



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 14, 2024 – 02:37 am GMT

PDB ID : 6HT9  
Title : Mouse fetuin-B in complex with crayfish astacin  
Authors : Gomis-Ruth, F.X.; Goulas, T.; Guevara, T.; Cuppari, A.  
Deposited on : 2018-10-03  
Resolution : 3.10 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.

The types of validation reports are described at

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

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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 : 1.8.4, CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.36  
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) : 2.36

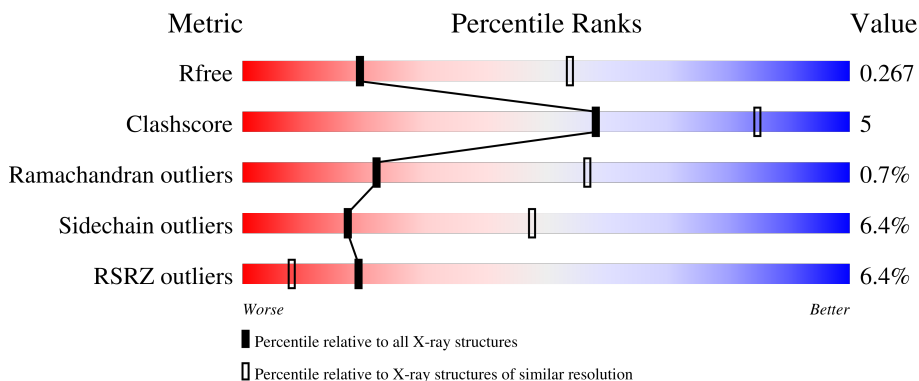
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.10 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	1094 (3.10-3.10)
Clashscore	141614	1184 (3.10-3.10)
Ramachandran outliers	138981	1141 (3.10-3.10)
Sidechain outliers	138945	1141 (3.10-3.10)
RSRZ outliers	127900	1067 (3.10-3.10)

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 of 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	251	 2% 71% 9% 20%
1	C	251	 2% 70% 8% 20%
2	B	378	 6% 66% 16% 16%
2	D	378	 9% 62% 15% 21%
3	E	2	 100%

## 2 Entry composition i

There are 7 unique types of molecules in this entry. The entry contains 8035 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 Astacin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	202	1612	1016	266	320	10	0	0	0
1	C	200	1590	1004	259	317	10	0	0	0

- Molecule 2 is a protein called Fetuin-B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	316	2409	1513	410	470	16	0	0	0
2	D	297	2288	1446	388	439	15	0	0	0

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	501	SER	-	expression tag	UNP Q9QXC1
B	502	ALA	-	expression tag	UNP Q9QXC1
B	503	HIS	-	expression tag	UNP Q9QXC1
B	504	HIS	-	expression tag	UNP Q9QXC1
B	505	HIS	-	expression tag	UNP Q9QXC1
B	506	HIS	-	expression tag	UNP Q9QXC1
B	507	HIS	-	expression tag	UNP Q9QXC1
B	508	HIS	-	expression tag	UNP Q9QXC1
D	501	SER	-	expression tag	UNP Q9QXC1
D	502	ALA	-	expression tag	UNP Q9QXC1
D	503	HIS	-	expression tag	UNP Q9QXC1
D	504	HIS	-	expression tag	UNP Q9QXC1
D	505	HIS	-	expression tag	UNP Q9QXC1
D	506	HIS	-	expression tag	UNP Q9QXC1
D	507	HIS	-	expression tag	UNP Q9QXC1
D	508	HIS	-	expression tag	UNP Q9QXC1

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

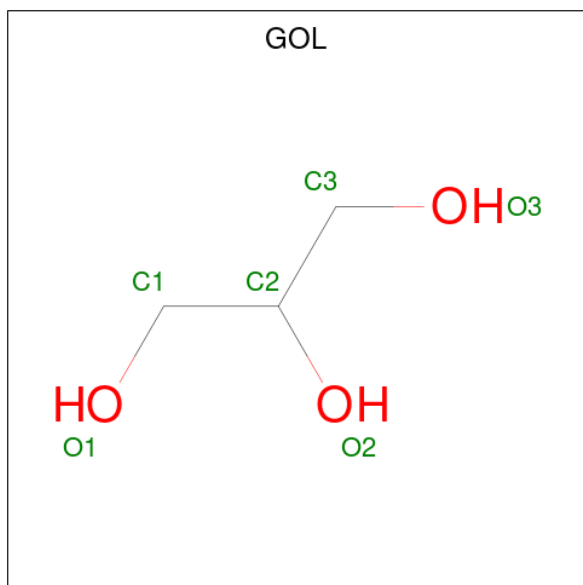


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace	
			Total	C	N				O
3	E	2	28	16	2	10	0	0	0

- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Zn		
4	A	1	1	1	0	0
4	C	1	1	1	0	0

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
5	A	1	6	3	3	0	0
5	B	1	6	3	3	0	0
5	B	1	6	3	3	0	0

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).



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

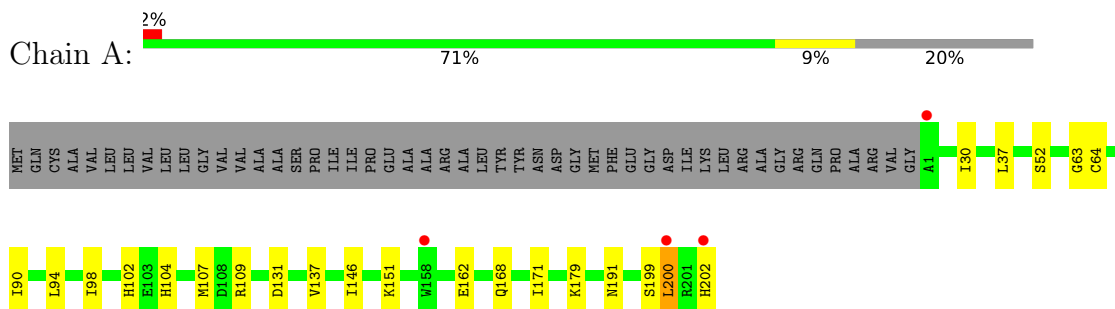
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	18	Total 18	O 18	0	0
7	B	11	Total 11	O 11	0	0
7	C	8	Total 8	O 8	0	0
7	D	9	Total 9	O 9	0	0

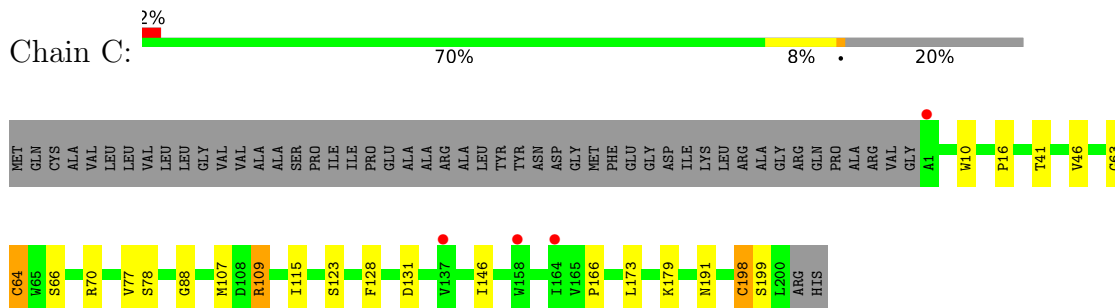
### 3 Residue-property plots [i](#)

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.

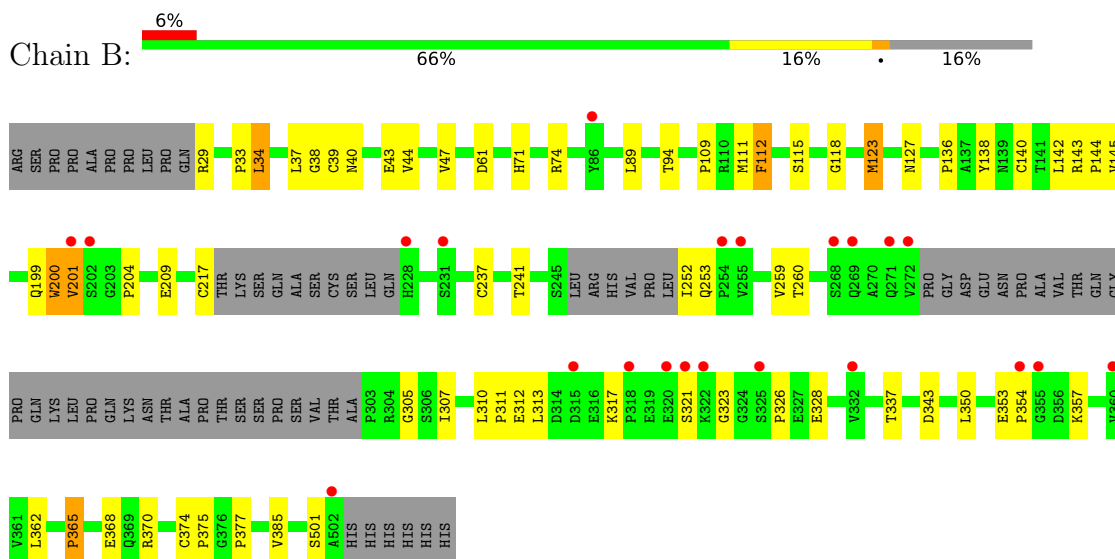
- Molecule 1: Astacin



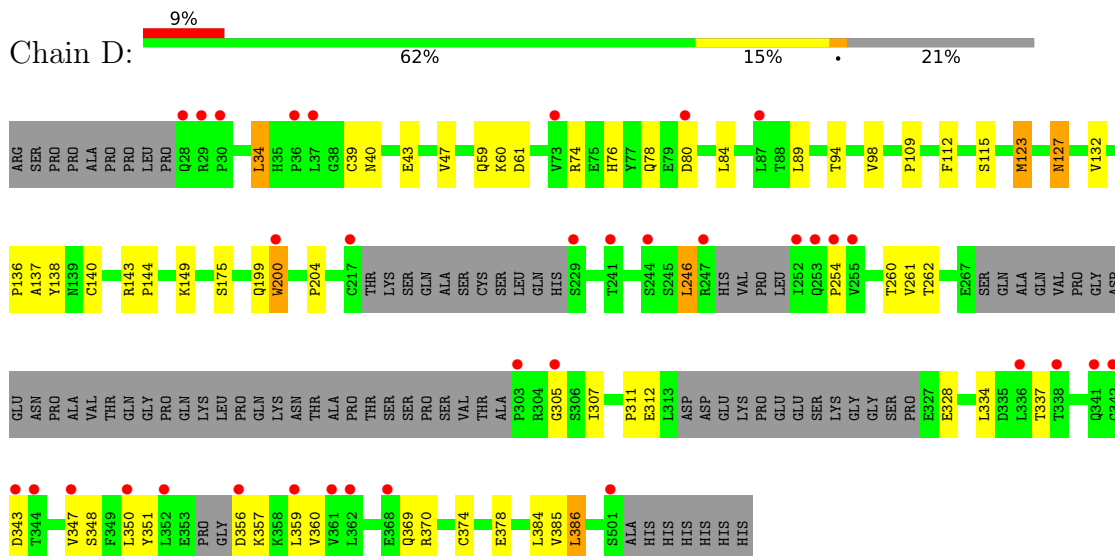
- Molecule 1: Astacin



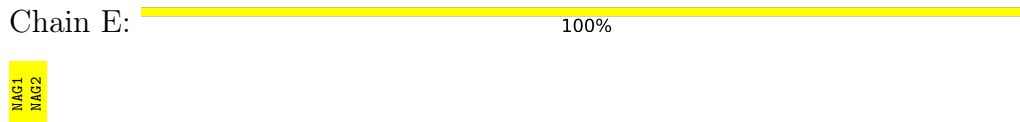
- Molecule 2: Fetuin-B



- Molecule 2: Fetuin-B



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



## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	83.40Å 85.80Å 168.70Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	34.12 – 3.10 84.35 – 3.10	Depositor EDS
% Data completeness (in resolution range)	100.0 (34.12-3.10) 100.0 (84.35-3.10)	Depositor EDS
$R_{merge}$	0.15	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.91 (at 3.13Å)	Xtrriage
Refinement program	BUSTER 2.10.3	Depositor
R, $R_{free}$	0.216 , 0.270 0.224 , 0.267	Depositor DCC
$R_{free}$ test set	643 reflections (2.84%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	95.6	Xtrriage
Anisotropy	0.183	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 95.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	0.022 for k,h,-l	Xtrriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	8035	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	101.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.43% 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: GOL, NAG, ZN

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	0.53	0/1653	0.67	0/2247
1	C	0.49	0/1630	0.64	0/2218
2	B	0.52	0/2466	0.72	0/3359
2	D	0.51	0/2340	0.69	0/3183
All	All	0.51	0/8089	0.69	0/11007

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	1612	0	1496	9	0
1	C	1590	0	1476	11	0
2	B	2409	0	2296	32	0
2	D	2288	0	2200	27	0
3	E	28	0	25	0	0
4	A	1	0	0	0	0
4	C	1	0	0	0	0
5	A	6	0	8	0	0
5	B	12	0	16	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	B	14	0	13	0	0
6	D	28	0	26	1	0
7	A	18	0	0	0	0
7	B	11	0	0	0	0
7	C	8	0	0	0	0
7	D	9	0	0	0	0
All	All	8035	0	7556	75	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 (75) 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)
2:B:39:CYS:H	2:B:374:CYS:HB2	1.44	0.81
2:B:323:GLY:HA2	2:B:328:GLU:HA	1.75	0.68
2:D:74:ARG:HH12	2:D:370:ARG:HA	1.59	0.67
2:D:347:VAL:HG13	2:D:350:LEU:HD12	1.77	0.66
2:B:337:THR:HG21	2:B:343:ASP:HB3	1.78	0.65
2:B:370:ARG:NH2	2:B:375:PRO:HA	2.12	0.65
2:B:123:MET:O	2:B:136:PRO:HD2	2.01	0.61
2:D:43:GLU:O	2:D:47:VAL:HG23	2.00	0.60
2:B:143:ARG:HG2	2:B:310:LEU:HB2	1.84	0.60
2:B:33:PRO:HG2	2:B:362:LEU:HD11	1.83	0.59
2:D:149:LYS:HD2	2:D:384:LEU:HD22	1.86	0.58
2:D:140:CYS:HB2	2:D:307:ILE:HG12	1.86	0.57
2:D:78:GLN:HE22	2:D:360:VAL:H	1.52	0.57
2:B:252:ILE:HG22	2:B:253:GLN:HG2	1.87	0.56
2:D:246:LEU:HB2	2:D:254:PRO:HD2	1.86	0.56
1:A:168:GLN:HB3	1:A:171:ILE:HD13	1.86	0.56
2:B:43:GLU:O	2:B:47:VAL:HG23	2.06	0.55
2:B:374:CYS:SG	2:B:374:CYS:O	2.65	0.55
2:D:132:VAL:HG21	2:D:351:TYR:CZ	2.42	0.55
2:D:123:MET:O	2:D:136:PRO:HD2	2.05	0.55
2:D:337:THR:HG21	2:D:343:ASP:HB3	1.90	0.54
1:A:94:LEU:O	1:A:98:ILE:HG13	2.08	0.54
2:B:40:ASN:HB2	2:B:377:PRO:HG2	1.91	0.53
2:B:144:PRO:HG2	2:B:312:GLU:HG2	1.91	0.53
2:B:118:GLY:HA3	2:B:142:LEU:HD23	1.92	0.52
2:B:337:THR:HG21	2:B:343:ASP:CB	2.40	0.52
2:B:138:TYR:O	2:B:305:GLY:HA3	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:39:CYS:H	2:D:374:CYS:HB2	1.76	0.50
1:C:88:GLY:HA2	1:C:146:ILE:HD11	1.92	0.50
2:D:59:GLN:HB2	2:D:98:VAL:HG11	1.93	0.50
2:D:144:PRO:HG2	2:D:312:GLU:HG2	1.92	0.50
1:A:63:GLY:HA3	2:B:199:GLN:HE21	1.77	0.50
2:B:71:HIS:HE2	2:B:501:SER:HB3	1.78	0.49
1:C:66:SER:HB2	1:C:77:VAL:HG22	1.94	0.49
2:B:34:LEU:HD13	2:B:74:ARG:HD2	1.94	0.49
2:D:94:THR:HA	2:D:109:PRO:HA	1.94	0.48
1:A:151:LYS:HB2	1:A:162:GLU:HG2	1.95	0.48
2:D:200:TRP:CH2	2:D:204:PRO:HB3	2.48	0.48
1:A:191:ASN:HB3	1:A:200:LEU:HD11	1.95	0.48
2:B:112:PHE:O	2:B:145:VAL:HG11	2.13	0.48
2:D:127:ASN:HB3	2:D:132:VAL:HB	1.96	0.48
2:B:71:HIS:NE2	2:B:501:SER:HB3	2.29	0.48
1:C:41:THR:HA	1:C:191:ASN:HD21	1.79	0.47
2:D:374:CYS:SG	2:D:374:CYS:O	2.73	0.47
1:A:63:GLY:HA2	2:B:201:VAL:CG2	2.45	0.46
2:B:94:THR:HA	2:B:109:PRO:HA	1.96	0.46
2:D:175:SER:HB2	2:D:261:VAL:HB	1.97	0.46
1:A:30:ILE:HA	1:A:90:ILE:HG21	1.98	0.45
2:B:143:ARG:HH21	2:B:311:PRO:HD2	1.81	0.45
2:B:74:ARG:HH12	2:B:370:ARG:HA	1.81	0.45
1:A:63:GLY:HA3	2:B:199:GLN:NE2	2.31	0.45
2:B:200:TRP:CH2	2:B:204:PRO:HB3	2.52	0.45
2:B:140:CYS:HB2	2:B:307:ILE:HG12	1.99	0.44
2:D:137:ALA:HB1	2:D:334:LEU:HD11	1.98	0.44
1:C:63:GLY:HA3	2:D:199:GLN:HE21	1.83	0.44
2:D:34:LEU:HB3	2:D:76:HIS:HB2	2.00	0.44
1:A:102:HIS:HB3	1:A:104:HIS:CE1	2.52	0.44
2:B:353:GLU:N	2:B:354:PRO:HD3	2.33	0.43
2:D:138:TYR:O	2:D:305:GLY:HA3	2.19	0.43
2:D:305:GLY:HA2	6:D:1002:NAG:H82	2.01	0.42
2:D:84:LEU:HD13	2:D:359:LEU:CD1	2.49	0.42
2:B:74:ARG:HG3	2:B:365:PRO:HG2	2.02	0.42
2:B:209:GLU:HA	2:B:237:CYS:O	2.20	0.42
1:C:64:CYS:HA	1:C:78:SER:O	2.20	0.42
2:D:34:LEU:H	2:D:34:LEU:HG	1.60	0.41
1:C:166:PRO:HD3	1:C:173:LEU:HD12	2.01	0.41
2:D:143:ARG:HH21	2:D:311:PRO:HD2	1.85	0.41
2:B:241:THR:HG22	2:B:259:VAL:HG22	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:109:ARG:NH2	1:C:128:PHE:HB3	2.35	0.41
1:C:198:CYS:HB2	1:C:199:SER:H	1.69	0.41
1:C:10:TRP:CE2	1:C:70:ARG:HB2	2.55	0.40
1:C:16:PRO:HA	1:C:46:VAL:O	2.21	0.40
1:C:109:ARG:NH2	1:C:115:ILE:HG13	2.36	0.40
2:D:378:GLU:HG2	2:D:386:LEU:HD22	2.03	0.40
2:B:38:GLY:O	2:B:44:VAL:HG21	2.21	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	200/251 (80%)	186 (93%)	13 (6%)	1 (0%)	29	64
1	C	198/251 (79%)	184 (93%)	14 (7%)	0	100	100
2	B	308/378 (82%)	275 (89%)	29 (9%)	4 (1%)	12	42
2	D	285/378 (75%)	263 (92%)	20 (7%)	2 (1%)	22	57
All	All	991/1258 (79%)	908 (92%)	76 (8%)	7 (1%)	22	57

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	313	LEU
2	D	40	ASN
1	A	199	SER
2	D	357	LYS
2	B	317	LYS
2	B	321	SER
2	B	326	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	175/211 (83%)	164 (94%)	11 (6%)	18	48
1	C	173/211 (82%)	166 (96%)	7 (4%)	31	65
2	B	269/339 (79%)	250 (93%)	19 (7%)	14	44
2	D	257/339 (76%)	238 (93%)	19 (7%)	13	42
All	All	874/1100 (80%)	818 (94%)	56 (6%)	17	48

All (56) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	37	LEU
1	A	52	SER
1	A	64	CYS
1	A	107	MET
1	A	109	ARG
1	A	131	ASP
1	A	137	VAL
1	A	146	ILE
1	A	179	LYS
1	A	200	LEU
1	A	202	HIS
2	B	29	ARG
2	B	34	LEU
2	B	37	LEU
2	B	61	ASP
2	B	89	LEU
2	B	111	MET
2	B	112	PHE
2	B	115	SER
2	B	123	MET
2	B	127	ASN
2	B	200	TRP
2	B	201	VAL
2	B	217	CYS

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Mol	Chain	Res	Type
2	B	260	THR
2	B	350	LEU
2	B	357	LYS
2	B	365	PRO
2	B	368	GLU
2	B	385	VAL
1	C	64	CYS
1	C	107	MET
1	C	109	ARG
1	C	123	SER
1	C	131	ASP
1	C	179	LYS
1	C	198	CYS
2	D	34	LEU
2	D	60	LYS
2	D	61	ASP
2	D	80	ASP
2	D	89	LEU
2	D	112	PHE
2	D	115	SER
2	D	123	MET
2	D	127	ASN
2	D	200	TRP
2	D	246	LEU
2	D	260	THR
2	D	262	THR
2	D	328	GLU
2	D	348	SER
2	D	356	ASP
2	D	369	GLN
2	D	385	VAL
2	D	386	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	191	ASN
2	B	59	GLN
2	B	199	GLN
2	B	381	ASN
1	C	35	GLN
1	C	191	ASN

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Mol	Chain	Res	Type
2	D	78	GLN
2	D	199	GLN
2	D	381	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

### 5.5 Carbohydrates [i](#)

2 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
3	NAG	E	1	3,2	14,14,15	0.40	0	17,19,21	1.42	2 (11%)
3	NAG	E	2	3	14,14,15	0.37	0	17,19,21	0.70	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
3	NAG	E	1	3,2	-	2/6/23/26	0/1/1/1
3	NAG	E	2	3	-	3/6/23/26	0/1/1/1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	1	NAG	O5-C1-C2	-4.66	103.93	111.29
3	E	1	NAG	O4-C4-C3	-2.22	105.21	110.35
3	E	2	NAG	C2-N2-C7	2.14	125.95	122.90

There are no chirality outliers.

All (5) torsion outliers are listed below:

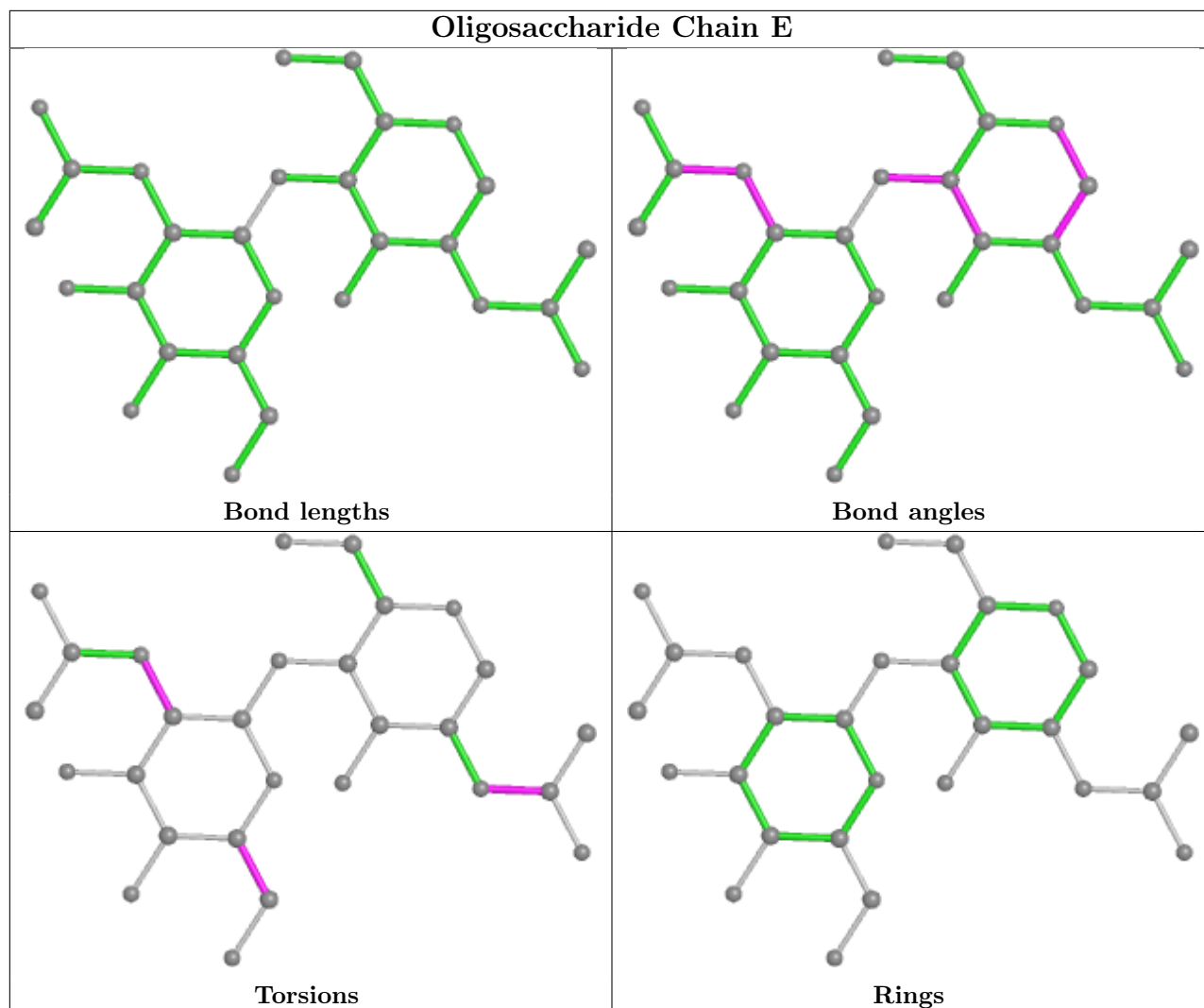
Mol	Chain	Res	Type	Atoms
3	E	2	NAG	O5-C5-C6-O6
3	E	1	NAG	C8-C7-N2-C2
3	E	2	NAG	C3-C2-N2-C7
3	E	2	NAG	C4-C5-C6-O6
3	E	1	NAG	O7-C7-N2-C2

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](#)

Of 8 ligands modelled in this entry, 2 are monoatomic - leaving 6 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
5	GOL	A	302	-	5,5,5	0.06	0	5,5,5	0.46	0
6	NAG	D	1001	2	14,14,15	0.35	0	17,19,21	0.56	0
6	NAG	B	1001	2	14,14,15	0.35	0	17,19,21	0.95	2 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	GOL	B	1005	-	5,5,5	0.11	0	5,5,5	0.37	0
6	NAG	D	1002	2	14,14,15	0.31	0	17,19,21	0.49	0
5	GOL	B	1004	-	5,5,5	0.26	0	5,5,5	0.38	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	GOL	A	302	-	-	0/4/4/4	-
6	NAG	D	1001	2	-	1/6/23/26	0/1/1/1
6	NAG	B	1001	2	-	1/6/23/26	0/1/1/1
5	GOL	B	1005	-	-	0/4/4/4	-
6	NAG	D	1002	2	-	1/6/23/26	0/1/1/1
5	GOL	B	1004	-	-	1/4/4/4	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	1001	NAG	C1-O5-C5	2.52	115.60	112.19
6	B	1001	NAG	C2-N2-C7	2.13	125.93	122.90

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	D	1002	NAG	O5-C5-C6-O6
6	D	1001	NAG	O5-C5-C6-O6
6	B	1001	NAG	C1-C2-N2-C7
5	B	1004	GOL	C1-C2-C3-O3

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	D	1002	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 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

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	202/251 (80%)	0.28	4 (1%) 65 44	57, 79, 97, 157	0
1	C	200/251 (79%)	0.30	4 (2%) 65 44	68, 90, 110, 133	0
2	B	316/378 (83%)	0.55	22 (6%) 16 7	65, 104, 168, 185	0
2	D	297/378 (78%)	0.64	35 (11%) 4 2	69, 112, 171, 186	0
All	All	1015/1258 (80%)	0.47	65 (6%) 19 8	57, 94, 156, 186	0

All (65) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	253	GLN	5.9
2	B	321	SER	5.6
2	B	228	HIS	5.6
2	B	269	GLN	5.0
2	D	37	LEU	4.6
2	B	318	PRO	4.5
2	B	320	GLU	3.9
2	D	342	GLY	3.9
2	D	36	PRO	3.8
2	B	325	SER	3.7
2	D	336	LEU	3.4
2	D	343	ASP	3.4
2	B	315	ASP	3.3
1	A	202	HIS	3.3
2	D	30	PRO	3.3
2	D	73	VAL	3.2
1	A	1	ALA	3.2
2	B	271	GLN	3.2
2	D	254	PRO	3.2
2	B	255	VAL	3.1
2	D	338	THR	3.0

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	C	158	TRP	2.9
2	B	272	VAL	2.9
2	D	87	LEU	2.8
2	B	201	VAL	2.8
2	D	200	TRP	2.8
2	D	501	SER	2.8
2	B	268	SER	2.8
1	A	200	LEU	2.8
1	C	137	VAL	2.8
2	B	202	SER	2.7
2	D	356	ASP	2.7
2	D	361	VAL	2.7
2	D	252	ILE	2.7
2	D	359	LEU	2.7
2	D	350	LEU	2.6
2	D	229	SER	2.6
2	D	244	SER	2.6
2	D	303	PRO	2.6
2	D	217	CYS	2.6
2	D	305	GLY	2.5
2	B	354	PRO	2.5
2	D	80	ASP	2.5
2	D	255	VAL	2.4
2	B	332	VAL	2.4
2	B	355	GLY	2.4
2	D	362	LEU	2.4
1	C	164	ILE	2.4
2	B	86	TYR	2.3
2	D	368	GLU	2.3
2	B	360	VAL	2.3
2	B	322	LYS	2.3
2	B	502	ALA	2.3
2	D	247	ARG	2.2
2	D	347	VAL	2.2
1	C	1	ALA	2.2
2	B	254	PRO	2.2
2	D	344	THR	2.1
2	D	29	ARG	2.1
2	B	231	SER	2.1
2	D	241	THR	2.1
2	D	341	GLN	2.1
1	A	158	TRP	2.1

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Mol	Chain	Res	Type	RSRZ
2	D	352	LEU	2.1
2	D	28	GLN	2.0

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

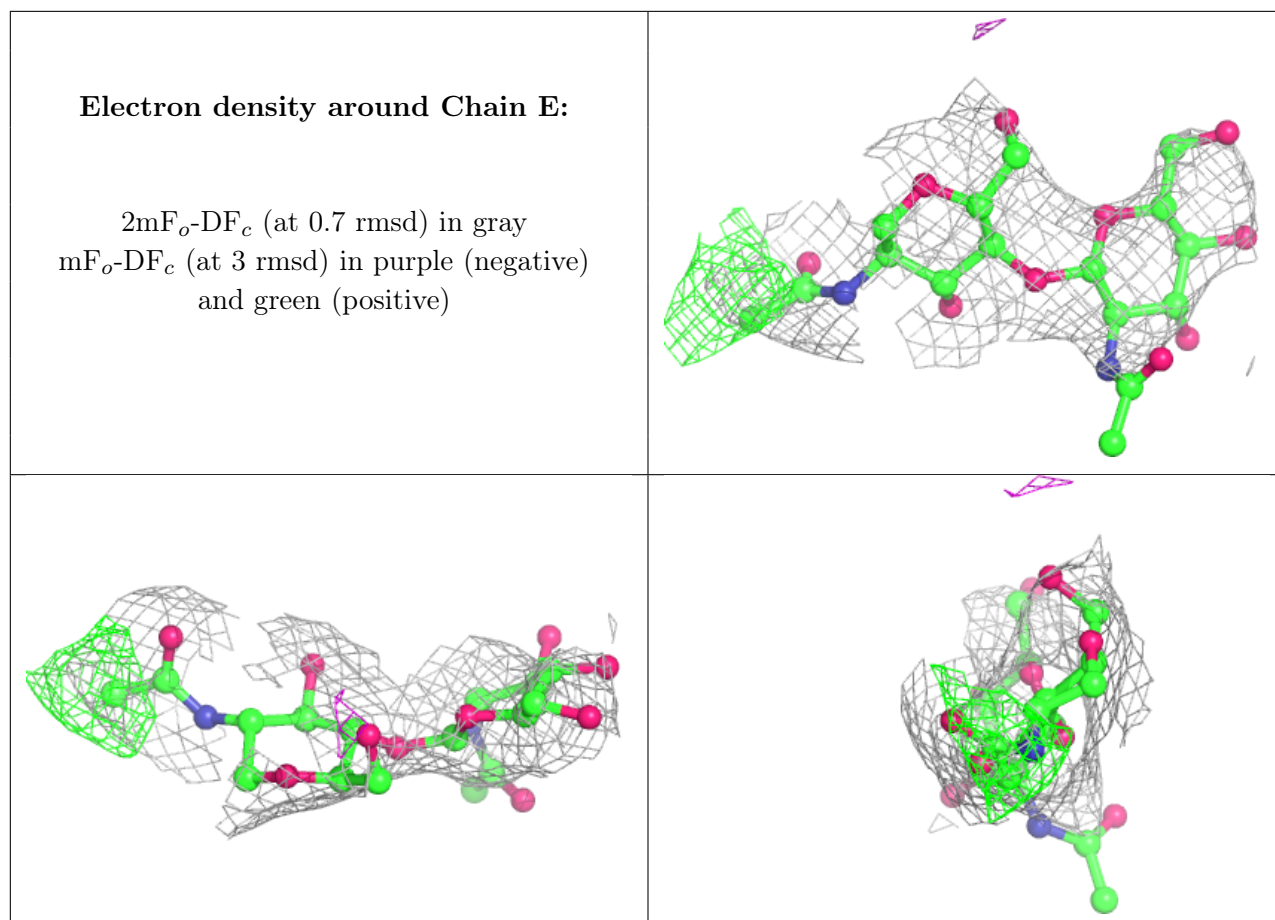
There are no non-standard protein/DNA/RNA residues in this entry.

## 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(Å <sup>2</sup> )	Q<0.9
3	NAG	E	1	14/15	0.74	0.23	141,148,155,162	0
3	NAG	E	2	14/15	0.82	0.29	168,173,180,180	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](#)

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	NAG	B	1001	14/15	0.61	0.26	149,155,162,162	0
6	NAG	D	1002	14/15	0.71	0.39	164,165,172,174	0
5	GOL	B	1005	6/6	0.74	0.23	110,111,112,113	0
5	GOL	B	1004	6/6	0.80	0.24	75,81,82,82	0
6	NAG	D	1001	14/15	0.83	0.25	154,161,162,165	0
5	GOL	A	302	6/6	0.89	0.26	97,97,97,98	0
4	ZN	A	301	1/1	0.99	0.18	64,64,64,64	0
4	ZN	C	301	1/1	0.99	0.17	72,72,72,72	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.