



wwPDB EM Validation Summary Report ⓘ

Mar 23, 2026 – 11:39 PM UTC

PDB ID : 9CTO / pdb_00009cto
EMDB ID : EMD-45913
Title : Full length EcPKS2 - acylated dataset with three ACP positions
Authors : Schubert, H.L.; Hill, C.P.
Deposited on : 2024-07-25
Resolution : 3.10 Å(reported)
Based on initial model : .

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

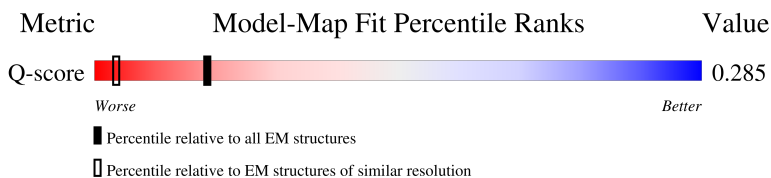
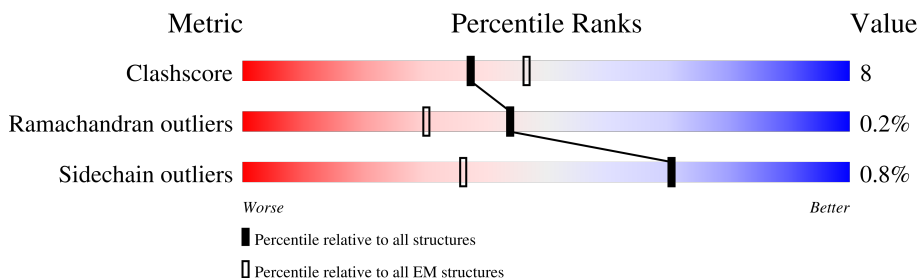
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.10 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	14724 (2.60 - 3.60)

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	2287	18% 83% 15% .
1	B	2287	14% 84% 14% .

2 Entry composition [i](#)

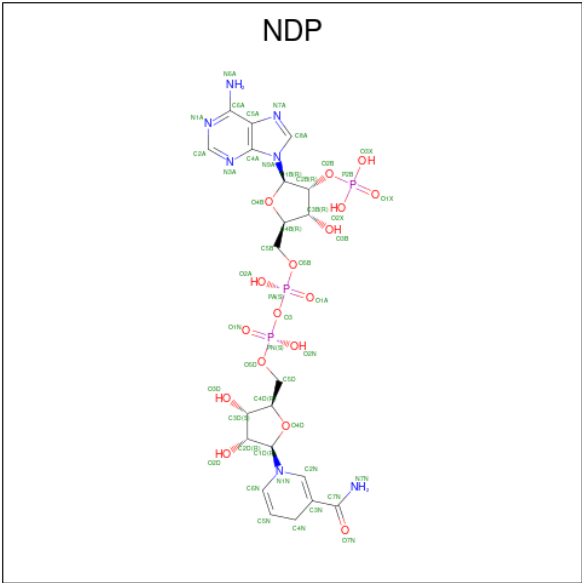
There are 3 unique types of molecules in this entry. The entry contains 69760 atoms, of which 34121 are hydrogens and 0 are deuteriums.

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 Polyketide synthase 2.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
1	A	2245	34773	11448	16717	3068	3426	114	84	0
1	B	2244	34745	11066	17306	2967	3298	108	2	0

- Molecule 2 is NADPH DIHYDRO-NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (CCD ID: NDP) (formula: C₂₁H₃₀N₇O₁₇P₃) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						AltConf
			Total	C	H	N	O	P	
2	A	1	74	21	26	7	17	3	0
2	B	1	74	21	26	7	17	3	0

- Molecule 3 is {S}-[2-[3-[(2 {R})-3,3-dimethyl-2-oxidanyl-4-phosphonooxy-butanoyl]amino]propanoylamino]ethyl] ethanethioate (CCD ID: 6VG) (formula: C₁₃H₂₅N₂O₈PS).

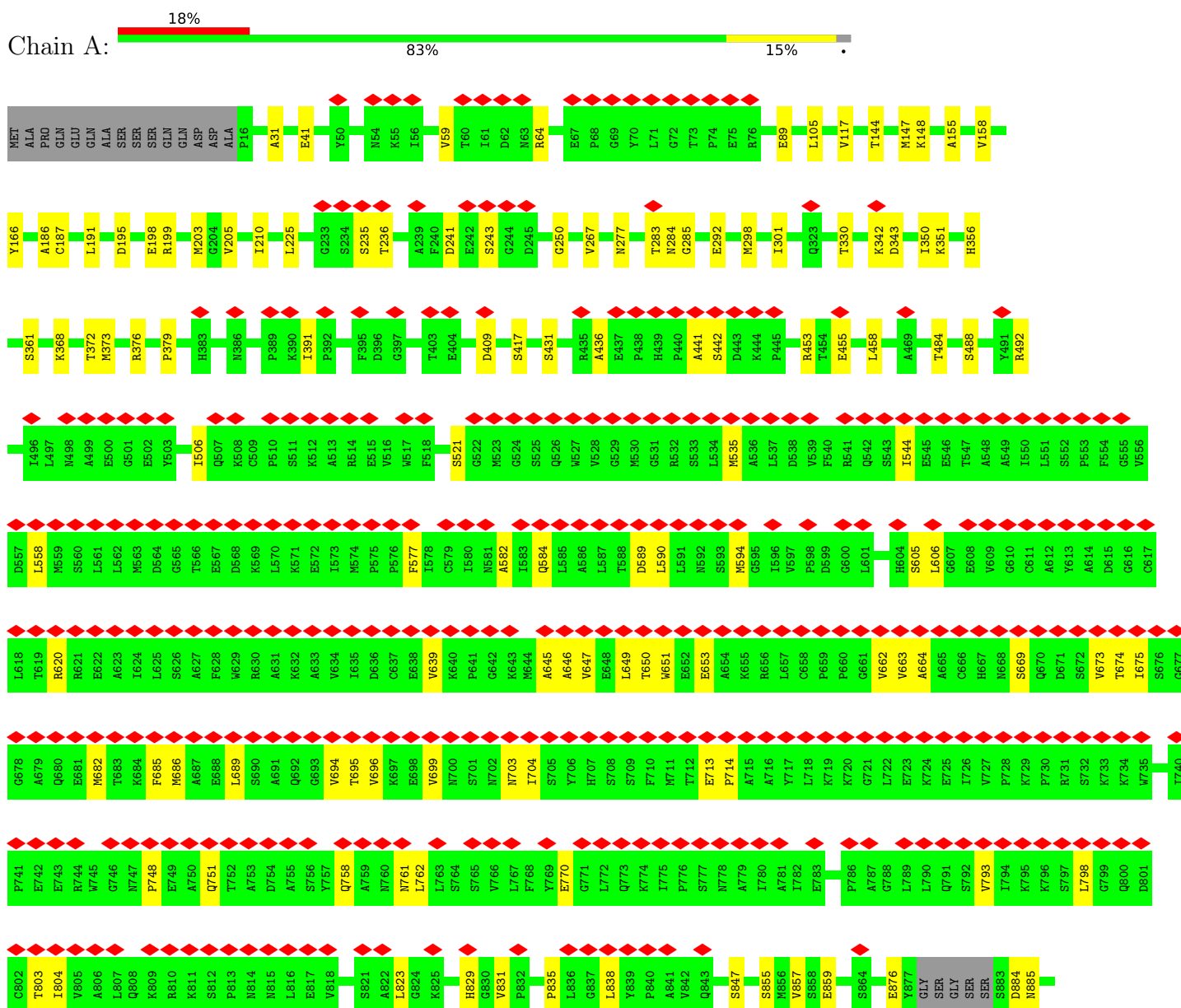


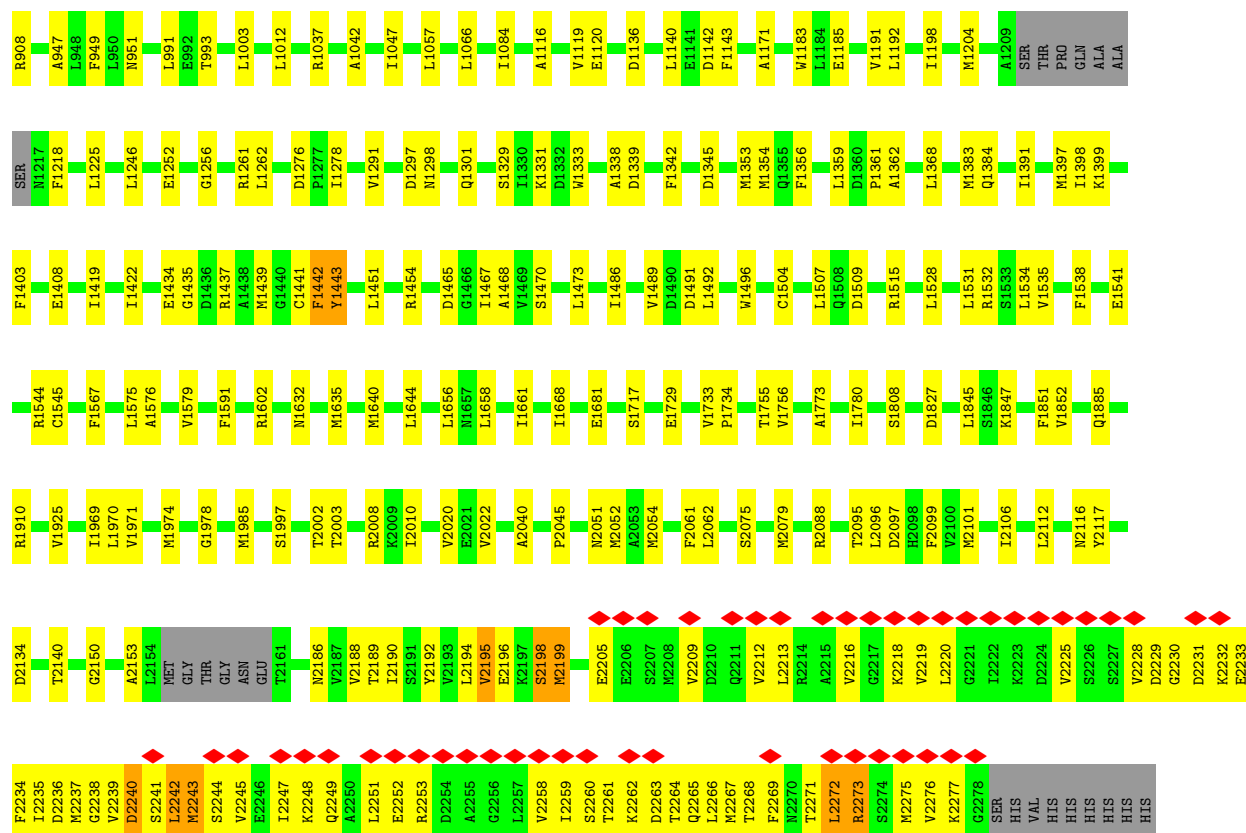
Mol	Chain	Residues	Atoms							AltConf
3	A	1	Total 47	C 13	H 23	N 2	O 7	P 1	S 1	1
3	B	1	Total 47	C 13	H 23	N 2	O 7	P 1	S 1	0

3 Residue-property plots

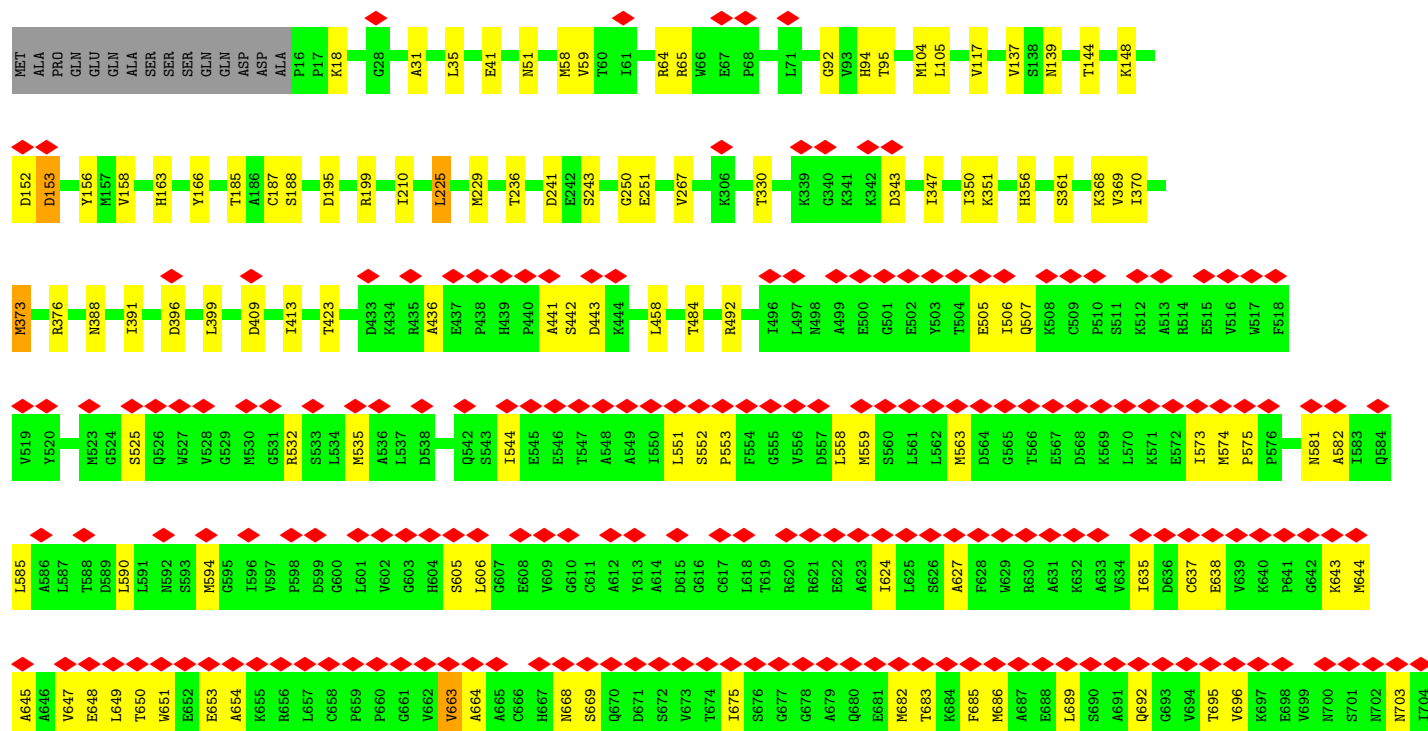
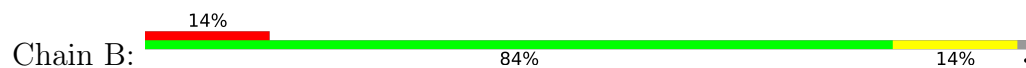
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Polyketide synthase 2





• Molecule 1: Polyketide synthase 2



E2205	E2206	V2209	L2213	R2214	V2219	D2229	G2230	D2231	I2235	V2239	S2240	L2241	L2242	M2243	I2247	R2253	M2267	L2272	G2278	SER	HIS	VAL	HIS	HIS	HIS	HIS	HIS	HIS
M2052	L2056	L2073	L2077	L2076	M2079	L2080	M2081	L2082	L2083	S2087	F2099	V2100	M2101	N2116	Y2117	E2125	R2131	Q2142	W2143	I2146	A2153	LEU	MET	GLY	THR	GLY	ASN	GLU
E1779	R1803	E1814	K1815	I1816	I1817	R1818	T1821	R1843	K1848	D1859	S1860	Q1863	T1868	R1875	Q1885	E1888	R1910	V1925	R1929	E1930	A1931	G1932	K1933	Q1944	C1961	V1971	M1977	G1978
M1439	G1440	Y1443	H1455	E1458	Q1459	I1460	M1461	H1462	A1468	L1473	L1474	I1486	V1489	K1512	R1515	V1527	L1531	L1543	R1544	C1545	I1560	F1567	V1571	R1572	K1573	D1574	R1659	D1660
R1270	D1276	P1277	I1278	E1283	V1291	T1294	M1298	E1308	Y1316	V1337	V1343	E1344	D1345	A1346	L1359	D1360	P1361	A1362	L1368	L1377	K1378	L1381	Q1382	M1383	Q1384	L1387	D1388	I1391
I1047	D1050	S1055	T1059	P1076	A1116	R1122	S1123	D1136	D1142	V1149	R1152	D1155	R1156	M1180	W1183	L1184	E933	N951	E976	T984	S985	S986	L990	T993	D994	Q995	D1008	K1009
H829	Q830	N834	L838	Y839	P840	A841	S847	V857	E876	Y877	GLY	SER	GLY	SER	SER	S883	L891	L901	V930	E931	F932	E933	N951	E976	T984	S985	S986	L990
S705	Y706	H707	S708	S709	F710	M711	T712	E713	P714	A715	A716	Y717	L718	K719	K720	I780	G721	L722	E723	K724	E725	I726	V727	P728	K729	P730	R731	S732
S765	V766	L767	F768	Y769	E770	G771	L772	Q773	K774	I775	P776	S777	N778	A779	I780	SER	A781	A785	G788	L789	L790	Q791	S792	V793	I794	K795	K796	S797
S705	Y706	H707	S708	S709	F710	M711	T712	E713	P714	A715	A716	Y717	L718	K719	K720	I780	G721	L722	E723	K724	E725	I726	V727	P728	K729	P730	R731	S732
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S705	Y706	H707	S708	S709	F710	M711	T712	E713	P714	A715	A716	Y717	L718	K719	K720	I780	G721	L722	E723	K724	E725	I726	V727	P728	K729	P730	R731	S732
S765	V766	L767	F768	Y769	E770	G771	L772	Q773	K774	I775	P776	S777	N778	A779	I780	SER	A781	A785	G788	L789	L790	Q791	S792	V793	I794	K795	K796	S797
S705	Y706	H707	S708	S709	F710	M711	T712	E713	P714	A715	A716	Y717	L718	K719	K720	I780	G721	L722	E723	K724	E725	I726	V727	P728	K729	P730	R731	S732
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S705	Y706	H707	S708	S709	F710	M711	T712	E713	P714	A715	A716	Y717	L718	K719	K720	I780	G721	L722	E723	K724	E725	I726	V727	P728	K729	P730	R731	S732
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S705	Y706	H707	S708	S709	F710	M711	T712	E713	P714	A715	A716	Y717	L718	K719	K720	I780	G721	L722	E723	K724	E725	I726	V727	P728	K729	P730	R731	S732
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S705	Y706	H707	S708	S709	F710	M711	T712	E713	P714	A715	A716	Y717	L718	K719	K720	I780	G721	L722	E723	K724	E725	I726	V727	P728	K729	P730	R731	S732
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S705	Y706	H707	S708	S709	F710	M711	T712	E713	P714	A715	A716	Y717	L718	K719	K720	I780	G721	L722	E723	K724	E725	I726	V727	P728	K729	P730	R731	S732
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S705	Y706	H707	S708	S709	F710	M711	T712	E713	P714	A715	A716	Y717	L718	K719	K720	I780	G721	L722	E723	K724	E725	I726	V727	P728	K729	P730	R731	S732
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S765	V766	L767	F768	Y769	E770	G771	L772	Q773	K774	I775	P776	S777	N778	A779	I780	SER	A781	A785	G788	L789	L790	Q791	S792	V793</				

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	168733	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)	800	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.779	Depositor
Minimum map value	-0.281	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.026	Depositor
Recommended contour level	0.0704	Depositor
Map size (Å)	317.99997, 317.99997, 317.99997	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	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: 6VG, SCY, NDP

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	0/18441	0.30	0/24958
1	B	0.14	0/17812	0.32	2/24120 (0.0%)
All	All	0.15	0/36253	0.31	2/49078 (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
1	A	0	4

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	B	2198	SER	N-CA-CB	5.90	120.47	110.49
1	B	2198	SER	CB-CA-C	5.07	120.50	110.42

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	2195	VAL	Mainchain
1	A	2205[B]	GLU	Mainchain
1	A	2273[A]	ARG	Sidechain

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	18056	16717	17948	304	0
1	B	17439	17306	17307	240	0
2	A	48	26	26	2	0
2	B	48	26	26	3	0
3	A	24	23	0	0	0
3	B	24	23	0	1	0
All	All	35639	34121	35307	532	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 8.

The worst 5 of 532 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:A:2241[B]:SER:C	1:A:2242[B]:LEU:N	1.87	1.33
1:A:949:PHE:HE2	1:A:2245[B]:VAL:HG23	1.15	1.05
1:A:285:GLY:HA3	1:A:2240[A]:ASP:CB	1.93	0.98
1:A:285:GLY:HA3	1:A:2240[A]:ASP:OD2	1.65	0.95
1:A:1329:SER:OG	1:A:2194:LEU:HD11	1.69	0.91

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	2319/2287 (101%)	2227 (96%)	85 (4%)	7 (0%)	36 67

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	2237/2287 (98%)	2146 (96%)	89 (4%)	2 (0%)	48	78
All	All	4556/4574 (100%)	4373 (96%)	174 (4%)	9 (0%)	44	73

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	2198	SER
1	A	2199[A]	MET
1	A	2199[B]	MET
1	A	186	ALA
1	A	1442	PHE

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	1966/1929 (102%)	1947 (99%)	19 (1%)	68	79
1	B	1891/1929 (98%)	1875 (99%)	16 (1%)	73	81
All	All	3857/3858 (100%)	3822 (99%)	35 (1%)	70	80

5 of 35 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	1404	LEU
1	B	1443	TYR
1	B	1961	CYS
1	A	2240[B]	ASP
1	A	2240[A]	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 30 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	2111	HIS
1	B	2051	ASN

Continued on next page...

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Mol	Chain	Res	Type
1	B	498	ASN
1	B	2186	ASN
1	B	1556	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
1	SCY	B	187	1	7,8,9	0.90	0	4,9,11	0.74	0
1	SCY	A	187	1	7,8,9	0.85	0	4,9,11	0.68	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
1	SCY	B	187	1	-	4/5/7/9	-
1	SCY	A	187	1	-	2/5/7/9	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	187	SCY	OCD-CD-SG-CB
1	A	187	SCY	CE-CD-SG-CB
1	B	187	SCY	N-CA-CB-SG
1	B	187	SCY	C-CA-CB-SG
1	B	187	SCY	OCD-CD-SG-CB

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	187	SCY	1	0
1	A	187	SCY	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

4 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	$\# Z > 2$
3	6VG	B	2302	1	18,23,24	0.34	0	22,30,33	1.10	2 (9%)
2	NDP	A	2301	-	51,52,52	2.38	9 (17%)	71,80,80	1.52	14 (19%)
2	NDP	B	2301	-	51,52,52	2.35	9 (17%)	71,80,80	1.52	16 (22%)

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
3	6VG	B	2302	1	-	13/27/29/30	-
2	NDP	A	2301	-	-	9/34/77/77	0/5/5/5
2	NDP	B	2301	-	-	4/34/77/77	0/5/5/5

The worst 5 of 18 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	2301	NDP	P2B-O2B	13.33	1.82	1.59
2	B	2301	NDP	P2B-O2B	13.04	1.82	1.59
2	A	2301	NDP	PA-O3	4.37	1.64	1.59
2	A	2301	NDP	PN-O5D	4.32	1.76	1.59
2	B	2301	NDP	PA-O3	4.24	1.64	1.59

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	2301	NDP	P2B-O2B-C2B	-4.64	111.04	123.43
2	B	2301	NDP	P2B-O2B-C2B	-4.57	111.22	123.43
2	B	2301	NDP	O2B-P2B-O1X	-3.59	96.54	109.33
2	A	2301	NDP	O2B-P2B-O1X	-3.58	96.59	109.33
2	A	2301	NDP	O3-PA-O1A	-3.32	100.73	110.70

There are no chirality outliers.

5 of 26 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	2301	NDP	C5B-O5B-PA-O1A
2	A	2301	NDP	C5B-O5B-PA-O3
2	B	2301	NDP	O4D-C1D-N1N-C6N
3	B	2302	6VG	C28-C29-C32-O33
3	B	2302	6VG	C28-C29-C32-C34

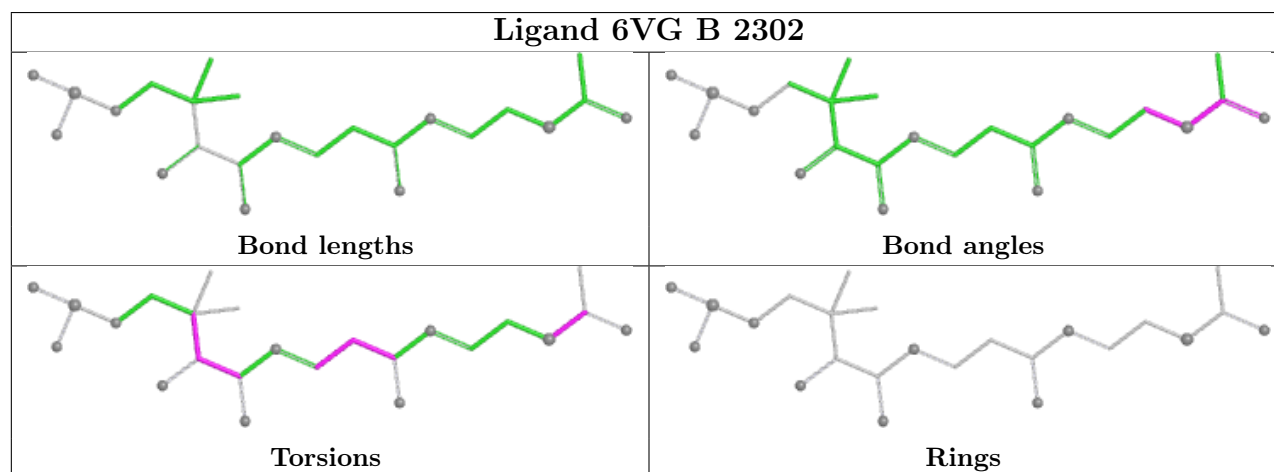
There are no ring outliers.

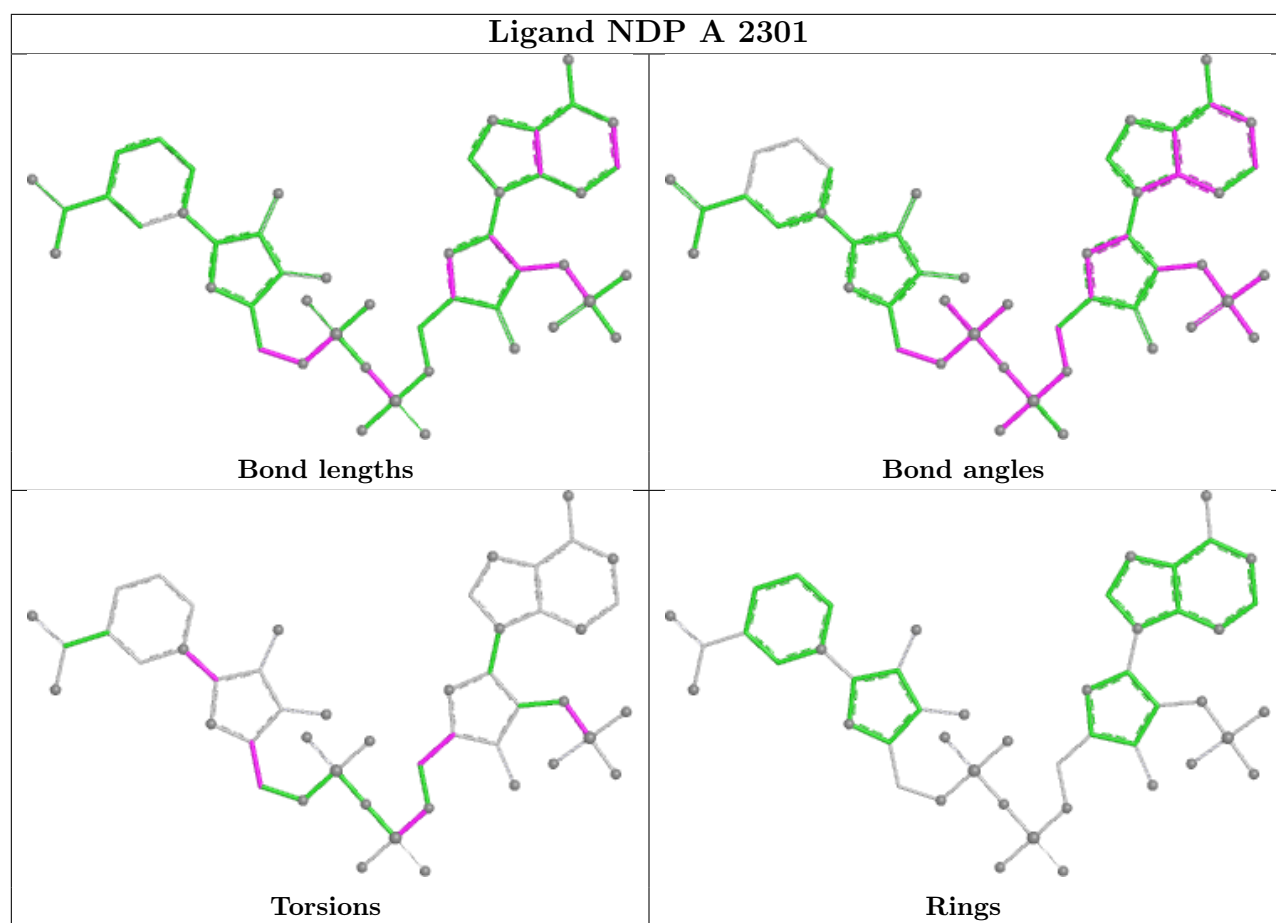
3 monomers are involved in 6 short contacts:

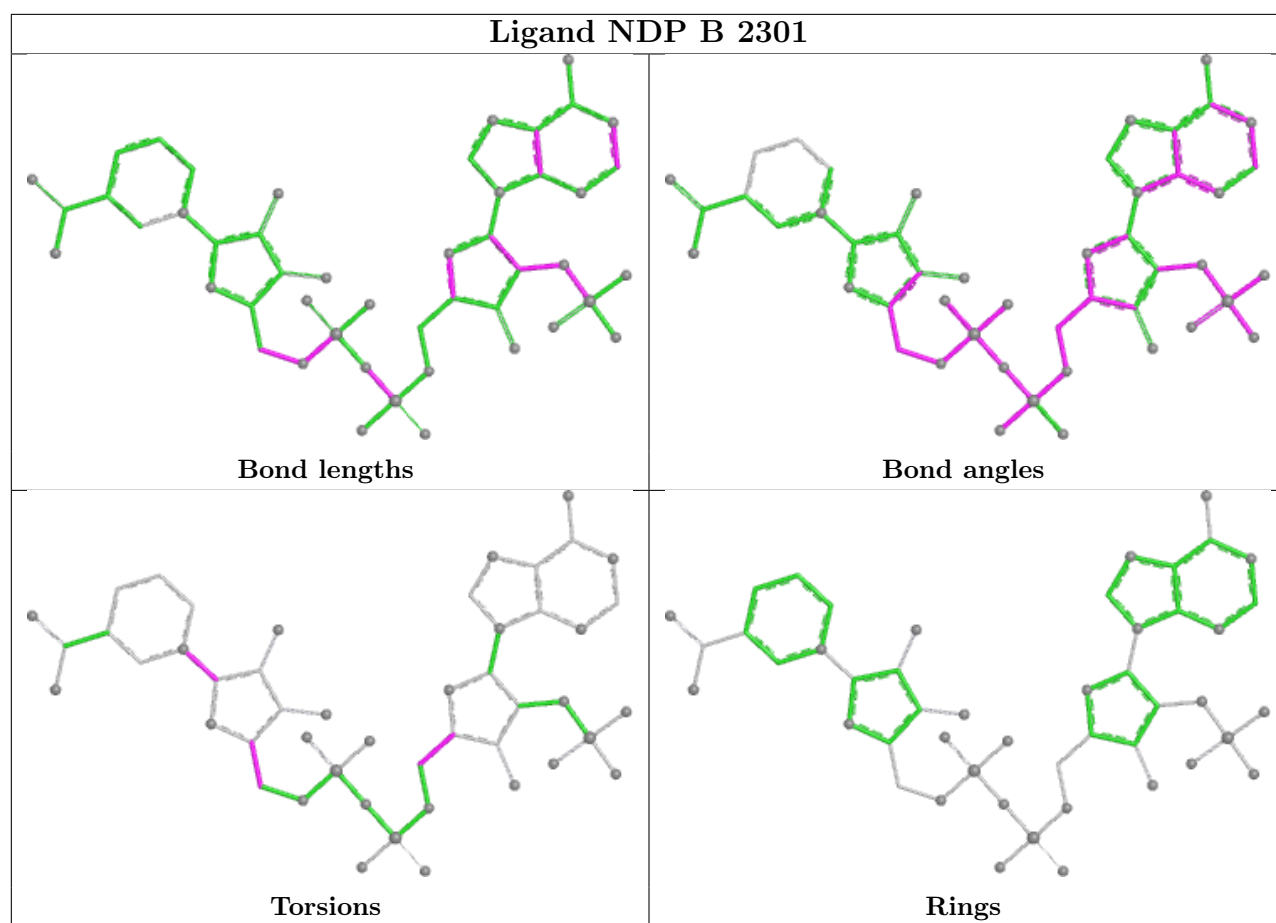
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	2302	6VG	1	0
2	A	2301	NDP	2	0
2	B	2301	NDP	3	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths,

bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.







5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	2241[B]:SER	C	2242[B]:LEU	N	1.87
1	A	2195:VAL	C	2196[A]:GLU	N	1.15

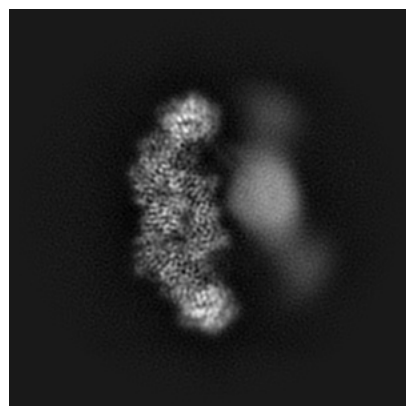
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-45913. These allow visual inspection of the internal detail of the map and identification of artifacts.

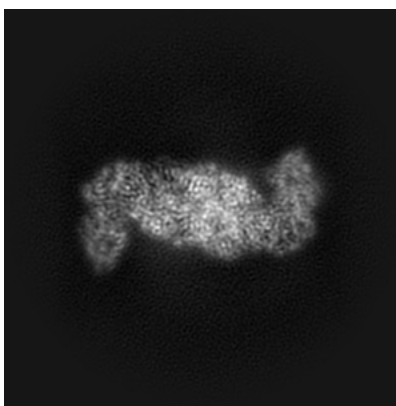
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

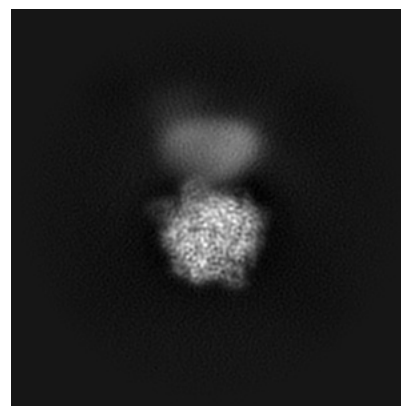
6.1.1 Primary map



X

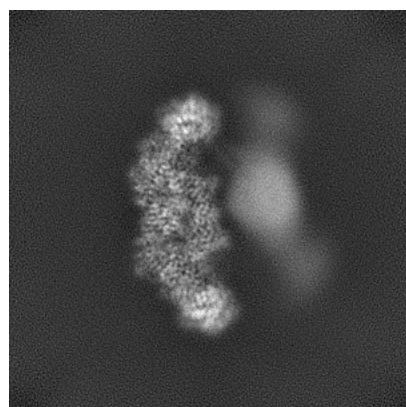


Y

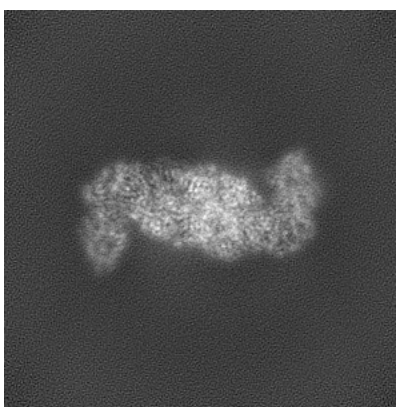


Z

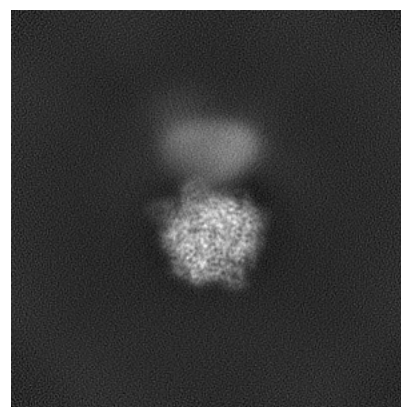
6.1.2 Raw map



X



Y

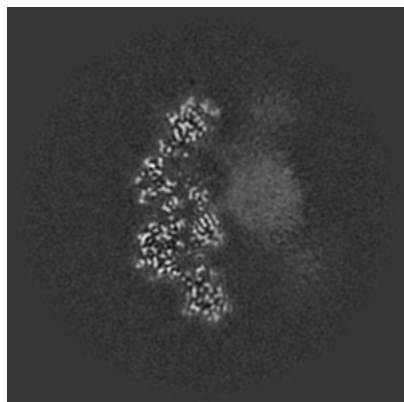


Z

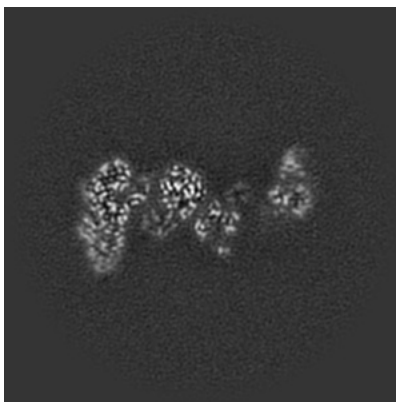
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

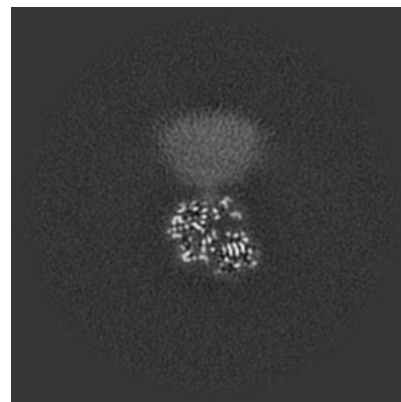
6.2.1 Primary map



X Index: 150

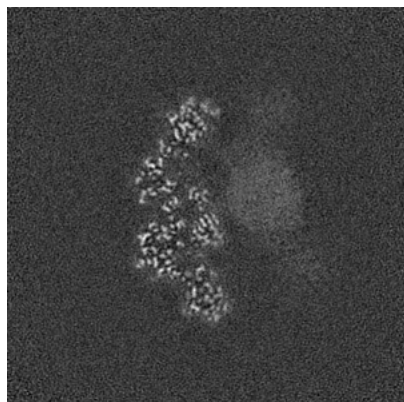


Y Index: 150

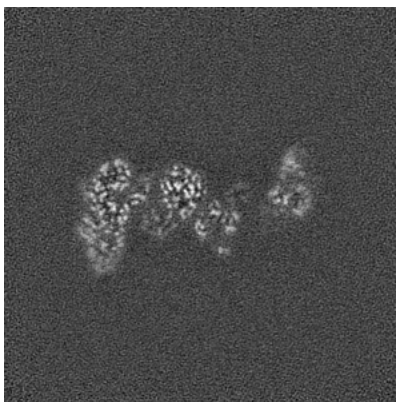


Z Index: 150

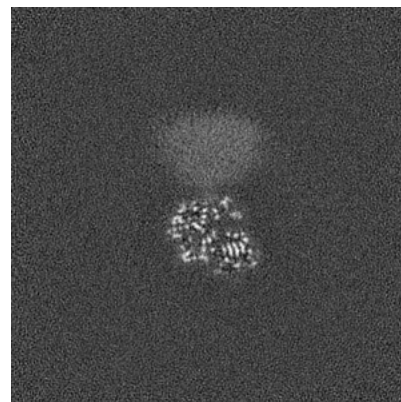
6.2.2 Raw map



X Index: 150



Y Index: 150

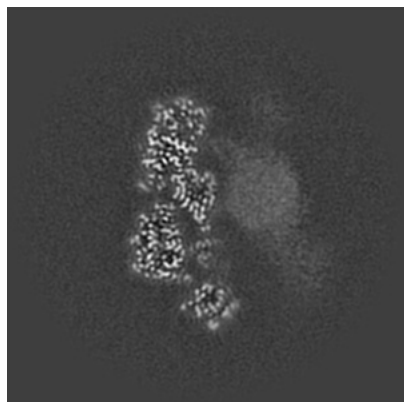


Z Index: 150

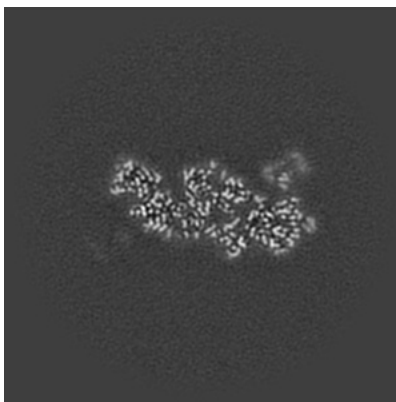
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

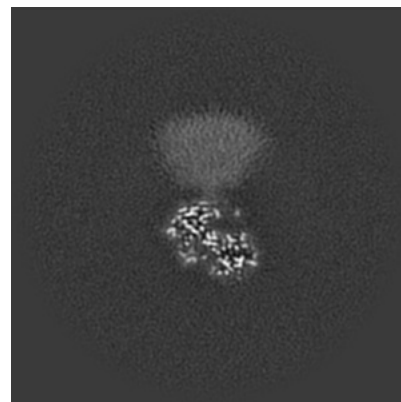
6.3.1 Primary map



X Index: 143

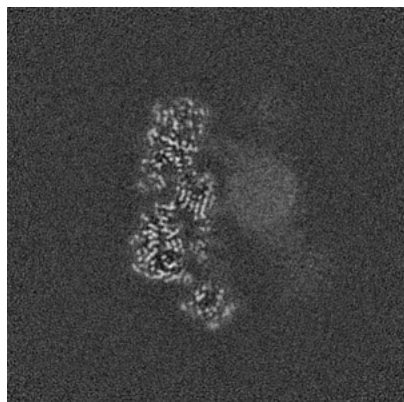


Y Index: 122

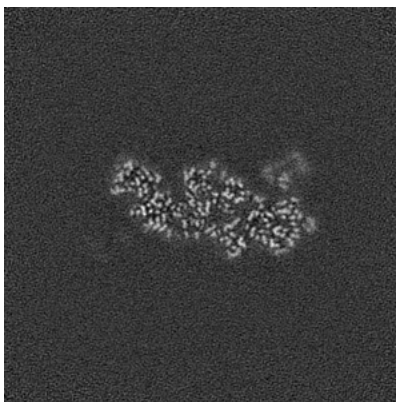


Z Index: 152

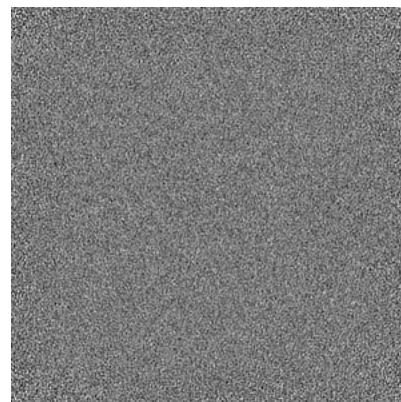
6.3.2 Raw map



X Index: 144



Y Index: 122

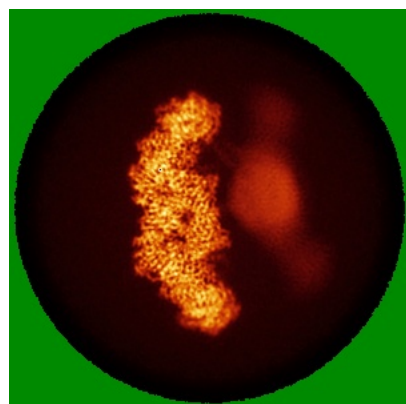


Z Index: 0

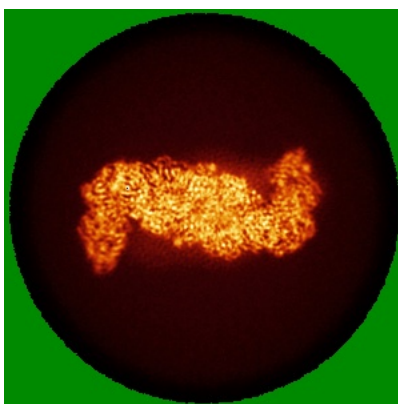
The images above show the largest variance slices of the map in three orthogonal directions.

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

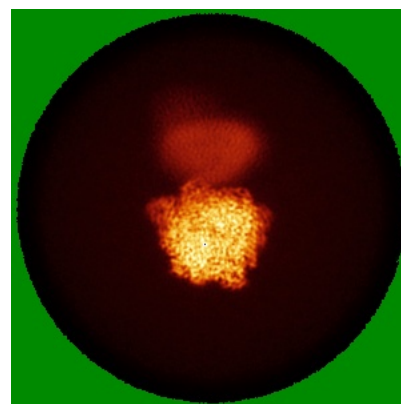
6.4.1 Primary map



X

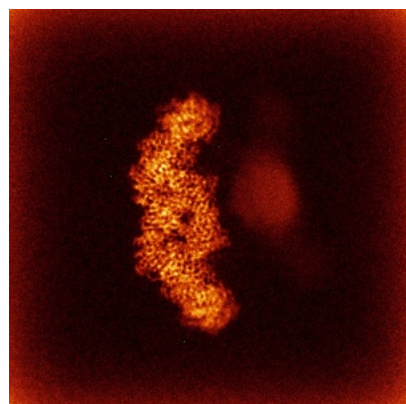


Y

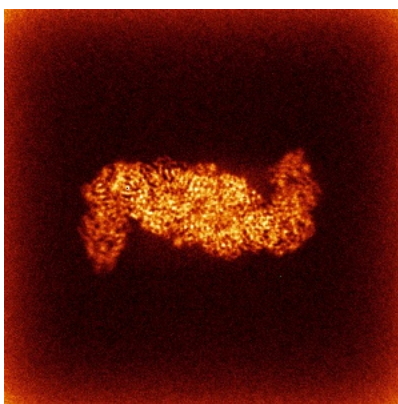


Z

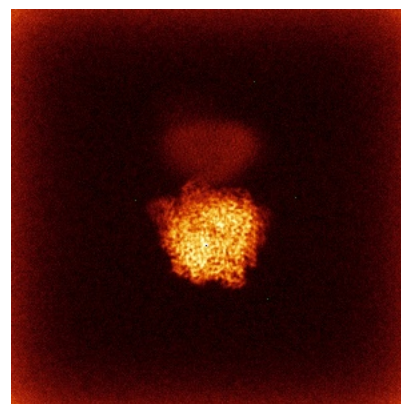
6.4.2 Raw map



X



Y

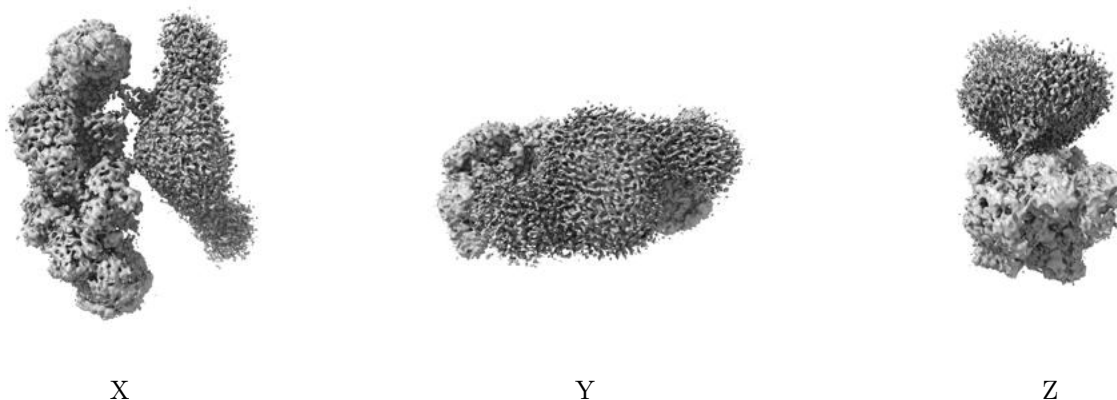


Z

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.

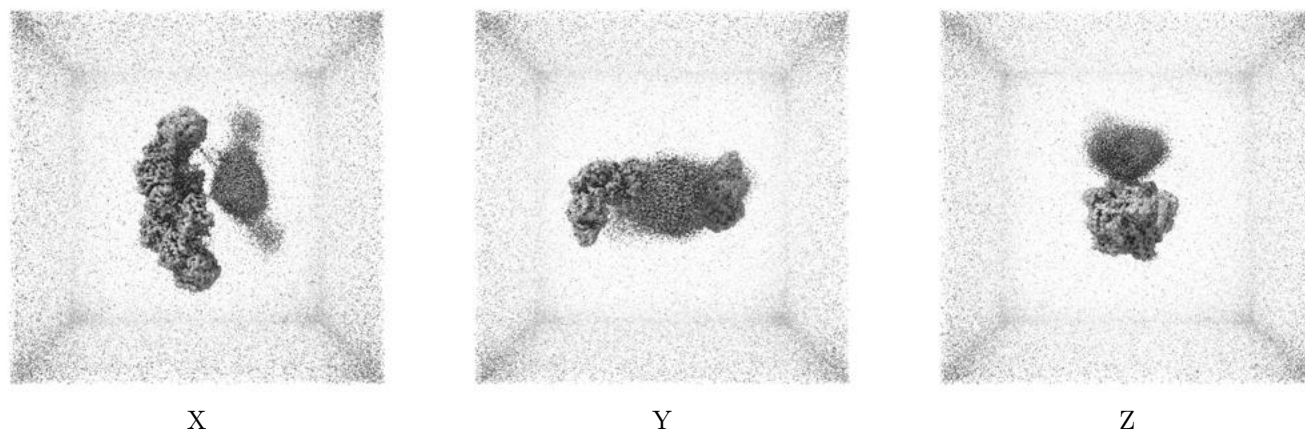
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0704. 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.

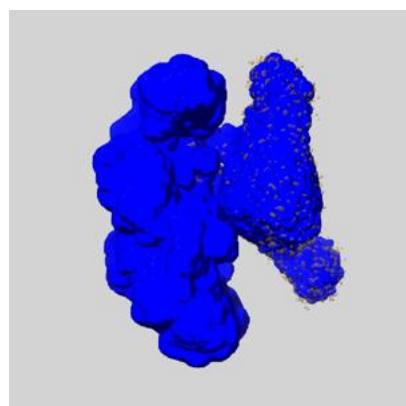
6.6 Mask visualisation [i](#)

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

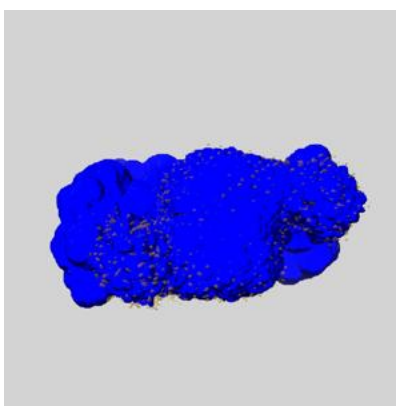
A mask typically either:

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

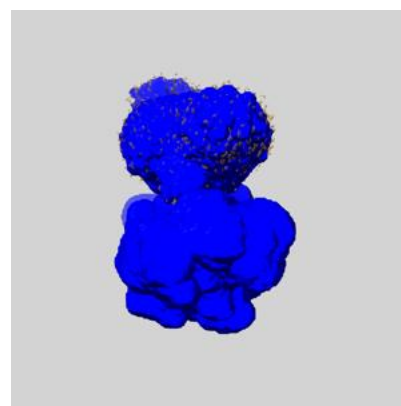
6.6.1 emd_45913_msk_1.map [i](#)



X



Y

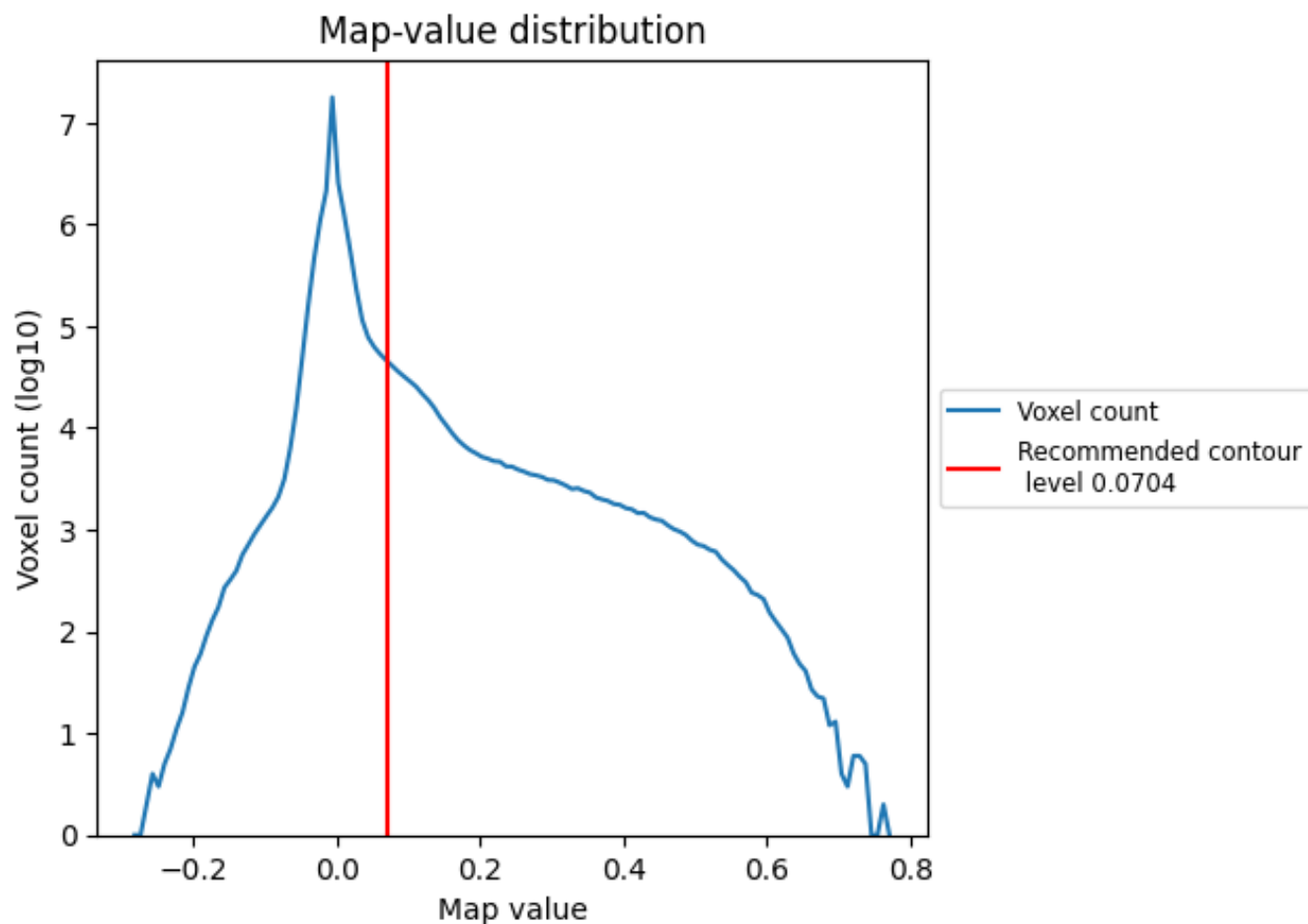


Z

7 Map analysis [i](#)

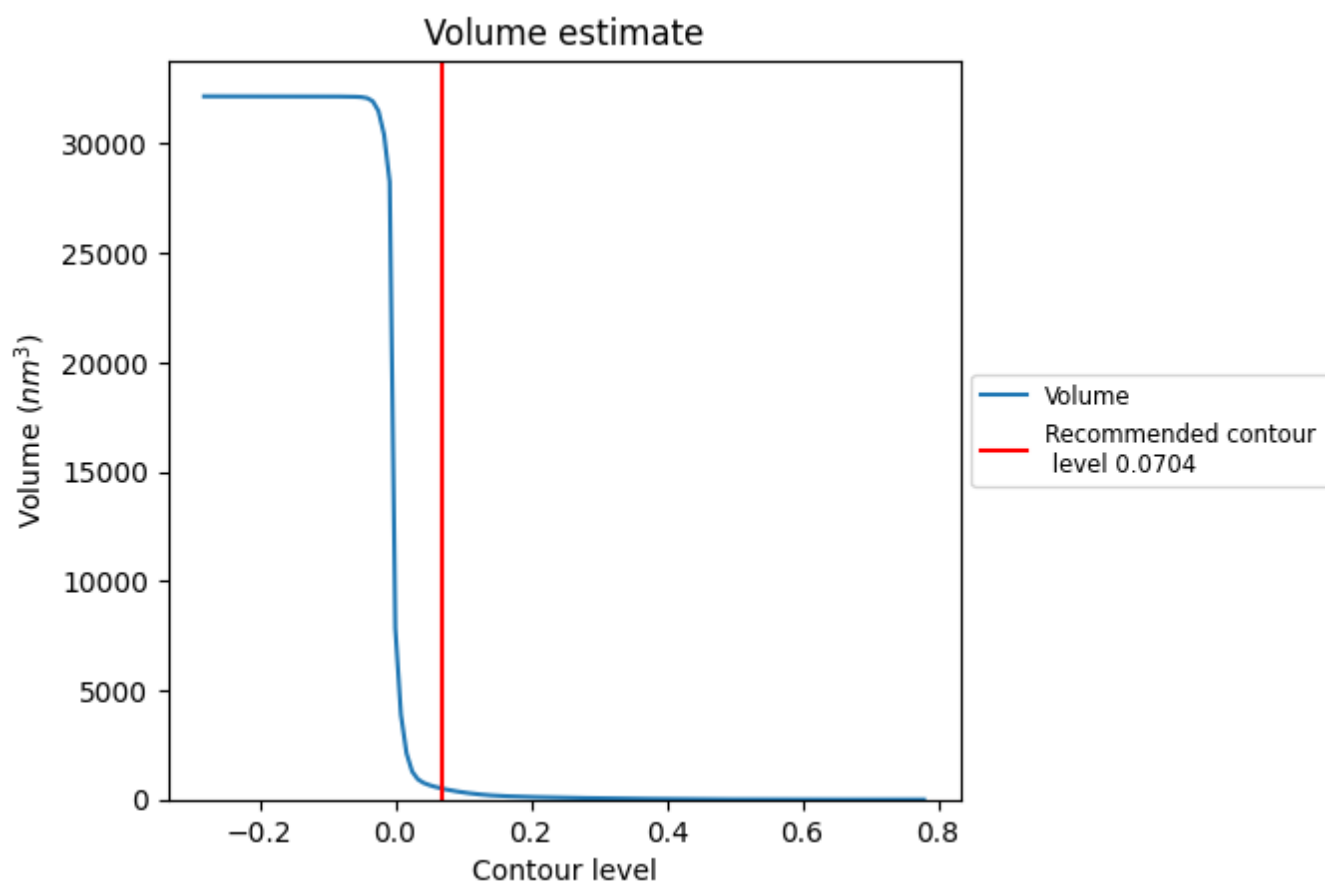
This section contains the results of statistical analysis of the map.

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.

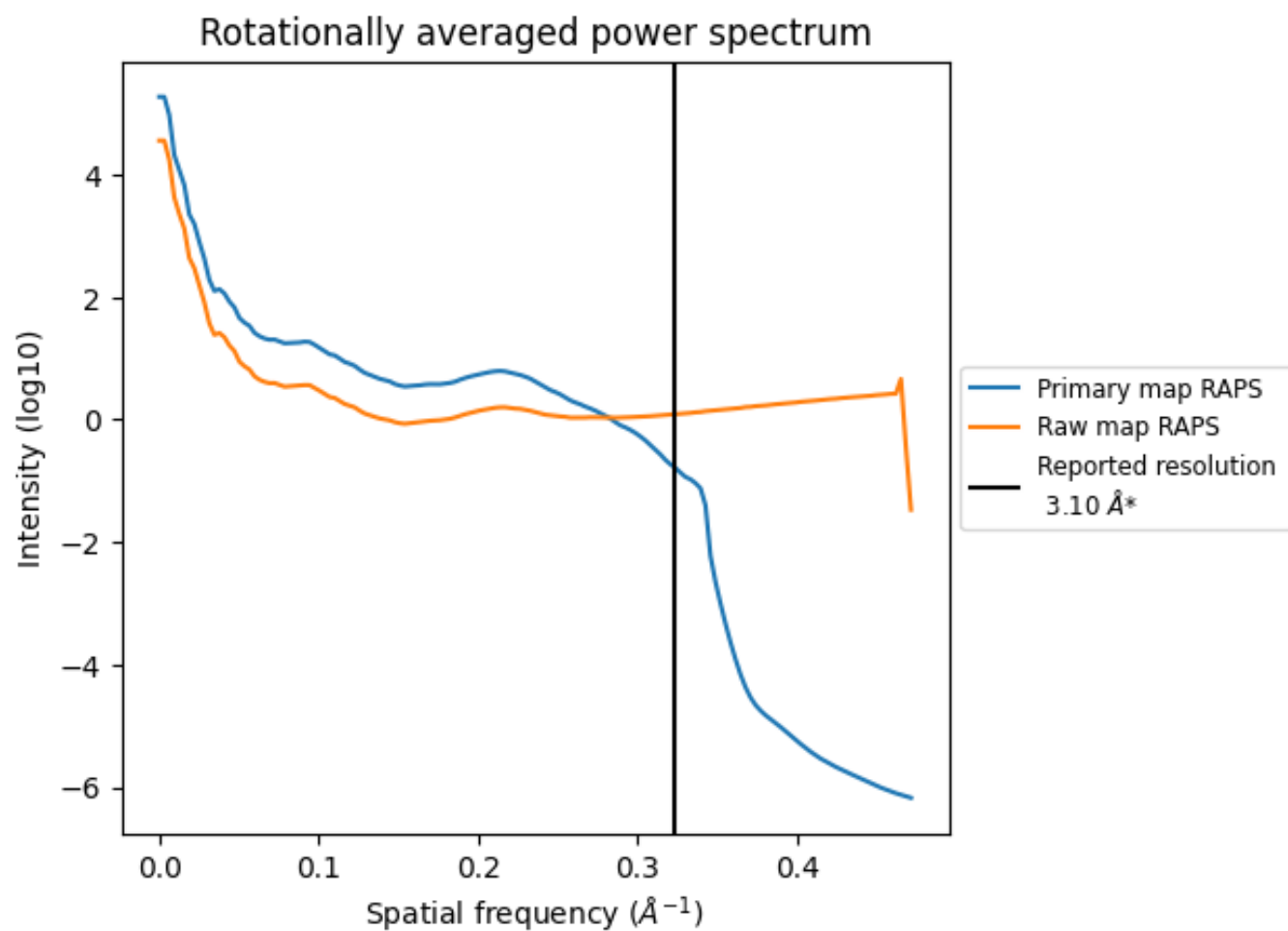
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 494 nm³; this corresponds to an approximate mass of 447 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 ⓘ

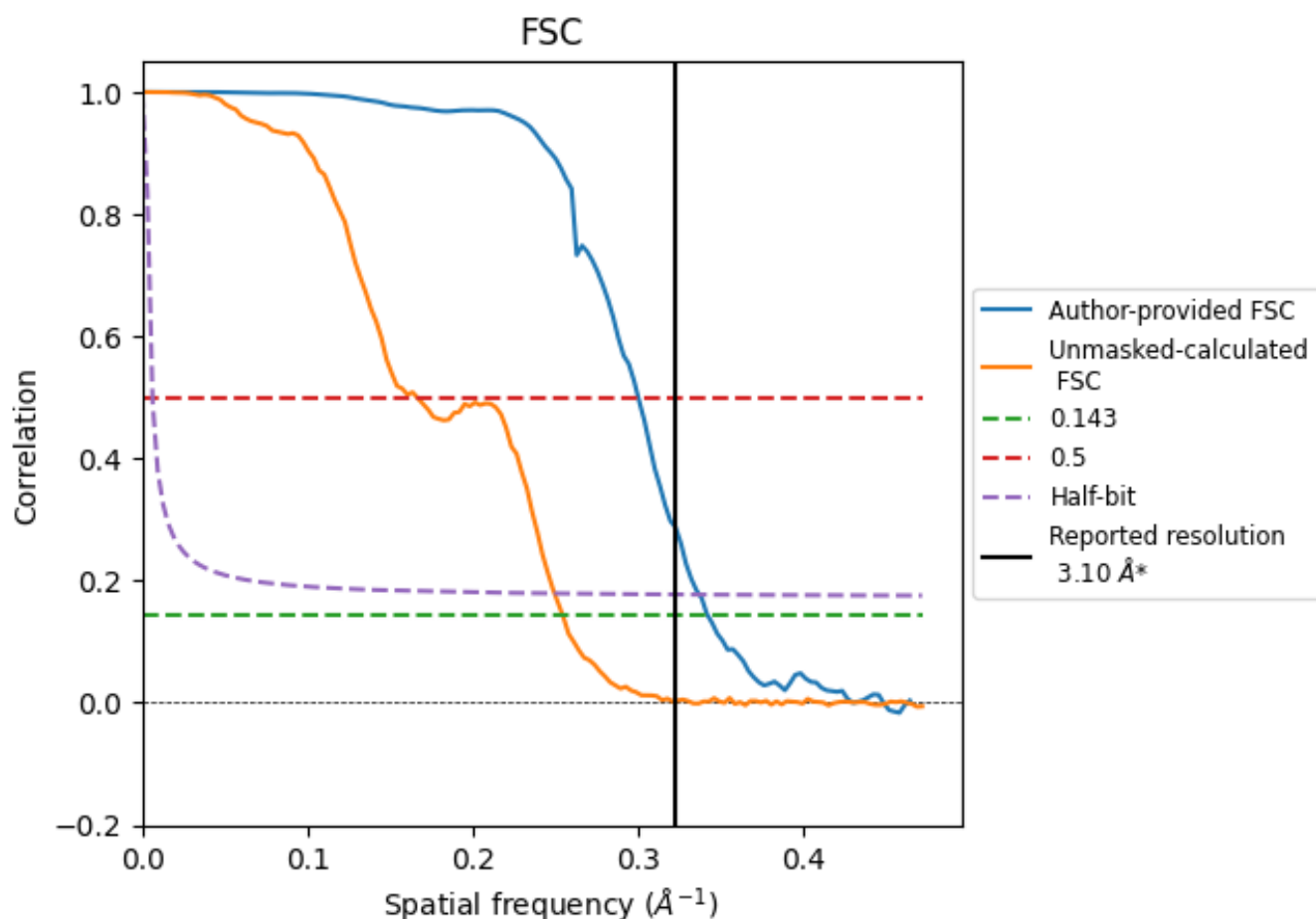


*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

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 0.323 Å⁻¹

8.2 Resolution estimates [i](#)

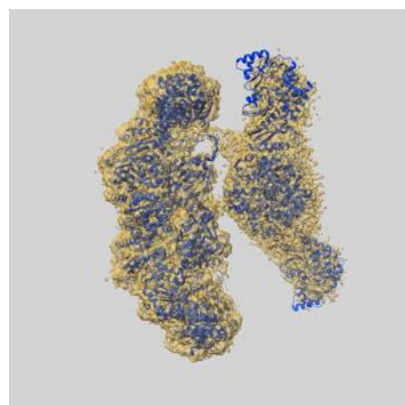
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	2.92	3.33	2.97
Unmasked-calculated*	3.93	6.01	4.01

*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 3.93 differs from the reported value 3.1 by more than 10 %

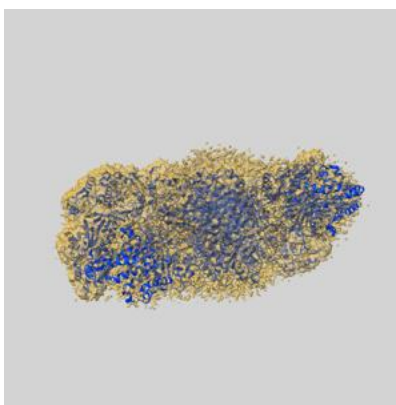
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-45913 and PDB model 9CTO. Per-residue inclusion information can be found in [section 3](#) on [page 5](#).

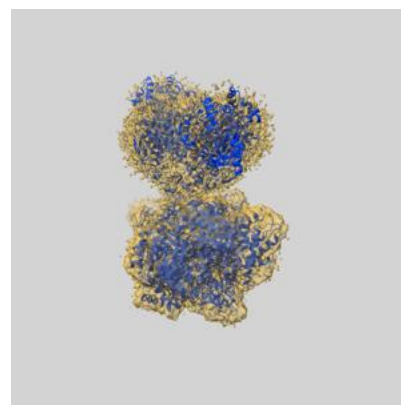
9.1 Map-model overlay [i](#)



X



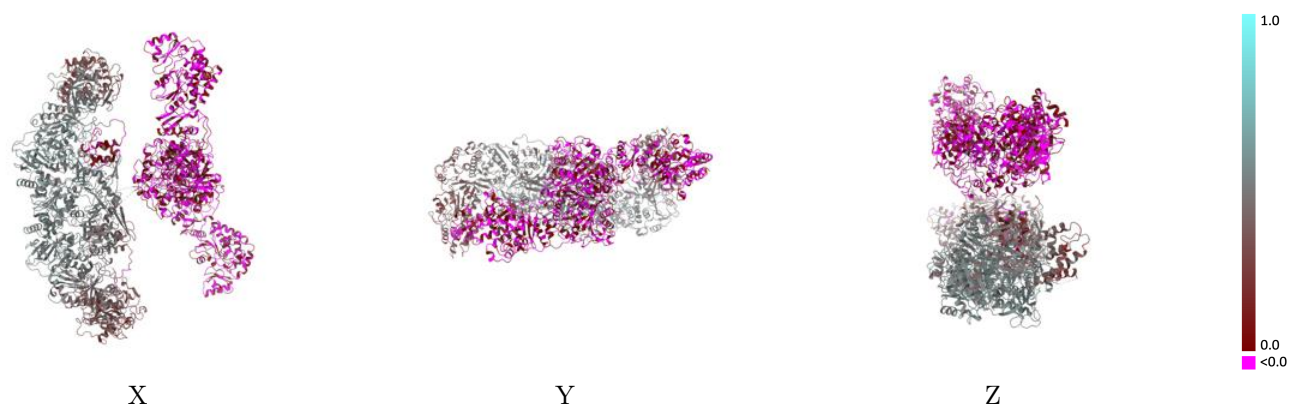
Y



Z

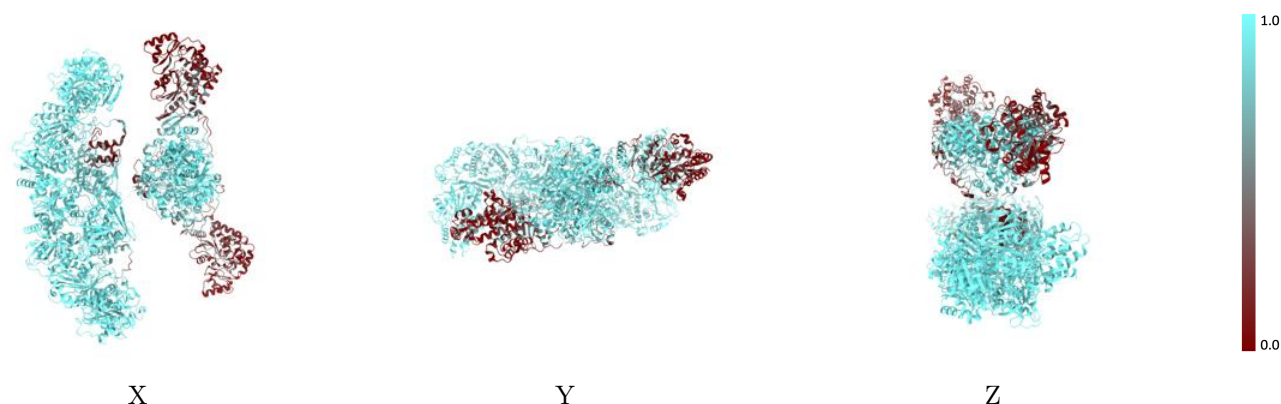
The images above show the 3D surface view of the map at the recommended contour level 0.0704 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



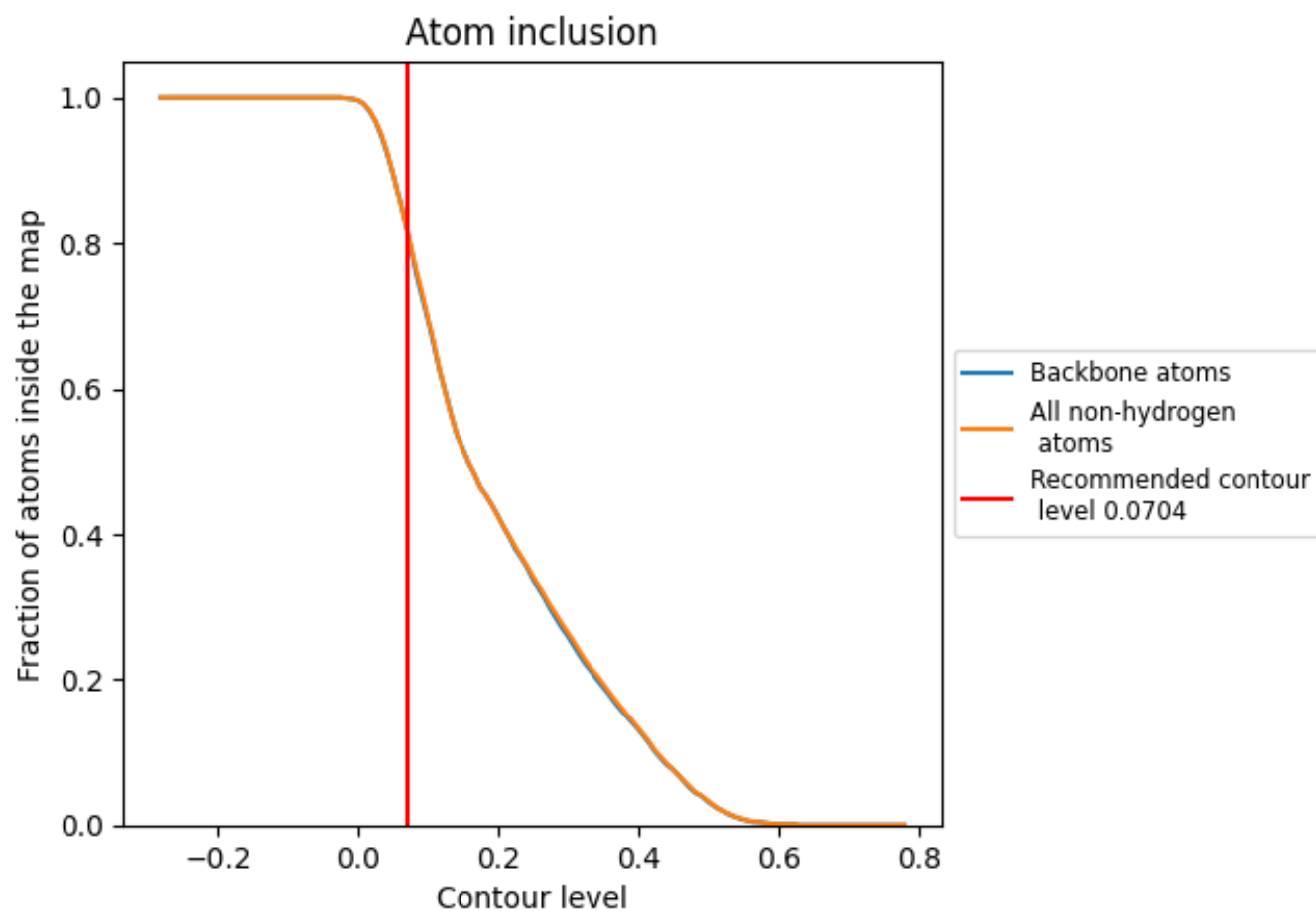
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0704).

9.4 Atom inclusion [i](#)



At the recommended contour level, 82% of all backbone atoms, 82% 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 (0.0704) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8160	0.2850
A	0.8020	0.3000
B	0.8280	0.2700

