



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 8, 2020 – 09:11 AM BST

PDB ID : 6ML8  
Title : Crystal structure of hemagglutinin from H1N1 Influenza A virus A/Denver/57 bound to the C05 antibody  
Authors : Seattle Structural Genomics Center for Infectious Disease (SSGCID)  
Deposited on : 2018-09-27  
Resolution : 2.92 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.13.1  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.13.1

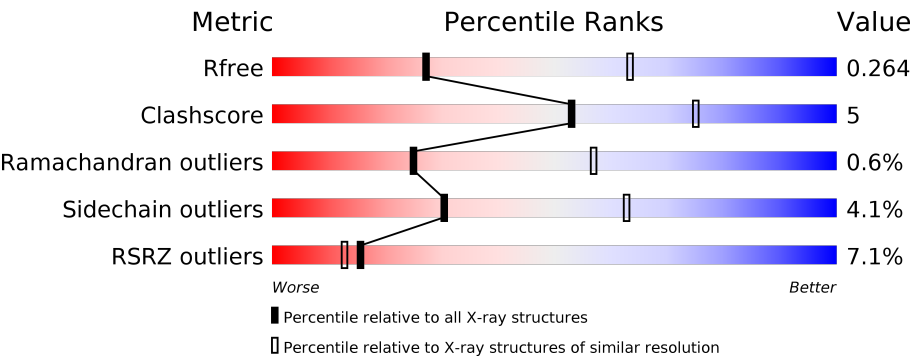
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.92 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)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	2307 (2.94-2.90)
Clashscore	141614	2531 (2.94-2.90)
Ramachandran outliers	138981	2462 (2.94-2.90)
Sidechain outliers	138945	2464 (2.94-2.90)
RSRZ outliers	127900	2248 (2.94-2.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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 electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	330	<div><div>%</div><div><div></div><div>79%</div><div>18%</div><div>.</div></div></div>
2	B	165	<div><div>6%</div><div><div></div><div>77%</div><div>18%</div><div>5%</div></div></div>
3	H	247	<div><div>7%</div><div><div></div><div>81%</div><div>11%</div><div>8%</div></div></div>
4	L	214	<div><div>16%</div><div><div></div><div>85%</div><div>13%</div><div>..</div></div></div>
5	C	4	<div><div></div><div><div></div><div>75%</div><div>25%</div></div></div>
6	D	3	<div><div></div><div><div></div><div>33%</div><div>67%</div></div></div>

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Mol	Chain	Length	Quality of chain
7	E	2	 100%

## 2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 6973 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 Hemagglutinin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	321	Total	C	N	O	S	0	2	0
			2487	1556	440	480	11			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	14	PHE	-	expression tag	UNP Q2IBI1
A	15	ALA	-	expression tag	UNP Q2IBI1
A	16	GLY	-	expression tag	UNP Q2IBI1
A	17	SER	-	expression tag	UNP Q2IBI1

- Molecule 2 is a protein called Hemagglutinin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	157	Total	C	N	O	S	0	0	0
			1167	729	203	228	7			

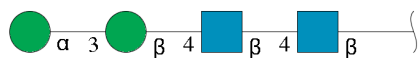
- Molecule 3 is a protein called C05 antibody Fab heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	H	227	Total	C	N	O	S	0	1	0
			1646	1030	276	332	8			

- Molecule 4 is a protein called C05 antibody Fab light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	L	212	Total	C	N	O	S	0	0	0
			1511	940	258	309	4			

- Molecule 5 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



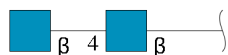
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	C	4	Total	C	N	O	0	0	0
			50	28	2	20			

- Molecule 6 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				ZeroOcc	AltConf	Trace
6	D	3	Total	C	N	O	0	0	0
			39	22	2	15			

- Molecule 7 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
7	E	2	Total	C	N	O	0	0	0
			28	16	2	10			

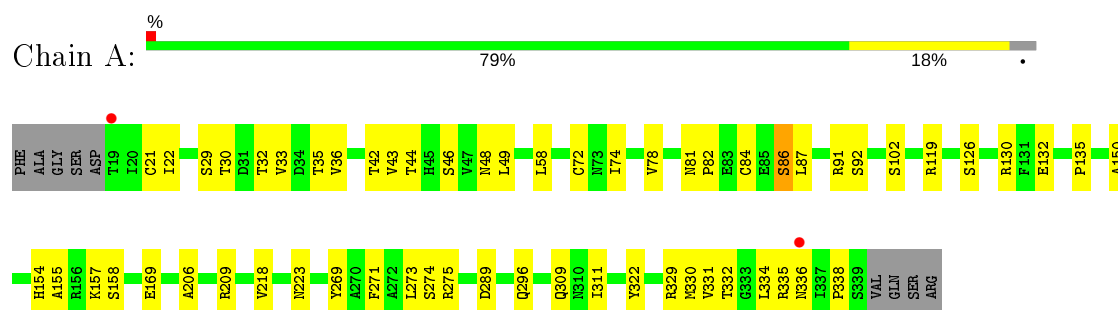
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	34	Total	O	0	0
			34	34		
8	B	1	Total	O	0	0
			1	1		
8	H	7	Total	O	0	0
			7	7		
8	L	3	Total	O	0	0
			3	3		

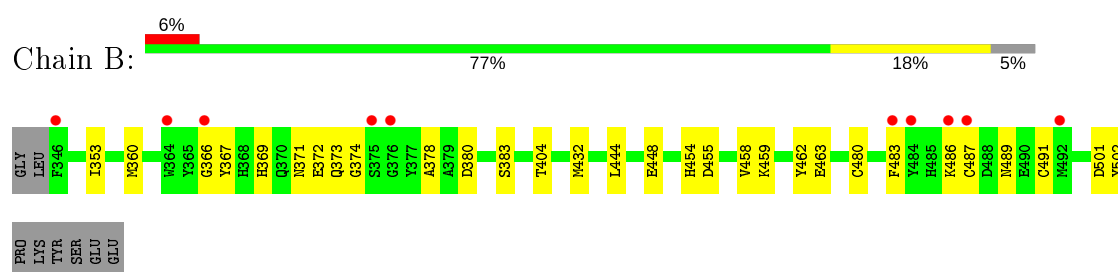
### 3 Residue-property plots [i](#)

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 electron 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 dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). 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.

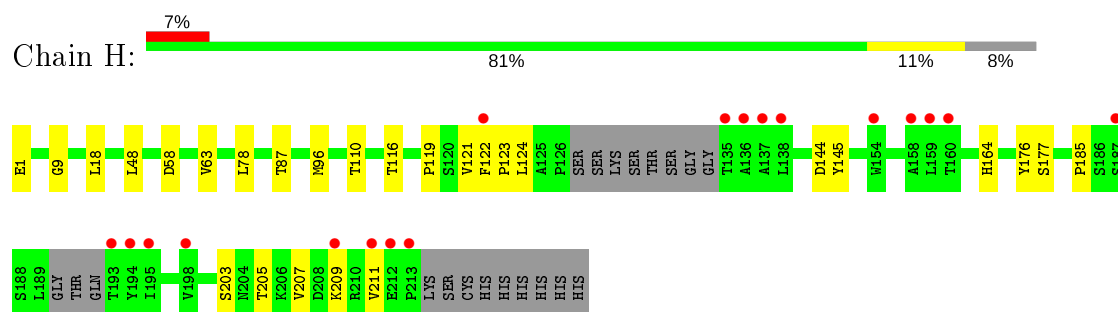
#### • Molecule 1: Hemagglutinin



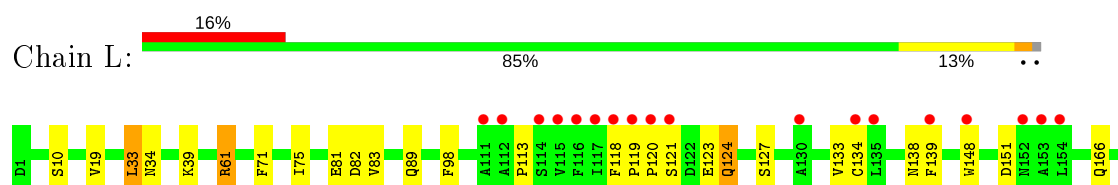
#### • Molecule 2: Hemagglutinin

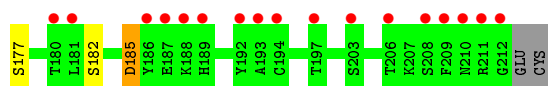


#### • Molecule 3: C05 antibody Fab heavy chain



#### • Molecule 4: C05 antibody Fab light chain





- Molecule 5: alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain C: 75% 25%



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

Chain D: 33% 67%



- Molecule 7: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain E: 100%



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 3 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	118.46Å 118.46Å 162.44Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	47.89 – 2.92 47.89 – 2.92	Depositor EDS
% Data completeness (in resolution range)	99.9 (47.89-2.92) 99.9 (47.89-2.92)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.96 (at 2.91Å)	Xtriage
Refinement program	PHENIX 1.14 _3219	Depositor
R, $R_{free}$	0.201 , 0.264 0.201 , 0.264	Depositor DCC
$R_{free}$ test set	1535 reflections (5.25%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	69.8	Xtriage
Anisotropy	0.104	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.27 , 56.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.023 for -h,-k,l	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	6973	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	87.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.06% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



## 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	A	0.33	0/2552	0.51	0/3489
2	B	0.30	0/1190	0.48	0/1611
3	H	0.33	0/1681	0.50	0/2294
4	L	0.28	0/1545	0.52	0/2113
All	All	0.31	0/6968	0.51	0/9507

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2487	0	2320	33	0
2	B	1167	0	1018	17	0
3	H	1646	0	1523	13	0
4	L	1511	0	1328	16	0
5	C	50	0	43	0	0
6	D	39	0	34	0	0
7	E	28	0	25	0	0
8	A	34	0	0	1	0
8	B	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	H	7	0	0	0	0
8	L	3	0	0	0	0
All	All	6973	0	6291	71	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 5.

All (71) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L:61:ARG:NH2	4:L:82:ASP:OD1	2.18	0.77
3:H:121:VAL:HG11	3:H:207:VAL:HG11	1.70	0.73
3:H:87:THR:HG23	3:H:110:THR:HA	1.76	0.66
1:A:74:ILE:HD12	1:A:119:ARG:HG2	1.75	0.66
2:B:371:ASN:ND2	2:B:487:CYS:O	2.27	0.66
1:A:82:PRO:HB2	1:A:154[A]:HIS:HB2	1.79	0.63
1:A:46:SER:OG	1:A:329:ARG:NH1	2.34	0.61
1:A:32:THR:HG22	1:A:42:THR:HG22	1.82	0.61
1:A:150:ALA:HA	1:A:158:SER:HB2	1.83	0.61
3:H:48:LEU:HD22	3:H:63:VAL:HG11	1.84	0.60
1:A:22:ILE:HD12	2:B:462:TYR:HA	1.84	0.59
4:L:113:PRO:HB3	4:L:139:PHE:HB3	1.85	0.58
1:A:206:ALA:O	1:A:209:ARG:NH1	2.37	0.58
1:A:86:SER:OG	1:A:130:ARG:NH1	2.37	0.58
1:A:43:VAL:HG11	1:A:331:VAL:HG13	1.87	0.56
1:A:36:VAL:HG12	2:B:448:GLU:HG3	1.88	0.54
1:A:49:LEU:HD21	1:A:330:MET:HE2	1.89	0.54
3:H:123:PRO:HD2	4:L:121:SER:HB2	1.88	0.54
1:A:35:THR:HB	2:B:448:GLU:HG2	1.90	0.53
1:A:33:VAL:HG12	1:A:329:ARG:HG2	1.90	0.53
1:A:218:VAL:HG13	1:A:223:ASN:HB3	1.90	0.52
4:L:182:SER:OG	4:L:185:ASP:OD1	2.27	0.52
2:B:366:GLY:HA3	2:B:378:ALA:O	2.08	0.52
1:A:74:ILE:O	1:A:78:VAL:HG22	2.10	0.51
2:B:369:HIS:NE2	2:B:374:GLY:O	2.43	0.51
1:A:322:TYR:OH	8:A:501:HOH:O	2.19	0.51
4:L:134:CYS:HB2	4:L:148:TRP:CZ2	2.45	0.50
3:H:119:PRO:HA	3:H:145:TYR:HB3	1.93	0.50
1:A:33:VAL:HG21	1:A:331:VAL:CG2	2.41	0.49
2:B:459:LYS:O	2:B:463:GLU:HG2	2.11	0.49
1:A:21:CYS:HA	2:B:480:CYS:HA	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:501:ASP:CG	2:B:502:TYR:H	2.16	0.48
1:A:218:VAL:HG22	1:A:223:ASN:HB2	1.95	0.48
2:B:380:ASP:OD2	2:B:383:SER:OG	2.21	0.48
2:B:360:MET:HE3	2:B:366:GLY:HA3	1.97	0.47
2:B:371:ASN:CG	2:B:372:GLU:H	2.18	0.47
4:L:124:GLN:O	4:L:127:SER:OG	2.23	0.46
1:A:155[A]:ALA:O	1:A:157:LYS:N	2.45	0.46
3:H:145:TYR:O	3:H:176:TYR:N	2.44	0.46
4:L:33:LEU:HD22	4:L:71:PHE:CG	2.51	0.46
3:H:122:PHE:HA	3:H:209:LYS:HE2	1.97	0.46
2:B:353:ILE:O	2:B:353:ILE:HG22	2.16	0.45
1:A:58:LEU:HA	1:A:296:GLN:NE2	2.31	0.45
4:L:19:VAL:HG22	4:L:75:ILE:HB	1.99	0.45
4:L:39:LYS:NZ	4:L:81:GLU:O	2.42	0.45
2:B:380:ASP:HB3	2:B:383:SER:HB2	1.99	0.44
1:A:87:LEU:HD11	1:A:91:ARG:HD3	1.99	0.44
1:A:29:SER:OG	1:A:43:VAL:O	2.36	0.44
3:H:119:PRO:HA	3:H:144:ASP:O	2.18	0.44
1:A:44:THR:HG22	1:A:336:ASN:OD1	2.17	0.44
2:B:373:GLN:HB2	2:B:489:ASN:OD1	2.17	0.44
1:A:309:GLN:OE1	1:A:311:ILE:N	2.50	0.43
4:L:118:PHE:HA	4:L:119:PRO:HD3	1.88	0.43
4:L:89:GLN:HB2	4:L:98:PHE:CD2	2.54	0.43
1:A:130:ARG:HB2	1:A:271:PHE:CD1	2.54	0.43
1:A:44:THR:HG23	1:A:334:LEU:O	2.19	0.42
1:A:48:ASN:HB2	1:A:329:ARG:HH21	1.85	0.42
3:H:122:PHE:CD2	4:L:124:GLN:HG3	2.55	0.42
1:A:132:GLU:HG3	1:A:269:TYR:CZ	2.54	0.41
1:A:126:SER:N	1:A:274:SER:O	2.52	0.41
4:L:133:VAL:HA	4:L:177:SER:O	2.20	0.41
1:A:132:GLU:OE1	1:A:135:PRO:HA	2.20	0.41
3:H:124:LEU:HB3	4:L:118:PHE:CD1	2.55	0.41
2:B:432:MET:HE2	2:B:432:MET:HB3	1.92	0.41
4:L:83:VAL:HG21	4:L:166:GLN:HB3	2.02	0.41
1:A:81:ASN:HB3	1:A:84:CYS:SG	2.60	0.41
3:H:164:HIS:NE2	4:L:138:ASN:OD1	2.51	0.41
3:H:9:GLY:HA2	3:H:18:LEU:HD21	2.02	0.41
2:B:454:HIS:O	2:B:458:VAL:HG22	2.21	0.41
1:A:72:CYS:O	1:A:102:SER:HB3	2.21	0.40
3:H:203:SER:OG	3:H:205:THR:OG1	2.30	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 X-ray entries followed by that with respect to entries of similar resolution.

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	321/330 (97%)	301 (94%)	19 (6%)	1 (0%)	41	70
2	B	155/165 (94%)	137 (88%)	17 (11%)	1 (1%)	25	57
3	H	221/247 (90%)	207 (94%)	12 (5%)	2 (1%)	17	46
4	L	210/214 (98%)	192 (91%)	17 (8%)	1 (0%)	29	60
All	All	907/956 (95%)	837 (92%)	65 (7%)	5 (1%)	25	57

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	486	LYS
3	H	211	VAL
4	L	120	PRO
3	H	185	PRO
1	A	338	PRO

### 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 X-ray entries followed by that with respect to entries of similar resolution.

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	268/290 (92%)	259 (97%)	9 (3%)	37	69
2	B	109/141 (77%)	103 (94%)	6 (6%)	21	51
3	H	173/207 (84%)	167 (96%)	6 (4%)	36	68
4	L	151/187 (81%)	143 (95%)	8 (5%)	22	53
All	All	701/825 (85%)	672 (96%)	29 (4%)	30	63

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	30	THR
1	A	86	SER
1	A	92	SER
1	A	169	GLU
1	A	273	LEU
1	A	275	ARG
1	A	289	ASP
1	A	332	THR
1	A	335	ARG
2	B	367	TYR
2	B	404	THR
2	B	444	LEU
2	B	455	ASP
2	B	483	PHE
2	B	491	CYS
3	H	1	GLU
3	H	58	ASP
3	H	78	LEU
3	H	96	MET
3	H	116	THR
3	H	177	SER
4	L	10	SER
4	L	33	LEU
4	L	34	ASN
4	L	61	ARG
4	L	123	GLU
4	L	124	GLN
4	L	151	ASP
4	L	185	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
3	H	197	ASN
4	L	79	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates ⓘ

9 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	$\# Z  > 2$
5	NAG	C	1	1,5	14,14,15	0.25	0	17,19,21	0.62	0
5	NAG	C	2	5	14,14,15	0.23	0	17,19,21	0.49	0
5	BMA	C	3	5	11,11,12	0.55	0	15,15,17	0.71	0
5	MAN	C	4	5	11,11,12	0.71	0	15,15,17	0.84	1 (6%)
6	NAG	D	1	1,6	14,14,15	0.38	0	17,19,21	0.66	1 (5%)
6	NAG	D	2	6	14,14,15	0.23	0	17,19,21	0.59	0
6	BMA	D	3	6	11,11,12	0.73	1 (9%)	15,15,17	1.17	1 (6%)
7	NAG	E	1	1,7	14,14,15	0.27	0	17,19,21	0.42	0
7	NAG	E	2	7	14,14,15	0.34	0	17,19,21	0.59	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
5	NAG	C	1	1,5	-	0/6/23/26	0/1/1/1
5	NAG	C	2	5	-	2/6/23/26	0/1/1/1
5	BMA	C	3	5	-	0/2/19/22	0/1/1/1
5	MAN	C	4	5	-	0/2/19/22	0/1/1/1
6	NAG	D	1	1,6	-	2/6/23/26	0/1/1/1
6	NAG	D	2	6	-	2/6/23/26	0/1/1/1
6	BMA	D	3	6	-	0/2/19/22	0/1/1/1
7	NAG	E	1	1,7	-	2/6/23/26	0/1/1/1
7	NAG	E	2	7	-	1/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	D	3	BMA	C1-C2	2.02	1.56	1.52

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	D	3	BMA	C1-O5-C5	2.67	115.81	112.19
6	D	1	NAG	C1-O5-C5	2.28	115.28	112.19
5	C	4	MAN	O2-C2-C3	-2.09	105.94	110.14

There are no chirality outliers.

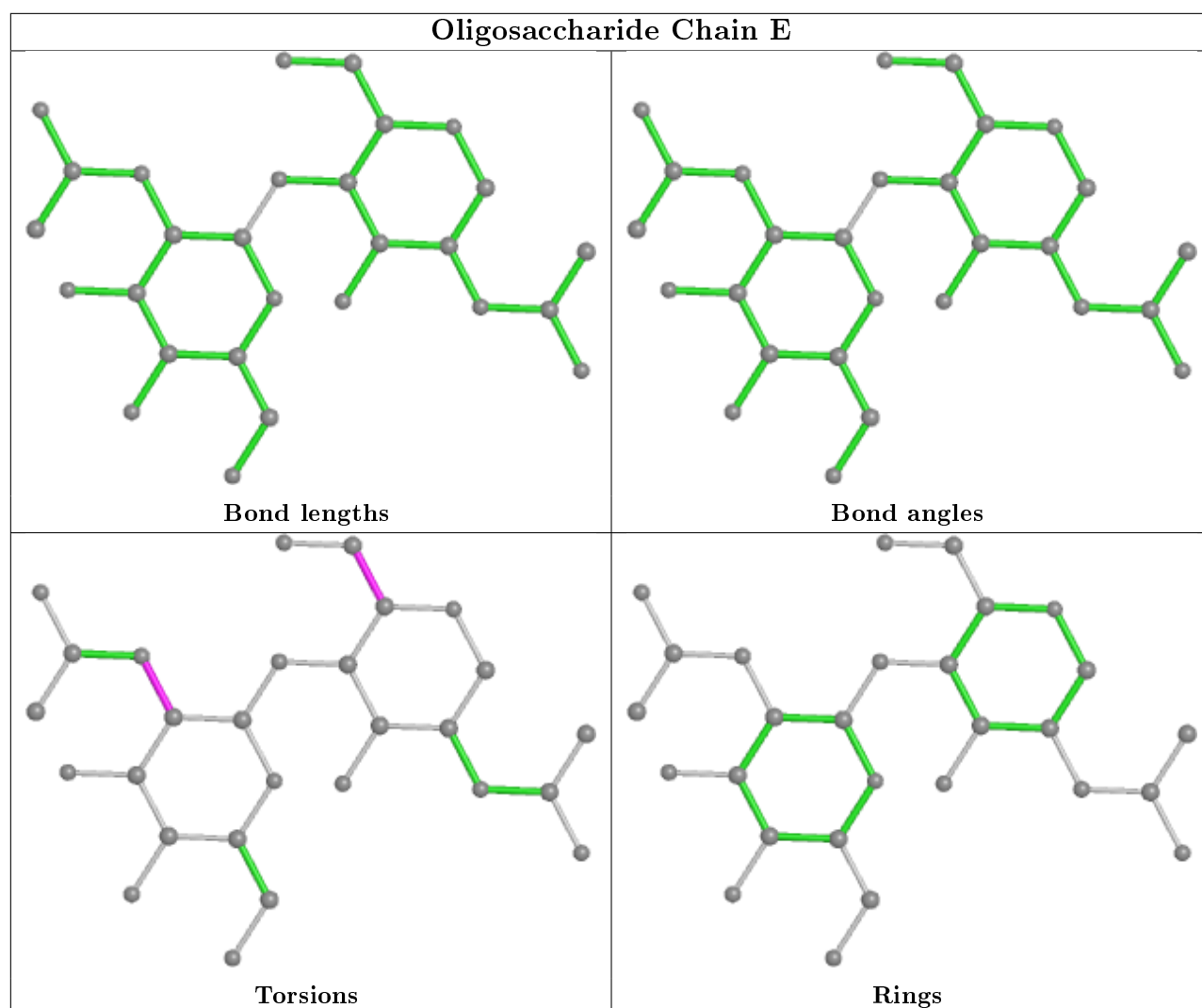
All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	D	2	NAG	O5-C5-C6-O6
7	E	1	NAG	O5-C5-C6-O6
6	D	1	NAG	O5-C5-C6-O6
7	E	1	NAG	C4-C5-C6-O6
6	D	1	NAG	C4-C5-C6-O6
6	D	2	NAG	C4-C5-C6-O6
5	C	2	NAG	C4-C5-C6-O6
5	C	2	NAG	O5-C5-C6-O6
7	E	2	NAG	C3-C2-N2-C7

There are no ring outliers.

No monomer is involved in short contacts.

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](#)

There are no ligands in this entry.

## 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 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	321/330 (97%)	-0.42	2 (0%) 89 89	32, 55, 117, 178	0
2	B	157/165 (95%)	0.25	10 (6%) 19 16	39, 121, 179, 213	0
3	H	227/247 (91%)	0.15	18 (7%) 12 10	36, 70, 174, 206	0
4	L	212/214 (99%)	0.54	35 (16%) 1 1	45, 88, 207, 244	0
All	All	917/956 (95%)	0.06	65 (7%) 16 13	32, 70, 182, 244	0

All (65) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	L	148	TRP	6.8
4	L	193	ALA	6.2
4	L	210	ASN	6.0
4	L	117	ILE	6.0
4	L	119	PRO	5.9
3	H	138	LEU	5.9
4	L	153	ALA	5.9
4	L	189	HIS	5.8
3	H	137	ALA	5.8
1	A	19	THR	5.8
3	H	159	LEU	5.7
4	L	194	CYS	5.4
4	L	121	SER	5.3
4	L	188	LYS	5.0
4	L	154	LEU	5.0
4	L	208	SER	4.7
4	L	181	LEU	4.7
4	L	186	TYR	4.6
2	B	484	TYR	4.6
3	H	195	ILE	4.5
4	L	111	ALA	4.4

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
2	B	346	PHE	4.4
2	B	375	SER	4.3
4	L	212	GLY	4.2
4	L	115	VAL	4.2
2	B	483	PHE	4.1
3	H	198	VAL	4.1
3	H	136	ALA	4.1
4	L	118	PHE	3.8
3	H	158	ALA	3.7
4	L	209	PHE	3.6
4	L	192	TYR	3.6
3	H	212	GLU	3.5
3	H	154	TRP	3.5
4	L	152	ASN	3.4
4	L	120	PRO	3.4
2	B	486	LYS	3.3
4	L	203	SER	3.2
2	B	376	GLY	3.1
3	H	160	THR	3.1
3	H	209	LYS	3.1
4	L	112	ALA	3.1
3	H	187	SER	3.1
4	L	135	LEU	3.0
2	B	364	TRP	2.9
4	L	187	GLU	2.8
4	L	134	CYS	2.8
4	L	206	THR	2.7
3	H	211	VAL	2.7
3	H	135	THR	2.7
2	B	487	CYS	2.7
3	H	193	THR	2.7
4	L	211	ARG	2.6
3	H	122	PHE	2.6
3	H	194	TYR	2.5
4	L	180	THR	2.4
4	L	130	ALA	2.2
3	H	213	PRO	2.2
2	B	366	GLY	2.2
4	L	114	SER	2.2
1	A	336	ASN	2.1
2	B	492	MET	2.1
4	L	116	PHE	2.1

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Mol	Chain	Res	Type	RSRZ
4	L	197	THR	2.0
4	L	139	PHE	2.0

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

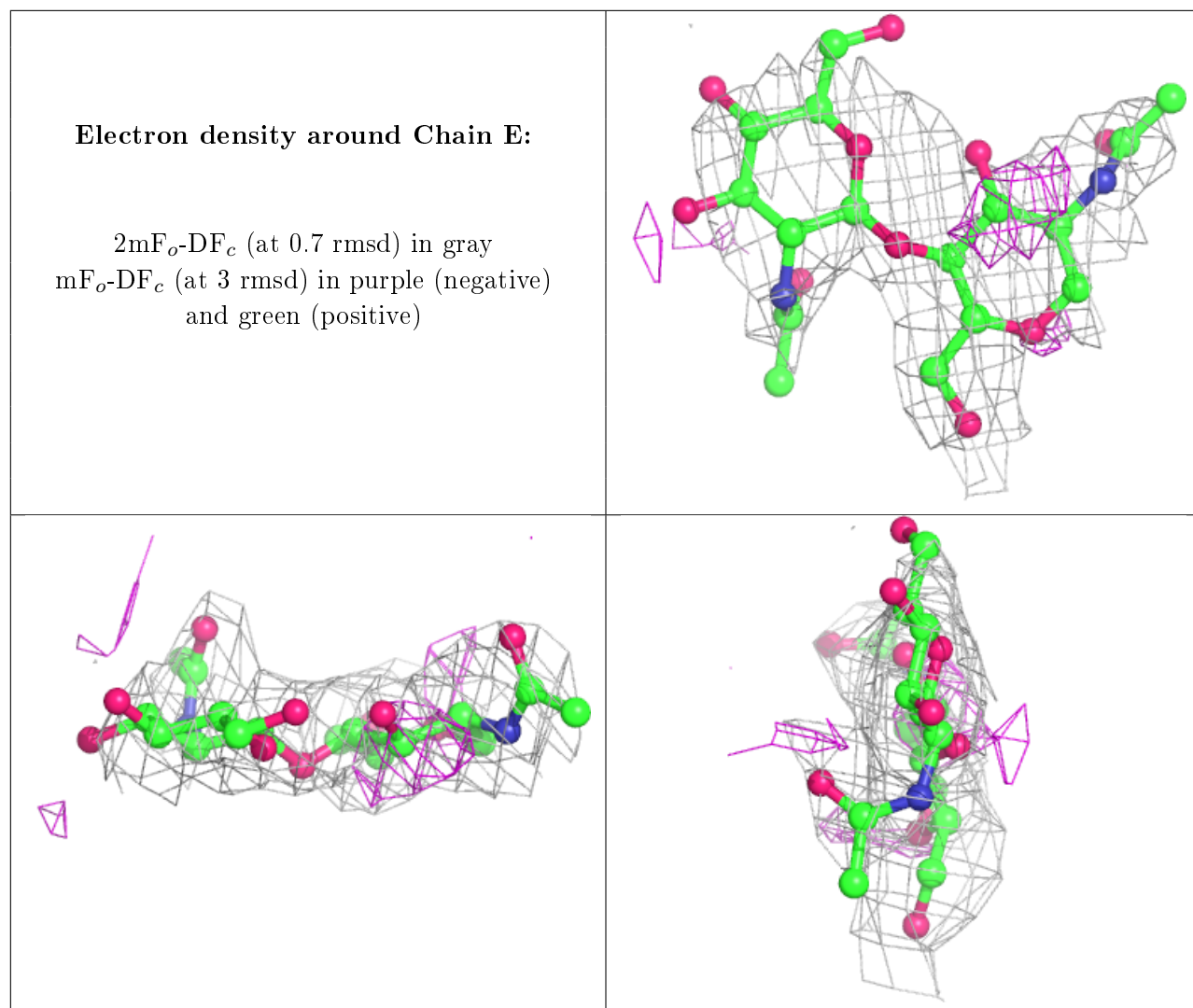
There are no non-standard protein/DNA/RNA residues in this entry.

## 6.3 Carbohydrates [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
6	BMA	D	3	11/12	0.62	0.24	140,155,161,163	0
6	NAG	D	2	14/15	0.72	0.27	130,140,155,163	0
7	NAG	E	1	14/15	0.78	0.40	86,112,131,148	0
5	MAN	C	4	11/12	0.81	0.32	133,140,143,143	0
7	NAG	E	2	14/15	0.85	0.43	145,154,158,161	0
5	BMA	C	3	11/12	0.87	0.11	111,119,128,128	0
5	NAG	C	2	14/15	0.92	0.18	78,90,105,111	0
6	NAG	D	1	14/15	0.93	0.11	56,73,86,106	0
5	NAG	C	1	14/15	0.95	0.13	38,59,75,81	0

The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.



## 6.4 Ligands [i](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.