```
                                   20                  40                  60                  80                  100                 120
                                    |                   |                   |                   |                   |                   |
MreB_MS1    M--------- ---------S A-DMAIDLGT ANTLVYV-KG RGIVLNEPSV VAIAEE---- ----KGKKKV LAVGDEAKMM LGRTPGYIQA IRP------- ---------L RDGVIA----
MreB_AMB1   MFS------- ---KLTGWMS A-DMAIDLGT ANTLVYV-KG RGIVLNEPSV VAIAEE---- ----KGKKKV LAVGDEAKMM LGRTPGYIQA IRP------- ---------L RDGVIA----
MreB_CAUCR  MFS------- ---SLFGVIS N-DIAIDLGT ANTLIYQ-KG KGIVLNEPSV VALRNV---- ----GGRKVV HAVGIEAKQM LGRTPGHMEA IRP------- ---------M RDGVIA----
MreB_ECOLI  MLK------- ---KFRGMFS N-DLSIDLGT ANTLIYV-KG QGIVLNEPSV VAIRQD---- --RAGSPKSV AAVGHDAKQM LGRTPGNIAA IRP------- ---------M KDGVIA----
MreB_MC1    MLS------- ---KLLGLFS T-DMAIDLGT ANTLVYV-RG KGIVLSEPSV VAIHES---- P-RHG--RKV LAVGNEAKRM LGRTPGNIVA TRP------- ---------M RDGVIA----
MreB_BACSU  MF-------- ------GIGA R-DLGIDLGT ANTLVFV-KG KGIVVREPSV VALQTD---- T------KSI VAVGNDAKNM IGRTPGNVVA LRP------- ---------M KDGVIA----
MreB_THEMA  MLR------- ---K------ --DIGIDLGT ANTLVFL-RG KGIVVNEPSV IAIDST---- T-G-----EI LKVGLEAKNM IGKTPATIKA IRP------- ---------M RDGVIA----
Mbl_BACSU   MF-------- ---------A R-DIGIDLGT ANVLIHV-KG KGIVLNEPSV VALDKN---- S-G-----KV LAVGEEARRM VGRTPGNIVA IRP------- ---------L KDGVIA----
MamK_AMB1   MSE------- ---GEGQAKN RLFLGIDLGT SHTAVMSSRG KKFLLK--SV VGYPKD---- VIGLKLLGRP YVVGDEAFEM ----RSYLDI RYP------- ---------L QDGVLSEISD
MamKc_MS1   MSE------- ---GEGQAKN RLFLGVDLGT SHTAVMSSRG KKFLLK--SV V-YPKD---- VIGLKLLGRP YVVGDEAFEM ----RSYLDI RYP------- ---------L QDGVLSEISD
MamKt_MRS1  MSE------- ---GEGQAKN RLFLGIDLGT SHTAVMTSRG KKFLLK--SV VGYPKD---- VIGLKLLGRP YVVGDEAFEM ----RSYLDL RYP------- ---------L QDGVLSEISD
MamK_MC1    MQS------- ---PAGNDK- QLFVGIDLGT SRTAIMTRRG VKTMVR--SV VGYPKD---- IIGVKILNNT VVIGQEALDN ----QAYLNL YYP------- ---------L ADGVLKETSE
ParM_ECOLI  M--------- ---------- -L-VFIDDGS TNIKLQWQES DGTIKQHISP NSFKREWAVS -FGDKKVFNY TLNG-EQYSF DPISPDAVVT TNIAWQYSDV NVVAVHHALL TSGLPV--SE
ParM_R100   M--------- ---------- -L-VFIDDGS T-IKLQWQES DGTIKQHISP NSFKREWAVS -FGDKKVFNY TLNG-EQYSF DPISPDAVVT TNI-WQYSDV NVVAVHHALL TSGLPV--SE
ParM_0157   M--------- ---------- -K-ICIDDGS TNIKLAWTEN -GERRNAISP NSFKSEWSAP -FGGTQPANY MLDG-VRYGF DPVSDRFVQT TDTQYQYSDV NVIAIHHALV KSGITP--QE
ParM_SDYSE  M--------- ---------- -LKVSCDDGS TNVKLAWLE- DGEVRTSLSG NSFKEGWNPG LFNAGKVYNY VVDE-KKYTY DLGSTAVIGT THVSYQYSTT NLLAIHHALL TSGLQP--QD
ParM_SERMA  MAELLKSESP VSPSVQDITE ALKIVVDDGS KAAKLVCLNE RNELVPLLTQ NSFVPDFRVR HEG-LNPFNY LIDGLERFSH HSESSNSLES TDVSHQYDEI SRLNVHHALH ASGLVP--QD
1ATN_ActinRab MDEDETTA-- ---------- ---LVCDNGS GLVKAGFAGD DAPRAVFPSI VGRPRHQGVM V---GMGQKD SYVGDEAQSK ----RGILTL KYP------- ---------I EHGIITNWD-
ACT_YEAST   MDS-EVAA-- ---------- ---LVIDNGS GMCKAGFAGD DAPRAVFPSI VGRPRHQGIM V---GMGQKD SYVGDEAQSK ----RGILTL RYP------- ---------I EHGIVTNWD-
Consensus   M--------- ---------- --DLGIDLGT ANTLVYV-KG KGIVLNEPSV VAFPKD---- --G-K-LKKV LAVGDEAKSM -GRTPGYIVA IRP------- ---------L RDGVIA----
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Phosphate 1

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                                   140                 160                 180                 200                 220                 240
                                    |                   |                   |                   |                   |                   |
MreB_MS1    -DFEVAEEMI KHFIRK-VHN RRSF-ASPLV IVCVPSGSTA VERRAIQESA ESAGARRVFL IEEPMAAAIG AGLP--VTEP TGSMVVDIGG GTTEVAVLSL GGIVYSRSVR V----GGDKM
MreB_AMB1   -DFEVAEEMI KHFIRK-VHN RRSF-ASPLV IVCVPSGSTA VERRAIQESA ESAGARRVFL IEEPMAAAIG AGLP--VTEP TGSMVVDIGG GTTEVAVLSL GGIVYSRSVR V----GGDKM
MreB_CAUCR  -DFEVAEEMI KYFIRK-VHN RKGF-VNPKV IVCVPSGATA VERRAINDSC LNAGARRVGL IDEPMAAAIG AGLP--IHEP TGSMVVDIGG GTTEVAVLSL SGIVYSRSVR V----GGDKM
MreB_ECOLI  -DFFVTEKML QHFIKQ-VHS NSFMRPSPRV LVCVPVGATQ VERRAIRESA QGAGAREVFL IEEPMAAAIG AGLP--VSEA TGSMVVDIGG GTTEVAVISL NGVVYSSSVR I----GGDRF
MreB_MC1    -DFTVTEAML KHFIRR-VHK RRFFH-SPRI IVCVPNGATP VERKAIRDSA ETAGAREVFL IEEPMAAAIG AGLP--VTDA SGSMVVDIGG GTSEVAIISL AGIVFSRSIR V----GGDKM
MreB_BACSU  -DYETTATMM KYYINQAIKN KGMFTRKPYV MVCVPSGITA VEERAVIDAT RQAGARDAYP IEEPFAAAIG ANLP--VWEP TGSMVVDIGG GTTEVAIISL GGIVTSQSIR V----AGDEM
MreB_THEMA  -DYTVALVML RYFINKAKGG MNLF--KPRV VIGVPIGITD VERRAILDAG LEAGASKVFL IEEPMAAAIG SNLN--VEEP SGNMVVDIGG GTTEVAVISL GSIVTWESIR I----AGDEM
Mbl_BACSU   -DFEVTEAML KHFINKL--N VKGLFSKPRM LICCPTNITS VEQKAIKEAA EKSGGKHVYL EEEPKVAAIG AGME--IFQP SGNMVVDIGG GTTDIAVISM GDIVTSSSIK M----AGDKF
MamK_AMB1   RDIEVARHLL THVVKSAEPG PND---EICA VIGVPARASA ANKALLLKMA QEV-VHTALV VSEPFMVGYG ------LDKL INTIIVDIGA GTTDIC--AL KGTVPGPEDQ VTLTKAGNYV
MamKc_MS1   RDIEVARHLL THVVKSAEPG PND---EICA VIGVPARASA ANKALLLKMA QEV-VHTALV VSEPFMVGYG ------LDKL INTIIVDIGA GTTDIC--AL KGTVPGPEDQ VTLTKAGNYV
MamKt_MRS1  RDIEVARHLL THVVKSAEPG AND---EICA VIGVPARASG ANKALLLKMA QEV-VHTALV VSEPFMVGYG ------LDKL NNTIIVDIGA GTTDIC--AL KGTVPGPEDQ VTLTKAGNYL
MamK_MC1    KDEMAAKELL KYVISQAKPQ GDE---QILG IVGVPARTSI YNKSQLLKIT DDL-MSMSMV VSEPFMVAYG ------LDKL NNAIIIDIGA GTIDIC--AM KGTVPSDKDQ ITLLKGGNYV
ParM_ECOLI  VDIVCTLPLT EYYDRNNQPN TENIERKKAN FRKKIT-LNG GD--TFT--- ----IKDVKV MPESIPAGYE VLQE--LDEL DSLLIIDLGG TTLDIS---- --QVMGKLSG ISKIYGDSSL
ParM_R100   VDIVCTLPLT EYYDRNNQPN TENIERKKAN FRKKI--LNG GD--TFT--- ----IKDVKV MPESIPAGYE VLQE--LDEL DSLLIIDLGG TTLDIS---- --QVMGKLSG ISK-YGDSSL
ParM_0157   VDVVVTLPLS EYFDTNAQPD MANINRKKAN VMRPVE-YQN GE--AFT--- ----IRNVRV MPESIPAGFK APAD--MSPF ESLLIVDLGG TTLDVA---- --KVQGQLAG ISQVFCDPHV
ParM_SDYSE  VELTVTLPVT EFFDNDNQPN EERIERKKAN VLREIS-LNK GE--TFK--- ----IKKVNV MPESLPAAFE LLKKDKVNKL ERSLIIDLGG TTLDCG---- --LILGAFEG ISEIRGYSEI
ParM_SERMA  VHLFVTLPLS QFYTALGETN IENIQRKKDN LMKPVERYLD GKRYSFN--- ----VLSVTV FPESLPAVTR ADEIEDIASF ESSLVIDLGG TTLDVA---- --SITGQLEQ ISKVKGFDRI
1ATN_ActinRab -DMEKIWHHT FYNELRVAPE EH-----PTL LTEAPLNPKA NREKMTQIMF ETFNVPAMYV AIQAVLSLYA SGR------- TTGIVLDSGD GVTHNVPIYE GYALPHAIMR LDL--AGRDL
ACT_YEAST   -DMEKIWHHT FYNELRVAPE EH-----PVL LTEAPMNPKS NREKMTQIMF ETFNVPAFYV SIQAVLSLYS SGR------- TTGIVLDSGD GVTHVVPIYA GFSLPHAILR IDL--AGRDL
Consensus   -DFEVTEHLL KYFIRKAVPN RENF--KPAV VVCVPSGATA VERRAIL-MA E-A-ARDVFV IEEPMAAAIG AGLP--VDEL TGSMVVDIGG GTTDVA--SL GGIVPGRSDR I----GGDKM
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Connect 1 Phosphate 2

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                                   260                 280                 300                 320                 340                 360
                                    |                   |                   |                   |                   |                   |
MreB_MS1    DEAIIAYIRR NH-NLLVGEG --SAERIKKE IGSACPPEDG EGRTMEIKGR -DLMNGVPKE LIISERQIAE SLAEPV---- ------GAII EAVKVALEHT APELAADIVD KGIVLTGGGA
MreB_AMB1   DEAIIAYIRR NH-NLLVGEG --SAERIKKE IGSACPPEDG EGRTMEIKGR -DLMNGVPKE LIISERQIAE SLAEPV---- ------GAII EAVKVALEHT APELAADIVD KGIVLTGGGA
MreB_CAUCR  DEAIISYMRR HH-NLLIGET --TAERIKKE IGTARAPADG EGLSIDVKGR -DLMQGVPRE VRISEKQAAD ALAEPV---- ------GQIV EAVKVALEAT PPELASDIAD KGIMLTGGGA
MreB_ECOLI  DEAIINYVRR NY-GSLIGEA --TAERIKHE IGSAYPGD-- EVREIEVRGR -NLAEGVPRG FTLNSNEILE ALQEPL---- ------TGIV SAVMVALEQC PPELASDISE RGMVLTGGGA
MreB_MC1    DEAIMAHVRR KY-SLLIGES --TAEMIKIK VGSAYPLE-- ERIEVEVKGR -DLINGVPKH QMISDPEILE ALQEPI---- ------NAIT EGVRTALECC PPELAADIVD RGIVLTGGGG
MreB_BACSU  DDAIINYIRK TY-NLMIGDR --TAEAIKME IGSAEAPE-- ESDNMEIRGR -DLLTGLPKT IEITGKEISN ALRDTV---- ------STIV EAVKSTLEKT PPELAADIMD RGIVLTGGGA
MreB_THEMA  DEAIVQYVRE TY-RVAIGER --TAERVKIE IGNVFPSKEN DELETTVSGI -DLSTGLPRK LTLKGGEVRE ALRSVV---- ------VAIV ESVRTTLEKT PPELVSDIIE RGIFLTGGGS
Mbl_BACSU   DMEILNYIKR EY-KLLIGER --TAEDIKIK VATVFPDARH E--EISIRGR -DMVSGLPRT ITVNSKEVEE ALRESV---- ------AVIV QAAKQVLERT PPELSADIID RGVIITGGGA
MamK_AMB1   DERLQNAILE RHPELQMNVN --VACAVKEQ FSFVGTPTEV ASFEFRAAGK -PVRADVTEP VKIA----CE AL---M---- ------PDII ESIETLLRSF QPEYQATVL- QNIVFAGGGS
MamKc_MS1   DERLQNAILE RHPELQMNVN --VACAVKEQ FSFVGTPTEV ASFEFRAAGK -PVRADVTEP VKIA----CE AL---M---- ------PDII ESIETLLRSF QPEYQATVL- QNIVFAGGGS
MamKt_MRS1  DERLQNAILE RHPELQMNTN --VACAVKEQ FSFVGARGEA ATFEFRAAGK -PVRCDVTES VKIA----CE AL---M---- ------PDII ESIEILLRSF QPEYQATVL- QNIVFAGGGS
MamK_MC1    DEVFTHAIAE SYPDVQITSY --IAQKIKEK HGFVGEPTEE VVVNLRAGGK -PMLHDVTRE LRFA----CE TI----I---- ------PDIL ESVEKLVLSF DPDNQQEAL- KNIILAGGGS
ParM_ECOLI  GVSLV----- ---------- ---TSAVKDA LSLARTKGSS YLADDIIIHR -KDNNYL--K QRINDENKIS IVTEAM---- ------NEAL RKLEQRVLNT LNEFSG--YT H-VMVIGGGA
ParM_R100   GVSLV----- ---------- ---TSAVKDA LSLARTKGSS YLADDIIIHR -KDNNYL--K QRINDENKIS IVTE-M---- ------NEAL RKLEQRVLNT LNEFSG--YT H-VMVIGGGA
ParM_0157   GVSLM----- ---------- ---ADAVLSV MATNGMRTSH HIANTIIEHR -HDEAWL--R QHIHNDAHYA SLMAVI---- ------REKE ETLKQRVIRA LAVFSG--YG R-VMVVGGGA
ParM_SDYSE  GTSRI----- ---------- ---THTVMNA LTKASTPCNY FIADELIKNR -HDNEYL--Q TLINDVAEIK NISHVI---- ------DREV KSLAESIRQE ISTFSG--MN R-IYLTGGGA
ParM_SERMA  GCSIV----- ---------- ---YDEISRY LESEKLNTSN AYIHHLVDNR -HDKSAL--K VA---EDKRD GVFDAV---- ------NSAV QKLQSKVIRA VTQVEE--RP HNVFLVGGGS
1ATN_ActinRab TDYLMKILTE RGYSFVTTAE REIVRDIKEK LCYVALDFEN EMATAASSSS LEKSYELPDG QVITIGNERF RCPETLFQPS FIGMESAGIH ETTYNSIMKC DIDIRKDLY- ANNVMSGGTT
ACT_YEAST   TDYLMKILSE RGYSFSTTAE REIVRDIKEK LCYVALDFEQ EMQTAAQSSS IEKSYELPDG QVITIGNERF RAPEALFHPS VLGLESAGID QTTYNSIMKC DVDVRKELY- GNIVMSGGTT
Consensus   DEAIINYIRE RH--LLIGE- --TAEAIKEE IGSAGPPTEG EGAEFEIKGR -DLMNGLPRE QRIN--EICE AL-EPV---- ------NAIV EAVEQALEKT PPELAADIYD RGIVLTGGGA
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Adenosine

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                                   380                 400                 420
                                    |                   |                   |
MreB_MS1    LLSNLDYVLR HAT------- -GLPVSIADD PLSCVALGTG RALEEMPKLK NVLTS-M--Y ---------- --
MreB_AMB1   LLSNLDYVLR HAT------- -GLPVSIADD PLSCVALGTG RALEEMPKLK NVLTS-M--Y ---------- --
MreB_CAUCR  LLRGLDAEIR DHT------- -GLPVTVADD PLSCVALGCG KVLEHPKWMK GVLESTL--A ---------- --
MreB_ECOLI  LLRNLDRLLM EET------- -GIPVVVAED PLTCVARGGG KALEMIDMHG GDLFSE---E ---------- --
MreB_MC1    LLRGLDRLIS EET------- -GLPVIVAED PLSCVVMGSG KALEELDAMS -DILTD---Q ---------- --
MreB_BACSU  LLRNLDKVIS EET------- -KMPVLIAED PLDCVAIGTG KALEHIHLFK GKT------R ---------- --
MreB_THEMA  LLRGLDTLLQ KET------- -GISVIRSEE PLTAVAKGAG MVLDKVNILK K--LQGA--G ---------- --
Mbl_BACSU   LLNGLDQLLA EEL------- -KVPVLVAEN PMDCVAIGTG VMLDNMDKLP KRKLS----- ---------- --
MamK_AMB1   RIRGLAAYVK EKLRPFG--- -DANVTCVKD PTFDGCRGAL RLAEELPPQY WRQLGDVSGS ---------- --
MamKc_MS1   RIRGLAAYVK EKLRPFG--- -DANVTCVKD PTFDGCRGAL RLAEELPPQY WRQLGDVSGS ---------- --
MamKt_MRS1  RIRGLAAYVK DKLRPFG--- -NADVTCVKD PTFDGCRGAL RLAEELPPQY WCQLGDVSGQ ---------- --
MamK_MC1    NLIGLDTVLT EGLKEYG--- -KVNVSRVAD PDFAGAAGAL KLATELPTEY WNQVGDIVGG ---------- --
ParM_ECOLI  EL--ICDAVK KHTQ-IR--- -DERFFKTNN SQYDLVNGMY -LIGN----- ---------- ---------- --
ParM_R100   EL--ICDAVK KHTQ-IR--- -DERFFKTNN SQYD-VNGMY -LIGN----- ---------- ---------- --
ParM_0157   EI--VATAIR EACG-V---- -NATFIADGV PQFALVNGLY -AMNK----- ---------- ---------- --
ParM_SDYSE  EL-------- ---------- ---------- ---------- ---------- ---------- ---------- --
ParM_SERMA  YL--IETAIR KH---FE--- -TAKVIMVDN PQFALSLAIA DTIYS----- ---------- ---------- --
1ATN_ActinRab MYPGIADRMQ KEITALAPST MKIKIIAPPE RKYSVWIG-G SILASLSTFQ QMWITKQEYD EAGPSIVHR- --
ACT_YEAST   MFPGIAERMQ KEITALAPSS MKVKIIAPPE RKYSVWIG-G SILASLTTFQ QMWISKQEYD ESGPSIVHHK CF
Consensus   LLRGLDAALK EET------- -GAPVIVAED PLFCVAIGAG KALEELP--K ---LS----- ---------- --
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Adenosine Connect 2