



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 05:06 PM UTC

PDB ID : 3U27 / pdb_00003u27
Title : Crystal structure of ethanolamine utilization protein EutL from *Leptotrichia buccalis* C-1013-b
Authors : Wu, R.; Gu, M.; Kerfeld, C.A.; Salmeen, A.; Joachimiak, A.; Midwest Center for Structural Genomics (MCSG)
Deposited on : 2011-10-01
Resolution : 1.85 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

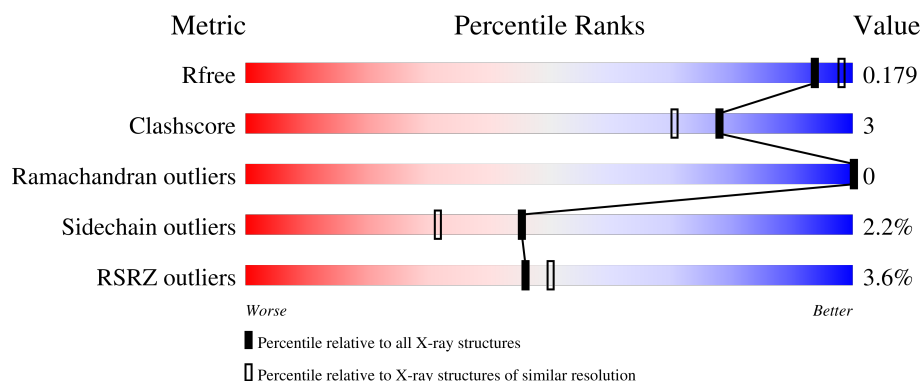
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.85 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.



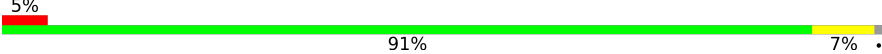
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	3428 (1.86-1.86)
Clashscore	190562	3579 (1.86-1.86)
Ramachandran outliers	187476	3553 (1.86-1.86)
Sidechain outliers	187428	3553 (1.86-1.86)
RSRZ outliers	180081	3429 (1.86-1.86)

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	220	2% 92% 6% ..
1	B	220	4% 92% 6% .
1	C	220	3% 95% . ..
1	D	220	4% 92% 6% ..
1	E	220	4% 94% 5% .

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Mol	Chain	Length	Quality of chain
1	F	220	 A horizontal bar chart showing the quality of chain 1. The bar is divided into three segments: a small red segment at the beginning labeled '5%', a long green segment in the middle labeled '91%', and a small yellow segment at the end labeled '7%'. A small grey dot is visible at the far right end of the bar.

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	GOL	F	302	-	-	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 10884 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 Microcompartments protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	C	218	Total	C	N	O	S	Se	0	2	0
			1608	1020	263	318	4	3			
1	A	217	Total	C	N	O	S	Se	0	2	0
			1604	1014	263	320	4	3			
1	B	217	Total	C	N	O	S	Se	0	3	0
			1612	1019	266	320	4	3			
1	D	218	Total	C	N	O	S	Se	0	1	0
			1603	1016	261	319	4	3			
1	E	218	Total	C	N	O	S	Se	0	2	0
			1603	1015	262	319	4	3			
1	F	218	Total	C	N	O	S	Se	0	4	0
			1622	1024	269	322	4	3			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-2	SER	-	expression tag	UNP C7NCS6
C	-1	ASN	-	expression tag	UNP C7NCS6
C	0	ALA	-	expression tag	UNP C7NCS6
A	-2	SER	-	expression tag	UNP C7NCS6
A	-1	ASN	-	expression tag	UNP C7NCS6
A	0	ALA	-	expression tag	UNP C7NCS6
B	-2	SER	-	expression tag	UNP C7NCS6
B	-1	ASN	-	expression tag	UNP C7NCS6
B	0	ALA	-	expression tag	UNP C7NCS6
D	-2	SER	-	expression tag	UNP C7NCS6
D	-1	ASN	-	expression tag	UNP C7NCS6
D	0	ALA	-	expression tag	UNP C7NCS6
E	-2	SER	-	expression tag	UNP C7NCS6
E	-1	ASN	-	expression tag	UNP C7NCS6
E	0	ALA	-	expression tag	UNP C7NCS6
F	-2	SER	-	expression tag	UNP C7NCS6
F	-1	ASN	-	expression tag	UNP C7NCS6

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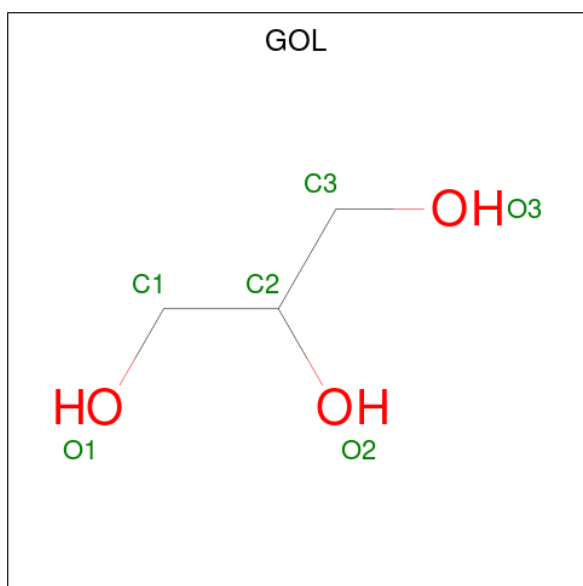
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Chain	Residue	Modelled	Actual	Comment	Reference
F	0	ALA	-	expression tag	UNP C7NCS6

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	C	2	Total 2 Ca 2	0	0
2	A	2	Total 2 Ca 2	0	0

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



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

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

- Molecule 4 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	C	2	Total	Na	0	0
			2	2		
4	A	1	Total	Na	0	0
			1	1		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	C	210	Total	O	0	0
			210	210		
5	A	214	Total	O	0	0
			214	214		
5	B	198	Total	O	0	0
			198	198		
5	D	194	Total	O	0	0
			194	194		
5	E	183	Total	O	0	0
			183	183		
5	F	172	Total	O	0	0
			172	172		

3 Residue-property plots [i](#)

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

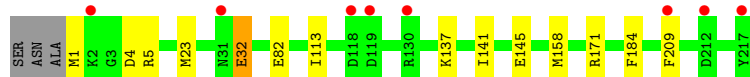
- Molecule 1: Microcompartments protein



- Molecule 1: Microcompartments protein



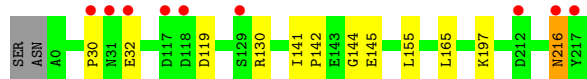
- Molecule 1: Microcompartments protein



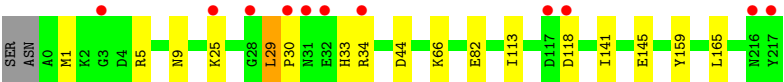
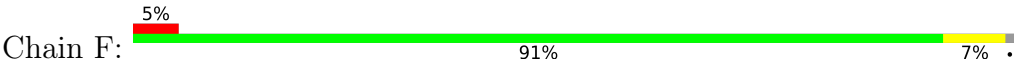
- Molecule 1: Microcompartments protein



- Molecule 1: Microcompartments protein



- Molecule 1: Microcompartments protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	100.85Å 105.64Å 101.55Å 90.00° 90.06° 90.00°	Depositor
Resolution (Å)	34.42 – 1.85 34.42 – 1.85	Depositor EDS
% Data completeness (in resolution range)	97.6 (34.42-1.85) 97.6 (34.42-1.85)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.03 (at 1.85Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.1_743)	Depositor
R, R_{free}	0.157 , 0.182 0.155 , 0.179	Depositor DCC
R_{free} test set	8843 reflections (4.89%)	wwPDB-VP
Wilson B-factor (Å ²)	21.9	Xtriage
Anisotropy	0.010	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 52.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.016 for -h,-l,-k 0.015 for -h,l,k 0.012 for k,h,-l 0.012 for -k,-h,-l 0.013 for l,k,-h 0.016 for l,h,k 0.017 for k,l,h 0.017 for k,-l,-h 0.017 for -l,-h,k 0.449 for h,-k,-l 0.014 for l,-k,h	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	10884	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.19% 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: GOL, NA, CA

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	0/1633	0.74	0/2217
1	B	0.44	0/1644	0.73	0/2231
1	C	0.45	0/1640	0.75	0/2225
1	D	0.45	0/1629	0.73	0/2211
1	E	0.43	0/1634	0.72	0/2217
1	F	0.45	0/1653	0.76	1/2242 (0.0%)
All	All	0.45	0/9833	0.74	1/13343 (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	F	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	29	LEU	CA-C-O	-5.52	114.47	120.87

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	F	29	LEU	Mainchain

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	1604	0	1586	10	0
1	B	1612	0	1599	11	0
1	C	1608	0	1595	7	0
1	D	1603	0	1581	11	0
1	E	1603	0	1588	8	0
1	F	1622	0	1608	11	0
2	A	2	0	0	0	0
2	C	2	0	0	0	0
3	A	18	0	24	2	0
3	B	6	0	8	3	0
3	C	12	0	16	1	0
3	D	6	0	8	0	0
3	F	12	0	16	4	0
4	A	1	0	0	0	0
4	C	2	0	0	0	0
5	A	214	0	0	0	0
5	B	198	0	0	3	0
5	C	210	0	0	2	0
5	D	194	0	0	2	0
5	E	183	0	0	1	0
5	F	172	0	0	3	0
All	All	10884	0	9629	54	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 3.

All (54) 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:D:213:ASN:HB3	1:D:216:ASN:HD22	1.28	0.99
1:F:82:GLU:OE1	3:F:302:GOL:H31	1.83	0.79
1:D:213:ASN:HB3	1:D:216:ASN:ND2	2.04	0.73
1:B:184:PHE:CE2	3:B:301:GOL:H31	2.24	0.72
1:E:216:ASN:N	1:E:216:ASN:OD1	2.24	0.69
1:B:141:ILE:HD12	1:B:145:GLU:HB3	1.77	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:66:LYS:NZ	5:F:509:HOH:O	2.26	0.65
1:D:141:ILE:HD12	1:D:145:GLU:HB3	1.80	0.64
1:C:82:GLU:OE1	3:C:302:GOL:H2	1.99	0.61
1:D:131:THR:HG21	1:D:147:LEU:HD22	1.88	0.55
1:C:129:SER:C	1:C:130:ARG:HD2	2.34	0.53
1:D:14:ARG:HG2	1:F:159:TYR:CD1	2.43	0.53
1:A:131:THR:HG21	1:A:147:LEU:HD22	1.91	0.53
1:F:5[A]:ARG:HG2	1:F:113:ILE:CD1	2.39	0.53
1:A:129:SER:C	1:A:130:ARG:HD2	2.34	0.52
1:E:142:PRO:HD2	1:E:145:GLU:HG3	1.93	0.52
1:F:34[B]:ARG:HG2	5:F:549:HOH:O	2.09	0.51
1:F:30:PRO:HG2	1:F:33:HIS:CG	2.46	0.51
1:A:82:GLU:OE1	3:A:304:GOL:H31	2.10	0.51
1:A:20:ASP:OD1	3:A:303:GOL:H2	2.11	0.51
1:F:9[B]:ASN:ND2	5:F:423:HOH:O	2.43	0.50
1:D:5:ARG:NE	5:D:488:HOH:O	2.21	0.50
1:E:141:ILE:HD12	1:E:145:GLU:HB2	1.94	0.50
1:B:1:MSE:HB2	1:B:4:ASP:OD2	2.11	0.49
1:B:145:GLU:HG3	5:B:416:HOH:O	2.13	0.49
1:F:141:ILE:HD12	1:F:145:GLU:HB2	1.95	0.48
1:E:119:ASP:OD2	5:E:385:HOH:O	2.20	0.48
1:D:145:GLU:HG3	5:D:419:HOH:O	2.13	0.48
1:B:158:MSE:HA	1:B:158:MSE:HE2	1.95	0.47
1:C:131:THR:HG21	1:C:147:LEU:HD22	1.97	0.47
1:A:107[B]:GLU:OE1	1:E:32:GLU:HG2	2.15	0.47
1:A:23:MSE:CE	1:D:162:ASP:HA	2.46	0.46
1:F:82:GLU:CD	3:F:302:GOL:H31	2.40	0.46
1:E:130:ARG:HD3	1:E:144:GLY:O	2.16	0.45
1:B:5[A]:ARG:HG2	1:B:113:ILE:CD1	2.47	0.45
1:D:19:VAL:HG22	1:D:23:MSE:HB3	1.99	0.44
1:B:184:PHE:CD2	3:B:301:GOL:H11	2.52	0.43
1:F:82:GLU:OE1	3:F:302:GOL:H11	2.18	0.43
1:D:39:LEU:HD12	1:D:39:LEU:C	2.43	0.43
1:B:82:GLU:OE1	3:B:301:GOL:H2	2.18	0.43
1:A:137:LYS:HE2	1:A:137:LYS:HB2	1.65	0.43
1:D:131:THR:CG2	1:D:147:LEU:HD22	2.48	0.43
1:A:158:MSE:HE2	1:A:158:MSE:HA	2.01	0.43
1:B:137:LYS:HE3	5:B:586:HOH:O	2.19	0.43
1:C:34:ARG:HD2	5:C:573:HOH:O	2.19	0.42
1:B:32[B]:GLU:CG	5:B:479:HOH:O	2.67	0.42
1:F:44:ASP:OD1	3:F:302:GOL:H11	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:104:ASP:OD2	5:C:600:HOH:O	2.21	0.41
1:A:118:ASP:OD2	1:A:120:SER:OG	2.37	0.41
1:C:39:LEU:C	1:C:39:LEU:HD12	2.46	0.41
1:C:14:ARG:HE	1:B:209:PHE:HE2	1.67	0.41
1:A:39:LEU:C	1:A:39:LEU:HD12	2.45	0.41
1:E:155:LEU:C	1:E:155:LEU:HD23	2.46	0.41
1:E:30:PRO:O	1:E:32:GLU:N	2.55	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	217/220 (99%)	212 (98%)	5 (2%)	0	100	100
1	B	218/220 (99%)	212 (97%)	6 (3%)	0	100	100
1	C	218/220 (99%)	214 (98%)	4 (2%)	0	100	100
1	D	217/220 (99%)	211 (97%)	6 (3%)	0	100	100
1	E	218/220 (99%)	211 (97%)	7 (3%)	0	100	100
1	F	220/220 (100%)	213 (97%)	7 (3%)	0	100	100
All	All	1308/1320 (99%)	1273 (97%)	35 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

The Analysed column shows the number of residues for which the sidechain conformation was

analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	164/161 (102%)	160 (98%)	4 (2%)	43	28
1	B	165/161 (102%)	161 (98%)	4 (2%)	43	28
1	C	164/161 (102%)	162 (99%)	2 (1%)	63	55
1	D	163/161 (101%)	158 (97%)	5 (3%)	35	20
1	E	163/161 (101%)	160 (98%)	3 (2%)	51	40
1	F	166/161 (103%)	162 (98%)	4 (2%)	43	28
All	All	985/966 (102%)	963 (98%)	22 (2%)	45	32

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	18	ASN
1	C	130	ARG
1	A	18	ASN
1	A	130	ARG
1	A	147	LEU
1	A	197	LYS
1	B	23	MSE
1	B	32[A]	GLU
1	B	32[B]	GLU
1	B	171	ARG
1	D	14	ARG
1	D	18	ASN
1	D	119	ASP
1	D	147	LEU
1	D	189	LEU
1	E	165	LEU
1	E	197	LYS
1	E	216	ASN
1	F	1	MSE
1	F	25	LYS
1	F	118	ASP
1	F	165	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	108	ASN

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Mol	Chain	Res	Type
1	D	31	ASN
1	D	216	ASN
1	E	74	ASN
1	F	108	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 16 ligands modelled in this entry, 7 are monoatomic - leaving 9 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	$\# Z > 2$
3	GOL	C	303	-	5,5,5	0.38	0	5,5,5	0.39	0
3	GOL	B	301	-	5,5,5	0.37	0	5,5,5	0.21	0
3	GOL	C	302	-	5,5,5	0.37	0	5,5,5	0.39	0
3	GOL	A	303	-	5,5,5	0.37	0	5,5,5	0.33	0
3	GOL	A	304	-	5,5,5	0.33	0	5,5,5	0.38	0
3	GOL	F	302	-	5,5,5	0.37	0	5,5,5	0.31	0
3	GOL	A	305	-	5,5,5	0.41	0	5,5,5	0.23	0
3	GOL	F	301	-	5,5,5	0.36	0	5,5,5	0.43	0
3	GOL	D	301	-	5,5,5	0.40	0	5,5,5	0.67	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
3	GOL	C	303	-	-	0/4/4/4	-
3	GOL	B	301	-	-	3/4/4/4	-
3	GOL	C	302	-	-	2/4/4/4	-
3	GOL	A	303	-	-	2/4/4/4	-
3	GOL	A	304	-	-	2/4/4/4	-
3	GOL	F	302	-	-	2/4/4/4	-
3	GOL	A	305	-	-	4/4/4/4	-
3	GOL	F	301	-	-	0/4/4/4	-
3	GOL	D	301	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (17) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	302	GOL	O1-C1-C2-C3
3	A	304	GOL	O1-C1-C2-C3
3	A	305	GOL	C1-C2-C3-O3
3	B	301	GOL	O1-C1-C2-O2
3	B	301	GOL	O1-C1-C2-C3
3	D	301	GOL	C1-C2-C3-O3
3	C	302	GOL	O1-C1-C2-O2
3	A	304	GOL	O1-C1-C2-O2
3	A	305	GOL	O1-C1-C2-C3
3	F	302	GOL	C1-C2-C3-O3
3	A	305	GOL	O2-C2-C3-O3
3	A	305	GOL	O1-C1-C2-O2
3	F	302	GOL	O2-C2-C3-O3
3	D	301	GOL	O2-C2-C3-O3
3	A	303	GOL	O1-C1-C2-O2
3	B	301	GOL	O2-C2-C3-O3
3	A	303	GOL	O1-C1-C2-C3

There are no ring outliers.

5 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	301	GOL	3	0
3	C	302	GOL	1	0
3	A	303	GOL	1	0
3	A	304	GOL	1	0
3	F	302	GOL	4	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, 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	214/220 (97%)	-0.34	5 (2%)	61	64	13, 21, 41, 64	5 (2%)
1	B	214/220 (97%)	-0.29	8 (3%)	45	49	11, 21, 42, 63	6 (2%)
1	C	215/220 (97%)	-0.32	6 (2%)	55	58	10, 21, 41, 65	5 (2%)
1	D	215/220 (97%)	-0.24	8 (3%)	45	49	13, 21, 41, 61	3 (1%)
1	E	215/220 (97%)	-0.16	9 (4%)	40	44	15, 23, 46, 79	3 (1%)
1	F	215/220 (97%)	-0.15	11 (5%)	33	36	14, 23, 48, 75	7 (3%)
All	All	1288/1320 (97%)	-0.25	47 (3%)	46	50	10, 21, 44, 79	29 (2%)

All (47) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	209[A]	PHE	9.7
1	F	34[A]	ARG	5.1
1	F	30	PRO	4.8
1	E	118	ASP	4.6
1	D	0	ALA	4.5
1	F	32	GLU	4.4
1	A	209	PHE	4.3
1	C	209[C]	PHE	4.2
1	E	32	GLU	4.0
1	B	209	PHE	3.9
1	A	118	ASP	3.9
1	F	118	ASP	3.8
1	E	31	ASN	3.7
1	E	216	ASN	3.7
1	E	30	PRO	3.7
1	B	118	ASP	3.6
1	C	0	ALA	3.5
1	B	119	ASP	3.4
1	D	118	ASP	3.2

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Mol	Chain	Res	Type	RSRZ
1	D	119	ASP	3.1
1	F	31	ASN	3.1
1	F	216	ASN	3.0
1	E	217	TYR	3.0
1	A	117	ASP	2.9
1	F	28	GLY	2.9
1	F	217	TYR	2.8
1	A	213	ASN	2.8
1	C	117	ASP	2.6
1	E	212	ASP	2.6
1	F	117	ASP	2.6
1	D	2	LYS	2.5
1	B	2	LYS	2.5
1	B	130	ARG	2.4
1	D	217	TYR	2.4
1	C	216	ASN	2.4
1	B	217	TYR	2.4
1	D	117	ASP	2.4
1	D	216	ASN	2.3
1	C	118	ASP	2.3
1	E	117	ASP	2.3
1	F	25	LYS	2.2
1	B	31	ASN	2.2
1	C	119	ASP	2.2
1	A	216	ASN	2.1
1	F	3	GLY	2.0
1	B	212	ASP	2.0
1	E	129	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 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	GOL	A	303	6/6	0.60	0.27	60,69,72,72	0
3	GOL	A	305	6/6	0.68	0.21	36,54,56,60	0
3	GOL	D	301	6/6	0.82	0.22	42,47,50,52	0
3	GOL	C	302	6/6	0.83	0.20	27,53,60,62	0
3	GOL	A	304	6/6	0.85	0.14	44,57,60,63	0
3	GOL	C	303	6/6	0.86	0.15	42,44,46,48	0
3	GOL	F	302	6/6	0.86	0.22	27,54,65,69	0
4	NA	C	306	1/1	0.87	0.21	36,36,36,36	0
3	GOL	B	301	6/6	0.89	0.14	28,50,53,60	0
3	GOL	F	301	6/6	0.89	0.14	43,50,53,54	0
4	NA	C	305	1/1	0.95	0.13	31,31,31,31	0
4	NA	A	306	1/1	0.98	0.12	30,30,30,30	0
2	CA	C	304	1/1	0.99	0.03	21,21,21,21	0
2	CA	C	301	1/1	1.00	0.11	3,3,3,3	1
2	CA	A	301	1/1	1.00	0.02	21,21,21,21	0
2	CA	A	302	1/1	1.00	0.02	14,14,14,14	0

6.5 Other polymers [i](#)

There are no such residues in this entry.