



## wwPDB EM Validation Summary Report ⓘ

Nov 2, 2024 – 10:06 PM EDT

PDB ID : 6MSB  
EMDB ID : EMD-9216  
Title : Cryo-EM structures and dynamics of substrate-engaged human 26S proteasome  
Authors : Mao, Y.D.  
Deposited on : 2018-10-16  
Resolution : 3.00 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](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:

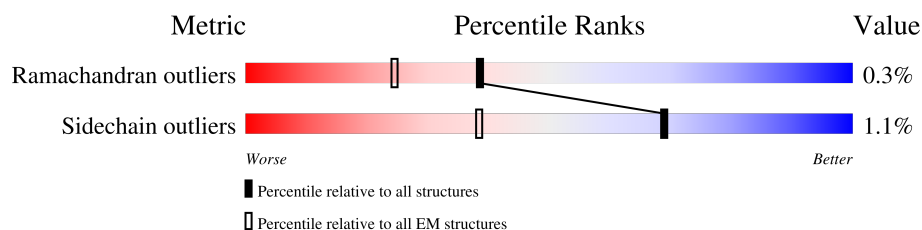
EMDB validation analysis	:	0.0.1.dev113
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

# 1 Overall quality at a glance

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

The reported resolution of this entry is 3.00 Å.

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



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

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	U	953	
2	V	534	
3	W	456	
4	X	422	
5	Y	389	
6	Z	324	
7	a	376	
8	b	377	
9	c	309	

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Mol	Chain	Length	Quality of chain
10	d	349	
11	e	70	
12	f	908	
13	A	433	
14	B	440	
15	C	398	
16	D	418	
17	E	403	
18	F	439	
19	u	76	
19	w	76	
20	G	245	
20	g	245	
21	H	233	
21	h	233	
22	I	260	
22	i	260	
23	J	247	
23	j	247	
24	K	240	
24	k	240	
25	L	268	
25	l	268	
26	M	254	
26	m	254	

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Mol	Chain	Length	Quality of chain
27	N	238	 80% 20%
27	n	238	 80% 20%
28	O	276	 80% 20%
28	o	276	 80% 20%
29	P	204	 100%
29	p	204	 100%
30	Q	201	 97% ..
30	q	201	 97% ..
31	R	262	 77% 23%
31	r	262	 77% 23%
32	S	240	 89% 11%
32	s	240	 89% 11%
33	T	263	 81% 18%
33	t	263	 81% 18%

## 2 Entry composition

There are 37 unique types of molecules in this entry. The entry contains 104938 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
1	U	812	Total	C	N	O	S	0	0
			6334	4023	1078	1189	44		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	V	508	Total	C	N	O	S	0	0
			3994	2530	712	738	14		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	W	456	Total	C	N	O	S	0	0
			3703	2339	635	704	25		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	X	380	Total	C	N	O	S	0	0
			3009	1918	509	570	12		

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

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

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

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

- Molecule 7 is a protein called 26S proteasome non-ATPase regulatory subunit 13.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	a	373	Total	C	N	O	S	0	0
			2995	1911	510	559	15		

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

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

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

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

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

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

- Molecule 11 is a protein called 26S proteasome complex subunit SEM1.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	e	40	Total	C	N	O	S	0	0
			334	200	55	77	2		

- Molecule 12 is a protein called 26S proteasome non-ATPase regulatory subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	f	889	Total	C	N	O	S	0	0
			6866	4315	1174	1331	46		

- Molecule 13 is a protein called 26S proteasome regulatory subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	A	394	Total	C	N	O	S	0	0
			3096	1951	543	584	18		

- Molecule 14 is a protein called 26S proteasome regulatory subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	B	384	Total	C	N	O	S	0	0
			3018	1901	515	587	15		

- Molecule 15 is a protein called 26S proteasome regulatory subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	C	363	Total	C	N	O	S	0	0
			2864	1808	515	525	16		

- Molecule 16 is a protein called 26S proteasome regulatory subunit 6B.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	D	380	Total	C	N	O	S	0	0
			3039	1923	524	579	13		

- Molecule 17 is a protein called 26S proteasome regulatory subunit 10B.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	E	375	Total	C	N	O	S	0	0
			2860	1796	512	536	16		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
18	F	376	Total	C	N	O	S	0	0
			2858	1802	496	545	15		

- Molecule 19 is a protein called Ubiquitin.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	u	76	Total	C	N	O	S	0	0
			603	378	107	117	1		
19	w	76	Total	C	N	O	S	0	0
			603	378	107	117	1		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
u	63	ARG	LYS	conflict	UNP P0CG47
w	63	ARG	LYS	conflict	UNP P0CG47

- Molecule 20 is a protein called Proteasome subunit alpha type-6.

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

- Molecule 21 is a protein called Proteasome subunit alpha type-2.

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

- Molecule 22 is a protein called Proteasome subunit alpha type-4.

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

- Molecule 23 is a protein called Proteasome subunit alpha type-7.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	J	239	Total	C	N	O	S	0	0
			1713	1062	311	335	5		
23	j	239	Total	C	N	O	S	0	0
			1704	1056	308	335	5		

- Molecule 24 is a protein called Proteasome subunit alpha type-5.

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

- Molecule 25 is a protein called Proteasome subunit alpha type-1.

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

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

- Molecule 26 is a protein called Proteasome subunit alpha type-3.

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

- Molecule 27 is a protein called Proteasome subunit beta type-6.

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

- Molecule 28 is a protein called Proteasome subunit beta type-7.

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

- Molecule 29 is a protein called Proteasome subunit beta type-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	P	204	Total	C	N	O	S	0	0
			1591	1013	265	294	19		
29	p	204	Total	C	N	O	S	0	0
			1591	1013	265	294	19		

- Molecule 30 is a protein called Proteasome subunit beta type-2.

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

- Molecule 31 is a protein called Proteasome subunit beta type-5.

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

- Molecule 32 is a protein called Proteasome subunit beta type-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	S	213	Total	C	N	O	S	0	0
			1641	1036	282	313	10		
32	s	213	Total	C	N	O	S	0	0
			1644	1039	282	313	10		

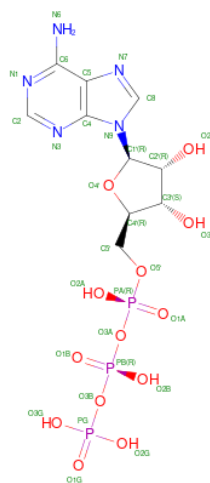
- Molecule 33 is a protein called Proteasome subunit beta type-4.

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

- Molecule 34 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

- Molecule 35 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: C<sub>10</sub>H<sub>16</sub>N<sub>5</sub>O<sub>13</sub>P<sub>3</sub>).



Mol	Chain	Residues	Atoms					AltConf
35	A	1	Total 31	C 10	N 5	O 13	P 3	0
35	B	1	Total 31	C 10	N 5	O 13	P 3	0
35	D	1	Total 31	C 10	N 5	O 13	P 3	0
35	E	1	Total 31	C 10	N 5	O 13	P 3	0

- Molecule 36 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	AltConf
36	A	1	Total Mg 1 1	0
36	B	1	Total Mg 1 1	0
36	D	1	Total Mg 1 1	0
36	E	1	Total Mg 1 1	0
36	F	1	Total Mg 1 1	0

- Molecule 37 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula:  $\text{C}_{10}\text{H}_{15}\text{N}_5\text{O}_{10}\text{P}_2$ ).

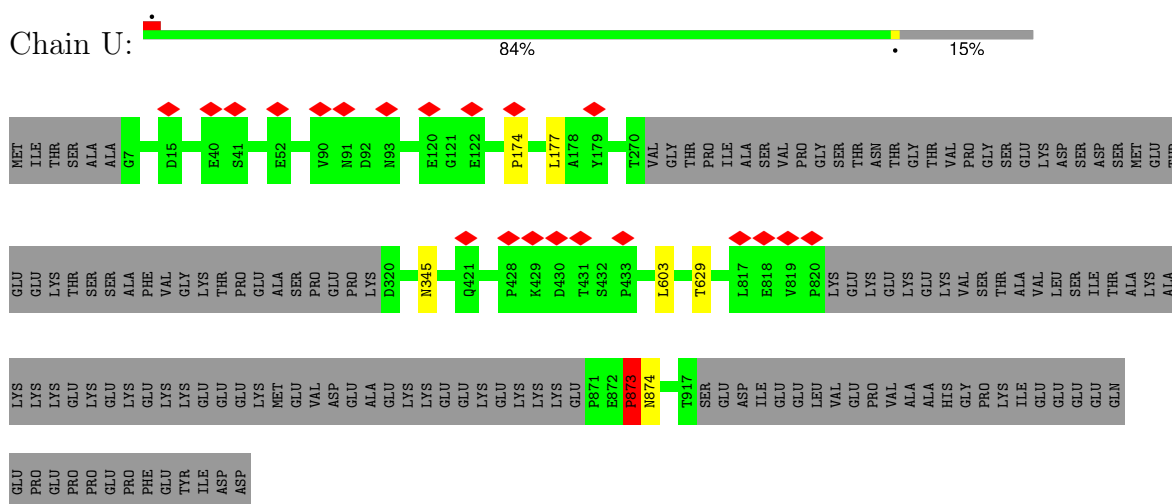


Mol	Chain	Residues	Atoms					AltConf
37	C	1	Total	C	N	O	P	0
			27	10	5	10	2	
37	F	1	Total	C	N	O	P	0
			27	10	5	10	2	

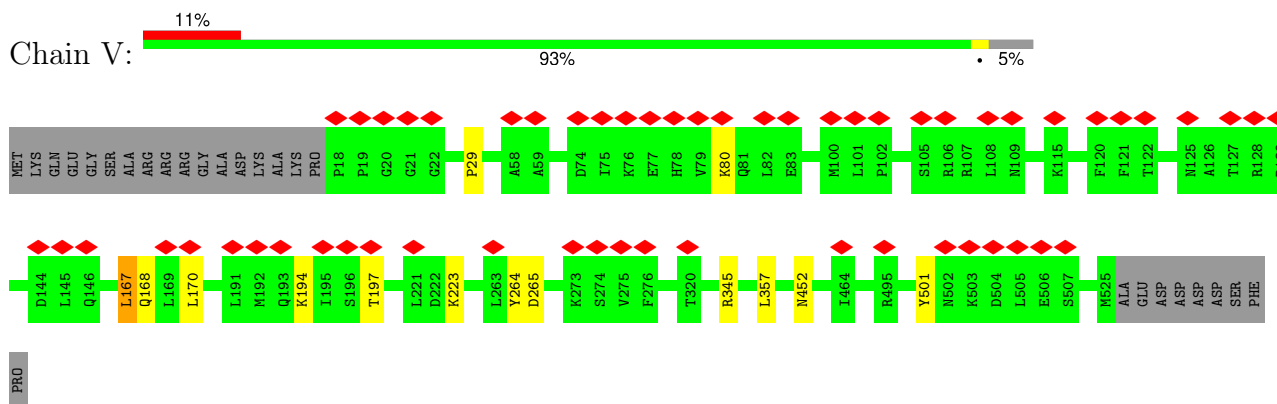
### 3 Residue-property plots

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

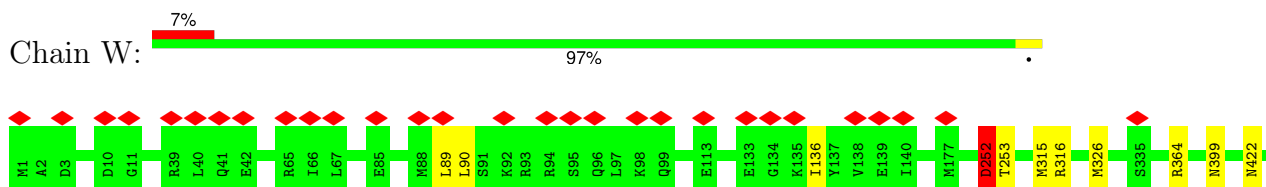
- Molecule 1: 26S proteasome non-ATPase regulatory subunit 1



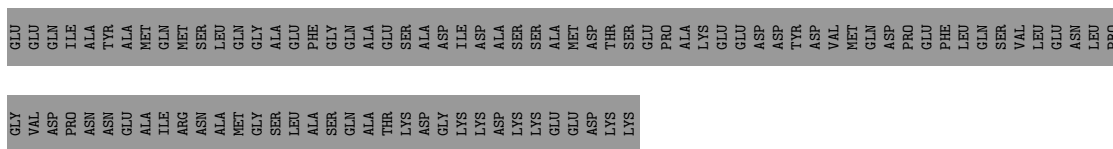
- Molecule 2: 26S proteasome non-ATPase regulatory subunit 3



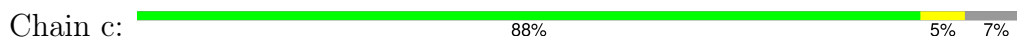
- Molecule 3: 26S proteasome non-ATPase regulatory subunit 12



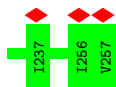
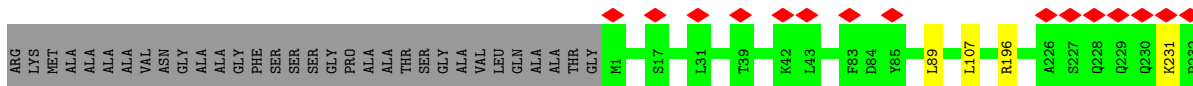
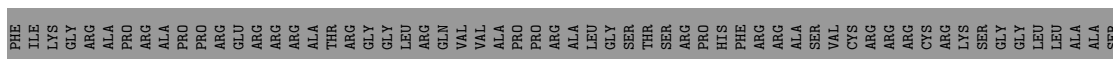




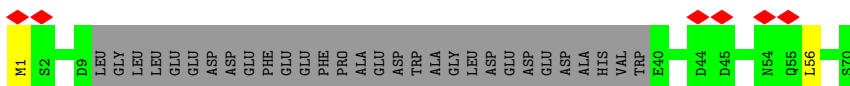
- Molecule 9: 26S proteasome non-ATPase regulatory subunit 14



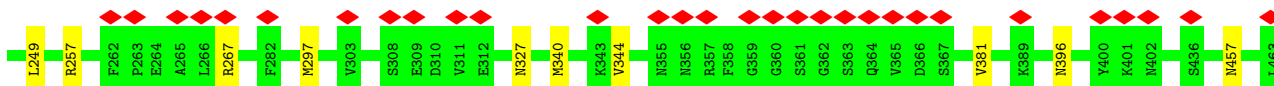
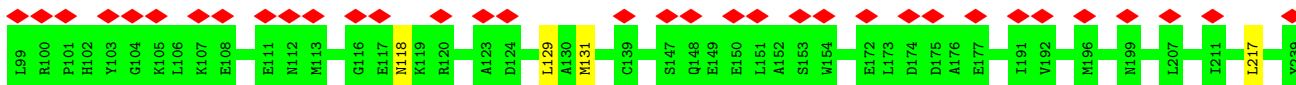
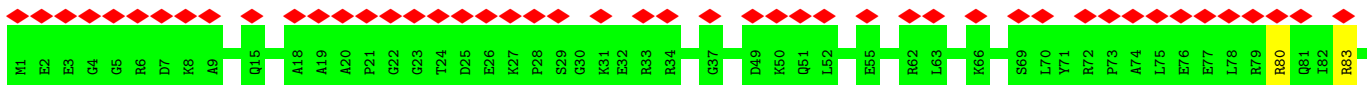
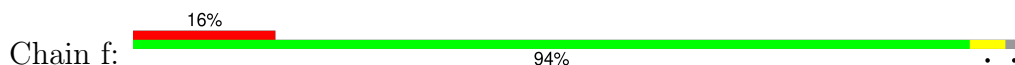
- Molecule 10: 26S proteasome non-ATPase regulatory subunit 8



- Molecule 11: 26S proteasome complex subunit SEM1



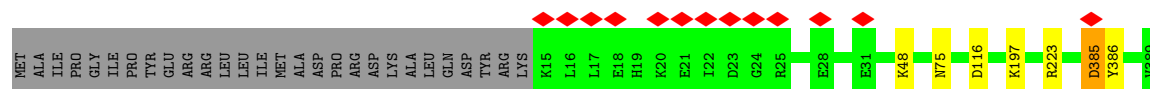
- Molecule 12: 26S proteasome non-ATPase regulatory subunit 2






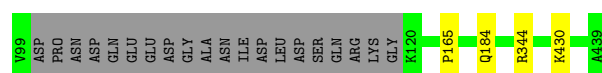
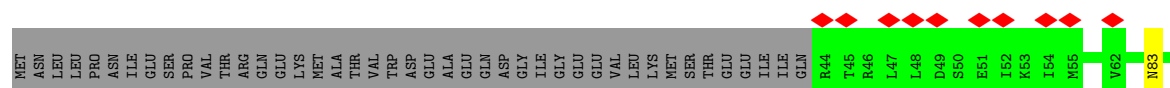


Chain E:  91% 7%



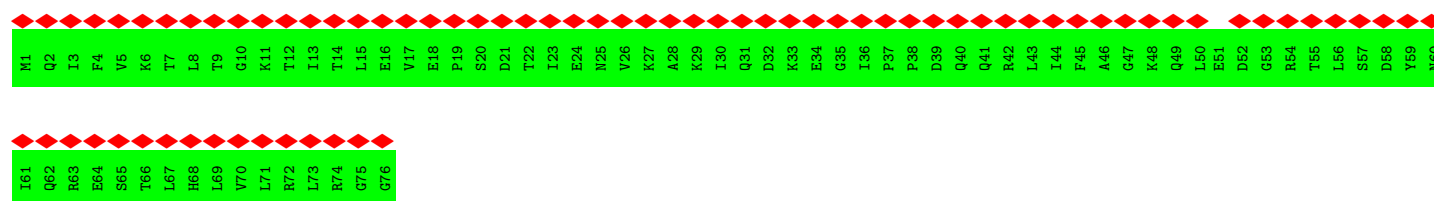
- Molecule 18: 26S proteasome regulatory subunit 6A

Chain F:  85% 14%




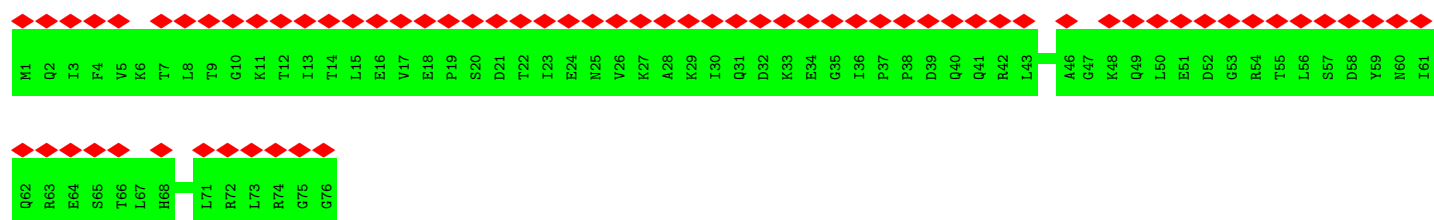
- Molecule 19: Ubiquitin

Chain u:  99% 100%



- Molecule 19: Ubiquitin

Chain w:  91% 100%



- Molecule 20: Proteasome subunit alpha type-6

Chain G:  98%



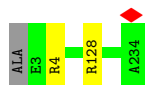
- Molecule 20: Proteasome subunit alpha type-6

Chain g:  98%



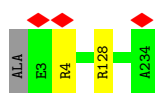
- Molecule 21: Proteasome subunit alpha type-2

Chain H: 99%



- Molecule 21: Proteasome subunit alpha type-2

Chain h: 99%



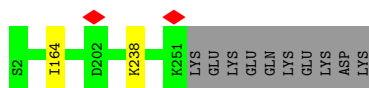
- Molecule 22: Proteasome subunit alpha type-4

Chain I: 95%



- Molecule 22: Proteasome subunit alpha type-4

Chain i: 95%



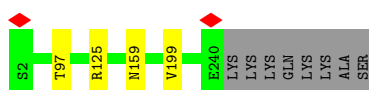
- Molecule 23: Proteasome subunit alpha type-7

Chain J: 95%



- Molecule 23: Proteasome subunit alpha type-7

Chain j: 95%



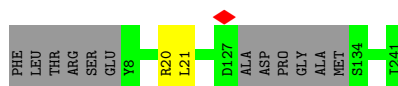
- Molecule 24: Proteasome subunit alpha type-5

Chain K:  94% • 5%




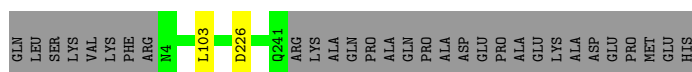
- Molecule 24: Proteasome subunit alpha type-5

Chain k:  94% • 5%




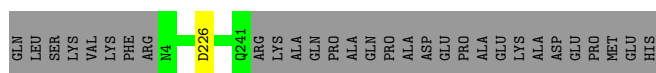
- Molecule 25: Proteasome subunit alpha type-1

Chain L:  88% • 11%



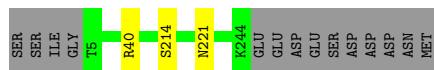
- Molecule 25: Proteasome subunit alpha type-1

Chain l:  88% • 11%



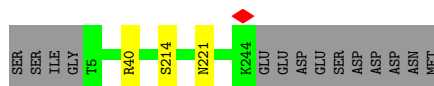
- Molecule 26: Proteasome subunit alpha type-3

Chain M:  93% • 6%




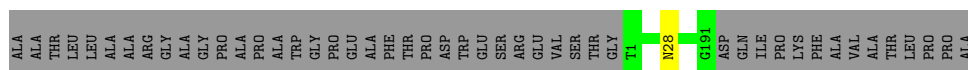
- Molecule 26: Proteasome subunit alpha type-3

Chain m:  93% • 6%




- Molecule 27: Proteasome subunit beta type-6

Chain N:  80% • 20%




- Molecule 27: Proteasome subunit beta type-6

Chain n:  80% 20%


ALA ALA THR LEU LEU ALA ALA ARG GLY GLY GLY PRO PRO ALA ALA TRP GLY GLY GLU ALA PHE THR PRO ASP TRP GLU SER ARG GLU VAL SER THR GLY T1 N28 G191 ASP GLN ILE PRO PRO LYS PHE ALA VAL ALA THR LEU PRO PRO ALA

- Molecule 28: Proteasome subunit beta type-7

Chain O:  80% 20%

ALA ALA VAL SER VAL TYR ALA PRO PRO VAL VAL GLY GLY PHE SER PHE ASP ASN CYS ARG ARG ASN ALA VAL LEU LEU GLU ALA ASP PHE ALA LYS LYS ARG GLY TYR LYS LEU LEU LYS VAL ARG LYS THR GLY T1 E220 ILE GLU VAL LEU GLU THR VAL GLN THR MET ASP THR SER

- Molecule 28: Proteasome subunit beta type-7

Chain o:  80% 20%

ALA ALA VAL SER VAL TYR ALA PRO PRO VAL VAL GLY GLY PHE SER PHE ASP ASN CYS ARG ARG ASN ALA VAL LEU LEU GLU ALA ASP PHE ALA LYS LYS ARG GLY TYR LYS LEU LEU LYS VAL ARG LYS THR GLY T1 E220 ILE GLU VAL LEU GLU THR VAL GLN THR MET ASP THR SER

- Molecule 29: Proteasome subunit beta type-3

Chain P:  100%

There are no outlier residues recorded for this chain.

- Molecule 29: Proteasome subunit beta type-3

Chain p:  100%

There are no outlier residues recorded for this chain.

- Molecule 30: Proteasome subunit beta type-2

Chain Q:  97% ..


H1 E2 Y3 L4 N82 L103 Q199 GLY SER

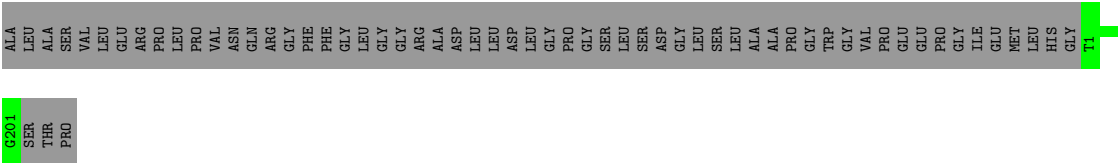
- Molecule 30: Proteasome subunit beta type-2

Chain q:  97% ..

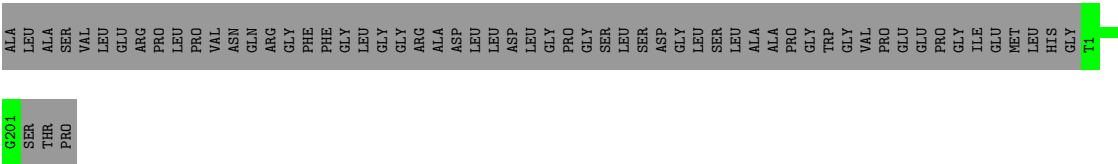
H1 E2 Y3 L4 N82 L103 Q199 GLY SER

- Molecule 31: Proteasome subunit beta type-5

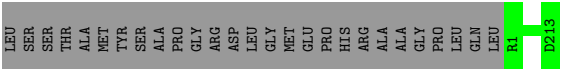
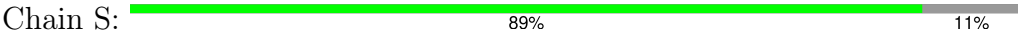
Chain R:  77% 23%



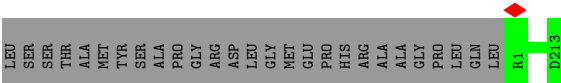
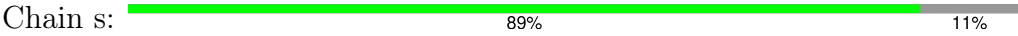
• Molecule 31: Proteasome subunit beta type-5



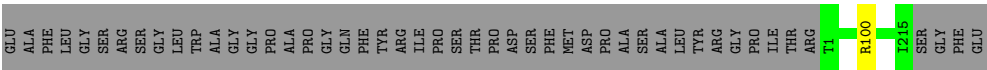
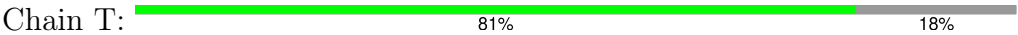
• Molecule 32: Proteasome subunit beta type-1



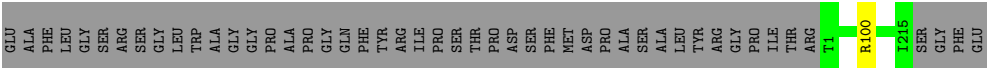
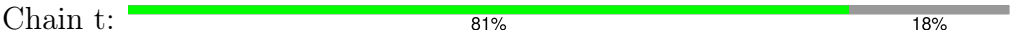
• Molecule 32: Proteasome subunit beta type-1



• Molecule 33: Proteasome subunit beta type-4



• Molecule 33: 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	105157	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 ( $e^-/\text{\AA}^2$ )	44	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	0.023	Depositor
Minimum map value	-0.006	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.0035	Depositor
Map size (Å)	411.0, 411.0, 411.0	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.685, 0.685, 0.685	Depositor

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	U	0.33	0/6449	0.58	4/8729 (0.0%)
2	V	0.34	0/4072	0.65	3/5510 (0.1%)
3	W	0.33	0/3751	0.63	2/5042 (0.0%)
4	X	0.32	0/3053	0.59	0/4115
5	Y	0.37	0/3173	0.62	0/4273
6	Z	0.32	0/2324	0.64	2/3150 (0.1%)
7	a	0.30	0/3053	0.60	1/4133 (0.0%)
8	b	0.29	0/1478	0.61	0/2001
9	c	0.37	0/2302	0.67	0/3110
10	d	0.33	0/2162	0.67	2/2919 (0.1%)
11	e	0.31	0/338	0.69	1/450 (0.2%)
12	f	0.32	0/6980	0.70	5/9433 (0.1%)
13	A	0.45	0/3148	0.65	2/4250 (0.0%)
14	B	0.42	0/3061	0.64	1/4129 (0.0%)
15	C	0.40	0/2902	0.63	1/3904 (0.0%)
16	D	0.44	0/3089	0.64	0/4168
17	E	0.40	0/2904	0.61	1/3924 (0.0%)
18	F	0.43	0/2896	0.59	0/3912
19	u	0.27	0/609	0.49	0/819
19	w	0.27	0/609	0.49	0/819
20	G	0.41	0/1859	0.56	0/2523
20	g	0.41	0/1859	0.56	0/2523
21	H	0.44	0/1743	0.53	0/2372
21	h	0.44	0/1743	0.53	0/2372
22	I	0.38	0/1942	0.58	1/2628 (0.0%)
22	i	0.37	0/1942	0.58	1/2628 (0.0%)
23	J	0.43	0/1737	0.59	0/2369
23	j	0.32	0/1728	0.55	0/2358
24	K	0.38	0/1747	0.57	1/2364 (0.0%)
24	k	0.37	0/1747	0.57	1/2364 (0.0%)
25	L	0.42	0/1885	0.61	2/2552 (0.1%)
25	l	0.42	0/1885	0.61	1/2552 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
26	M	0.41	0/1891	0.55	0/2552
26	m	0.41	0/1891	0.55	0/2552
27	N	0.36	0/1454	0.51	0/1967
27	n	0.36	0/1454	0.51	0/1967
28	O	0.38	0/1670	0.54	0/2265
28	o	0.38	0/1670	0.54	0/2265
29	P	0.38	0/1620	0.52	0/2184
29	p	0.38	0/1620	0.52	0/2184
30	Q	0.40	0/1603	0.57	1/2174 (0.0%)
30	q	0.40	0/1603	0.57	1/2174 (0.0%)
31	R	0.41	0/1579	0.51	0/2134
31	r	0.41	0/1579	0.51	0/2134
32	S	0.39	0/1671	0.51	0/2253
32	s	0.36	0/1674	0.51	0/2257
33	T	0.39	0/1700	0.54	0/2305
33	t	0.39	0/1700	0.54	0/2305
All	All	0.38	0/106549	0.60	34/144067 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	U	0	1
2	V	0	2
3	W	0	2
5	Y	0	1
6	Z	0	2
7	a	0	1
9	c	0	2
12	f	0	9
13	A	0	2
14	B	0	1
15	C	0	5
16	D	0	4
17	E	0	2
18	F	0	1
20	G	0	1
20	g	0	1
23	J	0	1
23	j	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
26	M	0	1
26	m	0	1
30	Q	0	1
30	q	0	1
All	All	0	43

There are no bond length outliers.

The worst 5 of 34 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	A	310	ASP	CB-CG-OD1	8.20	125.68	118.30
3	W	89	LEU	CA-CB-CG	7.57	132.70	115.30
11	e	56	LEU	CA-CB-CG	7.44	132.42	115.30
12	f	759	LEU	CA-CB-CG	6.86	131.09	115.30
1	U	603	LEU	CA-CB-CG	6.71	130.74	115.30

There are no chirality outliers.

5 of 43 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	U	873	PRO	Peptide
2	V	264	TYR	Peptide
2	V	501	TYR	Peptide
3	W	252	ASP	Peptide
3	W	315	MET	Peptide

## 5.2 Too-close contacts [i](#)

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

## 5.3 Torsion angles [i](#)

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

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	U	806/953 (85%)	738 (92%)	65 (8%)	3 (0%)	30	66
2	V	506/534 (95%)	453 (90%)	49 (10%)	4 (1%)	16	51
3	W	454/456 (100%)	407 (90%)	43 (10%)	4 (1%)	14	49
4	X	378/422 (90%)	353 (93%)	24 (6%)	1 (0%)	37	70
5	Y	376/389 (97%)	342 (91%)	34 (9%)	0	100	100
6	Z	284/324 (88%)	243 (86%)	41 (14%)	0	100	100
7	a	371/376 (99%)	337 (91%)	33 (9%)	1 (0%)	37	70
8	b	189/377 (50%)	175 (93%)	13 (7%)	1 (0%)	25	61
9	c	285/309 (92%)	244 (86%)	38 (13%)	3 (1%)	12	44
10	d	255/349 (73%)	216 (85%)	39 (15%)	0	100	100
11	e	36/70 (51%)	22 (61%)	14 (39%)	0	100	100
12	f	887/908 (98%)	715 (81%)	165 (19%)	7 (1%)	16	51
13	A	392/433 (90%)	342 (87%)	48 (12%)	2 (0%)	25	61
14	B	382/440 (87%)	348 (91%)	33 (9%)	1 (0%)	37	70
15	C	359/398 (90%)	333 (93%)	24 (7%)	2 (1%)	22	57
16	D	378/418 (90%)	334 (88%)	38 (10%)	6 (2%)	8	34
17	E	373/403 (93%)	335 (90%)	36 (10%)	2 (0%)	25	61
18	F	372/439 (85%)	338 (91%)	33 (9%)	1 (0%)	37	70
19	u	74/76 (97%)	73 (99%)	1 (1%)	0	100	100
19	w	74/76 (97%)	73 (99%)	1 (1%)	0	100	100
20	G	238/245 (97%)	223 (94%)	15 (6%)	0	100	100
20	g	238/245 (97%)	223 (94%)	15 (6%)	0	100	100
21	H	230/233 (99%)	224 (97%)	6 (3%)	0	100	100
21	h	230/233 (99%)	224 (97%)	6 (3%)	0	100	100
22	I	248/260 (95%)	229 (92%)	19 (8%)	0	100	100
22	i	248/260 (95%)	230 (93%)	18 (7%)	0	100	100
23	J	237/247 (96%)	218 (92%)	18 (8%)	1 (0%)	30	66
23	j	237/247 (96%)	220 (93%)	16 (7%)	1 (0%)	30	66
24	K	224/240 (93%)	211 (94%)	13 (6%)	0	100	100
24	k	224/240 (93%)	211 (94%)	13 (6%)	0	100	100
25	L	236/268 (88%)	221 (94%)	15 (6%)	0	100	100
25	l	236/268 (88%)	221 (94%)	15 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	M	238/254 (94%)	222 (93%)	16 (7%)	0	100	100
26	m	238/254 (94%)	222 (93%)	16 (7%)	0	100	100
27	N	189/238 (79%)	183 (97%)	6 (3%)	0	100	100
27	n	189/238 (79%)	183 (97%)	6 (3%)	0	100	100
28	O	218/276 (79%)	211 (97%)	7 (3%)	0	100	100
28	o	218/276 (79%)	211 (97%)	7 (3%)	0	100	100
29	P	202/204 (99%)	193 (96%)	9 (4%)	0	100	100
29	p	202/204 (99%)	193 (96%)	9 (4%)	0	100	100
30	Q	197/201 (98%)	181 (92%)	16 (8%)	0	100	100
30	q	197/201 (98%)	181 (92%)	16 (8%)	0	100	100
31	R	199/262 (76%)	188 (94%)	11 (6%)	0	100	100
31	r	199/262 (76%)	188 (94%)	11 (6%)	0	100	100
32	S	211/240 (88%)	204 (97%)	7 (3%)	0	100	100
32	s	211/240 (88%)	200 (95%)	11 (5%)	0	100	100
33	T	213/263 (81%)	203 (95%)	10 (5%)	0	100	100
33	t	213/263 (81%)	203 (95%)	10 (5%)	0	100	100
All	All	13391/15012 (89%)	12242 (91%)	1109 (8%)	40 (0%)	38	70

5 of 40 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	V	167	LEU
15	C	90	HIS
1	U	874	ASN
2	V	168	GLN
16	D	84	SER

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	U	692/816 (85%)	690 (100%)	2 (0%)	91	96
2	V	415/460 (90%)	409 (99%)	6 (1%)	62	83
3	W	416/416 (100%)	409 (98%)	7 (2%)	56	81
4	X	327/362 (90%)	320 (98%)	7 (2%)	48	77
5	Y	334/344 (97%)	331 (99%)	3 (1%)	75	89
6	Z	257/295 (87%)	252 (98%)	5 (2%)	52	79
7	a	333/336 (99%)	332 (100%)	1 (0%)	91	96
8	b	167/312 (54%)	167 (100%)	0	100	100
9	c	252/267 (94%)	242 (96%)	10 (4%)	27	61
10	d	231/293 (79%)	229 (99%)	2 (1%)	75	89
11	e	38/63 (60%)	37 (97%)	1 (3%)	41	72
12	f	745/763 (98%)	728 (98%)	17 (2%)	45	75
13	A	337/372 (91%)	327 (97%)	10 (3%)	36	69
14	B	339/385 (88%)	333 (98%)	6 (2%)	54	80
15	C	314/346 (91%)	306 (98%)	8 (2%)	42	73
16	D	333/366 (91%)	324 (97%)	9 (3%)	40	71
17	E	298/353 (84%)	295 (99%)	3 (1%)	73	88
18	F	296/379 (78%)	293 (99%)	3 (1%)	73	88
19	u	68/68 (100%)	68 (100%)	0	100	100
19	w	68/68 (100%)	68 (100%)	0	100	100
20	G	193/209 (92%)	193 (100%)	0	100	100
20	g	193/209 (92%)	193 (100%)	0	100	100
21	H	164/190 (86%)	162 (99%)	2 (1%)	67	86
21	h	164/190 (86%)	162 (99%)	2 (1%)	67	86
22	I	193/220 (88%)	192 (100%)	1 (0%)	86	94
22	i	193/220 (88%)	192 (100%)	1 (0%)	86	94
23	J	154/210 (73%)	151 (98%)	3 (2%)	52	79
23	j	152/210 (72%)	150 (99%)	2 (1%)	65	85
24	K	186/202 (92%)	185 (100%)	1 (0%)	86	94
24	k	186/202 (92%)	185 (100%)	1 (0%)	86	94
25	L	198/229 (86%)	198 (100%)	0	100	100
25	l	198/229 (86%)	198 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
26	M	192/211 (91%)	190 (99%)	2 (1%)	73	88
26	m	192/211 (91%)	190 (99%)	2 (1%)	73	88
27	N	148/180 (82%)	147 (99%)	1 (1%)	81	91
27	n	148/180 (82%)	147 (99%)	1 (1%)	81	91
28	O	177/227 (78%)	177 (100%)	0	100	100
28	o	177/227 (78%)	177 (100%)	0	100	100
29	P	173/173 (100%)	173 (100%)	0	100	100
29	p	173/173 (100%)	173 (100%)	0	100	100
30	Q	164/171 (96%)	162 (99%)	2 (1%)	67	86
30	q	164/171 (96%)	162 (99%)	2 (1%)	67	86
31	R	153/201 (76%)	153 (100%)	0	100	100
31	r	153/201 (76%)	153 (100%)	0	100	100
32	S	174/198 (88%)	174 (100%)	0	100	100
32	s	175/198 (88%)	175 (100%)	0	100	100
33	T	175/214 (82%)	174 (99%)	1 (1%)	84	93
33	t	175/214 (82%)	174 (99%)	1 (1%)	84	93
All	All	11147/12734 (88%)	11022 (99%)	125 (1%)	69	87

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

Mol	Chain	Res	Type
12	f	703	ARG
30	Q	4	LEU
14	B	48	LYS
27	N	28	ASN
24	k	20	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 118 such sidechains are listed below:

Mol	Chain	Res	Type
12	f	565	ASN
27	n	28	ASN
15	C	53	ASN
26	m	221	ASN
29	P	93	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

## 5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry ⓘ

Of 12 ligands modelled in this entry, 6 are monoatomic - leaving 6 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
35	ATP	B	501	36	28,33,33	0.80	0	34,52,52	1.19	1 (2%)
35	ATP	E	401	36	28,33,33	0.78	0	34,52,52	1.17	3 (8%)
35	ATP	D	501	36	28,33,33	0.78	0	34,52,52	1.29	4 (11%)
37	ADP	C	501	-	24,29,29	0.82	0	29,45,45	1.35	3 (10%)
37	ADP	F	501	36	24,29,29	0.81	0	29,45,45	1.19	2 (6%)
35	ATP	A	501	36	28,33,33	0.83	0	34,52,52	1.18	2 (5%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
35	ATP	B	501	36	-	3/18/38/38	0/3/3/3
35	ATP	E	401	36	-	2/18/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
35	ATP	D	501	36	-	4/18/38/38	0/3/3/3
37	ADP	C	501	-	-	4/12/32/32	0/3/3/3
37	ADP	F	501	36	-	5/12/32/32	0/3/3/3
35	ATP	A	501	36	-	1/18/38/38	0/3/3/3

There are no bond length outliers.

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	B	501	ATP	N3-C2-N1	-3.97	123.28	128.67
35	D	501	ATP	N3-C2-N1	-3.60	123.78	128.67
35	D	501	ATP	C4'-O4'-C1'	-3.59	106.64	109.92
35	E	401	ATP	N3-C2-N1	-3.59	123.80	128.67
37	C	501	ADP	N3-C2-N1	-3.54	123.87	128.67

There are no chirality outliers.

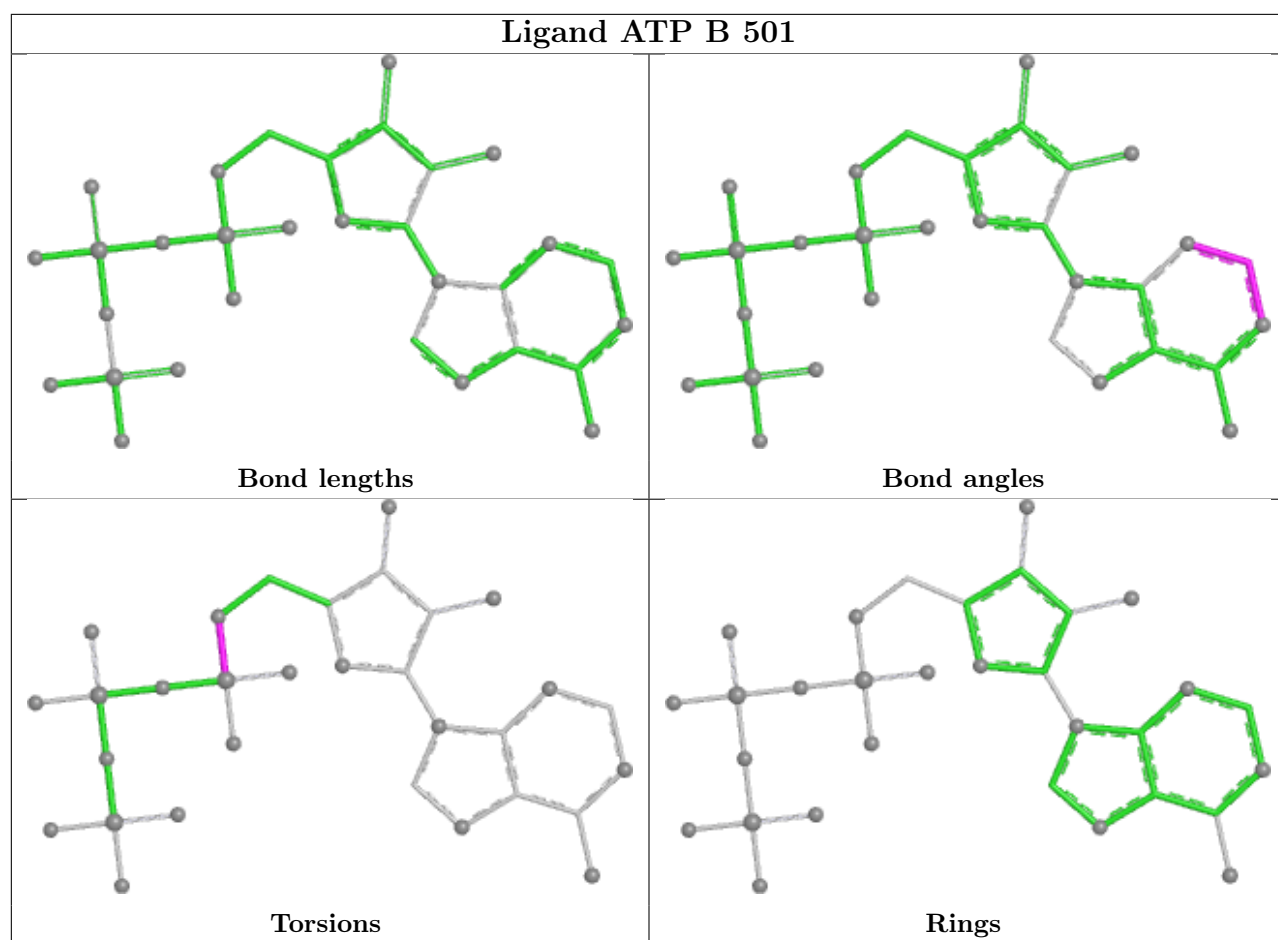
5 of 19 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
35	B	501	ATP	C5'-O5'-PA-O1A
35	B	501	ATP	C5'-O5'-PA-O2A
35	B	501	ATP	C5'-O5'-PA-O3A
37	C	501	ADP	PA-O3A-PB-O3B
37	C	501	ADP	C5'-O5'-PA-O2A

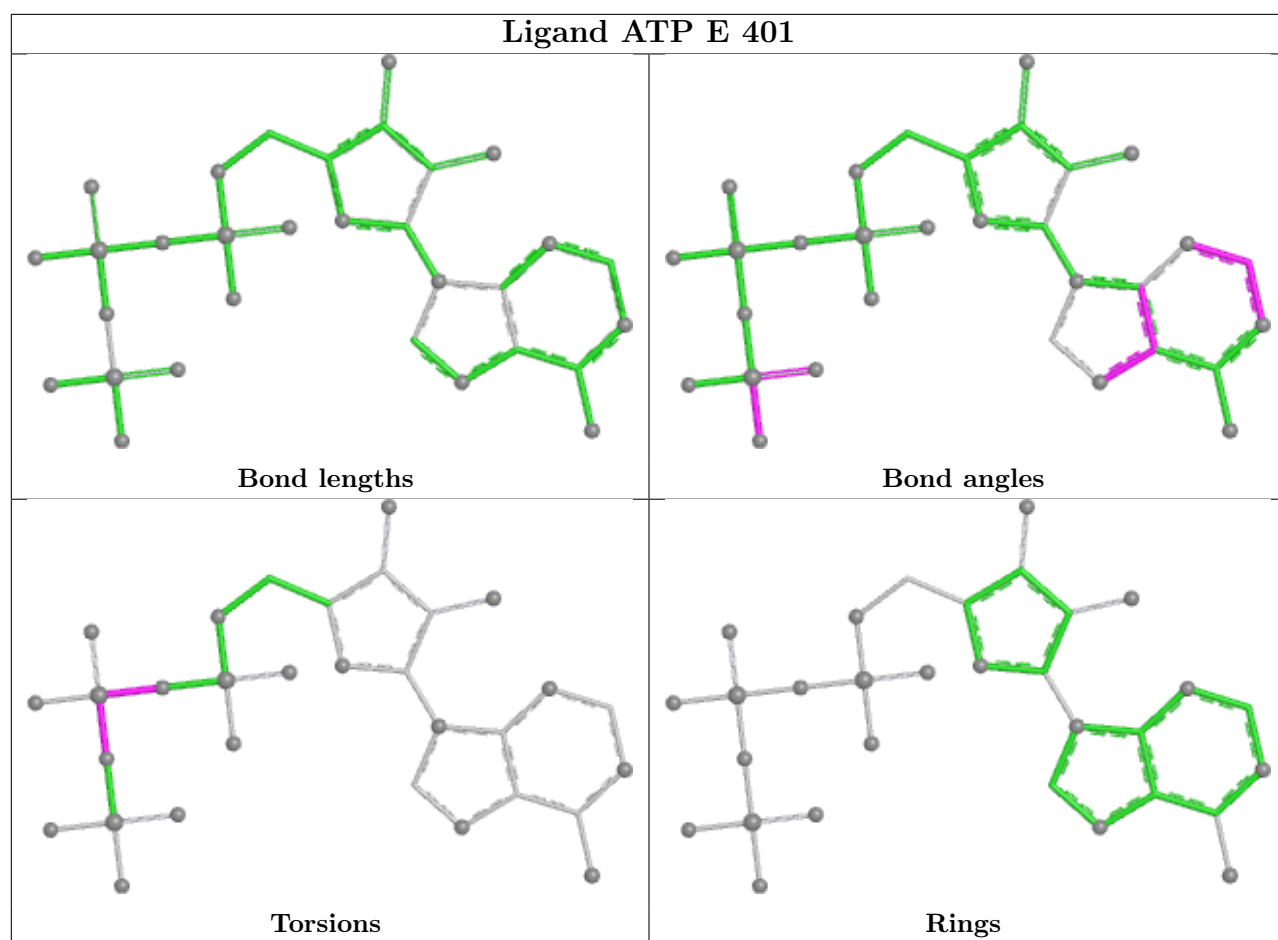
There are no ring outliers.

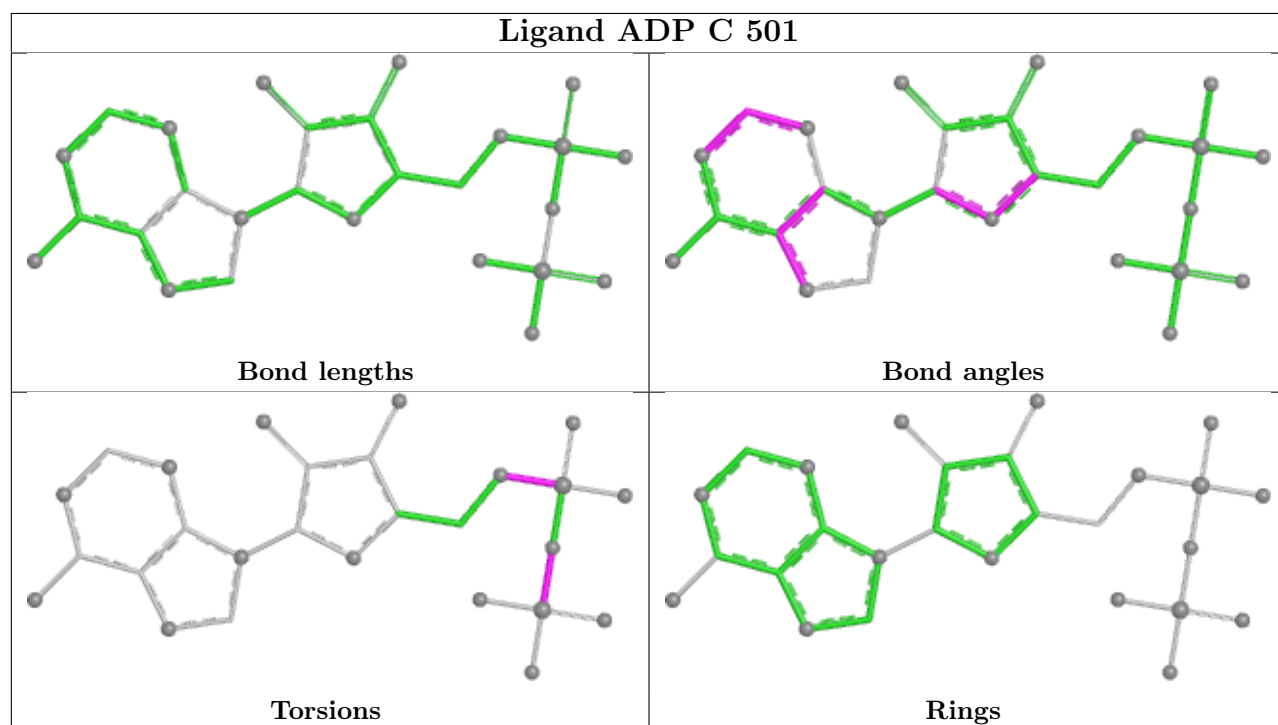
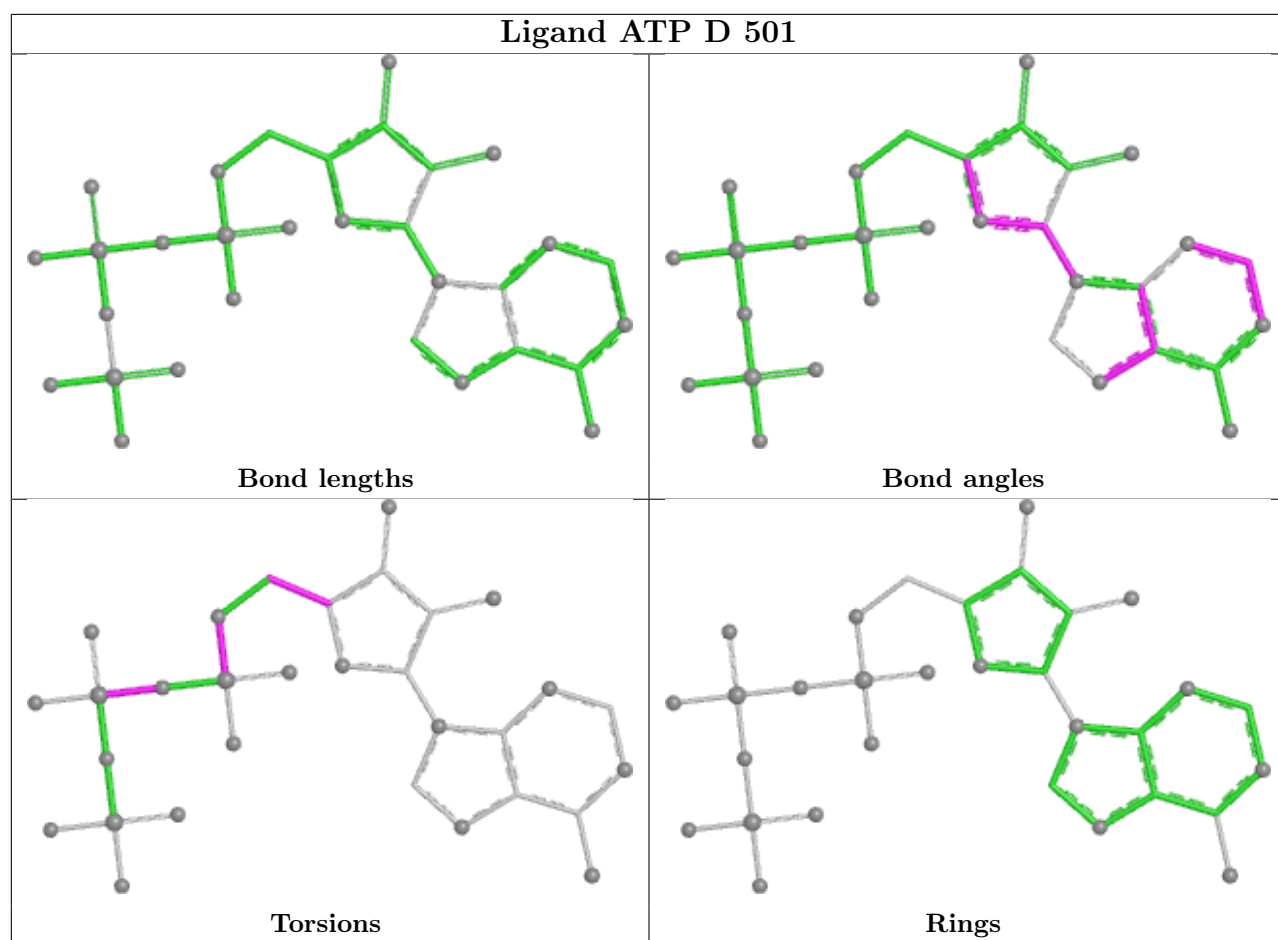
No monomer is involved in short contacts.

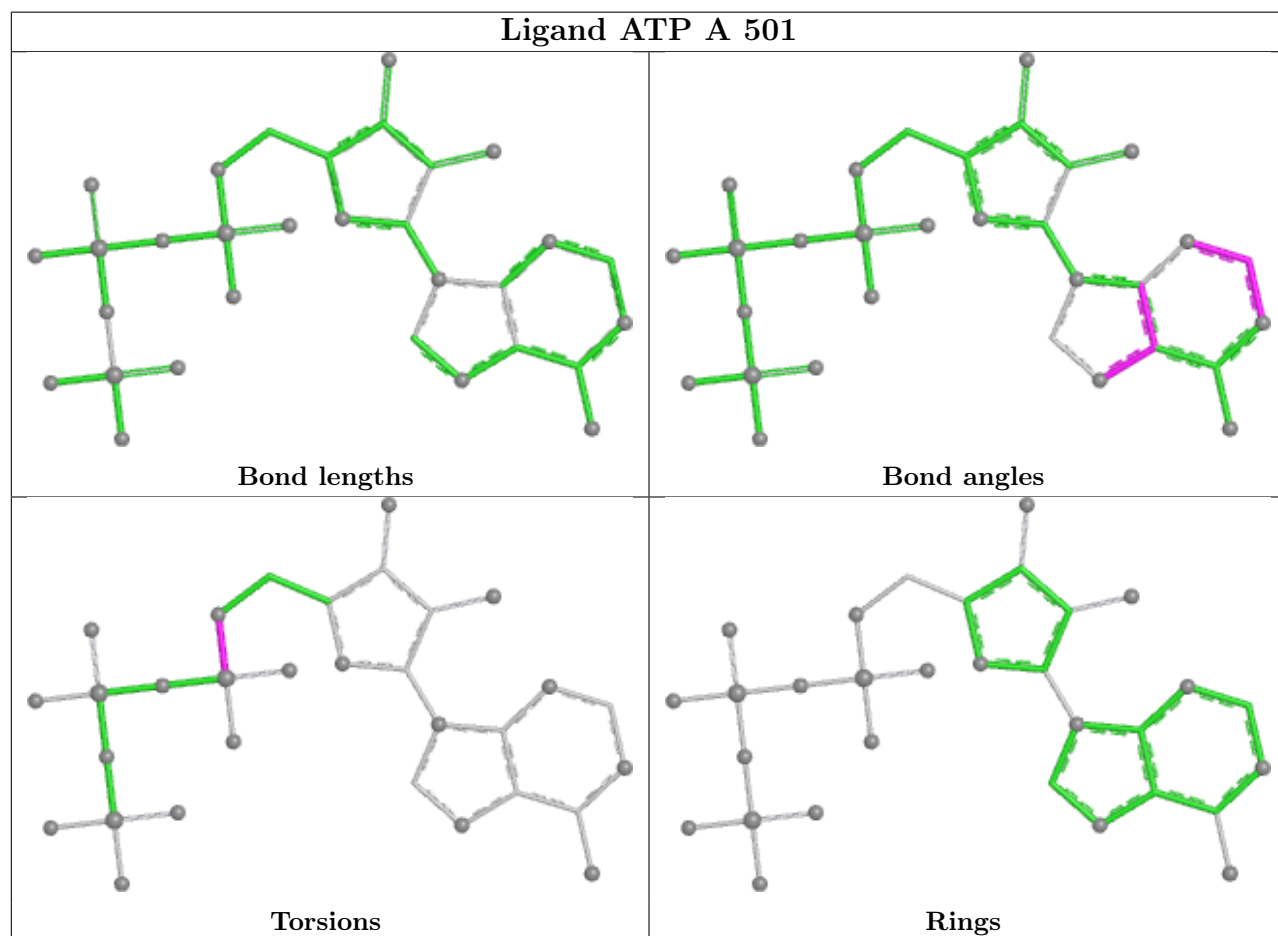
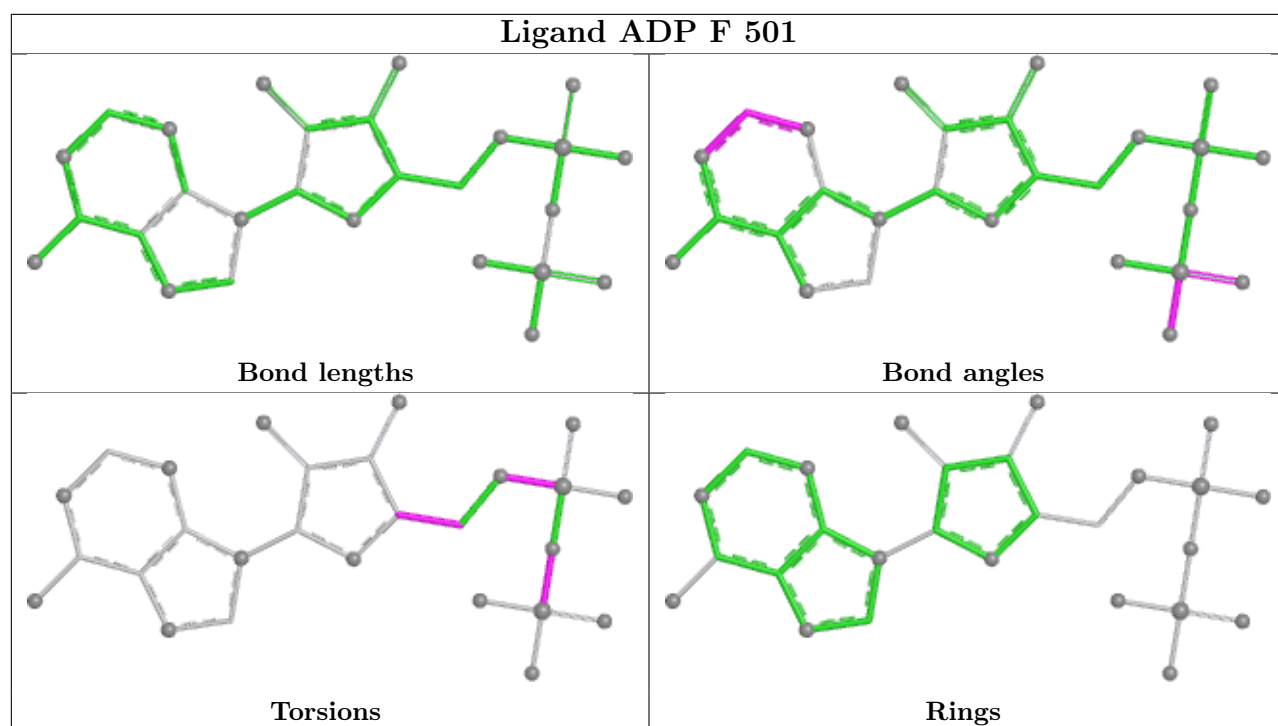
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.











## 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.

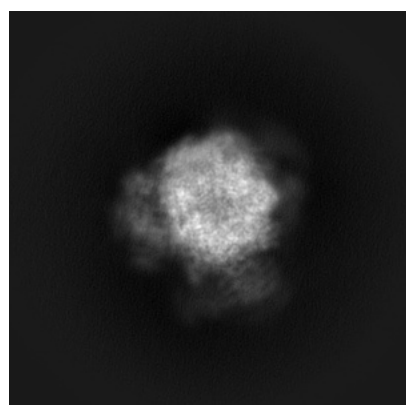
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-9216. These allow visual inspection of the internal detail of the map and identification of artifacts.

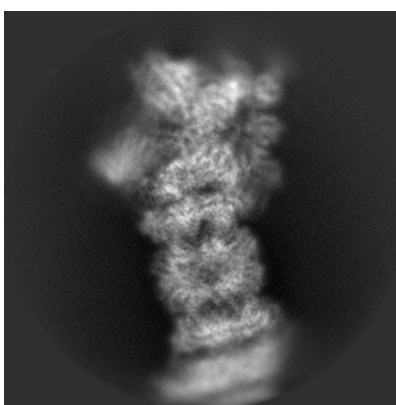
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

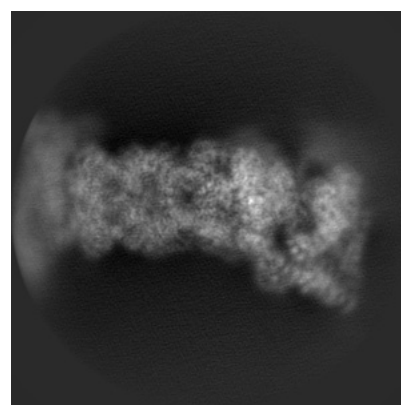
#### 6.1.1 Primary map



X



Y

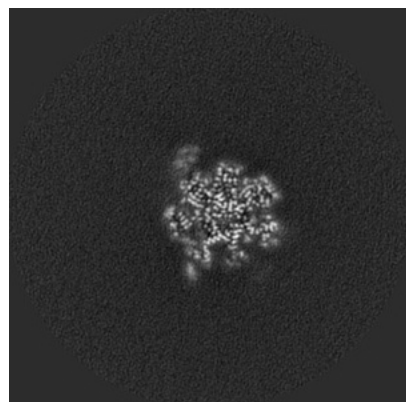


Z

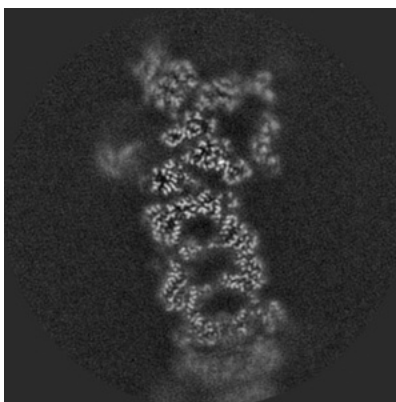
The images above show the map projected in three orthogonal directions.

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

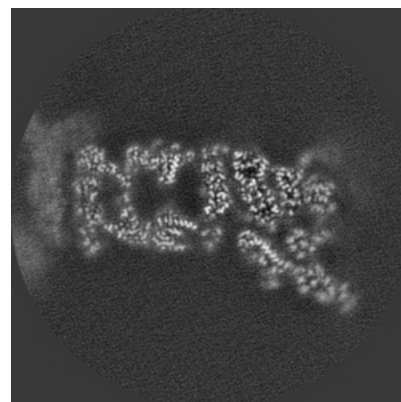
#### 6.2.1 Primary map



X Index: 300



Y Index: 300

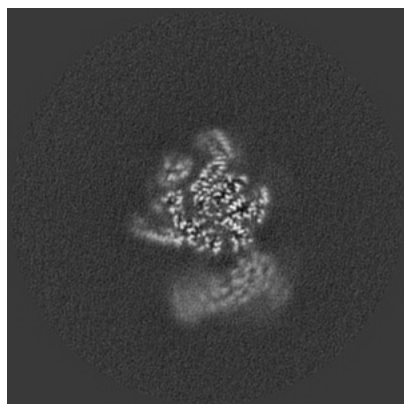


Z Index: 300

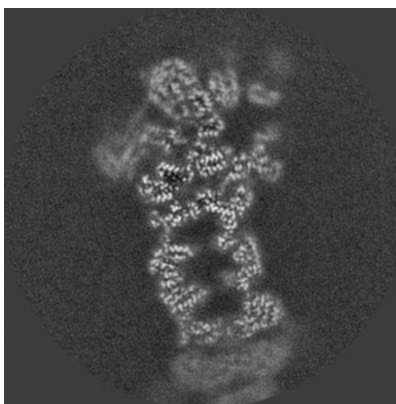
The images above show central slices of the map in three orthogonal directions.

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

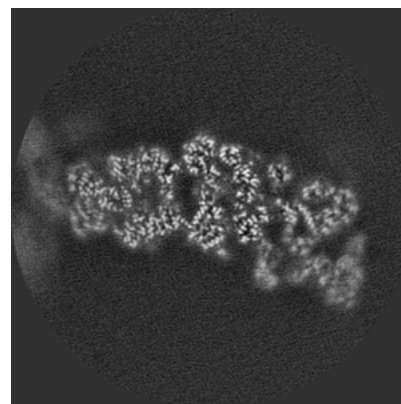
### 6.3.1 Primary map



X Index: 364



Y Index: 315

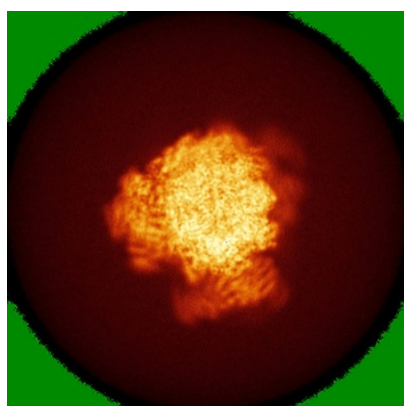


Z Index: 275

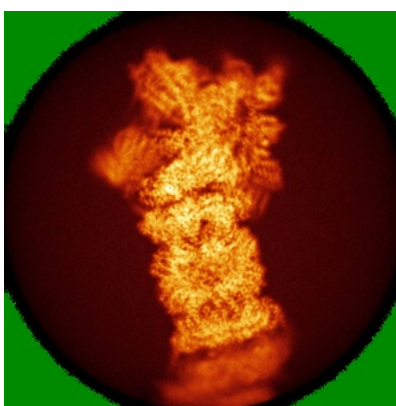
The images above show the largest variance slices of the map in three orthogonal directions.

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

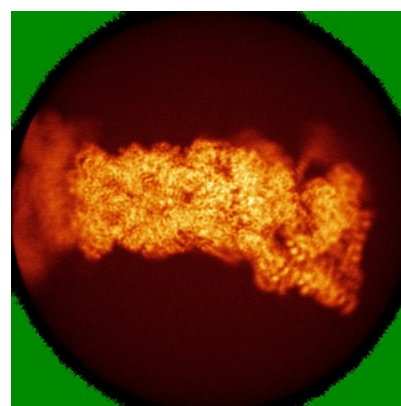
### 6.4.1 Primary map



X



Y

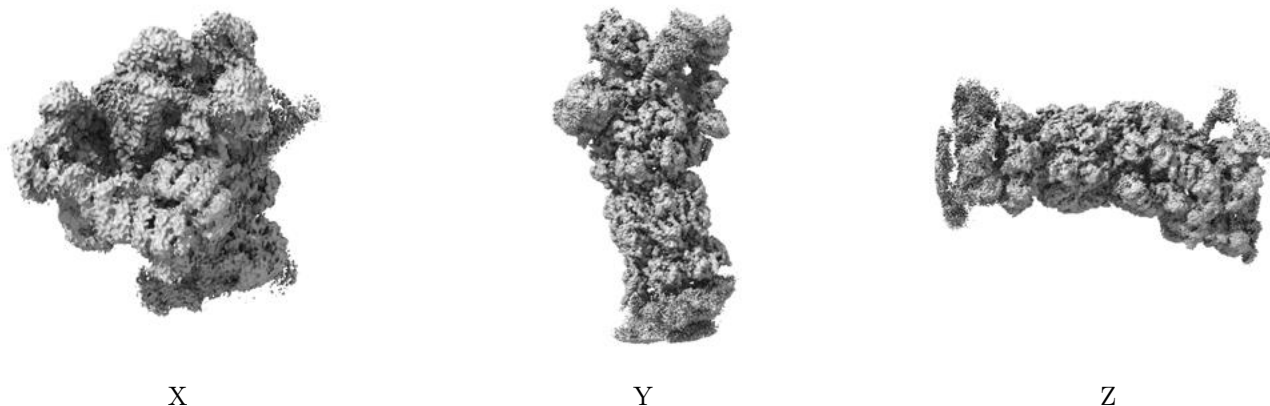


Z

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 0.0035. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

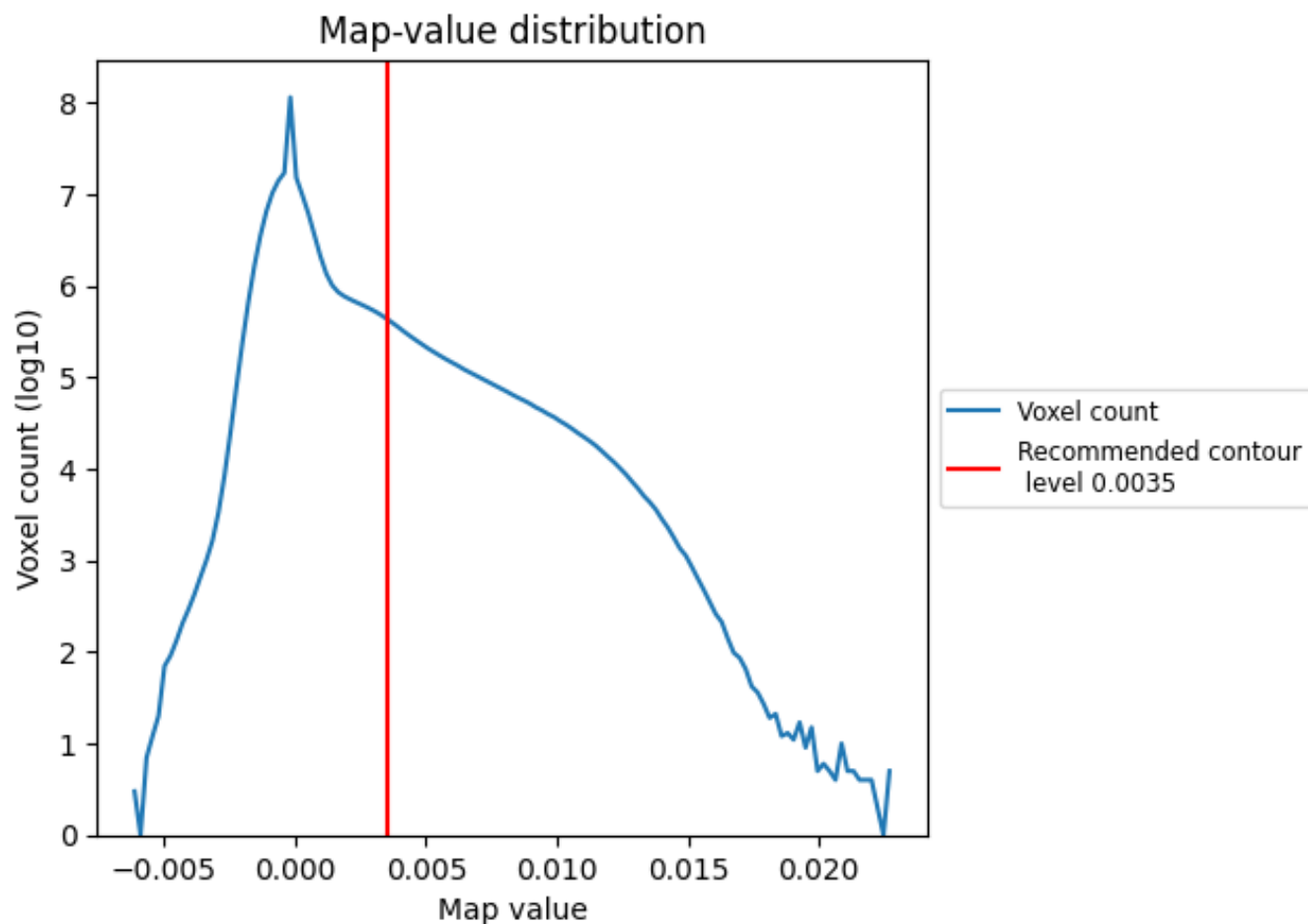
## 6.6 Mask visualisation [i](#)

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.

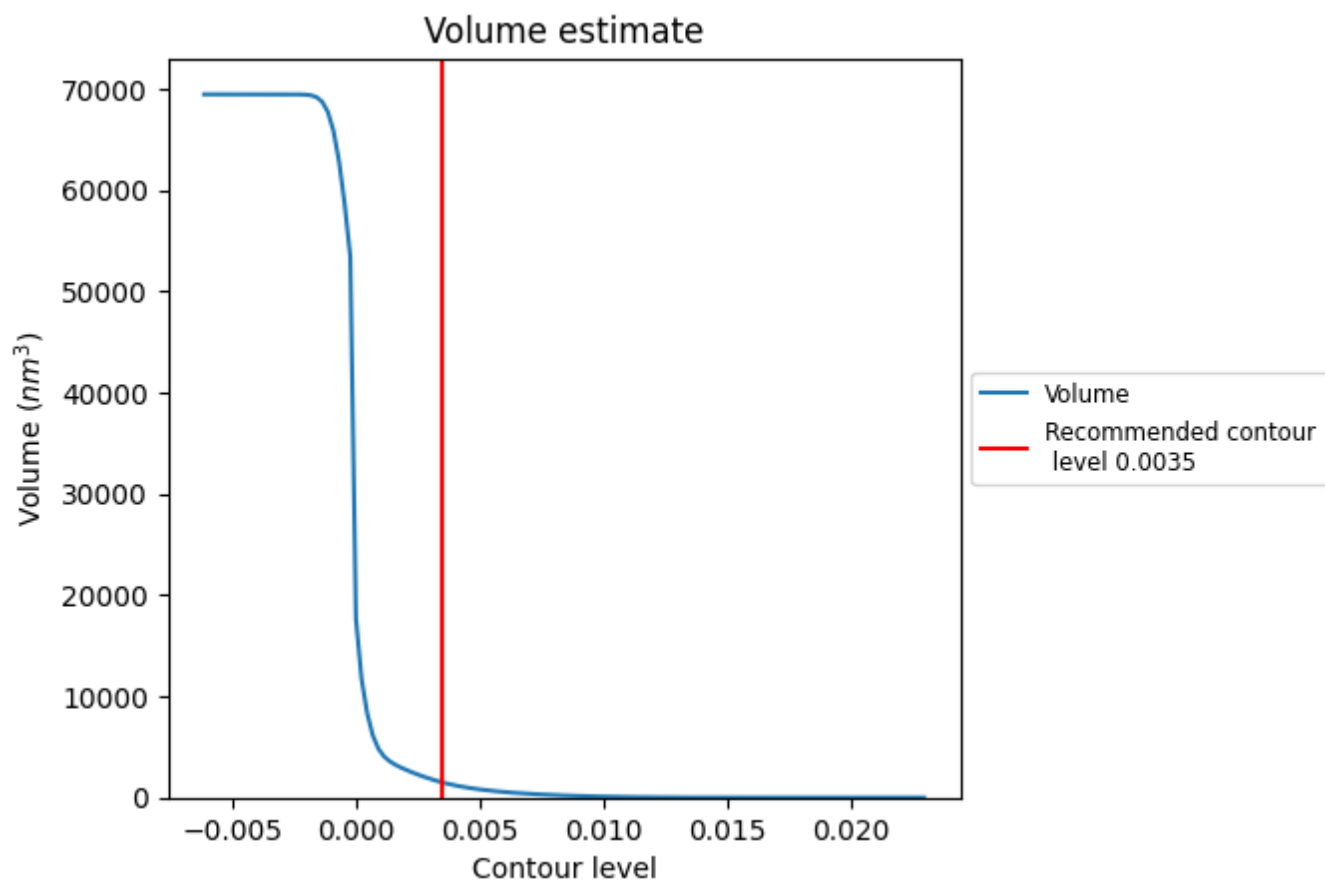
### 7.1 Map-value distribution [i](#)



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.



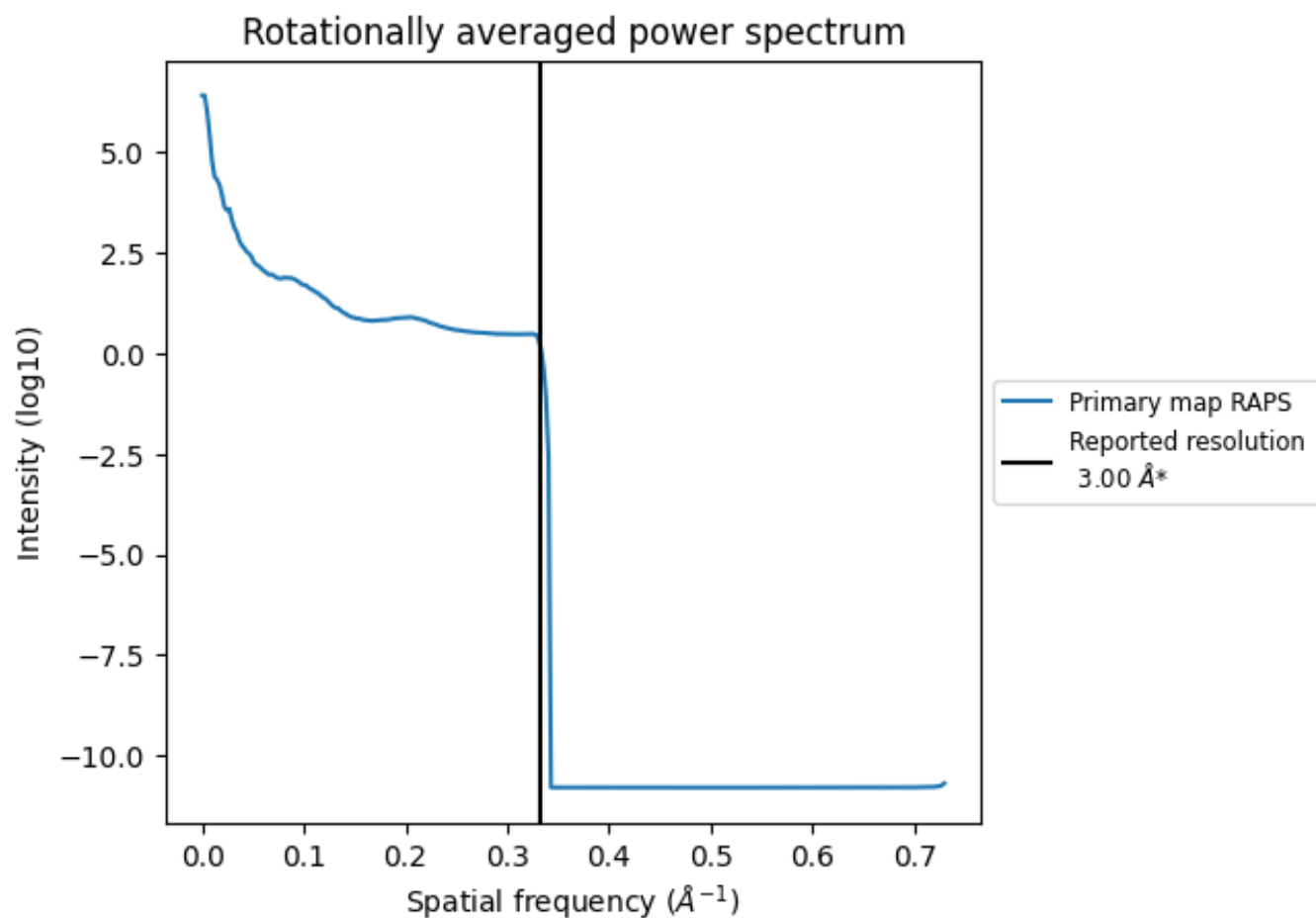
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1494 nm<sup>3</sup>; this corresponds to an approximate mass of 1350 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 0.333 Å<sup>-1</sup>

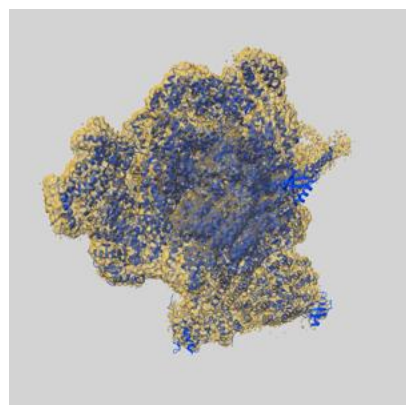
## 8 Fourier-Shell correlation

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

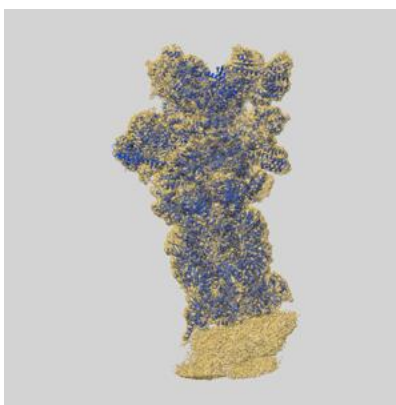
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-9216 and PDB model 6MSB. Per-residue inclusion information can be found in section 3 on page 13.

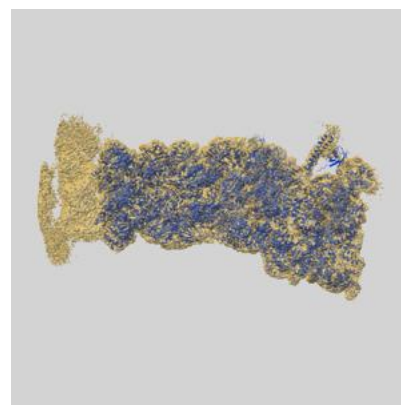
### 9.1 Map-model overlay [i](#)



X



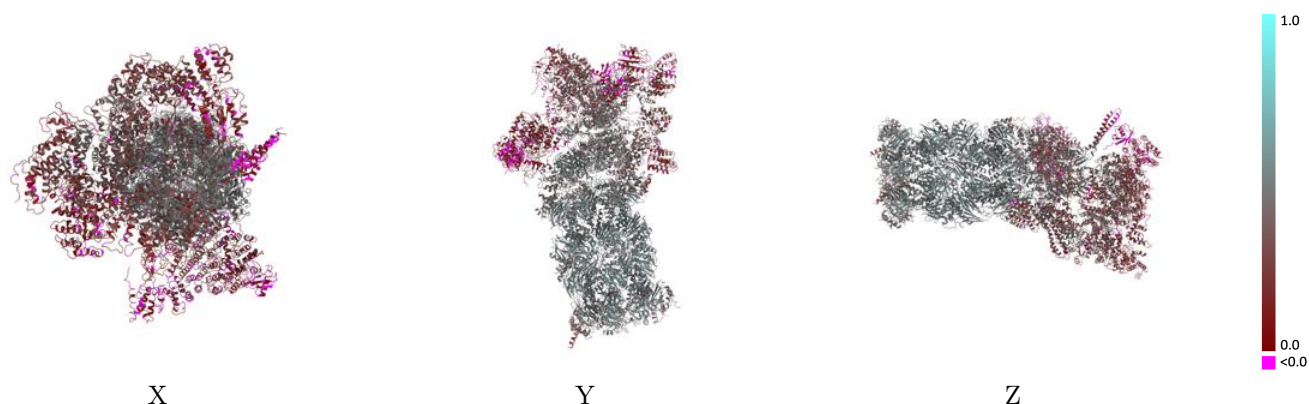
Y



Z

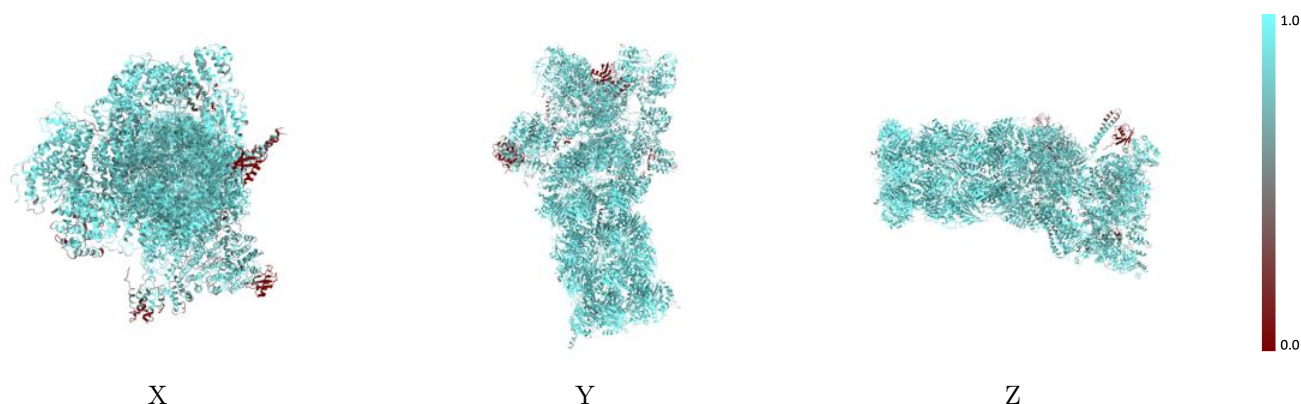
The images above show the 3D surface view of the map at the recommended contour level 0.0035 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



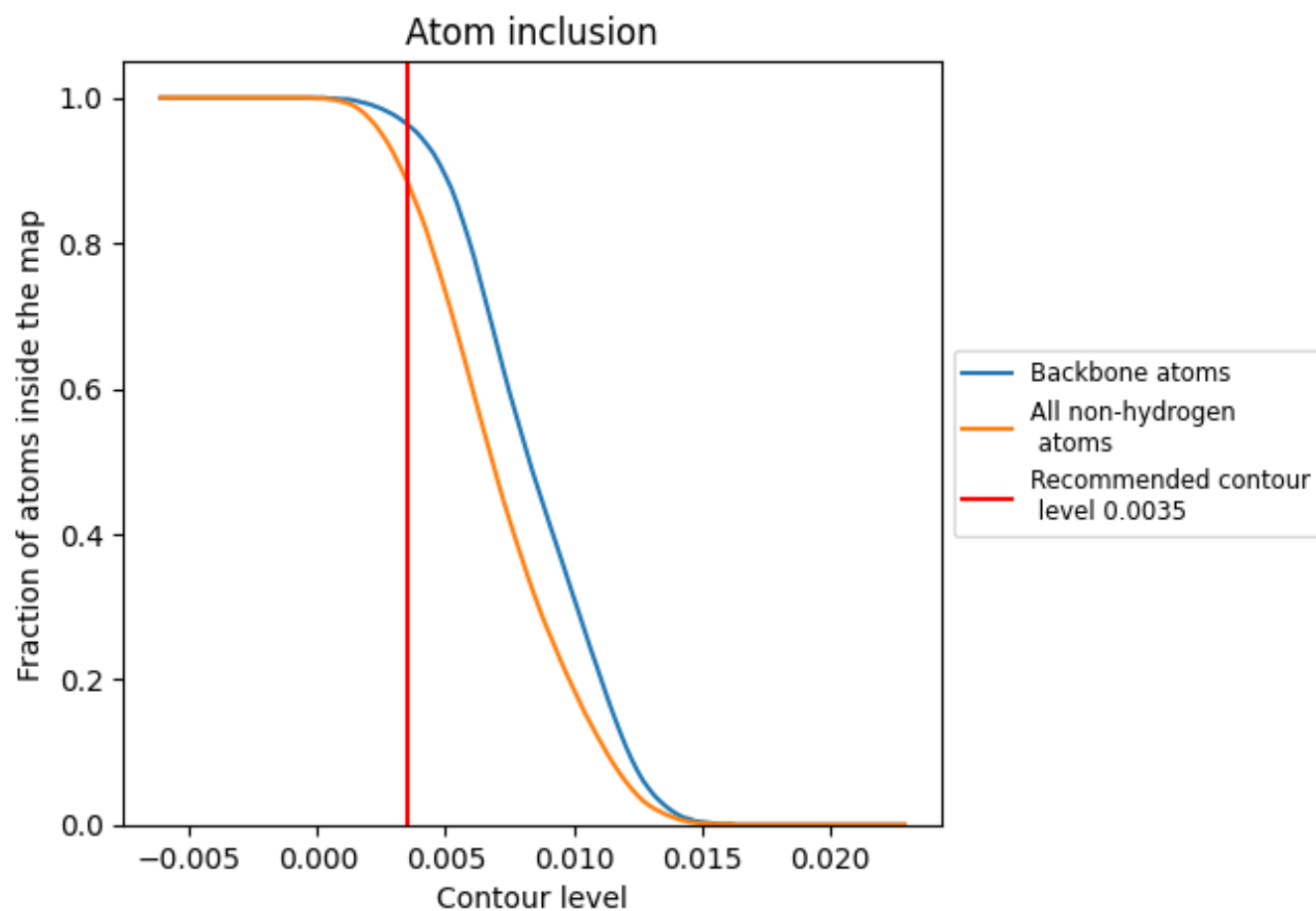
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0035).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 89% 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 (0.0035) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8860	 0.3890
A	 0.9040	 0.4330
B	 0.9080	 0.4270
C	 0.9130	 0.4390
D	 0.9020	 0.4280
E	 0.9030	 0.4250
F	 0.8980	 0.4340
G	 0.9460	 0.4920
H	 0.9550	 0.4990
I	 0.9460	 0.4700
J	 0.9560	 0.4710
K	 0.9470	 0.4850
L	 0.9530	 0.4930
M	 0.9410	 0.4780
N	 0.9640	 0.5170
O	 0.9780	 0.5130
P	 0.9670	 0.5180
Q	 0.9670	 0.5080
R	 0.9710	 0.5140
S	 0.9600	 0.5110
T	 0.9620	 0.5220
U	 0.8620	 0.2700
V	 0.7860	 0.2310
W	 0.7960	 0.2470
X	 0.8470	 0.3230
Y	 0.8940	 0.3210
Z	 0.8510	 0.3090
a	 0.8510	 0.2480
b	 0.8010	 0.1550
c	 0.8690	 0.3650
d	 0.8130	 0.2180
e	 0.7540	 0.1620
f	 0.7190	 0.1610
g	 0.9520	 0.4910
h	 0.9460	 0.4970



*Continued on next page...*

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Chain	Atom inclusion	Q-score
i	 0.9080	 0.4430
j	 0.9310	 0.4280
k	 0.9420	 0.4730
l	 0.9560	 0.4860
m	 0.9340	 0.4740
n	 0.9700	 0.5250
o	 0.9730	 0.5190
p	 0.9710	 0.5230
q	 0.9720	 0.5160
r	 0.9810	 0.5290
s	 0.9680	 0.5150
t	 0.9690	 0.5250
u	 0.0200	 -0.0160
w	 0.1080	 0.0120