



wwPDB EM Validation Summary Report ⓘ

Feb 2, 2025 – 01:12 am GMT

PDB ID : 9FMU
EMDB ID : EMD-50570
Title : Cryo-EM structure of human CD163 SRCR1-9 in complex with haptoglobin-hemoglobin
Authors : Andersen, C.B.F.; Kollman, J.M.
Deposited on : 2024-06-07
Resolution : 4.46 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.dev113
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) : 2.40

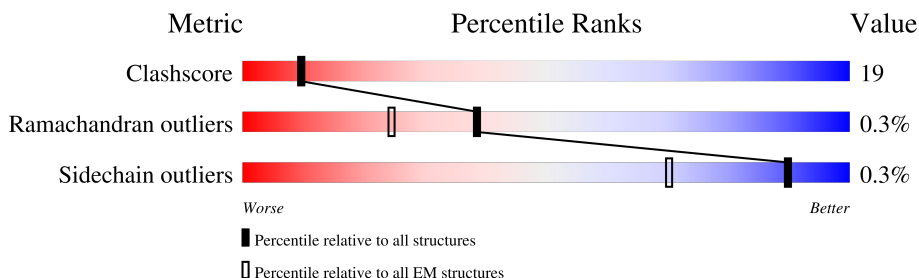
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.46 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	A	142	
2	B	147	
3	C	347	
4	D	1036	
4	E	1036	

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 14763 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 Hemopressin.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	141	Total	C	N	O	S	0	0
			1069	685	187	194	3		

- Molecule 2 is a protein called Spinorphin.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	146	Total	C	N	O	S	0	0
			1123	724	195	201	3		

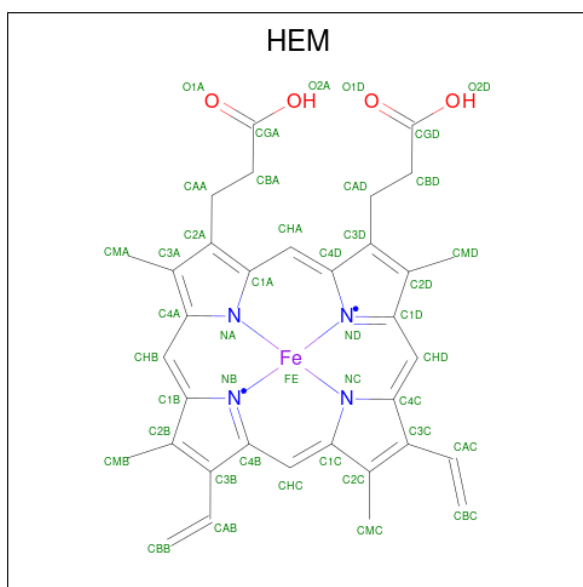
- Molecule 3 is a protein called Isoform 2 of Haptoglobin.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	254	Total	C	N	O	S	0	0
			1982	1265	334	373	10		

- Molecule 4 is a protein called Scavenger receptor cysteine-rich type 1 protein M130.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	738	Total	C	N	O	S	0	0
			5585	3433	1009	1081	62		
4	E	640	Total	C	N	O	S	0	0
			4845	2977	880	935	53		

- Molecule 5 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
5	A	1	Total	C	Fe	N	O	0
			43	34	1	4	4	
5	B	1	Total	C	Fe	N	O	0
			43	34	1	4	4	

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$) (labeled as "Ligand of Interest" by depositor).



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

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Mol	Chain	Residues	Atoms				AltConf
6	C	1	Total	C	N	O	0
			14	8	1	5	
6	D	1	Total	C	N	O	0
			14	8	1	5	
6	D	1	Total	C	N	O	0
			14	8	1	5	
6	E	1	Total	C	N	O	0
			14	8	1	5	

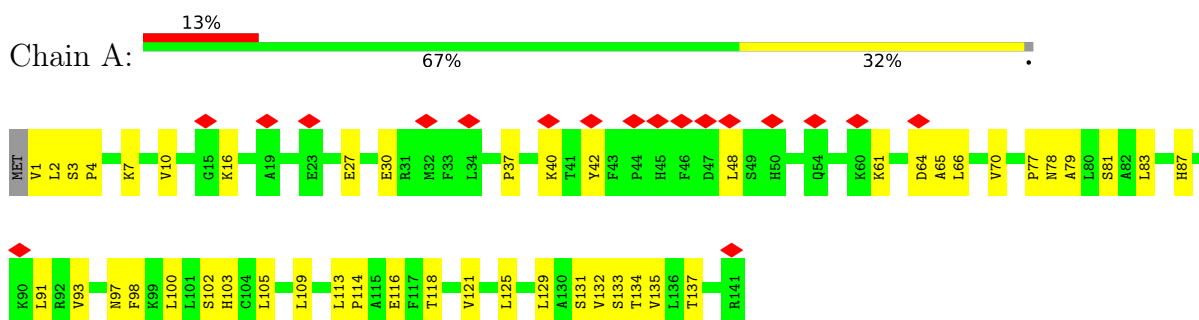
- Molecule 7 is CALCIUM ION (three-letter code: CA) (formula: Ca) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
7	D	2	Total	Ca	0
			2	2	
7	E	1	Total	Ca	0
			1	1	

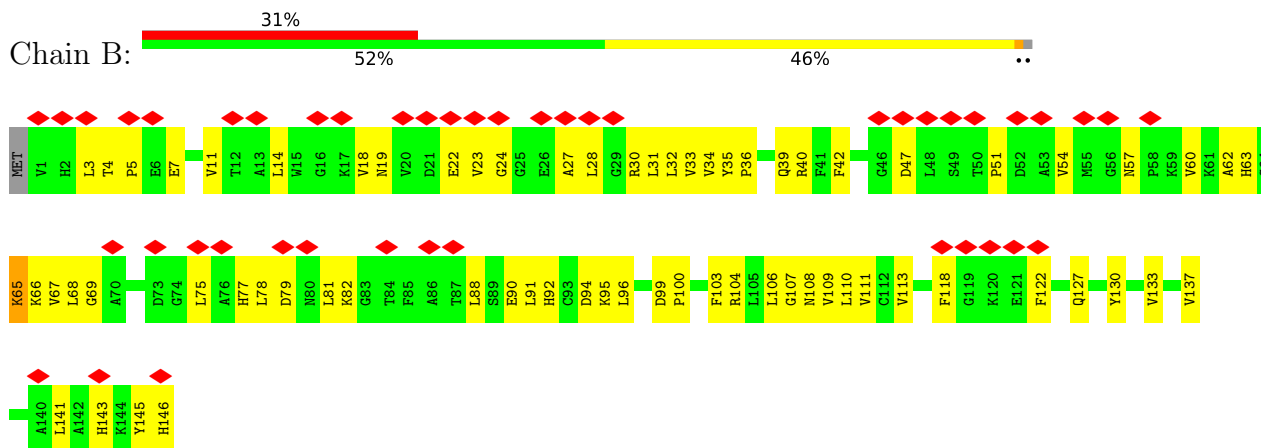
3 Residue-property plots

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

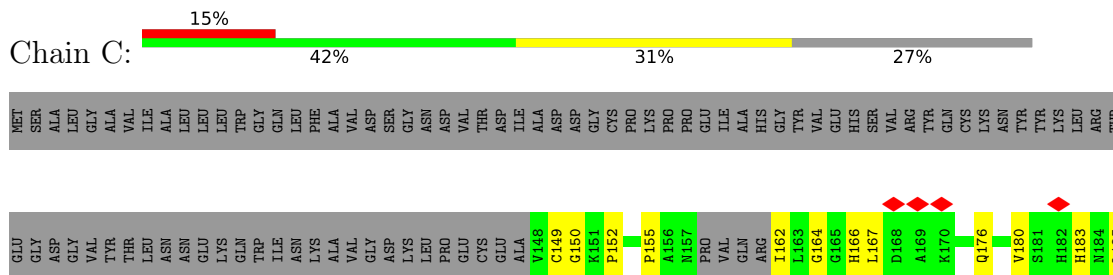
• Molecule 1: Hemopressin



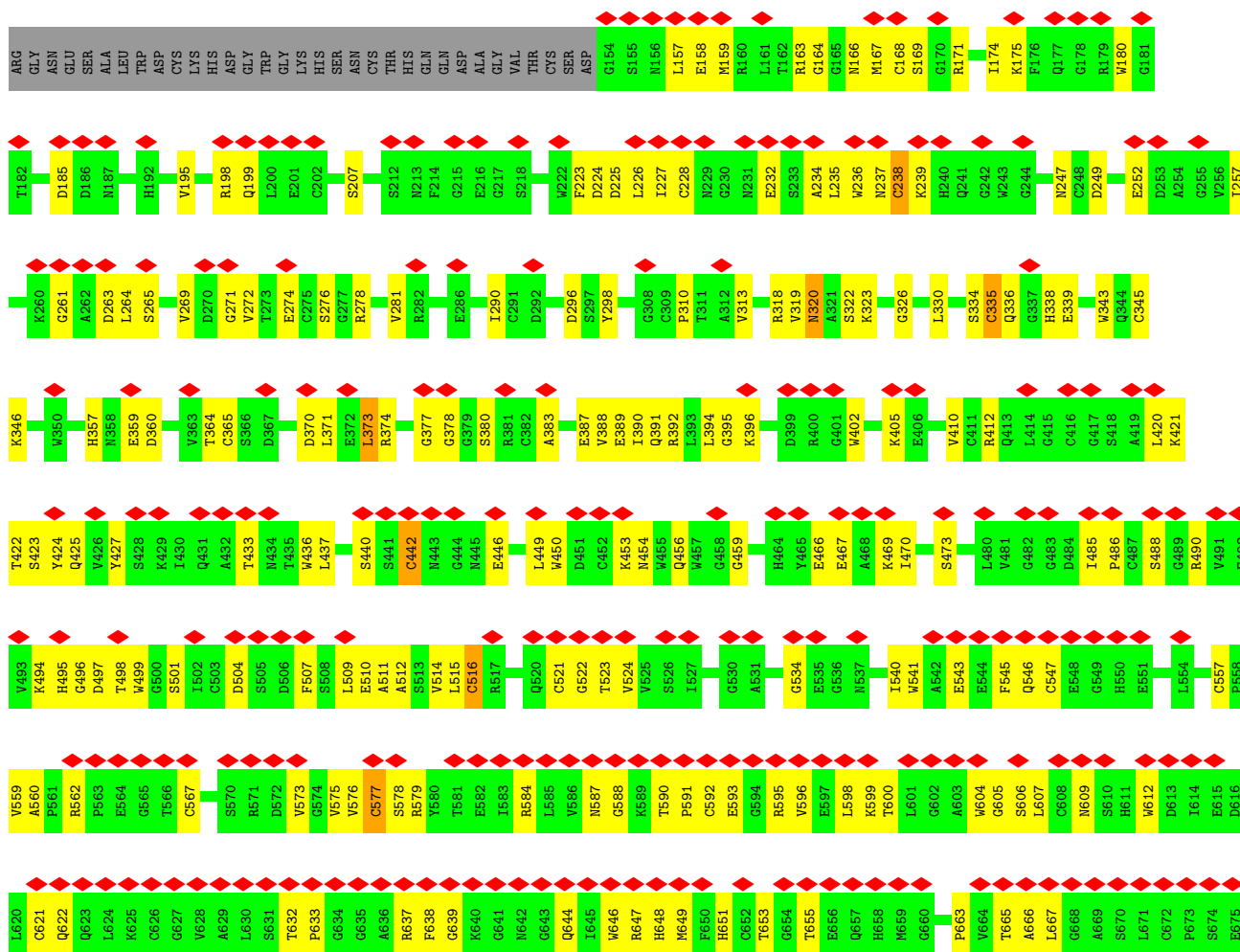
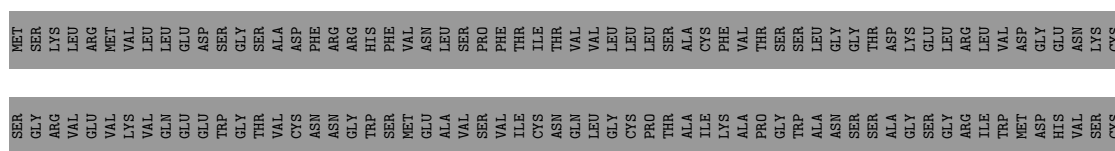
• Molecule 2: Spinorphin

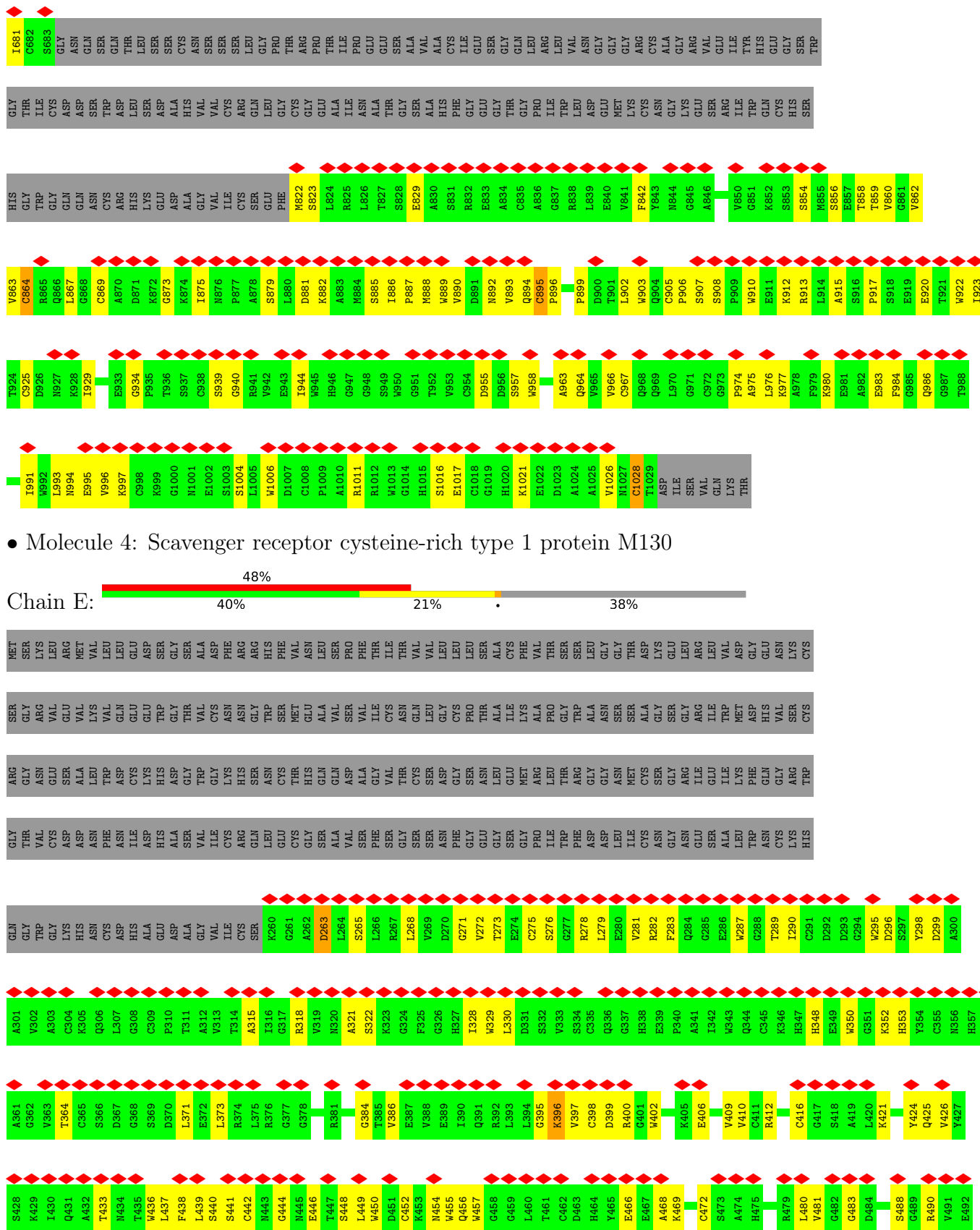


• Molecule 3: Isoform 2 of Haptoglobin



- Molecule 4: Scavenger receptor cysteine-rich type 1 protein M130





ASN	L867	Q806	C744	G684	Q623	P563	V493
LYS	G568	N807	D745	N855	L824	E564	K494
ILE	C969	C908	D746	Q686	K626	G565	H495
LEU	A870	R809	S747	Q687	C626	T566	G496
TRP	D871	H810	W748	Q688	G827	C567	D497
LEU	K372	K811	D749	T689	V828	S668	T498
ASN	G873	E812	L750	L890	A829	G500	W499
GLU	G874	E813	S751	SER	L630	H579	G501
VAL	K874	A814	D752	SER	S831	R571	I502
LYS	I875	A814	A753	CYS	T632	D572	C503
CYS	N876	G815	H754	ASN	P633	G573	D504
LYS	P877	V816	H755	SER	G634	S506	S506
GLY	P877	V816	V755	SER	G635	V575	D506
ASN	A878	I817		SER	A636	V576	F507
GLU	S879	C818	R758	LEU	R637	C577	S508
SER	L580	S819	Q759	GLY	F638	S578	L509
LEU	L580	E820	L760	PRO	G639	R579	
LEU	D881	F821	G761	THR	G640	T581	
TRP	K882		G762	ARG	G641	I582	
ASP	A883	L824	G763	PRO	N642	I583	
CYS	A883	R825	E764	PRO	G643	R584	
PRO	M884	L826	A765	ILE	Q644	L585	
ALA	S885	T827	E766	PRO	I645	V586	
ARG	I886	S828	I766	GLU	W646	N587	
TRP	P887	S828	A767	GLU	R647	G588	
GLY	M888	E829	A768	SER	G648	G589	
ASP	W889	A830	A768	GLY	M649	T590	
SER	V890	S831	T769	VAL	F650	P591	
GLY	D891	R832		ALA	H651	C592	
CYS	N892	E833	A772	CYS	T552	E593	
GLY	V893	E833	H773	ILE	G653	E593	
LYS	Q894	A834	F774	GLY	G654	G594	
GLU	Q894	A834	G775	GLY	T555	R595	
ASP	C895	C835	G775	GLY	E956	G597	
ALA	P896	A836	E776	Q718	Q657	L598	
ALA	K897	G837	G777	L719	H658	G598	
ALA	G398	R838	T778	R720	M659	T600	
VAL	G398	L839	G779	G721	G660	L601	
ASN	P899	L839	T779	V722	G661	G602	
GLN	D900	E940	P780	W722	D661	A603	
THR	D900	V841	I781	N723	C662	W604	
ASP	T901	F842	I781	G724	G666	C547	
ILE	L902	F843	W782	G724	L667	G608	
CYS	W903	T843	L783	G725	G668	N609	
SER	Q904	N844	D784	G726	V664	S610	
VAL	Q904	G845	A785	R727	S606	G549	
GLN	C905	A846	W786	G728	L607	H611	
LYS	F906	W847	E787	C728	T665	W612	
THR	S907	G848	K787	A729	A666	D613	
LYS	S908	T849	C788	G730	L667	C547	
PHE	P909	W850	W789	R731	G668	E548	
LYS	W910	G851	G790	H736	A669	G549	
ALA	E911	K852	K791	G738	S670	H611	
GLU	K912	S853	E792	S739	L671	W612	
PHE	R913	S854	E793	W740	C672	D613	
GLY	L914	M855	S793	Y735	G673	I614	
GLN	A915	S856	I795	H736	S674	E615	
	S916	S857	W796	E737	E675	C557	
	P917	T858	Q797	G738	A617	P558	
	S918	V859	C798	S739	H618	V559	
	E919	G860	H799	W740	V677	A560	
	E920	V862	S900	I742	Q676	P561	
	E920	V862	S900	I743	A678	L620	
	T921	V863	H801	G741	G682	G821	
	W922	C364	G802	T742		Q622	
	I923	R865	W803	I743	I681		
	C925	Q866	G804	I743	S683		
	D926		Q805				

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	38511	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 ($e^-/\text{\AA}^2$)	90	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	3.315	Depositor
Minimum map value	-1.605	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.088	Depositor
Recommended contour level	1	Depositor
Map size (\AA)	339.19998, 339.19998, 339.19998	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.06, 1.06, 1.06	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CA, NAG, 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	0.30	0/1097	0.58	0/1491
2	B	0.34	0/1153	0.64	0/1566
3	C	0.34	0/2029	0.63	2/2756 (0.1%)
4	D	0.37	5/5714 (0.1%)	0.74	13/7740 (0.2%)
4	E	0.32	1/4955 (0.0%)	0.70	10/6712 (0.1%)
All	All	0.34	6/14948 (0.0%)	0.69	25/20265 (0.1%)

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
4	D	0	1

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	577	CYS	CB-SG	-6.85	1.70	1.82
4	D	228	CYS	CB-SG	-6.10	1.71	1.82
4	D	516	CYS	CB-SG	-6.01	1.72	1.82
4	D	895	CYS	CB-SG	-5.57	1.72	1.81
4	E	547	CYS	CB-SG	-5.37	1.73	1.81

The worst 5 of 25 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	557	CYS	CA-CB-SG	11.95	135.51	114.00
4	E	547	CYS	CA-CB-SG	10.10	132.19	114.00
4	D	547	CYS	CA-CB-SG	9.96	131.94	114.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	516	CYS	CA-CB-SG	8.77	129.79	114.00
4	D	577	CYS	CA-CB-SG	8.01	128.42	114.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	D	442	CYS	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	1069	0	1072	39	0
2	B	1123	0	1118	65	0
3	C	1982	0	1955	86	0
4	D	5585	0	5214	209	0
4	E	4845	0	4541	172	0
5	A	43	0	30	6	0
5	B	43	0	30	5	0
6	C	28	0	26	0	0
6	D	28	0	26	2	0
6	E	14	0	13	0	0
7	D	2	0	0	0	0
7	E	1	0	0	0	0
All	All	14763	0	14025	561	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 19.

The worst 5 of 561 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)
4:D:590:THR:HG22	4:D:593:GLU:HG2	1.50	0.93
4:D:986:GLN:HE22	4:D:1021:LYS:HA	1.33	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:421:LYS:HG2	4:D:423:SER:H	1.40	0.85
3:C:349:ASP:OD1	3:C:350:THR:N	2.12	0.82
1:A:102:SER:HB2	1:A:129:LEU:HD13	1.62	0.82

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	139/142 (98%)	129 (93%)	10 (7%)	0	100	100
2	B	144/147 (98%)	139 (96%)	5 (4%)	0	100	100
3	C	250/347 (72%)	234 (94%)	16 (6%)	0	100	100
4	D	734/1036 (71%)	704 (96%)	27 (4%)	3 (0%)	30	68
4	E	636/1036 (61%)	609 (96%)	24 (4%)	3 (0%)	25	64
All	All	1903/2708 (70%)	1815 (95%)	82 (4%)	6 (0%)	38	72

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	E	686	GLN
4	D	263	ASP
4	D	320	ASN
4	D	422	THR
4	E	263	ASP

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	113/114 (99%)	113 (100%)	0	100	100
2	B	118/119 (99%)	117 (99%)	1 (1%)	79	84
3	C	217/294 (74%)	217 (100%)	0	100	100
4	D	602/849 (71%)	601 (100%)	1 (0%)	92	93
4	E	521/849 (61%)	519 (100%)	2 (0%)	89	90
All	All	1571/2225 (71%)	1567 (100%)	4 (0%)	90	91

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	65	LYS
4	D	647	ARG
4	E	396	LYS
4	E	647	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
4	E	657	GLN
4	E	754	HIS
4	D	237	ASN
4	D	648	HIS
4	D	986	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 10 ligands modelled in this entry, 3 are monoatomic - leaving 7 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
5	HEM	A	201	1	41,50,50	1.45	3 (7%)	45,82,82	1.16	3 (6%)
6	NAG	D	2004	4	14,14,15	0.67	0	17,19,21	1.11	2 (11%)
6	NAG	C	1001	3	14,14,15	0.76	0	17,19,21	0.80	0
5	HEM	B	201	2	41,50,50	1.51	6 (14%)	45,82,82	1.42	7 (15%)
6	NAG	C	1002	3	14,14,15	0.75	0	17,19,21	0.77	0
6	NAG	E	1102	4	14,14,15	0.79	0	17,19,21	0.75	0
6	NAG	D	2003	4	14,14,15	0.74	0	17,19,21	0.91	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	HEM	A	201	1	-	3/12/54/54	-
6	NAG	D	2004	4	-	2/6/23/26	0/1/1/1
6	NAG	C	1001	3	-	0/6/23/26	0/1/1/1
5	HEM	B	201	2	-	3/12/54/54	-
6	NAG	C	1002	3	-	0/6/23/26	0/1/1/1
6	NAG	E	1102	4	-	2/6/23/26	0/1/1/1
6	NAG	D	2003	4	-	2/6/23/26	0/1/1/1

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	201	HEM	C3C-C2C	-4.12	1.34	1.40
5	A	201	HEM	C3C-C2C	-4.06	1.34	1.40
5	A	201	HEM	C3C-CAC	3.74	1.55	1.47
5	B	201	HEM	C3C-CAC	3.73	1.55	1.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	201	HEM	CAB-C3B	2.89	1.55	1.47

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	201	HEM	CMB-C2B-C1B	2.93	129.50	125.04
5	B	201	HEM	CAD-CBD-CGD	-2.62	107.97	113.60
5	B	201	HEM	C1B-NB-C4B	2.61	107.77	105.07
5	B	201	HEM	CMC-C2C-C3C	2.56	129.47	124.68
6	D	2004	NAG	O5-C1-C2	-2.49	107.36	111.29

There are no chirality outliers.

5 of 12 torsion outliers are listed below:

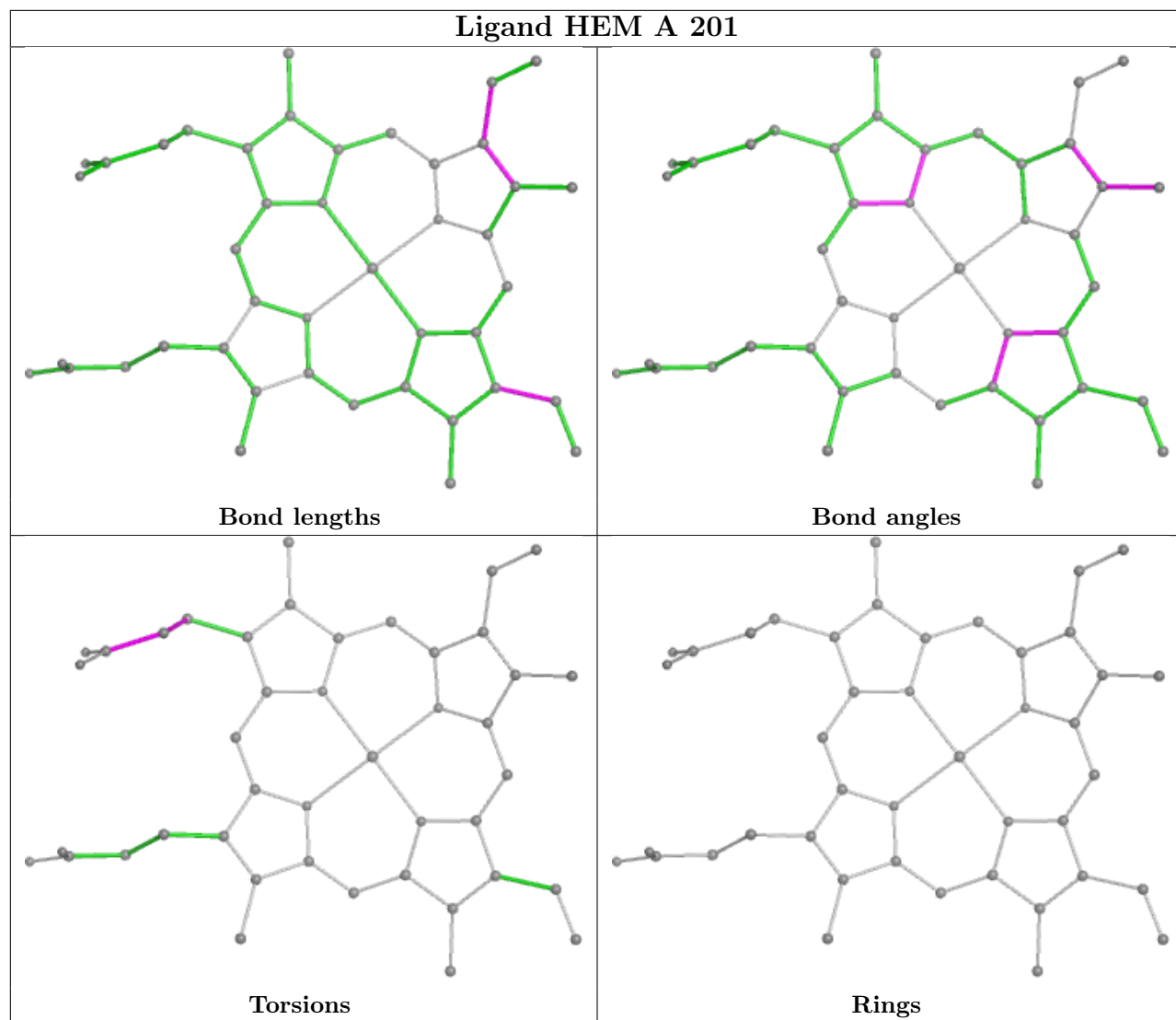
Mol	Chain	Res	Type	Atoms
6	D	2003	NAG	C8-C7-N2-C2
6	D	2003	NAG	O7-C7-N2-C2
6	D	2004	NAG	C8-C7-N2-C2
6	D	2004	NAG	O7-C7-N2-C2
6	E	1102	NAG	C8-C7-N2-C2

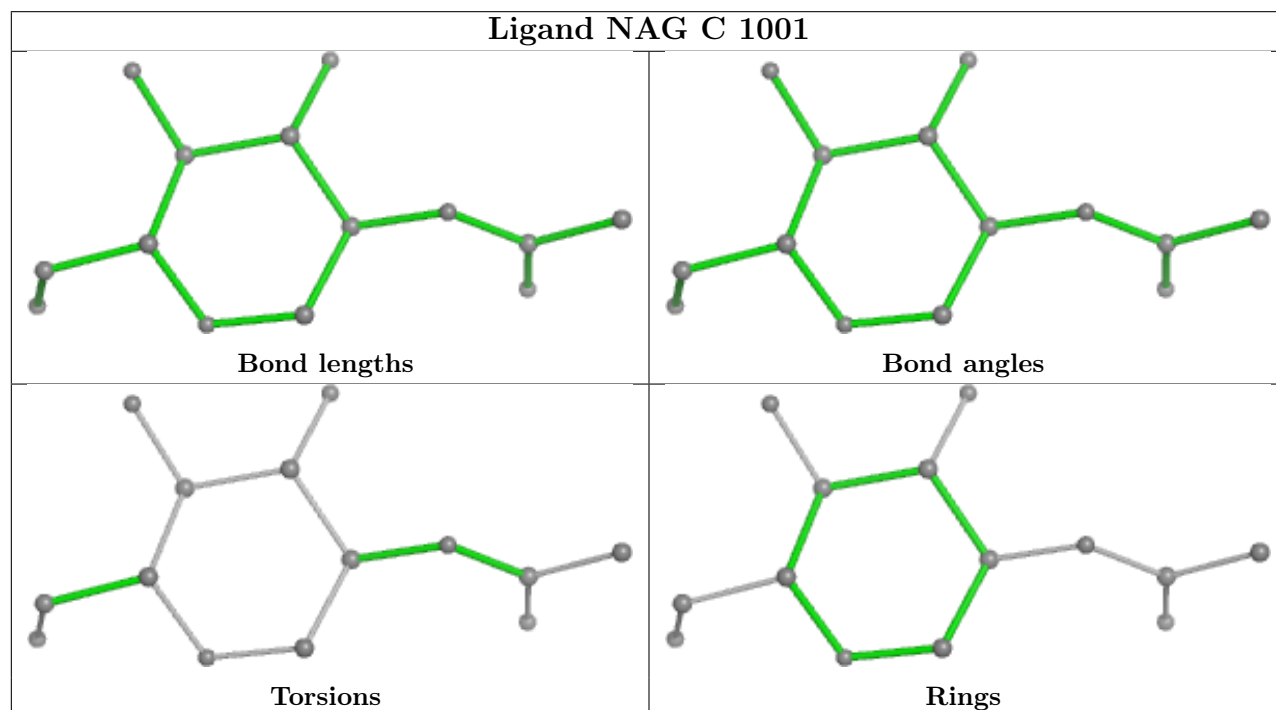
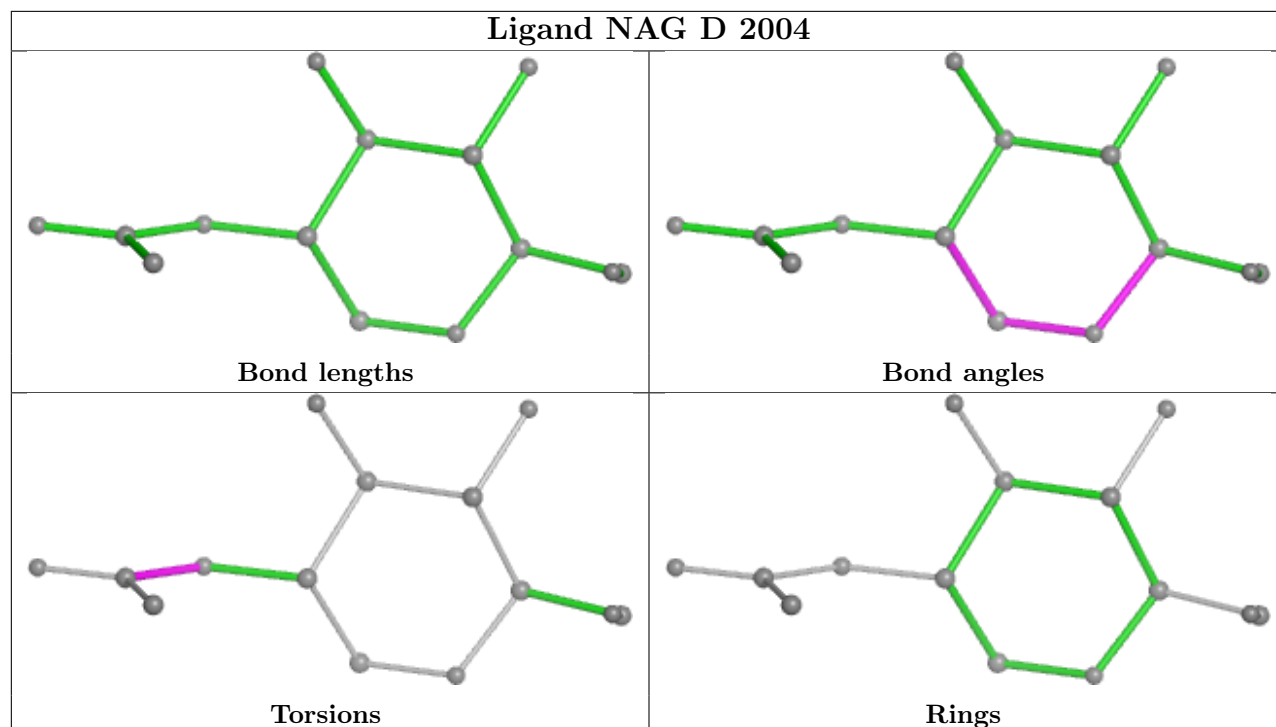
There are no ring outliers.

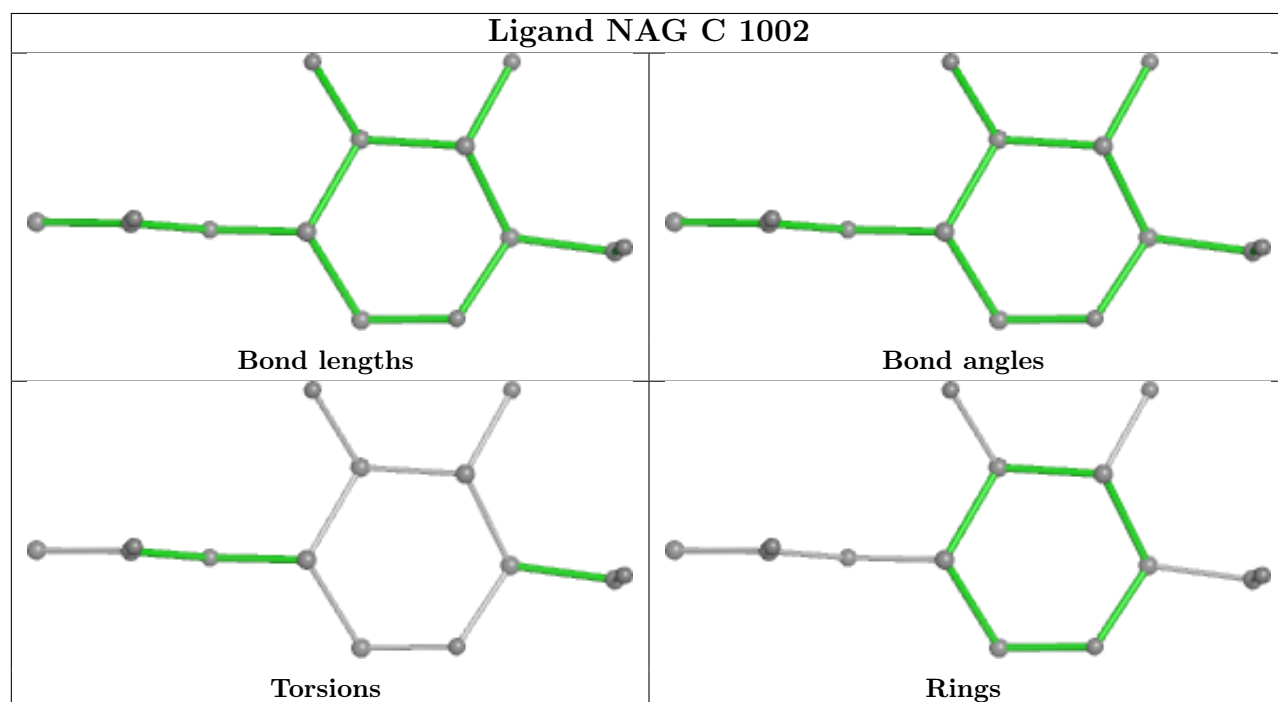
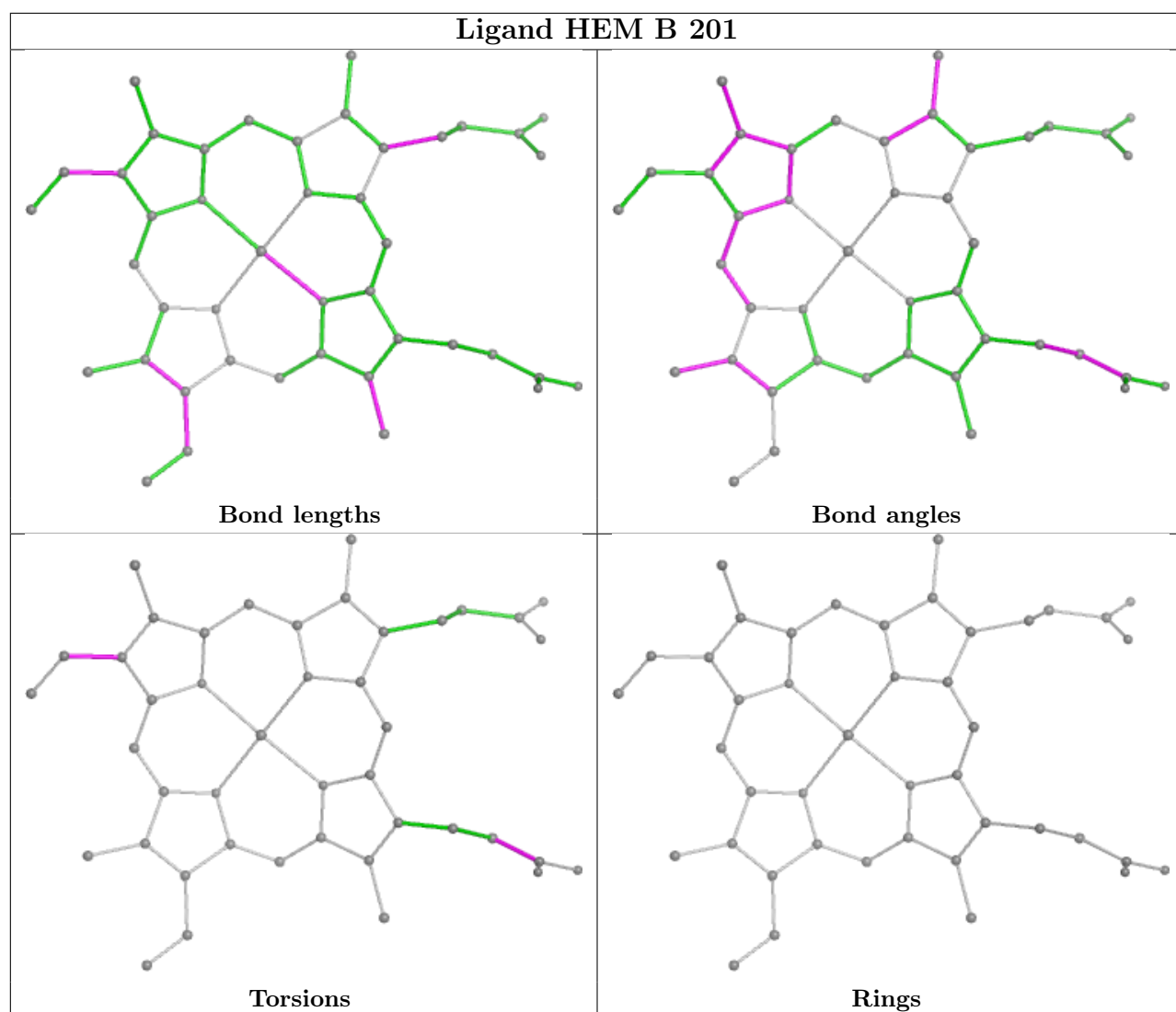
3 monomers are involved in 13 short contacts:

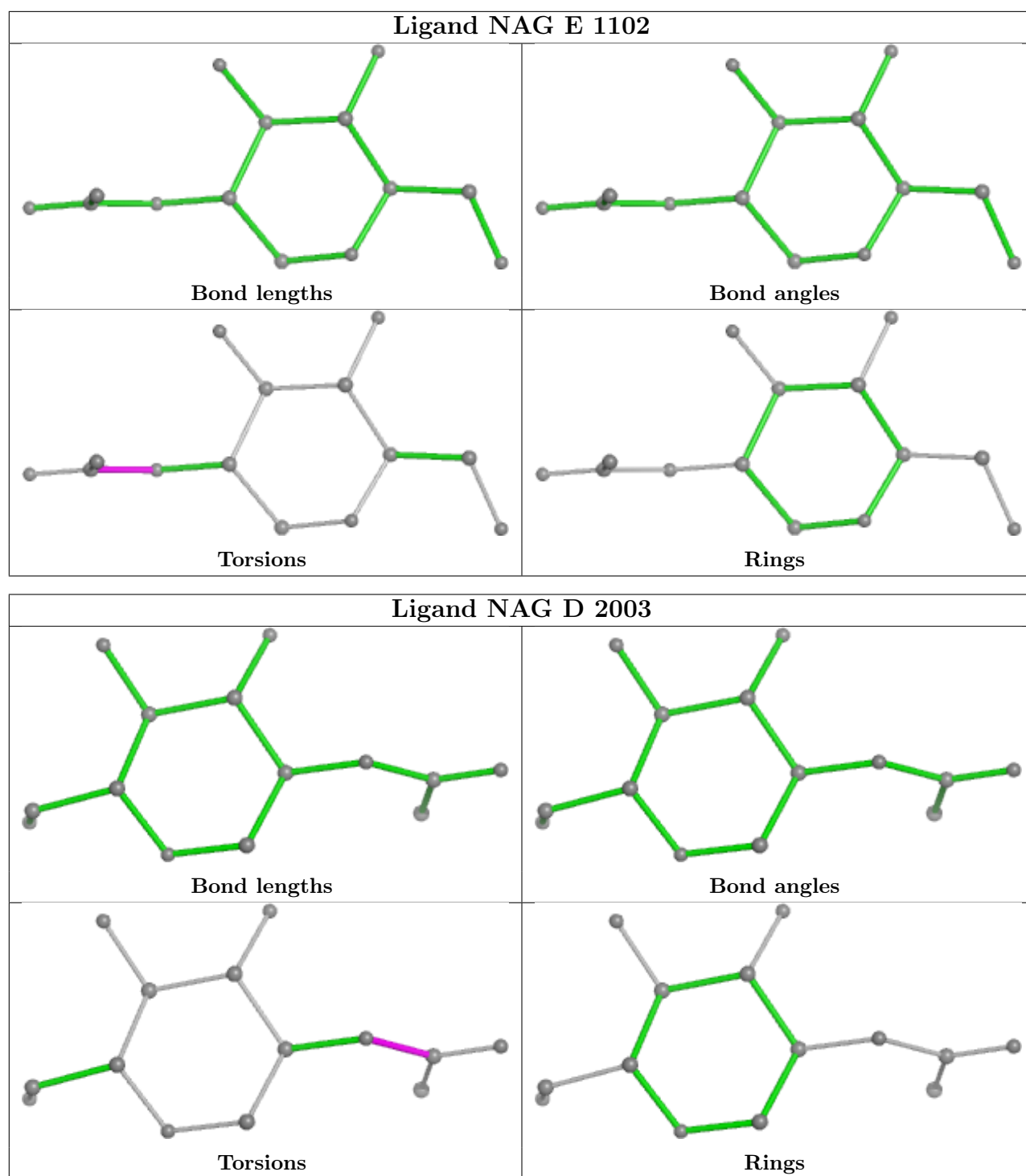
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	201	HEM	6	0
6	D	2004	NAG	2	0
5	B	201	HEM	5	0

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.

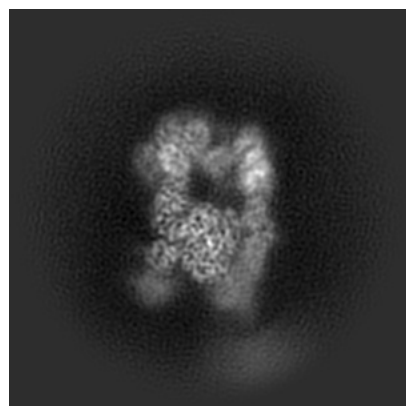
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-50570. These allow visual inspection of the internal detail of the map and identification of artifacts.

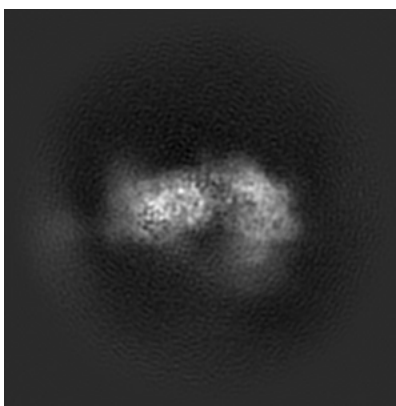
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

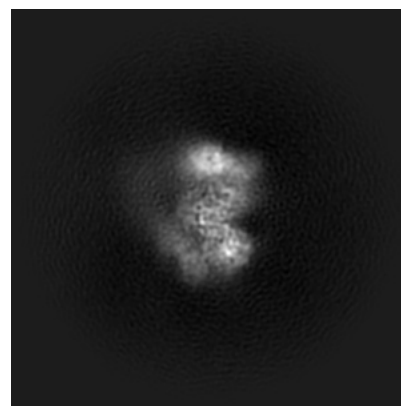
6.1.1 Primary map



X

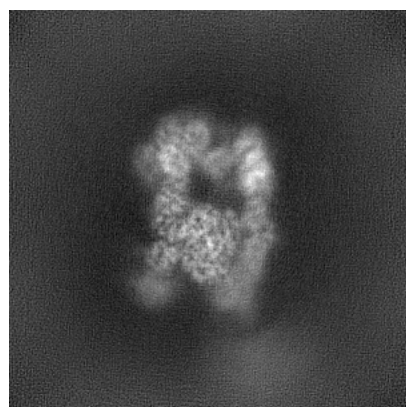


Y

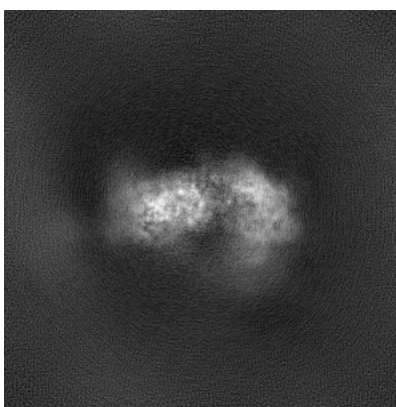


Z

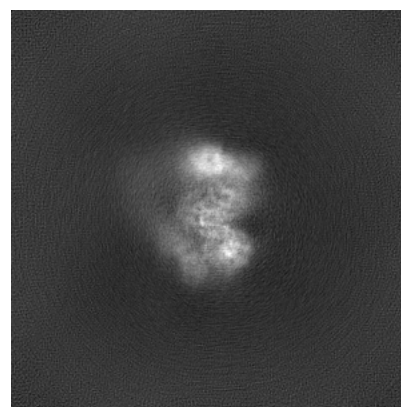
6.1.2 Raw map



X



Y

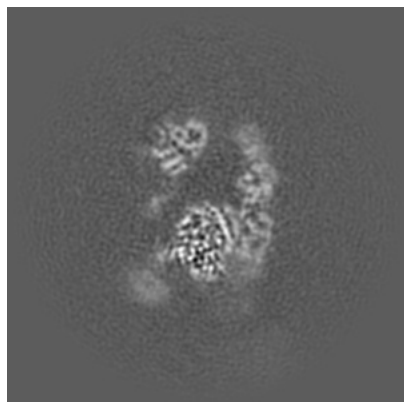


Z

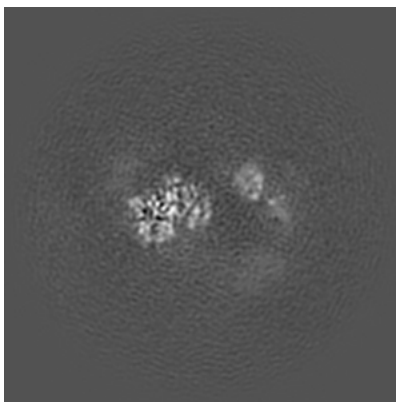
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

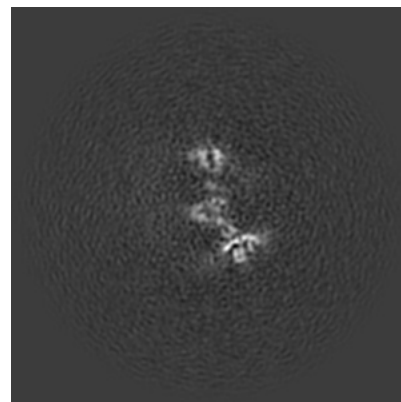
6.2.1 Primary map



X Index: 160

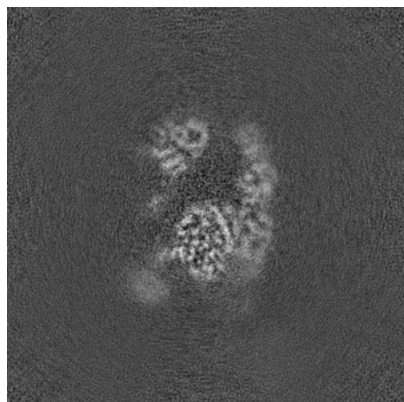


Y Index: 160

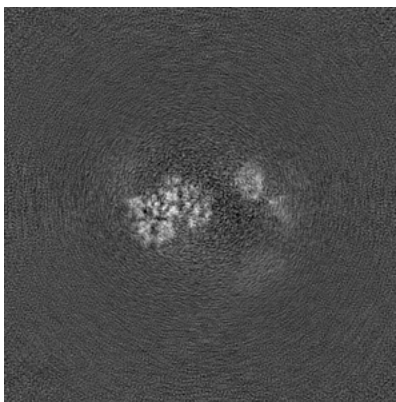


Z Index: 160

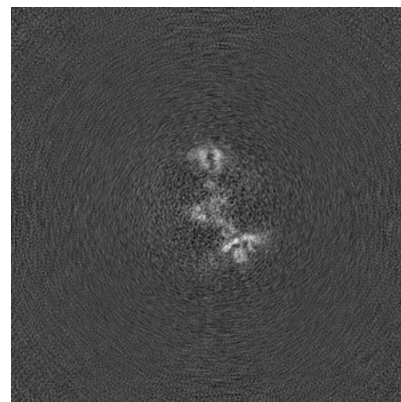
6.2.2 Raw map



X Index: 160



Y Index: 160

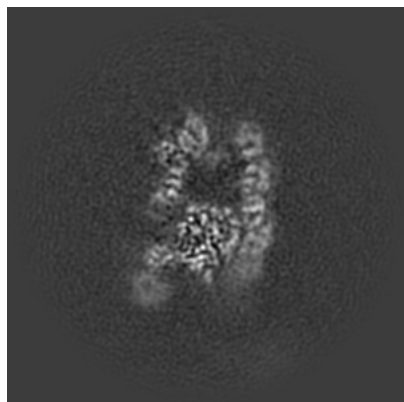


Z Index: 160

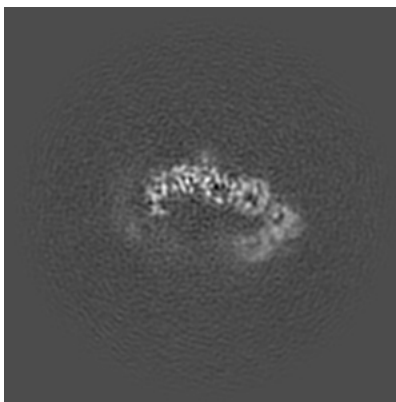
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

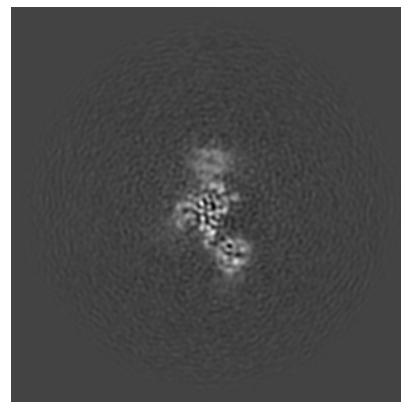
6.3.1 Primary map



X Index: 165

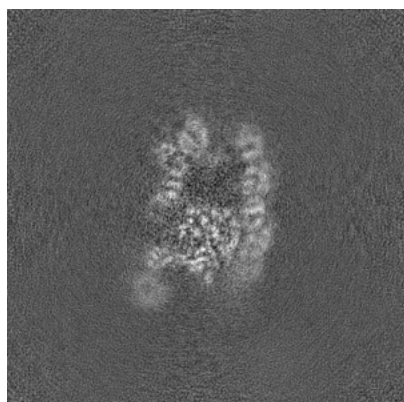


Y Index: 131

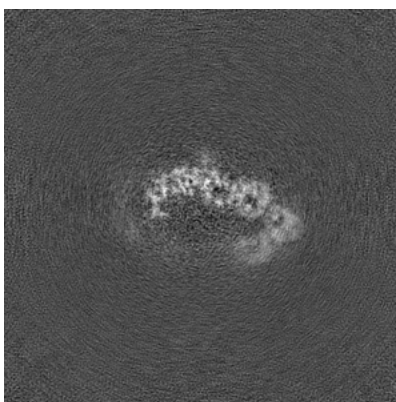


Z Index: 126

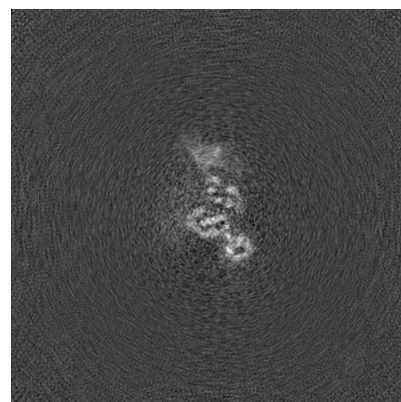
6.3.2 Raw map



X Index: 165



Y Index: 131

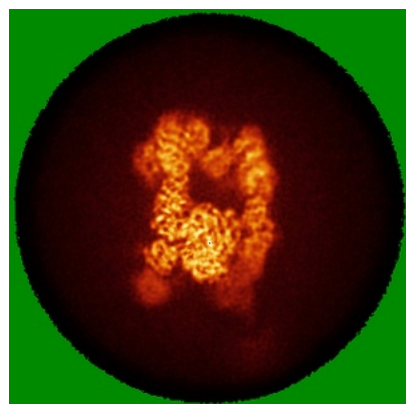


Z Index: 140

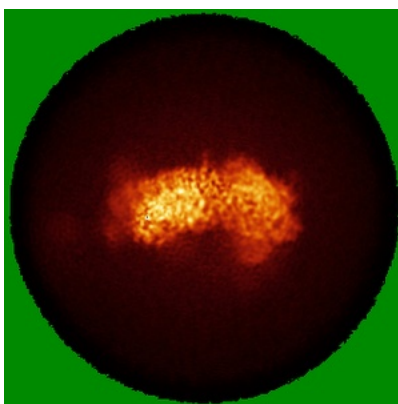
The images above show the largest variance slices of the map in three orthogonal directions.

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

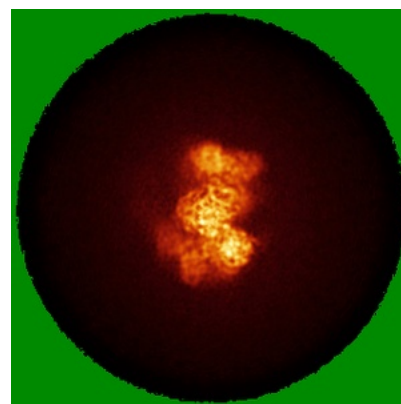
6.4.1 Primary map



X

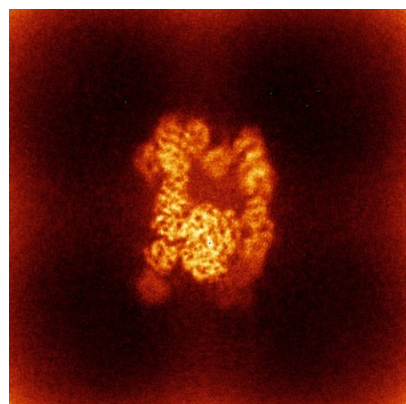


Y

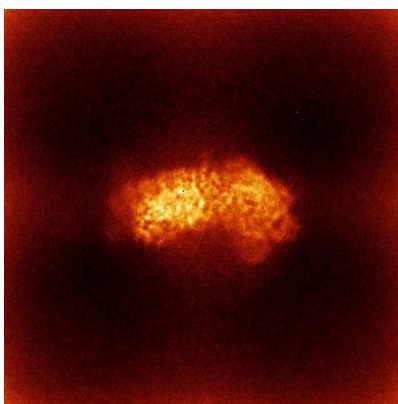


Z

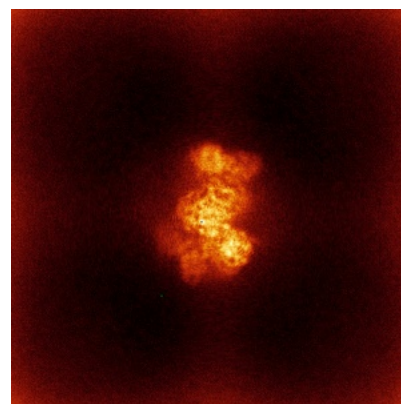
6.4.2 Raw map



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.

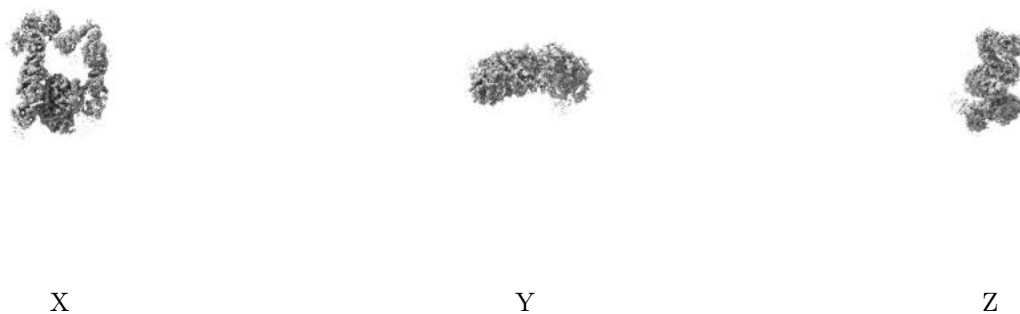
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 1.0. 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.

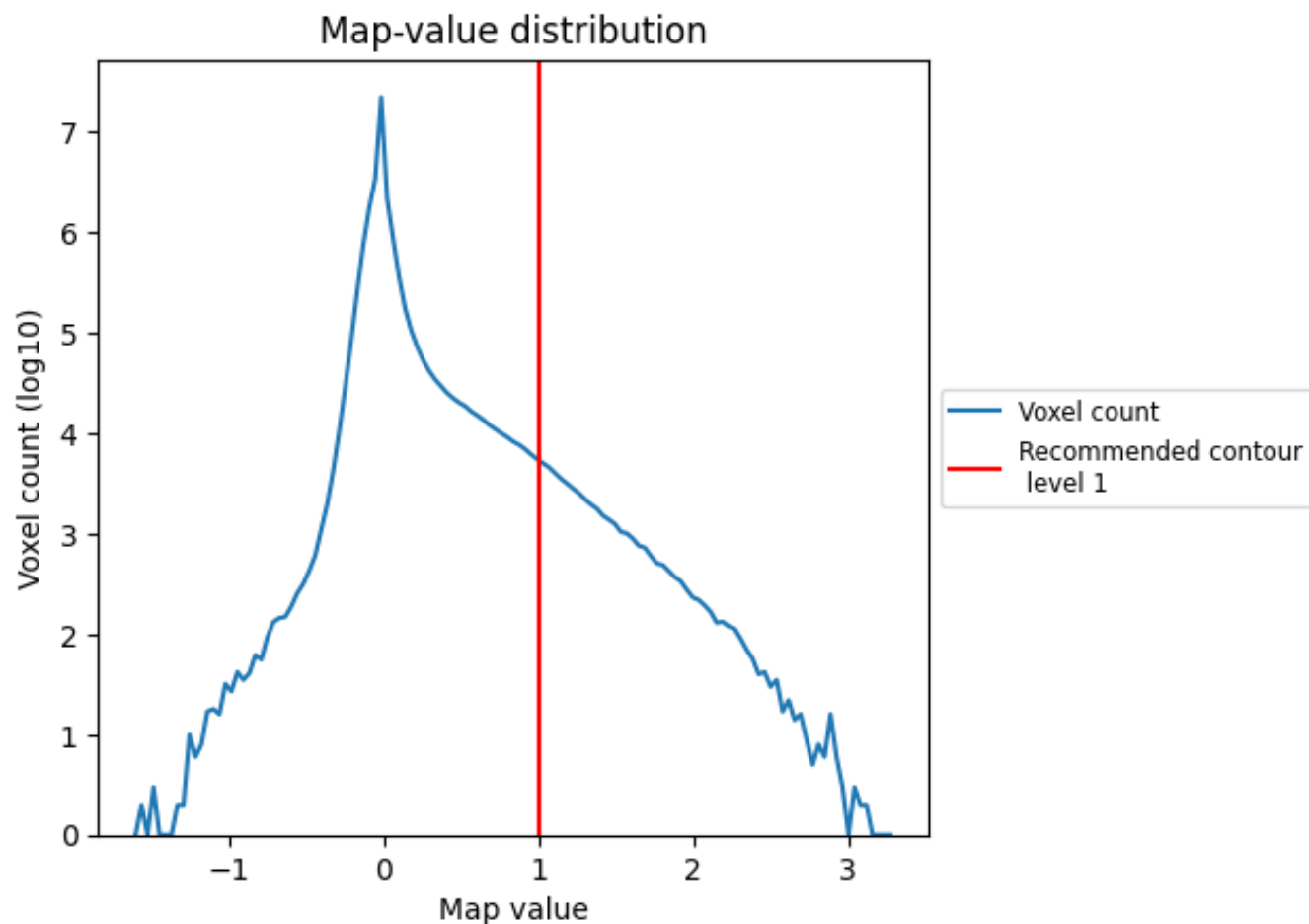
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

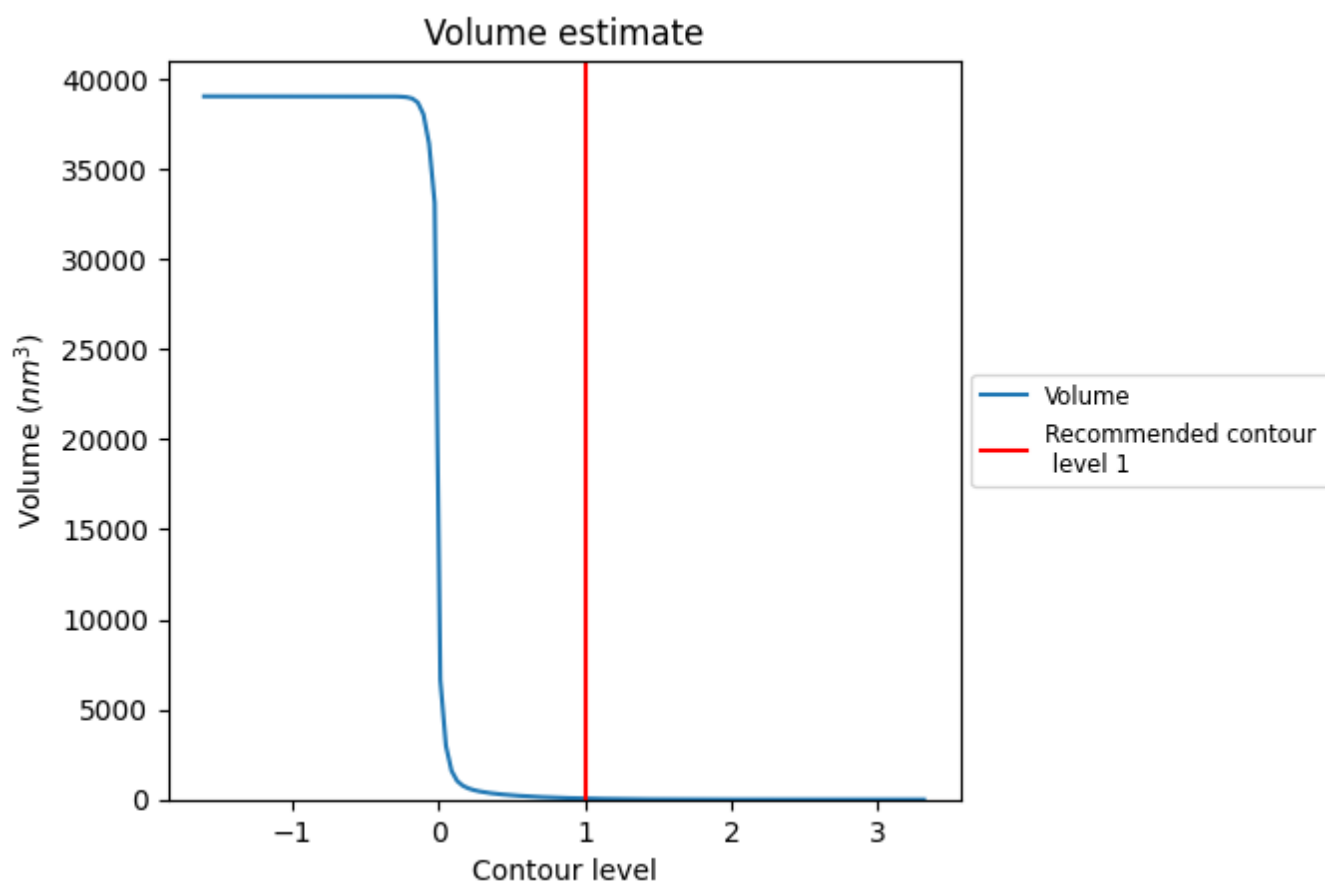
This section contains the results of statistical analysis of the map.

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.

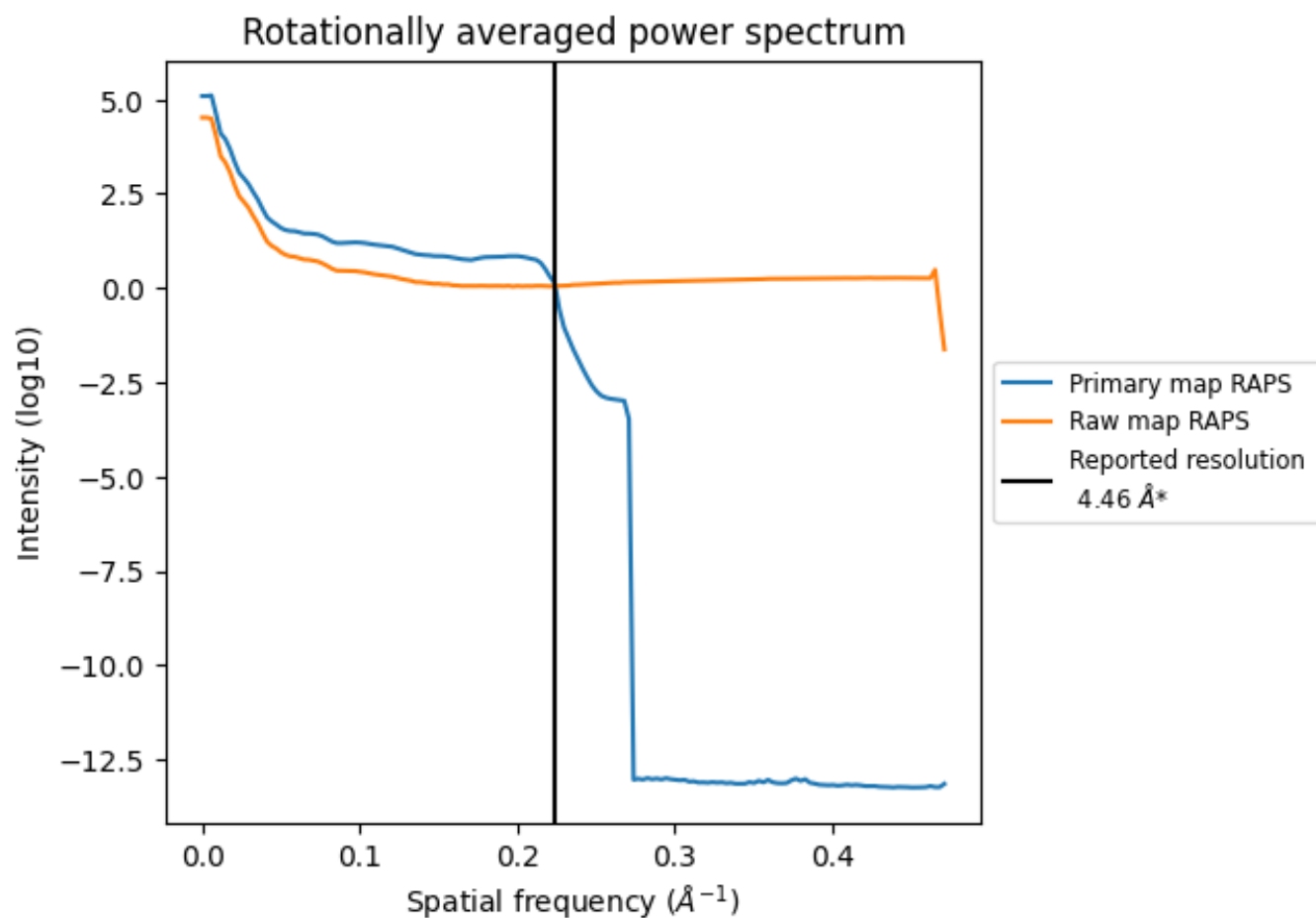
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 59 nm³; this corresponds to an approximate mass of 53 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 ⓘ

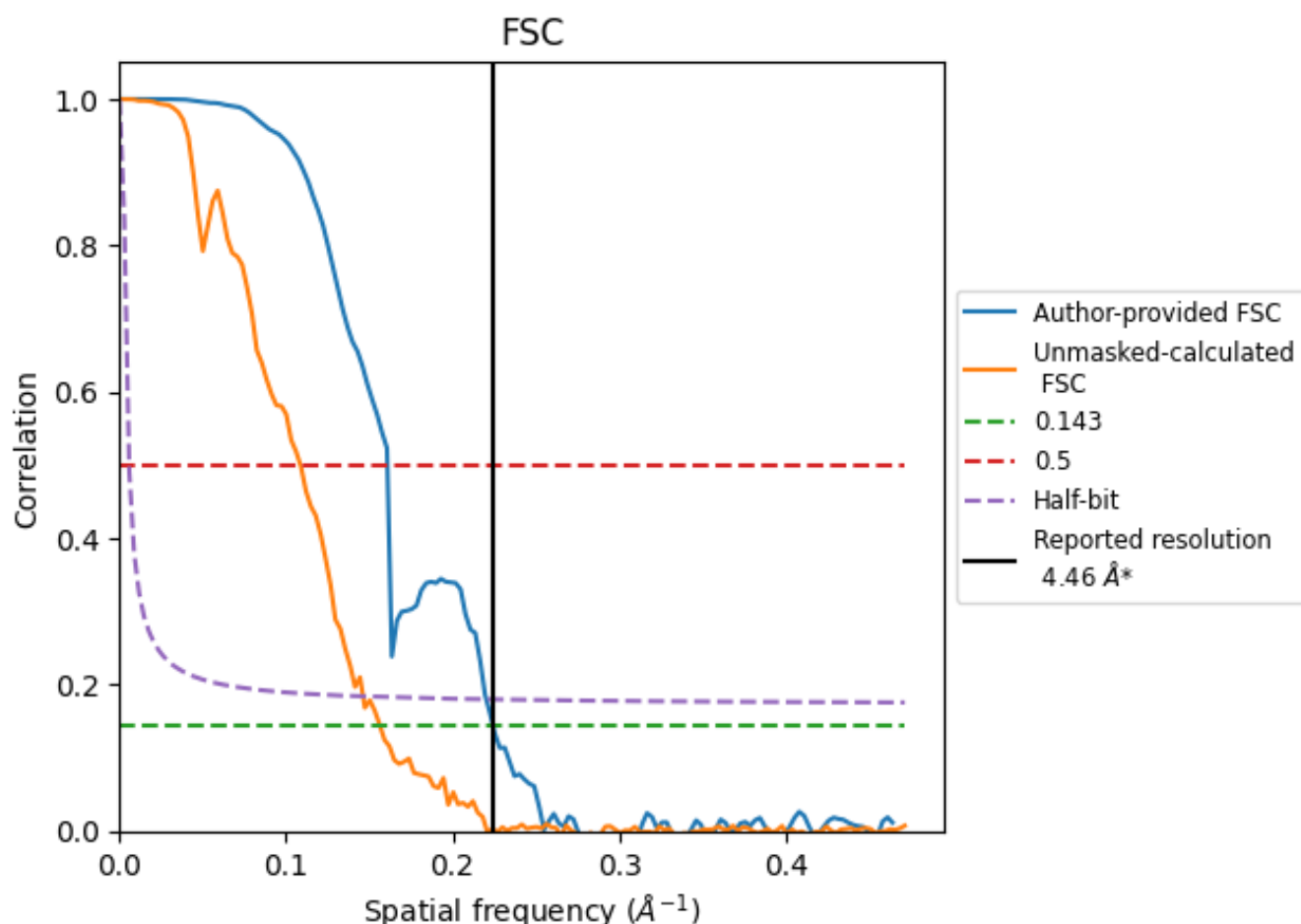


*Reported resolution corresponds to spatial frequency of 0.224 Å⁻¹

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 0.224 Å⁻¹

8.2 Resolution estimates [i](#)

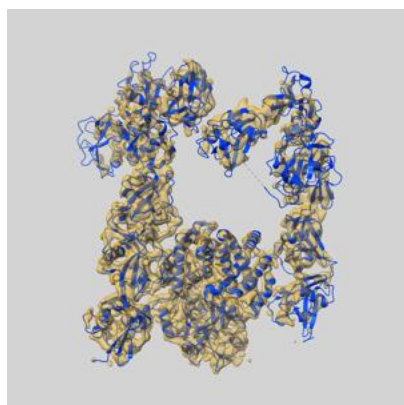
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.46	-	-
Author-provided FSC curve	4.46	6.22	4.54
Unmasked-calculated*	6.39	9.20	6.84

*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 6.39 differs from the reported value 4.46 by more than 10 %

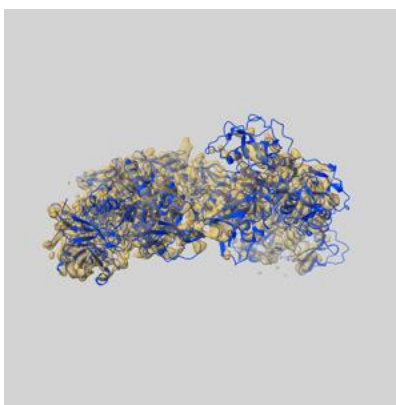
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-50570 and PDB model 9FMU. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

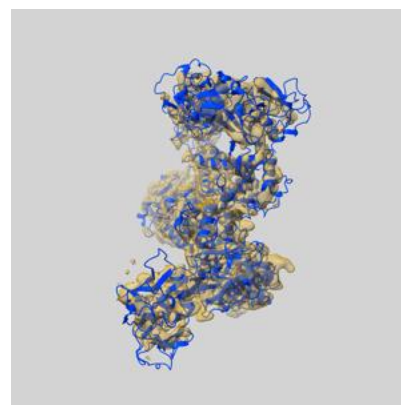
9.1 Map-model overlay [i](#)



X



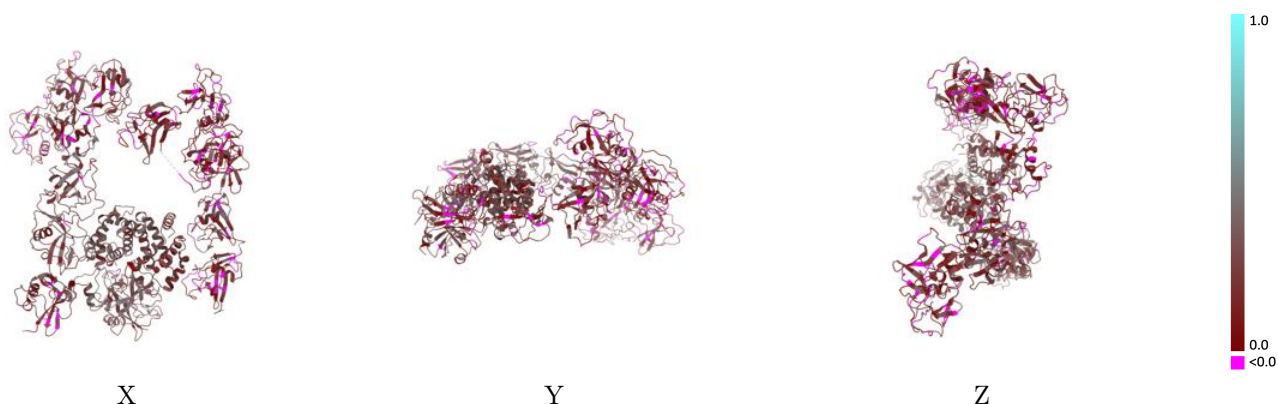
Y



Z

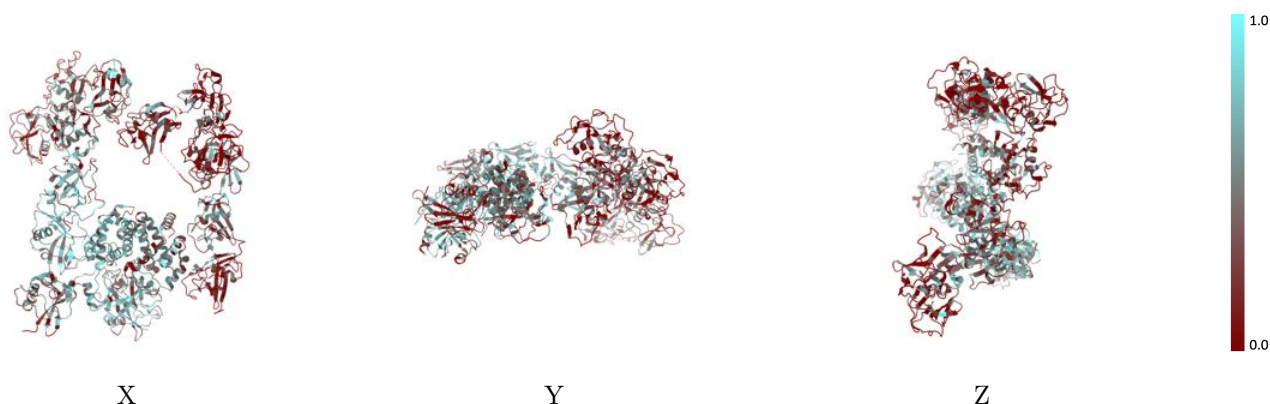
The images above show the 3D surface view of the map at the recommended contour level 1.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



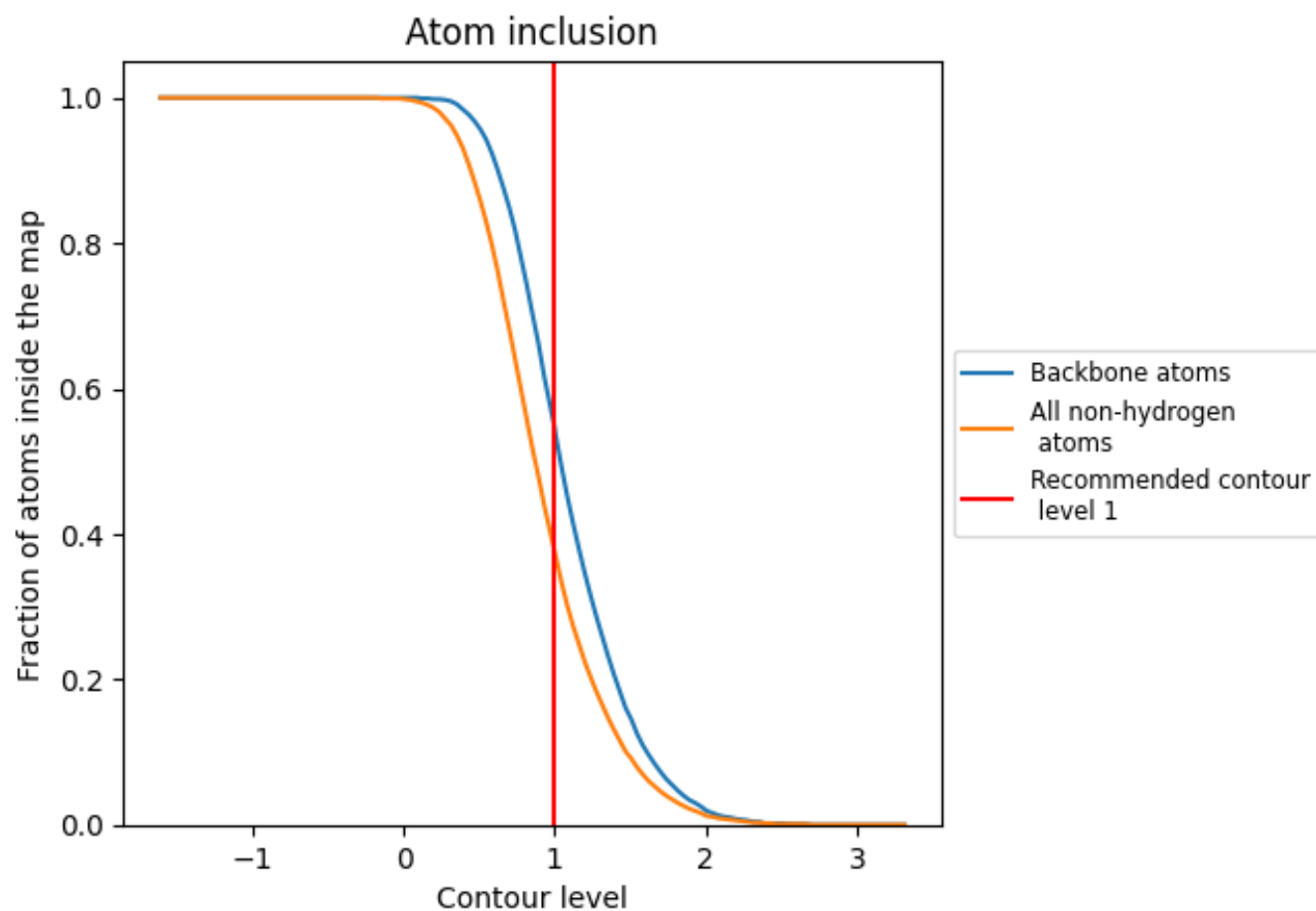
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (1).

9.4 Atom inclusion [i](#)



At the recommended contour level, 55% of all backbone atoms, 38% 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 (1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.3760	<div></div> 0.2330
A	<div></div> 0.5970	<div></div> 0.3190
B	<div></div> 0.4940	<div></div> 0.2800
C	<div></div> 0.5670	<div></div> 0.3160
D	<div></div> 0.3820	<div></div> 0.2330
E	<div></div> 0.2110	<div></div> 0.1660

