



wwPDB EM Validation Summary Report ⓘ

Nov 27, 2022 – 02:33 AM EST

PDB ID : 5W0S
EMDB ID : EMD-8750
Title : GroEL using cryoEM
Authors : Roh, S.H.; Chiu, W.
Deposited on : 2017-05-31
Resolution : 3.50 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

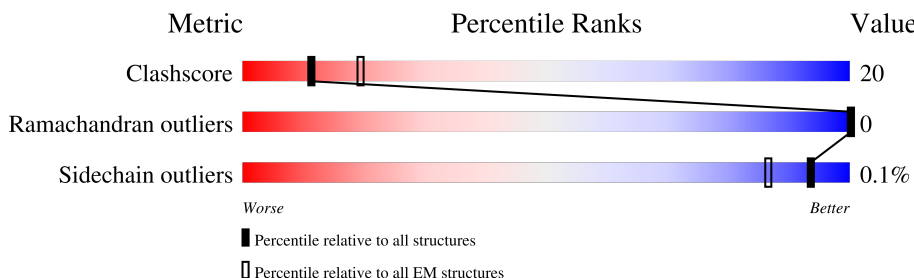
1 Overall quality at a glance

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	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	1-A	524	<div> <div>15%</div> <div>82%</div> <div>18%</div> </div>
1	1-B	524	<div> <div>15%</div> <div>82%</div> <div>18%</div> </div>
1	1-C	524	<div> <div>16%</div> <div>81%</div> <div>19%</div> </div>
1	1-D	524	<div> <div>15%</div> <div>82%</div> <div>18%</div> </div>
1	1-E	524	<div> <div>16%</div> <div>82%</div> <div>18%</div> </div>
1	1-F	524	<div> <div>16%</div> <div>83%</div> <div>17%</div> </div>
1	1-G	524	<div> <div>16%</div> <div>82%</div> <div>18%</div> </div>
1	1-H	524	<div> <div>16%</div> <div>82%</div> <div>18%</div> </div>

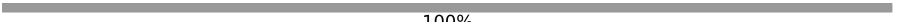
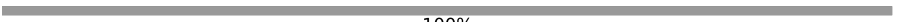
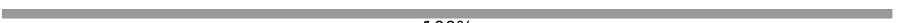




















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Mol	Chain	Length	Quality of chain
1	1-I	524	<div> <div>15%</div> <div>82%</div> <div>18%</div> </div>
1	1-J	524	<div> <div>15%</div> <div>83%</div> <div>17%</div> </div>
1	1-K	524	<div> <div>16%</div> <div>81%</div> <div>19%</div> </div>
1	1-L	524	<div> <div>15%</div> <div>82%</div> <div>18%</div> </div>
1	1-M	524	<div> <div>15%</div> <div>82%</div> <div>18%</div> </div>
1	1-N	524	<div> <div>15%</div> <div>82%</div> <div>18%</div> </div>
1	2-A	524	<div> <div>52%</div> <div>48%</div> </div>
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	<div> <div>56%</div> <div>43%</div> </div>
1	3-B	524	100%
1	3-C	524	100%
1	3-D	524	100%
1	3-E	524	100%

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Mol	Chain	Length	Quality of chain
1	3-F	524	 100%
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

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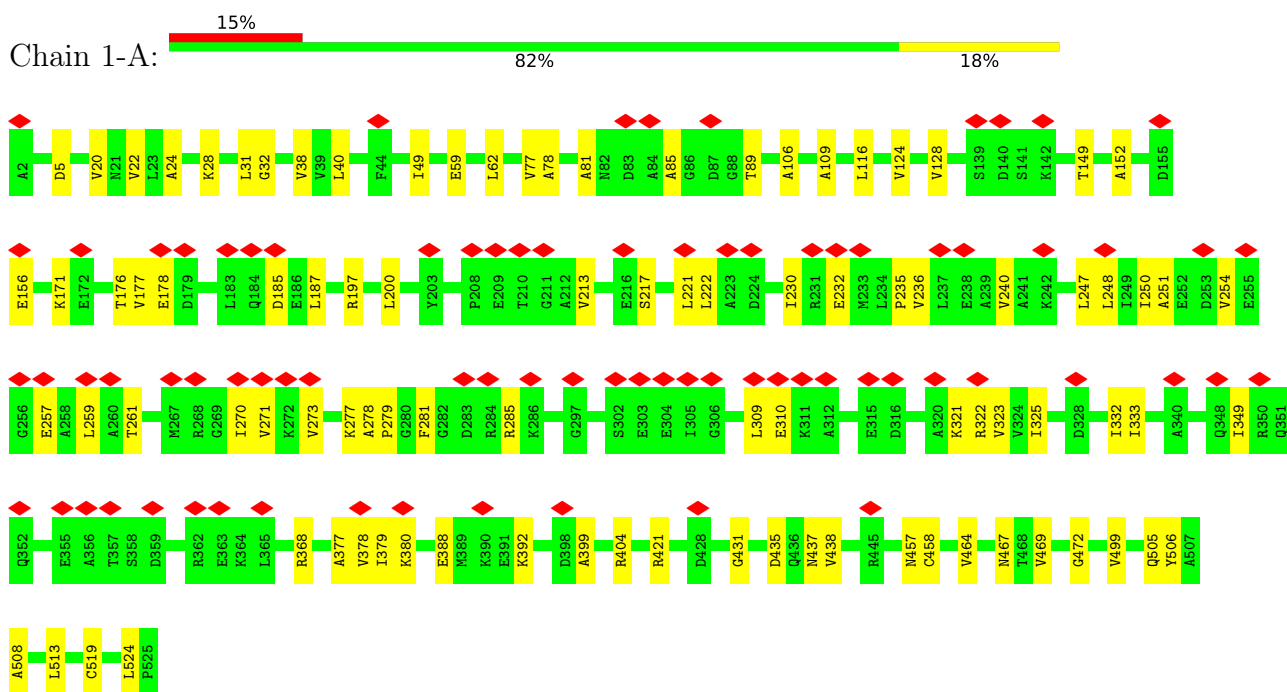
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Mol	Chain	Residues	Atoms		AltConf
2	1-M	5	Total	O	0
			5	5	
2	1-N	2	Total	O	0
			2	2	

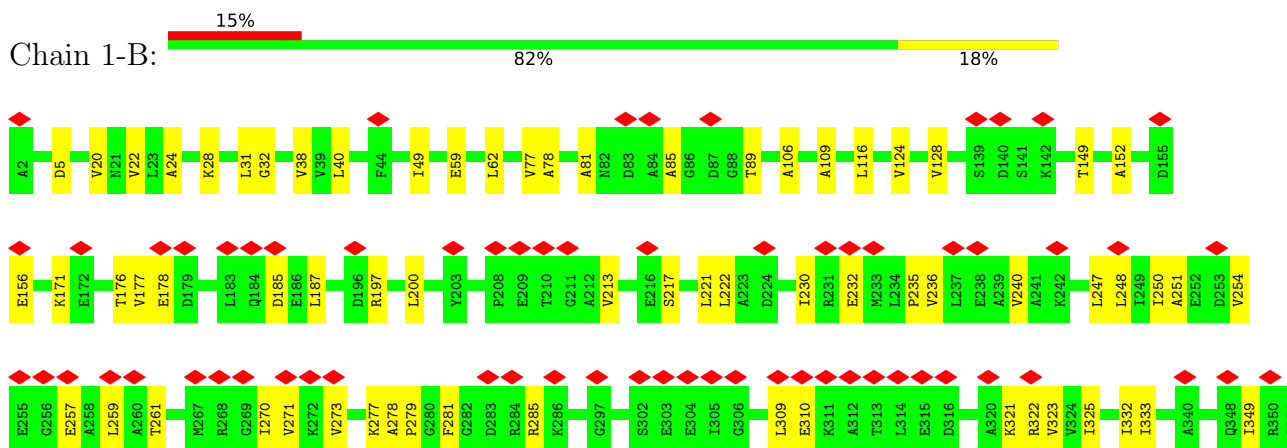
3 Residue-property plots

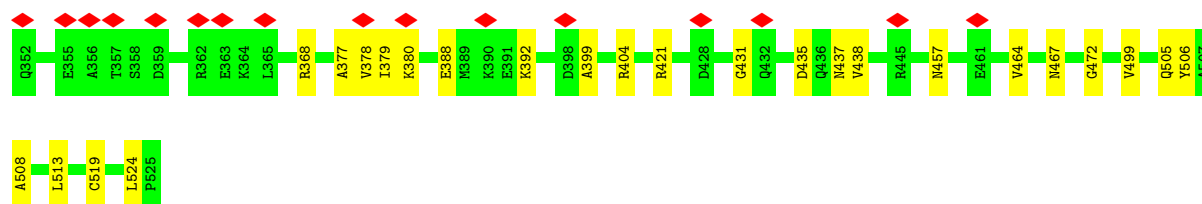
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. 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. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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

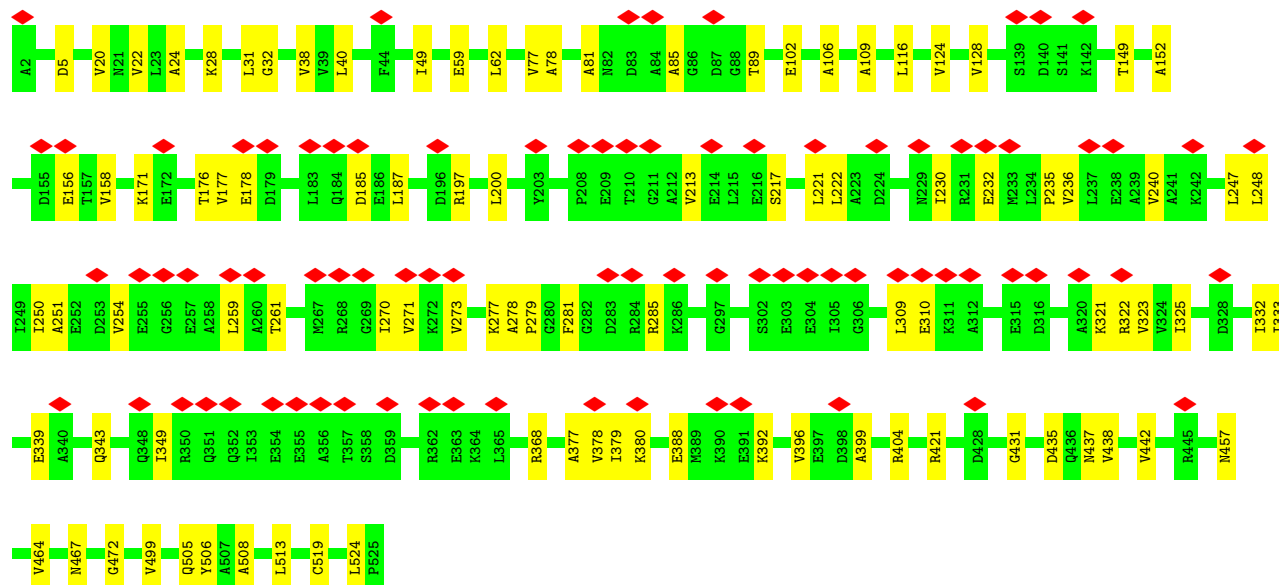
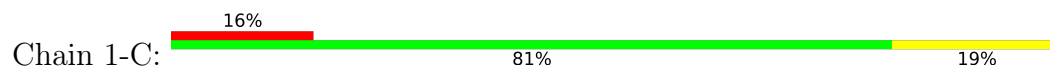


- Molecule 1: 60 kDa chaperonin

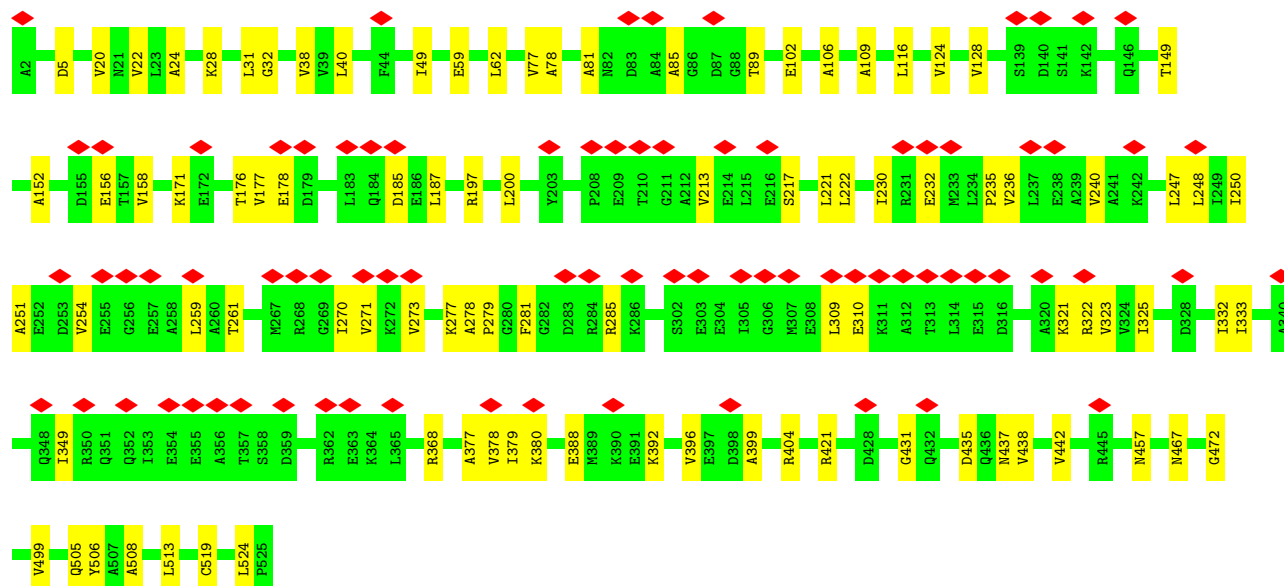
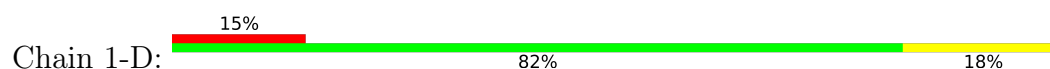




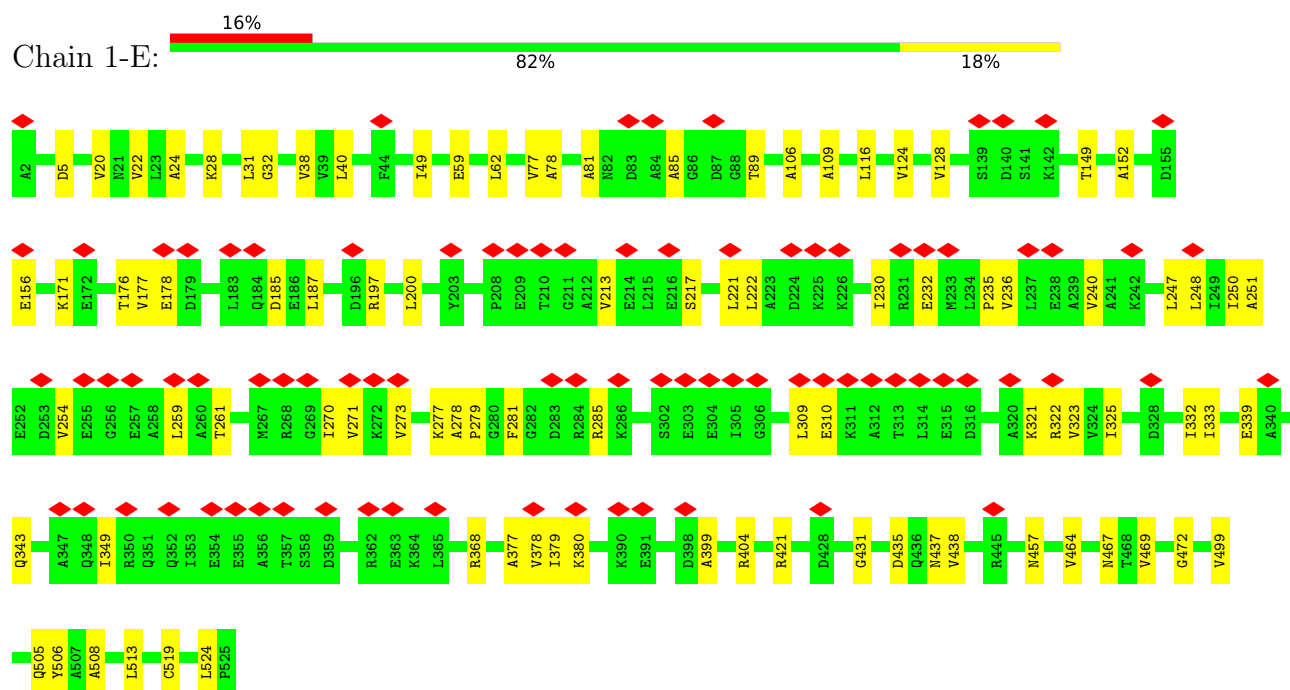
- Molecule 1: 60 kDa chaperonin



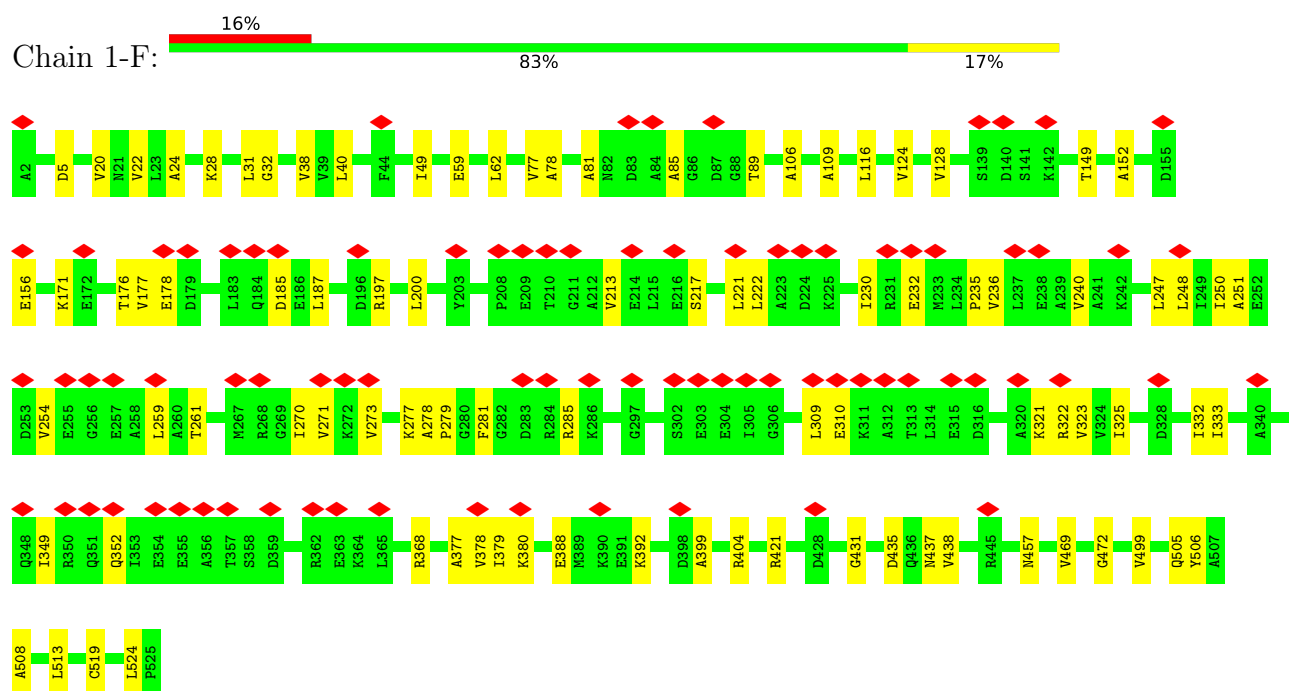
- Molecule 1: 60 kDa chaperonin



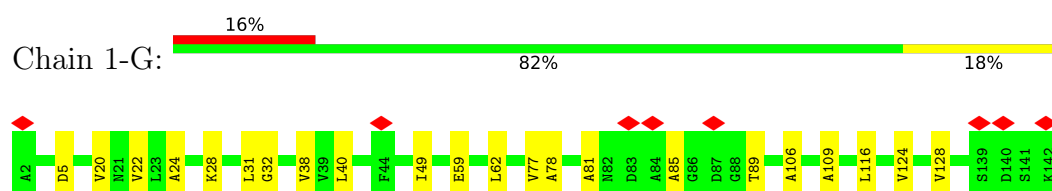
- Molecule 1: 60 kDa chaperonin

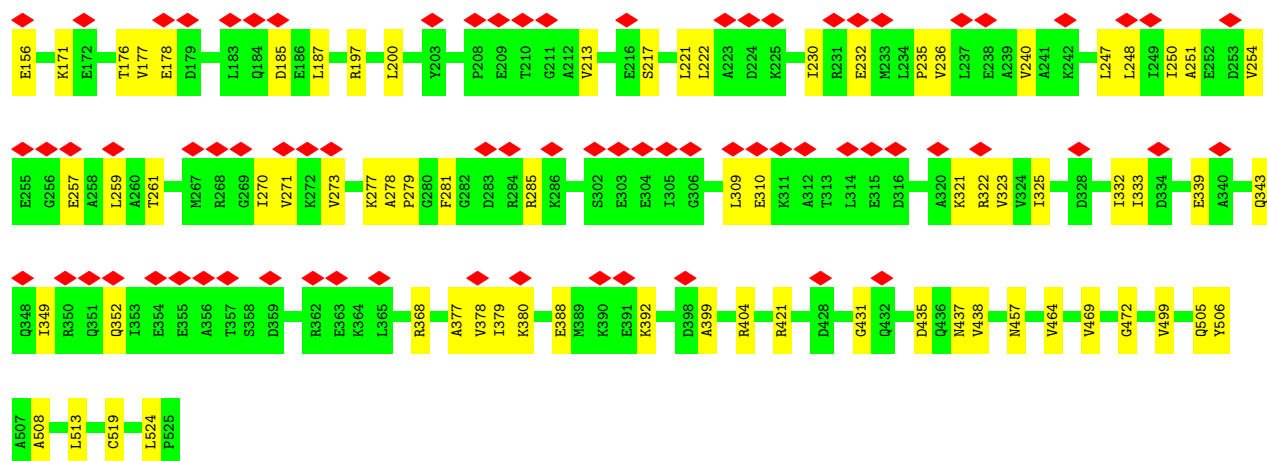


- Molecule 1: 60 kDa chaperonin

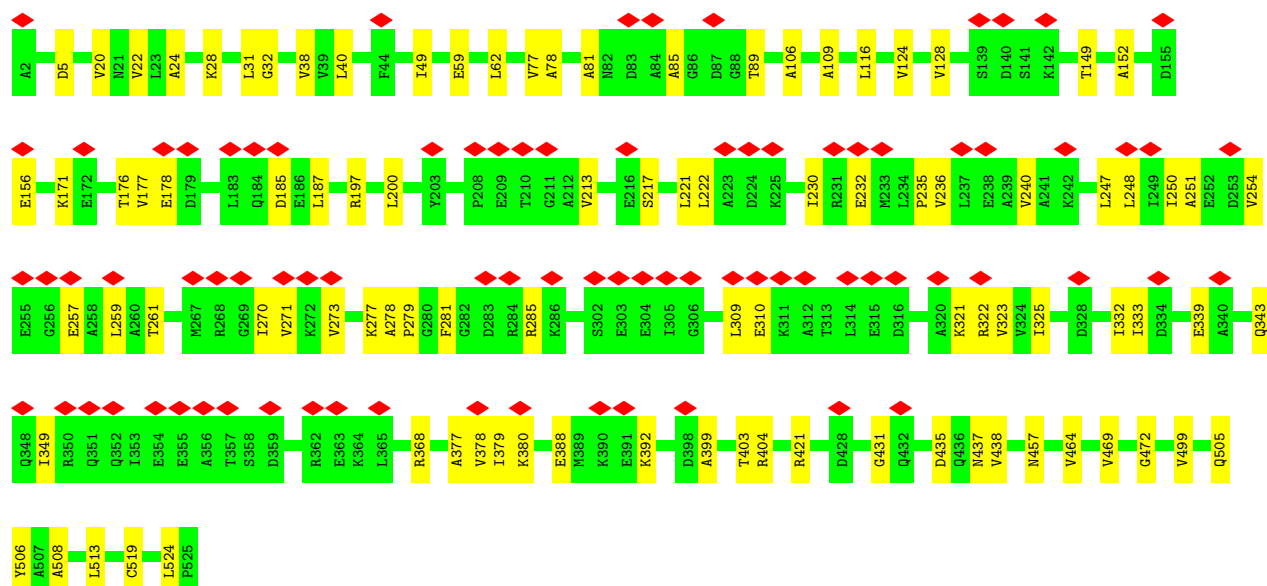
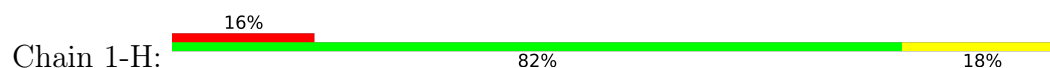


- Molecule 1: 60 kDa chaperonin

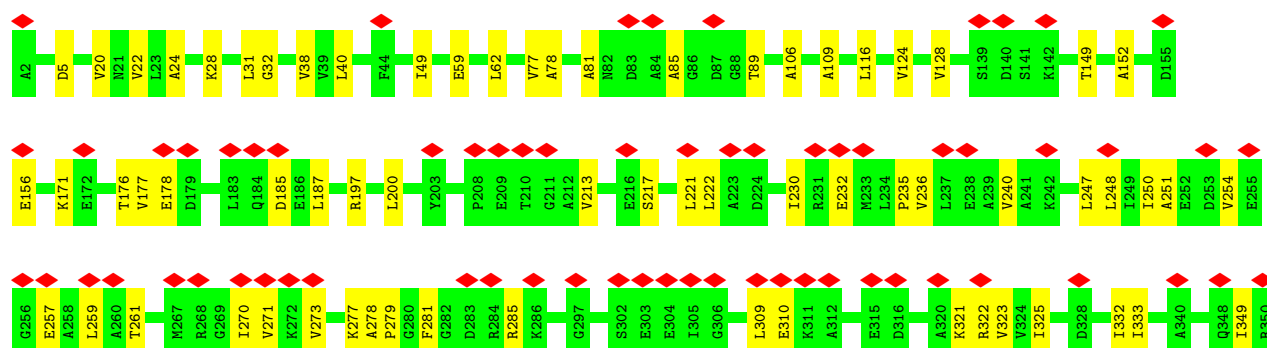
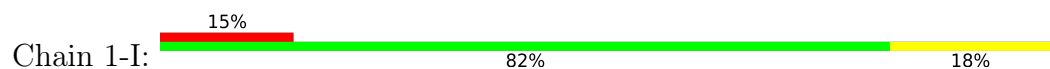


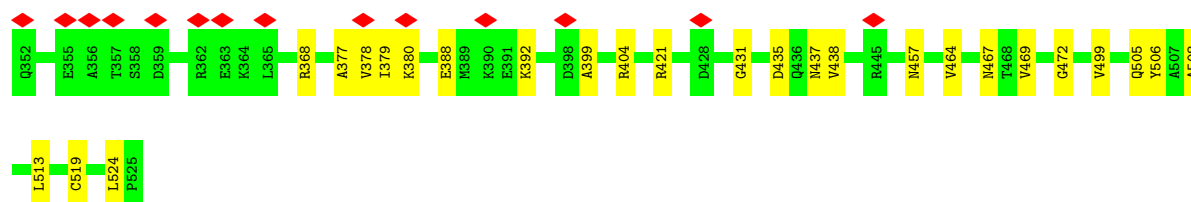


- Molecule 1: 60 kDa chaperonin

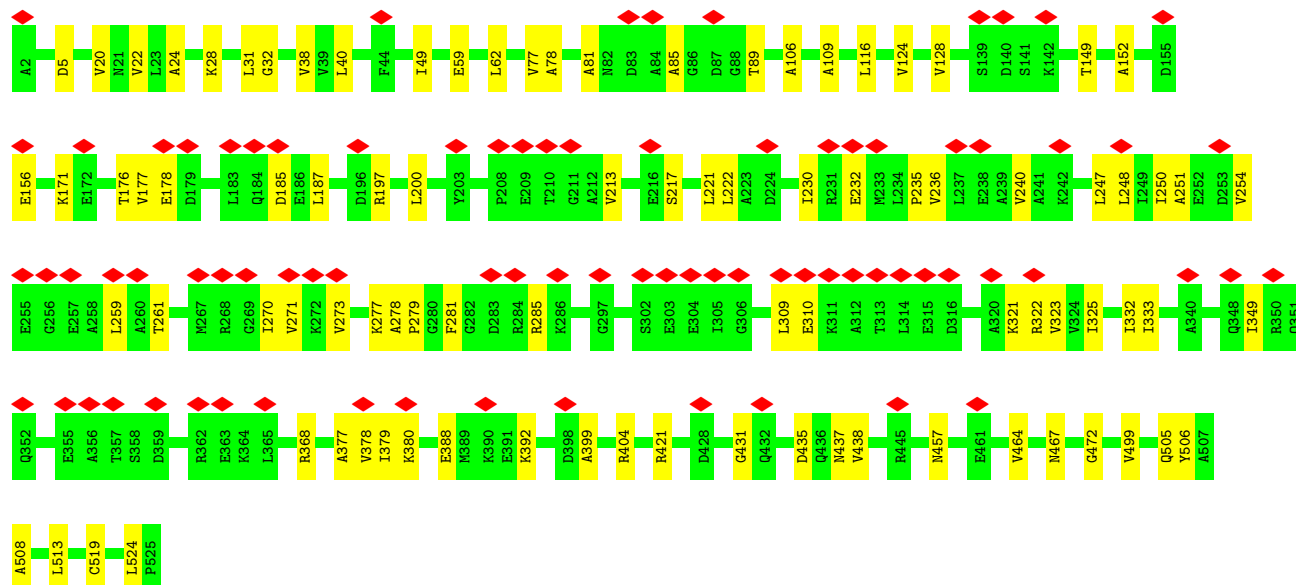
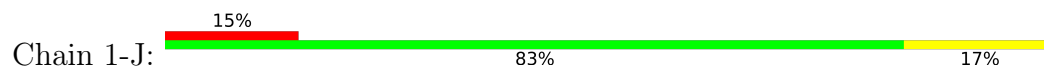


- Molecule 1: 60 kDa chaperonin

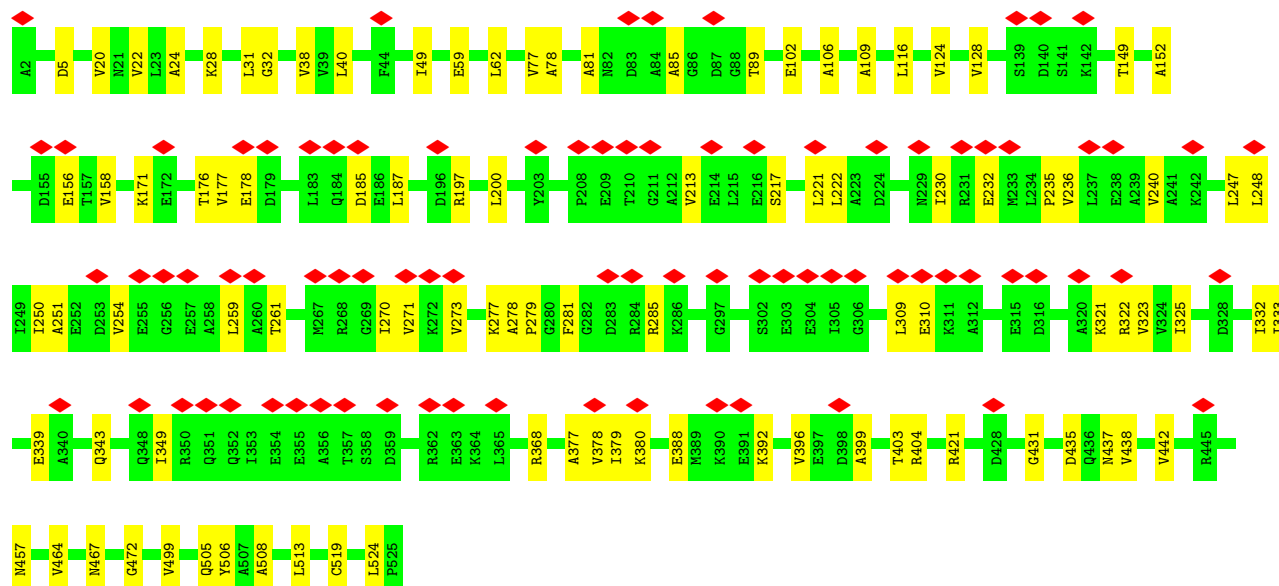
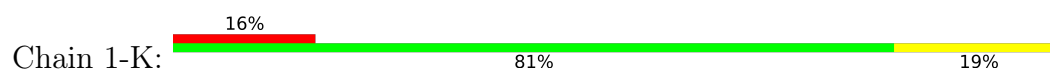




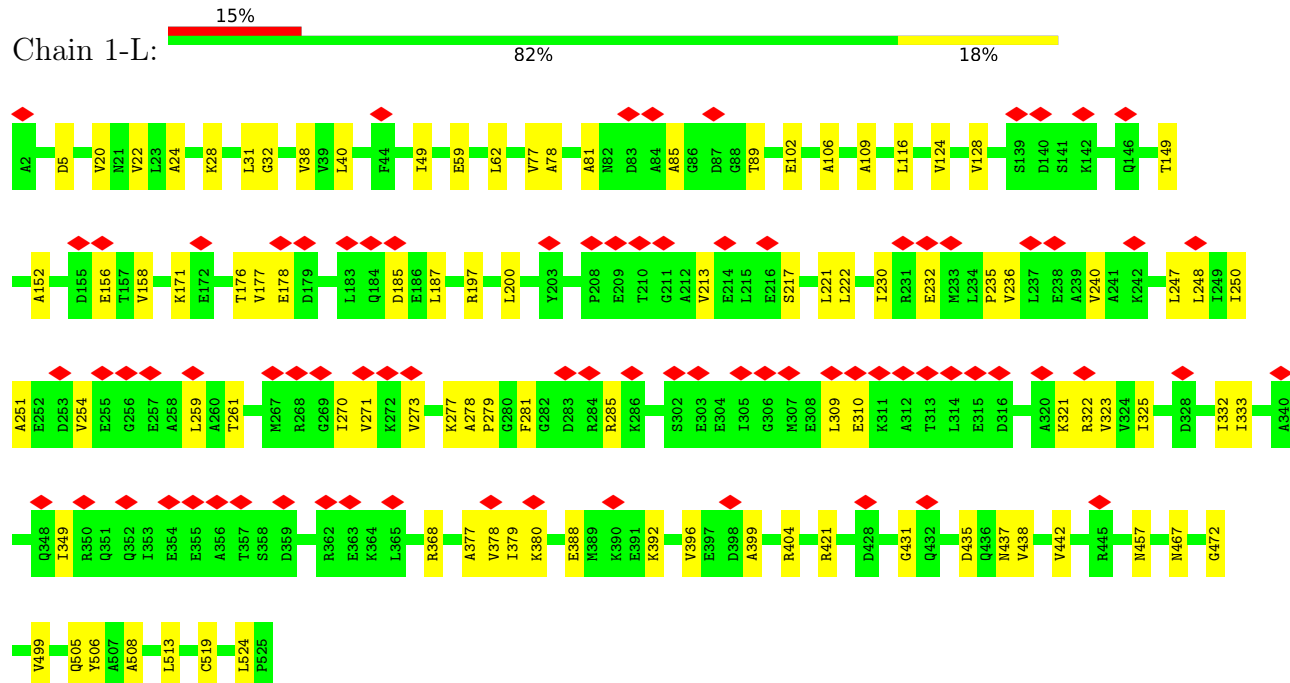
• Molecule 1: 60 kDa chaperonin



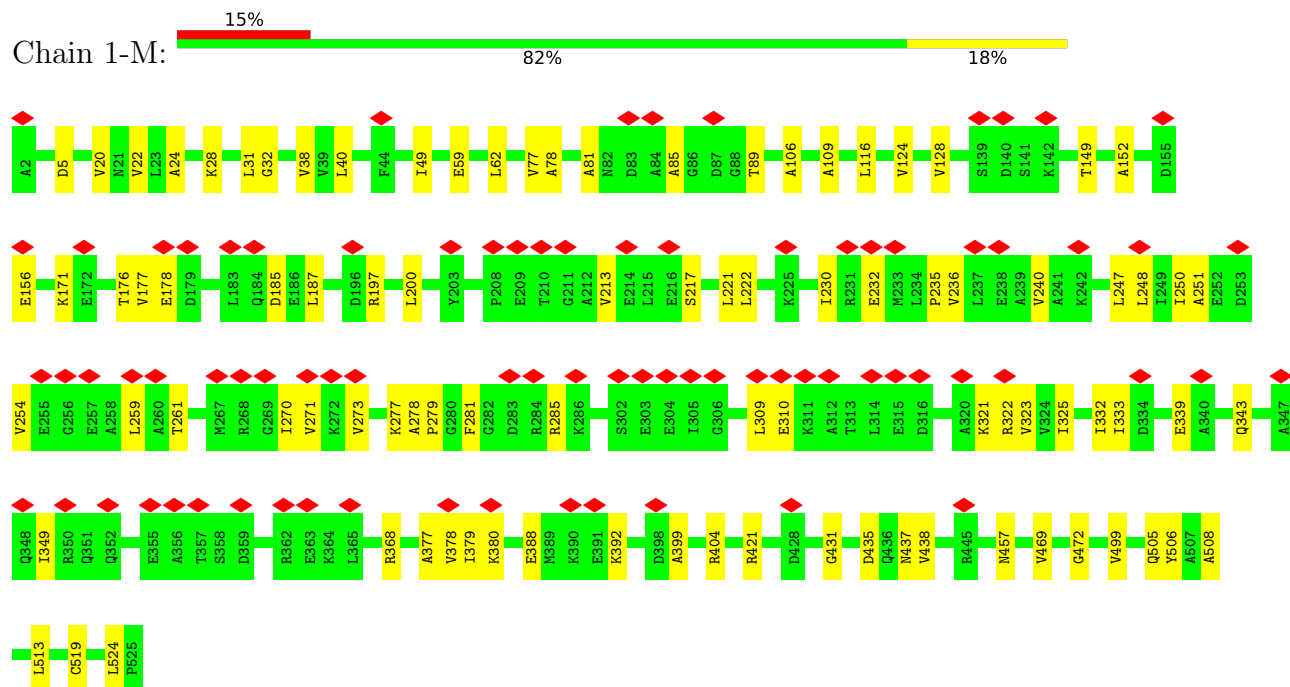
• Molecule 1: 60 kDa chaperonin



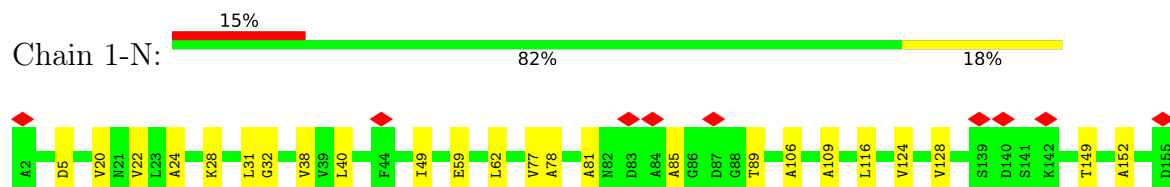
- Molecule 1: 60 kDa chaperonin

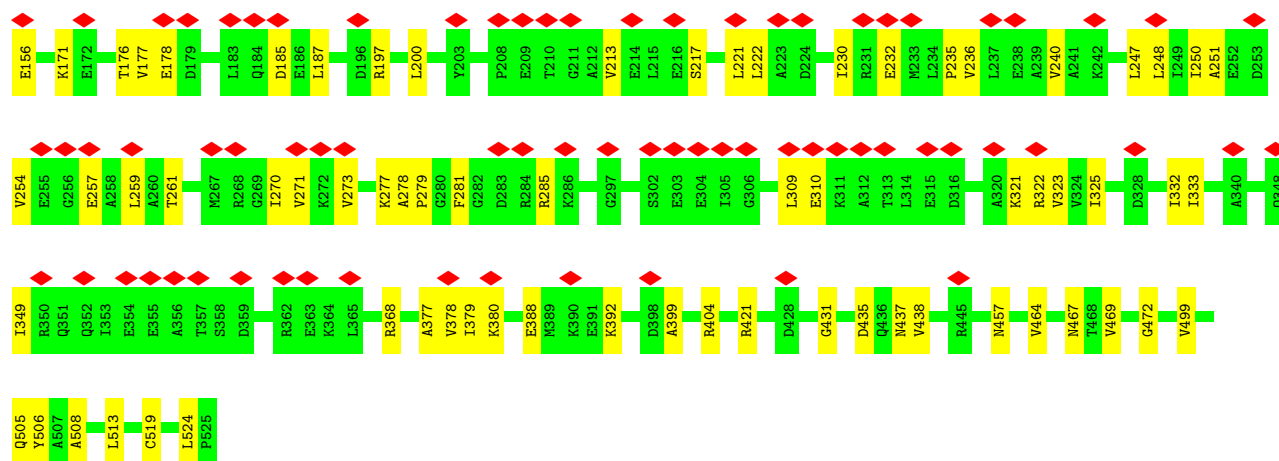


- Molecule 1: 60 kDa chaperonin



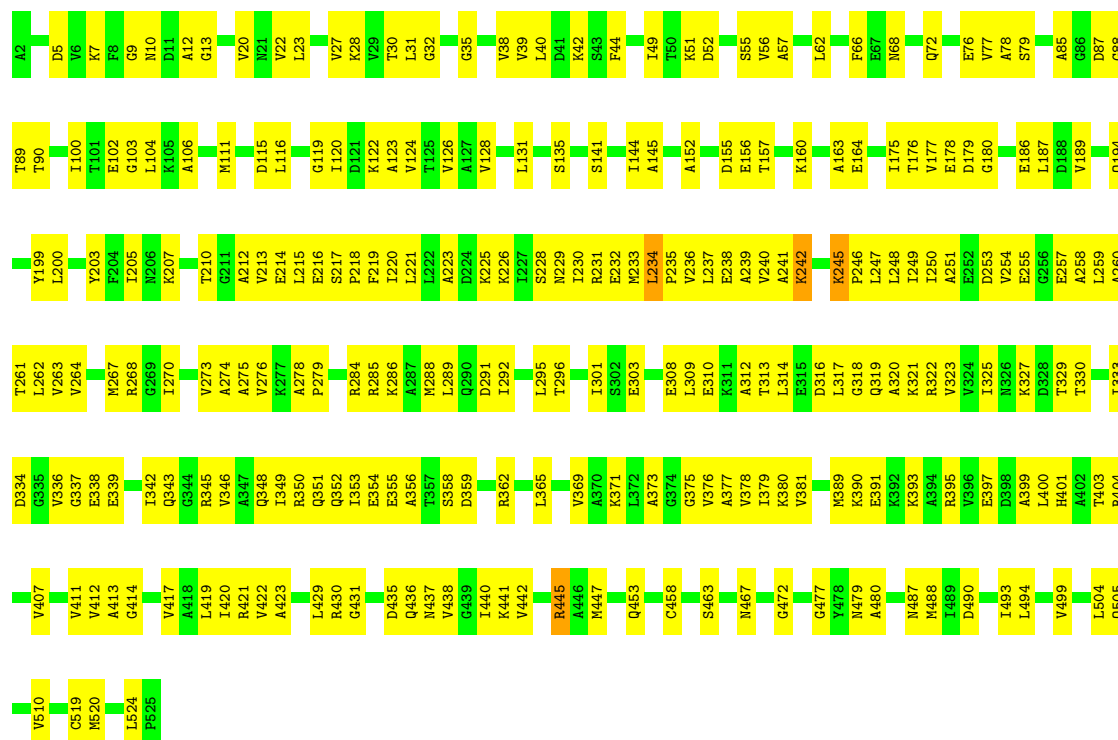
- Molecule 1: 60 kDa chaperonin





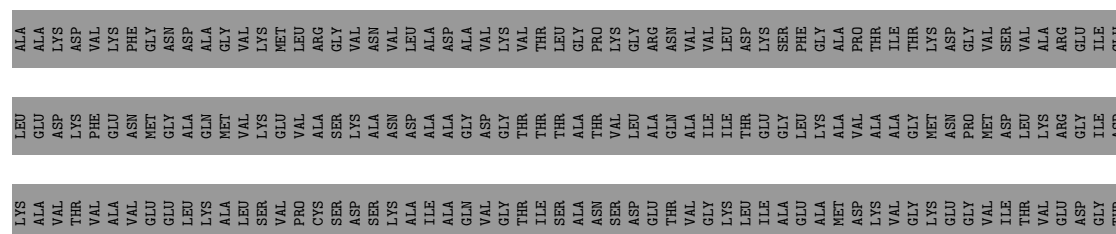
• Molecule 1: 60 kDa chaperonin

Chain 2-A:



• Molecule 1: 60 kDa chaperonin

Chain 2-B:

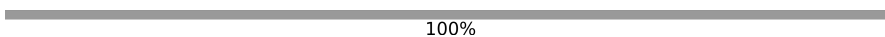




THR	VAL	ARG	SER	LYS	GLY	LYS	GLY	LYS
THR	VAL	ARG	SER	LYS	GLY	LYS	GLY	LYS
GLU	ALA	GLU	GLU	GLU	LEU	ALA	LEU	ALA
GLU	SER	LYS	GLU	GLU	LEU	GLY	GLN	VAL
TYR	LEU	LEU	ILE	GLY	GLN	PRO	GLU	THR
ASN	ALA	GLU	MET	GLY	GLU	LEU	LEU	ALA
MET	ASP	ARG	GLU	LEU	GLU	LEU	ASP	VAL
ILE	LEU	VAL	LEU	ILE	VAL	ILE	VAL	GLU
ASP	ARG	ALA	GLY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

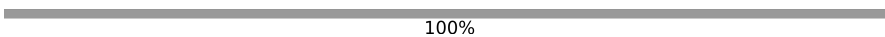
- Molecule 1: 60 kDa chaperonin

Chain 2-E:

[illegible]

- Molecule 1: 60 kDa chaperonin

Chain 2-F:

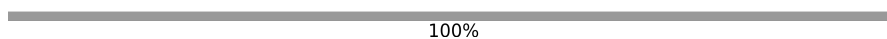


ALA	ALA	ALA	LYS	ASP	VAL	LYS	PHE	GLY	ASN	ASP	ALA	ALA	VAL	VAL	LYS	MET	LEU	ARG	GLY	VAL	ASN	VAL	LEU	VAL	ASP	ALA	ALA	VAL	LYS	VAL	VAL	THR	THR	LEU	GLY	PRO	PRO	LYS	GLY	LYS	ARG	ASN	VAL	VAL	VAL	LEU	LEU	ASP	LYS	LYS	SER	PHE	GLY	ALA	PRO	PRO	THR	THR	ILE	THR	THR	ASP	LYS	GLY	VAL	SER	VAL	ALA	ALA	ARG	GLU	ILE	GLU
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[illegible]

- Molecule 1: 60 kDa chaperonin

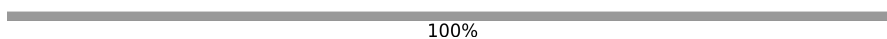
Chain 2-G:



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

- Molecule 1: 60 kDa chaperonin

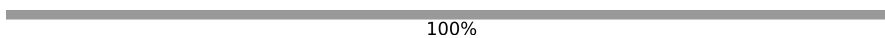
Chain 2-H:



[illegible]

- Molecule 1: 60 kDa chaperonin

Chain 2-I:

[illegible]

- Molecule 1: 60 kDa chaperonin

100%

[illegible]

- Molecule 1: 60 kDa chaperonin

100%

[illegible]

- Molecule 1: 60 kDa chaperonin

Chain 2-N:

100%

[illegible]

- Molecule 1: 60 kDa chaperonin

Chain 3-A:

56%

43%

N433	G344	R268	G192	V107	K2
N434	R345	G269	M193		A3
N435	V346	I270	Q194	P113	K4
N436	A347		F195	M114	V5
N437	Q348	V273	D196	D115	V6
V438	I349	K274	R197	L116	K7
G439	R350	A275	G198		
I440		V276	G199	G119	N10
K441	A356	R277	R200	I120	A12
		A278	S201	D121	A12
R445	R362	G280		K122	G13
	R363	G280	F204	A123	V14
E448	K364	F281	I205	V124	K15
	R365		N206	T125	M16
R452	Q366			V126	
	E367	R285	V213	A127	G19
C458	R368			V128	
G459	V369	M288	E216	E129	L23
E460	A370	L289	S217	E130	A24
	K371	Q290	F218	L131	
V469		D291	F219	K132	V27
	V376	L292	I220		K28
G472		A293	L221	S135	V99
	I379	T294	L222		T30
Y476	K380	L295	A223	A143	
G477	V381	T296	D224	I144	K34
Y478	G382		K225	A145	
	A383	I301	K226	Q146	N37
Y485			L227	V147	
G486	E388	T305	S228	G148	L40
N487	M389	G306	N229	T149	D41
M488		K307	T230		K42
	K392	E308	R231	N153	S43
M491	K393	L309	E232		F44
G492	A394	E310	N233	E156	
I493	R395	K311	L234		K51
L494	V396			I162	
D495		Q319	A239		V56
P496	L400	A320		M166	
		K321	K242	D167	D64
V499	T403	R322		K168	
	R404	V323	K245	V169	E67
Q505	A406	V324	T246	G170	
		L325	L247	K171	A78
A508		N326	L248	E172	
	E409	K327		G173	A81
A511	G410	G328	E252	V174	N82
	V411	T329	D253		
I515	V412	T330	V254	V177	A85
		T331	E255	E178	G86
V521	G414	T332		D179	D87
		T333	A258	G180	G88
	V417				T89
F525		G337	T261	D185	
	T420	E338	L262	E186	T100
	R421	E339	V263	L187	T101
		A340	N264	D188	E102
	A427	A341	G189	V189	G103
		T342	T286	V190	L104

- Molecule 1: 60 kDa chaperonin

Chain 3-D:

100%

[illegible]

- Molecule 1: 60 kDa chaperonin

Chain 3-E:

100%

[illegible]

[illegible]

- Molecule 1: 60 kDa chaperonin

Chain 3-F:  100%

[illegible]

- Molecule 1: 60 kDa chaperonin

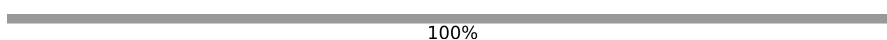
Chain 3-G: 100%

[illegible]

[illegible]

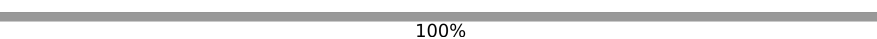
- Molecule 1: 60 kDa chaperonin

Chain 3-H:

[illegible]

- Molecule 1: 60 kDa chaperonin

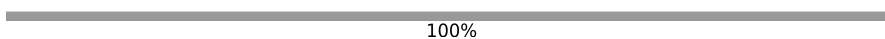
Chain 3-I:

[illegible]

[illegible]

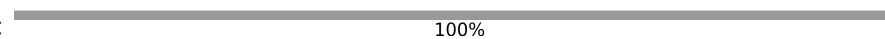
- Molecule 1: 60 kDa chaperonin

Chain 3-J:

[illegible]

- Molecule 1: 60 kDa chaperonin

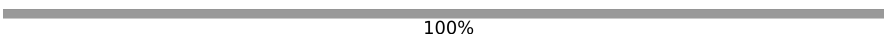
Chain 3-K:

[illegible]

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

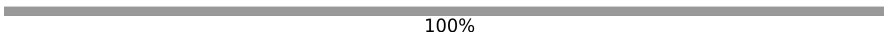
- Molecule 1: 60 kDa chaperonin

Chain 3-L:

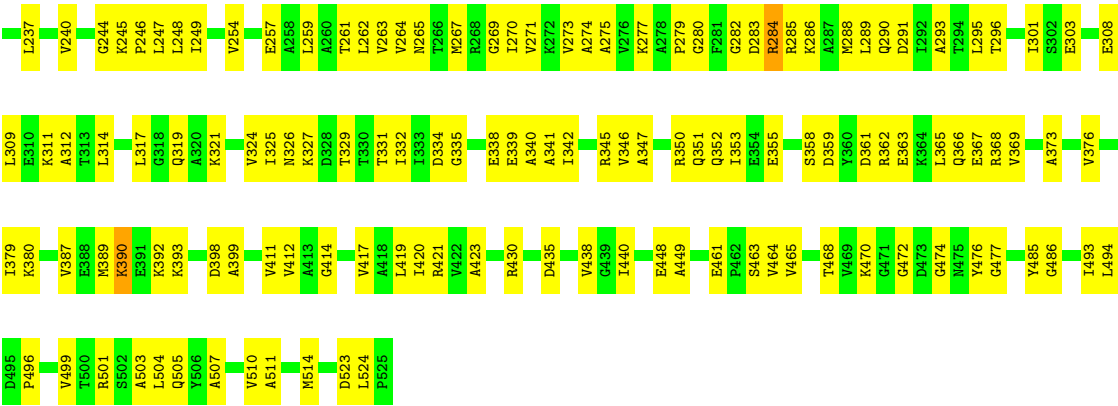
[illegible]

- Molecule 1: 60 kDa chaperonin

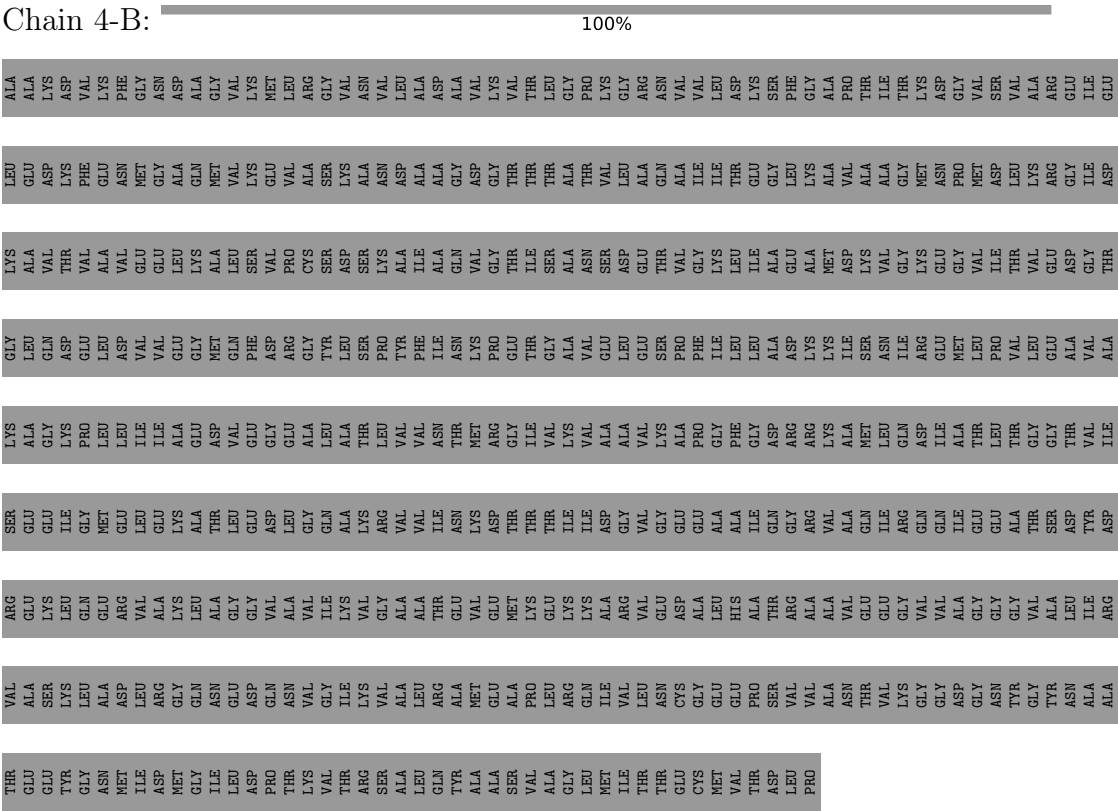
Chain 3-M:

[illegible]

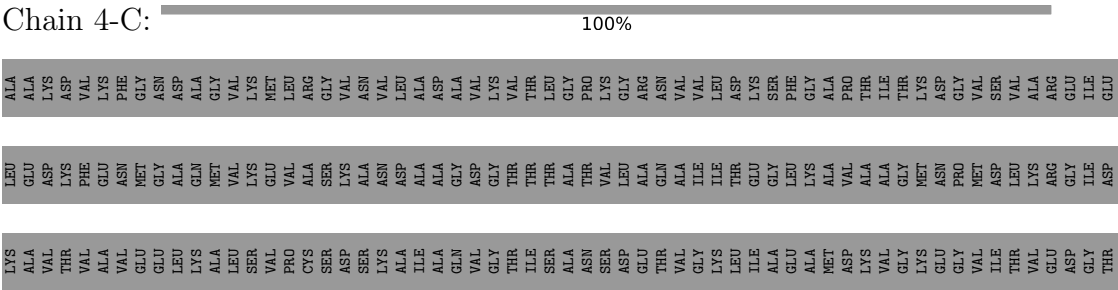




● Molecule 1: 60 kDa chaperonin



● Molecule 1: 60 kDa chaperonin



[illegible]

- Molecule 1: 60 kDa chaperonin

Chain 4-F: 100%

[illegible]

- Molecule 1: 60 kDa chaperonin

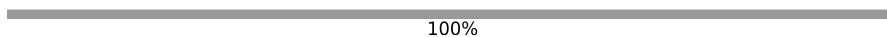
Chain 4-G: 100%

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

- Molecule 1: 60 kDa chaperonin

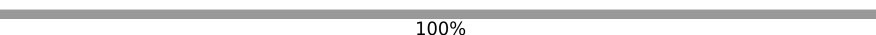
Chain 4-H:



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

- Molecule 1: 60 kDa chaperonin

Chain 4-I:



[illegible]

- Molecule 1: 60 kDa chaperonin

Chain 4-J: 100%

[illegible]

- Molecule 1: 60 kDa chaperonin

100%

- Molecule 1: 60 kDa chaperonin

100%



- Chain 4-M: 100%

[illegible]

- Chain 4-N: 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	ALA	GLY	LEU	MET	ILE	THR	THR	GLU	CYS	MET	VAL	THR	ASP	LEU	PRO
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

4 Experimental information

Property	Value	Source
EM 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	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.204	Depositor
Minimum map value	-0.111	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.012	Depositor
Recommended contour level	0.04	Depositor
Map size (Å)	295.2, 295.2, 295.2	wwPDB
Map dimensions	240, 240, 240	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.23, 1.23, 1.23	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 >5	RMSZ	# Z >5
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

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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 [i](#)

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

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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%)	76	88
1	3-A	404/404 (100%)	403 (100%)	1 (0%)	93	98
1	4-A	404/404 (100%)	400 (99%)	4 (1%)	76	88
All	All	6868/6868 (100%)	6859 (100%)	9 (0%)	93	98

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

Mol	Chain	Res	Type
1	4-A	284	ARG
1	4-A	390	LYS
1	2-A	445	ARG
1	3-A	225	LYS
1	4-A	226	LYS

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

Mol	Chain	Res	Type
1	2-A	146	GLN
1	4-A	505	GLN

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Mol	Chain	Res	Type
1	2-A	437	ASN
1	3-A	505	GLN
1	1-G	37	ASN

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 monosaccharides 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.

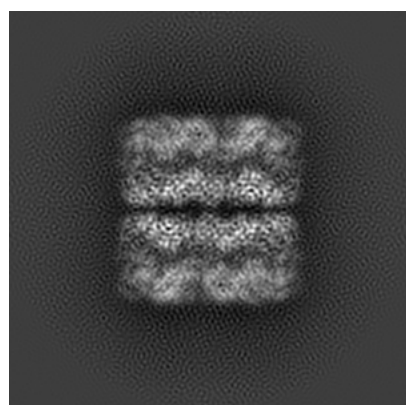
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8750. These allow visual inspection of the internal detail of the map and identification of artifacts.

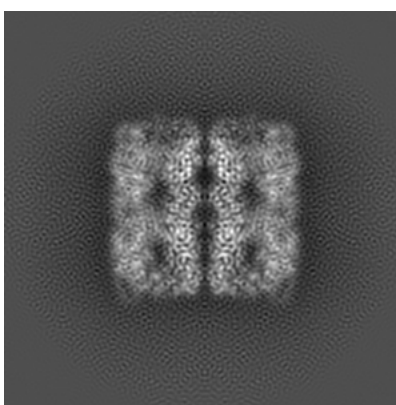
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

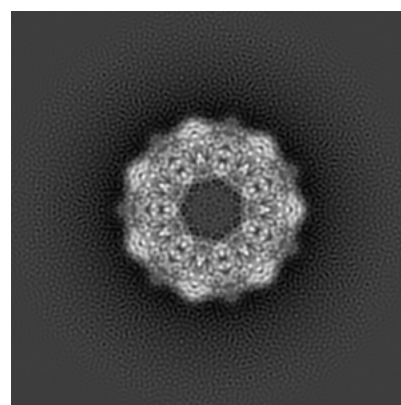
6.1.1 Primary map



X



Y

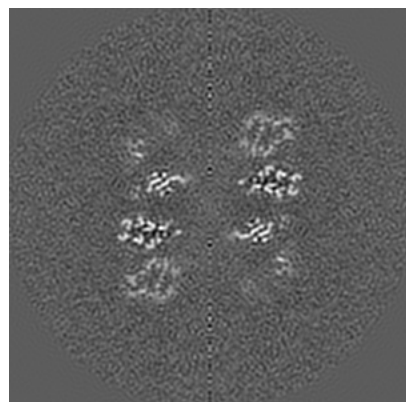


Z

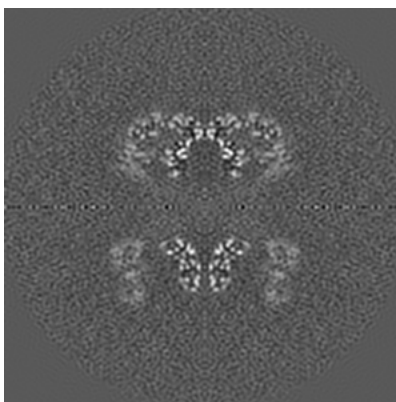
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

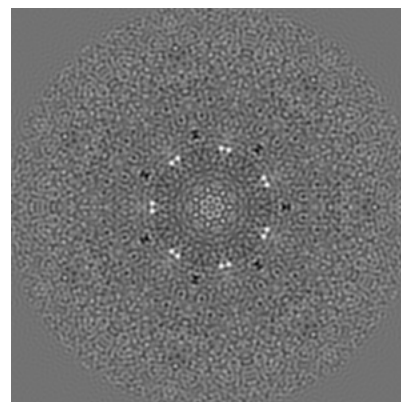
6.2.1 Primary map



X Index: 120



Y Index: 120

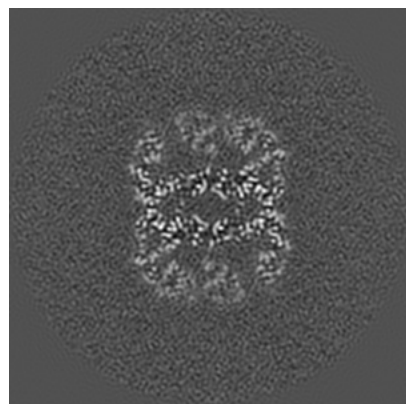


Z Index: 120

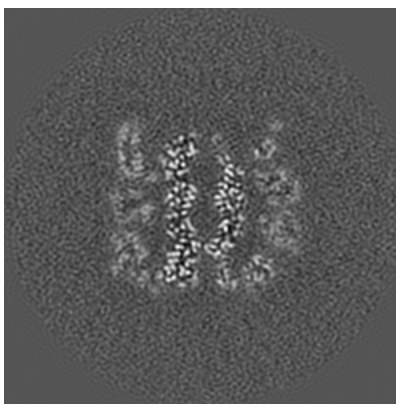
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

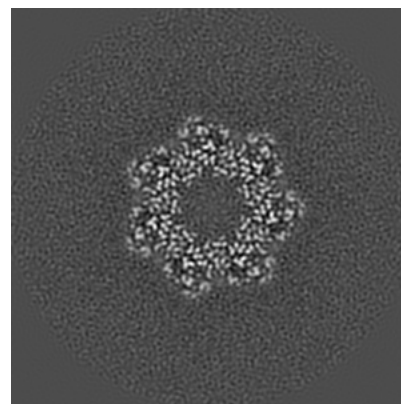
6.3.1 Primary map



X Index: 148



Y Index: 94

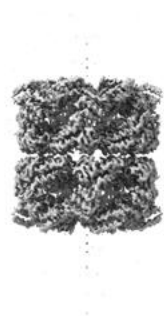


Z Index: 133

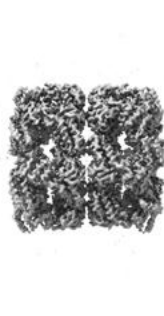
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views [i](#)

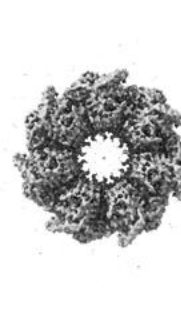
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.04. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

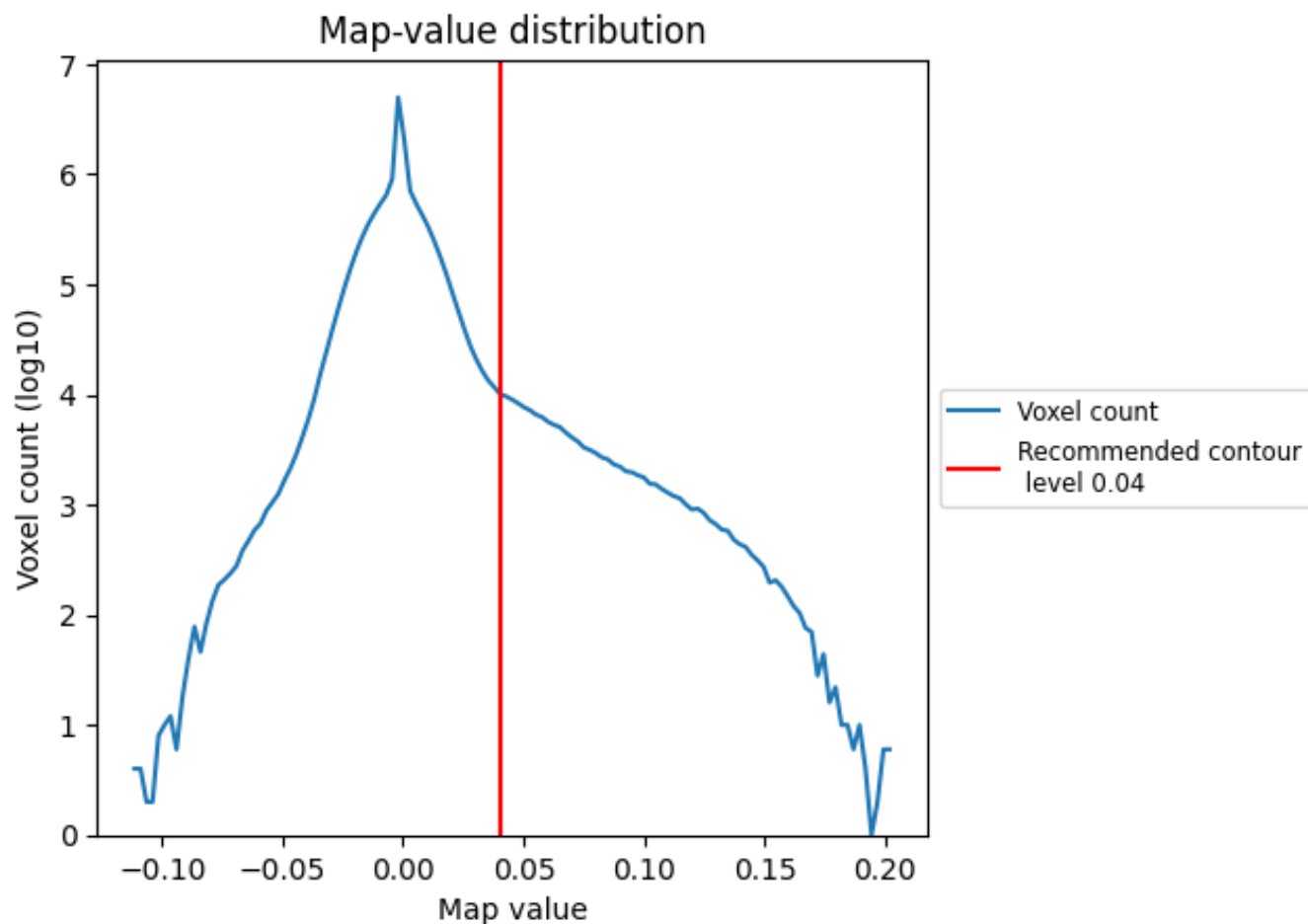
6.5 Mask visualisation

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

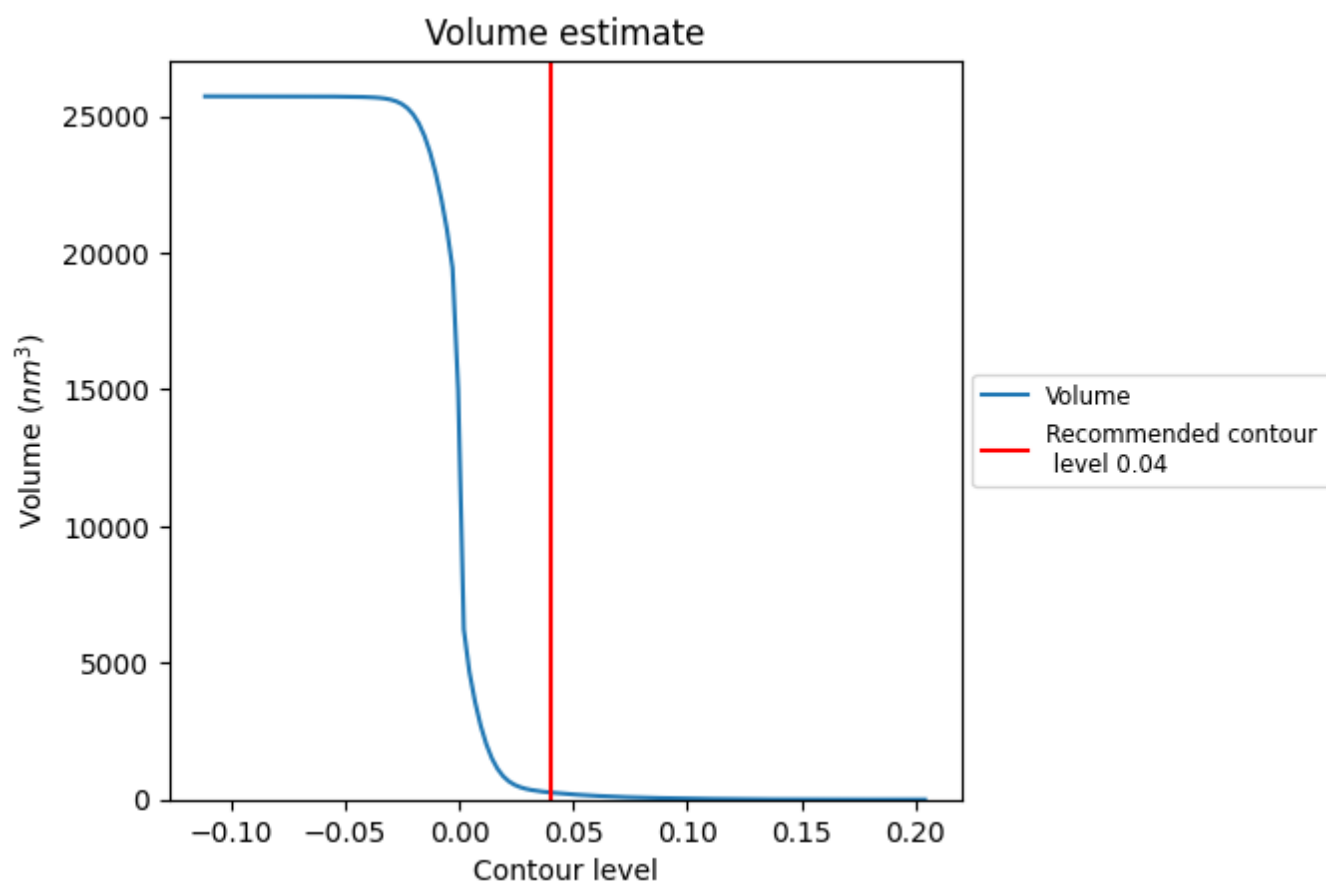
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

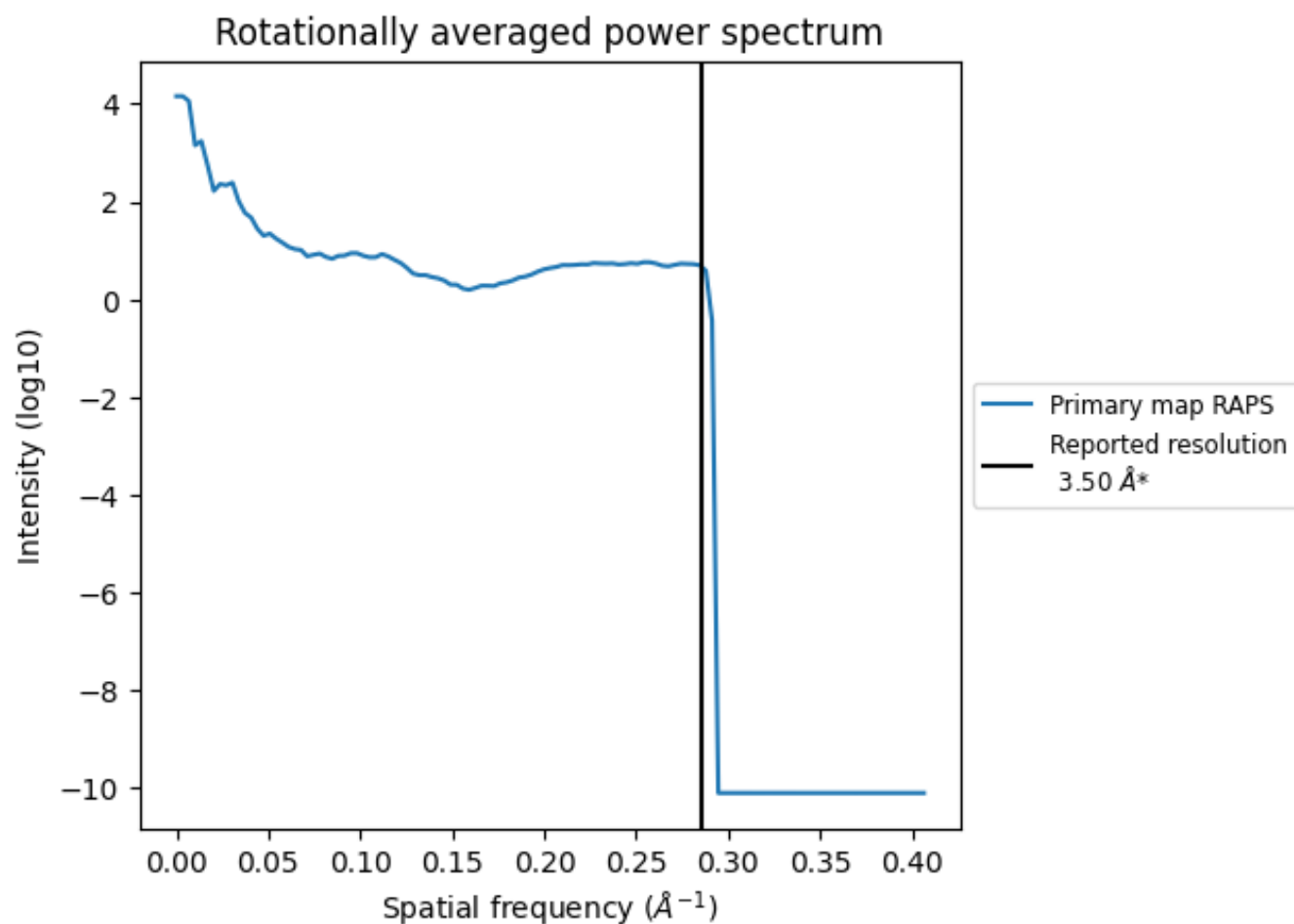
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 259 nm³; this corresponds to an approximate mass of 234 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

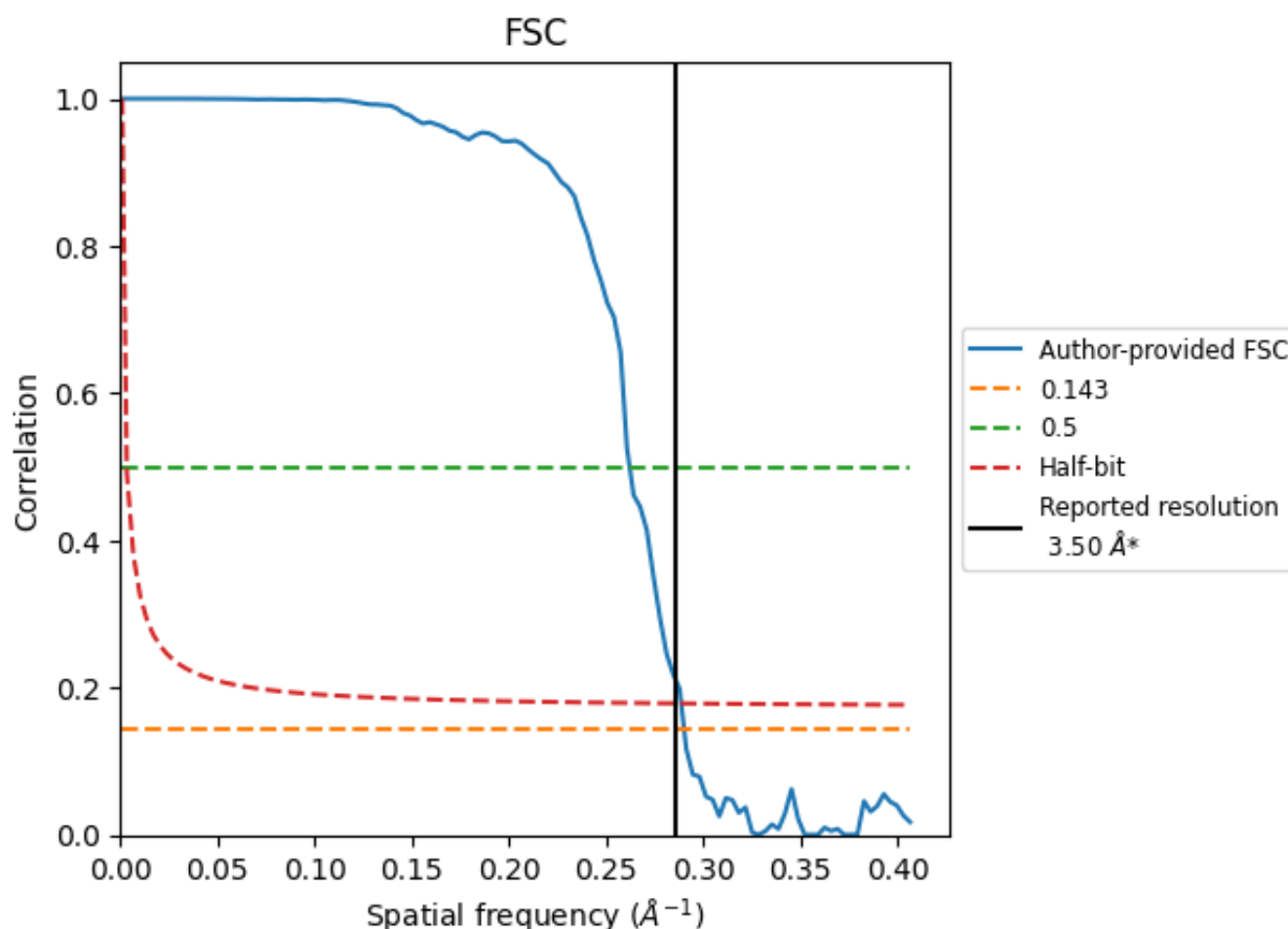


*Reported resolution corresponds to spatial frequency of 0.286 \AA^{-1}

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.286 \AA^{-1}

8.2 Resolution estimates [i](#)

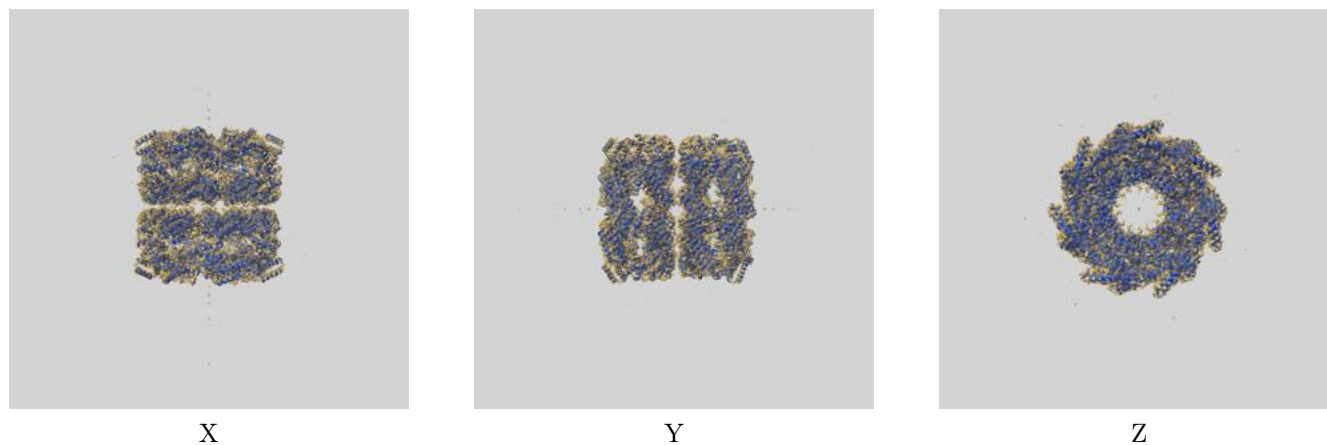
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	3.45	3.81	3.46
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-8750 and PDB model 5W0S. Per-residue inclusion information can be found in section [3](#) on page [8](#).

9.1 Map-model overlay [i](#)

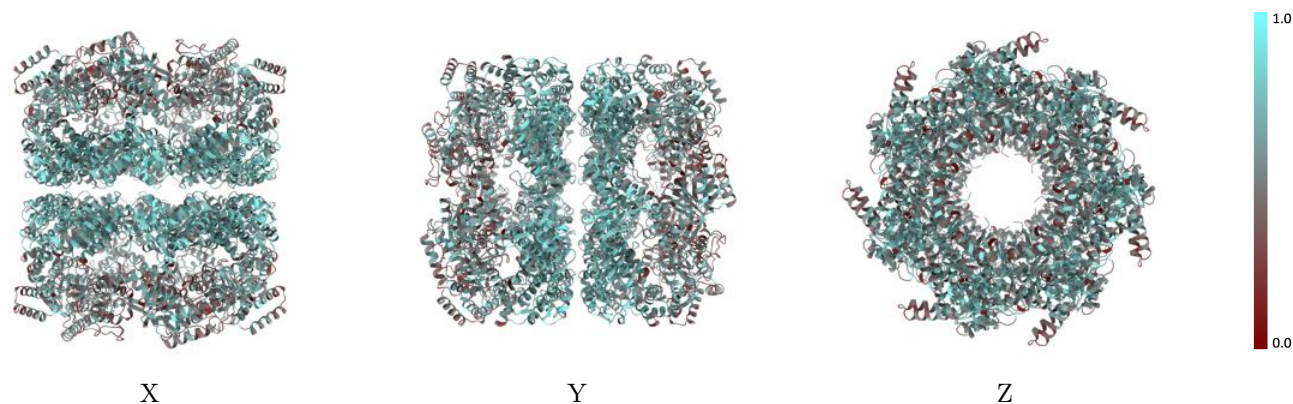


The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)

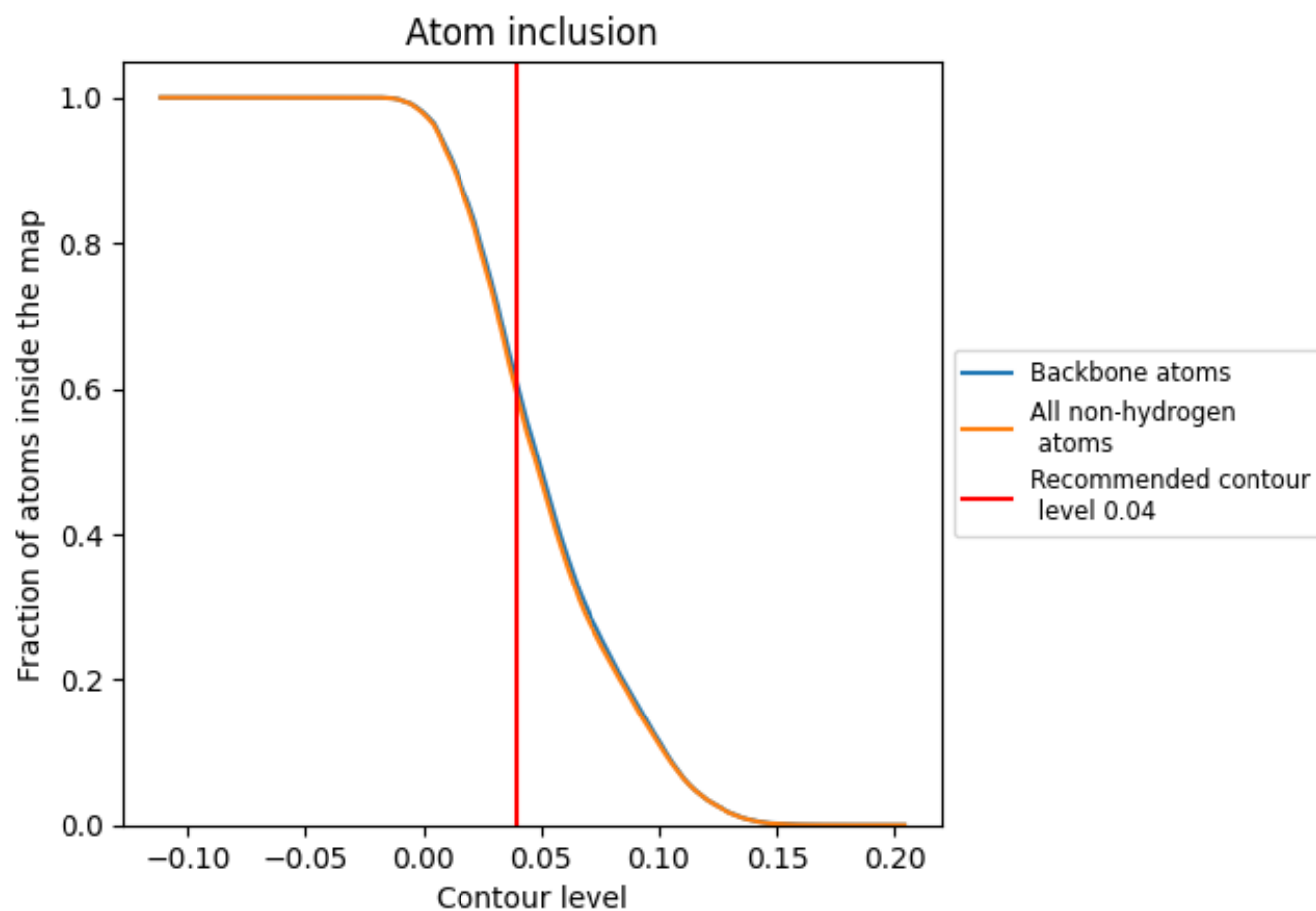
This section was not generated.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.04).

9.4 Atom inclusion [i](#)



At the recommended contour level, 61% of all backbone atoms, 59% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion
All	<div></div> 0.5898
A	<div></div> 0.5957
B	<div></div> 0.5965
C	<div></div> 0.5960
D	<div></div> 0.5963
E	<div></div> 0.5952
F	<div></div> 0.5944
G	<div></div> 0.5960
H	<div></div> 0.5960
I	<div></div> 0.5957
J	<div></div> 0.5960
K	<div></div> 0.5957
L	<div></div> 0.5960
M	<div></div> 0.5931
N	<div></div> 0.5950

