



wwPDB EM Validation Summary Report ⓘ

Nov 5, 2022 – 08:04 AM EDT

PDB ID : 5VFO
EMDB ID : EMD-8662
Title : Nucleotide-driven Triple-state Remodeling of the AAA-ATPase Channel in the Activated Human 26S Proteasome
Authors : Zhu, Y.; Wang, W.L.; Yu, D.; Ouyang, Q.; Lu, Y.; Mao, Y.
Deposited on : 2017-04-08
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:

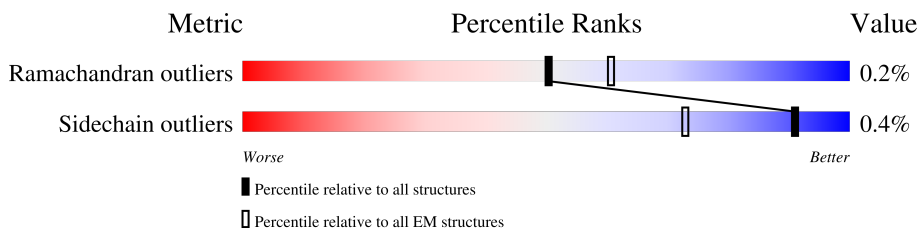
EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

1 Overall quality at a glance i

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)
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	G	240	38% (upper red bar), 99% (green bar), . (grey bar)
1	g	240	50% (upper red bar), 100% (green bar)
2	H	232	27% (upper red bar), 98% (green bar), .. (grey bar)
2	h	232	46% (upper red bar), 100% (green bar)
3	I	250	41% (upper red bar), 97% (green bar), .. (grey bar)
3	i	250	56% (upper red bar), 99% (green bar), . (grey bar)
4	J	243	45% (upper red bar), 97% (green bar), .. (grey bar)
4	j	243	60% (upper red bar), 97% (green bar), .. (grey bar)
5	K	234	41% (upper red bar), 94% (green bar), . . (grey bar)

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Mol	Chain	Length	Quality of chain
5	k	234	47% 97%
6	L	238	28% 100%
6	l	238	45% 100%
7	M	245	39% 97%
7	m	245	47% 98%
8	N	191	24% 99%
8	n	191	28% 100%
9	O	220	29% 98%
9	o	220	37% 99%
10	P	204	19% 100%
10	p	204	29% 100%
11	Q	199	32% 100%
11	q	199	31% 99%
12	R	201	20% 100%
12	r	201	25% 100%
13	S	213	30% 100%
13	s	213	26% 100%
14	T	215	24% 99%
14	t	215	24% 100%

2 Entry composition [i](#)

There are 14 unique types of molecules in this entry. The entry contains 47288 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 Proteasome subunit alpha type-6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	G	239	Total	C	N	O	S	0	0
			1820	1157	304	346	13		
1	g	240	Total	C	N	O	S	0	0
			1826	1160	305	348	13		

- Molecule 2 is a protein called Proteasome subunit alpha type-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	H	230	Total	C	N	O	S	0	0
			1688	1070	284	329	5		
2	h	232	Total	C	N	O	S	0	0
			1708	1081	289	333	5		

- Molecule 3 is a protein called Proteasome subunit alpha type-4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	I	248	Total	C	N	O	S	0	0
			1895	1195	324	368	8		
3	i	250	Total	C	N	O	S	0	0
			1912	1204	329	371	8		

- Molecule 4 is a protein called Proteasome subunit alpha type-7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	J	239	Total	C	N	O	S	0	0
			1704	1056	308	335	5		
4	j	239	Total	C	N	O	S	0	0
			1704	1056	308	335	5		

- Molecule 5 is a protein called Proteasome subunit alpha type-5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	K	228	1729	1086	284	349	10	0	0
5	k	228	1722	1080	284	348	10	0	0

- Molecule 6 is a protein called Proteasome subunit alpha type-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	L	238	1850	1159	334	346	11	0	0
6	l	238	1850	1159	334	346	11	0	0

- Molecule 7 is a protein called Proteasome subunit alpha type-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	M	240	1856	1178	314	353	11	0	0
7	m	240	1856	1178	314	353	11	0	0

- Molecule 8 is a protein called Proteasome subunit beta type-6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	N	191	1430	893	245	280	12	0	0
8	n	191	1430	893	245	280	12	0	0

- Molecule 9 is a protein called Proteasome subunit beta type-7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	O	220	1643	1033	280	318	12	0	0
9	o	220	1643	1033	280	318	12	0	0

- Molecule 10 is a protein called Proteasome subunit beta type-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	P	204	1585	1010	262	294	19	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	p	204	Total	C	N	O	S	0	0
			1585	1010	262	294	19		

- Molecule 11 is a protein called Proteasome subunit beta type-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	Q	199	Total	C	N	O	S	0	0
			1570	1006	265	290	9		
11	q	199	Total	C	N	O	S	0	0
			1570	1006	265	290	9		

- Molecule 12 is a protein called Proteasome subunit beta type-5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	R	201	Total	C	N	O	S	0	0
			1548	974	273	292	9		
12	r	201	Total	C	N	O	S	0	0
			1548	974	273	292	9		

- Molecule 13 is a protein called Proteasome subunit beta type-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	S	213	Total	C	N	O	S	0	0
			1641	1036	282	313	10		
13	s	213	Total	C	N	O	S	0	0
			1641	1036	282	313	10		

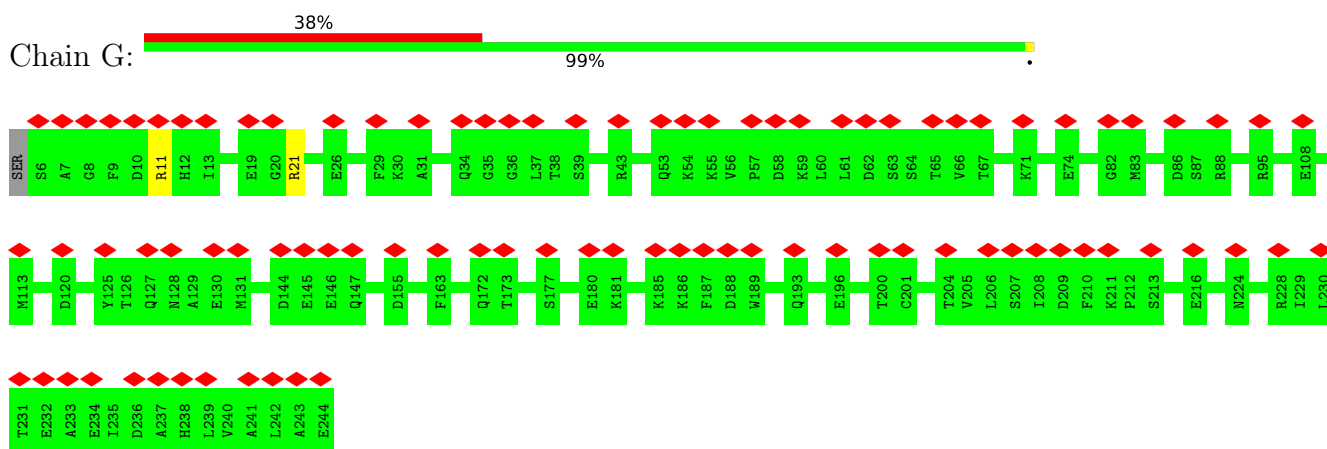
- Molecule 14 is a protein called Proteasome subunit beta type-4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	T	215	Total	C	N	O	S	0	0
			1667	1052	285	318	12		
14	t	215	Total	C	N	O	S	0	0
			1667	1052	285	318	12		

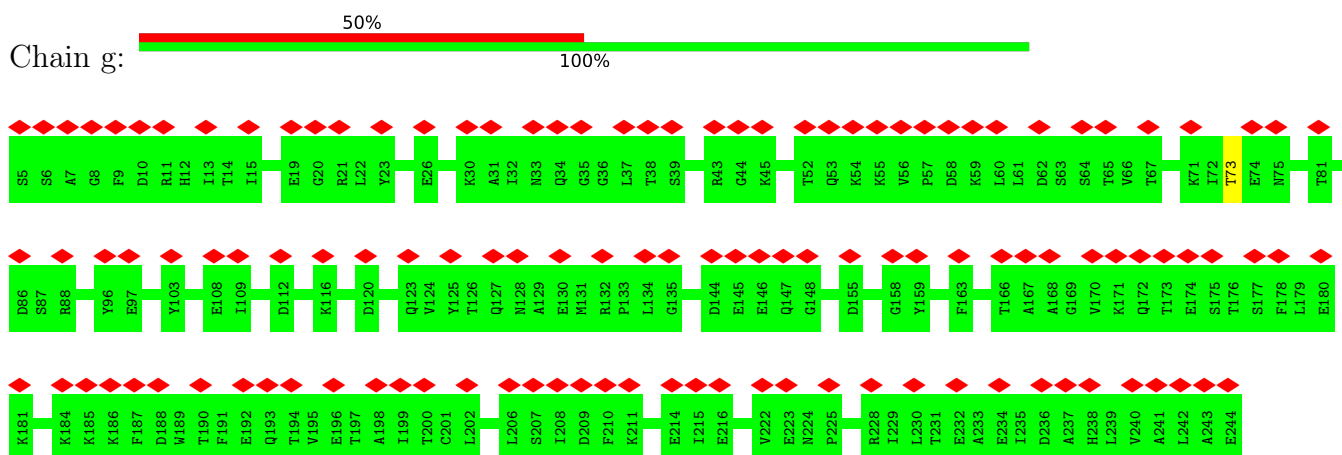
3 Residue-property plots [i](#)

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.

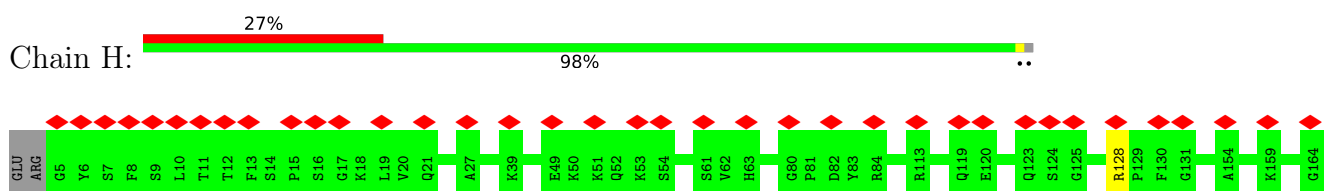
- Molecule 1: Proteasome subunit alpha type-6

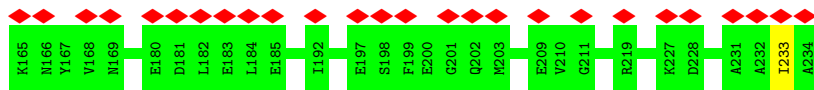


- Molecule 1: Proteasome subunit alpha type-6

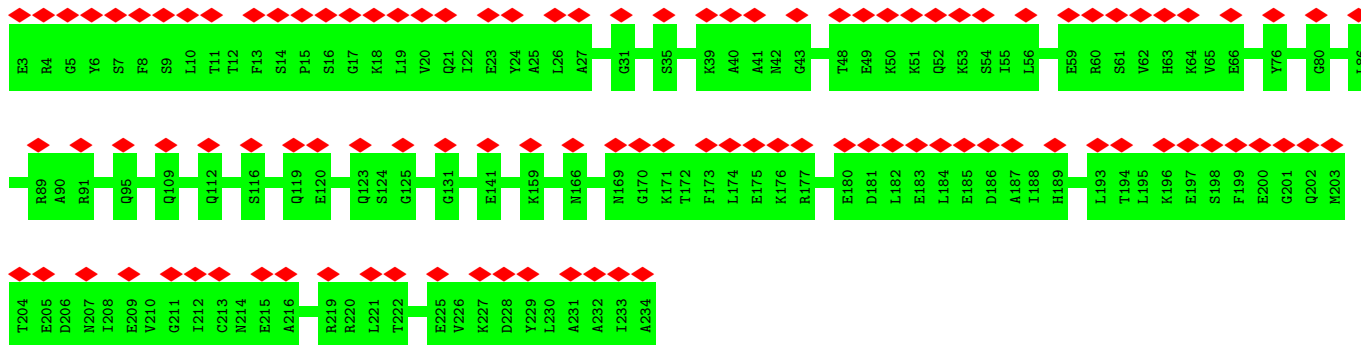


- Molecule 2: Proteasome subunit alpha type-2

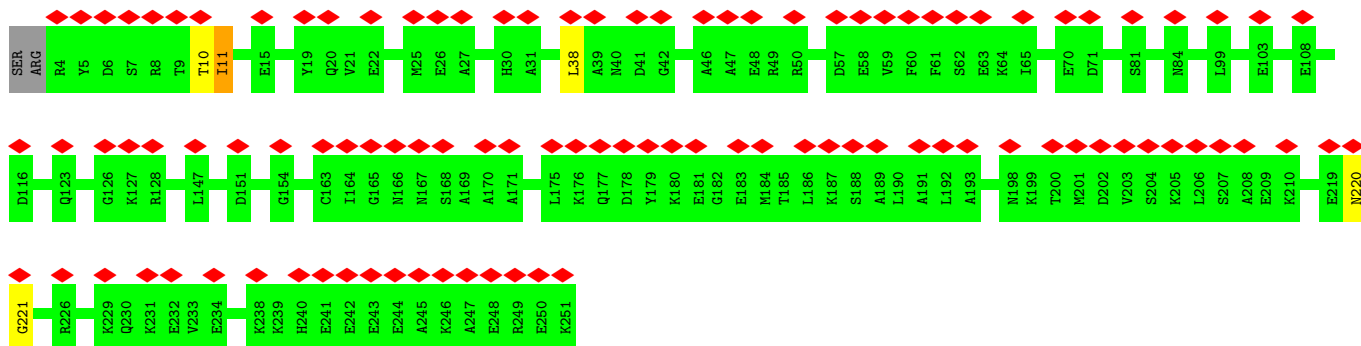
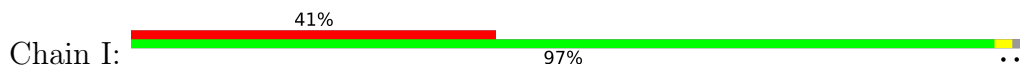




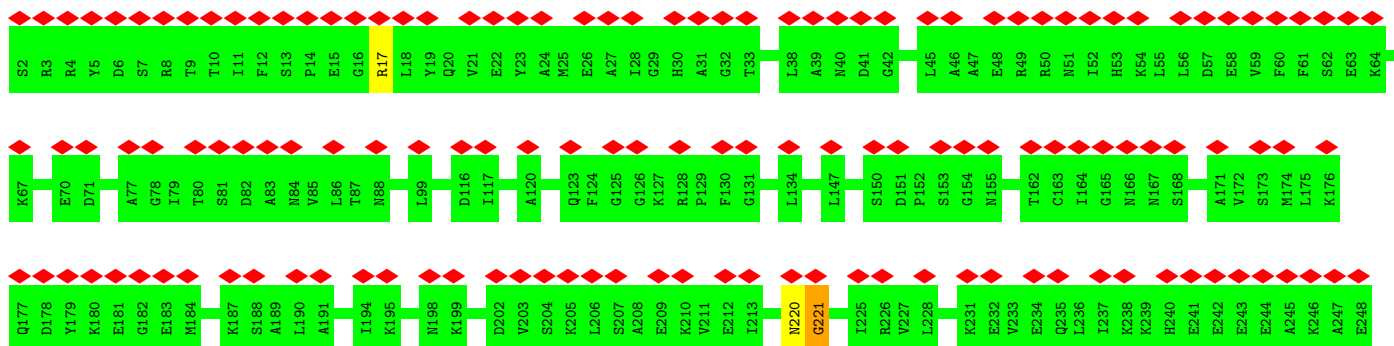
• Molecule 2: Proteasome subunit alpha type-2



• Molecule 3: Proteasome subunit alpha type-4

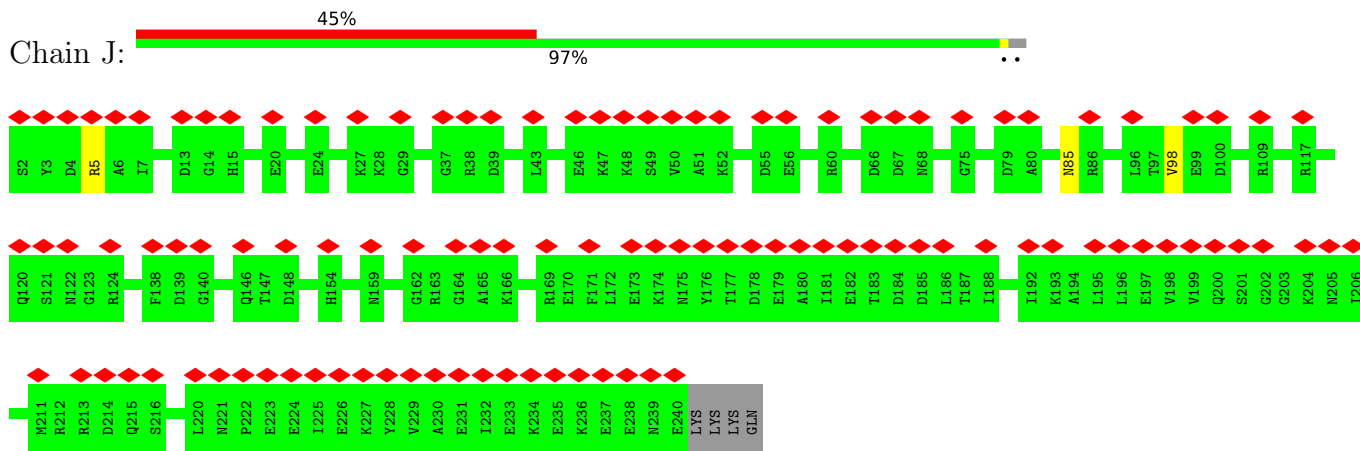


• Molecule 3: Proteasome subunit alpha type-4

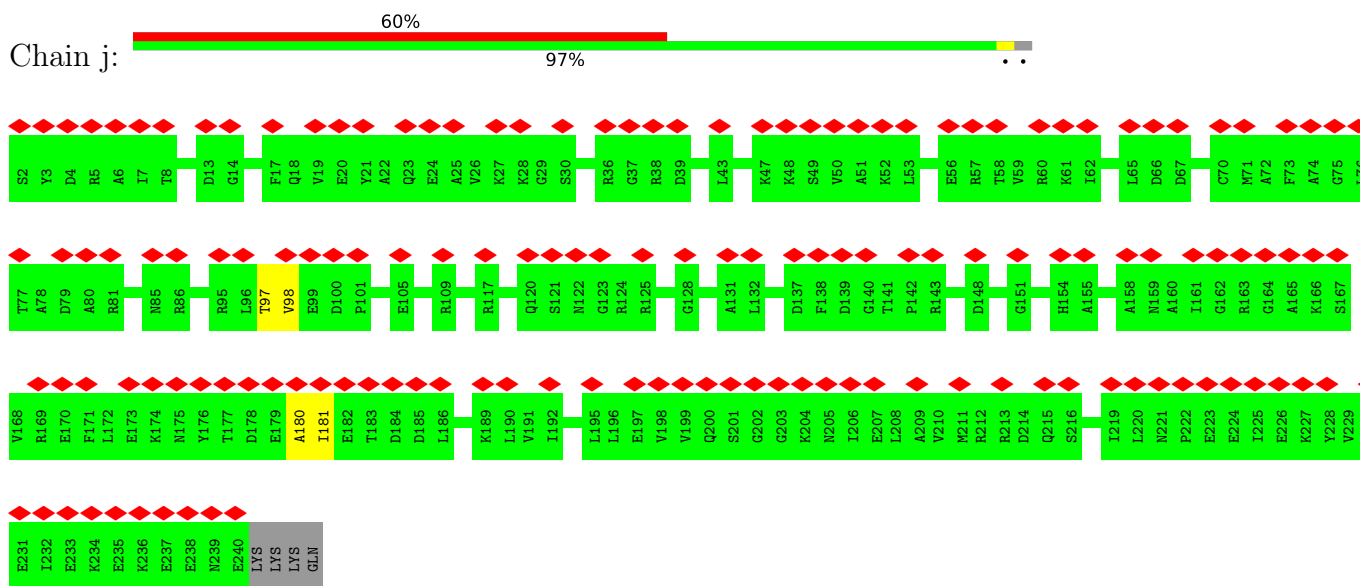




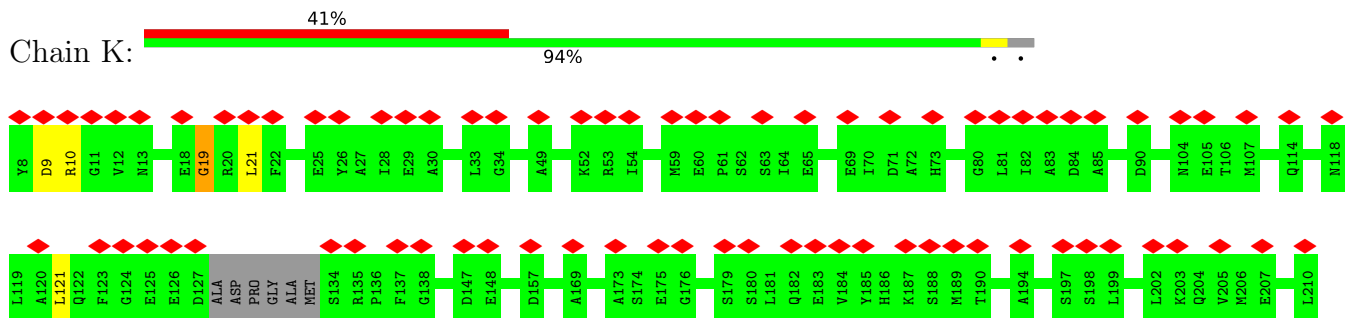
• Molecule 4: Proteasome subunit alpha type-7

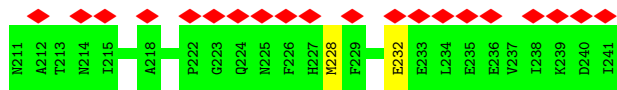


• Molecule 4: Proteasome subunit alpha type-7



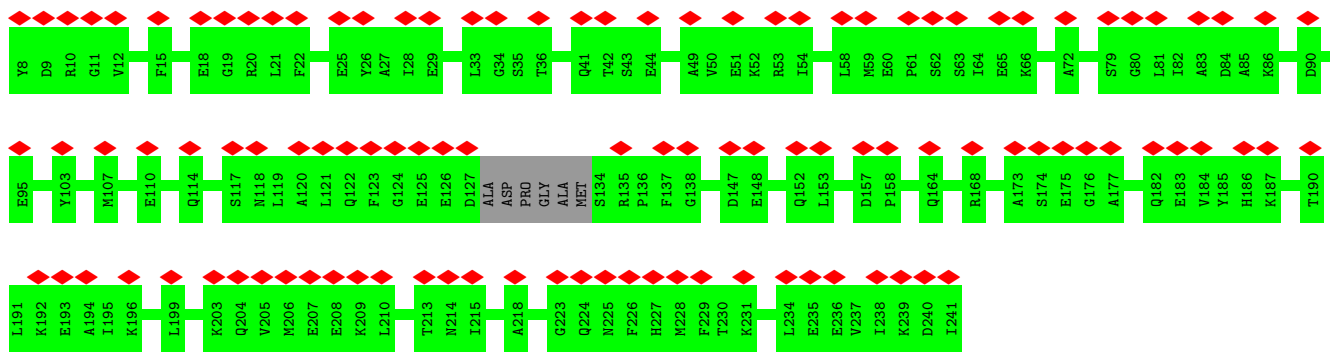
• Molecule 5: Proteasome subunit alpha type-5





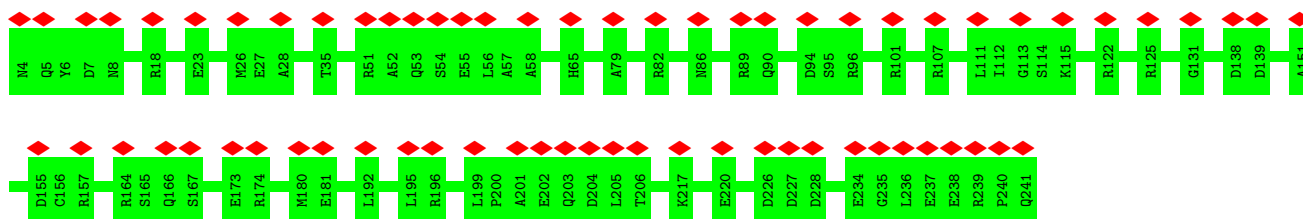
- Molecule 5: Proteasome subunit alpha type-5

Chain k: 47% 97%



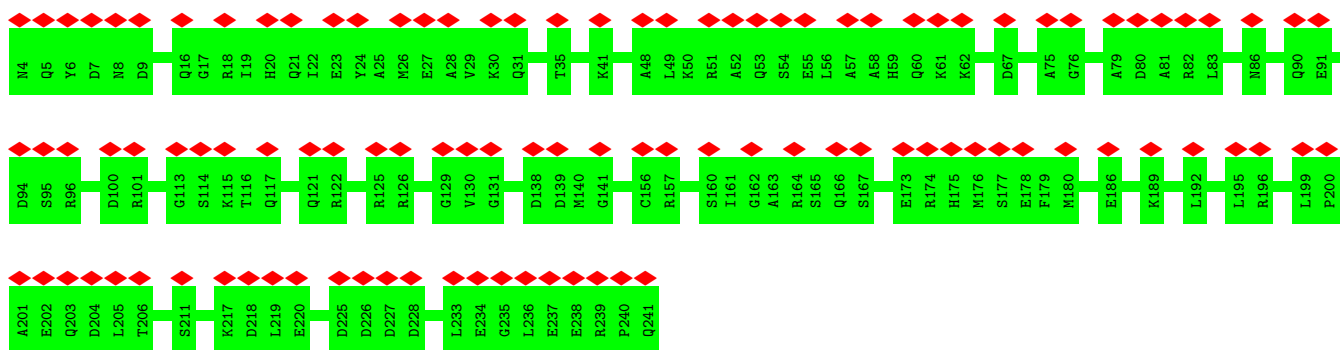
- Molecule 6: Proteasome subunit alpha type-1

Chain L: 28% 100%



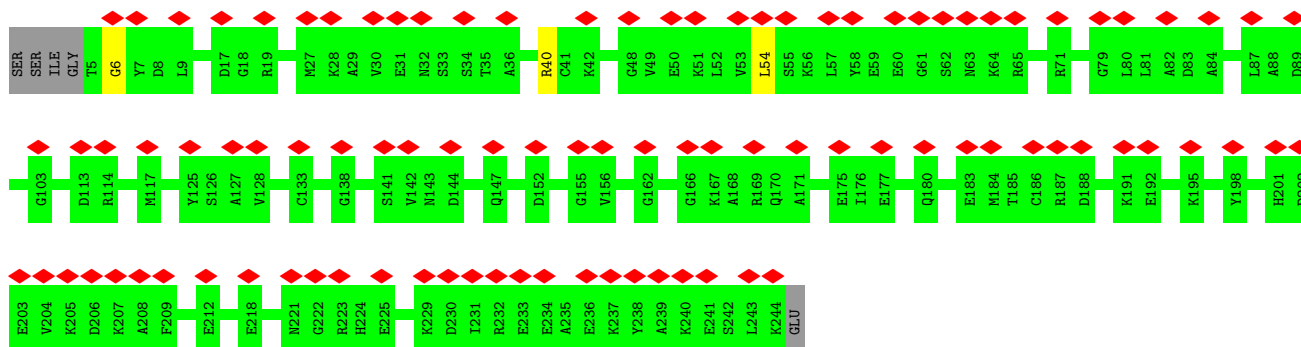
- Molecule 6: Proteasome subunit alpha type-1

Chain l: 45% 100%



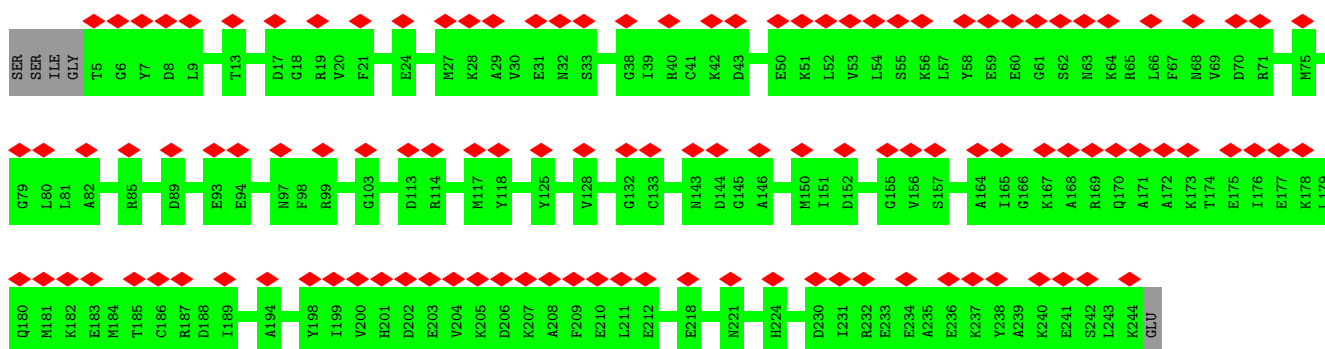
- Molecule 7: Proteasome subunit alpha type-3

Chain M: 39% 97%



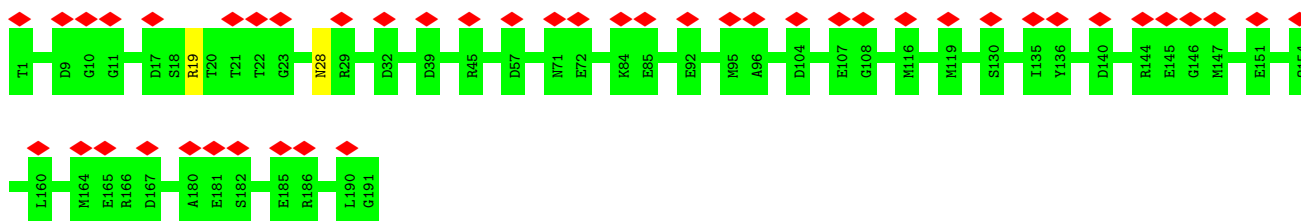
- Molecule 7: Proteasome subunit alpha type-3

Chain m: 47% 98%



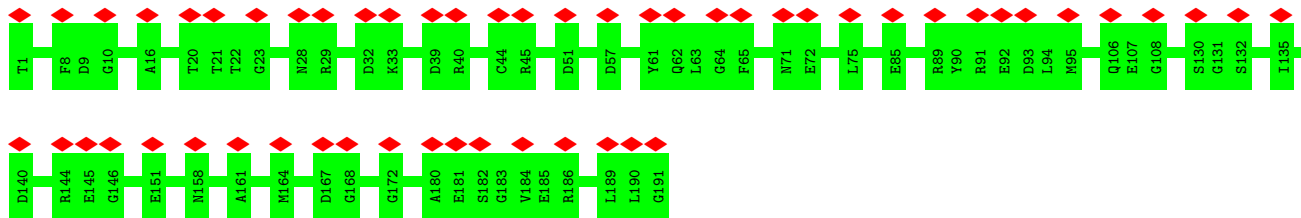
- Molecule 8: Proteasome subunit beta type-6

Chain N: 24% 99%

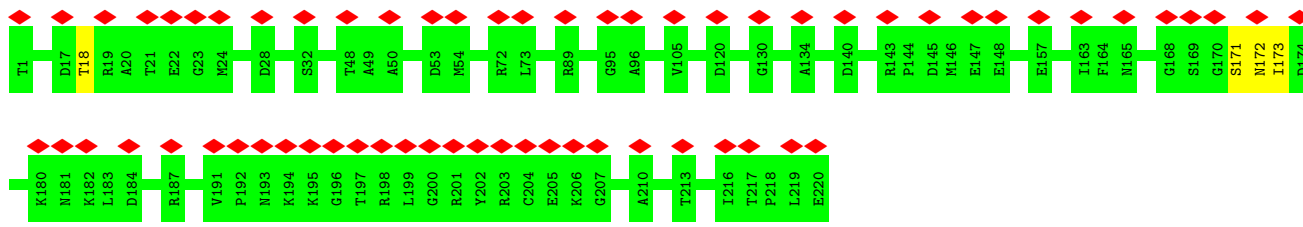


- Molecule 8: Proteasome subunit beta type-6

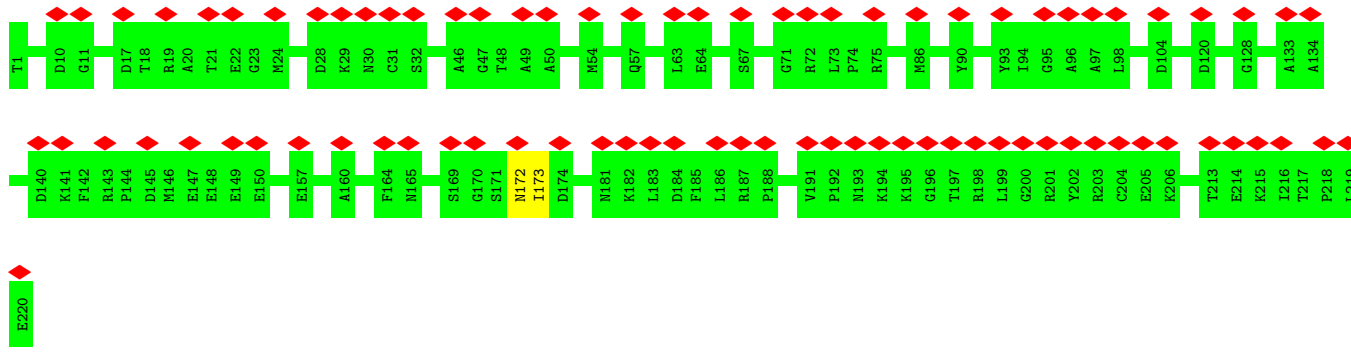
Chain n: 28% 100%



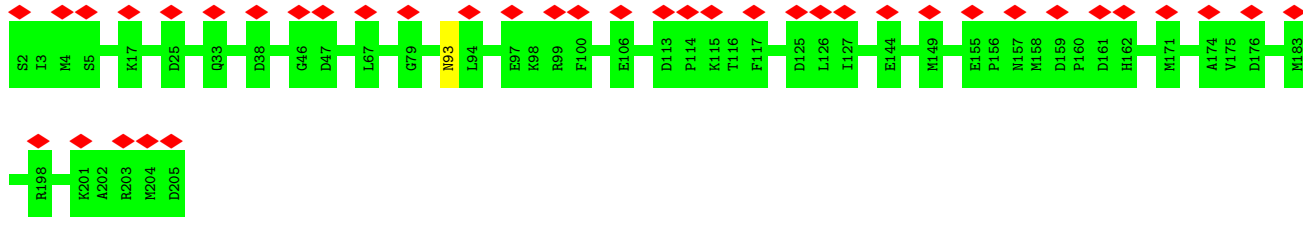
- Molecule 9: Proteasome subunit beta type-7



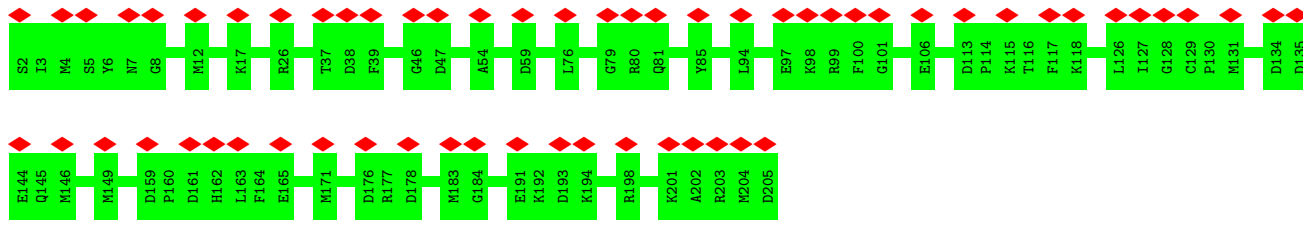
• Molecule 9: Proteasome subunit beta type-7



• Molecule 10: Proteasome subunit beta type-3

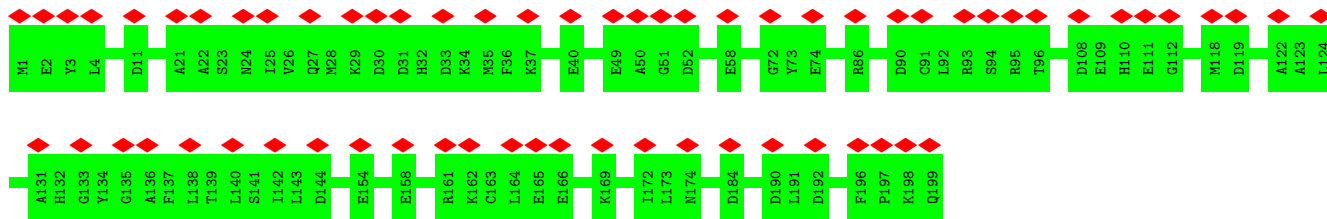


• Molecule 10: Proteasome subunit beta type-3

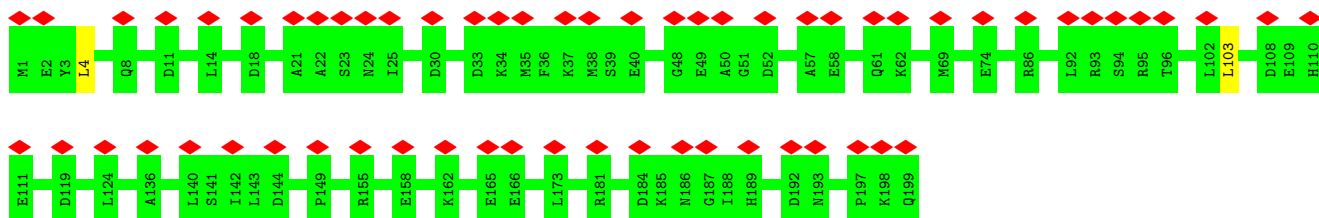


• Molecule 11: Proteasome subunit beta type-2

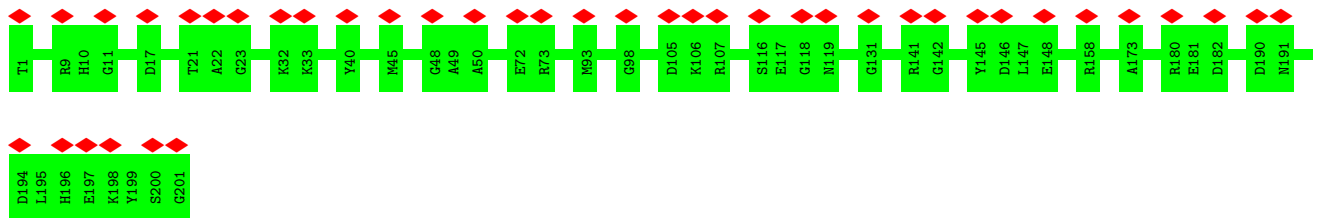




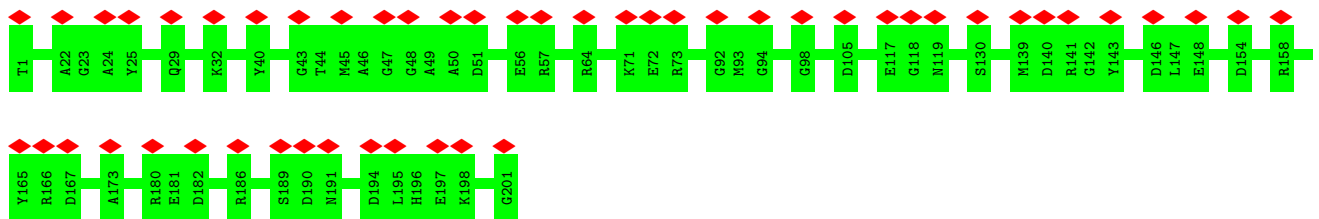
• Molecule 11: Proteasome subunit beta type-2



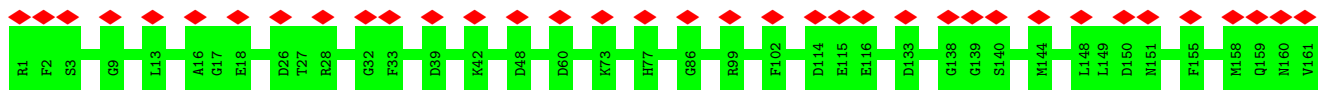
• Molecule 12: Proteasome subunit beta type-5

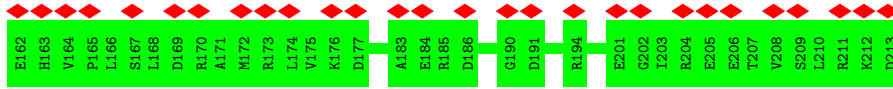


• Molecule 12: Proteasome subunit beta type-5

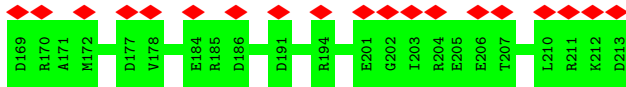
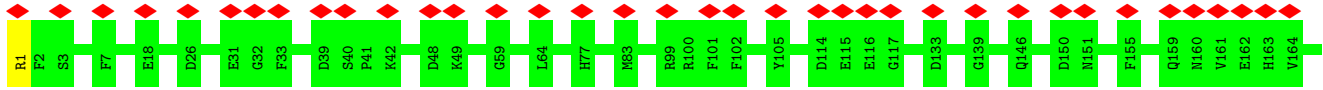


• Molecule 13: Proteasome subunit beta type-1

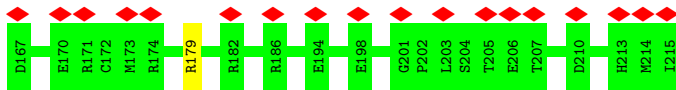
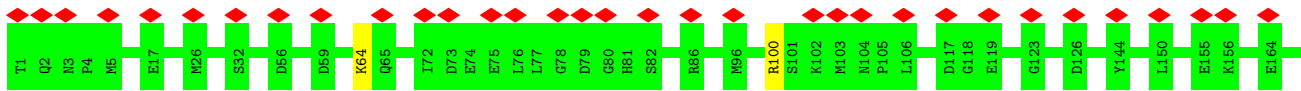




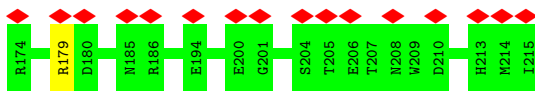
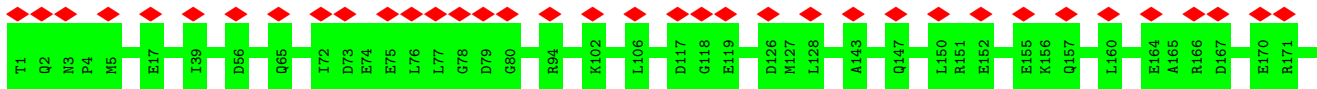
• Molecule 13: Proteasome subunit beta type-1



• Molecule 14: Proteasome subunit beta type-4



• Molecule 14: Proteasome subunit beta type-4



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	228086	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 ($e^-/\text{\AA}^2$)	30	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	0.027	Depositor
Minimum map value	-0.013	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	420.0, 420.0, 420.0	wwPDB
Map dimensions	560, 560, 560	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.75, 0.75, 0.75	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	G	0.45	0/1853	0.63	0/2515
1	g	0.42	0/1859	0.59	0/2523
2	H	0.47	0/1723	0.64	0/2346
2	h	0.44	0/1743	0.60	0/2372
3	I	0.46	0/1925	0.72	2/2606 (0.1%)
3	i	0.43	0/1942	0.67	0/2628
4	J	0.45	0/1728	0.65	0/2358
4	j	0.43	0/1728	0.58	0/2358
5	K	0.43	0/1755	0.69	2/2375 (0.1%)
5	k	0.40	0/1747	0.60	0/2364
6	L	0.47	0/1885	0.63	0/2552
6	l	0.45	0/1885	0.61	0/2552
7	M	0.49	0/1891	0.65	1/2552 (0.0%)
7	m	0.46	0/1891	0.60	0/2552
8	N	0.46	0/1454	0.59	0/1967
8	n	0.44	0/1454	0.58	0/1967
9	O	0.45	0/1670	0.60	0/2265
9	o	0.43	0/1670	0.62	0/2265
10	P	0.45	0/1614	0.56	0/2177
10	p	0.43	0/1614	0.56	0/2177
11	Q	0.49	0/1603	0.65	0/2174
11	q	0.47	0/1603	0.67	1/2174 (0.0%)
12	R	0.48	0/1579	0.56	0/2134
12	r	0.47	0/1579	0.55	0/2134
13	S	0.44	0/1671	0.58	0/2253
13	s	0.44	0/1671	0.57	0/2253
14	T	0.47	0/1700	0.57	0/2305
14	t	0.47	0/1700	0.58	0/2305
All	All	0.45	0/48137	0.61	6/65203 (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
3	I	0	3
3	i	0	2
4	j	0	1
5	K	0	4
9	O	0	2
9	o	0	1
All	All	0	13

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	K	21	LEU	C-N-CA	7.01	139.23	121.70
7	M	6	GLY	C-N-CA	6.49	137.91	121.70
3	I	38	LEU	CA-CB-CG	6.40	130.02	115.30
11	q	103	LEU	CA-CB-CG	5.85	128.76	115.30
5	K	19	GLY	C-N-CA	5.73	136.01	121.70

There are no chirality outliers.

5 of 13 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	I	10	THR	Peptide
3	I	220	ASN	Peptide
3	I	221	GLY	Peptide
5	K	19	GLY	Peptide
5	K	9	ASP	Peptide

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	G	237/240 (99%)	211 (89%)	26 (11%)	0	100	100
1	g	238/240 (99%)	217 (91%)	21 (9%)	0	100	100
2	H	228/232 (98%)	211 (92%)	16 (7%)	1 (0%)	34	72
2	h	230/232 (99%)	224 (97%)	6 (3%)	0	100	100
3	I	246/250 (98%)	220 (89%)	26 (11%)	0	100	100
3	i	248/250 (99%)	222 (90%)	25 (10%)	1 (0%)	34	72
4	J	237/243 (98%)	221 (93%)	15 (6%)	1 (0%)	34	72
4	j	237/243 (98%)	223 (94%)	11 (5%)	3 (1%)	12	48
5	K	224/234 (96%)	205 (92%)	18 (8%)	1 (0%)	34	72
5	k	224/234 (96%)	205 (92%)	19 (8%)	0	100	100
6	L	236/238 (99%)	225 (95%)	11 (5%)	0	100	100
6	l	236/238 (99%)	225 (95%)	11 (5%)	0	100	100
7	M	238/245 (97%)	218 (92%)	19 (8%)	1 (0%)	34	72
7	m	238/245 (97%)	222 (93%)	16 (7%)	0	100	100
8	N	189/191 (99%)	180 (95%)	8 (4%)	1 (0%)	29	68
8	n	189/191 (99%)	180 (95%)	9 (5%)	0	100	100
9	O	218/220 (99%)	204 (94%)	13 (6%)	1 (0%)	29	68
9	o	218/220 (99%)	205 (94%)	12 (6%)	1 (0%)	29	68
10	P	202/204 (99%)	188 (93%)	14 (7%)	0	100	100
10	p	202/204 (99%)	193 (96%)	9 (4%)	0	100	100
11	Q	197/199 (99%)	181 (92%)	16 (8%)	0	100	100
11	q	197/199 (99%)	181 (92%)	16 (8%)	0	100	100
12	R	199/201 (99%)	190 (96%)	9 (4%)	0	100	100
12	r	199/201 (99%)	188 (94%)	11 (6%)	0	100	100
13	S	211/213 (99%)	203 (96%)	8 (4%)	0	100	100
13	s	211/213 (99%)	205 (97%)	6 (3%)	0	100	100
14	T	213/215 (99%)	200 (94%)	13 (6%)	0	100	100
14	t	213/215 (99%)	202 (95%)	11 (5%)	0	100	100
All	All	6155/6250 (98%)	5749 (93%)	395 (6%)	11 (0%)	50	81

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	J	98	VAL
9	O	173	ILE
9	o	173	ILE
5	K	10	ARG
8	N	19	ARG

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	G	192/205 (94%)	190 (99%)	2 (1%)	76	88
1	g	193/205 (94%)	192 (100%)	1 (0%)	88	94
2	H	162/190 (85%)	161 (99%)	1 (1%)	86	94
2	h	164/190 (86%)	164 (100%)	0	100	100
3	I	191/210 (91%)	190 (100%)	1 (0%)	88	94
3	i	193/210 (92%)	192 (100%)	1 (0%)	88	94
4	J	152/207 (73%)	150 (99%)	2 (1%)	69	86
4	j	152/207 (73%)	152 (100%)	0	100	100
5	K	187/196 (95%)	186 (100%)	1 (0%)	88	94
5	k	186/196 (95%)	186 (100%)	0	100	100
6	L	198/204 (97%)	198 (100%)	0	100	100
6	l	198/204 (97%)	198 (100%)	0	100	100
7	M	192/202 (95%)	191 (100%)	1 (0%)	88	94
7	m	192/202 (95%)	192 (100%)	0	100	100
8	N	148/148 (100%)	147 (99%)	1 (1%)	84	93
8	n	148/148 (100%)	148 (100%)	0	100	100
9	O	177/181 (98%)	176 (99%)	1 (1%)	86	94
9	o	177/181 (98%)	177 (100%)	0	100	100
10	P	172/173 (99%)	171 (99%)	1 (1%)	86	94
10	p	172/173 (99%)	172 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	Q	164/170 (96%)	164 (100%)	0	100	100
11	q	164/170 (96%)	163 (99%)	1 (1%)	86	94
12	R	153/156 (98%)	153 (100%)	0	100	100
12	r	153/156 (98%)	153 (100%)	0	100	100
13	S	174/178 (98%)	174 (100%)	0	100	100
13	s	174/178 (98%)	173 (99%)	1 (1%)	86	94
14	T	175/178 (98%)	172 (98%)	3 (2%)	60	82
14	t	175/178 (98%)	174 (99%)	1 (1%)	86	94
All	All	4878/5196 (94%)	4859 (100%)	19 (0%)	91	96

5 of 19 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	g	73	THR
13	s	1	ARG
14	t	179	ARG
11	q	4	LEU
8	N	28	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 25 such sidechains are listed below:

Mol	Chain	Res	Type
8	N	154	GLN
3	i	167	ASN
10	p	93	ASN
3	i	146	GLN
5	k	114	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 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.

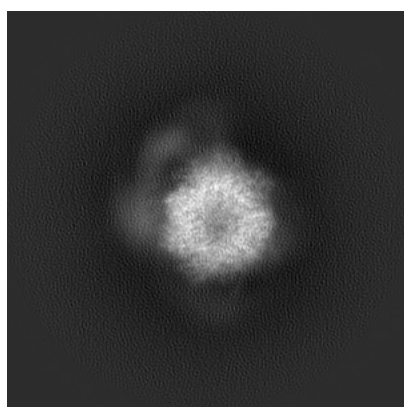
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8662. These allow visual inspection of the internal detail of the map and identification of artifacts.

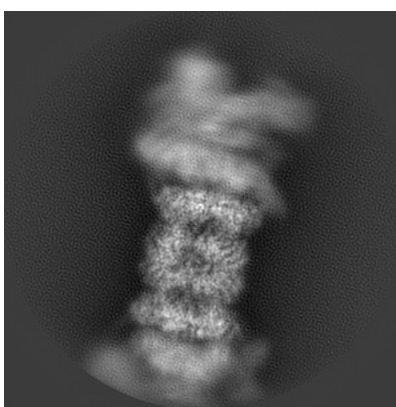
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

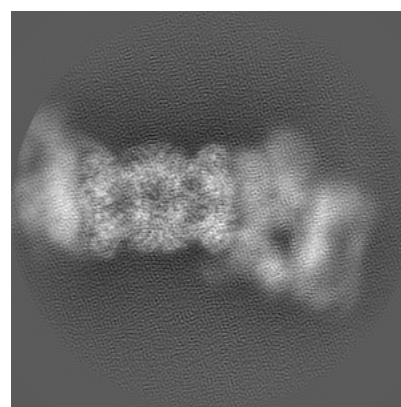
6.1.1 Primary map



X



Y

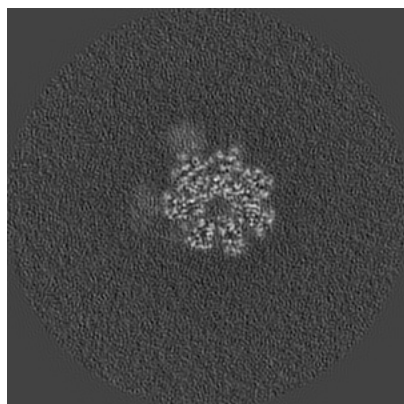


Z

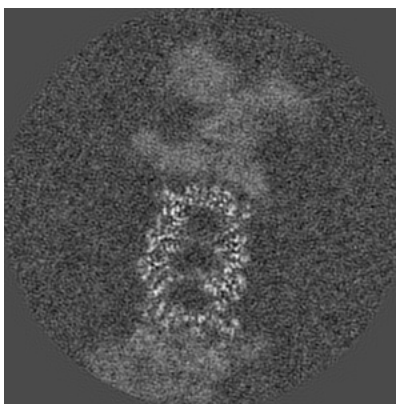
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

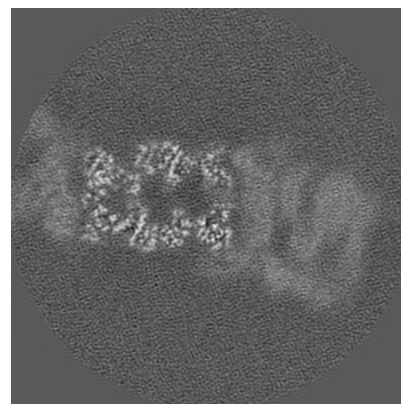
6.2.1 Primary map



X Index: 280



Y Index: 280

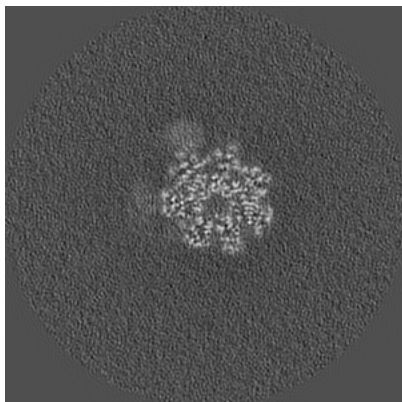


Z Index: 280

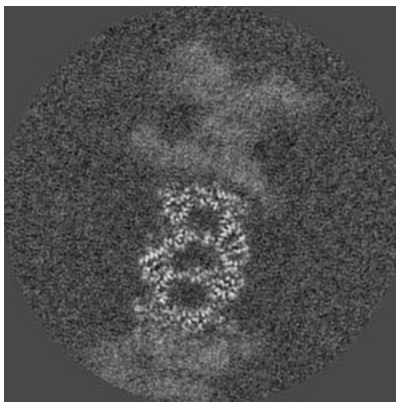
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

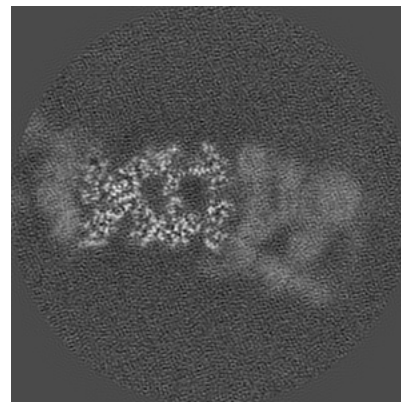
6.3.1 Primary map



X Index: 281



Y Index: 275



Z Index: 296

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

6.4 Orthogonal surface views [i](#)

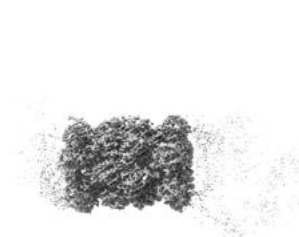
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.01. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

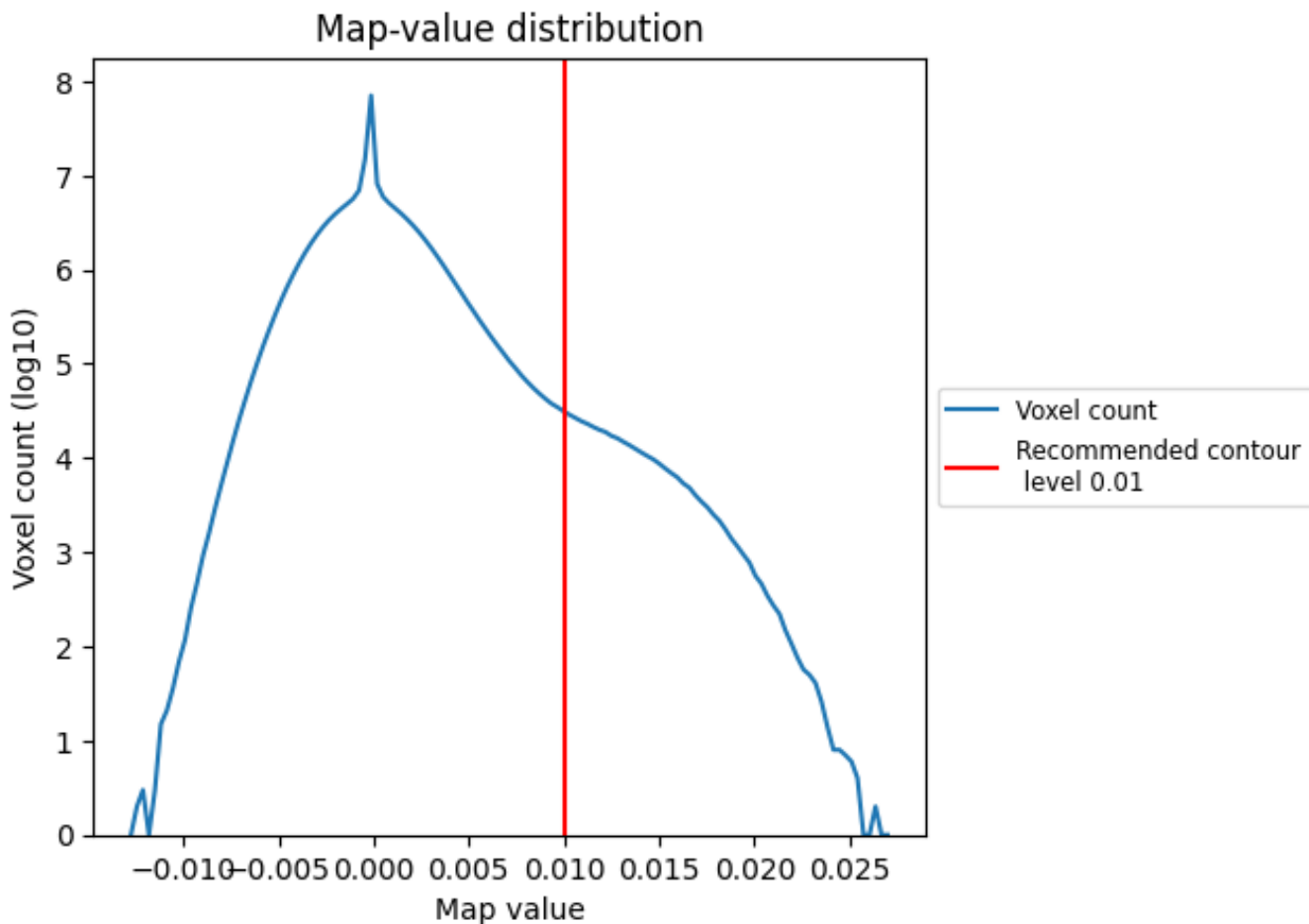
6.5 Mask visualisation

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

7 Map analysis [i](#)

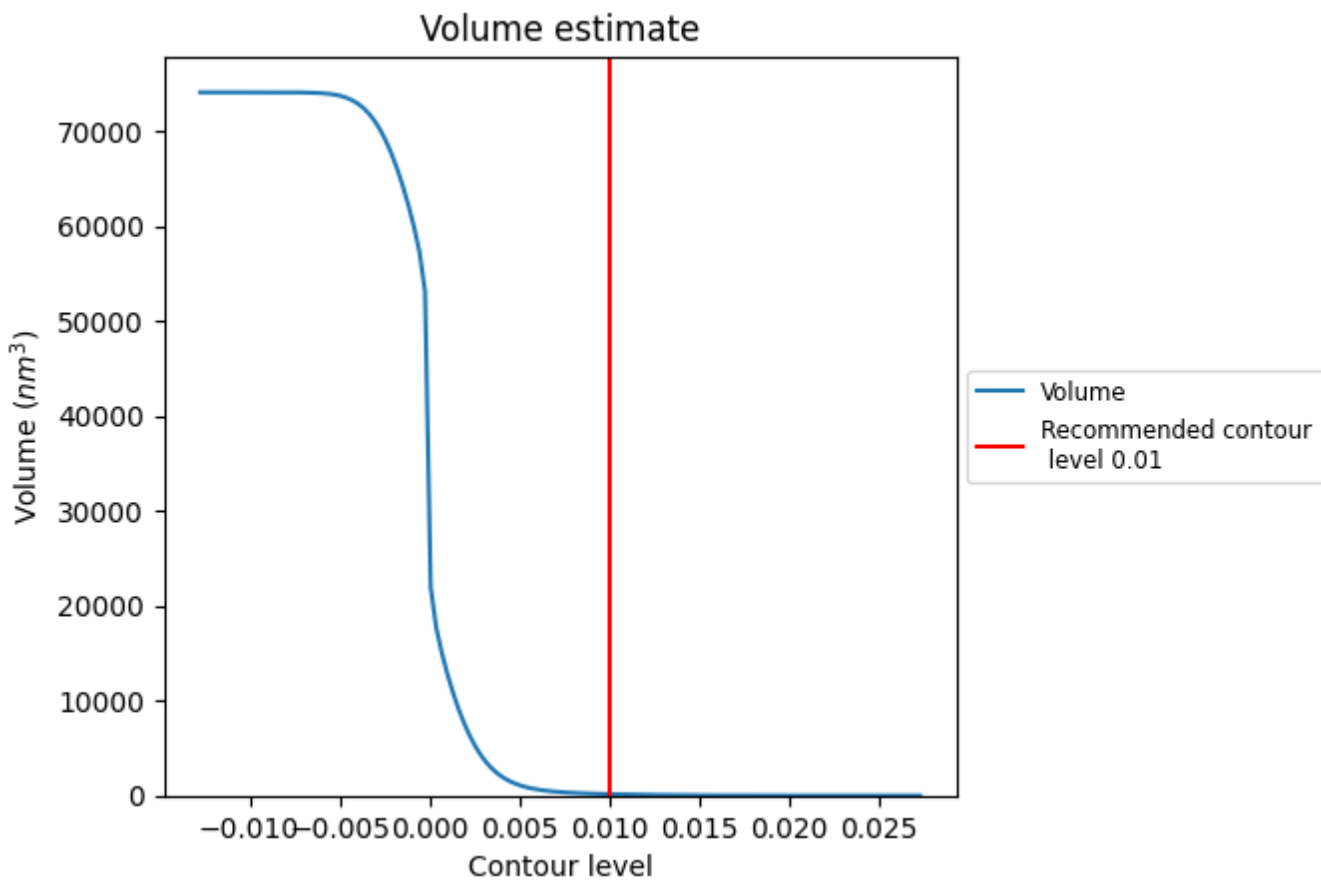
This section contains the results of statistical analysis of the map.

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.

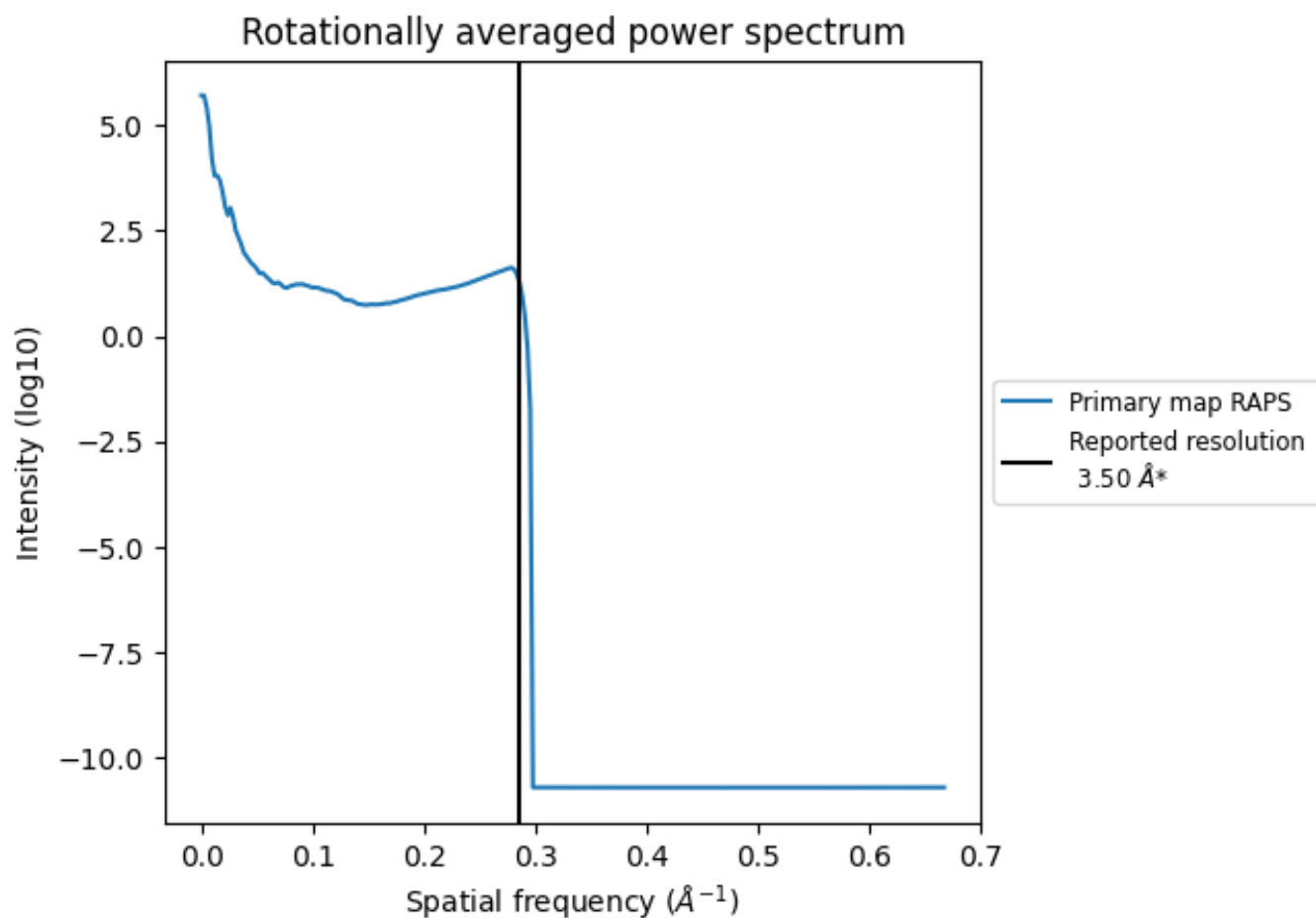
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 153 nm³; this corresponds to an approximate mass of 138 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 [i](#)



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

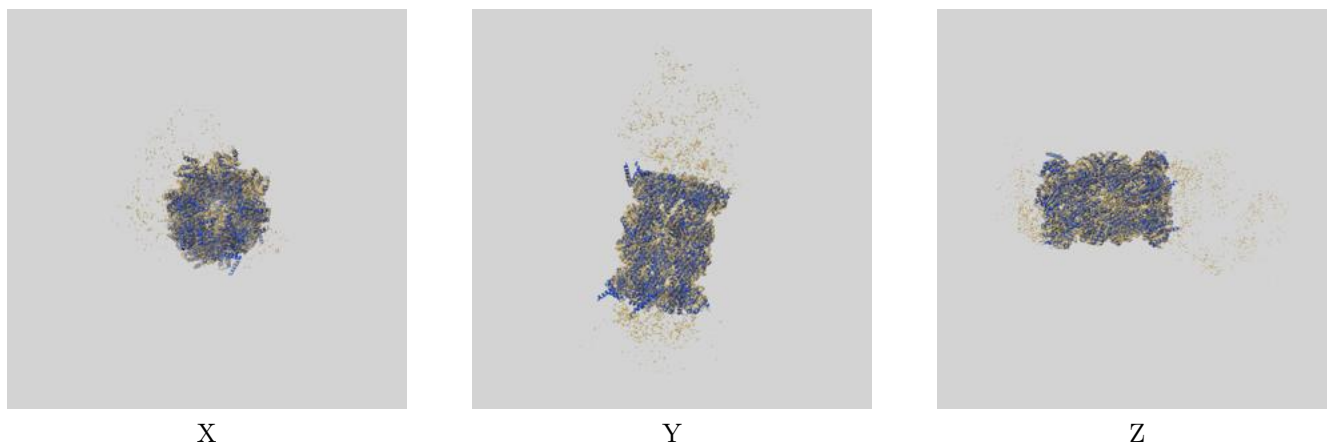
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

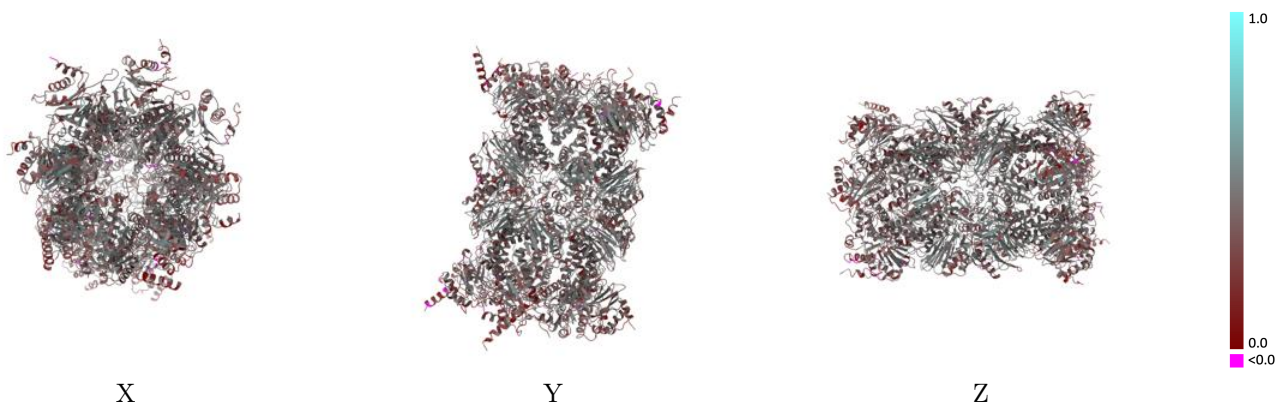
This section contains information regarding the fit between EMDB map EMD-8662 and PDB model 5VFO. Per-residue inclusion information can be found in section 3 on page 7.

9.1 Map-model overlay [i](#)



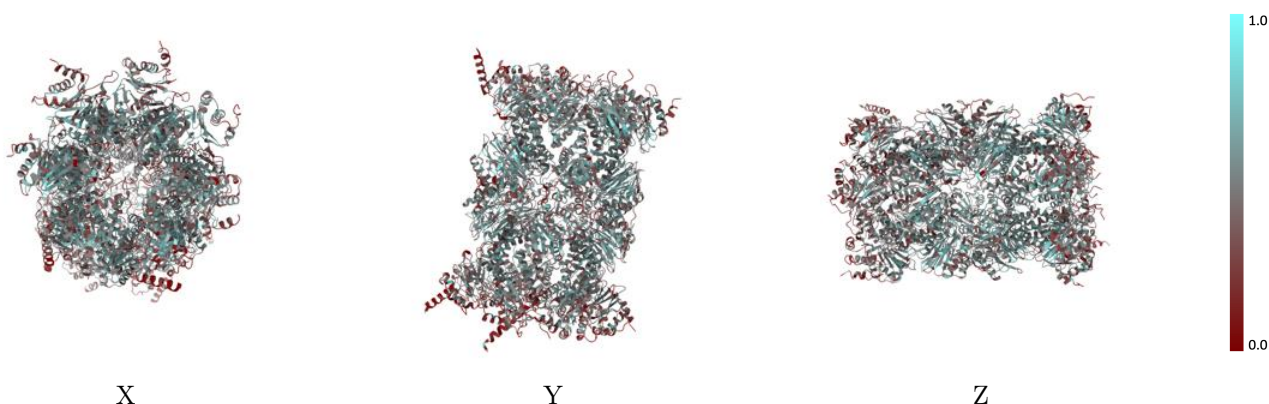
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



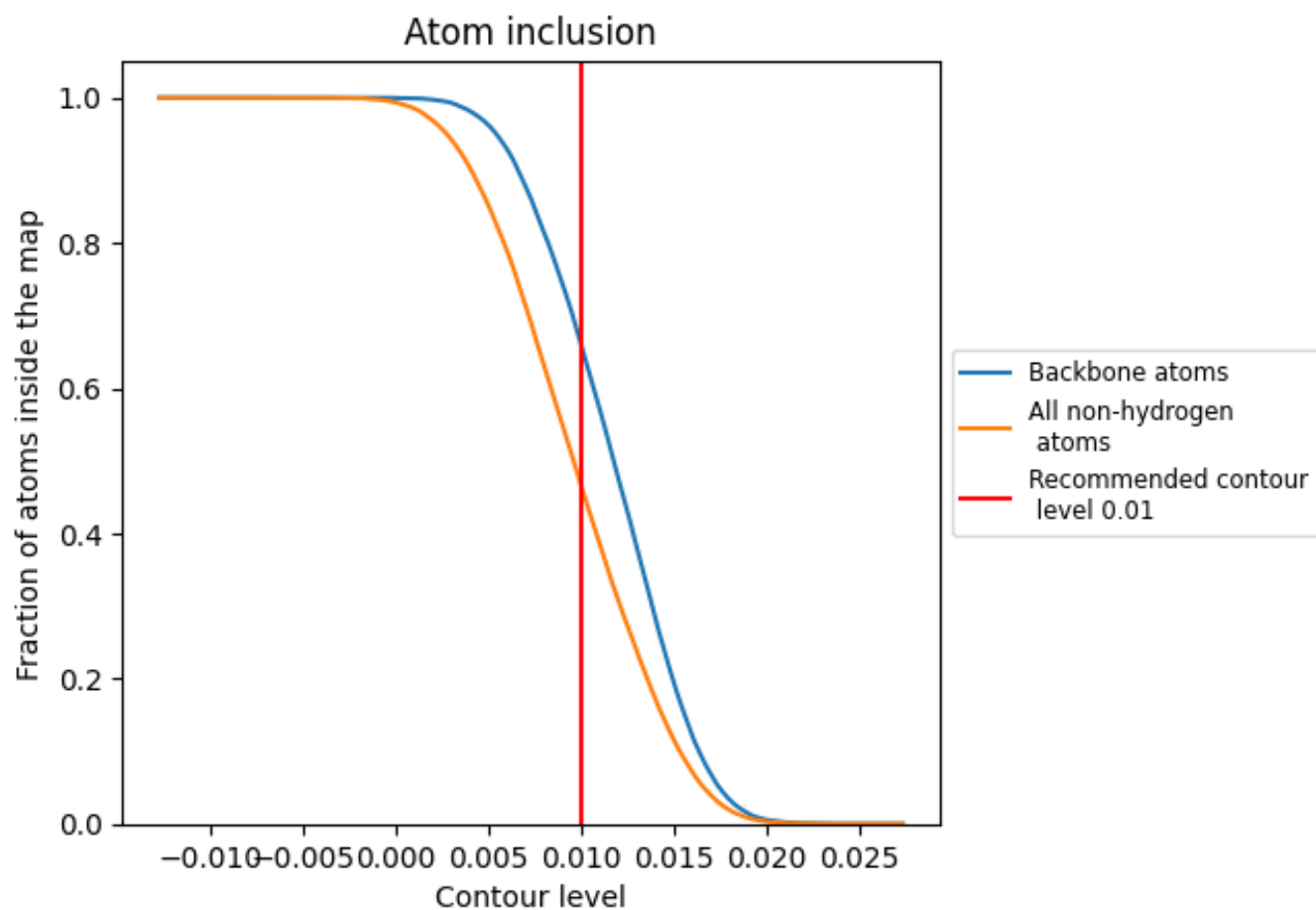
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.01).



























































9.4 Atom inclusion [i](#)



At the recommended contour level, 66% of all backbone atoms, 46% 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 (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.4632	 0.3940
G	 0.4559	 0.3890
H	 0.4904	 0.4030
I	 0.4459	 0.3710
J	 0.4190	 0.3650
K	 0.4328	 0.3660
L	 0.5003	 0.4000
M	 0.4612	 0.3780
N	 0.5279	 0.4240
O	 0.4820	 0.4190
P	 0.5289	 0.4320
Q	 0.4990	 0.4000
R	 0.5434	 0.4240
S	 0.4835	 0.4210
T	 0.5367	 0.4340
g	 0.3931	 0.3730
h	 0.4184	 0.3770
i	 0.3655	 0.3470
j	 0.3517	 0.3370
k	 0.4015	 0.3530
l	 0.4294	 0.3610
m	 0.4007	 0.3560
n	 0.5050	 0.4230
o	 0.4480	 0.3950
p	 0.4897	 0.4220
q	 0.4997	 0.4190
r	 0.5220	 0.4220
s	 0.4916	 0.4300
t	 0.5237	 0.4240

