



wwPDB EM Validation Summary Report ⓘ

Mar 27, 2026 – 09:54 PM UTC

PDB ID : 8QYV / pdb_00008qyv
EMDB ID : EMD-18764
Title : SWR1-hexasome complex
Authors : Jalal, A.S.B.; Wigley, D.B.
Deposited on : 2023-10-26
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:

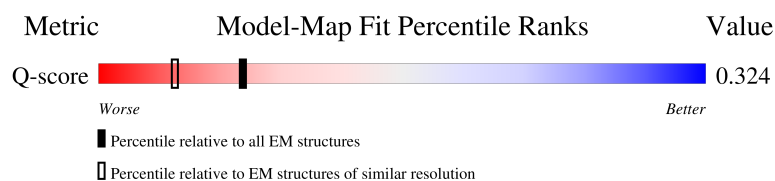
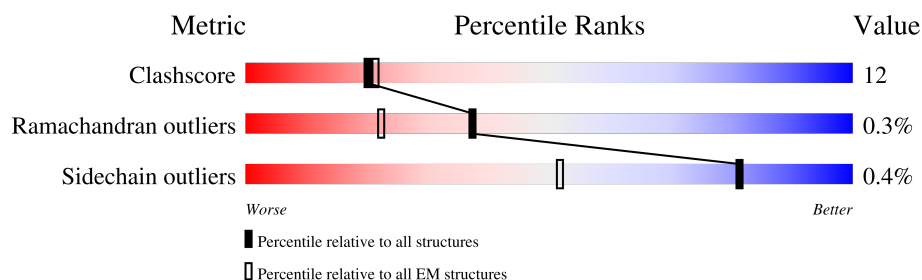
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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

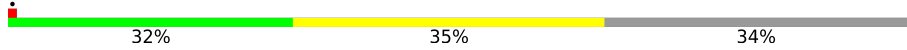
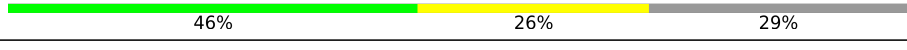
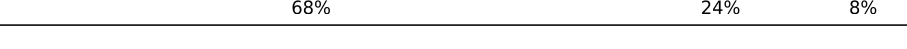
The reported resolution of this entry is 3.50 Å.

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	136	
1	B	136	
2	C	103	
2	D	103	

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Mol	Chain	Length	Quality of chain
3	E	132	
4	G	131	
5	I	118	
6	J	118	
7	M	1514	
8	P	303	
9	R	438	
10	S	280	
11	T	463	
11	V	463	
11	X	463	
12	U	471	
12	W	471	
12	Y	471	
13	Z	795	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
15	BEF	M	1602	-	-	X	-
15	BEF	R	502	-	-	X	-

2 Entry composition

There are 17 unique types of molecules in this entry. The entry contains 41998 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 Histone H3.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	90	Total	C	N	O	S	0	0
			728	461	136	130	1		
1	B	97	Total	C	N	O	S	0	0
			755	481	144	129	1		

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	120	MET	GLN	engineered mutation	UNP P61830
A	121	PRO	LYS	engineered mutation	UNP P61830
A	123	GLU	ASP	conflict	UNP P61830
A	125	GLN	LYS	engineered mutation	UNP P61830
B	120	MET	GLN	engineered mutation	UNP P61830
B	121	PRO	LYS	engineered mutation	UNP P61830
B	123	GLU	ASP	conflict	UNP P61830
B	125	GLN	LYS	engineered mutation	UNP P61830

- Molecule 2 is a protein called Histone H4.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	C	95	Total	C	N	O	0	0
			683	428	133	122		
2	D	71	Total	C	N	O	0	0
			521	326	100	95		

- Molecule 3 is a protein called Histone H2A.1.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	E	102	Total	C	N	O	0	0
			715	454	129	132		

- Molecule 4 is a protein called Histone H2B.1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	G	88	Total	C	N	O	S	0	0
			640	396	112	131	1		

- Molecule 5 is a DNA chain called DNA (118-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
5	I	118	Total	C	N	O	P	0	0
			2402	1139	436	709	118		

- Molecule 6 is a DNA chain called DNA (118-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
6	J	118	Total	C	N	O	P	0	0
			2436	1150	461	707	118		

- Molecule 7 is a protein called Helicase SWR1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	M	720	Total	C	N	O	S	0	0
			5562	3538	993	1005	26		

- Molecule 8 is a protein called SWR1-complex protein 5.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	P	108	Total	C	N	O	0	0
			872	537	168	167		

- Molecule 9 is a protein called Actin-like protein ARP6.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	R	411	Total	C	N	O	S	0	0
			3335	2156	544	619	16		

- Molecule 10 is a protein called Vacuolar protein sorting-associated protein 71.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	S	207	Total	C	N	O	S	0	0
			1675	1058	298	310	9		

- Molecule 11 is a protein called RuvB-like protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	T	439	Total	C	N	O	S	0	0
			3313	2090	573	640	10		
11	V	426	Total	C	N	O	S	0	0
			3245	2049	558	628	10		
11	X	441	Total	C	N	O	S	0	0
			3371	2128	581	653	9		

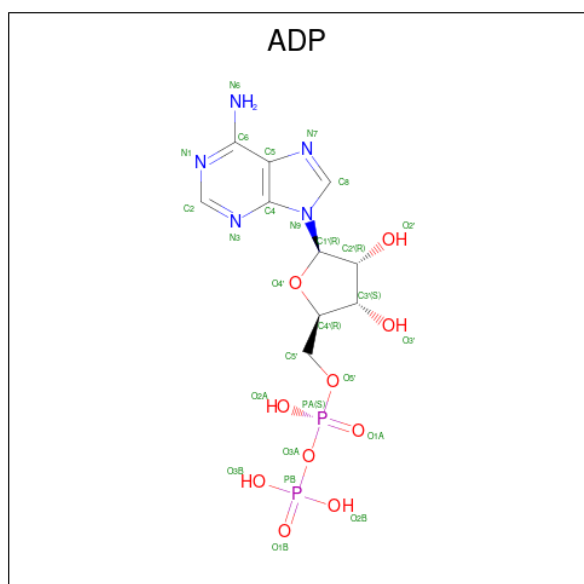
- Molecule 12 is a protein called RuvB-like protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	U	446	Total	C	N	O	S	0	0
			3424	2140	592	680	12		
12	W	433	Total	C	N	O	S	0	0
			3303	2074	569	649	11		
12	Y	443	Total	C	N	O	S	0	0
			3342	2091	581	659	11		

- Molecule 13 is a protein called Vacuolar protein sorting-associated protein 72.

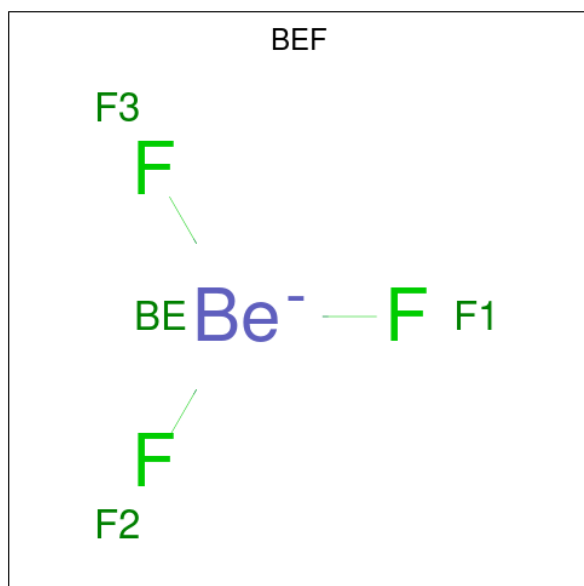
Mol	Chain	Residues	Atoms					AltConf	Trace
13	Z	178	Total	C	N	O	S	0	0
			1442	904	268	266	4		

- Molecule 14 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
14	M	1	Total	C	N	O	P	0
			27	10	5	10	2	
14	R	1	Total	C	N	O	P	0
			27	10	5	10	2	
14	T	1	Total	C	N	O	P	0
			27	10	5	10	2	
14	U	1	Total	C	N	O	P	0
			27	10	5	10	2	
14	V	1	Total	C	N	O	P	0
			27	10	5	10	2	
14	W	1	Total	C	N	O	P	0
			27	10	5	10	2	
14	X	1	Total	C	N	O	P	0
			27	10	5	10	2	
14	Y	1	Total	C	N	O	P	0
			27	10	5	10	2	

- Molecule 15 is BERYLLIUM TRIFLUORIDE ION (CCD ID: BEF) (formula: BeF₃) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			AltConf
15	M	1	Total	Be	F	0
			4	1	3	
15	R	1	Total	Be	F	0
			4	1	3	

- Molecule 16 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
16	M	1	Total 1	Mg 1	0
16	R	1	Total 1	Mg 1	0
16	T	1	Total 1	Mg 1	0
16	U	1	Total 1	Mg 1	0
16	V	1	Total 1	Mg 1	0
16	W	1	Total 1	Mg 1	0
16	X	1	Total 1	Mg 1	0
16	Y	1	Total 1	Mg 1	0

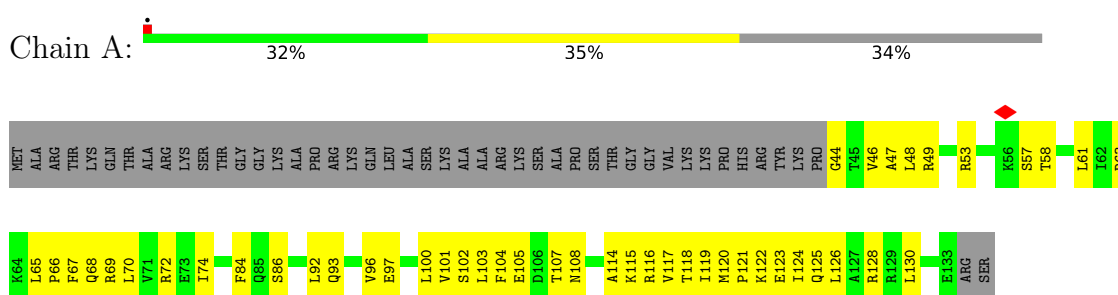
- Molecule 17 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
17	S	2	Total 2	Zn 2	0

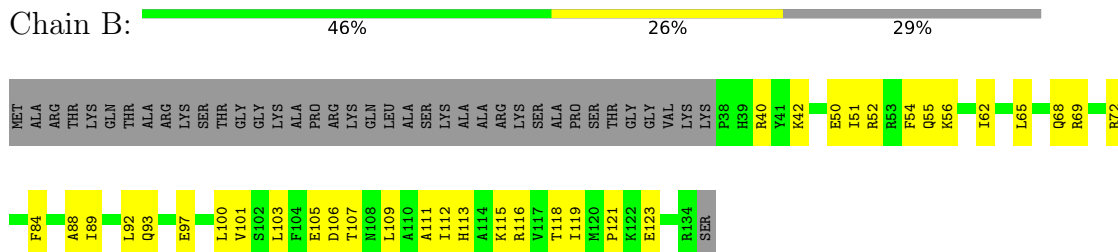
3 Residue-property plots [i](#)

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.

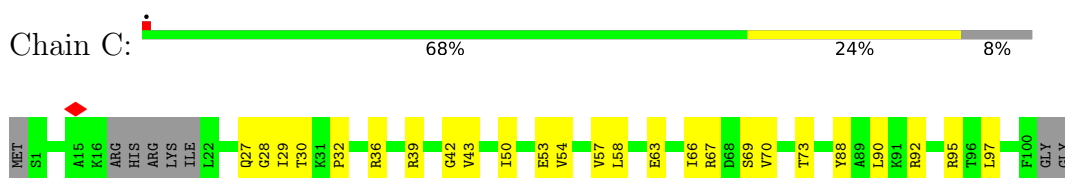
• Molecule 1: Histone H3



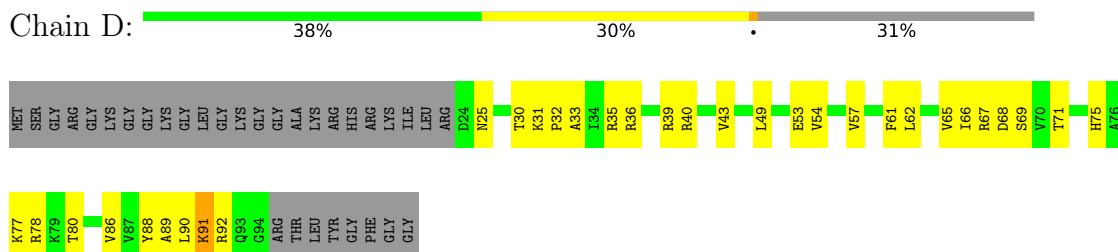
• Molecule 1: Histone H3



• Molecule 2: Histone H4

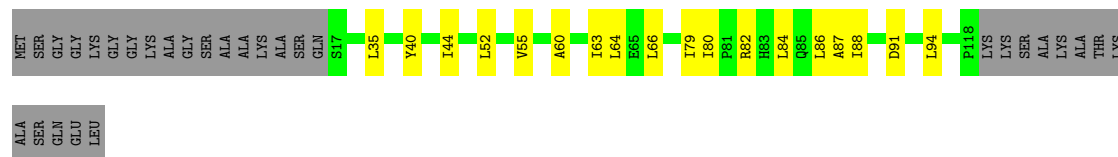


• Molecule 2: Histone H4

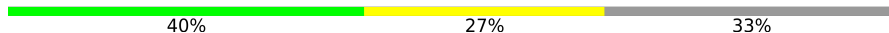


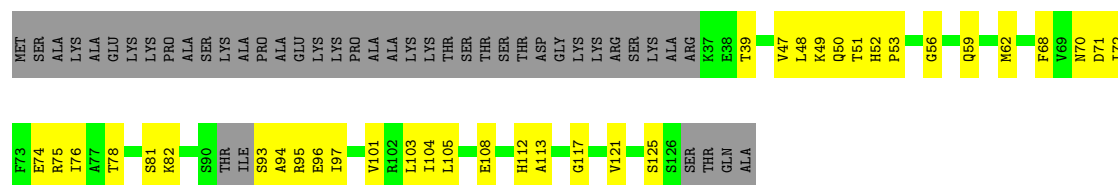
- Molecule 3: Histone H2A.1

Chain E:  64% 14% 23%

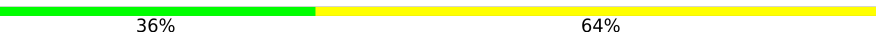


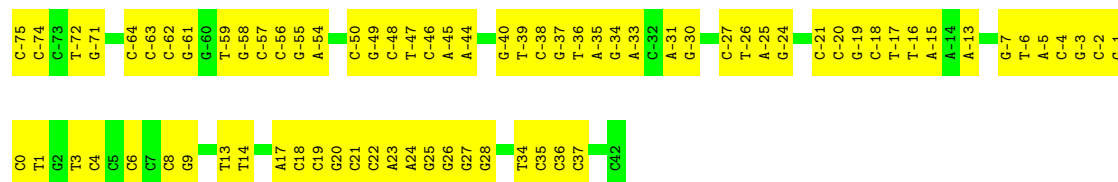
- Molecule 4: Histone H2B.1

Chain G:  40% 27% 33%



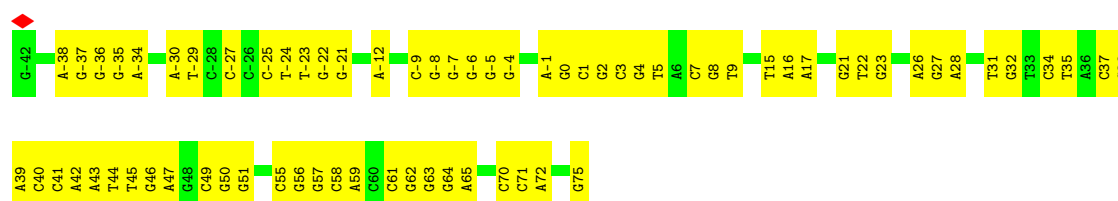
- Molecule 5: DNA (118-MER)

Chain I:  36% 64%



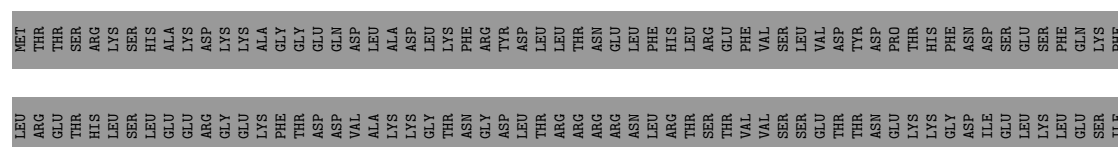
- Molecule 6: DNA (118-MER)

Chain J:  40% 60%

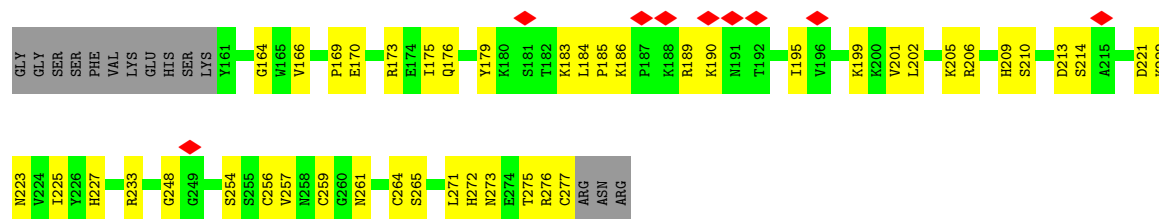


- Molecule 7: Helicase SWR1

Chain M:  34% 13% 52%



- Molecule 8: SWR1-complex protein 5



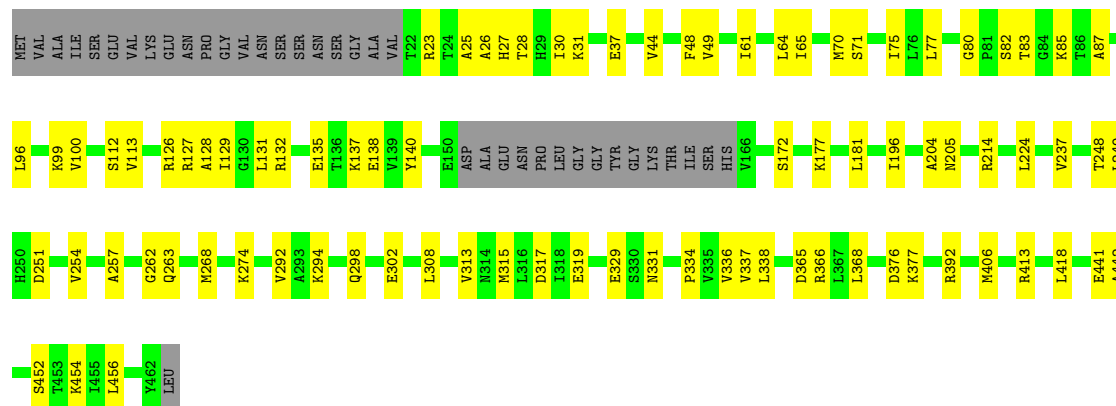
• Molecule 11: RuvB-like protein 1

Chain T: 75% 19% 5%



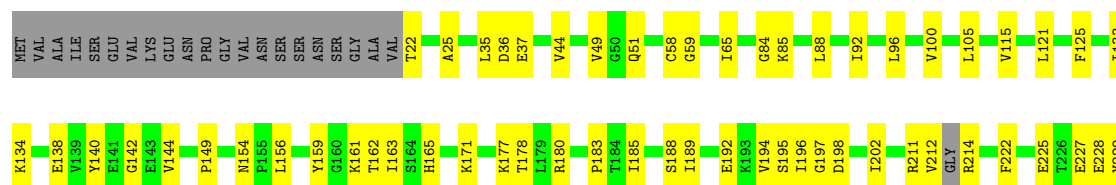
• Molecule 11: RuvB-like protein 1

Chain V: 74% 18% 8%

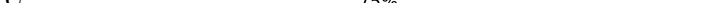


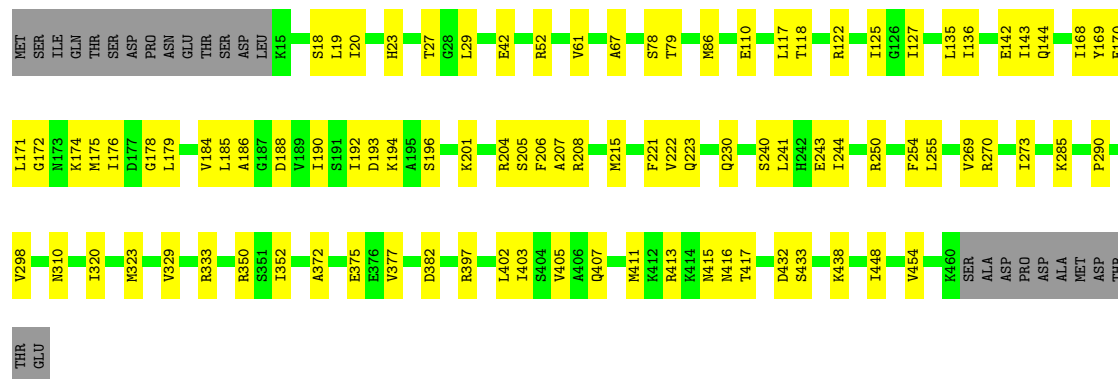
• Molecule 11: RuvB-like protein 1

Chain X: 71% 24% 5%

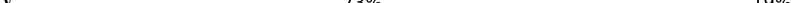


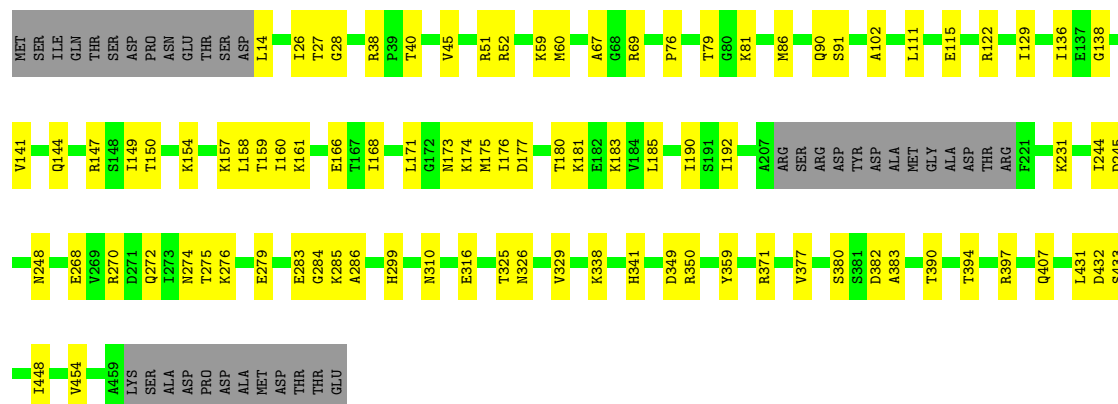
- Molecule 12: RuvB-like protein 2

Chain U:  75% 20% 5%

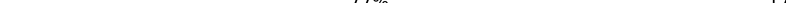


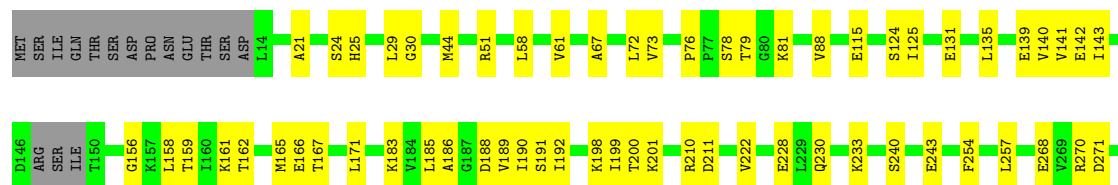
- Molecule 12: RuvB-like protein 2

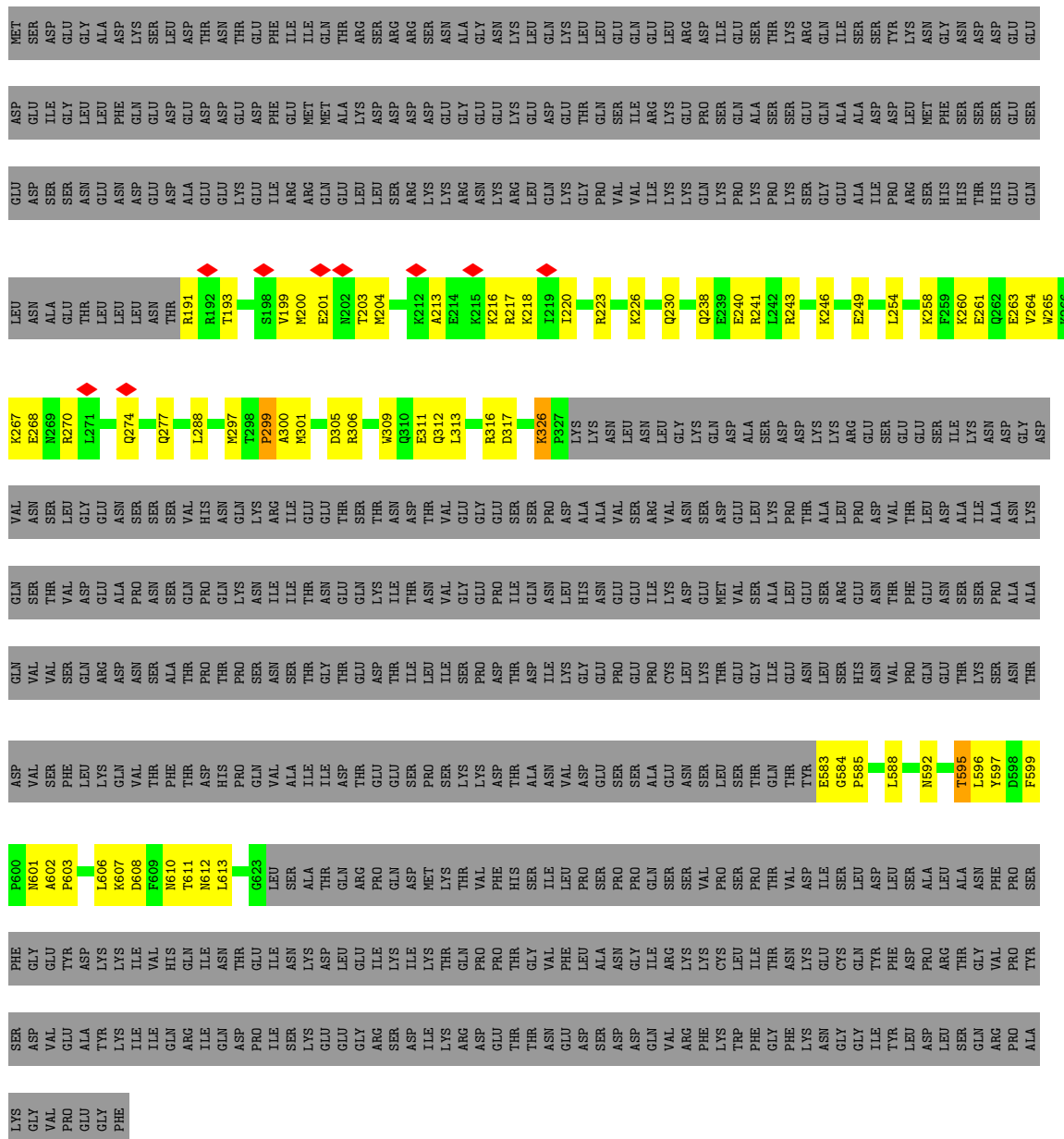
Chain W:  73% 19% 8%



- Molecule 12: RuvB-like protein 2

Chain Y:  77% 17% 6%





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	30312	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	300	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.047	Depositor
Minimum map value	-0.020	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.00197	Depositor
Map size (Å)	408.0, 408.0, 408.0	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.85, 0.85, 0.85	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: BEF, MG, ADP, 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	0.16	0/736	0.46	0/988
1	B	0.15	0/766	0.42	0/1032
2	C	0.12	0/688	0.37	0/921
2	D	0.14	0/525	0.39	0/709
3	E	0.12	0/725	0.32	0/992
4	G	0.16	0/646	0.42	0/873
5	I	0.18	0/2690	0.40	0/4145
6	J	0.16	0/2736	0.34	0/4225
7	M	0.12	0/5662	0.36	0/7672
8	P	0.14	0/882	0.47	0/1184
9	R	0.11	0/3429	0.31	0/4650
10	S	0.11	0/1705	0.35	0/2297
11	T	0.09	0/3351	0.26	0/4537
11	V	0.11	0/3282	0.30	0/4443
11	X	0.10	0/3412	0.30	0/4618
12	U	0.10	0/3462	0.30	0/4667
12	W	0.10	0/3339	0.28	0/4503
12	Y	0.09	0/3378	0.26	0/4561
13	Z	0.14	0/1464	0.48	2/1961 (0.1%)
All	All	0.12	0/42878	0.34	2/58978 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
7	M	0	1
8	P	0	1
All	All	0	2

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
13	Z	595	THR	CA-C-N	5.84	132.21	121.70
13	Z	595	THR	C-N-CA	5.84	132.21	121.70

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
7	M	871	MET	Peptide
8	P	236	THR	Peptide

5.2 Too-close contacts

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	728	0	762	49	0
1	B	755	0	767	31	0
2	C	683	0	676	21	0
2	D	521	0	525	32	0
3	E	715	0	692	14	0
4	G	640	0	617	29	0
5	I	2402	0	1323	65	0
6	J	2436	0	1322	71	0
7	M	5562	0	5438	159	0
8	P	872	0	877	26	0
9	R	3335	0	3256	122	0
10	S	1675	0	1703	66	0
11	T	3313	0	3405	69	0
11	V	3245	0	3365	67	0
11	X	3371	0	3487	79	0
12	U	3424	0	3493	72	0
12	W	3303	0	3385	67	0
12	Y	3342	0	3368	61	0
13	Z	1442	0	1438	47	0
14	M	27	0	12	1	0
14	R	27	0	12	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
14	T	27	0	12	1	0
14	U	27	0	12	1	0
14	V	27	0	12	2	0
14	W	27	0	12	2	0
14	X	27	0	12	3	0
14	Y	27	0	12	1	0
15	M	4	0	0	3	0
15	R	4	0	0	2	0
16	M	1	0	0	0	0
16	R	1	0	0	0	0
16	T	1	0	0	0	0
16	U	1	0	0	0	0
16	V	1	0	0	0	0
16	W	1	0	0	0	0
16	X	1	0	0	0	0
16	Y	1	0	0	0	0
17	S	2	0	0	0	0
All	All	41998	0	39995	1004	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 12.

The worst 5 of 1004 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)
7:M:994:ASN:HD21	7:M:997:ASN:HB2	1.36	0.91
5:I:-4:DC:N3	6:J:4:DG:N1	2.24	0.85
5:I:-75:DC:O2	6:J:75:DG:N2	2.10	0.85
7:M:871:MET:HG3	7:M:884:PHE:HB2	1.58	0.84
5:I:-4:DC:O2	6:J:4:DG:N2	2.10	0.84

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	88/136 (65%)	82 (93%)	6 (7%)	0	100	100
1	B	95/136 (70%)	92 (97%)	3 (3%)	0	100	100
2	C	91/103 (88%)	86 (94%)	4 (4%)	1 (1%)	11	43
2	D	69/103 (67%)	66 (96%)	2 (3%)	1 (1%)	9	38
3	E	100/132 (76%)	96 (96%)	4 (4%)	0	100	100
4	G	84/131 (64%)	82 (98%)	2 (2%)	0	100	100
7	M	718/1514 (47%)	645 (90%)	70 (10%)	3 (0%)	30	62
8	P	106/303 (35%)	89 (84%)	16 (15%)	1 (1%)	14	47
9	R	407/438 (93%)	390 (96%)	17 (4%)	0	100	100
10	S	201/280 (72%)	182 (90%)	17 (8%)	2 (1%)	12	44
11	T	433/463 (94%)	418 (96%)	14 (3%)	1 (0%)	43	74
11	V	422/463 (91%)	406 (96%)	16 (4%)	0	100	100
11	X	437/463 (94%)	419 (96%)	18 (4%)	0	100	100
12	U	444/471 (94%)	413 (93%)	29 (6%)	2 (0%)	24	57
12	W	429/471 (91%)	417 (97%)	12 (3%)	0	100	100
12	Y	439/471 (93%)	421 (96%)	18 (4%)	0	100	100
13	Z	174/795 (22%)	151 (87%)	20 (12%)	3 (2%)	7	35
All	All	4737/6873 (69%)	4455 (94%)	268 (6%)	14 (0%)	37	67

5 of 14 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	29	ILE
7	M	995	HIS
7	M	1068	VAL
8	P	237	THR
12	U	222	VAL

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	77/113 (68%)	76 (99%)	1 (1%)	61	72
1	B	74/113 (66%)	73 (99%)	1 (1%)	59	71
2	C	59/81 (73%)	59 (100%)	0	100	100
2	D	51/81 (63%)	50 (98%)	1 (2%)	48	67
3	E	65/99 (66%)	65 (100%)	0	100	100
4	G	66/109 (61%)	65 (98%)	1 (2%)	57	71
7	M	576/1376 (42%)	573 (100%)	3 (0%)	81	80
8	P	93/262 (36%)	93 (100%)	0	100	100
9	R	372/396 (94%)	371 (100%)	1 (0%)	86	83
10	S	195/261 (75%)	195 (100%)	0	100	100
11	T	357/391 (91%)	357 (100%)	0	100	100
11	V	354/391 (90%)	353 (100%)	1 (0%)	86	83
11	X	368/391 (94%)	367 (100%)	1 (0%)	86	83
12	U	378/403 (94%)	376 (100%)	2 (0%)	81	80
12	W	364/403 (90%)	364 (100%)	0	100	100
12	Y	359/403 (89%)	359 (100%)	0	100	100
13	Z	152/732 (21%)	150 (99%)	2 (1%)	61	72
All	All	3960/6005 (66%)	3946 (100%)	14 (0%)	81	81

5 of 14 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
9	R	241	GLU
12	U	206	PHE
13	Z	317	ASP
11	X	222	PHE
13	Z	200	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 36 such sidechains are listed below:

Mol	Chain	Res	Type
11	V	124	ASN
13	Z	605	ASN
11	V	205	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
11	X	260	GLN
9	R	61	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 20 ligands modelled in this entry, 10 are monoatomic - leaving 10 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
14	ADP	X	501	16	28,29,29	1.39	4 (14%)	43,45,45	1.88	8 (18%)
14	ADP	U	501	16	28,29,29	1.39	4 (14%)	43,45,45	1.85	8 (18%)
14	ADP	Y	501	16	28,29,29	1.40	4 (14%)	43,45,45	1.87	8 (18%)
14	ADP	M	1601	16	28,29,29	1.42	4 (14%)	43,45,45	1.84	10 (23%)
15	BEF	R	502	-	0,3,3	-	-	-	-	-
14	ADP	R	501	16	28,29,29	1.41	4 (14%)	43,45,45	1.83	9 (20%)
14	ADP	V	501	16	28,29,29	1.39	4 (14%)	43,45,45	1.82	7 (16%)
14	ADP	W	501	16	28,29,29	1.41	4 (14%)	43,45,45	1.83	8 (18%)
14	ADP	T	501	16	28,29,29	1.39	4 (14%)	43,45,45	1.81	8 (18%)
15	BEF	M	1602	7	0,3,3	-	-	-	-	-

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
14	ADP	X	501	16	-	3/16/32/32	0/3/3/3
14	ADP	U	501	16	-	2/16/32/32	0/3/3/3
14	ADP	Y	501	16	-	2/16/32/32	0/3/3/3
14	ADP	M	1601	16	-	4/16/32/32	0/3/3/3
14	ADP	R	501	16	-	3/16/32/32	0/3/3/3
14	ADP	V	501	16	-	3/16/32/32	0/3/3/3
14	ADP	W	501	16	-	4/16/32/32	0/3/3/3
14	ADP	T	501	16	-	3/16/32/32	0/3/3/3

The worst 5 of 32 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
14	R	501	ADP	C5-C4	4.69	1.47	1.39
14	M	1601	ADP	C5-C4	4.69	1.47	1.39
14	X	501	ADP	C5-C4	4.68	1.47	1.39
14	Y	501	ADP	C5-C4	4.67	1.47	1.39
14	U	501	ADP	C5-C4	4.67	1.47	1.39

The worst 5 of 66 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	X	501	ADP	C5-C4-N3	-6.21	118.16	126.72
14	Y	501	ADP	C5-C4-N3	-6.19	118.19	126.72
14	U	501	ADP	C5-C4-N3	-5.95	118.53	126.72
14	W	501	ADP	C5-C4-N3	-5.93	118.55	126.72
14	R	501	ADP	C5-C4-N3	-5.84	118.67	126.72

There are no chirality outliers.

5 of 24 torsion outliers are listed below:

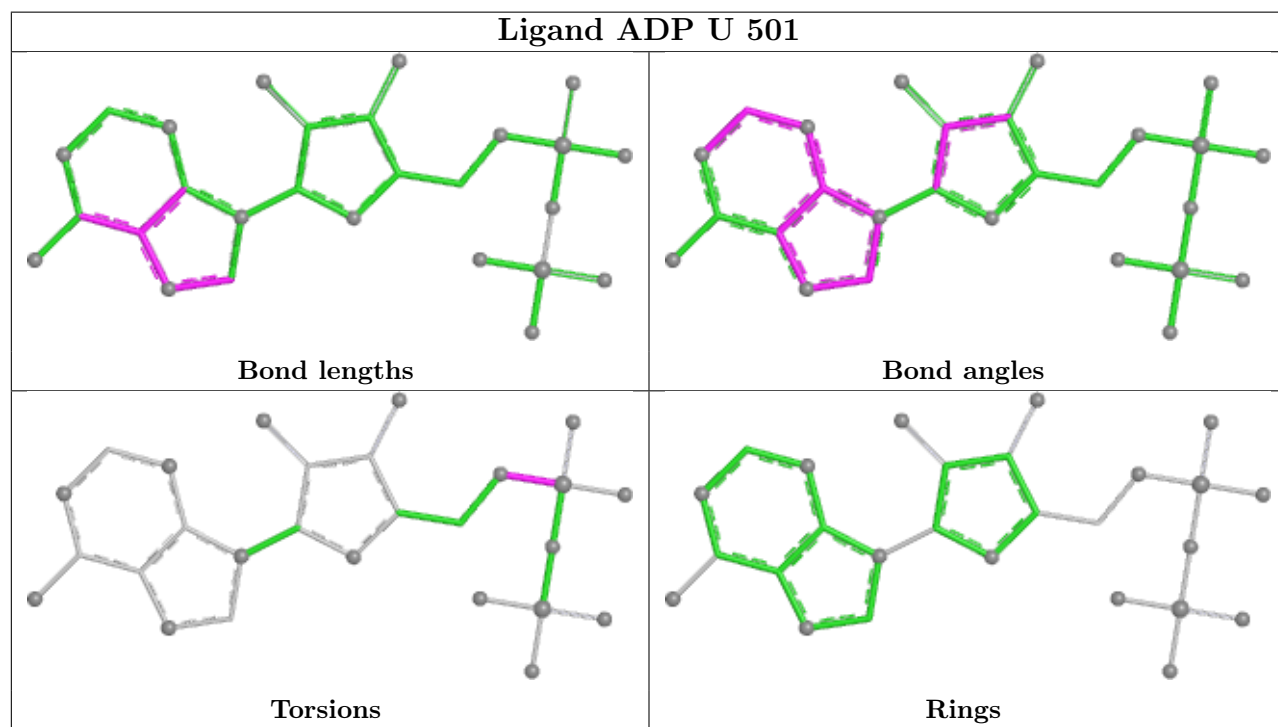
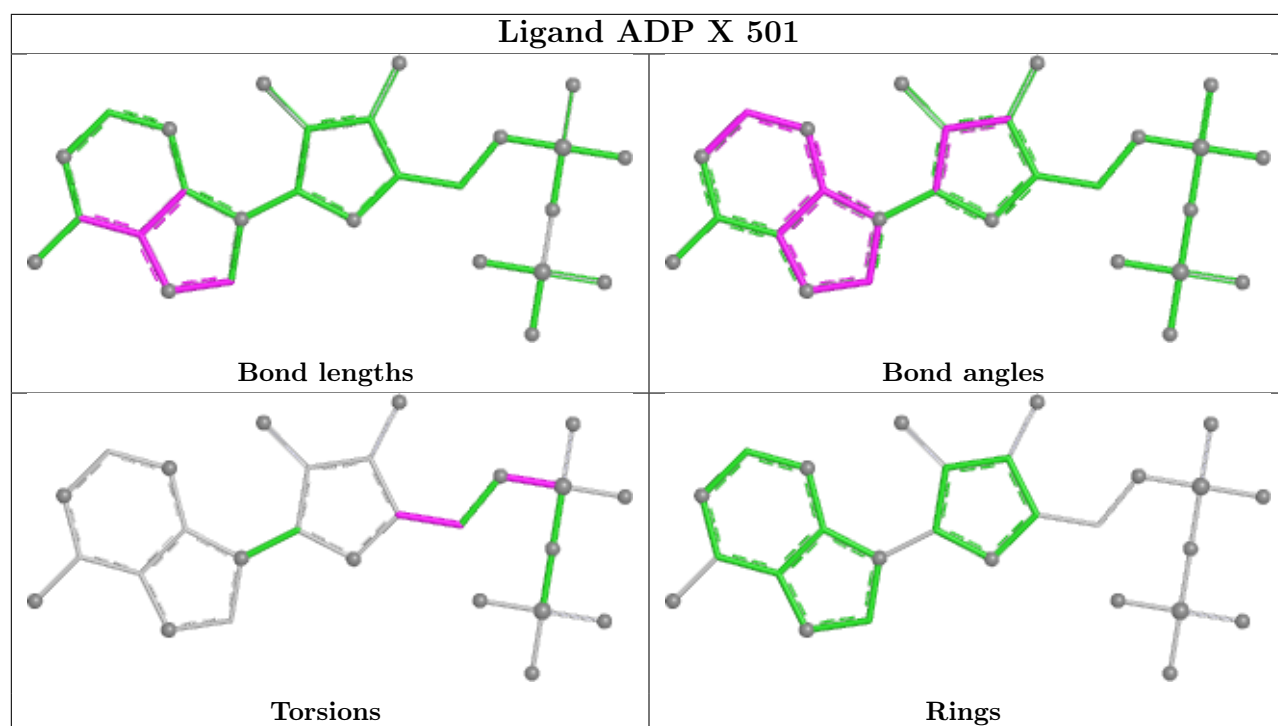
Mol	Chain	Res	Type	Atoms
14	M	1601	ADP	PB-O3A-PA-O5'
14	M	1601	ADP	C5'-O5'-PA-O2A
14	R	501	ADP	C5'-O5'-PA-O1A
14	T	501	ADP	C5'-O5'-PA-O1A
14	T	501	ADP	C5'-O5'-PA-O2A

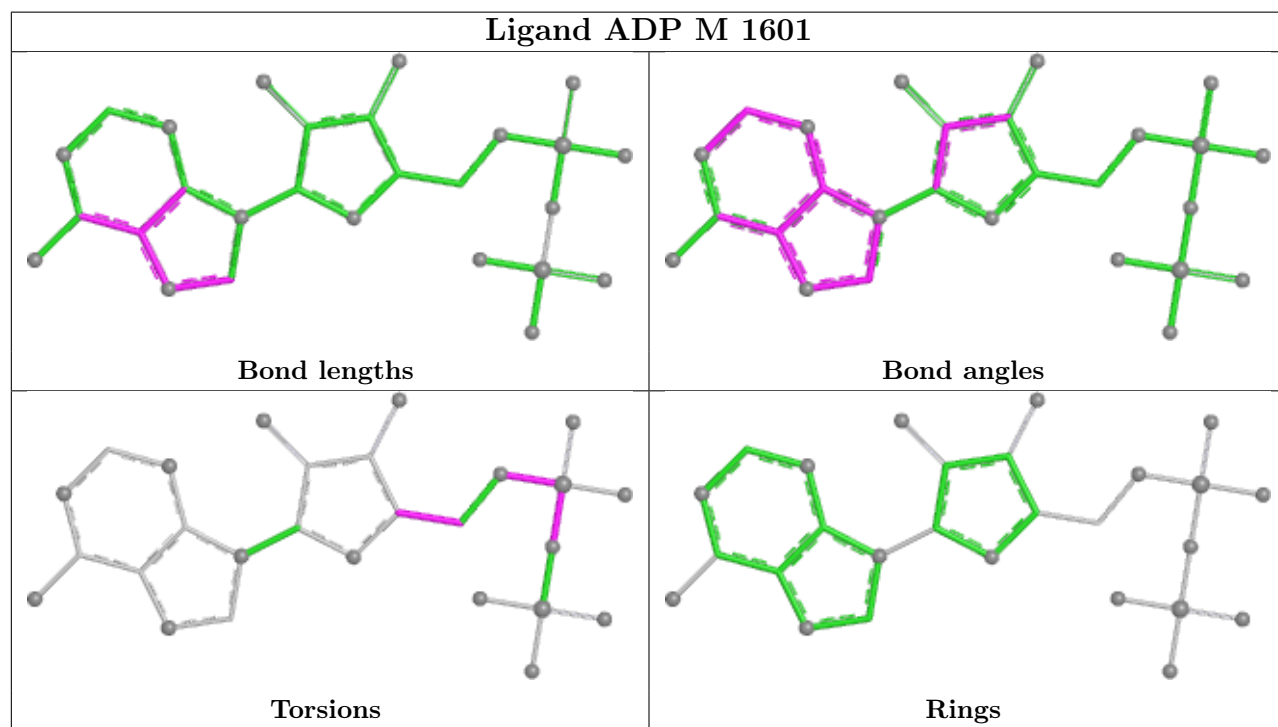
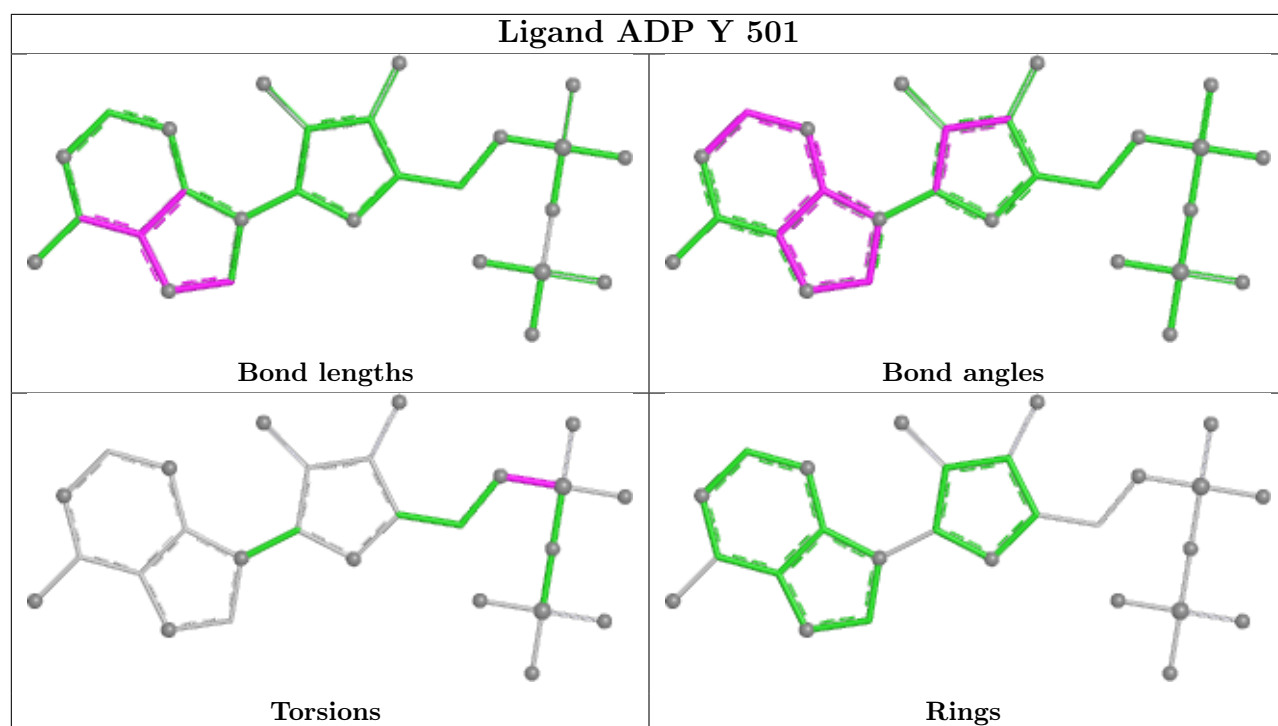
There are no ring outliers.

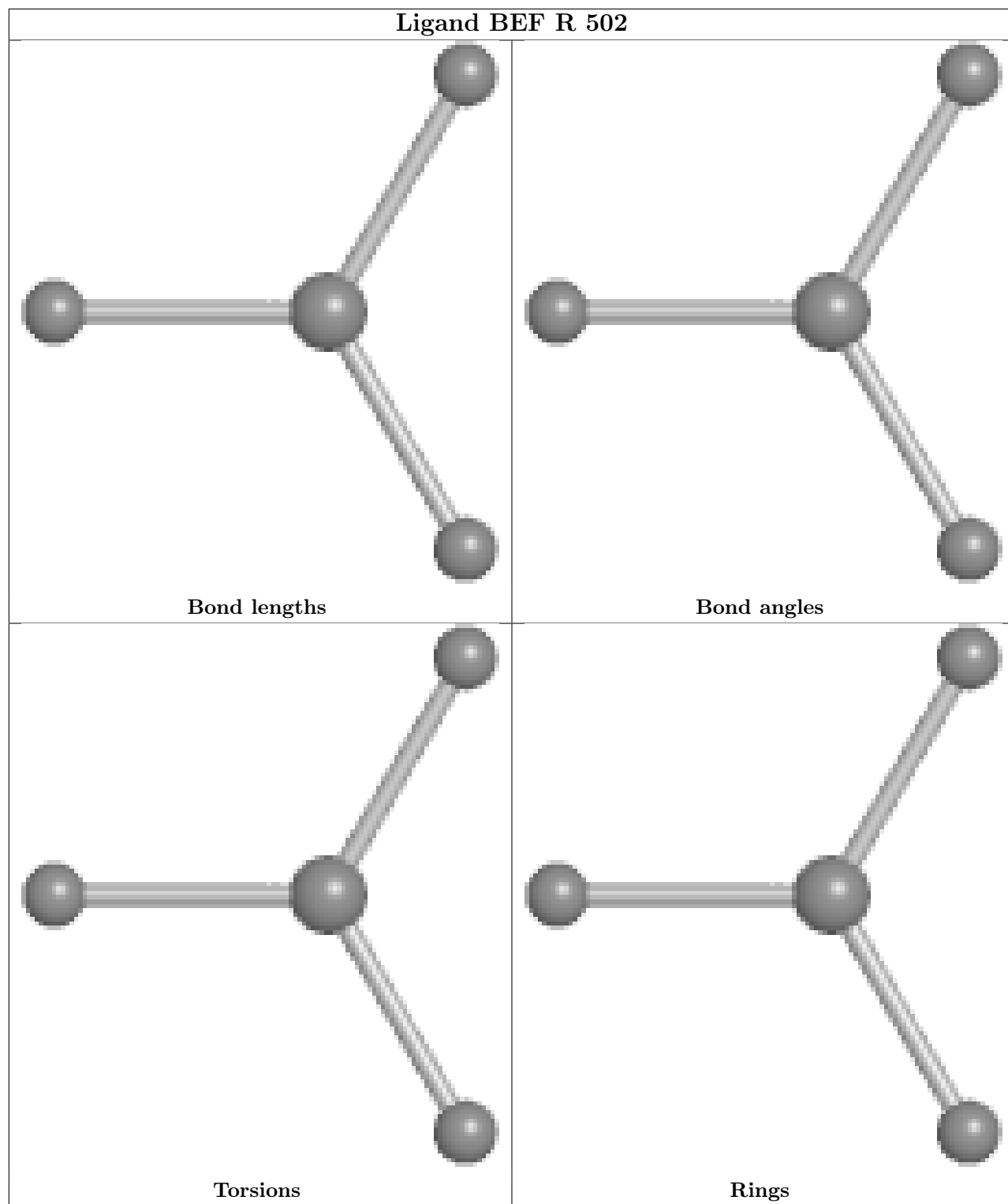
10 monomers are involved in 17 short contacts:

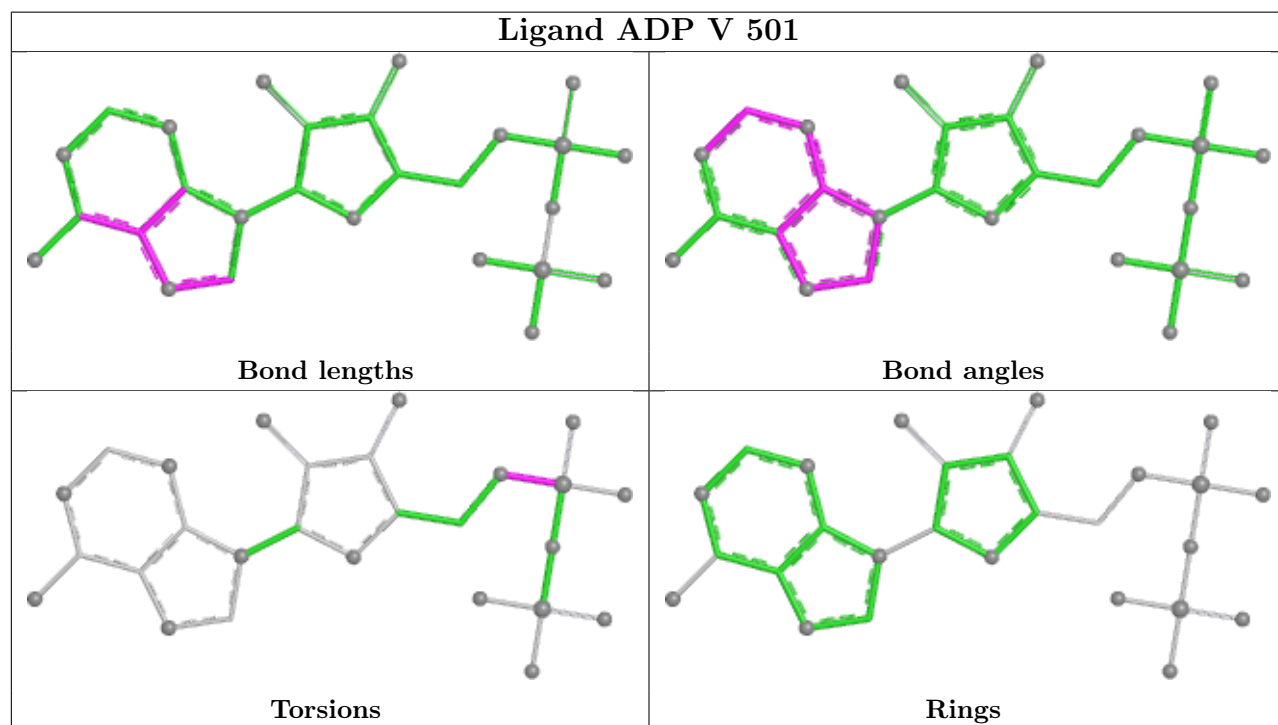
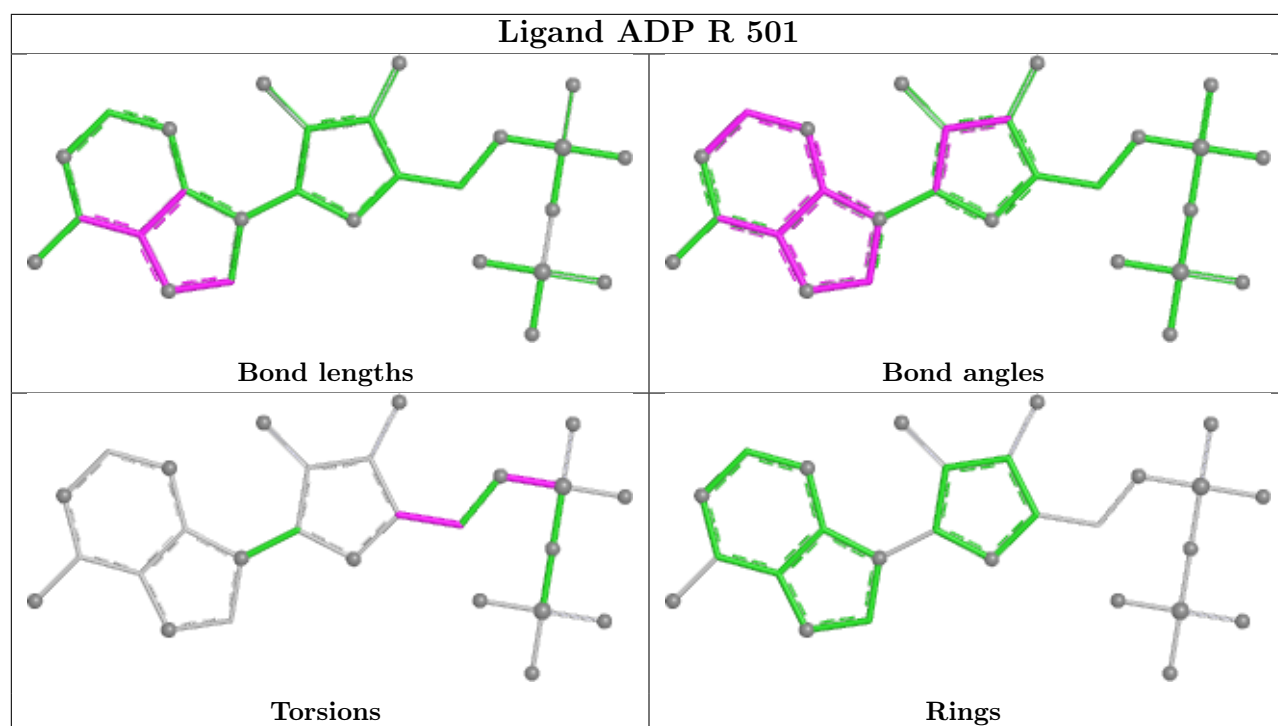
Mol	Chain	Res	Type	Clashes	Symm-Clashes
14	X	501	ADP	3	0
14	U	501	ADP	1	0
14	Y	501	ADP	1	0
14	M	1601	ADP	1	0
15	R	502	BEF	2	0
14	R	501	ADP	3	0
14	V	501	ADP	2	0
14	W	501	ADP	2	0
14	T	501	ADP	1	0
15	M	1602	BEF	3	0

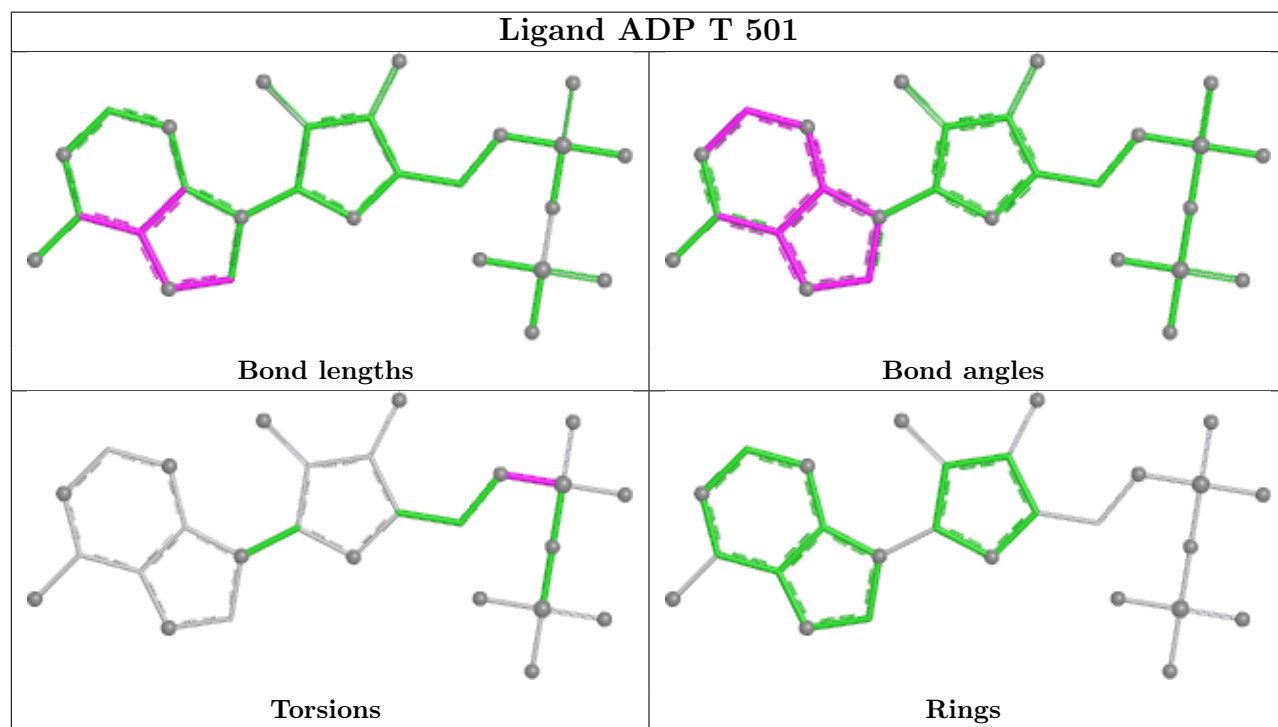
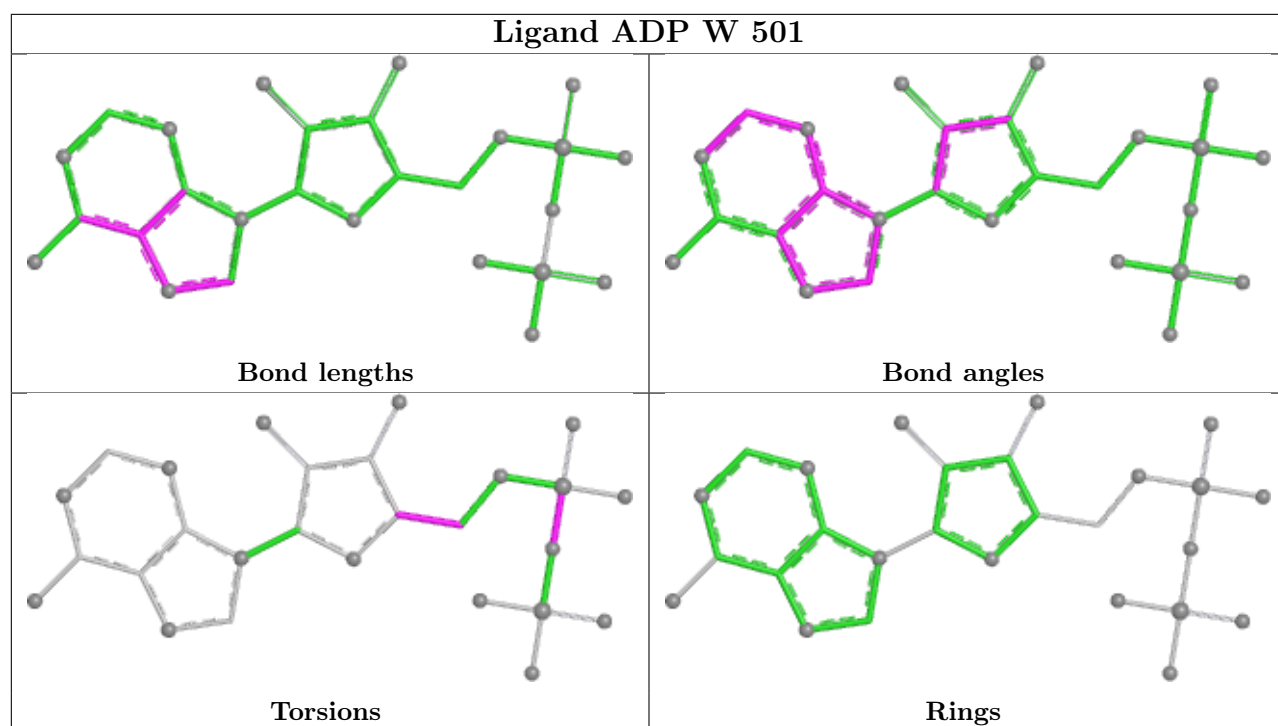
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

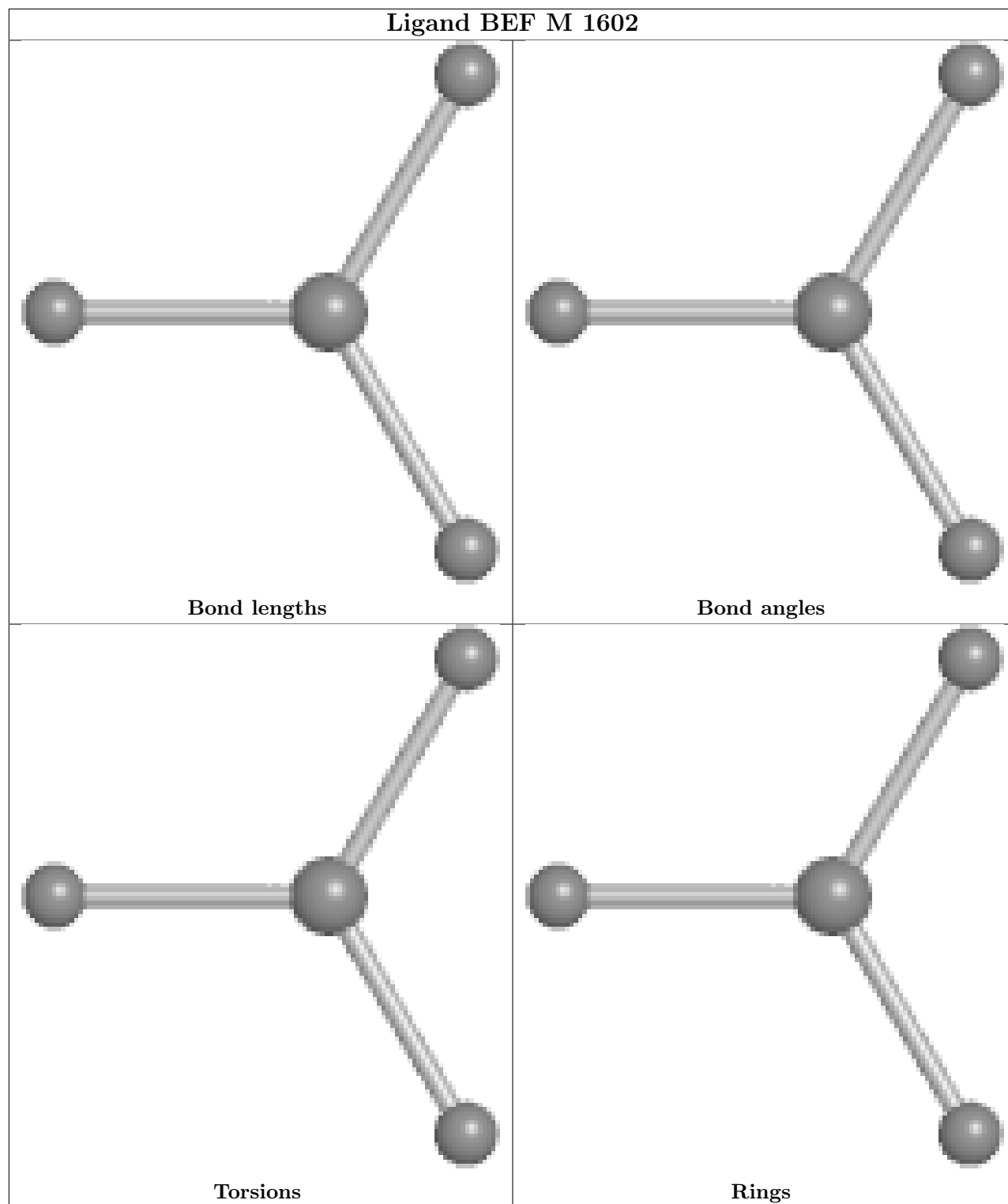












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

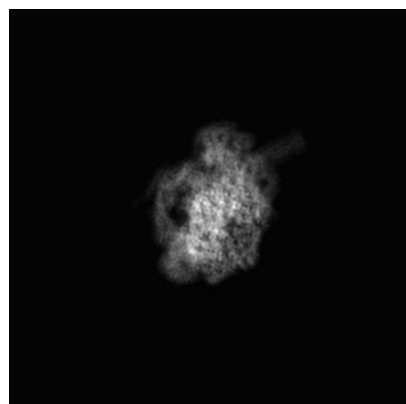
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-18764. These allow visual inspection of the internal detail of the map and identification of artifacts.

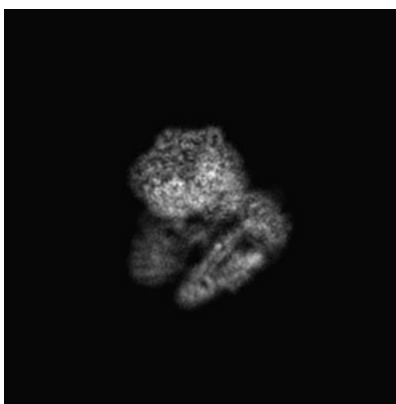
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

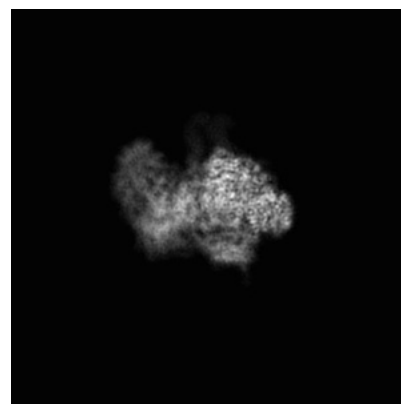
6.1.1 Primary map



X

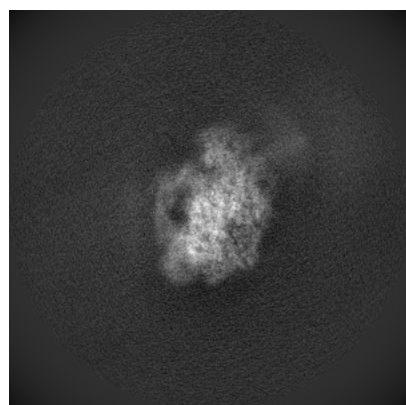


Y

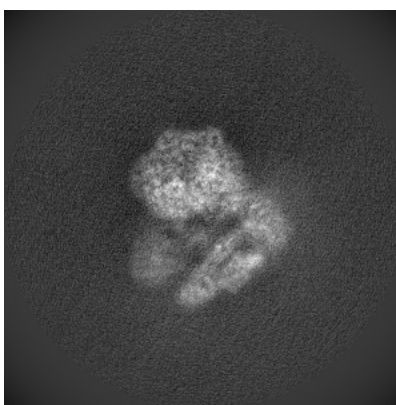


Z

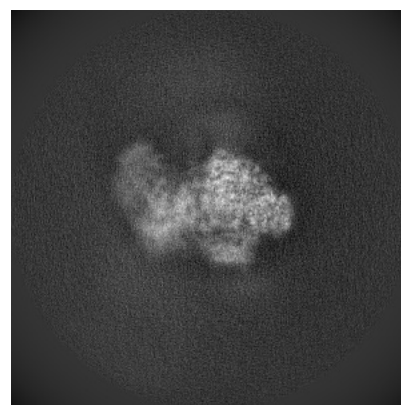
6.1.2 Raw map



X



Y

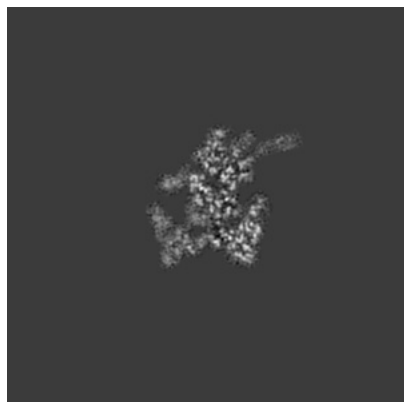


Z

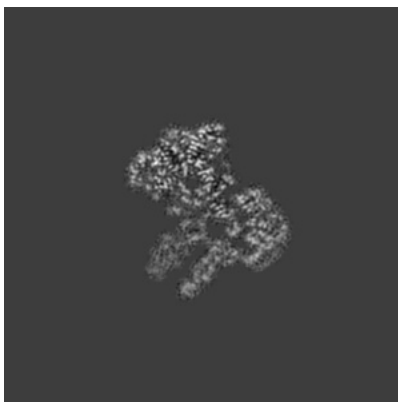
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

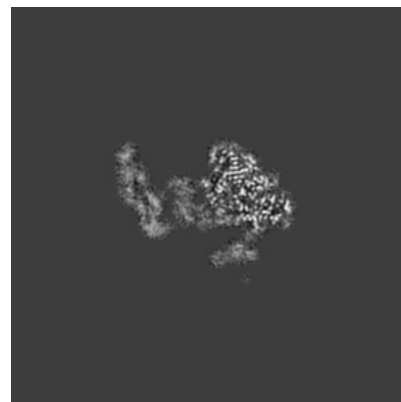
6.2.1 Primary map



X Index: 240

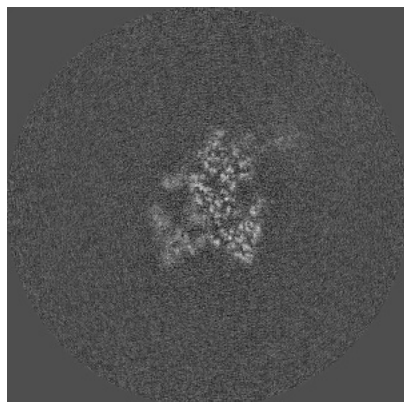


Y Index: 240

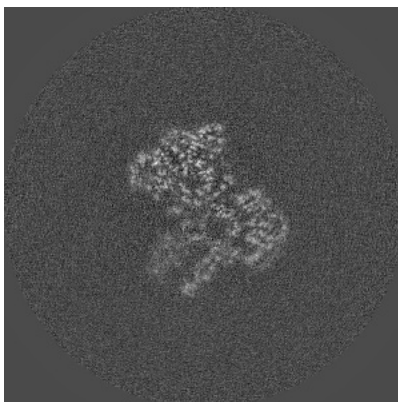


Z Index: 240

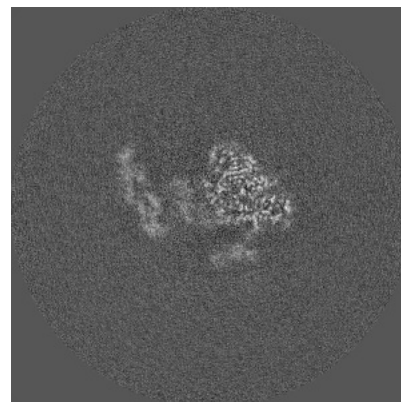
6.2.2 Raw map



X Index: 240



Y Index: 240

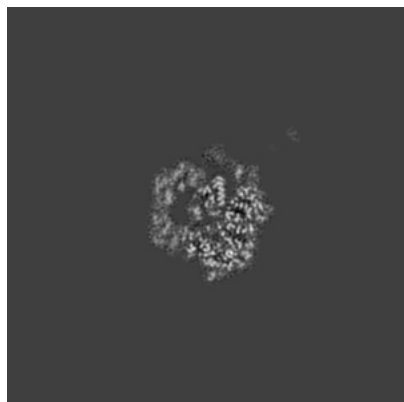


Z Index: 240

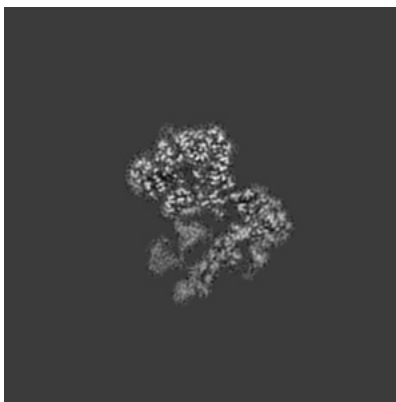
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

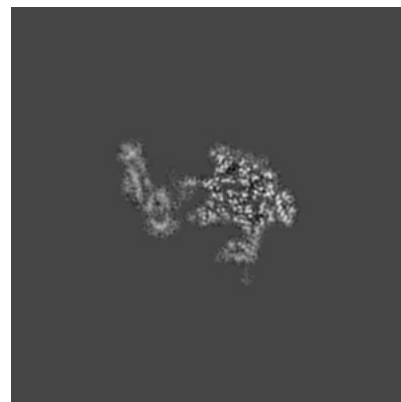
6.3.1 Primary map



X Index: 264

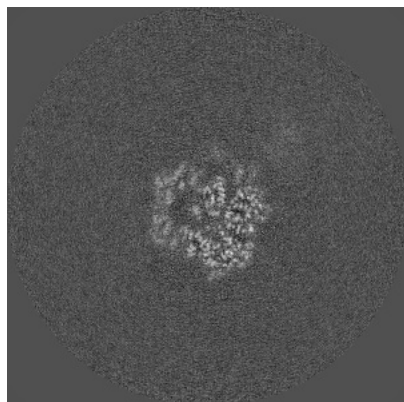


Y Index: 249

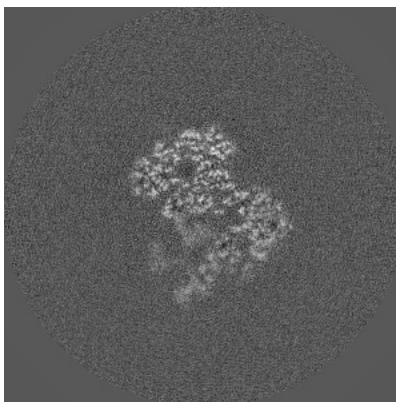


Z Index: 248

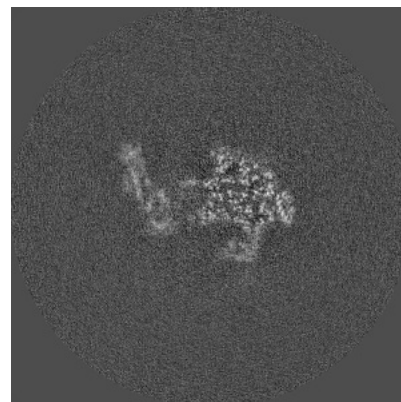
6.3.2 Raw map



X Index: 263



Y Index: 253

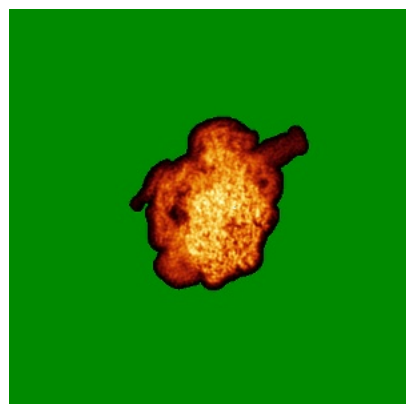


Z Index: 248

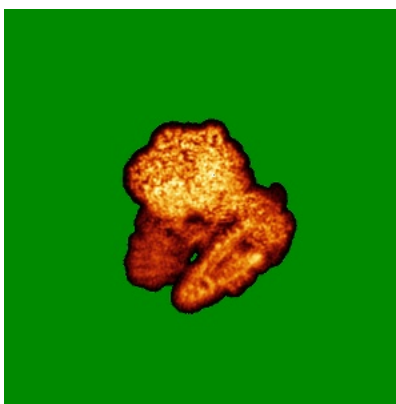
The images above show the largest variance slices of the map in three orthogonal directions.

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

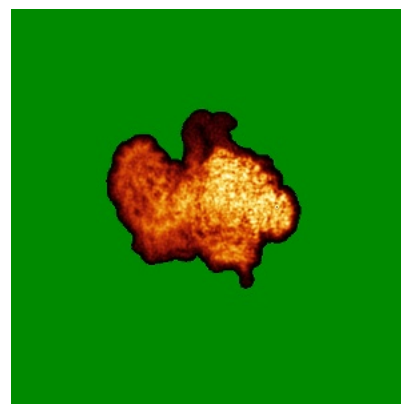
6.4.1 Primary map



X

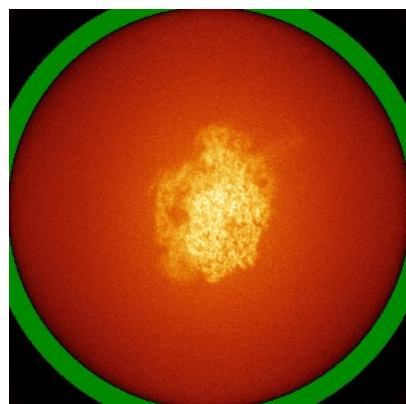


Y

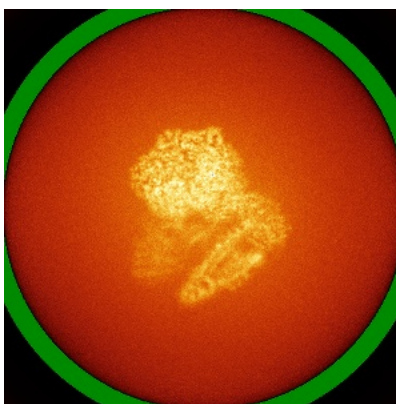


Z

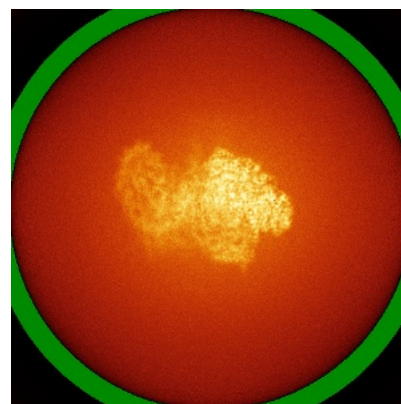
6.4.2 Raw map



X



Y

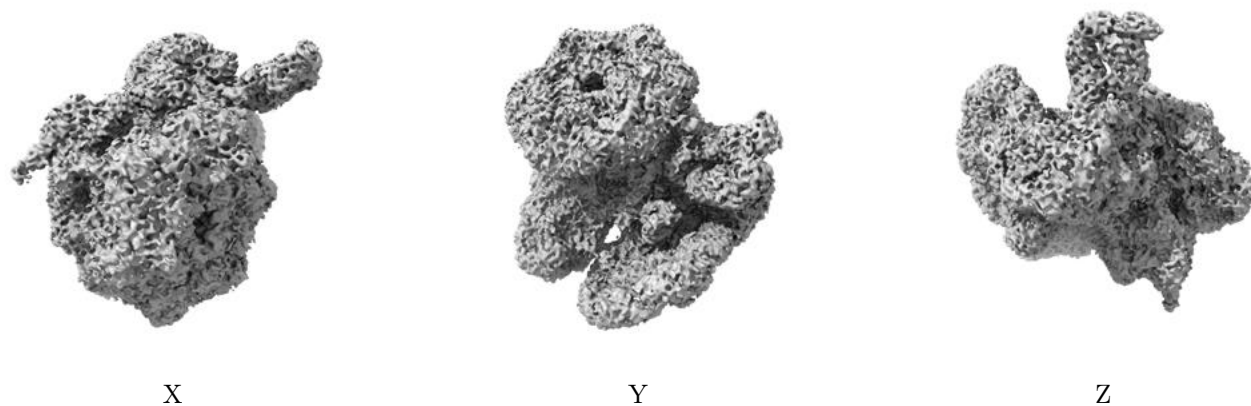


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

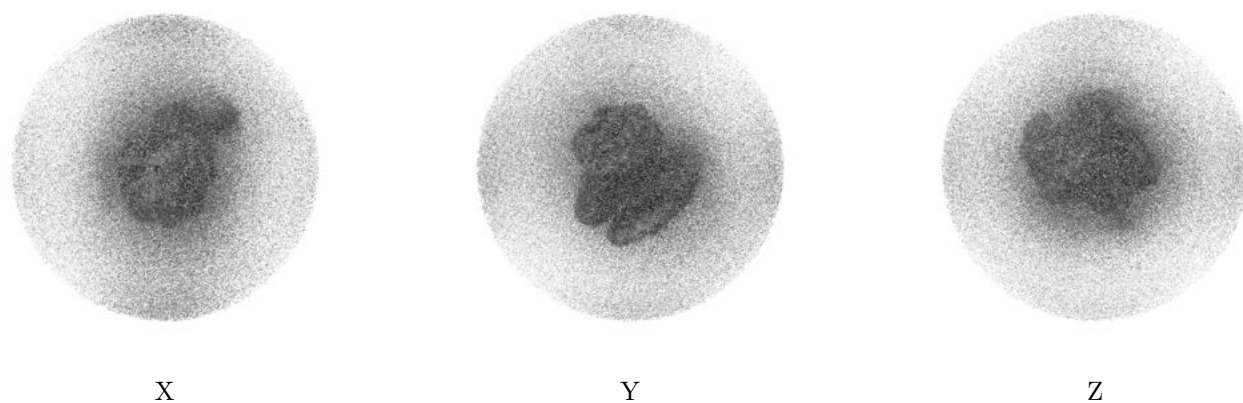
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.00197. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

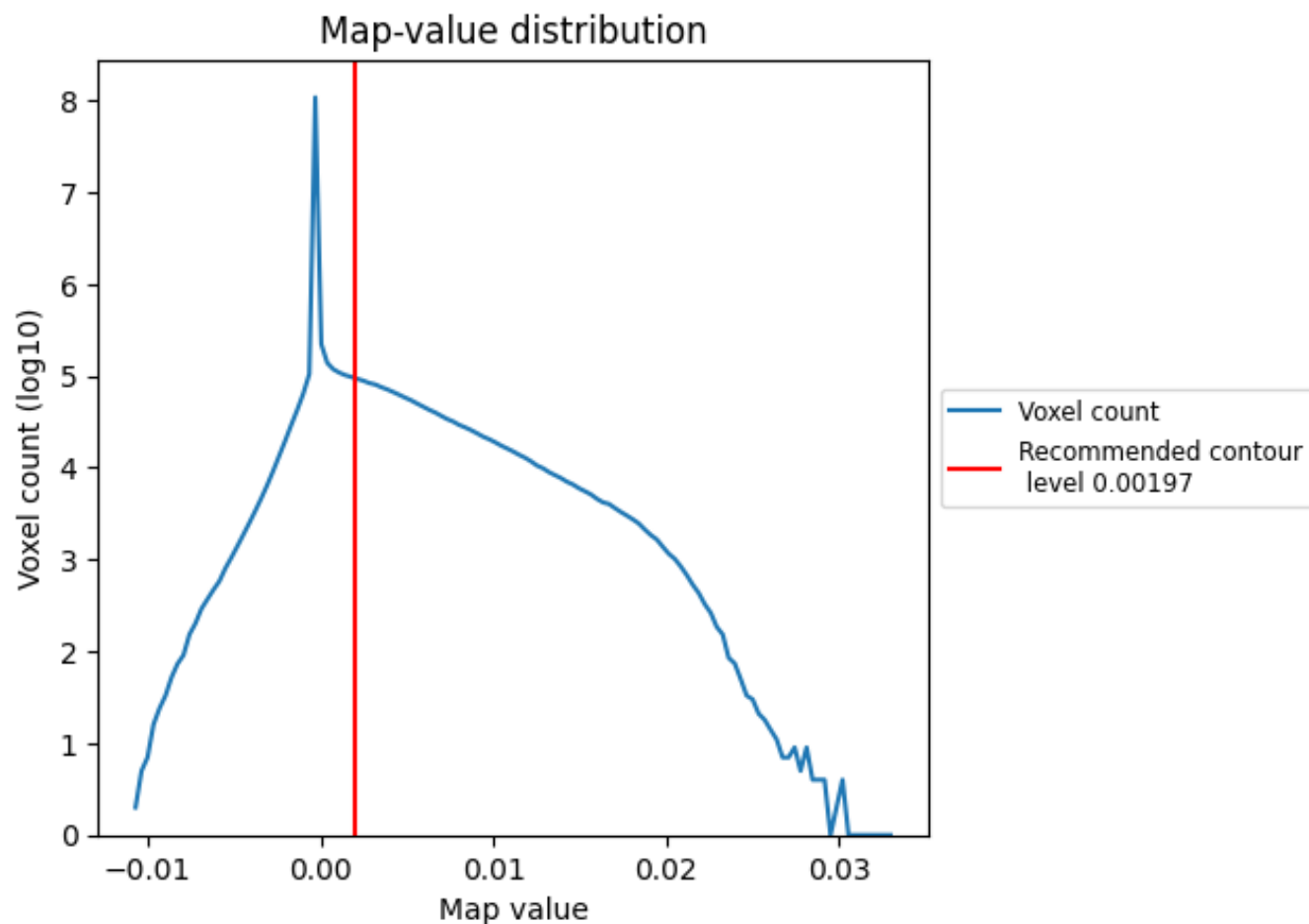
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

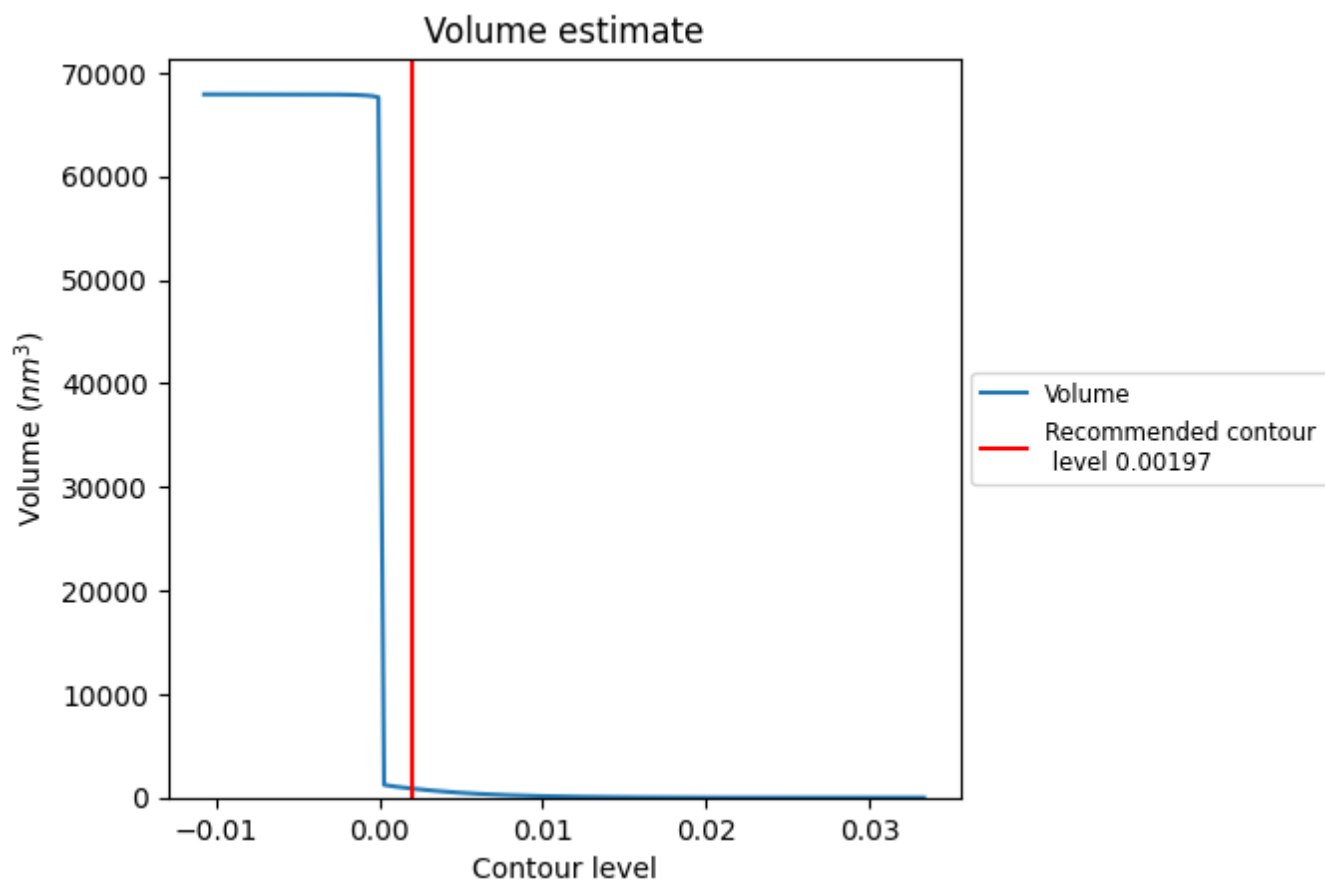
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

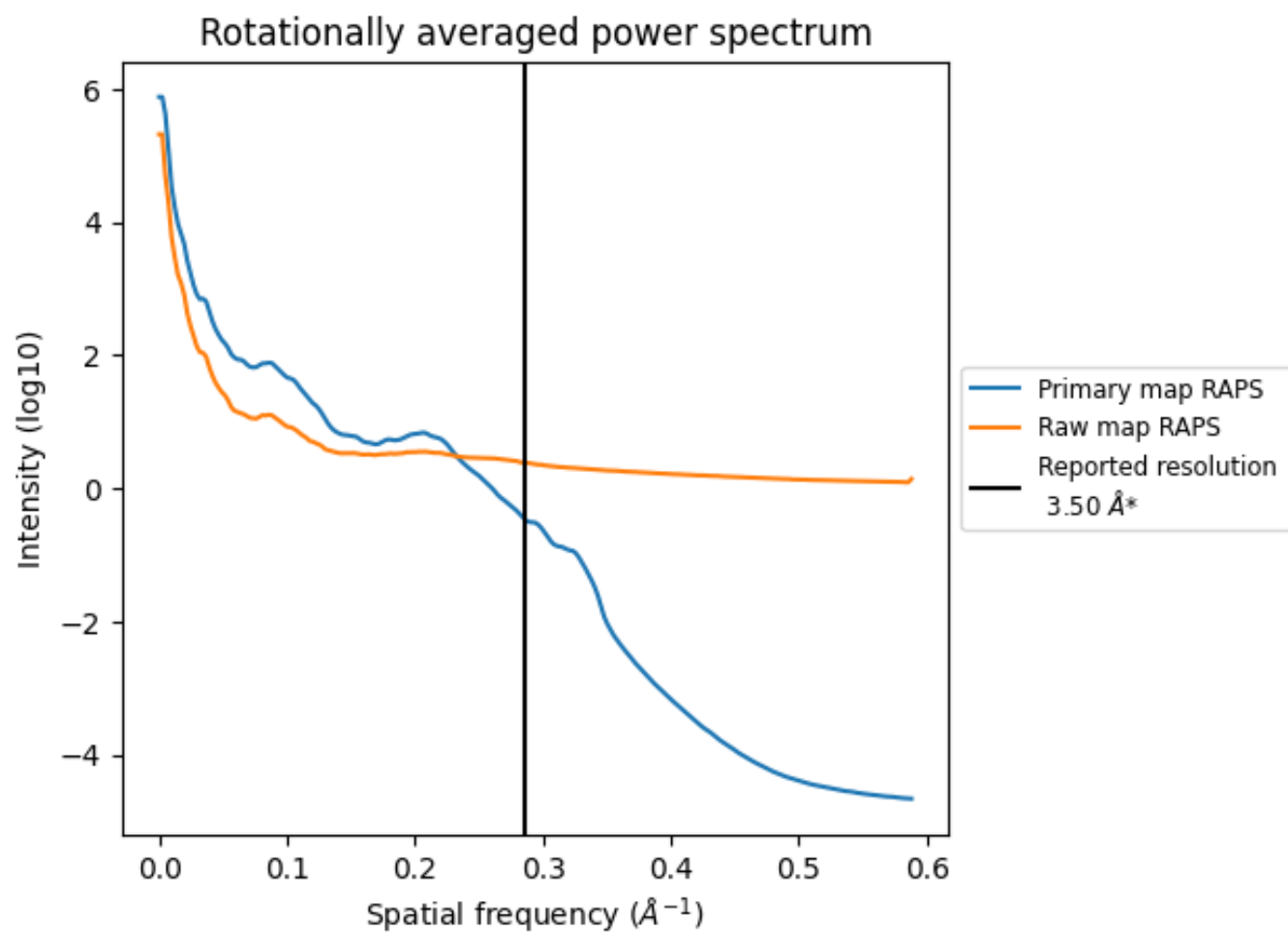
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 877 nm^3 ; this corresponds to an approximate mass of 792 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 ⓘ

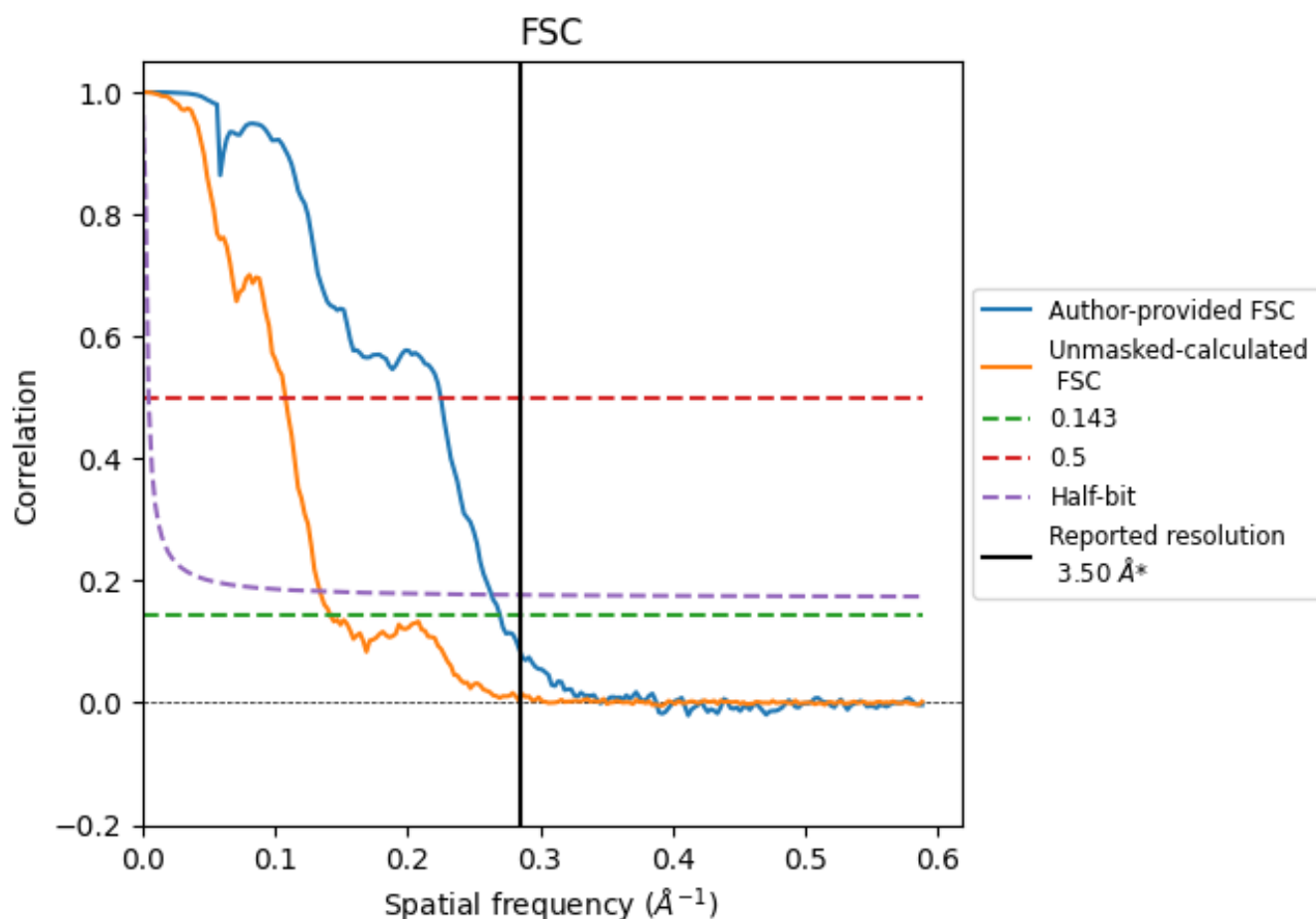


*Reported resolution corresponds to spatial frequency of 0.286 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.286 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

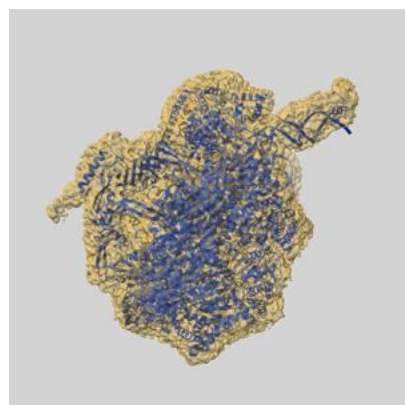
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	3.71	4.44	3.80
Unmasked-calculated*	7.05	9.26	7.46

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 7.05 differs from the reported value 3.5 by more than 10 %

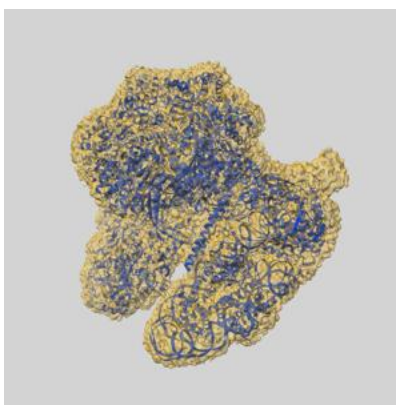
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-18764 and PDB model 8QYV. Per-residue inclusion information can be found in [section 3](#) on [page 9](#).

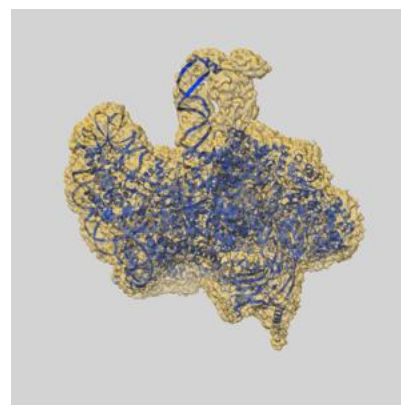
9.1 Map-model overlay [i](#)



X



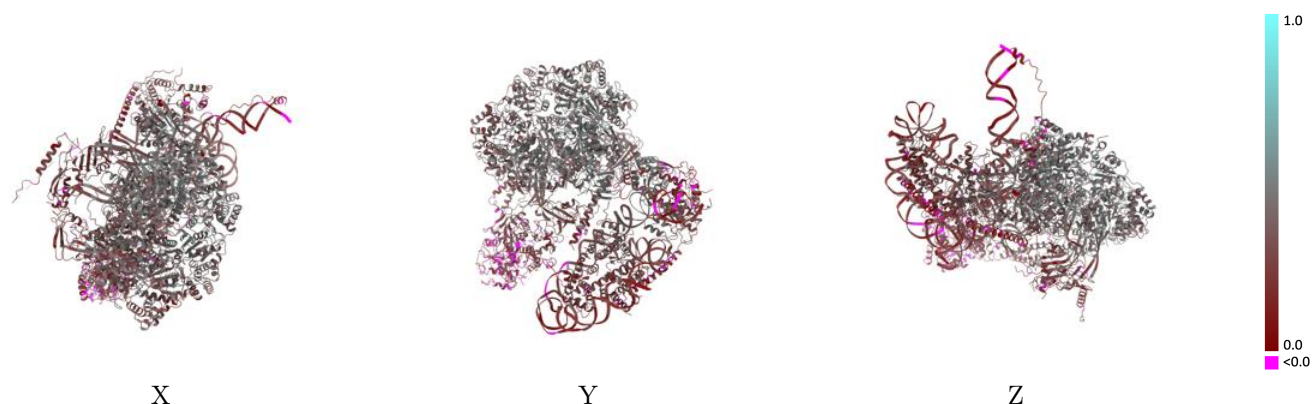
Y



Z

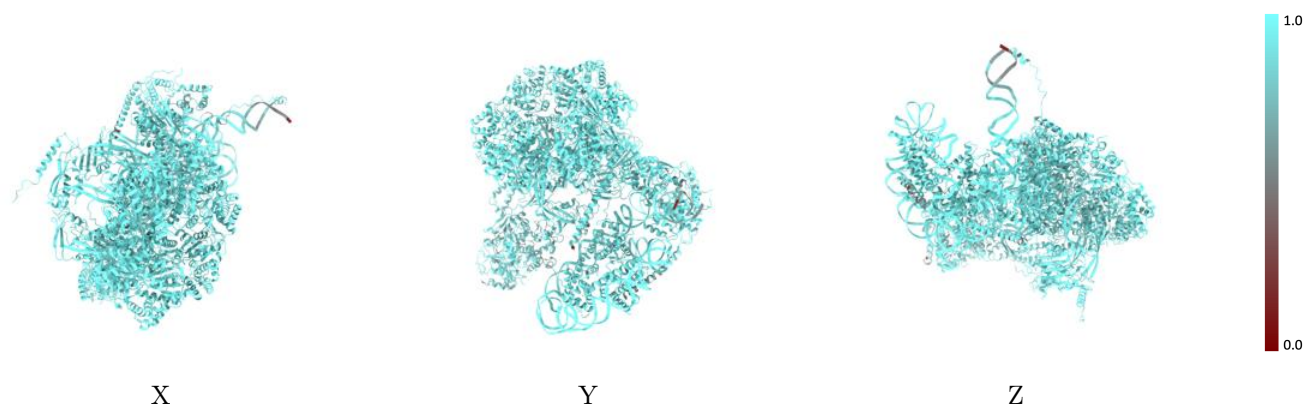
The images above show the 3D surface view of the map at the recommended contour level 0.00197 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



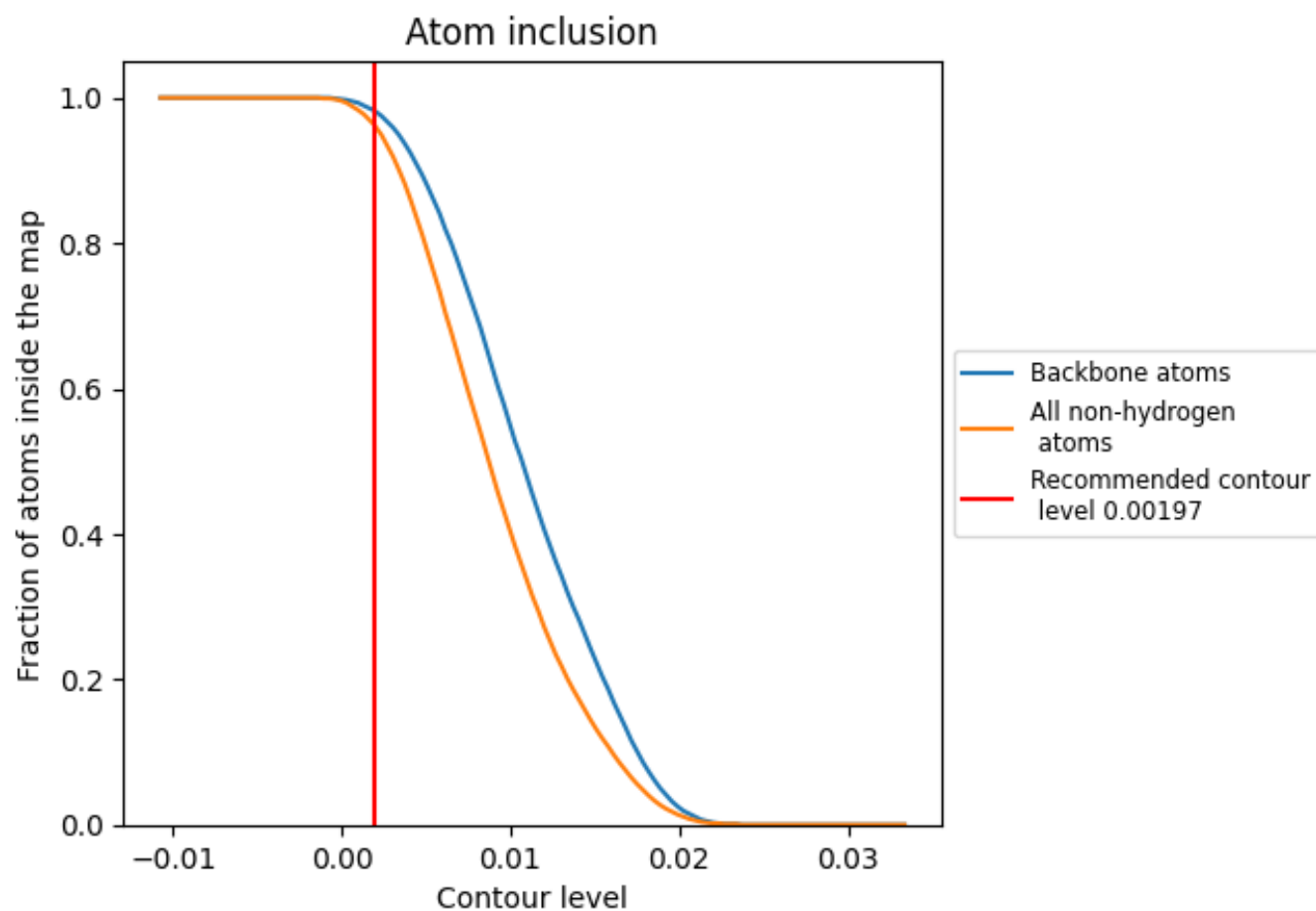
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.00197).

9.4 Atom inclusion ⓘ



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 (0.00197) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9620	 0.3240
A	 0.9390	 0.2020
B	 0.9660	 0.3430
C	 0.9480	 0.3370
D	 0.9900	 0.2290
E	 0.9790	 0.3250
G	 0.9750	 0.2710
I	 0.9650	 0.2320
J	 0.9540	 0.2230
M	 0.9690	 0.3560
P	 0.9050	 0.2890
R	 0.9310	 0.1390
S	 0.8190	 0.1680
T	 0.9860	 0.3840
U	 0.9780	 0.3980
V	 0.9890	 0.4490
W	 0.9890	 0.4330
X	 0.9820	 0.3850
Y	 0.9830	 0.3640
Z	 0.8840	 0.1730

