



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 06:33 PM GMT

PDB ID : 1BCS
Title : COMPLEX OF THE WHEAT SERINE CARBOXYPEPTIDASE, CPDW-II,
WITH THE MICROBIAL PEPTIDE ALDEHYDE INHIBITOR, CHYMO-
STATIN, AND ARGININE AT 100 DEGREES KELVIN
Authors : Bullock, T.L.; Remington, S.J.
Deposited on : 1995-11-03
Resolution : 2.08 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

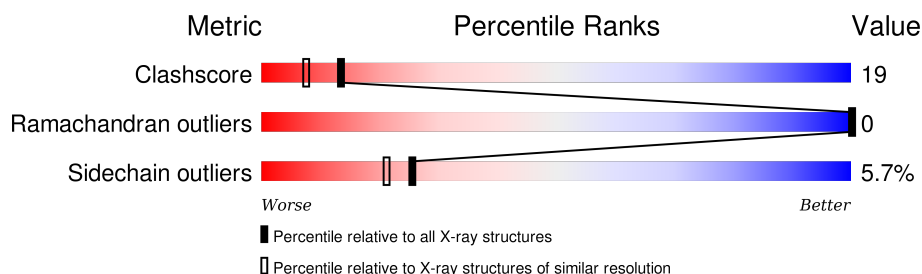
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.08 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))
Clashscore	102246	5101 (2.10-2.06)
Ramachandran outliers	100387	5048 (2.10-2.06)
Sidechain outliers	100360	5049 (2.10-2.06)

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 ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	263	 63% 27% 5% . .
2	B	160	 62% 27% 6% . .
3	C	4	 50% 50%

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
5	NAG	A	1131	X	-	X	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
6	NAG	A	1133	-	-	X	-
6	NDG	A	1134	X	-	-	-
7	NAG	B	2911	-	-	X	-
7	NAG	B	2912	X	-	-	-

2 Entry composition [i](#)

There are 10 unique types of molecules in this entry. The entry contains 3731 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 SERINE CARBOXYPEPTIDASE II.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	255	Total	C	N	O	S	0	0	0
			1999	1280	334	378	7			

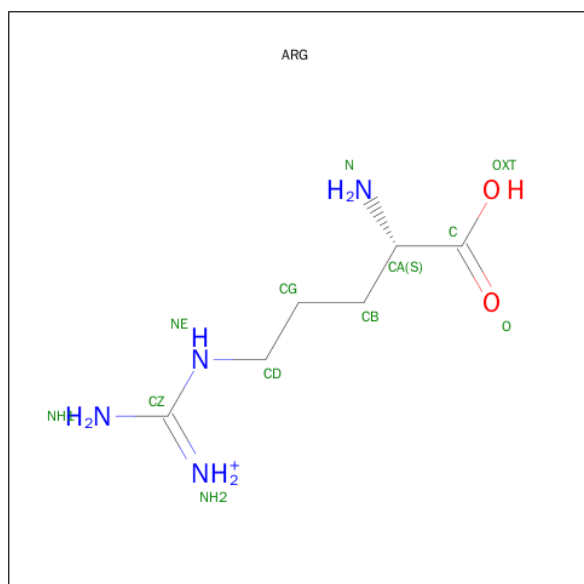
- Molecule 2 is a protein called SERINE CARBOXYPEPTIDASE II.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	153	Total	C	N	O	S	0	0	0
			1202	771	207	218	6			

- Molecule 3 is a protein called CHYMOSTATIN A.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	4	Total	C	N	O	0	0	0
			44	31	7	6			

- Molecule 4 is ARGinine (three-letter code: ARG) (formula: $C_6H_{15}N_4O_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			12	6	4	2		

- Molecule 5 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

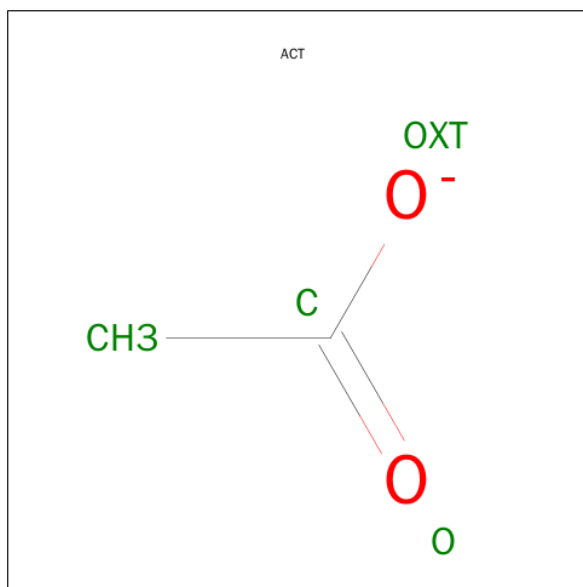
- Molecule 6 is a polymer of unknown type called SUGAR (3-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	3	Total	C	N	O	0	0
			38	22	2	14		

- Molecule 7 is a polymer of unknown type called SUGAR (2-MER).

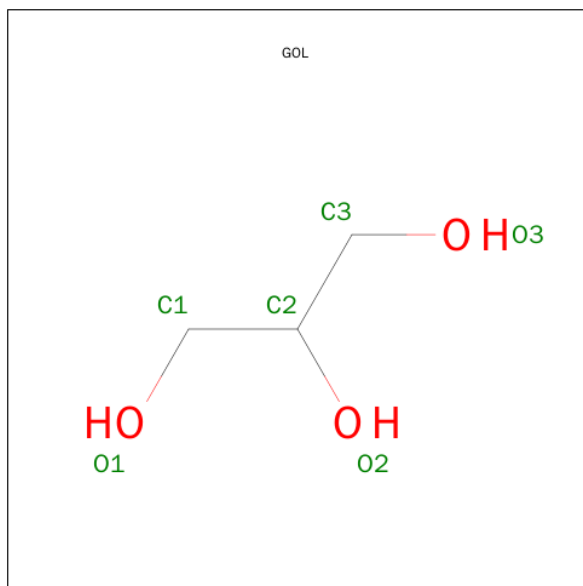
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	B	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 8 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 9 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



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

- Molecule 10 is water.

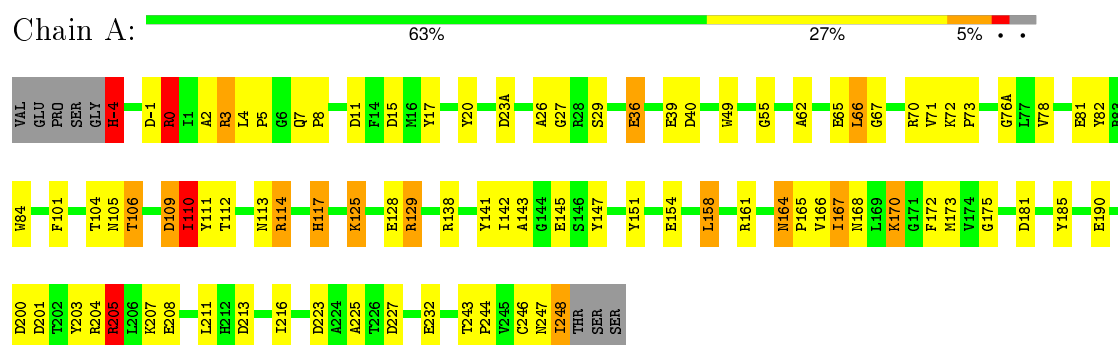
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	B	157	Total 157	O 157	0	0
10	C	1	Total 1	O 1	0	0
10	A	226	Total 226	O 226	0	0

3 Residue-property plots [i](#)

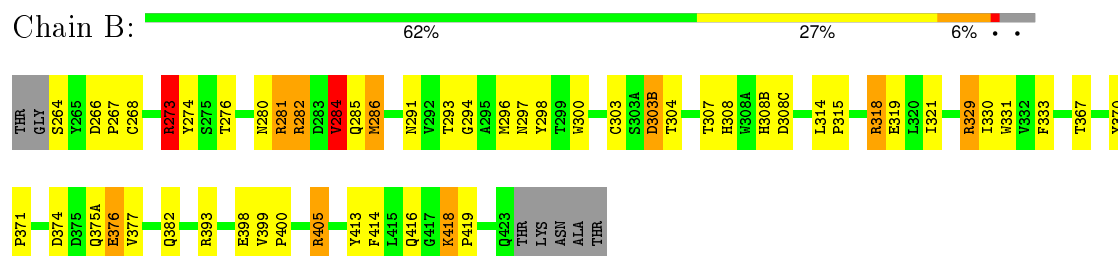
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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 ($\text{RSRZ} > 2$). 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.

Note EDS was not executed.

• Molecule 1: SERINE CARBOXYPEPTIDASE II



• Molecule 2: SERINE CARBOXYPEPTIDASE II



• Molecule 3: CHYMOSTATIN A



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	95.40Å 95.40Å 208.30Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	33.00 – 2.08	Depositor
% Data completeness (in resolution range)	(Not available) (33.00-2.08)	Depositor
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	TNT	Depositor
R, R_{free}	0.174 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3731	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

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, CSI, NAG, PHA, NDG, FUC, ACT

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	1.13	11/2062 (0.5%)	1.63	36/2814 (1.3%)
2	B	1.10	4/1242 (0.3%)	1.83	30/1702 (1.8%)
3	C	1.10	0/19	1.36	0/21
All	All	1.12	15/3323 (0.5%)	1.71	66/4537 (1.5%)

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
3	C	1	0
6	A	1	0
7	B	3	0
All	All	5	0

The worst 5 of 15 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	208	GLU	CD-OE1	8.44	1.34	1.25
2	B	398	GLU	CD-OE2	7.63	1.34	1.25
1	A	81	GLU	CD-OE1	7.49	1.33	1.25
1	A	232	GLU	CD-OE1	6.67	1.32	1.25
1	A	154	GLU	CD-OE2	6.63	1.32	1.25

The worst 5 of 66 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	114	ARG	NE-CZ-NH1	19.18	129.89	120.30
2	B	393	ARG	NE-CZ-NH2	-16.96	111.82	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	329	ARG	NE-CZ-NH1	16.47	128.54	120.30
2	B	393	ARG	NE-CZ-NH1	16.37	128.49	120.30
2	B	329	ARG	NE-CZ-NH2	-16.15	112.22	120.30

All (5) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
6	A	1134	NDG	C2
7	B	2912	NAG	C2,C5,C1
3	C	2	CSI	CB

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	1999	0	1853	74	0
2	B	1202	0	1135	55	0
3	C	44	0	36	3	0
4	A	12	0	12	1	0
5	A	14	0	13	7	0
6	A	38	0	34	9	0
7	B	28	0	24	10	0
8	B	4	0	3	1	0
9	A	6	0	8	1	0
10	A	226	0	0	5	0
10	B	157	0	0	6	0
10	C	1	0	0	0	0
All	All	3731	0	3118	121	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 19.

The worst 5 of 121 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:173:MET:HE1	2:B:414:PHE:HB2	1.42	1.01
1:A:0:ARG:HG3	1:A:17:TYR:CE2	2.08	0.88
1:A:113:ASN:ND2	5:A:1131:NAG:N2	2.26	0.83
1:A:5:PRO:HG2	2:B:284:VAL:HG12	1.64	0.78
2:B:374:ASP:HB3	10:B:3066:HOH:O	1.85	0.76

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	253/263 (96%)	243 (96%)	10 (4%)	0	100	100
2	B	151/160 (94%)	142 (94%)	9 (6%)	0	100	100
3	C	1/4 (25%)	1 (100%)	0	0	100	100
All	All	405/427 (95%)	386 (95%)	19 (5%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	205/215 (95%)	191 (93%)	14 (7%)	20	15
2	B	123/133 (92%)	118 (96%)	5 (4%)	37	36
3	C	2/2 (100%)	2 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	330/350 (94%)	311 (94%)	19 (6%)	25	20

5 of 19 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	170	LYS
1	A	204	ARG
2	B	273	ARG
1	A	167	ILE
2	B	284	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	217	HIS
2	B	308	HIS
1	A	247	ASN
1	A	117	HIS
1	A	233	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is 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	PHA	C	4	1,3	10,11,11	1.61	1 (10%)	10,13,13	2.39	1 (10%)

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	PHA	C	4	1,3	-	0/4/6/6	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	4	PHA	O-C	4.53	1.40	1.19

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	4	PHA	O-C-CA	-7.14	106.91	125.49

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	4	PHA	1	0

5.5 Carbohydrates

5 carbohydrates 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	$\# Z > 2$
6	FUC	A	1132	6	10,10,11	2.79	3 (30%)	14,14,16	3.50	8 (57%)
6	NAG	A	1133	6	14,14,15	1.28	2 (14%)	15,19,21	2.29	7 (46%)
6	NDG	A	1134	6	14,14,15	0.88	0	15,19,21	3.74	4 (26%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	NAG	B	2911	7	14,14,15	0.53	0	15,19,21	2.66	7 (46%)
7	NAG	B	2912	7	14,14,15	1.93	4 (28%)	15,19,21	3.94	8 (53%)

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
6	FUC	A	1132	6	-	0/0/17/20	0/1/1/1
6	NAG	A	1133	6	-	0/6/23/26	0/1/1/1
6	NDG	A	1134	6	1/1/5/7	0/6/23/26	0/1/1/1
7	NAG	B	2911	7	-	0/6/23/26	0/1/1/1
7	NAG	B	2912	7	3/3/5/7	0/6/23/26	0/1/1/1

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	1133	NAG	C1-C2	-2.99	1.48	1.52
6	A	1132	FUC	C2-C3	-2.51	1.49	1.52
6	A	1133	NAG	C3-C2	-2.02	1.47	1.52
6	A	1132	FUC	C4-C3	2.16	1.58	1.52
7	B	2912	NAG	C3-C2	2.98	1.59	1.52

The worst 5 of 34 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	1132	FUC	C2-C3-C4	-7.07	99.04	111.04
7	B	2911	NAG	O6-C6-C5	-4.53	96.38	111.33
6	A	1134	NDG	C4-C3-C2	-4.12	104.83	111.23
7	B	2911	NAG	C8-C7-N2	-3.60	109.22	116.11
6	A	1133	NAG	C3-C2-N2	-3.32	102.62	110.56

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
7	B	2912	NAG	C2
7	B	2912	NAG	C5
7	B	2912	NAG	C1
6	A	1134	NDG	C2

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 19 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	1132	FUC	2	0
6	A	1133	NAG	7	0
6	A	1134	NDG	3	0
7	B	2911	NAG	10	0
7	B	2912	NAG	4	0

5.6 Ligand geometry [i](#)

4 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
5	NAG	A	1131	-	14,14,15	1.04	1 (7%)	15,19,21	2.45	7 (46%)
4	ARG	A	426	-	5,11,11	1.15	1 (20%)	3,13,13	2.96	1 (33%)
9	GOL	A	450	-	5,5,5	0.48	0	5,5,5	0.56	0
8	ACT	B	461	-	1,3,3	4.39	1 (100%)	0,3,3	0.00	-

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	NAG	A	1131	-	1/1/5/7	0/6/23/26	1/1/1/1
4	ARG	A	426	-	-	0/5/11/11	0/0/0/0
9	GOL	A	450	-	-	0/4/4/4	0/0/0/0
8	ACT	B	461	-	-	0/0/0/0	0/0/0/0

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	1131	NAG	O5-C1	-2.26	1.39	1.43
4	A	426	ARG	CD-NE	-2.10	1.42	1.47
8	B	461	ACT	CH3-C	4.39	1.54	1.48

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	1131	NAG	C4-C3-C2	-2.74	106.96	111.23
5	A	1131	NAG	O7-C7-C8	-2.48	117.51	122.06
5	A	1131	NAG	O5-C5-C6	-2.18	102.62	107.35
5	A	1131	NAG	C1-O5-C5	2.06	114.86	112.25
5	A	1131	NAG	C8-C7-N2	3.28	122.39	116.11

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
5	A	1131	NAG	C2

There are no torsion outliers.

All (1) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	1131	NAG	C1-C2-C3-C4-C5-O5

4 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	1131	NAG	7	0
4	A	426	ARG	1	0
9	A	450	GOL	1	0
8	B	461	ACT	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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section will therefore be empty.

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.