wwPDB X-ray Structure Validation Summary Report (i)

Feb 1, 2016 – 01:45 PM GMT

PDB ID	:	3USU
Title	:	Crystal structure of Butea monosperma seed lectin
Authors	:	Abhilash, J.; Geethanandan, K.; Bharath, S.R.; Sadasivan, C.; Haridas, M.
Deposited on	:	2011-11-24
Resolution	:	2.46 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

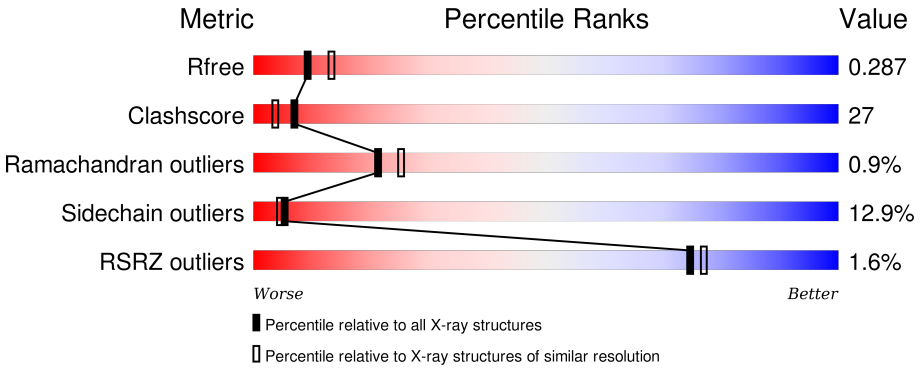
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.46 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}	91344	4776 (2.50-2.42)
Clashscore	102246	1030 (2.48-2.44)
Ramachandran outliers	100387	1024 (2.48-2.44)
Sidechain outliers	100360	1024 (2.48-2.44)
RSRZ outliers	91569	4787 (2.50-2.42)

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 <=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	256	51% 38% 9%
1	C	256	2% 58% 36%
1	E	256	3% 52% 37% 8%
1	G	256	% 52% 37% 8%
2	B	242	59% 34% 6%

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Mol	Chain	Length	Quality of chain
2	D	242	2% 63% 31% 5%
2	F	242	% 58% 35% 7%
2	H	242	2% 60% 34% 6%

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	ABU	A	280	-	-	X	X
5	ABU	B	276	-	-	X	X
5	ABU	C	282	-	-	X	X
5	ABU	D	278	-	-	-	X
5	ABU	E	284	-	-	-	X
5	ABU	E	288	-	-	X	X
5	ABU	F	290	-	-	X	X
5	ABU	G	286	-	-	-	X
7	GOL	D	285	-	-	-	X
8	BMA	B	304	-	-	X	-

2 Entry composition

There are 13 unique types of molecules in this entry. The entry contains 15748 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 Lectin Alpha chain.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	A	250	Total 1892	C 1227	N 296	O 369	0	0	0
1	C	250	Total 1892	C 1227	N 296	O 369	0	0	0
1	E	250	Total 1892	C 1227	N 296	O 369	0	0	0
1	G	250	Total 1892	C 1227	N 296	O 369	0	0	0

- Molecule 2 is a protein called Lectin Beta Chain.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	242	Total 1828	C 1184	N 287	O 357	0	0	0
2	D	242	Total 1828	C 1184	N 287	O 357	0	0	0
2	F	242	Total 1828	C 1184	N 287	O 357	0	0	0
2	H	242	Total 1828	C 1184	N 287	O 357	0	0	0

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	G	1	Total 1	Ca 1	0	0
3	D	1	Total 1	Ca 1	0	0
3	E	1	Total 1	Ca 1	0	0
3	H	1	Total 1	Ca 1	0	0

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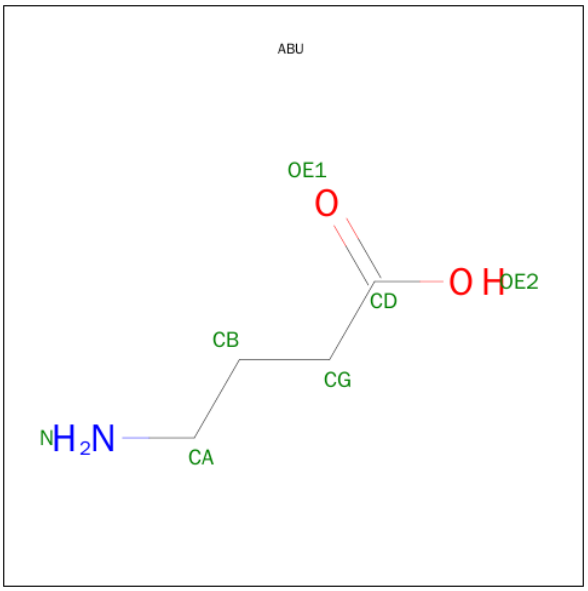
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total Ca 1 1	0	0
3	C	1	Total Ca 1 1	0	0
3	A	1	Total Ca 1 1	0	0
3	F	1	Total Ca 1 1	0	0

- Molecule 4 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	G	1	Total Mn 1 1	0	0
4	D	1	Total Mn 1 1	0	0
4	E	1	Total Mn 1 1	0	0
4	H	1	Total Mn 1 1	0	0
4	B	1	Total Mn 1 1	0	0
4	C	1	Total Mn 1 1	0	0
4	A	1	Total Mn 1 1	0	0
4	F	1	Total Mn 1 1	0	0

- Molecule 5 is GAMMA-AMINO-BUTANOIC ACID (three-letter code: ABU) (formula: $C_4H_9NO_2$).

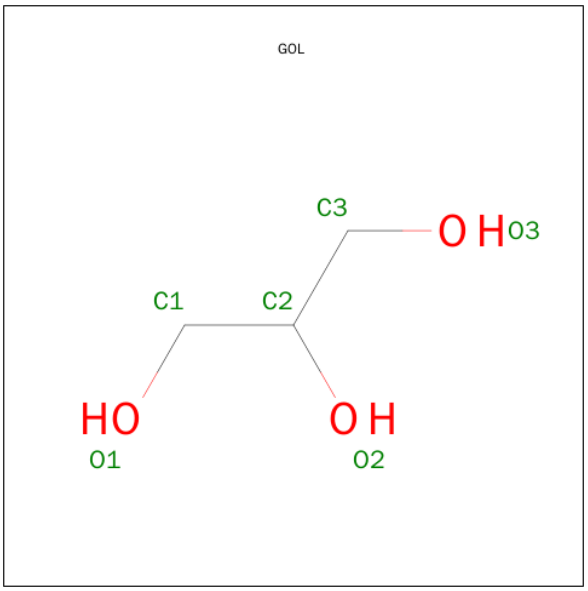


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C N O 7 4 1 2	0	0
5	B	1	Total C N O 7 4 1 2	0	0
5	C	1	Total C N O 7 4 1 2	0	0
5	D	1	Total C N O 7 4 1 2	0	0
5	E	1	Total C N O 7 4 1 2	0	0
5	E	1	Total C N O 7 4 1 2	0	0
5	F	1	Total C N O 7 4 1 2	0	0
5	G	1	Total C N O 7 4 1 2	0	0

- Molecule 6 is a polymer of unknown type called SUGAR (4-MER).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	4	Total C N O 49 28 2 19	0	0
6	C	4	Total C N O 49 28 2 19	0	0
6	E	4	Total C N O 49 28 2 19	0	0

- Molecule 7 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).

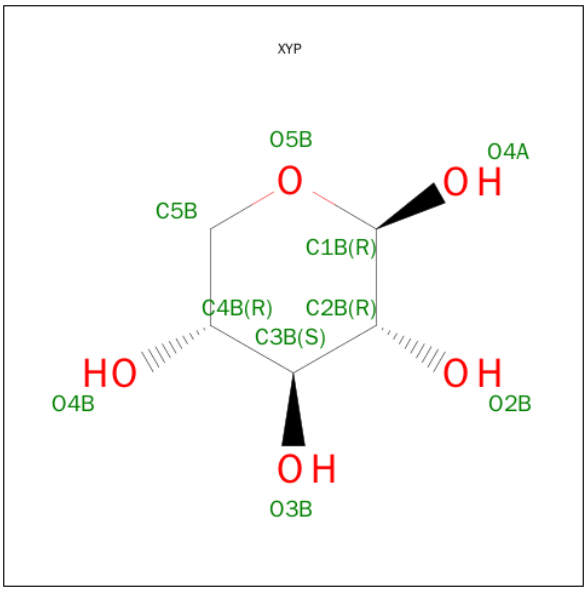


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	1	Total C O 6 3 3	0	0
7	B	1	Total C O 6 3 3	0	0
7	C	1	Total C O 6 3 3	0	0
7	D	1	Total C O 6 3 3	0	0
7	E	1	Total C O 6 3 3	0	0
7	E	1	Total C O 6 3 3	0	0
7	G	1	Total C O 6 3 3	0	0
7	H	1	Total C O 6 3 3	0	0

- Molecule 8 is a polymer of unknown type called SUGAR (5-MER).

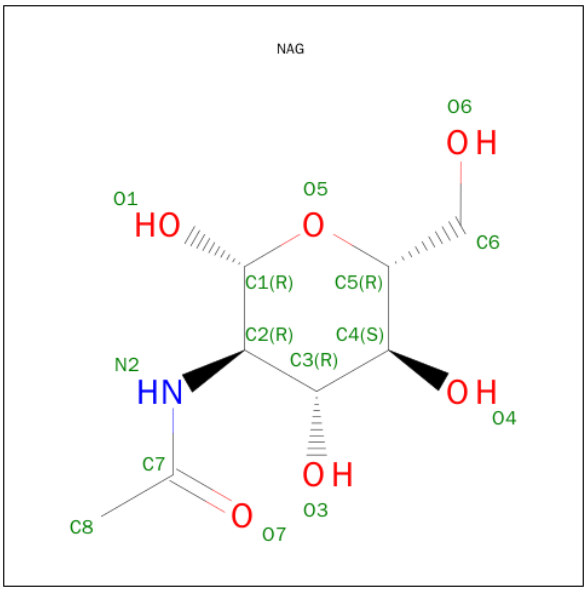
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	B	5	Total C N O 60 34 2 24	0	0

- Molecule 9 is SUGAR (BETA-D-XYLOPYRANOSE) (three-letter code: XYP) (formula: $C_5H_{10}O_5$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	B	1	Total C O 9 5 4	0	0

- Molecule 10 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

- Molecule 11 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
11	G	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 12 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
12	H	2	Total	C	N	O	0	0
			24	14	1	9		

- Molecule 13 is water.

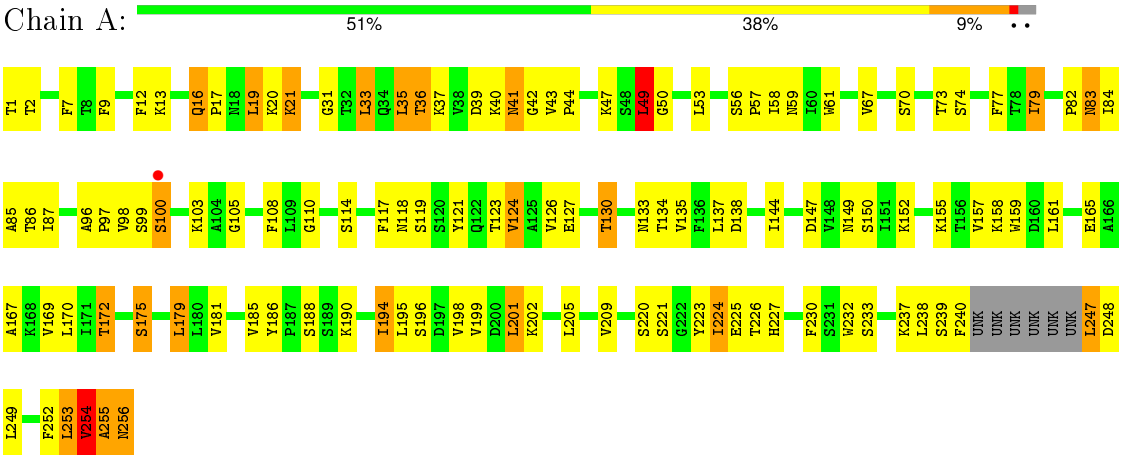
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
13	A	65	Total	O	0	0
			65	65		
13	B	70	Total	O	0	0
			70	70		
13	C	64	Total	O	0	0
			64	64		
13	D	47	Total	O	0	0
			47	47		
13	E	51	Total	O	0	0
			51	51		
13	G	60	Total	O	0	0
			60	60		
13	H	44	Total	O	0	0
			44	44		
13	F	65	Total	O	0	0
			65	65		

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 (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.

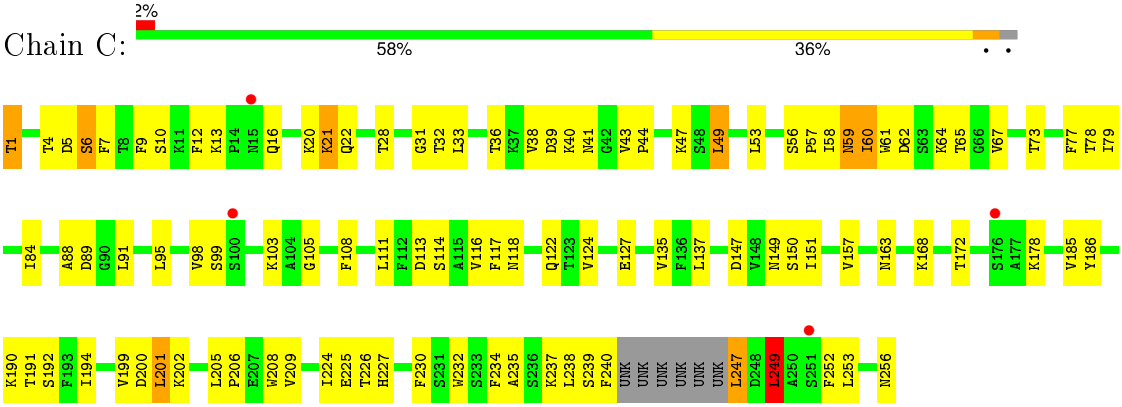
- Molecule 1: Lectin Alpha chain

Chain A:



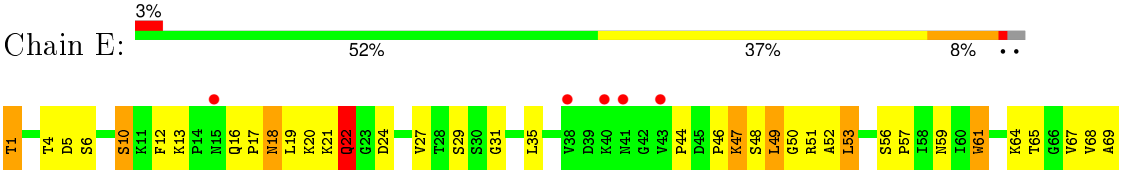
- Molecule 1: Lectin Alpha chain

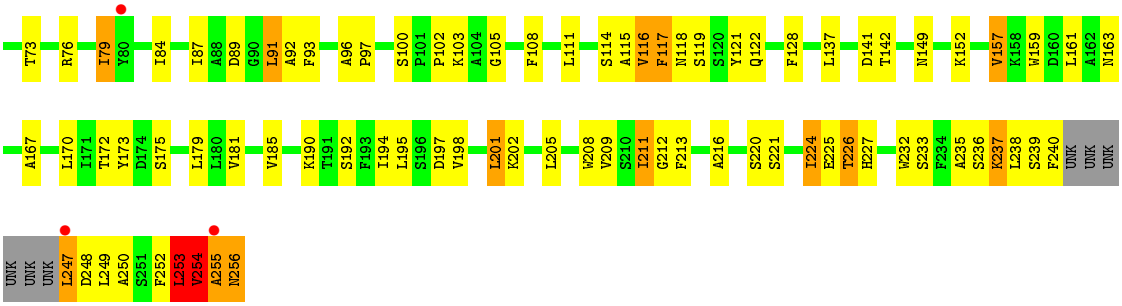
Chain C:



- Molecule 1: Lectin Alpha chain

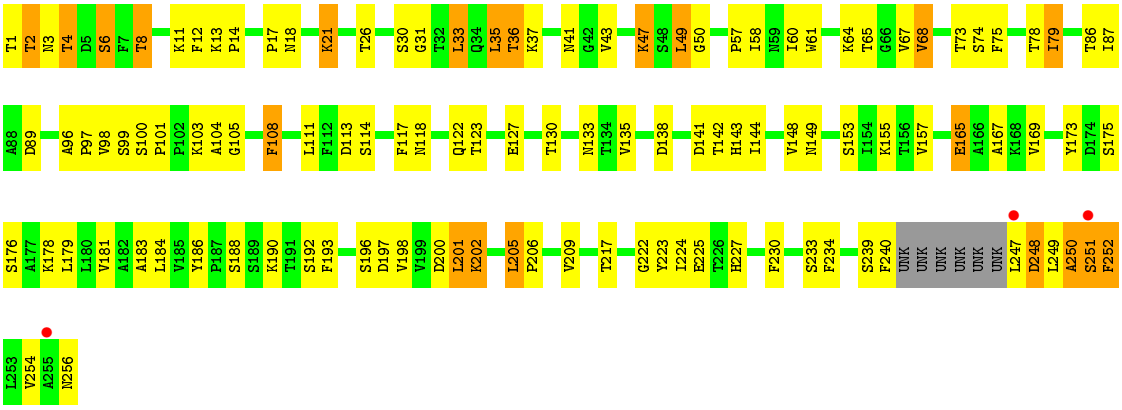
Chain E:





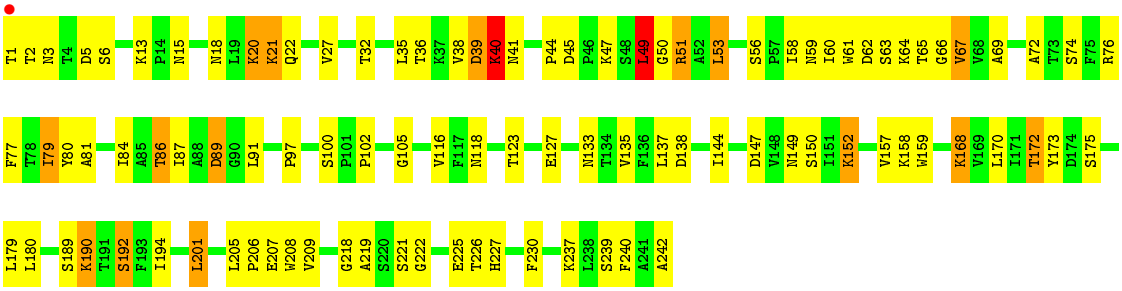
• Molecule 1: Lectin Alpha chain

Chain G:



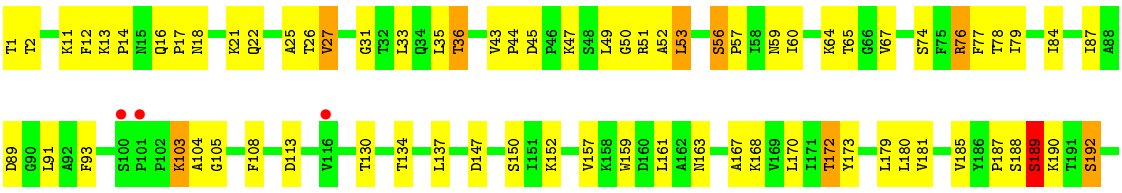
• Molecule 2: Lectin Beta Chain

Chain B:



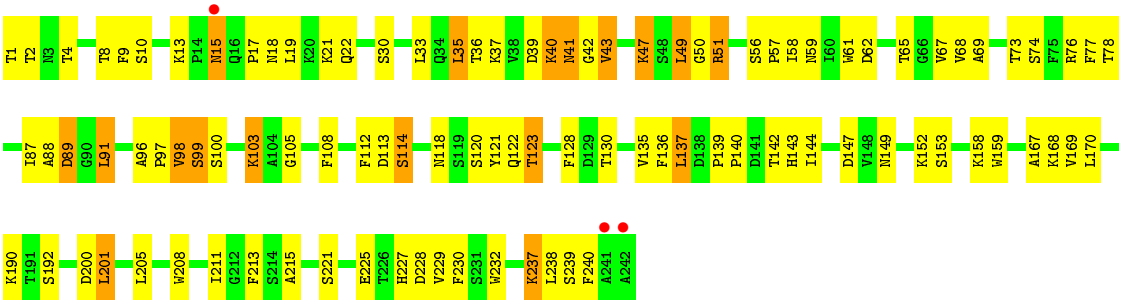
• Molecule 2: Lectin Beta Chain

Chain D:



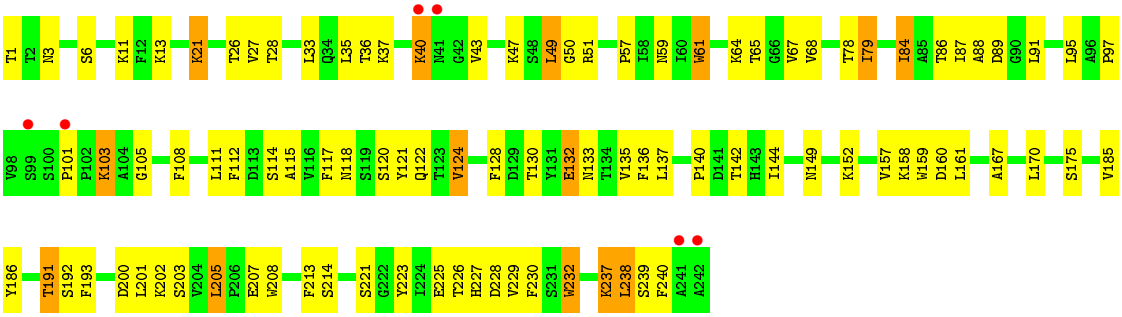
• Molecule 2: Lectin Beta Chain

Chain F:



• Molecule 2: Lectin Beta Chain

Chain H:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	78.45Å 78.91Å 101.85Å 74.30° 76.65° 86.88°	Depositor
Resolution (Å)	69.06 – 2.46 69.06 – 2.46	Depositor EDS
% Data completeness (in resolution range)	94.7 (69.06-2.46) 86.8 (69.06-2.46)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.99 (at 2.45Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.205 , 0.287 0.206 , 0.287	Depositor DCC
R_{free} test set	3944 reflections (5.27%)	DCC
Wilson B-factor (Å^2)	26.1	Xtriage
Anisotropy	0.245	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 45.2	EDS
Estimated twinning fraction	0.022 for -k,-h,-l	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.29$	Xtriage
Outliers	0 of 78775 reflections	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	15748	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 4.94% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: XYP, GOL, BMA, NAG, CA, MN, ABU, MAN, FUC

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	0.90	2/1939 (0.1%)	0.96	0/2646
1	C	0.79	3/1939 (0.2%)	0.91	1/2646 (0.0%)
1	E	0.77	2/1939 (0.1%)	0.89	3/2646 (0.1%)
1	G	0.74	1/1939 (0.1%)	0.89	0/2646
2	B	0.85	1/1875 (0.1%)	0.94	3/2560 (0.1%)
2	D	0.75	2/1875 (0.1%)	0.84	2/2560 (0.1%)
2	F	0.83	2/1875 (0.1%)	0.93	3/2560 (0.1%)
2	H	0.72	2/1875 (0.1%)	0.85	0/2560
All	All	0.80	15/15256 (0.1%)	0.90	12/20824 (0.1%)

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
1	C	0	1
1	E	0	1
All	All	0	3

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	232	TRP	CD2-CE2	5.96	1.48	1.41
2	H	61	TRP	CD2-CE2	5.95	1.48	1.41
1	C	208	TRP	CD2-CE2	5.78	1.48	1.41
1	E	61	TRP	CD2-CE2	5.58	1.48	1.41
2	D	232	TRP	CD2-CE2	5.58	1.48	1.41

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	39	ASP	CB-CG-OD1	7.57	125.11	118.30
1	E	253	LEU	CA-CB-CG	6.04	129.19	115.30
2	B	49	LEU	CA-CB-CG	-5.96	101.60	115.30
1	C	249	LEU	CA-CB-CG	5.89	128.84	115.30
1	E	253	LEU	CB-CG-CD2	-5.72	101.28	111.00

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	98	VAL	Peptide
1	C	247	LEU	Peptide
1	E	22	GLN	Peptide

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	1892	0	1874	128	0
1	C	1892	0	1875	97	0
1	E	1892	0	1875	112	0
1	G	1892	0	1875	114	0
2	B	1828	0	1809	108	0
2	D	1828	0	1810	80	0
2	F	1828	0	1810	96	0
2	H	1828	0	1810	112	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0
3	G	1	0	0	0	0
3	H	1	0	0	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	E	1	0	0	0	0
4	F	1	0	0	0	0
4	G	1	0	0	0	0
4	H	1	0	0	0	0
5	A	7	0	5	5	0
5	B	7	0	5	6	0
5	C	7	0	5	6	0
5	D	7	0	5	1	0
5	E	14	0	10	11	0
5	F	7	0	5	7	0
5	G	7	0	5	1	0
6	A	49	0	43	4	0
6	C	49	0	42	0	0
6	E	49	0	43	1	0
7	A	6	0	8	2	0
7	B	6	0	8	0	0
7	C	6	0	8	1	0
7	D	6	0	8	0	0
7	E	12	0	16	2	0
7	G	6	0	8	0	0
7	H	6	0	8	3	0
8	B	60	0	47	8	0
9	B	9	0	7	5	0
10	D	14	0	12	0	0
11	G	28	0	25	0	0
12	H	24	0	21	0	0
13	A	65	0	0	16	0
13	B	70	0	0	20	0
13	C	64	0	0	13	0
13	D	47	0	0	11	0
13	E	51	0	0	5	0
13	F	65	0	0	13	0
13	G	60	0	0	17	0
13	H	44	0	0	15	0
All	All	15748	0	15082	805	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 27.

The worst 5 of 805 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:H:238:LEU:HG	13:H:261:HOH:O	1.30	1.28
1:G:101:PRO:HD2	13:G:542:HOH:O	1.34	1.23
8:B:304:BMA:O2	9:B:306:XYP:C1B	1.87	1.21
7:H:289:GOL:H2	13:H:411:HOH:O	1.45	1.15
1:A:36:THR:HG21	1:A:227:HIS:HD2	1.04	1.13

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	246/256 (96%)	229 (93%)	12 (5%)	5 (2%)	9	7
1	C	246/256 (96%)	230 (94%)	13 (5%)	3 (1%)	16	17
1	E	246/256 (96%)	228 (93%)	15 (6%)	3 (1%)	16	17
1	G	246/256 (96%)	231 (94%)	12 (5%)	3 (1%)	16	17
2	B	240/242 (99%)	227 (95%)	11 (5%)	2 (1%)	24	28
2	D	240/242 (99%)	224 (93%)	15 (6%)	1 (0%)	39	49
2	F	240/242 (99%)	230 (96%)	9 (4%)	1 (0%)	39	49
2	H	240/242 (99%)	226 (94%)	14 (6%)	0	100	100
All	All	1944/1992 (98%)	1825 (94%)	101 (5%)	18 (1%)	21	25

5 of 18 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	41	ASN
1	A	255	ALA
2	B	40	LYS
1	C	178	LYS
1	E	253	LEU

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	210/210 (100%)	175 (83%)	35 (17%)	3 1
1	C	210/210 (100%)	190 (90%)	20 (10%)	11 12
1	E	210/210 (100%)	173 (82%)	37 (18%)	2 1
1	G	210/210 (100%)	179 (85%)	31 (15%)	4 3
2	B	202/202 (100%)	177 (88%)	25 (12%)	6 5
2	D	202/202 (100%)	181 (90%)	21 (10%)	9 10
2	F	202/202 (100%)	178 (88%)	24 (12%)	6 6
2	H	202/202 (100%)	182 (90%)	20 (10%)	10 10
All	All	1648/1648 (100%)	1435 (87%)	213 (13%)	5 4

5 of 213 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	192	SER
1	E	117	PHE
2	H	37	LYS
2	D	221	SER
1	E	27	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 33 such sidechains are listed below:

Mol	Chain	Res	Type
2	D	227	HIS
1	E	227	HIS
2	H	59	ASN
1	E	18	ASN
1	E	22	GLN

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)

21 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	NAG	A	301	1,6	14,14,15	0.68	0	15,19,21	1.54	3 (20%)
6	FUC	A	302	6	10,10,11	0.71	0	14,14,16	1.78	3 (21%)
6	NAG	A	303	6	14,14,15	0.56	0	15,19,21	2.25	4 (26%)
6	BMA	A	304	6	11,11,12	1.27	2 (18%)	14,15,17	2.10	6 (42%)
8	NAG	B	301	8,2	14,14,15	0.85	1 (7%)	15,19,21	2.49	2 (13%)
8	FUC	B	302	8	10,10,11	0.74	0	14,14,16	1.53	3 (21%)
8	NAG	B	303	8	14,14,15	1.01	1 (7%)	15,19,21	2.03	4 (26%)
8	BMA	B	304	8	11,11,12	2.31	3 (27%)	14,15,17	4.32	6 (42%)
8	MAN	B	305	8	11,11,12	6.15	8 (72%)	14,15,17	3.85	7 (50%)
6	NAG	C	301	1,6	14,14,15	0.55	0	15,19,21	1.33	2 (13%)
6	FUC	C	302	6	10,10,11	4.58	4 (40%)	14,14,16	4.52	6 (42%)
6	NAG	C	303	6	14,14,15	0.56	0	15,19,21	1.52	3 (20%)
6	BMA	C	304	6	11,11,12	0.79	0	14,15,17	1.11	0
6	NAG	E	301	1,6	14,14,15	1.14	2 (14%)	15,19,21	1.57	4 (26%)
6	FUC	E	302	6	10,10,11	0.76	0	14,14,16	1.37	2 (14%)
6	NAG	E	303	6	14,14,15	0.68	0	15,19,21	1.85	4 (26%)
6	BMA	E	304	6	11,11,12	0.79	0	14,15,17	1.45	3 (21%)
11	NAG	G	301	1,11	14,14,15	0.67	0	15,19,21	1.48	2 (13%)
11	NAG	G	303	11	14,14,15	0.87	1 (7%)	15,19,21	2.00	4 (26%)
12	NAG	H	301	12,2	14,14,15	1.34	3 (21%)	15,19,21	2.82	6 (40%)
12	FUC	H	302	12	10,10,11	3.90	3 (30%)	14,14,16	4.11	8 (57%)

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	NAG	A	301	1,6	-	0/6/23/26	0/1/1/1
6	FUC	A	302	6	-	0/0/17/20	0/1/1/1
6	NAG	A	303	6	-	0/6/23/26	0/1/1/1
6	BMA	A	304	6	-	0/2/19/22	0/1/1/1
8	NAG	B	301	8,2	-	0/6/23/26	0/1/1/1
8	FUC	B	302	8	-	0/0/17/20	0/1/1/1
8	NAG	B	303	8	-	0/6/23/26	0/1/1/1
8	BMA	B	304	8	-	0/2/19/22	0/1/1/1
8	MAN	B	305	8	-	0/2/19/22	0/1/1/1
6	NAG	C	301	1,6	-	0/6/23/26	0/1/1/1
6	FUC	C	302	6	-	0/0/17/20	0/1/1/1
6	NAG	C	303	6	-	0/6/23/26	0/1/1/1
6	BMA	C	304	6	-	0/2/19/22	0/1/1/1
6	NAG	E	301	1,6	-	0/6/23/26	0/1/1/1
6	FUC	E	302	6	-	0/0/17/20	0/1/1/1
6	NAG	E	303	6	-	0/6/23/26	0/1/1/1
6	BMA	E	304	6	-	0/2/19/22	0/1/1/1
11	NAG	G	301	1,11	-	0/6/23/26	0/1/1/1
11	NAG	G	303	11	-	0/6/23/26	0/1/1/1
12	NAG	H	301	12,2	-	0/6/23/26	0/1/1/1
12	FUC	H	302	12	-	0/0/17/20	0/1/1/1

The worst 5 of 28 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	C	302	FUC	C2-C3	-13.52	1.34	1.52
8	B	305	MAN	O5-C5	-11.05	1.19	1.43
8	B	305	MAN	C2-C3	-9.96	1.38	1.52
12	H	302	FUC	C4-C5	-7.84	1.36	1.52
8	B	305	MAN	C1-C2	-6.58	1.36	1.52

The worst 5 of 82 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
8	B	305	MAN	O3-C3-C4	-6.38	95.97	110.34
12	H	302	FUC	O3-C3-C2	-6.33	98.57	110.00
8	B	303	NAG	O4-C4-C3	-5.00	99.08	110.34
8	B	305	MAN	C3-C4-C5	-4.89	101.67	110.20
12	H	302	FUC	O4-C4-C5	-4.87	98.41	109.84

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

9 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	301	NAG	2	0
6	A	302	FUC	1	0
6	A	303	NAG	2	0
6	A	304	BMA	1	0
8	B	301	NAG	1	0
8	B	304	BMA	7	0
8	B	305	MAN	2	0
6	E	302	FUC	1	0
6	E	303	NAG	1	0

5.6 Ligand geometry (i)

Of 34 ligands modelled in this entry, 16 are monoatomic - leaving 18 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	$\#\|Z\| > 2$
7	GOL	A	277	-	5,5,5	0.29	0	5,5,5	0.57	0
5	ABU	A	280	-	3,6,6	0.33	0	3,6,6	0.46	0
5	ABU	B	276	-	3,6,6	0.42	0	3,6,6	0.29	0
7	GOL	B	281	-	5,5,5	0.35	0	5,5,5	0.84	0
9	XYP	B	306	-	9,9,10	2.45	3 (33%)	12,12,14	6.50	7 (58%)
5	ABU	C	282	-	3,6,6	0.29	0	3,6,6	0.16	0
7	GOL	C	283	-	5,5,5	0.37	0	5,5,5	0.65	0
5	ABU	D	278	-	3,6,6	0.26	0	3,6,6	0.68	0
7	GOL	D	285	-	5,5,5	0.32	0	5,5,5	0.62	0
10	NAG	D	301	2	14,14,15	1.81	3 (21%)	15,19,21	2.09	4 (26%)
7	GOL	E	279	-	5,5,5	0.32	0	5,5,5	1.12	1 (20%)
5	ABU	E	284	-	3,6,6	0.63	0	3,6,6	0.50	0
5	ABU	E	288	-	3,6,6	0.18	0	3,6,6	0.51	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
7	GOL	E	291	-	5,5,5	0.42	0	5,5,5	0.58	0
5	ABU	F	290	-	3,6,6	0.43	0	3,6,6	1.35	1 (33%)
5	ABU	G	286	-	3,6,6	0.39	0	3,6,6	0.33	0
7	GOL	G	287	-	5,5,5	0.29	0	5,5,5	0.30	0
7	GOL	H	289	-	5,5,5	0.32	0	5,5,5	0.44	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
7	GOL	A	277	-	-	0/4/4/4	0/0/0/0
5	ABU	A	280	-	-	0/2/4/4	0/0/0/0
5	ABU	B	276	-	-	0/2/4/4	0/0/0/0
7	GOL	B	281	-	-	0/4/4/4	0/0/0/0
9	XYP	B	306	-	-	0/0/14/17	0/1/1/1
5	ABU	C	282	-	-	0/2/4/4	0/0/0/0
7	GOL	C	283	-	-	0/4/4/4	0/0/0/0
5	ABU	D	278	-	-	0/2/4/4	0/0/0/0
7	GOL	D	285	-	-	0/4/4/4	0/0/0/0
10	NAG	D	301	2	-	0/6/23/26	0/1/1/1
7	GOL	E	279	-	-	0/4/4/4	0/0/0/0
5	ABU	E	284	-	-	0/2/4/4	0/0/0/0
5	ABU	E	288	-	-	0/2/4/4	0/0/0/0
7	GOL	E	291	-	-	0/4/4/4	0/0/0/0
5	ABU	F	290	-	-	0/2/4/4	0/0/0/0
5	ABU	G	286	-	-	0/2/4/4	0/0/0/0
7	GOL	G	287	-	-	0/4/4/4	0/0/0/0
7	GOL	H	289	-	-	0/4/4/4	0/0/0/0

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	D	301	NAG	C1-C2	-4.69	1.46	1.52
10	D	301	NAG	C3-C2	-3.63	1.43	1.52
10	D	301	NAG	C2-N2	2.65	1.51	1.46
9	B	306	XYP	C5B-C4B	2.78	1.58	1.52
9	B	306	XYP	C4B-C3B	3.01	1.56	1.52

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
9	B	306	XYP	O5B-C1B-C2B	-6.99	97.24	110.31
9	B	306	XYP	O4B-C4B-C3B	-6.00	98.05	110.12
9	B	306	XYP	O4B-C4B-C5B	-4.88	99.42	109.21
10	D	301	NAG	C2-N2-C7	-2.83	119.41	123.04
9	B	306	XYP	O3B-C3B-C2B	-2.59	105.32	110.00

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

13 monomers are involved in 50 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	277	GOL	2	0
5	A	280	ABU	5	0
5	B	276	ABU	6	0
9	B	306	XYP	5	0
5	C	282	ABU	6	0
7	C	283	GOL	1	0
5	D	278	ABU	1	0
7	E	279	GOL	2	0
5	E	284	ABU	3	0
5	E	288	ABU	8	0
5	F	290	ABU	7	0
5	G	286	ABU	1	0
7	H	289	GOL	3	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

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^{th} 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	250/256 (97%)	0.03	1 (0%)	93	93	12, 20, 30, 48	1 (0%)
1	C	250/256 (97%)	0.02	4 (1%)	74	77	12, 21, 39, 63	0
1	E	250/256 (97%)	0.26	8 (3%)	51	54	14, 24, 40, 59	0
1	G	250/256 (97%)	0.01	3 (1%)	81	83	14, 22, 35, 52	0
2	B	242/242 (100%)	-0.01	1 (0%)	93	93	11, 18, 26, 35	2 (0%)
2	D	242/242 (100%)	0.16	5 (2%)	67	70	15, 26, 41, 58	0
2	F	242/242 (100%)	-0.09	3 (1%)	81	83	14, 19, 28, 50	1 (0%)
2	H	242/242 (100%)	0.08	6 (2%)	61	63	17, 26, 39, 55	0
All	All	1968/1992 (98%)	0.06	31 (1%)	74	77	11, 22, 38, 63	4 (0%)

The worst 5 of 31 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	255	ALA	6.0
2	H	241	ALA	4.8
1	E	247	LEU	4.5
2	F	241	ALA	4.3
2	D	242	ALA	4.0

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

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

6.3 Carbohydrates

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains.

The B-factors column lists the minimum, median, 95^{th} 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	LLDF	B-factors(Å^2)	Q<0.9
6	FUC	A	302	10/11	0.95	0.18	0.45	33,35,37,37	0
6	NAG	E	301	14/15	0.92	0.15	0.36	24,26,28,30	0
6	NAG	C	301	14/15	0.90	0.13	-0.70	28,32,33,35	0
6	NAG	A	301	14/15	0.95	0.14	-0.72	26,29,31,32	0
8	NAG	B	301	14/15	0.93	0.13	-1.44	20,22,25,25	0
12	FUC	H	302	10/11	0.77	0.27	-	60,63,68,70	0
8	FUC	B	302	10/11	0.94	0.14	-	25,27,29,30	0
6	BMA	A	304	11/12	0.59	0.26	-	39,42,44,46	0
8	MAN	B	305	11/12	0.83	0.23	-	39,41,44,45	0
6	BMA	E	304	11/12	0.72	0.20	-	42,46,48,49	0
6	BMA	C	304	11/12	0.79	0.15	-	42,46,48,48	0
8	NAG	B	303	14/15	0.97	0.12	-	26,28,31,32	0
11	NAG	G	303	14/15	0.70	0.33	-	60,70,79,81	0
6	NAG	A	303	14/15	0.93	0.12	-	32,33,36,37	0
11	NAG	G	301	14/15	0.89	0.20	-	44,52,59,60	0
8	BMA	B	304	11/12	0.80	0.16	-	34,38,39,42	0
6	FUC	E	302	10/11	0.93	0.13	-	28,30,32,32	0
12	NAG	H	301	14/15	0.88	0.14	-	40,46,48,55	0
6	FUC	C	302	10/11	0.95	0.10	-	32,34,35,36	0
6	NAG	E	303	14/15	0.94	0.11	-	32,34,38,40	0
6	NAG	C	303	14/15	0.89	0.17	-	36,39,42,42	0

6.4 Ligands

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95^{th} 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	LLDF	B-factors(Å^2)	Q<0.9
5	ABU	F	290	7/7	0.93	0.30	9.06	14,16,20,22	0
5	ABU	E	288	7/7	0.91	0.40	9.04	32,36,38,38	0
5	ABU	D	278	7/7	0.92	0.29	8.10	29,30,33,35	0
5	ABU	C	282	7/7	0.93	0.30	5.44	29,30,33,34	0
5	ABU	B	276	7/7	0.92	0.31	4.91	27,30,34,35	0
5	ABU	G	286	7/7	0.95	0.27	3.21	31,33,35,37	0
5	ABU	E	284	7/7	0.88	0.26	3.18	25,28,33,33	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
7	GOL	D	285	6/6	0.90	0.20	2.55	32,33,33,34	0
5	ABU	A	280	7/7	0.95	0.21	2.16	22,24,27,28	0
7	GOL	E	279	6/6	0.94	0.19	1.40	31,32,33,35	0
7	GOL	A	277	6/6	0.91	0.18	1.02	30,33,34,36	0
7	GOL	C	283	6/6	0.94	0.18	0.47	25,25,26,26	0
7	GOL	H	289	6/6	0.89	0.16	0.23	29,31,31,34	0
7	GOL	G	287	6/6	0.94	0.15	-0.08	29,29,30,31	0
7	GOL	B	281	6/6	0.95	0.14	-0.67	20,21,22,23	0
7	GOL	E	291	6/6	0.93	0.13	-1.00	29,29,31,33	0
3	CA	H	272	1/1	0.96	0.11	-1.52	30,30,30,30	0
3	CA	C	266	1/1	0.99	0.11	-1.80	19,19,19,19	0
4	MN	C	267	1/1	0.99	0.09	-2.67	20,20,20,20	0
4	MN	H	273	1/1	0.98	0.09	-2.83	23,23,23,23	0
3	CA	B	260	1/1	0.99	0.10	-3.10	15,15,15,15	0
3	CA	A	264	1/1	0.98	0.09	-3.34	19,19,19,19	0
3	CA	E	262	1/1	0.99	0.06	-3.82	20,20,20,20	0
3	CA	D	268	1/1	0.97	0.08	-4.04	31,31,31,31	0
4	MN	A	265	1/1	1.00	0.09	-4.28	13,13,13,13	0
3	CA	G	270	1/1	0.98	0.05	-4.52	17,17,17,17	0
3	CA	F	274	1/1	0.96	0.07	-4.73	23,23,23,23	0
4	MN	E	263	1/1	0.97	0.06	-5.57	25,25,25,25	0
4	MN	B	261	1/1	0.99	0.07	-6.14	13,13,13,13	0
4	MN	D	269	1/1	0.99	0.04	-7.09	38,38,38,38	0
4	MN	F	275	1/1	0.99	0.07	-8.79	21,21,21,21	0
4	MN	G	271	1/1	1.00	0.05	-8.83	19,19,19,19	0
10	NAG	D	301	14/15	0.75	0.23	-	50,56,59,60	0
9	XYP	B	306	9/10	0.85	0.17	-	41,41,43,43	0

6.5 Other polymers (i)

There are no such residues in this entry.