



Full wwPDB EM Validation Report ⓘ

Mar 6, 2026 – 08:52 AM UTC

PDB ID : 7U8G / pdb_00007u8g
EMDB ID : EMD-26383
Title : Cryo-EM structure of the core human NADPH oxidase NOX2
Authors : Noreng, S.; Ota, N.; Sun, Y.; Masureel, M.; Payandeh, J.; Yi, T.; Koerber, J.T.
Deposited on : 2022-03-08
Resolution : 3.20 Å(reported)

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

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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

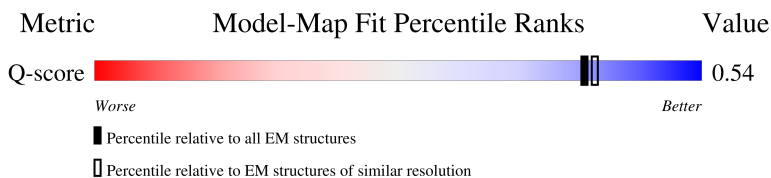
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 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	15020 (2.70 - 3.70)

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	864	 26% 70%
2	B	195	 58% 9% 32%
3	D	225	 51% 47%
4	E	217	 46% 5% 49%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 10108 atoms, of which 5062 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 EGFP, Cytochrome b-245 heavy chain chimera.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	260	Total	C	H	N	O	S	0	0
			4247	1387	2145	358	344	13		

There are 57 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-293	MET	-	initiating methionine	UNP A0A6M5E0N3
A	-292	SER	-	expression tag	UNP A0A6M5E0N3
A	-291	ALA	-	expression tag	UNP A0A6M5E0N3
A	-290	TRP	-	expression tag	UNP A0A6M5E0N3
A	-289	SER	-	expression tag	UNP A0A6M5E0N3
A	-288	HIS	-	expression tag	UNP A0A6M5E0N3
A	-287	PRO	-	expression tag	UNP A0A6M5E0N3
A	-286	GLN	-	expression tag	UNP A0A6M5E0N3
A	-285	PHE	-	expression tag	UNP A0A6M5E0N3
A	-284	GLU	-	expression tag	UNP A0A6M5E0N3
A	-283	LYS	-	expression tag	UNP A0A6M5E0N3
A	-282	GLY	-	expression tag	UNP A0A6M5E0N3
A	-281	GLY	-	expression tag	UNP A0A6M5E0N3
A	-280	GLY	-	expression tag	UNP A0A6M5E0N3
A	-279	SER	-	expression tag	UNP A0A6M5E0N3
A	-278	GLY	-	expression tag	UNP A0A6M5E0N3
A	-277	GLY	-	expression tag	UNP A0A6M5E0N3
A	-276	GLY	-	expression tag	UNP A0A6M5E0N3
A	-275	SER	-	expression tag	UNP A0A6M5E0N3
A	-274	GLY	-	expression tag	UNP A0A6M5E0N3
A	-273	GLY	-	expression tag	UNP A0A6M5E0N3
A	-272	SER	-	expression tag	UNP A0A6M5E0N3
A	-271	ALA	-	expression tag	UNP A0A6M5E0N3
A	-270	TRP	-	expression tag	UNP A0A6M5E0N3
A	-269	SER	-	expression tag	UNP A0A6M5E0N3
A	-268	HIS	-	expression tag	UNP A0A6M5E0N3
A	-267	PRO	-	expression tag	UNP A0A6M5E0N3
A	-266	GLN	-	expression tag	UNP A0A6M5E0N3

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-265	PHE	-	expression tag	UNP A0A6M5E0N3
A	-264	GLU	-	expression tag	UNP A0A6M5E0N3
A	-263	LYS	-	expression tag	UNP A0A6M5E0N3
A	-262	GLY	-	expression tag	UNP A0A6M5E0N3
A	-261	SER	-	expression tag	UNP A0A6M5E0N3
A	-260	GLY	-	expression tag	UNP A0A6M5E0N3
A	-75	GLN	HIS	conflict	UNP A0A6M5E0N3
A	-20	GLY	-	linker	UNP A0A6M5E0N3
A	-19	SER	-	linker	UNP A0A6M5E0N3
A	-18	GLY	-	linker	UNP A0A6M5E0N3
A	-17	GLU	-	linker	UNP A0A6M5E0N3
A	-16	ASN	-	linker	UNP A0A6M5E0N3
A	-15	LEU	-	linker	UNP A0A6M5E0N3
A	-14	TYR	-	linker	UNP A0A6M5E0N3
A	-13	PHE	-	linker	UNP A0A6M5E0N3
A	-12	GLN	-	linker	UNP A0A6M5E0N3
A	-11	GLY	-	linker	UNP A0A6M5E0N3
A	-10	GLY	-	linker	UNP A0A6M5E0N3
A	-9	SER	-	linker	UNP A0A6M5E0N3
A	-8	GLY	-	linker	UNP A0A6M5E0N3
A	-7	LEU	-	linker	UNP A0A6M5E0N3
A	-6	VAL	-	linker	UNP A0A6M5E0N3
A	-5	PRO	-	linker	UNP A0A6M5E0N3
A	-4	ARG	-	linker	UNP A0A6M5E0N3
A	-3	GLY	-	linker	UNP A0A6M5E0N3
A	-2	SER	-	linker	UNP A0A6M5E0N3
A	-1	GLY	-	linker	UNP A0A6M5E0N3
A	0	SER	-	linker	UNP A0A6M5E0N3
A	1	GLY	-	linker	UNP A0A6M5E0N3

- Molecule 2 is a protein called Cytochrome b-245 light chain.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	B	132	Total	C	H	N	O	S	0	0
			2081	679	1055	171	171	5		

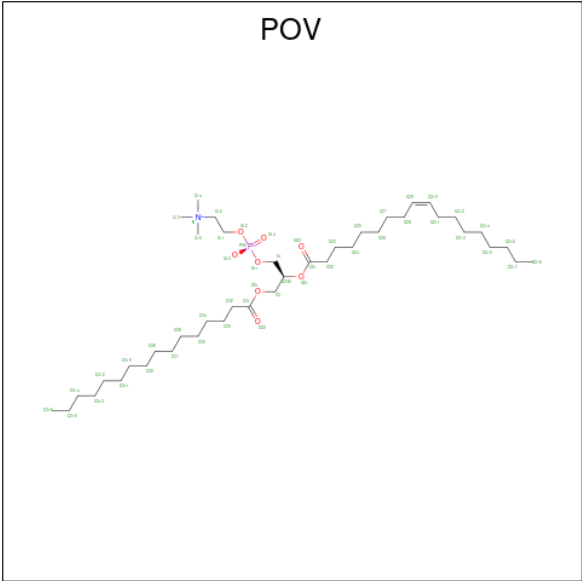
- Molecule 3 is a protein called 7G5 - heavy chain.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	D	119	Total	C	H	N	O	S	0	0
			1738	562	847	148	175	6		

- Molecule 4 is a protein called 7G5 - light chain.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
4	E	110	1640	520	814	138	165	3	0	0

- Molecule 5 is (2S)-3-(hexadecanoyloxy)-2-[(9Z)-octadec-9-enoyloxy]propyl 2-(trimethylammonio)ethyl phosphate (CCD ID: POV) (formula: C₄₂H₈₂NO₈P) (labeled as "Ligand of Interest" by depositor).



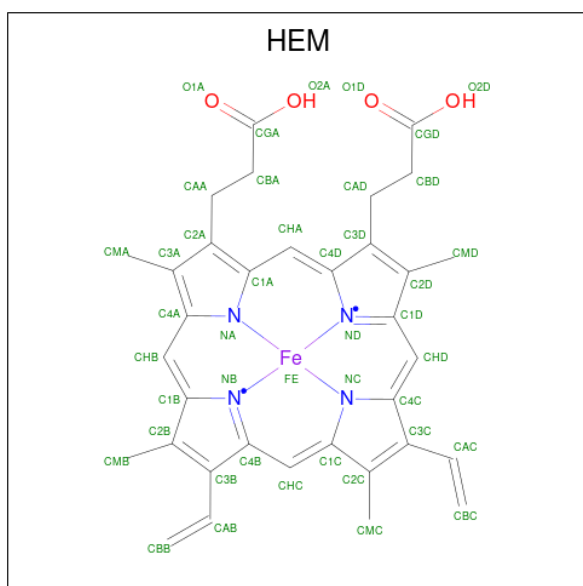
Mol	Chain	Residues	Atoms						AltConf
			Total	C	H	N	O	P	
5	A	1	68	20	40	1	6	1	0
5	A	1	62	19	36		6	1	0
5	B	1	42	13	23		5	1	0

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



Mol	Chain	Residues	Atoms					AltConf
6	A	1	Total	C	H	N	O	0
			28	8	14	1	5	
6	A	1	Total	C	H	N	O	0
			28	8	14	1	5	
6	A	1	Total	C	H	N	O	0
			28	8	14	1	5	

- Molecule 7 is PROTOPORPHYRIN IX CONTAINING FE (CCD ID: HEM) (formula: $C_{34}H_{32}FeN_4O_4$) (labeled as "Ligand of Interest" by depositor).

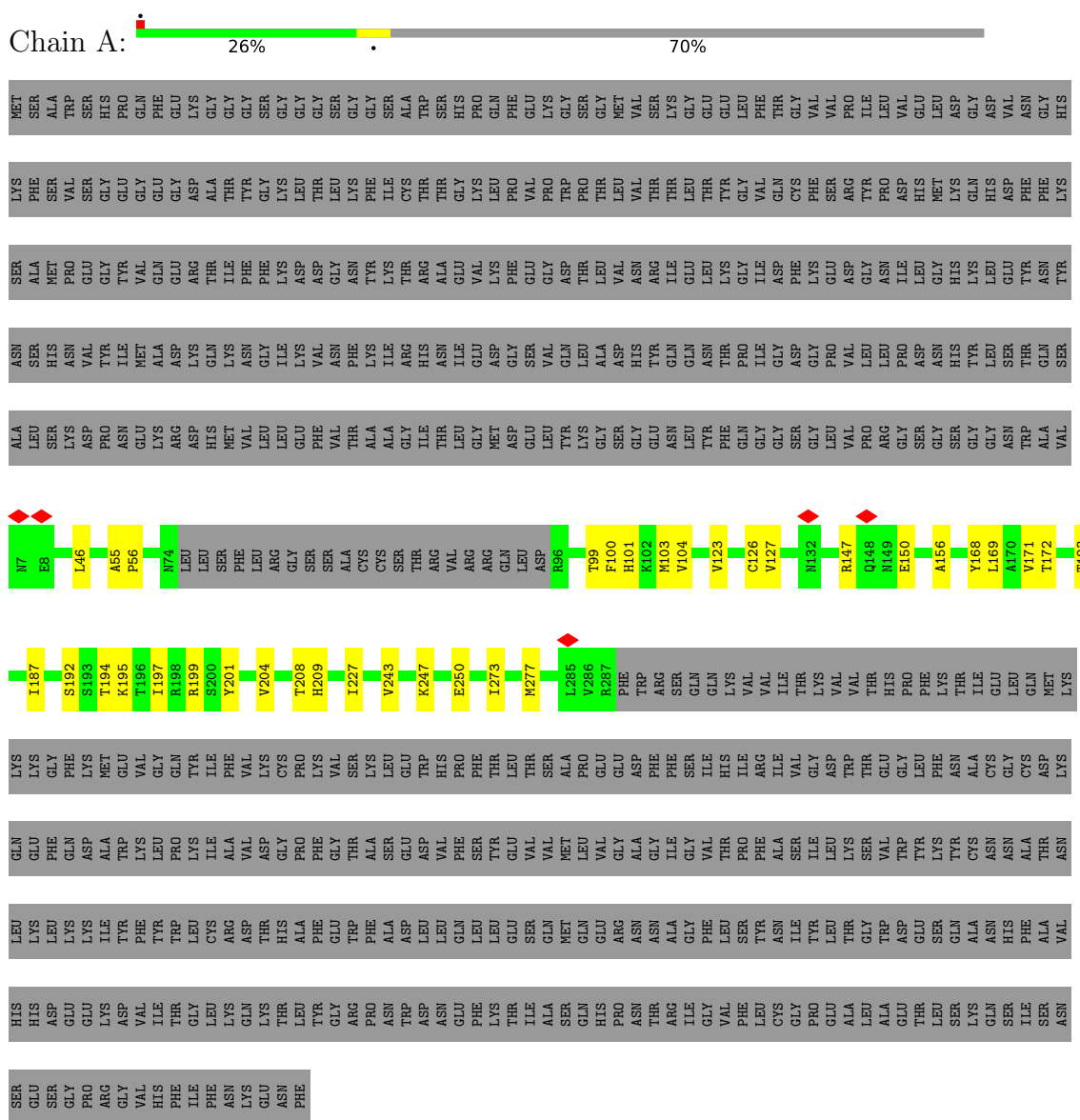


Mol	Chain	Residues	Atoms						AltConf
7	A	1	Total	C	Fe	H	N	O	0
			73	34	1	30	4	4	
7	A	1	Total	C	Fe	H	N	O	0
			73	34	1	30	4	4	

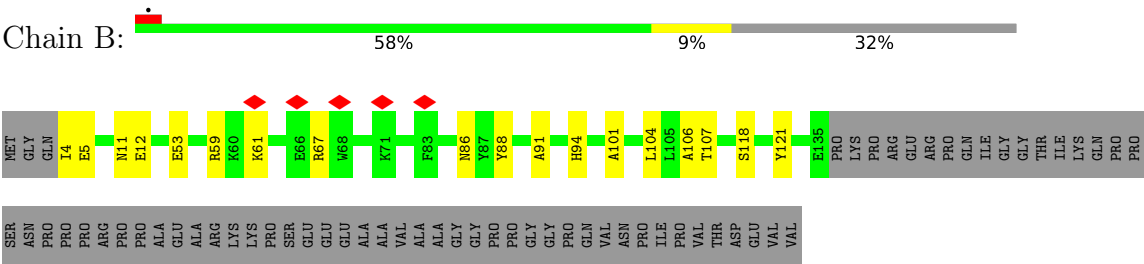
3 Residue-property plots

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

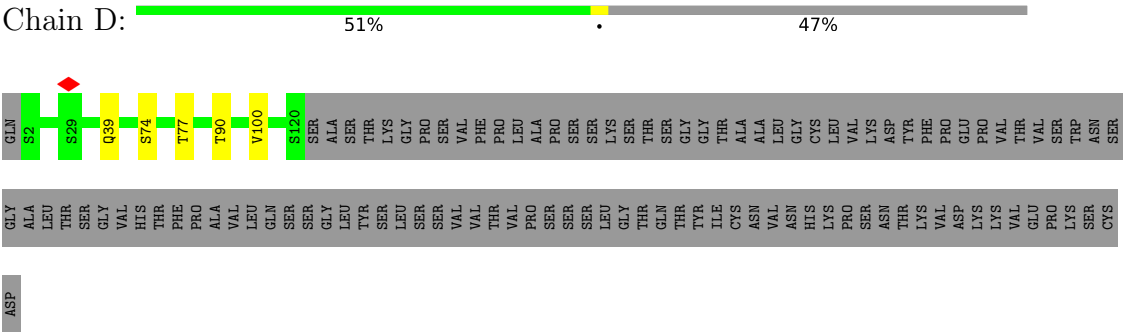
- Molecule 1: EGFP, Cytochrome b-245 heavy chain chimera



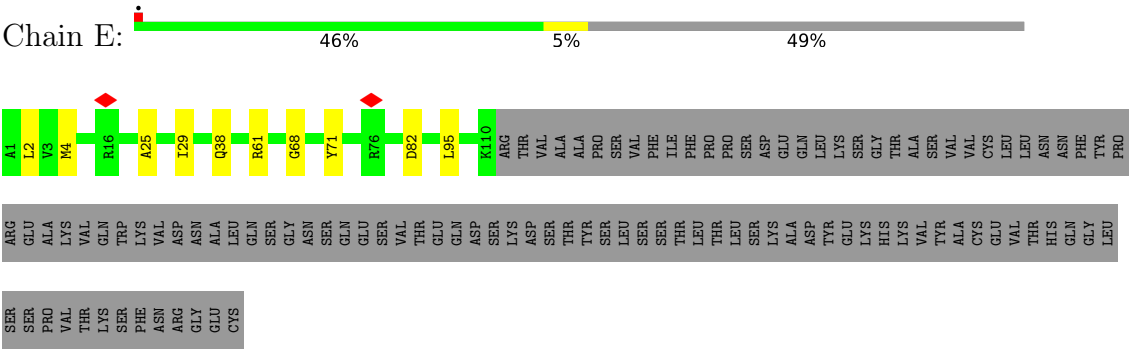
- Molecule 2: Cytochrome b-245 light chain



• Molecule 3: 7G5 - heavy chain



• Molecule 4: 7G5 - light chain



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	70486	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40.4	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	1.085	Depositor
Minimum map value	-0.611	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.017	Depositor
Recommended contour level	0.13	Depositor
Map size ($\text{\AA}$)	280.704, 280.704, 280.704	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.731, 0.731, 0.731	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NAG, POV, HEM

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	0/2161	0.32	0/2941
2	B	0.13	0/1053	0.24	0/1432
3	D	0.13	0/914	0.22	0/1243
4	E	0.14	0/842	0.26	0/1143
All	All	0.14	0/4970	0.28	0/6759

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2102	2145	2143	31	0
2	B	1026	1055	1054	14	0
3	D	891	847	846	4	0
4	E	826	814	814	7	0
5	A	54	76	72	2	0
5	B	19	23	20	0	0
6	A	42	42	39	0	0
7	A	86	60	60	9	0
All	All	5046	5062	5048	57	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.

All (57) 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:A:606:HEM:HMC1	7:A:606:HEM:HBC2	1.57	0.85
1:A:273:ILE:HG22	1:A:277:MET:HE2	1.63	0.80
7:A:607:HEM:HBC2	7:A:607:HEM:HHD	1.64	0.79
1:A:183:THR:O	1:A:187:ILE:HD12	1.87	0.74
1:A:201:TYR:OH	2:B:59:ARG:NH1	2.25	0.70
7:A:606:HEM:HBB2	7:A:606:HEM:HHC	1.80	0.64
1:A:147:ARG:NE	1:A:150:GLU:OE2	2.35	0.60
1:A:156:ALA:HB2	1:A:169:LEU:HD11	1.84	0.59
1:A:204:VAL:O	1:A:208:THR:HG22	2.04	0.57
7:A:607:HEM:HBB2	7:A:607:HEM:HMB2	1.86	0.56
3:D:39:GLN:OE1	4:E:38:GLN:NE2	2.38	0.56
1:A:273:ILE:CG2	1:A:277:MET:HE2	2.37	0.55
2:B:101:ALA:O	2:B:107:THR:OG1	2.16	0.53
3:D:74:SER:HB2	3:D:77:THR:HG22	1.88	0.53
1:A:100:PHE:O	1:A:104:VAL:HG23	2.08	0.53
1:A:168:TYR:O	1:A:172:THR:OG1	2.26	0.53
7:A:606:HEM:HBC2	7:A:606:HEM:CMC	2.32	0.52
1:A:209:HIS:NE2	7:A:606:HEM:NA	2.57	0.52
4:E:68:GLY:O	4:E:71:TYR:OH	2.22	0.51
4:E:2:LEU:HD21	4:E:29:ILE:CG2	2.40	0.51
7:A:607:HEM:HBB2	7:A:607:HEM:CMB	2.41	0.50
1:A:101:HIS:CD2	7:A:606:HEM:ND	2.80	0.50
1:A:123:VAL:O	1:A:127:VAL:HG23	2.11	0.50
1:A:99:THR:O	1:A:103:MET:HG3	2.12	0.49
2:B:91:ALA:O	2:B:118:SER:OG	2.29	0.49
1:A:250:GLU:OE2	3:D:100:VAL:HG21	2.12	0.49
2:B:59:ARG:NH2	2:B:61:LYS:O	2.45	0.49
2:B:104:LEU:HD23	2:B:106:ALA:H	1.78	0.48
2:B:11:ASN:ND2	2:B:53:GLU:O	2.46	0.47
2:B:11:ASN:OD1	2:B:67:ARG:NH2	2.40	0.47
1:A:194:THR:HG22	1:A:195:LYS:H	1.80	0.47
1:A:123:VAL:HG13	1:A:169:LEU:HD12	1.97	0.47
1:A:171:VAL:HG22	1:A:171:VAL:O	2.15	0.47
1:A:195:LYS:HG3	1:A:199:ARG:HH21	1.81	0.46
4:E:29:ILE:O	4:E:71:TYR:OH	2.34	0.46
4:E:4:MET:HE3	4:E:25:ALA:HB2	1.98	0.46
1:A:192:SER:HB2	1:A:208:THR:HG21	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:204:VAL:CG2	2:B:4:ILE:HD11	2.46	0.45
4:E:61:ARG:NH1	4:E:82:ASP:OD2	2.50	0.45
1:A:227:ILE:HD11	7:A:607:HEM:HMA3	2.01	0.43
2:B:59:ARG:HH11	2:B:59:ARG:HG2	1.84	0.43
3:D:90:THR:O	3:D:90:THR:HG23	2.18	0.43
1:A:194:THR:HG21	2:B:12:GLU:OE2	2.19	0.43
1:A:55:ALA:HB3	1:A:56:PRO:HD3	2.00	0.42
1:A:194:THR:HG22	1:A:195:LYS:N	2.35	0.42
1:A:192:SER:CB	1:A:208:THR:HG21	2.49	0.42
1:A:201:TYR:OH	2:B:5:GLU:HB2	2.20	0.41
5:A:601:POV:H15B	5:A:601:POV:O12	2.21	0.41
1:A:46:LEU:HD21	1:A:126:CYS:SG	2.61	0.41
2:B:53:GLU:OE1	2:B:94:HIS:CE1	2.73	0.41
1:A:197:ILE:HD12	1:A:197:ILE:H	1.86	0.41
1:A:183:THR:O	1:A:187:ILE:CD1	2.65	0.41
2:B:86:ASN:OD1	2:B:88:TYR:N	2.53	0.41
4:E:95:LEU:N	4:E:95:LEU:HD12	2.36	0.41
1:A:187:ILE:HD11	5:A:602:POV:H310	2.03	0.40
1:A:243:VAL:O	1:A:247:LYS:NZ	2.44	0.40
2:B:53:GLU:OE1	2:B:121:TYR:OH	2.37	0.40

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	256/864 (30%)	251 (98%)	5 (2%)	0	100	100
2	B	130/195 (67%)	129 (99%)	1 (1%)	0	100	100
3	D	117/225 (52%)	113 (97%)	4 (3%)	0	100	100
4	E	108/217 (50%)	103 (95%)	5 (5%)	0	100	100
All	All	611/1501 (41%)	596 (98%)	15 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	226/742 (30%)	226 (100%)	0	100	100
2	B	101/151 (67%)	101 (100%)	0	100	100
3	D	94/186 (50%)	94 (100%)	0	100	100
4	E	88/184 (48%)	88 (100%)	0	100	100
All	All	509/1263 (40%)	509 (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. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	7	ASN
1	A	74	ASN
2	B	35	GLN
2	B	94	HIS
3	D	39	GLN
3	D	81	GLN
4	E	38	GLN

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](#)

8 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
5	POV	A	601	-	27,27,51	1.29	2 (7%)	32,33,59	1.31	3 (9%)
6	NAG	A	604	1	14,14,15	0.22	0	17,19,21	0.44	0
6	NAG	A	603	1	14,14,15	0.23	0	17,19,21	1.16	3 (17%)
7	HEM	A	606	1	50,50,50	1.43	7 (14%)	67,82,82	1.18	4 (5%)
7	HEM	A	607	1	50,50,50	1.41	6 (12%)	67,82,82	1.15	4 (5%)
5	POV	B	201	-	15,18,51	1.30	1 (6%)	15,19,59	1.68	2 (13%)
5	POV	A	602	-	25,25,51	1.40	4 (16%)	28,28,59	1.53	3 (10%)
6	NAG	A	605	1	14,14,15	0.19	0	17,19,21	0.42	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
5	POV	A	601	-	-	5/28/28/55	-
6	NAG	A	604	1	-	2/6/23/26	0/1/1/1
6	NAG	A	603	1	-	1/6/23/26	0/1/1/1
7	HEM	A	606	1	-	3/14/54/54	-
7	HEM	A	607	1	-	1/14/54/54	-
5	POV	B	201	-	-	4/15/17/55	-
5	POV	A	602	-	-	7/24/24/55	-
6	NAG	A	605	1	-	2/6/23/26	0/1/1/1

All (20) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	A	606	HEM	FE-NB	3.79	2.06	1.94
7	A	606	HEM	FE-ND	3.52	2.05	1.94
7	A	607	HEM	FE-NB	3.35	2.05	1.94
5	A	602	POV	P-O12	3.27	1.67	1.54
7	A	607	HEM	FE-NA	3.25	2.05	1.95
5	A	601	POV	O31-C31	3.23	1.42	1.33
7	A	607	HEM	FE-ND	3.20	2.04	1.94
5	B	201	POV	O31-C31	3.14	1.42	1.33
5	A	602	POV	O31-C31	3.14	1.42	1.33
7	A	607	HEM	FE-NC	3.08	2.05	1.95
7	A	606	HEM	FE-NA	3.02	2.05	1.95
7	A	606	HEM	CAB-C3B	2.92	1.55	1.47
7	A	607	HEM	CAB-C3B	2.89	1.55	1.47
7	A	606	HEM	CAC-C3C	2.89	1.55	1.47
7	A	607	HEM	CAC-C3C	2.86	1.55	1.47
7	A	606	HEM	FE-NC	2.59	2.03	1.95
5	A	602	POV	P-O11	2.23	1.67	1.60
5	A	602	POV	P-O13	-2.17	1.46	1.54
5	A	601	POV	P-O11	2.09	1.67	1.59
7	A	606	HEM	C2A-C3A	-2.02	1.33	1.38

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	602	POV	C36-C35-C34	5.29	141.09	114.37
5	A	601	POV	C36-C35-C34	5.13	140.31	114.37
5	B	201	POV	C36-C35-C34	4.89	139.07	114.37
6	A	603	NAG	C6-C5-C4	2.97	120.31	113.02
7	A	606	HEM	C3B-C2B-C1B	2.90	108.59	106.41
5	B	201	POV	O31-C31-C32	2.66	119.94	111.83
5	A	601	POV	O31-C31-C32	2.61	119.78	111.83
5	A	602	POV	O31-C31-C32	2.59	119.72	111.83
6	A	603	NAG	O5-C5-C6	2.57	112.66	107.66
5	A	601	POV	O13-P-O14	-2.54	100.63	112.44
5	A	602	POV	O13-P-O14	-2.49	101.14	110.83
7	A	606	HEM	C3B-C4B-NB	-2.45	107.71	109.47
7	A	606	HEM	C1B-NB-C4B	2.40	108.05	105.21
7	A	607	HEM	C4D-ND-C1D	2.38	108.03	105.21
6	A	603	NAG	O5-C5-C4	2.23	116.25	110.83
7	A	606	HEM	C4D-ND-C1D	2.19	107.80	105.21
7	A	607	HEM	C3D-C4D-ND	-2.19	107.77	110.17
7	A	607	HEM	C2A-C1A-NA	-2.10	107.82	110.15

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	607	HEM	C1B-NB-C4B	2.06	107.64	105.21

There are no chirality outliers.

All (25) torsion outliers are listed below:

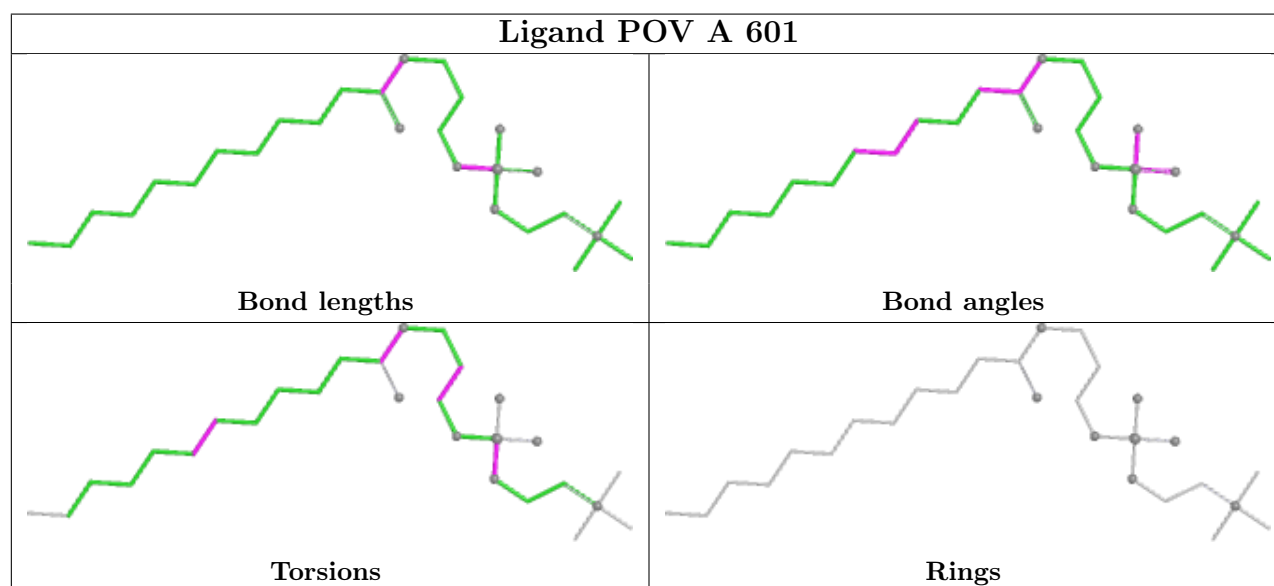
Mol	Chain	Res	Type	Atoms
6	A	604	NAG	O5-C5-C6-O6
6	A	603	NAG	O5-C5-C6-O6
6	A	604	NAG	C4-C5-C6-O6
5	A	601	POV	C32-C31-O31-C3
5	B	201	POV	C31-C32-C33-C34
5	A	601	POV	O32-C31-O31-C3
5	A	602	POV	C31-C32-C33-C34
5	A	602	POV	C32-C31-O31-C3
5	B	201	POV	C1-C2-C3-O31
5	A	602	POV	O32-C31-O31-C3
5	A	602	POV	C37-C38-C39-C310
5	A	601	POV	O11-C1-C2-C3
5	B	201	POV	C2-C1-O11-P
6	A	605	NAG	C1-C2-N2-C7
7	A	606	HEM	C4B-C3B-CAB-CBB
7	A	607	HEM	C4C-C3C-CAC-CBC
5	A	602	POV	C35-C36-C37-C38
5	B	201	POV	C36-C37-C38-C39
5	A	602	POV	O11-C1-C2-C3
5	A	601	POV	C11-O12-P-O13
5	A	601	POV	C35-C36-C37-C38
7	A	606	HEM	C4D-C3D-CAD-CBD
5	A	602	POV	C310-C311-C312-C313
7	A	606	HEM	C2D-C3D-CAD-CBD
6	A	605	NAG	C3-C2-N2-C7

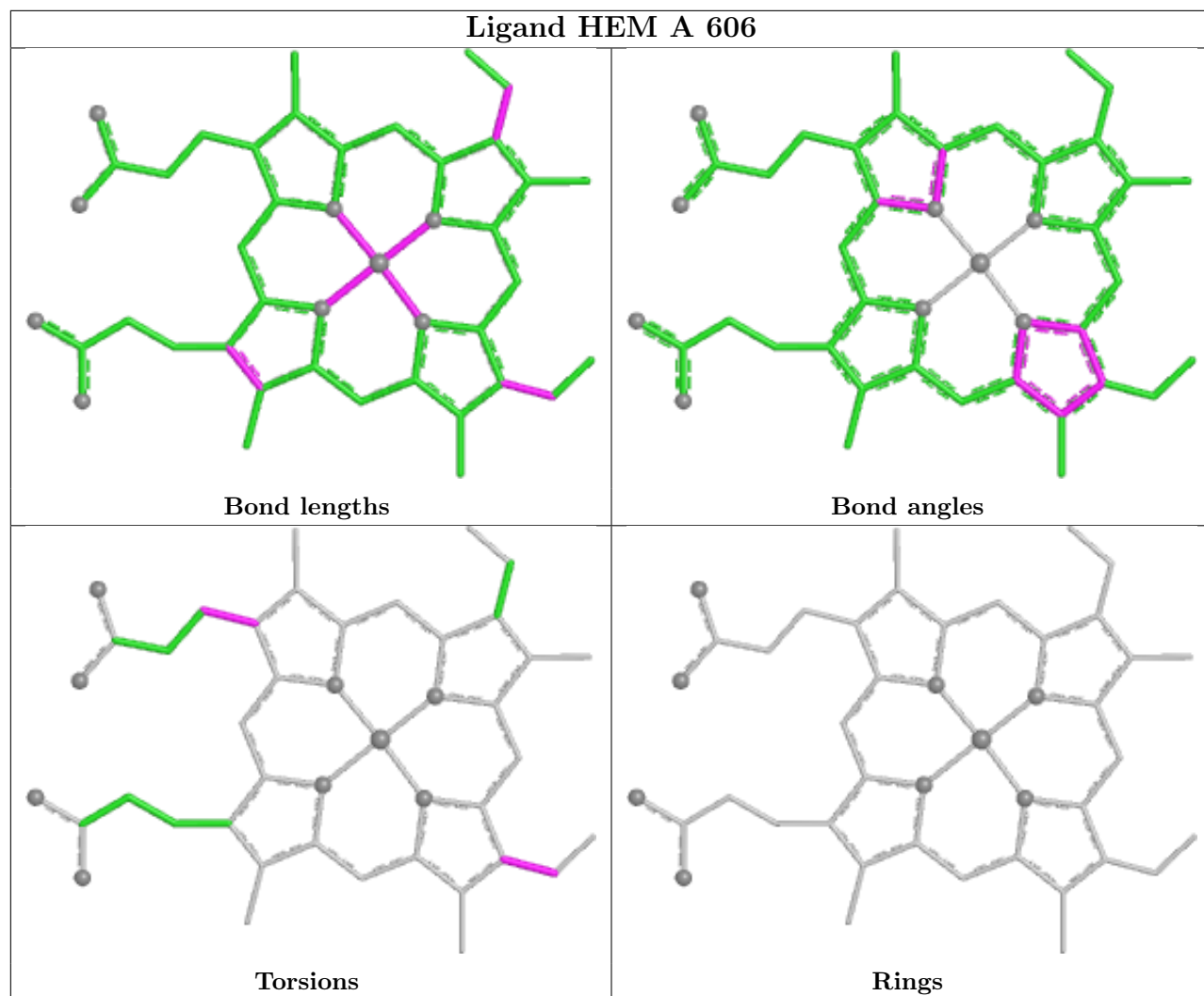
There are no ring outliers.

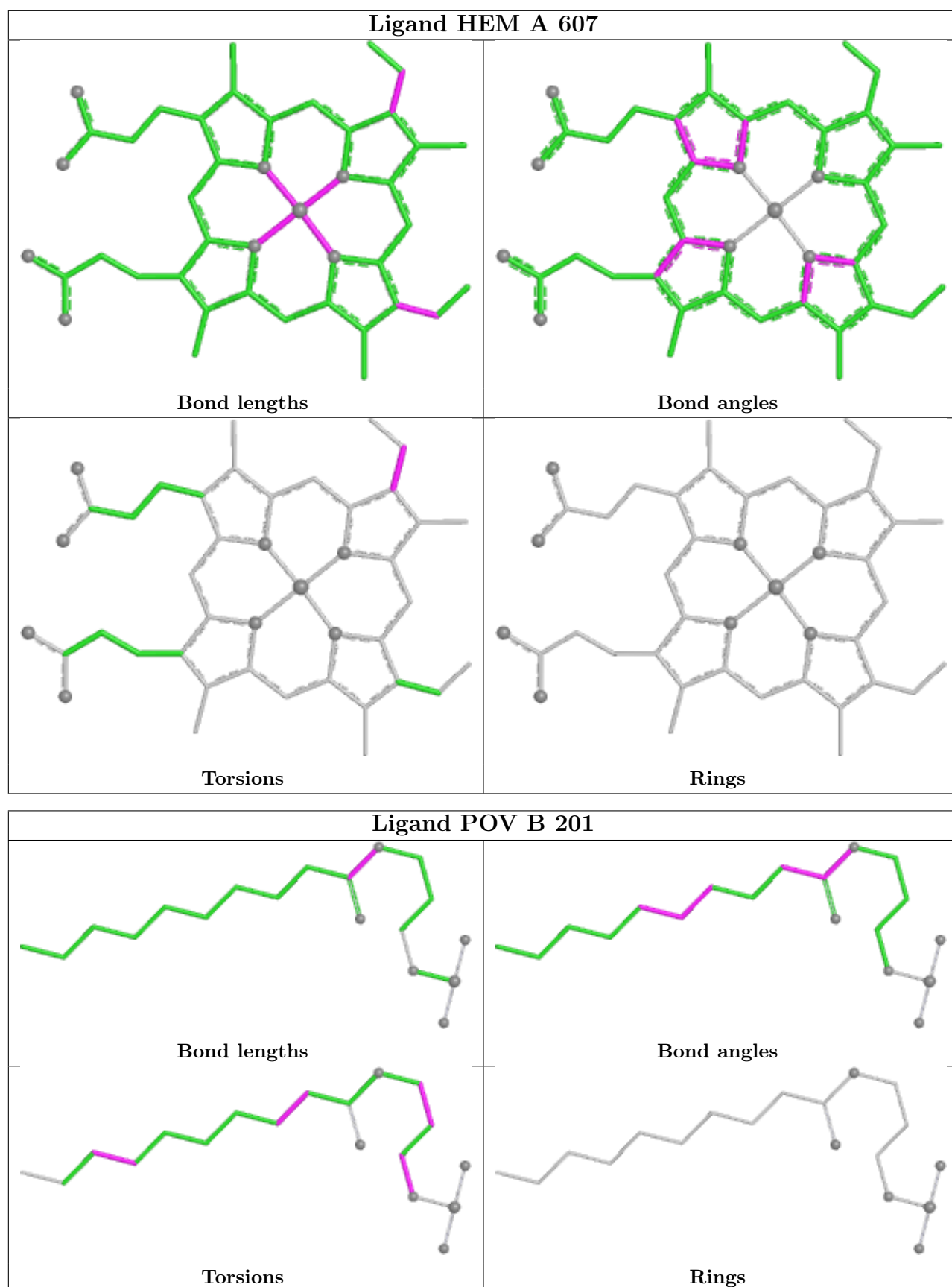
4 monomers are involved in 11 short contacts:

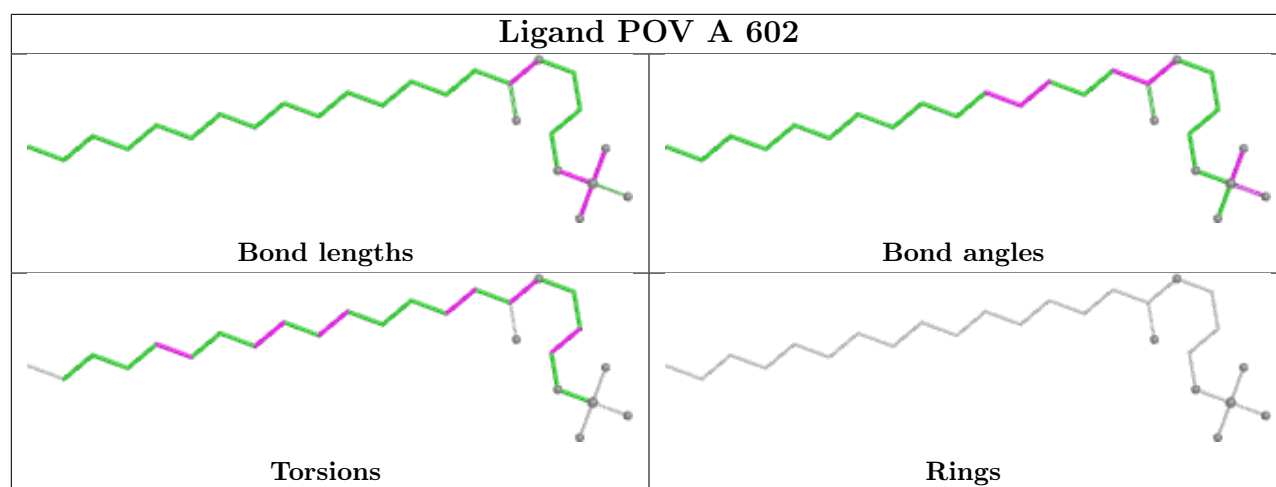
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	601	POV	1	0
7	A	606	HEM	5	0
7	A	607	HEM	4	0
5	A	602	POV	1	0

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.

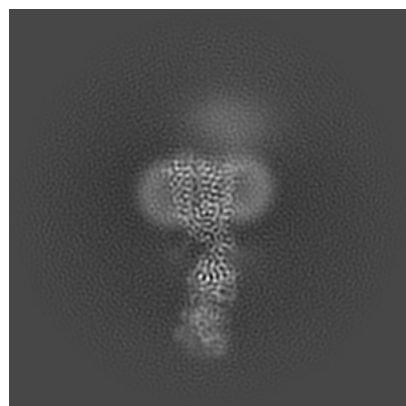
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-26383. These allow visual inspection of the internal detail of the map and identification of artifacts.

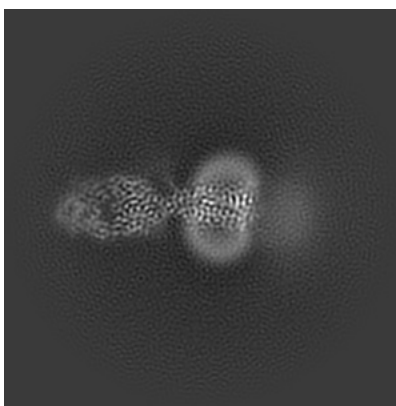
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

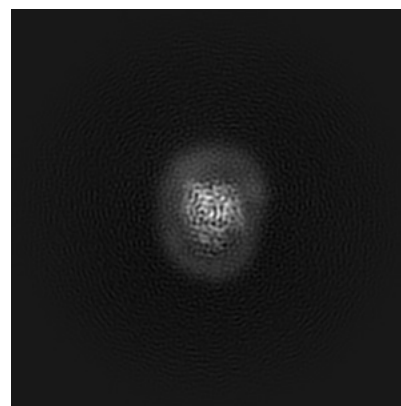
6.1.1 Primary map



X

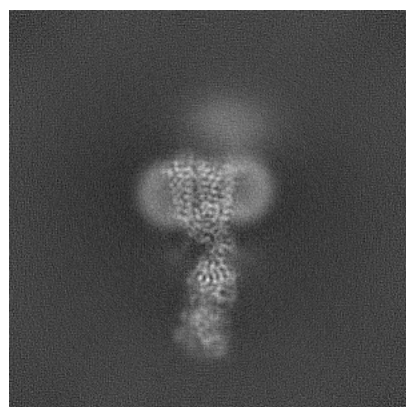


Y

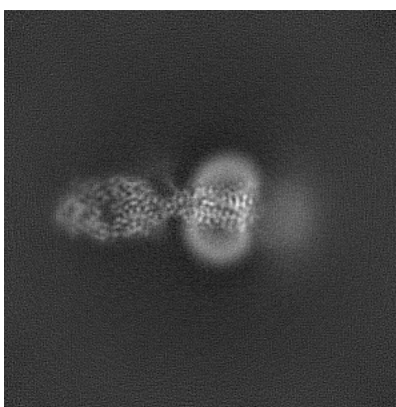


Z

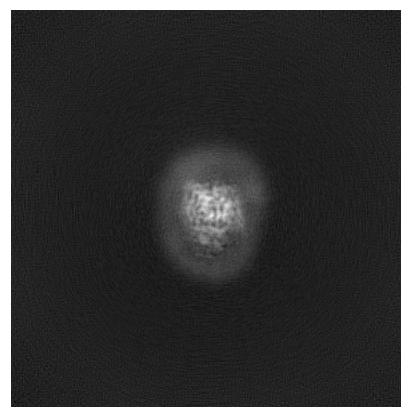
6.1.2 Raw map



X



Y

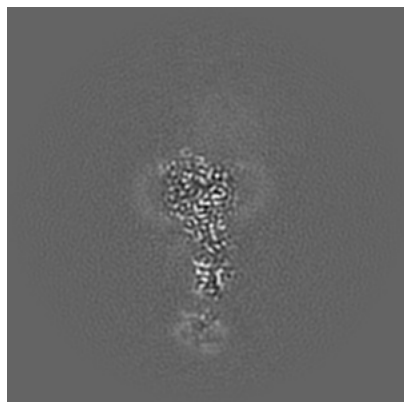


Z

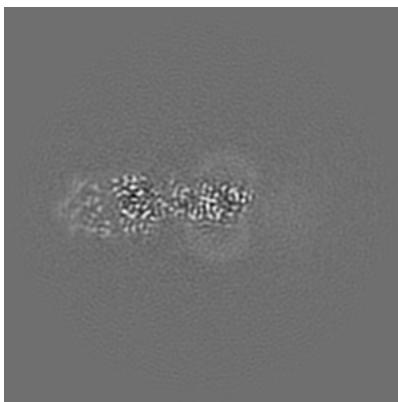
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

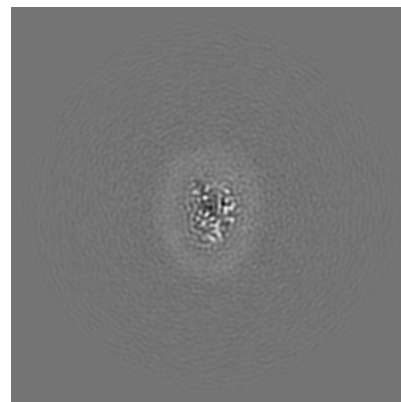
6.2.1 Primary map



X Index: 192

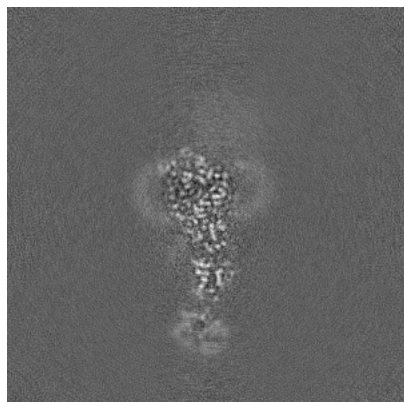


Y Index: 192

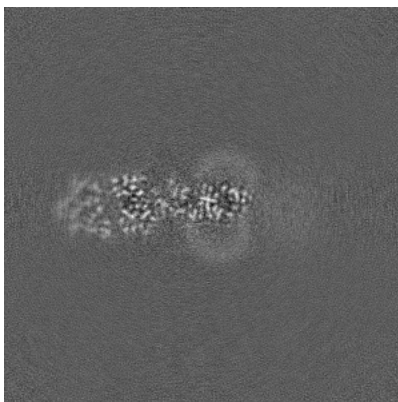


Z Index: 192

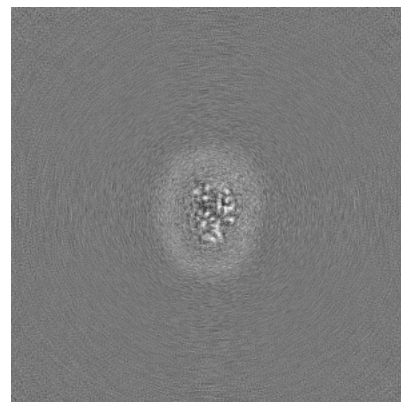
6.2.2 Raw map



X Index: 192



Y Index: 192

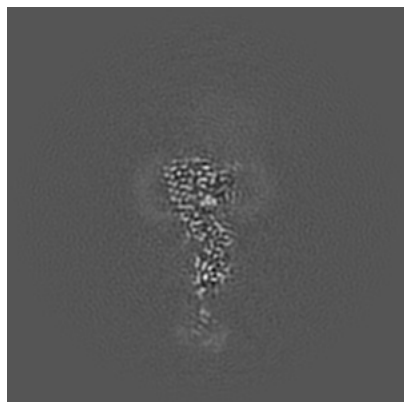


Z Index: 192

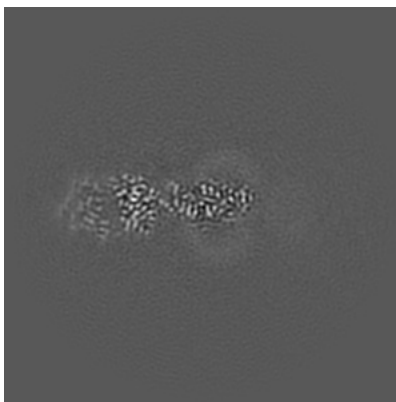
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

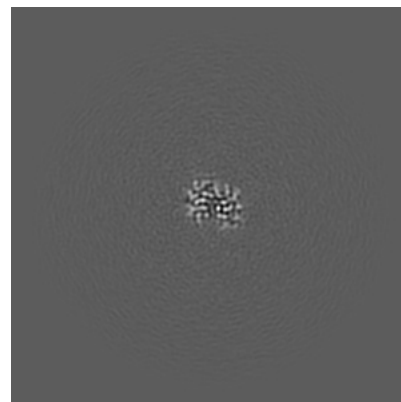
6.3.1 Primary map



X Index: 198

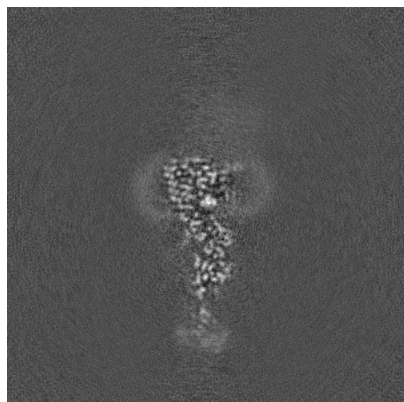


Y Index: 190

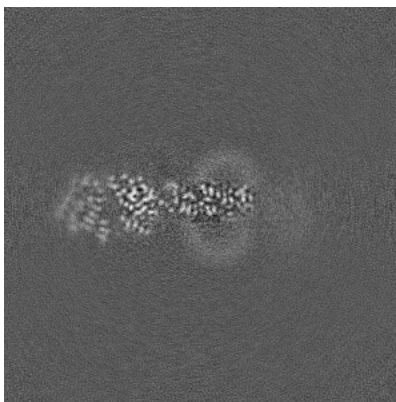


Z Index: 125

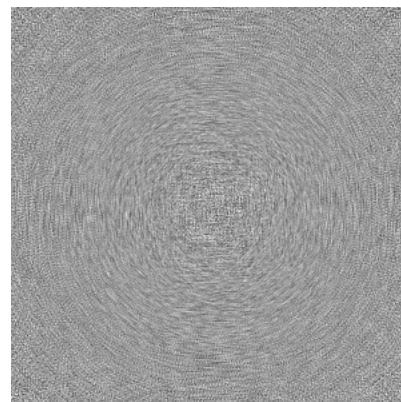
6.3.2 Raw map



X Index: 198



Y Index: 189

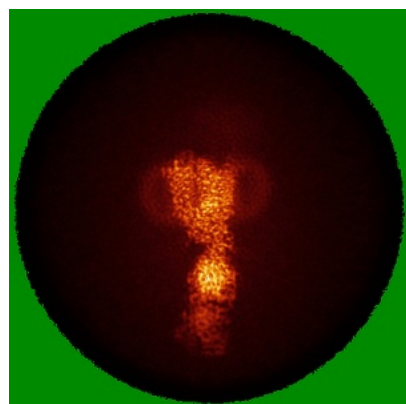


Z Index: 0

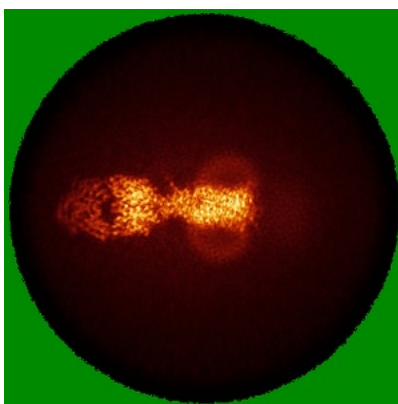
The images above show the largest variance slices of the map in three orthogonal directions.

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

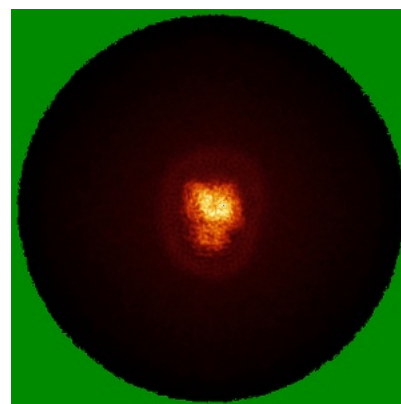
6.4.1 Primary map



X

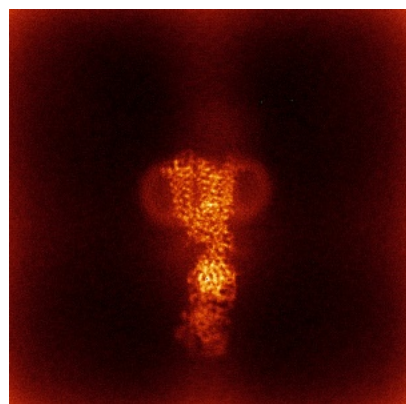


Y

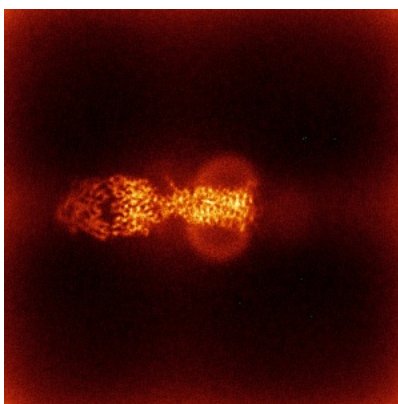


Z

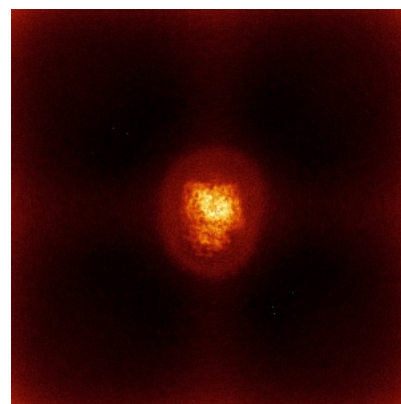
6.4.2 Raw map



X



Y

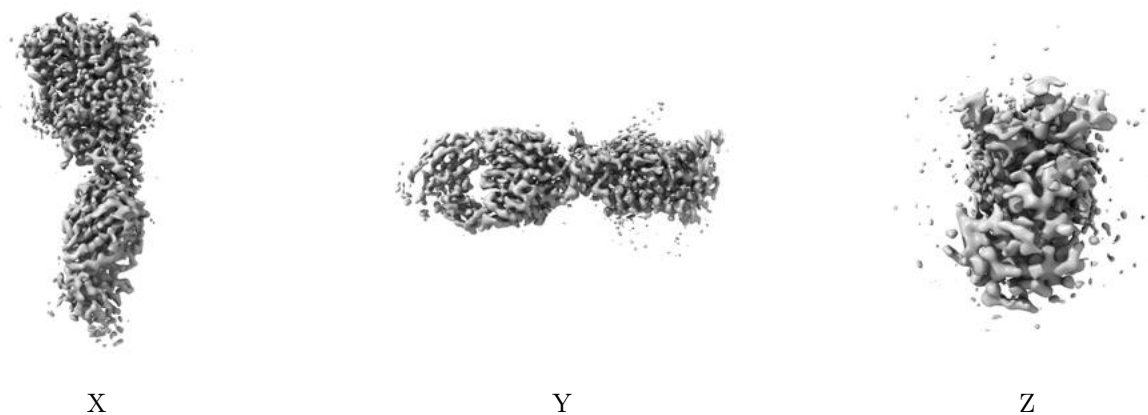


Z

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.

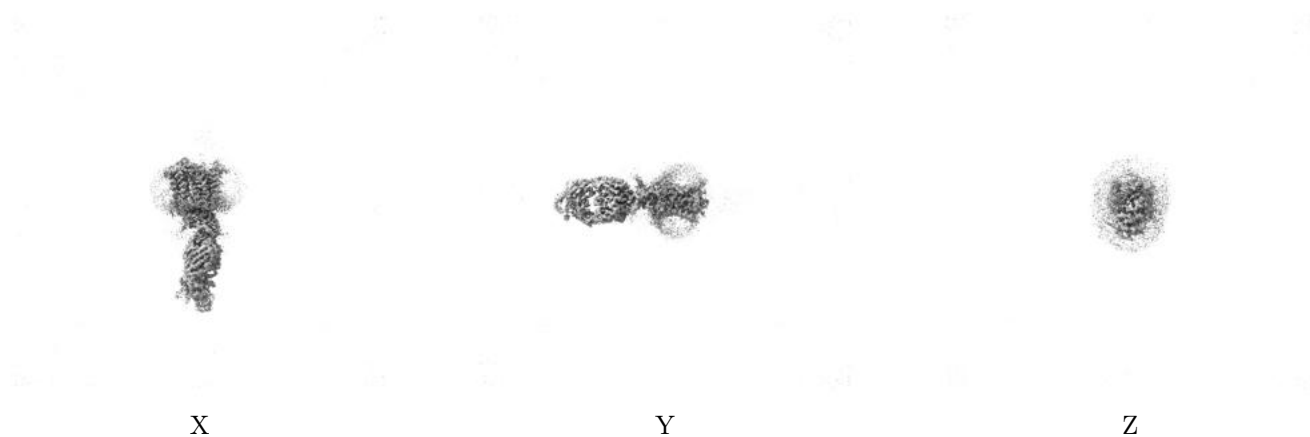
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.13. 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.

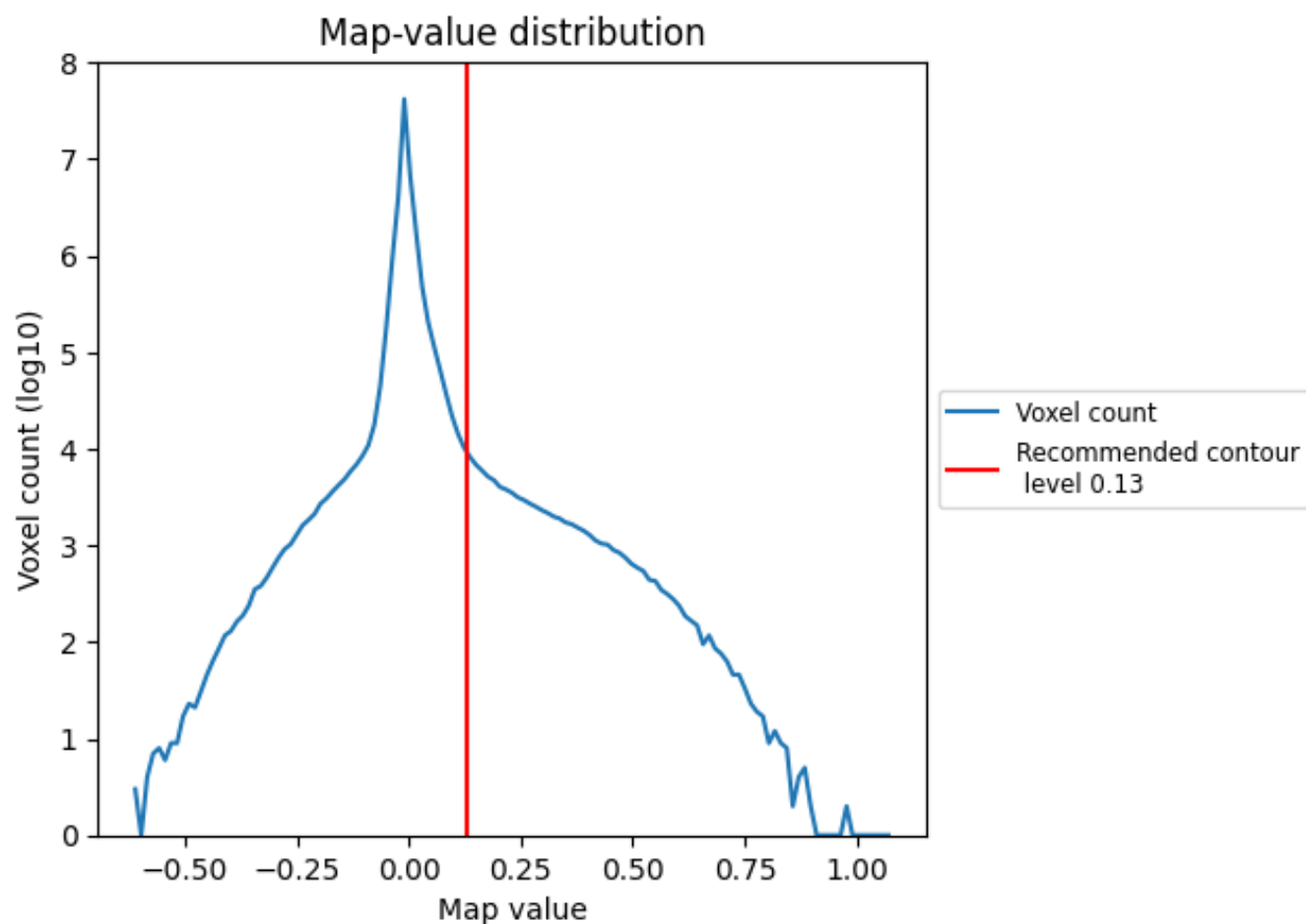
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

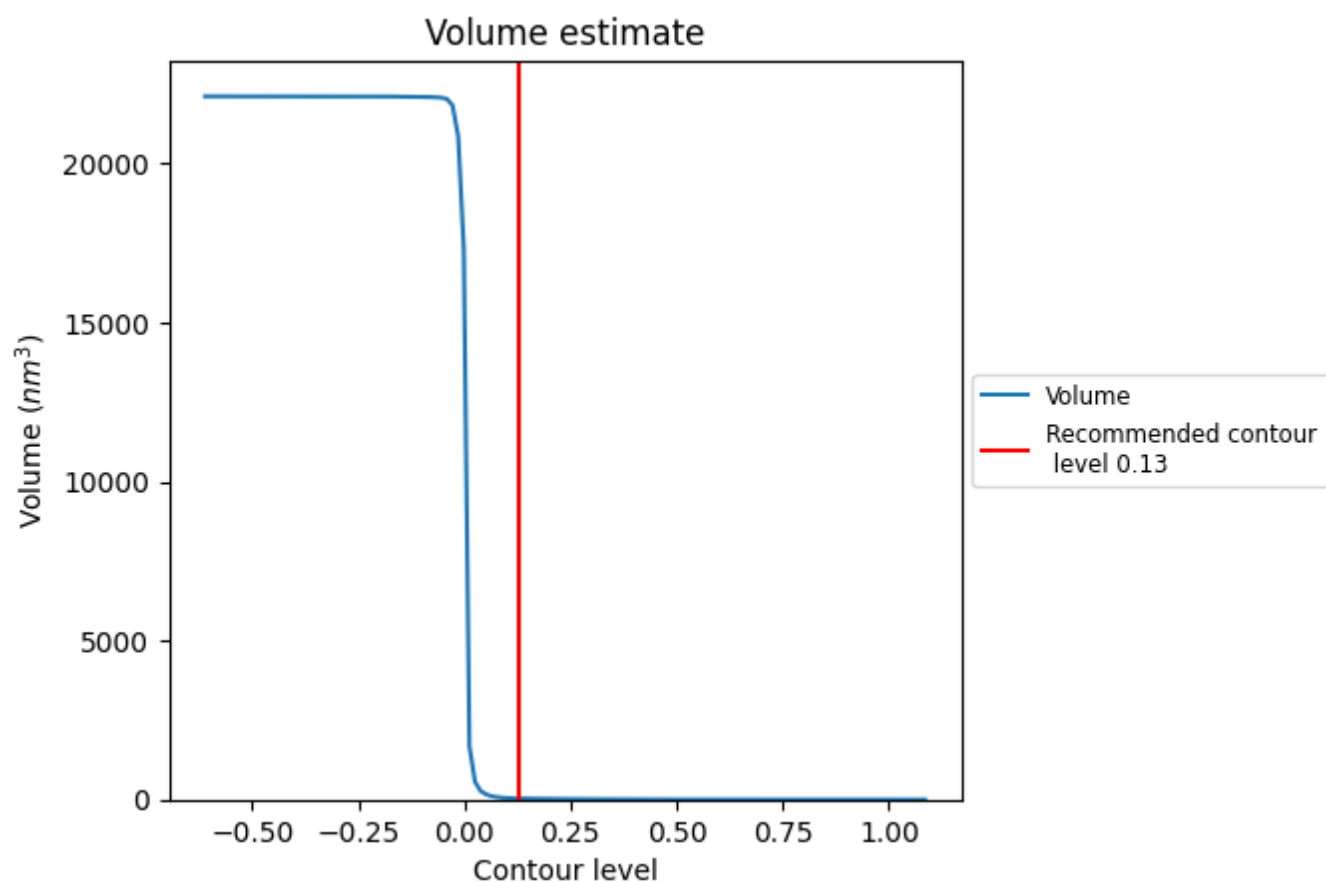
This section contains the results of statistical analysis of the map.

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.

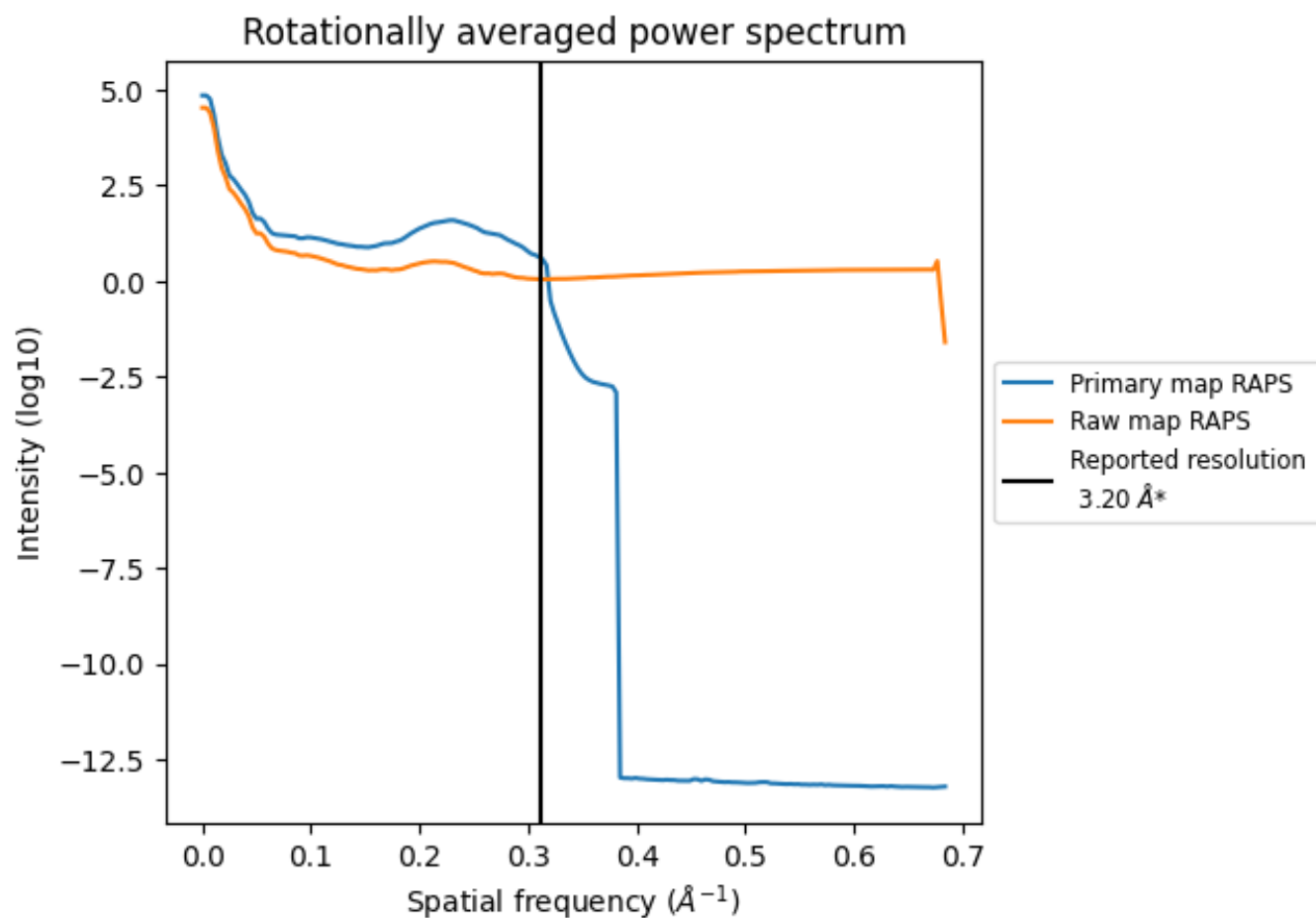
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 33 nm³; this corresponds to an approximate mass of 30 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 ⓘ

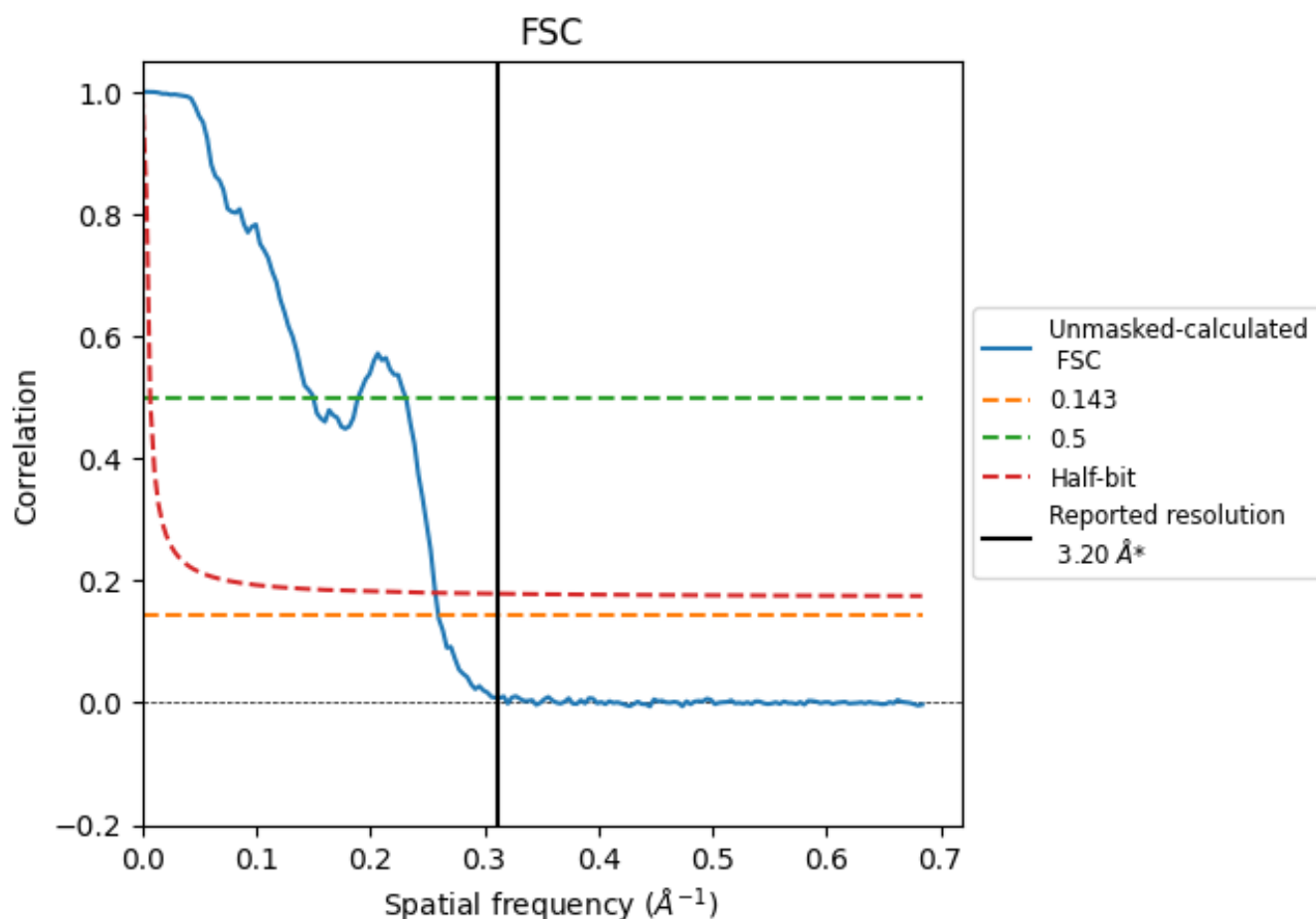


*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

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 0.312 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

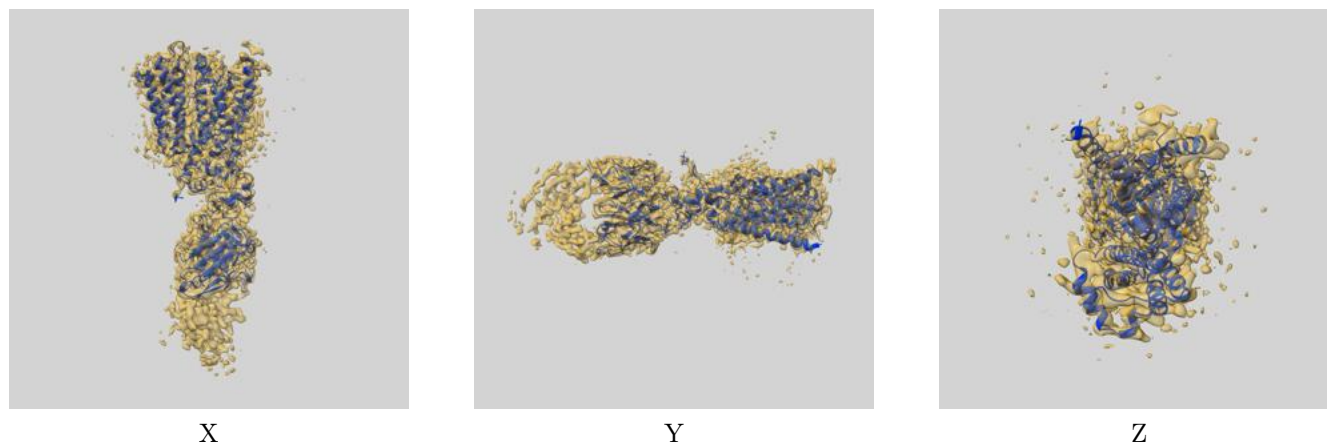
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.85	6.67	3.89

*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 3.85 differs from the reported value 3.2 by more than 10 %

9 Map-model fit [i](#)

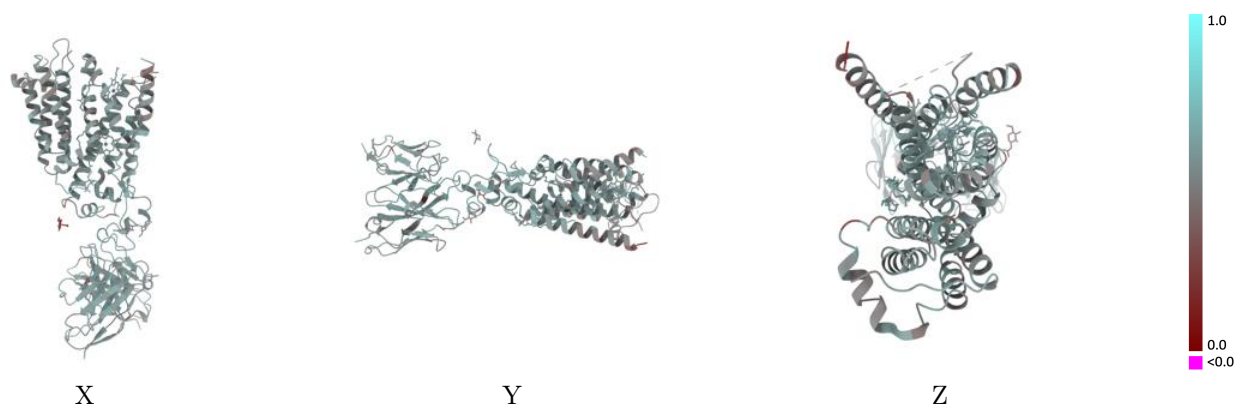
This section contains information regarding the fit between EMDB map EMD-26383 and PDB model 7U8G. Per-residue inclusion information can be found in [section 3](#) on [page 8](#).

9.1 Map-model overlay [i](#)



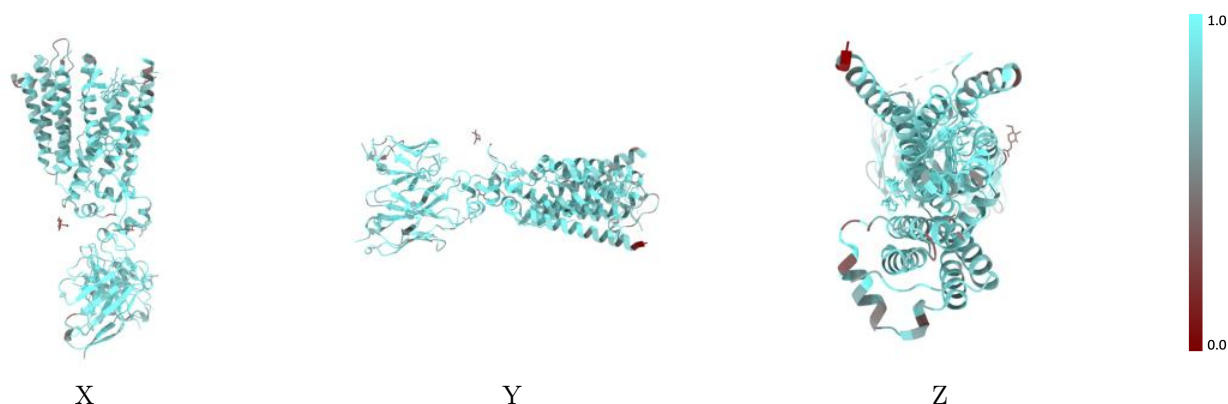
The images above show the 3D surface view of the map at the recommended contour level 0.13 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



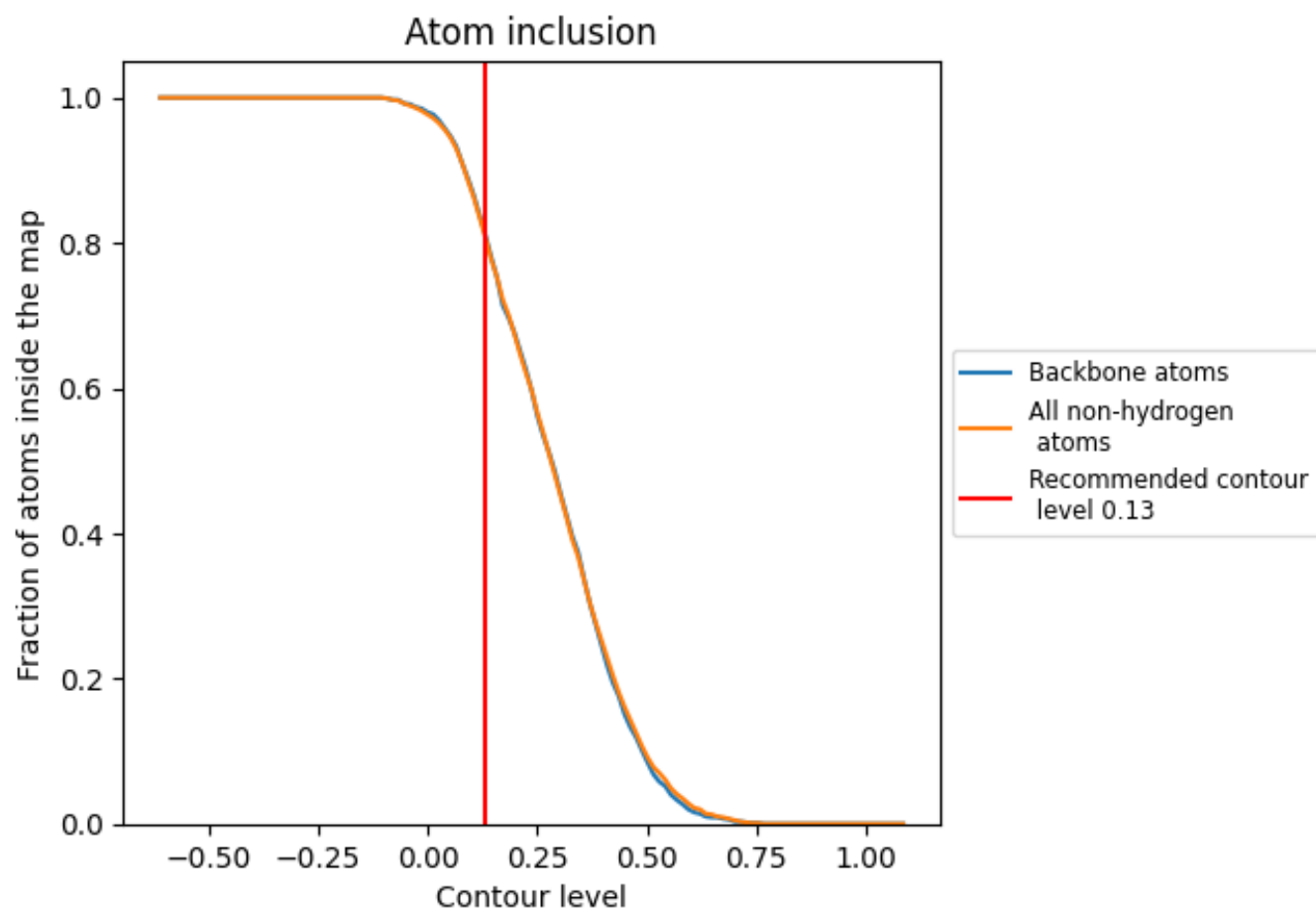
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.13).

9.4 Atom inclusion [i](#)



At the recommended contour level, 81% of all backbone atoms, 81% 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 (0.13) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8110	0.5400
A	0.8310	0.5410
B	0.7620	0.5230
D	0.8280	0.5480
E	0.8260	0.5510

