```
PBP1a_e.coli/1-     ------------------------------------------------------------------------------------------------------------
ponA1/1-827       1 VNNEGRHSRSTDDAREAAGRLGARENRPLANPPRPPVPPRSAVPPDDRLTAVLPPVRDGDIAPPIDVVRAALEGSPPPKPPPPPPPGRGG  90
ponA2/1-817         ------------------------------------------------------------------------------------------------------------

PBP1a_e.coli/1-     1 ----MKLNGKFPVKFVKYFLILAVCCILLGAGS---IY-------GLYRYIEPQLPDVA-----TLKDVRLQIPMQIYSADGELIAQYG-  70
ponA1/1-827        91 GGPSGPGGPSGPGR--QFR--INWKWVRRGSAIAVAVMVLLPLITFGMAYMIVD---VP-----EPGDIRTPQVSTILASDGSEIARIVP 168
ponA2/1-817         1 -MPELPTGPSAQPPRAVIVIKLAWCCLLASVLA---AALMFPVV-GGFGLMSNRASDVVANGSAALVEGEVPQVSTMVDAKGNTIAWLY-  84
                                                  Transglycosylase
PBP1a_e.coli/1-    71 -EKRRIPVTLDQIPPEMVKAFIATEDSRFYEHHGVDPVGIFRAASVALFSGHASQGASTITQQLARNFFLS------------PERTLMR 147
ponA1/1-827       169 PEGNRVDVKIDQIPVHVRDAVMAAEDRDFYSNPGFSWTGFLRAIKNNLFGGGGLQGGSTITQQYVKNALVGDER--------SGIGGLIR 250
ponA2/1-817        85 -SQRRFEVPSEQIANTMKLAIVSIEDKRFAEHNGVDWQGTLTGLSGYLSGNPDTRGGSTIEQQYVKNYQLLVVAQTDAERRAAIETTPAR 173

PBP1a_e.coli/1-   148 KIKEVFLAIRIEQLLTKDEILELYLNKIYLGYRAYGVGAAAQVYFGKTVDQLTLNEMAVIAGLPKAPSTFNPLYSMDRAVARRNVVLSRM 237
ponA1/1-827       251 KAKELVISTKMSGEWSKDAVLQAYLNIIYFGRGAYGISAASKAYFDKPVEQLDVAEGALLAALIQRPSTLDPAVDPEGAADRWNWVLDGM 340
ponA2/1-817       174 KLREIRMALTLDKTFTKPEILTRYLNLVSFGNGAYGIQDAAQTYFGVNASELNWQQAALLAGMVQSTSALNPYTNPDGALARRNLVLDTM 263

PBP1a_e.coli/1-   238 LDEGYITQQQFDQTRTEAINAN----------YHAPEIAFSAPY-------LSEMV---RQEMYNRYGESAYEDGYRIYTTITRKVQQAA 307
ponA1/1-827       341 VDIGALSQADRDAQVFPPT--------V------PPDYAFQQNQTTGPNGLIERQVTNELLDLFDINEQTLNTEGLQITTTIDPKAQEAA 416
ponA2/1-817       264 IQNIPQEAEALRAAKEQPLGILPQPNELPRGCIAAGDRAFFCDY-------VLEYL---ARAG--ISKEQVAKGGYLIKTTLDPDVQSSV 341

PBP1a_e.coli/1-   308 QQAVRNNVLDYDMRHGYRGPANVLWKVGESAWDNNKITDTLKALPTYGPLLPAAVTSANPQQATAMLADGSTVALSMEGVRWARPYRSDT 397
ponA1/1-827       417 VDAVDK------------------------------------------------------------------------------------ 422
ponA2/1-817       342 KSAIDSIA-----APDTPGVASVM-------------------------------SVIKPGKE-------SHPVL---AMASNRTYGLDT 385
                                                                                                  Transpeptidase
PBP1a_e.coli/1-   398 QQGPTPRKVTDVLQTGQQIWVRQVGDAWWLAQVPEVNSALVSINPQNGAVMALVGGFDFNQSKFNRATQALRQVGSNIKPFLYTAAMDKG 487
ponA1/1-827       423 ----------------------------YLEGQDPDMRAAVVSIDPRTGGIKAYYGGSDANGFDFAQAG---LPTGSSFKVFALVAALQQG 482
ponA2/1-817       386 ERGETMQPQPF-------------------------------------------SLVG----------------NGAGSVFKIFTVAAAMEMG 419

PBP1a_e.coli/1-   488 LTLASML----------------NDVPISRWDASAGSDWQPKNSPPQYAGPIRLRQGLGQSKNVVMVRAMRAMGVDYA--AEYLQRFGFP 559
ponA1/1-827       483 IGLGYQIDSG-PLEVNGIKIGNV---------------------EGEGCGTCSIAEALKRSLNTSYYRLMLKLENGPADVAEAAHDAGVA 550
ponA2/1-817       420 MGINTQLPVPARFEAKGLGSGGARGCPPATWCVQN---------AGGYRGSMSVTDALATSPNTAFAKLISQIGVQRA--VDMAVRLGLR 498

PBP1a_e.coli/1-   560 AQNIV---------------------HTESLALGSASFTPMQVARGYAVMANGGFLVDPWFISKIENDQGGVIFEAKPKVACPEC-DIPV 627
ponA1/1-827       551 -ESFPGVEHTLS-------EDGKGGPPNNGVVLGQYQSRVLDMASAYATLAASGVYHKPHFVEKVVNSSGQVLFDASKEDNGEERIDKAV 632
ponA2/1-817       499 SYAQPGTARDYDPESSESLADFVKRQNIGSFTLGPIEVNALELSNVAATLASGGTWCPPNPIAQVVDRNGNEVA-----VTTETC-EQVV 582

PBP1a_e.coli/1-   628 IYGDTQK-SNVLENNDVED--VAISREQQNVSVPMPQLEQA-----NQALVA---KTGAQEYAPHVIN---TPLAFLIKSALNTNIFGEP 703
ponA1/1-827       633 AD-------------NV----TSAMQPIAGWSRGH-------------------------------------------------NLA--- 653
ponA2/1-817       583 PEGLANTLANAMSKDDTGSGTAAASAGSVGWNLPMSGKTGTTEDNRSSAFLGFTNQYAAANYIYDDSPNPSELCSFPLRQCGSGNLFGG- 671

PBP1a_e.coli/1-   704 GWQGTGWRAGRDLQRRDIGGKTGTTNSSKDAWFSGYGP----------------------GVVTSVWIGFDDHRRNLGHTTASGA----- 766
ponA1/1-827       654 --------GGRPSAAKTGTVQLGDTGDNRDAWMVGYTP----------------------SLSTAVWVGTTEGVKPLVNKWGSPIYGSGL 713
ponA2/1-817       672 -------------------------NEPARTWFTAMKPIAESFGPVALPPTDPRYVDGGPGSRVPSVSGLTEEAARQRLKEAGFQ----- 731

PBP1a_e.coli/1-   767 IKDQISGYEGGAKSA-----QPAW----DAYM-KAVLEGVPEQPLTPPPGIVTVNIDRSTGQL---------------------------- 819
ponA1/1-827       714 PSDIWKATMDGALEGTDVESFPKPT-------EIGGYAGVPQAPAAPPPSAGPP---TDPGQPSVTVIQPTIEVAPGITIPIGPPTTVPV 793
ponA2/1-817       732 VADQASYVNSGARSGTVVGTTPSGQTIPGSIITIQLSNGIPPPP----PP--PVNIPLPGGPPEIGQT---V-----VEIPGLPPITVPV 807

PBP1a_e.coli/1-     ------------------------------------
ponA1/1-827       794 GPPPGAPGAPVGPGAPEVPVAPGAPGVPGAPPPP                                                          827
ponA2/1-817       808 LGPP------------------------PPPPPP                                                          817
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