



wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Sep 14, 2017 – 12:04 PM EDT

PDB ID : 5W0S
EMDB ID: : EMD-8750
Title : GroEL using cryoEM
Authors : Roh, S.H.; Chiu, W.
Deposited on : unknown
Resolution : 3.50 Å(reported)

This is a wwPDB/EMDataBank EM Map/Model Validation Summary Report
for a publicly released PDB/EMDB entry.

We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

MolProbity : 4.02b-467
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20029824

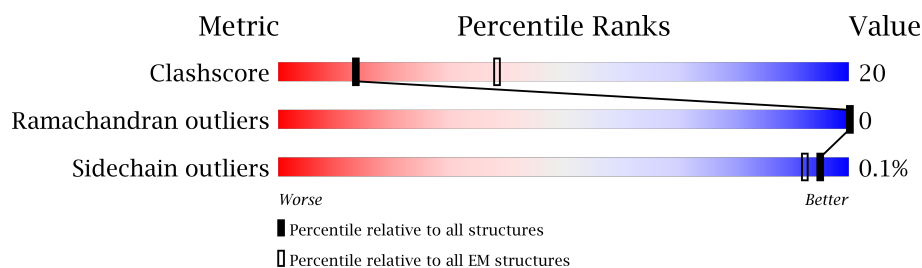
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.50 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.









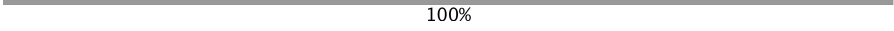
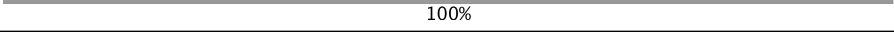
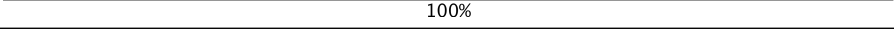
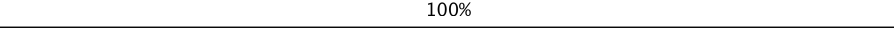
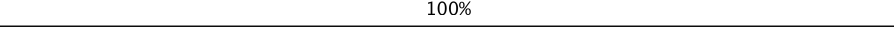
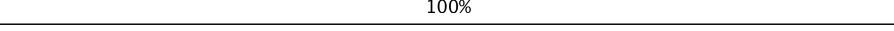
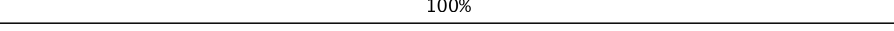
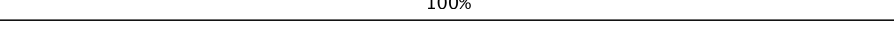
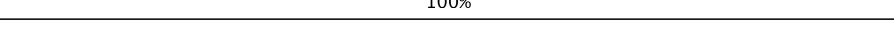
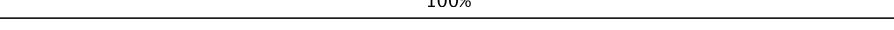
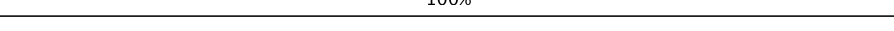
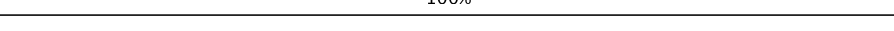
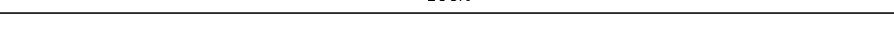
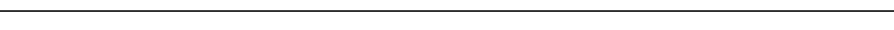

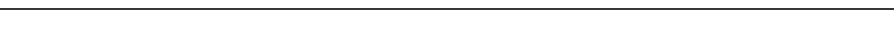
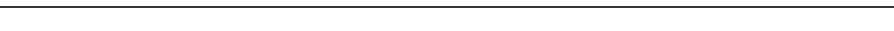


| Metric | Whole archive (#Entries) | EM structures (#Entries) |
|-----------------------|-----------------------------|-----------------------------|
| Clashscore | 125131 | 1336 |
| Ramachandran outliers | 121729 | 1120 |
| Sidechain outliers | 121581 | 1026 |

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$

| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 1 | 1-A | 524 | |
| 1 | 1-B | 524 | |
| 1 | 1-C | 524 | |
| 1 | 1-D | 524 | |
| 1 | 1-E | 524 | |
| 1 | 1-F | 524 | |
| 1 | 1-G | 524 | |
| 1 | 1-H | 524 | |
| 1 | 1-I | 524 | |

Continued on next page...

Continued from previous page...

| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|--|
| 1 | 1-J | 524 |  83% 17% |
| 1 | 1-K | 524 |  81% 19% |
| 1 | 1-L | 524 |  82% 18% |
| 1 | 1-M | 524 |  82% 18% |
| 1 | 1-N | 524 |  82% 18% |
| 1 | 2-A | 524 |  52% 48% |
| 1 | 2-B | 524 |  100% |
| 1 | 2-C | 524 |  100% |
| 1 | 2-D | 524 |  100% |
| 1 | 2-E | 524 |  100% |
| 1 | 2-F | 524 |  100% |
| 1 | 2-G | 524 |  100% |
| 1 | 2-H | 524 |  100% |
| 1 | 2-I | 524 |  100% |
| 1 | 2-J | 524 |  100% |
| 1 | 2-K | 524 |  100% |
| 1 | 2-L | 524 |  100% |
| 1 | 2-M | 524 |  100% |
| 1 | 2-N | 524 |  100% |
| 1 | 3-A | 524 |  56% 43% |
| 1 | 3-B | 524 |  100% |
| 1 | 3-C | 524 |  100% |
| 1 | 3-D | 524 |  100% |
| 1 | 3-E | 524 |  100% |
| 1 | 3-F | 524 |  100% |

Continued on next page...

Continued from previous page...

| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 1 | 3-G | 524 | 100% |
| 1 | 3-H | 524 | 100% |
| 1 | 3-I | 524 | 100% |
| 1 | 3-J | 524 | 100% |
| 1 | 3-K | 524 | 100% |
| 1 | 3-L | 524 | 100% |
| 1 | 3-M | 524 | 100% |
| 1 | 3-N | 524 | 100% |
| 1 | 4-A | 524 | 61% 39% |
| 1 | 4-B | 524 | 100% |
| 1 | 4-C | 524 | 100% |
| 1 | 4-D | 524 | 100% |
| 1 | 4-E | 524 | 100% |
| 1 | 4-F | 524 | 100% |
| 1 | 4-G | 524 | 100% |
| 1 | 4-H | 524 | 100% |
| 1 | 4-I | 524 | 100% |
| 1 | 4-J | 524 | 100% |
| 1 | 4-K | 524 | 100% |
| 1 | 4-L | 524 | 100% |
| 1 | 4-M | 524 | 100% |
| 1 | 4-N | 524 | 100% |

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 65574 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called 60 kDa chaperonin.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 1 | 1-A | 524 | Total | C | N | O | S | 0 | 0 |
| | | | 3851 | 2395 | 662 | 774 | 20 | | |
| 1 | 2-A | 524 | Total | C | N | O | S | 0 | 0 |
| | | | 3851 | 2395 | 662 | 774 | 20 | | |
| 1 | 3-A | 524 | Total | C | N | O | S | 0 | 0 |
| | | | 3851 | 2395 | 662 | 774 | 20 | | |
| 1 | 4-A | 524 | Total | C | N | O | S | 0 | 0 |
| | | | 3851 | 2395 | 662 | 774 | 20 | | |
| 1 | 1-B | 524 | Total | C | N | O | S | 0 | 0 |
| | | | 3851 | 2395 | 662 | 774 | 20 | | |
| 1 | 1-C | 524 | Total | C | N | O | S | 0 | 0 |
| | | | 3851 | 2395 | 662 | 774 | 20 | | |
| 1 | 1-D | 524 | Total | C | N | O | S | 0 | 0 |
| | | | 3851 | 2395 | 662 | 774 | 20 | | |
| 1 | 1-E | 524 | Total | C | N | O | S | 0 | 0 |
| | | | 3851 | 2395 | 662 | 774 | 20 | | |
| 1 | 1-F | 524 | Total | C | N | O | S | 0 | 0 |
| | | | 3851 | 2395 | 662 | 774 | 20 | | |
| 1 | 1-G | 524 | Total | C | N | O | S | 0 | 0 |
| | | | 3851 | 2395 | 662 | 774 | 20 | | |
| 1 | 1-H | 524 | Total | C | N | O | S | 0 | 0 |
| | | | 3851 | 2395 | 662 | 774 | 20 | | |
| 1 | 1-I | 524 | Total | C | N | O | S | 0 | 0 |
| | | | 3851 | 2395 | 662 | 774 | 20 | | |
| 1 | 1-J | 524 | Total | C | N | O | S | 0 | 0 |
| | | | 3851 | 2395 | 662 | 774 | 20 | | |
| 1 | 1-K | 524 | Total | C | N | O | S | 0 | 0 |
| | | | 3851 | 2395 | 662 | 774 | 20 | | |
| 1 | 1-L | 524 | Total | C | N | O | S | 0 | 0 |
| | | | 3851 | 2395 | 662 | 774 | 20 | | |
| 1 | 1-M | 524 | Total | C | N | O | S | 0 | 0 |
| | | | 3851 | 2395 | 662 | 774 | 20 | | |
| 1 | 1-N | 524 | Total | C | N | O | S | 0 | 0 |
| | | | 3851 | 2395 | 662 | 774 | 20 | | |

There are 14 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|------------|
| A | 13 | GLY | ARG | conflict | UNP Q6Q099 |
| B | 13 | GLY | ARG | conflict | UNP Q6Q099 |
| C | 13 | GLY | ARG | conflict | UNP Q6Q099 |
| D | 13 | GLY | ARG | conflict | UNP Q6Q099 |
| E | 13 | GLY | ARG | conflict | UNP Q6Q099 |
| F | 13 | GLY | ARG | conflict | UNP Q6Q099 |
| G | 13 | GLY | ARG | conflict | UNP Q6Q099 |
| H | 13 | GLY | ARG | conflict | UNP Q6Q099 |
| I | 13 | GLY | ARG | conflict | UNP Q6Q099 |
| J | 13 | GLY | ARG | conflict | UNP Q6Q099 |
| K | 13 | GLY | ARG | conflict | UNP Q6Q099 |
| L | 13 | GLY | ARG | conflict | UNP Q6Q099 |
| M | 13 | GLY | ARG | conflict | UNP Q6Q099 |
| N | 13 | GLY | ARG | conflict | UNP Q6Q099 |

- Molecule 2 is water.

| Mol | Chain | Residues | Atoms | AltConf |
|-----|-------|----------|------------------|---------|
| 2 | 1-A | 19 | Total O 19 19 | 0 |
| 2 | 1-B | 12 | Total O 12 12 | 0 |
| 2 | 1-C | 14 | Total O 14 14 | 0 |
| 2 | 1-D | 14 | Total O 14 14 | 0 |
| 2 | 1-E | 10 | Total O 10 10 | 0 |
| 2 | 1-F | 6 | Total O 6 6 | 0 |
| 2 | 1-G | 13 | Total O 13 13 | 0 |
| 2 | 1-H | 1 | Total O 1 1 | 0 |
| 2 | 1-I | 3 | Total O 3 3 | 0 |
| 2 | 1-J | 5 | Total O 5 5 | 0 |
| 2 | 1-K | 1 | Total O 1 1 | 0 |
| 2 | 1-L | 2 | Total O 2 2 | 0 |

Continued on next page...

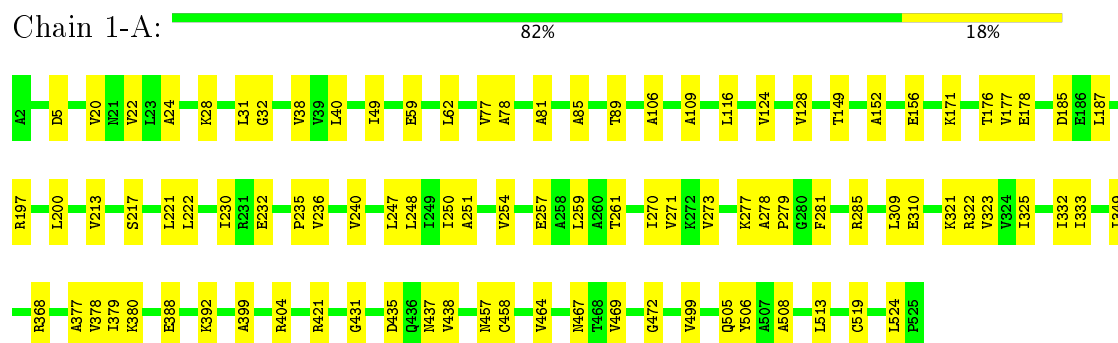
Continued from previous page...

| Mol | Chain | Residues | Atoms | | AltConf |
|-----|-------|----------|-------|---|---------|
| 2 | 1-M | 5 | Total | O | 0 |
| | | | 5 | 5 | |
| 2 | 1-N | 2 | Total | O | 0 |
| | | | 2 | 2 | |

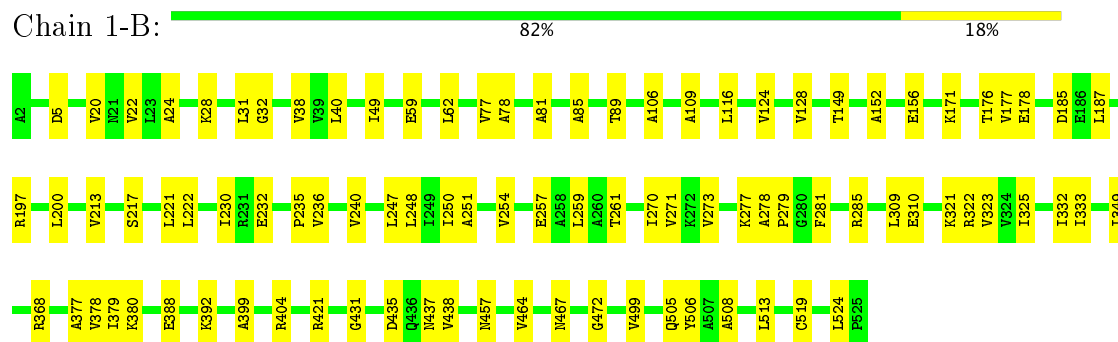
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

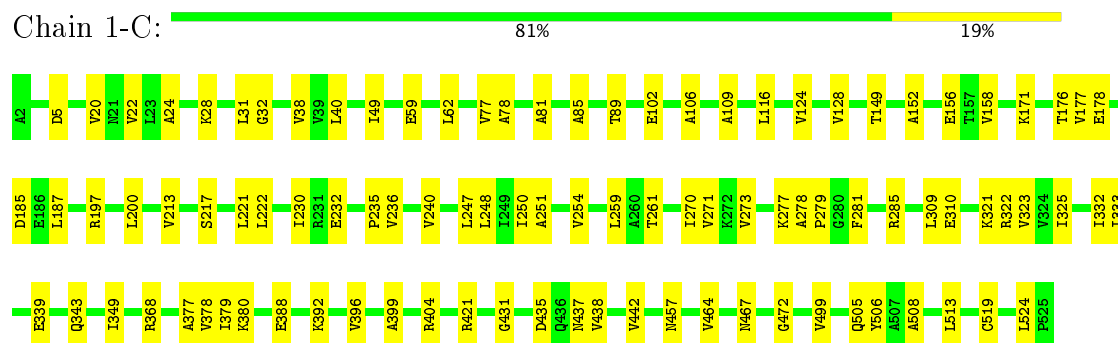
- Molecule 1: 60 kDa chaperonin



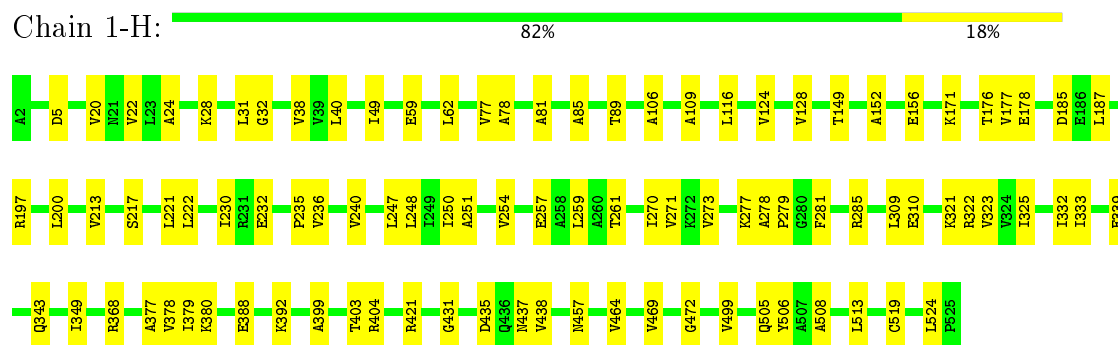
- Molecule 1: 60 kDa chaperonin



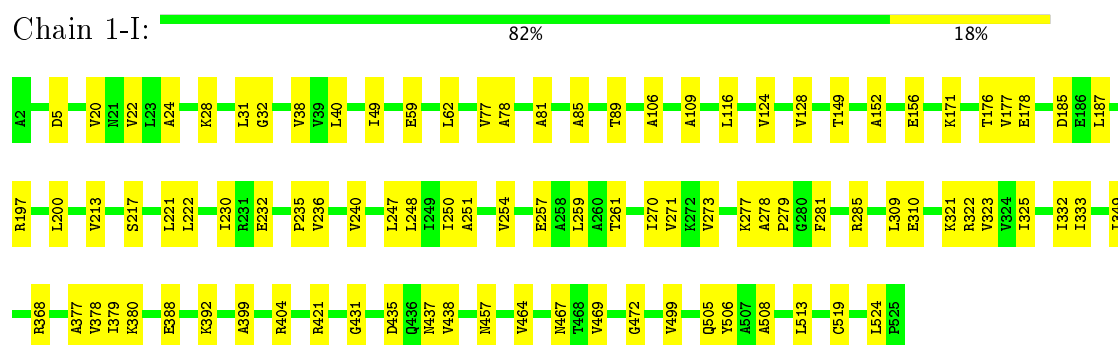
- Molecule 1: 60 kDa chaperonin



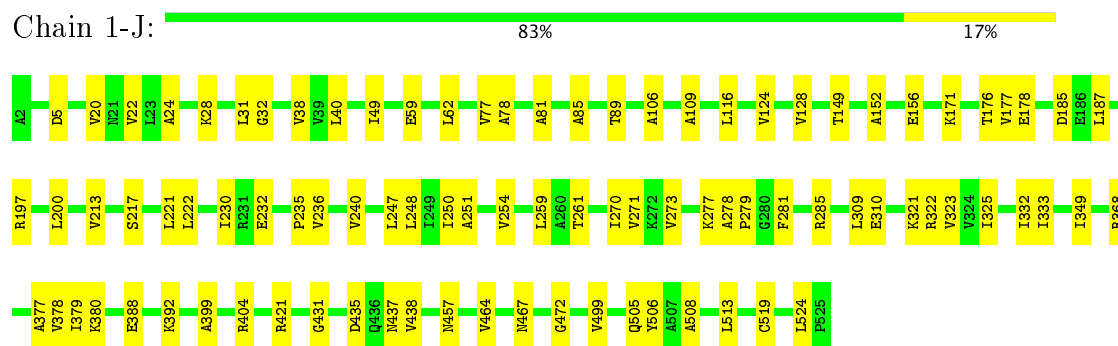
- Molecule 1: 60 kDa chaperonin



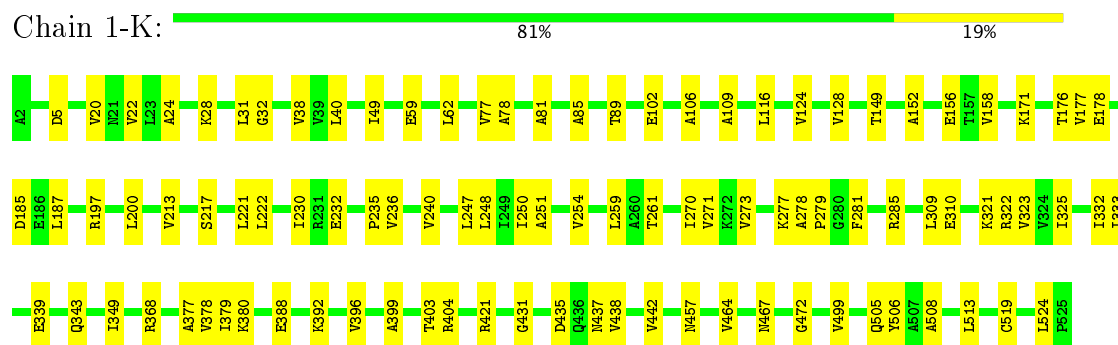
- Molecule 1: 60 kDa chaperonin



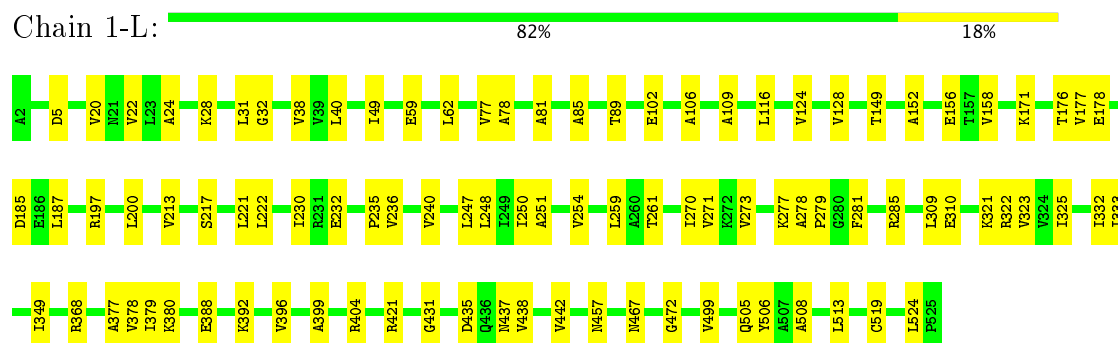
- Molecule 1: 60 kDa chaperonin



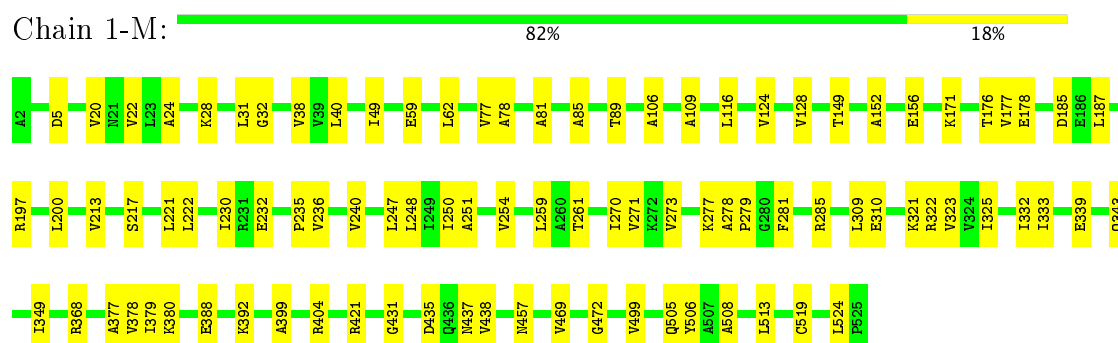
- Molecule 1: 60 kDa chaperonin



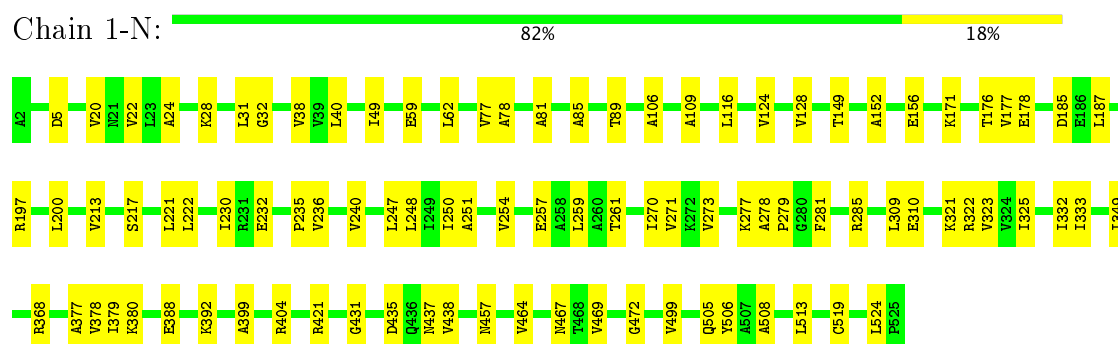
- Molecule 1: 60 kDa chaperonin



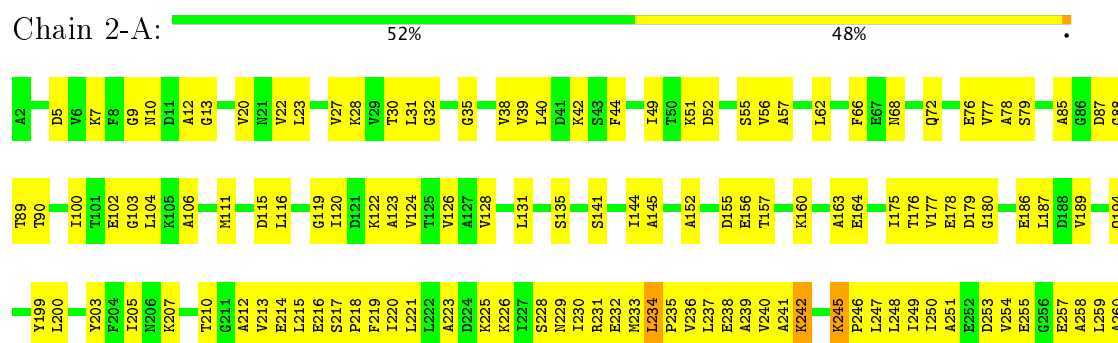
- Molecule 1: 60 kDa chaperonin

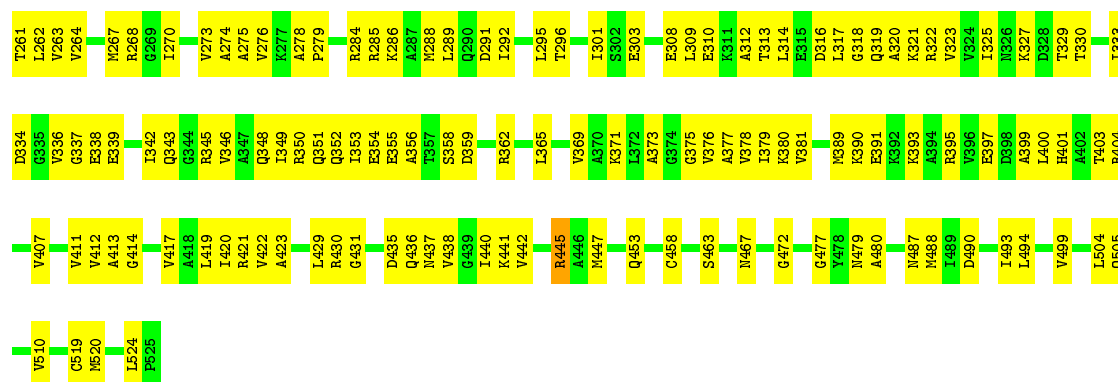


- Molecule 1: 60 kDa chaperonin



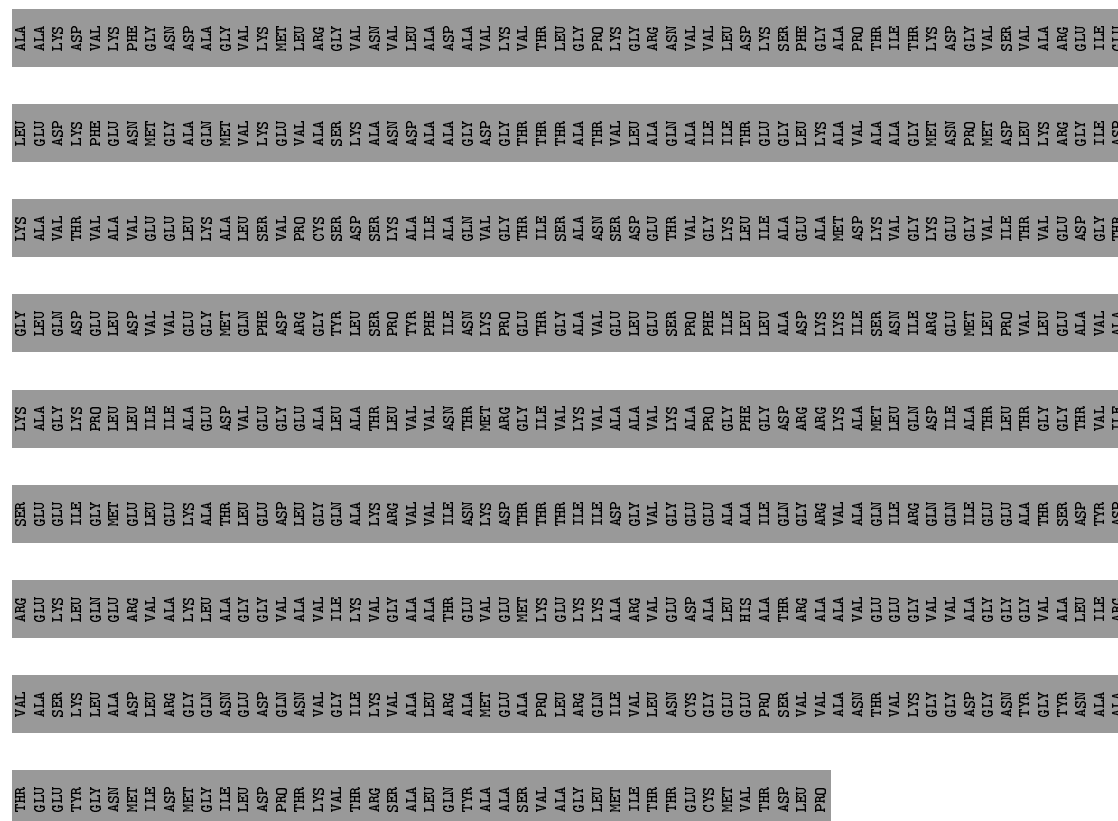
- Molecule 1: 60 kDa chaperonin





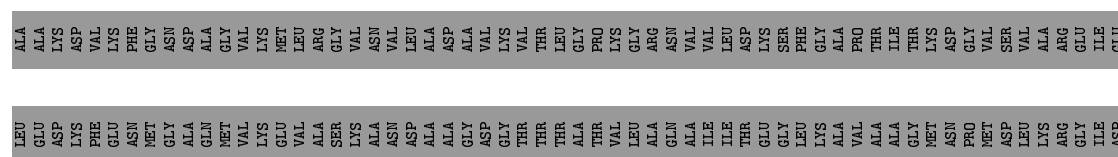
- Molecule 1: 60 kDa chaperonin

Chain 2-B:  100%



- Molecule 1: 60 kDa chaperonin

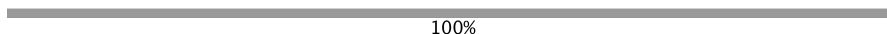
Chain 2-C:  100%



| | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|
| THR | VAL | ARG | SER | LYS | GLY | LYS |
| GLU | GLU | GLU | GLU | ALA | LEU | ALA |
| GLU | SER | LYS | GLU | GLY | GLN | VAL |
| TYR | LYS | LEU | ILE | LYS | ASP | THR |
| GLY | LEU | GLN | GLY | PRO | GLU | ALA |
| ASN | ALA | GLU | MET | LEU | LEU | ALA |
| MET | ASP | ARG | GLU | LEU | ASP | VAL |
| ILE | LEU | VAL | LEU | ILE | VAL | GLU |
| GLU | ARG | ALA | GLU | ILE | VAL | GLU |
| MET | GLY | LYS | GLY | ALA | GLY | LYS |
| ILE | ASN | ALA | THR | ASP | MET | ALA |
| LEU | GLU | GLY | LEU | VAL | GLN | LEU |
| PRO | ASP | GLY | GLU | GLU | PHE | SER |
| THR | GLN | VAL | ASP | GLY | ARG | PRO |
| ASN | ALA | ALA | LEU | ALA | GLY | CYS |
| VAL | VAL | ILE | GLN | LEU | TYR | SER |
| THR | ILE | LYS | ALA | ALA | LEU | ASP |
| ARG | ARG | LYS | LYS | THR | LEU | SER |
| SER | VAL | VAL | ARG | LEU | PRO | LYS |
| ALA | ALA | ALA | VAL | VAL | TYR | ALA |
| LEU | LEU | ALA | VAL | VAL | PHE | ILE |
| GLN | ARG | THR | ILE | ASN | ILE | ALA |
| TYR | ALA | GLU | ASN | THR | ASN | GLN |
| ALA | MET | VAL | LYS | MET | LYS | VAL |
| ALA | GLU | GLU | ASP | ARG | PRO | GLY |
| SER | ALA | MET | THR | GLY | GLU | THR |
| VAL | PRO | LYS | THR | ILE | THR | ILE |
| ALA | LEU | GLU | THR | VAL | GLY | SER |
| GLY | GLN | LYS | ILE | LYS | ALA | ALA |
| LEU | ARG | LYS | ILE | VAL | VAL | ASN |
| GLU | GLN | LYS | ILE | VAL | VAL | ASN |
| GLU | GLU | GLU | GLU | ALA | GLU | ASP |
| CYS | ASP | GLU | GLY | LYS | SER | THR |
| GLU | GLU | ALA | GLU | ALA | PRO | VAL |
| GLY | GLY | LEU | ALA | GLY | PHE | GLY |
| MET | GLU | LEU | ALA | GLY | ILE | LYS |
| VAL | GLU | HIS | ALA | PHE | LEU | LEU |
| THR | PRO | ALA | ILE | GLY | LEU | ILE |
| ASP | SER | THR | GLN | ASP | ALA | ALA |
| PRO | VAL | ARG | GLY | ARG | ASP | GLU |
| | ALA | ALA | VAL | LYS | LYS | ALA |
| | ALA | VAL | ALA | ILE | ASP | MET |
| | ASN | VAL | ALA | ALA | ILE | LYS |
| | THR | GLU | GLN | MET | SER | LYS |
| | VAL | GLU | ILE | LEU | ASN | VAL |
| | LYS | GLY | ARG | GLN | ILE | GLY |
| | GLY | VAL | GLN | ILE | ARG | LYS |
| | ASP | ALA | ILE | GLY | MET | GLY |
| | GLY | GLY | GLU | THR | LEU | VAL |
| | ASN | GLY | GLU | LEU | PRO | VAL |
| | TYR | GLY | ALA | THR | VAL | THR |
| | THR | VAL | THR | GLY | LEU | VAL |
| | TYR | ALA | SER | ASP | GLU | GLU |
| | ASN | LEU | THR | THR | ALA | ASP |
| | ALA | ILE | TYR | VAL | VAL | GLY |
| | ALA | ARG | ASN | ILE | VAL | THR |

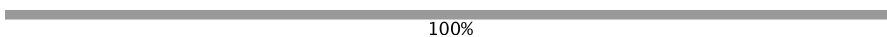
- Molecule 1: 60 kDa chaperonin

Chain 2-D:

[illegible]

- Molecule 1: 60 kDa chaperonin

Chain 2-E:



[illegible]

- Molecule 1: 60 kDa chaperonin

Chain 2-F: 100%

[illegible]

THR GLU GLU TYR GLY ASN MET ILE ASP MET GLY ILE LEU LEU ASP PRO THR LYS VAL THR ARG SER SER ALA LEU GLN TYR ALA ALA VAL VAL ALA GLY LEU MET ILE THR THR GLU CYS MET VAL THR ASP LEU PRO

- Molecule 1: 60 kDa chaperonin

Chain 2-G: 100%

[illegible]

- Molecule 1: 60 kDa chaperonin

Chain 2-H:  100%

[illegible]

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ARG | GLY | LYS | LEU | GLN | GLU | ARG | VAL | ALA | LYS | LEU | ALA | GLY | GLY | VAL | ALA | VAL | ILE | LYS | VAL | GLY | ALA | ALA | LYS | LYS | GLU | GLY | LYS | ALA | ARG | ARG | VAL | VAL | GLU | GLY | VAL | VAL | ALA | ALA | GLY | GLY | VAL | VAL | ALA | ALA | LEU | ILE | ARG |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| VAL | ALA | SER | LYS | LEU | ALA | ASP | LEU | ARG | GLY | GLN | ASN | GLU | ASP | GLN | ASN | VAL | VAL | GLY | GLY | LYS | ALA | VAL | LEU | ARG | ALA | ALA | MET | GLU | ALA | ALA | PRO | PRO | LEU | LEU | ARG | GLN | ILE | ILE | VAL | VAL | LEU | ASN | CYS | GLY | GLU | GLU | GLU | PRO | SER | VAL | VAL | VAL | ALA | ALA | ASN | ASN | THR | VAL | LYS | LYS | GLY | GLY | ASP | GLY | ASN | TYR | TYR | GLY | GLY | ASN | ASN | ALA | ALA |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| THR | GLU | GLU | TYR | GLY | ASN | MET | ILE | ASP | MET | GLY | ILE | LEU | ASP | PRO | THR | LYS | VAL | THR | ARG | SER | ALA | LEU | GLN | TYR | ALA | ALA | SER | VAL | ALA | GLY | LEU | MET | ILE | THR | THR | GLU | CYS | MET | VAL | THR | ASP | LEU | PRO |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

- Molecule 1: 60 kDa chaperonin

Chain 2-I: 100%

ALA ALA ALA ALA ALA ASP ASP LYS LYS PHE GLY GLY ASP ASP ALA ALA GLY VAL VAL LYS LYS MET NET LEU LEU ARG ARG GLY VAL VAL ASN ASN VAL VAL VAL VAL THR THR LEU LEU PRO PRO LYS LYS GLY GLY ARG ARG ASN ASN VAL VAL VAL VAL LEU LEU THR THR VAL VAL LEU LEU PRO PRO LYS LYS SER SER PHE PHE GLY GLY ALA ALA PRO PRO THR THR TLE TLE THR THR LYS LYS ASP ASP GLY GLY VAL VAL SER SER VAL VAL ALA ALA ARG ARG ARG ARG GLU GLU TLE TLE TLE TLE

LEU
GLU
ASP
ASP
LYS
PHE
GLU
GLU
ASN
MET
MET
GLY
ALA
ALA
GLN
MET
VAL
VAL
LYS
GLU
GLU
VAL
ALA
SER
LYS
LYS
ALA
ASN
ASN
ASP
ALA
ALA
ALA
GLY
ASP
GLY
THR
THR
THR
ALA
THR
VAL
LEU
ALA
ALA
GLN
ALA
ALA
ILE
ILE
THR
THR
GLU
GLY
LEU
LYS
LYS
ALA
ALA
VAL
VAL
ALA
ALA
ALA
GLY
MET
ASN
ASN
PRO
MET
MET
ASP
LEU
LYS
LYS
ARG
GLY
ILE
ILE
SER

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| LYS | ALA | VAL | THR | VAL | ALA | VAL | GLU | GLU | LEU | LYS | ALA | LEU | SER | VAL | PRO | CYS | SER | ASP | SER | LYS | ALA | ALA | ILE | ALA | GLN | VAL | GLY | THR | ILE | SER | ASN | SER | ASP | GLU | THR | VAL | GLY | LYS | LEU | ILE | ALA | GLU | ALA | NET | ASP | LYS | VAL | GLY | GLU | GLY | ILE | THR | VAL | GLU | ASP | GLY | THR |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

GLY
LEU
GLN
ASP
GLU
LEU
ASP
VAL
VAL
GLU
GLY
MET
GLN
PHE
ASP
ARG
GLY
TYR
LEU
SER
PRO
TYR
PHE
ILE
ASN
LYS
PRO
GLU
THR
GLY
ALA
VAL
GLU
LEU
GLU
SER
PRO
PHE
ILE
LYS
ILE
SER
ASN
ILE
ARG
GLU
MET
LEU
PRO
VAL
LEU
GLU
ALA
VAL

LYS ALA GLY LYS PRO LEU LEU ILE ILE ALA GLU ASP VAL GLY GLY ALA ALA LEU ALA THR LEU VAL VAL ASN THR MET ARG GLY ILE VAL LYS VAL VAL ALA ALA VAL LYS ALA PRO PHE GLY GLY GLY ASP ARG ARG LYS ALA MET LEU GLN ASP ILE ALA THR LEU THR GLY GLY THR VAL ILE

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| SER | GLU | GLU | ILE | GLY | GLU | GLU | GLU | LYS | ALA | THR | LEU | GLU | ASP | GLY | GLY | GLN | ALA | LYS | ARG | VAL | VAL | ILE | ASN | LYS | ASP | THR | THR | THR | ILE | ILE | ASP | GLY | VAL | GLY | GLU | GLU | ALA | ALA | ILE | GLN | GLY | ARG | VAL | VAL | GLN | GLN | ILE | ILE | THR | SER | ASP | THR | THR | ASP |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ARG | GLY | LYS | LEU | GLN | GLU | ARG | VAL | ALA | ALA | LYS | LEU | ALA | GLY | ILE | LYS | THR | GLU | GLU | GLU | MET | LYS | GLY | LYS | ALA | ARG | VAL | GLU | ASP | ALA | LEU | HIS | ALA | THR | ARG | ALA | VAL | VAL | GLU | GLY | GLY | VAL | ALA | ALA | ILE | PAC |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| VAL | ALA | SER | LYS | LEU | ALA | ASP | LEU | ARG | GLY | GLN | ASN | GLU | ASP | GLN | ASN | VAL | VAL | GLY | TYR | LYS | ASN | GLY | ASP | GLY | GLY | GLY | TYR | TYR | ASN | ALA | ALA |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| THR | GLU | GLU | TYR | GLY | ASN | MET | MET | ASP | MET | GLY | ILE | LEU | ASP | PRO | THR | LYS | THR | ARG | SER | ALA | LEU | GLN | TYR | ALA | ALA | SER | VAL | ALA | GLY | LEU | MET | ILE | THR | THR | GLU | CYS | MET | MET | VAL | THR | ASP | LEU | PRO |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

- Molecule 1: 60 kDa chaperonin

Chain 2-J: 100%

ALA
ALA
LYS
ASP
VAL
LYS
PHE
GLY
ASN
ASP
ALA
GLY
VAL
LYS
MET
LEU
ARG
GLY
VAL
ASN
VAL
LEU
VAL
ALA
ASP
ALA
VAL
LYS
LYS
GLY
GLY
ARG
ASN
VAL
VAL
LEU
LEU
LYS
LYS
SER
PHE
GLY
ALA
PRO
PRO
THR
ILE
THR
LYS
ASP
GLY
VAL
SER
VAL
ALA
ALA
ARG
GLU
ILE
Ile

LEU GLU ASP LYS PHE GLU ASN MET GLY GLN VAL VAL LYS GLU VAL ALA ALA SER LYS ALA ASP ASP ALA ALA GLY ASP GLY THR THR THR ALA THR VAL LEU LEU GLN ALA ALA ILE ILE THR THR GLY LEU LYS ALA VAL ALA ALA GLY MET ASN PRO MET ASP LEU LYS ARG GLY ILE ASP

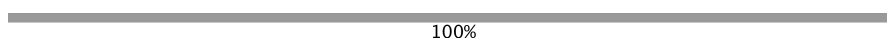
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| LYS | ALA | VAL | THR | VAL | ALA | VAL | GLU | GLU | LEU | LYS | ALA | LEU | SER | ASP | SER | LYS | ALA | ILE | ALA | GLN | GLY | THR | ILE | SER | ASN | SER | ASP | GLU | THR | VAL | GLY | LYS | LEU | ILE | ALA | GLU | ALA | MET | ASP | LYS | VAL | GLY | LYS | GLU | GLY | VAL | ILE | THR | VAL | GLU | ASP | GLY |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

GLY LEU GLN ASP ASP VAL VAL GLU MET GIN PHE ASP ARG TYR LEU SER PRO TYR PHE ILE ASN LYS PRD THR GLY ALA VAL GLU LEU SER GLU PRO PHE ILE LEU LEU LEU ALA ASP LYS LYS ILE ILE SER ASN ILE ARG GLU MET LEU PRO VAL LEU GLU ALA VAL

| | | | | |
|-----|-----|-----|-----|-----|
| THR | VAL | ARG | SER | LYS |
| GLU | ALA | GLU | GLU | ALA |
| GLU | SER | LYS | GLU | GLY |
| TYR | LYS | LEU | ILE | LYS |
| GLY | LEU | GLN | GLY | PRO |
| ASN | ALA | GLU | MET | LEU |
| MET | ASP | ARG | GLU | LEU |
| ILE | LEU | VAL | LEU | ILE |
| ASP | ARG | ALA | GLU | ILE |
| MET | GLY | LYS | LYS | ALA |
| GLY | GLN | LEU | ALA | GLU |
| ILE | ASN | LEU | THR | ASP |
| LEU | GLU | GLY | LEU | VAL |
| ASP | ASP | GLY | GLU | GLY |
| PRO | GLN | VAL | ASP | GLY |
| THR | ASN | ALA | LEU | GLU |
| LYS | VAL | VAL | GLY | ALA |
| VAL | GLY | ILE | GLN | LEU |
| THR | ILE | LYS | ALA | ALA |
| ARG | LYS | VAL | LYS | THR |
| SER | VAL | GLY | ARG | LEU |
| ALA | ALA | ALA | VAL | VAL |
| LEU | LEU | ALA | VAL | VAL |
| GLN | ARG | THR | ILE | ASN |
| TYR | ALA | GLU | ASN | THR |
| ALA | MET | VAL | LYS | MET |
| ALA | ALA | GLU | ASP | ARG |
| SER | SER | ALA | MET | GLY |
| VAL | PRO | LYS | THR | ILE |
| ALA | LEU | GLU | THR | VAL |
| GLY | ARG | LYS | ILE | LYS |
| ILE | GLN | LYS | ILE | VAL |
| ILE | ILE | ALA | ASP | ALA |
| THR | VAL | ARG | GLY | ALA |
| THR | LEU | VAL | VAL | VAL |
| GLU | ASN | GLU | GLY | LYS |
| THR | CYS | ASP | GLU | ALA |
| GLY | GLY | ALA | GLU | ALA |
| CYS | GLU | LEU | ALA | PRO |
| MET | MET | LEU | ALA | GLY |
| VAL | GLU | HIS | ALA | GLY |
| THR | PRO | ALA | ILE | PHE |
| THR | THR | THR | ALA | GLY |
| ASP | SER | THR | GLN | ASP |
| LEU | VAL | ARG | GLY | ARG |
| PRO | VAL | ALA | ARG | ARG |
| | ALA | ALA | VAL | LYS |
| | ASN | VAL | ALA | LYS |
| | THR | GLU | GLN | MET |
| | VAL | GLY | ILE | LEU |
| | LYS | GLY | ARG | GLN |
| | GLY | VAL | GLN | ASP |
| | ASP | ALA | ILE | ALA |
| | ASN | GLY | GLU | THR |
| | TYR | GLY | GLU | LEU |
| | THR | GLY | ALA | THR |
| | TYR | VAL | THR | GLY |
| | TYR | ALA | SER | GLY |
| | ASN | LEU | ASP | THR |
| | ALA | ILE | TYR | THR |
| | ALA | ARG | ASP | ILE |

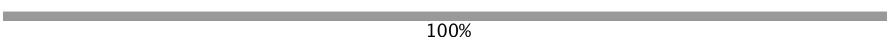
- Molecule 1: 60 kDa chaperonin

Chain 2-K:

[illegible]

- Molecule 1: 60 kDa chaperonin

Chain 2-L:

[illegible]

| | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|
| THR | VAL | ARG | SER | LYS | GLY | LYS |
| GLU | SER | GLU | GLU | ALA | LEU | ALA |
| GLU | GLU | GLU | GLU | GLY | GLN | VAL |
| THR | LYS | LEU | ILE | LYS | ASP | THR |
| GLY | LEU | GLN | GLY | PRO | GLU | VAL |
| ASN | ALA | GLU | MET | LEU | LEU | ALA |
| MET | ASP | ARG | GLU | LEU | ASP | VAL |
| ILE | LEU | VAL | LEU | ILE | VAL | GLU |
| GLU | ARG | ALA | GLU | ILE | VAL | GLU |
| MET | GLY | LYS | LYS | ALA | GLY | LYS |
| ILE | ASN | LEU | THR | ASP | MET | ALA |
| LEU | GLU | GLY | LEU | VAL | GLN | LEU |
| PRO | ASP | GLY | GLU | GLU | PHE | SER |
| THR | GLN | VAL | ASP | GLY | ARG | PRO |
| ASN | ALA | ALA | LEU | ALA | GLY | CYS |
| VAL | VAL | ILE | GLN | LEU | THR | SER |
| THR | ILE | LYS | ALA | ALA | LEU | ASP |
| ALA | ARG | THR | ILE | ASN | ILE | ALA |
| GLY | GLU | GLU | ASN | THR | ASN | GLN |
| LEU | ALA | VAL | LYS | VAL | LYS | VAL |
| GLU | MET | VAL | LYS | MET | PRO | GLY |
| ALA | GLU | GLU | ASP | ARG | PRO | GLY |
| ALA | ALA | MET | THR | GLY | GLU | THR |
| VAL | ALA | LYS | THR | ILE | THR | ILE |
| ALA | LEU | GLU | THR | VAL | GLY | SER |
| GLY | GLN | LYS | ILE | LYS | ALA | ALA |
| LEU | ARG | LYS | ILE | VAL | VAL | ASN |
| THR | GLN | THR | ILE | VAL | GLU | ASP |
| THR | ASN | GLU | GLY | VAL | GLU | THR |
| CYS | CYS | ASP | GLU | ALA | PRO | VAL |
| GLY | GLY | ALA | GLU | PRO | PHE | GLY |
| MET | GLU | LEU | ALA | GLY | ILE | LYS |
| VAL | GLU | HIS | ALA | PHE | LEU | LEU |
| THR | PRO | ALA | ILE | GLY | LEU | ILE |
| ASP | SER | THR | GLN | ASP | ALA | ALA |
| PRO | VAL | ARG | GLY | ARG | ASP | GLU |
| | ALA | ALA | VAL | LYS | LYS | ALA |
| | ASN | VAL | ALA | ALA | ILE | MET |
| | THR | GLU | GLN | MET | SER | LYS |
| | VAL | GLU | ILE | LEU | ASN | VAL |
| | LYS | GLY | ARG | GLN | ILE | GLY |
| | GLY | VAL | GLN | ILE | ARG | LYS |
| | ASP | ALA | ILE | THR | MET | GLY |
| | GLY | GLY | GLU | THR | LEU | VAL |
| | ASN | GLY | GLU | LEU | PRO | THR |
| | THR | GLY | ALA | THR | VAL | VAL |
| | VAL | VAL | THR | GLY | LEU | THR |
| | THR | ALA | THR | THR | GLU | VAL |
| | ASN | LEU | ASP | THR | ALA | ASP |
| | ALA | ARG | THR | ILE | VAL | GLY |

- Molecule 1: 60 kDa chaperonin

Chain 2-M: 100%

[illegible]

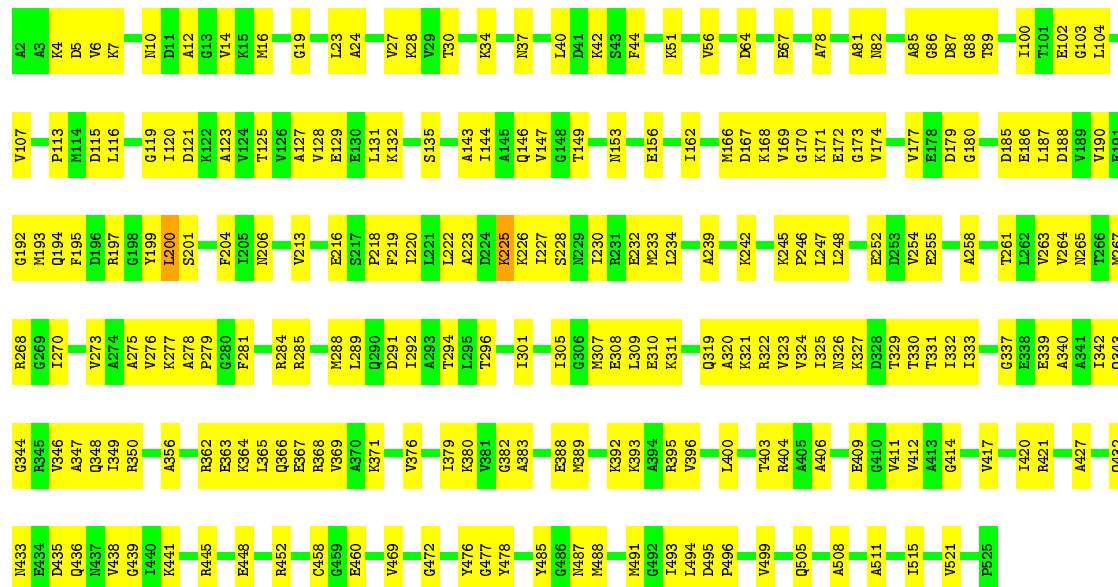
- Molecule 1: 60 kDa chaperonin

Chain 2-N:  100%

[illegible]

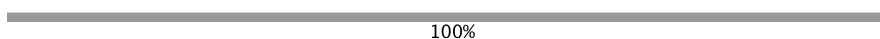
- Molecule 1: 60 kDa chaperonin

Chain 3-A:



- Molecule 1: 60 kDa chaperonin

Chain 3-B:



[illegible]

- Molecule 1: 60 kDa chaperonin

Chain 3-C: 100%

[illegible]

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| THR | GLU | GLU | TYR | GLY | ASN | MET | ILE | ASP | MET | GLY | ILE | LEU | ASP | PRO | THR | LYS | VAL | THR | ARG | SER | ALA | LEU | GLN | TYR | ALA | ALA | SER | VAL | VAL | ALA | GLY | LEU | MET | ILE | THR | THR | GLU | CYS | MET | VAL | THR | ASP | LEU | PRO |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

- Molecule 1: 60 kDa chaperonin

Chain 3-D: 100%

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ALA | ALA | ALA | LYS | ASP | VAL | LYS | PHE | GLY | ASN | ASP | ALA | GLY | VAL | LYS | MET | LEU | ARG | GLY | VAL | ASN | VAL | LEU | ALA | ASP | ALA | VAL | LYS | VAL | THR | THR | LEU | GLY | PRO | LYS | GLY | ARG | ASN | VAL | VAL | LEU | ASP | LYS | SER | PHE | GLY | ALA | PRO | THR | THR | LYS | ASP | GLY | VAL | SER | VAL | ALA | ALA | ARG | GLU | ILE | ILE |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

LEU
GLU
ASP
ASP
LYS
PHE
GLU
GLU
ASN
MET
MET
GLY
ALA
ALA
GLN
MET
VAL
VAL
LYS
GLU
GLU
VAL
ALA
SER
LYS
LYS
ALA
ASN
ASN
ASP
ALA
ALA
ALA
GLY
ASP
GLY
THR
THR
THR
ALA
THR
VAL
LEU
VAL
ALA
GLN
ALA
ALA
ILE
ILE
THR
THR
GLU
GLY
LEU
LYS
LYS
ALA
VAL
VAL
ALA
ALA
ALA
GLY
MET
ASN
MET
PRO
MET
ASP
LEU
LYS
ARG
GLY
ILE
SER

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| LYS | ALA | VAL | THR | VAL | ALA | VAL | GLU | GLU | LEU | LYS | ALA | LEU | SER | VAL | PRO | CYS | SER | ASP | SER | LYS | ALA | ILE | ILE | GLN | GLY | THR | ILE | SER | ASN | SER | ASP | GLU | THR | VAL | GLY | LYS | LEU | ILE | ALA | GLU | ALA | ASP | NET | LYS | VAL | GLY | GLU | ILE | THR | VAL | GLU | ASP | GLY | THR |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

GLY LEU GLN GLN ASP ASP ASP ASP VAL VAL VAL VAL GLU GLY GLY MET MET GLN PHE ASP ASP ARG ARG TYR LEU SER SER PRO TYR PHE PHE ILE ASN LYS PRO PRO GLU GLY THR GLY GLY ALA VAL VAL LEU LEU LEU LEU LEU LEU ALA ALA ASP LYS LYS LYS ILE ILE ILE SER SER ASN ASN ILE ILE ARG ARG GLU MET MET LEU PRO VAL VAL LEU LEU GLU GLU ALA ALA VAL VAL

LYS ALA GLY LYS PRO PRO LEU LEU LEU ILE ILE ALA ALA GLU GLU ASP VAL VAL GLU GLY GLY GLU ALA ALA LEU LEU ALA THR THR LEU VAL VAL VAL ASN THR THR MET ARG GLY ILE ILE VAL VAL LYS LYS VAL VAL ALA ALA ALA ALA VAL VAL LYS LYS ALA ALA PRO PRO GLY GLY PHE ASP GLY GLY ASP ARG ARG ARG LYS LYS ALA ALA MET MET LEU LEU GLN GLN ASP ASP ILE ILE ALA ALA THR THR LEU LEU THR THR GLY GLY THR THR VAL VAL

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| SER | GLU | GLU | ILE | GLY | MET | GLU | GLU | GLU | LYS | ALA | THR | LEU | GLU | ASP | LEU | GLY | GLN | ALA | LYS | ARG | VAL | VAL | ILE | ASN | LYS | ASP | THR | THR | ILE | ILE | ASP | GLY | VAL | GLY | GLU | GLU | ALA | ALA | ILE | GLN | GLY | ARG | VAL | GLN | GLN | ILE | ILE | GLU | ALA | THR | SER | ASP | TYR | ASP |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| ARG | GLU | LYS | GLY | LEU | GLN | GLU | ARG | VAL | ALA | LYS | LEU | ALA | GLY | GLY | VAL | ALA | VAL | ILE | LYS | VAL | GLY | ALA | ALA | ALA | LYS | LYS | GLU | THR | GLU | GLU | VAL | GLU | NET | LYS | GLY | LYS | ALA | ALA | ARG | VAL | VAL | ASP | GLU | ALA | LEU | HIS | ALA | THR | ARG | ALA | ALA | VAL | VAL | GLU | GLY | VAL | VAL | ALA | GLY | GLY | VAL | ALA | LEU | ILE | PC |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| VAL | ALA | SER | LYS | LEU | ALA | ASP | LEU | ARG | GLY | GLN | ASN | GLU | ASP | GLN | ASN | VAL | LEU | ALA | ARG | ALA | GLY | ILE | LYS | VAL | ALA | VAL | LEU | PRO | LEU | ARG | GLN | ILE | VAL | LEU | ASN | CYS | GLY | GLU | GLU | GLU | PRO | SER | VAL | VAL | VAL | ALA | ASN | THR | VAL | LYS | GLY | GLY | ASP | ASN | TYR | GLY | TYR | ASN | ALA | ALA |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| THR | GLU | GLU | TYR | GLY | ASN | MET | ILE | ASP | MET | GLY | ILE | LEU | ASP | PRO | THR | LYS | VAL | THR | ARG | SER | SER | ALA | LEU | GLN | TYR | ALA | ALA | SER | VAL | ALA | GLY | LEU | MET | ILE | THR | THR | GLU | CYS | MET | MET | VAL | THR | ASP | LEU | PRO |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

- Molecule 1: 60 kDa chaperonin

Chain 3-E:  100%

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ALA | ALA | ALA | LYS | ASP | VAL | LYS | PHE | GLY | ASN | ASP | ALA | GLY | VAL | LYS | VAL | MET | LEU | ARG | GLY | VAL | ASN | VAL | VAL | LEU | ALA | ALA | ASP | ALA | VAL | LYS | VAL | VAL | THR | THR | LEU | GLY | PRO | LYS | GLY | ARG | ASN | VAL | VAL | VAL | LEU | LYS | ASP | LYS | SER | PHE | GLY | ALA | PRO | THR | THR | ILE | LYS | ASP | GLY | VAL | SER | VAL | ALA | ALA | ARG | GLU | ILE | THR |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| LEU | GLU | ASP | LYS | PHE | GLU | ASN | MET | GLY | ALA | ALA | GLN | VAL | LYS | GLU | VAL | ALA | ALA | SER | LYS | ASN | ASP | ALA | ALA | GLY | ASP | GLY | THR | THR | THR | ALA | THR | VAL | LEU | ALA | GLN | ALA | ILE | ILE | THR | THR | GLU | GLY | LEU | LYS | ALA | VAL | VAL | ALA | ALA | GLY | ASN | PRO | MET | MET | ASP | LEU | LYS | ARG | GLY | ILE | STD |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| LYS | ALA | VAL | THR | VAL | ALA | VAL | GLU | GLU | LEU | LYS | ALA | LEU | SER | VAL | PRO | CYS | SER | ASP | SER | LYS | ALA | ALA | ILE | ALA | GLN | GLY | VAL | THR | THR | ILE | SER | ALA | ASN | SER | ASP | GLU | THR | VAL | GLY | LYS | LEU | ILE | ALA | ALA | GLU | MET | ASP | LYS | VAL | GLY | LYS | GLU | ILE | THR | VAL | GLU | ASP | GLY | THR |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

GLY
LEU
GLN
ASP
GLU
LEU
ASP
VAL
VAL
GLU
GLY
MET
GLN
PHE
ASP
ARG
GLY
TYR
LEU
SER
PRO
TYR
PHE
ILE
ASN
LYS
PRO
GLU
GLU
THR
GLY
ALA
VAL
LEU
GLU
SER
PRO
PHE
ILE
LYS
ILE
LYS
SER
ASN
ILE
ARG
GLU
MET
LEU
PRO
VAL
LEU
GLU
ALA
VAL

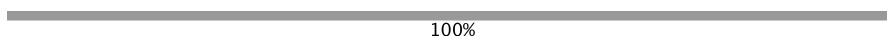
LYS ALA LYS GLY LYS PRO LEU LEU ILE ILE ALA ALA GLU ASP VAL VAL GLU GLY GLU ALA ALA LEU THR THR LEU VAL VAL ASN MET ARG GLY ILE VAL LYS VAL VAL ALA ALA VAL VAL LYS ALA PRO ARG ARG LYS ALA LYS ASP ASP ARG ARG LYS ALA THR THR LEU GLN ASP ILE ILE ALA ALA THR LEU THR GLY GLY THR THR VAL VAL ILE ILE

SER GLU GLU GLU ILE GLY MET GLU LEU GLU GLU LYS ALA ALA THR LEU LEU ASP ASP LEU GLY GLN ALA LYS ARG VAL VAL ILE ASN LYS ASP THR THR ILE ASP GLY VAL GLU GLU ALA ALA ALA GLN ARG ARG VAL VAL GLN GLN GLN ILE GLY GLU ALA THR SER SER TYR ASD

| | | | | |
|-----|-----|-----|-----|-----|
| THR | VAL | ARG | SER | LYS |
| GLU | ALA | GLU | GLU | ALA |
| GLU | SER | LYS | GLU | GLY |
| TYR | LYS | LEU | ILE | LYS |
| GLY | LEU | GLN | GLY | PRO |
| ASN | ALA | GLU | MET | LEU |
| MET | ASP | ARG | GLU | LEU |
| ILE | LEU | VAL | LEU | ILE |
| ASP | ARG | ALA | GLU | ILE |
| MET | GLY | LYS | LYS | ALA |
| GLY | GLN | LEU | ALA | GLU |
| ILE | ASN | LEU | THR | ASP |
| LEU | GLU | GLY | LEU | VAL |
| ASP | ASP | GLY | GLU | GLY |
| PRO | GLN | VAL | ASP | GLY |
| THR | ASN | ALA | LEU | GLU |
| LYS | VAL | VAL | GLY | ALA |
| VAL | GLY | ILE | GLN | LEU |
| THR | ILE | LYS | ALA | ALA |
| ARG | LYS | VAL | LYS | THR |
| SER | VAL | GLY | ARG | LEU |
| ALA | ALA | ALA | VAL | VAL |
| LEU | LEU | ALA | VAL | VAL |
| GLN | ARG | THR | ILE | ASN |
| TYR | ALA | GLU | ASN | THR |
| ALA | MET | VAL | LYS | MET |
| ALA | ALA | GLU | ASP | ARG |
| SER | SER | ALA | MET | GLY |
| VAL | PRO | LYS | THR | ILE |
| ALA | LEU | GLU | THR | VAL |
| GLY | ARG | LYS | ILE | LYS |
| ILE | GLN | LYS | ILE | VAL |
| ILE | ILE | ALA | ASP | ALA |
| THR | VAL | ARG | GLY | ALA |
| THR | LEU | VAL | VAL | VAL |
| THR | ASN | GLU | GLY | LYS |
| GLU | CYS | ASP | GLU | ALA |
| THR | GLY | ALA | GLU | ALA |
| CYS | GLY | LEU | ALA | PRO |
| MET | MET | LEU | ALA | GLY |
| VAL | GLU | HIS | ALA | GLY |
| THR | PRO | ALA | ILE | PHE |
| THR | THR | THR | ALA | GLY |
| ASP | SER | THR | GLN | ASP |
| LEU | VAL | ARG | GLY | ARG |
| PRO | VAL | ALA | ARG | ARG |
| | ALA | ALA | VAL | LYS |
| | ASN | VAL | ALA | LYS |
| | THR | GLU | GLN | MET |
| | VAL | GLY | ILE | LEU |
| | LYS | GLY | ARG | GLN |
| | GLY | VAL | GLN | ASP |
| | ASP | ALA | ILE | ALA |
| | ASN | GLY | GLU | THR |
| | TYR | GLY | GLU | LEU |
| | THR | GLY | ALA | THR |
| | TYR | VAL | THR | GLY |
| | TYR | ALA | SER | GLY |
| | ASN | LEU | ASP | THR |
| | ALA | ILE | TYR | THR |
| | ALA | ARG | ASP | ILE |

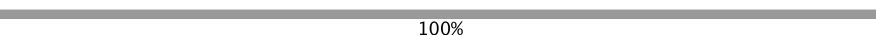
- Molecule 1: 60 kDa chaperonin

Chain 3-H:

[illegible]

- Molecule 1: 60 kDa chaperonin

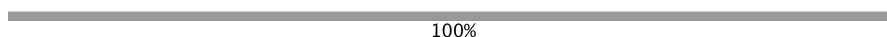
Chain 3-I:

[illegible]

| | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|
| THR | VAL | ARG | SER | LYS | GLY | LYS |
| GLU | GLU | GLU | GLU | ALA | LEU | ALA |
| GLU | SER | LYS | GLU | GLY | GLN | VAL |
| TYR | LYS | LEU | ILE | LYS | ASP | THR |
| GLY | LEU | GLN | GLY | PRO | GLU | ALA |
| ASN | ALA | GLU | MET | LEU | LEU | ALA |
| MET | ASP | ARG | GLU | LEU | ASP | VAL |
| ILE | LEU | VAL | ARG | ILE | VAL | GLU |
| GLU | ARG | ALA | GLU | ILE | VAL | GLU |
| MET | GLY | LYS | GLY | ALA | GLY | LYS |
| ILE | ASN | ALA | THR | ASP | MET | ALA |
| LEU | GLU | GLY | LEU | VAL | GLN | LEU |
| PRO | ASP | GLY | GLU | GLU | PHE | SER |
| THR | ASN | ALA | ASP | GLY | ARG | PRO |
| LYS | VAL | VAL | GLY | ALA | GLY | CYS |
| VAL | VAL | ILE | GLN | LEU | TYR | SER |
| THR | ILE | LYS | ALA | ALA | LEU | ASP |
| ARG | THR | THR | ILE | ASN | PHE | ILE |
| GLN | ARG | THR | ILE | ASN | ILE | ALA |
| TYR | ALA | GLU | ASN | THR | ASN | GLN |
| ALA | MET | VAL | LYS | MET | LYS | VAL |
| ALA | GLU | GLU | ASP | ARG | PRO | GLY |
| SER | ALA | MET | THR | GLY | GLU | THR |
| VAL | PRO | LYS | THR | ILE | THR | ILE |
| ALA | LEU | GLU | THR | VAL | GLY | SER |
| GLY | GLY | LYS | ILE | LYS | ALA | ALA |
| LEU | ARG | LYS | ILE | VAL | VAL | ASN |
| THR | ILE | ALA | ILE | ALA | GLU | SER |
| THR | LEU | VAL | GLY | VAL | GLU | ASP |
| THR | ASN | GLU | GLY | LYS | SER | THR |
| CYS | CYS | ASP | GLU | ALA | PRO | VAL |
| GLY | GLY | ALA | GLU | PRO | PHE | GLY |
| MET | GLU | LEU | ALA | GLY | ILE | LYS |
| VAL | GLU | HIS | ALA | PHE | LEU | LEU |
| THR | PRO | ALA | ILE | GLY | LEU | ILE |
| ASP | SER | THR | GLN | ASP | ALA | ALA |
| PRO | VAL | ARG | GLY | ARG | ASP | GLU |
| | ALA | ALA | VAL | LYS | LYS | ALA |
| | ASN | VAL | ALA | ALA | ILE | MET |
| | THR | GLU | GLN | MET | SER | LYS |
| | VAL | GLU | ILE | LEU | ASN | VAL |
| | LYS | GLY | ARG | GLN | ILE | GLY |
| | GLY | VAL | GLN | ILE | ARG | LYS |
| | ASP | ALA | ILE | ALA | MET | GLY |
| | GLY | GLY | GLU | THR | LEU | VAL |
| | ASN | GLY | GLU | LEU | PRO | ILE |
| | TYR | GLY | ALA | THR | VAL | THR |
| | THR | VAL | THR | GLY | LEU | VAL |
| | TYR | ALA | SER | THR | GLU | ASP |
| | ASN | LEU | ASP | THR | ALA | GLY |
| | ALA | ILE | THR | VAL | VAL | THR |
| | ALA | ARG | ASN | ILE | VAL | ASP |
| | | | | | | THR |

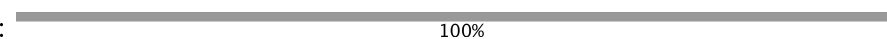
- Molecule 1: 60 kDa chaperonin

Chain 3-J:

[illegible]

- Molecule 1: 60 kDa chaperonin

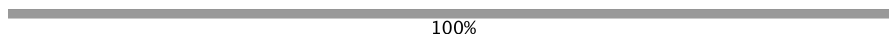
Chain 3-K:



[illegible]

- Molecule 1: 60 kDa chaperonin

Chain 3-L:

[illegible]

THR GLU GLU TYR GLY ASN MET ILE ASP MET GLY ILE LEU ASP PRO THR LYS VAL THR ARG SER SER ALA LEU GLN TYR ALA ALA SER VAL VAL ALA GLY LEU MET ILE THR THR GLU CYS MET MET VAL THR ASP LEU PRO

- Molecule 1: 60 kDa chaperonin

Chain 3-M: 100%

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ALA | ALA | LYS | ASP | VAL | LYS | PHE | GLY | ASN | ASP | ALA | GLY | VAL | LYS | LYS | MET | LEU | ARG | GLY | VAL | ASN | VAL | VAL | LEU | ALA | ASP | ALA | ALA | VAL | LYS | LYS | VAL | THR | THR | GLY | PRO | PRO | LYS | GLY | ARG | ASN | VAL | VAL | VAL | LEU | LEU | ASP | LYS | LYS | SER | PHE | GLY | ALA | ALA | PRO | THR | THR | THR | ILE | ILE | GLY | VAL | SER | SER | VAL | VAL | ALA | ALA | ARG | ARG | GLU | ILE | ILE |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| LEU | GLU | ASP | LYS | PHE | GLU | ASN | MET | GLY | ALA | GLN | VAL | VAL | LYS | GLU | VAL | ALA | SER | LYS | ALA | ALA | ASN | ASP | ASP | ALA | GLY | GLY | THR | THR | THR | THR | ALA | ALA | VAL | LEU | ALA | GLN | ALA | ILE | ILE | ILE | THR | THR | GLU | GLY | LEU | LYS | ALA | VAL | ALA | ALA | ALA | GLY | GLY | NET | ASN | PRO | NET | ASP | LEU | LYS | ARG | GLY | ILE |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| LYS | ALA | VAL | THR | VAL | ALA | VAL | GLU | LEU | LYS | ALA | LEU | VAL | SER | PRO | CYS | SER | ASP | SER | LYS | ALA | IIE | ALA | GLN | VAL | GLY | THR | IIE | SER | ASN | SER | ASP | GLU | THR | VAL | GLY | LYS | IIE | ALA | GLU | ALA | NET | ASP | LYS | VAL | GLY | LYS | GLU | GLY | VAL | IIE | THR | VAL | GLU | ASP | GLY |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

GLY LEU GLN ASP ASP VAL VAL GLU GLY MET GLN PHE ASP ARG GLY TYR LEU SER PRO TYR PHE ILE ASN LYS PRO PRO GLU THR GLY VAL ALA LEU LEU SER PRO PHE ILE LEU LEU ALA ASP LYS LYS ILE SER ASN ARG MET LEU PRO VAL LEU GLU ALA VAL

LYS ALA GLY LYS PRO LEU LEU LEU ILE ILE ALA ALA GLU ASP VAL VAL GLU GLY GLU ALA ALA LEU THR THR MET ARG ARG ILE ILE VAL VAL LYS PRO PRO PHE PHE GLY GLY ASP ARG ARG LYS LYS NET LEU LEU GLN ASP ILE ILE ALA ALA THR THR LEU GLY GLY THR VAL

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| SER | GLU | GLU | ILE | GLY | MET | LEU | LEU | GLU | GLY | LYS | ALA | THR | LEU | GLU | ASP | LEU | GLY | GLN | ALA | LYS | ARG | VAL | VAL | ILE | ILE | ASN | ASP | LYS | ASP | THR | THR | THR | ILE | ILE | ASP | GLY | VAL | GLY | GLU | GLU | ALA | ALA | ALA | ILE | GLN | GLY | ARG | VAL | GLN | GLN | GLN | GLN | ILE | GLN | ILE | GLY | GLU | ALA | ALA | THR | THR | ASP | SER | THR |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

ARG GLU LYS LEU GIN GLU ARG VAL ALA LYS LEU ALA GLY GLY VAL VAL VAL LYS LYS THR GLU GLU VAL MET LYS GLU LYS LYS LYS ARG ARG VAL ASP GLU LEU LEU HIS ALA THR ARG ALA ALA VAL VAL GLU GLU GLY VAL VAL GLY GLY ALA LEU ILE

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| VAL | ALA | SER | LYS | LEU | ALA | ASP | ARG | GLY | GLN | ASN | GLU | ASP | GLN | ASN | VAL | GLY | ILE | LYS | VAL | ALA | ALA | LEU | ARG | ALA | ALA | NET | GLU | THR | PRO | PRO | LEU | ARG | GLN | GLN | ILE | VAL | VAL | LEU | LEU | ASN | CYS | GLY | GLU | GLU | GLU | PRO | SER | VAL | VAL | VAL | ALA | ALA | ASN | THR | VAL | LYS | GLY | GLY | GLY | ASP | GLY | ASN | TYR | GLY | TYR | ASN | ASN | ALA |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| THR | GIU | GLU | TYR | GLY | ASN | MET | ILE | ASP | MET | GLY | ILE | LEU | ASP | PRO | THR | LYS | VAL | THR | ARG | SER | SER | ALA | LEU | GLN | TYR | ALA | ALA | SER | VAL | ALA | GLY | LEU | MET | ILE | THR | THR | GIU | CYS | MET | MET | VAL | THR | ASP | LEU | PRO |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

- Molecule 1: 60 kDa chaperonin

Chain 3-N:  100%

[illegible]

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| LEU | GLU | ASP | LYS | PHE | GLU | ASN | NET | MET | GLY | ALA | GLN | VAL | VAL | LYS | GLU | VAL | ALA | ALA | SER | LYS | ALA | ALA | ASP | ASN | ASP | ALA | ALA | GLY | GLY | THR | THR | THR | THR | LEU | ALA | GLN | ALA | ALA | ILE | ILE | THR | THR | GLU | GLY | LEU | ALA | ALA | LYS | LYS | ARG | GLY | ILE |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| LYS | ALA | VAL | THR | VAL | ALA | VAL | GLU | LEU | LYS | LEU | ALA | LEU | SER | VAL | PRO | CYS | SER | ASP | SER | LYS | ALA | ILE | ALA | GLN | VAL | GLY | THR | ILE | SER | ALA | ASN | SER | ASP | GLU | THR | VAL | GLY | LYS | LEU | ILE | ALA | GLU | ALA | MET | ASP | LYS | VAL | GLY | LYS | GLU | GLY | VAL | ILE | THR | VAL | GLU | ASP | GLY | THR |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| GLY | LEU | GLN | ASP | GLU | LEU | ASP | VAL | VAL | GLU | GLY | MET | GLN | GLN | PHE | ASP | ARG | GLY | TYR | LEU | LEU | PRO | PRO | TYR | PHE | ILE | PHE | ASN | LYS | PRO | PRO | GLU | GLU | THR | GLY | ALA | VAL | VAL | LEU | GLU | GLY | SER | PRO | PHE | ILE | ILE | LEU | LEU | ALA | ASP | LYS | LYS | ILE | ILE | SER | ASN | ARG | GLU | MET | LEU | PRO | VAL | LEU | GLU | ALA | VAL |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

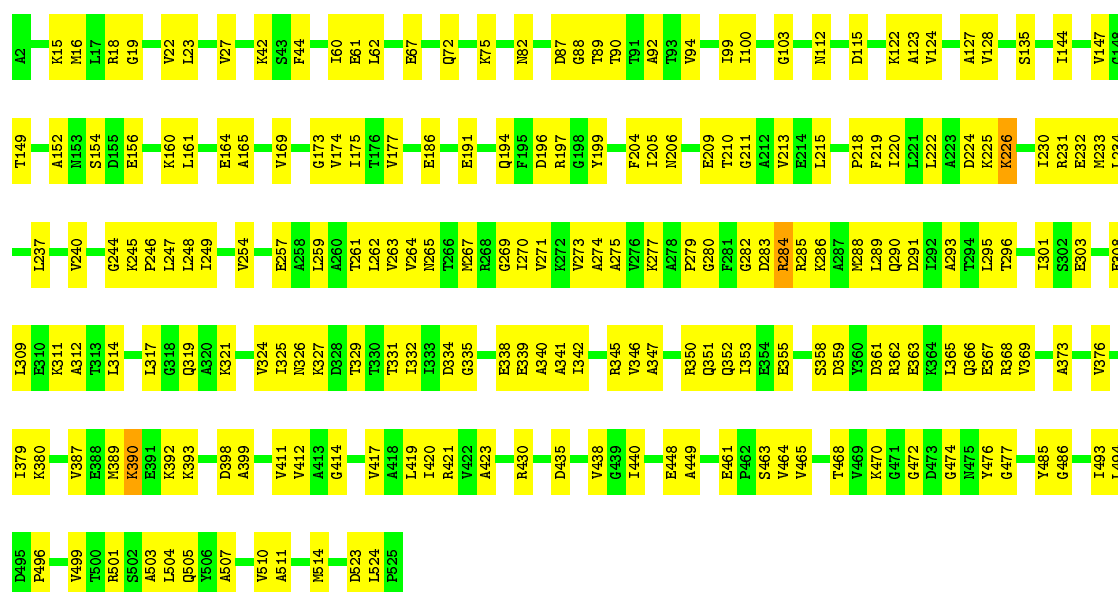
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| LYS | ALA | GLY | LYS | PRO | LEU | LEU | IIE | IIE | ALA | ALA | GLU | ASP | VAL | GLU | GLY | GLU | ALA | LEU | THR | ASN | THR | MET | ARG | GLY | IIE | VAL | LYS | VAL | ALA | ALA | VAL | LYS | PRO | GLY | PHE | GLY | ASP | ARG | ARG | LYS | MET | ALA | ALA | LEU | GLN | ASP | IIE | ALA | THR | LEU | THR | GLY | GLY | THR | VAL |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

[illegible]

[illegible]

- Molecule 1: 60 kDa chaperonin

Chain 4-A:  61% 39%



- Molecule 1: 60 kDa chaperonin

Chain 4-B:  100%

[illegible]

[illegible]

- Molecule 1: 60 kDa chaperonin

Chain 4-C: 100%

[illegible]

- Molecule 1: 60 kDa chaperonin

Chain 4-D: 100%

[illegible]

| | | | | |
|-----|-----|-----|-----|-----|
| THR | VAL | ARG | SER | LYS |
| GLU | ALA | GLU | GLU | ALA |
| GLU | SER | LYS | GLU | GLY |
| TYR | LYS | LEU | ILE | LYS |
| GLY | LEU | GLN | GLY | PRO |
| ASN | ALA | GLU | MET | LEU |
| MET | ASP | ARG | GLU | LEU |
| ILE | LEU | VAL | LEU | ILE |
| ASP | ARG | VAL | LEU | ILE |
| MET | GLY | LYS | LYS | ALA |
| GLY | GLN | LEU | ALA | GLU |
| ILE | ASN | LEU | THR | ASP |
| LEU | GLU | GLY | LEU | VAL |
| ASP | ASP | GLY | GLU | GLY |
| PRO | GLN | VAL | ASP | GLY |
| THR | ASN | ALA | LEU | GLU |
| LYS | VAL | VAL | GLY | ALA |
| VAL | GLY | ILE | GLN | LEU |
| THR | ILE | LYS | ALA | ALA |
| ARG | LYS | VAL | LYS | THR |
| SER | VAL | GLY | ARG | LEU |
| ALA | ALA | ALA | VAL | VAL |
| LEU | LEU | ALA | VAL | VAL |
| GLN | ARG | THR | ILE | ASN |
| TYR | ALA | GLU | ASN | THR |
| ALA | MET | VAL | LYS | MET |
| ALA | ALA | GLU | ASP | ARG |
| SER | SER | ALA | MET | GLY |
| VAL | PRO | LYS | THR | ILE |
| ALA | LEU | GLU | THR | VAL |
| GLY | ARG | LYS | ILE | LYS |
| ILE | GLN | LYS | ILE | VAL |
| ILE | ILE | ALA | ASP | ALA |
| THR | VAL | ARG | GLY | ALA |
| THR | LEU | VAL | VAL | VAL |
| THR | ASN | GLU | GLY | LYS |
| GLU | CYS | ASP | GLU | ALA |
| THR | GLY | ALA | GLU | ALA |
| CYS | GLY | LEU | ALA | PRO |
| MET | MET | LEU | ALA | GLY |
| VAL | GLU | HIS | ALA | GLY |
| THR | PRO | ALA | ILE | PHE |
| THR | THR | THR | ALA | GLY |
| ASP | SER | THR | GLN | ASP |
| LEU | VAL | ARG | GLY | ARG |
| PRO | VAL | ALA | ARG | ARG |
| | ALA | ALA | VAL | LYS |
| | ASN | VAL | ALA | LYS |
| | THR | GLU | GLN | MET |
| | VAL | GLY | ILE | LEU |
| | LYS | GLY | ARG | GLN |
| | GLY | VAL | GLN | ASP |
| | ASP | ALA | ILE | ALA |
| | ASN | GLY | GLU | THR |
| | TYR | GLY | GLU | LEU |
| | THR | GLY | ALA | THR |
| | TYR | VAL | THR | GLY |
| | TYR | ALA | SER | GLY |
| | ASN | LEU | ASP | THR |
| | ALA | ILE | TYR | THR |
| | ALA | ARG | ASP | ILE |

- Molecule 1: 60 kDa chaperonin

Chain 4-E: 100%

[illegible]

- Molecule 1: 60 kDa chaperonin

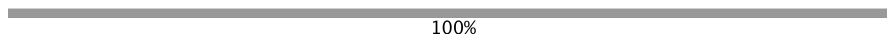
Chain 4-F:  100%

[illegible]

| | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|
| THR | VAL | ARG | SER | LYS | GLY | LYS |
| GLU | GLU | GLU | GLU | ALA | LEU | ALA |
| GLU | SER | LYS | GLU | GLY | GLN | VAL |
| TYR | LYS | LEU | ILE | LYS | ASP | THR |
| GLY | LEU | GLN | GLY | PRO | GLU | VAL |
| ASN | ALA | GLU | MET | LEU | LEU | ALA |
| MET | ASP | ARG | GLU | LEU | ASP | VAL |
| ILE | LEU | VAL | ARG | ILE | VAL | GLU |
| GLU | ARG | ALA | GLU | ILE | VAL | GLU |
| MET | GLY | LYS | GLY | ALA | GLY | LYS |
| ILE | ASN | ALA | THR | ASP | MET | ALA |
| LEU | GLU | GLY | LEU | VAL | GLN | LEU |
| PRO | ASP | GLY | GLU | GLU | PHE | SER |
| THR | GLN | VAL | ASP | GLY | ARG | PRO |
| ASN | ALA | ALA | LEU | ALA | GLY | CYS |
| VAL | VAL | ILE | GLN | LEU | TYR | SER |
| THR | ILE | LYS | ALA | ALA | LEU | ASP |
| ARG | ARG | LYS | LYS | THR | LEU | SER |
| SER | VAL | GLY | ARG | LEU | PRO | LYS |
| ALA | ALA | ALA | VAL | VAL | TYR | ALA |
| LEU | LEU | ALA | VAL | VAL | PHE | ILE |
| GLN | ARG | THR | ILE | ASN | ILE | ALA |
| TYR | ALA | GLU | ASN | THR | ASN | GLN |
| ALA | MET | VAL | LYS | MET | LYS | VAL |
| ALA | GLU | GLU | ASP | ARG | PRO | GLY |
| SER | ALA | MET | THR | GLY | GLU | THR |
| VAL | PRO | LYS | THR | ILE | THR | ILE |
| ALA | LEU | GLU | THR | VAL | GLY | SER |
| GLY | GLN | LYS | ILE | LYS | ALA | ALA |
| LEU | ARG | LYS | ILE | VAL | VAL | ASN |
| GLU | GLN | LYS | ILE | VAL | VAL | ASN |
| GLU | GLU | GLU | GLU | ALA | GLU | ASP |
| CYS | ASP | GLU | GLY | LYS | SER | THR |
| GLU | GLU | ALA | GLU | ALA | PRO | VAL |
| GLY | GLY | LEU | ALA | GLY | PHE | GLY |
| MET | GLU | LEU | ALA | GLY | ILE | LYS |
| VAL | GLU | HIS | ILE | PHE | LEU | LEU |
| THR | PRO | ALA | ILE | GLY | LEU | ILE |
| ASP | SER | THR | GLN | ASP | ALA | ALA |
| PRO | VAL | ARG | GLY | ARG | ASP | GLU |
| | ALA | ALA | VAL | ARG | LYS | ALA |
| | ALA | VAL | VAL | LYS | LYS | MET |
| | ASN | VAL | ALA | ALA | ILE | ASP |
| | THR | GLU | GLN | MET | SER | LYS |
| | VAL | GLU | ILE | LEU | ASN | VAL |
| | LYS | GLY | ARG | GLN | ILE | GLY |
| | GLY | VAL | GLN | ILE | ARG | LYS |
| | ASP | ALA | ILE | THR | MET | GLY |
| | GLY | GLY | GLU | THR | LEU | VAL |
| | ASN | GLY | GLU | LEU | PRO | ILE |
| | TYR | GLY | ALA | THR | VAL | THR |
| | THR | VAL | THR | GLY | LEU | VAL |
| | TYR | ALA | SER | THR | GLU | ASP |
| | ASN | LEU | ASP | THR | ALA | GLY |
| | ALA | ILE | THR | VAL | VAL | THR |
| | ALA | ARG | ASN | ILE | VAL | THR |

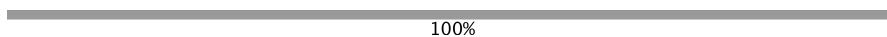
- Molecule 1: 60 kDa chaperonin

Chain 4-G:

[illegible]

- Molecule 1: 60 kDa chaperonin

Chain 4-H:



[illegible]

- Molecule 1: 60 kDa chaperonin

Chain 4-I:

100%

[illegible]

THR GLU GLU TYR GLY ASN MET ILE ASP MET GLY ILE LEU ASP PRO THR LYS VAL THR ARG SER SER ALA LEU GLN TYR ALA ALA SER VAL ALA GLY LEU MET ILE THR THR GLU CYS MET VAL THR ASP LEU PRO

- Molecule 1: 60 kDa chaperonin

Chain 4-J: 100%

[illegible]

- Molecule 1: 60 kDa chaperonin

Chain 4-K: 100%

[illegible]

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ARG | GLY | LYS | LEU | GLN | GLU | ARG | VAL | ALA | LYS | LEU | ALA | GLY | GLY | VAL | ALA | VAL | ILE | LYS | VAL | GLY | ALA | ALA | LYS | LYS | LYS | GLU | LYS | ALA | ARG | ARG | VAL | VAL | GLU | GLY | VAL | VAL | ALA | ALA | GLY | GLY | VAL | ALA | ALA | LEU | ILE | ARG |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| VAL | ALA | SER | LYS | LEU | ALA | ASP | LEU | ARG | GLY | GLN | ASN | GLU | ASP | GLN | ASN | VAL | VAL | GLY | GLY | LYS | ALA | VAL | LEU | ARG | ALA | ALA | MET | GLU | ALA | ALA | PRO | PRO | LEU | LEU | ARG | GLN | ILE | ILE | VAL | VAL | LEU | ASN | CYS | GLY | GLU | GLU | GLU | PRO | SER | VAL | VAL | VAL | ALA | ALA | ASN | ASN | THR | VAL | LYS | LYS | GLY | GLY | ASP | GLY | GLY | ASN | TYR | TYR | ASN | ASN | ALA | ALA |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| THR | GLU | GLU | TYR | GLY | ASN | MET | ILE | ASP | MET | GLY | ILE | LEU | ASP | PRO | THR | LYS | VAL | THR | ARG | SER | ALA | LEU | GLN | TYR | ALA | ALA | SER | VAL | ALA | GLY | LEU | MET | ILE | THR | THR | GLU | CYS | MET | VAL | THR | ASP | LEU | PRO |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

- Molecule 1: 60 kDa chaperonin

Chain 4-L:  100%

[illegible]

LEU
GLU
ASP
ASP
LYS
PHE
GLU
GLU
ASN
MET
MET
GLY
ALA
ALA
GLN
MET
VAL
VAL
LYS
GLU
GLU
VAL
ALA
SER
LYS
LYS
ALA
ASN
ASN
ASP
ALA
ALA
ALA
GLY
ASP
GLY
THR
THR
THR
ALA
THR
VAL
LEU
VAL
ALA
GLN
ALA
ALA
ILE
ILE
THR
THR
GLU
GLY
LEU
LYS
LYS
ALA
VAL
VAL
ALA
ALA
ALA
GLY
MET
ASN
PRO
MET
MET
ASP
LEU
LYS
ARG
GLY
ILE
SER

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| LYS | ALA | VAL | THR | VAL | ALA | VAL | GLU | GLU | LEU | LYS | ALA | LEU | SER | VAL | PRO | CYS | SER | ASP | SER | LYS | ALA | ALA | ILE | ALA | GLN | VAL | GLY | THR | ILE | SER | ASN | SER | ASP | GLU | THR | VAL | GLY | LYS | LEU | ILE | ALA | GLU | ALA | NET | ASP | LYS | VAL | GLY | LYS | GLU | GLY | VAL | ILE | THR | VAL | GLU | ASP | GLY | THR |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

GLY
LEU
GLN
ASP
GLU
LEU
ASP
VAL
VAL
GLU
GLY
MET
GLN
PHE
ASP
ARG
GLY
TYR
LEU
SER
PRO
TYR
PHE
ILE
ASN
LYS
PRO
GLU
THR
GLY
ALA
VAL
GLU
LEU
GLU
SER
PRO
PHE
ILE
LYS
ILE
SER
ASN
ILE
ARG
GLU
MET
LEU
PRO
VAL
LEU
GLU
ALA
VAL

LYS ALA GLY LYS PRO LEU LEU ILE ILE ALA GLU ASP VAL GLY GLY ALA ALA LEU THR LEU VAL VAL ASN THR MET ARG GLY ILE VAL LYS VAL VAL ALA ALA VAL LYS ALA PRO PHE GLY GLY ASP ARG ARG ARG LYS ALA MET LEU GLN ASP ILE ALA THR LEU THR GLY GLY THR VAL

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| SER | GLU | GLU | ILE | GLY | GLU | GLU | GLU | LYS | ALA | THR | LEU | GLU | ASP | GLY | GLY | GLN | ALA | LYS | ARG | VAL | VAL | ILE | ASN | LYS | ASP | THR | THR | THR | ILE | ILE | ASP | GLY | VAL | GLY | GLU | GLU | ALA | ALA | ILE | GLN | GLY | ARG | VAL | VAL | GLN | GLN | ILE | ILE | THR | SER | ASP | TYS | THR |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ARG | GIU | LEU | GLN | GIU | ARG | VAL | ALA | LYS | LEU | ALA | GLY | GLY | VAL | ALA | VAL | LYS | THR | GIU | VAL | GIU | LYS | LYS | GLU | LYS | ALA | VAL | VAL | ASP | ALA | LEU | ALA | HIS | THR | ARG | ALA | VAL | GIU | VAL | GLY | VAL | GLY | ALA | LEU | THR | ARG |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| VAL | ALA | SER | LYS | LEU | ALA | ASP | LEU | ARG | GLY | GLN | ASN | GLU | ASP | GLN | ASN | VAL | VAL | ILE | LYS | VAL | ALA | LEU | ARG | ALA | ALA | MET | GLU | ALA | ALA | PRO | PRO | LEU | LEU | GLN | ARG | ILE | ILE | VAL | VAL | VAL | LEU | ASN | CYS | GLY | GLU | GLU | GLU | PRO | PRO | SER | VAL | VAL | ALA | ALA | ASN | THR | THR | VAL | LYS | LYS | GLY | GLY | ASP | GLY | GLY | ASN | ASN | TYR | TYR | GLY | GLY | ASN | ALA | ALA |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| THR | GLU | GLU | TYR | GLY | ASN | MET | ILE | ASP | MET | GLY | ILE | LEU | ASP | PRO | THR | LYS | VAL | THR | ARG | SER | ALA | LEU | GLN | TYR | ALA | ALA | SER | SER | VAL | ALA | GLY | LEU | MET | ILE | THR | THR | GLU | CYS | MET | VAL | THR | ASP | LEU | PRO |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

- Molecule 1: 60 kDa chaperonin

Chain 4-M: 100%

ALA
ALA
LYS
ASP
VAL
LYS
PHE
GLY
ASN
ASP
ALA
GLY
VAL
LYS
MET
LEU
ARG
GLY
VAL
ASN
VAL
LEU
VAL
ALA
ASP
ALA
VAL
LYS
LYS
GLY
GLY
ARG
ASN
VAL
VAL
LEU
LEU
LYS
LYS
SER
PHE
GLY
ALA
PRO
PRO
THR
ILE
THR
LYS
ASP
GLY
VAL
SER
VAL
ALA
ALA
ARG
GLU
ILE
ILE

LEU GLU ASP LYS PHE GLU ASN MET GLY GLN VAL VAL LYS GLU VAL ALA ALA SER LYS ALA ASP ASP ALA ALA GLY ASP GLY THR THR THR ALA THR VAL LEU LEU GLN ALA ALA ILE ILE THR THR GLY LEU LYS ALA VAL ALA ALA GLY MET ASN PRO MET ASP LEU LYS ARG GLY ILE ASP

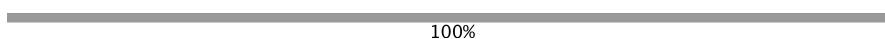
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| LYS | ALA | VAL | THR | VAL | ALA | VAL | GLU | GLU | LEU | LYS | ALA | LEU | SER | ASP | SER | LYS | ALA | ILE | ALA | GLN | GLY | THR | ILE | SER | ASN | SER | ASP | GLU | THR | VAL | GLY | LYS | LEU | ILE | ALA | GLU | ALA | MET | ASP | LYS | VAL | GLY | LYS | GLU | GLY | VAL | ILE | THR | VAL | GLU | ASP | GLY |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

[illegible]

| | | | | |
|-----|-----|-----|-----|-----|
| THR | VAL | ARG | SER | LYS |
| GLU | ALA | GLU | GLU | ALA |
| GLU | SER | LYS | GLU | GLY |
| TYR | LYS | LEU | ILE | LYS |
| GLY | LEU | GLN | GLY | PRO |
| ASN | ALA | GLU | MET | LEU |
| MET | ASP | ARG | GLU | LEU |
| ILE | LEU | VAL | LEU | ILE |
| ASP | ARG | ALA | GLU | ILE |
| MET | GLY | LYS | LYS | ALA |
| GLY | GLN | LEU | ALA | GLU |
| ILE | ASN | ALA | THR | ASP |
| LEU | GLU | GLY | LEU | VAL |
| GLY | ASN | ALA | THR | ASP |
| ARG | ASP | GLY | LEU | VAL |
| PRO | GLN | VAL | ASP | GLY |
| THR | ASN | ALA | LEU | ALA |
| LYS | VAL | VAL | GLY | ALA |
| VAL | GLY | ILE | GLN | LEU |
| THR | ILE | LYS | ALA | ALA |
| ARG | LYS | VAL | LYS | THR |
| SER | VAL | GLY | ARG | LEU |
| ALA | ALA | ALA | VAL | VAL |
| LEU | LEU | ALA | VAL | VAL |
| GLN | ARG | THR | ILE | ASN |
| TYR | ALA | GLU | ASN | THR |
| ALA | MET | VAL | LYS | MET |
| ALA | ALA | GLU | ASP | ARG |
| SER | ALA | MET | THR | GLY |
| VAL | PRO | LYS | THR | ILE |
| ALA | LEU | GLU | THR | VAL |
| GLY | ARG | LYS | ILE | LYS |
| LEU | GLN | LYS | ILE | VAL |
| MET | ILE | ALA | ASP | ALA |
| ILE | VAL | ARG | GLY | VAL |
| THR | LEU | VAL | VAL | VAL |
| THR | ASN | GLU | GLY | LYS |
| GLU | CYS | ASP | GLU | ALA |
| CYS | GLY | ALA | GLU | PRO |
| MET | GLU | LEU | ALA | GLY |
| VAL | GLU | HIS | ALA | PHE |
| THR | PRO | ALA | ILE | GLY |
| ASP | SER | THR | GLN | ASP |
| LEU | VAL | ARG | GLY | ARG |
| PRO | VAL | ALA | ARG | ARG |
| | ALA | VAL | VAL | LYS |
| | ASN | VAL | ALA | ALA |
| | THR | GLU | GLN | MET |
| | VAL | GLU | ILE | LEU |
| | LYS | GLY | ARG | GLN |
| | GLY | VAL | GLN | ASP |
| | GLY | ALA | ILE | ALA |
| | ASN | GLY | GLU | THR |
| | TYR | GLY | GLU | LEU |
| | TYR | VAL | THR | THR |
| | TYR | ALA | SER | GLY |
| | ASN | LEU | ASP | THR |
| | ALA | ILE | TYR | VAL |
| | ALA | ARG | ASP | ILE |

- Molecule 1: 60 kDa chaperonin

Chain 4-N:

[illegible]

4 Experimental information

| Property | Value | Source |
|--------------------------------------|---|-----------|
| Reconstruction method | SINGLE PARTICLE | Depositor |
| Imposed symmetry | POINT, D7 | Depositor |
| Number of particles used | 37367 | Depositor |
| Resolution determination method | FSC 0.143 CUT-OFF | Depositor |
| CTF correction method | PHASE FLIPPING AND AMPLITUDE CORRECTION | Depositor |
| Microscope | JEOL 3200FSC | Depositor |
| Voltage (kV) | 300 | Depositor |
| Electron dose ($e^-/\text{\AA}^2$) | 1.0 | Depositor |
| Minimum defocus (nm) | Not provided | Depositor |
| Maximum defocus (nm) | Not provided | Depositor |
| Magnification | Not provided | Depositor |
| Image detector | GATAN K2 SUMMIT (4k x 4k) | Depositor |

5 Model quality ⓘ

5.1 Standard geometry ⓘ

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

| Mol | Chain | Bond lengths | | Bond angles | |
|-----|-------|--------------|---------|-------------|----------------|
| | | RMSZ | # Z >2 | RMSZ | # Z >2 |
| 1 | 1-A | 0.39 | 0/3879 | 0.57 | 0/5237 |
| 1 | 1-B | 0.39 | 0/3879 | 0.57 | 0/5237 |
| 1 | 1-C | 0.39 | 0/3879 | 0.57 | 0/5237 |
| 1 | 1-D | 0.39 | 0/3879 | 0.57 | 0/5237 |
| 1 | 1-E | 0.39 | 0/3879 | 0.57 | 0/5237 |
| 1 | 1-F | 0.39 | 0/3879 | 0.57 | 0/5237 |
| 1 | 1-G | 0.39 | 0/3879 | 0.57 | 0/5237 |
| 1 | 1-H | 0.39 | 0/3879 | 0.57 | 0/5237 |
| 1 | 1-I | 0.39 | 0/3879 | 0.57 | 0/5237 |
| 1 | 1-J | 0.39 | 0/3879 | 0.57 | 0/5237 |
| 1 | 1-K | 0.39 | 0/3879 | 0.57 | 0/5237 |
| 1 | 1-L | 0.39 | 0/3879 | 0.57 | 0/5237 |
| 1 | 1-M | 0.39 | 0/3879 | 0.57 | 0/5237 |
| 1 | 1-N | 0.39 | 0/3879 | 0.57 | 0/5237 |
| 1 | 2-A | 0.53 | 0/3879 | 0.67 | 1/5237 (0.0%) |
| 1 | 3-A | 0.45 | 0/3879 | 0.59 | 1/5237 (0.0%) |
| 1 | 4-A | 0.39 | 0/3879 | 0.54 | 0/5237 |
| All | All | 0.40 | 0/65943 | 0.58 | 2/89029 (0.0%) |

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

| Mol | Chain | #Chirality outliers | #Planarity outliers |
|-----|-------|---------------------|---------------------|
| 1 | 1-A | 0 | 1 |
| 1 | 1-B | 0 | 1 |
| 1 | 1-C | 0 | 1 |
| 1 | 1-D | 0 | 1 |
| 1 | 1-E | 0 | 1 |
| 1 | 1-F | 0 | 1 |
| 1 | 1-G | 0 | 1 |
| 1 | 1-H | 0 | 1 |

Continued on next page...

Continued from previous page...

| Mol | Chain | #Chirality outliers | #Planarity outliers |
|-----|-------|---------------------|---------------------|
| 1 | 1-I | 0 | 1 |
| 1 | 1-J | 0 | 1 |
| 1 | 1-K | 0 | 1 |
| 1 | 1-L | 0 | 1 |
| 1 | 1-M | 0 | 1 |
| 1 | 1-N | 0 | 1 |
| All | All | 0 | 14 |

There are no bond length outliers.

All (2) bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(°) | Ideal(°) |
|-----|-------|-----|------|----------|-------|-------------|----------|
| 1 | 3-A | 200 | LEU | C-N-CA | -6.91 | 104.44 | 121.70 |
| 1 | 2-A | 234 | LEU | CA-CB-CG | 5.10 | 127.03 | 115.30 |

There are no chirality outliers.

5 of 14 planarity outliers are listed below:

| Mol | Chain | Res | Type | Group |
|-----|-------|-----|------|---------|
| 1 | 1-A | 32 | GLY | Peptide |
| 1 | 1-B | 32 | GLY | Peptide |
| 1 | 1-C | 32 | GLY | Peptide |
| 1 | 1-D | 32 | GLY | Peptide |
| 1 | 1-E | 32 | GLY | Peptide |

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 1 | 1-A | 3851 | 0 | 3970 | 58 | 0 |
| 1 | 1-B | 3851 | 0 | 3970 | 56 | 0 |
| 1 | 1-C | 3851 | 0 | 3970 | 58 | 0 |
| 1 | 1-D | 3851 | 0 | 3970 | 56 | 0 |
| 1 | 1-E | 3851 | 0 | 3970 | 56 | 0 |
| 1 | 1-F | 3851 | 0 | 3970 | 55 | 0 |
| 1 | 1-G | 3851 | 0 | 3970 | 58 | 0 |

Continued on next page...

Continued from previous page...

| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 1 | 1-H | 3851 | 0 | 3970 | 58 | 0 |
| 1 | 1-I | 3851 | 0 | 3970 | 57 | 0 |
| 1 | 1-J | 3851 | 0 | 3970 | 55 | 0 |
| 1 | 1-K | 3851 | 0 | 3970 | 59 | 0 |
| 1 | 1-L | 3851 | 0 | 3970 | 56 | 0 |
| 1 | 1-M | 3851 | 0 | 3970 | 55 | 0 |
| 1 | 1-N | 3851 | 0 | 3970 | 57 | 0 |
| 1 | 2-A | 3851 | 0 | 3970 | 234 | 0 |
| 1 | 3-A | 3851 | 0 | 3970 | 192 | 0 |
| 1 | 4-A | 3851 | 0 | 3970 | 148 | 0 |
| 2 | 1-A | 19 | 0 | 0 | 1 | 0 |
| 2 | 1-B | 12 | 0 | 0 | 0 | 0 |
| 2 | 1-C | 14 | 0 | 0 | 0 | 0 |
| 2 | 1-D | 14 | 0 | 0 | 0 | 0 |
| 2 | 1-E | 10 | 0 | 0 | 0 | 0 |
| 2 | 1-F | 6 | 0 | 0 | 0 | 0 |
| 2 | 1-G | 13 | 0 | 0 | 0 | 0 |
| 2 | 1-H | 1 | 0 | 0 | 0 | 0 |
| 2 | 1-I | 3 | 0 | 0 | 0 | 0 |
| 2 | 1-J | 5 | 0 | 0 | 0 | 0 |
| 2 | 1-K | 1 | 0 | 0 | 0 | 0 |
| 2 | 1-L | 2 | 0 | 0 | 0 | 0 |
| 2 | 1-M | 5 | 0 | 0 | 0 | 0 |
| 2 | 1-N | 2 | 0 | 0 | 0 | 0 |
| All | All | 65574 | 0 | 67490 | 1323 | 0 |

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 20.

The worst 5 of 1323 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|----------------|-----------------|--------------------------|-------------------|
| 1:A:176:THR:O | 1:A:377:ALA:HB3 | 1.56 | 1.04 |
| 1:A:221:LEU:O | 1:A:248:LEU:CB | 2.14 | 0.95 |
| 1:A:264:VAL:HA | 1:A:267:MET:HG2 | 1.51 | 0.92 |
| 1:A:197:ARG:HE | 1:A:279:PRO:HA | 1.35 | 0.92 |
| 1:A:237:LEU:O | 1:A:241:ALA:HB2 | 1.70 | 0.91 |

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|------------------|------------|----------|----------|-------------|-----|
| 1 | 1-A | 522/524 (100%) | 506 (97%) | 16 (3%) | 0 | 100 | 100 |
| 1 | 1-B | 522/524 (100%) | 506 (97%) | 16 (3%) | 0 | 100 | 100 |
| 1 | 1-C | 522/524 (100%) | 506 (97%) | 16 (3%) | 0 | 100 | 100 |
| 1 | 1-D | 522/524 (100%) | 506 (97%) | 16 (3%) | 0 | 100 | 100 |
| 1 | 1-E | 522/524 (100%) | 506 (97%) | 16 (3%) | 0 | 100 | 100 |
| 1 | 1-F | 522/524 (100%) | 506 (97%) | 16 (3%) | 0 | 100 | 100 |
| 1 | 1-G | 522/524 (100%) | 506 (97%) | 16 (3%) | 0 | 100 | 100 |
| 1 | 1-H | 522/524 (100%) | 506 (97%) | 16 (3%) | 0 | 100 | 100 |
| 1 | 1-I | 522/524 (100%) | 506 (97%) | 16 (3%) | 0 | 100 | 100 |
| 1 | 1-J | 522/524 (100%) | 506 (97%) | 16 (3%) | 0 | 100 | 100 |
| 1 | 1-K | 522/524 (100%) | 506 (97%) | 16 (3%) | 0 | 100 | 100 |
| 1 | 1-L | 522/524 (100%) | 506 (97%) | 16 (3%) | 0 | 100 | 100 |
| 1 | 1-M | 522/524 (100%) | 506 (97%) | 16 (3%) | 0 | 100 | 100 |
| 1 | 1-N | 522/524 (100%) | 506 (97%) | 16 (3%) | 0 | 100 | 100 |
| 1 | 2-A | 522/524 (100%) | 445 (85%) | 77 (15%) | 0 | 100 | 100 |
| 1 | 3-A | 522/524 (100%) | 452 (87%) | 70 (13%) | 0 | 100 | 100 |
| 1 | 4-A | 522/524 (100%) | 468 (90%) | 54 (10%) | 0 | 100 | 100 |
| All | All | 8874/8908 (100%) | 8449 (95%) | 425 (5%) | 0 | 100 | 100 |

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|------------------|-------------|----------|-------------|-----|
| 1 | 1-A | 404/404 (100%) | 404 (100%) | 0 | 100 | 100 |
| 1 | 1-B | 404/404 (100%) | 404 (100%) | 0 | 100 | 100 |
| 1 | 1-C | 404/404 (100%) | 404 (100%) | 0 | 100 | 100 |
| 1 | 1-D | 404/404 (100%) | 404 (100%) | 0 | 100 | 100 |
| 1 | 1-E | 404/404 (100%) | 404 (100%) | 0 | 100 | 100 |
| 1 | 1-F | 404/404 (100%) | 404 (100%) | 0 | 100 | 100 |
| 1 | 1-G | 404/404 (100%) | 404 (100%) | 0 | 100 | 100 |
| 1 | 1-H | 404/404 (100%) | 404 (100%) | 0 | 100 | 100 |
| 1 | 1-I | 404/404 (100%) | 404 (100%) | 0 | 100 | 100 |
| 1 | 1-J | 404/404 (100%) | 404 (100%) | 0 | 100 | 100 |
| 1 | 1-K | 404/404 (100%) | 404 (100%) | 0 | 100 | 100 |
| 1 | 1-L | 404/404 (100%) | 404 (100%) | 0 | 100 | 100 |
| 1 | 1-M | 404/404 (100%) | 404 (100%) | 0 | 100 | 100 |
| 1 | 1-N | 404/404 (100%) | 404 (100%) | 0 | 100 | 100 |
| 1 | 2-A | 404/404 (100%) | 400 (99%) | 4 (1%) | 80 | 91 |
| 1 | 3-A | 404/404 (100%) | 403 (100%) | 1 (0%) | 94 | 99 |
| 1 | 4-A | 404/404 (100%) | 400 (99%) | 4 (1%) | 80 | 91 |
| All | All | 6868/6868 (100%) | 6859 (100%) | 9 (0%) | 95 | 99 |

5 of 9 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | 3-A | 225 | LYS |
| 1 | 4-A | 390 | LYS |
| 1 | 4-A | 277 | LYS |
| 1 | 2-A | 327 | LYS |
| 1 | 4-A | 226 | LYS |

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 36 such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | 1-I | 37 | ASN |
| 1 | 1-K | 37 | ASN |

Continued on next page...

Continued from previous page...

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | 4-A | 37 | ASN |
| 1 | 1-J | 37 | ASN |
| 1 | 1-K | 505 | GLN |

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.