



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 08:42 PM UTC

PDB ID : 3IZN / pdb_00003izn
EMDB ID : EMD-5250
Title : Mm-cpn deltalid with ATP
Authors : Douglas, N.R.; Reissmann, S.; Zhang, J.; Chen, B.; Jakana, J.; Kumar, R.;
Chiu, W.; Frydman, J.
Deposited on : 2010-10-30
Resolution : 6.40 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:

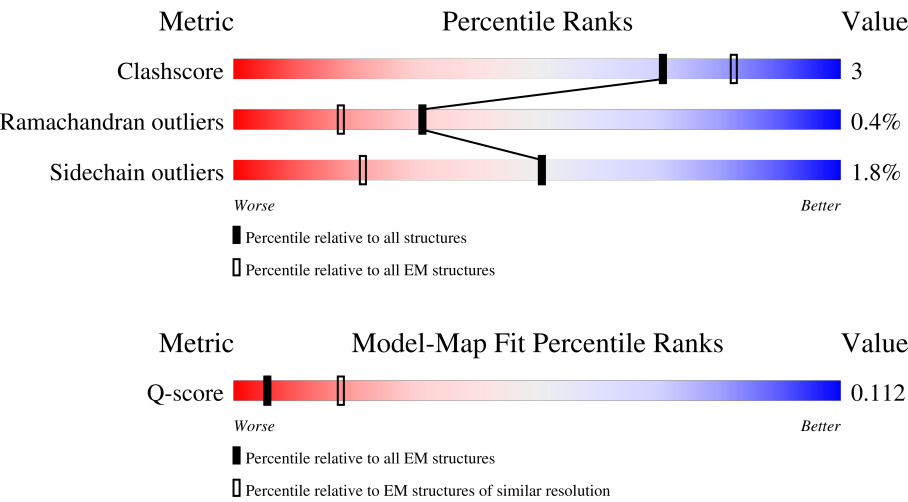
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 6.40 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	544 (5.90 - 6.90)

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	40% 89% 9% .
1	B	491	40% 90% 9% .
1	C	491	40% 89% 10% .
1	D	491	40% 90% 9% .

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Mol	Chain	Length	Quality of chain
1	E	491	40% 89%9%
1	F	491	40% 90%9%
1	G	491	40% 89%9%
1	H	491	40% 90%9%
1	I	491	41% 89%9%
1	J	491	40% 89%9%
1	K	491	41% 89%9%
1	L	491	40% 89%10%
1	M	491	41% 90%9%
1	N	491	40% 89%9%
1	O	491	41% 90%9%
1	P	491	40% 89%9%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 58640 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
			3665	2272	635	734	24		
1	B	491	Total	C	N	O	S	0	0
			3665	2272	635	734	24		
1	C	491	Total	C	N	O	S	0	0
			3665	2272	635	734	24		
1	D	491	Total	C	N	O	S	0	0
			3665	2272	635	734	24		
1	E	491	Total	C	N	O	S	0	0
			3665	2272	635	734	24		
1	F	491	Total	C	N	O	S	0	0
			3665	2272	635	734	24		
1	G	491	Total	C	N	O	S	0	0
			3665	2272	635	734	24		
1	H	491	Total	C	N	O	S	0	0
			3665	2272	635	734	24		
1	I	491	Total	C	N	O	S	0	0
			3665	2272	635	734	24		
1	J	491	Total	C	N	O	S	0	0
			3665	2272	635	734	24		
1	K	491	Total	C	N	O	S	0	0
			3665	2272	635	734	24		
1	L	491	Total	C	N	O	S	0	0
			3665	2272	635	734	24		
1	M	491	Total	C	N	O	S	0	0
			3665	2272	635	734	24		
1	N	491	Total	C	N	O	S	0	0
			3665	2272	635	734	24		
1	O	491	Total	C	N	O	S	0	0
			3665	2272	635	734	24		
1	P	491	Total	C	N	O	S	0	0
			3665	2272	635	734	24		

There are 80 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	235	GLU	-	expression tag	UNP Q877G8
A	236	THR	-	expression tag	UNP Q877G8
A	237	ALA	-	expression tag	UNP Q877G8
A	238	SER	-	expression tag	UNP Q877G8
A	239	GLU	-	expression tag	UNP Q877G8
B	726	GLU	-	expression tag	UNP Q877G8
B	727	THR	-	expression tag	UNP Q877G8
B	728	ALA	-	expression tag	UNP Q877G8
B	729	SER	-	expression tag	UNP Q877G8
B	730	GLU	-	expression tag	UNP Q877G8
C	1217	GLU	-	expression tag	UNP Q877G8
C	1218	THR	-	expression tag	UNP Q877G8
C	1219	ALA	-	expression tag	UNP Q877G8
C	1220	SER	-	expression tag	UNP Q877G8
C	1221	GLU	-	expression tag	UNP Q877G8
D	1708	GLU	-	expression tag	UNP Q877G8
D	1709	THR	-	expression tag	UNP Q877G8
D	1710	ALA	-	expression tag	UNP Q877G8
D	1711	SER	-	expression tag	UNP Q877G8
D	1712	GLU	-	expression tag	UNP Q877G8
E	2199	GLU	-	expression tag	UNP Q877G8
E	2200	THR	-	expression tag	UNP Q877G8
E	2201	ALA	-	expression tag	UNP Q877G8
E	2202	SER	-	expression tag	UNP Q877G8
E	2203	GLU	-	expression tag	UNP Q877G8
F	2690	GLU	-	expression tag	UNP Q877G8
F	2691	THR	-	expression tag	UNP Q877G8
F	2692	ALA	-	expression tag	UNP Q877G8
F	2693	SER	-	expression tag	UNP Q877G8
F	2694	GLU	-	expression tag	UNP Q877G8
G	3181	GLU	-	expression tag	UNP Q877G8
G	3182	THR	-	expression tag	UNP Q877G8
G	3183	ALA	-	expression tag	UNP Q877G8
G	3184	SER	-	expression tag	UNP Q877G8
G	3185	GLU	-	expression tag	UNP Q877G8
H	3672	GLU	-	expression tag	UNP Q877G8
H	3673	THR	-	expression tag	UNP Q877G8
H	3674	ALA	-	expression tag	UNP Q877G8
H	3675	SER	-	expression tag	UNP Q877G8
H	3676	GLU	-	expression tag	UNP Q877G8
I	4163	GLU	-	expression tag	UNP Q877G8
I	4164	THR	-	expression tag	UNP Q877G8
I	4165	ALA	-	expression tag	UNP Q877G8

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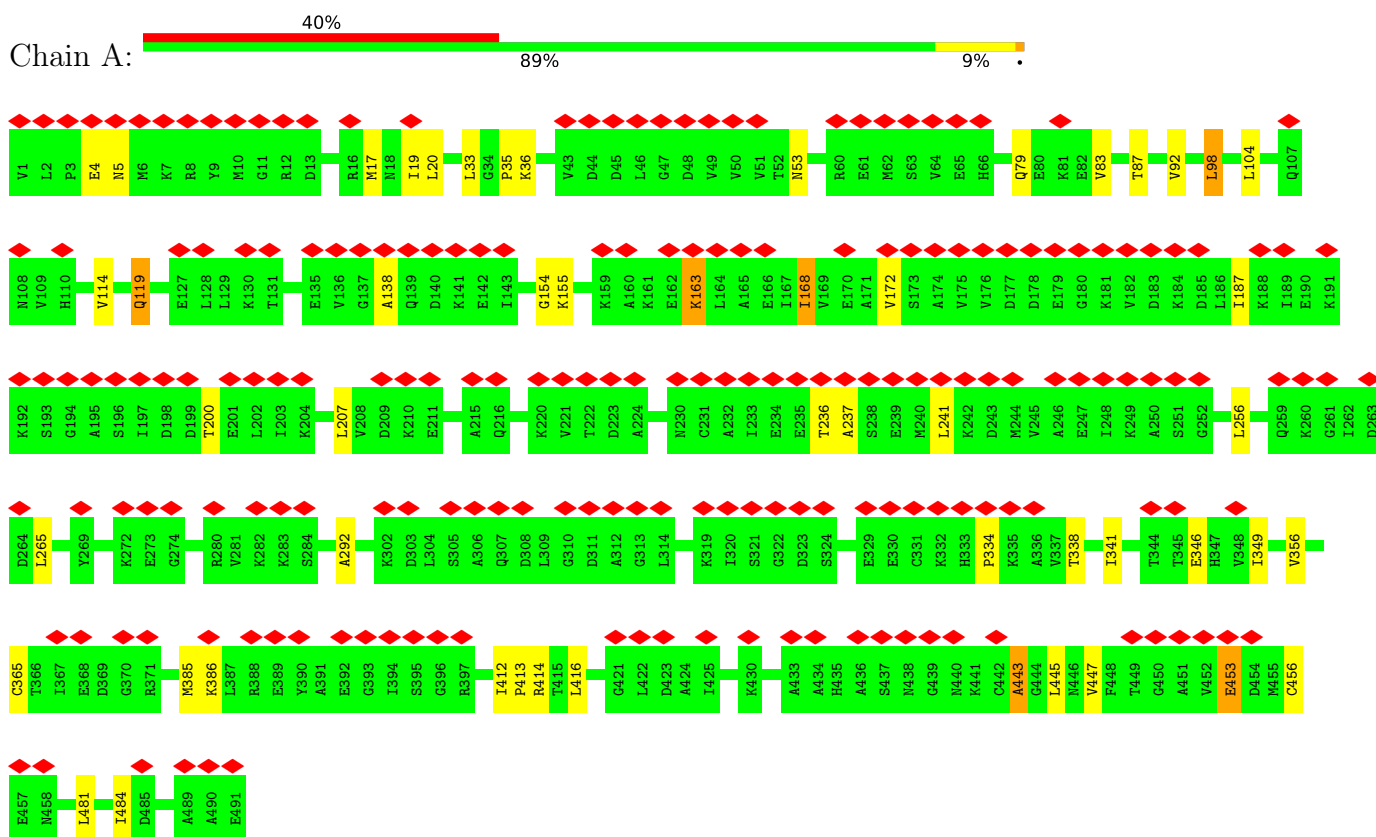
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Chain	Residue	Modelled	Actual	Comment	Reference
I	4166	SER	-	expression tag	UNP Q877G8
I	4167	GLU	-	expression tag	UNP Q877G8
J	4654	GLU	-	expression tag	UNP Q877G8
J	4655	THR	-	expression tag	UNP Q877G8
J	4656	ALA	-	expression tag	UNP Q877G8
J	4657	SER	-	expression tag	UNP Q877G8
J	4658	GLU	-	expression tag	UNP Q877G8
K	5145	GLU	-	expression tag	UNP Q877G8
K	5146	THR	-	expression tag	UNP Q877G8
K	5147	ALA	-	expression tag	UNP Q877G8
K	5148	SER	-	expression tag	UNP Q877G8
K	5149	GLU	-	expression tag	UNP Q877G8
L	5636	GLU	-	expression tag	UNP Q877G8
L	5637	THR	-	expression tag	UNP Q877G8
L	5638	ALA	-	expression tag	UNP Q877G8
L	5639	SER	-	expression tag	UNP Q877G8
L	5640	GLU	-	expression tag	UNP Q877G8
M	6127	GLU	-	expression tag	UNP Q877G8
M	6128	THR	-	expression tag	UNP Q877G8
M	6129	ALA	-	expression tag	UNP Q877G8
M	6130	SER	-	expression tag	UNP Q877G8
M	6131	GLU	-	expression tag	UNP Q877G8
N	6618	GLU	-	expression tag	UNP Q877G8
N	6619	THR	-	expression tag	UNP Q877G8
N	6620	ALA	-	expression tag	UNP Q877G8
N	6621	SER	-	expression tag	UNP Q877G8
N	6622	GLU	-	expression tag	UNP Q877G8
O	7109	GLU	-	expression tag	UNP Q877G8
O	7110	THR	-	expression tag	UNP Q877G8
O	7111	ALA	-	expression tag	UNP Q877G8
O	7112	SER	-	expression tag	UNP Q877G8
O	7113	GLU	-	expression tag	UNP Q877G8
P	7600	GLU	-	expression tag	UNP Q877G8
P	7601	THR	-	expression tag	UNP Q877G8
P	7602	ALA	-	expression tag	UNP Q877G8
P	7603	SER	-	expression tag	UNP Q877G8
P	7604	GLU	-	expression tag	UNP Q877G8

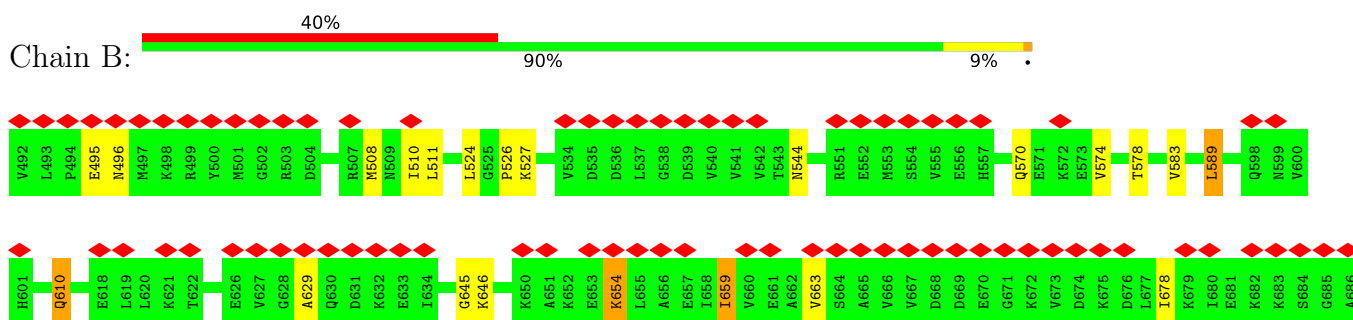
3 Residue-property plots

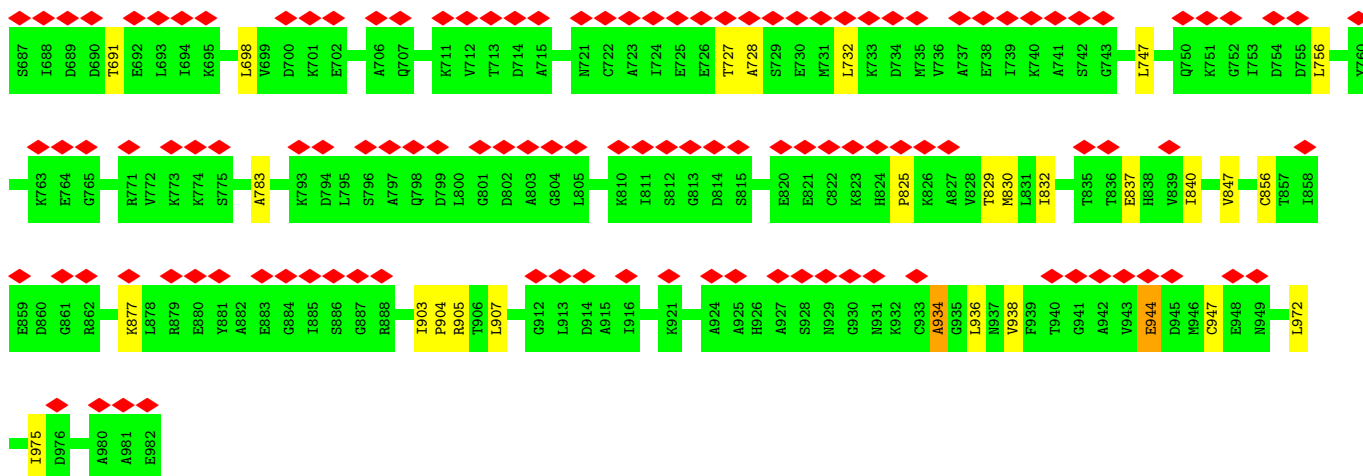
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

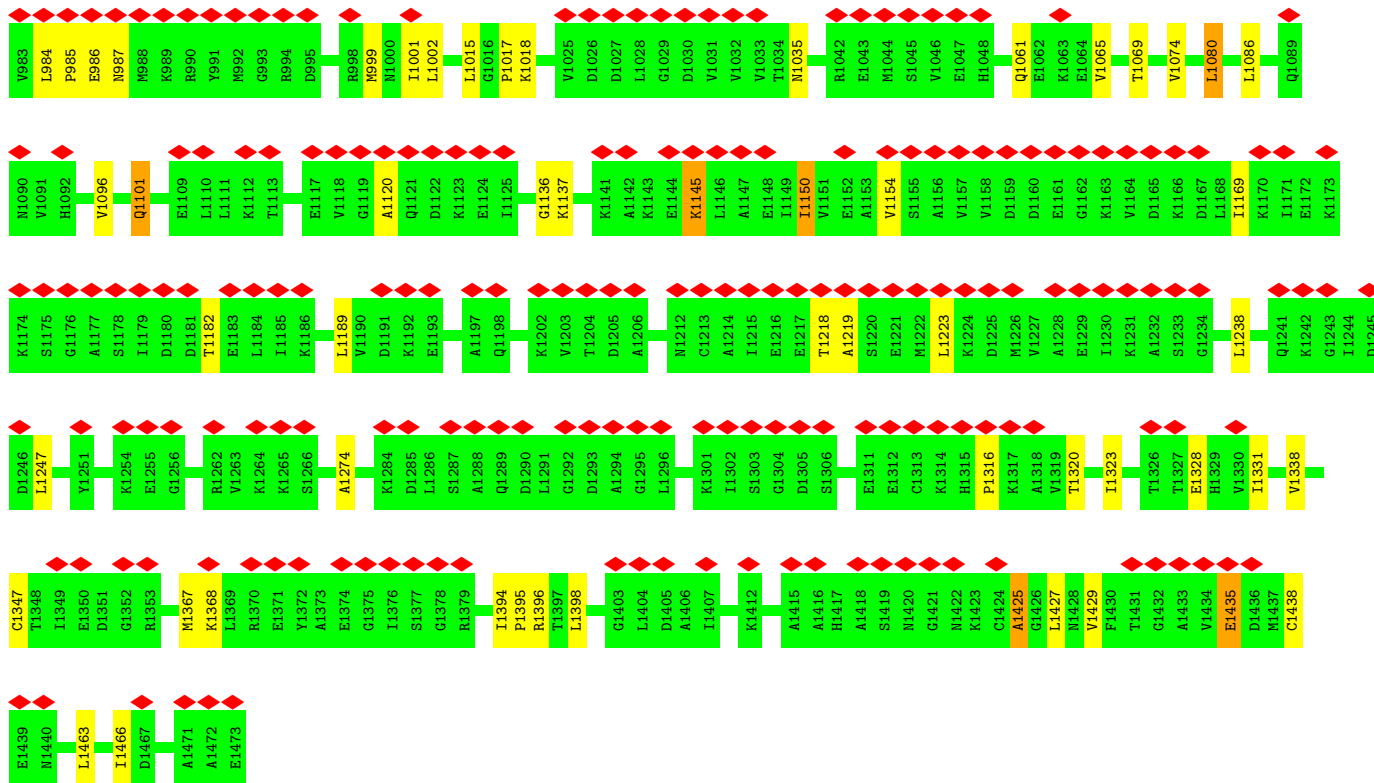
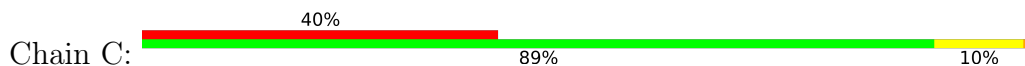


• Molecule 1: Chaperonin

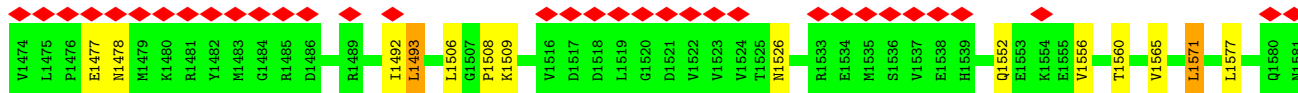
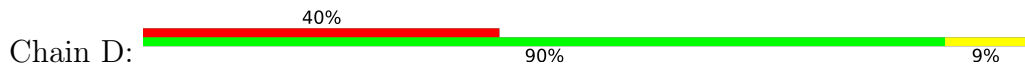


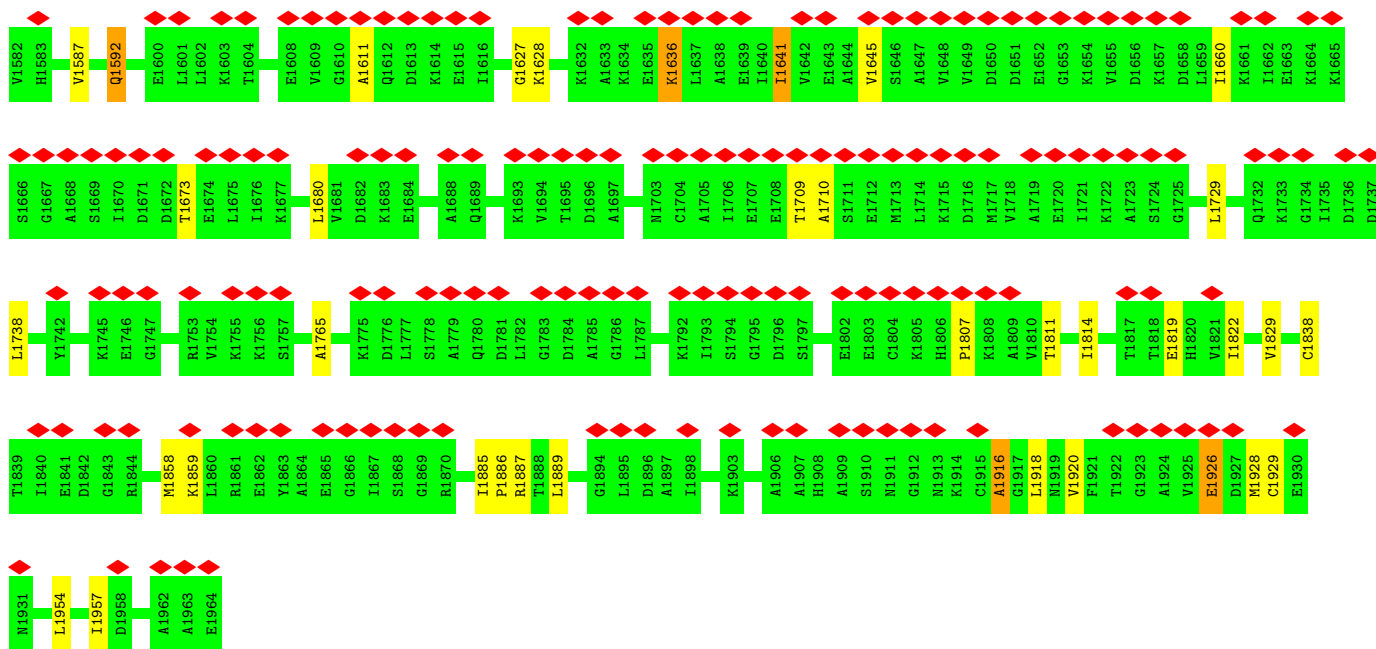


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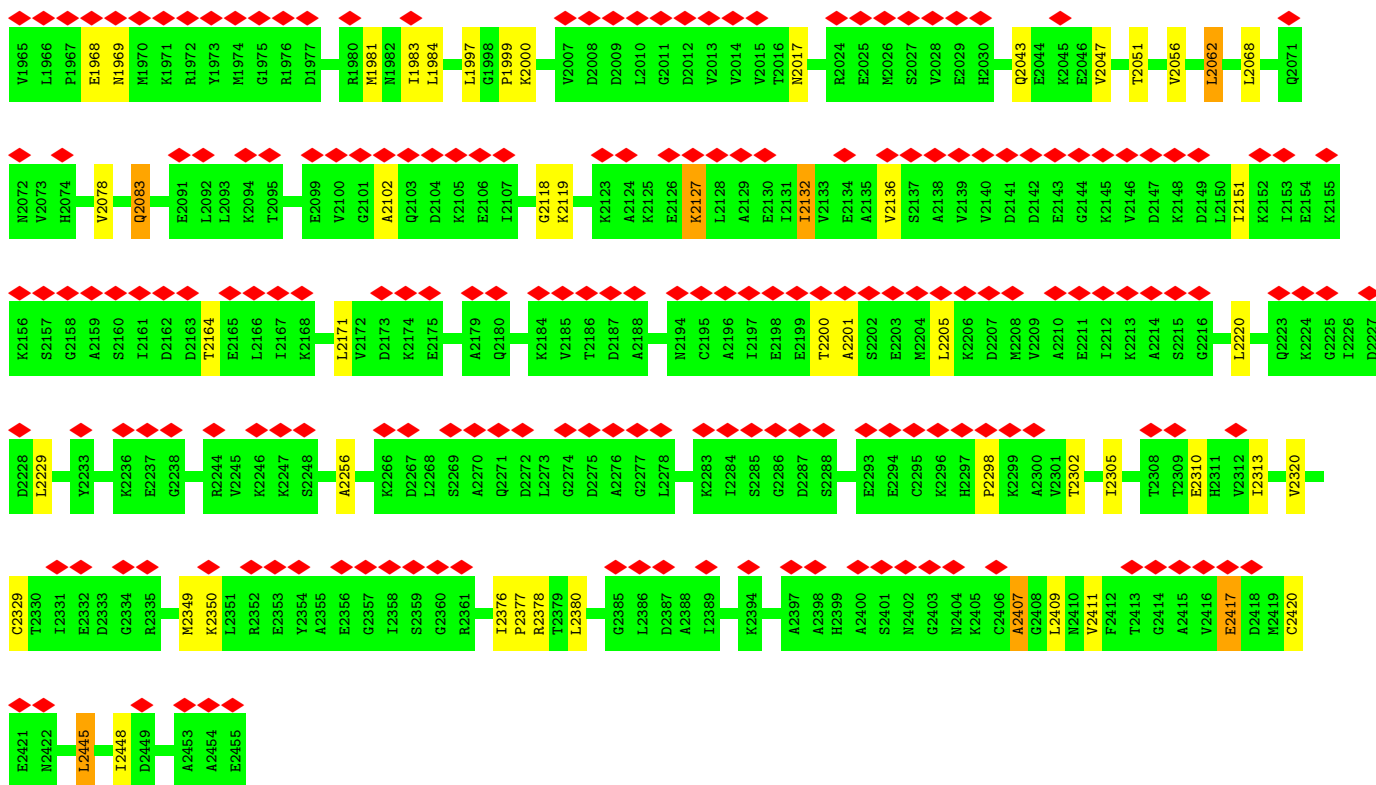
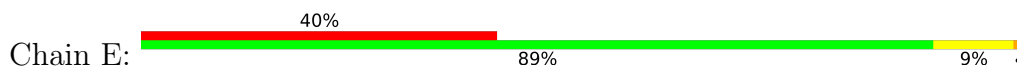


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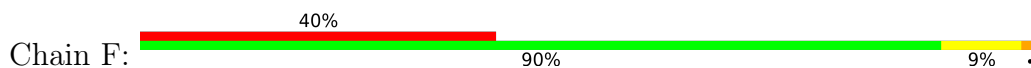


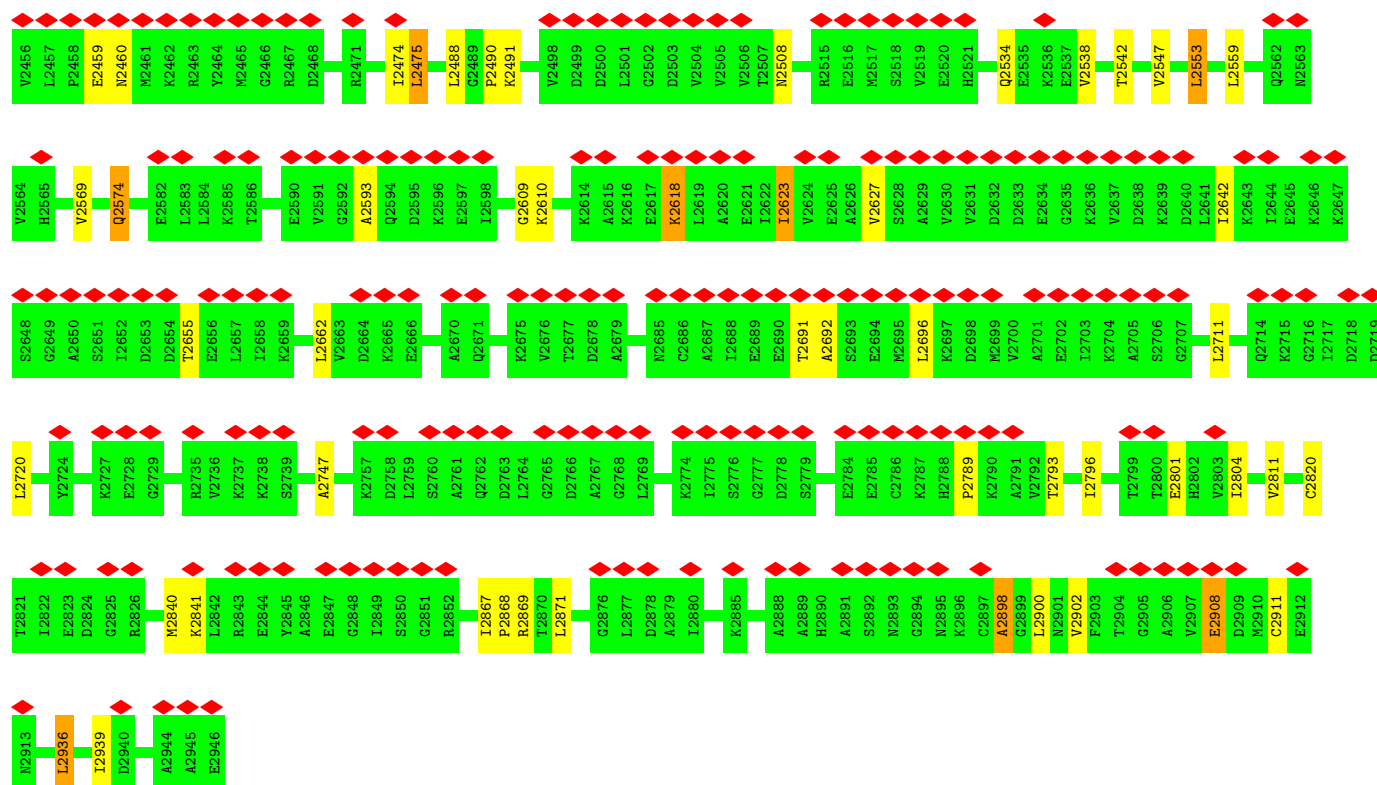


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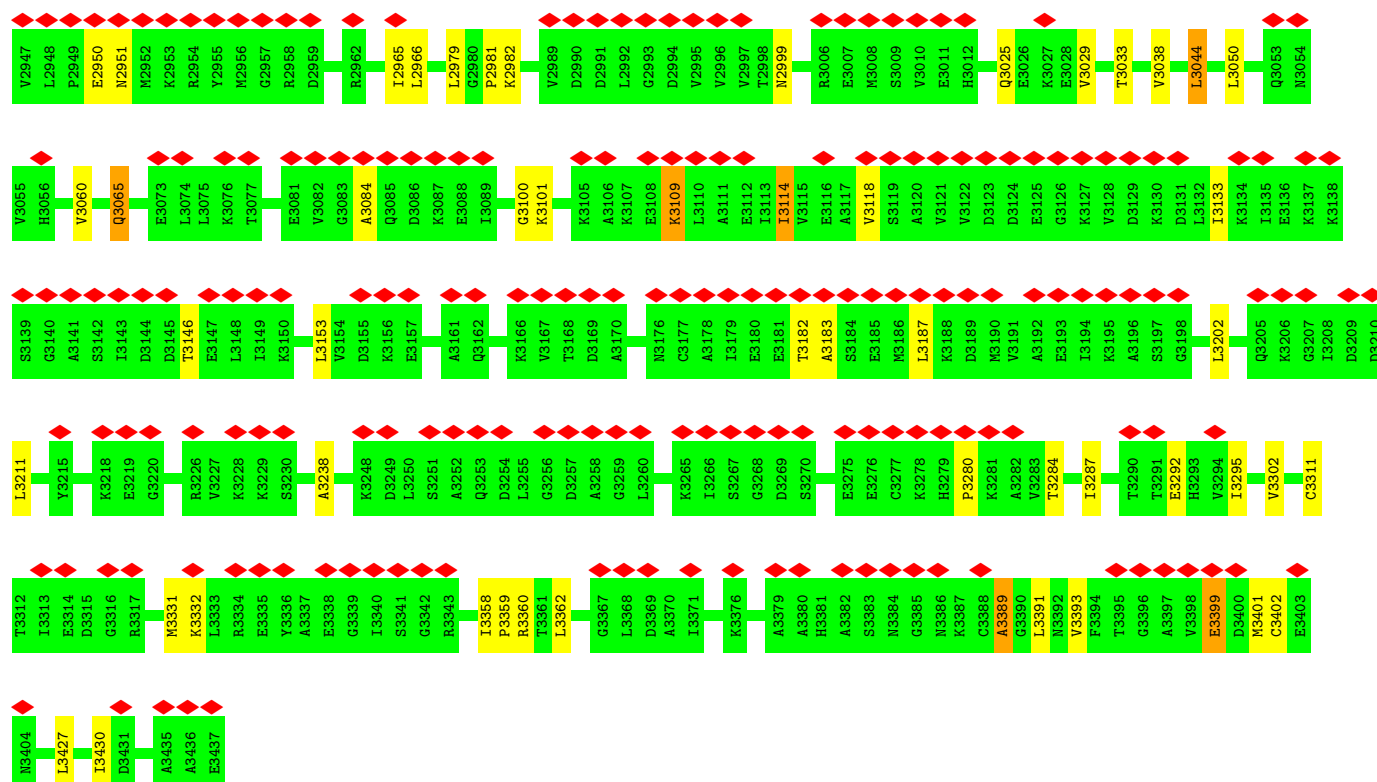
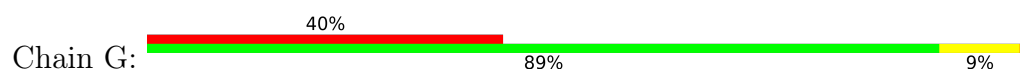


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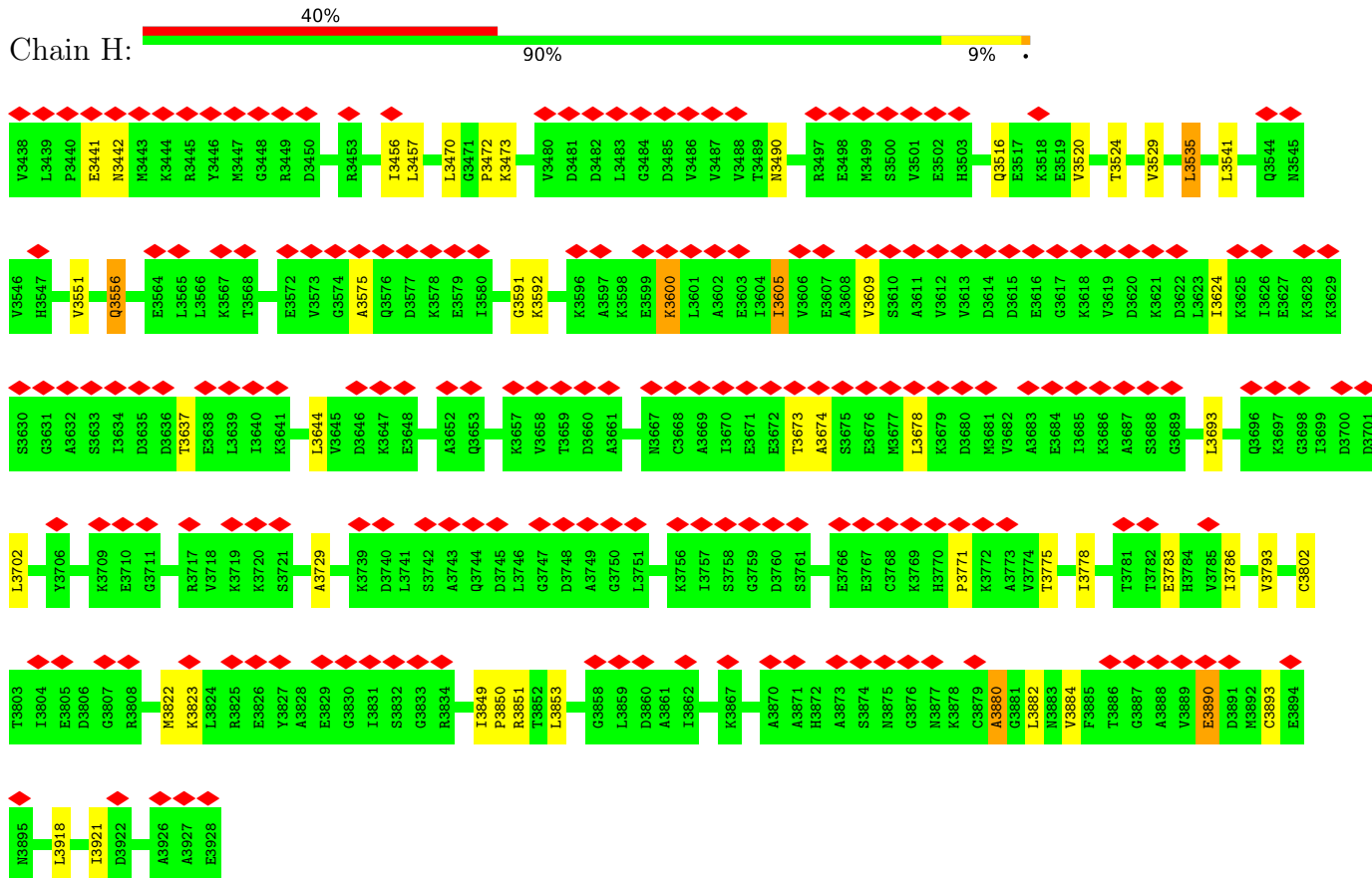




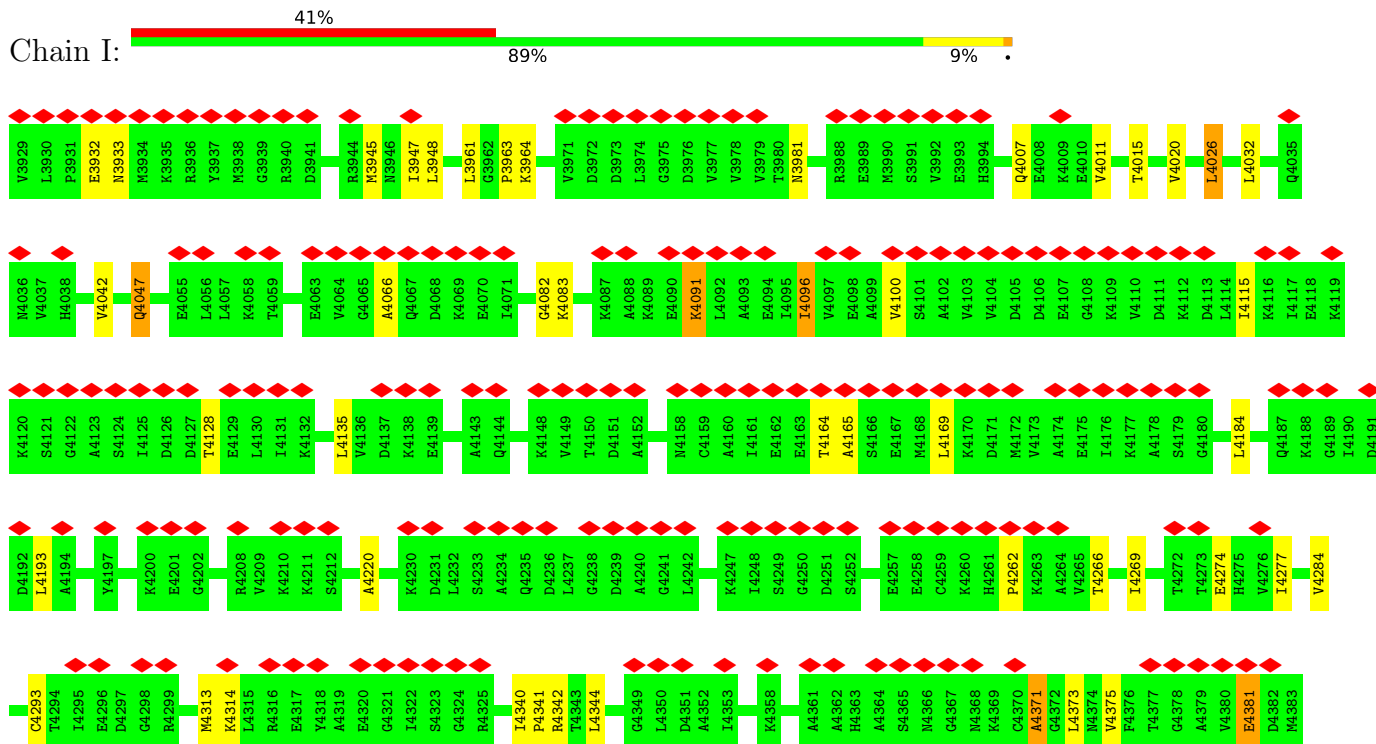
• Molecule 1: Chaperonin

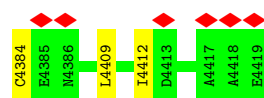


- Molecule 1: Chaperonin

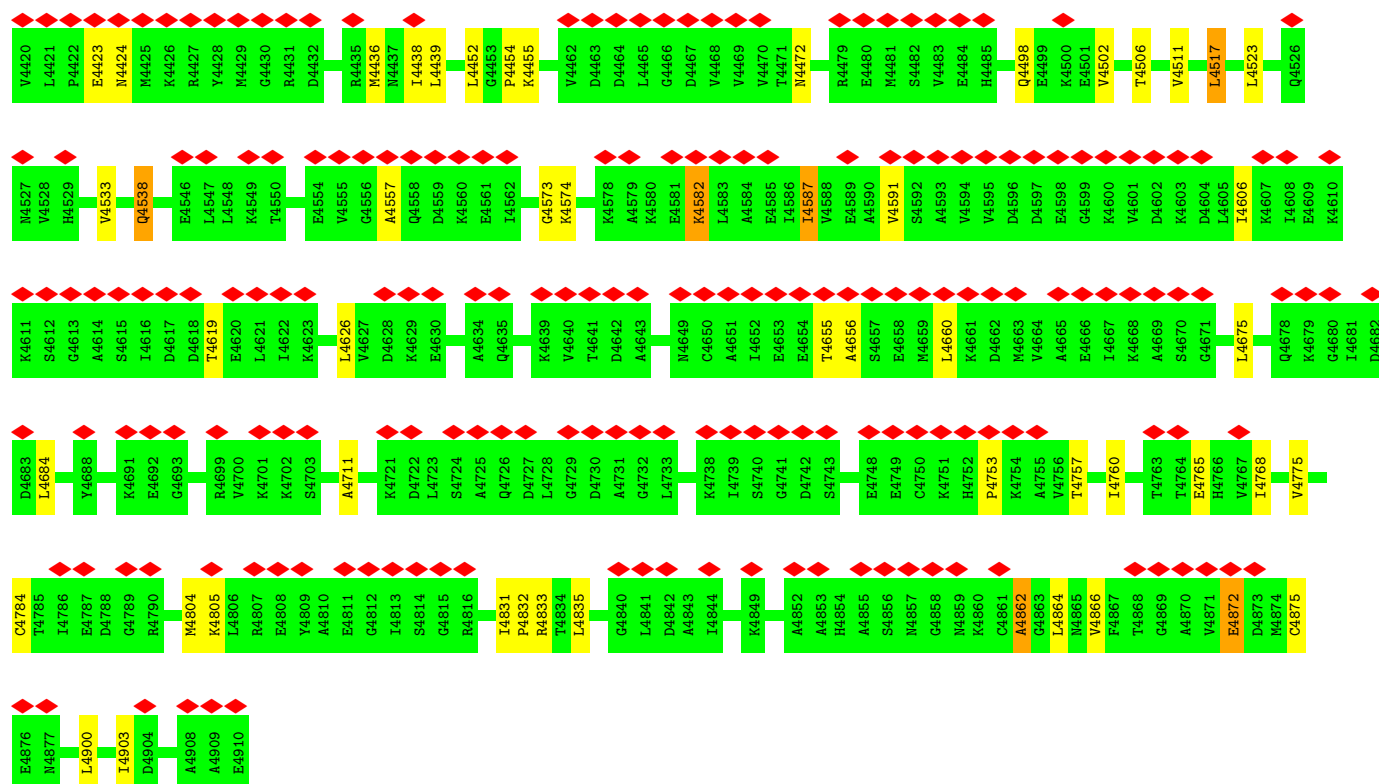
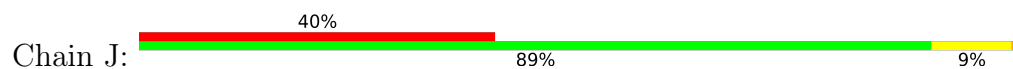


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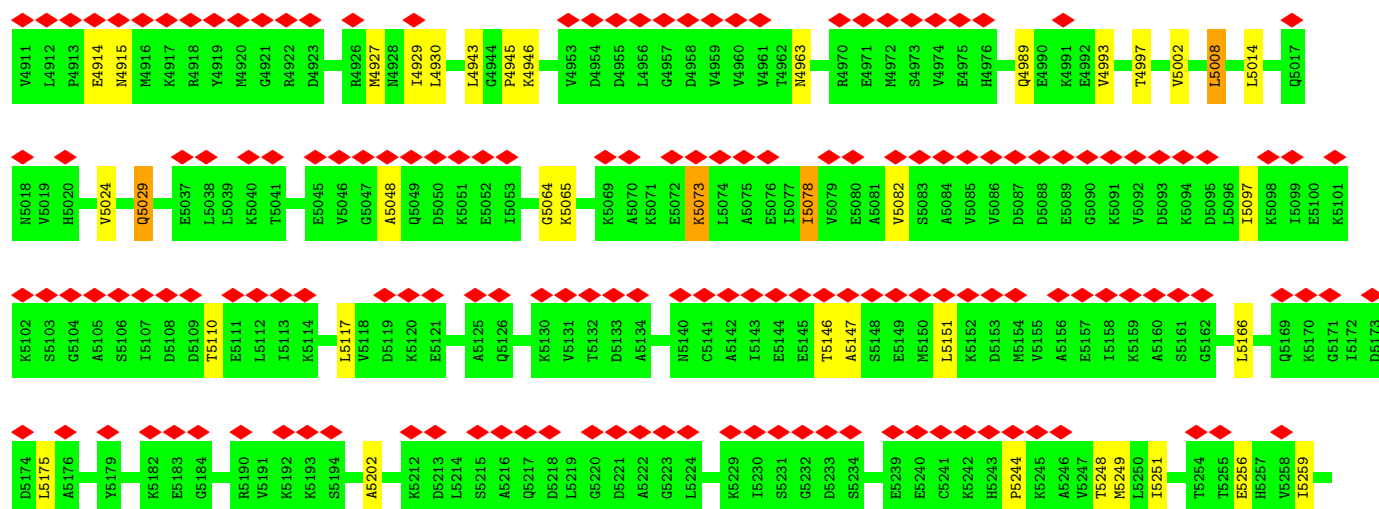
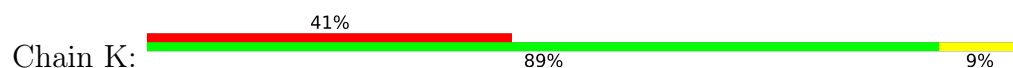


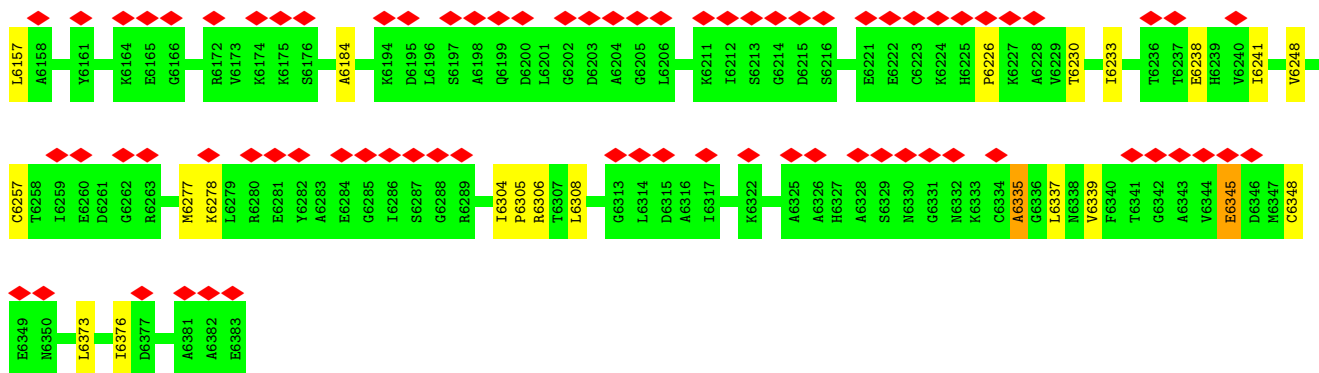


• Molecule 1: Chaperonin

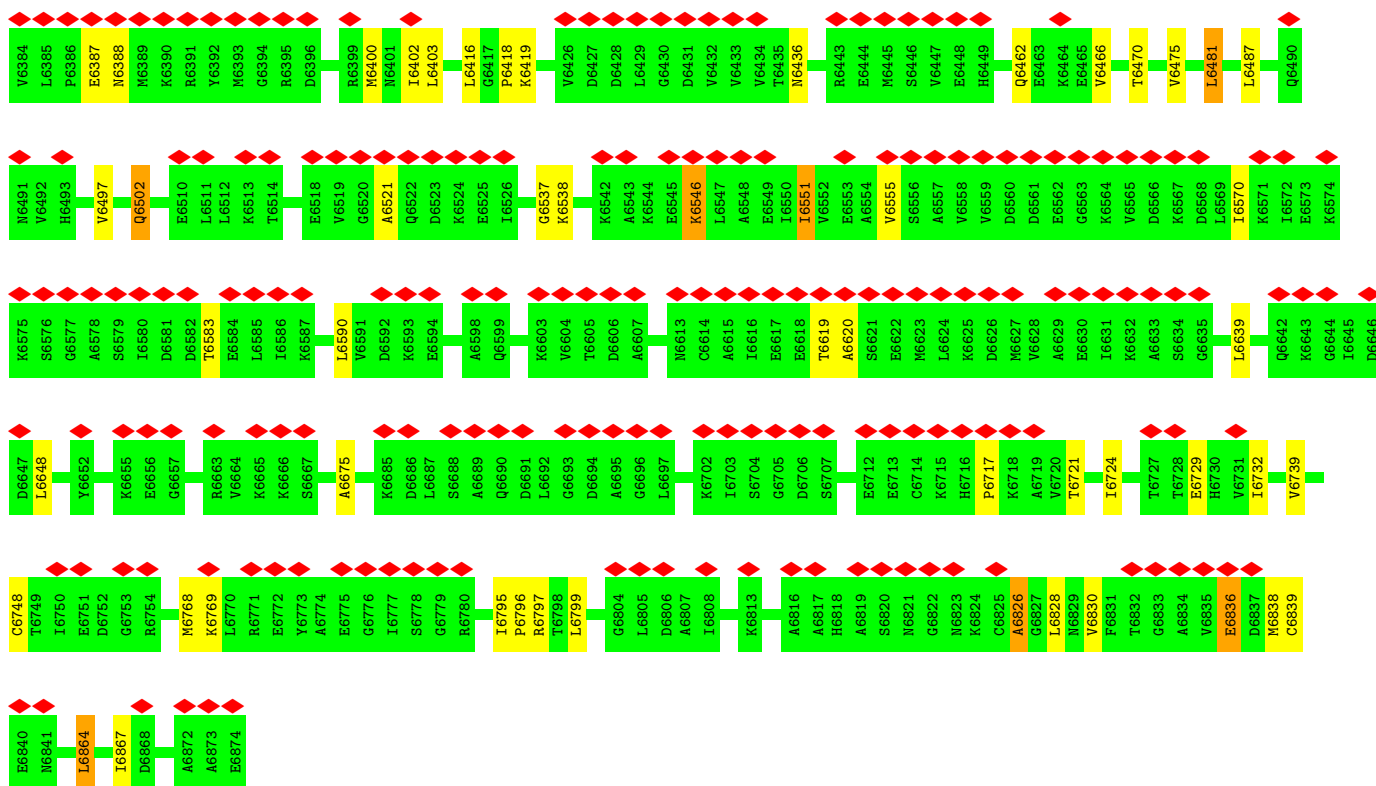
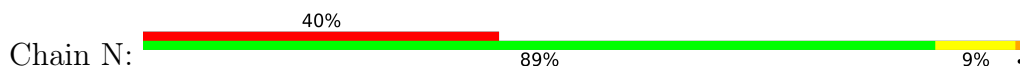


• Molecule 1: Chaperonin

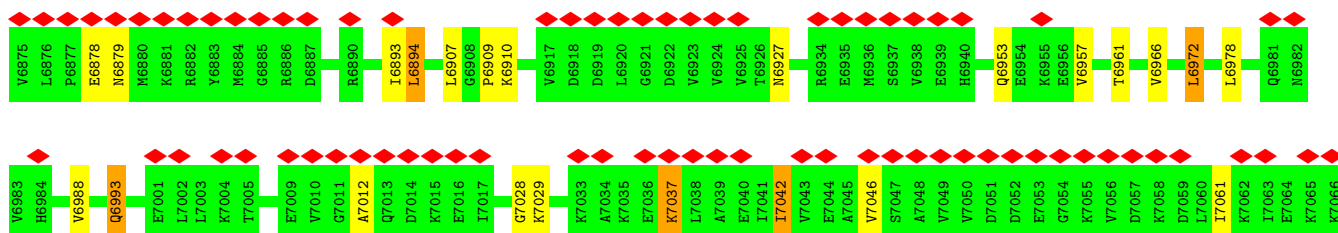
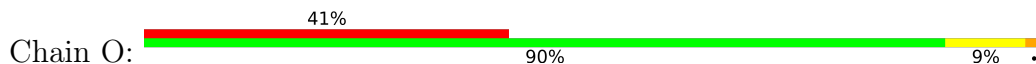


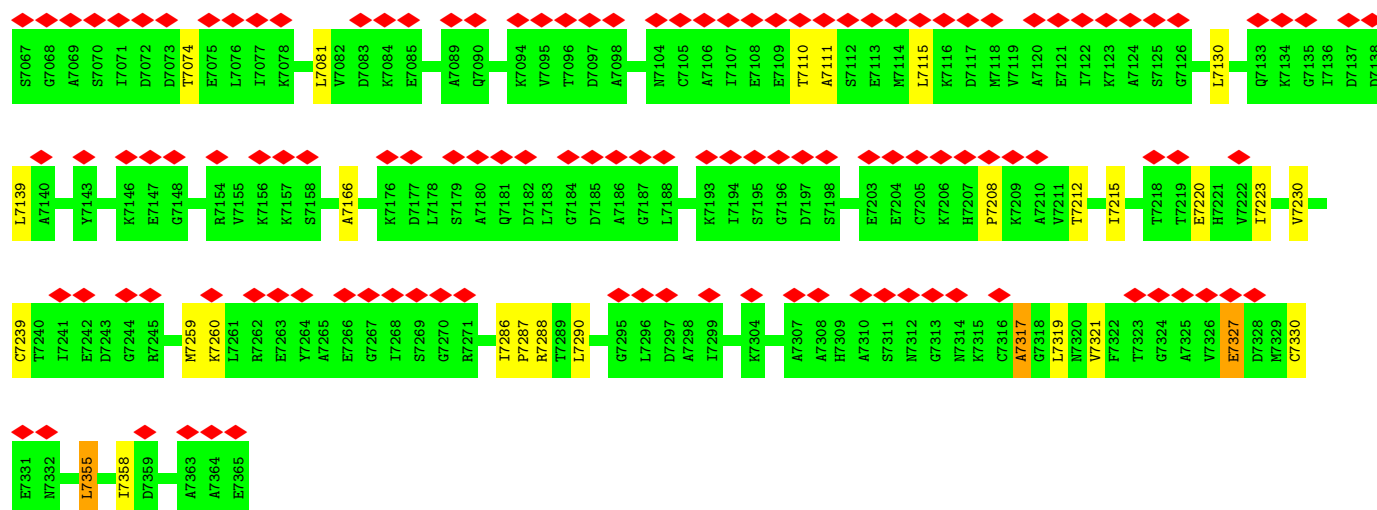


• Molecule 1: Chaperonin



• 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 10000 (10k x 10k)	Depositor
Maximum map value	2.733	Depositor
Minimum map value	-0.479	Depositor
Average map value	0.087	Depositor
Map value standard deviation	0.353	Depositor
Recommended contour level	1.58	Depositor
Map size ($\text{\AA}$)	289.44, 289.44, 289.44	wwPDB
Map dimensions	144, 144, 144	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	2.01, 2.01, 2.01	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	0.93	3/3686 (0.1%)	1.07	9/4961 (0.2%)
1	B	0.93	3/3686 (0.1%)	1.07	9/4961 (0.2%)
1	C	0.93	3/3686 (0.1%)	1.07	9/4961 (0.2%)
1	D	0.93	3/3686 (0.1%)	1.07	9/4961 (0.2%)
1	E	0.93	3/3686 (0.1%)	1.07	9/4961 (0.2%)
1	F	0.93	3/3686 (0.1%)	1.07	9/4961 (0.2%)
1	G	0.93	3/3686 (0.1%)	1.07	9/4961 (0.2%)
1	H	0.93	3/3686 (0.1%)	1.07	9/4961 (0.2%)
1	I	0.93	3/3686 (0.1%)	1.07	9/4961 (0.2%)
1	J	0.93	3/3686 (0.1%)	1.07	9/4961 (0.2%)
1	K	0.93	3/3686 (0.1%)	1.07	9/4961 (0.2%)
1	L	0.93	3/3686 (0.1%)	1.07	7/4961 (0.1%)
1	M	0.93	3/3686 (0.1%)	1.07	9/4961 (0.2%)
1	N	0.93	3/3686 (0.1%)	1.07	9/4961 (0.2%)
1	O	0.93	3/3686 (0.1%)	1.07	7/4961 (0.1%)
1	P	0.93	3/3686 (0.1%)	1.07	9/4961 (0.2%)
All	All	0.93	48/58976 (0.1%)	1.07	140/79376 (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 48 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	1916	ALA	C-O	7.19	1.33	1.24
1	F	2898	ALA	C-O	7.14	1.32	1.24
1	H	3880	ALA	C-O	7.14	1.32	1.24
1	K	5353	ALA	C-O	7.14	1.32	1.24
1	N	6826	ALA	C-O	7.14	1.32	1.24

The worst 5 of 140 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	1477	GLU	CA-C-O	-13.38	106.17	121.16
1	O	6878	GLU	CA-C-O	-13.38	106.17	121.16
1	A	4	GLU	CA-C-O	-13.36	106.20	121.16
1	B	495	GLU	CA-C-O	-13.36	106.20	121.16
1	I	3932	GLU	CA-C-O	-13.36	106.20	121.16

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	3665	0	3804	26	0
1	B	3665	0	3801	25	0
1	C	3665	0	3801	27	0
1	D	3665	0	3801	26	0
1	E	3665	0	3801	27	0
1	F	3665	0	3801	27	0
1	G	3665	0	3801	26	0
1	H	3665	0	3801	25	0
1	I	3665	0	3801	26	0
1	J	3665	0	3801	26	0
1	K	3665	0	3801	26	0
1	L	3665	0	3801	26	0
1	M	3665	0	3801	24	0
1	N	3665	0	3801	27	0
1	O	3665	0	3801	27	0
1	P	3665	0	3801	26	0
All	All	58640	0	60819	417	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 3.

The worst 5 of 417 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:C:1247:LEU:HD23	1:C:1247:LEU:C	2.17	0.70
1:J:4684:LEU:C	1:J:4684:LEU:HD23	2.17	0.70
1:P:7630:LEU:C	1:P:7630:LEU:HD23	2.17	0.70
1:F:2720:LEU:C	1:F:2720:LEU:HD23	2.17	0.69
1:G:3211:LEU:C	1:G:3211:LEU:HD23	2.17	0.69

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%)	468 (96%)	19 (4%)	2 (0%)	30	67
1	B	489/491 (100%)	468 (96%)	19 (4%)	2 (0%)	30	67
1	C	489/491 (100%)	468 (96%)	19 (4%)	2 (0%)	30	67
1	D	489/491 (100%)	468 (96%)	19 (4%)	2 (0%)	30	67
1	E	489/491 (100%)	468 (96%)	19 (4%)	2 (0%)	30	67
1	F	489/491 (100%)	468 (96%)	19 (4%)	2 (0%)	30	67
1	G	489/491 (100%)	468 (96%)	19 (4%)	2 (0%)	30	67
1	H	489/491 (100%)	468 (96%)	19 (4%)	2 (0%)	30	67
1	I	489/491 (100%)	468 (96%)	19 (4%)	2 (0%)	30	67
1	J	489/491 (100%)	468 (96%)	19 (4%)	2 (0%)	30	67
1	K	489/491 (100%)	468 (96%)	19 (4%)	2 (0%)	30	67
1	L	489/491 (100%)	468 (96%)	19 (4%)	2 (0%)	30	67
1	M	489/491 (100%)	468 (96%)	19 (4%)	2 (0%)	30	67
1	N	489/491 (100%)	468 (96%)	19 (4%)	2 (0%)	30	67
1	O	489/491 (100%)	468 (96%)	19 (4%)	2 (0%)	30	67
1	P	489/491 (100%)	468 (96%)	19 (4%)	2 (0%)	30	67
All	All	7824/7856 (100%)	7488 (96%)	304 (4%)	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	393/393 (100%)	386 (98%)	7 (2%)	51	67
1	B	393/393 (100%)	386 (98%)	7 (2%)	51	67
1	C	393/393 (100%)	386 (98%)	7 (2%)	51	67
1	D	393/393 (100%)	386 (98%)	7 (2%)	51	67
1	E	393/393 (100%)	386 (98%)	7 (2%)	51	67
1	F	393/393 (100%)	386 (98%)	7 (2%)	51	67
1	G	393/393 (100%)	386 (98%)	7 (2%)	51	67
1	H	393/393 (100%)	386 (98%)	7 (2%)	51	67
1	I	393/393 (100%)	386 (98%)	7 (2%)	51	67
1	J	393/393 (100%)	386 (98%)	7 (2%)	51	67
1	K	393/393 (100%)	386 (98%)	7 (2%)	51	67
1	L	393/393 (100%)	386 (98%)	7 (2%)	51	67
1	M	393/393 (100%)	386 (98%)	7 (2%)	51	67
1	N	393/393 (100%)	386 (98%)	7 (2%)	51	67
1	O	393/393 (100%)	386 (98%)	7 (2%)	51	67
1	P	393/393 (100%)	386 (98%)	7 (2%)	51	67
All	All	6288/6288 (100%)	6176 (98%)	112 (2%)	51	67

5 of 112 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	I	4026	LEU
1	P	7781	LEU
1	K	5008	LEU
1	P	7751	LYS
1	O	6972	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 96 such sidechains are listed below:

Mol	Chain	Res	Type
1	J	4715	ASN
1	L	5873	GLN
1	J	4891	GLN
1	K	5382	GLN
1	M	6188	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 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.

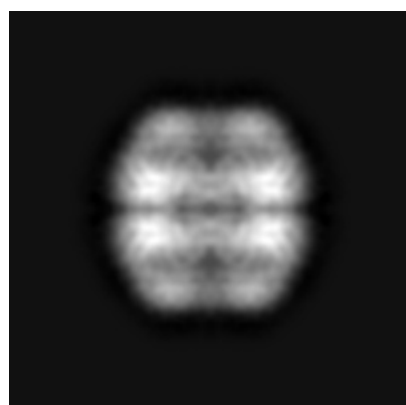
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-5250. These allow visual inspection of the internal detail of the map and identification of artifacts.

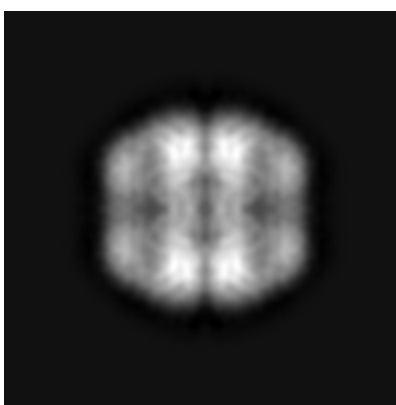
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

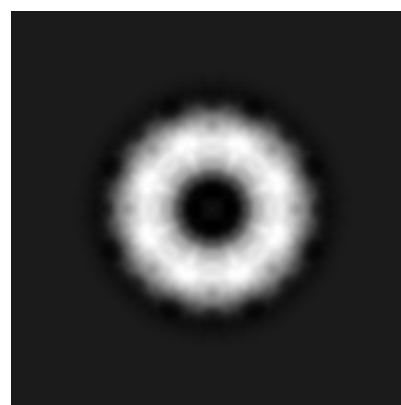
6.1.1 Primary map



X



Y



Z

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

6.2 Central slices [i](#)

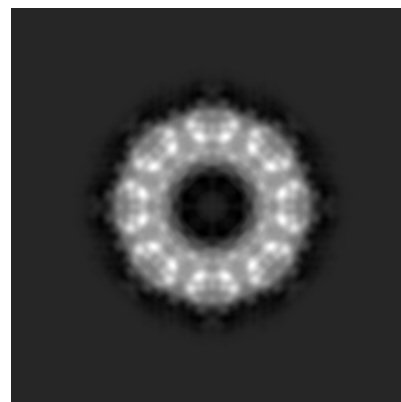
6.2.1 Primary map



X Index: 72



Y Index: 72

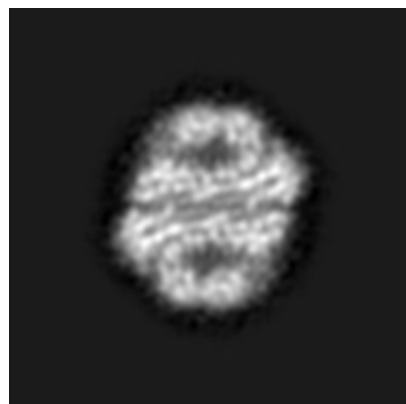


Z Index: 72

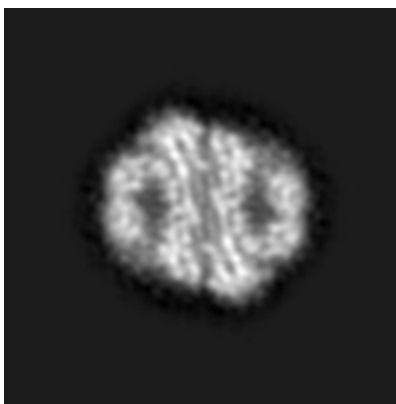
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 92



Y Index: 92

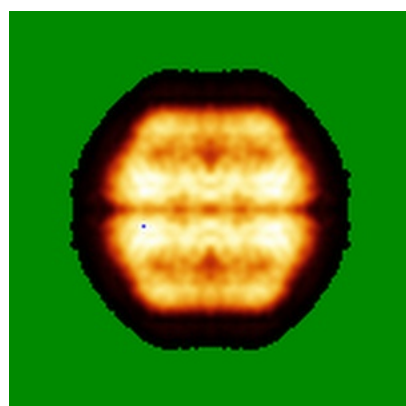


Z Index: 61

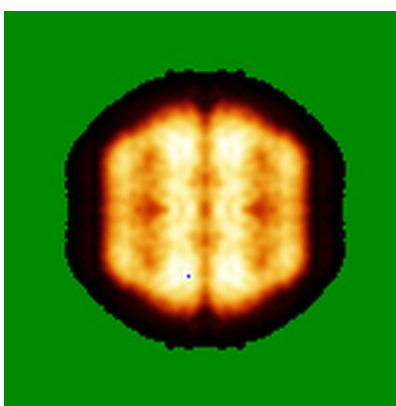
The images above show the largest variance slices of the map in three orthogonal directions.

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

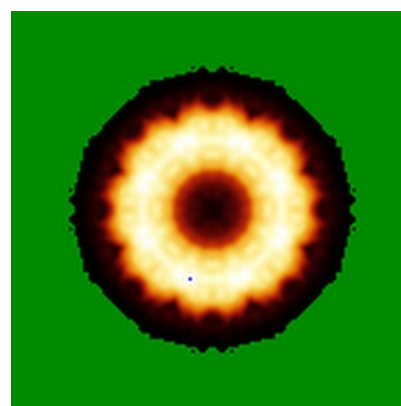
6.4.1 Primary map



X



Y

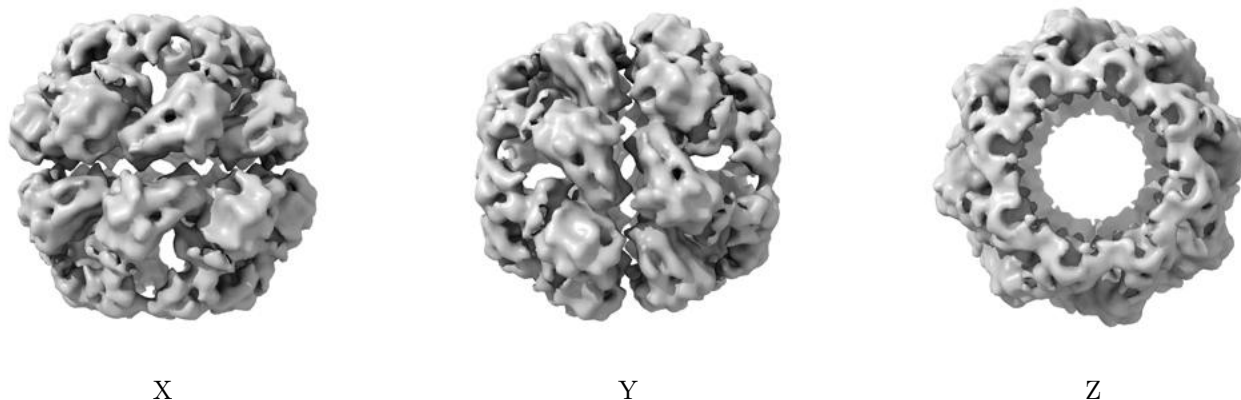


Z

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 [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 1.58. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

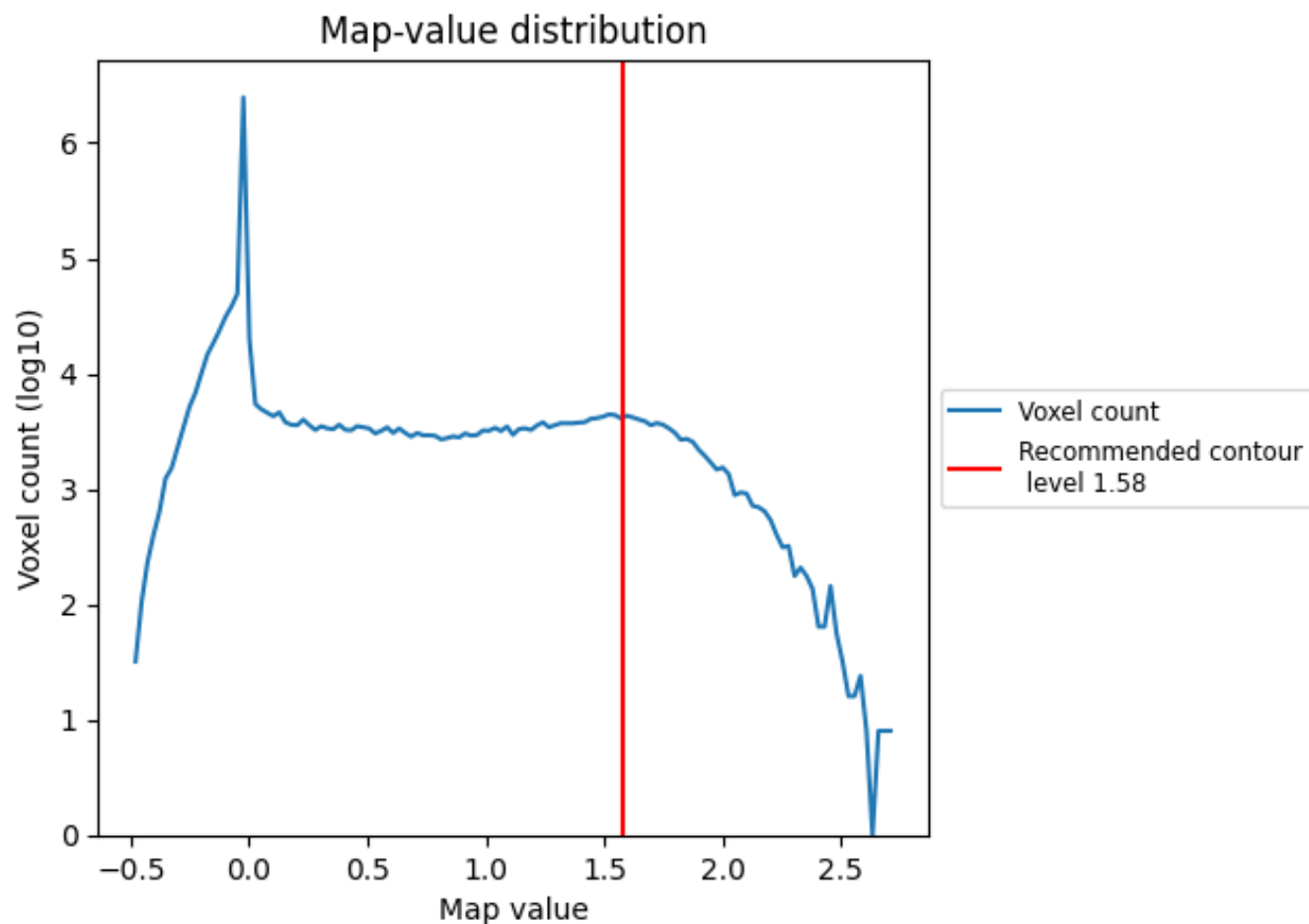
6.6 Mask visualisation [i](#)

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

7 Map analysis ⓘ

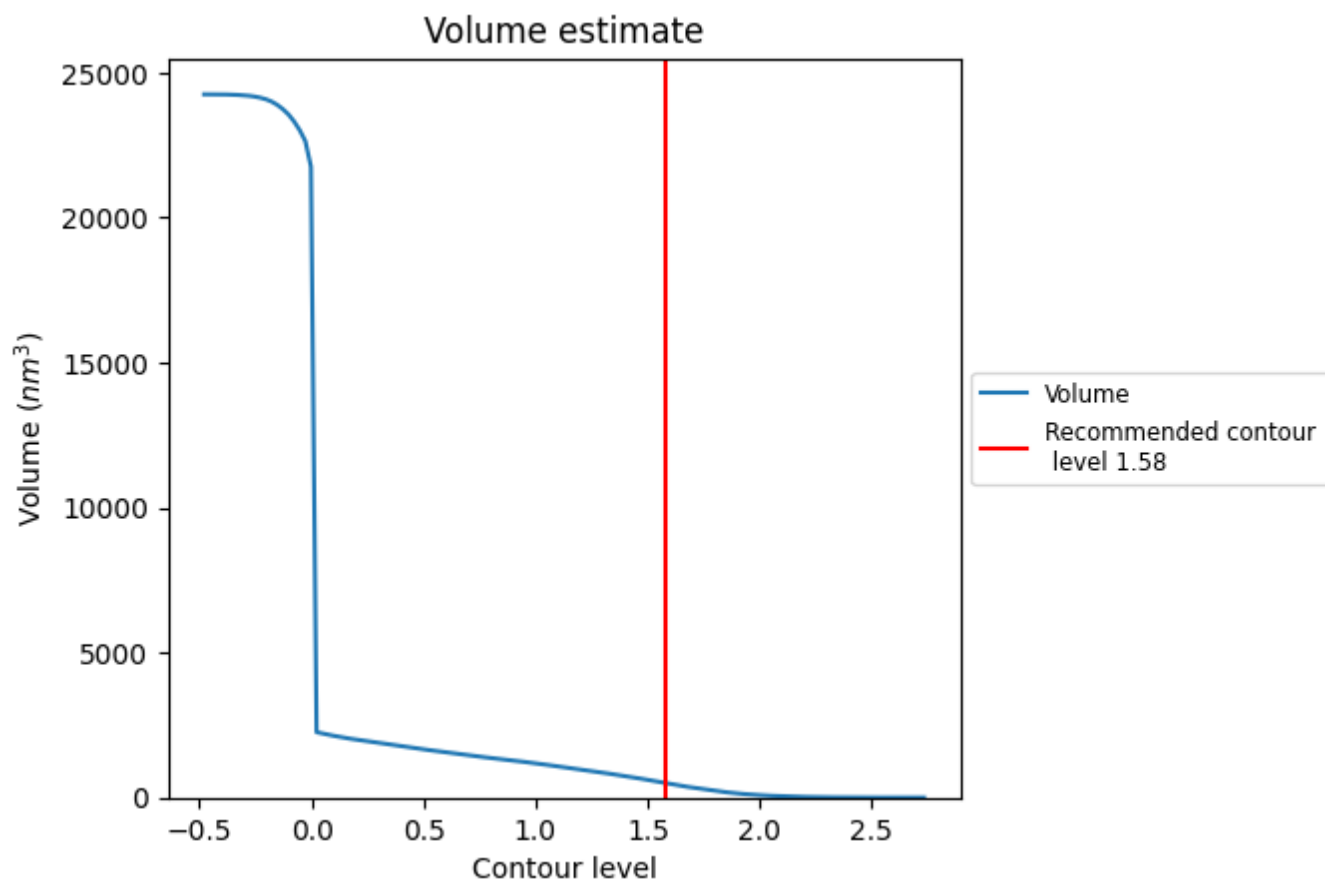
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution ⓘ



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.

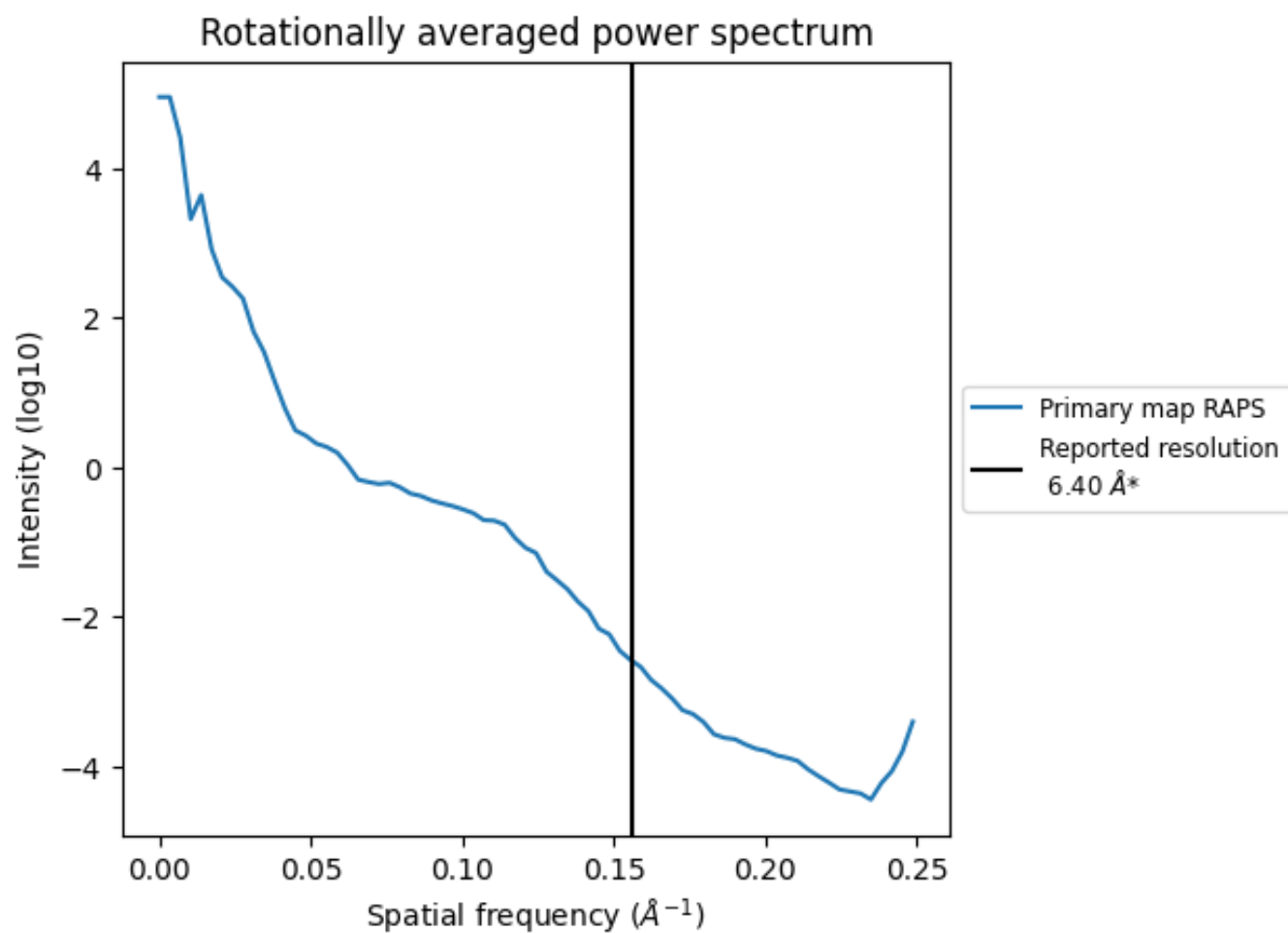
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 500 nm³; this corresponds to an approximate mass of 452 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 0.156 Å⁻¹

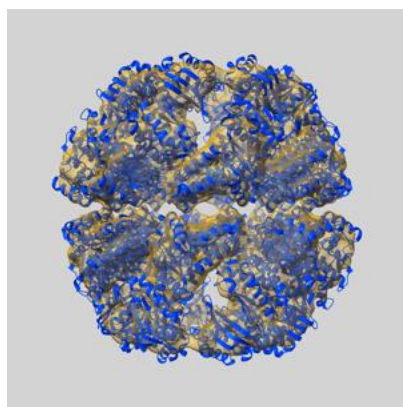
8 Fourier-Shell correlation

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

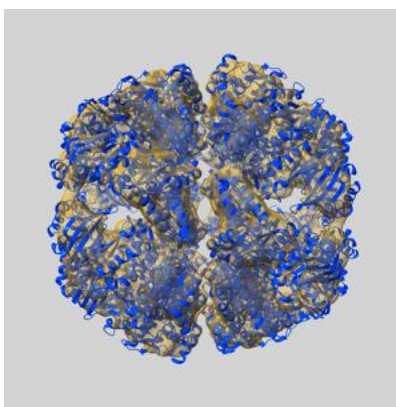
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-5250 and PDB model 3IZN. Per-residue inclusion information can be found in section [3](#) on page [7](#).

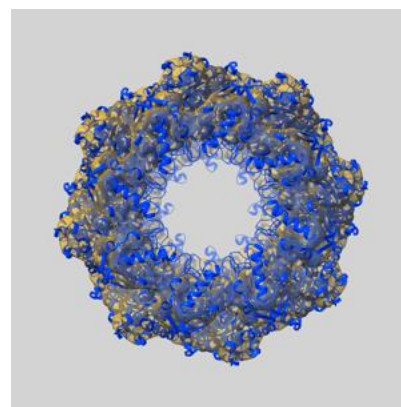
9.1 Map-model overlay [i](#)



X



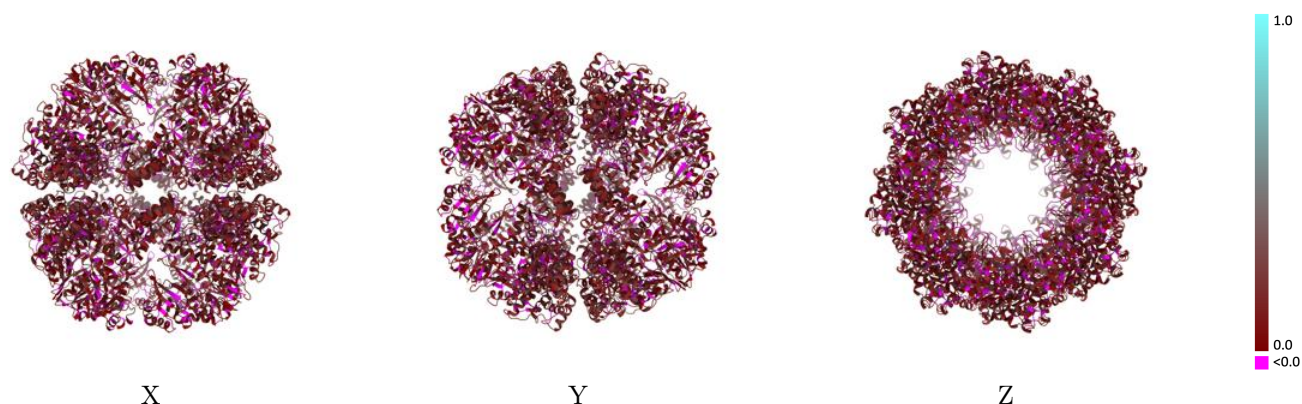
Y



Z

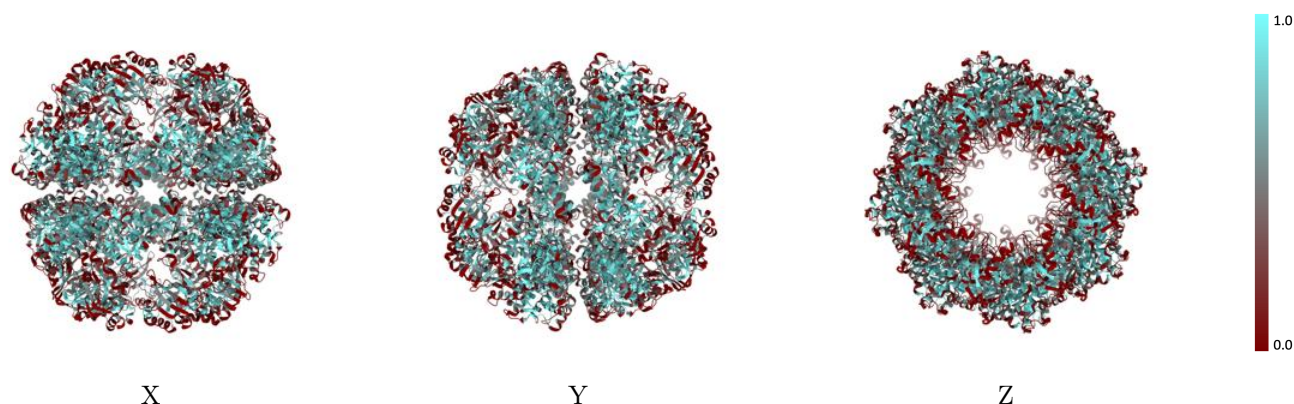
The images above show the 3D surface view of the map at the recommended contour level 1.58 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



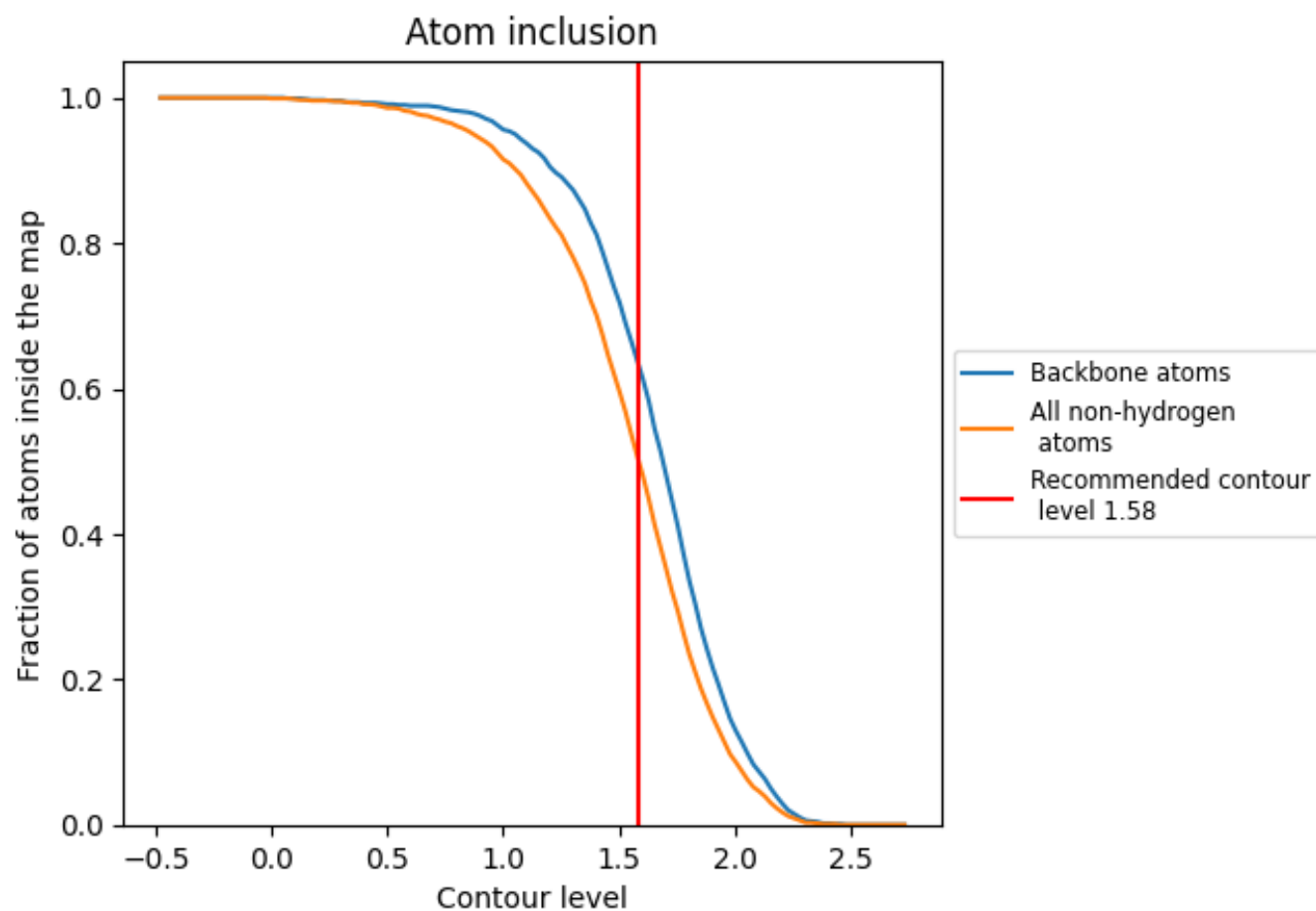
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (1.58).

9.4 Atom inclusion [i](#)



At the recommended contour level, 64% of all backbone atoms, 51% 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 (1.58) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5060	0.1120
A	0.5070	0.1120
B	0.5070	0.1130
C	0.5070	0.1130
D	0.5070	0.1130
E	0.5070	0.1120
F	0.5070	0.1130
G	0.5070	0.1120
H	0.5070	0.1120
I	0.5060	0.1110
J	0.5060	0.1110
K	0.5060	0.1110
L	0.5060	0.1120
M	0.5060	0.1110
N	0.5060	0.1110
O	0.5060	0.1100
P	0.5060	0.1100

1.0

0.0

<0.0