



## wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 12:02 PM UTC

PDB ID : 7DR6 / pdb\_00007dr6  
EMDB ID : EMD-30824  
Title : PA28alpha-beta in complex with immunoproteasome  
Authors : Cong, Y.; Xu, C.  
Deposited on : 2020-12-26  
Resolution : 4.10 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](mailto: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>.

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

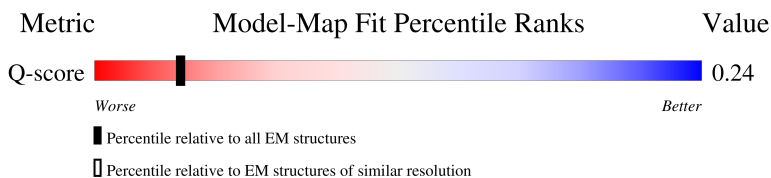
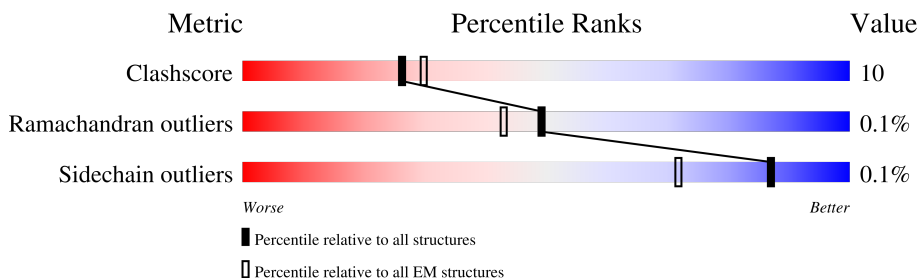
EMDB validation analysis : 0.0.1.dev132  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins)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

# 1 Overall quality at a glance i

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

The reported resolution of this entry is 4.10 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	6458 ( 3.60 - 4.60 )

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  $\geq 3$ , 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	L	246	21% (red), 74% (green), 22% (yellow), 1% (grey)
1	e	246	34% (red), 76% (green), 20% (yellow), 1% (grey)
2	M	234	22% (red), 79% (green), 18% (yellow), 1% (grey)
2	f	234	26% (red), 78% (green), 21% (yellow), 1% (grey)

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Mol	Chain	Length	Quality of chain
3	N	261	26% 72% 23% 6%
3	g	261	30% 73% 21% 6%
4	O	248	31% 69% 24% 6%
4	a	248	30% 68% 25% 6%
5	P	241	40% 75% 22% •
5	b	241	43% 66% 31% •
6	Q	263	32% 76% 14% 11%
6	c	263	34% 63% 26% 11%
7	R	255	24% 79% 15% 6%
7	d	255	40% 68% 26% 6%
8	A	239	50% 71% 17% 13%
8	D	239	55% 70% 15% • 13%
8	F	239	64% 68% 20% 12%
9	B	249	55% 71% 15% 14%
9	C	249	54% 67% 16% 17%
9	E	249	57% 69% 14% 16%
9	G	249	55% 63% 18% • 18%
10	H	205	27% 66% 34%
10	S	205	23% 68% 31%
11	I	201	26% 75% 24% •
11	T	201	22% 78% 20% •
12	J	241	23% 66% 23% 12%
12	U	241	24% 62% 26% 12%
13	K	264	23% 56% 26% 18%
13	V	264	24% 53% 28% • 18%

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Mol	Chain	Length	Quality of chain
14	W	219	<p>20% 67% 24% 9%</p>
14	Z	219	<p>21% 68% 23% 9%</p>
15	1	273	<p>20% 64% 16% 20%</p>
15	X	273	<p>20% 59% 21% 20%</p>
16	2	276	<p>18% 52% 21% 27%</p>
16	Y	276	<p>12% 54% 18% 27%</p>

## 2 Entry composition [i](#)

There are 16 unique types of molecules in this entry. The entry contains 59957 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	L	236	Total	C	N	O	S	0	0
			1850	1178	306	353	13		
1	e	238	Total	C	N	O	S	0	0
			1856	1181	308	354	13		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	M	226	Total	C	N	O	S	0	0
			1763	1127	298	332	6		
2	f	230	Total	C	N	O	S	0	0
			1793	1147	302	338	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	N	246	Total	C	N	O	S	0	0
			1936	1225	331	369	11		
3	g	246	Total	C	N	O	S	0	0
			1936	1225	331	369	11		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	O	232	Total	C	N	O	S	0	0
			1824	1149	322	348	5		
4	a	232	Total	C	N	O	S	0	0
			1824	1149	322	348	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	P	234	1790	1125	295	359	11	0	0
5	b	234	1790	1125	295	359	11	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	Q	235	1846	1156	330	349	11	0	0
6	c	235	1846	1156	330	349	11	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	R	240	1879	1191	321	356	11	0	0
7	d	240	1879	1191	321	356	11	0	0

- Molecule 8 is a protein called Proteasome activator complex subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	A	209	1684	1084	286	310	4	0	0
8	D	207	1678	1080	283	311	4	0	0
8	F	210	1695	1091	287	313	4	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	89	PRO	HIS	variant	UNP Q9UL46
D	89	PRO	HIS	variant	UNP Q9UL46
F	89	PRO	HIS	variant	UNP Q9UL46

- Molecule 9 is a protein called Proteasome activator complex subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	B	213	1720	1102	292	320	6	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
9	C	206	Total	C	N	O	S	0	0
			1663	1063	284	310	6		
9	E	208	Total	C	N	O	S	0	0
			1685	1078	287	314	6		
9	G	205	Total	C	N	O	S	0	0
			1654	1057	283	306	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	H	204	Total	C	N	O	S	0	0
			1594	1015	265	295	19		
10	S	204	Total	C	N	O	S	0	0
			1594	1015	265	295	19		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
11	I	198	Total	C	N	O	S	0	0
			1593	1023	270	292	8		
11	T	197	Total	C	N	O	S	0	0
			1584	1017	268	291	8		

- Molecule 12 is a protein called Proteasome subunit beta type-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	J	213	Total	C	N	O	S	0	0
			1645	1042	282	311	10		
12	U	213	Total	C	N	O	S	0	0
			1645	1042	282	311	10		

- Molecule 13 is a protein called Proteasome subunit beta type-4.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	K	216	Total	C	N	O	S	0	0
			1685	1065	289	319	12		
13	V	216	Total	C	N	O	S	0	0
			1682	1063	289	318	12		

- Molecule 14 is a protein called Proteasome subunit beta type-9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	W	199	1500	942	257	291	10	0	0
14	Z	199	1500	942	257	291	10	0	0

- Molecule 15 is a protein called Proteasome subunit beta type-10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	X	219	1611	1010	281	309	11	0	0
15	1	219	1611	1010	281	309	11	0	0

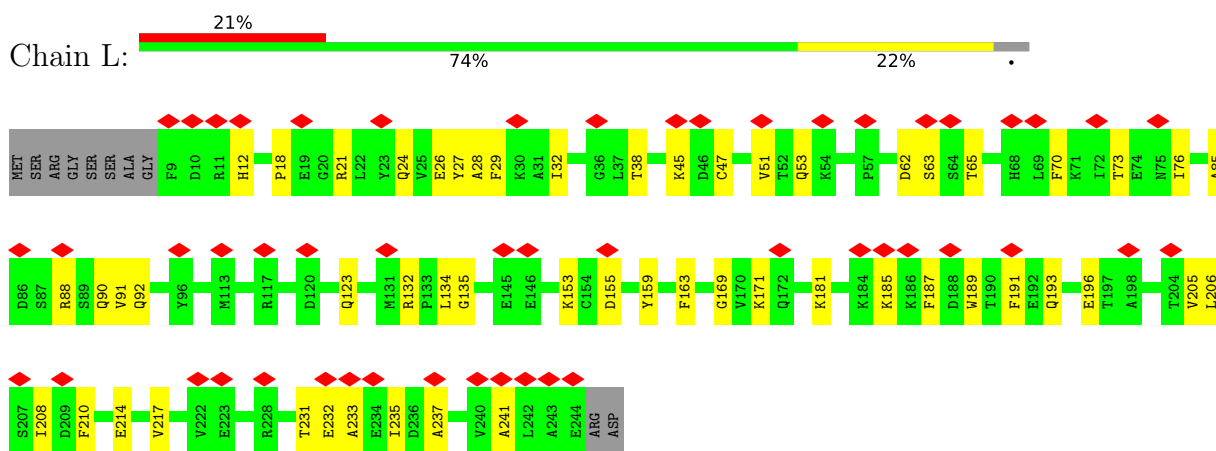
- Molecule 16 is a protein called Proteasome subunit beta type-8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	Y	201	1561	975	273	297	16	0	0
16	2	201	1561	975	273	297	16	0	0

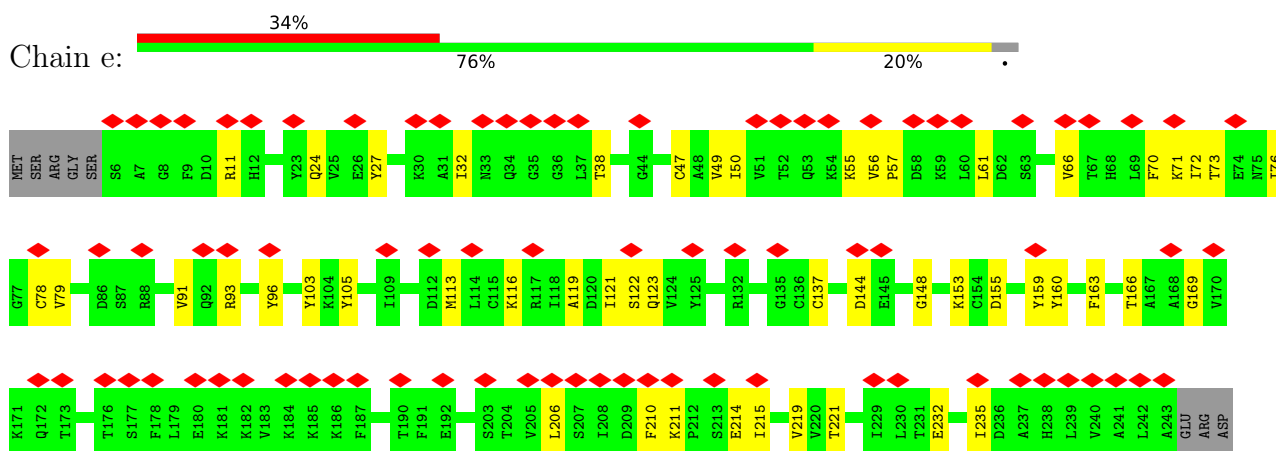
### 3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

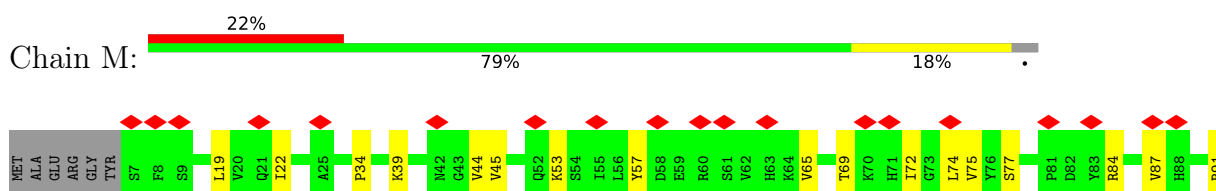
- Molecule 1: Proteasome subunit alpha type-6

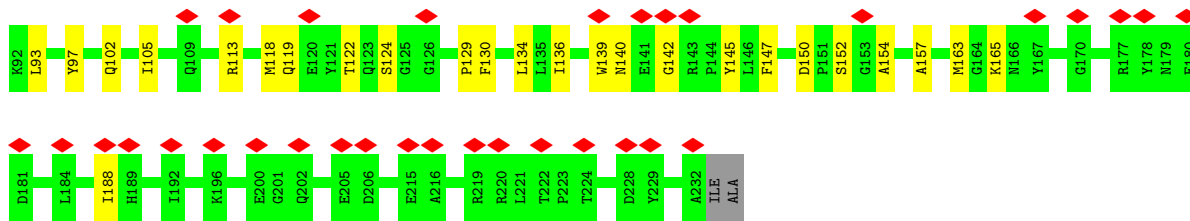


- Molecule 1: Proteasome subunit alpha type-6

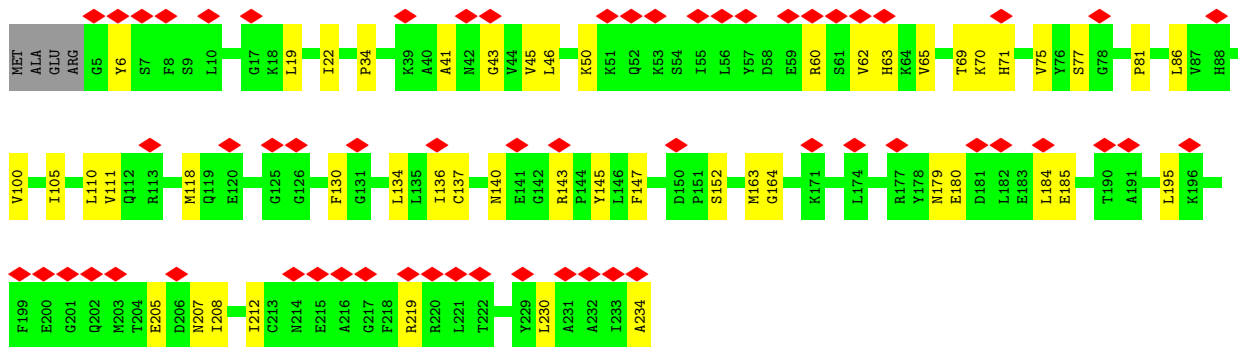
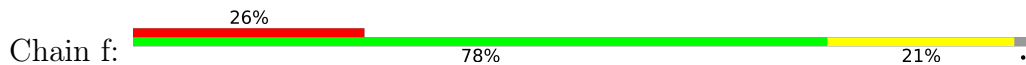


- Molecule 2: Proteasome subunit alpha type-2

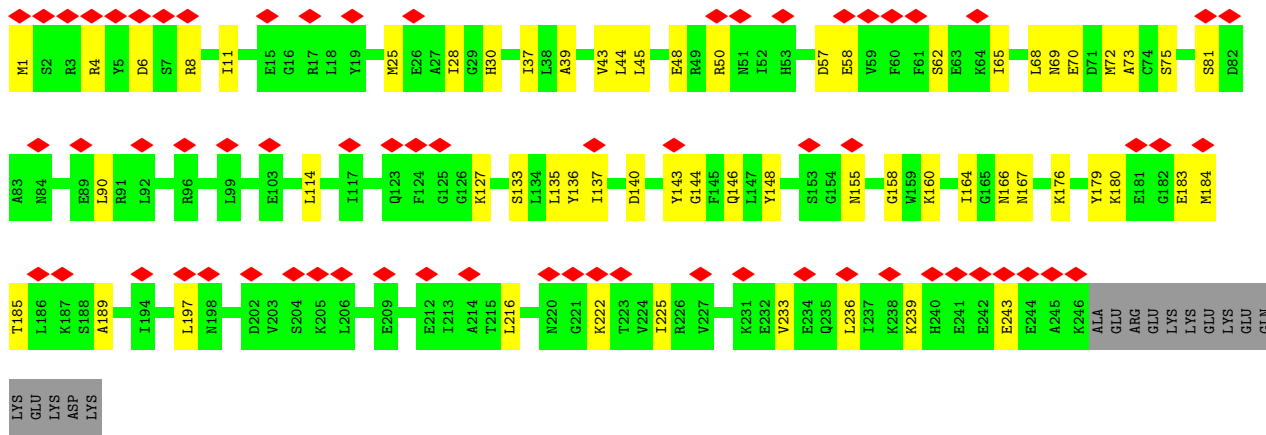




• Molecule 2: Proteasome subunit alpha type-2



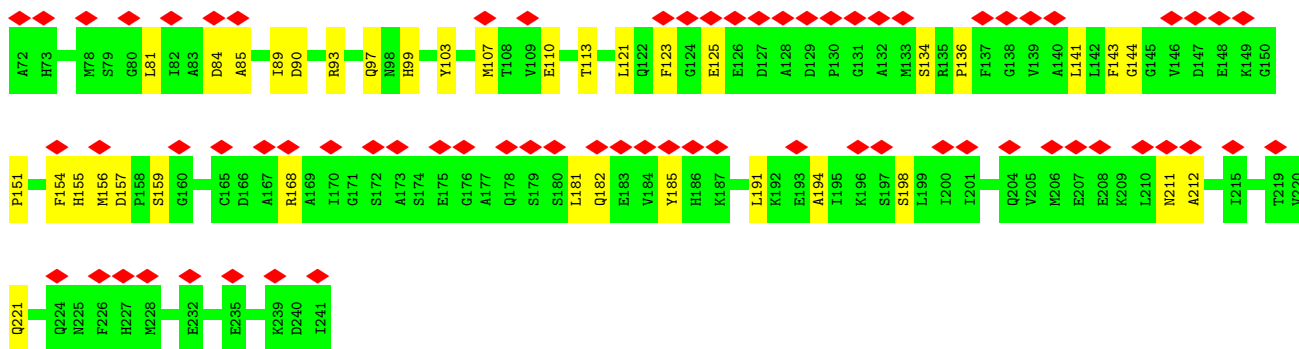
• Molecule 3: Proteasome subunit alpha type-4



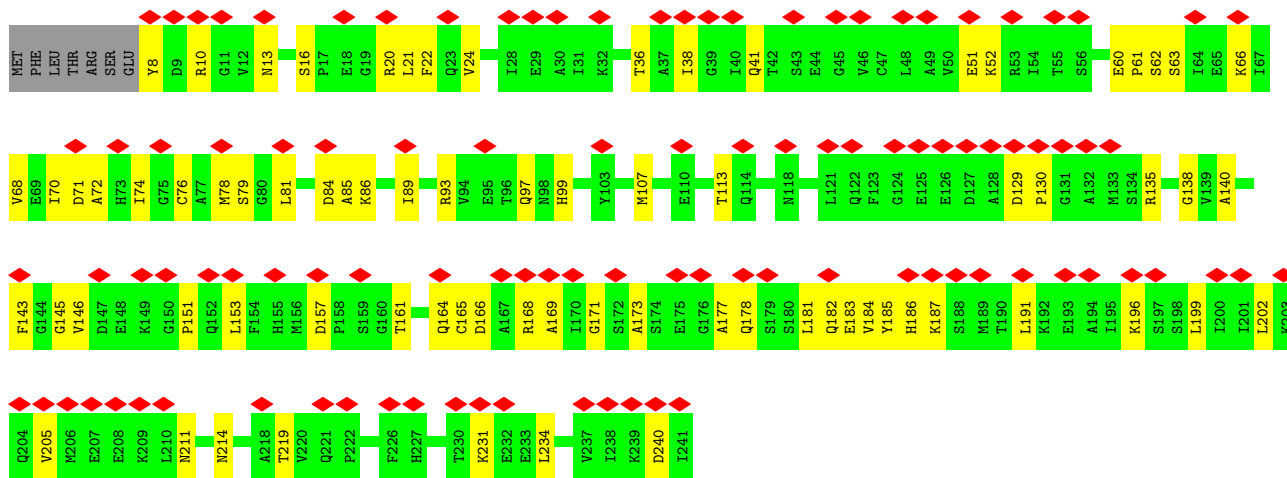
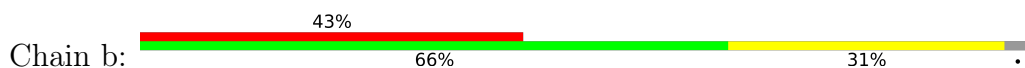
• Molecule 3: Proteasome subunit alpha type-4



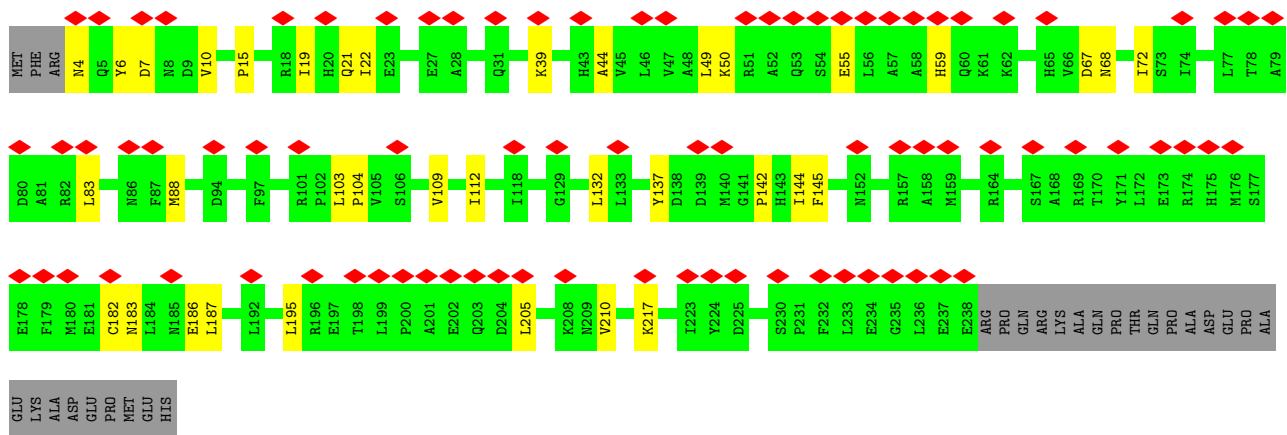
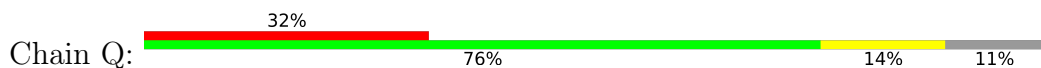




• Molecule 5: Proteasome subunit alpha type-5

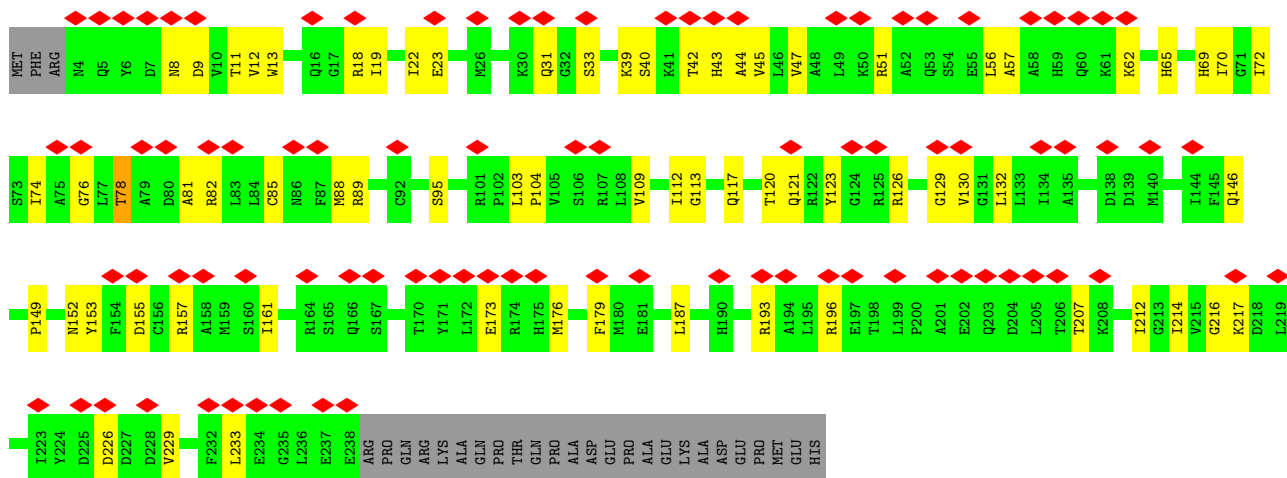


• Molecule 6: Proteasome subunit alpha type-1

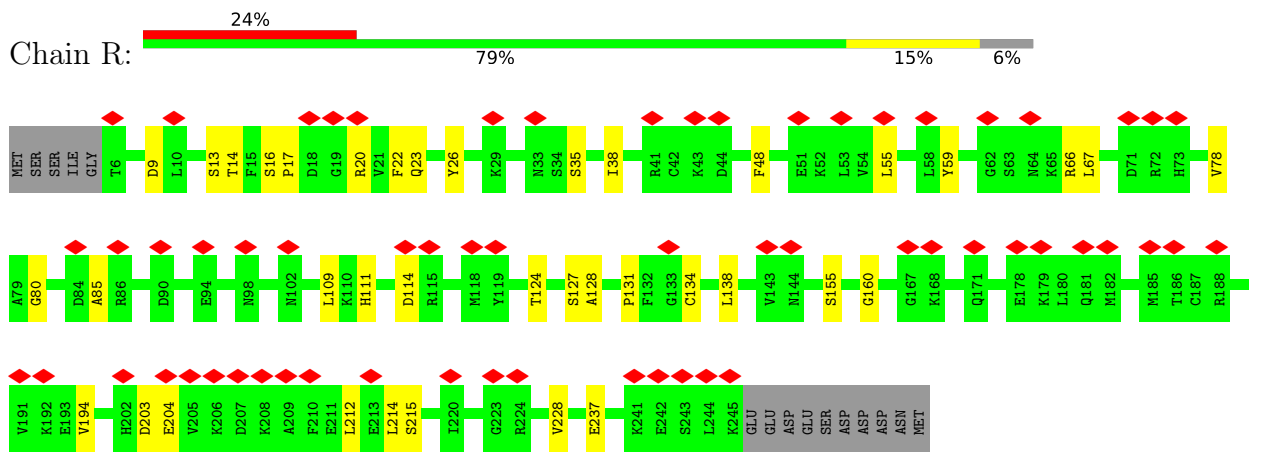


• Molecule 6: Proteasome subunit alpha type-1

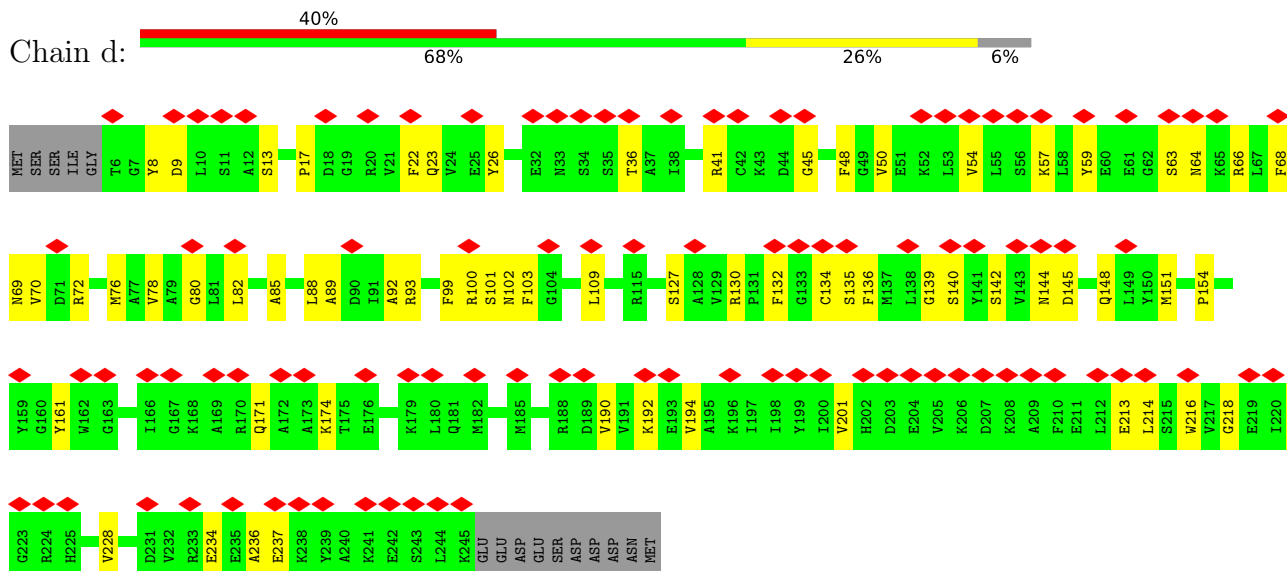




• Molecule 7: Proteasome subunit alpha type-3



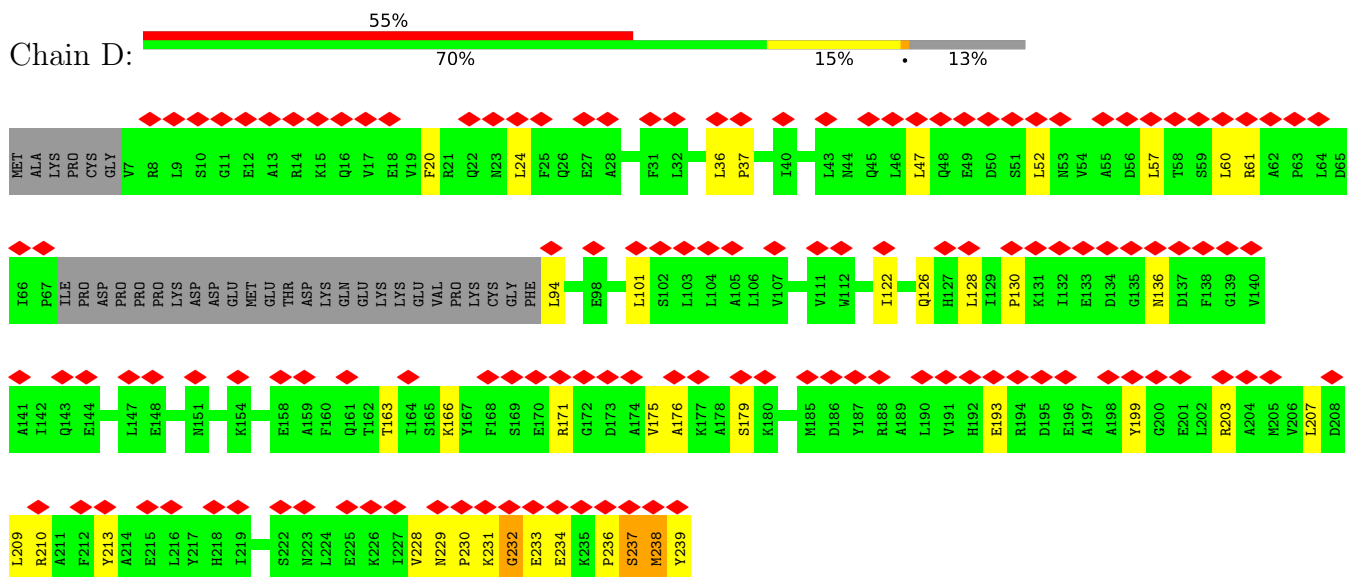
• Molecule 7: Proteasome subunit alpha type-3



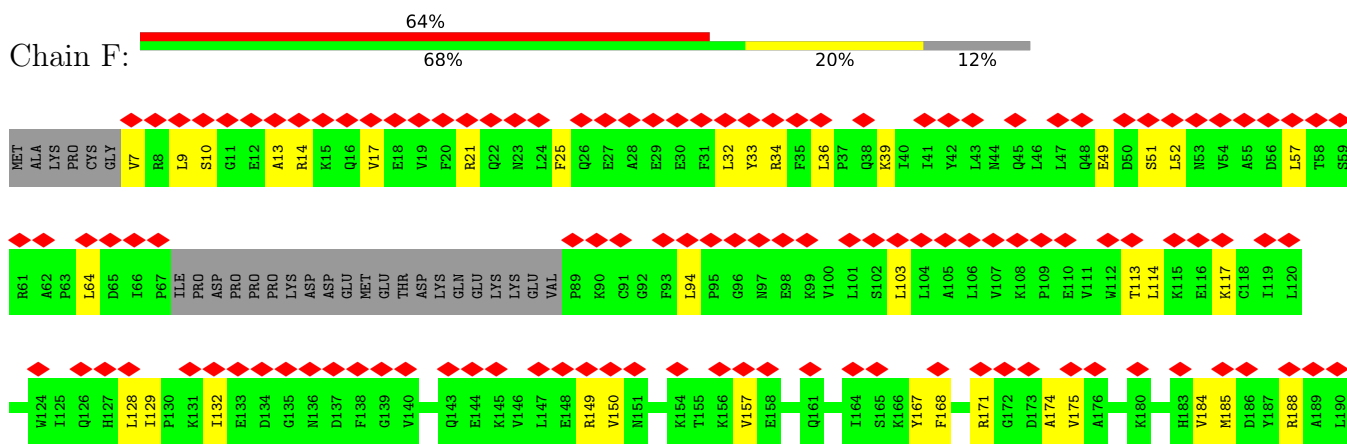
• Molecule 8: Proteasome activator complex subunit 2

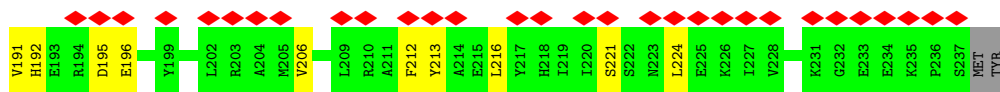


• Molecule 8: Proteasome activator complex subunit 2

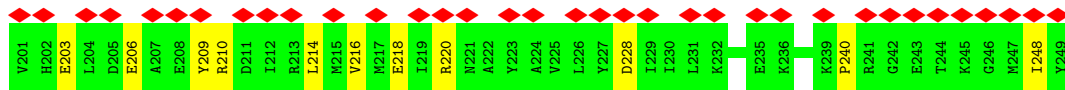
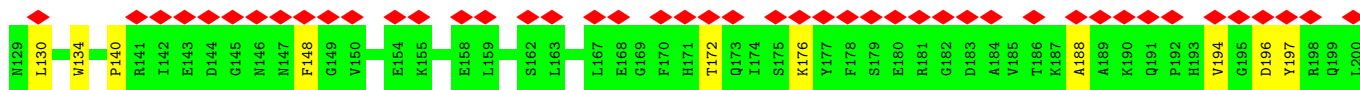
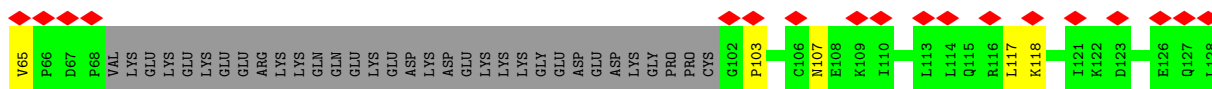
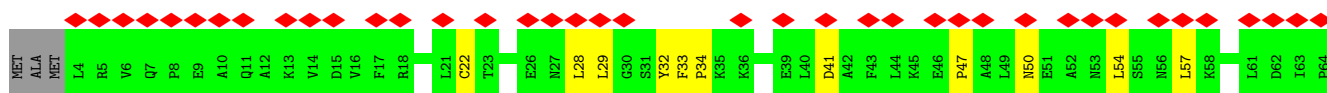


• Molecule 8: Proteasome activator complex subunit 2

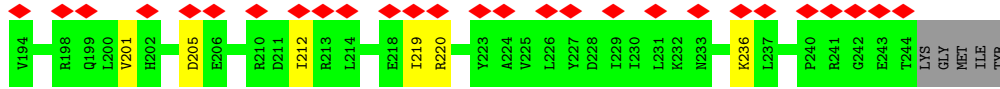
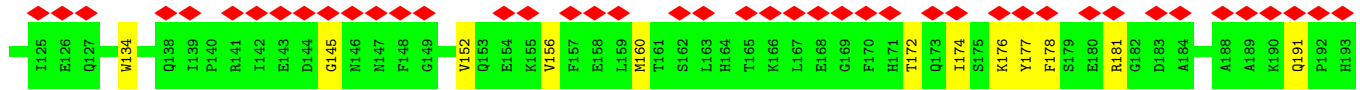
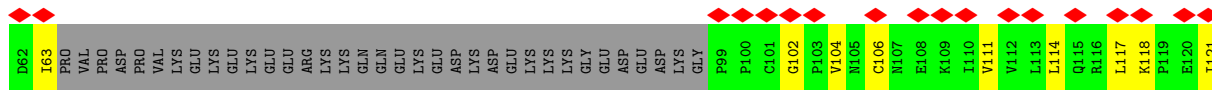
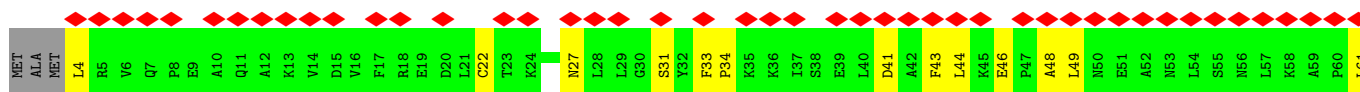




• Molecule 9: Proteasome activator complex subunit 1



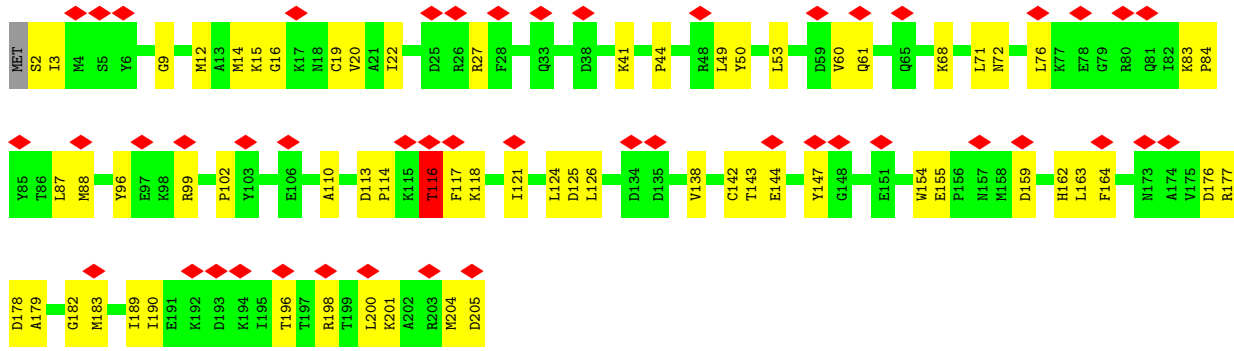
• Molecule 9: Proteasome activator complex subunit 1



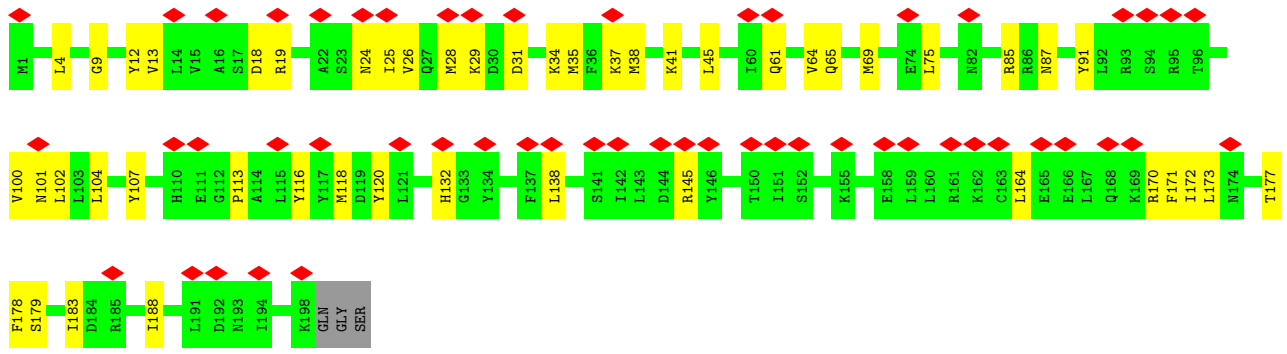
• Molecule 9: Proteasome activator complex subunit 1



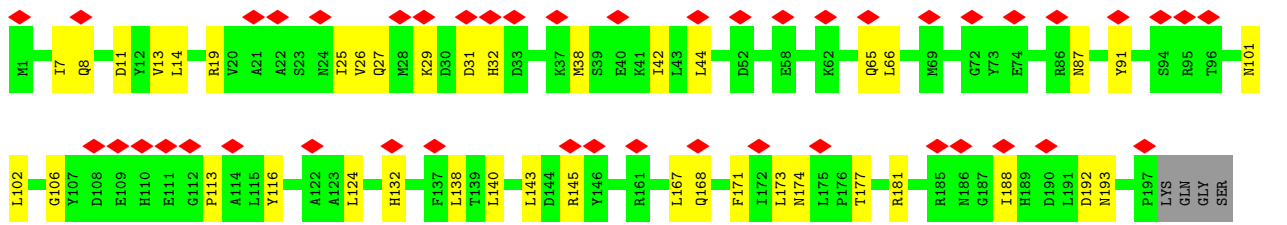
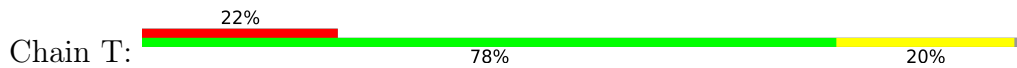




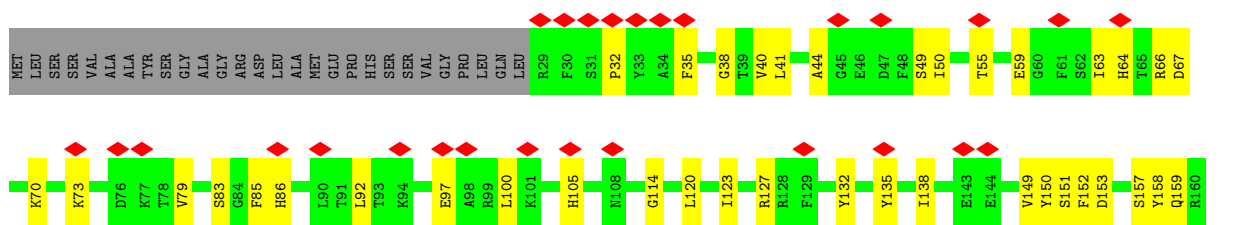
• Molecule 11: Proteasome subunit beta type-2

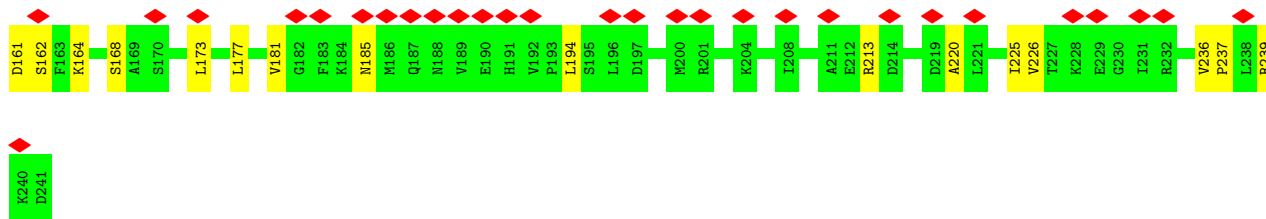


• Molecule 11: Proteasome subunit beta type-2

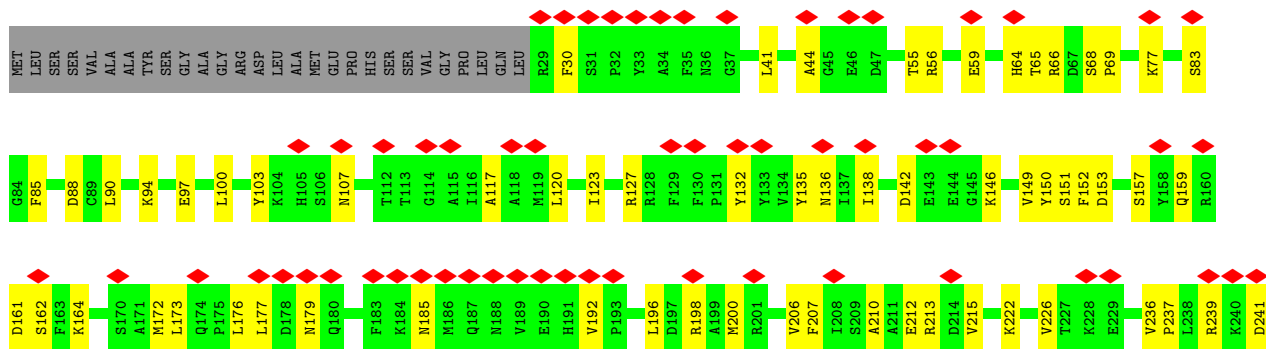


• Molecule 12: Proteasome subunit beta type-1

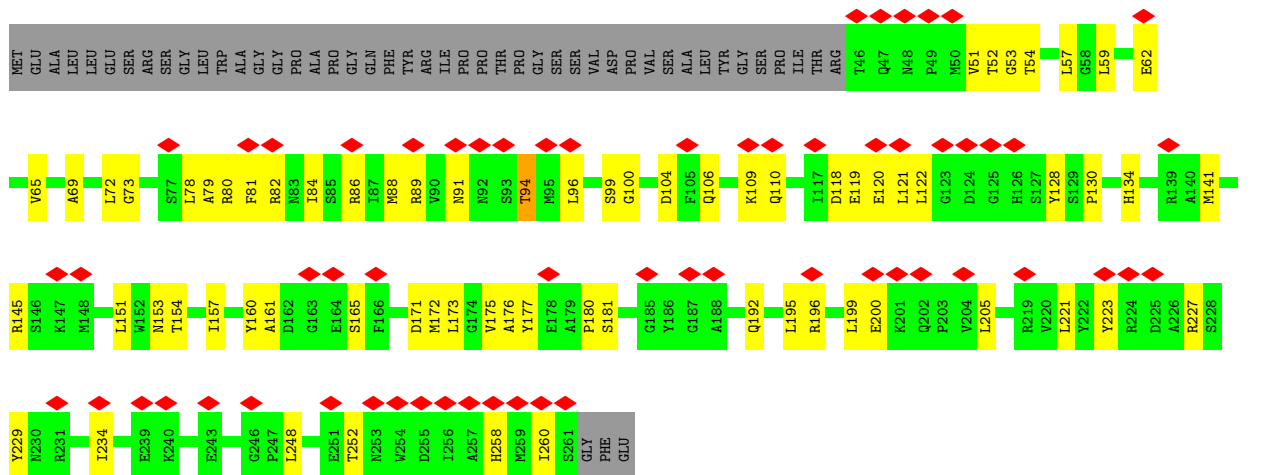




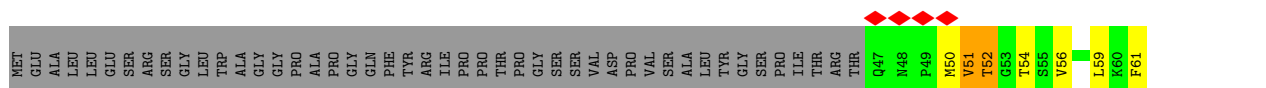
• Molecule 12: Proteasome subunit beta type-1

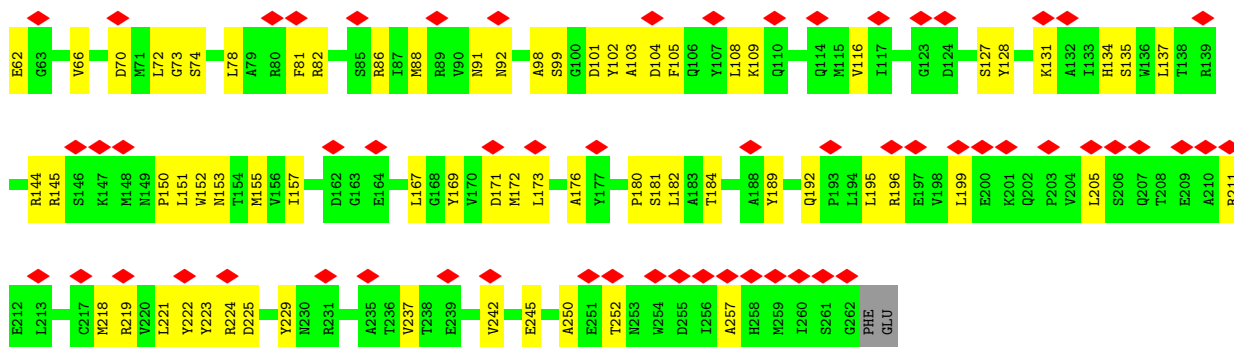


• Molecule 13: Proteasome subunit beta type-4

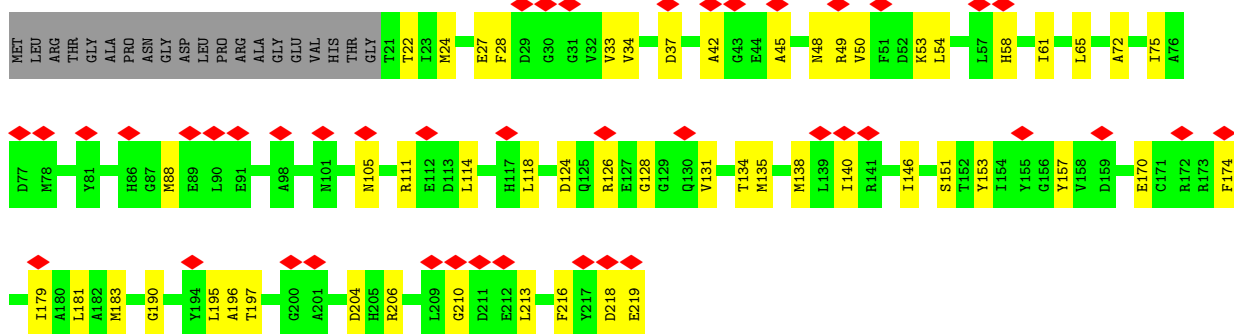


• Molecule 13: Proteasome subunit beta type-4

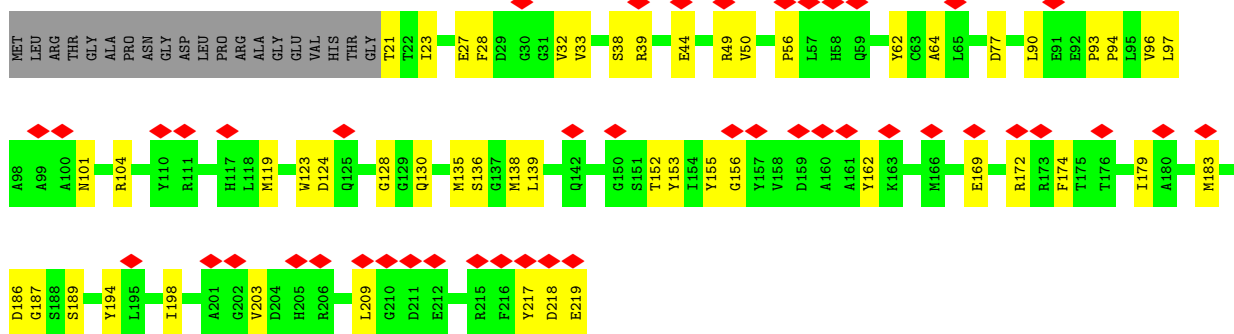




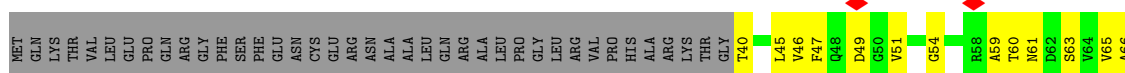
• Molecule 14: Proteasome subunit beta type-9

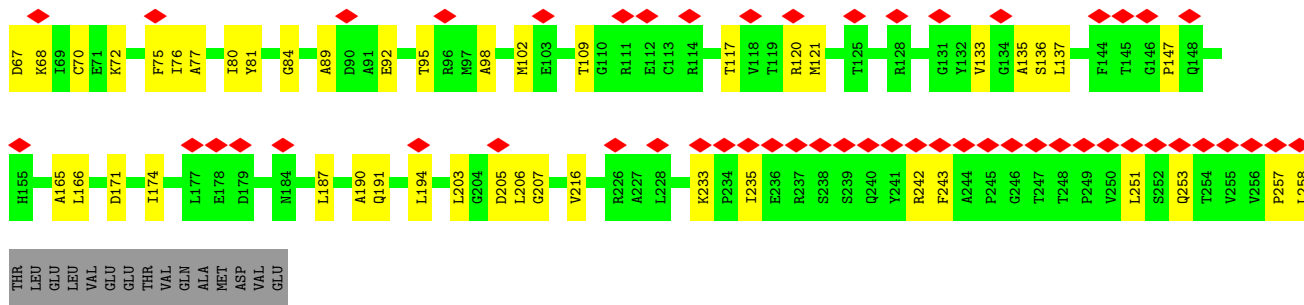


• Molecule 14: Proteasome subunit beta type-9

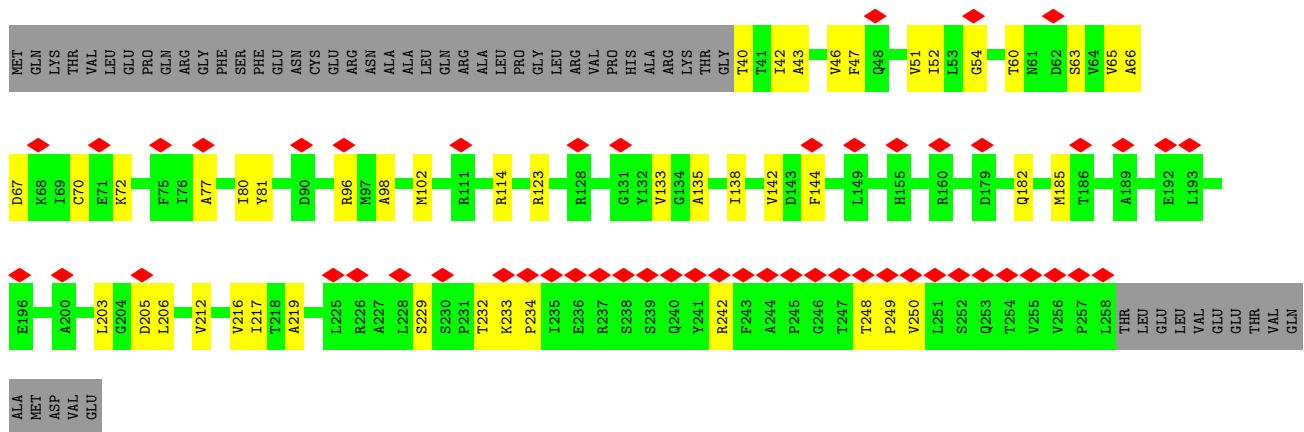


• Molecule 15: Proteasome subunit beta type-10

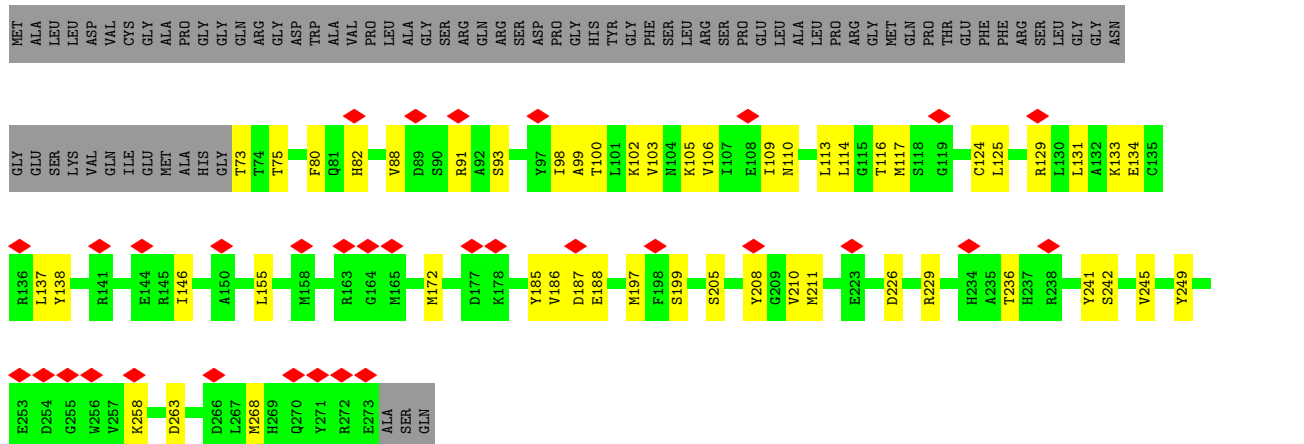


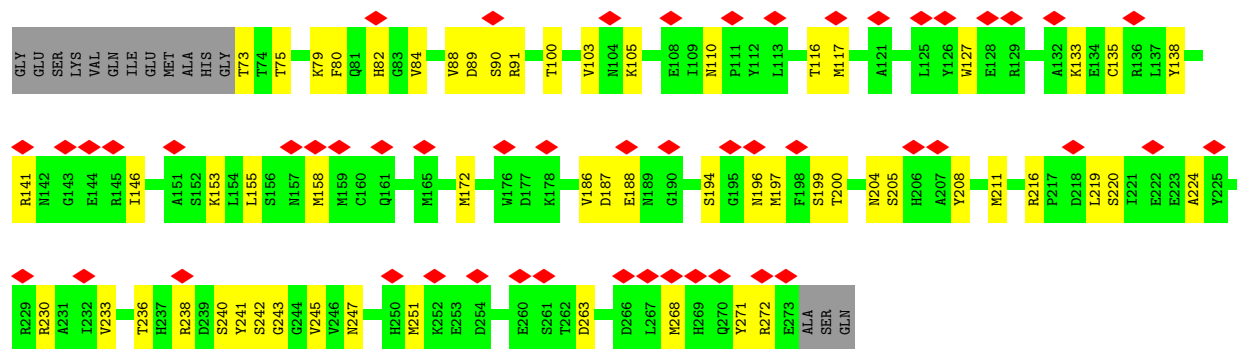


• Molecule 15: Proteasome subunit beta type-10



• Molecule 16: Proteasome subunit beta type-8





## 4 Experimental information i

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	45030	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 ( $e^-/\text{\AA}^2$ )	38	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	2.322	Depositor
Minimum map value	-1.426	Depositor
Average map value	0.012	Depositor
Map value standard deviation	0.108	Depositor
Recommended contour level	0.619	Depositor
Map size (Å)	337.408, 337.408, 337.408	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.318, 1.318, 1.318	Depositor

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	L	0.11	0/1884	0.36	0/2548
1	e	0.11	0/1890	0.35	0/2556
2	M	0.11	0/1801	0.32	0/2440
2	f	0.11	0/1832	0.36	1/2481 (0.0%)
3	N	0.11	0/1966	0.33	0/2648
3	g	0.12	0/1966	0.36	0/2648
4	O	0.14	0/1851	0.44	2/2501 (0.1%)
4	a	0.12	0/1851	0.40	1/2501 (0.0%)
5	P	0.12	0/1818	0.34	0/2455
5	b	0.10	0/1818	0.35	1/2455 (0.0%)
6	Q	0.11	0/1880	0.34	0/2541
6	c	0.12	0/1880	0.40	1/2541 (0.0%)
7	R	0.10	0/1914	0.31	0/2578
7	d	0.11	0/1914	0.34	0/2578
8	A	0.10	0/1714	0.28	0/2315
8	D	0.11	0/1708	0.32	0/2308
8	F	0.12	0/1726	0.32	0/2331
9	B	0.13	0/1751	0.32	0/2366
9	C	0.11	0/1692	0.34	0/2285
9	E	0.13	0/1713	0.34	0/2309
9	G	0.12	0/1681	0.35	0/2267
10	H	0.13	0/1623	0.44	0/2188
10	S	0.14	0/1623	0.41	0/2188
11	I	0.12	0/1627	0.38	1/2201 (0.0%)
11	T	0.11	0/1618	0.35	0/2190
12	J	0.12	0/1676	0.38	0/2258
12	U	0.13	0/1676	0.39	0/2258
13	K	0.12	0/1718	0.38	0/2324
13	V	0.15	0/1715	0.44	0/2319
14	W	0.12	0/1529	0.35	0/2071
14	Z	0.11	0/1529	0.33	0/2071
15	1	0.15	0/1637	0.42	0/2225
15	X	0.14	0/1637	0.40	0/2225
16	2	0.12	0/1592	0.38	0/2145

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
16	Y	0.13	0/1592	0.36	0/2145
All	All	0.12	0/61042	0.36	7/82460 (0.0%)

There are no bond length outliers.

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	c	78	THR	N-CA-C	7.16	120.13	111.82
5	b	187	LYS	CB-CA-C	-6.45	109.13	116.54
4	a	213	ARG	CB-CA-C	-5.54	110.17	116.54
2	f	41	ALA	CB-CA-C	-5.47	109.79	117.23
11	I	24	ASN	CB-CA-C	-5.27	110.52	116.63

There are no chirality outliers.

There are no planarity outliers.

## 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	L	1850	0	1859	36	0
1	e	1856	0	1866	35	0
2	M	1763	0	1759	26	0
2	f	1793	0	1787	29	0
3	N	1936	0	1961	61	0
3	g	1936	0	1961	37	0
4	O	1824	0	1851	52	0
4	a	1824	0	1851	42	0
5	P	1790	0	1773	32	0
5	b	1790	0	1773	51	0
6	Q	1846	0	1832	23	0
6	c	1846	0	1832	48	0
7	R	1879	0	1864	37	0
7	d	1879	0	1864	46	0
8	A	1684	0	1721	31	0
8	D	1678	0	1713	62	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	F	1695	0	1733	36	0
9	B	1720	0	1759	24	0
9	C	1663	0	1700	26	0
9	E	1685	0	1725	23	0
9	G	1654	0	1698	40	0
10	H	1594	0	1613	61	0
10	S	1594	0	1613	52	0
11	I	1593	0	1597	40	0
11	T	1584	0	1584	31	0
12	J	1645	0	1644	44	0
12	U	1645	0	1644	52	0
13	K	1685	0	1665	59	0
13	V	1682	0	1661	77	0
14	W	1500	0	1459	36	0
14	Z	1500	0	1459	46	0
15	1	1611	0	1624	30	0
15	X	1611	0	1624	47	0
16	2	1561	0	1516	43	0
16	Y	1561	0	1516	37	0
All	All	59957	0	60101	1214	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 10.

The worst 5 of 1214 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:N:25:MET:CE	8:D:236:PRO:HG3	1.51	1.40
12:U:69:PRO:HG3	12:U:222:LYS:NZ	1.34	1.38
3:N:25:MET:HE1	8:D:236:PRO:CG	1.61	1.30
10:H:140:GLY:O	10:H:143:THR:HG23	1.52	1.09
15:X:60:THR:HG22	15:X:65:VAL:HA	1.13	1.07

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	L	234/246 (95%)	220 (94%)	14 (6%)	0	100	100
1	e	236/246 (96%)	217 (92%)	19 (8%)	0	100	100
2	M	224/234 (96%)	217 (97%)	7 (3%)	0	100	100
2	f	228/234 (97%)	220 (96%)	8 (4%)	0	100	100
3	N	244/261 (94%)	234 (96%)	10 (4%)	0	100	100
3	g	244/261 (94%)	226 (93%)	17 (7%)	1 (0%)	30	65
4	O	230/248 (93%)	220 (96%)	10 (4%)	0	100	100
4	a	230/248 (93%)	218 (95%)	12 (5%)	0	100	100
5	P	232/241 (96%)	218 (94%)	14 (6%)	0	100	100
5	b	232/241 (96%)	224 (97%)	8 (3%)	0	100	100
6	Q	233/263 (89%)	217 (93%)	16 (7%)	0	100	100
6	c	233/263 (89%)	224 (96%)	9 (4%)	0	100	100
7	R	238/255 (93%)	230 (97%)	8 (3%)	0	100	100
7	d	238/255 (93%)	227 (95%)	11 (5%)	0	100	100
8	A	205/239 (86%)	204 (100%)	1 (0%)	0	100	100
8	D	203/239 (85%)	193 (95%)	9 (4%)	1 (0%)	24	61
8	F	206/239 (86%)	202 (98%)	4 (2%)	0	100	100
9	B	209/249 (84%)	202 (97%)	6 (3%)	1 (0%)	24	61
9	C	202/249 (81%)	198 (98%)	4 (2%)	0	100	100
9	E	204/249 (82%)	194 (95%)	9 (4%)	1 (0%)	24	61
9	G	201/249 (81%)	194 (96%)	4 (2%)	3 (2%)	8	39
10	H	202/205 (98%)	188 (93%)	14 (7%)	0	100	100
10	S	202/205 (98%)	185 (92%)	16 (8%)	1 (0%)	24	61
11	I	196/201 (98%)	186 (95%)	10 (5%)	0	100	100
11	T	195/201 (97%)	183 (94%)	12 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	J	211/241 (88%)	198 (94%)	13 (6%)	0	100	100
12	U	211/241 (88%)	197 (93%)	14 (7%)	0	100	100
13	K	214/264 (81%)	206 (96%)	7 (3%)	1 (0%)	24	61
13	V	214/264 (81%)	203 (95%)	11 (5%)	0	100	100
14	W	197/219 (90%)	185 (94%)	12 (6%)	0	100	100
14	Z	197/219 (90%)	191 (97%)	6 (3%)	0	100	100
15	1	217/273 (80%)	203 (94%)	13 (6%)	1 (0%)	24	61
15	X	217/273 (80%)	199 (92%)	17 (8%)	1 (0%)	24	61
16	2	199/276 (72%)	186 (94%)	13 (6%)	0	100	100
16	Y	199/276 (72%)	185 (93%)	14 (7%)	0	100	100
All	All	7577/8567 (88%)	7194 (95%)	372 (5%)	11 (0%)	49	81

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	D	232	GLY
15	1	63	SER
15	X	63	SER
9	G	240	PRO
9	G	241	ARG

### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	L	203/210 (97%)	203 (100%)	0	100	100
1	e	203/210 (97%)	203 (100%)	0	100	100
2	M	186/191 (97%)	186 (100%)	0	100	100
2	f	188/191 (98%)	188 (100%)	0	100	100
3	N	207/221 (94%)	207 (100%)	0	100	100
3	g	207/221 (94%)	207 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	O	196/211 (93%)	196 (100%)	0	100	100
4	a	196/211 (93%)	196 (100%)	0	100	100
5	P	196/203 (97%)	195 (100%)	1 (0%)	81	82
5	b	196/203 (97%)	196 (100%)	0	100	100
6	Q	201/225 (89%)	201 (100%)	0	100	100
6	c	201/225 (89%)	201 (100%)	0	100	100
7	R	198/212 (93%)	198 (100%)	0	100	100
7	d	198/212 (93%)	198 (100%)	0	100	100
8	A	183/212 (86%)	183 (100%)	0	100	100
8	D	183/212 (86%)	180 (98%)	3 (2%)	55	69
8	F	185/212 (87%)	185 (100%)	0	100	100
9	B	191/224 (85%)	191 (100%)	0	100	100
9	C	185/224 (83%)	185 (100%)	0	100	100
9	E	186/224 (83%)	186 (100%)	0	100	100
9	G	183/224 (82%)	183 (100%)	0	100	100
10	H	174/175 (99%)	174 (100%)	0	100	100
10	S	174/175 (99%)	173 (99%)	1 (1%)	78	80
11	I	169/171 (99%)	169 (100%)	0	100	100
11	T	168/171 (98%)	168 (100%)	0	100	100
12	J	177/198 (89%)	177 (100%)	0	100	100
12	U	177/198 (89%)	177 (100%)	0	100	100
13	K	178/215 (83%)	177 (99%)	1 (1%)	78	80
13	V	177/215 (82%)	175 (99%)	2 (1%)	65	74
14	W	153/167 (92%)	153 (100%)	0	100	100
14	Z	153/167 (92%)	153 (100%)	0	100	100
15	1	170/216 (79%)	170 (100%)	0	100	100
15	X	170/216 (79%)	170 (100%)	0	100	100
16	2	166/222 (75%)	166 (100%)	0	100	100
16	Y	166/222 (75%)	166 (100%)	0	100	100
All	All	6444/7206 (89%)	6436 (100%)	8 (0%)	87	89

5 of 8 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
13	V	52	THR
13	V	51	VAL
13	K	94	THR
8	D	238	MET
10	S	116	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 75 such sidechains are listed below:

Mol	Chain	Res	Type
10	S	188	HIS
16	2	82	HIS
12	U	107	ASN
15	X	61	ASN
9	G	7	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.

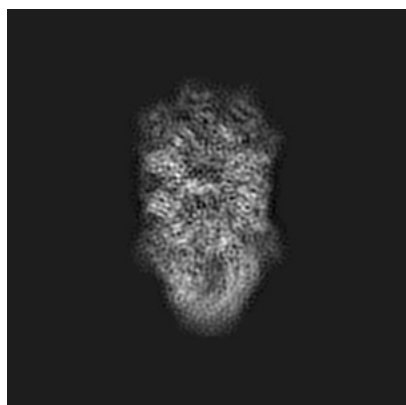
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-30824. These allow visual inspection of the internal detail of the map and identification of artifacts.

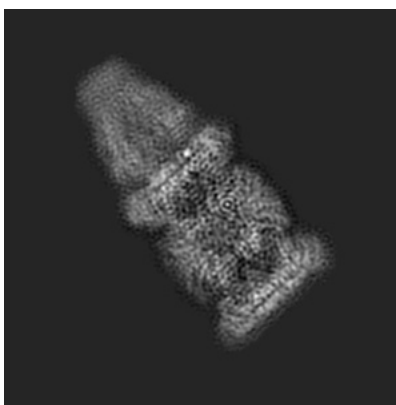
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

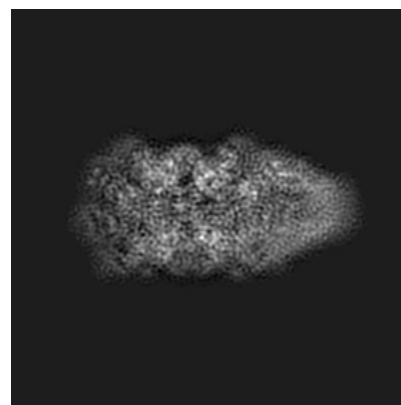
#### 6.1.1 Primary map



X



Y



Z

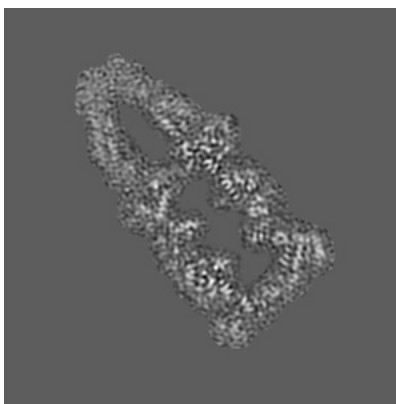
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

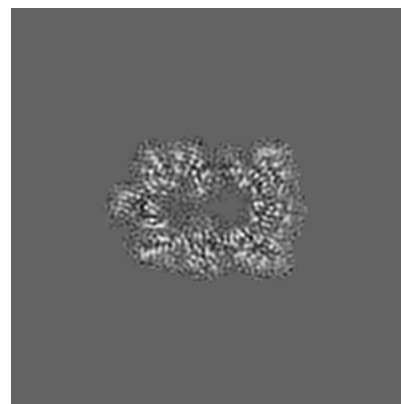
#### 6.2.1 Primary map



X Index: 128



Y Index: 128



Z Index: 128

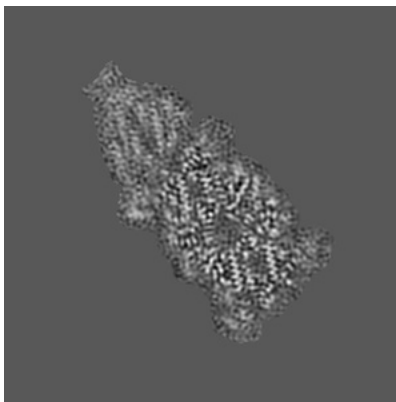
The images above show central slices of the map in three orthogonal directions.

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

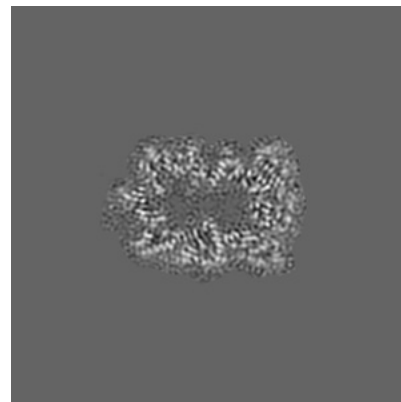
### 6.3.1 Primary map



X Index: 120



Y Index: 109

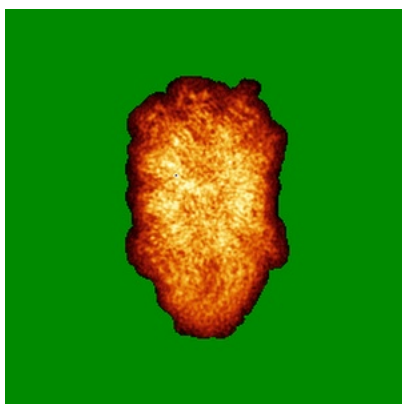


Z Index: 130

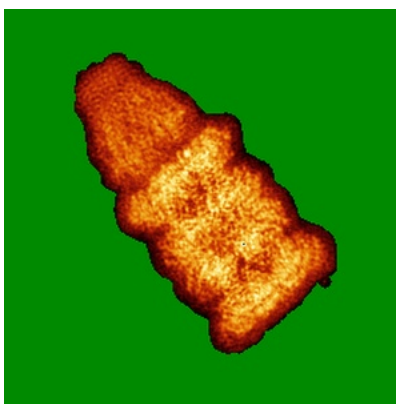
The images above show the largest variance slices of the map in three orthogonal directions.

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

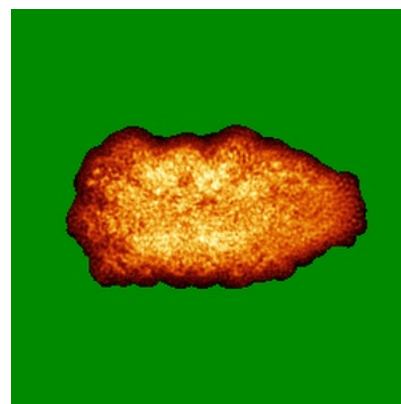
### 6.4.1 Primary map



X



Y

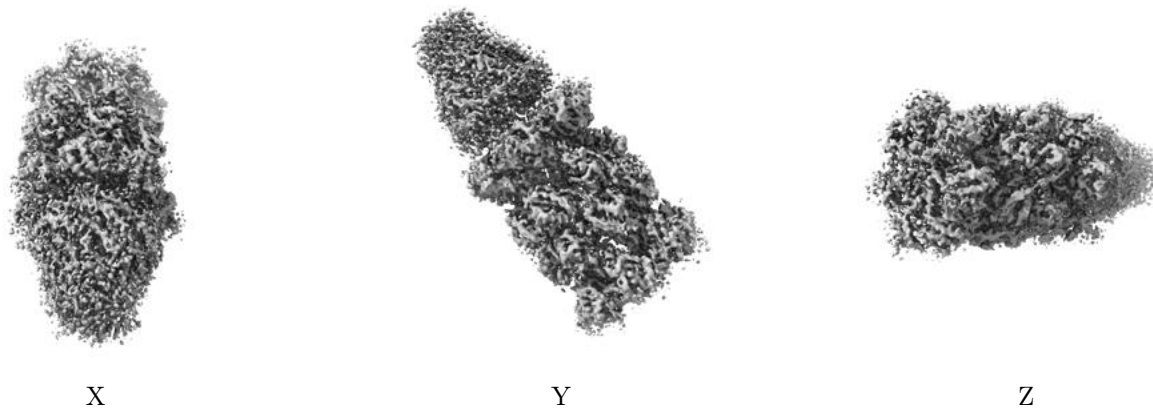


Z

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

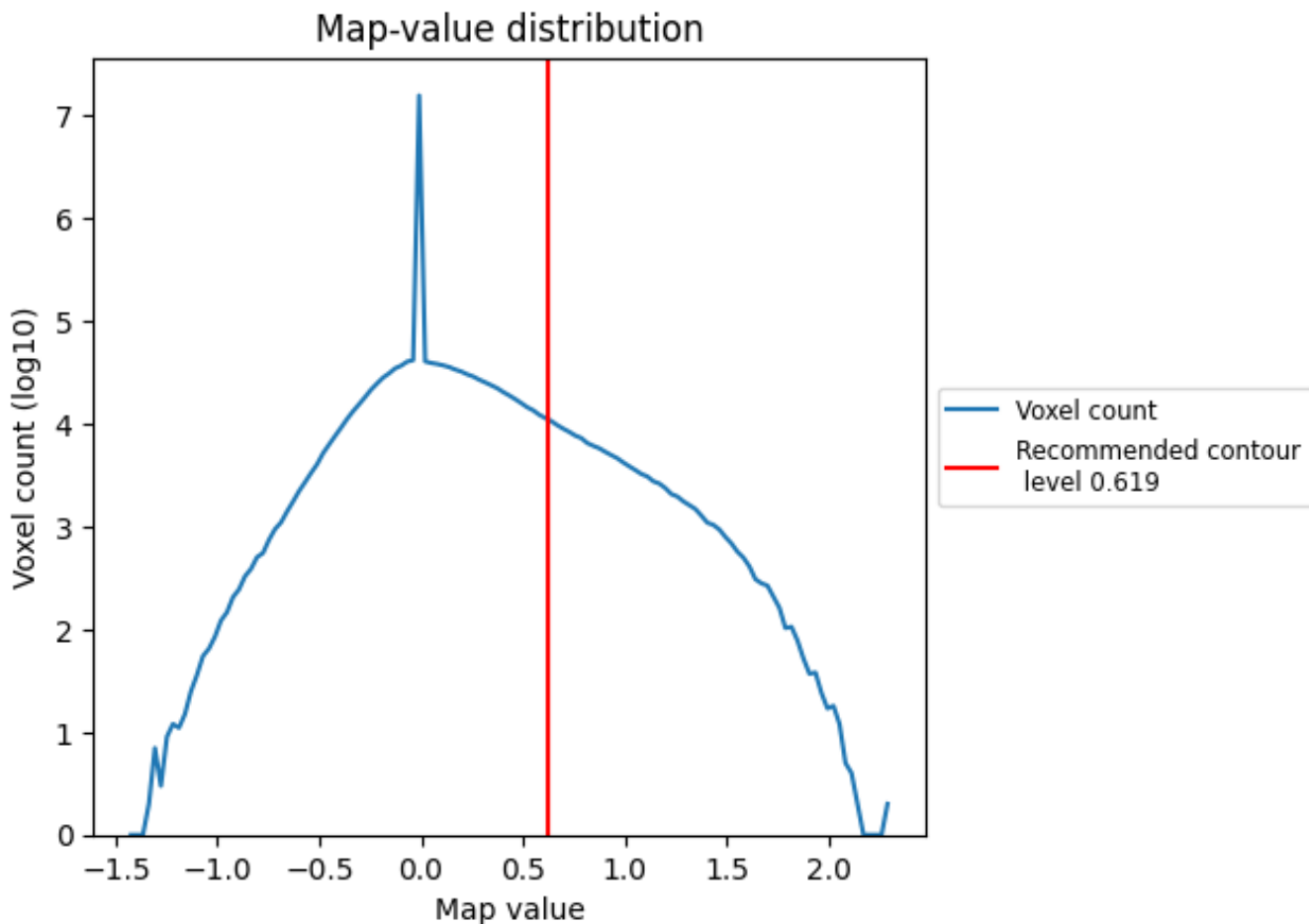
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

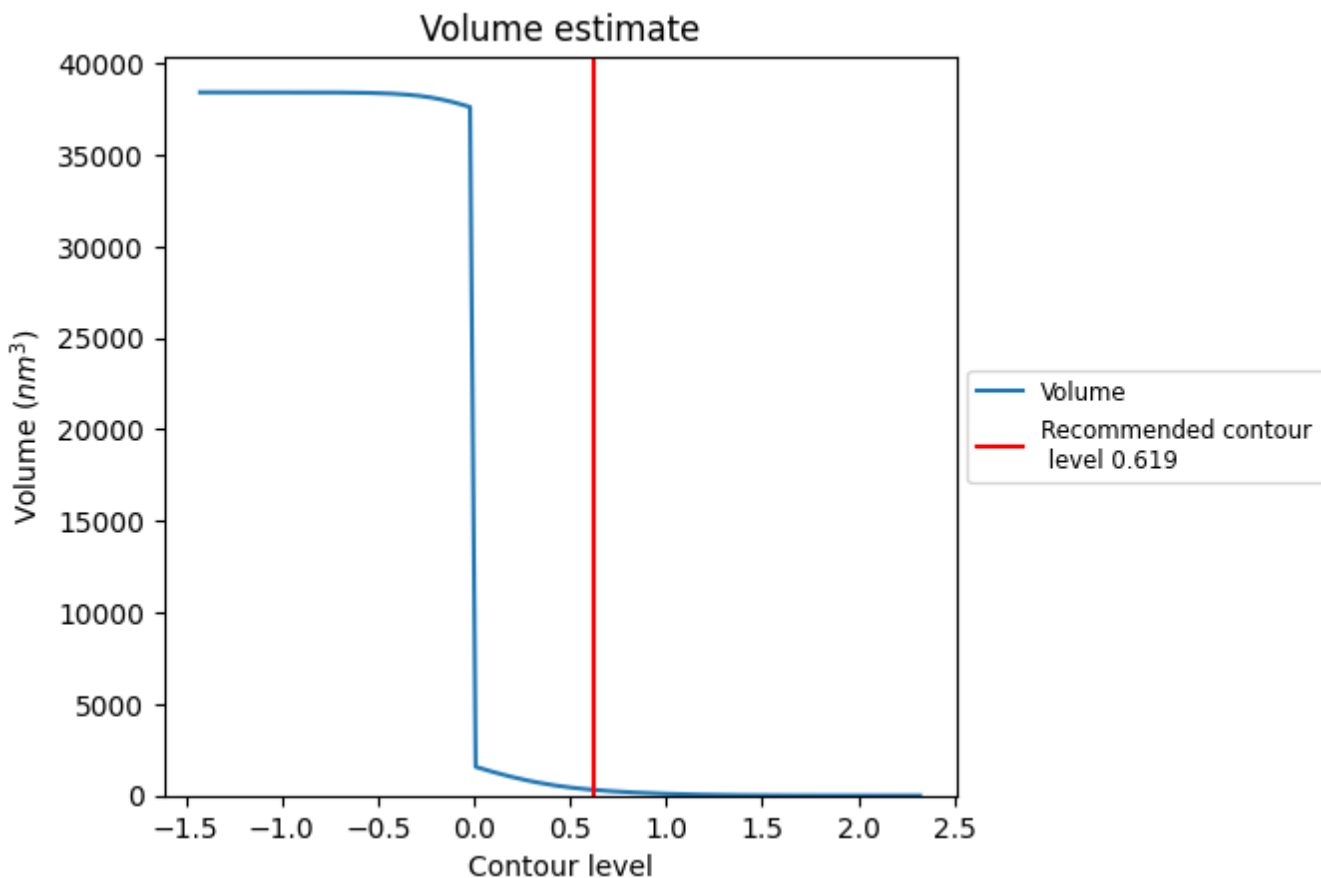
This section contains the results of statistical analysis of the map.

### 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.

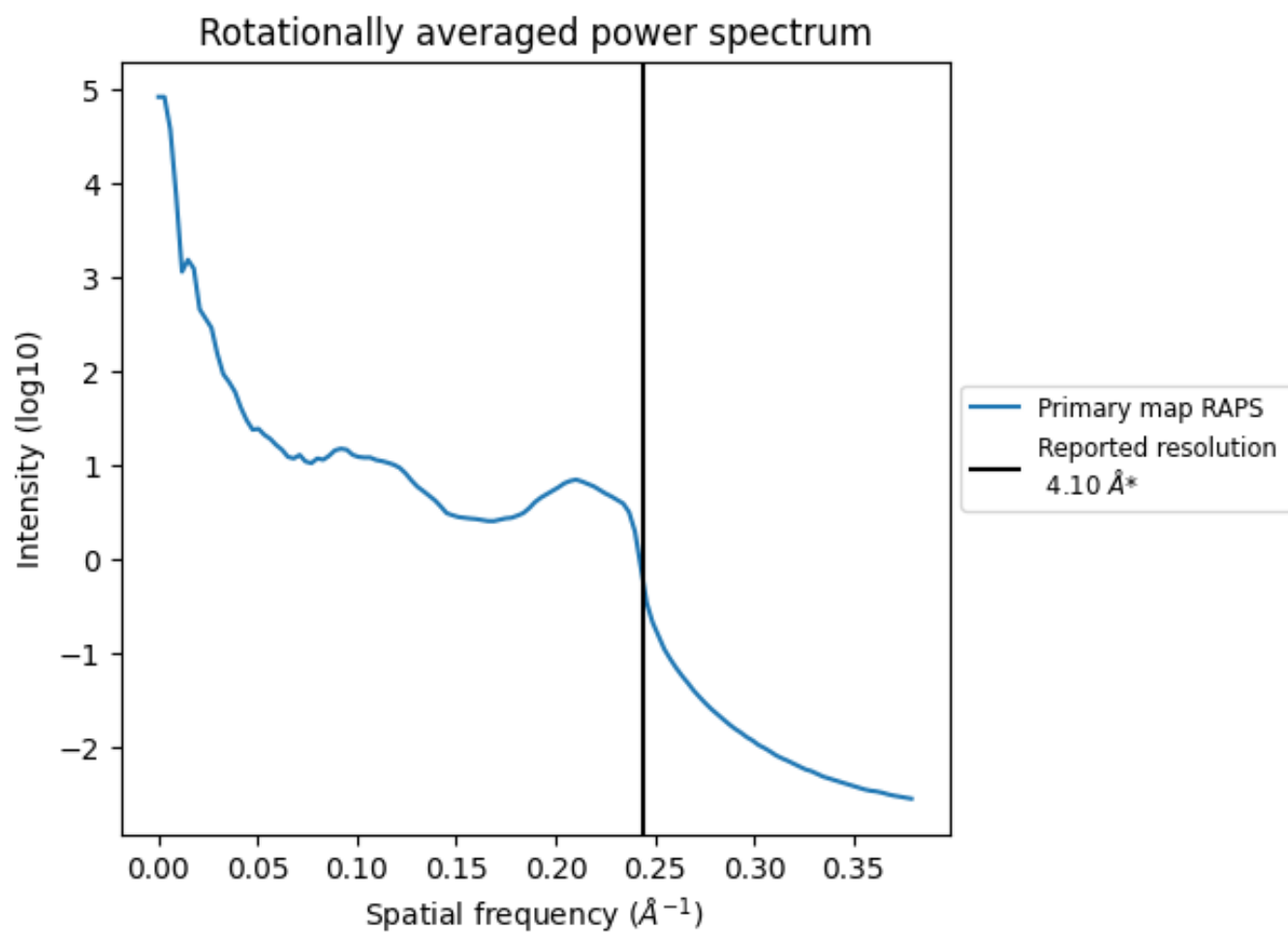
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 315 nm<sup>3</sup>; this corresponds to an approximate mass of 285 kDa.

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

### 7.3 Rotationally averaged power spectrum [i](#)



\*Reported resolution corresponds to spatial frequency of 0.244 Å<sup>-1</sup>

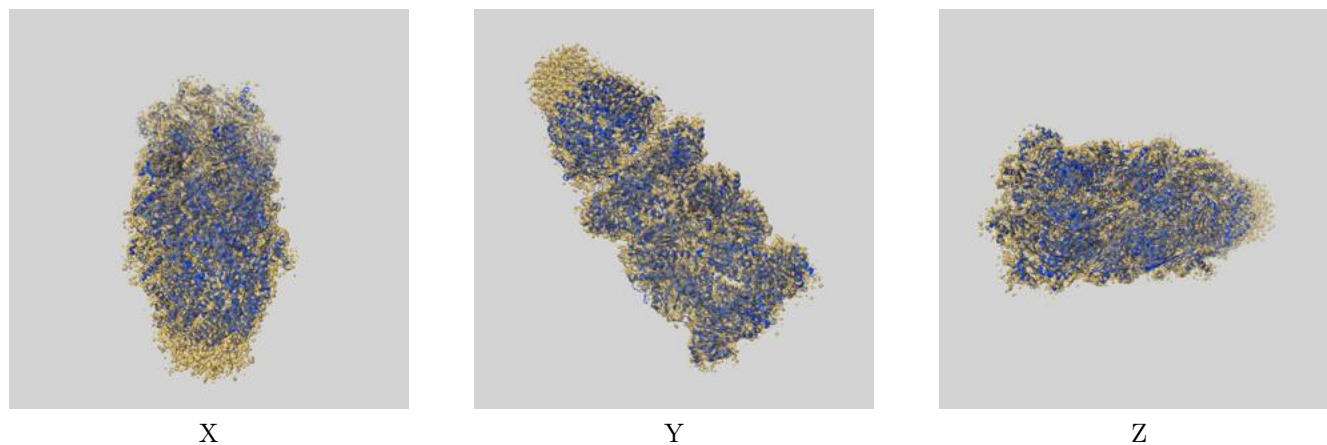
## 8 Fourier-Shell correlation

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

## 9 Map-model fit [i](#)

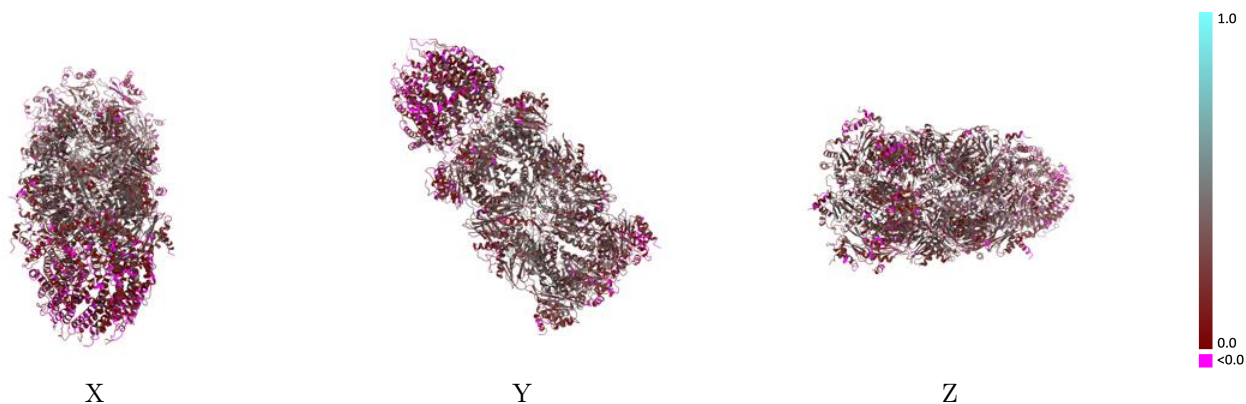
This section contains information regarding the fit between EMDB map EMD-30824 and PDB model 7DR6. Per-residue inclusion information can be found in section 3 on page 9.

### 9.1 Map-model overlay [i](#)



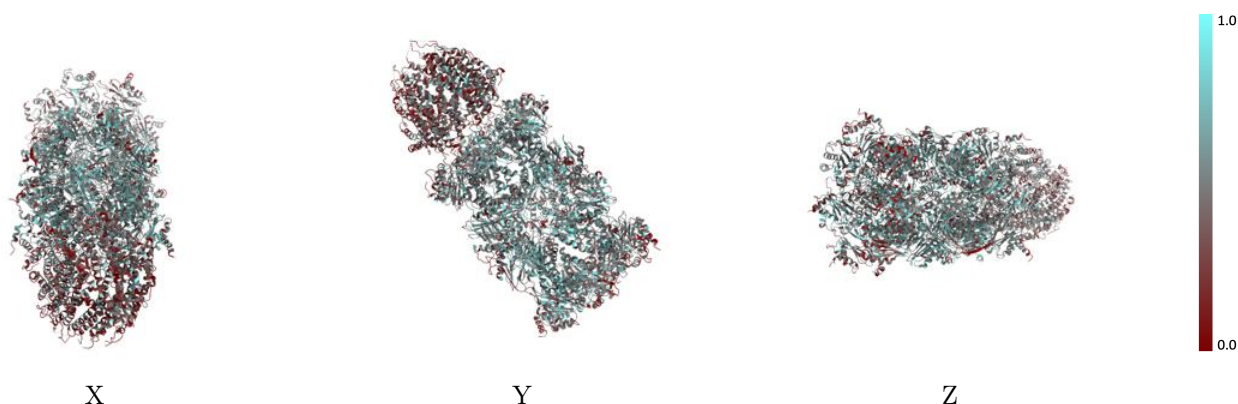
The images above show the 3D surface view of the map at the recommended contour level 0.619 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



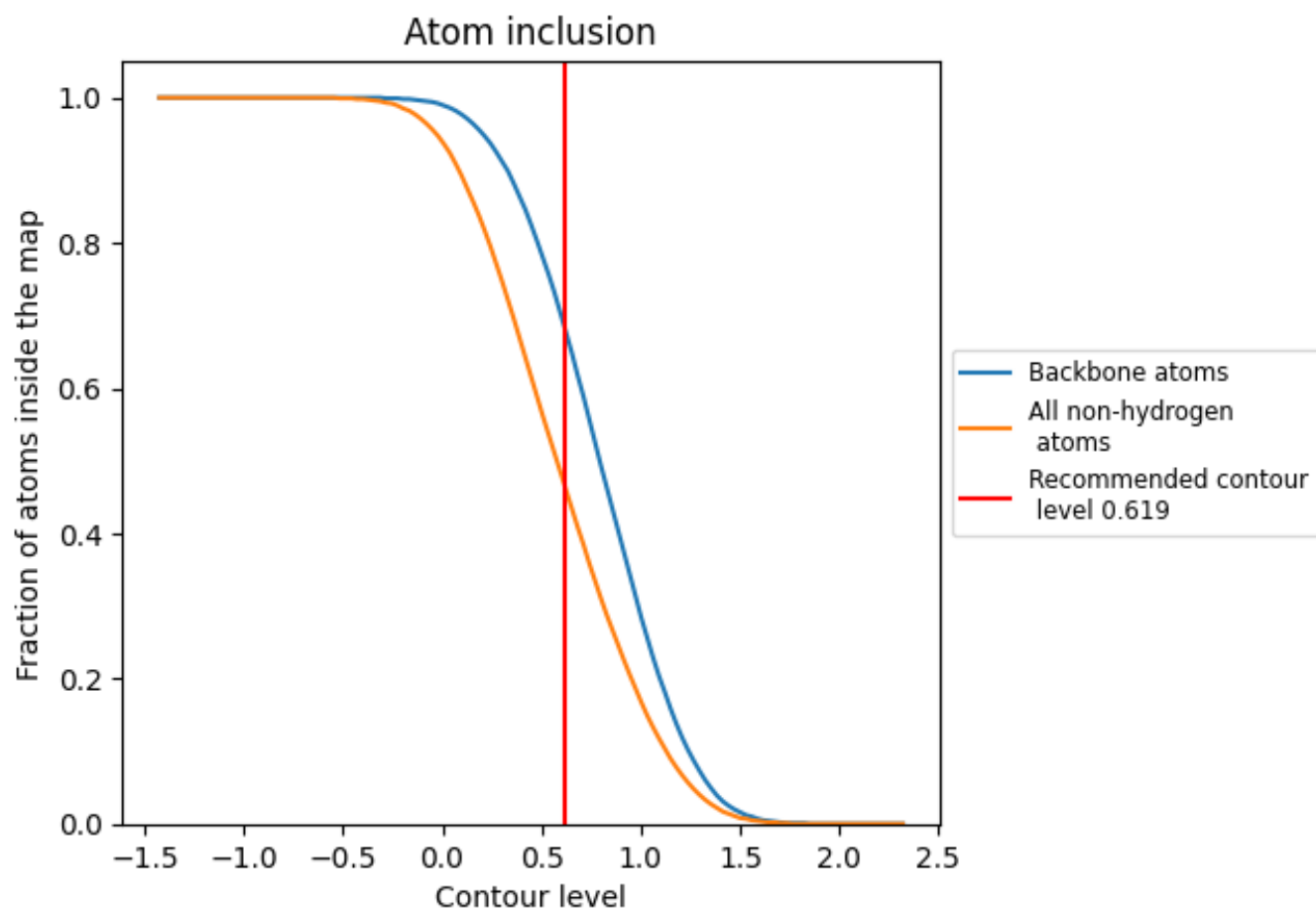
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.619).








































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 68% 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 (0.619) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.4640	 0.2400
1	 0.5170	 0.2920
2	 0.5310	 0.2430
A	 0.3710	 0.1670
B	 0.3290	 0.1390
C	 0.3180	 0.1130
D	 0.3310	 0.1600
E	 0.2950	 0.1240
F	 0.2720	 0.0870
G	 0.3160	 0.1060
H	 0.5310	 0.3120
I	 0.5090	 0.2890
J	 0.5110	 0.2890
K	 0.4960	 0.2680
L	 0.5200	 0.2840
M	 0.5310	 0.2810
N	 0.4950	 0.2640
O	 0.4830	 0.2330
P	 0.4240	 0.1750
Q	 0.4840	 0.2320
R	 0.5150	 0.2770
S	 0.5300	 0.3110
T	 0.5300	 0.2860
U	 0.4910	 0.2600
V	 0.5050	 0.2960
W	 0.5490	 0.3100
X	 0.5140	 0.3000
Y	 0.5570	 0.3170
Z	 0.5510	 0.2920
a	 0.4880	 0.2780
b	 0.4300	 0.2190
c	 0.4610	 0.2200
d	 0.4300	 0.1920
e	 0.4500	 0.2300
f	 0.5120	 0.2870
g	 0.4920	 0.2890

