



wwPDB EM Validation Summary Report ⓘ

Mar 28, 2026 – 06:11 PM UTC

PDB ID : 5VHH / pdb_00005vhh
EMDB ID : EMD-8675
Title : Conformational Landscape of the p28-Bound Human Proteasome Regulatory Particle
Authors : Lu, Y.; Wu, J.; Dong, Y.; Chen, S.; Sun, S.; Ma, Y.B.; Ouyang, Q.; Finley, D.; Kirschner, M.W.; Mao, Y.
Deposited on : 2017-04-13
Resolution : 6.10 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:

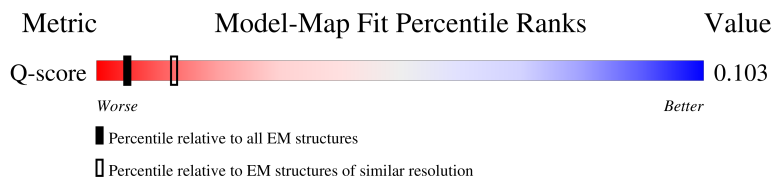
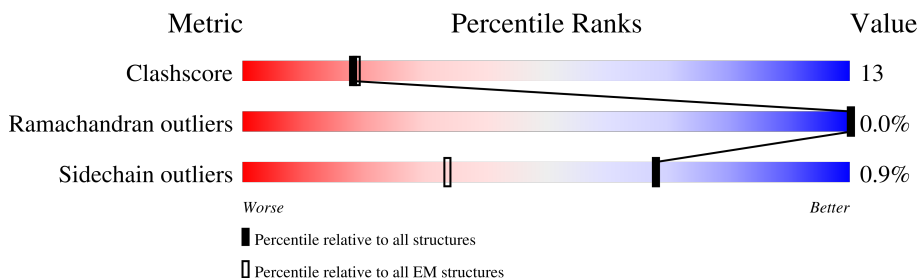
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 6.10 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	531 (5.60 - 6.60)

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	352	
2	B	340	
3	C	385	
4	D	368	

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Mol	Chain	Length	Quality of chain
5	E	379	
6	F	380	
7	U	935	
8	V	488	
9	W	456	
10	X	385	
11	Y	378	
12	Z	286	
13	a	374	
14	b	191	
15	c	287	
16	d	257	
17	e	70	
18	G	223	
19	f	848	

2 Entry composition

There are 20 unique types of molecules in this entry. The entry contains 55280 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 26S proteasome regulatory subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	341	Total	C	N	O	S	0	0
			2677	1690	473	497	17		

- Molecule 2 is a protein called 26S proteasome regulatory subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	330	Total	C	N	O	S	0	0
			2579	1624	437	506	12		

- Molecule 3 is a protein called 26S proteasome regulatory subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	342	Total	C	N	O	S	0	0
			2709	1701	493	501	14		

- Molecule 4 is a protein called 26S proteasome regulatory subunit 6B.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	344	Total	C	N	O	S	0	0
			2751	1744	480	517	10		

- Molecule 5 is a protein called 26S proteasome regulatory subunit 10B.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	345	Total	C	N	O	S	0	0
			2736	1715	490	515	16		

- Molecule 6 is a protein called 26S proteasome regulatory subunit 6A.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	359	Total	C	N	O	S	0	0
			2807	1772	487	531	17		

- Molecule 7 is a protein called 26S proteasome non-ATPase regulatory subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	U	845	Total	C	N	O	S	0	0
			6568	4169	1118	1236	45		

- Molecule 8 is a protein called 26S proteasome non-ATPase regulatory subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	V	488	Total	C	N	O	S	0	0
			3919	2487	695	723	14		

- Molecule 9 is a protein called 26S proteasome non-ATPase regulatory subunit 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	W	456	Total	C	N	O	S	0	0
			3703	2339	635	704	25		

- Molecule 10 is a protein called 26S proteasome non-ATPase regulatory subunit 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	X	385	Total	C	N	O	S	0	0
			3048	1939	515	582	12		

- Molecule 11 is a protein called 26S proteasome non-ATPase regulatory subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	Y	378	Total	C	N	O	S	0	0
			3115	1987	533	578	17		

- Molecule 12 is a protein called 26S proteasome non-ATPase regulatory subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	Z	286	Total	C	N	O	S	0	0
			2281	1457	392	427	5		

- Molecule 13 is a protein called 26S proteasome non-ATPase regulatory subunit 13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	a	374	Total	C	N	O	S	0	0
			3003	1915	511	562	15		

- Molecule 14 is a protein called 26S proteasome non-ATPase regulatory subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	b	191	Total	C	N	O	S	0	0
			1458	910	261	279	8		

- Molecule 15 is a protein called 26S proteasome non-ATPase regulatory subunit 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	c	287	Total	C	N	O	S	0	0
			2260	1430	389	422	19		

- Molecule 16 is a protein called 26S proteasome non-ATPase regulatory subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	d	257	Total	C	N	O	S	0	0
			2116	1371	346	390	9		

- Molecule 17 is a protein called 26S proteasome complex subunit SEM1.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	e	70	Total	C	N	O	S	0	0
			583	357	89	135	2		

- Molecule 18 is a protein called 26S proteasome non-ATPase regulatory subunit 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	G	219	Total	C	N	O	S	0	0
			1662	1036	294	323	9		

- Molecule 19 is a protein called 26S proteasome non-ATPase regulatory subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	f	686	Total	C	N	O	S	0	0
			5304	3335	901	1033	35		

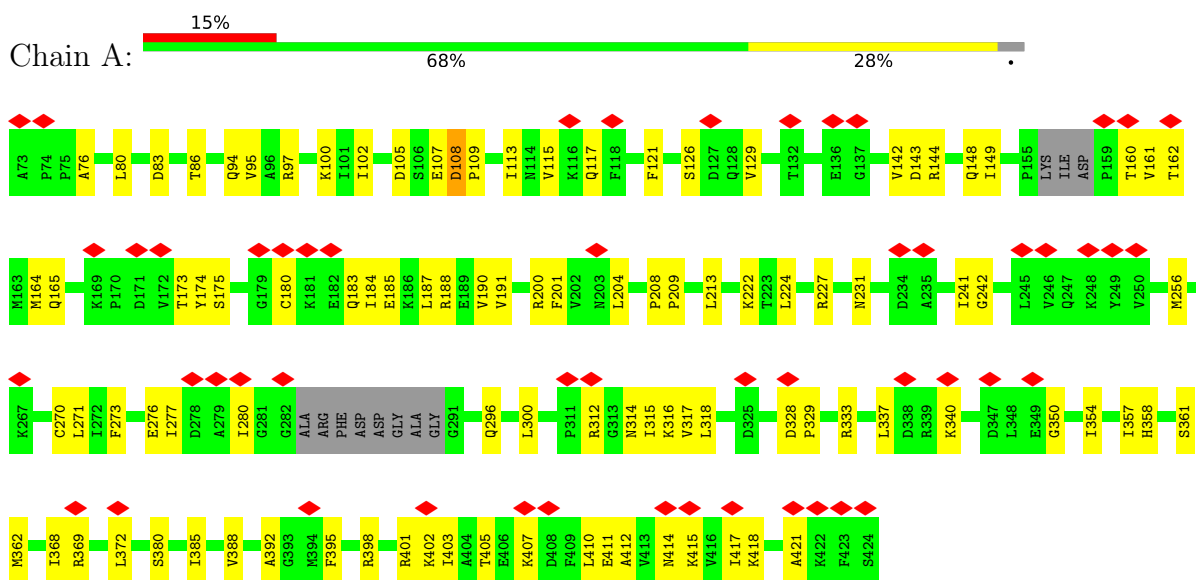
- Molecule 20 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
20	c	1	Total	Zn	0
			1	1	

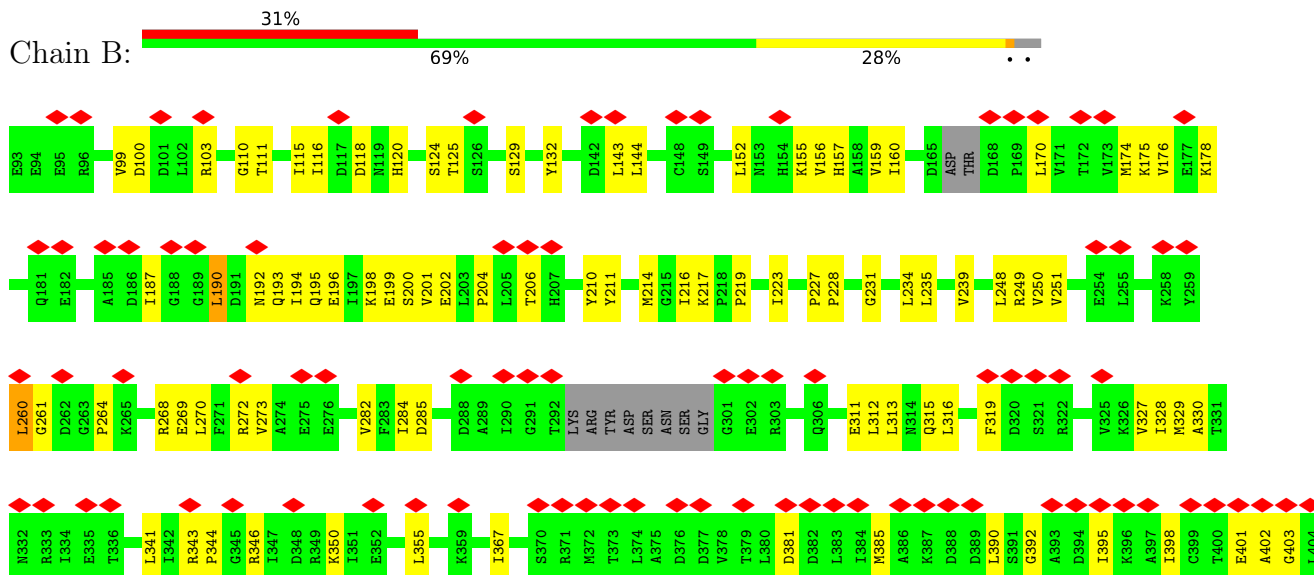
3 Residue-property plots

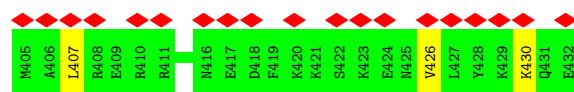
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 26S proteasome regulatory subunit 7

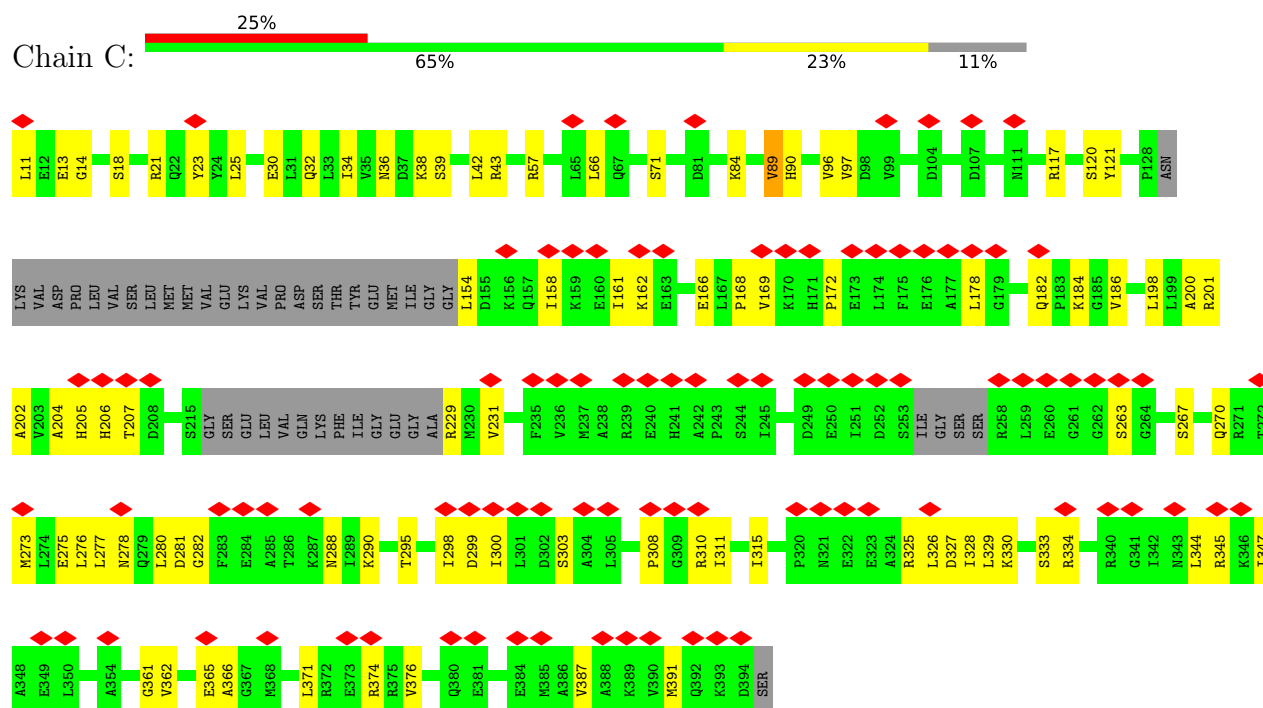


• Molecule 2: 26S proteasome regulatory subunit 4

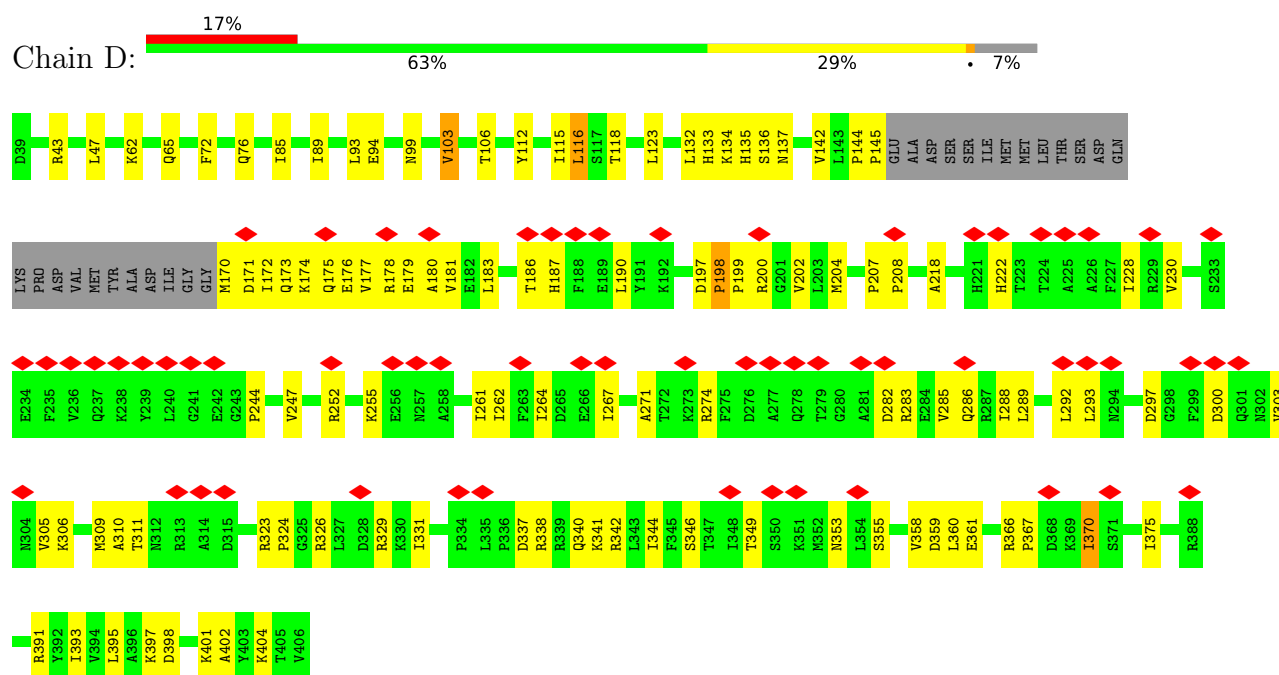




• Molecule 3: 26S proteasome regulatory subunit 8

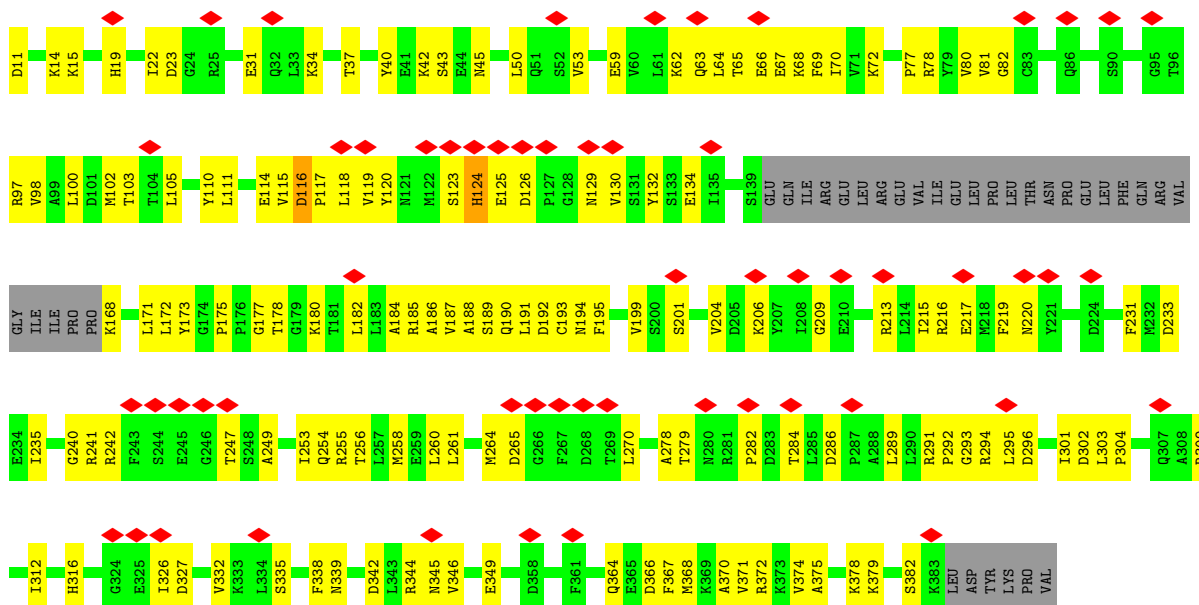


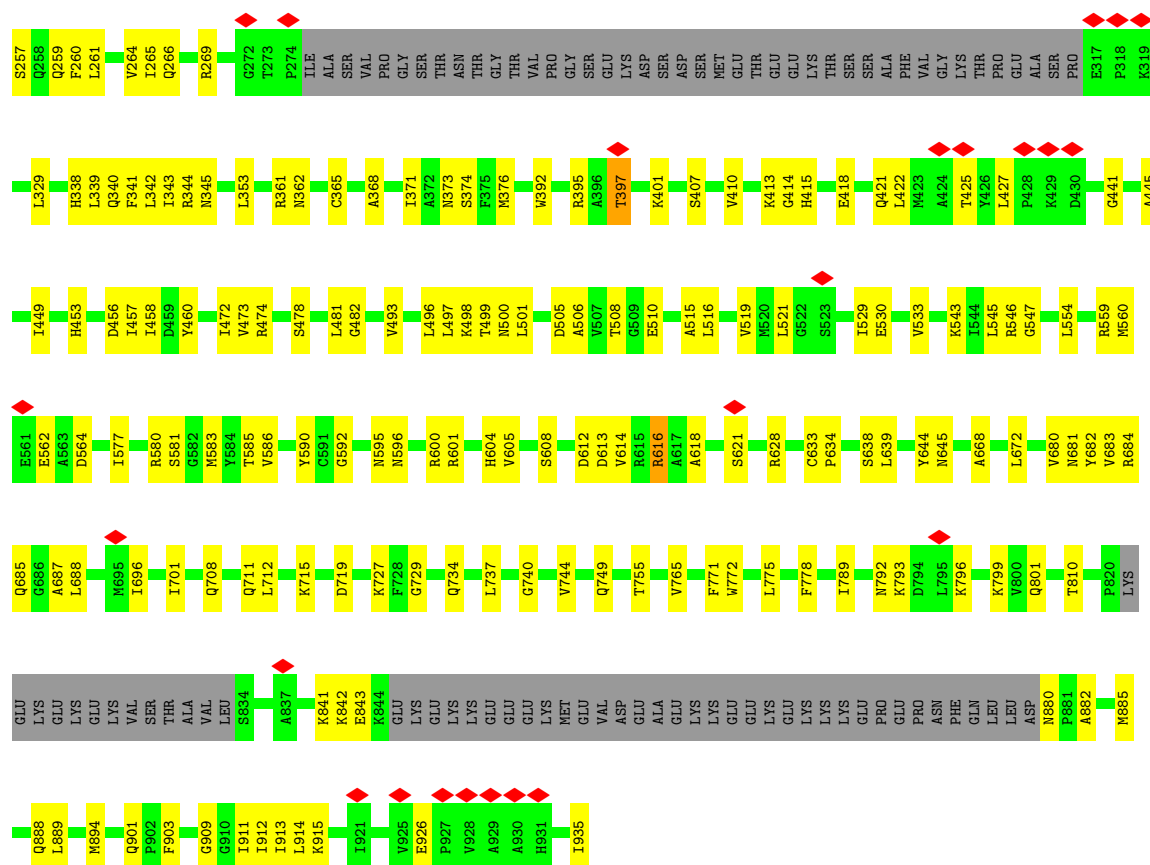
• Molecule 4: 26S proteasome regulatory subunit 6B



• Molecule 5: 26S proteasome regulatory subunit 10B



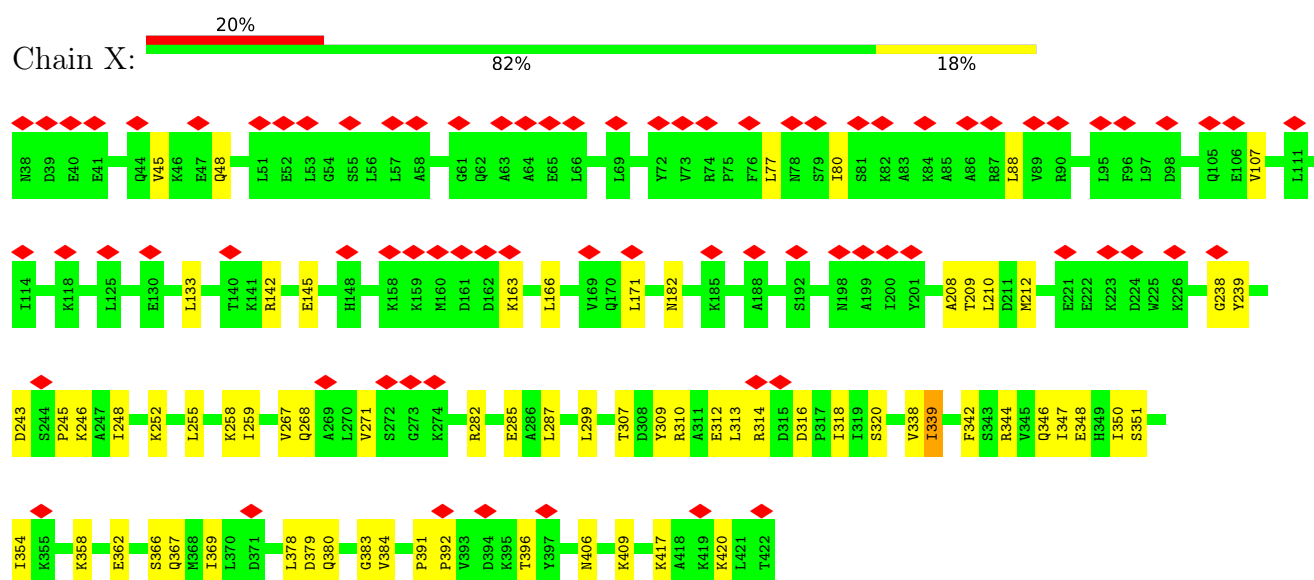




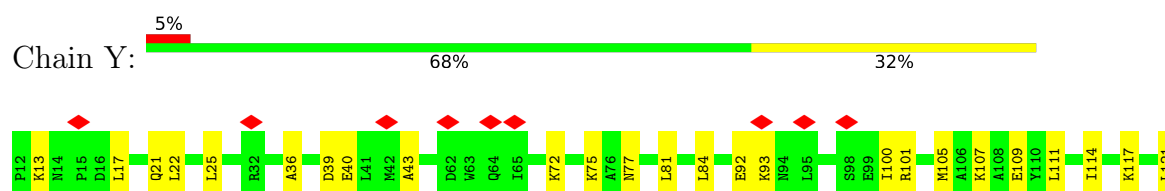
- Molecule 9: 26S proteasome non-ATPase regulatory subunit 12

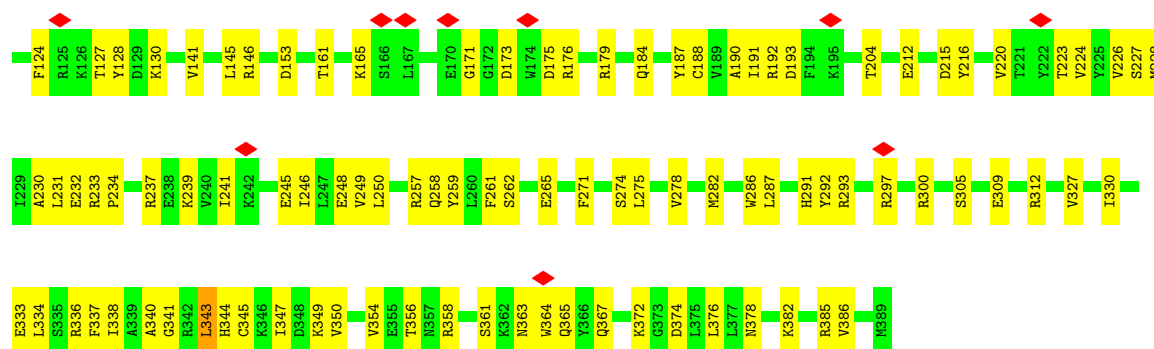


- Molecule 10: 26S proteasome non-ATPase regulatory subunit 11

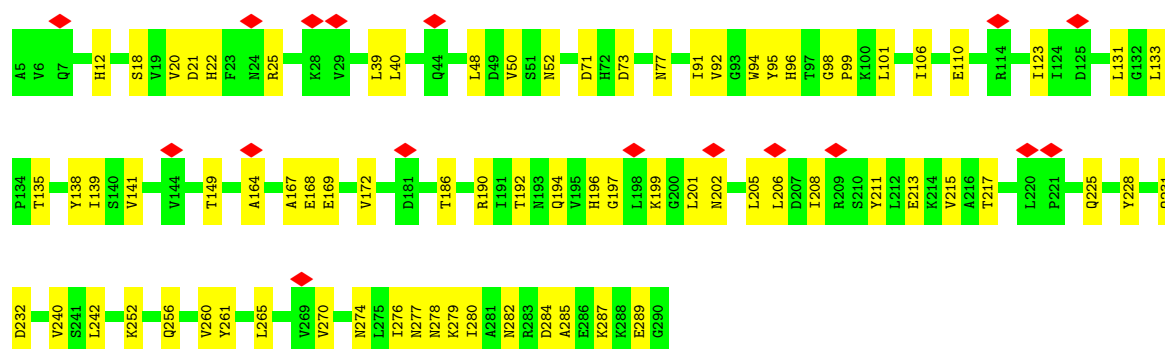


- Molecule 11: 26S proteasome non-ATPase regulatory subunit 6

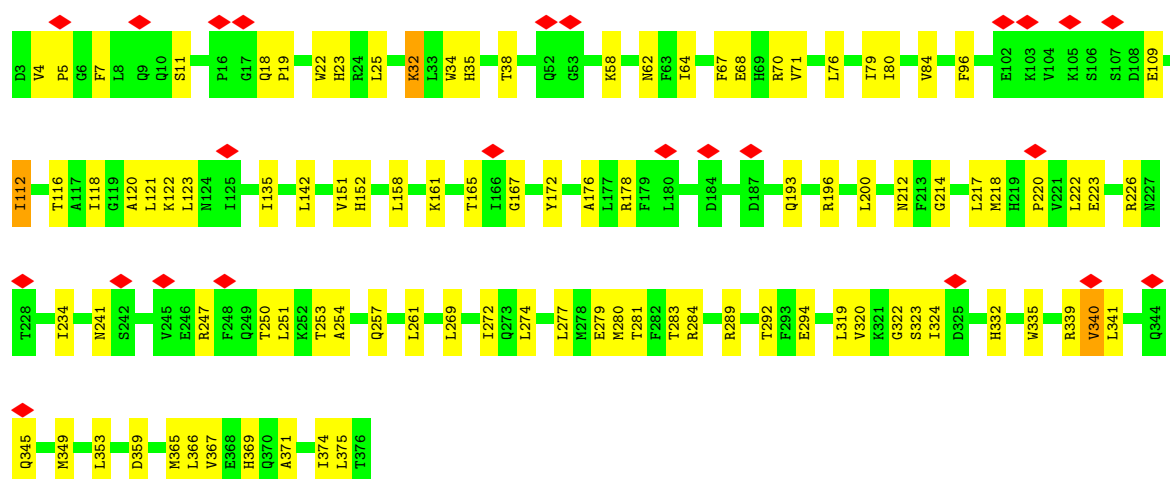




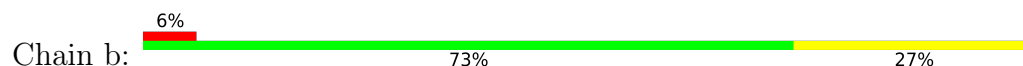
- Molecule 12: 26S proteasome non-ATPase regulatory subunit 7

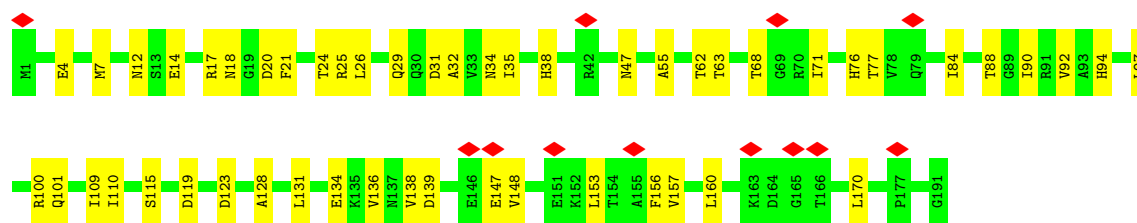


- Molecule 13: 26S proteasome non-ATPase regulatory subunit 13

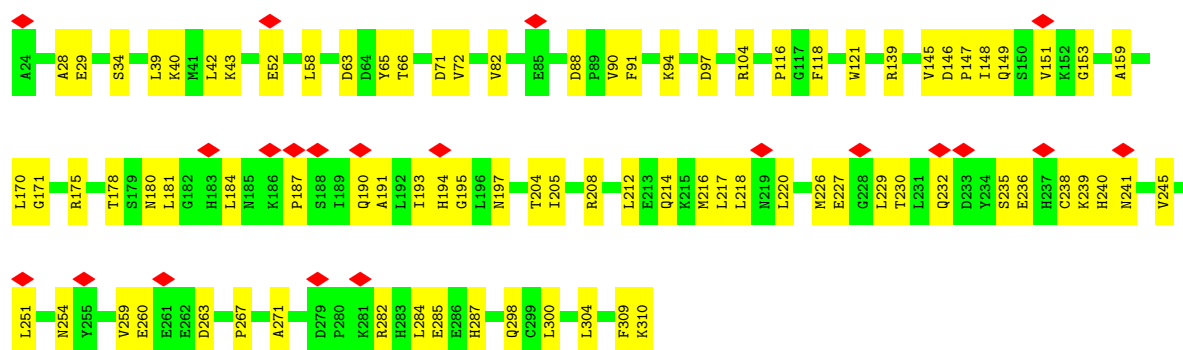


- Molecule 14: 26S proteasome non-ATPase regulatory subunit 4

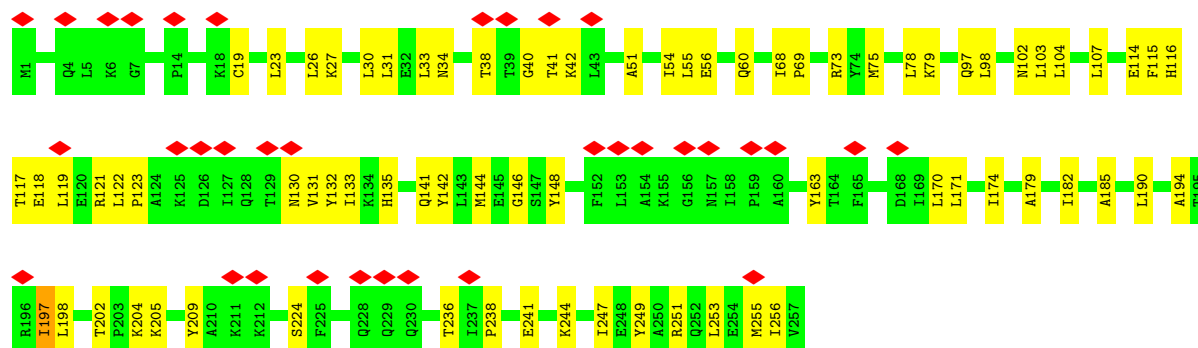




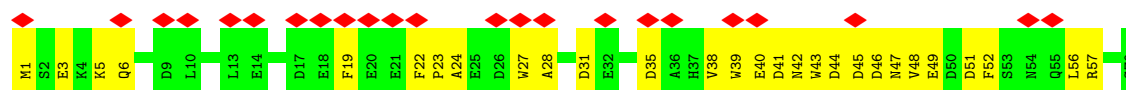
- Molecule 15: 26S proteasome non-ATPase regulatory subunit 14



- Molecule 16: 26S proteasome non-ATPase regulatory subunit 8

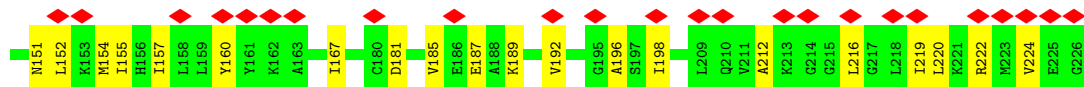
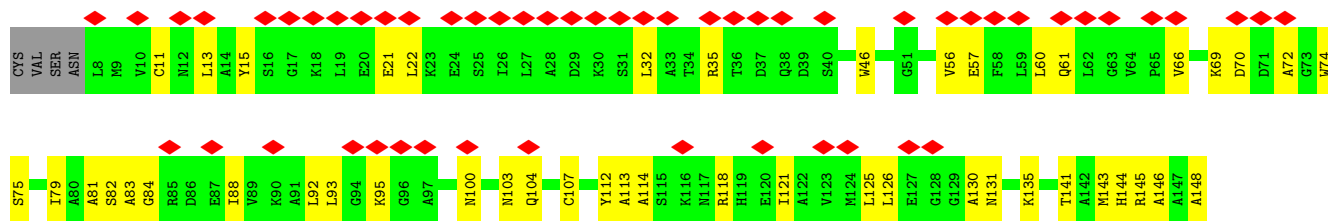


- Molecule 17: 26S proteasome complex subunit SEM1

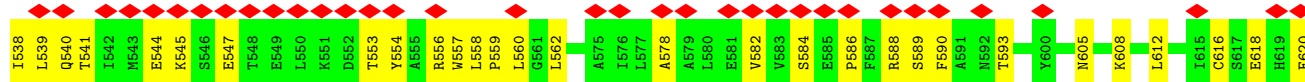
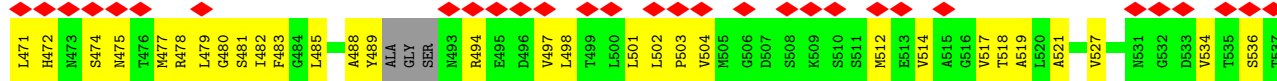
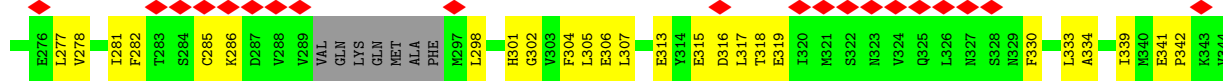
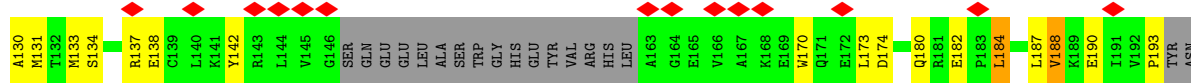
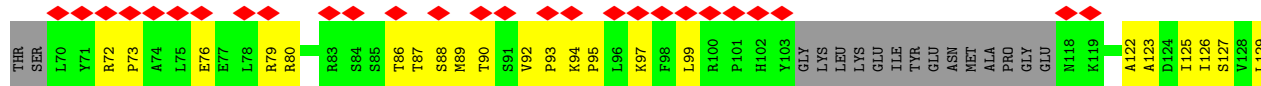
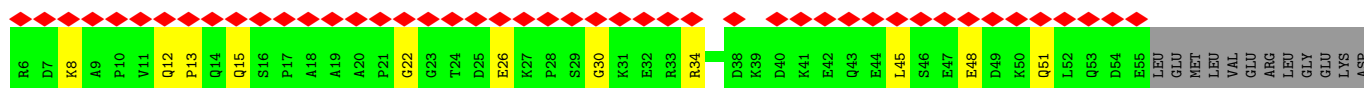
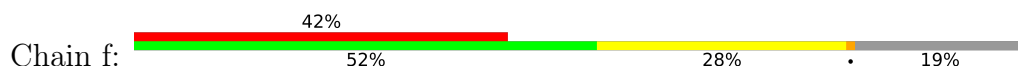


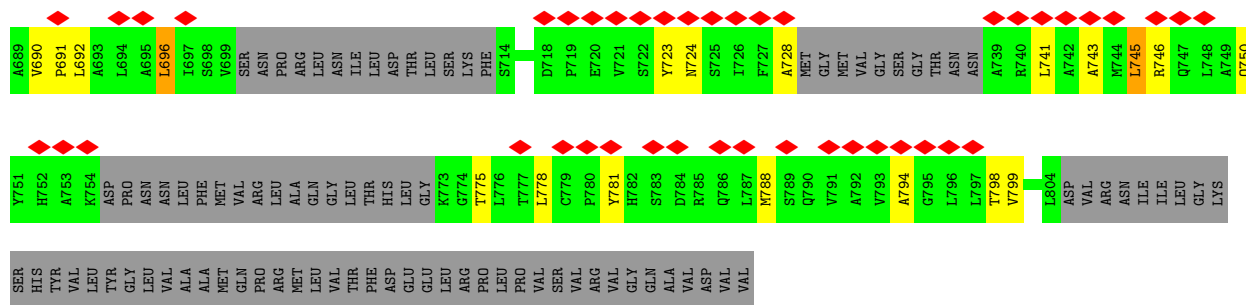
- Molecule 18: 26S proteasome non-ATPase regulatory subunit 10





• Molecule 19: 26S proteasome non-ATPase regulatory subunit 2





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	27629	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TECNAI ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	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	0.018	Depositor
Minimum map value	-0.007	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.004	Depositor
Map size (Å)	250.88, 250.88, 250.88	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.98, 0.98, 0.98	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN

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	0.11	0/2722	0.33	0/3673
2	B	0.10	0/2614	0.31	0/3527
3	C	0.10	0/2741	0.30	0/3681
4	D	0.11	0/2795	0.36	1/3773 (0.0%)
5	E	0.13	0/2775	0.37	2/3727 (0.1%)
6	F	0.09	0/2843	0.28	0/3827
7	U	0.09	0/6684	0.27	0/9043
8	V	0.15	0/3997	0.42	2/5399 (0.0%)
9	W	0.13	0/3750	0.35	2/5039 (0.0%)
10	X	0.08	0/3091	0.24	0/4165
11	Y	0.09	0/3173	0.26	0/4273
12	Z	0.09	0/2324	0.26	0/3150
13	a	0.09	0/3061	0.28	0/4144
14	b	0.09	0/1478	0.26	0/2001
15	c	0.09	0/2302	0.24	0/3110
16	d	0.09	0/2162	0.28	0/2919
17	e	0.09	0/596	0.25	0/805
18	G	0.07	0/1687	0.22	0/2279
19	f	0.12	0/5377	0.37	0/7248
All	All	0.11	0/56172	0.31	7/75783 (0.0%)

There are no bond length outliers.

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	V	188	SER	N-CA-C	-8.95	101.44	111.82
4	D	198	PRO	N-CA-C	8.88	121.53	110.70
5	E	116	ASP	N-CA-C	-7.16	102.99	113.16
8	V	262	SER	N-CA-C	-7.02	95.85	110.80
9	W	221	LYS	CA-C-N	6.80	134.52	121.54

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2677	0	2732	78	0
2	B	2579	0	2628	63	0
3	C	2709	0	2812	66	0
4	D	2751	0	2804	80	0
5	E	2736	0	2794	138	0
6	F	2807	0	2900	91	0
7	U	6568	0	6627	145	0
8	V	3919	0	3960	143	0
9	W	3703	0	3821	91	0
10	X	3048	0	3139	47	0
11	Y	3115	0	3120	86	0
12	Z	2281	0	2312	61	0
13	a	3003	0	3016	77	0
14	b	1458	0	1505	34	0
15	c	2260	0	2276	64	0
16	d	2116	0	2146	48	0
17	e	583	0	493	24	0
18	G	1662	0	1667	43	0
19	f	5304	0	5314	218	0
20	c	1	0	0	0	0
All	All	55280	0	56066	1467	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 13.

The worst 5 of 1467 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)
5:E:124:HIS:CD2	5:E:195:PHE:CE2	2.00	1.49
5:E:124:HIS:HD2	5:E:195:PHE:CE2	1.38	1.36
5:E:114:GLU:OE2	5:E:119:VAL:HG22	1.37	1.24

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:W:220:GLU:OE1	9:W:222:LEU:N	1.76	1.18
5:E:124:HIS:CD2	5:E:195:PHE:CZ	2.33	1.14

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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	335/352 (95%)	305 (91%)	30 (9%)	0	100	100
2	B	324/340 (95%)	293 (90%)	31 (10%)	0	100	100
3	C	334/385 (87%)	321 (96%)	13 (4%)	0	100	100
4	D	340/368 (92%)	316 (93%)	24 (7%)	0	100	100
5	E	341/379 (90%)	316 (93%)	25 (7%)	0	100	100
6	F	351/380 (92%)	332 (95%)	19 (5%)	0	100	100
7	U	837/935 (90%)	805 (96%)	32 (4%)	0	100	100
8	V	484/488 (99%)	429 (89%)	54 (11%)	1 (0%)	43	77
9	W	452/456 (99%)	413 (91%)	38 (8%)	1 (0%)	43	77
10	X	381/385 (99%)	374 (98%)	7 (2%)	0	100	100
11	Y	376/378 (100%)	358 (95%)	18 (5%)	0	100	100
12	Z	284/286 (99%)	268 (94%)	16 (6%)	0	100	100
13	a	372/374 (100%)	351 (94%)	21 (6%)	0	100	100
14	b	189/191 (99%)	174 (92%)	15 (8%)	0	100	100
15	c	285/287 (99%)	272 (95%)	13 (5%)	0	100	100
16	d	255/257 (99%)	237 (93%)	18 (7%)	0	100	100
17	e	68/70 (97%)	63 (93%)	5 (7%)	0	100	100
18	G	217/223 (97%)	213 (98%)	4 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	f	664/848 (78%)	591 (89%)	73 (11%)	0	100	100
All	All	6889/7382 (93%)	6431 (93%)	456 (7%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	W	221	LYS
8	V	190	ASP

5.3.2 Protein sidechains [i](#)

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	293/300 (98%)	291 (99%)	2 (1%)	76	81
2	B	289/298 (97%)	284 (98%)	5 (2%)	53	69
3	C	297/333 (89%)	294 (99%)	3 (1%)	68	78
4	D	301/321 (94%)	297 (99%)	4 (1%)	61	74
5	E	300/333 (90%)	298 (99%)	2 (1%)	76	81
6	F	307/326 (94%)	306 (100%)	1 (0%)	86	85
7	U	717/798 (90%)	710 (99%)	7 (1%)	68	78
8	V	422/422 (100%)	416 (99%)	6 (1%)	59	72
9	W	416/416 (100%)	413 (99%)	3 (1%)	76	81
10	X	331/331 (100%)	328 (99%)	3 (1%)	70	79
11	Y	334/334 (100%)	333 (100%)	1 (0%)	86	85
12	Z	257/257 (100%)	256 (100%)	1 (0%)	84	84
13	a	334/334 (100%)	331 (99%)	3 (1%)	70	79
14	b	167/167 (100%)	167 (100%)	0	100	100
15	c	252/252 (100%)	252 (100%)	0	100	100
16	d	231/231 (100%)	229 (99%)	2 (1%)	70	79
17	e	63/63 (100%)	62 (98%)	1 (2%)	55	70

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
18	G	174/178 (98%)	174 (100%)	0	100	100
19	f	579/714 (81%)	570 (98%)	9 (2%)	55	70
All	All	6064/6408 (95%)	6011 (99%)	53 (1%)	68	79

5 of 53 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
8	V	226	VAL
10	X	369	ILE
19	f	463	LEU
8	V	262	SER
9	W	211	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 99 such sidechains are listed below:

Mol	Chain	Res	Type
10	X	170	GLN
12	Z	273	HIS
10	X	375	HIS
11	Y	363	ASN
13	a	152	HIS

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](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
8	V	1
9	W	1
10	X	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	V	237:THR	C	238:ALA	N	3.86
1	W	205:ILE	C	206:SER	N	3.19
1	X	311:ALA	C	312:GLU	N	3.16

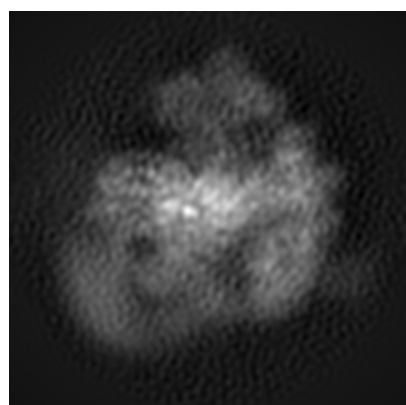
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8675. These allow visual inspection of the internal detail of the map and identification of artifacts.

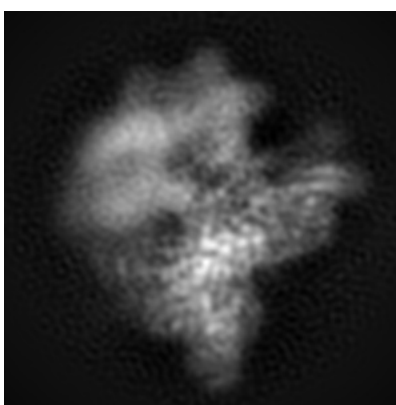
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

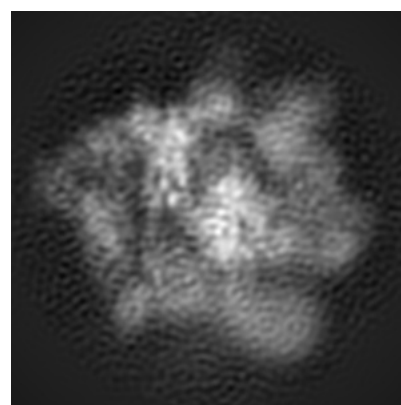
6.1.1 Primary map



X



Y

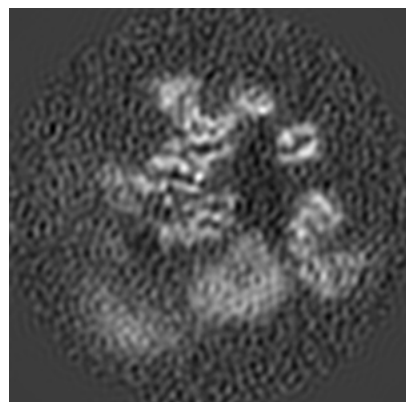


Z

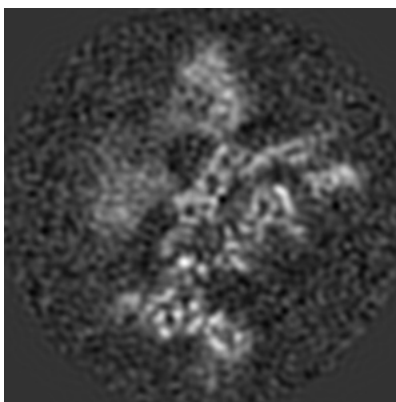
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

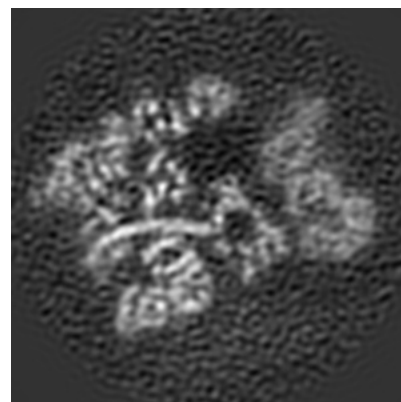
6.2.1 Primary map



X Index: 128



Y Index: 128

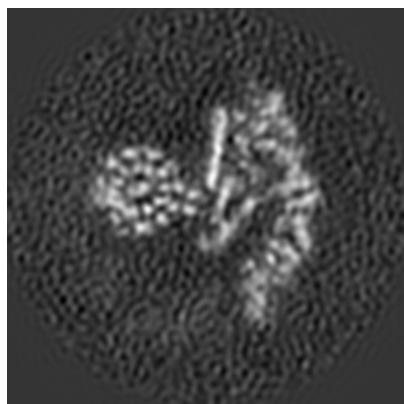


Z Index: 128

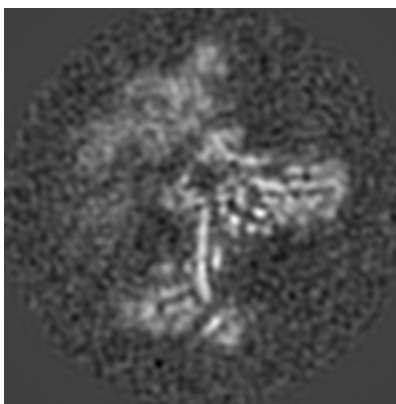
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

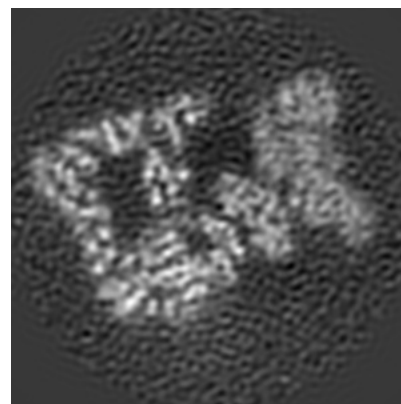
6.3.1 Primary map



X Index: 103



Y Index: 115

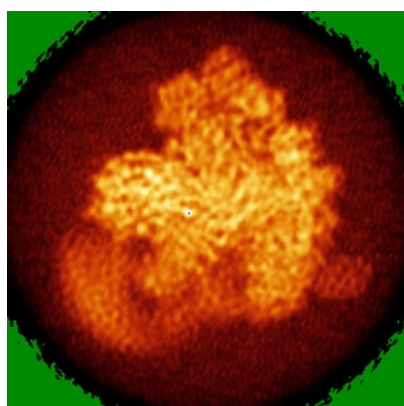


Z Index: 140

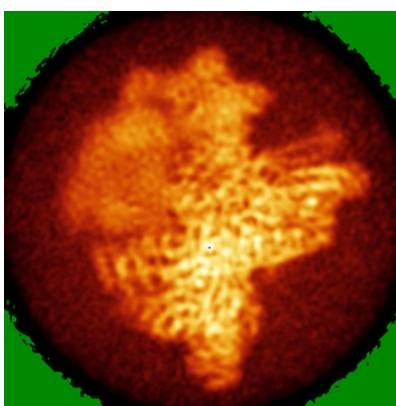
The images above show the largest variance slices of the map in three orthogonal directions.

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

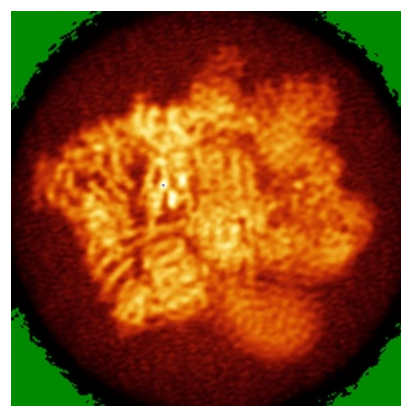
6.4.1 Primary map



X



Y

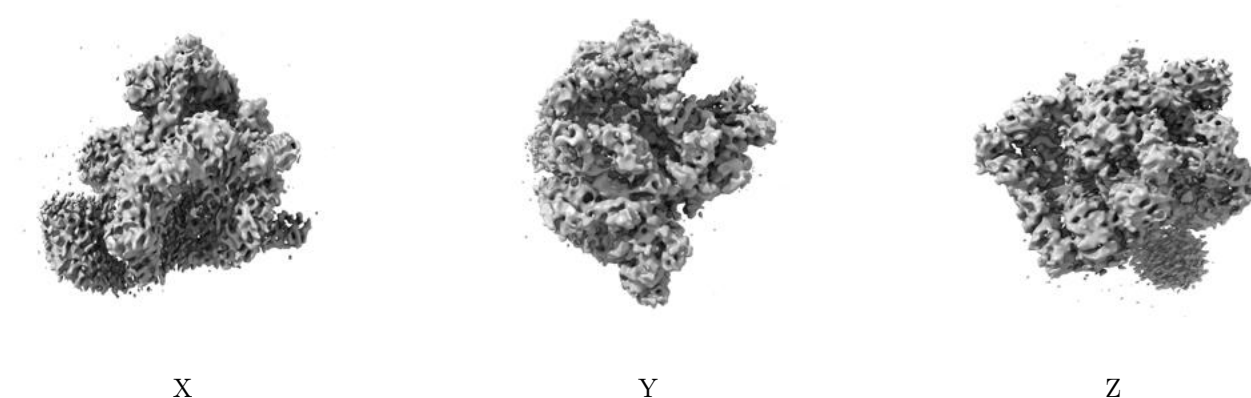


Z

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 0.004. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

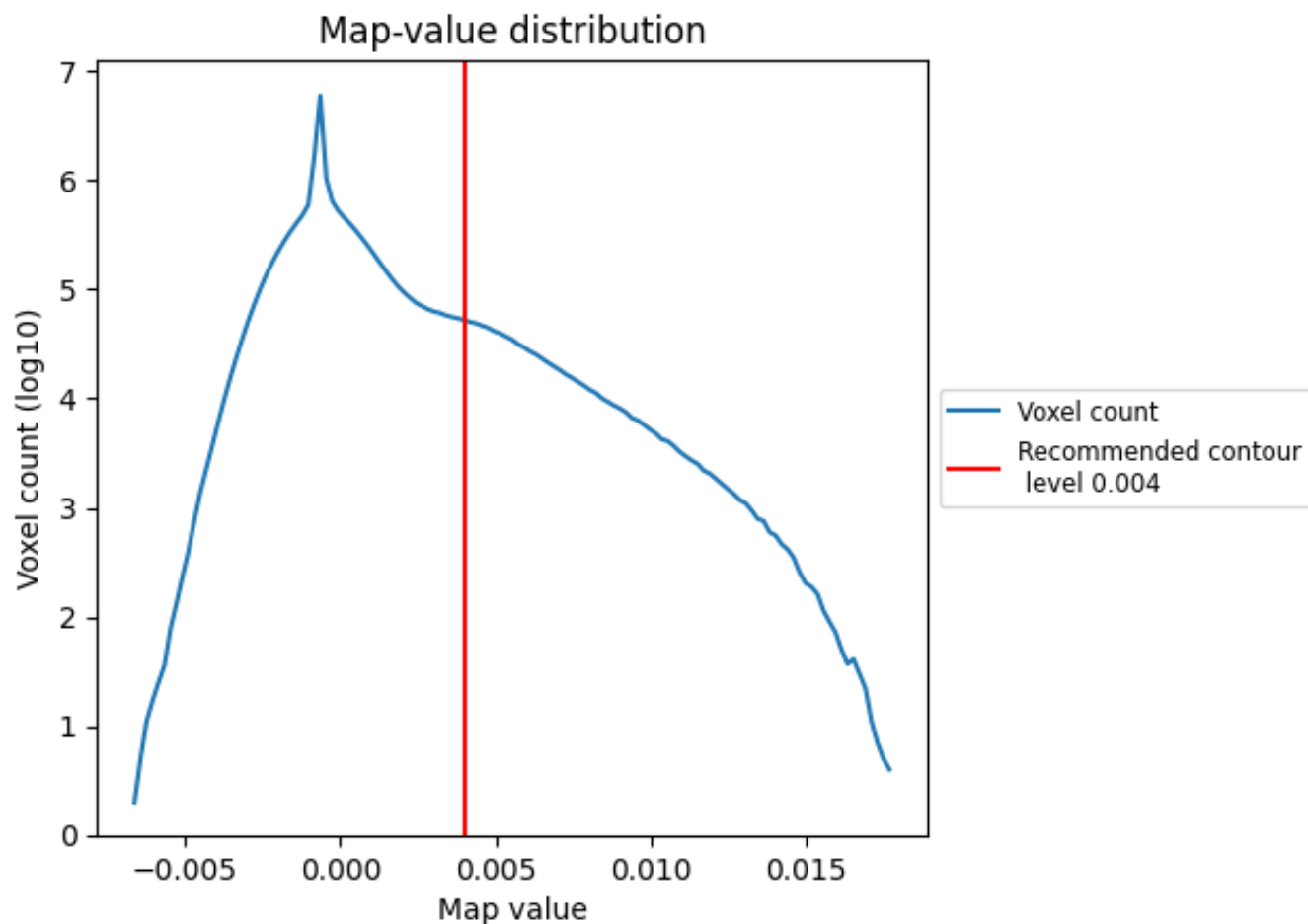
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

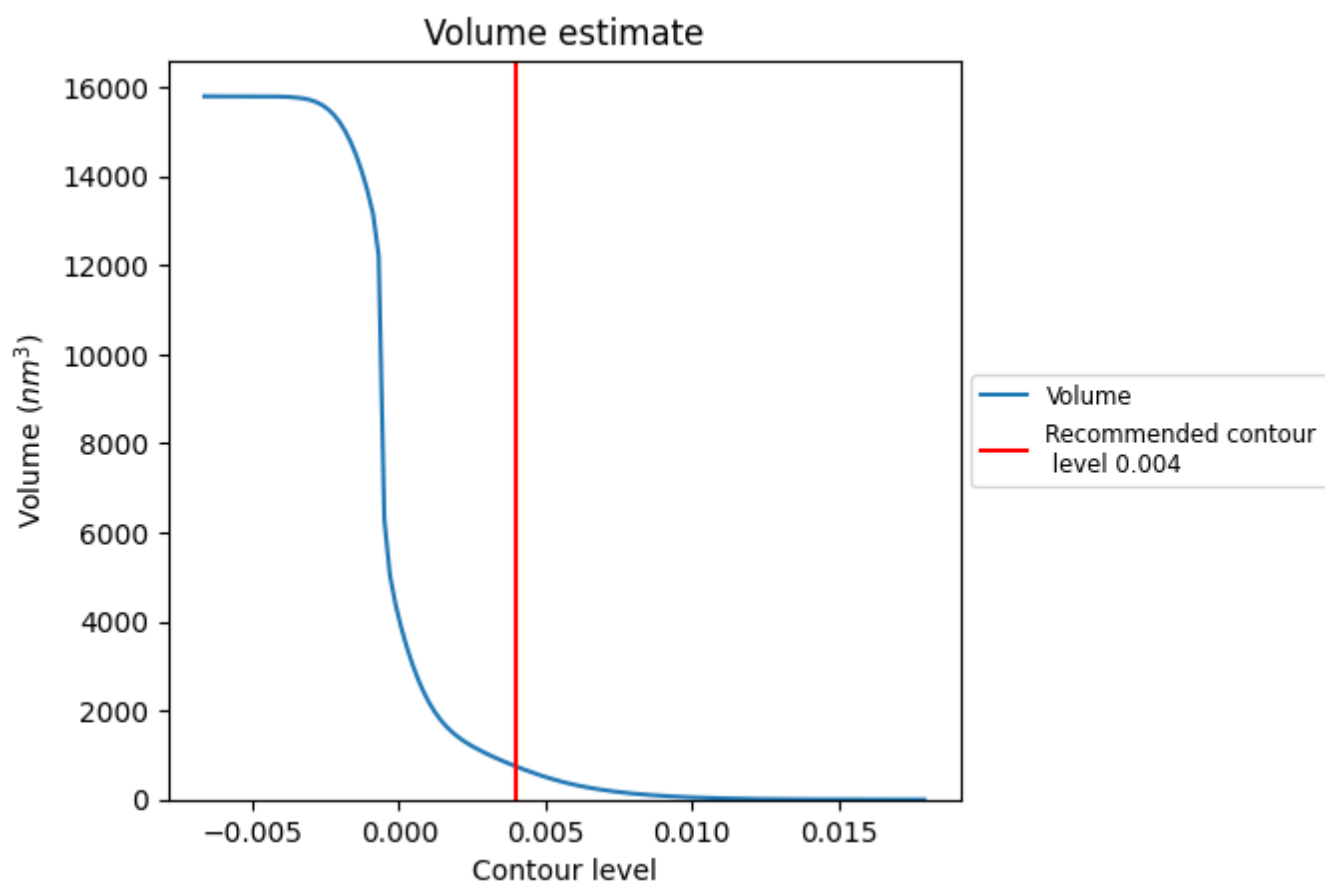
This section contains the results of statistical analysis of the map.

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.

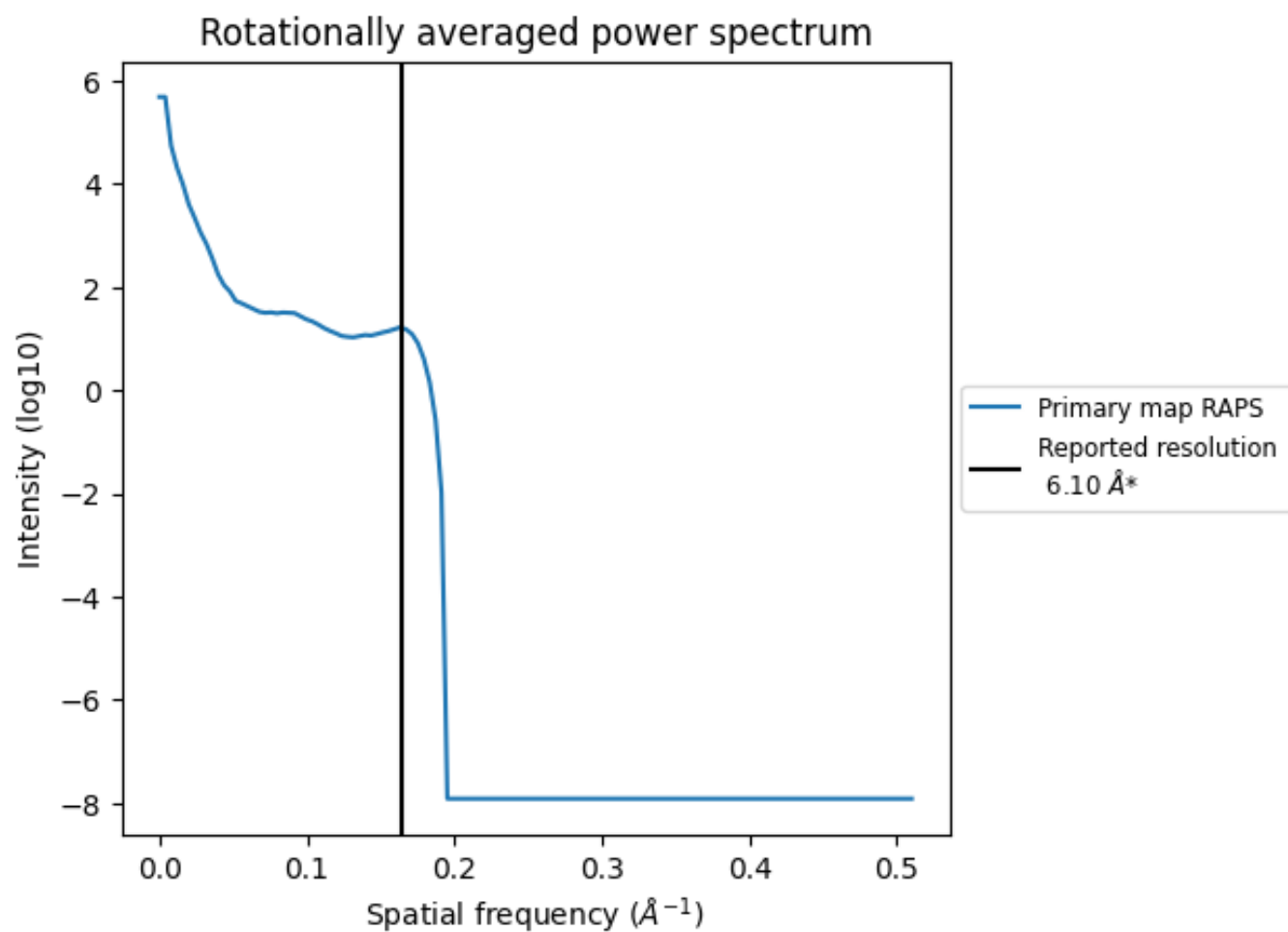
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 742 nm³; this corresponds to an approximate mass of 670 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 0.164 Å⁻¹

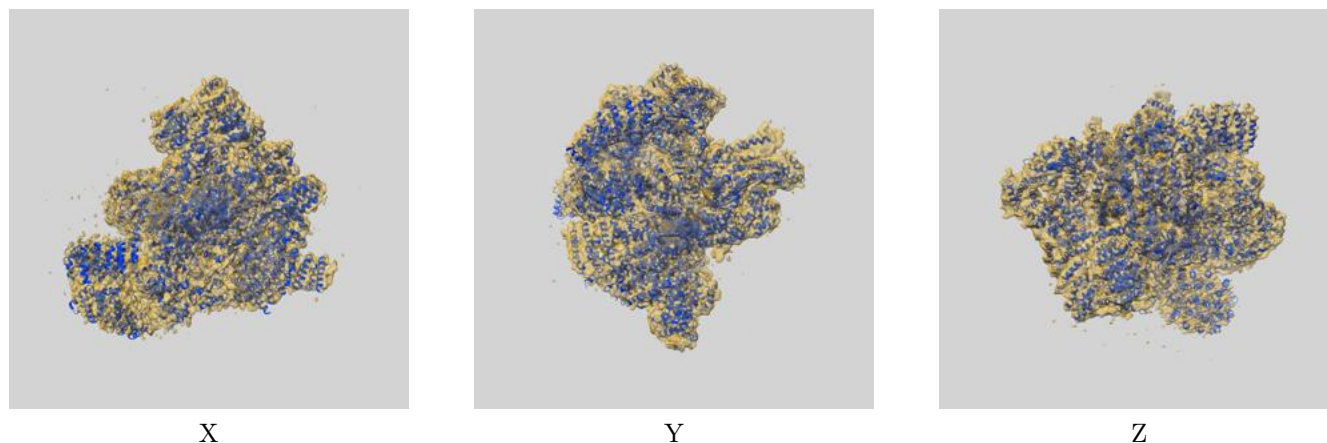
8 Fourier-Shell correlation

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-8675 and PDB model 5VHH. Per-residue inclusion information can be found in [section 3](#) on [page 7](#).

9.1 Map-model overlay [i](#)



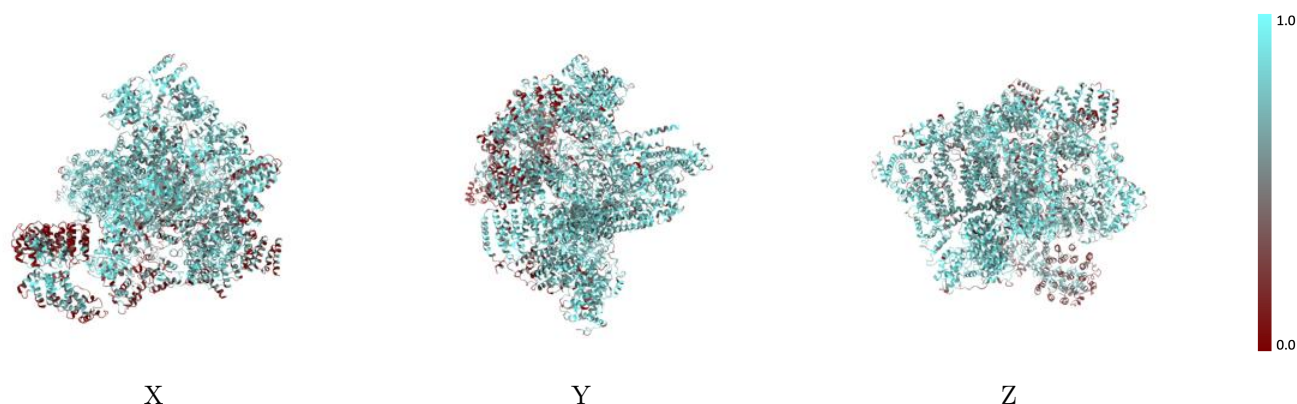
The images above show the 3D surface view of the map at the recommended contour level 0.004 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



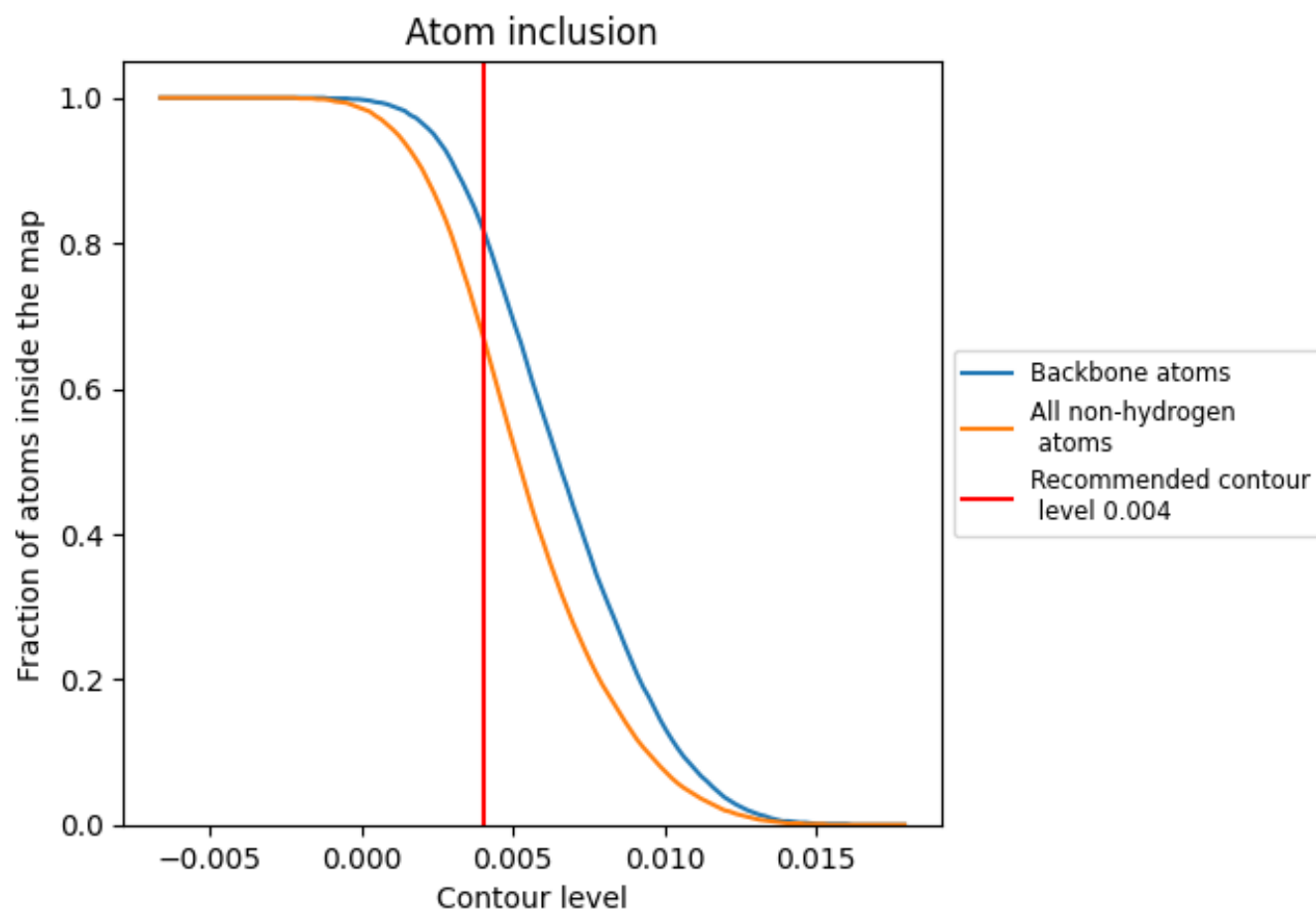
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.004).

9.4 Atom inclusion [i](#)



At the recommended contour level, 82% of all backbone atoms, 67% 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 (0.004) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6730	 0.1030
A	 0.7170	 0.0800
B	 0.5780	 0.0510
C	 0.5870	 0.0660
D	 0.6410	 0.0920
E	 0.6950	 0.0880
F	 0.7500	 0.1070
G	 0.5510	 0.0390
U	 0.8050	 0.1580
V	 0.6510	 0.1060
W	 0.6990	 0.1120
X	 0.6430	 0.1140
Y	 0.7680	 0.1310
Z	 0.7260	 0.1460
a	 0.7520	 0.1380
b	 0.7820	 0.1490
c	 0.7170	 0.1450
d	 0.7110	 0.1270
e	 0.4990	 0.0720
f	 0.4260	 0.0190

