



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 09:00 AM UTC

PDB ID : 6EPF / pdb_00006epf
EMDB ID : EMD-3916
Title : Ground state 26S proteasome (GS1)
Authors : Guo, Q.; Lehmer, C.; Martinez-Sanchez, A.; Rudack, T.; Beck, F.; Hartmann, H.; Hipp, M.S.; Hartl, F.U.; Edbauer, D.; Baumeister, W.; Fernandez-Busnadiego, R.
Deposited on : 2017-10-11
Resolution : 11.80 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

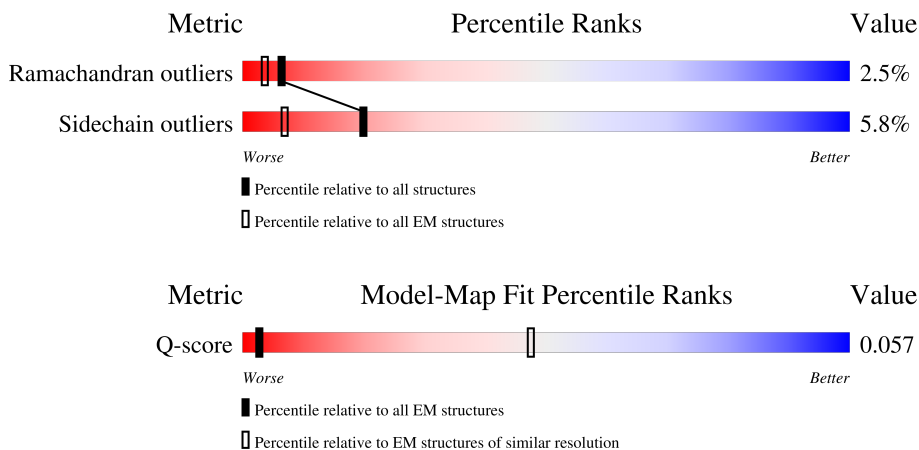
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 11.80 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.






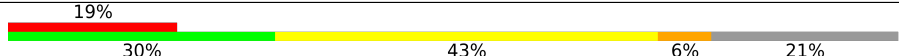
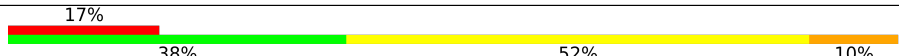
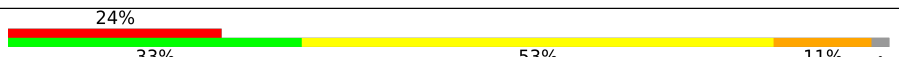
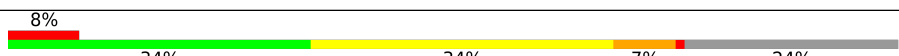
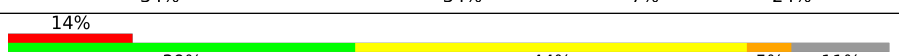
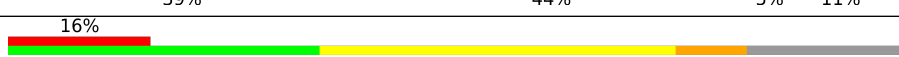

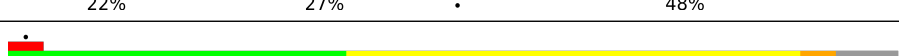
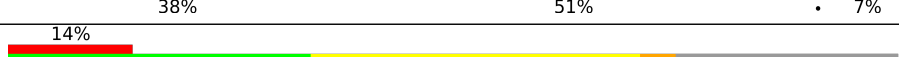
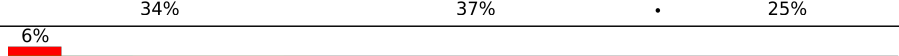
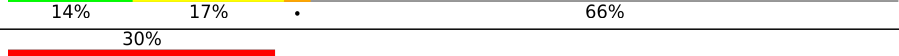

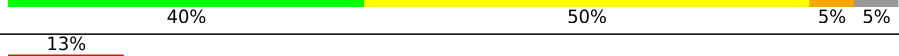
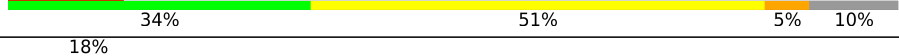

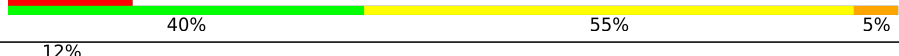

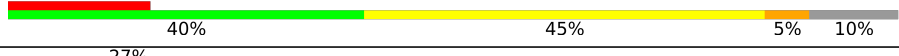
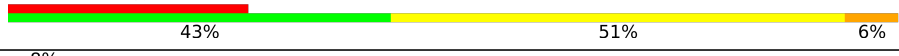



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	93 (11.30 - 12.30)

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	246	 7% 46% 48% 5%
2	B	234	 9% 43% 53% .
3	C	261	 8% 41% 47% 7% 5%
4	D	254	 11% 43% 51% . .
5	E	241	 5% 46% 47% . .

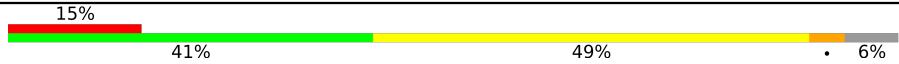

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Mol	Chain	Length	Quality of chain
6	F	263	
7	G	255	
8	1	238	
9	2	277	
10	3	205	
11	4	201	
12	5	263	
13	6	240	
14	7	263	
15	W	377	
16	V	310	
17	T	353	
18	Y	70	
19	Z	908	
20	N	953	
21	S	530	
22	P	456	
23	Q	422	
24	R	389	
25	U	320	
26	O	376	
27	H	433	
28	I	440	
29	K	418	
30	L	403	

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Mol	Chain	Length	Quality of chain
31	M	442	
32	J	406	

2 Entry composition [i](#)

There are 32 unique types of molecules in this entry. The entry contains 82757 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	A	246	1920	1215	322	369	14	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	234	1828	1166	311	344	7	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	249	1960	1238	337	374	11	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	D	246	1926	1209	340	371	6	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	E	233	1778	1114	296	358	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	F	238	1871	1170	337	353	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	G	245	1912	1212	326	362	12	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	1	202	1516	948	259	297	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	2	219	1651	1042	281	316	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	3	205	1600	1018	266	296	20	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	4	196	1572	1007	267	289	9	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	5	201	1560	984	272	295	9	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	6	213	1659	1050	284	315	10	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	7	216	1686	1065	292	317	12	0	0

- Molecule 15 is a protein called 26S proteasome subunit S5a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	W	195	1480	922	265	285	8	0	0

- Molecule 16 is a protein called Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	V	289	2272	1438	391	424	19	0	0

- Molecule 17 is a protein called Proteasome 26S subunit, non-ATPase 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	T	263	2149	1390	351	398	10	0	0

- Molecule 18 is a protein called RCG28037.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	Y	24	199	120	34	44	1	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	Z	896	6913	4342	1178	1346	47	0	0

- Molecule 20 is a protein called 26S proteasome non-ATPase regulatory subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	N	905	7082	4487	1193	1356	46	0	0

- Molecule 21 is a protein called Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	S	476	3844	2438	685	707	14	0	0

- Molecule 22 is a protein called Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	P	456	3706	2338	635	709	24	0	0

- Molecule 23 is a protein called 26S proteasome non-ATPase regulatory subunit 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	Q	422	3335	2116	567	639	13	0	0

- Molecule 24 is a protein called Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	R	389	3204	2042	542	600	20	0	0

- Molecule 25 is a protein called Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 7 (Predicted).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	U	288	2299	1470	395	428	6	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	O	376	3011	1918	514	564	15	0	0

- Molecule 27 is a protein called 26S proteasome regulatory subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	H	396	3113	1960	546	589	18	0	0

- Molecule 28 is a protein called 26S proteasome regulatory subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	I	385	3042	1913	516	598	15	0	0

- Molecule 29 is a protein called 26S proteasome regulatory subunit 6B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	K	391	3125	1978	535	599	13	0	0

- Molecule 30 is a protein called Proteasome 26S subunit, ATPase 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	L	389	3098	1947	552	582	17	0	0

- Molecule 31 is a protein called 26S proteasome regulatory subunit 6A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	M	415	3252	2038	561	635	18	0	0

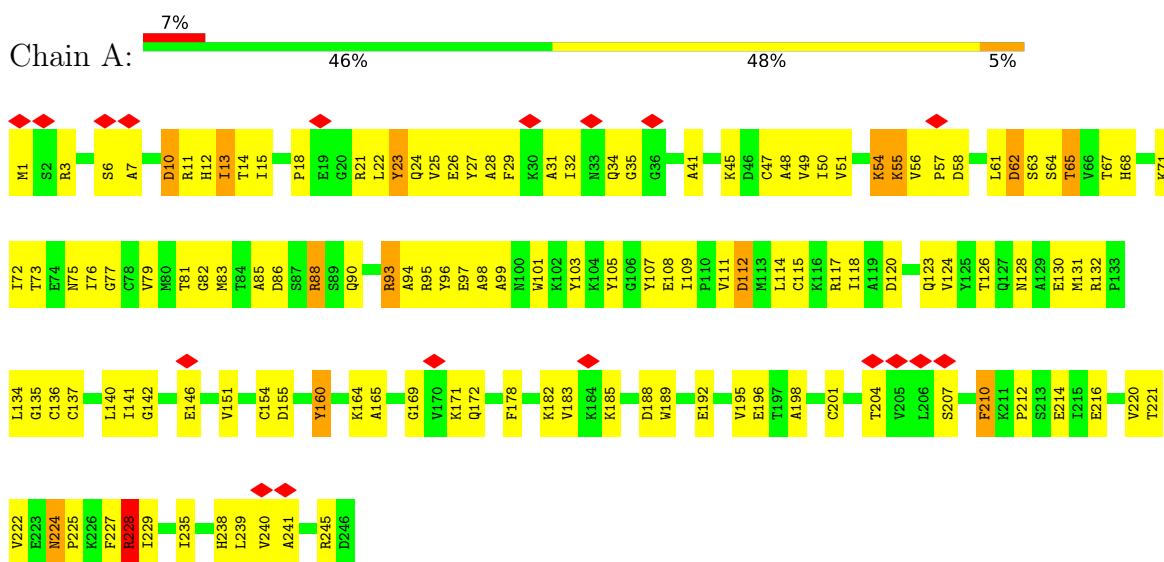
- Molecule 32 is a protein called 26S proteasome regulatory subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	J	406	3194	2006	569	599	20	0	0

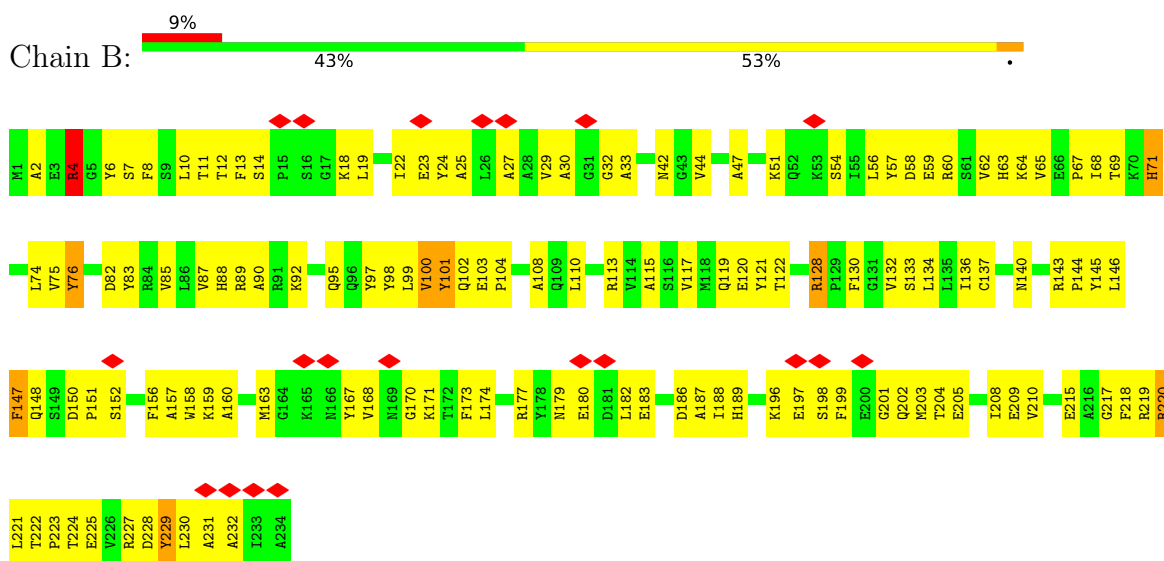
3 Residue-property plots

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.

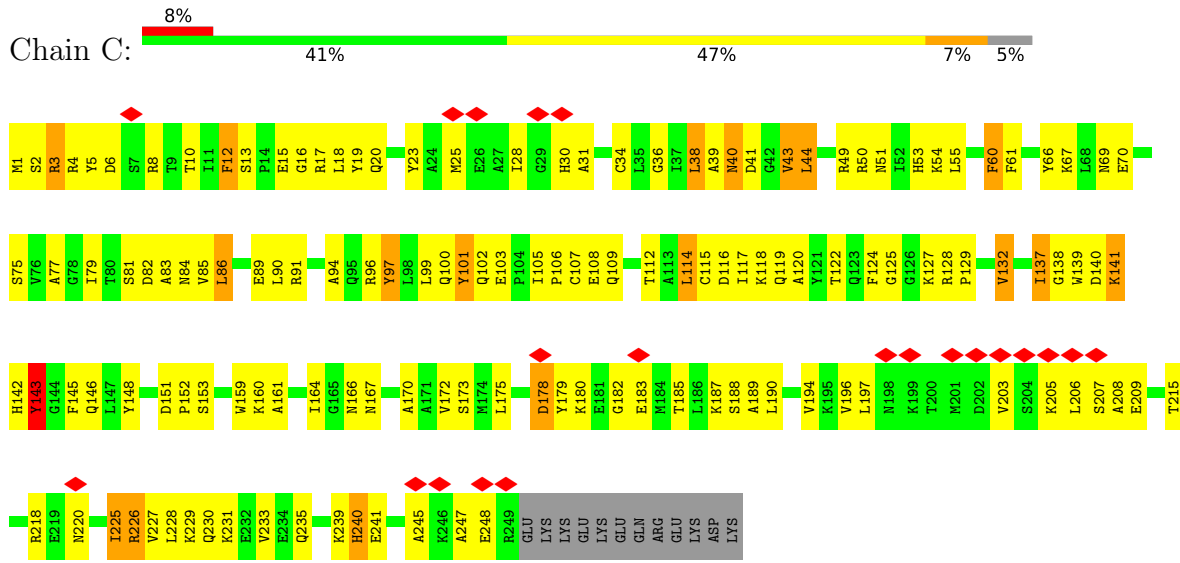
- Molecule 1: Proteasome subunit alpha type-6



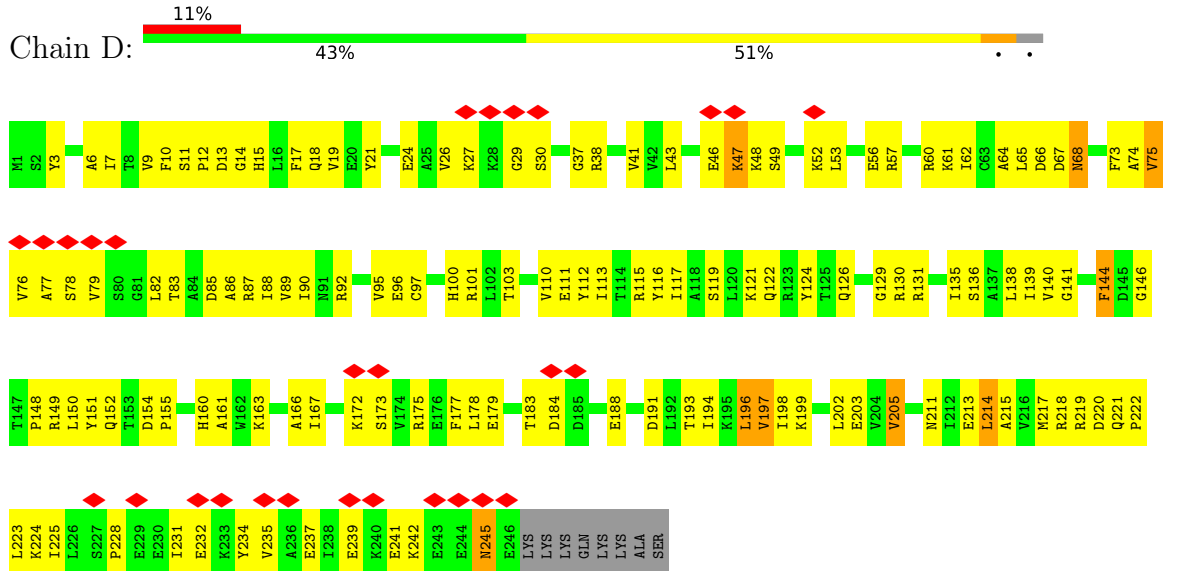
- Molecule 2: Proteasome subunit alpha type-2



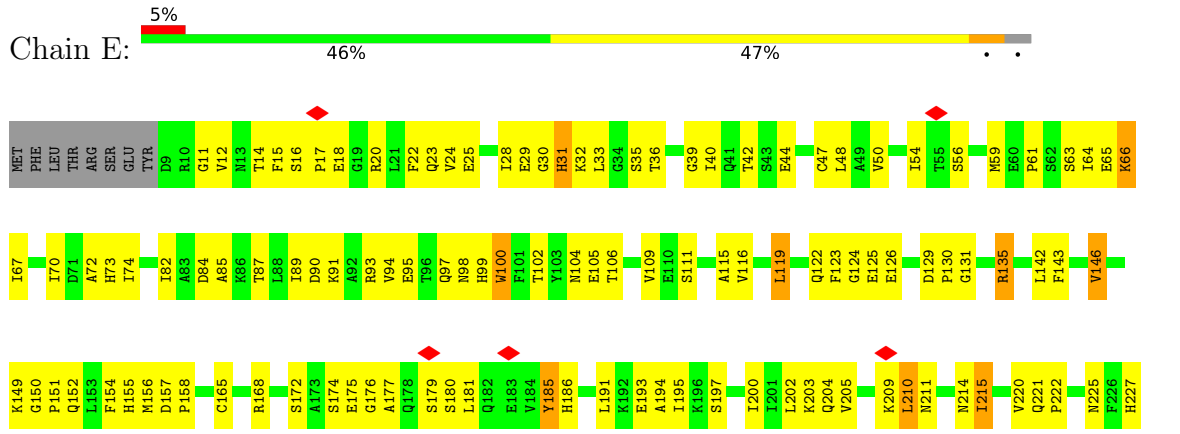
- Molecule 3: Proteasome subunit alpha type-4

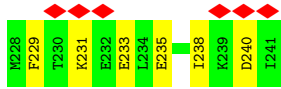


• Molecule 4: Proteasome subunit alpha type-7



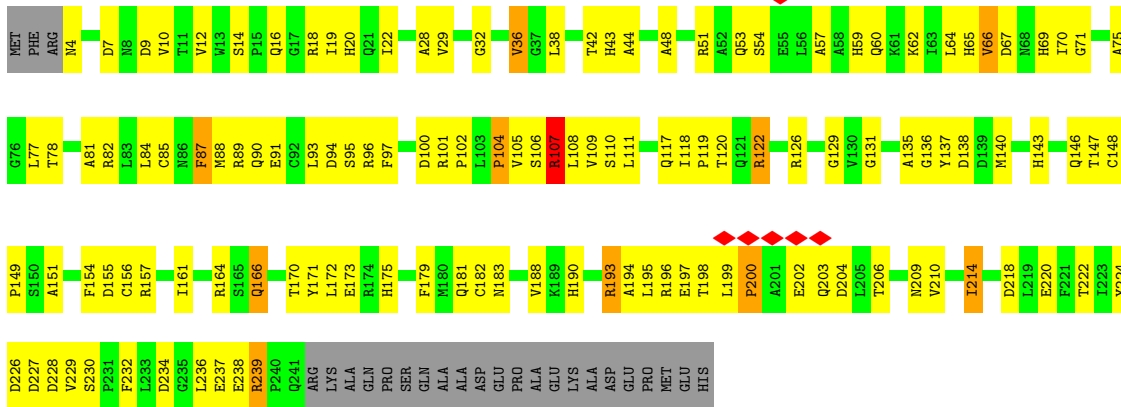
• Molecule 5: Proteasome subunit alpha type-5





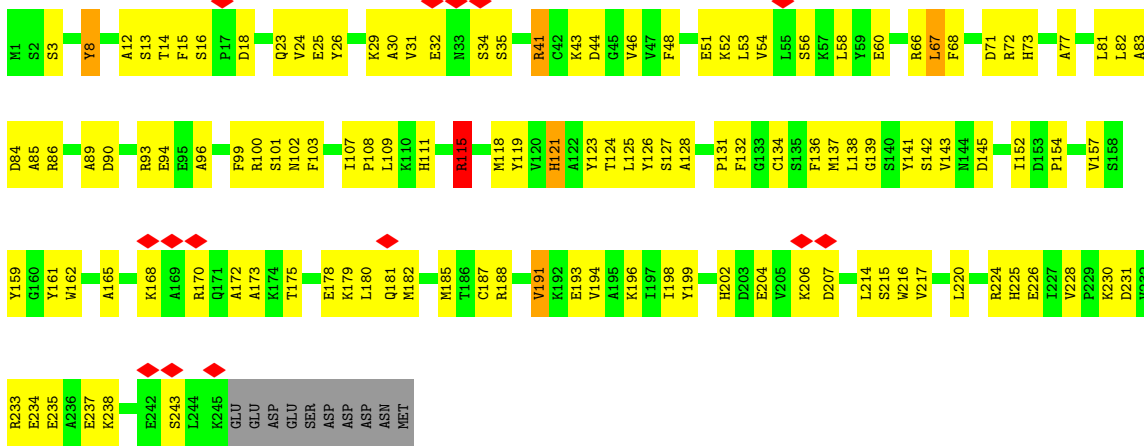
- Molecule 6: Proteasome subunit alpha type-1

Chain F: 41% 45% 10%



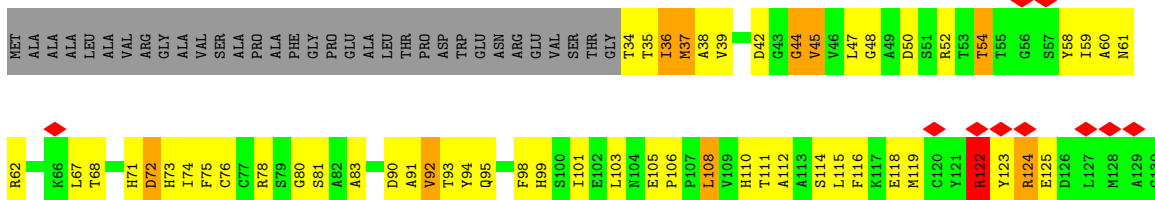
- Molecule 7: Proteasome subunit alpha type-3

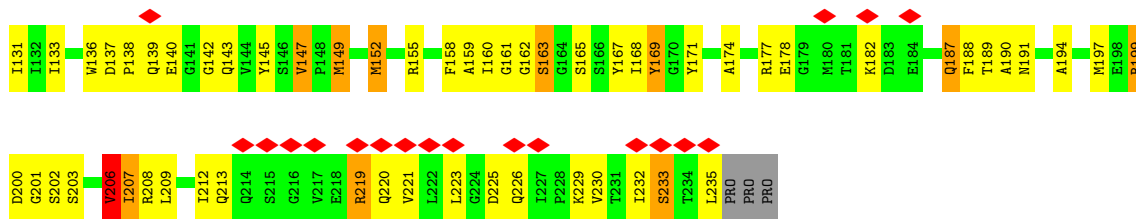
Chain G: 5% 47% 47%



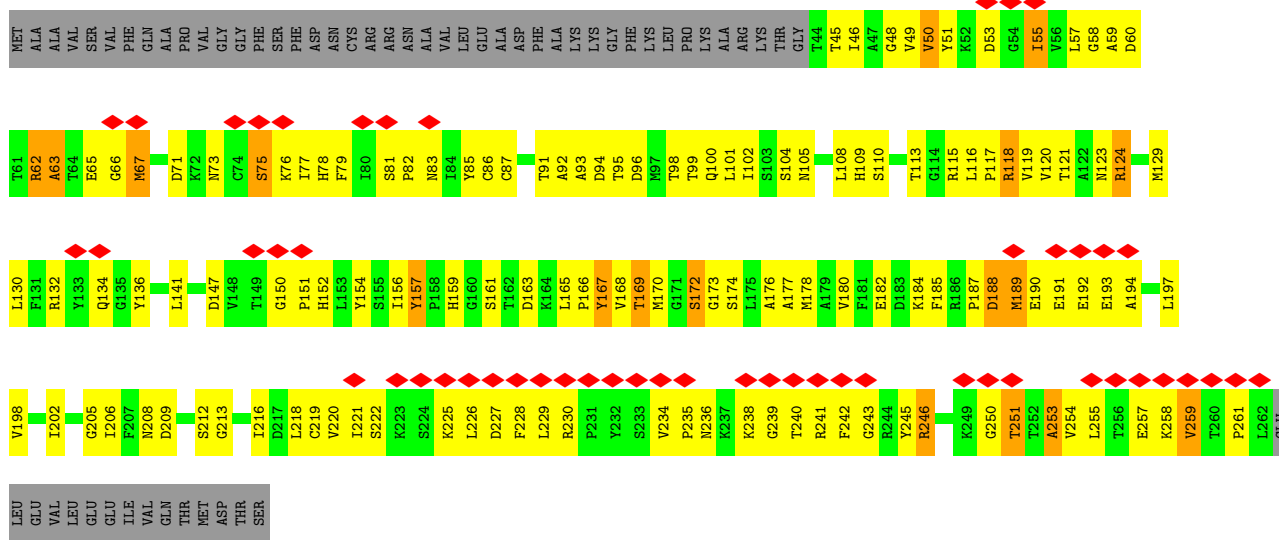
- Molecule 8: Proteasome subunit beta type-6

Chain 1: 12% 37% 39% 8% 15%

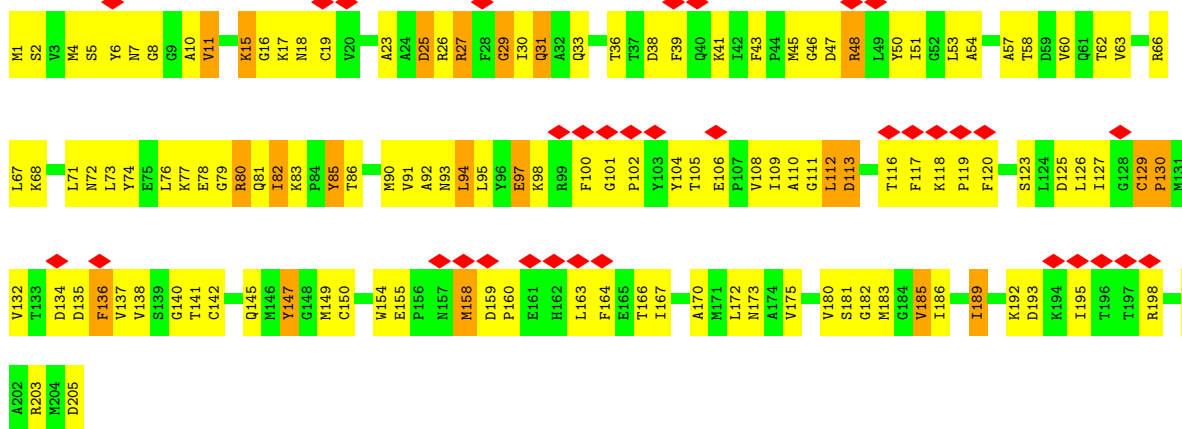




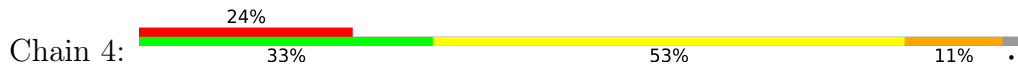
• Molecule 9: Proteasome subunit beta type-7

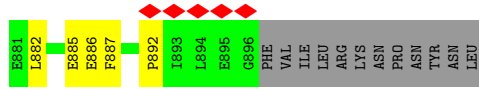


• Molecule 10: Proteasome subunit beta type-3

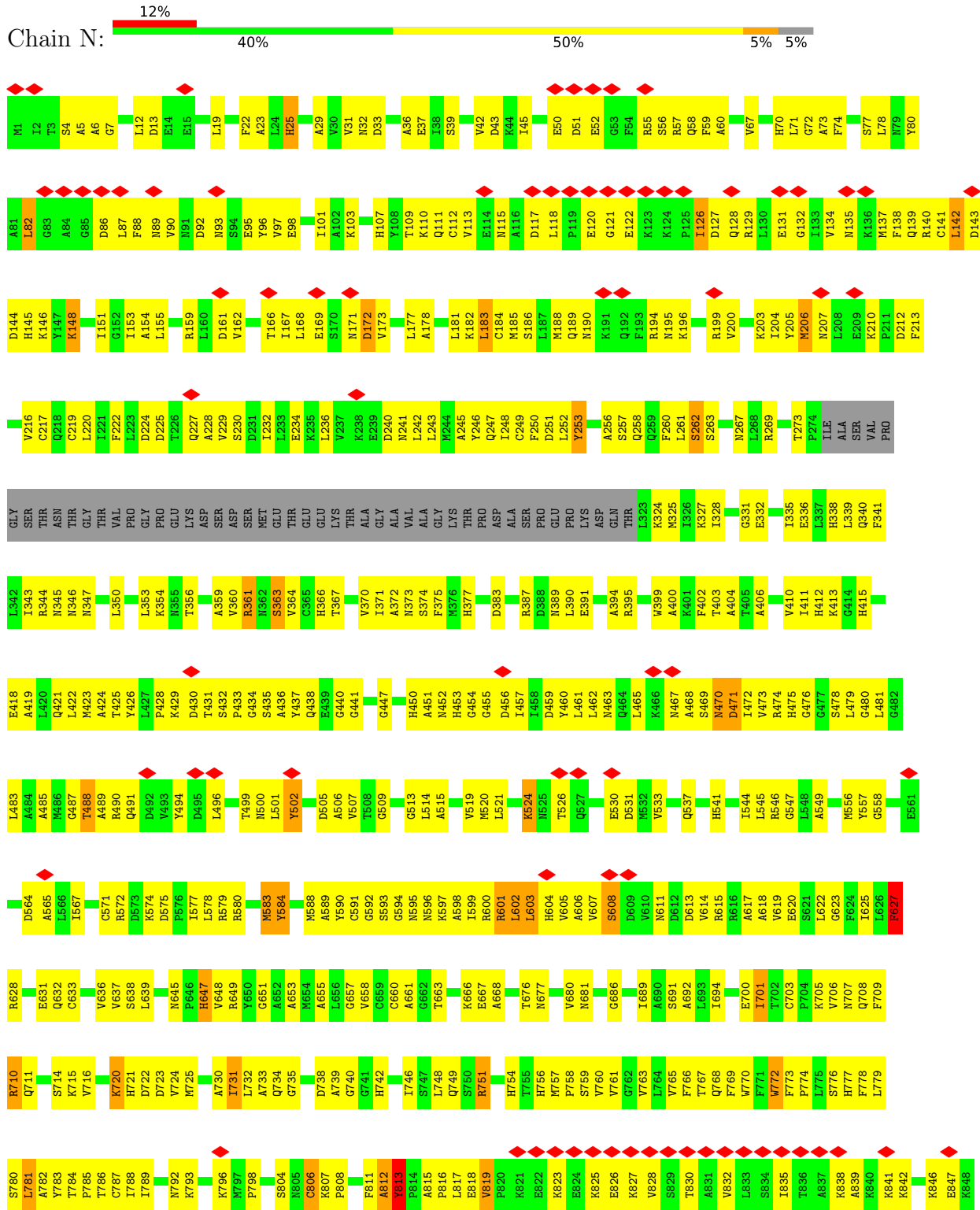


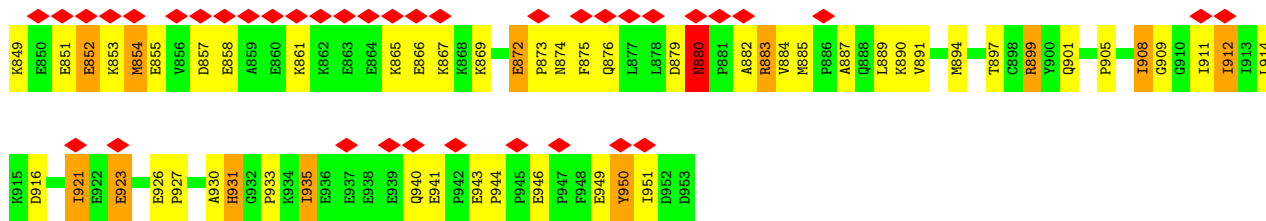
• Molecule 11: Proteasome subunit beta type-2



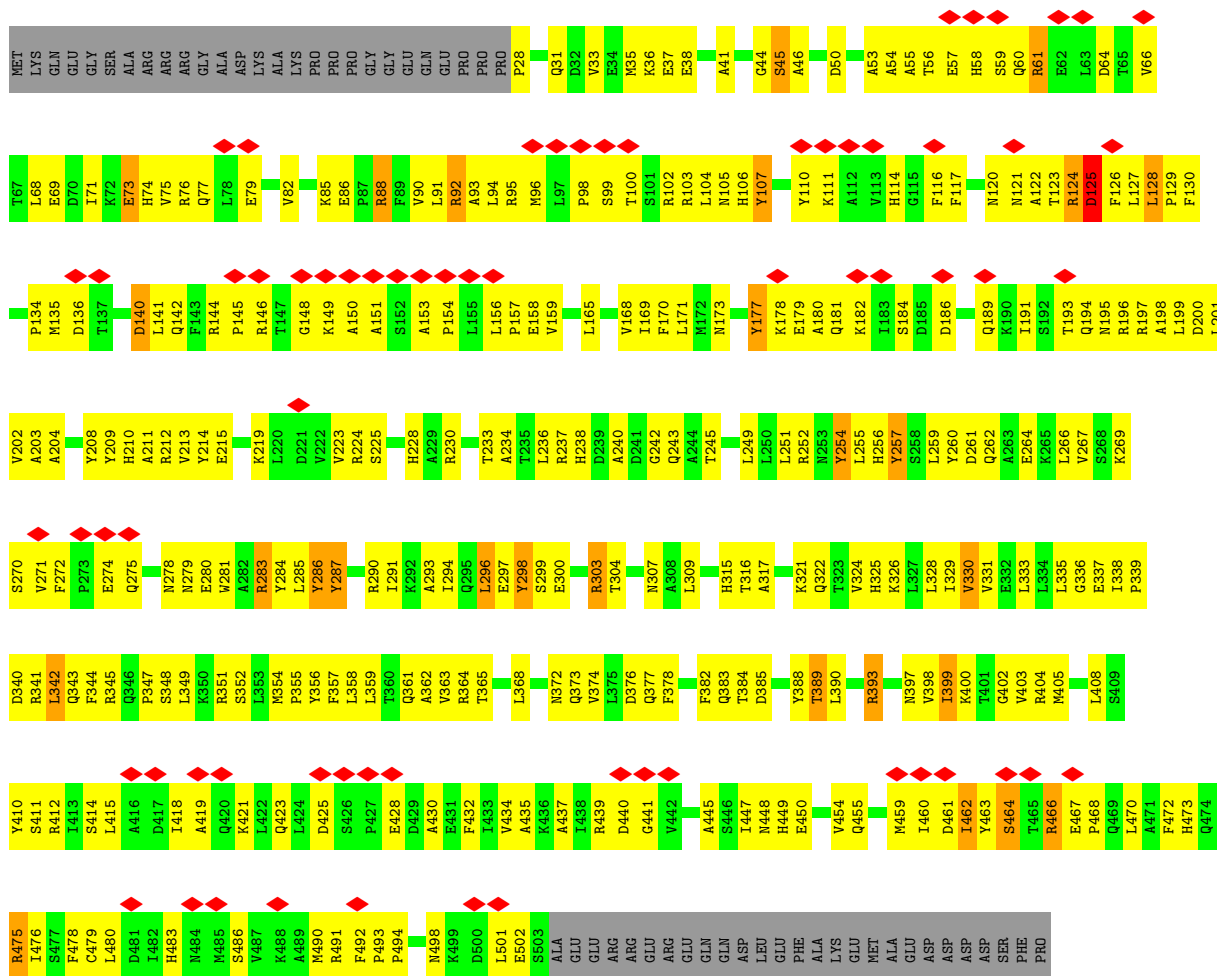


• Molecule 20: 26S proteasome non-ATPase regulatory subunit 1

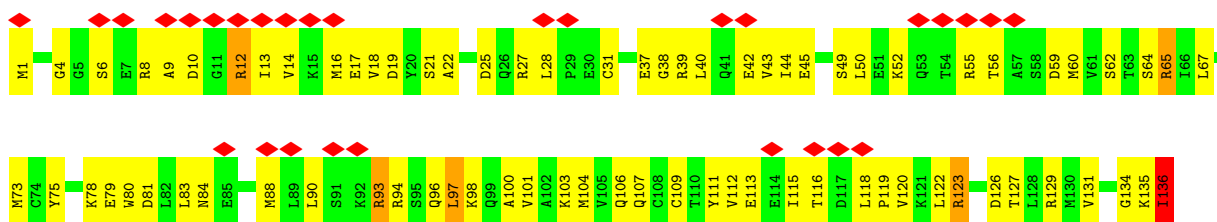


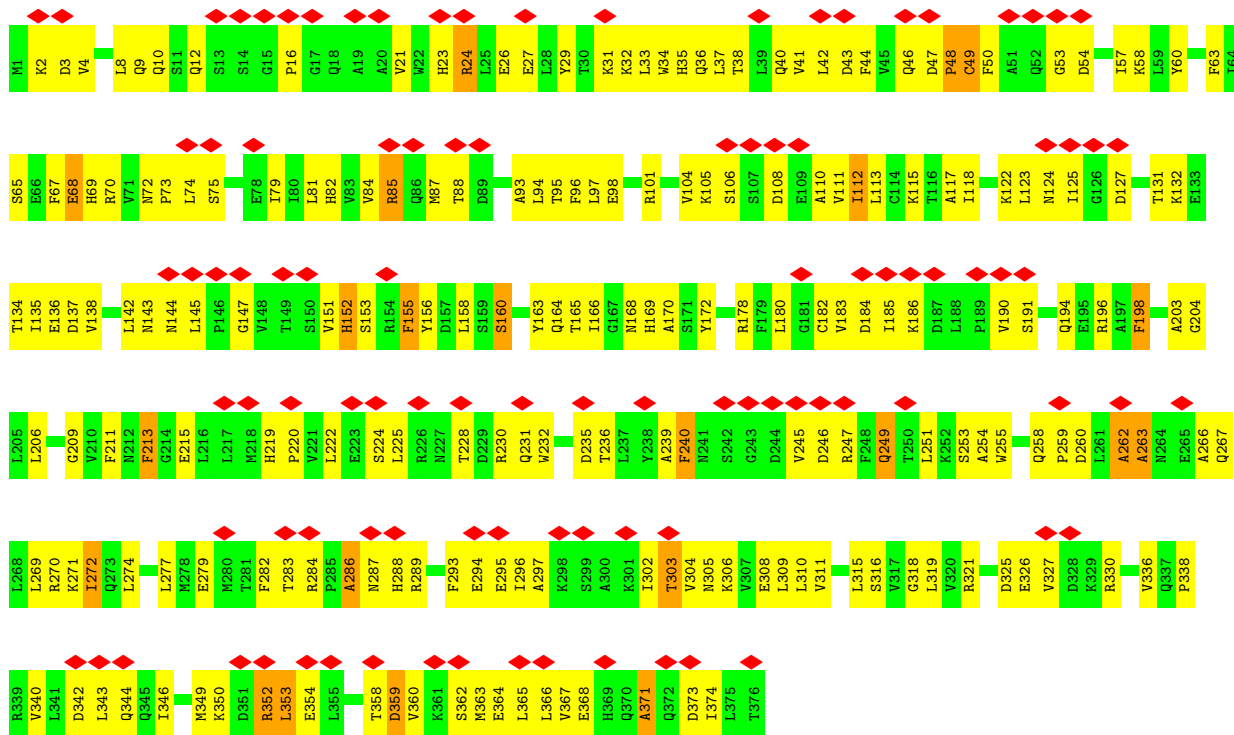


• Molecule 21: Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 3

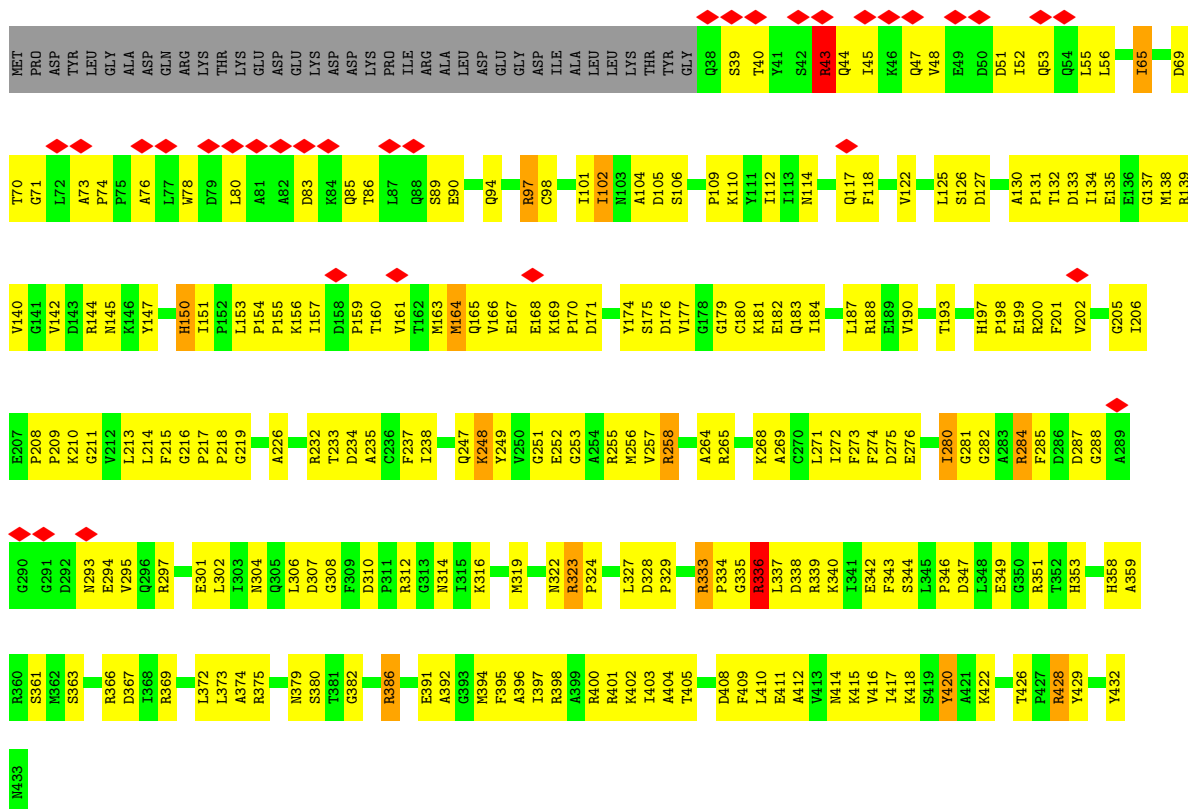


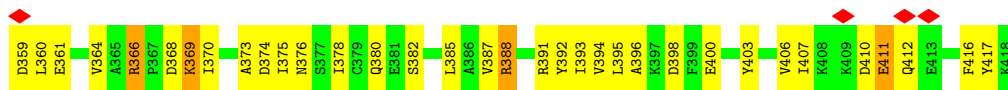
• Molecule 22: Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 12



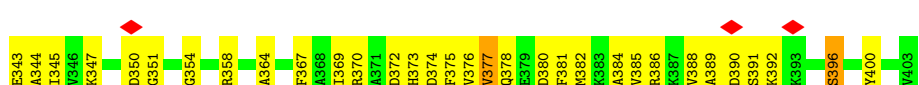
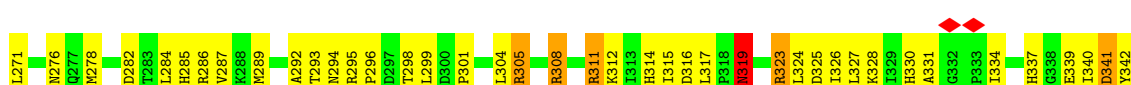
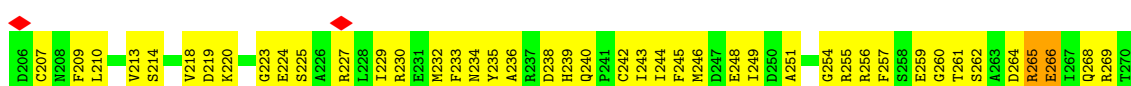
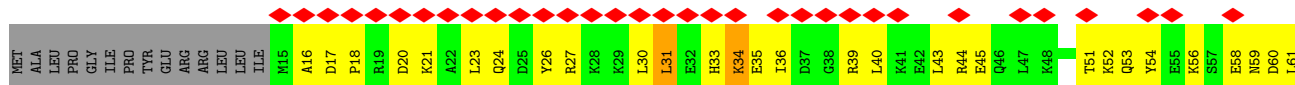


• Molecule 27: 26S proteasome regulatory subunit 7

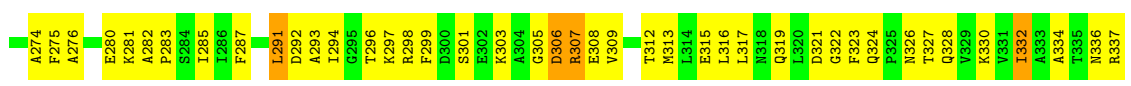
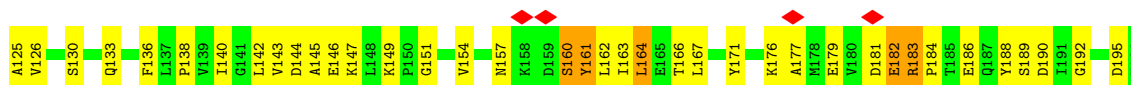
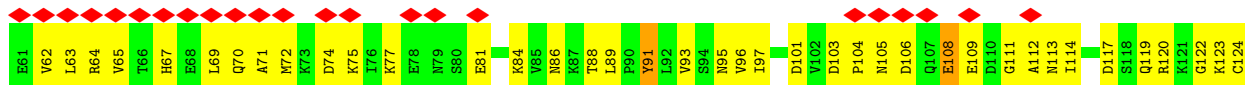


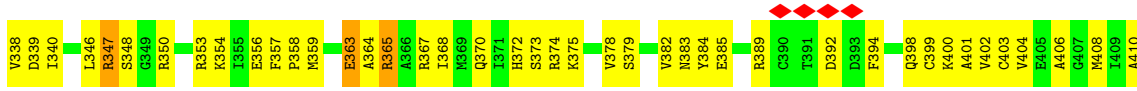


• Molecule 30: Proteasome 26S subunit, ATPase 6

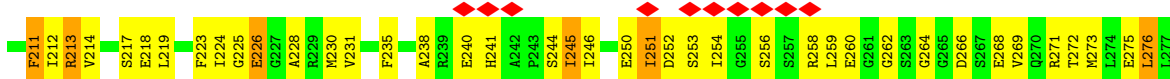
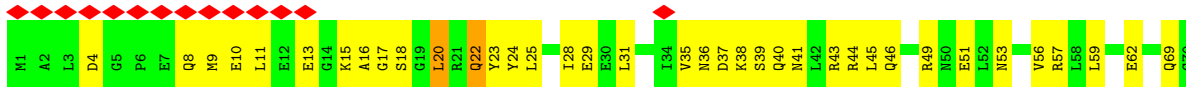


• Molecule 31: 26S proteasome regulatory subunit 6A





• Molecule 32: 26S proteasome regulatory subunit 8



4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	7393	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.8	Depositor
Minimum defocus (nm)	5000	Depositor
Maximum defocus (nm)	7000	Depositor
Magnification	42000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.860	Depositor
Minimum map value	-0.446	Depositor
Average map value	-0.037	Depositor
Map value standard deviation	0.171	Depositor
Recommended contour level	0.4	Depositor
Map size (Å)	307.80002, 307.80002, 307.80002	wwPDB
Map dimensions	90, 90, 90	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	3.4200003, 3.4200003, 3.4200003	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	A	2.30	74/1954 (3.8%)	2.46	120/2638 (4.5%)
2	B	2.25	62/1867 (3.3%)	2.55	151/2527 (6.0%)
3	C	2.32	82/1990 (4.1%)	2.50	137/2680 (5.1%)
4	D	2.31	74/1953 (3.8%)	2.50	135/2637 (5.1%)
5	E	2.73	66/1806 (3.7%)	2.54	133/2439 (5.5%)
6	F	2.34	83/1906 (4.4%)	2.47	137/2577 (5.3%)
7	G	2.23	61/1947 (3.1%)	2.41	118/2620 (4.5%)
8	1	2.28	52/1542 (3.4%)	2.58	125/2089 (6.0%)
9	2	2.28	63/1679 (3.8%)	2.52	124/2271 (5.5%)
10	3	2.23	51/1629 (3.1%)	2.63	139/2195 (6.3%)
11	4	2.31	67/1604 (4.2%)	2.51	121/2170 (5.6%)
12	5	2.55	69/1592 (4.3%)	2.55	121/2152 (5.6%)
13	6	2.26	58/1690 (3.4%)	2.54	119/2278 (5.2%)
14	7	2.33	72/1720 (4.2%)	2.54	133/2327 (5.7%)
15	W	2.35	56/1500 (3.7%)	2.56	112/2030 (5.5%)
16	V	2.32	90/2315 (3.9%)	2.60	194/3129 (6.2%)
17	T	2.23	66/2195 (3.0%)	2.50	177/2964 (6.0%)
18	Y	2.54	12/201 (6.0%)	2.55	12/266 (4.5%)
19	Z	2.32	282/7026 (4.0%)	2.66	644/9495 (6.8%)
20	N	2.31	287/7206 (4.0%)	2.57	600/9738 (6.2%)
21	S	2.35	160/3918 (4.1%)	2.62	339/5287 (6.4%)
22	P	2.26	131/3754 (3.5%)	2.56	309/5049 (6.1%)
23	Q	2.31	132/3381 (3.9%)	2.62	305/4558 (6.7%)
24	R	2.30	125/3263 (3.8%)	2.58	245/4393 (5.6%)
25	U	2.29	89/2344 (3.8%)	2.55	182/3178 (5.7%)
26	O	2.27	111/3066 (3.6%)	2.56	247/4148 (6.0%)
27	H	2.27	111/3166 (3.5%)	2.52	232/4275 (5.4%)
28	I	2.33	148/3085 (4.8%)	2.56	242/4158 (5.8%)
29	K	2.26	132/3178 (4.2%)	2.51	209/4290 (4.9%)
30	L	2.33	132/3146 (4.2%)	2.55	265/4233 (6.3%)
31	M	2.27	117/3293 (3.6%)	2.56	252/4436 (5.7%)
32	J	2.32	126/3236 (3.9%)	2.54	236/4347 (5.4%)
All	All	2.31	3241/84152 (3.9%)	2.56	6615/113574 (5.8%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	8
2	B	0	11
3	C	0	6
4	D	0	8
5	E	0	2
6	F	0	8
7	G	0	8
8	1	0	6
9	2	0	6
10	3	0	9
11	4	0	4
12	5	0	11
13	6	0	9
14	7	0	4
15	W	0	3
16	V	0	5
17	T	0	11
18	Y	0	1
19	Z	0	19
20	N	0	17
21	S	0	22
22	P	0	12
23	Q	0	10
24	R	0	12
25	U	0	6
26	O	0	9
27	H	0	11
28	I	0	12
29	K	0	11
30	L	0	11
31	M	0	8
32	J	0	11
All	All	0	291

The worst 5 of 3241 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	E	97	GLN	CG-CD	65.28	3.15	1.52
12	5	125	TYR	CG-CD1	18.96	1.79	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	5	125	TYR	CE2-CZ	17.77	1.80	1.38
12	5	125	TYR	CG-CD2	17.70	1.76	1.39
12	5	125	TYR	CD1-CE1	15.07	1.83	1.38

The worst 5 of 6615 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
19	Z	718	ASP	CA-C-O	-13.62	108.34	120.60
5	E	97	GLN	CB-CG-CD	13.50	135.55	112.60
29	K	302	ASN	CA-CB-CG	12.66	125.26	112.60
3	C	51	ASN	CA-CB-CG	-12.46	100.14	112.60
4	D	82	LEU	N-CA-C	-12.42	95.53	110.44

There are no chirality outliers.

5 of 291 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	103	TYR	Sidechain
1	A	160	TYR	Sidechain
1	A	23	TYR	Sidechain
1	A	88	ARG	Sidechain
1	A	93	ARG	Sidechain

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1920	0	1927	0	0
2	B	1828	0	1823	0	0
3	C	1960	0	1983	0	0
4	D	1926	0	1955	0	0
5	E	1778	0	1756	0	0
6	F	1871	0	1856	0	0
7	G	1912	0	1907	0	0
8	1	1516	0	1485	0	0
9	2	1651	0	1674	0	0
10	3	1600	0	1621	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	4	1572	0	1575	0	0
12	5	1560	0	1519	0	0
13	6	1659	0	1654	0	0
14	7	1686	0	1662	0	0
15	W	1480	0	1522	0	0
16	V	2272	0	2288	0	0
17	T	2149	0	2170	0	0
18	Y	199	0	180	0	0
19	Z	6913	0	6910	0	0
20	N	7082	0	7121	0	0
21	S	3844	0	3888	0	0
22	P	3706	0	3817	0	0
23	Q	3335	0	3435	0	0
24	R	3204	0	3204	0	0
25	U	2299	0	2334	0	0
26	O	3011	0	3042	0	0
27	H	3113	0	3162	0	0
28	I	3042	0	3098	0	0
29	K	3125	0	3151	0	0
30	L	3098	0	3171	0	0
31	M	3252	0	3321	0	0
32	J	3194	0	3311	0	0
All	All	82757	0	83522	0	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). Clashscore could not be calculated for this entry.

There are no clashes within the asymmetric unit.

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	244/246 (99%)	233 (96%)	7 (3%)	4 (2%)	7	38
2	B	232/234 (99%)	217 (94%)	13 (6%)	2 (1%)	14	51
3	C	247/261 (95%)	238 (96%)	8 (3%)	1 (0%)	30	67
4	D	244/254 (96%)	230 (94%)	11 (4%)	3 (1%)	10	44
5	E	231/241 (96%)	222 (96%)	9 (4%)	0	100	100
6	F	236/263 (90%)	216 (92%)	18 (8%)	2 (1%)	16	54
7	G	243/255 (95%)	225 (93%)	14 (6%)	4 (2%)	7	38
8	1	200/238 (84%)	169 (84%)	19 (10%)	12 (6%)	1	13
9	2	217/277 (78%)	184 (85%)	19 (9%)	14 (6%)	1	12
10	3	203/205 (99%)	167 (82%)	19 (9%)	17 (8%)	0	9
11	4	194/201 (96%)	172 (89%)	12 (6%)	10 (5%)	1	15
12	5	199/263 (76%)	179 (90%)	15 (8%)	5 (2%)	4	26
13	6	211/240 (88%)	182 (86%)	21 (10%)	8 (4%)	2	19
14	7	214/263 (81%)	188 (88%)	18 (8%)	8 (4%)	2	20
15	W	193/377 (51%)	171 (89%)	15 (8%)	7 (4%)	2	20
16	V	287/310 (93%)	264 (92%)	15 (5%)	8 (3%)	4	24
17	T	261/353 (74%)	234 (90%)	23 (9%)	4 (2%)	8	40
18	Y	22/70 (31%)	21 (96%)	1 (4%)	0	100	100
19	Z	894/908 (98%)	805 (90%)	64 (7%)	25 (3%)	4	24
20	N	901/953 (94%)	827 (92%)	50 (6%)	24 (3%)	4	25
21	S	474/530 (89%)	438 (92%)	24 (5%)	12 (2%)	4	26
22	P	454/456 (100%)	422 (93%)	23 (5%)	9 (2%)	6	31
23	Q	420/422 (100%)	390 (93%)	19 (4%)	11 (3%)	4	25
24	R	387/389 (100%)	367 (95%)	15 (4%)	5 (1%)	9	42
25	U	286/320 (89%)	263 (92%)	14 (5%)	9 (3%)	3	22
26	O	374/376 (100%)	346 (92%)	19 (5%)	9 (2%)	4	27
27	H	394/433 (91%)	348 (88%)	38 (10%)	8 (2%)	6	31
28	I	383/440 (87%)	349 (91%)	20 (5%)	14 (4%)	2	20
29	K	389/418 (93%)	356 (92%)	30 (8%)	3 (1%)	16	54
30	L	387/403 (96%)	359 (93%)	21 (5%)	7 (2%)	6	34
31	M	413/442 (93%)	380 (92%)	25 (6%)	8 (2%)	6	32
32	J	404/406 (100%)	369 (91%)	27 (7%)	8 (2%)	6	31

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	10438/11447 (91%)	9531 (91%)	646 (6%)	261 (2%)	6	26

5 of 261 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	D	75	VAL
8	1	45	VAL
8	1	81	SER
8	1	105	GLU
8	1	163	SER

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	210/210 (100%)	198 (94%)	12 (6%)	18	40
2	B	191/191 (100%)	183 (96%)	8 (4%)	26	48
3	C	209/221 (95%)	189 (90%)	20 (10%)	8	25
4	D	208/215 (97%)	199 (96%)	9 (4%)	26	47
5	E	195/203 (96%)	182 (93%)	13 (7%)	15	36
6	F	204/224 (91%)	196 (96%)	8 (4%)	28	49
7	G	202/212 (95%)	191 (95%)	11 (5%)	20	41
8	1	160/185 (86%)	145 (91%)	15 (9%)	8	26
9	2	180/227 (79%)	161 (89%)	19 (11%)	6	21
10	3	175/175 (100%)	159 (91%)	16 (9%)	9	27
11	4	167/172 (97%)	144 (86%)	23 (14%)	3	14
12	5	158/205 (77%)	142 (90%)	16 (10%)	7	23
13	6	179/200 (90%)	168 (94%)	11 (6%)	17	38
14	7	178/215 (83%)	162 (91%)	16 (9%)	9	27
15	W	168/312 (54%)	155 (92%)	13 (8%)	12	32
16	V	253/268 (94%)	240 (95%)	13 (5%)	21	42

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
17	T	233/298 (78%)	221 (95%)	12 (5%)	21	42
18	Y	22/63 (35%)	20 (91%)	2 (9%)	9	27
19	Z	753/765 (98%)	709 (94%)	44 (6%)	18	40
20	N	776/814 (95%)	735 (95%)	41 (5%)	20	41
21	S	414/458 (90%)	397 (96%)	17 (4%)	27	49
22	P	419/419 (100%)	398 (95%)	21 (5%)	22	43
23	Q	362/362 (100%)	340 (94%)	22 (6%)	17	38
24	R	345/345 (100%)	329 (95%)	16 (5%)	24	45
25	U	259/289 (90%)	248 (96%)	11 (4%)	26	48
26	O	334/334 (100%)	321 (96%)	13 (4%)	28	49
27	H	341/372 (92%)	326 (96%)	15 (4%)	25	47
28	I	341/385 (89%)	324 (95%)	17 (5%)	22	43
29	K	343/367 (94%)	323 (94%)	20 (6%)	18	40
30	L	341/353 (97%)	318 (93%)	23 (7%)	15	36
31	M	357/382 (94%)	342 (96%)	15 (4%)	26	48
32	J	352/352 (100%)	336 (96%)	16 (4%)	24	46
All	All	9029/9793 (92%)	8501 (94%)	528 (6%)	20	40

5 of 528 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
29	K	154	LEU
30	L	59	ASN
29	K	140	VAL
32	J	123	LEU
14	7	236	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

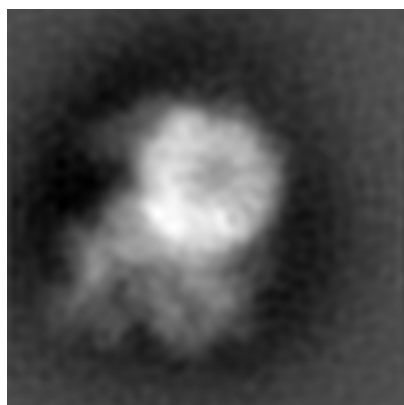
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3916. These allow visual inspection of the internal detail of the map and identification of artifacts.

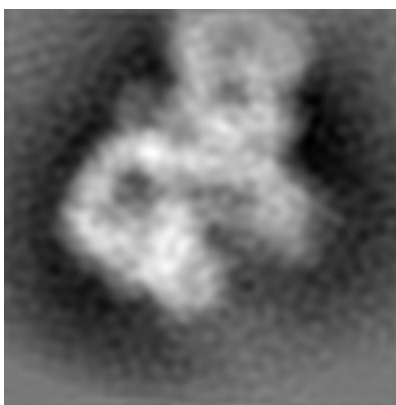
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

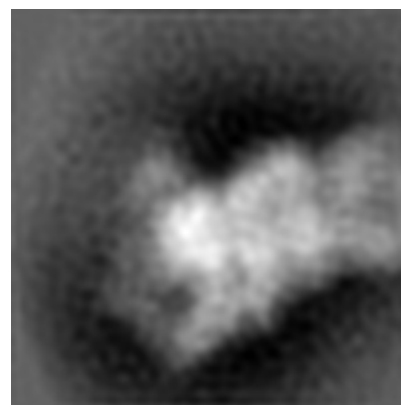
6.1.1 Primary map



X



Y

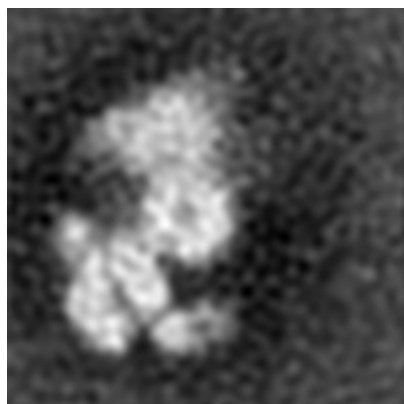


Z

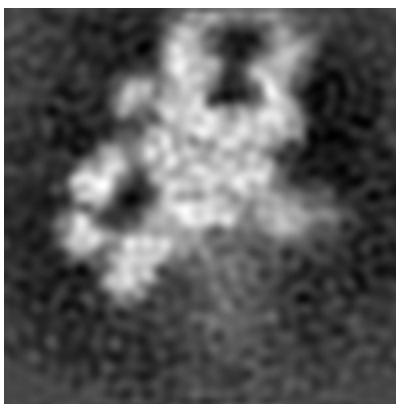
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

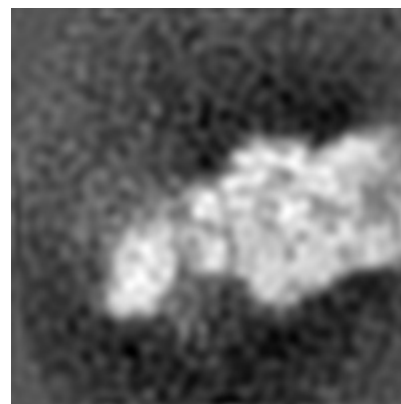
6.2.1 Primary map



X Index: 45



Y Index: 45

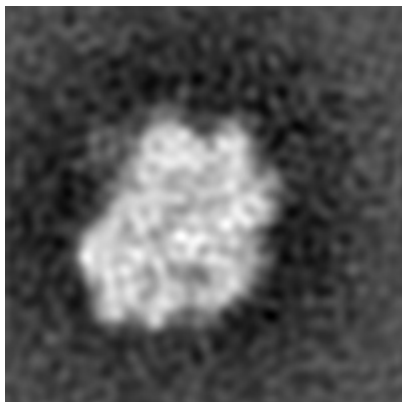


Z Index: 45

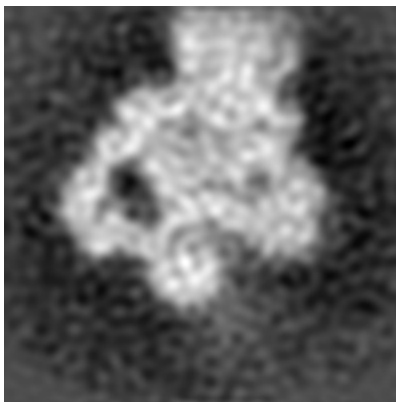
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [\(i\)](#)

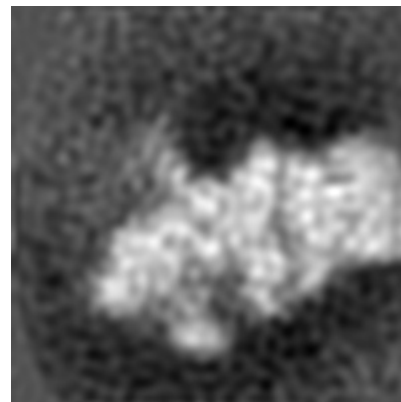
6.3.1 Primary map



X Index: 56



Y Index: 36

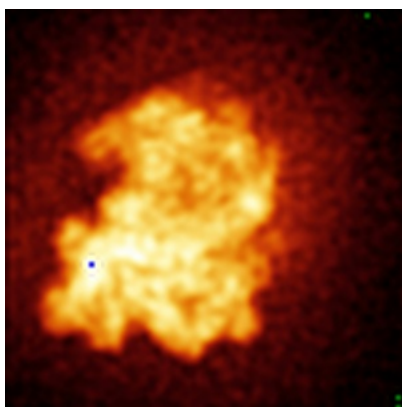


Z Index: 41

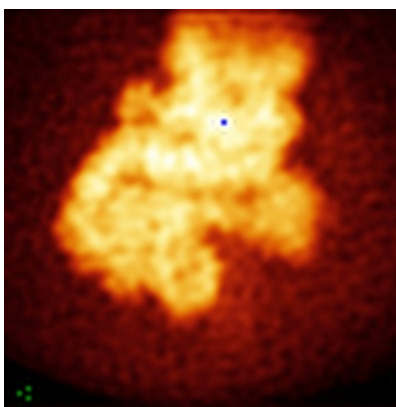
The images above show the largest variance slices of the map in three orthogonal directions.

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

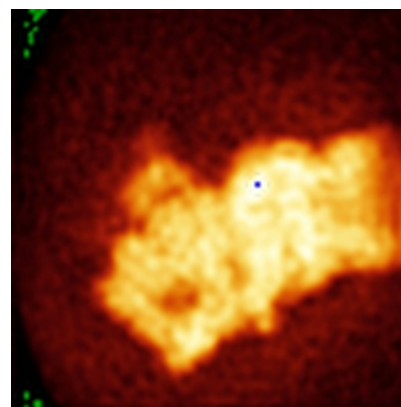
6.4.1 Primary map



X



Y

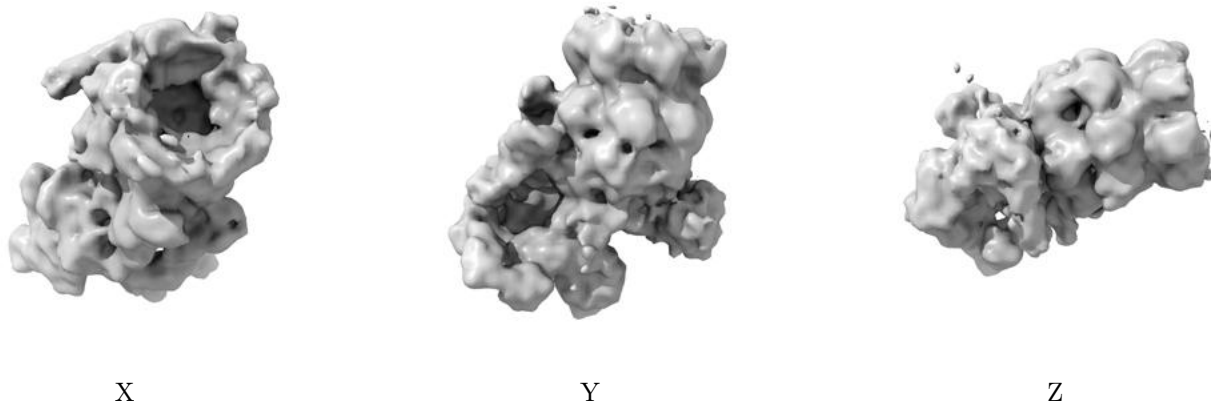


Z

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

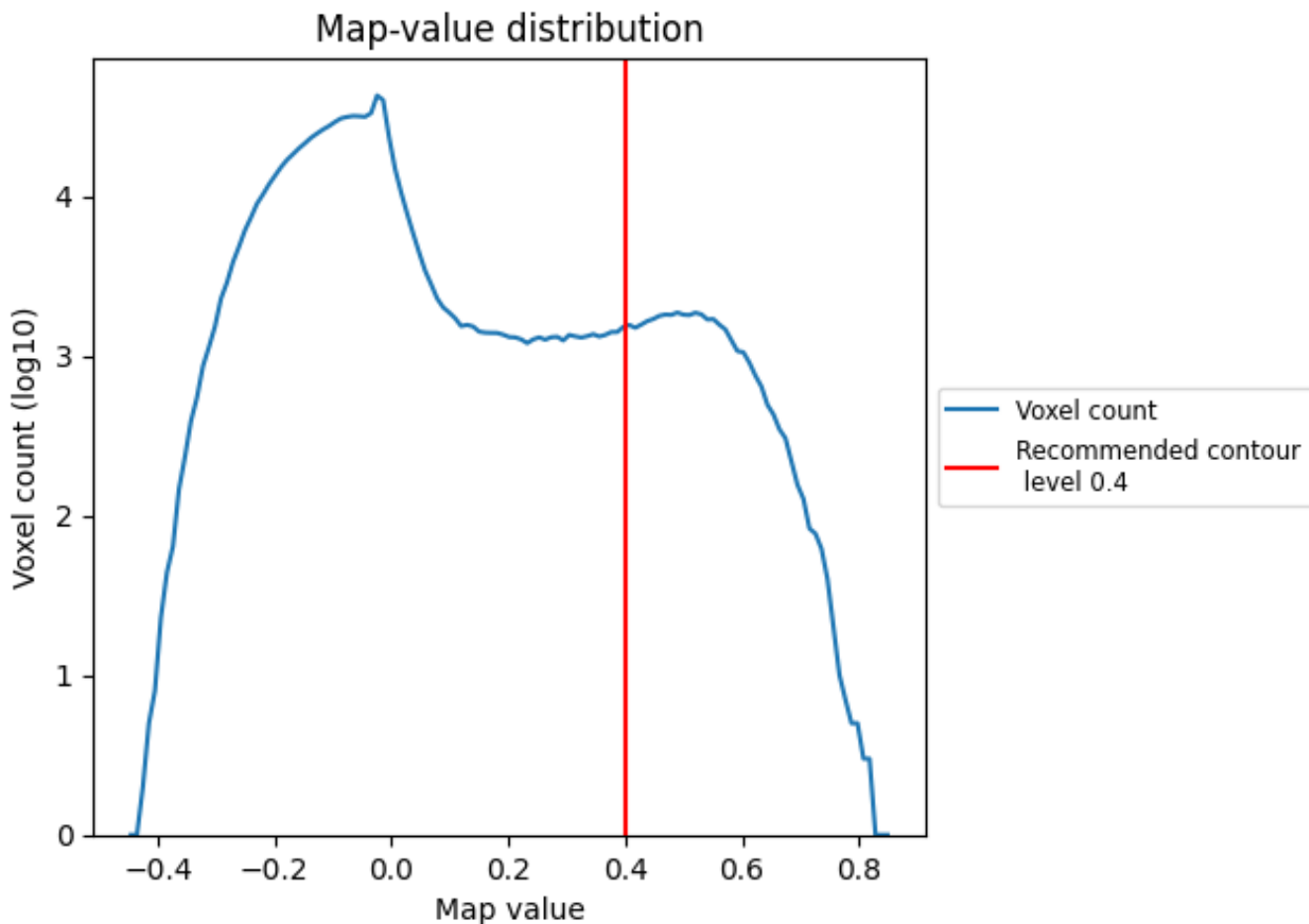
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

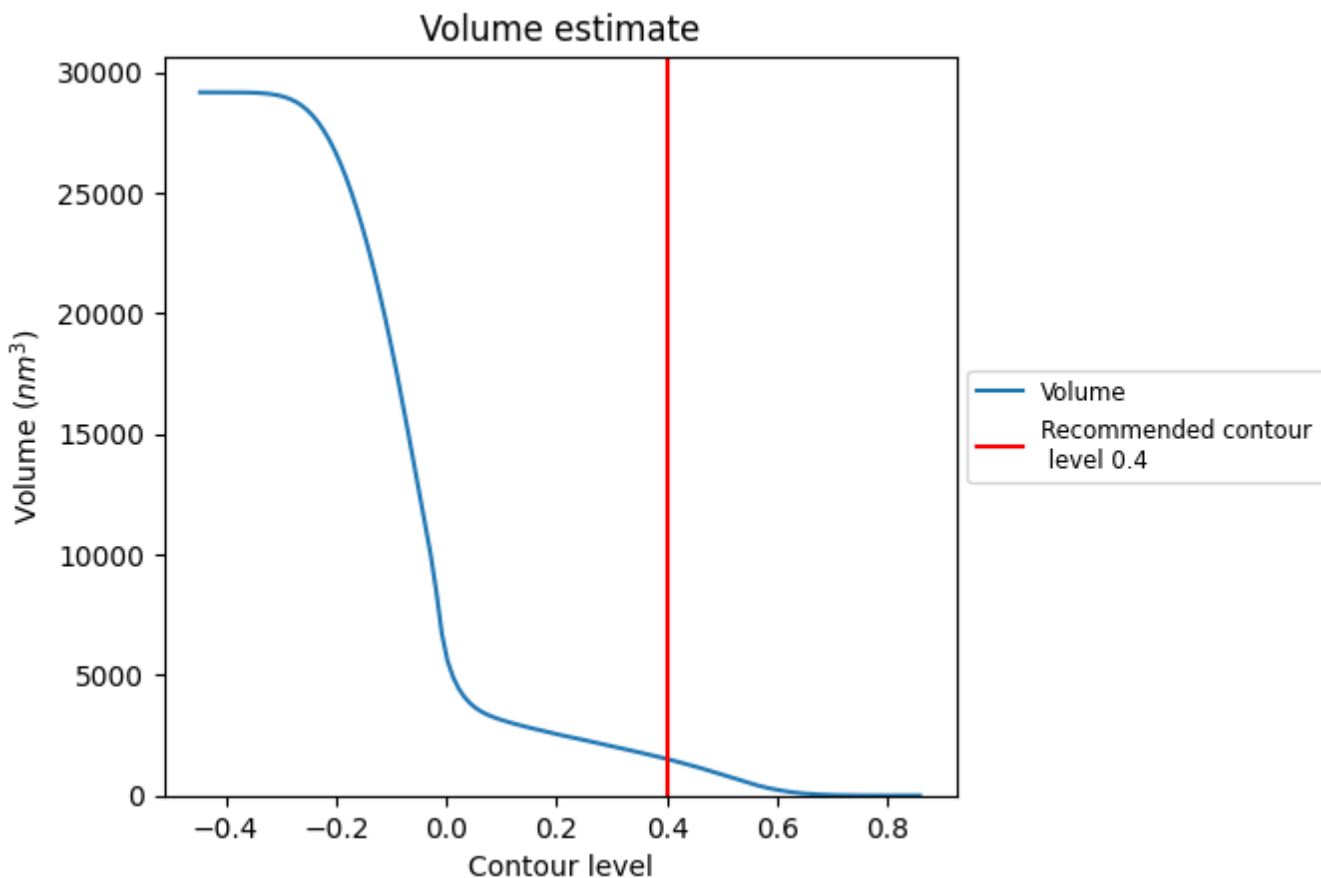
This section contains the results of statistical analysis of the map.

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.

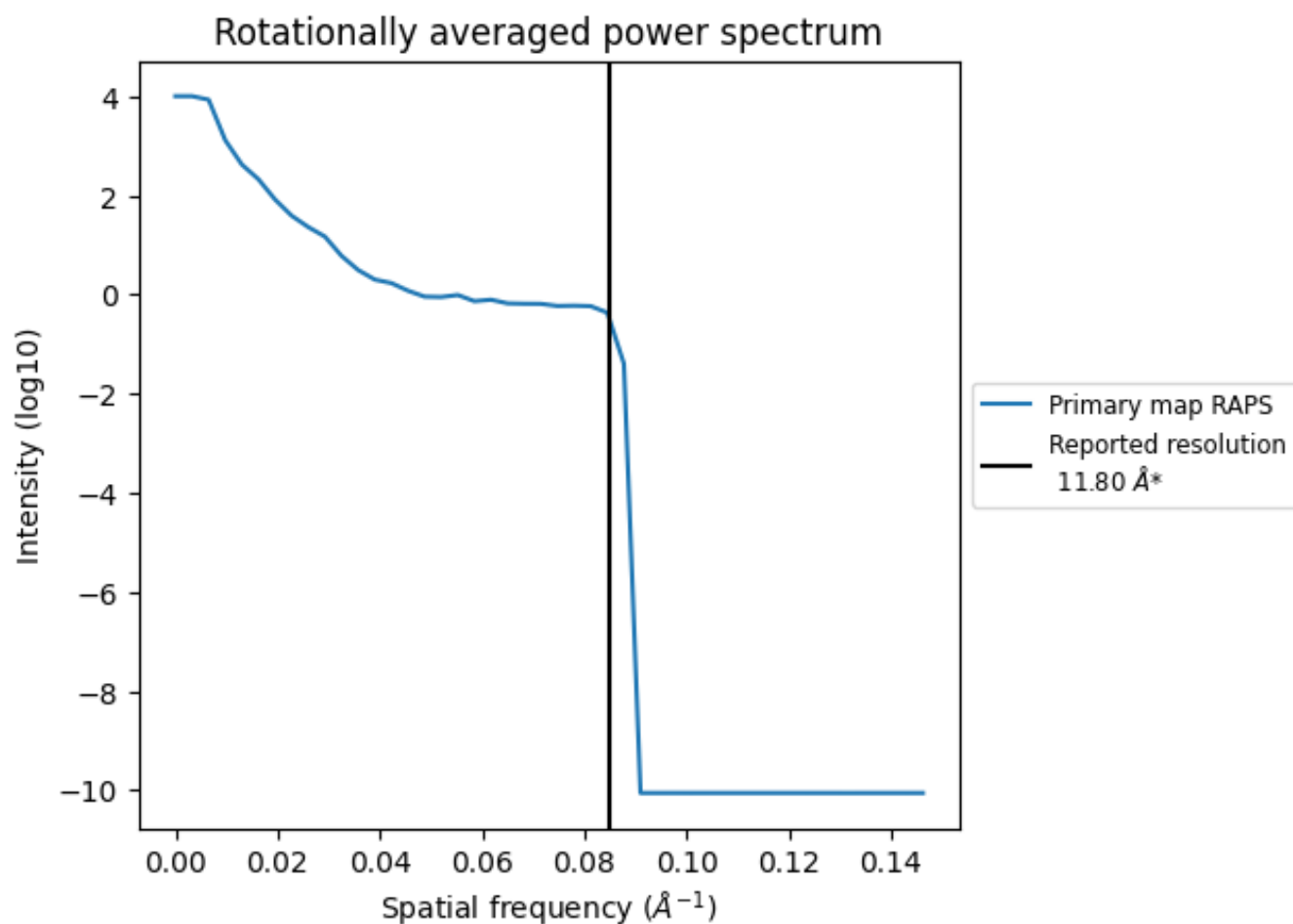
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1525 nm³; this corresponds to an approximate mass of 1377 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 0.085 Å⁻¹

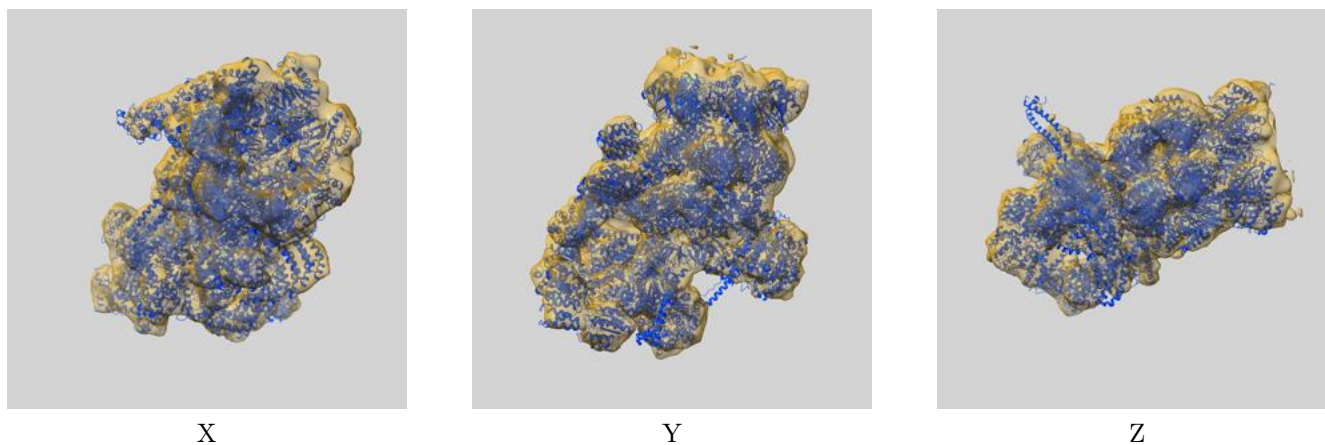
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

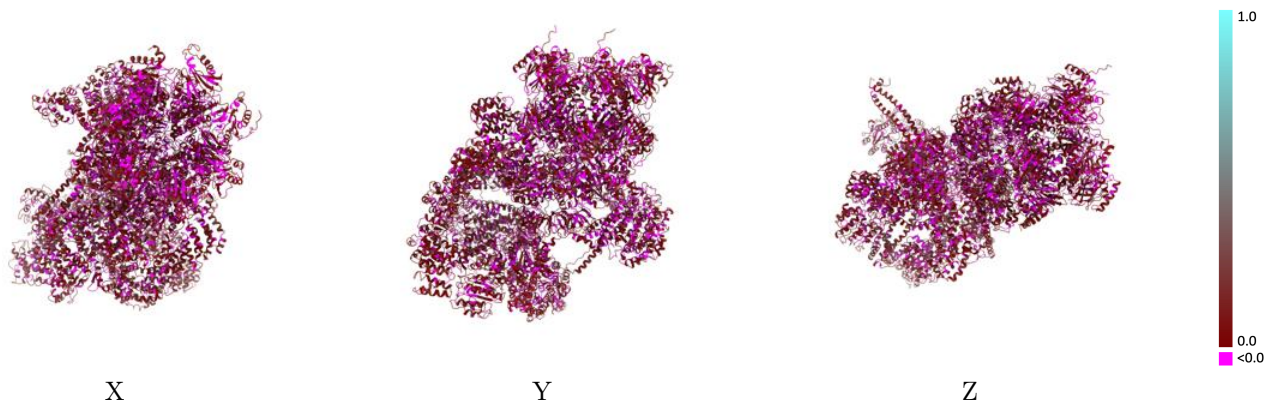
This section contains information regarding the fit between EMDB map EMD-3916 and PDB model 6EPF. Per-residue inclusion information can be found in section 3 on page 10.

9.1 Map-model overlay [i](#)



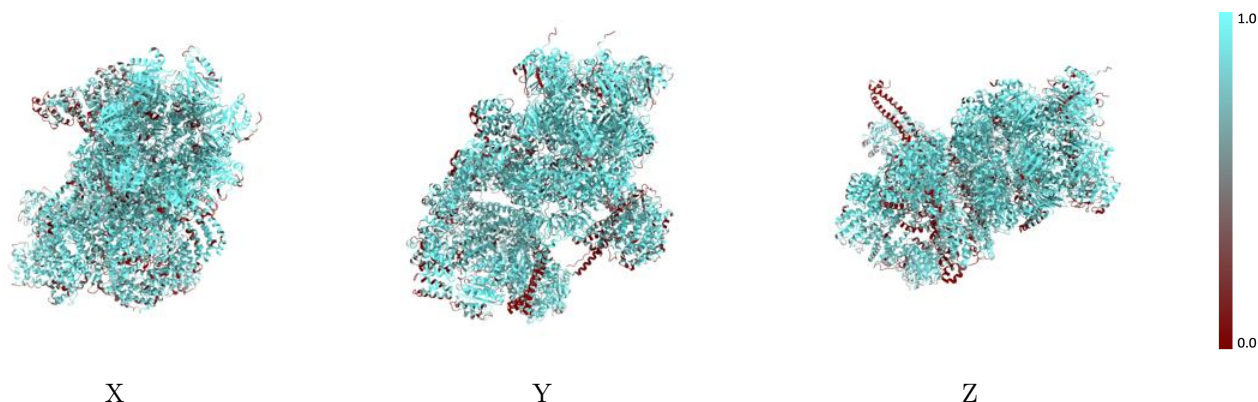
The images above show the 3D surface view of the map at the recommended contour level 0.4 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



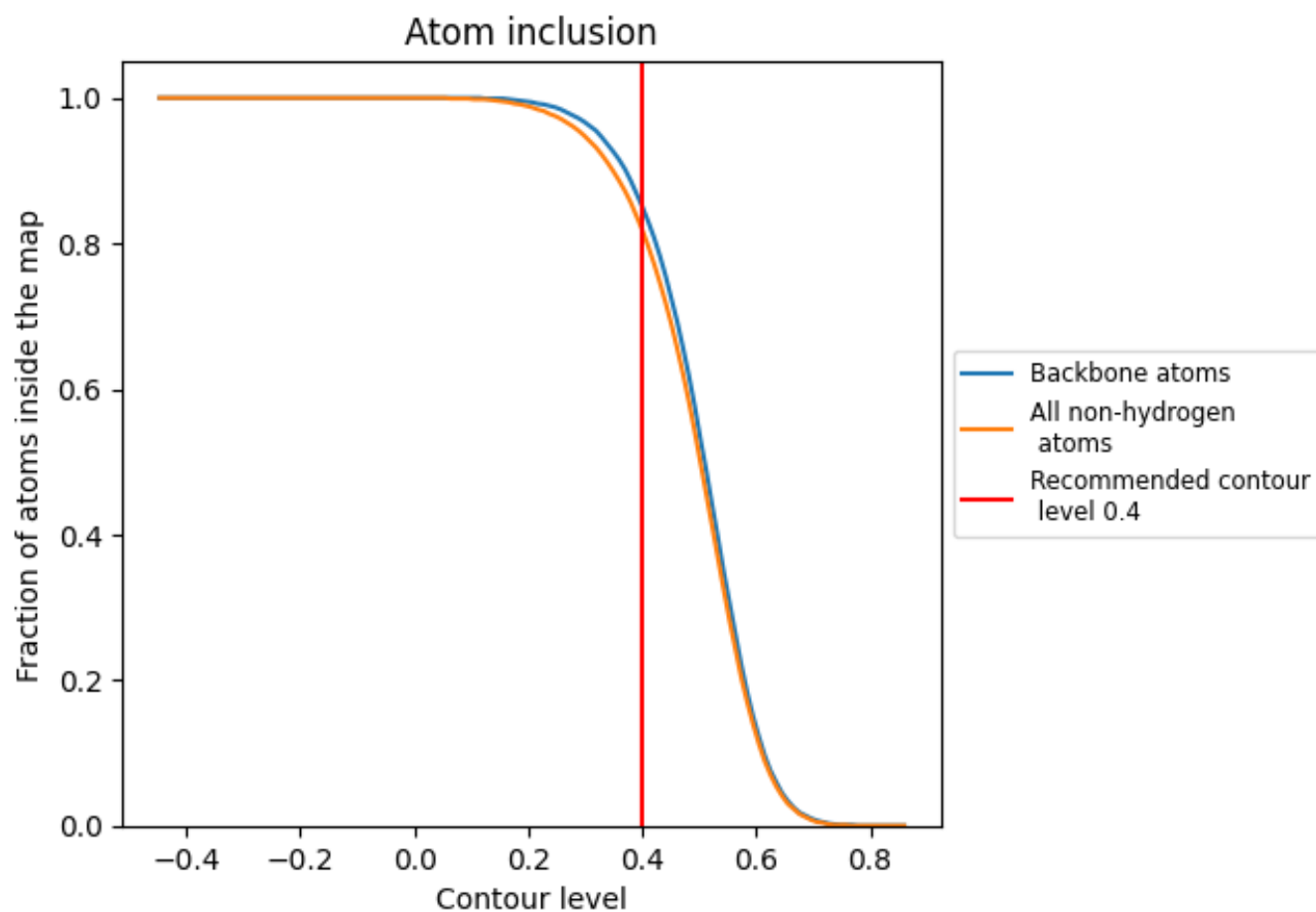
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.4).



































































9.4 Atom inclusion [i](#)



At the recommended contour level, 85% of all backbone atoms, 82% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8190	 0.0570
1	 0.8260	 0.0400
2	 0.7420	 0.0450
3	 0.7800	 0.0440
4	 0.7400	 0.0550
5	 0.8470	 0.0420
6	 0.7940	 0.0450
7	 0.7890	 0.0440
A	 0.8970	 0.0430
B	 0.8930	 0.0490
C	 0.8700	 0.0570
D	 0.8560	 0.0370
E	 0.9140	 0.0450
F	 0.9480	 0.0430
G	 0.9110	 0.0430
H	 0.8970	 0.0440
I	 0.8800	 0.0560
J	 0.8260	 0.0640
K	 0.8880	 0.0650
L	 0.8460	 0.0590
M	 0.8090	 0.0570
N	 0.8270	 0.0580
O	 0.6950	 0.0790
P	 0.7730	 0.0720
Q	 0.8060	 0.0750
R	 0.8390	 0.0730
S	 0.8270	 0.0560
T	 0.7750	 0.0810
U	 0.8000	 0.0610
V	 0.9360	 0.0670
W	 0.7790	 0.0790
Y	 0.7350	 0.0830
Z	 0.6670	 0.0460

