



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 07:56 PM GMT

PDB ID : 1HWN
Title : EBULIN COMPLEXED WITH GALACTOSE, TRIGONAL CRYSTAL FORM
Authors : Pascal, J.M.; Day, P.J.; Monzingo, A.F.; Ernst, S.R.; Robertus, J.D.
Deposited on : 2001-01-09
Resolution : 2.80 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<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) : 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

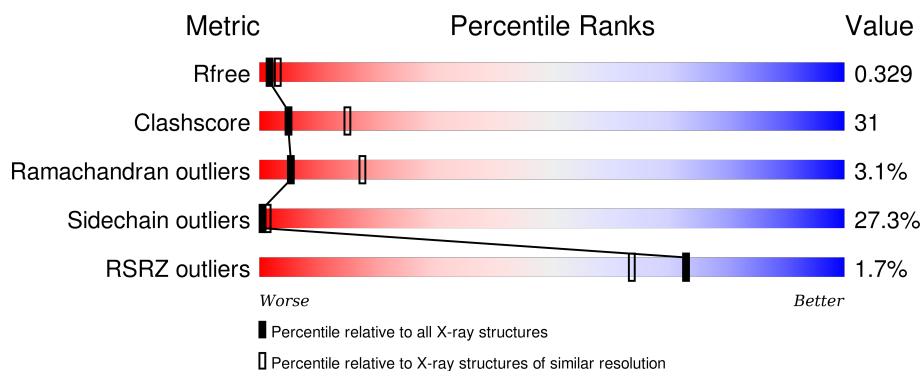
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

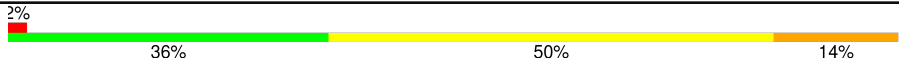
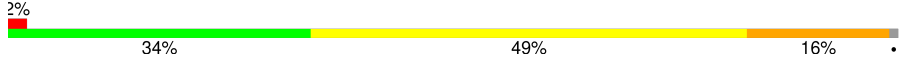
The reported resolution of this entry is 2.80 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	2393 (2.80-2.80)
Clashscore	102246	2827 (2.80-2.80)
Ramachandran outliers	100387	2782 (2.80-2.80)
Sidechain outliers	100360	2784 (2.80-2.80)
RSRZ outliers	91569	2404 (2.80-2.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments 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	254	 2% 36% 50% 14%
2	B	266	 2% 34% 49% 16% .

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
4	GAL	B	280	-	-	-	X
4	GAL	B	290	-	-	-	X

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 4133 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 EBULIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	254	Total	C	N	O	S	0	0	0
			2007	1267	344	391	5			

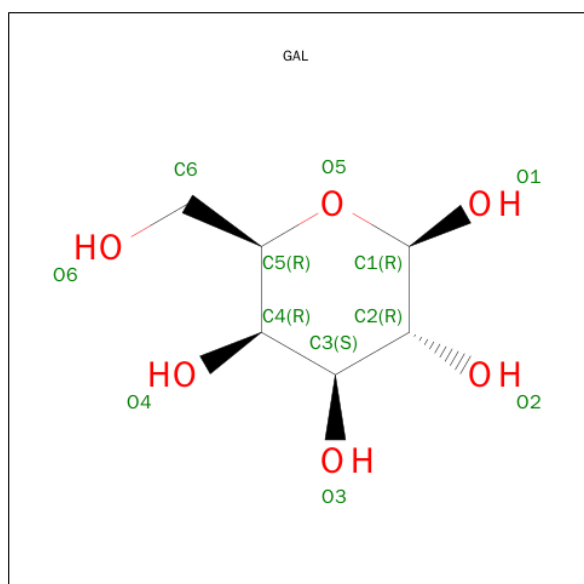
- Molecule 2 is a protein called EBULIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	263	Total	C	N	O	S	0	0	0
			2028	1253	359	400	16			

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

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

- Molecule 4 is SUGAR (D-GALACTOSE) (three-letter code: GAL) (formula: C₆H₁₂O₆).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	0
			12	6	6		
4	B	1	Total	C	O	0	0
			12	6	6		

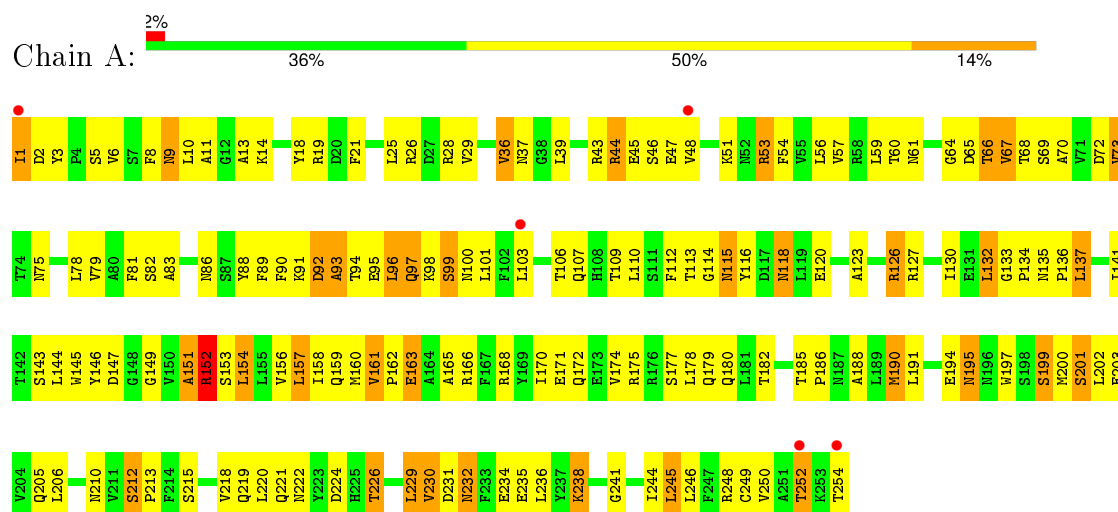
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	19	Total	O	0	0
			19	19		
5	B	27	Total	O	0	0
			27	27		

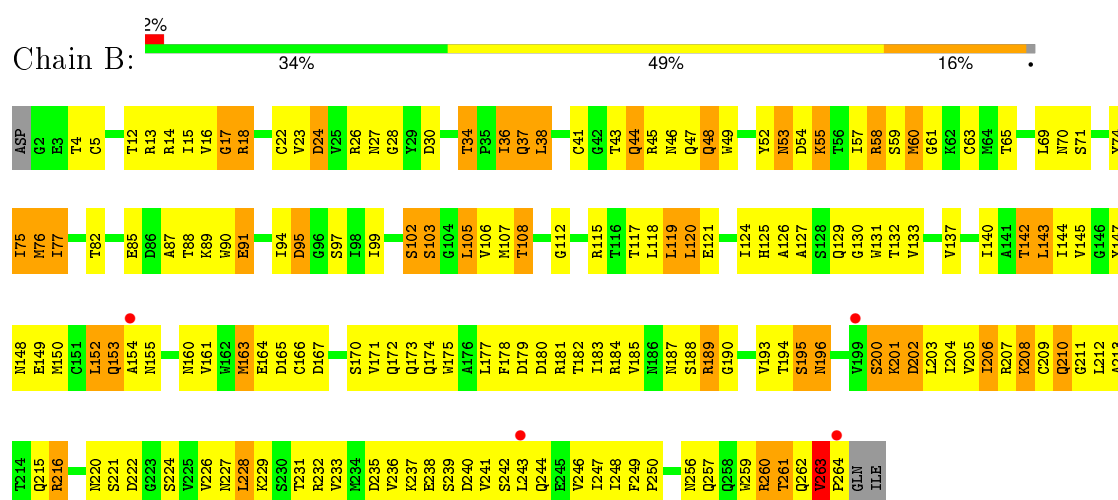
3 Residue-property plots

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: EBULIN



• Molecule 2: EBULIN



4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	73.60 Å 73.60 Å 190.90 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	30.00 – 2.80 36.13 – 2.70	Depositor EDS
% Data completeness (in resolution range)	(Not available) (30.00-2.80) 92.1 (36.13-2.70)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.94 (at 2.68 Å)	Xtriage
Refinement program	X-PLOR 3.851	Depositor
R, R_{free}	0.264 , 0.328 0.275 , 0.329	Depositor DCC
R_{free} test set	763 reflections (5.57%)	DCC
Wilson B-factor (Å ²)	36.8	Xtriage
Anisotropy	0.768	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 52.1	EDS
Estimated twinning fraction	0.036 for -h,-k,l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 17104 reflections	Xtriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	4133	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.35% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 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: GAL, 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	0.26	0/2044	0.42	0/2777
2	B	0.24	0/2065	0.44	0/2813
All	All	0.25	0/4109	0.43	0/5590

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

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	2007	0	1982	125	0
2	B	2028	0	1959	137	0
3	B	28	0	25	1	0
4	B	24	0	24	3	0
5	A	19	0	0	0	0
5	B	27	0	0	0	0
All	All	4133	0	3990	251	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 31.

All (251) close contacts within the same asymmetric unit are listed below, sorted by their clash

magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:263:VAL:HB	2:B:264:PRO:HD2	1.44	0.98
2:B:37:GLN:HB3	2:B:117:THR:HA	1.44	0.94
2:B:44:GLN:HG3	2:B:47:GLN:HG3	1.49	0.93
2:B:132:THR:HB	2:B:179:ASP:HB3	1.53	0.87
2:B:177:LEU:HD11	2:B:261:THR:HG21	1.57	0.86
2:B:45:ARG:HA	2:B:48:GLN:HE21	1.38	0.86
2:B:23:VAL:HG22	2:B:36:ILE:HD12	1.60	0.84
2:B:58:ARG:HB3	2:B:63:CYS:HA	1.58	0.84
1:A:127:ARG:HH12	1:A:195:ASN:HD21	1.25	0.82
1:A:134:PRO:HG3	1:A:178:LEU:HA	1.61	0.81
1:A:213:PRO:HG3	2:B:133:VAL:HG11	1.67	0.76
2:B:263:VAL:HB	2:B:264:PRO:CD	2.17	0.74
1:A:67:VAL:HG12	1:A:83:ALA:HB2	1.70	0.73
2:B:204:ILE:HD12	2:B:246:VAL:HG12	1.70	0.72
2:B:127:ALA:HB3	2:B:211:GLY:HA2	1.70	0.72
2:B:226:VAL:HG12	2:B:233:VAL:HG13	1.71	0.72
2:B:37:GLN:HA	2:B:118:LEU:HD23	1.71	0.72
2:B:235:ASP:HB3	2:B:257:GLN:HG2	1.73	0.71
2:B:200:SER:O	2:B:201:LYS:HB2	1.91	0.71
2:B:263:VAL:CB	2:B:264:PRO:HD2	2.18	0.70
2:B:124:ILE:H	2:B:129:GLN:HE22	1.41	0.69
1:A:218:VAL:HB	1:A:230:VAL:HG13	1.73	0.69
1:A:202:LEU:O	1:A:206:LEU:HB2	1.92	0.68
2:B:150:MET:HB2	2:B:163:MET:HG2	1.74	0.68
2:B:74:TYR:HA	2:B:119:LEU:HA	1.75	0.68
2:B:85:GLU:HG3	2:B:89:LYS:HE3	1.74	0.68
1:A:45:GLU:HA	1:A:48:VAL:HG12	1.74	0.68
2:B:209:CYS:HA	2:B:215:GLN:HE22	1.57	0.68
1:A:29:VAL:HG12	1:A:73:VAL:HG23	1.77	0.67
1:A:232:ASN:OD1	1:A:235:GLU:HB2	1.96	0.65
2:B:203:LEU:HA	2:B:247:ILE:HG22	1.77	0.64
2:B:126:ALA:HA	2:B:213:ALA:HA	1.78	0.64
1:A:191:LEU:O	1:A:194:GLU:HG2	1.98	0.64
1:A:61:ASN:OD1	1:A:65:ASP:HB2	1.98	0.63
1:A:161:VAL:HB	1:A:162:PRO:HD3	1.79	0.63
2:B:108:THR:HG23	2:B:129:GLN:HG2	1.78	0.63
1:A:202:LEU:HD12	1:A:203:GLU:N	2.14	0.63
2:B:183:ILE:O	2:B:193:VAL:HG23	1.98	0.63
1:A:115:ASN:OD1	1:A:118:ASN:HB2	1.98	0.63
2:B:256:ASN:HD21	4:B:290:GAL:H2	1.65	0.62
2:B:148:ASN:HB3	2:B:150:MET:HG3	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:15:ILE:HB	2:B:23:VAL:HG12	1.80	0.62
1:A:161:VAL:HB	1:A:162:PRO:CD	2.30	0.62
2:B:232:ARG:HB3	2:B:248:ILE:HB	1.81	0.61
2:B:154:ALA:HB2	2:B:175:TRP:CH2	2.36	0.61
1:A:154:LEU:HA	1:A:157:LEU:HD12	1.83	0.61
1:A:202:LEU:HD23	1:A:248:ARG:NH1	2.15	0.60
2:B:142:THR:HB	2:B:263:VAL:HA	1.83	0.60
1:A:45:GLU:HA	1:A:48:VAL:CG1	2.31	0.60
2:B:36:ILE:HG22	2:B:118:LEU:HB2	1.83	0.60
1:A:252:THR:HG22	2:B:5:CYS:H	1.67	0.59
1:A:94:THR:O	1:A:97:GLN:HG2	2.02	0.59
2:B:18:ARG:HG2	2:B:112:GLY:HA2	1.85	0.59
2:B:36:ILE:HD11	2:B:49:TRP:HZ2	1.66	0.59
2:B:154:ALA:HB1	2:B:206:ILE:HD13	1.85	0.58
1:A:134:PRO:HG3	1:A:178:LEU:HD23	1.86	0.58
1:A:218:VAL:HB	1:A:230:VAL:CG1	2.33	0.58
1:A:224:ASP:OD1	1:A:226:THR:HB	2.04	0.57
1:A:26:ARG:HG3	1:A:165:ALA:HB1	1.86	0.57
2:B:45:ARG:HA	2:B:48:GLN:NE2	2.15	0.57
2:B:201:LYS:HA	2:B:247:ILE:HD13	1.86	0.57
1:A:90:PHE:HB3	1:A:113:THR:HA	1.86	0.57
1:A:213:PRO:HG3	2:B:133:VAL:CG1	2.33	0.57
1:A:8:PHE:HB2	1:A:21:PHE:CD1	2.39	0.57
1:A:57:VAL:O	1:A:68:THR:HA	2.05	0.57
2:B:161:VAL:HG22	2:B:204:ILE:O	2.05	0.57
1:A:235:GLU:HG2	2:B:140:ILE:HD11	1.87	0.56
1:A:18:TYR:HD2	1:A:175:ARG:HG2	1.71	0.56
1:A:249:CYS:SG	1:A:250:VAL:N	2.78	0.56
2:B:226:VAL:HG12	2:B:233:VAL:HG22	1.86	0.56
1:A:123:ALA:HB2	1:A:151:ALA:HB3	1.87	0.56
1:A:19:ARG:HB2	1:A:175:ARG:CZ	2.36	0.56
1:A:26:ARG:HH21	1:A:165:ALA:HA	1.69	0.56
1:A:10:LEU:HD11	1:A:137:LEU:HD13	1.87	0.56
2:B:125:HIS:HB3	2:B:228:LEU:HB3	1.88	0.55
2:B:49:TRP:HB3	2:B:57:ILE:HG22	1.88	0.55
2:B:24:ASP:O	2:B:36:ILE:HD13	2.05	0.55
2:B:166:CYS:HA	2:B:173:GLN:HE22	1.71	0.55
2:B:224:SER:HB2	2:B:233:VAL:HG11	1.89	0.55
1:A:1:ILE:HG12	1:A:100:ASN:HB2	1.88	0.55
1:A:177:SER:HB2	1:A:182:THR:O	2.07	0.55
2:B:23:VAL:HG13	2:B:23:VAL:O	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:143:LEU:O	2:B:261:THR:HA	2.07	0.54
1:A:199:SER:O	1:A:202:LEU:HG	2.08	0.54
2:B:44:GLN:CG	2:B:47:GLN:HG3	2.33	0.54
1:A:59:LEU:HD11	1:A:161:VAL:HG21	1.89	0.54
1:A:39:LEU:HB2	1:A:245:LEU:HD23	1.90	0.54
2:B:45:ARG:NE	2:B:60:MET:HG3	2.23	0.53
1:A:156:VAL:O	1:A:160:MET:HB2	2.08	0.53
2:B:54:ASP:O	2:B:89:LYS:HD2	2.09	0.52
1:A:97:GLN:O	1:A:101:LEU:HB2	2.09	0.52
1:A:54:PHE:CZ	1:A:97:GLN:HB3	2.44	0.52
2:B:142:THR:HB	2:B:263:VAL:CA	2.39	0.52
1:A:201:SER:HA	1:A:245:LEU:HD12	1.91	0.52
1:A:6:VAL:HG21	1:A:25:LEU:HA	1.92	0.52
1:A:241:GLY:HA3	2:B:260:ARG:HH21	1.74	0.52
2:B:178:PHE:HB3	2:B:180:ASP:OD1	2.09	0.52
1:A:205:GLN:HE22	1:A:248:ARG:H	1.57	0.51
2:B:17:GLY:O	2:B:18:ARG:HB2	2.10	0.51
1:A:9:ASN:O	1:A:13:ALA:HB2	2.10	0.51
1:A:97:GLN:HB2	1:A:101:LEU:HD12	1.92	0.51
2:B:91:GLU:HB3	2:B:99:ILE:HG22	1.93	0.51
1:A:172:GLN:HB3	2:B:262:GLN:HE21	1.76	0.51
2:B:38:LEU:HD13	2:B:118:LEU:HD21	1.92	0.51
1:A:116:TYR:CD2	1:A:127:ARG:HD3	2.46	0.51
2:B:17:GLY:C	2:B:180:ASP:HB3	2.31	0.51
1:A:91:LYS:HB3	1:A:113:THR:HG22	1.92	0.51
2:B:95:ASP:HB3	2:B:228:LEU:HD11	1.91	0.51
1:A:144:LEU:CD2	1:A:149:GLY:HA2	2.41	0.51
2:B:52:TYR:HB2	2:B:54:ASP:OD1	2.10	0.50
1:A:137:LEU:HB2	1:A:160:MET:HE1	1.94	0.50
2:B:262:GLN:O	2:B:263:VAL:O	2.30	0.50
2:B:233:VAL:O	2:B:248:ILE:HA	2.11	0.50
2:B:210:GLN:HB2	2:B:212:LEU:HD13	1.92	0.50
1:A:206:LEU:HD12	2:B:5:CYS:SG	2.51	0.50
1:A:53:ARG:HH11	1:A:53:ARG:HG3	1.77	0.50
2:B:167:ASP:H	2:B:173:GLN:NE2	2.10	0.50
2:B:142:THR:HA	2:B:263:VAL:O	2.12	0.49
2:B:194:THR:HB	2:B:207:ARG:HG2	1.93	0.49
2:B:200:SER:O	2:B:201:LYS:CB	2.59	0.49
2:B:209:CYS:C	2:B:210:GLN:HG2	2.31	0.49
2:B:34:THR:O	2:B:76:MET:HB2	2.13	0.49
1:A:201:SER:HA	1:A:245:LEU:CD1	2.43	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:202:ASP:HB2	2:B:248:ILE:HD11	1.93	0.49
1:A:48:VAL:O	1:A:48:VAL:HG13	2.12	0.49
1:A:212:SER:HB2	1:A:234:GLU:OE2	2.12	0.49
1:A:53:ARG:NH1	1:A:96:LEU:HD21	2.28	0.49
2:B:127:ALA:HB3	2:B:211:GLY:CA	2.41	0.49
1:A:67:VAL:HG22	1:A:141:ILE:HG23	1.95	0.49
2:B:226:VAL:CG1	2:B:233:VAL:HG22	2.43	0.49
1:A:135:ASN:HB2	1:A:136:PRO:HD3	1.95	0.49
1:A:232:ASN:N	1:A:232:ASN:HD22	2.11	0.48
2:B:237:LYS:HG2	2:B:238:GLU:HG2	1.95	0.48
1:A:170:ILE:O	1:A:174:VAL:HG23	2.12	0.48
2:B:24:ASP:HB2	2:B:47:GLN:NE2	2.28	0.48
1:A:126:ARG:O	1:A:130:ILE:HD12	2.14	0.48
2:B:12:THR:C	2:B:13:ARG:HG2	2.33	0.48
1:A:110:LEU:HD13	1:A:112:PHE:CZ	2.47	0.48
1:A:202:LEU:HD23	1:A:248:ARG:CZ	2.44	0.48
1:A:100:ASN:HA	1:A:103:LEU:HG	1.95	0.48
1:A:180:GLN:HB2	1:A:182:THR:HG22	1.95	0.48
2:B:30:ASP:HB3	2:B:60:MET:HG2	1.96	0.48
1:A:249:CYS:SG	2:B:5:CYS:N	2.87	0.48
1:A:5:SER:HB3	1:A:56:LEU:HB2	1.95	0.47
1:A:172:GLN:HA	1:A:175:ARG:HB2	1.95	0.47
2:B:180:ASP:O	2:B:181:ARG:HB2	2.13	0.47
1:A:60:THR:HG23	1:A:64:GLY:O	2.15	0.47
2:B:153:GLN:HG2	2:B:164:GLU:HB2	1.97	0.47
3:B:268:NAG:O7	3:B:268:NAG:O5	2.33	0.47
2:B:171:VAL:HA	2:B:174:GLN:HG3	1.95	0.47
1:A:252:THR:CG2	2:B:5:CYS:HB2	2.45	0.47
1:A:53:ARG:HH12	1:A:96:LEU:HD21	1.80	0.47
2:B:41:CYS:HB3	2:B:137:VAL:HG11	1.97	0.47
1:A:151:ALA:O	1:A:152:ARG:C	2.54	0.46
1:A:188:ALA:HB3	1:A:222:ASN:O	2.15	0.46
1:A:60:THR:OG1	1:A:66:THR:HB	2.15	0.46
2:B:144:ILE:HG22	2:B:259:TRP:HE3	1.79	0.46
2:B:17:GLY:HA3	2:B:130:GLY:O	2.15	0.46
1:A:114:GLY:O	1:A:115:ASN:HB3	2.15	0.46
1:A:133:GLY:O	1:A:137:LEU:HB2	2.16	0.46
2:B:15:ILE:O	2:B:22:CYS:HA	2.16	0.46
1:A:163:GLU:OE1	1:A:194:GLU:HB2	2.16	0.46
1:A:53:ARG:HH11	1:A:96:LEU:HD11	1.81	0.46
2:B:90:TRP:HH2	2:B:120:LEU:HD21	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:53:ASN:C	2:B:55:LYS:H	2.20	0.45
1:A:158:ILE:O	1:A:162:PRO:HG2	2.16	0.45
1:A:101:LEU:HD23	1:A:101:LEU:HA	1.85	0.45
2:B:178:PHE:HB2	2:B:182:THR:O	2.17	0.45
2:B:118:LEU:HD11	2:B:131:TRP:CZ2	2.51	0.45
2:B:124:ILE:HG13	2:B:129:GLN:HE22	1.81	0.45
2:B:58:ARG:HB3	2:B:63:CYS:CA	2.40	0.45
2:B:49:TRP:HB3	2:B:57:ILE:CG2	2.47	0.44
2:B:140:ILE:HG22	2:B:142:THR:HG22	1.99	0.44
1:A:195:ASN:HD22	1:A:195:ASN:N	2.15	0.44
1:A:10:LEU:HB2	1:A:60:THR:O	2.18	0.44
2:B:99:ILE:HG13	2:B:106:VAL:HG12	1.98	0.44
1:A:238:LYS:HG2	2:B:177:LEU:CD1	2.48	0.44
2:B:226:VAL:CG1	2:B:233:VAL:HG13	2.46	0.44
1:A:144:LEU:HD22	1:A:149:GLY:HA2	2.00	0.44
2:B:188:SER:C	2:B:190:GLY:H	2.20	0.44
1:A:232:ASN:ND2	1:A:232:ASN:N	2.66	0.44
2:B:257:GLN:HG3	4:B:290:GAL:O2	2.18	0.44
1:A:230:VAL:HG21	1:A:236:LEU:HB2	1.99	0.44
2:B:220:ASN:HB3	2:B:222:ASP:OD1	2.18	0.43
1:A:98:LYS:H	1:A:98:LYS:HG3	1.64	0.43
1:A:172:GLN:HB3	2:B:262:GLN:NE2	2.32	0.43
2:B:41:CYS:CB	2:B:137:VAL:HG11	2.48	0.43
2:B:260:ARG:NH1	2:B:261:THR:O	2.51	0.43
2:B:144:ILE:HD12	2:B:152:LEU:HD23	2.01	0.43
1:A:166:ARG:HD2	1:A:197:TRP:CE2	2.53	0.43
2:B:160:ASN:H	2:B:160:ASN:HD22	1.66	0.43
1:A:229:LEU:HD12	1:A:229:LEU:H	1.83	0.43
1:A:120:GLU:OE2	1:A:127:ARG:HG3	2.19	0.43
1:A:137:LEU:HD21	1:A:157:LEU:HD23	2.00	0.43
2:B:108:THR:O	2:B:118:LEU:HD13	2.18	0.43
1:A:97:GLN:HE21	1:A:97:GLN:HB3	1.57	0.43
1:A:94:THR:OG1	1:A:96:LEU:HD23	2.19	0.42
1:A:197:TRP:HZ2	1:A:244:ILE:HG22	1.84	0.42
1:A:67:VAL:CG2	1:A:141:ILE:HG23	2.49	0.42
2:B:260:ARG:HD3	2:B:262:GLN:HE21	1.84	0.42
2:B:216:ARG:O	2:B:227:ASN:HA	2.19	0.42
1:A:159:GLN:HA	1:A:163:GLU:HB3	2.01	0.42
2:B:181:ARG:HD3	2:B:181:ARG:HA	1.78	0.42
1:A:44:ARG:H	1:A:44:ARG:HG3	1.66	0.42
2:B:235:ASP:CB	2:B:257:GLN:HG2	2.48	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:197:TRP:CH2	1:A:246:LEU:HB2	2.54	0.42
1:A:89:PHE:O	1:A:109:THR:HA	2.19	0.42
2:B:26:ARG:C	2:B:28:GLY:H	2.23	0.42
2:B:77:ILE:HD13	2:B:77:ILE:H	1.84	0.42
1:A:154:LEU:HA	1:A:154:LEU:HD13	1.87	0.42
1:A:72:ASP:HB3	1:A:75:ASN:OD1	2.20	0.42
2:B:27:ASN:H	4:B:280:GAL:H62	1.85	0.42
2:B:108:THR:OG1	2:B:121:GLU:HB2	2.20	0.42
1:A:202:LEU:HD12	1:A:202:LEU:C	2.39	0.42
2:B:85:GLU:O	2:B:89:LYS:HG2	2.19	0.42
1:A:70:ALA:O	1:A:79:VAL:HG12	2.19	0.42
2:B:263:VAL:O	2:B:264:PRO:C	2.58	0.42
2:B:75:ILE:CD1	2:B:118:LEU:HB3	2.50	0.42
2:B:226:VAL:HG12	2:B:233:VAL:CG1	2.46	0.42
2:B:85:GLU:O	2:B:88:THR:HG22	2.19	0.42
2:B:59:SER:C	2:B:61:GLY:H	2.23	0.42
2:B:65:THR:HA	2:B:87:ALA:O	2.20	0.41
2:B:126:ALA:HB1	2:B:211:GLY:O	2.19	0.41
2:B:160:ASN:N	2:B:205:VAL:HG12	2.34	0.41
1:A:26:ARG:CG	1:A:165:ALA:HB1	2.50	0.41
2:B:107:MET:CG	2:B:118:LEU:HD12	2.50	0.41
1:A:168:ARG:O	1:A:171:GLU:HB3	2.20	0.41
1:A:37:ASN:OD1	2:B:94:ILE:HG21	2.20	0.41
1:A:8:PHE:HB3	1:A:59:LEU:HD23	2.02	0.41
1:A:144:LEU:HD21	1:A:153:SER:HB2	2.03	0.41
1:A:170:ILE:HG23	1:A:190:MET:CE	2.50	0.41
1:A:132:LEU:HD11	1:A:186:PRO:HG3	2.03	0.41
2:B:124:ILE:HG13	2:B:129:GLN:NE2	2.35	0.41
2:B:195:SER:OG	2:B:196:ASN:N	2.54	0.41
1:A:234:GLU:O	1:A:238:LYS:HD3	2.20	0.41
2:B:160:ASN:OD1	2:B:203:LEU:HD13	2.22	0.41
1:A:8:PHE:HB2	1:A:21:PHE:CG	2.55	0.41
1:A:145:TRP:HD1	1:A:146:TYR:HD2	1.69	0.41
1:A:245:LEU:HA	1:A:245:LEU:HD13	1.88	0.40
1:A:81:PHE:CE2	1:A:88:TYR:HB2	2.56	0.40
1:A:200:MET:HE2	1:A:200:MET:HB3	1.86	0.40
2:B:14:ARG:O	2:B:133:VAL:HA	2.22	0.40
2:B:126:ALA:O	2:B:216:ARG:NH2	2.54	0.40
1:A:172:GLN:OE1	1:A:172:GLN:HA	2.21	0.40
2:B:240:ASP:OD2	2:B:243:LEU:HG	2.21	0.40
2:B:88:THR:HG23	2:B:89:LYS:HD3	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:92:ASP:O	1:A:93:ALA:C	2.58	0.40
2:B:249:PHE:CG	2:B:250:PRO:HD2	2.56	0.40
2:B:103:SER:O	2:B:105:LEU:HD22	2.21	0.40
1:A:3:TYR:HE1	1:A:54:PHE:H	1.69	0.40
1:A:99:SER:O	1:A:103:LEU:HD11	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	252/254 (99%)	218 (86%)	27 (11%)	7 (3%)	6	21
2	B	261/266 (98%)	212 (81%)	40 (15%)	9 (3%)	5	16
All	All	513/520 (99%)	430 (84%)	67 (13%)	16 (3%)	5	17

All (16) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	187	ASN
2	B	263	VAL
1	A	11	ALA
1	A	93	ALA
1	A	115	ASN
1	A	151	ALA
2	B	18	ARG
2	B	69	LEU
1	A	161	VAL
2	B	102	SER
2	B	189	ARG
2	B	201	LYS
1	A	152	ARG

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Mol	Chain	Res	Type
2	B	208	LYS
1	A	36	VAL
2	B	17	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	223/223 (100%)	166 (74%)	57 (26%)	0	2
2	B	228/231 (99%)	162 (71%)	66 (29%)	0	1
All	All	451/454 (99%)	328 (73%)	123 (27%)	0	1

All (123) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	ILE
1	A	2	ASP
1	A	9	ASN
1	A	14	LYS
1	A	28	ARG
1	A	36	VAL
1	A	43	ARG
1	A	44	ARG
1	A	46	SER
1	A	47	GLU
1	A	51	LYS
1	A	53	ARG
1	A	66	THR
1	A	67	VAL
1	A	69	SER
1	A	73	VAL
1	A	78	LEU
1	A	82	SER
1	A	86	ASN
1	A	92	ASP

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Mol	Chain	Res	Type
1	A	95	GLU
1	A	96	LEU
1	A	97	GLN
1	A	99	SER
1	A	106	THR
1	A	107	GLN
1	A	118	ASN
1	A	126	ARG
1	A	132	LEU
1	A	137	LEU
1	A	143	SER
1	A	147	ASP
1	A	152	ARG
1	A	154	LEU
1	A	157	LEU
1	A	163	GLU
1	A	179	GLN
1	A	185	THR
1	A	190	MET
1	A	195	ASN
1	A	199	SER
1	A	201	SER
1	A	210	ASN
1	A	212	SER
1	A	215	SER
1	A	219	GLN
1	A	220	LEU
1	A	221	GLN
1	A	226	THR
1	A	229	LEU
1	A	230	VAL
1	A	231	ASP
1	A	232	ASN
1	A	238	LYS
1	A	245	LEU
1	A	252	THR
1	A	254	THR
2	B	4	THR
2	B	16	VAL
2	B	24	ASP
2	B	34	THR
2	B	36	ILE

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Mol	Chain	Res	Type
2	B	37	GLN
2	B	38	LEU
2	B	43	THR
2	B	44	GLN
2	B	46	ASN
2	B	48	GLN
2	B	53	ASN
2	B	55	LYS
2	B	58	ARG
2	B	60	MET
2	B	70	ASN
2	B	71	SER
2	B	75	ILE
2	B	76	MET
2	B	77	ILE
2	B	82	THR
2	B	91	GLU
2	B	95	ASP
2	B	97	SER
2	B	102	SER
2	B	103	SER
2	B	105	LEU
2	B	108	THR
2	B	115	ARG
2	B	119	LEU
2	B	120	LEU
2	B	142	THR
2	B	143	LEU
2	B	145	VAL
2	B	147	TYR
2	B	149	GLU
2	B	152	LEU
2	B	153	GLN
2	B	155	ASN
2	B	163	MET
2	B	165	ASP
2	B	170	SER
2	B	172	GLN
2	B	184	ARG
2	B	185	VAL
2	B	189	ARG
2	B	195	SER

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Mol	Chain	Res	Type
2	B	196	ASN
2	B	200	SER
2	B	202	ASP
2	B	206	ILE
2	B	208	LYS
2	B	210	GLN
2	B	216	ARG
2	B	221	SER
2	B	228	LEU
2	B	229	LYS
2	B	231	THR
2	B	236	VAL
2	B	239	SER
2	B	241	VAL
2	B	242	SER
2	B	244	GLN
2	B	260	ARG
2	B	261	THR
2	B	263	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	86	ASN
1	A	107	GLN
1	A	135	ASN
1	A	195	ASN
1	A	196	ASN
1	A	221	GLN
2	B	27	ASN
2	B	48	GLN
2	B	70	ASN
2	B	129	GLN
2	B	159	ASN
2	B	173	GLN
2	B	215	GLN
2	B	256	ASN
2	B	262	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

2 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	$\# Z > 2$
3	NAG	B	267	3,2	14,14,15	0.45	0	15,19,21	0.70	1 (6%)
3	NAG	B	268	3	14,14,15	0.59	0	15,19,21	1.14	2 (13%)

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	NAG	B	267	3,2	-	0/6/23/26	0/1/1/1
3	NAG	B	268	3	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	267	NAG	C2-N2-C7	-2.24	120.16	123.04
3	B	268	NAG	C3-C4-C5	2.16	113.97	110.20
3	B	268	NAG	C1-O5-C5	2.55	115.48	112.25

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	B	268	NAG	1	0

5.6 Ligand geometry

2 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	GAL	B	280	-	12,12,12	0.30	0	17,17,17	0.34	0
4	GAL	B	290	-	12,12,12	0.30	0	17,17,17	0.36	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
4	GAL	B	280	-	-	0/2/22/22	0/1/1/1
4	GAL	B	290	-	-	0/2/22/22	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	280	GAL	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	290	GAL	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	254/254 (100%)	0.13	5 (1%) 68 58	7, 26, 48, 60	0
2	B	263/266 (98%)	0.25	4 (1%) 76 68	4, 29, 46, 63	0
All	All	517/520 (99%)	0.19	9 (1%) 73 63	4, 28, 47, 63	0

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	252	THR	2.9
2	B	199	VAL	2.8
1	A	254	THR	2.5
2	B	154	ALA	2.5
2	B	264	PRO	2.4
1	A	48	VAL	2.3
1	A	103	LEU	2.3
2	B	243	LEU	2.2
1	A	1	ILE	2.1

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](#)

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(\AA^2)	Q<0.9
3	NAG	B	267	14/15	0.87	0.20	-0.22	30,30,30,30	0
3	NAG	B	268	14/15	0.79	0.24	-	68,68,68,68	0

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(\AA^2)	Q<0.9
4	GAL	B	280	12/12	0.76	0.41	5.25	25,25,25,25	0
4	GAL	B	290	12/12	0.75	0.39	2.39	51,51,51,51	0

6.5 Other polymers [i](#)

There are no such residues in this entry.