```
         1              10                  20                  30                  40                  50                  60                  70                  80                  90                 100
GroEL  M A A K D V K F G N D - - A R V K M L R G V N V L A D A V K V T L G P K G R N V V L D K S F G A P T I T K D G V S V A R E I E L E D K F E N M G A Q M V K E V A S K A N D A A G D G T T T A T V L A Q A
α      - - - - E I V F - - D Q E S R R R L Q A G I N K V A D A V G V T L G P K G R N V V L E Q K F G V P Q V I N D G V S I A R A I E L K D P V E N A G A Q L I K E V A G R T N D A A G D G T T T A S V L A R E
β1     - - - - E L H F N K D M Q A L K R M Q A G V D K L A T V V G V T I G P K G R N V V L E S K F G A P K I V N D G V T I A R E V E L S D P V E N I G A T L V R Q A A A R T N D T A G D G T T T A T V L S A A
β2     - - - - E L H F N R N M E A L K K M Q A G V D K L A T V V G V T I G P K G R N V V L E S K F G S P K I V N D G V T I A R E V E L E D P V E N I G A K L V R Q A A A R T N D T A G D G T T T A T V L S A A

         101            110                 120                 130                 140                 150                 160                 170                 180                 190                 200
GroEL  I I T E G L A A V A A G M N P M D L K R G I D K A V T A A V E E L K A L S V P C S D S K A I A Q V G T I S A N S D E T V G K L I A E A M D K V G K E G V I T V E D G T G L Q D E L D V V E G M Q F D R G
α      M I H Y G L Q S V T A G A N P I A V K R G L D K T A E Y L V A K L K E H A K P V K G R D D I K N V A S I S A G N D N A I G E M I A D A L D K V G S N G V L S I E T S N S T E T V V E V Q E G M E I D R G
β1     F I A E G M K I V S A G T N P V Q L V R G M E K T V Q E L V K E L R K M S S V V Q T D K D L A N V A C V S A G G N T D I G S L I S D A M A K V G R T G V V T M E E G K T A E D A L I F V E G M Q F E R G
β2     F I A E G M K I V A A G T N P V Q L T R G M E K T V N A L V K E L K A A S S Q V H S D K D L S N V A S V S A G G N P D V G K L I S D A M A K V G R Q G V V T M E E S K T A E D A L I F V E G M Q F D R G

         201            210                 220                 230                 240                 250                 260                 270                 280                 290                 300
GroEL  Y L S P Y F I N K P E T G A V E L E S P F I L L A D K K I S N I R E M L P V L E A V A K A G K P L L I I A E D V E G E A L A T L V V N T M R G I V K V A A V K A P G F G D R R K A M L Q D I A T L T G G
α      Y I S P Q F V T N Q E R L L V E Y D N C R V L V T D Q K I D A I R D I I P I L E Q V T R L N A P L L I I A E D V S G E A L A T L V V N K L R G V L N V C A I K A P G F G E R R K S L L Q D I A I V T G A
β1     Y T S P Y F V T D P E R M I C E Y E N C K I L L V D K K I S T A R D I I T I L E S A I R G N Y P L L I M A E E V E Q E A L A T L V V N K L R G T L K V V A I K A P G F G E R R S S Y L E D I A I L T G G
β2     Y Y S P Y F V T D P E R M L A E Y E N C R I L L V D K K I S T A R D I I G I L E A A I R G N Y P L L I M A E D V E Q E A L A T L V V N K L R G T L K V V A V K A P G F G E R K S S Y L E D I A I L T G G

         301            310                 320                 330                 340                 350                 360                 370                 380                 390                 400
GroEL  T V I S E E I G M E L E K A T L E D L G Q A K R V V I N K D T T T I I D G V G E E A A I Q G R V A Q I R Q Q I E E A T S D Y D R E K L Q E R V A K L A G G V A V I K V G A A T E V E M K E K K A R V E D
α      E F I A K D L G M K V E Q A V V E Q L G V A R K V T V A N N T T T L I A D A A S K D E I E M R I A Q L K K E L A E T D S V Y D T E K L S E R I A K L S G G V A V I K V G A A T E A E L E D R K L R I E D
β1     T V V R D E M G V S L E Q A T D A V L G T A A K I T I T K E R T T V V G D G S T A A D V A A R V K Q I R N L Q M Q T D Q D Y E R E K L Q E R I A R L S G G V A I I Q V G A Q T E T E L K E K K L R V E D
β2     T V V K D E L G I T L E K A T E E V L G L A A K V S I S K E A T T I V G D G R T Q Q Q V E G R V K Q I R N L A A E T E Q E Y E K E K L N E R I A R L S G G V A I I Q V G A Q T E T E L K E K K L R V E D

         401            410                 420                 430                 440                 450                 460                 470                 480                 490                 500
GroEL  A L H A T R A A V E E G V V A G G G V A L I R V A S K L A D L R G - - Q N E D Q N V G I K V A L R A M E A P L R Q I V L N C G E E P S V V A N T V K G - - G D G N Y G Y N A A T E E Y G N M I D M G I L
α      A K N A T F A A V E G I V P G G G A A L L H L S E L V P A F K E T L T D A E E K L G A D I V M K S L R A P C R L I A D N A G V E G E V I V Q R L L G - - K P F E V G N A M I D K V E N L L D A G V I
β1     A L N A T R A A V E E G V V P G G G C T L L R L S E K V D V I K R R M T D P E Q Q M G A D I I K R A L C Y P I K L I A Q N A G V N G S V V M N E V M K N L D R P H Y G Y N A A T D S F E N L M E T G I I
β2     A L N A T K A A V E E G I V I G G G C T L L R L S Q K V D S I K E T L S N E E Q K M G A D I I K R A L S Y P I K L I A N N A G T N G S V V M Q R V M D N I D Q P Y Y G Y N A A T D T F E D L M E A G I I

         501            510                 520                 530
GroEL  D P T K V T R S A L Q Y A A S V A G L M I T T E C M V T D L P K
α      D P A K V T R N G L L N S V S I A G I M L T T Q A V M V E - - -
β1     D P S K V V R C S M E N A V S V A K T F L L A D V V V T E L K E
β2     D P T K V V R C S L E N A V S V A K T F L L A D V V V T E I - -
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**Fig. S1** Sequence alignment of Cpn60α, β1 and β2 and their homolog GroEL and residue number

| αα | | | | β1β1 | | | | β2β2 | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| Chain A | Chain B | Distance (Å) | Occupancy (%) | Chain A | Chain B | Distance (Å) | Occupancy (%) | Chain A | Chain B | Distance (Å) | Occupancy (%) |
| I6 (N)d | E63 (O) | 2.0 | 94 | E5 (OE1) | S65 (OG)d | 1.8 | 35 | L6 (O) | E63 (N)d | 2.0 | 83 |
| I6 (O) | K65 (N)d | 2.0 | 55 | E5 (OE1) | S65 (N)d | 2.1 | 13 | K74 (NZ)d | S44 (O) | 2.3 | 11 |
| Q74 (NE2)d | E43 (OE1) | 1.9 | 100 | Q78 (OE1) | A48 (N)d | 2.9 | 5 | K74 (NZ)d | G47 (O) | 2.4 | 56 |
| Q74 (NE2)d | G47 (O) | 2.2 | 95 | Q117 (OE1) | K36 (NZ)d | 2.1 | 22 | Q78 (OE1) | S48 (OG)d | 2.2 | 55 |
| E78 (OE2) | V48 (N)d | 2.2 | 57 | Q127 (OE1) | K392 (NZ) | 1.7 | 25 | R82 (NH1) | Q386 (O) | 2.1 | 18 |
| N114 (ND2)d | D489 (OD1) | 2.1 | 14 | R233 (NH2) | N246 (OD1) | 2.0 | 12 | R82 (NH2) | Q386 (O) | 2.1 | 18 |
| N114 (ND2)d | D489 (OD2) | 2.8 | 22 | E257 (OE2) | K274 (NZ)d | 2.3 | 43 | K228 (NZ)d | E218 (OE2) | 2.9 | 7 |
| D226 (O) | N183 (ND2)d | 2.0 | 92 | E259 (OE2) | T217 (OH)d | 1.7 | 98 | K228 (O) | N246 (ND2)d | 2.3 | 1 |
| D226 (OD2) | N183 (ND2)d | 2.5 | 83 | T263 (N)d | R270 (O) | 3.5 | 3 | A232 (N)d | T272 (OG1) | 1.9 | 39 |
| K228 (NZ)d | E180 (OE1) | 2.0 | 55 | L521 (O) | R38 (NH1)d | 2.2 | 16 | S515 (OG)d | Q386 (OE1) | 1.8 | 41 |
| E254 (OE2) | T181 (OG1)d | 1.8 | 95 | L522 (O) | N39 (N)d | 2.2 | 97 | L522 (O) | N39 (N)d | 1.7 | 93 |
| E254 (OE1) | S182 (OG)d | 1.7 | 100 | A523(O) | R38 (NH1)d | 2.4 | 8 | D524 (N)d | N39 (O) | 2.2 | 92 |
| D255 (OD2) | R212 (NH2)d | 2.6 | 57 | D524 (N)d | N39 (O) | 2.2 | 95 | V525 (O) | V41 (N)d | 1.7 | 85 |
| V256 (O) | R212 (NH2)d | 3.3 | 13 | V525 (O) | V41 (N)d | 2.0 | 92 | V527 (N)d | V41 (O) | 1.5 | 99 |
| G258 (N)d | E216 (OE2) | 1.9 | 23 | V527 (N)d | V41 (O) | 2.1 | 98 | V527 (O) | E43 (N)d | 2.0 | 94 |
| E259 (O) | N274 (ND2)d | 3.2 | 19 | V527 (O) | E43 (N)d | 2.2 | 54 | E529 (OE1) | K45 (NZ)d | 2.9 | 64 |
| E259 (OE2) | N274 (ND2)d | 1.8 | 60 | E529 (N)d | E43 (OE1) | 2.3 | 100 | | | | |
| T263 (OG1) | N274 (ND2)d | 2.1 | 31 | | | | | | | | |
| F283 (N)d | A386 (O) | 2.2 | 85 | | | | | | | | |
| R287 (NH1)d | N183 (OD1) | 2.3 | 19 | | | | | | | | |
| D306 (OD2) | N183 (N)d | 1.9 | 86 | | | | | | | | |
| D306 (OD1) | K382 (NZ)d | 2.2 | 14 | | | | | | | | |
| D306 (OD2) | K382 (NZ)d | 2.3 | 12 | | | | | | | | |
| T522 (O) | N39 (N)d | 1.9 | 85 | | | | | | | | |
| T522 (OG1)d | N39 (OD1) | 1.5 | 44 | | | | | | | | |
| Q524 (N)d | N39 (O) | 2.2 | 93 | | | | | | | | |
| M527 (N)d | V41 (O) | 1.8 | 98 | | | | | | | | |
| M527 (O) | E43 (N)d | 2.1 | 94 | | | | | | | | |

**Fig. S2** Residues forming H-bond at time 100 ns of MD simulation and %occupancy in last 20 ns