



wwPDB EM Validation Summary Report ⓘ

Nov 29, 2022 – 09:01 AM JST

PDB ID : 7W3K
EMDB ID : EMD-32283
Title : Structure of USP14-bound human 26S proteasome in substrate-inhibited state
SD4_USP14
Authors : Zhang, S.; Zou, S.; Yin, D.; Wu, Z.; Mao, Y.
Deposited on : 2021-11-25
Resolution : 3.60 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

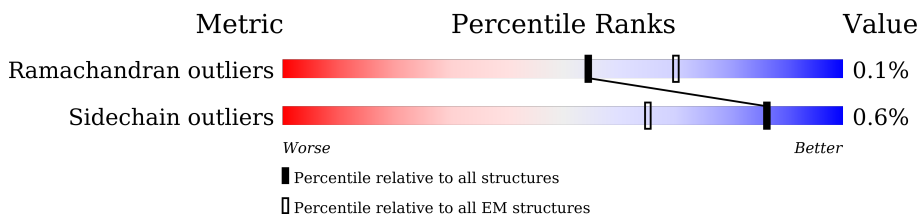
EMDB validation analysis : 0.0.1.dev43
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.3

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 3.60 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 ≥ 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	A	433	95% . 5%
2	B	440	93% 7%
3	E	403	96% ..
4	F	439	90% . 9%
5	G	246	98% .
5	g	246	99% .
6	H	234	99% .
6	h	234	99% .
7	I	261	94% . 5%

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Mol	Chain	Length	Quality of chain
7	i	261	95%
8	J	248	96%
8	j	248	96%
9	K	241	98%
9	k	241	97%
10	L	269	88% 11%
10	l	269	88% 12%
11	M	255	95% 5%
11	m	255	94% 6%
12	N	239	85% 15%
12	n	239	85% 15%
13	O	277	79% 21%
13	o	277	79% 21%
14	P	205	100%
14	p	205	99%
15	Q	201	99%
15	q	201	99%
16	R	263	76% 24%
16	r	263	76% 24%
17	S	241	88% 12%
17	s	241	88% 12%
18	T	264	81% 18%
18	t	264	82% 18%
19	x	494	27% 100%
20	y	76	41% 100%

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Mol	Chain	Length	Quality of chain
21	C	398	6% 99%
22	D	418	90% 9%
23	U	953	8% 91% 8%
24	W	456	9% 97%
25	X	422	89% 10%
26	Y	389	99%
27	Z	324	86% 12%
28	a	376	97%
29	b	377	51% 49%
30	c	310	91% 7%
31	d	350	23% 72% 27%
32	f	908	9% 97%
33	V	534	8% 83% 17%
34	e	70	71% 29%

2 Entry composition [i](#)

There are 37 unique types of molecules in this entry. The entry contains 110657 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 protease regulatory subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	413	3229	2034	566	611	18	0	0

- Molecule 2 is a protein called 26S protease regulatory subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	411	3207	2022	548	622	15	0	0

- Molecule 3 is a protein called 26S proteasome regulatory subunit 10B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	E	389	3097	1947	552	581	17	0	0

- Molecule 4 is a protein called 26S protease regulatory subunit 6A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	F	400	3133	1972	540	603	18	0	0

- Molecule 5 is a protein called Proteasome subunit alpha type-6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	G	240	1867	1187	312	355	13	0	0
5	g	244	1879	1193	318	355	13	0	0

- Molecule 6 is a protein called Proteasome subunit alpha type-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	H	232	Total	C	N	O	S	0	0
			1801	1149	304	342	6		
6	h	232	Total	C	N	O	S	0	0
			1805	1154	307	338	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	I	248	Total	C	N	O	S	0	0
			1933	1222	330	371	10		
7	i	250	Total	C	N	O	S	0	0
			1955	1234	336	375	10		

- Molecule 8 is a protein called Proteasome subunit alpha type-7.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	J	239	Total	C	N	O	S	0	0
			1861	1166	327	363	5		
8	j	239	Total	C	N	O	S	0	0
			1861	1168	332	356	5		

- Molecule 9 is a protein called Proteasome subunit alpha type-5.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	K	238	Total	C	N	O	S	0	0
			1813	1139	302	361	11		
9	k	234	Total	C	N	O	S	0	0
			1782	1119	295	357	11		

- Molecule 10 is a protein called Isoform Long of Proteasome subunit alpha type-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L	240	Total	C	N	O	S	0	0
			1876	1175	338	352	11		
10	l	238	Total	C	N	O	S	0	0
			1861	1165	335	350	11		

- Molecule 11 is a protein called Proteasome subunit alpha type-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	M	242	Total	C	N	O	S	0	0
			1890	1200	323	356	11		

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	m	240	Total	C	N	O	S	0	0
			1881	1193	321	356	11		

- Molecule 12 is a protein called Proteasome subunit beta type-6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	N	203	Total	C	N	O	S	0	0
			1521	954	259	296	12		
12	n	202	Total	C	N	O	S	0	0
			1510	947	258	293	12		

- Molecule 13 is a protein called Proteasome subunit beta type-7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	O	220	Total	C	N	O	S	0	0
			1645	1035	278	320	12		
13	o	220	Total	C	N	O	S	0	0
			1659	1044	283	320	12		

- Molecule 14 is a protein called Proteasome subunit beta type-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	P	204	Total	C	N	O	S	0	0
			1587	1010	264	294	19		
14	p	204	Total	C	N	O	S	0	0
			1591	1013	265	294	19		

- Molecule 15 is a protein called Proteasome subunit beta type-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	Q	199	Total	C	N	O	S	0	0
			1588	1017	270	292	9		
15	q	199	Total	C	N	O	S	0	0
			1578	1012	267	290	9		

- Molecule 16 is a protein called Proteasome subunit beta type-5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	R	201	Total	C	N	O	S	0	0
			1559	982	274	294	9		
16	r	201	Total	C	N	O	S	0	0
			1549	977	270	293	9		

- Molecule 17 is a protein called Proteasome subunit beta type-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	S	213	Total	C	N	O	S	0	0
			1641	1041	281	309	10		
17	s	213	Total	C	N	O	S	0	0
			1650	1044	283	313	10		

- Molecule 18 is a protein called Proteasome subunit beta type-4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	T	216	Total	C	N	O	S	0	0
			1683	1062	291	318	12		
18	t	216	Total	C	N	O	S	0	0
			1687	1064	291	320	12		

- Molecule 19 is a protein called Ubiquitin carboxyl-terminal hydrolase 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	x	494	Total	C	N	O	S	0	0
			3929	2485	647	769	28		

- Molecule 20 is a protein called Ubiquitin.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	y	76	Total	C	N	O	S	0	0
			601	378	105	117	1		

- Molecule 21 is a protein called Isoform 2 of 26S proteasome regulatory subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	C	396	Total	C	N	O	S	0	0
			3105	1954	558	576	17		

- Molecule 22 is a protein called 26S protease regulatory subunit 6B.

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

- Molecule 23 is a protein called 26S proteasome non-ATPase regulatory subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	U	872	6828	4328	1157	1298	45	0	0

- Molecule 24 is a protein called 26S proteasome non-ATPase regulatory subunit 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	W	446	3635	2302	622	687	24	0	0

- Molecule 25 is a protein called 26S proteasome non-ATPase regulatory subunit 11.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	Y	389	3202	2041	545	598	18	0	0

- Molecule 27 is a protein called 26S proteasome non-ATPase regulatory subunit 7.

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

- Molecule 28 is a protein called 26S proteasome non-ATPase regulatory subunit 13.

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

- Molecule 29 is a protein called 26S proteasome non-ATPase regulatory subunit 4.

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

- Molecule 30 is a protein called 26S proteasome non-ATPase regulatory subunit 14.

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

- Molecule 31 is a protein called 26S proteasome non-ATPase regulatory subunit 8.

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

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

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

- Molecule 33 is a protein called 26S proteasome non-ATPase regulatory subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	V	444	3612	2301	645	653	13	0	0

- Molecule 34 is a protein called 26S proteasome complex subunit DSS1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
34	e	50	425	260	65	100	0	0

- Molecule 35 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂) (labeled as "Ligand of Interest" by depositor).

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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
36	F	1	31	10	5	13	3	0

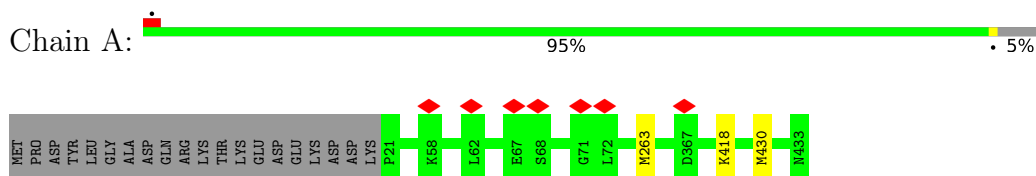
- Molecule 37 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

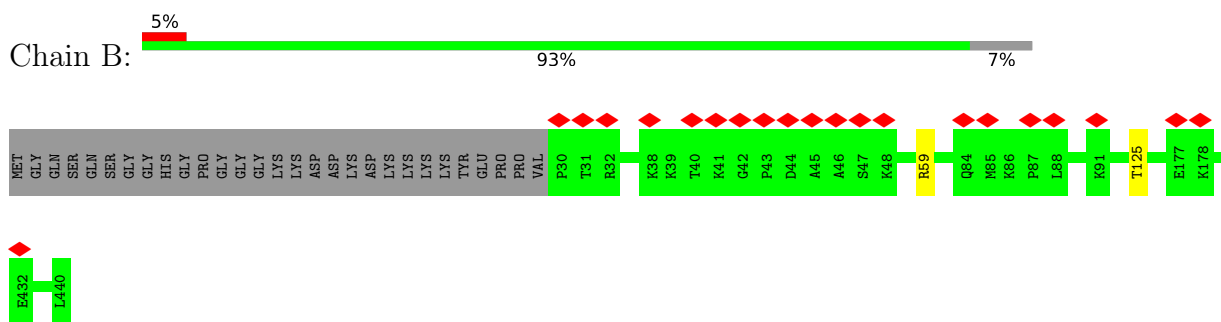
3 Residue-property plots [i](#)

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.

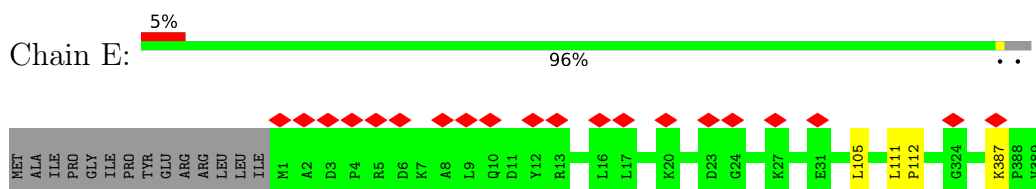
- Molecule 1: 26S protease regulatory subunit 7



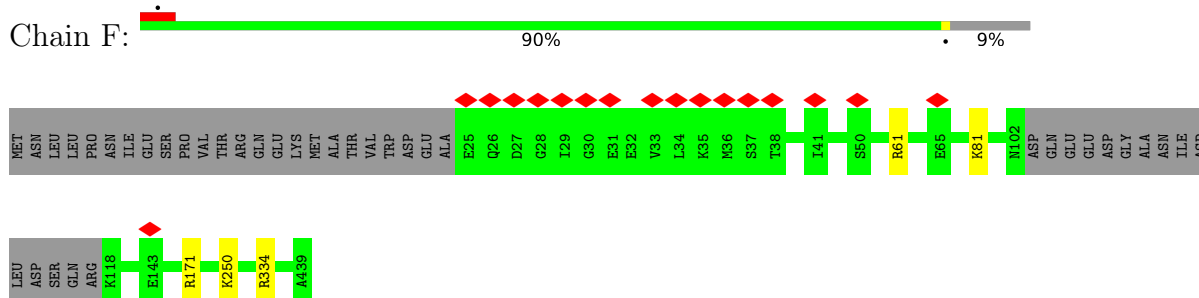
- Molecule 2: 26S protease regulatory subunit 4



- Molecule 3: 26S proteasome regulatory subunit 10B



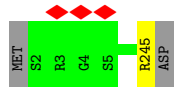
- Molecule 4: 26S protease regulatory subunit 6A



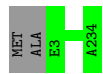
- Molecule 5: Proteasome subunit alpha type-6



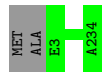
- Molecule 5: Proteasome subunit alpha type-6



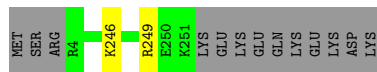
- Molecule 6: Proteasome subunit alpha type-2



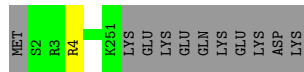
- Molecule 6: Proteasome subunit alpha type-2



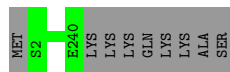
- Molecule 7: Proteasome subunit alpha type-4




- Molecule 7: Proteasome subunit alpha type-4

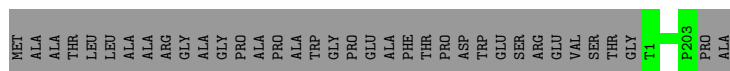


- Molecule 8: Proteasome subunit alpha type-7




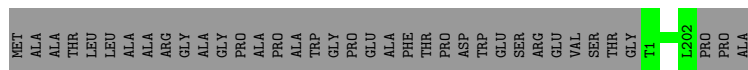
• Molecule 12: Proteasome subunit beta type-6

Chain N:  85% 15%




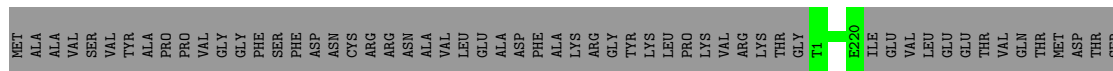
• Molecule 12: Proteasome subunit beta type-6

Chain n:  85% 15%




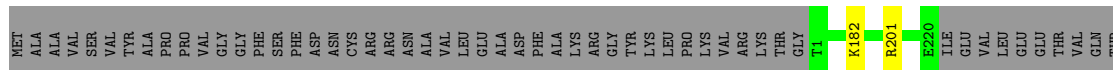
• Molecule 13: Proteasome subunit beta type-7

Chain O:  79% 21%



• Molecule 13: Proteasome subunit beta type-7

Chain o:  79% 21%



• Molecule 14: Proteasome subunit beta type-3

Chain P:  100%



• Molecule 14: Proteasome subunit beta type-3

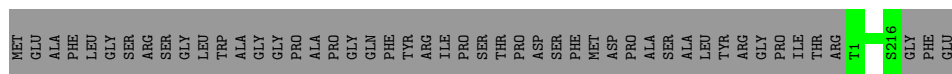
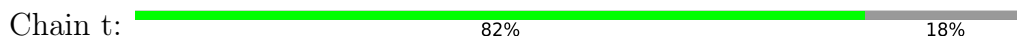
Chain p:  99%



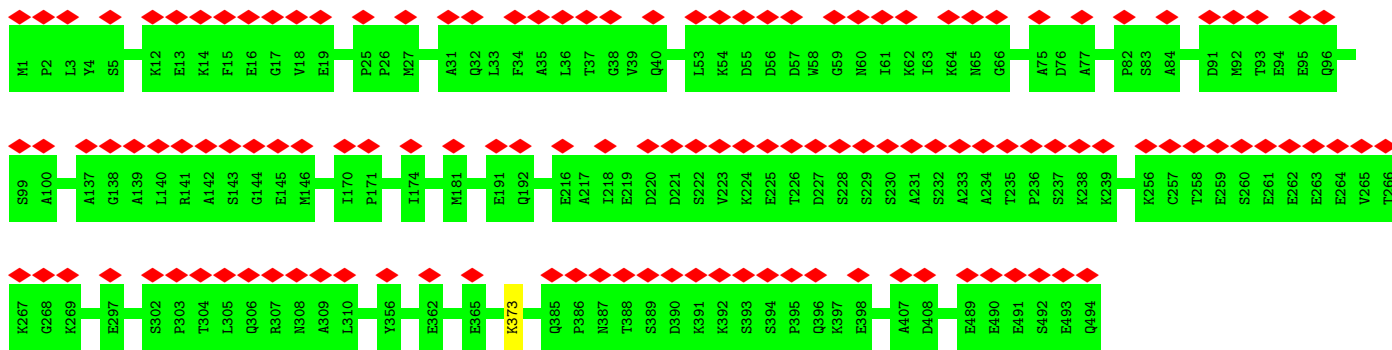
• Molecule 15: Proteasome subunit beta type-2

Chain Q:  99%

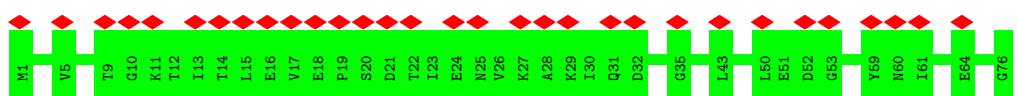
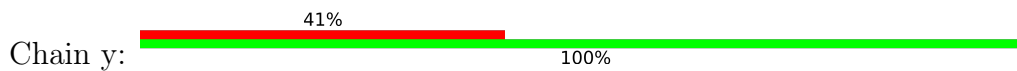
• Molecule 18: Proteasome subunit beta type-4



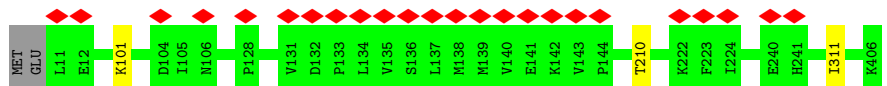
• Molecule 19: Ubiquitin carboxyl-terminal hydrolase 14



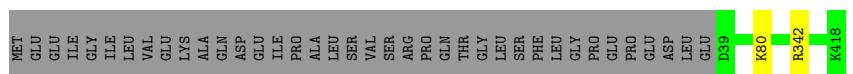
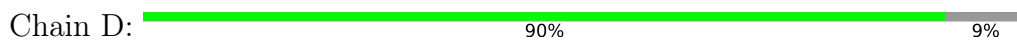
• Molecule 20: Ubiquitin



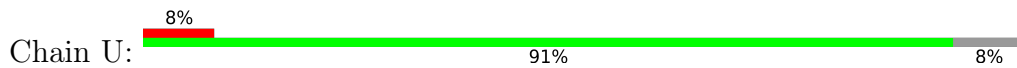
• Molecule 21: Isoform 2 of 26S proteasome regulatory subunit 8

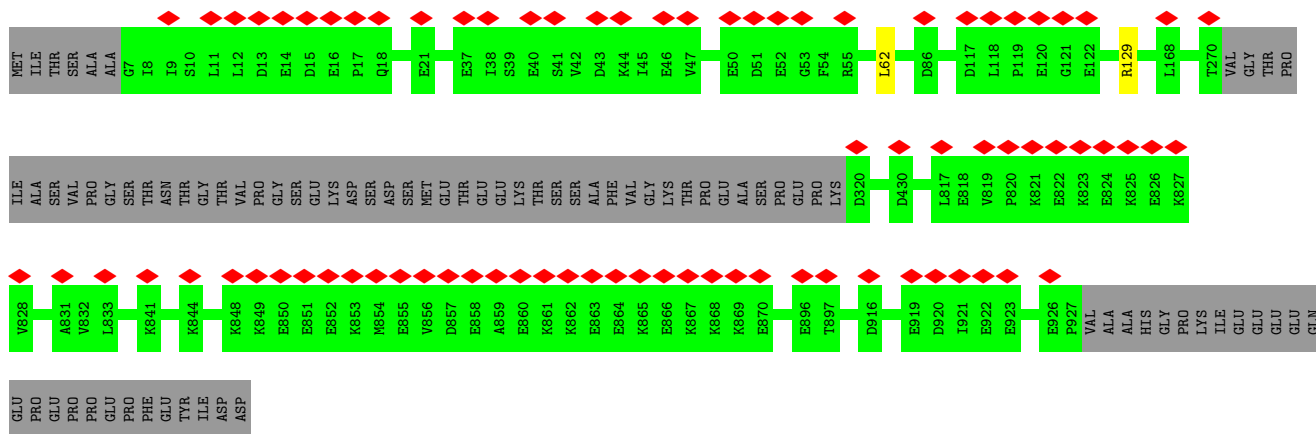


• Molecule 22: 26S protease regulatory subunit 6B



• Molecule 23: 26S proteasome non-ATPase regulatory subunit 1

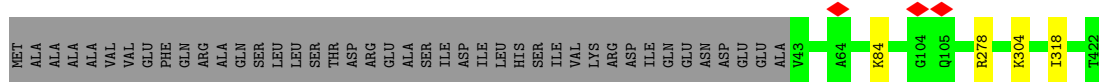
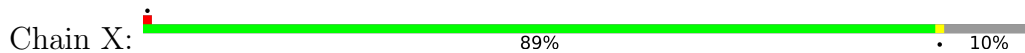




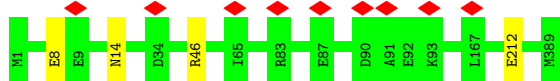
• Molecule 24: 26S proteasome non-ATPase regulatory subunit 12



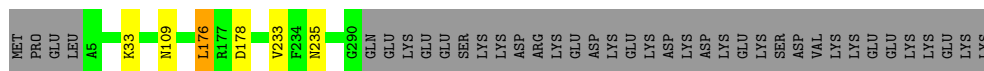
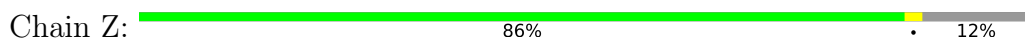
• Molecule 25: 26S proteasome non-ATPase regulatory subunit 11



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



• Molecule 27: 26S proteasome non-ATPase regulatory subunit 7



• Molecule 28: 26S proteasome non-ATPase regulatory subunit 13



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	74792	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	400	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.019	Depositor
Minimum map value	-0.004	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.005	Depositor
Map size (\AA)	438.4, 438.4, 438.4	wwPDB
Map dimensions	640, 640, 640	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	0.685, 0.685, 0.685	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.27	0/3283	0.61	2/4433 (0.0%)
2	B	0.27	0/3254	0.58	0/4388
3	E	0.28	0/3145	0.58	1/4233 (0.0%)
4	F	0.26	0/3173	0.57	0/4273
5	G	0.28	0/1901	0.53	0/2572
5	g	0.28	0/1913	0.52	0/2589
6	H	0.30	0/1840	0.54	0/2495
6	h	0.28	0/1844	0.52	0/2497
7	I	0.28	0/1963	0.53	0/2650
7	i	0.29	0/1985	0.56	0/2677
8	J	0.27	0/1887	0.55	0/2553
8	j	0.28	0/1887	0.57	0/2549
9	K	0.28	0/1841	0.54	1/2486 (0.0%)
9	k	0.26	0/1809	0.52	0/2444
10	L	0.28	0/1911	0.55	0/2584
10	l	0.27	0/1896	0.53	0/2565
11	M	0.29	0/1925	0.54	0/2592
11	m	0.29	0/1916	0.53	0/2580
12	N	0.28	0/1548	0.50	0/2097
12	n	0.28	0/1536	0.52	0/2080
13	O	0.27	0/1672	0.54	0/2267
13	o	0.28	0/1686	0.55	0/2282
14	P	0.28	0/1616	0.56	0/2180
14	p	0.28	0/1620	0.54	0/2184
15	Q	0.29	0/1621	0.52	0/2194
15	q	0.29	0/1611	0.52	0/2182
16	R	0.29	0/1590	0.54	0/2147
16	r	0.28	0/1580	0.55	0/2135
17	S	0.28	0/1671	0.56	0/2252
17	s	0.30	0/1680	0.55	0/2264
18	T	0.29	0/1716	0.54	0/2323
18	t	0.28	0/1720	0.54	0/2328

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
19	x	0.25	0/4002	0.51	0/5390
20	y	0.26	0/607	0.57	0/816
21	C	0.27	0/3146	0.59	0/4226
22	D	0.27	0/3089	0.58	0/4168
23	U	0.27	0/6945	0.57	1/9382 (0.0%)
24	W	0.26	0/3683	0.59	0/4952
25	X	0.26	0/3053	0.56	0/4115
26	Y	0.28	0/3261	0.63	0/4393
27	Z	0.26	0/2324	0.60	2/3150 (0.1%)
28	a	0.26	0/3053	0.59	1/4133 (0.0%)
29	b	0.29	0/1478	0.59	0/2001
30	c	0.27	0/2302	0.61	1/3110 (0.0%)
31	d	0.27	0/2162	0.57	0/2919
32	f	0.28	0/6980	0.62	1/9433 (0.0%)
33	V	0.26	0/3681	0.55	0/4969
34	e	0.29	0/437	0.46	0/595
All	All	0.27	0/112443	0.56	10/151827 (0.0%)

There are no bond length outliers.

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	c	184	LEU	CA-CB-CG	5.74	128.50	115.30
9	K	121	LEU	CA-CB-CG	5.63	128.25	115.30
32	f	502	LEU	CA-CB-CG	5.55	128.07	115.30
27	Z	176	LEU	CA-CB-CG	5.53	128.02	115.30
28	a	342	ASP	CB-CG-OD1	5.39	123.15	118.30

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

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	411/433 (95%)	375 (91%)	36 (9%)	0	100	100
2	B	409/440 (93%)	367 (90%)	42 (10%)	0	100	100
3	E	387/403 (96%)	359 (93%)	27 (7%)	1 (0%)	41	75
4	F	396/439 (90%)	373 (94%)	23 (6%)	0	100	100
5	G	238/246 (97%)	226 (95%)	12 (5%)	0	100	100
5	g	242/246 (98%)	232 (96%)	10 (4%)	0	100	100
6	H	230/234 (98%)	220 (96%)	10 (4%)	0	100	100
6	h	230/234 (98%)	219 (95%)	11 (5%)	0	100	100
7	I	246/261 (94%)	235 (96%)	11 (4%)	0	100	100
7	i	248/261 (95%)	238 (96%)	10 (4%)	0	100	100
8	J	237/248 (96%)	222 (94%)	15 (6%)	0	100	100
8	j	237/248 (96%)	229 (97%)	8 (3%)	0	100	100
9	K	236/241 (98%)	224 (95%)	12 (5%)	0	100	100
9	k	232/241 (96%)	223 (96%)	9 (4%)	0	100	100
10	L	238/269 (88%)	227 (95%)	11 (5%)	0	100	100
10	l	236/269 (88%)	230 (98%)	6 (2%)	0	100	100
11	M	240/255 (94%)	233 (97%)	7 (3%)	0	100	100
11	m	238/255 (93%)	234 (98%)	4 (2%)	0	100	100
12	N	201/239 (84%)	194 (96%)	7 (4%)	0	100	100
12	n	200/239 (84%)	196 (98%)	4 (2%)	0	100	100
13	O	218/277 (79%)	209 (96%)	9 (4%)	0	100	100
13	o	218/277 (79%)	208 (95%)	10 (5%)	0	100	100
14	P	202/205 (98%)	191 (95%)	11 (5%)	0	100	100
14	p	202/205 (98%)	194 (96%)	8 (4%)	0	100	100
15	Q	197/201 (98%)	191 (97%)	6 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	q	197/201 (98%)	190 (96%)	7 (4%)	0	100	100
16	R	199/263 (76%)	194 (98%)	5 (2%)	0	100	100
16	r	199/263 (76%)	193 (97%)	6 (3%)	0	100	100
17	S	211/241 (88%)	201 (95%)	10 (5%)	0	100	100
17	s	211/241 (88%)	205 (97%)	6 (3%)	0	100	100
18	T	214/264 (81%)	205 (96%)	9 (4%)	0	100	100
18	t	214/264 (81%)	206 (96%)	8 (4%)	0	100	100
19	x	492/494 (100%)	477 (97%)	15 (3%)	0	100	100
20	y	74/76 (97%)	72 (97%)	2 (3%)	0	100	100
21	C	394/398 (99%)	353 (90%)	40 (10%)	1 (0%)	41	75
22	D	378/418 (90%)	337 (89%)	41 (11%)	0	100	100
23	U	868/953 (91%)	828 (95%)	40 (5%)	0	100	100
24	W	444/456 (97%)	420 (95%)	22 (5%)	2 (0%)	29	68
25	X	378/422 (90%)	355 (94%)	22 (6%)	1 (0%)	41	75
26	Y	387/389 (100%)	349 (90%)	35 (9%)	3 (1%)	19	59
27	Z	284/324 (88%)	251 (88%)	33 (12%)	0	100	100
28	a	371/376 (99%)	340 (92%)	30 (8%)	1 (0%)	41	75
29	b	189/377 (50%)	179 (95%)	10 (5%)	0	100	100
30	c	285/310 (92%)	251 (88%)	34 (12%)	0	100	100
31	d	255/350 (73%)	217 (85%)	35 (14%)	3 (1%)	13	51
32	f	887/908 (98%)	795 (90%)	92 (10%)	0	100	100
33	V	442/534 (83%)	433 (98%)	9 (2%)	0	100	100
34	e	48/70 (69%)	41 (85%)	7 (15%)	0	100	100
All	All	13990/15458 (90%)	13141 (94%)	837 (6%)	12 (0%)	54	83

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	E	112	PRO
31	d	93	ALA
26	Y	8	GLU
26	Y	14	ASN
31	d	110	ASN

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	A	348/372 (94%)	347 (100%)	1 (0%)	92	97
2	B	357/385 (93%)	355 (99%)	2 (1%)	86	94
3	E	341/353 (97%)	339 (99%)	2 (1%)	86	94
4	F	344/379 (91%)	339 (98%)	5 (2%)	65	84
5	G	202/210 (96%)	202 (100%)	0	100	100
5	g	201/210 (96%)	200 (100%)	1 (0%)	88	95
6	H	187/191 (98%)	187 (100%)	0	100	100
6	h	188/191 (98%)	188 (100%)	0	100	100
7	I	202/221 (91%)	200 (99%)	2 (1%)	76	88
7	i	206/221 (93%)	205 (100%)	1 (0%)	88	95
8	J	197/211 (93%)	197 (100%)	0	100	100
8	j	196/211 (93%)	195 (100%)	1 (0%)	88	95
9	K	197/203 (97%)	196 (100%)	1 (0%)	88	95
9	k	195/203 (96%)	194 (100%)	1 (0%)	88	95
10	L	202/230 (88%)	200 (99%)	2 (1%)	76	88
10	l	201/230 (87%)	199 (99%)	2 (1%)	76	88
11	M	198/212 (93%)	197 (100%)	1 (0%)	88	95
11	m	198/212 (93%)	198 (100%)	0	100	100
12	N	158/181 (87%)	158 (100%)	0	100	100
12	n	156/181 (86%)	156 (100%)	0	100	100
13	O	178/228 (78%)	178 (100%)	0	100	100
13	o	181/228 (79%)	179 (99%)	2 (1%)	73	88
14	P	172/174 (99%)	172 (100%)	0	100	100
14	p	173/174 (99%)	172 (99%)	1 (1%)	86	94
15	Q	168/171 (98%)	168 (100%)	0	100	100
15	q	166/171 (97%)	166 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
16	R	156/202 (77%)	156 (100%)	0	100	100
16	r	154/202 (76%)	154 (100%)	0	100	100
17	S	175/199 (88%)	174 (99%)	1 (1%)	86	94
17	s	177/199 (89%)	177 (100%)	0	100	100
18	T	178/215 (83%)	177 (99%)	1 (1%)	86	94
18	t	179/215 (83%)	179 (100%)	0	100	100
19	x	439/439 (100%)	438 (100%)	1 (0%)	93	98
20	y	68/68 (100%)	68 (100%)	0	100	100
21	C	340/346 (98%)	338 (99%)	2 (1%)	86	94
22	D	333/366 (91%)	331 (99%)	2 (1%)	86	94
23	U	748/816 (92%)	747 (100%)	1 (0%)	93	98
24	W	410/416 (99%)	407 (99%)	3 (1%)	84	93
25	X	327/362 (90%)	324 (99%)	3 (1%)	78	90
26	Y	344/344 (100%)	343 (100%)	1 (0%)	92	97
27	Z	257/295 (87%)	251 (98%)	6 (2%)	50	76
28	a	333/336 (99%)	327 (98%)	6 (2%)	59	81
29	b	167/312 (54%)	167 (100%)	0	100	100
30	c	252/268 (94%)	247 (98%)	5 (2%)	55	79
31	d	231/294 (79%)	229 (99%)	2 (1%)	78	90
32	f	745/763 (98%)	739 (99%)	6 (1%)	81	91
33	V	390/460 (85%)	387 (99%)	3 (1%)	81	91
34	e	44/63 (70%)	44 (100%)	0	100	100
All	All	11959/13133 (91%)	11891 (99%)	68 (1%)	86	94

5 of 68 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
31	d	111	ARG
32	f	100	ARG
33	V	106	ARG
13	o	182	LYS
10	l	239	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
24	W	283	GLN
24	W	395	ASN
29	b	47	ASN
2	B	241	ASN
1	A	150	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](#)

Of 5 ligands modelled in this entry, 1 is monoatomic - leaving 4 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	ADP	B	501	-	24,29,29	0.96	1 (4%)	29,45,45	1.43	4 (13%)
36	ATP	E	501	-	26,33,33	0.61	0	31,52,52	0.75	2 (6%)
36	ATP	F	501	-	26,33,33	0.60	0	31,52,52	0.81	1 (3%)
35	ADP	A	501	-	24,29,29	0.95	1 (4%)	29,45,45	1.41	4 (13%)

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	ADP	B	501	-	-	4/12/32/32	0/3/3/3
36	ATP	E	501	-	-	7/18/38/38	0/3/3/3
36	ATP	F	501	-	-	9/18/38/38	0/3/3/3
35	ADP	A	501	-	-	5/12/32/32	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
35	B	501	ADP	C5-C4	2.51	1.47	1.40
35	A	501	ADP	C5-C4	2.44	1.47	1.40

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	B	501	ADP	C3'-C2'-C1'	4.00	107.01	100.98
35	A	501	ADP	PA-O3A-PB	-3.50	120.81	132.83
35	A	501	ADP	N3-C2-N1	-3.25	123.59	128.68
35	B	501	ADP	N3-C2-N1	-3.03	123.94	128.68
35	B	501	ADP	PA-O3A-PB	-2.80	123.20	132.83

There are no chirality outliers.

5 of 25 torsion outliers are listed below:

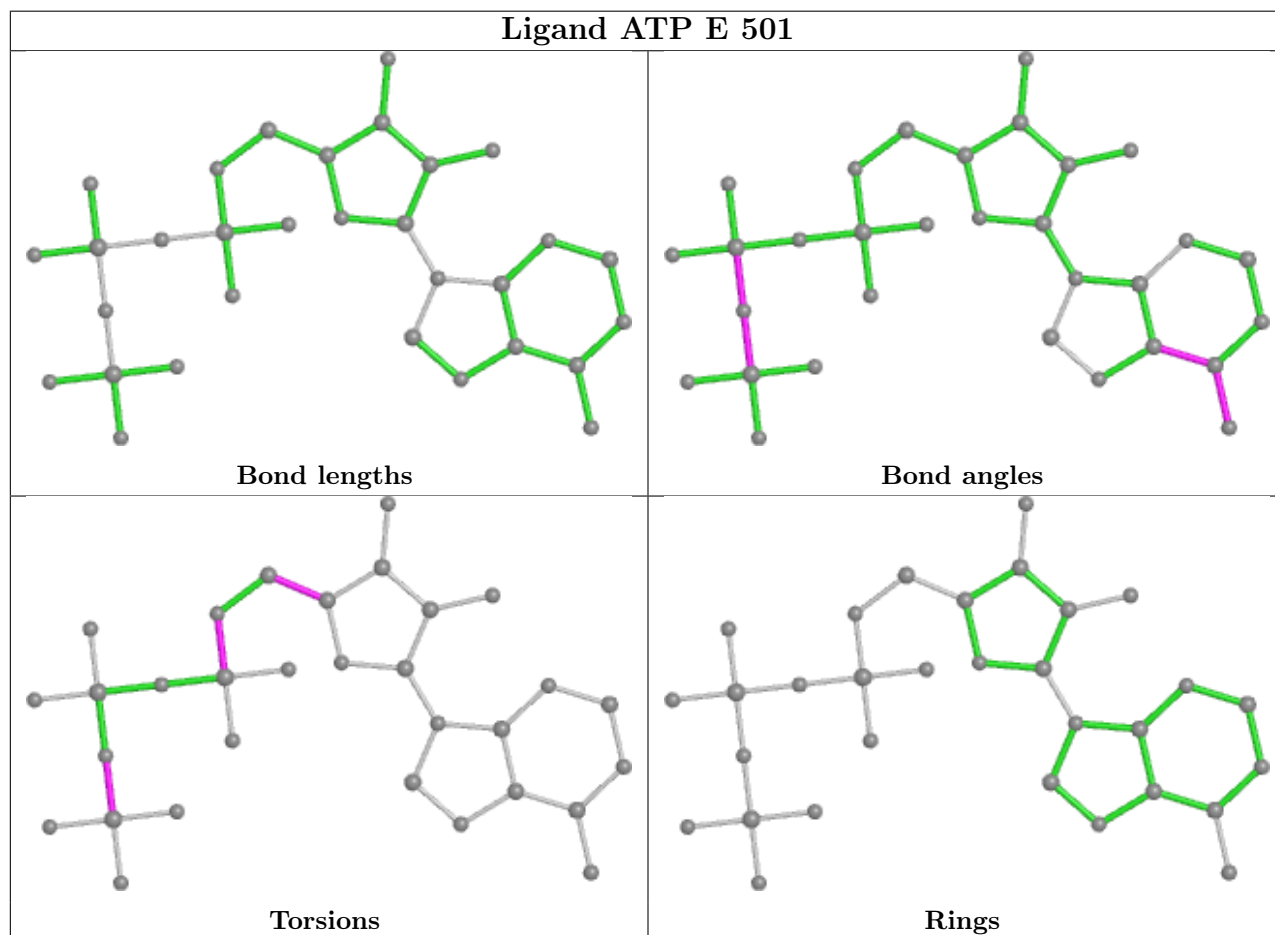
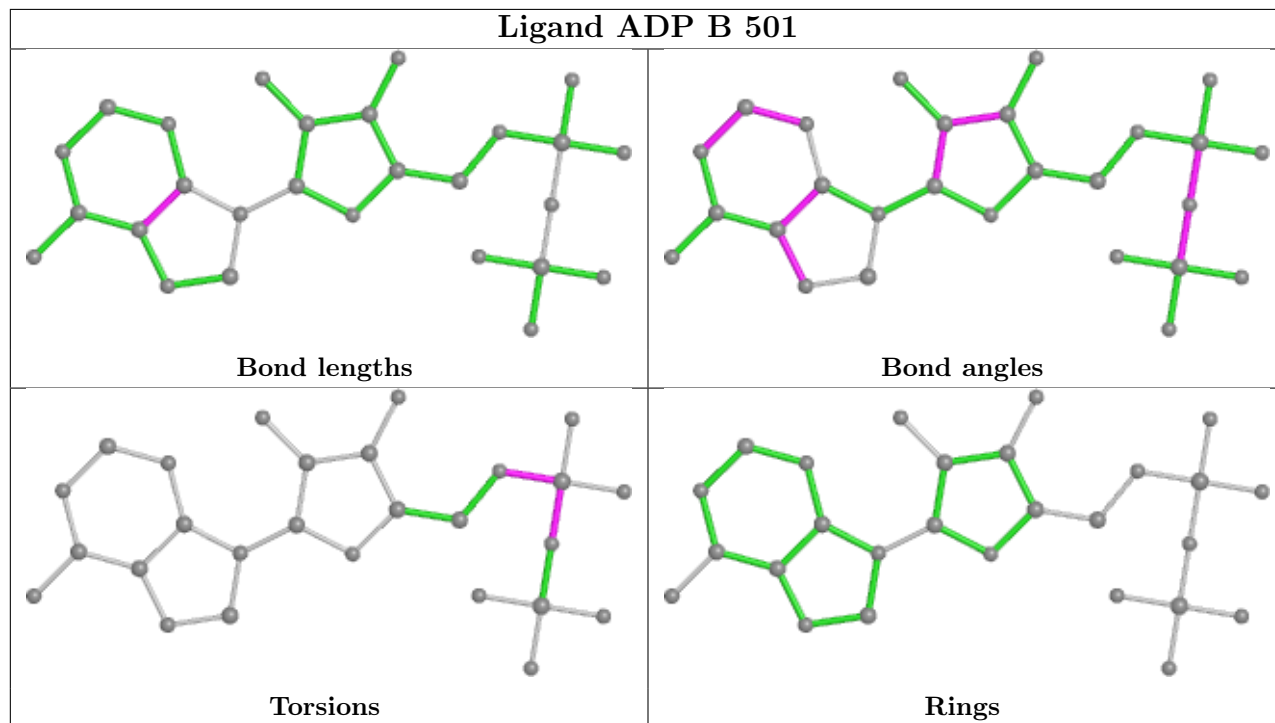
Mol	Chain	Res	Type	Atoms
35	A	501	ADP	C5'-O5'-PA-O1A
36	E	501	ATP	PB-O3B-PG-O3G
36	E	501	ATP	C5'-O5'-PA-O1A
36	E	501	ATP	C3'-C4'-C5'-O5'
36	F	501	ATP	PB-O3B-PG-O3G

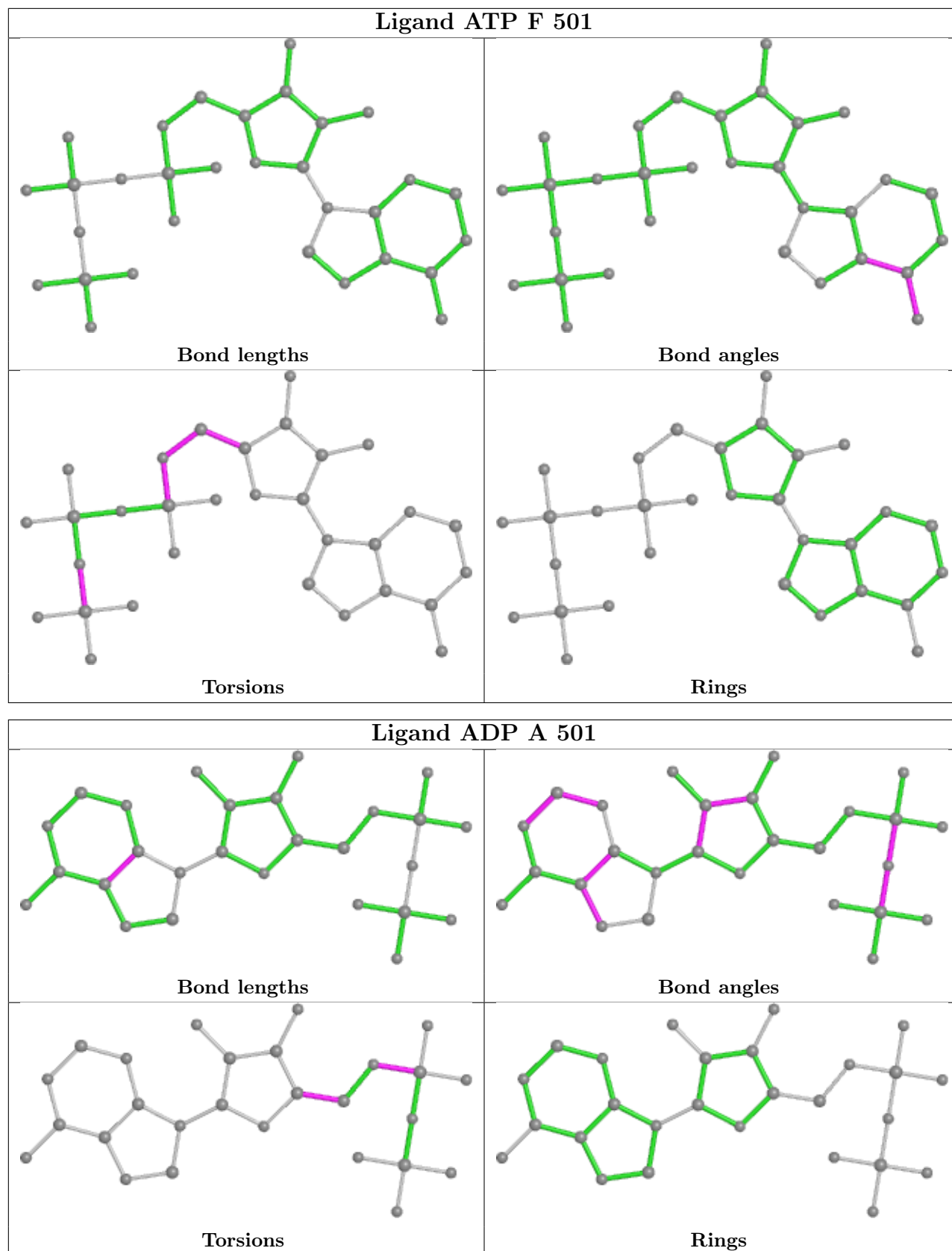
There are no ring outliers.

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.

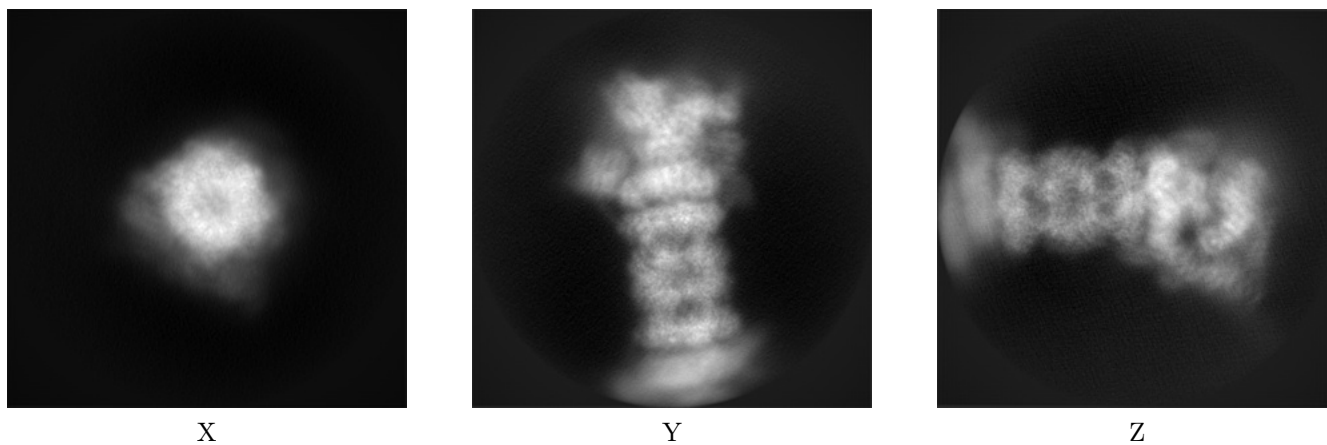
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-32283. 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](#)

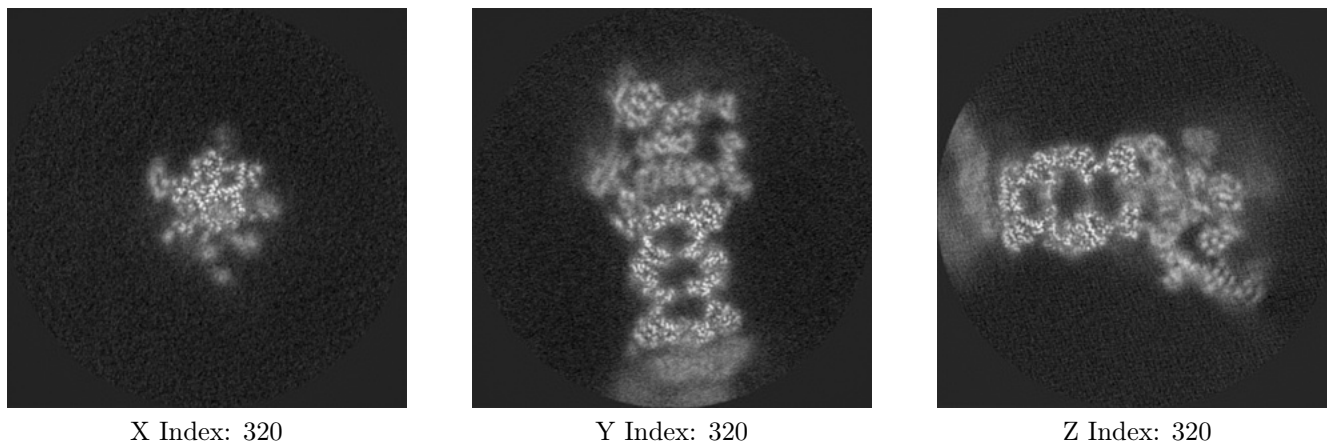
6.1.1 Primary map



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

6.2 Central slices [i](#)

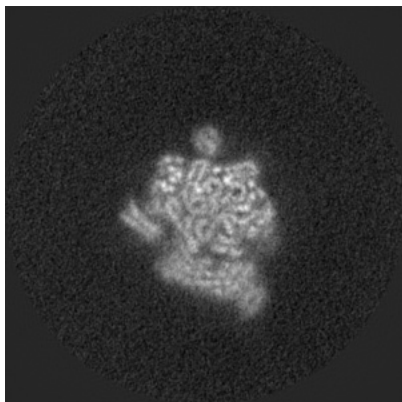
6.2.1 Primary map



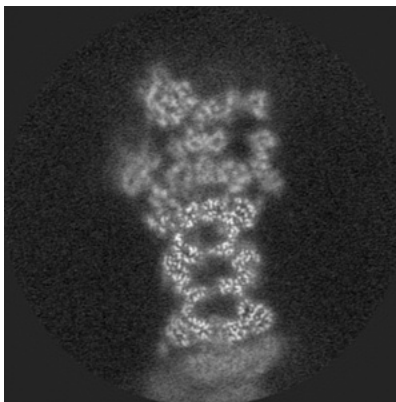
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

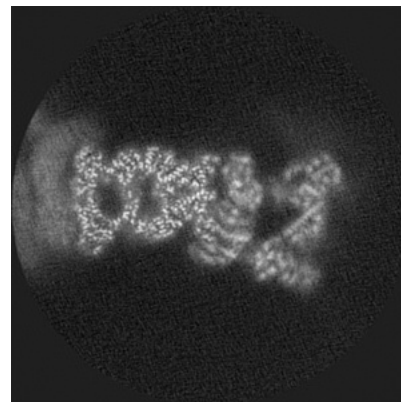
6.3.1 Primary map



X Index: 363



Y Index: 318



Z Index: 360

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

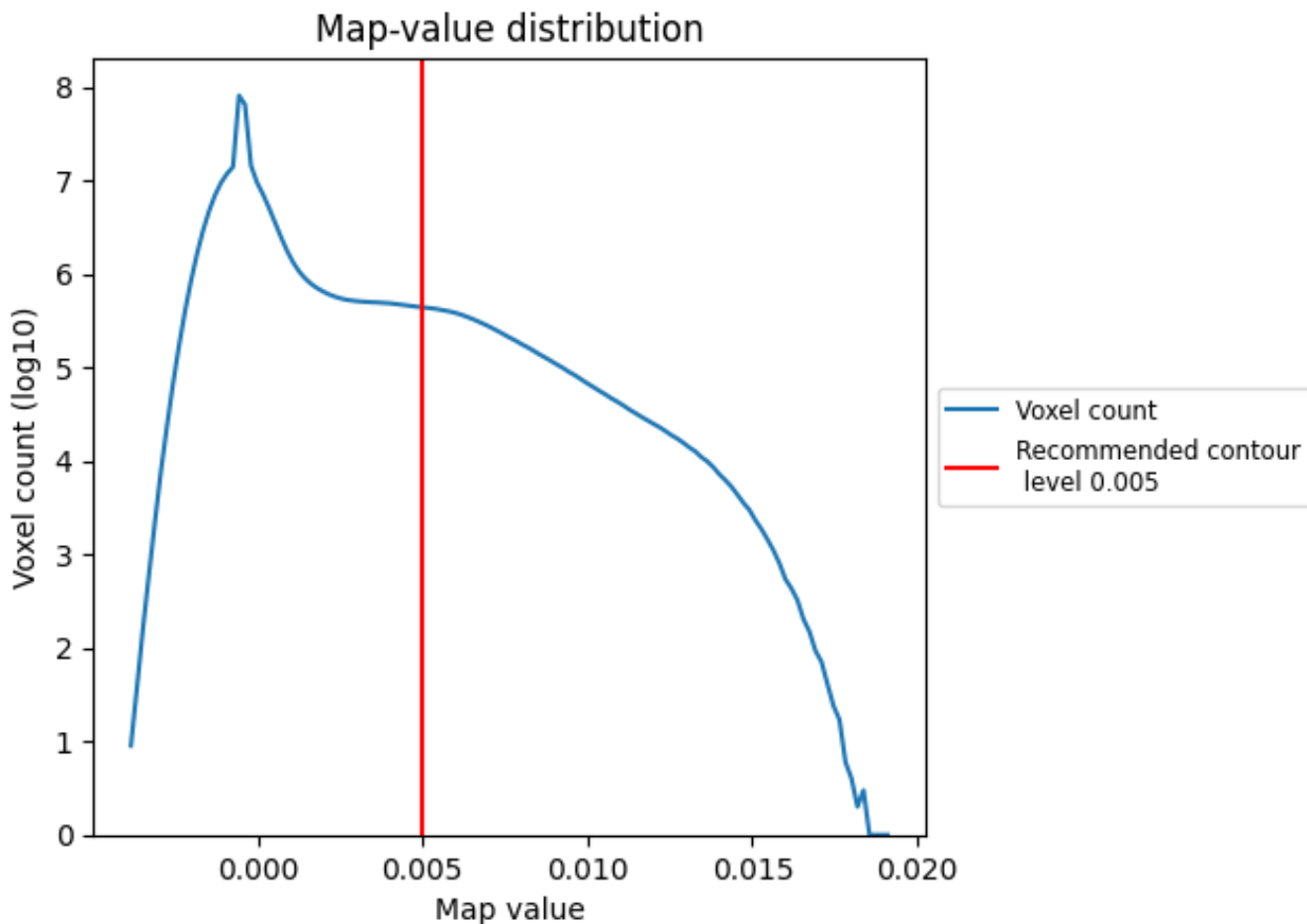
6.5 Mask visualisation

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

7 Map analysis [i](#)

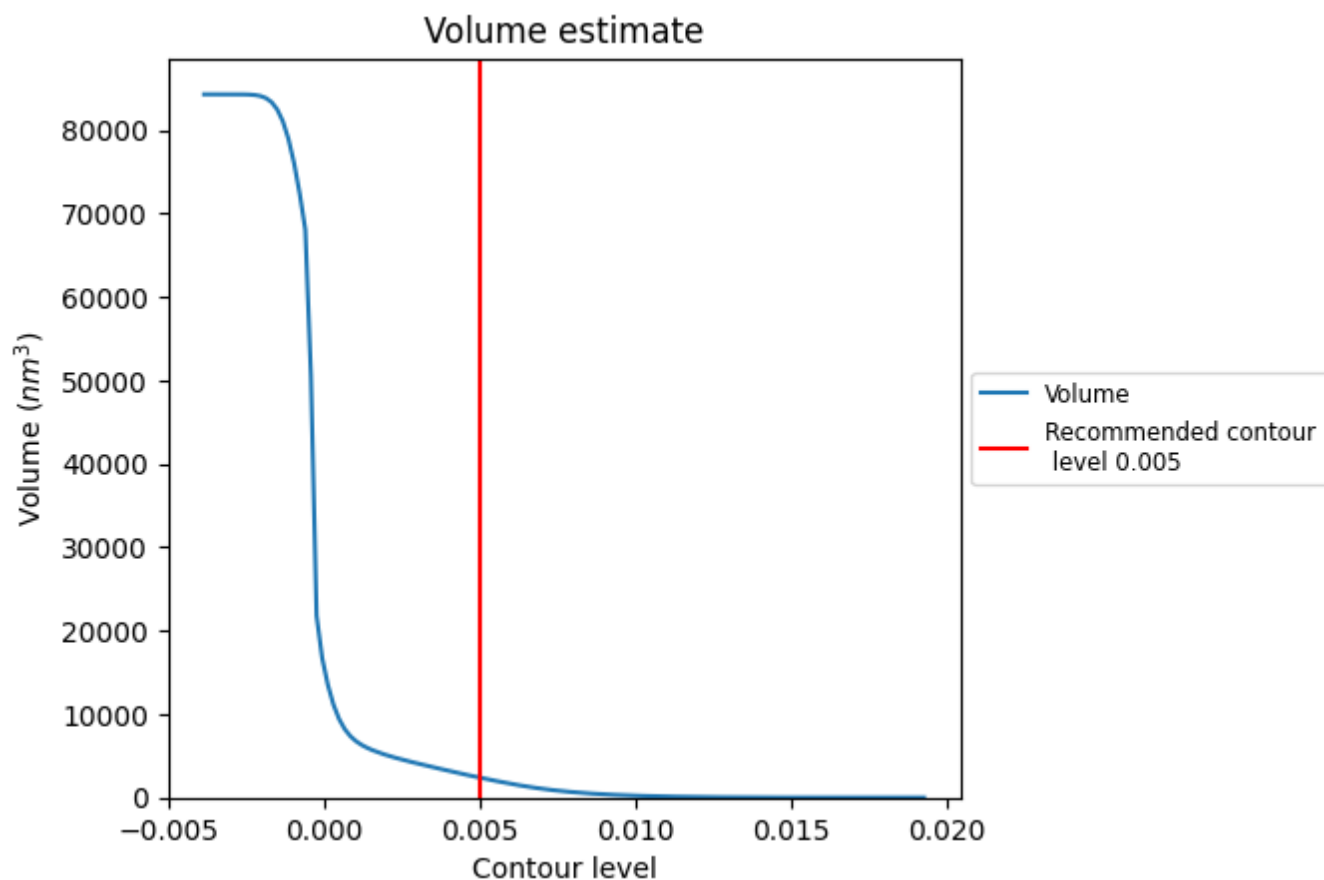
This section contains the results of statistical analysis of the map.

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.

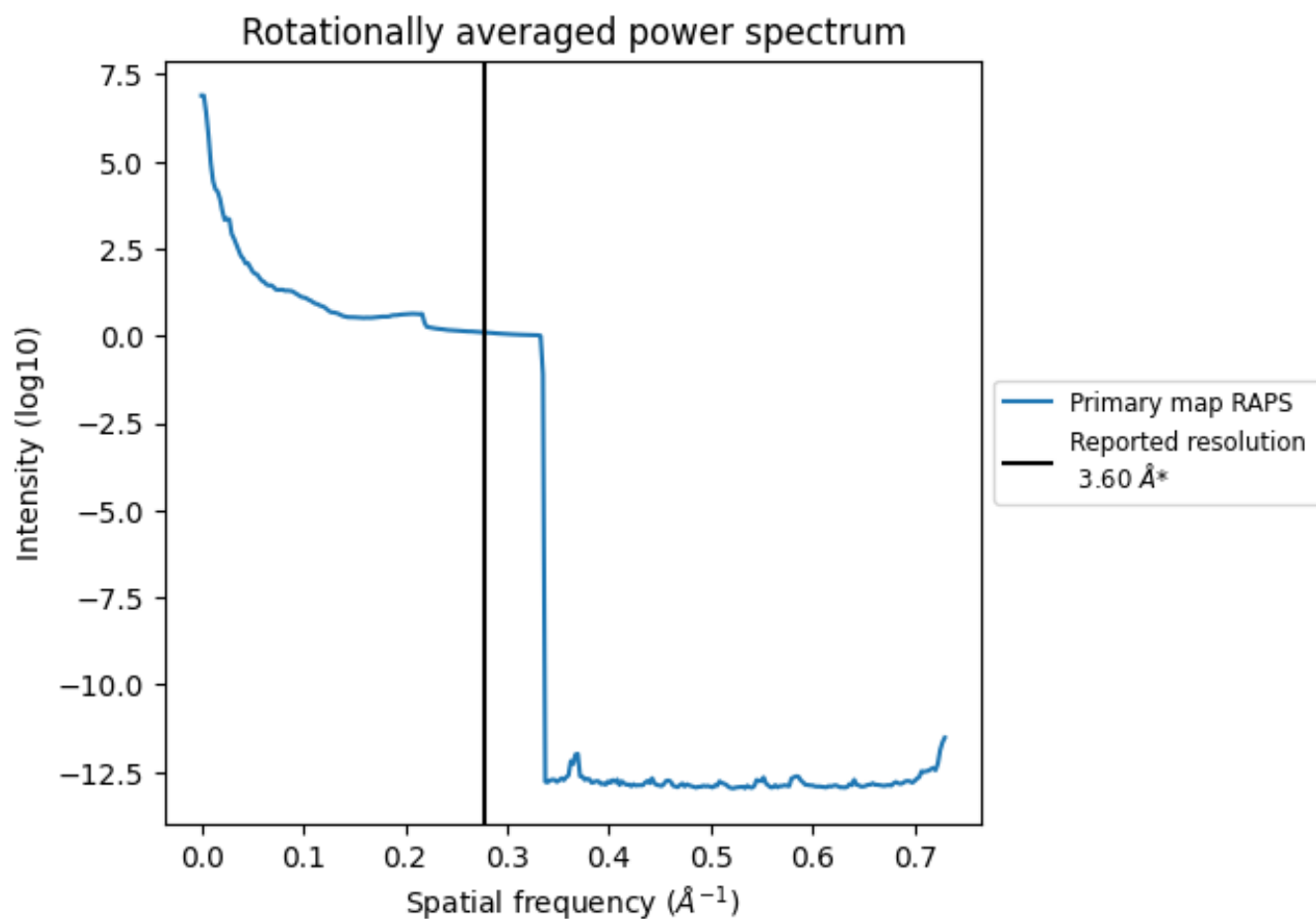
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2395 nm³; this corresponds to an approximate mass of 2164 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 0.278 Å⁻¹

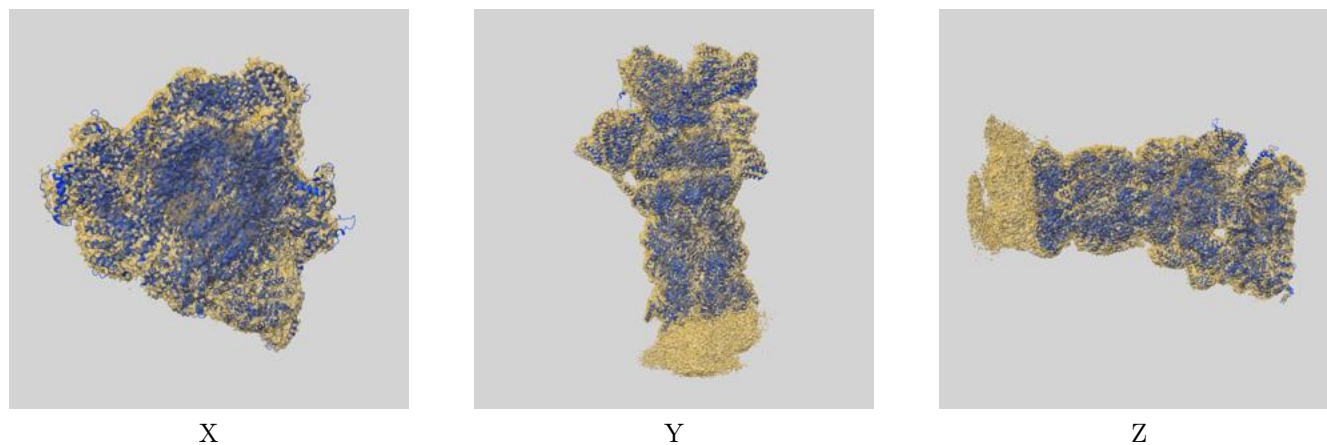
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

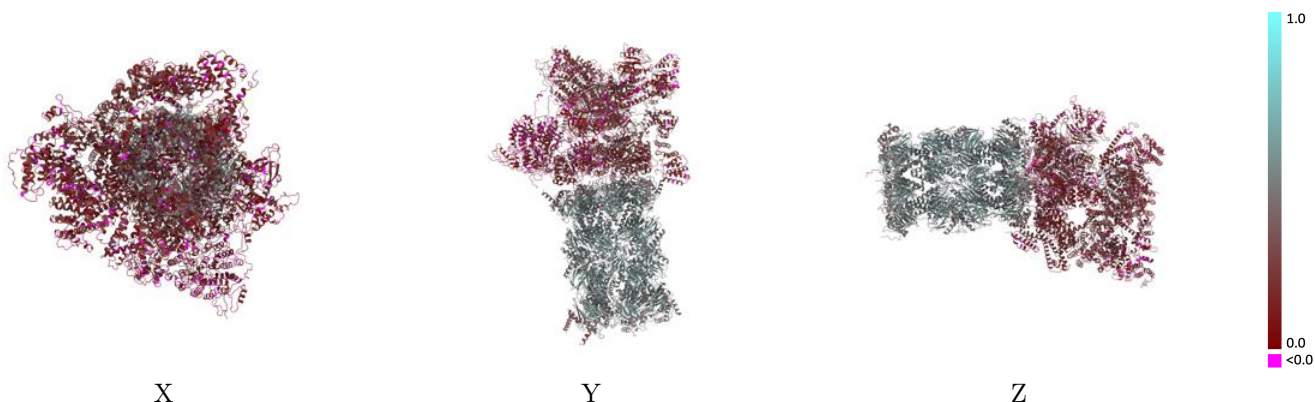
This section contains information regarding the fit between EMDB map EMD-32283 and PDB model 7W3K. Per-residue inclusion information can be found in section [3](#) on page [13](#).

9.1 Map-model overlay [i](#)



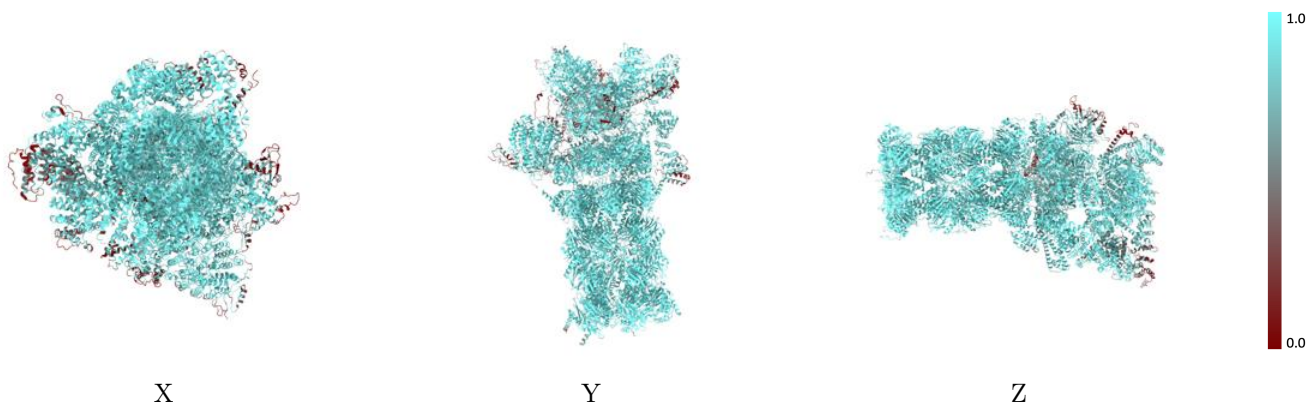
The images above show the 3D surface view of the map at the recommended contour level 0.005 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



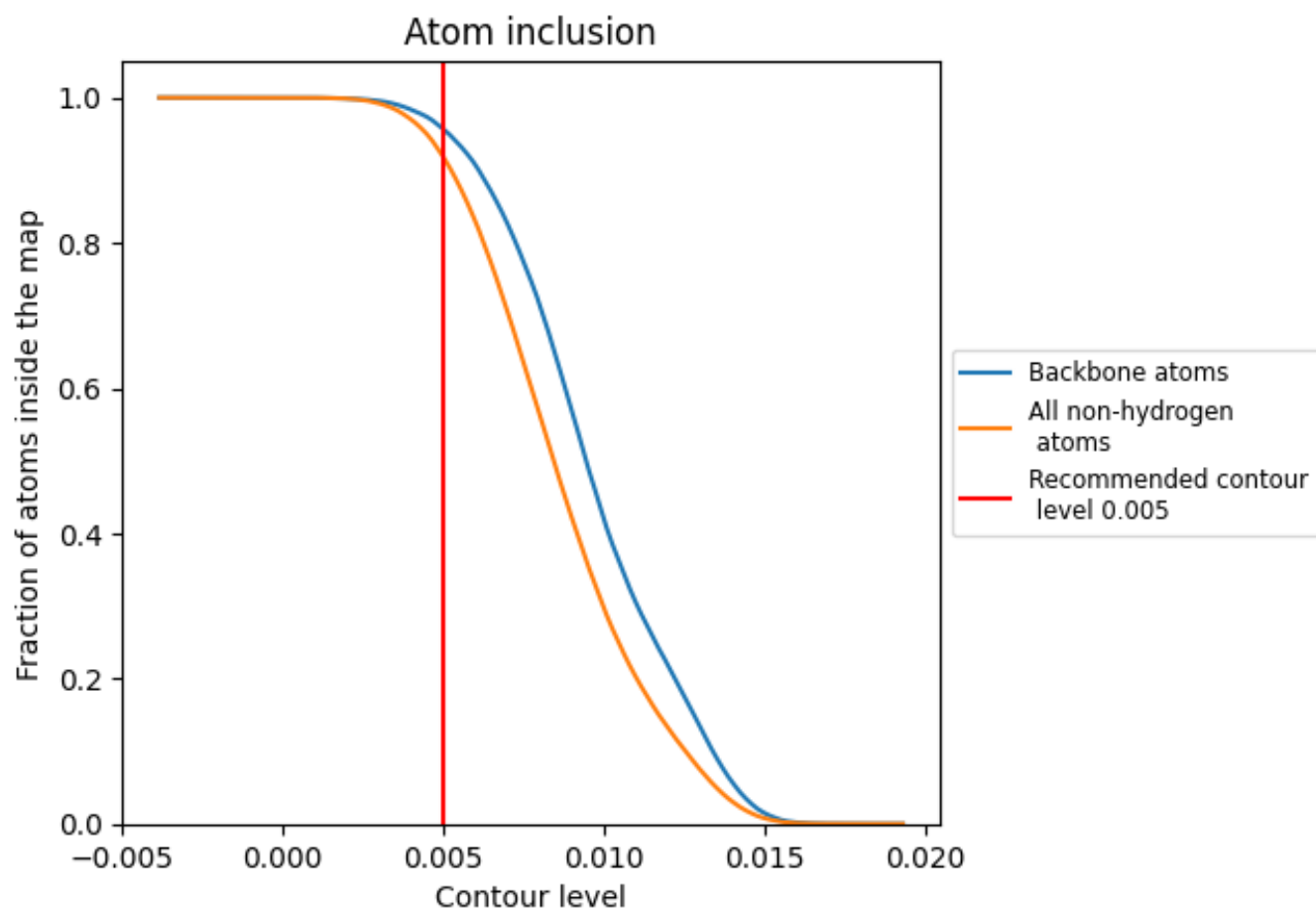
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.005).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 92% 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 (0.005) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9174	 0.3270
A	 0.9492	 0.1940
B	 0.9155	 0.1870
C	 0.8932	 0.1740
D	 0.9591	 0.1900
E	 0.9074	 0.2230
F	 0.9120	 0.2260
G	 0.9820	 0.4880
H	 0.9921	 0.4860
I	 0.9863	 0.4700
J	 0.9851	 0.4630
K	 0.9827	 0.4750
L	 0.9907	 0.4980
M	 0.9870	 0.4930
N	 0.9919	 0.5230
O	 0.9901	 0.5150
P	 0.9961	 0.5240
Q	 0.9910	 0.5170
R	 0.9934	 0.5180
S	 0.9900	 0.5200
T	 0.9884	 0.5290
U	 0.8528	 0.2040
V	 0.7969	 0.1900
W	 0.8241	 0.1880
X	 0.9489	 0.2290
Y	 0.9378	 0.2020
Z	 0.9711	 0.2330
a	 0.8732	 0.2050
b	 0.8924	 0.1780
c	 0.9485	 0.2450
d	 0.5906	 0.1610
e	 0.9212	 0.2010
f	 0.8590	 0.1340
g	 0.9664	 0.4920
h	 0.9836	 0.4970



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Chain	Atom inclusion	Q-score
i	 0.9593	 0.4750
j	 0.9598	 0.4480
k	 0.9740	 0.4840
l	 0.9807	 0.5070
m	 0.9734	 0.4940
n	 0.9926	 0.5310
o	 0.9908	 0.5270
p	 0.9930	 0.5240
q	 0.9942	 0.5230
r	 0.9953	 0.5250
s	 0.9895	 0.5170
t	 0.9829	 0.5240
x	 0.6730	 0.1490
y	 0.4899	 0.1130