



wwPDB EM Validation Summary Report ⓘ

May 5, 2025 – 01:43 pm BST

PDB ID : 9GU1 / pdb_00009gu1
EMDB ID : EMD-51569
Title : Human adult muscle nAChR in resting state in nanodisc with alpha-bungarotoxin
Authors : Li, A.; Pike, A.C.W.; Chi, G.; Webster, R.; Maxwell, S.; Liu, W.; Beeson, D.; Sauer, D.B.; Dong, Y.Y.
Deposited on : 2024-09-18
Resolution : 2.48 Å (reported)
Based on initial model : .

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev118
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0rc1
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.43.1

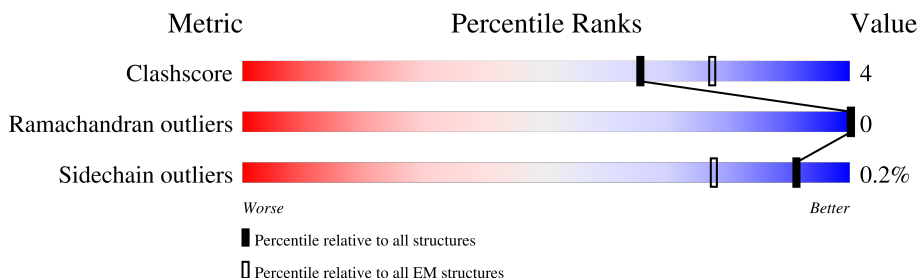
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.48 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.






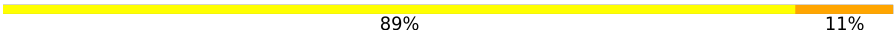
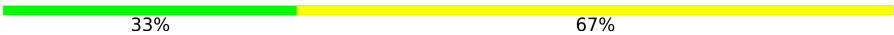


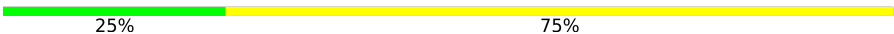
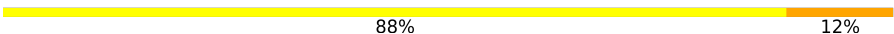
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	437	<div> <div>7%</div> <div>67%</div> <div>9%</div> <div>23%</div> </div>
1	L	437	<div> <div>7%</div> <div>70%</div> <div>7%</div> <div>23%</div> </div>
2	B	478	<div> <div>5%</div> <div>67%</div> <div>5%</div> <div>27%</div> </div>
3	C	213	<div> <div>13%</div> <div>93%</div> <div>6%</div> <div>.</div> </div>
3	G	213	<div> <div>22%</div> <div>88%</div> <div>10%</div> <div>.</div> </div>
4	D	496	<div> <div>5%</div> <div>65%</div> <div>9%</div> <div>25%</div> </div>
5	E	721	<div> <div>.</div> <div>44%</div> <div>5%</div> <div>51%</div> </div>
6	F	219	<div> <div>7%</div> <div>88%</div> <div>10%</div> <div>.</div> </div>

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Mol	Chain	Length	Quality of chain
6	H	219	
7	I	74	
7	J	74	
8	K	9	
9	M	3	
10	N	6	
11	O	2	
12	P	4	
13	Q	8	

2 Entry composition

There are 16 unique types of molecules in this entry. The entry contains 21896 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 Acetylcholine receptor subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	336	Total	C	N	O	S	0	0
			2665	1750	423	478	14		
1	L	337	Total	C	N	O	S	0	0
			2615	1709	420	474	12		

- Molecule 2 is a protein called Acetylcholine receptor subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	347	Total	C	N	O	S	0	0
			2756	1807	444	496	9		

- Molecule 3 is a protein called Fab35 light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	210	Total	C	N	O	S	0	0
			1575	989	258	322	6		
3	G	210	Total	C	N	O	S	0	0
			1568	986	258	318	6		

- Molecule 4 is a protein called Acetylcholine receptor subunit delta.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	371	Total	C	N	O	S	0	0
			2992	1962	492	526	12		

- Molecule 5 is a protein called Acetylcholine receptor subunit epsilon, Green fluorescent protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	355	Total	C	N	O	S	0	0
			2765	1805	442	508	10		

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	312H	ALA	-	linker	UNP Q04844
E	312I	PRO	-	linker	UNP Q04844
E	312J	PRO	-	linker	UNP Q04844
E	312K	VAL	-	linker	UNP Q04844
E	312L	ALA	-	linker	UNP Q04844
E	312M	THR	-	linker	UNP Q04844
E	312N	MET	-	linker	UNP Q04844
E	312O	VAL	-	linker	UNP Q04844
E	314Z	LEU	PHE	conflict	UNP P42212
E	315A	THR	SER	conflict	UNP P42212
E	321K	LEU	HIS	conflict	UNP P42212

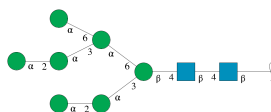
- Molecule 6 is a protein called Fab35 heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	214	Total	C	N	O	S	0	0
			1596	1009	272	307	8		
6	H	214	Total	C	N	O	S	0	0
			1590	1006	269	307	8		

- Molecule 7 is a protein called Alpha-bungarotoxin.

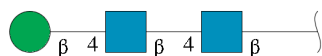
Mol	Chain	Residues	Atoms					AltConf	Trace
7	I	73	Total	C	N	O	S	0	0
			536	330	92	103	11		
7	J	73	Total	C	N	O	S	0	0
			536	330	92	103	11		

- Molecule 8 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



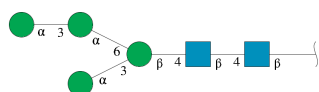
Mol	Chain	Residues	Atoms				AltConf	Trace
8	K	9	Total	C	N	O	0	0
			105	58	2	45		

- Molecule 9 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				AltConf	Trace
9	M	3	Total	C	N	O	0	0
			39	22	2	15		

- Molecule 10 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				AltConf	Trace
10	N	6	Total	C	N	O	0	0
			72	40	2	30		

- Molecule 11 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



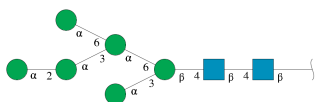
Mol	Chain	Residues	Atoms				AltConf	Trace
11	O	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 12 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



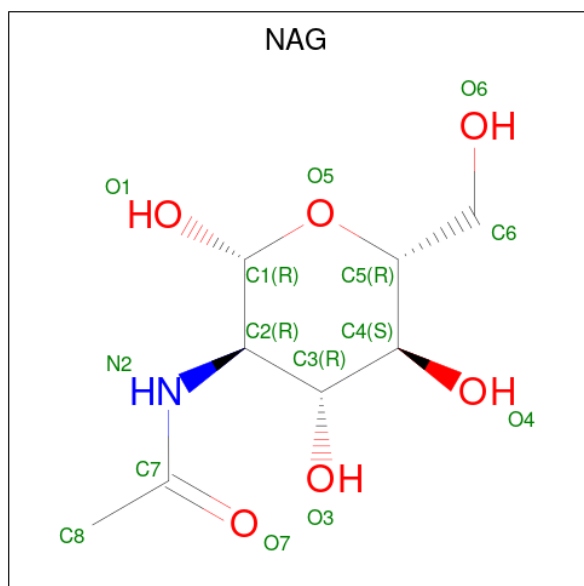
Mol	Chain	Residues	Atoms				AltConf	Trace
12	P	4	Total	C	N	O	0	0
			50	28	2	20		

- Molecule 13 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				AltConf	Trace
13	Q	8	Total	C	N	O	0	0
			94	52	2	40		

- Molecule 14 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



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

- Molecule 15 is COPPER (II) ION (CCD ID: CU) (formula: Cu).

Mol	Chain	Residues	Atoms		AltConf
15	L	1	Total	Cu	0
			1	1	

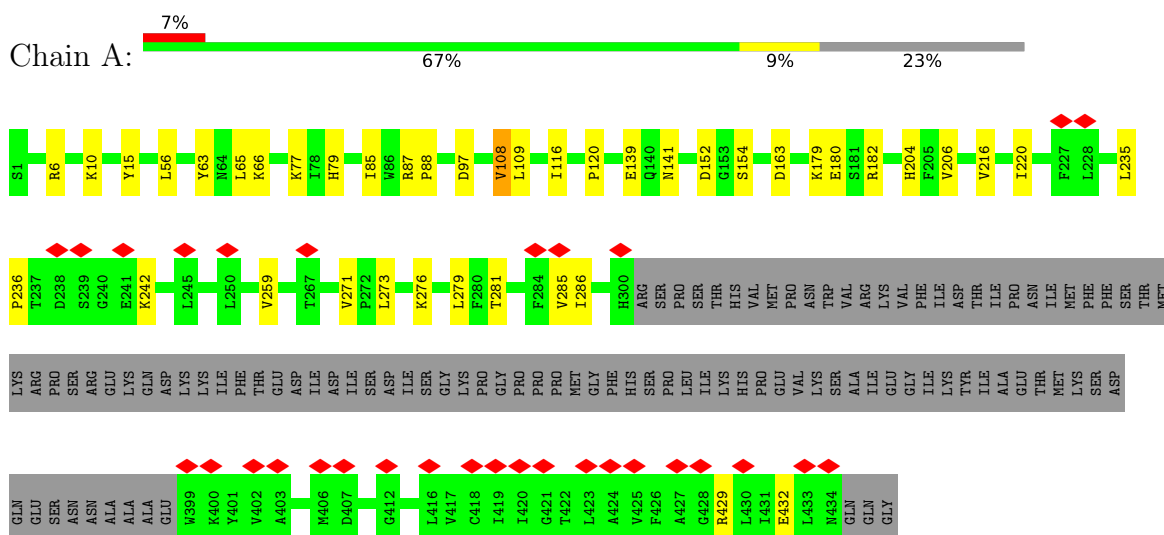
- Molecule 16 is water.

Mol	Chain	Residues	Atoms		AltConf
16	A	67	Total 67	O 67	0
16	B	36	Total 36	O 36	0
16	C	6	Total 6	O 6	0
16	D	45	Total 45	O 45	0
16	E	71	Total 71	O 71	0
16	F	7	Total 7	O 7	0
16	G	1	Total 1	O 1	0
16	H	5	Total 5	O 5	0
16	I	1	Total 1	O 1	0
16	J	1	Total 1	O 1	0
16	L	59	Total 59	O 59	0

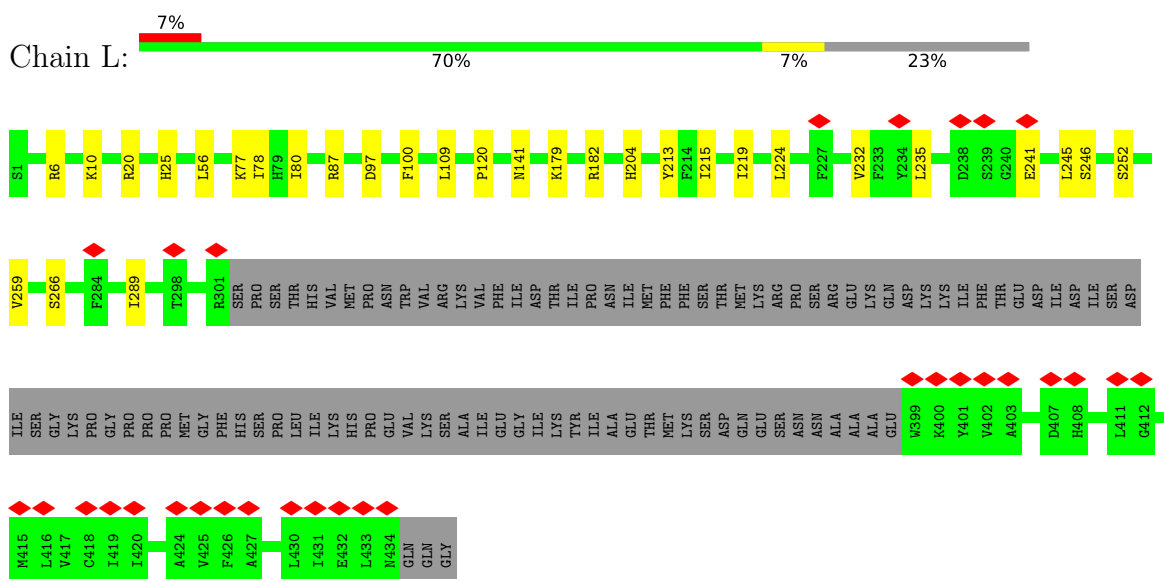
3 Residue-property plots

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

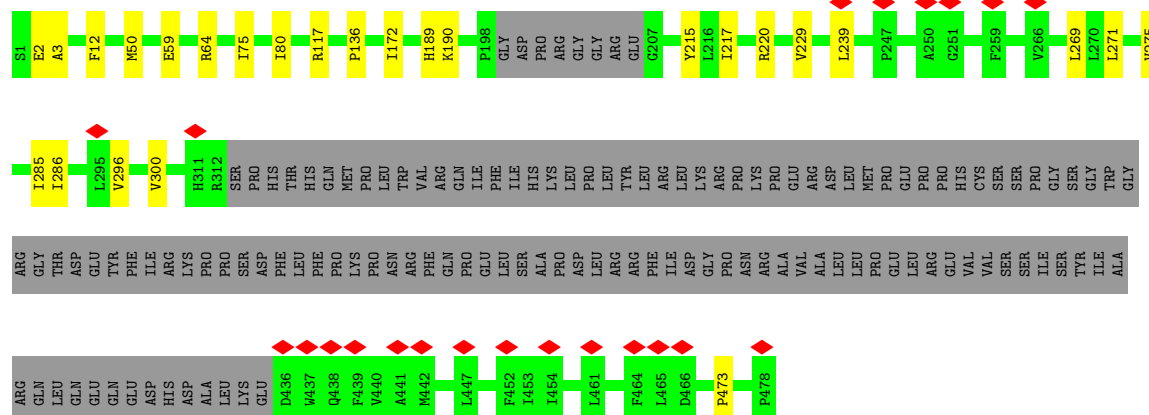
• Molecule 1: Acetylcholine receptor subunit alpha



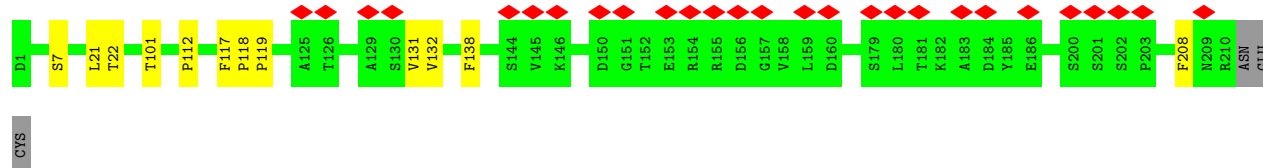
• Molecule 1: Acetylcholine receptor subunit alpha



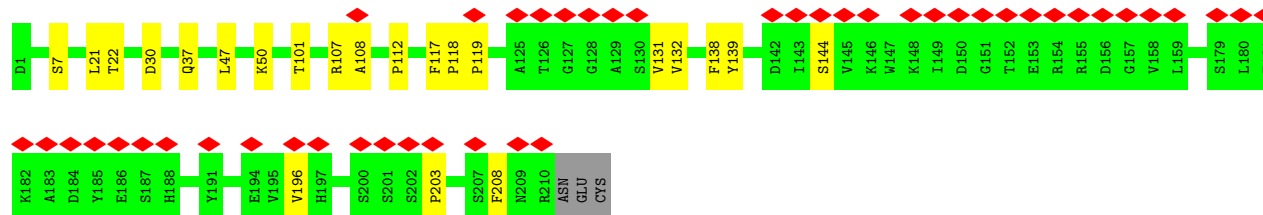
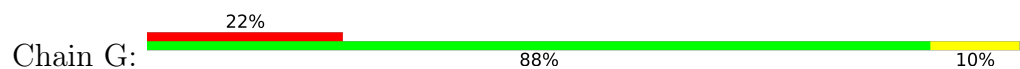
• Molecule 2: Acetylcholine receptor subunit beta



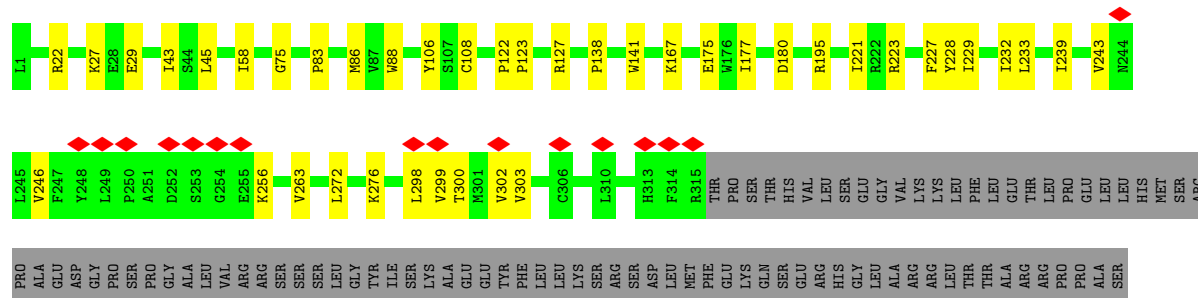
• Molecule 3: Fab35 light chain



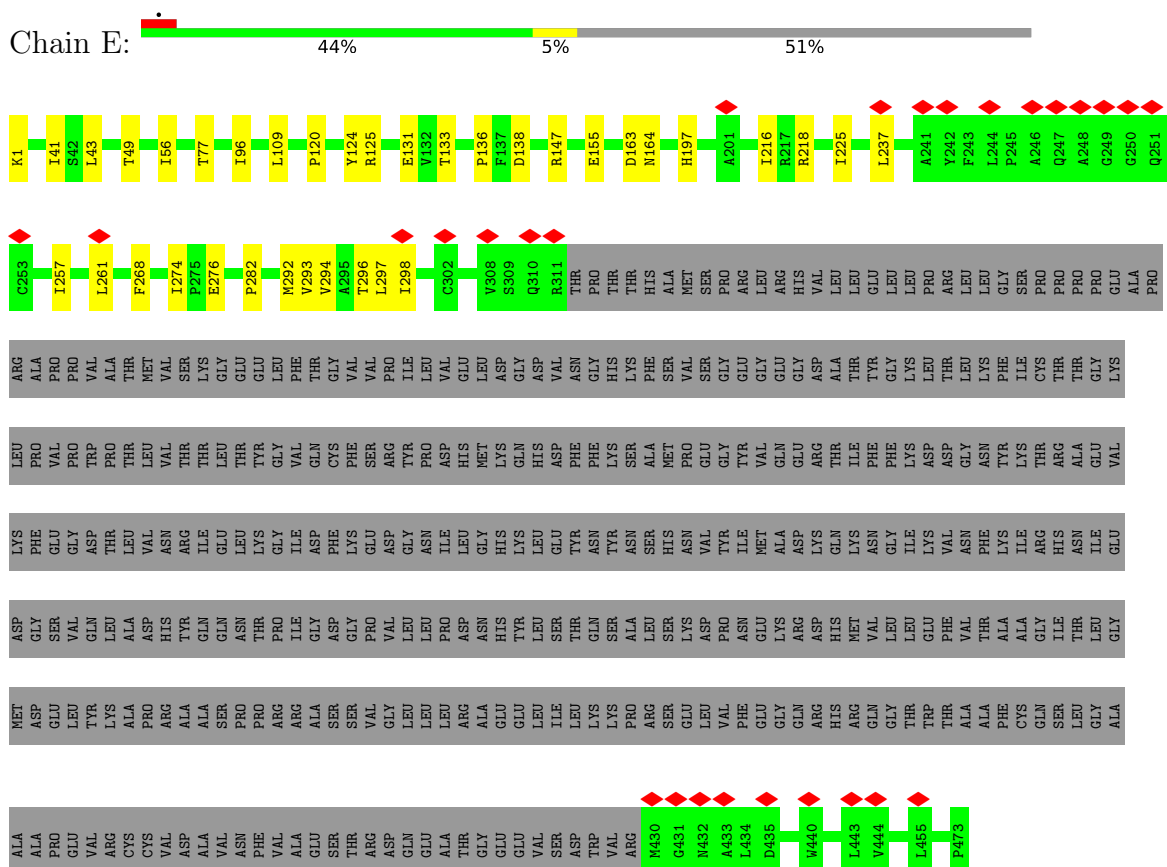
• Molecule 3: Fab35 light chain



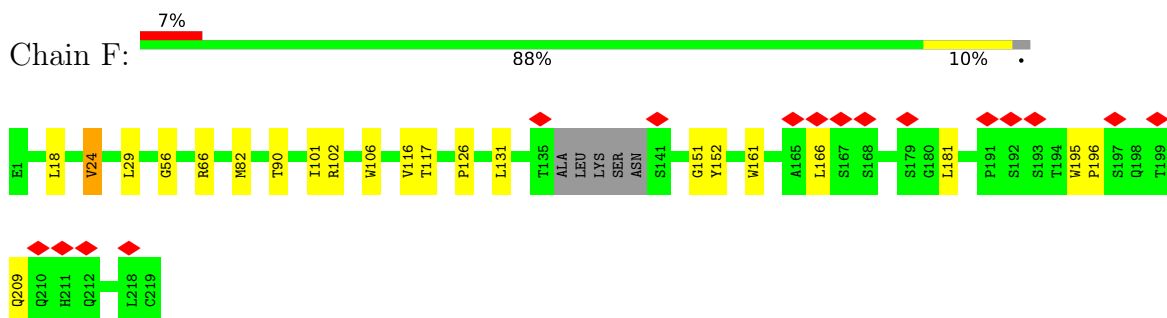
• Molecule 4: Acetylcholine receptor subunit delta



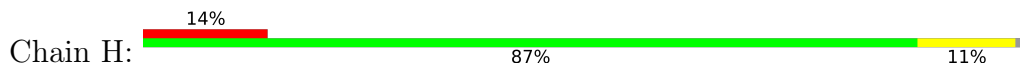
- Molecule 5: Acetylcholine receptor subunit epsilon, Green fluorescent protein.

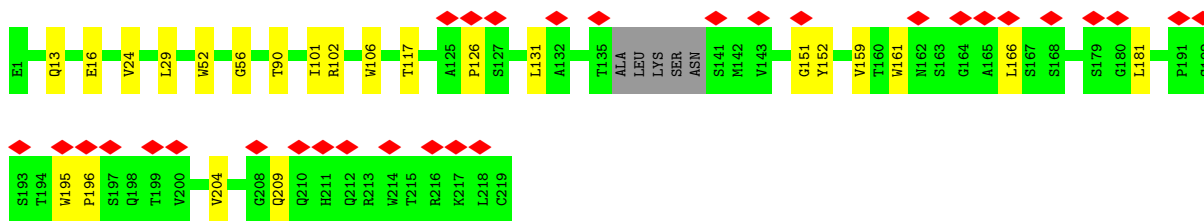


- Molecule 6: Fab35 heavy chain



- Molecule 6: Fab35 heavy chain





• Molecule 7: Alpha-bungarotoxin

Chain I: 92% 7% .



• Molecule 7: Alpha-bungarotoxin

Chain J: 89% 9% .



• Molecule 8: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain K: 89% 11%



• Molecule 9: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain M: 33% 67%



• Molecule 10: alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain N: 50% 50%



• Molecule 11: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain O:  100%



MAG1
MAG2

- Molecule 12: α -D-mannopyranose-(1-3)- β -D-mannopyranose-(1-4)-2-acetamido-2-deoxy- β -D-glucopyranose-(1-4)-2-acetamido-2-deoxy- β -D-glucopyranose

Chain P:  25%  75%

MAG1
MAG2
EM13
MAN4

- Molecule 13: α -D-mannopyranose-(1-2)- α -D-mannopyranose-(1-3)-[α -D-mannopyranose-(1-6)] α -D-mannopyranose-(1-6)-[α -D-mannopyranose-(1-3)] β -D-mannopyranose-(1-4)-2-acetamido-2-deoxy- β -D-glucopyranose-(1-4)-2-acetamido-2-deoxy- β -D-glucopyranose

Chain Q:  88%  12%

MAG1
MAG2
EM13
MAN4
MAN5
MAN6
MAN7
MAN8

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	319381	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	45	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	1.622	Depositor
Minimum map value	-0.857	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.025	Depositor
Recommended contour level	0.14	Depositor
Map size (Å)	404.35202, 404.35202, 404.35202	wwPDB
Map dimensions	486, 486, 486	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.832, 0.832, 0.832	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: BMA, CU, MAN, NAG

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	0/2733	0.38	0/3734
1	L	0.26	0/2680	0.35	0/3666
2	B	0.22	0/2829	0.34	0/3863
3	C	0.19	0/1607	0.39	0/2193
3	G	0.17	0/1600	0.35	0/2184
4	D	0.24	0/3076	0.36	0/4203
5	E	0.24	0/2834	0.34	0/3882
6	F	0.18	0/1637	0.39	0/2243
6	H	0.17	0/1631	0.38	0/2236
7	I	0.18	0/550	0.46	0/751
7	J	0.19	0/550	0.41	0/751
All	All	0.22	0/21727	0.37	0/29706

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 [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	2665	0	2670	32	0
1	L	2615	0	2563	24	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	2756	0	2750	17	0
3	C	1575	0	1497	8	0
3	G	1568	0	1491	16	0
4	D	2992	0	2996	29	0
5	E	2765	0	2712	25	0
6	F	1596	0	1526	12	0
6	H	1590	0	1515	13	0
7	I	536	0	507	3	0
7	J	536	0	507	4	0
8	K	105	0	88	1	0
9	M	39	0	34	2	0
10	N	72	0	61	2	0
11	O	28	0	25	0	0
12	P	50	0	43	0	0
13	Q	94	0	79	1	0
14	D	14	0	13	1	0
15	L	1	0	0	0	0
16	A	67	0	0	4	0
16	B	36	0	0	2	0
16	C	6	0	0	0	0
16	D	45	0	0	1	0
16	E	71	0	0	4	0
16	F	7	0	0	1	0
16	G	1	0	0	0	0
16	H	5	0	0	1	0
16	I	1	0	0	0	0
16	J	1	0	0	0	0
16	L	59	0	0	2	0
All	All	21896	0	21077	161	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 4.

The worst 5 of 161 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:489:ASN:ND2	4:D:491:GLN:OE1	2.24	0.70
3:C:132:VAL:HG11	6:F:131:LEU:HD13	1.74	0.68
1:A:66:LYS:NZ	3:G:30:ASP:OD2	2.27	0.68
5:E:124:TYR:OH	16:E:501:HOH:O	2.11	0.68
1:A:139:GLU:OE1	1:A:179:LYS:NZ	2.25	0.66

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	332/437 (76%)	323 (97%)	9 (3%)	0	100	100
1	L	333/437 (76%)	322 (97%)	11 (3%)	0	100	100
2	B	341/478 (71%)	331 (97%)	10 (3%)	0	100	100
3	C	208/213 (98%)	202 (97%)	6 (3%)	0	100	100
3	G	208/213 (98%)	202 (97%)	6 (3%)	0	100	100
4	D	367/496 (74%)	359 (98%)	8 (2%)	0	100	100
5	E	351/721 (49%)	341 (97%)	10 (3%)	0	100	100
6	F	210/219 (96%)	202 (96%)	8 (4%)	0	100	100
6	H	210/219 (96%)	202 (96%)	8 (4%)	0	100	100
7	I	71/74 (96%)	70 (99%)	1 (1%)	0	100	100
7	J	71/74 (96%)	69 (97%)	2 (3%)	0	100	100
All	All	2702/3581 (76%)	2623 (97%)	79 (3%)	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	301/402 (75%)	300 (100%)	1 (0%)	91	96

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	L	286/402 (71%)	286 (100%)	0	100	100
2	B	308/434 (71%)	308 (100%)	0	100	100
3	C	174/189 (92%)	174 (100%)	0	100	100
3	G	172/189 (91%)	172 (100%)	0	100	100
4	D	333/452 (74%)	333 (100%)	0	100	100
5	E	300/626 (48%)	299 (100%)	1 (0%)	91	96
6	F	174/191 (91%)	172 (99%)	2 (1%)	70	86
6	H	173/191 (91%)	172 (99%)	1 (1%)	84	93
7	I	63/65 (97%)	63 (100%)	0	100	100
7	J	63/65 (97%)	63 (100%)	0	100	100
All	All	2347/3206 (73%)	2342 (100%)	5 (0%)	91	97

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	108	VAL
5	E	197	HIS
6	F	24	VAL
6	F	209	GLN
6	H	209	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 22 such sidechains are listed below:

Mol	Chain	Res	Type
6	F	203	ASN
6	H	203	ASN
6	H	86	GLN
7	I	4	HIS
2	B	210	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

32 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
8	NAG	K	1	1,8	14,14,15	0.85	0	17,19,21	1.18	1 (5%)
8	NAG	K	2	8	14,14,15	0.82	0	17,19,21	1.09	2 (11%)
8	BMA	K	3	8	11,11,12	0.85	0	15,15,17	1.42	2 (13%)
8	MAN	K	4	8	11,11,12	0.82	0	15,15,17	1.30	3 (20%)
8	MAN	K	5	8	11,11,12	0.81	0	15,15,17	1.45	2 (13%)
8	MAN	K	6	8	11,11,12	0.83	1 (9%)	15,15,17	0.99	0
8	MAN	K	7	8	11,11,12	0.72	0	15,15,17	1.21	1 (6%)
8	MAN	K	8	8	11,11,12	0.82	1 (9%)	15,15,17	1.16	1 (6%)
8	MAN	K	9	8	11,11,12	0.78	0	15,15,17	1.04	1 (6%)
9	NAG	M	1	2,9	14,14,15	0.75	0	17,19,21	0.88	0
9	NAG	M	2	9	14,14,15	0.72	0	17,19,21	0.87	0
9	BMA	M	3	9	11,11,12	0.82	0	15,15,17	1.26	1 (6%)
10	NAG	N	1	10,4	14,14,15	0.82	0	17,19,21	1.08	2 (11%)
10	NAG	N	2	10	14,14,15	0.78	0	17,19,21	0.97	1 (5%)
10	BMA	N	3	10	11,11,12	0.85	0	15,15,17	1.52	2 (13%)
10	MAN	N	4	10	11,11,12	0.71	0	15,15,17	1.19	1 (6%)
10	MAN	N	5	10	11,11,12	0.74	0	15,15,17	1.11	1 (6%)
10	MAN	N	6	10	11,11,12	0.72	0	15,15,17	1.15	1 (6%)
11	NAG	O	1	11,5	14,14,15	0.75	0	17,19,21	0.79	0
11	NAG	O	2	11	14,14,15	0.71	0	17,19,21	0.81	0
12	NAG	P	1	5,12	14,14,15	0.82	0	17,19,21	1.09	2 (11%)
12	NAG	P	2	12	14,14,15	0.70	0	17,19,21	0.78	0
12	BMA	P	3	12	11,11,12	0.97	1 (9%)	15,15,17	1.71	4 (26%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
12	MAN	P	4	12	11,11,12	0.70	0	15,15,17	1.23	1 (6%)
13	NAG	Q	1	1,13	14,14,15	0.87	1 (7%)	17,19,21	1.14	1 (5%)
13	NAG	Q	2	13	14,14,15	0.83	0	17,19,21	1.07	2 (11%)
13	BMA	Q	3	13	11,11,12	0.84	0	15,15,17	1.30	1 (6%)
13	MAN	Q	4	13	11,11,12	0.78	0	15,15,17	1.41	2 (13%)
13	MAN	Q	5	13	11,11,12	0.85	0	15,15,17	1.25	1 (6%)
13	MAN	Q	6	13	11,11,12	0.75	0	15,15,17	1.22	1 (6%)
13	MAN	Q	7	13	11,11,12	0.77	0	15,15,17	1.02	1 (6%)
13	MAN	Q	8	13	11,11,12	0.83	1 (9%)	15,15,17	0.99	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
8	NAG	K	1	1,8	-	3/6/23/26	0/1/1/1
8	NAG	K	2	8	-	0/6/23/26	0/1/1/1
8	BMA	K	3	8	-	0/2/19/22	0/1/1/1
8	MAN	K	4	8	-	0/2/19/22	0/1/1/1
8	MAN	K	5	8	-	0/2/19/22	0/1/1/1
8	MAN	K	6	8	-	0/2/19/22	0/1/1/1
8	MAN	K	7	8	-	0/2/19/22	0/1/1/1
8	MAN	K	8	8	-	0/2/19/22	0/1/1/1
8	MAN	K	9	8	-	2/2/19/22	0/1/1/1
9	NAG	M	1	2,9	-	0/6/23/26	0/1/1/1
9	NAG	M	2	9	-	0/6/23/26	0/1/1/1
9	BMA	M	3	9	-	0/2/19/22	0/1/1/1
10	NAG	N	1	10,4	-	3/6/23/26	0/1/1/1
10	NAG	N	2	10	-	2/6/23/26	0/1/1/1
10	BMA	N	3	10	-	1/2/19/22	0/1/1/1
10	MAN	N	4	10	-	0/2/19/22	0/1/1/1
10	MAN	N	5	10	-	2/2/19/22	0/1/1/1
10	MAN	N	6	10	-	1/2/19/22	0/1/1/1
11	NAG	O	1	11,5	-	0/6/23/26	0/1/1/1
11	NAG	O	2	11	-	0/6/23/26	0/1/1/1
12	NAG	P	1	5,12	-	0/6/23/26	0/1/1/1
12	NAG	P	2	12	-	0/6/23/26	0/1/1/1
12	BMA	P	3	12	-	1/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
12	MAN	P	4	12	-	2/2/19/22	0/1/1/1
13	NAG	Q	1	1,13	-	4/6/23/26	0/1/1/1
13	NAG	Q	2	13	-	1/6/23/26	0/1/1/1
13	BMA	Q	3	13	-	0/2/19/22	0/1/1/1
13	MAN	Q	4	13	-	0/2/19/22	0/1/1/1
13	MAN	Q	5	13	-	0/2/19/22	0/1/1/1
13	MAN	Q	6	13	-	0/2/19/22	0/1/1/1
13	MAN	Q	7	13	-	2/2/19/22	0/1/1/1
13	MAN	Q	8	13	-	0/2/19/22	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	P	3	BMA	C2-C3	2.42	1.56	1.52
8	K	6	MAN	O5-C1	-2.11	1.40	1.43
8	K	8	MAN	O5-C1	-2.11	1.40	1.43
13	Q	8	MAN	O5-C1	-2.07	1.40	1.43
13	Q	1	NAG	O5-C1	-2.01	1.40	1.43

The worst 5 of 38 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	N	3	BMA	C1-O5-C5	4.85	118.77	112.19
8	K	3	BMA	C1-O5-C5	3.98	117.58	112.19
8	K	5	MAN	C1-O5-C5	3.90	117.48	112.19
13	Q	4	MAN	C1-O5-C5	3.82	117.36	112.19
12	P	4	MAN	C1-O5-C5	3.68	117.18	112.19

There are no chirality outliers.

5 of 24 torsion outliers are listed below:

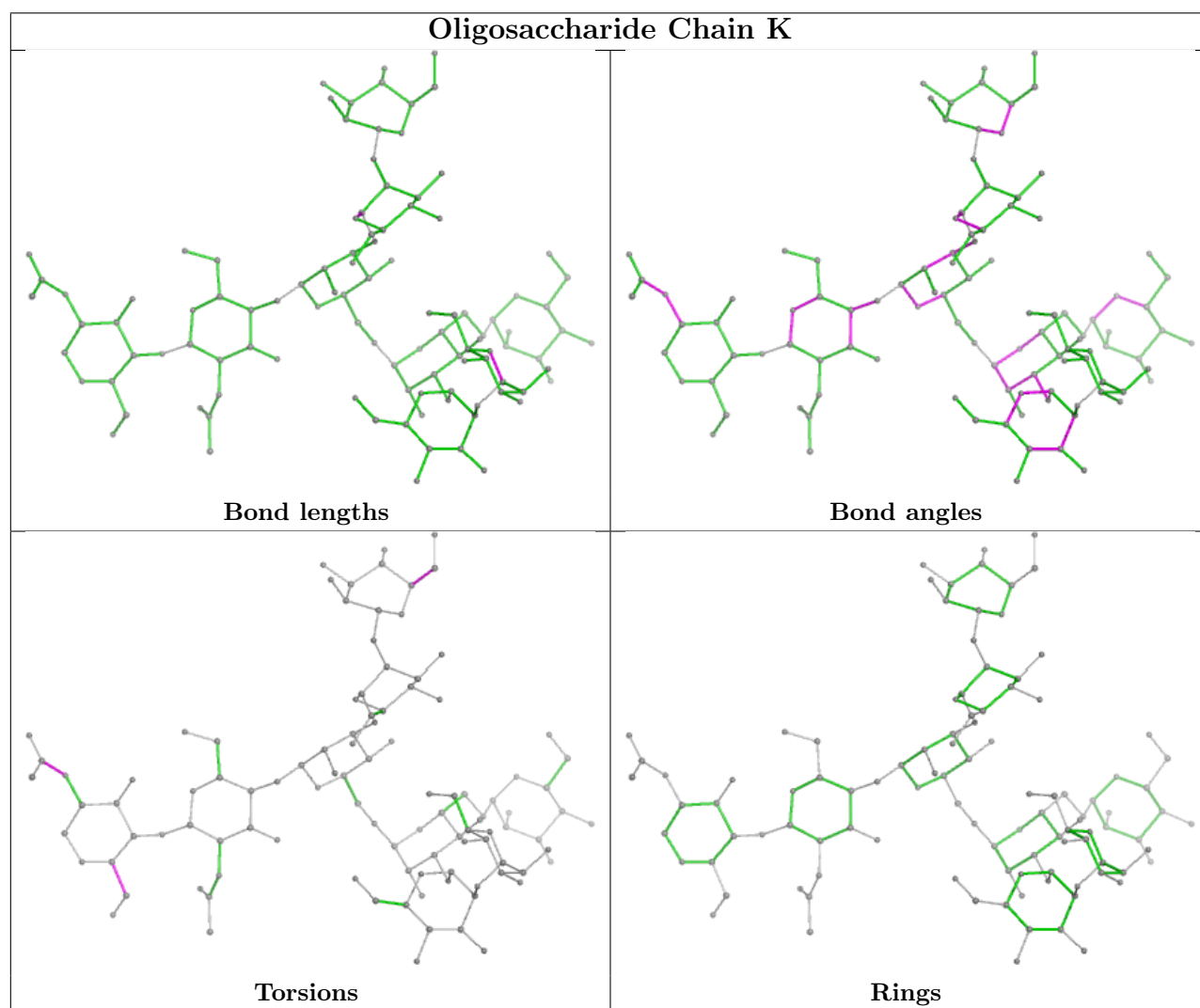
Mol	Chain	Res	Type	Atoms
13	Q	7	MAN	C4-C5-C6-O6
13	Q	7	MAN	O5-C5-C6-O6
13	Q	1	NAG	O5-C5-C6-O6
8	K	9	MAN	O5-C5-C6-O6
13	Q	1	NAG	C4-C5-C6-O6

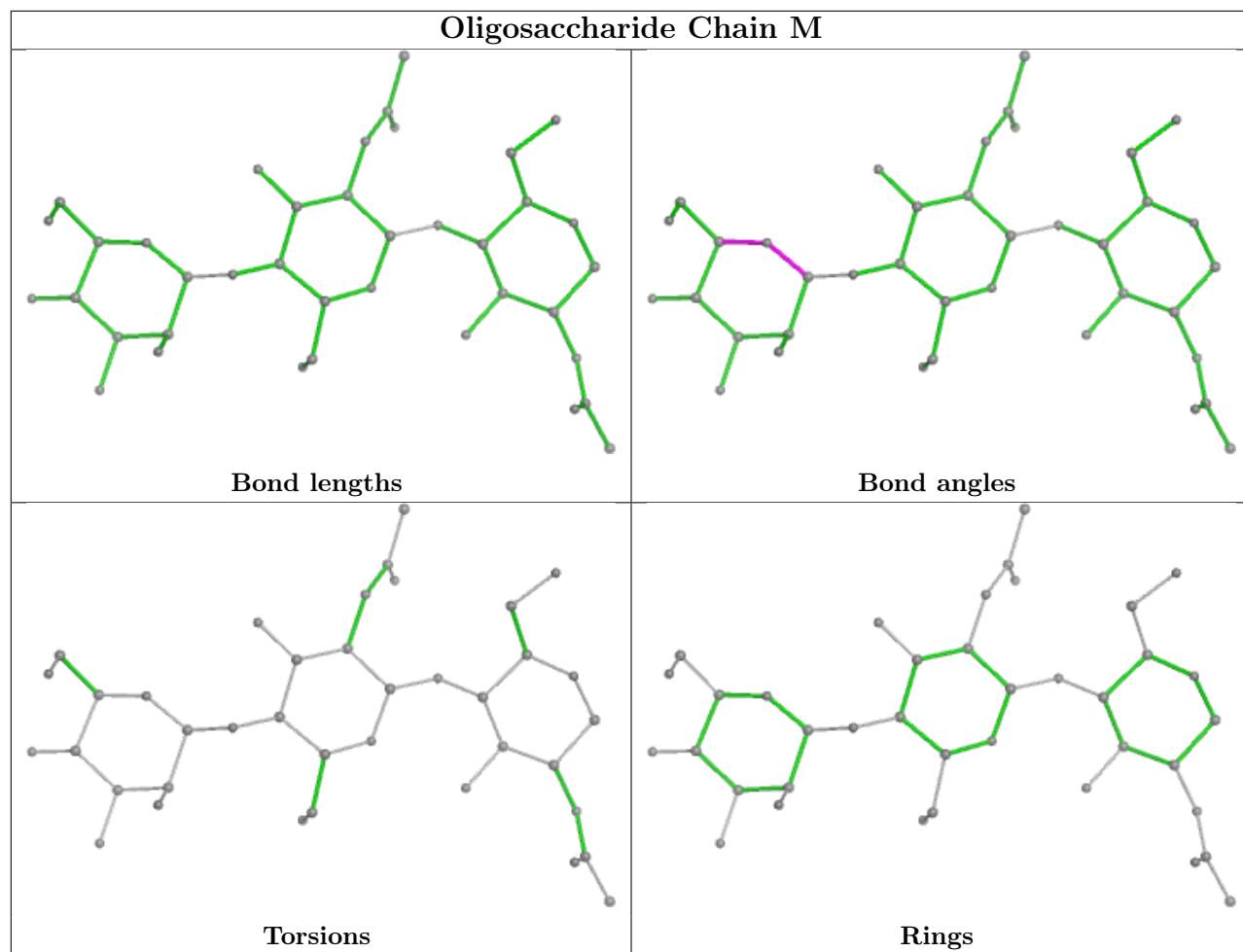
There are no ring outliers.

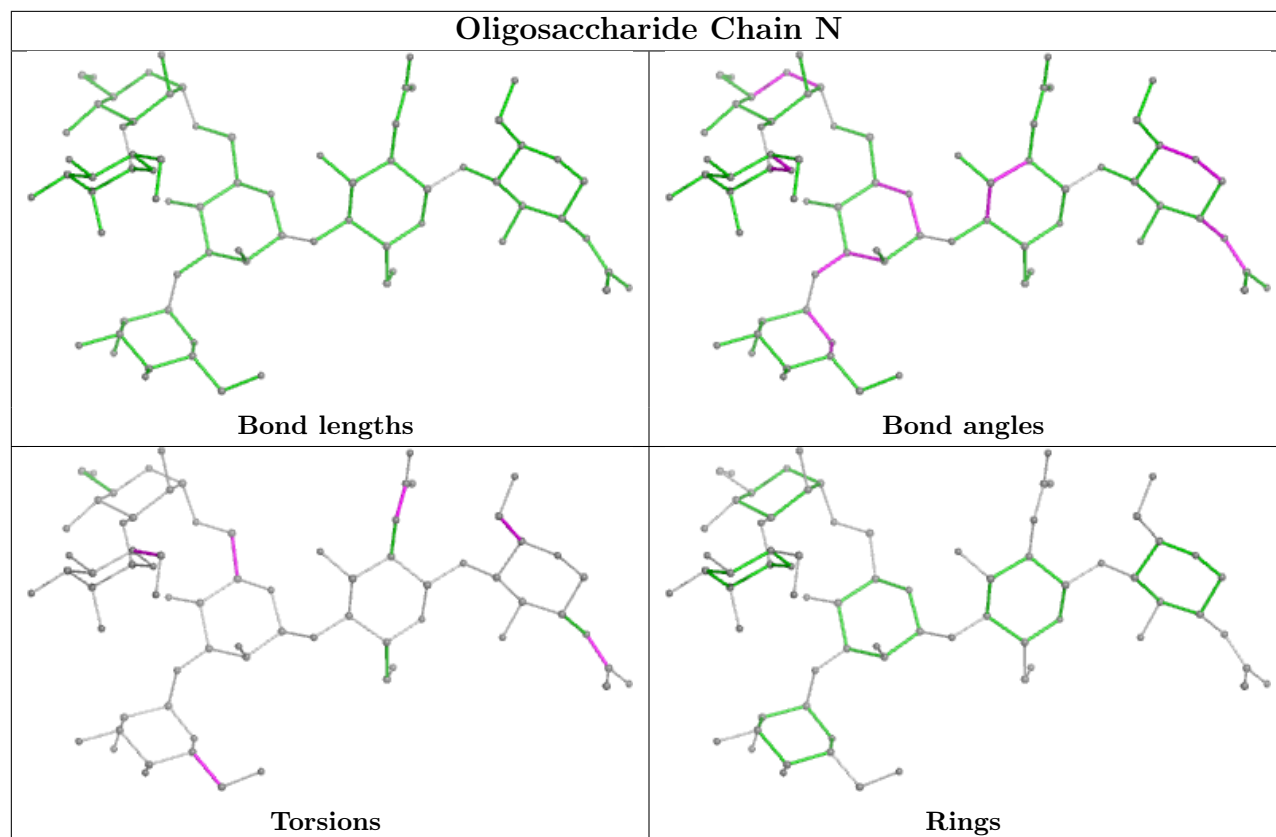
6 monomers are involved in 6 short contacts:

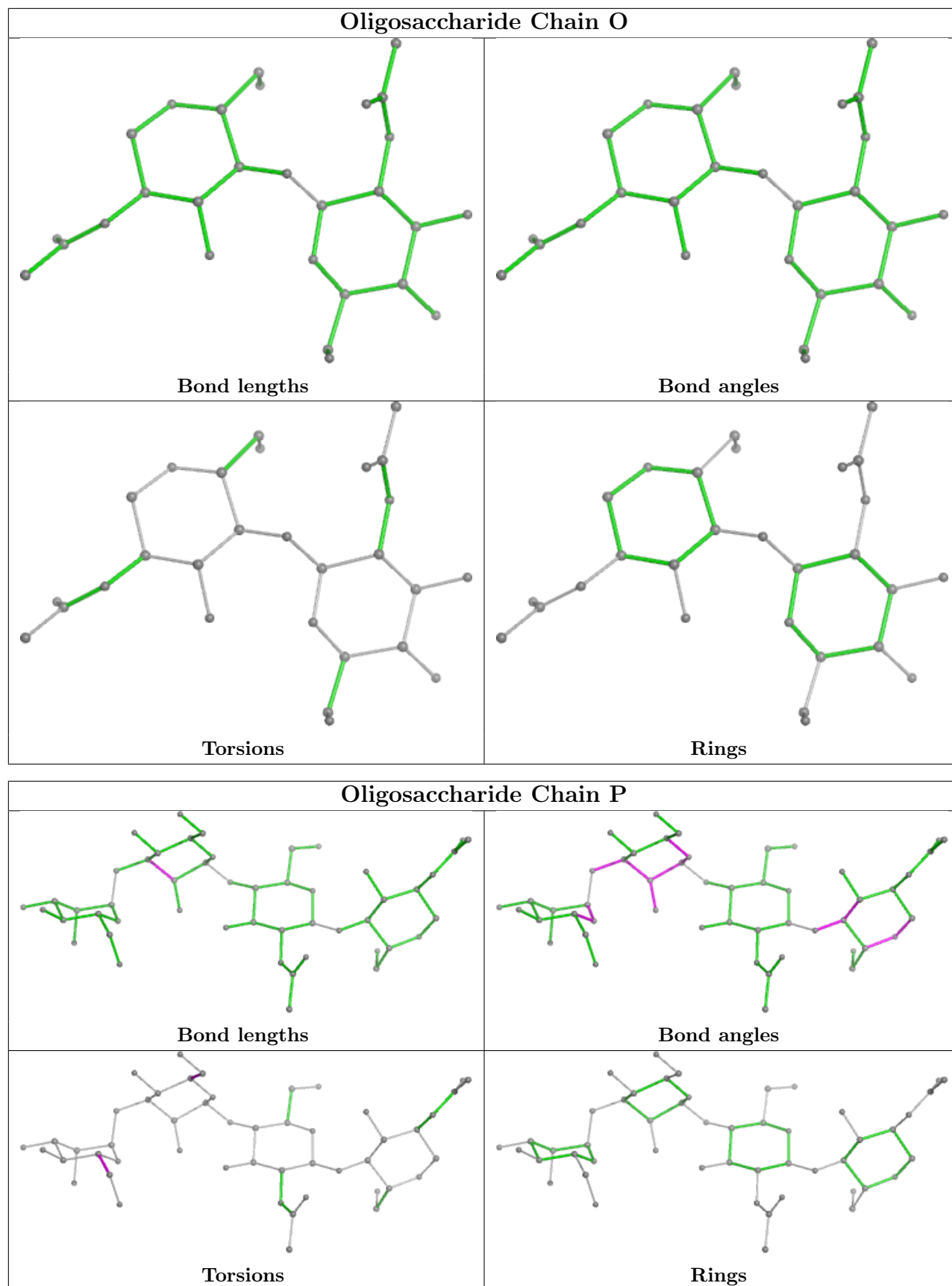
Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	M	1	NAG	2	0
10	N	3	BMA	1	0
10	N	4	MAN	1	0
13	Q	1	NAG	1	0
8	K	1	NAG	1	0
10	N	1	NAG	1	0

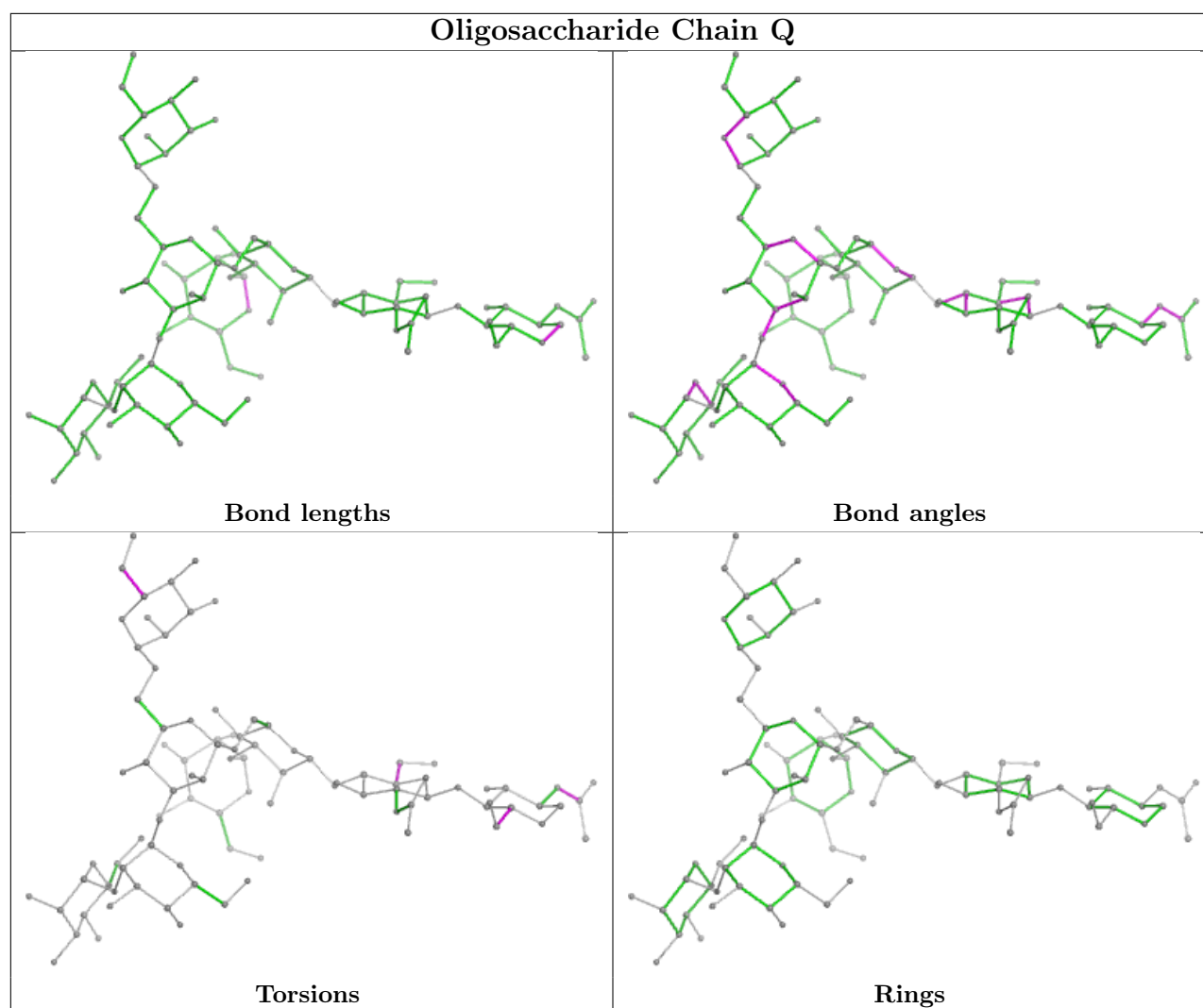
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.











5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 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	$\# Z > 2$
14	NAG	D	501	4	14,14,15	0.71	0	17,19,21	1.54	3 (17%)

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
14	NAG	D	501	4	-	1/6/23/26	0/1/1/1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	D	501	NAG	C2-N2-C7	4.17	128.84	122.90
14	D	501	NAG	C1-O5-C5	2.37	115.40	112.19
14	D	501	NAG	C1-C2-N2	2.11	114.09	110.49

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
14	D	501	NAG	C1-C2-N2-C7

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
14	D	501	NAG	1	0

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.

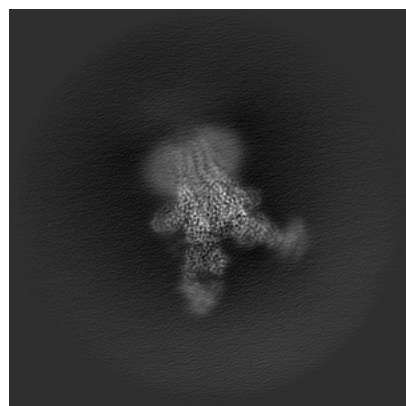
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-51569. These allow visual inspection of the internal detail of the map and identification of artifacts.

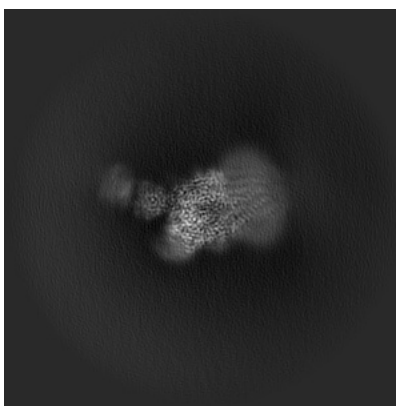
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

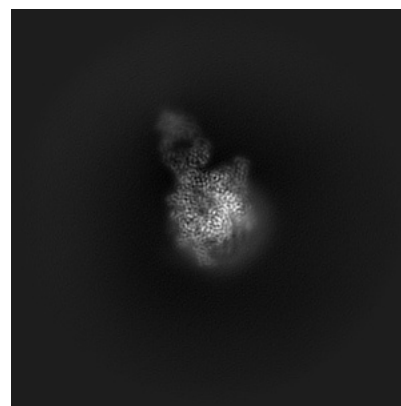
6.1.1 Primary map



X

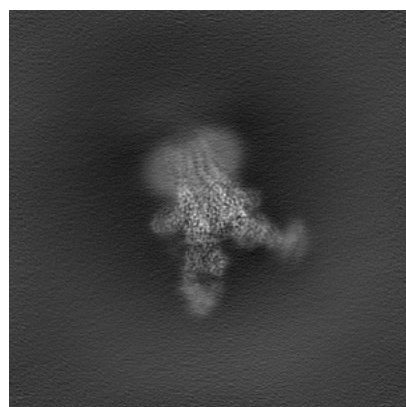


Y

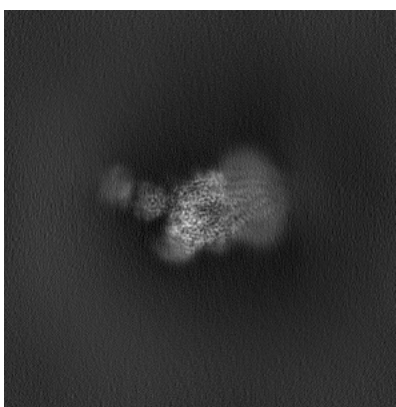


Z

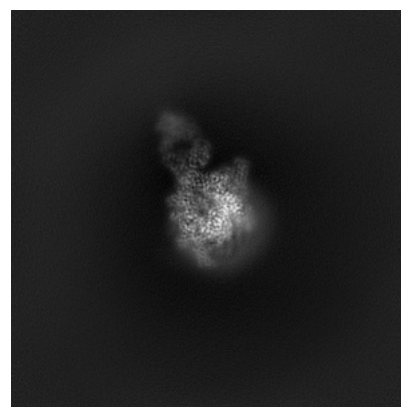
6.1.2 Raw map



X



Y

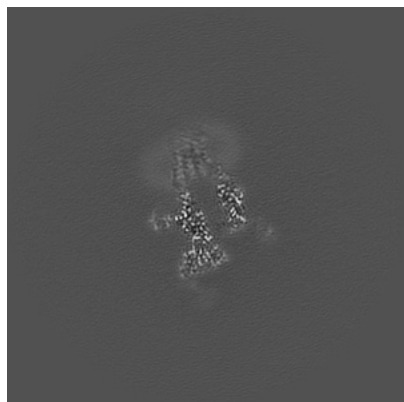


Z

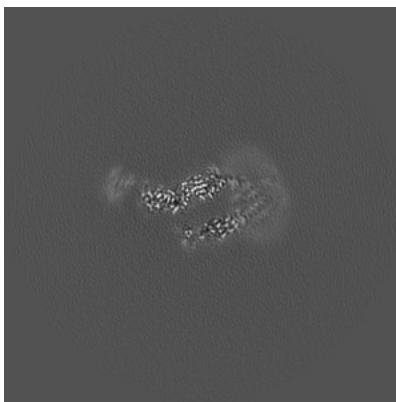
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

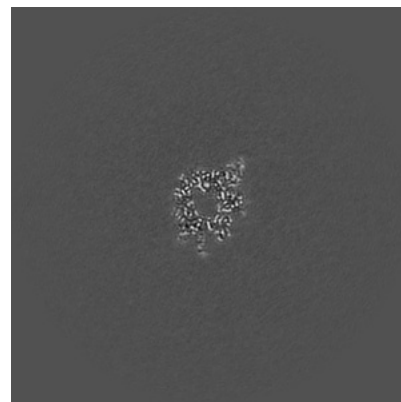
6.2.1 Primary map



X Index: 243

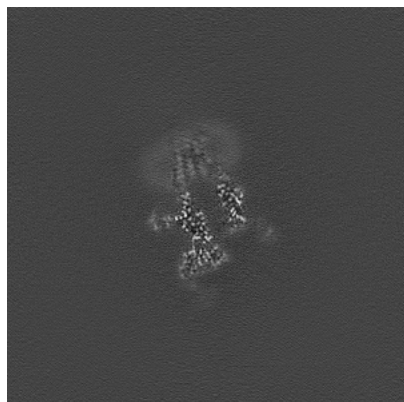


Y Index: 243

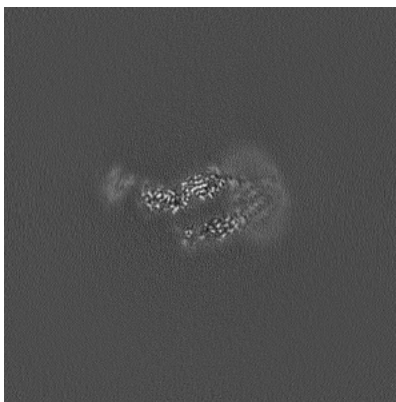


Z Index: 243

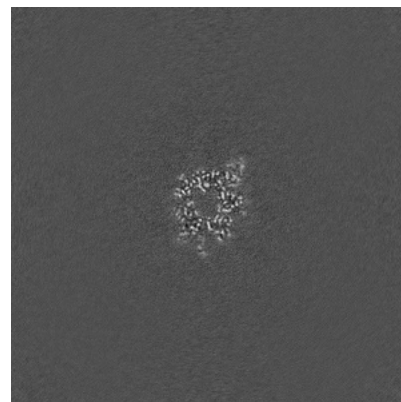
6.2.2 Raw map



X Index: 243



Y Index: 243

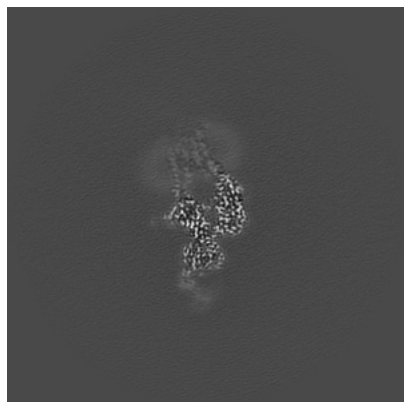


Z Index: 243

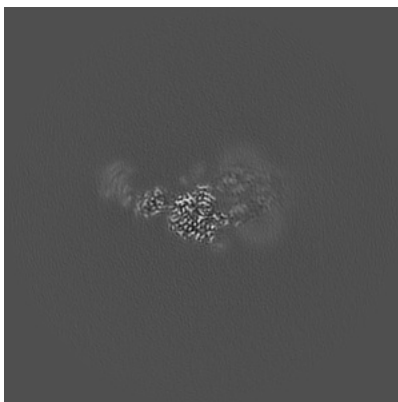
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

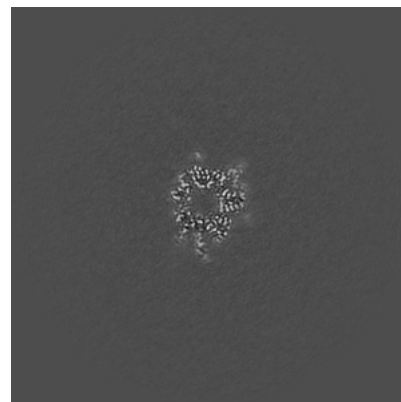
6.3.1 Primary map



X Index: 251

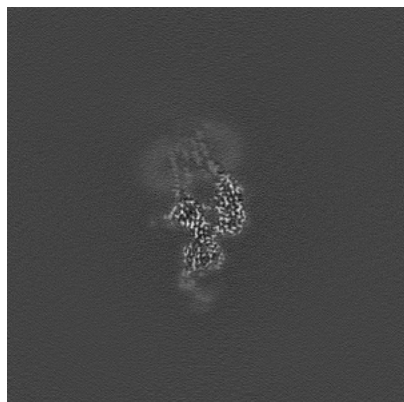


Y Index: 225

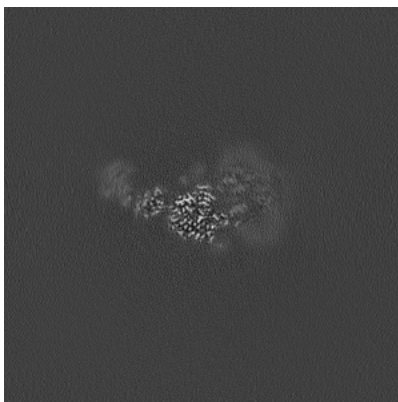


Z Index: 238

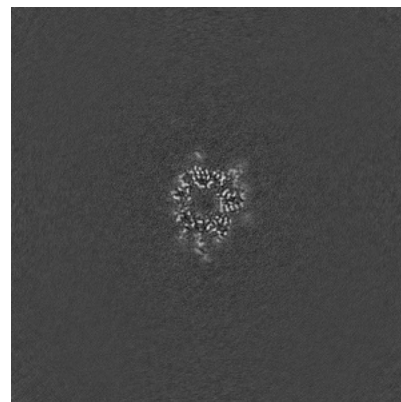
6.3.2 Raw map



X Index: 251



Y Index: 225

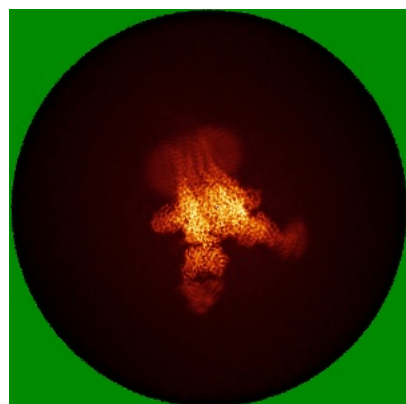


Z Index: 238

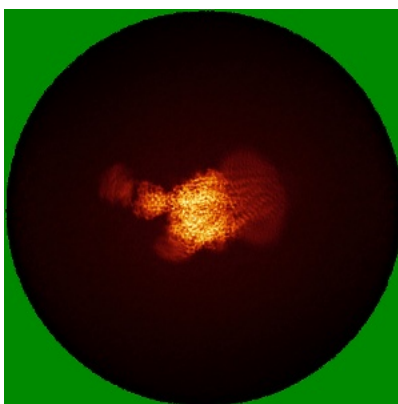
The images above show the largest variance slices of the map in three orthogonal directions.

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

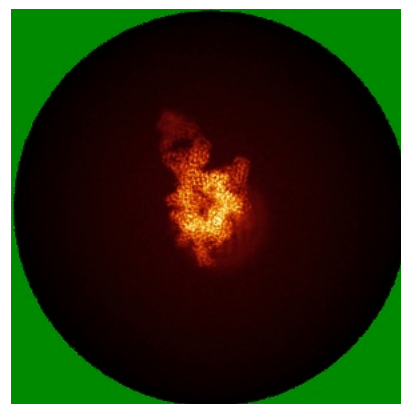
6.4.1 Primary map



X

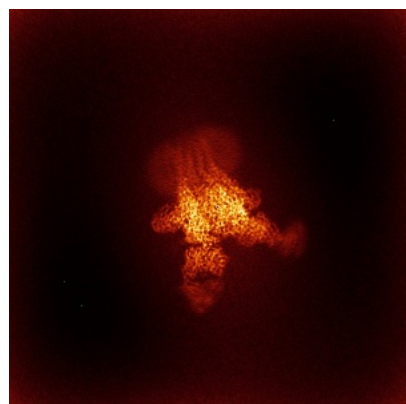


Y

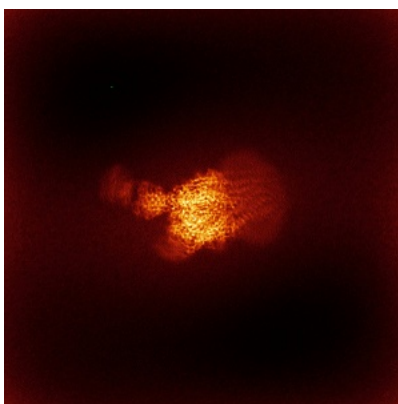


Z

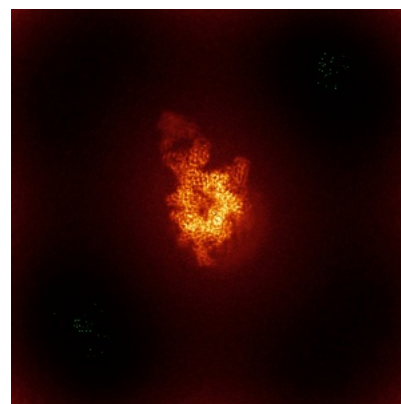
6.4.2 Raw map



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 0.14. 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.

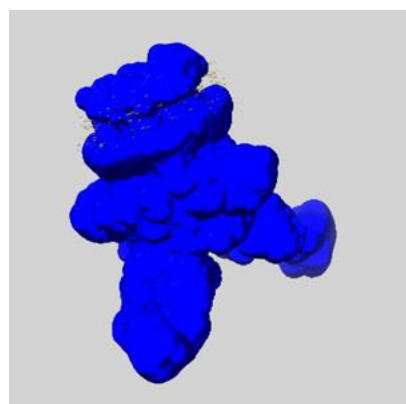
6.6 Mask visualisation [i](#)

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

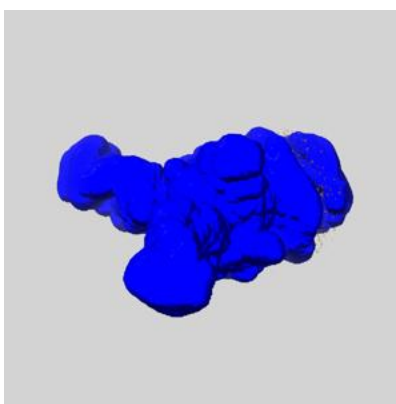
A mask typically either:

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

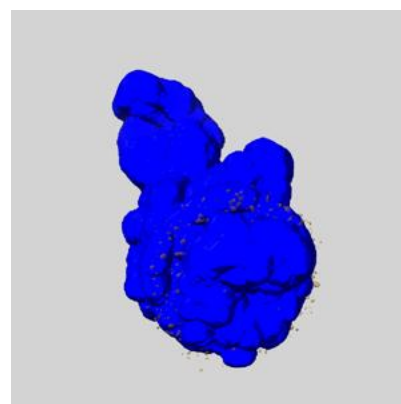
6.6.1 emd_51569_msk_1.map [i](#)



X

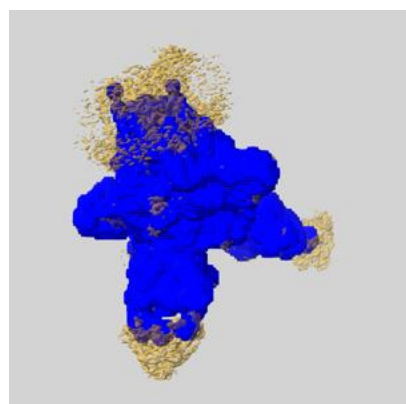


Y

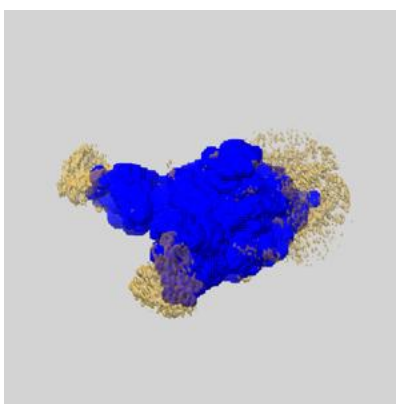


Z

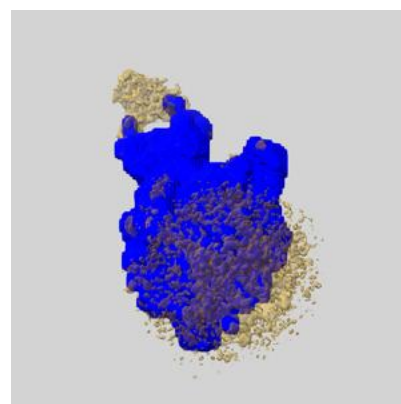
6.6.2 emd_51569_msk_2.map [i](#)



X



Y

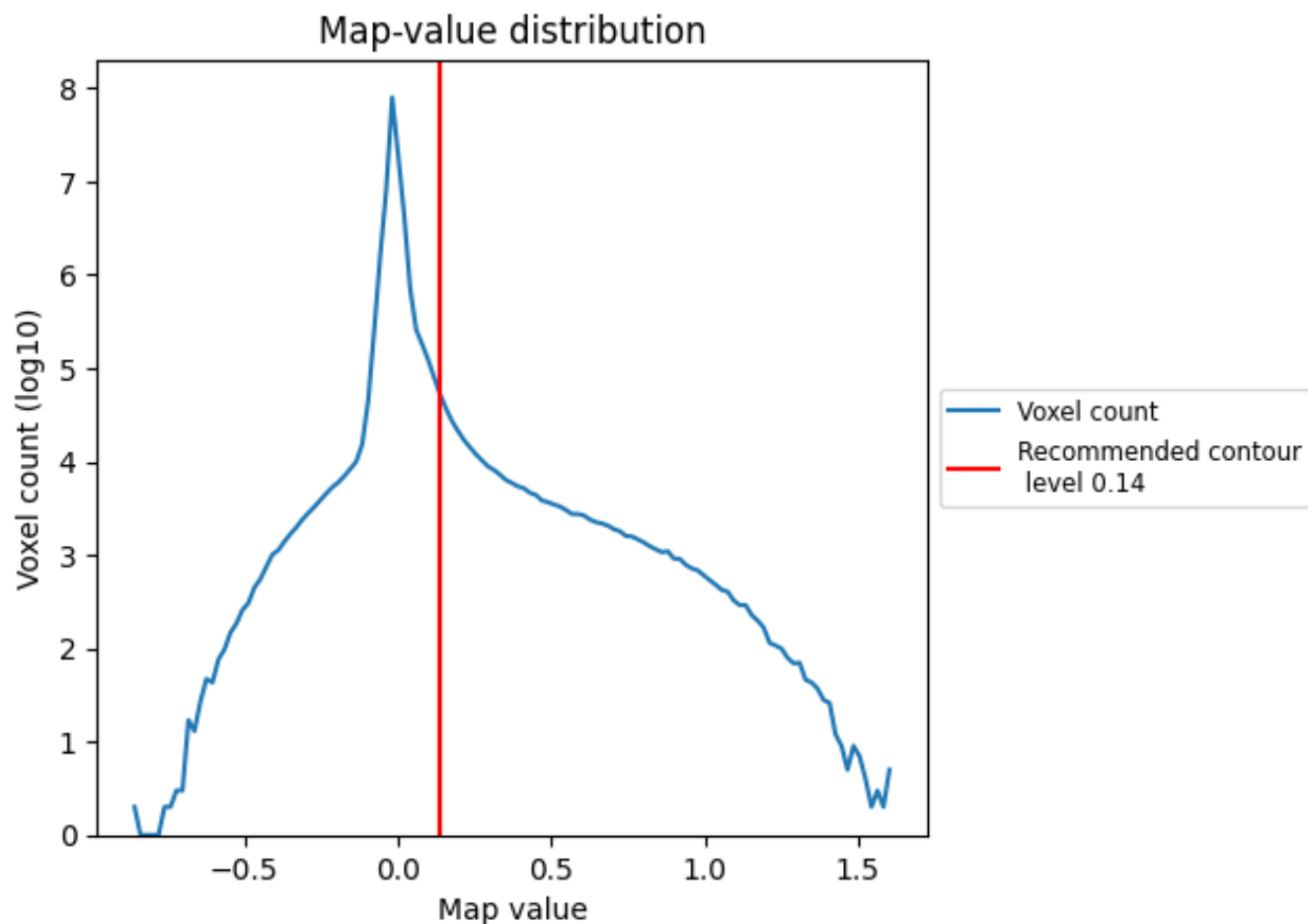


Z

7 Map analysis [i](#)

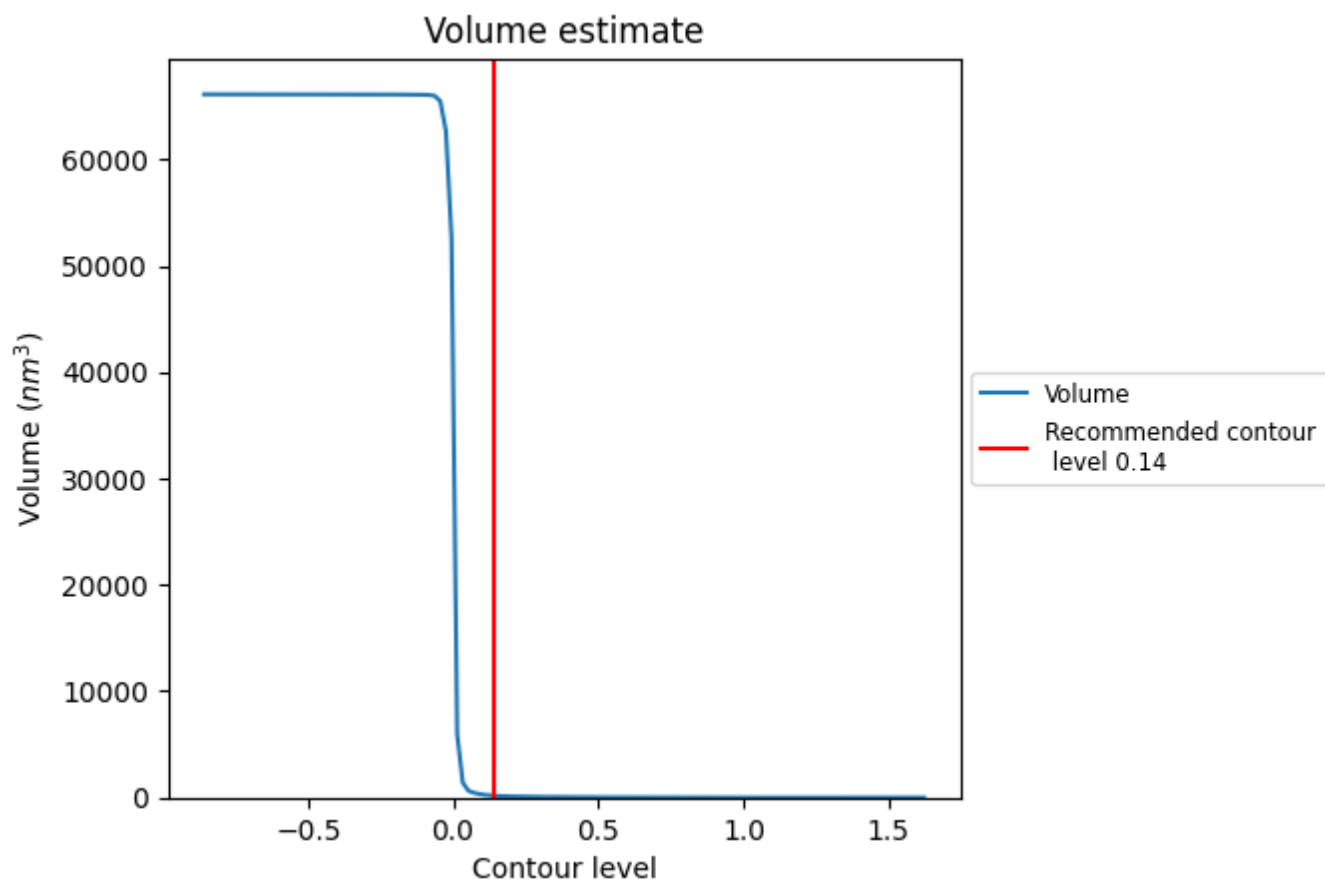
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

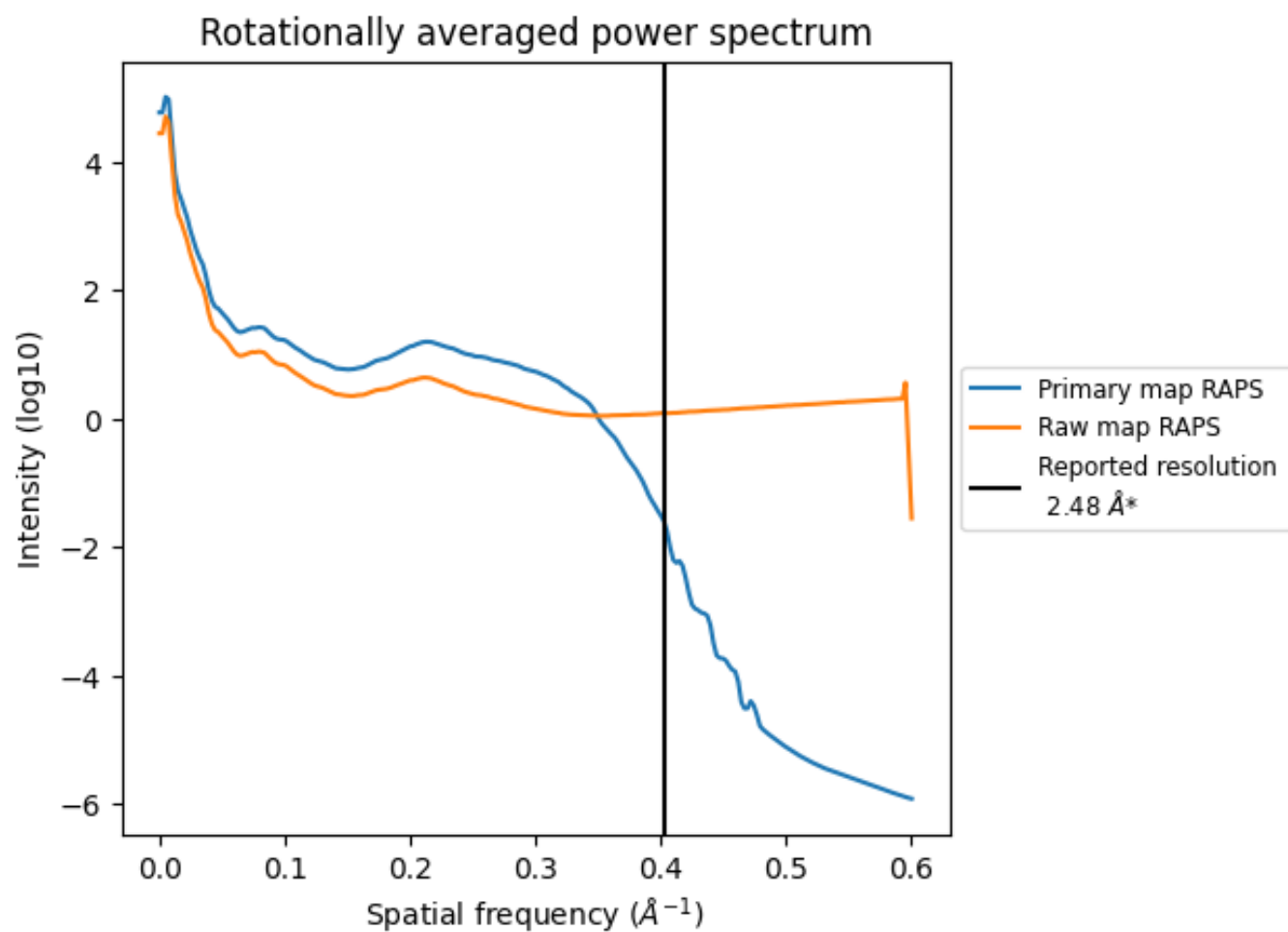
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 173 nm^3 ; this corresponds to an approximate mass of 157 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 ⓘ

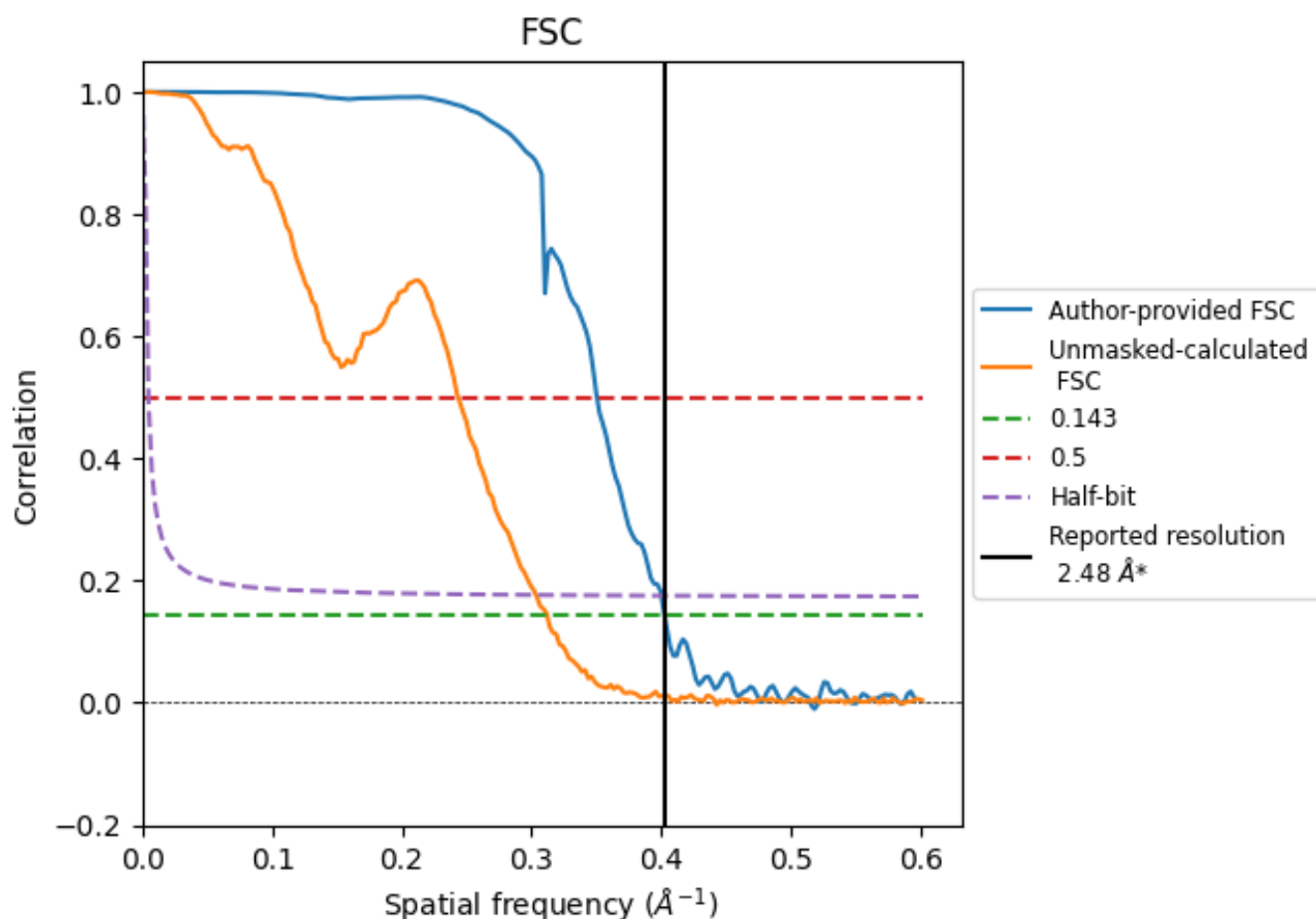


*Reported resolution corresponds to spatial frequency of 0.403 Å⁻¹

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 0.403 \AA^{-1}

8.2 Resolution estimates [i](#)

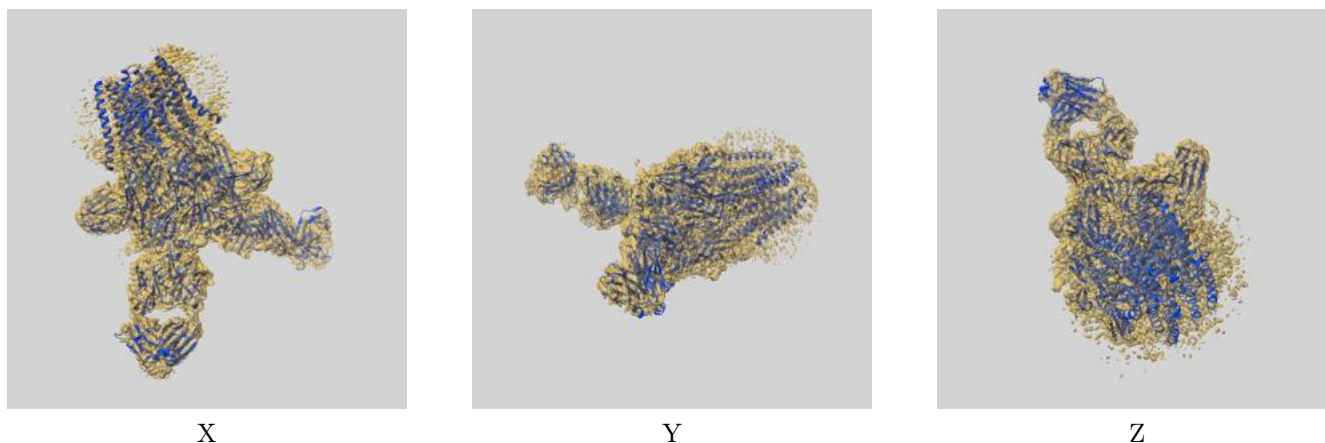
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.48	-	-
Author-provided FSC curve	2.48	2.85	2.50
Unmasked-calculated*	3.21	4.11	3.30

*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 3.21 differs from the reported value 2.48 by more than 10 %

9 Map-model fit [i](#)

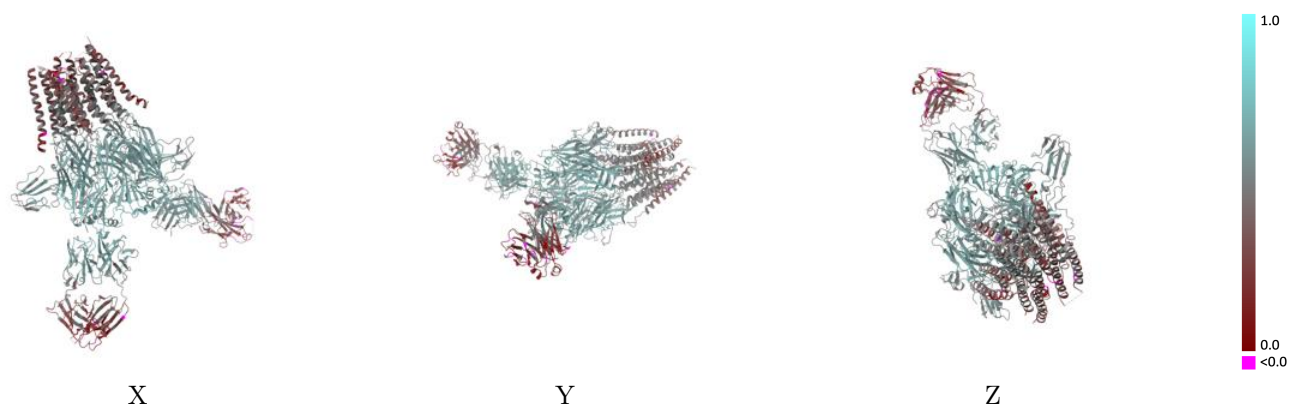
This section contains information regarding the fit between EMDB map EMD-51569 and PDB model 9GU1. Per-residue inclusion information can be found in section [3](#) on page [9](#).

9.1 Map-model overlay [i](#)



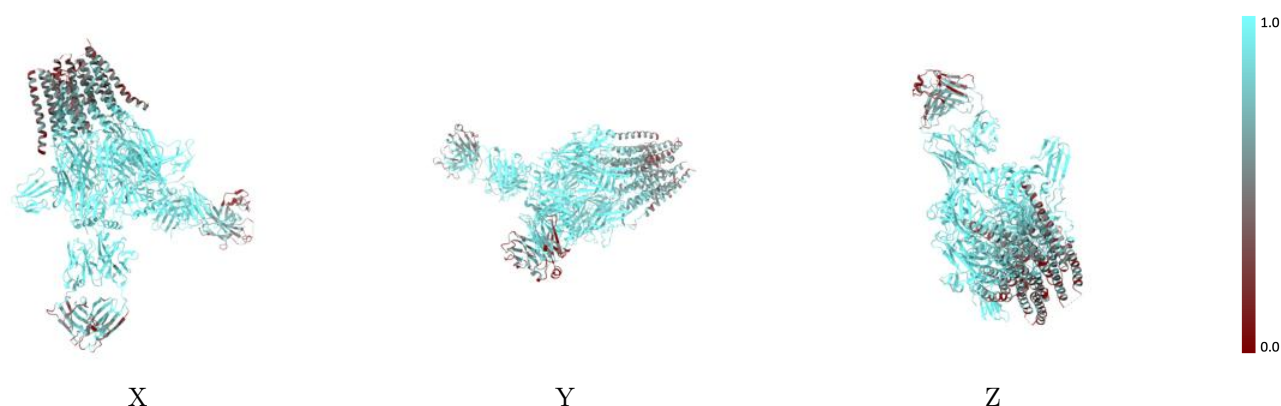
The images above show the 3D surface view of the map at the recommended contour level 0.14 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



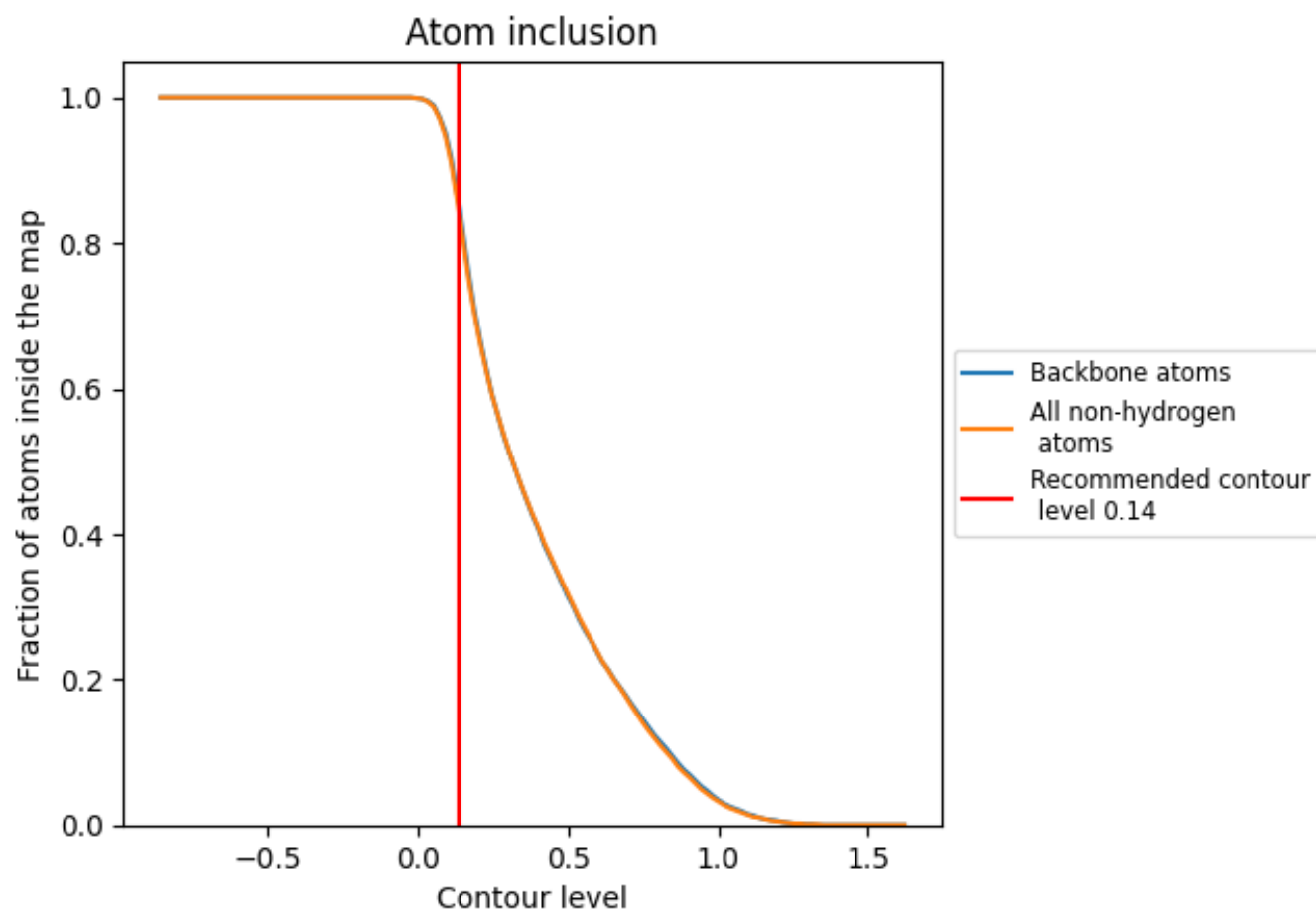
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.14).





































9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 83% 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 (0.14) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8340	 0.5060
A	 0.8450	 0.5440
B	 0.8390	 0.5300
C	 0.7940	 0.4470
D	 0.8590	 0.5390
E	 0.8470	 0.5300
F	 0.8440	 0.4510
G	 0.7160	 0.4070
H	 0.7750	 0.4100
I	 0.9530	 0.5250
J	 0.9640	 0.5450
K	 0.9710	 0.5620
L	 0.8490	 0.5470
M	 0.8970	 0.5250
N	 0.8750	 0.4950
O	 0.7860	 0.5230
P	 0.8800	 0.5020
Q	 0.9680	 0.5650

