



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 04:19 AM UTC

PDB ID : 3UJO / pdb_00003ujo
Title : Galactose-specific seed lectin from Dolichos lablab in complex with adenine and galactose
Authors : Shetty, K.N.; Latha, V.L.; Rao, R.N.; Nadimpalli, S.K.; Suguna, K.
Deposited on : 2011-11-08
Resolution : 2.00 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

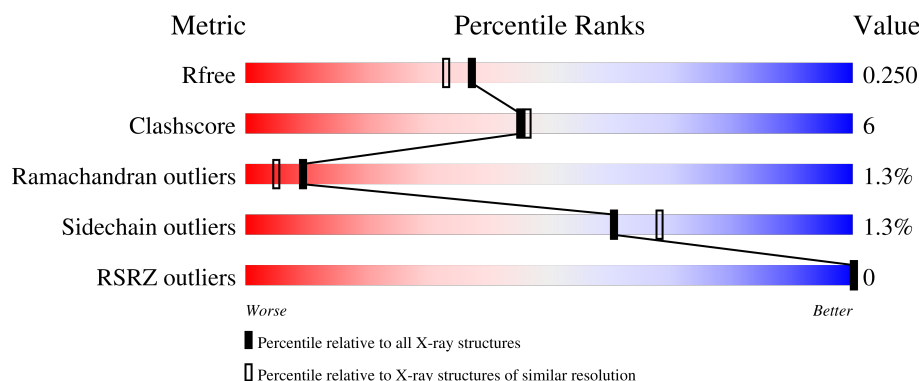
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

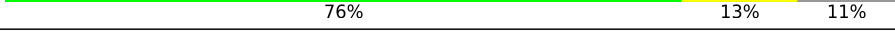
The reported resolution of this entry is 2.00 Å.

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}	180053	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	281	
1	B	281	
1	C	281	
1	D	281	

2 Entry composition [i](#)

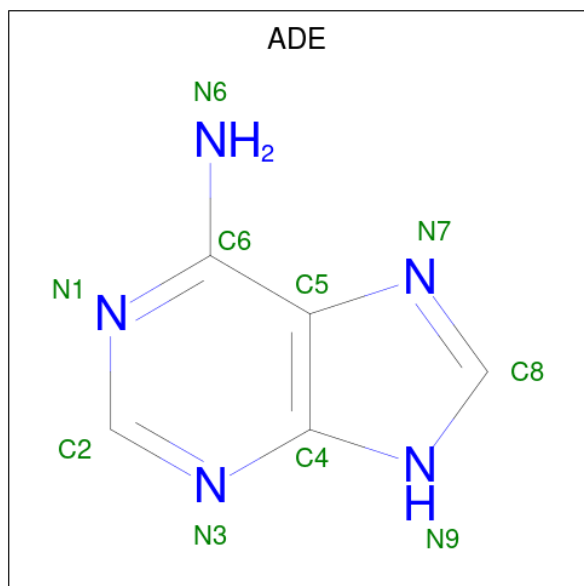
There are 8 unique types of molecules in this entry. The entry contains 7949 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Legume lectin.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	A	253	Total	C	N	O	0	0	0
			1926	1224	316	386			
1	B	253	Total	C	N	O	0	0	0
			1927	1224	317	386			
1	C	250	Total	C	N	O	0	0	0
			1904	1213	314	377			
1	D	250	Total	C	N	O	0	0	0
			1904	1213	314	377			

- Molecule 2 is ADENINE (CCD ID: ADE) (formula: C₅H₅N₅).



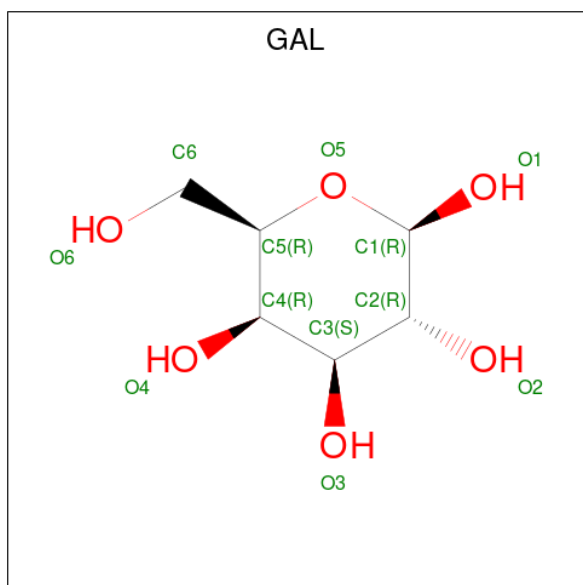
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	N	0	0
			10	5	5		
2	B	1	Total	C	N	0	0
			10	5	5		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	C	1	Total	C	N	0	0
			10	5	5		
2	D	1	Total	C	N	0	0
			10	5	5		

- Molecule 3 is beta-D-galactopyranose (CCD ID: GAL) (formula: C₆H₁₂O₆).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	1
			12	6	6		
3	B	1	Total	C	O	0	1
			12	6	6		
3	C	1	Total	C	O	0	1
			12	6	6		
3	D	1	Total	C	O	0	1
			12	6	6		

- Molecule 4 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Mn	0	0
			1	1		
4	B	1	Total	Mn	0	0
			1	1		
4	C	1	Total	Mn	0	0
			1	1		

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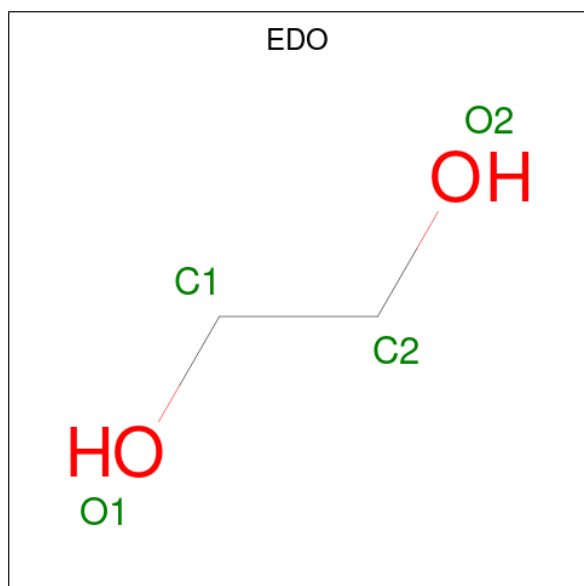
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	D	1	Total	Mn	0	0
			1	1		

- Molecule 5 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Ca	0	0
			1	1		
5	B	1	Total	Ca	0	0
			1	1		
5	C	1	Total	Ca	0	0
			1	1		
5	D	1	Total	Ca	0	0
			1	1		

- Molecule 6 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			4	2	2		
6	B	1	Total	C	O	0	0
			4	2	2		
6	C	1	Total	C	O	0	0
			4	2	2		
6	D	1	Total	C	O	0	0
			4	2	2		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	D	1	Total	C	O	0	0
			4	2	2		

- Molecule 7 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	B	1	Total	C	O	0	0
			7	4	3		
7	C	1	Total	C	O	0	0
			7	4	3		

- Molecule 8 is water.

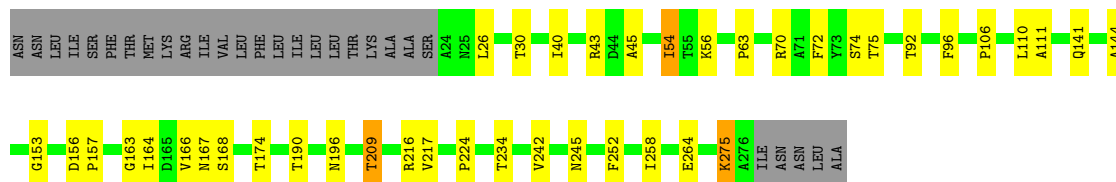
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	32	Total	O	0	0
			32	32		
8	B	43	Total	O	0	0
			43	43		
8	C	38	Total	O	0	0
			38	38		
8	D	45	Total	O	0	0
			45	45		

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

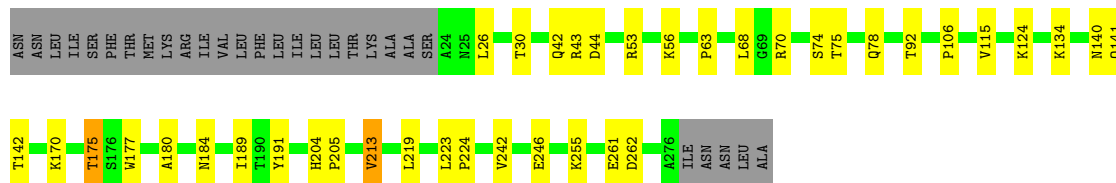
• Molecule 1: Legume lectin

Chain A: 



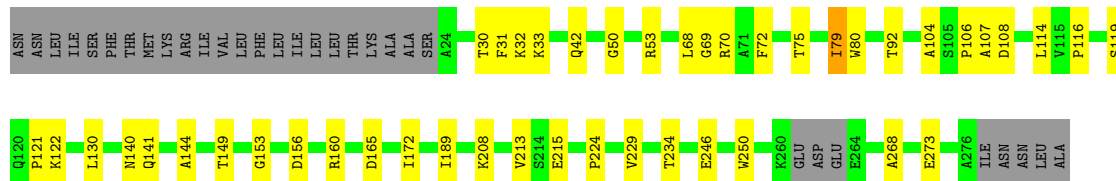
• Molecule 1: Legume lectin

Chain B: 



• Molecule 1: Legume lectin

Chain C: 



• Molecule 1: Legume lectin

Chain D: 





4 Data and refinement statistics

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, α , β , γ	89.78Å 89.78Å 123.89Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	42.20 – 2.00 42.20 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.6 (42.20-2.00) 99.8 (42.20-2.00)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.01 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.207 , 0.249 0.207 , 0.250	Depositor DCC
R_{free} test set	3794 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	30.0	Xtriage
Anisotropy	0.310	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 16.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.39$, $\langle L^2 \rangle = 0.21$	Xtriage
Estimated twinning fraction	0.470 for -h,-k,l 0.478 for h,-h-k,-l 0.470 for -k,-h,-l	Xtriage
Reported twinning fraction	0.253 for H, K, L 0.248 for -H, H+K, -L 0.248 for -h,-k,l 0.251 for K, H, -L	Depositor
Outliers	0 of 75267 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7949	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.44% 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, 0.333 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: GAL, EDO, ADE, CA, PEG, MN

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	0.43	0/1969	0.70	0/2683
1	B	0.41	0/1970	0.72	0/2683
1	C	0.40	0/1946	0.72	1/2649 (0.0%)
1	D	0.42	0/1946	0.75	2/2649 (0.1%)
All	All	0.42	0/7831	0.72	3/10664 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	32	LYS	N-CA-C	-7.05	106.58	114.62
1	D	156	ASP	N-CA-C	5.30	117.97	110.24
1	D	158	THR	N-CA-C	5.17	118.69	112.38

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	1926	0	1855	22	0
1	B	1927	0	1859	27	0
1	C	1904	0	1849	26	0
1	D	1904	0	1852	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	10	0	4	2	0
2	B	10	0	4	0	0
2	C	10	0	4	1	0
2	D	10	0	4	0	0
3	A	12	0	12	0	0
3	B	12	0	12	1	0
3	C	12	0	12	0	0
3	D	12	0	12	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
5	A	1	0	0	0	0
5	B	1	0	0	0	0
5	C	1	0	0	0	0
5	D	1	0	0	0	0
6	A	4	0	6	1	0
6	B	4	0	6	0	0
6	C	4	0	6	0	0
6	D	8	0	12	0	0
7	B	7	0	10	2	0
7	C	7	0	10	0	0
8	A	32	0	0	0	0
8	B	43	0	0	3	0
8	C	38	0	0	0	0
8	D	45	0	0	0	0
All	All	7949	0	7529	91	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 6.

All (91) 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:B:68:LEU:HD12	1:B:124:LYS:HG2	1.61	0.81
1:C:79:ILE:HD12	1:C:80:TRP:HD1	1.51	0.73
1:A:30:THR:OG1	1:B:26:LEU:HB2	1.89	0.71
1:C:172:ILE:HD12	1:C:215:GLU:HG2	1.79	0.63
1:A:216:ARG:HB3	1:C:208:LYS:HD3	1.81	0.62
1:B:219:LEU:HD22	1:B:223:LEU:HD12	1.82	0.62
1:D:160:ARG:HB2	1:D:177:TRP:O	2.00	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:53:ARG:HG2	1:B:246:GLU:HG2	1.82	0.61
1:A:196:ASN:HB2	1:A:216:ARG:HG3	1.82	0.61
1:D:51:LYS:HD2	1:D:248:LEU:HD22	1.83	0.60
1:A:63:PRO:HB2	1:A:242:VAL:HB	1.83	0.60
1:B:44:ASP:HB3	1:B:56:LYS:HG3	1.85	0.58
1:C:42:GLN:HB2	1:C:70:ARG:HB2	1.87	0.57
1:D:42:GLN:HB2	1:D:70:ARG:HB2	1.87	0.57
1:A:45:ALA:HB2	1:A:70:ARG:H	1.70	0.56
1:A:40:ILE:HD11	1:A:74:SER:HA	1.89	0.54
6:A:305:EDO:H12	1:B:26:LEU:HB3	1.89	0.54
1:C:31:PHE:HB2	1:C:250:TRP:H	1.74	0.53
1:B:205:PRO:HA	1:D:197:LEU:HD22	1.91	0.53
1:B:92:THR:HG22	1:B:189:ILE:HB	1.91	0.51
1:B:42:GLN:HB2	1:B:70:ARG:HB2	1.91	0.51
1:B:141:GLN:HB3	1:B:224:PRO:HD3	1.92	0.51
1:D:44:ASP:HB3	1:D:56:LYS:HG3	1.91	0.51
1:A:54:ILE:HD12	1:A:245:ASN:HB3	1.93	0.51
1:A:166:VAL:C	1:A:168:SER:H	2.19	0.50
1:D:97:ASN:HD22	1:D:184:ASN:ND2	2.10	0.50
1:D:188:LEU:HD21	1:D:267:LEU:HD11	1.92	0.50
1:C:79:ILE:HD12	1:C:80:TRP:CD1	2.41	0.50
1:B:43:ARG:HH12	1:B:124:LYS:HE2	1.77	0.49
1:D:167:ASN:ND2	1:D:222:VAL:HG13	2.27	0.49
1:B:175:THR:CG2	1:B:213:VAL:HG22	2.43	0.49
1:A:75:THR:HG23	1:B:75:THR:OG1	2.12	0.49
1:B:261:GLU:O	1:B:262:ASP:HB2	2.12	0.49
1:B:191:TYR:CZ	1:B:219:LEU:HG	2.48	0.48
7:B:306:PEG:H42	7:B:306:PEG:H21	1.44	0.48
1:A:141:GLN:HB3	1:A:224:PRO:HD3	1.95	0.48
1:C:70:ARG:HH21	1:C:130:LEU:HA	1.78	0.48
1:D:144:ALA:HB3	1:D:165:ASP:HB2	1.94	0.48
1:A:75:THR:HG22	1:B:74:SER:OG	2.13	0.48
1:A:153:GLY:H	1:A:156:ASP:HB2	1.78	0.48
1:C:53:ARG:HG2	1:C:246:GLU:HG2	1.95	0.47
1:C:114:LEU:HG	1:C:229:VAL:HG12	1.96	0.47
3:B:302[B]:GAL:O1	7:B:306:PEG:O4	2.27	0.47
1:C:42:GLN:OE1	1:C:121:PRO:HD3	2.15	0.47
1:C:153:GLY:H	1:C:156:ASP:HB2	1.80	0.47
1:C:30:THR:HG21	1:C:273:GLU:HG2	1.96	0.47
1:B:180:ALA:H	1:B:204:HIS:CE1	2.33	0.46
1:C:149:THR:HA	1:C:160:ARG:HD2	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:68:LEU:HD12	1:D:124:LYS:HA	1.97	0.46
1:B:26:LEU:HD11	1:B:255:LYS:HE3	1.97	0.46
1:B:63:PRO:HB2	1:B:242:VAL:HB	1.98	0.46
1:C:107:ALA:HA	1:C:108:ASP:HA	1.72	0.46
1:D:54:ILE:HG21	1:D:233:ALA:HB3	1.97	0.46
1:B:177:TRP:HE1	1:B:204:HIS:CE1	2.34	0.46
1:D:63:PRO:HG2	1:D:242:VAL:HB	1.98	0.46
1:D:219:LEU:HB3	1:D:223:LEU:HD12	1.97	0.45
1:D:68:LEU:HD13	1:D:124:LYS:HG2	1.98	0.45
1:D:54:ILE:O	1:D:69:GLY:HA3	2.17	0.45
1:D:92:THR:HB	1:D:252:PHE:HD1	1.81	0.45
1:D:167:ASN:HD21	1:D:222:VAL:HG13	1.82	0.45
1:A:163:GLY:HA3	1:A:174:THR:HG22	1.98	0.45
1:A:96:PHE:CD1	1:A:110:LEU:HD21	2.52	0.44
1:B:115:VAL:HG12	1:B:142:THR:HG23	2.00	0.44
1:A:26:LEU:HB2	1:B:30:THR:HB	1.99	0.44
1:C:116:PRO:HB2	1:C:119:SER:HB2	1.99	0.44
1:C:104:ALA:C	1:C:106:PRO:HD3	2.43	0.44
1:C:68:LEU:HD23	1:C:69:GLY:N	2.33	0.44
1:B:78:GLN:NE2	8:B:409:HOH:O	2.44	0.43
1:A:190:THR:OG1	2:A:301:ADE:N7	2.48	0.43
1:D:223:LEU:HD22	1:D:227:VAL:HG11	1.99	0.43
1:A:92:THR:HB	1:A:252:PHE:HD1	1.83	0.42
1:B:184:ASN:O	1:B:204:HIS:HD2	2.03	0.42
1:C:68:LEU:HG	1:C:234:THR:HG22	2.01	0.42
1:C:70:ARG:HD3	1:C:72:PHE:CE2	2.54	0.42
1:C:75:THR:OG1	1:D:75:THR:HG22	2.19	0.42
1:A:70:ARG:HB3	1:A:72:PHE:HE2	1.85	0.42
1:A:111:ALA:HB1	1:A:144:ALA:HB1	2.01	0.42
1:C:144:ALA:HB3	1:C:165:ASP:HB2	2.02	0.41
1:C:92:THR:HG22	1:C:189:ILE:HB	2.01	0.41
1:C:70:ARG:HD3	1:C:72:PHE:HE2	1.85	0.41
1:D:54:ILE:CG2	1:D:233:ALA:HB3	2.51	0.41
1:A:54:ILE:H	1:A:54:ILE:HG13	1.74	0.41
1:B:70:ARG:NH2	1:B:115:VAL:HG11	2.35	0.41
1:B:134:LYS:HD2	1:B:170:LYS:HD2	2.01	0.41
2:A:301:ADE:C2	2:C:301:ADE:C2	3.08	0.41
1:C:122:LYS:HE3	1:C:140:ASN:HB3	2.03	0.41
1:A:166:VAL:HG21	1:A:217:VAL:HG21	2.03	0.41
1:B:140:ASN:ND2	8:B:428:HOH:O	2.53	0.41
1:C:33:LYS:HD2	1:C:50:GLY:HA3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:74:SER:HB2	8:B:416:HOH:O	2.21	0.40
1:C:141:GLN:HB3	1:C:224:PRO:HD3	2.02	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	251/281 (89%)	222 (88%)	21 (8%)	8 (3%)	3	1
1	B	251/281 (89%)	237 (94%)	13 (5%)	1 (0%)	30	27
1	C	246/281 (88%)	226 (92%)	19 (8%)	1 (0%)	30	27
1	D	246/281 (88%)	229 (93%)	14 (6%)	3 (1%)	10	6
All	All	994/1124 (88%)	914 (92%)	67 (7%)	13 (1%)	9	5

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	56	LYS
1	A	157	PRO
1	A	258	ILE
1	A	167	ASN
1	C	268	ALA
1	A	43	ARG
1	A	275	LYS
1	D	273	GLU
1	A	209	THR
1	B	106	PRO
1	D	153	GLY
1	A	106	PRO
1	D	106	PRO

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	210/237 (89%)	204 (97%)	6 (3%)	37	40
1	B	210/237 (89%)	208 (99%)	2 (1%)	68	75
1	C	208/237 (88%)	206 (99%)	2 (1%)	68	75
1	D	208/237 (88%)	207 (100%)	1 (0%)	81	87
All	All	836/948 (88%)	825 (99%)	11 (1%)	61	68

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

Mol	Chain	Res	Type
1	A	54	ILE
1	A	164	ILE
1	A	209	THR
1	A	234	THR
1	A	264	GLU
1	A	275	LYS
1	B	175	THR
1	B	213	VAL
1	C	79	ILE
1	C	213	VAL
1	D	62	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	25	ASN
1	A	184	ASN
1	A	259	ASN
1	B	78	GLN
1	B	102	ASN
1	B	184	ASN
1	B	204	HIS
1	B	207	GLN

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Mol	Chain	Res	Type
1	C	35	ASN
1	C	99	GLN
1	C	120	GLN
1	C	135	ASN
1	C	204	HIS
1	C	265	ASN
1	D	78	GLN
1	D	99	GLN
1	D	184	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 23 ligands modelled in this entry, 8 are monoatomic - leaving 15 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	$\# Z > 2$
2	ADE	B	301	-	11,11,11	0.40	0	15,15,15	0.43	0
2	ADE	D	301	-	11,11,11	0.42	0	15,15,15	0.43	0
6	EDO	C	305	-	3,3,3	0.44	0	2,2,2	0.40	0
2	ADE	C	301	-	11,11,11	0.38	0	15,15,15	0.52	0
6	EDO	D	306	-	3,3,3	0.42	0	2,2,2	0.37	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	PEG	B	306	-	6,6,6	0.48	0	5,5,5	0.47	0
3	GAL	C	302[B]	-	12,12,12	0.54	0	17,17,17	0.79	0
3	GAL	B	302[B]	-	12,12,12	0.49	0	17,17,17	0.56	0
6	EDO	D	305	-	3,3,3	0.44	0	2,2,2	0.37	0
2	ADE	A	301	-	11,11,11	0.38	0	15,15,15	0.47	0
7	PEG	C	306	-	6,6,6	0.46	0	5,5,5	0.28	0
3	GAL	A	302[B]	-	12,12,12	0.54	0	17,17,17	0.58	0
6	EDO	B	305	-	3,3,3	0.43	0	2,2,2	0.34	0
6	EDO	A	305	-	3,3,3	0.36	0	2,2,2	0.46	0
3	GAL	D	302[B]	-	12,12,12	0.55	0	17,17,17	0.60	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
2	ADE	B	301	-	-	-	0/2/2/2
6	EDO	C	305	-	-	1/1/1/1	-
6	EDO	D	306	-	-	1/1/1/1	-
7	PEG	B	306	-	-	4/4/4/4	-
7	PEG	C	306	-	-	3/4/4/4	-
2	ADE	C	301	-	-	-	0/2/2/2
3	GAL	C	302[B]	-	-	2/2/22/22	0/1/1/1
3	GAL	B	302[B]	-	-	0/2/22/22	0/1/1/1
6	EDO	D	305	-	-	1/1/1/1	-
2	ADE	A	301	-	-	-	0/2/2/2
2	ADE	D	301	-	-	-	0/2/2/2
3	GAL	A	302[B]	-	-	2/2/22/22	0/1/1/1
6	EDO	B	305	-	-	1/1/1/1	-
6	EDO	A	305	-	-	1/1/1/1	-
3	GAL	D	302[B]	-	-	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.

All (16) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	B	306	PEG	C4-C3-O2-C2

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Mol	Chain	Res	Type	Atoms
3	A	302[B]	GAL	O5-C5-C6-O6
3	A	302[B]	GAL	C4-C5-C6-O6
7	B	306	PEG	O2-C3-C4-O4
6	D	305	EDO	O1-C1-C2-O2
3	C	302[B]	GAL	C4-C5-C6-O6
6	A	305	EDO	O1-C1-C2-O2
6	C	305	EDO	O1-C1-C2-O2
7	B	306	PEG	C1-C2-O2-C3
7	C	306	PEG	C1-C2-O2-C3
7	C	306	PEG	C4-C3-O2-C2
6	B	305	EDO	O1-C1-C2-O2
6	D	306	EDO	O1-C1-C2-O2
3	C	302[B]	GAL	O5-C5-C6-O6
7	C	306	PEG	O1-C1-C2-O2
7	B	306	PEG	O1-C1-C2-O2

There are no ring outliers.

5 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	301	ADE	1	0
7	B	306	PEG	2	0
3	B	302[B]	GAL	1	0
2	A	301	ADE	2	0
6	A	305	EDO	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [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	253/281 (90%)	-0.79	0 100 100	15, 45, 67, 69	14 (5%)
1	B	253/281 (90%)	-1.33	0 100 100	18, 24, 30, 38	14 (5%)
1	C	250/281 (88%)	-1.14	0 100 100	20, 30, 36, 38	14 (5%)
1	D	250/281 (88%)	-1.26	0 100 100	16, 27, 33, 35	14 (5%)
All	All	1006/1124 (89%)	-1.13	0 100 100	15, 29, 58, 69	56 (5%)

There are no RSRZ outliers to report.

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 oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	GAL	C	302[B]	12/12	0.98	0.05	30,30,31,31	12
3	GAL	D	302[B]	12/12	0.98	0.05	26,27,27,27	12
6	EDO	C	305	4/4	0.98	0.05	24,24,24,24	0
2	ADE	D	301	10/10	0.99	0.05	36,36,37,37	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	GAL	A	302[B]	12/12	0.99	0.05	28,29,29,29	12
3	GAL	B	302[B]	12/12	0.99	0.04	16,18,19,20	12
2	ADE	A	301	10/10	0.99	0.03	30,30,30,30	0
2	ADE	B	301	10/10	0.99	0.04	41,41,42,42	0
5	CA	A	304	1/1	0.99	0.04	49,49,49,49	0
6	EDO	A	305	4/4	0.99	0.03	20,20,21,21	0
6	EDO	B	305	4/4	0.99	0.03	26,26,26,27	0
2	ADE	C	301	10/10	0.99	0.04	27,27,27,27	0
6	EDO	D	305	4/4	0.99	0.03	26,26,26,26	0
6	EDO	D	306	4/4	0.99	0.04	28,28,28,29	0
7	PEG	B	306	7/7	0.99	0.03	20,21,22,22	0
7	PEG	C	306	7/7	0.99	0.03	28,28,29,29	0
4	MN	B	303	1/1	1.00	0.02	35,35,35,35	0
4	MN	C	303	1/1	1.00	0.04	36,36,36,36	0
4	MN	D	303	1/1	1.00	0.02	47,47,47,47	0
4	MN	A	303	1/1	1.00	0.06	57,57,57,57	0
5	CA	B	304	1/1	1.00	0.01	24,24,24,24	0
5	CA	C	304	1/1	1.00	0.01	31,31,31,31	0
5	CA	D	304	1/1	1.00	0.02	31,31,31,31	0

6.5 Other polymers

There are no such residues in this entry.