDI IKIFGYGADDGPAIMRLANWIDFR  
FKPIFEAWLKGLSKINRSDVDISEVDSKVPNELK GQLIRSVSFPYEGNTPYLVLNNPFGEED  
LSIDVASIQMKEKELLNKYSATEKTSVAPKATSSSFKESTTDVINDTITTIKSKSTDITNWFR  
DSTIGKAIKAVSPVESIRKMVTTTTVDTIIPKANASDSLTSLQALRVHAYGMQGLDLAAVNG  
LLSIESLVNDKMRVANGKATYTGDI EELIKWTGQAFGMVTTSDGPDRVKVVDWLYRRFLP  
VFKAFIVTARSVSTSITLSQIETLTATQRVQIANAIMGATDDEGISIWKAPSIFNIVGDMDSVE  
DLAKISLDEIKKEAETEVAEAPGKSKSAQIAGKNDAA SGRSFASRIIDNVKSTFNSATTKVT  
NWMENTSARVSQVIGRAREGVTDYTYTAKYKLGAGGELTPTGQTYGQLATGNGGVWEN  
IPMPQSNKSRDAAQATFKAVSEMTGVPVELLNIFCGIESSFNYN AKAPTSSAAGWFQFIKS  
TWKGM LAKYGAKFGIPADDENGLRFDPRINALMGAMFLRDNYEYLENALGRAPTDVD  
LYLAHFMPGAGARKFLTRDQNSIGAEIFPDQARANRSIFFKTDGSARTLGEIYQVMENKVA  
KFRRTGGKNANSQSLGKPKSTEELMND AATAKQKDMATDKELIGGAADTSITDSSNNKIG  
LGKIMSGMASPLRTNAPSMMLPGAPSSATDVSSGQQPVVDTGAATQATVRASQIEEQRKV  
VTSQDKAMLDIASEQLSVLKQFHADILNYIKNKAANPSAQTGQE QANTIAPSQRPGRVVD  
NRPLPIRLR

>sp|Q9T1X2|ENLYS\_BPMU Endolysin OS=Enterobacteria phage Mu GN=lys PE=2 SV=1

MAGIPKKLKAALLAVTIAGGGVGGYQEMTRQSLIHLENIAYMPYRDIAGVLTVCVGHTGP  
DIEMRRYSHAECMALLDSDLKPVYAAIDRLVRVLPYQKTALATFIFNTGVTAFSKSTLLK  
KLNAGDYAGARDQMARWVFAAGHKWKGLMNRREVEMAIWNIRGADDLRQ

>sp|P03726|EXLYS\_BPT7 Peptidoglycan hydrolase gp16 OS=Enterobacteria phage T7 GN=16  
PE=1 SV=1

MDKYDKNVPSDYDGLFQKAADANGVSYDLLR KVAWTESRFVPTAKSKTGPLGMMQFTK  
ATAKALGLRVTDGPD DDLRNPELAINAAKQLAGLVGKFDGDELKAALAYNQGEGR LGN  
PQLEAYSKGDFASISEGRNYMRNLLDVAKSPMAGQLETFFGGITPKGKGIPAEVGLAGIGH  
KQKVTQELPESTSFVDVKGIEQEATAKPFKDFWETHGETLDEYNSRSTFFGFKNAAEAELS  
NSVAGMAFRAGRLDNGFDVFKDTITPTRWNSHIWTPEELEKIRTEVKNPAYINVVTGGSPE  
NLDDLKLANENFENDSRAAEAGLGAKLSAGIIGAGVDPLSYVPMVGVGTGKGFKLINKAL  
VVGAE SAALNVASEGLR TSVAGGDADYAGAALGGFVFGAGMSAISDAVAAGLKRKPEA  
EFDNEFIGPMMRLEARETARNANSADLSRMNTENMKFEGEHNGVPYEDLPTERGAVVLH  
DGSVLSASNPINPKTLKEFSEVDPEKAARGIKLAGFTEIGLKTLSGDDADIRRV AIDLVRSP  
GMQSGASGKFGATASDIHERLHGTDQRTYNDLYKAMSDAMKDPEFSTGGAKMSREETRY  
TIYRRAALAIERPELQKALTPSERIVMDIIKRHFDTKRELMENPAIFGNTKAVSIFPESRHKG  
TYVPHVYDRHAKALMIQRYGAEGLQEGIARSWMNSYVSRPEVKARVDEMLKELHGVKE  
VTPEMVEKYAMD KAYGISHSDQFTNSSIIEENIEGLVGIENNSFLEARNLFDSDL SITMPDG  
QQFSVNDLRDFDMFRIMPAYDRRVNGDIAIMGSTGKTTKELKDEILALKAKAEGDGKKT  
GEVHALMDTVKILTGRARRNQDTVWETSLRAIN DLGFFAKNAYMGAQNITEIAGMIVTG  
NVRALGHGIPILRDTLYKSKPVSAKELKELHASLFGKEVDQLIRPKRADIVQRLREATDTG  
PAVANIVGTLKYSTQELAARSPWTKLLNGTTNYLLD AARQGM LGDVISATLTGKTTRWEK  
EGFLRGASVTPEQMAGIKSLIKEHMRGEGDGKFTVKDKQAFSMDPRAMD LWR LADKVA

DEAMLRPHKVSLSQDSHAFGALGKMVMQFKSFTIKSLNSKFLRTFYDGYKNNRAIDAALSI  
ITSMGLAGGFYAMAAHVKAYALPKEKRKEYLERALDPTMIAHAALSRSSQLGAPLAMVD  
LVGGVLFESSKMARSTILPKDTPKERDPNKPYSREVMGAMGSNLEQMPSAGFVANV  
GATLMNAAGVVNSPNKATEQDFMTGLMNSTKELVPNDPLTQQLVLKIYEANGVNLRRR  
K

>sp|Q37875|LYS\_BPP1 Lysozyme OS=Enterobacteria phage P1 GN=17 PE=1 SV=1

MKGKTAAGGGAICAIIVMITIVMGNNGVVRTNQAGLELIGNAEGCRRDPYMCAGVWTD  
GIGNTHGVTPGVRKTDQQAADWEKNILIAERCINQHFRGKDMPDNAFSAMTSAAFNMG  
CNSLRTYYSKARGMRVETSIHKWAQKGEWVNMCNHLPDFVNSNGVPLRGLKIRREKER  
QLCLTGLVNE

>sp|Q37979|AEPE\_BPA50 L-alanyl-D-glutamate peptidase OS=Listeria phage A500 GN=ply  
PE=1 SV=1

MALTEAWLIEKANRKLNAGGMYKITSKTRNVIKKMAKEGIYLCVAQGYRSTAEQNALY  
AQGRTPGAIVTNAKGGQSNHNYGVAVDLCLYTNDGKDVWESTTSRWKKVVAAMKAE  
GFKWGGDWKSFKDYPHFELCDAVSGEKIPAAATQNTNTNSNRYEGKVIDSAPLLPKMDFKS  
SPFRMYKVGTEFLVYDHNQYWYKTYIDDKLYMYKSFCDVVAKKDAKGRIKVIKSAK  
DLRIPVWNNIKLNSGKIKWYAPNVKLAWYNYRRGYLELWYPNDGWYYTAEYFLK

>sp|Q37976|AEPE\_BPA18 L-alanyl-D-glutamate peptidase OS=Listeria phage A118 GN=ply  
PE=2 SV=2

MTSYYYSRSLANVNKLADNTKAAARKLLDSESNIEVLIYETIRTKEQQAANVNSGAS  
QTMRSYHLVGQALDFVMAKGKTVDWGAYRSDKGKGFVAKAKSLGFEGGDDWSGFVD  
NPHLQFNYKGYGTDTFGKGASTSNSSKPSADTNTNSLGLVDYMNLNKLDSSFANRKKLA  
TSYGIKNYSGTATQNTTLLAKLKAGKPHTPASKNTYYTENPRKVKTIVQCDLYKSVDFTT  
KNQTTGGTFPPGTVFTISGMGKTKGGTPRLKTKSGYYLTANTKFKVKKI

>tr|B6SBV8|B6SBV8\_9CAUD Endolysin OS=Clostridium phage phiCD27 PE=1 SV=1

MKICITVGHSLKSGACTSADGVVNEYQYNKSLAPVLADTFRKEGHKVDVVICPEKQFKT  
KNEEKSYKIPRVNSGGYDLLIELHLNASNGQGKSEVLYYSNKGLEYATRICDKLGTVFK  
NRGAKLDKRLYLNSKPTAVLIESFFCDNKEDYDKAKKLGHEGIAKLIVEGVLNKNINNE  
GVKQMYKHTIVYDGEVDKISATVVGWGYNDGKILICDIKDYVPGQTQONLYVVGGGACE  
KISSITKEKFIMIKGNDRFDTLTKALDFINR

>sp|P03706|ENLYS\_LAMBDA Endolysin OS=Enterobacteria phage lambda GN=R PE=1 SV=1

MVEINNQRKAFLDMLAWSEGTDNGRQKTRNHGYDVIVGGELFTDYSHPKLVTLNPKL  
KSTGAGRYQLLSRWWDAYRKQLGLKDFSPKSQDAVALQQIKERGALPMDRGRDIRQAIDR  
CSNIWASLPGAGYGFQFEHKADSLIAKFKEAGGTVREIDV

>tr|D6QY02|D6QY02\_9CAUD Endolysin OS=Staphylococcus phage GH15 GN=lysGH15 PE=1  
SV=1

MAKTQAEINKRLDAYAKGTVDSPYRIKKATSYDPSFGVMEAGAIDADGYYHAQCQDLIT  
DYVLWLTNDKNVTRWGNKADQIKQSYGTGFKIHENKPSTVPKKGWIAVFTSGSYQQWGH  
GIVYDGGNTSTFTILEQNWNGYANKKPTKRVDNYYGLTHFIEIPVKAGTTVKKETAKKSA  
SKTPAPKKKATLKVSKNHINYTMKDRGKKEGPMVIHNDAGRSSGQQYENSLANAGYARY  
ANGIAHYYGSEGYVWEAIDAKNQIAWHTGDGTGANSNGNFRFAGIEVCQSMSASDAQFLK  
NEQAVFQFTAEEKFKEWGLTPNRKTVRLHMEFVPTACPHRSMVLHTGFNPVTQGRPSQAI  
MNKLDYFIKQIKNYMDKGTSSSTVVKDGTSSASTPATRPVTGSWKKNQYGTWYKPEN  
ATFVNGNQPIVTRIGSPFLNAPVGGNLPAGATIVYDEVCIQAGHIWIGYNAYNGDRVYCPV

RTCQGVPPNHIPGVAWGVFK

>sp|Q6QGP7|ENLYS\_BPT5 L-alanyl-D-glutamate peptidase OS=Escherichia phage T5 GN=lys PE=1 SV=1

MSFKFGKNSEKQLATVKPELQKVARRALELSPYDFTIVQGIRTVAQSAQNIANGTSFLKDP  
SKSKHITGDAIDFAPYINGKIDWNDLEAFWAVKKA FEQAGKELGIKLRFGADWNASGDY  
HDEIKRGTYDGGHVELV

>sp|O03979|ALYS\_BPDP1 Lysin OS=Pneumococcus phage Dp-1 GN=PAL PE=1 SV=1

MGVDIEKGVAVMQRKGRVSYSMDFRDGPDSDYDCSSSMYYALRSAGASSAGWAVNTEY  
MHAWLIENGYELISENAPWDAKRGDIFWGRKKGASAGAGGHTGMFIDSDNIIHCNYAYDG  
ISVNDHDERWYYAGQPYYYVYRLTNANAQPAEKKLWQKDATGFWYARANGTYPKDEF  
EYIEENKSWFYFDDQGYMLAEKWLKHTDGNWYWFDRDGYMATSWKRIGESWYYFNR  
DGSMVTGWIKYYDNWYYCDATNGDMKSNAFIRYNDGWYLLLPDGR LADKPQFTVEPD  
GLITAKV

>sp|P00806|ENLYS\_BPT7 Endolysin OS=Enterobacteria phage T7 GN=3.5 PE=1 SV=4

MARVQFKQRESTDAIFVHCSATKPSQNVGVREIRQWHKEQGWLVDVGYHFIKRDGTVEA  
GRDEMAVGS HAKGYNHNSIGVCLVGGIDDKGKFDANFTPAQMQLRSLLVTL LAKYEGA  
VLR AHHEVAPKACPSFDLKRWWEKNELVTS DRG

>sp|P07582|EXLYS\_BPPH6 Peptidoglycan hydrolase gp5 OS=Pseudomonas phage phi6 GN=P5 PE=1 SV=2

MSKDSAFAVQYSLRALGQKVRADGVVVGSETRAALDALPENQKKAIVELQALLPKAQS VG  
NNRVRFTTAEVDSAVARISQKIGVPASYQFLIPIENFV VAGGFETT VSGSFRGLGQFN RQT  
WDRLRRLGRNLPAFEEGSAQLNASLYAIGFLYLENKRAYEASF KGRVFTHEIAYLYHNQGA  
PAAEQYLTSGR LVYPKQSEAAVAVA AARNQHVKESWA

>tr|B6D7J9|B6D7J9\_9CAUD Gp26 OS=Listeria phage P40 PE=1 SV=1

MVLVLDISKWQPTVNYSGLKEDVGFVVIRSSNGTQKYDERLEQHAKGLDKVGM PFGLYH  
YALFEGGQDTINEANMLVSAYKKCRQLGA EPTFLFDYEEVKL KSGNVVNECQR FIDHVK  
GQTGVKVGLYAGDSFWKTHDLDKVKHDLRWVARYGVDNGK PSTKPSIPYDLWQYTSKG  
RIKAIASPVDMNTCSSDILNKLKGS KAPVKPAPKPTSPK PAKPAPKTTTKYVNTAHLNIR  
EKASADSKVLGVLNDSVQVISESGGWSKLKSGNKQVYVSSKYLSKSKTTPKAKPSSK  
QYYTIKSGDNLSYIAKKYKTTVKQIQNWNGIKDANKIYAGQKIRVK

>sp|P09963|ENLYS\_BPP22 Endolysin OS=Enterobacteria phage P22 GN=19 PE=1 SV=1

MMQISSNGITRLKREEGERLKAYS DSRGIPTIGVGH TGVKVDGNSVASGMTITAEKSSELLK  
EDLQWVEDAISSLVRVPLNQNQYDALCSLIFNIGKSAFAGSTVLRQLNLKNYQAAADAF L  
LWKKAGKDPDILLPRRRRERALFLS

>sp|Q38653|ALYS\_BPA51 Endolysin OS=Listeria phage A511 GN=PLY511 PE=2 SV=1

MVKYTVENKIIAGLPKGKLGANFVIAHETANSKSTIDNEVSYMTRNWKNAFVTHFVGG  
GGRVVQVANVNYVSWGAGQYANSYSYAQVELCRTSNATTFKKDYEVYCQLLVDLAKKA  
GIPITLDSGSKTSDKGIKSHKWVADKLG GTTHQDPYAYLSSWGISKAQFASDLAKVSGGG  
NTGTAPAKPSTPAPKPSTPSTNLDKLG LVDYMN AKKMDSSYSNRDKLAKQYGIANYSGTA  
SQNTLLSKIKGGAPKPSTPAPKPSTSTAKKIYFPPNKG NWSVYPTNKAPVKANAIGAINPT  
KFGGLTYTIQKDRNGVYEIQTDQFGRVQVY GAVIKK

>tr|D9ZNF3|D9ZNF3\_9CAUD Endolysin OS=Clostridium phage phiCTP1 GN=phiCTP1\_gp29 PE=1 SV=1

MKKIADISNLNGNVDV KLLFN LGYIGIIAKASEGGTFV DKYKQNYTNTKAQ GKITGAYH

FANFSTIAKAQQEANFFLNCAIAGTTPDFVVDLEQQCTGDITDACLAFLNIVAKKFKCVVY  
CNSSFIKEHLNSKICAYPLWIANYGVATPAFTLWTKYAMWQFTEKGQVSGISGYIDFSYITD  
EFIKYIKGEDEVENLVVYNDGADQRAAEYLADRLACPTINNARKFDYSNVKNVYAVGGN  
KEQYTSYLTTLIAGSTRYTTMQAVLDYIKNLK

>sp|P03639|E\_BPPHS Lysis protein E OS=Enterobacteria phage phiX174 (Isolate Sanger) GN=E  
PE=1 SV=2

MVRWTLWDTLAFLLLLSLLLPSLLIMFIPSTFKRPVSSWKALNLRKTLLMASSVRLKPLNC  
SRLPCVYAQETLTFLLTQKKTCVKNYVRKE

>sp|P16009|NEEDL\_BPT4 Peptidoglycan hydrolase gp5 OS=Enterobacteria phage T4 GN=5  
PE=1 SV=2

MEMISNNLNWFVGVVEDRMDPLKLGRVVRVVGVLHPPQRAQGDVMGIPTKLPWMSVI  
QPITSAAMSGIGGSVTGPVEGTRVYGHFLDKWKTNGIVLGTYYGGIVREKPNRLEGFSIPT  
GQYPRRLGNDTNVLNQGGEVGYDSSSNVIQDSNLDTAINPDDRPLSEIPTDDNPNMSMAE  
MLRRDEGLRLKVYWDTEGYPTIGIGHLIMKQPVRDMAQINKVLSKQVGREITGNPGSITM  
EEATTLFERDLADMQRDIKSHSKVGPVWQAVNRSRQMALENMAFQMGVGGVAKFNTML  
TAMLAGDWEKAYKAGRDSLWYQQTKGRASRVMTMILTGNLESYGVEVKTPARSLSAMAA  
TVAKSSDPADPPIPNDSRILFKEPVSSYKGEYPYVHTMETESGHIQEFDDTPGQERYRLVHP  
TGTYEEVSPSGRRTRKTVDNLYDITNADGNFLVAGDKKTNVGGSEIYYNMDNRLHQIDGS  
NTIFVRGDETKTVEGNGTILVKGNTIIVEGNADITVKGDATTLVEGNQNTNVNGNLSWK  
VAGTVDWDVGGDWTEKMASMSSISSGQYTIDGSRIDIG

>sp|P33486|LYS\_BPMV1 Lysozyme OS=Lactococcus phage mv1 GN=lysA PE=1 SV=3

MTKTYGVDVAVYQPIDLAAYHKAGASFAIVKLTEGVDYVNRGSRWTAPGLTTSTLMPT  
ISRSFGSSVSRAKKEAAYFLKEAKKQDISKKRMLWLDWEAGSGNVVTGSKSSNTAAILDF  
MDAIKAAGWRPGLYSGASLMRTAIDTKQVVKKYGTCLWVASYPTMAAVSTADFGYFRQ  
WTGSPSGSLPVTAWPGRRRERCSG

>sp|Q7Y2C9|EXLYS\_BPKMV Peptidoglycan hydrolase gp36 OS=Enterobacteria phage phiKMV  
GN=gp36 PE=1 SV=1

MAESQRASQELGINVGQTQLQPGQSARRGVRDSEVNYSGPSVGSQILDGILGAGQQIAGK  
WFEHNVQQEVLRRGERARMAGEAEEAVDSNVLAKPFVKGGWRKQDYRIAQADFLKMQ  
RFIANKGREMTPEEFRKYLSEATHVLDSTEGMNPNDALQALAQKQAEQFLGMQAKA  
YMDWSIDQAARGFRTQGNSILAKAVQAQATGDELSRQLSLEEAGLFYTNIMTSEDIPLEVR  
DKVGMQFLAASLDMNQRGIYEGLRDAGFLDSMSFDDRRALNGLYEKSKAQTRAKESMA  
TLRADADFQQRVANGAITDLAEVEAYSRRGMVEEGRWSDAQAI SFMTKAMTGLGNAQRM  
QGIMAALAEAGDINALHTLGTNVTEALEQWDKMQAANGSSLTDRLVQGTQLGLRLGTFFPK  
TYGESVGS AVRMIQAAKEGEANPELVNTLNSIFEQVASAQEINPSAGNVMLSGIPEAEQGA  
VAWALKQMKGIAPAQALREFSANA EVVKQMDEFKQNTKAFKDNLGKQVNDK FVN  
NIFGRAWNMLTGESDLSNNEAVLSMYRRATIDEANWLASDRKHAGLLTSDTGREALLEIA  
AANVRNRTIQVGEGRNLKEGDLFSRRDSAPLILPRGTAEQLFGTNDTETIGTVLAEQHKP  
HVEGLLGYKSVVAFEYDRTSGSLLAVEYDENGVALDRTRVDPQAVGKEVLKRNADKLNA  
MRGAEYGANVKVSGTDIRMNGGNSAGMLKQDVFNWRKELAQFEAYRGEAYKDADGYS  
VGLGHYLGSGNAGAGTTVTPEQAAQWFAEDTDRALDQGVRLADELGVTNNASILGLAG  
MAFQMGEGRARQFRNTFQAIKDRNKEAFEAGVRNSKWYTQTPDRAEAFIKRMAPHFDT  
PSQIGVDWYSAATAE

>sp|Q7Y2C0|ENLYS\_BPKMV SAR Endolysin OS=Enterobacteria phage phiKMV GN=45 PE=1

SV=1

MNKPLRGAALAAALAGLVALEGSETTAYRDIAGVPTICSGTTAGVKMGDKATPEQCYQM  
TIKDFQRFERIVLDAIKVPLNVNEQTALTFFCYNVGPVCTTSTAFKRFNQGRATEGCQALA  
MWNKVTINGQKVVSGLVNRNNAEIKQCLEPSSQYSSLLW

>sp|P13559|VLYS\_BPPRD Lysozyme OS=Enterobacteria phage PRD1 GN=XV PE=1 SV=2

MQYTLWDIISRVESNGNLKALRFEPEYYQRRMERSGDWDNSIIQNIRAANKCSLGTARMIY  
CSSWGAVQIMGFNLYLNGAFNLSVAHFMEANEAYQVNEFRRFLLKNGLTEYTPERLASDKA  
ARVKFAKVYNGAESYADLILQACQFYGVK

>sp|P15132|VG13\_BPPH2 Morphogenesis protein 1 OS=Bacillus phage phi29 GN=13 PE=1  
SV=2

MVYVSNKYLTSEMKVNAQYILNYLSSNGWTKQAICGMLGNMQSESTINPGLWQNLDE  
GNTSLGFGLVQWTPASNYINWANSQGLPYKDMSELKRIIWEVNNNAQWINLRDMTFKE  
YIKSTKTPRELAMIFLASYERPANPNQPERGDQAEYWYKNLSGGGGGGLQLAQFPMIINI  
SQGENGSFSHKGTLCIDFVGKTEKYPYAPCDCTCVWRGDASAYLAWTSDKEVMCADG  
SVRYITWVNVHESPLPFDVGKLLKKGDLMGHTGIGGNVTGDHWHFNVIDGKEYQGWTK  
KPDSCLAGTELHIYDVFVNNVEIINGNGYDWKTSWQDGDGGDGDNDNDNNTKDLI  
TLLSDALHGWKA

>tr|H2D0G4|H2D0G4\_9CAUD Endolysin OS=Salmonella phage SPN1S GN=SPN1S\_0028 PE=1  
SV=1

MDINQFRRASGINEQLAARWFPHITTAMNEFGITKPDDQAMFIAQVGHESGGFTRLQENF  
NYSVNGLSGFIRAGRITPDQANALGRKTYEKSPLERQRAIANLVYSKRMGNNGPGDGW  
NYRGRGLIQITGLNNYRDCGNGLKVDLVAQPELLAQDEYAARSAAWFFSSKGCMTYTG  
LVRVTQIINGGQNGIDRRTRYAAARKVLAL

>sp|P19385|LYS\_BPCP7 Lysozyme OS=Streptococcus phage Cp-7 GN=CPL7 PE=1 SV=2

MVKKNDLFVDVASHQGYDISGILEEAGTTNTIIVSESTSYLNPCLSAQVSQSNPIGFYHFA  
WFGGNEEEAEAEARYFLDNVPTQVKYLVLDYEDHASASVQRNTTACLRFMQIIAEAGYT  
PIYYSYKPFTLDNVDYQQILAQFPNSLWIAGYGLNDGTANFEYFPSMDGIRWWQYSSNPF  
DKNIVLLDDEKEDNINNENTLKSLETTVANEVIQGLWGNGQERYDSLANAGYDPQAVQDK  
VNEILNAREIADLTTVANEVIQGLWGNGQERYDSLANAGYDPQAVQDKVNEILNAREIAD  
LTTVANEVIQGLWGNGQERYDSLANAGYDPQAVQDKVNELLS

>sp|P27380|EXLYS\_BPPRD Transglycosylase OS=Enterobacteria phage PRD1 GN=VII PE=1  
SV=3

MSGALQWWETIGAASAQYNLDPRLVAGVVQTESSGNPRTTSGVGAMGLMQLMPATAKS  
LGVNTNAYDPTQNIYGAALLRENLDYGDVNTALLAYHGGTNQANWGAKTKSYPGKV  
MKNINLLFGNSGPVVTPAAGIAPVSGAQEMTAVNISDYTAPDLTGLTMGAGSPDFTGGAS  
GSWGEENIPWYRVDKHAVANAAGSAYDAVTDVAVSAPVEAAGNYALRGVVIIAAVAIVVVG  
LYFLFQDEINSAAMKMIPAGKAAGAAAKALA

## Non-Lyase for Bacterial Cell Wall

>sp|P23541|A2\_BPT5 Protein A2 OS=Escherichia phage T5 GN=A2 PE=1 SV=2

MTNAKTAKFAWNEENTQKAVSMYQQLINENGLDFANS DGLKEIAKAVGAASPVSVRSKL  
TSAKAYQKSDKPRKVG GSSIRKAHYVRVIAKHAIDSGIIKDADDLASLES AKLETLDAVA  
QLLGV ADEVKQAAGE

>sp|Q6QGT3|A1\_BPT5 Protein A1 OS=Escherichia phage T5 GN=A1 PE=1 SV=1

MVISA EKQTVILKMAADFN FYGKRLRATKLEV CDDISKMVYD TTKHSTAICDWLEANKP  
AKPKAAKVAKAIKNDERPEAAGIVSSTVEQWEVKQ GKRFIITSIQNNTFP HKNFLASLEQY  
AQFIGADLLVSKFIYNKNGFQNGEGADGIRYDSAFDKYICNKNVFLNRRFAFMAEINVLP  
TADYPLSGFAETATALNLEGLAIGAAKITAESVPALKGEIVRRMYSTGTATLKNYIQKAG  
QKAEALHNFGALIVEFDEDEGEFFVRQLETMDESGVFYDLNTCATPAGCYETTGHVGLGQ  
YGDIHAEKLD EEC AAASWGHGDTYGLVDILPKYQFVHDVHDFTSRNHHNRASGVFLA  
KQYAAGRDKVLDLIDTGRVLES MERDFSQTIIVESNHDLALSRLWDDR NANIKDDPANA  
ELYHRLNAAIYGAI AEKDDTFNVLDYALRKVAGCEFN AIFLTTDQSFKIAGIECGVHGHNG  
INGSRGNPKQFKKLGKLN TGHTHTASIYGGVYTAGVTGSLDMGYNVGASSWTQTHIITYA  
NGQRTLIDFKNGKFFA

>sp|P06022|ACTC\_BPMU Late transcription activator C OS=Enterobacteria phage Mu GN=C  
PE=1 SV=1

MQHDLFEHDP AIRQLIGHIDNIPAPELESRWPRS VVDLIDVLENELKRQNVSNPRELARKQ  
AVALSCFLGGRQFYIPCGDTILTALRDDLLYCQFN GRNMEELRRQYRLSQPQIYQIARQRK  
LHTRRHQPDLFSPETPK

>sp|P13304|ANTI\_H\_BPT4 Antiholin OS=Enterobacteria phage T4 GN=rI PE=1 SV=1

MALKATALFAM LGLSFVLSPIEANVDPHFDKFMESGIRHVYMLFENKSVESSEQFY SFMR  
TTYKNDPCSSDFECIERGAEMAQSYARIMNIKLETE

>sp|P32267|ASIA\_BPT4 10 kDa anti-sigma factor OS=Enterobacteria phage T4 GN=asiA PE=1  
SV=1

MNKNIDTVREIITVASILIKFSREDIVENRANFIAFLNEIGVTHEGRKLNQNSFRKIVSELTQE  
DKKTLIDEFNEGFE GVYRYLEMYTNK

>sp|Q9T1V1|BP48\_BPMU Baseplate protein gp48 OS=Enterobacteria phage Mu GN=Mup48  
PE=2 SV=1

MAVTPWQTAFLQLLPSGLAWNKSPDSKLSALAQ AISDVIATAADDARQMLRERFPSTSRW  
YLG EWESFLGLPDCTSENGTL SERQRAAANKMRMTGNLSRRFYEWLAAQYGFTVRLTDS  
TEGQWWTQVNIYGIKNYRNATVLDNVLTPLRVYESGALECLLEKYKPAHQIYKFVYHDG  
DN

>sp|P08986|BIMM\_BPT4 Immunity protein OS=Enterobacteria phage T4 GN=imm PE=1 SV=1

METLVAGSIFMVLVSGVLAI IYMLPWFIALMRGSKSTVGIFFASLLFNWSIIGWFITFIWSIA  
GETKKSAQPNQVIII REKE

>sp|P19060|BP06\_BPT4 Baseplate wedge protein gp6 OS=Enterobacteria phage T4 GN=6 PE=1  
SV=1

MANTPVNYQLTRTANA IPEIFVGGTFAEIKQNLIEWLNGQNEFLDYDFEGSRLNVLCDLLA  
YNTLYIQQFGNA AVYESFMRTANLRSSVVQAAQDNGYLP TSKSAAQTEIMLTCTDALNRN  
YITIPRGTRFLAYAKDTSVNPYNFVSREDVIAIRDKNNQYFPRLKLAQGRIVRTEIHYDKLTP

IIYDKNIDRNQVKLYVDGAEWINWTRKSMVHAGSTSTIYYMRETIDGNTEFYFGEGEISV  
NASEGALTANYIGGLKPTQNSTIVIEYISTNGADANGAVGFSYADTLTNITVININENPNDDP  
DFVGADGGGDPEDIERIRELGTIKRETQQRCVTATDYDTFVSERFGSIIQAVQTFDSTKPG  
YAFIAAKPKSGLYLTTVQREDIKNYLKDYNLAPITPSIISPNYLFIKTNLKVTYALNKLQESE  
QWLEGQIIDKIDRYYTEDVEIFNSSFAKSKMLTYVDDADHSVIGSSATIQMREVQNFYKT  
PEAGIKYNNQIKDRSMESNTFSFNNGRQVVPDTPGLEEDVLYDVRIVSTDRDSKIGKVII  
GPFASGDVTENENIQPYTGNDFNKLANSDGRDKYYVIGEINYPADVYWNIAKINLTSEKF  
EVQTIELYSDPTDDVIFTRDGLIVFENDLRPQYLTIDLEPISQ

>sp|Q9T1V3|BP46\_BPMU Baseplate protein gp46 OS=Enterobacteria phage Mu GN=Mup46  
PE=2 SV=1

MTDLAIWWTNGRGDIAQDGDMLTDDSLTTDVTISLFTDRRALDSDTLPDGSDDRRGWG  
DSYRDRPIGSRLWLLSREKATPDTLERARGYAEAELEWLKTAGRVSAINVRAEQLHQGWL  
YLYIALTLPDGSVIPYEFKAAFNGV

>sp|P13341|BP54\_BPT4 Baseplate tail-tube protein gp54 OS=Enterobacteria phage T4 GN=54  
PE=1 SV=1

MYSLEEFNNQAINADFQRNNMFSCVFATTPSTKSSSLISSISNFSYNNLGLNSDWLGLTQG  
DINQGITTLITAGTQKLIRKSGVSKYLIGAMSQRTVQSLGVSFTVGTYLIDFFNMAYNSSGL  
MIYSVKMPENRLSYETDWNYNPNRITGRELDPLVISFRMDSEACNYRAMQDWNVSVQ  
DPVTGLRALPQDVEADIQVNLHSRNLPHAVMFTMHSISVSAPELSYDGDNQITTFDVT  
AYRVMQAGAVDRQRALEWLESAAINGIQSVLGNSSGGVTGLSNLSRLSRLGGTAGSISNIN  
TMTGIVNSQSKILGAI

>sp|P19061|BP07\_BPT4 Baseplate wedge protein gp7 OS=Enterobacteria phage T4 GN=7 PE=1  
SV=1

MTVKAPSVTSLRISKLSANQVQVRWDDVGANFYFVEIAETKTNSGENLPSNQYRWINL  
GYTANNSFFFDDADPLTTYIIRVATAAQDFEQSDWIYTEEFETFATNAYTFQNMIEMLANK  
FIQEKFTLNNSDYVNFNNDTMAALMNESFQFSPSYVDVSSISNFIIGENEYHEIQGSIQQV  
CKDINRVYLMSEGILYLFERYQPVVKVSNDKGQTKAVKLFNDRVGYPLSKTVYYQSA  
NTTYVLGYDKIFYGRKSTDVRWSADDVRFSSQDITFAKLGDQLHLGFDVEIFATYATLPAN  
VYRIAEAITCTDDYIYVVARDKVRYIKTSNALIDFDPLSPTYSERLFEPDTMTITGNPKAVC  
YKMSDICDKVFALIIGEVELNANPRTSKIIDSADKGIYVLNHDEKTWKRVPFGNTEEERRRI  
QPGYANMSTDGKLVSLSSNFKFLSDNVVNDPETAACYQLIGAVKYEFFPREWLADKHYH  
MMAFIADETSDWETFTPQPMKYAEPFFNWSKKSNTRCWINNSDRAVVVYADLKYTKVI  
ENIPETSPDRLVHEYWDDGDCTIVMPNVKFTGFKKYASGMLFYKASGEIISYDFNYRVR  
DTVEIHWKPTVEFLKAFLQNEHETPWSPEEERGLADPDLRPLIGTMMPDSYLLQDSNFEA  
FCEAYIQYLSDGYGTQYNNLRNLIRNQYPREEHAWEYWLWSEIYKRNIYLNADKRDVARF  
FESRSYDFYSTKGIEASYKFLFKVLYNEEVEIEIESGAGTEYDIIVQSDSLTEDLVGQTIYTAT  
GRCNVTYIERSYSNGKLQWTVTIHNLGRLIAGQEVKAERLPSFEGEIRGVKGDLLQNN  
IDYINRSRSYYVMKIKSNLSSRWKSDVIRFVHPVGFGFIAITLLTMFINVGLTLKHTETIIN  
KYKNYKWDSGLPTEYADRIAKLTPTGEIEHDSVTGEAIYEPGPMAGVKYPLPDDYNAENN  
NSIFQGQLPSERRKLMSPFLDASGTTFAQFRDLVKNRKLKDNIGNPRDPENPTQVKIDE

>sp|P13339|BP48\_BPT4 Baseplate tail-tube protein gp48 OS=Enterobacteria phage T4 GN=48  
PE=1 SV=3

MAIVKEITADLIKKSgekisagqstksevgtktytaqfptgrasgndttedfqvtdlykng  
LLFTAYNMSSRDSGLRSMRSNYSSSSSILRTARNTISSTVSKLSNGLISNNNSGTISKSPIA



NILLPRSKSDVDTSSHRFNDVQESLISRGGGTATGVLSNIASTAVFGALESITQGIMADNNE  
QIYTTARSMYGGAENRTKVFTWDLTPRSTEDLMAIINIYQYFNYSYGETGKSQYAAEIKG  
YLDDWYRSTLIEPLSPEDAANKNTLFEKMTSSLTNVVLVSNPTVWMVKNFGATSKFDGK  
TEIFGPCQIQSIRFDKTPNGNFNGLAIAPNLPSTFTLEITMREIITLNRASLYAGTF

>sp|P16011|BP53\_BPT4 Baseplate wedge protein gp53 OS=Enterobacteria phage T4 GN=53  
PE=1 SV=1

MLFTFFDPIEYAAKTVNKNAPTIPMTDIFRNYKDYFKRALAGYRLRYYIKGSPRPEELAN  
AIYGNPQLYWVLLMCNDNYDPYYGWITSQEAAAYQASIQKYKNVGGDQIVYHVNENGEK  
FYNLISYDDNPYVWYDKGDKARKYPQYEGALAAVDTYEAAVLENEKLRQIKIIAKSDINS  
FMNDLIRIMEKSYGNDK

>sp|P19194|B\_BPCHP Internal scaffolding protein VP3 OS=Chlamydia phage 1 GN=ORF3 PE=1  
SV=1

MKFRTIYDEERPAPVLECKDESLCLAYQCTETSIEKLVKLANQNPSYLHAFAGDPTRQPEY  
GECPSPLDYQDALEIVARGEEAFYSLPANIRVNFNSPMEFLSWLEDPANYDEVEKLGLLDP  
EKVQIRKSKLQKDQKEEVSSEEK

>sp|Q6QGE9|BPPB3\_BPT5 Probable baseplate hub protein OS=Escherichia phage T5 GN=D16  
PE=2 SV=1

MKKILDSAKNYLNTHDKLKTACLIALELPSSSGSAATYIYLTDFRDVITYNGILYRSGKVK  
SISSHKQNRQLSIGSLSFTITGTAEDVLKLVQNGVSFLDRGITIHQAIINEEGNILPVPDPTD  
GPLLFFRGRITGGGIKDNVNTSGIGTSVITWNCNQQFYDFDRVNGRYTDDASHRGLEVVN  
GTLQPSNGAKRPEYQEDYGFFHSNKSTTILAKYQVKEERYKLQSKKKLFGLSRSYSLKKY  
YETVTKEVDLDFNLA AKFIPVVYGVQKIPGIPIFADTELNNPNIVYVYAFAGEIDGFLDF  
YIGDSPMICFDETDSDTRTCFGRKKIVGDTMHLRAAGTSTSQPSVHGQEYKYNDGNGDIR  
IWFTHGKPDQTAQAQLVDIAKKKGFYLQNGNGNGPEYWDSRYKLLDTAYAIVRFTINENR  
TEIPEISAEVQKKVKVYNSDGTIKADKTSLNGIWQLMDYLTSDRYGADITLDQFPLQKVI  
SEAKILDIIDESYQTSWQPYWRYVGVNDPLSENQIVQLNTILDTSESVFNKVVQGILESG  
GAINNLSGEYRITVEKYSTNPLRINFLDTYGDLDLSDTTGRNKFNSVQASLVDPALSWKTN  
SITFYNSKFKEQDKGLDKLQLSFANITNYTARSYADRELKKSRYSRTLSFSVPYKFIGIEP  
NDPIAFTYERYGWKDKFFLVDEVENTRDGKINLVLQYEGEDVFINSEQVDNSGNDIPDISN  
NVLPPRDFKYTPTPGGVVGAIGKNGELSWLPSLTNNVYYSIAHSGHVNPYIVQQLENNP  
NERMIQEIIGEPAGLAIFELRAVDINGRRSSPVTLVDLNSAKNLSVVSNFRVNTASGDVT  
EFVGPDVKLAWDKIPEEEIPEIYITLEIYDSQDRMLRSVRIEDVYTYDYLLTYNKADFALL  
NSGALGINRKLRFIRAEGENGEQSVGWATI

>sp|P09425|BP25\_BPT4 Baseplate wedge protein gp25 OS=Enterobacteria phage T4 GN=25  
PE=1 SV=1

MANINKLYSDIDPEMKMDWNKDVSRSGLRSIKNSLLGIITTRKGSRPFDPEFGCDLSDQL  
FENMTPLTADTVERNIESAVRNYEPRIDKLAVNVIPVYDDYTLIVEIRFSVIDNPDDIEQIKL  
QLASSNRV

>sp|Q6WHH0|BP27\_BPKVM Probable baseplate hub protein gp334 OS=Vibrio phage KVP40  
(isolate Vibrio parahaemolyticus/Japan/Matsuzaki/1991) GN=KVP40.0334 PE=1 SV=1

MFEMRSANPIENFVSKIHIRGLDFAASVENEITHMEIYESLNGLVSGMFMFKDSIGVVDTI  
RMTGFEAIDVEFASYVGEQANRVYQKSFRATGISRMPARTGGFETVLRFTNLLTLNDY  
VKRPYVFKKTSISNIIKAILDNLGDEKPEYEIETSLYQRDFVTKIGKPYDIKSIVDHASTDV  
NNSCKFMFYEDRDSVKFASLGSIRDKEYEYIIRKGADTGDGKWTSGNTNTITALRVVVKE

QSNMHEISSGLFGSRTYSHSLIRKKLTTKDVRNDYIAQVGILNDRAHMYTNELEFASEVP  
ETEQLNSIQLLPNDGFYEHDNKHPLGSIHGVSLMEETYLKAKQIIVEIPGNTNITVGDVVF  
LDYHAVTGENHSSLDASGRWIVHELKHRVEPNSFITTLLELSSDSSVNIAIAGSKK

>sp|P17172|BP27\_BPT4 Baseplate hub protein gp27 OS=Enterobacteria phage T4 GN=27 PE=1  
SV=4

MSMLQRPGYPNLSVKLFDSYDAWSNNRFVELAATITTLTMRDSLYGRNEGMLQFYDSKN  
IHTKMDGNEIIQISVANANDINNVKTRIYGCKHFSVSVDSKGDNIIEIELGTIHSIENLKFR  
PPFPDAGESIKEMLGVIYQDRLLTPAINAINAYVPDIPWTSTFENYLSYVREVALAVGSDK  
FVFWQDIMGVNMMDYDMMINQEPYPMIVGEPQLIGQFIQELKYPLAYDFVWLTKSNPH  
KRDPMKNATIYAHSFLDSSIPMITTGKGENSIVVSRSGAYSEM TYRNGYEEAIRLQTMAQY  
DGYAKCSTIGNFNLTGPKIIFNDSKNQFKTEFYVDEVIHELNNNSVTHLYMFTNATKLE  
TIDPVKVKNEFKSDTTTEESSSSNKQ

>sp|P08558|BP44\_BPMU Baseplate hub protein gp44 OS=Enterobacteria phage Mu GN=P PE=1  
SV=1

MSNTVTLRADGRLFTGWTSVSVTRSIESVAGYFELGVNVPPGTDLSGLAPGKKFTLEIGG  
QIVCTGYIDRRRQMTADSMKITVAGRDKTADLIDCAAVYSGGQWKNRTLEQIARDLCAP  
YGVTVRWELSDKESSAAFPGFTLDHSETVYEALVRASRARGVLMTSNAAGELVFSRAAST  
ATDELVLGENLLTDFEEDFRDRFSEYTVKGYARANGAEGDDIDAKSIVSRKGTATDSDVT  
RYRPMIIIADSKITAKDAQARALREQRRRLAKSITFEAEIDGWTRKDGQLWMPNLLVTIDA  
SKYAIKTELLVSKVTLILNDQDGLKTRVSLAPREGFLVPVESDRKNRKGGSNGGIDALV  
EDYYRRHPEKTPPWKE

>sp|P19727|CAPSB\_BPT7 Minor capsid protein 10B OS=Enterobacteria phage T7 GN=10 PE=1  
SV=1

MASMTGGQQMGTNQGKGVVAAGDKLALFLKVFGGEVLTAFARTSVTTSRHMVRSISSG  
KSAQFPVLGRTQAAYLAPGENLDDKRRKDIKHTEKVITIDGLLTADVLIYDIEDAMNHYDV  
RSEYTSQLGESLAMAADGAVLAEIAGLCNVESKYNENIEGLGTATVIETTQNKAALTDQV  
ALGKEIIAALTKARAALTKNYVPAADRVFYCDPDSYSAILAALMPNAANYAALIDPEKCSI  
RNVMGFEVVEVPHLTAGGAGTAREGTTGQKHVFPANKGEGNVKVAKDNVIGLFMHRSA  
VGTVKLRDLALERARRANFQADQIIAKYAMGHGGLRPEAAGAVVFQSGVMLGVASTVA  
ASPEEASVTSTEETLTPAQEAARTRAANKARKEAELAAATAEQ

>sp|P19192|CAPSD\_BPCHP Capsid protein VP1 OS=Chlamydia phage 1 GN=ORF1 PE=1 SV=2  
MAKGRKLPVSMKNRFSEVPTATIRSSFDKSHGYKTTFDMDYLVPFFVDEVLPGDTFSLSE  
THLCRLTTLVQPIMDNIQLTTQFFFVNRLLWDNWFESFITGGDEPVAWTSTNPANEYFVPQ  
VTSPDGGYAENSIYDYFGLPTKVANYRHQVPLRAYNLIFNEYRDENLQESLPVWTGDA  
DPKVDPTTGEESQEDDAVPYVYKLMRRNKRYDYFTSALPGLQKGPSVGIGITGGDSGRLP  
VHGLAIRSYLDDSSDDQFSFGVSYVNASQKWFTADGRLTSGMGSVPVGTGTFNFPIDNVV  
YPSYFGTTVAQTGSPSSSTPPFVKGDFPVYVDLAASSSVTINSLRNAITLQQWFEEKSARYG  
SRYVESVQGHFVHLDYRAQRPIYLGGSKSYVSVNPVQNSSTDSVSPQGNLSAYALST  
DTKHLFTKSFVEHGFVIGLLSATADLTYYQGLERQWSRFSRYDYYWPTFAHLGEQPVYNK  
EIYCQSDTVMDFSGSAVNDVPFGYQERYAEYRYKPSKVTGLFRSNATGTLDLSDWHLNQFA  
NLPTLNETFIQSNTPIDRALAVPDQPDFICDFYFNYRCIRPMPVYSVPGLRRI

>sp|P25477|CAPSD\_BPP2 Capsid proteins OS=Enterobacteria phage P2 GN=N PE=1 SV=1

MRQETRFKFNAYLSRVAELNGIDAGDVSKKFTVEPSVTQTLMNTMQESSDFLTRINIVPVS  
EMKGEKIGIGVTGSIASSTDTAGGTERQPKDFSKLASNKYECDQINFDFYIRYKTLDLWAR

YQDFQLRIRNAIIKRQSLDFIMAGFNGVKRAETSDRSSNPMLQDVAVGWLQKYRNEAPAR  
VMSKVTDEEGRTTSEVIRVVGKGGDYASLDALVMDATNNLIEPWYQEDPDLVVIVGRQLLA  
DKYFPIVNKEQDNSEMLAADVIISQKRIGNLPAVRVPYFPADAMLITKLENLSIYYMDDSH  
RRVIEENPKLDRVENYESMNIDYVVEDYAAGCLVEKIKVGFSTPAKATAEPGA

>sp|P03623|CAPSD\_BPPF3 Capsid protein G8P OS=Pseudomonas phage Pf3 GN=VIII PE=1  
SV=1

MQSVITDVTGQLTAVQADITTIGGAIIVLAAVVLGIRWIKAQFF

>sp|P85227|BP40\_BPPHE Virion protein 3 OS=Enterococcus phage phiEF24C GN=40 PE=1  
SV=2

MAIATNNSRVYASLQLKNKQDSMYLAIGKTTTPWTNEDAPPAPDPTTTTLTEVIGYKKVAR  
VSLCREYLPSSDKYPVVSYGSRKFTLIPDEDDGYKEQAWMVYVEAEITGDELPTGTFRQV  
GIHTDLVSKASSEKKALLPTDVTDAGILQFFENRQQNRTSDVILKEKFITMENKKSVKQ

>sp|P03622|CAPSD\_BPXF Capsid protein G8P OS=Xanthomonas phage Xf GN=VIII PE=1  
SV=1

SGVGDGVDVVSIAIEGAAGPIAAIGGAVLTMVGIKVKVWVRRAM

>sp|P22499|BOF\_BPP1 Modulator protein OS=Enterobacteria phage P1 GN=bof PE=1 SV=2

MKKRYTYTVKHGTLRALQEFADKHNVEVRREGGSKALRMYRPDGKWRTVVDFTNSVP  
QGVDRAFEWEQIIIDNALLLNAD

>sp|P10927|BP09\_BPT4 Baseplate wedge protein gp9 OS=Enterobacteria phage T4 GN=9 PE=1  
SV=1

MFIQEPKKLIDTGEIGNASTGDILFDGGNKINSDFNAIYNAFGDQRKMAVANGTGADGQII  
HATGYYQKHSITEYATPVKVGTRHDIDTSTVGKVIHERGELGDCVEFINSNGSISVTNPLTI  
QAIDSIKGVSGNLVVTSPYSKVTLCISSDNSTSVWNYSIESMFGQKESPAEGTWNISTSGS  
VDIPLFHRTEYNMAKLLVTCQSV DGRKIKTAEINILVDTVNSEVISSEYAVMRVGNETEDE  
IANIAFSIKENYVTATISSSTVGMRAAVKVIATQKIGVAQ

>sp|P49861|CAPSD\_BPHK7 Major capsid protein OS=Enterobacteria phage HK97 GN=5 PE=1  
SV=1

MSELALIQAIEESQQKMTQLFDAQKAEIESTGQVSKQLQSDLMKVQEELTKSGTRLFDL  
EQKLASGAENPGEKKSFSERAAEELIKSWDGKQGTFGAKTFNKSLGSDADSAGSLIQPMQ  
IPGIIMPGLRRLTIRDLLAQGRSSNALEYVREEVFTNNADVVAEKALKPESDITFSKQTAN  
VKTIAHWVQASRQVMDDAPMLQSYINNRLMYGLALKEEGQLLNGDGTGDNLEGLNKVA  
TAYDTSLNATGDTRADIIAHAIYQVTESEFSASGIVLNPRDWHNIALLKDNEGRYIFGGPQA  
FTSNIMWGLPVVPTKAQAAGTFTVGGFDMASQVWDRMDATVEVSREDRDNFVKNMLTI  
LCEERLALAHYRPTAIKGTFFSSGS

>sp|P03621|CAPSD\_BPPF1 Capsid protein G8P OS=Pseudomonas phage Pf1 GN=VIII PE=1  
SV=2

MKAMKQRIAKFSPVASFRNLCIAGSVTAATSLPAFAGVIDTSAVESAITDGQGMKAIGGY  
IVGALVILAVAGLIYSMLRKA

>sp|P15794|CAPSD\_BPPM2 Major capsid protein P2 OS=Pseudoalteromonas phage PM2 GN=II  
PE=1 SV=2

MRSFLNLNSIPNVAAGNSCSIKLPIGQTYEVIDLRYSGVTPSQIKNVRVELDGRLSTYKTL  
NDLILENTRHKR KIKAGVVSFHFVRPEMKGVNVTDLVQQRMFALGTVGLTTCEIKFDIDE  
AAAGPKLSAIAQKSVGTAPSWLTMRRNFFKQLNNGTTEIADLPRPVGYRIAAIHIKAAGV  
DAVEFQIDGTKWRDLLKKADNDYILEQY GKAVLDNTYTIDFMLEGDVYQSVLLDQMIQD

LRLKIDSTMDEQAEIIVEYMGVWSRNGF

>sp|P19062|BP08\_BPT4 Baseplate wedge protein gp8 OS=Enterobacteria phage T4 GN=8 PE=1 SV=1

MNDSSVIYRAIVTSKFRTEKMLNFYNSIGSGPDKNTIFITFGRSEPWSSNENEVGFAPPYPT  
DSVLGVTDMMWTHMMGTVKVLPMLDAVIPRRDWGDTRYDPYTFRINDIVVCNSAPYN  
ATESGAGWLVRCLDVPDTGMCSIASLTDKDECLKLGKWTSPARSMTPEGRGDAEGTI  
EPGDGYVWEYLFEIPPDVSINRCTNEYIVVPWPEELKEDPTRWGYEDNLTWQQDDFGLIY  
RVKANTIRFKAYLDSVYFPEAALPGNKGFRQISIITNPLEAKAHPNDPNVKAEKDYDPED  
LMRHSGEMIMENRPPIIMAMDQTEEINILFTF

>sp|P10928|BP10\_BPT4 Baseplate wedge protein gp10 OS=Enterobacteria phage T4 GN=10 PE=1 SV=1

MKQINIGNVVDDGTGDYLRKGGIKINENFDELYYELGDGDVPYSAGAWKTYNASSGQT  
LTAEWGKSYAINTSSGRVTINLPKGTVNDYNKIRARDVFATWVNPVTLVAASGDTIKGS  
AVPVEINVRFSDELVYCAPGRWEYVKNKQIDKITSSDISNVARKEFLVEVQQTDFLDVF  
RGTSYNVNNIRVKHRGNELYGDVFSNSDFGSPGENEGELVPLDGFNIRLRQPCNIGDTV  
QIETFMDGVSQWRSSYTRRQIRLLDSKLTSKTSLEGSIVTDLSTMKSIPFSAFGLIPGEPIN  
PNSLEVRFNIGILQELAGTVGMPLFHCVGADSDDEVECSVLGGTWEQSHTDYSVETDENG  
PEILHFDSVFEHGDIIITWFNNDLGTLLTKDEIIDETDNLYVSQGGVDISGDVNLDFDKI  
GWPVNEAVQSYQRAFNAVSNIFDTIYPIGTIYENAVNPNNPVTYMGFGSWKLFQGGKVLV  
GWNEDISDPNFALNNNDLDSGGNPSHTAGGTGGSTSVTLENANLPATETDEEVLIVDENG  
SVIVGGCQYDPDESGPIYTKYREAKASTNSTHTPPTSITNIQPYITVYRWIRIA

>sp|Q9T1V2|BP47\_BPMU Baseplate protein gp47 OS=Enterobacteria phage Mu GN=Mup47 PE=2 SV=1

MAYSPTLSSLIARTEQNIQRLPGSWPQAREKTLASAIAYAQAGLAAGCHEHISWVGRQIIP  
STADEDELLEHCRFWGVRRKQATAASGPLTVTTSAATTIPAGTRWQRADGVVYSLADTIVI  
DRAGTTEITVTLAAGEAGNTGENTLLTLITPVACVVSDAITVKGFSGGADIESAAELLSRL  
EYRVQYPPFGGNQFDYVRWAREVSGVTRAWCFPTWKGGGTGVVTFVMDNRSNIFPQPA  
DVERVADYIAGHTDPITGLIVGQPDGVNVTVFAPKAKPVNPRIYISPKTAELKQAITNAINT  
MFFNEVMPGGALAPSRIIRAVAGVTGLDDFEVRFPTIQRSENTELLTAGTIEWL

>sp|P51772|BPX\_BPP2 Baseplate protein X OS=Enterobacteria phage P2 GN=X PE=1 SV=1

MKTFALQGDTLDAICVRYYGRTEGVVETVLAANPGLAELGAVLPHGTAVELPDVQTAPVA  
ETVNLWE

>sp|P03633|B\_BPPHS Internal scaffolding protein B OS=Enterobacteria phage phiX174 (Isolate Sanger) GN=B PE=1 SV=1

MEQLTKNQAVATSQEAVQNQNEPQLRDENAHNDKSVHGVNLNPTYQAGLRRDAVQPDIEA  
ERKKRDEIEAGKSYCSRFFGGATCDDKSAQIYARFDKNDWRIQPAEFYRFHDAEVNTFGY  
F

>sp|P07579|CAPSD\_BPPH6 Major outer capsid protein OS=Pseudomonas phage phi6 GN=P8 PE=1 SV=1

MLLPVVARAAVPAIESAIAATPGLVSRIAAIGSKVSPSAILAAVKSNPVVAGLTLAQIGSTG  
YDAYQQLLENHPEVAEMLKDLSFKADEIQPDFIGNLGQYREELELVEDAARFVGGMSNLI  
RLRQALELDIKYYGLKMQLNDMGYRS

>sp|Q6QGD8|CAPSD\_BPT5 Major capsid protein OS=Escherichia phage T5 GN=D20 PE=1 SV=1

MTIDINKLKEELGLGDLAKSLEGLTAAQKAQEAERMKEQEEKELARMNDLVSKAVGED  
RKRLEEALVLSLDEKSKKSNELFAQTVEKQQETIVGLQDEIKSLLTAREGRSFVGDVA  
KALYGTQENFEDEVEKLVLLSYVMEKGVFETEHEGQRHLKAVNQSSSVEVSSESJETIFSQ  
RIIRDLQKELVVGALFEELPMSSKILTMLVEPDAGKATWVAASTYGTDTTTGEEVKGALKE  
IHFSTYKLAAKSFITDETEEDAIFSLPLLRKRLIEAHAVSIEEAFMTGDGSGKPKGLLTLAS  
EDSAKVVTEAKADGSVLVTAKTISKLRRLGRHGLKLSKLVLIVSMDAYYDLLEDEEWQ  
DVAQVGNDSVKLQGVGRIYGLPVVVSEYFPAKANSAEFAVIVYKDNFVMPRQRAVTV  
RERQAGKQRDAYYVTQRVNLQRYFANGVVSSTYAAAS

>sp|P03713|CAPSD\_LAMBDA Major capsid protein OS=Enterobacteria phage lambda GN=E  
PE=1 SV=1

MSMYTTAQLLAANEQKFKFDPLFLRLFFRESYPFTTEKVVLSQIPGLVNMALYVSPVSGE  
VIRSRGGSTSEFTPGYVVKPKHEVNPQMTLRRLPDEDPQNLADPAYRRRIIMQNMREEL  
AIAQVEEMQAVSAVLKGGKYTMTGEAFDPVEVDMGRSEENNITQSGGTEWSKRDKSTYDP  
TDDIEAYALNASGVVNIIVFDPKGVWALFRSFKAVKEKLDTRRGSNSELETAVKDLGKAVSY  
KGMVGDVAIVVYSGQYVENGVKKNFLPDNTMVLGNTQARGLRITYGCIQDADAQREGIN  
ASARYPKNWVTTGDPAREFTMIQSAPLMLLADPDEFVSVQLA

>sp|P04535|CAPSH\_BPT4 Major capsid protein OS=Enterobacteria phage T4 GN=gp23 PE=1  
SV=2

MTIKTKAELLNKWKPLLEGEGLPEIANSKQAIKIFENQEKFQTAPEYKDEKIAQAFGSF  
LTEAEIGGDHGYNATNIAAGQTSQAVTQIGPAVMGMVRRRAIPNLIAFDICGVQPMNSPTGQ  
VFALRAVYKDPVAAGAKEAFHPMYGPDAMFSGQGAACKKFPALAASTQTTVGDYIYTHFF  
QETGTVYLQASVQVTIDAGATDAAKLDAEIKKQMEAGALVEIAEGMATSIAELQEGFNDS  
TDNPWNEMGFRIDKQVIEAKSRQLKAAYSIELAQDLRAVHGMDADAELSGLATEIMLEI  
NREVVWDWINYSAQVVGKSGMTLTPGSKAGVDFDQDPIDIRGARWAGESFKALLFQIDKEAV  
EIARQTGRGEGNFIIASRNVVNLASVDTGISYAAQGLATGFSTDTTKSVFAGVLGGKYRV  
YIDQYAKQDYFTVGYKGNEMDAGIYYAPYVALTPLRGSDPKNFQPVMGFKTRYGIGINP  
FAESAAQAPASRIQSGMPSILNSLGKNAYFRRVYVKGI

>sp|P10929|BP11\_BPT4 Baseplate wedge protein gp11 OS=Enterobacteria phage T4 GN=11  
PE=1 SV=1

MSLLNKKAGVISRLADFLGFRPKTGDIDVMNRQSVGSVTISQLAKGFYEPNIESAINDVHN  
FSIKDVGTHITNKTVSPEGVSQTDYWAFSGTVTDDSLPPGSPITVLVFLPVSATTGMTAIE  
FVAKVRVALQEAIASFTAINSFKDHPDGSKLEVTYLDNQKHVLSYSTYGITISQEIISESK  
PGYGTWNLGAQTVTLDNQQTPTVYHFERTA

>sp|P13336|BP28\_BPT4 Baseplate structural protein gp28 OS=Enterobacteria phage T4 GN=28  
PE=1 SV=4

MNLNLILPLKKVLPISNKEVSIPKMGLKHYNILKDVKGPDENLKLIDSICPNLSPAEVDF  
VSIHLLEFNGKIKSRKEIDGYTYDINDVYVCQRLEFYQGNFTYFRPPGKFEQFLTVSDML  
SKCLLRVNDDEVKEINFLEMPAFVLKWARDIFTTLAIPGPNPITGIGNIIGLFE

>sp|Q9T1V4|BP45\_BPMU Baseplate puncturing device gp45 OS=Enterobacteria phage Mu  
GN=Mup45 PE=1 SV=1

MERVNDSALNRLTLPLMRRVRLMLARAVNVINDGRKVVQNLQVGLLDDEESDEVERLQ  
NYGHFSVPLPGAELIACVGAQRDQGIADVVEDRRYRPTNLEPGDAGIYHHEGHRIRLTK  
DGRCIITCKTVEVYADESMTVDTPRTTFTGDVEIQKGLGVKGSQFDSNITAPDAIINGKST  
DKHIHRGDSGGTTGPMQ

>sp|Q859Q5|CAPSD\_BPN4 Major capsid protein OS=Enterobacteria phage N4 PE=1 SV=2  
MLNYNAPT DGQKSSIDGANS DQM QTFFWLKKA IITARKEQYFMPLASVTNMPKH YGKTI  
KVYEVVPLDDRNDQ GIDASGATVNGNLYGSSKDIGNITSKLPLL TENGGRVNRVGF  
RIAREGSIHKFGFFYEFTQESIDFSD DGLMEHLSRELMNGATQITEAVLQKDLLAAAGTV  
LYAGAATSDATITGEGSTPSVVS YKNLMRLDQILTENRTPTQTTIITGSRMIDTKVIGATRVM  
YVGSELVPELKAMKDLFGNKAFIETQHYADAGTIMNGEVGSIDKFRIIQVPEMLHWAGAG  
AQATGANPGYRTSMVSGQEHYDVYPMLVVGDD SFTSIGFQTDGKSLKFTVMTKMPGKET  
ADRNDPYGETGFSSIKWYYGILVKRPERLALIKTVAPL

>sp|P26747|CAPSD\_BPP22 Major capsid protein OS=Enterobacteria phage P22 GN=5 PE=1  
SV=2  
MALNEGQIVTLAVDEIIETISAITPMAQKAKKYTPPAASMQRSSNTIWM PVEQESPTQEGW  
DLTDKATGLLELNVAVNMGEPDNDFFQLRADDLRDETAYRRRIQSAARKLANVELKVA  
NMAAEMGSLVITSPDAIGTNTADAWN FVADAEIIMFSRELN RDMGTSYFFNPQDYKKAG  
YDLTKRDIFGRIP EEA YRDGTIQRQVAGFDDVLRSPKLPVLT KSTATGITVSGAQSFKPVAW  
QLDNDGNKVNVDNRFATVTL SATTGMKRGDKISFAGVKFLGQMAKNVLAQDATFSVVR  
VVDGTHVEITPKPVALDDVSLSPEQRAYANVNTSLADAMAVN ILNVKDARTNVFWADDAI  
RIVSQPIPAHEL FAGMKTTSFSIPDVGLNGIFATQGDISTLSGLCRIALWYGVNATRPEAIG  
VGLPGQTA

>sp|P22535|CAPSD\_BPPRD Major capsid protein P3 OS=Enterobacteria phage PRD1 GN=III  
PE=1 SV=2  
MAQVQQLTPAQQAALRNQQAMAANLQARQIVLQQSYPVIQQVETQTFDPANRSVFDVTP  
ANVGIVKGFLVKVTAAITNNHATEAVALTDFGPANLVQRVIYDPDNQRHTETSGWHLHF  
VNTAKQGAPFLSSMVTDSPIKYGDVMNVIDAPATIAAGATGELTMYWVPLAYSETDLTG  
AVLANVPQSKQRLKLEFANNNTAFAAVGANPLEAIYQGAGAADCEFE EISYTVYQSYLDQ  
LPVGQNGYILPLIDLSTLYNLENSAQAGLTPNVDFV VQYANLYRYLSTIAVFDNGGSFNAG  
TDINYL SQR TANFS DTRKLDPKTWAAQTRRRRIATDFPKGVYYCDNRDKPIYTLQYGNVGF  
VVNPKTVNQNARLLMGY EYFTSRTELVNAGTISTT

>sp|P19896|CAPSP\_BPT4 Capsid vertex protein gp24 OS=Enterobacteria phage T4 GN=24 PE=1  
SV=2  
MAKINELLRESTTTNSNSIGRPNLVALTRATTKLIYSDIVATQRTNQPVAAFYGIKYL NPDNE  
FTFKTGATYAGEAGYVDREQITELTEESKLT LNKGDLFKYNNIVYKVLEDTPFATIEESDLE  
LALQIAIVLLKVRLFS DAASTSKFESSDSEIADARFQINKWQTAVKSRK LKTGITVELAQDL  
EANGFDAPNFLEDLLATEMADEINKDILQSLITVSKRYKVTGITDSGFIDLSYASAPEAGRS  
LYRMVCEMVSHIQKESTYTATFCVASARAAA ILAASGWLKHKPEDDKYLSQNAYGFLAN  
GLPLYCDTNSPLDYVIVGVVENIGEKEIVGSIFYAPYTEGLDLDDPEHVGA FKVVDPESL  
QPSIGLLVRYALSANPYTVAKDEKEARIIDGGDMDKMAGRS DLSVLLGVKLPKIIIDE

>sp|Q9T1S4|CAPSD\_BPAPS Major capsid protein OS=Acyrtosiphon pisum secondary  
endosymbiont phage 1 GN=24 PE=1 SV=3  
MANNLESNISQIVLKKFLPGFMSDIVLCKTVDRQLLSGEINSNTGDSVSFKRPHQFKSERTE  
TGDITGKDKNGLFSAKATGKVGKYITVAVEWTQIEEALKLNQLDQILSPIHERM VTDLETE  
LAHFMMNNGALS LGSPNTAIKKWADVAQTASFIKDIGIKTGENYAIMDPWSAQRLADAQS  
GLHAADQLVRTAWENAQISGNFGGIRALMSNGLASRKQGD FGAITVKTAPNVDYLSVK  
DSYQFTVALTGATPSKTGFLKAGDQLKFTSTHWLNQQSKQTLYNGSTAMSFTATVLEETN  
STASGDVTVKLSGVPIYDEKNSQYNAVD AKVKAGDAVSIIGTAKQMQMKNL FYNKFFCGL

GTIPLPKLHSLDSAVATYEGFSIRVHKYADGDANKQMMRFDLLPAYVCFNPHMGGQFFGN  
P

>sp|P03620|CAPSD\_BPIKE Capsid protein G8P OS=Enterobacteria phage IKe GN=VIII PE=1  
SV=1

MRVLSTVLAANKIALGAATMLVSAGSFAAEPNAATNYATEAMDSLKTQAIDLISQTPWPV  
VTTVVVAGLVIRLFKKFSSKAV

>sp|B2ZYY5|CAPSD\_BPMR2 Putative major capsid protein OS=Staphylococcus phage  
phiMR25 GN=orf47 PE=1 SV=1

MEQTQKLKLNLQHFASNNVKPQVFNPDNVMHEKKDGTLMNEFTTPILQEVMENSKIM  
QLGKYEPMEGTEKKFTFWADKPGAYWVGEGQKIETSKATWVNATMRAFKLGVLVPTKE  
FLNYTYSQFFEEMKPMIAEAFYKKFDEAGILNQGNPFGKSIAQSIEKTNKVIKGDFTQDN  
IIDLEALLEDELEANAFISKQNRSLLRKIVDPETKERIYDRNSDSLGLPVVNLKSSNLK  
RGELITGDFDKLIYGIPQLIEYKIDETAQLSTVKNEDGTPVNLFEQDMVAITCNYACSIAYR

>sp|Q37993|CAPSD\_BPCP1 Major capsid protein OS=Streptococcus phage Cp-1 GN=9 PE=1  
SV=1

MANKITTFLSGQTGKQISNIDLLNSIRTRASADYQADIPVLEGARINHATVPYQDFQKHAN  
EFFTALVNRIGSTVIKALTYENPLAIFKSETFEFGDTLQEIYVHPAEKKTIDAKSDVSPFKFA  
DTDIEAFYHTLNNENYERTFERAWIQKAFVSDMAFDEFVDKMFSTLLSSDTLDEYQAVR  
VYLRNHLRKSIIQTLKGNDDKITVAGTKIDETKQDFVVDNFQSLINLSKRFTIPSRTTFNNP  
VGVPNMTAIEDQYLVISAEFSTHLDMLLANAFNMDKASVLARTIVVDDFEKFTGEGANN  
GRKPVAFLISAKSIINKDKLVHMEAIRNPRNMTYNYFYHHHYMTSLSLFENIHFVYVEEA

>sp|P82889|CAPSD\_BPH75 Capsid protein G8P OS=Thermus phage PH75 GN=VIII PE=1 SV=1  
MDFNPSEVASQVTNYIAIAAAGVGVLALAIGLSAAWKYAKRFLKG

>sp|P03619|CAPSD\_BPIF1 Capsid protein G8P OS=Enterobacteria phage If1 GN=VIII PE=1  
SV=2

MKKSVVAKIIAGSTLVIGSSAFAADDATSQAKAAFDLTAQATEMSGYAWALVVLVVGATV  
GIKLFKKFVSRAS

>sp|A9CRA7|CAPSD\_BPMR1 Major capsid protein OS=Staphylococcus phage phiMR11  
GN=orf44 PE=1 SV=1

MPQGITKTSNQIIEVLAPMMQAQLEKKLRFASFAEVDSTLQGQPGDTLTFPAFVYSGDAQ  
VVAEGEKIPTDILETKKREAKIRKIAKGTSTIDEALLSGYGDPQGEQVRQHGLAHANKVD  
NDVLEALMGAKLTVNADITKLNGLQSAIDKFNDEDLEPMVLFINPLDAGKLRGDASTNFT  
RATELGDDIIVKGAFGALGAIIVRTNKLEAGTAILAKKGAVKLILKRDFFLVARDASTKT  
TALYSDKHVYVAYLYDESKAVKITKSGSLEM

>sp|Q9T1W1|CAPSD\_BPMU Major capsid protein OS=Enterobacteria phage Mu GN=T PE=1  
SV=1

MIVTPASIKALMTSWRKDFQGGLEDAPSQYNKIAMVVNSSTRSNTYGWLKGFPTLKEWV  
GKRTIQQMEAHGYSIANKTFEGTVGISRDDFEDDNLGIYAPIFQEMGRSAAVQPDELIFKLL  
KDGFTQPCYDQGNFFDKEHPVYPNVDGTGSVNTSNIVEQDSFSGLPFYLLDCSRAVKPLI  
FQERRKPELVARTRIDDDHVFMDNEFLFGASTRRAAGYGFWMMAVAVKGDLLDNLWKG  
WQLMRSFEGDGGKGLKLPHTHIVVPVGLEKAAEQLLNRELFADGNTTVSNEMKGLQL  
VVADYL

>sp|P08557|CIRCN\_BPMU DNA circularization protein N OS=Enterobacteria phage Mu GN=N  
PE=1 SV=2

MFEDALNAVNAVDRDKTGGGRKTTGKGTFRNVPFLVIEEQKQAGGRRLLVKREYPLRDTGG  
VNDLGKKLRSRTFSACILNSNAETARDEAGALMDALDAPGSGELVHPDFGTVDVMVDSW  
ECRTKADELNYYAFTVTVYPSLQDTAPDAETDTSAAVPAQAVAVTGS LGDTLSSVWQTVK  
DGTAAATAVMEAVTGVIDDISDAVDNLGVTQTVSGLMGSLSAMKGSVTSLINQPAMLIASS  
LMGALSGVSSLCDTRTAFSTWNRLAQRFFERRHAATAGRQGTITTSYNPVAEKNIATLNYV  
MLAAAQTYRAEAASQALTAALDFSRRMDNAARAPVLDAPSTTTGTASGASSTSATVTQG  
QLQLTAITPDGGFSQVSFSDSGTATPPVFESVSDIEKTTAMLGAALDSVILTASEQGFSTDSV  
QLTQLRLLVVADLEKRGLQLAGSESHHLPETLPAMVALYRFTGNSRNWQRLARRNGISNP  
LFVPGGVSIEVINE

>sp|P85500|COAT\_BPPAJ Structural protein OS=Pseudomonas phage PAJU2 PE=1 SV=2  
MKTNRAYSTLEV KALDDEKRVITGIASTPSPDRMQDVVEPKGAQFKLPIPLWQHNHDEPI  
GHVTEAKVTQKGIEVSVQLTQVEEPGKLDLDEAWQSIKSLVRLSIGFSAKEFEQIPG  
SWGLRFLSWEFELSAVTIPANA EATITSVKSIDREQRAALGIKSVVVRVTPAGASAIKTK  
TIKVPKQEGNDMKTAEQIAEFEATRVTKAAEMEAIMTKAAEAGETLDAEQSEQFDLLE  
AEIAAIDKHIGRLKQMKAQAANAKPVTEEAGAQRMANVKALDFKEVQVRAKNTQKLE  
PGIAFARAAKCLALGHLEHRDAIGIAKSLYDGDQSIIAATQRLVTKA AVAAATTS DATWAG  
PLVGDSETS VFADFVEYLRPQTILGRFGTNGIPSLRRVPRVPLIGQTSGGDGYWVGEGQAK  
PLTKDFFERKTLEPLKVANIAVATMEVIRDSSPSADVIIRDQLAAALRERLDIDFIDPAKAAV  
AGVSPASILNGVAGIPSSGNTADDVRADIRALFNAFIAANNAPTSGVWLM PATTALALSLM  
QNPLGQAEFFPGISM TGGTLFGLPVIVSEYIPTASAGAVVALVNASDIYLGDEGGVDLSMST  
EASLQMDNAPDNPTTASTVLVSLWQRNLVGFRAERAINWARRRASAVAYLTGVNWGAA

>sp|P11112|COMPL\_BPT4 Tail completion protein gp15 OS=Enterobacteria phage T4 GN=15  
PE=1 SV=2  
MFGYFYNSSFRRYATLMGDLFSNIQIKRQLES GDKFIRVPITYASKEHFMMKLNK WTSINS  
QEDVAKVETILPRINLHLVDFSYNAPFKTNILNQNLQKGATSVVSQYNPSP IKMIYELSIFT  
RYEDDMFQIVEQILPYFQPHFNTTMYEQFGNDIPFKRDIKIVLMSAAIDEAIDGDNLSRRRI  
EWSLTFEVNGW MYPPVDDAEGLIRTTYTDFHANTRDLPDGEGVFESVDSEV VPRDIDPED  
WDGTVKQTFTSNVNRPTPEPPGPRT

>sp|Q38200|COM\_BPD10 Translational activator com OS=Escherichia phage D108 GN=com  
PE=2 SV=2  
MKSIRCKNCNKLLFKADSFHIEIRCPRCKRHIIMLNACEHPTEKHCGKREKITHSDETVR  
Y

>sp|P07234|COAT\_BPGA Coat protein OS=Enterobacteria phage GA PE=1 SV=3  
MATLRSFVLVDNGGTGNVTVPVSNANGVAEWLSNNSRSQAYRVTASYRASGADKRKY  
AIKLEVPKIVTQVVNGVELPGSAWKAYASIDLTIFAATDDVTVISKSLAGLFKVG NPIAEA  
ISSQSGFYA

>sp|P03616|COAT\_BPPRR Coat protein OS=Pseudomonas phage PRR1 PE=1 SV=1  
AQLQNLVLKDREATPN DHTFVPRDIRDNVGEVVESTGVPIGESRFTISLRKTSNGRYKSTL  
KLVVPVVSQSTVNGIVTPVVVVRTSYVTVDYDARSTTKERNNFVGM IADALKADLMLV  
HDTIVNLQGVY

>sp|Q6QGE0|COMPL\_BPT5 Tail completion protein OS=Escherichia phage T5 GN=ORF136  
PE=2 SV=1  
MSLSDLARQIIKEQLDTASRENNKNTVVYSVETGLKDPTRDGTVAQVSFKFSKPV SQDLL  
NIRTASILKAVSSSLDLSGDLGALENLIQATAGKKSSVGKKRSTGRVQVNF GDPSDVEDGY



SGAVTGASGRFVSNSNMKIILEIVAKEYLIKDMKKAGAPLKFRTGRFANSLKIKDVMLRDS  
ETSKGSPELNVTYNYMTRPYSVFNPAVSTYRRLSLRPYPGARNPQKLIGEAIKAARDLIH  
SRYKIKVNQGT

>sp|P03630|COAT\_BPPP7 Coat protein OS=Pseudomonas phage PP7 PE=1 SV=1  
SKTIVLSVGEATRTLTEIQSTADRQIFEEKVGPLVGRRLRLTASLRQNGAKTAYRVNLKLDQA  
DVVDCSTSVCGELPKVRYTQVWVSHDVTIVANSTEASRKSPLYDLTKSLVVQATSEDLVVNL  
VPLGR

>sp|P03615|COAT\_BPQBE Coat protein OS=Enterobacteria phage Qbeta PE=1 SV=2  
MAKLETVTLGNIGKDGKQTLVLNPRGVNPTNGVASLSQAGAVPALEKRVTVSVSQPSRNR  
KNYKVQVKIQNPTACTANGSCDPSVTRQAYADVTFSTQYSTDEERAFVRTELAALLASP  
LLIDAIDQLNPAY

>sp|O21970|DARA\_BPP1 Defense against restriction protein A OS=Enterobacteria phage P1  
GN=darA PE=1 SV=1

MEQFNINKGMTIKPGLDVLPPPVTDDDEYRALMAGEDRYLMTESNTLEEIEATFFYDTPIH  
WCATDLLEAISSTRQLHRTMQAFVRALNQKLNGTGISAGSDKTGDVAQSGARAIGGAEI  
GRARNVNGLPVLPPIPLSDGQTISILFHSPTAENRITNSDTLVAFQFLNKKDVHTHTVAPMS  
GRDMTLAQVTMKLANLAEKNSAKFQRAQKKKKALVDEITQLQADSDQKEDAMSDLAD  
QVAAVEGQKADLEQKINAVASEADSLYEENERLQGEIDRLNRTGGRDTIAPAGMTGGHSR  
ALDRLASIKNRMHMDGEATLSNGASMKQFIGDGEGYIQLTDPDGSVYMIKAKSIQGV  
MADAIGKLFKAYKAGNVSEYLVQPEEHKPENVEPESAEDTGSSSPEPEVSVGAYRYALQM  
RPAAPGAIPEGNKAILPRPDEGDPYIEYARYGIATYDTPLSDQQMSEYDLKLLPREDSFDF  
LAKTLTNGPFGKYAQKALELATNSPDEFVMLKTQFQKTFPNIAFPGGAGTEKMVQSMIN  
ALQAEVGEITQPEPAPAQPDETVSEADAANKAIEYLNVMMDMQSTDMAEIRNARGNVR  
EAIAALQTAGRFEENEELVNGAARHLADLLVAIQKAGVAA

>sp|P36275|DECO\_BPP21 Head decoration protein OS=Enterobacteria phage P21 GN=shp PE=1  
SV=1

MVTKTITEQRAEVRIFAGNDPAHTATGSSGISSPTPALTPLMLDEATGKLVVWDGQKAGSA  
VGILVPLEGTETALTYKSGTFATEAIHWPEVDEHKKANAFAGSALSHAALP

>sp|P39232|DMD\_BPT4 Antitoxin Dmd OS=Enterobacteria phage T4 GN=dmd PE=1 SV=1  
MELVKVVFWMGWFKNESMFTKEITMMKDDVQWATTQYAEVNKALVKAFIDDKKVCED  
CRG

>sp|P03696|DNBI\_BPT7 Single-stranded DNA-binding protein gp2.5 OS=Enterobacteria phage  
T7 GN=2.5 PE=1 SV=1

MAKKIFTSALGTAEPYAYIAKPDYGNNEERGFNPRGVYKVDLTIPNKDPRCQRMVDEIVK  
CHEEAYAAAVEEYANPPAVARGKKPLKPYEGDMPFFDNGDGTTFKFKCYASFQDKKTK  
ETKHINLVVDSKGGKMEDVPIIGGGSKLVKYSVLPYKWNTAVGASVKLQLESVMLVE  
LATFGGGEDDWADEVEENGYVASGSAKASKPRDEESWDEDDEESEEADEDGDF

>sp|Q6QGE8|DIT\_BPT5 Distal tail protein OS=Escherichia phage T5 GN=D16 PE=1 SV=1  
MRLPDPYTNPEYPGLGFESVNLVDNDPMIRDELPNGKVKEVKISAQYWGINSYPELFPDE  
YAFILSRLLLEYKRTGDYLDVLLPQYEAFRVRGDTKSVTIPAGQKGSQIILNTNGTLTGQPK  
AGDLFKLSTHPKVYKITNFSSSGNVWNISLYPDLFITTTGSEKPVFNGLFRTKLMNGDSFG  
STLNNNGTYSGISLSLRESL

>sp|Q6QGD6|DECO\_BPT5 Decoration protein OS=Escherichia phage T5 GN=N5 PE=1 SV=1  
MIDYSGLRTIFGEKLPESHIFATVAAHKYVPSYAFRLRELGLSSAHTNRKVWKKFVEAYG

KAIPPAPPAPPLTSLKDLTASMSVEEGAALTLVSTATGGTGPYTYAWTKDGSPIPDASGATY  
TKPTAAAEDAGSYKVTVTDSKQVSKDSTTCAVTVNPTVPGG

>sp|O80164|DPA5\_BPR69 DNA polymerase processivity component OS=Enterobacteria phage  
RB69 GN=45 PE=1 SV=1

MKLSKDTIAILKNFASINSGILLSQGKFMTRAVNGTTYAEANISDEIDFDVALYDLNSFLSIL  
SLVSDDAEISMHTDGNIKIADTRSTVYWPAADKSTIVFPNKPIQFPVASVITEIKAEDLQQLL  
RVSRLQIDITIAITNKDGKIVINGYNKVEDSGLTRPKYSLTLTDYDGSNNFNFNINMANMK  
IQPGNYKVMLWGAGDKVAAKFESSQVSYVIAMEADSTHDF

>sp|P13320|DSBA\_BPT4 Double-stranded DNA-binding protein OS=Enterobacteria phage T4  
GN=dsbA PE=1 SV=1

MAKKEMVEFDEAIHGEDLAKFIKEASDHKLKISGYNELIKDIRIRAKDELGVDGKMFNRL  
LALYHKDNRDVFEAETEEVVELYDTVFSK

>sp|P69486|D\_BPPHS External scaffolding protein D OS=Enterobacteria phage phiX174 (Isolate  
Sanger) GN=D PE=1 SV=2

MSQVTEQSVRFQTALASIKLIQASAVLDLTEDDFDLTSNKVWIATDRSRARRCVEACVYG  
TLDFVGYPRFPAPVEFIAAVIAYVHPVNIQTACLIMEGAEFTENIINGVERPVKAAELFAFT  
LRVRAGNTDVLTDAAENVRQKLRAEGVM

>sp|P03744|FIB37\_BPT4 Long-tail fiber protein p37 OS=Enterobacteria phage T4 GN=37 PE=1  
SV=1

MATLKQIQFKRSKIAGTRPAASVLAEGELAINLKDRITFTKDDSGNIIDLGFAGGGQVDGN  
VTINGLLRLNGDYVQTGGMTVNGPIGSTDGVTGKIFRSTQGSFYARATNDTSNAHLWFEN  
ADGTERGVVIYARPQTTTDDGEIRLRVRQGTGSTANSEFYFRSINGGEFQANRILASDSLVTKR  
IAVDTVIHDAKAFGQYDSHSLVNYVYPGTGETNGVNYLRKVRKSGGTIYHEIVTAQTGL  
ADEVSWWSGDTPVFKLYGIRDDGRMIIRNSLALGTFTTNFPSSDYGNVGVMGDKYLVLG  
DTVTGLSYKKTGVFDLVGGGYSVASITPDSFRSTRKGFGRSEDQGATWIMPGTNAALLSV  
QTQADNNNAGDGQTHIGYNAGGKMNHYFRGTGQMNINTQQGMEINPGILKLVGTGSNNV  
QFYADGTISSIQPIKLDNEIFLTKSNNTAGLKFAGPSQVDGTRTIQWNGGTREGQNKNYVII  
KAWGNSFNATGDRSRETQVQVSDSQGYFYAHRKAPTGETIGRIEAQFAGDVYAKGIIA  
NGNFRVVGSSALAGNVMTSNGLQVGGSSITGQVKIGGTANALRIWNAEYGAIFRRSESN  
FYIIPNQNNEGESGDIHSSLRPVRIGLNDGMVGLGRDSFIVDQNNALTTINSNSRINANFRM  
QLGQSAYIDAECTDAVRPAGAGSFASQNNEDVRAPFYMNIIDRTDASAYVPILKQRYVQGN  
GCYSLGTLINNGNFRVHYHGGDNGSTGPQTADFGWEIFKNGDFISPRDLIAGKVRFDRT  
GNITGGSGNFANLNSTIESLKTDMSSYPGAPIPWPSDSVPAGFALMEGQTFDKSAYPKLA  
VAYPSGVIPDMRGQTIKPKSGRAVLSAEADGVKAHSHSASASSTDLGKTTSSFDYGTK  
GTNSTGGHTHSGSGSTSTNGEHSYIEAWNGTGVGGNKMSSYAISYRAGGSNTNAAGNH  
SHTFSFGTSSAGDHSVVGIGAHTHTVAIGSHGHTITVNSTGNTENTVKNIAFNIVRLA

>sp|P03743|FIB36\_BPT4 Long-ail fiber protein p36 OS=Enterobacteria phage T4 GN=36 PE=1  
SV=1

MADLKVGGSTTGGSVIWHQGNFPLNPAGDDVLYKSFKIYSEYNKPQAADNDFVSKANGGT  
YASKVTFNAGIQVPYAPNIMSPCGIYGGNGDGATFDKANIDIVSWYGVGFKSSFGSTGRTV  
VINTRNGDINTKGVVSAAGQVRSGAAPIAANDLTRKDYVDGAINVTANANSRVLRSR  
DTMTGNLTAPNFFSQNPASQPSHVPRFDQIVIKDSVQDFGYY

>sp|P03714|FII\_LAMBD Head-tail connector protein FII OS=Enterobacteria phage lambda  
GN=FII PE=1 SV=1

MADFDNLFDAAIARADETIRGYMGTSATITSGEQSGAVIRGVFDDPENISYAGQGVRVEGS  
SPSLFVRTDEVRQLRRGDTLTIGEENFWVDRVSPDDGGSCHLWLGRGVPPAVNRRR

>sp|P03709|FI\_LAMBDA DNA-packaging protein FI OS=Enterobacteria phage lambda GN=Fi  
PE=1 SV=1

MTKDELIARLRSLGEQLNRDVSLTGTKEELALRVAELKEELDDTDETAGQDTPLSRENVLT  
GHENEVGSAPQDVTVILDVSELVTVVALVKLHTDALHATRDEPVAFVLPGTAFRVSAGVAAE  
MTERGLARMQ

>sp|P03742|FIB35\_BPT4 Long-tail fiber protein Gp35 OS=Enterobacteria phage T4 GN=35  
PE=1 SV=4

MEKFMAEFGQGYVQTPFLSESNSVRYKISIAAGSCPLSTAGPSYVKFQDNPVGSQTFSAGLH  
LRVFDPSTGALVDSKSYAFSTSNDDTTSAAFVSFMSLNTNNRIVAILTSGKVNFPPEVVSCLR  
TAGTSAPSDSILSRFDVSYAAFYTSSKRAIALEHVKLSNRKSTDDYQITLDVVFDSLEDVG  
ATGFFRGTYESVEQFMSAVGGTNDIARLPTSAAISKLSYNLIPGDVLYLKAQLYADADL  
LALGTTNISIRFYNASNGYISSTQAEFTGQAGSWELKEDYVVVPENAVGFTIYAQRQAQAG  
QGGMRNLSFSEVSRNGGISKPAEFGVNGIRVNYICESASPPDIMVLPTQASSKTGKVFQGE  
FREV

>sp|Q6QGF0|FIBC\_BPT5 Probable central straight fiber OS=Escherichia phage T5 GN=D17  
PE=2 SV=1

MISNNAPAKMVLNSVLTGYTLAYIQHSIYSDYDVIGRSFWLKEGSNVTRRDFTGIDTFSVTI  
NNLKPTTTYEVQGAIFYDSIIDSELLNAQIGINLSDKQTFKMKSAPRITGARCESEPVDVGV  
GAPIVYIDTTGEADYCTIELKDNSNANNPWVYKYYV GALMPTIMFGGVPIGSYKVRISGQIS  
LPDGVITDSSGYEYPNVFEVRYNFVPPAAPINIVFKAARIADGKERYDLRVQWDWNRGA  
GANVREFVLSYIDSAEFVRTGWTKAQKINVGAAQSATIISFPWKVEHKFKVSSIAWGPDA  
QDVTDSAVQTFILNESTPLDNSFVNETGIEVNYAYIKGKIKDGSTWKQTFLLIDAATGAINIG  
LLDAEGKAPISFDPVKKIVNVDGSVITKTINAANFVMTNLTGQDNPAIYTQGKTWGDTKS  
GIWMGMDNVTAKPKLDIGNATQYIRYDGNILRISSEVVIGTPNGDIDIQTGIQKQTVFIYII  
GTSLPKPTSPAYPPSGWSKTPPNRTSNTQNIYCSGTGLDPVTNQLVSGTSSWSDVVQWSGT  
EGVDGRPGATGQRGPGMYSLAIANLTAWNDSQANSFFTSNFGSGPVKYDVLTEYKSGAP  
GTAFTRQWNGSAWTSPAMVLHGDMIVNGTVTASKIVANNAFLSQIGVNIIYDRAAALSSN  
PEGSYKMKIDLQNGYIHIR

>sp|P03748|FIBER\_BPT7 Tail fiber protein OS=Enterobacteria phage T7 GN=17 PE=1 SV=1

MANVIKTVLTYQLDGSNRDFNIPFEYLARKFVVVTLIGVDRKVLINTDYRFATRTTISLTK  
AWGPADGYTTIELRRVTSTTDRLVDFTDGSILRAYDLNVAQIQTMHVAEEARDLTTDTIGV  
NNDGHLDARGRRIVNLANAVDDRDAVPFGQLKTMNQNSWQARNEALQFRNEAETFRNQ  
AEGFKNESSTNATNTKQWRDETKGFRDEAKRFKNTAGQYATSAGNSASAAHQSEVNAEN  
SATASANSAHLAEQQADRAEREADKLENYNGLAGAIDKVDGTNVYWKGNHANGRLYM  
TTNGFDCGQYQQFFGGVTNRYSVMEWGDENGWLMYVQRREWTTAIGGNIQLVVGQII  
TQGGAMTGQLKLQNGHVLQLESASDKAHYILSKDGNRNNWYIGRSDNNNDCTFHYSYV  
HGTTTLTKQDYAVVNKHFHVQAVVATDGNIQGTKWGGKWLDAYLRDSFVAKSKAWTQ  
VWGSAGGGVSVTVSQDLRFRNIWIKCANNSSWNFFRTGPDGIYFIASDGGWLRFQIHSNG  
LGFKNIADSRSPNAIMVENE

>sp|P20345|FIB12\_BPPH2 Pre-neck appendage protein gp12 OS=Bacillus phage phi29 GN=12  
PE=1 SV=1

MSTKPELKRFEQFGEMMVQLYERYLPTAFDESLLLEKMNKIIHYLNEIGKVTNELIEEWN

KVMEWILNDGLEDLVKETLERWYEEGKFADLVIQVIDELKQFGVSVKTYGAKGDGVTDD  
IRAFEKAIESGFPVYVPYGTFMVSRGIKLPSTVLTGAGKRNAVIFMDSVGRGESLMYN  
QNVTTGNENIFLSSFTLDGNNKRLGQGISGIGGSRESNLSIRACHNVYIRDIEAVDCTLHGI  
DITCGGLDYPYLGDGTTAPNPSENIWIENCEATGFGDDGITTHHSQYINILNCYSHDPRLTA  
NCNGFEIDDGSRHVVLSSNNRSKGCYGGIEIKAHGDAAYNISINGHMSVEDVRSYNFRHI  
GHHAATDPQSVSAKNIVASNLVSIRPNNKRGFQDNATPRVLAVSAYYGVVINGLTGYTDDP  
NLLTETVVSQFRARNCSLNGVGLTGFSNSDNGIYVIGGSRGGDAVNISNVTLNNSGRYG  
VSIKGIENVSITNISGIGDGINSPVALVSTINSNPEISGLSSIGYPTAARVAGTDYNDGLTLFN  
GAFRASSTSSGKIHSEGFIMGSTSGCEASVSKSGVLTSSSSKTSSERSLIAGSSTSEAKGTYN  
TILGSLGAVADEQFAALISASQSRASGNHNLILSSYGINTTGSYKVNGGFEKINWELDSLNG  
RIKARDTVTGGNTWSDFAEYFESLDGQVIETGYLVTLEKKGIRKAEKGEKIIGVISETAGFV  
LGESSFEWQGAVLKNEFGGHIYEEVTTEDGVKFKRPLPSPDFPNKNYIPRSQRREWHVVG  
LLGQIAVRIDETVKQGHGIDAVGGVATDGDNFIVQEITTPYTKEKGYGVAIVLVK

>sp|Q775D6|FIBD\_BPBP Tail fiber receptor-binding protein OS=Bordetella phage BPP-1  
GN=mtd PE=1 SV=1

MSTAVQFRGGTTAQHATFTGAAREITVDTKNTVVVHDGATAGGFPLARHDLVKTAFIKA  
DKSAVAFTRTGNATASIKAGTIVEVNGKLVQFTADTAITMPALTAGTDYAIYVCDGTVRA  
DSNFSAPTGYTSTTARKVGGFHYAPGSNAAQAGGNTTAQINEYSLWDIKFRPAALDPRG  
MTLVAGAFWADIYLLGVNHLTDGTSKYNVTIADGSASPCKSTKFGGDGSAAYSDGAWYN  
FAEVMTHHGKRLPNYNEFQALAFGTTEATSSGGTDVPTTG VNGTGATSAWNIFTSKWGV  
VQASGLWTWGNFEGGVNGASEYTANTGGRGSVYAQPAAALFGGAWNGTSLSGSRAAL  
WYSGPSFSFAFFGARGVCDHLILE

>sp|Q9XJP3|FIBER\_BPSFV Tail fiber protein OS=Shigella phage Sf6 PE=1 SV=2

MTDIITNVVIGMPSQLFTMARSFKAVANGKIYIGKIDTDPVNPENQIQVYVENEDGSHVPA  
SQPIVINAAGYPVYNGQIVKFVTEQGHSMAYDAYGSQQFYFQNVLYKYPDQFGPDIEQ  
LAQSGKYSQDNTKGDAMIGVKQPLKAVLRTQHDKNKEAISILDFGVIDDGVTDNQAIQ  
NAIDAVASLPSGGELFIPASNQAVGYIVGSTLLIPGGVNIRGVGKASQLRAKSGLTGSVRLR  
SYSDTIGRYLRNIRVTGNNTCNGIDTNITAEDSVIRQVYGVWVFDNVMVNEVETAYLMQG  
LWHSKFIACQAGTCRVGLHFLGQCVSVSVSSCHFSGRGNYSADESFGIRIQPTYAWSSEAV  
RSEAILDSETMCIGFKNVYVHDCLDLHMEQLDLDYCGSTGVVIENVNGGFSFSNSWIA  
ADADGTEQFTGIYFRTPSTQSHKIVSGVHINTANKNTAANNQSIAIEQSAIFVFSVSGCTLT  
GDEWAVNIVDINECVSFDKCIFNKPLRYLRSGGVSVTDCYLAGITEVQKPEGRYNTYRGCS  
GVPSVNGIINVPVAVGATSGSAAIPNPGNLTYRVRSLFGDPASSGDKVSVSGVTINVTSP  
VGVALPSMVEYLAI

>sp|P18771|FIBP\_BPT4 Long-tail fiber proximal subunit OS=Enterobacteria phage T4 GN=34  
PE=1 SV=2

MAEIKREFRAEDGLDAGGDKIINVALADRTVGTGDNVDYLIQENTVQQYDPTRGYLKD  
FVIIYDNRFWAAINDIPKPAFNSGRWRALRTDANWITVSSGSYQLKSGEAISVNTAAGN  
DITFTLPSSPIDGDTIVLQDIGGKPGVNQVLIVAPVQSIVNFRGEQVRSVLMTHPKSQLVLIF  
SNRLWQMYVADYSREAIIVTPANTYQAQSNDFIVRRFTSAAPINVKLPRFANHGDIIINFVD  
LDKLNPLYHTIVTTYDETTVQEVGTHSIEGRTSIDGFLMFDDNEKLRWLFDGDSKARLRII  
TTNSNIRPNEEVMVFGANNGTQTIELKLPTNISVGDTVKISMNYMRKGQTVKIKAADED  
KIASSVQLLQFPKRSEYPPEAEWVTVQELVFNDENTNYVPVLELAYIEDSDGKYWVVQQNV  
PTVERVDSLNDSTRARLGVIALATQAQANVDLENSPQKELAITPETLANRTATETRRIARI

ATTAQVNQNTTFSFADDIIITPKKLNERTATETRRGVAEIATQQETNAGTDDTTIITPKKLQA  
RQGSESLSGIVTFVSTAGATPASSRELNGTNVYNKNTDNLVSPKALDQYKATPTQQGAVI  
LAVESEVIAGQSQGWANAVVTPETLHKKTSTDGRIGLIEIATQSEVNTGTDYTRAVTPKT  
LNDRRATESLSGIAEIATQVEFDAGVDDTRISTPLKIKTRFNSTDRTSVVALSGLVESGTLW  
DHYTLNILEANETQRGTLRVATQVEAAAGTLDNVLITPKKLLGTKSTEAQEGVIKVATQSE  
TVTGTSAANTAVSPKNLKWIAQSEPTWAATTAIRGFVKTSSGSITFVGNDTVGSTQDLELYE  
KNSYAVSPYELNRVLANYLPLKAKAADTNLLDGLDSSQFIRRDIAQTVNGSLTLTQQTNLS  
APLVSSSTGEFGGSLAANRTFTIRNTGAPTSIVFEKGPASGANPAQSMSIRVWGNQFGGGS  
DTTRSTVFEVGGDDTSHHFYSQRNKDGNIAFNINGTVMPININASGLMNVNGTATFGRSVT  
ANGEFISKSANAFRAINQDYGFFIRNDASNTYFLLTAAGDQTGGFNGLRPLLINNQSQTITI  
GGLIIAKGVNTINSGLTVNSRIRSQGTKTSPLYTRAPTSDTVGFWSIDINDSATYNQFPGY  
FKMVEKTNEVTGLPYLERGEEVKSPGTLTQFGNTLDSLYQDWITYPTTPEARTRWRTRTW  
QKTKNSWSSFVQVFDGGNPPQPSDIGALPSDNATMGNLTIRDFLRIGNVRIVPDPVVKTVK  
FEWVE

>sp|P10930|FIB12\_BPT4 Short tail fiber protein gp12 OS=Enterobacteria phage T4 GN=12 PE=1  
SV=3

MSNNTYQHVS NESRYVKFDPTDTNFPPEITDVQAAIAAISPAGVNGVPDASSTTKGILFIPT  
EQEVIDGTNNTKAVTPATLATRLSYPNATETVYGLTRYSTNDEAIAAGVNNESSITPAKFTVA  
LNNAFETRVSTESSNGVIKISSLPQALAGADTTAMTPLKTQQLAIKLIQIAPSETTATESD  
QGVVQLATVAQVRQGTREGYAI SPYTFMNSSSTEYKGVIKLGTQSEVNSNNASVAVTG  
ATLN GRGSTTSMRGVVKLT TTAGS QSGGDASSALAWNADVIQQRGGQIYGTLRIEDTFTI  
ANGGANITGTVRMTGGYIQGNRIVTQNEIDRTIPVGAIMMWAADSLPSDAWRFC HGGTVS  
ASDCPLYASRIGTRYGGNPSNPGLPDMRGLFVRGSGRGSHTLNPVNGNDQFGKPRLGVG  
CTGGYVGEVQIQMSYHKHAGGFGEHDDLGAFGNTRRSNFVGT RKGLDWDNRSYFTN  
DGYEIDPESQRNSKYTLNRPELIGNETRPWNISLNYIHKVKE

>sp|P13390|FIBL1\_BPT5 L-shaped tail fiber protein pb1 OS=Escherichia phage T5 GN=1 PE=1  
SV=3

MAITKIILQQMVTMDQNSITASKYPKYTVVLSNSISSITAADVTS AIESSKASGPAKQSEIN  
AKQSELNAKDSENEAEISATSSQQSATQSASSATASANSAKAAKTSETNANN SKNAKTSE  
TNAASSASSASSFATAAENSARA AKTSETNAGNSAQAADASKTAAANSATAAKTSETNAK  
KSETAAKTSETNAKTSENKAKKEYLDMASELSPVTQYDWPVGTNNNSVYVKI AKLTDPG  
AVSCHLTLMITNGGNYGSSYGNIDFVEISARGLNDARGVTS ENITKFLSVRRLGSPNLAWD  
NQLRYGLVEGDGYFEVWCYQRAFIKETRVAVLAQTGRTELYIPEGFVSQDTQPSGFIESLA  
ARIYDQVNKPTKADL GLENAMLVGAFGLGGNGLSYSSVQSNVDLINKLKANGGQYWRA  
ARESGANVDINDHGS GFYSHCGDTHAAINVQYNTGIVKVLATTDNRNLASDIVYANTLYGT  
ANKPSKSDVGLGNVTNDAQVKKAGDVMSGDLDIRKETPSIRLKSTQGN AHLWFMNNDG  
GERGVIWSPPNNGSLGEIHIRAKTSDGTSTGDFIVRHDGRIEAKDAKISYKISSRTAEFSND  
DTNTAATNLRVSGKQHTPIMLVRSDSNVSVGFKLNMNAKLLGIDIDGDLAFGENPDHK  
QNSKIVTRKMMDAGFSVAGLMDFTNGFAGPWEAKNISDQELDLNSLMIKKSDPGSIRVY  
QCVSAGGGNITNKPSGIGGNFILYVESIRKVGDTDFTNRQRLFGTDLNREFTRYCSNGTW  
SAWRESVVS GMNQDVS VKSMSVSGRLSGNELSVGGAGVLNGLVGGGATSKMPSSDK  
GIVIGRSIVREGGEGRLILSSSGGTDRLQLRPAGATSLDNQVEISCT SASAGDTKISFGQG  
AAIRCNNAGSPIISAKAGQMIYFRPNGDGISEGQMILSPNGDLVVKGGVNSKEIDVTASQS  
LPLKETTATTGIGVNFIGDSATECSFGIENTAGGS AVFHNYTRGASNSVTKNNQLLGGYGS

RPWLGSTYTEHSNAALHFLGAGDTSATNHGGWIRLLVTPKGTISDRVPAFRLSDNGDLW  
LVPDGAMHSDLGLVRSIETLNAAVPRFNAPSIQDGRGLKIVAPQAPEIDLIAPRGSGASAPAI  
RAMWCDGSLADTTRYIGATQPGSTFYIGASGHGKFDMSMRGSVAIKSAGGWGPTSTPTQ  
VVLETCESGSISRLPRWGVHDHNGTLMADMADNRYNLGWGSGRVKQVYAVNGTINTSDARL  
KNDVRAMSDPETEAAKAIKEIGFWTWKEQADMNDIREHCGLTVQRAIEIMESFGLDPFK  
YGFICYDKWDEHTVVSEYGPANEDGTENPIYKTIAGDHYSFRLEELNLFIAKGFEARLSAI  
EDKLG

>sp|O80297|G3P\_BPIF1 Attachment protein G3P OS=Enterobacteria phage If1 GN=III PE=1  
SV=1

MKKIIIALFFAPFFTHATDAECLSKPAFDGTLNVDWKEGDSRYANFENCIYELSGIGIGYD  
NDTSCNGHWTPVRAADGSGNGGDDNSSGGGSGNGDSGNNSTPDTVTPGQTVNLPSDLSTL  
SIPANVVKSDSIGSQFSLYTNASCTMCSGYLNSNADSIANITETVKADYNQPDWFEQ  
TDSGDNHVKILQNSYKAVSYNVEKQSDVNNPTYINYSYSVNVKQVSYDTSNVCIMNWE  
TFQNKCDASRAVLITDTVTPSYSRNITIQSNINYQGSNGSGGSGGSGGSGNDGGGTGNG  
NGTGDFDYVKMANANKDALTESFDLSALQADTGASLDGSVQGTLDLSLGSFSDSIGGLVG  
NGSAISGEFAGSSAAMNAIGEGDKSPLDLSLFLKDGLFPALPEFKQCTPFVAFPGKEYEFII  
ECKYIDMFKGIFAFILYFWTFVTVYDSFSGILRKGRG

>sp|Q858F5|FIBER\_BPE15 Tail fiber protein OS=Salmonella phage epsilon15 PE=1 SV=1

MTVSTEVVDHNDYTGNGVTTSPYTFRIFKKSLLVQVVDLNNITELILDYTVTGAGG  
YTCGDVVLSSPLANGYQISISRELPTQETDLRNQGKFFAEVHENAFLKTLMLIQVRSW  
LSLALRKPSFVANYDLAGNYIRNLRDPSRPQDAATKNYVDNLSEGNSYADNLFRTLR  
VPEKINTLPSSLDRAKIPAFDSNGNAIVIPQSGSASDVLIELAKPSGSLVGFSSNNYNP  
GMVGEKLNQNVYPTDAPFYAPTDGTSATTALQSAITHCEGKNAVLCINKSFSVSDSLSIS  
SPLCVFAMNEQCGIVSSAPAGHAAVIFNGDNICWNGGFIRGLNQSSSTIRQDGVLLNGND  
CVLDNVSINGFFAKGLHTSNADGSGVGIRDYGRNTISKCRVEYNKFGISLEGKDGWVLG  
NYVSNHYRMSSEAKPWDDTSNYWDGIVGGGEWLVGATGYLIDGNEFEDNGQSGIYAGG  
NGGIFAKNRITNNHHGNWNRGIDFGVVQRLANSVYENIITDNIVHNNRAANIWLAGVR  
DSIINNNSWFTDDYRSMFAGNFDACVCLTLADGGEKAAPTGNQVNGNRCKTLESDDQI  
SGFTLNITDARGNQVRDNVLSPIGEAYIPNELYAVNNIDIPTEFAFTPQLIGGSGVTLGNSS  
GKLTANGNVFSLSLISAQSVSSPSGLTIGYIPGLSGTSVRHHNVRTEFYNNLNTTMQRAQ  
PYVNIGDSADQLRVYRLADGLSKDDLLEYFMSNSDLRMVGDIEIEPYNFSRSVTVVGHF  
CTSDVMSTELNRLGTDIYNFARGGASDVEVAMSQEAITRQYAPVGG SIPASGSVALTPTE  
VGIFWNGATGKCFGGIDGTFSTTLVNAAGTGETQLVFTRDSAGSAVSSTATFAMRPYTRF  
NTNTIPAGRKHSRHRDDIYVWGRNSTDYTRYVSELHTMVANMHTQRFVICPEFPYDTE  
TTGTTGATNLAALNNNLKADFPDNYCQISGVDLLQNFKSKYNPAYAGDVTDIANGITPRS  
LREDNLHPSETLQPNGLYIGAKVNADFAQFIKSKGWGG

>sp|P12528|FIBER\_BPP22 Tail fiber protein OS=Enterobacteria phage P22 GN=9 PE=1 SV=1

MTDITANVVSNRPIFTESRSFKAVANGKIYIGQIDTPVNPANQIPVYIENEDGSHVQITQ  
PLIINAAGKIVYNGQLVKIVTVQGHSMAYDANGSQVDYIANVLKYDPDQYSIEADKKFK  
YSVKLSDYPTLQDAASA AVDGLLIDRDYNFYGGGETVDFGGKVLTIIECKAKFIGDGNLIFTK  
LGKGSRIAGVFMESTTTPWVIKPWDNDQWLTDAAAVVATLKQSKTDGYQPTVSDYVKF  
PGIETLLPPNAKGNITSTLEIRECIGVEVHRASGLMAGFLFRGCHFCMVDANNPSGGKD  
GIITFENLSGDWKGKNYVIGGRSYGSVSSAQFLRNNGGFERDGGVIGFTSYRAGESGVK  
TWQGTVGSTTSRNYNLQFRDSVVIYPVWDGFDLGADTDMNPELDRPGDYPIQYPLHQL

PLNHLIDNLLVRGALGVGFGMDGKGMYSNITVEDCAGSGAYLLTHESVFTNIAIIDTNTK  
DFQANQIYISGACRVNGLRLIGIRSTDGQGLTIDAPNSTVSGITGMVDPSRINVANLAE EGL  
GNIRANSFGYDSAAIKLRIHKLSKTLDSGALYSHINGGAGSGSAYTQLTAISGSTPDAVSLK  
VNHKDCRGAEIPFVPDIASDDFIKSSCFLPYWENNSTSLKALVKKPNGELVRLTLATL

>sp|Q7Y5D9|FIBL2\_BPT5 L-shaped tail fiber protein p132 OS=Escherichia phage T5  
GN=ORF125 PE=2 SV=1

MSTENRVIDLVVDENVPYGLLMQFMDVDDSVYPSTSKPVDLTDFSLRGSIKSSLEDGAET  
VASFTTAIVDAAQGVASISLPVSAVTTIASKASKERDRYNPRQLAGYYDVIITRTAVGSAA  
SSFRIMEGKVYISDGVTQ

>sp|P03661|G3P\_BPF1 Attachment protein G3P OS=Enterobacteria phage fd GN=III PE=1  
SV=1

MKKLLFAIPLVVPFYSHSAETVESCLAKPHTENSFTNVWKDDKTLDRYANYEGCLWNATG  
VVVCTGDETQCYGTWVPIGLAIPENEGGGSEGGGSEGGGSEGGGSKPPEYGDTPIPGYTY  
INPLDGTYPGTEQNPANPNPSLEESQPLNTFMFQNNRFRNRQGALTVYTGVTQTGDPV  
KTYYYQYTPVSSKAMYDAYWNGKFRDCAFHSGFNEDPFVCEYQGQSSDLPQPPVNAGGG  
SGGGSGGGSEGGGSEGGGSEGGGSEGGGSGGGSGGDFDYEKMANANKGAMTENADE  
NALQSDAKGKLDVATDYGAAIDGFIGDVSGLANGNGATGDFAGSNSQMAQVGDGDNPS  
LMNNFRQYLPSLPQSVVECRPYVFGAGKPYEFSIDCDKINLFRGVFAFLLYVATFMYVFSTF  
ANILRNKES

>sp|P03657|G1P\_BPF1 Gene 1 protein OS=Enterobacteria phage f1 GN=I PE=1 SV=1

MAVYFVTGKLGSGKTLVSVGKIQDKIVAGCKIATNLDLRLQNLQPVGRAKTPRVLRIIPDK  
PSISDLLAIGRGNDSDENKNGLLVLDECGTWFNTRSWNDKERQPIIDWFLHARKLGWDI  
IFLVQDLSIVDKQARSALAENVVYCRRLDRITLPFVGTLYSLITGSKMPLPKLHVGVVVKYG  
DSQLSPTVERWLYTGKNLYNAYDTKQAFSSNYDSGVYSYLTPLYSHGRYFKPLNLGQKM  
KLTKIYLLKFSRVLCLAIGFASAFTYSYITQPKPEVKKVVSQTYDFDKFTIDSSQRLNLSYR  
YVFKDSKGLINSDDLQKQGYSLTYIDLCTVSIKKGNSNEIVKCN

>sp|P03663|G3P\_BPIKE Attachment protein G3P OS=Enterobacteria phage IKe GN=III PE=1  
SV=1

MKRKIIAISLFLYIPLSNADNWESITKSYTGFASKTVESKDKDGKPVKKEVITQADLTAC  
NDAKASAQNVFNQIKLTLSTGTPNSQFRLVTGDTVCVYNGSPGEKTESWSIRAQVEGDIQR  
SVPDEEPSEQTPEEICEAKPPIDGVFNNVFKGDEGGFYINYNGCEYEATGVTVCQNDGTVC  
SSSAWKPTGYVPESGEPSSSPLKDGDGTGGTGEGGSDTGGDTGGGDTGGGSTGGDTGGSS  
GGGSSGGGSSGGSTGKSLTKEDVTAIHAVSPSIGDAVKDSLTEDNDQYDNQKKADEQSA  
KASASVSDAISDGMRGVGNFVDDFGGESSQYGTGNSEMDLSVSLAKGQLGIDREGHGSA  
WESFLNDGALRPSIPTGHGCTNFVMYQGSVYQIEIGCDKLNDIKSVLSWVMYCLTFWYVF  
QSVTSLLRKGEQ

>sp|P03670|G5P\_BPIKE DNA-Binding protein G5P OS=Enterobacteria phage IKe GN=V PE=1  
SV=1

MLTVEIHDSQVSVKERSGVSQKSGKPYTIREQEAYIDLGGVYPALFNFNLEDGQQPYPAK  
YRLHPASFKINNFQVAVGRVLLESVK

>sp|P03666|G4P\_BPF1 Virion export protein OS=Enterobacteria phage f1 GN=IV PE=1 SV=1

MKLLNVINFVFLMFVSSSSFAQVIEMNNSLRDFVTWYSKQTGESVIVSPDVKGTVTYSS  
DVKPENLRDFFISVLRANFDMVGSIPSIIQKYNPNNQDYIDELPSSDNQEYDDNSAPSGG  
FFVPQNDNVTQTFKINNVRAKDLIRVVELFVKSNTSKSSNVLSVDGSNLLVVSAPKDILDN

LPQFLSTVDLPTDQILIEGLIFEVQQGDALDFSFAAGSQRGTVAGGVNTDRLTSVLSSAGGS  
FGIFNGDVLGLSVRALKTNSHSHKILSVPRILTLSGQKGSISVGQNVPFITGRVTGESANVNN  
PFQTVRQNVGISMSVFPVAMAGGNIVLDITSKADSLSSSTQASDVITNQRSIATTVNLRDG  
QTLGLGLTDYKNTSQDSGVPFLSKIPLIGLLFSSRSDSNEESTLYVLVKATIVRAL

>sp|P03672|G5P\_BPPF3 DNA-Binding protein G5P OS=Pseudomonas phage Pf3 GN=V PE=1  
SV=1

MNIQITFTDSVRQGTSKGNPYTFQEGFLHLEDKPFPLQCQFFVESVIPAGSYQVPYRINVN  
NGRPELAFDFKAMKRA

>sp|P69538|G9P\_BPM13 Tail virion protein G9P OS=Enterobacteria phage M13 GN=IX PE=1  
SV=1

MSVLVYSFASFVLGWCLRSGITYFTRLMETSS

>sp|P11128|FUS\_BPPH6 Fusion protein P6 OS=Pseudomonas phage phi6 GN=P6 PE=1 SV=3

MSIFSSLFKVIKKVISKVVATLKKIKKIWPLLLIVAIIFYFAPYLAGFFTSAGFTGIGGIFSSIAT  
TITPTLTSFLSTAWSGVGSLASTAWSGFQSLGMGTQLAVVSGAAALIAPEETAQLVTEIGTT  
VGDIAGTIIGGVAKALPGWIWIAAGGLAVWALWPSSDSKE

>sp|P68676|G5P\_BPPHL DNA-Binding protein G5P OS=Xanthomonas phage phiLf GN=V PE=1  
SV=1

MKVQIMSSAVAVRSFPAREGKPATHFREQTA AVLREGDFPLPFTIGLDEDEDQPPYGEGFYIIDP  
KSLQNNKFGGLEFGRRIRLIPDLTAKLQQPAKVG

>sp|P69532|G6P\_BPM13 Head virion protein G6P OS=Enterobacteria phage M13 GN=VI PE=1  
SV=1

MPVLLGIPLLLRFLGFLLVTLFGYLLTFLKKGFGKIAIAISLFLALIIGLNSILVGYLSDISAQL  
PSDFVQGVQLILPSNALPCFYVILSVKAAIFIFDVKQKIVSYLDWDK

>sp|P69535|G7P\_BPM13 Tail virion protein G7P OS=Enterobacteria phage M13 GN=VII PE=1  
SV=1

MEQVADFDTIYQAMIQISVVLCFALGIIAGGQR

>sp|P06023|GAM\_BPMU Putative DNA ends protecting protein gam OS=Enterobacteria phage  
Mu GN=gam PE=1 SV=2

MAKPAKRIKSAAYVPQNRDAVITDIKRIGDLQREASRLETEMNDAIAEITEKFAARIAPI  
KTDIETLSKGVQGWCEANRDELNNGGKVKTNANLVTGDVSWRVRPPSVSIRGMDAVMETL  
ERLGLQRFIRTKQEINKEAILLEPKAVAGVAGITVKSIEDFSIIPFEQEAGI

>sp|O80294|G5P\_BPIF1 DNA-Binding protein G5P OS=Enterobacteria phage If1 GN=V PE=1  
SV=3

MSELGNLETTVTGKIKRFNNGGGYTYTTVVSPAADAYSFPPVIRIKSKKSLGRVGDEIADI  
HCRITGYERSFPYTDKQTGEQSRGFNVDMLELLE

>sp|P03671|G5P\_BPPF1 DNA-Binding protein G5P OS=Pseudomonas phage Pf1 GN=V PE=1  
SV=1

MNMFATQGGVVELWVTKTDYTTSTKTGEIYASVQSIAPIPEGARGNAKGFEISEYNIEPTL  
LDAIVFEGQPVLCKFASVVRPTQDRFGRITNTQVLVDLLAVGGKPMAPTAQAPARPQAQA  
QAPRPAQQPQGQDKQDKSPDAKA

>sp|P03702|GAM\_LAMBDA Host-nuclease inhibitor protein gam OS=Enterobacteria phage  
lambda GN=gam PE=1 SV=1

MDINTETEIKQKHS�TPFPVFLISPAFRGRYFHSYFRSSAMNAYYIQDRLEAQSWARHYQQ  
LAREEKEAELADDMEKGLPQHLFESLCIDHLQRHGASKKSITRAFDDDDVEFQERMAEHIR



YMVETIAHHQVDIDSEV

>sp|P00276|GLRX\_BPT4 Glutaredoxin OS=Enterobacteria phage T4 GN=NRDC PE=1 SV=1  
MFKVYGYDSNIHKCVYCDNAKRLTLVKKQPFEFINIMPEKGVFDDEKIAELLTKLGRDQTQI  
GLTMPQVFAPDGGSHIGGFDQLREYFK

>sp|Q38494|GEMA\_BPMU GemA protein OS=Enterobacteria phage Mu GN=gemA PE=1 SV=2  
MSRTSLIKLIHVARRELQLDDDTYRAFLMQKTGKISCRELTVTQLEQVLGAMKERGFKKQ  
NKYPRRRFKGHVTPREKVYKIWQQMAEDGFITDGGDVALDKYVQRLTAKRNGGQGVST  
LAWCHGDTLLTVLETLKQWHIRCIREAFSRHGLPLPVSPSGRELRGYDAMTAAYAHARKT  
RRMAQ

>sp|P03776|GP04\_BPT7 Gene 0.4 protein OS=Enterobacteria phage T7 PE=1 SV=1  
MSTTNVQYGLTAQTVLFYSDMVRFCFNWSLAMAQLKELYENNKAI ALES AE

>sp|P79677|GP38\_BPMU Putative sheath terminator protein OS=Enterobacteria phage Mu  
GN=Mup38 PE=2 SV=2  
MLKIKPAAGKAIRDPLTMKLLASEGEEKPRNSFWIRRLAAGDVVEVGSTENTADDDAAP  
KKRSKSK

>sp|P04538|GP68\_BPT4 Prohead assembly protein gp68 OS=Enterobacteria phage T4 GN=gp68  
PE=1 SV=1

MLLIPETHELVLNVEALPEAQGRFDELSSALNKDDINTIVENMLDDETDLAVALASINEN  
MPLNEFIVKHVSARGEITRTKDRKTRERNAFQTTGLSKAKRRQIARKATKTKIANPAGQSR  
AQRKRKKALKRRKALGLS

>sp|P03751|GP73\_BPT7 Protein 7.3 OS=Enterobacteria phage T7 GN=7.3 PE=1 SV=1  
MGKKVKKAVKKVTKSVKKVVKEGARPVKQVAGGLAGGTGEAQMVEVPQAAAQIV  
DVPEKEVSTEDEAQTESGRKKARAGGKKSLSVARSSGGGINI

>sp|Q09YD1|GP38\_BPLP0 Gene product 38 OS=Lactococcus phage P008 GN=orf38 PE=1  
SV=1

MYTAEEREQIIDIVDKMSLLRQDFDGAFTWIKENVAMPDFDFDGEQQFISDLKQLVKINALK  
FGKIYEGVLN

>sp|Q01261|GPG\_BPMU Putative capsid assembly protein G OS=Enterobacteria phage Mu  
GN=G PE=2 SV=1

MSLDMNVAVDVRRIQLALDELGTVTRDRAIPRVMAAALLSSTEQA FERQADPDTGKGWE  
AWSDSWLAWRQDHGFVPGSILTLHGDLARSITTDYQDYALIGSPKIYAAIHQWGGTPDM  
APRPAGVPARPYMGLDKTGEQEIFDAIRKRVSAALRQ

>sp|O48449|GP171\_BPSPP Major tail protein 17.1 OS=Bacillus phage SPP1 PE=1 SV=1  
MPETPIMGQDVKYLFQSIDAATGSAPLPAYQTDGSVSGERELFDEQTKNGRILGPGSVAD  
SGEVTYYGKRGDAGQKAIEDAYQNGKQIKFWRVDTVKNENDKYDAQFGFAYIESREYSD  
GVEGAVEISISLQVIGELKNGEIDTLPEEIVNVSKGGYDFQQPGQTTGEAPGTV P AP

>sp|P03780|GP12\_BPT7 Inhibitor of dGTPase OS=Enterobacteria phage T7 GN=1.2 PE=1 SV=1  
MGRLYSGNLA AFKAATNKLFLQLDLAVIYDDWYDAYTRKDCIRLRIEDRSNGLIDTSTFYH  
HDEDVLFNMCTDWLNHMYDQLKDWK

>sp|P03724|GP14\_BPT7 Internal virion protein gp14 OS=Enterobacteria phage T7 GN=14 PE=1  
SV=1

MCWAAAIPIAISGAQAISGQNAQAKMIAAQTAAGRRQAMEIMRQTNIQNADLSLQARSKL  
EEASAELTSQNMQKVQAIGSIRAAIGESMLEGSSMDRIKRVTEGQFIREANMVTENYRRD  
YQAIFAQQLGGTQSAASQIDEIYKSEQKQKSKLQMVLDPLAIMGSSAASAYASGAFDSKST

TKAPIVAAKGTKTGR

>sp|P03725|GP15\_BPT7 Internal virion protein gp15 OS=Enterobacteria phage T7 GN=15 PE=1 SV=1

MSKIESALQAAQPGLSRLRGGAGGMGYRAATTQAEQPRSSLLDTIGRFAKAGADMYTAK  
EQRARDLADERSNEIIRKLTPEQRREALNNGTLLYQDDPYAMEALRVKTGRNAAYLVDDD  
VMQKIKEGVFRTREEMEEYRHSRLQEGAKVYAEQFGIDPEDVDYQRFNGDITERNISLY  
GAHDNFLSQQAQKGAIMNSRVELNGVLQDPDMLRRPDSADFFEKYIDNGLVTGAIPSDA  
QATQLISQAFSDASSRAGGADFLMRVGDKKVTLNGATTTYRELIGEEQWNALMVTAQRS  
QFETDAKLNEQYRLKINSALNQEDPRTAWEMLQGIKAELDKVQPDEQMTTPQREWLIASQ  
EQVQNQMNAWTKAQAKALDDSMKSMNKLDVIDKQFQKRINGEWWSTDFKDMPVNENT  
GEFKHSDMVNYANKKLAEIDSMDIPDGAKDAMKLYLQADSKDGAFRTAIGTMVTDAG  
QEWSAAVINGKLPERTPAMDALRRIRNADPQLIAALYPDQAEFLTMDMMDKQGIDPQVI  
LDADRLTVKRSKEQRFEDDKAFESALNASKAPEIARMPASLRESARKIYDSVKYRSGNES  
MAMEQMTKFLKESTYTFTGDDVDGDTVGVIPKNMMQVNSDPKSWEQGRDILEEARKGII  
ASNPWITNKQLTMYSQGDSIYLMDDTTGQVRVRYDKELLSKVWSENQKKLEEKAREKALA  
DVNKRAPIVAATKAREAAKRVREKRKQTPKFIYGRKE

>sp|Q01259|GPF\_BPMU Putative capsid assembly protein F OS=Enterobacteria phage Mu GN=F PE=2 SV=2

MPQQTIDLAYAARLPPKEAVAYFRAKGYNITWNWYEQ LADAHARAFTVAKATRMVLT  
IREEVERAVSEGITREEFRTLAPRLQKLGWWGKQIIVDAEGNAKEIELGSPRRLATIYNVN  
TRTAYGAGRYAQMMNTADLYPYWQYVAVMDGRTRPEHARLHNMFQYDDIFWQTHYPP  
NGWNCRCRVRALSAARMKELGLQVSYGASFMNTREVDAGTDESTGEIFRTSSTTFDNGR  
VKMTPDVGWSYNPGSAAFQTDQALIRKLV EVRDAQLREQVVQTLNNSRERQLAFSLWL  
KRLAGSRQTGHEIRALGFMTGSVAEAVYQRTGNMPARLLVMNGKSLATTADAALKPEDL  
QRLPSLMAKPQAVLWDRENHQLLYVVATRDGTARIVVRTSQTVGRQNDRADVLV SISRVS  
AQSLEAAIADGMIDVLEGHVEV NK

>sp|Q38278|GP19\_BPLC2 Gene product 19 OS=Lactococcus phage c2 GN=e19 PE=1 SV=1

MINLQNKKLDIKEFLQELGFTVSLDYEREPMGVMFAEIHPIVSQVSNNSAIYQSFR TLEIEL  
MVICTEETENSLYRAVQLLSDEHYIYANTITDNTNIIKLRGNYYD

>sp|P03735|GT\_LAMBDA Tail assembly protein GT OS=Enterobacteria phage lambda GN=T PE=1 SV=2

MFLKTESFEHNGVTVTLSELSALQRIEHLALMKRQAEQAESDSNRKFTVEDAIRTGAF LVA  
MSLWHNHPQKTQMP SMNEAVKQIEQEVLTWPT EAI SHAENVVYRLSGMYEFV VNNAPE  
QTEDAGPAEPVSAGKVF DGELSFALKLAREMGRPDWRAML AGMSSTEYADWHRFYSTH  
YFHDVLLDMHFSGLTYTVLSLFFSDPDMHPLDFSLN RREADEEPEDDVL MQKAAGLAG  
GVRFGPDGNEVIPASPDVADMTEDDV MLMTVSEGIAGGVRYG

>sp|P03644|G\_BPG4 Major spike protein G OS=Enterobacteria phage G4 GN=G PE=1 SV=1

MFQKFISKHNAPINSTQLAATKTPAVAAPVLSV PNLRSRSTILINATTTAVTTHSGLCHVVRID  
ETNPTNHHALS IAGSLSNVPADMIAFAIRFEVADGVVPTAVPALYDVYPIETFNNGKAISFK  
DAVTIDSHPRTVGNDVYAGIMLWSNAWTA STISGVLSVNQVNREATVLQPLK

>sp|P31281|G\_BPAL3 Major spike protein G OS=Enterobacteria phage alpha3 GN=G PE=1 SV=1

MYQNFVTKHDTAIQTSRFSVTGNVIPAAPTGNIPVINGGSITAERAVV NLYANMNVSTSSD  
GSFIVAMKVDTSPTDPNCVISAGVNLSFAGTSYPIVGIVRFESASEQPTS IAGSEVEHYPIEM

SVGSGGVCSARDCATVDIHPRTSGNNVFGVICSSAKWTSGRVIGTIATTQVIHEYQVLQPLK

>sp|P18056|HOC\_BPT4 Highly immunogenic outer capsid protein OS=Enterobacteria phage T4 GN=hoc PE=1 SV=1

MTFTVDITPKTPTGVIDETKQFTATPSGQTGGGTITYAWSVDNVPQDGAEATFSYVLKGA  
GQKTIKVVATNTLSEGGPETAEATTTITVKNKTQTTTLAVTPASPAAGVIGTPVQFTAALAS  
QPDGASATYQWYVDDSQVGGETNSTFSYTPPTSGVKRIKCVAQVTATDYDALSVTSNEVS  
LTVNKKTMNPQVTLTPPSINVQDASATFTANVTGAPEEAQITYSWKKDSSPVEGSTNVY  
TVDTSSVGSQTIEVTATVTAADYNPVTVTKTGNVTVTAKVAPEPEGELPYVHPLPHRSSAY  
IWCWWVMDEIQKMTEEGKDWKTDDPDSKYLHRYTLQKMMKDYPEVDVQESRNGY  
IIHKTALETGIIYTYP

>sp|Q7Y2C1|HOLIN\_BPKMV Pinholin OS=Enterobacteria phage phiKMV GN=44 PE=1 SV=1  
MMLDTATEAGKGTAVTGVGIAVYSPYEIASLCAAVLTALYVGAQLITLLPKMLDSIAELR  
RRFKK

>sp|P09962|HOLIN\_BPP2 Holin OS=Enterobacteria phage P22 GN=13 PE=1 SV=1  
MKKMPEKHDLTAMMAAKEQGIGAILAFAMAYLRGRYNGGAFKKTLDATMCAIIAWFI  
RDLLVFAGLSSNLAYIASVFIGYIGTDSIGSLIKRFAAKKAGVDDANQQ

>sp|Q6R6U4|HOLIN\_BPT5 Holin OS=Escherichia phage T5 GN=C1 PE=2 SV=1  
MVLVRGGYKLEKFLQLLVLLQEAKDPASLLKRLTILVAVIIFLVSNTSEVMSFLKTFSTS  
AVLQDVQTRIDNFPNVAREKSMVLFSTGADAVFVVKYKPDANDYSNIIAWESNAQLD  
RADLADKAVNKTSSELYRRHLEGFNYASDLTVKVNKYMGNIPSFKNVIFNYIYTCPYFNL  
NNIYAGYIGIAWRDKPVDIADSEQFKEYLTKLCSPQQRSLGRSI

>sp|P51773|HOLIN\_BPP2 Holin OS=Enterobacteria phage P2 GN=Y PE=1 SV=1  
MTAEKSVLSLFMIGVLIVVGKVLGAGGEPITPRLFIGRMLLGGFVSMVAGVVLVQFPDLSL  
PAVCGIGSMLGIAGYQVIEIAIQRRFKGRGKQ

>sp|P06808|HOLIN\_BPT4 Holin OS=Enterobacteria phage T4 GN=t PE=1 SV=1  
MAAPRISFSPDILFGVLDRLFKDNATGKVLASRVAVVILLFIMAIVWYRGDSFFEYKQSK  
YETYSEIIEKERTARFESVALEQLQIVHISSEADFSVYFRPKNLNYFVDIIAYEGKLPSTISE  
KSLGGYPVDKTMDEYTVHLNGRHYYSNSKFAFLPTKKPTPEINMYSCPYFNLDNIYAGT  
ITMYWYRNDHISNDRLESICAQAARILGRAK

>sp|P03646|H\_BPPHS Minor spike protein H OS=Enterobacteria phage phiX174 (Isolate Sanger)  
GN=H PE=1 SV=1

MFGAIAGGIASALAGGAMSKLFGGGQKAASGGIQQDVLATDNNTVGMGDAGIKSAIQGS  
NVPNPDEAAPS FVSGAMAKAGKGLLEGTLQAGTSAVSDKLLDLVGLGGKSAADK GKDT  
RDYLA AAFP ELNAWERAGADASSAGMVDAGFENQKELTKMQLDNQKEIAEMQNETQKE  
IAGIQSATS RQNTKDQVYAQNEMLAYQQKESTARVASIMENTNLSKQQVSEIMRQMLTQ  
AQTAGQYFTNDQIKEMTRKVS AEVDLVHQQTQNQRYGSSHIGATAKDISNVVTD AASGV  
VDIFHGIDKAVADTWNNFWKDGKADGIGSNLSRK

>sp|P19193|H\_BPCHP Minor spike protein H OS=Chlamydia phage 1 GN=ORF2 PE=1 SV=2  
MSFAENVGRFIGNSVNSVGSVIGDGLKGFNSTQSISSAKQANLLNNLPLPSLDNVLNIGMF  
GGLASGLLSYRAAKKQNKVMQDIANRQMAFQERMSSTAVRRHVEDLKKAGLNPLLAGL  
GSASTPQGAFYSPVNPMEGLNSAISVADKVFYDQRLAHADFQGR LNSAMS VVQLASAV  
QDYKRNYGKFGEVAYWFD RYAGKLLPAMLFYLF RKHPVGRAVSAANS GYAVAKGAKGV  
NFKFSNMSSTAVQRHNSRYNVSKGWRR

>sp|P03719|IPI2\_BPT4 Internal protein II OS=Enterobacteria phage T4 GN=ipi2 PE=1 SV=2  
MKTYQEFIGAEARVGAGKLEAAVNKKAHSFHDLDPKDRKKLVSLYIDRERILALPGANEGK  
QAKPLNAVEKKIDNFASKFGMSMDDLQAAIEAAKAIKDK

>sp|P69592|J\_BPPHS DNA-binding protein J OS=Enterobacteria phage phiX174 (Isolate Sanger)  
GN=J PE=1 SV=2  
MSKGGKRSRGARPRPQLRGTKGKRKGARLWYVGGQQF

>sp|P03785|ITAS\_BPT7 Inhibitor of toxin/antitoxin system OS=Enterobacteria phage T7 GN=4.5  
PE=1 SV=1  
MSNVAETIRLSDTADQWNRVHINVRNGKATMVYRWKDSKSSKNHTQRM TLTDEQALR  
LVNALTKA AVTAIHEAGRVNEAMAILDKIDN

>sp|P03046|KIL\_BPMU Protein kil OS=Enterobacteria phage Mu GN=kil PE=2 SV=3  
MARNIKMATDAQNW LQARGSHVNESYLGVARPILEITYPPVELVKN AVRIMEHKSGVARS  
VWTARLNGCQIIWR

>sp|Q856K7|KU\_BPMCO Protein Ku OS=Mycobacterium phage Corndog GN=87 PE=1 SV=1  
MRSVGNVDLTIGLVTPVKMVGVSSEHDRKASMYHPHEDGNFGKIKMPKLCEDCGEVV  
PTADIAKGFEEGGDIVILTADELASIAAATGAALEVPQFVKAEQINPMLFANENIYRLVPDP  
KRGRQAATTYLMVRHILVSQELVGVVQYTRWGRNRLGVLDVEPSDDGGVLVIRNMMWA  
DELIRSTEGIVPTNVTEDDIDPRLLPVMA SVVESMTGDWDPTAYTD RYTEQLSEAITAKAQ  
GDEIATVASESGKAIDDVSDLLAKLEASIQKKAPAKKATARRKTA

>sp|Q853W0|KU\_BPMOM Protein Ku OS=Mycobacterium phage Omega GN=206 PE=1 SV=1  
MRAVWTGAVNFGLVNPVKMYAATEEHDLKGHLAHVQDGGRIRYHKVCETCGEVHTA  
DLGKVFVEVDGQTALLTDEDLAELPSENNKVIDVVEFVPAGEVDPILLDKPYYLNAEGSVR  
PYALLARTLSADAKVAIVRVTLRSKEHLAVLRVTGKNEVTLQTLRWPDEVREPDFPKLDN  
KPELSEAELKVAAMLVDELSAPFNPDKHQD TYKVELRALVESKLEPVEVPEDVSGLLAKL  
EASVKPKQAKPDIRTWAKAQGFKISARGRIPKDIVDKYEGAMA

>sp|Q38162|LLP\_BPT5 Lytic conversion lipoprotein OS=Escherichia phage T5 GN=llp PE=1  
SV=1  
MKKLFLAMAVLLSACSTFGPKDIKCEAYYMQDHVKYKANVFDRKGD MFLVSPIMAYG  
SFWAPVSYFTEGNTCEGVF

>sp|P22915|MOTA\_BPT4 Middle transcription regulatory protein motA OS=Enterobacteria phage  
T4 GN=motA PE=1 SV=1  
MSKVTYI IKASNDVLNEKTATILITIAKKDFITAAEVRE VHPDLGN AVVNSNIGVLIKKGLV  
EKSGDGLIITGEAQDIISNAATLYAQENAPELLKKRATRKAREITSDMEEDKDMLKLLDK  
NGFVLKKVEIYRSNYLAILEKRTNGIRNFEINNGNM RIFGYKMMEHHIQKFTDIGMSCKI  
AKNGNVYLDIKRSAENIEAVITVASEL

>sp|P23848|MOR\_BPMU Middle operon regulator OS=Enterobacteria phage Mu GN=mor PE=1  
SV=1  
MTEDLFGDLQDDTILAHLDNPAEDTSRFPALLAELNDLLRGELSRLGVDP AHSLEIVVAIC  
KHLGGGQVYIPRGQALDSLIRD LRIW NDFNGRNVSELTRYGVTFNTVYKAIRRMRLKY  
RQYQPSLL

>sp|P15556|NDD\_BPT4 Nucleoid disruption protein OS=Enterobacteria phage T4 GN=ndd PE=1  
SV=2  
MKYMTVTDLNDAGATVIGTIKGGEWFLGTPHKDILSKPGFYFLVSKLGGPFSNPCVSARF  
YVGNQRSKQGFSAVLSHIRQRSQLARTIANNVPPYTVFYLPASKMKPLTTGFGKQLAL

AFTRNHHSEYQTL EEMNRMLADNFKFVLQAY

>sp|Q6WHG9|NEEDL\_BPKVM Protein Gp5 OS=Vibrio phage KVP40 (isolate Vibrio parahaemolyticus/Japan/Matsuzaki/1991) GN=5 PE=1 SV=1

MFMGLDGFEEWWTGVVEDRTTDP LKLGRIKVRMIGLHPDKKSSEQGIRTEELLWVHPMQS  
LDNAAMNGIGNAPIGVVEGTWVFGFFRDKLRQDAVAMGVLP GIPEDLPNGSVGFNDPNE  
KYPLADKLN EPD TNRLARNDVDPDVYDESQSQTAFDNGEAPYVYRPHPIIASKRAAEEKE  
IPLAGYNAEGPKYDEKGPYAAQYPYNHVRESESGHIHEIDDTEGAERLHTYHRTGT FEEI  
HPDGSRVTKIIGDDFEIVHKNQNVYIKGNL NITVVG DATFYCQQNVTQQIDGDLKQHVKG  
NVDQHVEMNVTQTVDKDVTQVVHQNV TQTVDMNVTQTVHQNV TQTVDGDVNQTVGG  
NVQSNVTGDY TQNISGNYTITVGGSMSSES VSSSYTRSAASISDDGGGATLNLGSAALDG  
TTVSLG

>sp|P35837|NEEDL\_BPP22 Tail needle protein gp26 OS=Enterobacteria phage P22 GN=26 PE=1 SV=2

MADPSLNNPVVIQATRLDASILPRNVFSKSYLLYVIAQGT DVGAIAGKANEAGQGAYDAQ  
VKNDEQDVELADHEARIKQLRIDVDDHESRITANTKAITALNVRVT TAEGEIASLQTNVSA  
LDGRVTTAENNISALQADYVSKTATTSQSLASPLNVTTSSYSVGGK KVLGARQTGWTAATG  
TANKGVFDADLTF AVSDTYTQSEIQAIANALITERRR TKALEDALRAHGLID

>sp|P11110|NECK1\_BPT4 Neck protein gp13 OS=Enterobacteria phage T4 GN=13 PE=1 SV=1

MSGYNPQNPKELKDVILRRLGAPIINVELTPDQIYDCIQRALELYGEYHFDGLNKGFHV FY  
VGDDEERYKTGVFDLRGSNVFAVTRILRTNIGSITSMDGNATYPWF TDFLLGMAGINGGM  
GTSCNRFYGPNAFGADLGYFTQLTSYMGMMQDMLSPIPDFWFNSANEQLKVMGNFQKY  
DLIIVESWTKSYIDTNKMVGNTVGYGTVGPQDSWLSERYNNPDHNLVGRVVGQDPNVK  
QGAYNNRWVKDYATALAKELNGQILARHQGMMLPGGVTIDGQRLIEEARLEKEALREEL  
YLLDPPFGILVG

>sp|P06020|NER\_BPMU Negative regulator of transcription OS=Enterobacteria phage Mu GN=ner PE=1 SV=3

MCSNEKARDWHRADVIAGLKKRKL SLSALS RQFGYAPTTLANALERHWP KGEQIIANAL  
ETKPEVIWPSRYQAGE

>sp|P11111|NECK2\_BPT4 Neck protein gp14 OS=Enterobacteria phage T4 GN=14 PE=1 SV=1

MATYDKNLF AKLENRTGYSQTNETEILNPYVNFNHYKNSQILADVLVAESIQMRGVECY Y  
VPREYVSPDLIFGEDLKNKFTKAWKFAAYLNSFEGYEGAKSFFSNFGMQVQDEV TLSINP  
NLFKHQVNGKEPKEGDLIYFPMDNSLFEINWVEPYDPFYQLGQNAIRKITAGKFIYSGEEI  
NPVLQKNEGINIPEFSELELNAVRNLNGIH DINIDQYAEVDQINSEAKEYVEPYVVVNNRG  
KSFESSPFDFND FMD

>sp|P03775|OCR\_BPT7 Overcome classical restriction gp0.3 OS=Enterobacteria phage T7 GN=0.3 PE=1 SV=1

MAMSNMTYNNVFDHAYEMLKENIRYDDIRDTDDLHDAIHMAADNAVPHYYADIFSVMA  
SEGIDLEFEDSGLMPDTKD VIRILQARIYEQLTIDLWEDAEDLLNEYLEEVEEYEEDEE

>sp|P11126|P1\_BPPH6 Major inner protein P1 OS=Pseudomonas phage phi6 GN=P1 PE=1 SV=1

MFNLKVKDLNGSARGLTQAF AIGELKNQLSVGALQLPLQFTRTFSASMTSELLWEV GKG  
IDPVMYARLFFQYAQAGGALSVD ELVNQFTEYHQSTACNPEIWRKLTAYITGSSNRAIKAD  
AVGKVPPTAILEQLRTLAPSEHEL FHHITDFVCHVLSPLGFILPDAAYVYRVGRTATYPNFY  
ALVDCVRASDLRRMLTALSSVDSKMLQATFKAKGALAPALISQHLANAATTAFERSRGNF  
DANAVVSSVLTILGRLWSPSTPKELDPSARLRNTNGIDQLRSNLALFIAYQDMVKQRGRAE

VIFSDEELSSTIIPWFIEAMSEVSPFKLRPINETTSYIGQTS AIDHMGQPSHVVVYEDWQFAK  
EITAFTPVKLANNSNQRFLDVEPGISDRMSATLAPIGNTFAVSAFVKNRTAVYEAVSQRGTV  
NSNGAEMTLGFPSVVERDYALDRDPMVAIAALRTGIVDESLEARASNDLKRSMFNYYAAV  
MHYAVAHNPEVVVSEHQGVAAEQGSLYLWNVRTEL RIPVGYNAIEGGSIRTPEPLEAIAY  
NKPIQPSEVLQAKVLDLANHTTSIHIWPWHEASTE FAYEDAYSVTIRNKRYTAEVKEFELL  
GLGQRRERVRILKPTVAHAIIQMWYSWFVEDDRTLAAARRTSRDDAEKLAIDGRRMQNA  
VTLLRKIEMIGTTGIGASAVHLAQSRIVDQMAGRGLIDDSSDLHVGINRHRIRIWAGLAVL  
QMMGLLSRSEAEALTKVLGDSNALGMVVATTDIDPSL

>sp|Q6QGH9|OBP\_BPT5 Putative replication origin binding protein OS=Escherichia phage T5  
GN=obp PE=1 SV=1

MFSILQGHAGFSRDLATGIWREIKAEDYTFAKRFSKEHPEGK PASM PFKFDVIEEHDPQSL  
AEMLPLMRRLTSDPHIVAVRGRCLAPKNNVRRKKGNFVSNPSNIIAMDVDGILDTGGYD  
KFNLVGMARHIIKMLNSISED MFPLDAGFIAHASSSAGLKPGIRMHLMLESNVKVTQGQL  
KFLFTSINDSSKQKFGFDIADLAYYSVQLHYFADPLFSDGIVDPFKAESKPRLVYVKGSKV  
NLPNNLVDYETTRGEFKEEFYSLLDQIKGKKIASDKVEETISELEEADDGVYLRIPKLYHR  
ALEDGVDFAWLEREIKPALSEYIATKDNSRNIQDYFNNGRKQALKAFVNNSKREIPLNLKG  
VPLKLEVDSPPEVPYLKINIVPPKGHITFVKASLGTGKTTAVTKWLDAGVLPGNFLAVTN  
TRALVSSNAKKFSAGQYDKSVDMLNFKRGAIDRMSTTIHSLHKFKSFIGQIDTIFIDECDV  
MNDLLFAPVVKQRRECIQVLRDILMTAKTVILSDGDISAETIEAYGSLIDFDKPVAFYNHHR  
KMLSKAHAYEFPDESSIWVALQTSLEMGEKSILVSDCGPDELNEKGMALRRNTGALVKEI  
HSNSTSDVDIRRIDYTTNELIDQQIDCLLCSPSVTSGVDFNYFDNVFVITRTSNQAPNMRF  
QAIRRDRGAQNIYYFIDKSTSGFSAGSEQYNIDEGWLELAQQLYARRRELES RNYTSTLRY  
YLLDQGATIDIFSESWG TIEGAGKEYTEERIKAILHSTPDYCAPRHADAYEAKLLLRYYYH  
LESIKDVTVEHVEQYIKDKPNDRAAFFHKMHMFWE DIKKCSNVTIKPFIEALKGKKKDF  
FLKTGQSANPKYARMYLGMMGIGKDMNTENIVDWYRTYCKIECMPIPFKFMTEEERAM  
AEEVMSELGATNEDA

>sp|P22536|P5\_BPPRD Spike protein P5 OS=Enterobacteria phage PRD1 GN=V PE=1 SV=2

MANQQIGGSTVTYNGAIPMGGPVAINSVIEIAGTEVLVDLKL DYATGKISGVQTLYIDLRDF  
LGDVTVTMPDTGQRITARAGTQGYYPVLSTNLMKFIVSATIDGK FPMNFINFPIALGVWPS  
GIKGDKGDGPAGPGAGGTVVVEDSGASFGESLLDTTSEPGKILVKRISGGSGITVTDYGDQ  
VEIEASGGGGGGGGVTDALSLMYSTSTGGP ASIAANALDFDL SGALTVNSVGTGLTKSA  
AGIQLAAGKSGLYQITMTVKNNTVTTGNYLLRVKYGSSDFV VACPASSL TAGGTISLLIYC  
NVLGVPSLDV LKFSLCNDGAALS NYIIN TAAKIN

>sp|P11129|P3\_BPPH6 Spike protein P3 OS=Pseudomonas phage phi6 GN=P3 PE=1 SV=1

MRYQGINEWLGGAKKLT TANGEIGAIYLSAAPPTDAARADAKAVDFTAGWPSAIVDCAD  
ATRAKQNYLWVGDNVVHIGAKHVPLLDLWGGTGD AWQQFVGYACPMLDL CRAWGLGY  
ASASVTTGSLQGYQPSAFLDVEQQQFAKDNLNLYGDNCLDLATSSSAQRAFLEQCMGCA  
LPEDCIFGWYVKMDWEGSAVADAYAAIRVQGFATV MAPWQSVGGAGYVYARVPQKGA  
WMGVNLLAYVHGTSGQPAYGIPMTLSGFTGNMGQVASKWLMPLLMIVDPHV VQILAA  
LGVKRGTKSDPRTTDVYADPKVPASRISGPMINGTVAPPATIPATIPVPLAPLGGAGGPGAQ  
GFQVYPVFTWGLPEFMTDVTIEGTVTADSNGLHVVD DVRNYVWNGTALAAIEQVNAAD  
GRVTLTDSERAQLASLTVRTASLRQQLSVGADPLSKTSIWRR AQKADYD LLSQQIIEADTV  
KNLPAVTFAQANKAAGGQSETLWHQMYRVNDIAGDQVTAIQITGTMATGIRWSATAGGL  
VVD ADEQDAVIAISSGKPVKNSSDLPTADAVNYLFGITADDMPGIVSSQKEMNSEFEEGFL

QKARLWNPRKLVENVQNAYFLMVYARDRKQFHSLVASSLAMAKLGVSTRACKESYGC  
>sp|P27378|P2\_BPPRD Adsorption protein P2 OS=Enterobacteria phage PRD1 GN=II PE=1 SV=3

MANFNVPKLGVFPVAAVFDIDNVPEDSSATGSRWLPSIYQGGNYWGGGPQALHAQVSNF  
DSSNRLPYNPRTEENNPAGNCAFAFNPFQYISNISSAQSVHRRYIGIDLNDEPLFSPNAASIT  
NGGNPTMSQDTGYHNIGPINTAYKAEIFRPVNPLPMSDTAPDPETLEPGQTEPLIKSDGVYS  
NSGIASFIFDRPVTEPNPNWPPLPPPVIPIIYPTPALGIGAAAAYGFGYQVTVYRWEEIPVEFI  
ADPETCPAQPTTDKVIIRTDLNPEGSPCAYEAGIILVRQTSNPMNAVAGRLVPYVEDIAVDI  
FLTGKFFTLNPLRITNNYFADDEVKENTVTIGNYTTTLSSAYYAVYKTDGYGGATCFIASG  
GAGISALVQLQDNSVLDVLYYSLPLSLGGSKAAIDEWVANNCGLFPMSGGLDKTTLLEIPR  
RQLEAINPQDGPQYDLFILDDSGAYASFSSFIGYPEAAYYVAGAATFMDVENPDEIIFILRN  
GAGWYACEIGDALKIADDEFDSVDYFAYRGGVMFIGSARYTEGGDPLPIKYRAIIPGLPRG  
RLPRVVLEYQAVGMSFIPCQTHCLGKGGIISKV

>sp|P11123|P7\_BPPH6 Assembly protein P7 OS=Pseudomonas phage phi6 GN=P7 PE=1 SV=1  
MTLYLVPLDSADKELPALASKAGVTLEIEFLHELWPHLSGGQIVIAALNANNLAILNRH  
MSTLLVELPVAVMAVPGASYRSDWNMIAHALPSEDWITLSNKMLKSGLLANDTVQGEKR  
SGAEPLSPNVYTDALSRLGIATAHAIPVEPEQPFVDVDEVSA

>sp|Q06253|PHD\_BPP1 Antitoxin phd OS=Enterobacteria phage P1 GN=phd PE=1 SV=1  
MQSINFRTARGNLSEVLNNVEAGEEVEITRRGREPAVIVSKATFEAYKKAALDAEFASLFD  
TLDSTNKELVNR

>sp|P27379|PKG6\_BPPRD Packaging efficiency factor P6 OS=Enterobacteria phage PRD1  
GN=VI PE=1 SV=1

MDTEEIKEEMQEAAEAAIENAVETAETAIAKAEGAAAAAEQSAEQAAVMAATLAASV  
EANAAQQAIEHSEQVQTQEEKISWLENQVMAMASNLQMMQEAVTALTVSQSLTPEPSPVP  
AVEVEAMPEAVTVEILPESAGDQQAEPVPSVGDQQETAPRKRFRAI

>sp|P27388|PKG22\_BPPRD Packaging protein P22 OS=Enterobacteria phage PRD1 GN=XXII  
PE=1 SV=1

MQLITDMAEWSSKPFPRPDMSLTGWLAFVGLIIVAILWQQIIRFII

>sp|P27387|PKG20\_BPPRD Packaging protein P20 OS=Enterobacteria phage PRD1 GN=XX  
PE=1 SV=1

MVNWELLKNPINWLIVILMLTIAGMAATLVCNHFGKNAVTSE

>sp|P26744|PORTL\_BPP22 Portal protein OS=Enterobacteria phage P22 GN=1 PE=1 SV=2  
MADNENRLESILSRFDADWTASDEARREAKNDLFFSRVSQWDDWLSQYTTLQYRGQFD  
VVRPVVRKLVSEMRQNPIDVLYRPKDARPDAADVLMGMYRTDMRHNTAKIAVNIAVRE  
QIEAGVGAWRLVTDYEDQSPTSNNQVIRREPIHSACSHVIWDSNSKLMDKSDARHCTVIH  
SMSQNGWEDFAEKYDLADDDIPSFQNPNDWVFPWLTQDTIQIAEFYEVVEKKETAFIYQD  
PVTGEPVSYFKRDIKDVIDDLADSGFIKIAERQIKRRRVYKSIITCTAVLKDKQLIAGEHIPV  
PVFGEWGFVEDKEVYEGVVRLTKDGQRLRNMIMSFNADIVARTPKKKPFVPEQIAGFEH  
MYDGNDDYPYLLNRTDENSGLPTQPLAYYENPEVPQANAYMLEAATS AVKEVATLGV  
DTEAVNGGQVAFDTVNQLNMRADLETYVFQDNLATAMRRDGEIYQSIVNDIYDVPRNVTI  
TLEDGSEKDVQLMAEVVDLATGEKQVLNDIRGRYECYTDVGPSFQSMKQQRNRAEILELL  
GKTPQGTPEYQLLLLQYFTLLDGKGVEMMRDYANKQLIQMGVKKPETPEEQWLVEAQ  
QAKQGQDPAMVQAQGVLLQGQAELAKAQNQTLSLQIDAAKVEAQNLNAARIAEIFN  
NMDLSKQSEFREFLKTVASFQQDRSEDARANAELLKGDQTHKQRMDIANILQSQRQN

QPSGSVAETPQ

>sp|P03728|PORTL\_BPT7 Portal protein OS=Enterobacteria phage T7 GN=8 PE=1 SV=1  
MAEKRTGLAEDGAKSVYERLKNDRAPYETRAQNCAQYTIPSLFPKDSNASTDYQTPWQ  
AVGARGLNNLASKLMLALFPMQTMRLTISEYEAKQLLSDPDGLAKVDEGLSMVERIIM  
NYIESNSYRVTLFEALKQLVAVGNVLLYLPEPEGSNYNPMKLYRLSSYVVQRDAFGNVLQ  
MVTRDQIAFGALPEDIRKAVEGQGGGKKADETIDVYTHIYLDEDSGEYLRVEEVEGMEVQ  
GSDGTYPKACPYIPIRMVRLDGESYGRSYIEEYLGDLRSLENLQEAIVKMSMISSKVIGLV  
NPAGITQPRRLTKAQTGDFVTGRPEDISFLQLEKQADFTVAKAVSDAIEARLSFAFMLNSAV  
QRTGERVTAAEIRYVASELEDTLGGVYSILSQELQLPLVRVLLKQLQATQQIPELPKEAVEPT  
ISTGLEAIGRGQDLKLERCVTAWAALAPMRDDPDINLAMIKLRIANAIGIDTSGILLTEEQ  
KQQKMAQQSMQMGMDNGAAALAQGMAAQATASPEAMAAAADSVGLQPGI

>sp|P25480|PORTL\_BPP2 Probable portal protein OS=Enterobacteria phage P2 GN=Q PE=1  
SV=1  
MSKKKGKTPQAAKTMTASGPKMEAFFGEPVPLDRRDILDYVECISNGRWYEPVVSFT  
GLAKSLRAAVHSSPIYVKNILASTFIPHPWLSQQDFSRFVLDLFLVFGNAFLEKRYSTTGK  
VIRLETSPAKYTRRGVEEDVYWWVPSFNEPTAFAPGSVFHLLPEPDINQELYGLPEYLSALN  
SAWLNESATLFRKYYENGAHAGYIMYVTDVAVQDRNDIEMLRNMMVKSGRNNFNKLF  
LYAPQKADGIKIPLSEVATKDDFFNIKKASAADLLDAHRIPFQLMGGKPEVNGSLGDIEK  
VAKVFVRNELIPLQDRIREINGWLGQEVIRFKNYSLDTDND

>sp|P04332|PORTL\_BPPH2 Portal protein OS=Bacillus phage phi29 GN=10 PE=1 SV=1  
MARKRSNTYRSINEIQRQKRNRWFIHYLNYLQSLAYQLFEWENLPPTINPSFLEKSIHQFG  
YVGFYKDPVISYIACNGALSGQRDVYNQATVFRAASPVYQKEFKLYNYRDMKEEDMGV  
VIYNNDMAFPTTPTLELFAAELAELEKIIISVNQNAQKTPVLIRANDNNQLSLKQVYNQYE  
GNAPVIFAHEALSDSIEVFKTDAPYVVDKLNQKNAVWNEMMTFLGIKNANLEKKERM  
VTDEVSSNDEQIESSGTVFLKSREEACEKINELYGLNVKVKFRYDIVEQMRRELQQIENVS  
RGTS DGETNE

>sp|P13334|PORTL\_BPT4 Portal protein gp20 OS=Enterobacteria phage T4 GN=20 PE=1 SV=2  
MKFNVLSLFAPWAKMDERNFKDQEKEDLVSITAPKLDDGAREFEVSSNEAASPYNAAFQT  
IFGSYEPGMKTTRELIDTYRNLNMNNYEVDNAVSEIVSDAIVYEDDTEVVALNLDKSKFSPK  
IKNMMLDEFSDVLNHLFSQRKGSDFRFRWYVDSRIFFHKIIDPKRKPKEGIKELRRLDPRQV  
QYVREIITETEAGTKIVKGYKEYFIYDTAHESYACDGRMYEAGTKIKIPKAAVVYAHSLV  
DCCGKNIIGYLHRAVKPANQLKLEDAVVYIRITRAPDRRVWYVDTGNMPARKAAEHMQ  
HVMNTMKNRVYDASTGKIKNQQHNMSMTEDYWLQRRDGKAVTEVDTLPGADNTGN  
MEDIRWFRQALYMALRVPLSRIPQDQGGVMFDSGTSITRDELTFKAFIRELQHKFEEVFL  
DPLKTNLLKGIITEDEWNDEINNIKIEFHRDSYFAELKEAEILERRINMLTMAEFIGKYIS  
HRTAMKDILQMTDEEIEQEAKQIEEESKEARFQDPDQEEDF

>sp|Q6QGD5|PORTL\_BPT5 Portal protein OS=Escherichia phage T5 GN=ORF141 PE=1 SV=1  
MGFKSWITEKLNPGQRIIRDMEPVSHRTNRKPFTTGQAYSKIEILNRTANMVIDSAAECSYT  
VGDKYNIVTYANGVKTCTLDTLNVRPNPFMDISTFRRLVVTDLLFEGCAYIYWDGTSLY  
HVPAALMQVEADANKFIKFIKFNQINRVDEIIFIKDNSYVCGTNSQISGQSRVATVIDSLE  
KRSKMLNFKEKFLDNGTVIGLILETDEILNKKLRERKQEELQLDYNPSTGQSSVLILDGGM  
KAKPYSQISSFKDLDFKEDIEGFNKSICLAFGVPQVLLDGGNNANIRPNIELFYMTIIPML  
NKLTSSLTFFFGYKITPNTKEVAALTPDKEAEAKHLTSLVNNGIITGNEARSELNLEPLDDE  
QMNKIRIPANVAGSATGVSGQEGGRPKGSTEGD



>sp|P03710|PORTL\_LAMBD Portal protein B OS=Enterobacteria phage lambda GN=B PE=1 SV=1

MKTPTIPTLLGPDGMTSLREYAGYHGGGSGFGGQLRSWNPPSESVDAALLPNFTRGNAR  
ADDLVRNNGYAANAIQLHQDHIVGSFFRLSHRPSWRYLGIGEEEEARAFSREVEAAWKEFA  
EDDCCCIDVERKRTFTMMIREGVAMHAFNGELFVQATWDTSSSRLFRTQFRMVSPKRISN  
PNNTGDSRNCRAGVQINDSGAALGYVSEDGYPGWMPQKWTWIPRELPGGRASFIHVFE  
PVEDGQTRGANVFYSVMEQMKMLDTLQNTQLQSAIVKAMYAATIESELDTQSAMDFILG  
ANSQEQRERLTGWIGEIAAYYAAAPVRLGGAKVPHLMPGDSLNLQTAQDNDNGYSVFEQ  
SLLRYIAAGLGVSYEQLSRNYAQMSYSTARASANESWAYFMGRRKFVASRQASQMFLCW  
LEEAIVRRVVTLPKARFSFQEARSAWGNCDWIGSGRMAIDGLKEVQEAVMLIEAGLSTY  
EKECAKRGDDYQEIFAQQVRETMERRAAGLKPPAWAAAAFESGLRQSTEEEEKSDSRAA

>sp|P54309|PORTL\_BPSPP Portal protein OS=Bacillus phage SPP1 GN=6 PE=1 SV=1

MADIYPLGKTHTEELNEIIVESAKEIAEPDTTMIQKLIDEHNPEPLLKGVRYMYCENDIEKK  
RRTYYDAAGQQLVDDTKTNNRTSHAWHKLFDQKTQYLVGEPVTFTSDNKTLLLEYVNE  
LADDDFDDILNETVKNMSNKGIEYWHPFVDEEGEFDYVIFPAEEMIVVYKDNTRRDILFA  
LRYYSYKIMGEETQKAELYTDTHVYYYEKIDGVYQMDYSYGENNPRPHMTKGGQAIG  
WGRVPIIPFKNNEEMVSDLKFKDLIDNYDSITSSTMDSFSDFFQIVYVLKNYDGENPKF  
TANLRYHSVIKVS GDGGVDTLRAEIPVDSAAKELERIQDELYKSAQAVDNPETIGGGATG  
PALENLYALLDLKANMAERKIRAGLRLFFWFFAEYLRNTGKGFNPKELTMTFTRTRIQ  
NDSEIVQSLVQGVTTGIMSKETAVARNPFVQDPEELARIEEEMNQYAEMQGNLLDDEGG  
DDDLEEDDPNAGAAESGGAGQVS

>sp|Q9T1W5|PORTL\_BPMU Portal protein OS=Enterobacteria phage Mu GN=H PE=1 SV=1

MGRILDISGQPFDFDEMQRSDDELAMVMKRTQEHPSGVTNRAAQMLRDAERGDLT  
QADLAFDMEEKDTHLSELSKRLAIQALEWRIAPARDASAQEKDADMLNEYLHDA  
WFEDALFDAGDAILKGYSMQEIEWGWLKMRVPVALHHRDPALFCANPDNLNELRLRD  
ASYHGLELQPFGWFMHRAKSRTGYVGTNGLVRTLIWPFIFKNYSVRDFAEFLEIYGLPMR  
VGKYPTGSTNREKATLMQAVMDIGRRAGGIIPMGMTLDFQSAADGQSDPFMAMIGWAEK  
AISKAILGGTLTTEAGDKGARSLGEVHDEVREIRNADVGQLARSINRDLIYPLLALNSDS  
TIDINRLPGIVFDTSEAGDITALSDAIPKLAAGMRIPVSWIQEKLHIPQPVGDEAVFTIQPVV  
PDNGSQKEAALSAEDIPQEDDIDRMGVSPEDWQRSVDPLLKPVIFSVLKDGPEAAMNKA  
ASLYPQMDDAELIDMLTRAIFVADIWGRLDAAADH

>sp|P03037|RANT\_BPP22 Antirepressor protein ant OS=Enterobacteria phage P22 GN=ant PE=1 SV=1

MNSIAILEAVNTSYVPFNGQHVLTA MVAGVAYVAMKPVVDNIGLSWSSQVQKLLKMKDK  
FNYVDIDMVAGDMKKRLMGCIPLKKNLNGWLF SINPEKVRADIRDKLIK YQEECFVLYDY  
WTKGKAENPRKKTSDERTPLRDAVNMLVSKKHLMYPEAYAMIHQRFNVE SIEELEASQI  
PLAVEYIHRVVLEGEFIGKQEKKTNDLSAKEANSLVWLWDYANRSQALFRELYPAMRQIQ  
SNYSYKCYDYGHEFSYIIGIARDVLINHTRDVIDNEPDGPTNLSAWMRLKDKELPSSLHRY

>sp|P03036|RCRO\_BP434 Regulatory protein cro OS=Enterobacteria phage 434 GN=CRO PE=1 SV=1

MQTLSERLKKRRIALKMTQTELATKAGVKQQSIQLIEAGVTKRPRFLFEIAMALNCDPVW  
LQYGTKRGKAA

>sp|P09964|RCRO\_BPP22 Regulatory protein cro OS=Enterobacteria phage P22 GN=cro PE=1 SV=1

MYKKDVIDHFGTQRAVAKALGISDAAVSQWKEVIPEKDAYRLEIVTAGALKYQENAYRQ  
AA

>sp|Q9T216|RDF\_BPPHC Recombination directionality factor OS=Streptomyces phage phiC31  
GN=3 PE=1 SV=2

MAKRSIWAGDEDNKPKKRETYADDTVGRFHSGYSETNERGKVVVPVALDKWRISTGEQSV  
ADAVAQLFGGTPVENEESTSENFIDVFTDRPKVPVIEADGIHWDMLKWLNGKLKHHCDG  
FDFVSHADEEMIGQPCGCPKLFDERKAAAKEYDAPNPAITVTFTLADDPDELGRFKFQTGS  
WTLFKVLHEAEDDVERVGKGGAVLANLELELVEYTPKRGPMRNKLVSYKPTITVLKSY  
NDAIAD

>sp|P35926|REF\_BPP1 Recombination enhancement function protein OS=Enterobacteria phage  
P1 GN=ref PE=1 SV=1

MKTIEQKIEQCRKWQKAARERAIARQREKLADPVWRESQYQKMRDTLDRRIAKQKERPP  
ASKTRKSAVKIKSRGLKGRTPAEERRIANALGALPCACYMHGVISNEVSLHHIAGRTAP  
GCHKKQLPLCRWHHQAAPAEVREKYPWLVPHADGVVGGKKEFTLLNKSEMELLADA  
YEMANIMH

>sp|P69702|REGA\_BPT4 Translation repressor protein OS=Enterobacteria phage T4 GN=regA  
PE=1 SV=1

MIEITLKKPEDFLKVKETLTRMGIANNKDKVLYQSCHILQKKGLYIVHFKEMLRMDGRQ  
VEMTEEDEVRRDSIAWLLLEDWGLIEIVPGQRTFMKDLTNNFRVISFKQKHEWKLVPKYTIG  
N

>sp|P23207|RBP5\_BPT5 Receptor-binding protein OS=Escherichia phage T5 GN=oad PE=1  
SV=2

MSFFAGKLNKLSILSLRRGSGGDTNQHINPDSQTIFHSDMSHVIITETHSTGLRLDQGAGD  
YYWSEMPSRVTQLHNNDPNRVVLTEIEFSDGSRHMLSGMSMGVGAAYGIINPQIMSQG  
GLKTQITASADLSLDVGYFNTGTSGTIPQKLRDGTGCQHMFGAFSGRRGFASSAMYLGA  
ALYKSAWSGSGYVADAGTLTIPSDYVRHPGARNFGFNAIYVRGRSCNRVLYGMEGPNY  
TTGGAVQGASSSGALNFTYNPSNPESPKYSVGFARADPTNYAYWESMGDPNDSANGPIGI  
YSEHLGIYPSKITWYVTNLVYNGSGYNIDGGLFNGNDIKLSPREIIKGVNVNNTSWKFINF  
IEKNFNVGNRADFRDVGCNLSKDSPSTGISGIATFGLPTTESNNAPSIKGGNVGGLHANVV  
SIYNFLPSASWYVSSNPPKIGNNYGDVWSENLLPLRLLGGSGSTILSGNIVFQNGSVHVG  
TVGLDLNSSRNGAIVCTMEFIDDTWLSAGGIGCFNPTEMLSQGAEYGDSTRFRIGGNTINK  
KLHQILSLPAGEYVPFFTIKGTVVNACKLQAAAYNPTPYWVWVGLPGSVGQTGYTTLTYM  
RNDGNNNISIWLDSMSNIIGMKACLPNIKLIQRLT

>sp|P03045|REGN\_LAMBDA Antitermination protein N OS=Enterobacteria phage lambda GN=N  
PE=1 SV=3

MDAQTRRRERRAEKQAQWKAANPLLVGVSAPVNRPILSLNRKPKSRVESALNPIDLTVL  
AEYHKQIESNLQRIERKNQRTWYSKPGERGITCSGRQKIKGKSIPLI

>sp|P06019|REPC\_BPMU Repressor protein c OS=Enterobacteria phage Mu GN=repc PE=1  
SV=2

MKSNFIEKNNTEKSIWCSPQEIMAADGMPGSVAGVHYRANVQGWTKQKKEGVKGGKAV  
EYDVMSMPTKEREQVIAHLGLSTPDTGAQANEKQDSELINKLTTTLINMIEELEPDEARK  
ALKLLSKGGLLALMPLVFNEQKLYSFIGFSQQSIQTLMMLDALPEEKREILSKYGIHEQES  
VVVPSQEPQEVKKAV

>sp|P03050|RARC\_BPP22 Transcriptional repressor arc OS=Enterobacteria phage P22 GN=arc

PE=1 SV=1

MKGMSKMPQFNLRWPREVLDLVRKVAEENGRSVNSEIYQRMESFKKEGRIGA

>sp|P04891|REGN\_BPP22 Probable regulatory protein N OS=Enterobacteria phage P22 GN=N  
PE=1 SV=2

MTVITYGKSTFAGNAKTRRHERRRKLAIERDTICNIIDSIFGCDAPDASQEVKAKRIDRVTK  
AISLAGTRQKEVEGGSVLLPGVALYAAGHRKSKQITAR

>sp|P03040|RCRO\_LAMBD Regulatory protein cro OS=Enterobacteria phage lambda GN=cro  
PE=1 SV=1

MEQRITLKDYAMRFGQTKTAKDLGVYQSAINKAIHAGRKIFLTINADGSVYAEVVKPFPSN  
KTTA

>sp|P07243|REGN\_BPPH3 Probable regulatory protein N OS=Enterobacteria phage phi21 GN=N  
PE=1 SV=1

MVTIVWKESKGTAKSRYKARRAELIAERRSNEALARKIALKLSGCVRADKAASLGLSRCK  
KAEEVERKQNRYYKPRSEMGVTCVGRQKIKLGSKPLI

>sp|P03631|REPA\_BPPHS Replication-associated protein A OS=Enterobacteria phage phiX174  
(Isolate Sanger) GN=A PE=1 SV=1

MVRSYYPSECHADYFDFERIEALKPAIEACGISTLSQSPMLGFHKQMDNRIKLEELSRM  
QGVEFDNGDMYVDGHKAASDVRDEFVSVTEKLMDELAQCYNVLPQLDINNTIDHRPEG  
DEKWFLNEKTVTQFCRKLAAERPLKDIRDEYNYPKKKGIKDECSRLEASTMKSRRGFA  
IQRLMNAMRQAHADGWFIWFDLTLADDRLEAFYDNPALRDYFRDIGRMVLAEGRK  
ANDSHADCYQYFCVPEYGTANGLRHLHFHAVHFMRTLPTGSVDPNFGRRVRNRRQLNSLQN  
TWPYGYSMPIAVRYTQDAFSRSGWLWPVDAKGEPLKATSYMAVGFYVAKYVNKKSMDM  
LAAKGLGAKWNNLSLTKLSLLPKLFRIRMSRNFGMKMLTMTNLSTECLIQLTKLGYD  
ATPFNQILKQNAKREMLRLGKVTVADVLAAQPVTNLLKFMRASIKMIGVSNLQSFAS  
MTQKLTLSDISDESKNYLDKAGITTA CLRISKWTAGGK

>sp|P07040|REPC\_BPD10 Repressor c protein OS=Escherichia phage D108 GN=repc PE=2  
SV=1

MMSFEIKEWFNAKELEGMPGVPKLATNITRKAVAEDWVKRQRHGGKGVAYEYHINSLPE  
ETRRAIKGASLSDKPVHTSIVHTVDERLIYAMSFLTPDEQAAAVEIIRVAGIKGLMPTIVSKD  
KALEALGITVEQQKTLQTLQALPPEKVVREILSQYEGKEHNFPVRENDVKKAV

>sp|P03047|REGQ\_LAMBD Antitermination protein Q OS=Enterobacteria phage lambda GN=Q  
PE=1 SV=1

MRLESVAKFHSPKSPMMSDSPRATASDSLSTGTDVMAAMGMAQSQAGFGMAAFCGKHEL  
SQNDKQKAINYLMQFAHKVSGKYRGVAKLEGNTKAKVLQVLATFAYADYCRSAATPGA  
RCRDCHGTGRAVDIAKTELWGRVVEKECGRCKGVGYSRMPASAAYRAVTMLIPNLTQPT  
WSRTVKPLYDALVVQCHKEESIADNILNAVTR

>sp|P03049|RMNT\_BPP22 Regulatory protein mnt OS=Enterobacteria phage P22 GN=mnt PE=1  
SV=3

MARDDPHFNFRMPMEVREKLFRAEANGRSMNSELLQIVQDALS KPSPTGYRND AERL  
ADEQSELVKKMVFDTLKDLYKKT

>sp|P03034|RPC1\_LAMBD Repressor protein cI OS=Enterobacteria phage lambda GN=cI PE=1  
SV=2

MSTKKKPLTQEQLDARRLKAIYEKKKKNELGLSQESVADKMGMGQSGVGALFNGINALN  
AYNAALLAKILKVSVEEFSPSIAREIYEMYEA VSMQPSLRSEYEYPVFSHVQAGMFSPELR

TFTKGDAERWVSTTKKASDSAFWLEVEGNSMTAPTGSKPSFPDGMLLILVDPEQAVEPGDF  
CIARLGGDEFTFKKLIRDSGQVFLQPLNPQYPMIPCNESCSVVGKVIASQWPEETFG  
>sp|P03042|RPC2\_LAMBD Transcriptional activator II OS=Enterobacteria phage lambda GN=cII  
PE=1 SV=1  
MVRANKRNEALRIESALLNKIAMLGTEKTAEAVGVVDSQISRWKRDWIPKFSMLLAVLE  
WGVVDDDMARLARQVAAILTNKKRPAATERSEQIQMEF  
>sp|P08707|RPC1\_BP186 Repressor protein CI OS=Enterobacteria phage 186 GN=CI PE=1  
SV=2  
MRIDSLGWSNVLDLDRICEAYGFSQKIQLANHFDIASSSLSNRYTRGAISYDFAAHCALET  
GANLQWLLTGEGEAFVNNRESSDAKRIEGFTLSEEILKSDKQLSVDAQFFTKPLTDGMAIR  
SEGKIYFVVDKQASLSDGLWLVDIEGAISIRELTKLPGRKLVAGGKVPFECGIDDIKTLGRV  
VGVYSEVN  
>sp|P69202|RPC2\_BPP22 Repressor protein C2 OS=Enterobacteria phage P22 GN=C2 PE=1  
SV=1  
MNTQLMGERIRARRKKLIRQAALGKMVGVSNVAISQWERSETEPNGENLLALSALQC  
SPDYLLKGDLSQTNVAYHSRHEPRGSYPLISWVSAGQWMEAVEPYHKRAIENWHDTTVD  
CSEDSFWLDVQGDMSMTAPAGLSIPEGMIILVDPEVEPRNGKLVVAKLEGENEATFKKLVMD  
AGRKFLKPLNPQYPMIEINGNCKIIGVVVDAKLANLP  
>sp|P04524|RP55\_BPT4 RNA polymerase sigma factor OS=Enterobacteria phage T4 GN=55  
PE=1 SV=1  
MSETKPKYNYVNNKELLQAIIDWKTELANNKDPNKVVRQNDTIGLAIMLIAEGLSKRFNF  
SGYTQSWKQEMIADGIEASIKGLHNFDETKYKNPHAYITQACFNAAFVQRIKKERKEVAKK  
YSYFVHNVDYDRDDDMVALVDETFIQDIYDKMTHYEEESTYRTPGAEEKSVVDDSPSLDFL  
YEAND  
>sp|P18681|RPC3\_BPHK0 Regulatory protein CIII OS=Enterobacteria phage HK022 GN=CIII  
PE=1 SV=1  
MMHFQLAGSGVMSAFYPHESELSRRVKQLIRAAKKQLEALCAMK  
>sp|P07879|RPBA\_BPT4 15 kDa RNA polymerase-binding protein OS=Enterobacteria phage T4  
GN=rpba PE=1 SV=2  
MTKITVNYTVVDVKDIQPKHVRSESNPQNQNKIRRAWVLSLSDNAMEVIQNKIKSAPARHA  
YYEAIDREVS NKWIELMRKHTTESL NAGAKFIMTSCGERLEDDYCGNADERLIVAAQIVA  
ETIAADFNR  
>sp|P03044|RPC3\_LAMBD Protease inhibitor III OS=Enterobacteria phage lambda GN=cIII  
PE=1 SV=1  
MQYAIAGWPVAGCPSESLERITRKLRLDVGWKRLIDILNQPGVPKNGSNTYGYPD  
>sp|P13121|RPC1\_BPP1 Repressor protein C1 OS=Enterobacteria phage P1 GN=C1 PE=1 SV=1  
MINYVYGEQLYQEFVFRDLFLKAVARAQHVDAAASDGRPVRPVVLPFKETDSIQAEID  
KWTLMARELEQYPDLNIPKTILYPVNPILRGVRKVTTYQTEAVNSVNMTAGRIIHLIDKDIR  
IQKSAGINEHSAKYIENLEATKELMKQYPEDEKFRMRVHGFSETMLRVHYISSSPNYNDG  
KSVSYHVLLCGVFICDETLRDGIIINGEFEKAKFSLYDSIEPIICDRWPQAKIYRLADIENVK  
KQIAITREEKKVKSAAASVTRSRKTKKGQPVNDNPESAQ  
>sp|P03716|SCAF\_BPT7 Capsid assembly scaffolding protein OS=Enterobacteria phage T7  
GN=9 PE=1 SV=1  
MAESNADVYASFGVNSAVMSGGSVEEHEQNMLALDVAARDGDDAIELASDEVETERDLY

DNSDPFGQEDDEGRIQVRIGDGSEPTDVDTGEEGVEGTEGSEEFPLGETPEELVAASEQL  
GEHEEGFQEMINIAAERGMSVETIEAIQREYEENEELSAESYAKLAEIGYTKAFIDSYIRGQ  
EALVEQYVNSVIEYAGGRERFDALYNHLETHNPEAAQSLDNALTNRDLATVKAIINLAGES  
RAKAFGRKPTRSVTNRAIPAKPQATKREGFADRSEMIKAMSDPRYRTDANYRRQVEQKVI  
DSNF

>sp|P04534|SCAF\_BPT4 Capsid assembly scaffolding protein OS=Enterobacteria phage T4  
GN=22 PE=1 SV=2

MLKEQLIAEAQKIDASVALDSIFESVNISPEAKETFGTVFEATVKQHAKLAESHIKIAEK  
AEEVEKNKEEAEEKAEEKIAEQASKFIDHLAKEWLAENKLAVDKGIKAELEFESMLGGLK  
ELFVEHNVVPEESVDVVAEMEEELQEHKEESPRLFEELNMRDAYINYVQREVALSESTK  
DLTESQKEKVSALVEGMDYSDAFSSKLSAIVEMVKKSNKDESTITESINTPDTEAAGLNFB  
TEAVEDKAAQGAEDIVSVYAKVASRF

>sp|Q05222|SCAF\_BPML5 Probable capsid assembly scaffolding protein OS=Mycobacterium  
phage L5 GN=16 PE=1 SV=2

MSDNPTPESTPEAETPEVEKPMEPQGVFDEAYVQSLRQEAAAARVAKKDAVEAAEARV  
KAEYEAKLAERDTAYTELQNLGQAWIELEKVVYLSLDAKVPNDKVRFAFVEILEGNDRDSI  
AESVKSRLLELVGGFGNKTPSPAFDPSQGRGGKPIPLNGDPIEAIKAAVGIKK

>sp|Q38580|SCAF\_BPSPP Capsid assembly scaffolding protein OS=Bacillus phage SPP1 GN=11  
PE=1 SV=1

MSLKEQLGEELYGQVLAKLGEGAKLVDISDGSFIPKEKFDVNSEKKSLEQQLTDRDQQL  
QELSTKATGHDELSAKIADLQKANEAKQAFEAEKQLKYEHALETALRDSGAKNPKAV  
KALLDTESIKLDGDKLLGFEDQIKALKEQEDYLFKGTPEPNGGVQGTTPPGKGADLGGGLPT  
KKNPFKQGPDFNLTEQGILFRENPELAKKLQAEAQ

>sp|P0DJY6|S2\_BPMU Tail fiber protein S' OS=Enterobacteria phage Mu GN=S' PE=2 SV=1

MPKSTIIQNLGLQETVNQASGALQQNQNGADIPGKDTFTKNIGACRAYSAWLNIGGDSQV  
WTTAQFISWLESQGAFNHPYWMCKGSWAYANNKVITDTGCGNICLAGAVVEVIGTRGAM  
TIRVTTTPSTSSGGGITNAQFTYINHGDAYAPGWRRDYNTKNQOPAFALGQTGSTVGNDA  
VGWNWNSGVYANIGGASTLILHFNMTGSCPAVQFRVNYRNGGIFYRSARDGYGFED  
WSEIYTTTRKPSAGDVGAYTQAECNSRFITGIRLGLSSVQTWNGPGWSDRSGYVVTGSV  
NGNRDELIDTTQARPIQYCINGTWYNAGSI

>sp|Q9T1V0|S1\_BPMU Tail fiber protein S OS=Enterobacteria phage Mu GN=S PE=2 SV=1

MFYIDNDSGVTVMPPVSAQRSIVRWFSEGDGNNVITWPGMDWFNIVQAELLNTLEEAG  
IQPDKTKLNQLALSIAKAIMSNNALLIKNNLSEIKTAGASAQRTARENLDIYDASLNKKGLV  
QLTSATDSPSETLAATAKAVKIAMDANARLAKDRNGADIPNKPLFIQNLGLQETVNRAR  
NAVQKNGDTLSGGLTFENDSILAWIRNTDWAKIGFKNDADSDTDSYMWFFETGDNGNEYF  
KWRKQSTTTKDLMLNKWDALSVLVNAIVNGEVISKSANGLRIAYGNYGFFIRNDGSNT  
YFMLTNSGDNMGTYNGLRPLWINNATGAVSMGRGLNVSGDTLSDRFAINSSNGMWIQMR  
DNNAIFGKNIVNTDSAQALLRQNHADRKFMIIGGLGNKQFGIYMINNSRTANGTDGQAYM  
DNNGNWLCGAQVIPGNANFDSRYVRDVRGLTQSLTGGLSRDYKAPSGHVITGFHTNGD  
WEMQGGDDKVYIRPVQKNINGTWYNVASA

>sp|P25478|SCAF\_BPP2 Capsid assembly scaffolding protein OS=Enterobacteria phage P2  
GN=0 PE=1 SV=1

MAKKVSKFFRIGVEGDTCDGRVISAQDIQEMAETFDPRVYGCRINLEHLRGILPDGIFKRY  
GDVAELKAEKIDDDSAKLGKVALFAKITPTDDLIAMNKAAQKVYTSMEIQPNFANTGKC

YLVGLAVTDDPASLGTEYLEFCRTAKHNPLNRFKLSPENLISVATPVELEFEDLPETVFTALT  
EKVKSIFGRKQASDDARLNDVHEAVTAVAEHVQEKLSATEQRLAEMETAFSALKQEVTDR  
ADETSQAFTRLKNSLDHTESLTQQRRSKATGGGGDALMTNC

>sp|P13848|SCAF\_BPPH2 Capsid assembly scaffolding protein OS=Bacillus phage phi29 GN=7  
PE=1 SV=1

MPLKPEEHEDILNKLLDPELAQSERTEALQQLRVNYGSFVSEYNDLTKSHEKLAAEKDDLI  
VSNSKLFQRQIGLTDKQEEDHKKADISETITIEDLEAK

>sp|P0DJY3|SGS\_BPT7 Protein suppressor of silencing OS=Enterobacteria phage T7 GN=5.5  
PE=1 SV=1

MAMTKKFKVSVFDVTAKMSSDVQAILEKDMLHLCKQVGSAGIIVPNGKQKEMIVQFLTHG  
MEGLMTFVVRTSFREAIKDMHEEYADKDSFKQSPATVREVF

>sp|Q9T1X1|SPAN1\_BPMU Probable spanin, inner membrane subunit OS=Enterobacteria phage  
Mu GN=Mup23 PE=2 SV=1

MTFASKSLLLA AVFTAVLSGGLWHRLDSTRHDNQT LRRELQTEQQARHTAEWLLHGQEQ  
TMQVFSAIRAANRAARLADETEHHDAAKEKITTAITGDNCSTRPVAVAADRLRELEKTRR  
AIGGDPARN

>sp|Q37935|SPAN2\_LAMBD Spanin, outer lipoprotein subunit OS=Enterobacteria phage lambda  
GN=Rz1 PE=1 SV=1

MLKLMMLCVMMLPLVVVGCTSKQSVSQCVKPPPPAWIMQPPPDWQTPLNGIISPSESG

>sp|P00726|SPAN1\_LAMBD Spanin, inner membrane subunit OS=Enterobacteria phage lambda  
GN=Rz PE=1 SV=1

MSRVTAIISALVICIIVCLSWAVNHYRDNAITYKAQRDKNARELKLANAAITDMQMRQRD  
VAALDAKYTKELADAKAENDALRDDVAAGRRLHIKAVCQSVREATTASGVDNAASPRL  
ADTAERDYFTLRERLITMQKQLEGTQKYINEQCR

>sp|Q38504|SSB\_BPPH2 Single-strand-binding protein OS=Bacillus phage phi29 GN=5 PE=1  
SV=1

MENTNIVKATFDTETLEGQIKIFNAQTGGGQSFKNLPDGTIIEANAIAQYKQVSDTYGDAK  
EETVTTIFAADGSLYSASKTVAEAAASDLIDLVTTRHKLETFKVKVVQGTSSKGNVFFSLQLS  
L

>sp|P39230|SPAC\_BPT4 Protein spackle OS=Enterobacteria phage T4 GN=sp PE=1 SV=1

MKKFIFATIFALASCAAQPAMAGYDKDLCEWSMTADQTEVETQIEADIMNIVKRDRPEMK  
AEVQKQLKSGGVMQYNYVLYCDKNFNKNIIAEVVGE

>sp|P31340|SPIKE\_BPP2 Spike protein OS=Enterobacteria phage P2 GN=V PE=1 SV=2

MNTLANIQELARALRN MIRTGIIVETDLNAGRCRVQTGGMCTDWLQWLTHRAGRSRTW  
WAPSVGEQVLILAVGGELDTAFVLPGIYSGDNPSPSVSADALHIRFPDGAVIEYEPETSALT  
VSGIKTASVTASGSVTATVPVVMVKA STRVTLDTPEVVCTNRLITGTLEVQKGGTMRGNIE  
HTGGELSSNGKVLHTHKHPGDSGGTTGSPL

>sp|P20376|SSDNA\_BPT5 Probable ssDNA-binding protein OS=Escherichia phage T5 GN=D11  
PE=2 SV=1

MAKSWGETTGGSNDKIEFLKFNNGITRVRIVSGVLPYVYWL TNKEGSVAPFECLRFNRD  
KESFVRGKADPVHELGF FEKELDKDGNRVPLPKPKKNYIAFVIDRSDNKLKVMVKATILK  
GIQSIMKQLNLATPFIDIDISIEKKGKGFDT EYDVQQAAMQFQIKLQDPNSAESKQYAADV  
DLIGEAMCDEDGDIIFEKVPSLEQTYPVPTYEEQKEAIQAFMEGRENKDDDAKSGNSNA  
GSQKGIDQEAASDLDD

>sp|P85502|STRU2\_BPPAJ Structural protein 2 OS=Pseudomonas phage PAJU2 PE=1 SV=2  
MAYDTSAPFLGSKDPRVLYNNAENMDVAMNSVEQERWMDRGPQRPPPLPRWTYWGMEQ  
NYNRFISNSAWELPLVYVDGSPLTVERSSQVIERDGNLYSVKLPASFPVELSGTWSADEPL  
LVFRSDQSLRQELAEQNGGTLVGWKRTQLSASIDTIQQLADSIPIRVWEFAELVSDKPSDP  
ATWNWTPAFQAMVDTAESYMQSSGAKQITCYAGPGTFLIDSIVWRSGVHMYFGGAELKA  
HPDSIDGNLNLATLKLSDIGFYGPGIVNGDKDSFDPEHRQHGIHCVAKKVVKVLDLFIENIG  
SSSVFSLGDGVIFRPTIPEGDFQCEDCEVSGCTFSNIERQCITVESGFNIRILSNGFYNSTYAA  
LDIENAGYTMGDVDGVIFQGNIDGCLYGVTAVTYQPVDAQRNIVCGGNIYKNVMDAYH  
FRGCSNVKVGYGDIAEVSRYGAIYSDGATTVSNIEISDFTTSGGTYGVYAQTTSGGSFNRI  
KLSTLKITGTSTSPITVQSTSGLRIEEVDVLINTGAGVVIQNCASPIIRNLKMGAVTLSVPA  
VSFIGTTTNPVGGGLDIAGFTVGVSVTTSATTTIHSLSNNVFAGVATPWSVNPNGYIKGQFS  
GTFTMNAASMNVNSVGMNVTSSVVRLIPTNAAAATLQAGSKMAWVVNSASSNNVSFR  
VQTADGTAAAGTETFAFVIENL

>sp|Q9XJR3|SPIKE\_BPPM2 Spike protein P1 OS=Pseudoalteromonas phage PM2 GN=I PE=1  
SV=1  
MIVKKKLAAGEFAETFKNGNNTIHKAVGELVLRAYGADGGEGRLTIVRQGVSIKGMNYTS  
VMLHTEYAQEIEYWVGDLDYSFQEQTTSKRDVNSFQIPLRDGVRELLPEDASRNRAKISPK  
VDIWIGGENMTALNGIVDGGKFEAGQEFQINTFGSVNYWVSDEEIRVFKKEYSARAKYQAQ  
NEGRTALEANNVPPFDIDVPELDGVPFSLKARVRHKSXGVDGLGDYTSISVKPAFYITEG  
DETTDTLIKYTSYGSTGSHSGYDFDNTLDVMVTLASGVHRVFPVETELDYDAVQEVQH  
DWYDESFTTFIEVYSDDPLLVKGYAQILMERT

>sp|P85501|STRU1\_BPPAJ Structural protein 1 OS=Pseudomonas phage PAJU2 PE=1 SV=2  
MATDSLGLTLVDLIANTGGFERGMDAAERRIASSTTRAFQRQEQAERLVGRIDPVAGAIN  
RLVQEQTLELRFHRSGLIIPAGEFERLNRILNDQLDAVQRGNREMASGAMSARQYQAALRG  
VPAQFTDIAVSLASGQQPLTVLLQQGGQLKDMFGGVVPAARALGGYIAGLVNPITGLAAS  
VGVLGISFIDAEREAFAFNKAIFAGNNAAGVSGSGLSQIAEQASAVAGSLSSANKAAIALA  
SSGKVAASQLQSLTEATIAIAQFTGKEVDDVAKSLSAMGDSATDAAAKISEQYGLLTYEQY  
QVIKSIDEQNSQRALDVLGEELNRNAQERLQYRESLSDIERDWIDIKTAINSYAAVRSE  
IFPNQNNQIEQIRILRTRQEGGVLGAVSSAFGFGENSTESLQQQLDSLQKQRDAAAKQAE  
EQAKITKSNQDRVDASREWEEKENEKYLSSRVKMEKEISAARELGRKAGLNEIEIEDRIAQI  
RKSYYEKPSSRSGSLDAGQRMLDSLQYASMQAQLATEKLGTQAQALVQWEQQQLAD  
LKSRGSLADQKALLANADLITAQLKRNAALEDELNTRKEIQKTLDDYKRLNESLRTDAE  
KQLDLTRQRFEILDKARQAGISDDDYRRTAERIVSSSTTKAPTFSGVDVAVVAGPQGELDKL  
DKAQEDLEAWYEQLEILNENREKRAELNASWDEQELKLKQEHEDAMAAIEQSRQQITL  
SANEQFFGNLSGLAKTFFGEQSGLYKAAFVAEKSFIAIAKTLINVPKTASDAYSAMAGIPVIG  
PALGIAAAAAAVTAQLAQVAAVKNVNLGMAHDGIDAVPETGTWLLQKGERVTTAETSA  
KLDKTLDDVRSNQSQQGAPTINLIEDRSRAGQVNTRRQDDQYIIDVVADLFGDGRTSKA  
IGSSFGRMRRSGT

>sp|P09386|STXB\_BP933 Shiga-like toxin 2 subunit B OS=Enterobacteria phage 933W  
GN=stxB2 PE=1 SV=1  
MKKMFMAVLFALASVNAAMAADCAKKGKIEFSKYNEDDTFTVKVDGKEYWTSRWNLQPL  
LQSAQLTGMTVTIKSSTCESGSGFAEVQFNND

>sp|P85503|STRU3\_BPPAJ Structural protein 3 OS=Pseudomonas phage PAJU2 PE=1 SV=2  
MAKNNVVKAQGTDLFYFIDPDTHVVMNAGCITSLSGIDTSIDQIETTCLNETARSYVAGLAT

PGTATFSINTNPQDPVHIRLLELKNAGVSLDWAVGWSDGTSAPTAVLDSSGEYDFDVPADR  
SWLLFEGYMNSFSFEFAQNAVVTSSIGIQVSGEPVLIPKSTS

>sp|P09385|STXA\_BP933 Shiga-like toxin 2 subunit A OS=Enterobacteria phage 933W  
GN=stxA2 PE=1 SV=2

MKCILFKWVLCLLGFSSVSYREFTIDFSTQQSYVSSLNSIRTEISTPLEHISQGTTSVSVIN  
HTPPGSYFAVDIRGLDVYQARFDHLRLIIEQNNLYVAGFVNTATNTFYRFSDFTHISVPGVT  
TVSMTTDDSSYTTLQRVAALERSGMQISRHSLVSSYLALMEFSGNTMTRDASRAVLRVFTV  
TAEALRFRQIQREFRQALSETAPVYTMTPGDVDLTLNWGRISNVLPEYRGEDGVRVGRISF  
NNISAILGTAVILNCHHQGARSVRVNEESQPECQITGDRPVKINNTLWESNTAAAFNR  
KSQFLYTTGK

>sp|Q6QGE3|TAIL1\_BPT5 Minor tail protein OS=Escherichia phage T5 GN=ORF133 PE=2  
SV=1

MFYSLMRESKIVIEYDGRGYHFDALSNYDASTSFQEFKTLRRTIHNRTNYADSIINAQDPSS  
ISLAINFSTLIESNFFDWMGFTREGNSLFLPRNTPNIEPIMFNMYIINHNNNSCIYFENCYVST  
VDFSLDKSIPILNVGIESGKFSEVSTFRDGYTITQGEVLPYSAPAVYTNSSPLPALISASMSFQ  
QQCSWREDRNIFDINKIYTNKRAYVNEMNASATLAFYYVKRLVGDKFLNLDPETRTPLIIK  
NKYVSITFPLARISKRLNFSLDLYQVEYDVIPTADSDPVEINFFGERK

>sp|P13771|TARGB\_BPD10 ATP-dependent target DNA activator B OS=Escherichia phage D108  
GN=B PE=2 SV=2

MNISDIRAGLRTLVEEETTFKQIALESGLSTGTISSFINDKYNGDNERVSQMLQRWLEKY  
HAVAELPEPPRFVETQTVKQIWTSMRFASLTESIADVCGNPGVVGKTEAAREYRRTNNNVW  
MITITPSCASVLECLTELAFELGMNDAPRRKGPLSRALRRRLEGTQGLVIIDEADHLGAEVL  
EELRLLQESTRTGLVLMGNHRVYSNMTGGNRTVEFARLFSRIAKRTAINKTKKADVKAIA  
DAWQINGENELELLQQAQKPGALRILNHSLRLAAMTAHGKGERVNEDYLRQAFRELDL  
DVDISTLLRN

>sp|P0DJY4|TAPFS\_BPMU Probable tail assembly protein FS-gp41 OS=Enterobacteria phage  
Mu GN=Mup41 PE=2 SV=1

MDEMNLGPEAQELHDSIVAEIQSGVLKLDGLPFGTGDETEMQYDVTLRELTAGDMIDA  
QAAAEKLVMSKEGPVLVSSPSRMGLEMLRRQIASVGCIKGPLSMALIRKLSVDDFQRLSL  
ATEMYDMAVAASLTQERGGEWLRCRNDIEKAATAIGVILKSGPEWALSPLSRFFRHCQQ  
AKTLSQYHR

>sp|P03681|TERM\_BPPH2 DNA terminal protein OS=Bacillus phage phi29 GN=3 PE=1 SV=1

MARSPRIRIKDNDKAEYARLVKNTKAKIARTKKKYGVDLTAEIDIPDLDSFETRAQFNKW  
KEQASSFTNRANMRYQFEKNAYGVVASKAKIAEIERNTKEVQRLVDEKIKAMKDKEYYA  
GGKPQGTIEQRIAMTSPAHTVGINRPHDFDFSKVRSYRLRTLEESMEMRTDPQYYEKKMI  
QLQLNFIKSVESFNSFDAADELIEELKKIPPDDFYELFLRISEISFEEFDSEGNTVENVEGN  
VYKILSYLEQYRRGDFDLSLKGK

>sp|P03740|TFA\_LAMB Tail fiber assembly protein OS=Enterobacteria phage lambda GN=tfa  
PE=1 SV=1

MAFRMSEQPRTIKIYNLLAGTNEFIGEGDAYIPPHTGLPANSTDIAPPDIPAGFVAVFNSDEA  
SWHLVEDHRGKTVYDVASGDALFISELGPLPENFTWLSPGGEYQKWNGTAWVKDTEAEK  
LFRIREAEETKKSMLQVASEHIAPLQDAADLEIATKEETSLLLEAWKKYRVLLNRVDTSTAP  
DIEWPAVPVME

>sp|P04445|TF1\_BPSP1 Transcription factor 1 OS=Bacillus phage SP01 GN=TF1 PE=1 SV=1



MNKTELIKAI AQDTELTQVSVSKMLASF EKITTETVAKGDKVQLTGFLNIKPVARQARKGF  
NPQTQEALEIAPSVGVSVKPGESLKKAAEGLKYEDFAK

>sp|P09009|TERM\_BPPRD DNA terminal protein OS=Enterobacteria phage PRD1 GN=VIII  
PE=1 SV=1

MAKKKPVEKNGLVYKEFQKQVSNLKKAGLIPKTL DV RKVKPTKHYKGLVSKYKDVATG  
GAKLAAIPNPAVIETLEARGESI I K K G G KAYL KARQQINQRGQIVNPFTVRVTKRGEV VRR  
YRKTTPPEGKPVYITQRELPIKFENMEQWLTELKAAGFQLQPGEQIYFTFNGNYSRRTYTSF  
DEAFNKFMTYDIIDAVAGKLVKVEDEADLVKSVGFQRISGPEAKAYNRNRIVLPEMQFSQA  
AKKKYKRRQKRGYGSKGV

>sp|P03738|TIPL\_LAMBD Tail tip protein L OS=Enterobacteria phage lambda GN=L PE=1  
SV=1

MQDIRQETLNECTRAEQSASVVLWEIDLTEVGGERYFFCNEQNEKGEPVTWQGRQYQPY  
PIQGS GFELNGKGTSTRPTLTVSNLYGMVTGMAEDMQSLVGGTVVRRKVYARFLDAVNF  
VNGNSYADPEQEVISRWRIEQCSELSAVSASFVLSTPTETDGAVFPGRIMLANTCTWTYRG  
DECGYSGPAVADEYDQPTSDITKDKCSKCLSGCKFRNNVGNFGGFLSINKLSQ

>sp|Q6QGE7|TMP\_BPT5 Probable tape measure protein OS=Escherichia phage T5 GN=D18-19  
PE=1 SV=1

MTDKLIRELLIDVKQKGATR TAKSIENVSDALENAAA SELTNEQLGKMPRTLYSIERAAD  
RAAKSLTKMQASRG MAGITKSIDGIGDKLDYLAIQ LIEVTDKLEIGFDGVSRSVKAMGND  
VAAATEKVQDRLYDTNRALGGTSKGFNDTAGAAGRASRALGNTSGSARGATRDFAAMA  
KIGGRLPIMYAALASNVFVLQTAFESLKVGDQLNRLEQFGTIVGTMTGTPVQTLALS LQN  
ATNGAISFEEAMRQASSASAYGFDSEQLEQFGLVARRAAAVLGVDMTDALNRVIKGVSKQ  
EIELLDELGV TIRLNDAYENYVKQLNATSTGIKYTVDSLTTYQKQAYANEVIAESTRRFG  
YLDDALKATSWEQFAANANSALRSLQQAATYLNPMVMDTLN TFLYQTKSSQMRVSAMA  
RSASAKTTPAENV TALIENAVGAREDLDTYLKESEERVKKAQELKQQLDDLKAKQAATAP  
IANALTAGGIGGDES NKLVVQLTNELARQNKEIEERTKTEKVL RQAVQDTGEALLRNGKL  
AEQLGAKMKYADTAVPGDKGVFEVDPN NLKAVSEIQKNFD FLKSSSDTANNIRMAASSI  
TNAKKASSDLNSVVKAVEDT SKVTGQSADTLVKNLNLGFSSLDQMKA AQGLSEYVTA  
MDKSEQNALEVAKRKDEVYNQTKDKAKAEAAAREVLLRQQQEQLTAAKALLAINPNDP  
EALKQVAKIETEILNTKAQGFENAKKTKDYTDKILGVDREIALLNDR TMTSTQYRLAQLR  
LELQLEQEKTELYSKQADGQAKVEQSRAQAQISREIWEAEKQGTASHVSALMDALEVS  
QTQRNVTGQS QILTERLSILQQLELSKGNTEEELKYRNEIYKTSAALEQLKKQRESQMQ  
QQVGSSVGATYTP TTGLIGEDKDFADMQNRMASYDQAISKLSELN SEATAVAQSMGNLTN  
AMIQFSQGS LDTTSMIASGMQTVASMIQYSTSQVSAIDQAIAAEQKRDGKSEASKAKLK  
KLEAEK LKIQQDAAKKQIIIQTAVAVMQAATAVPYPFSIPLMVAAGLAGALALAQASSASG  
MSSIADSGADTTQYLTLGERQKNVDVSMQASSGELSYLRGDKGIGNANSFVPR AEGGMM  
YPGVSYQMGEHGTEVVTPMVP MKATPN DQLSDGSKTTSGRP IILNISTMDAASFRDFASN  
NSTAFRDAVELALNENGTTLKSLGNS

>sp|Q9T1V6|TMP\_BPMU Probable tape measure protein OS=Enterobacteria phage Mu  
GN=Mup42 PE=2 SV=1

MTGKRLKASVIIDLNGNLSRRSRQYSNQINALSRSGQSSLRALRMEVVRVSGAIDRMGSL  
STRTFRMLSAGALGIAGVGYTANKLFIGAAAQREQQIIAMNSLYHGDKVRAQAMMAWA  
KQNAKDTTWGLSGVLDEIRSSKGFGMTDEQTKQFITMLQDQGAMHGWDLPTAQGASLQ  
LKQMFARQQITAADANLLTGYGINVYQALADATGTDVKKIRD LGTKGKLG MKSILTVFRT

LSEQSKGAQASAMNSWDGMFAQMEANLLEFRIKVANS GP FEEIKNEMRRVLNWHDMAD  
KSGELDALAENIGQKFLTTFRTVKISAQELWRWLKPGKDALAWVDQNI VSLKKLA AVLVS  
VWLANKALRAGWAVAKPSWQVASYPFKTGRRMWRW MRNRKRGGQAGLPVPDAMTSET  
LLQGIGIQRVFVINWPRGFGDYSGGGRRVRS GGRMAPLLPRQPLLSGPQPLALPAPRPV  
LALPPP GVPVTARPAPLPLPGKSGLLSRLAGSAAGQLVTGTVGKLADAGRAVGGWFSGIG  
NKLAGSAIGRVVTKGAGALGWMGKGAGRALSRLGGPVMGALQLAPVLMDEQASTHEK  
AGAIGSTAGAWLGGAVGSLAGPLGTVAGATLGSVAGEYLG GFVTDLYQKWTATDKEPQE  
QKVNAEASLRVELGEGRLRTSSRVTEDGMGLNIYAGDNYITGW

>sp|P03749|TIPJ\_LAMBD Tip attachment protein J OS=Enterobacteria phage lambda GN=J  
PE=1 SV=1

MGKGS SKGHTPREAKDNLKSTQLLSVIDAISEGPIEGPVDGLKSVLLNSTPVL DTEGNTNI  
SGVTVVFRAGEQEQTPEGFESSGSETVLGTEVKYDTPITRTIT SANIDRLRFTFGVQALVE  
TTSKGDRNPSEVRLLVQIQRN GGWVTEKDITIKGKTTSQYLASVVMGNLPPRPFNIRMRR  
MTPDSTTDQLQNKTLWSSYTEIIDVKQCY PNTALVGVQVDSEQFGSQVSRNYHLRGRIL  
QVPSNYPNQTRQYSGIWDGTFKPAYSNNMAWCLWDM LTHPRYGMGKRLGAADV DKA  
LYVIGQYCDQSPDGFEGGTEPRITCNAYLTTQRKA WDVLSDFCSAMRCMPVWNGQTLTF  
VQDRPSDKTWTYNRSNVVMPDDGAPFRYSFSALKDRHNAVEVNWIDPNNGWETATELV  
EDTQAIARYGRNVTKMDAFGCTSRGQAHRAGLWLIKTE LLETQTVDFSVGAEGLRHVPG  
DVIEICDDDYAGISTGGRVLAVNSQTRTLTLDREITL PSSGTALISLVDGSGNPVSVEVQSVT  
DGVKVKVSRVPDGVAEYSVWELKLPTLRQRLFR CVSIRENDDGTYAITAVQHVPEKEAIV  
DNGAHFDGEQSGTVNGVTPPAVQHLTA EVTADSGEYQVLARWDTPKVVKGV SFLRLRTV  
TADDGSERLVSTARTTETTYRFTQLALGNYRLTVRAVNAWGQQGDPASVSFRIAAPAAPSR  
IELTPGYFQITATPHLAVYDPTVQFEFWFSEKQIADIRQVETSTRYLGTALYWIAASINIKPG  
HDYYFYIRSVNTV GKSAFVEAVGRASDDAEGYLDFFK GKITESH LGKELLEKVELTEDNA  
SRLEEF SKWKDASDKWNAMWAVKIEQTKDGKHYVAGIGLSMEDTEEGKLSQFLVAANR  
IAFIDPANGNETPMFVAQGNQIFMNDVFLKRLTAPTITSGGNPPAFSLTPDGKLTAKNADISG  
SVNANSGLTNSVTIAENCTINGTLRAEKIVGDIVKAASAAFP RQRESSVDWPSGTRT VTVT  
DDHPFDRQIVLPLTFRGSKRTVSGRTTYSMCY LKVL MNGAVIYDGAANEAVQVFSRIVD  
MPAGRGNVILTFTLTSTRHSADIPPYTFASDVQVMVIKKQALGISVV

>sp|P03736|TMP\_LAMBD Tape measure protein OS=Enterobacteria phage lambda GN=H PE=1  
SV=1

MAEPVGD LVVDLSLDAARFDEQMARVRRHFSGTESDAKKTA AVVEQSLSRQALAAQKA  
GISVGQYKAAMRMLPAQFTDVATQLAGGQSPWLILLQQGGQVKDSFGGMIPMFRGLAGA  
ITLPMVGATSLAVATGALAYAWYQGNSTLSDFNKT LVLSGNQAGLTADRMLVLSRAGQAA  
GLTFNQTS ELSALVKAGVSGEAQIASISQSVARFSSASGVEVDKVAEAFGKLT TDPTSGLT  
AMARQFHNVS AEQIAYVAQLQRSGDEAGALQA ANEAATKGFDDQTRRLKENMG TLETW  
ADRTARAFKSMWDAVLDIGRPDTAQEMLIKAEAA YKKADDIWNLRKDDYFVNDEARAR  
YWDREKARLAL EAARKKAEQQTQQDKNAQQQSDTEASRLKYTEEAQKAYERLQTPLE  
KYTARQEELNKAL KDGKILQADYNTLMAAAKKDYEA TLKPKQSSVKVSAGDRQEDSA  
HAALLTLQAE LRTLEKHAGANEKISQQRDLWKAESQFAVLEEAAQRRQLSAQEKSLLAH  
KDETLEYKRQLAALGDKVTYQERLNALAQQADKFAQQQRAKRAAIDAKSRGLTDRQAE  
REATEQRLKEQY GDNPLALNNVMSEQKKTWAAEDQLRGNWMAGL KSGWSEWEESATD  
SMSQVKSAAATQTFD GIAQNMAAMLTGSEQNWR SFTRSVLSMMTEILLKQAMVGIVGSIG  
SAIGGAVGGGASASGGTAIQAAA AKFHFATGGFTGTGGKYEPAGIVHRGEFVFTKEATSRI

GVGNYRLMRGYATGGYVGTTPGSMADSRSQASGTFEQNNHVVINNDGTNGQIGPAALKA  
VYDMARKGARDEIQTQMRDGGGLFSSGGGR

>sp|Q9T1V8|TRP\_BPMU Probable tail terminator protein OS=Enterobacteria phage Mu  
GN=Mup37 PE=2 SV=1

MLEETEAAALLARVRELFGATLRQVEPLTGTWTNEDVHRLFLAPPSVFLAWMGCGEGRTR  
REVESRWAFFVVAELLNAGEPVNRPGIYQIVERLIAGVNGQTFGPTTGMRLTQVRNLCDDN  
RINAGVVLYGVLFSGTTPLPSVVDLDSLDDYERHWQTKFPDETPEFAAHINVNQEKDH  
DAEN

>sp|P13331|TTTT\_BPT4 Tail tube terminator protein OS=Enterobacteria phage T4 GN=3 PE=1  
SV=3

MSQALQQIFNQANTTNFVVSIPHSNTTSAFTLNAQSVPIPGIRIPVTDVTGPFGLGRAQRP  
GVTFEYDPLIVRFIVDEELKSWIGMYEWMLGTSNYLTGENTAQKTGPEYITLYILDNSKTEI  
VMSINFYKPWVSDLSEVEFSYTEDSDPALVCTATIPYTYFQVEKDGKIIAEV

>sp|P03732|TTTT\_LAMBD Tail tube terminator protein OS=Enterobacteria phage lambda GN=U  
PE=1 SV=1

MKHTELRAAVLDALEKHDTGATFFDGRPAVFDEADFPAAVAVYLTGAEYTGEELSDTWQA  
ELHIEVFLPAQVPDSELDAWMESRIYPVMSDIPALSDLITSMVASGYDYRRDDDAGLWSSA  
DLTYVITYEM

>sp|P03747|TUBE2\_BPT7 Tail tubular protein gp12 OS=Enterobacteria phage T7 GN=12 PE=1  
SV=1

MALISQSIKNLKGGISQQPDILRYPDQGSRVNGWSSETGLQKRPLVFLNTLGDNGALG  
QAPYIHLINRDEHEQYYAVFTGSGIRVFDLSGNEKQVRYPNGSNYIKTANPRNDLRMVTVA  
DYTFIVNRNVVAQKNTKSVNLPNYPNQDGLINVRGGQYGRELIVHINGKDVAKYKIPDG  
SQPEHVNNTDAQWLAEEELAKQMRTNLSDWTVNVGQGFIVTAPSGQQIDSFTTKDGYAD  
QLINPVTHYAQSFSKLPPNAPNGYMKIVGDASKSADQYYVRYDAERKVVWTETLGWNT  
EDQVLWETMPHALVRAADGNDFKWLWESPKSCGDVDTNPWPSFVGSINDVFFFRNRL  
GFLSGENIILSRTAKYFNFPASIANLSDDDDPIDVAVSTNRMAILKYAVPFSEELLIWSDEAQF  
VLTASGTLTSKSVELNLTQFDVQDRARPFGIGRNVYFASPRSSFTSIHRYAVQDVSSVKN  
AEDITSHVPNYIPNGVFSICSGTENFCSVLSHGDPKIFMYKFLYLNEELRQQSWSHWDF  
GENVQVLACQSISSDMYVILRNEFNFTFLARISFTKNAIDLQGEPYRAFMDMKIRYTIPTGT  
YNDDTFTTSIHPTIYGANFGRGKITVLEPDGKITVFEQPTAGWNSDPWLRLSGNLEGRMV  
YIGFNINFVYEFKFLIKQTADDGSTSTEDIGRLQLRRRAWVNYENSGTFDIYVENQSSNWK  
YTMAGARLGSNTLRAGRLNLGTGQYRFPVVGNAKFNTVYILSDETTPLNIIGCGWEGNY  
LRRSSGI

>sp|P79678|TSP\_BPMU Tail sheath protein OS=Enterobacteria phage Mu GN=L PE=1 SV=1

MSDISFNAIPSDVRVPLTYIEFDNSNAVSGTPAPRQRVLMFGQSGSKASAAPNVPVIRIRSGS  
QASAAFQGSMLALMADAFLNANRVAELWCIPQGNGTGNAAVGEISLSGTAGENGLSVT  
YIAGQRLAVSVAAGATGAALADLLVARIKQPDLPVTAEVRADSGDDDDTHADVLSAKFT  
GALSVDVRWNYAYAGETTPYGIITAFKAASGKNGNPDISASIAGMGDLQYKYIVMPYTDE  
PNLNLRLTELQERWGPVNQADGFAVTVLSGTYGDISTFGVSRNDHLISCMGIAGAPEPSYL  
YAATLCAVASQALSIDPARPLQTLPLGRMPPAVGDRFTWSERNALLFDGISTFNVDGGE  
MQUIERMITMYRTNKYGSDPSYLVNNTIATLSYLRYSRTRITQKFPNYKLASDGTRFATG  
QAVVTPSVIKTELLALFEEWENAGLVEDFDTFKEELYVARNKDDKDRDLVLCGPNLINQF  
RIFAAQVQFIL

>sp|P79679|TUBE\_BPMU Tail tube protein OS=Enterobacteria phage Mu GN=M PE=2 SV=1  
MAGNQRQGVAFIRVNGMELESMEGASFTPSGITREEVTGSRVYGWKGGKPRAAKVECKIP  
GGGPIGLDEIIDWENITVEFQADTGETWMLANAWQADEPKNDGGEISLVLMKQSKRIA

>sp|P41063|TUM\_BP186 SOS operon TUM protein OS=Enterobacteria phage 186 GN=TUM  
PE=1 SV=3

MDRELNEHVMIERVEMARLTAEGTCQERDREIALNLIAEIARGNLMKNNNFSVVFSAPPV  
GETFAKEGKVKVNITLDDKQKIGQPVIDAFQCELTKRIQSVFPSTRVTVKKGSMGTVELM  
GFDKDSREALDSILQEVEDESWR

>sp|P22501|TSP\_BPP2 Tail sheath protein OS=Enterobacteria phage P2 GN=FI PE=1 SV=2

MSDYHHGVQVLEINEGTRVISTVSTAIVGMVCTASDADAETFPNKPVLITNVQSAISKAG  
KKGTLAASLQAIADQSKPVTVMRVEDGTGDDEETKLAQTVSNIIGTTDENGQYTGLKA  
MLAAESVTGVKPRILGVPGLDTKEVAVALASVCQKLRAFQYISAWGCKTISEVKAYRQNF  
SQRELMVIWPDFLAWDTVTSTTATAYATARALGLRAKIDQEQGWKTLNSVGVNGVTGIS  
ASVFWDLQESGTDADLLNESGVTTLIRRDGFRFWGNRTCSDPLFLFENYTRTAQVVADT  
MAEAHMWAVDKPITATLIRDIVDGINAKFRELKTNGYIVDATCWFSEESNDAETLKAGKL  
YIDYDTPVPLENLTLRQRITDKYLANLVTSVNSN

>sp|P13333|TUBE\_BPT4 Tail tube protein gp19 OS=Enterobacteria phage T4 GN=19 PE=1  
SV=1

MFVDDVTRAFESGDFARPRLFQVEISYLGQNFTFQCKATALPAGIVEKIPVGFMRKINVA  
GDRTFDDWTVTVMNDEAHDARQKFVDWQSIAGQGNEITGGKPAEYKKSIVRQYARD  
AKTVTKEIEIKGLWPTNVGELQLDWDSNNEIQTFEVTLALDYWE

>sp|P03733|TUBE\_LAMBDA Tail tube protein OS=Enterobacteria phage lambda GN=V PE=1  
SV=1

MPVNPMPVKGAGTTLWVYKSGDPYANPLSDVDWSRLAKVKDLTPGELTAESYDDS  
YLDEDEDADWTATGQGQKSAGDTSFTLAWMPGEGQQAALLAWFNEGDTRAYKIRFPNGT  
VDVFRGWVSSIGKAVTAKEVITRTVKVTNVGRPSMAEDRSTVTAATGMTVTPASTSVVKG  
QSTTLTVAFAQPEGVTDKSFRAVSADKTKATVSVSGMTITVNGVAAGKVNIPVVSNGEFAA  
VAEITVTAS

>sp|P0DJY5|U2\_BPMU Tail fiber assembly protein U' OS=Enterobacteria phage Mu GN=U'  
PE=2 SV=1

MMHLKNITAGNPKTKEQYQLTKQFNKWLTYTEDGKNWYEEQKNFQPDTLKMVYDHNG  
VIICIEKDVSAINPEGANVVEVPDITANRRADISGKWMFKDGVVIKRTYTEEEQRQQAENE  
KQSLQLVRDKTQLWDSQLRLGIISDENKQKLTWMLYAQKVESTDTSSLPVTFPEQPE

>sp|P03746|TUBE1\_BPT7 Tail tubular protein gp11 OS=Enterobacteria phage T7 GN=11 PE=1  
SV=1

MRSYDMNVETAELSANDILASIGEPVSTLEGDANADAANARRILNKINRQIQSRGWT  
FNIEEGITLLPDVYSNLIVYSDDYLSLMSTSGQSIYVNRGGYVYDRTSQSDRFDSGITVNIIR  
LRDYDEMPECFRYWIVTKASRQFNRRFFGAPEVEGVLQEEDEARRLCMEYEMDYGGY  
NMLDGDFTSGLLTR

>sp|P14739|UNGI\_BPPB2 Uracil-DNA glycosylase inhibitor OS=Bacillus phage PBS2 GN=UGI  
PE=1 SV=1

MTNLSDIIEKETGKQLVIQESILMLPEEVEEVIGNKPESDILVHTAYDESTDENVMMLLTSAP  
EYKPWALVIQDSNGENKIKML

>sp|P13332|TSP\_BPT4 Tail sheath protein OS=Enterobacteria phage T4 GN=18 PE=1 SV=5

MTLLSPGIELKETTQSTVVNNSTGTAALAGKFQWGPAFQIKQVTNEVDLVNTFGQPTAE  
TADYFMSAMNFLQYGNDLRVVRAVDRDTAKNSSPIAGNIDYTISTPGSNYAVGDKITVKY  
VSDDIETEGKITEVDADGKIKKINIPTGKNYAKAKEVGEYPTLGSNWTAEISSSSSGLAAVI  
TLGKIITDSGILLAEIENAEAAMTAVDFQANLKKYGIPGVVALYPGELGDKIEIEIVSKADYA  
KGASALLPIYPGGGTRASTAKAVFGYGPQTDSQYAIIVRRNDAIVQSVVLSTKRGEKDIYD  
SNIYIDFFAKGGSEYIFATAQNWPEGFSGILTLGGSSNAEVTAGDLMEAWDFFADRESV  
DVQLFIAGSCAGESLETASTVQKHVVSIGDARQDCLVLCSPPRETVVGPVTRAVDNLVN  
WRTAAGSYTDNNFNISSTYAAIDGNHKYQYDKYNDVNRWVPLAADIAGLCARTDNVSQT  
WMSPAGYNRGQILNVIKLAIETRQAQRDRLYQEAINPVTGTGGDGYVLYGDKTATSVSP  
FDRINVRRLFNMLKTNIGRSSKYRLFELNNAFTRSSFRTETAQYLQGNKALGGIYEYRVVC  
DTTNNTPSVIDRNEFVATFYIQPARSINYITLNFVATATGADDFDELTLGAG

>sp|Q6QGE1|TTTT\_BPT5 Tail tube terminator protein OS=Escherichia phage T5 GN=ORF135  
PE=2 SV=1

MDHRTSIAQAMVDRISKQMDGSQPDEYFNNLYGNVSRQTYKFEEIREFPYVAVHIGTETG  
QYLPSSGQQWMFLELPILVYDKEKTDIQEQLEKLVADIKTVIDTGGNLEYTVSKPNGSTFPC  
EATDMIITSVSTDEGLLAPYGLAEINVTVRYQPFRSLRR

>sp|P85992|TUBE\_BPSK9 Tail tube protein OS=Serratia phage KSP90 PE=1 SV=2

MATVNEFRGAMSRGGGVQRQHRWRVTISFPSFAASADQTRDVCLLAVTTNTPTGQLGEIL  
VPWGGRELFPFGDRRFEALPITFINVVNNGPYNSMEVWQQYINGSESNRASANPDEYFRD  
VVLELLDANDNVTKTWTLQGAWPQNLGQLELDMSAMDSYTQFTCDLRYFQAVSDRSR

>sp|P22502|TUBE\_BPP2 Tail tube protein OS=Enterobacteria phage P2 GN=FII PE=1 SV=2

MAMPRLKLMNVFLNGYSYQGVAKSVTLPKLTRKLENYRGAGMNGSAPVDLGLDDDA  
LSMEWSLGGFPDSVIWELYAATGVDAVPIRFAGSYQRDDTGETVAVEVVMRGRQKEIDTG  
EGKQGEDTESKISVVCTYFRLTMDGKELVEIDTINMIEKVNGVDRLEQHRRNIGL

>sp|Q6QGE2|TUBE\_BPT5 Tail tube protein OS=Escherichia phage T5 GN=N4 PE=1 SV=1

MSLQLLRNTRIFVSTVKTGHNKNTQEILVQDDISWGQDSNSTDITVNEAGPRPTRGSKRF  
NDSLNAEWSFSTYILPYKDKNTSKQIVPDYMLWHALSSGRAINLEGGTGAHNNATNFM  
VNFKDNSYHELAMLHIYILTDKTSYIDSCQINQAEVNVDIEDIGRVTWSGNGNQLIPLDE  
QPFDPDQIGIDDETYMTIQGSYIKNKLTLKIKDMDTNKSYDIPITGGTFTINNNITYLTPNV  
MSRVTIPIGSFTGAFELTGLTAYLNDKSLGSMELYKDLIKTLKVNRFEIALVLGGEYDDE  
RPAAILVAKQAHVNIPTIETDDVLGTSVEFKAIPSDLDAGDEGYLGFSSKYTRTTINNLIVN  
GDGATDAVTAITVKSAGNVTTLNRSATLQMSVEVTPSSARNKEVTWAITAGDAATINATGL  
LRADASKTGAVTVEATAKDGGSGVKGTKVITVTAGG

>sp|P03610|VASS\_BPMS2 Assembly protein OS=Enterobacteria phage MS2 GN=A PE=1 SV=1

MRAFSTLDRENETFVPSVRVYADGETEDNSFSLKYRSNWTPGRFNSTGAKTKQWHYPSP  
YSRGALSVTSIDQGAYKRSGSSWGRPYEEKAGFGFSLDARSCYSLFPVSQNLTYIEVPQNV  
ANRASTEVLQKVTQGNFNLGVALAEARSTASQLATQTIALVKAYTAARRGNWRQALRYL  
ALNEDRKFRSKHVAGRWLELQFGWLPLMSDIQGAYEMLTKVHLQEFLPMRAVRQVGTNI  
KLDGRLSYPAANFQTTCNISRRIVIWFYINDARLAWLSSLGILNPLGIVWEKVPFSFVVDW  
LLPVGNMLEGLTAPVGCYSMSGTVTDVITGESIISVDAPYGWTVERQGTAKAQISAMHRG  
VQSVWPTTGAYVKSPFSMVHTLDALALIRQLSR

>sp|P21680|VDHR\_BP186 Protein dhr OS=Enterobacteria phage 186 GN=dhr PE=1 SV=1

MSRDELRIVLGAMIPNMEEGFEEKTRDGAIRVDPEWECCKEFDGLKAEIHKQLKSKPAV  
VFGYS

>sp|Q01146|VG16\_BPP22 DNA transfer protein gp16 OS=Enterobacteria phage P22 GN=16 PE=1 SV=1

MKVTANGKTFNFPDGTSTEDIGAAVDEYFAGQASAAETQPAEQQEPPQQPEQSLMQRAG  
DLLTGGQSAGQIAEQAGRGLVNIPFDVLQGGASLINAISQGLGGPKVLDVYRVPVDRPTDP  
YAQAGESIGGYLIPGAGVAGNMAIGSVAEANQQGDFAGNVAKNAAVNLGAQGLLSGAA  
KLVGRGITAARGEIAPEARQLIDTAESMGVKPMTSDMIKPGNAFTRSLMQGGEGALLGTG  
GKRAEQYAIRSKLLGDYFDRVGGYNPDDIVKSMTSTVGGRKNAAGAVRDEIVNRMGSAP  
VGTNSINAIDTNIARLEKLGTSADQRLLTALKNLKSELNSGNVDFDLLQHRTAFRTNVQ  
GDAMVFPNQAKAATNMVENAMTRDLRNVGKSLGPQAASKYLKSNDSFANIYNKVLNK  
RISNTLNKARSEYTPELINTVVFSRKPSDIKRIWSSLDNKGKDAMRAAYISKIAEKTGDSAP  
KFITEVNKLKAQSGGEIYNTIFSGRHMKELDALHDVLRQTARSDSANVVTQTGQALANPV  
RLGAAIPTLGKSLAAEAGYGLAMRVYESKPIRNMLLRLANTKPGTPAYERALNQAATAVR  
PLLANEATRQ

>sp|P17171|VG40\_BPT4 Head formation protein OS=Enterobacteria phage T4 GN=40 PE=1 SV=1

MNKDDLDDLEIIDESPSSGEEERKERLFNESLKIISAMENVIQEIVIKLEDGSTHIVYVT  
KLDWVDGKVVMDFAVLDQERKAELAPHVEKCITMQLQDAFNKRSKKKFKFF

>sp|Q01074|VG07\_BPP22 DNA transfer protein gp7 OS=Enterobacteria phage P22 GN=7 PE=1 SV=2

MLYAFTLGRKLRGEEPSYPEKGGKGGADKSAKYAAEAQKYAADLQNNQFNTIMNNLKP  
TPLADKYIGSLEGLSSLEGQALNNYNSQQYQDLAQARYQNLAAAEATGGLGSTAT  
SNQLSAIAPTLGQQWLSGQMNNYQNLANIGLALQGQANAGQTYANNMSQISQQAAL  
AAANANRPSAMQSAIGGGASGAIAGAGLAKLIGSSTPWGAAIGGGIGLLGSLF

>sp|P03686|VG17\_BPPH2 Early protein GP17 OS=Bacillus phage phi29 GN=17 PE=1 SV=2

MNNYQLTINEVIDIINTNTEINKLVAKKENLFPTDLYDLKQELIAIILNSDFALSSIKRVLL  
VTVEELGTQDNDEDELEDDLDGEIDRVYIDKDGIRFDVPRETSPHVDKSIVTFNDELLE  
ANKIAKSIQEHDFNDKAIEEAELKIFKNHLPSIYSMKKENK

>sp|P03679|VG1\_BPPH2 Early protein GP1 OS=Bacillus phage phi29 GN=1 PE=1 SV=2

MGKIFDQEKRLGRTWKNSKWNQGIAPVDGDLKMIDLELEKMTKLEHENKLMKNAL  
YELSRMENNDYATWVIKVLFGGAPHGAK

>sp|Q05286|VG71\_BPML5 Repressor-like immunity protein OS=Mycobacterium phage L5 GN=71 PE=1 SV=1

MSGKIQHKAVVPAPSRIPLTLSEIEDLRRKGFNQTEIAELYGVTRQAVSWHKKTYGGRLTT  
RQIVQQNWPWDTRKPHDKSKAFQRLRDHGEYMRVGSFRTMSKDKKRLLSWWKMLRD  
DDLVLFDPSIEPYEGMAGGGFRYVPRGIEDDLLIRVNEHTNLTAEGELLWSWPDDIEEL  
LSEP

>sp|Q38008|VLYS\_BPCP1 Holin OS=Streptococcus phage Cp-1 GN=CPH1 PE=1 SV=1

MLYNIMLEVAKGDYITILFALILFDITGFLKAWKWKVTDTSWTGLKGVIKHTLTFIFYFVA  
VFLTYIHAMAVGQILLVIINLYYALSIMENLAVMGVFIPKFMTARVQEELQKYTAQLDAGK  
DLLEEFKGEKK

>sp|P04537|UVSY\_BPT4 Recombination protein uvsY OS=Enterobacteria phage T4 GN=UvsY PE=1 SV=3

MRLEDLQEELKKDVFIDSTKLQYEAANNVMLYSKWLKHSIKKEMLRIEAQKKVALKA  
RLDYSSGRGDGDEFMSMDRYEKSEMKTVLSADKDVLDVSLQYWGILLDFCSGALDAIK

SRGFAIKHIQDMRAFEAGK

>sp|P15236|VFIL\_BP186 Protein fil OS=Enterobacteria phage 186 GN=fil PE=1 SV=1

MLKSEPSFASLLVKQSPGMHYGHGWIAGKDGKRWHPCRSQSELLKGLKTKSPKSSGFLII  
RIVHFVIKGVKHVTR

>sp|P03695|VHED\_BPT4 Single-stranded DNA-binding protein OS=Enterobacteria phage T4  
GN=32 PE=1 SV=1

MFKRKSTAELAAQMAKLNKNGKGFSSSEDKGEWKLKLDNAGNGQAVIRFLPSKNDEQAPF  
AILVNHGFKKNGKWIETCSSTHGDYDSCPVCQYISKNDLYNTDNKEYSLVKRKTSYWA  
NILVVKDPAAPENEGKVFYRFGKKIWDKINAMIAVDVEMGETPVDVTCPWEGANFVLK  
VKQVSGFSNYDESKFLNQAIPNIDDESFKELFEQMVDLSEMTSKDKFKSFEELNTKFGQ  
VMGTAVMGGAAATAAKKADKVADDLDAFNVDVDFNTKTEDDFMSSSSGSSSSADDTDL  
DLLNDL

>sp|P27382|VP11\_BPPRD Infectivity protein P11 OS=Enterobacteria phage PRD1 GN=XI PE=1  
SV=2

MEKVKAWLIKYKWWIVAIGGLAAFLLLKNRGGGSGGGGEYMGVSGPVPYQQAGSGAV  
DNTMALAALQANTQLSAQNAQLQAQMDASRLQLETQLNIETLAADNAHYSTQSQLQLG  
MAQVDLSKYLGDLOSTTSTALAGMQSDTAKYQSNQLQAENIRANTSLAEIDAQKYIVGK  
QADIAYQAKTERRGQDYGFALGLLNFGGKFF

>sp|P27391|VP30\_BPPRD Minor capsid protein P30 OS=Enterobacteria phage PRD1 GN=XXX  
PE=1 SV=3

MALINPQFPYAGPVPPIPGPAPTETMPLLNYRVEGRIAGIQARQFMPFLQGPHRAVAEQTY  
HAIGTGIQMGQTFNQPLINTQEG

>sp|P07695|VCOX\_BPP2 Regulatory protein cox OS=Enterobacteria phage P2 GN=cox PE=1  
SV=1

MSKQVTLMTDAIPYQEFALIGKSTGAVRRMIDKGLPVIDMTDPQSASGRAGEYWVYL  
PAWNNGLKLAYESRPKEIRDGWLMLGLGEP

>sp|P09676|VASS\_BPSP Maturation protein OS=Enterobacteria phage SP PE=2 SV=1

MPTLPRGLRFGSNGEVLNDFEALWPPERHTVDLSNGTCKLTGYITNLPGYSDIFPNKGVTA  
ARTPYRSTVPVNHLYRPTTVEYIPDGTYVRLDGHVKFEGDLVNGSVDLTNLFVISLAAQ  
GGFDYQSVIGPRFSARFSAFSTKYGVLLGEGRETLKYLLLVRRMREGYRAVRRGDLKRL  
RNVISTFEPSTIKGRARAQFSQTYRDKLTGNKVEVRPSEGKWNSSSASDLWLEFRYGLM  
PLFYDIQSVMEDFMRVHKKIAKIQRFSAGHGKLETVSSRFYDPVHFSLEVTAVLQRRHRW  
GVIIQDTGSFATFNNGRLVPVKDWKTAAFALLNPAEVAWEVTPYSFVVDWFVNVGDMLE  
QMGQLYRHVDVVDGFDRKDIKLSVSVRVLTDVAHVASFQLRQAKLLHSYYSRVHTVA  
FPQISPQLDTEIRSVKHVIDSIALLTQRVKR

>sp|P03682|VG4\_BPPH2 Late genes activator OS=Bacillus phage phi29 GN=4 PE=1 SV=1

MPKTQRGIYHNLKESEYVASNTDVTFFFSSSELYLNKFLDGYQEYRKKFNKKIERVAVTPW  
NMDMLADITFYSEVEKRGFHAWLKGDNATWREHVHYALRIMTKPNTLDWSRIQKPRLRE  
RRKSMV

>sp|P03701|VLOM\_LAMBD Outer membrane protein lom OS=Enterobacteria phage lambda  
GN=lom PE=1 SV=1

MRNVCIAVAVFAALAVTVTPARAEGGHGTFTVGYFQVKPGTLPSSLGGDTGVSHLKGIN  
KYRYELTDSVGVMAASLGFASKKSSTVMTGEDTFHYESLRGRYVSVMAGPVLQISKQVS  
AYAMAGVAHSRWSGSTMDYRKTEITPGYMKETTARDESAMRHTSVAWSAGIQINPAAS

VVVDIAYEGSGSGDWRTDGFIVGVGYKF

>sp|P07696|VPB\_BPP2 Replication gene B protein OS=Enterobacteria phage P2 GN=B PE=2 SV=1

MTVMTLNLVEKQPAAMRRIIGKHLAVPRWQDTCDYNNQMMERERLTVCFHAQLKQRHA  
TMCFEEMNDVERERLVCAIDELRGAFSKRRQVGASEYAYISFLTVSQRRTLFMHAGLTEKE  
FNQPYWRINEESCYWRDALFRALRELFSLFEYAPTILTSVKPEQYLH

>sp|A8E283|VPN7\_BPPHE Tail fiber protein OS=Enterococcus phage phiEF24C GN=EF031 PE=1 SV=1

MNKLVKRRFQAGLGSEIKRVYKEGQQINTLLLAQVIQVNYKYNTVDLLALQHKEVFQNS  
YANEGRF SARLPMEFGGRNIVGQPYGQVNPIAVGTVVLVGFINSKDKMPIVISVYNNNDV  
SKQLSRTQFSNSDPKDLELIGDMHQKFSLYPSLTYDSVDGEGGRVVTFSGKSFIADFDTKEV  
ANSSTTDAGYGTKYEDLETSYNNGLIEPMKGRAPNVLFKHQGVLDGKPDLDHLLI  
HINPDGTYRTSMMNKEEDWRTL FEMTPDGRVKLRKQDSINIDGGIEISELGINNEGFVYLR  
NGDMDLEVRKDGIIYSQGLFTADVLSVYDKLNGLSIQIKETNGQLEIIANGVEEQNGK  
ISELSTEITIVAGKVESKVTKEVQDMIDSSFVDMSDAIKKAQEDADKANKVIADMSSDNR  
LTPSEKIDLLKEWDIINKNEPSYLEQAETYEVDSDKYTAKYNSLELFVTPILADMESTSSVD  
GATLRKTFNSY YTARIALLNSISKKLDGITEAMKKASQASLDATQAMADASQAKIDADN  
ANKLISDIASDNKLTPEKYQLKKEWDVIVKEYPTTIAQAEKYAVDTAEY TAKYKALELFV  
EPLFKDMDETSIVDGERLRATFSYYASKIALLKEVTDSA KTELDAYGNKISVMETNITQT  
SEAITLLATRVQTVEDGVQSNKAQIEIQAEQISQKVTASEVKGIVDDSINNLTGGTNLFVI  
KTQTAGLLNENDGT VGTAVDNSVSDYIKVNQKTPYIATLYGNTGTNMIITDWYDKNRTF  
ISGEAVADSGDFSKKYVSPENAVYARVSYKKANSVNIKFEAGTKATDYSPSWEDIKGDQTA  
LEEYIKKVEEQAKKAQQDAENAKNDAENANNAIADMSNDNMLAPNEKKQILLQWEQIK  
TEYPINLDQATKFGVSSQYTTAYNALDEYLKPIADMTTTSVVVGSTLRNTFNYYDKR  
TTLLNRISDVAKNVADKAQETADTINDNLQNI GGYNVYVGFSSGDNMLPRLMIKNVGYTYL  
GSSTTEFIDSMVAVKGDATTQPFDYTVGTS DKEIAGGGLADYRMKEVKEGQWL TASANV  
QVIDGGSARLAIYTLEGDNWVGSNSTPIQVSDGLKRVVAQRKVTGLTKGVLIRIESADTNV  
KEFRFGNVQLEVGIIPTWKKSDIDIQEDINNVQNIKTYTAWANDLQGLDFTREKVEGKT  
YMYVGTSMKSDSNYS DYTWRLTDEHIEGQINGKEGAWIYSPTAPTNP SQGLIWVDLSKV  
PNQPKRWVDSETGWVALTPEEVKDLPWGEDGTNLADWVAQAEQRISSDSIINTVLGSEDF  
TSVFDTKANTDLDNLATYEDLDSIKEDYNRLIKEGINGIDFTPYVTNSELQQLKDSFNFSV  
QQAGGVNMLKNSLGFSGLDFWDGTVGKNLLPNSTWNLGFGRWGGASIASFEILPPEDDK  
PTSHILGSIGSRSSSTKEIGNRPHPLKVNSGETY TISFDYKEEALAYDKDRPILVVRNYPDKDT  
DQWMEYSIEGWAVMANGSTTDLTVWRRFTKFTIGTSGYLDILPKTIVESWTHRSFWREL  
KIEEGSQATTWVPNKEDGAFTGGIVETTQTEELANLGFSGFVSSKR PSSSLTQSVELPEIG  
ANLEYSLSFYMKVTTDNPVADFKCGIRVYEGDTLTYTLGIEDATQPIPLGFQYKLVFTPTS  
TSTKIEMFVENGQEASVIISGIMYNIGNIPLKWQYPSEIYNTNVKIDINGVTVKNNQTDGY  
TMITPQEFSGYSRIDGNIERIFTLNGQVTEVKMLKAEKRITMEPVSVFAMNTVTDTKRIRG  
WAFVPSFE

>sp|P04529|UVSX\_BPT4 Recombination and repair protein OS=Enterobacteria phage T4 GN=UVSX PE=1 SV=2

MSDLKSRLIKASTSKLTAELTASKEFFNEKD VVRTKIPMMNIALSGEITGGMQSGLLILAGPS  
KSFKSNFGLTMVSSYMRQYPDAVCLFYDSEFGITPAYLRSMGVDPERVIHTPVQSLEQLRI  
DMVNQLDAIERGEKVVVFIDSLGNLASKKETEDALNEKVVS DMTRAKTMKSLFRIVTPY



FSTKNIPCIAINHTYETQEMFSKTVMGGGTGPMYSADTVFIIGKRQIKDGSDDLQGYQFVLN  
VEKSRTVKEKSKFFIDVKFDGGIDPYSGLLDMALELGFVVKPKNGWYAREFLDEETGEMI  
REEKSWRAKDTNCTTFWGPLFKHQPFDAIKRAYQLGAIDSNEIVEAEVDELINSKVEKF  
KSPEKSKSAADLETDLQLSDMEEFNE

>sp|P07394|VASS\_BPGA Assembly protein OS=Enterobacteria phage GA GN=A PE=2 SV=1  
MFPKSNIDRNYKVKLISYDKKGLVSDSFEQVENYLFQNRSTTYKPGYIRDRFRPTNF  
WNGYRCFNQPVGTFTRKLSGGRQVADYGIVNPNKFTANSQHLGDNMVIYPGPF SINIDQ  
RASVEVLNKLQSNNLIGVAIAEAKMTASLLAKQSIALIRAYTAAKRGNWREVLSQLLISE  
HRFRAPAKDLGGRWLELQYGWLPLMSDLKAAAYDLLTQTKLPAFMPLRVTRTVGGTHNY  
KVRNVESAGDTWSYRHRLSVNYRIWYFISDPRLAWASSLGLLNPLEIYWEKTPWSFVVD  
WFLPVGNLIEAMSNPLGLDIISGKTWQLESKLNATLPASGWSGTAKLTAYAKAYDRSTFY  
SFPTPLPYVKSPLSGLHLANALALINQLKR

>sp|P25475|VPL\_BPP2 Head completion/stabilization protein OS=Enterobacteria phage P2  
GN=L PE=2 SV=1

MMTLIIPRKEAPVSGEGTVVIPQPAGDEPVIKNTFFFPDIDPKRVRERMRLEQTVAPARLRE  
AIKSGMAETNAELYEYREQKIAAGFTRLADV PADDIDGESIKVFYERAVCAMATASLYER  
YRGVDASAKGDKKADSIDSTIDELWRDMRWAVARIQ GKPRCIVS QI

>sp|P13338|VG33\_BPT4 RNA polymerase-associated protein Gp33 OS=Enterobacteria phage T4  
GN=33 PE=1 SV=1

MTQFSLNDIRPVDETGLSEKELSIKKEKDEIAKLLDRQENGFIEK MVEEFGMSYLEATTAF  
LEENSIPETQFAKFIPSGIIEKIQSEAIDENLLRPSVVRCEKTNTLDFLL

>sp|P13342|VG59\_BPT4 Protein Gp59 OS=Enterobacteria phage T4 GN=59 PE=1 SV=1

MIKLMPAGGERYIDGKS VYKLYLMIKQH MNGKYDV I KYNWCMRVSDAAYQKRRDKYF  
FQKLSEKYK LKELALIFISNLVANQDAWIGDISDADALVFYREYIGRLKQIKFKFEEDIRNIY  
YFSKKVEVSAFKEIFEYNPKVQSSYIFKLLQSNII SFETFILLDSFLNIIDKHDEQTDNLVWN  
NYSIKLKAYRKILNIDSQKAKNVFIETVK SCKY

>sp|P08767|VGF\_BPAL3 Capsid protein OS=Enterobacteria phage alpha3 GN=F PE=1 SV=2

MSNVQTSAREIVDLSHLAFDCGMLGRLKTVSWTPVIAGDSFELDAVGALRLSPLRRGLA  
IDSKVDFFTFYIPHRHVYGDQWIQFMRDGVNAQPLPSVTCNRYPDHAGYVGTIVPANNRI  
PKFLHQSYLNIYNNYFRAPWMPERTEANPSNLNEDDARYRFRCCHLKNIWSAPLPPETKL  
AEEMGIESNSIDIMGLQAAYAQLHTEQERTYFMQRYRDVISSFGGSTS YDADNRPLLVMH  
TDFWASGYDVDGTDQSSLGQFSGRVQQTFFKHSVPRFFVPEHGVMMLALIRFPPI SPLEHH  
YLAGKSQLTYTDLAGDPALIGNLPPREISYRDLFRDGRSGIKIKVAESI WYRTHPDYVNFKY  
HDLHGPFPLDDAPGTSTGDNLQEAILVRHQDYDACFQSQQLLQWNKQARYNVSVYRHM  
PTVRDSIMTS

>sp|P27383|VP17\_BPPRD Protein P17 OS=Enterobacteria phage PRD1 GN=XVII PE=1 SV=1

MMGKGFEMMVASAIRAAGINPDELMEKANTLVHNLNYQLDRFGQRLDSIDSRLSVIEKA  
LDISPAEKPDNQP ELTGITFEGDNNDQ

>sp|P05460|VPSU\_BPP4 Polarity suppression protein OS=Enterobacteria phage P4 GN=psu  
PE=1 SV=3

MESTALQAFDTCQNNKAAWLQRKNELAAAEQEYLRLLSGEGRNV SRLDEL RNIEVRK  
WQVNQAAGRYIRSHEAVQHISIRDRLNDFMQQHGTALAAALAPELMGYSELTAIARNCAI  
QRATDALREALLSWLAKGEKINYSAQSDILTTIGFRPDVASVDDSREKFTPAQNMIFSRK  
SAQLASRQSV

>sp|P03690|VR2A\_BPT4 Protein rIIA OS=Enterobacteria phage T4 GN=rIIA PE=2 SV=2  
MIITTEKETILGNGSKSKAFSITASPKVFILSSDLYTNKIRAVVRELITNMIDAHALNGNPE  
KFIIQVPGRLDPRFVCRDFGPGMSDFDIQGDDNSPGLYNSYFSSSKAESNDFIGGFGLGSKS  
PFSYTDTSITSYHKGEIRGYVAYMDGDGPQIKPTFVKEMGPDDKTGIEIVVPVEEKDFRNF  
AYEVSYIMRPFKDLAIINGLDREIDYFPDFDDYYGVNPERYWPDRGGLYAIYGGIVYPIDG  
VIRDRNWLSIRNEVNYIKFPMGSLDIAPSREALSLDDRTRKNIIERVKELSEKAFNEDVKRF  
KESTSPRHTYRELMKMGYSARDYMISNSVKFTTKNLSYKKMQSMFEPDSKLCNAGVVY  
EVNLDPRLKRIKQSHETS AVASSYRLFGINTTKINIVIDNIKNRVNIVRGLARALDDSEFNNT  
LNIHHNERLLFINPEVESQIDLLPDIMAMFESDEVNIHYLSEIEALVKSYPKVVKSKAPRPK  
AATAFKFEIKDGRWEKRNLYRLTSEADEITGYVAYMHRSDIFSMDGTTSLCHPSMNLIRM  
ANLIGINEFYVIRPLLQKKVKELGQCQCIFEALRDLYVDAFDDVDYDKYVGYSSSAKRYID  
KIIKYPELDFMMKYFSIDEVSEEYTRLANMVSSLQGVYFNGGKDTIGHDIWTVTNLFDVL  
SNNASKNSDKMVAEFTKKFRIVSDFIGYRNSLSDDDEVSQIAKTMKALAA

>sp|P68660|W\_LAMBD Head completion protein OS=Enterobacteria phage lambda GN=W  
PE=1 SV=1  
MTRQEELAAARAALHDLMTGKRVATVQKDGRRVEFTATS VSDLKKYIAELEVQ TGMTQR  
RRGPAGFYV

>sp|P26748|VG08\_BPP22 Scaffolding protein OS=Enterobacteria phage P22 GN=8 PE=1 SV=1  
MEPTTEIQATEDLTLSGDHAAASADSLVVDNANDNAGQEEGFIVLKDDETAPKQDPAKN  
AEFARRRIERKRQRELEQQMEAVKRGELPESLRVNPDLPPQPDINAYLSEEGLAKYDYDNS  
RALAAFNAANTEWLMKAQDARSNAVAEQGRKTQEFTQSAQYVEAARKHYDAAEKLNI  
PDYQEKEDAFMQLVPPAVGADIMRLFPEKSAALMYHLGANPEKARQLLAMDGQSALIEL  
TRLSERLTLKPRGKQISSAPPADQPITGDVSAANKDAIRKQMDAAASKGDVETYRKLKAK  
LKGIR

>sp|P17313|VG31\_BPT4 Capsid assembly protein Gp31 OS=Enterobacteria phage T4 GN=31  
PE=1 SV=1  
MSEVQQLPIRAVGEYVILVSEPAQAGDEEVTE SGLIIGKRVQGEVPEL CVVH SVGPDVPEG  
FCEVGDLTSLPVGQIRNVPHPFVALGLKQPKKQKFVTCHYKAIPCLYK

>sp|P04532|VG57\_BPT4 Tail fiber assembly helper protein OS=Enterobacteria phage T4 GN=57  
PE=1 SV=3  
MSEQTVEQKLSAEIVTLKSRILDTQDQAARLMEESKILQGT LAEIARAVGITGDTIKVEEIV  
EAVKNLTAESADEAKDEE

>sp|P27384|VP31\_BPPRD Penton protein P31 OS=Enterobacteria phage PRD1 GN=XXXI PE=1  
SV=1  
MNVNPNQMTVTPVYNGCDSGEGPQSVRGYF DAVAGENVKYDLTYLADTQGFTGVQCI  
YIDNAENDGA FEIDVEETGRIKCPAGKQGYFPLLVPGRAKFVARHLGSGKKS VPLFFLN  
TIAQGVW

>sp|P03704|VRPI\_BPT7 Bacterial RNA polymerase inhibitor OS=Enterobacteria phage T7 GN=2  
PE=1 SV=1  
MSNVNTGSLVDNKKFWATVESSEHSFEVPIYAETLDEALELAEWQYVPAGFEVTRVRC  
VAPK

>sp|P13310|VS\_BPT4 Valyl--tRNA ligase modifier OS=Enterobacteria phage T4 GN=vs PE=1  
SV=1  
MTKILVLCIGLISFSASASADTSYTEIREYVNR TAADYCGKNKACQAEFAQKLIYAYKDGE

RDKSSRYKNDTLLKRYAKKWNTLECSVAEEKDKAACHSMVDRLVDSYNRGLSTR  
>sp|P10104|WAC\_BPT4 Fibrin OS=Enterobacteria phage T4 GN=wac PE=1 SV=5  
MTDIVLNDLPFVDGPPAEGQSRISWIKNGEELGADTQYGSEGSMNRPTVSVLRNVEVLD  
KNIGILKTSLETANSDIKTIQGILDVSGDIEALAQIGINKKDISDLKTLTSEHTEILNGTNNTV  
DSILADIGPFNAEANSVYRTIRNDLLWIKRELQYTGQDINGLPVVGPNSSGMKHIINNT  
DVITSQGIRLSELETKFIESDVGSLTIEVGNLREELGPKPPSFSQNVYSRLNEIDTKQTTVES  
DISAIKTSIGYPGNNISIITSVNTNTDNIA SINLELNQSGGIKQRLTVIETSIGSDDIPSSIKGQIK  
DNTTSIESLNGIVGENTSSGLRANVSWLNQIVGTDSSGGQPSPPGSLN RVSTIETS VSGLN  
NAVQNLQVEIGNNSAGIKGQVVALNTLVNGTNPNGSTVEERGLTNSIKANETNIASVTQEV  
NTAKGNISLQGDVQALQEAGYIPEAPRDGQAYVRKDGEWVFLSTFLSPA  
>sp|P27392|VP16\_BPPRD Protein P16 OS=Enterobacteria phage PRD1 GN=XVI PE=1 SV=1  
MDKKKLLYWVGGGLVLILWLWFRNRPAQVASNWEGPPYMTYNQPQAGSVTLPVAGY  
TSPSPTLPNRNRSCGCNPAVSAAMAQGADLASKLTD SITSQLNDYASSLNDY LASQAGV  
>sp|Q9ZX29|WHIB\_BPMT4 Probable transcriptional regulator WhiBTM4 OS=Mycobacterium  
phage TM4 GN=whiBTM4 PE=1 SV=1  
MHMHMGDPSAICAQTDPPELWFPDKGQSTRDAKRMCMRCPLLDECRALALRDPHLVGV  
WGGLSAQERRRIRKGASA  
>sp|Q37958|P4\_BPPM2 Protein P4 OS=Pseudoalteromonas phage PM2 GN=IV PE=1 SV=1  
MQKPSGKGLKYFAYGVAISAAGAILAEYVRDWMRKPKAKS  
>sp|P13302|IPI3\_BPT4 Internal protein III OS=Enterobacteria phage T4 GN=ipi3 PE=1 SV=1  
MKTYQEFIAEASVVKAKGINKDEWYRSNGFDPKTAPIERYLATKASDFKAFaweGLR  
WRTDLNIEVDGLKFAHIEDVVASNLDSEFVKADADLRRWNLKLFSKQKGPKFV PKAGKW  
VIDNKLAKAVNFAGLEFAKHKSSWKGLDAMAFRKEFADVMTKGGFKAEIDTSKGKFKD  
ANIQYAYAVANAARGNS  
>sp|P03759|REXB\_LAMBDA Protein rexB OS=Enterobacteria phage lambda GN=rexB PE=1  
SV=1  
MRNRIMPGVYIIPYVIVSICYLLFRHYIPGVSFSAHRDGLGATLSSYAGTMIAILIAALTFL  
IGSRTRRLAKIREYGYMTSVVIVYALS FVELGALFFCGLLLLSSISGYMIPTIAIGIASASFIHI  
CILVFQLYNL TREQE  
>sp|P03718|IPI1\_BPT4 Internal protein I OS=Enterobacteria phage T4 GN=ipi1 PE=1 SV=1  
MKTFKEFTSTTTPVSTITEATLTSEVIKANKGREGKPMISLVDGEEIKGTVYLG DGWSAKK  
DGATIVISPAEETALFKAKHISAAHLKIIAKNLL  
>sp|P85987|CAPSD\_BPSK1 Major capsid protein OS=Serratia phage KSP100 PE=1 SV=2  
MAAYQTYTMAGIKEDFADWVSNISPEYTPLISMIRKFPVHNTMFQWQWDVLKDVDTEN  
QHNEASDAKDVELPTTVVQNYVQIMRKVVFVSDSANAVSSHGREKELFYQLKKA AKEL  
KRDNEGIFLLKDRAGDAGSATKPRLTASFGSLIDASMKKTADLDEATLFEMTAKLYTEGA  
DPTLIMYHPSNANFFASLQEKSGTRMRIFENDKRFVKQVEYIVDPLGQELKCIPNRWCPED  
ATYIFNPSDLGMAVLRAPKKVALAKSGSAEKYMIEQEVGFRLNNPKAAALIIGKYKEGGN  
GGGESVKS  
>sp|P85989|CAPSD\_BPSK9 Major capsid protein OS=Serratia phage KSP90 PE=1 SV=2  
MSKKLVTEEMRTQWLPVLEKKSEQIQPLTAENVS VRLLNQNAEWN AKNLGESEGPSSVN  
ANVGKWPVLIDMAKRLAPNNIAMDFGVQPLAGPDGQIFALRARQGVGDASNTQQR  
KELFMEEAQTNYSGDQTTVHSGDPSGFSQADIEGSGTEVSSYGKAMDTVKA EQLGSPTQ  
PWARVGITIQKATVTA KSRGLYADYSHEL RQDMMAIHGEDVDAILSDVMVTEIQAEMNRE

FIRTMNFTAVRFKKFGTNGVVDVAADVSGRWALEKWKYLVMLEVEANGVVDTRRGK  
ANRVLCSNVASALAMAGMLDYSALNVQAQLAVDPTGQTFAGVLSNGMRVYIDPYAVA  
EYITLAYKGTALDAGIYFAPYVPLEMYRTQGETTFAPRMAFKTRYGIAANPFVQIPANQD  
PQVYVTEGIAKDTNVIYFRKGLIKNLY

>sp|Q04754|COAT\_BPLH Major capsid protein OS=Lactococcus phage LL-H GN=g34 PE=1  
SV=3

MTVVLDKDLARIDEEYKADSQVWSYLTGGNGVTQRFRGHNEVRINKLSGFVDATAYKR  
GQDNARKTISVGKETVKLTHEDWFGYDLQDFMDENGAYTVENVVREHNKMITIPHRD  
KVAVQKLFDSAAKKATDSITKDNALDAYDTAEAYMFDNEVPGGFVMFVSSAYYTALKQS  
AAVTRTFSTDGTMVINGIDRRVAQLDGGVPIVRVSSDRLKGLGITNHVNFILTPLSAIAPIVK  
YDSVSVIDPSTDRSGNRWTIKGLSYDAIVLDNAKKGIYVAATAGV

>sp|P26596|MCP\_BPF41 Major capsid protein OS=Lactococcus phage F4-1 GN=MCP PE=1  
SV=1

MKLDYNSREIFFGNEALIVADMSKGINGKPEFTNHKIVAGLVSVMEDQAETNSYPADD  
VPDHGVKKGATLLQGEMVFIQTDQALKEDILGQRTENGLGWSPTGNWTKCVQYLIKQ  
RKRDKVTGEFVDGYRVVYPNLTPTAEATKESETDSVDGVDPIQWTLAVQATESDIYLNQ  
GKKVPAIEYEWGEQAKDFVKKMESGLFIMQPDTVLAGAITLVAPVIPNVTATKGNNDGT  
IVVPDTLKDSSKGGTVKVTSVIKDAHGKVATNGQLAPGVYIVTFSADGYEDVTAGVSVTD  
HS

>sp|D6RRG1|ORF4\_BPKPP Structural protein ORF4 OS=Pseudomonas phage KPP10 PE=1  
SV=1

MRPIPSLQNNFEYTDLTEPMILIPNVWGLTQQLGIFGVDRTTQESVTLEEITKSFGLMEDIH  
RGARHQVGRDYDRQMRTFAVPHFTYDDYITPRDIQGKRAYGKQELETLDQVRMRKLERL  
RGTHAATMEFARMHTLVTKPYTPNNTVGGATGYDWYQEFGKTRFEVNFELDTPTTNIL  
EKSELVYAHMQDEAYTGGVVGDVIAICSPFFSKLISHPTVVEAYKYASQPQILRERLRA  
RGFDARYREFYFGNVLYIEYRGGFQGRPGGEKRRYVPAGEAVFIPGSGTEDLFKTFAPAS  
KFEHVNTPGEESYAFEYVDPKGEFLEINSETNFINVLMYPQLVVKGKAA

>sp|D6RRG7|ORF10\_BPKPP Structural protein ORF10 OS=Pseudomonas phage KPP10 PE=1  
SV=1

MAGRTSTYAPNQVTIVINHAASGISHTLTGFSEDSIVSVERLVDTFTEYVGADDTHTRVFN  
ANSGARATVSLAQTSESNVLTFLHEFDREAMSADGMFEMLIKDNSGRSLYFSDEAYIAVI  
PQGGFSNQMNTRDWVISMNTTTFQHGGNQKVSPATADTLTALGVNLDARWL

>sp|P14819|RPC1\_BPPH8 Repressor protein CI OS=Enterobacteria phage phi80 GN=CI PE=1  
SV=2

MSSISERIKFLLAREGLKQRDLAEALSTSPQTVNNWIKRDALSREAAQQISEKFGYSLDWL  
LNREGSPKKDLESNIPPESEWGTVDWDKNTPLPDDEVEVPFLKDIEFACGDGRVHDEDH  
NGFKLRFSKATLRRVGANSDGSVLCFPASGDSMEPVIPDGATVAVDGTGNKRVIDGELYAI  
NQGDLKRIKQLYRKPGGKILIRSINRDYDDEEADVEIIGFVFWYSVLRVRR

>sp|P15238|RPC\_BP163 Repressor protein C OS=Rhizobium phage 16-3 GN=C PE=1 SV=4

MHKGTFHMSRLTDTLAAKLEEAGITQAELARRVQSQQAINNLFAGRAASSMVWRELAR  
ELGIDEQEMRQMMTEAGRDPKVTSLAGLRKYRAVLPSPREPFPIRQQEHLPRPNATIGEE  
TNMEPRKKKLLPVLGEAVGGEDGEYIFNGSVLDYVDCPPSLENVNPAYAVYIDGESMVPR  
FRPGETVWVHPTKPPRRGDDVVIQIHPDNEDDGAPPRGFVKEFVGWTANKLVLQQYNPT  
KKIEFTREQVVSVHPILAGKYW

>sp|P06153|RPC\_BPPH1 Immunity repressor protein OS=Bacillus phage phi105 PE=1 SV=2  
MTVGQRIKAIRKERKLTQVQLAEKANLSRSYLADIERDRYNPSLSTLEAVAGALGIQVSAI  
VGEETLIKEEQAEYNSKEEKDIAKRMEEIRKDLEKSDGLSFSGEPMSQEAVESLMEAMEHI  
VRQTQRINKKYTPKKYRNDDQE

>sp|B2ZYZ1|TAIL\_BPMR2 Putative tail protein OS=Staphylococcus phage phiMR25 GN=orf53  
PE=1 SV=1  
MANMKNSNDRIILFRKAGEKVDATKMLFLTEYGLSHEADTDTEDTMDGSYNTGGSVEST  
MSGTAKMFYGDFFADEIEDAVVDRVLYEAWEVESRIPGKNGDATKFKAKYFQGFHNKFE  
LKAANGIDEYEYEGVNGRFQRFATLPEAVTKKLKATGYRFHDTTKADALTGEDLTAI  
PQPKVDSSTVTPGEV

>sp|A9CRB8|TAIL\_BPMR1 Putative tail protein OS=Staphylococcus phage phiMR11 GN=orf50  
PE=1 SV=1  
MAQDKYIVALQIADKDLAKKLTIEEATLLGSLAEGGHTISNDLAEIQQGKKDYSRNSVEE  
EIKLTLDDVVPDGKQLALKESVKQFKQLRVWIWETKKRDGKHHGVFAYVVIEHEWSFD  
DEDNKIEITAKVKFNSADGTINDLPKEWLNPSALAPVVEFEDMNAYEDSYENRTKKTAG  
SSDLSM

>sp|Q05234|VG27\_BPML5 Minor tail protein Gp27 OS=Mycobacterium phage L5 GN=27 PE=1  
SV=1  
MITDTIVELEGVNGERFNLTGDAQVYLATDVEGCFYDPPVKVVVEEPGNYPGARYLSHR  
ALKRDIVFGVVILNDAKQGPRSWLSRDSEWRKAWAFNRTCKLYVTTTPDSGTRYLKLALFE  
SPTVKMDTDPRGKPLEVTVMSCIAYPDWFYEDDKVFSAKTKTDTRFDPSFWTPWPWEE  
LPKETLRIKVGREQGGLNPTDQYIFPKWTVPGSTEKVPNFPWPFPPNVIPIWETAPFTQFVI  
PDYSFEDEEFRNRRLKTPGLIYGENCIDTDRREEQIASESGSPVWARMNGVRFNSIPPYT  
EEAEFVIDASGCAPGQVVTLRRLTRPWSRCWGLE

>sp|Q05235|VG28\_BPML5 Minor tail protein Gp28 OS=Mycobacterium phage L5 GN=28 PE=1  
SV=2  
MSGLTSVREAEDLWQKIQLRRCRERKHPDVELRDGDFRLRGLVAGERVLEWFEIEN  
ETGTCTLQLSLSHYLAKWVMDHRGRAKRNVIINIEKQGARWTGMMDHRYVIKTDAGDA  
YIEIVFLHDFEQTKHIRVWCNPFLRPELQFPKVVIFGPAKWCLLVTLFVNLLRLETSLWTL  
PDDPTDINEWMGSPFNANWRNIVKPFPLADNSPVTMVFSRFGTFYDTAKKILEDHQLTL  
TCRRYIKDRDPHPFEDLKGLWGIDPVEDLLQKIPLRDGCVVWDIEDNSGWTQTAFGGG  
WLTGFVRGMVQLAGDGQVEGVDVFTGDYTFPGEYYSPWFMGTSPHAPHVVFEEGPLTGI  
KSSEFSYYEATDTSFLAGGQSAPGINEGIALVNIIGDLLTSFINSQLAALGAVGGAILPPL  
GGLLDAVLQPLYSDVFGAFMEVPTLRAMGISLPISGLEDIVTGLGDFHYFENMADGAMKA  
FTLSAFAAIASQIHKTRARTHTLKVSDAAPYIFAPKPYGHCWIGDRVGTSLGYPVEHQL  
FVERIRKVKYRIDKDKGMKPLEIEIGYREPKNPALHILEEIKRVNGALGTAGIL

>sp|P20344|VG85\_BPPH2 Head fiber protein OS=Bacillus phage phi29 GN=8.5 PE=1 SV=1  
MMVSFTARAKSNVMAYRLLAYSQGDDIIEISHAAENTIPDYVAVKDVDKGDLTQVNMYP  
LAAWQVIAGSDIKVGDNLTTGKDGTAVPTDDPSTVFGYAVEEAQEGQLVTLVISRSKEISIE  
VDDIKDAGDTGKRLKINTPSGARNIIENEDAKALINGETTNTNKKNLQDLLFSDGNVKA  
FLQATTTDENKTALQQLVSNADVGLLSGNPTSDNKINLRMTMIGAGVPYSLPAATTTTIG  
GVKKGAAVTASTATDVATAVKDLNSLITVLKNAGIIS

>sp|P85225|VPN1\_BPPHE Putative tail sheath protein OS=Enterococcus phage phiEF24C PE=1  
SV=2

MAVEQFPRKKVSRPHEITVDTSGIGGSSSSSDKTLMLVGS AKGGKPDTVYRFRNYQQAK  
QVLRSGDLLDAIELAWNASDVNTASAGDILAVRVEDAKNATLTKGGLTFASTIYGVDANEI  
QVALEDNNLHTKRLTVAFSKDGYKKVFDNLGKIFSIQYKGSEAQANFTIAQDSISKKATT  
LTLNVGSEPESTTEVMKYELGQGVYSETNVLVSAINSLPDWEAKFFPIGDKNLPTDALEAV  
TKVDVKTEAVFVGALAGDIAKQLEYNDYVTVAVDATKPVEDFELTNLTGGSDGTAPESWA  
NKFPLLANEGGYLVPLTDKQAVHSEALAFVKDRDNGDPMRIIVGGGTNETVEESITRAT  
NLRDPRASLVGFSGTRKMDDGRLKLPGYMMASQIAGIASGLEVGEAITFKHFNVTSVDR  
VFESSQLDMLNESGVISIEFVRNRTLAFRVVQDVTTYNDKSDPVKNEMSVGEANDFLVSE  
LKIELDNFIGTKVIDTSASLIKNFIQSFLDNKKRAREIQDYTPPEVQVVLEGDVASISMTV  
MPIRSLNKITVQLVYKQQILTA

>sp|P03715|VSOC\_BPT4 Small outer capsid protein OS=Enterobacteria phage T4 GN=soc PE=1 SV=1

MASTRGYVNIKTFEQKLDGNKKIEGKEISVAFPLYSDVHKISGAHYQTFPSEKAAAYSTVYE  
ENQRTEWIAANEDLWKVTG

>sp|Q05278|VG06\_BPML5 Minor tail protein Gp6 OS=Mycobacterium phage L5 GN=6 PE=1 SV=2

MADLGNPLDLEMLCLVTGRDFRWTIDYPWGPGELEFLELETGGEHNALHQVYVTGATGGT  
YTLNVNGTNTPAIDYNDVSENPPQGLAGDIQDALDAAVGAGNAVVHPVSLFPAWTLNFNL  
NASKPLTEQLVNTINKAANDFFDTFDQLLGV DVEMTVTDTLNFKLKVTSRRSFDEVGVVT  
FAVDVTSQAVINFFNSVAELTGAVNTVNVDFYWNRTYDIEFTGSLGLQPIATTADITNLAG  
TSKAVSVTVVEPGKKRLTIWPFTVNGETATIKVESEEADKIPNRCRWQLVHMPTGEAAGG  
DAKQLGRVYRQPR

>sp|Q05223|VG17\_BPML5 Major head protein Gp17 OS=Mycobacterium phage L5 GN=17 PE=1 SV=2

MAVNPDRTPFLGVNDPKVAQTGDSMFEGYLEPEQAQDYFAEAEKISIVQQFAQKIPMGT  
TGQKIPHWTGDVSASWIGEGDMKPITKGNMTSQTIAPHKIATIFVASAETVRANPANYLGT  
MRTKVATAFAMAFDAAINGTDSPPFTFLAQTTKEVSLVDPDGTGSNADLTVYDAVAVNA  
LSLLVNAGKKWHTLLDDITEPILNGAKDKSGRPLFIESTYTEENSPFRLGRIVARPTILSDH  
VASGTVVGYQGDFRQLVWGQVGGLSFDVTDQATLNLGTPQAPNFVSLWQHNLVAVRVE  
AEYAFHCNDKDAFVKL TNVDATEA

>sp|Q05233|VG26\_BPML5 Minor tail protein Gp26 OS=Mycobacterium phage L5 GN=26 PE=1 SV=2

MPNSAGVEVARISVKVSPNTKEFRRELKTELEKIERELKGDVEINGHLDAQAQKADFKRM  
MMQLKTEAAKGVHVPVDVTVDKKSKKGGLLGGLLGGSRGLGDLGDDAEKASSQVQHL  
GKSFLGLTRA AWIGVGIVAVAAPLVGIVAGLLAGLPSLLSAFGAGAGVVALGMDGIKAAAS  
TLAPTLETVKA AVSSTFQQGLTPVFQQLGPM LTAITPNLQNVASGLVNMAGSITDVITQAP  
GLQQIQNILTKTGEFFTGLGPVLATGTQAF LTLNAGANSFGTLLAPLQEFTNGFNDMVNR  
VTSNGVFEGAMQGLSQT LGSVLNLFNRLMESGLQAMGQLGGPLSTFINGFGDLFVSLMP  
ALTSVSGLIGNVLGTLGTQLAPIV TALTPAFQTLASTLGTMLTGALQALGPILTQVATLIGTT  
LNTALQALQPMLPSLMQSFQQISDVLVTS LAPHIPALATALGQVAGAVLQLAPTIISTLVPAF  
VQLVPKVAELVPTIVNLVQSFANLMPVVLPLAQALVSVAGAVIQVGVSIGGALIGALANLT  
EIISNVIKKVSEWVSSFSSGAQQIAAKAAELPGMIQSALANLMAIGLQAGKDLVQGLINGI  
GGMVSAAVNKAKELASSVAGAVKGF L GIESPSKLFTEYGGQFTAEGFGNGMEAGFKPVIER  
AKDLAAELSRAMESGTDPSGILAGLDQNELKQMLAALEEKRLKVEKNGIPKGDKAGR

EALQNQLDQIQAQKDILSYQRDRIKNESEYGDMAGEDPLVKAASGLMSAPVDFAKATGK  
QFLSDIGISGDGFISKAITTEGIQYIFQIGSVDEALSIKDREESKNALSVVGR

>sp|P85226|VPN2\_BPPHE Putative major capsid protein OS=Enterococcus phage phiEF24C  
PE=1 SV=2

MTEKKNTERQLTSVQEEVIKGFITTYGYPESQTDAAALRREFLDDQITMLTWADGDLSF  
YRDITKRPATSTVAKYDVYLAHGRVGHTRFTREIGVAPISDPNLRQKTVNMKYVSDTKNM  
SIATGLVNNIEDPMRILTDDAISVVAKTIEWASFYGSDLSENPDAGSGLEFDGLAKLIDKH  
NVLDAKGASLTEALLNQASVLVGKGYGTPTDAYMPIGVQADFNQQLDRQVQVVISDNG  
QNATMGFNVKGFNSARGFIRLHGSTVMELEQILDENRMQLPNAPQKATVKATLEAGTKG  
KFRDEDLTIDTEYKVVVVSDDAESAPSDVASVVIDDKKKQVKLEITINMYQARPQYVAI  
YRKGLETGLFYQIARVPASKAVEGVITFIDVNDIPEADVFVVGELTPSVVHLFELLPMMRL  
PLAQVNASVTFVLWYGALALRAPKKWARIKNVKYIATGNVFN

>sp|P18683|VNUN\_BPHK0 Transcription termination factor nun OS=Enterobacteria phage  
HK022 GN=nun PE=1 SV=1

MLMVKKTIYVNPDSGQNRKVS DRGLTSRDRRRIARWEKRIAYALKNGVTPGFNAIDDGPE  
YKINEDPMDKVDKALATPFPRDVEKIEDEKYEDVMHRVVNHAHQRNPNKKWS

>sp|Q05229|VG23\_BPML5 Major tail protein Gp23 OS=Mycobacterium phage L5 GN=23 PE=1  
SV=2

MAENDDAVLTAAGVYVYVGAAGTAAPTALLKTIDLSKPETWTGATGWTSVGHTSRGTL  
PEFGFEGGESEVKGSWQKKKLREITTEDPIDYVTVLLHQFDEQSLGLYYGPNASETPGVFG  
VKTGQTNEKAVLVVIEDGDMRLGHHAHKAGVRRDDAIELPIDDLAALPVRFTYLDHEDE  
LPFSWINEDLFNVPEVPEG