



wwPDB EM Validation Summary Report ⓘ

Mar 22, 2025 – 06:59 am GMT

PDB ID : 9F61
EMDB ID : EMD-50206
Title : Structure of the Chlamydomonas reinhardtii respiratory complex IV from respiratory supercomplex
Authors : Waltz, F.; Righetto, R.; Kotecha, A.; Engel, B.D.
Deposited on : 2024-04-30
Resolution : 2.55 Å(reported)

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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.dev117
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.41.5

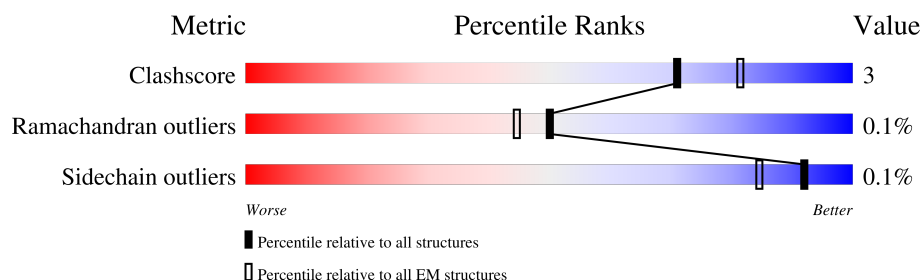
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.55 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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 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	3A	505	
2	3B	284	
3	3C	153	
4	3D	382	
5	3E	175	
6	3F	96	
7	3G	125	
8	3H	148	

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Mol	Chain	Length	Quality of chain
9	3I	101	
10	3J	105	
11	3K	58	
12	3L	87	

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
18	CUA	3C	301	-	-	X	-

2 Entry composition

There are 20 unique types of molecules in this entry. The entry contains 14224 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 Cytochrome c oxidase subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	3A	504	Total	C	N	O	S	0	0
			3888	2600	618	643	27		

- Molecule 2 is a protein called Cytochrome c oxidase polypeptide II.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	3B	141	Total	C	N	O	S	0	0
			1169	774	188	201	6		

- Molecule 3 is a protein called cytochrome-c oxidase.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3C	153	Total	C	N	O	S	0	0
			1212	776	206	223	7		

- Molecule 4 is a protein called Cytochrome c oxidase subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3D	266	Total	C	N	O	S	0	0
			2079	1373	334	351	21		

- Molecule 5 is a protein called Cox5b.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	3E	90	Total	C	N	O	S	0	0
			737	478	114	144	1		

- Molecule 6 is a protein called Cox5c.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	3F	86	Total	C	N	O	S	0	0
			706	456	122	126	2		

- Molecule 7 is a protein called Cox6a.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	3G	91	Total	C	N	O	S	0	0
			733	484	120	124	5		

- Molecule 8 is a protein called Cox6b.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	3H	114	Total	C	N	O	S	0	0
			954	606	159	185	4		

- Molecule 9 is a protein called Cox7c.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	3I	72	Total	C	N	O	0	0
			594	393	98	103		

- Molecule 10 is a protein called Cytochrome c oxidase subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	3J	104	Total	C	N	O	S	0	0
			816	522	144	147	3		

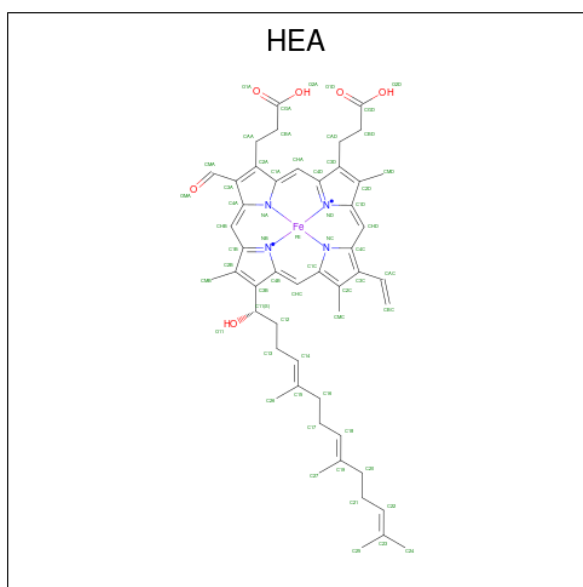
- Molecule 11 is a protein called Cox7a.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	3K	47	Total	C	N	O	0	0
			382	249	63	70		

- Molecule 12 is a protein called CoxIn.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	3L	78	Total	C	N	O	S	0	0
			627	405	104	114	4		

- Molecule 13 is HEME-A (three-letter code: HEA) (formula: $C_{49}H_{56}FeN_4O_6$).



Mol	Chain	Residues	Atoms					AltConf
13	3A	1	Total 60	C 49	Fe 1	N 4	O 6	0
13	3A	1	Total 60	C 49	Fe 1	N 4	O 6	0

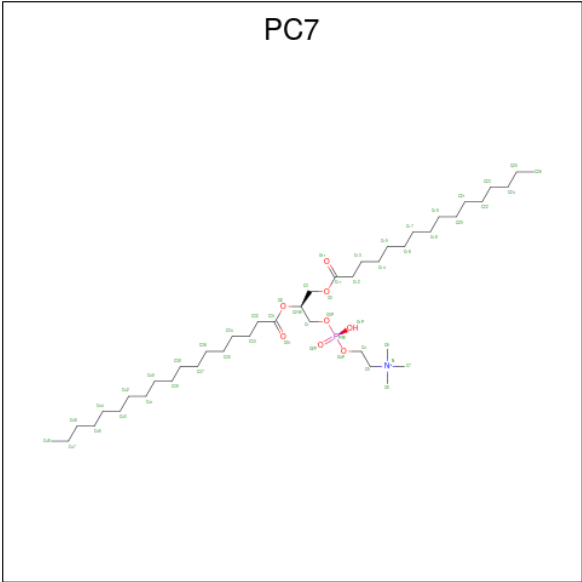
- Molecule 14 is COPPER (II) ION (three-letter code: CU) (formula: Cu).

Mol	Chain	Residues	Atoms		AltConf
14	3A	1	Total	Cu	0
			1	1	

- Molecule 15 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

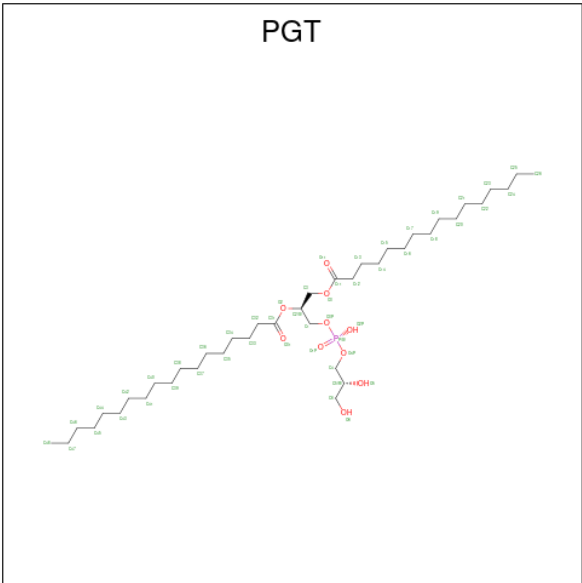
Mol	Chain	Residues	Atoms		AltConf
15	3A	1	Total	Mg	0
			1	1	

- Molecule 16 is (7S)-4-HYDROXY-N,N,N-TRIMETHYL-9-OXO-7-[(PALMITOYLOXY)METHYL]-3,5,8-TRIOXA-4-PHOSPHAHEXACOSAN-1-AMINIUM 4-OXIDE (three-letter code: PC7) (formula: C₄₂H₈₅NO₈P).



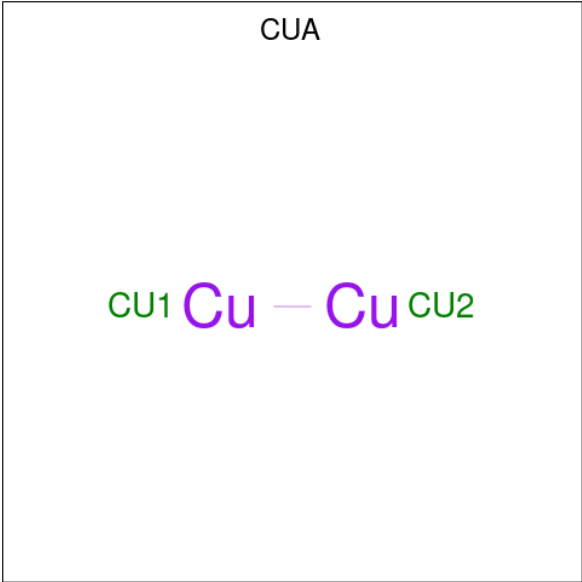
Mol	Chain	Residues	Atoms					AltConf
16	3A	1	Total	C	N	O	P	0
			27	17	1	8	1	

- Molecule 17 is (1S)-2-[[[(2R)-2,3-DIHYDROXYPROPYL]OXY}(HYDROXY)PHOSPHORYL]OXY}-1-[(PALMITOYLOXY)METHYL]ETHYL STEARATE (three-letter code: PGT) (formula: C₄₀H₇₉O₁₀P).



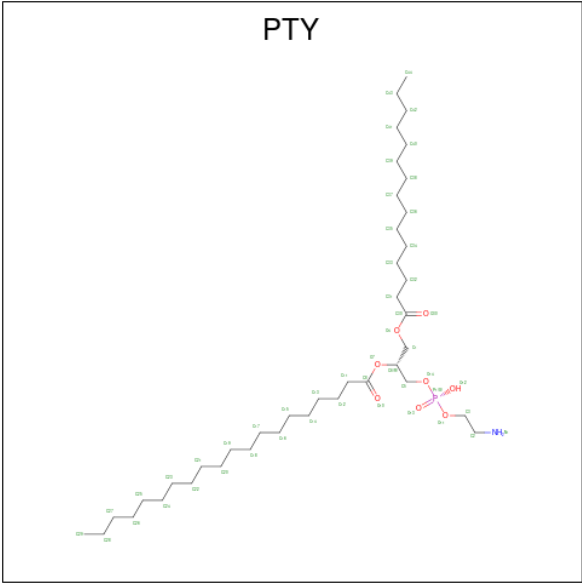
Mol	Chain	Residues	Atoms				AltConf
17	3A	1	Total	C	O	P	0
			33	22	10	1	

- Molecule 18 is DINUCLEAR COPPER ION (three-letter code: CUA) (formula: Cu₂).



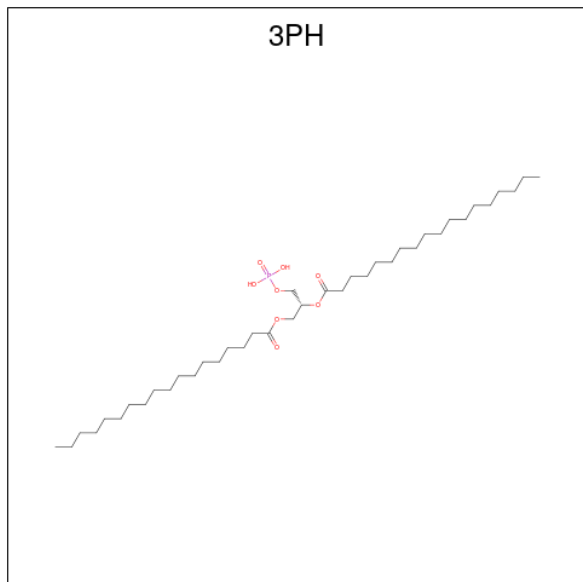
Mol	Chain	Residues	Atoms		AltConf
18	3C	1	Total	Cu	0
			2	2	

- Molecule 19 is PHOSPHATIDYLETHANOLAMINE (three-letter code: PTY) (formula: C₄₀H₈₀NO₈P).



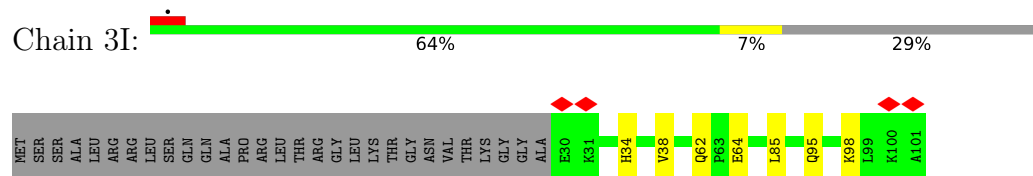
Mol	Chain	Residues	Atoms					AltConf
19	3D	1	Total	C	N	O	P	0
			35	25	1	8	1	
19	3F	1	Total	C	N	O	P	0
			34	24	1	8	1	

- Molecule 20 is 1,2-DIACYL-GLYCEROL-3-SN-PHOSPHATE (three-letter code: 3PH) (formula: $C_{39}H_{77}O_8P$).

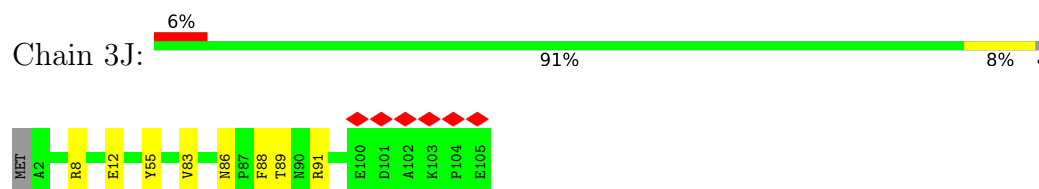


Mol	Chain	Residues	Atoms				AltConf
			Total	C	O	P	
20	3D	1	32	23	8	1	0
20	3I	1	42	33	8	1	0

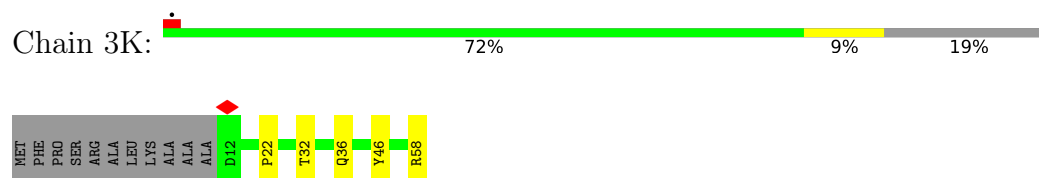
- Molecule 9: Cox7c



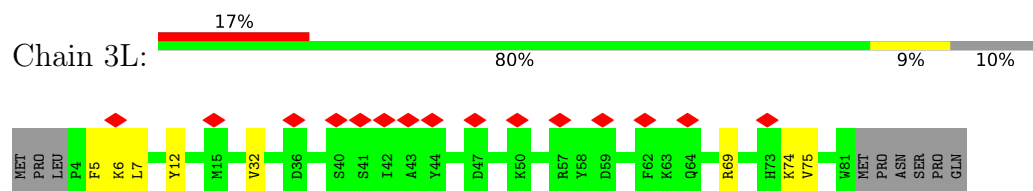
- Molecule 10: Cytochrome c oxidase subunit



- Molecule 11: Cox7a



- Molecule 12: CoxIn



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	83443	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)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	TFS FALCON 4i (4k x 4k)	Depositor
Maximum map value	0.836	Depositor
Minimum map value	-0.521	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.020	Depositor
Recommended contour level	0.127	Depositor
Map size (Å)	589.6, 589.6, 589.6	wwPDB
Map dimensions	588, 588, 588	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0027211, 1.0027211, 1.0027211	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PC7, MG, 3PH, HEA, CU, CUA, PGT, PTY

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	3A	0.34	0/4011	0.56	1/5484 (0.0%)
2	3B	0.30	0/1204	0.52	0/1641
3	3C	0.32	0/1237	0.55	0/1676
4	3D	0.32	0/2152	0.50	0/2937
5	3E	0.32	0/757	0.60	0/1029
6	3F	0.30	0/726	0.46	0/974
7	3G	0.30	0/762	0.55	1/1038 (0.1%)
8	3H	0.32	0/980	0.55	0/1325
9	3I	0.32	0/619	0.50	0/839
10	3J	0.31	0/839	0.53	0/1143
11	3K	0.32	0/392	0.51	0/531
12	3L	0.30	0/645	0.56	0/875
All	All	0.32	0/14324	0.54	2/19492 (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	3G	0	1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	3G	74	LEU	CA-CB-CG	6.43	130.08	115.30
1	3A	417	LEU	CA-CB-CG	6.25	129.68	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
7	3G	114	TRP	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	3A	3888	0	3936	32	0
2	3B	1169	0	1191	12	0
3	3C	1212	0	1243	14	0
4	3D	2079	0	2039	19	0
5	3E	737	0	706	1	0
6	3F	706	0	685	3	0
7	3G	733	0	708	5	0
8	3H	954	0	900	6	0
9	3I	594	0	553	7	0
10	3J	816	0	807	6	0
11	3K	382	0	367	5	0
12	3L	627	0	604	15	0
13	3A	120	0	108	2	0
14	3A	1	0	0	0	0
15	3A	1	0	0	0	0
16	3A	27	0	28	2	0
17	3A	33	0	36	1	0
18	3C	2	0	0	4	0
19	3D	35	0	43	2	0
19	3F	34	0	41	0	0
20	3D	32	0	37	0	0
20	3I	42	0	60	0	0
All	All	14224	0	14092	94	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 3.

The worst 5 of 94 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)
1:3A:265:THR:HG21	12:3L:5:PHE:CE2	1.39	1.53
3:3C:124:CYS:SG	18:3C:301:CUA:CU1	1.27	1.24
1:3A:265:THR:CG2	12:3L:5:PHE:CE2	2.35	1.10
1:3A:265:THR:HG21	12:3L:5:PHE:CD2	1.92	1.03
1:3A:265:THR:HG21	12:3L:5:PHE:CZ	2.05	0.91

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	3A	502/505 (99%)	490 (98%)	12 (2%)	0	100	100
2	3B	139/284 (49%)	135 (97%)	4 (3%)	0	100	100
3	3C	151/153 (99%)	145 (96%)	6 (4%)	0	100	100
4	3D	264/382 (69%)	254 (96%)	10 (4%)	0	100	100
5	3E	88/175 (50%)	85 (97%)	2 (2%)	1 (1%)	12	15
6	3F	84/96 (88%)	80 (95%)	4 (5%)	0	100	100
7	3G	87/125 (70%)	80 (92%)	7 (8%)	0	100	100
8	3H	112/148 (76%)	108 (96%)	4 (4%)	0	100	100
9	3I	70/101 (69%)	67 (96%)	3 (4%)	0	100	100
10	3J	102/105 (97%)	100 (98%)	2 (2%)	0	100	100
11	3K	45/58 (78%)	44 (98%)	1 (2%)	0	100	100
12	3L	76/87 (87%)	72 (95%)	4 (5%)	0	100	100
All	All	1720/2219 (78%)	1660 (96%)	59 (3%)	1 (0%)	50	61

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	3E	28	TRP

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	3A	408/409 (100%)	408 (100%)	0	100	100
2	3B	132/224 (59%)	132 (100%)	0	100	100
3	3C	137/137 (100%)	137 (100%)	0	100	100
4	3D	211/294 (72%)	211 (100%)	0	100	100
5	3E	79/137 (58%)	79 (100%)	0	100	100
6	3F	66/72 (92%)	66 (100%)	0	100	100
7	3G	75/100 (75%)	74 (99%)	1 (1%)	65	79
8	3H	103/132 (78%)	103 (100%)	0	100	100
9	3I	58/80 (72%)	58 (100%)	0	100	100
10	3J	83/84 (99%)	83 (100%)	0	100	100
11	3K	39/46 (85%)	39 (100%)	0	100	100
12	3L	65/74 (88%)	65 (100%)	0	100	100
All	All	1456/1789 (81%)	1455 (100%)	1 (0%)	92	98

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
7	3G	109	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 11 ligands modelled in this entry, 2 are monoatomic - leaving 9 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$
13	HEA	3A	602	1	57,67,67	2.06	15 (26%)	61,103,103	2.46	23 (37%)
19	PTY	3F	101	-	33,33,49	0.54	0	36,38,54	0.47	0
17	PGT	3A	606	-	32,32,50	0.59	0	35,38,56	0.52	0
18	CUA	3C	301	-	0,1,1	-	-	-	-	-
16	PC7	3A	605	-	26,26,51	0.66	0	32,34,59	0.65	0
13	HEA	3A	601	1	57,67,67	2.05	16 (28%)	61,103,103	2.43	25 (40%)
20	3PH	3D	302	-	31,31,47	0.75	1 (3%)	35,36,52	0.79	1 (2%)
20	3PH	3I	201	-	41,41,47	0.65	1 (2%)	45,46,52	0.66	1 (2%)
19	PTY	3D	301	-	34,34,49	0.57	0	37,39,54	0.47	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
13	HEA	3A	602	1	-	4/32/76/76	-
19	PTY	3F	101	-	-	10/37/37/53	-
17	PGT	3A	606	-	-	12/37/37/55	-
16	PC7	3A	605	-	-	22/30/30/55	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
13	HEA	3A	601	1	-	7/32/76/76	-
20	3PH	3D	302	-	-	10/33/33/49	-
20	3PH	3I	201	-	-	9/43/43/49	-
19	PTY	3D	301	-	-	15/38/38/53	-

The worst 5 of 33 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	3A	602	HEA	C3B-C2B	5.44	1.47	1.34
13	3A	601	HEA	C3B-C2B	5.36	1.46	1.34
13	3A	602	HEA	C3C-C2C	5.13	1.47	1.40
13	3A	601	HEA	C3C-C2C	4.93	1.47	1.40
13	3A	601	HEA	CHC-C4B	4.89	1.47	1.35

The worst 5 of 50 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	3A	602	HEA	C3D-C4D-ND	6.84	116.98	110.36
13	3A	601	HEA	C3D-C4D-ND	6.22	116.38	110.36
13	3A	602	HEA	C2B-C1B-NB	5.74	116.75	109.88
13	3A	601	HEA	C2D-C1D-ND	5.72	116.61	109.84
13	3A	601	HEA	C2B-C1B-NB	5.50	116.47	109.88

There are no chirality outliers.

5 of 89 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
13	3A	602	HEA	C3B-C11-C12-C13
13	3A	602	HEA	O11-C11-C12-C13
13	3A	602	HEA	C15-C16-C17-C18
13	3A	602	HEA	C19-C20-C21-C22
16	3A	605	PC7	C2-C1-O3P-P

There are no ring outliers.

6 monomers are involved in 11 short contacts:

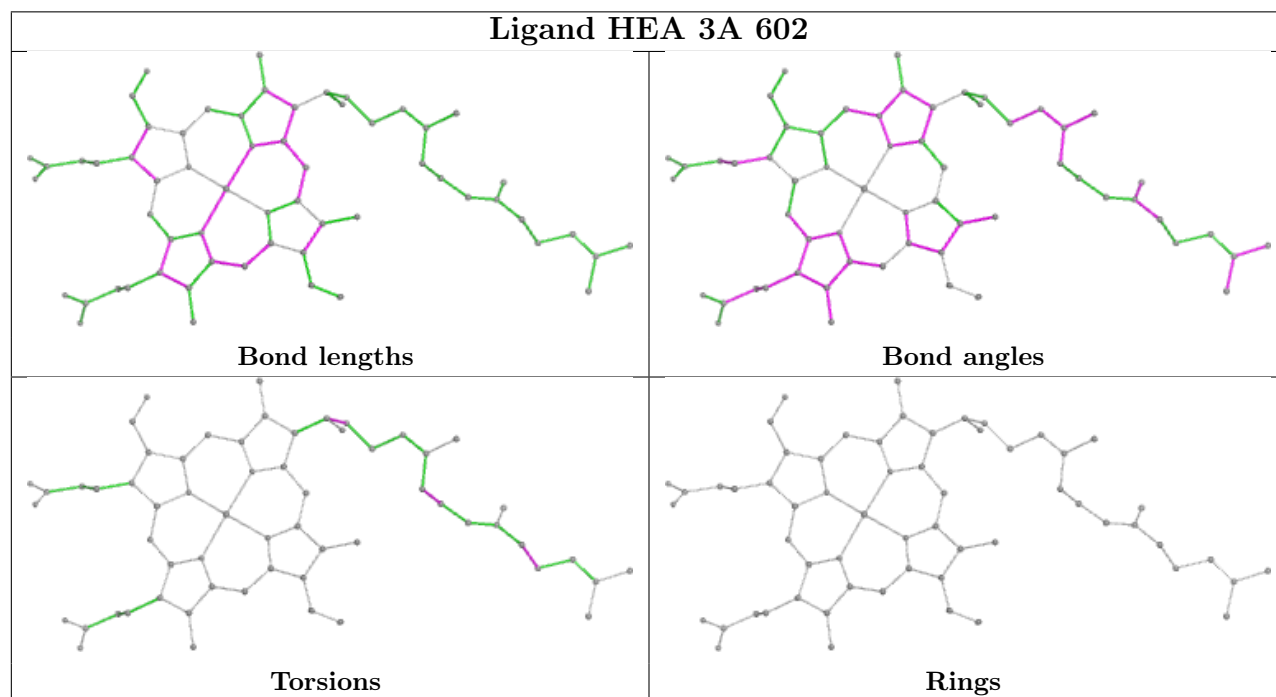
Mol	Chain	Res	Type	Clashes	Symm-Clashes
13	3A	602	HEA	1	0
17	3A	606	PGT	1	0
18	3C	301	CUA	4	0

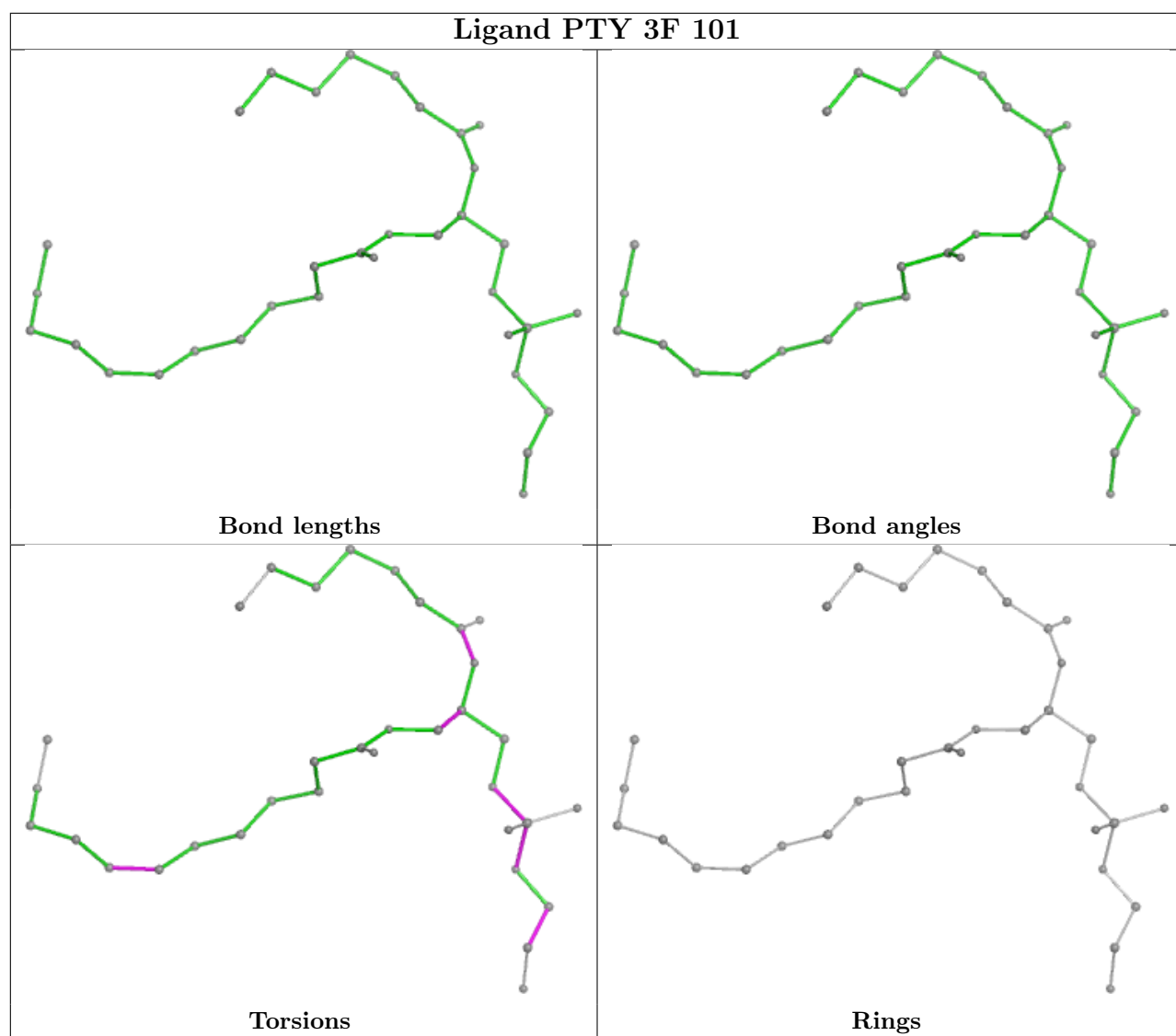
Continued on next page...

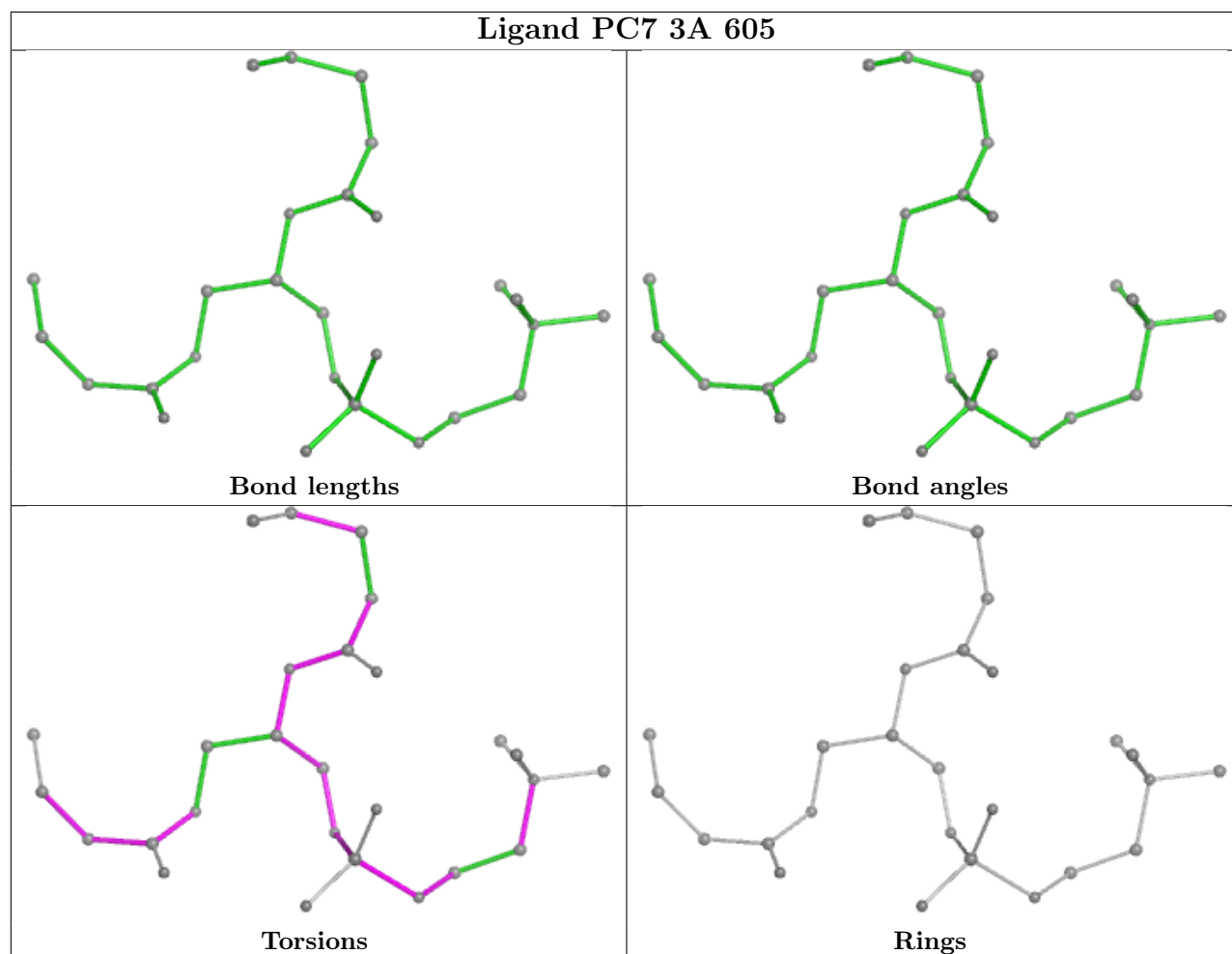
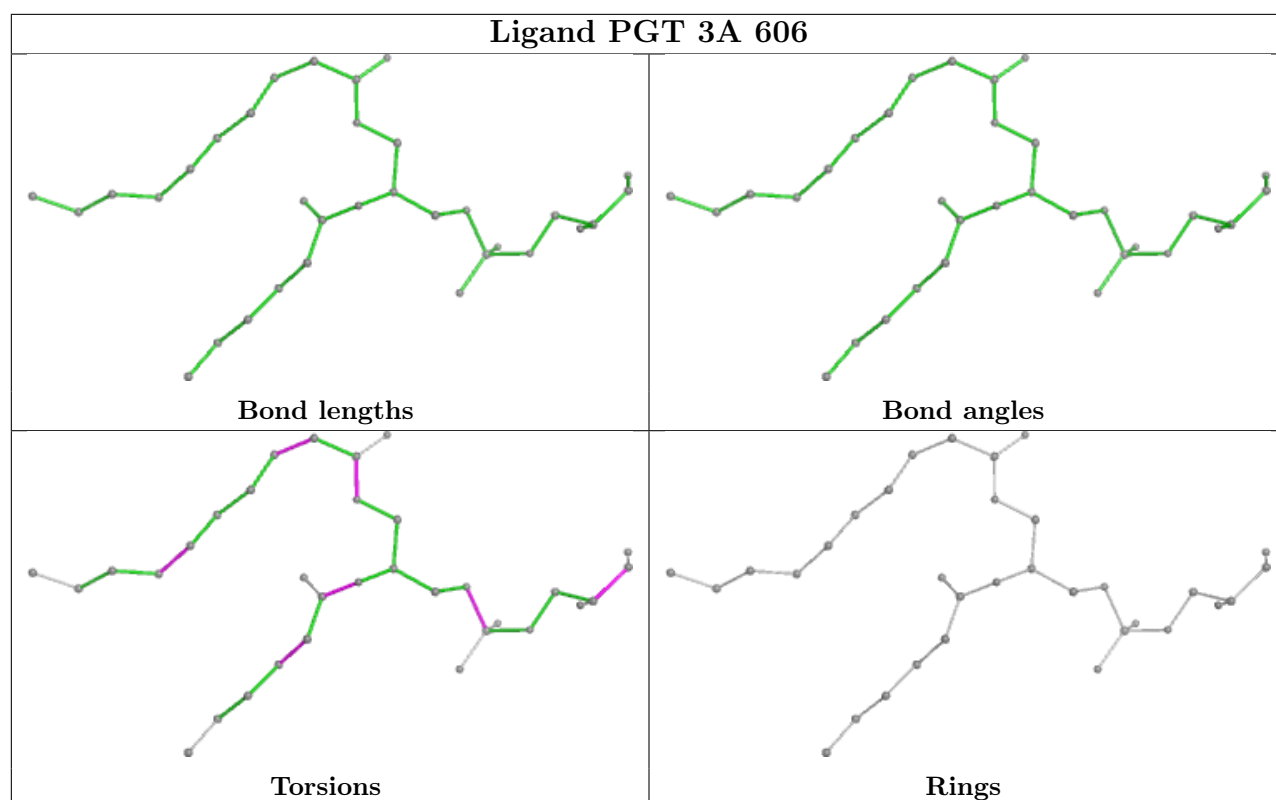
Continued from previous page...

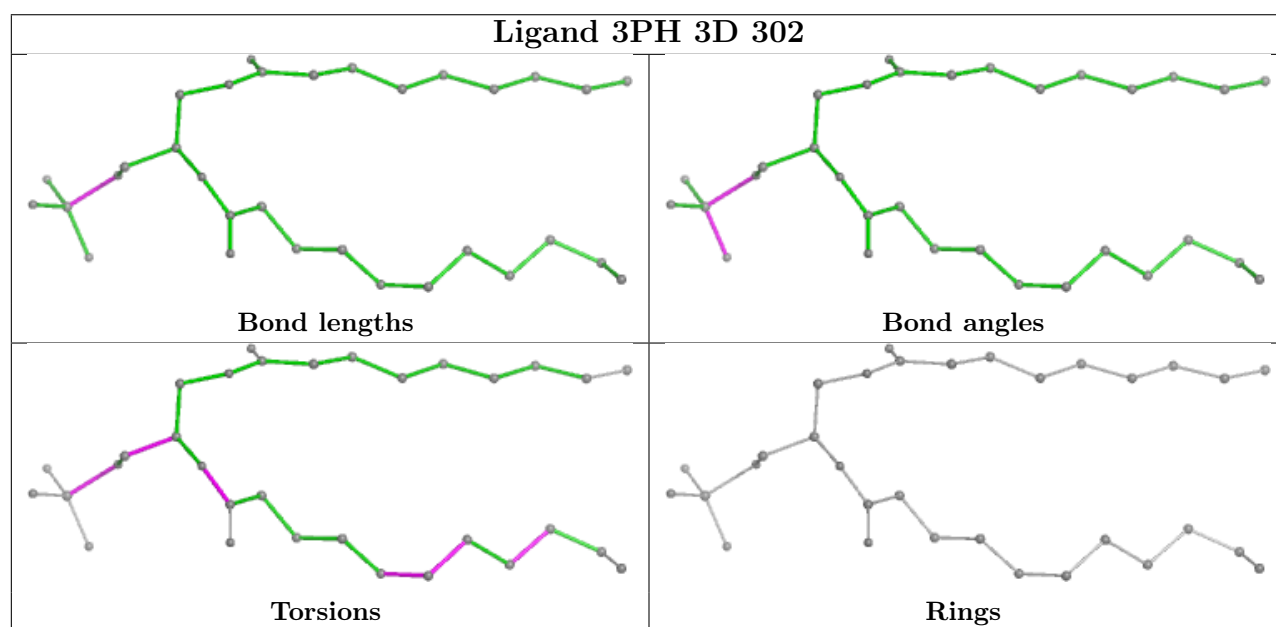
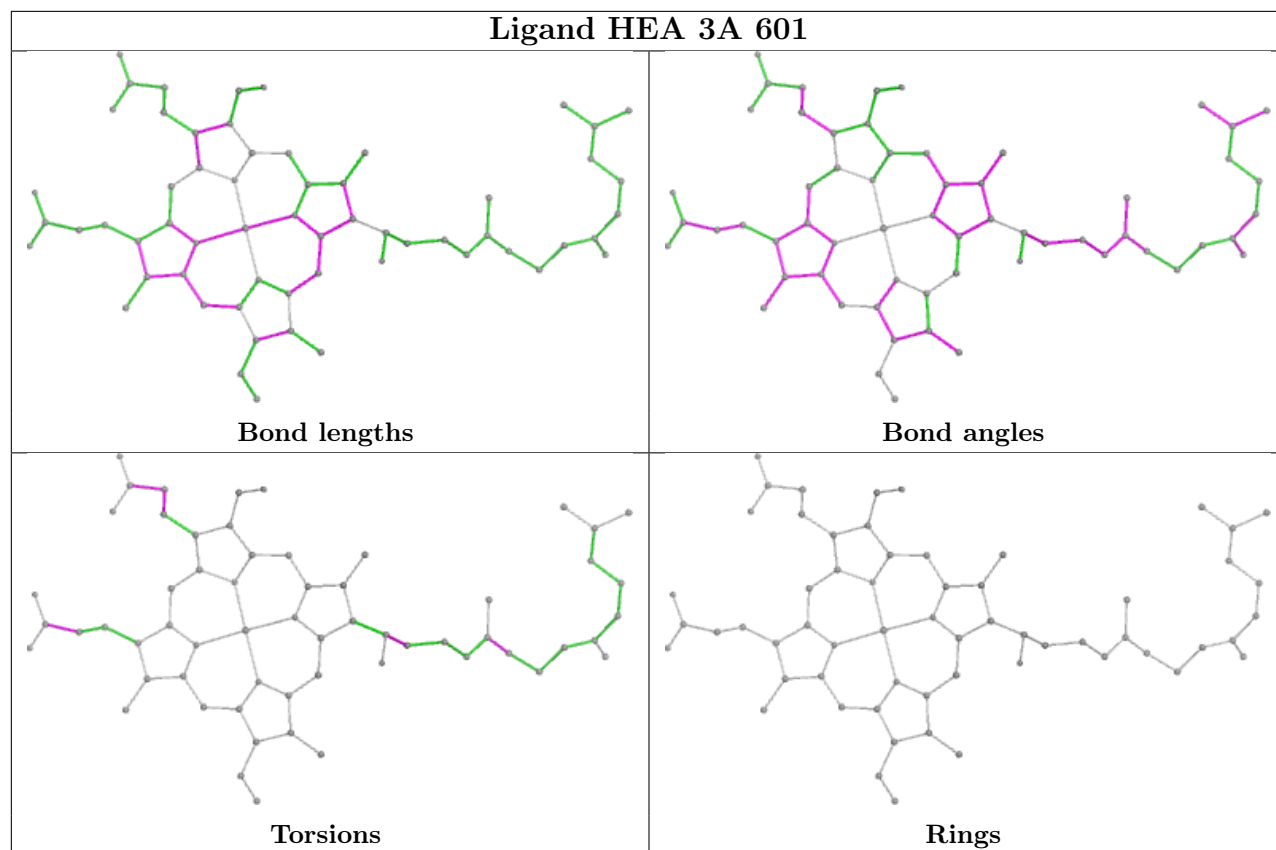
Mol	Chain	Res	Type	Clashes	Symm-Clashes
16	3A	605	PC7	2	0
13	3A	601	HEA	1	0
19	3D	301	PTY	2	0

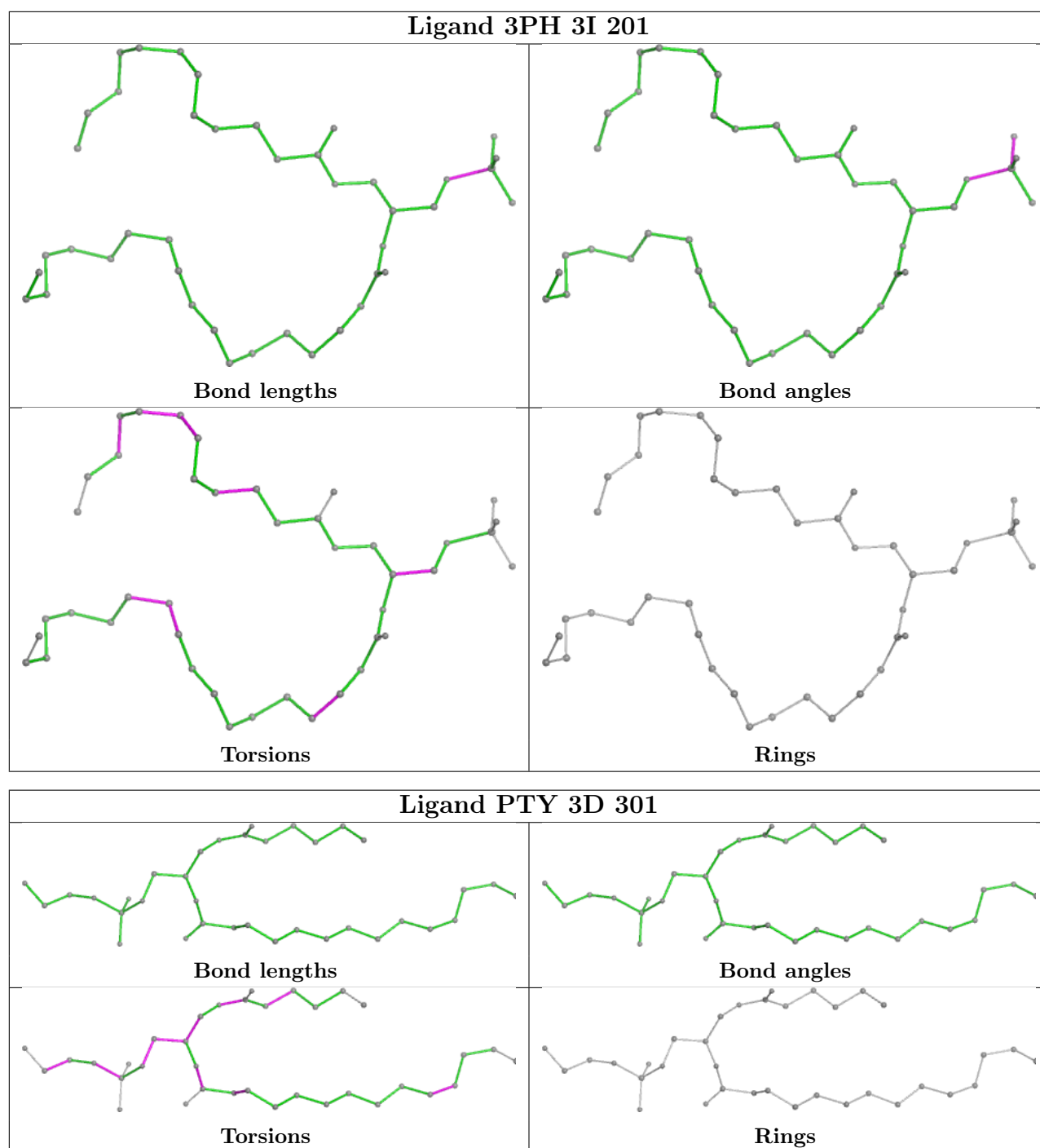
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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











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.

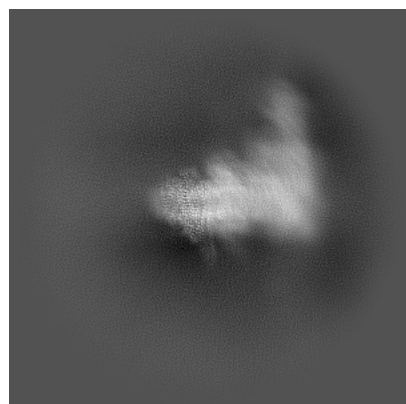
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-50206. These allow visual inspection of the internal detail of the map and identification of artifacts.

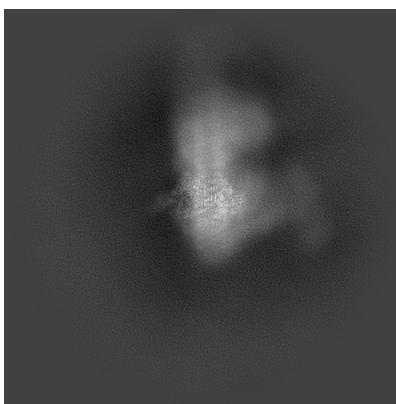
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

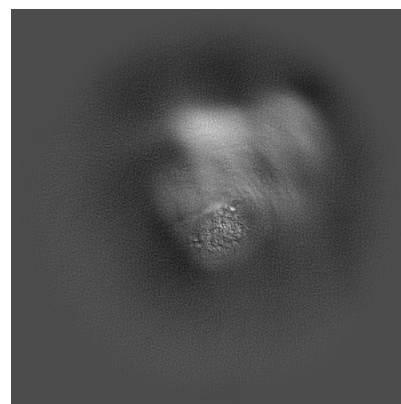
6.1.1 Primary map



X

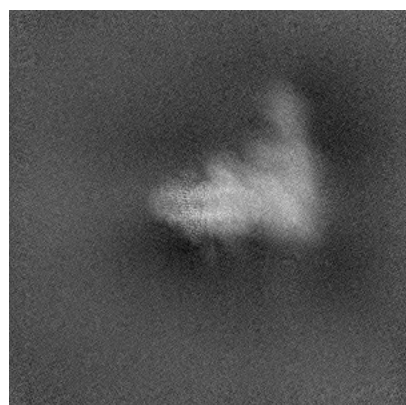


Y

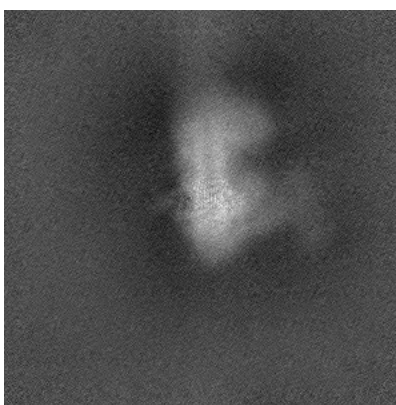


Z

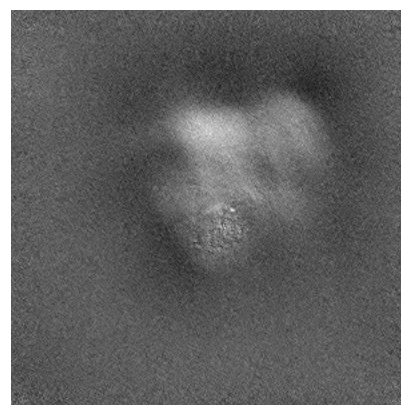
6.1.2 Raw map



X



Y

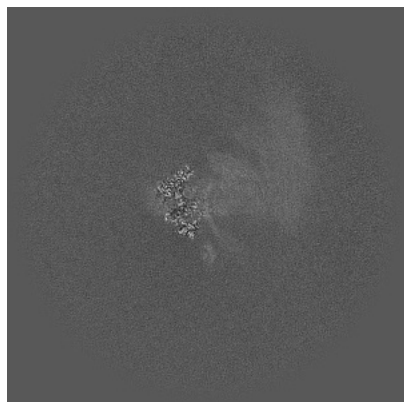


Z

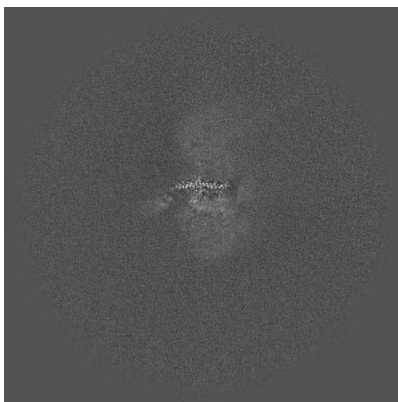
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

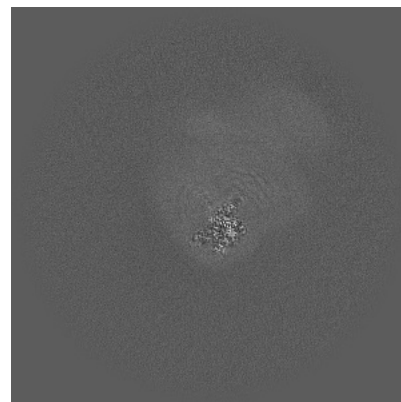
6.2.1 Primary map



X Index: 294

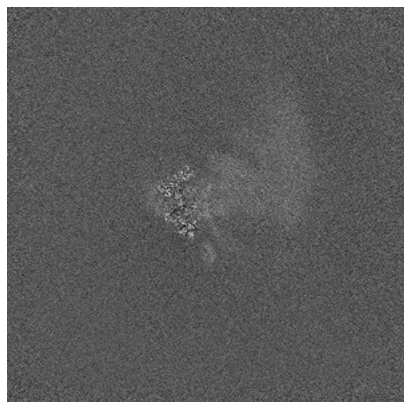


Y Index: 294



Z Index: 294

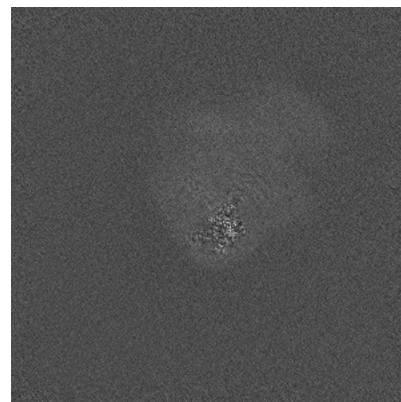
6.2.2 Raw map



X Index: 294



Y Index: 294

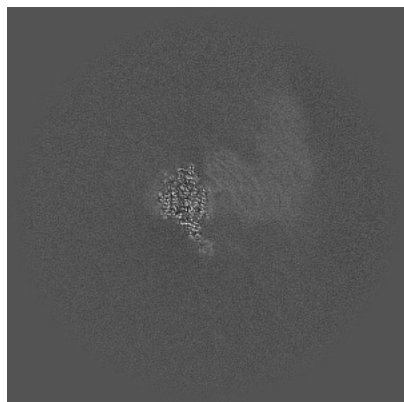


Z Index: 294

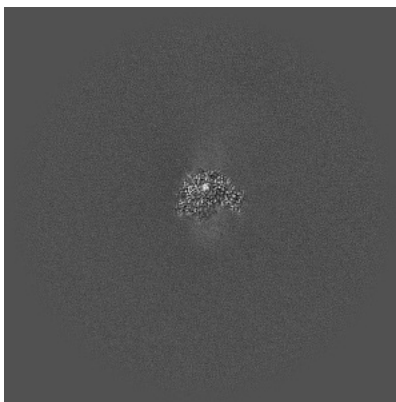
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

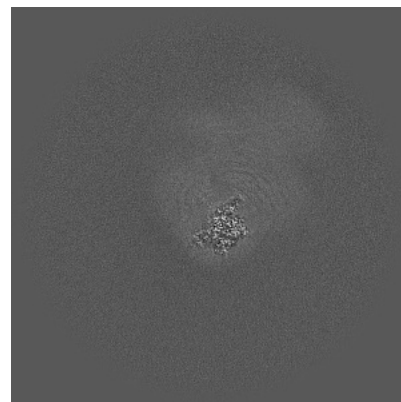
6.3.1 Primary map



X Index: 307

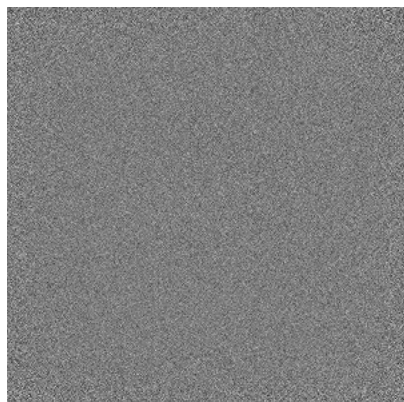


Y Index: 260

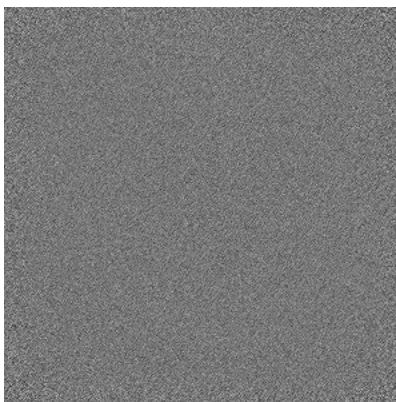


Z Index: 290

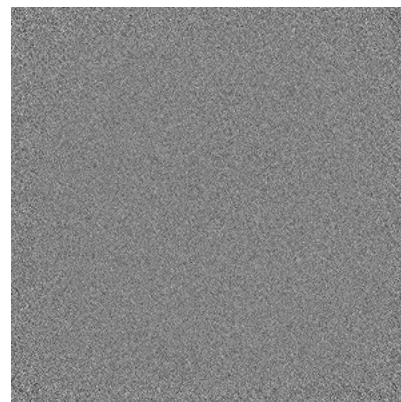
6.3.2 Raw map



X Index: 0



Y Index: 0

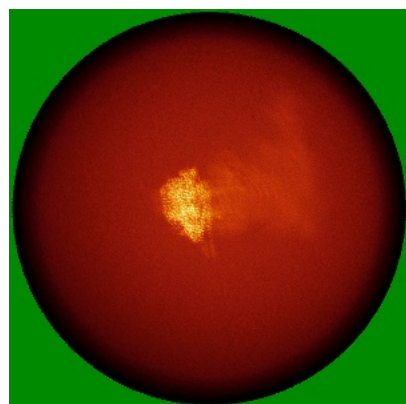


Z Index: 0

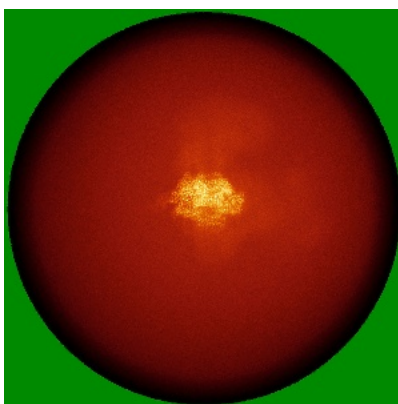
The images above show the largest variance slices of the map in three orthogonal directions.

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

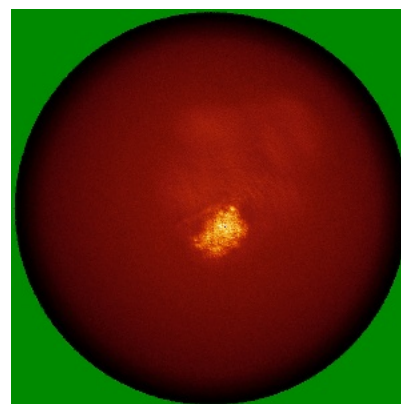
6.4.1 Primary map



X

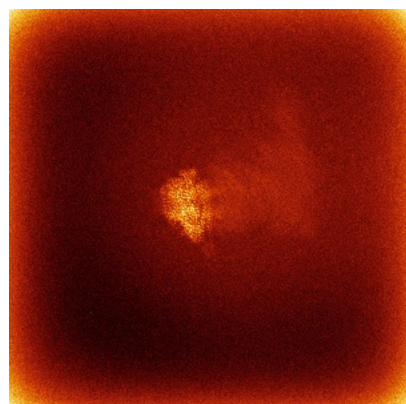


Y

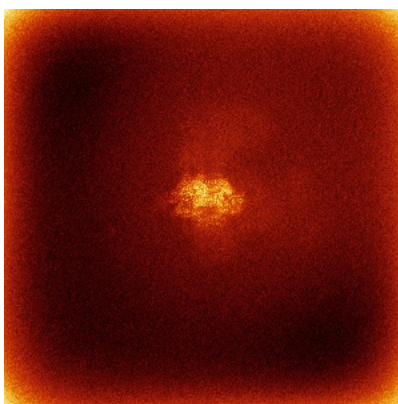


Z

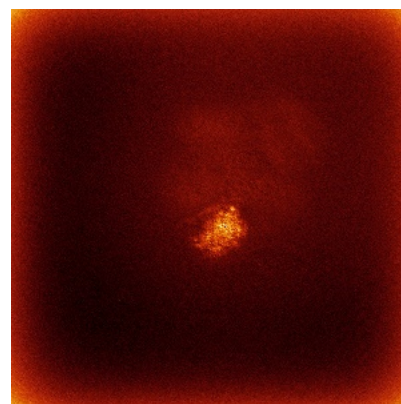
6.4.2 Raw map



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.

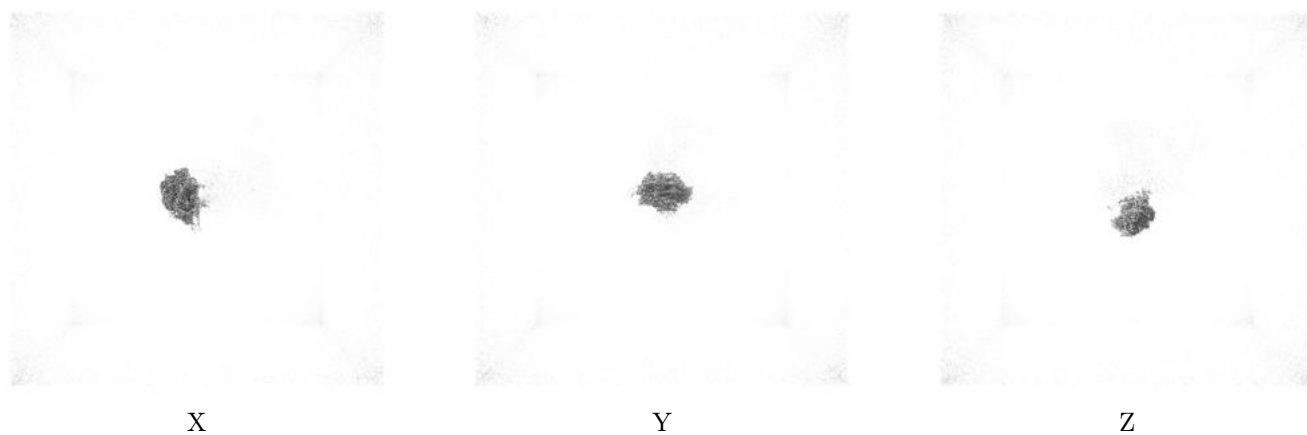
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.127. 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.

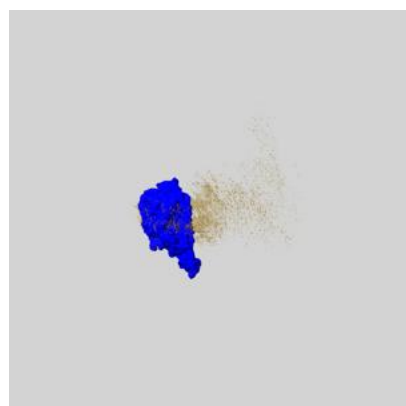
6.6 Mask visualisation [i](#)

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

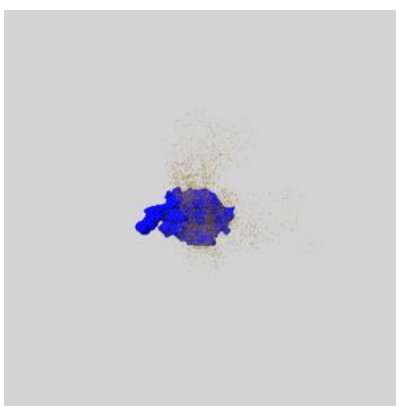
A mask typically either:

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

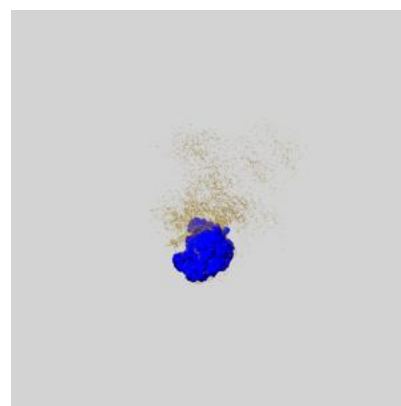
6.6.1 emd_50206_msk_1.map [i](#)



X



Y

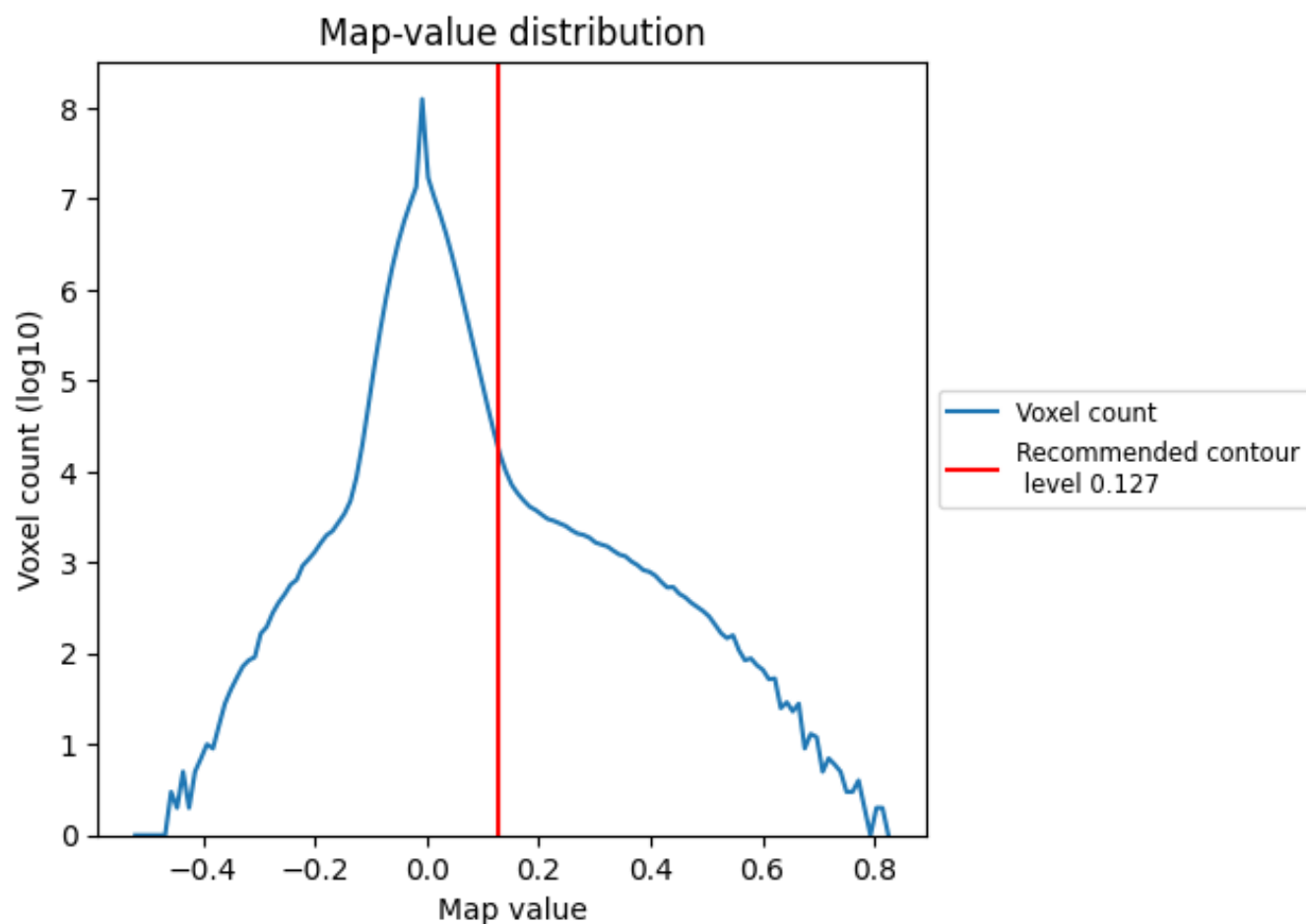


Z

7 Map analysis [i](#)

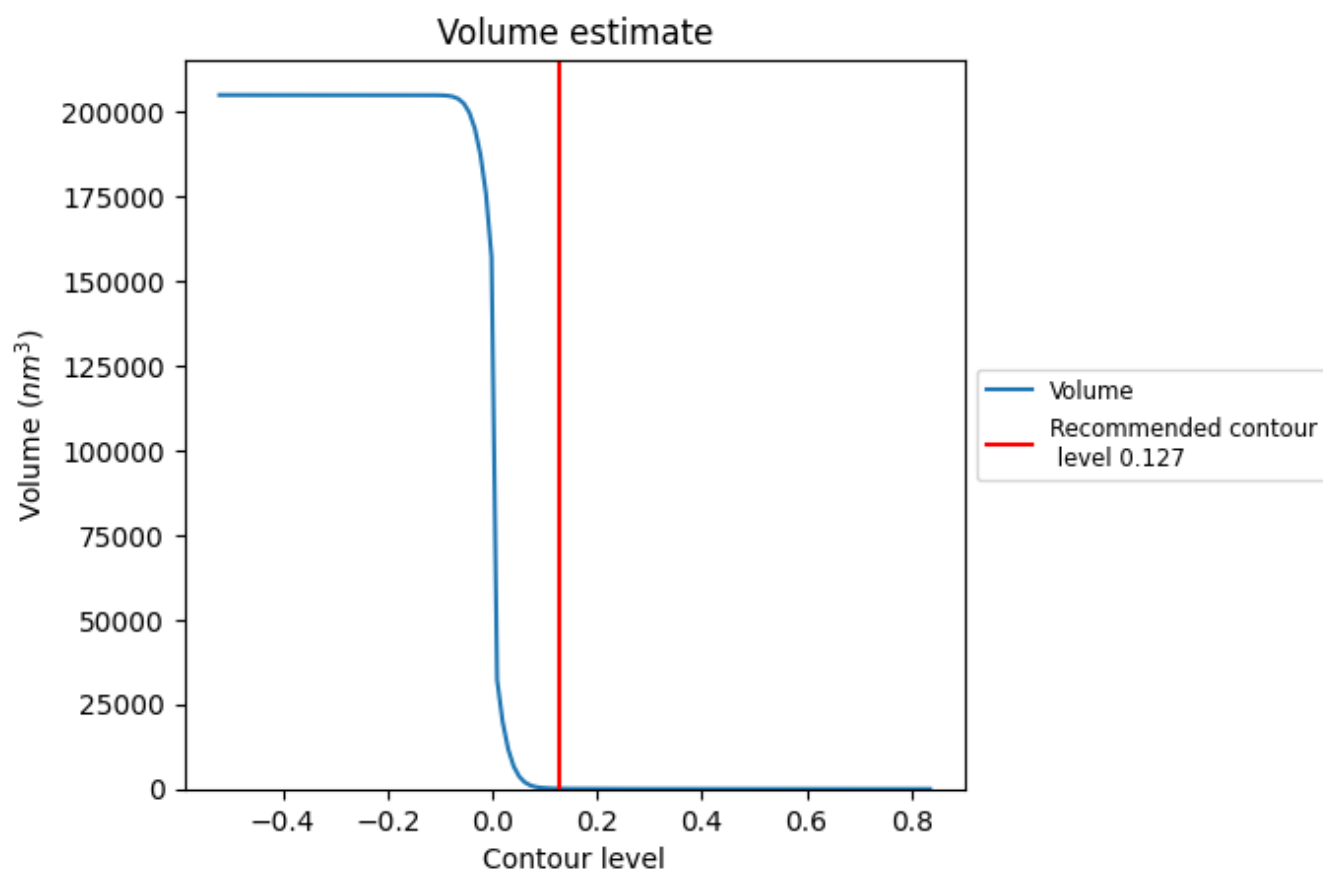
This section contains the results of statistical analysis of the map.

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.

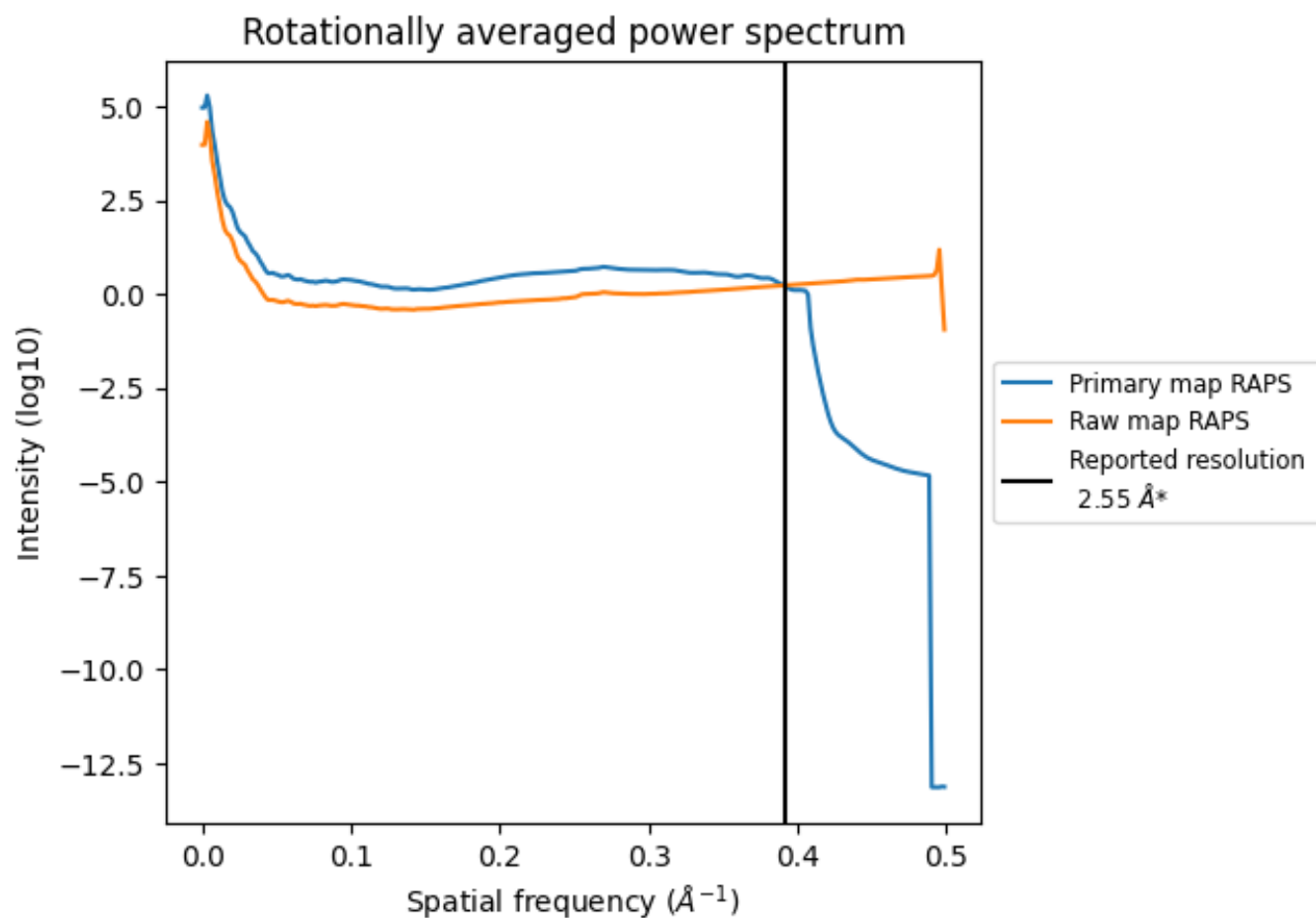
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 101 nm³; this corresponds to an approximate mass of 91 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 ⓘ

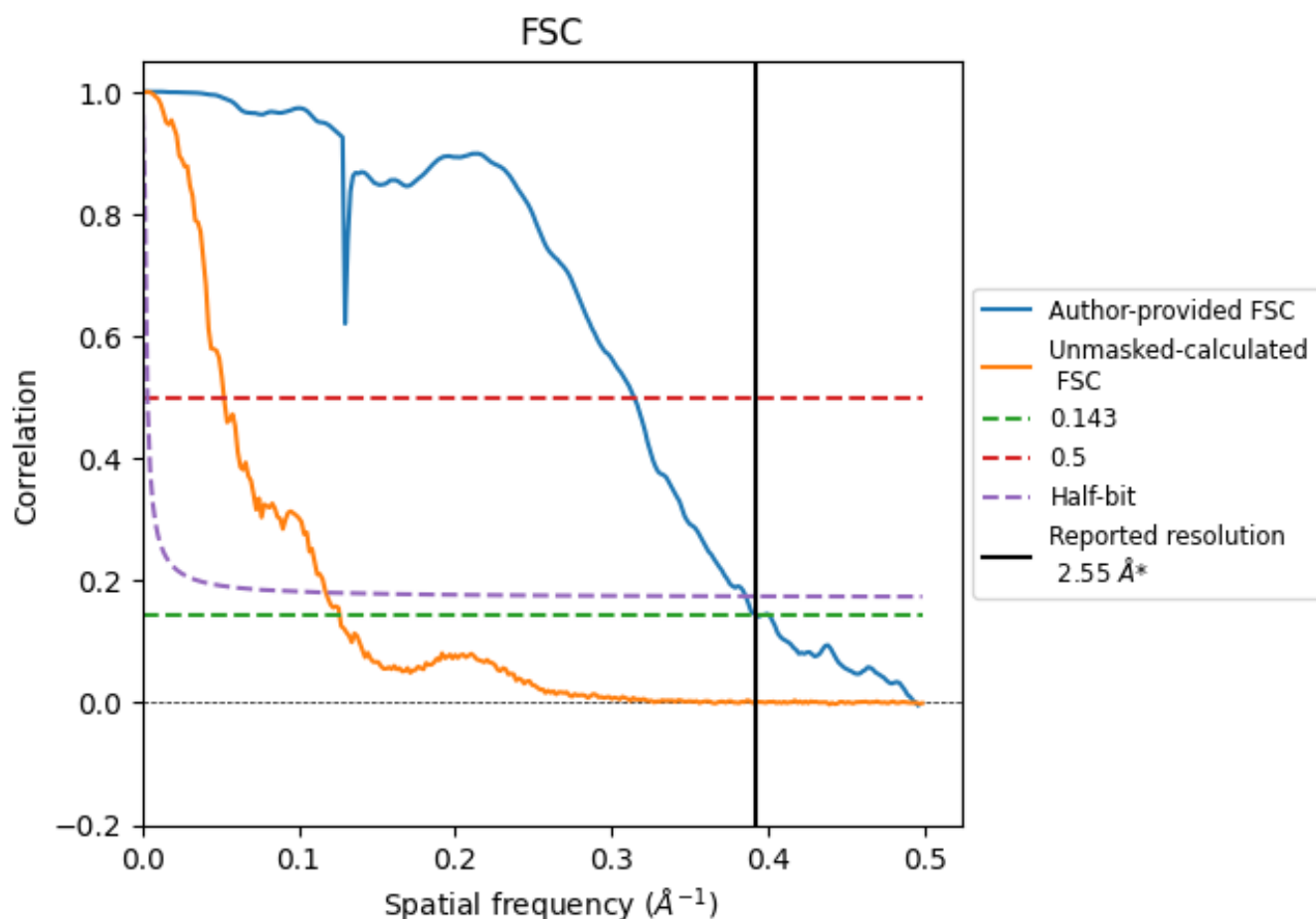


*Reported resolution corresponds to spatial frequency of 0.392 \AA^{-1}

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 0.392 \AA^{-1}

8.2 Resolution estimates [i](#)

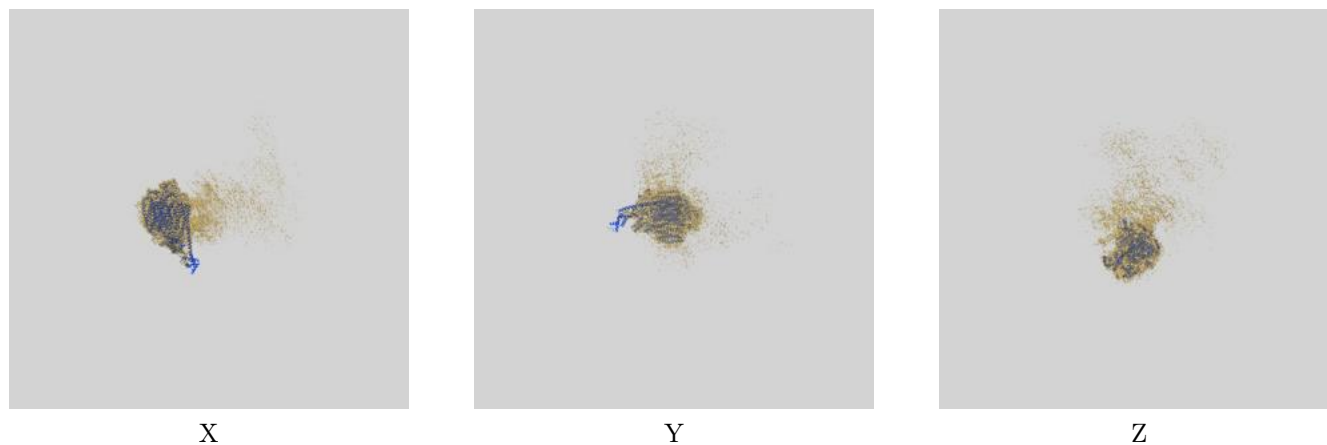
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.55	-	-
Author-provided FSC curve	2.55	3.18	2.59
Unmasked-calculated*	7.92	19.16	8.51

*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 7.92 differs from the reported value 2.55 by more than 10 %

9 Map-model fit [i](#)

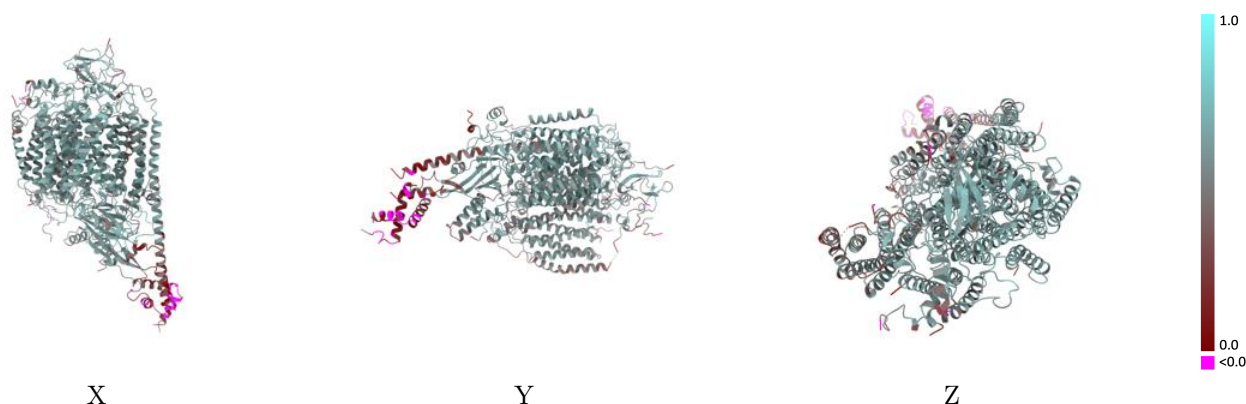
This section contains information regarding the fit between EMDB map EMD-50206 and PDB model 9F61. Per-residue inclusion information can be found in section 3 on page 10.

9.1 Map-model overlay [i](#)



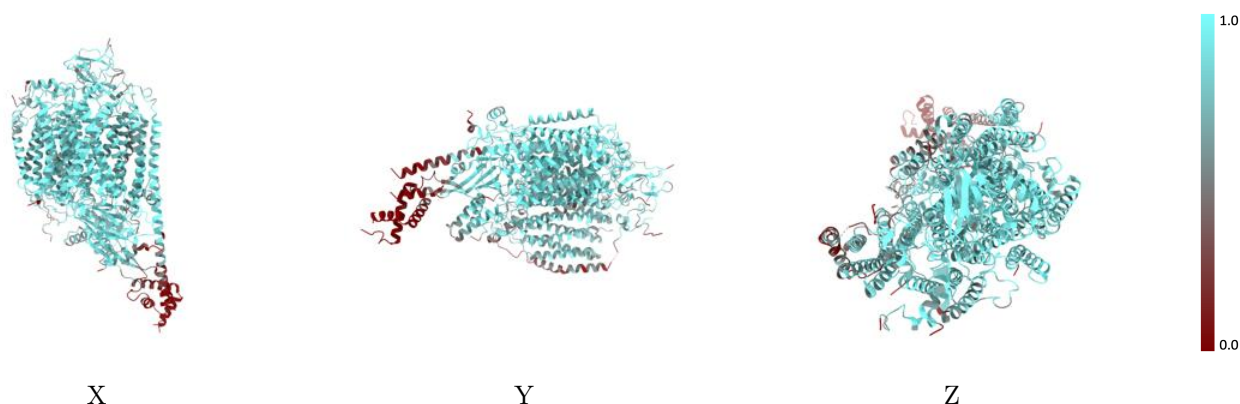
The images above show the 3D surface view of the map at the recommended contour level 0.127 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



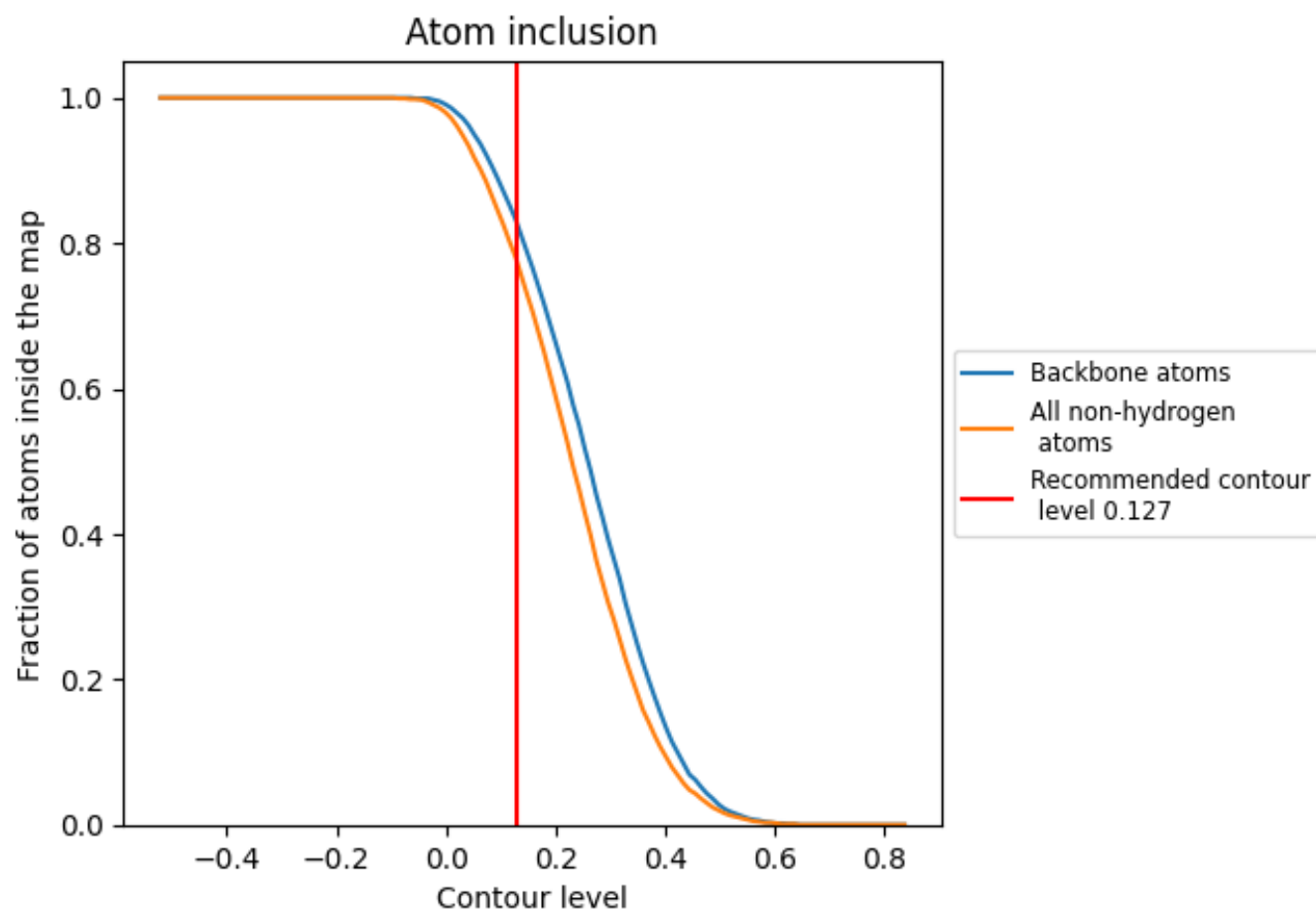
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.127).

9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 78% 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 (0.127) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.7800	<div></div> 0.5320
3A	<div></div> 0.9110	<div></div> 0.6020
3B	<div></div> 0.7710	<div></div> 0.5270
3C	<div></div> 0.7140	<div></div> 0.4890
3D	<div></div> 0.8340	<div></div> 0.5570
3E	<div></div> 0.7500	<div></div> 0.5220
3F	<div></div> 0.6600	<div></div> 0.4480
3G	<div></div> 0.5750	<div></div> 0.4520
3H	<div></div> 0.5280	<div></div> 0.3930
3I	<div></div> 0.7720	<div></div> 0.5480
3J	<div></div> 0.8340	<div></div> 0.5600
3K	<div></div> 0.7680	<div></div> 0.5140
3L	<div></div> 0.6220	<div></div> 0.4520

1.0

0.0

<0.0