



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 04:28 PM UTC

PDB ID : 7W3A / pdb_00007w3a
EMDB ID : EMD-32275
Title : Structure of USP14-bound human 26S proteasome in substrate-engaged state
ED4_USP14
Authors : Zhang, S.; Zou, S.; Yin, D.; Wu, Z.; Mao, Y.
Deposited on : 2021-11-25
Resolution : 3.50 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

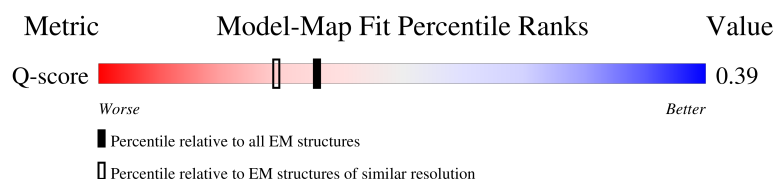
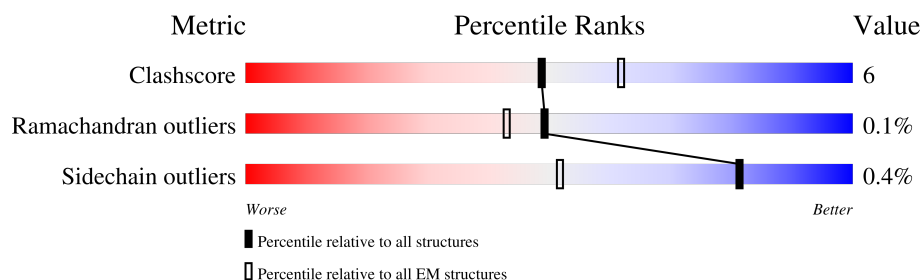
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

The reported resolution of this entry is 3.50 Å.

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



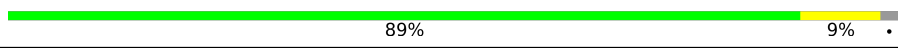
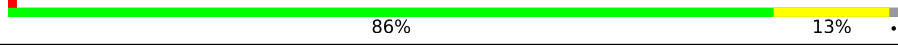
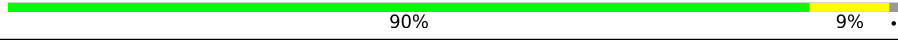
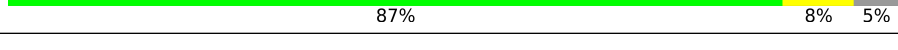
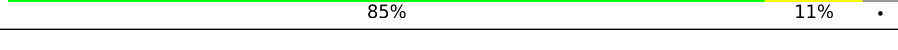
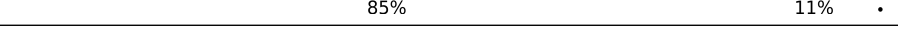
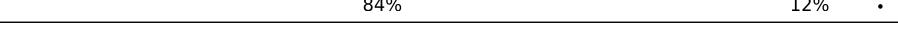
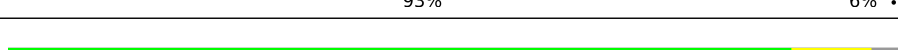
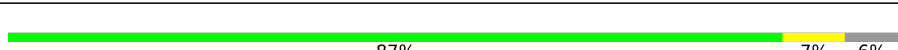
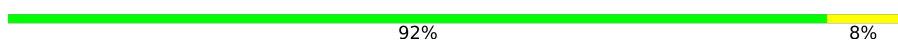
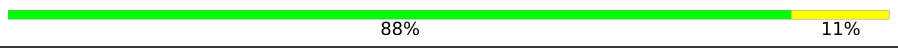
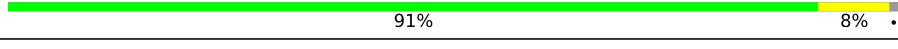
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	13950 (3.00 - 4.00)

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

Mol	Chain	Length	Quality of chain
1	A	433	
2	B	440	
3	C	398	
4	D	418	

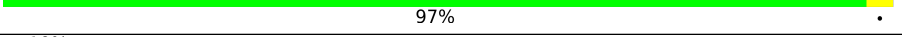
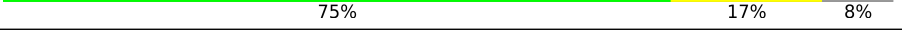
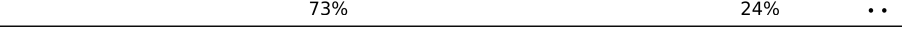
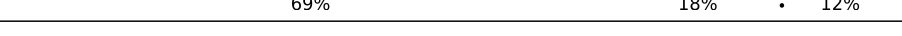
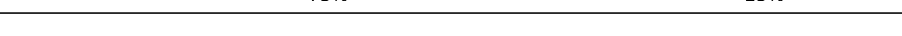
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Mol	Chain	Length	Quality of chain
5	E	403	
6	F	439	
7	G	246	
7	g	246	
8	H	234	
8	h	234	
9	I	261	
9	i	261	
10	J	248	
10	j	248	
11	K	241	
11	k	241	
12	L	269	
12	l	269	
13	M	255	
13	m	255	
14	N	239	
14	n	239	
15	O	277	
15	o	277	
16	P	205	
16	p	205	
17	Q	201	
17	q	201	
18	R	263	

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Mol	Chain	Length	Quality of chain
18	r	263	
19	S	241	
19	s	241	
20	T	264	
20	t	264	
21	v	34	
22	x	494	
23	y	76	
24	U	953	
25	V	534	
26	W	456	
27	X	422	
28	Y	389	
29	Z	324	
30	a	376	
31	b	377	
32	c	310	
33	d	350	
34	f	908	
35	e	70	

2 Entry composition

There are 38 unique types of molecules in this entry. The entry contains 110889 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
1	A	413	Total	C	N	O	S	0	0
			3229	2034	566	611	18		

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

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

- Molecule 3 is a protein called Isoform 2 of 26S proteasome regulatory subunit 8.

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

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

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

- Molecule 5 is a protein called 26S proteasome regulatory subunit 10B.

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

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

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

- Molecule 7 is a protein called Proteasome subunit alpha type-6.

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

- Molecule 8 is a protein called Proteasome subunit alpha type-2.

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

- Molecule 9 is a protein called Proteasome subunit alpha type-4.

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

- Molecule 10 is a protein called Proteasome subunit alpha type-7.

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

- Molecule 11 is a protein called Proteasome subunit alpha type-5.

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

- Molecule 12 is a protein called Isoform Long of Proteasome subunit alpha type-1.

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

- Molecule 13 is a protein called Proteasome subunit alpha type-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	242	Total	C	N	O	S	0	0
			1890	1200	323	356	11		
13	m	240	Total	C	N	O	S	0	0
			1881	1193	321	356	11		

- Molecule 14 is a protein called Proteasome subunit beta type-6.

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

- Molecule 15 is a protein called Proteasome subunit beta type-7.

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

- Molecule 16 is a protein called Proteasome subunit beta type-3.

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

- Molecule 17 is a protein called Proteasome subunit beta type-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	199	Total	C	N	O	S	0	0
			1588	1017	270	292	9		

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Mol	Chain	Residues	Atoms					AltConf	Trace
17	q	199	Total	C	N	O	S	0	0
			1578	1012	267	290	9		

- Molecule 18 is a protein called Proteasome subunit beta type-5.

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

- Molecule 19 is a protein called Proteasome subunit beta type-1.

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

- Molecule 20 is a protein called Proteasome subunit beta type-4.

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

- Molecule 21 is a protein called Substrate.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	v	34	Total	C	N	O	0	0
			170	102	34	34		

- Molecule 22 is a protein called Ubiquitin carboxyl-terminal hydrolase 14.

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

- Molecule 23 is a protein called Ubiquitin.

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

- Molecule 24 is a protein called 26S proteasome non-ATPase regulatory subunit 1.

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

- Molecule 25 is a protein called 26S proteasome non-ATPase regulatory subunit 3.

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

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

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

- Molecule 27 is a protein called 26S proteasome non-ATPase regulatory subunit 11.

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

- Molecule 28 is a protein called 26S proteasome non-ATPase regulatory subunit 6.

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

- Molecule 29 is a protein called 26S proteasome non-ATPase regulatory subunit 7.

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

- Molecule 30 is a protein called 26S proteasome non-ATPase regulatory subunit 13.

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

- Molecule 31 is a protein called 26S proteasome non-ATPase regulatory subunit 4.

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

- Molecule 32 is a protein called 26S proteasome non-ATPase regulatory subunit 14.

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

- Molecule 33 is a protein called 26S proteasome non-ATPase regulatory subunit 8.

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

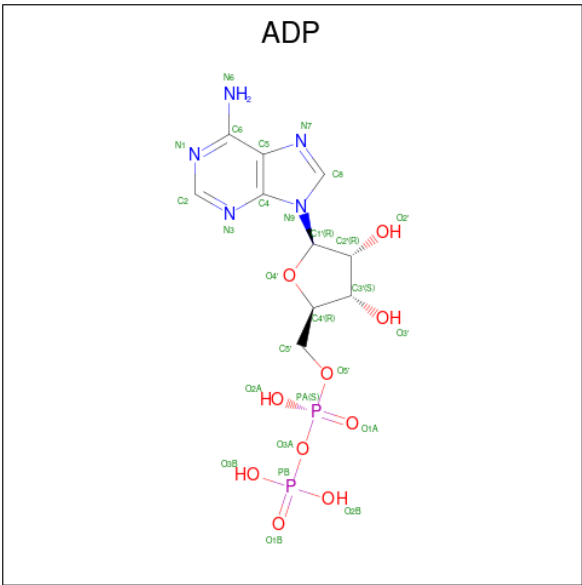
- Molecule 34 is a protein called 26S proteasome non-ATPase regulatory subunit 2.

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

- Molecule 35 is a protein called 26S proteasome complex subunit DSS1.

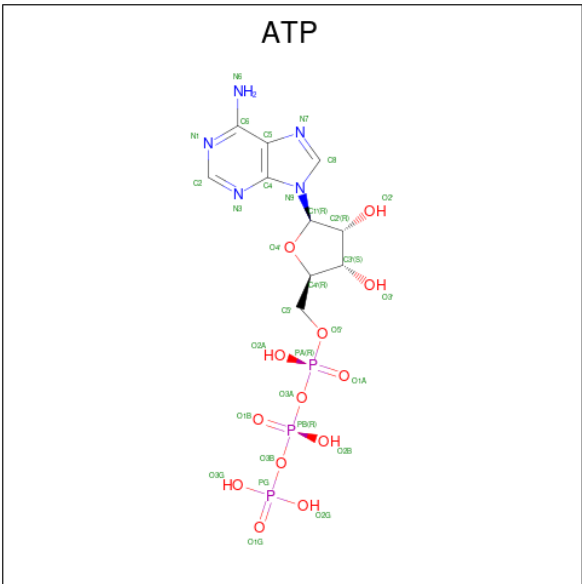
Mol	Chain	Residues	Atoms				AltConf	Trace
35	e	50	Total	C	N	O	0	0
			425	260	65	100		

- Molecule 36 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
36	A	1	Total	C	N	O	P	0
			27	10	5	10	2	
36	B	1	Total	C	N	O	P	0
			27	10	5	10	2	

- Molecule 37 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$) (labeled as "Ligand of Interest" by depositor).



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

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

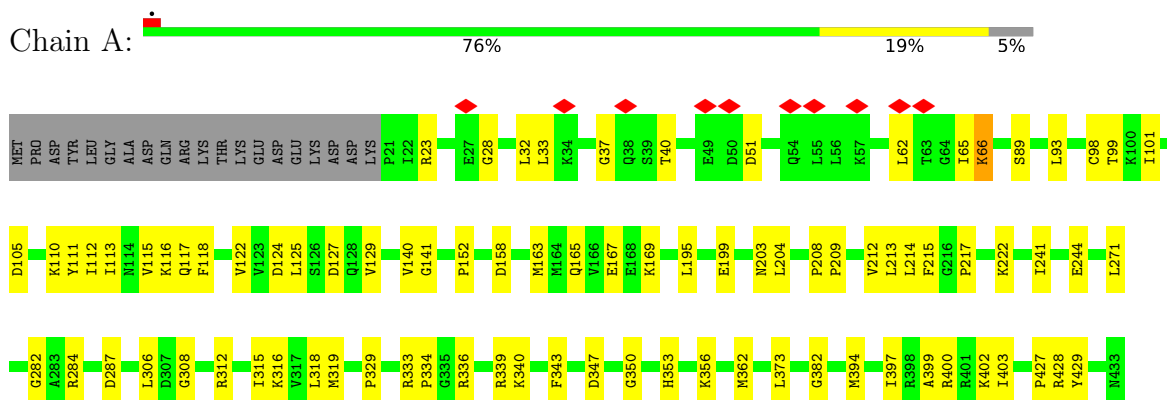
- Molecule 38 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

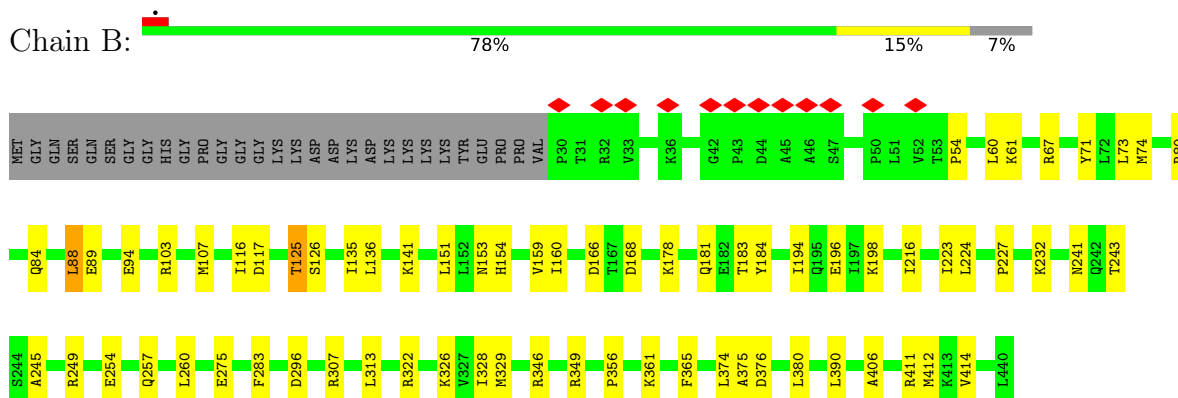
3 Residue-property plots

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.

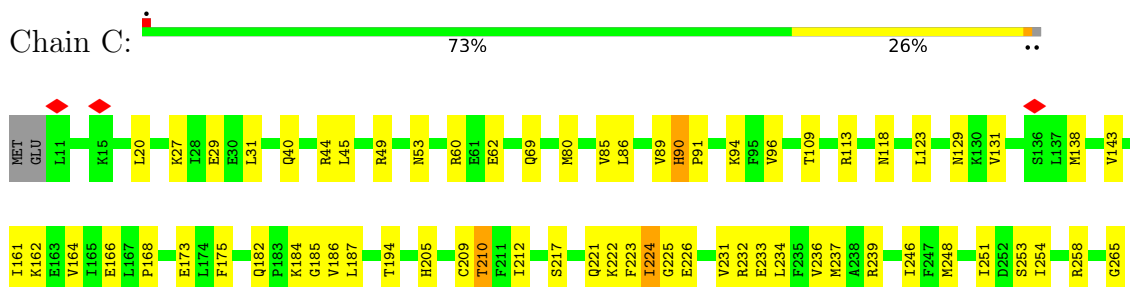
• Molecule 1: 26S protease regulatory subunit 7



• Molecule 2: 26S protease regulatory subunit 4



• Molecule 3: Isoform 2 of 26S proteasome regulatory subunit 8



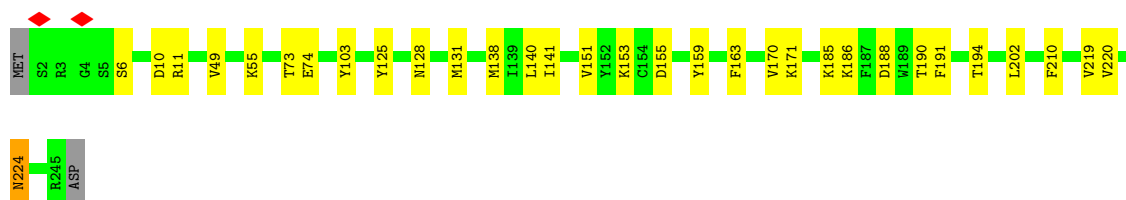
- Molecule 7: Proteasome subunit alpha type-6

Chain G:  89% 9%



- Molecule 7: Proteasome subunit alpha type-6

Chain g:  86% 13%



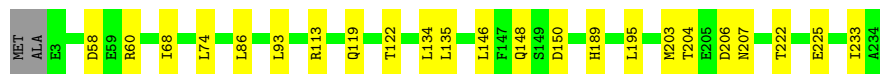
- Molecule 8: Proteasome subunit alpha type-2

Chain H:  90% 9%



- Molecule 8: Proteasome subunit alpha type-2

Chain h:  89% 10%



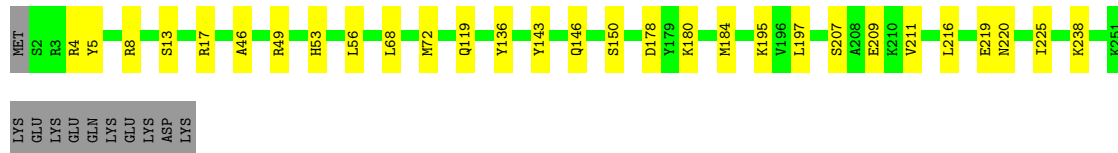
- Molecule 9: Proteasome subunit alpha type-4

Chain I:  87% 8% 5%



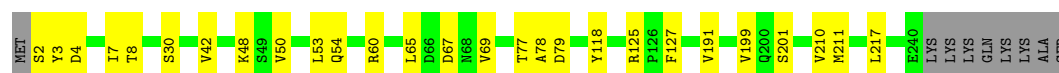
- Molecule 9: Proteasome subunit alpha type-4

Chain i:  85% 11%



- Molecule 10: Proteasome subunit alpha type-7

Chain J:  85% 11%

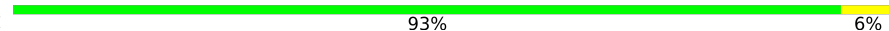


- Molecule 10: Proteasome subunit alpha type-7

Chain j:  84% 12%



- Molecule 11: Proteasome subunit alpha type-5

Chain K:  93% 6%



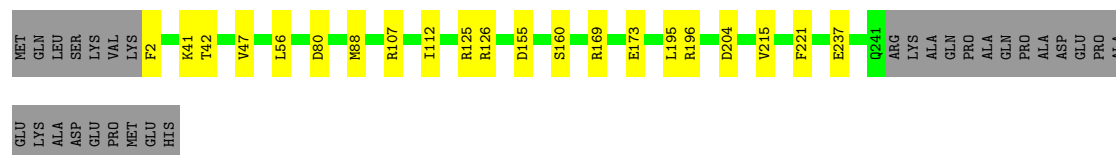
- Molecule 11: Proteasome subunit alpha type-5

Chain k:  88% 9%



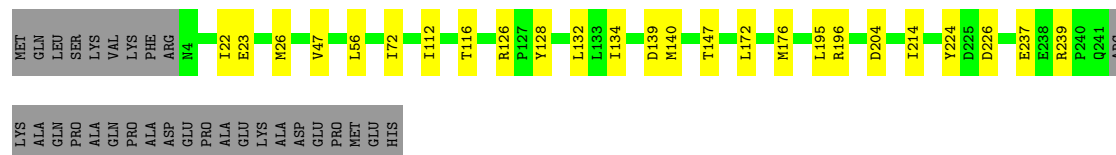
- Molecule 12: Isoform Long of Proteasome subunit alpha type-1

Chain L:  81% 8% 11%



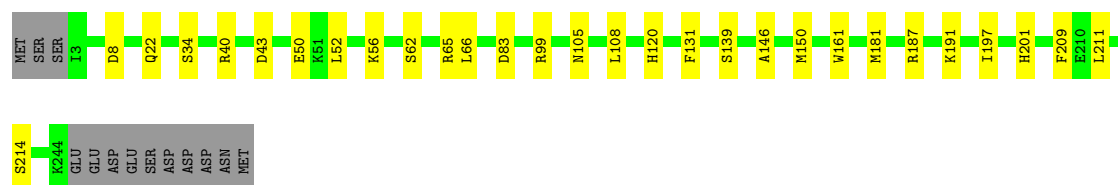
- Molecule 12: Isoform Long of Proteasome subunit alpha type-1

Chain l:  79% 9% 12%



- Molecule 13: Proteasome subunit alpha type-3

Chain M:  84% 11% 5%



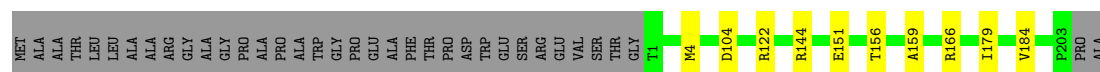
- Molecule 13: Proteasome subunit alpha type-3

Chain m:  87% 7% 6%



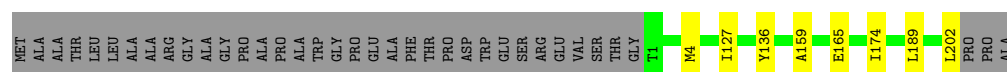
- Molecule 14: Proteasome subunit beta type-6

Chain N:  81% 15%



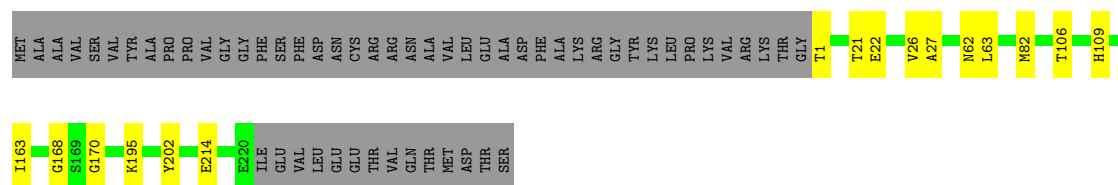
- Molecule 14: Proteasome subunit beta type-6

Chain n:  81% 15%



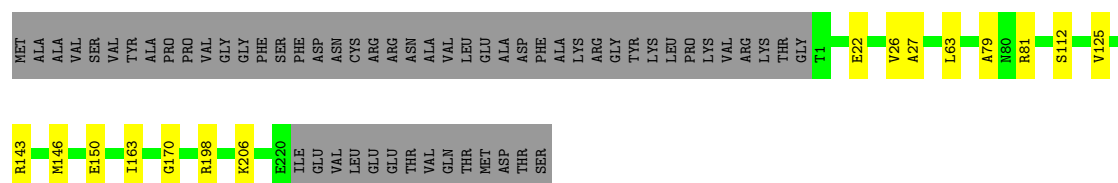
- Molecule 15: Proteasome subunit beta type-7

Chain O:  74% 6% 21%



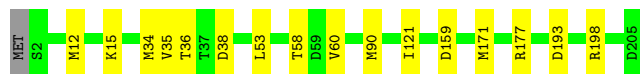
- Molecule 15: Proteasome subunit beta type-7

Chain o:  74% 5% 21%



- Molecule 16: Proteasome subunit beta type-3

Chain P:  92% 8%



- Molecule 16: Proteasome subunit beta type-3

Chain p:  88% 11%



- Molecule 17: Proteasome subunit beta type-2

Chain Q:  88% 11%



- Molecule 17: Proteasome subunit beta type-2

Chain q:  91% 8%



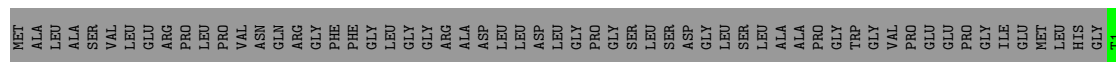
- Molecule 18: Proteasome subunit beta type-5

Chain R:  71% 6% 24%



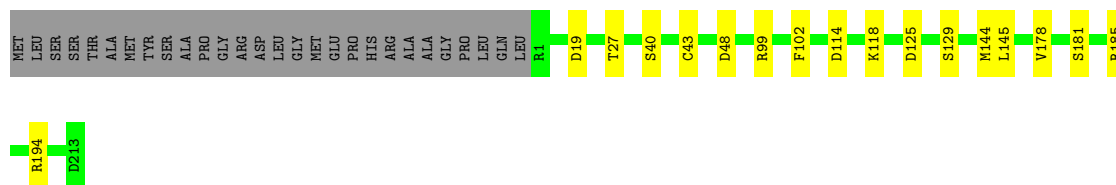
- Molecule 18: Proteasome subunit beta type-5

Chain r:  72% 5% 24%



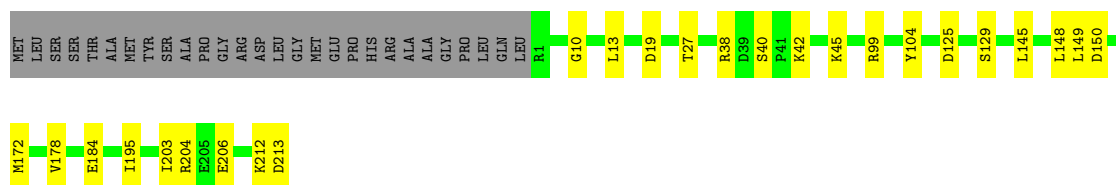
- Molecule 19: Proteasome subunit beta type-1

Chain S:  81% 7% 12%



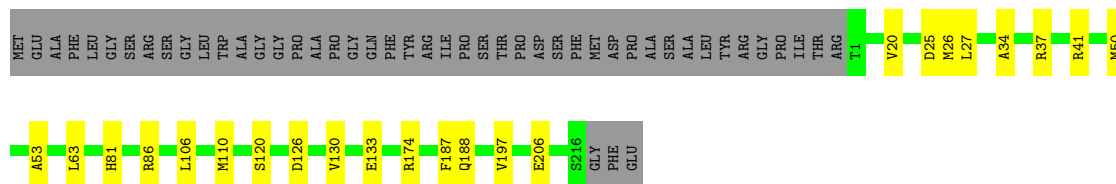
- Molecule 19: Proteasome subunit beta type-1

Chain s:  78% 10% 12%



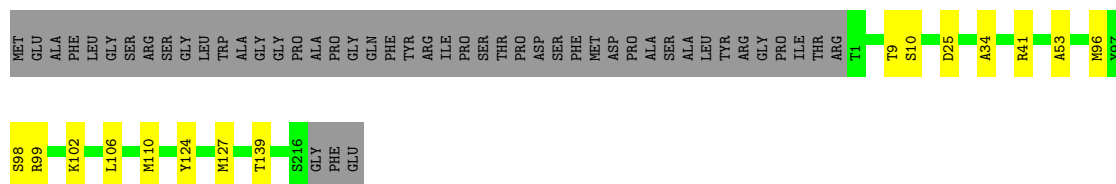
- Molecule 20: Proteasome subunit beta type-4

Chain T:  73% 9% 18%

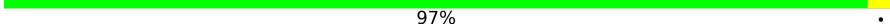


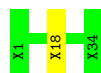
- Molecule 20: Proteasome subunit beta type-4

Chain t:  76% 6% 18%



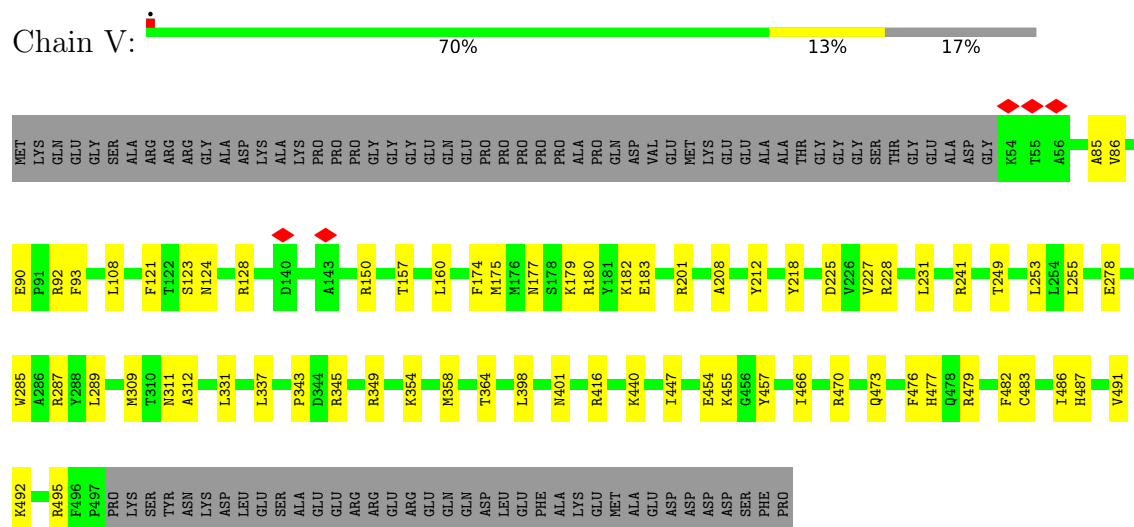
- Molecule 21: Substrate

Chain v:  97% .

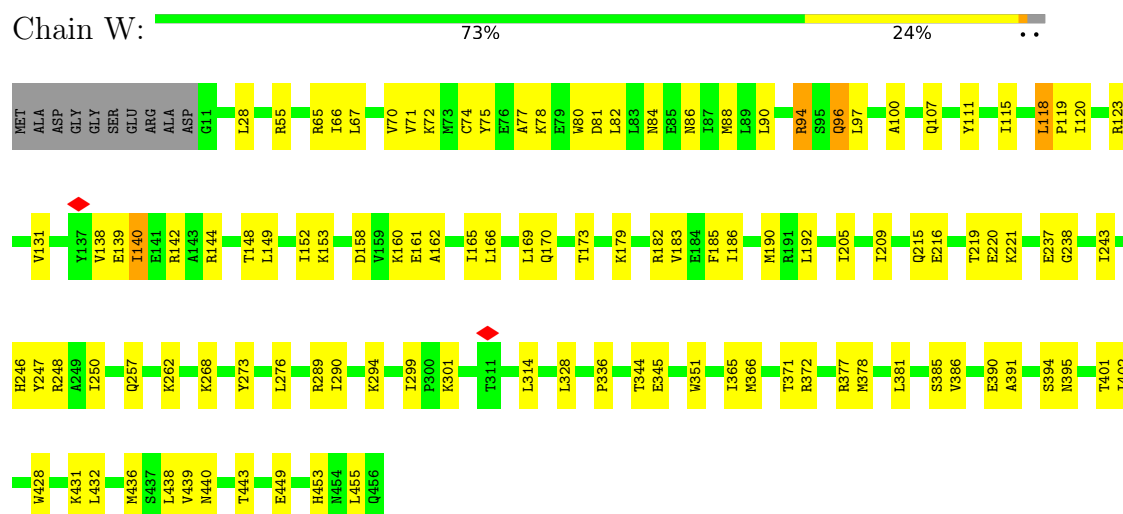


- Molecule 22: Ubiquitin carboxyl-terminal hydrolase 14

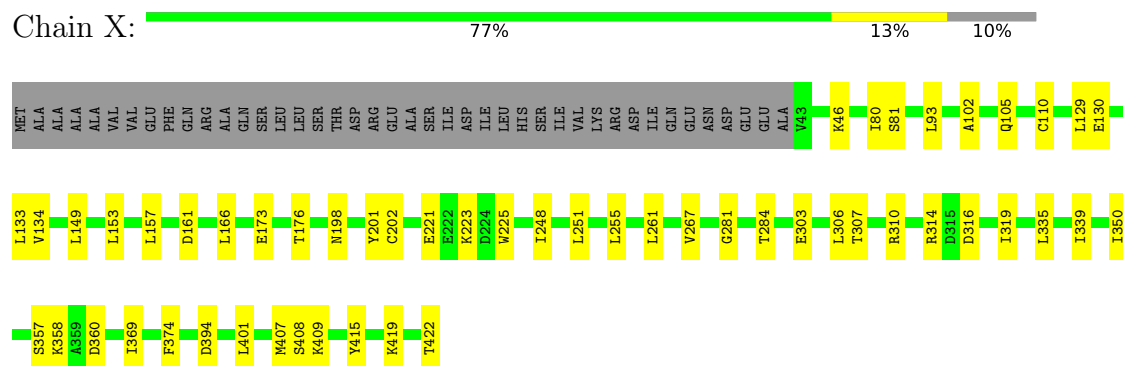
Chain x:  10% 81% 18%



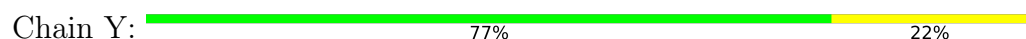
• Molecule 26: 26S proteasome non-ATPase regulatory subunit 12



• Molecule 27: 26S proteasome non-ATPase regulatory subunit 11

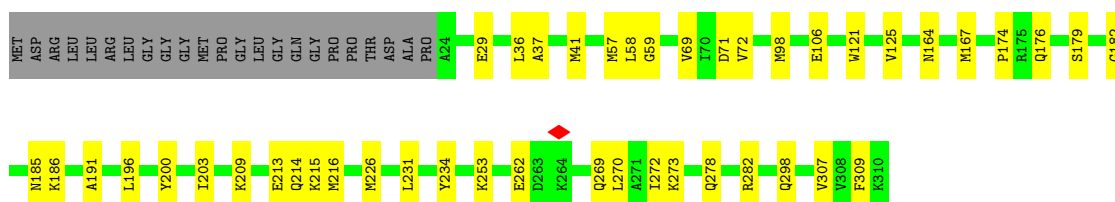


• Molecule 28: 26S proteasome non-ATPase regulatory subunit 6

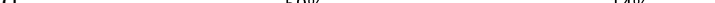


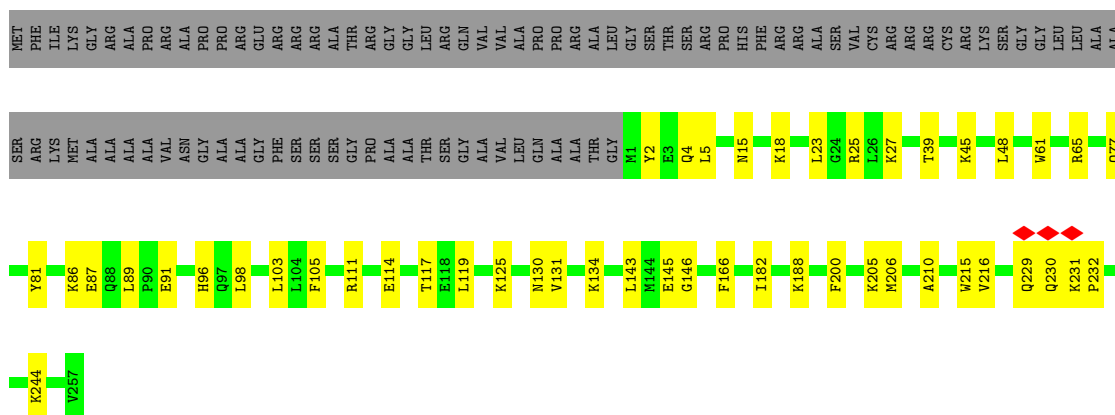
- Molecule 32: 26S proteasome non-ATPase regulatory subunit 14

Chain c: 78% 15% 7%

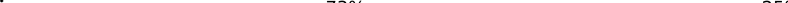


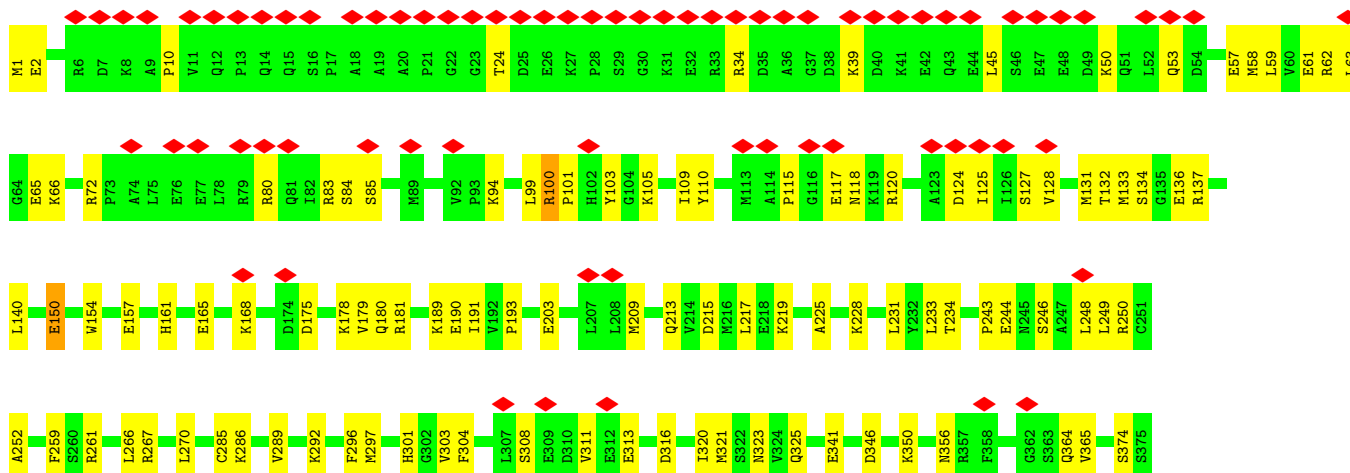
- Molecule 33: 26S proteasome non-ATPase regulatory subunit 8

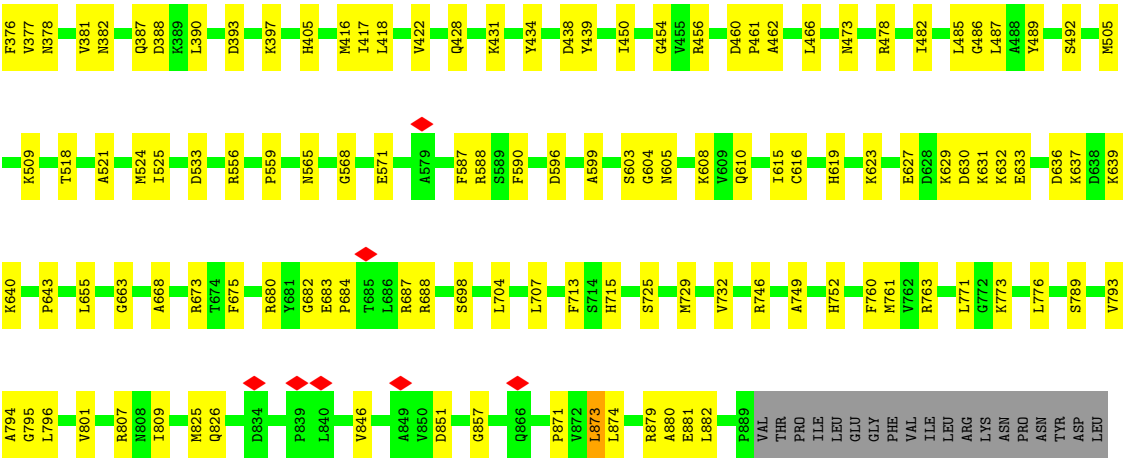
Chain d:  59% 14% 27%



- Molecule 34: 26S proteasome non-ATPase regulatory subunit 2

Chain f:  9% 73% 25%





● Molecule 35: 26S proteasome complex subunit DSS1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	66910	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	0.024	Depositor
Minimum map value	-0.005	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.005	Depositor
Map size (Å)	438.4, 438.4, 438.4	wwPDB
Map dimensions	640, 640, 640	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: ATP, ZN, 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	A	0.18	0/3283	0.47	0/4433
2	B	0.18	0/3254	0.48	0/4388
3	C	0.19	0/3146	0.50	0/4226
4	D	0.21	0/3089	0.50	0/4168
5	E	0.17	0/3145	0.46	1/4233 (0.0%)
6	F	0.16	0/3173	0.42	0/4273
7	G	0.19	0/1901	0.43	0/2572
7	g	0.17	0/1913	0.45	2/2589 (0.1%)
8	H	0.17	0/1840	0.38	0/2495
8	h	0.17	0/1844	0.40	0/2497
9	I	0.17	0/1963	0.41	0/2650
9	i	0.17	0/1985	0.42	0/2677
10	J	0.17	0/1887	0.40	0/2553
10	j	0.17	0/1887	0.41	0/2549
11	K	0.17	0/1841	0.34	0/2486
11	k	0.15	0/1809	0.36	0/2444
12	L	0.17	0/1911	0.33	0/2584
12	l	0.16	0/1896	0.33	0/2565
13	M	0.16	0/1925	0.37	0/2592
13	m	0.17	0/1916	0.40	0/2580
14	N	0.16	0/1548	0.31	0/2097
14	n	0.17	0/1536	0.33	0/2080
15	O	0.16	0/1672	0.37	0/2267
15	o	0.15	0/1686	0.37	0/2282
16	P	0.18	0/1616	0.40	0/2180
16	p	0.17	0/1620	0.41	0/2184
17	Q	0.16	0/1621	0.35	0/2194
17	q	0.16	0/1611	0.35	0/2182
18	R	0.15	0/1590	0.34	0/2147
18	r	0.18	0/1580	0.38	0/2135
19	S	0.17	0/1671	0.37	0/2252
19	s	0.17	0/1680	0.39	0/2264

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
20	T	0.17	0/1716	0.36	0/2323
20	t	0.16	0/1720	0.37	0/2328
22	x	0.15	0/4002	0.37	0/5390
23	y	0.17	0/607	0.47	0/816
24	U	0.19	0/6945	0.53	1/9382 (0.0%)
25	V	0.18	0/3681	0.42	0/4969
26	W	0.20	0/3683	0.55	3/4952 (0.1%)
27	X	0.19	0/3053	0.46	0/4115
28	Y	0.23	0/3261	0.55	0/4393
29	Z	0.20	0/2324	0.52	0/3150
30	a	0.18	0/3053	0.48	0/4133
31	b	0.20	0/1478	0.53	0/2001
32	c	0.21	0/2302	0.53	0/3110
33	d	0.20	0/2162	0.56	0/2919
34	f	0.20	0/6980	0.53	2/9433 (0.0%)
35	e	0.21	0/437	0.48	0/595
All	All	0.18	0/112443	0.45	9/151827 (0.0%)

There are no bond length outliers.

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	g	224	ASN	CA-C-N	-7.81	112.86	120.83
7	g	224	ASN	C-N-CA	-7.81	112.86	120.83
26	W	96	GLN	CB-CA-C	-6.21	109.42	116.63
34	f	99	LEU	CA-C-N	5.67	135.63	121.80
34	f	99	LEU	C-N-CA	5.67	135.63	121.80

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3229	0	3261	55	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	3207	0	3278	46	0
3	C	3105	0	3219	68	0
4	D	3039	0	3076	59	0
5	E	3097	0	3174	44	0
6	F	3133	0	3220	49	0
7	G	1867	0	1867	14	0
7	g	1879	0	1872	19	0
8	H	1801	0	1773	15	0
8	h	1805	0	1798	12	0
9	I	1933	0	1923	16	0
9	i	1955	0	1955	17	0
10	J	1861	0	1846	19	0
10	j	1861	0	1865	20	0
11	K	1813	0	1796	10	0
11	k	1782	0	1766	14	0
12	L	1876	0	1856	14	0
12	l	1861	0	1839	16	0
13	M	1890	0	1880	17	0
13	m	1881	0	1868	9	0
14	N	1521	0	1494	7	0
14	n	1510	0	1483	6	0
15	O	1645	0	1648	10	0
15	o	1659	0	1681	11	0
16	P	1587	0	1598	13	0
16	p	1591	0	1609	15	0
17	Q	1588	0	1584	14	0
17	q	1578	0	1569	10	0
18	R	1559	0	1523	11	0
18	r	1549	0	1506	8	0
19	S	1641	0	1639	12	0
19	s	1650	0	1645	16	0
20	T	1683	0	1662	14	0
20	t	1687	0	1666	8	0
21	v	170	0	44	1	0
22	x	3929	0	3915	59	0
23	y	601	0	629	16	0
24	U	6828	0	6884	98	0
25	V	3612	0	3682	48	0
26	W	3635	0	3762	71	0
27	X	3009	0	3113	36	0
28	Y	3202	0	3204	56	0
29	Z	2281	0	2312	44	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	a	2995	0	3012	50	0
31	b	1458	0	1505	28	0
32	c	2260	0	2276	31	0
33	d	2116	0	2146	33	0
34	f	6866	0	6866	149	0
35	e	425	0	328	12	0
36	A	27	0	12	1	0
36	B	27	0	12	0	0
37	C	31	0	12	3	0
37	D	31	0	12	0	0
37	E	31	0	12	2	0
37	F	31	0	12	1	0
38	c	1	0	0	0	0
All	All	110889	0	111189	1279	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

The worst 5 of 1279 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:U:890:LYS:HG3	24:U:891:VAL:HG23	1.66	0.77
25:V:309:MET:HE1	25:V:331:LEU:HB3	1.66	0.77
34:f:58:MET:HG2	34:f:62:ARG:HE	1.51	0.73
34:f:127:SER:HA	34:f:131:MET:HB3	1.69	0.73
2:B:74:MET:HE2	34:f:610:GLN:HA	1.71	0.72

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	411/433 (95%)	361 (88%)	48 (12%)	2 (0%)	24	57
2	B	409/440 (93%)	367 (90%)	42 (10%)	0	100	100
3	C	394/398 (99%)	351 (89%)	39 (10%)	4 (1%)	12	44
4	D	378/418 (90%)	337 (89%)	40 (11%)	1 (0%)	36	67
5	E	387/403 (96%)	357 (92%)	30 (8%)	0	100	100
6	F	396/439 (90%)	360 (91%)	36 (9%)	0	100	100
7	G	238/246 (97%)	225 (94%)	13 (6%)	0	100	100
7	g	242/246 (98%)	234 (97%)	8 (3%)	0	100	100
8	H	230/234 (98%)	216 (94%)	14 (6%)	0	100	100
8	h	230/234 (98%)	220 (96%)	10 (4%)	0	100	100
9	I	246/261 (94%)	234 (95%)	12 (5%)	0	100	100
9	i	248/261 (95%)	238 (96%)	10 (4%)	0	100	100
10	J	237/248 (96%)	225 (95%)	12 (5%)	0	100	100
10	j	237/248 (96%)	226 (95%)	11 (5%)	0	100	100
11	K	236/241 (98%)	229 (97%)	7 (3%)	0	100	100
11	k	232/241 (96%)	223 (96%)	9 (4%)	0	100	100
12	L	238/269 (88%)	225 (94%)	13 (6%)	0	100	100
12	l	236/269 (88%)	224 (95%)	12 (5%)	0	100	100
13	M	240/255 (94%)	232 (97%)	8 (3%)	0	100	100
13	m	238/255 (93%)	235 (99%)	3 (1%)	0	100	100
14	N	201/239 (84%)	197 (98%)	4 (2%)	0	100	100
14	n	200/239 (84%)	194 (97%)	6 (3%)	0	100	100
15	O	218/277 (79%)	212 (97%)	6 (3%)	0	100	100
15	o	218/277 (79%)	209 (96%)	9 (4%)	0	100	100
16	P	202/205 (98%)	197 (98%)	5 (2%)	0	100	100
16	p	202/205 (98%)	195 (96%)	7 (4%)	0	100	100
17	Q	197/201 (98%)	191 (97%)	6 (3%)	0	100	100
17	q	197/201 (98%)	192 (98%)	5 (2%)	0	100	100
18	R	199/263 (76%)	194 (98%)	5 (2%)	0	100	100
18	r	199/263 (76%)	194 (98%)	5 (2%)	0	100	100
19	S	211/241 (88%)	205 (97%)	6 (3%)	0	100	100
19	s	211/241 (88%)	202 (96%)	9 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	T	214/264 (81%)	206 (96%)	8 (4%)	0	100	100
20	t	214/264 (81%)	206 (96%)	8 (4%)	0	100	100
22	x	492/494 (100%)	469 (95%)	22 (4%)	1 (0%)	43	74
23	y	74/76 (97%)	73 (99%)	1 (1%)	0	100	100
24	U	868/953 (91%)	785 (90%)	83 (10%)	0	100	100
25	V	442/534 (83%)	432 (98%)	10 (2%)	0	100	100
26	W	444/456 (97%)	415 (94%)	28 (6%)	1 (0%)	43	74
27	X	378/422 (90%)	357 (94%)	21 (6%)	0	100	100
28	Y	387/389 (100%)	349 (90%)	35 (9%)	3 (1%)	16	49
29	Z	284/324 (88%)	243 (86%)	41 (14%)	0	100	100
30	a	371/376 (99%)	345 (93%)	26 (7%)	0	100	100
31	b	189/377 (50%)	170 (90%)	19 (10%)	0	100	100
32	c	285/310 (92%)	244 (86%)	41 (14%)	0	100	100
33	d	255/350 (73%)	222 (87%)	33 (13%)	0	100	100
34	f	887/908 (98%)	778 (88%)	107 (12%)	2 (0%)	43	74
35	e	48/70 (69%)	41 (85%)	7 (15%)	0	100	100
All	All	13990/15458 (90%)	13036 (93%)	940 (7%)	14 (0%)	49	79

5 of 14 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	329	PRO
3	C	224	ILE
4	D	416	PHE
22	x	87	VAL
34	f	100	ARG

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	349/372 (94%)	344 (99%)	5 (1%)	59	71
2	B	357/385 (93%)	353 (99%)	4 (1%)	65	74
3	C	340/346 (98%)	338 (99%)	2 (1%)	78	79
4	D	333/366 (91%)	331 (99%)	2 (1%)	78	79
5	E	341/353 (97%)	341 (100%)	0	100	100
6	F	344/379 (91%)	344 (100%)	0	100	100
7	G	202/210 (96%)	201 (100%)	1 (0%)	81	80
7	g	201/210 (96%)	200 (100%)	1 (0%)	81	80
8	H	187/191 (98%)	187 (100%)	0	100	100
8	h	188/191 (98%)	188 (100%)	0	100	100
9	I	202/221 (91%)	202 (100%)	0	100	100
9	i	206/221 (93%)	206 (100%)	0	100	100
10	J	197/211 (93%)	197 (100%)	0	100	100
10	j	196/211 (93%)	196 (100%)	0	100	100
11	K	197/203 (97%)	197 (100%)	0	100	100
11	k	195/203 (96%)	195 (100%)	0	100	100
12	L	202/230 (88%)	202 (100%)	0	100	100
12	l	201/230 (87%)	201 (100%)	0	100	100
13	M	198/212 (93%)	198 (100%)	0	100	100
13	m	198/212 (93%)	197 (100%)	1 (0%)	81	80
14	N	158/181 (87%)	158 (100%)	0	100	100
14	n	156/181 (86%)	156 (100%)	0	100	100
15	O	178/228 (78%)	178 (100%)	0	100	100
15	o	181/228 (79%)	181 (100%)	0	100	100
16	P	172/174 (99%)	172 (100%)	0	100	100
16	p	173/174 (99%)	173 (100%)	0	100	100
17	Q	168/171 (98%)	168 (100%)	0	100	100
17	q	166/171 (97%)	166 (100%)	0	100	100
18	R	156/202 (77%)	156 (100%)	0	100	100
18	r	154/202 (76%)	154 (100%)	0	100	100
19	S	175/199 (88%)	175 (100%)	0	100	100
19	s	177/199 (89%)	177 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
20	T	178/215 (83%)	178 (100%)	0	100	100
20	t	179/215 (83%)	179 (100%)	0	100	100
22	x	439/439 (100%)	438 (100%)	1 (0%)	87	85
23	y	68/68 (100%)	68 (100%)	0	100	100
24	U	748/816 (92%)	748 (100%)	0	100	100
25	V	390/460 (85%)	390 (100%)	0	100	100
26	W	410/416 (99%)	409 (100%)	1 (0%)	87	85
27	X	327/362 (90%)	327 (100%)	0	100	100
28	Y	344/344 (100%)	331 (96%)	13 (4%)	29	55
29	Z	257/295 (87%)	250 (97%)	7 (3%)	39	62
30	a	333/336 (99%)	331 (99%)	2 (1%)	78	79
31	b	167/312 (54%)	167 (100%)	0	100	100
32	c	252/268 (94%)	251 (100%)	1 (0%)	84	81
33	d	231/294 (79%)	231 (100%)	0	100	100
34	f	745/763 (98%)	742 (100%)	3 (0%)	84	81
35	e	44/63 (70%)	42 (96%)	2 (4%)	24	50
All	All	11960/13133 (91%)	11914 (100%)	46 (0%)	81	81

5 of 46 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
28	Y	212	GLU
29	Z	151	THR
28	Y	213	LEU
29	Z	144	VAL
29	Z	176	LEU

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

Mol	Chain	Res	Type
8	h	169	ASN
34	f	53	GLN
22	x	308	ASN
33	d	229	GLN
30	a	231	GLN

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 7 ligands modelled in this entry, 1 is 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$
36	ADP	B	501	-	28,29,29	1.40	4 (14%)	43,45,45	1.88	8 (18%)
37	ATP	E	501	-	32,33,33	0.45	0	48,52,52	0.29	0
37	ATP	F	501	-	32,33,33	0.47	0	48,52,52	0.33	0
37	ATP	D	501	-	32,33,33	0.48	0	48,52,52	0.30	0
36	ADP	A	501	-	28,29,29	1.40	4 (14%)	43,45,45	1.83	10 (23%)
37	ATP	C	501	-	32,33,33	0.52	0	48,52,52	0.38	0

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
36	ADP	B	501	-	-	5/16/32/32	0/3/3/3
37	ATP	E	501	-	-	4/22/38/38	0/3/3/3
37	ATP	F	501	-	-	3/22/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
37	ATP	D	501	-	-	10/22/38/38	0/3/3/3
36	ADP	A	501	-	-	2/16/32/32	0/3/3/3
37	ATP	C	501	-	-	6/22/38/38	0/3/3/3

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
36	B	501	ADP	C5-C4	4.72	1.47	1.39
36	A	501	ADP	C5-C4	4.60	1.47	1.39
36	B	501	ADP	C5-C6	2.65	1.48	1.41
36	A	501	ADP	C5-C6	2.58	1.48	1.41
36	B	501	ADP	C5-N7	-2.40	1.34	1.39

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	B	501	ADP	C5-C4-N3	-6.02	118.42	126.72
36	A	501	ADP	C5-C4-N3	-5.86	118.65	126.72
36	B	501	ADP	N3-C4-N9	4.89	135.48	127.17
36	A	501	ADP	N3-C4-N9	4.59	134.98	127.17
36	B	501	ADP	C2-N3-C4	3.74	120.95	111.83

There are no chirality outliers.

5 of 30 torsion outliers are listed below:

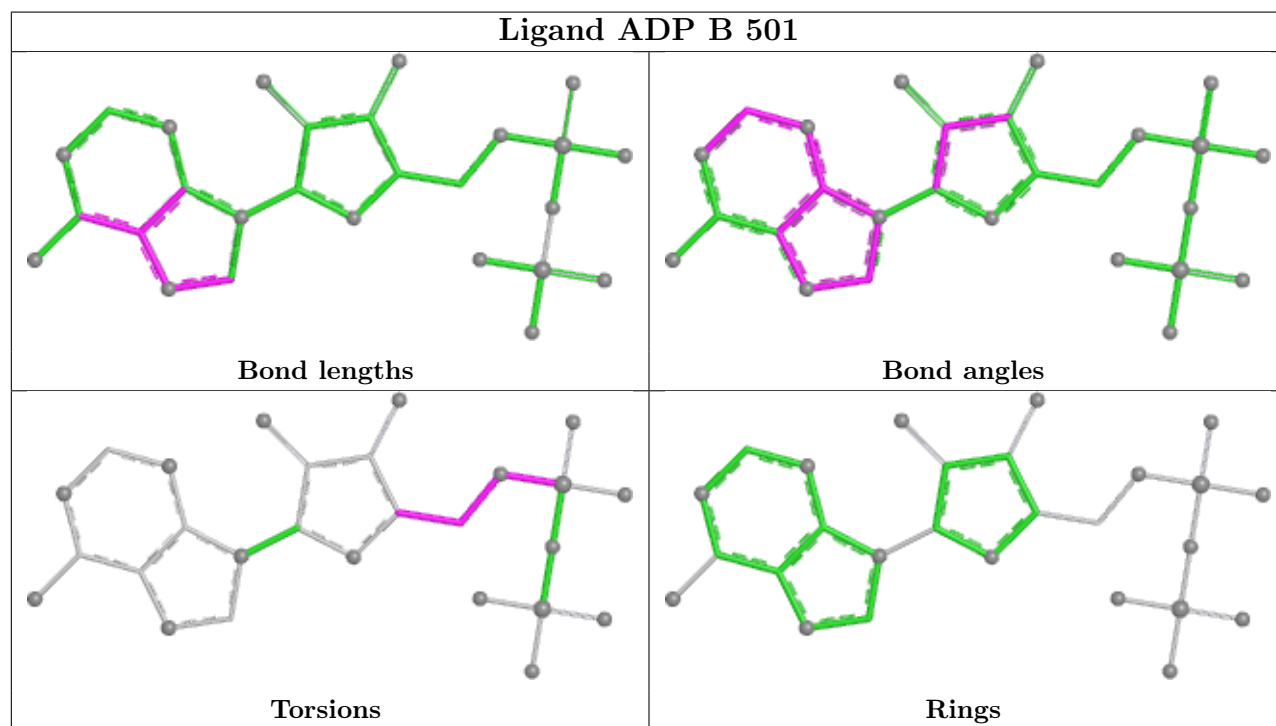
Mol	Chain	Res	Type	Atoms
36	A	501	ADP	C5'-O5'-PA-O3A
36	B	501	ADP	C5'-O5'-PA-O2A
36	B	501	ADP	C5'-O5'-PA-O3A
36	B	501	ADP	C3'-C4'-C5'-O5'
37	C	501	ATP	C5'-O5'-PA-O2A

There are no ring outliers.

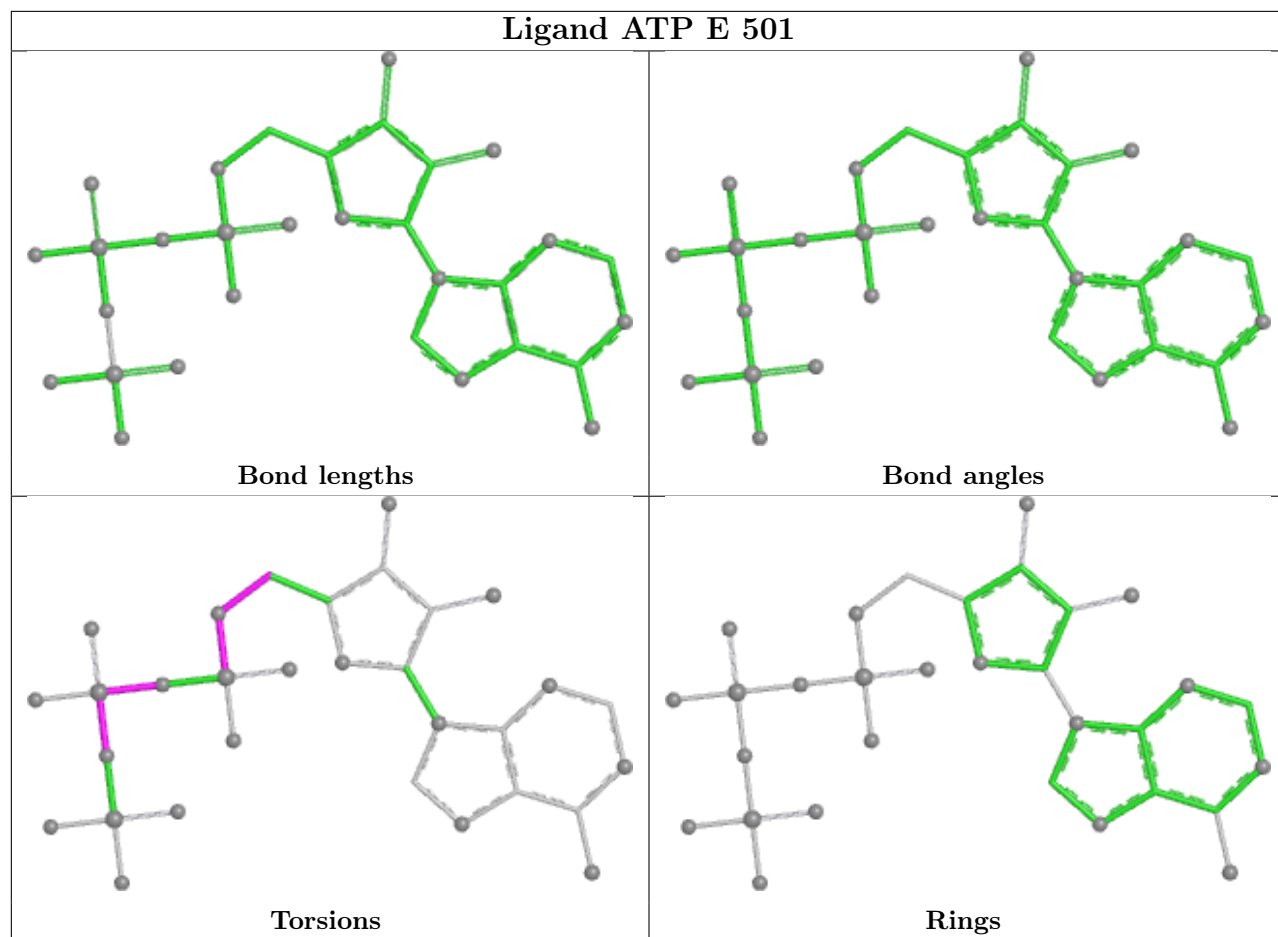
4 monomers are involved in 7 short contacts:

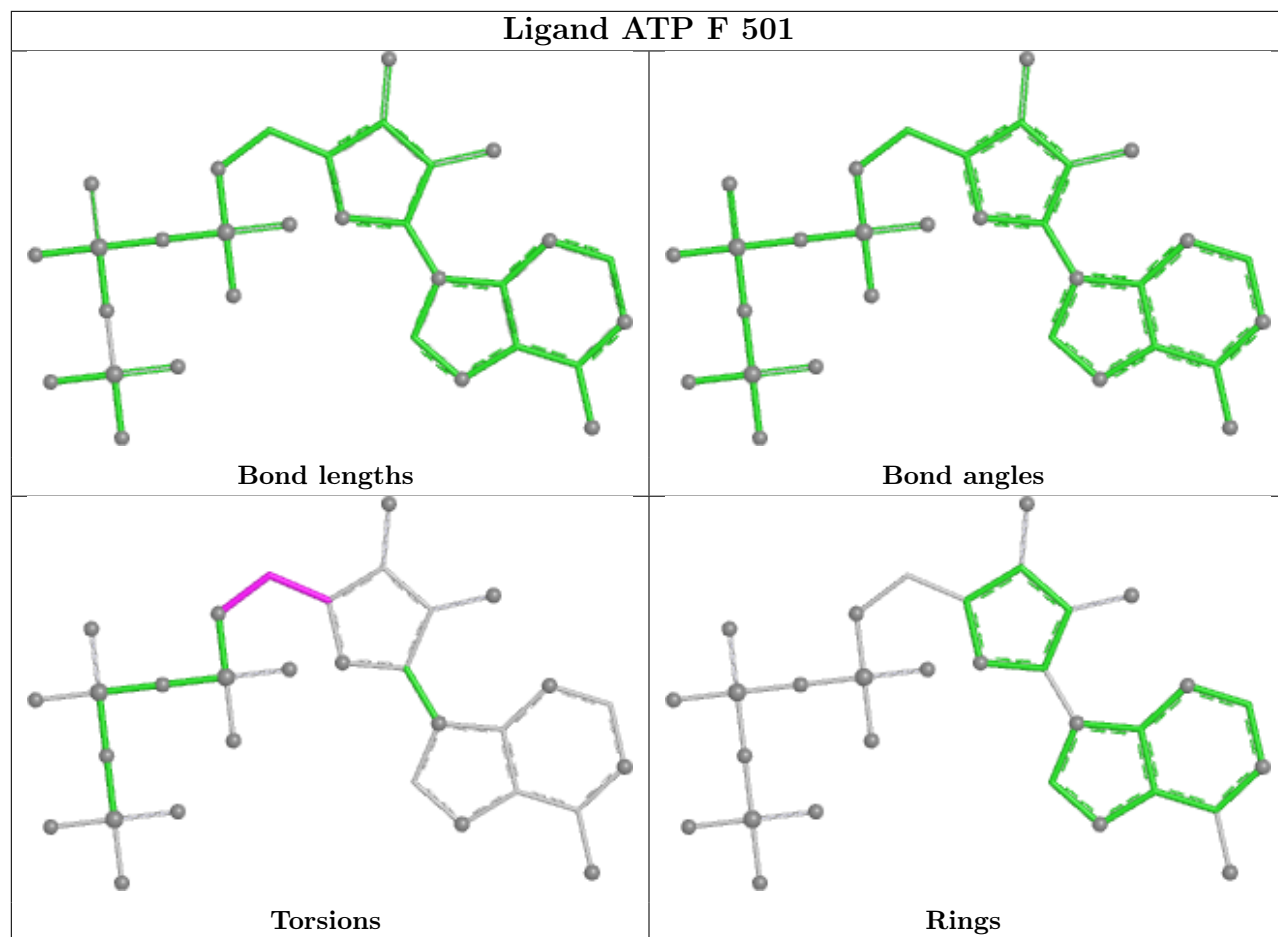
Mol	Chain	Res	Type	Clashes	Symm-Clashes
37	E	501	ATP	2	0
37	F	501	ATP	1	0
36	A	501	ADP	1	0
37	C	501	ATP	3	0

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.

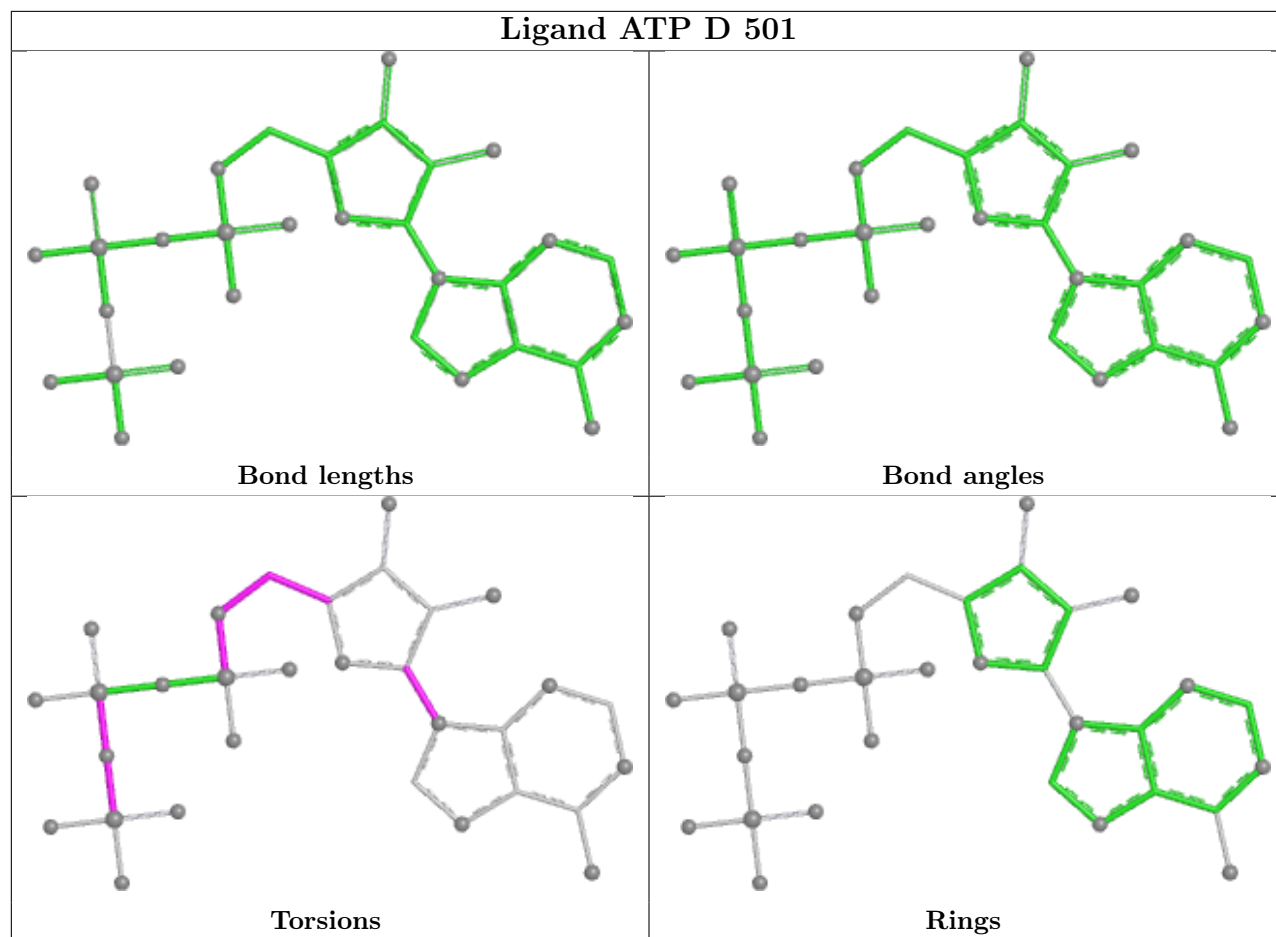


Ligand ATP E 501

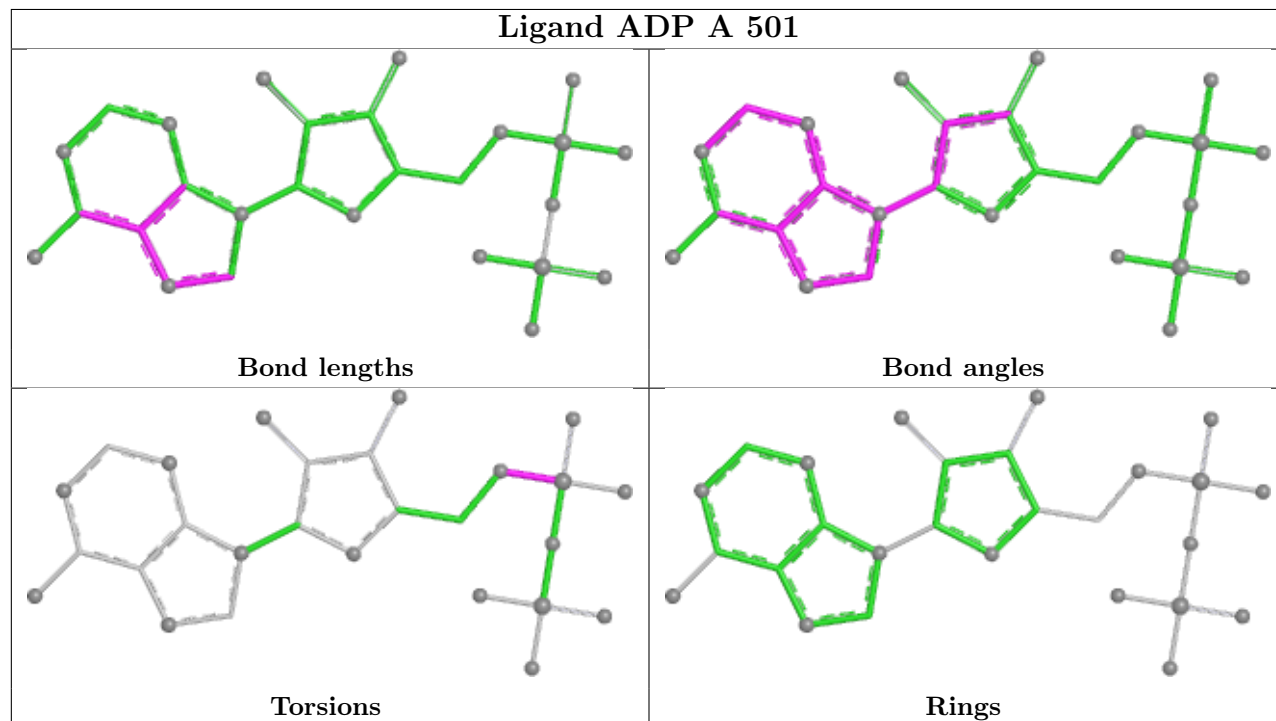


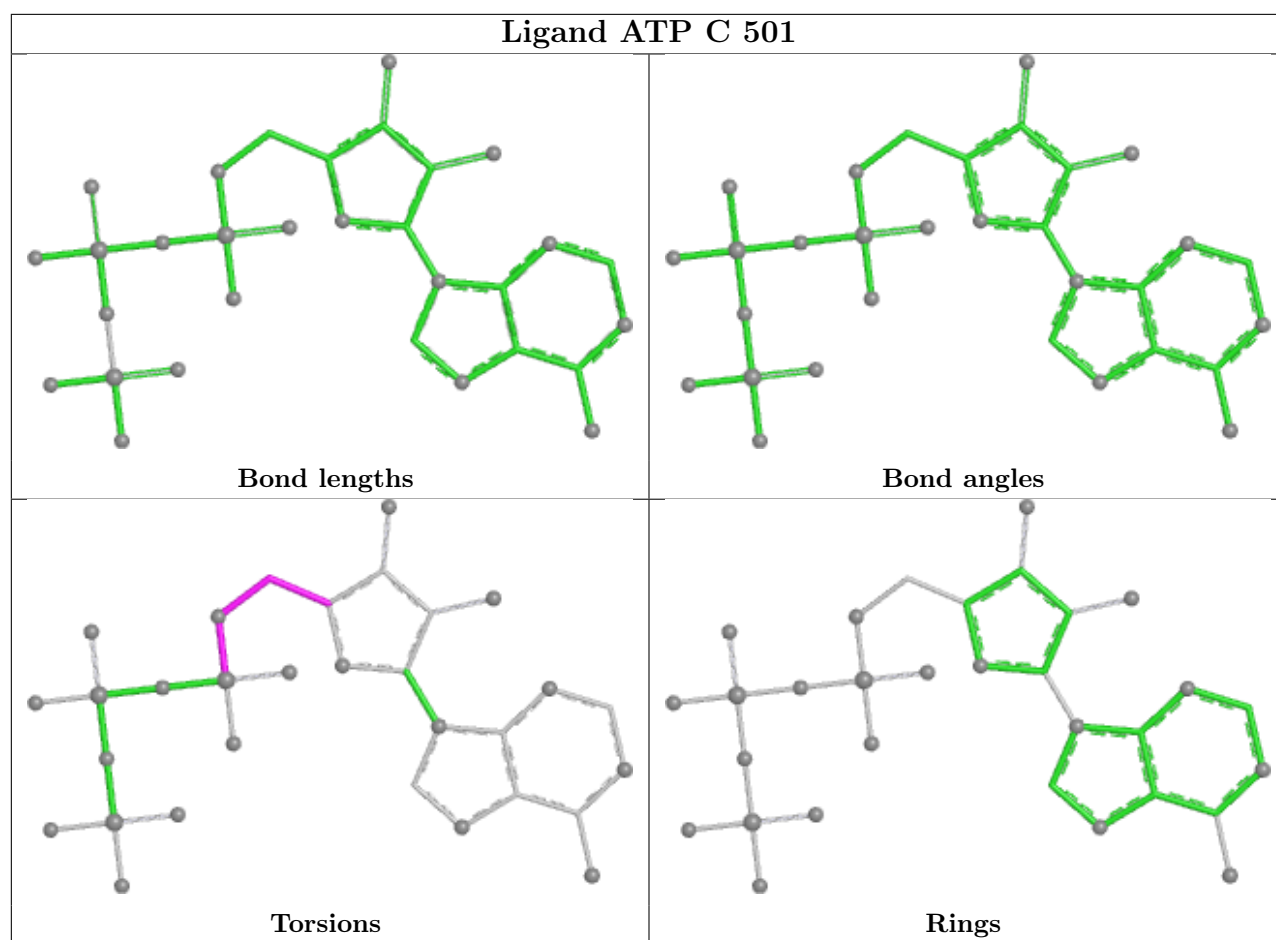


Ligand ATP D 501



Ligand ADP A 501





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.

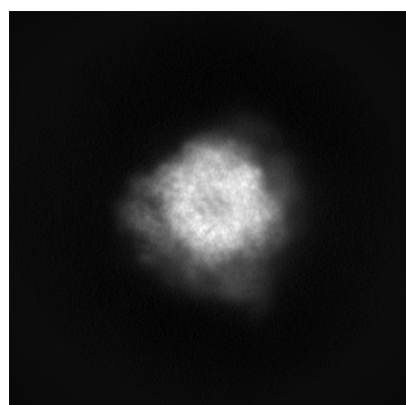
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-32275. 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](#)

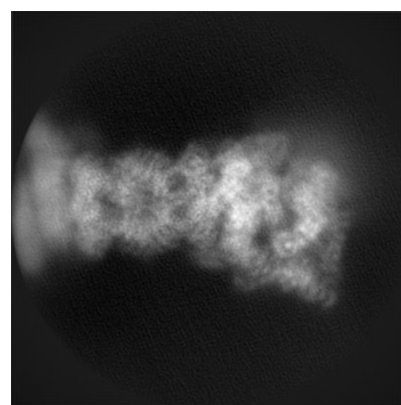
6.1.1 Primary map



X



Y

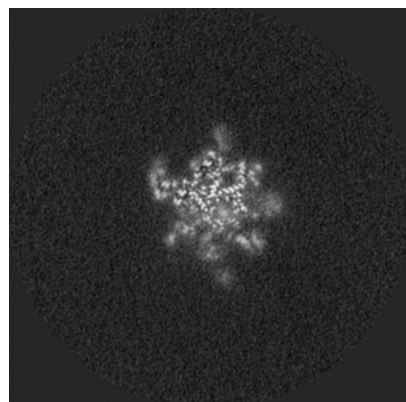


Z

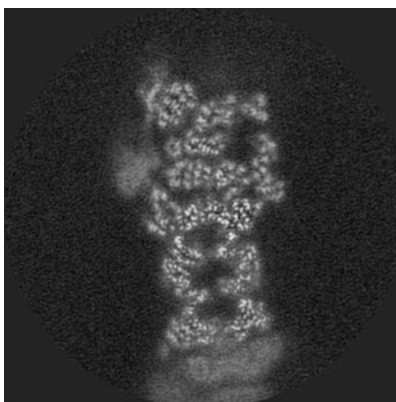
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

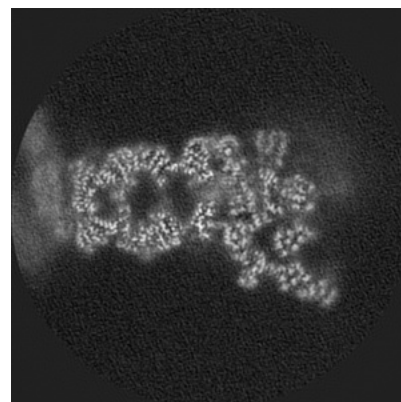
6.2.1 Primary map



X Index: 320



Y Index: 320

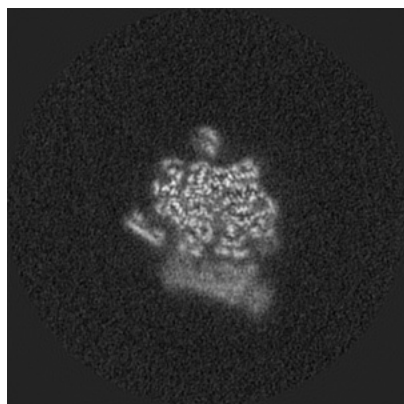


Z Index: 320

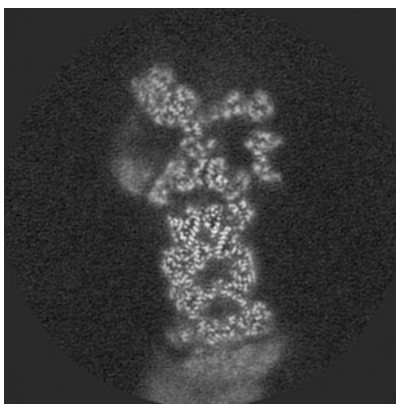
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

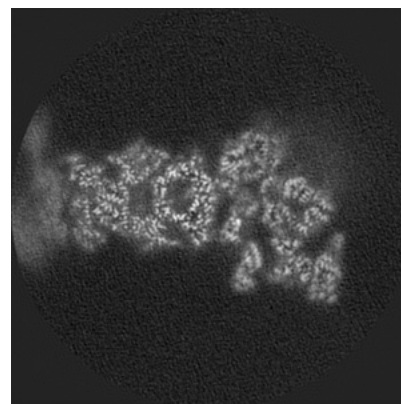
6.3.1 Primary map



X Index: 359



Y Index: 302

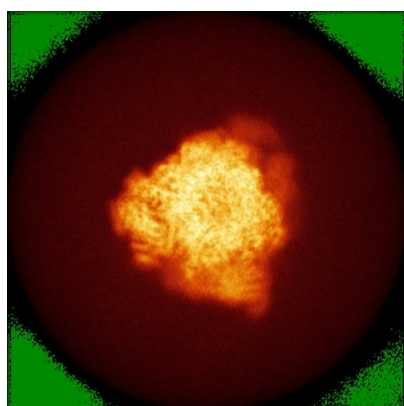


Z Index: 298

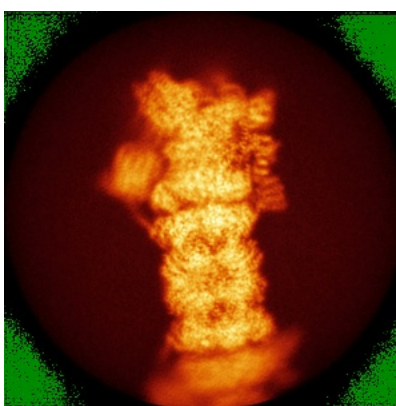
The images above show the largest variance slices of the map in three orthogonal directions.

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

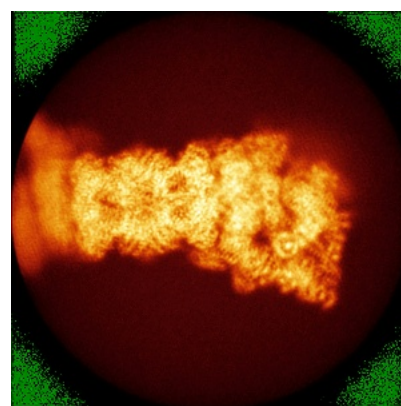
6.4.1 Primary map



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

This section was not generated.

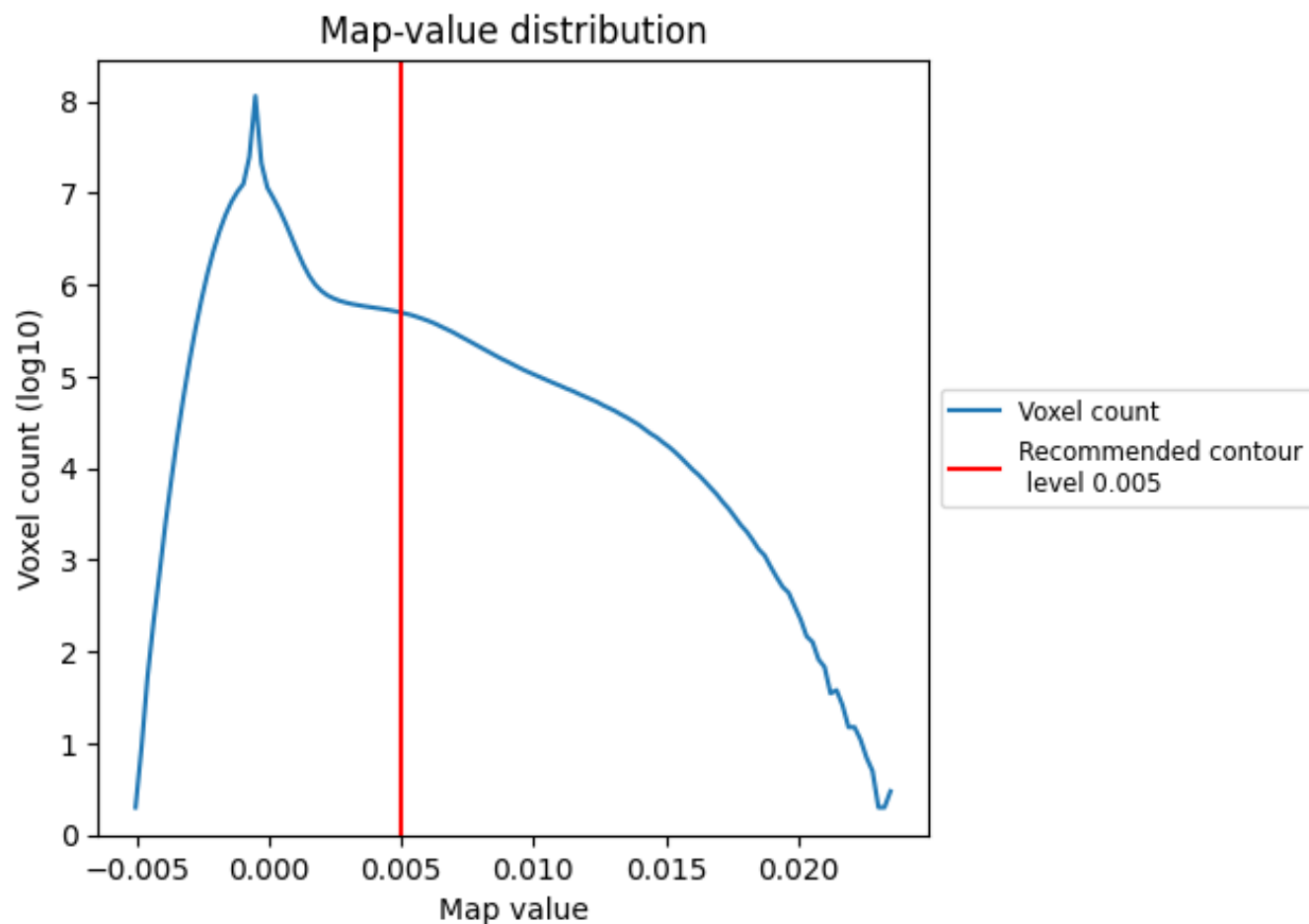
6.6 Mask visualisation

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

7 Map analysis [i](#)

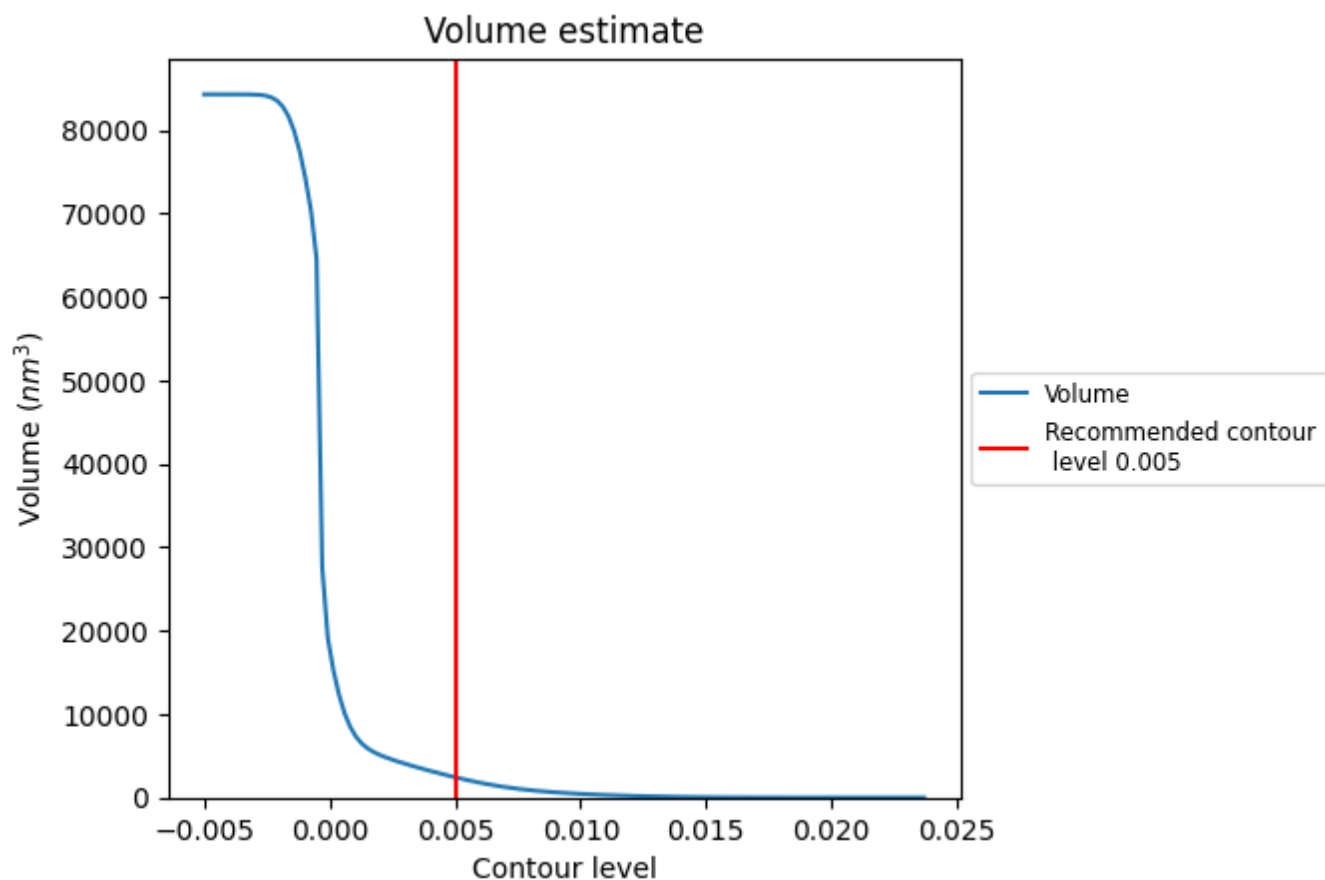
This section contains the results of statistical analysis of the map.

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.

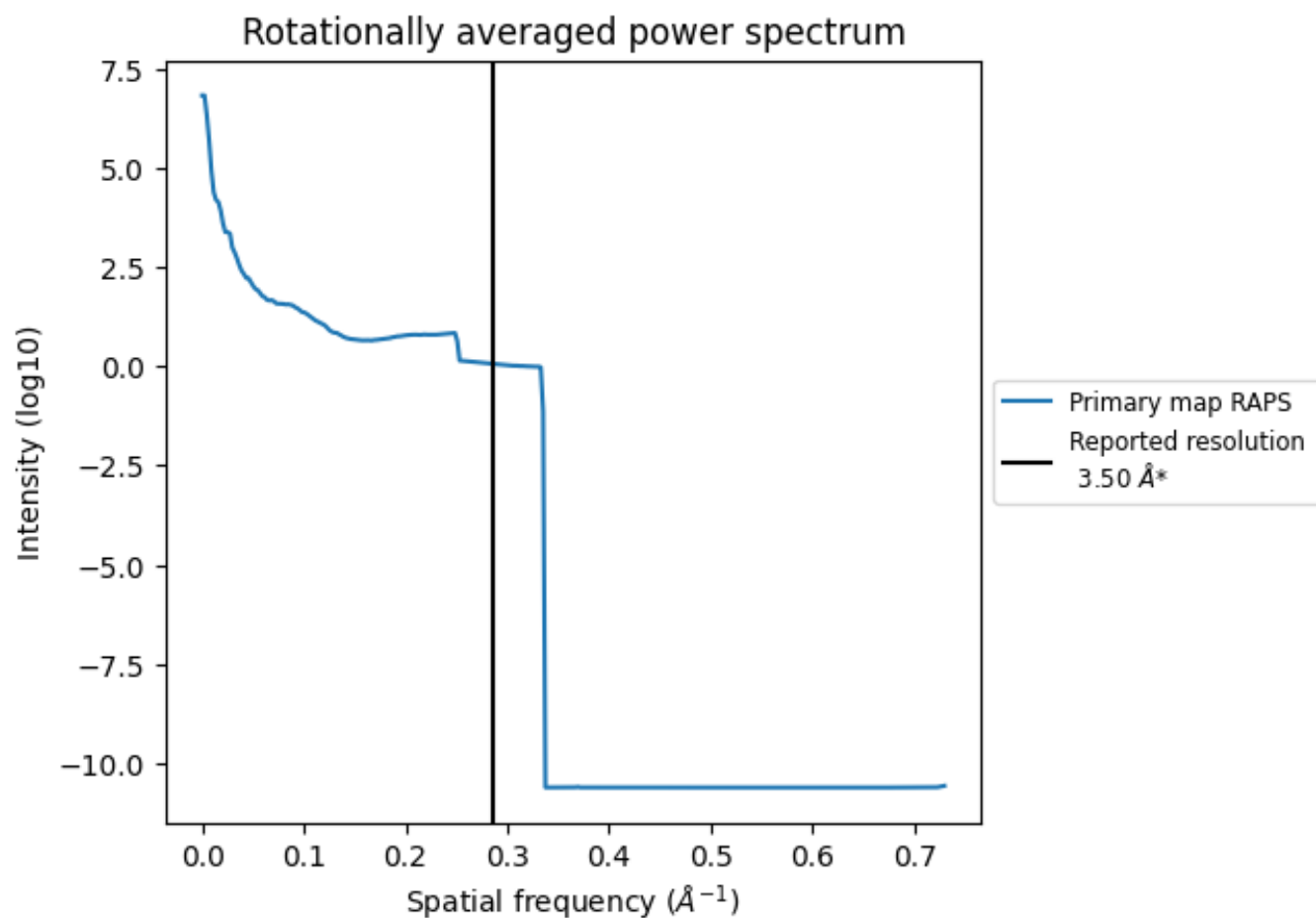
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2426 nm³; this corresponds to an approximate mass of 2191 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ



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

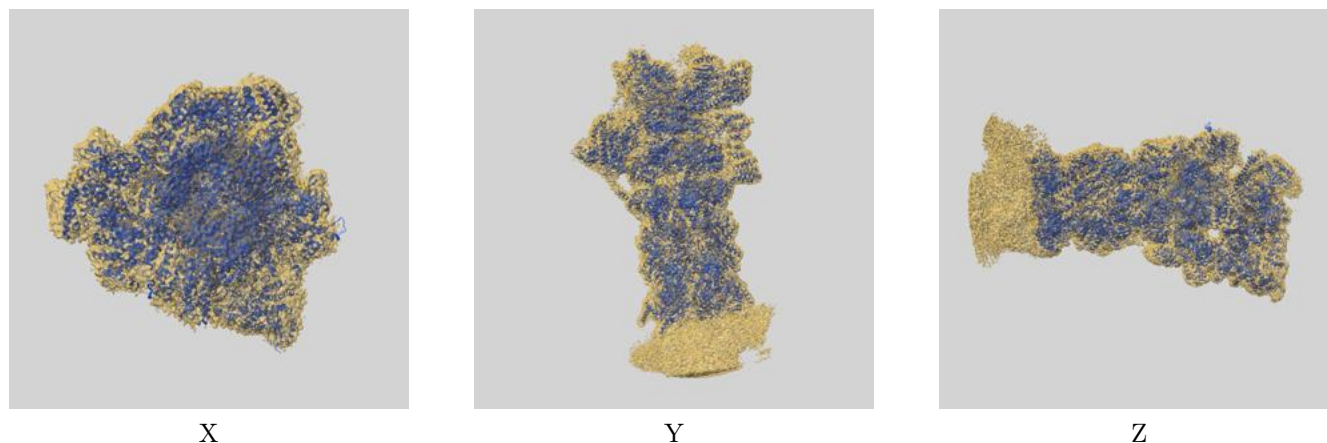
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

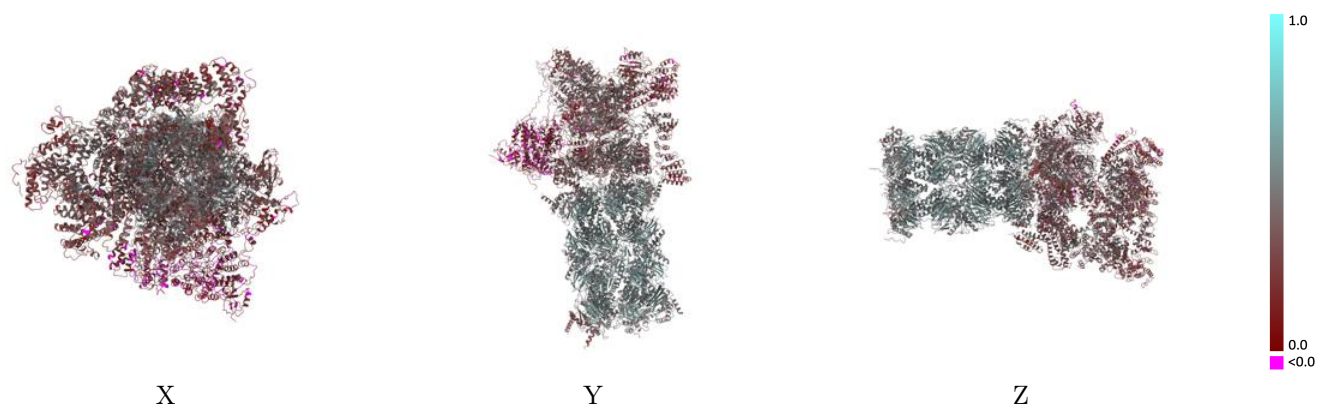
This section contains information regarding the fit between EMDB map EMD-32275 and PDB model 7W3A. Per-residue inclusion information can be found in section [3](#) on page [13](#).

9.1 Map-model overlay [i](#)



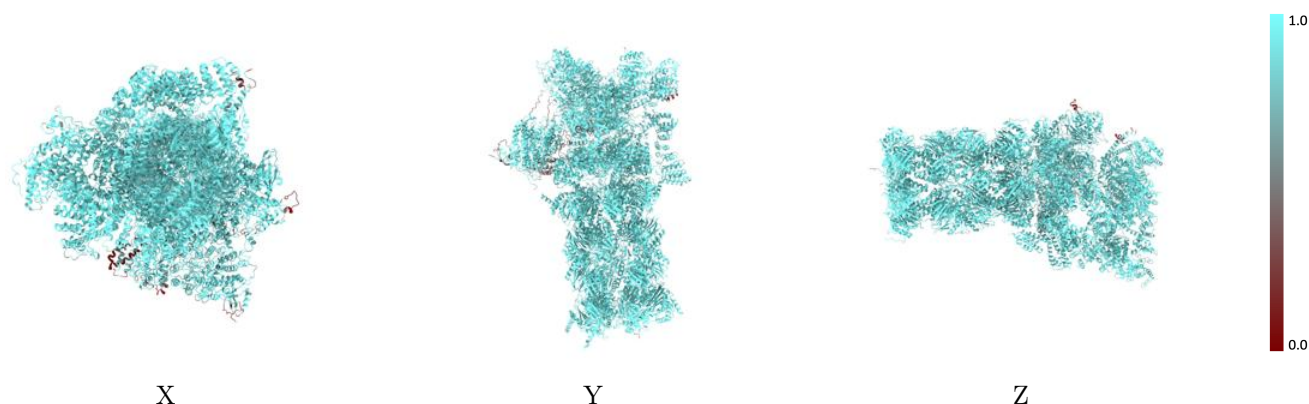
The images above show the 3D surface view of the map at the recommended contour level 0.005 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



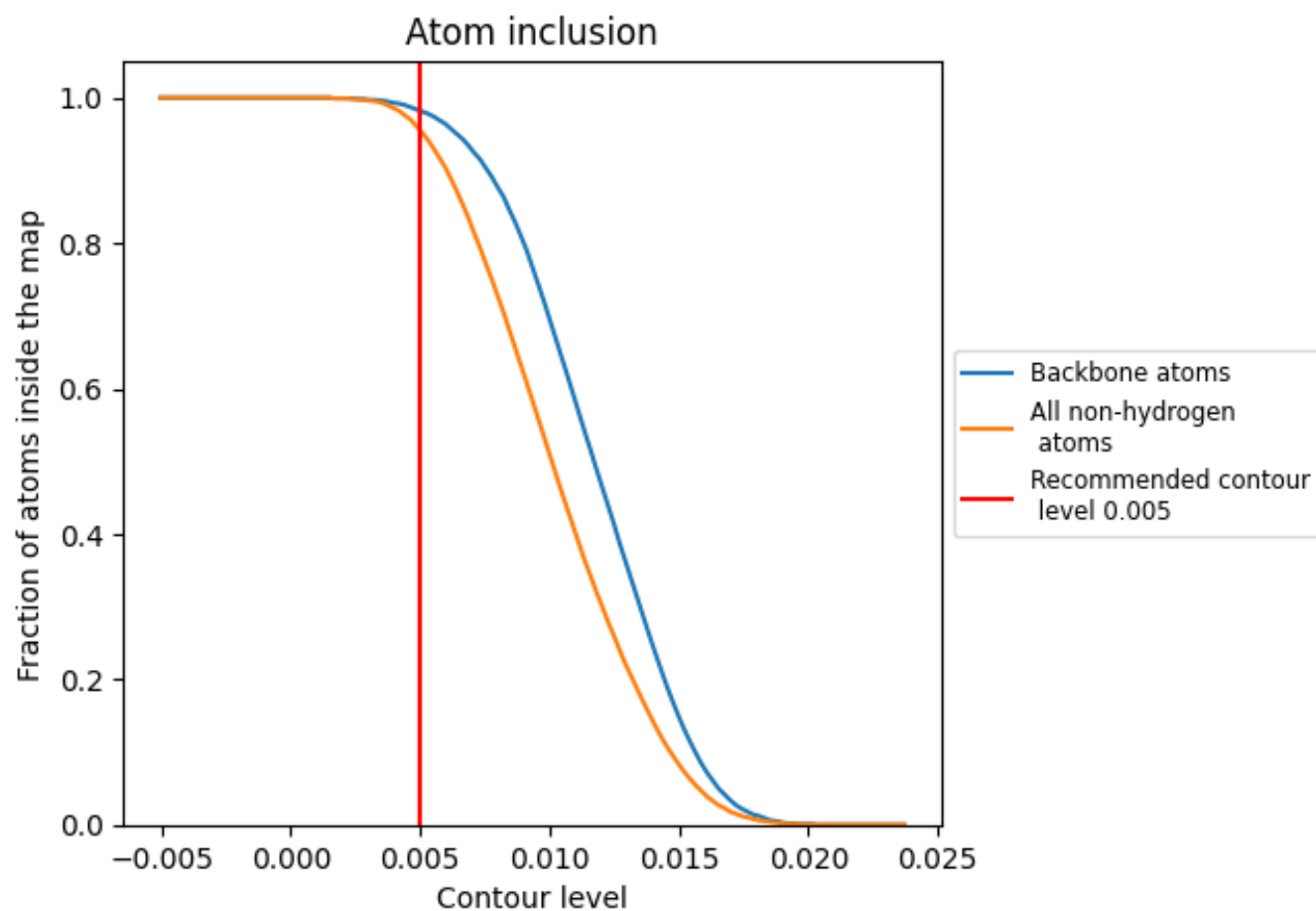
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 98% of all backbone atoms, 96% 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	 0.9550	 0.3900
A	 0.9430	 0.3320
B	 0.9250	 0.3000
C	 0.9630	 0.3300
D	 0.9730	 0.3670
E	 0.9580	 0.3680
F	 0.9420	 0.3660
G	 0.9870	 0.4970
H	 0.9890	 0.4940
I	 0.9840	 0.4810
J	 0.9810	 0.4780
K	 0.9840	 0.4900
L	 0.9920	 0.5040
M	 0.9870	 0.5010
N	 0.9880	 0.5190
O	 0.9930	 0.5120
P	 0.9920	 0.5220
Q	 0.9900	 0.5170
R	 0.9950	 0.5210
S	 0.9930	 0.5090
T	 0.9860	 0.5260
U	 0.9230	 0.3270
V	 0.9500	 0.3300
W	 0.9310	 0.2950
X	 0.9610	 0.3500
Y	 0.9540	 0.3300
Z	 0.9730	 0.3350
a	 0.9460	 0.2830
b	 0.9470	 0.2680
c	 0.9660	 0.3420
d	 0.9250	 0.2580
e	 0.9450	 0.3200
f	 0.8630	 0.1480
g	 0.9780	 0.4950
h	 0.9830	 0.4980



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Chain	Atom inclusion	Q-score
i	 0.9740	 0.4700
j	 0.9690	 0.4350
k	 0.9770	 0.4740
l	 0.9890	 0.5060
m	 0.9780	 0.4930
n	 0.9950	 0.5270
o	 0.9900	 0.5170
p	 0.9940	 0.5220
q	 0.9950	 0.5190
r	 0.9960	 0.5250
s	 0.9900	 0.5130
t	 0.9880	 0.5220
v	 0.9880	 0.3420
x	 0.8520	 0.2700
y	 0.9410	 0.3260