



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 08:43 AM UTC

PDB ID : 5VFO / pdb_00005vfo
EMDB ID : EMD-8662
Title : Nucleotide-driven Triple-state Remodeling of the AAA-ATPase Channel in the Activated Human 26S Proteasome
Authors : Zhu, Y.; Wang, W.L.; Yu, D.; Ouyang, Q.; Lu, Y.; Mao, Y.
Deposited on : 2017-04-08
Resolution : 3.50 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

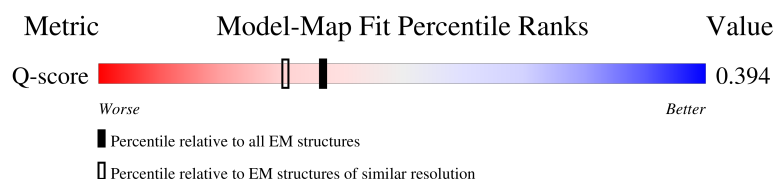
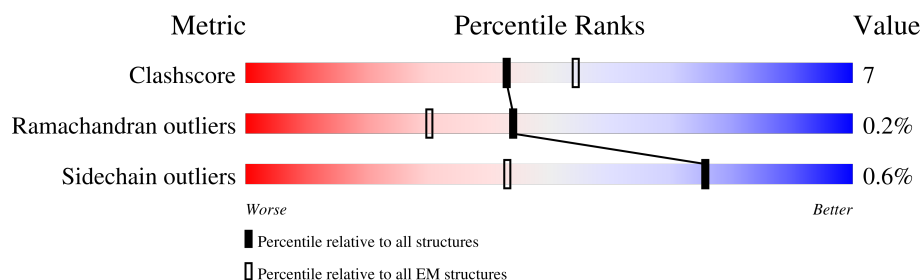
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.50 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	13950 (3.00 - 4.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	G	240	
1	g	240	
2	H	232	
2	h	232	

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Mol	Chain	Length	Quality of chain
3	I	250	41% 76% 22%
3	i	250	56% 76% 22%
4	J	243	45% 80% 18%
4	j	243	60% 82% 16%
5	K	234	41% 76% 20%
5	k	234	47% 79% 18%
6	L	238	28% 79% 20%
6	l	238	45% 86% 14%
7	M	245	39% 72% 26%
7	m	245	47% 80% 18%
8	N	191	24% 86% 13%
8	n	191	28% 87% 13%
9	O	220	29% 81% 18%
9	o	220	37% 81% 18%
10	P	204	19% 87% 13%
10	p	204	29% 83% 17%
11	Q	199	32% 79% 21%
11	q	199	31% 84% 15%
12	R	201	20% 80% 20%
12	r	201	25% 84% 16%
13	S	213	30% 85% 15%
13	s	213	26% 85% 15%
14	T	215	24% 89% 11%
14	t	215	24% 88% 12%

2 Entry composition [i](#)

There are 14 unique types of molecules in this entry. The entry contains 47288 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

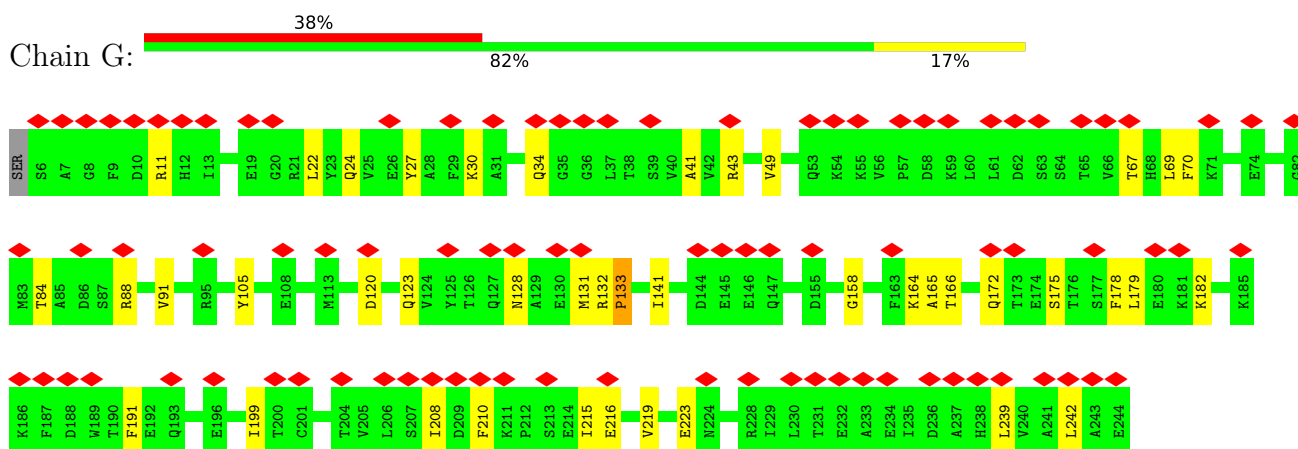
- Molecule 14 is a protein called Proteasome subunit beta type-4.

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

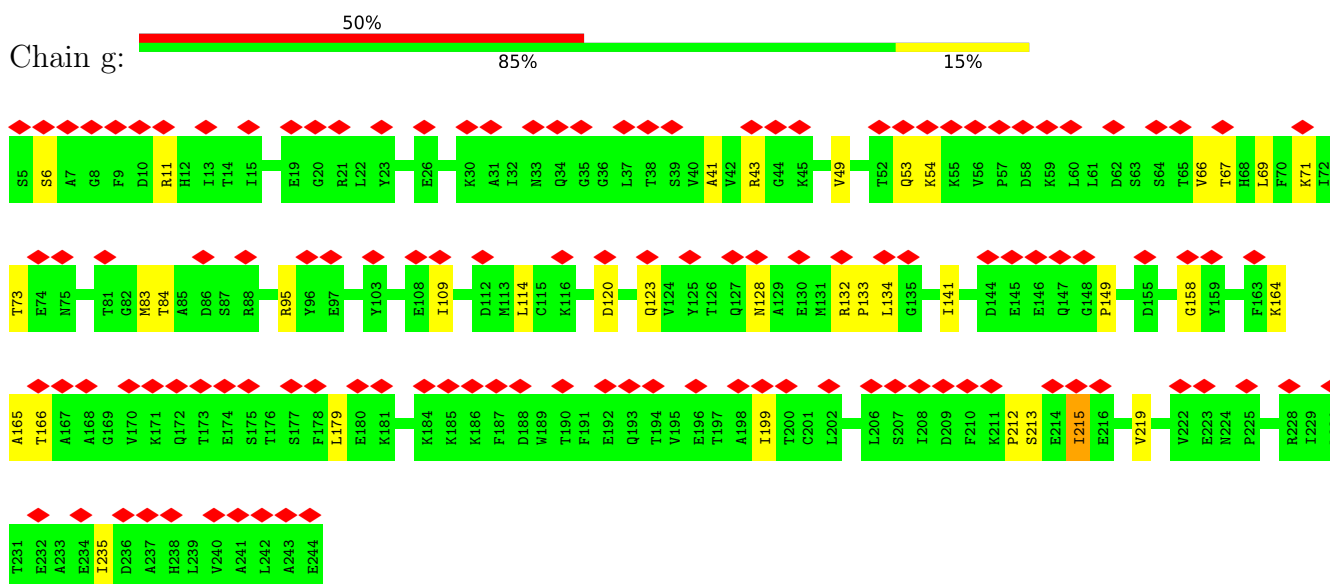
3 Residue-property plots

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.

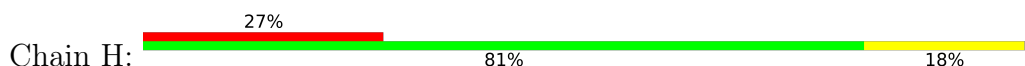
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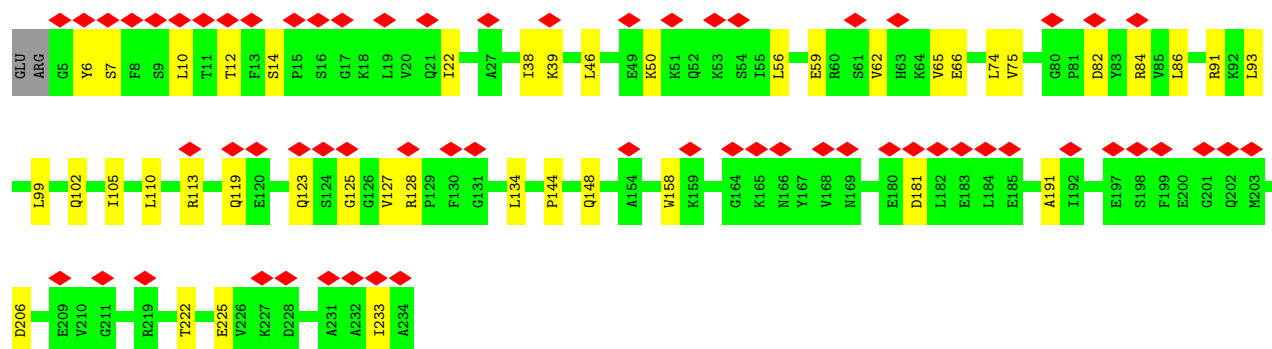


- Molecule 1: Proteasome subunit alpha type-6

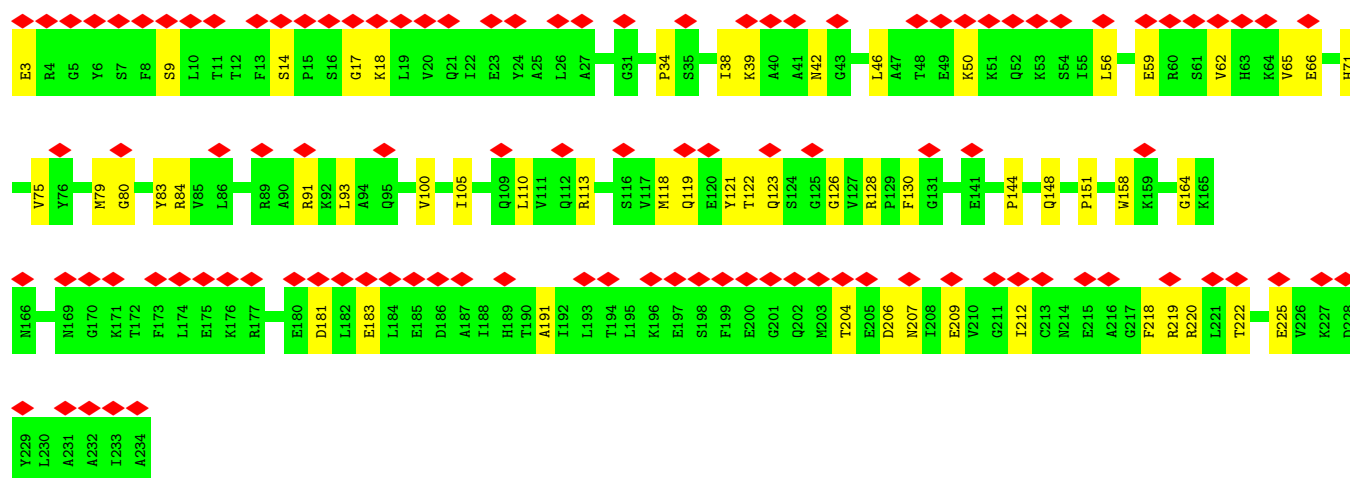
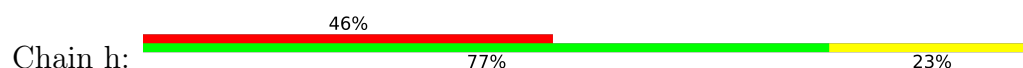


- Molecule 2: Proteasome subunit alpha type-2

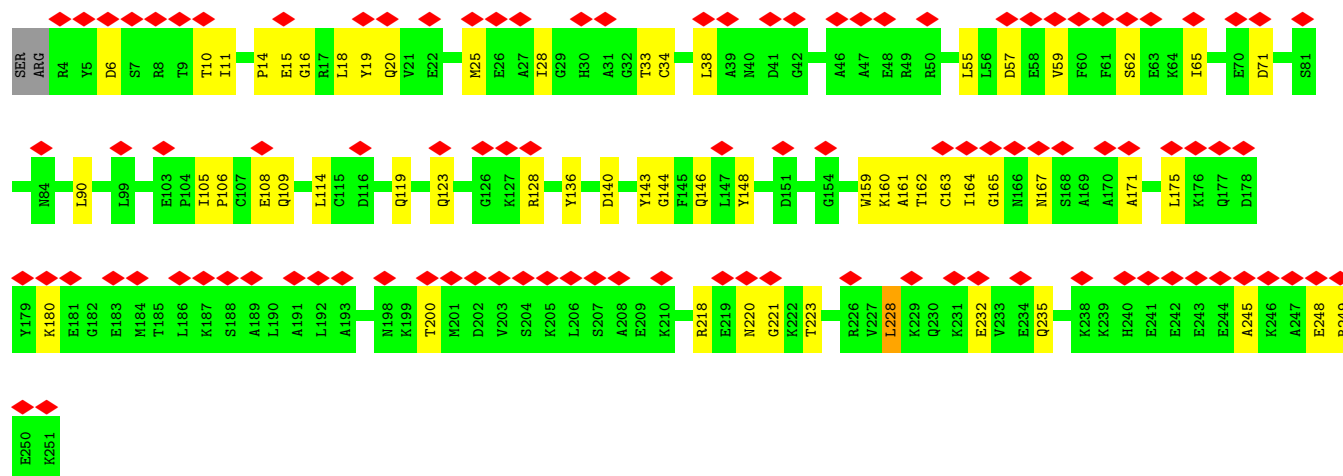
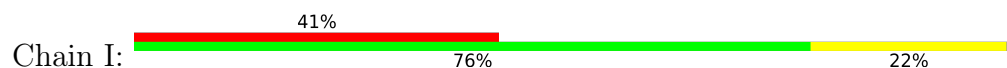




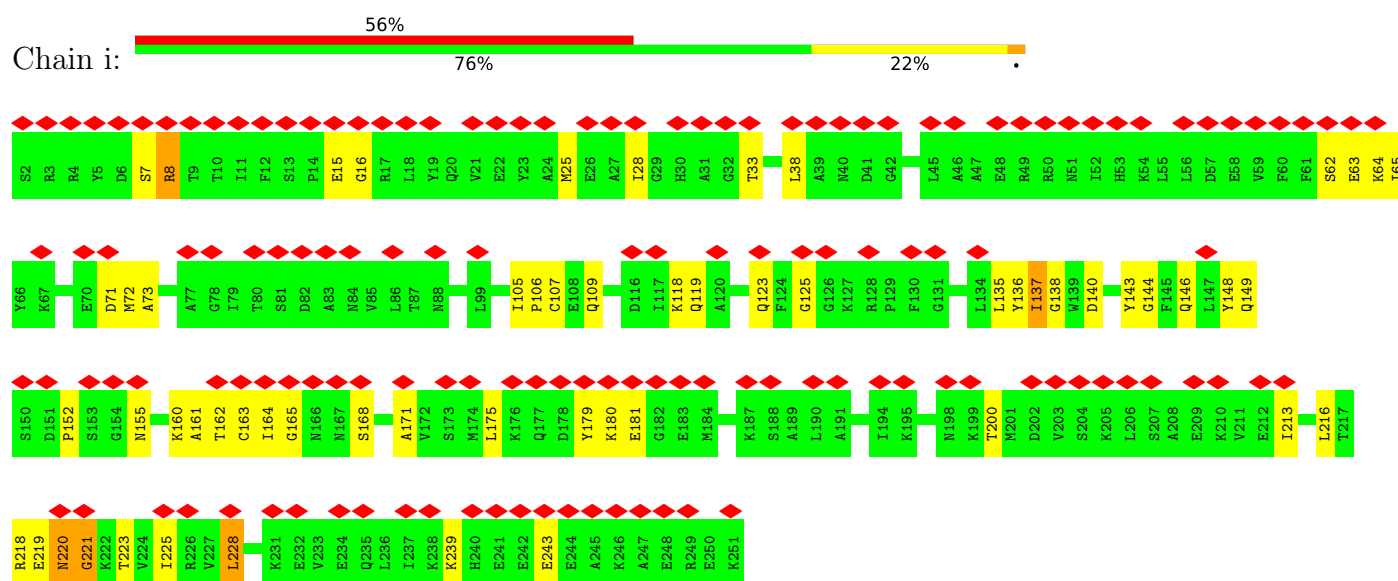
• Molecule 2: Proteasome subunit alpha type-2



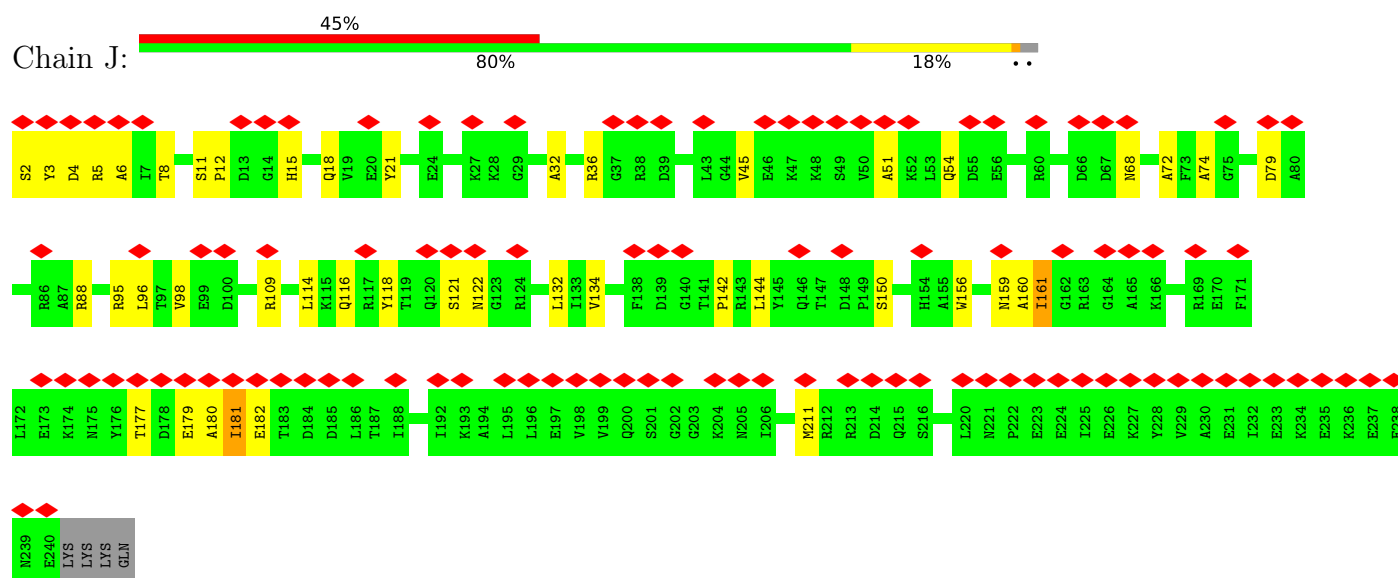
• Molecule 3: Proteasome subunit alpha type-4



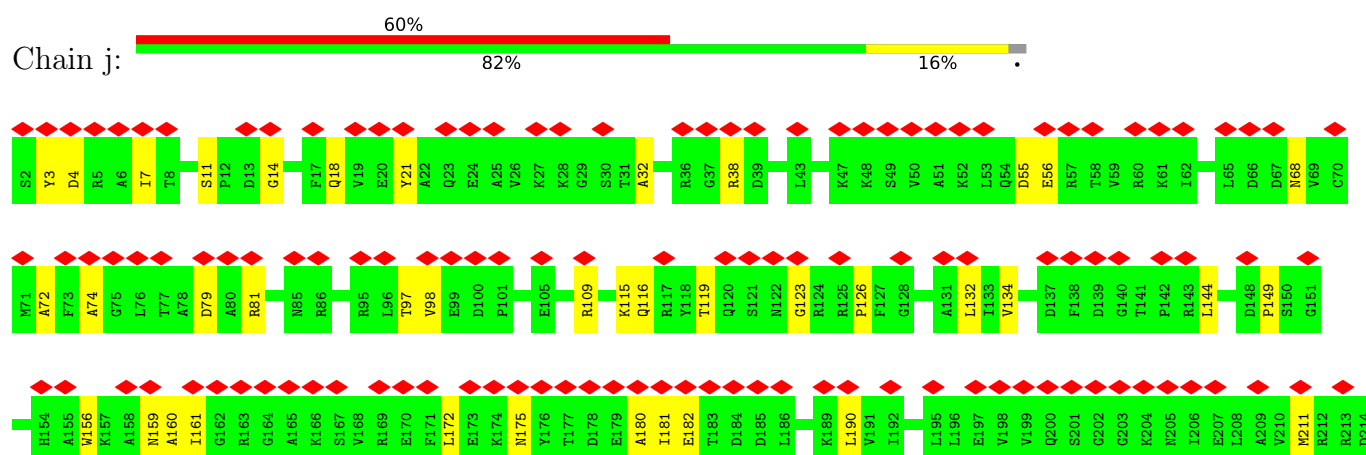
• Molecule 3: Proteasome subunit alpha type-4

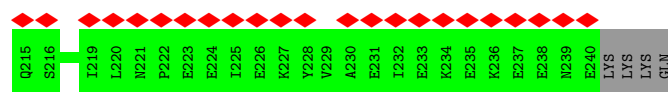


• Molecule 4: Proteasome subunit alpha type-7

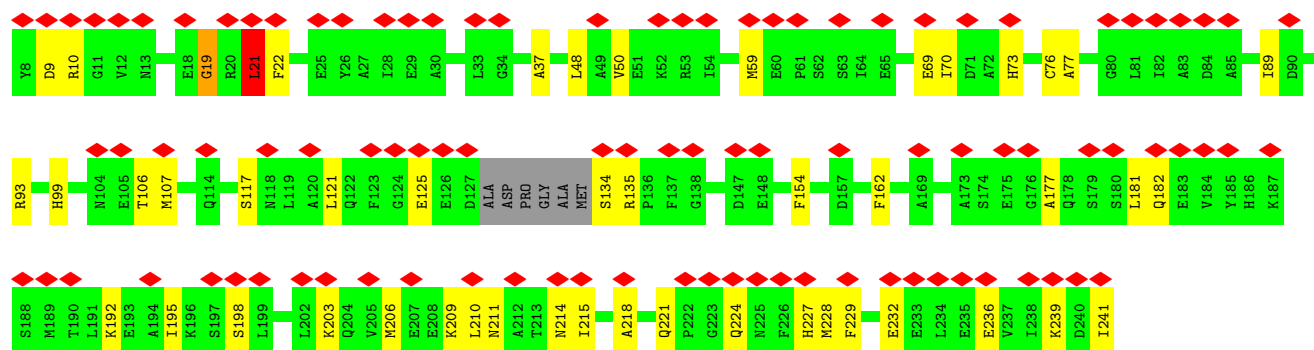
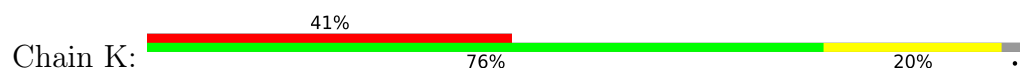


• Molecule 4: Proteasome subunit alpha type-7

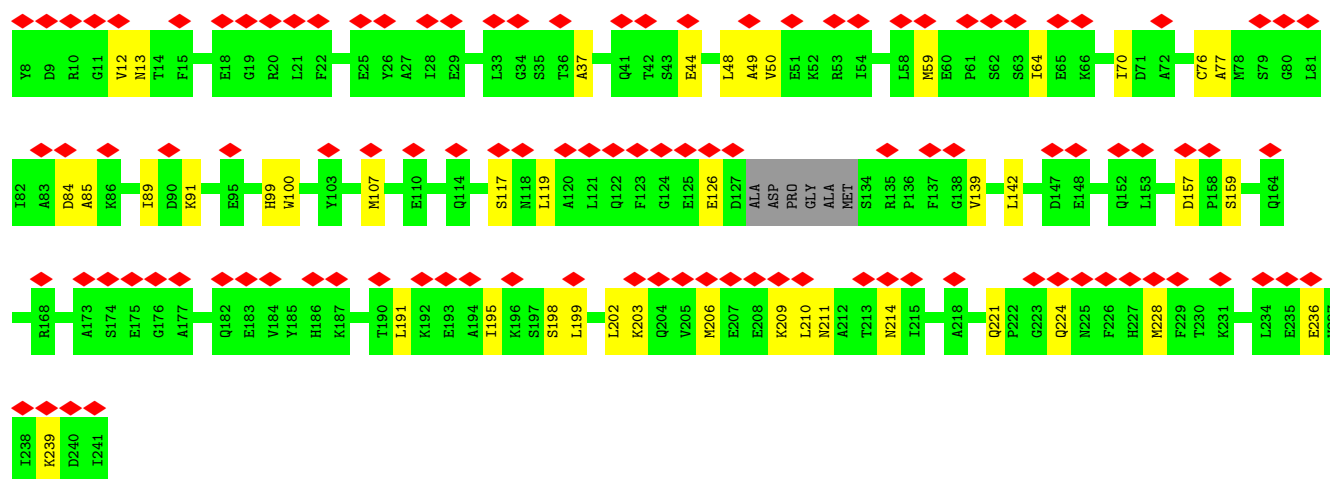
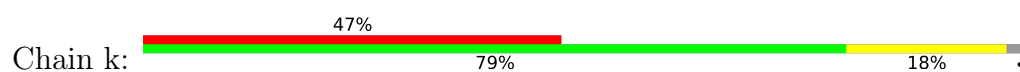




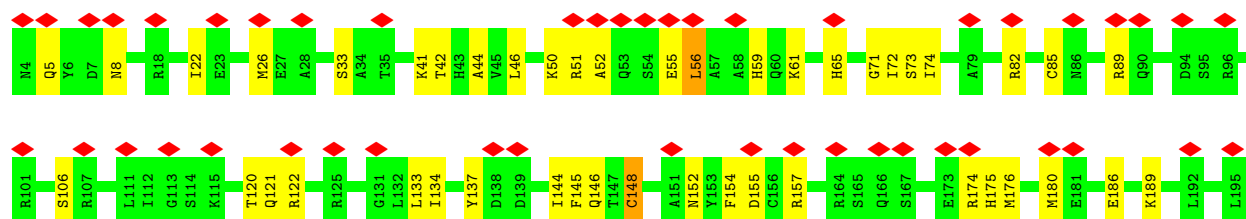
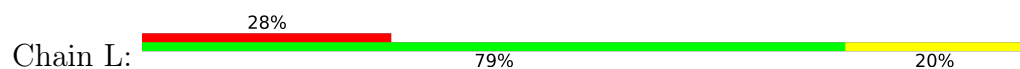
• Molecule 5: Proteasome subunit alpha type-5



• Molecule 5: Proteasome subunit alpha type-5

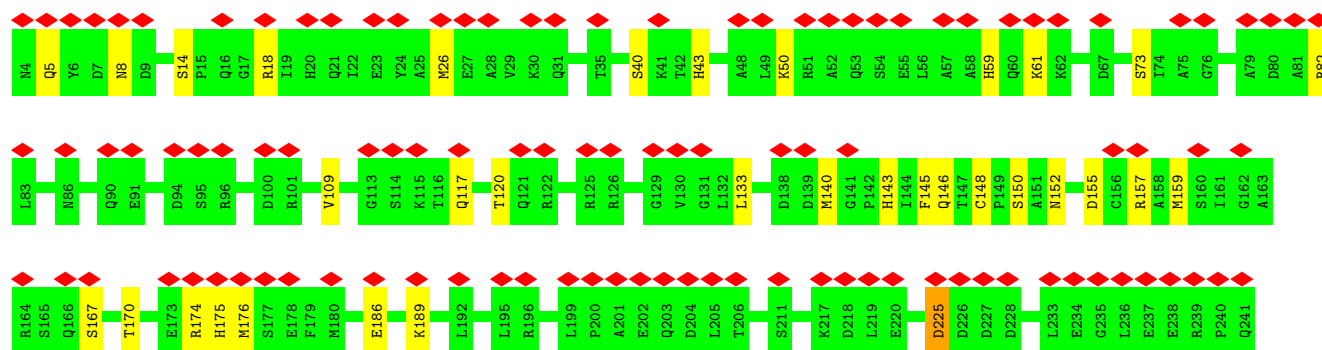
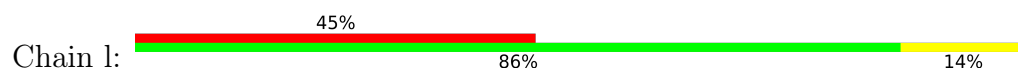


• Molecule 6: Proteasome subunit alpha type-1

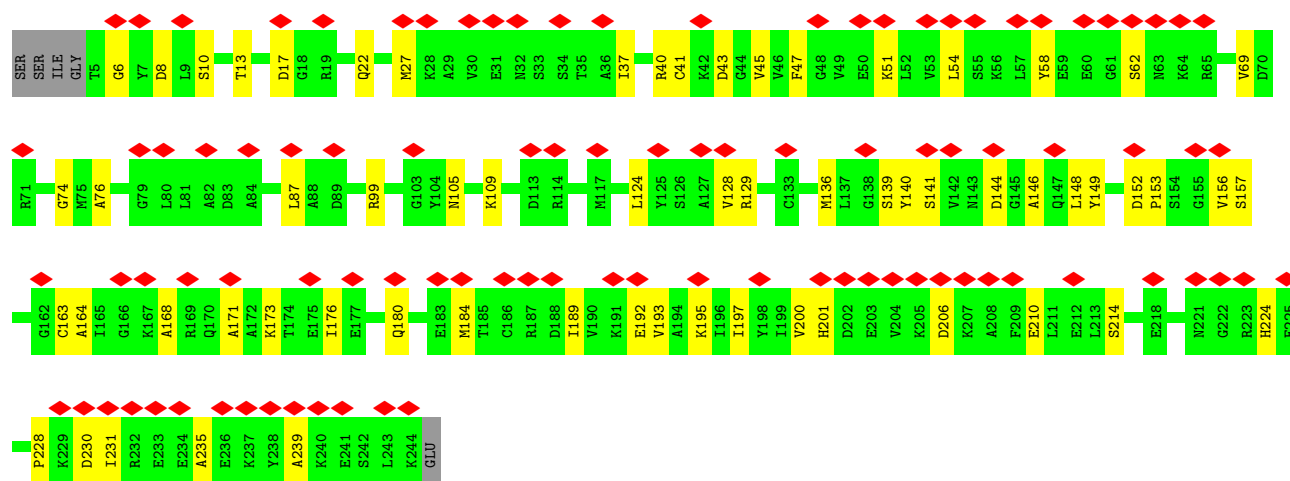
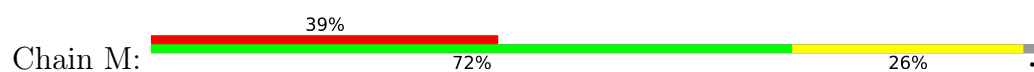




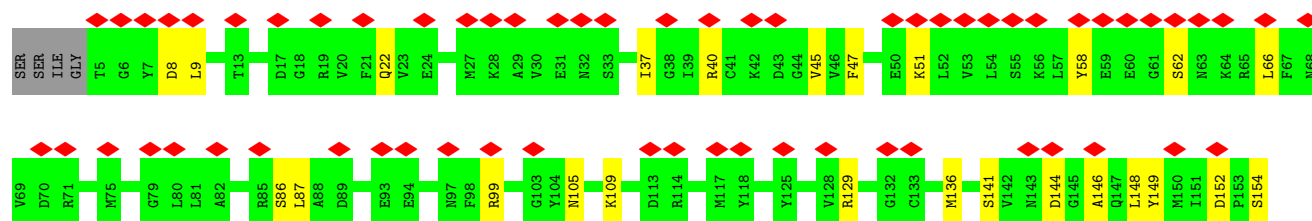
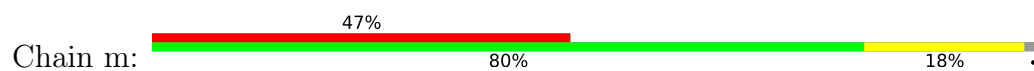
• Molecule 6: Proteasome subunit alpha type-1

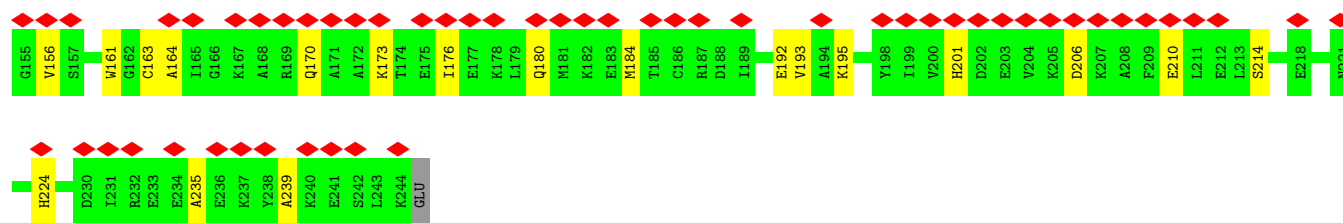


• Molecule 7: Proteasome subunit alpha type-3

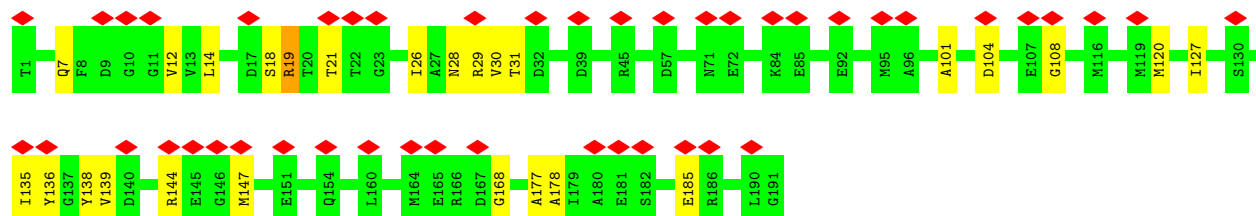
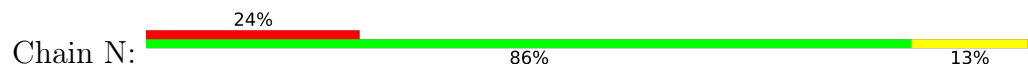


• Molecule 7: Proteasome subunit alpha type-3

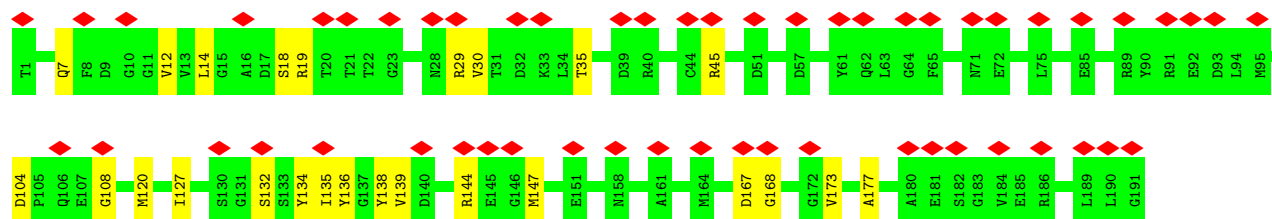
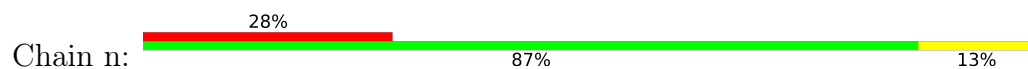




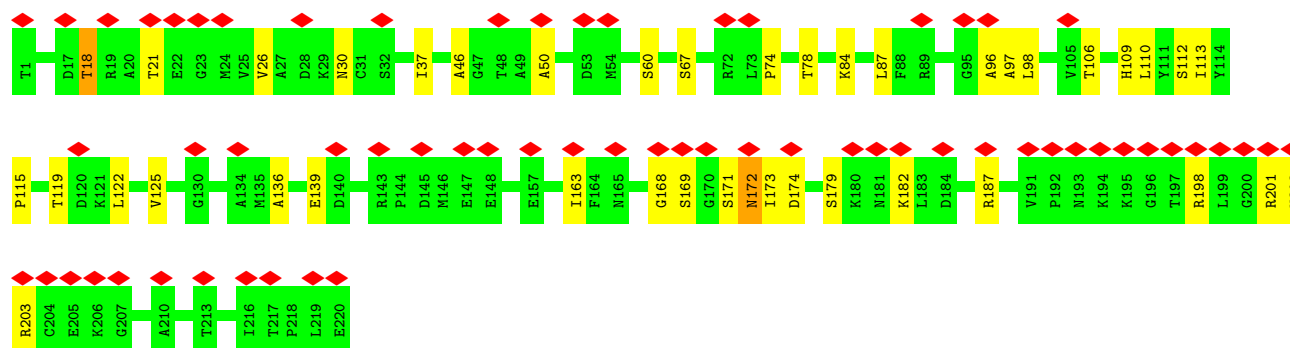
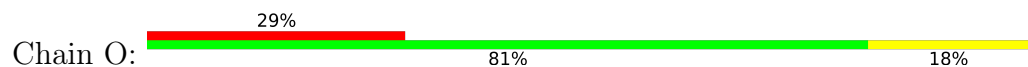
- Molecule 8: Proteasome subunit beta type-6



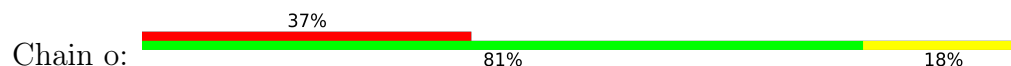
- Molecule 8: Proteasome subunit beta type-6

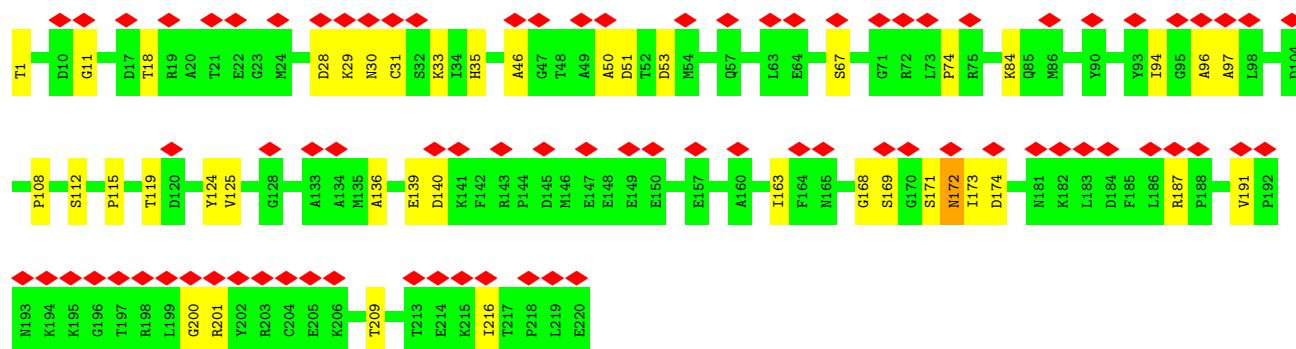


- Molecule 9: Proteasome subunit beta type-7

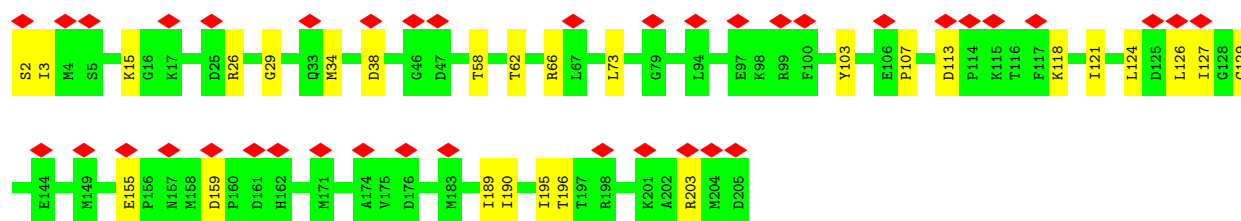
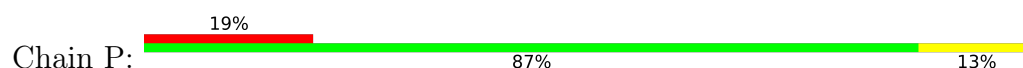


- Molecule 9: Proteasome subunit beta type-7

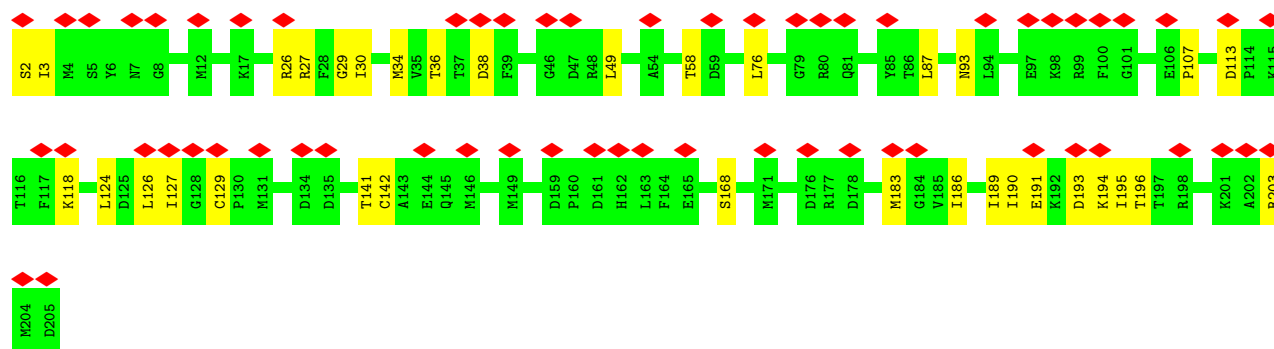
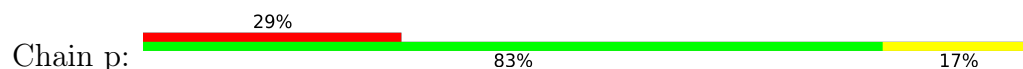




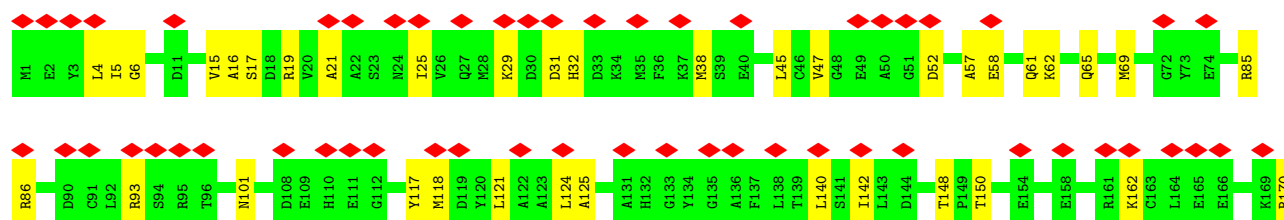
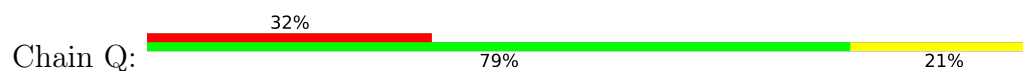
• Molecule 10: Proteasome subunit beta type-3

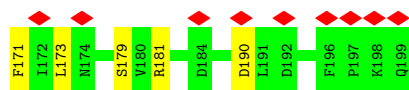


• Molecule 10: Proteasome subunit beta type-3

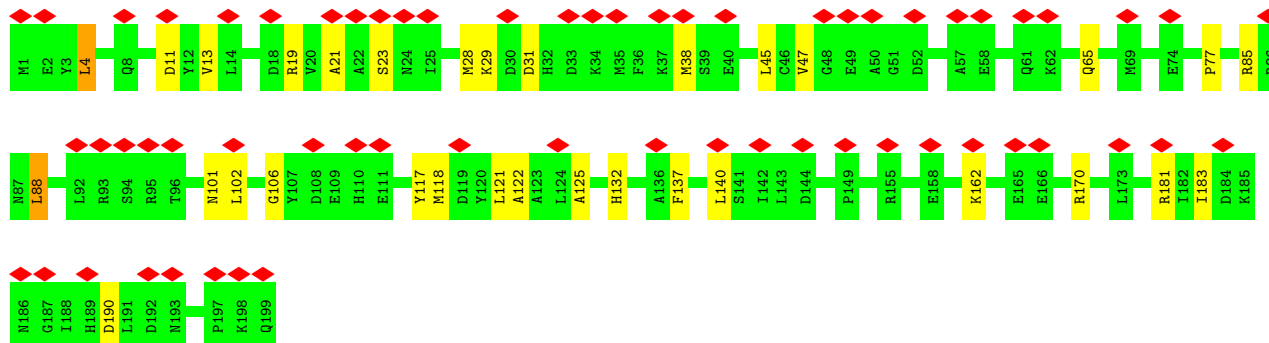
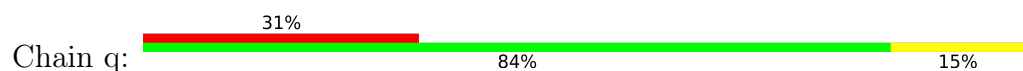


• Molecule 11: Proteasome subunit beta type-2

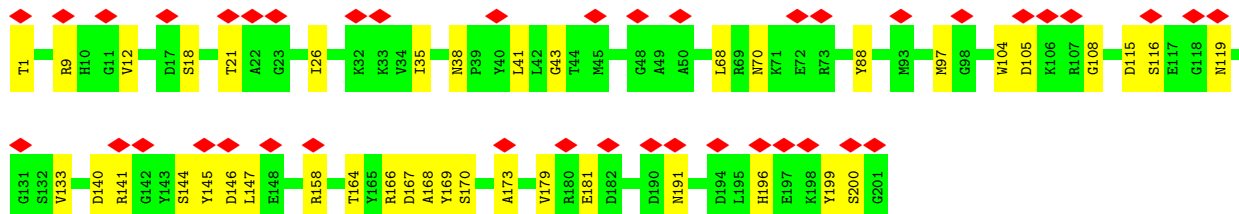
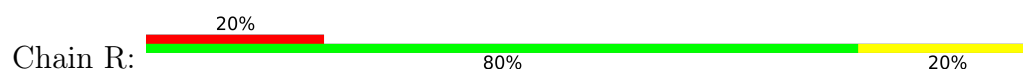




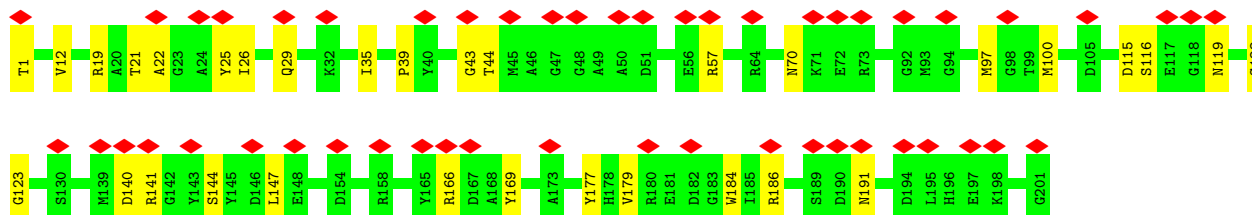
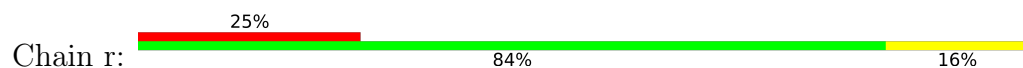
• Molecule 11: Proteasome subunit beta type-2



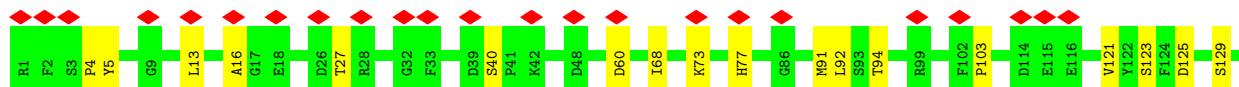
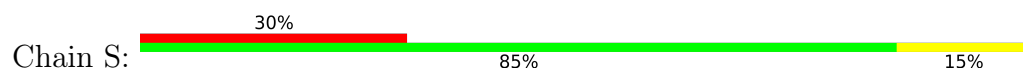
• Molecule 12: Proteasome subunit beta type-5

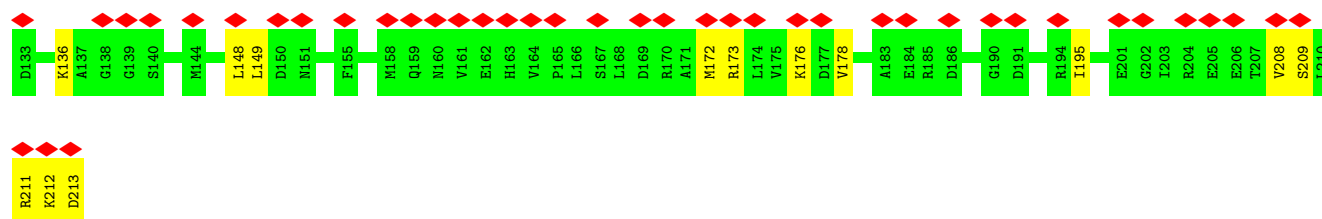


• Molecule 12: Proteasome subunit beta type-5

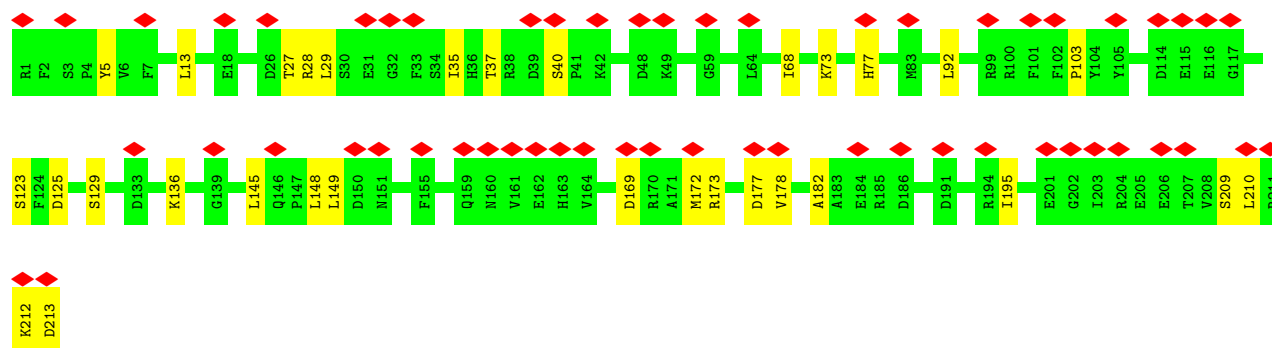
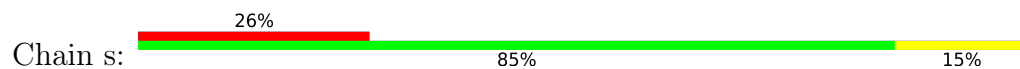


• Molecule 13: Proteasome subunit beta type-1

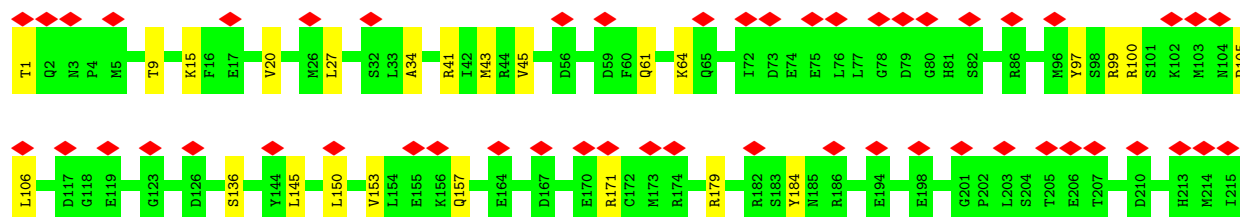
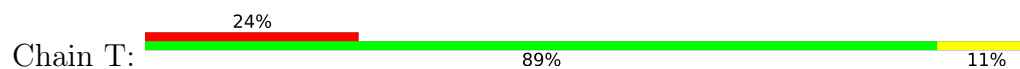




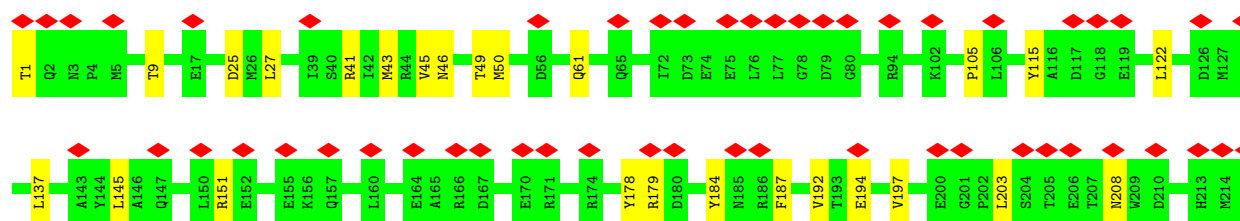
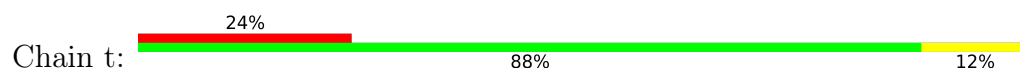
• Molecule 13: Proteasome subunit beta type-1



• Molecule 14: Proteasome subunit beta type-4



• Molecule 14: Proteasome subunit beta type-4



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	228086	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TECNAI ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.027	Depositor
Minimum map value	-0.013	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	420.0, 420.0, 420.0	wwPDB
Map dimensions	560, 560, 560	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.75, 0.75, 0.75	Depositor

5 Model quality

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	G	0.40	0/1853	0.72	2/2515 (0.1%)
1	g	0.38	0/1859	0.65	1/2523 (0.0%)
2	H	0.40	0/1723	0.68	3/2346 (0.1%)
2	h	0.37	0/1743	0.61	2/2372 (0.1%)
3	I	0.42	0/1925	0.79	4/2606 (0.2%)
3	i	0.38	0/1942	0.70	2/2628 (0.1%)
4	J	0.40	0/1728	0.74	4/2358 (0.2%)
4	j	0.35	0/1728	0.59	0/2358
5	K	0.40	0/1755	0.79	4/2375 (0.2%)
5	k	0.36	0/1747	0.59	0/2364
6	L	0.43	0/1885	0.66	3/2552 (0.1%)
6	l	0.39	0/1885	0.63	2/2552 (0.1%)
7	M	0.41	0/1891	0.73	2/2552 (0.1%)
7	m	0.38	0/1891	0.64	0/2552
8	N	0.41	0/1454	0.63	0/1967
8	n	0.39	0/1454	0.60	0/1967
9	O	0.40	0/1670	0.61	2/2265 (0.1%)
9	o	0.38	0/1670	0.64	2/2265 (0.1%)
10	P	0.41	0/1614	0.54	0/2177
10	p	0.39	0/1614	0.56	2/2177 (0.1%)
11	Q	0.44	0/1603	0.65	0/2174
11	q	0.44	0/1603	0.67	0/2174
12	R	0.41	0/1579	0.55	0/2134
12	r	0.40	0/1579	0.54	0/2134
13	S	0.39	0/1671	0.56	0/2253
13	s	0.39	0/1671	0.56	0/2253
14	T	0.40	0/1700	0.58	0/2305
14	t	0.40	0/1700	0.59	0/2305
All	All	0.40	0/48137	0.64	35/65203 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
3	I	0	3
3	i	0	2
4	j	0	1
5	K	0	4
9	O	0	2
9	o	0	1
All	All	0	13

There are no bond length outliers.

The worst 5 of 35 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	K	21	LEU	CA-C-N	9.74	139.23	121.70
5	K	21	LEU	C-N-CA	9.74	139.23	121.70
1	G	223	GLU	N-CA-C	-9.38	103.93	114.62
7	M	6	GLY	CA-C-N	9.01	137.91	121.70
7	M	6	GLY	C-N-CA	9.01	137.91	121.70

There are no chirality outliers.

5 of 13 planarity outliers are listed below:

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

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	G	1820	0	1791	26	0
1	g	1826	0	1796	21	0
2	H	1688	0	1575	26	0
2	h	1708	0	1594	32	0
3	I	1895	0	1833	35	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	i	1912	0	1851	35	0
4	J	1704	0	1517	29	0
4	j	1704	0	1517	27	0
5	K	1729	0	1680	28	0
5	k	1722	0	1673	27	0
6	L	1850	0	1822	32	0
6	l	1850	0	1822	22	0
7	M	1856	0	1814	41	0
7	m	1856	0	1814	31	0
8	N	1430	0	1398	18	0
8	n	1430	0	1398	15	0
9	O	1643	0	1644	26	0
9	o	1643	0	1644	25	0
10	P	1585	0	1598	18	0
10	p	1585	0	1598	22	0
11	Q	1570	0	1547	30	0
11	q	1570	0	1547	20	0
12	R	1548	0	1499	28	0
12	r	1548	0	1499	22	0
13	S	1641	0	1618	17	0
13	s	1641	0	1618	17	0
14	T	1667	0	1628	15	0
14	t	1667	0	1628	18	0
All	All	47288	0	45963	615	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 7.

The worst 5 of 615 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)
3:I:119:GLN:HE21	3:I:123:GLN:HE22	1.24	0.82
13:s:27:THR:HB	13:s:40:SER:H	1.53	0.73
13:S:27:THR:HB	13:S:40:SER:H	1.56	0.70
3:I:38:LEU:HG	3:I:160:LYS:HB3	1.75	0.68
5:k:91:LYS:HE2	5:k:119:LEU:HD11	1.75	0.67

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	G	237/240 (99%)	211 (89%)	26 (11%)	0	100	100
1	g	238/240 (99%)	217 (91%)	21 (9%)	0	100	100
2	H	228/232 (98%)	211 (92%)	16 (7%)	1 (0%)	30	62
2	h	230/232 (99%)	224 (97%)	6 (3%)	0	100	100
3	I	246/250 (98%)	220 (89%)	26 (11%)	0	100	100
3	i	248/250 (99%)	222 (90%)	25 (10%)	1 (0%)	30	62
4	J	237/243 (98%)	221 (93%)	15 (6%)	1 (0%)	30	62
4	j	237/243 (98%)	223 (94%)	11 (5%)	3 (1%)	9	39
5	K	224/234 (96%)	205 (92%)	18 (8%)	1 (0%)	30	62
5	k	224/234 (96%)	205 (92%)	19 (8%)	0	100	100
6	L	236/238 (99%)	225 (95%)	11 (5%)	0	100	100
6	l	236/238 (99%)	225 (95%)	11 (5%)	0	100	100
7	M	238/245 (97%)	218 (92%)	19 (8%)	1 (0%)	30	62
7	m	238/245 (97%)	222 (93%)	16 (7%)	0	100	100
8	N	189/191 (99%)	180 (95%)	8 (4%)	1 (0%)	24	57
8	n	189/191 (99%)	180 (95%)	9 (5%)	0	100	100
9	O	218/220 (99%)	204 (94%)	13 (6%)	1 (0%)	24	57
9	o	218/220 (99%)	205 (94%)	12 (6%)	1 (0%)	24	57
10	P	202/204 (99%)	188 (93%)	14 (7%)	0	100	100
10	p	202/204 (99%)	193 (96%)	9 (4%)	0	100	100
11	Q	197/199 (99%)	181 (92%)	16 (8%)	0	100	100
11	q	197/199 (99%)	181 (92%)	16 (8%)	0	100	100
12	R	199/201 (99%)	190 (96%)	9 (4%)	0	100	100
12	r	199/201 (99%)	188 (94%)	11 (6%)	0	100	100
13	S	211/213 (99%)	203 (96%)	8 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
13	s	211/213 (99%)	205 (97%)	6 (3%)	0	100	100
14	T	213/215 (99%)	200 (94%)	13 (6%)	0	100	100
14	t	213/215 (99%)	202 (95%)	11 (5%)	0	100	100
All	All	6155/6250 (98%)	5749 (93%)	395 (6%)	11 (0%)	44	74

5 of 11 Ramachandran outliers are listed below:

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

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	G	192/205 (94%)	188 (98%)	4 (2%)	47	66
1	g	193/205 (94%)	188 (97%)	5 (3%)	40	62
2	H	162/190 (85%)	162 (100%)	0	100	100
2	h	164/190 (86%)	164 (100%)	0	100	100
3	I	191/210 (91%)	189 (99%)	2 (1%)	68	75
3	i	193/210 (92%)	191 (99%)	2 (1%)	68	75
4	J	152/207 (73%)	151 (99%)	1 (1%)	76	78
4	j	152/207 (73%)	152 (100%)	0	100	100
5	K	187/196 (95%)	186 (100%)	1 (0%)	81	80
5	k	186/196 (95%)	185 (100%)	1 (0%)	81	80
6	L	198/204 (97%)	196 (99%)	2 (1%)	68	75
6	l	198/204 (97%)	198 (100%)	0	100	100
7	M	192/202 (95%)	190 (99%)	2 (1%)	68	75

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	m	192/202 (95%)	191 (100%)	1 (0%)	81	80
8	N	148/148 (100%)	147 (99%)	1 (1%)	76	78
8	n	148/148 (100%)	148 (100%)	0	100	100
9	O	177/181 (98%)	176 (99%)	1 (1%)	78	79
9	o	177/181 (98%)	177 (100%)	0	100	100
10	P	172/173 (99%)	172 (100%)	0	100	100
10	p	172/173 (99%)	172 (100%)	0	100	100
11	Q	164/170 (96%)	163 (99%)	1 (1%)	78	79
11	q	164/170 (96%)	162 (99%)	2 (1%)	63	73
12	R	153/156 (98%)	153 (100%)	0	100	100
12	r	153/156 (98%)	153 (100%)	0	100	100
13	S	174/178 (98%)	174 (100%)	0	100	100
13	s	174/178 (98%)	174 (100%)	0	100	100
14	T	175/178 (98%)	174 (99%)	1 (1%)	78	79
14	t	175/178 (98%)	175 (100%)	0	100	100
All	All	4878/5196 (94%)	4851 (99%)	27 (1%)	76	79

5 of 27 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
11	Q	25	ILE
1	g	73	THR
7	m	87	LEU
1	g	66	VAL
1	g	141	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 66 such sidechains are listed below:

Mol	Chain	Res	Type
11	q	132	HIS
13	s	146	GLN
14	t	213	HIS
8	N	158	ASN
8	N	28	ASN

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.

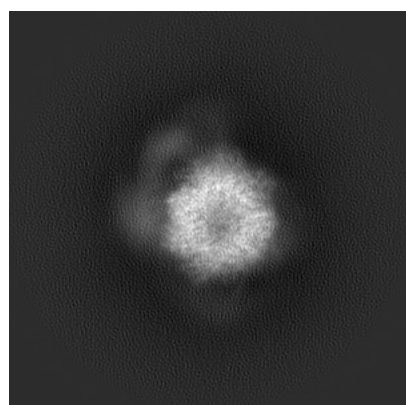
6 Map visualisation [i](#)

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

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

6.1 Orthogonal projections [i](#)

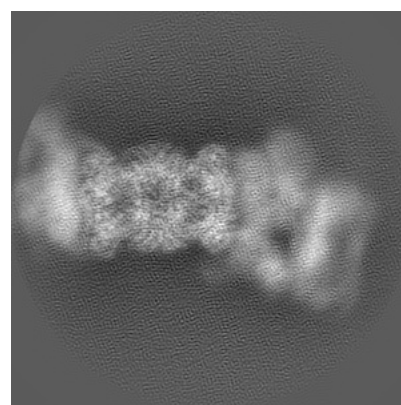
6.1.1 Primary map



X



Y

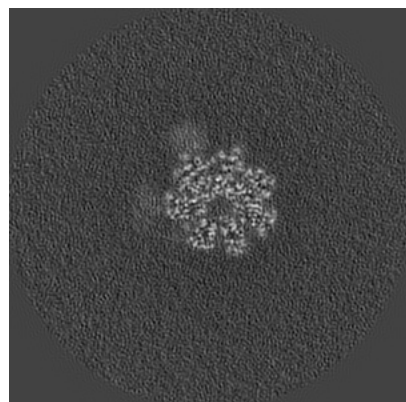


Z

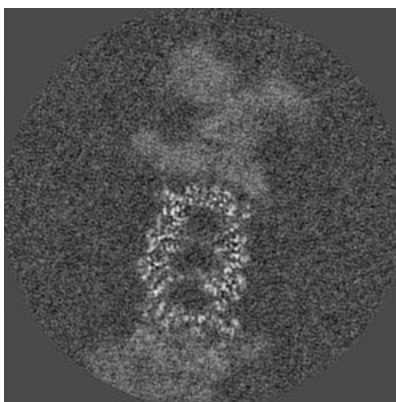
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

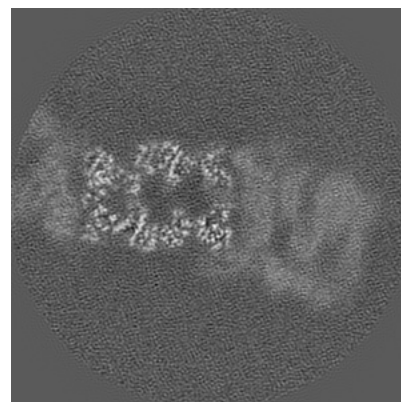
6.2.1 Primary map



X Index: 280



Y Index: 280

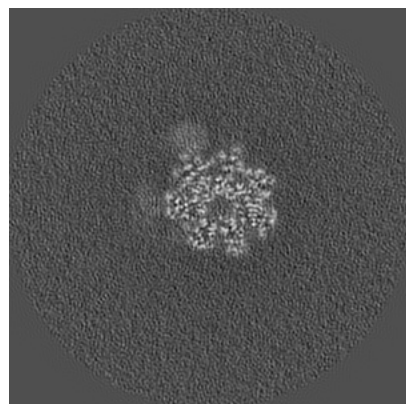


Z Index: 280

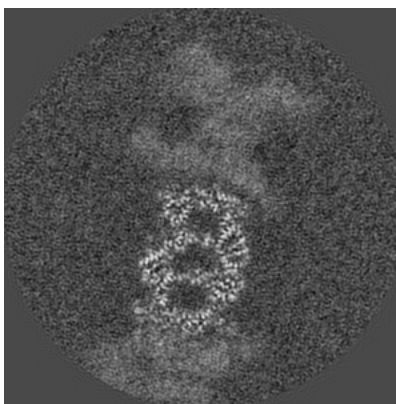
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

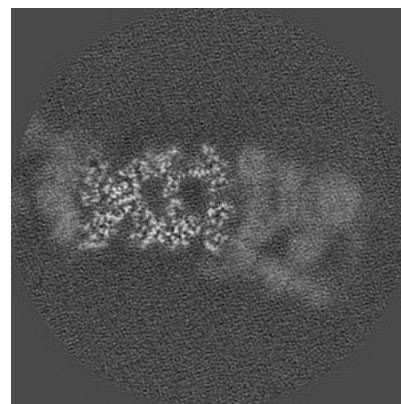
6.3.1 Primary map



X Index: 281



Y Index: 275

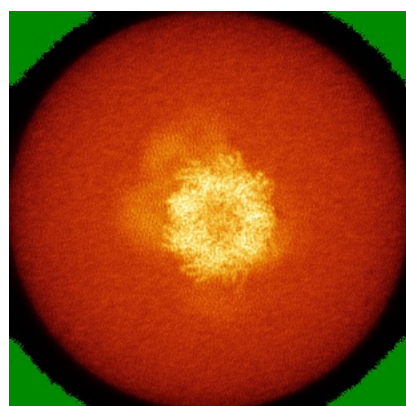


Z Index: 296

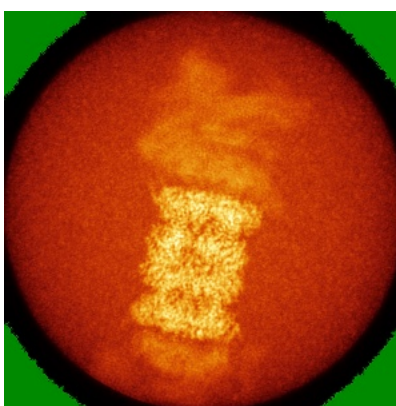
The images above show the largest variance slices of the map in three orthogonal directions.

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

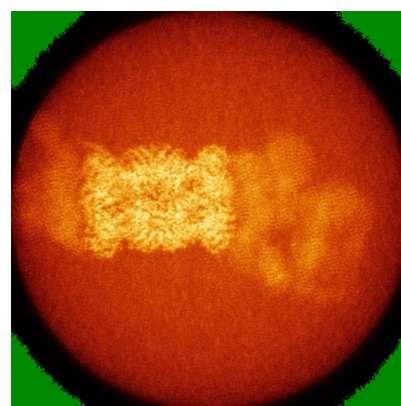
6.4.1 Primary map



X



Y

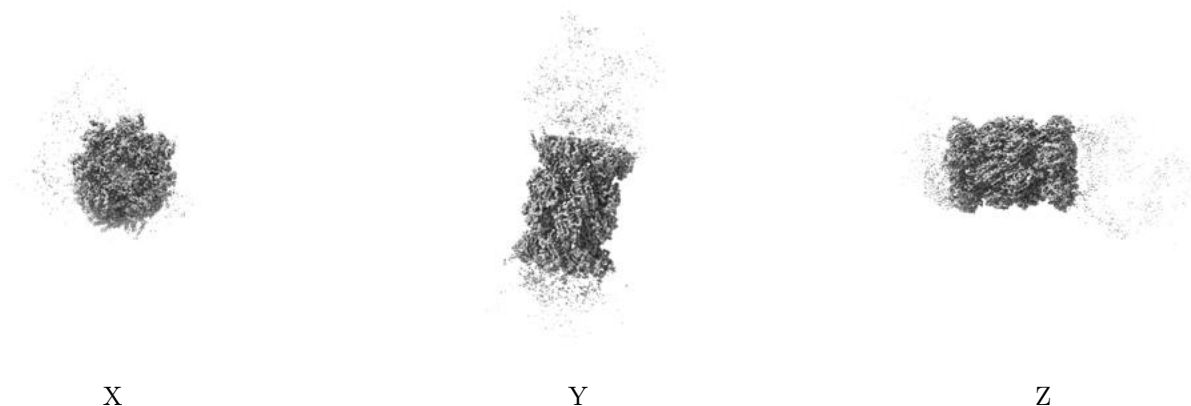


Z

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

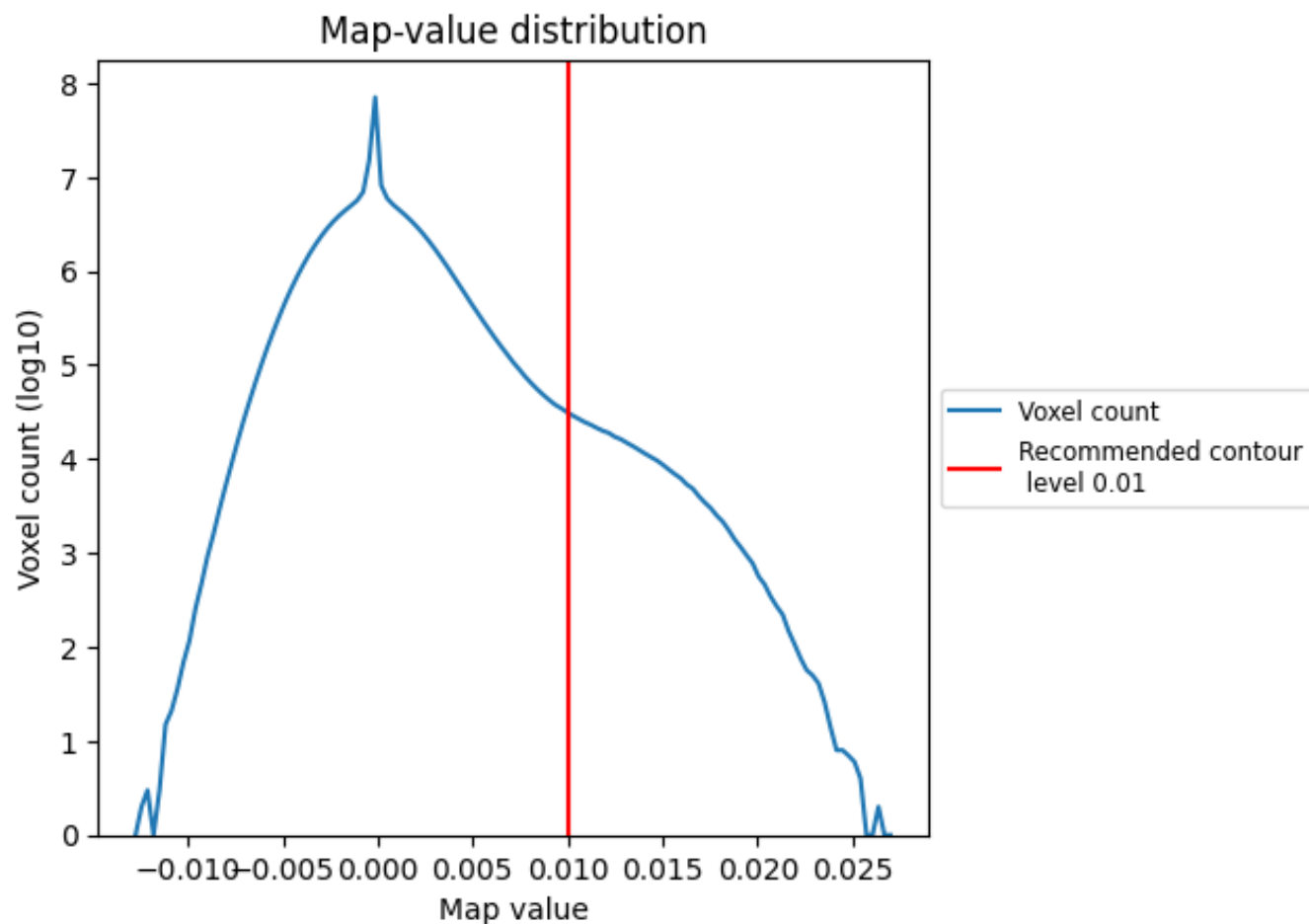
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

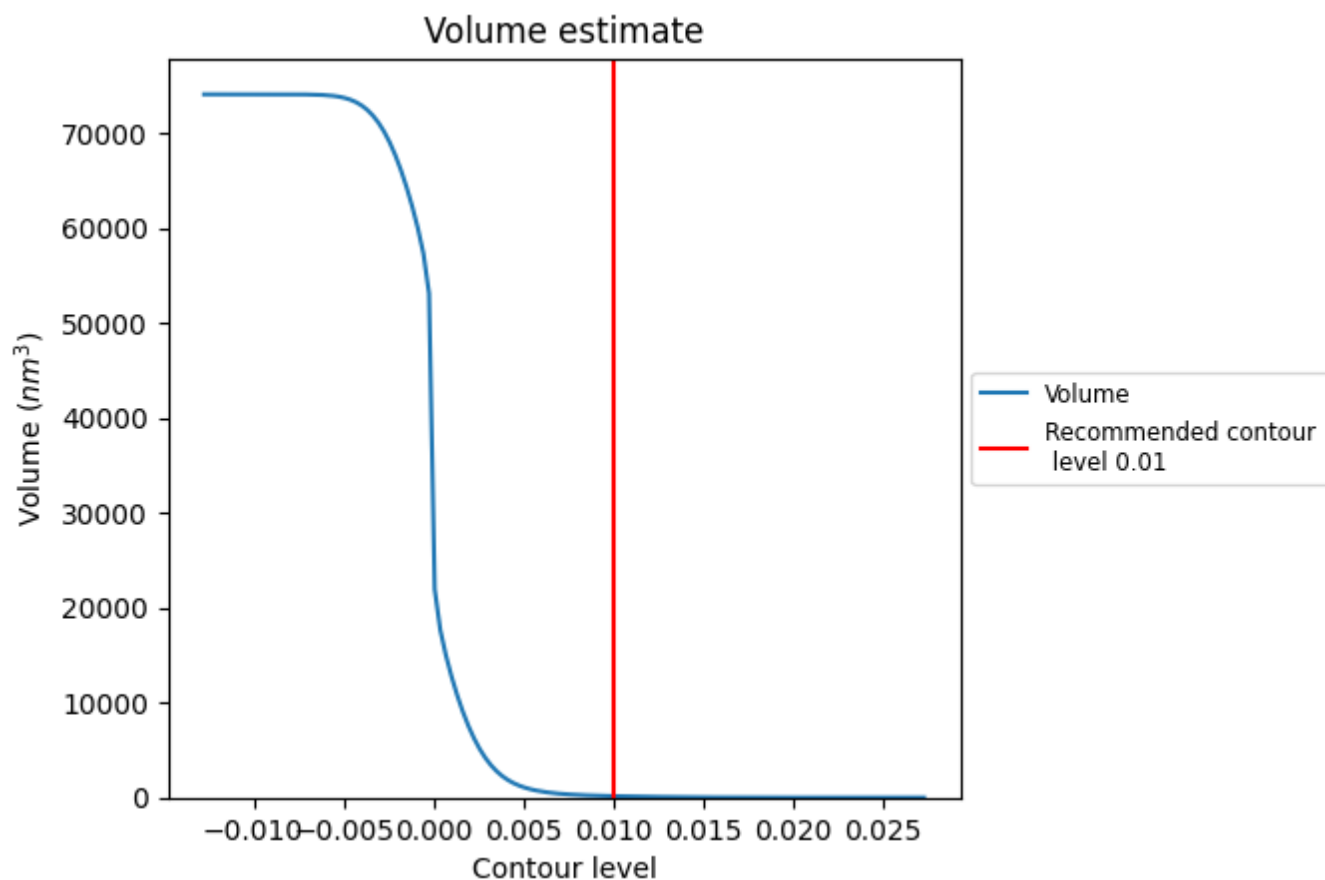
This section contains the results of statistical analysis of the map.

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.

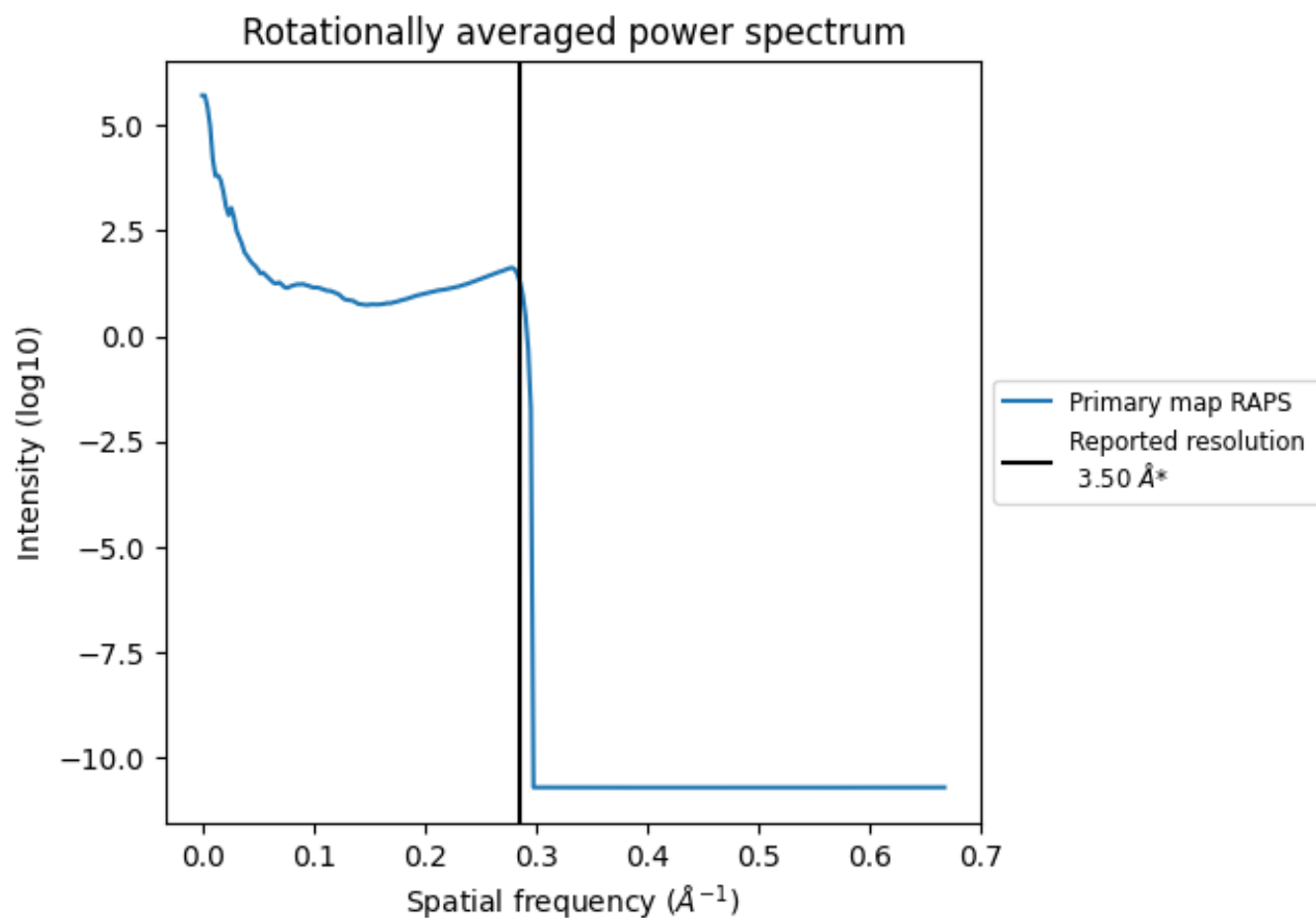
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 153 nm^3 ; this corresponds to an approximate mass of 138 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.286 Å⁻¹

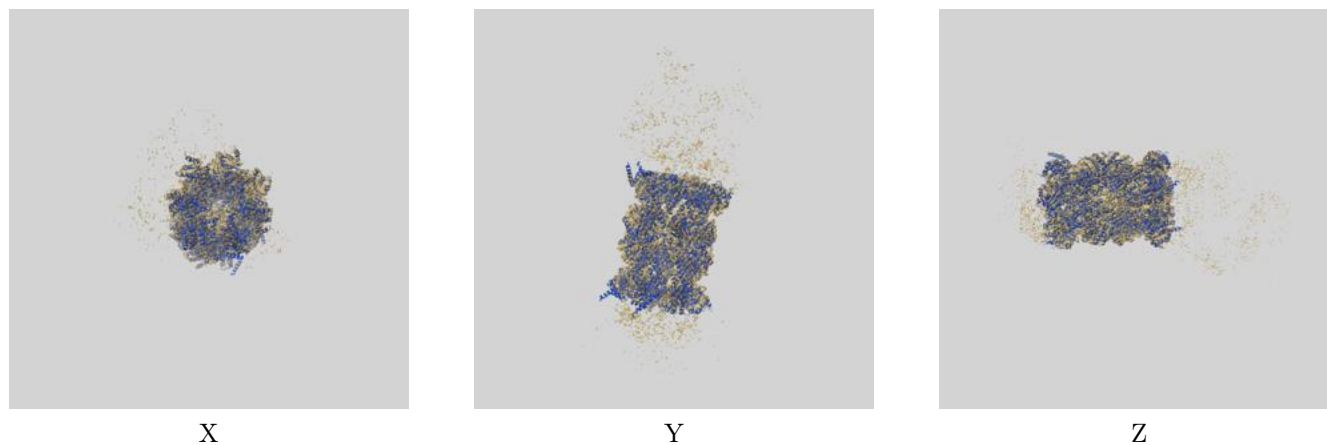
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

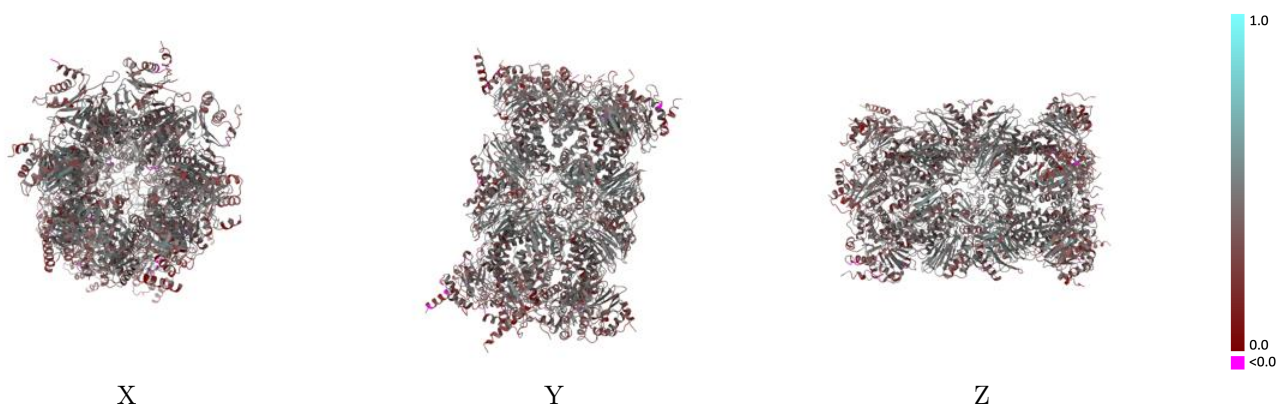
This section contains information regarding the fit between EMDB map EMD-8662 and PDB model 5VFO. Per-residue inclusion information can be found in [section 3](#) on [page 7](#).

9.1 Map-model overlay [i](#)



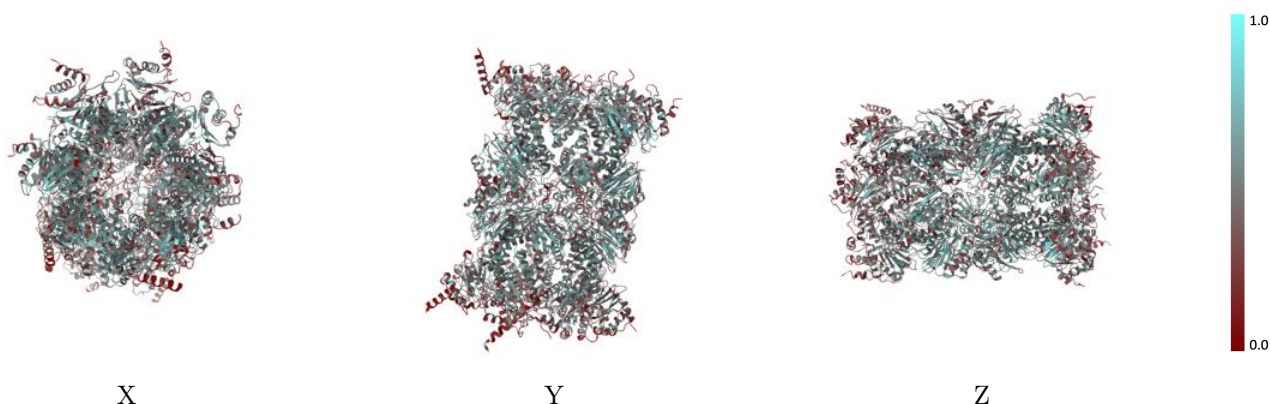
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



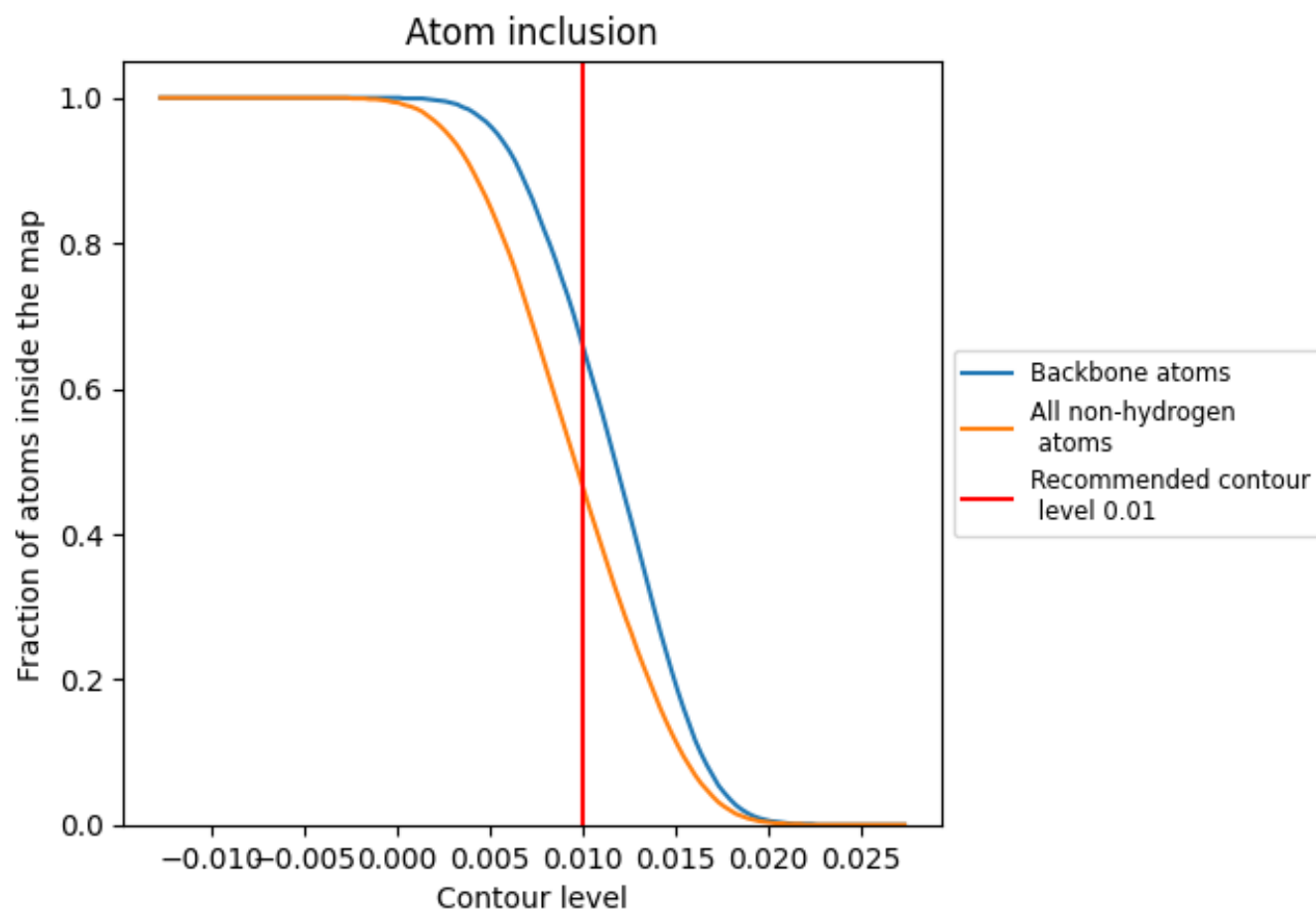
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

9.4 Atom inclusion [i](#)



At the recommended contour level, 66% of all backbone atoms, 46% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.4630	 0.3940
G	 0.4560	 0.3890
H	 0.4900	 0.4030
I	 0.4460	 0.3710
J	 0.4190	 0.3650
K	 0.4330	 0.3660
L	 0.5000	 0.4000
M	 0.4610	 0.3780
N	 0.5280	 0.4240
O	 0.4820	 0.4190
P	 0.5290	 0.4320
Q	 0.4990	 0.4000
R	 0.5430	 0.4240
S	 0.4830	 0.4210
T	 0.5370	 0.4340
g	 0.3930	 0.3730
h	 0.4180	 0.3770
i	 0.3650	 0.3470
j	 0.3520	 0.3370
k	 0.4020	 0.3530
l	 0.4290	 0.3610
m	 0.4010	 0.3560
n	 0.5050	 0.4230
o	 0.4480	 0.3950
p	 0.4900	 0.4220
q	 0.5000	 0.4190
r	 0.5220	 0.4220
s	 0.4920	 0.4300
t	 0.5240	 0.4240

