



Full wwPDB EM Validation Report ⓘ

Mar 10, 2026 – 12:09 AM UTC

PDB ID : 8JD0 / pdb_00008jd0
EMDB ID : EMD-36171
Title : Cryo-EM structure of mGlu2-mGlu3 heterodimer in presence of NAM563
Authors : Wang, X.; Wang, M.; Xu, T.; Feng, Y.; Han, S.; Lin, S.; Zhao, Q.; Wu, B.
Deposited on : 2023-05-12
Resolution : 3.30 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

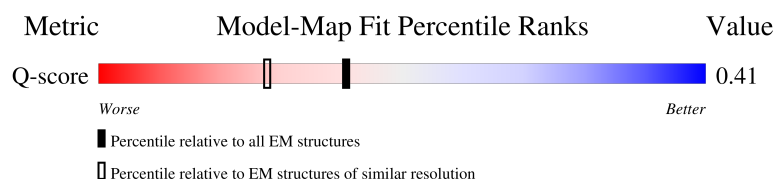
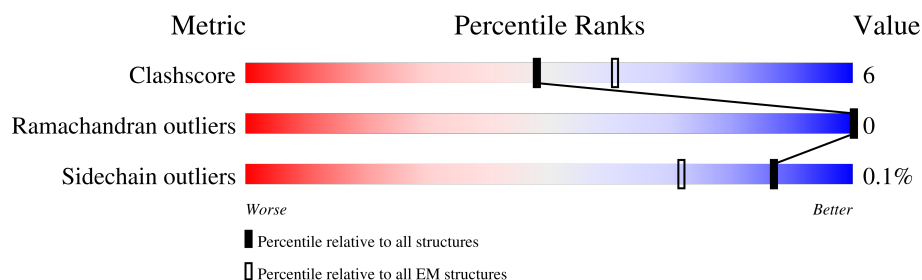
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.30 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	15087 (2.80 - 3.80)

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	2	993	13% 68% 10% 23%
2	3	993	13% 66% 11% 23%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 11264 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 Metabotropic glutamate receptor 2,Peptidyl-prolyl cis-trans isomerase FKBP1A.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	2	766	Total	C	N	O	S	0	0
			5377	3398	956	990	33		

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
2	9	ASP	-	expression tag	UNP Q14416
2	10	TYR	-	expression tag	UNP Q14416
2	11	LYS	-	expression tag	UNP Q14416
2	12	ASP	-	expression tag	UNP Q14416
2	13	ASP	-	expression tag	UNP Q14416
2	14	ASP	-	expression tag	UNP Q14416
2	15	ASP	-	expression tag	UNP Q14416
2	16	GLY	-	expression tag	UNP Q14416
2	17	ALA	-	expression tag	UNP Q14416
2	18	PRO	-	expression tag	UNP Q14416
2	873	LEU	-	linker	UNP Q14416
2	874	GLU	-	linker	UNP Q14416
2	875	VAL	-	linker	UNP Q14416
2	876	LEU	-	linker	UNP Q14416
2	877	PHE	-	linker	UNP Q14416
2	878	GLN	-	linker	UNP Q14416
2	879	GLY	-	linker	UNP Q14416
2	880	PRO	-	linker	UNP Q14416
2	988	PHE	-	expression tag	UNP P62942
2	989	ALA	-	expression tag	UNP P62942
2	990	ALA	-	expression tag	UNP P62942
2	991	ALA	-	expression tag	UNP P62942
2	992	HIS	-	expression tag	UNP P62942
2	993	HIS	-	expression tag	UNP P62942
2	994	HIS	-	expression tag	UNP P62942
2	995	HIS	-	expression tag	UNP P62942
2	996	HIS	-	expression tag	UNP P62942

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Chain	Residue	Modelled	Actual	Comment	Reference
2	997	HIS	-	expression tag	UNP P62942
2	998	HIS	-	expression tag	UNP P62942
2	999	HIS	-	expression tag	UNP P62942
2	1000	HIS	-	expression tag	UNP P62942
2	1001	HIS	-	expression tag	UNP P62942

- Molecule 2 is a protein called Metabotropic glutamate receptor 3, Serine/threonine-protein kinase mTOR.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	3	765	Total	C	N	O	S	0	0
			5567	3528	963	1041	35		

There are 41 discrepancies between the modelled and reference sequences:

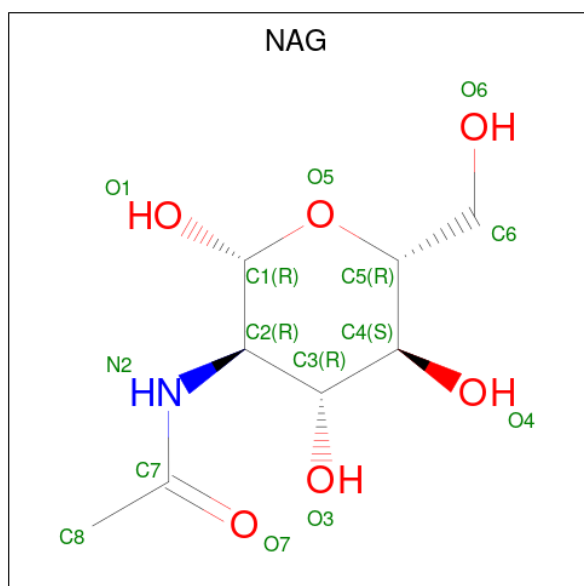
Chain	Residue	Modelled	Actual	Comment	Reference
3	-8	ASP	-	expression tag	UNP Q14832
3	-7	TYR	-	expression tag	UNP Q14832
3	-6	LYS	-	expression tag	UNP Q14832
3	-5	ASP	-	expression tag	UNP Q14832
3	-4	ASP	-	expression tag	UNP Q14832
3	-3	ASP	-	expression tag	UNP Q14832
3	-2	ASP	-	expression tag	UNP Q14832
3	-1	LYS	-	expression tag	UNP Q14832
3	0	GLY	-	expression tag	UNP Q14832
3	1	ALA	-	expression tag	UNP Q14832
3	2	PRO	-	expression tag	UNP Q14832
3	3	TRP	-	expression tag	UNP Q14832
3	4	SER	-	expression tag	UNP Q14832
3	5	HIS	-	expression tag	UNP Q14832
3	6	PRO	-	expression tag	UNP Q14832
3	7	GLN	-	expression tag	UNP Q14832
3	8	PHE	-	expression tag	UNP Q14832
3	9	GLU	-	expression tag	UNP Q14832
3	10	LYS	-	expression tag	UNP Q14832
3	11	GLY	-	expression tag	UNP Q14832
3	12	SER	-	expression tag	UNP Q14832
3	13	GLY	-	expression tag	UNP Q14832
3	14	SER	-	expression tag	UNP Q14832
3	15	TRP	-	expression tag	UNP Q14832
3	16	SER	-	expression tag	UNP Q14832
3	17	HIS	-	expression tag	UNP Q14832

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Chain	Residue	Modelled	Actual	Comment	Reference
3	18	PRO	-	expression tag	UNP Q14832
3	19	GLN	-	expression tag	UNP Q14832
3	20	PHE	-	expression tag	UNP Q14832
3	21	GLU	-	expression tag	UNP Q14832
3	22	LYS	-	expression tag	UNP Q14832
3	880	LEU	-	linker	UNP Q14832
3	881	GLU	-	linker	UNP Q14832
3	882	VAL	-	linker	UNP Q14832
3	883	LEU	-	linker	UNP Q14832
3	884	PHE	-	linker	UNP Q14832
3	885	GLN	-	linker	UNP Q14832
3	886	GLY	-	linker	UNP Q14832
3	887	PRO	-	linker	UNP Q14832
3	983	GLU	-	expression tag	UNP A0A8V8TRG9
3	984	PHE	-	expression tag	UNP A0A8V8TRG9

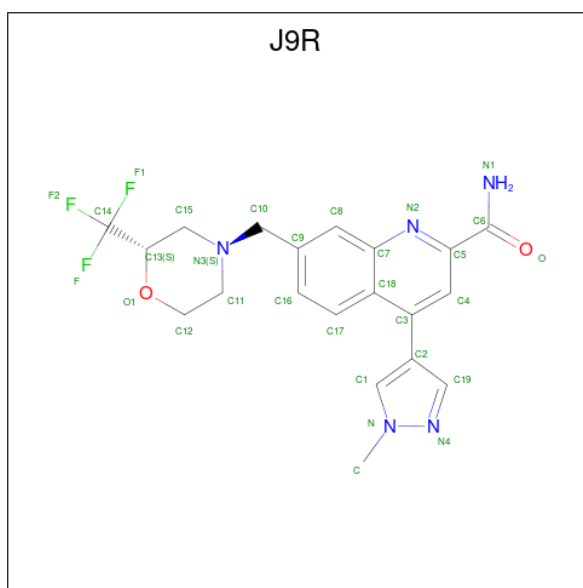
- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				AltConf
3	2	1	Total	C	N	O	0
			14	8	1	5	
3	3	1	Total	C	N	O	0
			14	8	1	5	

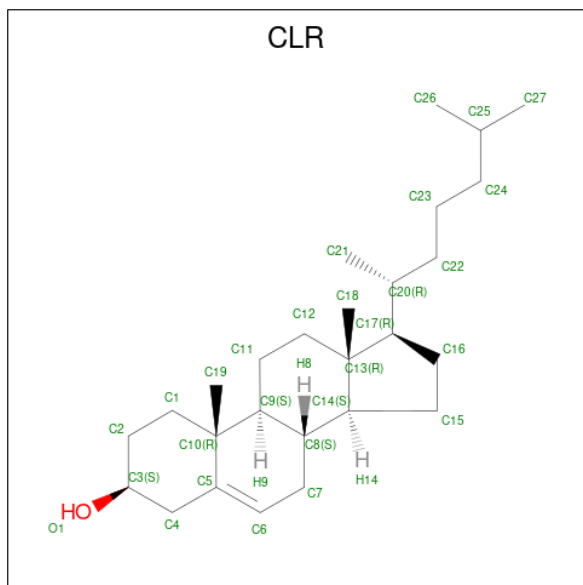
- Molecule 4 is 4-(1-methylpyrazol-4-yl)-7-[[2 {S}]-2-(trifluoromethyl)morpholin-4-yl]methyl]quinoline-2-carboxamide (CCD ID: J9R) (formula: $C_{20}H_{20}F_3N_5O_2$) (labeled as "Ligand of

Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
4	2	1	Total	C	F	N	O	0
			30	20	3	5	2	

- Molecule 5 is CHOLESTEROL (CCD ID: CLR) (formula: $C_{27}H_{46}O$).



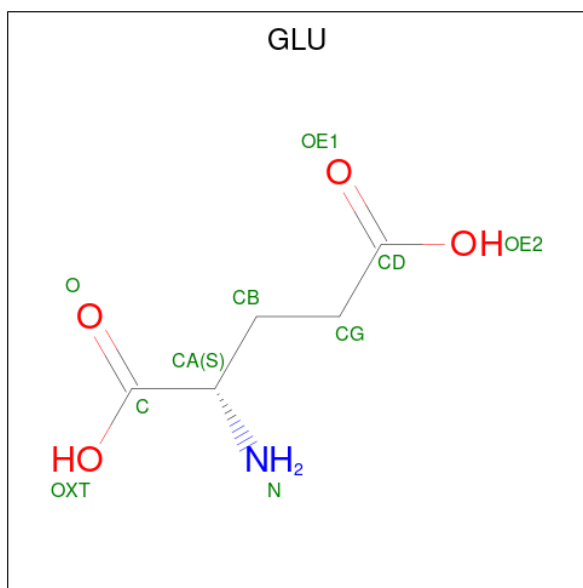
Mol	Chain	Residues	Atoms			AltConf
5	2	1	Total	C	O	0
			28	27	1	
5	2	1	Total	C	O	0
			28	27	1	

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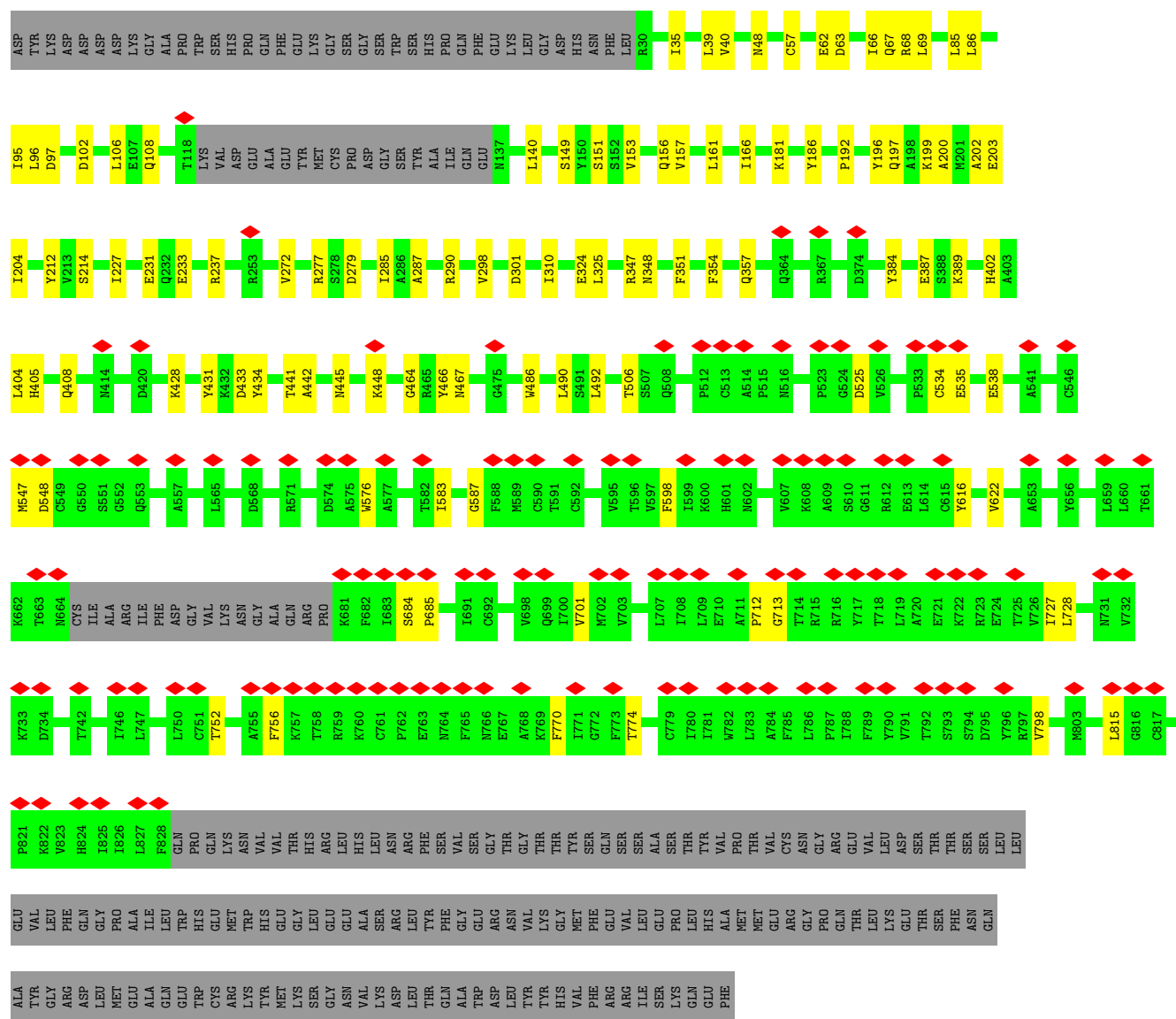
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Mol	Chain	Residues	Atoms			AltConf
5	2	1	Total	C	O	0
			28	27	1	
5	2	1	Total	C	O	0
			28	27	1	
5	3	1	Total	C	O	0
			28	27	1	
5	3	1	Total	C	O	0
			28	27	1	
5	3	1	Total	C	O	0
			28	27	1	
5	3	1	Total	C	O	0
			28	27	1	

- Molecule 6 is GLUTAMIC ACID (CCD ID: GLU) (formula: $C_5H_9NO_4$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
6	3	1	Total	C	N	O	0
			10	5	1	4	



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	460025	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	70	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	6.599	Depositor
Minimum map value	-4.131	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.065	Depositor
Recommended contour level	0.5	Depositor
Map size ($\text{\AA}$)	385.56, 385.56, 385.56	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.071, 1.071, 1.071	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NAG, CLR, J9R

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	2	0.10	0/5497	0.25	0/7521
2	3	0.08	0/5684	0.24	0/7751
All	All	0.09	0/11181	0.24	0/15272

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	2	5377	0	4783	57	0
2	3	5567	0	5073	65	0
3	2	14	0	13	0	0
3	3	14	0	13	0	0
4	2	30	0	0	1	0
5	2	112	0	184	8	0
5	3	140	0	230	6	0
6	3	10	0	5	2	0
All	All	11264	0	10301	128	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

All (128) 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)
1:2:685:ALA:HB2	5:2:1106:CLR:H3	1.67	0.75
1:2:698:LEU:HD22	5:2:1103:CLR:H152	1.70	0.73
1:2:634:LEU:HD21	5:2:1104:CLR:H71	1.77	0.67
1:2:293:ALA:HB3	1:2:316:THR:HA	1.76	0.67
5:2:1104:CLR:H261	5:2:1105:CLR:H271	1.78	0.65
2:3:227:ILE:O	2:3:231:GLU:HG2	1.98	0.63
2:3:102:ASP:HB2	2:3:156:GLN:HG3	1.81	0.62
1:2:139:VAL:HG12	1:2:141:GLY:H	1.65	0.61
2:3:214:SER:HB2	2:3:272:VAL:HG12	1.81	0.61
2:3:63:ASP:HA	2:3:67:GLN:HG3	1.80	0.61
1:2:96:THR:O	1:2:100:GLU:HG2	2.01	0.60
1:2:79:LEU:HD23	1:2:82:VAL:HB	1.85	0.59
2:3:48:ASN:HB3	2:3:57:CYS:HB2	1.86	0.58
2:3:35:ILE:HD11	2:3:347:ARG:HD2	1.85	0.57
2:3:534:CYS:SG	2:3:535:GLU:N	2.72	0.56
1:2:421:ASP:O	1:2:425:ASN:ND2	2.36	0.56
1:2:59:ILE:HD13	1:2:348:PHE:HB2	1.87	0.56
1:2:419:TYR:HD2	1:2:420:LYS:HD2	1.70	0.56
2:3:153:VAL:O	2:3:157:VAL:HG23	2.06	0.55
1:2:276:ARG:HB2	1:2:303:VAL:HA	1.88	0.55
1:2:32:LEU:HD13	1:2:392:LEU:HD13	1.87	0.55
1:2:81:GLY:O	1:2:405:ARG:NH1	2.40	0.54
1:2:395:MET:HG3	1:2:418:LEU:HD13	1.89	0.54
5:3:1003:CLR:H17	5:3:1004:CLR:H161	1.90	0.53
1:2:328:ALA:O	1:2:332:GLN:HG2	2.08	0.53
1:2:186:PRO:HG3	1:2:451:GLY:HA3	1.90	0.53
2:3:622:VAL:HG21	2:3:815:LEU:HB2	1.91	0.53
1:2:79:LEU:HD22	1:2:84:LEU:HD11	1.89	0.52
2:3:202:ALA:HB1	2:3:237:ARG:HD2	1.91	0.52
5:3:1003:CLR:H161	5:3:1004:CLR:H221	1.91	0.52
2:3:86:LEU:HG	2:3:405:HIS:HB2	1.92	0.51
2:3:538:GLU:HB3	2:3:548:ASP:HA	1.92	0.51
2:3:68:ARG:NH2	2:3:387:GLU:OE2	2.44	0.51
5:2:1103:CLR:H272	5:2:1106:CLR:H242	1.93	0.51
2:3:40:VAL:HG21	2:3:140:LEU:HG	1.94	0.50
2:3:441:THR:OG1	2:3:448:LYS:NZ	2.44	0.50
5:2:1104:CLR:H152	2:3:701:VAL:HG11	1.93	0.50
1:2:41:HIS:HB2	1:2:92:CYS:HB3	1.93	0.50
1:2:225:GLU:O	1:2:229:ARG:HG2	2.11	0.50
2:3:68:ARG:NH1	2:3:149:SER:OG	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:342:ASN:HB3	1:2:345:PHE:HB2	1.94	0.49
2:3:199:LYS:HA	2:3:233:GLU:HG2	1.94	0.49
1:2:72:ILE:HG12	1:2:78:LEU:HD23	1.94	0.49
2:3:285:ILE:HG21	2:3:310:ILE:HG22	1.95	0.49
1:2:175:LYS:NZ	1:2:181:PHE:O	2.46	0.49
2:3:616:TYR:HE2	5:3:1007:CLR:H9	1.78	0.48
2:3:442:ALA:HB3	2:3:445:ASN:HB2	1.95	0.48
2:3:287:ALA:HA	2:3:290:ARG:HE	1.78	0.48
2:3:85:LEU:HD13	2:3:402:HIS:HD2	1.77	0.48
2:3:196:TYR:HB2	2:3:466:TYR:HE2	1.78	0.48
1:2:95:ASP:HB3	1:2:150:GLN:HG3	1.95	0.47
5:2:1106:CLR:H272	5:2:1106:CLR:H161	1.96	0.47
2:3:149:SER:OG	6:3:1001:GLU:OE2	2.33	0.47
2:3:186:TYR:HE1	2:3:428:LYS:HA	1.80	0.47
2:3:348:ASN:HB3	2:3:351:PHE:HB2	1.97	0.46
1:2:204:TRP:HE1	1:2:496:PRO:HA	1.80	0.46
1:2:32:LEU:HD22	1:2:137:THR:HG21	1.96	0.46
2:3:433:ASP:OD1	2:3:434:TYR:N	2.48	0.46
5:3:1003:CLR:H211	5:3:1003:CLR:H241	1.97	0.46
2:3:324:GLU:OE2	2:3:389:LYS:NZ	2.49	0.46
1:2:180:TYR:HE1	1:2:416:ARG:HA	1.81	0.46
1:2:512:VAL:N	1:2:521:LEU:O	2.49	0.46
2:3:200:ALA:O	2:3:204:ILE:HG22	2.17	0.45
2:3:490:LEU:HD21	2:3:492:LEU:HD12	1.99	0.45
2:3:598:PHE:CE1	5:3:1007:CLR:H112	2.51	0.45
1:2:285:LEU:HD22	1:2:287:ALA:HB2	1.97	0.45
2:3:192:PRO:HG3	2:3:464:GLY:HA2	1.97	0.45
2:3:161:LEU:HD22	2:3:166:ILE:HD12	1.99	0.45
2:3:324:GLU:O	2:3:467:ASN:N	2.49	0.45
2:3:547:MET:N	2:3:547:MET:SD	2.90	0.45
2:3:203:GLU:OE1	2:3:486:TRP:NE1	2.47	0.45
1:2:395:MET:HG2	1:2:422:PHE:CD2	2.52	0.45
1:2:297:TRP:NE1	1:2:468:TYR:OH	2.42	0.44
1:2:304:VAL:HG11	1:2:458:TYR:HE1	1.82	0.44
1:2:640:GLY:HA2	4:2:1102:J9R:O	2.17	0.44
2:3:85:LEU:HD13	2:3:402:HIS:CD2	2.52	0.44
1:2:591:ARG:HD3	1:2:591:ARG:HA	1.73	0.44
1:2:49:ASP:OD1	1:2:49:ASP:N	2.50	0.44
1:2:221:ILE:HA	1:2:224:PHE:HB3	1.98	0.44
2:3:192:PRO:HD2	2:3:325:LEU:HD21	1.99	0.44
2:3:583:ILE:O	2:3:587:GLY:N	2.40	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:146:ASP:OD1	1:2:146:ASP:N	2.40	0.44
1:2:199:LEU:HD23	1:2:204:TRP:HE3	1.83	0.44
2:3:684:SER:OG	2:3:685:PRO:HD3	2.18	0.44
1:2:172:LEU:HB2	1:2:183:ARG:HH21	1.83	0.43
2:3:212:TYR:O	2:3:506:THR:OG1	2.28	0.43
2:3:272:VAL:O	2:3:298:VAL:N	2.50	0.43
2:3:712:PRO:HB3	2:3:727:ILE:HG22	1.99	0.43
2:3:325:LEU:HD13	2:3:389:LYS:HE3	2.01	0.43
2:3:67:GLN:HE22	2:3:384:TYR:HE1	1.66	0.43
1:2:510:LYS:H	1:2:522:CYS:HB2	1.83	0.43
2:3:408:GLN:HE21	2:3:408:GLN:HB3	1.64	0.43
2:3:151:SER:OG	6:3:1001:GLU:O	2.30	0.43
2:3:106:LEU:HG	2:3:156:GLN:HB3	1.99	0.43
1:2:429:ASP:HB3	1:2:433:ARG:HH21	1.84	0.43
2:3:66:ILE:HG13	2:3:354:PHE:HB2	2.01	0.43
2:3:62:GLU:OE1	2:3:357:GLN:NE2	2.52	0.42
1:2:223:ALA:HA	1:2:226:LEU:HB2	2.00	0.42
2:3:181:LYS:NZ	2:3:431:TYR:OH	2.50	0.42
2:3:197:GLN:OE1	2:3:301:ASP:N	2.51	0.42
1:2:285:LEU:O	1:2:285:LEU:HD23	2.19	0.42
1:2:637:LEU:HD21	5:2:1104:CLR:H213	2.00	0.42
2:3:525:ASP:OD1	2:3:525:ASP:N	2.53	0.42
1:2:400:CYS:HB3	1:2:407:CYS:HB3	1.81	0.41
1:2:105:PHE:HD1	1:2:136:ILE:HG13	1.85	0.41
1:2:250:PHE:HA	1:2:253:VAL:HG12	2.02	0.41
1:2:453:TYR:HD2	1:2:474:TRP:HD1	1.67	0.41
2:3:576:TRP:NE1	2:3:798:VAL:HG13	2.35	0.41
1:2:375:GLU:HB3	1:2:378:ILE:HG12	2.03	0.41
2:3:752:THR:O	2:3:756:PHE:HB2	2.20	0.41
1:2:509:VAL:HA	1:2:522:CYS:HB2	2.01	0.41
2:3:227:ILE:HD12	2:3:227:ILE:HA	1.93	0.41
1:2:684:LEU:HD13	5:3:1006:CLR:H17	2.03	0.41
2:3:69:LEU:HG	2:3:95:ILE:HG21	2.02	0.41
1:2:61:ARG:NE	1:2:375:GLU:OE1	2.39	0.41
1:2:615:LEU:HD12	1:2:615:LEU:HA	1.92	0.41
1:2:697:TRP:HA	1:2:700:VAL:HG22	2.03	0.41
2:3:48:ASN:ND2	2:3:97:ASP:OD2	2.50	0.41
2:3:96:LEU:HD22	2:3:108:GLN:HG2	2.03	0.41
2:3:277:ARG:NH2	2:3:279:ASP:OD1	2.43	0.41
1:2:334:LEU:HD23	1:2:334:LEU:HA	1.97	0.40
2:3:713:GLY:H	2:3:728:LEU:H	1.69	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:3:770:PHE:O	2:3:774:THR:HG23	2.21	0.40
1:2:455:ILE:HG21	1:2:480:LEU:HD21	2.02	0.40
2:3:39:LEU:HD13	2:3:404:LEU:HD23	2.02	0.40
1:2:220:GLY:HA3	1:2:269:PHE:CE2	2.57	0.40
2:3:140:LEU:HD12	2:3:140:LEU:HA	1.98	0.40
1:2:485:ILE:HB	1:2:488:ALA:HB3	2.04	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	2	760/993 (76%)	721 (95%)	39 (5%)	0	100	100
2	3	759/993 (76%)	733 (97%)	26 (3%)	0	100	100
All	All	1519/1986 (76%)	1454 (96%)	65 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	2	471/813 (58%)	471 (100%)	0	100	100
2	3	533/867 (62%)	533 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	1004/1680 (60%)	1004 (100%)	0	87	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 (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	2	97	HIS
1	2	191	GLN
1	2	390	HIS
2	3	332	GLN
2	3	405	HIS

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](#)

13 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
5	CLR	3	1005	-	31,31,31	0.28	0	48,48,48	0.37	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	CLR	3	1006	-	31,31,31	0.28	0	48,48,48	0.44	0
3	NAG	3	1002	2	14,14,15	0.21	0	17,19,21	0.44	0
5	CLR	2	1103	-	31,31,31	0.27	0	48,48,48	0.39	0
5	CLR	2	1105	-	31,31,31	0.29	0	48,48,48	0.40	0
5	CLR	3	1004	-	31,31,31	0.29	0	48,48,48	0.37	0
5	CLR	2	1104	-	31,31,31	0.30	0	48,48,48	0.44	0
4	J9R	2	1102	-	33,33,33	2.86	10 (30%)	47,49,49	1.82	7 (14%)
3	NAG	2	1101	1	14,14,15	0.22	0	17,19,21	0.43	0
5	CLR	3	1003	-	31,31,31	0.28	0	48,48,48	0.40	0
5	CLR	3	1007	-	31,31,31	0.29	0	48,48,48	0.39	0
5	CLR	2	1106	-	31,31,31	0.28	0	48,48,48	0.50	0
6	GLU	3	1001	-	8,9,9	1.06	0	8,11,11	1.12	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	CLR	3	1005	-	-	0/10/68/68	0/4/4/4
5	CLR	3	1006	-	-	0/10/68/68	0/4/4/4
3	NAG	3	1002	2	-	2/6/23/26	0/1/1/1
5	CLR	2	1103	-	-	3/10/68/68	0/4/4/4
5	CLR	2	1105	-	-	0/10/68/68	0/4/4/4
5	CLR	3	1004	-	-	1/10/68/68	0/4/4/4
5	CLR	2	1104	-	-	0/10/68/68	0/4/4/4
4	J9R	2	1102	-	-	6/18/28/28	0/4/4/4
3	NAG	2	1101	1	-	2/6/23/26	0/1/1/1
5	CLR	3	1003	-	-	1/10/68/68	0/4/4/4
5	CLR	3	1007	-	-	0/10/68/68	0/4/4/4
5	CLR	2	1106	-	-	5/10/68/68	0/4/4/4
6	GLU	3	1001	-	-	4/9/9/9	-

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	2	1102	J9R	C10-N3	-10.96	1.26	1.47
4	2	1102	J9R	C6-N1	6.85	1.45	1.33
4	2	1102	J9R	C15-N3	-5.00	1.38	1.46
4	2	1102	J9R	C18-C7	-3.56	1.36	1.42
4	2	1102	J9R	C11-N3	-2.96	1.38	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	2	1102	J9R	O1-C13	-2.90	1.39	1.43
4	2	1102	J9R	O-C6	-2.80	1.18	1.24
4	2	1102	J9R	C1-N	-2.63	1.31	1.34
4	2	1102	J9R	O1-C12	-2.40	1.38	1.44
4	2	1102	J9R	C3-C2	2.04	1.53	1.49

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	2	1102	J9R	C-N-N4	5.84	124.71	120.03
4	2	1102	J9R	C19-N4-N	5.47	107.41	104.41
4	2	1102	J9R	C5-C6-N1	3.89	120.05	116.22
4	2	1102	J9R	C-N-C1	-3.09	124.84	127.94
4	2	1102	J9R	C1-N-N4	-2.88	110.45	112.08
4	2	1102	J9R	C6-C5-N2	2.16	119.35	117.04
4	2	1102	J9R	C18-C7-N2	-2.02	120.66	122.80

There are no chirality outliers.

All (24) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	2	1102	J9R	C4-C5-C6-N1
4	2	1102	J9R	C4-C5-C6-O
6	3	1001	GLU	N-CA-CB-CG
6	3	1001	GLU	C-CA-CB-CG
3	2	1101	NAG	C8-C7-N2-C2
3	2	1101	NAG	O7-C7-N2-C2
3	3	1002	NAG	C8-C7-N2-C2
3	3	1002	NAG	O7-C7-N2-C2
4	2	1102	J9R	N2-C5-C6-N1
4	2	1102	J9R	N2-C5-C6-O
5	3	1004	CLR	C22-C23-C24-C25
5	2	1106	CLR	C22-C23-C24-C25
5	3	1003	CLR	C20-C22-C23-C24
5	2	1106	CLR	C17-C20-C22-C23
5	2	1106	CLR	C13-C17-C20-C22
4	2	1102	J9R	C9-C10-N3-C15
5	2	1106	CLR	C16-C17-C20-C22
4	2	1102	J9R	C9-C10-N3-C11
5	2	1103	CLR	C16-C17-C20-C22
5	2	1103	CLR	C13-C17-C20-C22
6	3	1001	GLU	OE1-CD-CG-CB

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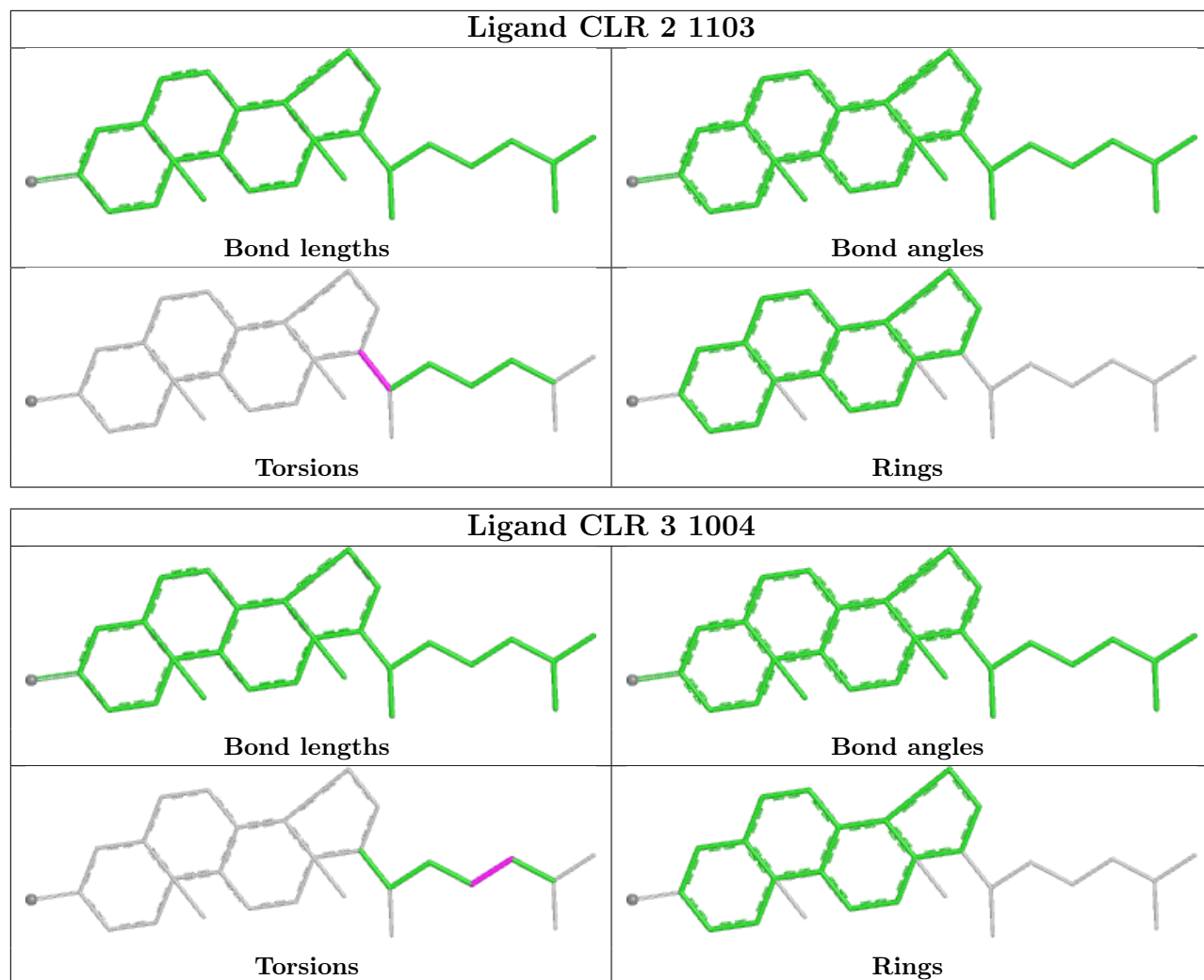
Mol	Chain	Res	Type	Atoms
6	3	1001	GLU	OE2-CD-CG-CB
5	2	1103	CLR	C13-C17-C20-C21
5	2	1106	CLR	C13-C17-C20-C21

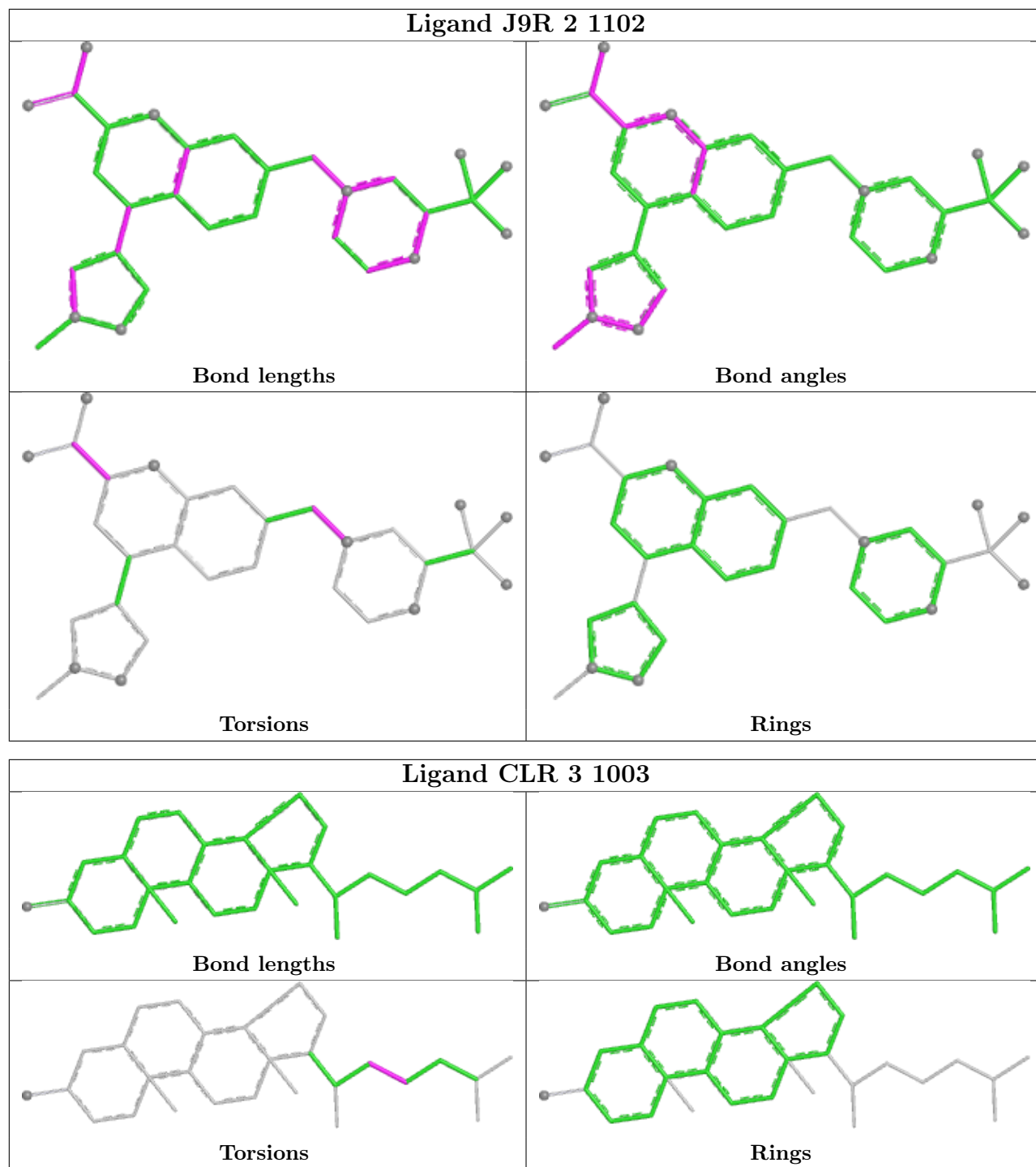
There are no ring outliers.

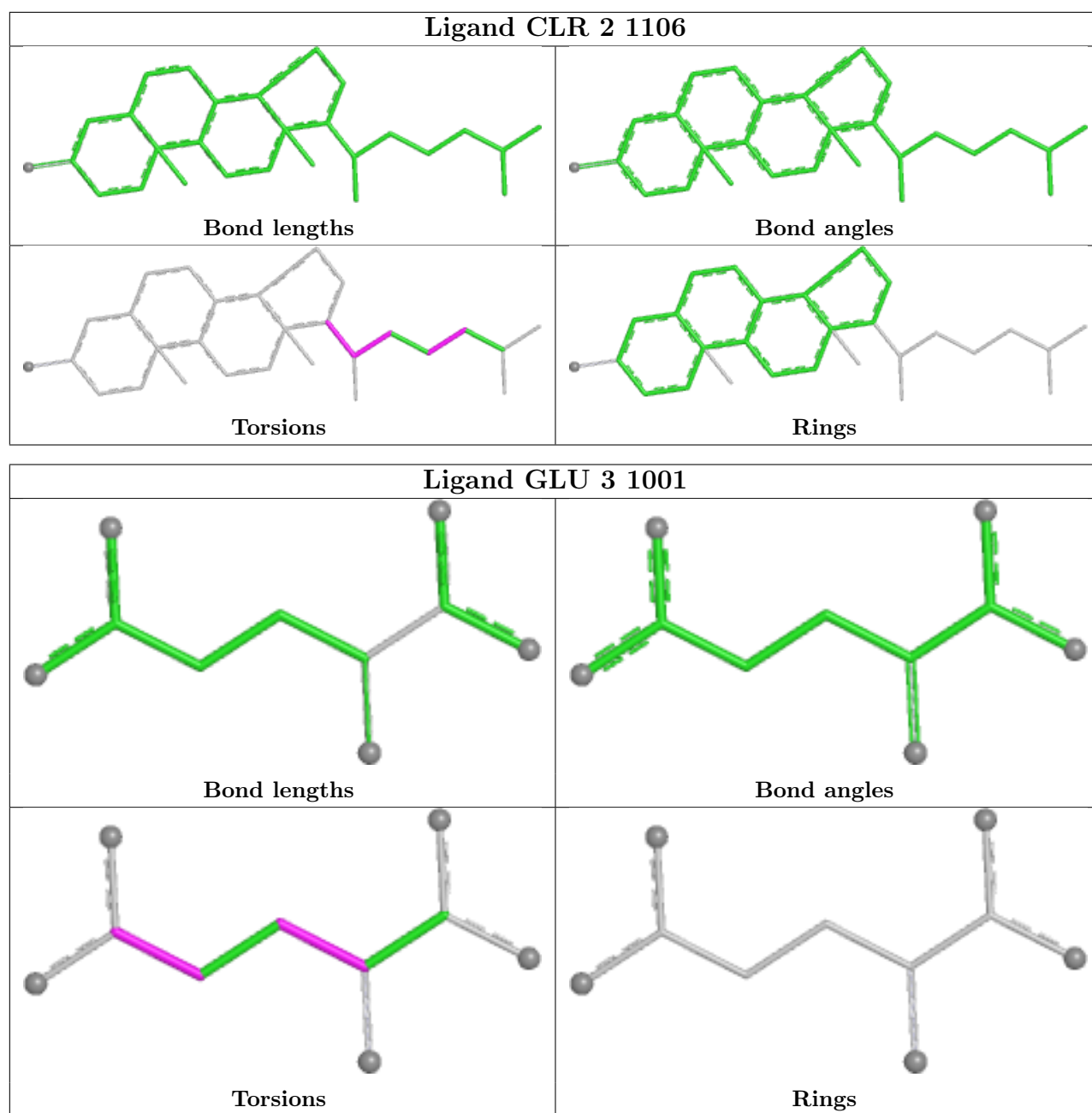
10 monomers are involved in 17 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	3	1006	CLR	1	0
5	2	1103	CLR	2	0
5	2	1105	CLR	1	0
5	3	1004	CLR	2	0
5	2	1104	CLR	4	0
4	2	1102	J9R	1	0
5	3	1003	CLR	3	0
5	3	1007	CLR	2	0
5	2	1106	CLR	3	0
6	3	1001	GLU	2	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.

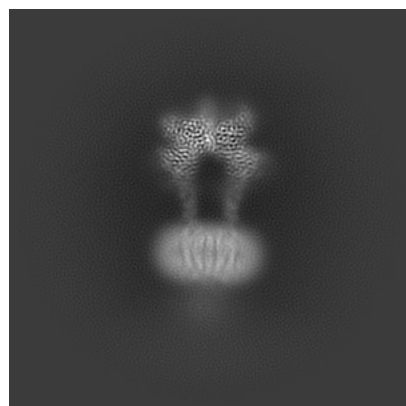
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-36171. These allow visual inspection of the internal detail of the map and identification of artifacts.

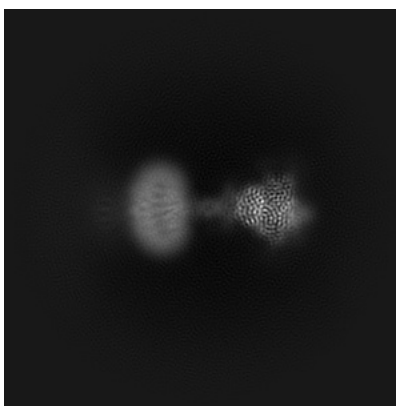
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

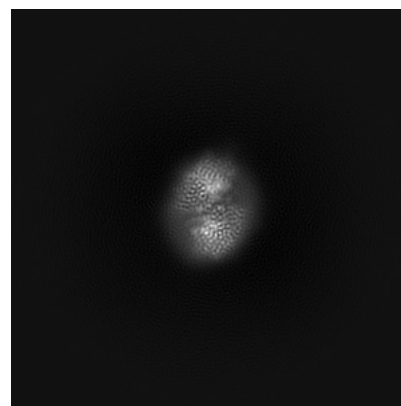
6.1.1 Primary map



X

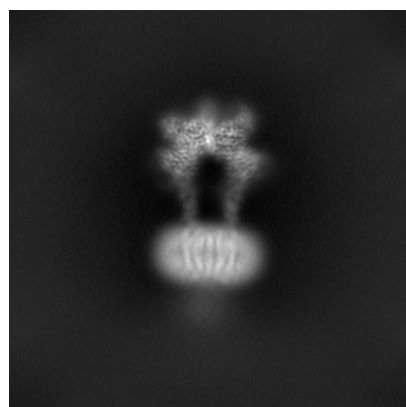


Y

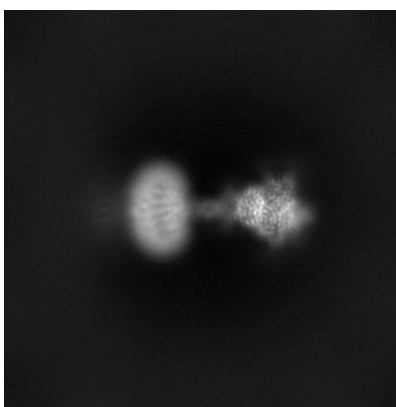


Z

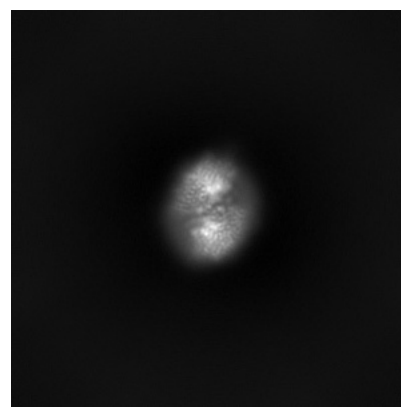
6.1.2 Raw map



X



Y

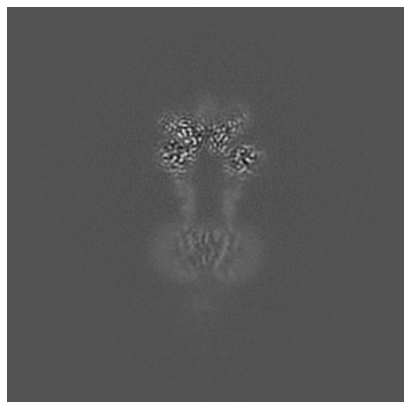


Z

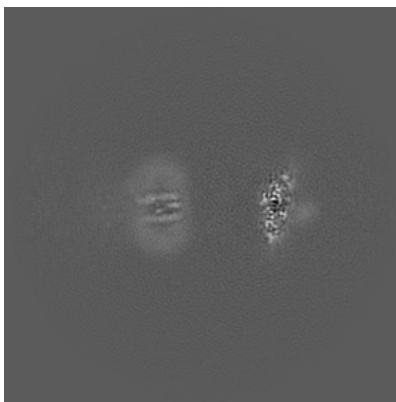
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

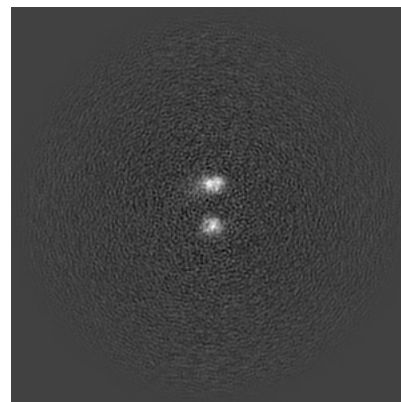
6.2.1 Primary map



X Index: 180

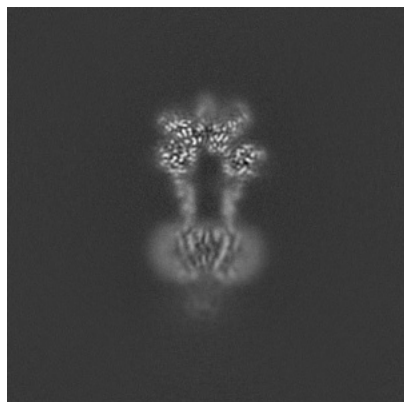


Y Index: 180

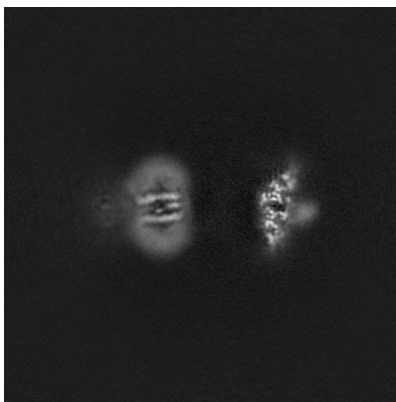


Z Index: 180

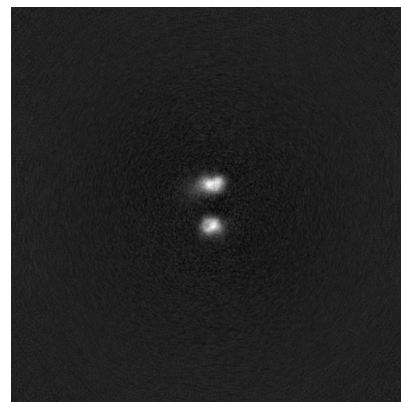
6.2.2 Raw map



X Index: 180



Y Index: 180

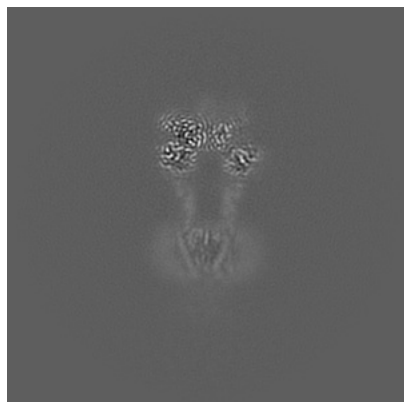


Z Index: 180

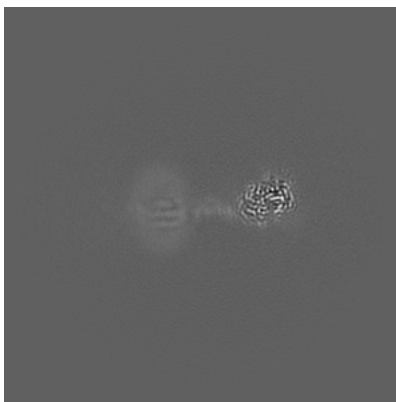
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

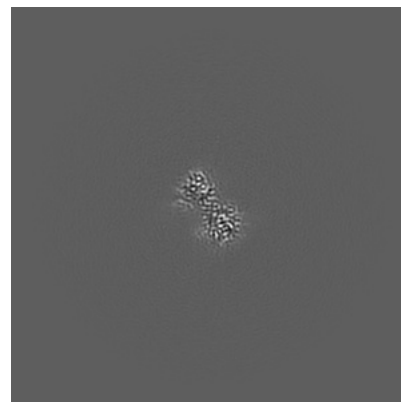
6.3.1 Primary map



X Index: 182

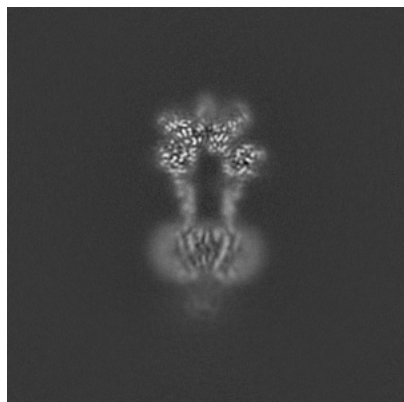


Y Index: 158

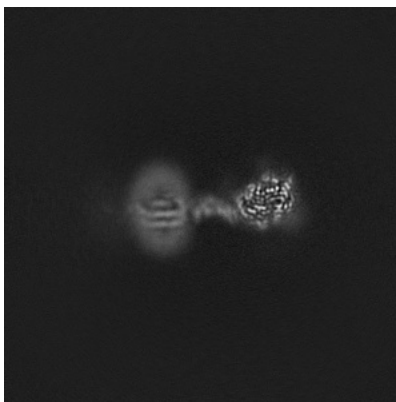


Z Index: 243

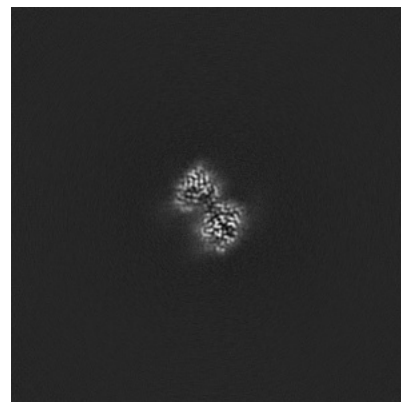
6.3.2 Raw map



X Index: 180



Y Index: 159

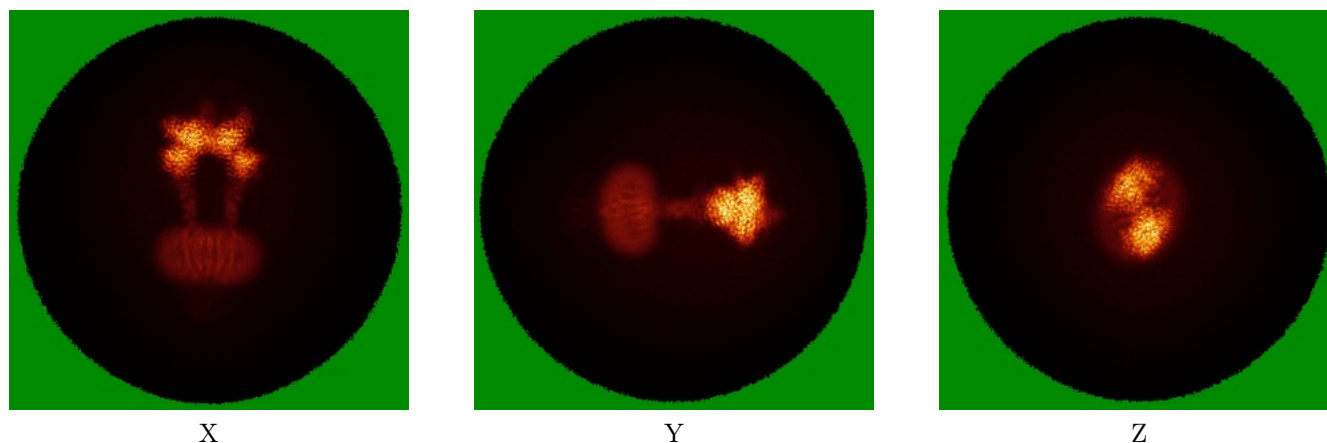


Z Index: 247

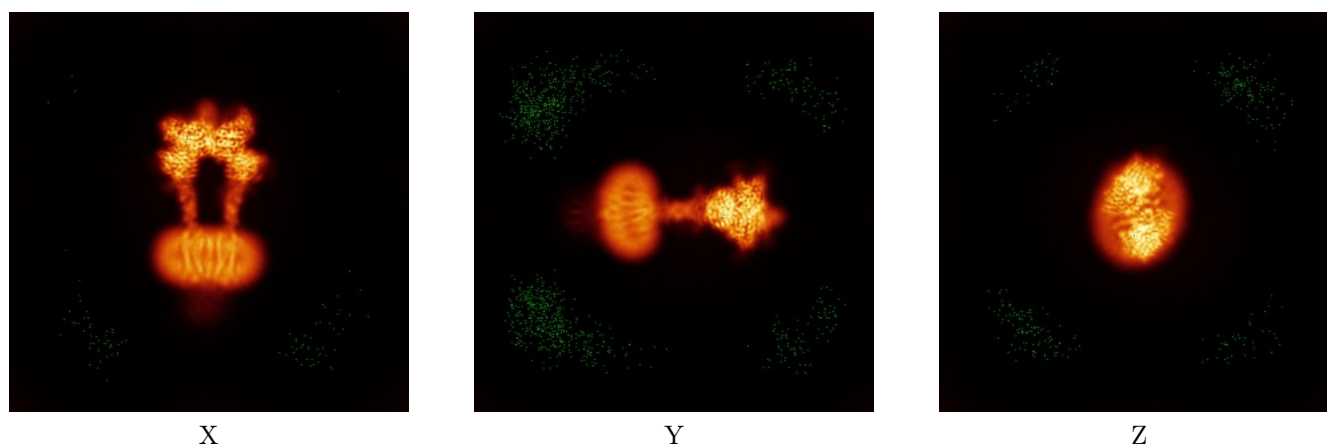
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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.

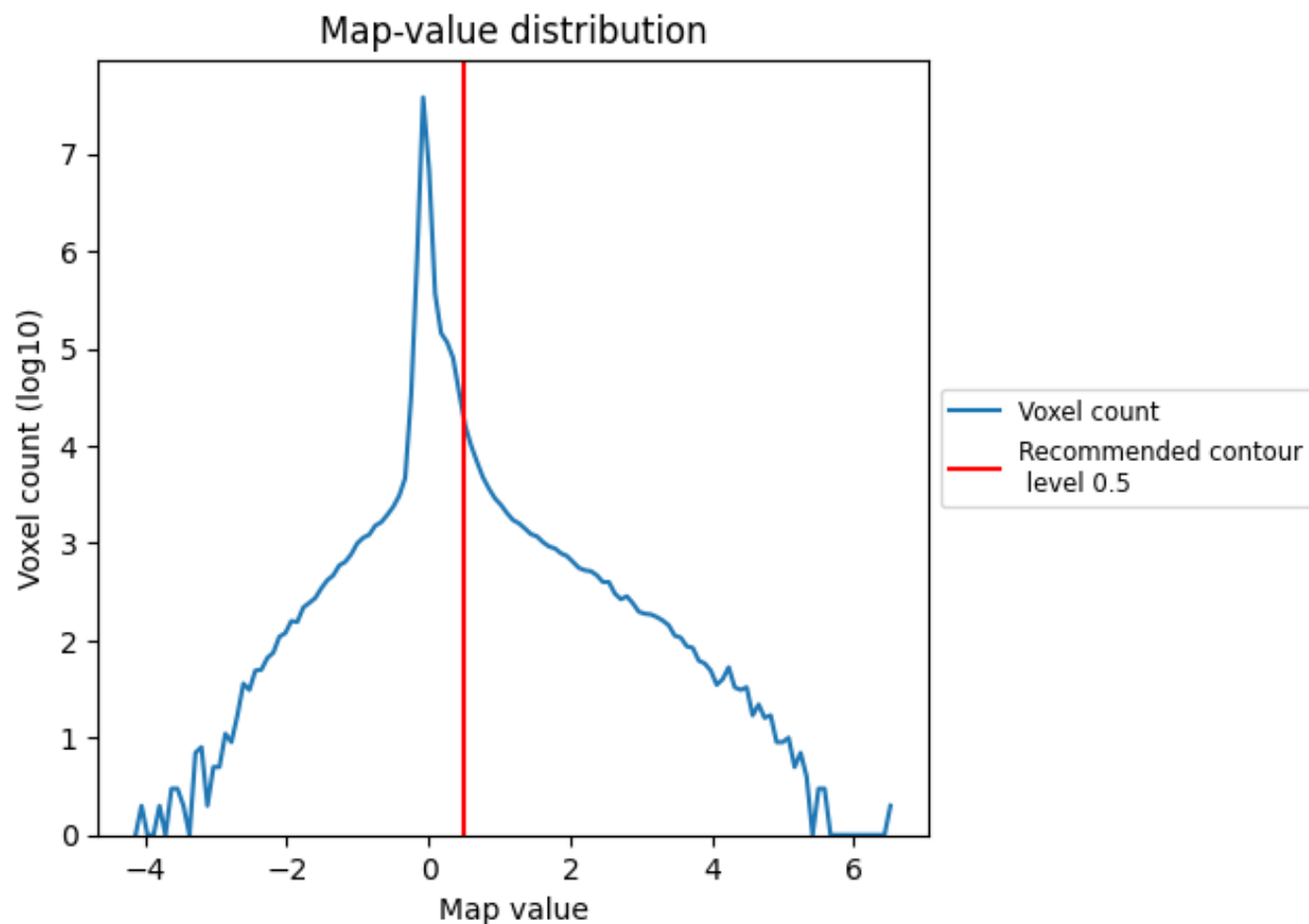
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

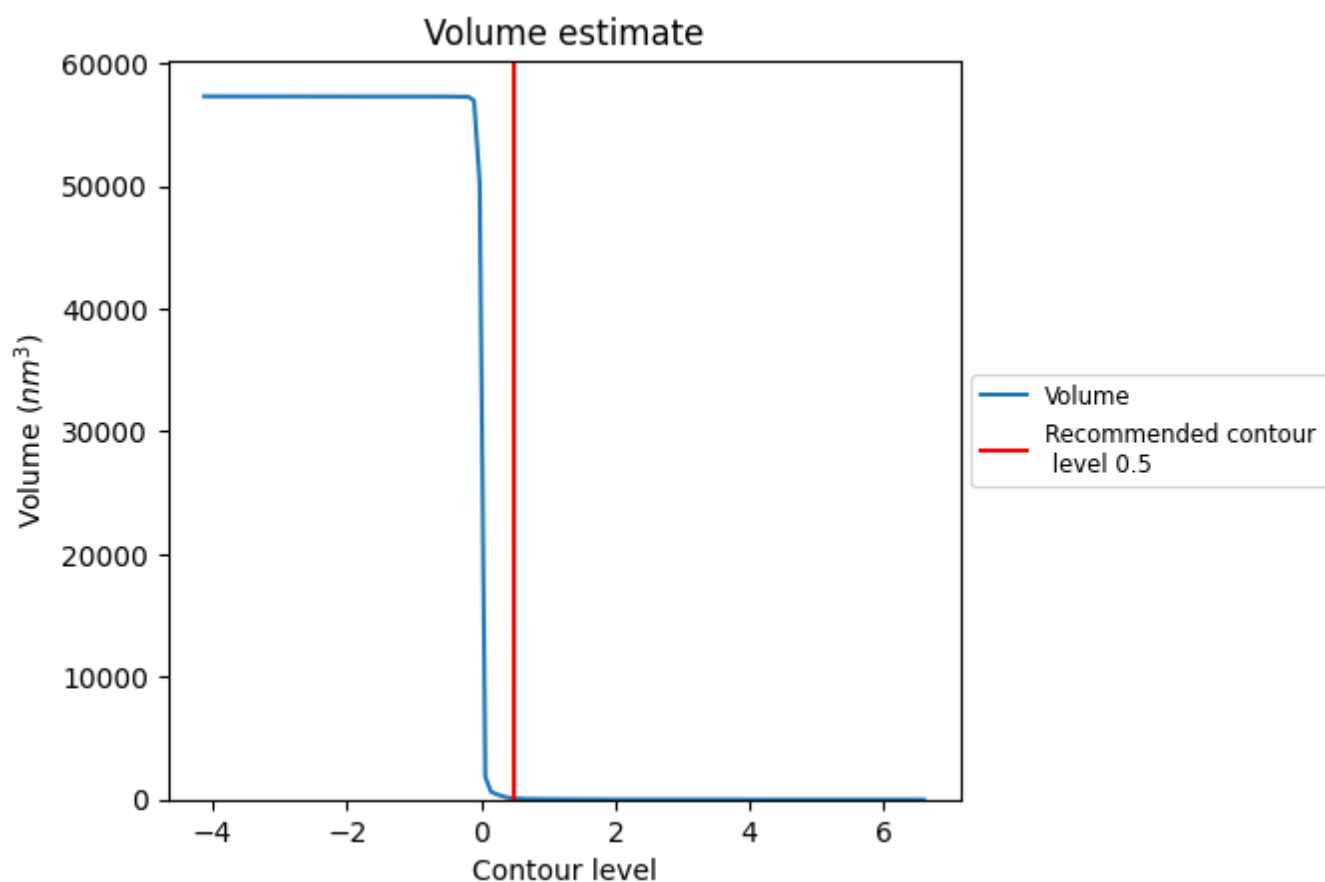
This section contains the results of statistical analysis of the map.

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.

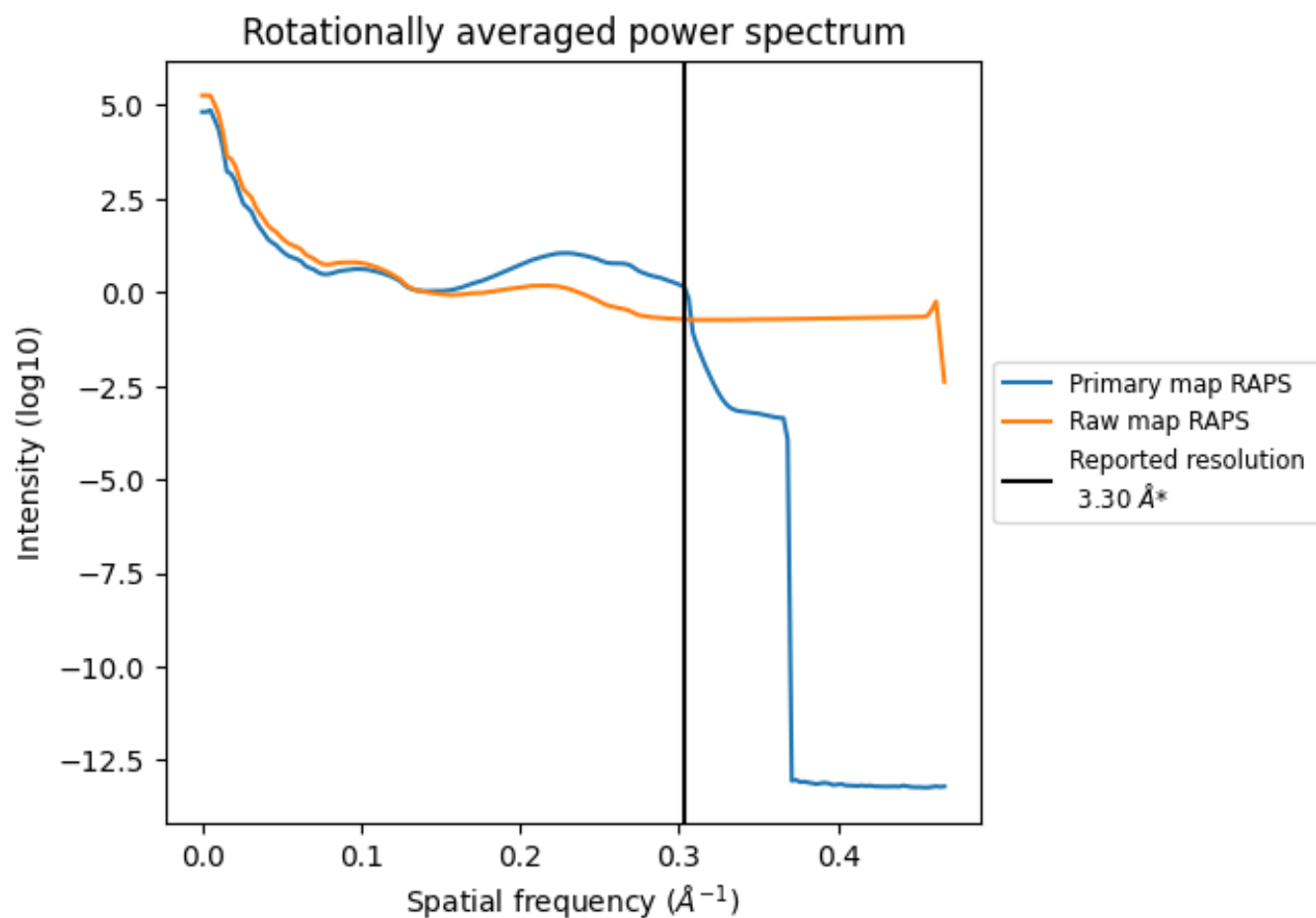
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 90 nm³; this corresponds to an approximate mass of 81 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 ⓘ

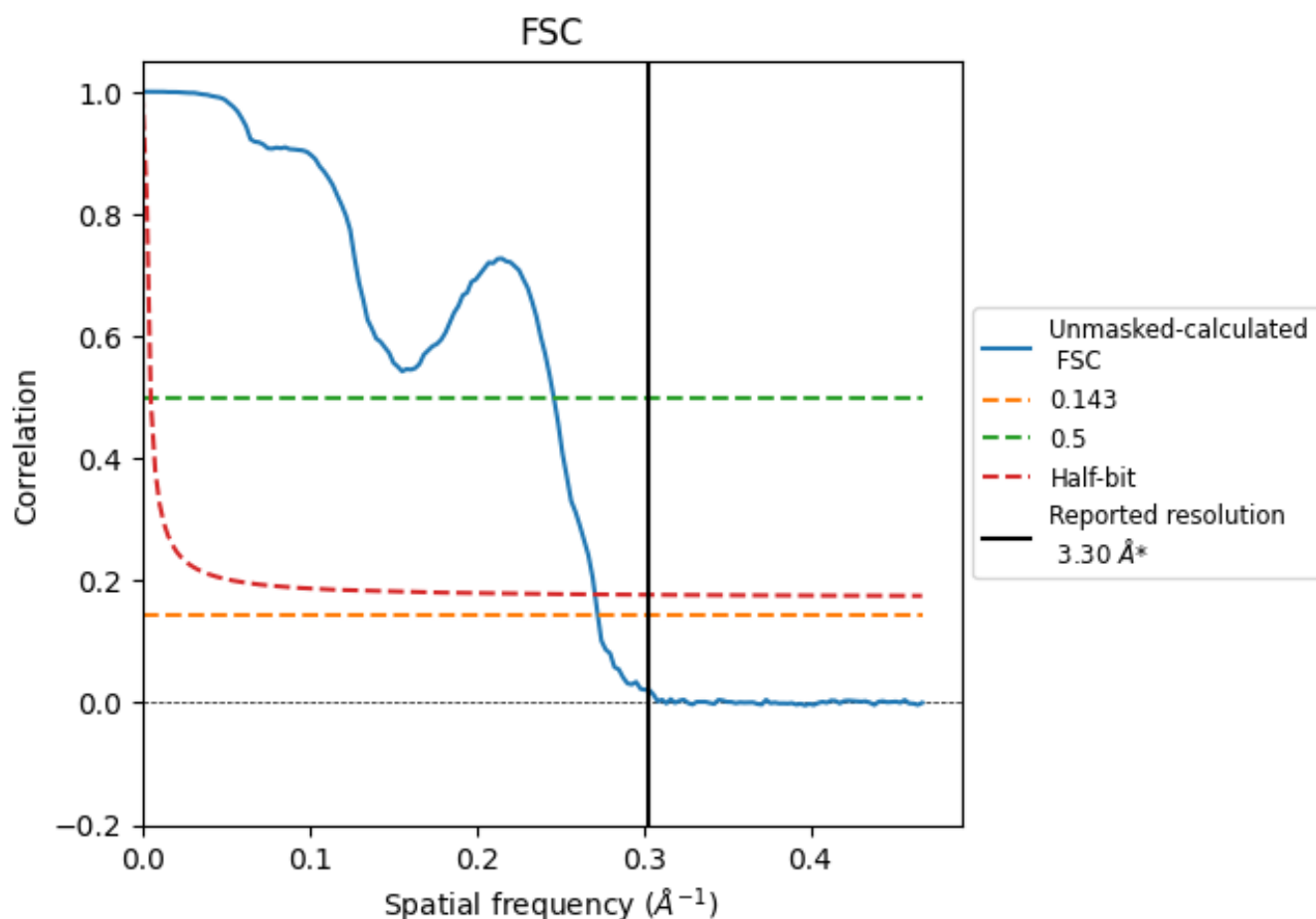


*Reported resolution corresponds to spatial frequency of 0.303 Å⁻¹

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 $0.303 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.67	4.06	3.69

*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 3.67 differs from the reported value 3.3 by more than 10 %

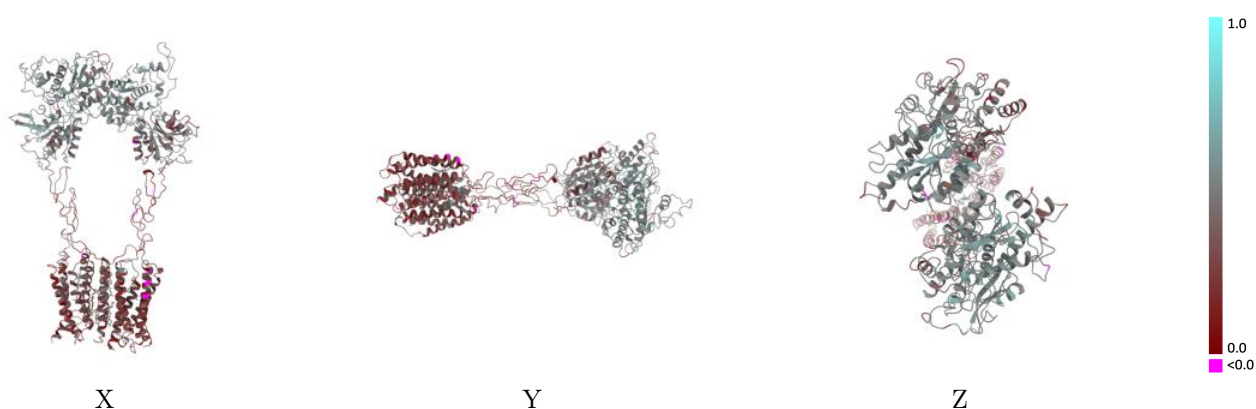
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-36171 and PDB model 8JD0. Per-residue inclusion information can be found in section 3 on page 8.

9.1 Map-model overlay [i](#)

This section was not generated.

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

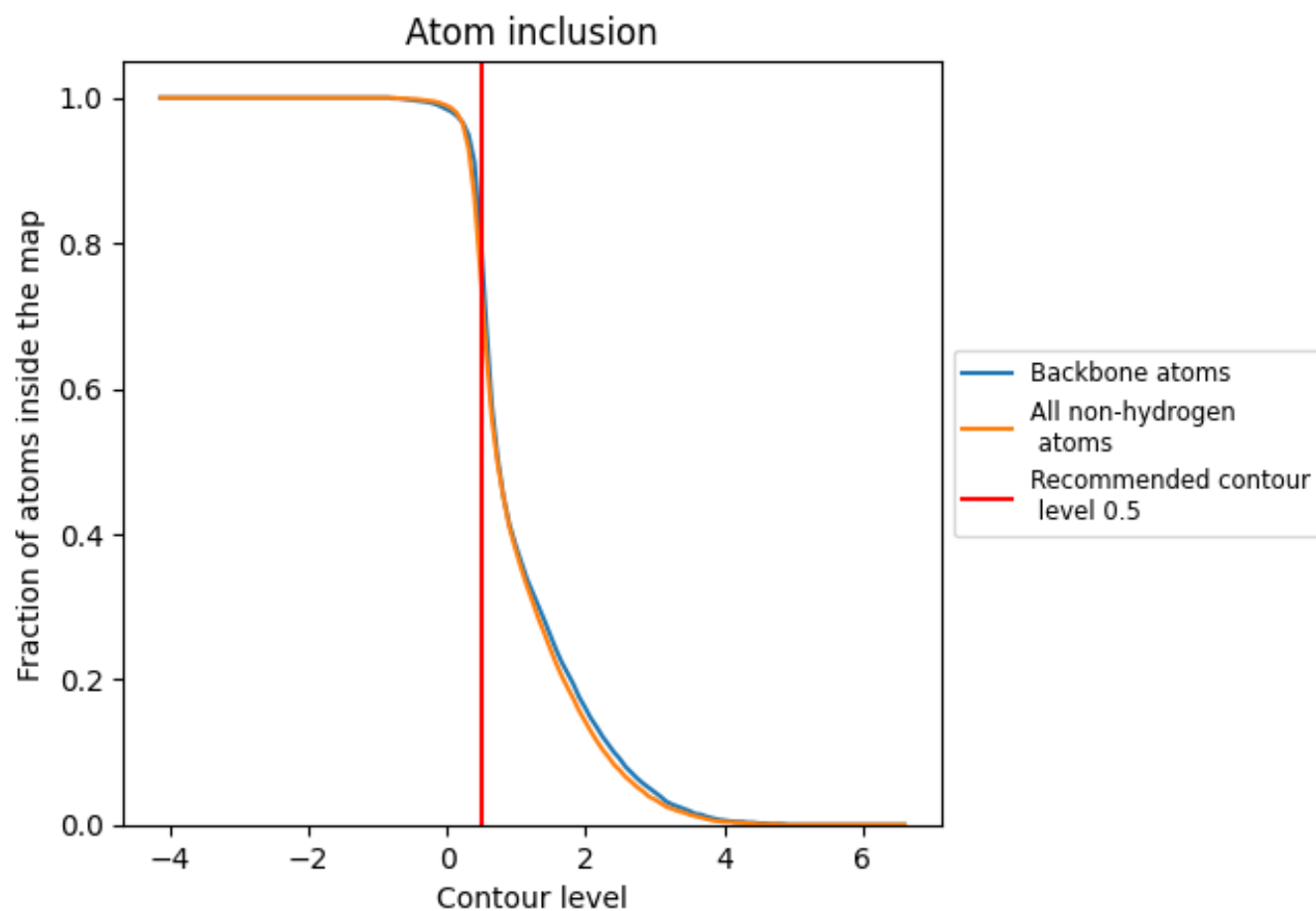


The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 74% 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 (0.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7380	0.4100
2	0.7360	0.4010
3	0.7390	0.4180

