



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 01:39 AM UTC

PDB ID : 8E5B / pdb_00008e5b
EMDB ID : EMD-27909
Title : Human L-type voltage-gated calcium channel Cav1.3 in the presence of Amiodarone and Sofosbuvir at 3.3 Angstrom resolution
Authors : Gao, S.; Yao, X.; Yan, N.
Deposited on : 2022-08-20
Resolution : 3.30 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.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

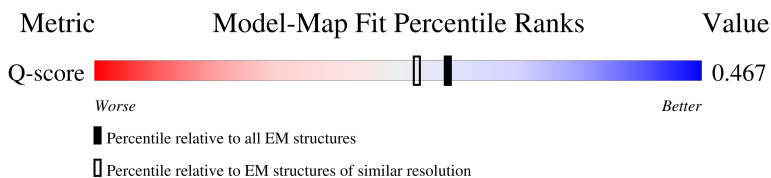
1 Overall quality at a glance

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	A	2161	
2	D	1103	
3	C	484	
4	B	3	

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Mol	Chain	Length	Quality of chain
5	E	2	100% 50% 50%
5	G	2	50% 100%
5	H	2	50% 100%
6	F	4	50% 25% 25% 50%

2 Entry composition [i](#)

There are 10 unique types of molecules in this entry. The entry contains 20310 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 Voltage-dependent L-type calcium channel subunit alpha-1D.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1230	Total	C	N	O	S	0	0
			9900	6517	1597	1715	71		

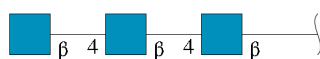
- Molecule 2 is a protein called Voltage-dependent calcium channel subunit alpha-2/delta-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	D	948	Total	C	N	O	S	0	0
			7570	4803	1269	1467	31		

- Molecule 3 is a protein called Voltage-dependent L-type calcium channel subunit beta-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	324	Total	C	N	O	S	0	0
			2575	1619	467	479	10		

- Molecule 4 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				AltConf	Trace
4	B	3	Total	C	N	O	0	0
			42	24	3	15		

- Molecule 5 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



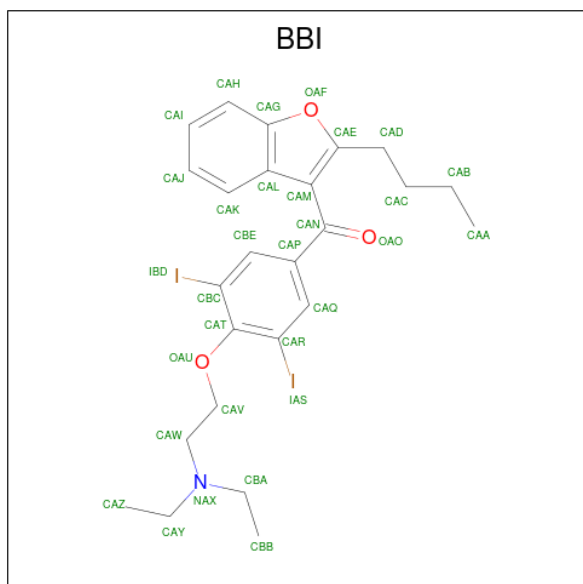
Mol	Chain	Residues	Atoms				AltConf	Trace
5	E	2	Total 28	C 16	N 2	O 10	0	0
5	G	2	Total 28	C 16	N 2	O 10	0	0
5	H	2	Total 28	C 16	N 2	O 10	0	0

- Molecule 6 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



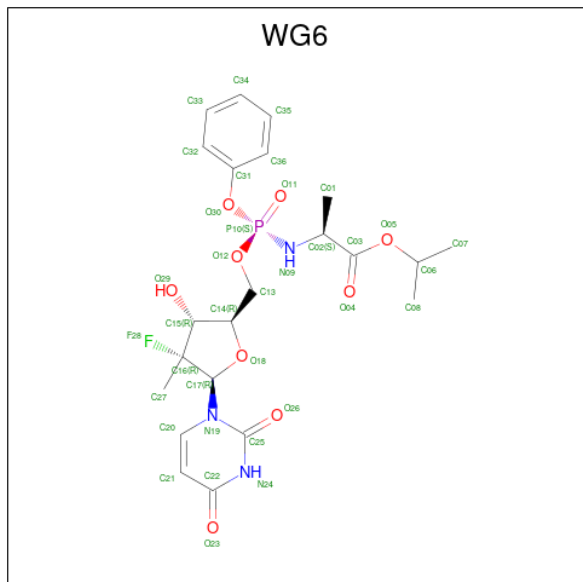
Mol	Chain	Residues	Atoms				AltConf	Trace
6	F	4	Total	C	N	O	0	0
			56	32	4	20		

- Molecule 7 is (2-butyl-1-benzofuran-3-yl){4-[2-(diethylamino)ethoxy]-3,5-diiodophenyl}methanone (CCD ID: BBI) (formula: $\text{C}_{25}\text{H}_{29}\text{I}_2\text{NO}_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
7	A	1	Total	C	I	N	O	0
			31	25	2	1	3	

- Molecule 8 is Sofosbuvir (CCD ID: WG6) (formula: $C_{22}H_{29}FN_3O_9P$) (labeled as "Ligand of Interest" by depositor).

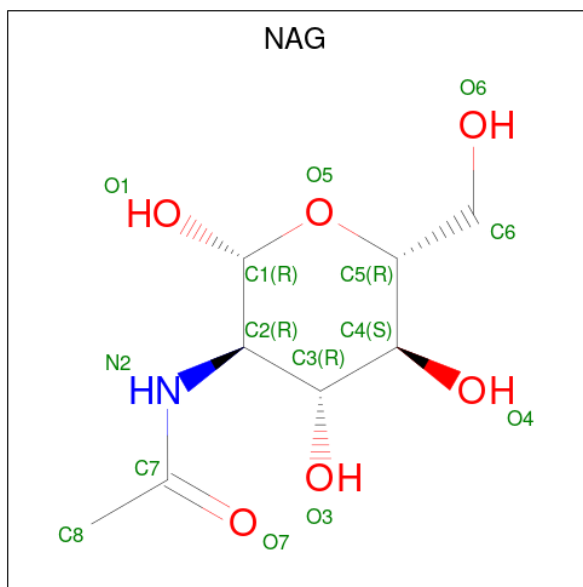


Mol	Chain	Residues	Atoms						AltConf
			Total	C	F	N	O	P	
8	A	1	36	22	1	3	9	1	0

- Molecule 9 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		AltConf
9	A	1	Total	Ca	0
			1	1	
9	D	1	Total	Ca	0
			1	1	

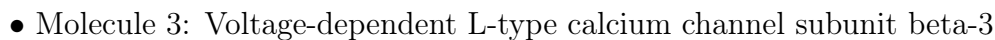
- Molecule 10 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



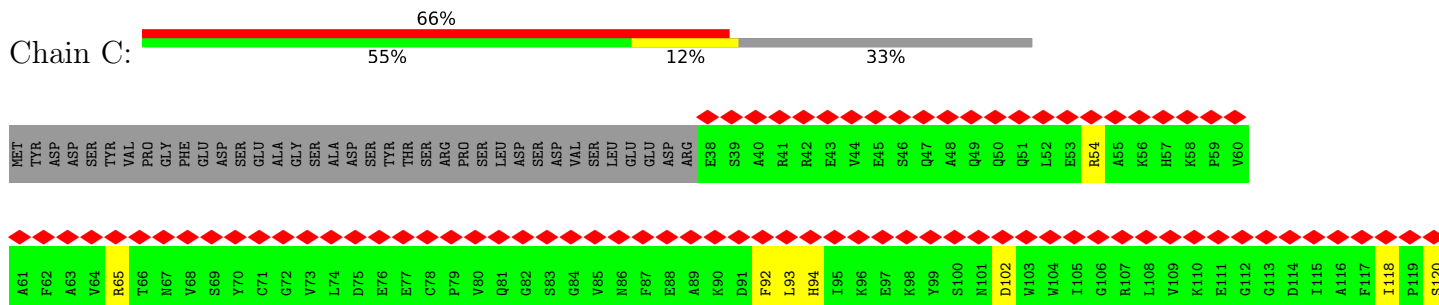
Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
10	D	1	14	8	1	5	0



Chain D:



Chain C:



LYS	SER	H361	Q301	S241	V181	P121
	ASP	HIS	R302	S242	L182	Q122
ASP	ARG	PRO	L303	A243	V183	R123
SER	HIS	ALA	I304	R244	G184	L124
TYR	LEU	PRO	R305	S245	P185	E125
	GLU	GLY	S306	S246	S186	S126
	ASP	GLY	R307	I247	L187	I127
	TYR	LEU	G308	A248	K188	R128
	ALA	LEU	K309	E249	G189	L129
	ASP	LEU	S310	V250	Y190	K130
	ALA	PRO	Q311	Q251	E191	Q131
	GLN	SER	M312	S252	V192	E132
	ASP	ALA	M313	E253	T193	Q133
	LEU	ILE	H314	I254	D194	K134
	TYR	PRO	L315	E255	M195	A135
	GLN	GLY	T316	R256	M196	R136
	PRO	LEU	V317	I257	Q197	R137
	ARG	ASN	Q318	F258	K198	S138
	GLN	GLN	M319	E259	A199	G139
	HIS	LEU	M320	L260	L200	M140
	THR	LEU	A321	A261	F201	P141
	SER	GLY	Y322	K262	D202	S142
	GLY	ARG	D323	S263	F203	S143
	PRO	GLY	K324	L264	L204	L144
	ALA	HIS	L325	Q265	K205	S145
	ASN	GLU	L326	L266	H206	D146
	GLY	HIS	V326	L266	R207	I147
	SER	SER	Q327	V267	F208	G148
	ASP	PRO	C328	V268	D209	M149
	PRO	LEU	P329	L269	G210	R150
	GLN	GLU	P330	D270	R211	S151
	ASP	ASP	E331	A271	I212	S152
	GLU	LEU	S332	D272	S213	P153
	ALA	MET	F333	T273	I214	P154
	GLN	ASP	D334	I274	T215	P155
	ASP	SER	V335	N275	R216	S156
	SER	ASP	I336	H276	V217	L157
	GLU	ALA	L337	P277	T218	A158
	ASN	SER	D338	A278	A219	K159
	SER	SER	E339	Q279	D220	Q160
	ASP	ARG	N340	L280	L221	K161
	ARG	ASN	Q341	A281	S222	Q162
	GLN	GLN	L342	K282	L223	K163
	TRP	ALA	E343	T283	A224	Q164
	GLN	THR	D344	S284	K225	A165
	ARG	GLY	A345	L285	R226	E166
	ASN	SER	C346	A286	S227	H167
	PRO	SER	E347	P287	V228	P168
	TRP	GLN	H348	I288	L229	P169
	ARG	ARG	L349	I289	N230	P170
			A350	V290	N231	Y171
			E351	F291	P232	D172
			Y352	V292	G233	V173
			L353	K293	K234	V174
			E354	V294	R235	P175
			V355	S295	T236	S176
			Y356	S296	I237	M177
			W357	P297	L238	R178
			R358	K298	E239	P179
			A359	V299	R240	V180
			T360	L300		

- Molecule 4: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



MAG1
MAG2
MAG3

- Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



MAG1
MAG2

- Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

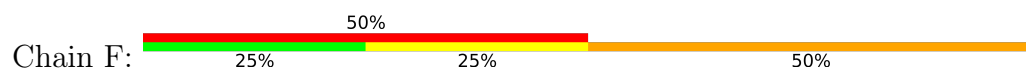


MAG1
MAG2

- Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 6: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	69718	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1900	Depositor
Maximum defocus (nm)	2100	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.152	Depositor
Minimum map value	-0.088	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.025	Depositor
Map size (Å)	311.91998, 311.91998, 311.91998	wwPDB
Map dimensions	280, 280, 280	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.114, 1.114, 1.114	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CA, NAG, WG6, BBI

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	0.13	0/10127	0.30	0/13716
2	D	0.14	0/7728	0.28	0/10477
3	C	0.10	0/2624	0.25	0/3544
All	All	0.13	0/20479	0.28	0/27737

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	A	9900	0	10071	139	0
2	D	7570	0	7370	88	0
3	C	2575	0	2619	41	0
4	B	42	0	37	2	0
5	E	28	0	25	1	0
5	G	28	0	25	0	0
5	H	28	0	25	1	0
6	F	56	0	49	4	0
7	A	31	0	29	10	0
8	A	36	0	0	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	A	1	0	0	0	0
9	D	1	0	0	0	0
10	D	14	0	13	0	0
All	All	20310	0	20263	277	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 7.

The worst 5 of 277 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1391:THR:HG22	1:A:1393:PRO:HD2	1.59	0.84
1:A:377:MET:HG2	1:A:378:GLY:H	1.45	0.80
2:D:822:ILE:HD11	2:D:868:THR:HG21	1.66	0.76
1:A:1187:ARG:HH21	1:A:1494:PRO:HB3	1.52	0.75
1:A:377:MET:HE1	1:A:381:LEU:HD23	1.69	0.75

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	1214/2161 (56%)	1154 (95%)	60 (5%)	0	100	100
2	D	936/1103 (85%)	891 (95%)	45 (5%)	0	100	100
3	C	322/484 (66%)	312 (97%)	10 (3%)	0	100	100
All	All	2472/3748 (66%)	2357 (95%)	115 (5%)	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	A	1086/1902 (57%)	1086 (100%)	0	100	100
2	D	837/971 (86%)	837 (100%)	0	100	100
3	C	287/426 (67%)	287 (100%)	0	100	100
All	All	2210/3299 (67%)	2210 (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. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1381	ASN
2	D	472	GLN
3	C	275	ASN
3	C	149	ASN
3	C	206	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](#)

13 monosaccharides 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
4	NAG	B	1	4,2	14,14,15	0.47	0	17,19,21	0.51	0
4	NAG	B	2	4	14,14,15	0.44	0	17,19,21	1.32	2 (11%)
4	NAG	B	3	4	14,14,15	0.35	0	17,19,21	0.45	0
5	NAG	E	1	5,2	14,14,15	0.47	0	17,19,21	0.51	0
5	NAG	E	2	5	14,14,15	0.50	0	17,19,21	0.80	0
6	NAG	F	1	6,2	14,14,15	0.31	0	17,19,21	0.53	0
6	NAG	F	2	6	14,14,15	0.18	0	17,19,21	0.46	0
6	NAG	F	3	6	14,14,15	1.01	1 (7%)	17,19,21	1.73	3 (17%)
6	NAG	F	4	6	14,14,15	0.51	0	17,19,21	1.35	2 (11%)
5	NAG	G	1	5,2	14,14,15	0.26	0	17,19,21	0.42	0
5	NAG	G	2	5	14,14,15	0.25	0	17,19,21	0.52	0
5	NAG	H	1	5,2	14,14,15	0.55	0	17,19,21	0.41	0
5	NAG	H	2	5	14,14,15	0.23	0	17,19,21	0.42	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
4	NAG	B	1	4,2	-	0/6/23/26	0/1/1/1
4	NAG	B	2	4	-	5/6/23/26	0/1/1/1
4	NAG	B	3	4	-	4/6/23/26	0/1/1/1
5	NAG	E	1	5,2	-	4/6/23/26	0/1/1/1
5	NAG	E	2	5	-	4/6/23/26	0/1/1/1
6	NAG	F	1	6,2	-	2/6/23/26	0/1/1/1
6	NAG	F	2	6	-	0/6/23/26	0/1/1/1
6	NAG	F	3	6	-	4/6/23/26	0/1/1/1
6	NAG	F	4	6	-	5/6/23/26	0/1/1/1
5	NAG	G	1	5,2	-	2/6/23/26	0/1/1/1
5	NAG	G	2	5	-	2/6/23/26	0/1/1/1
5	NAG	H	1	5,2	-	2/6/23/26	0/1/1/1
5	NAG	H	2	5	-	4/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	F	3	NAG	O5-C1	3.19	1.49	1.43

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	F	3	NAG	C1-O5-C5	4.64	118.40	112.19
6	F	3	NAG	C2-N2-C7	4.58	129.04	122.90
6	F	4	NAG	C2-N2-C7	4.58	129.04	122.90
4	B	2	NAG	C2-N2-C7	4.54	128.99	122.90
6	F	4	NAG	C1-C2-N2	2.22	113.93	110.43

There are no chirality outliers.

5 of 38 torsion outliers are listed below:

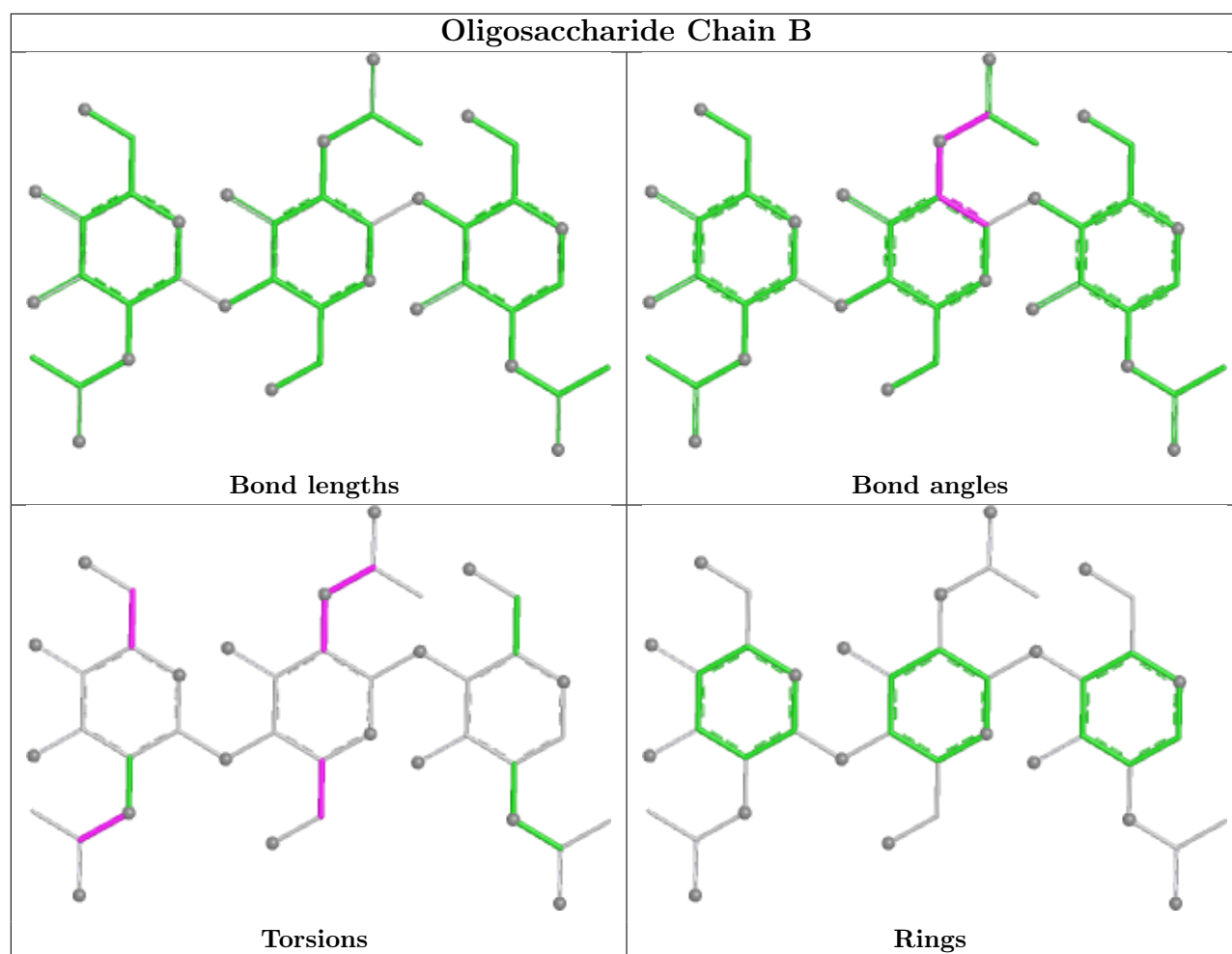
Mol	Chain	Res	Type	Atoms
5	G	1	NAG	O5-C5-C6-O6
4	B	3	NAG	C4-C5-C6-O6
5	E	2	NAG	C4-C5-C6-O6
5	G	2	NAG	O5-C5-C6-O6
5	G	1	NAG	C4-C5-C6-O6

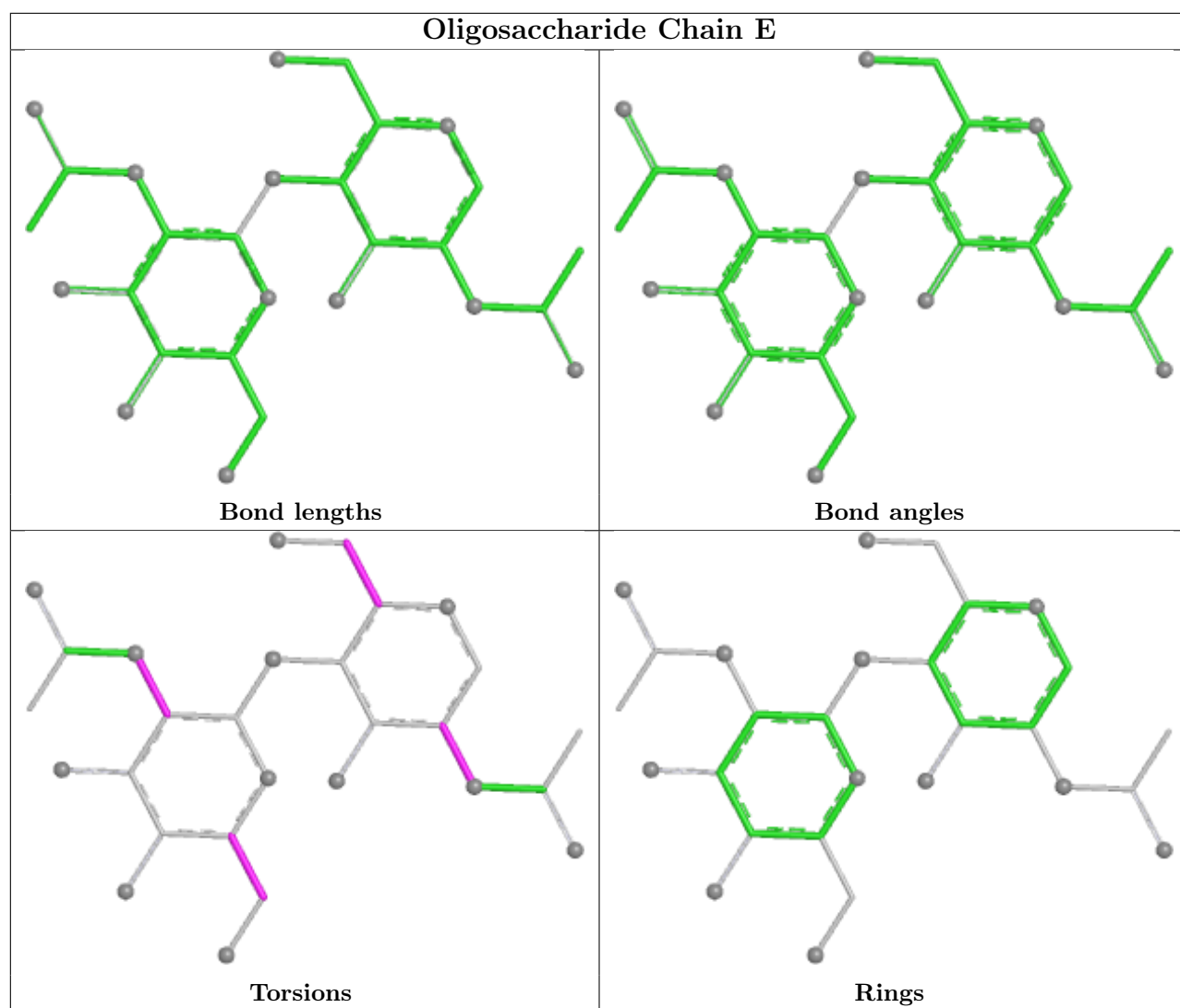
There are no ring outliers.

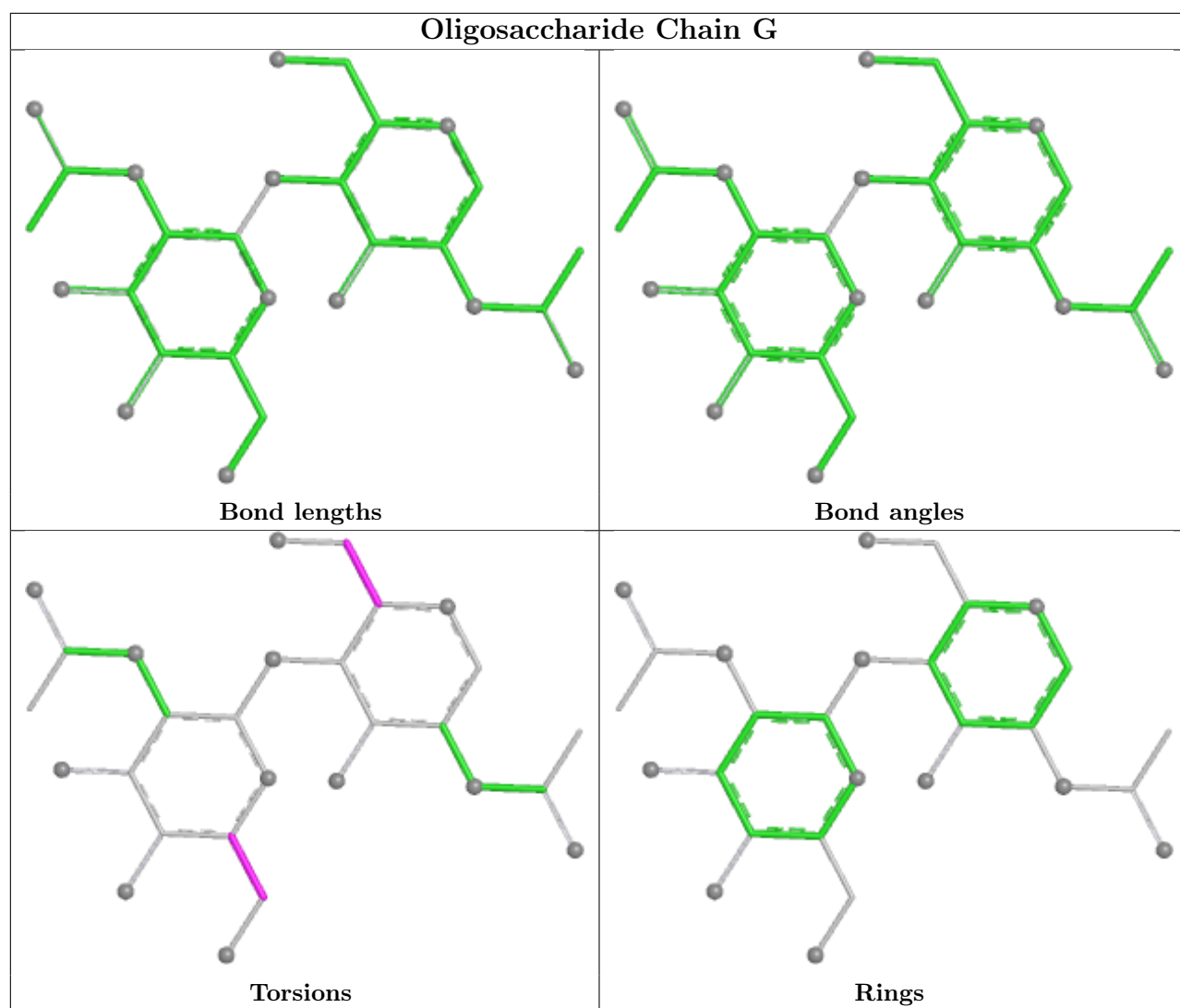
8 monomers are involved in 8 short contacts:

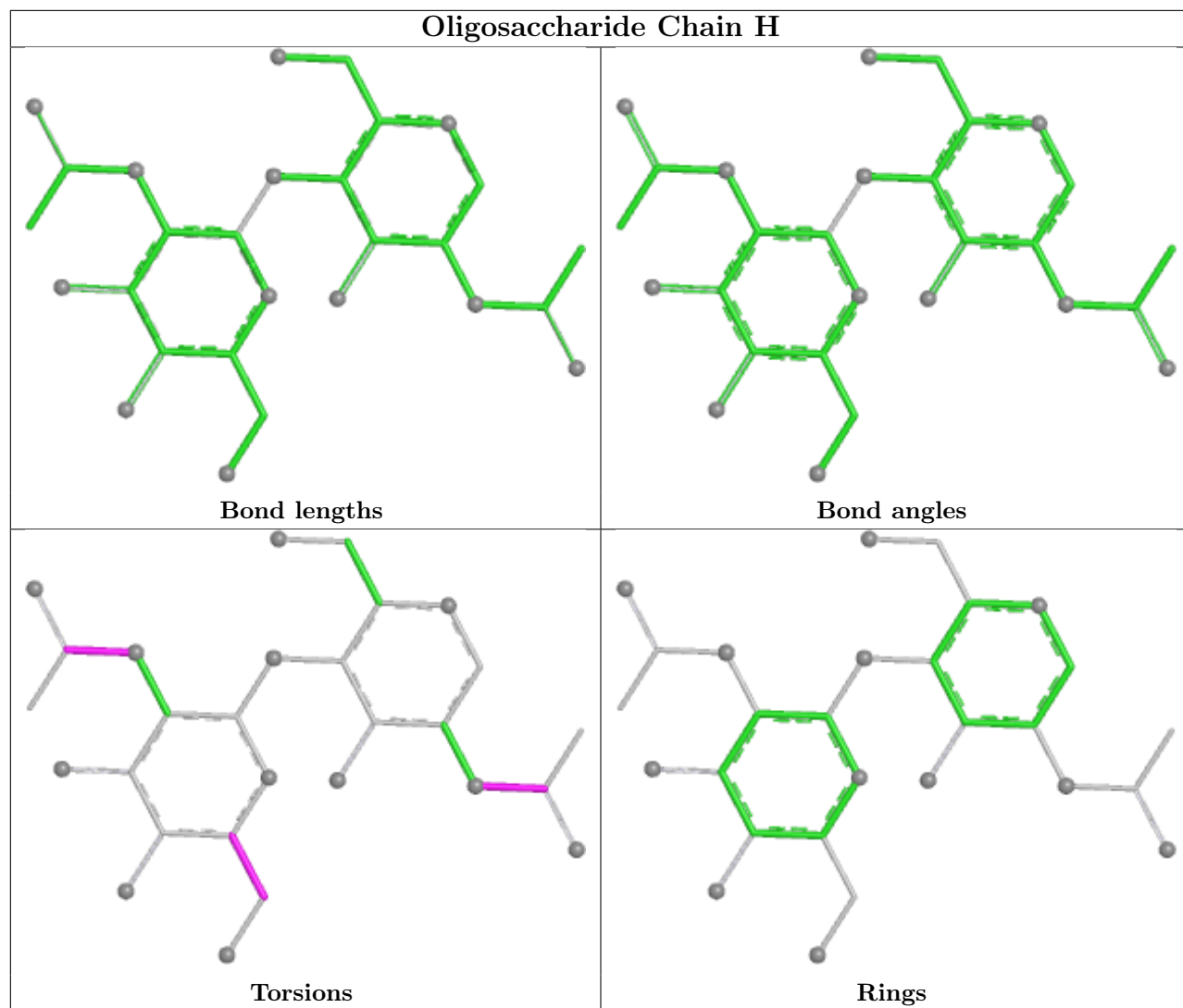
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	F	1	NAG	2	0
6	F	4	NAG	1	0
5	E	1	NAG	1	0
4	B	1	NAG	1	0
5	H	2	NAG	1	0
5	H	1	NAG	1	0
6	F	3	NAG	1	0
4	B	2	NAG	1	0

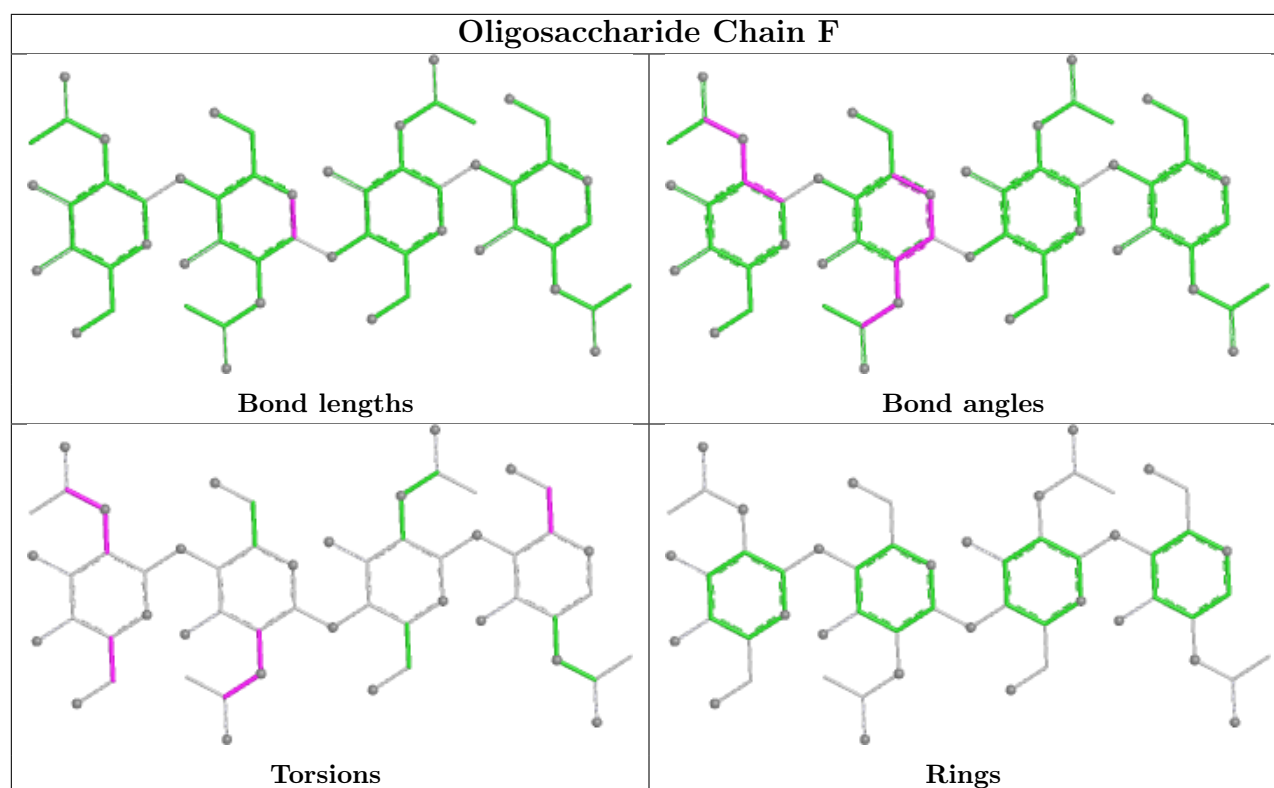
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.











5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 2 are monoatomic - leaving 3 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
10	NAG	D	1201	2	14,14,15	0.38	0	17,19,21	0.50	0
8	WG6	A	2202	-	34,38,38	3.39	15 (44%)	46,56,56	2.58	15 (32%)
7	BB1	A	2201	-	33,33,33	1.52	5 (15%)	44,45,45	1.98	5 (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
10	NAG	D	1201	2	-	2/6/23/26	0/1/1/1
8	WG6	A	2202	-	-	15/28/48/48	0/3/3/3
7	BBI	A	2201	-	-	9/22/22/22	0/3/3/3

The worst 5 of 20 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	2202	WG6	P10-O30	11.41	1.71	1.58
8	A	2202	WG6	P10-N09	8.62	1.72	1.61
8	A	2202	WG6	C17-N19	5.94	1.61	1.46
7	A	2201	BBI	OAF-CAE	-5.65	1.30	1.38
8	A	2202	WG6	P10-O12	5.19	1.71	1.57

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	2202	WG6	O18-C17-N19	10.67	117.80	108.23
7	A	2201	BBI	CAD-CAE-CAM	-8.40	125.67	133.84
7	A	2201	BBI	OAF-CAE-CAD	6.38	124.89	115.22
8	A	2202	WG6	O05-C03-C02	5.84	120.61	110.83
7	A	2201	BBI	CAG-OAF-CAE	5.48	111.45	106.04

There are no chirality outliers.

5 of 26 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	A	2201	BBI	CAR-CAT-OAU-CAV
7	A	2201	BBI	CAV-CAW-NAX-CBA
8	A	2202	WG6	N09-C02-C03-O04
8	A	2202	WG6	N09-C02-C03-O05
8	A	2202	WG6	C03-C02-N09-P10

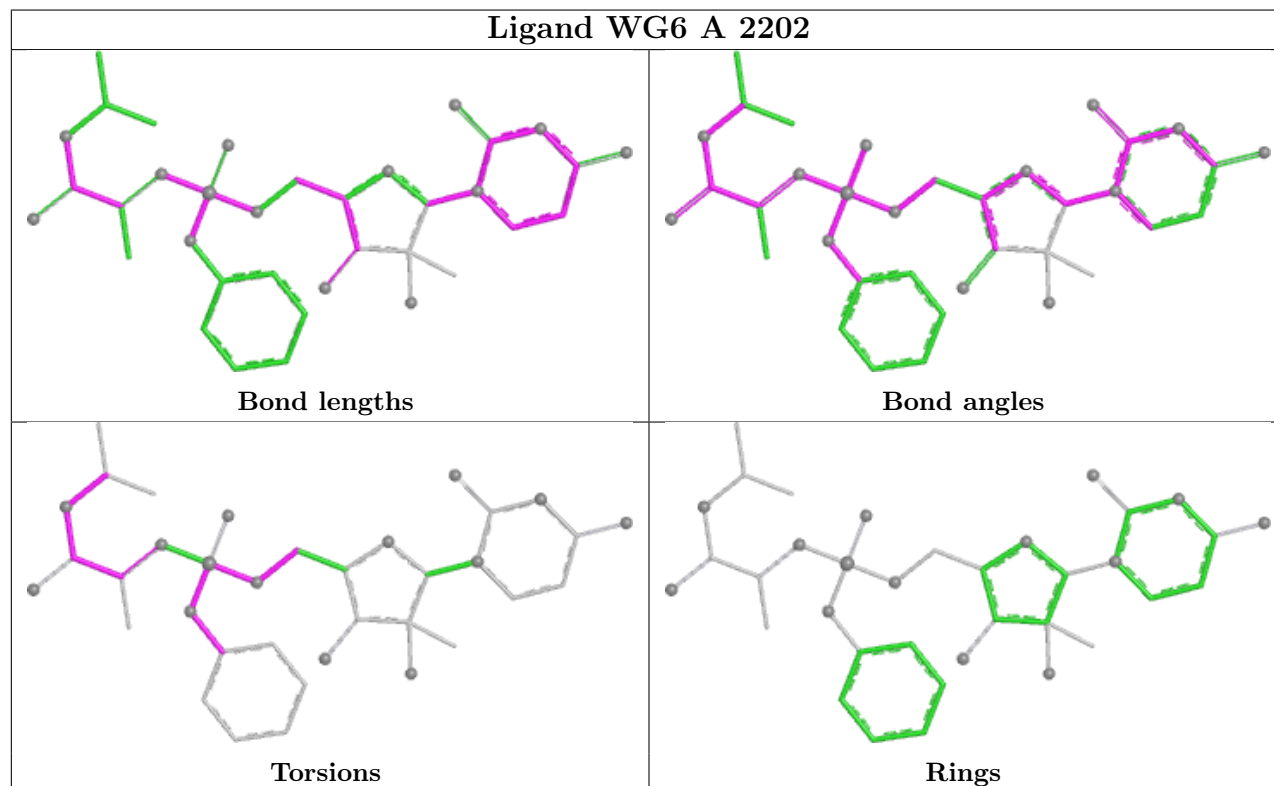
There are no ring outliers.

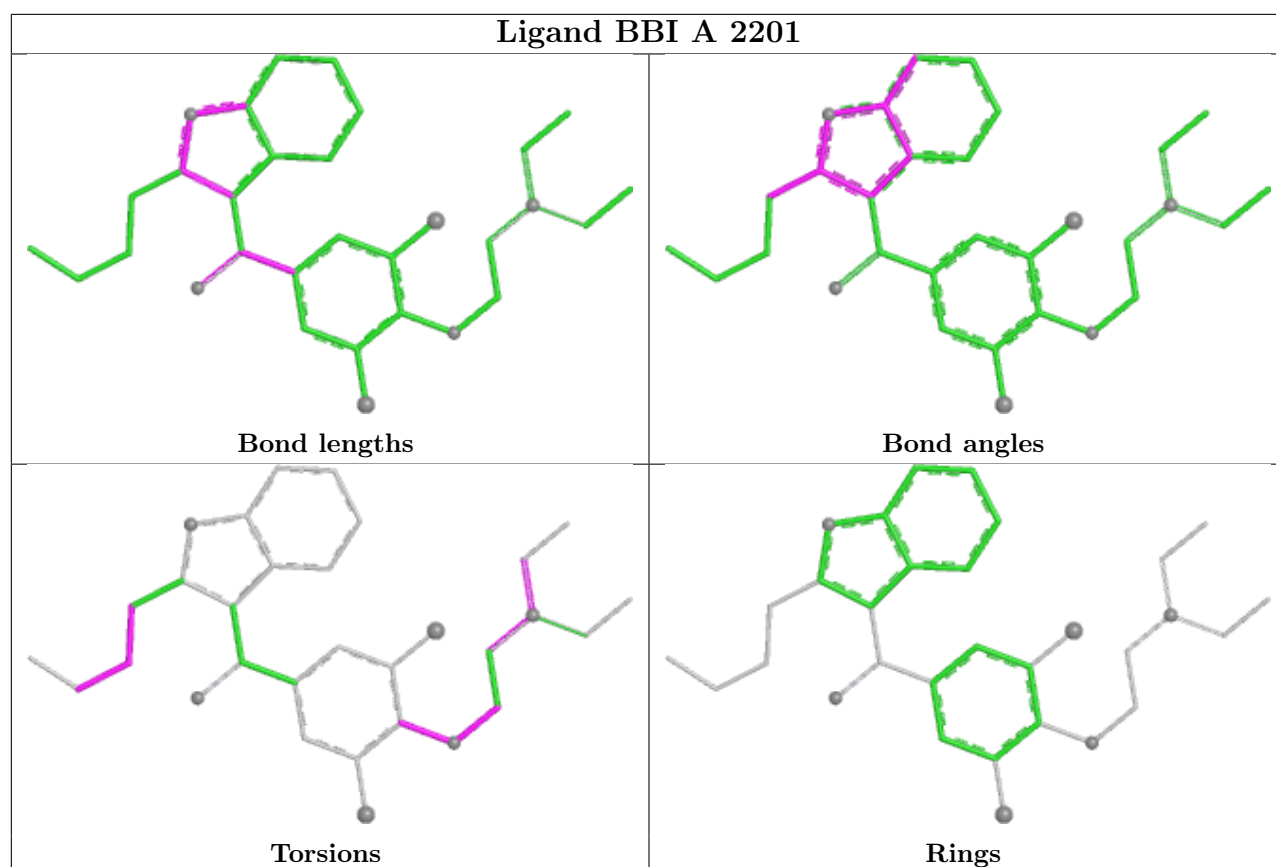
2 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	A	2202	WG6	4	0
7	A	2201	BBI	10	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.

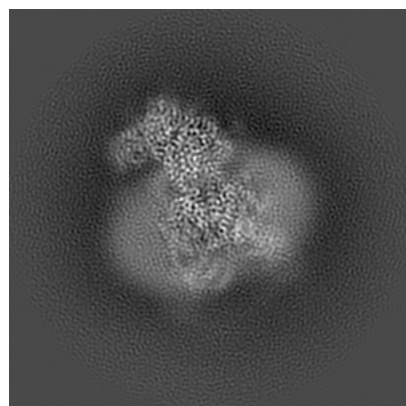
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-27909. These allow visual inspection of the internal detail of the map and identification of artifacts.

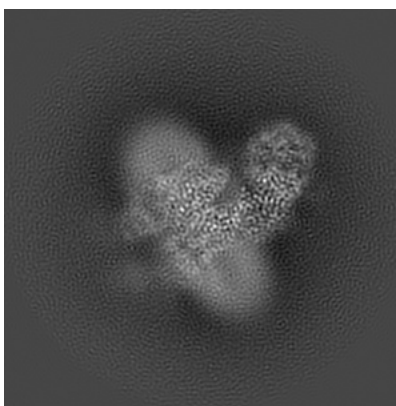
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

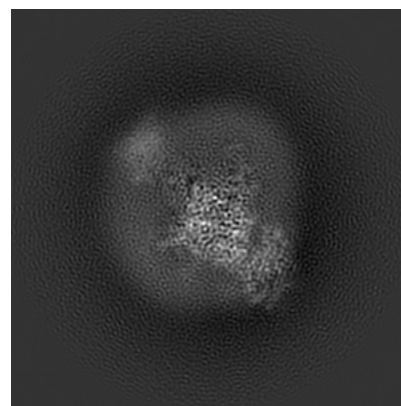
6.1.1 Primary map



X

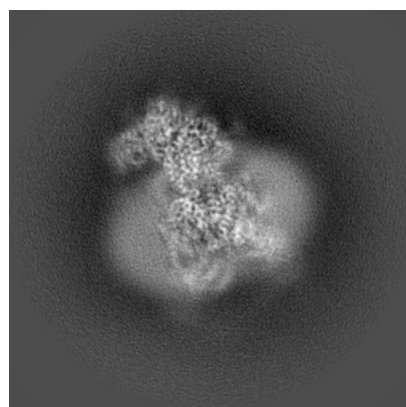


Y

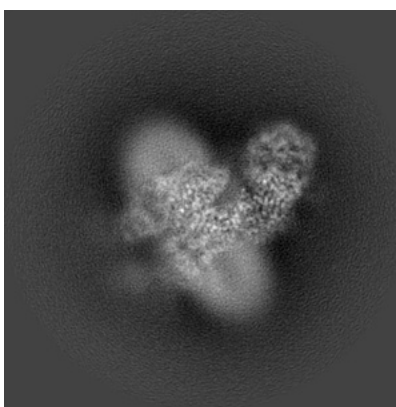


Z

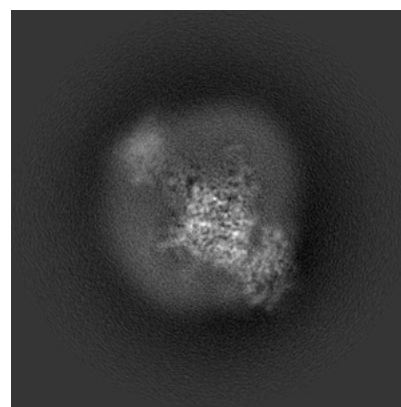
6.1.2 Raw map



X



Y

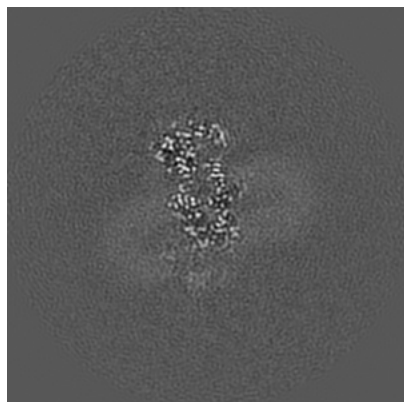


Z

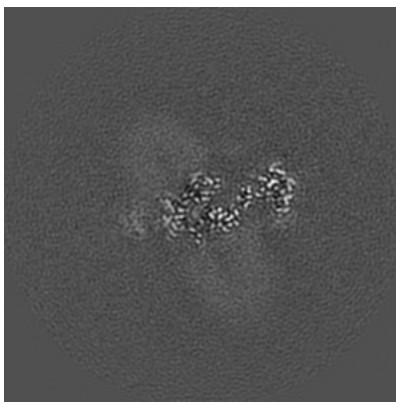
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

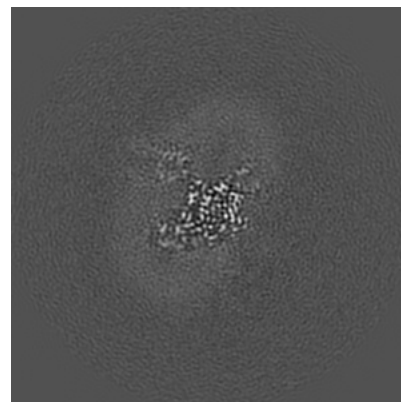
6.2.1 Primary map



X Index: 140

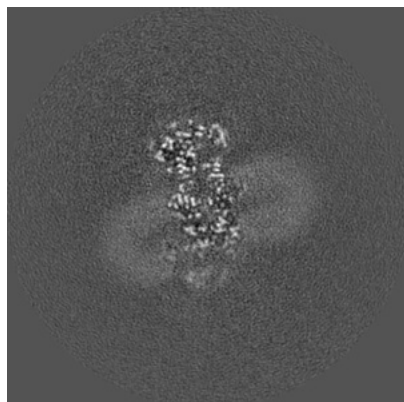


Y Index: 140

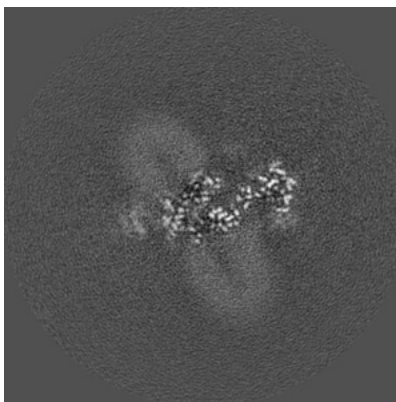


Z Index: 140

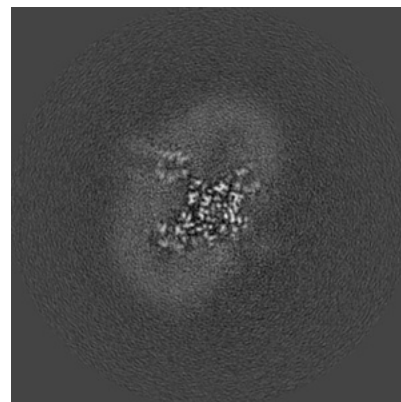
6.2.2 Raw map



X Index: 140



Y Index: 140

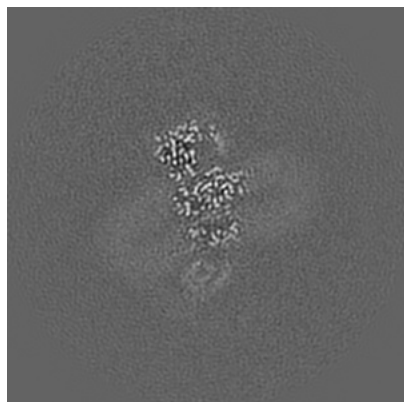


Z Index: 140

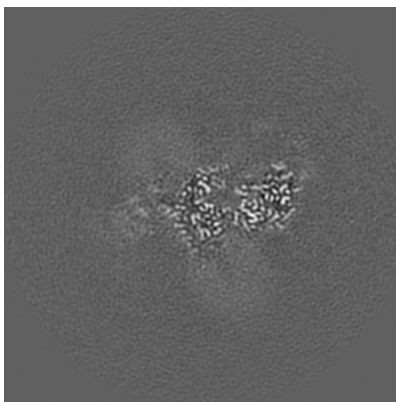
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

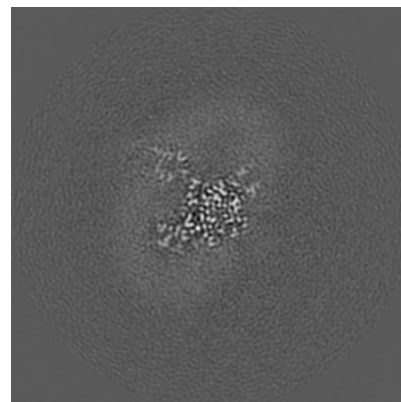
6.3.1 Primary map



X Index: 135

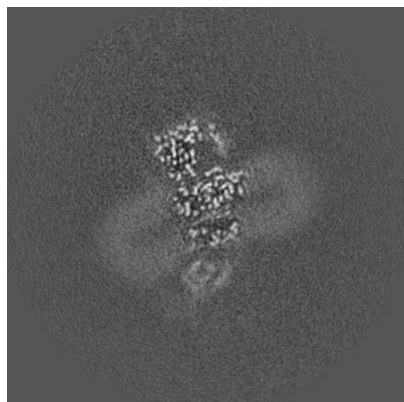


Y Index: 130

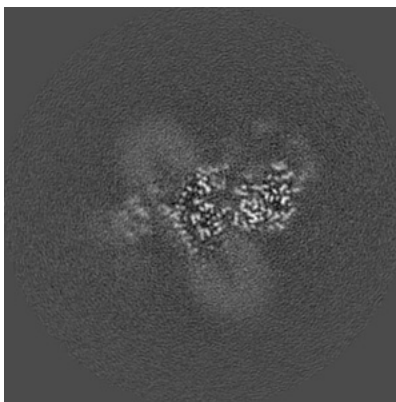


Z Index: 141

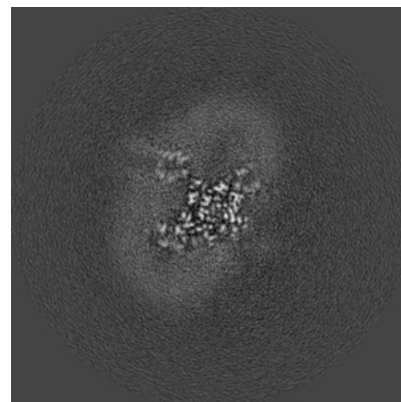
6.3.2 Raw map



X Index: 135



Y Index: 130

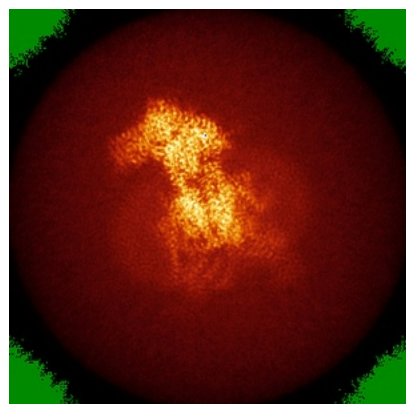


Z Index: 140

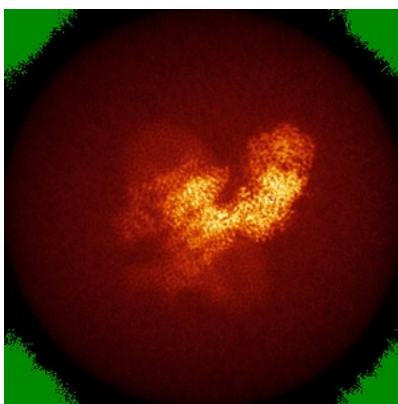
The images above show the largest variance slices of the map in three orthogonal directions.

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

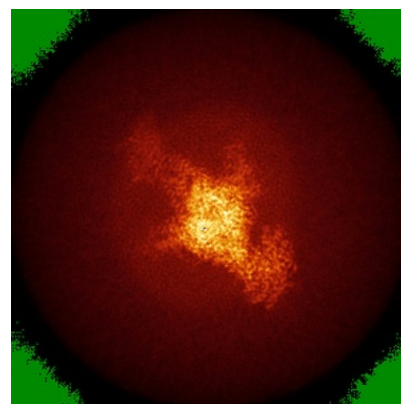
6.4.1 Primary map



X

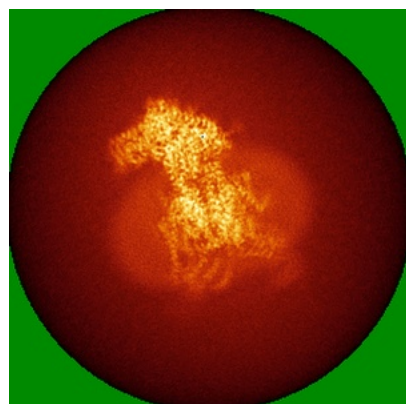


Y

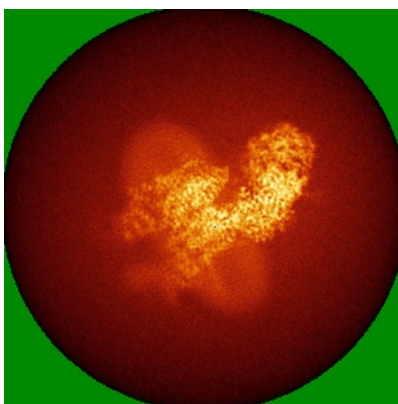


Z

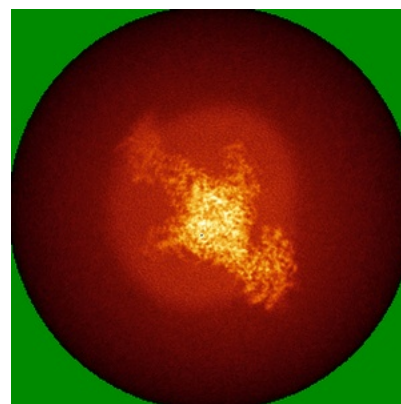
6.4.2 Raw map



X



Y



Z

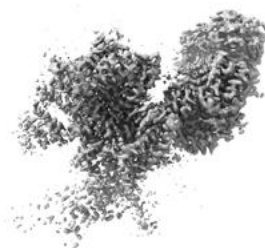
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.025. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

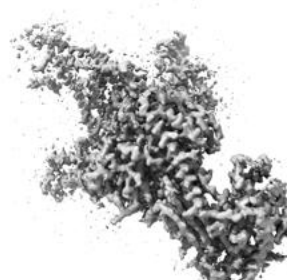
6.5.2 Raw map



X



Y



Z

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.

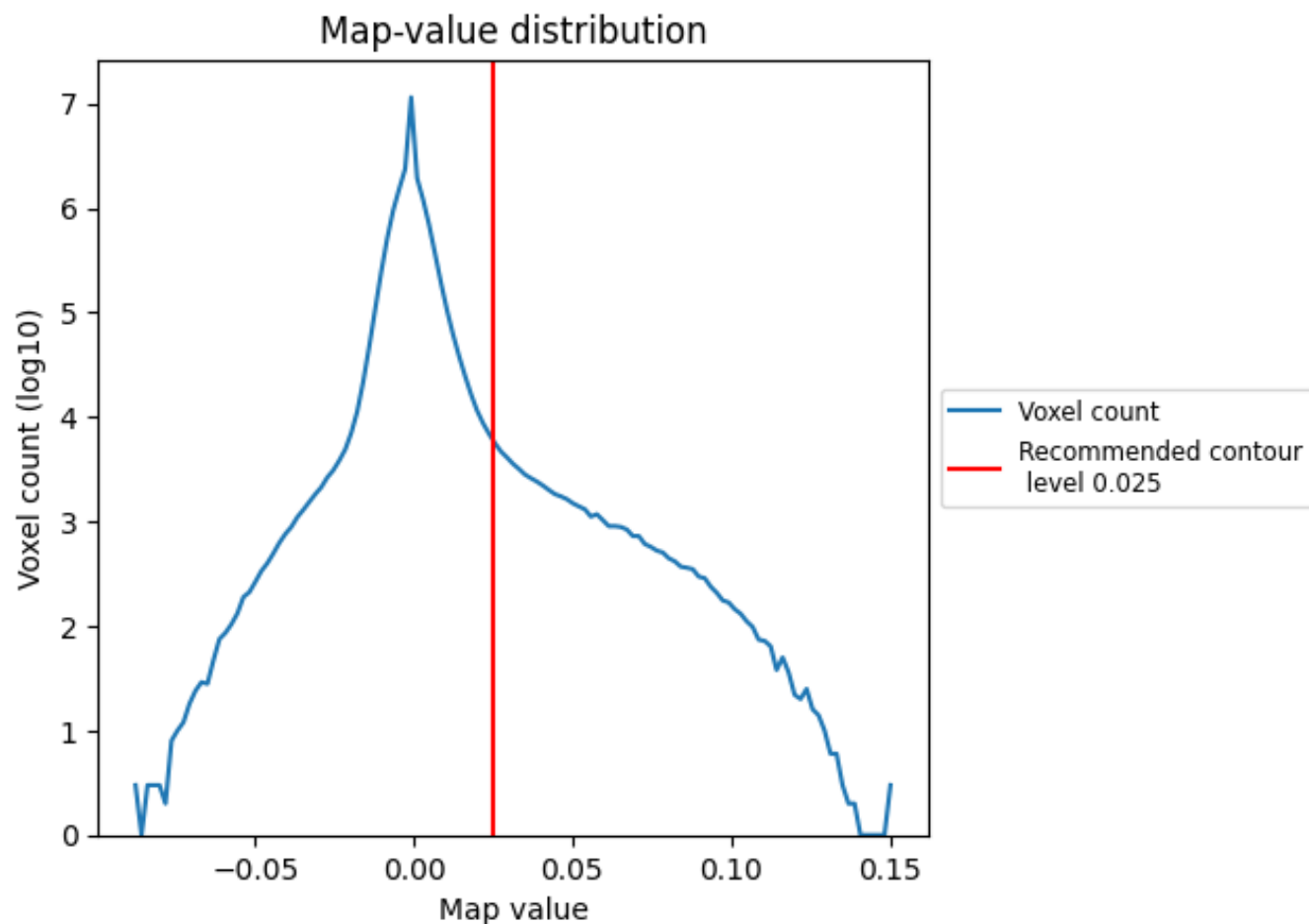
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

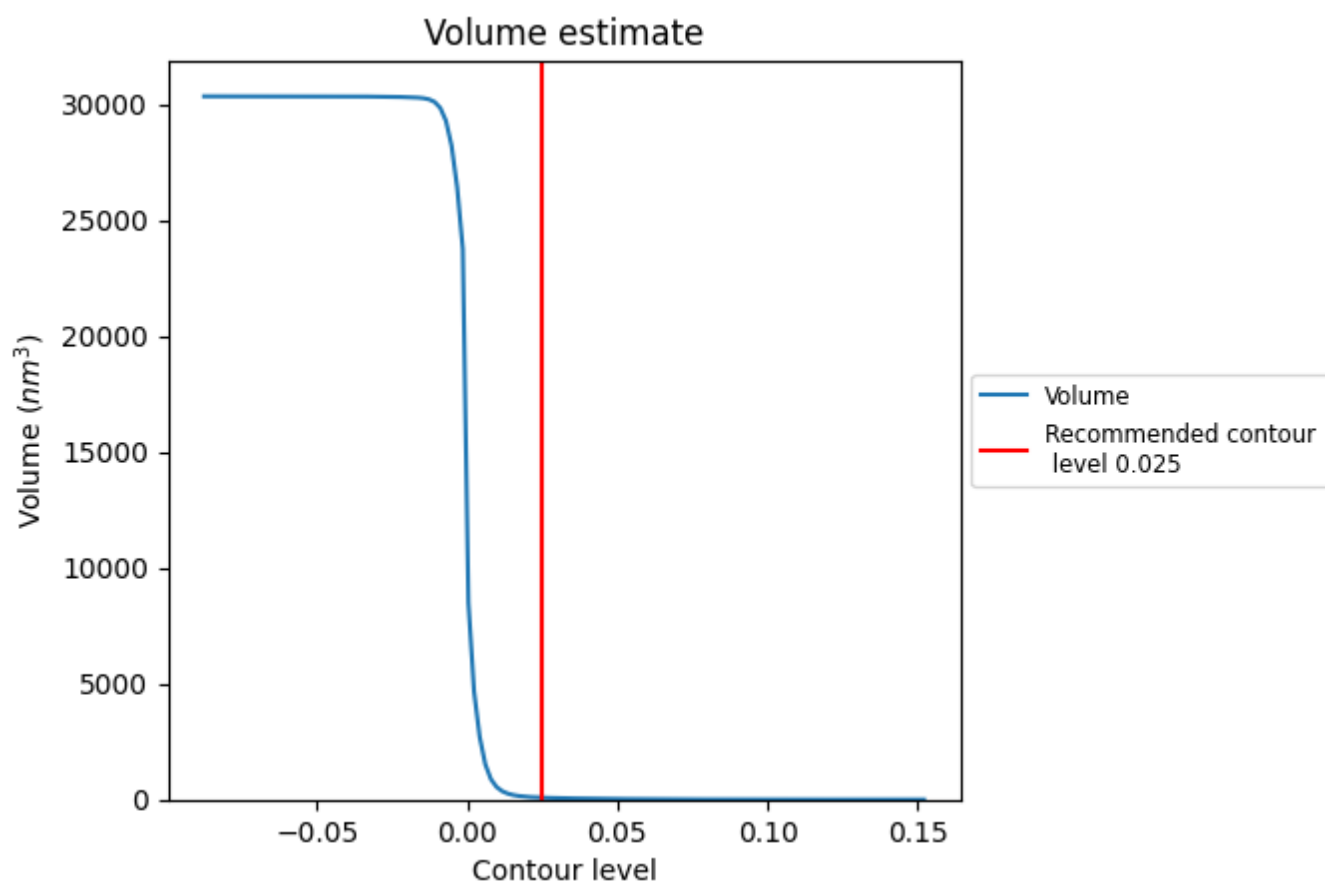
This section contains the results of statistical analysis of the map.

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.

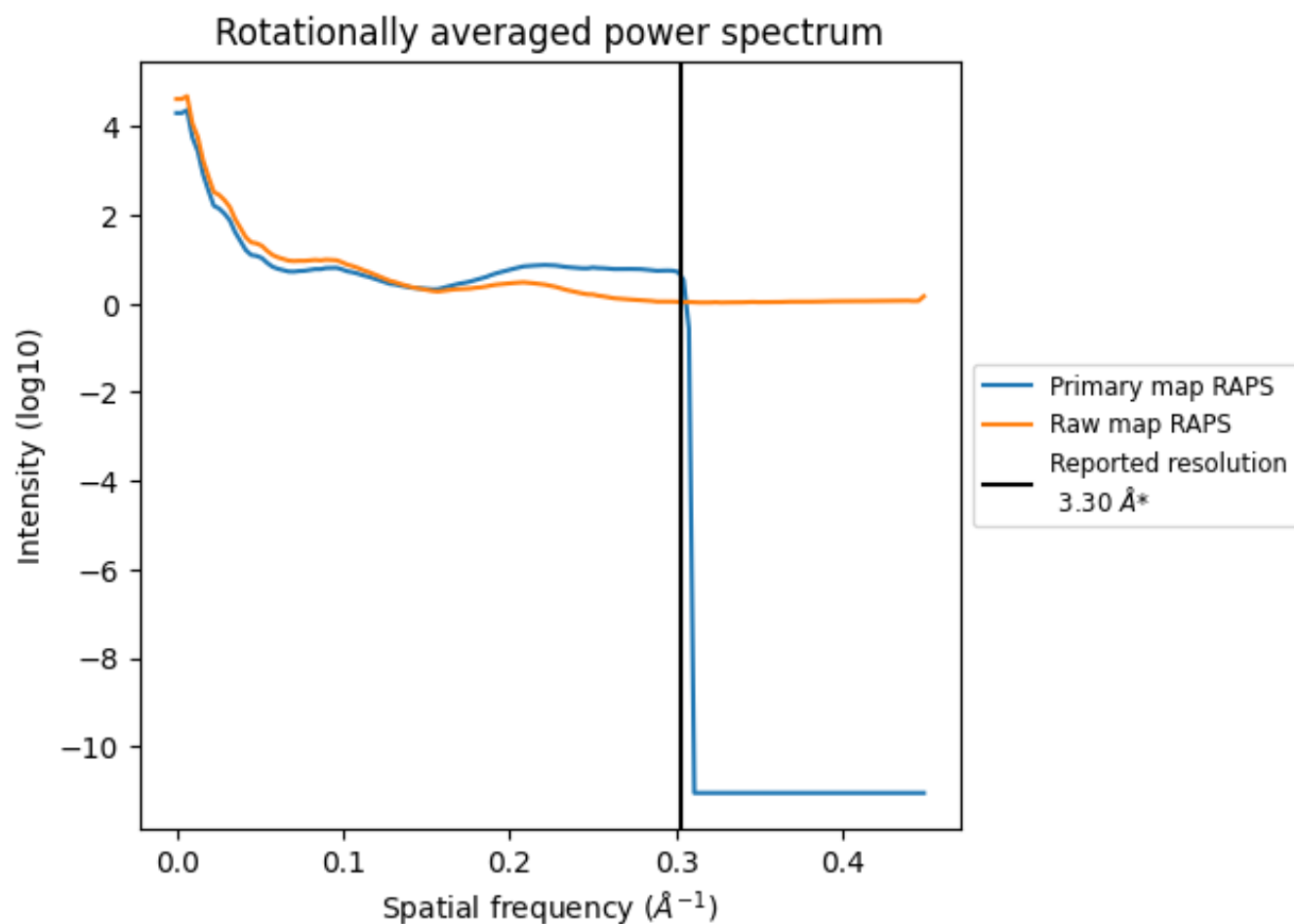
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 82 nm³; this corresponds to an approximate mass of 74 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 ⓘ

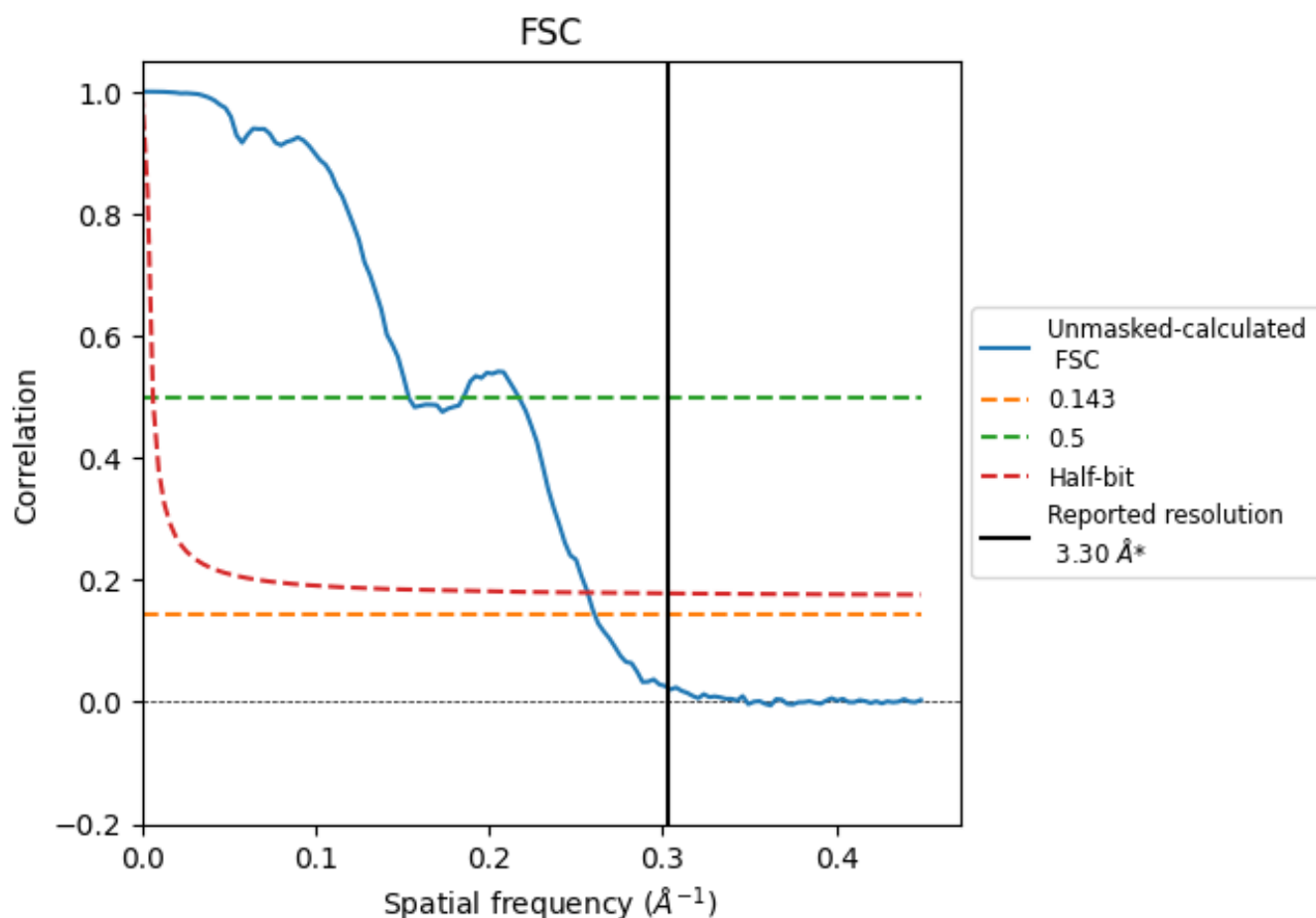


*Reported resolution corresponds to spatial frequency of 0.303 Å⁻¹

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 Å⁻¹

8.2 Resolution estimates [i](#)

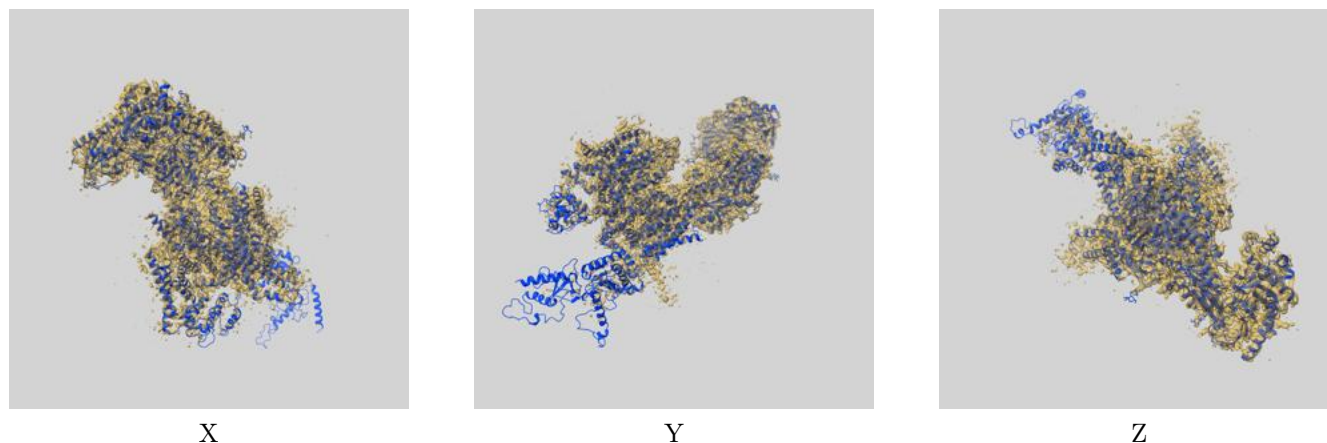
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.83	6.51	3.89

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

9 Map-model fit [i](#)

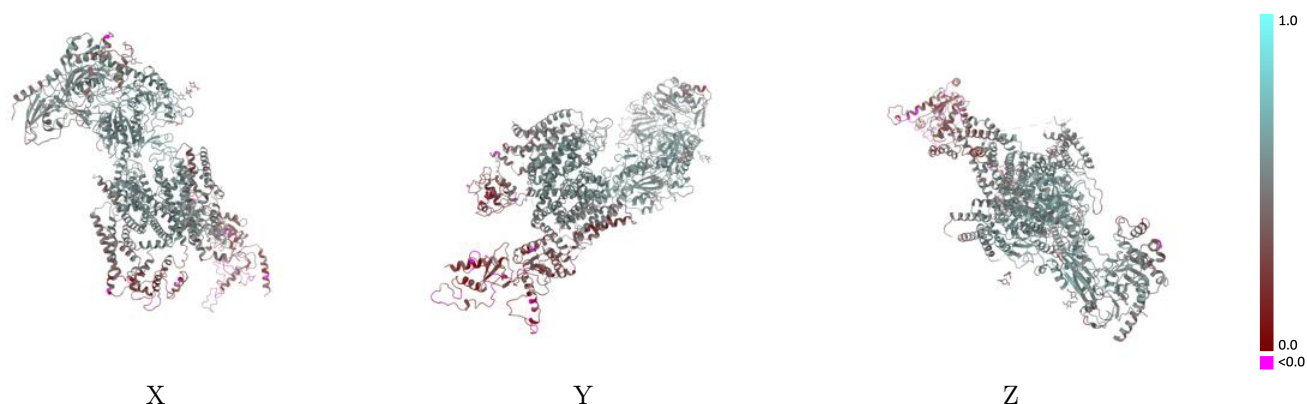
This section contains information regarding the fit between EMDB map EMD-27909 and PDB model 8E5B. Per-residue inclusion information can be found in section [3](#) on page [8](#).

9.1 Map-model overlay [i](#)



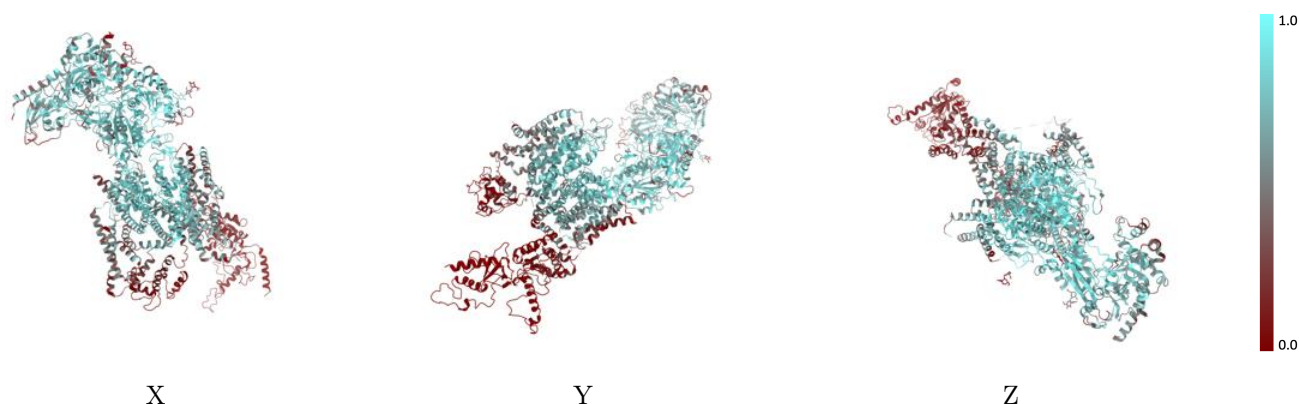
The images above show the 3D surface view of the map at the recommended contour level 0.025 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



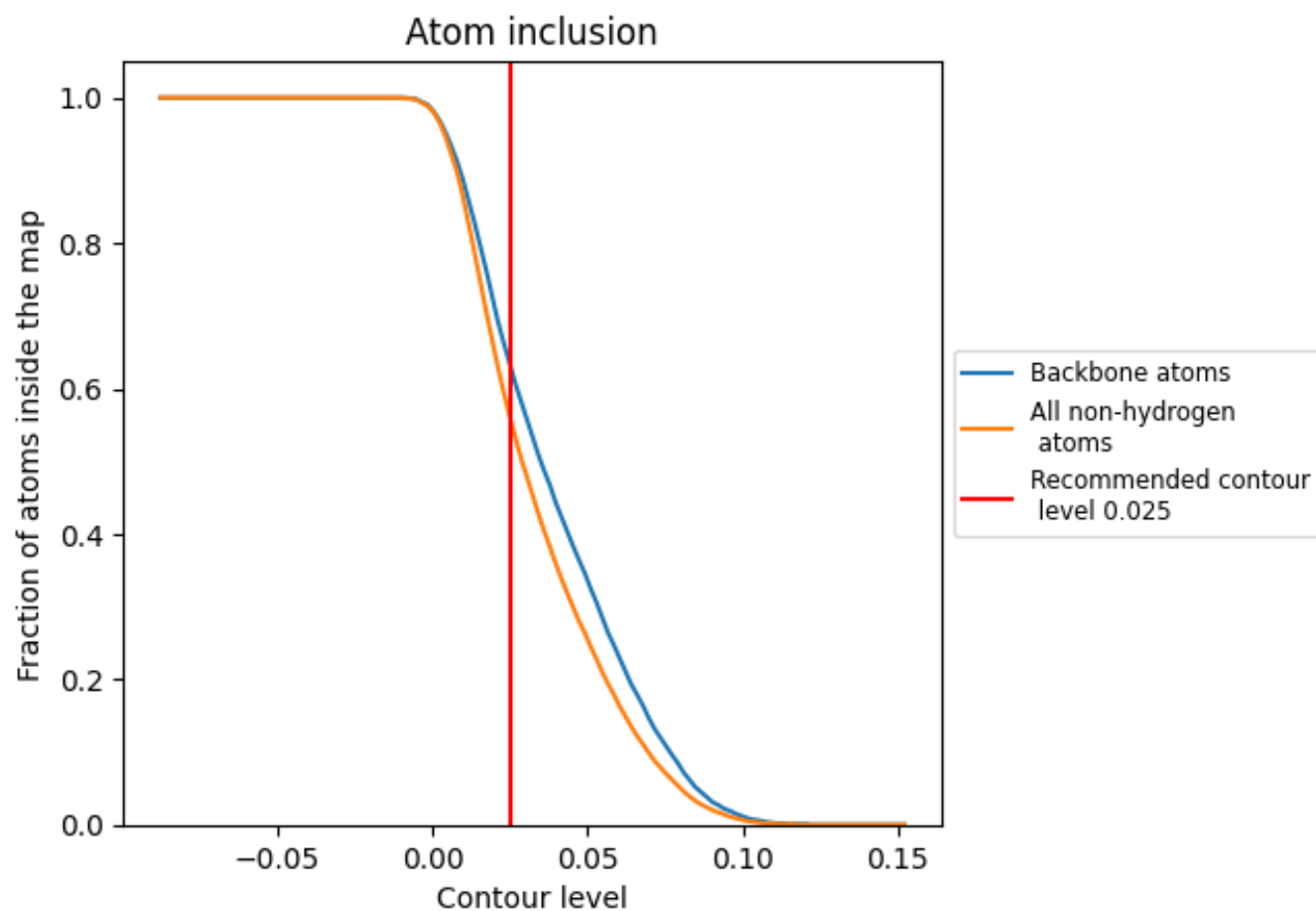
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.025).

9.4 Atom inclusion [i](#)



At the recommended contour level, 63% of all backbone atoms, 56% 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 (0.025) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5600	0.4670
A	0.5770	0.4800
B	0.3570	0.3880
C	0.0430	0.2340
D	0.7160	0.5310
E	0.1430	0.3180
F	0.5000	0.4650
G	0.3570	0.3770
H	0.4640	0.4610

1.0

0.0

<0.0