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logo
                    MRI.YVI                      P.Y                    N                P.A..G.LRQ..TALESL.AQ
            Mᵉˢ...ᴿᴵˡ·ᵞᴵᴵᴿᴿᴱᴱᴱ...          ...P.Y...          MᴱᴱᴬᵠLᴿᴬᴴ...          Nˢ...ᴬˢᴬᴾ...ᴬᴬᴾˢᴬᴬᴾ..ᴿᴿˢᴿᴬᴿYᵀ..

sleC        ...........MIHILYLA..........HDL.............SD......PAIRR.......RVLTLLAGGARVT....       31
exoL        ...........MLQILYLA..........QDL.............AD......PAVRR.......RTLTLVAGGARVT....       31
sleD        ......ME.GPGHSGIRTLIVI.......PCL.............NE......AKTIEGL......LV....                 29
exoA        ......MS.SDELTSTSSLIVI.......PCL.............NE......ASHIEAL......IE....                 29
dpsQ        .......MQMLP................                                                            5
gelQ        .......MTDQT................                                                            5
spsQ        .......MEASP................                                                            5
pslH        ........MRILWIL.............PYS..............PW......PTTSGGKTRQYHLLRSLAARGHRITVLLHS       42
sleW        ....MINARGETMARFTVVI........PYY..............QK......QHGVLG......RALASVFAQ.......         36
exoW        ........MAKLTVVI............PYY..............QK......EPGILR......RALASVFAQ.......         28
sleE        MTDN.TVTGTQYLKTVD..IGI.......CTY..............RR......PALVA.....TL.LSLFELD......         38
exoM        ........MPNETLHID..IGV.......CTY..............RR......PELAE.....TL.RSLAAMN......         31
pslC        .........MRCALVI............PTR..............NA......GAHLD......RLLPALAAQ.......         26
gelL        ........MTGPRISVVI..........PHY..............ND......LEGLT......KCLESIDRQ.......         29
dpsL        ........MSTPRISVVI..........PHY..............ND......PQSLR......LCLDALERQ.......         29
spsL        ........MSAPRISVVI..........PHY..............ND......PDSLR......QCLDALQHQ.......         29
sleU        .......MVSGSQPICVII.........AAK..............NA......SDTID......IAIRSALAE.......         31
exoU        ........MTAAAPTDVCIII.......SAK..............NA......ADTIA......RAVASALAE.......         32
sleF        ......MENLTSPPDISFVI........AAY..............NA......ADTIE......AAVQSALDQ.......         33
exoO        ......MNPPAIDKVPDVTFVV......AAY..............NS......ADTIV......RAIESALAQ.......         35
gumD        ........MLLA................DLSS............ATYTTSSPRLLSK..YSAAADLV........             29
gelB        ........MNAFEAQRAFEE........QLRAY..........AAPKQSAMPAFRRS.TVRMILYTE........             40
dpsB        ........MNAFEAQRAFEE........QLRAH..........SRVTPSAAPVWRRS.TLRMVLYTE........             40
spsB        ........MNAFEAQRAFEE........QLRAH..........ARSAPSAAPMLRRS.TIRMILYTE........             40
pslI        .......MRIGLDYRTVG..........................SSPHSGISRQVY.AMEQ..A.......                 28
pslF        .......MRIALLA.PLPPEKNGIADYASHFRNALQGLGIEVATPLAGVAADSANIASRLDSVDWNAFDLVHAELGGGRLGEFI.ALRE..L....  81
gumI        MSASASLPVTRAAAAPRITVLFSTEKPNANT.NPYLTQLYDALP....DAVQPRFFSMRDALLSRYDVLHLHWPEYLLRHPSKMGTLAKQACAALLL..M.........  93
gelK        ...........................MAEATEAAH...............TTGKRLKMCLAASGGGHLRQILDLESVWRE.......  39
dpsK        ...........................MAEANAVDG...............KASKPLKMCLAASGGGHLRQILDLESVWRE.......  39
spsK        ...............MGDG........MAEATVTEA...............KAGKPLKMCLAASGGGHLRQILDLESVWKE.......  43
gumH        ........MKVVHVVRQFHPSIGG.......MEEVVLNVA...........RQHQANSAD.TVEIVTLDRVFTDPSAQLTQ.......  54
gumM        ..................MHGQPAG..............VET.......                                       10
consensus
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logo                      IVVAD SPD T D VRALA            QEGGR
         (sequence logo)

sleC       ..........................LAGFR......RGQNRLA....EIEGV...............VPVVLGET..........ADGQ.....FL   62
exoL       ..........................LAGFR......RGDNPLA....AIDGV...............EPIELGTT..........ADGR.....FA   62
sleD       ...............KFTGAMQGRLFRIVADGGSTDGTRDIVAAFA....AKDER...............VTL.................DGD..     69
exoA       ...............KLRPSLTPLNARVVIADGGSTDGTREIARRLA....TEDPR...............VLF.................DGA..     69
dpsQ       ................TPDVSILVVAFNSTEYIEDCLRGIA....EGAGK...............TPHEVLLI..........DNGD.....       47
gelQ       ................LPHVSVLVVAYHSTDFIRQCVDGIA....AAAPN...............TPYEILMI..........DNGG.....       47
spsQ       ................TPDVSILVVAYHSAPFIGQCIRGIA....AAAQG...............TAHEILLI..........DNGG.....       47
pslH       KQPVSAEDRQALEPFLERLVVLPRRPLRSLSTLLAALFAPYPLLASVNGLS....AELQR...............TATELLRE...........P......  107
sleW       ...........T.........YQDFDLVIVDDESPYPIDQELAELS....QEQKD...............RIL.....................       70
exoW       ...........T.........LEDFHVLVIDDESPYPIADELAGLA....QEERE...............RIT.....................       62
sleE       .........VPE.........GVKVRLIVADNDEEPSAKASVDRLR....ETAPF...............EIT.....................       74
exoM       .........VPE.........RARLRVIVADNDAEPSARALVEGLR....PEMPF...............DIL.....................       67
pslC       .........R..........RQPDSILVVDSRSSDDTVERFRAFG.......AR...............VEV.....................       57
gelL       .........TID.........RGSFEIIVGDNNSPCGIAA.VEA.....VVAGR...............GRV.....................       62
dpsL       .........TIG.........RDAFEIIVGDNNSPCGLAA.VEA.....AVAGR...............ARI.....................       62
spsL       .........TIG.........REAFEIIVGDNNSPCGLAA.VEA.....AVAGR...............ARI.....................       62
sleU       .........P..........E.VGEVVVIDDGSTDTTSDVAHAAD....DGTGR...............LRV.....................       64
exoU       .........P..........E.AAEVVVIDDGSTDDSASVARAAD....DGTGR...............LNV.....................       65
sleF       .........Q..........GVTLEVIVVDDRSADDTIPFVEAIA....AIDPR...............VRL.....................       67
exoO       .........E..........GVTVEVVVDDCSADATPALVA.A....IPDPR...............VRL.....................       67
gumD       ........LR.......VFDLTMVVASGLIAYRIVFGTWVPAAPYRVAI...A.......................gumTT                   66
gelB       ........LL.......LIDSIAILASYFYFAACMRDSNWLSLAGVNVGI...FLLPITL...........GT..............AIAS         87
dpsB       ........LL.......LLDSLSILAGFHVAAGTRDGNWLSLAGINVGV...FLLPIAL...........GT..............ALAS         87
spsB       ........LL.......LLDSIAILLGFYIAACSRDGNWLSLAGVNVGI...FLLPITL...........GT..............ALAS         87
pslI       .........LE......SLPGTQVTRFTV..APLDDPLRQRAVCPPWGCPRTAMHQPHQ....RLRFEAGFLPRAL.....RE....QDIDLYI.....ST  94
pslF       .........RK......RFPRLPLSATVHDP...ERMVWRRE.RLPWPLNLLERLPSPL....PQAAVVLADPLTL.....RE....ERAVAQGLTRLVTL 150
gumI       .........KL......QLTGTPVVRTLHNLAPHEDRGWRERALLRWIDQLTR.......................RW....IRIN........       137
gelK       .........HD......YFFVTEDTAL..........GRSLA.......EKHPVELVGHYALGQARLGHPFKMLGGALRNLRQSLAIVRRHKPDVVIS    105
dpsK       .........HD......YFFVTEDTAL..........GRSLA.......EKHPVELVEHYALGQAKLGHPLRMLGGAWRNLRQSLSILRRHKPDVVIS    105
spsK       .........HD......YFFVTEDTAL..........GRSLA.......EKHSVALVDHYALGQAKLGHPLRMLGGAWRNLRQSLSIIRKHKPDVVIS    109
gumH       .........HE......VHQGLPITRI..........GYRGS.......SRYPIAPS...VLGAIRSADVVHLHGIDFFYDYLALTKPLHGKPMVVST    117
gumM       ................................A...........TVSPATPA...Q.........................GVVIPLGGFPVLSTT     35
consensus                           *              *
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logo
        [sequence logo]

sleC   QRMAAVA.....KASLSLGKV............................LNG..I...............PAPDVVLARNLEMLAL..........AKRAM......SIYSG   108
exoL   QRIGAVA.....RACLSLQRQ............................LGH..V...............RKPDVIIARNLEMLAV..........ARRAV......AFFGG   108
sleD   ...................................................LAN.PK...............RIQSAGINLAVA.....................TFGED    91
exoA   ...................................................LDN.PK...............RIQSAAVNRAVA......................ELGAG    91
dpsQ   GRTEALV.....RQRFHHVRI............................VPSEGN...............IGFGAGNNRLAA......................QAA..    84
gelQ   GDTEAFV.....RAELPQVRI............................VPSEGN...............IGFGAGNNRCAA......................HAR..    84
spsQ   GDTEAVV.....RAEFPHVRI............................VPSEGN...............IGFGAGNNRCAA......................HAR..    84
pslH   ...............WDVVQ.............................VEHSYS...............FQPYERPLRDAGQPFVLTEHNVESSLGAATYD......RLP..   153
sleW   ...............................................VIKQAN...............AGPG..GARNTG.....................LD.....NVPDG    93
exoW   ...............................................VIRQPN...............GGPG..GARNTG.....................LD.....NVPAD    85
sleE   ...............................................YVHCPK...............SNIS..IARNAC.....................LS.....ECK.    95
exoM   ...............................................YVHCPH...............SNIS..IARNCC.....................LD.....NST.    88
pslC   ...............................................IEP.AS...............FNHG..GTRRWA.....................SQ.....QVE.    77
gelL   ...............................................VPV.LE...............KGAG..PARNGA....................AA.....AAR.    82
dpsL   ...............................................VTI.LE...............KGAG..PARNGA....................AA.....AAR.    82
spsL   ...............................................VTI.LE...............KGAG..PARNGA....................AA.....EAQ.    82
sleU   ...............................................VRFDVN...............RGPS..AARNHA....................IS.....ISS.    85
exoU   ...............................................VRFEEN...............RGPA..AARNHA....................IA.....ISH.    86
sleF   ...............................................LALEEN...............RGPG..GARNAG....................IE.....AAT.    88
exoO   ...............................................IALDRN...............RGPG..GARNAG....................IG.....AAR.    88
gumD   LLYSVICFALFPLYRSWRGRGLLSELMVLGGAFGGVFALFAVHALIVQVGE.........QVS....RG.......WVGLWFVGG...LVSLVAARTLLRGFLNHLRTQG   153
gelB   GTYSLESLRHP..........IS......GVKNILSAFLFSILIVLLGS..YLLTTELPLS....RI...QLGAGALMT...VVLLMA...GRLVFRRHVRAMT   160
dpsB   GTYSLNCLRYP..........VS......GVKSIFSAFFFSIFVVLLGS..YLLTAELPLS....RV...QLAEGAILS...LVLLMV...GRLMFRRHVRAVT   160
spsB   GTYSLSCLRYP..........VS......GVKSIFSAFFFSVFIVLLGS..YLLTAELPLS....RL...QLGEGVLLA...LSLVTI...CRLGFRWHVRALT   160
pslI   FNMG.....LPLPPR.................PPGV.....RYALLIHDLFQ..ITLKN.................YHANR.L...KALVYRV.    137
pslF   TGLGGECLARRMRLP................PGRV.....E..VINHGNL..EIATVPLP.................SLDTLR.LLY.FGFIYRGKG   203
gumI   ......ATTPVR................PPFT.....D..TILHGHYRDWFATMEQS...................TTLPGR.LLH.FGLIRPYKG   183
gelK   TGAGAVYF..................................TALFA...............................KLFGAKFIH.....IESFAR.FDHPSAFGKMVKG   146
dpsK   TGAGAVYF..................................TALLA...............................KLSGAKFVH.....IESFAR.FDHPSAFGKMVKG   146
spsK   TGAGAVYF..................................TALLA...............................KLSGAKFVH.....IESFAR.FDHPSAFGKMVKG   150
gumH   HG....GF.............................FHTAYASRMKQIWFQTLTR.......TSALAYARVIATSEND......GDLFAK.VVAPSRLRVIENG   175
gumM   QEAFALDL.............................FHALAAHQPRRVFFANTNFIVQCQALRARMQAPAVRIVNDGIG......MDLAAR.LIHGRRFAGNLNG   105
consensus                                                                             *
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         [sequence logo]

sleC  RPALVYECLDIH.................RLLLHEGKPGQMLNAAQRYFA.RDAKLLVTSSPAFVE.............HYFKPVSG.....L..........DLPV  169
exoL  TVPIVYECLDIH.................RLMLRKDIVGRMLRAAESQLG.KDARLLITSSPAFIE.............HYFRPLSG.....I..........GAPP  169
sleD  FDYLI..RIDAH.................GDYPDDYCQRLIEDAERTGA.DSVVVAMDTVGHGLF.............QKAT................  140
exoA  SDYLI..RIDAH.................GTYPDDYCERLVEDALATGA.DSVVVAMQTVGFSTF.............QKAT................  140
dpsQ  GPLLL..LVNPD.................AIPQPGAIDQLVTFAKQHPE.AAAWG.....GRSYS.............PSGD.....L.EPAN....FMSLPT  139
gelQ  GQYMM..LVNPD.................AVPQPGALDRLVAFARAHPE.AAAWG.....GRSYD.............TAGK.....L.DPGN....FLPLPT  139
spsQ  APRLL..LVNPD.................AIPRPGAIDLLVAFAKAHPD.AAAWG.....GRSYF.............PNGQ.....L.DHAN....FLPLPT  139
pslH  GWALP..FVRYD.................QWRYRRWERRVMSQAAAV......VA.....VTE.............KDARQLGA.....M.........LGRPV  200
sleW  TDYVA..FLDSD.................DIWTPDHLRNAAFALTTYGG.ECYWASMQASDEFYY.............HFAISELE.....K.NEGA....ARLSEK  157
exoW  SDFVA..FLDSD.................DVWTPDHLLNAYQSMTRFDA.DCYWASITGGDAFYY.............HFGVADLE.....K.SETV....TRLSES  149
sleE  ADYLA..FIDDD.................ETAPPHWLAALLEKADETGA.ETVLG....PVTAVY.............RDNAPGW......M.KRGD....FH..ST  152
exoM  GDFLA..FLDDD.................ETVSGDWLTRLLETARTTGA.AAVLG....PVRAHY.............GPTAPRW......M.RSGD....FH..ST  145
pslC  ADALI..YLTQD.................AIPASPDSFANLLDEL.YAEA.DIGVA....YGRQLP.............HPGAGLLG.....A.QARR....FNYPPE  137
gelL  GEVLA..FTDSD.................CVVAPGWLAGGVAQVAPG...RFVGG....HMFVIK.............PEGPLSGA.........E...AL..EL  134
dpsL  GEILA..FTDSD.................CVVEPGWLAGGTTRVAPG...RFIGG....HMYVRK.............PEGPPNGA.........E...AL..EM  134
spsL  GEILA..FTDSD.................CVVEPGWLAGGVAHVAPG...RFVGG....HMYVLK.............PEGRLTGA.........E...AL..EM  134
sleU  APLIS..ILDAD.................DFFFHGRFAAMLADDDW....DLVAD....NIAFIQ.............QSVPGASS.....M.QPAR....FE..PQ  140
exoU  SPLIG..VLDAD.................DFFFPGRLGQLLSQDGW....DFIAD....NIAFID.............AAQAATAH.....G.RIDR....FA..PT  141
sleF  GRWIA..VLDSD.................DVIRPERSACMMCRAEAANA.DIAVD....NLDVVY.............TDGRPMET.....M.FPEE....FL..EE  146
exoO  GRWIA..VLDSD.................DTVRPDRLRRMIERADAAGA.QIAVD....NLDVVS.............LDGRSLR......M.FSEA....EL..AR  145
gumD  VDV...QRVVVVGLRHPVMK.......ISHYLSRNPWVGMNMVGYFRTPY.DLAVA....EQRQGLPCLGDPDELIEYLKNNQVEQVWISLPLGERDHIKQLLQRLDRYP  248
gelB  GDKLLDELVIIDGVSLDLASDAVALDARIINLSPNPRDPQMLHR.LGT....TVIG....FDRVVVACT.............EEHRAVWALLLKGMNIKGE.........  239
dpsB  GGRLLDELVIIDGVSLDVAGNAVALDARIINLSPNPRDPQMLHR.LGT....TVIG....FDRVIVACT.............KEHRAVWALLLKGMNIKGE.........  239
spsB  RGTLLDELVIVDGVALEVASGAVALDARIINLTPNPRDPQMLHR.LGT....TVVG....FDRVVVACT.............EEHRAVWALLLKGMNIKGE.........  239
pslI  ...............SD.YLSIAYALRVADRVWTPSQYSADEAVRLFPGVAG....KVRVLPNQVDGFAGE.......P.....A..........  190
pslF  IEDLLE..........ALAD.LFAS.......APEM.........RQ....RVRLT.LAGGTAA.......E....M..........  237
gumI  VEVLLD..........VMRD.VQDPRLSLRIVGNPATPQM.........RT....LVETA..CAQD.............A..........  224
gelK  IATISI..........VQS...P.........ALKQIWPDAEL.......FD....PFRM.................  173
dpsK  IATVTI..........VQS...A.........ALKETWPDAEL.......FD....PFRL.................  173
spsK  IATVTI..........VQS...A.........ALKQTWPDAEL.......FD....PFRL.................  177
gumH  VDVEKY..........AGQ.............GA.....RA....PGRT.................  192
gumM  TDLIPY..........LCR.............EA.....AQ....PLKF.................  122

consensus      *        *
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logo
                    LP F A L RR       G           G P Y R  F       R F DE  L        LL S    ED DLF         R RA  A R  YA   P
              P  V  VF V E N L N      EL A    TP  Y  R  S   VYR BY  L  AE  F        D L PAYEW         P  P       Y   L G A

sleC    LLQENKVLALDDTIAAT..PR....PRAPA..PGEP.WKIGWFGALRCRKSLEILAEFARRMEGRVEIILRGRPAYSEFADFDGFVA.AAPH..VHFHGPYKNPEDLAA.    266
exoL    MLLENKVLEIDGTVERRTASP....AKSPP..PGAP.WKIGWFGALRCRRSLALLAEFSRKMEGRFEIVLRGRPAYSEFDDFDGFVR.NEPF..MRFEGAYRNPEDLAE.    268
sleD    ......AIAQNSKLGNG.GSK....HREGA..KGHW.IDHGHHALMRIAA.........FDAVGGYDESFS....HN..EDAELDF......RLRKSGFRIWMTD....    210
exoA    ......AFAQNSKLGNG.GSK....HRTGA..VGHW.AEHGHHALMRIEA.........FKAVGGYDESFS....HN..EDAELDY......RLGKAGYRIWMTD....    210
dpsQ    PADFLTAIFNARALRSG.GLQ....EGATT..PGAVEVLNGGFMMVRTDV.........WQAIGGFDESFF...LYS..EEIDLFQ......RIRTLGHKVLVDP...    217
gelQ    PMDFVASIVSARRLRRG.GLA....EDATE..PGPVDVLNGGFMMVRADV.........WREIGGFDESFF...LYS..EEVDMFK......RIRERGYAVLVDP...    217
spsQ    VRDFVVSIFSSSPMRRG.GLP....ADATA..PGPVEVLNGGFMMVDARV.........WREIDGFDEGFF...LYS..EEIDLFQ......RIRARGYSVLVDP...    217
pslH    PVVVNGVDCE................HFATA..RPTPEAQRVLFL.............GNY..EYAP.......NV.DAVEWMLDEILPRVWAHCPEARMSVCG...    263
sleW    PLVIELPDLASVMLRNW.......SFLHL..SCMV.IGRPLF............EKIRFDPALR...LAA..EDVLFFC........DSILASKRTLLCD...    222
exoW    PLVVELPELQDVMLKNW.......SFLHM..SCMV.IGRKLF............EKVRFEATLK...LAA..EDVLFFC........DCVLASKRVVLCD...    214
sleE    .....VPVWVNGEIITG.Y.......TCNT.LLRMEAP........SVKGRRFALALG..QSGG..EDTHFFS......HLHAAGGRIVFAE...    212
exoM    ....LPVWAKGEIRTG.Y.......TCNA.LLRRDAA........SLLGRRFKLSLG..KSGG..EDTDFFT......GMHCAGGTIAFSP...    205
pslC    SRSKRLADASELGIKT..........CFS.SDSF.SAYRSDA.......LAAVGDFPE..D..VIGS.EDAYVAA......RLLQAGYAVRYAA...    201
gelL    ....AVAFDNEGYVRR.A.....QYTVT.ANLF.VMRADFE........RVGEFR......TGVS.EDMEWCH......RAIAKGLTIDYAA...    193
dpsL    ....ALAFDNEGYVRR.T.....QFTVT.ANLF.VMRADFE........RVGGFR......VGVS.EDMEWCH......RAIASGLTINYAP...    193
spsL    ....ALAFDNEGYVRR.A.....KFTVT.ANLF.VMRADFE........RVGGFR......TGVS.EDLEWCH......RAIATGLAIDYAP...    193
sleU    ARFLSLTEFVEGNISRP.GVE....RGETG.FLKP.VIRRAFL........DKHALRYDE..A..LRLG.EDYELYV......RALAAGARYKVIR.    210
exoU    PRLIDLVGFVEGNISRR.GVR....RGEIG.FLKP.LMRRAFL........DQHGLRYNE..T..LRLG.EDYDLYA......RALANGARYKIIH.    211
sleF    RPVLTLEDFISSNILFR.S.....TFNFG.YMKP.MFRRDFL........NNEALRFRE..D..IRIG.EDYILLA......SALAAGGLCVIEP...    214
exoO    LPQLTLPAFIESNVLFR.S.....EHNFG.YMKP.IFERRFL........ENQQLRFDE..A..LRIG.EDYILLA......SALACGGRCAVEP....    213
gumD    INVKLVPDLFDFGLLNQSAEQIGSVPVINLRQGGVD..RDNYF..........VVAK.A....LQDKILAVI...............ALMGLWPLMLA    314
gelB    ...ILVPQFNALGAIGVDAYD.GKDTLVVSQGPLS..MPN...........RAKK..R...ALDLLITVP...............AVLALAPLMIL    298
dpsB    ...ILVPQFNALGAIGVDAFD.GKDTLVVSQGPLN..MPN...........RAKK..R...ALDLAITVP...............AVLALAPLMIL    298
spsB    ...ILVPQFNALGAIGVDSYE.GKDTLVVSQGPLN..MPN...........RAKK..R...ALDLLITVP...............AVLALAPLMIV    298
pslI    .......DLSA.............RGLP..PRYWL.........LVGT..R...E..LRKNVPWFVSA.....WTRARAQAPGVPPLVLV    237
pslF    ......AFGA.............GGN...YLYQL.........KAQI..A...ELGLADAIDWNLNL...........AAADIPRTIQA    279
gumI    .......RISA.................L.........LAYV..E...E...................PVLAREVSA    244
gelK    ......LD.............TPRP..PKQAL.........TFAT...............VGATLPFPRLVQA    201
dpsK    ......LD.............TPRP..PKQAL.........IFAT...............VGATLPFPRLVQA    201
spsK    ......LD.............TPRP..PKQAL.........TFAT...............VGATLPFPRLVQA    205
gumH    .......MLY.............FGRW.SVNKG.........LIET..L...EL..LQA...............ALTRDPQWRLIIA    227
gumM    .......FLL.............GGRP..GVGKT.........AAAT..L...TGTLGQQV...............VGMCDGYGEFAAA    160
consensus                                   *                 *              **         *
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logo
          AG V                QYGH L      R              S  L                    R ARL   A   GRG  L   V  A  G R    AYGR  RE      E    PQ   E
     V   I KLE  EPDCV L KE     AQ  H YS           N  F  EL LLF  R    Y    F F    F  G         L     A R  R     T  P I W    F  L  PQ  VLEGA

sleC    ........IYNEVQF.TWAIDFFEEG.........QNSSWLLP.........NRLYEGCLYGTLPIALAG.........TETARFIE........K.RNIGFVLQQAGA        330
exoL    ........IYGEVHF.TWAIDFFEEG.........QNSAWLLP.........NRLYEGCRHGRIPIAMKG.........TETARFLS........V.RSIGLVLEGADV        332
sleD    ........KTRM.........TYYPR.........ASVMPLFKQY.........LAYGRGRAKNLL.........KH....RSIPKIRQM....IPLAVLPVFIF           263
exoA    ........KTSM.........VYYPR.........AKLVPLFWQY.........FGYGRGRAKNFL.........KH....RAMPGLRQM....LPLAVAPIAFG           263
dpsQ    ........SVKVVHN.TG..SGQSMS.........QNRLMY.......LTTGRMHYARKHFGALGTL.............ATGCALWLIAAKYT.LVGA.......           275
gelQ    ........GVAVVHD.AG..SGHSLS.........SSRIMF.......MTTGRMHYARKHFTKGGAL.............VTGWAIWLAALKYQ.LLGS.......           275
spsQ    ........AVGVVHD.TG..GGHSLS.........PTRVLF.......LTTGRMHYARKHFGHVGAV.............VTGWALWANAAKYV.VIGG.......           275
pslH    ........YALPA...EWAQRWSDPR.........IEWQGFVPDLLQLQSSSSVFLAALRHG.GGSKLKVLEALAAGLPLASTAQGVSGLELRDGED.YLGGESAEQLA.       350
sleW    ........DAGAMRG.MGVNIFHSID.........NTSPEFLRQQ....FNT...WVALDTLEGRFSRRP.ADVASIASYKNTARKQALWSQAGNLK.RRK...APEFG.       301
exoW    ........AAGAVRG.EGLNIFHSID.........NDSPQFLKQQ....FNT...WVALDTLEGRYRNRP.KAMEAIRSYKHTARRQALWSQARRIK.RRK...LPQFD.       293
sleE    ........DAV.......LSEPVP.........ENRASFL.........WLAKRRFRSGQ................THGRVLAEKKPGAR.RVVQVVKAGSK.             264
exoM    ........EAW.......VHEPVP.........ENRASLA.........WLAKRRFRSGQ................THGRLLAEKAHGLR.QAWNIALAGAK.             257
pslC    ........SAE.......VYHSHD.........YRLLEEFRRY....FDIGVFYGRERWIRAAFGGAG.GE..GKR..YVLAEIQALRAAGA.LY.RVPEIALRSAF.         273
gelL    ........QAS.......VGHPPR.........RDW...........EALLV.............................KTRRIQRELYLFYK.ERPQ....GRL.         231
dpsL    ........DAS.......VGHPPR.........PDW...........SALLV.............................KTRRIQRELYLFNI.ERPK....GRL.         231
spsL    ........EAS.......VGHPPR.........PDW...........ATLLV.............................KTRRIQRELFLFNI.ERPR....GRL.         231
sleU    ........HCG.......YGAIVR.........GNSLSGRHRT....EDLRLLYEADRAILAGCRLSA.EETAILR..EHEKHIRAKFELRHFLD.TKKQ...KGVS.         282
exoU    ........SCG.......YAAVVR.........GNSLSGSHRT....IDLKRLYEADRAILAGSRLSS.DAEAAVR..RHERHIRDRYELRHFLD.LKNQ...QGFG.         283
sleF    ........KPG.......YIYNIR.........EGSISRVLEL....HHVEAMMRADEEFLSHYTLLP.AA..MDA..QQ.ARARSLRLAHNFLT.LVENIKRRSVL.         286
exoO    ........SAG.......YIYHIR.........EGSISRVLRL....DHIDAMIAADEAFLRRYALDG.LA..QKM..QH.RRMRGFREARSFLV.LVEQLKKRSLA.         285
gumD    IAVGVKMSSPGPVF...FRQR....R.......HGLGGR..EFYMFKFRSMRVHDDHGTT.......IQQATKNDTR..ITRFGSFLRRSSLDEL...PQ.....IFN         389
gelB    VAIAIKLESPGPVL...FAQD....R.......VGRGNR..LFKILKFRSMRQALCDANG......NVSASRDDDR..ITKVGRFIRKTSIDEL...PQ.....LLN         373
dpsB    VAILIKLESPGPVL...FAQD....R.......VGRGNR..LFKIMKFRSMRVTLCDANG......NVSASRDDDR..ITKVGRFIRKTSIDEL...PQ.....LLN         373
spsB    VAILIKLESPGPVF...FAQD....R.......VGRGNR..LFKILKFRSMRVALCDANG......NVSASRDDDR..ITKVGRIIRKTSIDEL...PQ.....LLN         373
pslI    GS...LDHLP.......EEQRGLPGL........HALGGLDDAELHALYRQAERLWQPSYAEGFGLP.VVEALSVGTP.VAVASGTSLDEVTPPSAPRF.S...PSDGA         322
pslF    HH...VMVLP.......YRES.............KKLGLLGQQR..G..TSGALSWAAACGRGA..I.TS...........DARAFAEEVASGNGAIYPQ....GDVA         342
gumI    CE...LVVLP.......YKQM.............HNSGTLLLAL..SLARPVLAPWSESN.................AAIADEVGPGWVFLYEG....EFDAA         301
gelK    VL...DLKRAGGLPGKLILQYGDQALTDPGIPDVEIRPTIPFDE.LQLMLRDADIVICH...GGTGSL..VTALRAGCR.....VIAFPRRFDLGEHYDDHQ..EEIAQT       295
dpsK    VL...DLKRAGGLPGKLILQYGDQDLPDPGIPDVEIRRTIPFDD.LQLLLRDADMVICH...GGTGSL..VTALRAGCR.....VVAFPRRHDLGEHYDDHQ..EEIAQT       295
spsK    VL...DLKRAGGLPGKLVLQYGDQDLADPGIPDVEIRRTIPFDD.LQLLLRDADMVICH...GGTGSL..VTALRAGCR.....VVAFPRRHDLGEHYDDHQ..EEIAQT       299
gumH    GR...EYDLNEADLRKAIAERGLQDK........VQLSMSPSQQQLCALMQQAQFFVCLSRHEGFGIA.AVEAMSAGLIPILSDIPPFVRLATESG..........QGV        314
gumM    GE...G.......LAERINRSGADVL........LVAFGNPLQERWILDHSEA.....LQVPLVFGVG.ALLDFLSG...TAKRAPNWVRRLHMEW..........MYR        232
consensus
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| logo | | |

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logo      <sequence logo>

sleC      DDLAALFN................RMTP......QTYADAFH........TLSATDRKQWLT....DRDDCRLLVQQLSSLAKSASGHAREAQF.............  390
exoL      ESLATVLG................PLTP......NCYADAAE........RISRCNPGSWVF....DRTDCEALVRQLATLTLQAPQTVPVVAM.............  392
sleD      ALLSLVHWAALIPLGLWIAACVGYGLWMAIGQKNPYGPLAAFSAMVMHLAWSTGF.....WLE....LLKFRGRK....AVS.......................  332
exoA      ALLAIVNWMAVVPVGVWAAACLGYGVWMALGQRNPYGPLAAVAAMVMHLAWSAGF.....WRE....LLDFRRRV....A.........................  330
dpsQ      .....ALW................RLSP....RTGTRYKELS......NGWRAVFSNPGRWWS...GYPRR....................................  312
gelQ      .....LLA................PLLP....KKRERLTAVS......RAWAPVVRERRRWWA....GYPAKK...................................  313
spsQ      .....LLG................RLSP....RRAARWNALR......DAWSIVFGQPRRWWH....GWRDHVRT.................................  315
pslH      ...NAVVRLLQDPAQARAL.......GE....NGRAYVRRAH.........DWSV....AASQLEQVY...AGLAEGAPACA.........................  402
sleW      ...LLLKWAMRDPALLRAA....FELGA....GKIVRSR............................IRQYGAVEAT.............................  329
exoW      ...LLARWLWRDPRLIGSA....AELAV....GKLSR....................................................................  319
sleE      ...VLYC.........ALF....AALSG....FNAVRRNRYALRGALHMGSMSGAFGVRE...........IRQYGAVEAT.........................  314
exoM      ...SGFC.........ATA....AVLCF....PSAARRNRFALRAVLHAGVISGLLGLKE...........IEQYGAREVT.SA.......................  309
pslC      ...KLLGYRLGQ......LE....RHLPV.....ALKRRI.S.........MFPGYWK...............................................  303
gelL      ...RWLARSALQPALLPSDA..AKILR....TSTTQGARAKA..........LLTACRLRFWKS...G.VGLLQLLGRPA.........................  288
dpsL      ...RWLVRSVAQPAMIPQDV..AKILR....TPGTKGARLAA..........VTTLVRLRLWRG...G.AGLLQLLGRDI.........................  288
spsL      ...RWLARSTLQPALIPADT..AKILR....TPGTRGSRIAA..........VGTLVRLRFWRA...G.AGLLQLLGRPI.........................  288
sleU      ...GALSHALARLPALPAIT...RGIWS....DKTARFRKAAP...VRD........VRYLLD....GTP.VS................................  329
exoU      ...RAFGYALTHPAALPAII...GGILA....DKTERFRPSGS...PAPVALGGKGDVRYLLE....TLA.VDQP.....QK.......................  342
sleF      ...GALKTTIRDPAVLG.......HLRM....PIAVRLRRLRDAV.FAPAANTG...VKRQIS........................................  331
exoO      ...GALKTALADPFALR.......HLSM....PIAARLRRLAARF.VHPSSHSA...PRAAPV....TAAAERSPLGNDPRISKG....................  348
gumD      VLGGSMSIVGPRPHAAQHNT...............................H.YEKLI..NHYMQRHYVKPGITGWAQVNGFRGETPELRTMKKRIQYDLDYIRRWSLWLDIRI  469
gelB      VLRGDMSVVGPRPHALGSRAAD.............................HYFWEID..ERYWHRHTLKPGMTGLAQVRGFRGATDRRIDLTNRLQANMEYIDGWDIWRDITI  456
dpsB      VLRGDMSVVGPRPHALGSRAAD.............................HLFWEID..ERYWHRHTLKPGMTGLAQVRGFRGATDRRVDLTNRLQADMEYIDGWDIWRDITI  456
spsB      VLRGDMSVVGPRPHALGSRAAN.............................HLFWEID..ERYWHRHTLKPGMTGLAQIRGFRGATDRRVDLTNRLQADMEYIDGWDIWRDVTI  456
pslI      ALERLMLRLADAPREASAEELI.............................AWAAR..FNREAY.......RQRLAALIEELS........................  367
pslF      ALSEQLLNLAREPRLAQAWAER.............................AGAIG.HART.WPR..........TALRFQALFNDMVGTVHGT.............  395
gumI      LLSGMLDQVRAAPRG...................................PAPDL.SQRD.WPR..........IGGQLHYRTYLEALGKDGAAL..............  349
gelK      FADRGLLQAVRDERELGAAVA..............AAK.....ATEPR..L..ATTDHTA.........LAARL.RTLLAEWGAKR...................  348
dpsK      FADRGLLQAVRDERQLGAAVE..............AAK.....ATEPQ..L..ATTDHTA.........LAARL.RQLLAQWSAKR...................  348
spsK      FADRGLLHAVRDERELGAAVE..............AAK.....ATEPQ..L..ATTDHTA.........LAGRL.RELLAQWSAKR...................  352
gumH      IVNRDRIQAAADSVQALALQAD...............ADFDAR......RTATMAYV..ARYDWRH.........VVGRYIDEYHAALGTPRTQEAVR........  380
gumM      LL.........................................NEPRRLL..KRYSWDL..........LVFFRTCLRAG......KQLA.................  263

consensus     *        *                                          *
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logo
              LEKTLRVIVH.SNAF.
sleC          .....SPV........       393
exoL          .....AGSSHKEGGFL       403
sleD          ...............        332
exoA          ...............        330
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
gumD          IVLTAVRVLGQKTAY.       484
gelB          LFKTLRVIVH.SNAF.       470
dpsB          LFKTLRVIVH.SNAF.       470
spsB          LFKTLRVIVH.SNAF.       470
pslI          ...............        367
pslF          ...............        395
gumI          ...............        349
gelK          ...............        348
dpsK          ...............        348
spsK          ...............        352
gumH          ...............        380
gumM          ...............        263
consensus
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X̄	non-conserved
X	≥ 50% conserved