



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 06:50 AM UTC

PDB ID : 8JSP / pdb_00008jsp
EMDB ID : EMD-36626
Title : Ulotaront(SEP-363856)-bound Serotonin 1A (5-HT1A) receptor-Gi complex
Authors : Xu, Z.; Guo, L.L.; Zhao, C.; Shen, S.Y.; Sun, J.P.; Shao, Z.H.
Deposited on : 2023-06-20
Resolution : 3.65 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.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

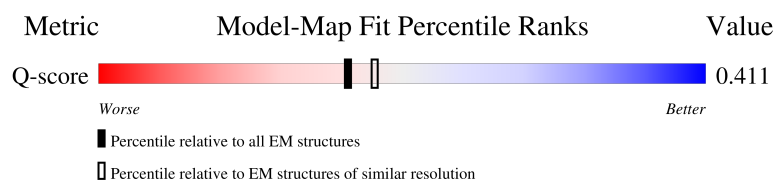
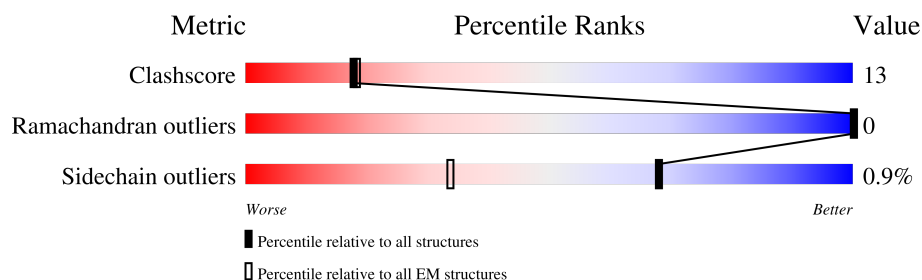
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.65 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	11564 (3.15 - 4.15)

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	351	
2	B	328	
3	E	250	
4	G	45	

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Mol	Chain	Length	Quality of chain
5	R	381	 A horizontal bar chart showing the quality of chain R. The bar is divided into three segments: a red segment at the beginning (approximately 5% of the total length), a green segment (56%), a yellow segment (18%), and a grey segment at the end (25%). A small black dot is located on the yellow segment, near the end of the bar.

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 8599 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(i) subunit alpha-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	216	Total	C	N	O	S	0	0
			1743	1111	291	329	12		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	47	ASN	SER	engineered mutation	UNP P63096
A	203	ALA	GLY	engineered mutation	UNP P63096
A	245	ALA	GLU	engineered mutation	UNP P63096
A	326	SER	ALA	engineered mutation	UNP P63096

- 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	B	328	Total	C	N	O	S	0	0
			2516	1554	452	489	21		

- Molecule 3 is a protein called ScFv16.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	E	227	Total	C	N	O	S	0	0
			1717	1098	290	320	9		

- Molecule 4 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	G	45	Total	C	N	O	S	0	0
			347	218	60	66	3		

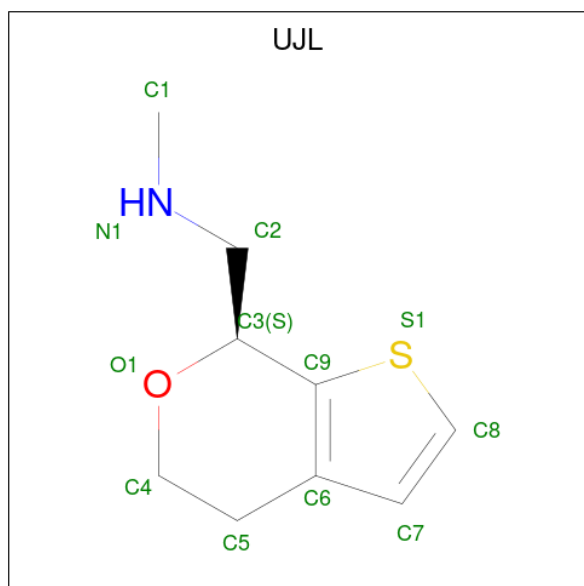
- Molecule 5 is a protein called 5-hydroxytryptamine receptor 1A.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	R	286	Total	C	N	O	S	0	0
			2264	1490	376	381	17		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	125	TRP	LEU	conflict	UNP P08908

- Molecule 6 is 1-[(7 {S})-5,7-dihydro-4 {H}-thieno[2,3-c]pyran-7-yl]- {N}-methyl-methanamine (CCD ID: UJL) (formula: C₉H₁₃NOS) (labeled as "Ligand of Interest" by depositor).

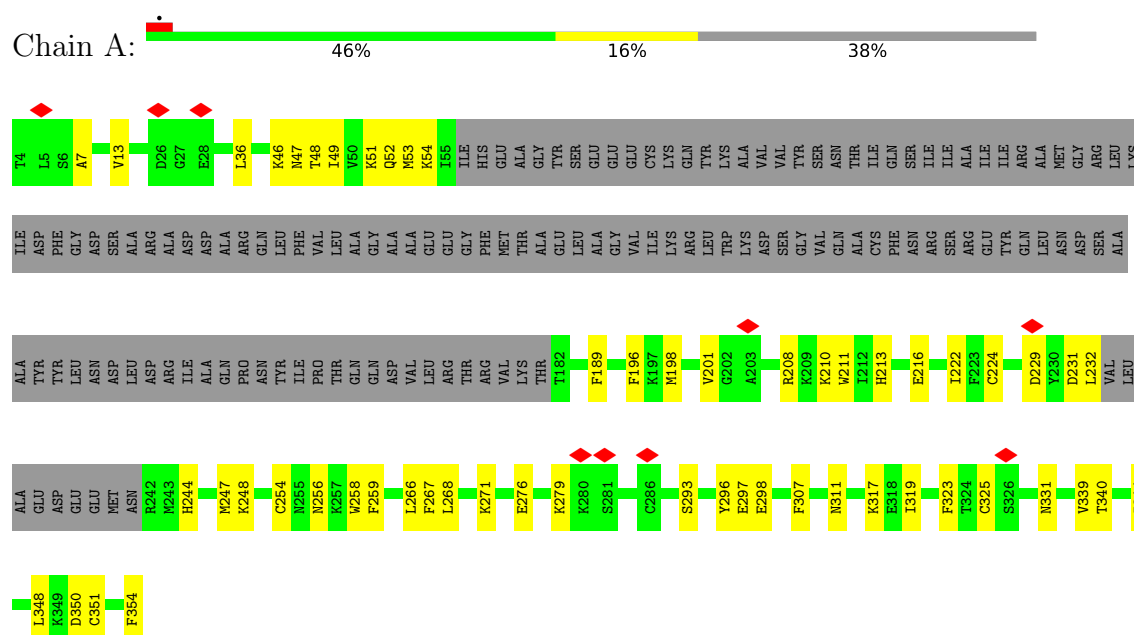


Mol	Chain	Residues	Atoms					AltConf
6	R	1	Total	C	N	O	S	0
			12	9	1	1	1	

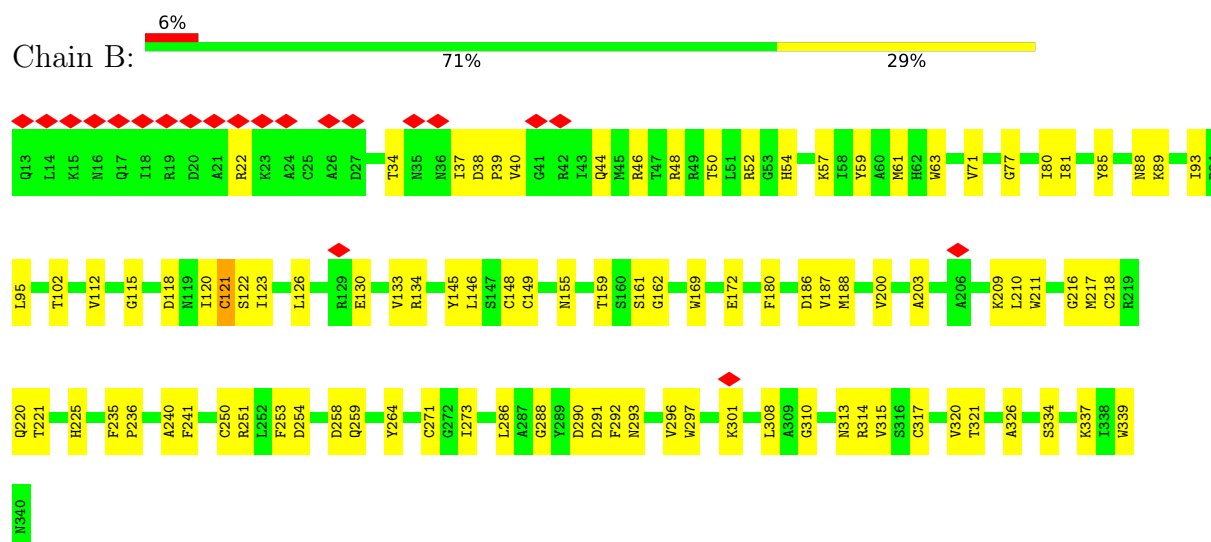
3 Residue-property plots

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: Guanine nucleotide-binding protein G(i) subunit alpha-1



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



Chain E:

Amino Acid	Category
F203	Red
S204	Red
G205	Red
S206	Red
G207	Red
A211	Red
F212	Red
T213	Red
T215	Red
I216	Red
S217	Red
R218	Red
L219	Red
E220	Red
A221	Red
E222	Red
D223	Red
V224	Red
G225	Red
V226	Red
Y227	Red
Y228	Red
C229	Red
M230	Red
Q231	Red
H232	Red
L233	Red
E234	Red
Y235	Red
P236	Red
L237	Red
T238	Red
F239	Red
G240	Red
A241	Red
G242	Red
T243	Red
K244	Red
L245	Red
E246	Red
L247	Red
Lys	Red
ALA	Red
ALA	Red
ALA	Red
F68	Green
T69	Green
I70	Green
S71	Green
R72	Green
D73	Green
M74	Green
C75	Green
K76	Green
N77	Green
T78	Green
L79	Green
F80	Green
L81	Green
K82	Green
M83	Green
T84	Green
S85	Green
L86	Green
R87	Green
S88	Green
E89	Green
D90	Green
T91	Green
M93	Green
Y94	Green
S95	Green
C96	Green
V97	Green
R98	Green
S99	Green
I100	Green
Y101	Green
Y102	Green
F108	Green
W111	Green
G112	Green
Q113	Green
G114	Green
T115	Green
T116	Green
L117	Green
T118	Green
Val	Green
SER	Green
SER	Green
GLY	Green
GLY	Green
GLY	Green
GLY	Green
GLY	Green
Val	Green
SER	Green
A196	Green
S197	Green
G198	Green
V199	Green
P200	Green
D201	Green
R202	Green
V2	Yellow
Q3	Yellow
I4	Yellow
V5	Yellow
E6	Yellow
S7	Yellow
O8	Yellow
C9	Yellow
G10	Yellow
L11	Yellow
V12	Yellow
Q13	Yellow
P14	Yellow
G15	Yellow
G16	Yellow
S17	Yellow
R18	Yellow
K19	Yellow
L20	Yellow
C22	Yellow
S23	Yellow
A24	Yellow
S25	Yellow
G26	Yellow
F27	Yellow
A28	Yellow
F29	Yellow
S30	Yellow
S31	Yellow
F32	Yellow
W36	Yellow
V37	Yellow
R38	Yellow
K39	Yellow
A40	Yellow
P41	Yellow
E42	Yellow
K43	Yellow
G44	Yellow
L45	Yellow
E46	Yellow
W47	Yellow
V48	Yellow
A49	Yellow
Y50	Yellow
I51	Yellow
S52	Yellow
S53	Yellow
G54	Yellow
Y60	Yellow
A61	Yellow
D62	Yellow
T63	Yellow
V64	Yellow
K65	Yellow
G66	Yellow

Chain G:

Color	Percentage
Red	18%
Green	82%
Yellow	18%

Q18 L19 K20 M21 E22 A23 N24 I25 D26 R27 I28 A33 L37 M38 L51 F61 F62

Chain R:

56% 18% 25%

ALA GLY GLY GLY ALA ALA CYS ALA ASN ALA VAL ARG GLN ASP ASP GLY ALA LEU VAL VAL VAL ILE GLU VAL HIS ARG VAL ASN SER LYS GLU HIS LEU PRO LEU PRO PRO SER GLU ALA GLY PRO THR PRO CYS ALA PRO ALA SER PHE ARG ARG K324 R327 R328 A329 E330 A331

K332 R333 R334 M335 A336 L337 A338 R339 K342 T346 I349 F361 F362 L368 C371 S374 M377 I385 N396 P397 V398 I399 Y400 A401 Y402 D406 F407 Q408 K412 I415

Y35 Q36 V37 T39 I47 F48 L78 D82 L83 R84 R85 R86 R87 L88 R89 L90 V98 L99 N100 K101 W102 C109 D110 I113 A114 L115 D116 V117 L118 C119 G120 T121 I130 R134 I138 P141 A153 I157 I169 P170 M172 T177

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	313570	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 ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.389	Depositor
Minimum map value	-0.967	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.032	Depositor
Recommended contour level	0.145	Depositor
Map size (Å)	235.52, 235.52, 235.52	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.92, 0.92, 0.92	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: UJL

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	0.26	0/1772	0.44	0/2375
2	B	0.29	0/2563	0.44	0/3475
3	E	0.19	0/1761	0.45	2/2391 (0.1%)
4	G	0.16	0/353	0.35	0/477
5	R	0.38	0/2317	0.60	1/3154 (0.0%)
All	All	0.29	0/8766	0.49	3/11872 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	234	GLU	CA-C-N	-8.63	113.22	122.89
3	E	234	GLU	C-N-CA	-8.63	113.22	122.89
5	R	85	VAL	N-CA-CB	5.22	116.10	110.62

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1743	0	1742	43	0
2	B	2516	0	2425	77	0
3	E	1717	0	1647	61	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	G	347	0	350	12	0
5	R	2264	0	2357	56	0
6	R	12	0	0	1	0
All	All	8599	0	8521	229	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 (229) 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)
2:B:121:CYS:HB3	2:B:146:LEU:HD22	1.48	0.95
1:A:247:MET:HE1	1:A:307:PHE:HA	1.66	0.76
3:E:47:TRP:NE1	3:E:49:ALA:O	2.20	0.74
1:A:344:ILE:HD11	5:R:141:PRO:HD3	1.70	0.73
5:R:85:VAL:HB	5:R:119:CYS:HB3	1.71	0.73
2:B:288:GLY:HA3	2:B:315:VAL:HG11	1.71	0.73
5:R:102:TRP:H	5:R:185:ASP:H	1.38	0.72
3:E:6:GLU:HA	3:E:22:CYS:HA	1.74	0.70
5:R:113:ILE:HD11	5:R:189:ILE:HG12	1.72	0.69
1:A:276:GLU:HA	1:A:279:LYS:HZ3	1.58	0.69
1:A:210:LYS:HG3	2:B:188:MET:HE1	1.75	0.69
2:B:37:ILE:O	2:B:301:LYS:NZ	2.24	0.69
1:A:189:PHE:HD2	1:A:196:PHE:HB2	1.57	0.68
1:A:229:ASP:HA	1:A:232:LEU:HD13	1.74	0.68
2:B:80:ILE:HD13	2:B:89:LYS:HZ1	1.57	0.68
3:E:67:ARG:NH2	3:E:85:SER:O	2.26	0.68
3:E:231:GLN:HE21	3:E:238:THR:H	1.41	0.68
3:E:51:ILE:HD11	3:E:70:ILE:HG12	1.75	0.67
2:B:240:ALA:HA	2:B:254:ASP:HA	1.76	0.66
2:B:71:VAL:HG12	2:B:81:ILE:HG12	1.76	0.66
5:R:82:ASP:O	5:R:85:VAL:HG13	1.96	0.65
2:B:80:ILE:HD13	2:B:89:LYS:NZ	2.11	0.65
5:R:181:ARG:NH1	5:R:188:THR:O	2.25	0.64
3:E:20:LEU:HB2	3:E:81:LEU:HB2	1.79	0.64
1:A:189:PHE:HE2	1:A:198:MET:HE3	1.61	0.63
2:B:200:VAL:HG12	2:B:210:LEU:HA	1.81	0.63
3:E:232:HIS:CD2	3:E:237:LEU:HD21	2.34	0.63
1:A:340:THR:HG23	5:R:141:PRO:HG2	1.79	0.62
5:R:169:ILE:HG13	5:R:170:PRO:HD3	1.82	0.62
1:A:52:GLN:OE1	1:A:331:ASN:ND2	2.32	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:173:TYR:HB3	3:E:232:HIS:HB3	1.82	0.61
2:B:337:LYS:HB2	2:B:339:TRP:HE1	1.65	0.61
3:E:29:PHE:O	3:E:72:ARG:NH2	2.34	0.61
3:E:142:GLN:NE2	3:E:243:THR:OG1	2.33	0.60
2:B:39:PRO:HB3	2:B:301:LYS:HG2	1.84	0.60
1:A:276:GLU:HG3	1:A:279:LYS:HZ3	1.66	0.60
2:B:115:GLY:HA3	2:B:121:CYS:HA	1.83	0.60
2:B:209:LYS:HG2	2:B:221:THR:HG22	1.84	0.60
1:A:196:PHE:HE1	1:A:339:VAL:HG21	1.66	0.59
1:A:213:HIS:HB3	1:A:258:TRP:CZ3	2.38	0.59
3:E:234:GLU:HB3	3:E:236:PRO:HD3	1.83	0.59
5:R:201:PHE:HD1	5:R:205:TYR:HD2	1.50	0.59
3:E:60:TYR:HB3	3:E:64:VAL:HG23	1.84	0.59
2:B:39:PRO:HD3	2:B:301:LYS:HE2	1.85	0.58
3:E:5:VAL:HG23	3:E:23:SER:HB3	1.84	0.58
1:A:36:LEU:HD13	1:A:222:ILE:HD11	1.84	0.58
2:B:34:THR:HG23	4:G:38:MET:HE1	1.85	0.58
3:E:167:HIS:CD2	3:E:168:SER:H	2.22	0.58
3:E:171:ASN:HB2	3:E:173:TYR:HE1	1.68	0.57
2:B:162:GLY:HA2	2:B:186:ASP:HB2	1.86	0.57
2:B:259:GLN:OE1	4:G:27:ARG:NH2	2.37	0.57
2:B:264:TYR:HB3	2:B:297:TRP:CZ3	2.39	0.57
3:E:199:VAL:HG23	3:E:201:ASP:H	1.69	0.57
1:A:7:ALA:HB3	3:E:232:HIS:HE1	1.69	0.57
3:E:38:ARG:O	3:E:46:GLU:N	2.37	0.56
2:B:159:THR:OG1	2:B:169:TRP:NE1	2.32	0.56
1:A:216:GLU:OE2	1:A:258:TRP:HB3	2.05	0.56
2:B:220:GLN:HA	4:G:22:GLU:HG3	1.87	0.56
5:R:101:LYS:HA	5:R:185:ASP:HB2	1.86	0.56
4:G:33:ALA:O	4:G:37:LEU:HG	2.05	0.56
1:A:348:LEU:HG	5:R:138:ILE:HD12	1.87	0.56
2:B:61:MET:HG2	2:B:317:CYS:SG	2.47	0.55
5:R:36:GLN:NE2	5:R:98:VAL:O	2.39	0.55
2:B:22:ARG:HG2	4:G:27:ARG:HH22	1.72	0.55
5:R:47:ILE:HG12	5:R:90:LEU:HB3	1.89	0.55
3:E:12:VAL:HG21	3:E:18:ARG:HB2	1.88	0.55
3:E:40:ALA:HB3	3:E:43:LYS:HB2	1.89	0.54
3:E:32:PHE:CD2	3:E:98:ARG:HD2	2.42	0.54
1:A:271:LYS:HD3	1:A:325:CYS:HB3	1.90	0.54
2:B:22:ARG:HA	4:G:27:ARG:HH22	1.72	0.54
2:B:310:GLY:O	2:B:337:LYS:NZ	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:308:LEU:HB3	2:B:339:TRP:CH2	2.43	0.53
3:E:36:TRP:CE2	3:E:81:LEU:HD11	2.43	0.53
1:A:244:HIS:HB3	1:A:248:LYS:HZ1	1.74	0.53
5:R:102:TRP:NE1	5:R:109:CYS:HB2	2.24	0.53
2:B:187:VAL:HG12	2:B:203:ALA:HB2	1.91	0.53
3:E:70:ILE:HG13	3:E:81:LEU:HD23	1.91	0.53
5:R:84:MET:O	5:R:85:VAL:C	2.51	0.53
1:A:311:ASN:HD22	1:A:319:ILE:HD11	1.74	0.53
5:R:88:LEU:HB3	5:R:115:LEU:HD12	1.90	0.52
3:E:45:LEU:HD12	3:E:239:PHE:CE2	2.45	0.52
1:A:47:ASN:OD1	1:A:48:THR:N	2.41	0.52
5:R:172:MET:HE3	5:R:172:MET:HA	1.90	0.52
1:A:254:CYS:O	1:A:317:LYS:NZ	2.43	0.52
3:E:174:LEU:HD11	3:E:229:CYS:SG	2.50	0.52
3:E:32:PHE:CE1	3:E:100:ILE:HD12	2.45	0.52
1:A:276:GLU:HG3	1:A:279:LYS:NZ	2.25	0.51
3:E:41:PRO:HA	3:E:93:MET:HE1	1.93	0.51
5:R:408:GLN:O	5:R:412:LYS:HG2	2.10	0.51
2:B:130:GLU:HB2	2:B:134:ARG:HH21	1.75	0.51
1:A:47:ASN:HB2	1:A:51:LYS:NZ	2.25	0.51
1:A:208:ARG:HA	1:A:211:TRP:NE1	2.25	0.51
1:A:7:ALA:HB2	3:E:235:TYR:CD1	2.46	0.51
5:R:78:LEU:HD11	5:R:396:ASN:HD21	1.76	0.50
2:B:308:LEU:HB3	2:B:339:TRP:CZ3	2.46	0.50
2:B:50:THR:HG23	2:B:337:LYS:HD3	1.93	0.50
2:B:146:LEU:HA	2:B:161:SER:HA	1.93	0.50
2:B:308:LEU:HD13	2:B:339:TRP:CE3	2.46	0.50
3:E:5:VAL:O	3:E:23:SER:N	2.44	0.50
2:B:250:CYS:HB2	2:B:264:TYR:HB2	1.93	0.50
3:E:95:TYR:HD2	3:E:111:TRP:HE3	1.59	0.50
2:B:130:GLU:HB2	2:B:134:ARG:NH2	2.27	0.49
2:B:180:PHE:HE1	2:B:216:GLY:HA2	1.77	0.49
3:E:230:MET:HB3	3:E:239:PHE:CD2	2.48	0.49
1:A:344:ILE:HG12	5:R:141:PRO:HG3	1.94	0.49
5:R:331:ALA:HA	5:R:334:LYS:NZ	2.28	0.49
5:R:37:VAL:HG23	5:R:38:ILE:HD12	1.95	0.48
5:R:183:ASP:OD1	5:R:183:ASP:N	2.43	0.48
3:E:12:VAL:HB	3:E:86:LEU:HD21	1.95	0.48
3:E:94:TYR:HB2	3:E:115:THR:OG1	2.13	0.48
3:E:100:ILE:HG12	3:E:102:TYR:HE1	1.78	0.48
3:E:158:SER:HA	3:E:213:THR:HA	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:256:ASN:HB3	1:A:259:PHE:HB2	1.95	0.48
5:R:153:ALA:O	5:R:157:ILE:HG12	2.13	0.48
2:B:57:LYS:HG3	2:B:59:TYR:HE1	1.78	0.48
2:B:77:GLY:C	2:B:95:LEU:HD12	2.39	0.48
2:B:145:TYR:OH	2:B:188:MET:HE2	2.13	0.47
5:R:85:VAL:O	5:R:86:SER:C	2.56	0.47
3:E:157:ILE:HG12	3:E:243:THR:HG21	1.96	0.47
5:R:406:ASP:OD1	5:R:407:PHE:N	2.47	0.47
1:A:231:ASP:O	1:A:232:LEU:HD12	2.14	0.47
2:B:155:ASN:OD1	2:B:172:GLU:HG2	2.14	0.47
3:E:189:ILE:HG13	3:E:194:ASN:O	2.15	0.47
2:B:93:ILE:HD11	2:B:133:VAL:HG21	1.96	0.47
2:B:112:VAL:HG23	2:B:126:LEU:HD11	1.96	0.47
5:R:361:PHE:HA	5:R:385:ILE:HG23	1.96	0.47
2:B:271:CYS:HB2	2:B:290:ASP:HB2	1.97	0.47
5:R:200:THR:HA	5:R:362:PHE:HE2	1.80	0.46
2:B:220:GLN:NE2	2:B:258:ASP:OD2	2.48	0.46
3:E:178:LEU:HD12	3:E:226:VAL:O	2.16	0.46
2:B:225:HIS:HE2	2:B:251:ARG:HG3	1.81	0.46
3:E:6:GLU:OE2	3:E:114:GLY:N	2.30	0.46
3:E:67:ARG:HH21	3:E:86:LEU:HA	1.80	0.46
3:E:93:MET:HB3	3:E:95:TYR:HE1	1.81	0.46
5:R:85:VAL:HG22	5:R:86:SER:N	2.29	0.46
2:B:264:TYR:HB3	2:B:297:TRP:HZ3	1.79	0.45
3:E:177:PHE:HB2	3:E:228:TYR:HB2	1.97	0.45
5:R:85:VAL:HB	5:R:119:CYS:CB	2.44	0.45
1:A:268:LEU:HD13	1:A:323:PHE:HE1	1.80	0.45
3:E:99:SER:HG	3:E:108:PHE:H	1.60	0.45
5:R:333:ARG:O	5:R:337:LEU:HD23	2.17	0.45
3:E:15:GLY:HA2	3:E:85:SER:HA	1.97	0.45
5:R:399:ILE:HG13	5:R:400:TYR:CD2	2.51	0.45
1:A:266:LEU:HD12	1:A:267:PHE:H	1.80	0.45
3:E:100:ILE:HG12	3:E:102:TYR:CE1	2.51	0.45
1:A:48:THR:O	1:A:52:GLN:HG2	2.17	0.45
2:B:187:VAL:HA	2:B:203:ALA:HA	1.98	0.45
2:B:217:MET:HE2	4:G:18:GLN:OE1	2.16	0.45
2:B:122:SER:OG	2:B:123:ILE:N	2.50	0.45
2:B:290:ASP:HA	2:B:314:ARG:HG3	1.98	0.45
1:A:244:HIS:O	1:A:248:LYS:HG3	2.17	0.45
2:B:217:MET:HG3	2:B:218:CYS:N	2.32	0.45
3:E:108:PHE:O	3:E:111:TRP:NE1	2.43	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:85:TYR:CD1	4:G:61:PHE:HE1	2.35	0.45
3:E:94:TYR:HB2	3:E:115:THR:HG1	1.81	0.44
3:E:97:VAL:HG11	3:E:108:PHE:CD2	2.53	0.44
5:R:100:ASN:C	5:R:101:LYS:HD2	2.42	0.44
5:R:115:LEU:O	5:R:116:ASP:C	2.61	0.44
1:A:201:VAL:HB	1:A:211:TRP:CH2	2.53	0.44
2:B:235:PHE:CD2	2:B:236:PRO:HD2	2.52	0.44
3:E:32:PHE:CD1	3:E:100:ILE:HD12	2.53	0.44
5:R:335:MET:O	5:R:339:ARG:HG2	2.18	0.44
2:B:286:LEU:HD23	2:B:296:VAL:HG12	2.00	0.44
1:A:54:LYS:HA	1:A:189:PHE:HE1	1.83	0.43
5:R:121:THR:OG1	6:R:501:UJL:S1	2.76	0.43
5:R:346:THR:O	5:R:349:ILE:HG22	2.18	0.43
2:B:180:PHE:HB3	2:B:211:TRP:CZ3	2.53	0.43
3:E:69:THR:HG23	3:E:82:GLN:HB2	2.00	0.43
1:A:350:ASP:OD1	1:A:351:CYS:N	2.51	0.43
3:E:50:TYR:HB3	3:E:235:TYR:OH	2.18	0.43
5:R:202:GLY:HA2	5:R:206:ILE:HD13	2.00	0.43
1:A:13:VAL:HG12	2:B:88:ASN:HD21	1.83	0.43
2:B:121:CYS:HB3	2:B:146:LEU:CD2	2.34	0.43
2:B:149:CYS:CB	2:B:159:THR:HG22	2.49	0.43
2:B:291:ASP:OD1	2:B:293:ASN:HB2	2.19	0.43
3:E:87:ARG:HE	3:E:87:ARG:HB3	1.68	0.43
5:R:331:ALA:HA	5:R:334:LYS:HZ3	1.84	0.43
5:R:398:VAL:HA	5:R:402:TYR:HD2	1.83	0.43
3:E:200:PRO:HB2	3:E:202:ARG:HE	1.83	0.43
2:B:44:GLN:HG3	2:B:46:ARG:HG3	2.00	0.43
2:B:264:TYR:HB3	2:B:297:TRP:CE3	2.54	0.43
3:E:187:LEU:HD21	3:E:190:TYR:CD2	2.54	0.43
5:R:329:ALA:O	5:R:333:ARG:NE	2.50	0.43
2:B:54:HIS:CB	2:B:334:SER:HB2	2.49	0.43
3:E:53:SER:HA	3:E:72:ARG:NH1	2.34	0.43
5:R:223:ARG:HD2	5:R:223:ARG:HA	1.78	0.42
5:R:368:LEU:HD13	5:R:377:MET:SD	2.59	0.42
5:R:206:ILE:H	5:R:206:ILE:HD12	1.83	0.42
2:B:22:ARG:HA	4:G:27:ARG:NH2	2.35	0.42
1:A:276:GLU:HA	1:A:279:LYS:NZ	2.31	0.42
2:B:38:ASP:OD1	2:B:38:ASP:N	2.44	0.42
5:R:201:PHE:CD1	5:R:205:TYR:HD2	2.34	0.42
1:A:49:ILE:HG13	1:A:224:CYS:SG	2.60	0.42
5:R:361:PHE:HD1	5:R:385:ILE:HG22	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:292:PHE:HB3	2:B:313:ASN:C	2.44	0.42
1:A:296:TYR:CE2	1:A:297:GLU:HG2	2.55	0.42
3:E:61:ALA:HB3	3:E:64:VAL:HG22	2.01	0.42
5:R:39:THR:HG22	5:R:98:VAL:HG22	2.02	0.42
5:R:415:ILE:HD13	5:R:415:ILE:HA	1.90	0.42
5:R:78:LEU:HD21	5:R:396:ASN:OD1	2.20	0.41
1:A:293:SER:OG	1:A:298:GLU:OE1	2.21	0.41
1:A:354:PHE:OXT	5:R:342:LYS:HD2	2.21	0.41
3:E:195:LEU:HD11	3:E:199:VAL:HG21	2.00	0.41
2:B:48:ARG:HG3	4:G:61:PHE:HB3	2.02	0.41
2:B:235:PHE:N	2:B:240:ALA:O	2.38	0.41
2:B:250:CYS:SG	2:B:273:ILE:HD13	2.61	0.41
2:B:320:VAL:HG23	2:B:326:ALA:O	2.19	0.41
2:B:145:TYR:O	2:B:162:GLY:N	2.33	0.41
2:B:180:PHE:HB3	2:B:211:TRP:CH2	2.56	0.41
3:E:150:THR:O	3:E:219:LEU:HD11	2.20	0.41
5:R:200:THR:HG22	5:R:362:PHE:CD2	2.56	0.41
5:R:116:ASP:O	5:R:117:VAL:C	2.62	0.41
2:B:40:VAL:HG11	4:G:51:LEU:HD21	2.02	0.41
2:B:241:PHE:CZ	2:B:253:PHE:HB2	2.56	0.41
5:R:102:TRP:H	5:R:185:ASP:N	2.12	0.41
5:R:130:ILE:HG22	5:R:134:ARG:HE	1.85	0.41
1:A:53:MET:HB3	1:A:189:PHE:CZ	2.56	0.41
2:B:63:TRP:CE3	2:B:321:THR:HG22	2.56	0.41
2:B:326:ALA:HB2	4:G:61:PHE:CE2	2.56	0.41
5:R:87:VAL:HG12	5:R:88:LEU:HD12	2.03	0.41
2:B:118:ASP:N	2:B:118:ASP:OD1	2.54	0.41
5:R:110:ASP:OD2	5:R:172:MET:HE1	2.21	0.41
1:A:46:LYS:HB3	1:A:46:LYS:HE3	1.88	0.40
3:E:18:ARG:HB3	3:E:83:MET:HE3	2.04	0.40
3:E:176:TRP:HB2	3:E:189:ILE:CG2	2.51	0.40
2:B:52:ARG:O	2:B:52:ARG:HG3	2.22	0.40
2:B:102:THR:OG1	2:B:148:CYS:HA	2.21	0.40
2:B:118:ASP:O	2:B:120:ILE:N	2.50	0.40
3:E:20:LEU:HB3	3:E:81:LEU:HD12	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	210/351 (60%)	201 (96%)	9 (4%)	0	100	100
2	B	326/328 (99%)	301 (92%)	25 (8%)	0	100	100
3	E	223/250 (89%)	212 (95%)	11 (5%)	0	100	100
4	G	43/45 (96%)	41 (95%)	2 (5%)	0	100	100
5	R	282/381 (74%)	265 (94%)	17 (6%)	0	100	100
All	All	1084/1355 (80%)	1020 (94%)	64 (6%)	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	A	192/303 (63%)	192 (100%)	0	100	100
2	B	272/272 (100%)	271 (100%)	1 (0%)	84	79
3	E	181/201 (90%)	181 (100%)	0	100	100
4	G	37/37 (100%)	37 (100%)	0	100	100
5	R	245/316 (78%)	238 (97%)	7 (3%)	37	56
All	All	927/1129 (82%)	919 (99%)	8 (1%)	68	73

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	121	CYS
5	R	83	LEU
5	R	85	VAL
5	R	86	SER
5	R	89	VAL
5	R	113	ILE
5	R	115	LEU
5	R	118	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	322	HIS
2	B	142	HIS
2	B	183	HIS
3	E	113	GLN
3	E	142	GLN
3	E	231	GLN
5	R	54	ASN
5	R	146	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand is 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	$\# Z > 2$
6	UJL	R	501	-	10,13,13	0.36	0	9,17,17	1.03	1 (11%)

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
6	UJL	R	501	-	-	0/3/13/13	0/2/2/2

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	R	501	UJL	C3-C2-N1	2.46	115.46	111.07

There are no chirality outliers.

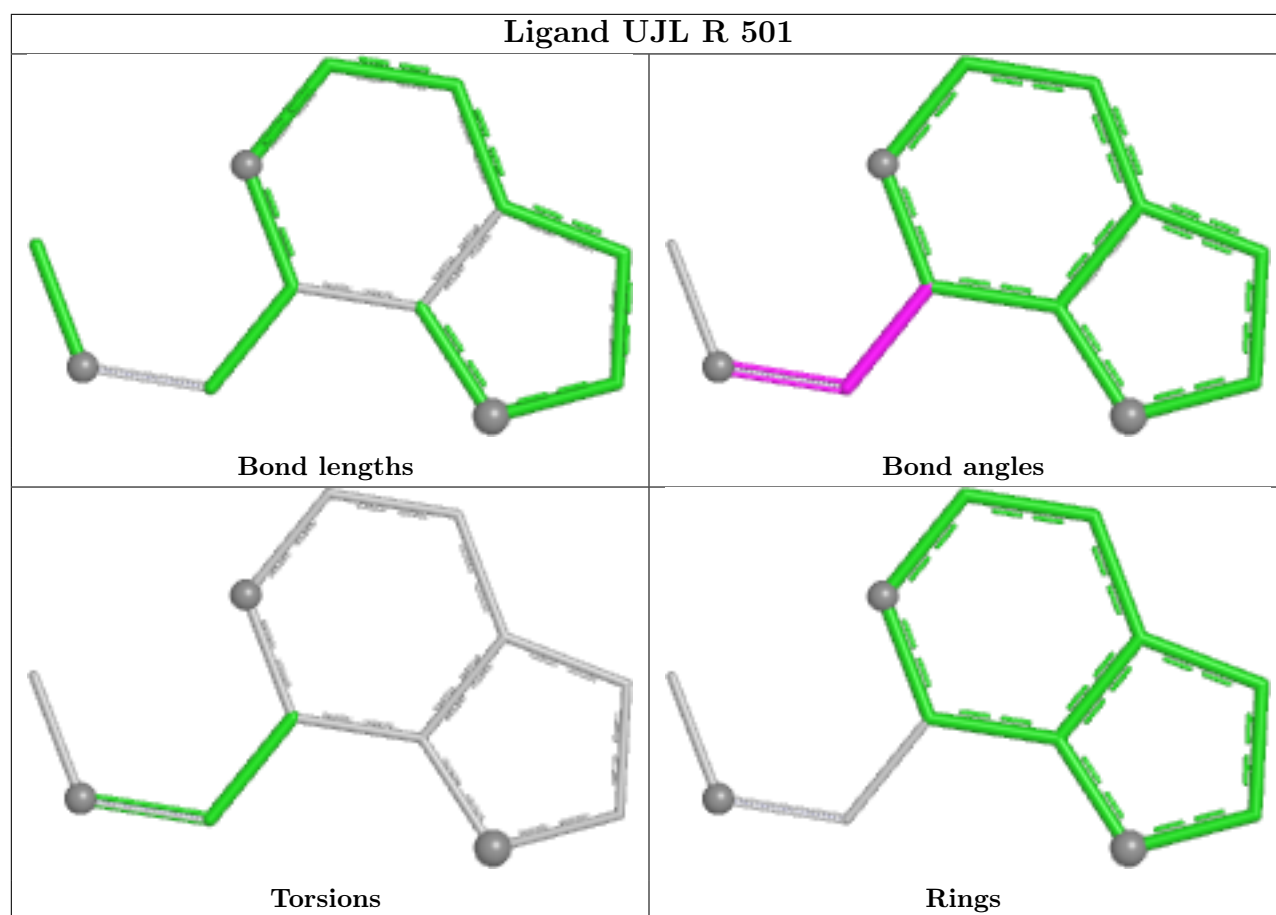
There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	R	501	UJL	1	0

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

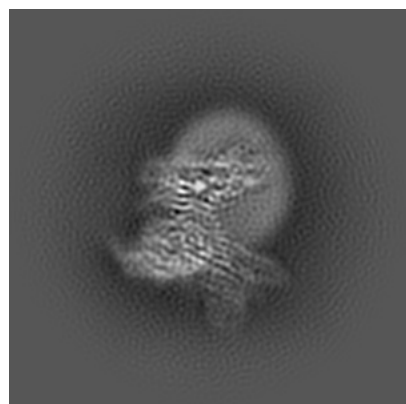
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-36626. These allow visual inspection of the internal detail of the map and identification of artifacts.

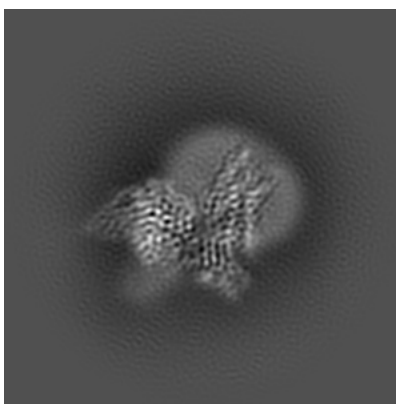
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

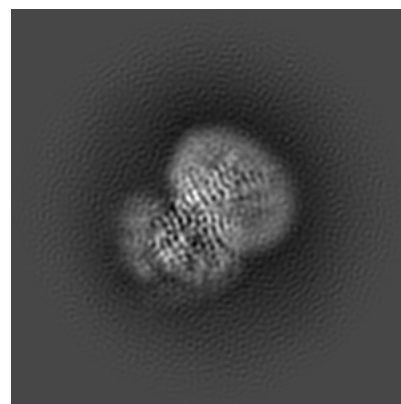
6.1.1 Primary map



X

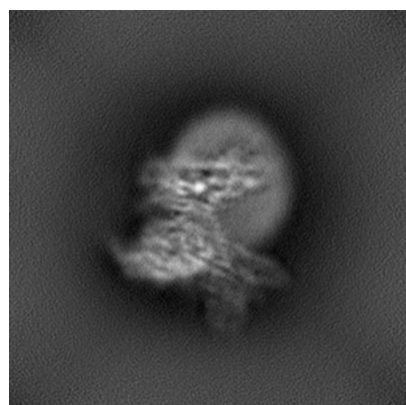


Y

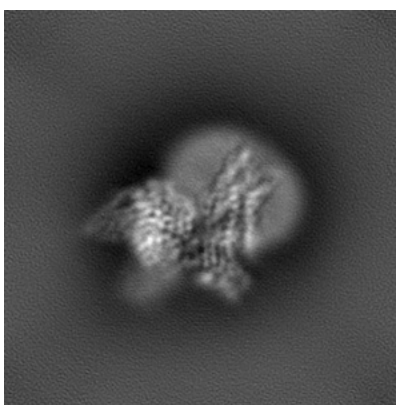


Z

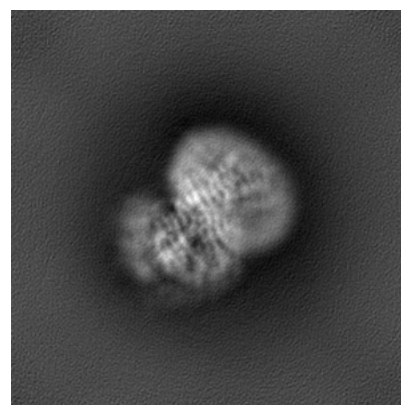
6.1.2 Raw map



X



Y

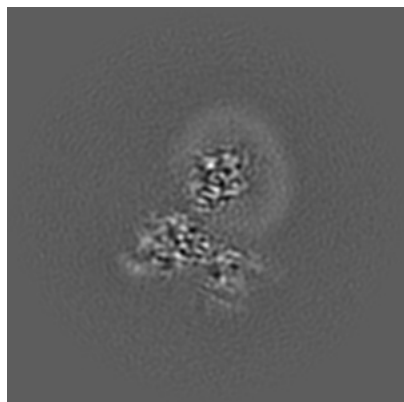


Z

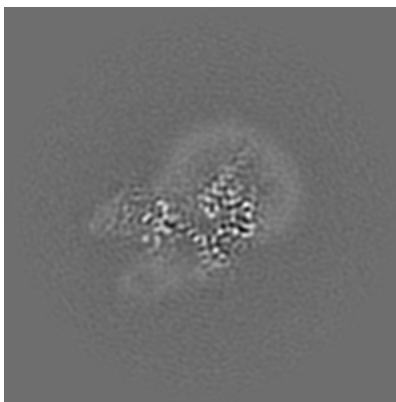
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

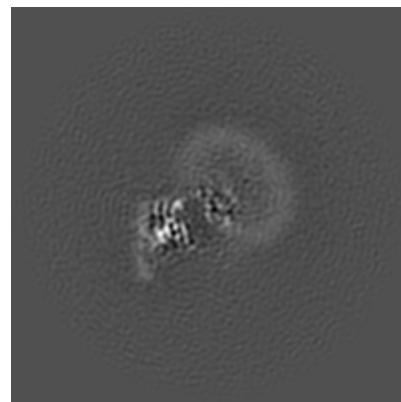
6.2.1 Primary map



X Index: 128

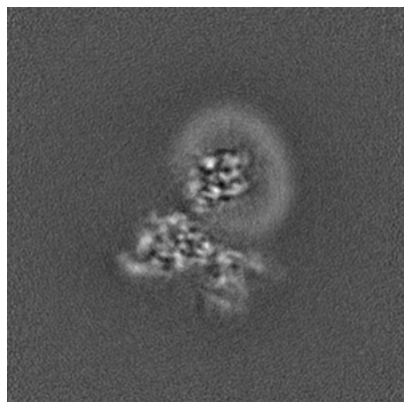


Y Index: 128

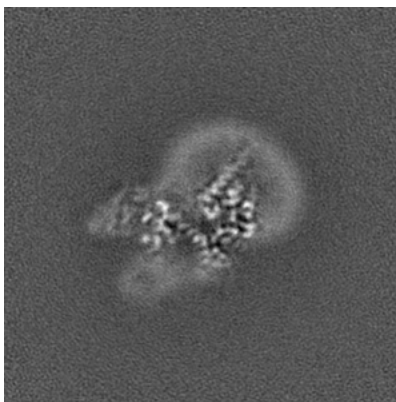


Z Index: 128

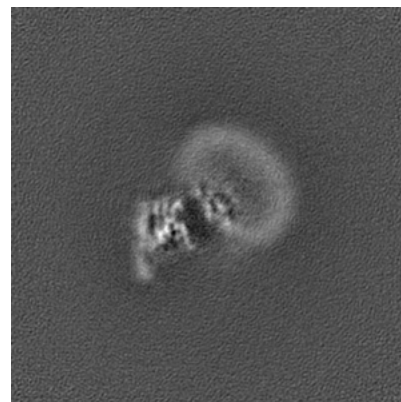
6.2.2 Raw map



X Index: 128



Y Index: 128

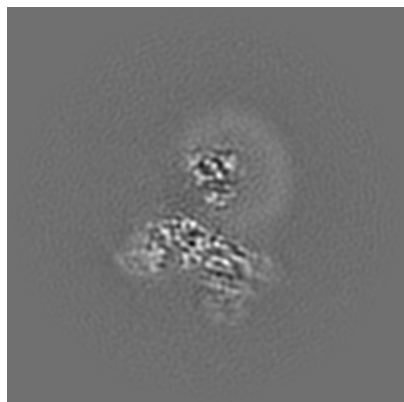


Z Index: 128

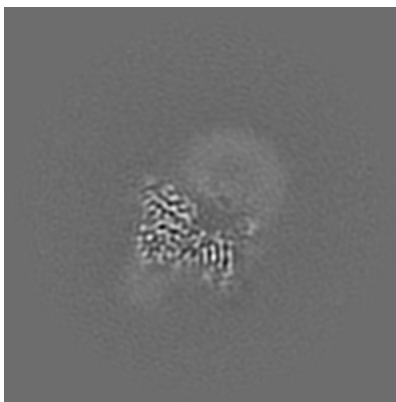
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

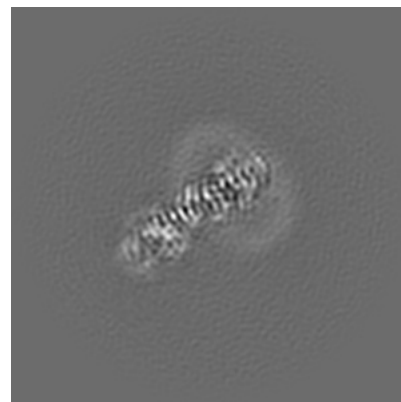
6.3.1 Primary map



X Index: 121

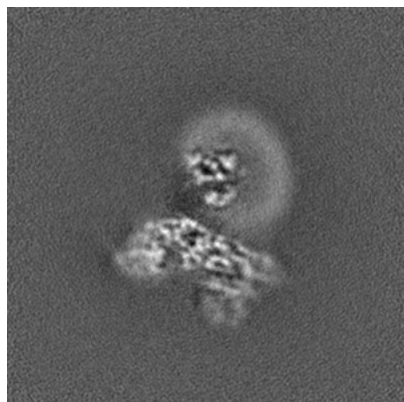


Y Index: 112

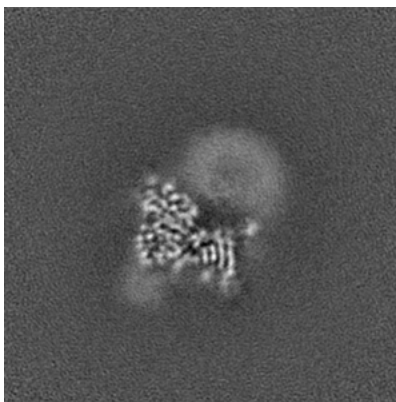


Z Index: 144

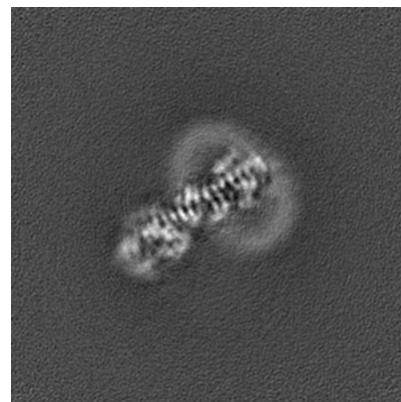
6.3.2 Raw map



X Index: 121



Y Index: 111

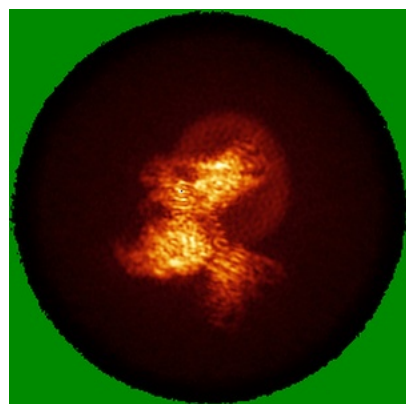


Z Index: 144

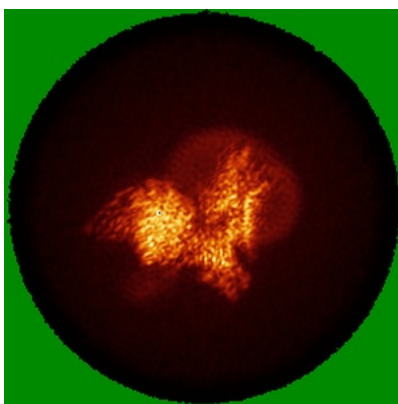
The images above show the largest variance slices of the map in three orthogonal directions.

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

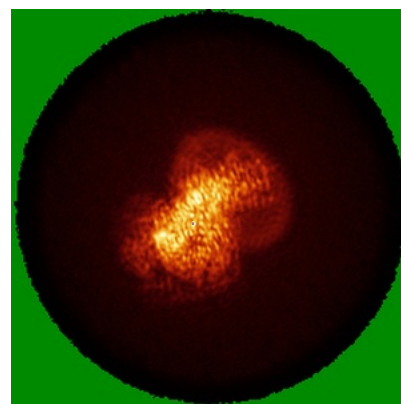
6.4.1 Primary map



X



Y

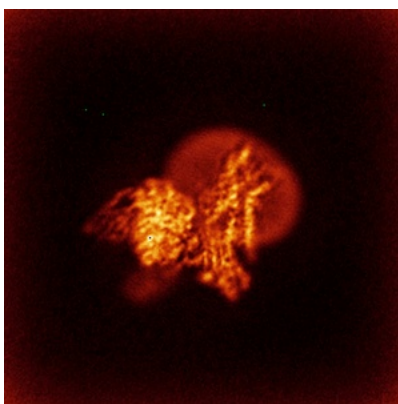


Z

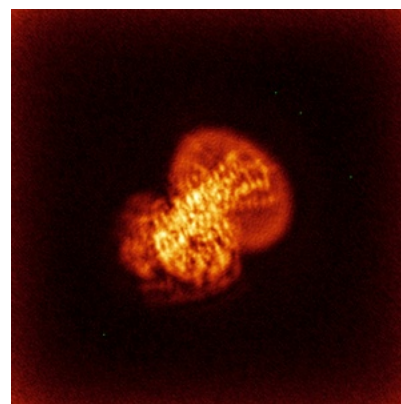
6.4.2 Raw map



X



Y

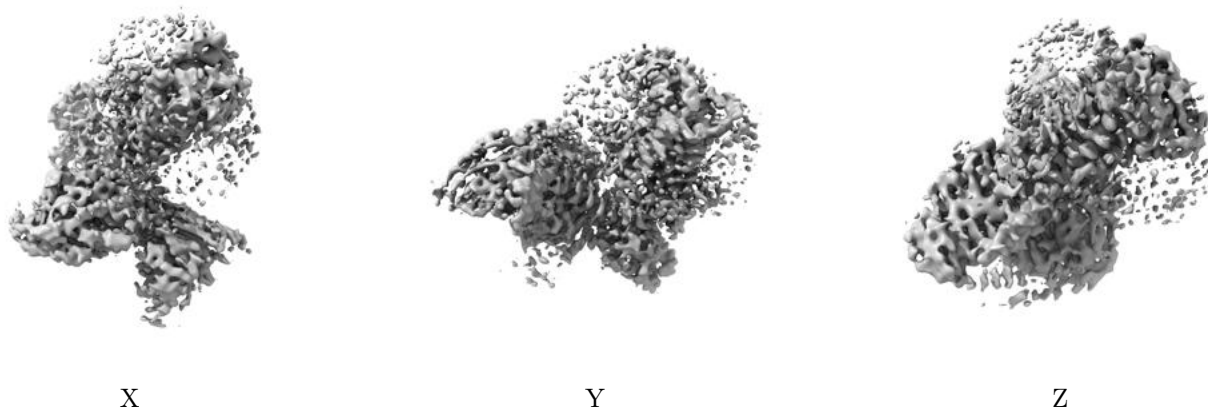


Z

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.

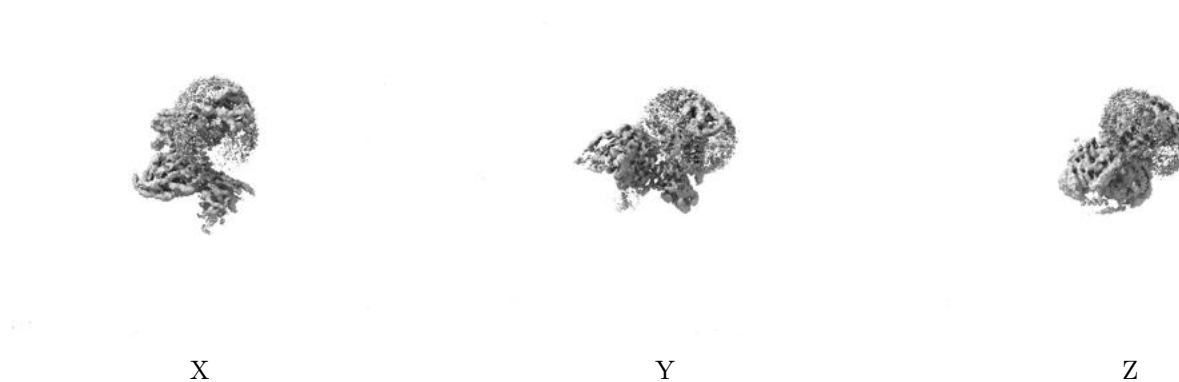
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.145. 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.

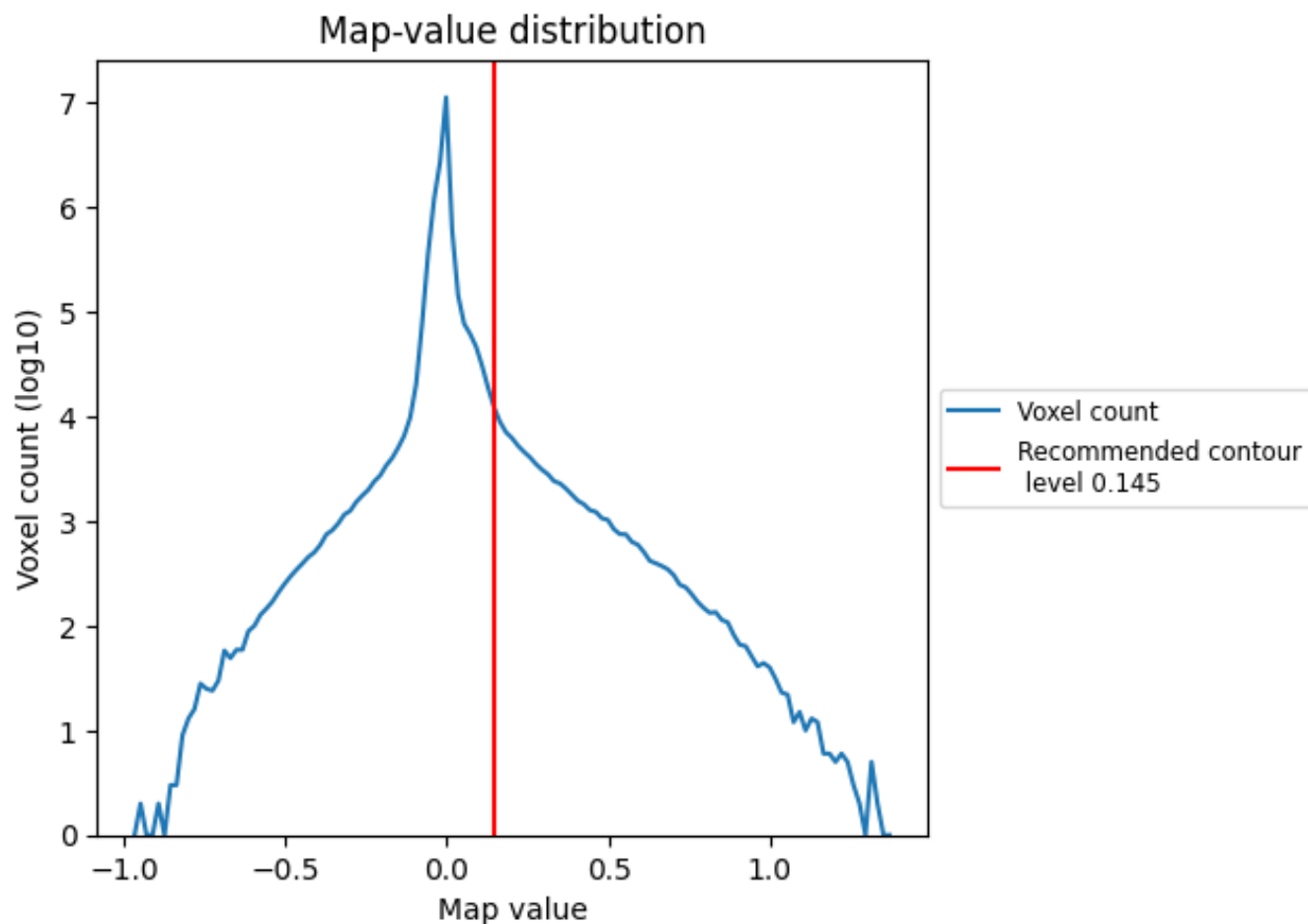
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

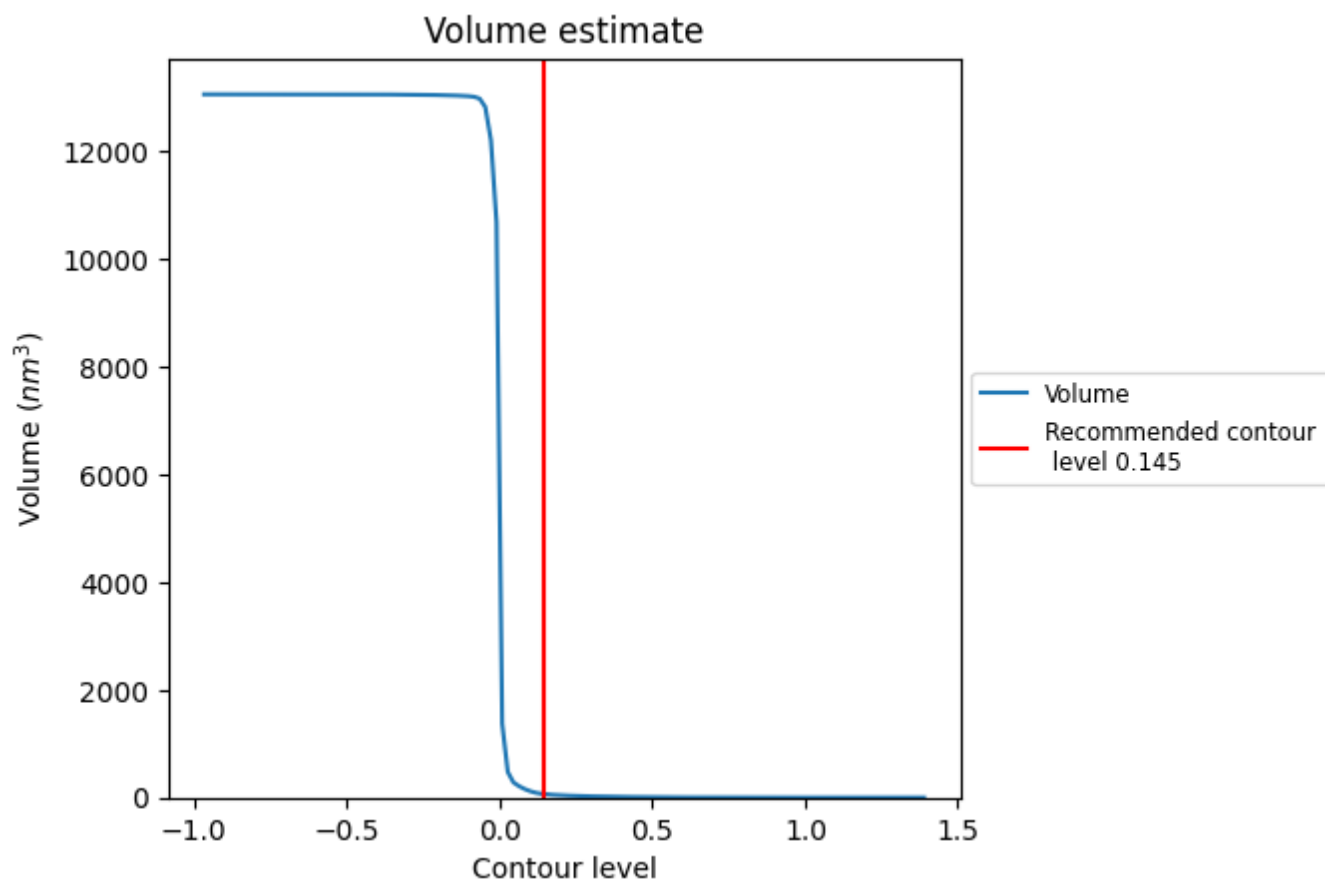
This section contains the results of statistical analysis of the map.

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.

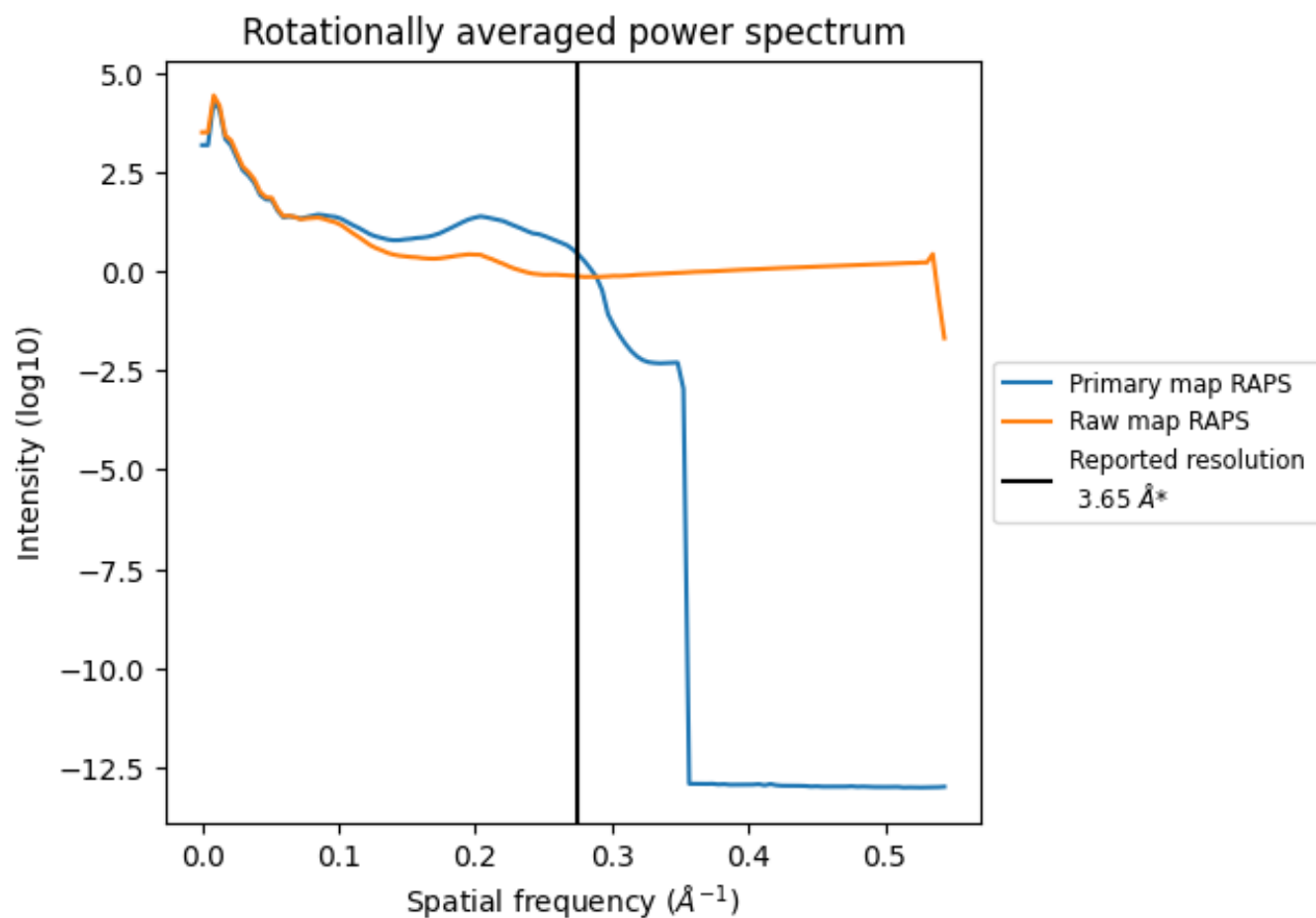
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 65 nm^3 ; this corresponds to an approximate mass of 59 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 ⓘ

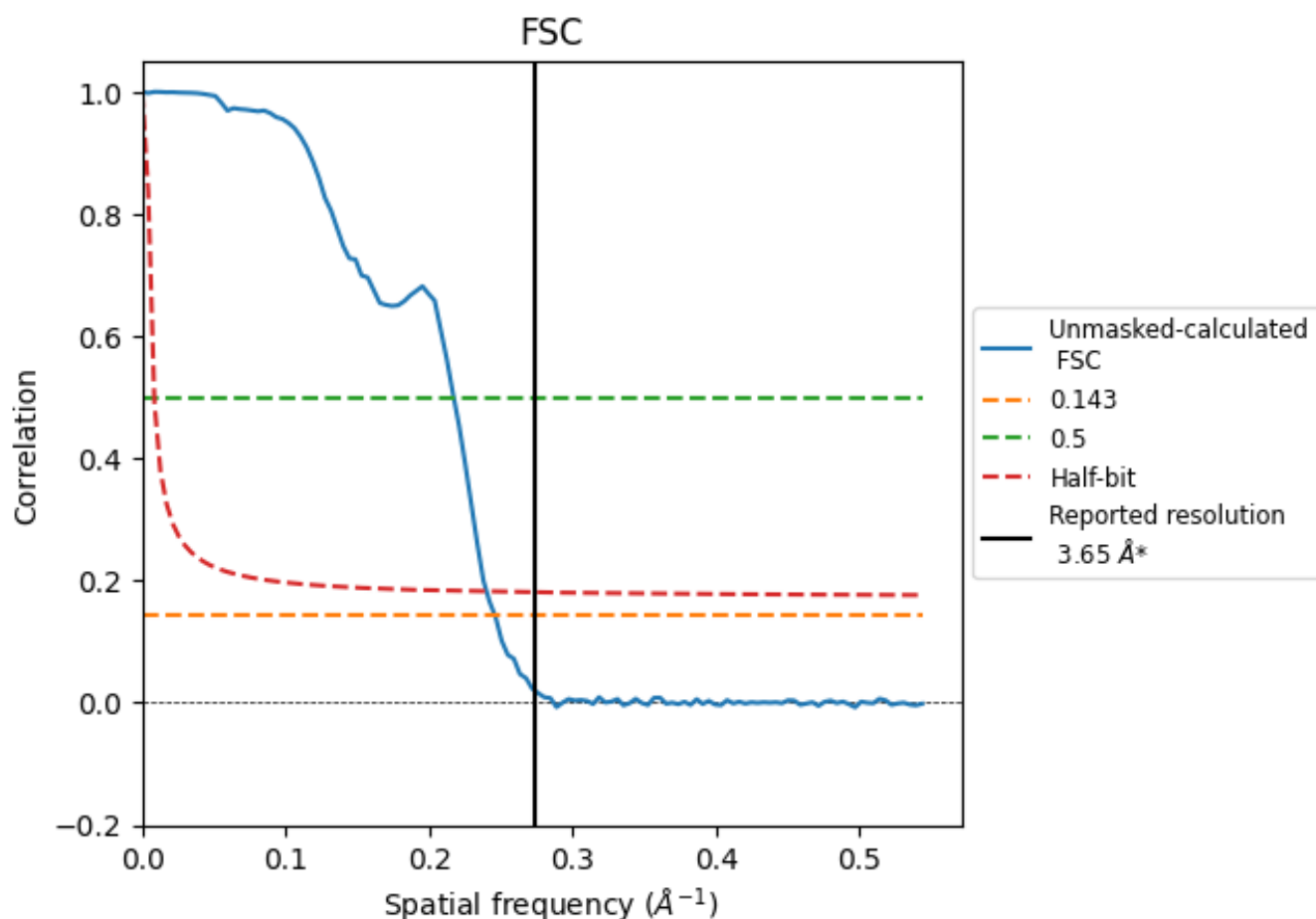


*Reported resolution corresponds to spatial frequency of 0.274 Å⁻¹

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 0.274 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

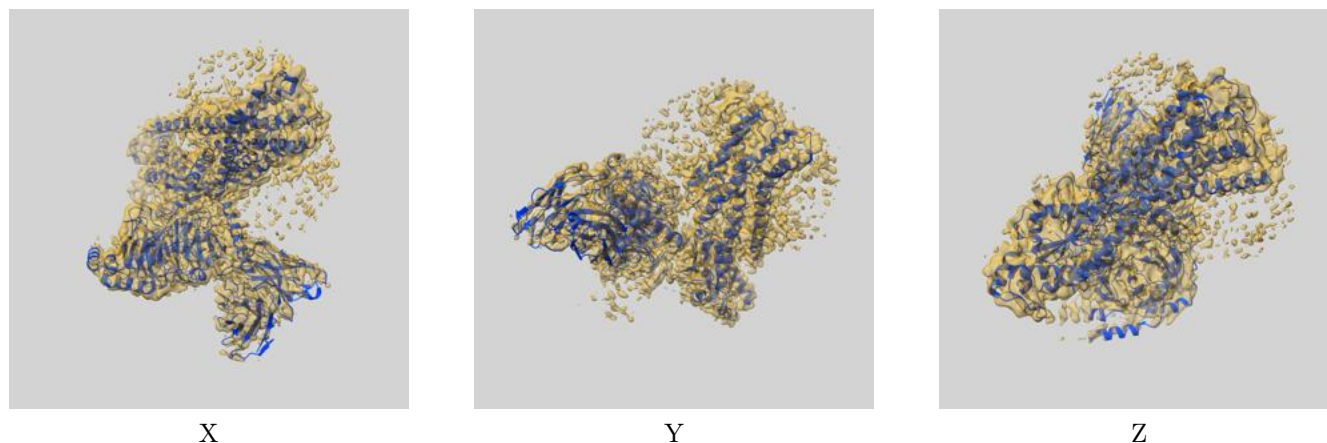
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.65	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.07	4.61	4.17

*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 4.07 differs from the reported value 3.65 by more than 10 %

9 Map-model fit [i](#)

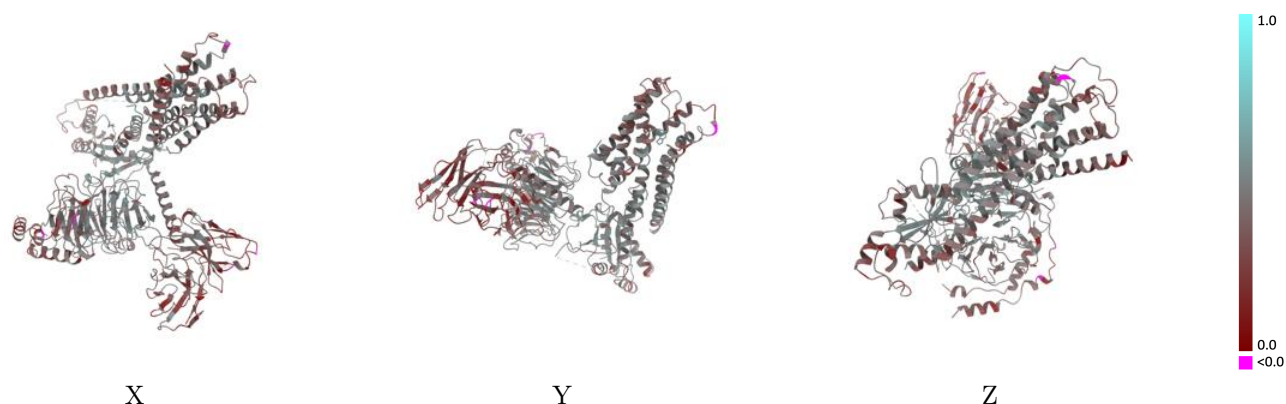
This section contains information regarding the fit between EMDB map EMD-36626 and PDB model 8JSP. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

9.1 Map-model overlay [i](#)



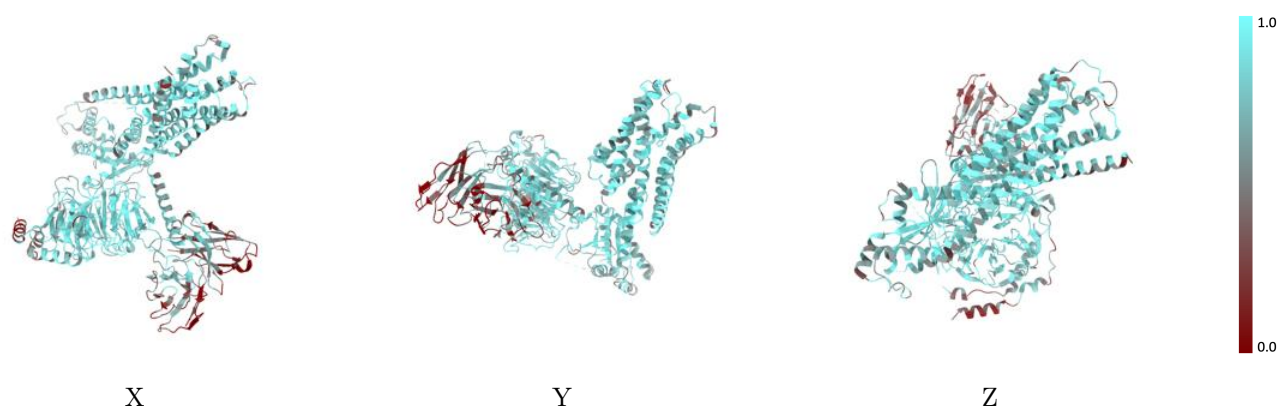
The images above show the 3D surface view of the map at the recommended contour level 0.145 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



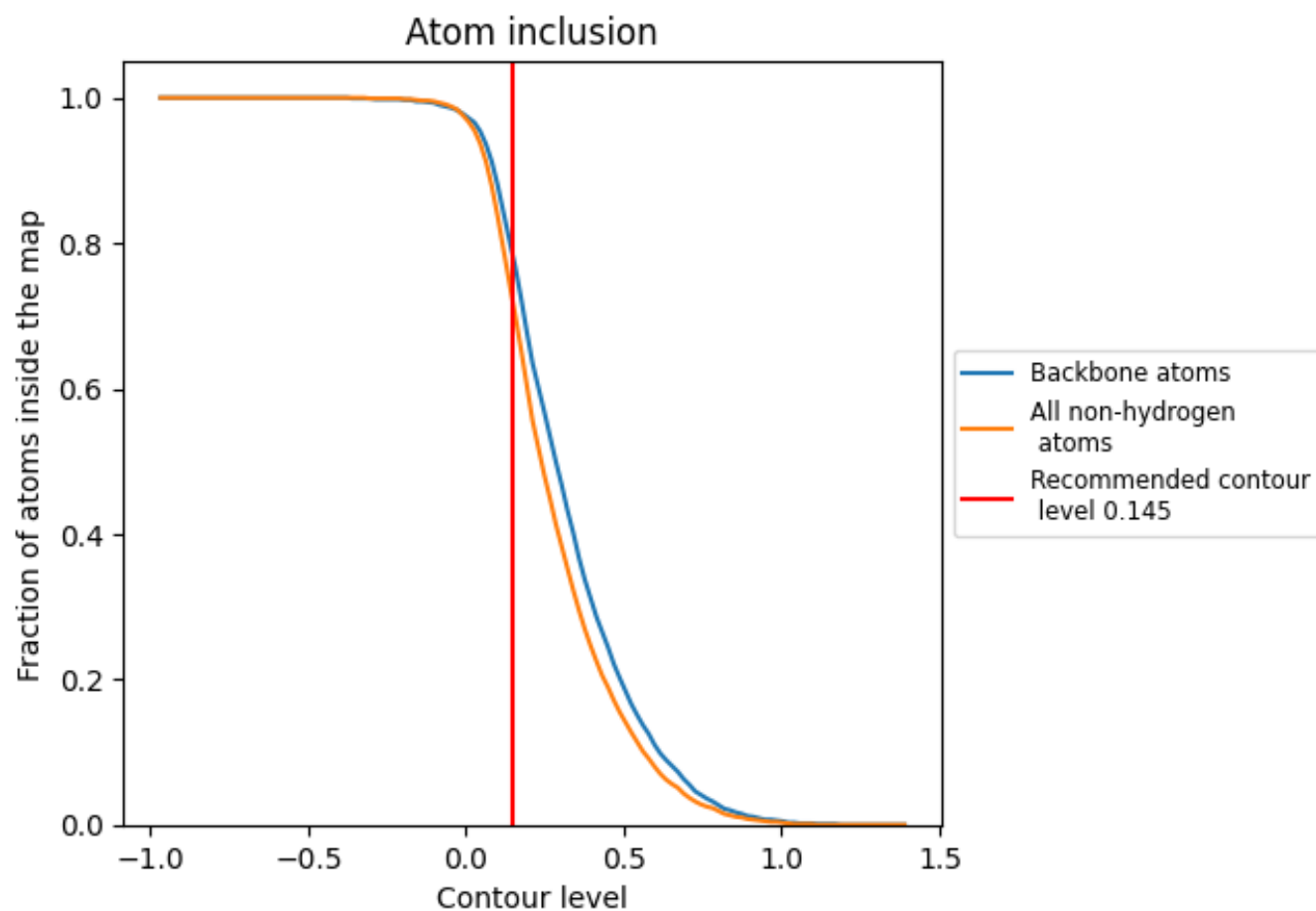
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.145).

9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 73% 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 (0.145) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7270	0.4110
A	0.7810	0.4380
B	0.8200	0.4400
E	0.4580	0.3230
G	0.6490	0.3820
R	0.7990	0.4300

