



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 18, 2026 – 03:44 AM UTC

PDB ID : 9TPF / pdb_00009tpf
Title : The structure of the orthorhombic crystal form of the type II ribosome inactivating protein from Winter Aconite Eranthis hyemalis.
Authors : Cooper, J.B.; Palmer, R.A.
Deposited on : 2025-12-18
Resolution : 1.80 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

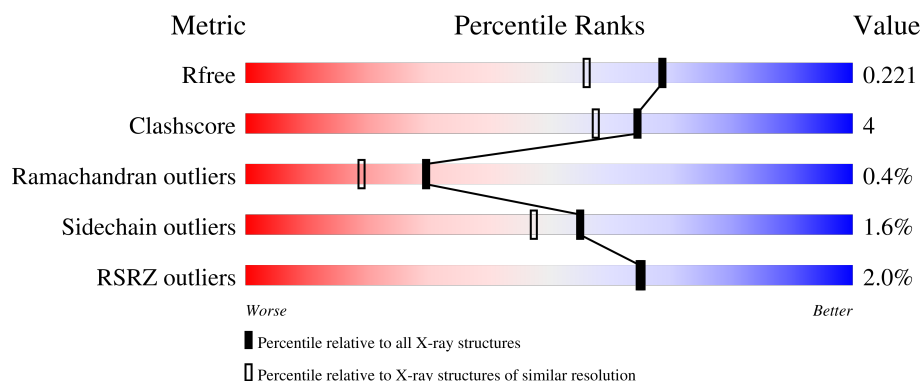
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

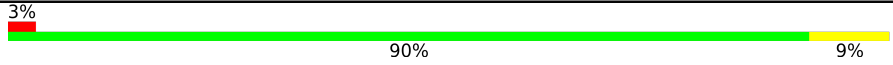
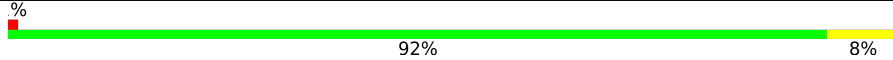
The reported resolution of this entry is 1.80 Å.

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	7662 (1.80-1.80)
Clashscore	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)
RSRZ outliers	180081	7663 (1.80-1.80)

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	241	
2	B	262	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	NAG	B	303	-	-	X	-

2 Entry composition [i](#)

There are 10 unique types of molecules in this entry. The entry contains 4739 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.

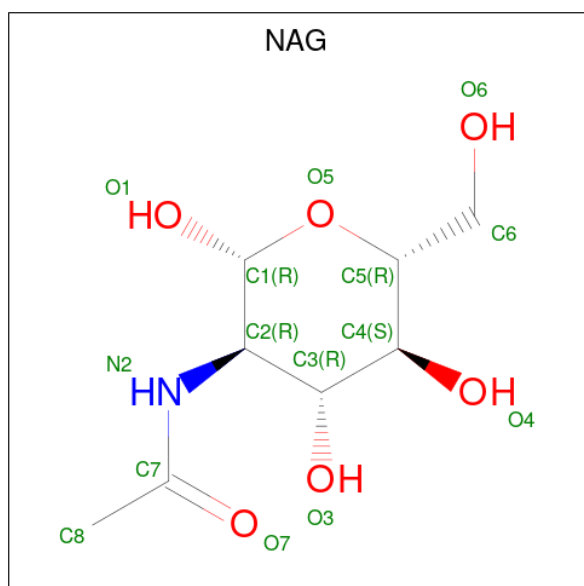
- Molecule 1 is a protein called N-glycosidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	241	Total	C	N	O	S	0	3	0
			1916	1221	338	354	3			

- Molecule 2 is a protein called Lectin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	261	Total	C	N	O	S	0	0	0
			2025	1252	352	408	13			

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



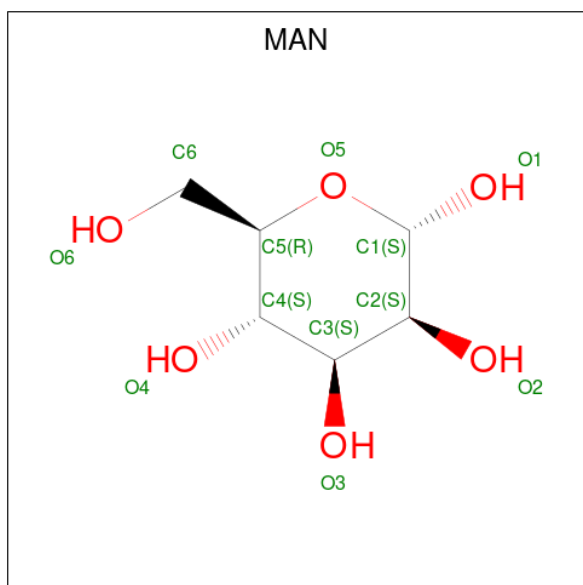
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		

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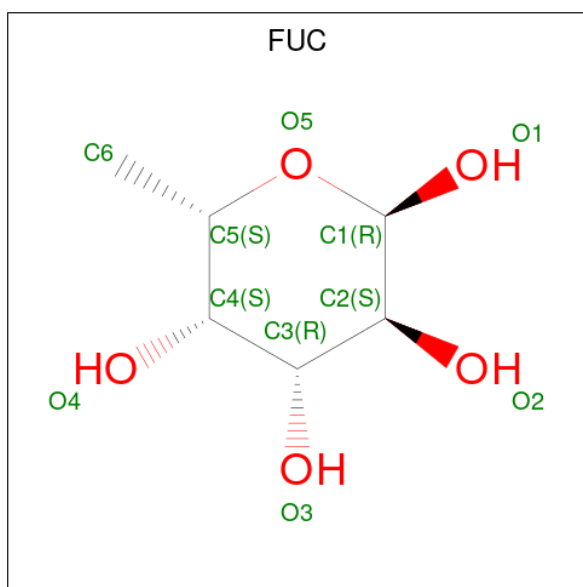
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	B	1	Total	C	N	O	0	0
			14	8	1	5		
3	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 4 is alpha-D-mannopyranose (CCD ID: MAN) (formula: C₆H₁₂O₆).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			11	6	5		

- Molecule 5 is alpha-L-fucopyranose (CCD ID: FUC) (formula: C₆H₁₂O₅).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			10	6	4		

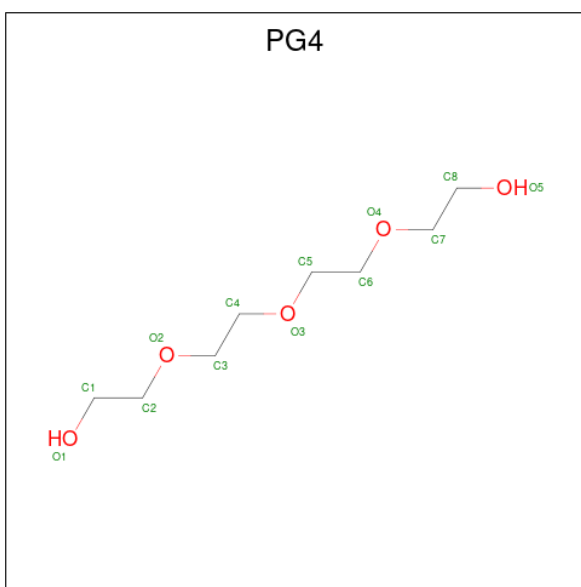
- Molecule 6 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	2	Total	Zn	0	0
			2	2		
6	B	1	Total	Zn	0	0
			1	1		

- Molecule 7 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

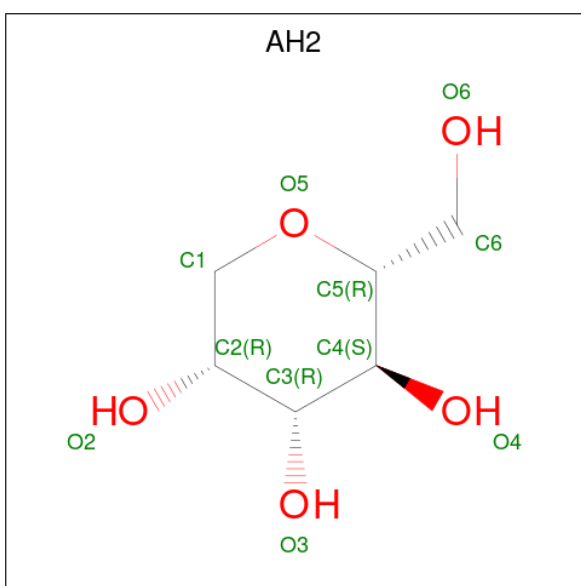
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	1	Total	Cl	0	0
			1	1		

- Molecule 8 is TETRAETHYLENE GLYCOL (CCD ID: PG4) (formula: C₈H₁₈O₅).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	B	1	Total	C	O	0	0
			13	8	5		
8	B	1	Total	C	O	0	0
			13	8	5		

- Molecule 9 is 1-deoxy-alpha-D-mannopyranose (CCD ID: AH2) (formula: C₆H₁₂O₅).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	B	1	Total	C	O	0	0
			11	6	5		

- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	320	Total 320	O 320	0	0
10	B	360	Total 360	O 360	0	0

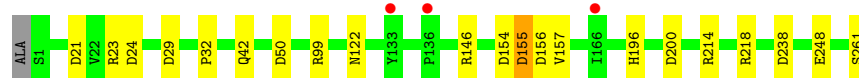
3 Residue-property plots [i](#)

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: N-glycosidase



- Molecule 2: Lectin



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	80.59Å 95.47Å 96.34Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.73 – 1.80 47.73 – 1.80	Depositor EDS
% Data completeness (in resolution range)	100.0 (47.73-1.80) 100.0 (47.73-1.80)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.48 (at 1.79Å)	Xtriage
Refinement program	Servalcat 0.4.105	Depositor
R, R_{free}	0.182 , 0.233 (Not available) , 0.221	Depositor DCC
R_{free} test set	3452 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å ²)	30.0	Xtriage
Anisotropy	0.742	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 35.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.023 for -h,l,k	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	4739	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.61% 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: MAN, FUC, AH2, PG4, NAG, CL, 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	0.83	0/1969	1.26	5/2682 (0.2%)
2	B	0.88	0/2066	1.26	10/2816 (0.4%)
All	All	0.85	0/4035	1.26	15/5498 (0.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
2	B	0	3
All	All	0	4

There are no bond length outliers.

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	130	ASP	CA-CB-CG	6.91	119.51	112.60
1	A	38	GLN	N-CA-CB	-6.39	99.98	110.52
2	B	248	GLU	CB-CG-CD	6.13	123.02	112.60
2	B	238	ASP	CA-CB-CG	6.01	118.61	112.60
2	B	21	ASP	CA-CB-CG	5.91	118.51	112.60
2	B	155	ASP	CA-CB-CG	5.80	118.40	112.60
2	B	29	ASP	CA-CB-CG	5.74	118.34	112.60
1	A	159	ARG	NE-CZ-NH1	-5.73	115.77	121.50
1	A	98	PHE	CB-CA-C	5.37	115.81	110.33
1	A	18	GLN	N-CA-CB	-5.36	102.24	110.12
2	B	24	ASP	CA-CB-CG	5.31	117.91	112.60
2	B	32	PRO	CB-CA-C	-5.29	104.46	111.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	154	ASP	CA-CB-CG	5.08	117.68	112.60
2	B	156	ASP	CA-CB-CG	5.01	117.61	112.60
2	B	200	ASP	CA-CB-CG	5.00	117.61	112.60

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	206	ARG	Sidechain
2	B	146	ARG	Sidechain
2	B	214	ARG	Sidechain
2	B	23	ARG	Sidechain

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	1916	0	1901	9	0
2	B	2025	0	1930	10	0
3	A	28	0	25	6	0
3	B	28	0	26	10	0
4	A	11	0	10	2	0
5	A	10	0	10	1	0
6	A	2	0	0	0	0
6	B	1	0	0	0	0
7	A	1	0	0	0	0
8	B	26	0	36	0	0
9	B	11	0	0	1	0
10	A	320	0	0	5	0
10	B	360	0	0	3	0
All	All	4739	0	3938	29	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

All (29) 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:122:ASN:HD21	3:B:303:NAG:C1	0.94	1.55
2:B:122:ASN:ND2	3:B:303:NAG:C1	1.75	1.50
3:A:302:NAG:O4	4:A:303:MAN:C1	1.82	1.26
3:B:303:NAG:O4	3:B:304:NAG:C1	1.82	1.26
3:A:301:NAG:O3	5:A:304:FUC:C1	2.07	1.02
3:A:302:NAG:HO4	4:A:303:MAN:C1	1.69	1.02
1:A:119:GLU:HG2	10:A:623:HOH:O	1.65	0.94
2:B:122:ASN:HD21	3:B:303:NAG:C2	1.89	0.85
3:B:303:NAG:HO4	3:B:304:NAG:C1	1.86	0.84
1:A:180[B]:ARG:HD3	1:A:211:GLN:O	1.89	0.72
2:B:122:ASN:CG	3:B:303:NAG:C1	2.62	0.70
3:B:303:NAG:C4	3:B:304:NAG:C1	2.68	0.70
1:A:180[A]:ARG:NH2	2:B:261:SER:O	2.24	0.70
1:A:83:THR:HG21	1:A:104:ARG:NH2	2.11	0.65
3:B:303:NAG:O4	3:B:304:NAG:C2	2.48	0.60
3:A:301:NAG:C8	10:A:410:HOH:O	2.50	0.59
2:B:196:HIS:ND1	10:B:401:HOH:O	2.31	0.58
1:A:41[B]:GLN:HG2	10:A:566:HOH:O	2.03	0.57
2:B:122:ASN:ND2	3:B:303:NAG:C2	2.59	0.56
2:B:155:ASP:HB2	2:B:157:VAL:HG22	1.88	0.54
3:A:301:NAG:H83	10:A:410:HOH:O	2.08	0.54
1:A:83:THR:HG21	1:A:104:ARG:CZ	2.36	0.54
3:B:304:NAG:O4	9:B:305:AH2:O2	2.26	0.53
2:B:50:ASP:HB2	10:B:590:HOH:O	2.08	0.53
2:B:218:ARG:HD2	10:B:643:HOH:O	2.11	0.50
1:A:214:SER:O	1:A:215:TYR:HB2	2.13	0.47
1:A:209:TRP:HD1	1:A:217:VAL:CG1	2.29	0.45
3:A:301:NAG:H82	10:A:543:HOH:O	2.18	0.43
1:A:111:ASN:HD22	1:A:111:ASN:H	1.70	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	242/241 (100%)	233 (96%)	7 (3%)	2 (1%)	16	6
2	B	259/262 (99%)	256 (99%)	3 (1%)	0	100	100
All	All	501/503 (100%)	489 (98%)	10 (2%)	2 (0%)	30	19

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	47	VAL
1	A	229	GLY

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	208/205 (102%)	202 (97%)	6 (3%)	37	25
2	B	226/226 (100%)	224 (99%)	2 (1%)	70	67
All	All	434/431 (101%)	426 (98%)	8 (2%)	55	43

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	SER
1	A	79	LEU
1	A	114	ASN
1	A	133	ASP
1	A	180[A]	ARG
1	A	180[B]	ARG
2	B	42	GLN
2	B	99	ARG

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	32	HIS

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Mol	Chain	Res	Type
1	A	111	ASN
1	A	150	GLN
1	A	172	ASN
2	B	40	GLN
2	B	91	ASN
2	B	122	ASN
2	B	172	GLN
2	B	252	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](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 13 ligands modelled in this entry, 4 are monoatomic - leaving 9 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	FUC	A	304	-	10,10,11	0.79	0	14,14,16	1.31	2 (14%)
3	NAG	B	303	-	14,14,15	0.63	0	17,19,21	1.26	2 (11%)
8	PG4	B	301	-	12,12,12	1.04	0	11,11,11	0.77	0
8	PG4	B	302	-	12,12,12	0.90	0	11,11,11	0.54	0
3	NAG	B	304	-	14,14,15	0.42	0	17,19,21	1.29	2 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	MAN	A	303	-	11,11,12	1.15	1 (9%)	15,15,17	1.61	4 (26%)
3	NAG	A	301	-	14,14,15	0.63	0	17,19,21	1.14	1 (5%)
9	AH2	B	305	-	11,11,11	0.86	1 (9%)	15,15,15	1.27	2 (13%)
3	NAG	A	302	-	14,14,15	0.36	0	17,19,21	0.88	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	FUC	A	304	-	-	-	0/1/1/1
3	NAG	B	303	-	-	0/6/23/26	0/1/1/1
8	PG4	B	301	-	-	2/10/10/10	-
8	PG4	B	302	-	-	3/10/10/10	-
3	NAG	B	304	-	-	0/6/23/26	0/1/1/1
4	MAN	A	303	-	-	2/2/19/22	0/1/1/1
3	NAG	A	301	-	-	2/6/23/26	0/1/1/1
9	AH2	B	305	-	-	0/2/19/19	0/1/1/1
3	NAG	A	302	-	-	0/6/23/26	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	303	MAN	C2-C3	3.27	1.57	1.52
9	B	305	AH2	C4-C5	2.13	1.57	1.53

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	303	NAG	C2-N2-C7	3.48	127.56	122.90
4	A	303	MAN	C1-C2-C3	3.20	114.31	109.64
9	B	305	AH2	C3-C4-C5	3.06	115.78	110.23
4	A	303	MAN	C1-O5-C5	2.98	116.17	112.19
5	A	304	FUC	O5-C1-C2	2.97	117.89	110.79
3	B	304	NAG	O5-C1-C2	-2.92	106.77	111.29
3	B	303	NAG	C1-C2-N2	2.63	114.58	110.43
4	A	303	MAN	O2-C2-C3	2.60	115.54	110.15
5	A	304	FUC	C1-O5-C5	2.57	119.03	112.97
4	A	303	MAN	O5-C1-C2	2.56	116.89	110.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	302	NAG	C1-C2-N2	2.42	114.24	110.43
3	A	301	NAG	C1-O5-C5	-2.39	108.98	112.19
9	B	305	AH2	C1-O5-C5	2.16	115.08	112.19
3	B	304	NAG	C3-C4-C5	2.12	114.08	110.23

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	303	MAN	O5-C5-C6-O6
4	A	303	MAN	C4-C5-C6-O6
3	A	301	NAG	C8-C7-N2-C2
3	A	301	NAG	O7-C7-N2-C2
8	B	302	PG4	O3-C5-C6-O4
8	B	302	PG4	O4-C7-C8-O5
8	B	302	PG4	C5-C6-O4-C7
8	B	301	PG4	O2-C3-C4-O3
8	B	301	PG4	C5-C6-O4-C7

There are no ring outliers.

7 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	304	FUC	1	0
3	B	303	NAG	9	0
3	B	304	NAG	5	0
4	A	303	MAN	2	0
3	A	301	NAG	4	0
9	B	305	AH2	1	0
3	A	302	NAG	2	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	241/241 (100%)	0.10	7 (2%) 53 53	21, 37, 59, 102	3 (1%)
2	B	261/262 (99%)	-0.03	3 (1%) 78 78	27, 35, 52, 78	0
All	All	502/503 (99%)	0.03	10 (1%) 65 65	21, 35, 57, 102	3 (0%)

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	166	ILE	4.4
1	A	1	ALA	4.3
1	A	209	TRP	4.0
1	A	213	ILE	3.9
1	A	215	TYR	3.2
1	A	241	ALA	3.0
1	A	99	PRO	2.2
2	B	136	PRO	2.1
1	A	217	VAL	2.0
2	B	133	TYR	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](#)

There are no oligosaccharides in this entry.

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
9	AH2	B	305	11/11	0.44	0.15	96,115,122,129	0
4	MAN	A	303	11/12	0.50	0.14	97,111,117,119	0
5	FUC	A	304	10/11	0.86	0.10	60,69,72,72	0
3	NAG	B	304	14/15	0.86	0.11	64,73,81,86	0
3	NAG	A	302	14/15	0.90	0.10	52,62,77,84	0
3	NAG	A	301	14/15	0.92	0.08	36,46,49,53	0
8	PG4	B	302	13/13	0.93	0.11	40,51,83,92	0
6	ZN	B	306	1/1	0.94	0.07	98,98,98,98	0
3	NAG	B	303	14/15	0.95	0.07	34,41,44,46	0
6	ZN	A	307	1/1	0.96	0.08	82,82,82,82	0
8	PG4	B	301	13/13	0.96	0.07	27,38,49,53	0
7	CL	A	306	1/1	0.99	0.04	36,36,36,36	0
6	ZN	A	305	1/1	1.00	0.01	34,34,34,34	0

6.5 Other polymers [i](#)

There are no such residues in this entry.