



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 09:42 PM UTC

PDB ID : 6EF2 / pdb_00006ef2
EMDB ID : EMD-9044
Title : Yeast 26S proteasome bound to ubiquitinated substrate (5T motor state)
Authors : de la Pena, A.H.; Goodall, E.A.; Gates, S.N.; Lander, G.C.; Martin, A.
Deposited on : 2018-08-15
Resolution : 4.27 Å(reported)
Based on initial model : 5MPC

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

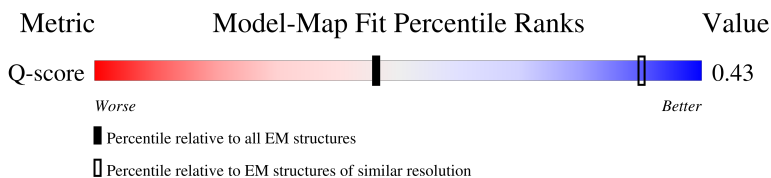
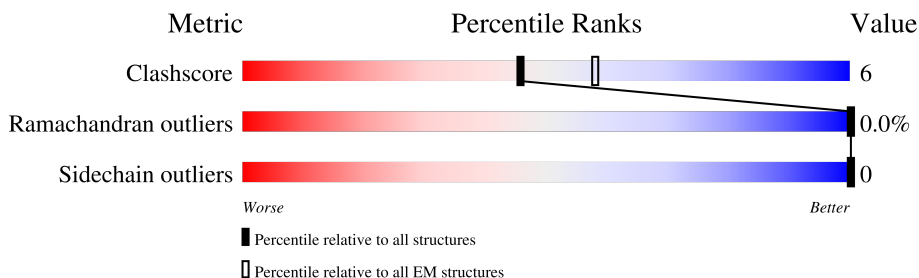
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.27 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.





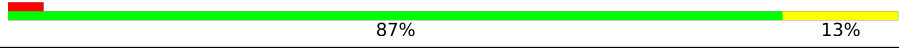



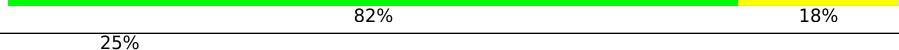
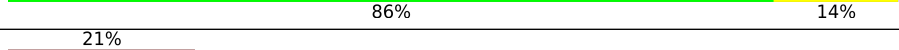
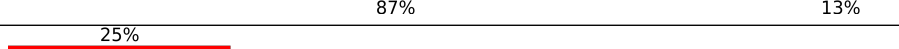
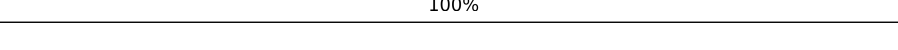
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	4567 (3.77 - 4.76)

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	238	 83% 17%
2	B	249	 88% 12%
3	C	241	 9% 85% 15%
4	D	241	 9% 88% 12%

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Mol	Chain	Length	Quality of chain
5	E	247	 89%11%
6	F	232	 88%12%
7	G	246	 87%13%
8	H	273	 12%80%17%
9	I	260	 81%19%
10	J	262	 7%78%22%
11	K	259	 7%82%18%
12	L	264	 25%86%14%
13	M	270	 21%87%13%
14	s	16	 25%100%

2 Entry composition

There are 16 unique types of molecules in this entry. The entry contains 24659 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	238	Total	C	N	O	S	0	0
			1835	1169	309	349	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	249	Total	C	N	O	S	0	0
			1816	1164	308	341	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	241	Total	C	N	O	S	0	0
			1795	1140	301	352	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	241	Total	C	N	O	S	0	0
			1782	1121	309	348	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	247	Total	C	N	O	S	0	0
			1869	1173	319	370	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	232	Total	C	N	O	S	0	0
			1739	1097	307	331	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	246	Total	C	N	O	S	0	0
			1778	1135	313	326	4		

- Molecule 8 is a protein called 26S proteasome regulatory subunit 7 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	265	Total	C	N	O	S	0	0
			1986	1246	358	369	13		

- Molecule 9 is a protein called 26S proteasome regulatory subunit 4 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	260	Total	C	N	O	S	0	0
			1958	1230	337	382	9		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	262	Total	C	N	O	S	0	0
			1976	1242	358	363	13		

- Molecule 11 is a protein called 26S proteasome regulatory subunit 6B homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	259	Total	C	N	O	S	0	0
			1956	1231	351	367	7		

- Molecule 12 is a protein called 26S proteasome subunit RPT4.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	264	Total	C	N	O	S	0	0
			1860	1189	315	348	8		

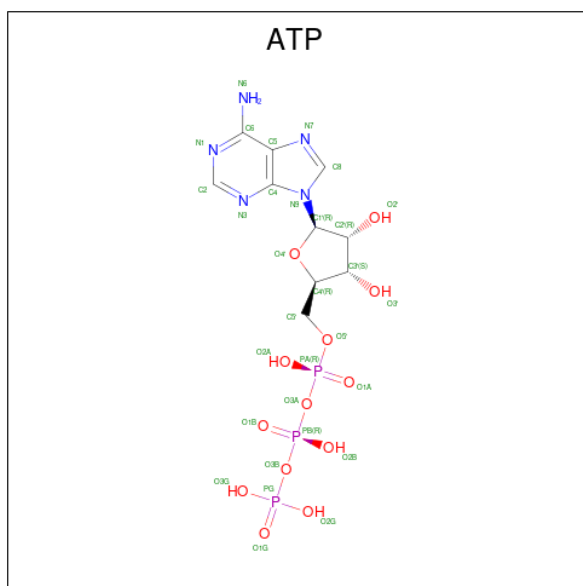
- Molecule 13 is a protein called 26S proteasome regulatory subunit 6A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	270	Total	C	N	O	S	0	0
			2035	1272	356	400	7		

- Molecule 14 is a protein called model substrate polypeptide.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	s	16	Total	C	N	O	0	0
			96	58	18	20		

- Molecule 15 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).



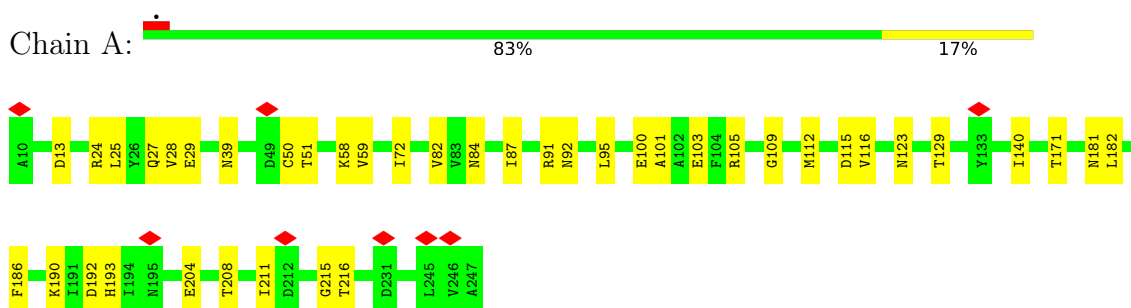


Mol	Chain	Residues	Atoms					AltConf
16	K	1	Total	C	N	O	P	0
			27	10	5	10	2	
16	L	1	Total	C	N	O	P	0
			27	10	5	10	2	

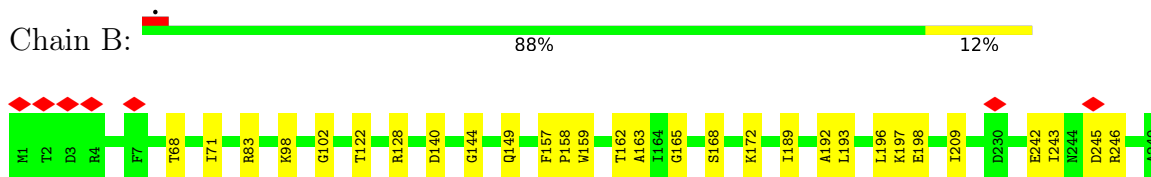
3 Residue-property plots [i](#)

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

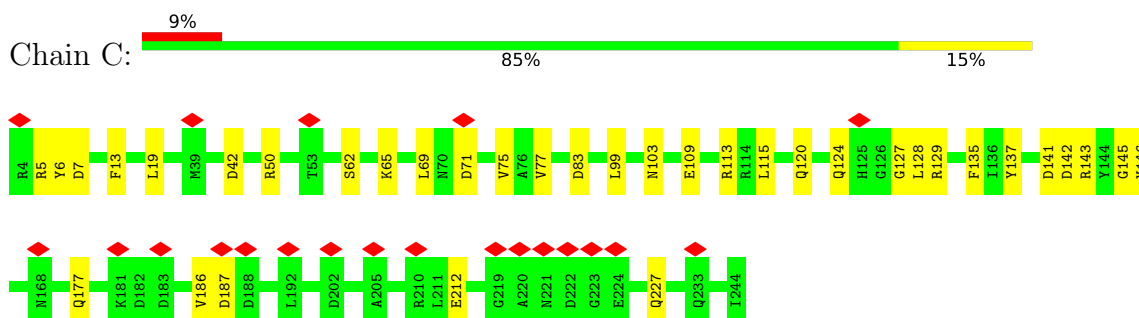
- Molecule 1: Proteasome subunit alpha type-1



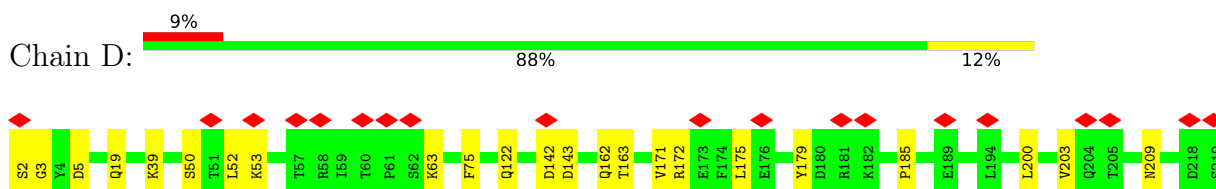
- Molecule 2: Proteasome subunit alpha type-2



- Molecule 3: Proteasome subunit alpha type-3



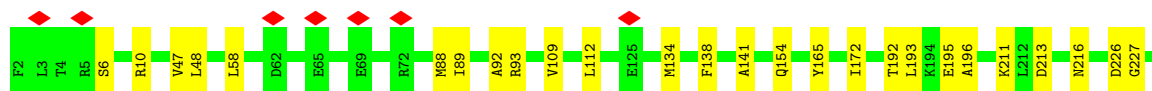
- Molecule 4: Proteasome subunit alpha type-4





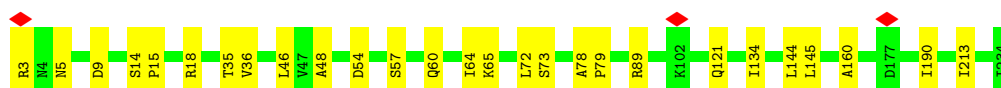
- Molecule 5: Proteasome subunit alpha type-5

Chain E: 89% 11%



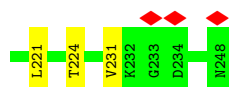
- Molecule 6: Proteasome subunit alpha type-6

Chain F: 88% 12%



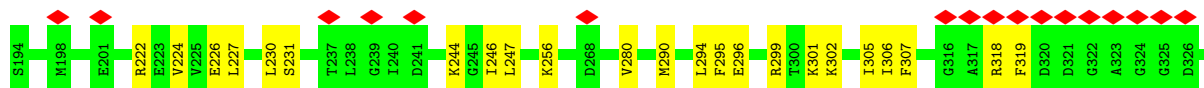
- Molecule 7: Probable proteasome subunit alpha type-7

Chain G: 87% 13%



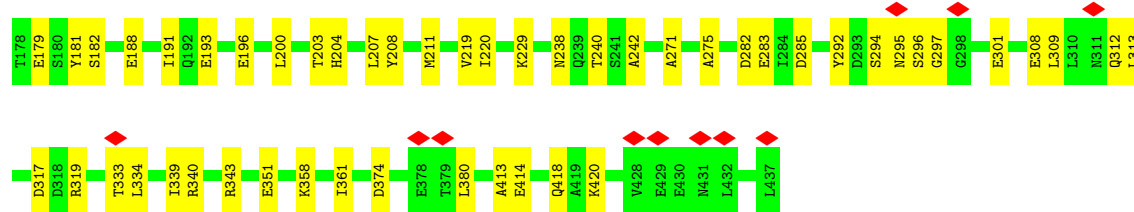
- Molecule 8: 26S proteasome regulatory subunit 7 homolog

Chain H: 12% 80% 17%

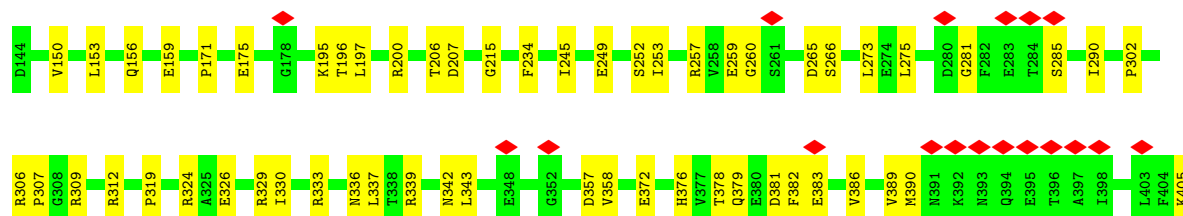
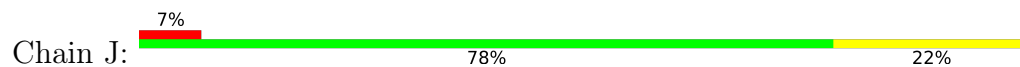


- Molecule 9: 26S proteasome regulatory subunit 4 homolog

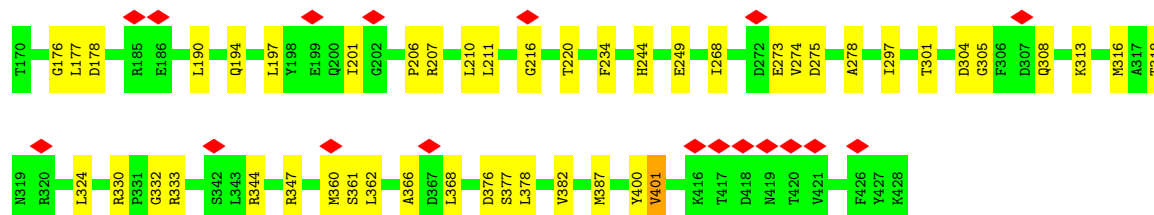
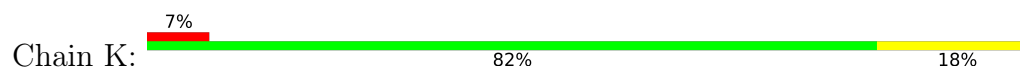
Chain I: 81% 19%



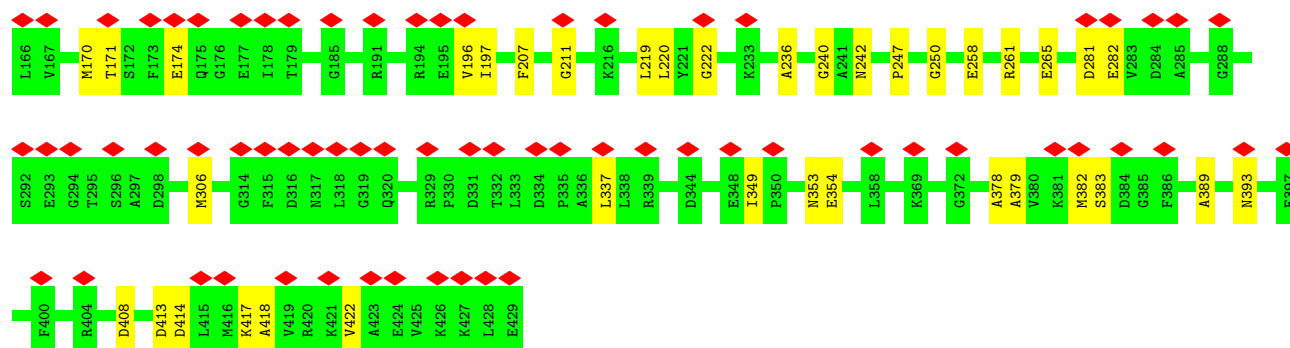
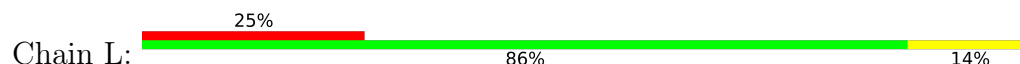
- Molecule 10: 26S proteasome regulatory subunit 8 homolog



- Molecule 11: 26S proteasome regulatory subunit 6B homolog

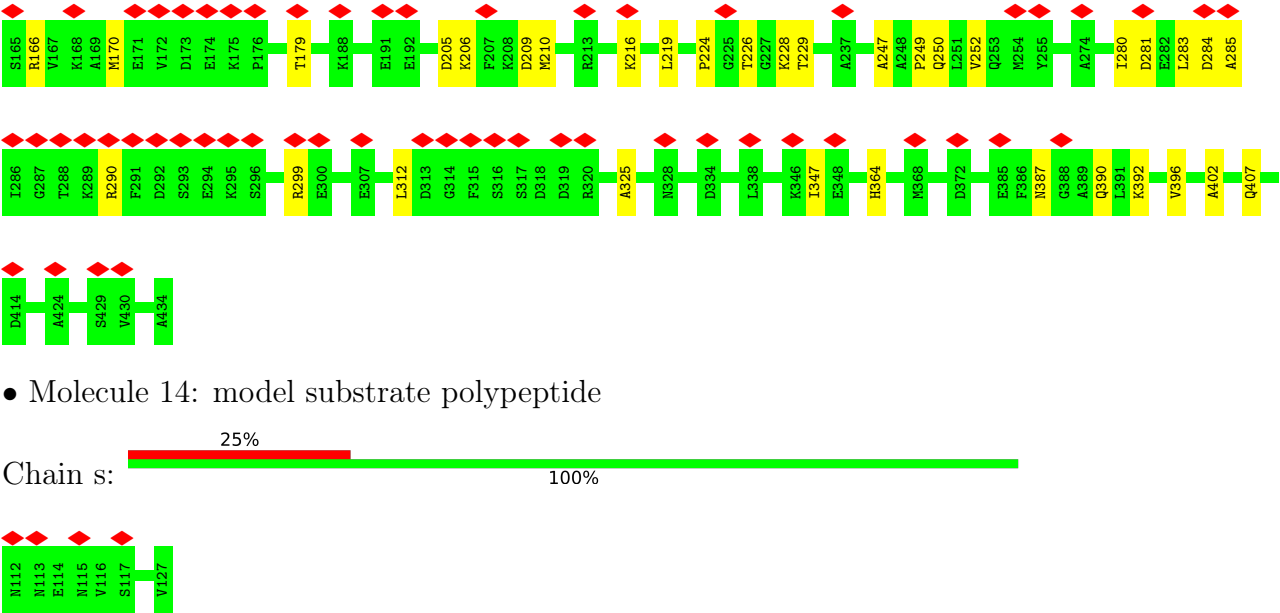


- Molecule 12: 26S proteasome subunit RPT4



- Molecule 13: 26S proteasome regulatory subunit 6A





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	47349	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION; CTF correction was performed by Relion during reconstruction	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	-1500	Depositor
Maximum defocus (nm)	-3000	Depositor
Magnification	29000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.192	Depositor
Minimum map value	0.000	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.04	Depositor
Map size (Å)	350.19998, 350.19998, 350.19998	wwPDB
Map dimensions	340, 340, 340	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.03, 1.03, 1.03	Depositor

5 Model quality

5.1 Standard geometry

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

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	0.46	0/1873	0.51	0/2544
2	B	0.48	0/1852	0.51	0/2519
3	C	0.42	0/1825	0.47	0/2488
4	D	0.43	0/1811	0.49	0/2472
5	E	0.48	0/1896	0.49	0/2561
6	F	0.49	0/1766	0.47	0/2393
7	G	0.44	0/1816	0.49	0/2474
8	H	0.43	0/2016	0.52	0/2724
9	I	0.51	0/1981	0.55	0/2673
10	J	0.52	0/2003	0.57	0/2696
11	K	0.47	0/1982	0.53	0/2681
12	L	0.33	0/1891	0.49	0/2578
13	M	0.35	0/2062	0.53	0/2785
14	s	0.37	0/95	0.59	0/129
All	All	0.45	0/24869	0.51	0/33717

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
2	B	0	1
11	K	0	1
All	All	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	157	PHE	Peptide
11	K	401	VAL	Peptide

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	1835	0	1781	28	0
2	B	1816	0	1796	17	0
3	C	1795	0	1720	23	0
4	D	1782	0	1706	17	0
5	E	1869	0	1818	17	0
6	F	1739	0	1722	16	0
7	G	1778	0	1672	19	0
8	H	1986	0	1958	29	0
9	I	1958	0	1960	37	0
10	J	1976	0	2018	36	0
11	K	1956	0	1948	33	0
12	L	1860	0	1747	23	0
13	M	2035	0	1998	30	0
14	s	96	0	88	0	0
15	H	31	0	12	3	0
15	I	31	0	12	3	0
15	J	31	0	12	2	0
15	M	31	0	12	6	0
16	K	27	0	12	2	0
16	L	27	0	12	0	0
All	All	24659	0	24004	301	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 301 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)
11:K:304:ASP:OD2	11:K:330:ARG:NH2	2.14	0.81
8:H:385:ARG:NH1	8:H:411:CYS:O	2.15	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:330:ILE:O	10:J:333:ARG:NH1	2.15	0.78
11:K:206:PRO:O	11:K:313:LYS:NZ	2.18	0.77
9:I:414:GLU:O	9:I:418:GLN:NE2	2.18	0.77

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	236/238 (99%)	205 (87%)	31 (13%)	0	100	100
2	B	247/249 (99%)	216 (87%)	30 (12%)	1 (0%)	30	66
3	C	239/241 (99%)	207 (87%)	32 (13%)	0	100	100
4	D	239/241 (99%)	211 (88%)	28 (12%)	0	100	100
5	E	245/247 (99%)	217 (89%)	28 (11%)	0	100	100
6	F	230/232 (99%)	206 (90%)	24 (10%)	0	100	100
7	G	244/246 (99%)	219 (90%)	25 (10%)	0	100	100
8	H	261/273 (96%)	226 (87%)	35 (13%)	0	100	100
9	I	258/260 (99%)	211 (82%)	47 (18%)	0	100	100
10	J	260/262 (99%)	222 (85%)	38 (15%)	0	100	100
11	K	257/259 (99%)	226 (88%)	31 (12%)	0	100	100
12	L	262/264 (99%)	218 (83%)	44 (17%)	0	100	100
13	M	268/270 (99%)	226 (84%)	42 (16%)	0	100	100
14	s	14/16 (88%)	11 (79%)	3 (21%)	0	100	100
All	All	3260/3298 (99%)	2821 (86%)	438 (13%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	158	PRO

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	190/203 (94%)	190 (100%)	0	100	100
2	B	184/208 (88%)	184 (100%)	0	100	100
3	C	177/201 (88%)	177 (100%)	0	100	100
4	D	185/213 (87%)	185 (100%)	0	100	100
5	E	192/204 (94%)	192 (100%)	0	100	100
6	F	178/191 (93%)	178 (100%)	0	100	100
7	G	168/203 (83%)	168 (100%)	0	100	100
8	H	202/230 (88%)	202 (100%)	0	100	100
9	I	205/223 (92%)	205 (100%)	0	100	100
10	J	207/220 (94%)	207 (100%)	0	100	100
11	K	197/219 (90%)	197 (100%)	0	100	100
12	L	169/218 (78%)	169 (100%)	0	100	100
13	M	207/224 (92%)	207 (100%)	0	100	100
14	s	8/11 (73%)	8 (100%)	0	100	100
All	All	2469/2768 (89%)	2469 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 26 such sidechains are listed below:

Mol	Chain	Res	Type
8	H	339	GLN
9	I	311	ASN
13	M	362	GLN
9	I	192	GLN
9	I	370	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 ⓘ

6 ligands are modelled in this entry.

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$
15	ATP	M	501	-	32,33,33	1.26	4 (12%)	48,52,52	1.74	7 (14%)
15	ATP	I	501	-	32,33,33	1.27	4 (12%)	48,52,52	1.75	9 (18%)
15	ATP	H	501	-	32,33,33	1.30	5 (15%)	48,52,52	1.64	9 (18%)
15	ATP	J	501	-	32,33,33	1.26	4 (12%)	48,52,52	1.72	8 (16%)
16	ADP	K	501	-	28,29,29	1.38	5 (17%)	43,45,45	1.87	10 (23%)
16	ADP	L	501	-	28,29,29	1.33	5 (17%)	43,45,45	1.83	10 (23%)

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
15	ATP	M	501	-	-	3/22/38/38	0/3/3/3
15	ATP	I	501	-	-	0/22/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
15	ATP	H	501	-	-	2/22/38/38	0/3/3/3
15	ATP	J	501	-	-	7/22/38/38	0/3/3/3
16	ADP	K	501	-	-	3/16/32/32	0/3/3/3
16	ADP	L	501	-	-	2/16/32/32	0/3/3/3

The worst 5 of 27 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
16	L	501	ADP	C5-C4	4.21	1.46	1.39
16	K	501	ADP	C5-C4	4.18	1.46	1.39
15	M	501	ATP	C5-C4	4.16	1.46	1.39
15	H	501	ATP	C5-C4	4.08	1.46	1.39
15	I	501	ATP	C5-C4	3.82	1.45	1.39

The worst 5 of 53 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	J	501	ATP	C5-C4-N3	-5.87	118.64	126.72
16	K	501	ADP	C5-C4-N3	-5.81	118.72	126.72
15	M	501	ATP	C5-C4-N3	-5.78	118.75	126.72
16	L	501	ADP	C5-C4-N3	-5.51	119.13	126.72
15	I	501	ATP	C5-C4-N3	-5.44	119.22	126.72

There are no chirality outliers.

5 of 17 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
15	H	501	ATP	C5'-O5'-PA-O1A
15	J	501	ATP	PB-O3B-PG-O2G
15	J	501	ATP	C5'-O5'-PA-O3A
15	M	501	ATP	C5'-O5'-PA-O1A
16	K	501	ADP	C5'-O5'-PA-O1A

There are no ring outliers.

5 monomers are involved in 16 short contacts:

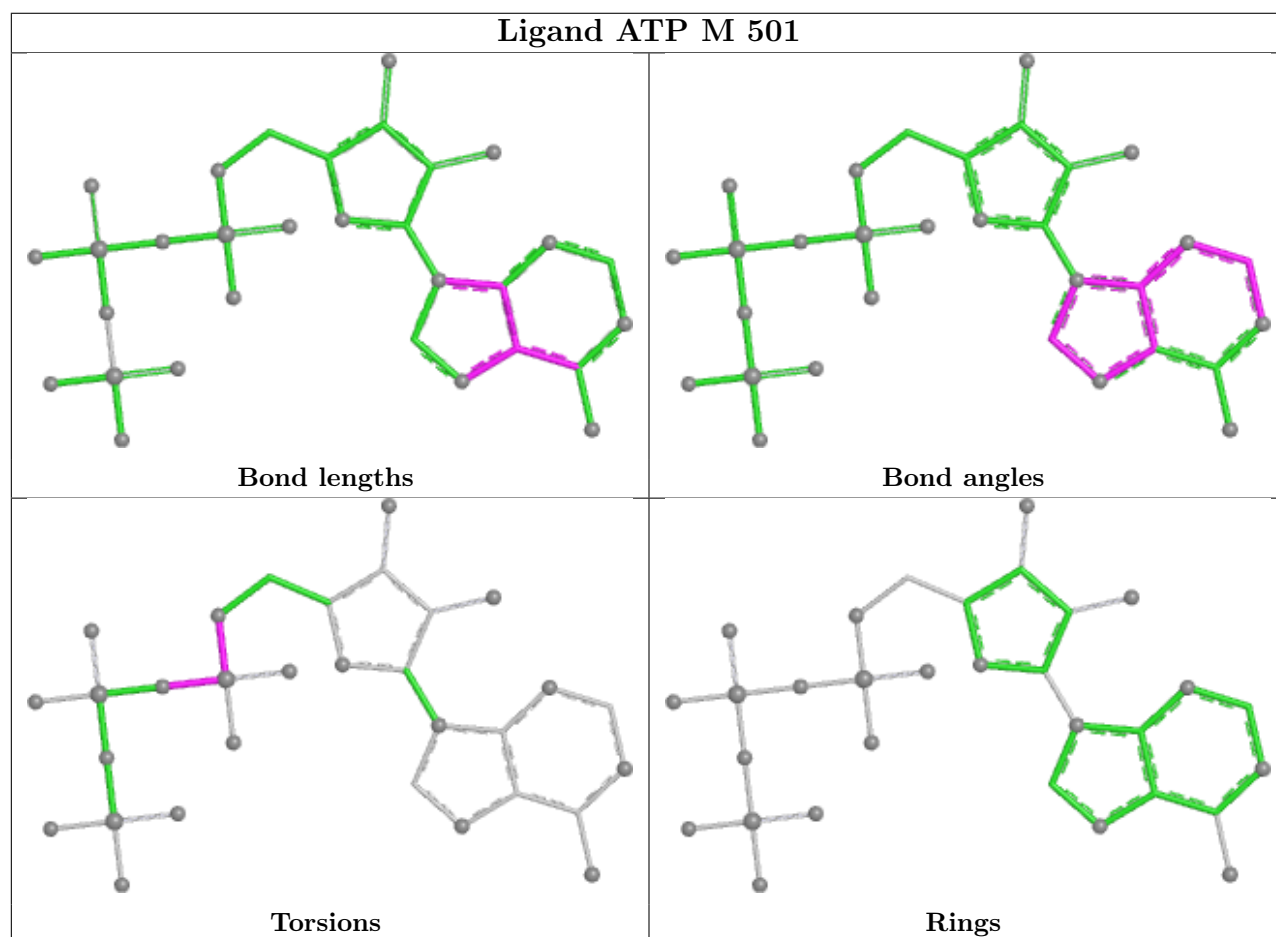
Mol	Chain	Res	Type	Clashes	Symm-Clashes
15	M	501	ATP	6	0
15	I	501	ATP	3	0
15	H	501	ATP	3	0

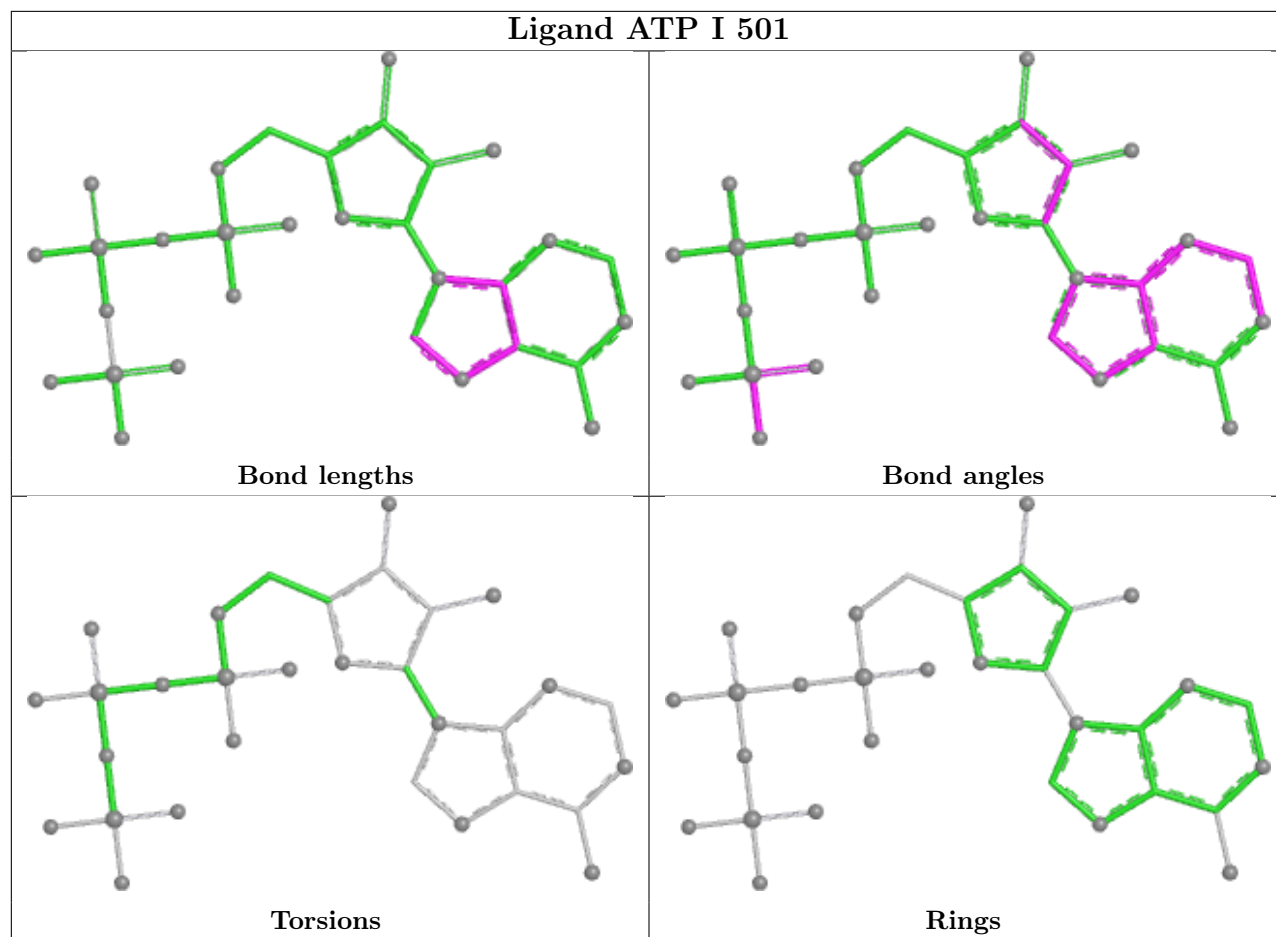
Continued on next page...

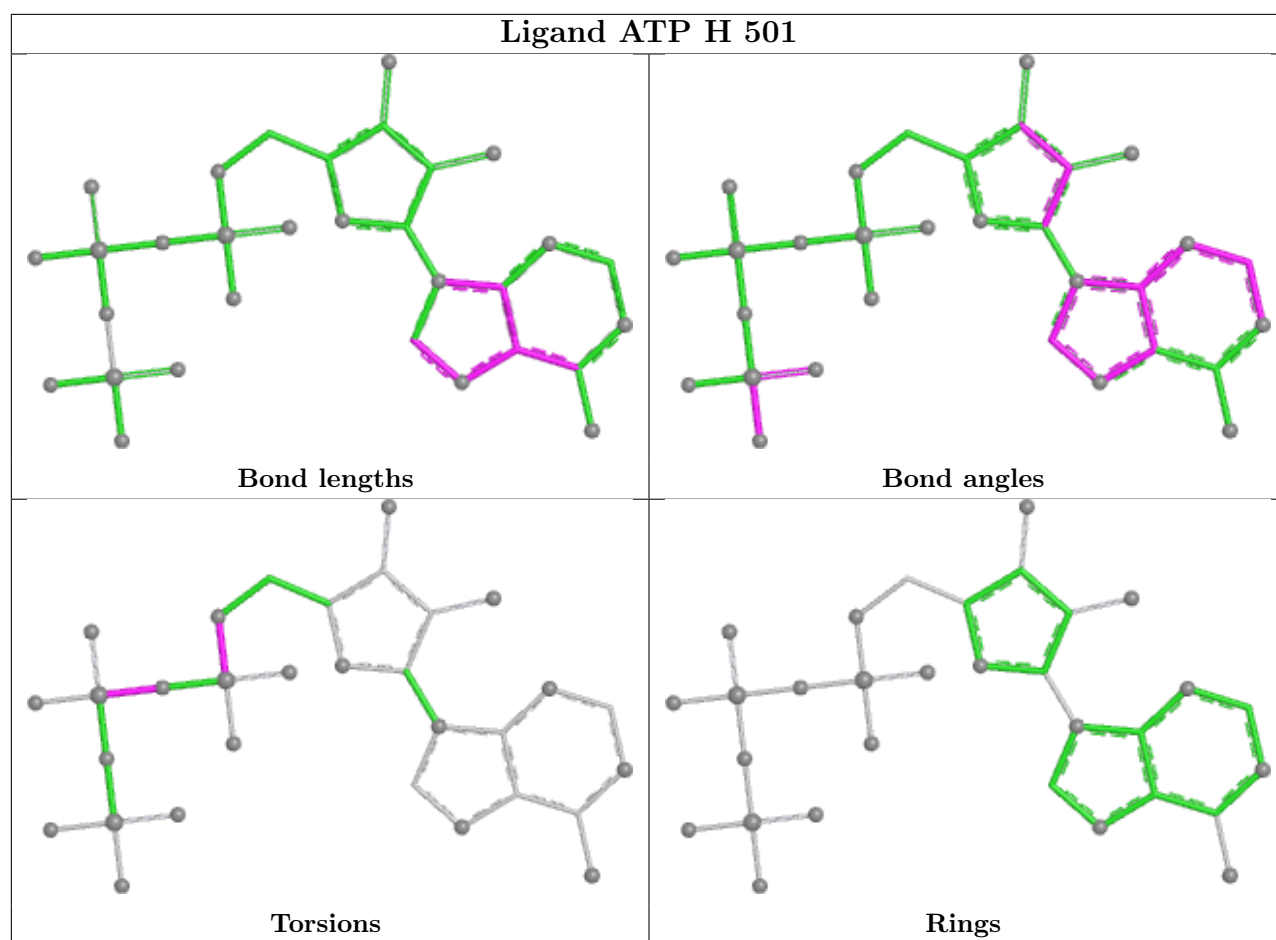
Continued from previous page...

Mol	Chain	Res	Type	Clashes	Symm-Clashes
15	J	501	ATP	2	0
16	K	501	ADP	2	0

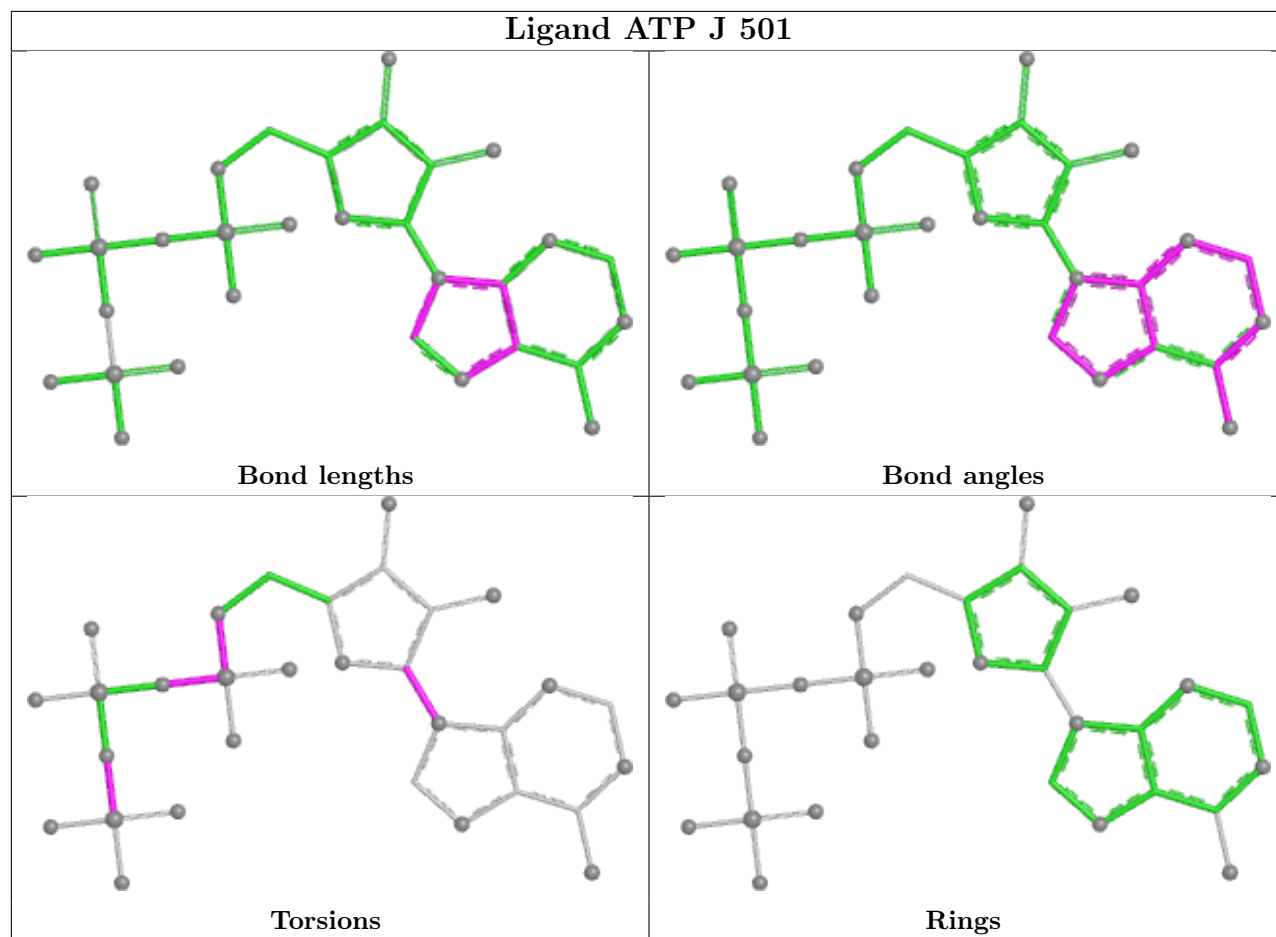
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.



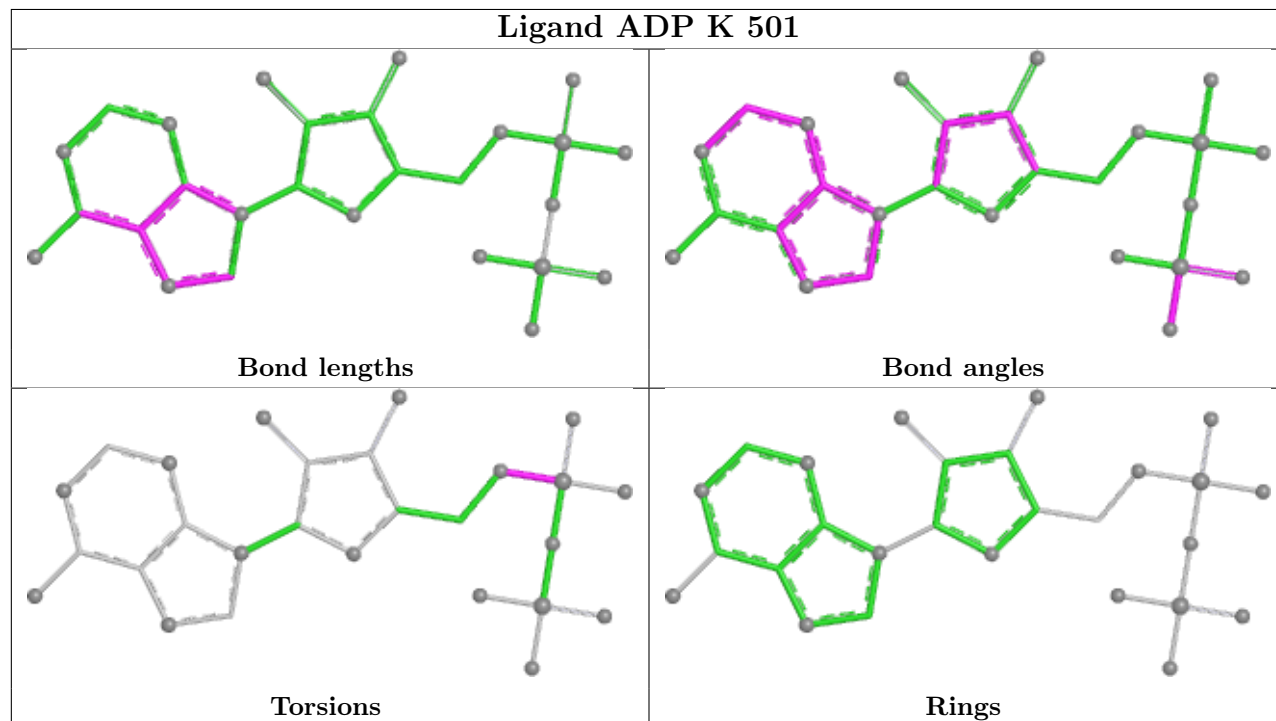


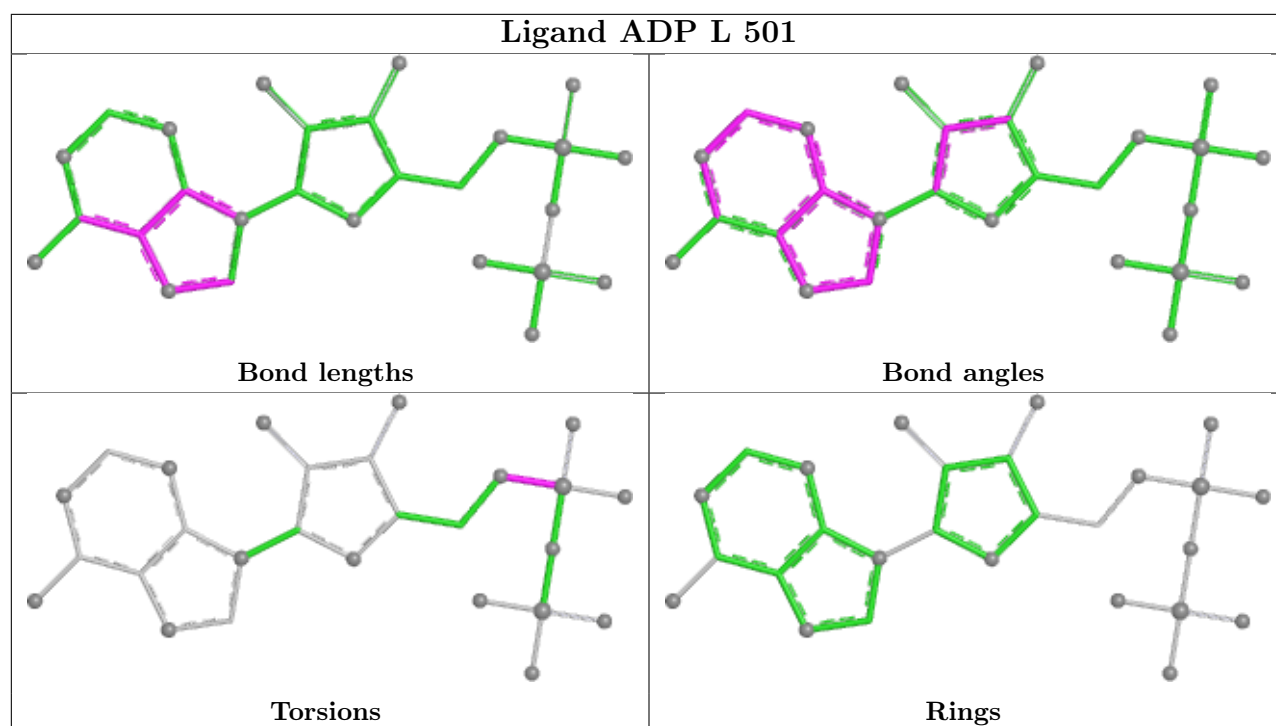


Ligand ATP J 501



Ligand ADP K 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.

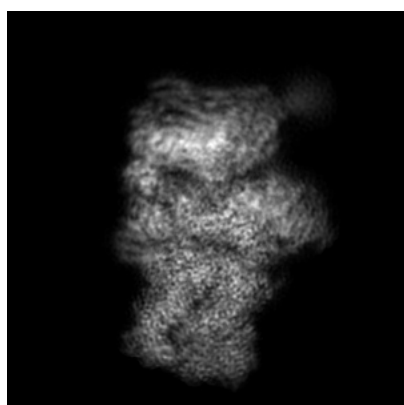
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-9044. These allow visual inspection of the internal detail of the map and identification of artifacts.

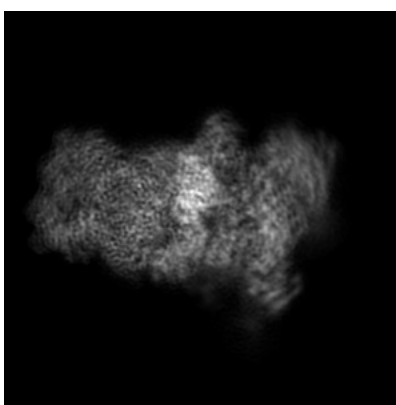
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

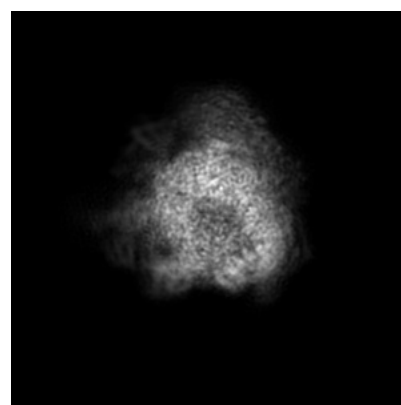
6.1.1 Primary map



X



Y

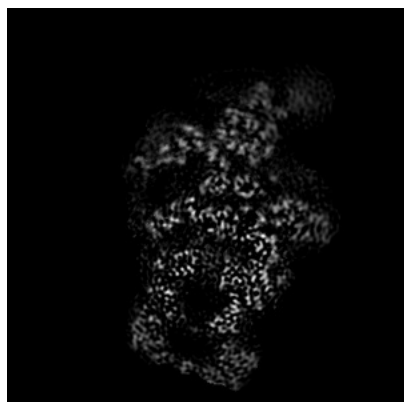


Z

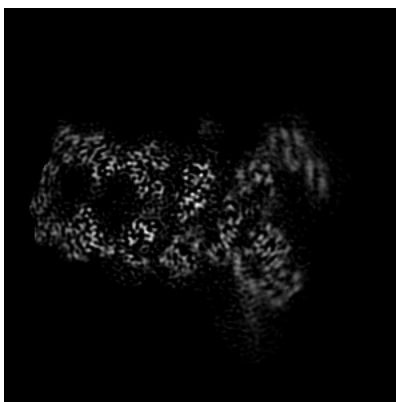
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

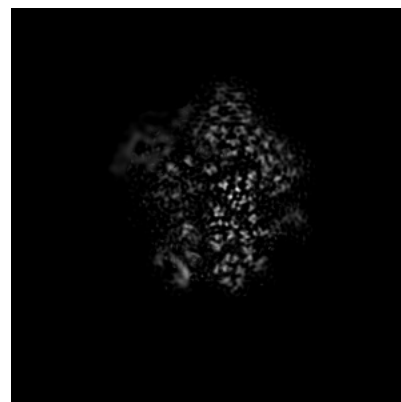
6.2.1 Primary map



X Index: 170



Y Index: 170

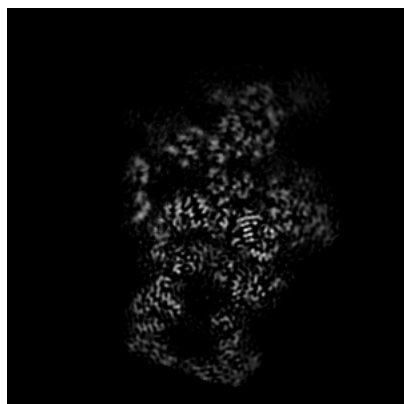


Z Index: 170

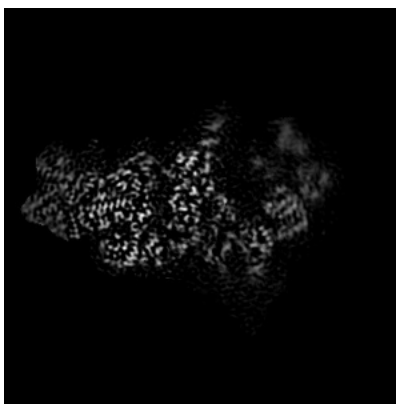
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

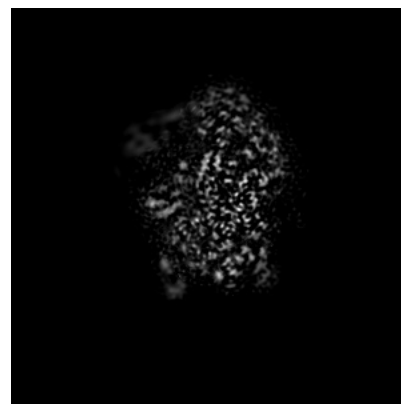
6.3.1 Primary map



X Index: 175



Y Index: 193

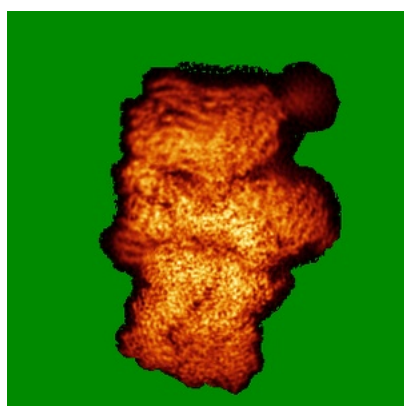


Z Index: 162

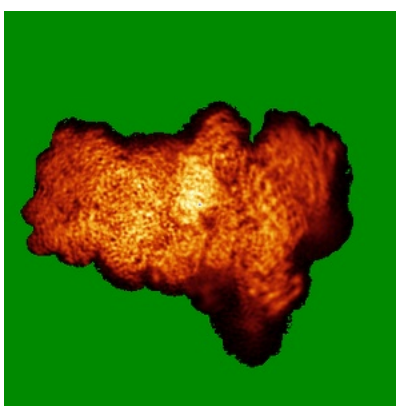
The images above show the largest variance slices of the map in three orthogonal directions.

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

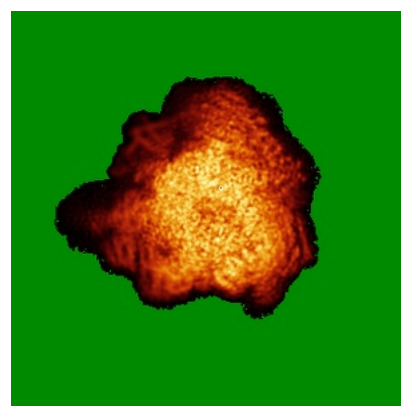
6.4.1 Primary map



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.

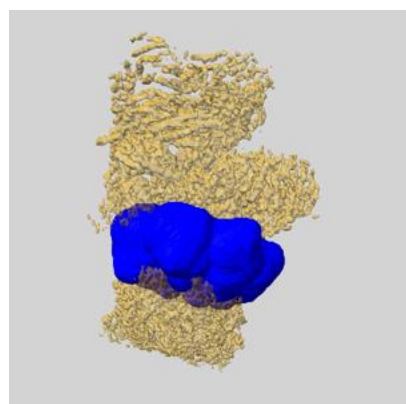
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

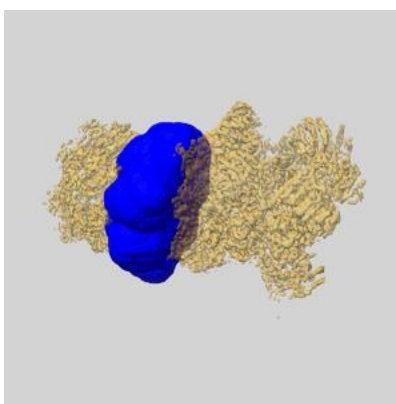
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

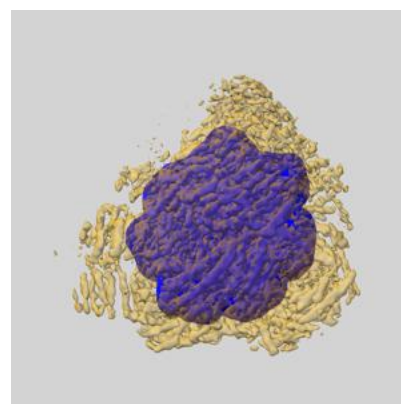
6.6.1 emd_9044_msk_1.map [i](#)



X

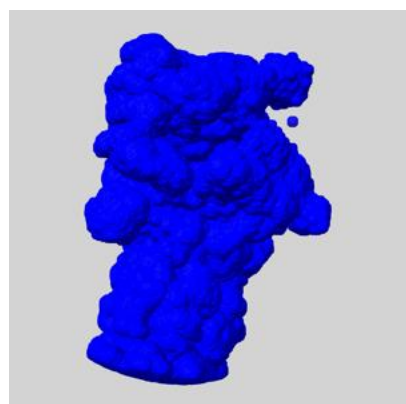


Y

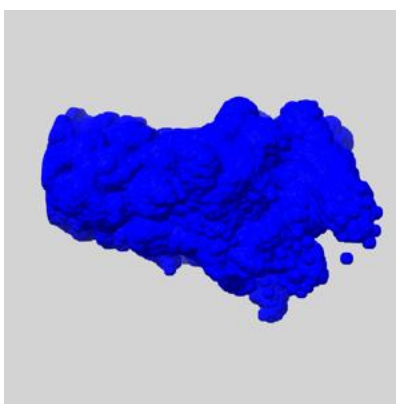


Z

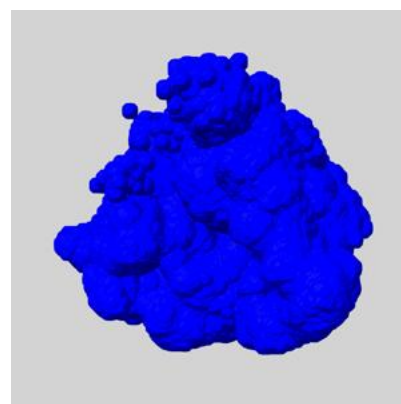
6.6.2 emd_9044_msk_2.map [i](#)



X

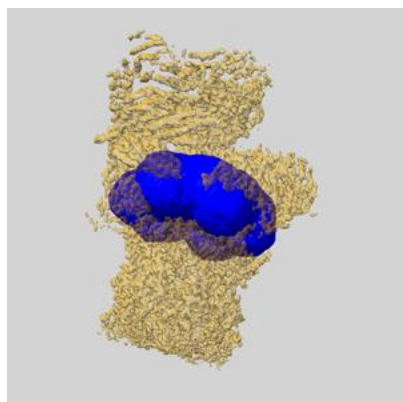


Y

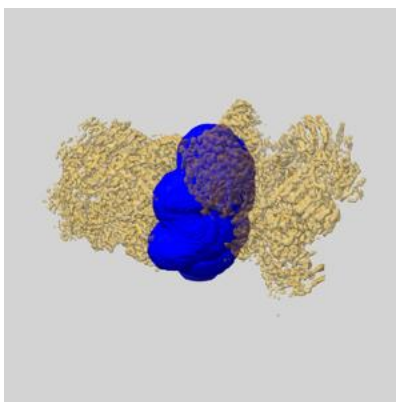


Z

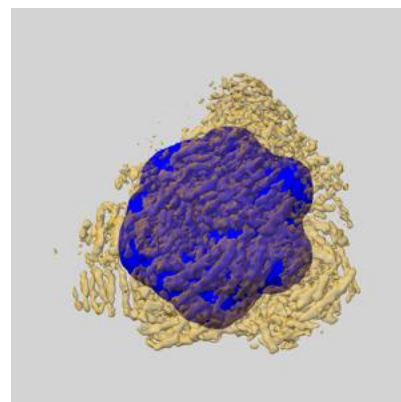
6.6.3 emd_9044_msk_3.map [i](#)



X



Y

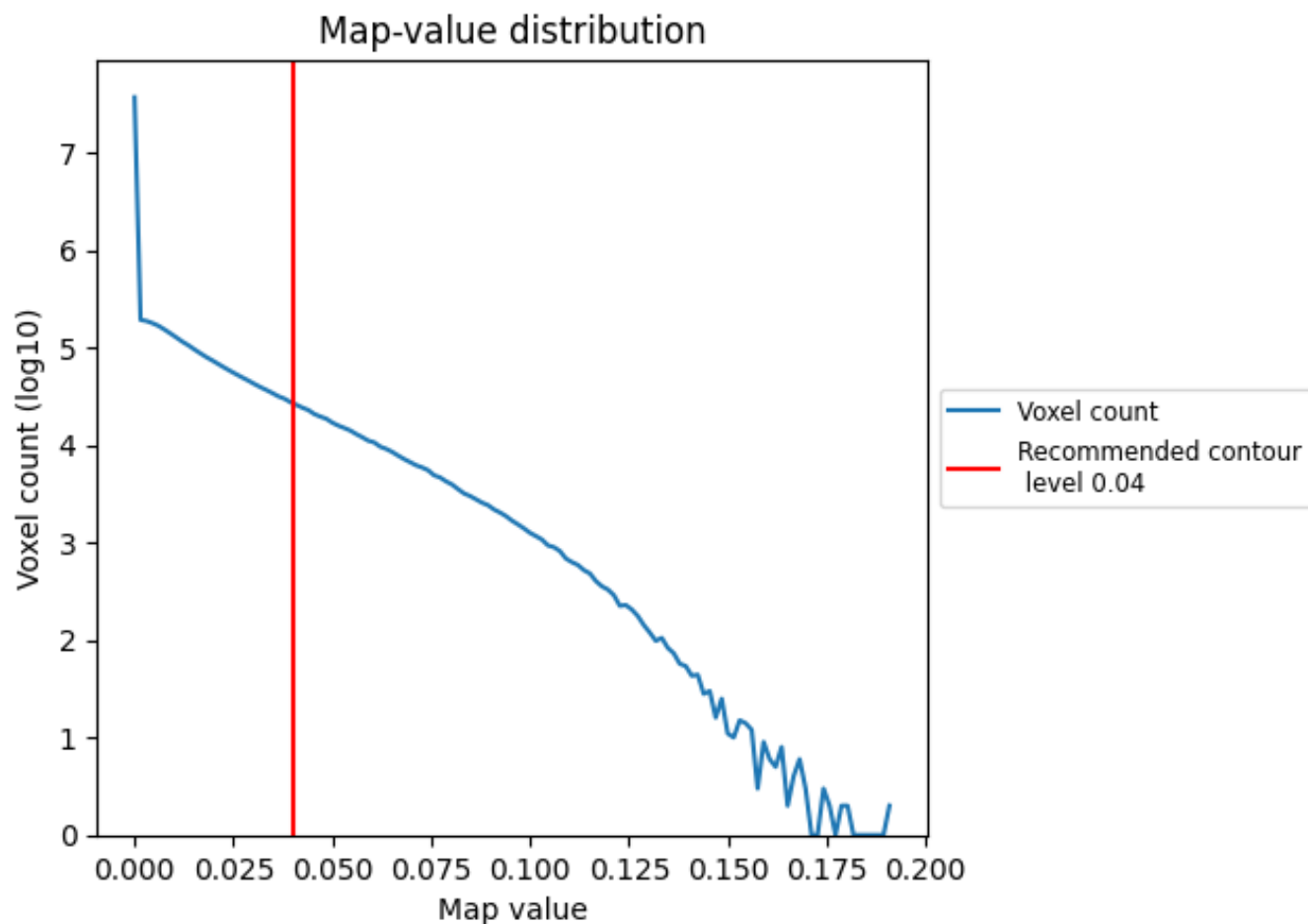


Z

7 Map analysis [i](#)

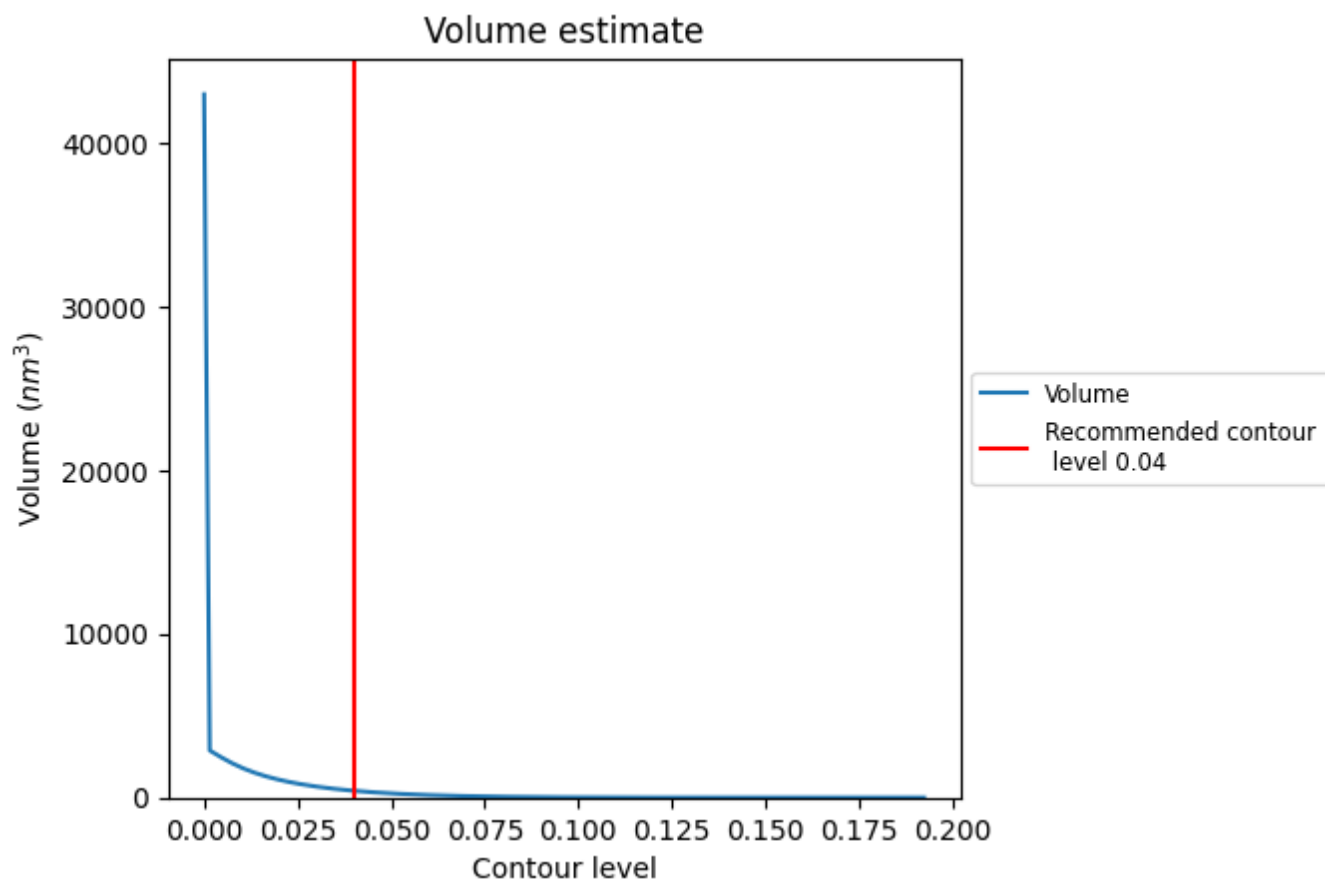
This section contains the results of statistical analysis of the map.

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.

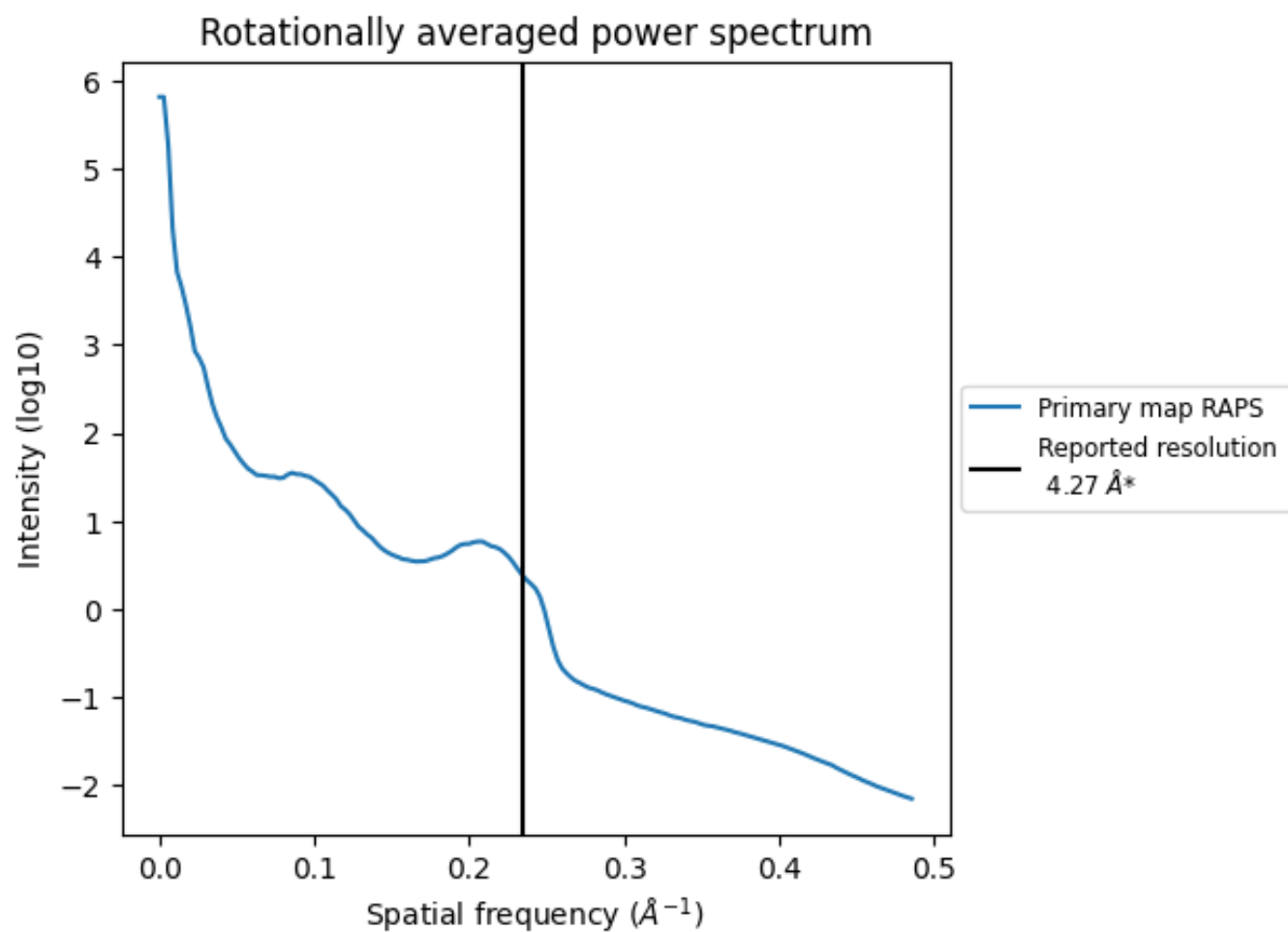
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 416 nm^3 ; this corresponds to an approximate mass of 375 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 0.234 Å⁻¹

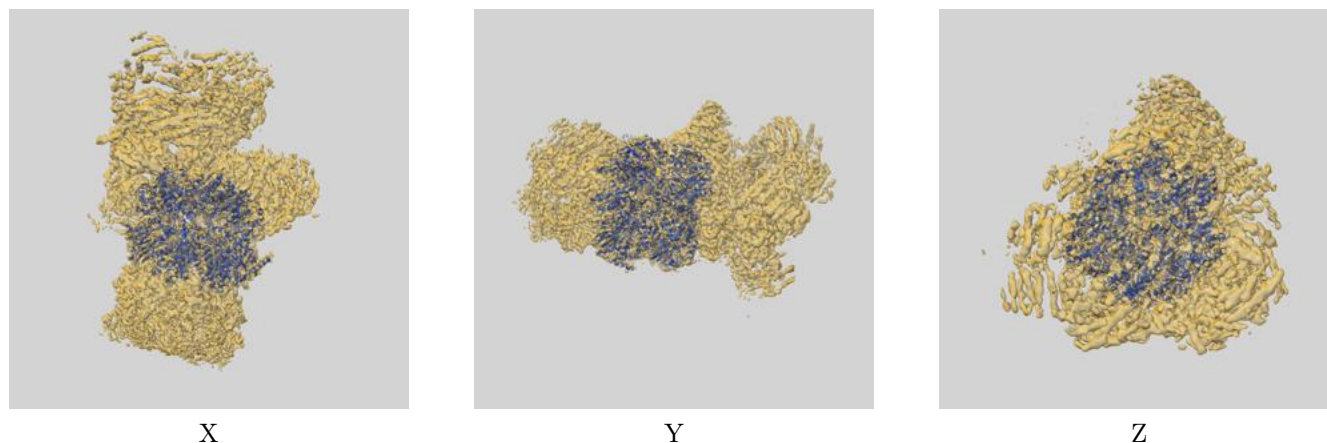
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

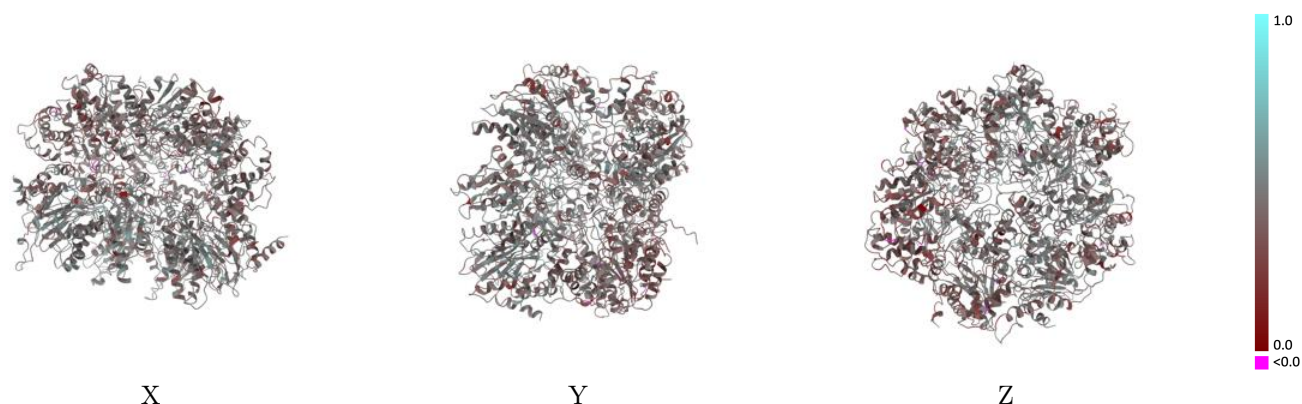
This section contains information regarding the fit between EMDB map EMD-9044 and PDB model 6EF2. Per-residue inclusion information can be found in section [3](#) on page [8](#).

9.1 Map-model overlay [i](#)



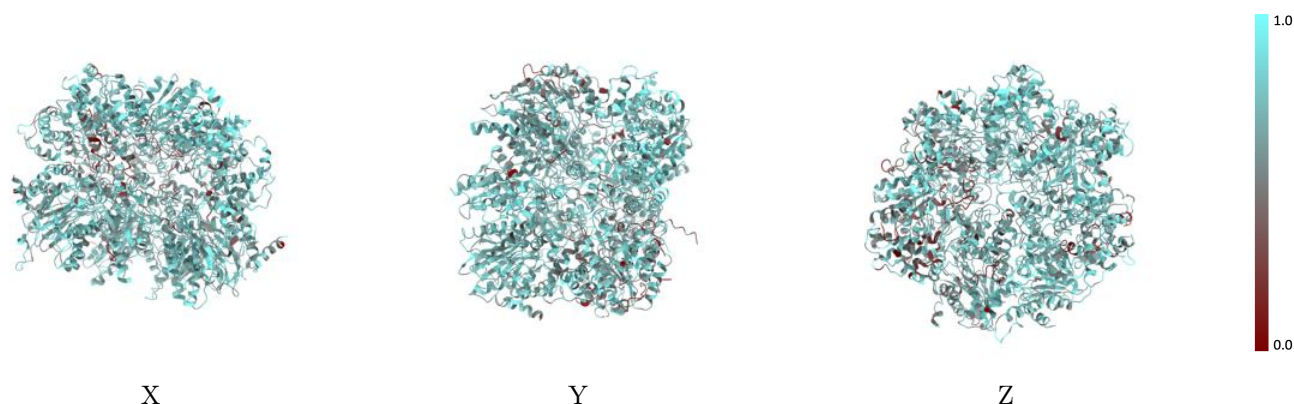
The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



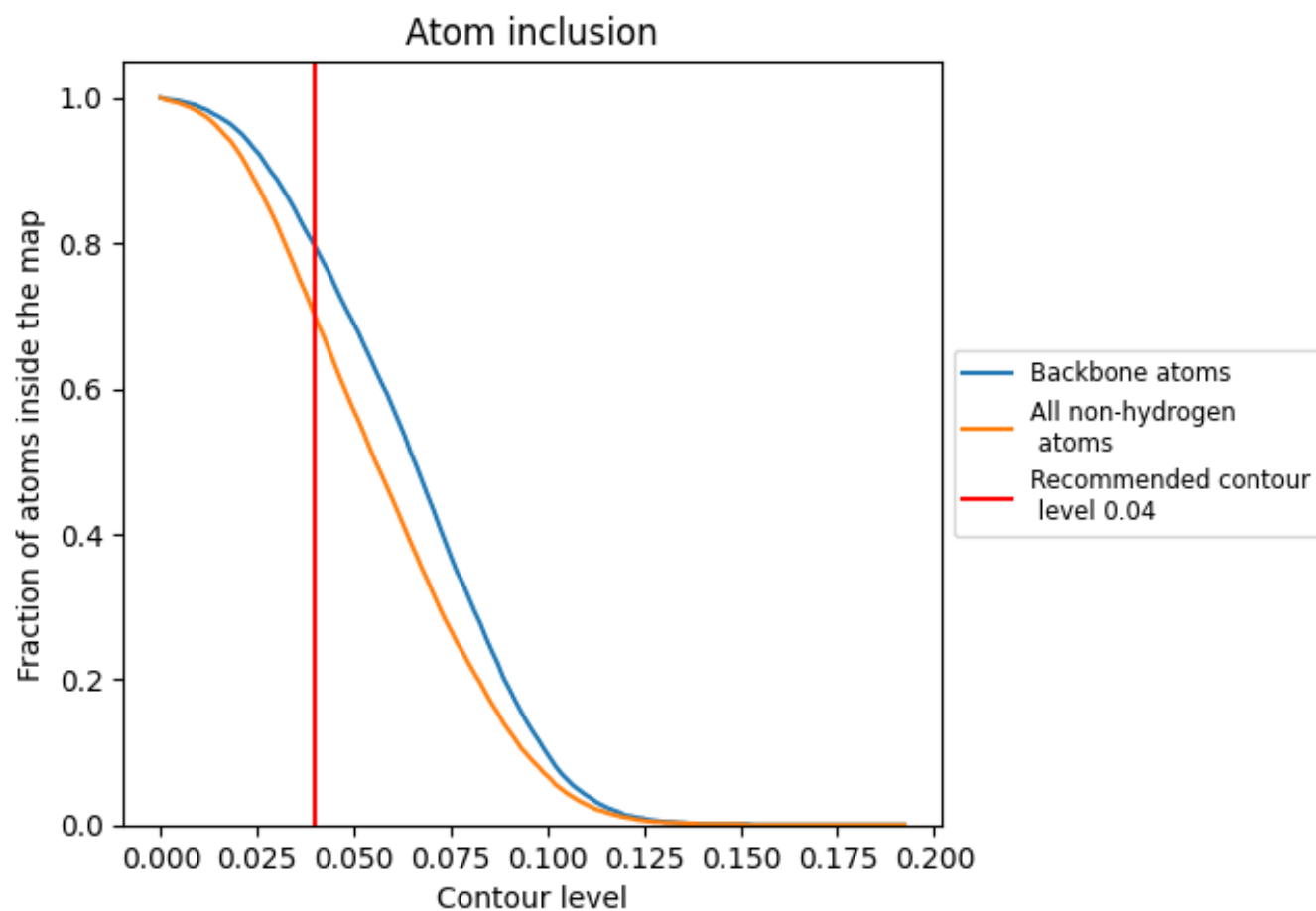
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.04).































9.4 Atom inclusion ⓘ



At the recommended contour level, 80% of all backbone atoms, 70% 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 (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6990	 0.4300
A	 0.7210	 0.4440
B	 0.7410	 0.4620
C	 0.6850	 0.4570
D	 0.6850	 0.4350
E	 0.7210	 0.4520
F	 0.7490	 0.4570
G	 0.7370	 0.4620
H	 0.6730	 0.4090
I	 0.7490	 0.4340
J	 0.7310	 0.4250
K	 0.7270	 0.4180
L	 0.5760	 0.3740
M	 0.6120	 0.3720
s	 0.6350	 0.4620

