



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 06:40 AM UTC

PDB ID : 5LN3 / pdb_00005ln3
EMDB ID : EMD-4089
Title : The human 26S Proteasome at 6.8 Ang.
Authors : Schweitzer, A.; Beck, F.; Sakata, E.; Unverdorben, P.
Deposited on : 2016-08-03
Resolution : 6.80 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:

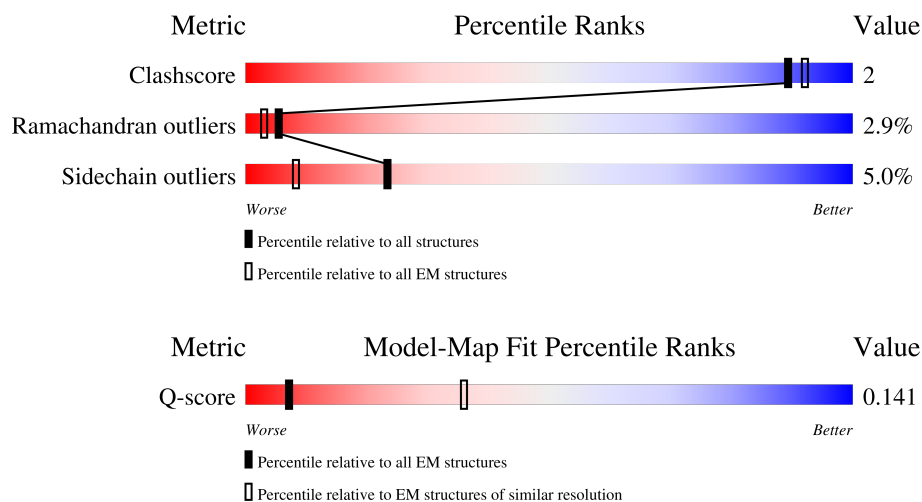
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 6.80 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))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	503 (6.30 - 7.30)

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	Z	908	79% 33% 48% 6% 13%
2	1	239	27% 45% 39% 5% 10%
3	2	277	15% 37% 37% 5% 20%
4	3	205	32% 43% 46% 10%

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Mol	Chain	Length	Quality of chain
5	4	201	
6	5	263	
7	6	241	
8	7	264	
9	A	246	
10	B	234	
11	C	261	
12	D	248	
13	E	241	
14	F	263	
15	G	255	
16	H	433	
17	I	440	
18	J	406	
19	K	418	
20	L	389	
21	M	439	
22	N	953	
23	O	376	
24	P	456	
25	Q	422	
26	R	389	
27	S	534	
28	T	350	
29	U	324	

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Mol	Chain	Length	Quality of chain
30	V	310	22% 35% 41% 5% 19%
31	W	377	21% 22% 24% 51%
32	Y	70	16% 16% 14% 70%

2 Entry composition

There are 32 unique types of molecules in this entry. The entry contains 78323 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 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	Z	794	Total	C	N	O	S	0	0
			6146	3893	1043	1166	44		

- Molecule 2 is a protein called Proteasome subunit beta type-6.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	214	Total	C	N	O	S	0	0
			1607	1006	274	315	12		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	222	Total	C	N	O	S	0	0
			1676	1055	285	324	12		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	205	Total	C	N	O	S	0	0
			1599	1018	266	295	20		

- Molecule 5 is a protein called Proteasome subunit beta type-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	194	Total	C	N	O	S	0	0
			1554	994	265	286	9		

- Molecule 6 is a protein called Proteasome subunit beta type-5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	5	195	Total	C	N	O	S	0	0
			1509	951	265	284	9		

- Molecule 7 is a protein called Proteasome subunit beta type-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	6	213	Total	C	N	O	S	0	0
			1654	1047	284	313	10		

- Molecule 8 is a protein called Proteasome subunit beta type-4.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	7	218	Total	C	N	O	S	0	0
			1705	1076	293	324	12		

- Molecule 9 is a protein called Proteasome subunit alpha type-6.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	A	239	Total	C	N	O	S	0	0
			1874	1190	312	359	13		

- Molecule 10 is a protein called Proteasome subunit alpha type-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	B	234	Total	C	N	O	S	0	0
			1826	1166	309	344	7		

- Molecule 11 is a protein called Proteasome subunit alpha type-4.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	C	261	Total	C	N	O	S	0	0
			2069	1304	356	398	11		

- Molecule 12 is a protein called Proteasome subunit alpha type-7.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	D	248	Total	C	N	O	S	0	0
			1961	1229	349	377	6		

- Molecule 13 is a protein called Proteasome subunit alpha type-5.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	E	232	Total	C	N	O	S	0	0
			1770	1112	293	354	11		

- Molecule 14 is a protein called Proteasome subunit alpha type-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	F	233	Total	C	N	O	S	0	0
			1837	1153	331	341	12		

- Molecule 15 is a protein called Proteasome subunit alpha type-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	G	242	Total	C	N	O	S	0	0
			1894	1200	323	360	11		

- Molecule 16 is a protein called 26S protease regulatory subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	H	378	Total	C	N	O	S	0	0
			2962	1865	522	558	17		

- Molecule 17 is a protein called 26S protease regulatory subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	I	362	Total	C	N	O	S	0	0
			2840	1782	483	562	13		

- Molecule 18 is a protein called 26S protease regulatory subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	J	373	Total	C	N	O	S	0	0
			2929	1839	525	548	17		

- Molecule 19 is a protein called 26S protease regulatory subunit 6B.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	K	379	Total	C	N	O	S	0	0
			3032	1919	523	577	13		

- Molecule 20 is a protein called 26S protease regulatory subunit 10B.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	L	361	Total	C	N	O	S	0	0
			2862	1797	512	537	16		

- Molecule 21 is a protein called 26S protease regulatory subunit 6A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	M	389	Total	C	N	O	S	0	0
			3046	1914	526	589	17		

- Molecule 22 is a protein called 26S proteasome non-ATPase regulatory subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	N	836	Total	C	N	O	S	0	0
			6508	4130	1106	1229	43		

- Molecule 23 is a protein called 26S proteasome non-ATPase regulatory subunit 13.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	O	376	Total	C	N	O	S	0	0
			3020	1926	514	564	16		

- Molecule 24 is a protein called 26S proteasome non-ATPase regulatory subunit 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	P	422	Total	C	N	O	S	0	0
			3447	2185	589	651	22		

- Molecule 25 is a protein called 26S proteasome non-ATPase regulatory subunit 11.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
26	R	374	Total	C	N	O	S	0	0
			3084	1967	527	573	17		

- Molecule 27 is a protein called 26S proteasome non-ATPase regulatory subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	S	338	Total	C	N	O	S	0	0
			2757	1761	489	497	10		

- Molecule 28 is a protein called 26S proteasome non-ATPase regulatory subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	T	253	Total	C	N	O	S	0	0
			2056	1332	337	378	9		

- Molecule 29 is a protein called 26S proteasome non-ATPase regulatory subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	U	272	Total	C	N	O	S	0	0
			2183	1401	373	403	6		

- Molecule 30 is a protein called 26S proteasome non-ATPase regulatory subunit 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	V	252	Total	C	N	O	S	0	0
			1986	1261	342	366	17		

- Molecule 31 is a protein called 26S proteasome non-ATPase regulatory subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	W	185	Total	C	N	O	S	0	0
			1420	885	255	272	8		

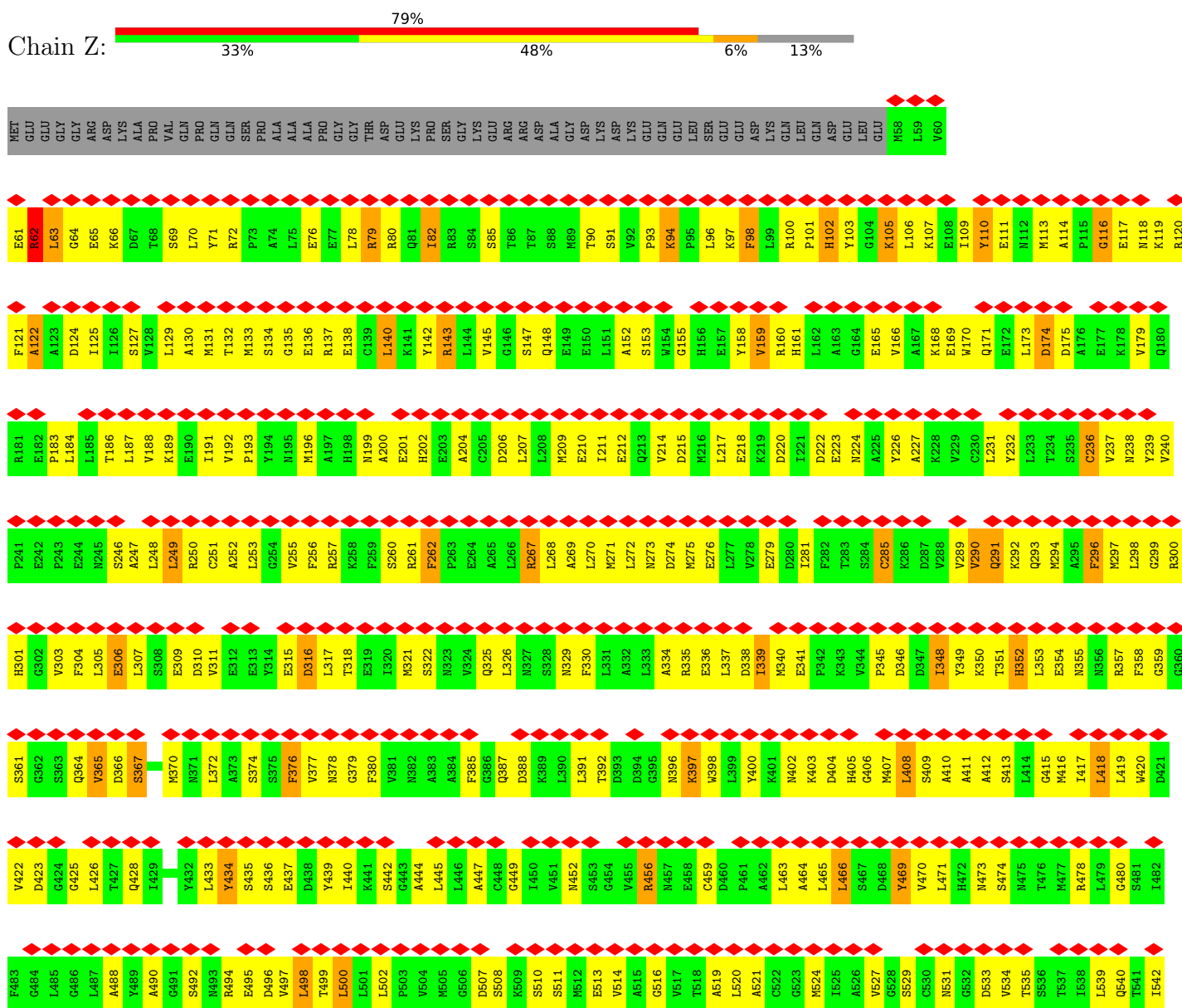
- Molecule 32 is a protein called 26S proteasome complex subunit DSS1.

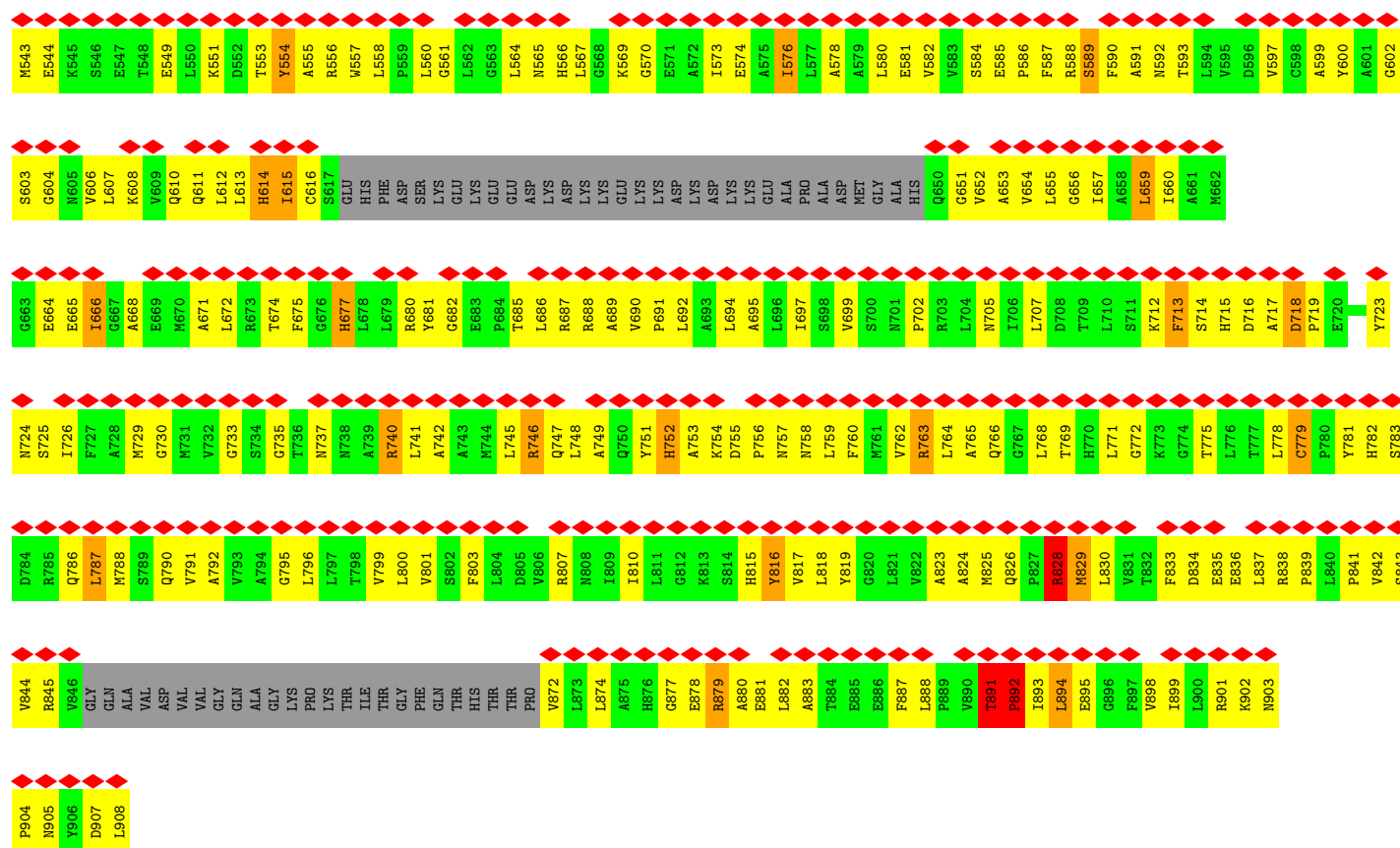
Mol	Chain	Residues	Atoms					AltConf	Trace
32	Y	21	Total	C	N	O	S	0	0
			175	106	30	38	1		

3 Residue-property plots

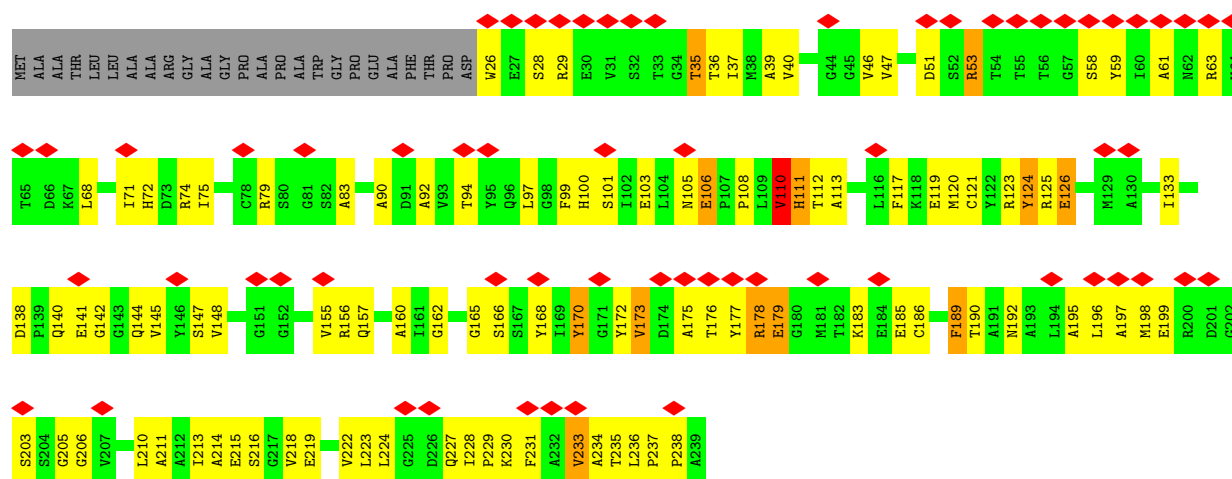
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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 2



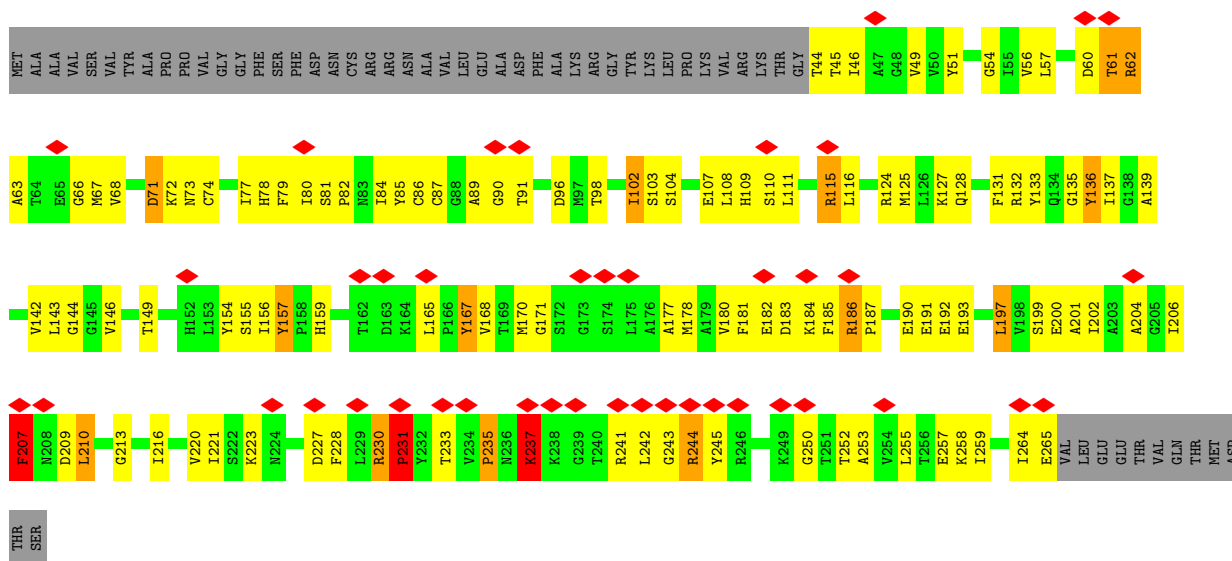


• Molecule 2: Proteasome subunit beta type-6

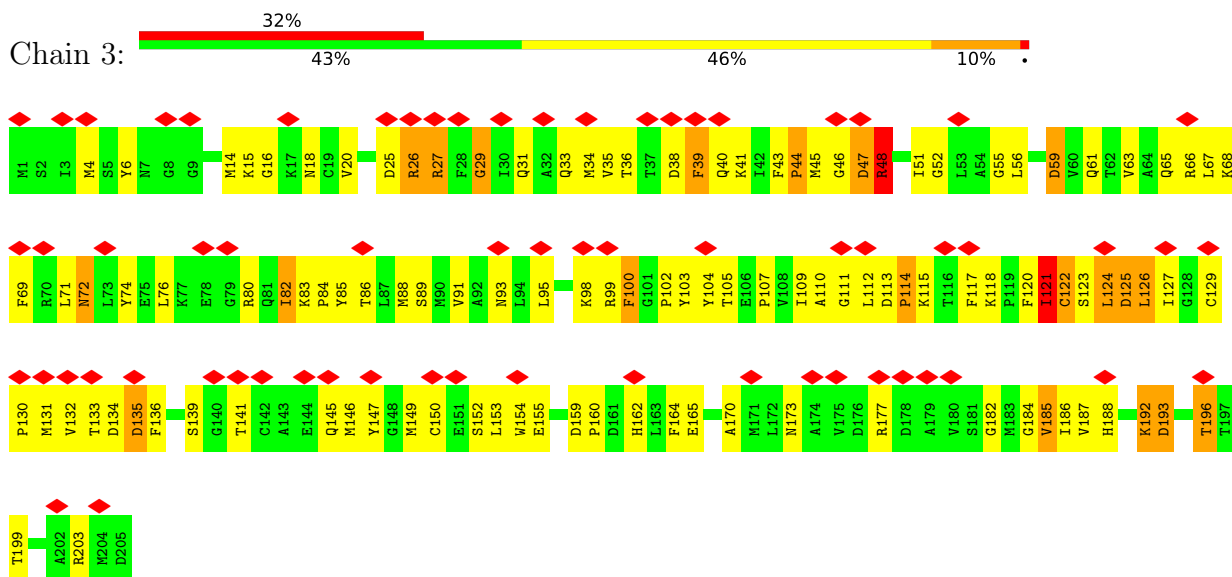


• Molecule 3: Proteasome subunit beta type-7

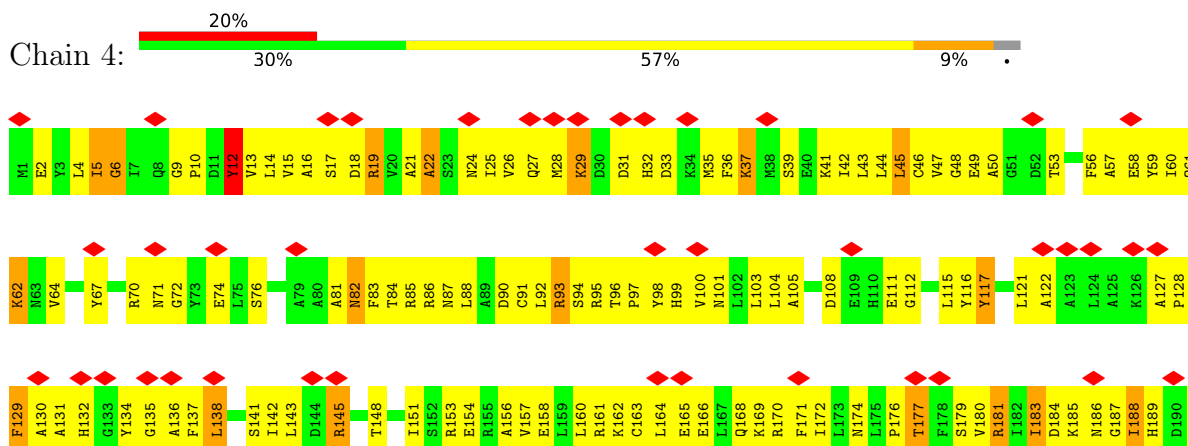


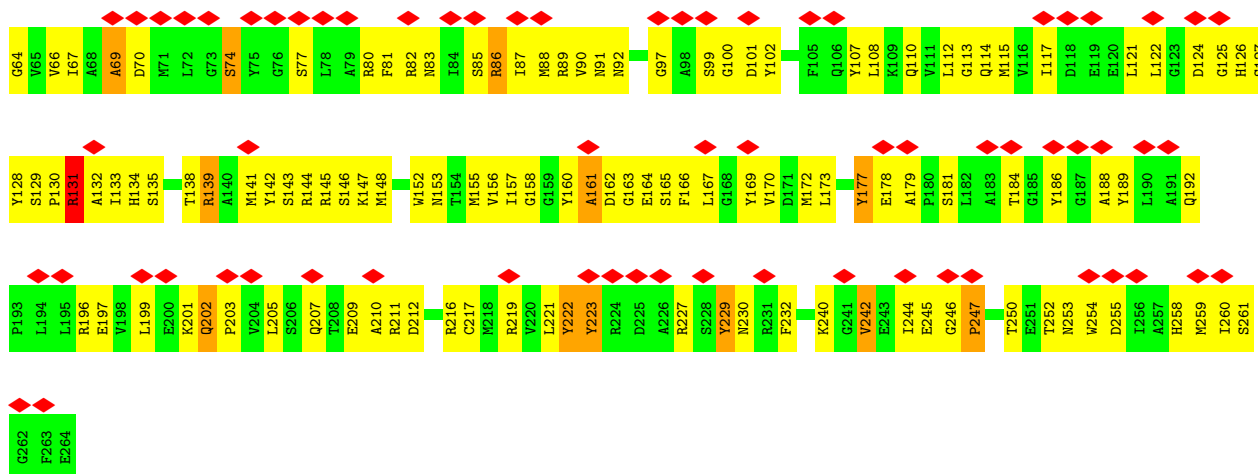


• Molecule 4: Proteasome subunit beta type-3

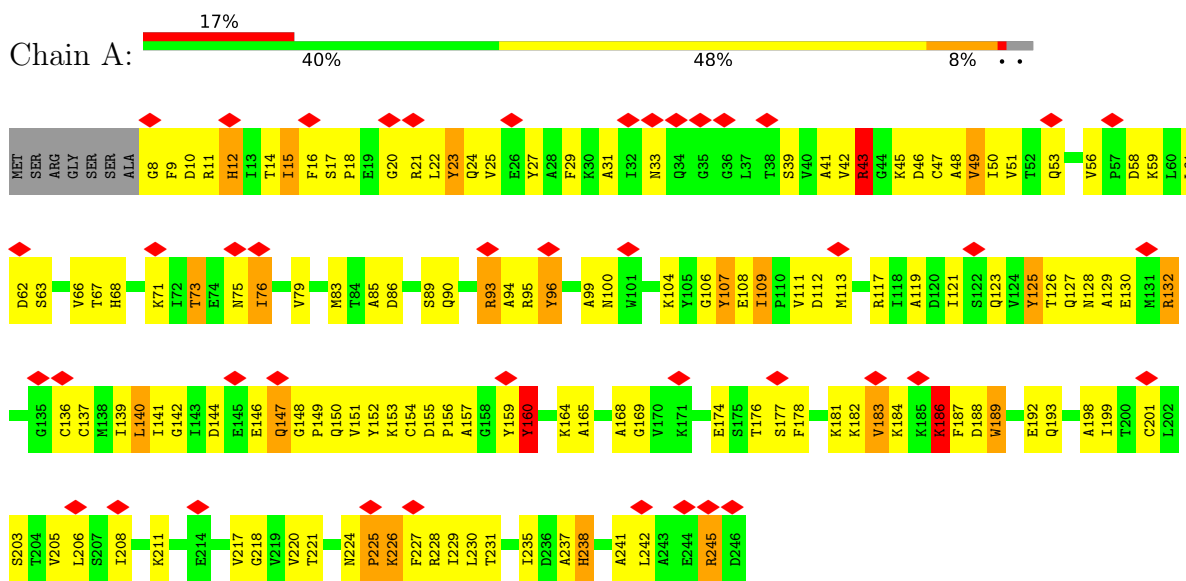


• Molecule 5: Proteasome subunit beta type-2

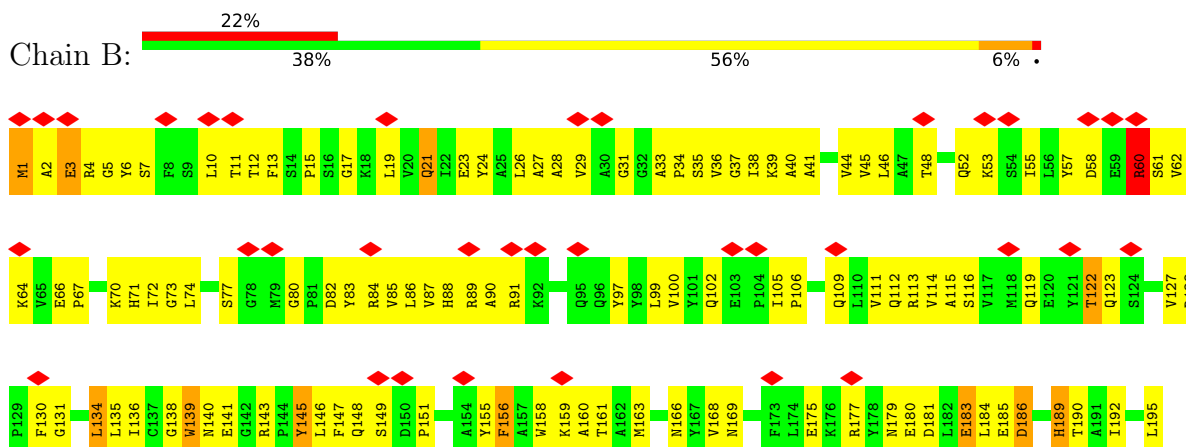


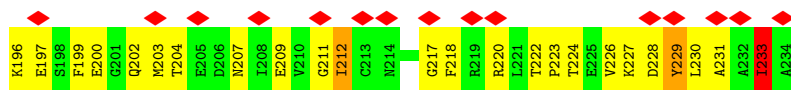


• Molecule 9: Proteasome subunit alpha type-6

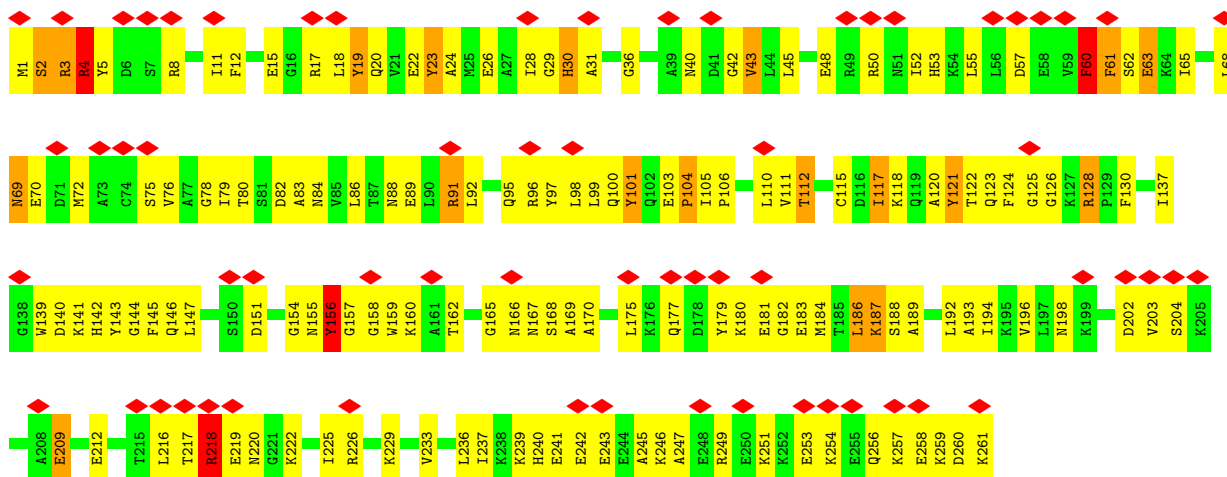
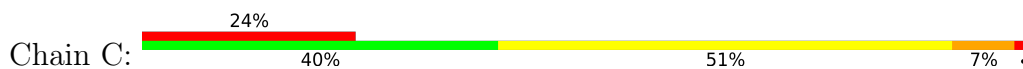


• Molecule 10: Proteasome subunit alpha type-2

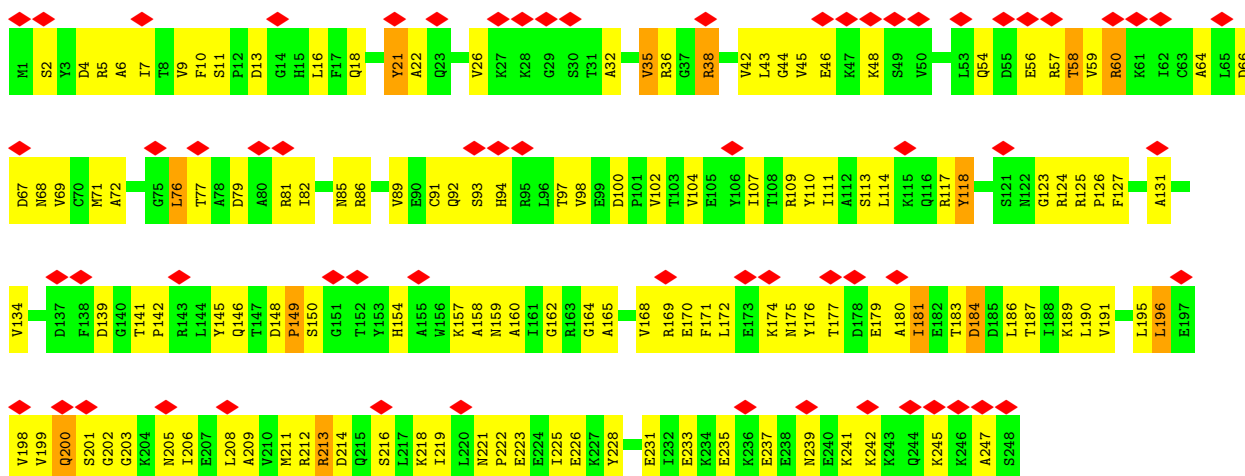
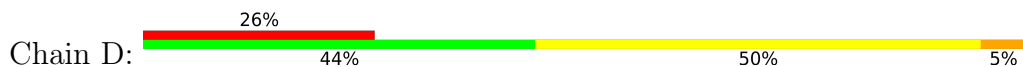




• Molecule 11: Proteasome subunit alpha type-4

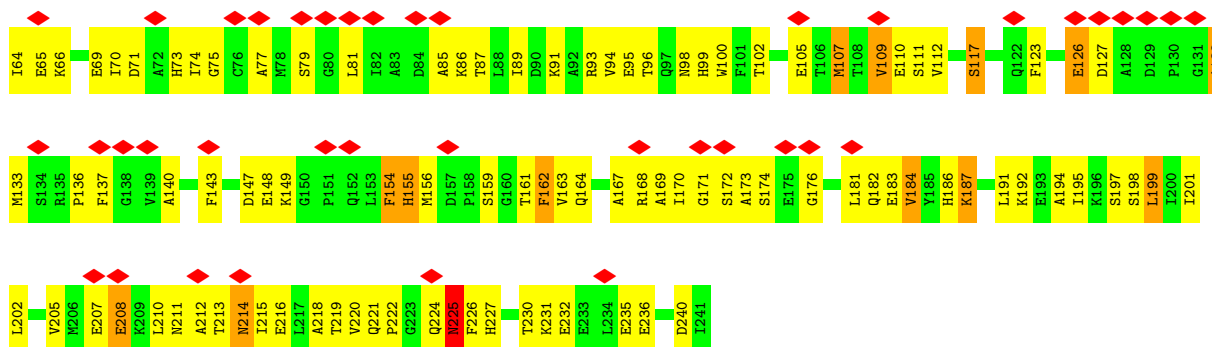


• Molecule 12: Proteasome subunit alpha type-7

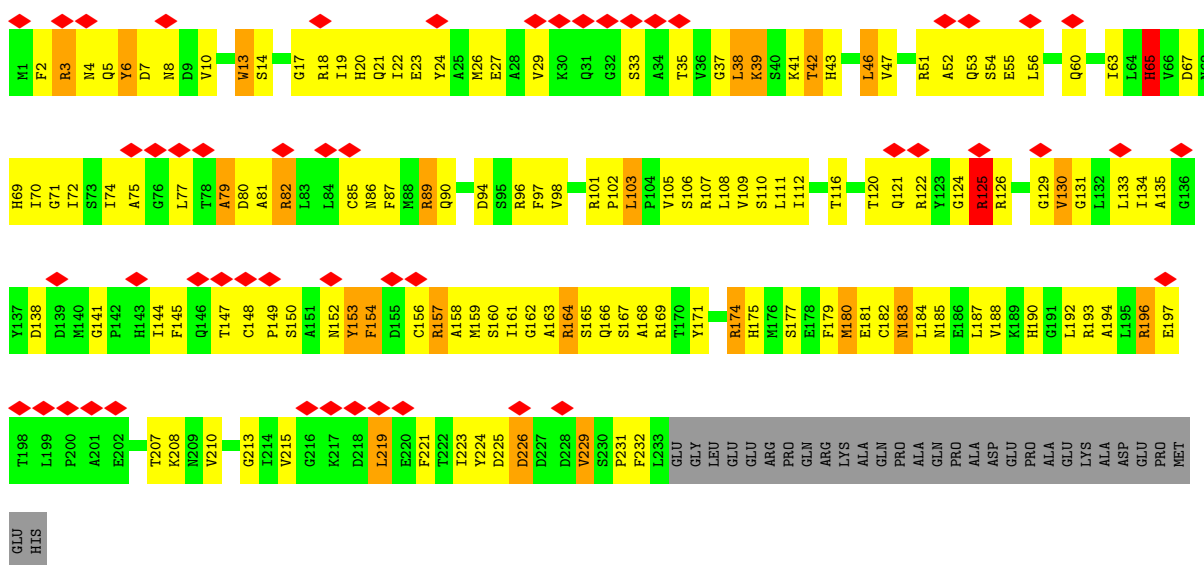


• Molecule 13: Proteasome subunit alpha type-5

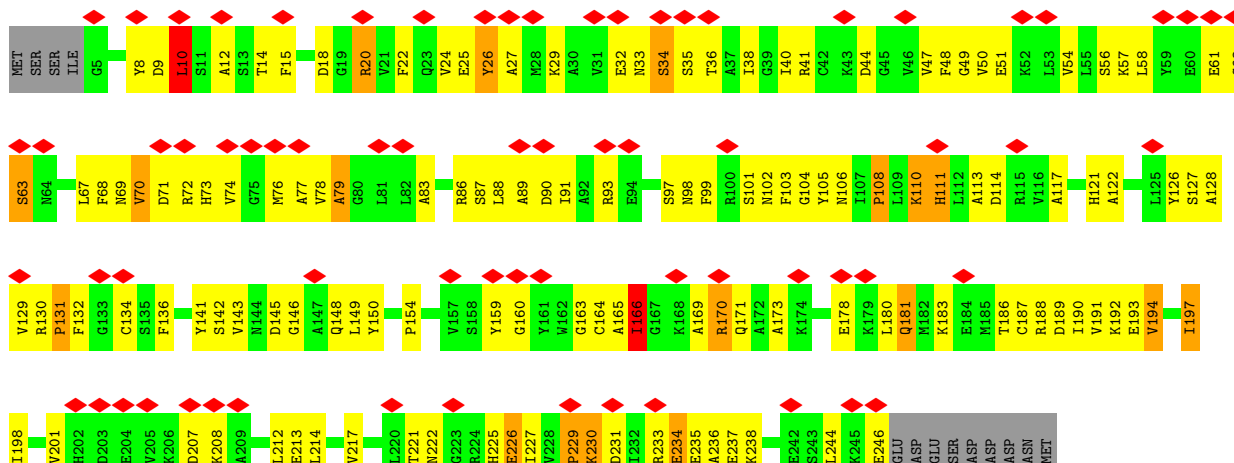
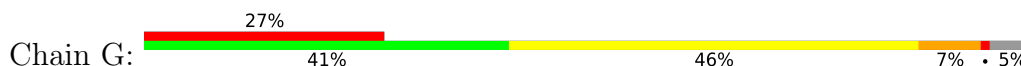




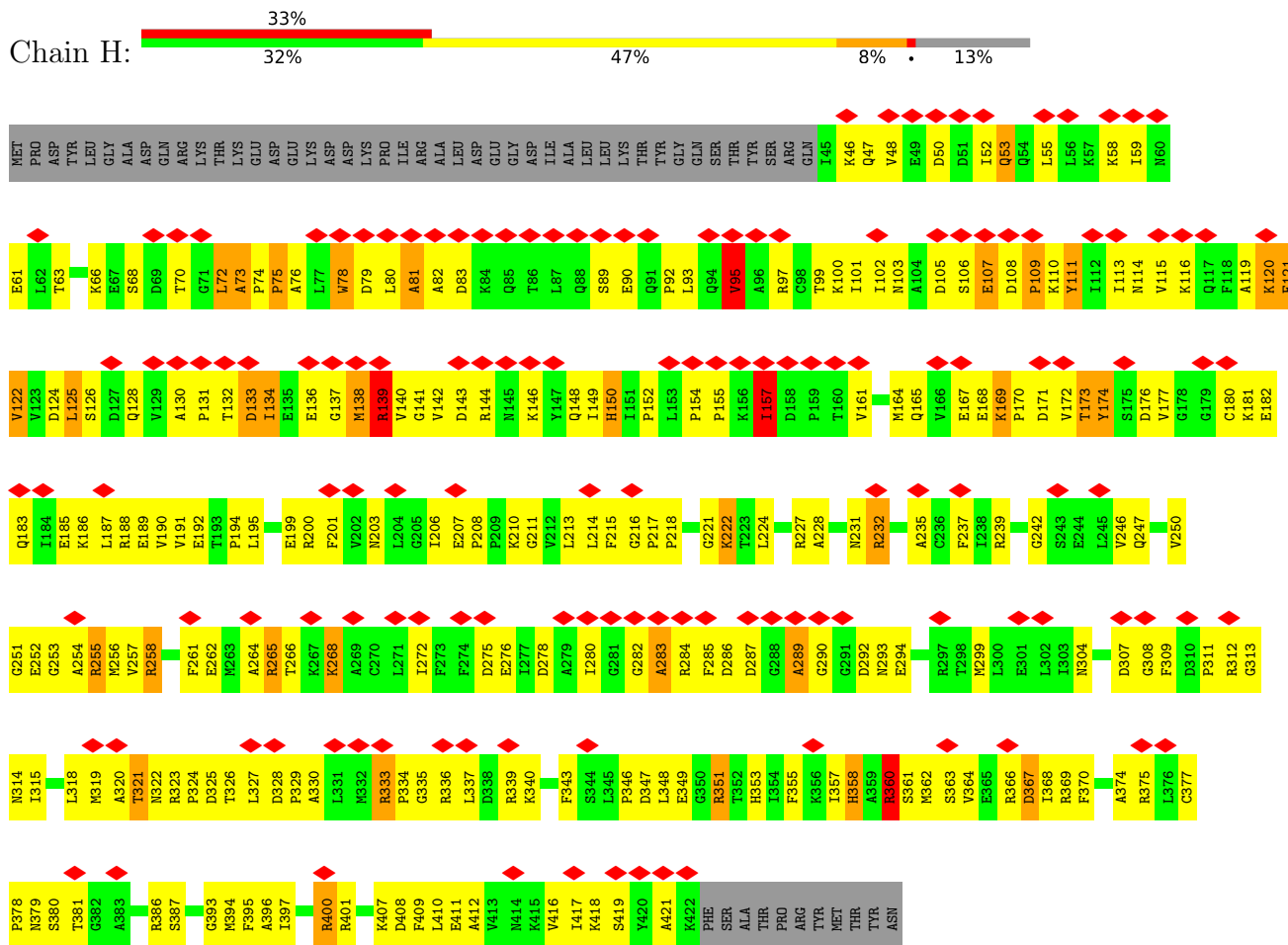
• Molecule 14: Proteasome subunit alpha type-1



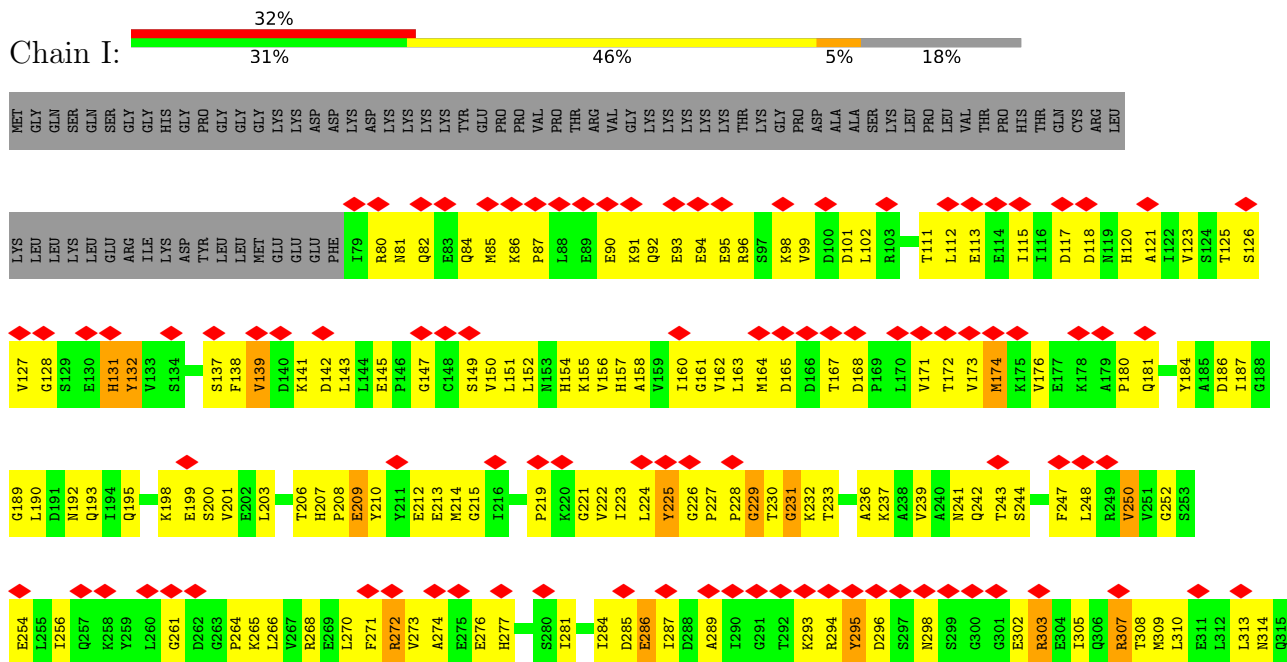
• Molecule 15: Proteasome subunit alpha type-3

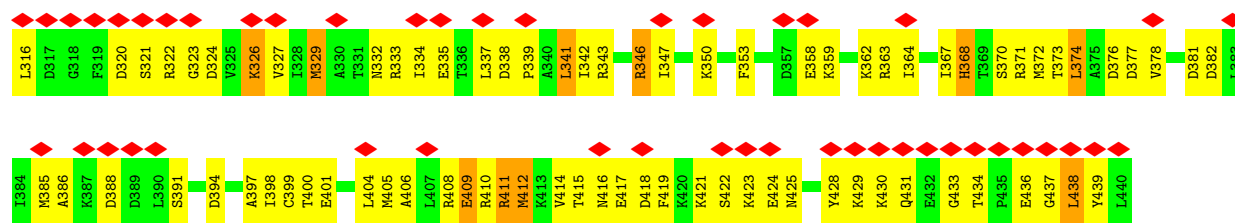


Chain H:

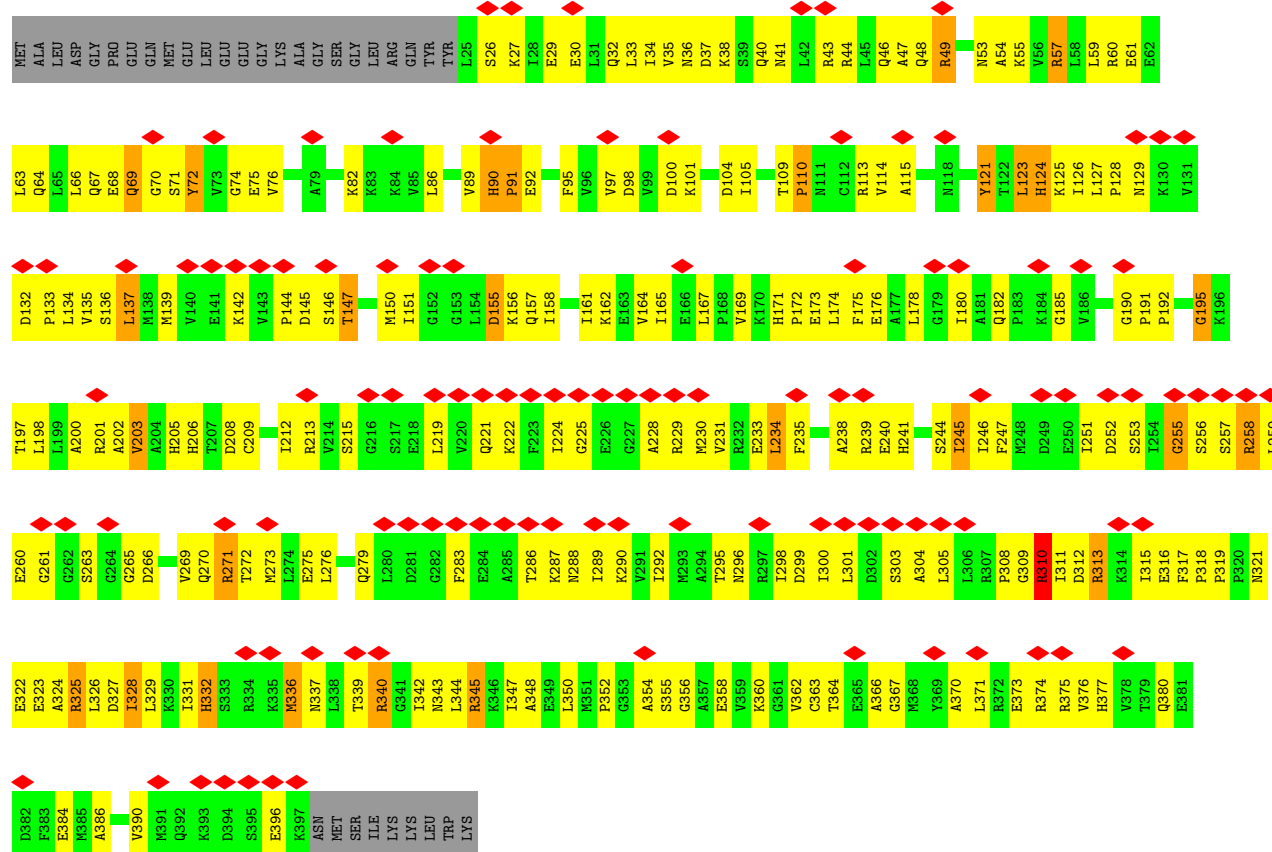


Chain I:

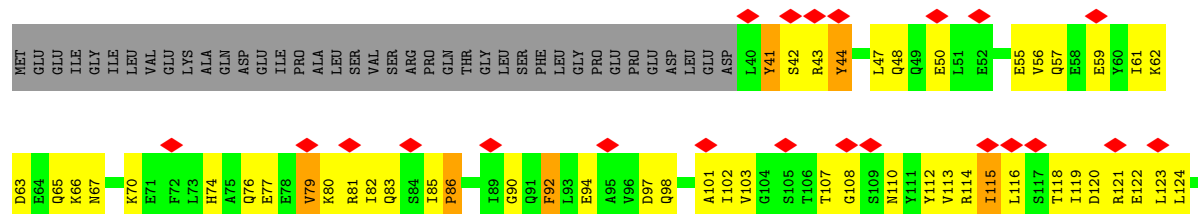




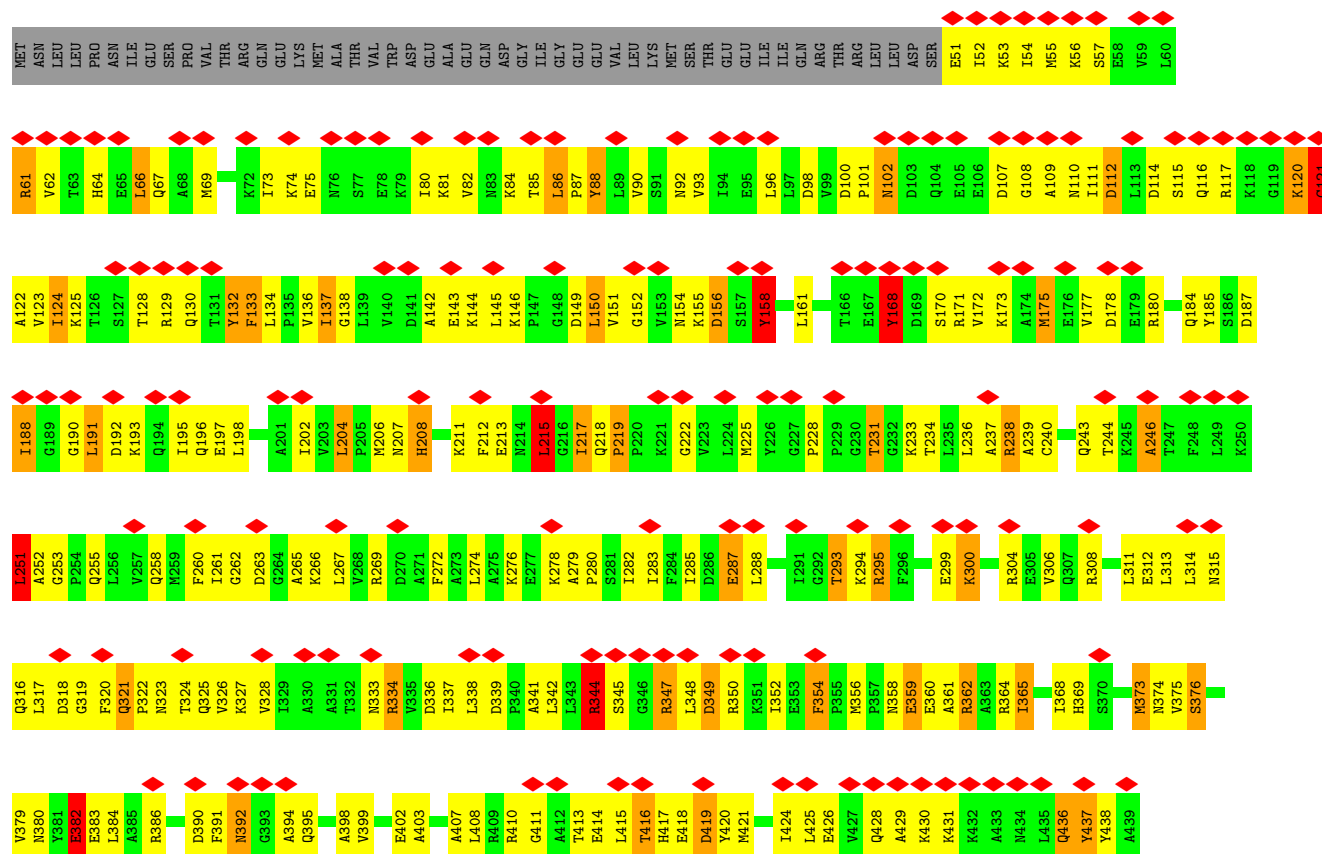
• Molecule 18: 26S protease regulatory subunit 8



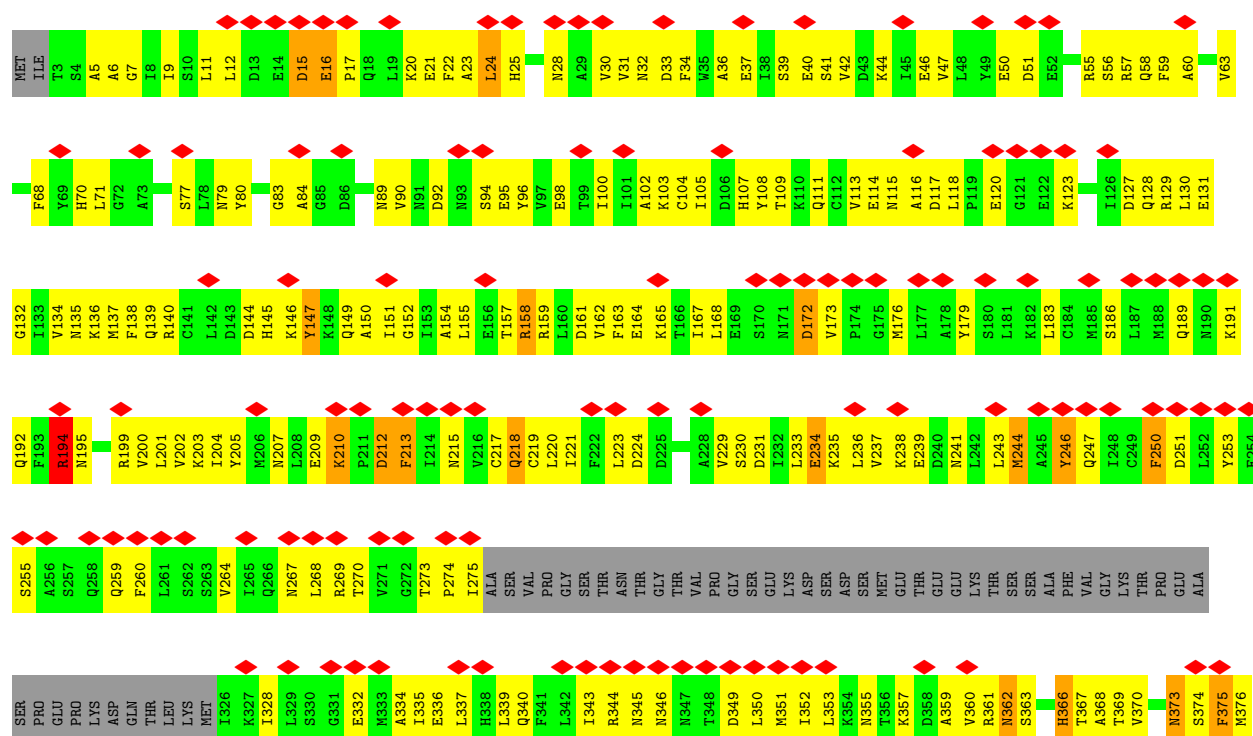
• Molecule 19: 26S protease regulatory subunit 6B

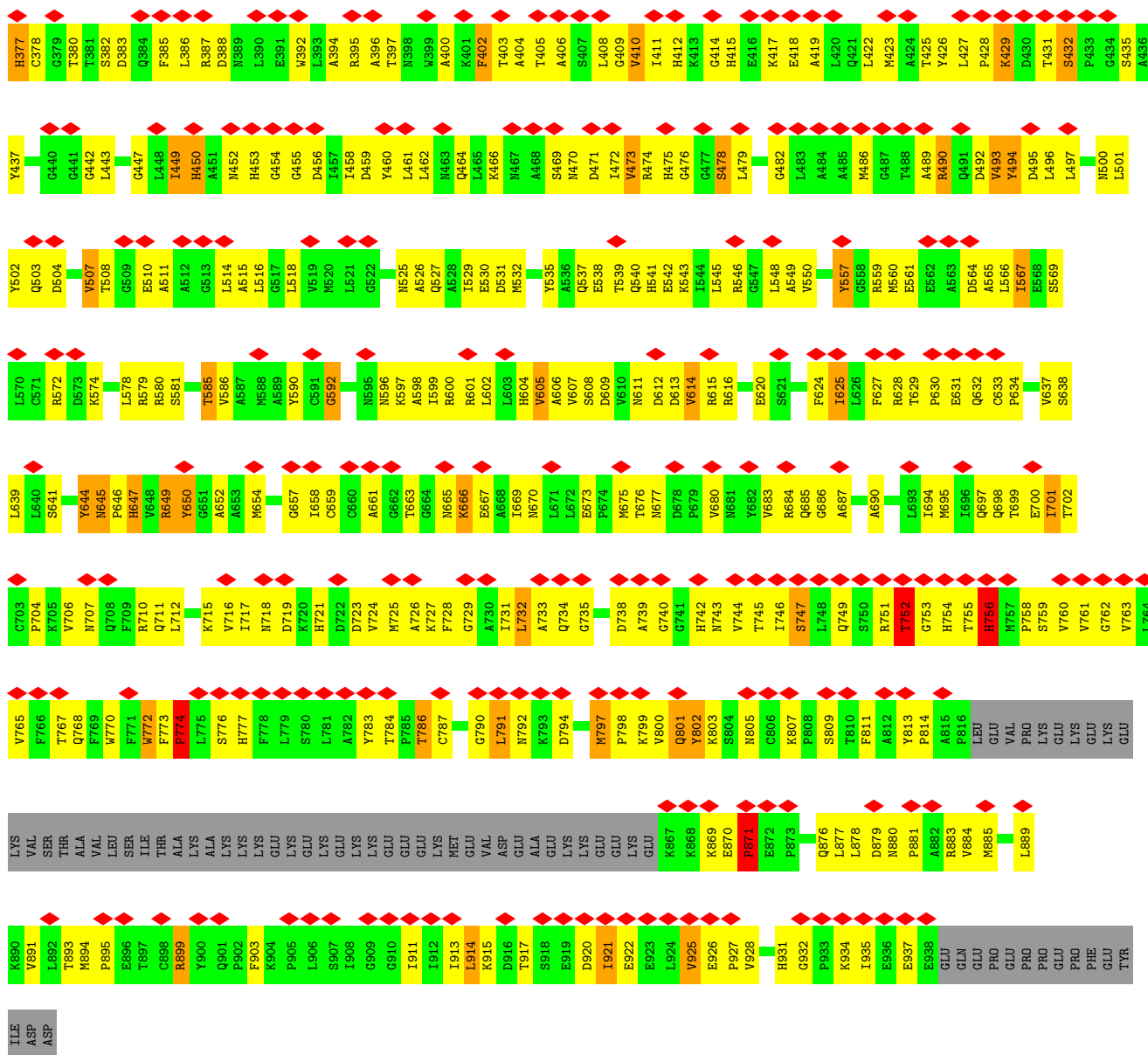




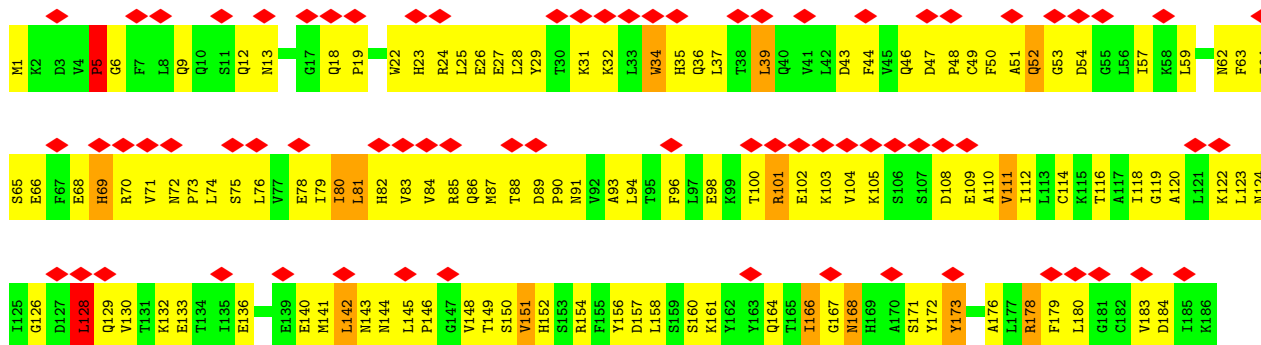


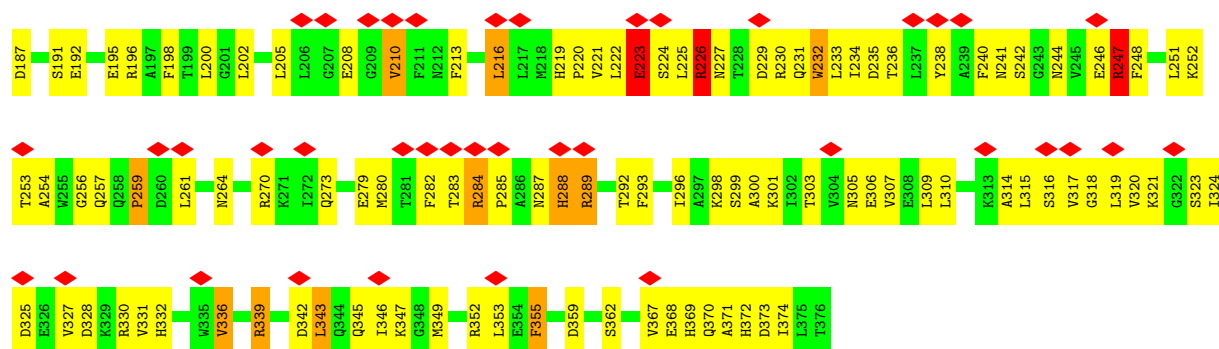
• Molecule 22: 26S proteasome non-ATPase regulatory subunit 1



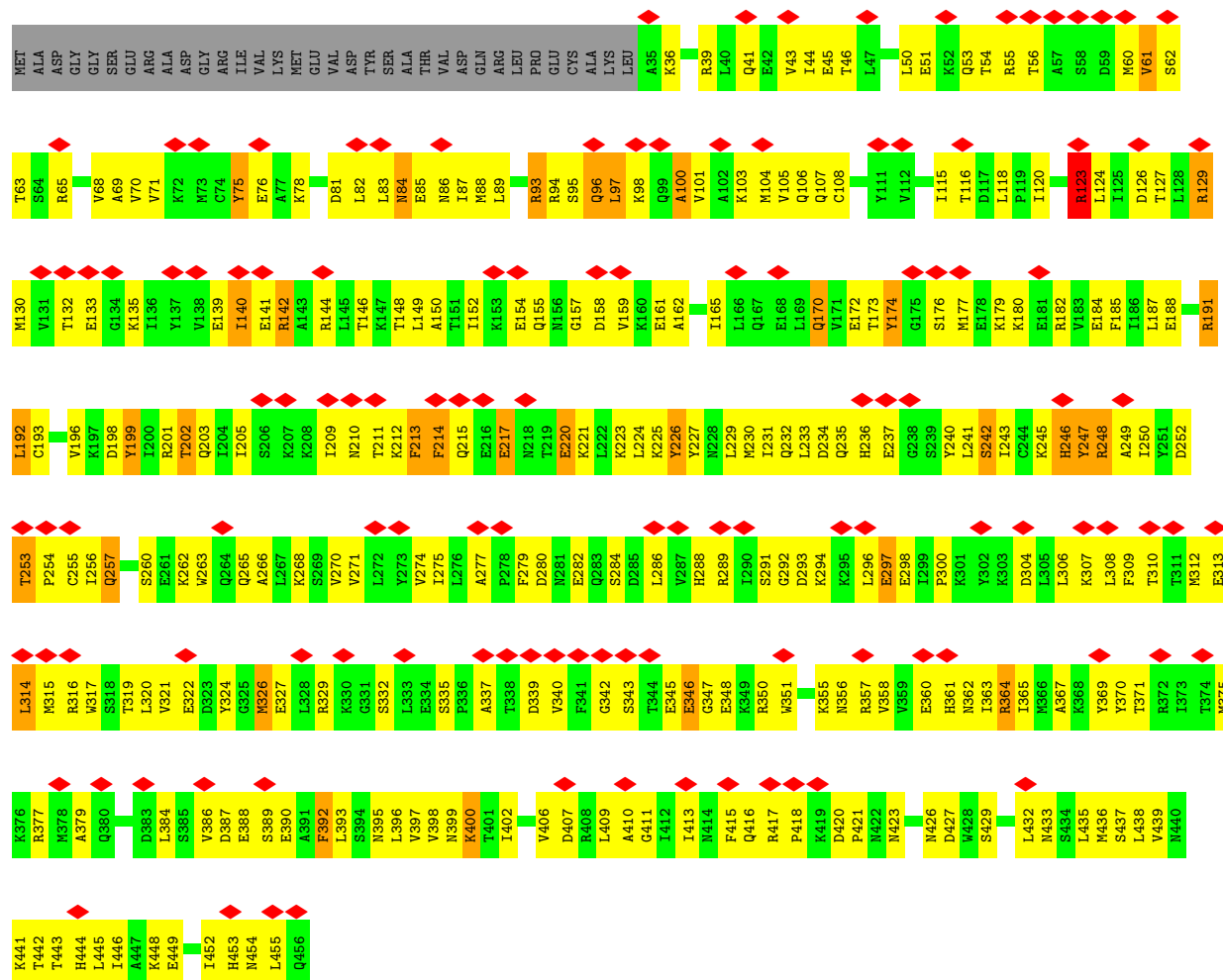


- Molecule 23: 26S proteasome non-ATPase regulatory subunit 13



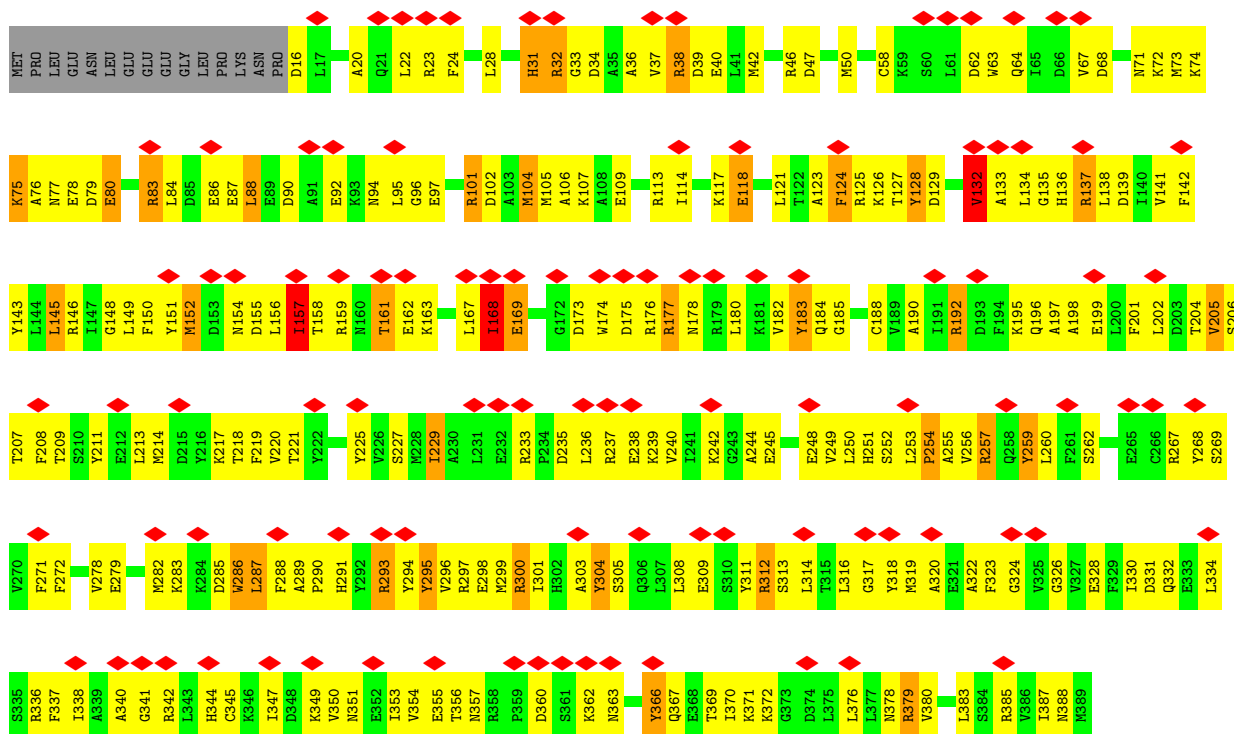


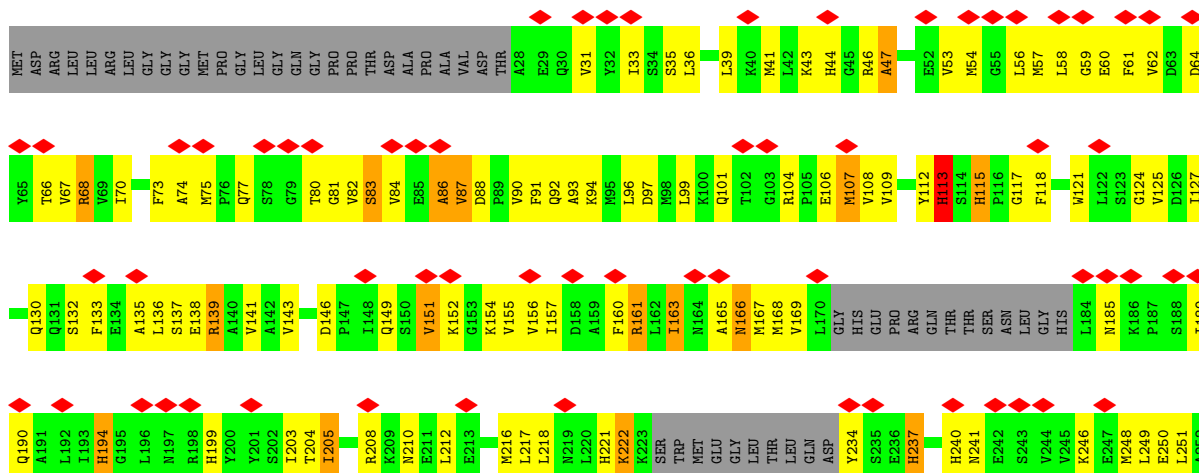
• Molecule 24: 26S proteasome non-ATPase regulatory subunit 12

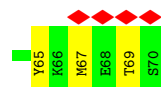


• Molecule 25: 26S proteasome non-ATPase regulatory subunit 11









4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	252000	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 ($e^-/\text{\AA}^2$)	45	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.549	Depositor
Minimum map value	-0.463	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.012	Depositor
Recommended contour level	0.088	Depositor
Map size (Å)	604.80005, 604.80005, 604.80005	wwPDB
Map dimensions	280, 280, 280	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.16, 2.16, 2.16	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	Z	2.35	257/6249 (4.1%)	2.64	550/8457 (6.5%)
2	1	2.32	61/1637 (3.7%)	2.50	112/2218 (5.0%)
3	2	2.42	79/1703 (4.6%)	2.47	113/2305 (4.9%)
4	3	2.36	82/1628 (5.0%)	2.39	96/2194 (4.4%)
5	4	2.44	83/1585 (5.2%)	2.46	112/2144 (5.2%)
6	5	2.33	71/1538 (4.6%)	2.45	97/2078 (4.7%)
7	6	2.41	79/1684 (4.7%)	2.48	104/2268 (4.6%)
8	7	2.28	60/1739 (3.5%)	2.42	107/2351 (4.6%)
9	A	2.35	84/1908 (4.4%)	2.45	125/2578 (4.8%)
10	B	2.35	82/1865 (4.4%)	2.53	146/2524 (5.8%)
11	C	2.34	92/2099 (4.4%)	2.44	138/2818 (4.9%)
12	D	2.36	88/1987 (4.4%)	2.44	136/2673 (5.1%)
13	E	2.31	78/1797 (4.3%)	2.52	136/2426 (5.6%)
14	F	2.45	90/1872 (4.8%)	2.51	137/2529 (5.4%)
15	G	2.34	77/1929 (4.0%)	2.42	112/2597 (4.3%)
16	H	2.30	127/3009 (4.2%)	2.45	214/4061 (5.3%)
17	I	2.29	115/2881 (4.0%)	2.51	220/3887 (5.7%)
18	J	2.36	138/2966 (4.7%)	2.54	222/3989 (5.6%)
19	K	2.35	135/3082 (4.4%)	2.50	221/4157 (5.3%)
20	L	2.35	121/2906 (4.2%)	2.50	210/3913 (5.4%)
21	M	2.31	124/3087 (4.0%)	2.51	226/4160 (5.4%)
22	N	2.34	270/6626 (4.1%)	2.57	541/8970 (6.0%)
23	O	2.27	110/3078 (3.6%)	2.58	259/4165 (6.2%)
24	P	2.33	160/3493 (4.6%)	2.60	280/4696 (6.0%)
25	Q	2.31	137/3381 (4.1%)	2.55	250/4558 (5.5%)
26	R	2.31	122/3140 (3.9%)	2.53	229/4228 (5.4%)
27	S	2.40	122/2808 (4.3%)	2.60	237/3791 (6.3%)
28	T	2.23	73/2097 (3.5%)	2.47	139/2830 (4.9%)
29	U	2.37	101/2223 (4.5%)	2.55	189/3006 (6.3%)
30	V	2.28	73/2020 (3.6%)	2.50	134/2724 (4.9%)
31	W	2.38	64/1439 (4.4%)	2.52	94/1947 (4.8%)
32	Y	2.39	6/177 (3.4%)	2.53	11/233 (4.7%)
All	All	2.34	3361/79633 (4.2%)	2.52	5897/107475 (5.5%)

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	Z	0	19
2	1	0	3
3	2	0	5
4	3	0	3
5	4	0	7
6	5	0	6
7	6	0	9
8	7	0	9
9	A	0	10
10	B	0	3
11	C	0	9
12	D	0	5
14	F	0	8
15	G	0	4
16	H	1	12
17	I	0	5
18	J	0	10
19	K	0	19
20	L	0	11
21	M	0	12
22	N	1	16
23	O	0	8
24	P	0	13
25	Q	0	12
26	R	0	18
27	S	0	11
28	T	0	8
29	U	0	7
30	V	0	3
31	W	0	3
32	Y	0	1
All	All	2	269

The worst 5 of 3361 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	N	7	GLY	CA-C	-13.08	1.37	1.52
7	6	148	ALA	CA-C	-11.96	1.38	1.52
3	2	167	TYR	CA-C	-11.86	1.37	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	E	47	CYS	CA-C	-11.63	1.38	1.52
7	6	187	GLN	C-N	11.60	1.47	1.33

The worst 5 of 5897 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	7	52	THR	CA-C-N	16.54	132.90	121.65
8	7	52	THR	C-N-CA	16.54	132.90	121.65
25	Q	380	GLN	CA-C-N	14.39	135.95	119.98
25	Q	380	GLN	C-N-CA	14.39	135.95	119.98
24	P	315	MET	N-CA-C	-13.85	96.10	113.55

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
16	H	311	PRO	CA
22	N	752	THR	CA

5 of 269 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	Z	110	TYR	Sidechain
1	Z	120	ARG	Sidechain
1	Z	143	ARG	Sidechain
1	Z	62	ARG	Sidechain
1	Z	79	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	Z	6146	0	6189	25	0
2	1	1607	0	1567	2	0
3	2	1676	0	1695	5	0
4	3	1599	0	1621	10	0
5	4	1554	0	1559	8	0
6	5	1509	0	1477	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	6	1654	0	1653	3	0
8	7	1705	0	1674	4	0
9	A	1874	0	1879	10	0
10	B	1826	0	1823	11	0
11	C	2069	0	2099	9	0
12	D	1961	0	2000	3	0
13	E	1770	0	1760	9	0
14	F	1837	0	1834	11	0
15	G	1894	0	1877	12	0
16	H	2962	0	3027	15	0
17	I	2840	0	2881	13	0
18	J	2929	0	3044	8	0
19	K	3032	0	3072	10	0
20	L	2862	0	2924	14	0
21	M	3046	0	3116	19	0
22	N	6508	0	6533	19	0
23	O	3020	0	3041	13	0
24	P	3447	0	3567	7	0
25	Q	3335	0	3435	8	0
26	R	3084	0	3086	17	0
27	S	2757	0	2819	7	0
28	T	2056	0	2096	6	0
29	U	2183	0	2223	9	0
30	V	1986	0	2014	9	0
31	W	1420	0	1463	4	0
32	Y	175	0	159	0	0
All	All	78323	0	79207	277	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 2.

The worst 5 of 277 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)
23:O:128:LEU:H	23:O:128:LEU:HD22	1.58	0.68
20:L:85:ARG:HE	30:V:47:ALA:HA	1.59	0.67
1:Z:261:ARG:HH21	1:Z:267:ARG:HH12	1.43	0.65
28:T:184:GLU:HG2	28:T:188:MET:HE1	1.79	0.65
17:I:303:ARG:HE	17:I:307:ARG:HH22	1.43	0.65

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	Z	788/908 (87%)	698 (89%)	66 (8%)	24 (3%)	3	23
2	1	212/239 (89%)	187 (88%)	19 (9%)	6 (3%)	4	24
3	2	220/277 (79%)	206 (94%)	9 (4%)	5 (2%)	5	28
4	3	203/205 (99%)	184 (91%)	14 (7%)	5 (2%)	4	26
5	4	192/201 (96%)	173 (90%)	13 (7%)	6 (3%)	3	22
6	5	193/263 (73%)	177 (92%)	12 (6%)	4 (2%)	5	30
7	6	211/241 (88%)	185 (88%)	15 (7%)	11 (5%)	1	15
8	7	216/264 (82%)	193 (89%)	17 (8%)	6 (3%)	4	24
9	A	237/246 (96%)	219 (92%)	15 (6%)	3 (1%)	9	42
10	B	232/234 (99%)	210 (90%)	14 (6%)	8 (3%)	3	21
11	C	259/261 (99%)	239 (92%)	11 (4%)	9 (4%)	3	20
12	D	246/248 (99%)	221 (90%)	21 (8%)	4 (2%)	7	38
13	E	230/241 (95%)	210 (91%)	13 (6%)	7 (3%)	3	23
14	F	231/263 (88%)	213 (92%)	12 (5%)	6 (3%)	4	25
15	G	240/255 (94%)	217 (90%)	18 (8%)	5 (2%)	5	30
16	H	376/433 (87%)	320 (85%)	32 (8%)	24 (6%)	1	12
17	I	360/440 (82%)	331 (92%)	18 (5%)	11 (3%)	3	22
18	J	371/406 (91%)	342 (92%)	18 (5%)	11 (3%)	3	23
19	K	377/418 (90%)	328 (87%)	39 (10%)	10 (3%)	4	25
20	L	359/389 (92%)	319 (89%)	32 (9%)	8 (2%)	5	29
21	M	387/439 (88%)	336 (87%)	37 (10%)	14 (4%)	2	20
22	N	830/953 (87%)	758 (91%)	50 (6%)	22 (3%)	4	25
23	O	374/376 (100%)	331 (88%)	26 (7%)	17 (4%)	2	17
24	P	420/456 (92%)	390 (93%)	21 (5%)	9 (2%)	5	30
25	Q	420/422 (100%)	389 (93%)	23 (6%)	8 (2%)	6	32

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	R	372/389 (96%)	338 (91%)	26 (7%)	8 (2%)	5	29
27	S	336/534 (63%)	305 (91%)	20 (6%)	11 (3%)	3	21
28	T	249/350 (71%)	226 (91%)	14 (6%)	9 (4%)	2	20
29	U	266/324 (82%)	252 (95%)	12 (4%)	2 (1%)	16	54
30	V	246/310 (79%)	227 (92%)	15 (6%)	4 (2%)	7	38
31	W	183/377 (48%)	170 (93%)	7 (4%)	6 (3%)	3	21
32	Y	19/70 (27%)	18 (95%)	1 (5%)	0	100	100
All	All	9855/11432 (86%)	8912 (90%)	660 (7%)	283 (3%)	5	23

5 of 283 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	Z	303	VAL
1	Z	306	GLU
1	Z	365	VAL
1	Z	891	THR
2	1	110	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	Z	670/763 (88%)	642 (96%)	28 (4%)	26	48
2	1	167/181 (92%)	158 (95%)	9 (5%)	20	41
3	2	183/228 (80%)	176 (96%)	7 (4%)	29	50
4	3	174/174 (100%)	162 (93%)	12 (7%)	14	36
5	4	165/171 (96%)	159 (96%)	6 (4%)	31	52
6	5	151/202 (75%)	144 (95%)	7 (5%)	24	46
7	6	178/199 (89%)	167 (94%)	11 (6%)	16	38
8	7	180/215 (84%)	167 (93%)	13 (7%)	13	35
9	A	205/210 (98%)	197 (96%)	8 (4%)	28	49

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	B	191/191 (100%)	181 (95%)	10 (5%)	21	42
11	C	221/221 (100%)	200 (90%)	21 (10%)	8	25
12	D	211/211 (100%)	205 (97%)	6 (3%)	38	60
13	E	194/203 (96%)	185 (95%)	9 (5%)	24	46
14	F	200/224 (89%)	193 (96%)	7 (4%)	32	53
15	G	199/212 (94%)	186 (94%)	13 (6%)	15	37
16	H	324/372 (87%)	300 (93%)	24 (7%)	13	33
17	I	318/385 (83%)	304 (96%)	14 (4%)	25	47
18	J	325/352 (92%)	308 (95%)	17 (5%)	21	42
19	K	332/366 (91%)	309 (93%)	23 (7%)	14	36
20	L	315/341 (92%)	300 (95%)	15 (5%)	23	44
21	M	333/379 (88%)	316 (95%)	17 (5%)	21	42
22	N	710/816 (87%)	674 (95%)	36 (5%)	21	42
23	O	336/336 (100%)	321 (96%)	15 (4%)	24	46
24	P	389/416 (94%)	370 (95%)	19 (5%)	22	43
25	Q	362/362 (100%)	350 (97%)	12 (3%)	33	55
26	R	330/344 (96%)	310 (94%)	20 (6%)	17	38
27	S	299/460 (65%)	288 (96%)	11 (4%)	30	51
28	T	222/294 (76%)	213 (96%)	9 (4%)	27	49
29	U	245/295 (83%)	234 (96%)	11 (4%)	24	46
30	V	221/268 (82%)	211 (96%)	10 (4%)	24	46
31	W	163/312 (52%)	155 (95%)	8 (5%)	22	43
32	Y	19/63 (30%)	19 (100%)	0	100	100
All	All	8532/9766 (87%)	8104 (95%)	428 (5%)	23	43

5 of 428 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
19	K	158	GLN
22	N	210	LYS
29	U	38	VAL
19	K	303	VAL
21	M	61	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 235 such sidechains are listed below:

Mol	Chain	Res	Type
20	L	305	ASN
30	V	199	HIS
22	N	876	GLN
30	V	130	GLN
28	T	221	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 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.

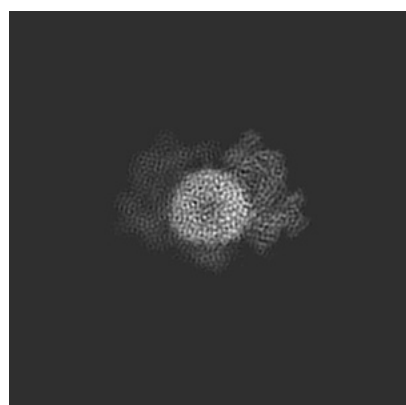
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4089. These allow visual inspection of the internal detail of the map and identification of artifacts.

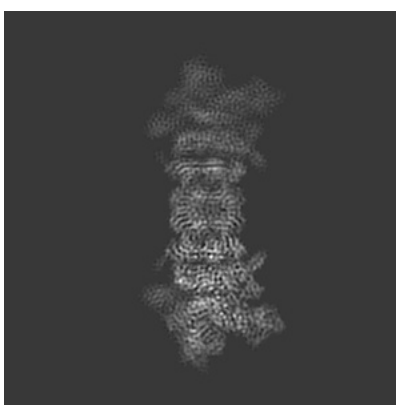
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

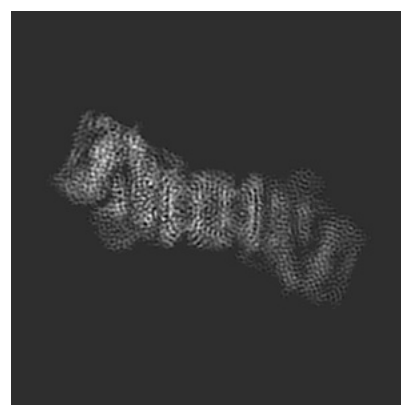
6.1.1 Primary map



X



Y

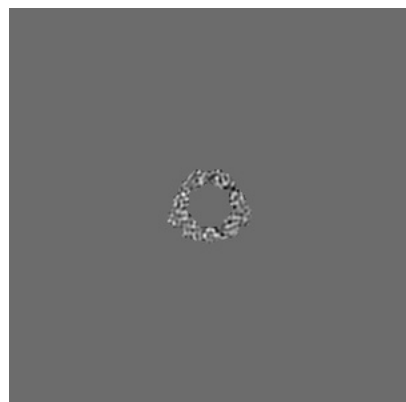


Z

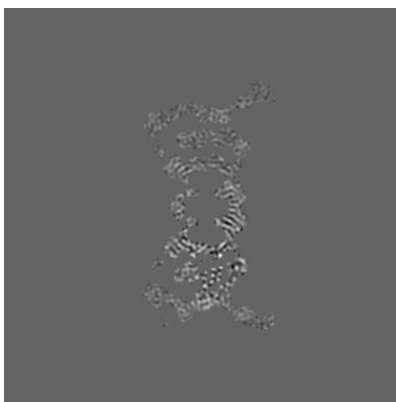
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 140



Y Index: 140



Z Index: 140

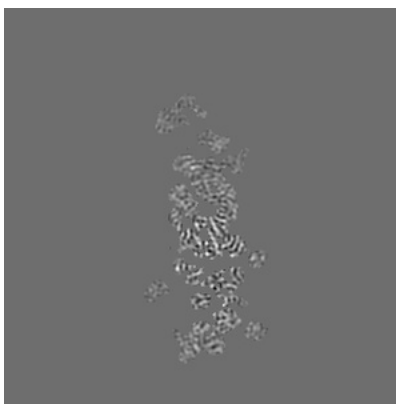
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 111



Y Index: 153

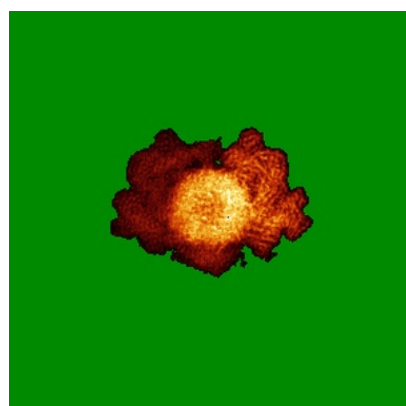


Z Index: 134

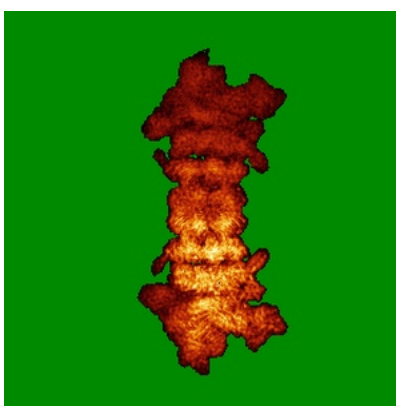
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



X



Y

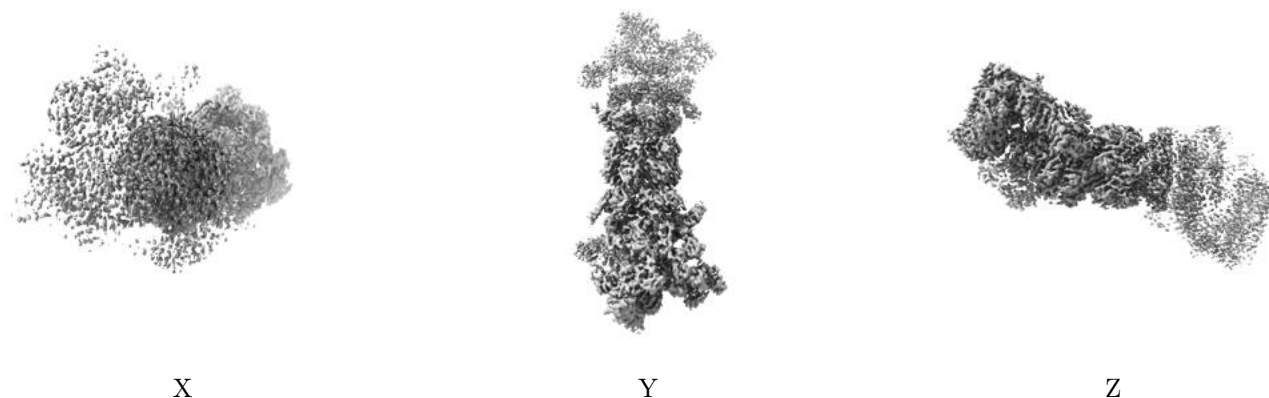


Z

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

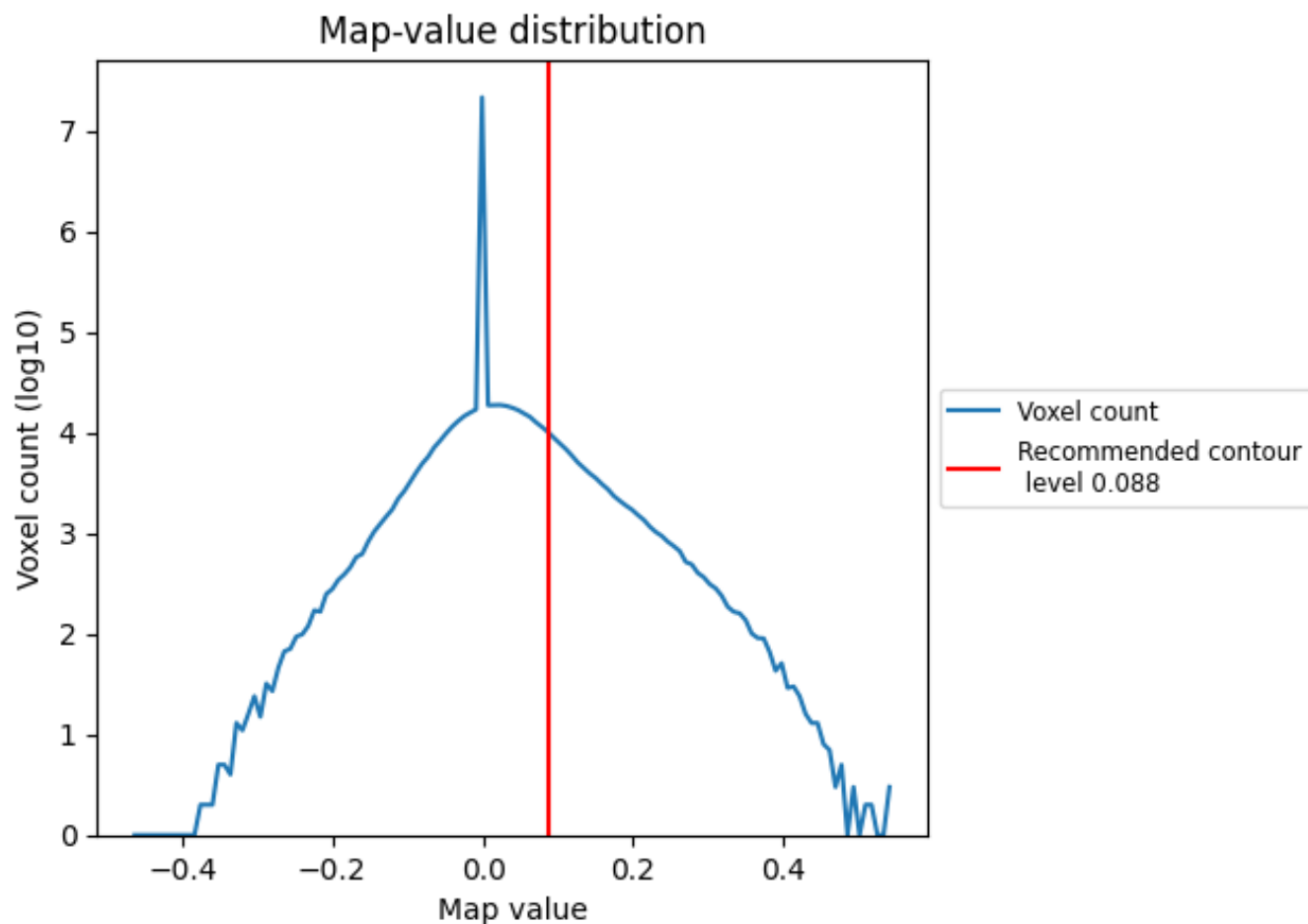
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

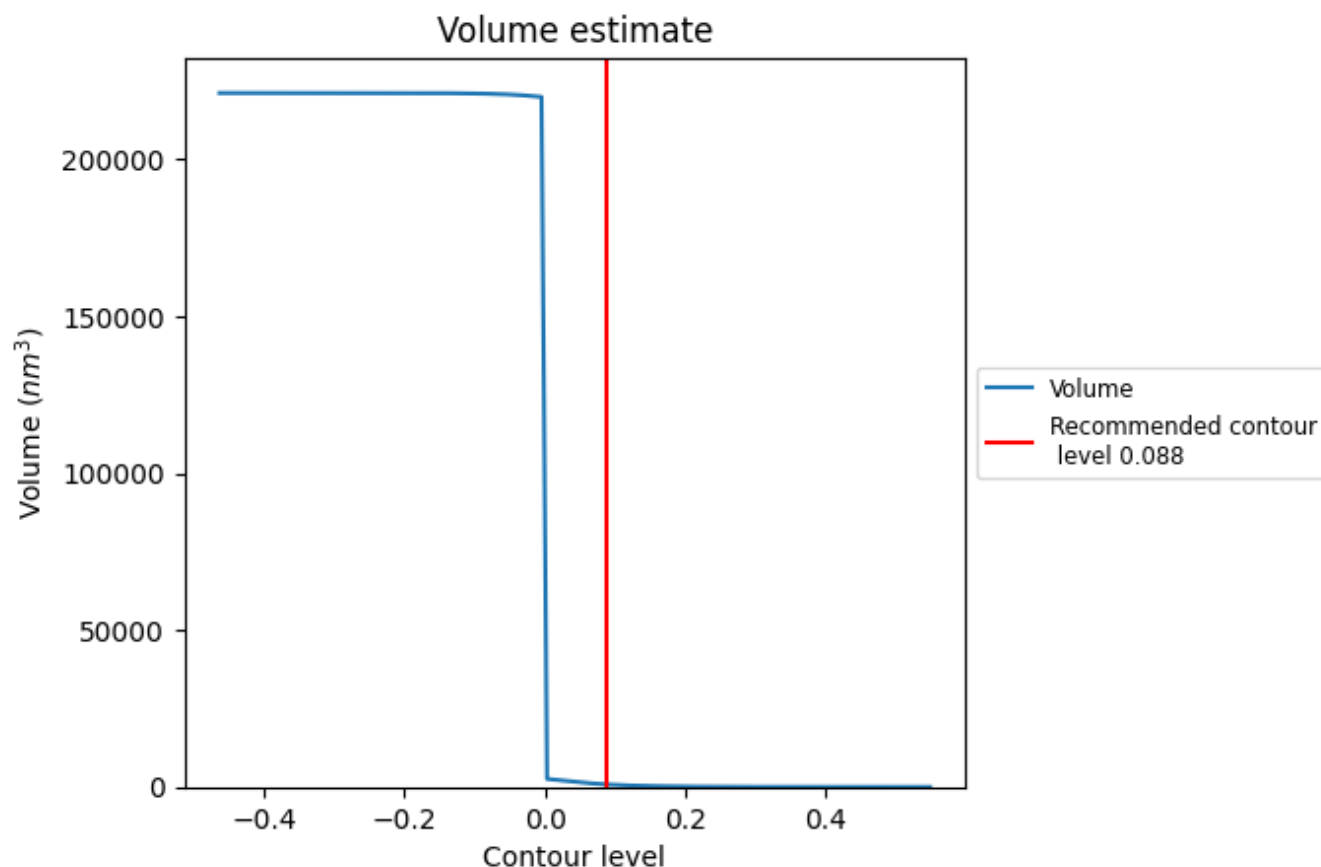
This section contains the results of statistical analysis of the map.

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.

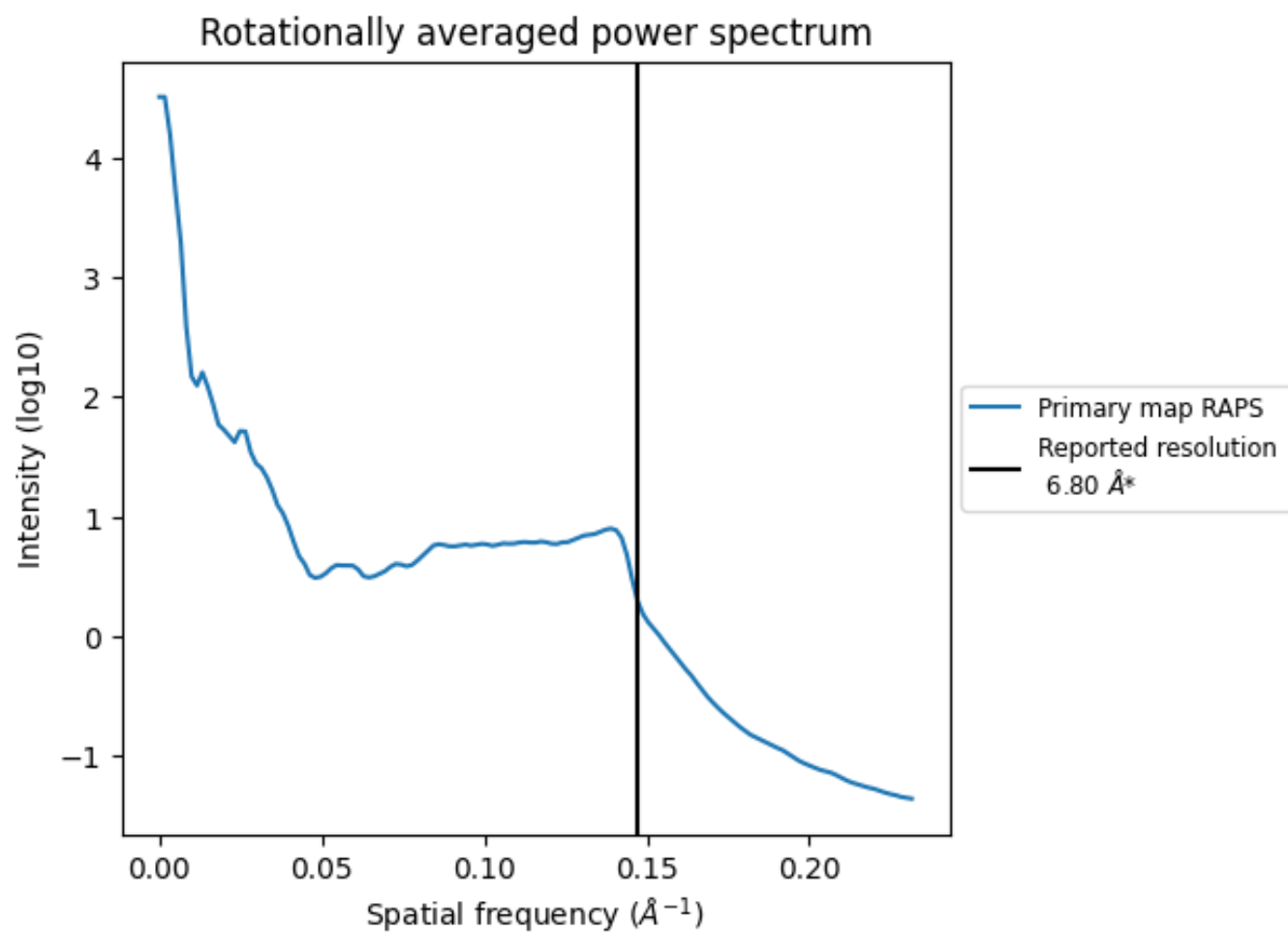
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 815 nm³; this corresponds to an approximate mass of 737 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 0.147 Å⁻¹

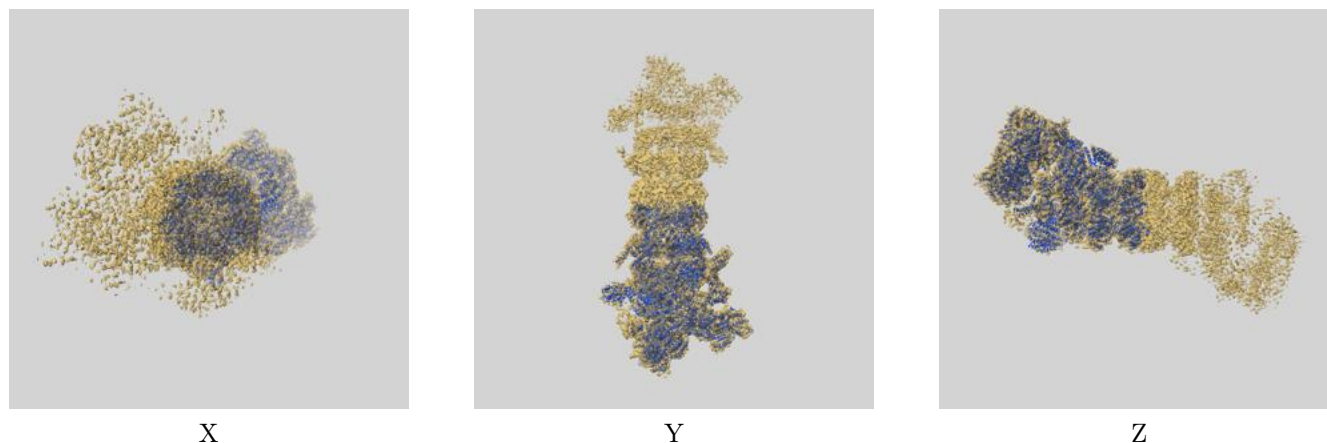
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

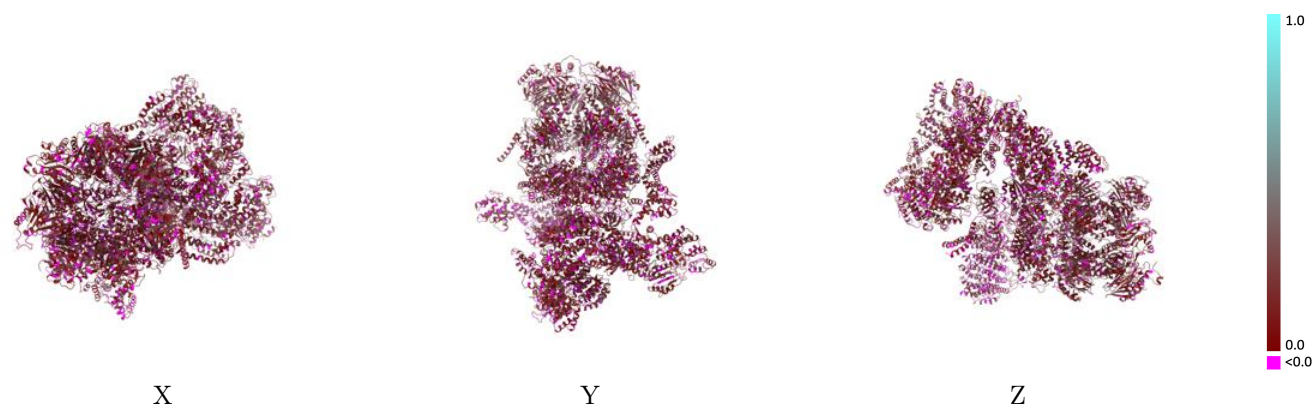
This section contains information regarding the fit between EMDB map EMD-4089 and PDB model 5LN3. Per-residue inclusion information can be found in [section 3](#) on [page 10](#).

9.1 Map-model overlay [i](#)



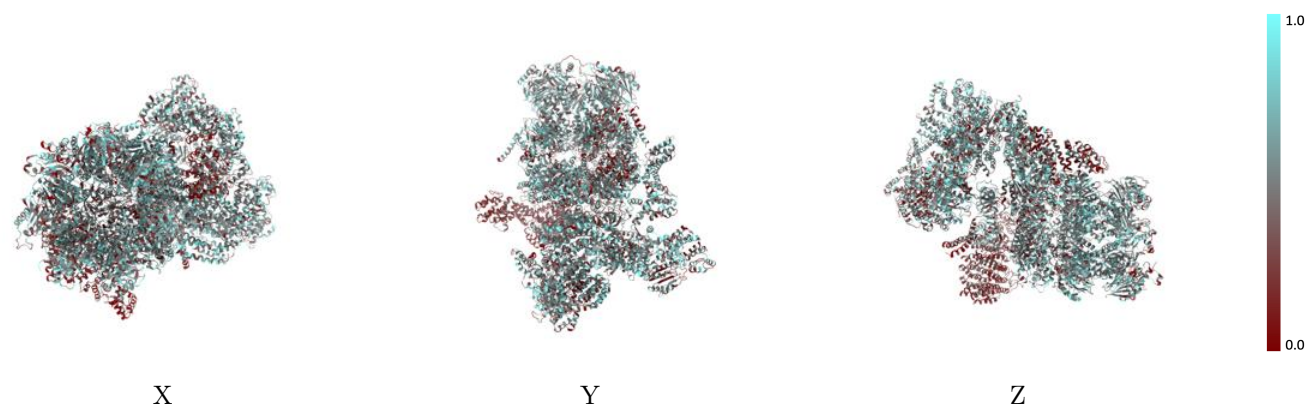
The images above show the 3D surface view of the map at the recommended contour level 0.088 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



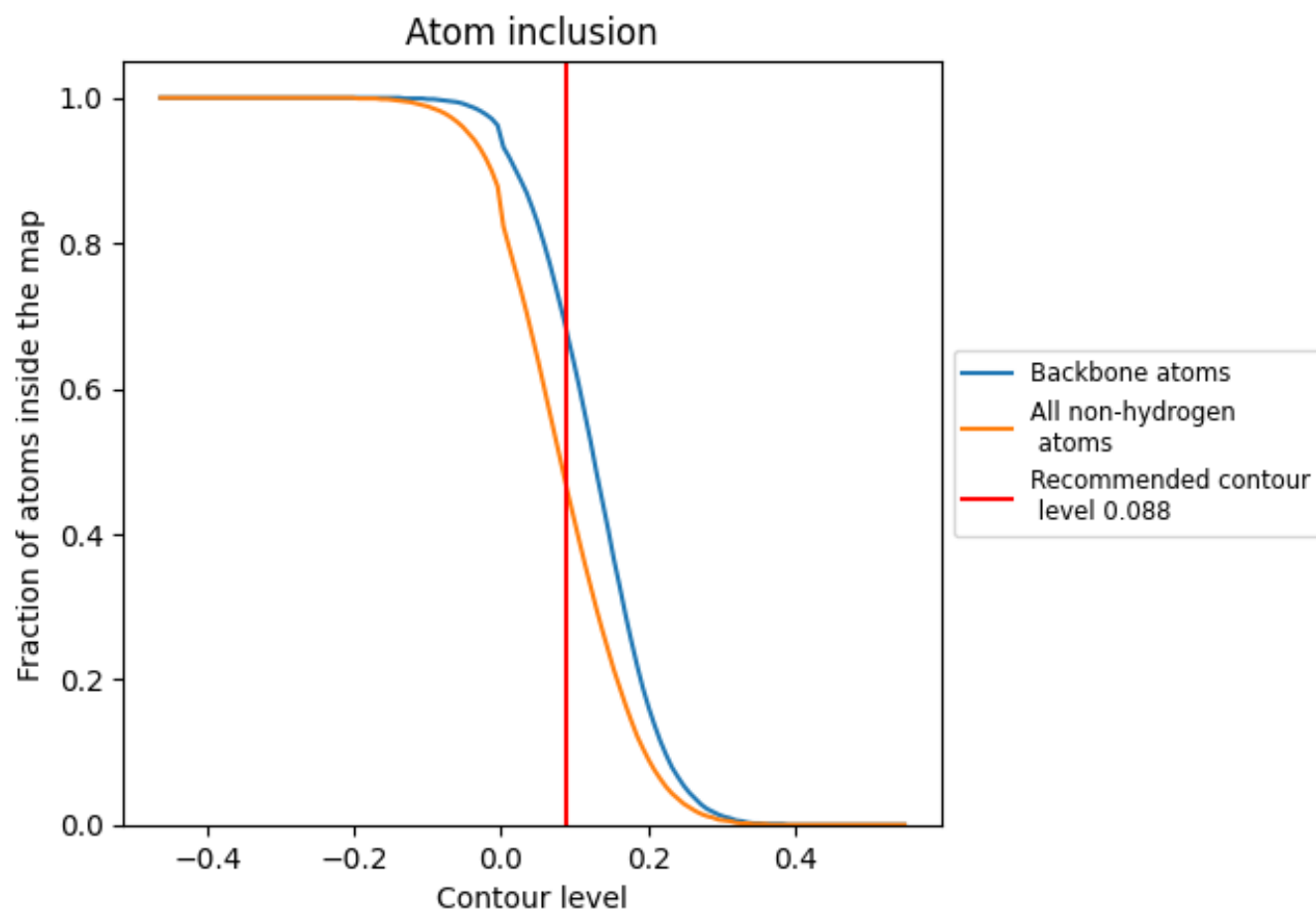
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.088).

9.4 Atom inclusion [i](#)



At the recommended contour level, 68% of all backbone atoms, 47% 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 (0.088) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.4690	 0.1410
1	 0.5060	 0.1540
2	 0.5600	 0.1950
3	 0.4990	 0.1550
4	 0.5600	 0.1640
5	 0.5640	 0.1700
6	 0.5020	 0.1640
7	 0.5170	 0.1590
A	 0.5950	 0.1790
B	 0.5610	 0.1630
C	 0.5370	 0.1670
D	 0.5360	 0.1720
E	 0.5460	 0.1610
F	 0.5460	 0.1660
G	 0.5310	 0.1520
H	 0.4650	 0.1340
I	 0.4550	 0.1290
J	 0.5020	 0.1470
K	 0.5100	 0.1440
L	 0.4880	 0.1450
M	 0.4550	 0.1350
N	 0.4460	 0.1440
O	 0.5270	 0.1330
P	 0.5200	 0.1320
Q	 0.3150	 0.1120
R	 0.5370	 0.1380
S	 0.5000	 0.1440
T	 0.5110	 0.1360
U	 0.5420	 0.1560
V	 0.5210	 0.1530
W	 0.4300	 0.1420
Y	 0.4420	 0.1600
Z	 0.1150	 0.0640

