Full wwPDB EM Validation Report ⓘ

Nov 6, 2025 – 04:39 PM JST

PDB ID	:	9VJE / pdb_00009vje
EMDB ID	:	EMD-65110
Title	:	Cryo-EM structure of 5-HT1AR-GoA in complex with buspirone
Authors	:	Wang, C.; Cao, C.
Deposited on	:	2025-06-19
Resolution	:	2.47 Å(reported)

This is a Full wwPDB EM Validation 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:

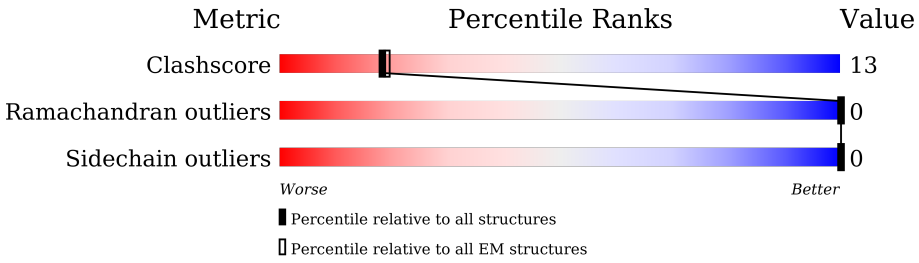
EMDB validation analysis	:	0.0.1.dev129
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4-5-2 with Phenix2.0
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive 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)	:	2.46

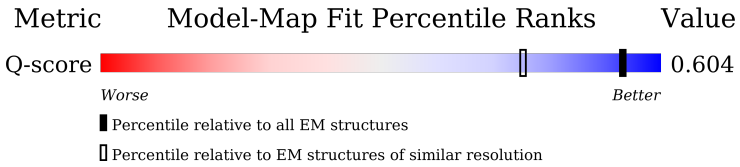
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 2.47 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	210492	15764	-
Ramachandran outliers	207382	16835	-
Sidechain outliers	206894	16415	-
Q-score	-	25397	6086 (1.98 - 2.97)

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 <=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	B	354	46% 15% 39%
2	C	358	7% 62% 32% 7%
3	D	71	23% 59% 18% 23%
4	E	251	6% 59% 34% 8%

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Mol	Chain	Length	Quality of chain
5	R	549	

2 Entry composition (i)

There are 8 unique types of molecules in this entry. The entry contains 8698 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 Guanine nucleotide-binding protein G(o) subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	216	Total	C	N	O	S	0	0
			1680	1072	288	311	9		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	3	SER	CYS	conflict	UNP P09471
B	47	ASN	SER	conflict	UNP P09471
B	204	ALA	GLY	conflict	UNP P09471
B	246	ALA	GLU	conflict	UNP P09471
B	249	LYS	MET	conflict	UNP P09471
B	326	SER	ALA	conflict	UNP P09471

- Molecule 2 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	334	Total	C	N	O	S	0	0
			2556	1578	458	499	21		

There are 19 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-17	MET	-	initiating methionine	UNP P62873
C	-16	HIS	-	expression tag	UNP P62873
C	-15	HIS	-	expression tag	UNP P62873
C	-14	HIS	-	expression tag	UNP P62873
C	-13	HIS	-	expression tag	UNP P62873
C	-12	HIS	-	expression tag	UNP P62873
C	-11	HIS	-	expression tag	UNP P62873
C	-10	LEU	-	expression tag	UNP P62873
C	-9	GLU	-	expression tag	UNP P62873
C	-8	VAL	-	expression tag	UNP P62873

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-7	LEU	-	expression tag	UNP P62873
C	-6	PHE	-	expression tag	UNP P62873
C	-5	GLN	-	expression tag	UNP P62873
C	-4	GLY	-	expression tag	UNP P62873
C	-3	PRO	-	expression tag	UNP P62873
C	-2	GLY	-	expression tag	UNP P62873
C	-1	SER	-	expression tag	UNP P62873
C	0	SER	-	expression tag	UNP P62873
C	1	GLY	-	expression tag	UNP P62873

- Molecule 3 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	55	Total	C	N	O	S	0	0
			399	251	69	76	3		

- Molecule 4 is a protein called ScFv16.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	232	Total	C	N	O	S	0	0
			1781	1129	295	347	10		

- Molecule 5 is a protein called Soluble cytochrome b562,5-hydroxytryptamine receptor 1A.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	R	276	Total	C	N	O	S	0	0
			2167	1434	357	359	17		

There are 55 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	-126	ASP	-	expression tag	UNP P0ABE7
R	-125	TYR	-	expression tag	UNP P0ABE7
R	-124	LYS	-	expression tag	UNP P0ABE7
R	-123	ASP	-	expression tag	UNP P0ABE7
R	-122	ASP	-	expression tag	UNP P0ABE7
R	-121	ASP	-	expression tag	UNP P0ABE7
R	-120	ASP	-	expression tag	UNP P0ABE7
R	-119	ALA	-	expression tag	UNP P0ABE7
R	-118	LYS	-	expression tag	UNP P0ABE7
R	-117	LEU	-	expression tag	UNP P0ABE7

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Chain	Residue	Modelled	Actual	Comment	Reference
R	-116	GLN	-	expression tag	UNP P0ABE7
R	-115	THR	-	expression tag	UNP P0ABE7
R	-114	MET	-	expression tag	UNP P0ABE7
R	-113	HIS	-	expression tag	UNP P0ABE7
R	-112	HIS	-	expression tag	UNP P0ABE7
R	-111	HIS	-	expression tag	UNP P0ABE7
R	-110	HIS	-	expression tag	UNP P0ABE7
R	-109	HIS	-	expression tag	UNP P0ABE7
R	-108	HIS	-	expression tag	UNP P0ABE7
R	-107	HIS	-	expression tag	UNP P0ABE7
R	-106	HIS	-	expression tag	UNP P0ABE7
R	-105	HIS	-	expression tag	UNP P0ABE7
R	-104	HIS	-	expression tag	UNP P0ABE7
R	-103	GLU	-	expression tag	UNP P0ABE7
R	-102	ASN	-	expression tag	UNP P0ABE7
R	-101	LEU	-	expression tag	UNP P0ABE7
R	-100	TYR	-	expression tag	UNP P0ABE7
R	-99	PHE	-	expression tag	UNP P0ABE7
R	-98	GLN	-	expression tag	UNP P0ABE7
R	-97	GLY	-	expression tag	UNP P0ABE7
R	-96	GLY	-	expression tag	UNP P0ABE7
R	-95	THR	-	expression tag	UNP P0ABE7
R	-94	THR	-	expression tag	UNP P0ABE7
R	-93	MET	-	expression tag	UNP P0ABE7
R	-92	ALA	-	expression tag	UNP P0ABE7
R	-91	ASP	-	expression tag	UNP P0ABE7
R	-90	LEU	-	expression tag	UNP P0ABE7
R	-89	GLU	-	expression tag	UNP P0ABE7
R	-88	ASP	-	expression tag	UNP P0ABE7
R	-87	ASN	-	expression tag	UNP P0ABE7
R	-86	TRP	-	expression tag	UNP P0ABE7
R	9	ILE	HIS	conflict	UNP P0ABE7
R	13	LEU	-	linker	UNP P0ABE7
R	14	GLY	-	linker	UNP P0ABE7
R	15	SER	-	linker	UNP P0ABE7
R	16	THR	-	linker	UNP P0ABE7
R	17	LEU	-	linker	UNP P0ABE7
R	18	GLU	-	linker	UNP P0ABE7
R	19	VAL	-	linker	UNP P0ABE7
R	20	LEU	-	linker	UNP P0ABE7
R	21	PHE	-	linker	UNP P0ABE7
R	22	GLN	-	linker	UNP P0ABE7

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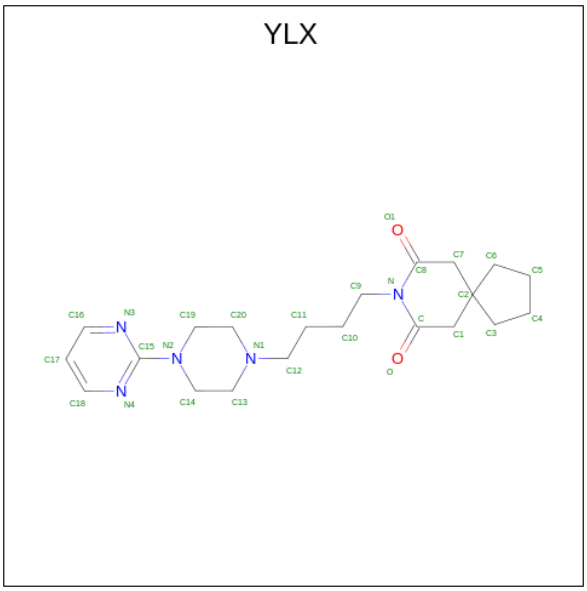
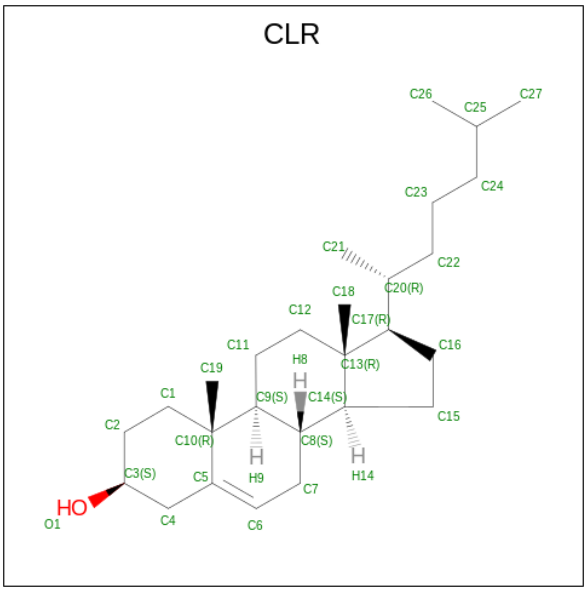
Chain	Residue	Modelled	Actual	Comment	Reference
R	23	GLY	-	linker	UNP P0ABE7
R	24	PRO	-	linker	UNP P0ABE7
R	125	TRP	LEU	conflict	UNP P08908

- Molecule 6 is Buspirone (CCD ID: YLX) (formula: $C_{21}H_{31}N_5O_2$) (labeled as "Ligand of Interest" by depositor).



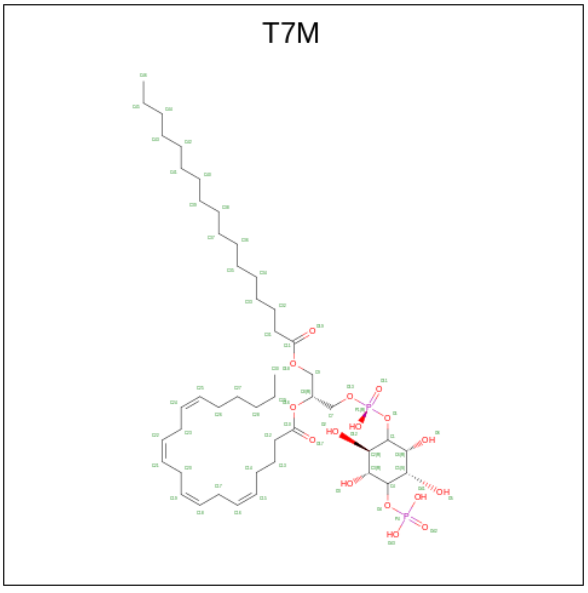
Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
6	R	1	28	21	5	2	0

- Molecule 7 is CHOLESTEROL (CCD ID: CLR) (formula: $C_{27}H_{46}O$).



Mol	Chain	Residues	Atoms			AltConf
7	R	1	Total	C	O	0
			28	27	1	
7	R	1	Total	C	O	0
			28	27	1	

- Molecule 8 is (2R)-1-(heptadecanoyloxy)-3-{[(R)-hydroxy{[(1R,2R,3R,4R,5S,6R)-2,3,5,6-tetrahydroxy-4-(phosphonooxy)cyclohexyl]oxy}phosphoryl]oxy}propan-2-yl (5Z,8Z,11Z,14Z)-icosa-5,8,11,14-tetraenoate (CCD ID: T7M) (formula: $C_{46}H_{82}O_{16}P_2$).



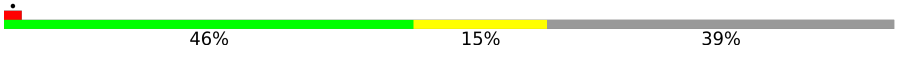
Mol	Chain	Residues	Atoms				AltConf
8	R	1	Total	C	O	P	0
			31	13	16	2	

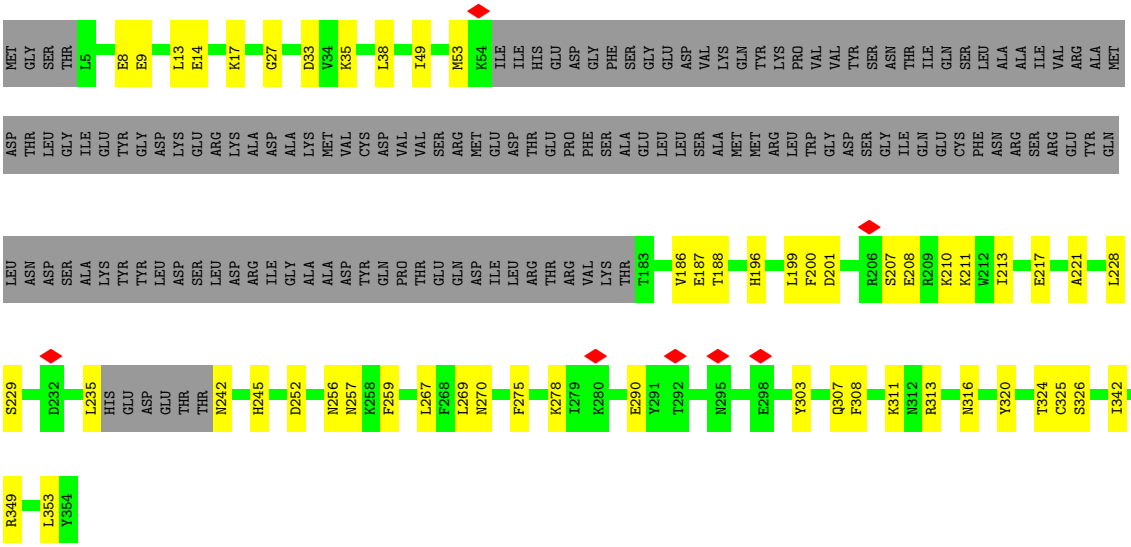
3 Residue-property plots (i)

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

• Molecule 1: Guanine nucleotide-binding protein G(o) subunit alpha

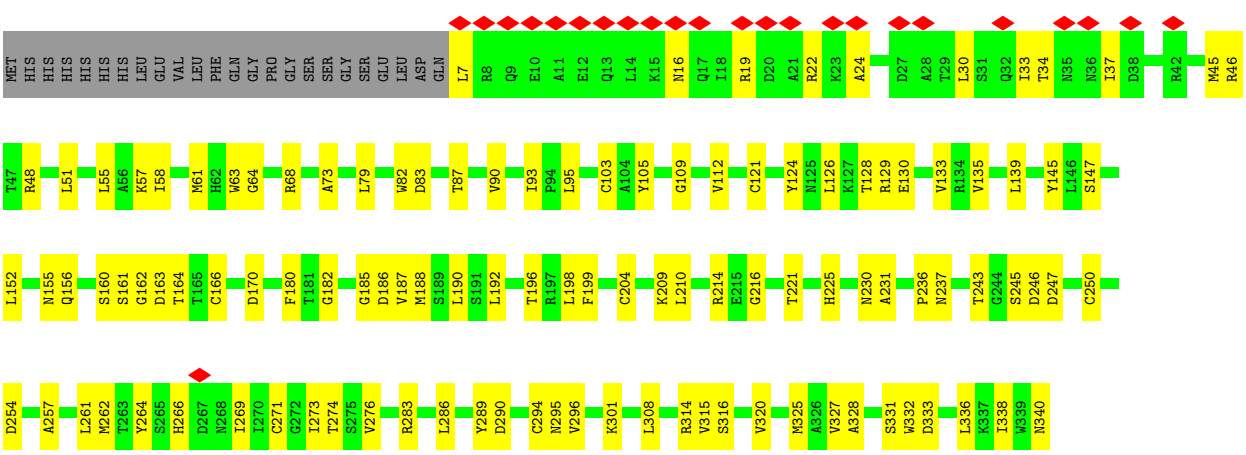
Chain B:





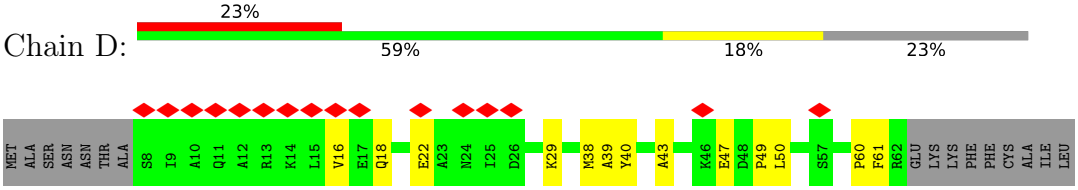
• Molecule 2: Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1

Chain C:



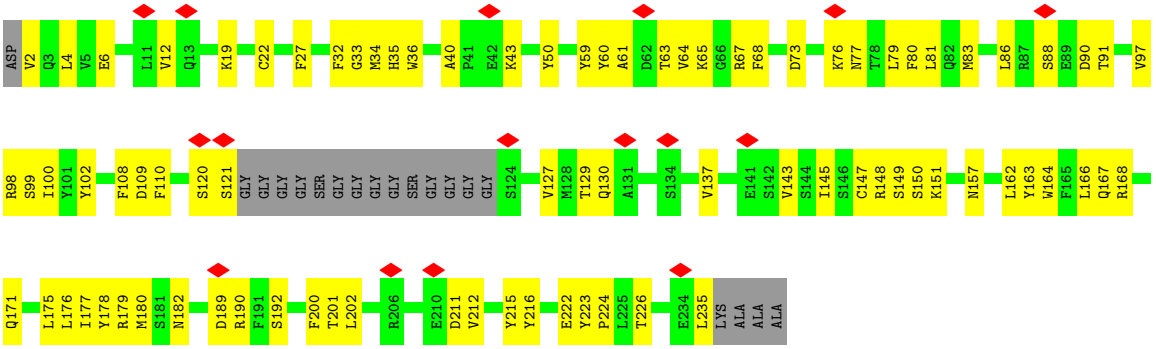
• Molecule 3: Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2

Chain D:



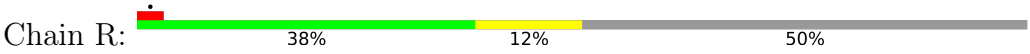
• Molecule 4: ScFv16

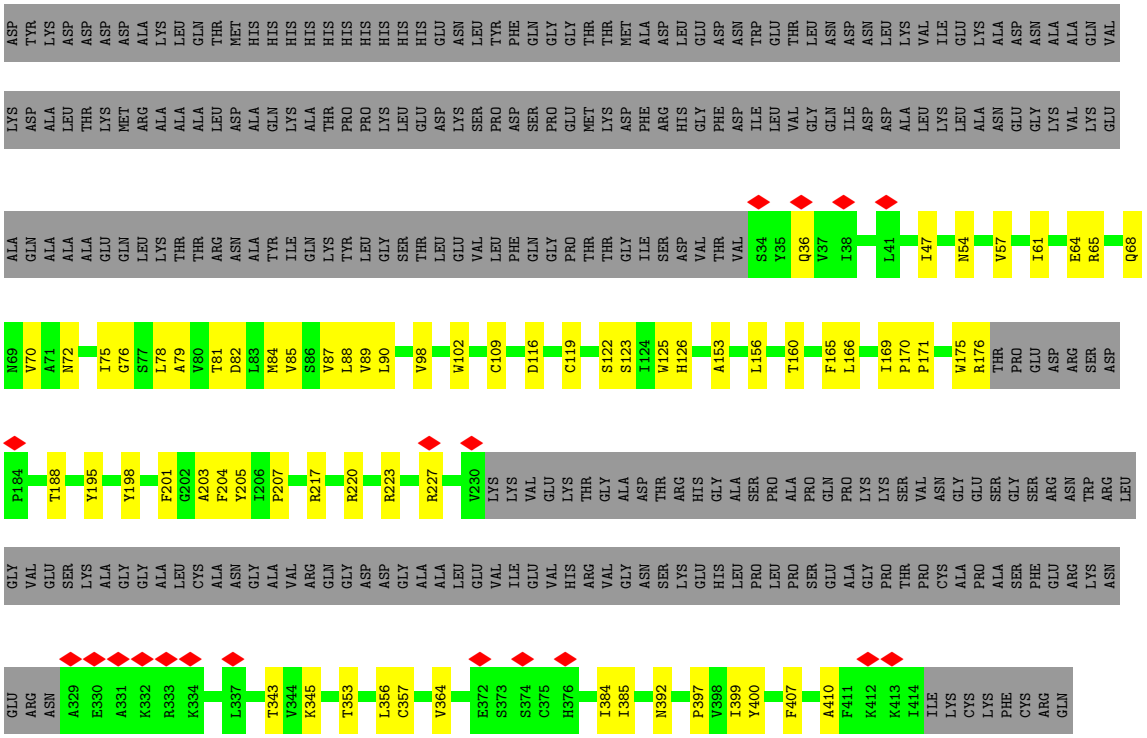
Chain E:



• Molecule 5: Soluble cytochrome b562,5-hydroxytryptamine receptor 1A

Chain R:





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	291653	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	50	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	18000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	4.734	Depositor
Minimum map value	-3.118	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.074	Depositor
Recommended contour level	0.5	Depositor
Map size (Å)	291.91998, 291.91998, 291.91998	wwPDB
Map dimensions	356, 356, 356	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.81999993, 0.81999993, 0.81999993	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: YLX, CLR, T7M

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	B	0.19	0/1708	0.32	0/2301
2	C	0.22	0/2603	0.38	0/3532
3	D	0.16	0/405	0.34	0/551
4	E	0.21	0/1824	0.46	2/2472 (0.1%)
5	R	0.21	0/2217	0.36	0/3018
All	All	0.21	0/8757	0.38	2/11874 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	E	222	GLU	CA-C-N	-8.08	102.08	121.80
4	E	222	GLU	C-N-CA	-8.08	102.08	121.80

There are no chirality outliers.

There are no planarity outliers.

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	B	1680	0	1654	37	0
2	C	2556	0	2454	81	0
3	D	399	0	383	11	0
4	E	1781	0	1713	56	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	R	2167	0	2265	49	0
6	R	28	0	0	1	0
7	R	56	0	92	9	0
8	R	31	0	15	1	0
All	All	8698	0	8576	222	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 13.

All (222) 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:E:167:GLN:NE2	4:E:171:GLN:O	2.10	0.83
5:R:47:ILE:HG12	5:R:90:LEU:HB3	1.63	0.80
2:C:48:ARG:HG3	2:C:340:ASN:HD22	1.47	0.79
4:E:175:LEU:HD21	4:E:178:TYR:HB3	1.63	0.79
5:R:217:ARG:HG2	5:R:220:ARG:HH21	1.46	0.78
2:C:198:LEU:HD13	2:C:210:LEU:HD11	1.62	0.78
2:C:271:CYS:HB2	2:C:290:ASP:HB2	1.65	0.77
2:C:294:CYS:HB3	2:C:308:LEU:HB2	1.65	0.77
5:R:85:VAL:HG22	5:R:119:CYS:HB3	1.65	0.76
2:C:58:ILE:O	2:C:316:SER:OG	2.03	0.76
2:C:112:VAL:HG13	2:C:126:LEU:HD11	1.69	0.74
2:C:45:MET:HE3	2:C:308:LEU:HD11	1.69	0.73
2:C:22:ARG:NH2	2:C:221:THR:O	2.21	0.72
2:C:245:SER:OG	2:C:247:ASP:OD1	2.06	0.72
2:C:254:ASP:HB2	2:C:261:LEU:HD11	1.71	0.71
2:C:79:LEU:HB3	2:C:93:ILE:HB	1.72	0.71
5:R:70:VAL:HG13	5:R:153:ALA:HB2	1.71	0.71
1:B:9:GLU:OE2	4:E:157:ASN:ND2	2.24	0.71
5:R:356:LEU:HD22	7:R:502:CLR:H241	1.75	0.69
1:B:188:THR:HB	1:B:199:LEU:HB3	1.75	0.69
2:C:79:LEU:HB2	2:C:95:LEU:HD21	1.75	0.68
2:C:51:LEU:HB2	2:C:336:LEU:HB2	1.75	0.68
4:E:2:VAL:HG22	4:E:27:PHE:HB3	1.76	0.68
1:B:308:PHE:HA	1:B:311:LYS:HZ1	1.58	0.67
2:C:325:MET:HE2	3:D:60:PRO:HD2	1.74	0.67
1:B:307:GLN:O	1:B:311:LYS:NZ	2.27	0.67
2:C:147:SER:OG	2:C:187:VAL:O	2.13	0.66
2:C:128:THR:OG1	2:C:130:GLU:O	2.13	0.66
2:C:225:HIS:NE2	2:C:243:THR:OG1	2.29	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:67:ARG:NH2	4:E:90:ASP:OD2	2.28	0.65
2:C:250:CYS:HB2	2:C:264:TYR:HB2	1.79	0.64
1:B:213:ILE:HG21	1:B:257:ASN:HD21	1.62	0.63
5:R:201:PHE:HA	5:R:205:TYR:HB2	1.79	0.63
5:R:65:ARG:HA	5:R:68:GLN:HG3	1.80	0.63
2:C:112:VAL:HG22	2:C:126:LEU:HD21	1.81	0.63
5:R:125:TRP:CE2	5:R:207:PRO:HG3	2.35	0.62
5:R:357:CYS:HB3	5:R:392:ASN:HB2	1.82	0.62
1:B:252:ASP:OD2	1:B:256:ASN:ND2	2.33	0.62
2:C:37:ILE:HD12	2:C:283:ARG:HH12	1.62	0.61
5:R:102:TRP:NE1	5:R:109:CYS:HB2	2.15	0.61
2:C:64:GLY:HA2	2:C:105:TYR:CD2	2.35	0.61
5:R:122:SER:O	5:R:126:HIS:ND1	2.28	0.61
2:C:331:SER:OG	2:C:333:ASP:OD1	2.19	0.61
5:R:353:THR:HG21	5:R:399:ILE:HD11	1.83	0.61
1:B:27:GLY:HA3	2:C:55:LEU:HD13	1.83	0.61
2:C:333:ASP:HB2	5:R:65:ARG:HH11	1.66	0.60
2:C:340:ASN:ND2	3:D:61:PHE:HB2	2.16	0.60
2:C:225:HIS:ND1	2:C:245:SER:OG	2.35	0.60
2:C:30:LEU:HD23	2:C:262:MET:HB2	1.82	0.60
5:R:54:ASN:ND2	5:R:82:ASP:HB2	2.17	0.59
1:B:228:LEU:HG	1:B:269:LEU:HB3	1.84	0.59
2:C:320:VAL:HG22	2:C:327:VAL:HG22	1.83	0.59
4:E:168:ARG:HB2	4:E:171:GLN:HE21	1.68	0.59
5:R:81:THR:O	5:R:85:VAL:HG23	2.03	0.59
5:R:166:LEU:O	5:R:198:TYR:OH	2.12	0.58
4:E:34:MET:HB3	4:E:79:LEU:HD22	1.85	0.58
2:C:192:LEU:HD23	2:C:199:PHE:HB3	1.85	0.58
4:E:130:GLN:HE22	4:E:216:TYR:HA	1.68	0.58
2:C:124:TYR:CE1	2:C:135:VAL:HG22	2.39	0.58
4:E:129:THR:HB	4:E:148:ARG:HB2	1.84	0.58
1:B:13:LEU:HG	1:B:17:LYS:HE2	1.85	0.58
2:C:333:ASP:O	5:R:65:ARG:NH1	2.36	0.58
1:B:49:ILE:O	1:B:53:MET:HG2	2.05	0.57
5:R:345:LYS:HA	7:R:502:CLR:H42	1.84	0.57
1:B:252:ASP:OD2	1:B:313:ARG:NH1	2.37	0.57
1:B:252:ASP:HB2	1:B:311:LYS:HD2	1.87	0.57
2:C:188:MET:HE3	2:C:204:CYS:SG	2.45	0.56
2:C:236:PRO:HB2	3:D:40:TYR:CE2	2.41	0.56
1:B:242:ASN:HD22	1:B:245:HIS:CD2	2.23	0.56
4:E:63:THR:HG23	4:E:64:VAL:HG13	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:121:CYS:HB3	2:C:139:LEU:HD12	1.87	0.56
2:C:266:HIS:HB3	2:C:269:ILE:HG13	1.86	0.56
5:R:64:GLU:HG3	5:R:410:ALA:HB1	1.88	0.56
5:R:54:ASN:HD22	5:R:79:ALA:HA	1.70	0.56
2:C:61:MET:HE3	2:C:328:ALA:HB3	1.88	0.55
5:R:156:LEU:O	5:R:160:THR:HG23	2.06	0.55
5:R:61:ILE:HD12	5:R:76:GLY:HA3	1.89	0.55
2:C:90:VAL:HG13	4:E:102:TYR:HB2	1.89	0.55
2:C:126:LEU:HA	2:C:133:VAL:HG22	1.89	0.54
8:R:504:T7M:O11	8:R:504:T7M:O6	2.25	0.54
5:R:176:ARG:NH1	5:R:188:THR:O	2.40	0.54
2:C:45:MET:HE1	2:C:286:LEU:HD21	1.90	0.54
4:E:149:SER:OG	4:E:151:LYS:O	2.19	0.54
4:E:166:LEU:HB2	4:E:176:LEU:HD11	1.91	0.53
1:B:353:LEU:HD22	5:R:343:THR:HG23	1.90	0.53
1:B:267:LEU:N	1:B:320:TYR:O	2.41	0.53
1:B:8:GLU:OE2	4:E:163:TYR:OH	2.17	0.53
2:C:24:ALA:O	3:D:29:LYS:NZ	2.41	0.53
2:C:73:ALA:HB2	2:C:103:CYS:HB3	1.90	0.53
4:E:12:VAL:HG11	4:E:86:LEU:HD13	1.91	0.53
1:B:316:ASN:ND2	1:B:349:ARG:HD3	2.24	0.52
2:C:166:CYS:HB2	2:C:180:PHE:HB2	1.90	0.52
4:E:120:SER:OG	4:E:121:SER:N	2.42	0.52
4:E:164:TRP:CE2	4:E:202:LEU:HB2	2.45	0.51
2:C:254:ASP:HB3	2:C:257:ALA:HB3	1.92	0.51
4:E:178:TYR:CZ	4:E:182:ASN:HB3	2.45	0.51
5:R:357:CYS:CB	5:R:392:ASN:HB2	2.41	0.51
2:C:57:LYS:HD2	2:C:332:TRP:CG	2.46	0.51
5:R:223:ARG:HD2	5:R:227:ARG:CZ	2.40	0.51
2:C:105:TYR:CZ	2:C:109:GLY:HA2	2.45	0.51
5:R:36:GLN:HG2	5:R:98:VAL:HG13	1.93	0.51
1:B:14:GLU:HA	1:B:17:LYS:HE3	1.93	0.50
1:B:208:GLU:OE1	1:B:210:LYS:NZ	2.43	0.50
4:E:32:PHE:CD1	4:E:98:ARG:HG2	2.46	0.50
4:E:40:ALA:HB3	4:E:43:LYS:HB2	1.93	0.50
2:C:274:THR:OG1	2:C:315:VAL:O	2.15	0.50
4:E:32:PHE:CD1	4:E:100:ILE:HB	2.47	0.49
2:C:250:CYS:SG	2:C:273:ILE:HD13	2.52	0.49
4:E:190:ARG:NE	4:E:211:ASP:OD2	2.46	0.49
4:E:64:VAL:HB	4:E:68:PHE:CD2	2.47	0.49
4:E:137:VAL:HG12	4:E:143:VAL:HG21	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:229:SER:HB2	1:B:278:LYS:HD3	1.95	0.48
4:E:50:TYR:HD2	4:E:59:TYR:HD2	1.61	0.48
4:E:33:GLY:N	4:E:99:SER:O	2.46	0.48
5:R:61:ILE:HD11	5:R:407:PHE:HZ	1.78	0.48
2:C:162:GLY:HA2	2:C:186:ASP:HB3	1.95	0.48
5:R:57:VAL:HG21	5:R:397:PRO:HB3	1.95	0.48
5:R:72:ASN:HD22	5:R:407:PHE:HE2	1.61	0.48
2:C:145:TYR:OH	2:C:188:MET:HE1	2.14	0.48
4:E:35:HIS:NE2	4:E:223:TYR:OH	2.46	0.48
4:E:68:PHE:CE1	4:E:83:MET:HG2	2.49	0.48
4:E:127:VAL:HB	4:E:150:SER:HB3	1.95	0.47
2:C:33:ILE:HG22	3:D:38:MET:HE3	1.95	0.47
5:R:87:VAL:HG23	5:R:88:LEU:HG	1.96	0.47
2:C:161:SER:HB3	2:C:163:ASP:OD1	2.14	0.47
1:B:316:ASN:HD22	1:B:349:ARG:HD3	1.79	0.47
4:E:4:LEU:HD11	4:E:98:ARG:HB2	1.97	0.47
2:C:130:GLU:CD	2:C:130:GLU:H	2.23	0.47
7:R:503:CLR:H221	7:R:503:CLR:H162	1.57	0.46
3:D:47:GLU:O	3:D:49:PRO:HD3	2.15	0.46
2:C:16:ASN:HA	2:C:19:ARG:HG2	1.98	0.46
4:E:177:ILE:HA	4:E:182:ASN:O	2.15	0.46
5:R:345:LYS:HG3	7:R:502:CLR:H192	1.96	0.46
2:C:231:ALA:HB1	2:C:276:VAL:HG22	1.98	0.46
7:R:502:CLR:H262	7:R:502:CLR:H232	1.75	0.45
2:C:286:LEU:HG	2:C:296:VAL:HG22	1.98	0.45
2:C:7:LEU:HD22	3:D:16:VAL:HG21	1.97	0.45
5:R:171:PRO:HD3	5:R:195:TYR:CE1	2.50	0.45
1:B:217:GLU:HG3	1:B:259:PHE:HB3	1.98	0.45
2:C:87:THR:HG22	2:C:87:THR:O	2.17	0.45
5:R:170:PRO:HB3	5:R:175:TRP:HE3	1.82	0.45
1:B:270:ASN:HA	1:B:324:THR:OG1	2.17	0.45
7:R:502:CLR:H183	7:R:502:CLR:H20	1.85	0.45
1:B:325:CYS:O	1:B:326:SER:OG	2.26	0.45
2:C:130:GLU:HA	4:E:27:PHE:HB2	1.98	0.45
5:R:384:ILE:HA	7:R:503:CLR:H112	1.99	0.45
4:E:73:ASP:HB3	4:E:76:LYS:HB2	1.98	0.44
1:B:33:ASP:OD1	1:B:196:HIS:HD2	2.00	0.44
1:B:38:LEU:HB2	1:B:199:LEU:HD11	1.98	0.44
2:C:156:GLN:HE22	2:C:214:ARG:NH2	2.16	0.44
3:D:18:GLN:O	3:D:22:GLU:HG2	2.18	0.44
4:E:4:LEU:HD12	4:E:110:PHE:HD2	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:51:LEU:HB3	2:C:82:TRP:CE3	2.53	0.44
4:E:61:ALA:HB3	4:E:64:VAL:HG22	1.98	0.44
4:E:212:VAL:HG21	4:E:235:LEU:HG	2.00	0.44
4:E:224:PRO:O	4:E:226:THR:HG23	2.18	0.44
1:B:221:ALA:HB2	1:B:342:ILE:HD13	1.99	0.44
1:B:186:VAL:HB	1:B:201:ASP:HB3	2.00	0.44
3:D:39:ALA:O	3:D:43:ALA:CB	2.66	0.44
4:E:97:VAL:HG11	4:E:108:PHE:CD2	2.53	0.44
5:R:78:LEU:HB2	5:R:126:HIS:HB3	1.98	0.44
4:E:60:TYR:HB2	4:E:65:LYS:HG3	2.00	0.43
5:R:75:ILE:HG12	5:R:400:TYR:HB3	2.00	0.43
4:E:147:CYS:HB2	4:E:164:TRP:CH2	2.53	0.43
4:E:162:LEU:HD13	4:E:200:PHE:CD2	2.53	0.43
5:R:72:ASN:ND2	5:R:407:PHE:HE2	2.15	0.43
4:E:73:ASP:O	4:E:77:ASN:N	2.52	0.43
4:E:88:SER:O	4:E:91:THR:HG22	2.19	0.43
5:R:364:VAL:HG21	5:R:385:ILE:HD13	2.01	0.43
5:R:85:VAL:HG12	5:R:90:LEU:CD1	2.49	0.43
1:B:187:GLU:HG2	1:B:200:PHE:HD2	1.84	0.43
2:C:46:ARG:NH2	2:C:48:ARG:HD3	2.33	0.43
2:C:180:PHE:CE1	2:C:216:GLY:HA2	2.53	0.43
4:E:19:LYS:HE2	4:E:80:PHE:CD1	2.53	0.43
7:R:502:CLR:H232	7:R:502:CLR:H211	1.80	0.43
5:R:165:PHE:O	5:R:169:ILE:HG12	2.18	0.43
2:C:61:MET:HE1	2:C:63:TRP:CD1	2.55	0.42
2:C:48:ARG:HG3	2:C:340:ASN:ND2	2.25	0.42
2:C:271:CYS:SG	2:C:289:TYR:HB3	2.60	0.42
4:E:179:ARG:O	4:E:180:MET:C	2.62	0.42
4:E:211:ASP:O	4:E:215:TYR:OH	2.20	0.42
4:E:6:GLU:HA	4:E:22:CYS:HA	2.02	0.42
1:B:228:LEU:HB3	1:B:275:PHE:HB2	2.01	0.42
2:C:290:ASP:HA	2:C:314:ARG:HG3	2.02	0.42
4:E:36:TRP:NE1	4:E:81:LEU:HB2	2.34	0.42
1:B:207:SER:HB3	2:C:186:ASP:OD1	2.20	0.42
1:B:235:LEU:HD12	1:B:235:LEU:HA	1.88	0.42
2:C:160:SER:HB3	2:C:190:LEU:HD21	2.01	0.42
2:C:164:THR:HG22	2:C:185:GLY:C	2.45	0.42
2:C:182:GLY:C	2:C:209:LYS:HE3	2.45	0.42
1:B:213:ILE:HD12	1:B:213:ILE:HA	1.95	0.42
1:B:290:GLU:OE2	1:B:303:TYR:OH	2.38	0.42
2:C:155:ASN:ND2	2:C:170:ASP:OD1	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:189:ASP:OD1	4:E:189:ASP:N	2.52	0.42
2:C:48:ARG:HD3	2:C:48:ARG:HA	1.85	0.41
7:R:503:CLR:H183	7:R:503:CLR:H20	1.83	0.41
1:B:252:ASP:CB	1:B:311:LYS:HD2	2.49	0.41
2:C:48:ARG:N	2:C:338:ILE:O	2.52	0.41
4:E:223:TYR:O	4:E:223:TYR:CD2	2.72	0.41
2:C:230:ASN:HD21	2:C:246:ASP:CG	2.28	0.41
4:E:109:ASP:OD1	4:E:110:PHE:N	2.53	0.41
4:E:175:LEU:HD11	4:E:178:TYR:HA	2.01	0.41
4:E:192:SER:O	4:E:202:LEU:HD12	2.20	0.41
2:C:45:MET:SD	3:D:50:LEU:HD22	2.60	0.41
5:R:89:VAL:HG21	5:R:116:ASP:HA	2.03	0.41
5:R:116:ASP:OD2	6:R:501:YLX:N1	2.53	0.41
5:R:203:ALA:O	5:R:207:PRO:HG2	2.20	0.41
5:R:204:PHE:C	5:R:207:PRO:HD2	2.45	0.41
2:C:129:ARG:O	4:E:98:ARG:NH1	2.47	0.41
2:C:152:LEU:HD12	2:C:196:THR:HB	2.03	0.41
4:E:83:MET:HB3	4:E:86:LEU:HD21	2.02	0.41
1:B:35:LYS:HB3	1:B:200:PHE:HE1	1.86	0.40
2:C:289:TYR:CE2	2:C:295:ASN:HB2	2.56	0.40
2:C:34:THR:O	2:C:301:LYS:NZ	2.51	0.40
5:R:170:PRO:N	5:R:171:PRO:HD2	2.36	0.40
4:E:145:ILE:O	4:E:201:THR:HA	2.22	0.40
1:B:211:LYS:HD3	1:B:211:LYS:HA	1.73	0.40
2:C:68:ARG:NE	2:C:83:ASP:OD1	2.48	0.40
5:R:84:MET:HE2	5:R:84:MET:HB3	1.87	0.40
2:C:237:ASN:HB3	3:D:40:TYR:CD1	2.57	0.40
5:R:82:ASP:OD1	5:R:123:SER:OG	2.32	0.40
5:R:125:TRP:CZ2	5:R:207:PRO:HG3	2.57	0.40

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	B	210/354 (59%)	202 (96%)	8 (4%)	0	100	100
2	C	332/358 (93%)	313 (94%)	19 (6%)	0	100	100
3	D	53/71 (75%)	53 (100%)	0	0	100	100
4	E	228/251 (91%)	214 (94%)	14 (6%)	0	100	100
5	R	270/549 (49%)	259 (96%)	11 (4%)	0	100	100
All	All	1093/1583 (69%)	1041 (95%)	52 (5%)	0	100	100

There are no Ramachandran outliers to report.

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	B	177/308 (58%)	177 (100%)	0	100	100
2	C	275/298 (92%)	275 (100%)	0	100	100
3	D	38/58 (66%)	38 (100%)	0	100	100
4	E	196/201 (98%)	196 (100%)	0	100	100
5	R	233/458 (51%)	233 (100%)	0	100	100
All	All	919/1323 (70%)	919 (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 (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	196	HIS
1	B	242	ASN
1	B	316	ASN
2	C	75	GLN
2	C	156	GLN
2	C	340	ASN
4	E	39	GLN
4	E	82	GLN

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Mol	Chain	Res	Type
4	E	113	GLN
4	E	130	GLN
4	E	159	ASN
4	E	171	GLN
5	R	54	ASN

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

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	$\#\|Z\| > 2$
7	CLR	R	503	-	31,31,31	0.65	0	48,48,48	1.32	6 (12%)
8	T7M	R	504	-	31,31,64	2.64	7 (22%)	43,46,79	1.30	5 (11%)
7	CLR	R	502	-	31,31,31	0.60	0	48,48,48	1.29	4 (8%)
6	YLX	R	501	-	31,31,31	0.33	0	40,43,43	0.87	2 (5%)

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
7	CLR	R	503	-	-	6/10/68/68	0/4/4/4
8	T7M	R	504	-	-	14/25/49/84	0/1/1/1
7	CLR	R	502	-	-	5/10/68/68	0/4/4/4
6	YLX	R	501	-	-	0/11/48/48	0/4/4/4

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	R	504	T7M	P4-O4	12.46	1.82	1.59
8	R	504	T7M	P1-O13	3.08	1.71	1.59
8	R	504	T7M	O4-C4	-3.02	1.33	1.44
8	R	504	T7M	P1-O1	2.80	1.67	1.60
8	R	504	T7M	C5-C4	2.23	1.58	1.52
8	R	504	T7M	C3-C4	2.19	1.58	1.52
8	R	504	T7M	O13-C7	-2.04	1.36	1.44

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
7	R	503	CLR	C13-C17-C20	-4.24	112.85	119.49
7	R	502	CLR	C13-C17-C20	-3.97	113.26	119.49
8	R	504	T7M	C5-C4-C3	-3.46	105.87	110.85
6	R	501	YLX	C8-N-C	3.06	125.03	124.07
7	R	502	CLR	C13-C14-C8	-2.87	110.13	114.38
8	R	504	T7M	O4-P4-O42	-2.84	98.44	109.39
8	R	504	T7M	O16-C10-C12	2.72	116.09	111.09
6	R	501	YLX	C4-C3-C2	-2.70	101.67	105.68
8	R	504	T7M	O12-P1-O11	2.55	124.87	112.24
7	R	503	CLR	C13-C14-C8	-2.45	110.75	114.38
8	R	504	T7M	O43-P4-O41	2.27	116.33	107.64
7	R	503	CLR	C8-C7-C6	-2.26	109.49	112.73
7	R	503	CLR	C2-C3-C4	-2.16	107.34	110.31
7	R	502	CLR	C11-C9-C10	-2.14	110.26	113.08
7	R	502	CLR	C10-C9-C8	-2.14	109.53	112.73
7	R	503	CLR	C11-C9-C10	-2.03	110.41	113.08
7	R	503	CLR	C11-C12-C13	-2.02	109.32	112.78

There are no chirality outliers.

All (25) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	R	504	T7M	C2-C1-O1-P1
8	R	504	T7M	C4-O4-P4-O42
7	R	503	CLR	C13-C17-C20-C21
7	R	502	CLR	C13-C17-C20-C22
7	R	503	CLR	C13-C17-C20-C22
7	R	502	CLR	C13-C17-C20-C21
8	R	504	T7M	O19-C11-O18-C9
7	R	503	CLR	C16-C17-C20-C21
8	R	504	T7M	C31-C11-O18-C9
8	R	504	T7M	C12-C10-O16-C8
7	R	503	CLR	C17-C20-C22-C23
7	R	503	CLR	C16-C17-C20-C22
8	R	504	T7M	C7-O13-P1-O1
7	R	503	CLR	C21-C20-C22-C23
7	R	502	CLR	C16-C17-C20-C21
8	R	504	T7M	O17-C10-O16-C8
8	R	504	T7M	O13-C7-C8-C9
7	R	502	CLR	C16-C17-C20-C22
7	R	502	CLR	C22-C23-C24-C25
8	R	504	T7M	C6-C1-O1-P1
8	R	504	T7M	C7-O13-P1-O12
8	R	504	T7M	O13-C7-C8-O16
8	R	504	T7M	C8-C7-O13-P1
8	R	504	T7M	O16-C8-C9-O18
8	R	504	T7M	C7-C8-C9-O18

There are no ring outliers.

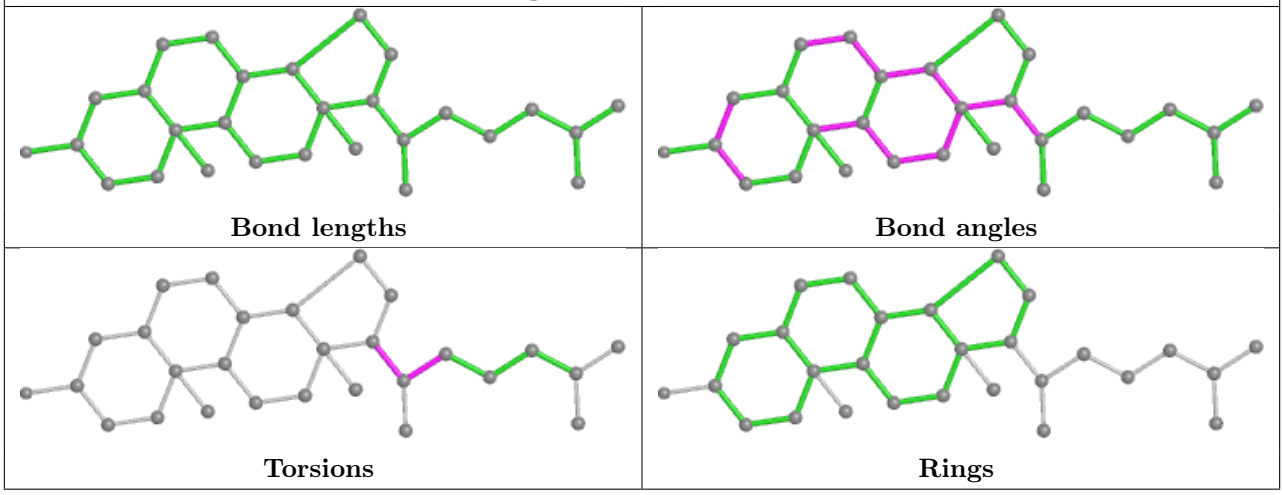
4 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	R	503	CLR	3	0
8	R	504	T7M	1	0
7	R	502	CLR	6	0
6	R	501	YLX	1	0

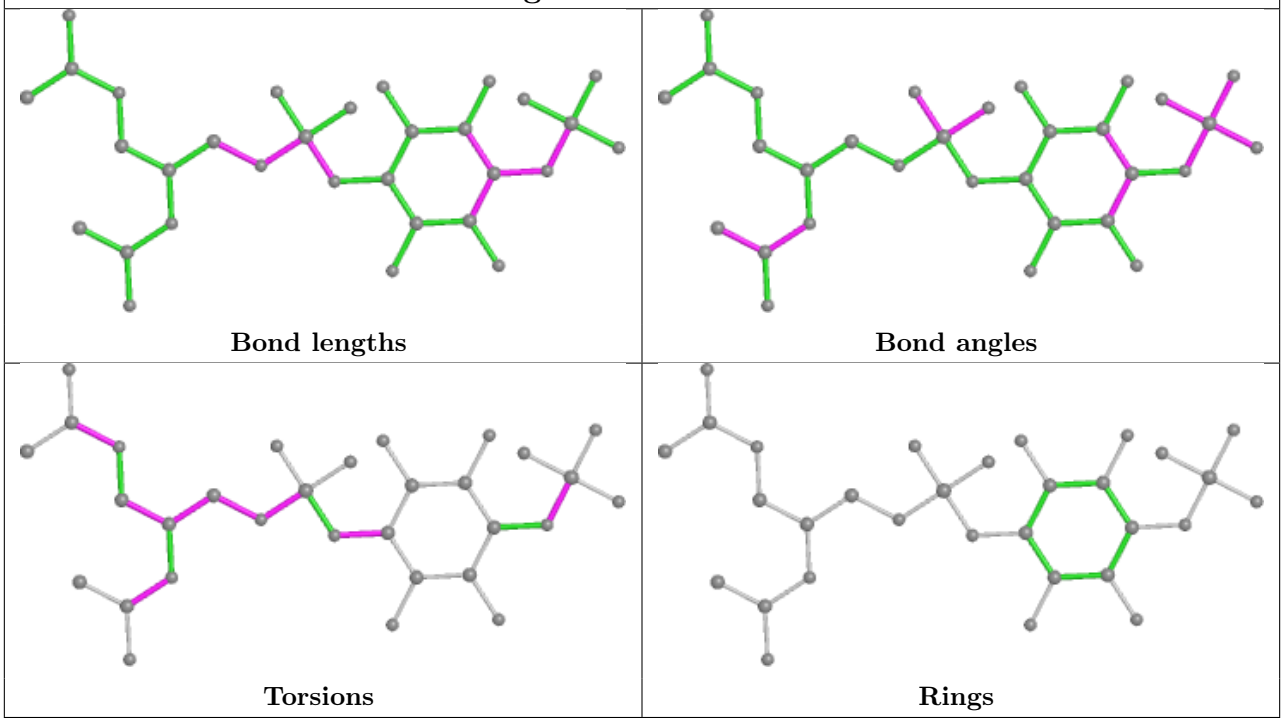
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

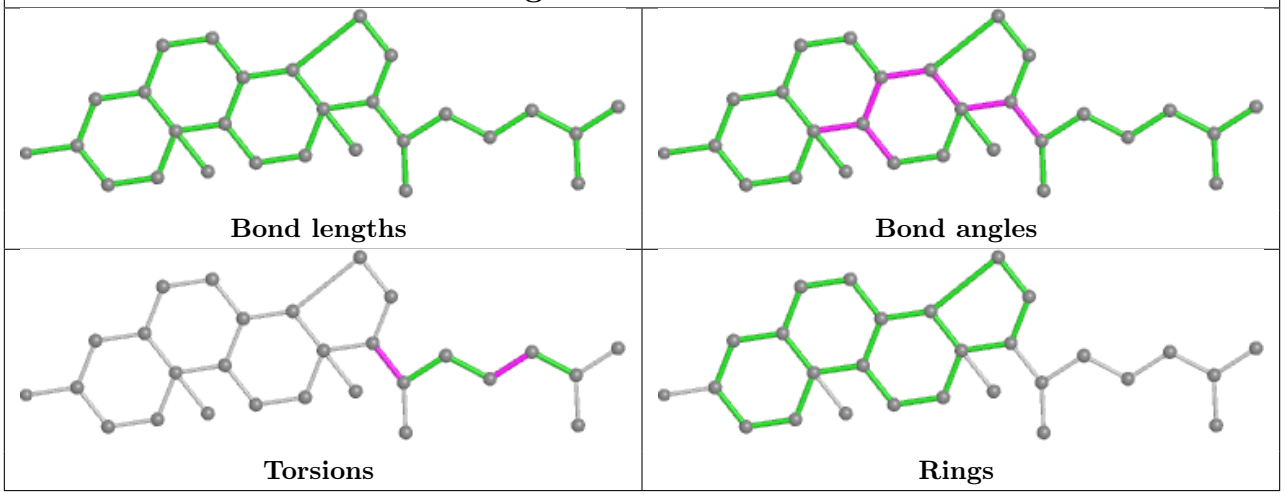
Ligand CLR R 503



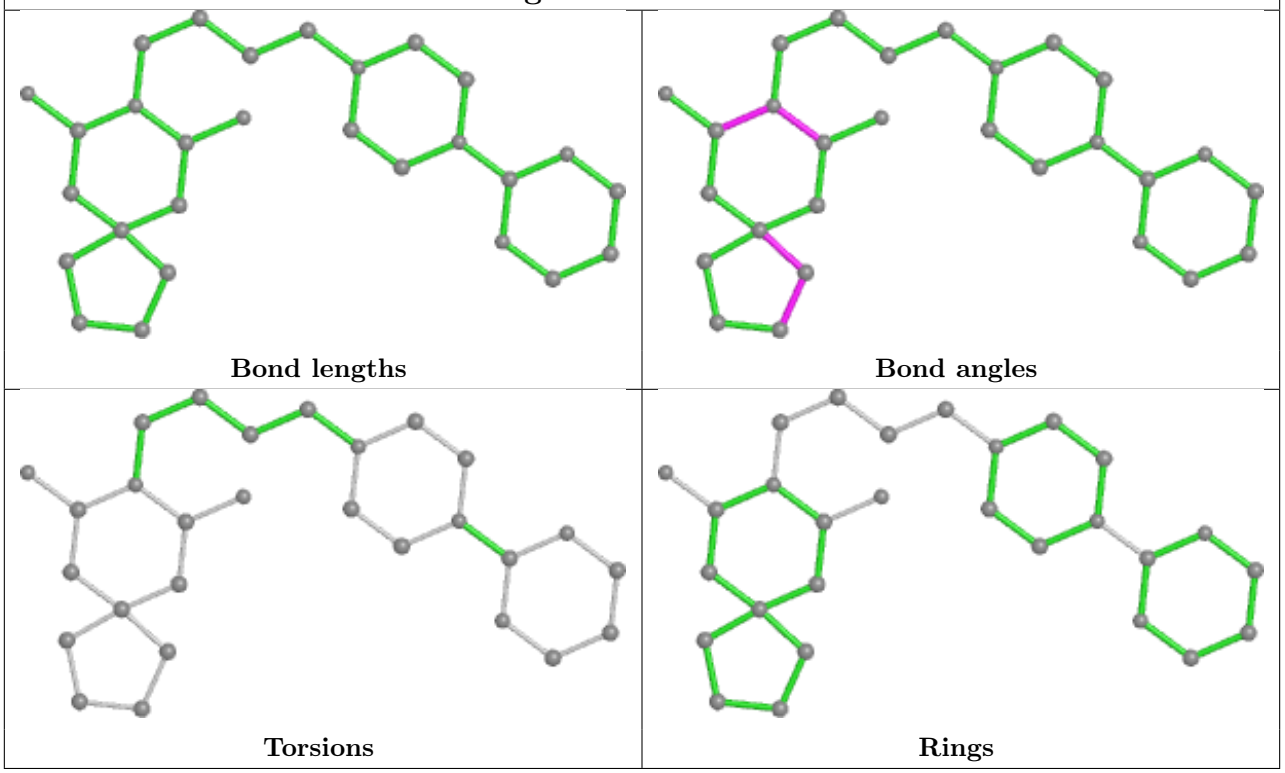
Ligand T7M R 504



Ligand CLR R 502



Ligand YLX R 501



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.

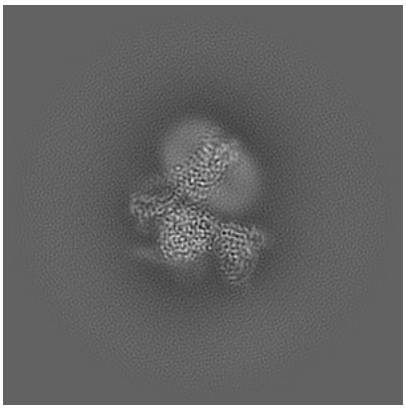
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-65110. These allow visual inspection of the internal detail of the map and identification of artifacts.

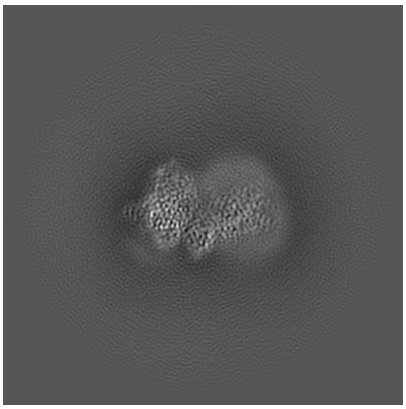
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

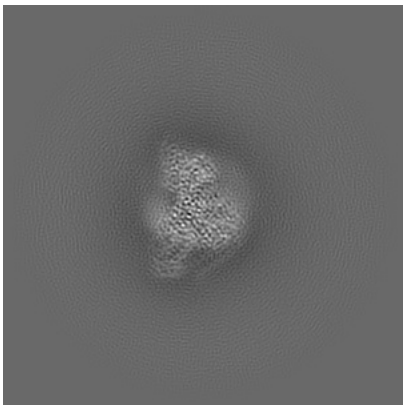
6.1.1 Primary map



X

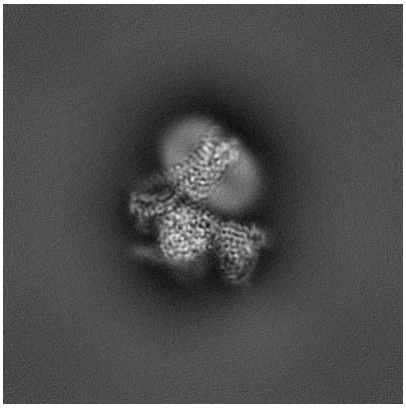


Y

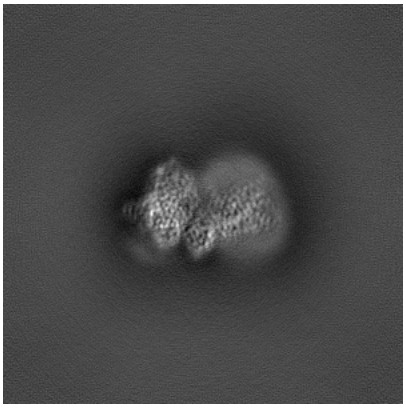


Z

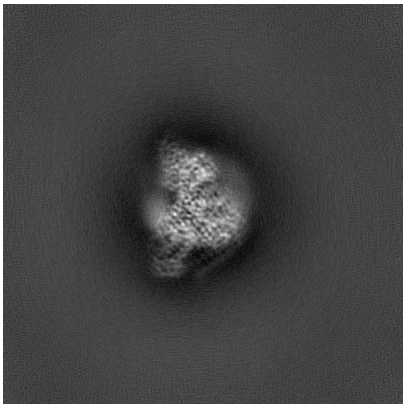
6.1.2 Raw map



X



Y

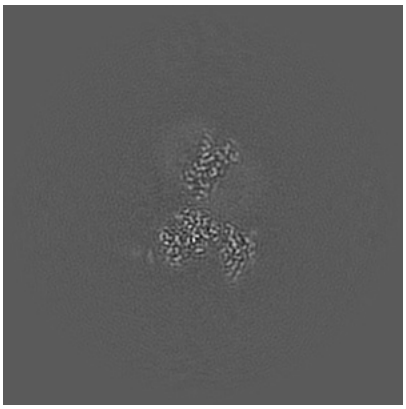


Z

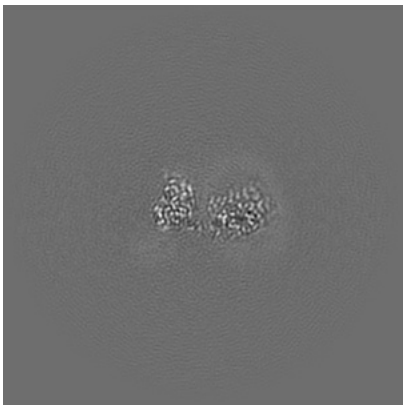
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

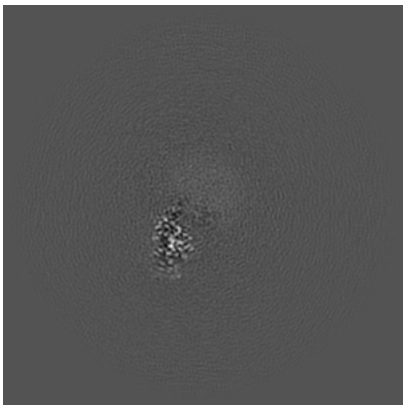
6.2.1 Primary map



X Index: 178

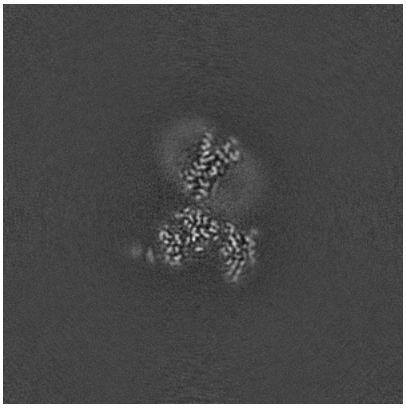


Y Index: 178

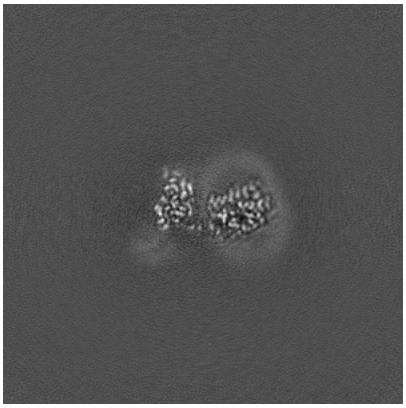


Z Index: 178

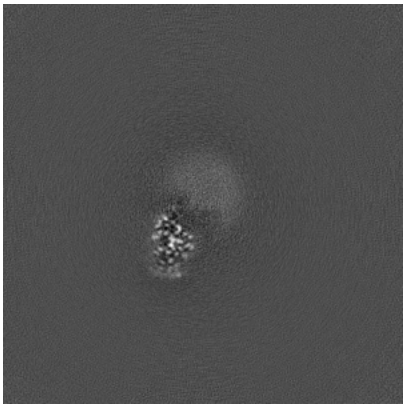
6.2.2 Raw map



X Index: 178



Y Index: 178

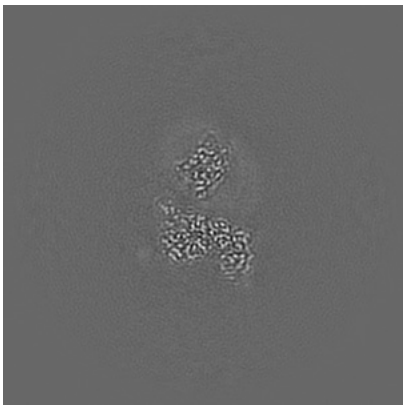


Z Index: 178

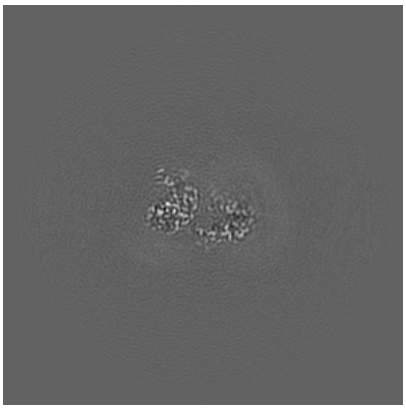
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

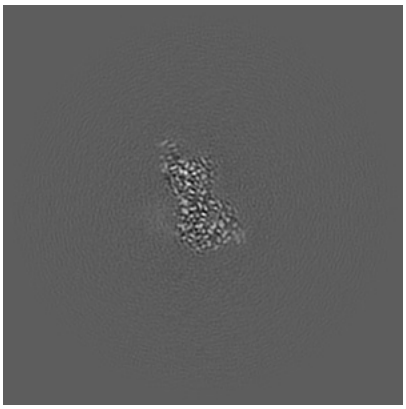
6.3.1 Primary map



X Index: 169

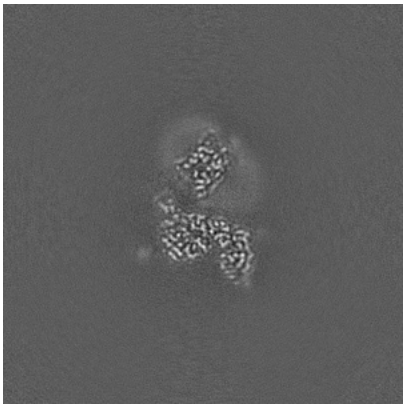


Y Index: 169

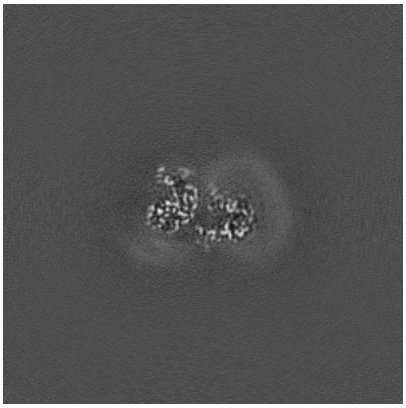


Z Index: 147

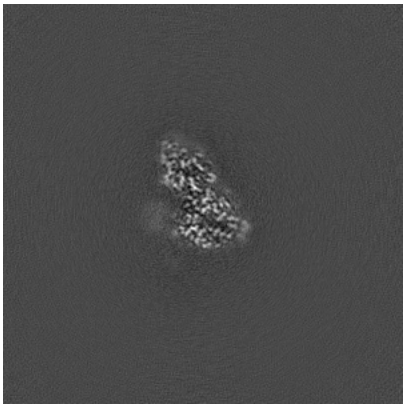
6.3.2 Raw map



X Index: 169



Y Index: 169

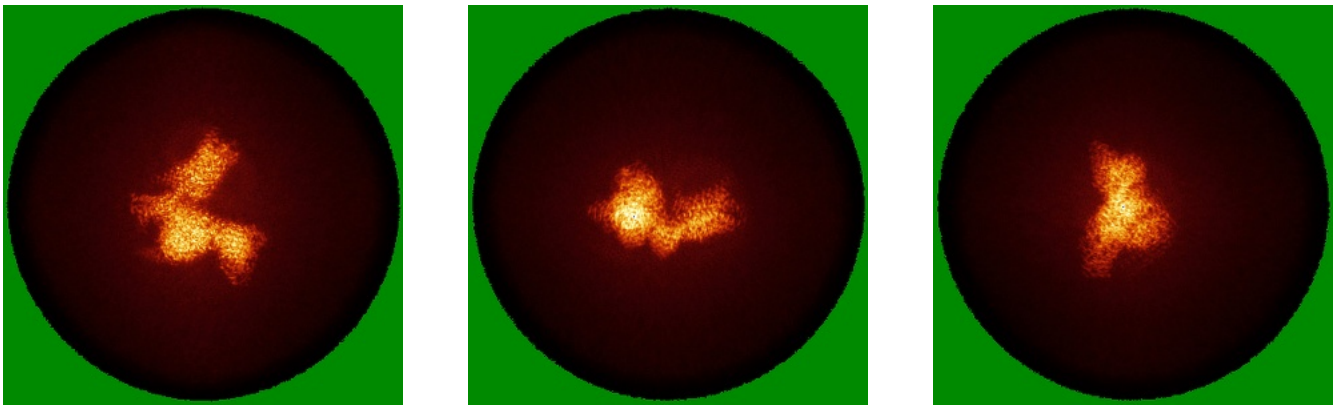


Z Index: 150

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

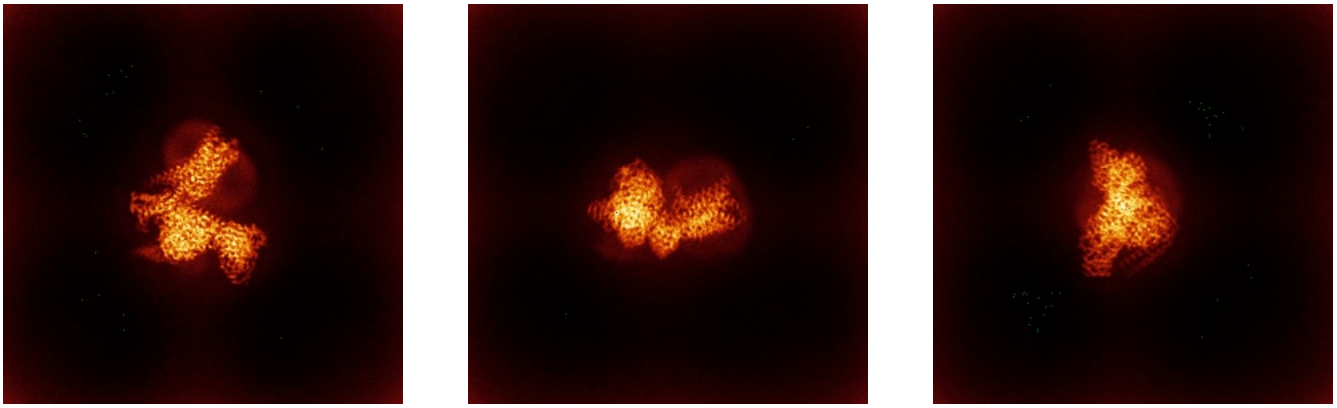
6.4 Orthogonal standard-deviation projections (False-color) (i)

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)

This section was not generated.

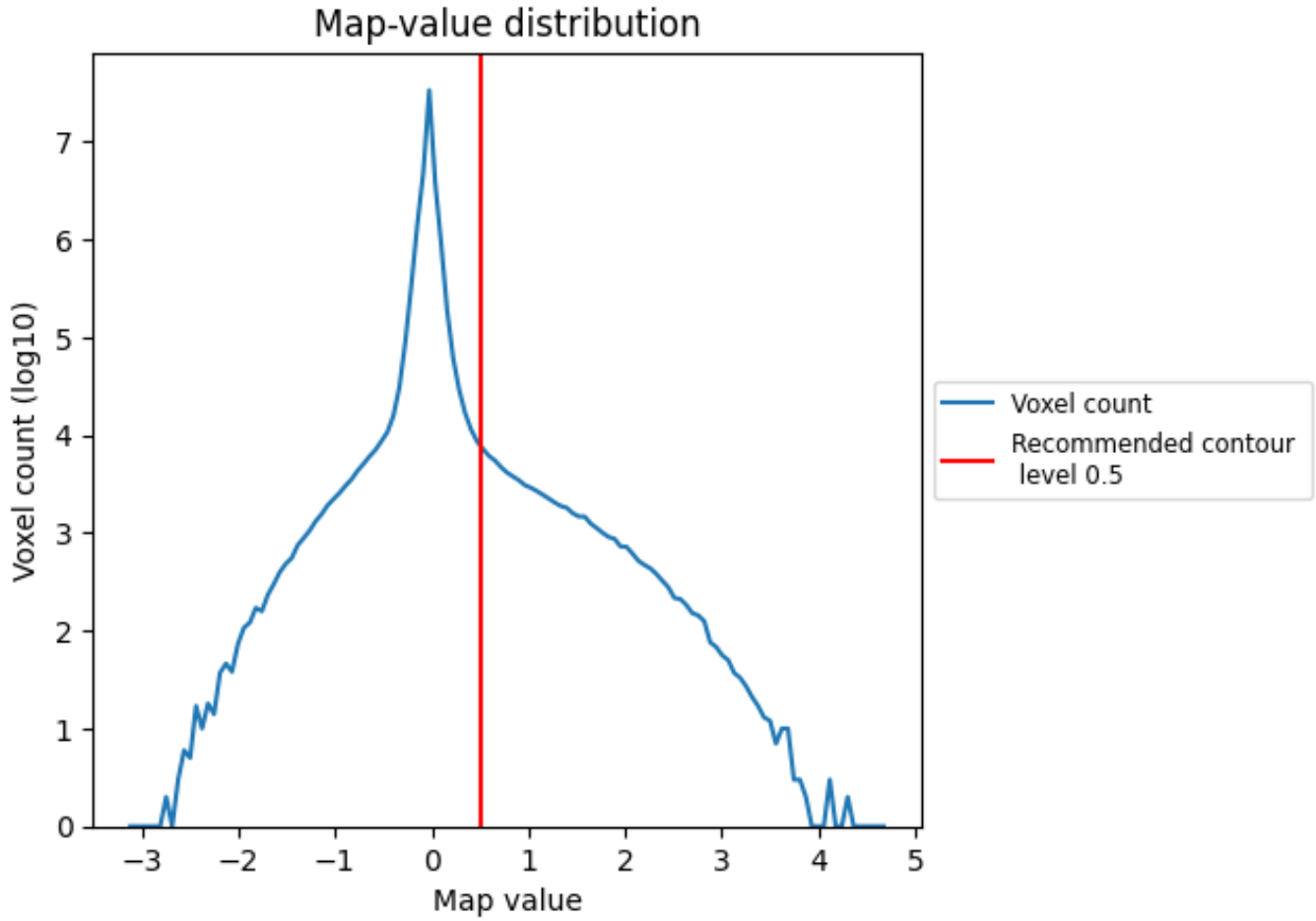
6.6 Mask visualisation (i)

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

7 Map analysis

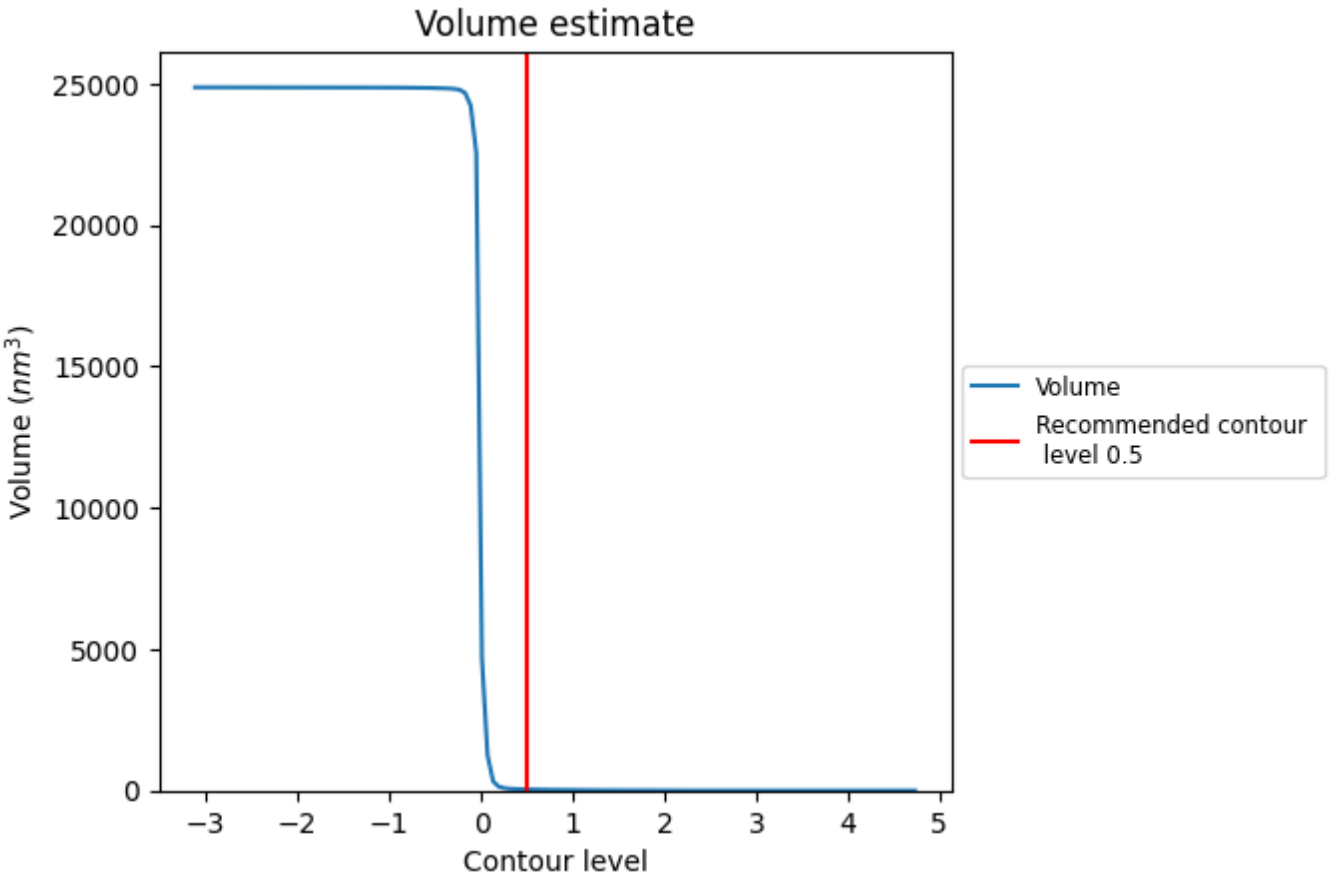
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

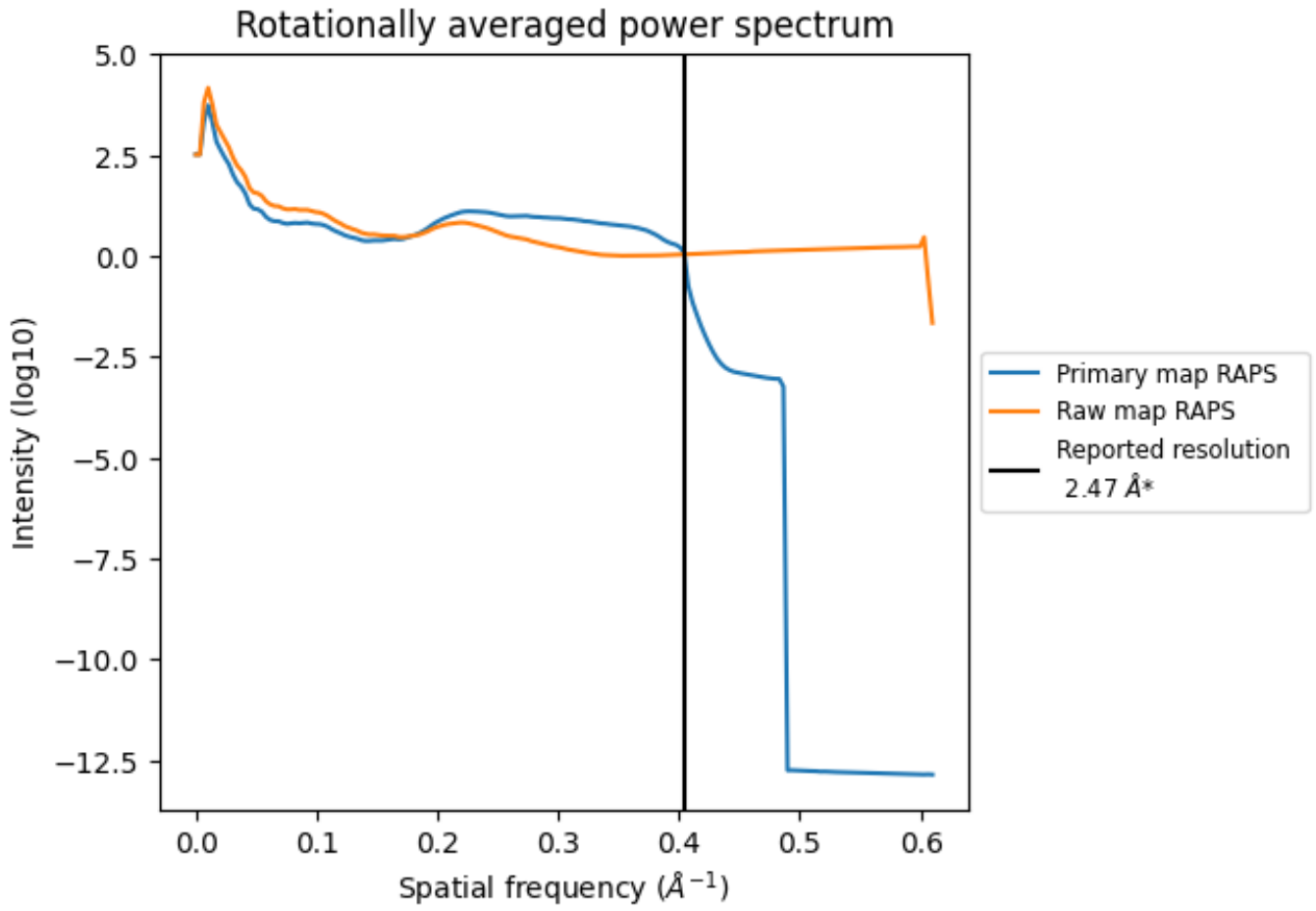
7.2 Volume estimate



The volume at the recommended contour level is 40 nm^3; this corresponds to an approximate mass of 37 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 (i)

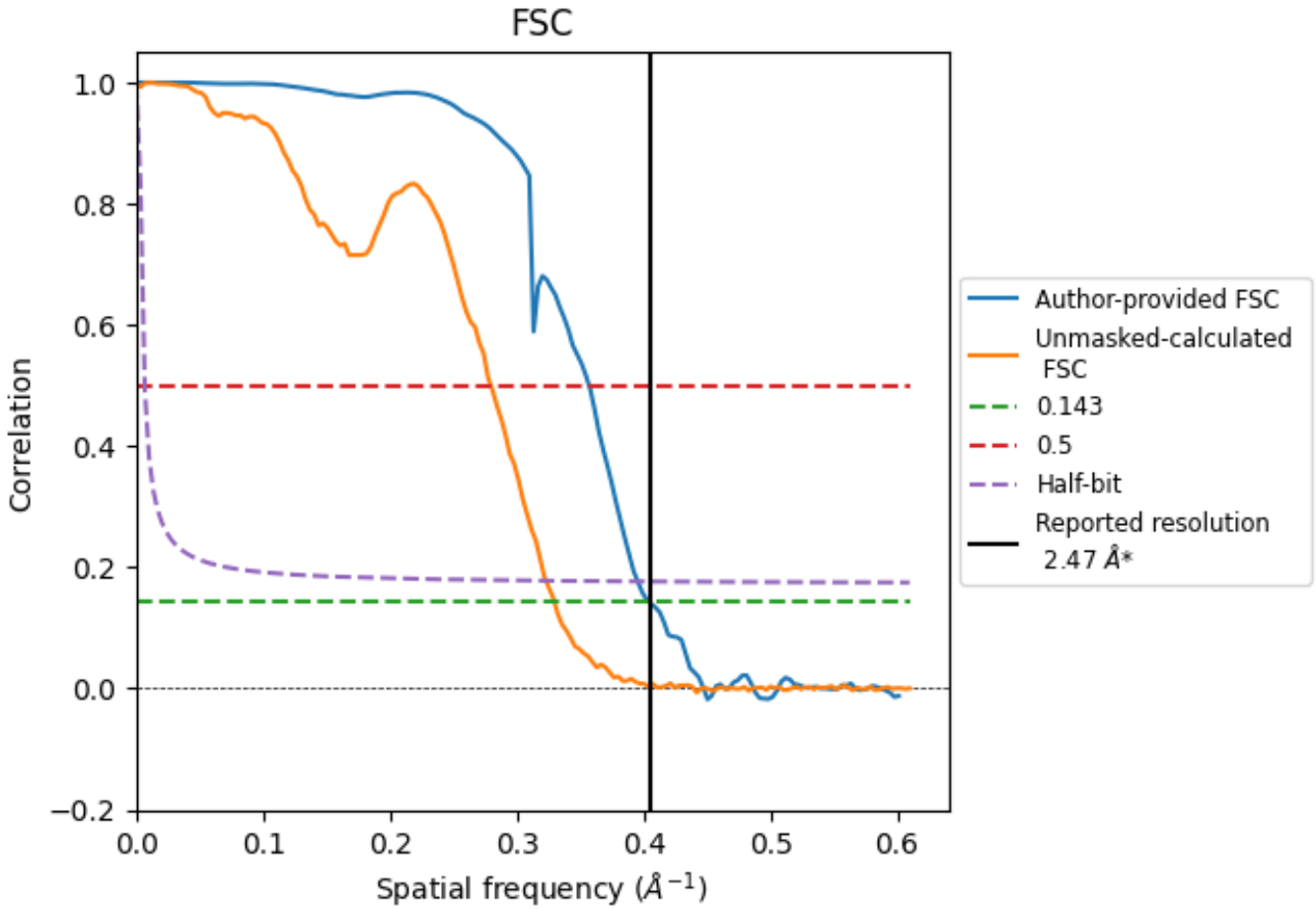


*Reported resolution corresponds to spatial frequency of 0.405 Å^{-1}

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.405 Å^{-1}

8.2 Resolution estimates (i)

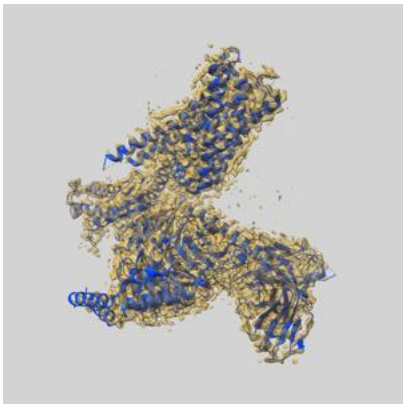
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.47	-	-
Author-provided FSC curve	2.47	2.80	2.53
Unmasked-calculated*	3.03	3.58	3.10

*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 3.03 differs from the reported value 2.47 by more than 10 %

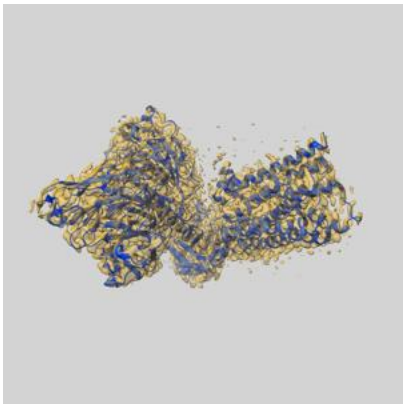
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-65110 and PDB model 9VJE. Per-residue inclusion information can be found in section 3 on page 9.

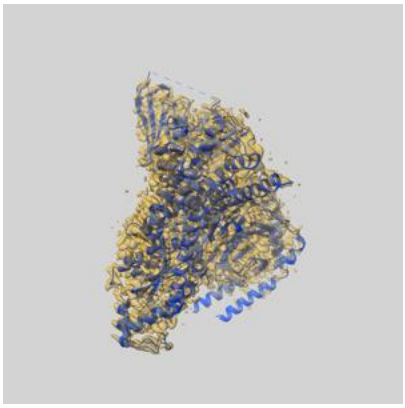
9.1 Map-model overlay



X



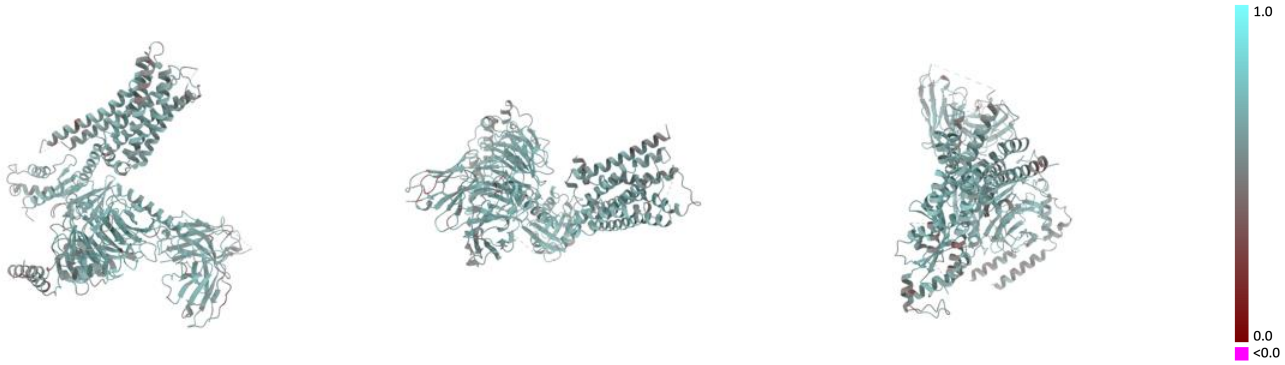
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.5 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.

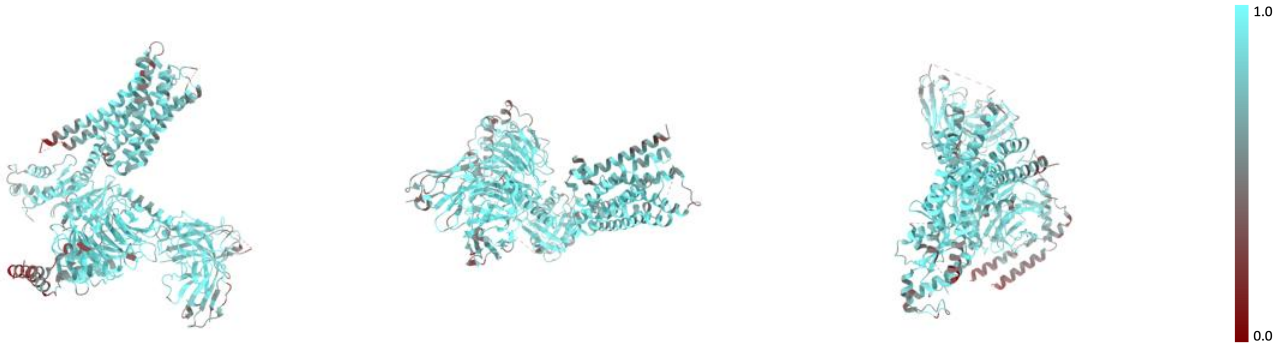
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according 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.

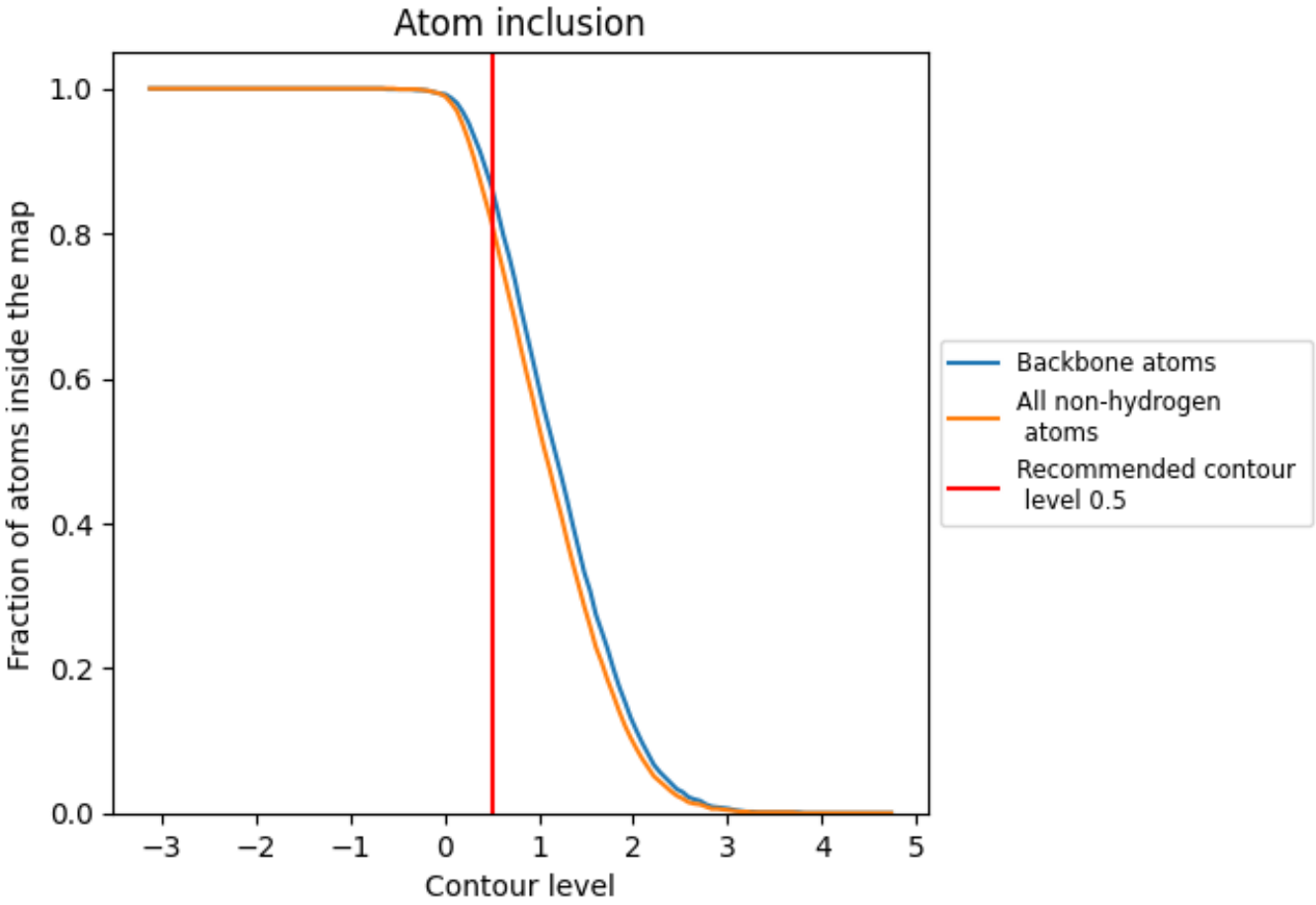
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.5).

9.4 Atom inclusion (i)



At the recommended contour level, 86% of all backbone atoms, 82% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8160	0.6040
B	0.8370	0.6110
C	0.8690	0.6350
D	0.5840	0.5360
E	0.8090	0.5910
R	0.7860	0.5880