


Protein	Sequence	Score
neuB	0
gumD	0
gelB	0
dpsB	0
spsB	0
crdSMYFSAEGDVQSVLYVNLTTIAIGAILFALLADPRKMV.DRLAFSIIMLLSLGVYIVWRATDTLPPPEL	66
bcsBI	0
bcsAI	MSEVQSSAPAESWFGFRFSNKILSLRG....ASYVVGALGLCALLAA..TMVTLSLNEQMIVALVCVAVFFIVGRRKSRRTQVFLEVL SALVSLRYLTWRLTETLDFDT.	102
bcsABII-AMYGTWFTTGKVTDLLARTGLDRVPVWVPVVLGVVLMFV..GSVRIDPALQGWVSVGTVTLLLVLNRRRRGRGITVFLMMLSLLVSLRYIVWRLTATVQFSN.	99
pslF	0
gumI	0
pelFMTEH.....	4
pslI	0
gelK	0
dpsK	0
spsK	0
gumH	0
gumM	0
hasA	0
sleD	0
exoA	0
icaA	0
pgaC	0
sleC	0
exoL	0
alg8	0
pmHASMNTLS...QAIIKA.....YNSN.....	14
epsH	0
epsJ	0
dpsQ	0
gelQ	0
spsQ	0
pslH	0
sleW	0
exoW	0
sleE	0
exoM	0
pslC	0
gelL	0
dpsL	0
spsL	0
sleU	0
exoU	0
sleF	0
exoO	0
consensus		

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neuBW.....L.....E.....Y.....K.....L.....E.....P.....V.....P.....S.....L.....L.....S.....D.....P.....P.....V.....L.....L.....D.....R.....S.....B	0
gumD	0
gelB	0
dpsB	0
spsB	0
crdS	SLETLWCYTYFTF.ELISVLYAMGSILILLRRTDWSAVADQGEAYLAGNPHAPLVDVFICTYNEPLNVLEKSIIAAQAMDYPRL.....RVF.V.CDDTR.....R	159
bcsBI	0
bcsAIWTQGILGVTLLLAELYALYMLFLSYFQTISPLH.RAPLPLPANPDEWPTVDIFIPTYDEALSIVRLTVLGALGIDWPPDK.....VNVY.I.LDDGR.....R	192
bcsABII-AWLQTALAVLLLLLAEAYALMTLCLSIFYQMAWPLR.RREHPLPEDMAQWPSVDVFVPSYNEELSLVRSTVLGALDLDWPADR.....LNVY.I.LDDGR.....R	189
pslF	0
gumITAPTAPVADVCL.....LLEGTWPYVRGGVSSWVNQL.....ILG.....LPDLT.....FSVFFI.GGQKDAY.GKRH	61
pelF	15
pslIMRI.GLDYRTVGSSPH	0
gelK	0
dpsK	0
spsK	0
gumHMKV.VHVVR....Q..	9
gumM	0
hasA	0
sleD	0
exoA	0
icaA	0
pgaC	0
sleC	0
exoL	0
alg8	0
pmHASDYQLALKLFEKSAEIYGRKI...VEFQITKCK.....EKLSAHPSPVNSAHLNVNKEEKV.....NVCDSPLDIATQLLLSNVKKLVLSNSE.....	92
epsH	0
epsJ	0
dpsQ	0
gelQ	0
spsQ	0
pslH	0
sleW	0
exoW	0
sleE	0
exoM	0
pslC	0
gelL	0
dpsL	0
spsL	0
sleU	0
exoU	0
sleF	0
exoO	0
consensus	0

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neuB	0	
gumD	0	
gelB	0	
dpsB	0	
spsB	0	
crdS	GEVRTYCEAVGVNYV...TRPDNKHAKAGNLNNALLHTNALEEVSDFIM.....VLDAD...FAPQANFLRRVTG.....LFSDPKVAVVQTPQ...F	238	
bcsBI	0	
bcsAI	EEFARFAEACGARYI...ARPDNAHAKAGNLNYAIKHTT....GDHIL.....ILDCD...HIPTRAFLQISMGW.....MVSDSNIALLQTPH...H	267	
bcsABII-A	KAFHDFAVEAGAGYI...IRAENNHAKAGNLNHALAVTD....SPFAV.....IFDCD...HVPTRGFLRRITIGW.....MMADPNLALLQTPH...H	264	
pslFMRIALL...A.PLPPEKNGIADYASHFRNALQGLGIEVATPLAGVA..A...D...SANIAS.....RL..D.....S	54	
gumI	LPVTRAAAAPRITVL...FSTEKPNANT.NPYLTQLYDALP...DAVQPRFFSM..R...D...ALLSRY.....DV..L.....H	65	
pelF	YPIPDNVLHIEEHFLETAWSSPNPQTRQGSSETEKALRDLHR...FFHYPETPDVEEGDALLDLAEGRIGREDFLHSKASWEAITAGYERYCTDPSF..V.....N	158	
pslI	SGISRQVYAMEQA.LE...SLPGTQV.....TR...FTVAPL.....DDPLR.....QRA..V.....C	55	
gelKMAEATEAAH...TTGKRLKM.....CL.....AASGGGHLRQILDLES..VWREH...D	41	
dpsKMAEANAVDG...KASKPLKM.....CL.....AASGGGHLRQILDLES..VWREH...D	41	
spsKMGDGMAEATVTEA...KAGKPLKM.....CL.....AASGGGHLRQILDLES..VWKEH...D	45	
gumH	..FHPSIGGMEEVVLNVA...RQHQANSA.....D.....TVEIVTLDRVFTDPSA..QLTQH...E	56	
gumM	..MHGQPAGVET.....	10	
hasA	0	
sleD	0	
exoA	0	
icaA	0	
pgaC	0	
sleC	0	
exoL	0	
alg8	0	
pmHASKNTLKNKWK.....LLTEKKSENA..EVRAVALVPKDFPK.....D.....LVL..APLPDHVND	138	
epsH	0	
epsJ	0	
dpsQ	0	
gelQ	0	
spsQ	0	
pslH	0	
sleW	0	
exoW	0	
sleE	0	
exoM	0	
pslC	0	
gelL	0	
dpsL	0	
spsL	0	
sleU	0	
exoU	0	
sleF	0	
exoO	0	
consensus	0	

logo

neuB	0
gumD	0
gelB	0
dpsB	0
spsB	0
crdS	YFNSDPIQHN LGI.DKSFVDDQRVFFDV.....FQPAKDAVG.CAFCV.GTSFVVRRAAVNGIGGFPSDALSEDM.....LLTYRL.....	311
bcsBI	0
bcsAI	FYSPPDFQRNLAV.GYRTPPEGNLFYGV.....IQDGNDFWD.ATFFC.GSCAILRRKAIEEIGGFATETVTEDA.....HTALRM.....	340
bcsABII-A	FYAPDPFQRNLAV.GMHVPPEGNMFYGL.....VQDGNDFWD.ATFFC.GSCAILRREAVMGIGGFATETVTEDA.....HTALKM.....	337
pslF	VDW.....NAFDLVHAE LGGGR...LG.....EFI.....ALRELKRFRPRLPLSATVHDP.....	97
gumI	LHW.....PEYLLRHPSKMGTL...AK.....QACA.....ALLLMKLQLTGTPVVRTLHNL.....APH.....	112
pelF	YFWTLR.....SMQAPVFMLAEAAARRMPR...ARMLHS...I.STGYA.G...LLGCILQRRWGCRYLLSEHGI.....YTK.....	219
pslI	PPWGCPRT.....AMHQPHQRLRFEAGFLPR...ALREQDIDLYI.STFNM.G...LPLPPRPPGVRYALLIHDL.....FQI.....	120
gelK	YFFVTEDTALGRSLAEKHPVELVGHYALGQARLGHPFKMLGGA...LRN...LRQSLAIVRRHKPDVVISTGAGAVYF.TALFA.....	118
dpsK	YFFVTEDTALGRSLAEKHPVELVEHYALGQAKLGHPRLMLGGA...WRN...LRQSLSIILRRHKPDVVISTGAGAVYF.TALLA.....	118
spsK	YFFVTEDTALGRSLAEKHSVALVDHYALGQAKLGHPRLMLGGA...WRN...LRQSLSIILRRHKPDVVISTGAGAVYF.TALLA.....	122
gumH	VHQGLPITRIGYRGSSRYPIAPS...VLGAIRSADVVHLHGID...FFY...DYLALTKPLHGKPMVVSTHG...GFFHTAYAS.....	128
gumMATVSPATPA...Q.....GVVIPLGGFPVLSTTQEAFALDLFHALAAH.....	50
hasA	0
sleD	0
exoA	0
icaA	0
pgaC	0
sleC	0
exoL	0
alg8	0
pmHAS	FTWYKKRKKRLGI.....KPEHQHVGLSIIVTTFNRPAILSITLACLNVNQKTHYPFEVIVTDDGSQEDLSPIIRQYENKLDIRYVRQKDNGFQA	227
epsH	0
epsJ	0
dpsQ	0
gelQ	0
spsQ	0
pslH	0
sleW	0
exoW	0
sleE	0
exoM	0
pslC	0
gelL	0
dpsL	0
spsL	0
sleU	0
exoU	0
sleF	0
exoO	0
consensus		

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neuB	8
gumD	LTMVVASGLI	64
gelB	SIAILASFYF	78
dpsB	SLSILAGFHV	78
spsB	SIAILLGFYI	78
crdS	WRG.NF..	TLTQRLHYLHGLFCWLSKPFILCLLLAPSIYWLTGVSA....	L....QVDELMF..M.K.....LGLSSLALFWTYSTWISGKRTLPLFTEVTH.ALT.	445
bcsBI	0
bcsAI	GSG..L..	KLQQLCYLSAMTSFFFFAIPRVIFLASPLAFLFFSQNIIAASPLAVGVYAIPHMF..HSI.....	ATAAKVNKGWRYSFWSVEVETVM.....ALF.	476
bcsABII-A	GAG..L..	RWEQRLCYLSAMSHFLFAIPRLTFLVSPLAFLFLGQNIIAASPLAISVYALPHIF..HSV.....	ITLSRIEGRWRYSFWSSEIYETSL.....ALF.	473
pslF	TRLVTL.TG....	LG.....GECLARRMRL.....PPGRVEVINHGNL.....	EIATVPL.PSLDTLRL.LYFG	196
gumI	ATTPV.....RPPFTDTILHGHY.....	RDWFATMEQ.STTLPGR.LHFG	176
pelF	NPIVALYEGNRQRQVL.....	DGAEPRTTRV.....IPNGIDL.....	DAWTGALERRPPGIPPVV.GLVG	324
pslI	DEAVRLFPG.....	VAGKVRV.....LPNQVDGFAGEPADLSARGLPPTYWLLVG.....	TRELKKNVPWFVSAWTRARAQ.APGVPPLV.LVGS	239
gelK	.LFGAK..FIHIESFA.....	RFDHPSAFGK.....MVKGIATISIVQSPA.....	LKQIWPDAEL...FDPFRM.LDTP	177
dpsK	.LSGAK..FVHIESFA.....	RFDHPSAFGK.....MVKGIATVTIVQSAA.....	LKETWPADEL...FDPFRL.LDTP	177
spsK	.LSGAK..FVHIESFA.....	RFDHPSAFGK.....MVKGIATVTIVQSAA.....	LKETWPADEL...FDPFRL.LDTP	181
gumH	.VIATS..ENDGDLFA.....	KVVAPSRLRV.....IENGVDVEKYAGQ.....	GA...RAPGRTMLYFG	197
gumM	.RIVND..GIGMDLAA.....	RLIHGRRFAG.....NLNGTDLIPYLCR.....	EA...AQPLKFFLLGG	127
hasAMRTLK.....	NLITVVAFSIF.WVLLIYVNVYLF..GAK.....	G.SLSIY.GFLLIAYLL.....VKMSLSFF.....	54
sleD	0
exoA	0
icaAMH..VFN.FLLFY.PIFMSIYWI.....	VGSIYYFF.....	27
pgaC	MINRIVSFFILCLVLCIPLCVAYF..HSGEL..MMR.FVFFW.PFFMSIMWI.....	VGGVYFWV.....	54
sleC	0
exoL	0
alg8MMETYK.....	RGLAEATGWLVL.....	SL..LMVLALAVPKTVFDA....D	37
pmHASL..DWRLEQFE.....	KTENLRLSDSPFRFFAAGNVAFAKKWLNKSGFFDEEFN..HWGGEDVEFGYRLFYRGSFFKTIDGIMAYHQEPPGKENET....D		405
epsH	0
epsJ	0
dpsQ	0
gelQ	0
spsQ	0
pslH	0
sleW	0
exoW	0
sleE	0
exoM	0
pslC	0
gelL	0
dpsL	0
spsL	0
sleU	0
exoU	0
sleF	0
exoO	0
consensus	0

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neuBGIKPRG.....SSMTC.....FIIAEAGVNHN.GD...LQLAK.....ELVYAAKESGADAVKFQTFKADTLVNKTVEKAHEYQKN.	74
gumDTTLL.....YSVIC.....FALFPLYRSWR.GR...GLLSE.....LMV....LGGAFGGVFALFAVHALI...VQVGE.....	117
gelB	ITLGTAIASGT.....YSLES.....LRHP.....IS.....GVKNILSAFLFSILI...VLLGSYLLTT	125
dpsB	IALGTALASGT.....YSLNC.....LRYP.....VS.....GVKSIFSAFFFSIFV...VLLGSYLLTA	125
spsB	ITLGTALASGT.....YSLSC.....LRYP.....VS.....GVKSIFSAFFFSVFI...VLLGSYLLTA	125
crdS	.AVPITIT.....LFQAIR.....KPFGRPFK.VTEKGGDRSQVRVHL...PTAIFFAFVTLSSAVSIVLAVYGLDAPSEL.....SSRDCL..	517
bcsBI	0
bcsAI	.LVRVTIV.....TML.....FPSKGKFN.VTEKGGVLEREEFDLTATYPNIIFAIIMA.LGILLRGLYALIFQHLDIIS.....ERAYAL..	548
bcsABII-A	.LVRITIV.....TLL.....QPHKGKFN.VTDKGGLLARGYFDWDVAVPNVILAGVLC.AALLRGVFGIVWQFHDRLA.....LQSFIL..	545
pslF	FIYRGKGIEDL....LEALADLFAS.....APEMRQVRVRLTLAGGTAAEMAFGAGG.....NYLYQLKAQIAELGLADAIDW.....NLNLAA..	270
gumI	LIRPYKGVEVL....LDVMRDVQDPRLSLRIVGNPATPQMRTLVTETACAQD...ARISA.....LLAYVEE.....	235
pelF	RVVPIKDVKTF.....IRAMRGVVSA.....MPEAEGWIVGPEE.....EDP.....DYASECRSLVASLGLQDKVKF.....LGFR....	386
pslI	.L.....DH.....LPEEQRG.....LPGLHALGG.LDDAEL.....HALY....	268
gelK	RPPKQALTFAT.....VGATLP.....FPRLVQAVL.....DLK.....RAGGLPGKLILQYGDQALTDP.....GIPDVE..	233
dpsK	RPPKQALIFAT.....VGATLP.....FPRLVQAVL.....DLK.....RAGGLPGKLILQYGDQDLDPD.....GIPDVE..	233
spsK	RPPKQALTFAT.....VGATLP.....FPRLVQAVL.....DLK.....RAGGLPGKLVLQYGDQDLADP.....GIPDVE..	237
gumH	RWSVNKGLIETLEL..LQA.ALTRDP.....QWRLIIAGR.....EYD.....LNEADLRKAIAERGLQDK.....V..	251
gumM	RPGVGKTAATLTGTLGQQVVGMCDG.....YGEFAAAGE.....G.....LAERINRSGADVL.....L..	177
hasAYKPF.....	58
sleDMEG.....	3
exoAMSS.....	3
icaAIKEKPFNRS.....LLVK.....	40
pgaCYRERHWPWG.....ENAPA.....	68
sleCM.....	1
exoLM.....	1
alg8	SK...DFI.....LLIGA.....VGI..WR.....YSMGG.....	57
pmHAS	REAGKNIT.....LDIMRE.....KVPYIYRKL.....LPIED.....	433
epsH	0
epsJ	0
dpsQ	0
gelQ	0
spsQ	0
pslH	0
sleWMIN.....	3
exoW	0
sleEMTD.....NTVTG.....	8
exoMM.....	1
pslC	0
gelL	0
dpsL	0
spsL	0
sleU	0
exoU	0
sleFM.....	1
exoOMNP.....	3
consensus		

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	NEPESSTQYEMLKALELSE..EDHYLLSELANSLGIEFMST.GFDEQSID.....FLISLGVKR.....LKIPS.....	135
neuB	..QVSRGWVGLWFVGGVLVLAARTLLRGFLNHLRTQGVDV....QRVVV.....VGLRHPVMK.....	170
gumD	ELPLSRIQLGAGALMTVVLLMA...GRLVFRRHVRAMTGDK.LLDELVII.....DGVSLDLAS.....	180
gelsB	ELPLSRVQLAEGAILSLLVLLMV...GRLMFRRHVRRAVTGGR.LLDELVII.....DGVSLDVAG.....	180
dpsB	ELPLSRLQLGEGVLLALSLVTI...CRLGFRWHVRALTRGT.LLDELVIV.....DGVALEVAS.....	180
spsB	NL....IWSAVAMVIAFTSFICCIELPR.FGKEEMIGVDFRGQLRSASST.....RPVRIT...GLSTENITLAAPVSSSDVKDVFVPEAGWMRISPAE.....	603
crdS		0
bcsBI	NC....IWSVISLIILMAVISVGRETQK.LRQSHRIE.....AQ.....IPVTVYDYGDNSSHGITEDVSMGG.....VAIHLPWREVTPDHP...V	622
bcsAI	NT....LWVVISLIIVLASIAVGRETRQ.TRNAPRVS.....VR.....LPVVVTDAGHRQMEGHTHDISLGG.....LAVGTR..LATPDMVGGEV	620
bcsABII-A	AD.....IPRTIQAHHVMVL.PYRE.SKKLGL.....LGQQRG.....TSGALSWAAACGRGAITS DARAF A.....EEVAS.....	330
pslF	PV.....LAREVSACELVVL.PYKQ.MHNSGT.....LLLALS LA.....RPVLAPWSESN.....AAIA.....DEVGP.....	288
gumI	.R.....IGEVLPLQLGLMVLTSISE.AQPL.V.....ILEAWAAG.....APVVSSDVGSCRELIEGAD...A.....EDRAL.....	443
pelF	.R.....QAERLWQP.....SYAE.GFGL.P.....VVEALSVG.....TPVAVASGTS LDEVTPPSA.....	313
pslI	IRPTIPFDE.LQLMLRDADIVICH...G.GTGSL.....VTALRAG.....CR.....V.....IAFP.....RRFDL.....	281
gelK	IRRTIPFDD.LQLLLRDADMVICH...G.GTGSL.....VTALRAG.....CR.....V.....VAFP.....RRHDL.....	281
dpsK	IRRTIPFDD.LQLLLRDADMVICH...G.GTGSL.....VTALRAG.....CR.....V.....VAFP.....RRHDL.....	285
spsK	QLSMSPSQQLCALMQQAQFFVCLSRHE.GFGIA.....AVEAMSAG.....LIPILSDI.....PPFV.....RLATE.....	309
gumH	VAFGNPLQERWILDHSEA....LQVPL.VFGVG.....ALLDFLSG.....TAKRA.....PNWV.....RRLHM.....	227
gumMKGRAGQ.YKVAAIIPSYNED.AESLL.....ETLKS VQQQ.....T.....	92
hasAPG.HSG.IRTLIVIPCLNEA.KTIEG.....LLVKFTGAM.....Q.....	36
sleDDE.LTS.TSSLIVIPCLNEA.SHIEA.....LIEKLRPSL.....T.....	36
exoASEHQVQV.EGISFLLACYNES.ETVQD.....TLSSVLSLE.....Y.....	74
icaAPQLKDN.PSISIIIPCFNEE.KNVEE.....TIHAALAQR.....Y.....	102
pgaCIHILYL..AHDLS DPAIRRR.VLTL.....LAGGARV.....T.....LA.....	33
sleCLQILYL..AQDLADPAVRRR.TLTL.....VAGGARV.....T.....LA.....	33
exoLVHFLRGMLFLHVVPYRRR.V.....RQLGSAADPSHVFLMVT SFRI.....DAL T.....TA.....	105
alg8SHINRV.PLVSIYIPAYNC..ANYIQ.....RCVDSALNQ.....T.....	466
pmHASMET.PAVSLLVAVYNT..ETYIR.....TCLESLRNQ.....T.....	30
epsHMI.PLVSIIVPMYNV..EPFIE.....ECIDSLLRQ.....T.....	29
epsJMQMLP.....	5
dpsQMTDQT.....	5
gelQMEASP.....	5
spsQMRILWILPYSPW..PTTSGG.KTRQYHLLRSLAARGHRITVLLHSKQPVS AEDRQA.....LE.....	55
pslHARGETM.ARFTVVIPYYQKQ.HGVLG.....RALASVFAQ.....T.....	37
sleWM.AKLTVVIPYYQKE.PGILR.....RALASVFAQ.....T.....	29
exoWTQYLKT.VD..IGICTYRR..PALVA.....TL.LSLFELD.....V.....PE.....	41
sleEPNETLH.ID..IGVCTYRR..PELAE.....TL.RSLAAMN.....V.....PE.....	34
exoMMRCALVIPTRNA..GAHLD.....RLLPALAAQ.....R.....	27
pslCMTG.PRISVVIPHYND..LEGLT.....KCLESIDRQ.....T.....ID.....	32
gelLMST.PRISVVIPHYND..PQSLR.....LCLDALERQ.....T.....IG.....	32
dpsLMSA.PRISVVIPHYND..PDSL R.....QCLDALQH Q.....T.....IG.....	32
spsLMVSGS.QPICVIIIAAKNA..SDTID.....IAIRSALAE.....P.....	32
sleUMTAAAP.TDVCIIISAKNA..ADTIA.....RAVASALAE.....P.....	33
exoUENLTSP.PDISFVIAAYNA..ADTIE.....AAVQSALDQ.....Q.....	34
sleFPAIDKV.PDVT FVVAAYNS..ADTIV.....RAIESALAQ.....E.....	36
exoO		
consensus		

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	G E Y V D S I D E T A Y S A G S R F S P S R L R L A S R S R			
neuB	GEITNVPYLQHCASKKLPLIISTG.....	MCDLQEV RVAIDTVKPYYG.....	NSL.....SDYL 185
gumD	ISHYLSRNPWVG.....	MNMVGYFRTPYDL..AVAEQR 201
gelB	DAVA.....	L...DARIINLSPNPRDP.....	QMLHR.LGT...T..VIGFDR 214
dpsB	NAVA.....	L...DARIINLSPNPRDP.....	QMLHR.LGT...T..VIGFDR 214
spsB	GAVA.....	L...DARIINLTPNPRDP.....	QMLHR.LGT...T..VVGFD 214
crdS	HAQNSGKFDIHPSDEQ.....	RRSILRLLFR 629
bcsBI			MKMVSLIALLVF 12
bcsAI		QVVIHAVLDGEEMNLPATMIRS..AQGKAVFTWS.....ISNIQVEAAVVRVFVGRADAWLQ.....	WNNYEDDRPLRSL....WSLILSIKALFRR	703
bcsABII-A		TVRYDSARDGIHVGVPARVLDA..RDGTLRLRWA.....VRDLEDERQVVSVMVFGRNDAWAG.....	WADFAPDRPLRSL....AMVFRSIGGLLR	701
pslF	GNGAIYPQ.....GDVAALSEQLLNLAEPRLAQAWAER.....	AGAI.....GHARTWPRTALRFQALFNDM..VGTVHGT..	395
gumI	GWVFLYEGE.....FDAALLSGMLDQVRAAPRG.....	PAPD.....LSQRDWPRIGQLHYRTYLEA..LGKDGAAL	349
pelF	GRAGEVVAI.....ADPQATSRAILALLRNP.....	Q.....RWQA.....AQAV....GLQ RVERYYTEALMLGRYRGLYR	501
pslI	PRFSP.....SDGAALERLMLRLADAPREASAEELI.....	AWAA.....RFNRE..AYRQRLAALIEEL.....	366
gelK	GEHYDDHQEE.....IAQTFADRGLLQAVRDERELGAAVA...AAKATEPR.....	LATTDHTALAARL.RTLLAEWGAKR.....	348
dpsK	GEHYDDHQEE.....IAQTFADRGLLQAVRDERQLGAAVE...AAKATEPQ.....	LATTDHTALAARL.RQLLAQWSAKR.....	348
spsK	GEHYDDHQEE.....IAQTFADRGLLHAVRDERELGAAVE...AAKATEPQ.....	LATTDHTALAGRL.RELLAQWSAKR.....	352
gumH	SG.....QGVIVNRDRIQAAADSVQALALQADADFDARRATMAY.....	VARYDWRHVVGRIYIDEYHAALGTPRTQEAVR	380
gumM	EW.....MYRLL.....NEPRRL.....	LKRYSDLLVFFRTCLRAG.....KQLA..	263
hasA	YPLAEIYVVDGSADETGI..KRIEDYVRDTG.....	122
sleD	GRLFRIVVADGGSTDGTRD..IVAFA.....A.....	62
exoA	PLNARVVIADGGSTDGTRE..IARRLA...T.....	62
icaA	PEKEIIIINDGSSDNTAE..IIYDFK...K.....	99
pgaC	ENIEVIAVNDGSTDKTRA..ILDRMA...A.....	127
sleC	GFRRGQNRLA..EIEGVVPVVLGETADGQF....LQRM.....AAVAK	70
exoL	GFRRGDNPLA..AIDGVEPIELGTTADGRF....AQRI.....GAVAR	70
alg8	MVYRSVIREAIDSGYPTTVVCSIVEMSDEVLVRSLEWKMNP.....	146
pmHAS	VVDLEVCI CNDGSTDNTLE..VINKLYGN.NPRVR.....	498
epsH	MDNIEIIIVNDGSSADASPD..IAEEYAKM.DNRFK.....	62
epsJ	LSDIEIILVNDGTPDRSGE..IAEDYAKR.DARIR.....	61
dpsQ	TPDVSILVVFNSSTEYIED..CLRGIAEG.AGKTPHEVLLIDNGDGRT.....EALVR	55
gelQ	LPHVSVLVVAYHSTDFIRQ..CVDGIAAAA.APNTPYEILMIDNGGGDT.....EAFVR	55
spsQ	TPDVSILVVAYHSAFIGQ..CIRGIAAAA.AQGTAEILLIDNGGGDT.....EAVVR	55
pslHPFLERLVVLP RPLRSLSTLLAALFAPYPLLA..SVNGLSAE.LQRTATELLREP.....		107
sleW	YQDFDLVIVDDESPYPIDQ..ELAELSQE.QKDRIL.....	70
exoW	LEDHFVLVIDDESPYPIAD..ELAGLAQE.ERERIT.....	62
sleE	GVKVRLIVADNDDEEPSAKA..SVDRLRET.APFEIT.....	74
exoM	RARLRVIVADNDNAEPSARA..LVEGLRPE.MPFDIL.....	67
pslC	RQPDSILVVDSRSSDDTVE..RFRAFG...ARVEV.....	57
gelL	RGSFEIIVGDNNSPCGIAA...VEA..VV.AGRGRV.....	62
dpsL	RDAFEIIVGDNNSPCGLAA...VEA..AV.AGRARI.....	62
spsL	REAFEIIVGDNNSPCGLAA...VEA..AV.AGRARI.....	62
sleU	E.VGEVVVIDDGSTDTTSD..VAHAADDG.TGRLRV.....	64
exoU	E.AAEVVVIDDGSTDDSAS..VARAADDG.TGRLNV.....	65
sleF	GVTLEVIVVDDRSADDTIP..FVEAIAAI.DPRVRL.....	67
exoO	GVTVEVVVVDDCSADATPA..LVA..AIP.DPRVRL.....	67
consensus			*	

neuB
gumD
gelB
dpsB
spsB
crdS
bcsBI
bcsAI
bcsABII-A
pslF
gumI
pelF
pslI
gelK
dpsK
spsK
gumH
gumM
hasA
sleD
exoA
icaA
pgaC
sleC
exoL
alg8
pmHAS
epsH
epsJ
dpsQ
gelQ
spsQ
pslH
sleW
exoW
sleE
exoM
pslC
gelL
dpsL
spsL
sleU
exoU
sleF
exoO
consensus

[illegible]

neuB

[illegible]

logo


	STGPR F Y RR F E R E R E F Y S E D D Y F F E E L B S A N L P B C H E G S L V A D S Y F A C M	
neuB	LPGPDHLASM...DPEE.....M.....KNL..VQSIR..DAETVLGSGEKKPSDNELPIRALVRRSITLRRDLVKGAQISKEDLILLRPGTGIAPSEIS	332
gumD	SPGPVFFRQR...RHGLGGREFYMFKFRSMRVHDDHG.TTI..QQATKNDTRITRFGSFLRRSSLDELPIQIFNVLG.....GSM	395
gelB	SPGPVLFAQD...RVGRGNRLFILKILKFRSMRQALCDA.NGN..VSASRDDDRIKVGGRFIRKTSIDELPQLLNVLRL.....GDM	379
dpsB	SPGPVLFAQD...RVGRGNRLFILKILKFRSMRVTLCDAN.NGN..VSASRDDDRIKVGGRFIRKTSIDELPQLLNVLRL.....GDM	379
spsB	SPGPVFFAQD...RVGRGNRLFILKILKFRSMRVALCDA.NGN..VSASRDDDRIKVGRIIRKTSIDELPQLLNVLRL.....GDM	379
crdS	654
bcsBI	AFGPLSFD.....I.....NPI.....FFV.....SGNRLN...FNFA.....SG.....S.....	196
bcsAI	745
bcsABII-A	QFGPVSF.....I.....DPL.....YFT.....GDNKLN...FHFA.....GE.....YR.....	914
pslF	395
gumI	349
pelF	507
pslI	367
gelK	348
dpsK	348
spsK	352
gumH	380
gumM	263
hasA	S.VTGNIL.....VCSGPLSVYRREVVPNIDRYINQTFGLGIPVSGD.....DR.....CLTNYATDLGKT.....	273
sleD	REGAKGHW.....IDHGHHALMRIAFAFVAVGG.Y.DESFSHNEDAELDF.....RLRKS.....GFRIWMTDKTRM.....	214
exoA	RTGAUGHW.....AEHGHHALMRIAFAFVAVGG.Y.DESFSHNEDAELDY.....RLGKA.....GYRIWMTDKTSM.....	214
icaA	S.LAGAIN.....TISGVFTLFKKSALKDVGW.DTD.MITEDIAVSW.....KLHLF.....DY.....EI.....	241
pgaC	R.IYGNVF.....TVSGVIAAFRRSALAEVGY.W.SDD.MITEDIDISW.....KLQLN.....QW.....TI.....	270
sleC	APAPGEPWKIGWFGALRCRKSLEILAFAFARRME.GRV.EIIL..RGRPAYSEFADFDFGVA....AAP...HVFHF.....GP.....YKNPE.....	262
exoL	SPPPGAPWKIGWFGALRCRRSLALLAEFSRKME.GRF.EIVL..RGRPAYSEFDDFDGFVR....NEP...FMRFE.....GA.....YRNPE.....	264
alg8	.TD.....VENDHLE....HWRL..GRF.KF...LTGDDKSSWFS.....LMRL.....GY.....DT.....	310
pmHAS	.REKLTTA.....MIAHHFRMFTIRAWHLT.DGF.NEKIE..NAVYDMFLKLSEVGKFKHLNKCYNRVVLHGD.....NT.....SI.....	645
epsHEHY.....IKALFEGKVRGFSWNKL.YRR.S.MIE..AH....RLSFPLRGELEHVEDQFFSFRAHFF.....AR.....SV.....	201
epsJTEQ.....LKHAEHTRFIWYVWRYL.YRR.E.LFE..RA....NLLFDEDIR..FAEDSPFNLSAFRE.....AE.....RV.....	201
dpsQ	ATTPGAVE.....VLNGGFMMVRTDVWQAI.GGF.DESFF.LYSEEIDLFQ.....RIRTL.....GH.....KV.....	213
gelQ	ATEPGPVD.....VLNGGFMMVRADVWREI.GGF.DESFF.LYSEEIDLFQ.....RIRER.....GY.....AV.....	213
spsQ	ATAPGPVE.....VLNGGFMMVDARVWREI.DGF.DEGFF.LYSEEIDLFQ.....RIRAR.....GY.....SV.....	213
pslH	ATARPTPE.....AQRVLFL.....GNY...EY.AP....NVDAVEWML.....DEILP.RVWAHCP.....EA.....RM.....	259
sleW	LHLSCMV.....IGRPLF.....EK.IRF.DPALR.LAAEDVLFFC.....DSILA.....SK.....RT.....	218
exoW	LHMSCMV.....IGRKLF.....EK.VRF.EATLK.LAAEDVLFFC.....DCVLA.....SK.....RV.....	210
sleE	...TCNT.....LLRMEAP.....SVKG.RRF.ALALGQSGGEDTHFFS.....HLHAA.....GG.....RI.....	208
exoM	...TCNA.....LLRRDAA.....SLLG.RRF.KLSLGKSGGEDTDFFT.....GMHCA.....GG.....TI.....	201
pslC	CFSSDSF.....SAYRSDA....LAAV.GDF.PE..DVGISEDAYVAA.....RLLQA.....GY.....AV.....	197
gelL	TVTANLF.....VMRADFE.....RVGE.FR.....TGVSEDMEWCH.....RAIAK.....GL.....TI.....	189
dpsL	TVTANLF.....VMRADFE.....RVGG.FR.....TGVSEDLEWCH.....RAIAS.....GL.....TI.....	189
spsL	TVTANLF.....VMRADFE.....RVGG.FR.....TGVSEDLEWCH.....RAIAT.....GL.....AI.....	189
sleU	ETGFLKP.....VIRRAFL.....DKHA.LRY.DE..ALRLGEDYELYV.....RALAA.....GA.....RY.....	206
exoU	EIGFLKP.....LMRRAFL.....DQHG.LRY.NE..TLRLGEDYDLYA.....RALAN.....GA.....RY.....	207
sleF	NFGYMKP.....MFRRDFL.....NNEA.LRF.RE..DIRIGEDYILLA.....SALAA.....GG.....LC.....	210
exoO	NFGYMKP.....IFERRFL.....ENQQ.LRF.DE..ALRIGEDYILLA.....SALAC.....GG.....RC.....	209
consensus		

Protein	Sequence	Score
neuB	NIVGSRSLSMNL.SAGTTLLWEHIEA.....	356
gumD	SIVGPRPHAAQHNT..H.YEKLINHYMQ.....	420
gelB	SVVGPRPHALGSRAADHYFWEIDERYWH.....	407
dpsB	SVVGPRPHALGSRAADHLFWEIDERYWH.....	407
spsB	SVVGPRPHALGSRAANHFLWEIDERYWH.....	407
crdS	654
bcsBIKGCAD.PTNGLQWASVSEH.SQLQITTIPLPPRR..QLARLPQ..PFFDKTVRQKVVIPFVLAQTFDPEVLKASGIIASWFGQQTDFR.G.VN.....F...	282
bcsAI	745
bcsABII-ARDCND.LFNEILWARISDM.SRITLTTVRITPER..KLSRLPA..PFFDPNQRSTLRVPVVLDPATGDRGALRAAGLVASWFGRIADFR.K.LS.....F...	1000
pslF	395
gumI	349
pelF	507
pslI	367
gelK	348
dpsK	348
spsK	352
gumH	380
gumM	263
hasAVYQSTAK.....CITDVPDK.....MSTYLKQQNRWNKSFFRESII.....SVKKIM..N.....NPFVALWLTILEVS...	329
sleDTYYPRAS.....VMPLFKQYLAYGRGRAKNLLK.....HRSIPKIRQ.....MIPLAVLPV...F...	261
exoAVYYPRAK.....LVPLFWQYFYGYGRGRAKNFLK.....HRAMPGLRQ.....MLPLAVAPI...A...	261
icaAKYEPRAL.....CWMLVPET.....IGGLWKQRVRWAQGGHEVLLR.....DFWPTI..K.....TKKLSLYIL.....	293
pgaCFYEPRAL.....CWILMPET.....LKGLWKQRLRWAQGGGAEVFLK.....NMTRLW..R.....KENFRMWPL.....	322
sleCDLAAIYNEVQFTWAIDFFEEGQNSSWLLPN.....RLYEGCLYGTLPAL.....AGTE.....	311
exoLDLAEIYGEVHFTWAIDFFEEGQNSAWLLPN.....RLYEGCRHGRIPIAM.....KGTE.....	313
alg8FYVPDAAINT...VEHPPEKSFIKASR.....KLMYRWYGNLNRQNSR.....ALKLGARRLGWFTMLVLFDQRVSMWTSLLGLVVA	384
pmHASKKLGIQKKNHVFVVVN..Q..SLN.....RQGITYYNYDEFDDL.....ESRK...YIF...NKTAEQEEIDI...	699
epsHSYV.....KT..PLYHYRIHLSSI.....VQR...YQKKLFESGLALYETNAAF...	240
epsJKML.....DE..GLYIYRENPNSL.....TEIP...YKPAMDEHLQKQYQAKIAF...	241
dpsQLVDPSVKVVHNTG..SGQSMSQNRLMY.....LTTGRMHYARKHFGALGTL.....ATGCALWL.IAAK...	269
gelQLVDPGVAVVHDAG..SGHSLSSSRIMF.....MTTGRMHYARKHFTKGGAL.....VTGWAIWL.AALK...	269
spsQLVDPAVGVVHDTG..GGHSLSPTRVLF.....LTTGRMHYARKHFGHVAV.....VTGWALWA.NAAK...	269
pslHSVCGYALPA..EWAQRWSDPRIEQGFVPDLLQLQSSSSVFLAALRHG.GGSKLKVL.....EALAAGLP...LAS..TAQGVSGLE.LRDG...	337
sleWLLCDDAGAMRGMGVNIFHSIDNTSPEFLRQQ...FNT...WVALDTLEGRFSRRP.....ADVASIAS...YKN..TARKQALWS.QAGN...	291
exoWVLCDAAGAVRGEGLNIFHSIDNDSPQFLKQQ...FNT...WVALDTLEGRYRNRP.....KAMEAIRS...YKH..TARRQALWS.QARR...	283
sleEVFAEDAV.....LSEPVPENRASFL.....WLAKRRFRSGQ.....THGRVLAE.KKPG...	251
exoMAFSPEAW.....VHEPVPENRASLA.....WLAKRRFRSGQ.....THGRLLAE.KAHG...	244
pslCRYAASAE.....VYHSHDYRLLEEFRRY...FDIGVFYGRERWIRAAFGGAG.....GE..GKR...YV..LAEIQALRA.AGA...	260
gelLDYAAQAS.....VGHPPRRDW.....EALLV.....KTRRIQRE.LYLF...	222
dpsLNYAPDAS.....VGHPPRPDW.....SALLV.....KTRRIQRE.LYLF...	222
spsLDYAPEAS.....VGHPPRPDW.....ATLLV.....KTRRIQRE.LFLF...	222
sleUKVIRHCG.....YGAIVRGNSLSGRHRT...EDLRLLYEADRAILAGCRLSA.....EETAILR.....EH..EKHIRAKFE.LRHF...	272
exoUKIIHSCG.....YAAVVRGNSLSGSHRT...IDLKRLYEADRAILAGSRLSS.....DAEA AVR.....RH..ERHIRDRYE.LRHF...	273
sleFVIEPKPG.....YIYNIREGSISRVLRL...HHVEAMMRADEEFLSHYTLLP...AA..MDA.....QQ...ARARSLRL.AHNF...	273
exoOAVEPSAG.....YIYHIREGSISRVLRL...DHIDAMIAADEAFLRRYALDG.....LA..QKM.....QH...RRMRGFRE.ARSF...	272
consensus		

logo

neuBRHYVKPGITGWAQVNGFRGETPELRTMKKRIQYDLDYIRRWLSLWDIRIIV	356
gumDRHTLKPGMTGLAQVRGFRGATDRRIDLTNRLQANMEYIDGWDIWRDITILF	471
gelBRHTLKPGMTGLAQVRGFRGATDRRIDLTNRLQANMEYIDGWDIWRDITILF	458
dpsBRHTLKPGMTGLAQVRGFRGATDRRIDLTNRLQADMEYIDGWDIWRDITILF	458
spsBRHTLKPGMTGLAQIRGFRGATDRRVDLTNRLQADMEYIDGWDIWRDVTILF	458
crdSLMEVANPSDPNGTVLLV.....TGRDRDEVITASKGIGF	654
bcsBIPVFSTIPQTGNAIVVGVADELPAALGRPSVSGPT.....LMEVANPSDPNGTVLLV.....TGRDRDEVITASKGIGF	350
bcsAIPVSTTIPASGNAVEVGVNLPVDAEGGRP..AGPM.....LAEVANPNDRWGTVLVV.....TGRTAQEVEVAARALVF	745
bcsABII-APVSTTIPASGNAVEVGVNLPVDAEGGRP..AGPM.....LAEVANPNDRWGTVLVV.....TGRTAQEVEVAARALVF	1066
pslF	395
gumI	349
pelF	507
pslI	367
gelK	348
dpsK	348
spsK	352
gumH	380
gumM	263
hasAMFMMMLVYSVVD.....F.....FVGVNREFDWLRVLAFVLVIIF	362
sleDIFALLSLVHWAALIPLGLWIAACVGY.GLWMAIG.....QKNPYGPLAA.....FSAMVMHLAWSTGFWLELLKF	325
exoAFGALLAIVNWMAVVPVGVWAAACLG.GVWMAIG.....QRNPYGPLAA.....VAAMVMHLAWSAGFWRELLDF	325
icaAMFEQIASITWVYIV.....LCYLSFLVITANI.....LDYTYL..K.....YSFSIFFSSFTMTFINIIQF	348
pgaCFFEYCLTTIWAF.....TCLVGFIIYAVQL.....AGVPLNIE.L.....THIAATHTAGILLCTLCLLQF	377
sleCTARFIEKRNIGFVLQAGADDL.....AALFNRMTPTQYADAFHT.....LSATDRKQWLTDRDDCRL	370
exoLTARFLSVRSIGLVLEGADVESL.....ATVLGPLTPNCYADAAER.....ISRCNPGSWVFDRTDCEAL	372
alg8	ILASLKYSIAFLLVYLLWIGLTRLVLTLLLSLSGHRIGPAY...PLILYYNQIVGALVKIYVFFRLDRQSWTR...QPT...KLERGLASQFQRFNAWSSRAMTF	480
pmHASLKDIKIIQNKDAKIAV..SIFYPNTLNLVKKLNNIIEYNKNIFVIVLHVDKNHLTPDIKKEILAFYH...KH...QVNILLNNDISYYTSNRLIK	787
epsHLQE.....NNKLEEYRKELDTFIV...LH...SSICMLNEWKT.SGSRRLFE	280
epsJYNH.....YGLAGACKEDLNVYIC...RH...QLP	265
dpsQYTLVGA.....ALW.....RLSPRTGTR.YKELS.....NGWRAVFSNPGRWWSGYPR	311
gelQYQLLGS.....LLA.....PLLPKKRER.LTAVS.....RAWAPVVRERRRRWWAGYPA	311
spsQYVVIGG.....LLG.....RLSPRRAAR.WNALR.....DAWSIVFGQPRRWWHGWDRD	311
pslHEDYLGGESAEQLANAVVRLQLDPAQARAL.....GENGRAY.VRRAH.....DWSVAASQ	386
sleWLKRRK...APEFGLLLKWAMRDPALLRAA.....FELGAGKIVR.SR	329
exoWIKRRK...LPQFDLLARWLWRDPRLIGSA.....AELAVGKLSR	319
sleEARRVVQVVKAGSKVLYC.....ALF.....AALSGFNAVR.RNRYALRGALHMGSMGAFGVRE	304
exoMLRQAWNIALAGAKSGFC.....ATA.....AVLCFPASAAR.RNRFALRAVLHAGVISGLLGLKE	297
pslCLYRVPEIALRSAFKLLGYRLGQ.....LE.....RHLPV...AL.KRRI.S.....MFPGYWK	303
gelLYKERPQ...GRLRWLARSALQPALLPSDA.....AKILRTSTTQ.GARAKA.....LLTACRLRFWKSG.VG	279
dpsLNIERPQ...GRLRWLVRSAQPAMIPQDV.....AKILRTPGTR.GARLAA.....VTTLVRLRLWRGG.AG	279
spsLNIERPQ...GRLRWLARSALQPAMIPQDV.....AKILRTPGTR.GSRIAA.....VGTLVRLRFWRAG.AG	279
sleULDTKKQ...KGVSGALSHALARLPALPAIT.....RGIWSDKTAR.FRKAAP...VRD.....VRYLLDGTP	327
exoULDLKNQ...QGFGRAFGYALHTHPALPAII.....GGILADKTER.FRPSGS...PAPVALGGKGDVRYLLETLA	336
sleFLTLVENIKRRSVLGALKTTIRDPAVLG.....HLRMPPIAVR.LRRLRDAV.FAPAANTG...VKRQIS	331
exoOLVLVEQLKKRSLAGALKTALADPFALR.....HLSMPIAAR.LRRLAARF.VHPSSSHA...PRAAPVTA	334
consensus		

logo

			
neuB	356
gumD	LTA.....	474
gelB	CTL.....	461
dpsB	CTL.....	461
spsB	CTL.....	461
crdS	654
bcsBI	GSS.....ALPVASRMDVAPIDVAPRLANDAP.....	SFIPTSRPVRLGELVPVSALQGEQYTPGVLSVPFRVSPDLYTWRDRPYKLNVRFRAPDG	436
bcsAI	745
bcsABII-A	SPD.....TLGGVASKVVSVDVSLETRHPYDAP.....	AFVPTDRPVRFGEVLGAADLQGGGFAPAGMTLPFHLPPDLYTWRGRPFLLNMWVRAPGG	1152
pslF	395
gumI	349
pelF	507
pslI	367
gelK	348
dpsK	348
spsK	352
gumH	380
gumM	263
hasA	IVALCRNIHYMLKHPLSFLLSPFYGVL.....	HLFVLQPLKL.....YSLFTIRNA.....DWGTR.....KKLL.....	417
sleD	RG.....RKAVS.....	332
exoA	RR.....RVA.....	330
icaA	TVALFIDSRYEKKNIVGLIFLSWYPTL.....	YWVINAAVVIMAFPKALKRKKGGYA.....TWSSP.....DRGNIQ.R	412
pgaC	IVSLMIENRYEHNLTSSLFWIIFPVI.....	FWMLSLATTLVSFTRVMLMPKKQRA.....RWVSP.....DRGILR.G	441
sleC	.VQQLS...SLAKSASGHAREA.....QF...SPV.....	393
exoL	.VRQLA...TLTLQAPQTVPVV.....AM...AGSSHKEGG.....	401
alg8SAASIFVAV.....	489
pmHAS	TEAHLNINKLSQLNLNCEYIIFDNHDSLFVKND SYAYMKKYDVGMNFSALTHDWIEKINAH..	PPFKKLIKTYFNDND.....LKSMN.....VKGASQ.G	876
epsHKLRNVGVICADPVFQESLSKTGT.....	APFDA.....KRSCLLLMAYRM...IPFVAMASAVYQR.....VIEYKMR.....NRG.....	344
epsJMLLANACASPNSPKDIKKKIR.....	QI.....LSYDMVRQAVRH...TPFQHEKLLRGERLVLALCKWRLTFLIKLFFE.....QRGTMK.G	339
dpsQ	R.....	312
gelQ	KK.....	313
spsQ	HVRT.....	315
pslH	LEQVY...AGLAEGAPACA.....	402
sleW	329
exoW	319
sleE	IRQYGAVEAT.....	314
exoM	IEQYGAREVT.SA.....	309
pslC	303
gelL	LLQLLGRPA.....	288
dpsL	LLQLLGRDI.....	288
spsL	LLQLLGRPI.....	288
sleU	VS.....	329
exoU	VDQP.....QK.....	342
sleF	331
exoO	ERSPLGNDPRISKG.....	348
consensus			

logo

			
neuB		356
gumDVRVLGQKTAY.....		484
gelBRVIVH.SNAF.....		470
dpsBRVIVH.SNAF.....		470
spsBRVIVH.SNAF.....		470
crdS		654
bcsBI	PILDVARSHLDVGIN...NTYLQSYSLRE...QSSVVDQLLRRVGVGTQNAGVEQHTLTIPPWMVFGQDQLQFYFDAAPLAQPGCRPGPSLIHMSVDPDSTIDLSNAYH		539
bcsAI	PVVVDLETSRVDVSLN...NNYLQSYTLSP...PGLWRKWSE...RLVNQHAGAVGHVTALPPWLLFGQNQLQFNFDARPIDRGACRRTPGDIHMSVDSDSLDFRRGYH		745
bcsABII-A	PVVVDLETSRVDVSLN...NNYLQSYTLSP...PGLWRKWSE...RLVNQHAGAVGHVTALPPWLLFGQNQLQFNFDARPIDRGACRRTPGDIHMSVDSDSLDFRRGYH		1252
pslF		395
gumI		349
pelF		507
pslI		367
gelK		348
dpsK		348
spsK		352
gumH		380
gumM		263
hasA		417
sleD		332
exoA		330
icaA		412
pgaC		441
sleC		393
exoL	.FL.....		403
alg8LLTIV.....		494
pmHAS	MFMTYALAHELLTIIKEVITSCQSIDSVPYNTEDIWFQFALLILEKKTGHVFNKTSTLTYPWERKLQWTNEQIES...AKRGENIPVNKFIINSITL.....		972
epsH		344
epsJ	SAKQA.....		344
dpsQ		312
gelQ		313
spsQ		315
pslH		402
sleW		329
exoW		319
sleE		314
exoM		309
pslC		303
gelL		288
dpsL		288
spsL		288
sleU		329
exoU		342
sleF		331
exoO		348
consensus			

logo



neuB	356
gumD	484
gelB	470
dpsB	470
spsB	470
crdS	654
bcsBI	ITRMPNLAYMASAGYPFTTYADLSRSAVVLPDHPNGTVVVSAYLDLMGFMGATTWYPVSGVDIVSADHVSDVADRNLIVLSTL..SNSADVSALLANSAYQISDGRLHMGL	647
bcsAI	745
bcsABII-A	FAEMPNLSYFAEAAFPFSRMADLSETTVVLPDHPDTGTTGAFLDLMGFFGASTWYPAAGVTVMGADEVAHTPPKGDIVVLGTAAQLGGAASGLLARSPYVIHDRHITVGQ	1362
pslF	395
gumI	349
pelF	507
pslI	367
gelK	348
dpsK	348
spsK	352
gumH	380
gumM	263
hasA	417
sleD	332
exoA	330
icaA	412
pgaC	441
sleC	393
exoL	403
alg8	494
pmHAS	972
epsH	344
epsJ	344
dpsQ	312
gelQ	313
spsQ	315
pslH	402
sleW	329
exoW	319
sleE	314
exoM	309
pslC	303
gelL	288
dpsL	288
spsL	288
sleU	329
exoU	342
sleF	331
exoO	348
consensus		

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neuB	356
gumD	484
gelB	470
dpsB	470
spsB	470
crdS	654
bcsBI	RSTLSGVWNIFQDPMSVMSNTHPTEVETTLSGGVGAMVEAESPLASGRTVLALLSGDGQGLDNLVQILGQRKNQAKVQGDVLVAHGDDLTSYRSSPLYTVGTVPLWLIPD	757
bcsAI	745
bcsABII-A	RMGLQGIWYLFQDHDHAGLKDGVTANLNAPIAEAGVLLAAQSPYDSQRSVVAFTGDTPERIHDLVLSLRNKGDLPSLQGDVLKNGDRFTSYRTAPVYTVGSLPLWLRLD	1472
pslF	395
gumI	349
pelF	507
pslI	367
gelK	348
dpsK	348
spsK	352
gumH	380
gumM	263
hasA	417
sleD	332
exoA	330
icaA	412
pgaC	441
sleC	393
exoL	403
alg8	494
pmHAS	972
epsH	344
epsJ	344
dpsQ	312
gelQ	313
spsQ	315
pslH	402
sleW	329
exoW	319
sleE	314
exoM	309
pslC	303
gelL	288
dpsL	288
spsL	288
sleU	329
exoU	342
sleF	331
exoO	348
consensus		

logo

neuB	356
gumD	484
gelB	470
dpsB	470
spsB	470
crdS	654
bcsBI	WYMHNHPPFRVIVVGLVGCLLVVAVLV...RALFRHAMFRRRQLQEERQKS	804
bcsAI	745
bcsABII-A	WFLGHHPSALYLAGLAGAGLAALGVWAWLRGWSRKRIARDDLTGEL....	1518
pslF	395
gumI	349
pelF	507
pslI	367
gelK	348
dpsK	348
spsK	352
gumH	380
gumM	263
hasA	417
sleD	332
exoA	330
icaA	412
pgaC	441
sleC	393
exoL	403
alg8	494
pmHAS	972
epsH	344
epsJ	344
dpsQ	312
gelQ	313
spsQ	315
pslH	402
sleW	329
exoW	319
sleE	314
exoM	309
pslC	303
gelL	288
dpsL	288
spsL	288
sleU	329
exoU	342
sleF	331
exoO	348
consensus		

 non-conserved
 ≥ 50% conserved