

```

10      20      30      40      50      60      70      80      90      100     110     120
AtClpD  ---MVLVSSPGLTLHSH---RLLSAS---SSSHVTSI---AASSSSFSASVILGISLNRNTHREFTPTNTRRPFQQRK
BsClpC  -----
AtClpC1 MMTATRVLQASTPSS---LACYQR---NVPGRSGRRSRVKKMCSQVQVGLRMQVCGVGNNAITDILGK---R--QDHF-SKVRQAMNVPEK
AtClpC2 MWWS---IALLTLPFPFGPRGVQAEKYRFRPGCVMMSSLKAFLVRIQATYR-REFRGRVKMSSQAPILLITQSSGSRAPSAIDVGLRE---S--PGDL-VKKYKLAQSSGPK
AtClpB3 MATATT---A---TAAFS---GV---VSVGTETRTIYSSSHLQPSAIFPAKPSVFKSLKIKQS---ARLT-RRLDHRFPVVFCE
EcClpB  -----

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130     140     150     160     170     180     190     200     210     220     230     240
AtClpD  KKFPPSSVFRFETETERLALSLQEKASLGDVHGHMIIAGLHLDPRDQCFLGSGHITDQEDAEVWVSLRDEANSRDSKQEEASVHYSKSTDMFSELSNRVAFDSEARVTFMDC
BsClpC  ---SFRFETETERLALSLQEKASLGDVHGHMIIAGLHLDPRDQCFLGSGHITDQEDAEVWVSLRDEANSRDSKQEEASVHYSKSTDMFSELSNRVAFDSEARVTFMDC
AtClpC1 ASRTFVKAMERFETETAKAVVLAQEAELALGHNVGVEEILLCHLGGQVIAALVPSGQVGNLAKDAFVWVSLRDEANSRDSKQEEASVHYSKSTDMFSELSNRVAFDSEARVTFMDC
AtClpC2 ASRCVFKAMERFETETAKAVVLAQEAELALGHNVGVEEILLCHLGGQVIAALVPSGQVGNLAKDAFVWVSLRDEANSRDSKQEEASVHYSKSTDMFSELSNRVAFDSEARVTFMDC
AtClpB3 ASSNSGRITQCEPTEAWOSVLSVPEVAKENKQOIVFTHLMKALDEQRNDAKRIEFSKIQVNTNVLKATENGICRQKVIYGDAAAGSLMGRLDEALFQARQAFKDLND
EcClpB  ---MRLDRNRFQALALAPAGSLALGHNDGFEPLIMSAALNQQEVSVPFLVPSAGINAGQLTDINQALNR---LQVVEGTGGVQPSQDLVRVNLNCDKIAQRKQD

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250     260     270     280     290     300     310     320     330     340     350     360
AtClpD  QVLAPEHAFVAFD-SRFGKQLRFDQFQISERSLKSATESIRKQSVI---D---QDFEGVYEAELRYKQDLTAAREGKLDPVIGRDEETRRCTQLLRRRT
BsClpC  SVVSEHLLVLAFAE-SRFGKQLRFDQFQISERSLKSATESIRKQSVN---D---QGAEDRQAKIKVPLDTEAREGKLDPVIGRDEETRRCTQLLRRRT
AtClpC1 NVYGEHLLVLAFAE-SRFGKQLRFDQFQISERSLKSATESIRKQSVN---D---QGAEDRQAKIKVPLDTEAREGKLDPVIGRDEETRRCTQLLRRRT
AtClpC2 NVYGEHLLVLAFAE-SRFGKQLRFDQFQISERSLKSATESIRKQSVN---D---QGAEDRQAKIKVPLDTEAREGKLDPVIGRDEETRRCTQLLRRRT
AtClpB3 SVVSEHLLVLAFAE-SRFGKQLRFDQFQISERSLKSATESIRKQSVI---D---QDFEGVYEAELRYKQDLTAAREGKLDPVIGRDEETRRCTQLLRRRT
EcClpB  NFVSEHLLVLAFAE-SRFGKQLRFDQFQISERSLKSATESIRKQSVN---D---QGAEDRQAKIKVPLDTEAREGKLDPVIGRDEETRRCTQLLRRRT

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370     380     390     400     410     420     430     440     450     460     470     480
AtClpD  KNNFVLLGEAGVCGKTAIABGLAITSIAEASAPGFTLAKRIMSLDGLDLAGARQCELEAVVATISSEV---KSGVILFDIVHTLIGSGVWGRNGKSGGIDHANIHKPSVGRGEIQGAS
BsClpC  KNNFVLLGEPGVGKTAIABGLAQLKNNFVLLGRVRLVLDGMGLVAGKYRGEFEERLKLKIMET---RQSDGHTLFDIVHTLIGAGAA---EGAIIDANILKPSLARGEIQGAI
AtClpC1 KNNFVLLGEPGVGKTAIABGLAQRASGDVPEETGRKVTITLDGMGLVAGKYRGEFEERLKLKIMET---RQSDGHTLFDIVHTLIGAGAA---EGAIIDANILKPSLARGEIQGAI
AtClpC2 KNNFVLLGEPGVGKTAIABGLAQRASGDVPEETGRKVTITLDGMGLVAGKYRGEFEERLKLKIMET---RQSDGHTLFDIVHTLIGAGAA---EGAIIDANILKPSLARGEIQGAI
AtClpB3 KNNFVLLGEPGVGKTAIABGLAQRITVGDVPEETMNNKRLVLDGMGLVAGAKYRGEFEERLKLKIMET---RQSDGHTLFDIVHTVWVAGAT---EGAIIDANILKPSLARGEIQGAI
EcClpB  KNNFVLLGEPGVGKTAIVGCLAQRITVGPVPEETGRKRVVLDGMGLVAGAKYRGEFEERLKLKIMET---RQSDGHTLFDIVHTVWVAGAT---EGAIIDANILKPSLARGEIQGAI

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490     500     510     520     530     540     550     560     570     580     590     600
AtClpD  TLLDEYRKYIEKDPALERRFPQVDFVDPVETDITQLLGLRERYEHHVAVTDEALVAAALSRYSIDRFLDPDKAIDLIDEAGSIVRLASPTFPPNDELQORDEVERKEDAVALQSS
BsClpC  TLLDEYRKYIEKDPALERRFPQVDFVDPVETDITQLLGLRERYEHHVAVTDEALVAAALSRYSIDRFLDPDKAIDLIDEAGSIVRLASPTFPPNDELQORDEVERKEDAVALQSS
AtClpC1 TLLDEYRKYIEKDPALERRFPQVDFVDPVETDITQLLGLRERYEHHVAVTDEALVAAALSRYSIDRFLDPDKAIDLIDEAGSIVRLASPTFPPNDELQORDEVERKEDAVALQSS
AtClpC2 TLLDEYRKYIEKDPALERRFPQVDFVDPVETDITQLLGLRERYEHHVAVTDEALVAAALSRYSIDRFLDPDKAIDLIDEAGSIVRLASPTFPPNDELQORDEVERKEDAVALQSS
AtClpB3 TLLDEYRKYIEKDPALERRFPQVDFVDPVETDITQLLGLRERYEHHVAVTDEALVAAALSRYSIDRFLDPDKAIDLIDEAGSIVRLASPTFPPNDELQORDEVERKEDAVALQSS
EcClpB  TLLDEYRKYIEKDPALERRFPQVDFVDPVETDITQLLGLRERYEHHVAVTDEALVAAALSRYSIDRFLDPDKAIDLIDEAGSIVRLASPTFPPNDELQORDEVERKEDAVALQSS

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Hsp70-binding domain

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610     620     630     670     680     690     700     710     720
AtClpD  ---YVCEIKTVQAM---H---EVLSSRSKQDDGDAIS---DESCE---VY---ESSLPPAGDDPEILVGGPDITAVASVMSVGTIV
BsClpC  ---FERASLRDREIFRQVEDTKKS---WK---E---QGGENSEVVDIIAVSVSWGIV
AtClpC1 ---FERASLRDREIFRQVSAIQAL---GKMSKRA---S---TGEEGPVAVESDIOHVSWSGTIV
AtClpC2 ---FERASLRDREILKAEIANVLSR---GVEKARV---N---AEMGFPEVSDIOHVAVWGIV
AtClpB3 DAKSRRLNRITETLVLLKEQAELETQVEHRSVMSRLQSKIEIDRWLQIQAEREYDILNRAAEKLYGSINSLQRQNEKELNELYSS---KAGFPVEVCGSDIACHVSKVGTIV
EcClpB  DASKRRLDMLNELSDKERQYSELEEEVKAEKASLSGTAKAELEQAKIATEARRVGLDARMSELQVKIPELEQAEATQLE---GK---MRLLENKVDABEAVLAWVGTIV

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730     740     750     760     770     780     790     800     810     820     830     840
AtClpD  QGITADEKRLIMSLDGRVGVGQDEAVVAISRAVRSRVLKDPDRTIAVMTLGGPTGVGKTELAKALANFDSEESVRLDMDSVEMERTVSKLIGSPPGYGVYEGGOLTEAVRR
BsClpC  RYVTAQEDKRLIMENLISRVIGQDEAVVAISRAVRSRAGLKDPEPRTIAVMTLGGPTGVGKTELAKALANFDSEESVRLDMDSVEMERTVSKLIGSPPGYGVYEGGOLTEAVRR
AtClpC1 EHVSTDESDKRLIMELHRRVIGQDEAVVAISRAIRARVGLKNRPIASFTISSGPTGVGKTELAKALAAAYFGSEEMIRLDMSEMERHTVSKLIGSPPGYGVYEGGOLTEAVRR
AtClpC2 RYVSTDESDKRLIMELHRRVIGQDEAVVAISRAIRARVGLKNRPIASFTISSGPTGVGKTELAKALAAAYFGSEEMIRLDMSEMERHTVSKLIGSPPGYGVYEGGOLTEAVRR
AtClpB3 SKLQOESRDKRLIMELHRRVIGQDEAVVAISRAIRARVGLKNRPIASFTISSGPTGVGKTELAKALANFDSEEMIRLDMSEMERHTVSKLIGSPPGYGVYEGGOLTEAVRR
EcClpB  SRMSESERKRLIMELHRRVIGQDEAVVAISRAIRARVGLKNRPIASFTISSGPTGVGKTELAKALANFDSEEMIRLDMSEMERHTVSKLIGSPPGYGVYEGGOLTEAVRR

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ClpP-binding loop

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850     860     870     880     890     930     940     950     960
AtClpD  RPYVTVLDFDEIEKAHPDVFNLIQLLEDGRLLDQSGRVDVFNKNTLIMTSNVGSSLAIEKGRHSGIGFLLDDDEAASVYKQALVWELKLVYFPELINRIDEVIVFROLKQAMMIFLN
BsClpC  RPYVTVLDFDEIEKAHPDVFNLIQLLEDGRLLDQSGRVDVFNKNTLIMTSNVGSSLAIEKGRHSGIGFLLDDDEAASVYKQALVWELKLVYFPELINRIDEVIVFROLKQAMMIFLN
AtClpC1 RPYVTVLDFDEIEKAHPDVFNLIQLLEDGRLLDQSGRVDVFNKNTLIMTSNVGSSVIEKGRHSGIGFLLDDDEKDSVYKQALVWELKLVYFPELINRIDEVIVFROLKQAMMIFLN
AtClpC2 RPYVTVLDFDEIEKAHPDVFNLIQLLEDGRLLDQSGRVDVFNKNTLIMTSNVGSSVIEKGRHSGIGFLLDDDEKDSVYKQALVWELKLVYFPELINRIDEVIVFROLKQAMMIFLN
AtClpB3 RPYVTVLDFDEIEKAHPDVFNLIQLLEDGRLLDQSGRVDVFNKNTLIMTSNVGSSVIEKGRHSGIGFLLDDDEKDSVYKQALVWELKLVYFPELINRIDEVIVFROLKQAMMIFLN
EcClpB  RPYVTVLDFDEIEKAHPDVFNLIQLLEDGRLLDQSGRVDVFNKNTLIMTSNVGSSVIEKGRHSGIGFLLDDDEKDSVYKQALVWELKLVYFPELINRIDEVIVFROLKQAMMIFLN

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970     980     990     1000    1010    1020    1030    1040    1050    1060
AtClpD  IMLDQKSRVAVLGVGVSPPVKEKILCKQGVDEYNGARPLRRITVEIIVDPSEAFVGSKFGFVAVLVDITDNPSTVRSPTDSTRIVDKTYSIA
BsClpC  IMLDQKSRVAVLGVGVSPPVKEKILCKQGVDEYNGARPLRRITVEIIVDPSEAFVGSKFGFVAVLVDITDNPSTVRSPTDSTRIVDKTYSIA
AtClpC1 IMLDQKSRVAVLGVGVSPPVKEKILCKQGVDEYNGARPLRRARLMLLEDSEAFVAREKEGVSIVYVDAEAGVNVLNGSGSPTTFLSLEE---Q---DLSLVA
AtClpC2 IMLDQKSRVAVLGVGVSPPVKEKILCKQGVDEYNGARPLRRARLMLLEDSEAFVAREKEGVSIVYVDAEAGVNVVSTGTRVGRVDFAEAEAM---EPPILPIL
AtClpB3 IMLDQKSRVAVLGVGVSPPVKEKILCKQGVDEYNGARPLRRARLMLLEDSEAFVAREKEGVSIVYVDAEAGVNVVSTGTRVGRVDFAEAEAM---EPPILPIL
EcClpB  IMLDQKSRVAVLGVGVSPPVKEKILCKQGVDEYNGARPLRRARLMLLEDSEAFVAREKEGVSIVYVDAEAGVNVVSTGTRVGRVDFAEAEAM---EPPILPIL

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