



Full wwPDB EM Validation Report ⓘ

Mar 6, 2026 – 07:05 AM UTC

PDB ID : 8HGP / pdb_00008hgp
EMDB ID : EMD-34745
Title : The EREG-bound EGFR/HER2 ectodomain complex
Authors : Zhang, Z.; Bai, X.
Deposited on : 2022-11-15
Resolution : 4.53 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

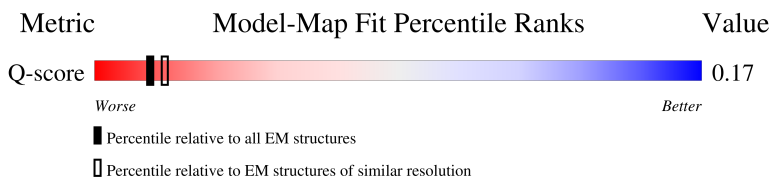
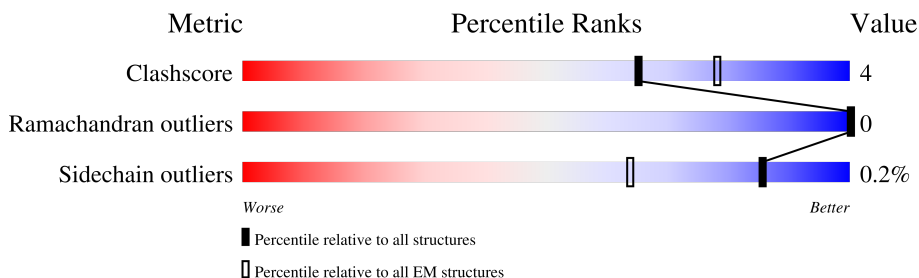
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

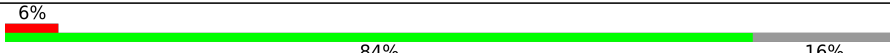
The reported resolution of this entry is 4.53 Å.

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	2491 (4.03 - 5.03)

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	B	745	
2	A	736	
3	C	49	
4	D	4	

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Mol	Chain	Length	Quality of chain
5	E	2	

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 9169 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 Receptor tyrosine-protein kinase erbB-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	563	Total	C	N	O	S	0	0
			4345	2701	783	812	49		

There are 52 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	694	GLY	-	expression tag	UNP P04626
B	695	GLY	-	expression tag	UNP P04626
B	696	SER	-	expression tag	UNP P04626
B	697	GLU	-	expression tag	UNP P04626
B	698	ASN	-	expression tag	UNP P04626
B	699	LEU	-	expression tag	UNP P04626
B	700	TYR	-	expression tag	UNP P04626
B	701	PHE	-	expression tag	UNP P04626
B	702	GLN	-	expression tag	UNP P04626
B	703	GLY	-	expression tag	UNP P04626
B	704	GLY	-	expression tag	UNP P04626
B	705	GLY	-	expression tag	UNP P04626
B	706	SER	-	expression tag	UNP P04626
B	707	ALA	-	expression tag	UNP P04626
B	708	GLN	-	expression tag	UNP P04626
B	709	LEU	-	expression tag	UNP P04626
B	710	GLU	-	expression tag	UNP P04626
B	711	LYS	-	expression tag	UNP P04626
B	712	GLU	-	expression tag	UNP P04626
B	713	LEU	-	expression tag	UNP P04626
B	714	GLN	-	expression tag	UNP P04626
B	715	ALA	-	expression tag	UNP P04626
B	716	LEU	-	expression tag	UNP P04626
B	717	GLU	-	expression tag	UNP P04626
B	718	LYS	-	expression tag	UNP P04626
B	719	GLU	-	expression tag	UNP P04626
B	720	ASN	-	expression tag	UNP P04626
B	721	ALA	-	expression tag	UNP P04626

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Chain	Residue	Modelled	Actual	Comment	Reference
B	722	GLN	-	expression tag	UNP P04626
B	723	LEU	-	expression tag	UNP P04626
B	724	GLU	-	expression tag	UNP P04626
B	725	TRP	-	expression tag	UNP P04626
B	726	GLU	-	expression tag	UNP P04626
B	727	LEU	-	expression tag	UNP P04626
B	728	GLN	-	expression tag	UNP P04626
B	729	ALA	-	expression tag	UNP P04626
B	730	LEU	-	expression tag	UNP P04626
B	731	GLU	-	expression tag	UNP P04626
B	732	LYS	-	expression tag	UNP P04626
B	733	GLU	-	expression tag	UNP P04626
B	734	LEU	-	expression tag	UNP P04626
B	735	ALA	-	expression tag	UNP P04626
B	736	GLN	-	expression tag	UNP P04626
B	737	SER	-	expression tag	UNP P04626
B	738	ASN	-	expression tag	UNP P04626
B	739	SER	-	expression tag	UNP P04626
B	740	LEU	-	expression tag	UNP P04626
B	741	GLU	-	expression tag	UNP P04626
B	742	VAL	-	expression tag	UNP P04626
B	743	LEU	-	expression tag	UNP P04626
B	744	PHE	-	expression tag	UNP P04626
B	745	GLN	-	expression tag	UNP P04626

- Molecule 2 is a protein called Epidermal growth factor receptor.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	568	Total	C	N	O	S	0	0
			4391	2709	784	845	53		

There are 53 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	684	GLY	-	expression tag	UNP P00533
A	685	GLY	-	expression tag	UNP P00533
A	686	SER	-	expression tag	UNP P00533
A	687	GLU	-	expression tag	UNP P00533
A	688	ASN	-	expression tag	UNP P00533
A	689	LEU	-	expression tag	UNP P00533
A	690	TYR	-	expression tag	UNP P00533
A	691	PHE	-	expression tag	UNP P00533

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Chain	Residue	Modelled	Actual	Comment	Reference
A	692	GLN	-	expression tag	UNP P00533
A	693	GLY	-	expression tag	UNP P00533
A	694	GLY	-	expression tag	UNP P00533
A	695	GLY	-	expression tag	UNP P00533
A	696	SER	-	expression tag	UNP P00533
A	697	ALA	-	expression tag	UNP P00533
A	698	ALA	-	expression tag	UNP P00533
A	699	GLN	-	expression tag	UNP P00533
A	700	LEU	-	expression tag	UNP P00533
A	701	LYS	-	expression tag	UNP P00533
A	702	LYS	-	expression tag	UNP P00533
A	703	LYS	-	expression tag	UNP P00533
A	704	LEU	-	expression tag	UNP P00533
A	705	GLN	-	expression tag	UNP P00533
A	706	ALA	-	expression tag	UNP P00533
A	707	LEU	-	expression tag	UNP P00533
A	708	LYS	-	expression tag	UNP P00533
A	709	LYS	-	expression tag	UNP P00533
A	710	LYS	-	expression tag	UNP P00533
A	711	ASN	-	expression tag	UNP P00533
A	712	ALA	-	expression tag	UNP P00533
A	713	GLN	-	expression tag	UNP P00533
A	714	LEU	-	expression tag	UNP P00533
A	715	LYS	-	expression tag	UNP P00533
A	716	TRP	-	expression tag	UNP P00533
A	717	LYS	-	expression tag	UNP P00533
A	718	LEU	-	expression tag	UNP P00533
A	719	GLN	-	expression tag	UNP P00533
A	720	ALA	-	expression tag	UNP P00533
A	721	LEU	-	expression tag	UNP P00533
A	722	LYS	-	expression tag	UNP P00533
A	723	LYS	-	expression tag	UNP P00533
A	724	LYS	-	expression tag	UNP P00533
A	725	LEU	-	expression tag	UNP P00533
A	726	ALA	-	expression tag	UNP P00533
A	727	GLN	-	expression tag	UNP P00533
A	728	SER	-	expression tag	UNP P00533
A	729	ASN	-	expression tag	UNP P00533
A	730	SER	-	expression tag	UNP P00533
A	731	LEU	-	expression tag	UNP P00533
A	732	GLU	-	expression tag	UNP P00533
A	733	VAL	-	expression tag	UNP P00533

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Chain	Residue	Modelled	Actual	Comment	Reference
A	734	LEU	-	expression tag	UNP P00533
A	735	PHE	-	expression tag	UNP P00533
A	736	GLN	-	expression tag	UNP P00533

- Molecule 3 is a protein called Proepiregulin.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	41	Total	C	N	O	S	0	0
			327	202	56	61	8		

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



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

- 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	C	N	O	0	0
			28	16	2	10		

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆) (labeled as "Ligand of Interest" by depositor).

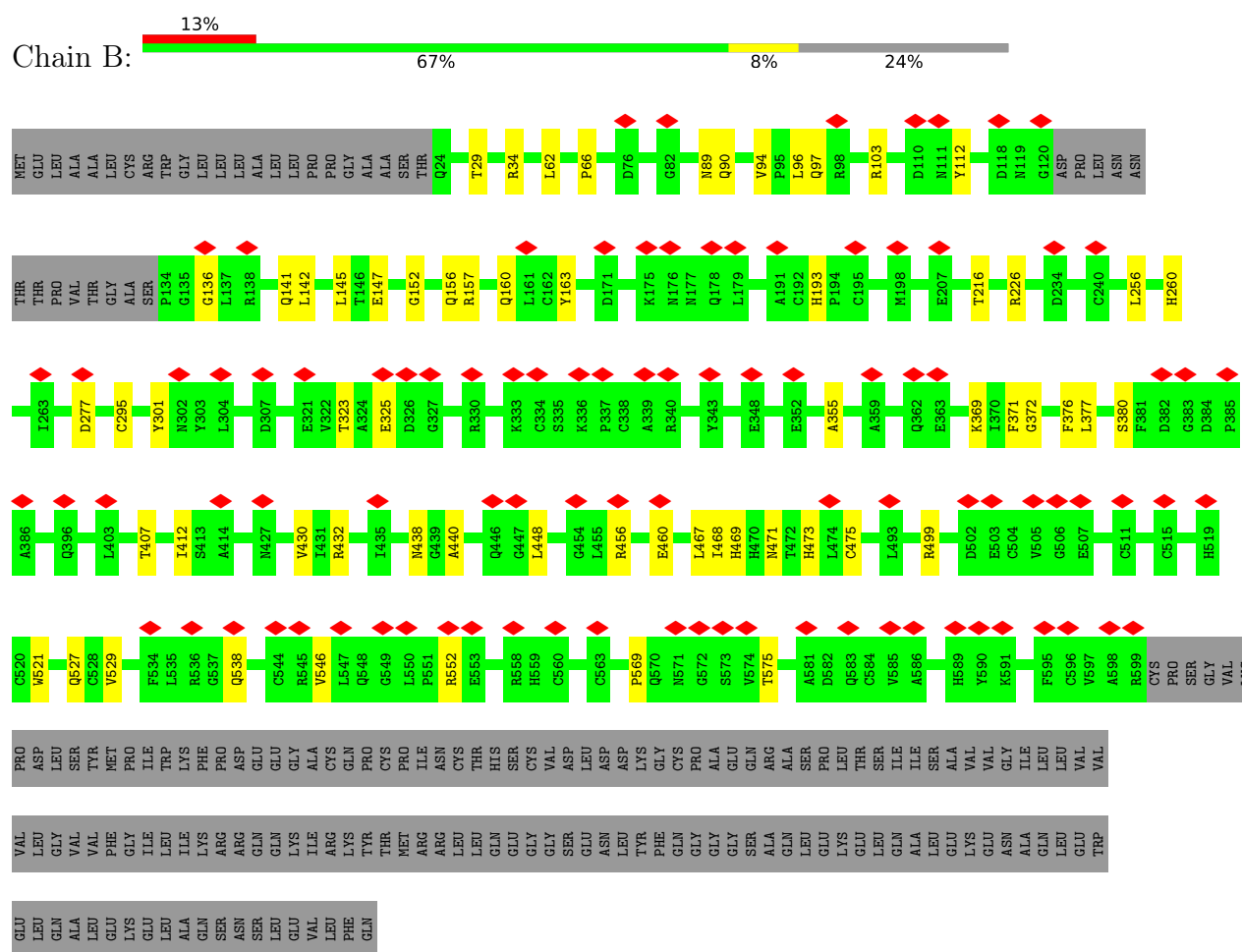


Mol	Chain	Residues	Atoms				AltConf
6	A	1	Total	C	N	O	0
			14	8	1	5	
6	A	1	Total	C	N	O	0
			14	8	1	5	

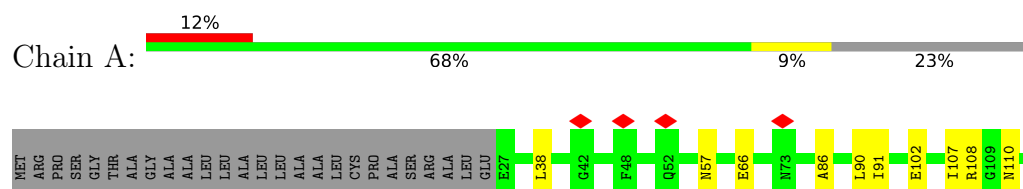
3 Residue-property plots

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: Receptor tyrosine-protein kinase erbB-2



• Molecule 2: Epidermal growth factor receptor





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	273388	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60.8	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.047	Depositor
Minimum map value	-0.002	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.016	Depositor
Recommended contour level	0.145	Depositor
Map size ($\text{\AA}$)	410.88, 410.88, 410.88	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.07, 1.07, 1.07	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, NAG, 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	B	0.15	0/4446	0.39	0/6046
2	A	0.15	0/4472	0.42	0/6043
3	C	0.12	0/334	0.35	0/447
All	All	0.15	0/9252	0.40	0/12536

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	B	4345	0	4165	36	0
2	A	4391	0	4250	37	0
3	C	327	0	290	0	0
4	D	50	0	43	1	0
5	E	28	0	25	0	0
6	A	28	0	26	1	0
All	All	9169	0	8799	72	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.

All (72) 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:B:521:TRP:HE1	1:B:529:VAL:HB	1.63	0.63
2:A:371:ILE:HD12	2:A:407:ILE:HG12	1.83	0.60
2:A:468:ASN:HA	2:A:494:ARG:HD3	1.85	0.59
2:A:350:SER:HB2	2:A:372:LEU:HD12	1.85	0.58
2:A:38:LEU:HD12	2:A:90:LEU:HD21	1.85	0.57
1:B:552:ARG:HE	1:B:569:PRO:HB3	1.70	0.57
2:A:319:GLU:HB3	2:A:324:ARG:HD2	1.85	0.57
1:B:34:ARG:NH2	1:B:438:ASN:OD1	2.40	0.55
1:B:372:GLY:H	1:B:407:THR:HG1	1.54	0.55
2:A:57:ASN:HD21	6:A:801:NAG:H62	1.71	0.54
1:B:66:PRO:HA	1:B:90:GLN:HB2	1.90	0.54
1:B:376:PHE:HB2	1:B:412:ILE:HA	1.90	0.53
1:B:136:GLY:HA3	1:B:160:GLN:HG3	1.89	0.53
2:A:438:LEU:HB3	2:A:461:VAL:HG22	1.91	0.53
1:B:301:TYR:OH	1:B:432:ARG:NH1	2.42	0.52
2:A:309:ARG:O	2:A:429:ARG:NH1	2.43	0.52
1:B:260:HIS:HB3	1:B:295:CYS:HB2	1.91	0.52
2:A:199:CYS:HA	2:A:207:CYS:HA	1.92	0.52
1:B:29:THR:HG22	1:B:440:ALA:HB2	1.92	0.52
2:A:190:CYS:SG	2:A:191:ASP:N	2.83	0.52
1:B:546:VAL:O	1:B:552:ARG:NH2	2.44	0.51
2:A:472:ALA:HB1	2:A:490:ILE:HD13	1.91	0.51
2:A:458:ASP:HA	2:A:486:GLN:HE22	1.75	0.50
1:B:147:GLU:OE1	1:B:226:ARG:NH2	2.44	0.49
2:A:509:LEU:HD21	2:A:527:ARG:HH11	1.77	0.49
1:B:456:ARG:NH2	1:B:538:GLN:OE1	2.46	0.49
1:B:468:ILE:HG23	1:B:471:ASN:HD22	1.75	0.49
2:A:91:ILE:HG22	2:A:124:ASN:HD21	1.77	0.49
1:B:473:HIS:HA	1:B:499:ARG:HH21	1.78	0.48
2:A:66:GLU:HG2	2:A:90:LEU:HB3	1.95	0.48
1:B:277:ASP:OD1	2:A:110:ASN:ND2	2.46	0.48
2:A:516:TRP:H	2:A:522:ASP:HB3	1.79	0.48
1:B:216:THR:OG1	1:B:226:ARG:NH1	2.47	0.47
2:A:280:ASN:HB2	2:A:283:GLY:H	1.79	0.47
2:A:102:GLU:HB3	2:A:138:ARG:HH21	1.80	0.47
2:A:280:ASN:ND2	2:A:283:GLY:O	2.48	0.47
2:A:119:LEU:HB3	2:A:148:VAL:HG22	1.96	0.47
2:A:384:THR:HG21	4:D:1:NAG:HN2	1.80	0.47
2:A:529:VAL:HG21	2:A:539:CYS:H	1.79	0.47
1:B:475:CYS:HB2	1:B:499:ARG:HD2	1.95	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:62:LEU:O	1:B:89:ASN:ND2	2.43	0.46
2:A:530:SER:HB2	2:A:554:GLU:HG2	1.98	0.46
2:A:119:LEU:HD21	2:A:137:MET:HE1	1.97	0.46
2:A:415:THR:HB	2:A:446:THR:HG22	1.99	0.45
1:B:103:ARG:NH1	1:B:256:LEU:O	2.39	0.44
2:A:445:ILE:HG13	2:A:469:LEU:HD13	1.99	0.44
1:B:163:TYR:OH	1:B:193:HIS:O	2.27	0.44
1:B:407:THR:HA	1:B:432:ARG:HB2	2.00	0.43
2:A:402:THR:HA	2:A:427:ARG:HB2	2.01	0.43
2:A:477:TRP:HA	2:A:480:LEU:HD23	2.00	0.43
2:A:118:ALA:HB2	2:A:146:GLY:HA3	2.01	0.43
2:A:407:ILE:HG22	2:A:443:LEU:HD21	2.01	0.43
1:B:467:LEU:HG	1:B:469:HIS:HD2	1.84	0.43
1:B:430:VAL:HG23	1:B:460:GLU:HB3	2.01	0.42
2:A:350:SER:HA	2:A:370:HIS:HB2	2.01	0.42
1:B:97:GLN:NE2	1:B:141:GLN:OE1	2.53	0.42
1:B:355:ALA:HB2	1:B:377:LEU:HB2	2.01	0.42
1:B:323:THR:HG22	1:B:325:GLU:H	1.85	0.42
1:B:369:LYS:HE2	1:B:371:PHE:HE1	1.85	0.42
1:B:521:TRP:HB2	1:B:527:GLN:HB3	2.01	0.42
2:A:136:PRO:HB3	2:A:206:ASN:HD21	1.85	0.41
2:A:86:ALA:HA	2:A:108:ARG:HB2	2.02	0.41
2:A:494:ARG:NE	2:A:498:SER:OG	2.45	0.41
2:A:271:ASN:ND2	2:A:274:THR:OG1	2.53	0.41
1:B:112:TYR:HA	1:B:152:GLY:H	1.86	0.41
1:B:156:GLN:HG2	1:B:157:ARG:HG3	2.03	0.41
2:A:107:ILE:HB	2:A:143:ILE:HG12	2.03	0.41
1:B:94:VAL:HG12	1:B:96:LEU:HG	2.03	0.40
1:B:142:LEU:HD13	1:B:145:LEU:HD23	2.02	0.40
1:B:355:ALA:HB1	1:B:380:SER:HB2	2.02	0.40
1:B:448:LEU:N	1:B:471:ASN:OD1	2.45	0.40
1:B:552:ARG:HG3	1:B:575:THR:HG21	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

entries.

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	559/745 (75%)	516 (92%)	43 (8%)	0	100	100
2	A	566/736 (77%)	511 (90%)	55 (10%)	0	100	100
3	C	39/49 (80%)	38 (97%)	1 (3%)	0	100	100
All	All	1164/1530 (76%)	1065 (92%)	99 (8%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	484/637 (76%)	484 (100%)	0	100	100
2	A	500/629 (80%)	498 (100%)	2 (0%)	84	82
3	C	37/44 (84%)	37 (100%)	0	100	100
All	All	1021/1310 (78%)	1019 (100%)	2 (0%)	85	85

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	509	LEU
2	A	510	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	48	HIS
1	B	57	GLN
1	B	319	ASN
1	B	437	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	470	HIS
1	B	589	HIS
2	A	47	HIS
2	A	57	ASN
2	A	158	ASN
2	A	206	ASN
2	A	271	ASN
2	A	358	HIS
2	A	370	HIS
2	A	422	ASN
2	A	432	GLN
2	A	433	HIS
2	A	486	GLN
2	A	540	ASN

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 ⓘ

6 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	D	1	2,4	14,14,15	0.25	0	17,19,21	0.61	0
4	NAG	D	2	4	14,14,15	0.31	0	17,19,21	0.70	0
4	BMA	D	3	4	11,11,12	0.85	0	15,15,17	0.74	0
4	MAN	D	4	4	11,11,12	1.08	2 (18%)	15,15,17	1.30	2 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	NAG	E	1	5,1	14,14,15	0.53	0	17,19,21	1.05	1 (5%)
5	NAG	E	2	5	14,14,15	0.36	0	17,19,21	0.50	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	D	1	2,4	-	2/6/23/26	0/1/1/1
4	NAG	D	2	4	-	1/6/23/26	0/1/1/1
4	BMA	D	3	4	-	0/2/19/22	0/1/1/1
4	MAN	D	4	4	-	1/2/19/22	1/1/1/1
5	NAG	E	1	5,1	-	2/6/23/26	0/1/1/1
5	NAG	E	2	5	-	1/6/23/26	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	4	MAN	O5-C5	2.34	1.48	1.43
4	D	4	MAN	C1-C2	2.07	1.57	1.52

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	4	MAN	C1-O5-C5	4.15	117.75	112.19
5	E	1	NAG	C2-N2-C7	3.19	127.17	122.90
4	D	4	MAN	O2-C2-C3	-2.11	105.78	110.15

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	D	1	NAG	C8-C7-N2-C2
4	D	1	NAG	O7-C7-N2-C2
5	E	2	NAG	O5-C5-C6-O6
4	D	4	MAN	O5-C5-C6-O6
5	E	1	NAG	C1-C2-N2-C7
5	E	1	NAG	C3-C2-N2-C7
4	D	2	NAG	C4-C5-C6-O6

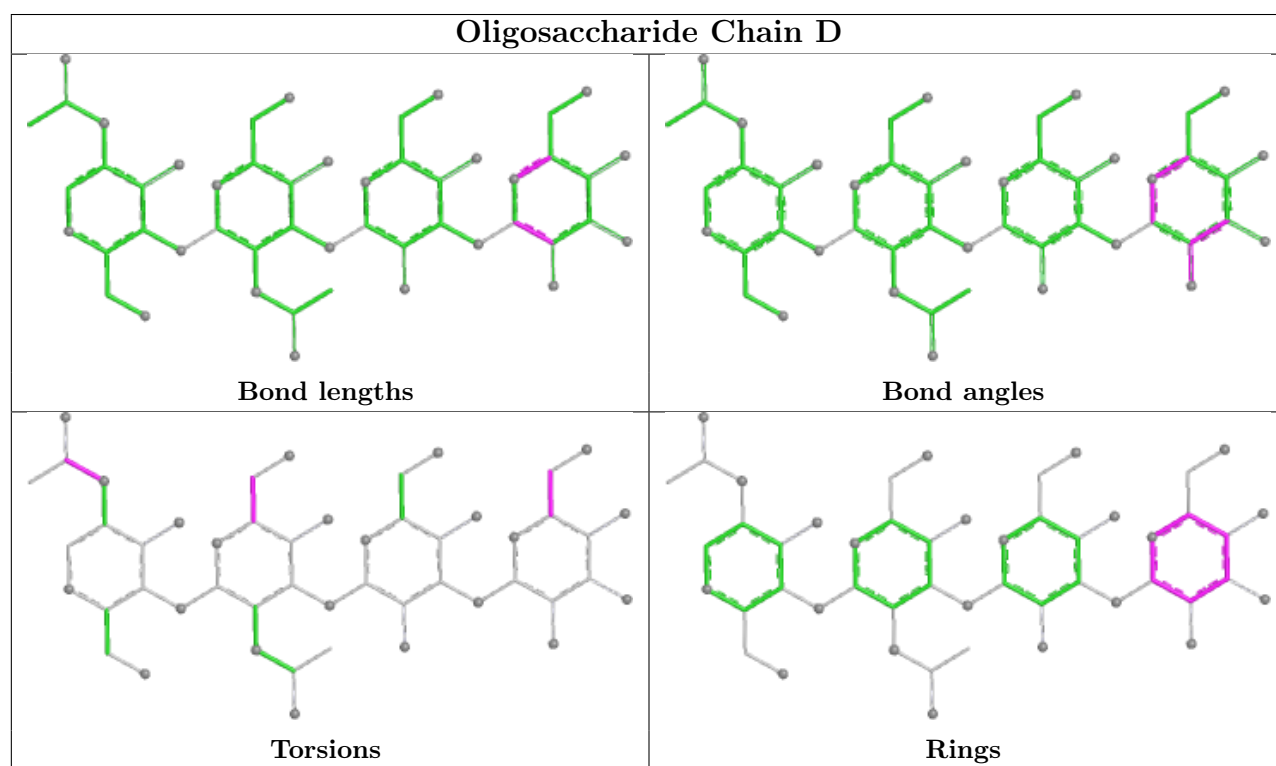
All (1) ring outliers are listed below:

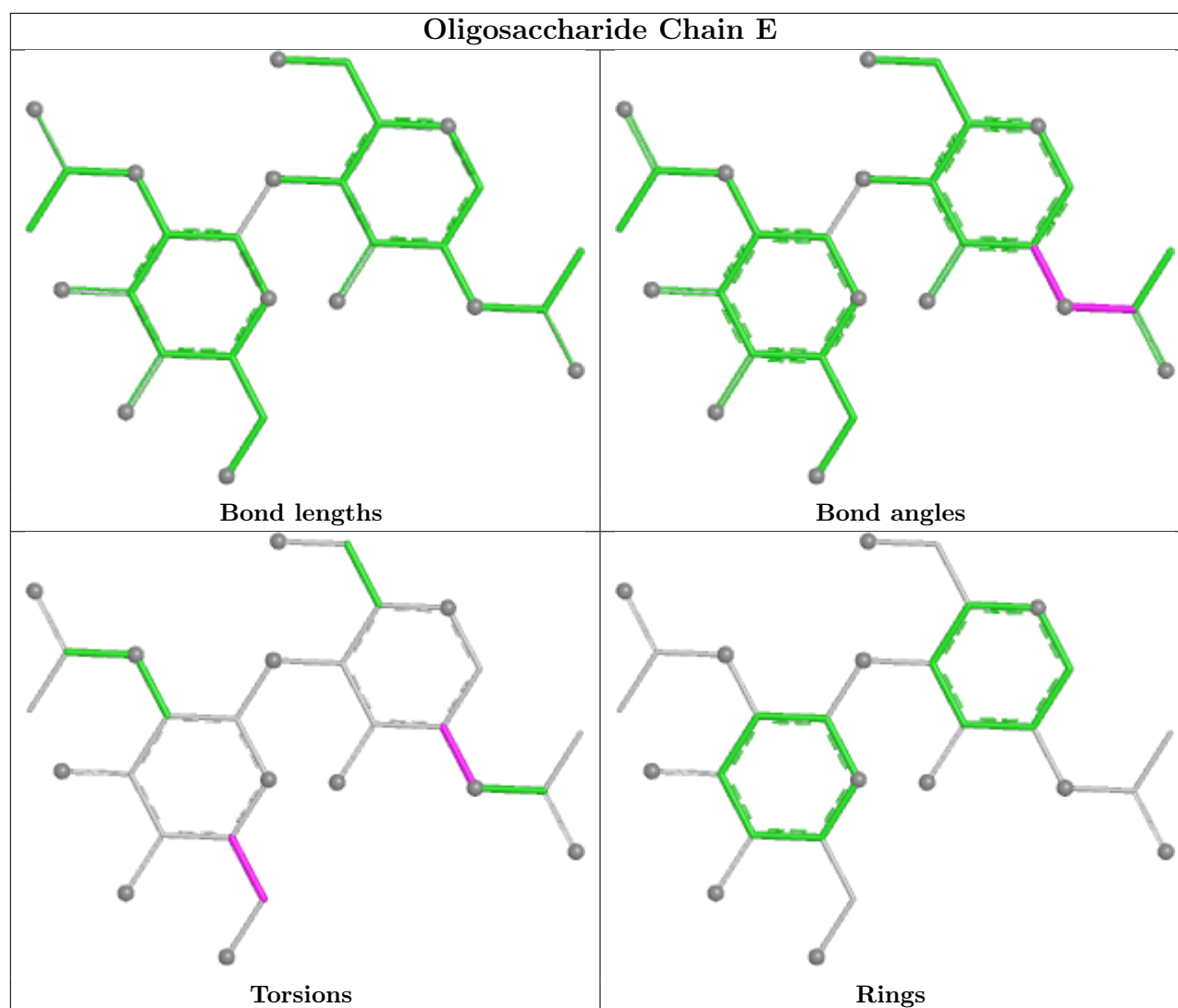
Mol	Chain	Res	Type	Atoms
4	D	4	MAN	C1-C2-C3-C4-C5-O5

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	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](#)

2 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
6	NAG	A	801	2	14,14,15	0.41	0	17,19,21	0.45	0
6	NAG	A	802	2	14,14,15	0.98	1 (7%)	17,19,21	2.36	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
6	NAG	A	801	2	-	2/6/23/26	0/1/1/1
6	NAG	A	802	2	-	6/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	802	NAG	C1-C2	3.10	1.56	1.52

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	802	NAG	C2-N2-C7	8.26	133.96	122.90
6	A	802	NAG	C1-C2-N2	4.13	116.95	110.43
6	A	802	NAG	C8-C7-N2	2.08	119.57	116.12

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	801	NAG	C4-C5-C6-O6
6	A	802	NAG	C4-C5-C6-O6
6	A	801	NAG	O5-C5-C6-O6
6	A	802	NAG	O5-C5-C6-O6
6	A	802	NAG	C8-C7-N2-C2
6	A	802	NAG	O7-C7-N2-C2
6	A	802	NAG	C1-C2-N2-C7
6	A	802	NAG	C3-C2-N2-C7

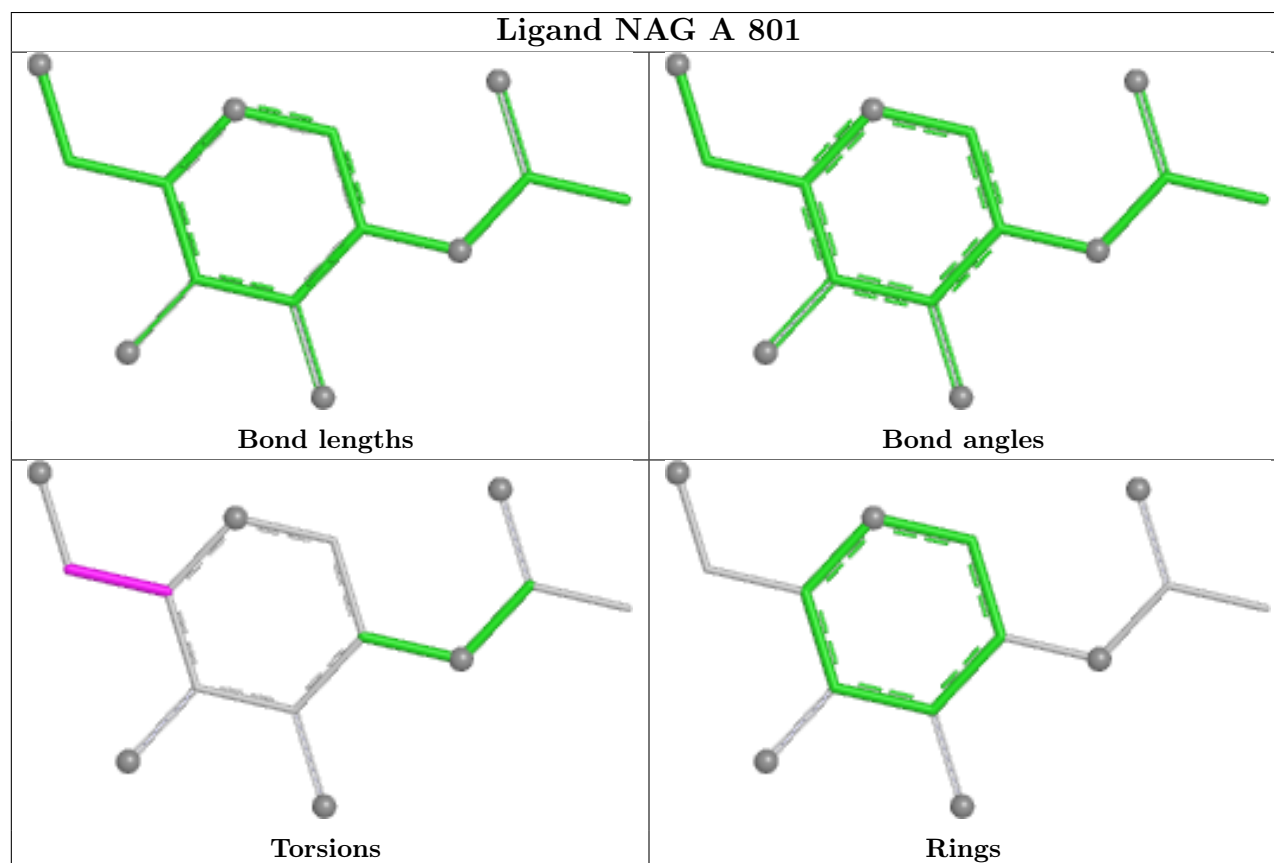
There are no ring outliers.

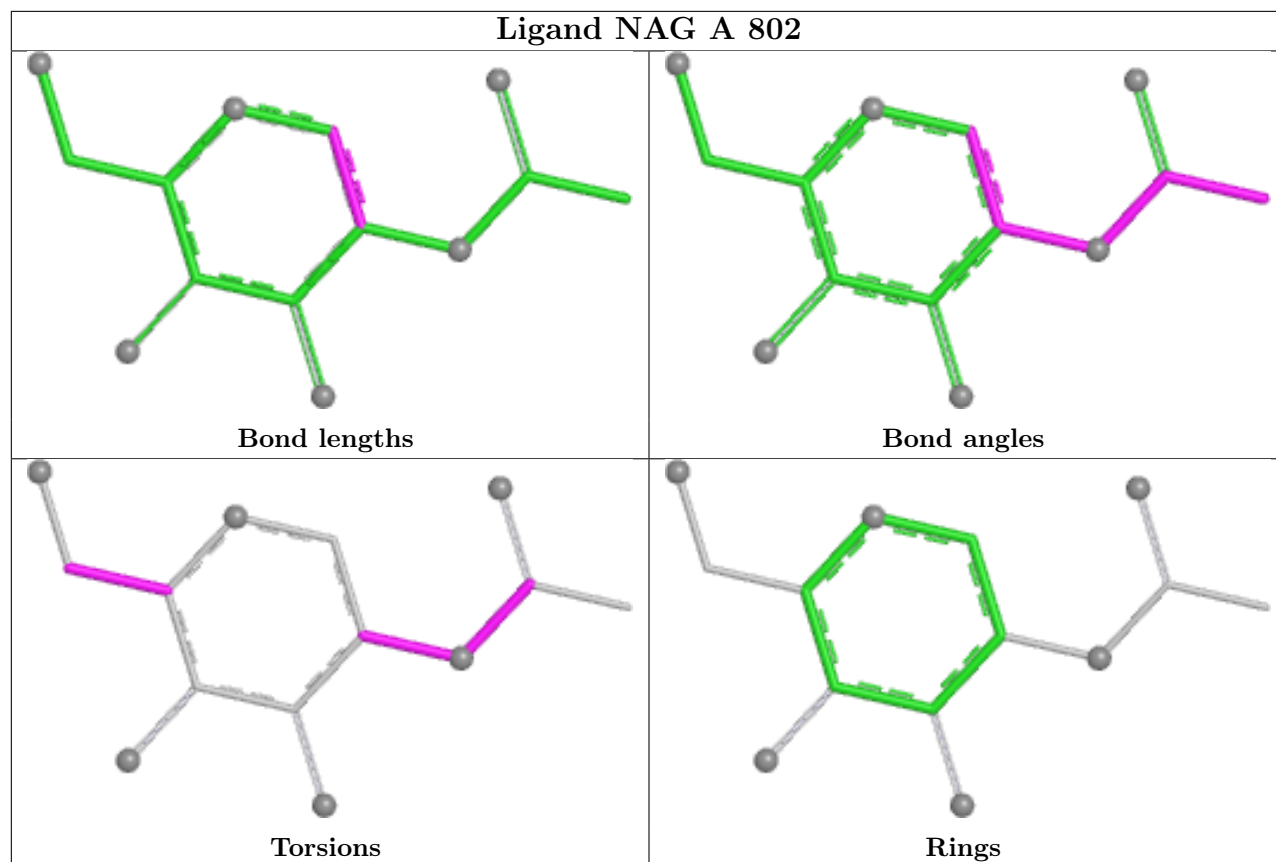
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	801	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 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.

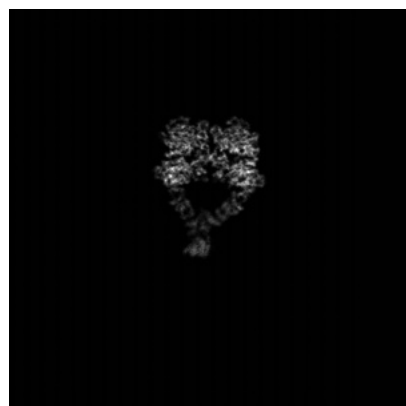
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-34745. 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](#)

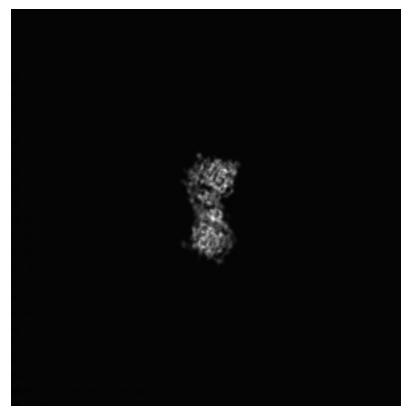
6.1.1 Primary map



X

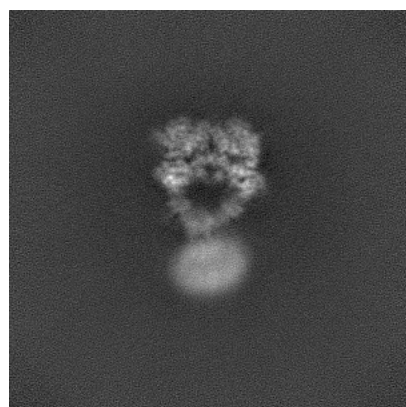


Y

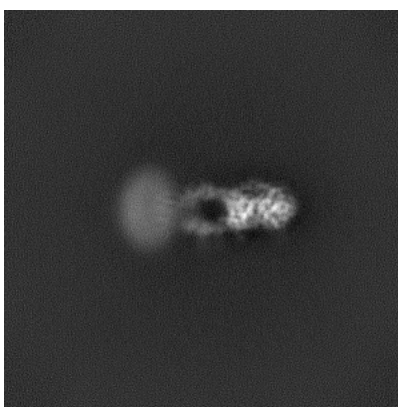


Z

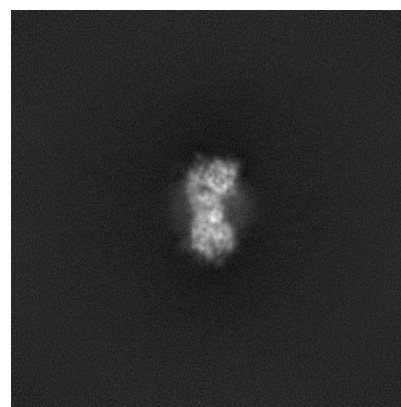
6.1.2 Raw map



X



Y



Z

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

6.2 Central slices [i](#)

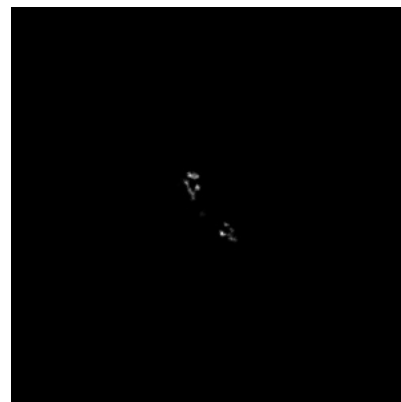
6.2.1 Primary map



X Index: 192

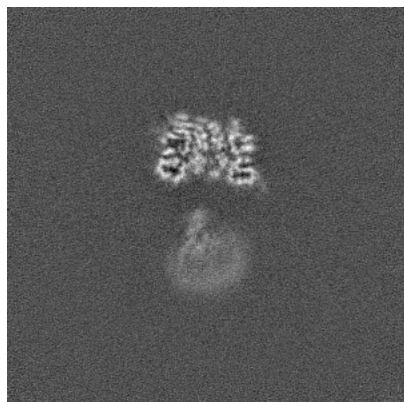


Y Index: 192

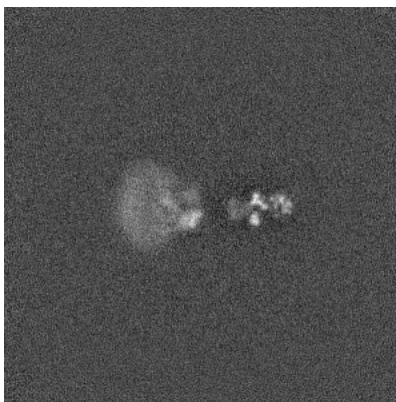


Z Index: 192

6.2.2 Raw map



X Index: 192



Y Index: 192



Z Index: 192

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

6.3 Largest variance slices [i](#)

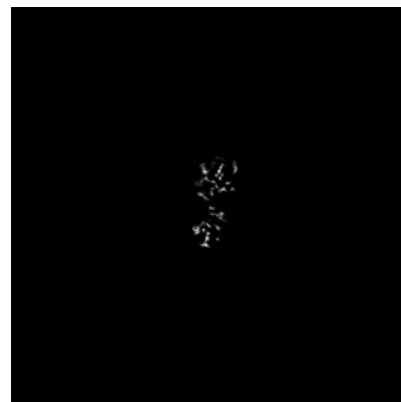
6.3.1 Primary map



X Index: 193



Y Index: 226

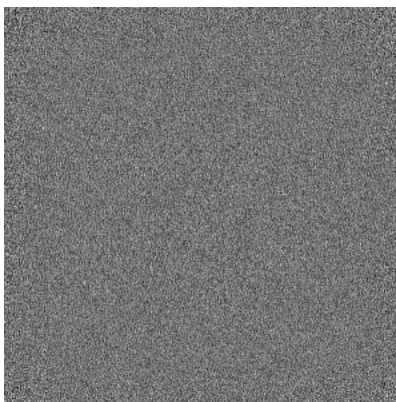


Z Index: 251

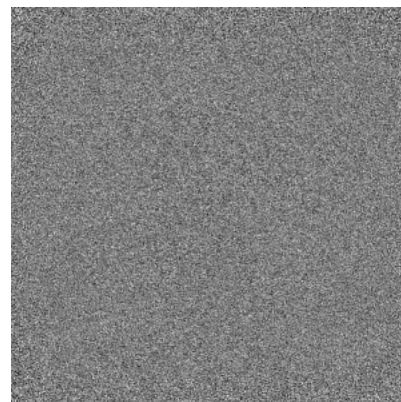
6.3.2 Raw map



X Index: 193



Y Index: 0

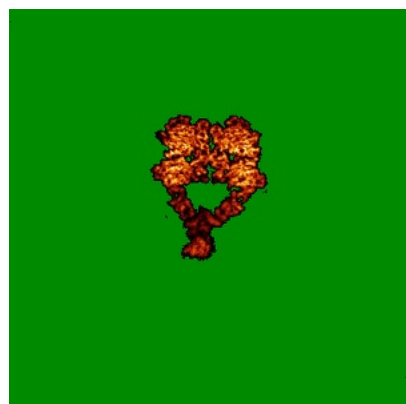


Z Index: 0

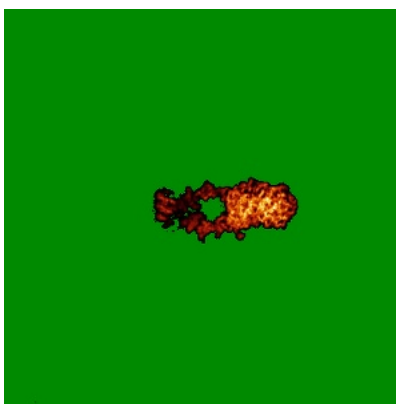
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



X

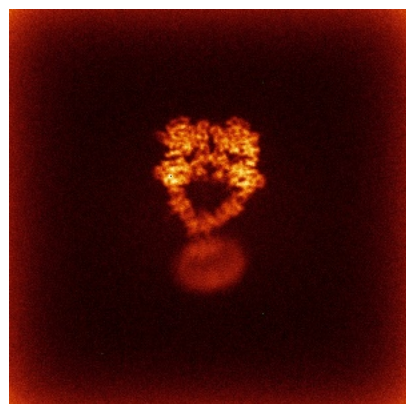


Y

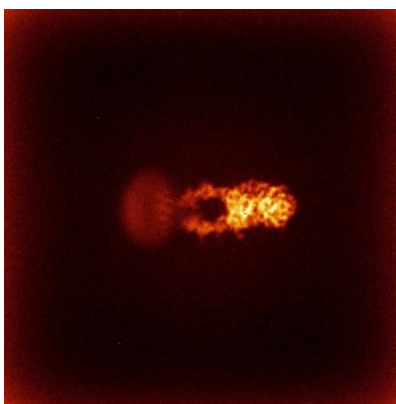


Z

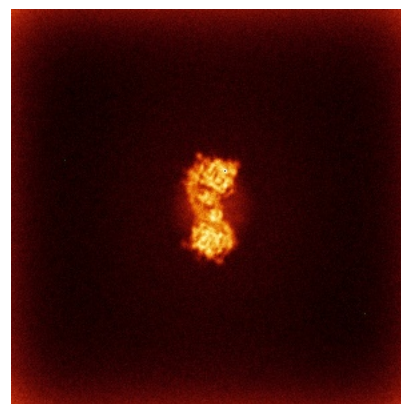
6.4.2 Raw map



X



Y

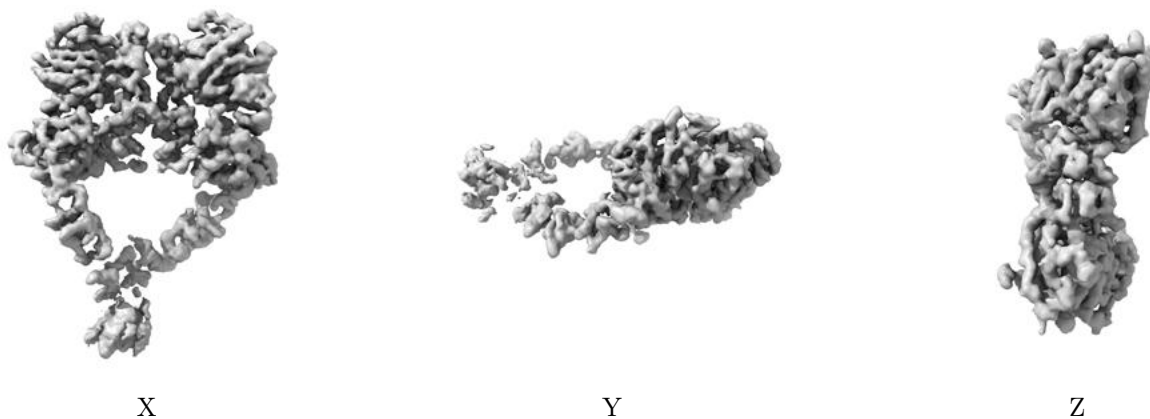


Z

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

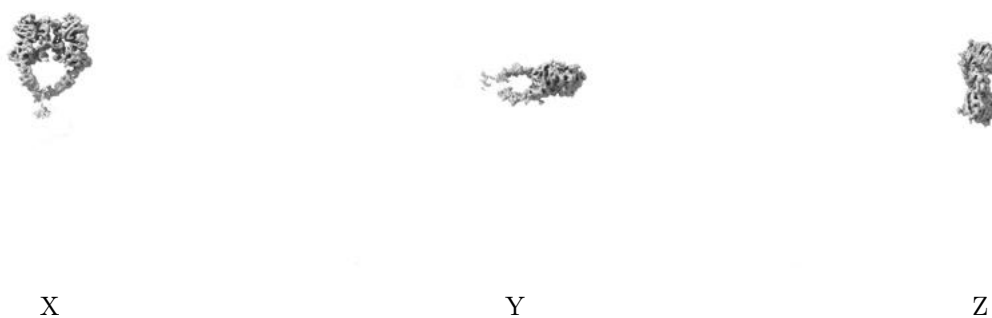
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.145. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

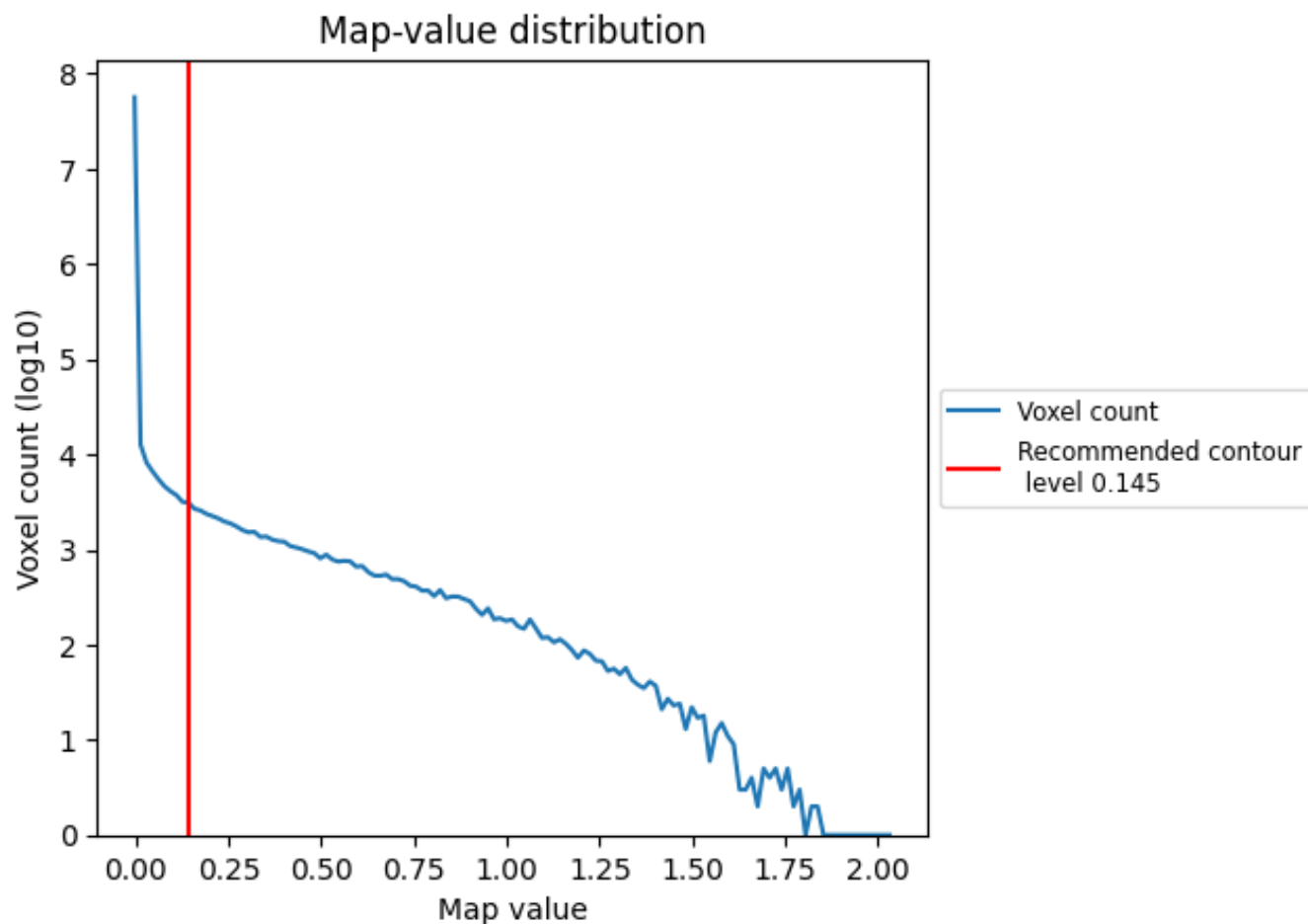
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

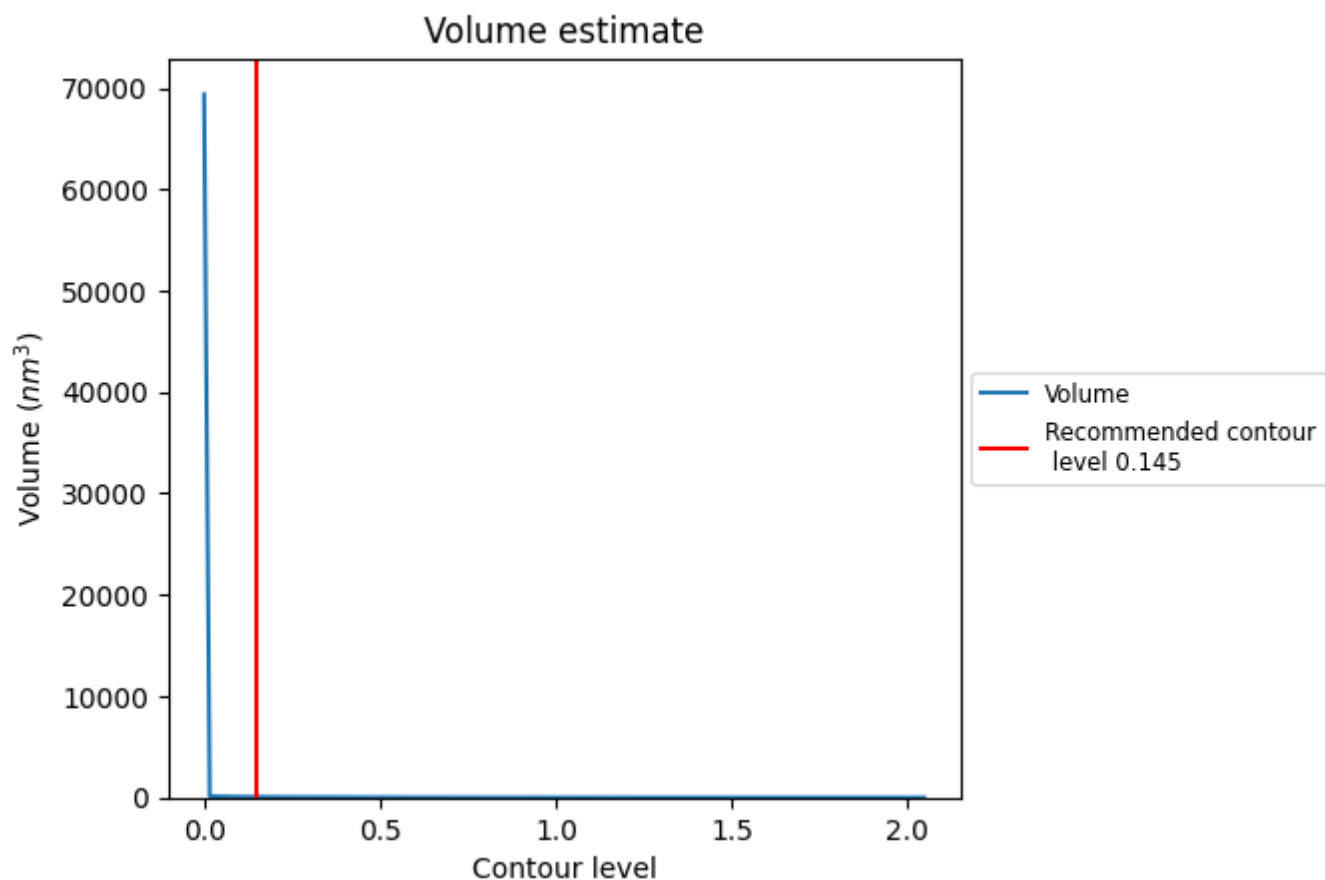
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

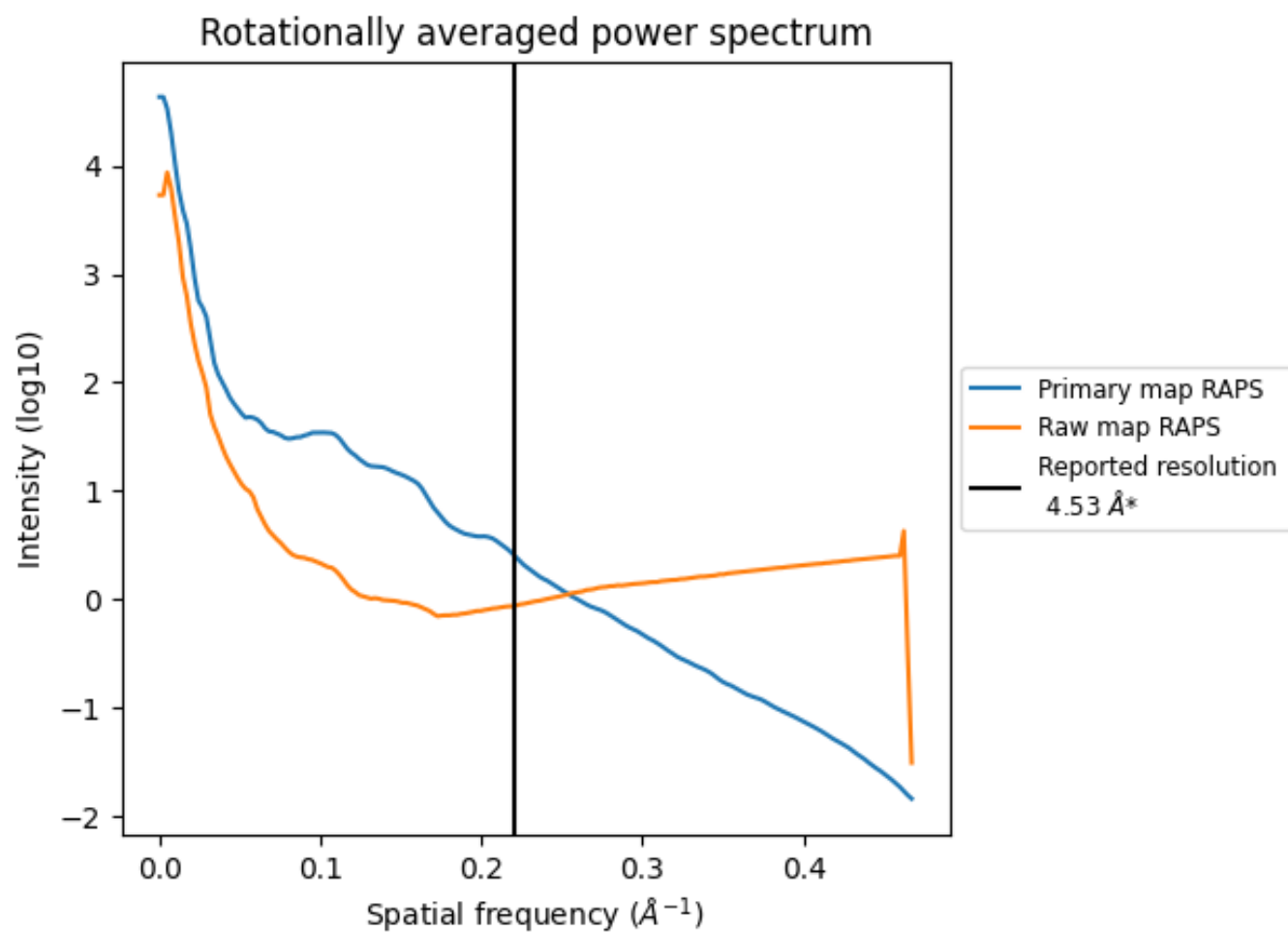
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 66 nm^3 ; this corresponds to an approximate mass of 59 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

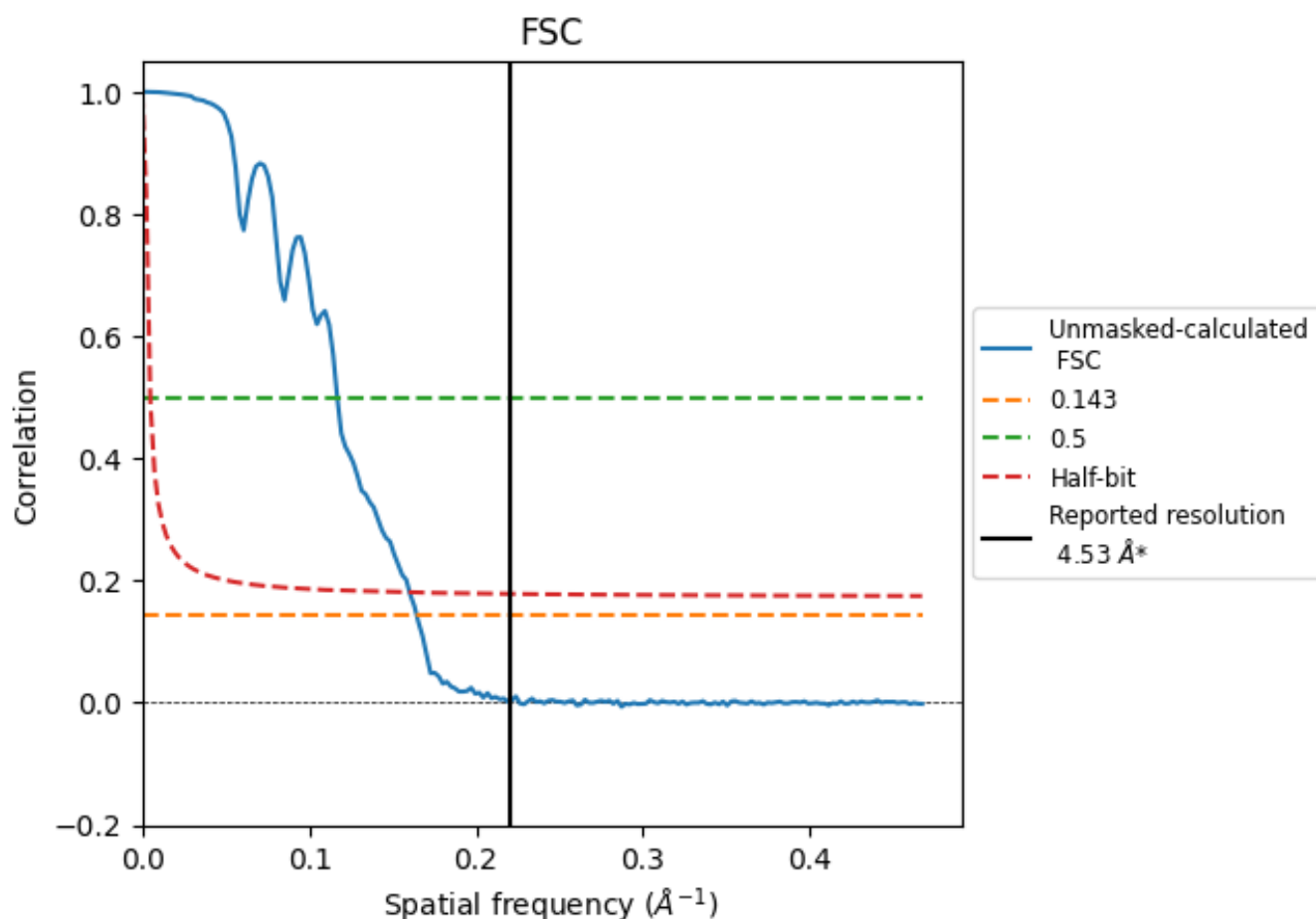


*Reported resolution corresponds to spatial frequency of 0.221 $\text{\AA}^{-1}$

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 0.221 Å⁻¹

8.2 Resolution estimates [i](#)

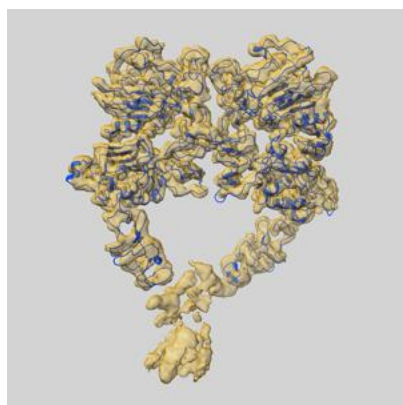
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.53	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	6.08	8.55	6.24

*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 6.08 differs from the reported value 4.53 by more than 10 %

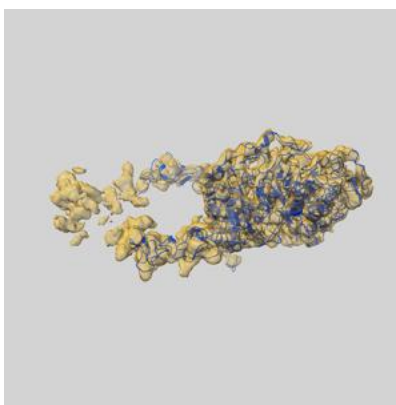
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-34745 and PDB model 8HGP. Per-residue inclusion information can be found in section [3](#) on page [9](#).

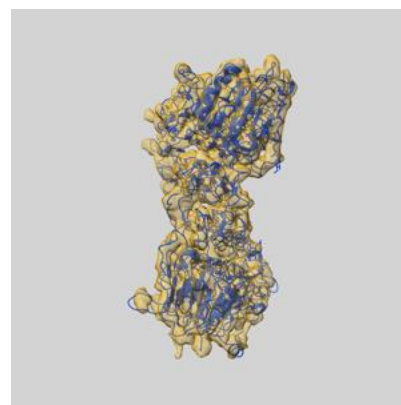
9.1 Map-model overlay [i](#)



X



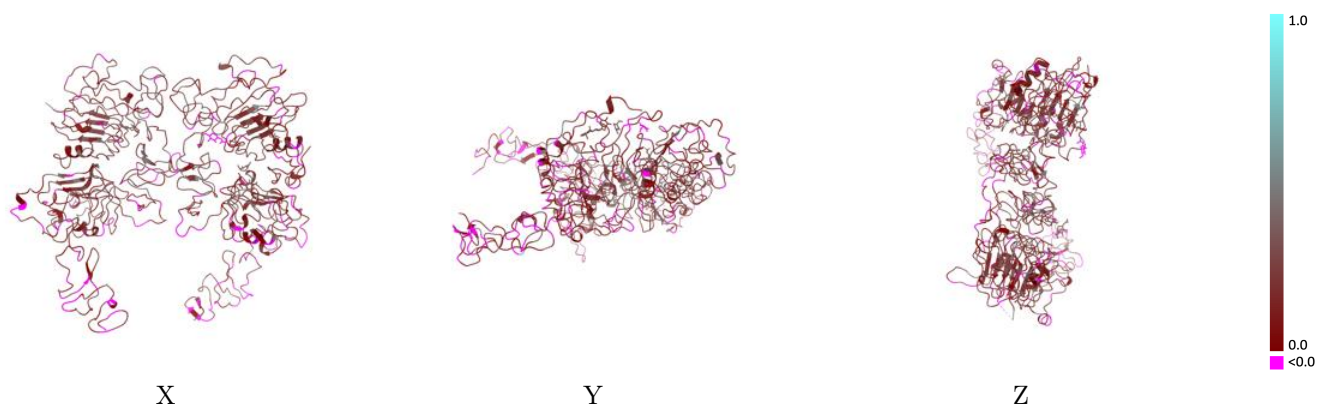
Y



Z

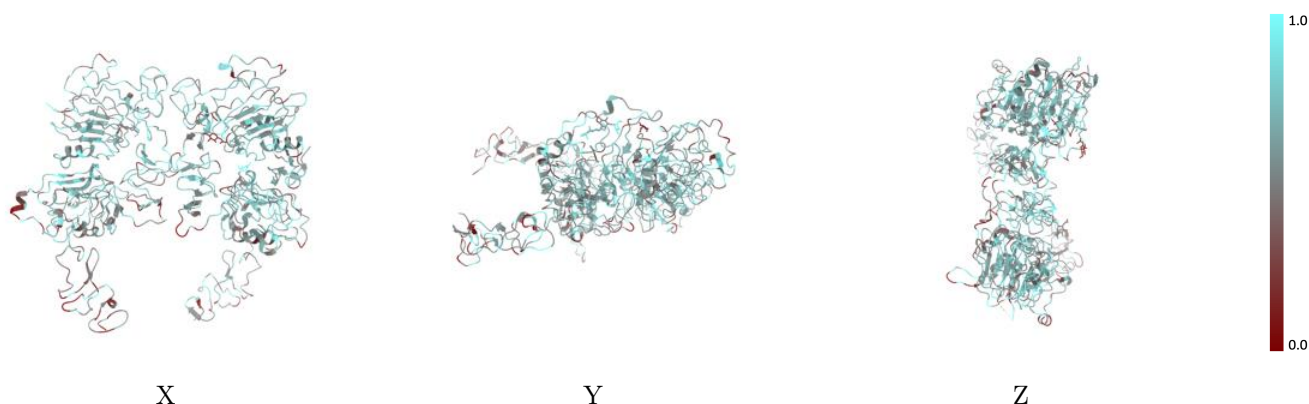
The images above show the 3D surface view of the map at the recommended contour level 0.145 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



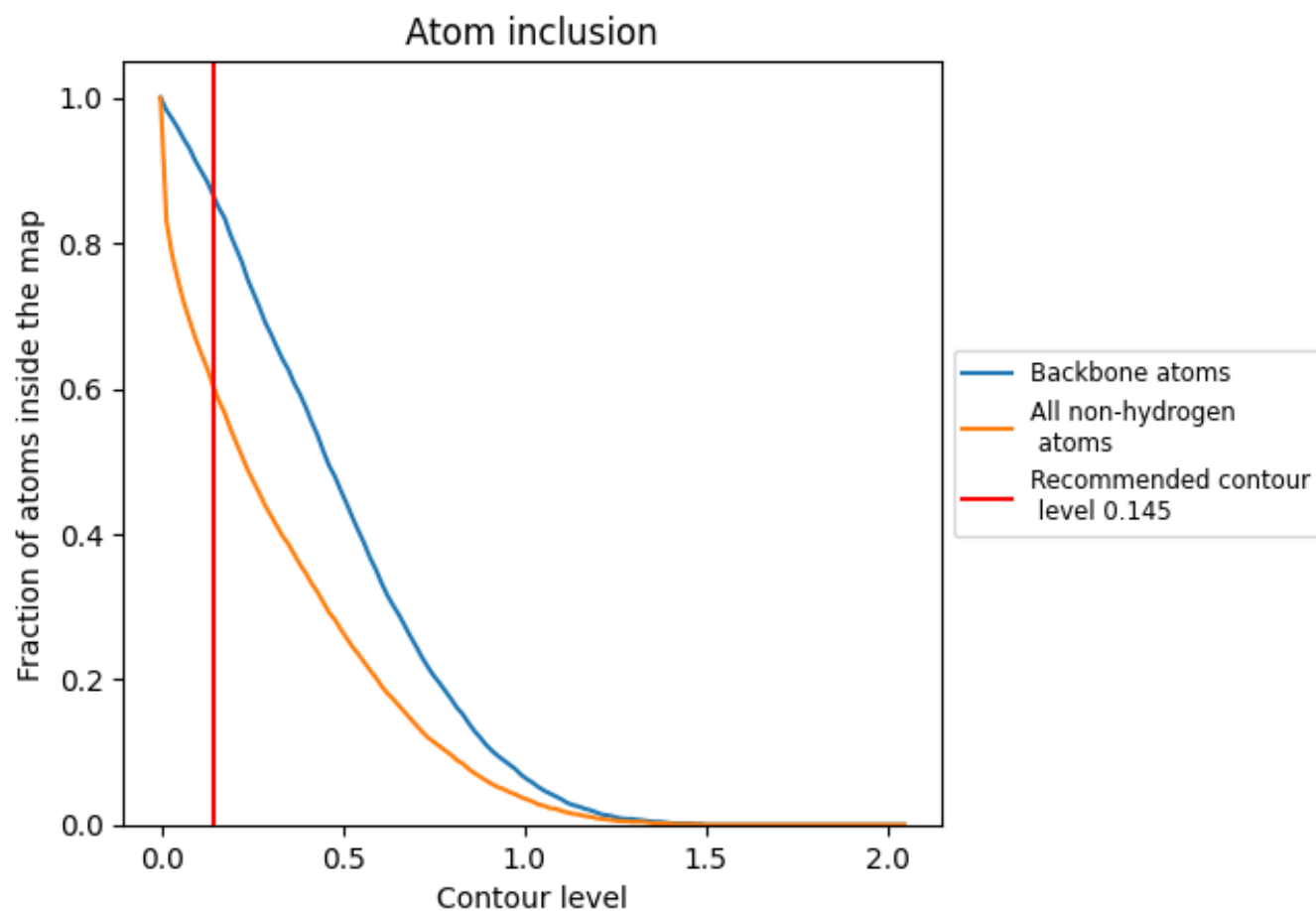
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.145).

9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 60% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.145) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6000	0.1700
A	0.5960	0.1600
B	0.6030	0.1810
C	0.5960	0.1340
D	0.7400	0.2790
E	0.5710	0.3110

