



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 04:06 PM UTC

PDB ID : 6HT9 / pdb_00006ht9
Title : Mouse fetuin-B in complex with crayfish astacin
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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

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>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

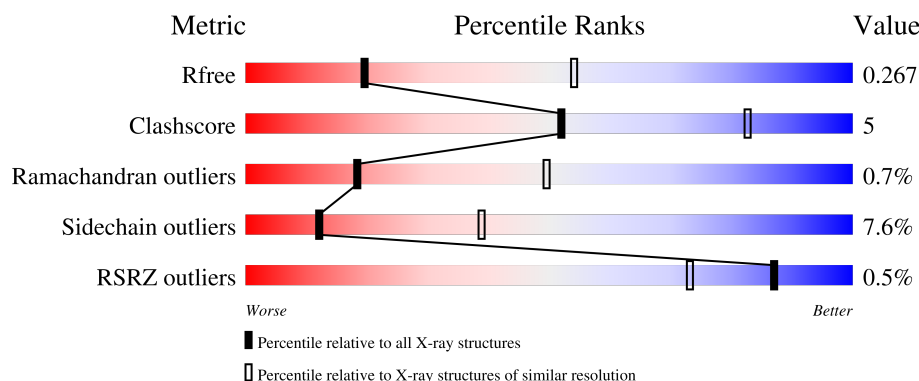
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

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}	180053	1456 (3.10-3.10)
Clashscore	190562	1539 (3.10-3.10)
Ramachandran outliers	187476	1467 (3.10-3.10)
Sidechain outliers	187428	1467 (3.10-3.10)
RSRZ outliers	180081	1456 (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 ≥ 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	
1	C	251	
2	B	378	
2	D	378	
3	E	2	

2 Entry composition

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
1	A	202	Total	C	N	O	S	0	0	0
			1612	1016	266	320	10			
1	C	200	Total	C	N	O	S	0	0	0
			1590	1004	259	317	10			

- Molecule 2 is a protein called Fetuin-B.

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

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.

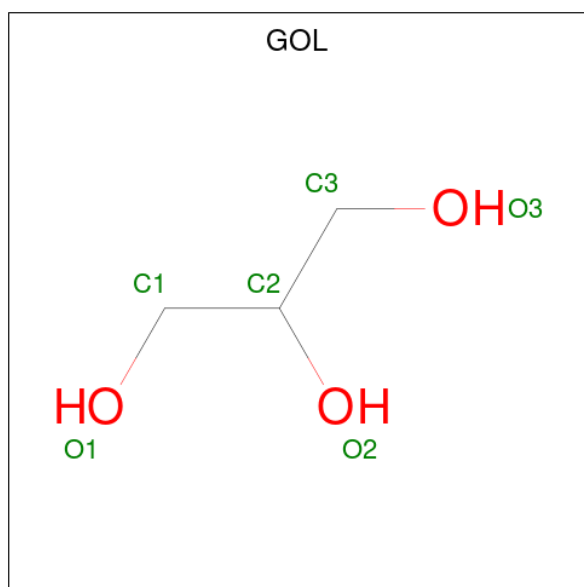


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	E	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 4 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 5 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



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

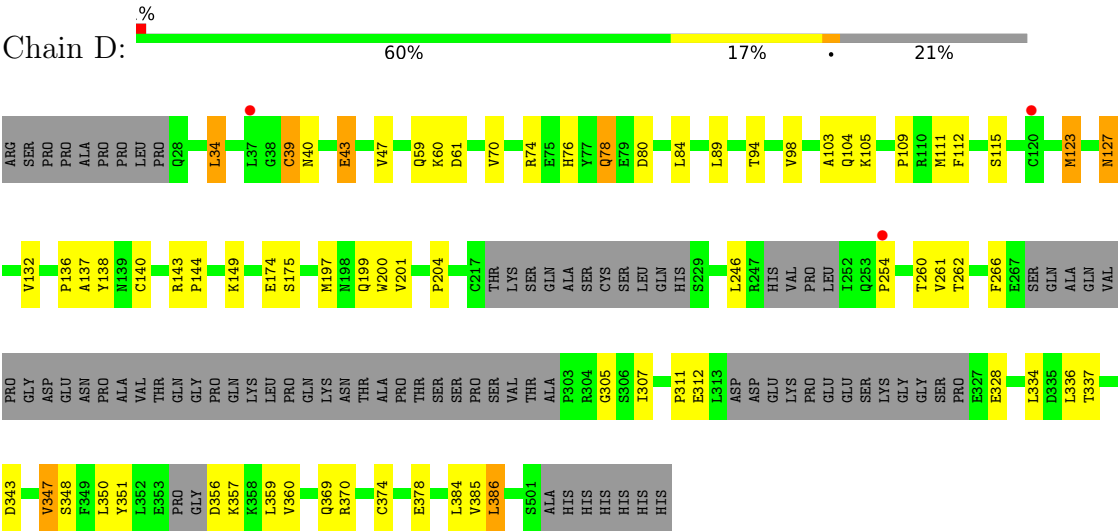
- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



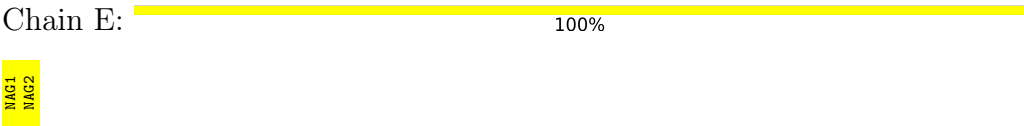
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	B	1	Total	C	N	O	0	0
			14	8	1	5		
6	D	1	Total	C	N	O	0	0
			14	8	1	5		
6	D	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 7 is water.

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



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



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	83.40Å 85.80Å 168.70Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	34.12 – 3.10 34.12 – 3.10	Depositor EDS
% Data completeness (in resolution range)	100.0 (34.12-3.10) 99.9 (34.12-3.10)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.91 (at 3.13Å)	Xtriage
Refinement program	BUSTER 2.10.3	Depositor
R, R_{free}	0.216 , 0.270 0.223 , 0.267	Depositor DCC
R_{free} test set	643 reflections (2.84%)	wwPDB-VP
Wilson B-factor (Å ²)	95.6	Xtriage
Anisotropy	0.183	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 85.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.022 for k,h,-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	8035	wwPDB-VP
Average B, all atoms (Å ²)	101.0	wwPDB-VP

Xtriage'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.*

¹Intensities estimated from amplitudes.

²Theoretical 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 ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, GOL, 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	0.91	0/1653	1.29	5/2247 (0.2%)
1	C	0.86	0/1630	1.25	1/2218 (0.0%)
2	B	0.89	1/2466 (0.0%)	1.30	15/3359 (0.4%)
2	D	0.89	1/2340 (0.0%)	1.28	13/3183 (0.4%)
All	All	0.89	2/8089 (0.0%)	1.28	34/11007 (0.3%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	197	MET	SD-CE	5.69	1.93	1.79
2	D	197	MET	SD-CE	5.56	1.93	1.79

All (34) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	70	VAL	N-CA-CB	7.07	119.06	111.00
2	B	352	LEU	N-CA-C	-6.49	101.18	110.59
2	B	201	VAL	N-CA-C	-6.36	106.09	111.56
2	D	39	CYS	CA-C-N	6.31	133.59	121.54
2	D	39	CYS	C-N-CA	6.31	133.59	121.54
2	B	350	LEU	CA-C-N	6.19	131.38	122.35
2	B	350	LEU	C-N-CA	6.19	131.38	122.35
1	A	71	ILE	N-CA-C	-5.89	103.63	110.05
2	D	43	GLU	CA-C-N	5.67	127.71	120.56
2	D	43	GLU	C-N-CA	5.67	127.71	120.56
2	B	48	ALA	CA-C-N	5.58	126.13	119.94
2	B	48	ALA	C-N-CA	5.58	126.13	119.94
2	D	266	PHE	CA-CB-CG	5.56	119.36	113.80
2	D	201	VAL	N-CA-C	-5.54	106.40	111.67
2	D	103	ALA	CA-C-N	5.50	129.07	120.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	103	ALA	C-N-CA	5.50	129.07	120.82
2	D	266	PHE	CA-C-N	5.44	131.49	121.70
2	D	266	PHE	C-N-CA	5.44	131.49	121.70
1	A	131	ASP	CA-CB-CG	5.43	118.03	112.60
1	A	108	ASP	CA-CB-CG	5.31	117.91	112.60
2	B	72	ASP	CA-CB-CG	5.30	117.90	112.60
2	B	375	PRO	N-CA-C	-5.27	106.67	113.57
2	B	328	GLU	CA-C-N	5.23	127.24	120.44
2	B	328	GLU	C-N-CA	5.23	127.24	120.44
2	B	43	GLU	CA-C-N	5.22	127.14	120.56
2	B	43	GLU	C-N-CA	5.22	127.14	120.56
1	C	71	ILE	N-CA-C	-5.21	104.37	110.05
2	D	78	GLN	CA-C-N	5.17	127.17	120.44
2	D	78	GLN	C-N-CA	5.17	127.17	120.44
2	B	347	VAL	CA-C-N	5.10	127.53	120.29
2	B	347	VAL	C-N-CA	5.10	127.53	120.29
1	A	32	SER	CA-C-N	5.06	125.46	119.94
1	A	32	SER	C-N-CA	5.06	125.46	119.94
2	D	70	VAL	N-CA-CB	5.01	117.47	111.31

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	1612	0	1496	10	0
1	C	1590	0	1476	12	0
2	B	2409	0	2296	33	0
2	D	2288	0	2200	29	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
6	B	14	0	13	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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	79	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 (79) 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:HE2	2:B:336:LEU:HD12	1.81	0.61
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: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:B:374:CYS:SG	2:B:374:CYS:O	2.65	0.54
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:D:123:MET:HE2	2:D:336:LEU:HD12	1.98	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:104:GLN:H	2:D:104:GLN:CD	2.24	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
1:A:38:GLU:CD	1:C:35:GLN:HE22	2.27	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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 ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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%)	24	57
1	C	198/251 (79%)	184 (93%)	14 (7%)	0	100	100
2	B	308/378 (82%)	275 (89%)	29 (9%)	4 (1%)	9	35
2	D	285/378 (75%)	263 (92%)	20 (7%)	2 (1%)	18	49
All	All	991/1258 (79%)	908 (92%)	76 (8%)	7 (1%)	18	49

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

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Mol	Chain	Res	Type
2	B	321	SER
2	B	326	PRO

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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%)	162 (93%)	13 (7%)	13	40
1	C	173/211 (82%)	163 (94%)	10 (6%)	18	48
2	B	269/339 (79%)	247 (92%)	22 (8%)	10	36
2	D	257/339 (76%)	236 (92%)	21 (8%)	10	36
All	All	874/1100 (80%)	808 (92%)	66 (8%)	12	39

All (66) 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	130	ILE
1	A	131	ASP
1	A	137	VAL
1	A	146	ILE
1	A	171	ILE
1	A	179	LYS
1	A	200	LEU
1	A	202	HIS
2	B	34	LEU
2	B	37	LEU
2	B	61	ASP
2	B	70	VAL
2	B	89	LEU
2	B	110	ARG

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Mol	Chain	Res	Type
2	B	111	MET
2	B	112	PHE
2	B	115	SER
2	B	123	MET
2	B	174	GLU
2	B	190	LEU
2	B	201	VAL
2	B	217	CYS
2	B	260	THR
2	B	341	GLN
2	B	347	VAL
2	B	350	LEU
2	B	368	GLU
2	B	380	GLU
2	B	385	VAL
2	B	386	LEU
1	C	35	GLN
1	C	64	CYS
1	C	107	MET
1	C	109	ARG
1	C	123	SER
1	C	130	ILE
1	C	131	ASP
1	C	171	ILE
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	105	LYS
2	D	111	MET
2	D	112	PHE
2	D	115	SER
2	D	123	MET
2	D	127	ASN
2	D	174	GLU
2	D	260	THR
2	D	262	THR
2	D	328	GLU
2	D	347	VAL

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Mol	Chain	Res	Type
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 (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	104	HIS
1	A	118	GLN
1	A	191	ASN
2	B	151	HIS
2	B	165	ASN
2	B	198	ASN
2	B	339	ASN
2	B	381	ASN
1	C	35	GLN
1	C	184	GLN
1	C	191	ASN
2	D	68	ASN
2	D	78	GLN
2	D	165	ASN
2	D	198	ASN
2	D	199	GLN
2	D	339	ASN
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	0.39	0	17,19,21	1.45	2 (11%)
3	NAG	E	2	3	14,14,15	0.39	0	17,19,21	0.73	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	-	4/6/23/26	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	-4.76	103.93	111.29
3	E	2	NAG	C2-N2-C7	2.28	125.95	122.90
3	E	1	NAG	O4-C4-C3	-2.19	105.21	110.38

There are no chirality outliers.

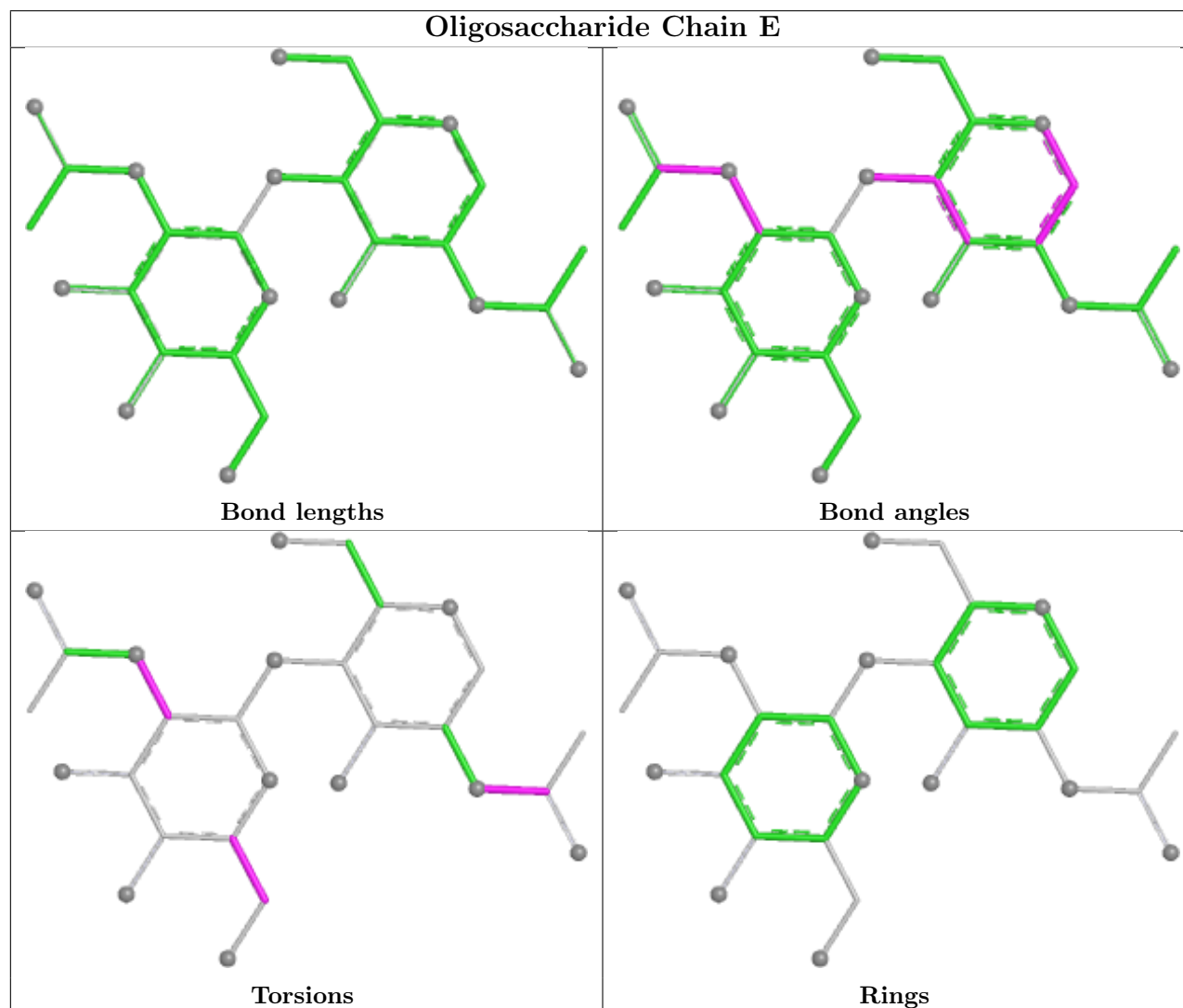
All (6) torsion outliers are listed below:

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	2	NAG	C1-C2-N2-C7
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	B	1004	-	5,5,5	0.26	0	5,5,5	0.37	0
5	GOL	A	302	-	5,5,5	0.06	0	5,5,5	0.48	0
6	NAG	B	1001	2	14,14,15	0.37	0	17,19,21	0.99	2 (11%)
6	NAG	D	1001	2	14,14,15	0.37	0	17,19,21	0.59	0
5	GOL	B	1005	-	5,5,5	0.11	0	5,5,5	0.38	0
6	NAG	D	1002	2	14,14,15	0.32	0	17,19,21	0.50	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	GOL	B	1004	-	-	0/4/4/4	-
5	GOL	A	302	-	-	0/4/4/4	-
6	NAG	B	1001	2	-	1/6/23/26	0/1/1/1
6	NAG	D	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

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	2.55	115.60	112.19
6	B	1001	NAG	C2-N2-C7	2.26	125.93	122.90

There are no chirality outliers.

All (3) torsion outliers are listed below:

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

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, 95th 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 ²)	Q<0.9
1	A	202/251 (80%)	-0.35	0	100	100	57, 79, 97, 157	0
1	C	200/251 (79%)	-0.35	0	100	100	68, 90, 110, 133	0
2	B	316/378 (83%)	-0.05	2 (0%)	85	70	65, 104, 168, 185	0
2	D	297/378 (78%)	0.10	3 (1%)	79	61	69, 112, 171, 186	0
All	All	1015/1258 (80%)	-0.13	5 (0%)	87	73	57, 94, 156, 186	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	252	ILE	2.5
2	D	254	PRO	2.4
2	B	317	LYS	2.0
2	D	120	CYS	2.0
2	D	37	LEU	2.0

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

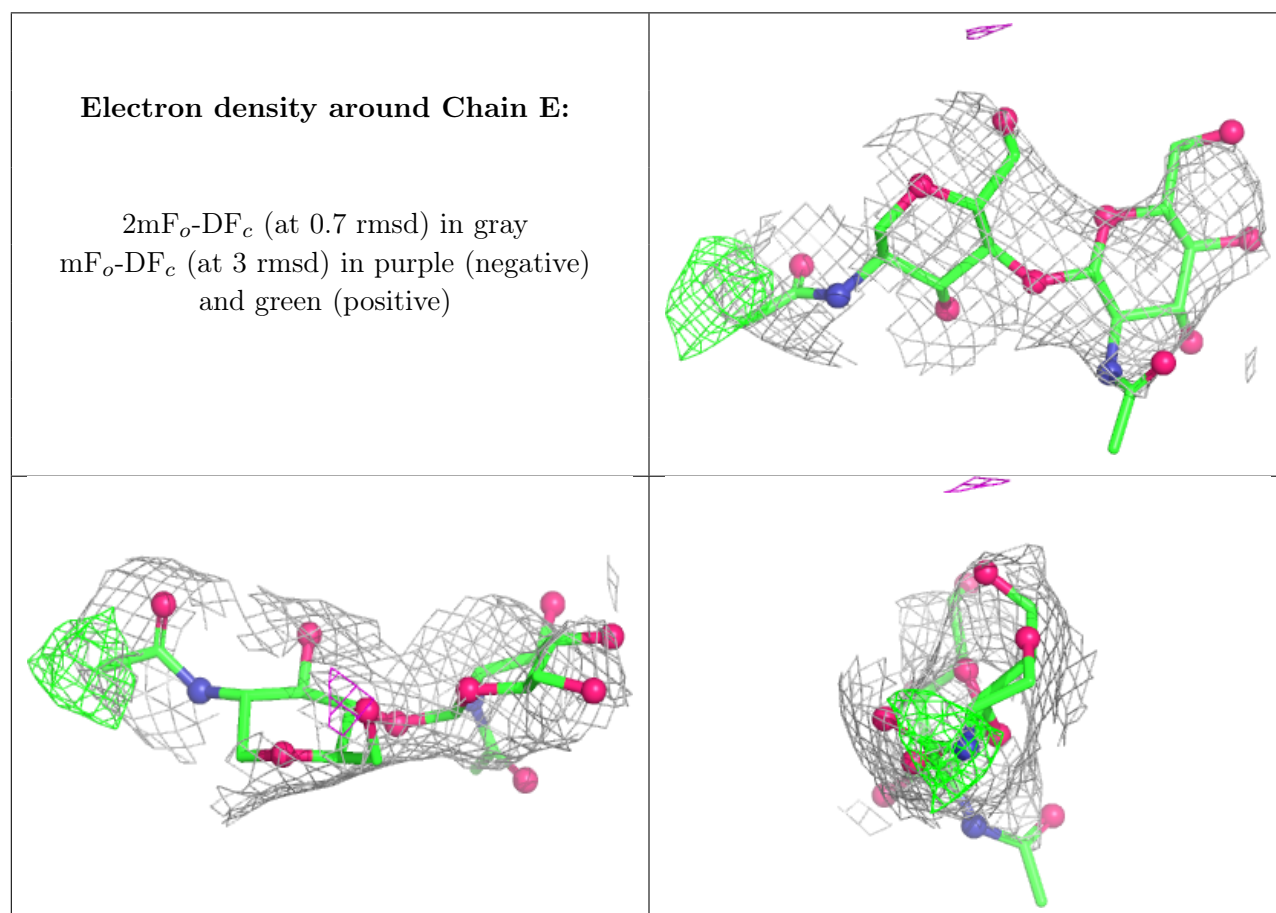
There are no non-standard protein/DNA/RNA residues in this entry.

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, 95th 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 ²)	Q<0.9
3	NAG	E	2	14/15	0.67	0.11	168,173,180,180	0
3	NAG	E	1	14/15	0.77	0.13	141,148,155,162	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, 95th 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 ²)	Q<0.9
6	NAG	D	1001	14/15	0.62	0.10	154,161,162,165	0
6	NAG	B	1001	14/15	0.66	0.11	149,155,162,162	0
6	NAG	D	1002	14/15	0.79	0.10	164,165,172,174	0
5	GOL	B	1004	6/6	0.82	0.10	75,81,82,82	0
5	GOL	B	1005	6/6	0.85	0.14	110,111,112,113	0
5	GOL	A	302	6/6	0.90	0.10	97,97,97,98	0
4	ZN	A	301	1/1	1.00	0.04	64,64,64,64	0
4	ZN	C	301	1/1	1.00	0.03	72,72,72,72	0

6.5 Other polymers [i](#)

There are no such residues in this entry.