



wwPDB EM Validation Summary Report ⓘ

Mar 25, 2026 – 01:19 AM UTC

PDB ID : 9GU2 / pdb_00009gu2
EMDB ID : EMD-51570
Title : Human adult muscle nAChR in desensitised state in nanodisc with 100 uM acetylcholine
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 : 2.73 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:

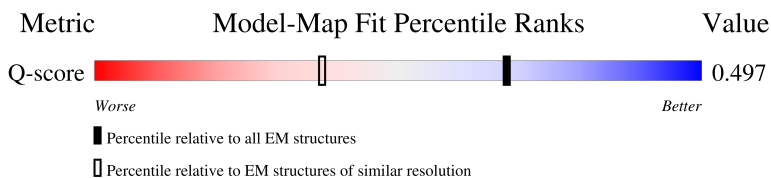
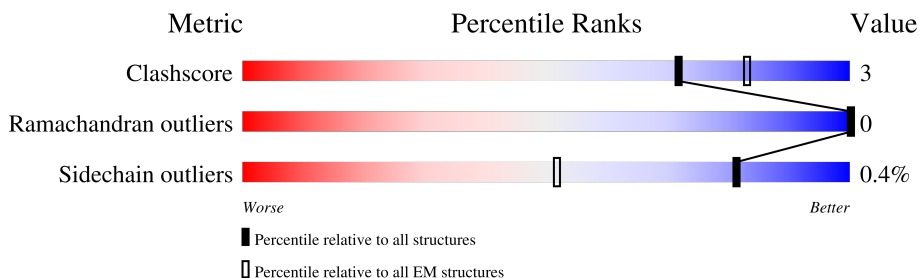
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
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 2.73 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	10432 (2.23 - 3.23)

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	<p>14% (red), 73% (green), 8% (yellow), 18% (grey)</p>
1	L	437	<p>12% (red), 70% (green), 12% (yellow), 18% (grey)</p>
2	B	478	<p>9% (red), 69% (green), 10% (yellow), 21% (grey)</p>
3	D	496	<p>8% (red), 75% (green), 7% (yellow), 18% (grey)</p>

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Mol	Chain	Length	Quality of chain
4	E	721	<p>7% 49% 46%</p>
5	C	213	<p>24% 95% 7%</p>
5	G	213	<p>29% 92% 7%</p>
6	F	219	<p>13% 89% 11%</p>
6	H	219	<p>17% 90% 10%</p>
7	I	7	<p>29% 29% 43%</p>
7	O	7	<p>86% 14%</p>
8	J	4	<p>50% 25% 50% 25%</p>
8	N	4	<p>25% 75%</p>
9	K	7	<p>29% 43% 57%</p>
10	M	2	<p>100%</p>

2 Entry composition [i](#)

There are 14 unique types of molecules in this entry. The entry contains 21623 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
			Total	C	N	O	S		
1	A	357	Total	C	N	O	S	3	0
			2797	1825	453	506	13		
1	L	357	Total	C	N	O	S	0	0
			2774	1815	446	499	14		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	378	Total	C	N	O	S	1	0
			2951	1926	486	529	10		

- Molecule 3 is a protein called Acetylcholine receptor subunit delta.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	D	407	Total	C	N	O	S	0	0
			3268	2142	539	576	11		

- Molecule 4 is a protein called Acetylcholine receptor subunit epsilon, Green fluorescent protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	E	387	Total	C	N	O	S	0	0
			2948	1916	475	547	10		

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	333L	ALA	-	linker	UNP Q04844
E	333M	PRO	-	linker	UNP Q04844
E	333N	PRO	-	linker	UNP Q04844
E	333O	VAL	-	linker	UNP Q04844
E	333P	ALA	-	linker	UNP Q04844
E	333Q	THR	-	linker	UNP Q04844

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Chain	Residue	Modelled	Actual	Comment	Reference
E	333R	MET	-	linker	UNP Q04844
E	333S	VAL	-	linker	UNP Q04844
E	336D	LEU	PHE	conflict	UNP P42212
E	336E	THR	SER	conflict	UNP P42212
E	342O	LEU	HIS	conflict	UNP P42212

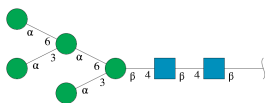
- Molecule 5 is a protein called Fab35 light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	C	212	1565	984	256	319	6	0	0
5	G	212	1553	979	258	310	6	0	0

- Molecule 6 is a protein called Fab35 heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	F	219	1633	1028	279	318	8	0	0
6	H	219	1624	1025	276	315	8	0	0

- Molecule 7 is an oligosaccharide called 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.



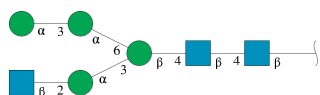
Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
7	I	7	83	46	2	35	0	0
7	O	7	83	46	2	35	0	0

- Molecule 8 is an oligosaccharide called alpha-D-mannopyranose-(1-6)-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
			Total	C	N	O		
8	J	4	50	28	2	20	0	0
8	N	4	50	28	2	20	0	0

- Molecule 9 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



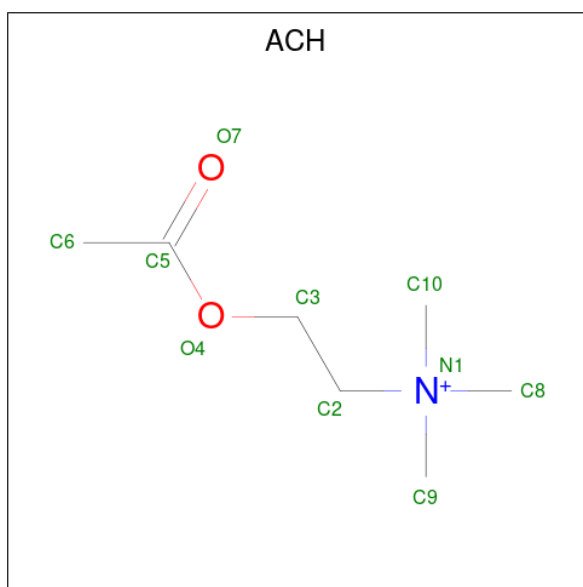
Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
9	K	7	86	48	3	35	0	0

- Molecule 10 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



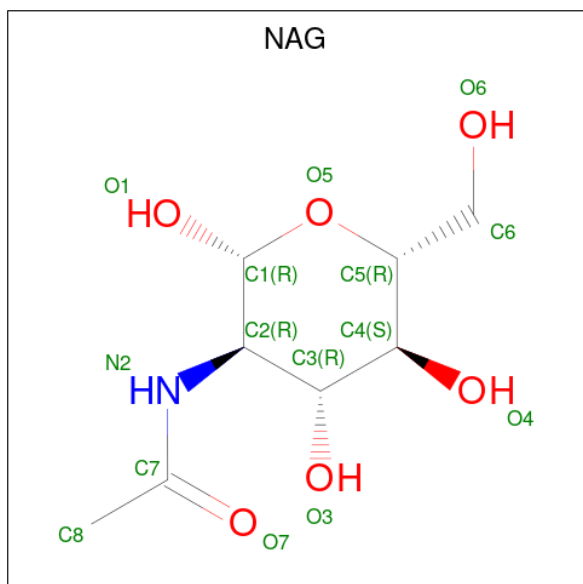
Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
10	M	2	28	16	2	10	0	0

- Molecule 11 is ACETYLCHOLINE (CCD ID: ACH) (formula: C₇H₁₆NO₂).



Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
11	A	1	10	7	1	2	0
11	L	1	10	7	1	2	0

- Molecule 12 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	
12	D	1	14	8	1	5	0

- Molecule 13 is COPPER (II) ION (CCD ID: CU) (formula: Cu).

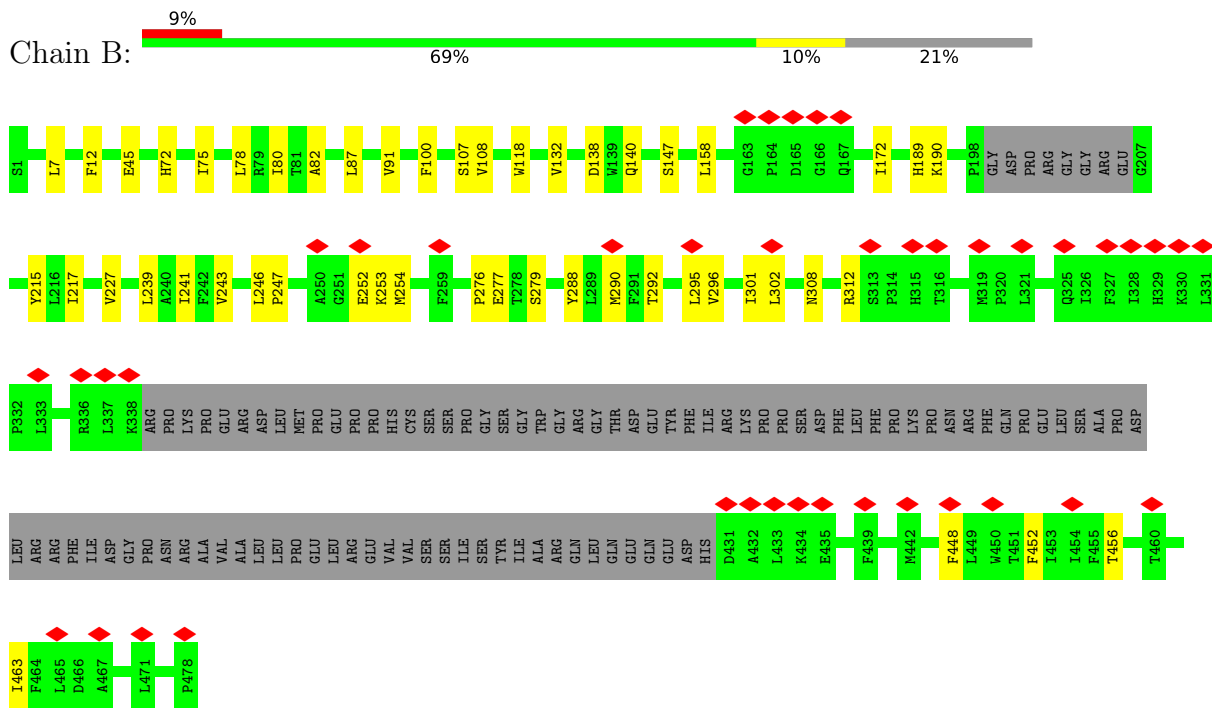
Mol	Chain	Residues	Atoms		AltConf
13	L	1	Total 1	Cu 1	0

- Molecule 14 is water.

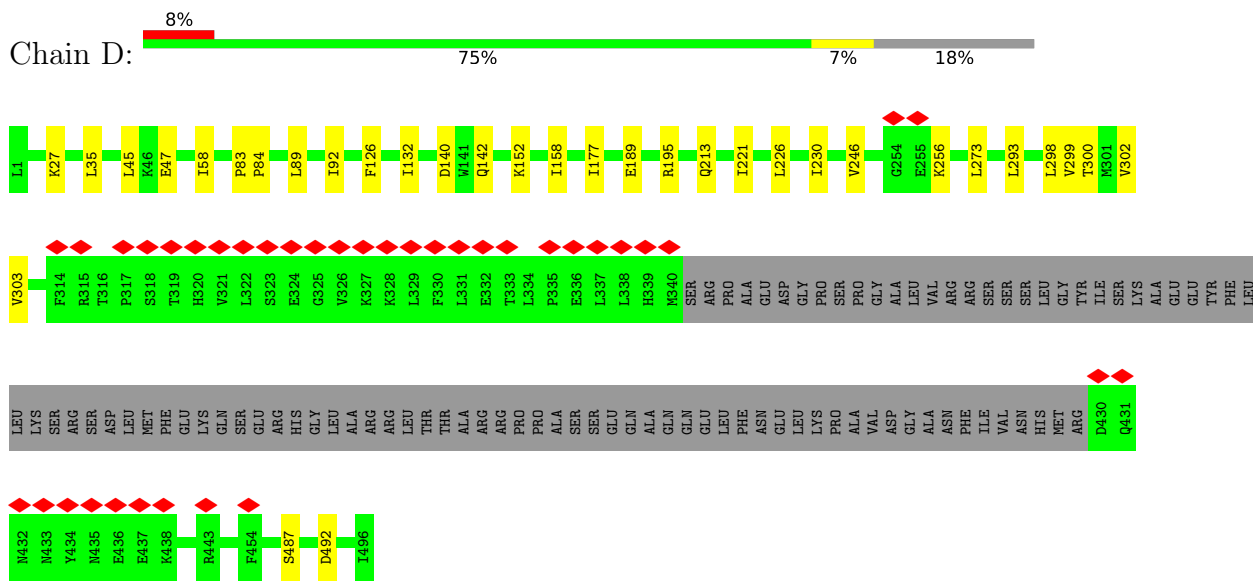
Mol	Chain	Residues	Atoms		AltConf
14	A	20	Total 20	O 20	0
14	B	5	Total 5	O 5	0
14	D	16	Total 16	O 16	0
14	E	31	Total 31	O 31	0
14	L	20	Total 20	O 20	0
14	C	1	Total 1	O 1	0
14	F	2	Total 2	O 2	0

GLY

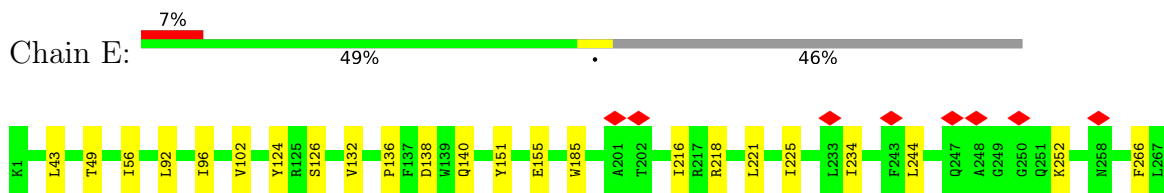
• Molecule 2: Acetylcholine receptor subunit beta

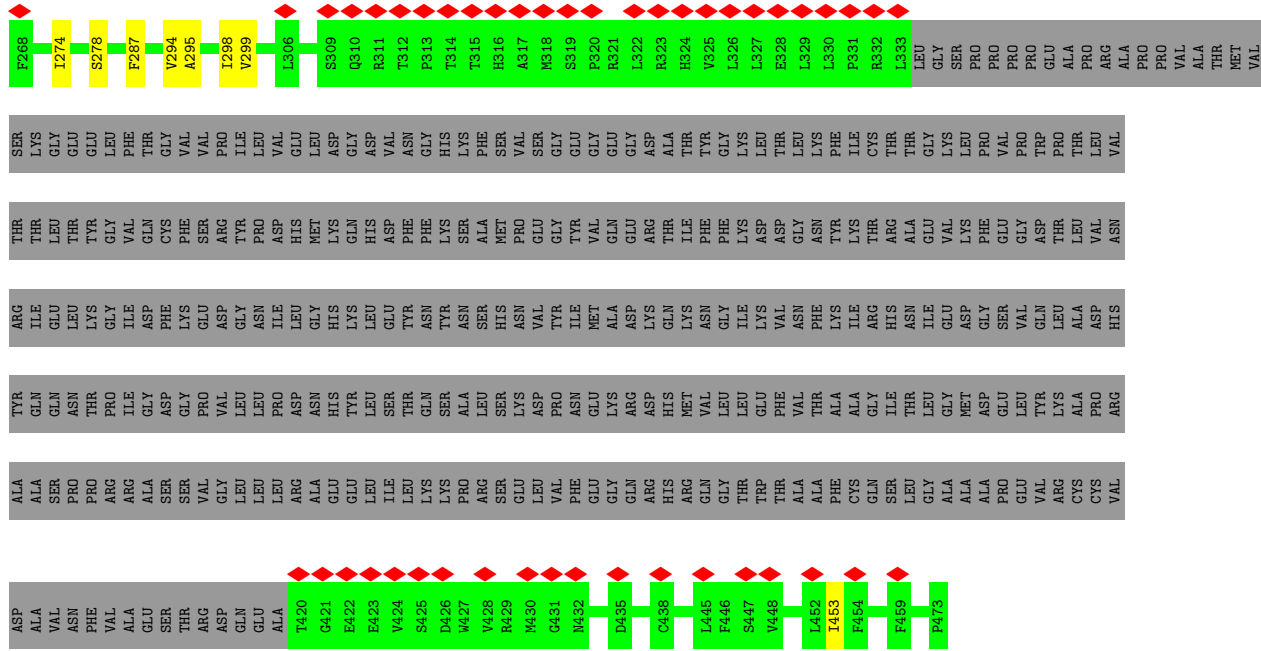


• Molecule 3: Acetylcholine receptor subunit delta

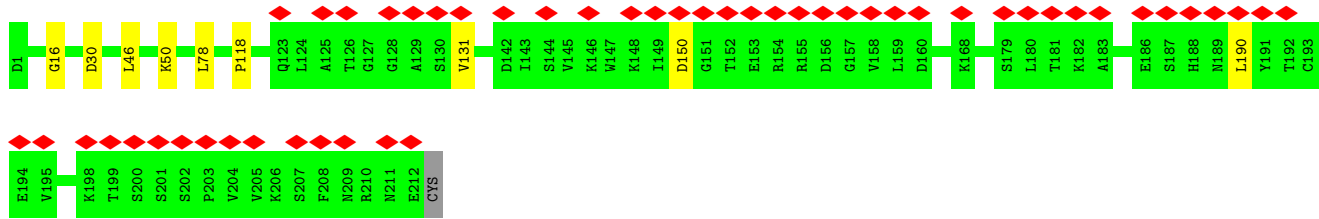


• Molecule 4: Acetylcholine receptor subunit epsilon, Green fluorescent protein

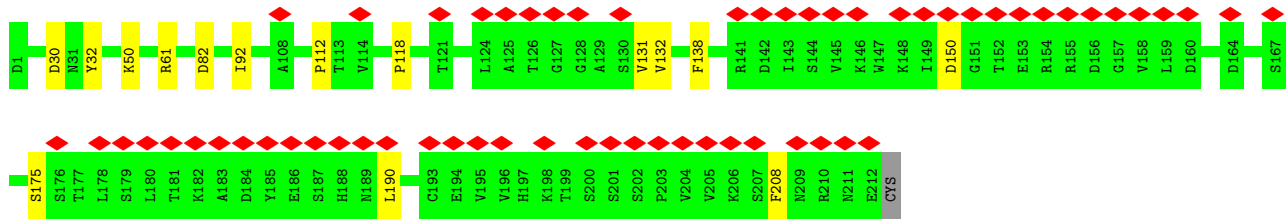




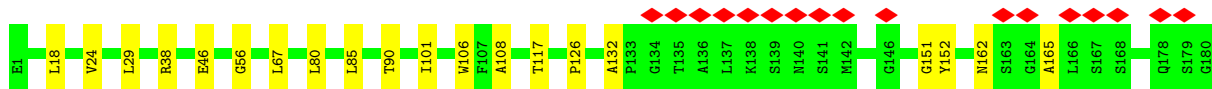
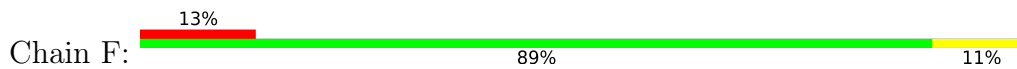
• Molecule 5: Fab35 light chain

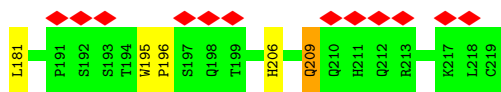


• Molecule 5: Fab35 light chain

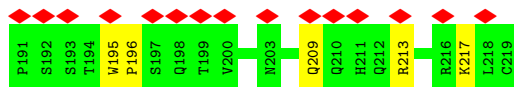
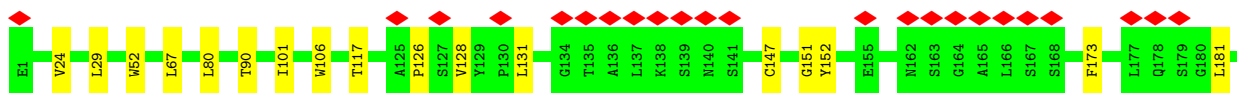
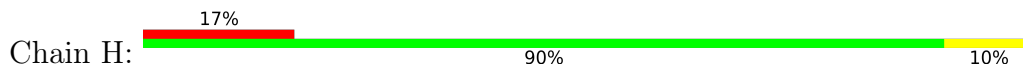


• Molecule 6: Fab35 heavy chain

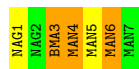
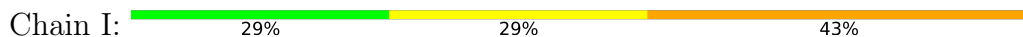




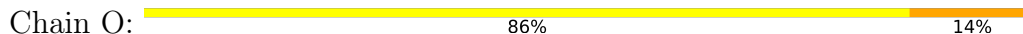
- Molecule 6: Fab35 heavy chain



- Molecule 7: 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



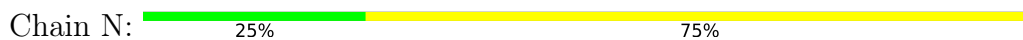
- Molecule 7: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose




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

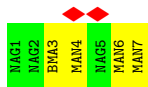


- Molecule 8: alpha-D-mannopyranose-(1-6)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 9: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain K: 



- Molecule 10: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain M: 



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	175800	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2400	Depositor
Magnification	130000	Depositor
Image detector	TFS FALCON 4i (4k x 4k)	Depositor
Maximum map value	3.722	Depositor
Minimum map value	-2.143	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.058	Depositor
Recommended contour level	0.3	Depositor
Map size (Å)	397.872, 397.872, 397.872	wwPDB
Map dimensions	432, 432, 432	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.921, 0.921, 0.921	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, ACH, NAG, CU, MAN

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	0.11	0/2871	0.27	0/3932
1	L	0.11	0/2845	0.26	0/3892
2	B	0.10	0/3031	0.26	0/4145
3	D	0.11	0/3359	0.28	0/4591
4	E	0.11	0/3020	0.27	0/4145
5	C	0.10	0/1597	0.30	0/2185
5	G	0.10	0/1585	0.30	0/2165
6	F	0.11	0/1675	0.30	0/2296
6	H	0.10	0/1665	0.30	0/2283
All	All	0.11	0/21648	0.28	0/29634

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	2797	0	2725	24	0
1	L	2774	0	2709	31	0
2	B	2951	0	2899	31	0
3	D	3268	0	3270	23	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	E	2948	0	2835	18	0
5	C	1565	0	1460	6	0
5	G	1553	0	1439	9	0
6	F	1633	0	1549	14	0
6	H	1624	0	1539	12	0
7	I	83	0	70	3	0
7	O	83	0	70	1	0
8	J	50	0	43	2	0
8	N	50	0	43	0	0
9	K	86	0	73	0	0
10	M	28	0	25	1	0
11	A	10	0	16	1	0
11	L	10	0	16	1	0
12	D	14	0	13	0	0
13	L	1	0	0	0	0
14	A	20	0	0	0	0
14	B	5	0	0	0	0
14	C	1	0	0	0	0
14	D	16	0	0	0	0
14	E	31	0	0	0	0
14	F	2	0	0	0	0
14	L	20	0	0	0	0
All	All	21623	0	20794	145	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 3.

The worst 5 of 145 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:L:66:LYS:NZ	5:C:30:ASP:OD2	2.23	0.71
1:A:63:TYR:OH	5:G:50:LYS:NZ	2.23	0.71
1:L:63:TYR:OH	5:C:50:LYS:NZ	2.27	0.68
1:A:66:LYS:NZ	5:G:30:ASP:OD2	2.26	0.67
2:B:246:LEU:HD12	2:B:247:PRO:HD2	1.77	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	355/437 (81%)	345 (97%)	10 (3%)	0	100	100
1	L	351/437 (80%)	341 (97%)	10 (3%)	0	100	100
2	B	373/478 (78%)	361 (97%)	12 (3%)	0	100	100
3	D	403/496 (81%)	392 (97%)	11 (3%)	0	100	100
4	E	383/721 (53%)	369 (96%)	14 (4%)	0	100	100
5	C	210/213 (99%)	203 (97%)	7 (3%)	0	100	100
5	G	210/213 (99%)	201 (96%)	9 (4%)	0	100	100
6	F	217/219 (99%)	208 (96%)	9 (4%)	0	100	100
6	H	217/219 (99%)	208 (96%)	9 (4%)	0	100	100
All	All	2719/3433 (79%)	2628 (97%)	91 (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	305/402 (76%)	304 (100%)	1 (0%)	86	92
1	L	301/402 (75%)	299 (99%)	2 (1%)	76	85
2	B	320/434 (74%)	318 (99%)	2 (1%)	78	87
3	D	364/452 (80%)	364 (100%)	0	100	100
4	E	311/626 (50%)	311 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	C	168/189 (89%)	167 (99%)	1 (1%)	78	87
5	G	161/189 (85%)	160 (99%)	1 (1%)	78	87
6	F	177/191 (93%)	176 (99%)	1 (1%)	78	87
6	H	174/191 (91%)	173 (99%)	1 (1%)	78	87
All	All	2281/3076 (74%)	2272 (100%)	9 (0%)	81	90

5 of 9 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	G	131	VAL
6	H	209	GLN
1	L	1	SER
1	L	155	VAL
5	C	131	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 23 such sidechains are listed below:

Mol	Chain	Res	Type
1	L	115	HIS
5	C	137	ASN
1	L	159	ASN
5	C	209	ASN
1	A	159	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

31 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
7	NAG	I	1	1,7	14,14,15	0.73	0	17,19,21	0.91	0
7	NAG	I	2	7	14,14,15	0.75	0	17,19,21	0.96	0
7	BMA	I	3	7	11,11,12	0.84	0	15,15,17	1.20	1 (6%)
7	MAN	I	4	7	11,11,12	0.71	0	15,15,17	1.28	1 (6%)
7	MAN	I	5	7	11,11,12	0.67	0	15,15,17	1.28	1 (6%)
7	MAN	I	6	7	11,11,12	0.95	1 (9%)	15,15,17	1.62	2 (13%)
7	MAN	I	7	7	11,11,12	0.77	0	15,15,17	0.90	0
8	NAG	J	1	8,2	14,14,15	0.72	0	17,19,21	1.03	2 (11%)
8	NAG	J	2	8	14,14,15	0.69	0	17,19,21	0.86	0
8	BMA	J	3	8	11,11,12	0.84	0	15,15,17	1.21	1 (6%)
8	MAN	J	4	8	11,11,12	0.70	0	15,15,17	1.10	1 (6%)
9	NAG	K	1	9,3	14,14,15	0.73	0	17,19,21	0.92	0
9	NAG	K	2	9	14,14,15	0.71	0	17,19,21	0.98	0
9	BMA	K	3	9	11,11,12	0.80	0	15,15,17	1.46	1 (6%)
9	MAN	K	4	9	11,11,12	0.69	0	15,15,17	1.08	1 (6%)
9	NAG	K	5	9	14,14,15	0.69	0	17,19,21	0.76	0
9	MAN	K	6	9	11,11,12	0.74	0	15,15,17	1.19	1 (6%)
9	MAN	K	7	9	11,11,12	0.71	0	15,15,17	1.06	1 (6%)
10	NAG	M	1	4,10	14,14,15	0.68	0	17,19,21	1.34	2 (11%)
10	NAG	M	2	10	14,14,15	0.74	0	17,19,21	1.40	2 (11%)
8	NAG	N	1	4,8	14,14,15	0.73	0	17,19,21	1.10	1 (5%)
8	NAG	N	2	8	14,14,15	0.69	0	17,19,21	0.79	0
8	BMA	N	3	8	11,11,12	0.80	0	15,15,17	1.22	1 (6%)
8	MAN	N	4	8	11,11,12	0.72	0	15,15,17	1.08	1 (6%)
7	NAG	O	1	1,7	14,14,15	0.75	0	17,19,21	1.18	2 (11%)
7	NAG	O	2	7	14,14,15	0.75	0	17,19,21	0.92	1 (5%)
7	BMA	O	3	7	11,11,12	0.83	0	15,15,17	1.17	1 (6%)
7	MAN	O	4	7	11,11,12	0.73	0	15,15,17	1.20	1 (6%)
7	MAN	O	5	7	11,11,12	0.73	0	15,15,17	1.01	1 (6%)
7	MAN	O	6	7	11,11,12	0.72	0	15,15,17	1.08	1 (6%)
7	MAN	O	7	7	11,11,12	0.77	0	15,15,17	0.94	1 (6%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	NAG	I	1	1,7	-	0/6/23/26	0/1/1/1
7	NAG	I	2	7	-	1/6/23/26	0/1/1/1
7	BMA	I	3	7	-	0/2/19/22	0/1/1/1
7	MAN	I	4	7	-	2/2/19/22	0/1/1/1
7	MAN	I	5	7	-	0/2/19/22	0/1/1/1
7	MAN	I	6	7	-	2/2/19/22	0/1/1/1
7	MAN	I	7	7	-	0/2/19/22	0/1/1/1
8	NAG	J	1	8,2	-	1/6/23/26	0/1/1/1
8	NAG	J	2	8	-	0/6/23/26	0/1/1/1
8	BMA	J	3	8	-	0/2/19/22	0/1/1/1
8	MAN	J	4	8	-	2/2/19/22	0/1/1/1
9	NAG	K	1	9,3	-	3/6/23/26	0/1/1/1
9	NAG	K	2	9	-	2/6/23/26	0/1/1/1
9	BMA	K	3	9	-	2/2/19/22	0/1/1/1
9	MAN	K	4	9	-	2/2/19/22	0/1/1/1
9	NAG	K	5	9	-	0/6/23/26	0/1/1/1
9	MAN	K	6	9	-	2/2/19/22	0/1/1/1
9	MAN	K	7	9	-	0/2/19/22	0/1/1/1
10	NAG	M	1	4,10	-	2/6/23/26	0/1/1/1
10	NAG	M	2	10	-	4/6/23/26	0/1/1/1
8	NAG	N	1	4,8	-	0/6/23/26	0/1/1/1
8	NAG	N	2	8	-	1/6/23/26	0/1/1/1
8	BMA	N	3	8	-	2/2/19/22	0/1/1/1
8	MAN	N	4	8	-	0/2/19/22	0/1/1/1
7	NAG	O	1	1,7	-	4/6/23/26	0/1/1/1
7	NAG	O	2	7	-	0/6/23/26	0/1/1/1
7	BMA	O	3	7	-	0/2/19/22	0/1/1/1
7	MAN	O	4	7	-	2/2/19/22	0/1/1/1
7	MAN	O	5	7	-	2/2/19/22	0/1/1/1
7	MAN	O	6	7	-	0/2/19/22	1/1/1/1
7	MAN	O	7	7	-	1/2/19/22	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	I	6	MAN	O5-C1	-2.26	1.39	1.43

The worst 5 of 28 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	K	3	BMA	C1-O5-C5	4.01	117.56	112.19
7	I	5	MAN	C1-O5-C5	3.86	117.35	112.19
10	M	2	NAG	C2-N2-C7	3.69	127.84	122.90
7	I	6	MAN	C1-C2-C3	3.68	115.00	109.64
7	O	1	NAG	C2-N2-C7	3.67	127.81	122.90

There are no chirality outliers.

5 of 37 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
10	M	1	NAG	C1-C2-N2-C7
10	M	2	NAG	C1-C2-N2-C7
7	I	4	MAN	C4-C5-C6-O6
7	O	5	MAN	O5-C5-C6-O6
9	K	4	MAN	O5-C5-C6-O6

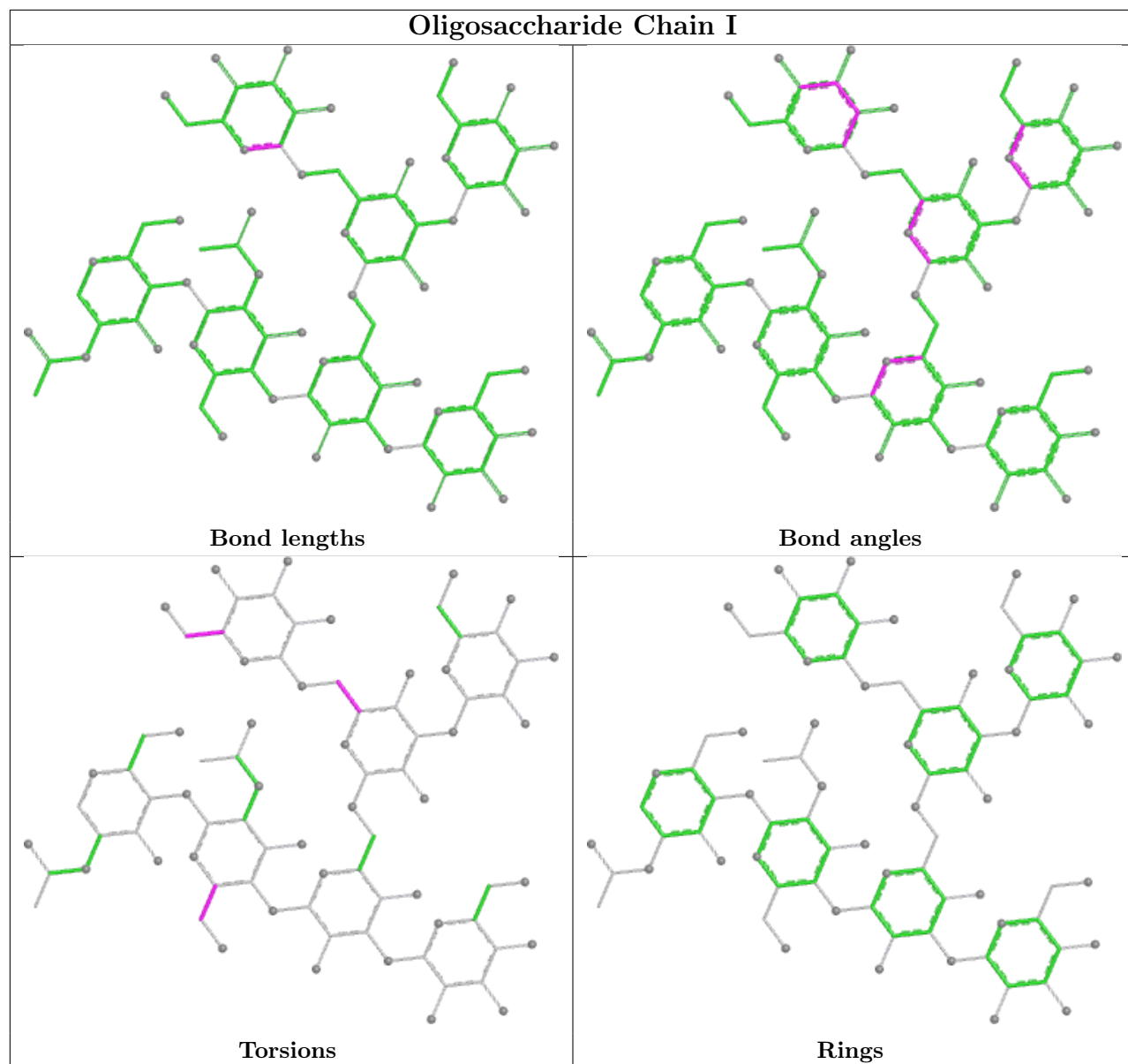
All (1) ring outliers are listed below:

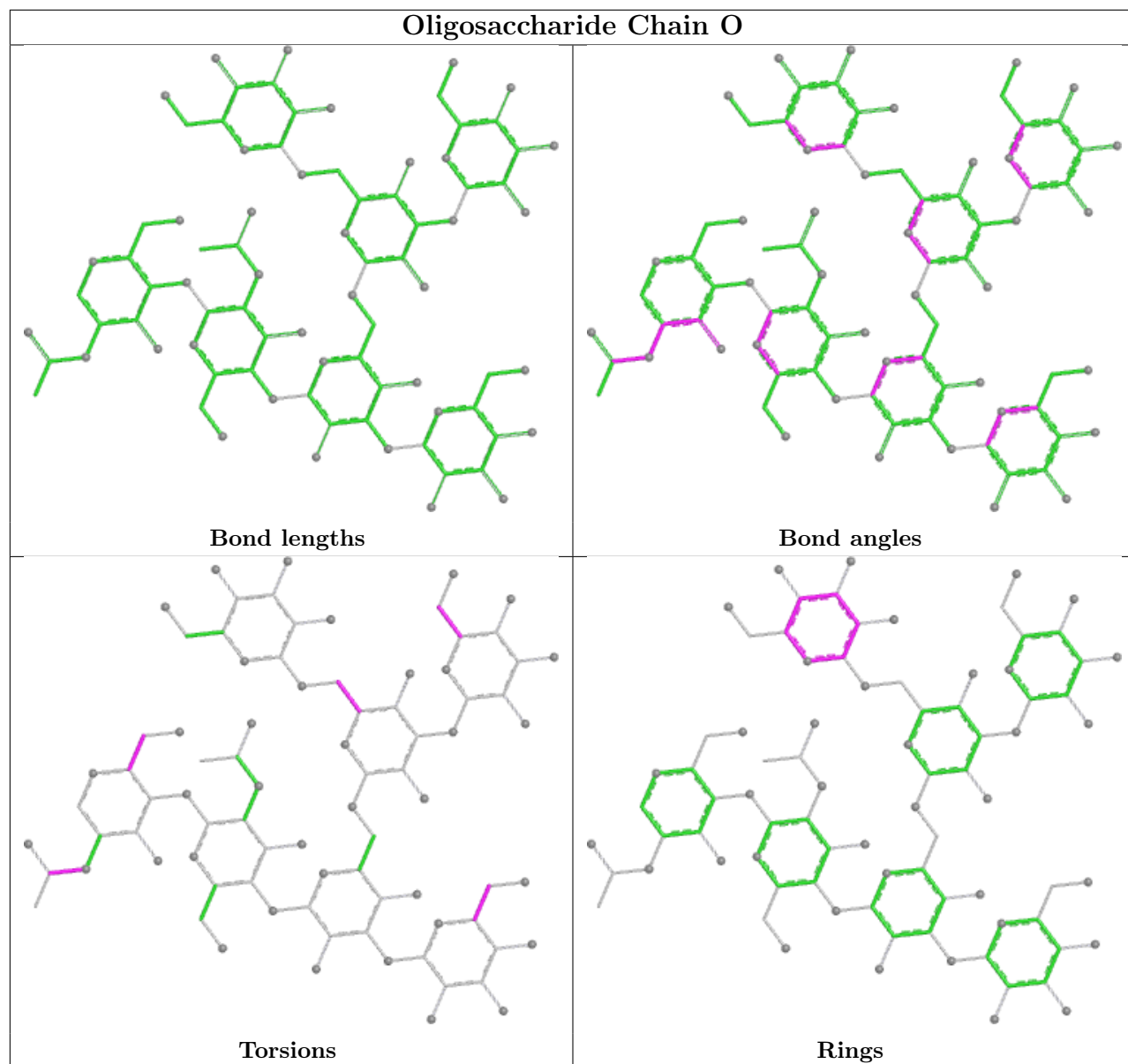
Mol	Chain	Res	Type	Atoms
7	O	6	MAN	C1-C2-C3-C4-C5-O5

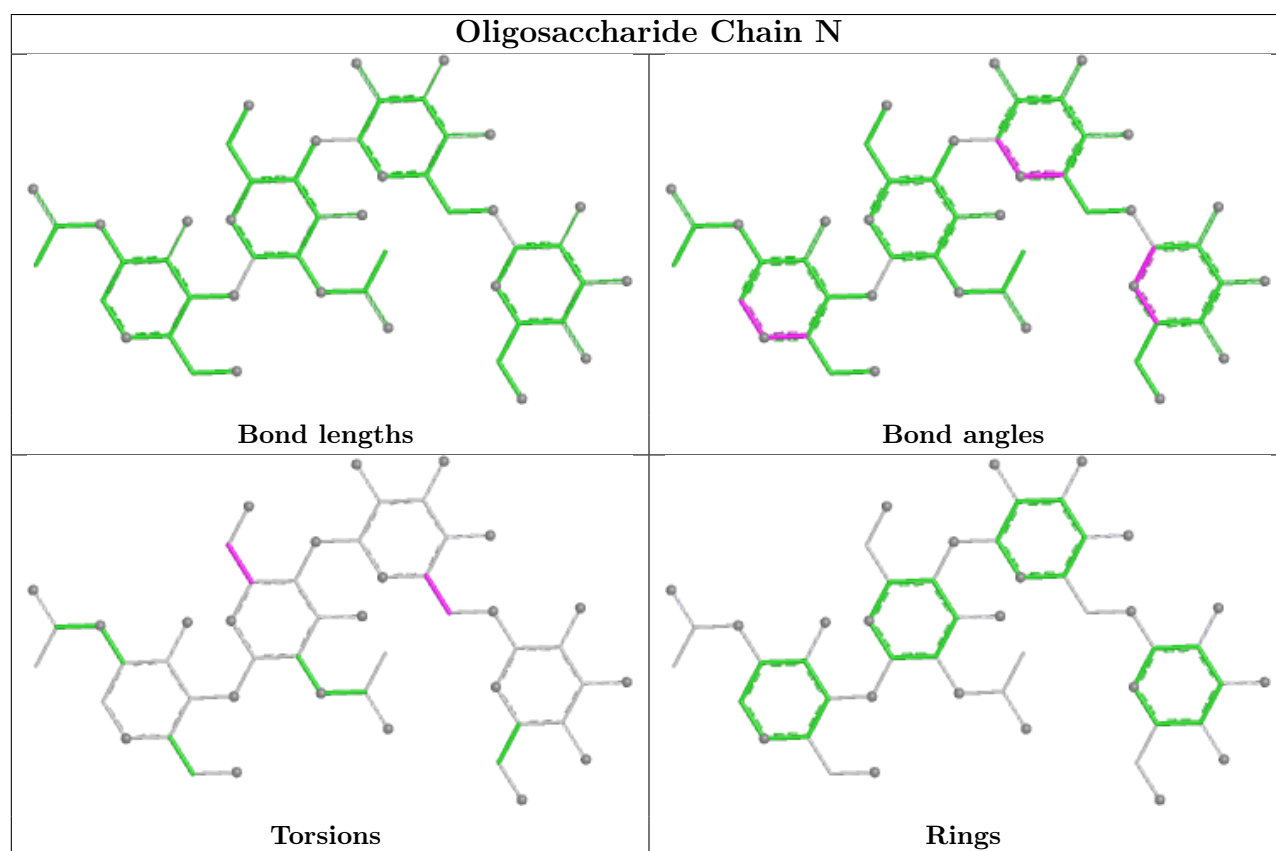
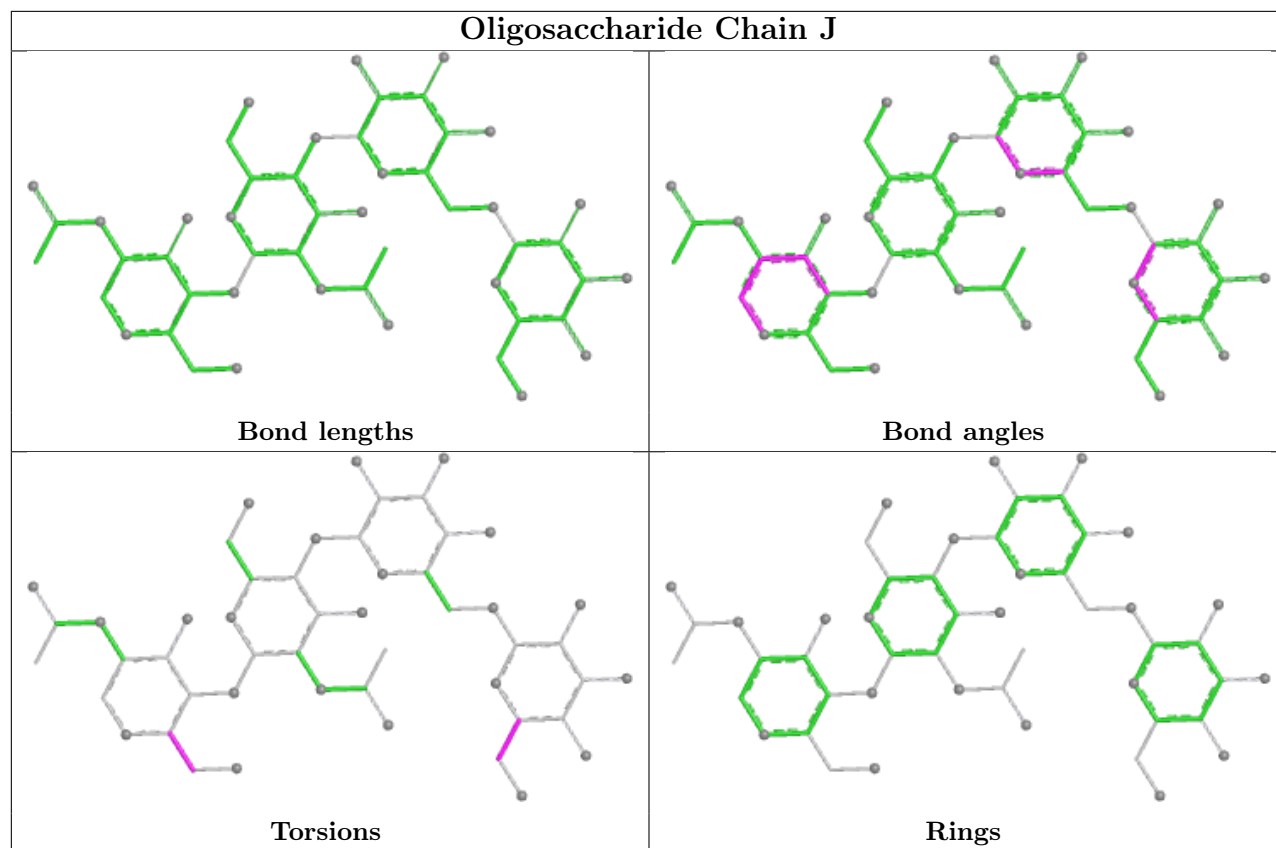
8 monomers are involved in 7 short contacts:

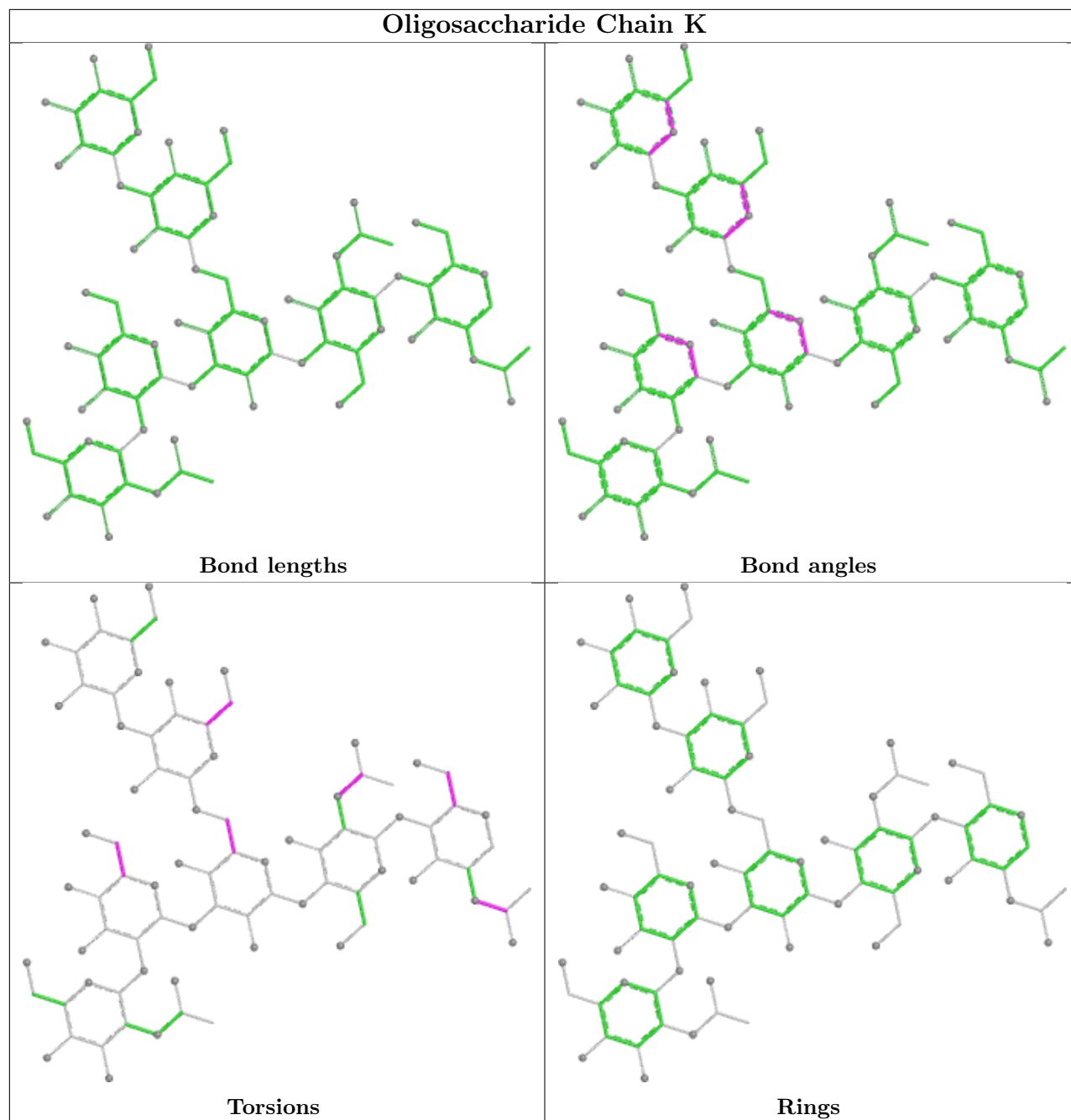
Mol	Chain	Res	Type	Clashes	Symm-Clashes
10	M	1	NAG	1	0
7	I	3	BMA	1	0
7	I	1	NAG	1	0
7	O	1	NAG	1	0
10	M	2	NAG	1	0
8	J	1	NAG	2	0
7	I	4	MAN	1	0
7	I	6	MAN	1	0

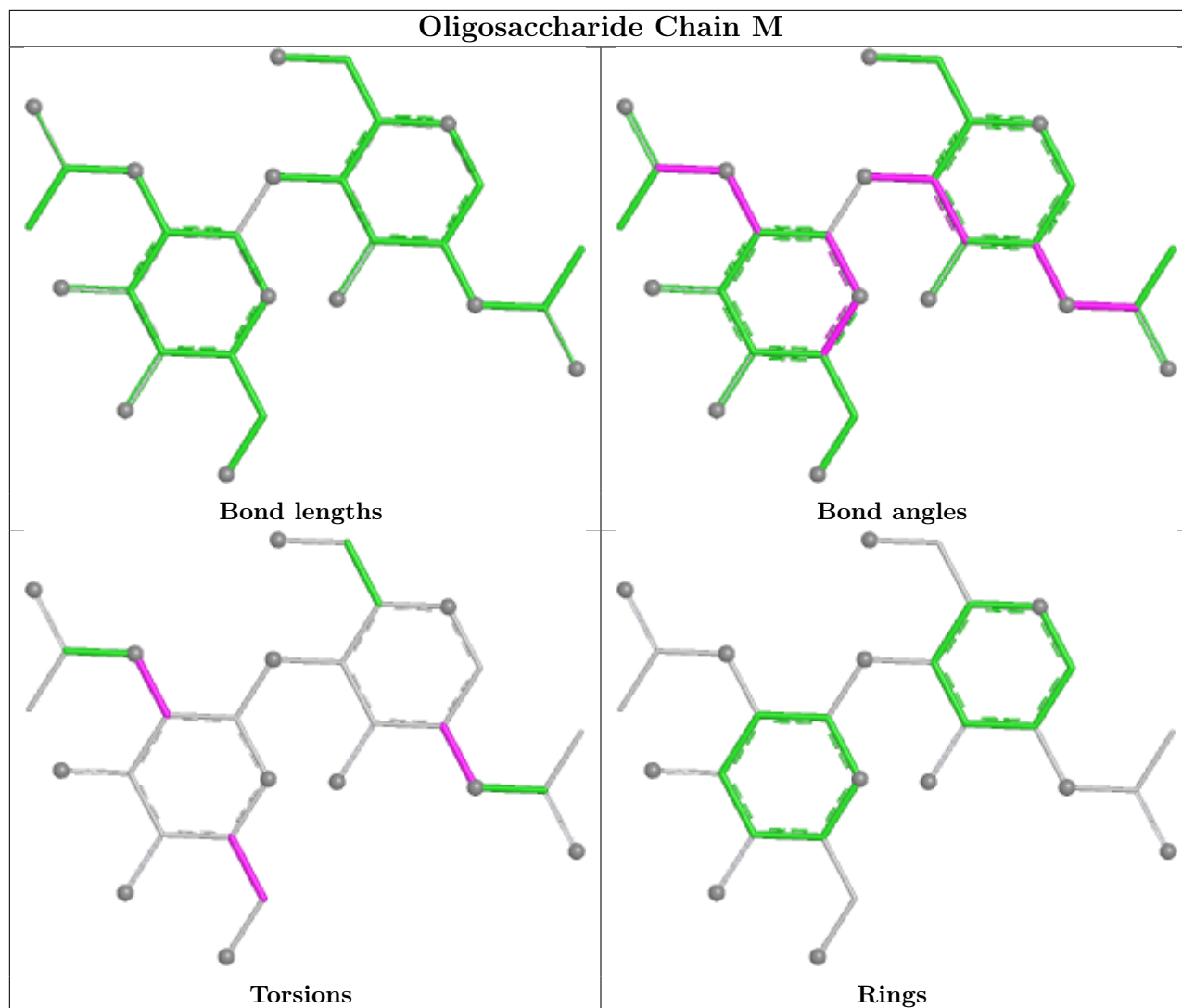
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.











5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 1 is 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	$\# Z > 2$
11	ACH	A	500	-	9,9,9	0.11	0	12,12,12	0.19	0
11	ACH	L	501	-	9,9,9	0.11	0	12,12,12	0.18	0
12	NAG	D	501	3	14,14,15	0.69	0	17,19,21	0.87	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
11	ACH	A	500	-	-	3/7/7/7	-
11	ACH	L	501	-	-	0/7/7/7	-
12	NAG	D	501	3	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
11	A	500	ACH	C3-C2-N1-C10
11	A	500	ACH	C3-C2-N1-C8
11	A	500	ACH	C3-C2-N1-C9

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
11	A	500	ACH	1	0
11	L	501	ACH	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.

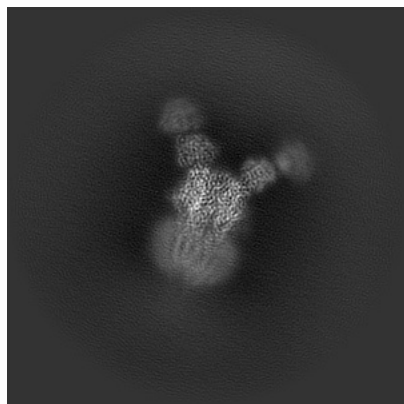
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-51570. These allow visual inspection of the internal detail of the map and identification of artifacts.

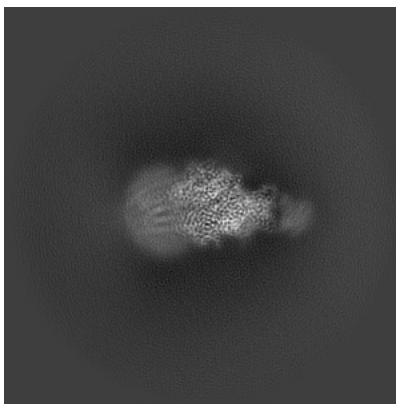
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

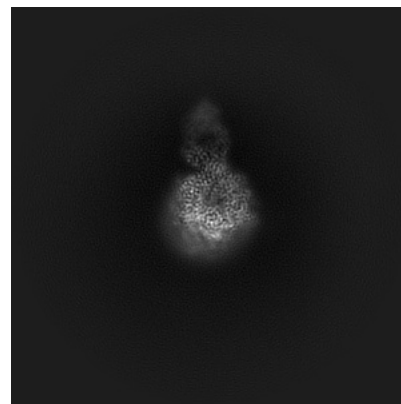
6.1.1 Primary map



X

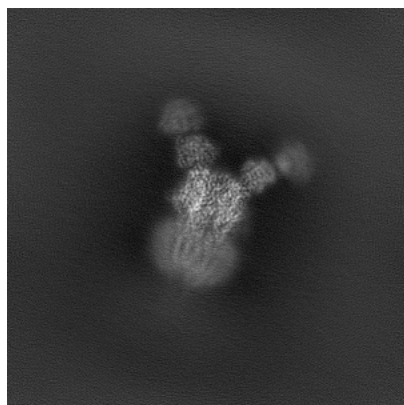


Y

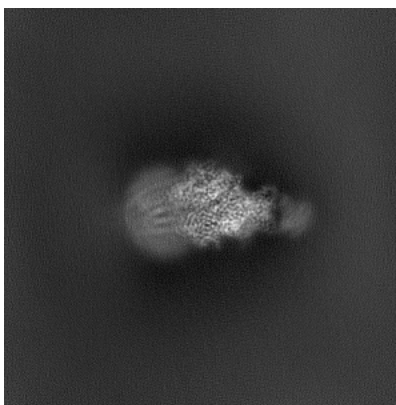


Z

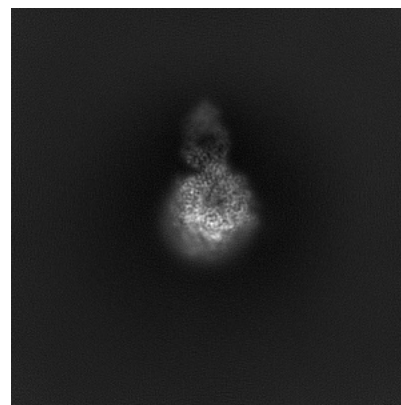
6.1.2 Raw map



X



Y

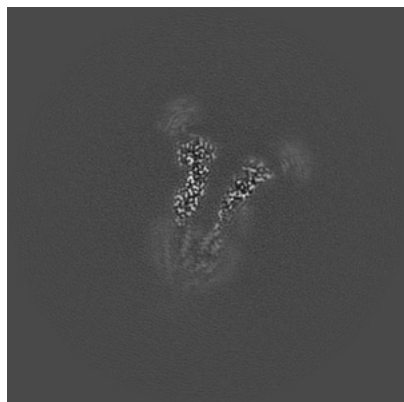


Z

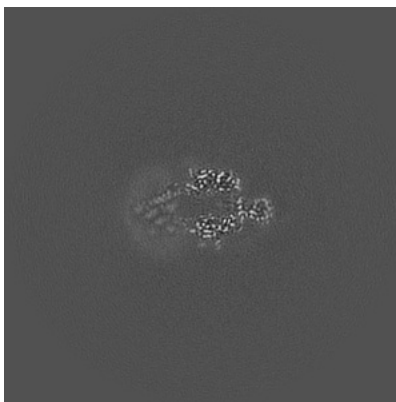
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

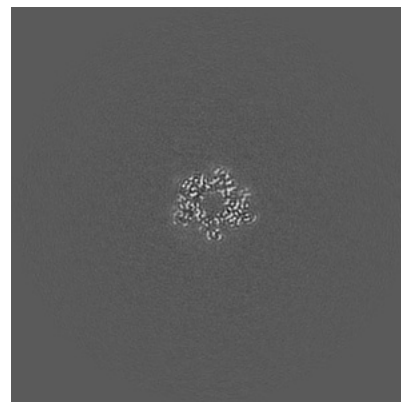
6.2.1 Primary map



X Index: 216

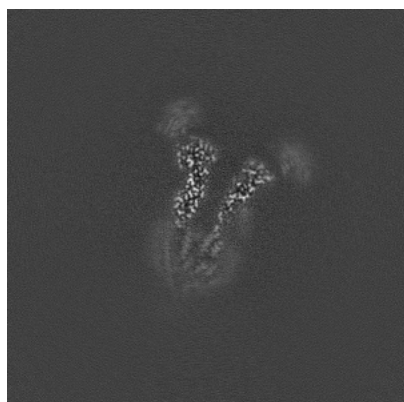


Y Index: 216

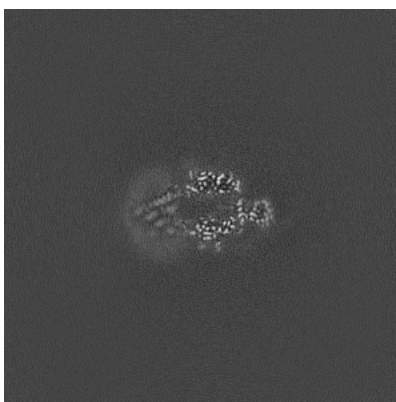


Z Index: 216

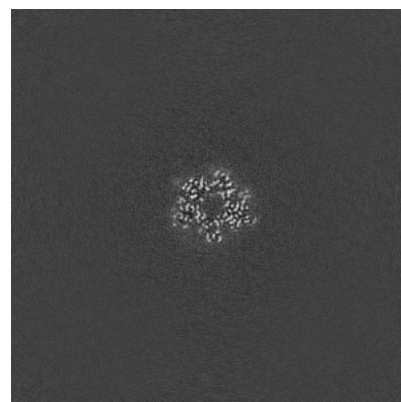
6.2.2 Raw map



X Index: 216



Y Index: 216

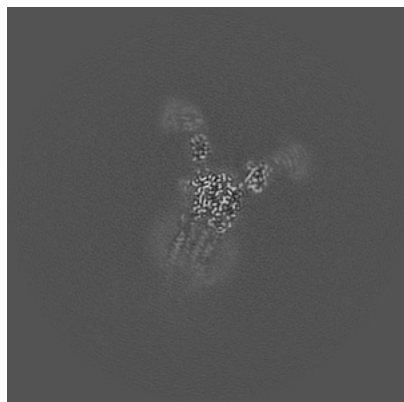


Z Index: 216

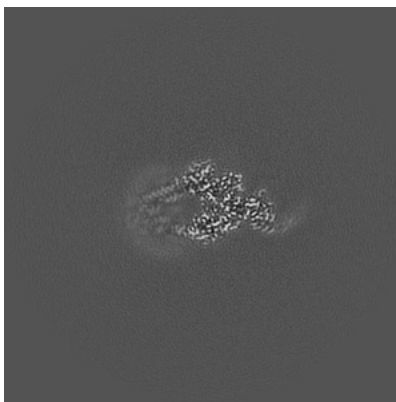
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

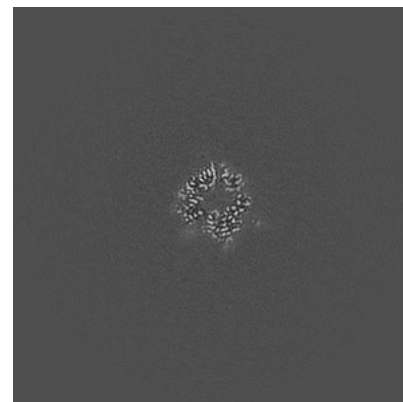
6.3.1 Primary map



X Index: 200



Y Index: 206

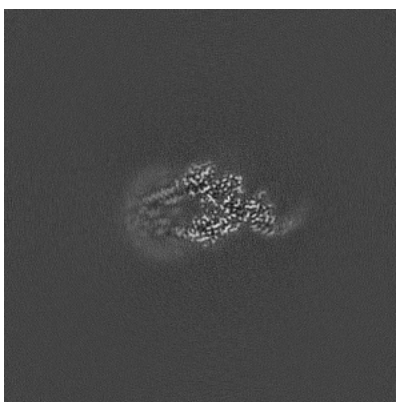


Z Index: 228

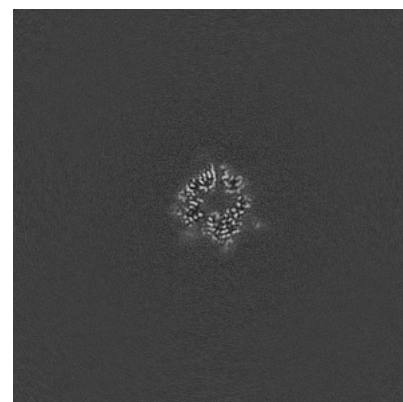
6.3.2 Raw map



X Index: 201



Y Index: 206

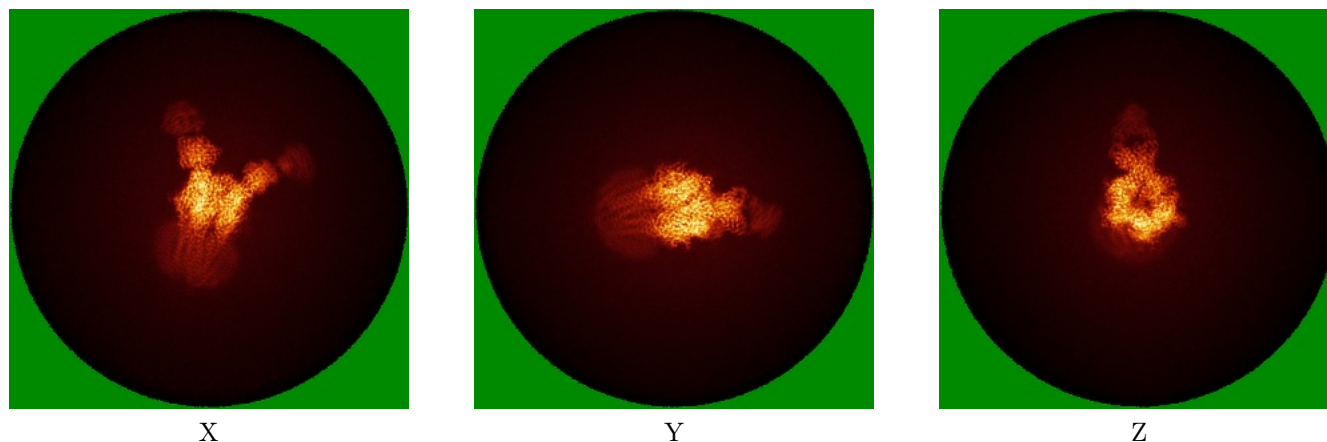


Z Index: 228

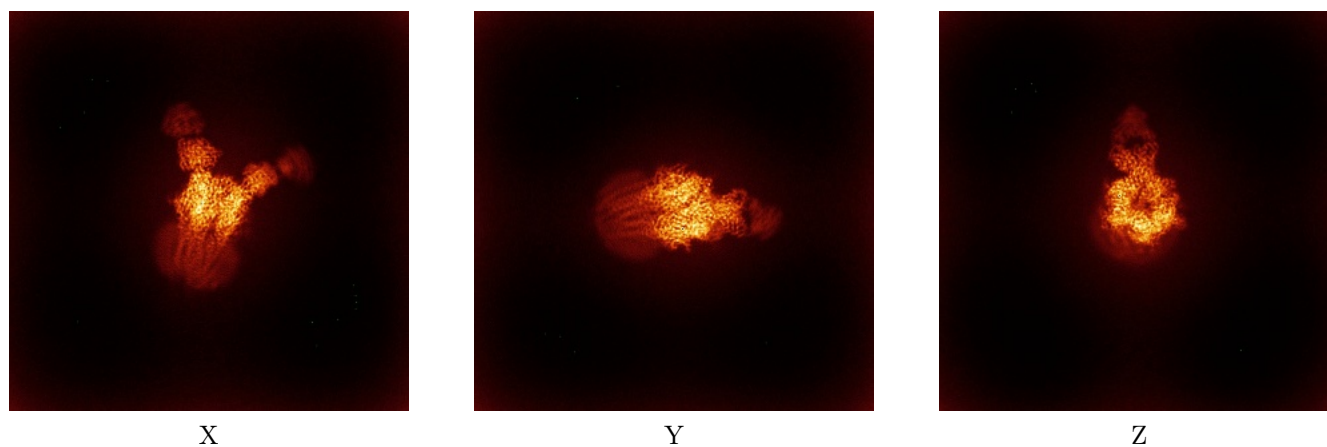
The images above show the largest variance slices of the map in three orthogonal directions.

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](#)

6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.3. 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.

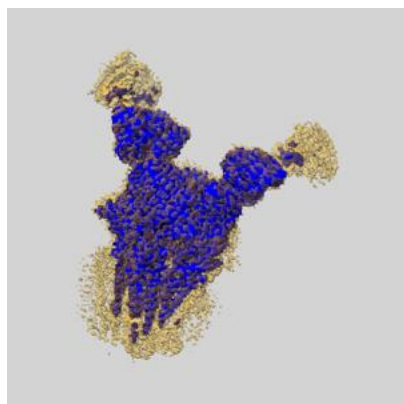
6.6 Mask visualisation [i](#)

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

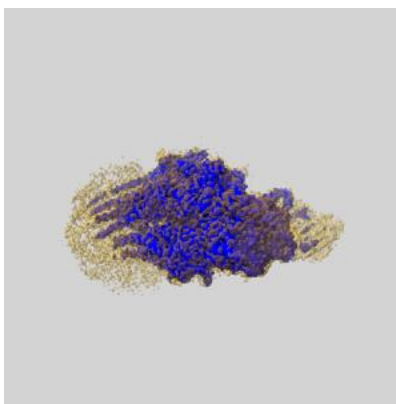
A mask typically either:

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

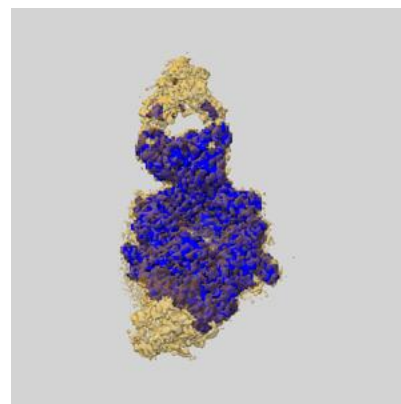
6.6.1 emd_51570_msk_1.map [i](#)



X

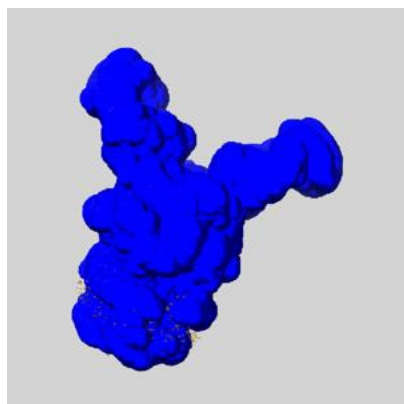


Y



Z

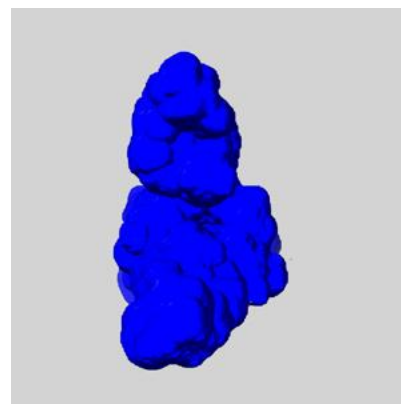
6.6.2 emd_51570_msk_2.map [i](#)



X



Y

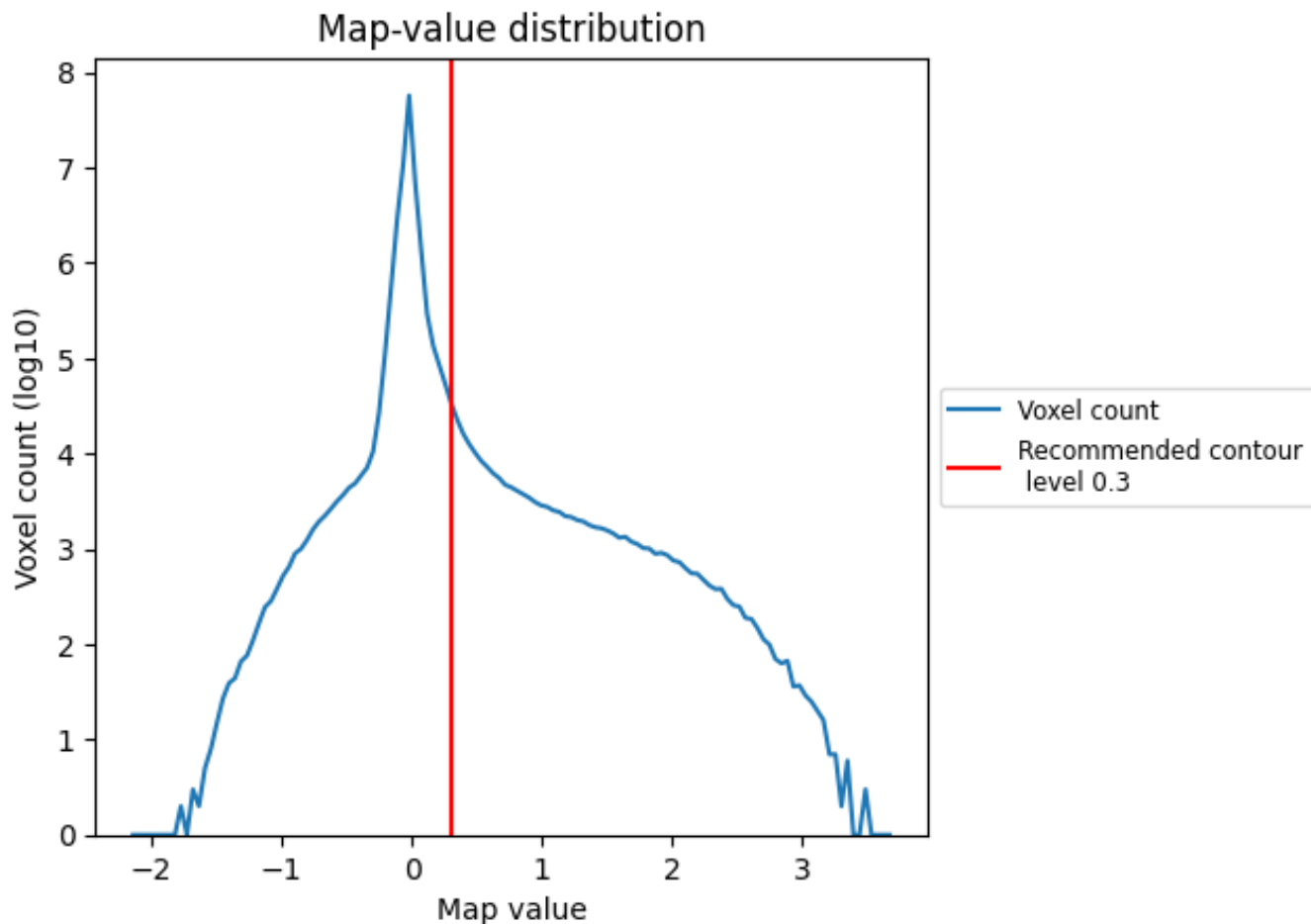


Z

7 Map analysis [i](#)

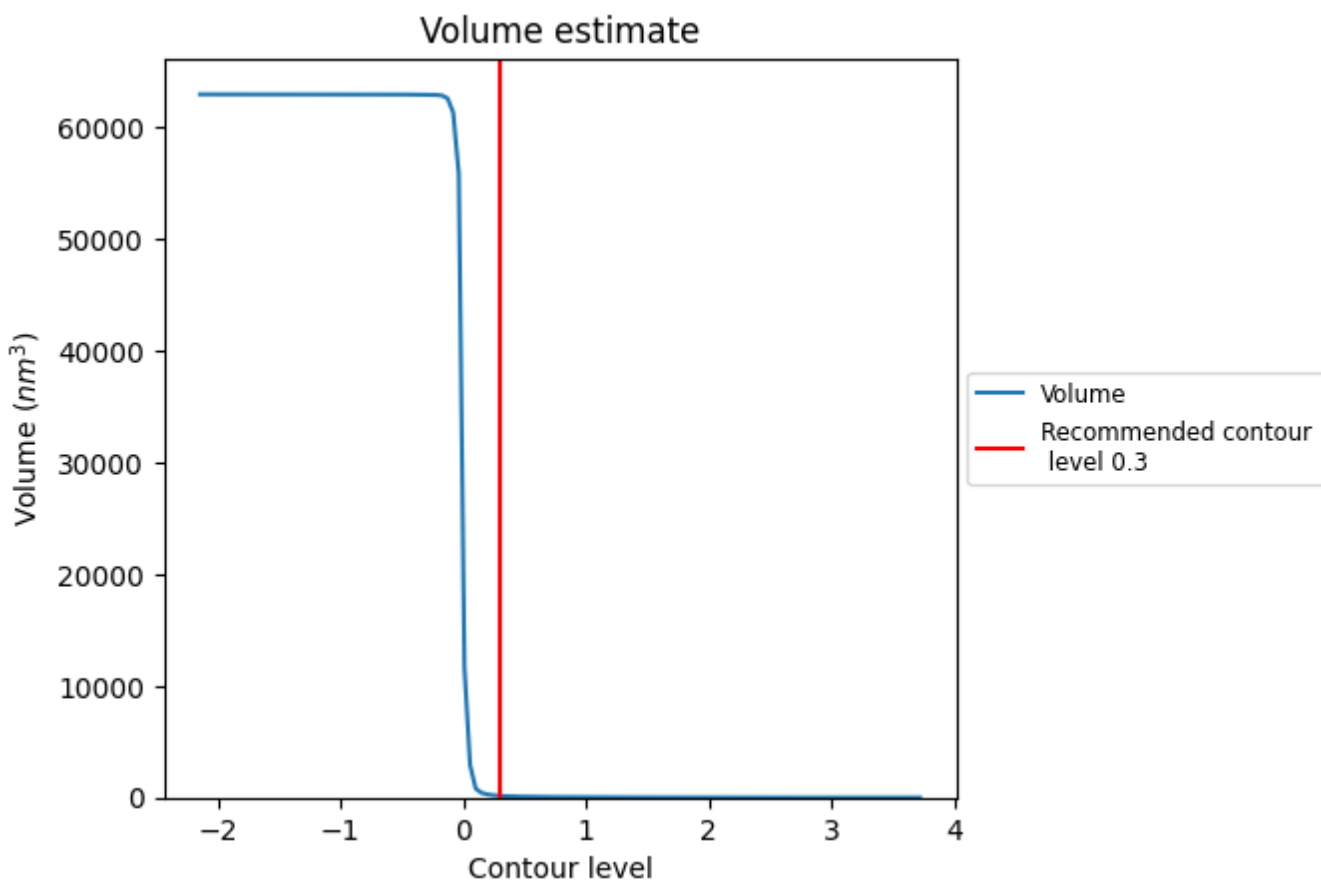
This section contains the results of statistical analysis of the map.

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.

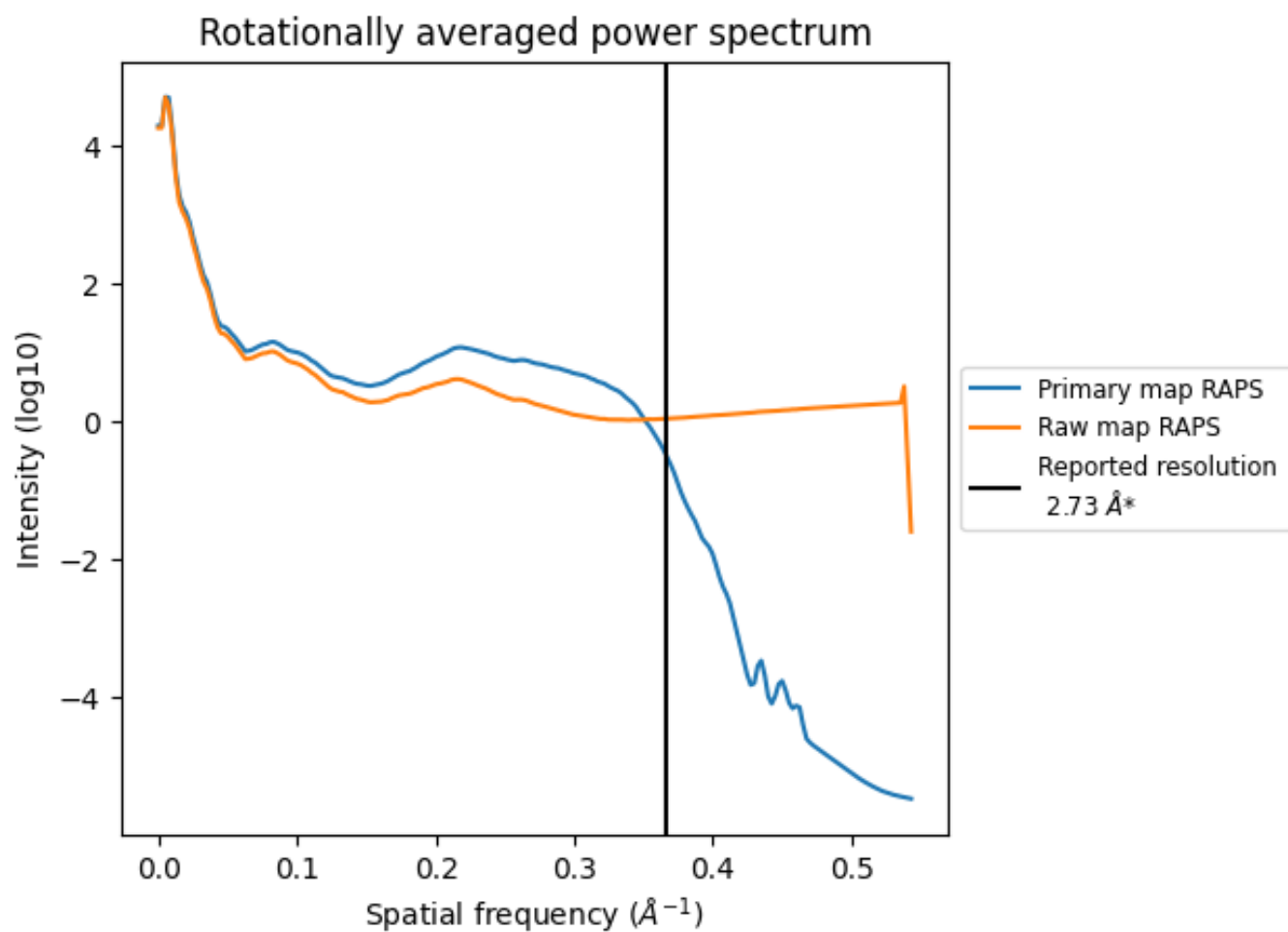
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 153 nm³; this corresponds to an approximate mass of 139 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum i

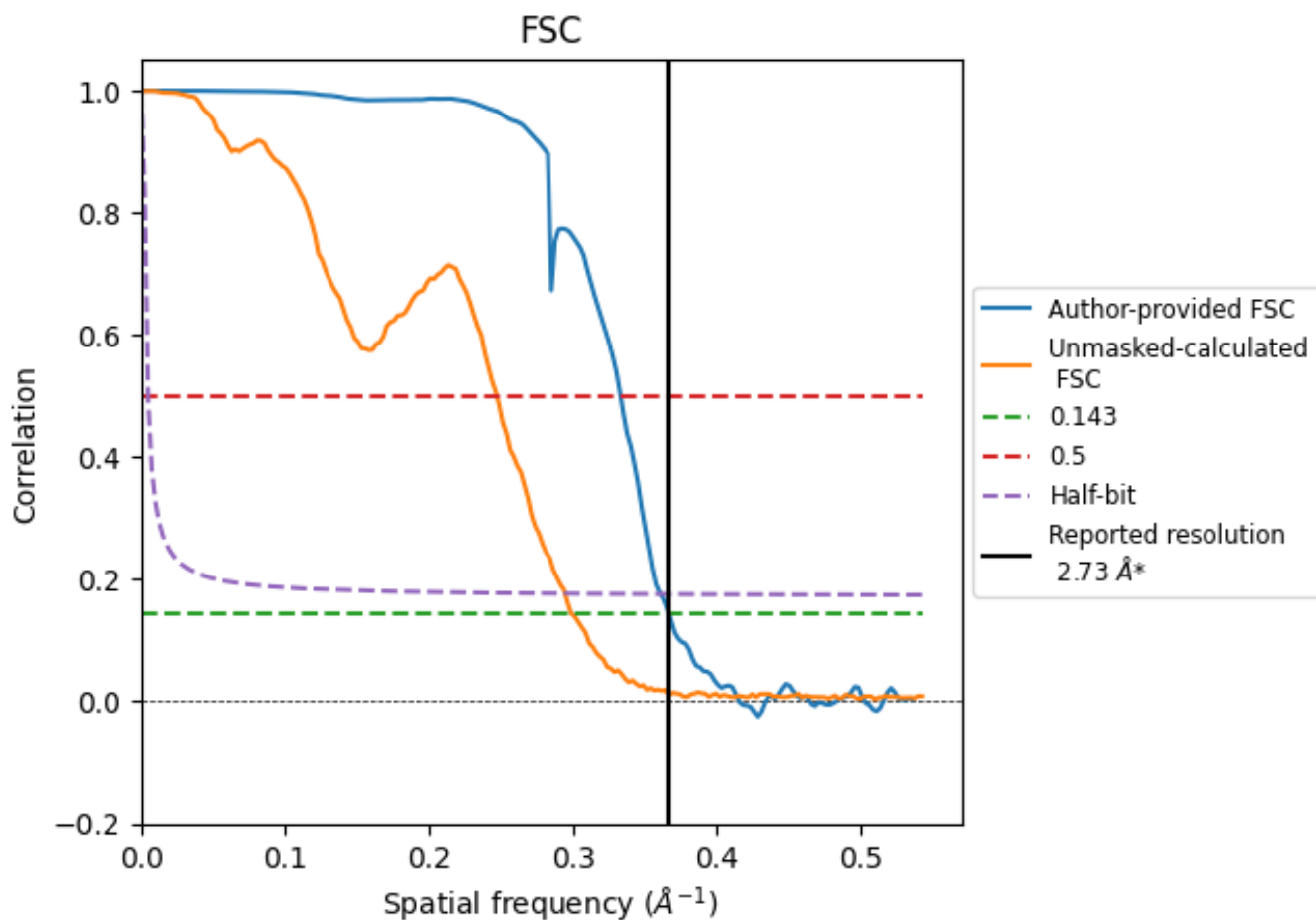


*Reported resolution corresponds to spatial frequency of 0.366 Å⁻¹

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 0.366\AA^{-1}

8.2 Resolution estimates [i](#)

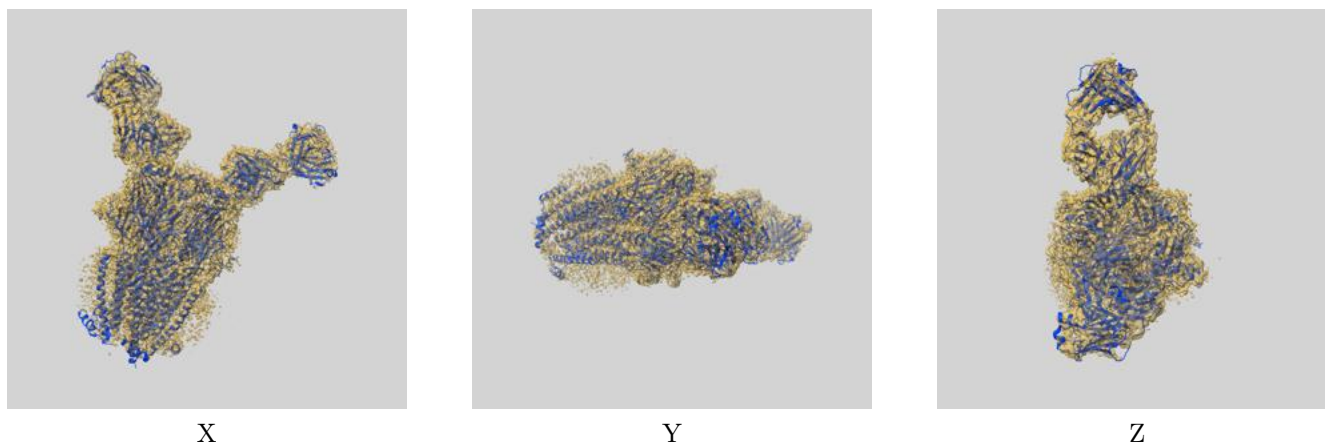
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.73	-	-
Author-provided FSC curve	2.72	3.00	2.77
Unmasked-calculated*	3.34	4.05	3.39

*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 3.34 differs from the reported value 2.73 by more than 10 %

9 Map-model fit [i](#)

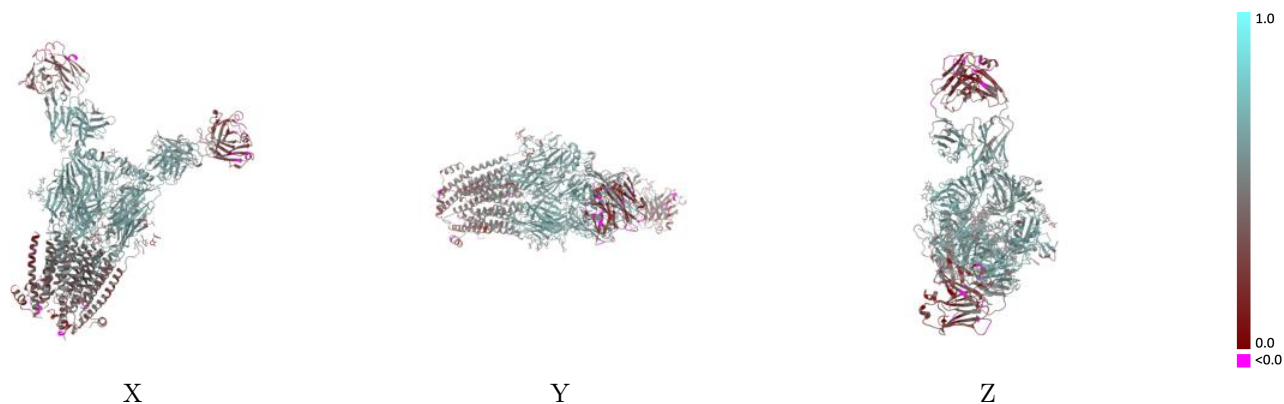
This section contains information regarding the fit between EMDB map EMD-51570 and PDB model 9GU2. Per-residue inclusion information can be found in section 3 on page 9.

9.1 Map-model overlay [i](#)



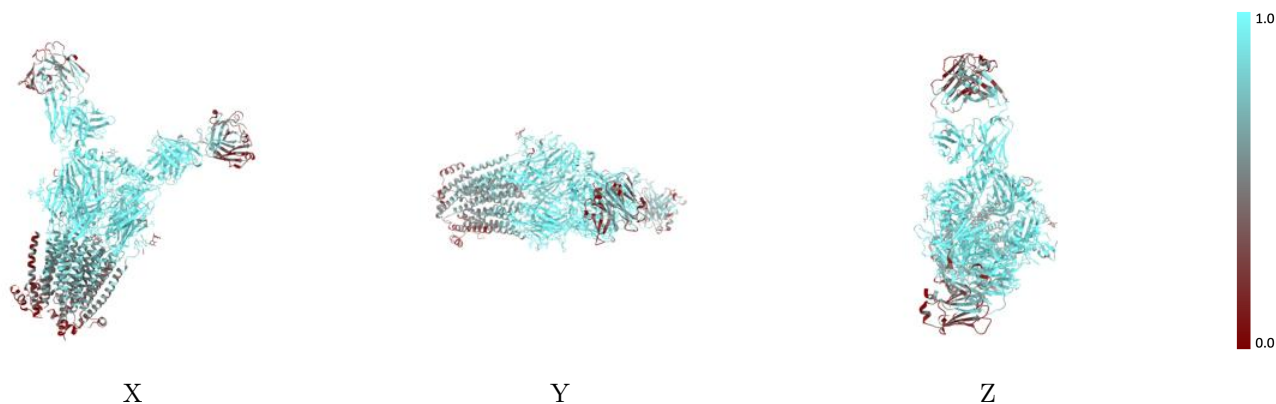
The images above show the 3D surface view of the map at the recommended contour level 0.3 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



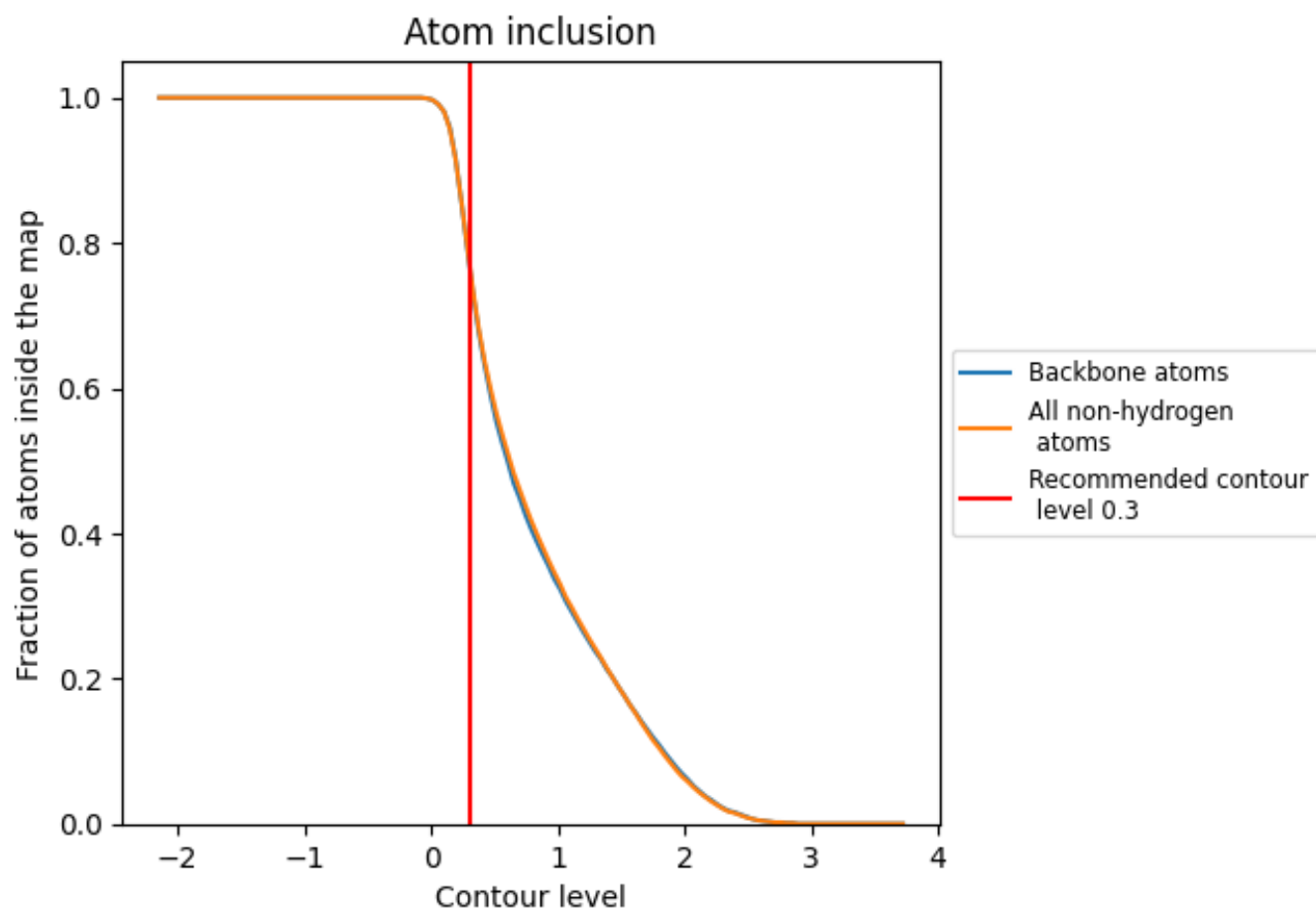
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.3).

































9.4 Atom inclusion [i](#)



At the recommended contour level, 77% of all backbone atoms, 78% 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 (0.3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7750	 0.4970
A	 0.7830	 0.5270
B	 0.7910	 0.5040
C	 0.6970	 0.4470
D	 0.8220	 0.5330
E	 0.7970	 0.5230
F	 0.7700	 0.4550
G	 0.6770	 0.4090
H	 0.7410	 0.4310
I	 0.9400	 0.5360
J	 0.6000	 0.3320
K	 0.7210	 0.4170
L	 0.7990	 0.5370
M	 0.7860	 0.4430
N	 0.9000	 0.4710
O	 0.9760	 0.5590

