



## Full wwPDB EM Validation Report ⓘ

Nov 14, 2022 – 02:43 PM JST

PDB ID : 6J2X  
EMDB ID : EMD-9772  
Title : Yeast proteasome in resting state (C1-a)  
Authors : Cong, Y.  
Deposited on : 2019-01-03  
Resolution : 3.80 Å (reported)

This is a Full wwPDB EM Validation 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:

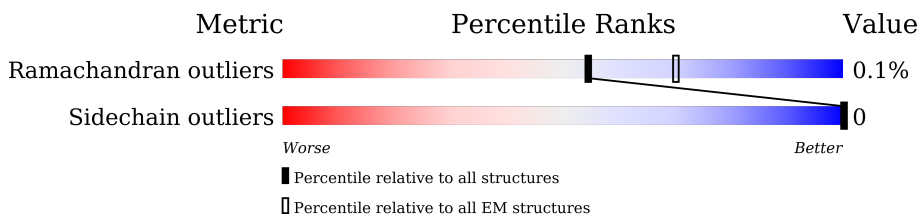
EMDB validation analysis : 0.0.1.dev43  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.31.2

# 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 3.80 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	1	215	
1	b	215	
2	2	261	
2	i	261	
3	3	205	
3	h	205	
4	4	198	
4	g	198	
5	5	287	

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Mol	Chain	Length	Quality of chain
5	f	287	74% 26%
6	6	241	92% 8%
6	e	241	92% 8%
7	7	266	88% 12%
7	a	266	88% 12%
8	A	252	96%
8	c	252	96%
9	B	250	100%
9	j	250	100%
10	C	258	95% 5%
10	d	258	95% 5%
11	D	254	95% 5%
11	n	254	95% 5%
12	E	260	93% 7%
12	m	260	93% 7%
13	F	234	100%
13	l	234	100%
14	G	288	84% 16%
14	k	288	85% 15%
15	H	467	76% 24%
16	I	437	83% 17%
17	J	405	92% 8%
18	K	428	88% 11%
19	L	437	85% 15%
20	M	434	84% 15%

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Mol	Chain	Length	Quality of chain
21	N	945	
22	O	393	
23	P	445	
24	Q	434	
25	R	429	
26	S	523	
27	T	274	
28	U	338	
29	V	306	
30	W	268	
31	X	156	
32	Y	89	
33	Z	993	

## 2 Entry composition [i](#)

There are 33 unique types of molecules in this entry. The entry contains 106176 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 beta type-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	1	205	Total	C	N	O	S	0	0
			1576	996	261	312	7		
1	b	205	Total	C	N	O	S	0	0
			1576	996	261	312	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	2	222	Total	C	N	O	S	0	0
			1684	1061	293	323	7		
2	i	222	Total	C	N	O	S	0	0
			1684	1061	293	323	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	3	204	Total	C	N	O	S	0	0
			1581	1010	258	305	8		
3	h	204	Total	C	N	O	S	0	0
			1581	1010	258	305	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	4	198	Total	C	N	O	S	0	0
			1585	1005	269	305	6		
4	g	198	Total	C	N	O	S	0	0
			1585	1005	269	305	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	5	212	Total	C	N	O	S	0	0
			1644	1045	280	312	7		
5	f	212	Total	C	N	O	S	0	0
			1644	1045	280	312	7		

- Molecule 6 is a protein called PROTEASOME COMPONENT C5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	6	222	Total	C	N	O	S	0	0
			1757	1115	303	335	4		
6	e	222	Total	C	N	O	S	0	0
			1757	1115	303	335	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	7	233	Total	C	N	O	S	0	0
			1824	1154	312	351	7		
7	a	233	Total	C	N	O	S	0	0
			1824	1154	312	351	7		

- Molecule 8 is a protein called Proteasome subunit alpha type-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	A	243	Total	C	N	O	S	0	0
			1921	1221	322	370	8		
8	c	243	Total	C	N	O	S	0	0
			1921	1221	322	370	8		

- Molecule 9 is a protein called Proteasome subunit alpha type-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	B	250	Total	C	N	O	S	0	0
			1915	1219	315	377	4		
9	j	250	Total	C	N	O	S	0	0
			1915	1219	315	377	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	C	244	Total	C	N	O	S	0	0
			1904	1201	321	379	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
10	d	244	Total	C	N	O	S	0	0
			1904	1201	321	379	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
11	D	241	Total	C	N	O	S	0	0
			1890	1181	331	374	4		
11	n	241	Total	C	N	O	S	0	0
			1890	1181	331	374	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	E	242	Total	C	N	O	S	0	0
			1861	1162	314	378	7		
12	m	242	Total	C	N	O	S	0	0
			1861	1162	314	378	7		

- Molecule 13 is a protein called Proteasome subunit alpha type-6.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	F	233	Total	C	N	O	S	0	0
			1795	1129	312	350	4		
13	l	233	Total	C	N	O	S	0	0
			1795	1129	312	350	4		

- Molecule 14 is a protein called Probable proteasome subunit alpha type-7.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	G	243	Total	C	N	O	S	0	0
			1888	1201	328	355	4		
14	k	244	Total	C	N	O	S	0	0
			1896	1205	330	357	4		

- Molecule 15 is a protein called 26S proteasome regulatory subunit 7 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	H	355	Total	C	N	O	S	0	0
			2787	1755	500	515	17		

- Molecule 16 is a protein called 26S PROTEASE REGULATORY SUBUNIT 4 HOMOLOG.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	I	362	2822	1773	471	563	15	0	0

- Molecule 17 is a protein called 26S proteasome regulatory subunit 8 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	J	373	2928	1837	527	547	17	0	0

- Molecule 18 is a protein called 26S proteasome regulatory subunit 6B homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	K	381	3019	1898	530	581	10	0	0

- Molecule 19 is a protein called 26S proteasome subunit RPT4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	L	371	2937	1852	519	554	12	0	0

- Molecule 20 is a protein called 26S proteasome regulatory subunit 6A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	M	367	2866	1799	503	553	11	0	0

- Molecule 21 is a protein called 26S proteasome regulatory subunit RPN2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	N	849	6562	4174	1099	1261	28	0	0

- Molecule 22 is a protein called 26S proteasome regulatory subunit RPN9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	O	387	3182	2047	520	606	9	0	0

- Molecule 23 is a protein called 26S PROTEASOME REGULATORY SUBUNIT RPN5.



Mol	Chain	Residues	Atoms					AltConf	Trace
23	P	432	Total	C	N	O	S	0	0
			3545	2260	592	684	9		

- Molecule 24 is a protein called 26S proteasome regulatory subunit RPN6.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Q	431	Total	C	N	O	S	0	0
			3471	2205	574	676	16		

- Molecule 25 is a protein called 26S proteasome regulatory subunit RPN7.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	R	400	Total	C	N	O	S	0	0
			3218	2051	527	630	10		

- Molecule 26 is a protein called 26S proteasome regulatory subunit RPN3.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	S	475	Total	C	N	O	S	0	0
			3894	2488	653	738	15		

- Molecule 27 is a protein called 26S proteasome regulatory subunit RPN12.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	T	272	Total	C	N	O	S	0	0
			2235	1432	355	441	7		

- Molecule 28 is a protein called 26S proteasome regulatory subunit RPN8.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	U	255	Total	C	N	O	S	0	0
			2061	1312	352	391	6		

- Molecule 29 is a protein called Ubiquitin carboxyl-terminal hydrolase RPN11.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	V	258	Total	C	N	O	S	0	0
			2025	1273	344	395	13		

- Molecule 30 is a protein called 26S proteasome regulatory subunit RPN10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	W	197	1534	962	269	300	3	0	0

- Molecule 31 is a protein called 26S proteasome regulatory subunit RPN13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	X	111	906	586	148	169	3	0	0

- Molecule 32 is a protein called 26S proteasome complex subunit SEM1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
32	Y	27	236	143	39	54	0	0

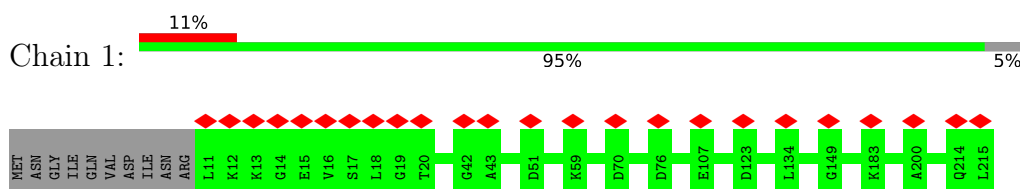
- Molecule 33 is a protein called 26S proteasome regulatory subunit RPN1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	Z	813	6290	3995	1029	1237	29	0	0

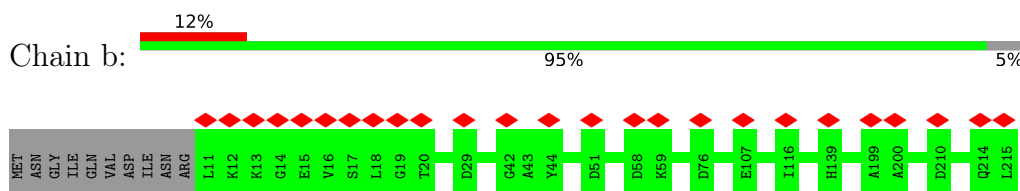
### 3 Residue-property plots [i](#)

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.

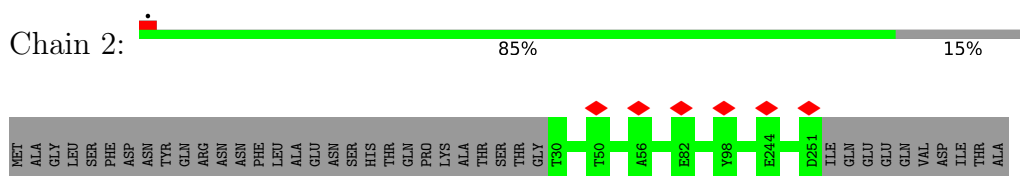
- Molecule 1: Proteasome subunit beta type-1



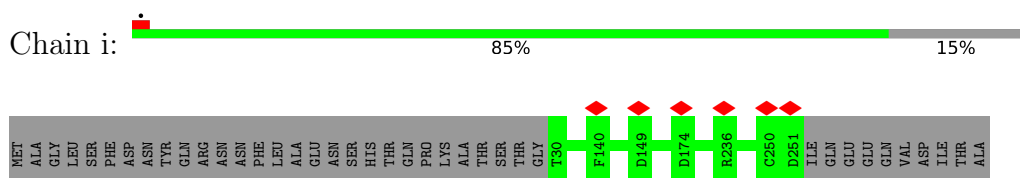
- Molecule 1: Proteasome subunit beta type-1



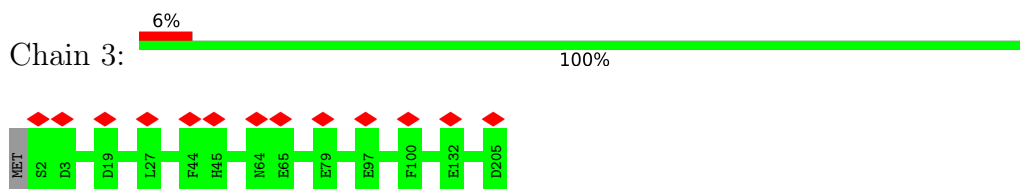
- Molecule 2: Proteasome subunit beta type-2



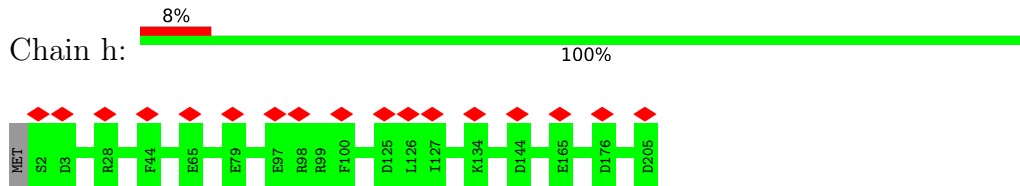
- Molecule 2: Proteasome subunit beta type-2



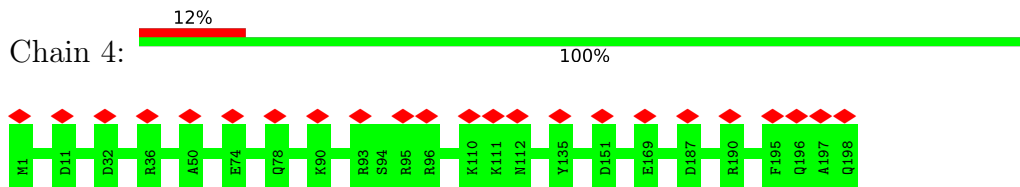
- Molecule 3: Proteasome subunit beta type-3



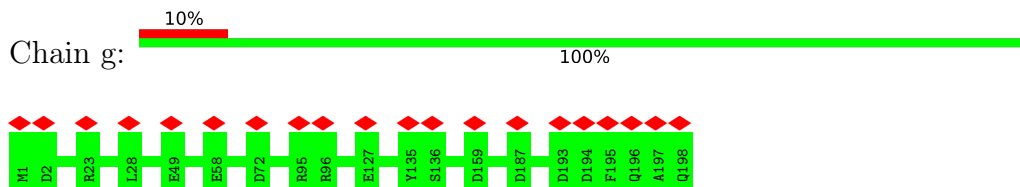
• Molecule 3: Proteasome subunit beta type-3



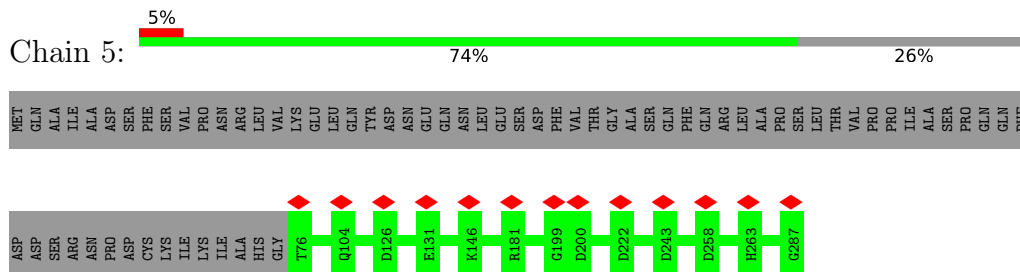
• Molecule 4: Proteasome subunit beta type-4



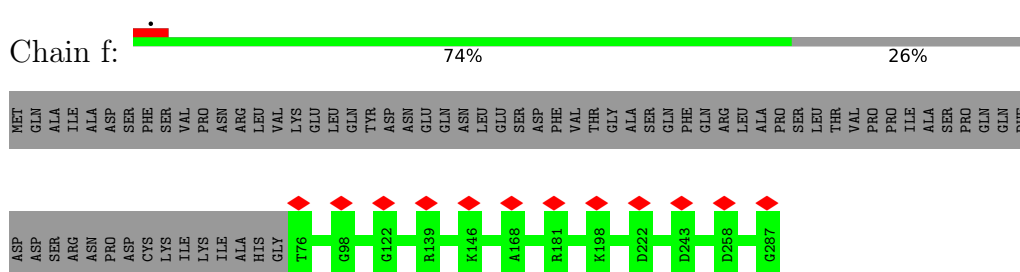
• Molecule 4: Proteasome subunit beta type-4



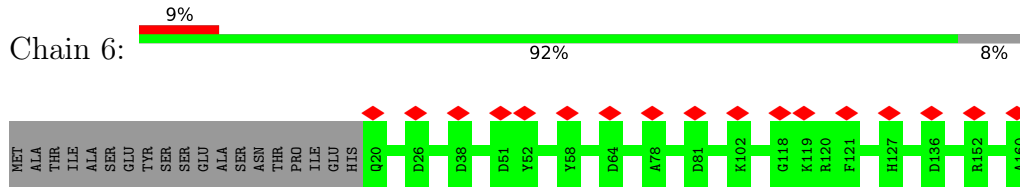
• Molecule 5: Proteasome subunit beta type-5



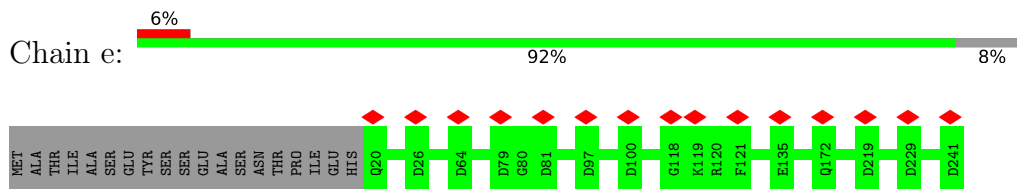
• Molecule 5: Proteasome subunit beta type-5



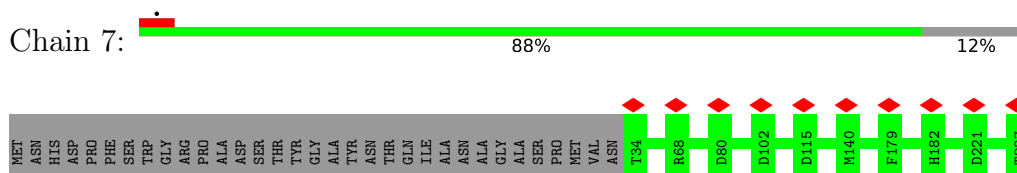
• Molecule 6: PROTEASOME COMPONENT C5



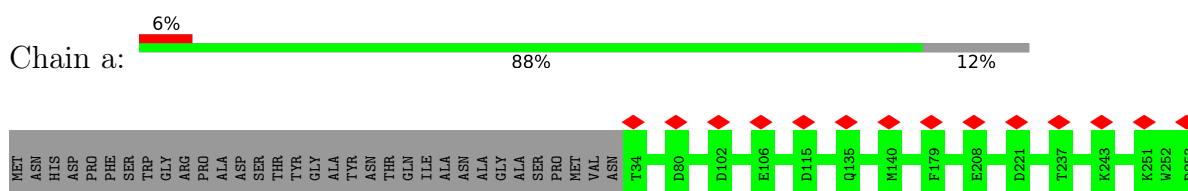
• Molecule 6: PROTEASOME COMPONENT C5



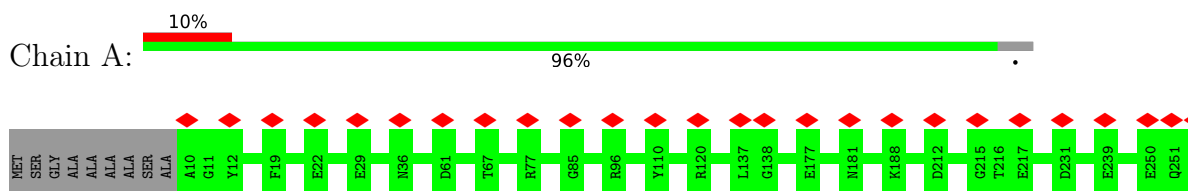
• Molecule 7: Proteasome subunit beta type-7



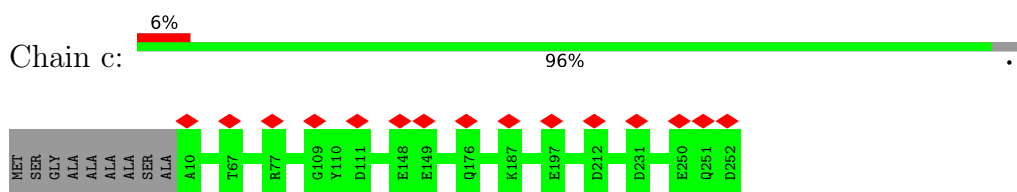
• Molecule 7: Proteasome subunit beta type-7



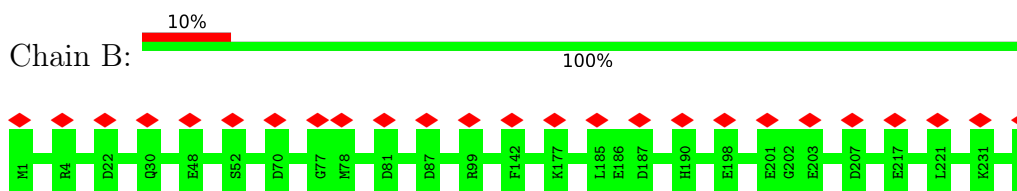
• Molecule 8: Proteasome subunit alpha type-1



• Molecule 8: Proteasome subunit alpha type-1



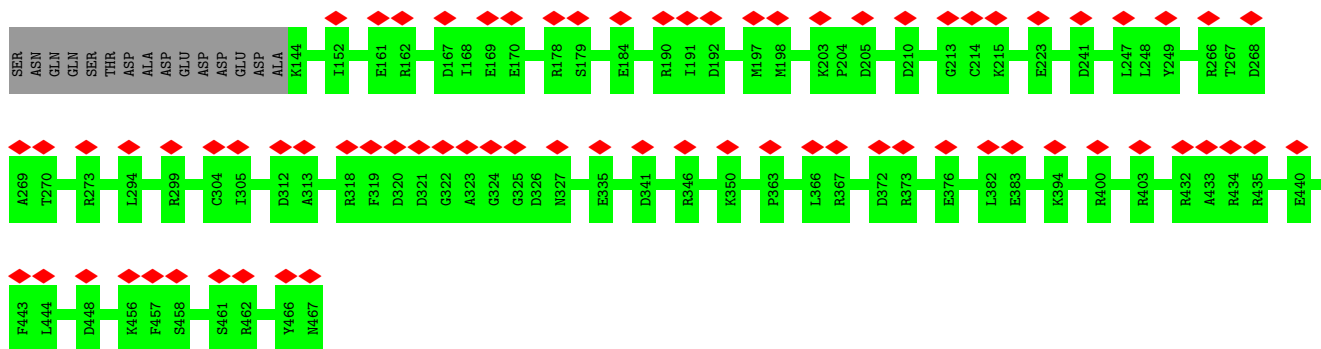
• Molecule 9: Proteasome subunit alpha type-2



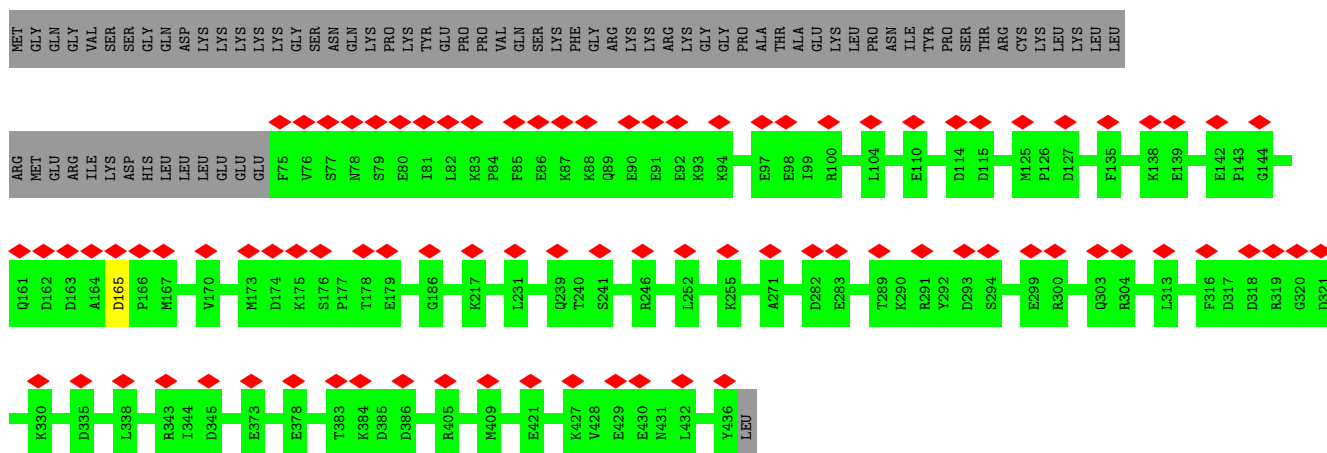
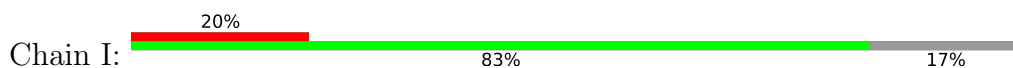
• Molecule 9: Proteasome subunit alpha type-2



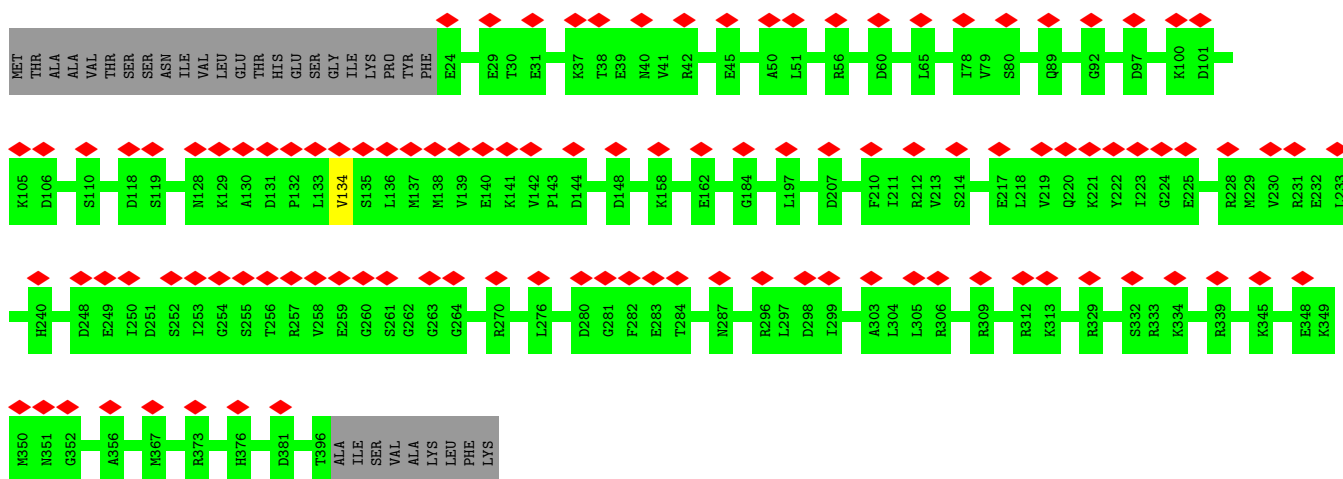
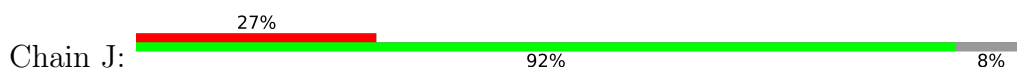




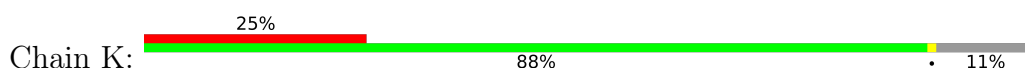
• Molecule 16: 26S PROTEASE REGULATORY SUBUNIT 4 HOMOLOG



• Molecule 17: 26S proteasome regulatory subunit 8 homolog



• Molecule 18: 26S proteasome regulatory subunit 6B homolog



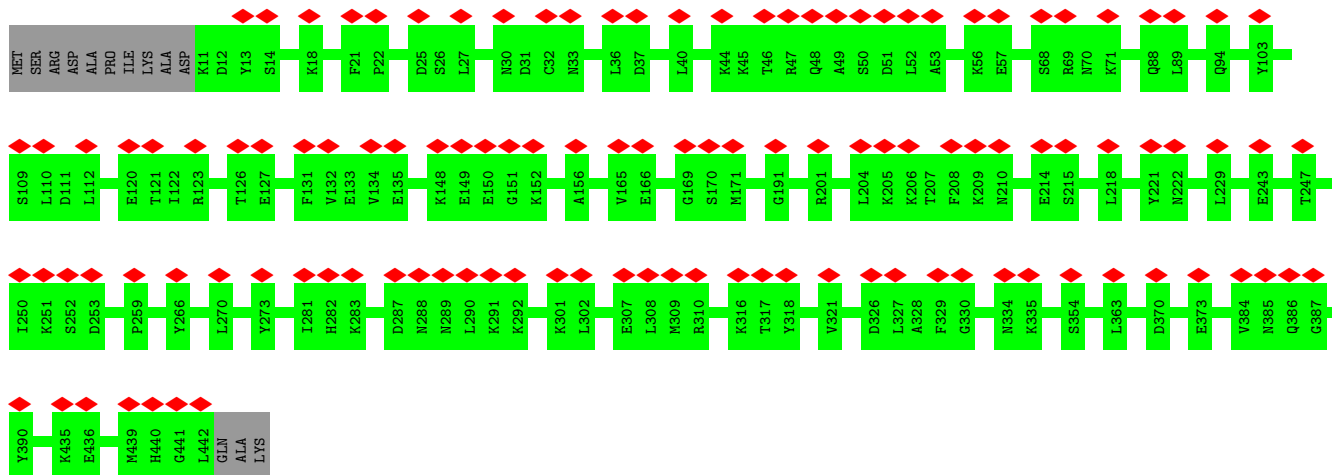




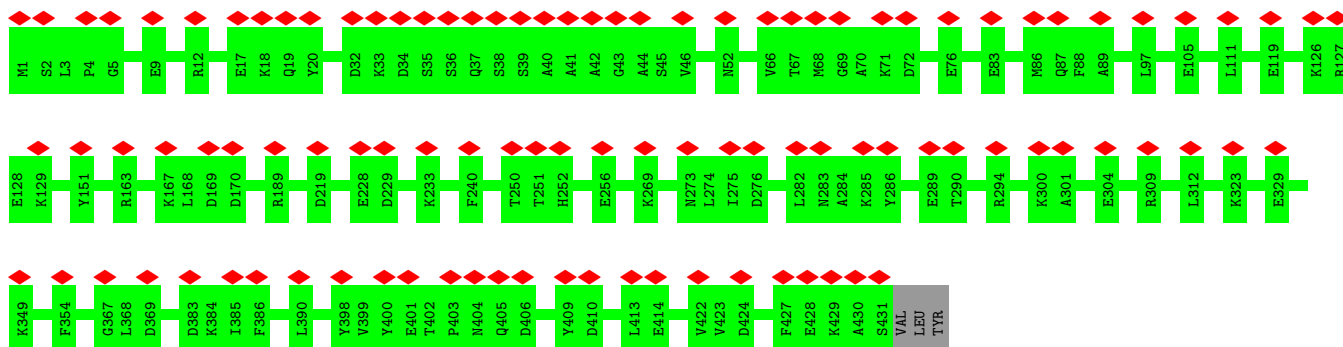




• Molecule 23: 26S PROTEASOME REGULATORY SUBUNIT RPN5

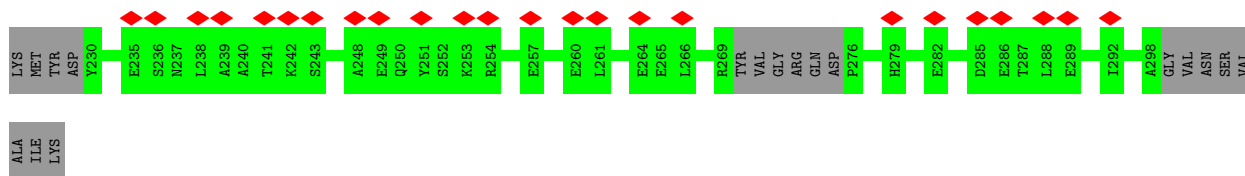


• Molecule 24: 26S proteasome regulatory subunit RPN6

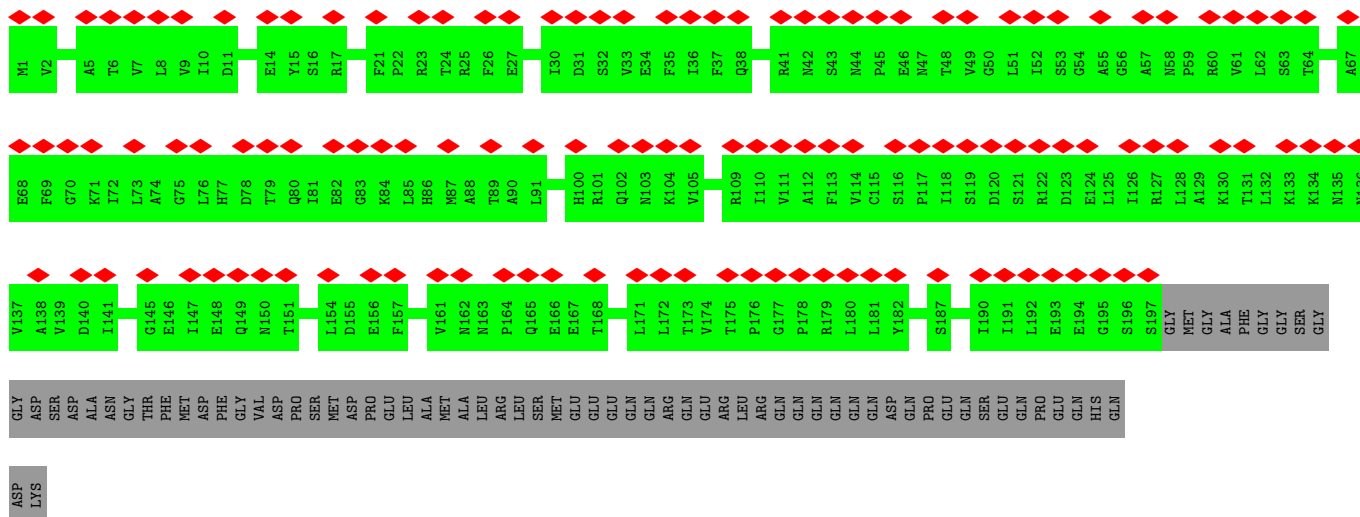
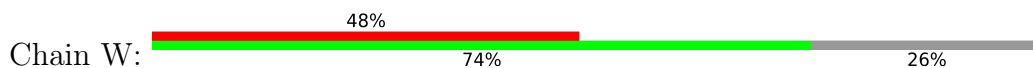




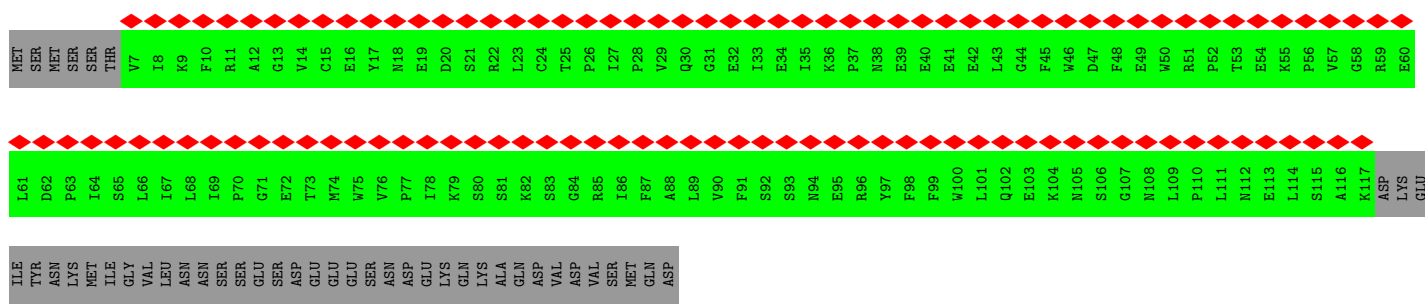




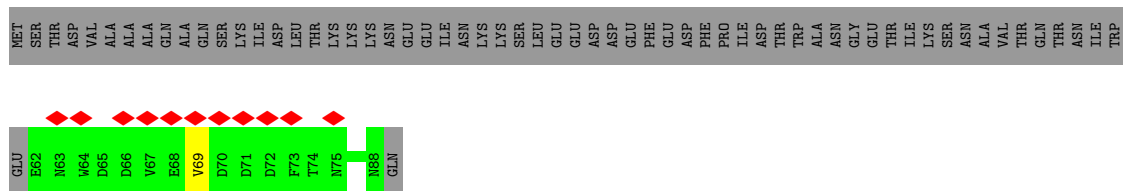
• Molecule 30: 26S proteasome regulatory subunit RPN10



• Molecule 31: 26S proteasome regulatory subunit RPN13



• Molecule 32: 26S proteasome complex subunit SEM1



• Molecule 33: 26S proteasome regulatory subunit RPN1



V783	D843	M903	A963
S784	A844	L904	E964
V785	L845	N905	L965
S786	F846	A906	E966
D787	I847	G907	T967
P788	T848	I908	D968
Q789	R849	R909	E969
M790	L850	P910	Y970
K791	A851	K911	I971
V792	Q852	F912	S972
F793	G853	I913	Y973
D794	L854	L914	T974
T795	L855	A915	S975
L796	H856	L916	H976
T797	L857	N917	I977
R798	G858	D918	E978
F799	K859	E919	G979
S800	G860	G920	V980
H801	T861	E921	V981
D802	M862	P922	I982
A803	T863	I923	L983
D804	M864	K924	K984
L805	D865	V925	K985
E806	V866	N926	N986
V807	F867	V927	P987
S808	N868	R928	D988
M809	D869	V929	Y989
N810	A870	G930	R990
S811	H871	Q931	E991
I812	V872	ALA	E992
F813	L873	VAL	E993
A814	N874	THR	
M815	K875	VAL	
G816	V876	GLY	
L817	T877	GLN	
C818	L878	ALA	
G819	A879	GLY	
A820	S880	ARG	
G821	I881	PRO	
M823	T822	LYS	
N824	T883	ILE	
A825	T884	GLY	
R826	A885	TRP	
L827	V886	ILE	
A828	G887	THR	
Q829	L888	GLN	
L830	V889	SER	
L831	S890	THR	
R832	P891	THR	
Q833	S892	GLY	
L834	F893	ILE	
A835	M894	TRP	
S836	L895	ILE	
Y837	K896	GLN	
Y838	H897	SER	
R840	H898	THR	
E841	Q899	THR	
Q842	L900	THR	
	F901	THR	
	Y902		
		P954	
		V955	
		L956	
		L957	
		N958	
		H959	
		G960	
		E961	
		R962	



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	49507	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	2.766	Depositor
Minimum map value	-1.268	Depositor
Average map value	0.010	Depositor
Map value standard deviation	0.098	Depositor
Recommended contour level	0.704	Depositor
Map size (Å)	474.47998, 474.47998, 474.47998	wwPDB
Map dimensions	360, 360, 360	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	1	0.24	0/1605	0.42	0/2171
1	b	0.23	0/1605	0.43	0/2171
2	2	0.23	0/1715	0.42	0/2326
2	i	0.23	0/1715	0.42	0/2326
3	3	0.24	0/1611	0.40	0/2174
3	h	0.24	0/1611	0.41	0/2174
4	4	0.23	0/1613	0.39	0/2173
4	g	0.23	0/1613	0.39	0/2173
5	5	0.23	0/1681	0.39	0/2274
5	f	0.23	0/1681	0.40	0/2274
6	6	0.24	0/1795	0.40	0/2420
6	e	0.24	0/1795	0.40	0/2420
7	7	0.24	0/1855	0.42	0/2514
7	a	0.24	0/1855	0.41	0/2514
8	A	0.24	0/1959	0.39	0/2652
8	c	0.24	0/1959	0.39	0/2652
9	B	0.24	0/1952	0.41	0/2642
9	j	0.24	0/1952	0.40	0/2642
10	C	0.23	0/1934	0.40	0/2618
10	d	0.24	0/1934	0.40	0/2618
11	D	0.22	0/1919	0.39	0/2598
11	n	0.23	0/1919	0.39	0/2598
12	E	0.23	0/1886	0.39	0/2541
12	m	0.23	0/1886	0.40	0/2541
13	F	0.24	0/1823	0.41	0/2463
13	l	0.24	0/1823	0.43	0/2463
14	G	0.24	0/1928	0.39	0/2603
14	k	0.23	0/1936	0.39	0/2614
15	H	0.24	0/2834	0.40	0/3816
16	I	0.26	1/2860 (0.0%)	0.41	0/3856
17	J	0.23	0/2964	0.39	0/3981
18	K	0.33	1/3062 (0.0%)	0.41	0/4132
19	L	0.32	1/2981 (0.0%)	0.40	0/4008
20	M	0.24	0/2903	0.41	0/3909

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
21	N	0.23	0/6670	0.39	0/9023
22	O	0.23	0/3243	0.39	0/4374
23	P	0.23	0/3599	0.38	0/4854
24	Q	0.23	0/3527	0.36	0/4748
25	R	0.23	0/3272	0.38	0/4412
26	S	0.23	0/3966	0.37	0/5355
27	T	0.23	0/2279	0.38	0/3077
28	U	0.23	0/2087	0.37	0/2811
29	V	0.23	0/2054	0.42	0/2770
30	W	0.23	0/1557	0.40	0/2111
31	X	0.23	0/931	0.40	0/1262
32	Y	0.22	0/239	0.37	0/322
33	Z	0.23	0/6404	0.39	0/8686
All	All	0.24	3/107992 (0.0%)	0.40	0/145856

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
18	K	265	ALA	C-N	12.60	1.58	1.34
19	L	274	GLU	C-N	11.88	1.56	1.34
16	I	165	ASP	C-N	6.37	1.46	1.34

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

## 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	1	203/215 (94%)	194 (96%)	9 (4%)	0	100	100
1	b	203/215 (94%)	191 (94%)	12 (6%)	0	100	100
2	2	220/261 (84%)	214 (97%)	6 (3%)	0	100	100
2	i	220/261 (84%)	211 (96%)	9 (4%)	0	100	100
3	3	202/205 (98%)	194 (96%)	8 (4%)	0	100	100
3	h	202/205 (98%)	195 (96%)	7 (4%)	0	100	100
4	4	196/198 (99%)	187 (95%)	9 (5%)	0	100	100
4	g	196/198 (99%)	190 (97%)	6 (3%)	0	100	100
5	5	210/287 (73%)	200 (95%)	10 (5%)	0	100	100
5	f	210/287 (73%)	201 (96%)	9 (4%)	0	100	100
6	6	220/241 (91%)	213 (97%)	7 (3%)	0	100	100
6	e	220/241 (91%)	212 (96%)	8 (4%)	0	100	100
7	7	231/266 (87%)	219 (95%)	12 (5%)	0	100	100
7	a	231/266 (87%)	226 (98%)	5 (2%)	0	100	100
8	A	241/252 (96%)	235 (98%)	6 (2%)	0	100	100
8	c	241/252 (96%)	234 (97%)	7 (3%)	0	100	100
9	B	248/250 (99%)	240 (97%)	8 (3%)	0	100	100
9	j	248/250 (99%)	239 (96%)	9 (4%)	0	100	100
10	C	242/258 (94%)	233 (96%)	9 (4%)	0	100	100
10	d	242/258 (94%)	234 (97%)	8 (3%)	0	100	100
11	D	239/254 (94%)	232 (97%)	7 (3%)	0	100	100
11	n	239/254 (94%)	231 (97%)	8 (3%)	0	100	100
12	E	240/260 (92%)	230 (96%)	10 (4%)	0	100	100
12	m	240/260 (92%)	230 (96%)	10 (4%)	0	100	100
13	F	231/234 (99%)	222 (96%)	9 (4%)	0	100	100
13	l	231/234 (99%)	217 (94%)	14 (6%)	0	100	100
14	G	241/288 (84%)	232 (96%)	9 (4%)	0	100	100
14	k	242/288 (84%)	233 (96%)	9 (4%)	0	100	100
15	H	351/467 (75%)	313 (89%)	38 (11%)	0	100	100
16	I	360/437 (82%)	324 (90%)	36 (10%)	0	100	100
17	J	371/405 (92%)	344 (93%)	26 (7%)	1 (0%)	41	74
18	K	379/428 (89%)	338 (89%)	39 (10%)	2 (0%)	29	66

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	L	369/437 (84%)	339 (92%)	30 (8%)	0	100	100
20	M	363/434 (84%)	325 (90%)	37 (10%)	1 (0%)	41	74
21	N	843/945 (89%)	810 (96%)	33 (4%)	0	100	100
22	O	385/393 (98%)	342 (89%)	43 (11%)	0	100	100
23	P	430/445 (97%)	395 (92%)	35 (8%)	0	100	100
24	Q	429/434 (99%)	404 (94%)	25 (6%)	0	100	100
25	R	398/429 (93%)	355 (89%)	41 (10%)	2 (0%)	29	66
26	S	473/523 (90%)	452 (96%)	20 (4%)	1 (0%)	47	79
27	T	270/274 (98%)	245 (91%)	25 (9%)	0	100	100
28	U	245/338 (72%)	238 (97%)	7 (3%)	0	100	100
29	V	252/306 (82%)	231 (92%)	20 (8%)	1 (0%)	34	70
30	W	195/268 (73%)	183 (94%)	12 (6%)	0	100	100
31	X	109/156 (70%)	96 (88%)	13 (12%)	0	100	100
32	Y	25/89 (28%)	20 (80%)	4 (16%)	1 (4%)	3	28
33	Z	807/993 (81%)	753 (93%)	53 (7%)	1 (0%)	51	83
All	All	13383/15139 (88%)	12596 (94%)	777 (6%)	10 (0%)	54	83

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
17	J	134	VAL
18	K	158	ILE
18	K	160	VAL
20	M	167	VAL
25	R	26	VAL
25	R	241	ILE
29	V	165	ILE
32	Y	69	VAL
33	Z	442	VAL
26	S	83	PRO

### 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	1	169/178 (95%)	169 (100%)	0	100	100
1	b	169/178 (95%)	169 (100%)	0	100	100
2	2	181/214 (85%)	181 (100%)	0	100	100
2	i	181/214 (85%)	181 (100%)	0	100	100
3	3	172/173 (99%)	172 (100%)	0	100	100
3	h	172/173 (99%)	172 (100%)	0	100	100
4	4	175/175 (100%)	175 (100%)	0	100	100
4	g	175/175 (100%)	175 (100%)	0	100	100
5	5	169/235 (72%)	169 (100%)	0	100	100
5	f	169/235 (72%)	169 (100%)	0	100	100
6	6	185/201 (92%)	185 (100%)	0	100	100
6	e	185/201 (92%)	185 (100%)	0	100	100
7	7	199/224 (89%)	199 (100%)	0	100	100
7	a	199/224 (89%)	199 (100%)	0	100	100
8	A	207/210 (99%)	207 (100%)	0	100	100
8	c	207/210 (99%)	207 (100%)	0	100	100
9	B	209/209 (100%)	209 (100%)	0	100	100
9	j	209/209 (100%)	209 (100%)	0	100	100
10	C	203/216 (94%)	203 (100%)	0	100	100
10	d	203/216 (94%)	203 (100%)	0	100	100
11	D	213/226 (94%)	213 (100%)	0	100	100
11	n	213/226 (94%)	213 (100%)	0	100	100
12	E	198/215 (92%)	198 (100%)	0	100	100
12	m	198/215 (92%)	198 (100%)	0	100	100
13	F	192/193 (100%)	192 (100%)	0	100	100
13	l	192/193 (100%)	192 (100%)	0	100	100
14	G	200/239 (84%)	200 (100%)	0	100	100
14	k	201/239 (84%)	201 (100%)	0	100	100
15	H	303/399 (76%)	303 (100%)	0	100	100
16	I	319/385 (83%)	319 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
17	J	325/352 (92%)	325 (100%)	0	100	100
18	K	334/374 (89%)	334 (100%)	0	100	100
19	L	317/377 (84%)	317 (100%)	0	100	100
20	M	315/375 (84%)	315 (100%)	0	100	100
21	N	713/797 (90%)	713 (100%)	0	100	100
22	O	363/368 (99%)	363 (100%)	0	100	100
23	P	405/415 (98%)	405 (100%)	0	100	100
24	Q	388/391 (99%)	388 (100%)	0	100	100
25	R	351/379 (93%)	351 (100%)	0	100	100
26	S	447/489 (91%)	447 (100%)	0	100	100
27	T	254/256 (99%)	254 (100%)	0	100	100
28	U	234/308 (76%)	234 (100%)	0	100	100
29	V	227/268 (85%)	227 (100%)	0	100	100
30	W	171/230 (74%)	171 (100%)	0	100	100
31	X	101/144 (70%)	101 (100%)	0	100	100
32	Y	26/81 (32%)	26 (100%)	0	100	100
33	Z	692/850 (81%)	692 (100%)	0	100	100
All	All	11630/13054 (89%)	11630 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (100) such sidechains are listed below:

Mol	Chain	Res	Type
2	2	95	HIS
2	2	115	HIS
3	3	169	GLN
4	4	65	GLN
5	5	263	HIS
6	6	55	ASN
6	6	178	GLN
6	6	216	GLN
7	7	35	GLN
7	7	145	ASN
2	i	115	HIS
2	i	122	HIS

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
2	i	143	HIS
3	h	169	GLN
4	g	112	ASN
4	g	191	GLN
5	f	254	HIS
6	e	55	ASN
6	e	216	GLN
7	a	153	GLN
10	C	147	GLN
11	D	-224	HIS
12	E	23	GLN
13	F	41	ASN
13	F	52	ASN
14	G	90	ASN
14	G	127	ASN
14	G	182	HIS
14	G	183	HIS
8	c	37	GLN
8	c	181	ASN
10	d	120	GLN
11	n	16	HIS
13	l	117	GLN
13	l	210	ASN
14	k	121	GLN
14	k	183	HIS
15	H	95	HIS
15	H	98	GLN
15	H	265	ASN
17	J	25	GLN
17	J	47	GLN
17	J	52	ASN
17	J	181	GLN
17	J	278	GLN
18	K	238	ASN
18	K	285	GLN
18	K	302	GLN
18	K	375	ASN
19	L	302	GLN
20	M	125	GLN
21	N	34	GLN
21	N	226	ASN
21	N	267	GLN

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
21	N	375	HIS
21	N	564	ASN
21	N	719	ASN
21	N	738	GLN
21	N	747	HIS
22	O	122	HIS
22	O	354	GLN
23	P	78	GLN
23	P	348	HIS
23	P	349	ASN
23	P	417	HIS
24	Q	106	GLN
24	Q	145	HIS
24	Q	150	GLN
24	Q	226	HIS
24	Q	346	ASN
24	Q	379	GLN
25	R	73	ASN
26	S	177	ASN
26	S	227	ASN
26	S	283	GLN
26	S	311	GLN
26	S	321	GLN
26	S	334	HIS
26	S	450	ASN
26	S	459	GLN
26	S	469	ASN
27	T	92	ASN
27	T	127	GLN
28	U	75	ASN
28	U	193	GLN
28	U	302	GLN
29	V	73	GLN
29	V	126	GLN
29	V	181	ASN
29	V	190	HIS
29	V	279	HIS
30	W	108	GLN
30	W	184	ASN
31	X	38	ASN
31	X	94	ASN
33	Z	391	ASN

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Mol	Chain	Res	Type
33	Z	532	HIS
33	Z	763	HIS
33	Z	810	ASN
33	Z	976	HIS

### 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 monosaccharides 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.

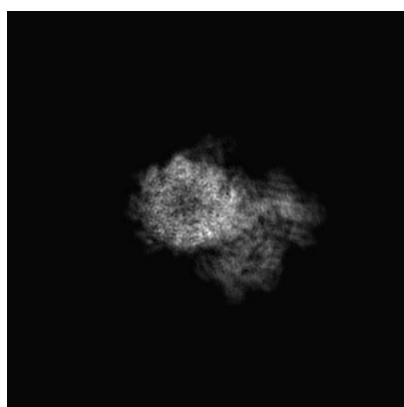
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-9772. These allow visual inspection of the internal detail of the map and identification of artifacts.

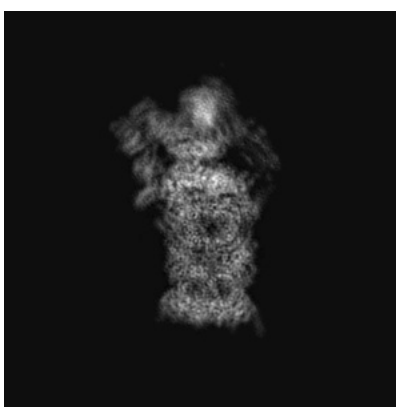
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

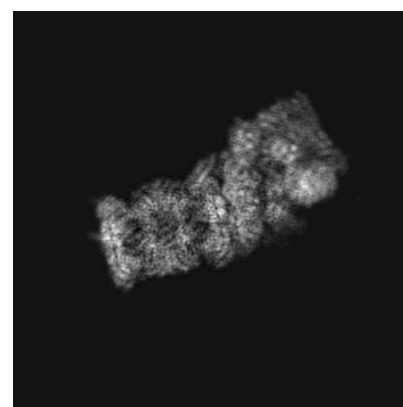
#### 6.1.1 Primary map



X



Y

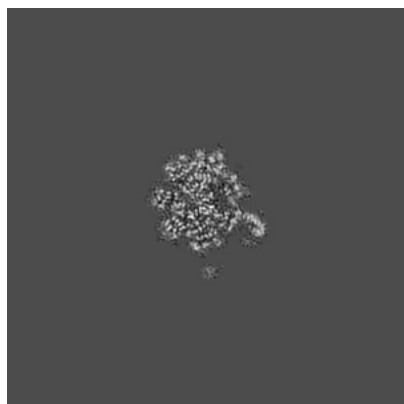


Z

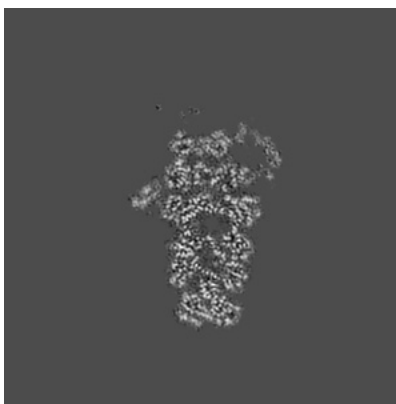
The images above show the map projected in three orthogonal directions.

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

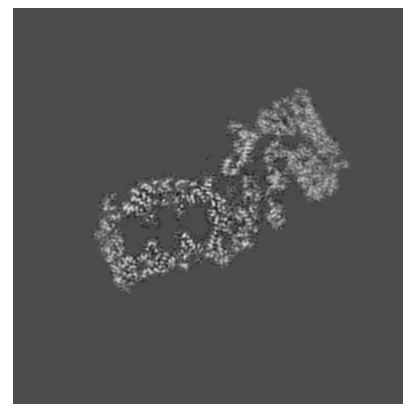
#### 6.2.1 Primary map



X Index: 180



Y Index: 180

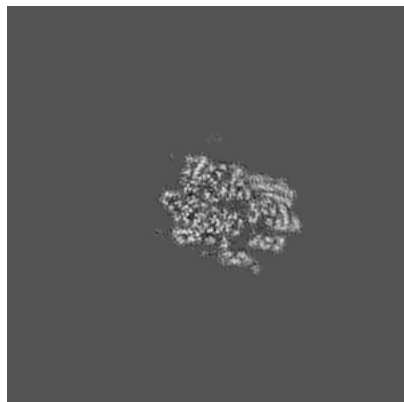


Z Index: 180

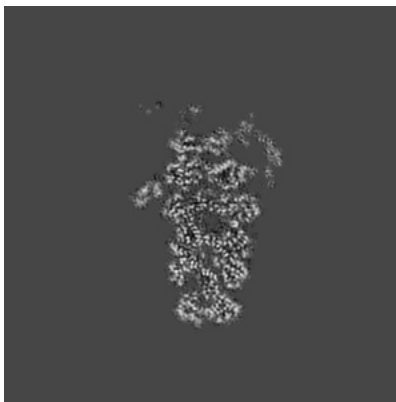
The images above show central slices of the map in three orthogonal directions.

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

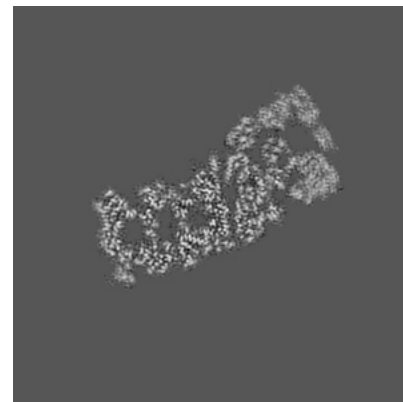
### 6.3.1 Primary map



X Index: 204



Y Index: 182



Z Index: 172

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

## 6.4 Orthogonal surface views [i](#)

### 6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.704. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

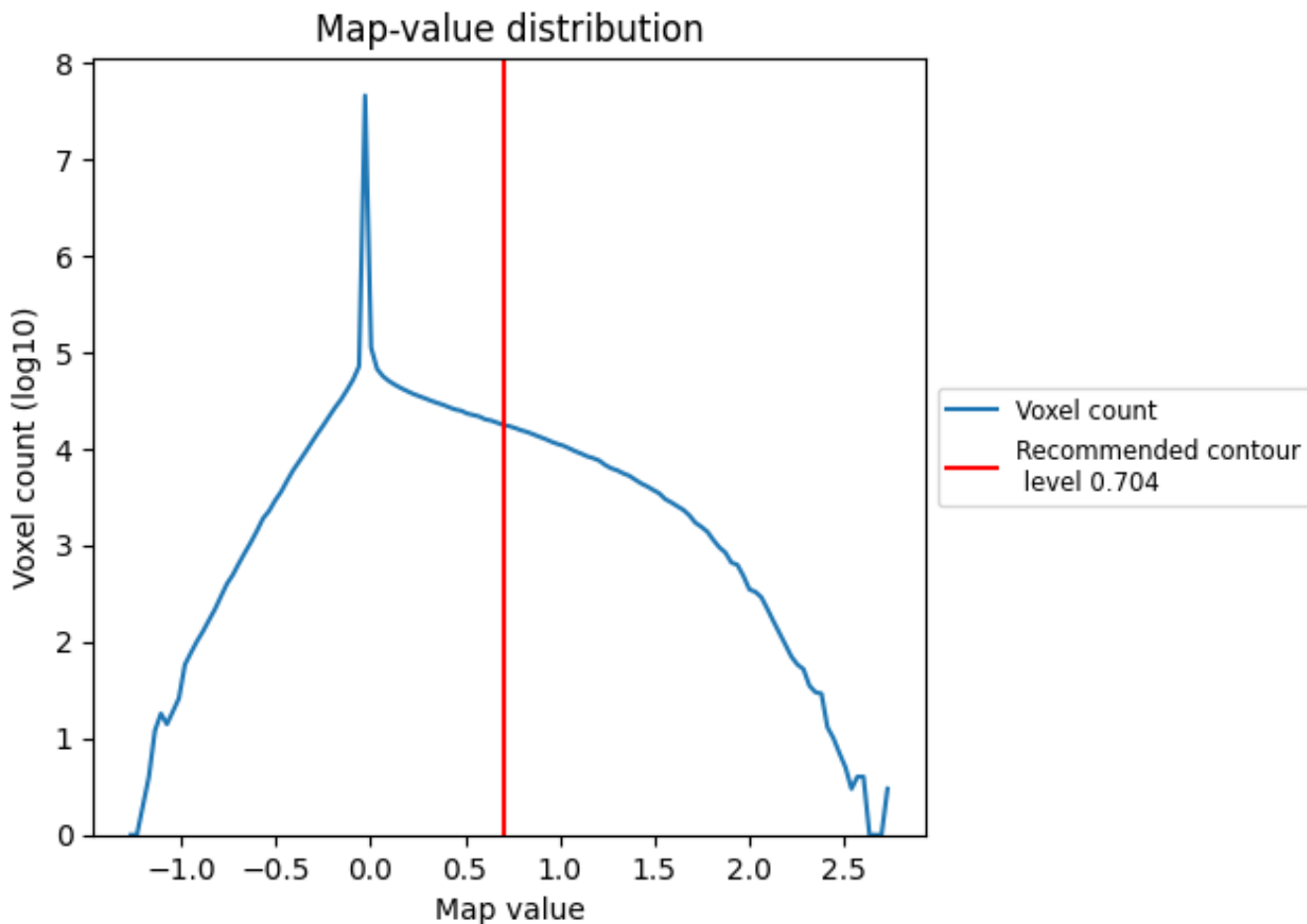
## 6.5 Mask visualisation

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

## 7 Map analysis [i](#)

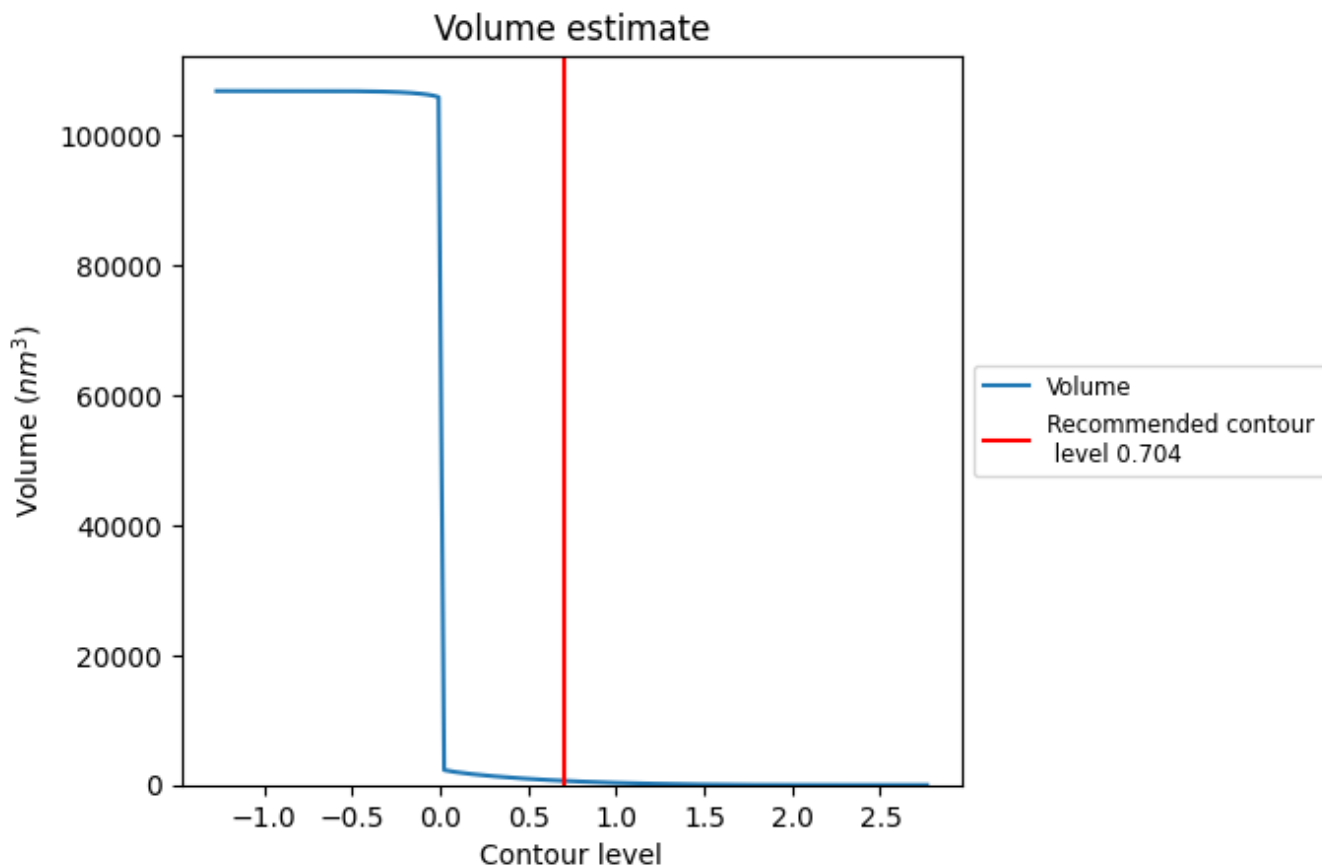
This section contains the results of statistical analysis of the map.

### 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.

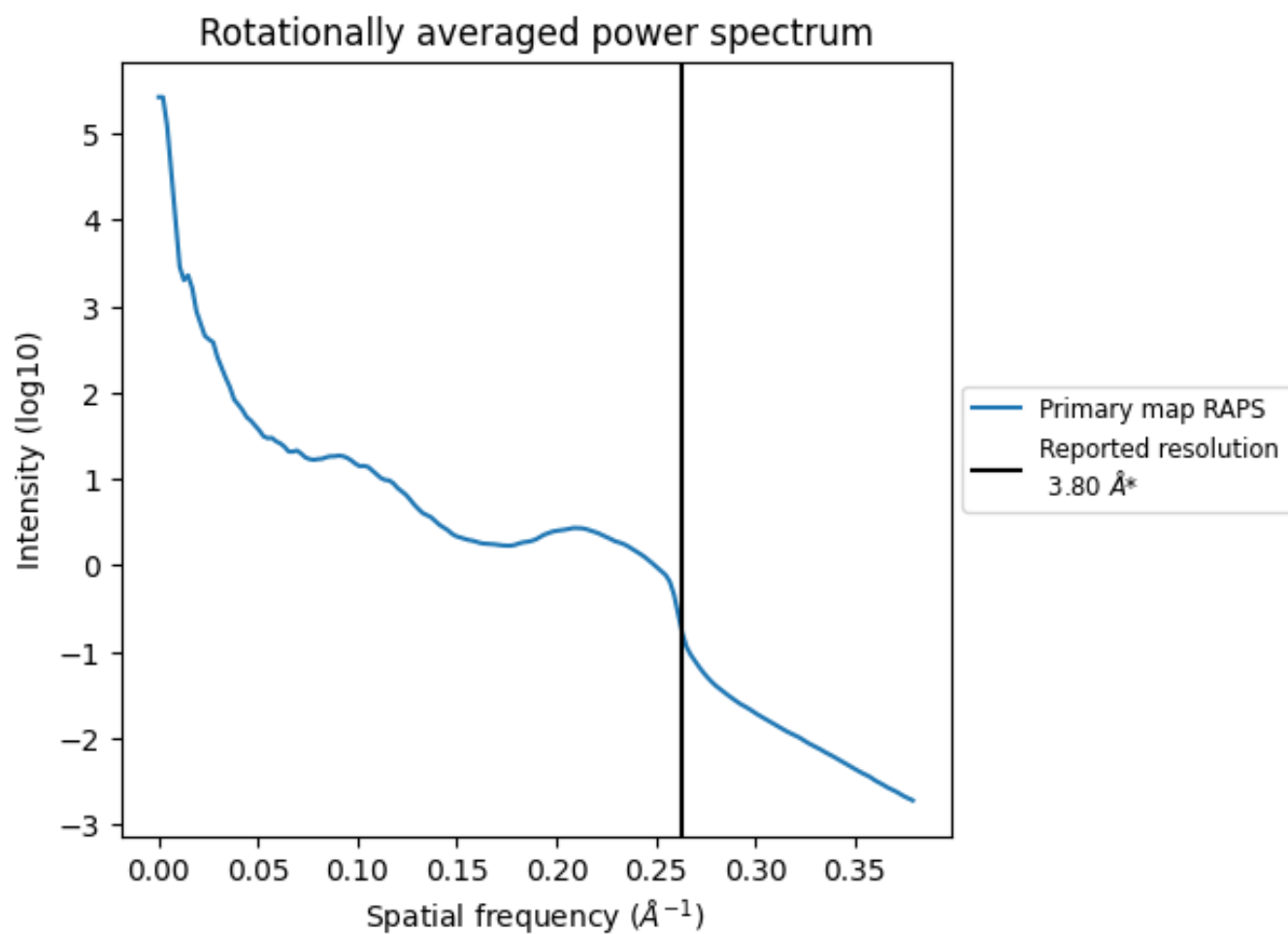
## 7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 639 nm<sup>3</sup>; this corresponds to an approximate mass of 578 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 0.263 Å<sup>-1</sup>



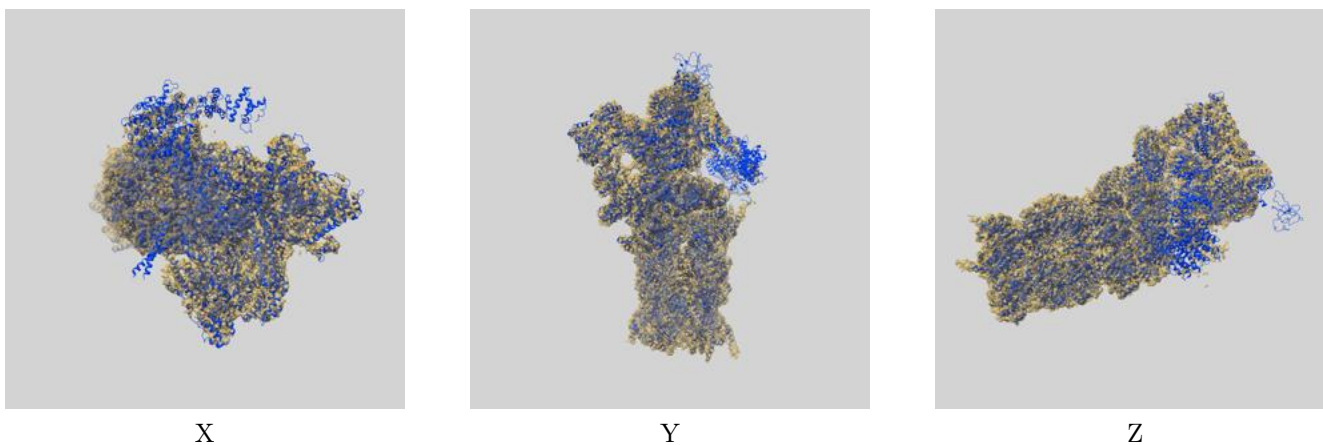
## 8 Fourier-Shell correlation

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

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

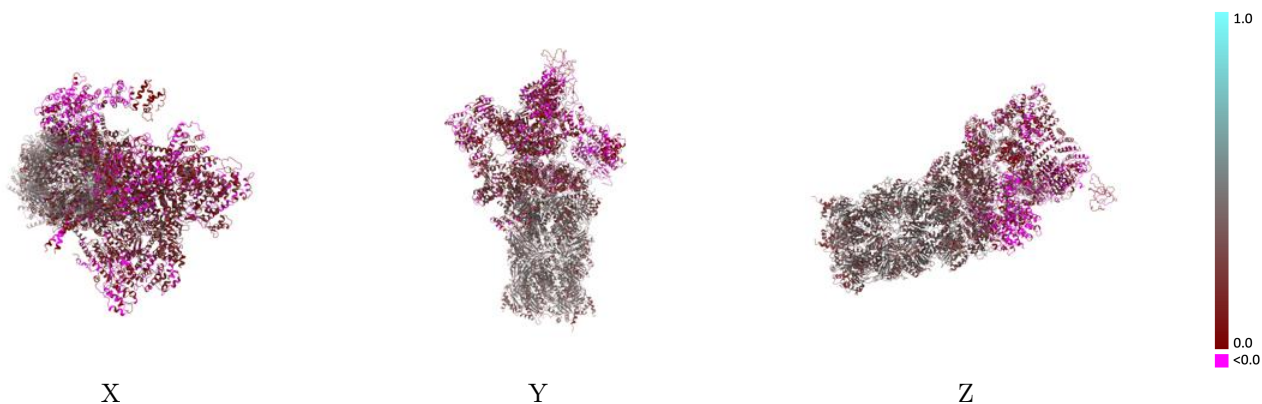
This section contains information regarding the fit between EMDB map EMD-9772 and PDB model 6J2X. Per-residue inclusion information can be found in section 3 on page 11.

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



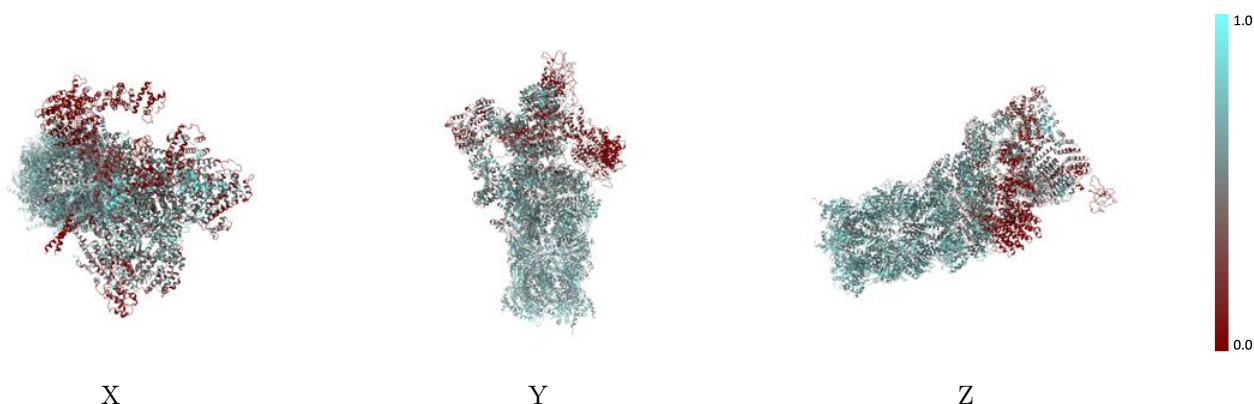
The images above show the 3D surface view of the map at the recommended contour level 0.704 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



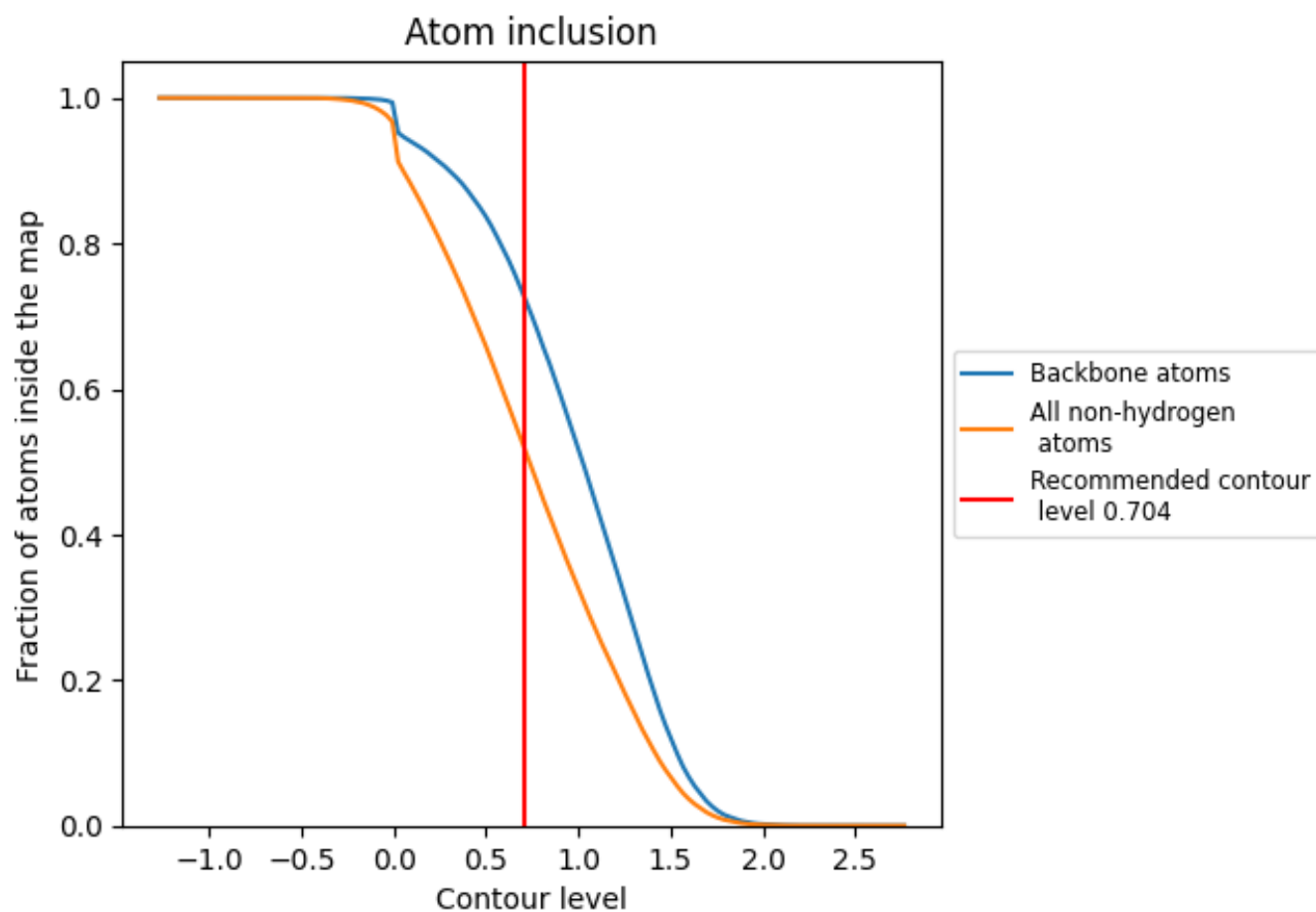
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.704).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 73% of all backbone atoms, 52% 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 (0.704) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5214	 0.2420
1	 0.6253	 0.3670
2	 0.6594	 0.3730
3	 0.6452	 0.3700
4	 0.6115	 0.3420
5	 0.6613	 0.3550
6	 0.6365	 0.3430
7	 0.6435	 0.3790
A	 0.6175	 0.3540
B	 0.6095	 0.3600
C	 0.6237	 0.3390
D	 0.6423	 0.3390
E	 0.6268	 0.3330
F	 0.6271	 0.3530
G	 0.6292	 0.3590
H	 0.5433	 0.2570
I	 0.5287	 0.2360
J	 0.5019	 0.1970
K	 0.5237	 0.2320
L	 0.5209	 0.2460
M	 0.5187	 0.2360
N	 0.4398	 0.1000
O	 0.3485	 0.1030
P	 0.5192	 0.1610
Q	 0.5561	 0.2120
R	 0.5127	 0.1640
S	 0.3778	 0.1010
T	 0.2564	 0.0860
U	 0.5285	 0.1690
V	 0.5043	 0.1680
W	 0.3062	 0.0750
X	 0.0011	 -0.0020
Y	 0.4522	 0.0930
Z	 0.0293	 -0.0050
a	 0.6564	 0.3740



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Chain	Atom inclusion	Q-score
b	 0.6234	 0.3560
c	 0.6631	 0.3260
d	 0.6769	 0.3360
e	 0.6510	 0.3580
f	 0.6644	 0.3700
g	 0.6173	 0.3470
h	 0.6510	 0.3720
i	 0.6600	 0.3770
j	 0.6658	 0.3450
k	 0.6570	 0.3410
l	 0.6634	 0.3390
m	 0.6416	 0.3340
n	 0.6791	 0.3320