



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 21, 2017 – 10:07 AM EDT

PDB ID : 5DG1
Title : Sugar binding protein - human galectin-2
Authors : Su, J.Y.; Si, Y.L.
Deposited on : unknown
Resolution : 3.20 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

<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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20029824
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : rb-20029824

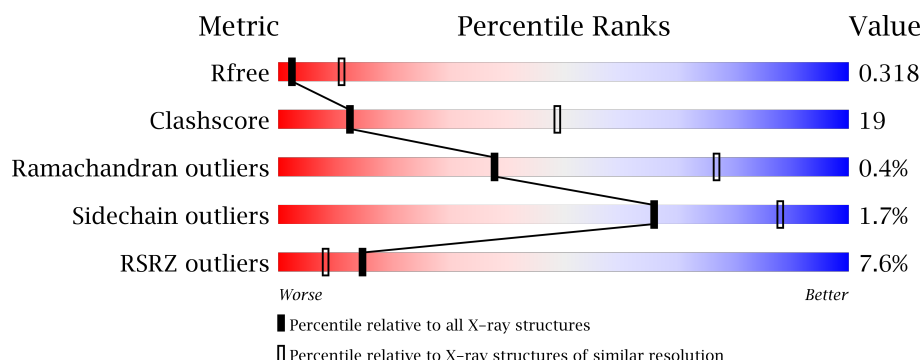
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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}	100719	1015 (3.22-3.18)
Clashscore	112137	1009 (3.20-3.20)
Ramachandran outliers	110173	1118 (3.22-3.18)
Sidechain outliers	110143	1117 (3.22-3.18)
RSRZ outliers	101464	1020 (3.22-3.18)

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.

Mol	Chain	Length	Quality of chain
1	A	135	<div> <div>2%</div> <div>64%</div> <div>31%</div> <div>..</div> </div>
1	B	135	<div> <div>22%</div> <div>51%</div> <div>39%</div> <div>6%</div> <div>...</div> </div>
1	C	135	<div> <div>0%</div> <div>74%</div> <div>22%</div> <div>.</div> </div>
1	D	135	<div> <div>0%</div> <div>70%</div> <div>24%</div> <div>..</div> </div>
1	H	135	<div> <div>8%</div> <div>73%</div> <div>21%</div> <div>..</div> </div>

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Mol	Chain	Length	Quality of chain
1	I	135	

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
2	GAL	C	201	-	-	-	X
2	GAL	H	201	-	-	-	X
2	GAL	I	201	-	-	X	X
3	BGC	C	202	-	-	-	X
3	BGC	H	202	-	-	X	X
3	BGC	I	202	-	-	-	X

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5945 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 Galectin-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	129	Total	C	N	O	S	0	0	0
			992	622	171	194	5			
1	B	130	Total	C	N	O	S	0	0	0
			918	581	161	173	3			
1	C	130	Total	C	N	O	S	0	0	0
			1004	630	171	198	5			
1	D	129	Total	C	N	O	S	0	0	0
			1000	628	169	198	5			
1	H	129	Total	C	N	O	S	0	0	0
			978	614	170	190	4			
1	I	129	Total	C	N	O	S	0	0	0
			984	622	167	190	5			

There are 18 discrepancies between the modelled and reference sequences:

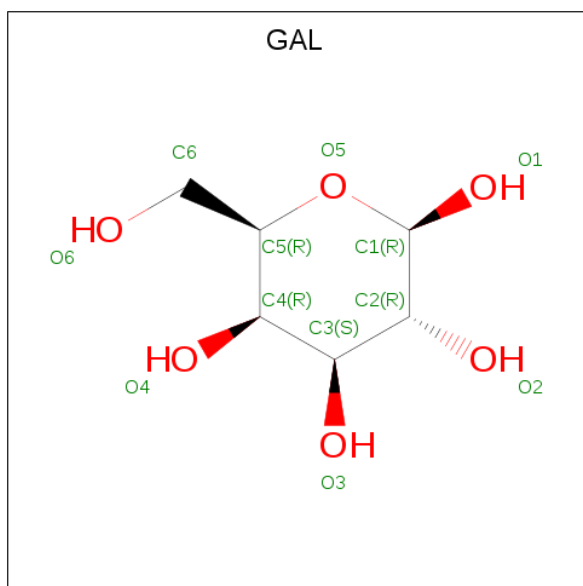
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	expression tag	UNP P05162
A	2	SER	-	expression tag	UNP P05162
A	3	HIS	-	expression tag	UNP P05162
B	1	GLY	-	expression tag	UNP P05162
B	2	SER	-	expression tag	UNP P05162
B	3	HIS	-	expression tag	UNP P05162
C	1	GLY	-	expression tag	UNP P05162
C	2	SER	-	expression tag	UNP P05162
C	3	HIS	-	expression tag	UNP P05162
D	1	GLY	-	expression tag	UNP P05162
D	2	SER	-	expression tag	UNP P05162
D	3	HIS	-	expression tag	UNP P05162
H	1	GLY	-	expression tag	UNP P05162
H	2	SER	-	expression tag	UNP P05162
H	3	HIS	-	expression tag	UNP P05162
I	1	GLY	-	expression tag	UNP P05162
I	2	SER	-	expression tag	UNP P05162

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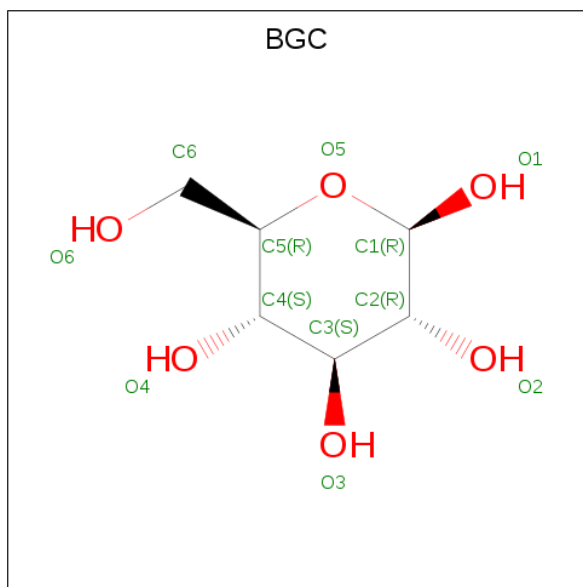
Chain	Residue	Modelled	Actual	Comment	Reference
I	3	HIS	-	expression tag	UNP P05162

- Molecule 2 is BETA-D-GALACTOSE (three-letter code: GAL) (formula: $C_6H_{12}O_6$).



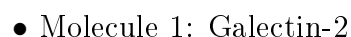
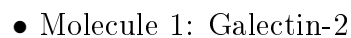
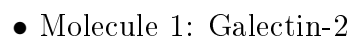
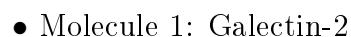
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	C	1	Total	C	O	0	0
			11	6	5		
2	H	1	Total	C	O	0	0
			11	6	5		
2	I	1	Total	C	O	0	0
			11	6	5		

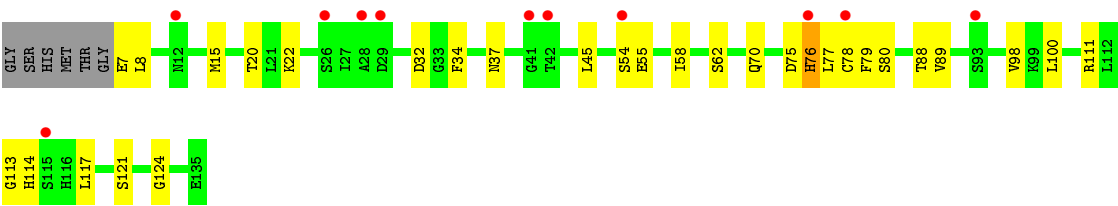
- Molecule 3 is BETA-D-GLUCOSE (three-letter code: BGC) (formula: $C_6H_{12}O_6$).



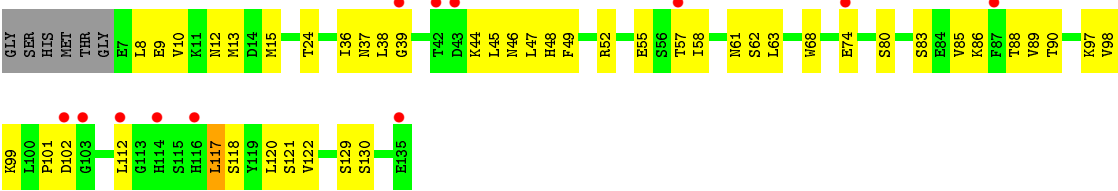
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	C	1	Total	C	O	0	0
			12	6	6		
3	H	1	Total	C	O	0	0
			12	6	6		
3	I	1	Total	C	O	0	0
			12	6	6		

- Molecule 1: Galectin-2





● Molecule 1: Galectin-2



4 Data and refinement statistics

Property	Value	Source
Space group	P 2 ₁ 2 ₁ 2 ₁	Depositor
Cell constants a, b, c, α , β , γ	38.50Å 106.78Å 182.11Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.06 – 3.20 46.06 – 3.20	Depositor EDS
% Data completeness (in resolution range)	99.1 (46.06-3.20) 96.5 (46.06-3.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.25 (at 3.19Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.297 , 0.321 0.297 , 0.318	Depositor DCC
R_{free} test set	1309 reflections (11.51%)	DCC
Wilson B-factor (Å ²)	46.3	Xtriage
Anisotropy	0.747	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 76.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	5945	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 43.38 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 1.7783e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² Theoretical 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: BGC, GAL

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	0.45	1/1014 (0.1%)	0.51	1/1365 (0.1%)
1	B	0.44	2/937 (0.2%)	0.72	2/1257 (0.2%)
1	C	0.25	0/1025	0.42	0/1377
1	D	0.28	0/1020	0.42	0/1370
1	H	0.26	0/998	0.43	0/1341
1	I	0.32	0/1006	0.48	0/1354
All	All	0.34	3/6000 (0.1%)	0.51	3/8064 (0.0%)

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	B	0	3
1	C	0	1
1	H	0	3
1	I	0	1
All	All	0	8

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	101	PRO	N-CD	5.20	1.55	1.47
1	B	26	SER	C-N	5.16	1.46	1.34
1	A	81	PRO	N-CD	5.08	1.54	1.47

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	100	LEU	C-N-CD	5.71	140.39	128.40
1	A	80	SER	C-N-CD	5.53	140.00	128.40
1	B	26	SER	O-C-N	5.03	130.74	122.70

There are no chirality outliers.

All (8) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	118	SER	Peptide
1	B	69	GLY	Peptide
1	B	85	VAL	Peptide
1	C	112	LEU	Peptide
1	H	75	ASP	Peptide
1	H	76	HIS	Peptide
1	H	78	CYS	Peptide
1	I	102	ASP	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	992	0	938	43	0
1	B	918	0	821	51	3
1	C	1004	0	962	22	0
1	D	1000	0	965	25	0
1	H	978	0	931	44	0
1	I	984	0	936	38	1
2	C	11	0	10	4	0
2	H	11	0	10	1	0
2	I	11	0	10	5	1
3	C	12	0	10	0	0
3	H	12	0	10	22	0
3	I	12	0	10	0	1
All	All	5945	0	5613	216	3

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.

All (216) 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:H:55:GLU:CG	3:H:202:BGC:H5	1.73	1.17
1:H:55:GLU:HG2	3:H:202:BGC:C5	1.74	1.15
1:B:119:TYR:HB3	1:B:120:LEU:HA	1.16	1.14
1:H:55:GLU:HG2	3:H:202:BGC:H5	1.16	1.14
1:H:113:GLY:HA2	1:H:114:HIS:HB2	1.11	1.08
1:H:55:GLU:HA	3:H:202:BGC:H6C2	1.43	1.00
1:H:55:GLU:CB	3:H:202:BGC:H5	1.90	0.99
1:H:113:GLY:HA2	1:H:114:HIS:CB	1.90	0.97
1:B:119:TYR:HB3	1:B:120:LEU:CA	1.96	0.95
1:B:51:PRO:HA	1:B:58:ILE:HA	1.51	0.93
1:B:113:GLY:O	1:B:114:HIS:HB2	1.70	0.92
1:A:12:ASN:O	1:D:8:LEU:HD23	1.71	0.91
1:B:123:ARG:HG3	1:B:123:ARG:HH11	1.38	0.88
1:C:35:VAL:HB	1:C:123:ARG:HB3	1.56	0.87
1:B:76:HIS:O	1:B:76:HIS:ND1	2.09	0.85
1:H:55:GLU:HA	3:H:202:BGC:C6	2.07	0.84
1:A:8:LEU:HD22	1:A:128:MET:CE	2.11	0.79
1:H:55:GLU:CA	3:H:202:BGC:H6C2	2.13	0.77
1:A:8:LEU:HD22	1:A:128:MET:HE2	1.66	0.77
1:B:96:PHE:HE1	1:B:117:LEU:HD21	1.49	0.77
1:H:55:GLU:HG2	3:H:202:BGC:C6	2.14	0.77
1:I:8:LEU:HD12	1:I:9:GLU:H	1.49	0.77
1:I:8:LEU:HD12	1:I:9:GLU:N	1.99	0.76
1:B:119:TYR:CB	1:B:120:LEU:HA	2.03	0.76
1:B:34:PHE:O	1:B:51:PRO:HD2	1.87	0.74
1:H:55:GLU:HA	3:H:202:BGC:C5	2.18	0.74
1:A:7:GLU:HG3	1:A:8:LEU:H	1.52	0.73
1:C:37:ASN:HB2	1:C:121:SER:HB3	1.72	0.72
1:D:35:VAL:HB	1:D:123:ARG:HB2	1.72	0.72
1:C:24:THR:HB	1:C:130:SER:HB3	1.72	0.72
1:D:123:ARG:HH11	1:D:123:ARG:HG3	1.55	0.71
1:B:96:PHE:CE1	1:B:117:LEU:HD21	2.26	0.71
1:A:15:MET:HB3	1:A:117:LEU:HB2	1.74	0.70
1:A:76:HIS:CD2	1:A:76:HIS:H	2.09	0.69
1:I:85:VAL:HG23	1:I:101:PRO:HG3	1.74	0.69
1:B:123:ARG:HG3	1:B:123:ARG:NH1	2.09	0.68
1:H:113:GLY:CA	1:H:114:HIS:HB2	2.06	0.68
1:B:52:ARG:N	1:B:57:THR:O	2.27	0.67
1:H:22:LYS:HG2	1:H:88:THR:HG23	1.76	0.67
1:A:9:GLU:OE2	1:A:119:TYR:OH	2.08	0.67
1:I:88:THR:HB	1:I:99:LYS:HB3	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:80:SER:O	1:I:83:SER:OG	2.12	0.67
1:I:10:VAL:CG2	1:I:120:LEU:HD22	2.24	0.67
1:B:36:ILE:HB	1:B:49:PHE:HB3	1.77	0.66
1:I:37:ASN:HB2	1:I:121:SER:HB3	1.77	0.66
1:A:85:VAL:HG23	1:A:101:PRO:HG3	1.76	0.66
1:H:55:GLU:HB3	3:H:202:BGC:H5	1.76	0.66
1:B:59:VAL:HA	1:B:73:ARG:H	1.59	0.65
1:B:38:LEU:HB2	1:B:47:LEU:HB3	1.78	0.65
1:B:99:LYS:C	1:B:100:LEU:HD12	2.17	0.65
1:I:10:VAL:HG23	1:I:120:LEU:HD22	1.79	0.64
1:A:76:HIS:CE1	1:A:104:HIS:CE1	2.86	0.64
1:A:8:LEU:CD2	1:A:128:MET:HE3	2.27	0.64
1:B:98:VAL:C	1:B:105:GLU:CB	2.66	0.64
1:D:15:MET:HB3	1:D:117:LEU:HB2	1.78	0.64
1:C:115:SER:OG	1:C:116:HIS:N	2.29	0.64
1:C:6:GLY:HA3	1:C:123:ARG:HA	1.79	0.63
1:C:71:GLU:OE1	2:C:201:GAL:C6	2.47	0.63
1:I:39:GLY:HA3	1:I:45:LEU:HA	1.81	0.62
1:C:71:GLU:OE1	2:C:201:GAL:O6	2.14	0.62
1:D:36:ILE:HB	1:D:49:PHE:HB3	1.82	0.62
1:A:8:LEU:CD2	1:A:128:MET:CE	2.77	0.62
1:C:71:GLU:OE1	2:C:201:GAL:H61	2.00	0.62
1:I:90:THR:HB	1:I:97:LYS:HB3	1.81	0.61
1:A:35:VAL:HB	1:A:123:ARG:HB2	1.82	0.61
1:A:7:GLU:HG3	1:A:8:LEU:N	2.16	0.60
1:D:123:ARG:HH11	1:D:123:ARG:CG	2.14	0.60
1:I:15:MET:HB3	1:I:117:LEU:HB3	1.83	0.60
1:A:76:HIS:HE1	1:A:104:HIS:CE1	2.18	0.59
1:H:55:GLU:HG2	3:H:202:BGC:C4	2.32	0.59
1:H:55:GLU:CA	3:H:202:BGC:C6	2.78	0.59
1:B:19:SER:HA	1:B:135:GLU:HA	1.85	0.59
1:H:113:GLY:CA	1:H:114:HIS:CB	2.74	0.59
1:I:24:THR:HB	1:I:130:SER:HB3	1.85	0.59
1:A:7:GLU:CG	1:A:8:LEU:H	2.15	0.58
1:C:31:THR:HG21	1:C:125:GLY:HA3	1.84	0.58
1:D:7:GLU:OE1	1:D:7:GLU:HA	2.03	0.58
1:A:88:THR:HB	1:A:99:LYS:HB2	1.85	0.58
1:H:55:GLU:CB	3:H:202:BGC:C5	2.74	0.58
1:I:36:ILE:HB	1:I:49:PHE:HB3	1.86	0.58
1:A:11:LYS:O	1:D:8:LEU:HD22	2.04	0.57
1:A:58:ILE:HD11	1:A:79:PHE:CE2	2.39	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:76:HIS:CD2	1:A:76:HIS:N	2.73	0.57
1:H:54:SER:O	3:H:202:BGC:H6C2	2.05	0.57
1:H:55:GLU:CA	3:H:202:BGC:C5	2.84	0.56
1:B:42:THR:CG2	1:B:119:TYR:OH	2.54	0.56
1:H:55:GLU:HG2	3:H:202:BGC:H6C1	1.88	0.56
1:B:42:THR:HG22	1:B:119:TYR:OH	2.06	0.55
1:I:8:LEU:HB3	1:I:122:VAL:HB	1.87	0.55
1:D:24:THR:HB	1:D:130:SER:HB3	1.88	0.55
1:H:55:GLU:HG2	3:H:202:BGC:O4	2.06	0.55
1:H:54:SER:C	3:H:202:BGC:H6C2	2.27	0.55
1:A:58:ILE:HD11	1:A:79:PHE:HE2	1.72	0.54
1:C:88:THR:HB	1:C:99:LYS:HB3	1.88	0.54
1:I:48:HIS:HD1	1:I:68:TRP:HZ3	1.55	0.54
1:B:85:VAL:HG12	1:B:86:LYS:H	1.72	0.54
1:A:8:LEU:HD22	1:A:128:MET:HE3	1.83	0.54
1:B:53:PHE:C	1:B:56:SER:H	2.12	0.54
1:B:123:ARG:HH11	1:B:123:ARG:CG	2.15	0.53
1:D:43:ASP:HB2	1:D:65:GLY:HA2	1.90	0.53
1:I:68:TRP:CE3	2:I:201:GAL:H62	2.42	0.53
1:B:83:SER:O	1:B:84:GLU:HB2	2.08	0.53
1:B:50:ASN:HB3	1:B:59:VAL:HB	1.90	0.53
1:I:10:VAL:HG23	1:I:120:LEU:CD2	2.39	0.53
1:B:38:LEU:HD12	1:B:47:LEU:HD23	1.90	0.52
1:C:74:GLU:HG3	1:C:106:LEU:HD22	1.90	0.52
1:H:15:MET:HB3	1:H:117:LEU:HB2	1.92	0.52
1:B:100:LEU:HD13	1:B:104:HIS:O	2.10	0.52
1:H:55:GLU:CG	3:H:202:BGC:C6	2.87	0.52
1:C:10:VAL:HB	1:C:120:LEU:HB3	1.92	0.51
1:H:62:SER:OG	1:H:111:ARG:NH1	2.41	0.51
1:B:120:LEU:H	1:B:120:LEU:HD23	1.76	0.51
1:C:38:LEU:HG	1:C:117:LEU:HD13	1.91	0.51
1:H:55:GLU:CG	3:H:202:BGC:C5	2.53	0.51
1:D:123:ARG:NH1	1:D:123:ARG:CG	2.73	0.50
1:C:52:ARG:NH2	2:C:201:GAL:O4	2.44	0.50
1:A:76:HIS:HD2	1:A:76:HIS:H	1.57	0.50
1:H:32:ASP:OD1	1:H:54:SER:HB2	2.11	0.50
1:D:89:VAL:HG22	1:D:98:VAL:HG22	1.93	0.50
1:H:88:THR:O	1:H:98:VAL:HA	2.11	0.50
1:A:51:PRO:HB3	1:A:79:PHE:HZ	1.77	0.50
1:B:32:ASP:O	1:B:53:PHE:HD2	1.94	0.50
1:C:27:ILE:HD13	1:C:53:PHE:HZ	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:10:VAL:CG2	1:I:120:LEU:HB3	2.42	0.49
1:B:84:GLU:O	1:B:85:VAL:O	2.31	0.49
1:D:52:ARG:NH2	2:H:201:GAL:H2	2.28	0.49
1:A:7:GLU:CG	1:A:8:LEU:N	2.73	0.49
1:I:48:HIS:CE1	2:I:201:GAL:H4	2.47	0.49
1:H:79:PHE:O	1:H:80:SER:OG	2.28	0.49
1:A:98:VAL:HB	1:A:106:LEU:HB3	1.96	0.48
1:A:51:PRO:HB3	1:A:79:PHE:CZ	2.48	0.48
1:I:24:THR:O	1:I:129:SER:N	2.36	0.48
1:H:22:LYS:CG	1:H:88:THR:HG23	2.43	0.48
1:I:52:ARG:HH22	2:I:201:GAL:H2	1.78	0.48
1:A:79:PHE:HB3	1:A:101:PRO:HG2	1.95	0.48
1:I:89:VAL:HG22	1:I:98:VAL:HG13	1.95	0.47
1:B:112:LEU:HD12	1:B:112:LEU:H	1.78	0.47
1:H:37:ASN:HB3	1:H:45:LEU:HD22	1.95	0.47
1:H:58:ILE:HD12	1:H:76:HIS:O	2.13	0.47
1:H:70:GLN:O	1:H:111:ARG:NH2	2.46	0.47
1:A:37:ASN:HB3	1:A:45:LEU:HD22	1.95	0.47
1:B:100:LEU:O	1:B:103:GLY:N	2.47	0.47
1:B:46:ASN:HD21	1:B:114:HIS:HD2	1.63	0.47
1:C:15:MET:HB3	1:C:117:LEU:HB2	1.97	0.47
1:B:50:ASN:O	1:B:59:VAL:N	2.48	0.46
1:A:100:LEU:HB3	1:A:101:PRO:HD2	1.96	0.46
1:I:48:HIS:HE1	2:I:201:GAL:H4	1.80	0.46
1:I:45:LEU:HB2	1:I:63:LEU:HB3	1.98	0.46
1:I:62:SER:HB2	1:I:112:LEU:HD13	1.97	0.46
1:B:123:ARG:NH1	1:B:123:ARG:CG	2.73	0.46
1:B:28:ALA:HB3	1:B:31:THR:CG2	2.45	0.46
1:D:90:THR:OG1	1:D:97:LYS:HB3	2.15	0.46
1:C:120:LEU:HD22	1:C:131:PHE:CE1	2.51	0.46
1:I:10:VAL:HG21	1:I:120:LEU:HD22	1.98	0.46
1:A:46:ASN:HD21	1:A:114:HIS:HB2	1.79	0.46
1:I:10:VAL:HG23	1:I:120:LEU:HB3	1.98	0.46
1:I:13:MET:O	1:I:118:SER:HA	2.16	0.46
1:C:94:ASP:OD1	1:C:94:ASP:N	2.39	0.45
1:B:120:LEU:N	1:B:120:LEU:HD23	2.31	0.45
1:H:55:GLU:N	3:H:202:BGC:H6C2	2.31	0.45
1:B:80:SER:CB	1:B:81:PRO:HA	2.46	0.45
1:D:94:ASP:N	1:D:94:ASP:OD1	2.50	0.45
1:I:46:ASN:ND2	1:I:112:LEU:O	2.48	0.45
1:A:24:THR:HB	1:A:130:SER:OG	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:100:LEU:HD12	1:B:100:LEU:N	2.31	0.45
1:D:74:GLU:HG3	1:D:106:LEU:HD13	1.99	0.45
1:B:37:ASN:O	1:B:120:LEU:HB2	2.17	0.44
1:A:102:ASP:OD1	1:A:103:GLY:N	2.50	0.44
1:C:40:GLN:NE2	1:C:116:HIS:O	2.42	0.44
1:D:102:ASP:OD1	1:D:103:GLY:N	2.50	0.44
1:H:89:VAL:HG22	1:H:98:VAL:HG22	1.98	0.44
1:H:7:GLU:OE1	1:I:12:ASN:HB3	2.17	0.44
1:B:34:PHE:CG	1:B:126:PHE:HB2	2.53	0.44
1:D:45:LEU:HB2	1:D:63:LEU:HB3	2.00	0.44
1:I:117:LEU:HA	1:I:117:LEU:HD22	1.79	0.44
1:B:28:ALA:HB3	1:B:125:GLY:HA3	1.99	0.44
1:H:20:THR:HG23	1:H:88:THR:CG2	2.48	0.44
1:D:134:LYS:O	1:D:135:GLU:HB2	2.18	0.44
1:A:21:LEU:O	1:A:88:THR:HA	2.18	0.43
1:B:96:PHE:HE1	1:B:117:LEU:CD2	2.25	0.43
1:H:37:ASN:HB2	1:H:121:SER:HB3	1.99	0.43
1:I:85:VAL:HG23	1:I:101:PRO:CG	2.47	0.43
1:B:41:GLY:HA2	1:B:119:TYR:CE1	2.54	0.43
1:I:68:TRP:CZ3	2:I:201:GAL:H62	2.54	0.43
1:D:32:ASP:OD1	1:D:54:SER:OG	2.35	0.43
1:A:19:SER:HA	1:A:135:GLU:HG2	2.02	0.42
1:H:55:GLU:CA	3:H:202:BGC:H5	2.43	0.42
1:I:38:LEU:HB3	1:I:47:LEU:HB3	2.01	0.42
1:I:44:LYS:HA	1:I:44:LYS:HD2	1.97	0.42
1:I:48:HIS:HB3	1:I:61:ASN:O	2.19	0.42
1:A:76:HIS:CE1	1:A:104:HIS:ND1	2.87	0.42
1:D:88:THR:HB	1:D:99:LYS:HB3	2.00	0.42
1:B:28:ALA:HB3	1:B:31:THR:HG21	2.00	0.42
1:A:52:ARG:NH2	1:C:32:ASP:OD2	2.51	0.42
1:B:13:MET:SD	1:B:120:LEU:CD2	3.07	0.42
1:B:91:PHE:HE1	1:B:110:ASN:ND2	2.17	0.42
1:H:77:LEU:CA	1:H:100:LEU:CD1	2.97	0.42
1:H:34:PHE:HA	1:H:124:GLY:HA3	2.01	0.41
1:A:112:LEU:HD23	1:A:114:HIS:CE1	2.55	0.41
1:H:8:LEU:HD12	1:H:8:LEU:HA	1.80	0.41
1:A:100:LEU:HB3	1:A:101:PRO:CD	2.51	0.41
1:H:77:LEU:CA	1:H:100:LEU:HD13	2.50	0.41
1:B:34:PHE:CD1	1:B:34:PHE:C	2.94	0.41
1:B:53:PHE:CE1	1:B:80:SER:CB	3.03	0.41
1:A:32:ASP:OD2	1:C:123:ARG:NH1	2.43	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:63:LEU:HD22	1:C:30:GLY:HA2	2.03	0.41
1:D:15:MET:HB2	1:D:15:MET:HE2	1.85	0.41
1:B:34:PHE:HA	1:B:124:GLY:HA3	2.03	0.41
1:A:130:SER:HB3	1:D:132:LYS:HG3	2.03	0.41
1:D:37:ASN:HB3	1:D:45:LEU:HD22	2.02	0.41
1:A:21:LEU:HD23	1:A:38:LEU:HD11	2.03	0.41
1:I:55:GLU:O	1:I:57:THR:HG23	2.21	0.40
1:B:63:LEU:HD12	1:B:64:ASP:N	2.36	0.40
1:I:58:ILE:HB	1:I:74:GLU:HG3	2.04	0.40
1:A:17:PRO:HD3	1:A:115:SER:O	2.21	0.40
1:D:100:LEU:HD11	1:D:106:LEU:HD11	2.04	0.40

All (3) 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)
1:B:54:SER:O	3:I:202:BGC:O6[4_674]	1.83	0.37
1:B:55:GLU:CG	2:I:201:GAL:O2[4_674]	1.87	0.33
1:B:29:ASP:OD1	1:I:86:LYS:CE[4_574]	2.15	0.05

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	127/135 (94%)	125 (98%)	2 (2%)	0	100	100
1	B	128/135 (95%)	111 (87%)	14 (11%)	3 (2%)	7	40
1	C	128/135 (95%)	120 (94%)	8 (6%)	0	100	100
1	D	127/135 (94%)	124 (98%)	3 (2%)	0	100	100
1	H	127/135 (94%)	118 (93%)	9 (7%)	0	100	100
1	I	127/135 (94%)	124 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	764/810 (94%)	722 (94%)	39 (5%)	3 (0%)	38 77

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	83	SER
1	B	85	VAL
1	B	84	GLU

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	110/119 (92%)	109 (99%)	1 (1%)	82 94
1	B	92/119 (77%)	85 (92%)	7 (8%)	15 51
1	C	113/119 (95%)	113 (100%)	0	100 100
1	D	113/119 (95%)	111 (98%)	2 (2%)	64 87
1	H	107/119 (90%)	107 (100%)	0	100 100
1	I	109/119 (92%)	108 (99%)	1 (1%)	82 94
All	All	644/714 (90%)	633 (98%)	11 (2%)	66 88

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	LEU
1	B	32	ASP
1	B	53	PHE
1	B	76	HIS
1	B	102	ASP
1	B	115	SER
1	B	117	LEU
1	B	120	LEU
1	D	8	LEU

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Mol	Chain	Res	Type
1	D	112	LEU
1	I	117	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	50	ASN
1	A	76	HIS
1	A	104	HIS
1	B	114	HIS
1	D	76	HIS
1	H	12	ASN
1	I	40	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](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

6 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
2	GAL	C	201	3	11,11,12	1.37	1 (9%)	13,15,17	0.83	1 (7%)
3	BGC	C	202	2	12,12,12	2.29	6 (50%)	17,17,17	1.05	1 (5%)
2	GAL	H	201	3	11,11,12	1.36	1 (9%)	13,15,17	0.82	1 (7%)
3	BGC	H	202	2	12,12,12	2.30	6 (50%)	17,17,17	1.05	1 (5%)
2	GAL	I	201	3	11,11,12	1.37	1 (9%)	13,15,17	0.84	1 (7%)
3	BGC	I	202	1,2	12,12,12	2.29	6 (50%)	17,17,17	1.05	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
2	GAL	C	201	3	-	0/2/19/22	0/1/1/1
3	BGC	C	202	2	-	0/2/22/22	0/1/1/1
2	GAL	H	201	3	-	0/2/19/22	0/1/1/1
3	BGC	H	202	2	-	0/2/22/22	0/1/1/1
2	GAL	I	201	3	-	0/2/19/22	0/1/1/1
3	BGC	I	202	1,2	-	0/2/22/22	0/1/1/1

All (21) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	H	202	BGC	C4-C3	-3.12	1.44	1.52
3	C	202	BGC	C4-C3	-3.10	1.44	1.52
3	I	202	BGC	C4-C3	-3.09	1.44	1.52
3	C	202	BGC	O1-C1	-2.40	1.31	1.39
3	I	202	BGC	O1-C1	-2.38	1.31	1.39
3	H	202	BGC	O1-C1	-2.38	1.31	1.39
3	I	202	BGC	C3-C2	-2.09	1.47	1.52
3	H	202	BGC	C3-C2	-2.04	1.47	1.52
3	C	202	BGC	C3-C2	-2.03	1.47	1.52
3	I	202	BGC	O3-C3	2.96	1.49	1.43
3	H	202	BGC	O3-C3	2.97	1.49	1.43
3	C	202	BGC	O3-C3	2.97	1.49	1.43
2	H	201	GAL	O5-C5	3.36	1.50	1.43
2	I	201	GAL	O5-C5	3.37	1.50	1.43
2	C	201	GAL	O5-C5	3.38	1.50	1.43
3	H	202	BGC	O4-C4	3.40	1.50	1.43
3	I	202	BGC	O4-C4	3.41	1.50	1.43
3	C	202	BGC	O4-C4	3.42	1.50	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	I	202	BGC	O5-C1	3.83	1.50	1.43
3	C	202	BGC	O5-C1	3.85	1.50	1.43
3	H	202	BGC	O5-C1	3.85	1.50	1.43

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	202	BGC	O5-C1-C2	-2.67	105.60	110.04
3	I	202	BGC	O5-C1-C2	-2.67	105.60	110.04
3	H	202	BGC	O5-C1-C2	-2.67	105.61	110.04
2	H	201	GAL	C1-C2-C3	2.66	113.02	109.65
2	C	201	GAL	C1-C2-C3	2.67	113.04	109.65
2	I	201	GAL	C1-C2-C3	2.71	113.09	109.65

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 34 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	201	GAL	4	0
2	H	201	GAL	1	0
3	H	202	BGC	22	0
2	I	201	GAL	5	1
3	I	202	BGC	0	1

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, 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	129/135 (95%)	0.24	3 (2%) 61 46	13, 31, 69, 108	0
1	B	130/135 (96%)	1.31	30 (23%) 1 1	28, 70, 126, 165	0
1	C	130/135 (96%)	0.23	1 (0%) 86 77	14, 26, 61, 94	0
1	D	129/135 (95%)	0.44	2 (1%) 72 59	17, 42, 75, 98	0
1	H	129/135 (95%)	0.74	11 (8%) 11 7	21, 47, 85, 102	0
1	I	129/135 (95%)	1.10	12 (9%) 9 6	28, 61, 109, 142	0
All	All	776/810 (95%)	0.68	59 (7%) 15 8	13, 47, 98, 165	0

All (59) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	107	THR	6.1
1	B	59	VAL	4.2
1	I	57	THR	4.2
1	I	39	GLY	4.1
1	B	57	THR	4.0
1	I	112	LEU	3.9
1	I	87	PHE	3.9
1	B	58	ILE	3.9
1	H	28	ALA	3.7
1	B	72	GLN	3.7
1	B	78	CYS	3.5
1	H	76	HIS	3.5
1	B	28	ALA	3.4
1	B	76	HIS	3.3
1	H	78	CYS	3.1
1	I	116	HIS	3.0
1	B	106	LEU	3.0
1	I	43	ASP	2.9
1	B	21	LEU	2.9

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Mol	Chain	Res	Type	RSRZ
1	I	114	HIS	2.8
1	I	135	GLU	2.8
1	B	93	SER	2.8
1	I	74	GLU	2.7
1	B	115	SER	2.7
1	B	54	SER	2.6
1	B	56	SER	2.6
1	B	95	LYS	2.6
1	I	103	GLY	2.5
1	D	114	HIS	2.5
1	B	60	CYS	2.5
1	H	12	ASN	2.5
1	B	80	SER	2.5
1	D	109	PRO	2.5
1	B	73	ARG	2.4
1	H	41	GLY	2.4
1	H	115	SER	2.4
1	B	114	HIS	2.4
1	B	75	ASP	2.4
1	H	93	SER	2.3
1	B	94	ASP	2.3
1	H	29	ASP	2.3
1	B	35	VAL	2.3
1	B	61	ASN	2.3
1	I	102	ASP	2.3
1	B	89	VAL	2.3
1	A	135	GLU	2.3
1	A	83	SER	2.3
1	I	42	THR	2.2
1	B	81	PRO	2.2
1	B	102	ASP	2.2
1	B	118	SER	2.2
1	H	42	THR	2.1
1	B	29	ASP	2.1
1	B	113	GLY	2.1
1	B	48	HIS	2.1
1	A	78	CYS	2.0
1	C	135	GLU	2.0
1	H	26	SER	2.0
1	H	54	SER	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 carbohydrates 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. 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, 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	LLDF	B-factors(Å ²)	Q<0.9
3	BGC	C	202	12/12	0.42	0.74	12.01	96,107,113,120	0
3	BGC	H	202	12/12	0.34	0.71	7.81	111,119,125,133	0
2	GAL	H	201	11/12	0.74	0.50	3.63	105,108,111,113	0
2	GAL	C	201	11/12	0.78	0.34	2.06	90,94,98,102	0
3	BGC	I	202	12/12	0.35	0.75	1.96	127,137,145,155	0
2	GAL	I	201	11/12	0.72	0.43	1.05	113,116,123,126	0

6.5 Other polymers [i](#)

There are no such residues in this entry.