Full wwPDB EM Validation Report ⓘ

Jun 12, 2025 – 05:19 PM EDT

PDB ID	:	9D5M / pdb_00009d5m
EMDB ID	:	EMD-46579
Title	:	Apo ACE full dimer 1 prepared by chameleon
Authors	:	Mancl, J.M.; Tang, W.J.
Deposited on	:	2024-08-13
Resolution	:	3.05 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:

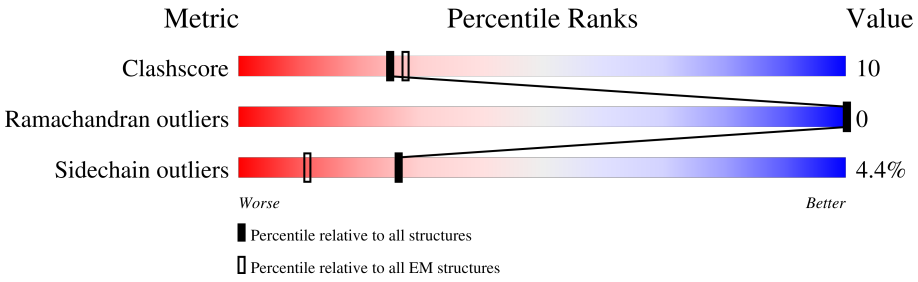
EMDB validation analysis	:	0.0.1.dev118
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4-5-2 with Phenix2.0rc1
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson 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 3.05 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 <=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	1241	71% 25%
1	B	1241	71% 24%
2	D	3	67% 33% 67%
2	N	3	33% 100%
2	P	3	67% 67% 33%
3	F	4	50% 25% 75%
4	G	2	100%
4	H	2	50% 100%

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Mol	Chain	Length	Quality of chain
4	I	2	100%
4	L	2	100%
4	Q	2	100% 100%
4	R	2	100% 100%
4	S	2	50% 50%
4	U	2	50% 50%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 20031 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.

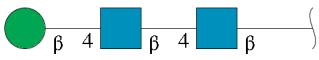
- Molecule 1 is a protein called Angiotensin-converting enzyme.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1201	Total	C	N	O	S	0	0
			9784	6273	1673	1795	43		
1	B	1199	Total	C	N	O	S	0	0
			9773	6267	1671	1792	43		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1207	HIS	-	expression tag	UNP P12821
A	1208	HIS	-	expression tag	UNP P12821
A	1209	HIS	-	expression tag	UNP P12821
A	1210	HIS	-	expression tag	UNP P12821
A	1211	HIS	-	expression tag	UNP P12821
A	1212	HIS	-	expression tag	UNP P12821
B	1207	HIS	-	expression tag	UNP P12821
B	1208	HIS	-	expression tag	UNP P12821
B	1209	HIS	-	expression tag	UNP P12821
B	1210	HIS	-	expression tag	UNP P12821
B	1211	HIS	-	expression tag	UNP P12821
B	1212	HIS	-	expression tag	UNP P12821

- Molecule 2 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
2	D	3	Total	C	N	O	0	0
			39	22	2	15		
2	N	3	Total	C	N	O	0	0
			39	22	2	15		

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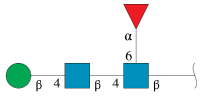
Mol	Chain	Residues	Atoms				AltConf	Trace
2	P	3	Total	C	N	O	0	0
			39	22	2	15		

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

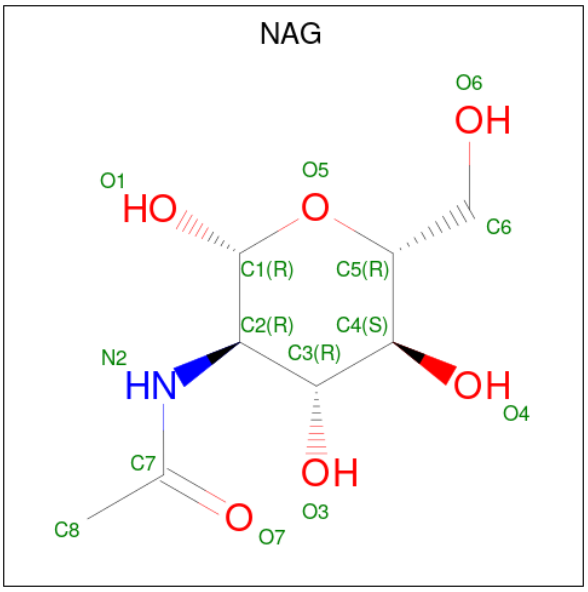


Mol	Chain	Residues	Atoms				AltConf	Trace
3	F	4	Total	C	N	O	0	0
			49	28	2	19		

- Molecule 4 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
4	G	2	Total	C	N	O	0	0
			28	16	2	10		
4	H	2	Total	C	N	O	0	0
			28	16	2	10		
4	I	2	Total	C	N	O	0	0
			28	16	2	10		
4	L	2	Total	C	N	O	0	0
			28	16	2	10		
4	Q	2	Total	C	N	O	0	0
			28	16	2	10		
4	R	2	Total	C	N	O	0	0
			28	16	2	10		
4	S	2	Total	C	N	O	0	0
			28	16	2	10		
4	U	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



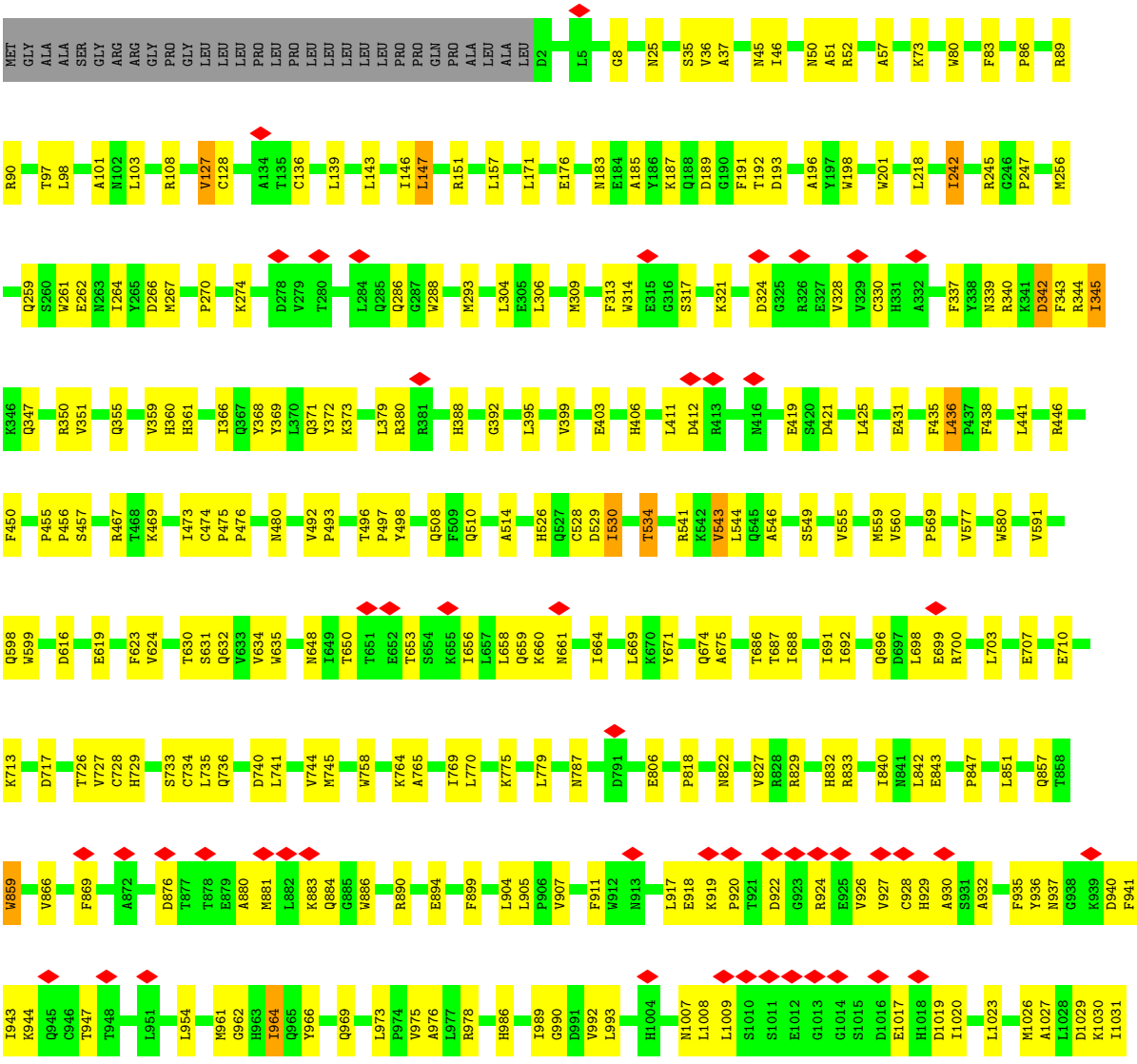
Mol	Chain	Residues	Atoms				AltConf
5	A	1	Total	C	N	O	0
			14	8	1	5	
5	A	1	Total	C	N	O	0
			14	8	1	5	
5	A	1	Total	C	N	O	0
			14	8	1	5	
5	B	1	Total	C	N	O	0
			14	8	1	5	
5	B	1	Total	C	N	O	0
			14	8	1	5	
5	B	1	Total	C	N	O	0
			14	8	1	5	

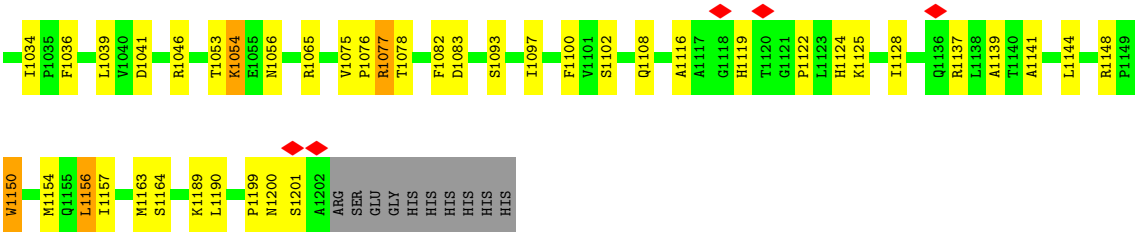
3 Residue-property plots (i)

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: Angiotensin-converting enzyme

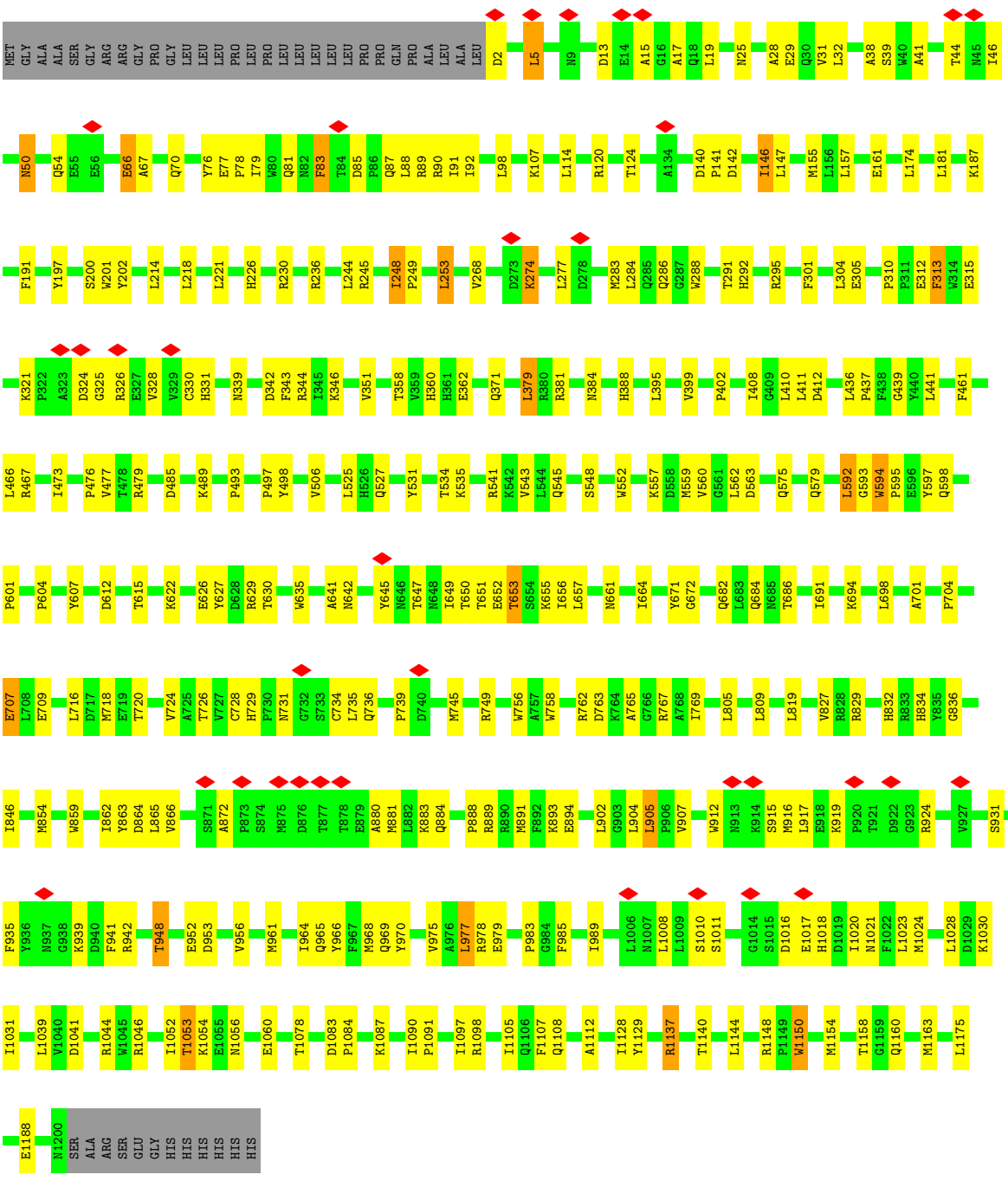
Chain A:





• Molecule 1: Angiotensin-converting enzyme

Chain B:

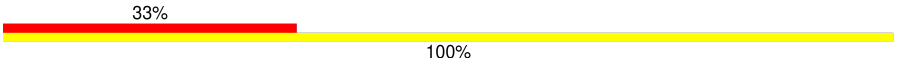


• Molecule 2: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain D:

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

Chain N:



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

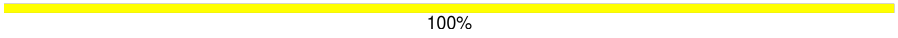
Chain P:

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

Chain F:

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

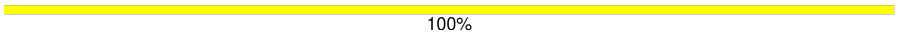
Chain G:



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

Chain H:

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

Chain I: 

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

Chain L: 

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

Chain Q: 

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

Chain R: 

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

Chain S: 

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

Chain U: 

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	51497	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	52.82	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.675	Depositor
Minimum map value	-0.455	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.017	Depositor
Recommended contour level	0.06	Depositor
Map size (Å)	297.36, 297.36, 297.36	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.826, 0.826, 0.826	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: BMA, FUC, 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	0/10084	0.39	0/13733
1	B	0.29	0/10073	0.40	0/13718
All	All	0.28	0/20157	0.40	0/27451

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	9784	0	9377	203	0
1	B	9773	0	9365	201	0
2	D	39	0	34	2	0
2	N	39	0	34	2	0
2	P	39	0	34	2	0
3	F	49	0	43	0	0
4	G	28	0	25	0	0
4	H	28	0	25	0	0
4	I	28	0	25	0	0
4	L	28	0	25	0	0
4	Q	28	0	25	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	R	28	0	25	1	0
4	S	28	0	25	0	0
4	U	28	0	25	0	0
5	A	42	0	39	1	0
5	B	42	0	39	0	0
All	All	20031	0	19165	404	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 10.

All (404) 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:339:ASN:HD21	1:B:342:ASP:HB2	1.42	0.83
1:A:368:TYR:HA	1:A:544:LEU:HD21	1.59	0.82
1:B:728:CYS:HA	1:B:734:CYS:HA	1.59	0.81
1:A:543:VAL:HG21	1:A:559:MET:HB2	1.62	0.79
1:A:1039:LEU:HD11	1:A:1065:ARG:HA	1.63	0.78
1:A:441:LEU:HD11	1:A:467:ARG:HA	1.67	0.75
1:A:406:HIS:HB2	1:A:411:LEU:HD23	1.68	0.74
1:A:337:PHE:HE2	1:A:344:ARG:HD3	1.52	0.74
1:A:598:GLN:HE22	1:B:479:ARG:H	1.33	0.74
1:B:342:ASP:OD2	1:B:344:ARG:NH2	2.22	0.71
1:A:745:MET:HE1	1:A:758:TRP:HB2	1.72	0.71
1:B:749:ARG:HH21	1:B:864:ASP:HB3	1.56	0.70
1:A:851:LEU:HB3	1:A:859:TRP:HB2	1.72	0.69
1:A:372:TYR:HE1	1:A:380:ARG:HA	1.58	0.69
1:A:829:ARG:HD3	1:A:842:LEU:HD11	1.73	0.69
1:B:236:ARG:O	1:B:684:GLN:NE2	2.26	0.68
1:A:992:VAL:HG13	1:A:993:LEU:HD12	1.76	0.67
1:A:962:GLY:HA3	1:A:990:GLY:HA2	1.76	0.67
1:A:1150:TRP:HE1	1:A:1154:MET:HE2	1.60	0.66
1:B:441:LEU:HD11	1:B:467:ARG:HA	1.77	0.66
1:A:770:LEU:HB2	1:A:1082:PHE:HB2	1.75	0.66
1:B:1108:GLN:NE2	1:B:1154:MET:SD	2.69	0.66
1:B:85:ASP:OD2	1:B:87:GLN:NE2	2.29	0.66
1:B:371:GLN:NE2	1:B:545:GLN:OE1	2.29	0.65
1:B:829:ARG:NE	1:B:1188:GLU:OE2	2.31	0.64
1:B:642:ASN:HA	1:B:645:TYR:CD2	2.33	0.64
1:B:645:TYR:HD1	1:B:653:THR:HG22	1.64	0.63
1:B:694:LYS:NZ	1:B:979:GLU:OE1	2.23	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:635:TRP:CD1	1:B:664:ILE:HD11	2.33	0.63
1:A:899:PHE:HE1	1:A:904:LEU:HD12	1.64	0.63
1:B:881:MET:O	1:B:884:GLN:NE2	2.29	0.63
1:B:916:MET:O	1:B:919:LYS:NZ	2.31	0.62
1:A:98:LEU:HD22	1:A:101:ALA:HB3	1.82	0.61
1:A:337:PHE:HB2	1:A:342:ASP:HB3	1.82	0.61
1:A:361:HIS:HD2	1:A:392:GLY:HA3	1.64	0.61
1:B:575:GLN:OE1	1:B:579:GLN:NE2	2.31	0.61
1:B:249:PRO:HG3	1:B:601:PRO:HG3	1.82	0.60
1:B:120:ARG:NH2	2:P:1:NAG:O7	2.33	0.60
1:B:915:SER:OG	1:B:916:MET:N	2.34	0.60
1:A:857:GLN:HB3	1:A:1036:PHE:CD2	2.37	0.60
1:B:902:LEU:HD11	1:B:1128:ILE:HG22	1.82	0.60
1:B:157:LEU:HD13	1:B:476:PRO:HB2	1.81	0.60
1:B:70:GLN:HG3	1:B:98:LEU:HD11	1.84	0.60
1:B:762:ARG:NH2	1:B:854:MET:O	2.34	0.60
1:B:381:ARG:NH2	1:B:548:SER:OG	2.35	0.59
1:B:641:ALA:HB1	1:B:645:TYR:CZ	2.38	0.59
1:B:557:LYS:HB2	1:B:563:ASP:HB3	1.84	0.59
1:B:652:GLU:O	1:B:656:ILE:HG13	2.02	0.59
1:B:718:MET:HE3	1:B:1091:PRO:HA	1.85	0.59
1:B:305:GLU:HG3	1:B:534:THR:HG23	1.83	0.58
1:B:25:ASN:HB3	2:N:1:NAG:O5	2.02	0.58
1:B:904:LEU:HB3	1:B:965:GLN:NE2	2.18	0.58
1:A:1019:ASP:OD1	1:A:1124:HIS:NE2	2.35	0.58
1:B:718:MET:HG2	1:B:769:ILE:HG23	1.84	0.58
1:B:29:GLU:HG3	2:N:1:NAG:H62	1.86	0.58
1:A:632:GLN:HE22	1:A:937:ASN:HA	1.69	0.57
1:B:1105:ILE:HD11	1:B:1163:MET:HE2	1.85	0.57
1:B:76:TYR:HA	1:B:79:ILE:HD13	1.86	0.57
1:B:83:PHE:H	1:B:89:ARG:NH1	2.03	0.57
1:B:87:GLN:O	1:B:91:ILE:HD12	2.04	0.57
1:A:328:VAL:HG13	1:A:330:CYS:H	1.70	0.57
1:B:888:PRO:HA	1:B:891:MET:HB3	1.87	0.57
1:A:259:GLN:HG3	1:A:438:PHE:CD2	2.40	0.57
1:A:139:LEU:HA	1:A:143:LEU:HB2	1.87	0.56
1:A:343:PHE:HB3	1:A:366:ILE:HD12	1.86	0.56
1:A:827:VAL:HG22	1:A:866:VAL:HG21	1.87	0.56
1:B:863:TYR:HA	1:B:866:VAL:HG12	1.87	0.56
1:A:25:ASN:HB3	2:D:1:NAG:O5	2.04	0.56
1:A:1077:ARG:NH1	1:A:1083:ASP:OD1	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:248:ILE:HD12	1:B:253:LEU:HD21	1.87	0.56
1:A:337:PHE:CE2	1:A:344:ARG:HD3	2.37	0.56
1:A:151:ARG:NH2	1:A:266:ASP:OD2	2.39	0.56
1:B:17:ALA:HB1	1:B:88:LEU:HD21	1.86	0.56
1:A:321:LYS:HG3	1:A:324:ASP:HB3	1.88	0.56
1:B:90:ARG:HB3	1:B:379:LEU:HD11	1.86	0.56
1:B:328:VAL:HG23	1:B:330:CYS:H	1.71	0.56
1:B:339:ASN:OD1	1:B:342:ASP:N	2.37	0.55
1:B:604:PRO:HG2	1:B:607:TYR:HB2	1.88	0.55
1:A:631:SER:HA	1:A:634:VAL:HG12	1.87	0.55
1:B:77:GLU:HB2	1:B:78:PRO:HD3	1.87	0.55
1:A:728:CYS:HA	1:A:734:CYS:HA	1.88	0.55
1:A:339:ASN:C	1:A:340:ARG:HD3	2.32	0.55
1:A:806:GLU:OE2	1:A:1046:ARG:NH2	2.40	0.55
1:B:2:ASP:HB3	1:B:5:LEU:HB2	1.89	0.55
1:B:292:HIS:O	1:B:292:HIS:ND1	2.39	0.55
1:A:193:ASP:HB3	1:A:196:ALA:H	1.70	0.55
1:B:201:TRP:HZ3	1:B:497:PRO:HG2	1.73	0.55
1:B:321:LYS:NZ	1:B:328:VAL:O	2.40	0.54
1:B:626:GLU:OE1	1:B:629:ARG:NH2	2.40	0.54
1:A:1026:MET:HE2	1:A:1026:MET:HA	1.89	0.54
1:A:624:VAL:HG23	1:A:691:ILE:HG21	1.88	0.54
1:B:645:TYR:HB3	1:B:657:LEU:HD12	1.87	0.54
1:B:615:THR:HG21	1:B:682:GLN:HB3	1.90	0.54
1:B:467:ARG:HE	1:B:473:ILE:HD11	1.72	0.54
1:B:543:VAL:HG21	1:B:559:MET:HB2	1.89	0.53
1:A:368:TYR:O	1:A:372:TYR:HD2	1.91	0.53
1:A:598:GLN:NE2	1:B:479:ARG:O	2.42	0.53
1:B:645:TYR:CE2	1:B:657:LEU:HA	2.43	0.53
1:B:1017:GLU:O	1:B:1021:ASN:ND2	2.31	0.53
1:A:157:LEU:HD13	1:A:476:PRO:HB2	1.90	0.53
1:A:270:PRO:HB3	1:A:580:TRP:CH2	2.43	0.53
1:A:425:LEU:HB3	1:A:577:VAL:HB	1.89	0.53
1:A:347:GLN:HE22	1:A:359:VAL:HG23	1.74	0.53
1:B:360:HIS:CG	1:B:399:VAL:HG21	2.44	0.53
1:A:45:ASN:O	1:A:50:ASN:ND2	2.42	0.52
1:A:469:LYS:HB2	1:B:461:PHE:HE2	1.73	0.52
1:B:202:TYR:HD2	1:B:384:ASN:HD21	1.56	0.52
1:B:594:TRP:CD1	1:B:594:TRP:N	2.76	0.52
1:A:36:VAL:HG12	1:A:337:PHE:CD1	2.44	0.52
1:A:379:LEU:HD13	1:A:549:SER:HA	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:687:THR:O	1:A:691:ILE:HG12	2.09	0.52
1:A:147:LEU:HD22	1:A:256:MET:HA	1.91	0.52
1:B:218:LEU:HD13	1:B:436:LEU:HD13	1.92	0.52
1:A:35:SER:HA	1:A:57:ALA:HB1	1.91	0.52
1:A:635:TRP:CD1	1:A:664:ILE:HD11	2.45	0.52
1:B:305:GLU:O	1:B:541:ARG:NH1	2.43	0.52
1:B:726:THR:HG22	1:B:736:GLN:HB3	1.90	0.52
1:A:735:LEU:HD23	1:A:740:ASP:CG	2.35	0.52
1:A:880:ALA:HA	1:A:883:LYS:HE2	1.91	0.52
1:A:306:LEU:HD13	1:A:541:ARG:HG2	1.90	0.52
1:A:926:VAL:HG12	1:A:927:VAL:N	2.25	0.52
1:B:291:THR:OG1	1:B:295:ARG:NH1	2.43	0.52
1:A:309:MET:HE3	1:A:314:TRP:HE1	1.74	0.52
1:A:274:LYS:HD3	1:A:419:GLU:HB3	1.92	0.51
1:A:941:PHE:HB3	1:A:964:ILE:HG23	1.92	0.51
1:A:101:ALA:HA	1:A:108:ARG:HE	1.76	0.51
1:A:412:ASP:N	1:A:412:ASP:OD1	2.40	0.51
1:B:81:GLN:O	1:B:89:ARG:NH2	2.30	0.51
1:A:1108:GLN:OE1	1:A:1164:SER:N	2.43	0.51
1:A:881:MET:HE1	1:A:954:LEU:HD12	1.91	0.51
1:A:859:TRP:CD1	1:A:859:TRP:C	2.88	0.51
1:A:930:ALA:HB3	1:A:944:LYS:HZ3	1.75	0.51
1:B:28:ALA:HB1	1:B:32:LEU:HD12	1.91	0.51
1:B:983:PRO:O	1:B:1098:ARG:HB2	2.11	0.51
1:B:905:LEU:HB2	1:B:968:MET:HE3	1.93	0.51
1:B:1137:ARG:HA	1:B:1140:THR:HG22	1.92	0.51
1:B:142:ASP:O	1:B:146:ILE:HG22	2.12	0.50
1:B:872:ALA:HB1	1:B:1018:HIS:CE1	2.46	0.50
1:A:528:CYS:SG	1:A:529:ASP:N	2.85	0.50
1:A:313:PHE:O	1:A:317:SER:OG	2.21	0.50
1:A:369:TYR:O	1:A:373:LYS:HB2	2.12	0.50
1:A:886:TRP:HA	1:A:890:ARG:HD3	1.94	0.50
1:A:1034:ILE:HG23	1:A:1100:PHE:CE2	2.47	0.49
1:B:1112:ALA:HB2	1:B:1158:THR:HG23	1.94	0.49
1:A:361:HIS:CD2	1:A:392:GLY:HA3	2.47	0.49
1:A:543:VAL:HG22	1:A:555:VAL:HG13	1.93	0.49
1:B:661:ASN:O	1:B:664:ILE:HG22	2.12	0.49
1:B:736:GLN:HG2	1:B:739:PRO:HD2	1.94	0.49
1:B:328:VAL:HG11	1:B:346:LYS:HE2	1.93	0.49
1:A:247:PRO:HB2	1:A:474:CYS:HB2	1.95	0.49
1:B:970:TYR:CE2	1:B:978:ARG:HG2	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:201:TRP:CZ3	1:A:497:PRO:HG2	2.48	0.49
1:A:869:PHE:HB2	1:A:1017:GLU:OE1	2.13	0.49
1:A:187:LYS:NZ	1:A:192:THR:O	2.41	0.49
1:A:876:ASP:OD1	1:A:876:ASP:N	2.46	0.49
1:A:288:TRP:HD1	1:A:293:MET:HE2	1.78	0.49
1:A:598:GLN:HE22	1:B:479:ARG:N	2.05	0.49
1:A:691:ILE:HD12	1:A:976:ALA:HB3	1.95	0.48
1:A:818:PRO:O	1:A:822:ASN:ND2	2.45	0.48
1:A:883:LYS:HE3	1:A:884:GLN:HG2	1.95	0.48
1:B:161:GLU:HG3	1:B:477:VAL:HG21	1.95	0.48
1:A:514:ALA:HB2	1:A:560:VAL:HG13	1.94	0.48
1:A:350:ARG:H	1:A:355:GLN:HG2	1.78	0.48
1:B:283:MET:HG3	1:B:288:TRP:CD1	2.49	0.48
1:B:292:HIS:HD1	1:B:295:ARG:HB2	1.79	0.48
1:B:328:VAL:HG21	1:B:346:LYS:HD3	1.95	0.48
1:B:948:THR:N	1:B:953:ASP:OD2	2.43	0.48
1:A:128:CYS:HA	1:A:136:CYS:HB2	1.94	0.48
1:A:1200:ASN:OD1	1:A:1201:SER:N	2.46	0.48
1:B:214:LEU:HD21	1:B:506:VAL:HG11	1.95	0.48
1:B:310:PRO:HG2	1:B:313:PHE:CZ	2.49	0.48
1:A:245:ARG:HG2	1:A:591:VAL:HG11	1.95	0.48
1:A:421:ASP:OD1	1:A:526:HIS:NE2	2.46	0.48
1:A:729:HIS:N	1:A:733:SER:O	2.39	0.48
1:B:827:VAL:HG22	1:B:866:VAL:HG21	1.96	0.48
1:A:713:LYS:NZ	1:A:717:ASP:OD2	2.47	0.48
1:A:127:VAL:HG12	1:A:143:LEU:HD11	1.96	0.47
1:A:973:LEU:HD11	1:A:1144:LEU:O	2.14	0.47
1:B:187:LYS:HA	1:B:191:PHE:O	2.14	0.47
1:B:966:TYR:CD2	1:B:989:ILE:HG13	2.49	0.47
1:A:935:PHE:HB2	1:A:940:ASP:HB2	1.96	0.47
1:B:916:MET:N	1:B:916:MET:SD	2.87	0.47
1:B:83:PHE:HD1	1:B:83:PHE:HA	1.63	0.47
1:A:928:CYS:SG	1:A:929:HIS:N	2.87	0.47
1:B:965:GLN:HE22	1:B:969:GLN:NE2	2.13	0.47
1:A:198:TRP:HZ3	1:A:446:ARG:HE	1.62	0.47
1:A:1029:ASP:C	1:A:1031:ILE:H	2.22	0.47
1:B:1046:ARG:HA	1:B:1046:ARG:HD3	1.78	0.47
1:A:1141:ALA:HB3	1:A:1157:ILE:HG13	1.97	0.47
1:B:38:ALA:HB1	1:B:54:GLN:HA	1.95	0.47
1:B:907:VAL:HG21	1:B:961:MET:HE3	1.96	0.47
1:B:13:ASP:O	1:B:17:ALA:N	2.40	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:304:LEU:HA	1:A:534:THR:HA	1.97	0.46
1:B:1016:ASP:OD1	1:B:1016:ASP:N	2.48	0.46
1:A:340:ARG:HA	1:A:373:LYS:HD3	1.96	0.46
1:B:1053:THR:OG1	1:B:1054:LYS:N	2.48	0.46
1:A:661:ASN:O	1:A:664:ILE:HG22	2.16	0.46
1:B:641:ALA:HB1	1:B:645:TYR:OH	2.15	0.46
1:B:805:LEU:O	1:B:809:LEU:HG	2.15	0.46
2:D:1:NAG:H61	2:D:2:NAG:C7	2.46	0.46
1:A:201:TRP:HZ3	1:A:497:PRO:HG2	1.80	0.46
1:A:1093:SER:O	1:A:1093:SER:OG	2.29	0.46
1:A:86:PRO:O	1:A:90:ARG:HG2	2.15	0.46
1:A:881:MET:CE	1:A:954:LEU:HD12	2.46	0.46
1:A:961:MET:HE3	1:A:961:MET:HA	1.98	0.46
1:B:324:ASP:OD1	1:B:325:GLY:N	2.48	0.46
1:B:720:THR:O	1:B:724:VAL:HG22	2.15	0.46
1:B:245:ARG:O	1:B:595:PRO:HD2	2.15	0.46
1:B:575:GLN:O	1:B:579:GLN:HG2	2.16	0.46
1:A:648:ASN:HA	1:A:922:ASP:OD1	2.16	0.46
1:A:775:LYS:HB3	1:A:775:LYS:HE3	1.73	0.46
1:A:924:ARG:NH1	1:A:926:VAL:O	2.48	0.46
1:B:592:LEU:HD23	1:B:592:LEU:HA	1.68	0.46
1:B:889:ARG:CZ	1:B:912:TRP:HB3	2.46	0.46
1:B:437:PRO:O	1:B:441:LEU:HB2	2.15	0.45
1:B:834:HIS:CD2	1:B:865:LEU:HD22	2.51	0.45
1:A:8:GLY:HA2	5:A:1301:NAG:H82	1.97	0.45
1:A:83:PHE:H	1:A:89:ARG:NH2	2.13	0.45
1:A:304:LEU:HD21	1:A:530:ILE:HG22	1.97	0.45
1:A:37:ALA:HA	1:A:337:PHE:HE1	1.81	0.45
1:A:765:ALA:O	1:A:769:ILE:HG12	2.17	0.45
1:A:847:PRO:HB3	1:A:1199:PRO:HG3	1.98	0.45
1:B:439:GLY:HA2	1:B:498:TYR:CD2	2.51	0.45
1:A:176:GLU:HG2	1:A:456:PRO:HB3	1.99	0.45
1:A:843:GLU:OE2	1:A:1189:LYS:HD2	2.17	0.45
1:A:455:PRO:C	1:A:457:SER:H	2.25	0.45
1:A:692:ILE:O	1:A:696:GLN:HB2	2.17	0.45
1:B:201:TRP:CZ3	1:B:497:PRO:HG2	2.51	0.45
1:A:932:ALA:HB1	1:A:964:ILE:HD11	1.99	0.45
1:A:966:TYR:HE2	1:A:989:ILE:HG13	1.82	0.45
1:B:284:LEU:HD21	1:B:351:VAL:HG21	1.99	0.45
1:B:765:ALA:O	1:B:769:ILE:HG12	2.17	0.45
1:A:36:VAL:HG12	1:A:337:PHE:CE1	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:259:GLN:NE2	1:A:498:TYR:OH	2.50	0.45
1:A:1189:LYS:HB3	1:A:1189:LYS:HE3	1.78	0.45
1:B:1008:LEU:HD23	1:B:1008:LEU:HA	1.81	0.45
1:A:634:VAL:HG13	1:A:635:TRP:CD1	2.52	0.44
1:B:626:GLU:O	1:B:630:THR:HG22	2.17	0.44
1:A:73:LYS:HD2	1:A:98:LEU:HD12	1.97	0.44
1:A:80:TRP:HA	1:A:83:PHE:HZ	1.83	0.44
1:A:218:LEU:HD13	1:A:436:LEU:HD23	1.99	0.44
1:A:635:TRP:HB3	1:A:936:TYR:CE2	2.52	0.44
1:A:943:ILE:HD12	1:A:944:LYS:H	1.82	0.44
1:A:313:PHE:HZ	1:A:345:ILE:HD11	1.80	0.44
1:A:1046:ARG:HD3	1:A:1046:ARG:HA	1.76	0.44
1:B:197:TYR:O	1:B:200:SER:OG	2.31	0.44
1:A:630:THR:HG21	1:A:671:TYR:CZ	2.52	0.44
1:B:157:LEU:HD11	1:B:477:VAL:HG13	2.00	0.44
1:B:274:LYS:HE3	1:B:274:LYS:HB3	1.70	0.44
1:B:866:VAL:HG11	1:B:1028:LEU:HD11	2.00	0.44
1:A:919:LYS:HD3	1:A:919:LYS:HA	1.80	0.44
1:A:907:VAL:HG11	1:A:911:PHE:HD2	1.81	0.44
1:B:161:GLU:OE1	1:B:607:TYR:OH	2.27	0.44
1:B:1052:ILE:HG12	1:B:1060:GLU:HG3	2.00	0.44
1:A:1029:ASP:OD1	1:A:1030:LYS:N	2.51	0.44
1:B:15:ALA:O	1:B:19:LEU:HG	2.18	0.44
1:B:939:LYS:HG3	1:B:941:PHE:CE2	2.52	0.44
1:A:51:ALA:HB3	1:A:52:ARG:NH1	2.33	0.44
1:A:371:GLN:HB3	1:A:544:LEU:HD22	1.99	0.44
1:B:50:ASN:OD1	1:B:50:ASN:N	2.51	0.44
1:B:535:LYS:H	1:B:535:LYS:HD3	1.83	0.44
1:B:729:HIS:HA	1:B:756:TRP:CZ2	2.53	0.44
1:B:1083:ASP:N	1:B:1084:PRO:HD2	2.33	0.44
1:B:1144:LEU:HD13	1:B:1148:ARG:HG3	2.00	0.44
1:A:894:GLU:OE2	1:A:894:GLU:HA	2.18	0.44
1:A:1076:PRO:HD3	1:A:1200:ASN:HD22	1.82	0.44
1:B:758:TRP:O	1:B:762:ARG:HG2	2.18	0.44
1:B:120:ARG:O	1:B:124:THR:HG22	2.18	0.43
1:B:301:PHE:CZ	1:B:395:LEU:HD13	2.53	0.43
1:A:446:ARG:NH2	1:A:496:THR:O	2.51	0.43
1:A:969:GLN:HE22	1:A:1139:ALA:HB1	1.83	0.43
1:A:1027:ALA:O	1:A:1031:ILE:HB	2.19	0.43
1:B:39:SER:HA	1:B:54:GLN:OE1	2.18	0.43
1:B:657:LEU:HD22	1:B:716:LEU:HD22	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:645:TYR:OH	1:B:656:ILE:HG22	2.19	0.43
1:A:45:ASN:HB3	1:A:50:ASN:HD21	1.83	0.43
1:A:1019:ASP:CG	1:A:1124:HIS:HE2	2.27	0.43
1:A:1116:ALA:HB2	1:A:1137:ARG:HH21	1.82	0.43
1:B:81:GLN:C	1:B:89:ARG:HH12	2.26	0.43
1:B:597:TYR:CE2	1:B:598:GLN:HG3	2.53	0.43
1:A:686:THR:HG21	1:A:1148:ARG:NH1	2.32	0.43
1:B:1010:SER:OG	1:B:1011:SER:N	2.51	0.43
1:A:1008:LEU:HD12	1:A:1008:LEU:HA	1.73	0.43
1:B:408:ILE:HG23	1:B:410:LEU:HD23	1.99	0.43
1:B:763:ASP:O	1:B:767:ARG:HB2	2.18	0.43
1:B:889:ARG:O	1:B:893:LYS:HG3	2.19	0.43
1:A:360:HIS:CG	1:A:399:VAL:HG21	2.52	0.43
1:A:492:VAL:HB	1:A:493:PRO:HD3	2.00	0.43
1:A:1041:ASP:OD1	1:A:1097:ILE:N	2.50	0.43
1:B:698:LEU:HB3	1:B:701:ALA:HB3	2.01	0.43
1:B:1020:ILE:HD13	1:B:1020:ILE:HA	1.83	0.43
1:A:1023:LEU:HD23	1:A:1023:LEU:HA	1.76	0.43
1:B:331:HIS:HB2	1:B:346:LYS:HZ2	1.83	0.43
1:B:439:GLY:HA2	1:B:498:TYR:HD2	1.84	0.43
1:A:917:LEU:HD12	1:A:918:GLU:HG3	2.00	0.43
1:A:924:ARG:HH12	1:A:927:VAL:HA	1.84	0.43
1:A:1122:PRO:HB2	1:A:1125:LYS:HG2	2.00	0.43
1:A:80:TRP:HA	1:A:83:PHE:CZ	2.53	0.42
1:A:936:TYR:HD1	1:A:978:ARG:HD2	1.83	0.42
1:B:915:SER:HB2	1:B:942:ARG:HD3	2.01	0.42
1:A:267:MET:H	1:A:267:MET:HG2	1.66	0.42
1:A:475:PRO:HA	1:A:476:PRO:HD3	1.90	0.42
1:A:309:MET:HE2	1:A:309:MET:HB3	1.66	0.42
1:A:832:HIS:HB2	1:A:840:ILE:HG22	2.00	0.42
1:B:114:LEU:HD23	1:B:174:LEU:HD23	2.01	0.42
1:B:202:TYR:O	1:B:552:TRP:NE1	2.35	0.42
1:B:1087:LYS:O	1:B:1091:PRO:HD2	2.20	0.42
1:A:688:ILE:O	1:A:692:ILE:HG12	2.19	0.42
1:A:1141:ALA:HB2	1:A:1156:LEU:HB3	2.02	0.42
1:B:535:LYS:H	1:B:535:LYS:CD	2.33	0.42
1:B:543:VAL:CG2	1:B:559:MET:HB2	2.49	0.42
1:B:859:TRP:O	1:B:862:ILE:HG22	2.20	0.42
1:A:726:THR:O	1:A:764:LYS:HD2	2.19	0.42
1:B:331:HIS:HB2	1:B:346:LYS:NZ	2.35	0.42
1:A:660:LYS:HE2	1:A:660:LYS:HB2	1.88	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:699:GLU:O	1:A:700:ARG:HG2	2.19	0.42
1:A:1116:ALA:HB2	1:A:1137:ARG:NH2	2.35	0.42
1:B:651:THR:O	1:B:655:LYS:HG2	2.20	0.42
1:B:905:LEU:H	1:B:905:LEU:HG	1.65	0.42
1:A:306:LEU:HA	1:A:541:ARG:HH11	1.85	0.42
1:A:656:ILE:O	1:A:659:GLN:HG3	2.19	0.42
1:A:1077:ARG:HD3	1:A:1083:ASP:OD2	2.19	0.42
1:B:441:LEU:HG	1:B:466:LEU:HB3	2.00	0.42
1:B:672:GLY:HA3	1:B:698:LEU:HD21	2.02	0.42
1:B:975:VAL:HG22	1:B:978:ARG:NH1	2.35	0.42
1:A:698:LEU:N	1:A:787:ASN:OD1	2.44	0.42
1:B:92:ILE:HD13	1:B:92:ILE:HA	1.83	0.42
1:A:313:PHE:CZ	1:A:345:ILE:HD11	2.55	0.42
1:A:650:THR:OG1	1:A:653:THR:OG1	2.26	0.42
1:A:1020:ILE:HD13	1:A:1020:ILE:HA	1.96	0.42
1:A:1150:TRP:CZ2	1:A:1163:MET:HE3	2.54	0.42
1:B:28:ALA:HA	1:B:31:VAL:HG22	2.02	0.42
1:A:395:LEU:H	1:A:395:LEU:HG	1.71	0.41
1:B:226:HIS:CE1	1:B:594:TRP:CD1	3.08	0.41
1:B:880:ALA:O	1:B:883:LYS:HG2	2.20	0.41
1:A:242:ILE:HA	1:A:599:TRP:CH2	2.55	0.41
1:A:975:VAL:HG23	1:A:978:ARG:HH21	1.84	0.41
1:B:985:PHE:CZ	1:B:1150:TRP:HD1	2.38	0.41
1:A:187:LYS:HA	1:A:191:PHE:O	2.20	0.41
1:A:261:TRP:O	1:A:264:ILE:HG22	2.20	0.41
1:A:919:LYS:HD2	1:A:920:PRO:HD2	2.03	0.41
1:B:691:ILE:HG12	1:B:977:LEU:HD13	2.01	0.41
4:Q:1:NAG:H3	4:Q:2:NAG:N2	2.36	0.41
4:R:1:NAG:H4	4:R:2:NAG:N2	2.35	0.41
1:A:403:GLU:OE2	1:A:403:GLU:C	2.64	0.41
1:A:436:LEU:HA	1:A:436:LEU:HD12	1.85	0.41
1:B:98:LEU:HD23	1:B:98:LEU:HA	1.79	0.41
1:B:479:ARG:NH2	1:B:485:ASP:OD1	2.28	0.41
2:P:1:NAG:H61	2:P:2:NAG:H83	2.01	0.41
1:A:262:GLU:OE2	1:A:431:GLU:HB2	2.20	0.41
1:A:274:LYS:HE2	1:A:274:LYS:HB3	1.81	0.41
1:A:966:TYR:CE2	1:A:989:ILE:HG13	2.56	0.41
1:B:230:ARG:HH22	1:B:593:GLY:HA2	1.85	0.41
1:B:630:THR:HG21	1:B:671:TYR:CZ	2.56	0.41
1:B:819:LEU:HG	1:B:1031:ILE:HD12	2.02	0.41
1:A:97:THR:HG23	1:A:189:ASP:OD2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:315:GLU:H	1:B:315:GLU:HG2	1.64	0.41
1:B:1024:MET:HE2	1:B:1175:LEU:HD11	2.03	0.41
1:B:1097:ILE:HD12	1:B:1097:ILE:HA	1.89	0.41
1:A:546:ALA:O	1:A:549:SER:OG	2.32	0.41
1:A:623:PHE:HE1	1:A:674:GLN:HB3	1.85	0.41
1:A:658:LEU:HD23	1:A:658:LEU:HA	1.75	0.41
1:A:710:GLU:HG2	1:A:779:LEU:HD11	2.01	0.41
1:B:560:VAL:HG23	1:B:562:LEU:HD23	2.02	0.41
1:A:623:PHE:CZ	1:A:675:ALA:HB2	2.55	0.41
1:A:700:ARG:O	1:A:703:LEU:HD12	2.21	0.41
1:B:41:ALA:O	1:B:46:ILE:HD11	2.21	0.41
1:B:146:ILE:HD11	1:B:155:MET:HG3	2.01	0.41
1:B:489:LYS:O	1:B:493:PRO:HD2	2.21	0.41
1:B:832:HIS:ND1	1:B:836:GLY:O	2.54	0.41
1:B:1030:LYS:HD2	1:B:1107:PHE:CZ	2.56	0.41
1:A:833:ARG:HE	1:A:833:ARG:HB2	1.73	0.41
1:B:44:THR:HG23	1:B:326:ARG:HH21	1.86	0.41
1:B:647:THR:O	1:B:924:ARG:HB2	2.20	0.41
1:B:745:MET:HE2	1:B:854:MET:HA	2.02	0.41
1:B:862:ILE:HD12	1:B:862:ILE:HA	1.98	0.41
1:B:872:ALA:HB1	1:B:1018:HIS:NE2	2.35	0.41
1:A:183:ASN:ND2	1:A:450:PHE:O	2.47	0.41
1:A:964:ILE:HD13	1:A:964:ILE:HA	1.83	0.41
1:A:1053:THR:HG22	1:A:1054:LYS:H	1.85	0.41
1:B:140:ASP:HA	1:B:141:PRO:HA	1.87	0.41
1:B:313:PHE:HE1	1:B:343:PHE:HD2	1.69	0.41
1:B:686:THR:HG21	1:B:1148:ARG:HH22	1.85	0.40
1:B:704:PRO:HD2	1:B:707:GLU:HG3	2.03	0.40
1:B:883:LYS:HB3	1:B:883:LYS:HE2	1.82	0.40
1:B:916:MET:SD	1:B:919:LYS:HE3	2.61	0.40
1:B:1023:LEU:HA	1:B:1023:LEU:HD23	1.78	0.40
1:A:259:GLN:HG2	1:A:435:PHE:HD1	1.85	0.40
1:A:369:TYR:HA	1:A:372:TYR:CE2	2.56	0.40
1:B:304:LEU:HD12	1:B:304:LEU:HA	1.91	0.40
1:B:652:GLU:H	1:B:652:GLU:HG3	1.70	0.40
1:A:510:GLN:HG2	1:A:569:PRO:HG2	2.03	0.40
1:A:616:ASP:OD2	1:A:619:GLU:N	2.37	0.40
1:A:736:GLN:O	1:A:741:LEU:HB2	2.20	0.40
1:B:277:LEU:HD22	1:B:402:PRO:HG3	2.04	0.40
1:B:310:PRO:HB2	1:B:312:GLU:OE1	2.22	0.40
1:B:411:LEU:HD13	1:B:412:ASP:N	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:881:MET:HE3	1:B:881:MET:HB2	1.98	0.40
1:B:66:GLU:HG3	1:B:67:ALA:N	2.35	0.40
1:B:358:THR:O	1:B:362:GLU:HG2	2.22	0.40
1:B:627:TYR:HD1	1:B:671:TYR:CD2	2.39	0.40
1:A:103:LEU:HD21	1:A:185:ALA:HB2	2.03	0.40
1:B:244:LEU:HD23	1:B:244:LEU:HA	1.83	0.40
1:B:964:ILE:HA	1:B:964:ILE:HD13	1.85	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	1199/1241 (97%)	1122 (94%)	77 (6%)	0	100	100
1	B	1197/1241 (96%)	1129 (94%)	68 (6%)	0	100	100
All	All	2396/2482 (96%)	2251 (94%)	145 (6%)	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	1040/1071 (97%)	1000 (96%)	40 (4%)	28	55

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	B	1039/1071 (97%)	987 (95%)	52 (5%)	20 47
All	All	2079/2142 (97%)	1987 (96%)	92 (4%)	26 51

All (92) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	46	ILE
1	A	127	VAL
1	A	146	ILE
1	A	147	LEU
1	A	171	LEU
1	A	242	ILE
1	A	286	GLN
1	A	342	ASP
1	A	345	ILE
1	A	351	VAL
1	A	388	HIS
1	A	436	LEU
1	A	473	ILE
1	A	480	ASN
1	A	508	GLN
1	A	530	ILE
1	A	534	THR
1	A	543	VAL
1	A	669	LEU
1	A	707	GLU
1	A	727	VAL
1	A	744	VAL
1	A	859	TRP
1	A	905	LEU
1	A	947	THR
1	A	964	ILE
1	A	986	HIS
1	A	1007	ASN
1	A	1009	LEU
1	A	1054	LYS
1	A	1056	ASN
1	A	1075	VAL
1	A	1077	ARG
1	A	1078	THR
1	A	1102	SER
1	A	1119	HIS

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Mol	Chain	Res	Type
1	A	1128	ILE
1	A	1150	TRP
1	A	1156	LEU
1	A	1190	LEU
1	B	5	LEU
1	B	50	ASN
1	B	66	GLU
1	B	83	PHE
1	B	107	LYS
1	B	146	ILE
1	B	147	LEU
1	B	181	LEU
1	B	221	LEU
1	B	248	ILE
1	B	253	LEU
1	B	268	VAL
1	B	274	LYS
1	B	286	GLN
1	B	313	PHE
1	B	379	LEU
1	B	388	HIS
1	B	525	LEU
1	B	527	GLN
1	B	531	TYR
1	B	592	LEU
1	B	594	TRP
1	B	612	ASP
1	B	622	LYS
1	B	649	ILE
1	B	650	THR
1	B	653	THR
1	B	707	GLU
1	B	709	GLU
1	B	731	ASN
1	B	735	LEU
1	B	846	ILE
1	B	894	GLU
1	B	905	LEU
1	B	917	LEU
1	B	931	SER
1	B	935	PHE
1	B	948	THR

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Mol	Chain	Res	Type
1	B	952	GLU
1	B	956	VAL
1	B	977	LEU
1	B	1039	LEU
1	B	1041	ASP
1	B	1044	ARG
1	B	1053	THR
1	B	1056	ASN
1	B	1078	THR
1	B	1090	ILE
1	B	1129	TYR
1	B	1137	ARG
1	B	1150	TRP
1	B	1160	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (36) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	22	GLN
1	A	87	GLN
1	A	217	GLN
1	A	285	GLN
1	A	347	GLN
1	A	355	GLN
1	A	361	HIS
1	A	365	HIS
1	A	388	HIS
1	A	471	GLN
1	A	588	ASN
1	A	598	GLN
1	A	606	ASN
1	A	632	GLN
1	A	736	GLN
1	A	824	HIS
1	A	1042	GLN
1	A	1056	ASN
1	A	1110	HIS
1	B	22	GLN
1	B	34	GLN
1	B	164	HIS
1	B	263	ASN
1	B	285	GLN

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Mol	Chain	Res	Type
1	B	331	HIS
1	B	347	GLN
1	B	586	GLN
1	B	632	GLN
1	B	636	ASN
1	B	644	ASN
1	B	817	GLN
1	B	824	HIS
1	B	913	ASN
1	B	969	GLN
1	B	1004	HIS
1	B	1196	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

29 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	$\#\|Z\| > 2$
2	NAG	D	1	1,2	14,14,15	0.72	0	17,19,21	1.49	4 (23%)
2	NAG	D	2	2	14,14,15	0.72	0	17,19,21	1.99	3 (17%)
2	BMA	D	3	2	11,11,12	0.87	0	15,15,17	2.11	2 (13%)
3	NAG	F	1	1,3	14,14,15	0.78	0	17,19,21	1.17	1 (5%)
3	NAG	F	2	3	14,14,15	0.79	1 (7%)	17,19,21	2.19	4 (23%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
3	BMA	F	3	3	11,11,12	0.84	0	15,15,17	2.00	4 (26%)
3	FUC	F	4	3	10,10,11	0.75	0	14,14,16	1.01	0
4	NAG	G	1	4,1	14,14,15	0.82	0	17,19,21	1.66	5 (29%)
4	NAG	G	2	4	14,14,15	0.71	0	17,19,21	1.32	2 (11%)
4	NAG	H	1	4,1	14,14,15	0.75	0	17,19,21	1.26	1 (5%)
4	NAG	H	2	4	14,14,15	0.72	0	17,19,21	0.92	1 (5%)
4	NAG	I	1	4,1	14,14,15	0.74	0	17,19,21	1.53	3 (17%)
4	NAG	I	2	4	14,14,15	0.72	0	17,19,21	1.39	1 (5%)
4	NAG	L	1	4,1	14,14,15	0.75	0	17,19,21	0.83	0
4	NAG	L	2	4	14,14,15	0.73	0	17,19,21	0.86	0
2	NAG	N	1	1,2	14,14,15	0.69	0	17,19,21	0.97	0
2	NAG	N	2	2	14,14,15	0.74	0	17,19,21	1.21	1 (5%)
2	BMA	N	3	2	11,11,12	0.82	0	15,15,17	2.07	2 (13%)
2	NAG	P	1	1,2	14,14,15	0.78	0	17,19,21	1.08	0
2	NAG	P	2	2	14,14,15	0.76	0	17,19,21	1.32	2 (11%)
2	BMA	P	3	2	11,11,12	0.85	0	15,15,17	2.19	3 (20%)
4	NAG	Q	1	4,1	14,14,15	0.75	0	17,19,21	1.43	3 (17%)
4	NAG	Q	2	4	14,14,15	0.83	0	17,19,21	2.28	2 (11%)
4	NAG	R	1	4,1	14,14,15	0.72	0	17,19,21	1.08	2 (11%)
4	NAG	R	2	4	14,14,15	0.80	0	17,19,21	1.30	3 (17%)
4	NAG	S	1	4,1	14,14,15	0.78	0	17,19,21	0.97	1 (5%)
4	NAG	S	2	4	14,14,15	0.73	0	17,19,21	0.93	0
4	NAG	U	1	4,1	14,14,15	0.70	0	17,19,21	1.24	1 (5%)
4	NAG	U	2	4	14,14,15	0.69	0	17,19,21	0.85	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
2	NAG	D	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	D	2	2	-	3/6/23/26	0/1/1/1
2	BMA	D	3	2	-	1/2/19/22	0/1/1/1
3	NAG	F	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	F	2	3	-	0/6/23/26	0/1/1/1
3	BMA	F	3	3	-	0/2/19/22	0/1/1/1
3	FUC	F	4	3	-	-	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	G	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	G	2	4	-	4/6/23/26	0/1/1/1
4	NAG	H	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	H	2	4	-	0/6/23/26	0/1/1/1
4	NAG	I	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	I	2	4	-	2/6/23/26	0/1/1/1
4	NAG	L	1	4,1	-	1/6/23/26	0/1/1/1
4	NAG	L	2	4	-	0/6/23/26	0/1/1/1
2	NAG	N	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	N	2	2	-	2/6/23/26	0/1/1/1
2	BMA	N	3	2	-	1/2/19/22	0/1/1/1
2	NAG	P	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	P	2	2	-	2/6/23/26	0/1/1/1
2	BMA	P	3	2	-	2/2/19/22	0/1/1/1
4	NAG	Q	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	Q	2	4	-	4/6/23/26	0/1/1/1
4	NAG	R	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	R	2	4	-	3/6/23/26	0/1/1/1
4	NAG	S	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	S	2	4	-	0/6/23/26	0/1/1/1
4	NAG	U	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	U	2	4	-	3/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	F	2	NAG	C1-C2	2.17	1.55	1.52

All (51) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	Q	2	NAG	C2-N2-C7	8.17	133.85	122.90
2	P	3	BMA	C1-O5-C5	6.90	121.43	112.19
2	D	3	BMA	C1-O5-C5	6.69	121.15	112.19
2	N	3	BMA	C1-O5-C5	6.39	120.75	112.19
3	F	2	NAG	C1-O5-C5	6.19	120.48	112.19
2	D	2	NAG	C2-N2-C7	5.96	130.89	122.90
3	F	3	BMA	C1-O5-C5	5.71	119.84	112.19
4	I	1	NAG	C1-O5-C5	3.85	117.34	112.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	I	2	NAG	C2-N2-C7	3.84	128.05	122.90
4	U	1	NAG	C2-N2-C7	3.74	127.91	122.90
3	F	2	NAG	C3-C4-C5	-3.70	103.52	110.23
2	D	1	NAG	O5-C1-C2	-3.53	105.83	111.29
3	F	1	NAG	C1-O5-C5	3.53	116.92	112.19
4	H	1	NAG	C2-N2-C7	3.51	127.60	122.90
2	P	2	NAG	C2-N2-C7	3.48	127.57	122.90
3	F	2	NAG	O5-C1-C2	3.47	116.67	111.29
4	G	2	NAG	C2-N2-C7	3.37	127.42	122.90
4	Q	1	NAG	O5-C1-C2	-3.18	106.37	111.29
4	Q	1	NAG	C3-C4-C5	3.15	115.95	110.23
4	G	1	NAG	O4-C4-C3	-3.08	103.12	110.38
4	G	1	NAG	C4-C3-C2	2.92	115.29	111.02
4	G	1	NAG	C2-N2-C7	2.90	126.78	122.90
2	D	2	NAG	C1-O5-C5	2.90	116.07	112.19
4	R	2	NAG	C1-C2-N2	2.82	114.88	110.43
3	F	2	NAG	O4-C4-C5	2.80	116.21	109.32
2	N	2	NAG	C2-N2-C7	2.79	126.64	122.90
4	R	2	NAG	O5-C1-C2	-2.78	106.99	111.29
4	Q	2	NAG	C8-C7-N2	2.77	120.71	116.12
4	I	1	NAG	C4-C3-C2	-2.68	107.10	111.02
2	P	2	NAG	O5-C1-C2	-2.52	107.39	111.29
2	D	2	NAG	O7-C7-N2	2.47	126.34	121.98
4	G	2	NAG	O5-C1-C2	-2.47	107.47	111.29
2	D	1	NAG	C4-C3-C2	2.45	114.61	111.02
2	D	3	BMA	C2-C3-C4	2.45	115.16	110.86
2	D	1	NAG	O4-C4-C3	-2.45	104.61	110.38
4	G	1	NAG	O5-C1-C2	-2.44	107.52	111.29
3	F	3	BMA	C3-C4-C5	2.41	114.61	110.23
2	P	3	BMA	C3-C4-C5	2.41	114.60	110.23
4	R	1	NAG	O3-C3-C2	-2.27	104.69	109.40
2	P	3	BMA	C2-C3-C4	2.26	114.84	110.86
2	N	3	BMA	C2-C3-C4	2.23	114.78	110.86
4	S	1	NAG	C2-N2-C7	2.19	125.84	122.90
3	F	3	BMA	C2-C3-C4	2.14	114.63	110.86
4	R	2	NAG	C1-O5-C5	2.14	115.05	112.19
4	I	1	NAG	O4-C4-C3	2.11	115.36	110.38
4	H	2	NAG	O5-C1-C2	-2.11	108.02	111.29
3	F	3	BMA	O3-C3-C2	-2.06	105.84	110.05
4	R	1	NAG	O5-C1-C2	-2.06	108.10	111.29
4	G	1	NAG	C6-C5-C4	2.06	118.08	113.02
2	D	1	NAG	C3-C4-C5	2.04	113.93	110.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	Q	1	NAG	O4-C4-C3	-2.03	105.59	110.38

There are no chirality outliers.

All (38) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	2	NAG	C3-C2-N2-C7
2	P	3	BMA	O5-C5-C6-O6
4	I	1	NAG	O5-C5-C6-O6
2	D	1	NAG	C8-C7-N2-C2
2	D	1	NAG	O7-C7-N2-C2
4	Q	1	NAG	C8-C7-N2-C2
4	Q	1	NAG	O7-C7-N2-C2
4	Q	2	NAG	C8-C7-N2-C2
4	Q	2	NAG	O7-C7-N2-C2
4	R	2	NAG	C8-C7-N2-C2
4	R	2	NAG	O7-C7-N2-C2
4	U	2	NAG	C8-C7-N2-C2
4	U	2	NAG	O7-C7-N2-C2
2	D	3	BMA	O5-C5-C6-O6
4	G	2	NAG	O5-C5-C6-O6
4	I	1	NAG	C4-C5-C6-O6
2	D	2	NAG	O5-C5-C6-O6
4	U	2	NAG	O5-C5-C6-O6
4	Q	2	NAG	O5-C5-C6-O6
4	R	2	NAG	O5-C5-C6-O6
2	N	3	BMA	O5-C5-C6-O6
2	P	2	NAG	C1-C2-N2-C7
4	G	2	NAG	C1-C2-N2-C7
4	H	1	NAG	C1-C2-N2-C7
4	U	1	NAG	C1-C2-N2-C7
2	P	3	BMA	C4-C5-C6-O6
2	N	2	NAG	C3-C2-N2-C7
4	I	2	NAG	C3-C2-N2-C7
4	Q	2	NAG	C3-C2-N2-C7
4	G	2	NAG	C4-C5-C6-O6
4	L	1	NAG	O5-C5-C6-O6
2	D	2	NAG	C4-C5-C6-O6
2	N	2	NAG	C1-C2-N2-C7
4	I	2	NAG	C1-C2-N2-C7
2	P	2	NAG	C3-C2-N2-C7
4	G	2	NAG	C3-C2-N2-C7

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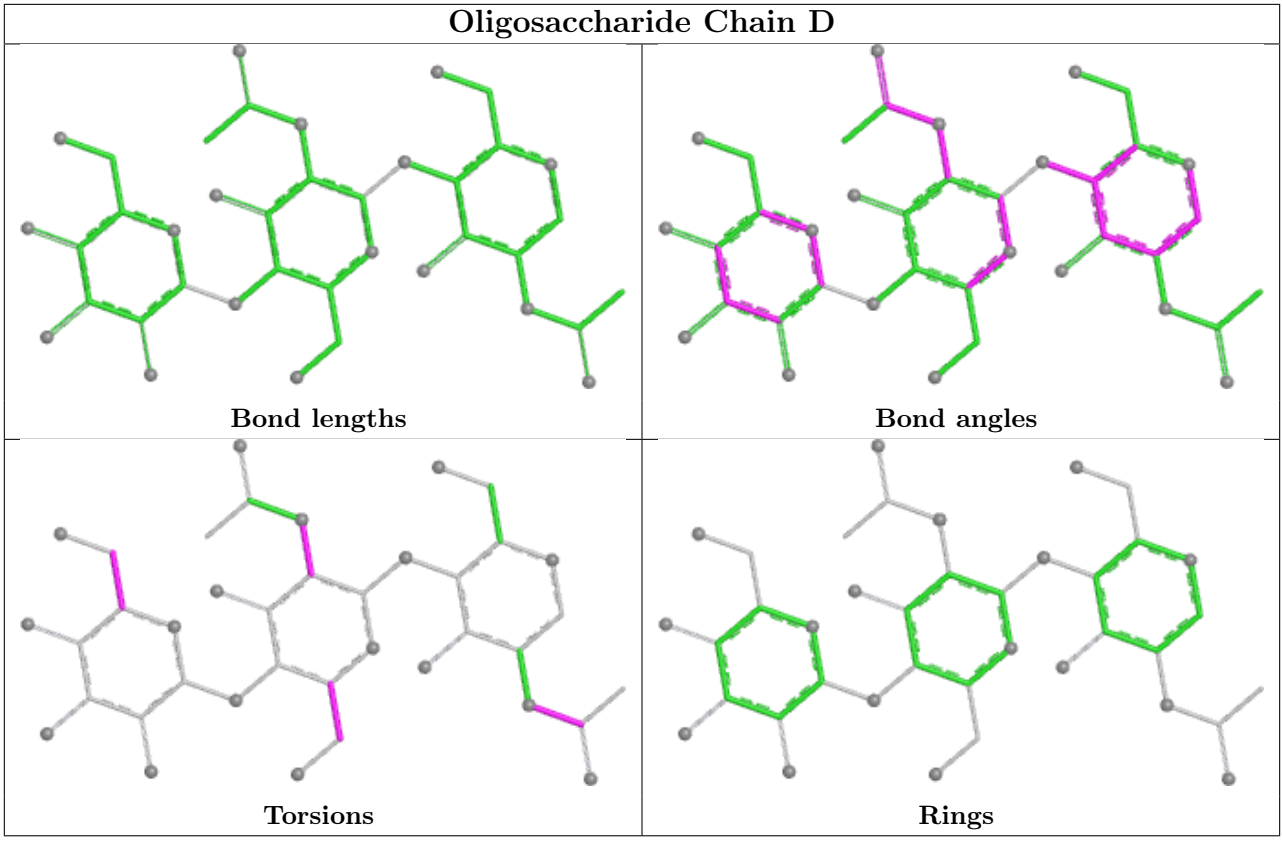
Mol	Chain	Res	Type	Atoms
4	H	1	NAG	C3-C2-N2-C7
4	U	1	NAG	C3-C2-N2-C7

There are no ring outliers.

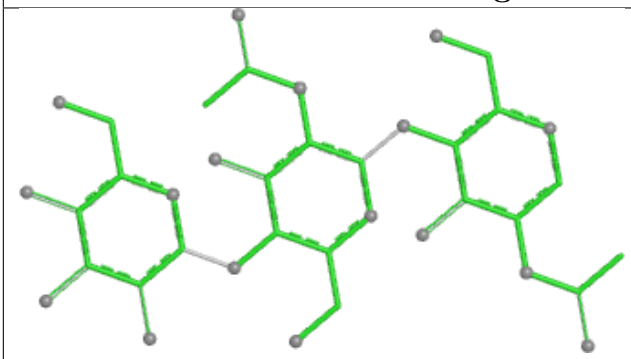
9 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	N	1	NAG	2	0
2	P	2	NAG	1	0
4	Q	2	NAG	1	0
4	R	2	NAG	1	0
2	P	1	NAG	2	0
4	R	1	NAG	1	0
2	D	2	NAG	1	0
4	Q	1	NAG	1	0
2	D	1	NAG	2	0

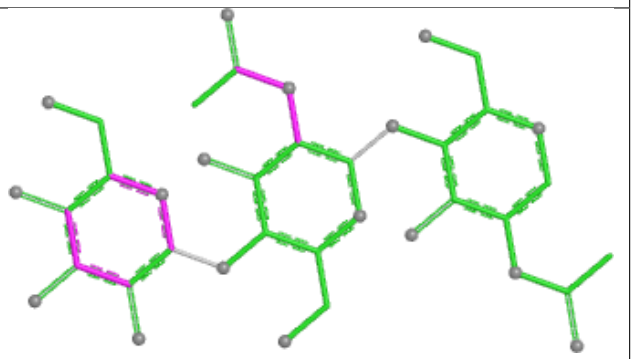
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.



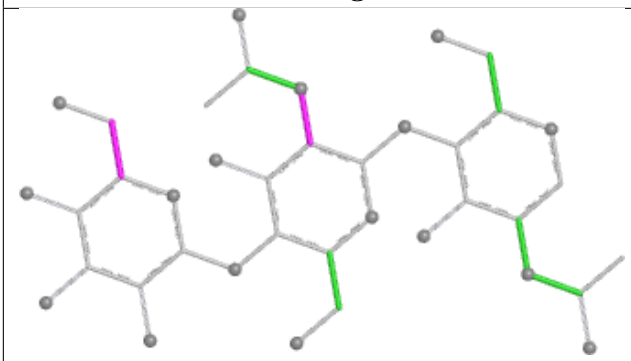
Oligosaccharide Chain N



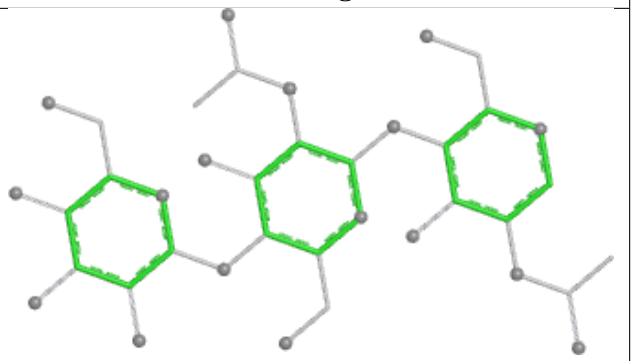
Bond lengths



Bond angles

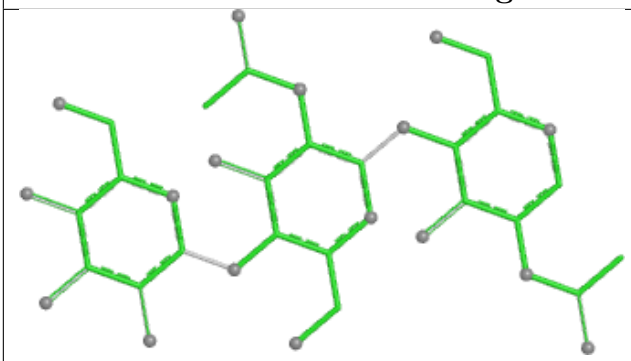


Torsions

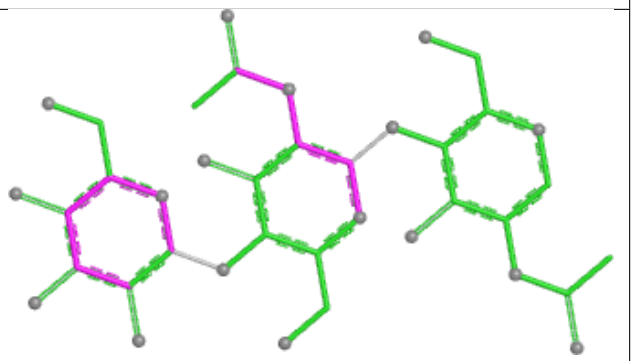


Rings

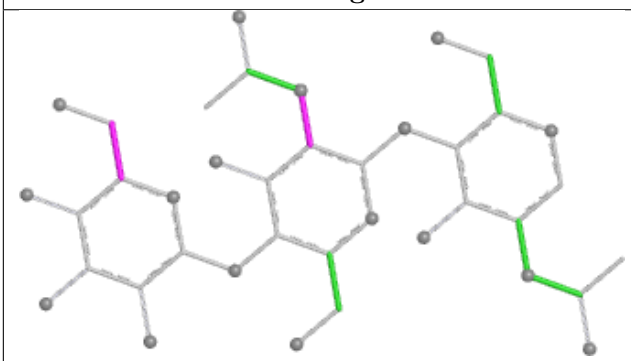
Oligosaccharide Chain P



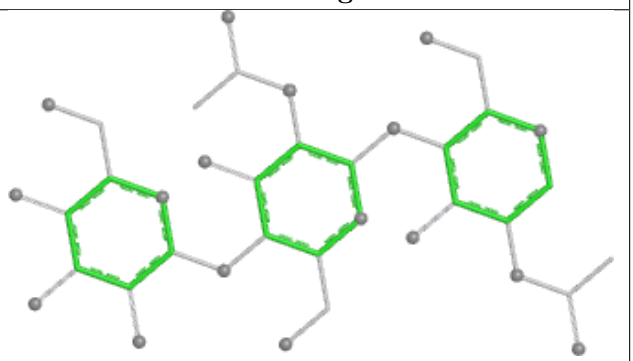
Bond lengths



Bond angles

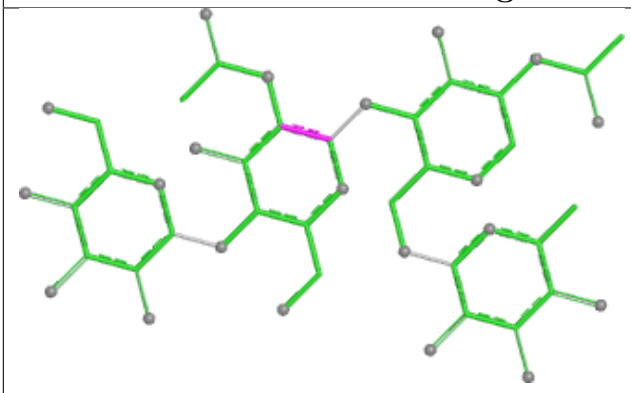


Torsions

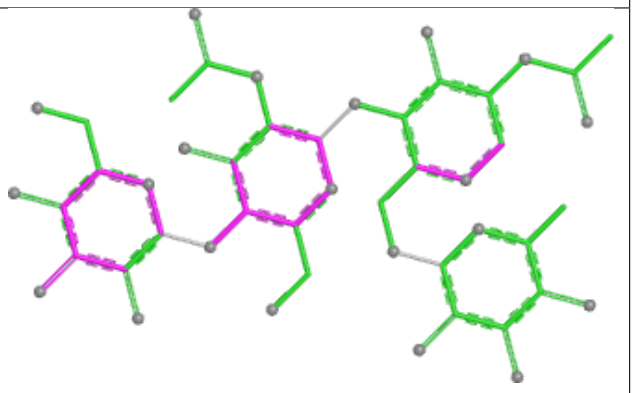


Rings

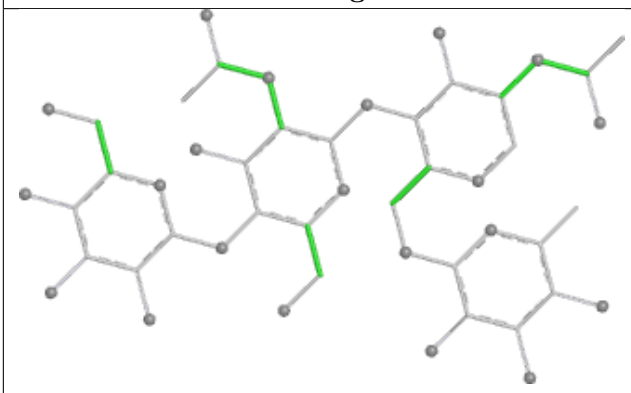
Oligosaccharide Chain F



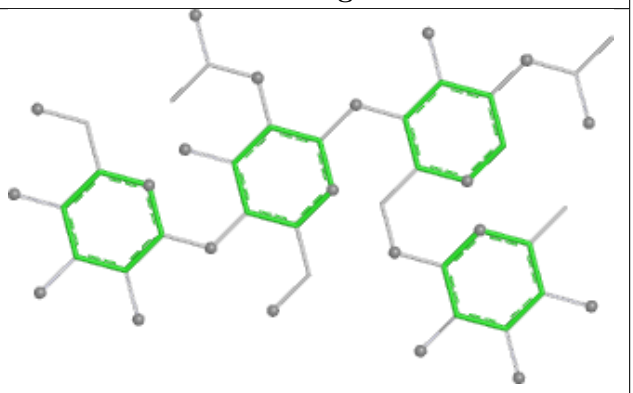
Bond lengths



Bond angles

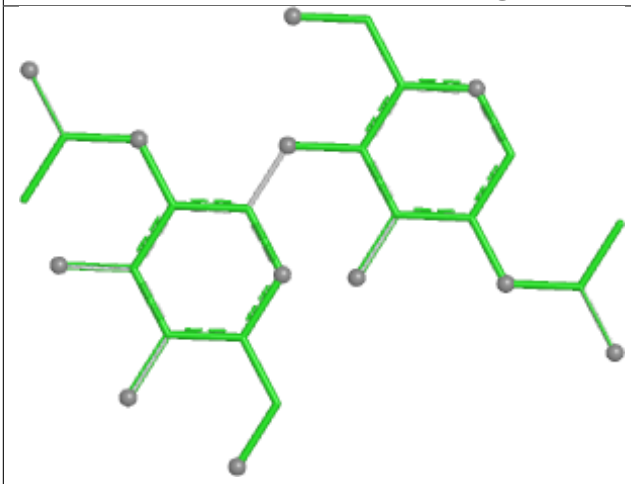


Torsions

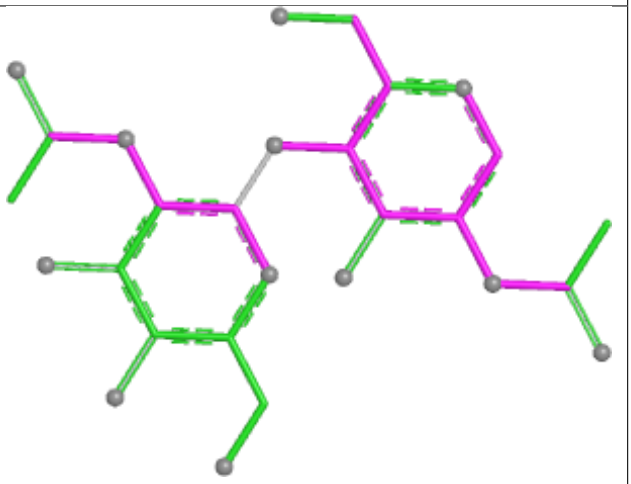


Rings

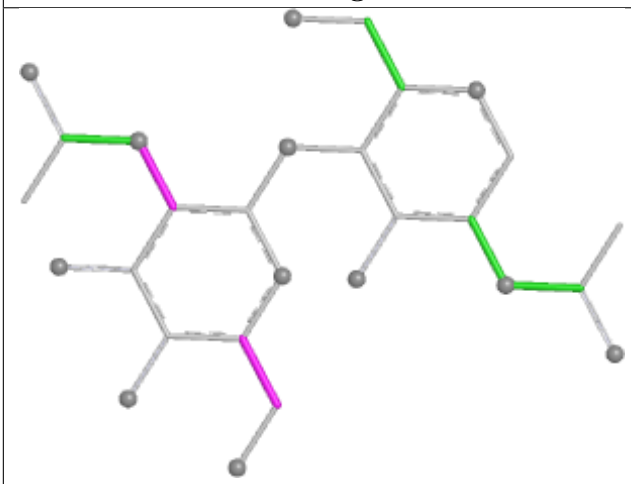
Oligosaccharide Chain G



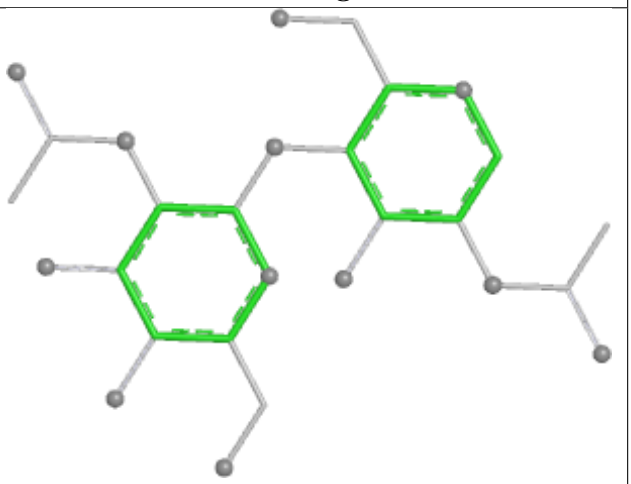
Bond lengths



Bond angles

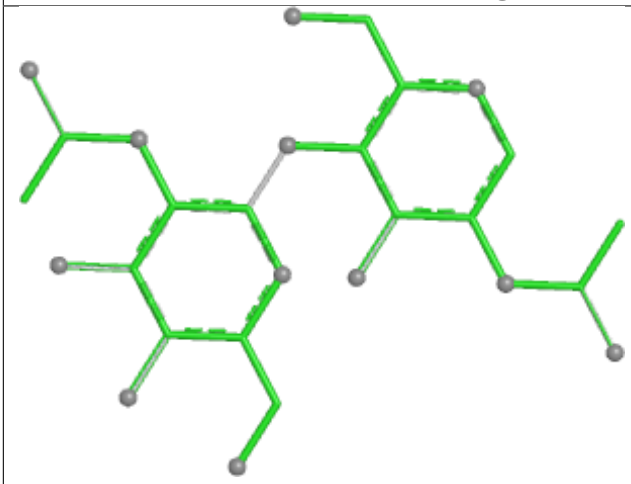


Torsions

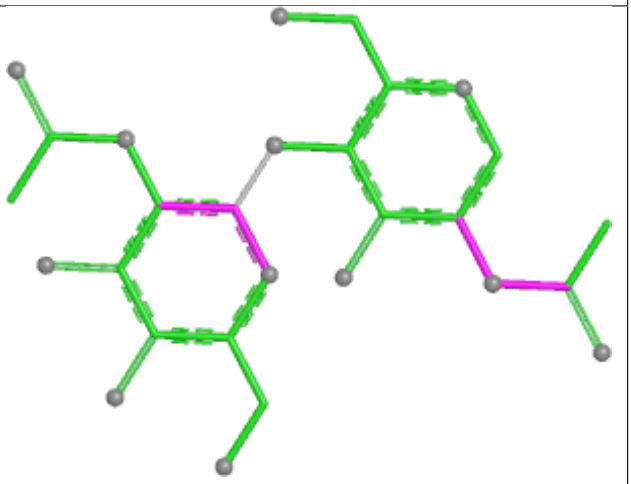


Rings

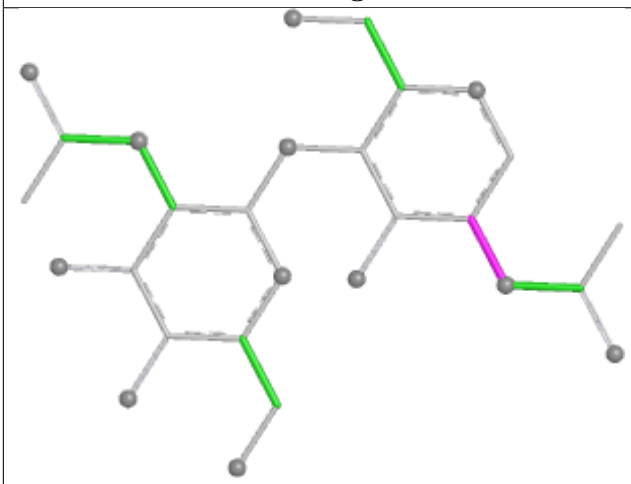
Oligosaccharide Chain H



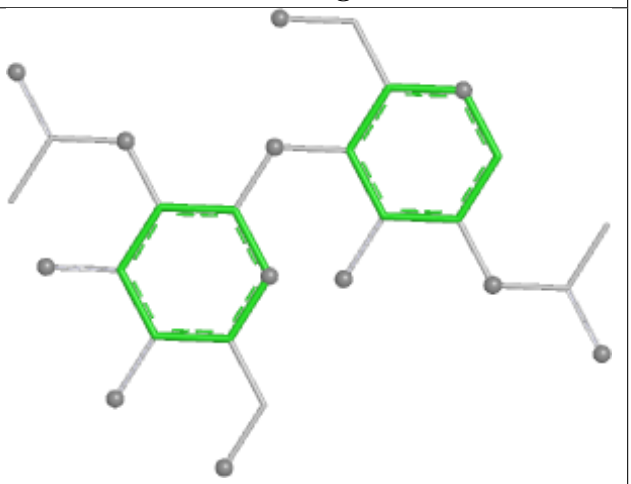
Bond lengths



Bond angles

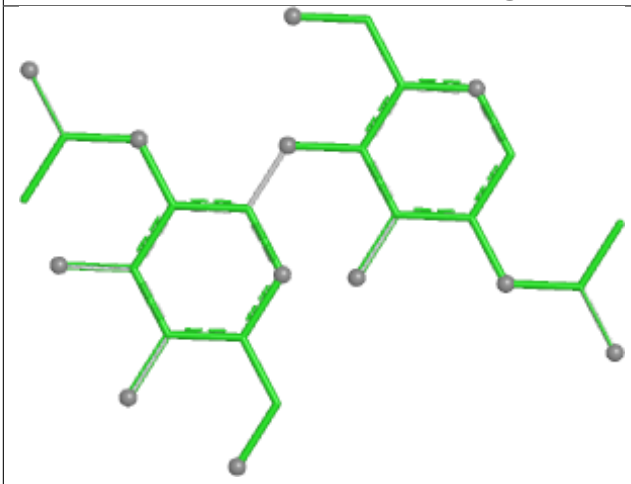


Torsions

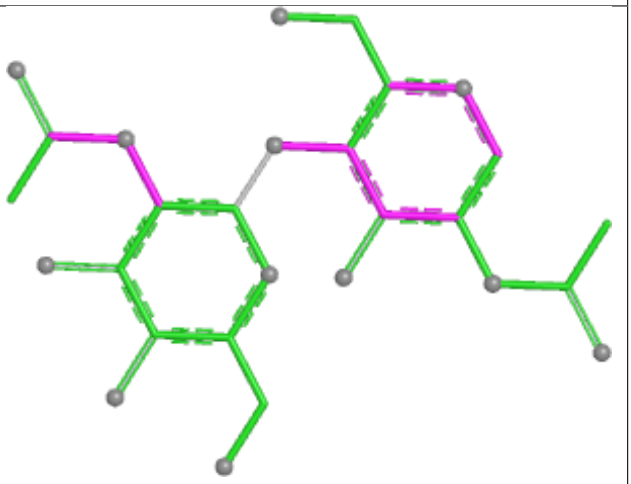


Rings

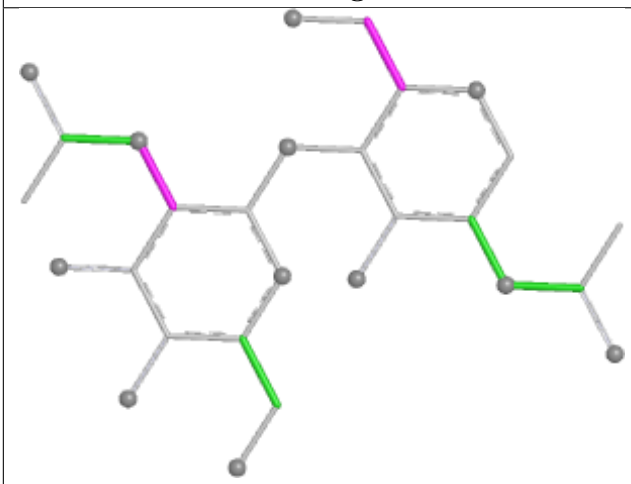
Oligosaccharide Chain I



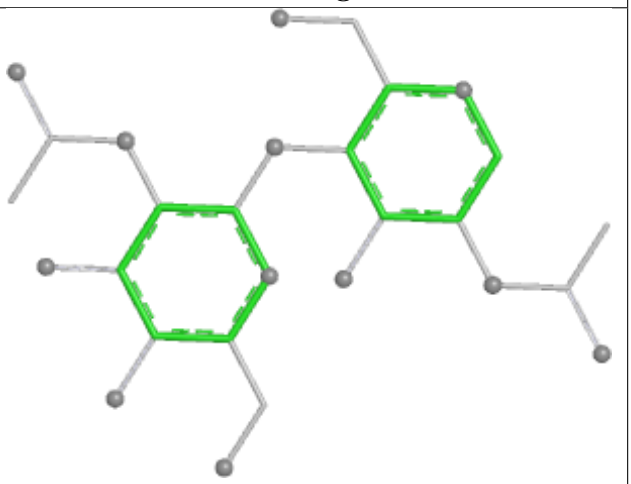
Bond lengths



Bond angles

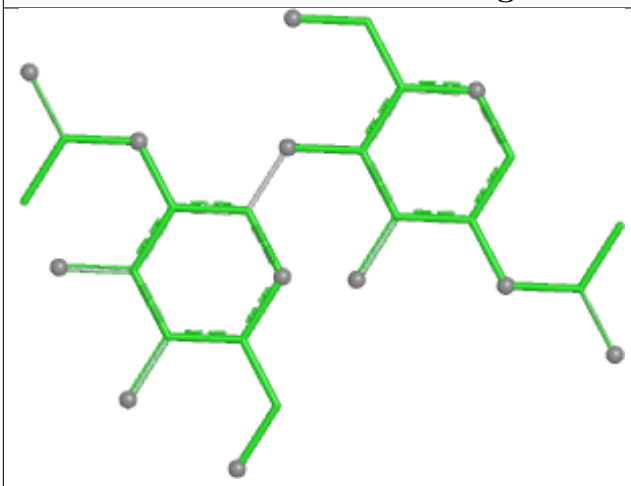


Torsions

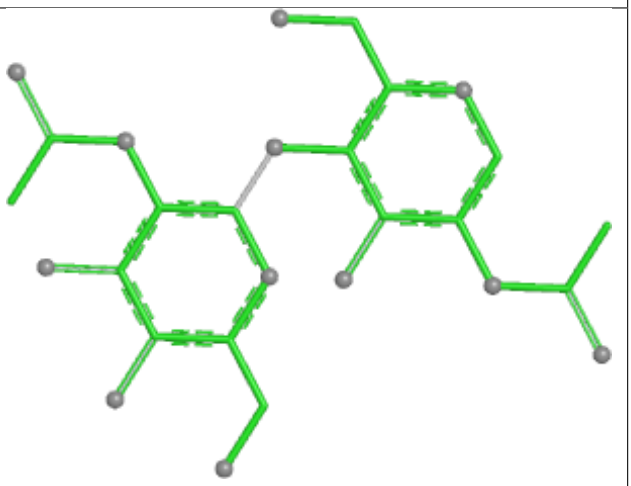


Rings

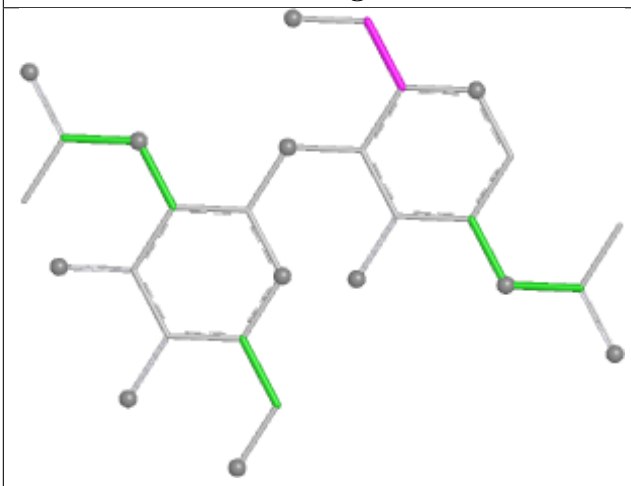
Oligosaccharide Chain L



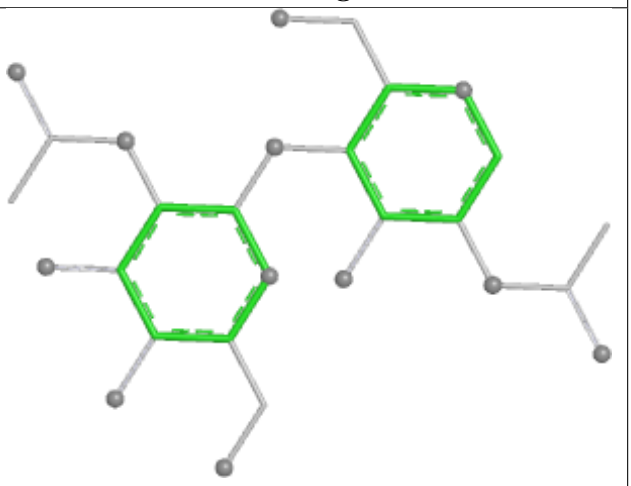
Bond lengths



Bond angles

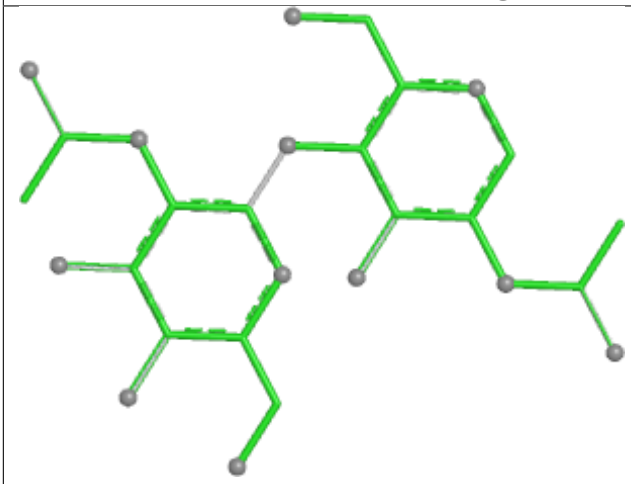


Torsions

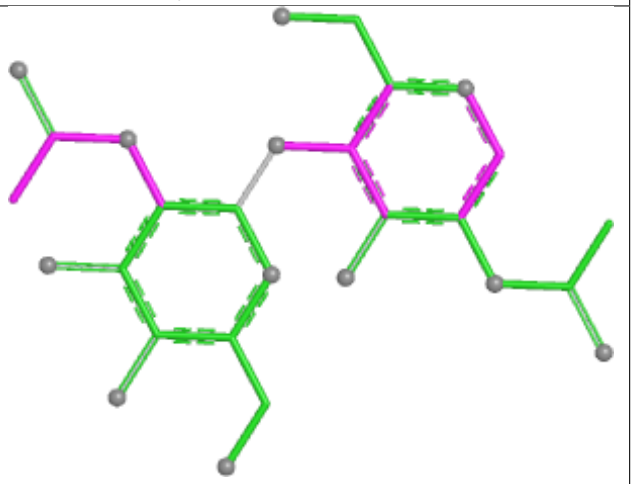


Rings

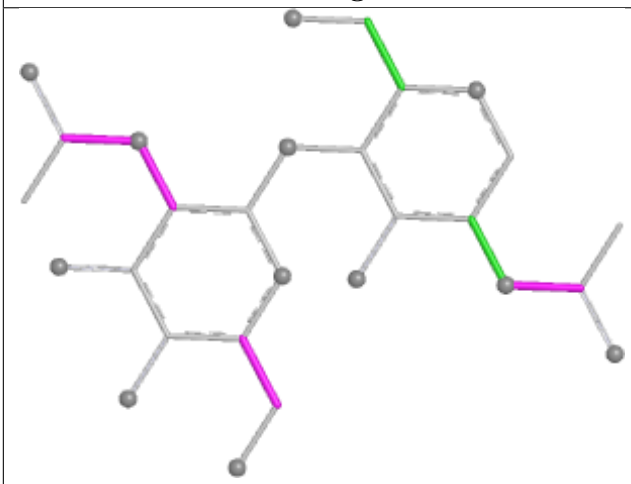
Oligosaccharide Chain Q



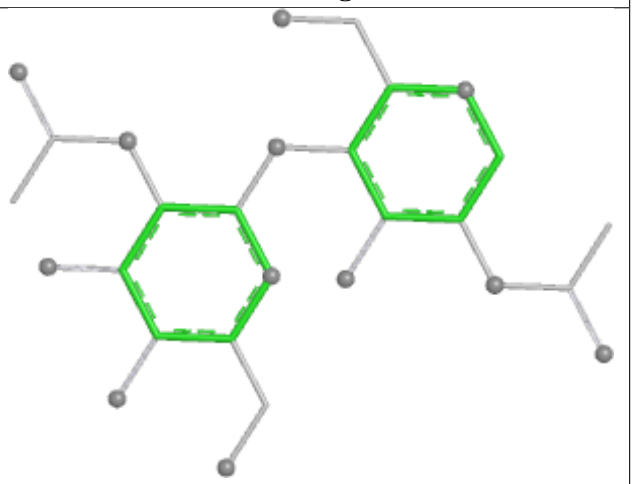
Bond lengths



Bond angles

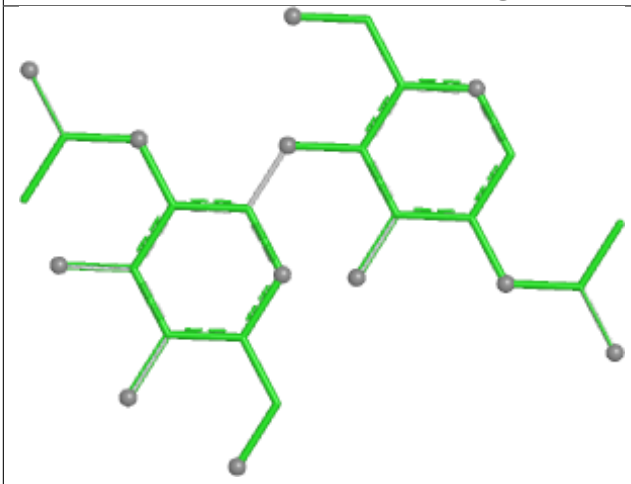


Torsions

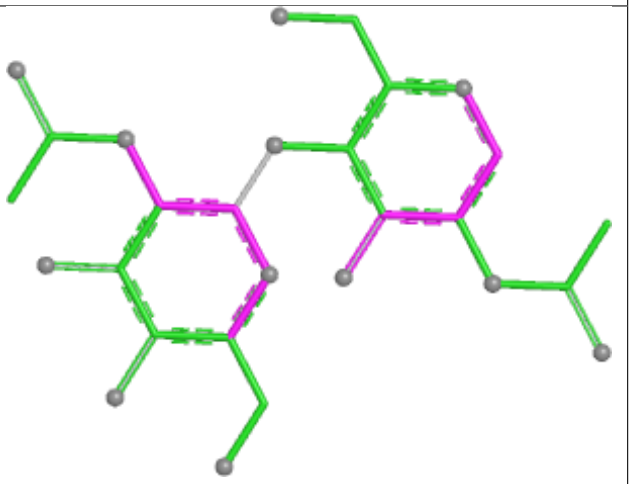


Rings

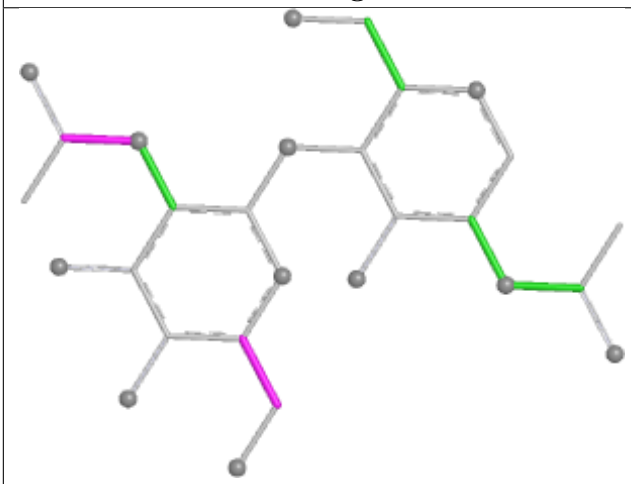
Oligosaccharide Chain R



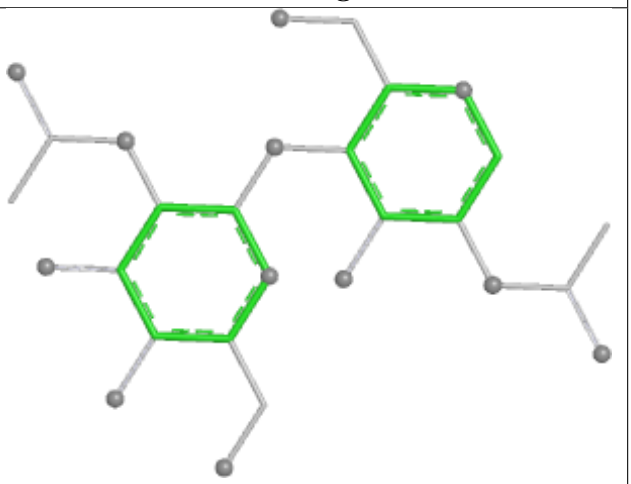
Bond lengths



Bond angles

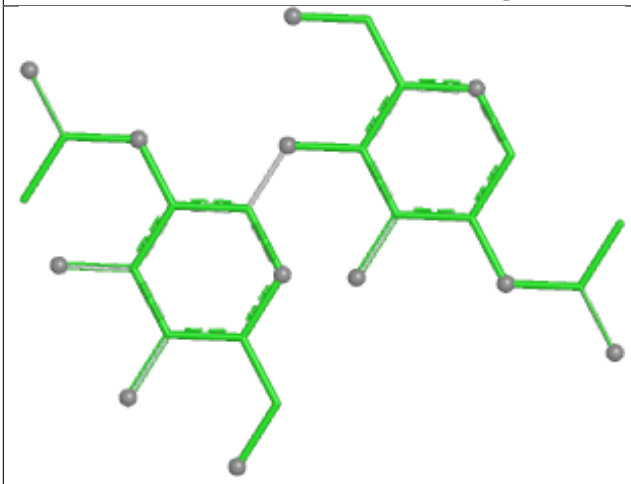


Torsions

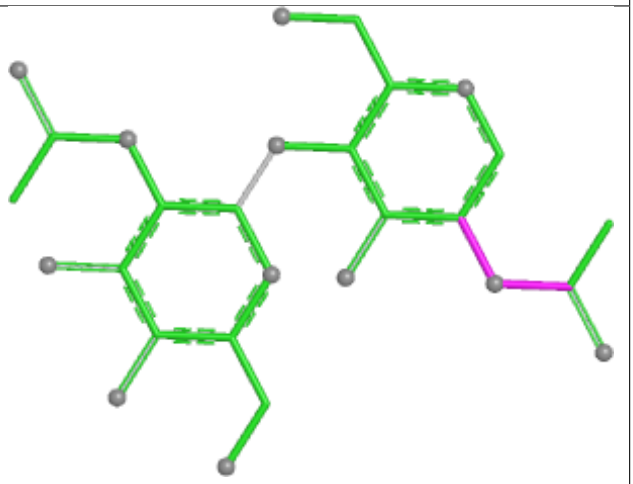


Rings

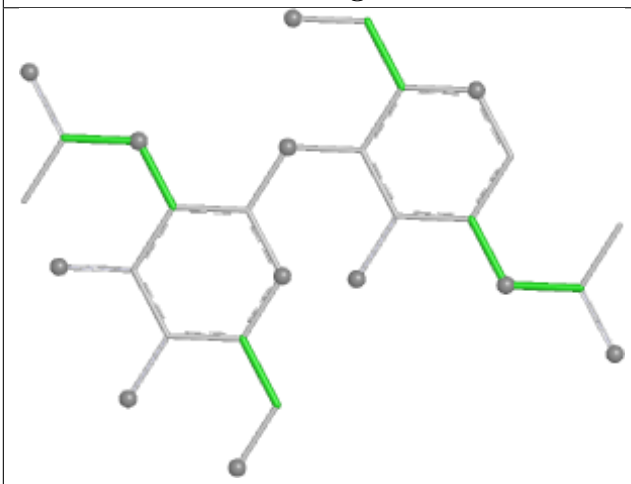
Oligosaccharide Chain S



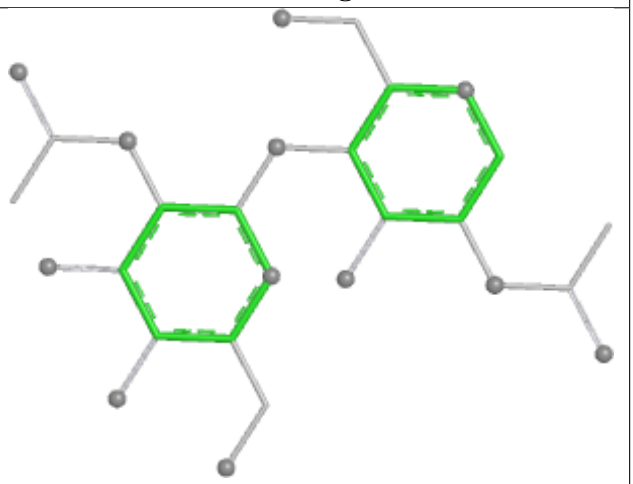
Bond lengths



Bond angles

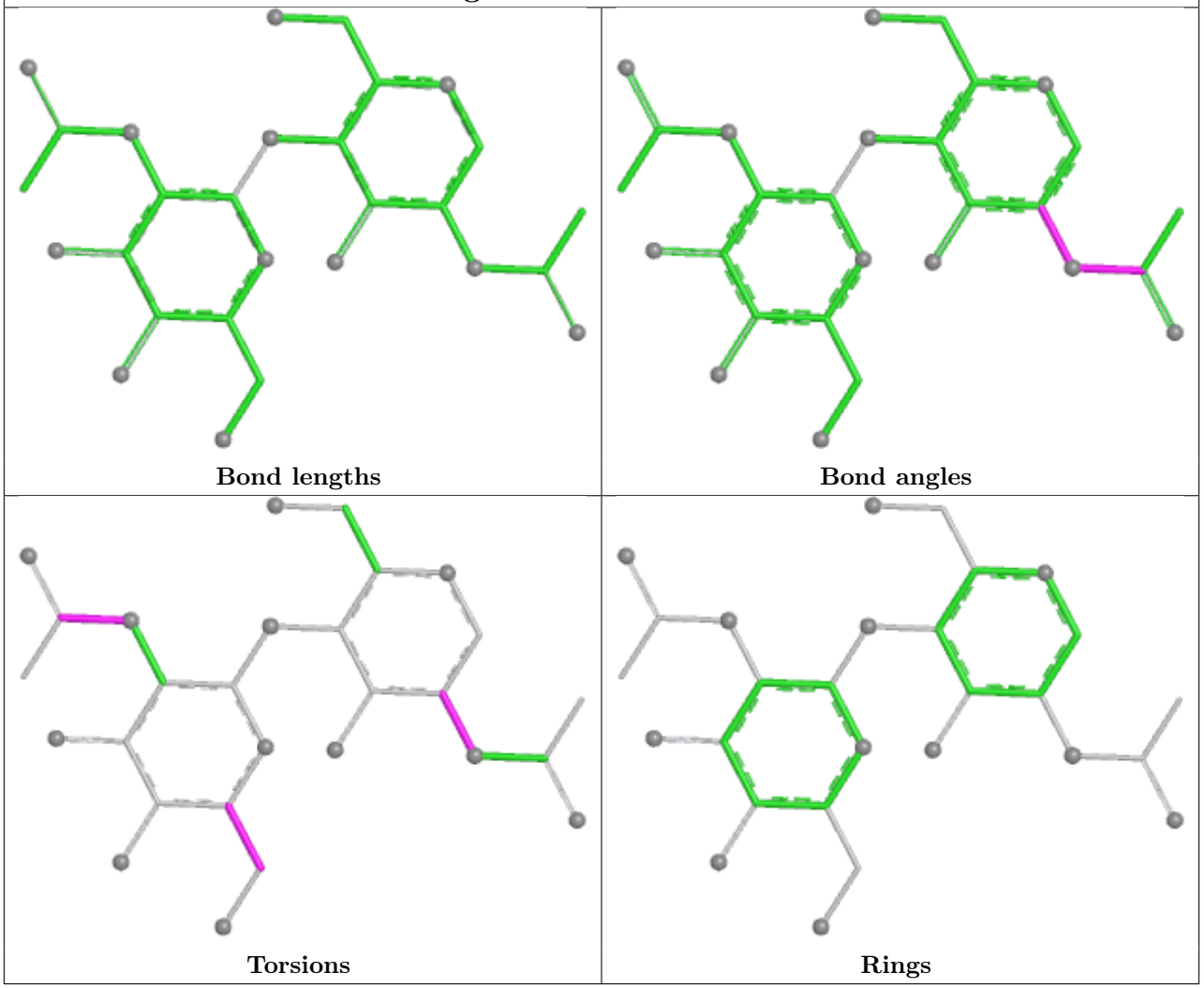


Torsions



Rings

Oligosaccharide Chain U



5.6 Ligand geometry (i)

6 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
5	NAG	A	1303	1	14,14,15	0.73	0	17,19,21	0.79	0
5	NAG	A	1302	1	14,14,15	0.72	0	17,19,21	0.89	0
5	NAG	B	1302	1	14,14,15	0.73	0	17,19,21	0.70	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
5	NAG	A	1301	1	14,14,15	0.72	0	17,19,21	0.80	0
5	NAG	B	1301	1	14,14,15	0.72	0	17,19,21	0.80	0
5	NAG	B	1303	1	14,14,15	0.76	0	17,19,21	0.92	1 (5%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	NAG	A	1303	1	-	1/6/23/26	0/1/1/1
5	NAG	A	1302	1	-	2/6/23/26	0/1/1/1
5	NAG	B	1302	1	-	0/6/23/26	0/1/1/1
5	NAG	A	1301	1	-	1/6/23/26	0/1/1/1
5	NAG	B	1301	1	-	1/6/23/26	0/1/1/1
5	NAG	B	1303	1	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	B	1303	NAG	O5-C1-C2	-2.79	106.97	111.29

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	1302	NAG	O5-C5-C6-O6
5	A	1303	NAG	O5-C5-C6-O6
5	B	1301	NAG	O5-C5-C6-O6
5	A	1301	NAG	O5-C5-C6-O6
5	A	1302	NAG	C4-C5-C6-O6

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	1301	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.

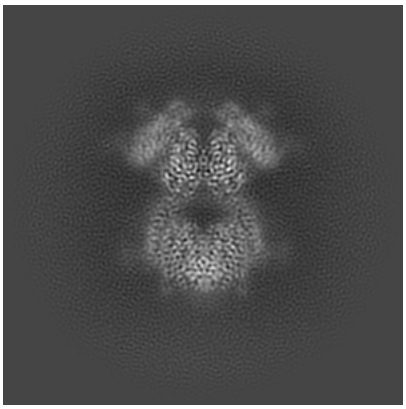
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-46579. These allow visual inspection of the internal detail of the map and identification of artifacts.

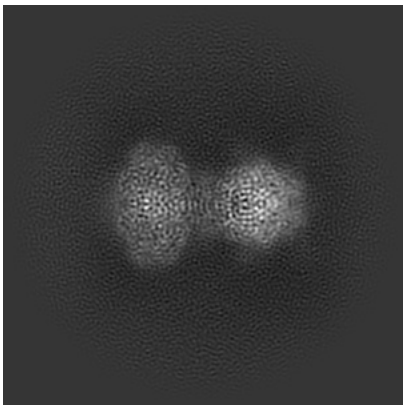
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

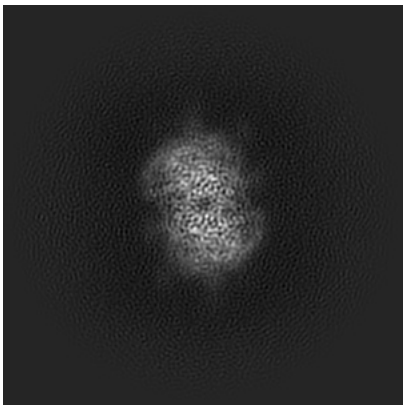
6.1.1 Primary map



X

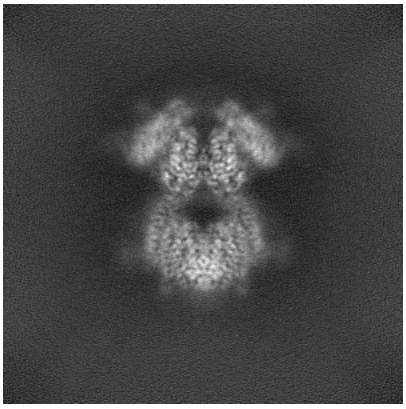


Y

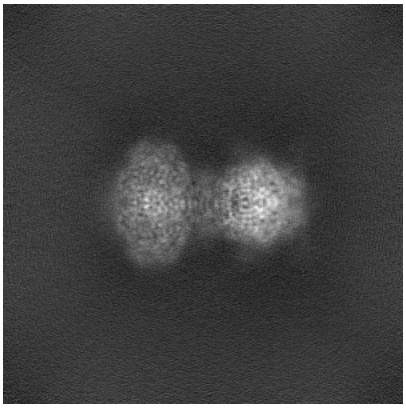


Z

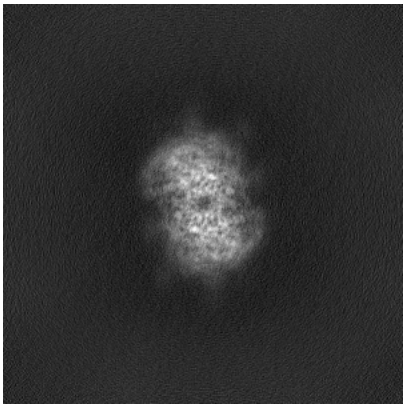
6.1.2 Raw map



X



Y

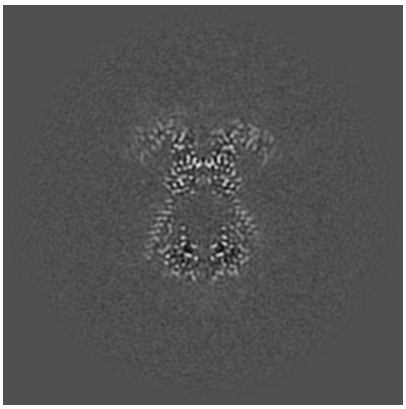


Z

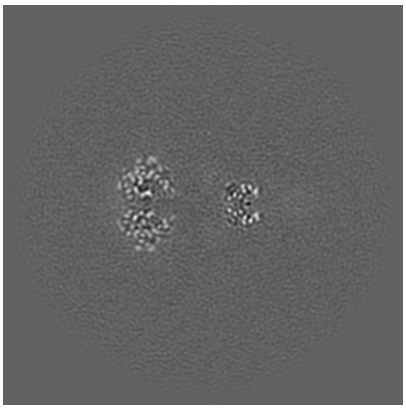
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

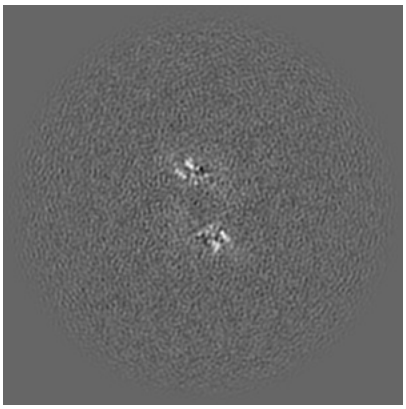
6.2.1 Primary map



X Index: 180

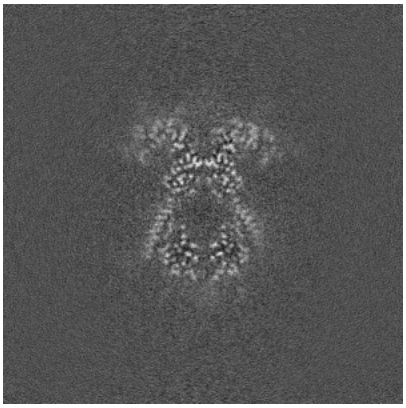


Y Index: 180

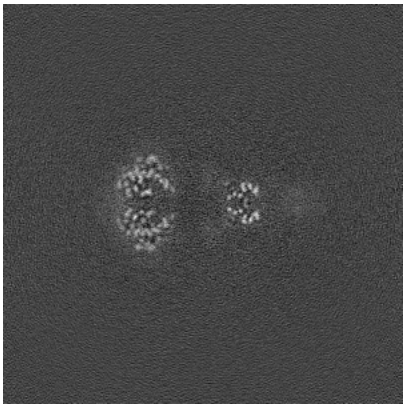


Z Index: 180

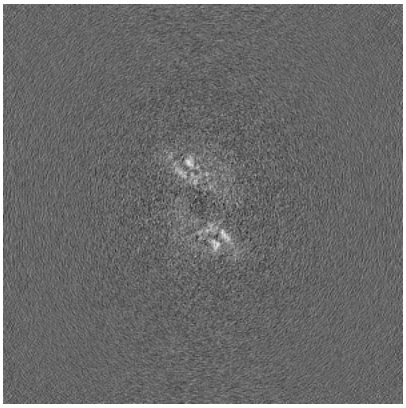
6.2.2 Raw map



X Index: 180



Y Index: 180

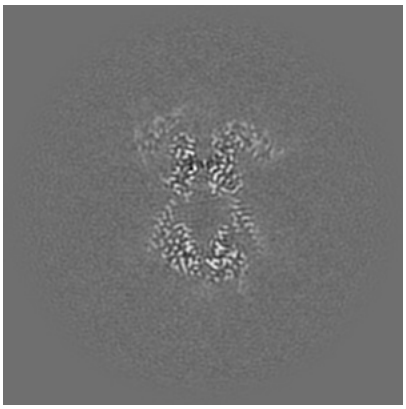


Z Index: 180

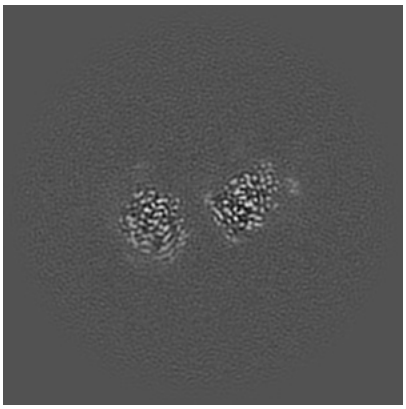
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

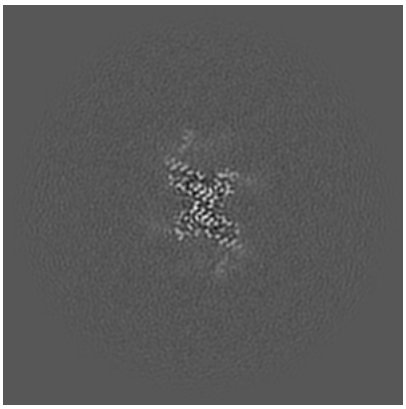
6.3.1 Primary map



X Index: 177

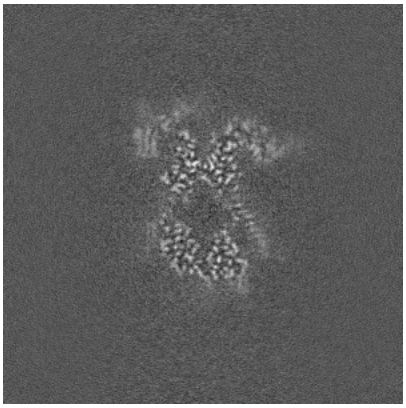


Y Index: 194

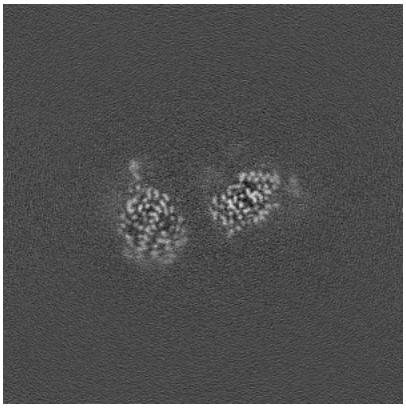


Z Index: 214

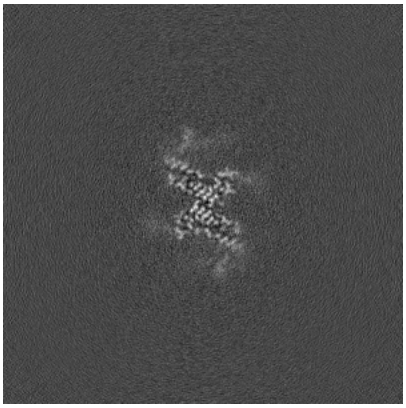
6.3.2 Raw map



X Index: 175



Y Index: 191

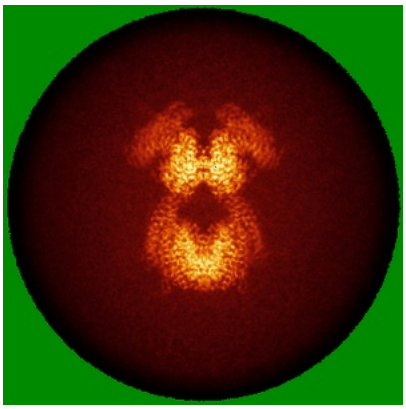


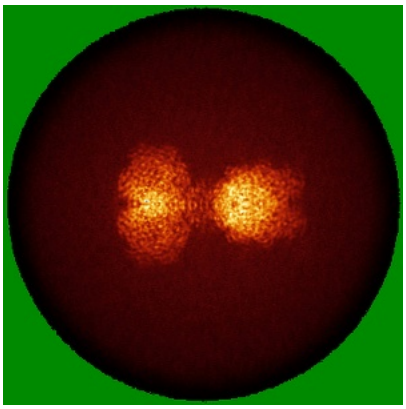
Z Index: 214

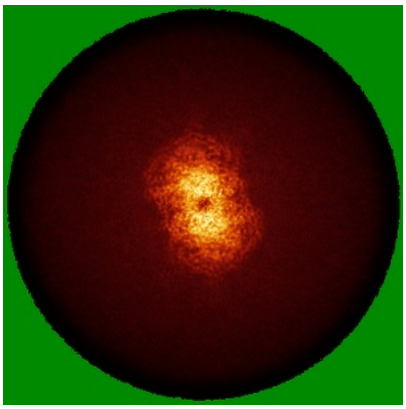
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

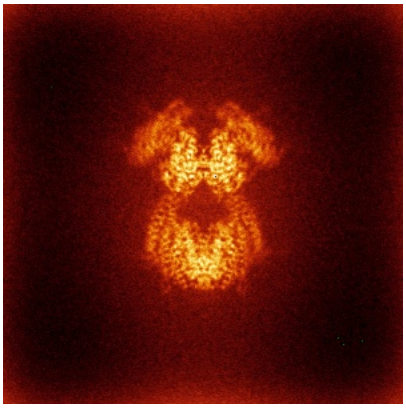
6.4.1 Primary map

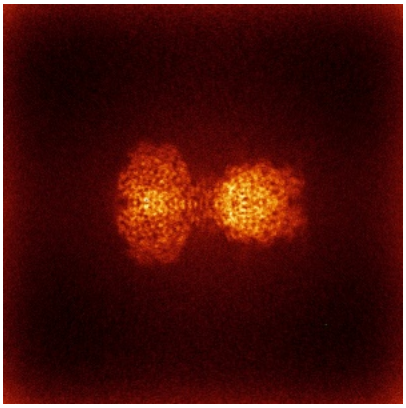

X

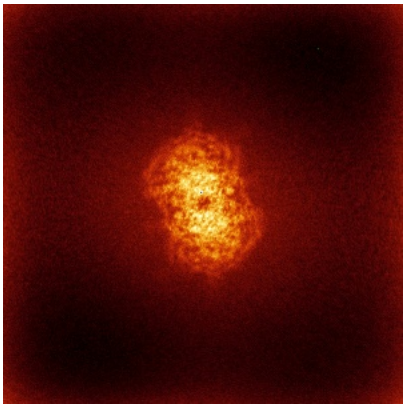

Y


Z

6.4.2 Raw map


X

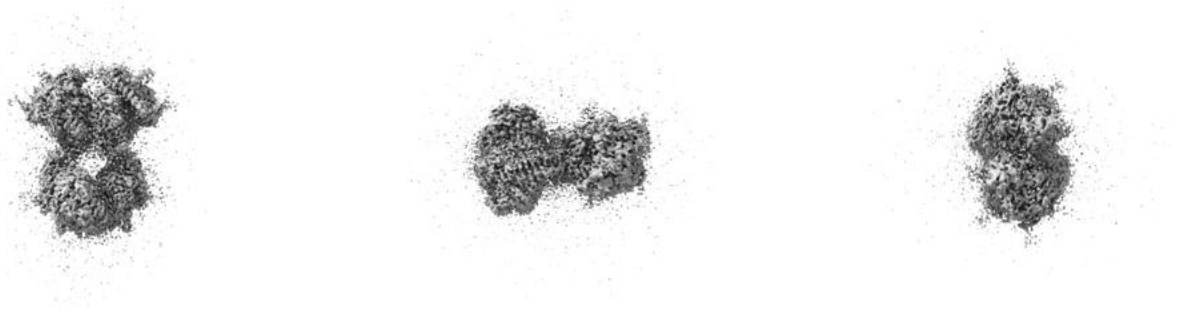

Y


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)

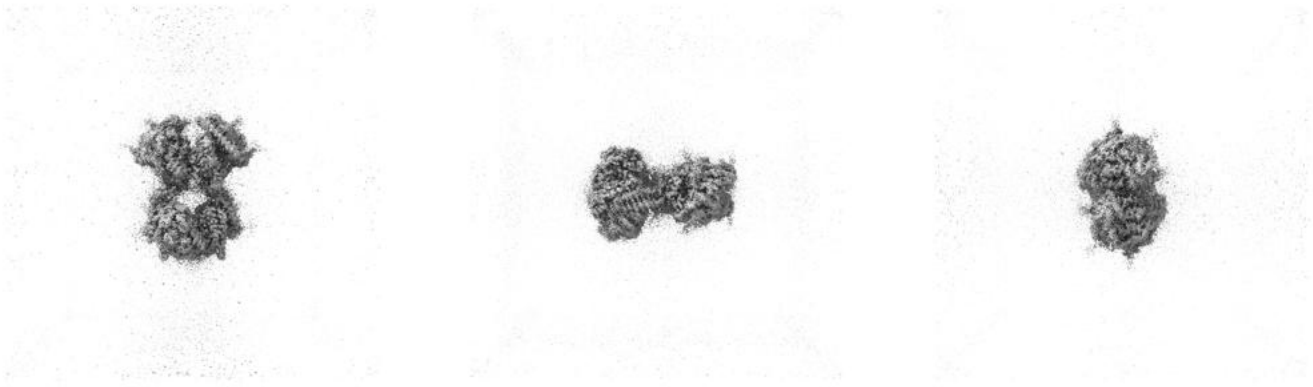
6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.06. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X Y Z

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

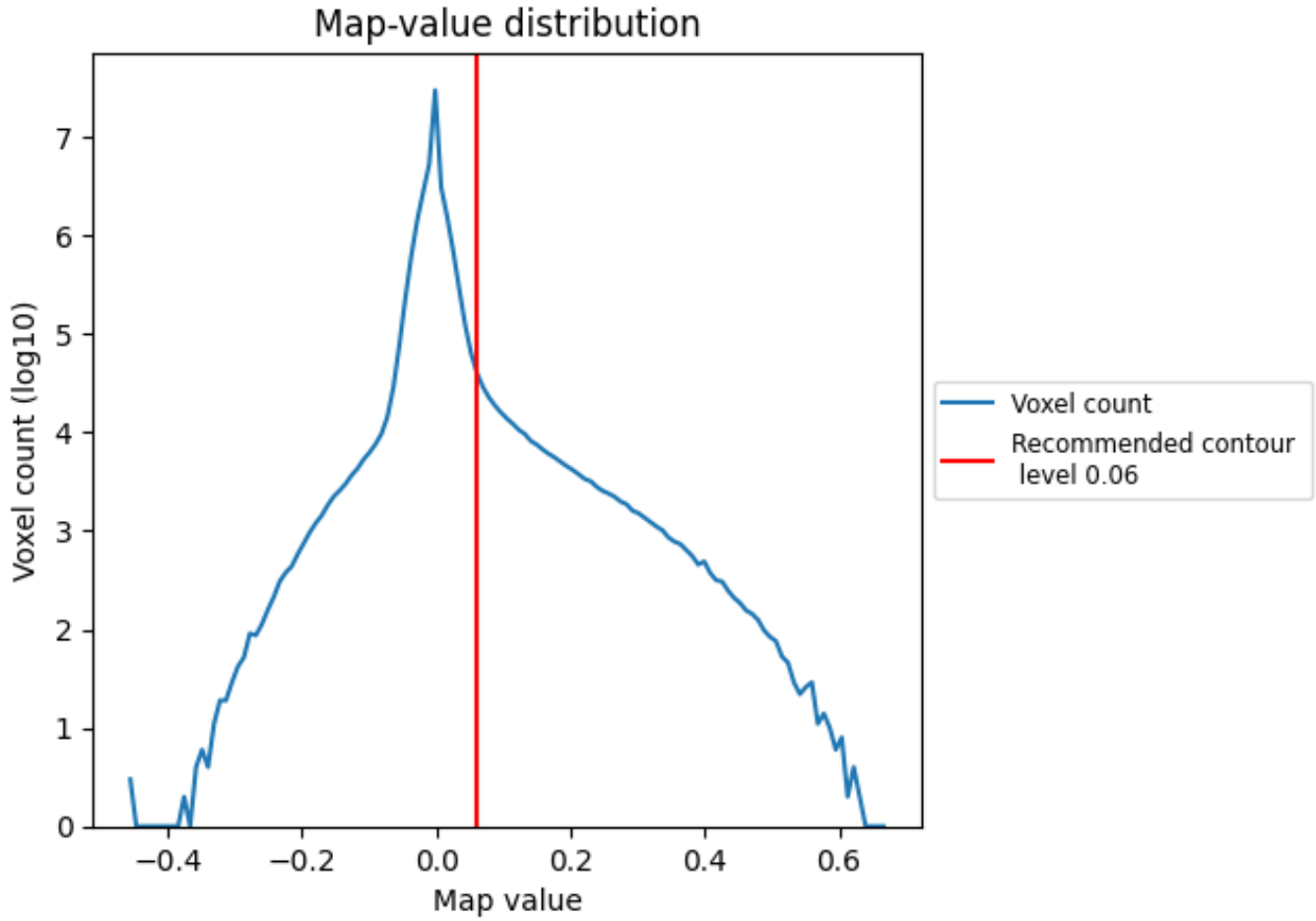
6.6 Mask visualisation (i)

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

7 Map analysis

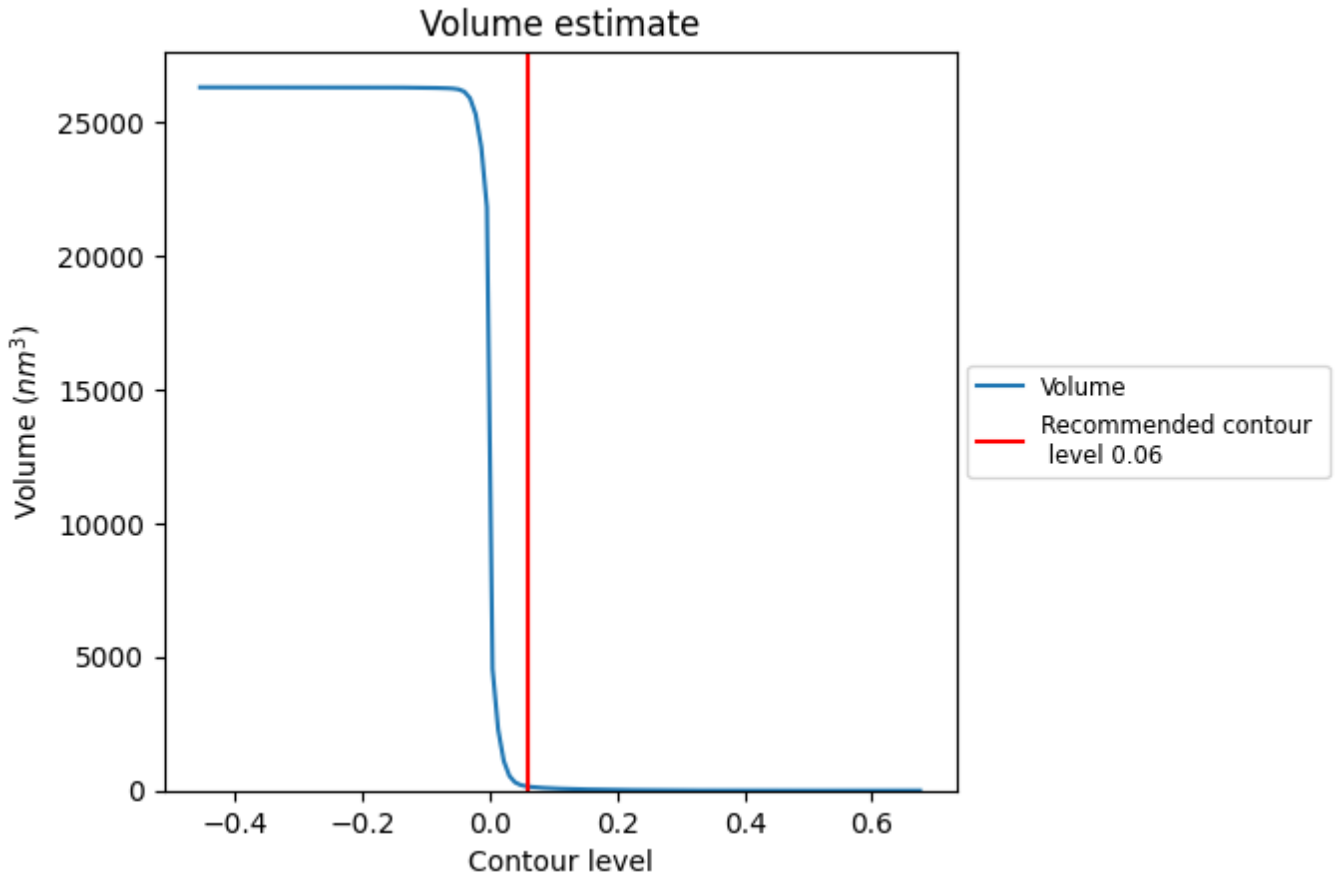
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

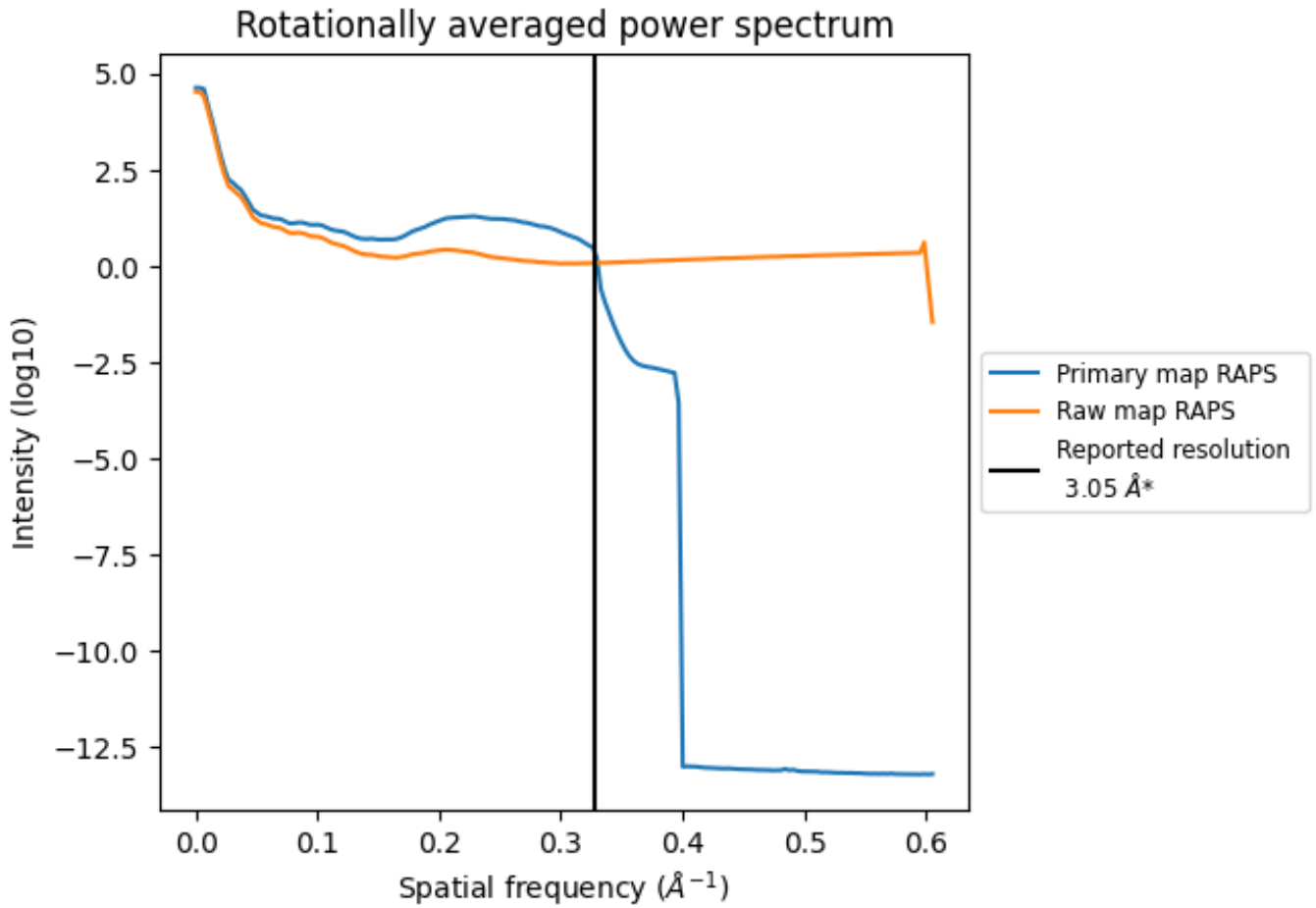
7.2 Volume estimate



The volume at the recommended contour level is 151 nm^3; this corresponds to an approximate mass of 136 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)

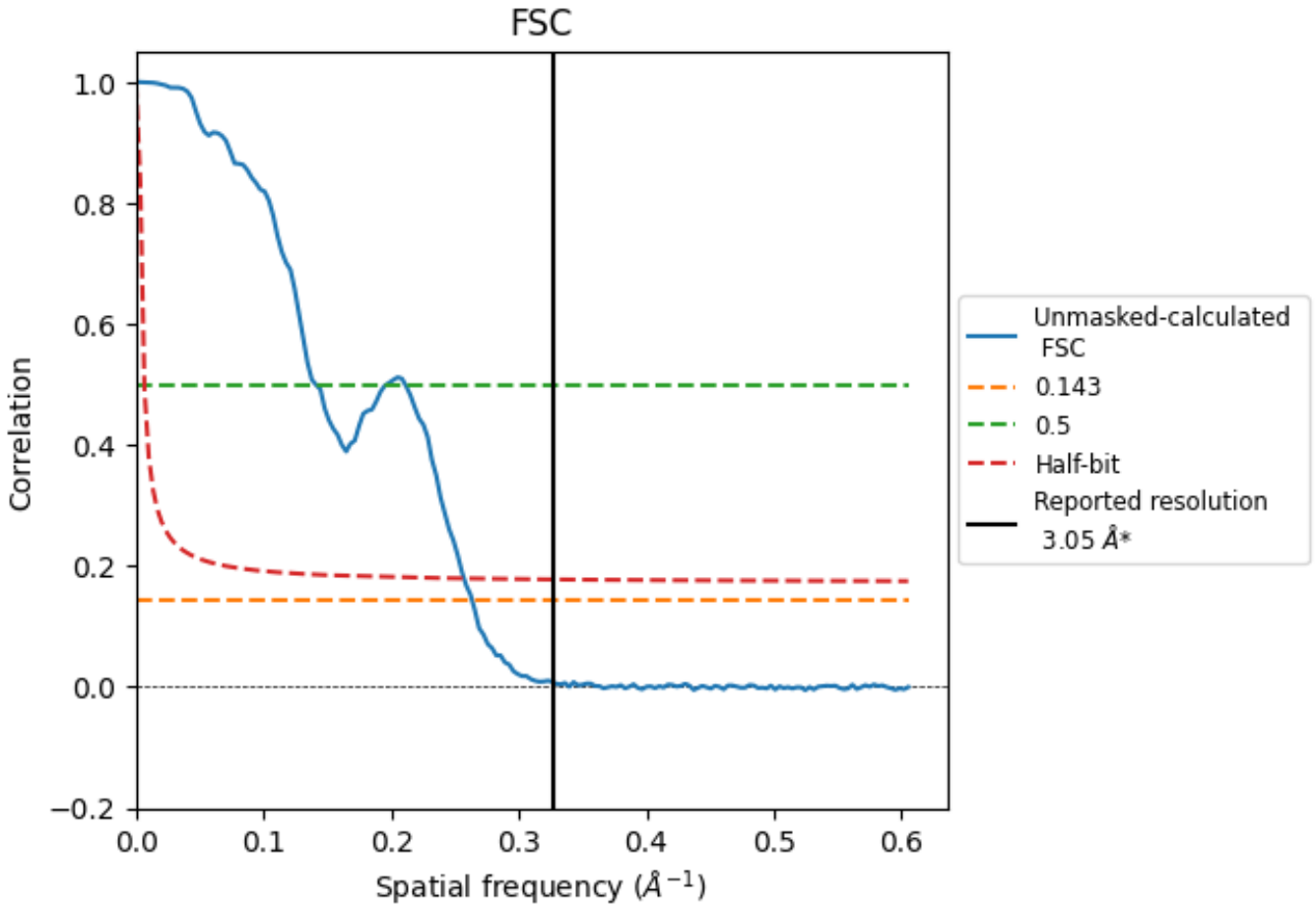


*Reported resolution corresponds to spatial frequency of 0.328 $Å^{-1}$

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.328 Å^{-1}

8.2 Resolution estimates (i)

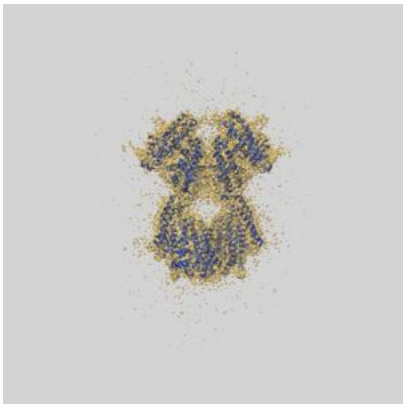
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.05	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.80	7.09	3.89

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.80 differs from the reported value 3.05 by more than 10 %

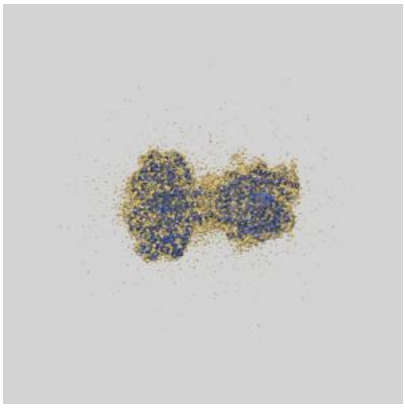
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-46579 and PDB model 9D5M. Per-residue inclusion information can be found in section 3 on page 7.

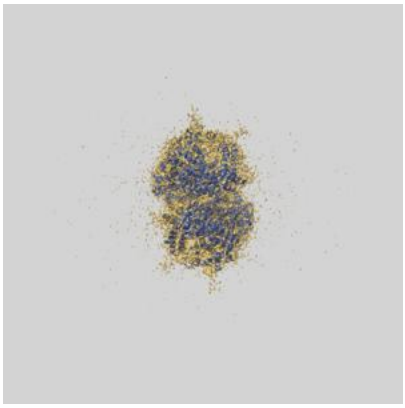
9.1 Map-model overlay



X



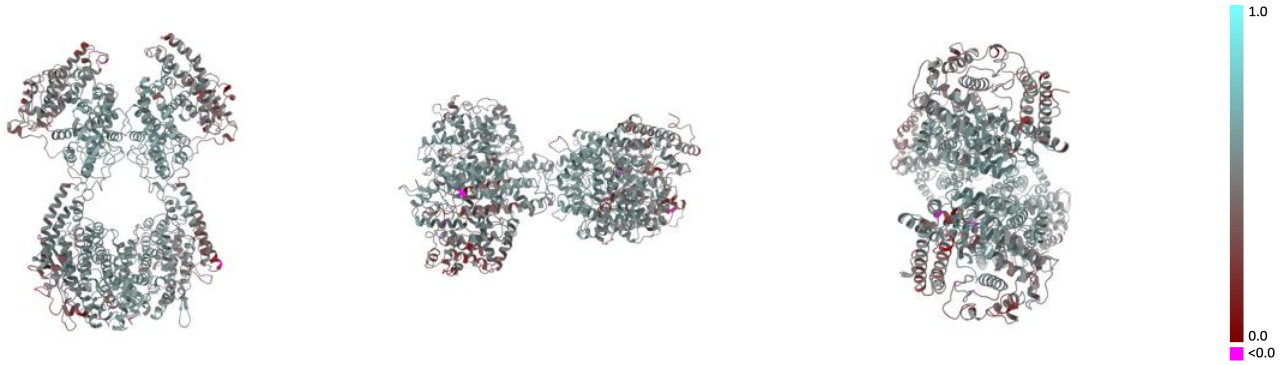
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.06 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.

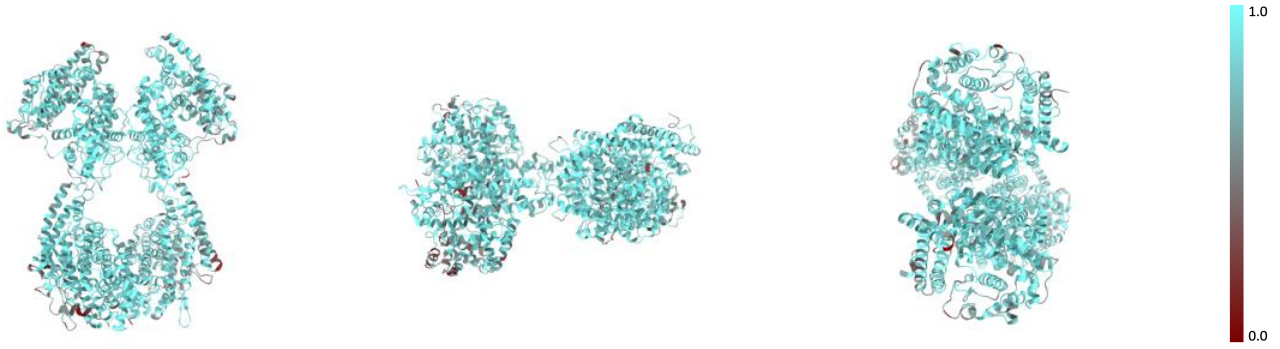
9.2 Q-score mapped to coordinate model



X Y Z

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

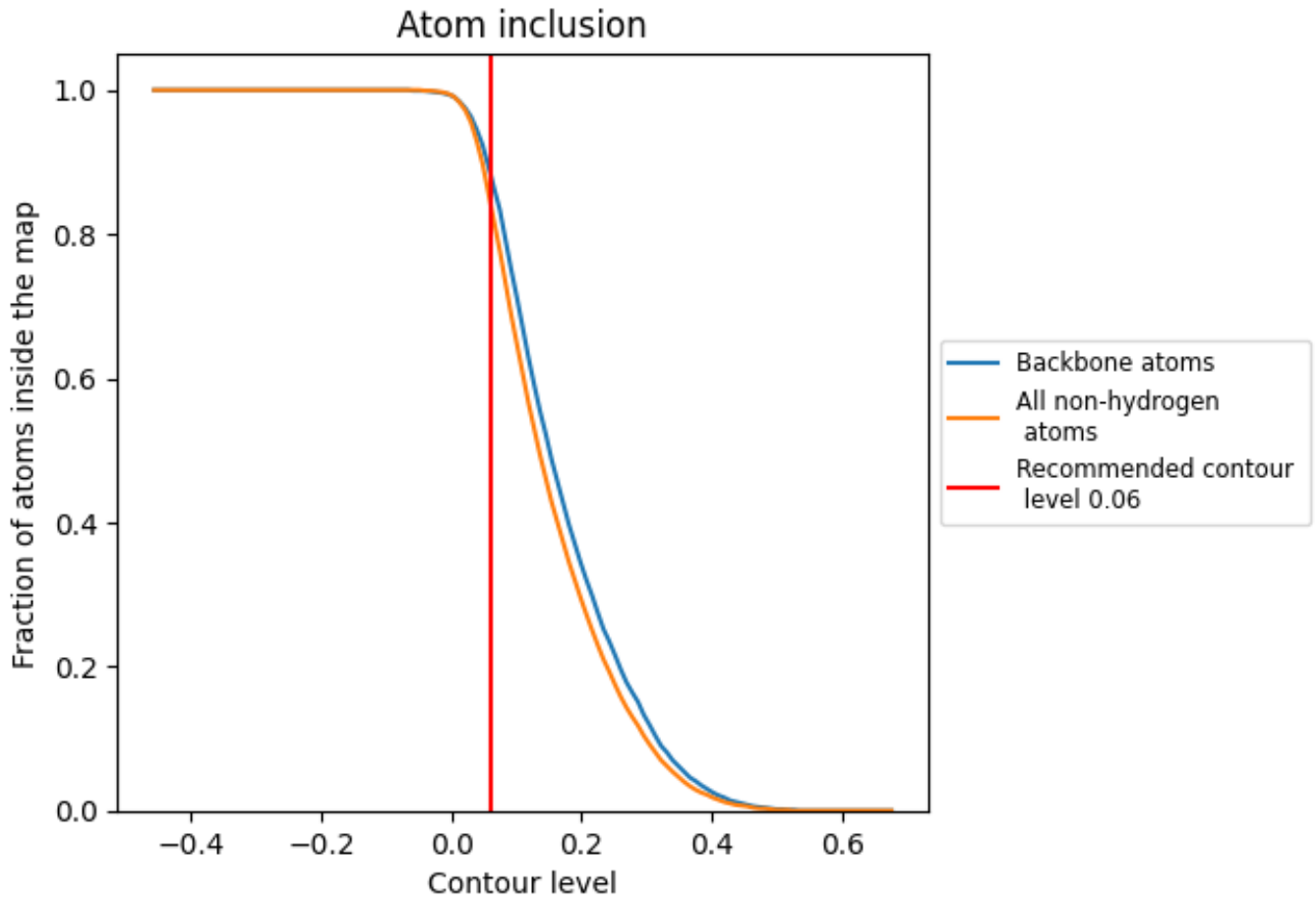
9.3 Atom inclusion mapped to coordinate model



X Y Z

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 (0.06).

9.4 Atom inclusion (i)



At the recommended contour level, 88% of all backbone atoms, 84% 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 (0.06) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8440	0.5040
A	0.8450	0.5020
B	0.8580	0.5140
D	0.4360	0.2400
F	0.4900	0.3250
G	0.5000	0.2710
H	0.3570	0.2660
I	0.6790	0.3900
L	0.4640	0.2430
N	0.5640	0.3560
P	0.3590	0.2470
Q	0.2500	0.0540
R	0.3570	0.3050
S	0.7500	0.4530
U	0.5000	0.4110