



wwPDB EM Validation Summary Report ⓘ

Oct 5, 2024 – 06:34 PM EDT

PDB ID : 5VFT
EMDB ID : EMD-8667
Title : Nucleotide-driven Triple-state Remodeling of the AAA-ATPase Channel in the Activated Human 26S Proteasome
Authors : Zhu, Y.; Wang, W.L.; Yu, D.; Ouyang, Q.; Lu, Y.; Mao, Y.
Deposited on : 2017-04-09
Resolution : 7.00 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:

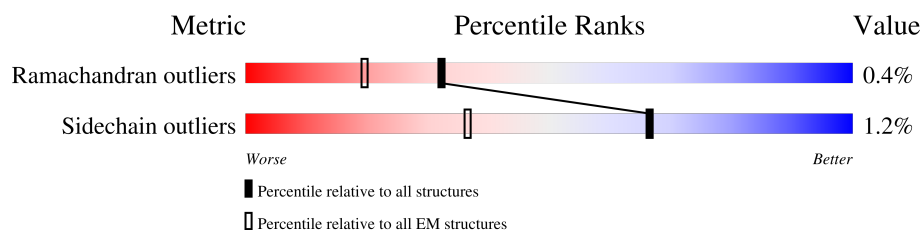
EMDB validation analysis : 0.0.1.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

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 7.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	U	911	
2	V	480	
3	W	456	
4	X	380	
5	Y	378	
6	Z	286	
7	a	373	
8	b	191	
9	c	287	

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Mol	Chain	Length	Quality of chain
10	d	257	77% 98%
11	e	70	26% 34% 66%
12	A	361	53% 98%
13	B	341	59% 97%
14	C	384	57% 96%
15	D	380	65% 97%
16	E	353	61% 99%
17	F	377	53% 93%
18	G	240	20% 99%
18	g	240	14% 100%
19	H	232	22% 99%
19	h	232	19% 100%
20	I	250	28% 99%
20	i	250	26% 99%
21	J	243	21% 97%
21	j	243	20% 98%
22	K	234	18% 95%
22	k	234	15% 95%
23	L	238	14% 98%
23	l	238	12% 100%
24	M	245	15% 97%
24	m	245	17% 97%
25	N	191	14% 100%
25	n	191	9% 99%
26	O	220	15% 100%

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Mol	Chain	Length	Quality of chain
26	o	220	
27	P	204	
27	p	204	
28	Q	199	
28	q	199	
29	R	201	
29	r	201	
30	S	213	
30	s	213	
31	T	215	
31	t	215	
32	f	908	

2 Entry composition

There are 33 unique types of molecules in this entry. The entry contains 96994 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 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	U	806	Total	C	N	O	S	0	0
			6287	3990	1075	1178	44		

- Molecule 2 is a protein called 26S proteasome non-ATPase regulatory subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	V	480	Total	C	N	O	S	0	0
			3852	2444	684	710	14		

- Molecule 3 is a protein called 26S proteasome non-ATPase regulatory subunit 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	W	236	Total	C	N	O	S	0	0
			1940	1237	331	361	11		

- Molecule 4 is a protein called 26S proteasome non-ATPase regulatory subunit 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	X	81	Total	C	N	O	S	0	0
			647	414	107	124	2		

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

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

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

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

- Molecule 7 is a protein called Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 13, isoform CRA_a.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	a	373	Total	C	N	O	S	0	0
			2993	1910	509	559	15		

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

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

- Molecule 9 is a protein called 26S proteasome non-ATPase regulatory subunit 14.

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

- Molecule 10 is a protein called 26S proteasome non-ATPase regulatory subunit 8.

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

- Molecule 11 is a protein called sem1.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	e	24	Total	C	N	O	S	0	0
			197	121	34	40	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	A	361	Total	C	N	O	S	0	0
			2835	1788	501	528	18		

- Molecule 13 is a protein called 26S proteasome regulatory subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	B	341	Total	C	N	O	S	0	0
			2662	1671	453	526	12		

- Molecule 14 is a protein called 26S proteasome regulatory subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	C	384	Total	C	N	O	S	0	0
			3015	1894	540	564	17		

- Molecule 15 is a protein called 26S proteasome regulatory subunit 6B.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	D	380	Total	C	N	O	S	0	0
			3040	1923	524	580	13		

- Molecule 16 is a protein called 26S proteasome regulatory subunit 10B.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	E	353	Total	C	N	O	S	0	0
			2790	1755	494	525	16		

- Molecule 17 is a protein called 26S proteasome regulatory subunit 6A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	F	366	Total	C	N	O	S	0	0
			2863	1802	496	549	16		

- Molecule 18 is a protein called Proteasome subunit alpha type-6.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	G	240	Total	C	N	O	S	0	0
			1825	1160	304	348	13		
18	g	240	Total	C	N	O	S	0	0
			1826	1160	305	348	13		

- Molecule 19 is a protein called Proteasome subunit alpha type-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	H	232	Total	C	N	O	S	0	0
			1708	1081	289	333	5		
19	h	232	Total	C	N	O	S	0	0
			1708	1081	289	333	5		

- Molecule 20 is a protein called Proteasome subunit alpha type-4.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	I	250	Total	C	N	O	S	0	0
			1912	1204	329	371	8		
20	i	250	Total	C	N	O	S	0	0
			1912	1204	329	371	8		

- Molecule 21 is a protein called Proteasome subunit alpha type-7.

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

- Molecule 22 is a protein called Proteasome subunit alpha type-5.

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

- Molecule 23 is a protein called Proteasome subunit alpha type-1.

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

- Molecule 24 is a protein called Proteasome subunit alpha type-3.

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

- Molecule 25 is a protein called Proteasome subunit beta type-6.

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

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

- Molecule 26 is a protein called Proteasome subunit beta type-7.

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

- Molecule 27 is a protein called Proteasome subunit beta type-3.

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

- Molecule 28 is a protein called Proteasome subunit beta type-2.

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

- Molecule 29 is a protein called Proteasome subunit beta type-5.

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

- Molecule 30 is a protein called Proteasome subunit beta type-1.

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

- Molecule 31 is a protein called Proteasome subunit beta type-4.

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

- Molecule 32 is a protein called 26S proteasome non-ATPase regulatory subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	f	689	Total	C	N	O	S	0	0
			5319	3343	904	1037	35		

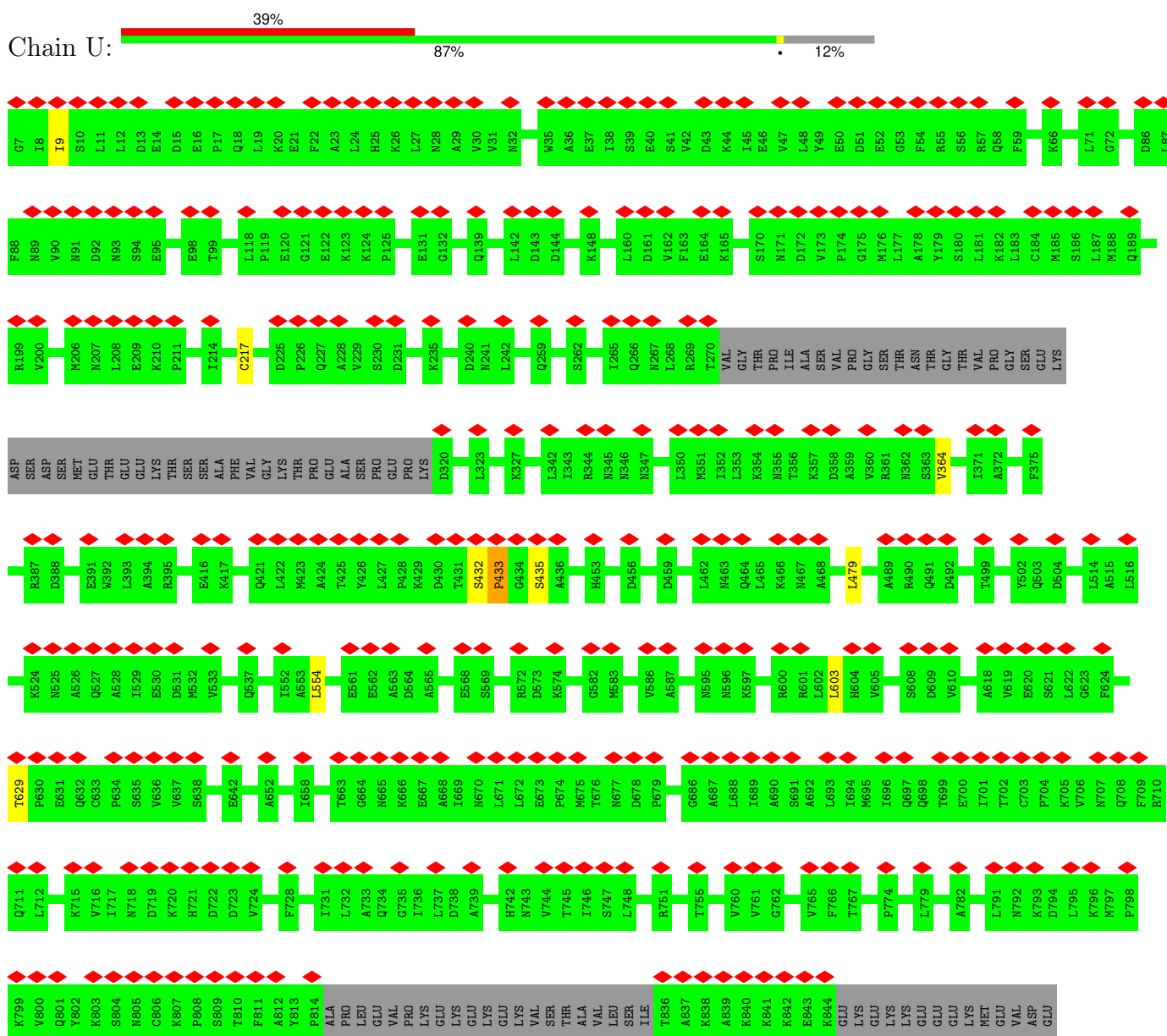
- Molecule 33 is ZINC ION (three-letter code: ZN) (formula: Zn).

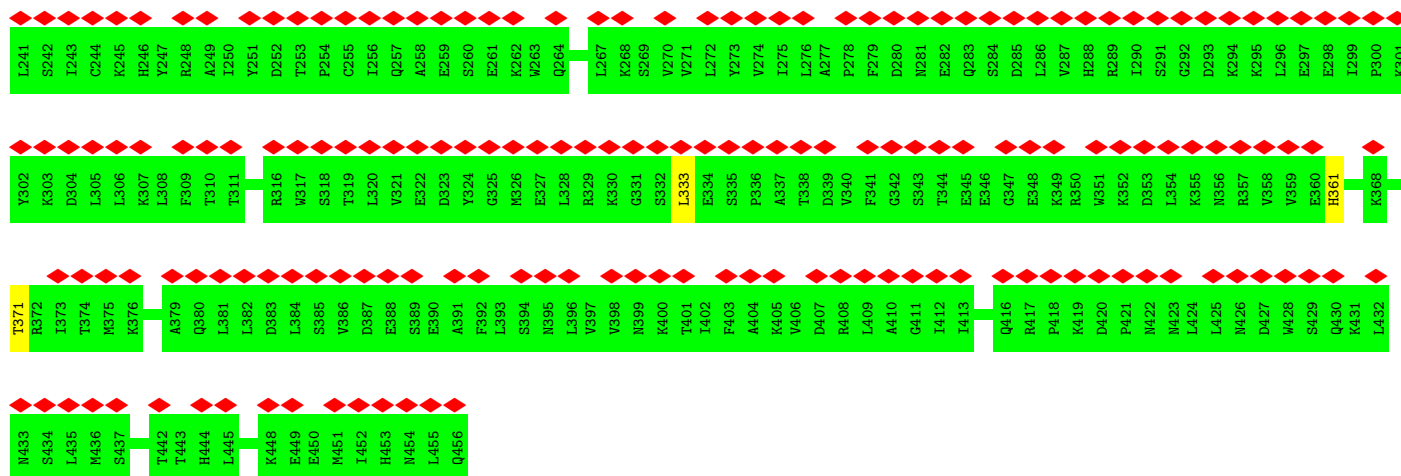
Mol	Chain	Residues	Atoms		AltConf
33	c	1	Total	Zn	0
			1	1	

3 Residue-property plots

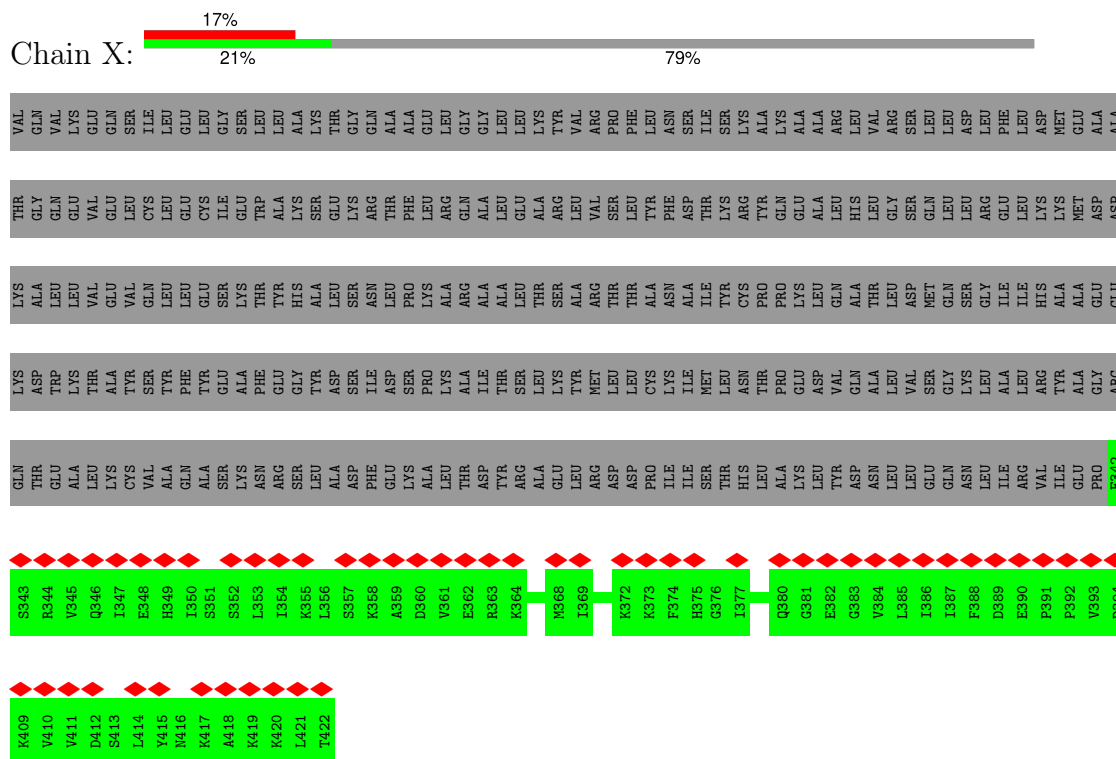
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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 1

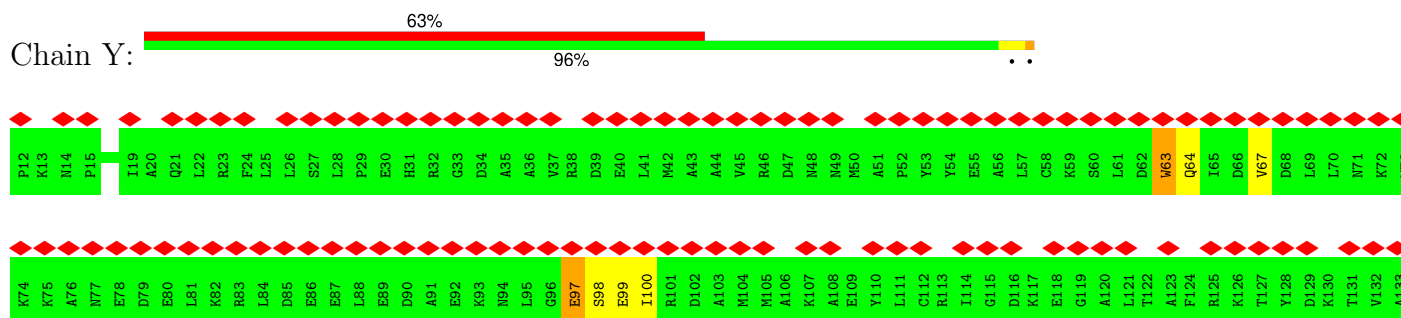


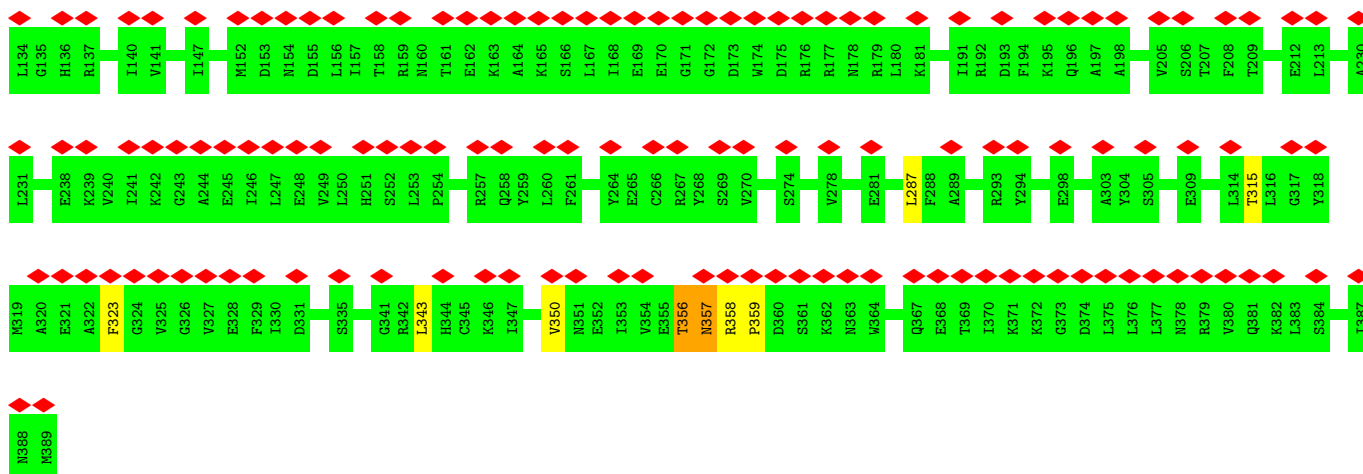


• Molecule 4: 26S proteasome non-ATPase regulatory subunit 11

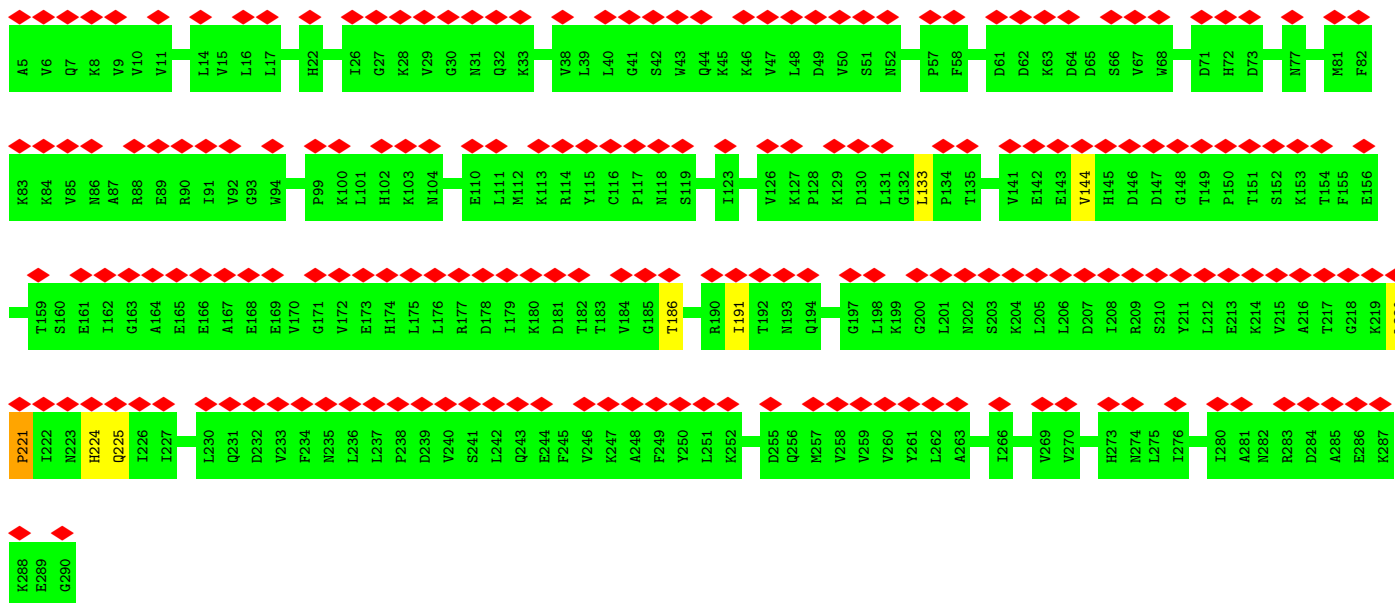


• Molecule 5: 26S proteasome non-ATPase regulatory subunit 6

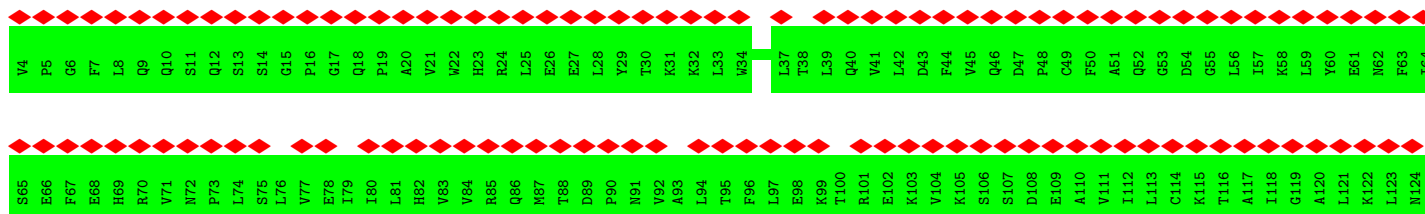
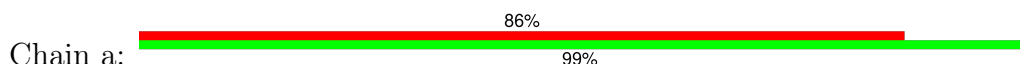


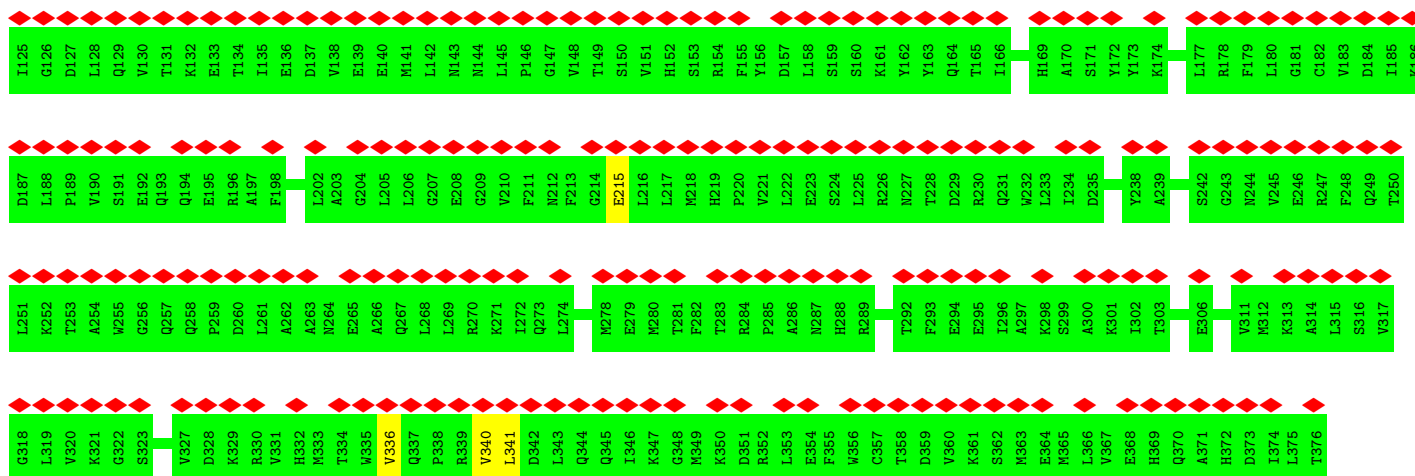


- Molecule 6: 26S proteasome non-ATPase regulatory subunit 7

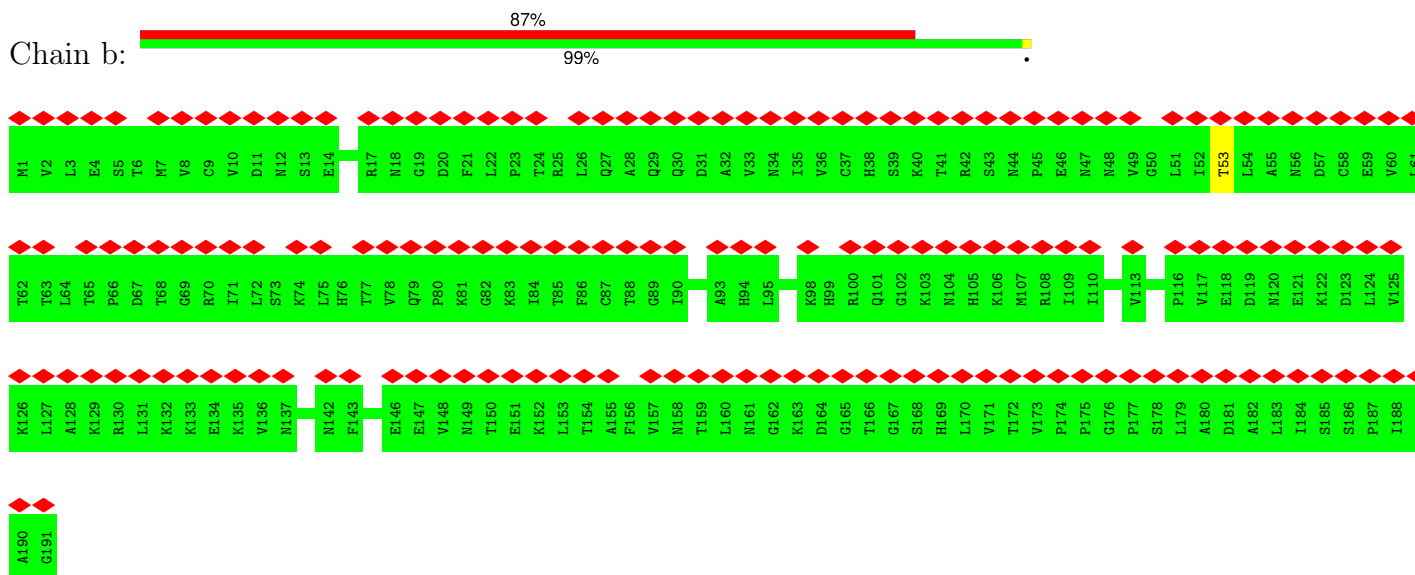


- Molecule 7: Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 13, isoform CRA_a

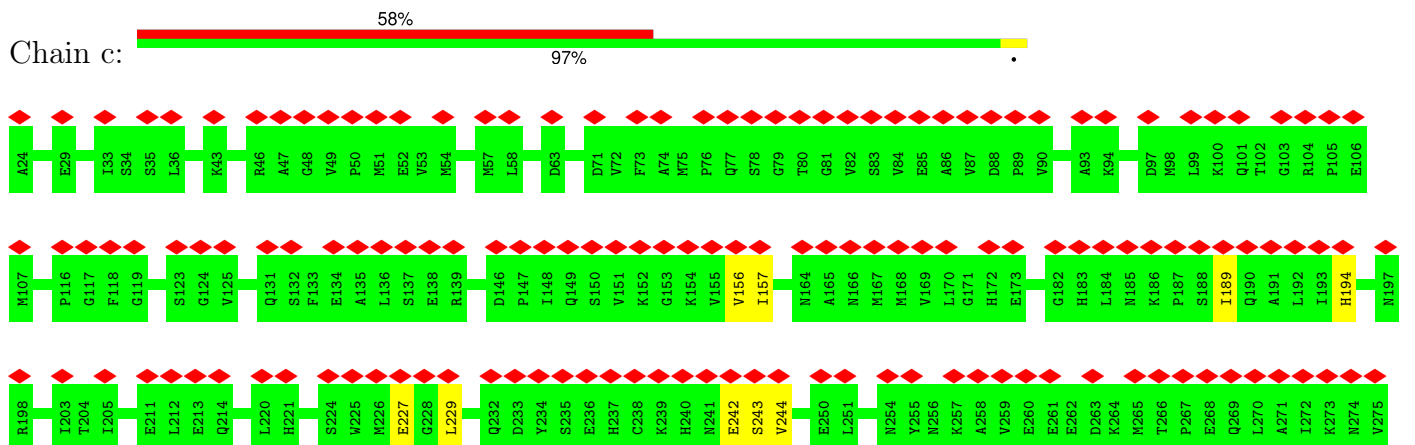


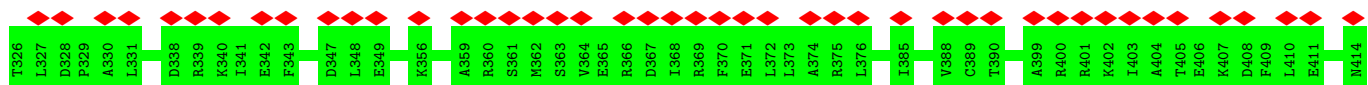


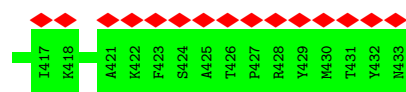
- Molecule 8: 26S proteasome non-ATPase regulatory subunit 4



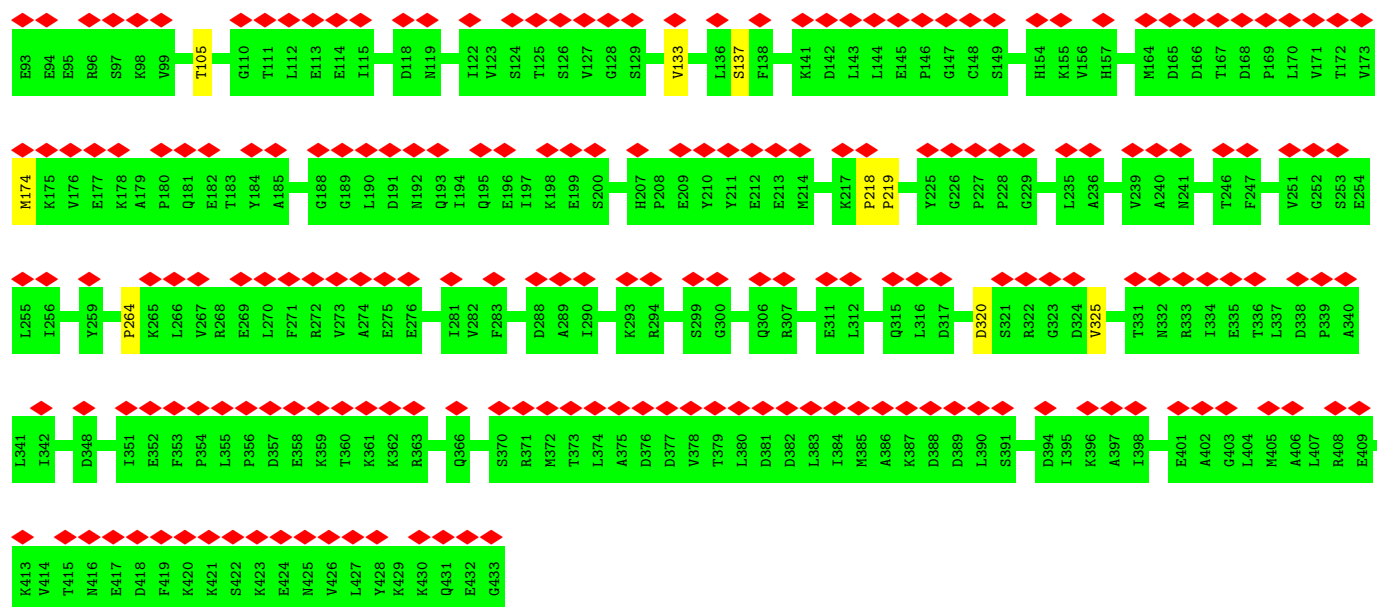
- Molecule 9: 26S proteasome non-ATPase regulatory subunit 14



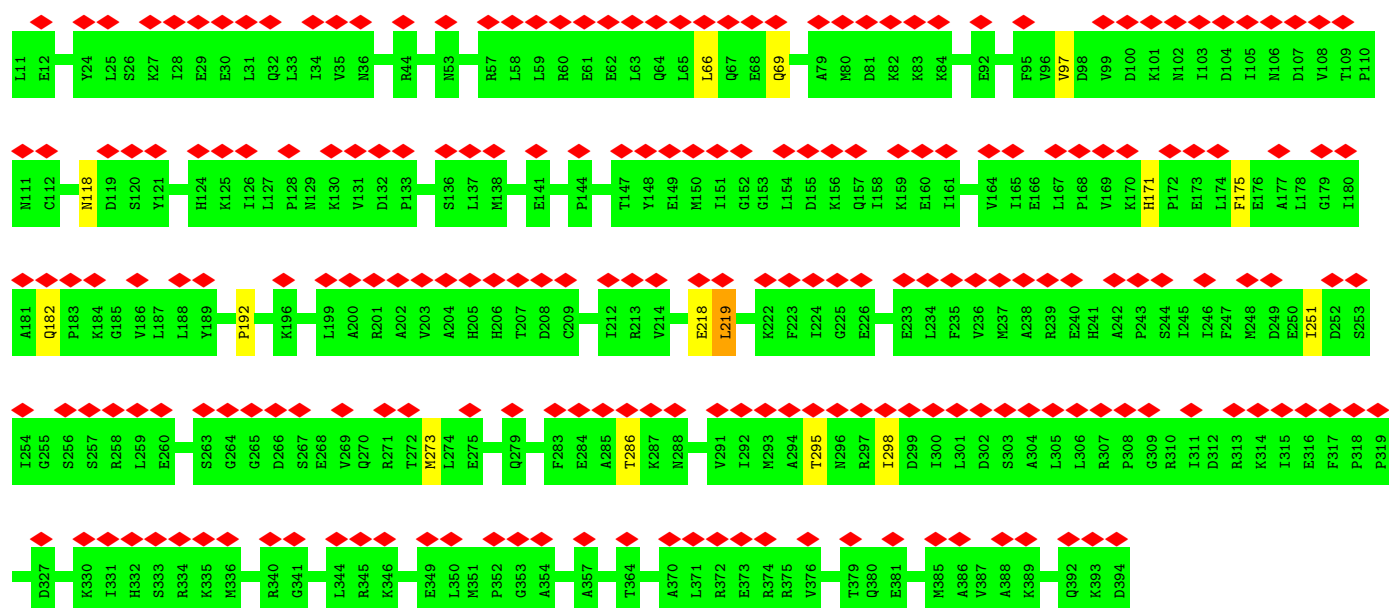




- Molecule 13: 26S proteasome regulatory subunit 4



- Molecule 14: 26S proteasome regulatory subunit 8

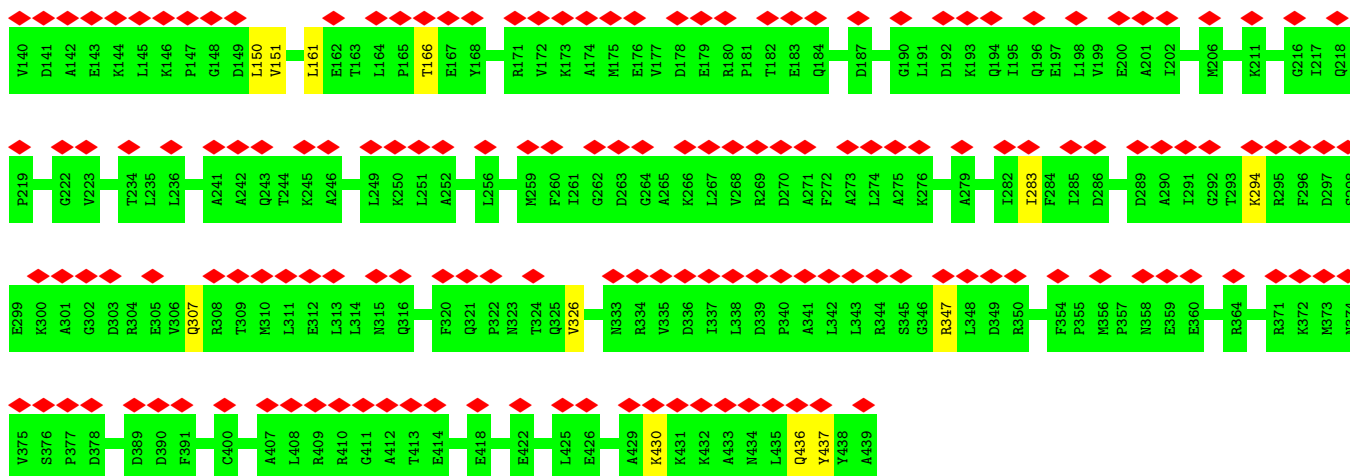


- Molecule 15: 26S proteasome regulatory subunit 6B

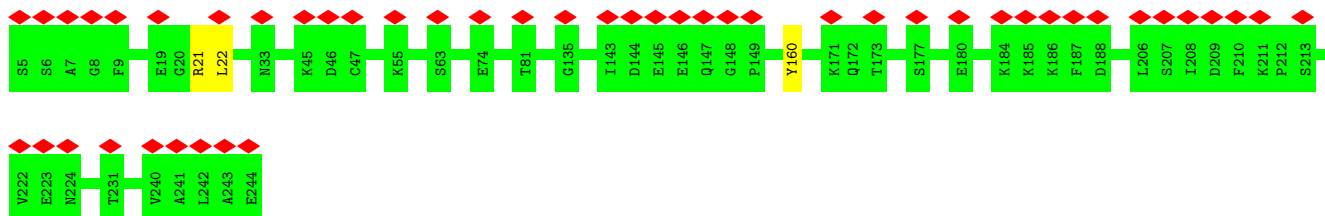
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G340	A341	D342	L343	R344	N345	V346	E349	A350	G351	M352	R356	A357	D358	H359	E365	M368	K369	A370	V371	R372	K373	V374	A375	D376	S377	K378	R379	L380	E381	S382	K383	L384	D385	Y386	K387	P388	V389																
N262	Q263	M264	D265	G266	F267	D268	T269	L270	H271	R272	A278	T279	N280	R281	P282	D283	P287	A288	P292	G293	R294	L295	D296	I301	D302	L303	E306	Q307	A308	R309	L310	D311	K314	I315	T321	K322	H323	G324	E325	I326	D327	Y328	E329	A330	K333	L334	S335	D336	G337	F338	N339		
A186	L191	D192	C193	M194	F195	L196	S200	S201	S202	L203	V204	D205	K206	Y207	T208	G209	E210	S211	A212	R213	L214	I215	R216	E217	W218	F219	Y221	A222	R223	D224	H225	Q226	P227	C228	T235	D236	A237	L238	G239	G240	R241	S248	A249	D250	R251	E252	T253	Q254	R255	T256	L257	M258	E259
R109	Y110	L111	P112	R113	E114	V115	D116	P117	L118	V119	Y120	M121	M122	S123	H124	E125	I126	P127	G128	M129	V130	E134	I135	G136	G137	L138	Q141	L145	P152	M155	P156	E157	Q160	R161	V162	I165	K168	G169	Y173	G174	P175	P176	G177	K180	T181	L182	L183	A184	R185				
T37	K38	Q39	Y40	E41	K42	S43	E44	M45	D46	L47	K48	A49	S52	V53	G58	E59	V60	L61	K62	Q63	L64	T65	E66	E67	K68	A73	T74	N75	G76	P77	R78	Y79	V80	V81	G82	C83	R84	R85	Q86	L87	D88	K89	S90	K91	L92	K93	P94	G95	T96	L100	T104	L107	M108

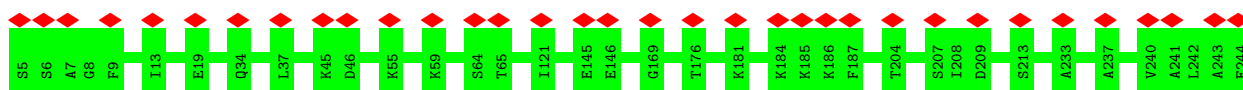
T63	H64	E65	L66	Q67	A68	M69	K70	D71	T72	W73	K74	E75	S76	T77		R80	K81	V82		P87		M92	V93	I94	E95	L96	L97	D98	V99	D100	P101	M102	D103	GLN	GLU	GLU	GLY	ASP	ASP	GLY	ALA	ASN	ILE	ASP	ASP	LEU	ASP	S115	Q116	R117	K118	G119	K120	C121		K125		T128	R129		I137	
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	--	-----	-----	-----	--	-----	--	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	------	--	------	--	------	------	--	------	--



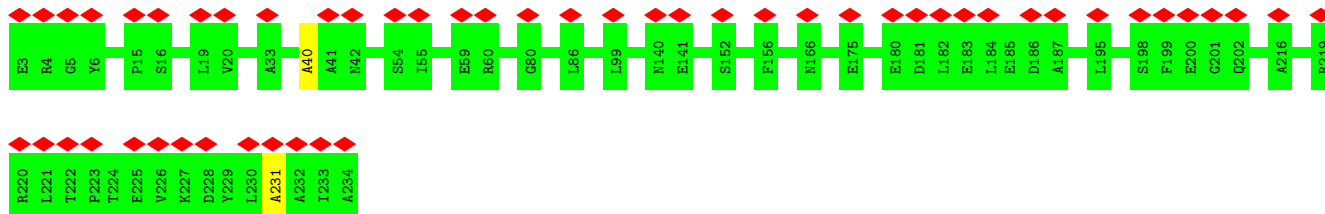
• Molecule 18: Proteasome subunit alpha type-6



• Molecule 18: Proteasome subunit alpha type-6

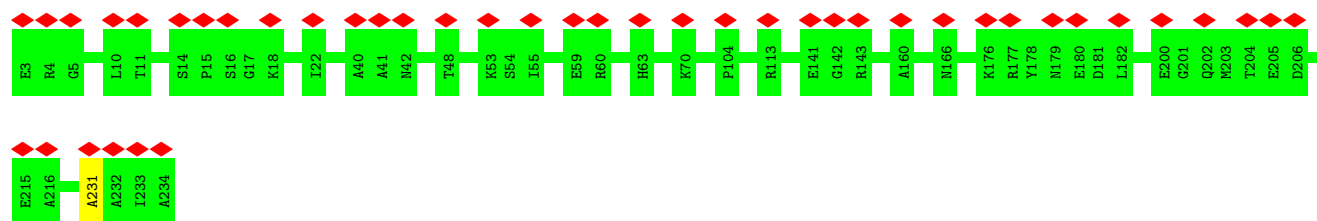


• Molecule 19: Proteasome subunit alpha type-2



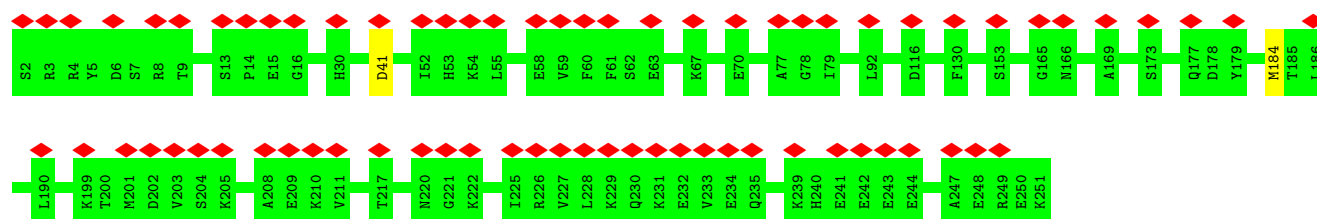
• Molecule 19: Proteasome subunit alpha type-2





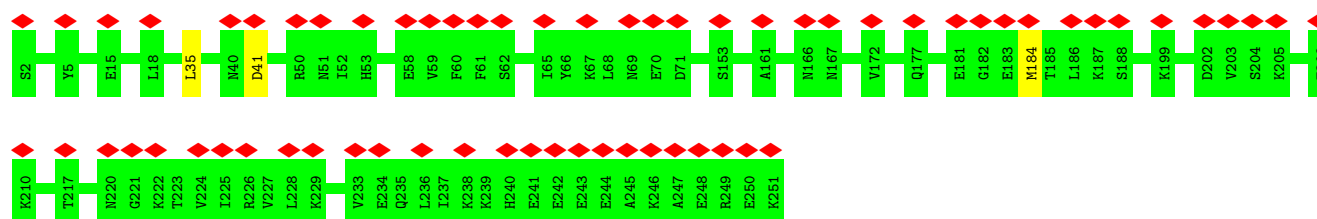
• Molecule 20: Proteasome subunit alpha type-4

Chain I: 28% 99%



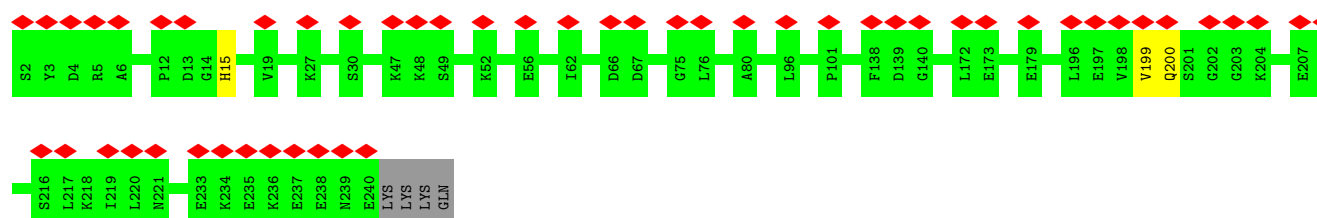
• Molecule 20: Proteasome subunit alpha type-4

Chain i: 26% 99%



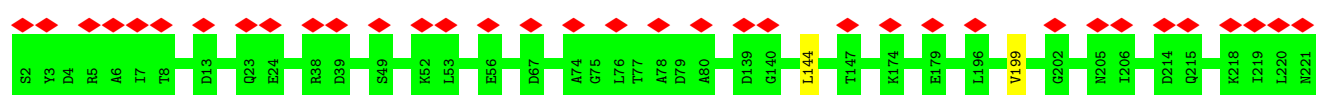
• Molecule 21: Proteasome subunit alpha type-7

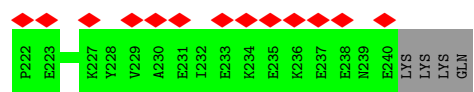
Chain J: 21% 97%



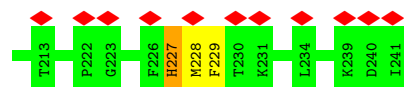
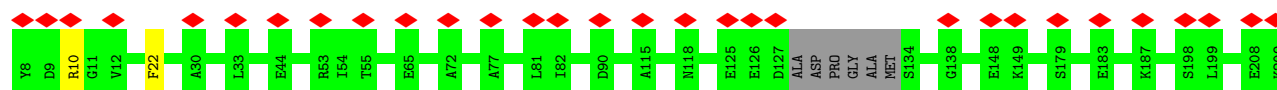
• Molecule 21: Proteasome subunit alpha type-7

Chain j: 20% 98%

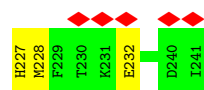
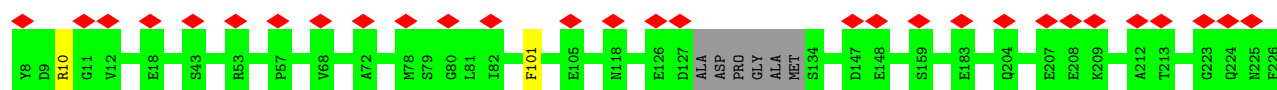




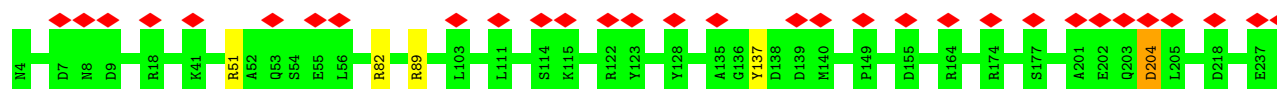
- Molecule 22: Proteasome subunit alpha type-5



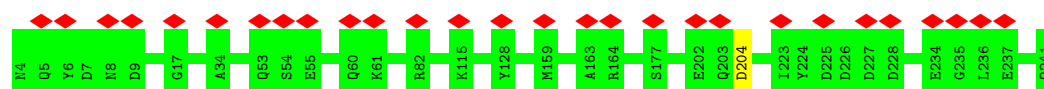
- Molecule 22: Proteasome subunit alpha type-5



- Molecule 23: Proteasome subunit alpha type-1

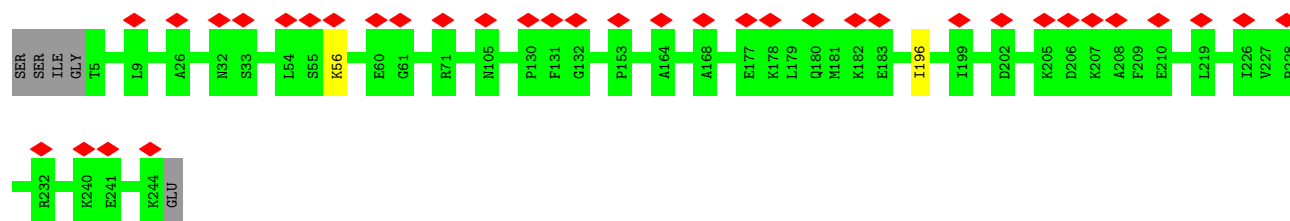


- Molecule 23: Proteasome subunit alpha type-1

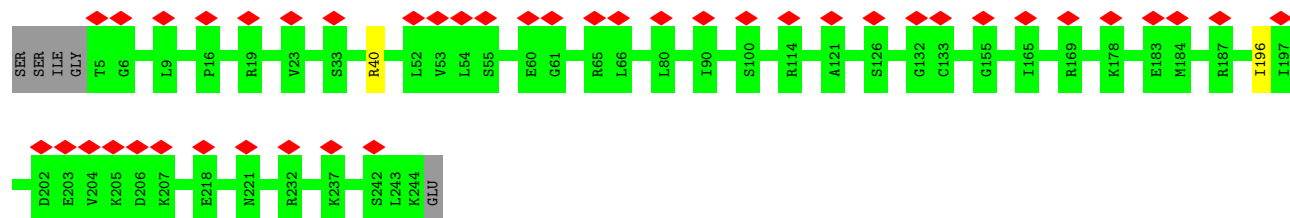


- Molecule 24: Proteasome subunit alpha type-3

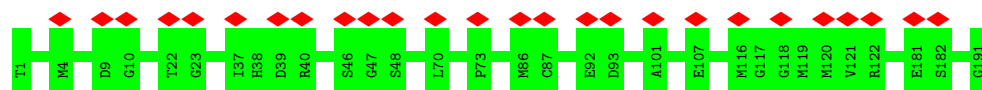




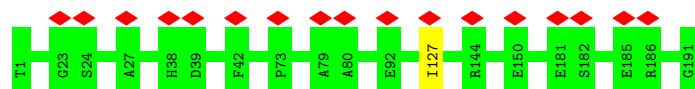
- Molecule 24: Proteasome subunit alpha type-3



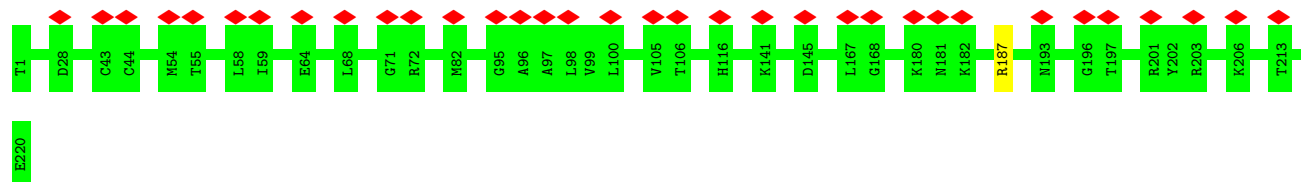
- Molecule 25: Proteasome subunit beta type-6



- Molecule 25: Proteasome subunit beta type-6

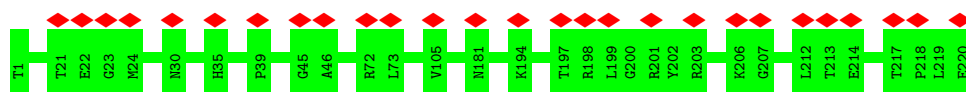


- Molecule 26: Proteasome subunit beta type-7

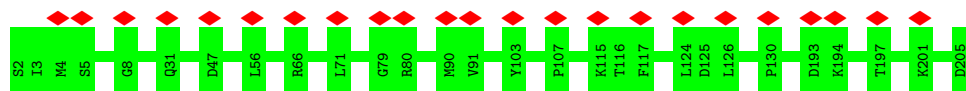


- Molecule 26: Proteasome subunit beta type-7

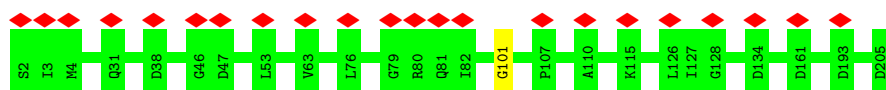




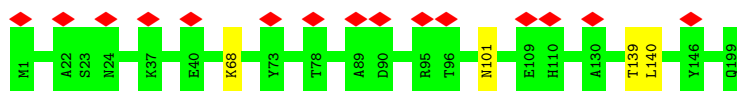
- Molecule 27: Proteasome subunit beta type-3



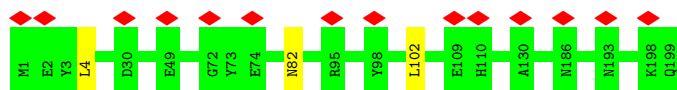
- Molecule 27: Proteasome subunit beta type-3



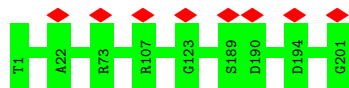
- Molecule 28: Proteasome subunit beta type-2



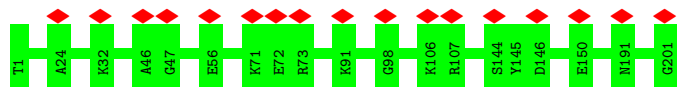
- Molecule 28: Proteasome subunit beta type-2



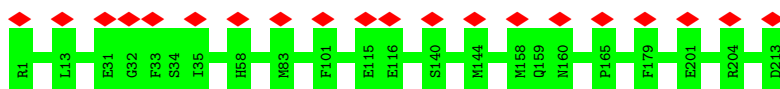
- Molecule 29: Proteasome subunit beta type-5



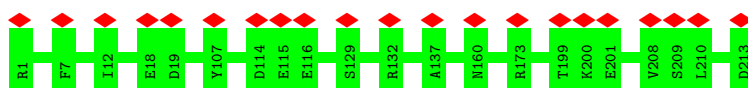
- Molecule 29: Proteasome subunit beta type-5



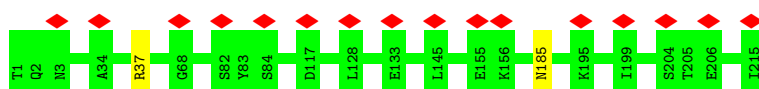
- Molecule 30: Proteasome subunit beta type-1



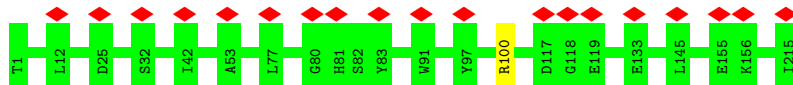
- Molecule 30: Proteasome subunit beta type-1



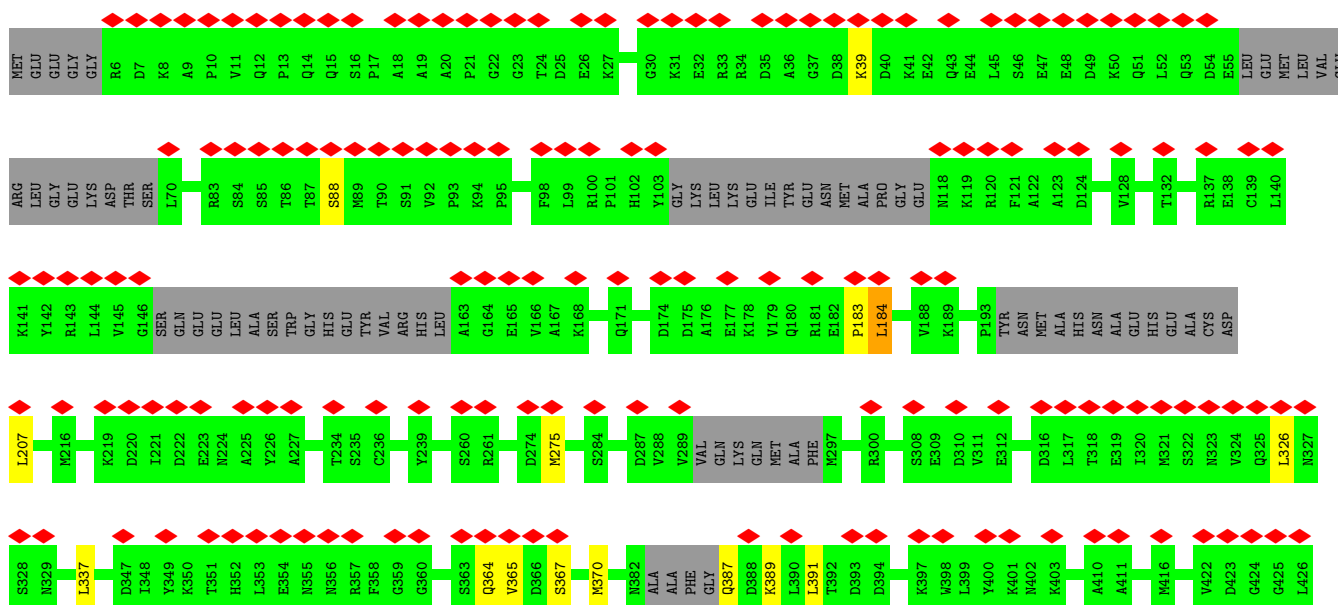
- Molecule 31: Proteasome subunit beta type-4

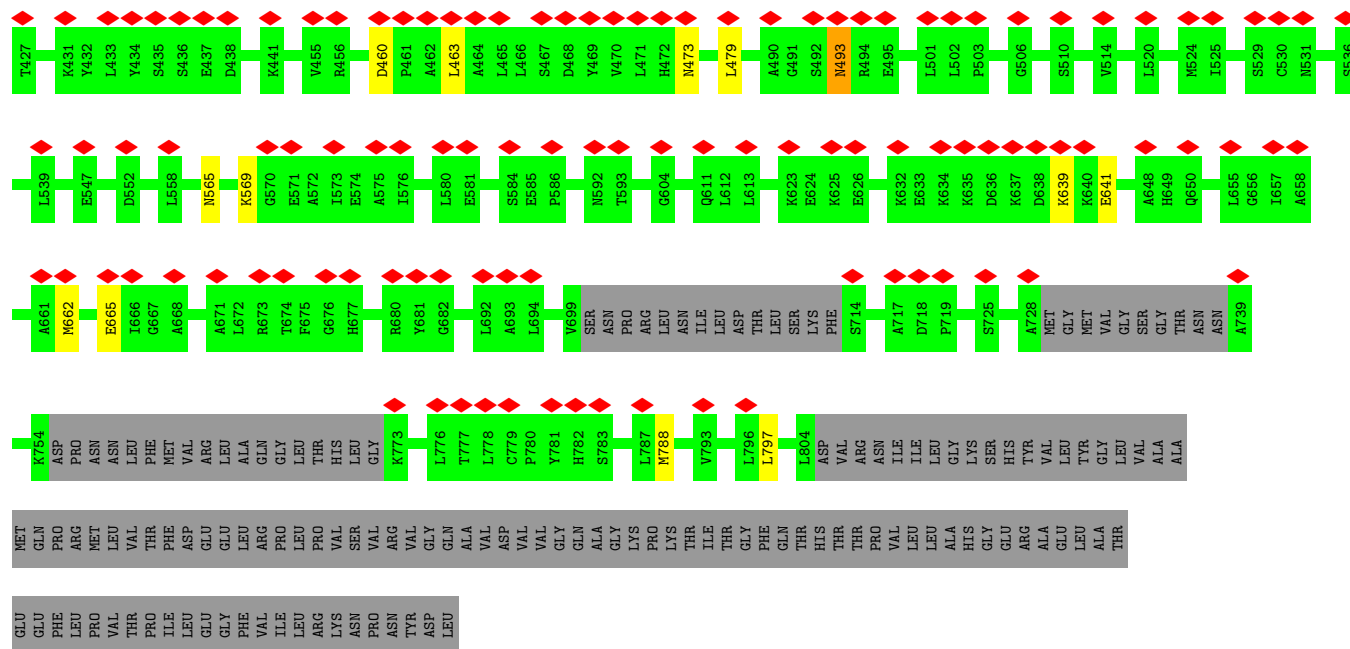


- Molecule 31: Proteasome subunit beta type-4



- Molecule 32: 26S proteasome non-ATPase regulatory subunit 2





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	15536	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TECNAI ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.008	Depositor
Minimum map value	-0.003	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.003	Depositor
Map size (Å)	420.0, 420.0, 420.0	wwPDB
Map dimensions	560, 560, 560	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.75, 0.75, 0.75	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	U	0.24	0/6396	0.42	0/8646
2	V	0.25	0/3929	0.46	0/5309
3	W	0.24	0/1975	0.46	0/2659
4	X	0.22	0/655	0.40	0/877
5	Y	0.23	0/3173	0.44	1/4273 (0.0%)
6	Z	0.23	0/2324	0.51	1/3150 (0.0%)
7	a	0.24	0/3051	0.45	0/4130
8	b	0.25	0/1478	0.43	0/2001
9	c	0.25	0/2302	0.51	0/3110
10	d	0.26	0/2162	0.51	0/2919
11	e	0.24	0/198	0.52	0/258
12	A	0.27	0/2886	0.53	0/3899
13	B	0.27	0/2700	0.55	0/3645
14	C	0.25	0/3054	0.49	0/4107
15	D	0.26	0/3090	0.52	0/4168
16	E	0.25	0/2835	0.48	0/3821
17	F	0.26	0/2903	0.54	0/3912
18	G	0.36	0/1858	0.58	0/2521
18	g	0.33	0/1859	0.58	0/2523
19	H	0.37	0/1743	0.60	0/2372
19	h	0.35	0/1743	0.59	1/2372 (0.0%)
20	I	0.36	0/1942	0.62	2/2628 (0.1%)
20	i	0.34	0/1942	0.63	3/2628 (0.1%)
21	J	0.38	0/1728	0.60	0/2358
21	j	0.34	0/1728	0.57	1/2358 (0.0%)
22	K	0.35	0/1747	0.61	0/2364
22	k	0.34	0/1747	0.63	1/2364 (0.0%)
23	L	0.37	0/1885	0.59	1/2552 (0.0%)
23	l	0.33	0/1885	0.58	0/2552
24	M	0.38	0/1891	0.58	0/2552
24	m	0.34	0/1891	0.57	0/2552
25	N	0.35	0/1454	0.53	0/1967

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
25	n	0.35	0/1454	0.55	0/1967
26	O	0.34	0/1670	0.53	0/2265
26	o	0.34	0/1670	0.53	0/2265
27	P	0.35	0/1614	0.53	0/2177
27	p	0.35	0/1614	0.53	0/2177
28	Q	0.38	0/1603	0.60	0/2174
28	q	0.40	0/1603	0.65	1/2174 (0.0%)
29	R	0.38	0/1579	0.52	0/2134
29	r	0.36	0/1579	0.51	0/2134
30	S	0.35	0/1671	0.54	0/2253
30	s	0.33	0/1671	0.53	0/2253
31	T	0.37	0/1700	0.55	0/2305
31	t	0.36	0/1700	0.53	0/2305
32	f	0.31	0/5393	0.68	1/7271 (0.0%)
All	All	0.31	0/98675	0.54	13/133401 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	U	0	3
2	V	0	4
5	Y	0	2
6	Z	0	1
9	c	0	1
10	d	0	1
12	A	0	1
13	B	0	2
14	C	0	1
15	D	0	1
16	E	0	1
17	F	0	2
18	G	0	1
19	H	0	2
21	J	0	2
21	j	0	1
22	K	0	1
22	k	0	3
23	L	0	2
23	l	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
24	M	0	1
26	O	0	1
27	p	0	1
28	Q	0	2
28	q	0	1
All	All	0	39

There are no bond length outliers.

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	Z	220	LEU	C-N-CD	-11.96	94.29	120.60
20	i	35	LEU	CA-CB-CG	6.83	131.01	115.30
28	q	4	LEU	CB-CG-CD2	5.70	120.69	111.00
19	h	231	ALA	C-N-CA	5.69	135.93	121.70
20	i	41	ASP	CB-CG-OD1	5.68	123.41	118.30

There are no chirality outliers.

5 of 39 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	U	432	SER	Peptide
1	U	433	PRO	Peptide
1	U	435	SER	Peptide
2	V	54	LYS	Peptide
2	V	57	ALA	Peptide

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

The Analysed column shows the number of residues for which the backbone conformation was

analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	U	798/911 (88%)	729 (91%)	67 (8%)	2 (0%)	37	73
2	V	478/480 (100%)	412 (86%)	60 (13%)	6 (1%)	10	43
3	W	234/456 (51%)	213 (91%)	21 (9%)	0	100	100
4	X	79/380 (21%)	75 (95%)	4 (5%)	0	100	100
5	Y	376/378 (100%)	331 (88%)	36 (10%)	9 (2%)	5	27
6	Z	284/286 (99%)	252 (89%)	30 (11%)	2 (1%)	19	57
7	a	371/373 (100%)	340 (92%)	28 (8%)	3 (1%)	16	55
8	b	189/191 (99%)	178 (94%)	11 (6%)	0	100	100
9	c	285/287 (99%)	241 (85%)	39 (14%)	5 (2%)	7	35
10	d	255/257 (99%)	220 (86%)	33 (13%)	2 (1%)	16	55
11	e	20/70 (29%)	16 (80%)	4 (20%)	0	100	100
12	A	359/361 (99%)	303 (84%)	54 (15%)	2 (1%)	22	60
13	B	339/341 (99%)	298 (88%)	38 (11%)	3 (1%)	14	52
14	C	382/384 (100%)	318 (83%)	60 (16%)	4 (1%)	13	49
15	D	378/380 (100%)	325 (86%)	51 (14%)	2 (0%)	25	64
16	E	351/353 (99%)	299 (85%)	51 (14%)	1 (0%)	37	73
17	F	362/377 (96%)	315 (87%)	45 (12%)	2 (1%)	22	60
18	G	238/240 (99%)	223 (94%)	15 (6%)	0	100	100
18	g	238/240 (99%)	226 (95%)	12 (5%)	0	100	100
19	H	230/232 (99%)	213 (93%)	17 (7%)	0	100	100
19	h	230/232 (99%)	214 (93%)	16 (7%)	0	100	100
20	I	248/250 (99%)	236 (95%)	12 (5%)	0	100	100
20	i	248/250 (99%)	228 (92%)	20 (8%)	0	100	100
21	J	237/243 (98%)	215 (91%)	21 (9%)	1 (0%)	30	68
21	j	237/243 (98%)	222 (94%)	15 (6%)	0	100	100
22	K	224/234 (96%)	204 (91%)	19 (8%)	1 (0%)	30	68
22	k	224/234 (96%)	203 (91%)	21 (9%)	0	100	100
23	L	236/238 (99%)	222 (94%)	14 (6%)	0	100	100
23	l	236/238 (99%)	222 (94%)	14 (6%)	0	100	100
24	M	238/245 (97%)	221 (93%)	17 (7%)	0	100	100
24	m	238/245 (97%)	220 (92%)	18 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
25	N	189/191 (99%)	179 (95%)	10 (5%)	0	100	100
25	n	189/191 (99%)	181 (96%)	8 (4%)	0	100	100
26	O	218/220 (99%)	210 (96%)	8 (4%)	0	100	100
26	o	218/220 (99%)	210 (96%)	8 (4%)	0	100	100
27	P	202/204 (99%)	194 (96%)	8 (4%)	0	100	100
27	p	202/204 (99%)	186 (92%)	16 (8%)	0	100	100
28	Q	197/199 (99%)	179 (91%)	18 (9%)	0	100	100
28	q	197/199 (99%)	177 (90%)	20 (10%)	0	100	100
29	R	199/201 (99%)	189 (95%)	10 (5%)	0	100	100
29	r	199/201 (99%)	191 (96%)	8 (4%)	0	100	100
30	S	211/213 (99%)	203 (96%)	8 (4%)	0	100	100
30	s	211/213 (99%)	202 (96%)	9 (4%)	0	100	100
31	T	213/215 (99%)	204 (96%)	9 (4%)	0	100	100
31	t	213/215 (99%)	201 (94%)	12 (6%)	0	100	100
32	f	669/908 (74%)	579 (86%)	82 (12%)	8 (1%)	11	44
All	All	12369/13423 (92%)	11219 (91%)	1097 (9%)	53 (0%)	32	68

5 of 53 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	U	364	VAL
2	V	58	ALA
2	V	81	GLN
2	V	193	GLN
2	V	197	THR

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	U	685/779 (88%)	679 (99%)	6 (1%)	75	83

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	V	414/414 (100%)	402 (97%)	12 (3%)	37	56
3	W	218/416 (52%)	215 (99%)	3 (1%)	62	75
4	X	74/327 (23%)	74 (100%)	0	100	100
5	Y	334/334 (100%)	326 (98%)	8 (2%)	44	62
6	Z	257/257 (100%)	252 (98%)	5 (2%)	52	69
7	a	333/333 (100%)	332 (100%)	1 (0%)	91	92
8	b	167/167 (100%)	166 (99%)	1 (1%)	84	88
9	c	252/252 (100%)	249 (99%)	3 (1%)	67	78
10	d	231/231 (100%)	229 (99%)	2 (1%)	75	83
11	e	22/22 (100%)	22 (100%)	0	100	100
12	A	308/308 (100%)	303 (98%)	5 (2%)	58	73
13	B	298/298 (100%)	294 (99%)	4 (1%)	65	77
14	C	332/332 (100%)	321 (97%)	11 (3%)	33	52
15	D	333/333 (100%)	322 (97%)	11 (3%)	33	52
16	E	308/308 (100%)	306 (99%)	2 (1%)	84	88
17	F	312/321 (97%)	302 (97%)	10 (3%)	34	53
18	G	192/205 (94%)	190 (99%)	2 (1%)	73	82
18	g	193/205 (94%)	193 (100%)	0	100	100
19	H	164/190 (86%)	164 (100%)	0	100	100
19	h	164/190 (86%)	164 (100%)	0	100	100
20	I	193/210 (92%)	193 (100%)	0	100	100
20	i	193/210 (92%)	193 (100%)	0	100	100
21	J	152/207 (73%)	152 (100%)	0	100	100
21	j	152/207 (73%)	152 (100%)	0	100	100
22	K	186/196 (95%)	182 (98%)	4 (2%)	47	65
22	k	186/196 (95%)	185 (100%)	1 (0%)	86	89
23	L	198/204 (97%)	195 (98%)	3 (2%)	60	75
23	l	198/204 (97%)	198 (100%)	0	100	100
24	M	192/202 (95%)	191 (100%)	1 (0%)	86	89
24	m	192/202 (95%)	190 (99%)	2 (1%)	73	82
25	N	148/148 (100%)	148 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
25	n	148/148 (100%)	147 (99%)	1 (1%)	81	87
26	O	177/181 (98%)	177 (100%)	0	100	100
26	o	177/181 (98%)	177 (100%)	0	100	100
27	P	172/173 (99%)	172 (100%)	0	100	100
27	p	172/173 (99%)	172 (100%)	0	100	100
28	Q	164/170 (96%)	162 (99%)	2 (1%)	67	78
28	q	164/170 (96%)	163 (99%)	1 (1%)	84	88
29	R	153/156 (98%)	153 (100%)	0	100	100
29	r	153/156 (98%)	153 (100%)	0	100	100
30	S	174/178 (98%)	174 (100%)	0	100	100
30	s	174/178 (98%)	174 (100%)	0	100	100
31	T	175/178 (98%)	173 (99%)	2 (1%)	70	80
31	t	175/178 (98%)	174 (99%)	1 (1%)	84	88
32	f	580/763 (76%)	559 (96%)	21 (4%)	30	50
All	All	10339/11391 (91%)	10214 (99%)	125 (1%)	66	78

5 of 125 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
14	C	219	LEU
32	f	387	GLN
15	D	418	LYS
32	f	370	MET
32	f	565	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 92 such sidechains are listed below:

Mol	Chain	Res	Type
19	H	119	GLN
20	i	53	HIS
20	I	53	HIS
25	N	154	GLN
22	k	114	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no 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](#)

There are no chain breaks in this entry.

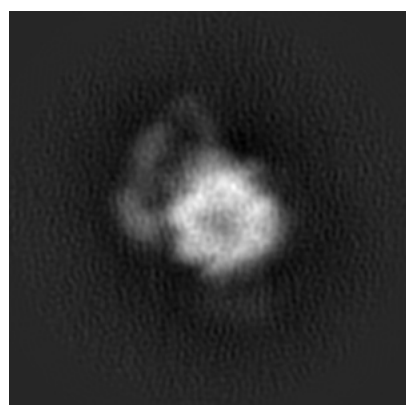
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8667. These allow visual inspection of the internal detail of the map and identification of artifacts.

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

6.1 Orthogonal projections [i](#)

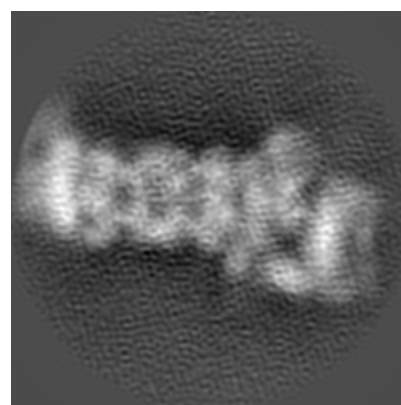
6.1.1 Primary map



X



Y

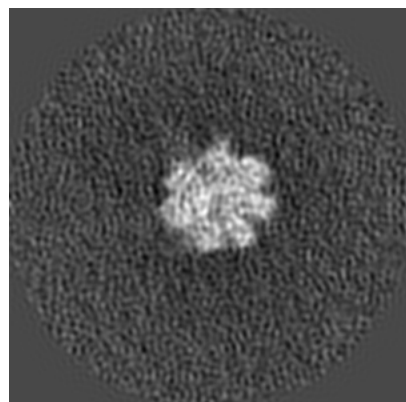


Z

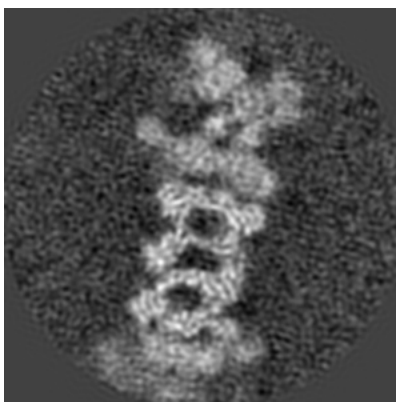
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 280



Y Index: 280

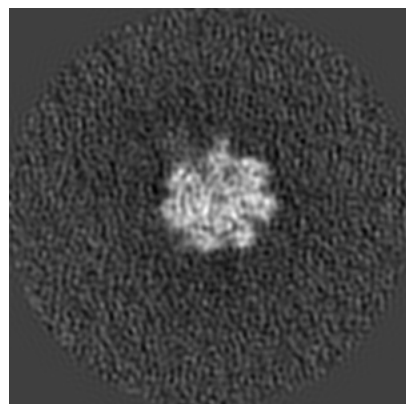


Z Index: 280

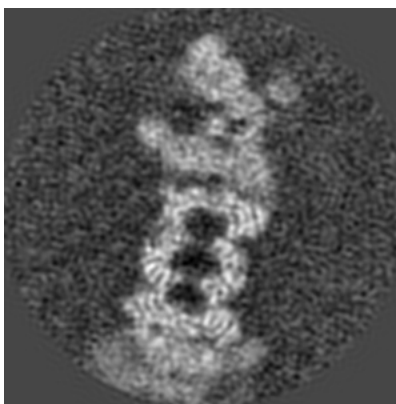
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

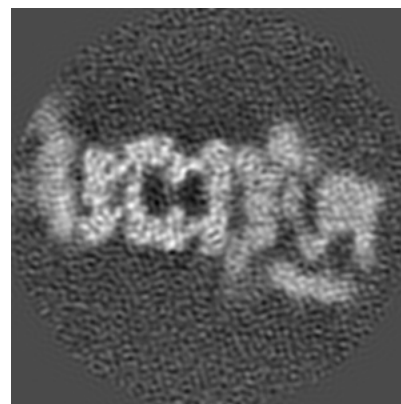
6.3.1 Primary map



X Index: 283



Y Index: 290

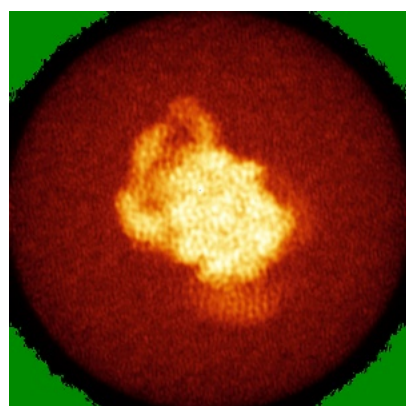


Z Index: 283

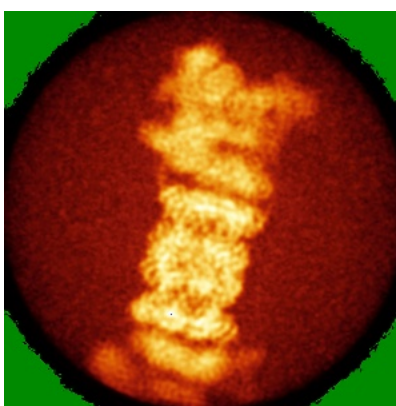
The images above show the largest variance slices of the map in three orthogonal directions.

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

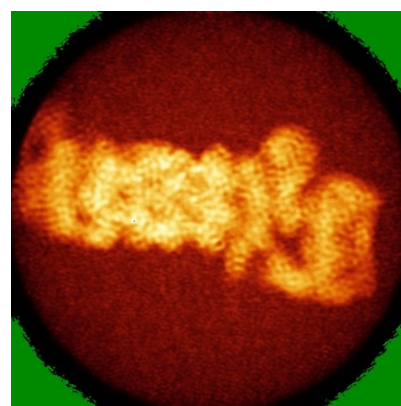
6.4.1 Primary map



X



Y

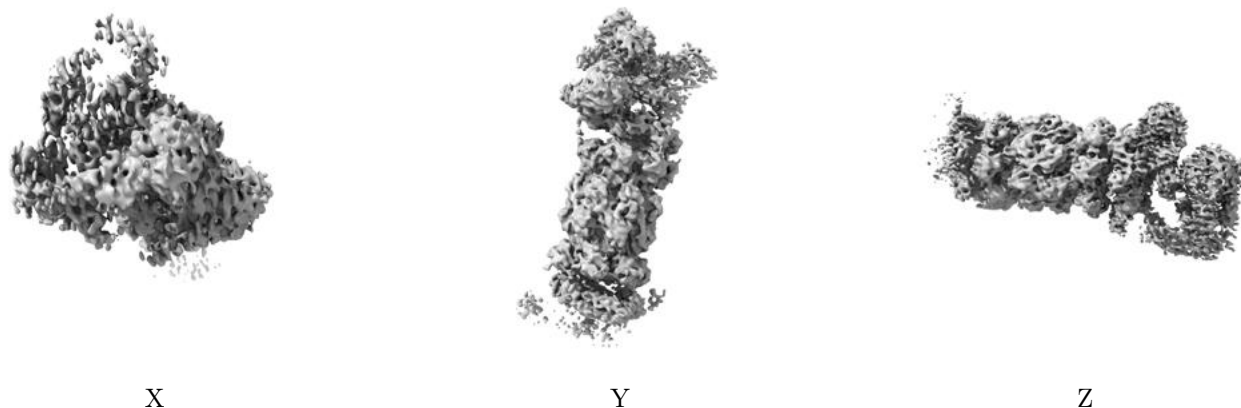


Z

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

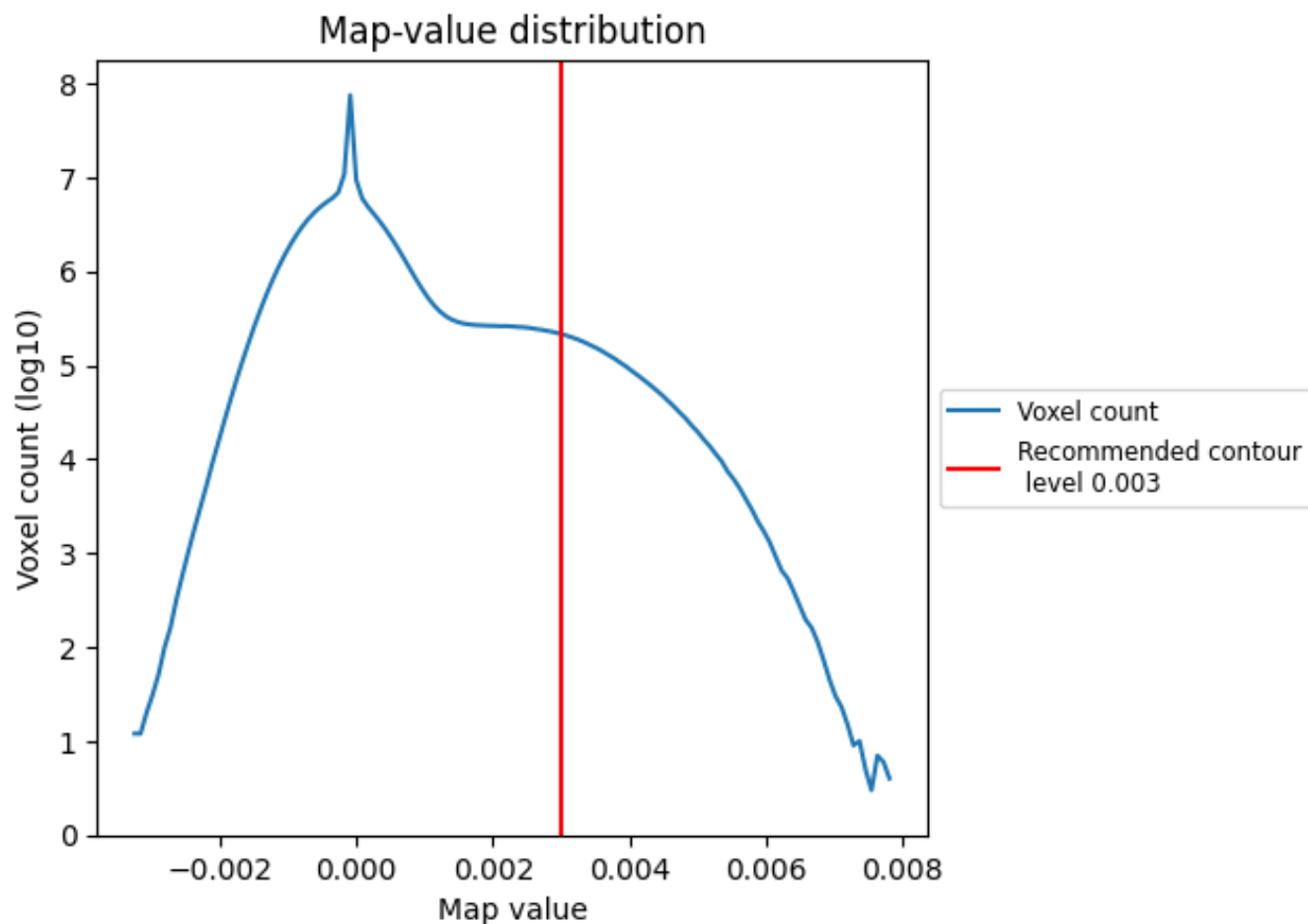
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

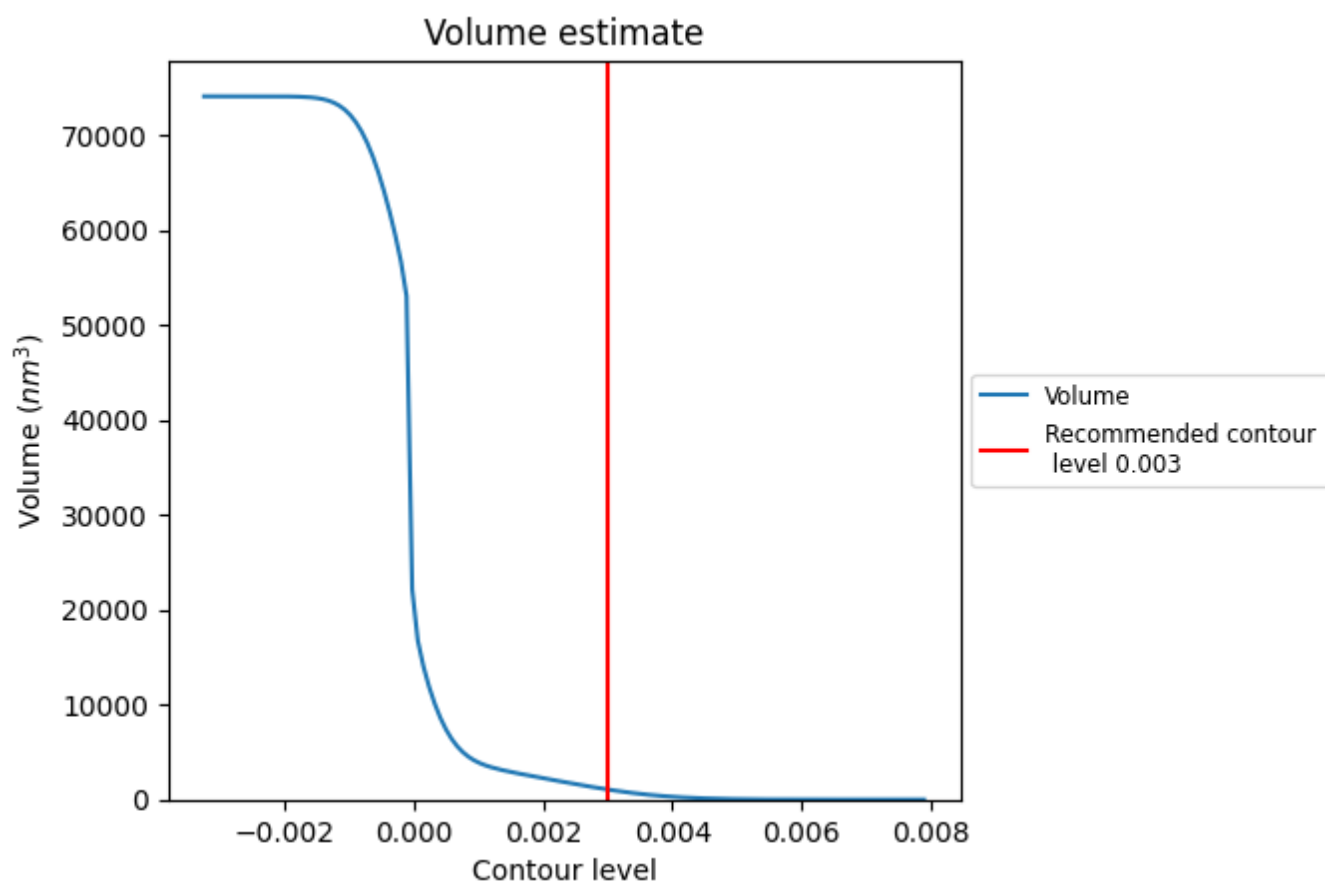
This section contains the results of statistical analysis of the map.

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 1064 nm³; this corresponds to an approximate mass of 961 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.

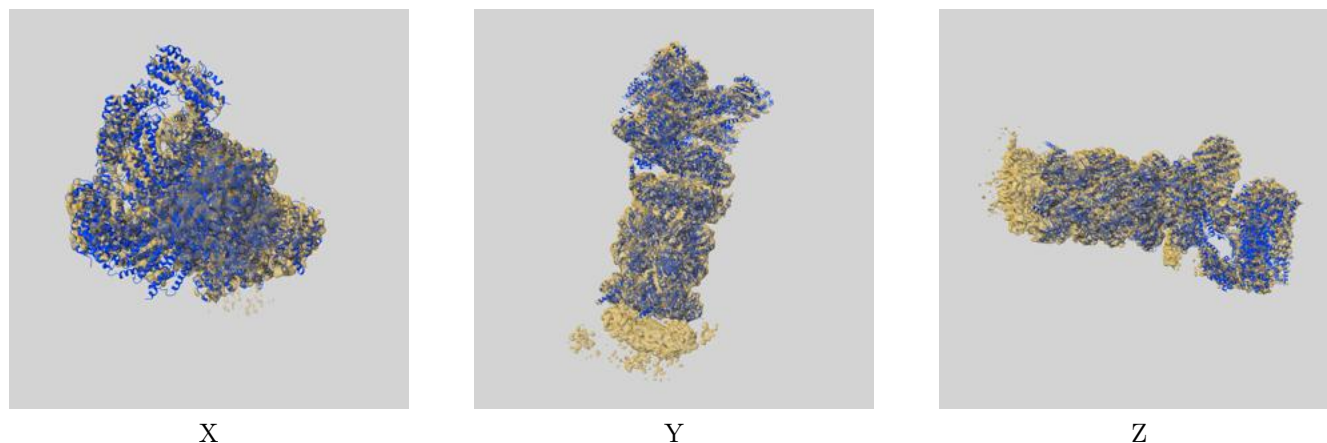
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

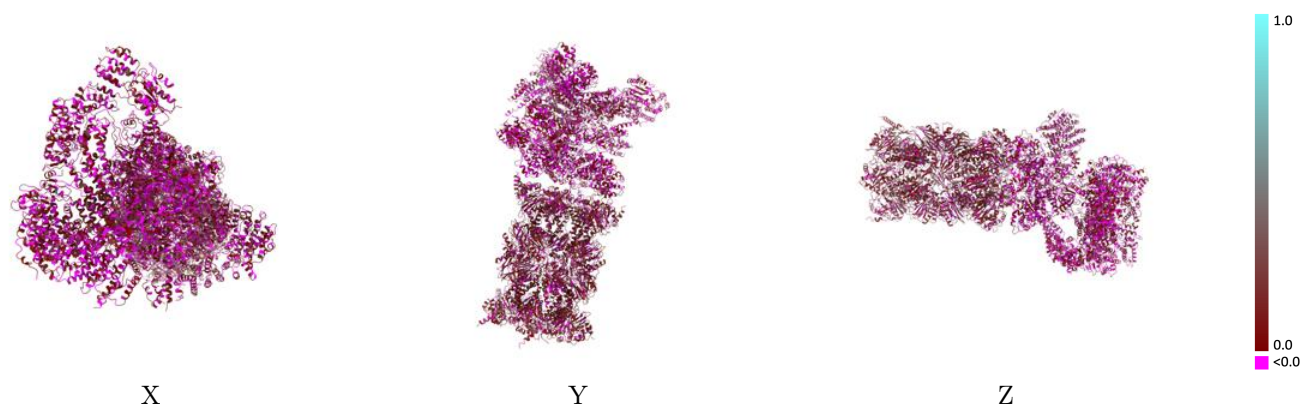
This section contains information regarding the fit between EMDB map EMD-8667 and PDB model 5VFT. Per-residue inclusion information can be found in section 3 on page 11.

9.1 Map-model overlay [i](#)



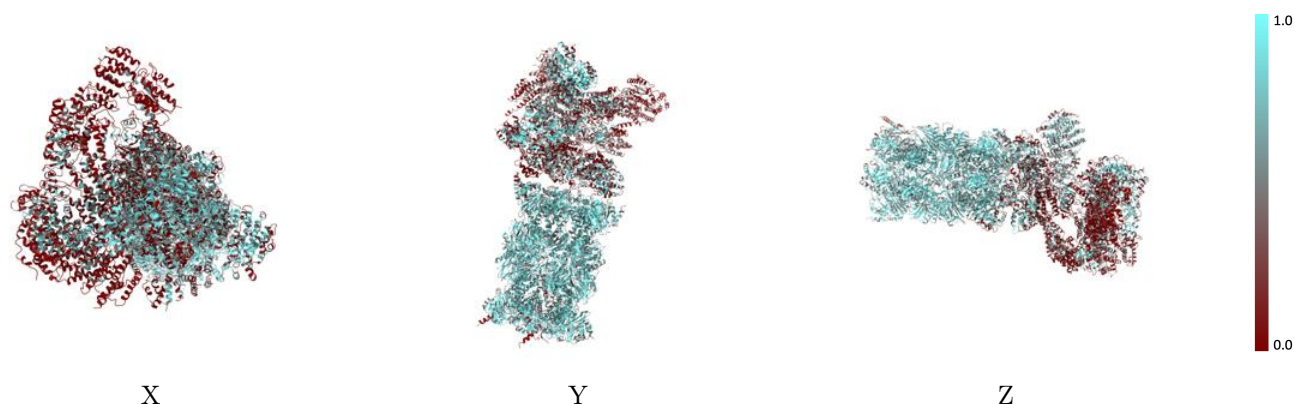
The images above show the 3D surface view of the map at the recommended contour level 0.003 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



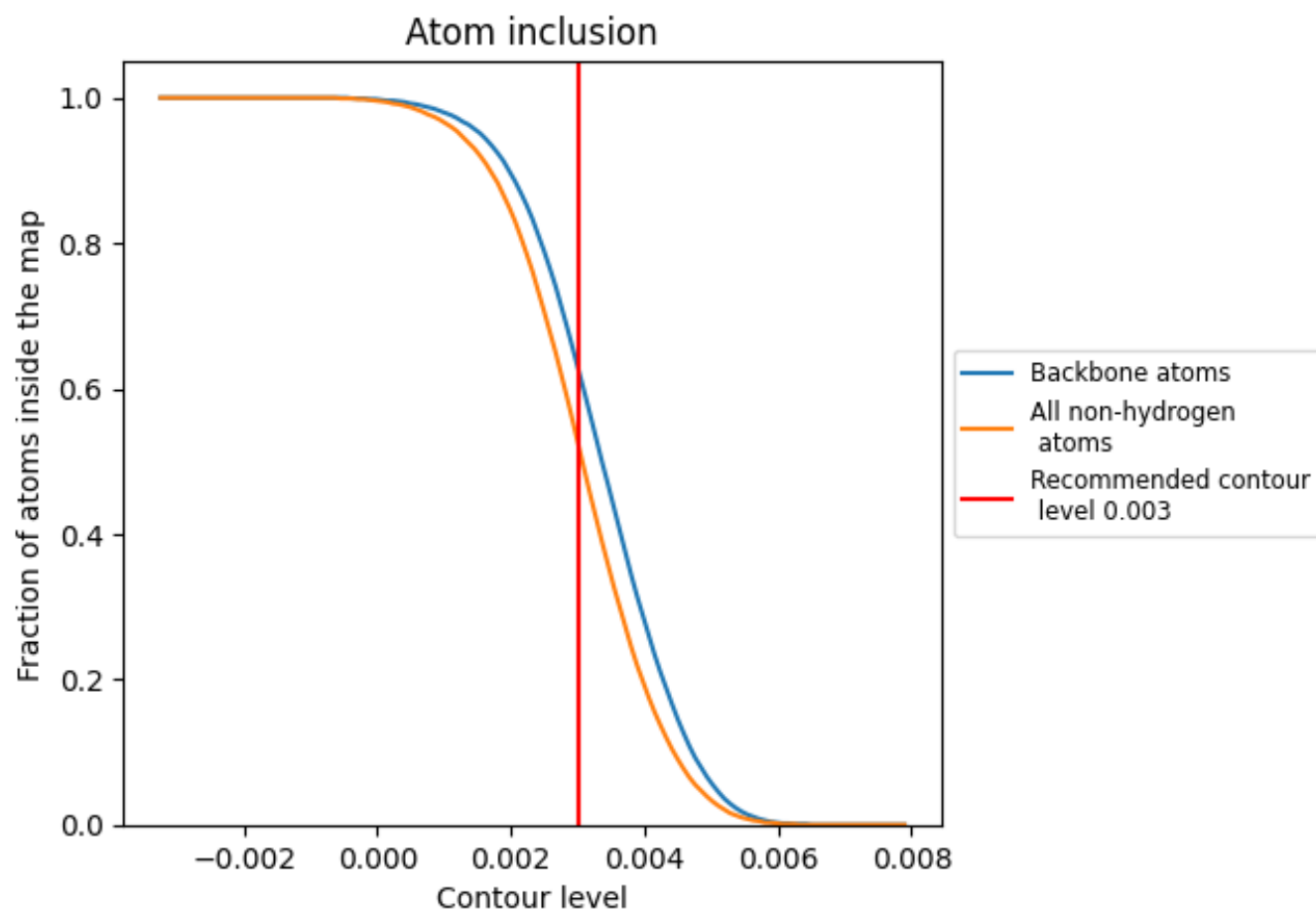
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.003).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 63% of all backbone atoms, 53% 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 (0.003) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5270	 0.0860
A	 0.4110	 0.0520
B	 0.3570	 0.0310
C	 0.3820	 0.0460
D	 0.3210	 0.0300
E	 0.3460	 0.0490
F	 0.3880	 0.0470
G	 0.6550	 0.1240
H	 0.6350	 0.1190
I	 0.6130	 0.1090
J	 0.6850	 0.1340
K	 0.6840	 0.1080
L	 0.7250	 0.1150
M	 0.7020	 0.1220
N	 0.7350	 0.1150
O	 0.7110	 0.1090
P	 0.7430	 0.1080
Q	 0.7380	 0.1360
R	 0.7750	 0.1420
S	 0.7410	 0.1350
T	 0.7500	 0.1290
U	 0.5030	 0.0500
V	 0.2900	 0.0350
W	 0.2100	 0.0430
X	 0.2220	 0.0750
Y	 0.3370	 0.0310
Z	 0.2680	 0.0460
a	 0.1390	 0.0500
b	 0.1350	 0.0560
c	 0.3500	 0.0820
d	 0.2240	 0.0360
e	 0.2470	 0.0240
f	 0.5170	 0.0680
g	 0.7340	 0.1350
h	 0.6780	 0.1260



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Chain	Atom inclusion	Q-score
i	 0.6040	 0.1370
j	 0.7050	 0.1300
k	 0.7070	 0.1280
l	 0.7220	 0.1160
m	 0.6900	 0.1180
n	 0.7560	 0.1400
o	 0.7210	 0.1440
p	 0.7310	 0.1080
q	 0.7700	 0.1410
r	 0.7680	 0.1310
s	 0.7430	 0.1220
t	 0.7770	 0.1290