



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 05:57 AM UTC

PDB ID : 5VHF / pdb_00005vhf
EMDB ID : EMD-8674
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 : 5.70 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:

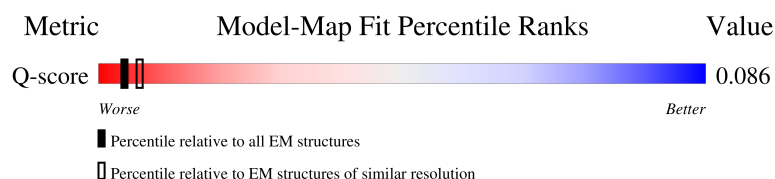
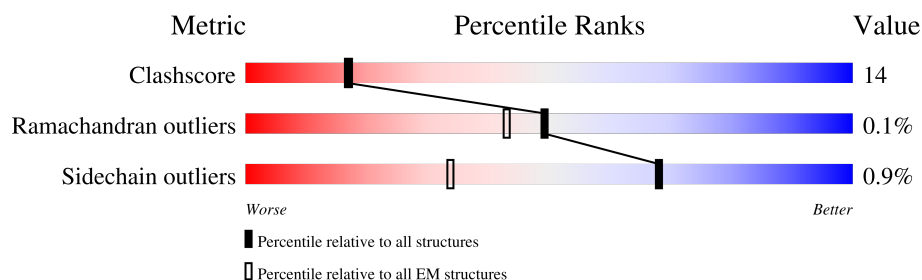
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 5.70 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	503 (5.20 - 6.20)

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	223	95% 69% 29% .
2	A	352	74% 66% 31% .
3	B	340	78% 69% 28% ..
4	C	385	65% 64% 25% 11%

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Mol	Chain	Length	Quality of chain
5	D	368	
6	E	379	
7	F	380	
8	U	841	
9	V	183	
10	W	456	
11	X	385	
12	Y	378	
13	Z	286	
14	a	374	
15	b	191	
16	c	287	
17	d	136	
18	e	70	
19	f	848	

2 Entry composition

There are 20 unique types of molecules in this entry. The entry contains 51096 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 non-ATPase regulatory subunit 10.

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

- Molecule 2 is a protein called 26S proteasome regulatory subunit 7.

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

- Molecule 3 is a protein called 26S proteasome regulatory subunit 4.

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

- Molecule 4 is a protein called 26S proteasome regulatory subunit 8.

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

- Molecule 5 is a protein called 26S proteasome regulatory subunit 6B.

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

- Molecule 6 is a protein called 26S proteasome regulatory subunit 10B.

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

- Molecule 7 is a protein called 26S proteasome regulatory subunit 6A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	F	359	Total	C	N	O	S	0	0
			2808	1772	488	531	17		

- Molecule 8 is a protein called 26S proteasome non-ATPase regulatory subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	U	751	Total	C	N	O	S	0	0
			5829	3696	1001	1088	44		

- Molecule 9 is a protein called 26S proteasome non-ATPase regulatory subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	V	183	Total	C	N	O	S	0	0
			1480	949	260	265	6		

- Molecule 10 is a protein called 26S proteasome non-ATPase regulatory subunit 12.

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

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

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

- Molecule 12 is a protein called 26S proteasome non-ATPase regulatory subunit 6.

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

- Molecule 13 is a protein called 26S proteasome non-ATPase regulatory subunit 7.

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

- Molecule 14 is a protein called 26S proteasome non-ATPase regulatory subunit 13.

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

- Molecule 15 is a protein called 26S proteasome non-ATPase regulatory subunit 4.

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

- Molecule 16 is a protein called 26S proteasome non-ATPase regulatory subunit 14.

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

- Molecule 17 is a protein called 26S proteasome non-ATPase regulatory subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	d	136	Total	C	N	O	S	0	0
			1109	720	176	209	4		

- Molecule 18 is a protein called 26S proteasome complex subunit SEM1.

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

- 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		

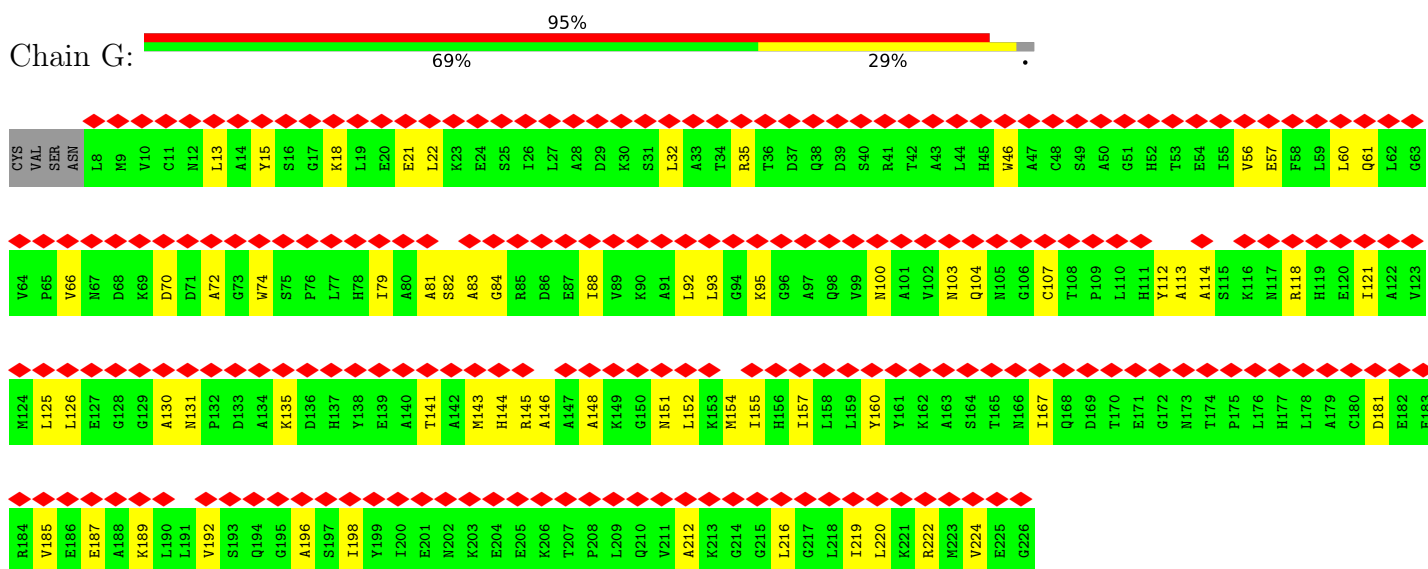
- Molecule 20 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

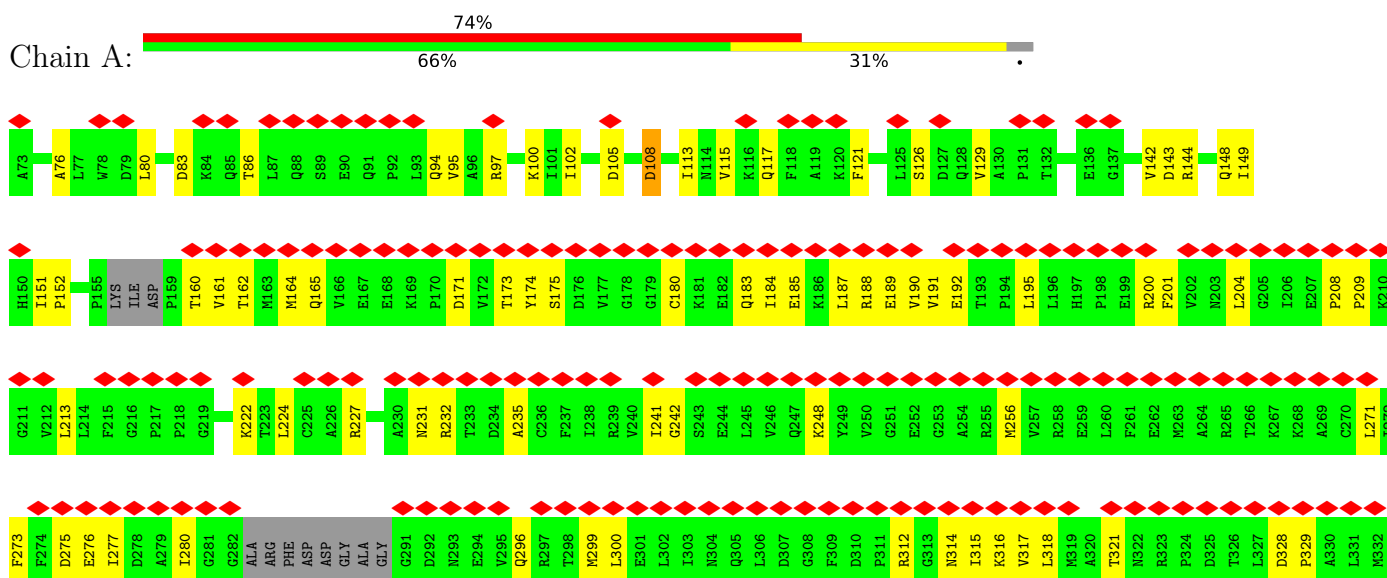
3 Residue-property plots

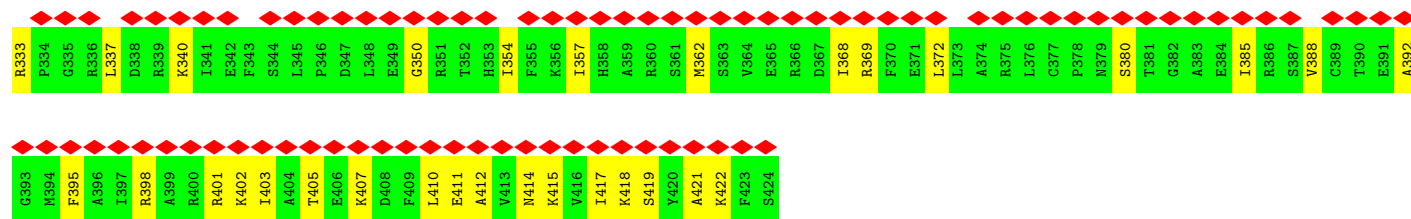
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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 non-ATPase regulatory subunit 10

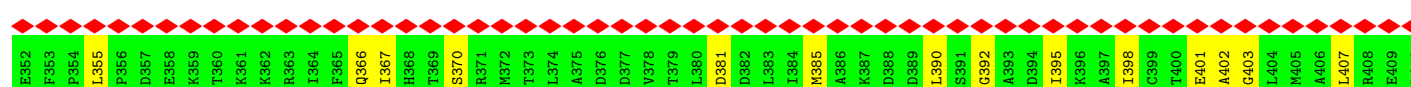
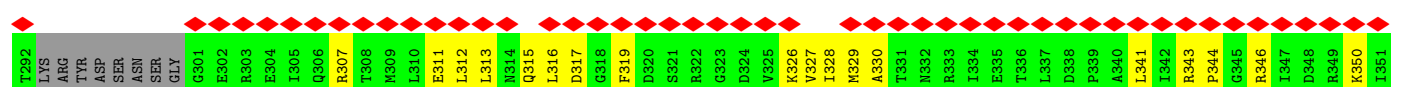
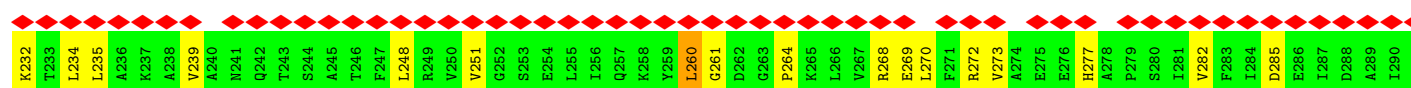
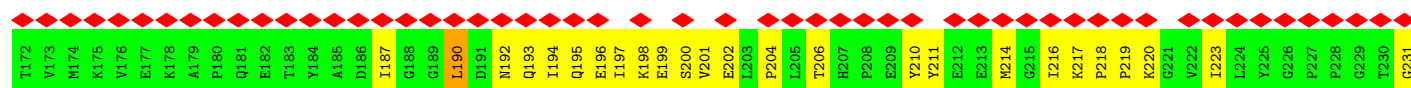
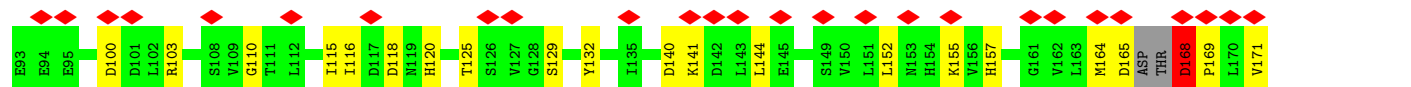
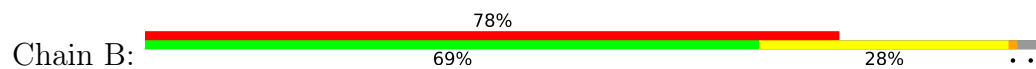


- Molecule 2: 26S proteasome regulatory subunit 7

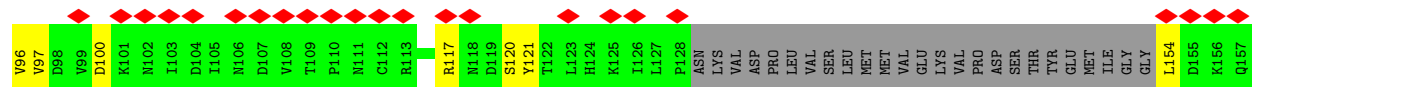
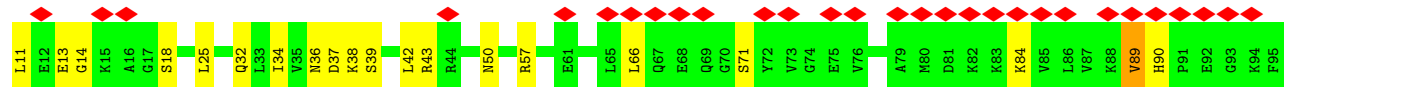




• Molecule 3: 26S proteasome regulatory subunit 4

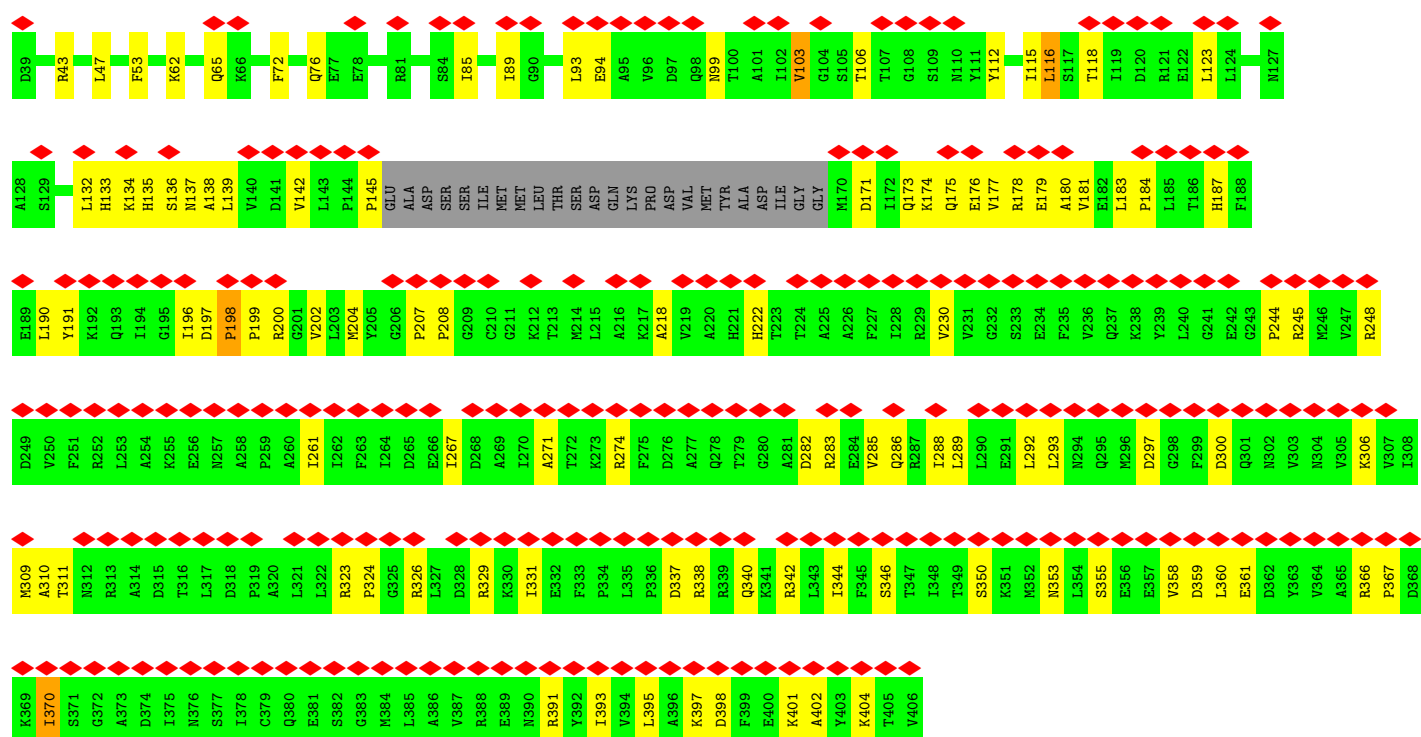


• Molecule 4: 26S proteasome regulatory subunit 8

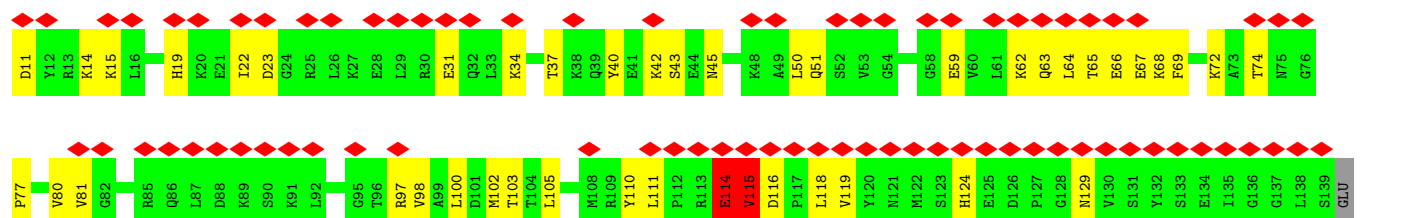


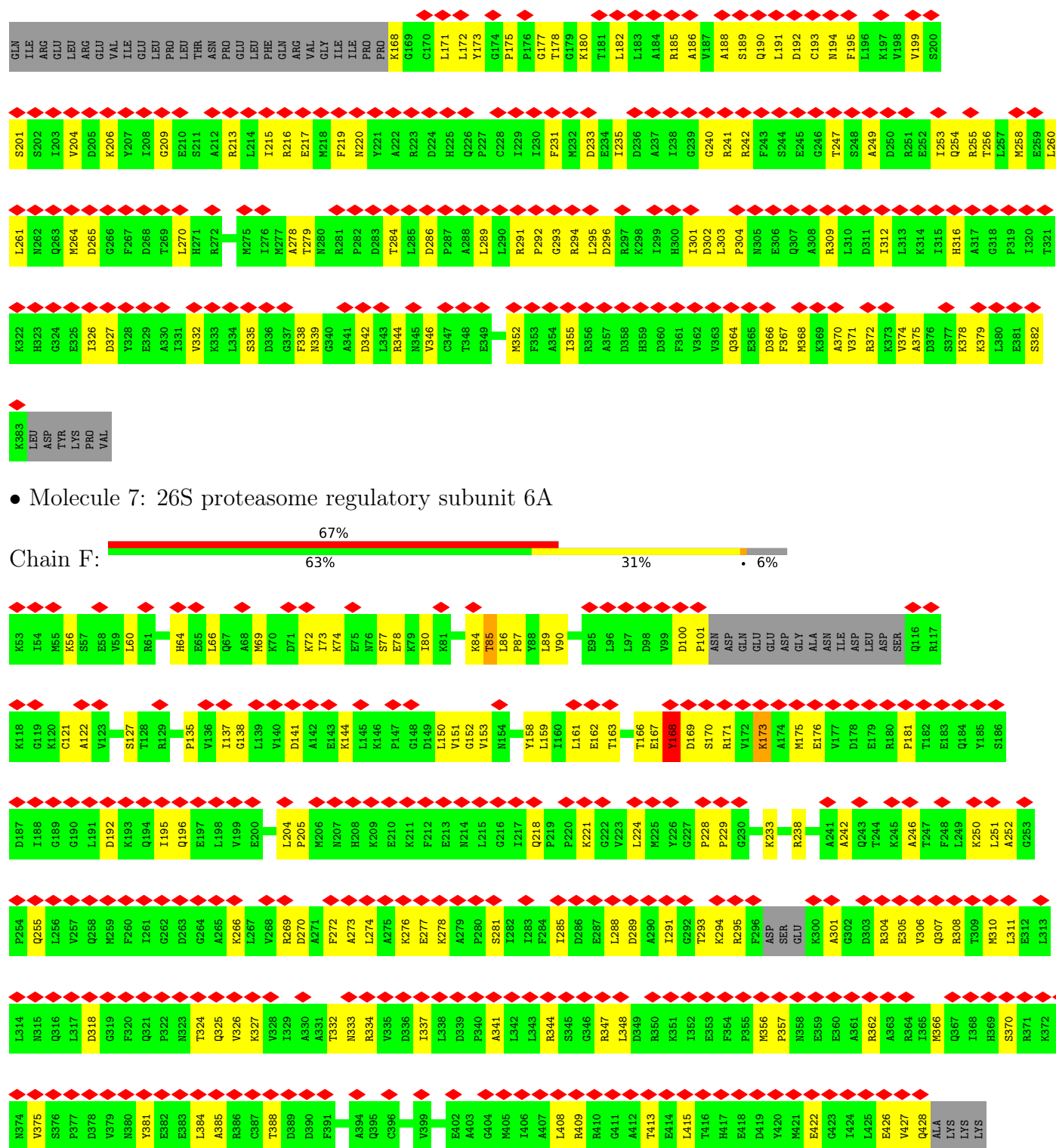


• Molecule 5: 26S proteasome regulatory subunit 6B



• Molecule 6: 26S proteasome regulatory subunit 10B





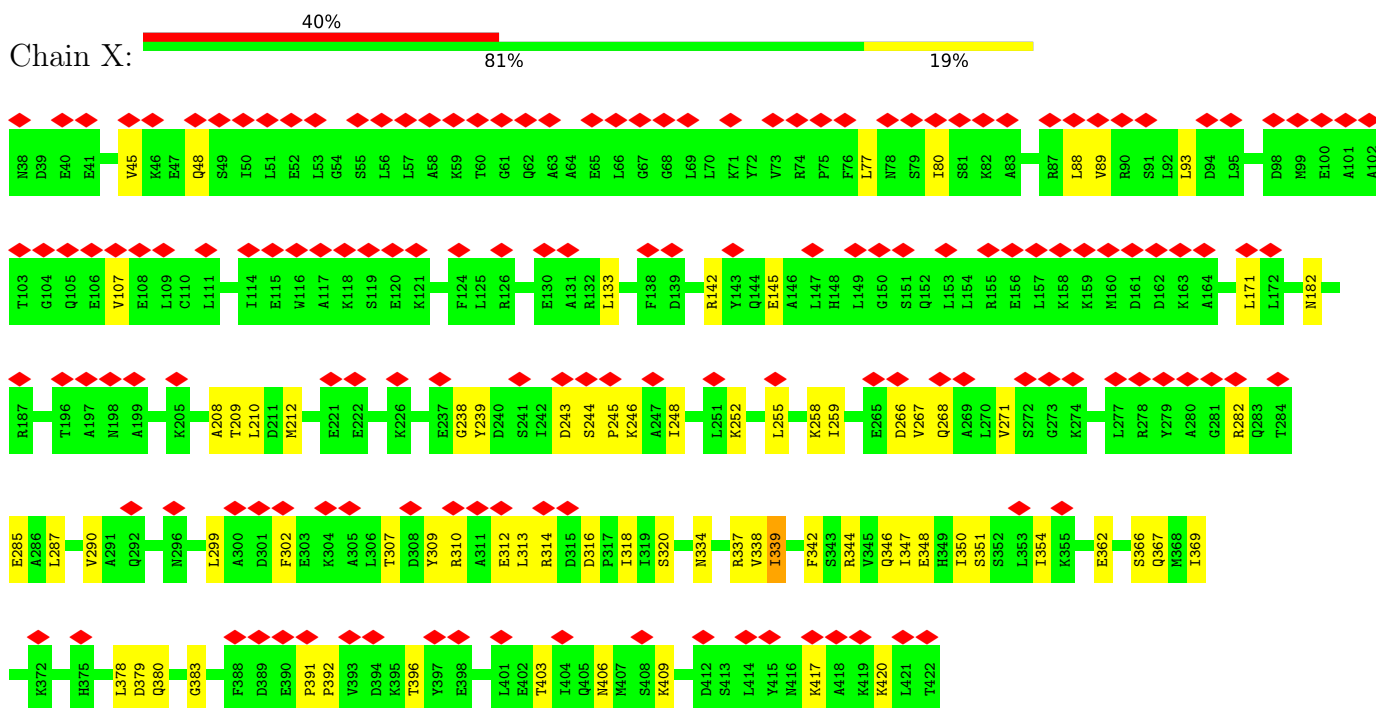
• Molecule 8: 26S proteasome non-ATPase regulatory subunit 1



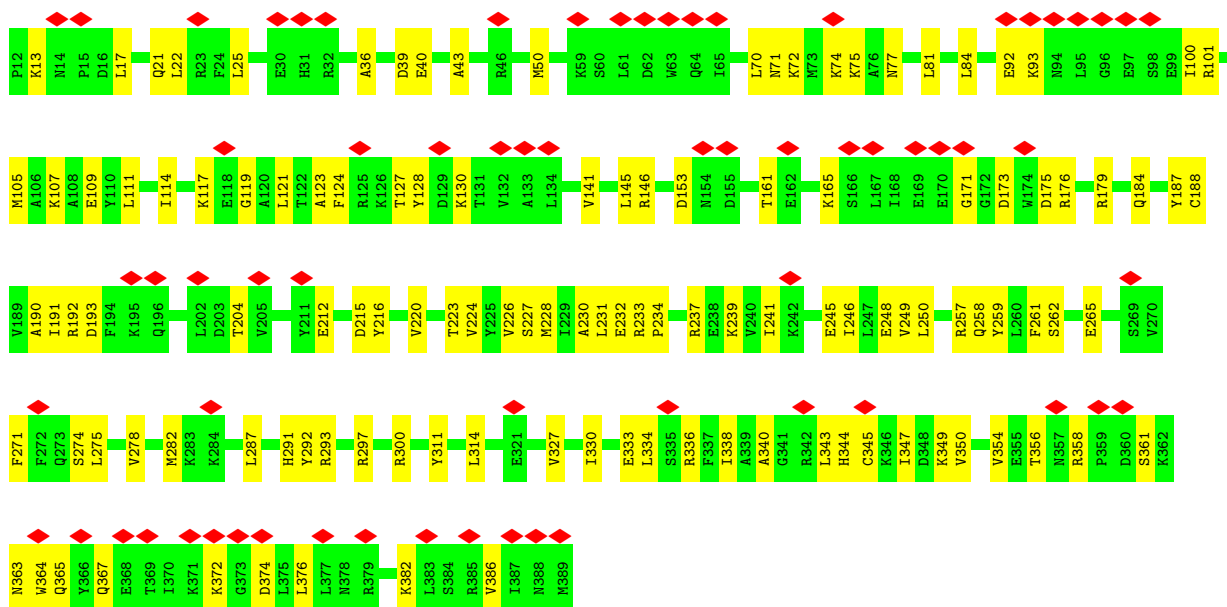
- Molecule 10: 26S proteasome non-ATPase regulatory subunit 12



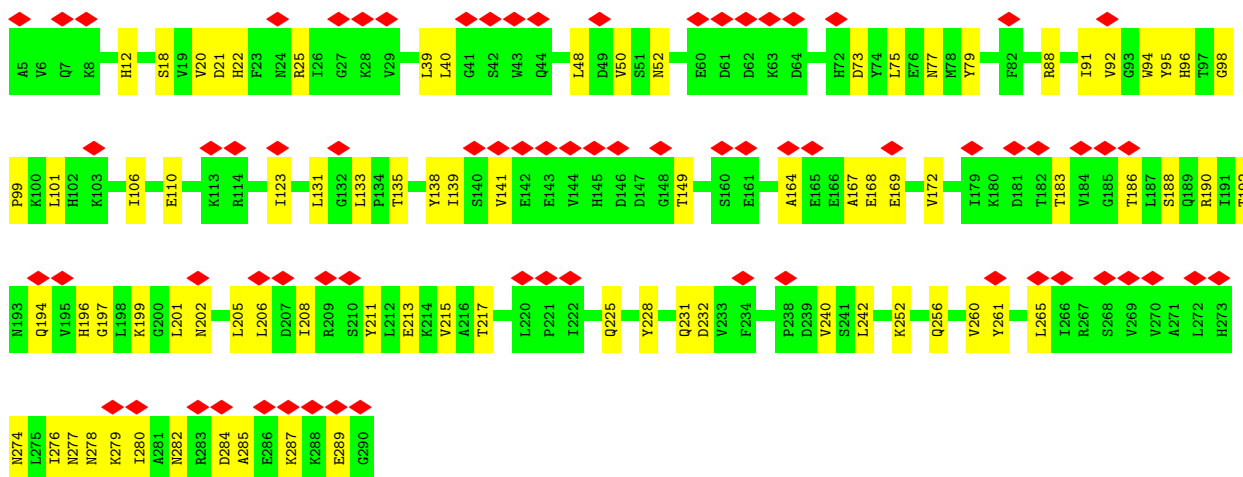
- Molecule 11: 26S proteasome non-ATPase regulatory subunit 11



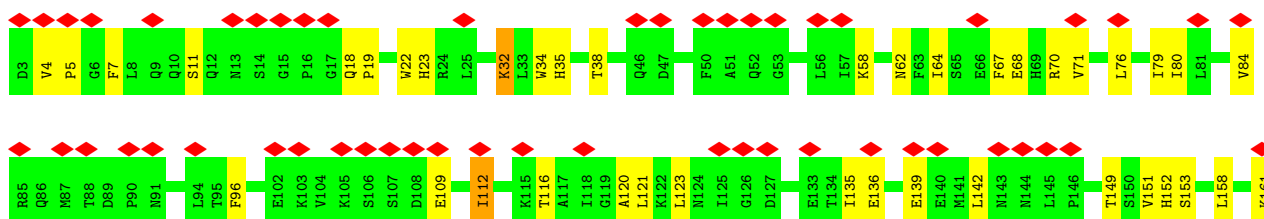
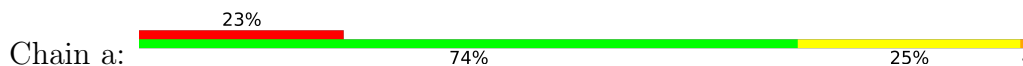
- Molecule 12: 26S proteasome non-ATPase regulatory subunit 6

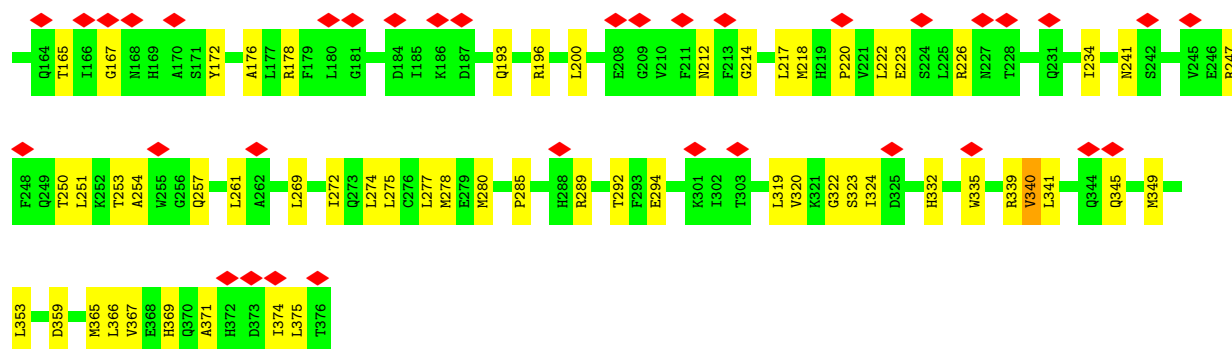


• Molecule 13: 26S proteasome non-ATPase regulatory subunit 7

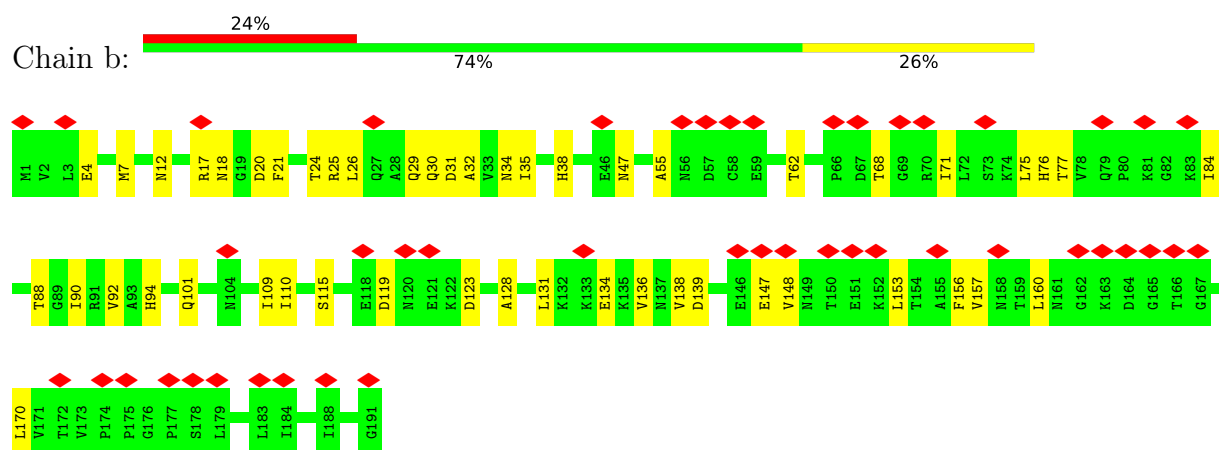


• Molecule 14: 26S proteasome non-ATPase regulatory subunit 13

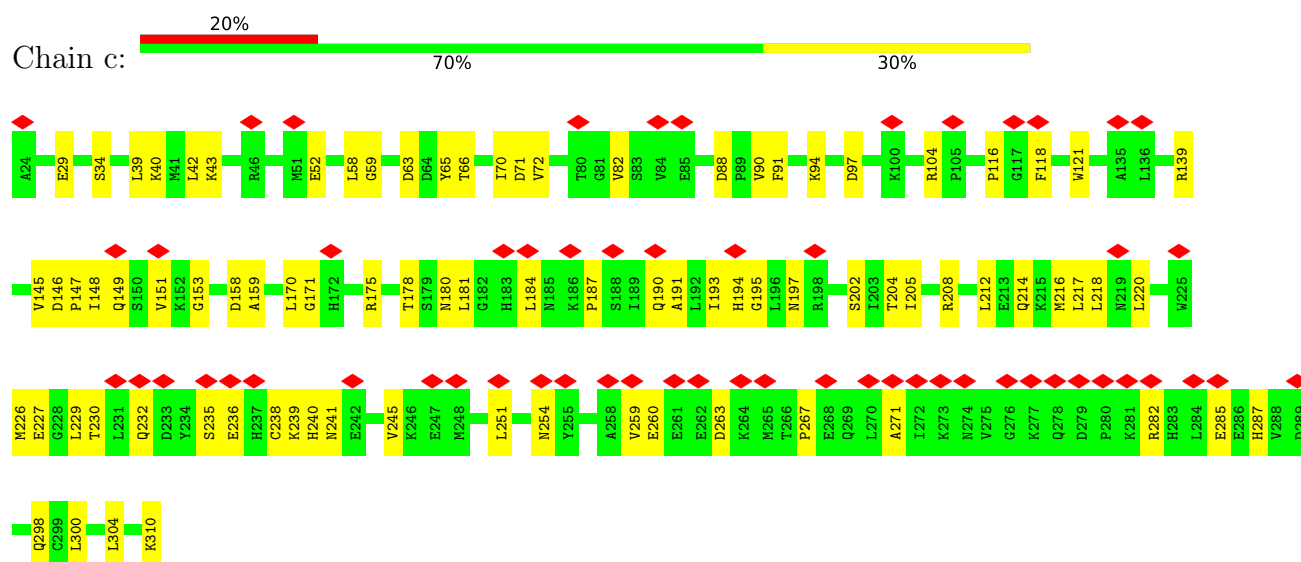




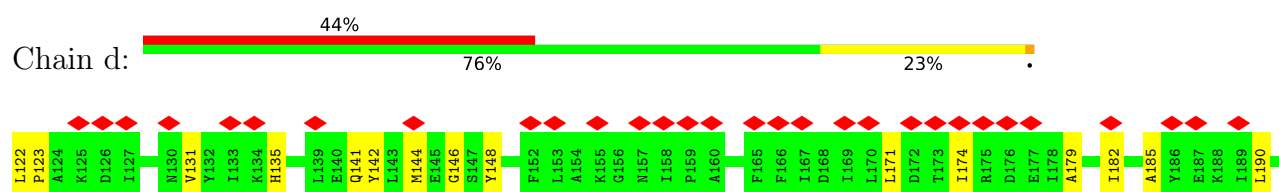
• Molecule 15: 26S proteasome non-ATPase regulatory subunit 4

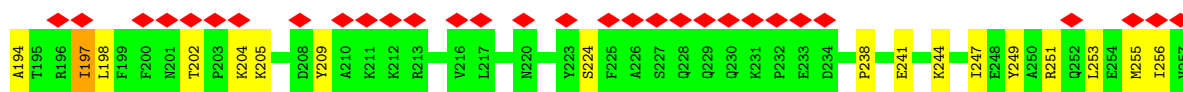


• Molecule 16: 26S proteasome non-ATPase regulatory subunit 14

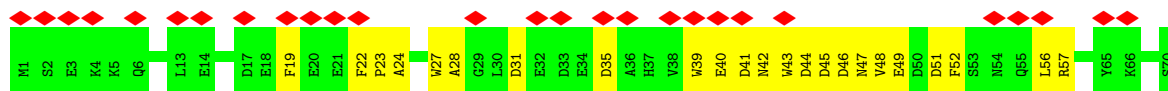
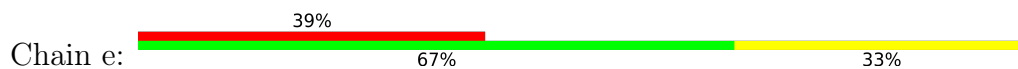


• Molecule 17: 26S proteasome non-ATPase regulatory subunit 8

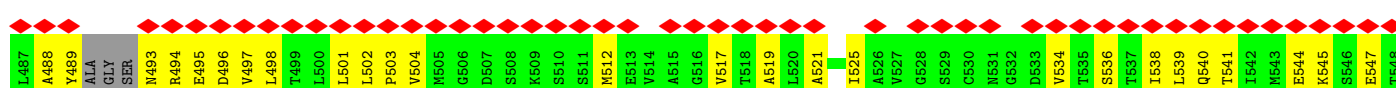
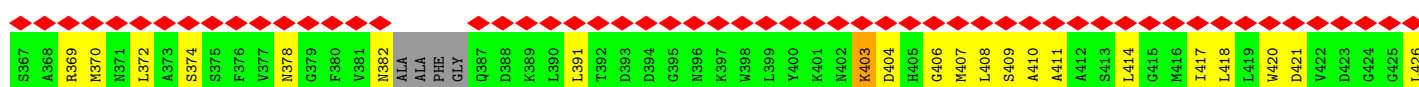
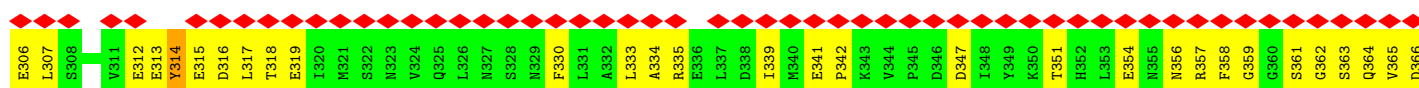
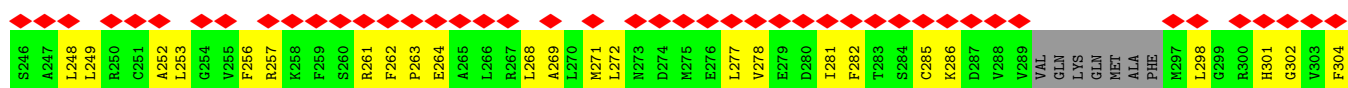
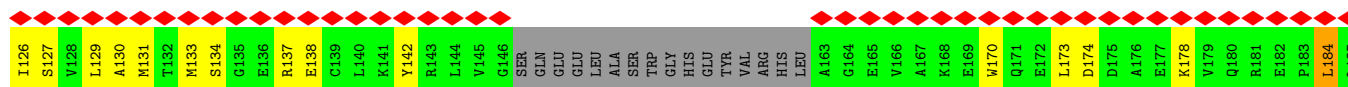
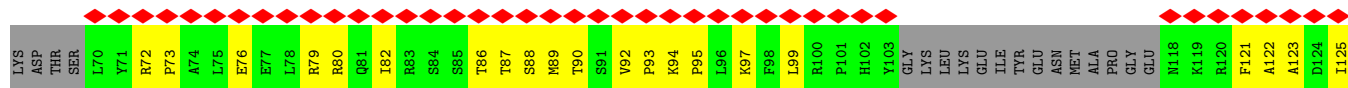
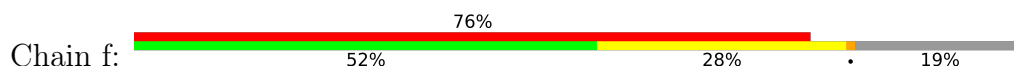




• Molecule 18: 26S proteasome complex subunit SEM1



• 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	39520	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	0.012	Depositor
Minimum map value	-0.004	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.004	Depositor
Map size ($\text{\AA}$)	250.88, 250.88, 250.88	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.98, 0.98, 0.98	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	G	0.07	0/1687	0.22	0/2279
2	A	0.11	0/2722	0.34	0/3673
3	B	0.11	0/2615	0.47	2/3530 (0.1%)
4	C	0.10	0/2741	0.30	0/3681
5	D	0.12	0/2795	0.37	1/3773 (0.0%)
6	E	0.39	3/2775 (0.1%)	0.43	6/3727 (0.2%)
7	F	0.11	0/2845	0.32	0/3832
8	U	0.09	0/5930	0.28	0/8021
9	V	0.10	0/1507	0.30	0/2029
10	W	0.11	0/3750	0.31	1/5039 (0.0%)
11	X	0.08	0/3091	0.24	0/4165
12	Y	0.09	0/3173	0.27	0/4273
13	Z	0.10	0/2324	0.26	0/3150
14	a	0.09	0/3061	0.28	0/4144
15	b	0.09	0/1478	0.26	0/2001
16	c	0.08	0/2302	0.24	0/3110
17	d	0.10	0/1134	0.29	0/1534
18	e	0.09	0/596	0.28	0/805
19	f	0.12	0/5377	0.38	0/7248
All	All	0.13	3/51903 (0.0%)	0.32	10/70014 (0.0%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	E	115	VAL	N-CA	13.55	1.63	1.46
6	E	115	VAL	CA-C	12.18	1.68	1.52
6	E	114	GLU	C-N	5.52	1.41	1.33

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	168	ASP	CA-C-N	-13.30	103.21	119.84
3	B	168	ASP	C-N-CA	-13.30	103.21	119.84
5	D	198	PRO	N-CA-C	9.56	122.36	110.70
6	E	115	VAL	CA-C-N	-8.41	101.28	121.80
6	E	115	VAL	C-N-CA	-8.41	101.28	121.80

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	G	1662	0	1667	41	0
2	A	2677	0	2732	85	0
3	B	2579	0	2628	65	0
4	C	2709	0	2812	71	0
5	D	2751	0	2804	78	0
6	E	2736	0	2794	122	0
7	F	2808	0	2902	124	0
8	U	5829	0	5920	137	0
9	V	1480	0	1527	48	0
10	W	3703	0	3821	97	0
11	X	3048	0	3139	50	0
12	Y	3115	0	3120	84	0
13	Z	2281	0	2312	63	0
14	a	3003	0	3016	74	0
15	b	1458	0	1505	32	0
16	c	2260	0	2276	63	0
17	d	1109	0	1114	20	0
18	e	583	0	493	19	0
19	f	5304	0	5315	262	0
20	c	1	0	0	0	0
All	All	51096	0	51897	1429	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 14.

The worst 5 of 1429 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)
19:f:486:GLY:HA2	19:f:489:TYR:CD1	1.31	1.57
19:f:486:GLY:CA	19:f:489:TYR:HD1	1.44	1.31
19:f:486:GLY:CA	19:f:489:TYR:CD1	2.14	1.29
6:E:115:VAL:CG1	6:E:118:LEU:HB2	1.72	1.19
6:E:124:HIS:CD2	6:E:195:PHE:CE2	2.31	1.19

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	G	217/223 (97%)	214 (99%)	3 (1%)	0	100	100
2	A	335/352 (95%)	301 (90%)	34 (10%)	0	100	100
3	B	326/340 (96%)	294 (90%)	30 (9%)	2 (1%)	21	59
4	C	334/385 (87%)	313 (94%)	21 (6%)	0	100	100
5	D	340/368 (92%)	317 (93%)	23 (7%)	0	100	100
6	E	341/379 (90%)	311 (91%)	28 (8%)	2 (1%)	21	59
7	F	353/380 (93%)	329 (93%)	23 (6%)	1 (0%)	36	72
8	U	743/841 (88%)	714 (96%)	29 (4%)	0	100	100
9	V	181/183 (99%)	170 (94%)	11 (6%)	0	100	100
10	W	452/456 (99%)	414 (92%)	38 (8%)	0	100	100
11	X	381/385 (99%)	375 (98%)	6 (2%)	0	100	100
12	Y	376/378 (100%)	357 (95%)	19 (5%)	0	100	100
13	Z	284/286 (99%)	267 (94%)	17 (6%)	0	100	100
14	a	372/374 (100%)	351 (94%)	21 (6%)	0	100	100
15	b	189/191 (99%)	174 (92%)	15 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
16	c	285/287 (99%)	271 (95%)	14 (5%)	0	100	100
17	d	134/136 (98%)	123 (92%)	11 (8%)	0	100	100
18	e	68/70 (97%)	64 (94%)	4 (6%)	0	100	100
19	f	664/848 (78%)	597 (90%)	67 (10%)	0	100	100
All	All	6375/6862 (93%)	5956 (93%)	414 (6%)	5 (0%)	49	83

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	B	169	PRO
3	B	168	ASP
7	F	168	TYR
6	E	114	GLU
6	E	115	VAL

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	G	174/178 (98%)	174 (100%)	0	100	100
2	A	293/300 (98%)	291 (99%)	2 (1%)	76	80
3	B	289/298 (97%)	285 (99%)	4 (1%)	59	71
4	C	297/333 (89%)	294 (99%)	3 (1%)	68	77
5	D	301/321 (94%)	297 (99%)	4 (1%)	61	73
6	E	300/333 (90%)	298 (99%)	2 (1%)	76	80
7	F	308/326 (94%)	305 (99%)	3 (1%)	68	77
8	U	639/720 (89%)	633 (99%)	6 (1%)	70	77
9	V	164/164 (100%)	164 (100%)	0	100	100
10	W	416/416 (100%)	413 (99%)	3 (1%)	76	80
11	X	331/331 (100%)	328 (99%)	3 (1%)	70	77

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	Y	334/334 (100%)	333 (100%)	1 (0%)	86	85
13	Z	257/257 (100%)	256 (100%)	1 (0%)	84	83
14	a	334/334 (100%)	331 (99%)	3 (1%)	70	77
15	b	167/167 (100%)	167 (100%)	0	100	100
16	c	252/252 (100%)	252 (100%)	0	100	100
17	d	121/121 (100%)	119 (98%)	2 (2%)	53	68
18	e	63/63 (100%)	62 (98%)	1 (2%)	55	69
19	f	579/714 (81%)	567 (98%)	12 (2%)	47	65
All	All	5619/5962 (94%)	5569 (99%)	50 (1%)	68	77

5 of 50 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
11	X	339	ILE
17	d	190	LEU
19	f	745	LEU
11	X	369	ILE
14	a	32	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 89 such sidechains are listed below:

Mol	Chain	Res	Type
12	Y	251	HIS
14	a	241	ASN
12	Y	363	ASN
13	Z	273	HIS
15	b	34	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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
10	W	1
11	X	1

All chain breaks are listed below:

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

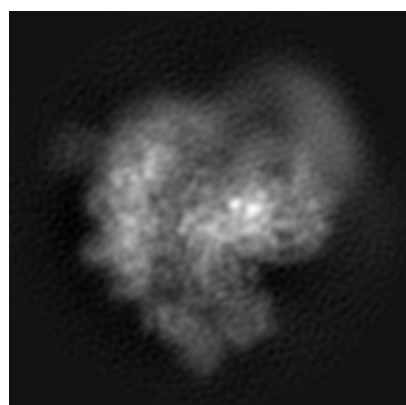
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8674. These allow visual inspection of the internal detail of the map and identification of artifacts.

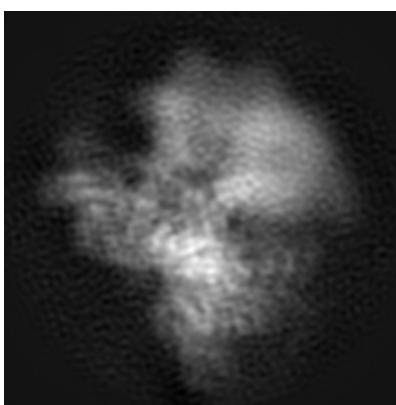
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

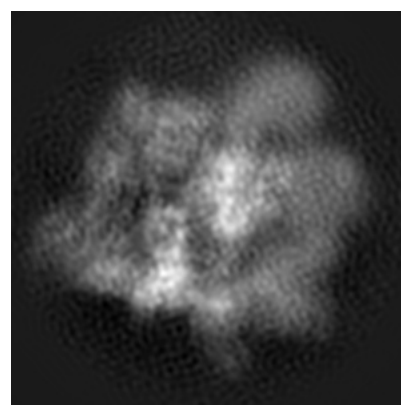
6.1.1 Primary map



X



Y

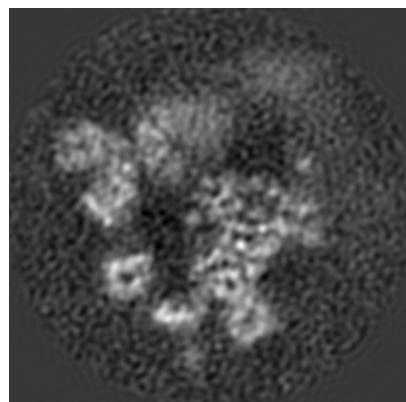


Z

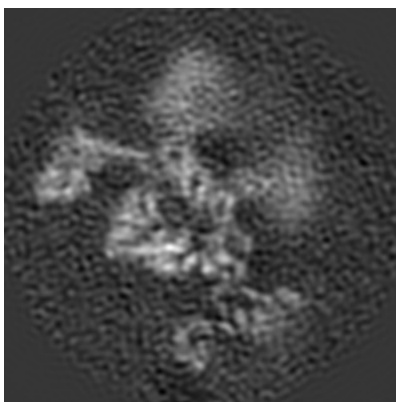
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

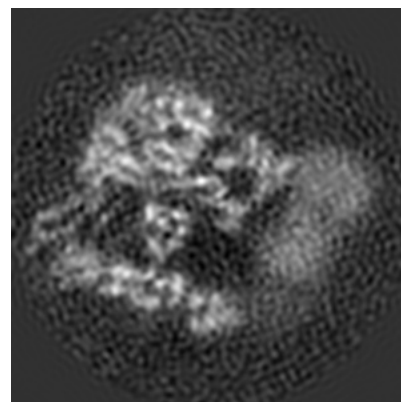
6.2.1 Primary map



X Index: 128



Y Index: 128

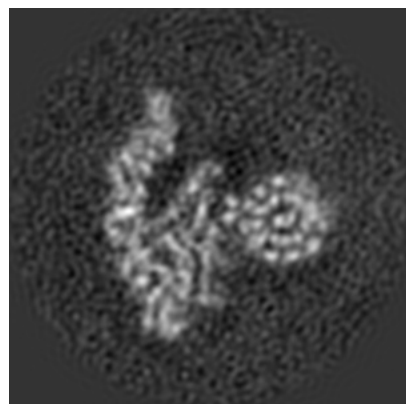


Z Index: 128

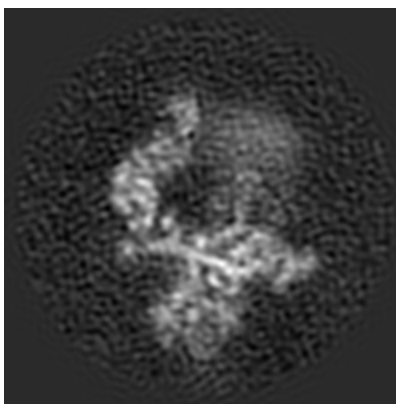
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

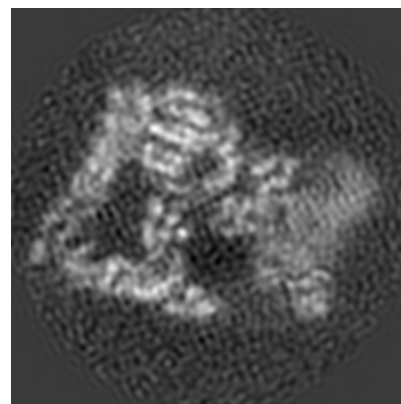
6.3.1 Primary map



X Index: 105



Y Index: 79

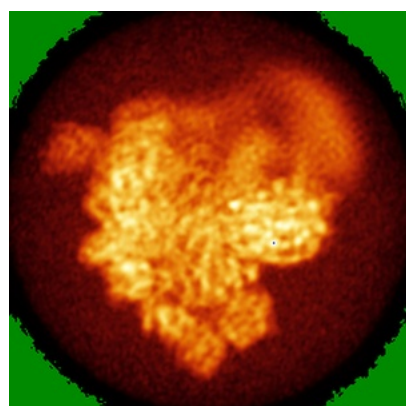


Z Index: 118

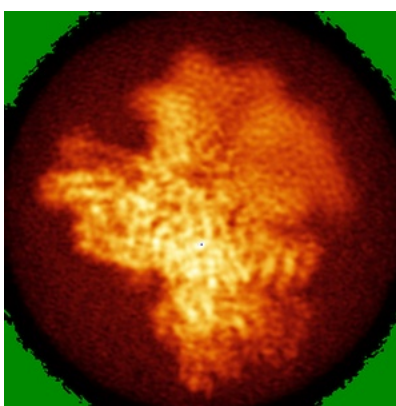
The images above show the largest variance slices of the map in three orthogonal directions.

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

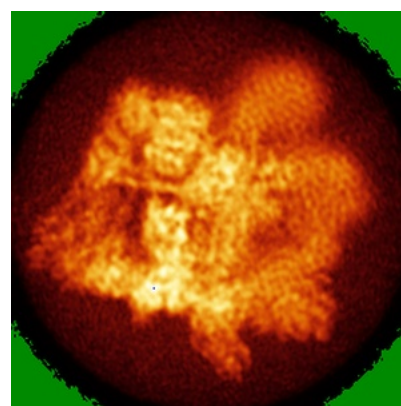
6.4.1 Primary map



X



Y

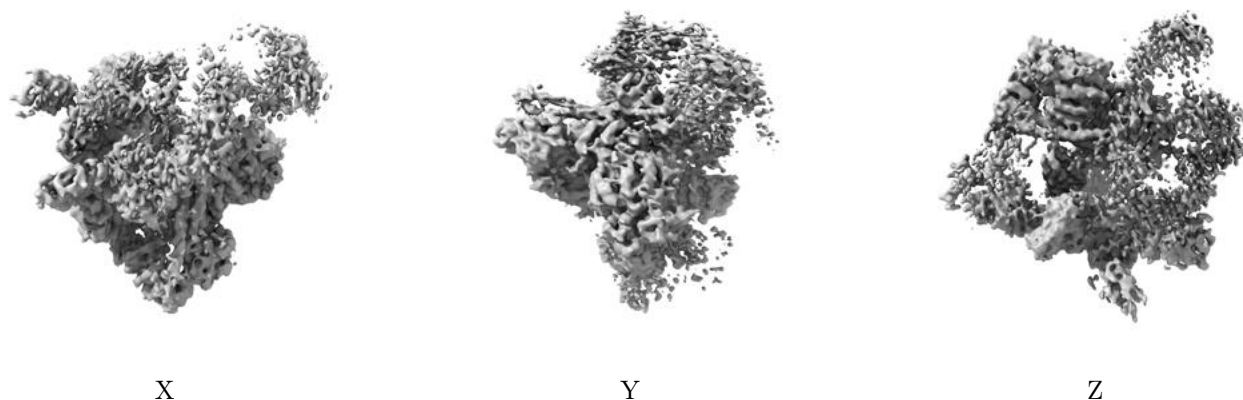


Z

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

6.5 Orthogonal surface views [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.

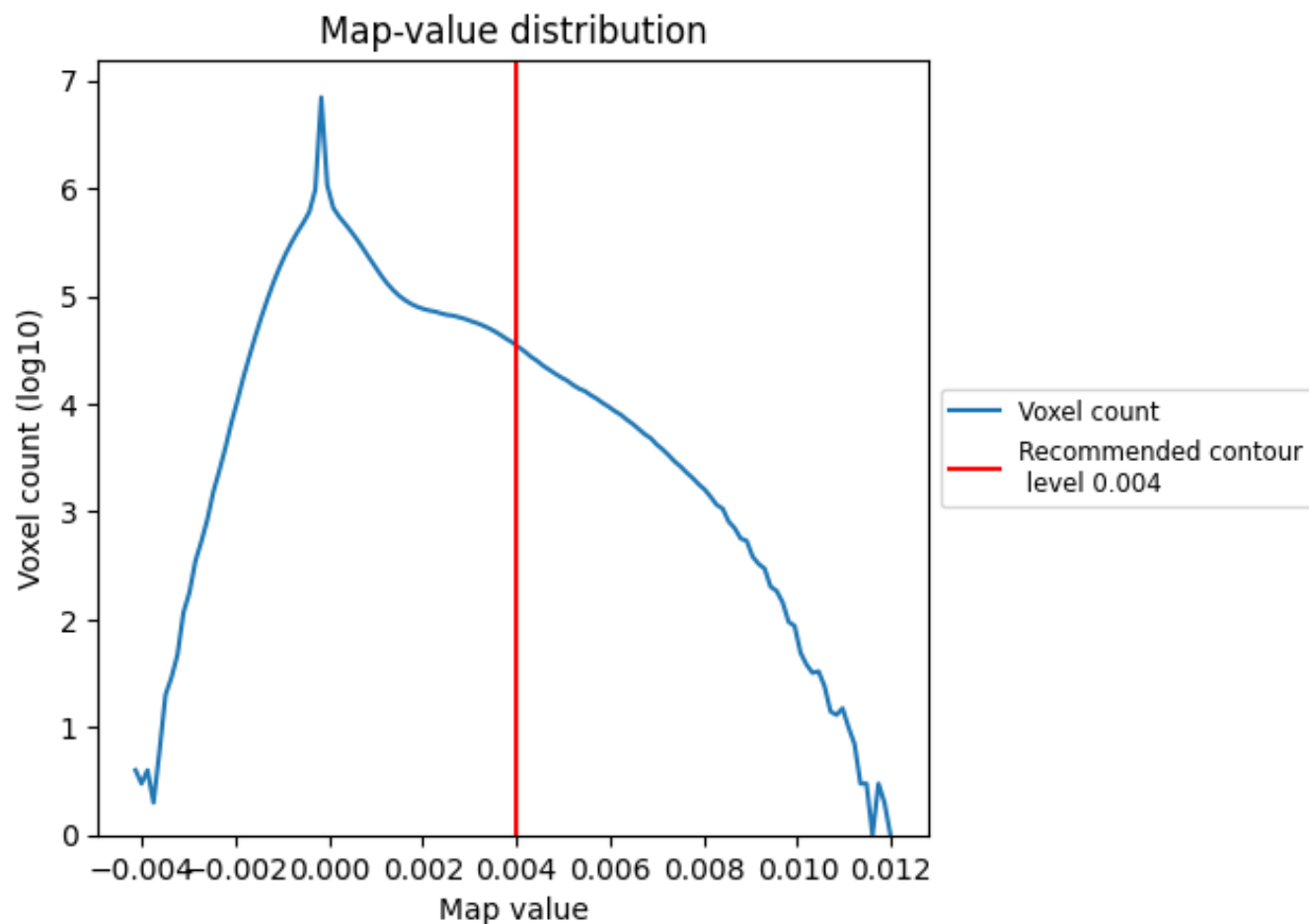
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

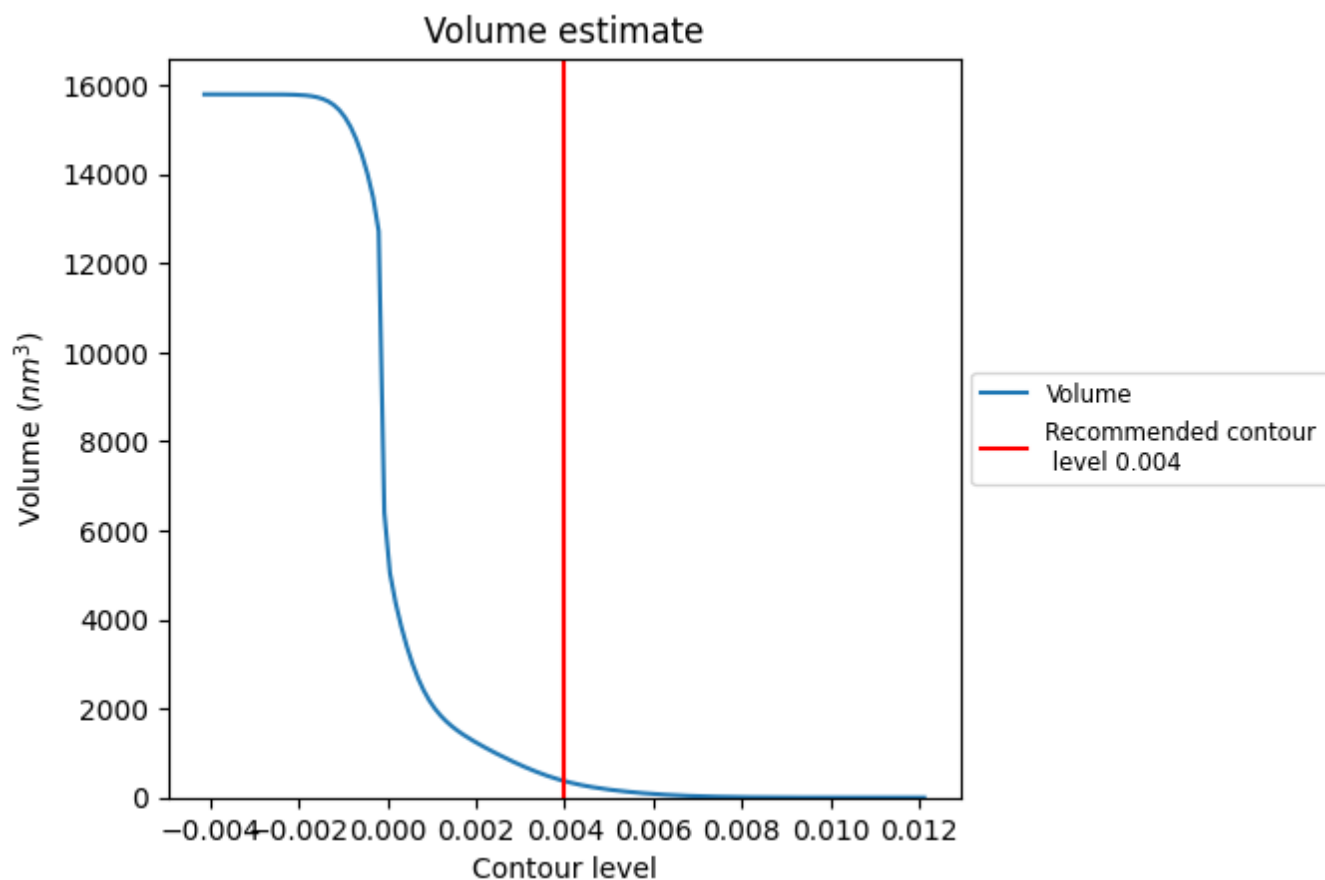
This section contains the results of statistical analysis of the map.

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.

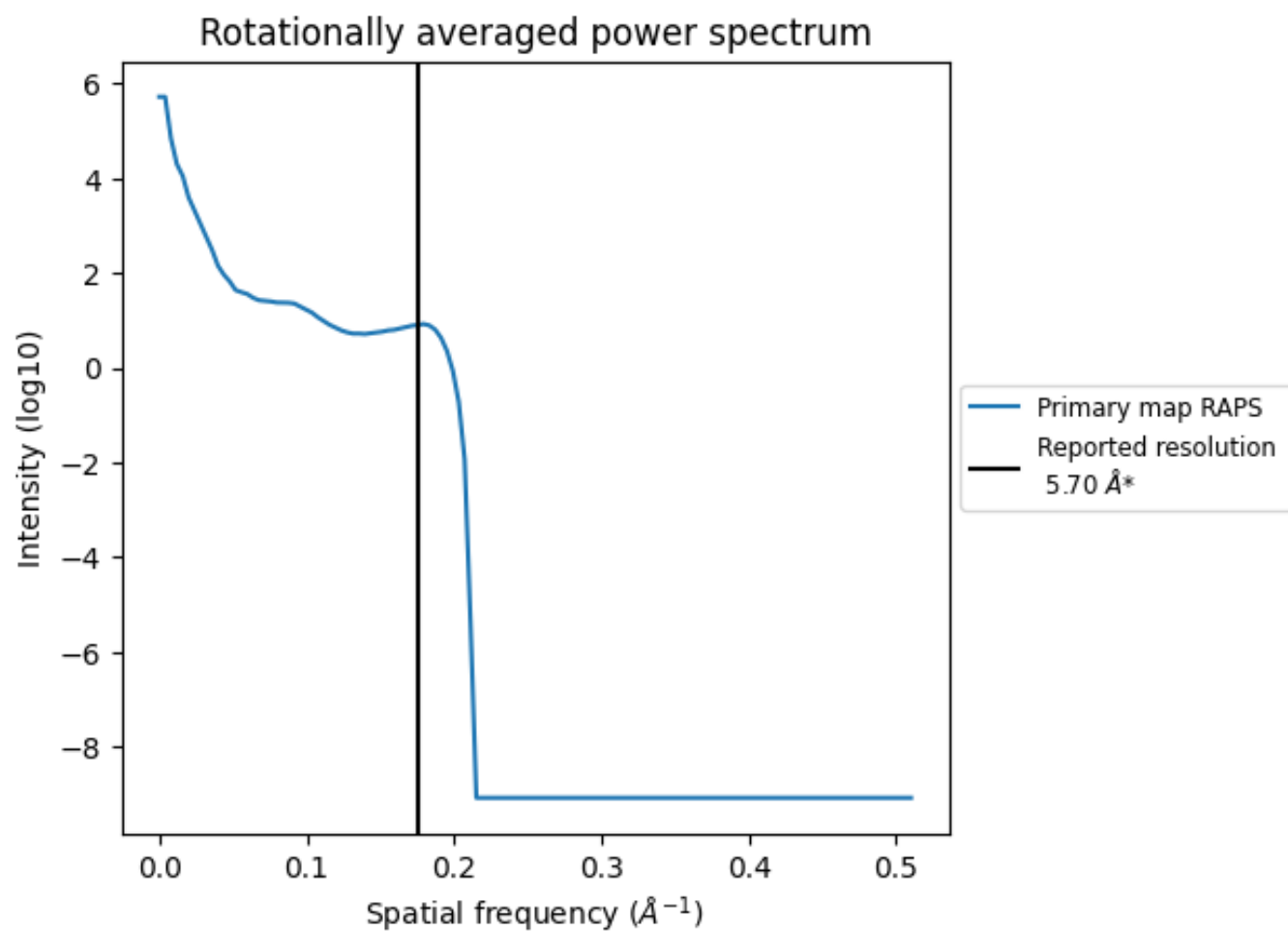
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 369 nm³; this corresponds to an approximate mass of 334 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 0.175 Å⁻¹

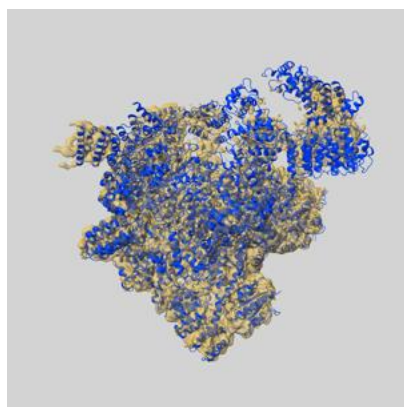
8 Fourier-Shell correlation

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

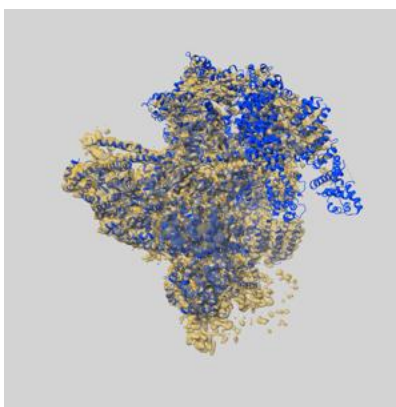
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-8674 and PDB model 5VHF. Per-residue inclusion information can be found in [section 3](#) on [page 7](#).

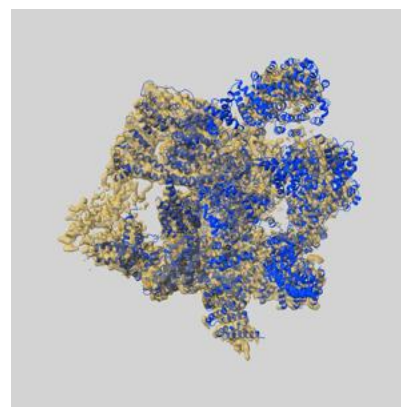
9.1 Map-model overlay [i](#)



X



Y



Z

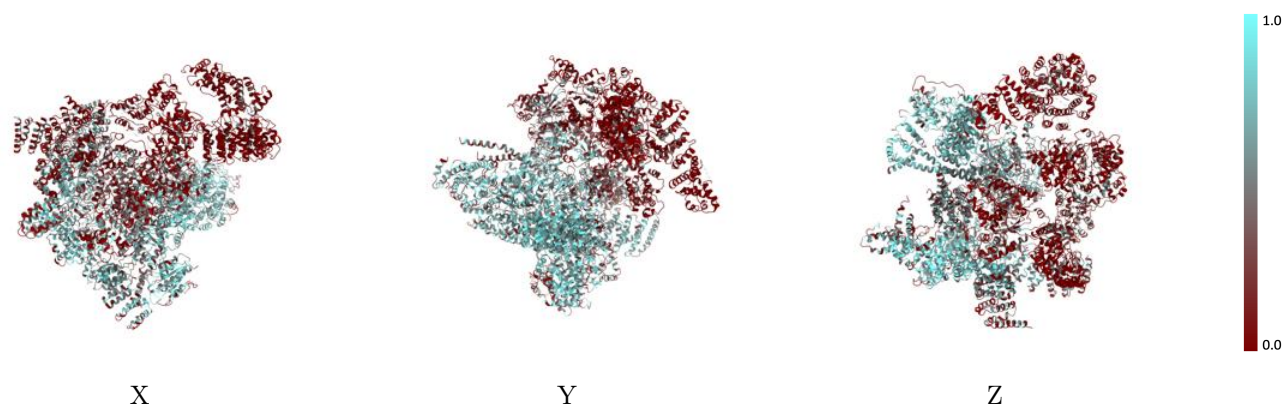
The images above show the 3D surface view of the map at the recommended contour level 0.004 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



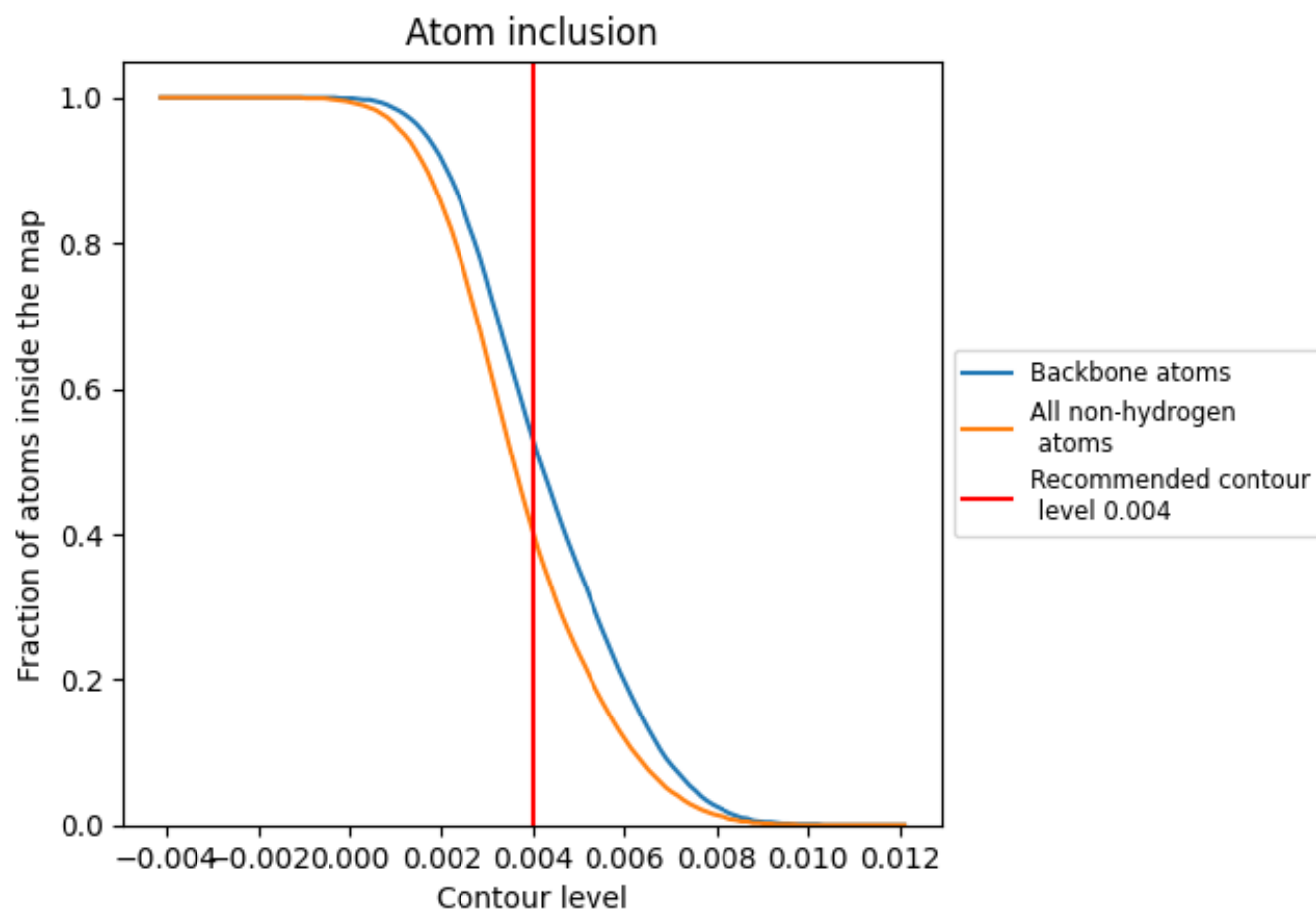
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 53% of all backbone atoms, 40% 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	 0.4040	 0.0860
A	 0.2110	 0.0390
B	 0.1730	 0.0260
C	 0.2290	 0.0480
D	 0.2500	 0.0730
E	 0.2600	 0.0650
F	 0.2620	 0.0620
G	 0.0260	 0.0200
U	 0.6630	 0.1360
V	 0.5860	 0.1130
W	 0.5570	 0.1070
X	 0.4940	 0.1080
Y	 0.6730	 0.1310
Z	 0.5750	 0.1310
a	 0.5910	 0.1310
b	 0.5870	 0.1110
c	 0.5910	 0.1460
d	 0.4510	 0.1050
e	 0.4870	 0.0640
f	 0.0680	 0.0160

