Full wwPDB X-ray Structure Validation Report (i)

Jun 17, 2024 – 11:02 AM EDT

PDB ID	:	3SOV
Title	:	The structure of a beta propeller domain in complex with peptide S
Authors	:	Wang, W.; Bourhis, E.; Zhang, Y.; Rouge, L.; Wu, Y.; Franke, Y.; Cochran, A.G.
Deposited on	:	2011-06-30
Resolution	:	1.27 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 (i) 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 (i)) were used in the production of this report:

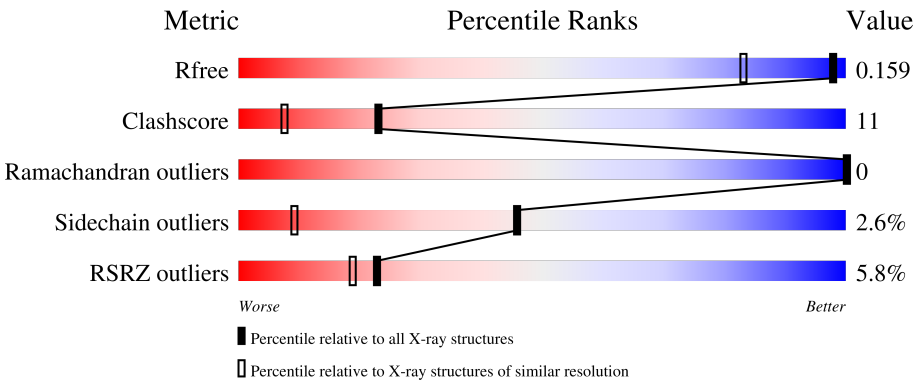
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.27 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	1850 (1.30-1.26)
Clashscore	141614	1926 (1.30-1.26)
Ramachandran outliers	138981	1860 (1.30-1.26)
Sidechain outliers	138945	1859 (1.30-1.26)
RSRZ outliers	127900	1807 (1.30-1.26)

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 <=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	318	4%, 83%, 12%, • •
2	Z	9	44%, 56%, 11%, 11%, 22%

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	A	400	-	-	X	-
3	NAG	A	500	-	-	X	-
4	FUC	A	402	-	-	X	-
4	FUC	A	403	-	-	X	-

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 3050 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 Low-density lipoprotein receptor-related protein 6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	306	2566	1630	434	489	13	0	17	0

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	17	ALA	-	expression tag	UNP O75581
A	18	GLY	-	expression tag	UNP O75581
A	19	SER	-	expression tag	UNP O75581
A	327	ASN	-	expression tag	UNP O75581
A	328	SER	-	expression tag	UNP O75581
A	329	HIS	-	expression tag	UNP O75581
A	330	HIS	-	expression tag	UNP O75581
A	331	HIS	-	expression tag	UNP O75581
A	332	HIS	-	expression tag	UNP O75581
A	333	HIS	-	expression tag	UNP O75581
A	334	HIS	-	expression tag	UNP O75581

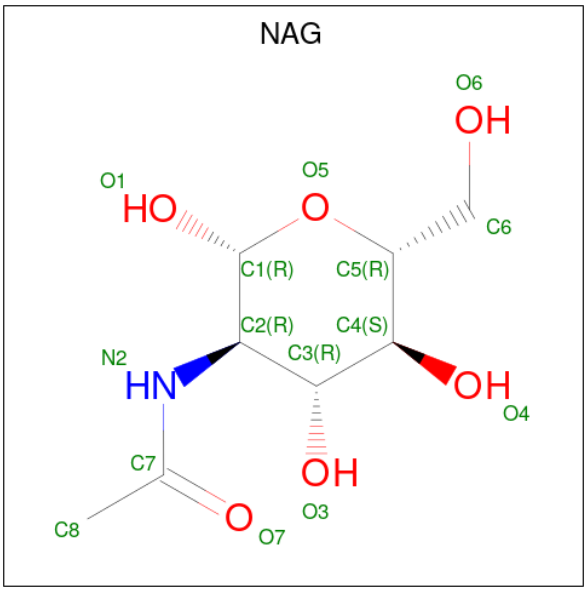
- Molecule 2 is a protein called Sclerostin.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	Z	7	59	38	12	9	0	1	0

There are 2 discrepancies between the modelled and reference sequences:

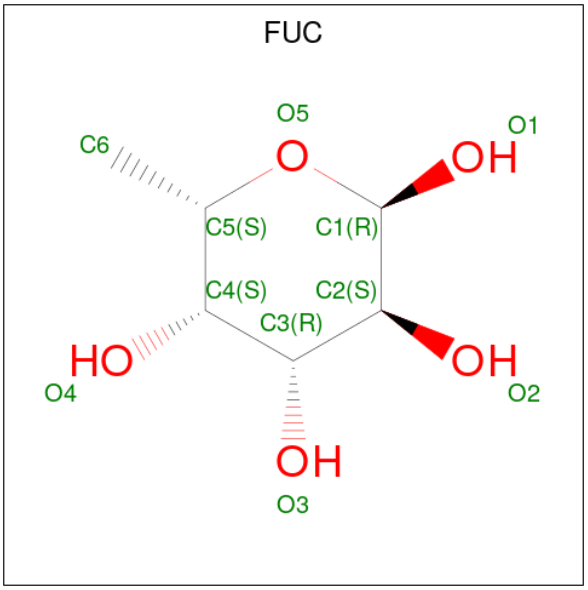
Chain	Residue	Modelled	Actual	Comment	Reference
Z	37	ACE	-	acetylation	UNP Q9BQB4
Z	45	NH2	-	amidation	UNP Q9BQB4

- Molecule 3 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		
3	A	1	14	8	1	5	0	0
			Total	C	N	O		
3	A	1	14	8	1	5	0	0

- Molecule 4 is alpha-L-fucopyranose (three-letter code: FUC) (formula: $C_6H_{12}O_5$).



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

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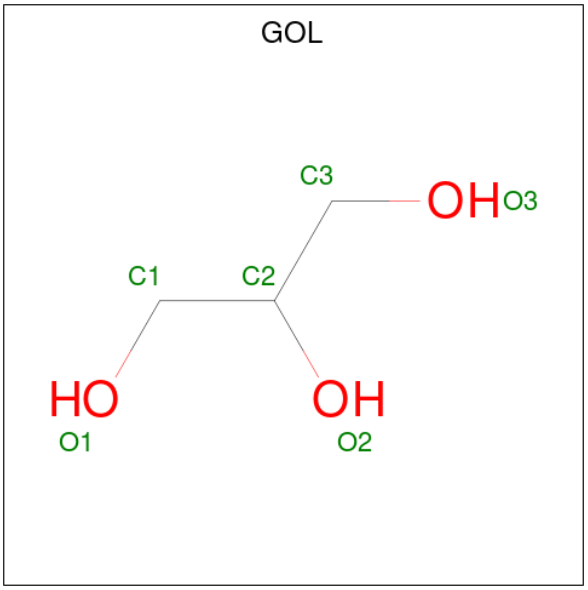
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 10 6 4	0	0
4	A	1	Total C O 10 6 4	0	0

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 6 is water.

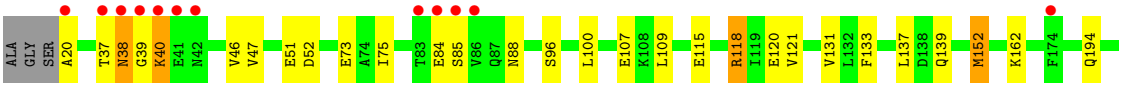
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	334	Total O 334 334	0	2
6	Z	5	Total O 5 5	0	0

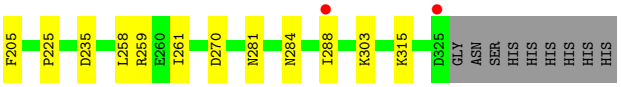
3 Residue-property plots (i)

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: Low-density lipoprotein receptor-related protein 6

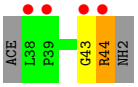
Chain A:





• Molecule 2: Sclerostin

Chain Z:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	103.57Å 47.09Å 68.72Å 90.00° 97.68° 90.00°	Depositor
Resolution (Å)	26.77 – 1.27 43.90 – 1.27	Depositor EDS
% Data completeness (in resolution range)	98.0 (26.77-1.27) 98.0 (43.90-1.27)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.99 (at 1.27Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.6.4_486)	Depositor
R, R_{free}	0.153 , 0.180 0.157 , 0.159	Depositor DCC
R_{free} test set	4310 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å^2)	15.9	Xtriage
Anisotropy	0.116	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 48.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	3050	wwPDB-VP
Average B, all atoms (Å^2)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.40% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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, FUC, 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	0.78	1/2629 (0.0%)	0.85	5/3573 (0.1%)
2	Z	0.72	0/59	0.97	0/79
All	All	0.78	1/2688 (0.0%)	0.85	5/3652 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	107	GLU	CD-OE1	-5.32	1.19	1.25

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	270	ASP	CB-CG-OD2	-6.09	112.82	118.30
1	A	118[A]	ARG	NE-CZ-NH2	-5.71	117.45	120.30
1	A	118[B]	ARG	NE-CZ-NH2	-5.71	117.45	120.30
1	A	152[A]	MET	CG-SD-CE	-5.51	91.39	100.20
1	A	152[B]	MET	CG-SD-CE	-5.51	91.39	100.20

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	2566	0	2464	42	0
2	Z	59	0	65	4	0
3	A	28	0	26	22	0
4	A	40	0	40	18	1
5	A	18	0	24	1	0
6	A	334	0	0	18	1
6	Z	5	0	0	1	0
All	All	3050	0	2619	61	1

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 11.

All (61) 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:281:ASN:HD21	3:A:500:NAG:C1	1.14	1.56
1:A:281:ASN:ND2	3:A:500:NAG:C1	1.85	1.40
3:A:400:NAG:O6	4:A:401:FUC:C1	1.74	1.34
3:A:400:NAG:O4	4:A:403:FUC:C1	1.86	1.24
3:A:500:NAG:O3	4:A:501:FUC:C1	1.94	1.16
3:A:400:NAG:O3	4:A:402:FUC:C1	2.00	1.08
3:A:400:NAG:HO4	4:A:403:FUC:C1	1.66	1.04
1:A:281:ASN:HD21	3:A:500:NAG:C2	1.80	0.94
2:Z:43:GLY:HA2	6:Z:605:HOH:O	1.73	0.87
1:A:20:ALA:HB3	1:A:37:THR:CG2	2.09	0.83
1:A:137:LEU:HD23	6:A:845:HOH:O	1.76	0.83
1:A:281:ASN:ND2	3:A:500:NAG:C2	2.42	0.80
1:A:20:ALA:HB3	1:A:37:THR:HG22	1.64	0.78
1:A:281:ASN:CG	3:A:500:NAG:C1	2.52	0.78
3:A:400:NAG:C4	4:A:403:FUC:C1	2.64	0.74
3:A:400:NAG:C6	4:A:401:FUC:C1	2.66	0.74
3:A:400:NAG:HO3	4:A:402:FUC:C1	1.99	0.73
1:A:194:GLN:NE2	6:A:761:HOH:O	2.21	0.73
1:A:52:ASP:OD2	2:Z:44:ARG:NE	2.26	0.68
1:A:259[A]:ARG:NH2	6:A:834[A]:HOH:O	2.24	0.68
3:A:500:NAG:C3	4:A:501:FUC:C1	2.72	0.68
1:A:235[B]:ASP:OD1	6:A:688:HOH:O	2.16	0.63
1:A:315:LYS:HD2	6:A:717:HOH:O	1.98	0.62
1:A:137:LEU:CD2	6:A:845:HOH:O	2.43	0.61
1:A:85:SER:HB2	6:A:934:HOH:O	2.02	0.60
3:A:400:NAG:O3	4:A:402:FUC:C2	2.51	0.58
1:A:20:ALA:HB3	1:A:37:THR:HG23	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:284:ASN:HB3	4:A:501:FUC:O4	2.06	0.56
3:A:400:NAG:C3	4:A:402:FUC:C1	2.85	0.54
1:A:51:GLU:OE1	2:Z:44:ARG:NH2	2.40	0.54
1:A:38:ASN:HA	1:A:40:LYS:HD3	1.92	0.51
1:A:100[A]:LEU:C	1:A:100[A]:LEU:HD12	2.30	0.51
1:A:194:GLN:CD	6:A:761:HOH:O	2.47	0.51
1:A:120[A]:GLU:CD	6:A:835:HOH:O	2.50	0.50
1:A:118[A]:ARG:NH2	1:A:131:VAL:HG21	2.27	0.50
3:A:400:NAG:O3	4:A:402:FUC:H5	2.13	0.49
1:A:281:ASN:OD1	3:A:500:NAG:C1	2.60	0.48
1:A:40:LYS:H	1:A:40:LYS:CD	2.26	0.47
1:A:39:GLY:HA3	1:A:261[A]:ILE:O	2.15	0.47
1:A:46:VAL:HG12	1:A:47:VAL:HG23	1.96	0.47
3:A:500:NAG:O3	4:A:501:FUC:C2	2.61	0.47
3:A:400:NAG:O3	4:A:402:FUC:C5	2.64	0.46
1:A:96:SER:HB2	1:A:115[A]:GLU:HG3	1.98	0.46
1:A:194:GLN:NE2	6:A:846:HOH:O	2.49	0.45
1:A:118[A]:ARG:NH2	6:A:694:HOH:O	2.46	0.45
1:A:73:GLU:OE1	6:A:604:HOH:O	2.21	0.45
1:A:258[A]:LEU:HD13	1:A:259[A]:ARG:N	2.31	0.45
1:A:162:LYS:HE3	6:A:845:HOH:O	2.17	0.45
3:A:400:NAG:HO4	4:A:402:FUC:H5	1.82	0.45
1:A:139:GLN:NE2	6:A:756:HOH:O	2.46	0.45
3:A:400:NAG:H4	4:A:403:FUC:C1	2.44	0.44
1:A:133:PHE:HE1	1:A:152[B]:MET:CE	2.31	0.44
1:A:288:ILE:O	1:A:288:ILE:HG22	2.17	0.43
1:A:109[B]:LEU:O	1:A:121:VAL:HA	2.19	0.43
4:A:403:FUC:O2	6:A:818:HOH:O	2.22	0.43
1:A:85:SER:CB	6:A:934:HOH:O	2.61	0.42
1:A:75:ILE:HD13	1:A:100[B]:LEU:HD13	2.01	0.42
1:A:235[B]:ASP:OD1	6:A:852:HOH:O	2.22	0.42
1:A:118[A]:ARG:NH1	6:A:933:HOH:O	2.53	0.41
2:Z:44:ARG:HG2	2:Z:44:ARG:HH11	1.86	0.40
1:A:225:PRO:O	5:A:336:GOL:H2	2.22	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:403:FUC:O4	6:A:748:HOH:O[4_444]	2.17	0.03

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	321/318 (101%)	296 (92%)	25 (8%)	0	100	100
2	Z	6/9 (67%)	5 (83%)	1 (17%)	0	100	100
All	All	327/327 (100%)	301 (92%)	26 (8%)	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	281/273 (103%)	275 (98%)	6 (2%)	53	15
2	Z	6/5 (120%)	5 (83%)	1 (17%)	2	0
All	All	287/278 (103%)	280 (98%)	7 (2%)	46	11

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	38	ASN
1	A	40	LYS
1	A	84	GLU
1	A	88	ASN
1	A	205	PHE
1	A	303	LYS
2	Z	44	ARG

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

Mol	Chain	Res	Type
1	A	276	GLN
1	A	281	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

9 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	$\#\|Z\| > 2$
4	FUC	A	402	-	10,10,11	0.63	0	14,14,16	1.40	2 (14%)
4	FUC	A	403	-	10,10,11	1.45	1 (10%)	14,14,16	3.46	12 (85%)
4	FUC	A	501	-	10,10,11	0.68	0	14,14,16	1.94	5 (35%)
3	NAG	A	500	-	14,14,15	0.53	0	17,19,21	1.65	5 (29%)
5	GOL	A	336	-	5,5,5	0.34	0	5,5,5	0.73	0
3	NAG	A	400	-	14,14,15	0.50	0	17,19,21	2.01	3 (17%)
5	GOL	A	337	-	5,5,5	0.52	0	5,5,5	0.78	0
5	GOL	A	338	-	5,5,5	0.25	0	5,5,5	0.58	0
4	FUC	A	401	-	10,10,11	0.55	0	14,14,16	1.26	3 (21%)

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
4	FUC	A	402	-	-	-	0/1/1/1
4	FUC	A	403	-	-	-	0/1/1/1
4	FUC	A	501	-	-	-	0/1/1/1
3	NAG	A	500	-	-	0/6/23/26	0/1/1/1
5	GOL	A	336	-	-	1/4/4/4	-
3	NAG	A	400	-	-	0/6/23/26	0/1/1/1
5	GOL	A	337	-	-	1/4/4/4	-
5	GOL	A	338	-	-	2/4/4/4	-
4	FUC	A	401	-	-	-	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	403	FUC	O2-C2	3.15	1.49	1.43

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	400	NAG	C1-O5-C5	-6.75	103.14	112.19
4	A	403	FUC	C2-C3-C4	5.74	120.96	110.86
4	A	403	FUC	O2-C2-C1	4.90	120.44	109.22
4	A	403	FUC	C1-O5-C5	4.47	123.50	112.97
4	A	403	FUC	O2-C2-C3	4.39	119.24	110.15
4	A	403	FUC	O5-C1-C2	4.19	120.78	110.79
4	A	403	FUC	O4-C4-C5	3.24	116.88	109.74
4	A	501	FUC	C2-C3-C4	-3.21	105.21	110.86
4	A	403	FUC	O5-C5-C6	3.16	114.26	107.40
4	A	501	FUC	C1-C2-C3	3.10	114.16	109.64
4	A	501	FUC	O5-C1-C2	3.10	118.17	110.79
3	A	500	NAG	C6-C5-C4	-2.94	105.81	113.02
4	A	402	FUC	C1-C2-C3	2.86	113.81	109.64
3	A	500	NAG	C1-C2-N2	2.81	114.87	110.43
4	A	403	FUC	C1-C2-C3	-2.77	105.61	109.64
4	A	401	FUC	O5-C5-C4	2.70	114.41	109.55
3	A	500	NAG	O5-C5-C6	2.67	112.85	107.66
3	A	400	NAG	O7-C7-N2	2.59	126.56	121.98
3	A	400	NAG	C8-C7-N2	-2.55	111.89	116.12
4	A	403	FUC	C6-C5-C4	2.51	117.67	113.08

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	A	402	FUC	O5-C1-C2	2.49	116.73	110.79
3	A	500	NAG	O7-C7-C8	-2.43	117.73	122.05
4	A	501	FUC	C1-O5-C5	2.39	118.59	112.97
4	A	501	FUC	O5-C5-C6	-2.36	102.28	107.40
3	A	500	NAG	O7-C7-N2	2.23	125.92	121.98
4	A	403	FUC	O4-C4-C3	2.22	115.61	110.38
4	A	403	FUC	C3-C4-C5	2.22	113.18	109.81
4	A	401	FUC	C6-C5-C4	-2.17	109.12	113.08
4	A	403	FUC	O3-C3-C4	-2.14	105.34	110.38
4	A	401	FUC	O2-C2-C1	-2.07	104.49	109.22

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	338	GOL	O1-C1-C2-C3
5	A	338	GOL	O1-C1-C2-O2
5	A	336	GOL	O2-C2-C3-O3
5	A	337	GOL	O2-C2-C3-O3

There are no ring outliers.

7 monomers are involved in 26 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	402	FUC	7	0
4	A	403	FUC	5	1
4	A	501	FUC	4	0
3	A	500	NAG	9	0
5	A	336	GOL	1	0
3	A	400	NAG	13	0
4	A	401	FUC	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	306/318 (96%)	-0.05	14 (4%)	32	28	11, 18, 38, 56	0
2	Z	7/9 (77%)	2.29	4 (57%)	0	0	16, 24, 50, 57	0
All	All	313/327 (95%)	0.00	18 (5%)	23	19	11, 18, 39, 57	0

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	86	VAL	6.4
1	A	41	GLU	6.0
1	A	288	ILE	4.7
2	Z	38	LEU	4.6
2	Z	44	ARG	4.6
1	A	42	ASN	4.4
2	Z	43	GLY	4.3
1	A	39	GLY	3.9
1	A	325	ASP	3.4
1	A	38	ASN	3.4
1	A	40	LYS	3.1
1	A	174[A]	PHE	2.8
1	A	85	SER	2.8
1	A	84	GLU	2.7
1	A	83	THR	2.6
2	Z	39	PRO	2.5
1	A	20	ALA	2.2
1	A	37	THR	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 monosaccharides 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
3	NAG	A	500	14/15	0.75	0.28	32,35,42,45	0
5	GOL	A	336	6/6	0.78	0.15	36,45,48,48	0
4	FUC	A	403	10/11	0.81	0.14	29,33,39,46	0
4	FUC	A	501	10/11	0.83	0.26	30,33,36,39	0
4	FUC	A	401	10/11	0.83	0.10	25,33,38,44	0
4	FUC	A	402	10/11	0.87	0.14	41,48,51,57	0
3	NAG	A	400	14/15	0.91	0.10	20,24,26,27	0
5	GOL	A	337	6/6	0.92	0.12	17,29,35,35	0
5	GOL	A	338	6/6	0.92	0.17	26,34,47,50	0

6.5 Other polymers (i)

There are no such residues in this entry.