



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 05:52 AM UTC

PDB ID : 3IZK / pdb_00003izk
EMDB ID : EMD-5247
Title : Mm-cpn rls deltalid with ATP
Authors : Douglas, N.R.; Reissmann, S.; Zhang, J.; Chen, B.; Jakana, J.; Kumar, R.;
Chiu, W.; Frydman, J.
Deposited on : 2010-10-29
Resolution : 4.90 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:

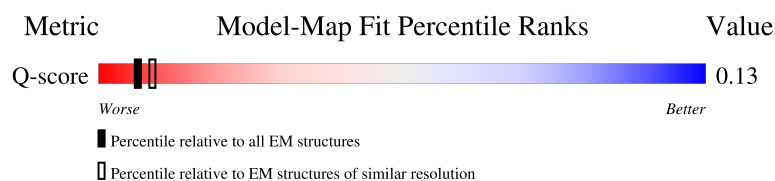
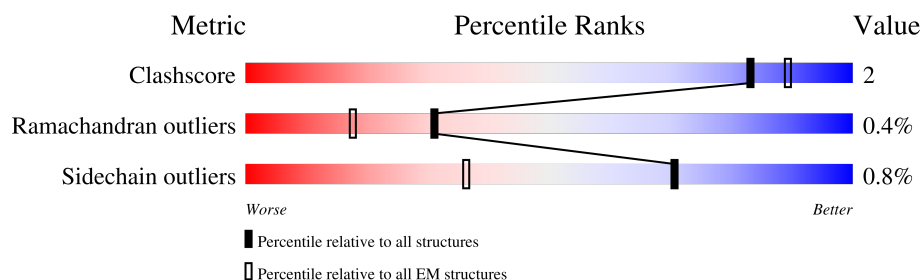
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

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 4.90 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	1274 (4.40 - 5.40)

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	A	491	27% 93% 7%
1	B	491	26% 93% 7%
1	C	491	27% 92% 7%
1	D	491	26% 92% 7%

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Mol	Chain	Length	Quality of chain
1	E	491	27% 92% 8%
1	F	491	26% 93% 7%
1	G	491	27% 93% 7%
1	H	491	26% 93% 7%
1	I	491	27% 93% 7%
1	J	491	27% 93% 7%
1	K	491	27% 93% 7%
1	L	491	27% 93% 7%
1	M	491	26% 92% 7%
1	N	491	27% 92% 7%
1	O	491	26% 93% 7%
1	P	491	27% 93% 6%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 58448 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 Chaperonin.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	491	Total	C	N	O	S	0	0
			3653	2266	633	730	24		
1	B	491	Total	C	N	O	S	0	0
			3653	2266	633	730	24		
1	C	491	Total	C	N	O	S	0	0
			3653	2266	633	730	24		
1	D	491	Total	C	N	O	S	0	0
			3653	2266	633	730	24		
1	E	491	Total	C	N	O	S	0	0
			3653	2266	633	730	24		
1	F	491	Total	C	N	O	S	0	0
			3653	2266	633	730	24		
1	G	491	Total	C	N	O	S	0	0
			3653	2266	633	730	24		
1	H	491	Total	C	N	O	S	0	0
			3653	2266	633	730	24		
1	I	491	Total	C	N	O	S	0	0
			3653	2266	633	730	24		
1	J	491	Total	C	N	O	S	0	0
			3653	2266	633	730	24		
1	K	491	Total	C	N	O	S	0	0
			3653	2266	633	730	24		
1	L	491	Total	C	N	O	S	0	0
			3653	2266	633	730	24		
1	M	491	Total	C	N	O	S	0	0
			3653	2266	633	730	24		
1	N	491	Total	C	N	O	S	0	0
			3653	2266	633	730	24		
1	O	491	Total	C	N	O	S	0	0
			3653	2266	633	730	24		
1	P	491	Total	C	N	O	S	0	0
			3653	2266	633	730	24		

There are 144 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	235	GLU	-	linker	UNP Q877G8
A	236	THR	-	linker	UNP Q877G8
A	237	ALA	-	linker	UNP Q877G8
A	238	SER	-	linker	UNP Q877G8
A	239	GLU	-	linker	UNP Q877G8
A	299	ALA	THR	engineered mutation	UNP Q877G8
A	300	ALA	ASN	engineered mutation	UNP Q877G8
A	302	ALA	LYS	engineered mutation	UNP Q877G8
A	303	ALA	ASP	engineered mutation	UNP Q877G8
B	726	GLU	-	linker	UNP Q877G8
B	727	THR	-	linker	UNP Q877G8
B	728	ALA	-	linker	UNP Q877G8
B	729	SER	-	linker	UNP Q877G8
B	730	GLU	-	linker	UNP Q877G8
B	790	ALA	THR	engineered mutation	UNP Q877G8
B	791	ALA	ASN	engineered mutation	UNP Q877G8
B	793	ALA	LYS	engineered mutation	UNP Q877G8
B	794	ALA	ASP	engineered mutation	UNP Q877G8
C	1217	GLU	-	linker	UNP Q877G8
C	1218	THR	-	linker	UNP Q877G8
C	1219	ALA	-	linker	UNP Q877G8
C	1220	SER	-	linker	UNP Q877G8
C	1221	GLU	-	linker	UNP Q877G8
C	1281	ALA	THR	engineered mutation	UNP Q877G8
C	1282	ALA	ASN	engineered mutation	UNP Q877G8
C	1284	ALA	LYS	engineered mutation	UNP Q877G8
C	1285	ALA	ASP	engineered mutation	UNP Q877G8
D	1708	GLU	-	linker	UNP Q877G8
D	1709	THR	-	linker	UNP Q877G8
D	1710	ALA	-	linker	UNP Q877G8
D	1711	SER	-	linker	UNP Q877G8
D	1712	GLU	-	linker	UNP Q877G8
D	1772	ALA	THR	engineered mutation	UNP Q877G8
D	1773	ALA	ASN	engineered mutation	UNP Q877G8
D	1775	ALA	LYS	engineered mutation	UNP Q877G8
D	1776	ALA	ASP	engineered mutation	UNP Q877G8
E	2199	GLU	-	linker	UNP Q877G8
E	2200	THR	-	linker	UNP Q877G8
E	2201	ALA	-	linker	UNP Q877G8
E	2202	SER	-	linker	UNP Q877G8
E	2203	GLU	-	linker	UNP Q877G8
E	2263	ALA	THR	engineered mutation	UNP Q877G8
E	2264	ALA	ASN	engineered mutation	UNP Q877G8

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Chain	Residue	Modelled	Actual	Comment	Reference
E	2266	ALA	LYS	engineered mutation	UNP Q877G8
E	2267	ALA	ASP	engineered mutation	UNP Q877G8
F	2690	GLU	-	linker	UNP Q877G8
F	2691	THR	-	linker	UNP Q877G8
F	2692	ALA	-	linker	UNP Q877G8
F	2693	SER	-	linker	UNP Q877G8
F	2694	GLU	-	linker	UNP Q877G8
F	2754	ALA	THR	engineered mutation	UNP Q877G8
F	2755	ALA	ASN	engineered mutation	UNP Q877G8
F	2757	ALA	LYS	engineered mutation	UNP Q877G8
F	2758	ALA	ASP	engineered mutation	UNP Q877G8
G	3181	GLU	-	linker	UNP Q877G8
G	3182	THR	-	linker	UNP Q877G8
G	3183	ALA	-	linker	UNP Q877G8
G	3184	SER	-	linker	UNP Q877G8
G	3185	GLU	-	linker	UNP Q877G8
G	3245	ALA	THR	engineered mutation	UNP Q877G8
G	3246	ALA	ASN	engineered mutation	UNP Q877G8
G	3248	ALA	LYS	engineered mutation	UNP Q877G8
G	3249	ALA	ASP	engineered mutation	UNP Q877G8
H	3672	GLU	-	linker	UNP Q877G8
H	3673	THR	-	linker	UNP Q877G8
H	3674	ALA	-	linker	UNP Q877G8
H	3675	SER	-	linker	UNP Q877G8
H	3676	GLU	-	linker	UNP Q877G8
H	3736	ALA	THR	engineered mutation	UNP Q877G8
H	3737	ALA	ASN	engineered mutation	UNP Q877G8
H	3739	ALA	LYS	engineered mutation	UNP Q877G8
H	3740	ALA	ASP	engineered mutation	UNP Q877G8
I	4163	GLU	-	linker	UNP Q877G8
I	4164	THR	-	linker	UNP Q877G8
I	4165	ALA	-	linker	UNP Q877G8
I	4166	SER	-	linker	UNP Q877G8
I	4167	GLU	-	linker	UNP Q877G8
I	4227	ALA	THR	engineered mutation	UNP Q877G8
I	4228	ALA	ASN	engineered mutation	UNP Q877G8
I	4230	ALA	LYS	engineered mutation	UNP Q877G8
I	4231	ALA	ASP	engineered mutation	UNP Q877G8
J	4654	GLU	-	linker	UNP Q877G8
J	4655	THR	-	linker	UNP Q877G8
J	4656	ALA	-	linker	UNP Q877G8
J	4657	SER	-	linker	UNP Q877G8

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Chain	Residue	Modelled	Actual	Comment	Reference
J	4658	GLU	-	linker	UNP Q877G8
J	4718	ALA	THR	engineered mutation	UNP Q877G8
J	4719	ALA	ASN	engineered mutation	UNP Q877G8
J	4721	ALA	LYS	engineered mutation	UNP Q877G8
J	4722	ALA	ASP	engineered mutation	UNP Q877G8
K	5145	GLU	-	linker	UNP Q877G8
K	5146	THR	-	linker	UNP Q877G8
K	5147	ALA	-	linker	UNP Q877G8
K	5148	SER	-	linker	UNP Q877G8
K	5149	GLU	-	linker	UNP Q877G8
K	5209	ALA	THR	engineered mutation	UNP Q877G8
K	5210	ALA	ASN	engineered mutation	UNP Q877G8
K	5212	ALA	LYS	engineered mutation	UNP Q877G8
K	5213	ALA	ASP	engineered mutation	UNP Q877G8
L	5636	GLU	-	linker	UNP Q877G8
L	5637	THR	-	linker	UNP Q877G8
L	5638	ALA	-	linker	UNP Q877G8
L	5639	SER	-	linker	UNP Q877G8
L	5640	GLU	-	linker	UNP Q877G8
L	5700	ALA	THR	engineered mutation	UNP Q877G8
L	5701	ALA	ASN	engineered mutation	UNP Q877G8
L	5703	ALA	LYS	engineered mutation	UNP Q877G8
L	5704	ALA	ASP	engineered mutation	UNP Q877G8
M	6127	GLU	-	linker	UNP Q877G8
M	6128	THR	-	linker	UNP Q877G8
M	6129	ALA	-	linker	UNP Q877G8
M	6130	SER	-	linker	UNP Q877G8
M	6131	GLU	-	linker	UNP Q877G8
M	6191	ALA	THR	engineered mutation	UNP Q877G8
M	6192	ALA	ASN	engineered mutation	UNP Q877G8
M	6194	ALA	LYS	engineered mutation	UNP Q877G8
M	6195	ALA	ASP	engineered mutation	UNP Q877G8
N	6618	GLU	-	linker	UNP Q877G8
N	6619	THR	-	linker	UNP Q877G8
N	6620	ALA	-	linker	UNP Q877G8
N	6621	SER	-	linker	UNP Q877G8
N	6622	GLU	-	linker	UNP Q877G8
N	6682	ALA	THR	engineered mutation	UNP Q877G8
N	6683	ALA	ASN	engineered mutation	UNP Q877G8
N	6685	ALA	LYS	engineered mutation	UNP Q877G8
N	6686	ALA	ASP	engineered mutation	UNP Q877G8
O	7109	GLU	-	linker	UNP Q877G8

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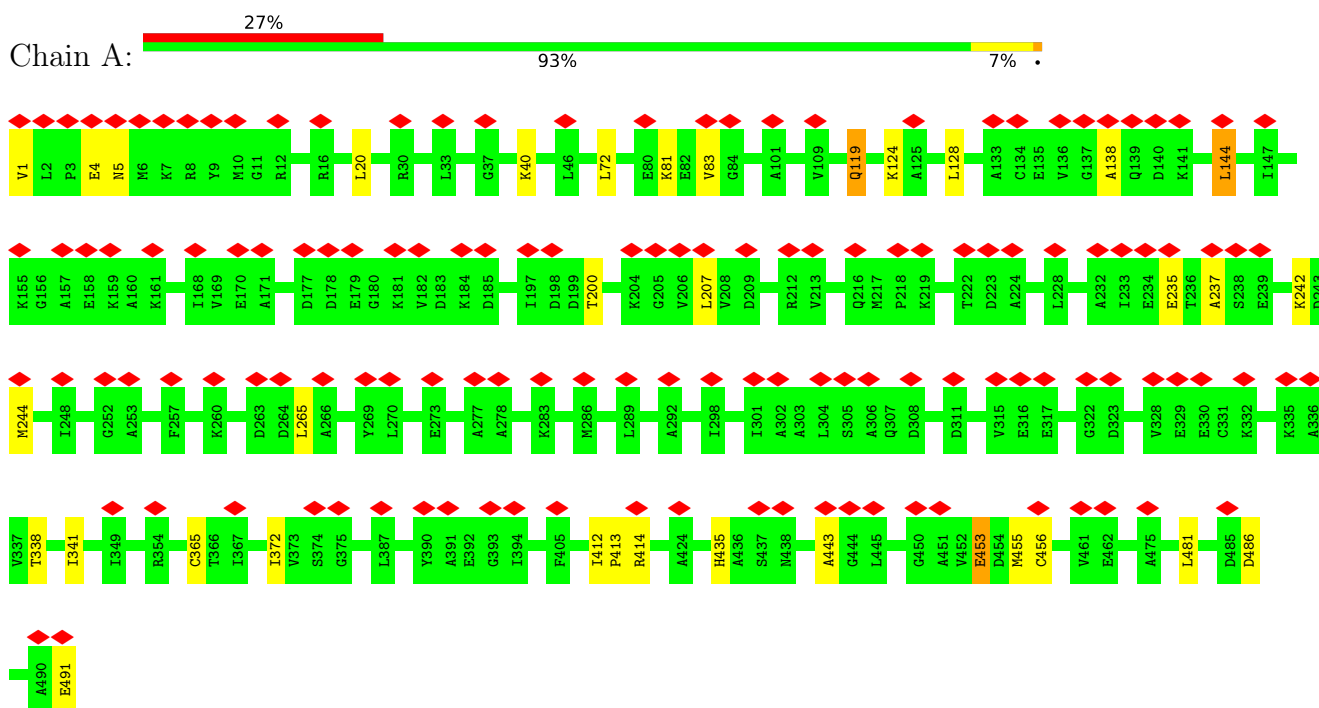
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Chain	Residue	Modelled	Actual	Comment	Reference
O	7110	THR	-	linker	UNP Q877G8
O	7111	ALA	-	linker	UNP Q877G8
O	7112	SER	-	linker	UNP Q877G8
O	7113	GLU	-	linker	UNP Q877G8
O	7173	ALA	THR	engineered mutation	UNP Q877G8
O	7174	ALA	ASN	engineered mutation	UNP Q877G8
O	7176	ALA	LYS	engineered mutation	UNP Q877G8
O	7177	ALA	ASP	engineered mutation	UNP Q877G8
P	7600	GLU	-	linker	UNP Q877G8
P	7601	THR	-	linker	UNP Q877G8
P	7602	ALA	-	linker	UNP Q877G8
P	7603	SER	-	linker	UNP Q877G8
P	7604	GLU	-	linker	UNP Q877G8
P	7664	ALA	THR	engineered mutation	UNP Q877G8
P	7665	ALA	ASN	engineered mutation	UNP Q877G8
P	7667	ALA	LYS	engineered mutation	UNP Q877G8
P	7668	ALA	ASP	engineered mutation	UNP Q877G8

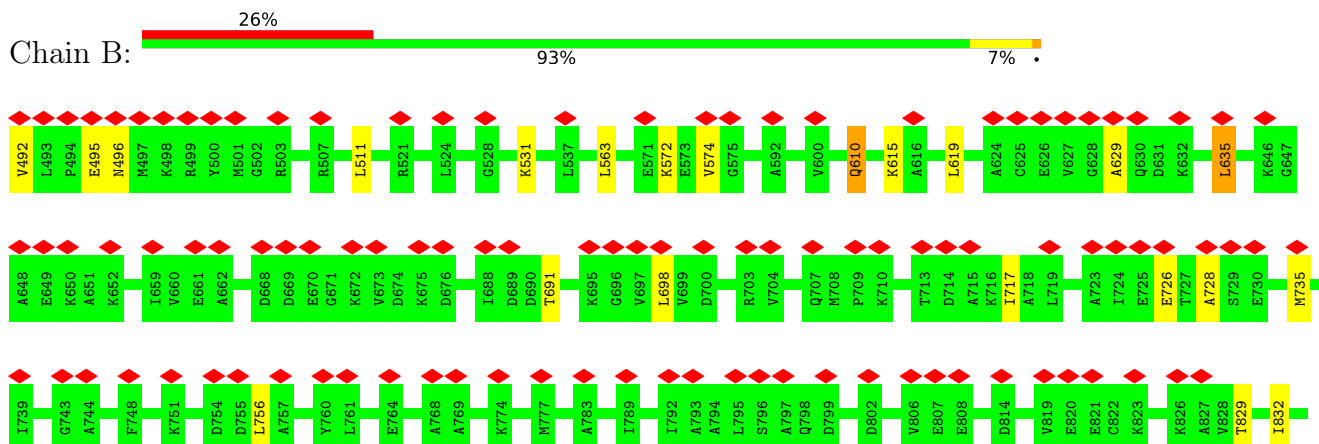
3 Residue-property plots

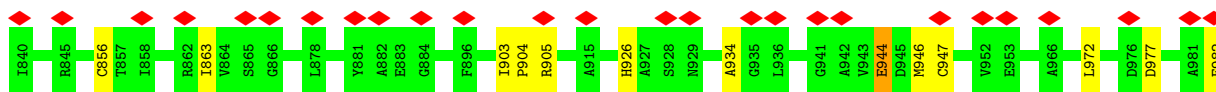
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Chaperonin

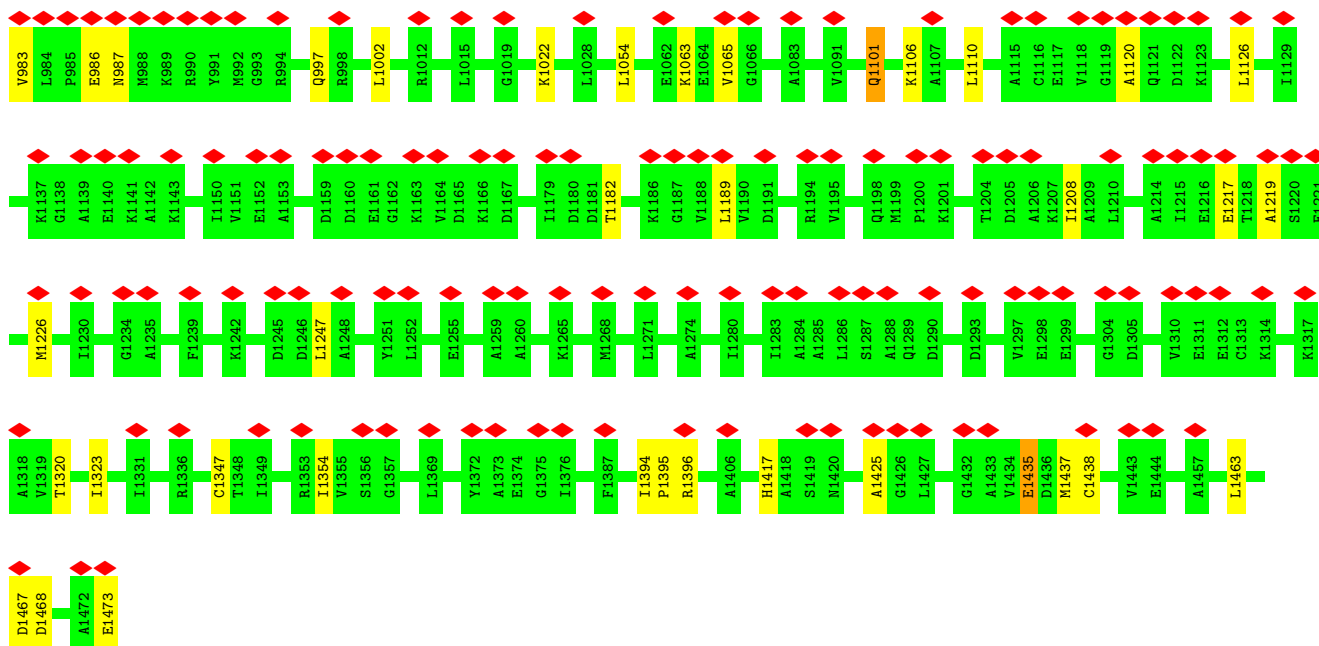
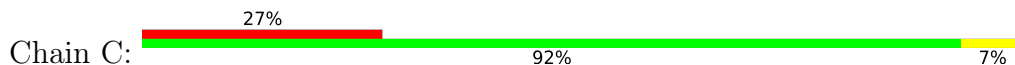


- Molecule 1: Chaperonin

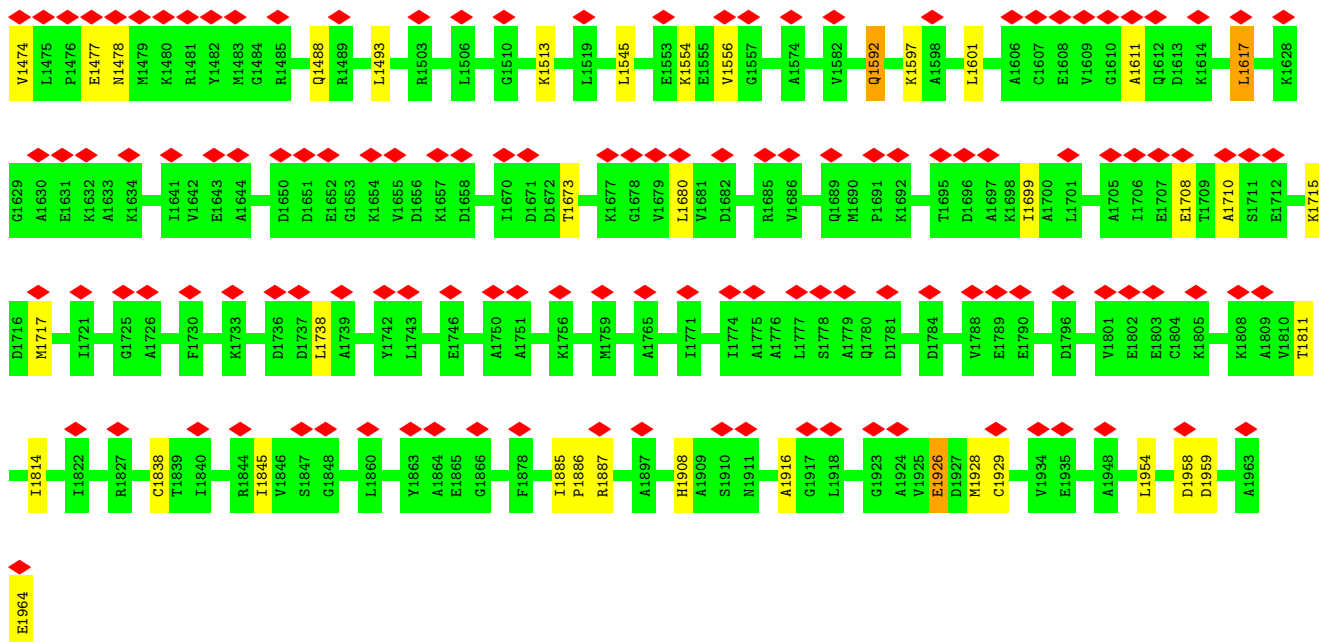




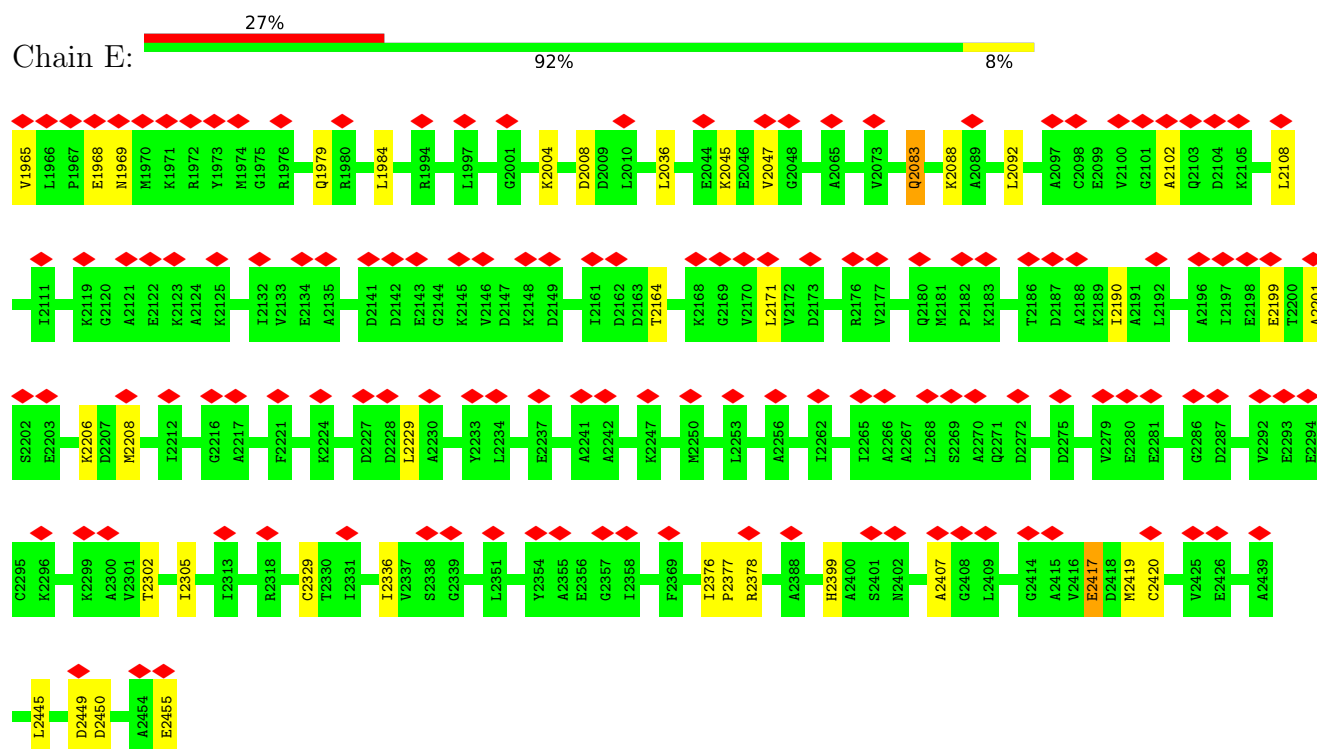
• Molecule 1: Chaperonin



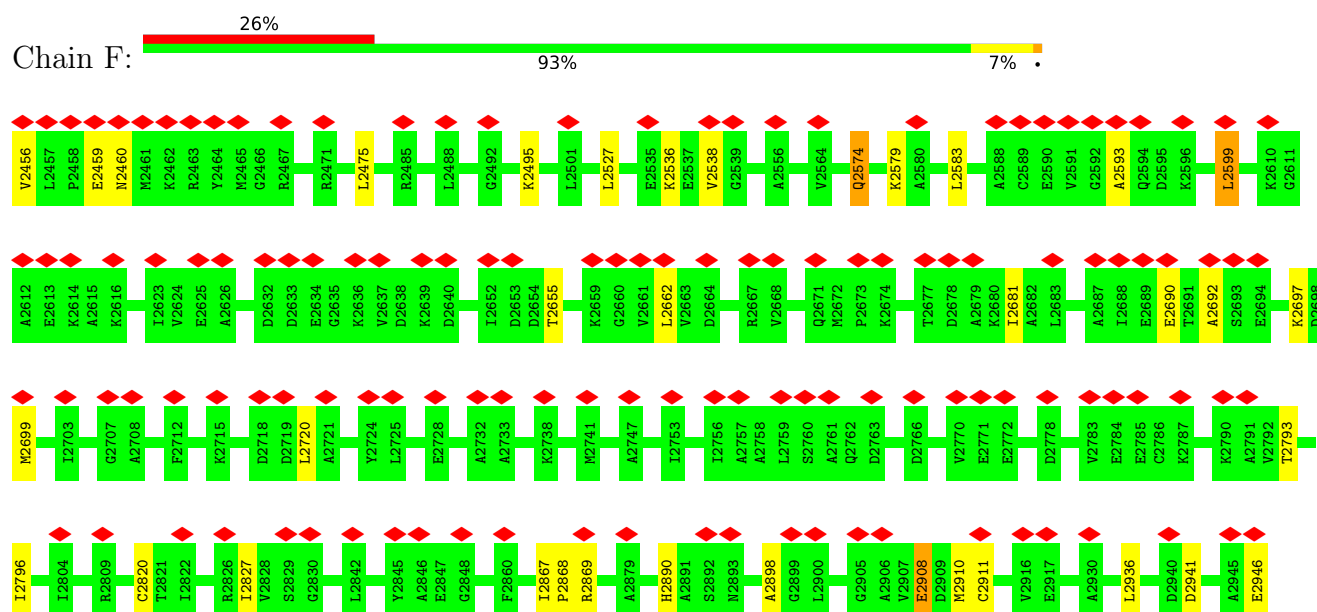
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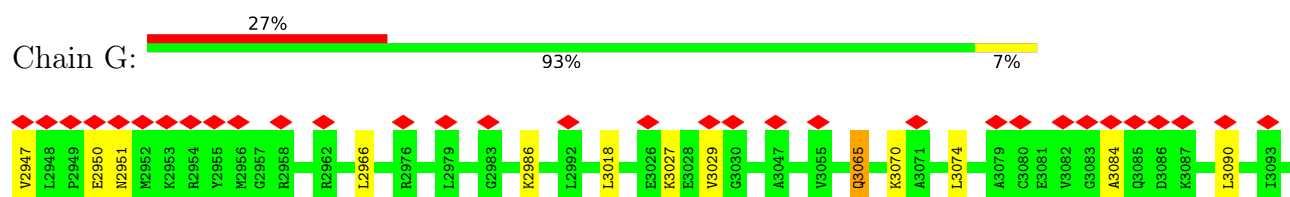
- Molecule 1: Chaperonin

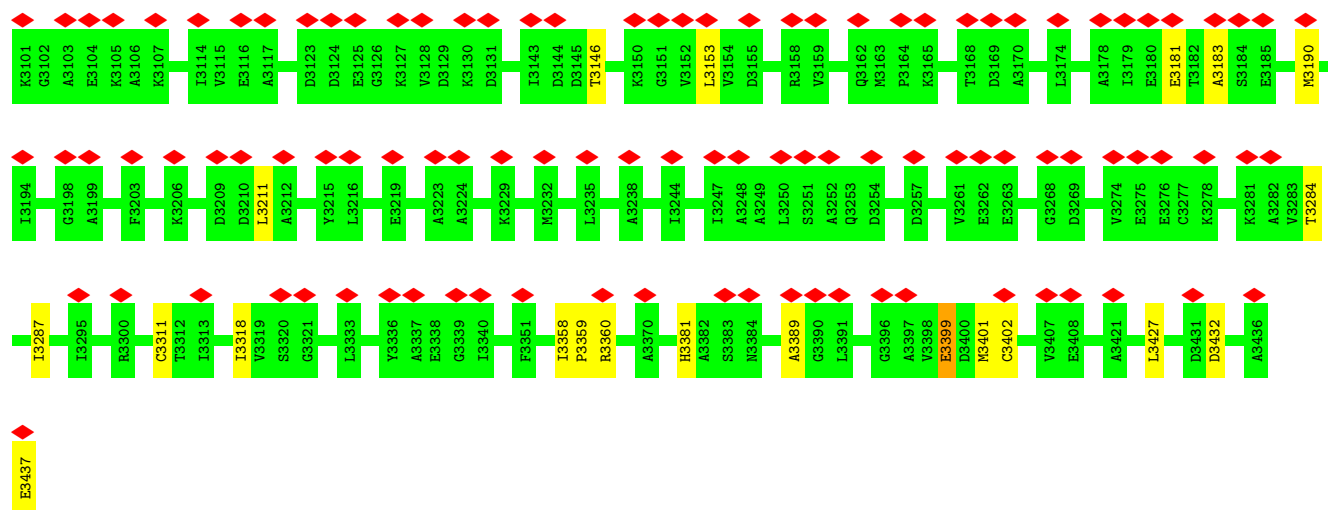


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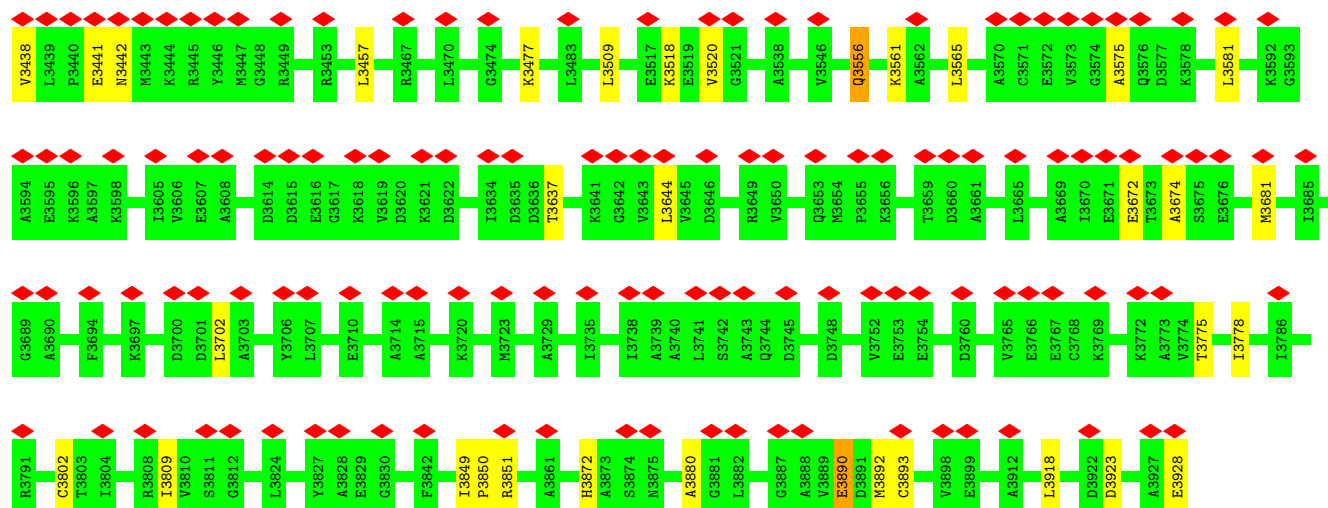
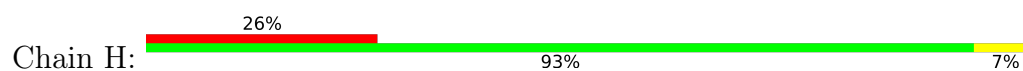


- Molecule 1: Chaperonin

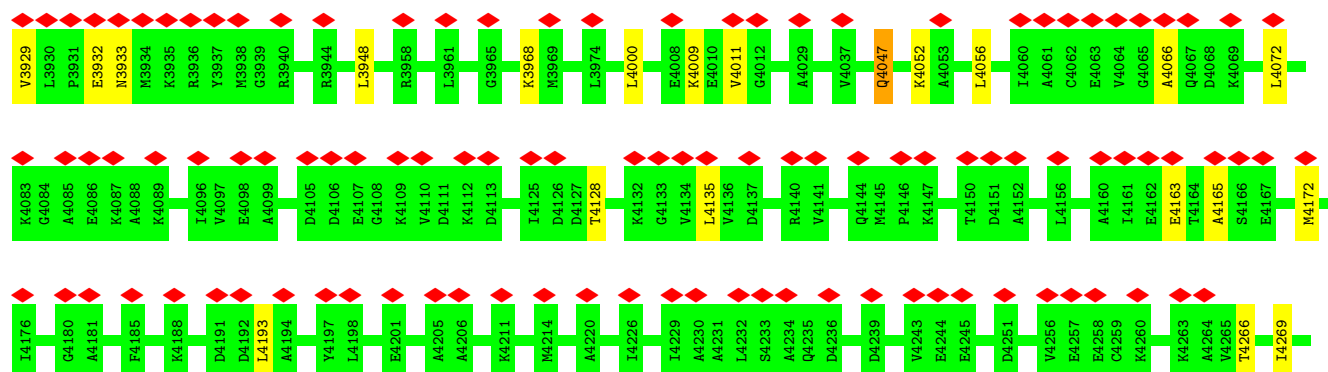


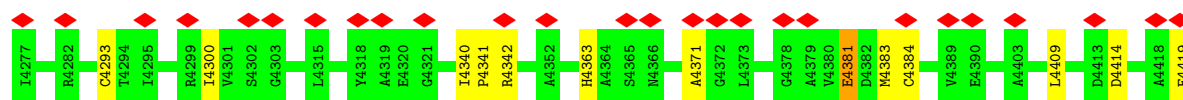


• Molecule 1: Chaperonin

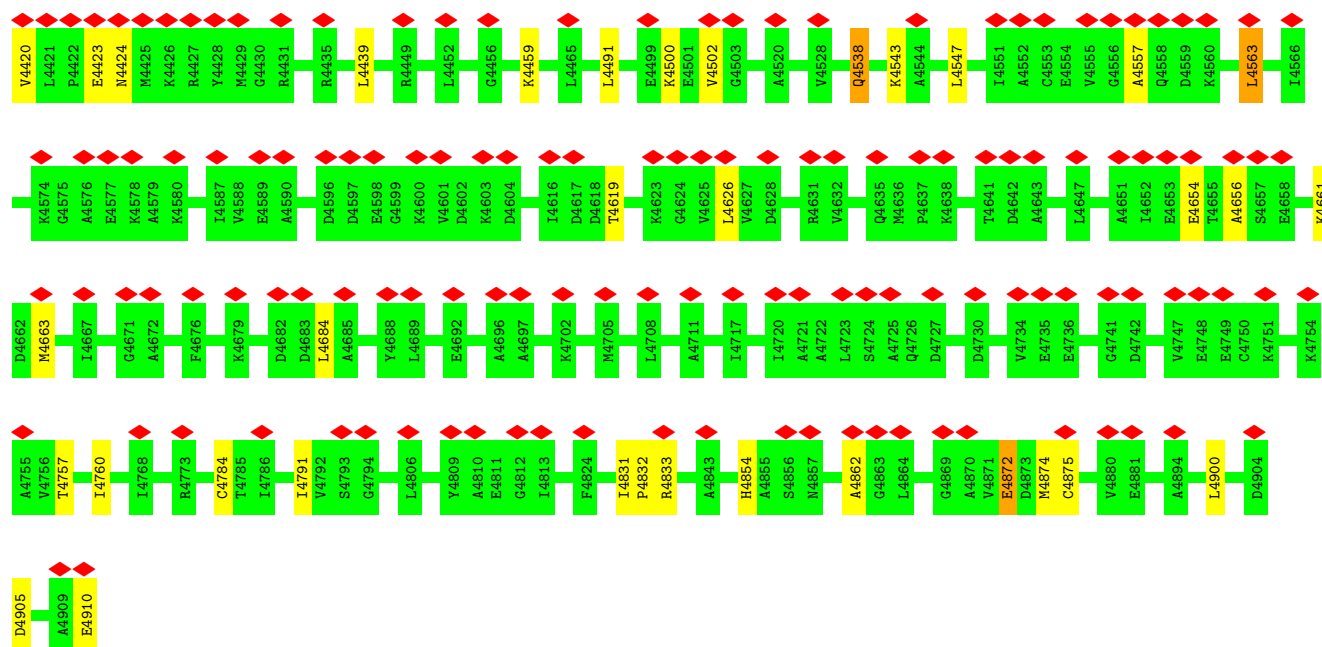
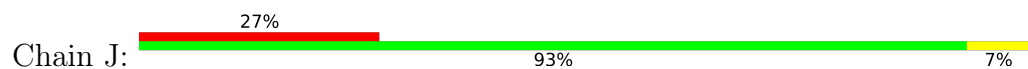


• Molecule 1: Chaperonin

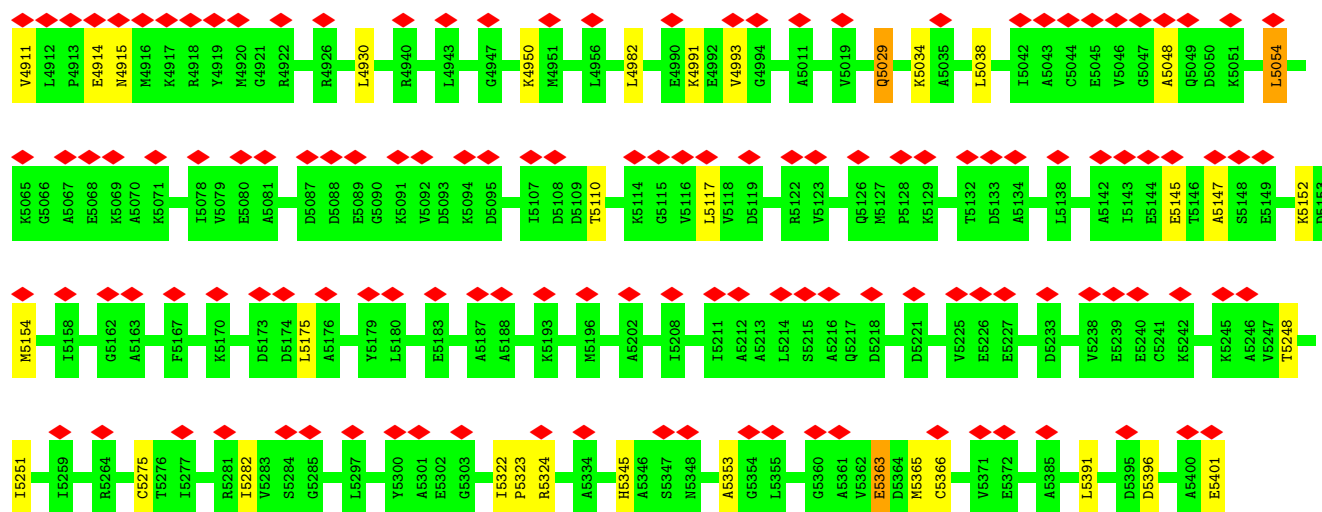




• Molecule 1: Chaperonin

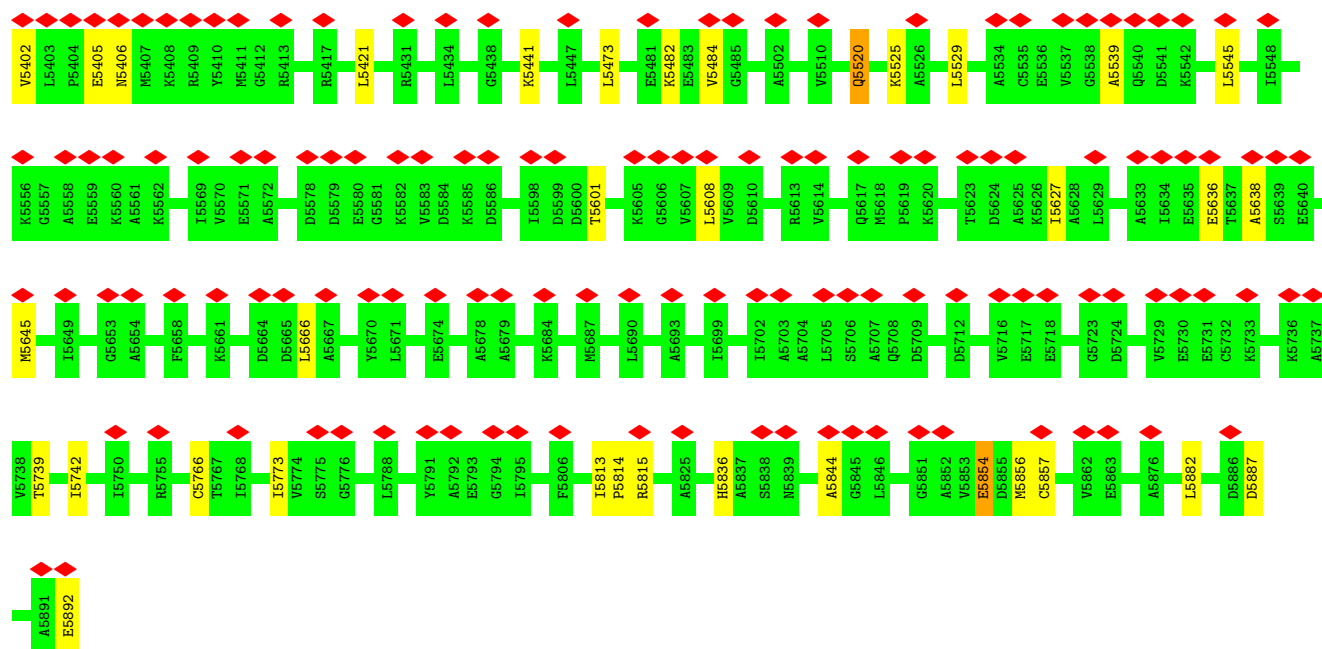


• Molecule 1: Chaperonin

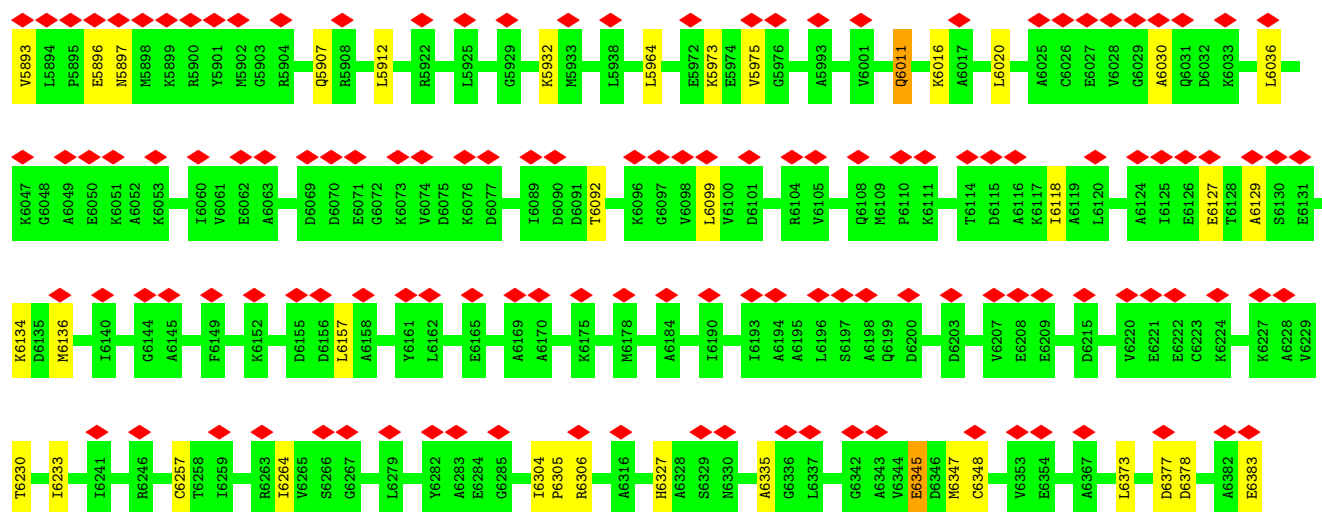


• Molecule 1: Chaperonin

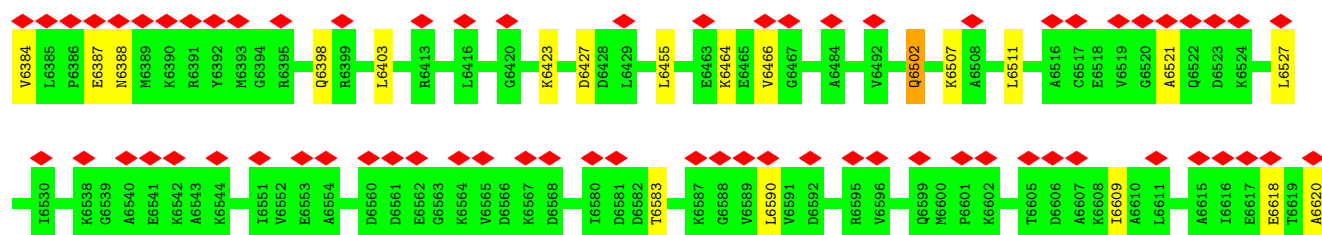


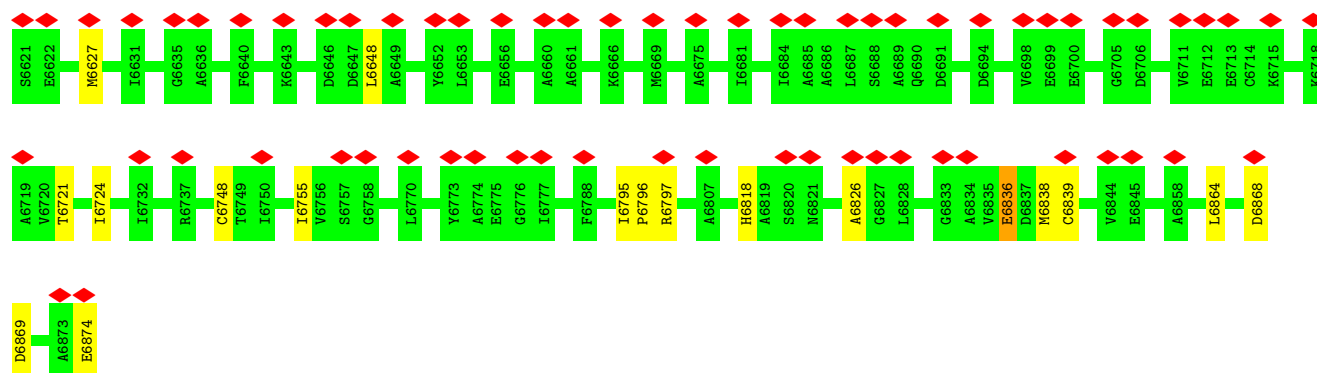


• Molecule 1: Chaperonin

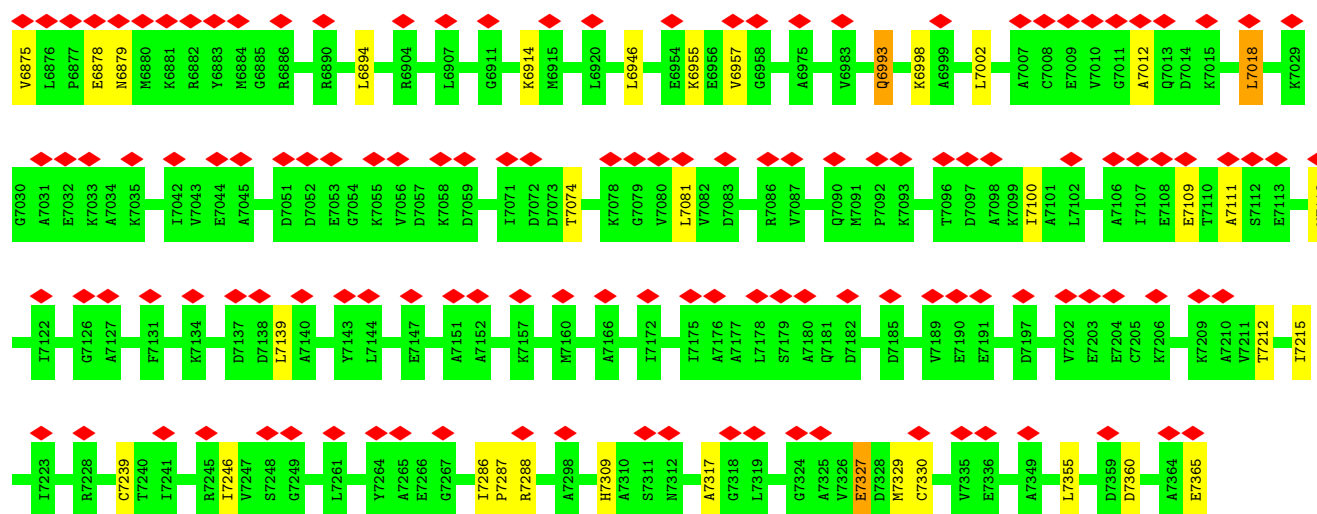


• Molecule 1: Chaperonin

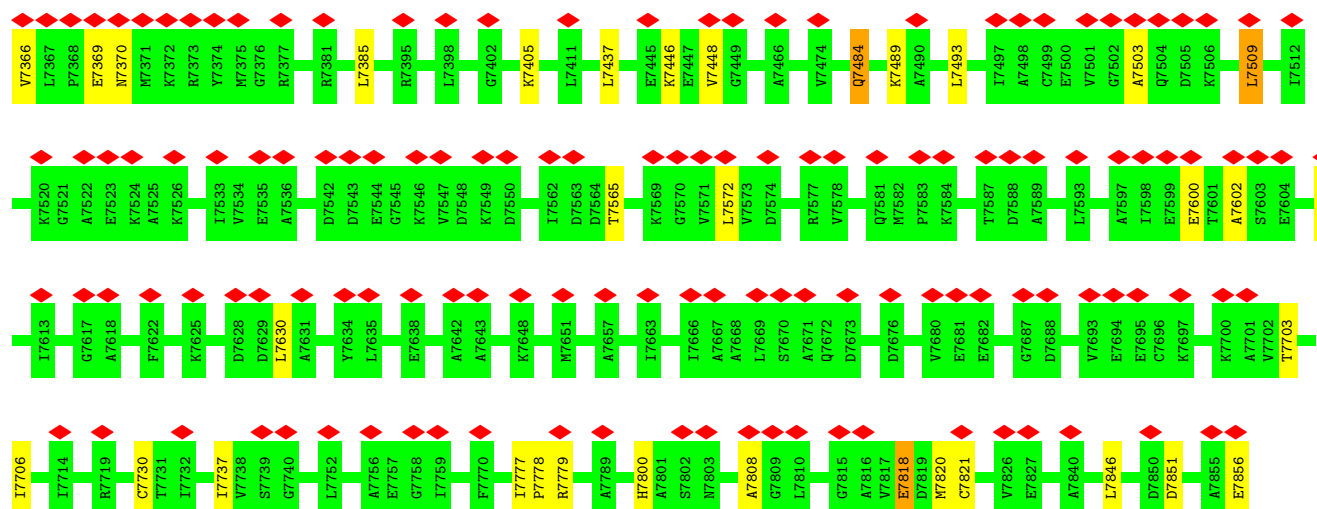




• Molecule 1: Chaperonin



• Molecule 1: Chaperonin



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, D8	Depositor
Number of particles used	Not provided	
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	Not provided	
Microscope	JEOL 3200FSC	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	Not provided	
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN ULTRASCAN 4000 (4k x 4k)	Depositor
Maximum map value	1.330	Depositor
Minimum map value	-0.698	Depositor
Average map value	0.022	Depositor
Map value standard deviation	0.108	Depositor
Recommended contour level	0.4	Depositor
Map size ($\text{\AA}$)	266.0, 266.0, 266.0	wwPDB
Map dimensions	200, 200, 200	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.33, 1.33, 1.33	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	A	0.94	4/3674 (0.1%)	1.07	8/4946 (0.2%)
1	B	0.94	4/3674 (0.1%)	1.07	8/4946 (0.2%)
1	C	0.94	4/3674 (0.1%)	1.07	8/4946 (0.2%)
1	D	0.94	4/3674 (0.1%)	1.07	8/4946 (0.2%)
1	E	0.94	4/3674 (0.1%)	1.07	8/4946 (0.2%)
1	F	0.94	4/3674 (0.1%)	1.07	8/4946 (0.2%)
1	G	0.94	4/3674 (0.1%)	1.07	8/4946 (0.2%)
1	H	0.94	4/3674 (0.1%)	1.07	8/4946 (0.2%)
1	I	0.94	4/3674 (0.1%)	1.07	8/4946 (0.2%)
1	J	0.94	4/3674 (0.1%)	1.07	8/4946 (0.2%)
1	K	0.94	4/3674 (0.1%)	1.07	8/4946 (0.2%)
1	L	0.94	4/3674 (0.1%)	1.07	8/4946 (0.2%)
1	M	0.94	4/3674 (0.1%)	1.07	8/4946 (0.2%)
1	N	0.94	4/3674 (0.1%)	1.07	8/4946 (0.2%)
1	O	0.94	4/3674 (0.1%)	1.07	8/4946 (0.2%)
1	P	0.94	4/3674 (0.1%)	1.07	8/4946 (0.2%)
All	All	0.94	64/58784 (0.1%)	1.07	128/79136 (0.2%)

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	A	0	3
1	B	0	3
1	C	0	3
1	D	0	3
1	E	0	3
1	F	0	3
1	G	0	3
1	H	0	3
1	I	0	3

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	J	0	3
1	K	0	3
1	L	0	3
1	M	0	3
1	N	0	3
1	O	0	3
1	P	0	3
All	All	0	48

The worst 5 of 64 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	H	3880	ALA	C-O	8.44	1.33	1.23
1	K	5353	ALA	C-O	8.44	1.33	1.23
1	O	7317	ALA	C-O	8.44	1.33	1.23
1	A	443	ALA	C-O	8.43	1.33	1.23
1	C	1425	ALA	C-O	8.43	1.33	1.23

The worst 5 of 128 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	4	GLU	CA-C-O	-12.96	106.14	120.92
1	G	2950	GLU	CA-C-O	-12.96	106.14	120.92
1	N	6387	GLU	CA-C-O	-12.96	106.14	120.92
1	B	495	GLU	CA-C-O	-12.96	106.14	120.92
1	D	1477	GLU	CA-C-O	-12.96	106.14	120.92

There are no chirality outliers.

5 of 48 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	119	GLN	Mainchain
1	A	138	ALA	Mainchain
1	A	453	GLU	Mainchain
1	B	610	GLN	Mainchain
1	B	629	ALA	Mainchain

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	A	3653	0	3794	20	0
1	B	3653	0	3791	20	0
1	C	3653	0	3791	20	0
1	D	3653	0	3791	22	0
1	E	3653	0	3791	22	0
1	F	3653	0	3791	21	0
1	G	3653	0	3791	18	0
1	H	3653	0	3791	18	0
1	I	3653	0	3791	18	0
1	J	3653	0	3791	21	0
1	K	3653	0	3791	21	0
1	L	3653	0	3791	19	0
1	M	3653	0	3791	21	0
1	N	3653	0	3791	21	0
1	O	3653	0	3791	20	0
1	P	3653	0	3791	19	0
All	All	58448	0	60659	288	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 2.

The worst 5 of 288 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:B:572:LYS:HE2	1:B:572:LYS:HA	1.79	0.65
1:K:4991:LYS:HE2	1:K:4991:LYS:HA	1.79	0.65
1:D:1554:LYS:HE2	1:D:1554:LYS:HA	1.79	0.64
1:M:5973:LYS:HA	1:M:5973:LYS:HE2	1.79	0.64
1:H:3518:LYS:HE2	1:H:3518:LYS:HA	1.79	0.64

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	A	489/491 (100%)	477 (98%)	10 (2%)	2 (0%)	30	67
1	B	489/491 (100%)	477 (98%)	10 (2%)	2 (0%)	30	67
1	C	489/491 (100%)	477 (98%)	10 (2%)	2 (0%)	30	67
1	D	489/491 (100%)	477 (98%)	10 (2%)	2 (0%)	30	67
1	E	489/491 (100%)	477 (98%)	10 (2%)	2 (0%)	30	67
1	F	489/491 (100%)	477 (98%)	10 (2%)	2 (0%)	30	67
1	G	489/491 (100%)	477 (98%)	10 (2%)	2 (0%)	30	67
1	H	489/491 (100%)	477 (98%)	10 (2%)	2 (0%)	30	67
1	I	489/491 (100%)	477 (98%)	10 (2%)	2 (0%)	30	67
1	J	489/491 (100%)	477 (98%)	10 (2%)	2 (0%)	30	67
1	K	489/491 (100%)	477 (98%)	10 (2%)	2 (0%)	30	67
1	L	489/491 (100%)	477 (98%)	10 (2%)	2 (0%)	30	67
1	M	489/491 (100%)	477 (98%)	10 (2%)	2 (0%)	30	67
1	N	489/491 (100%)	477 (98%)	10 (2%)	2 (0%)	30	67
1	O	489/491 (100%)	477 (98%)	10 (2%)	2 (0%)	30	67
1	P	489/491 (100%)	477 (98%)	10 (2%)	2 (0%)	30	67
All	All	7824/7856 (100%)	7632 (98%)	160 (2%)	32 (0%)	31	67

5 of 32 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	5	ASN
1	B	496	ASN
1	C	987	ASN
1	D	1478	ASN
1	E	1969	ASN

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	A	389/389 (100%)	386 (99%)	3 (1%)	73	78
1	B	389/389 (100%)	386 (99%)	3 (1%)	73	78
1	C	389/389 (100%)	386 (99%)	3 (1%)	73	78
1	D	389/389 (100%)	386 (99%)	3 (1%)	73	78
1	E	389/389 (100%)	386 (99%)	3 (1%)	73	78
1	F	389/389 (100%)	386 (99%)	3 (1%)	73	78
1	G	389/389 (100%)	386 (99%)	3 (1%)	73	78
1	H	389/389 (100%)	386 (99%)	3 (1%)	73	78
1	I	389/389 (100%)	386 (99%)	3 (1%)	73	78
1	J	389/389 (100%)	386 (99%)	3 (1%)	73	78
1	K	389/389 (100%)	386 (99%)	3 (1%)	73	78
1	L	389/389 (100%)	386 (99%)	3 (1%)	73	78
1	M	389/389 (100%)	386 (99%)	3 (1%)	73	78
1	N	389/389 (100%)	386 (99%)	3 (1%)	73	78
1	O	389/389 (100%)	386 (99%)	3 (1%)	73	78
1	P	389/389 (100%)	386 (99%)	3 (1%)	73	78
All	All	6224/6224 (100%)	6176 (99%)	48 (1%)	70	78

5 of 48 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	J	4547	LEU
1	L	5545	LEU
1	J	4563	LEU
1	K	5054	LEU
1	M	6020	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 49 such sidechains are listed below:

Mol	Chain	Res	Type
1	J	4542	GLN
1	L	5540	GLN
1	J	4558	GLN
1	L	5508	GLN
1	M	6011	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 oligosaccharides 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.

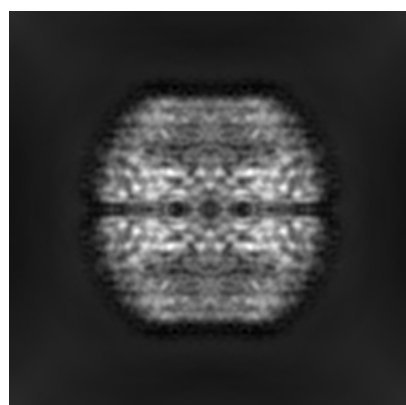
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-5247. These allow visual inspection of the internal detail of the map and identification of artifacts.

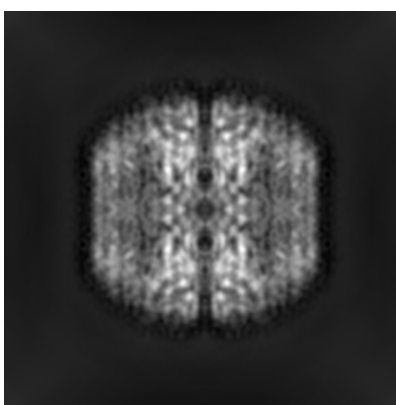
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

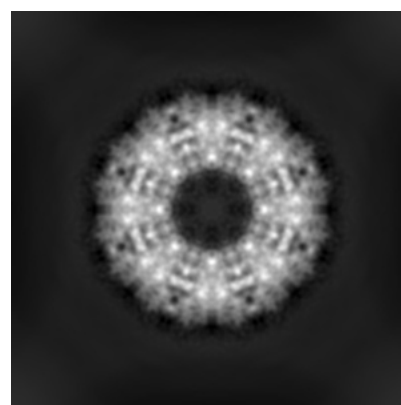
6.1.1 Primary map



X



Y

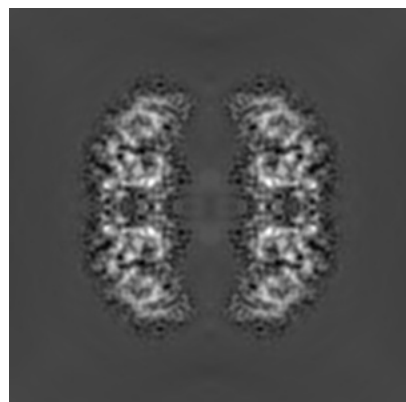


Z

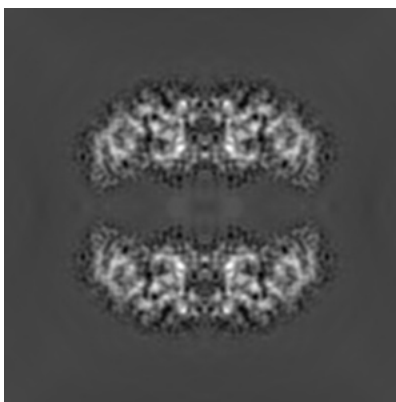
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

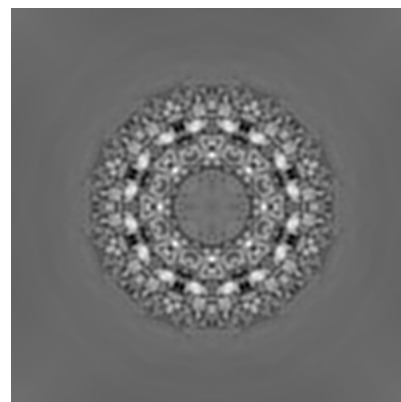
6.2.1 Primary map



X Index: 100



Y Index: 100

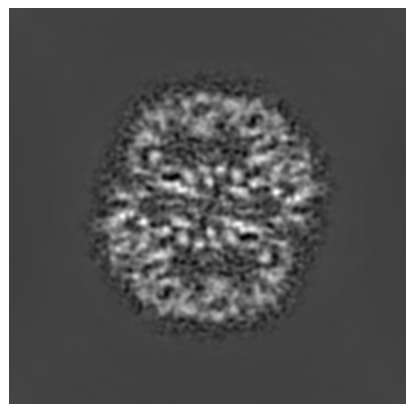


Z Index: 100

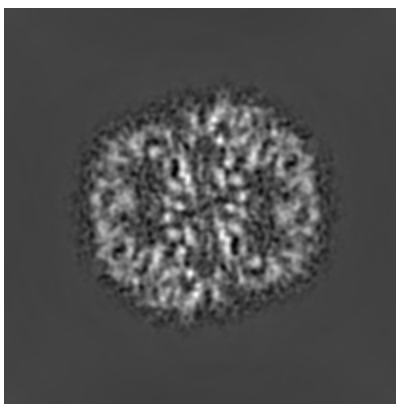
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

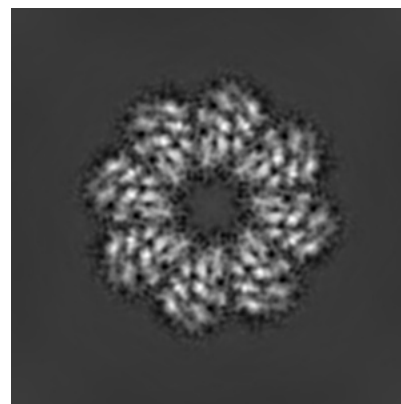
6.3.1 Primary map



X Index: 71



Y Index: 129

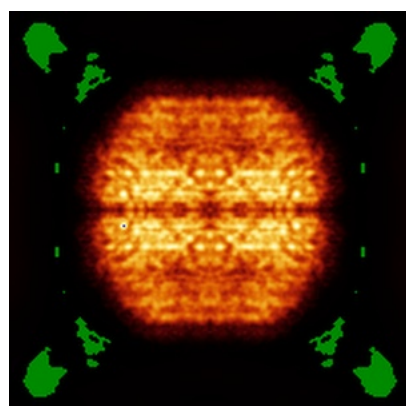


Z Index: 118

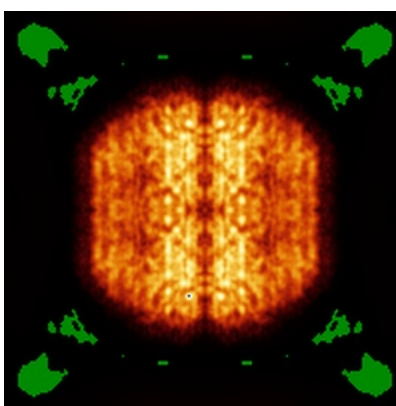
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

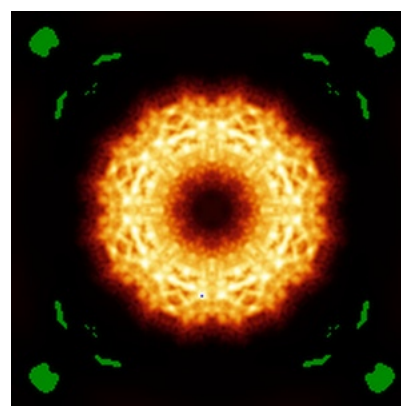
6.4.1 Primary map



X



Y



Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views

This section was not generated.

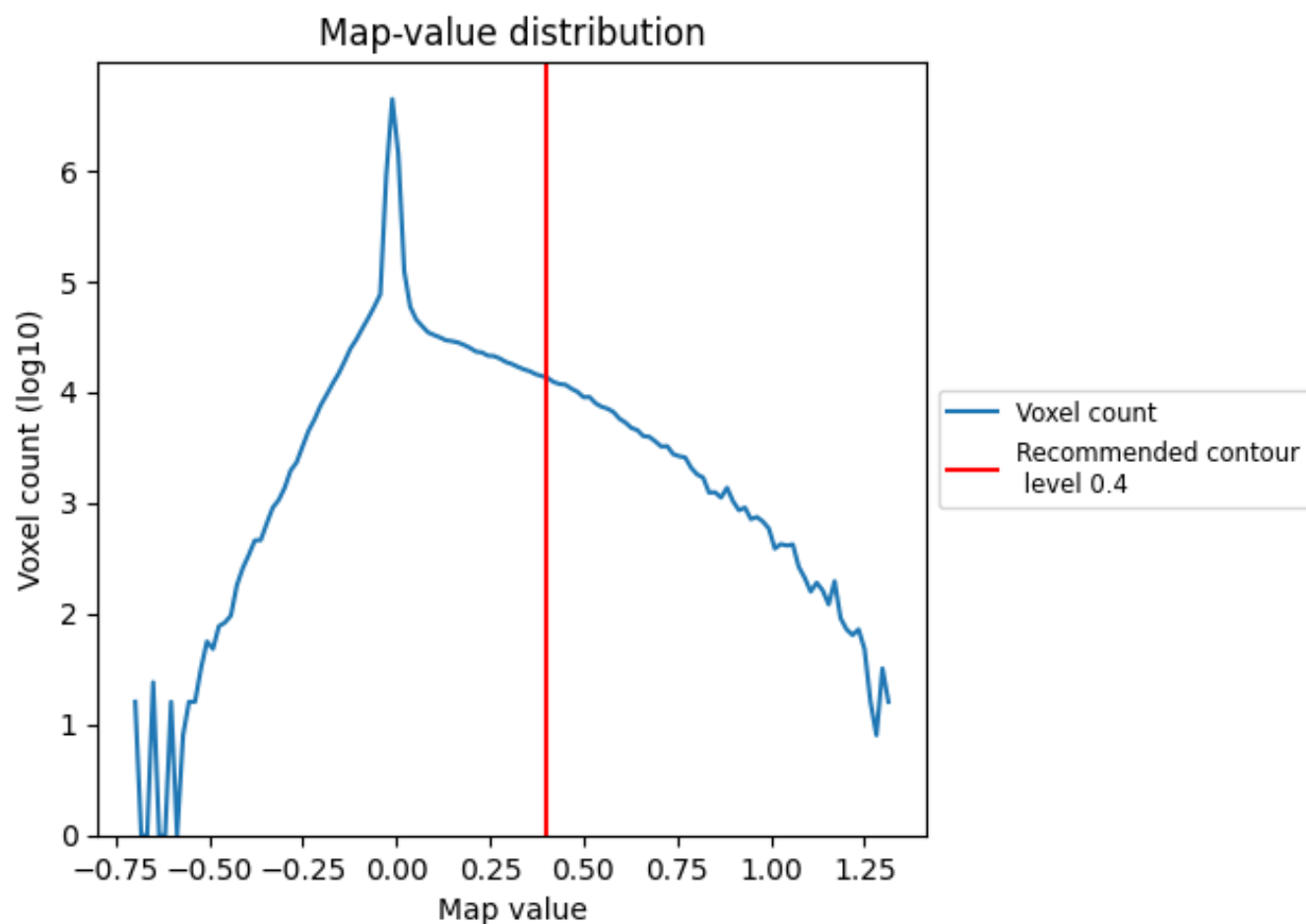
6.6 Mask visualisation

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

7 Map analysis [i](#)

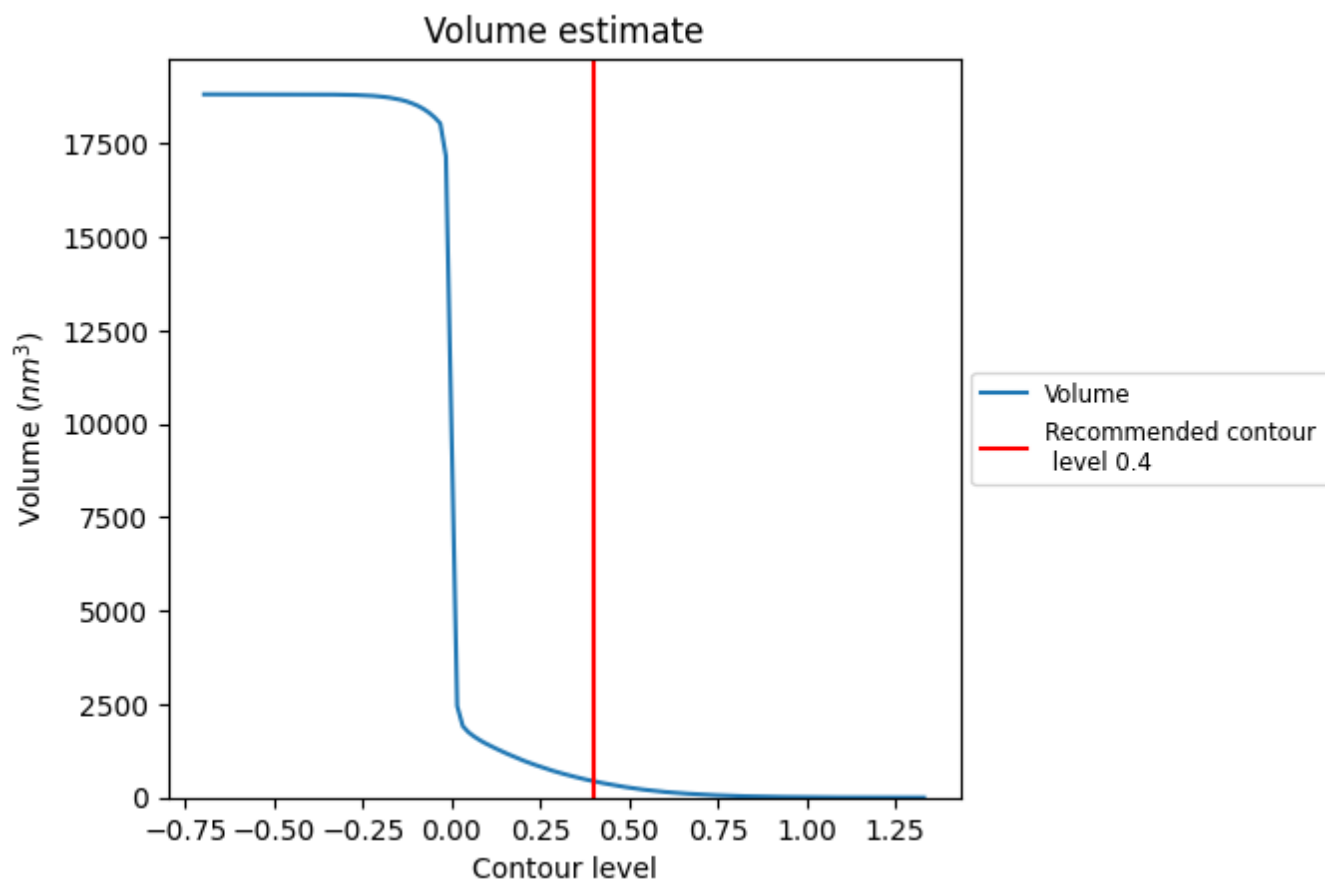
This section contains the results of statistical analysis of the map.

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.

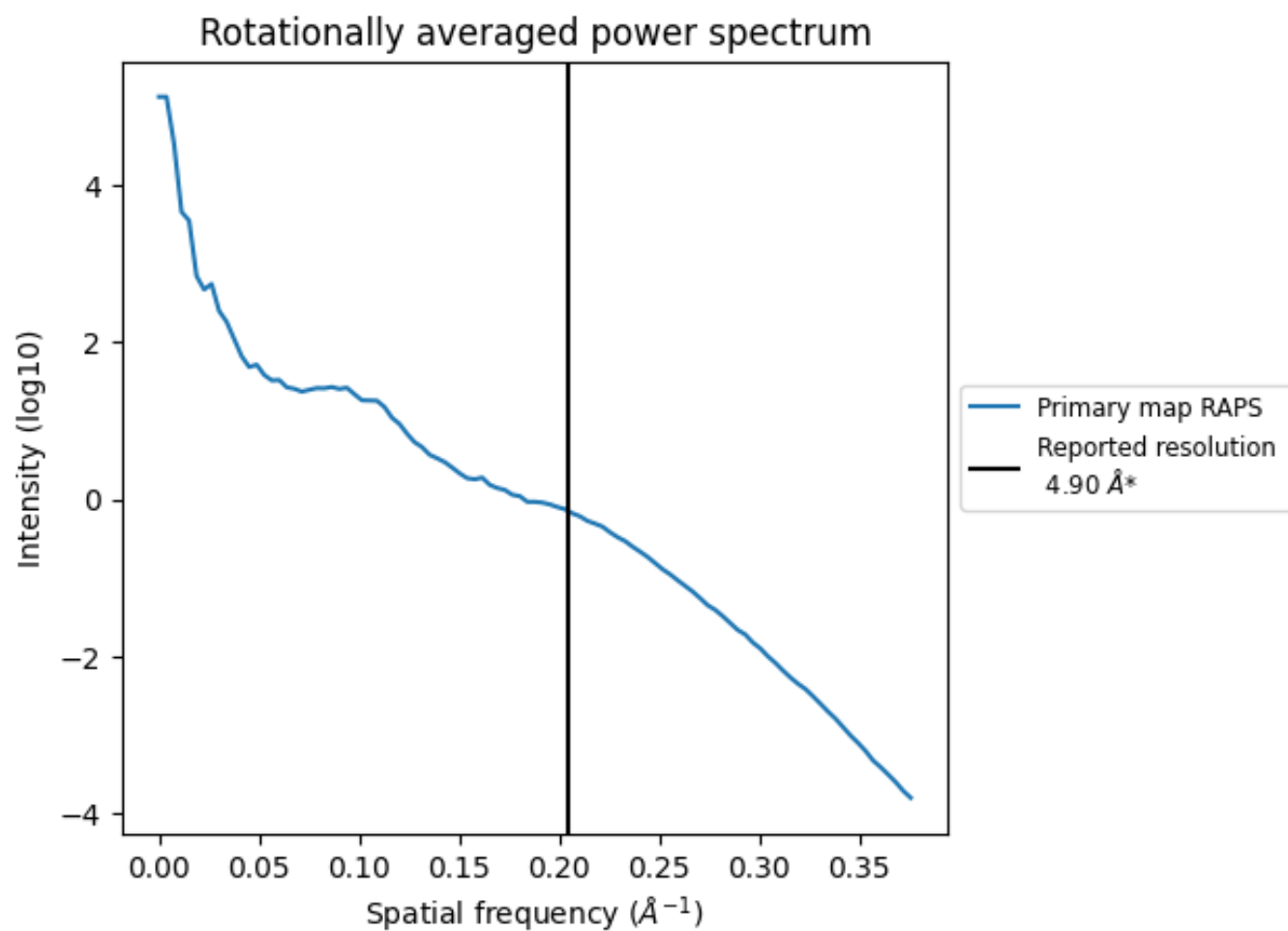
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 438 nm³; this corresponds to an approximate mass of 395 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 0.204 Å⁻¹

8 Fourier-Shell correlation ⓘ

This section was not generated. No FSC curve or half-maps provided.

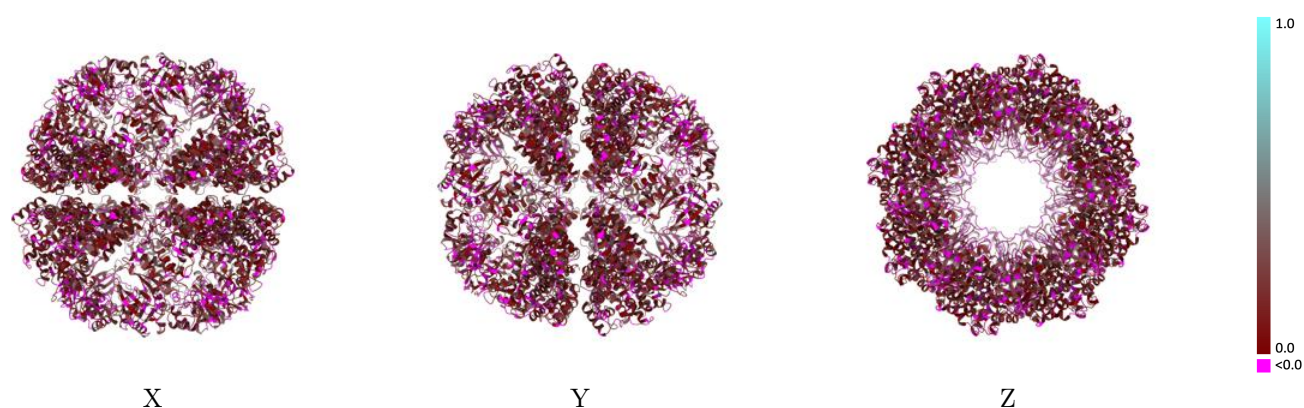
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-5247 and PDB model 3IZK. Per-residue inclusion information can be found in section 3 on page 9.

9.1 Map-model overlay [i](#)

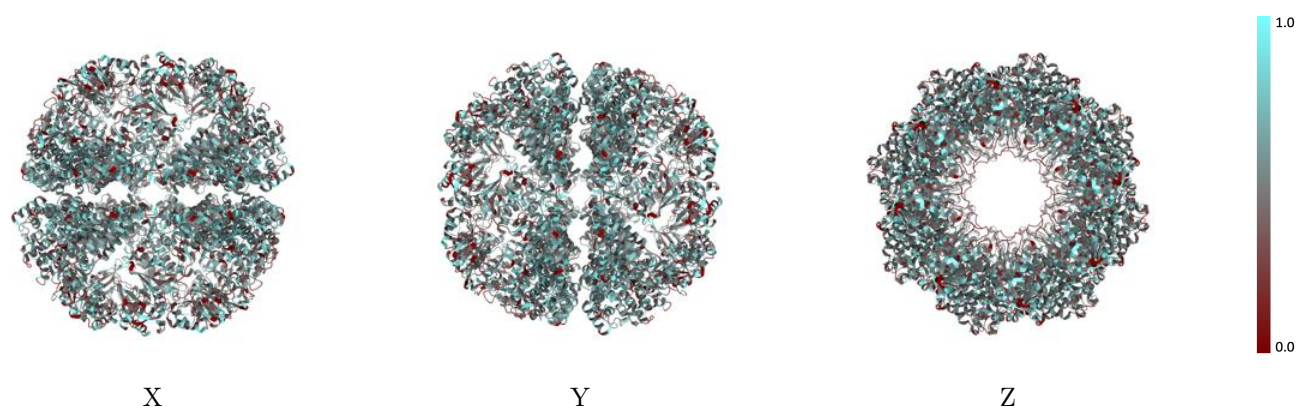
This section was not generated.

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



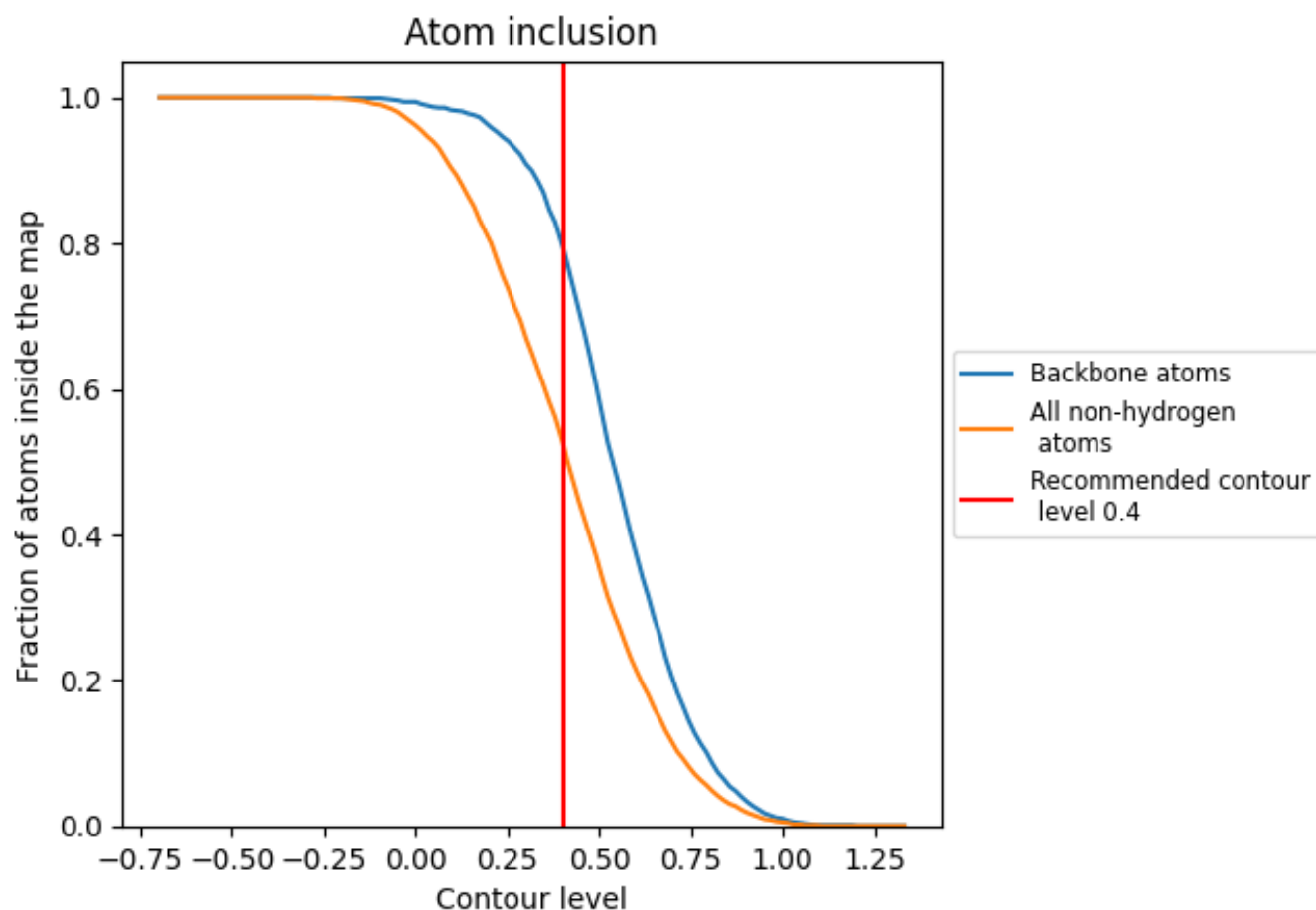
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

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 (0.4).

9.4 Atom inclusion [i](#)



At the recommended contour level, 80% of all backbone atoms, 53% 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 (0.4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5270	 0.1300
A	 0.5260	 0.1300
B	 0.5270	 0.1310
C	 0.5260	 0.1310
D	 0.5270	 0.1300
E	 0.5260	 0.1300
F	 0.5270	 0.1310
G	 0.5260	 0.1290
H	 0.5280	 0.1320
I	 0.5270	 0.1300
J	 0.5270	 0.1290
K	 0.5280	 0.1310
L	 0.5260	 0.1310
M	 0.5280	 0.1320
N	 0.5260	 0.1300
O	 0.5280	 0.1300
P	 0.5270	 0.1290

