Full wwPDB X-ray Structure Validation Report ⓘ

Aug 22, 2023 – 04:31 PM EDT

PDB ID	:	3BY0
Title	:	Crystal structure of Siderocalin (NGAL, Lipocalin 2) W79A-R81A complexed with Ferric Enterobactin
Authors	:	Clifton, M.C.; Pizzaro, J.C.; Strong, R.K.
Deposited on	:	2008-01-15
Resolution	:	2.57 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:

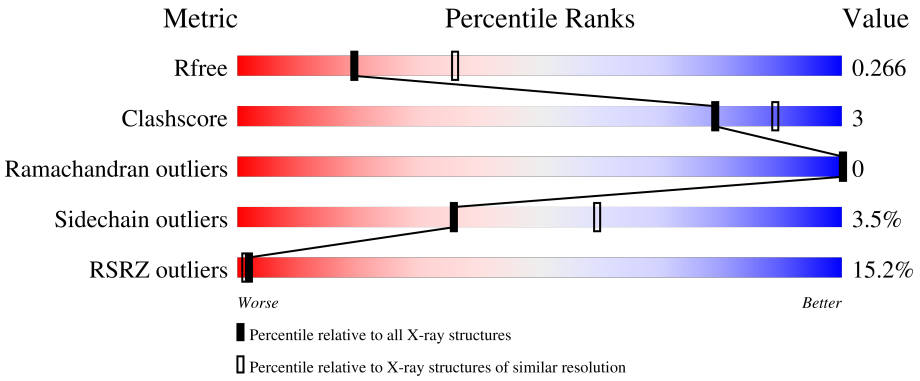
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.57 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}	130704	3676 (2.60-2.56)
Clashscore	141614	4049 (2.60-2.56)
Ramachandran outliers	138981	3979 (2.60-2.56)
Sidechain outliers	138945	3979 (2.60-2.56)
RSRZ outliers	127900	3614 (2.60-2.56)

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 <=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	198	5% 81% 6% • 12%
1	B	198	31% 77% 9% 14%
1	C	198	4% 74% 13% • 12%

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 4403 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 Neutrophil gelatinase-associated lipocalin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	174	Total	C	N	O	S	0	2	0
			1405	909	232	260	4			
1	B	171	Total	C	N	O	S	4	1	0
			1362	883	222	253	4			
1	C	174	Total	C	N	O	S	0	5	0
			1432	926	240	262	4			

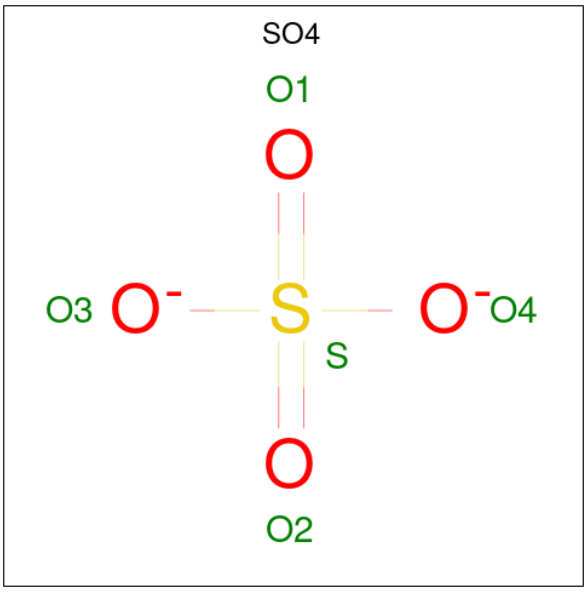
There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	79	ALA	TRP	engineered mutation	UNP P80188
A	81	ALA	ARG	engineered mutation	UNP P80188
A	87	SER	CYS	engineered mutation	UNP P80188
B	79	ALA	TRP	engineered mutation	UNP P80188
B	81	ALA	ARG	engineered mutation	UNP P80188
B	87	SER	CYS	engineered mutation	UNP P80188
C	79	ALA	TRP	engineered mutation	UNP P80188
C	81	ALA	ARG	engineered mutation	UNP P80188
C	87	SER	CYS	engineered mutation	UNP P80188

- Molecule 2 is FE (III) ION (three-letter code: FE) (formula: Fe).

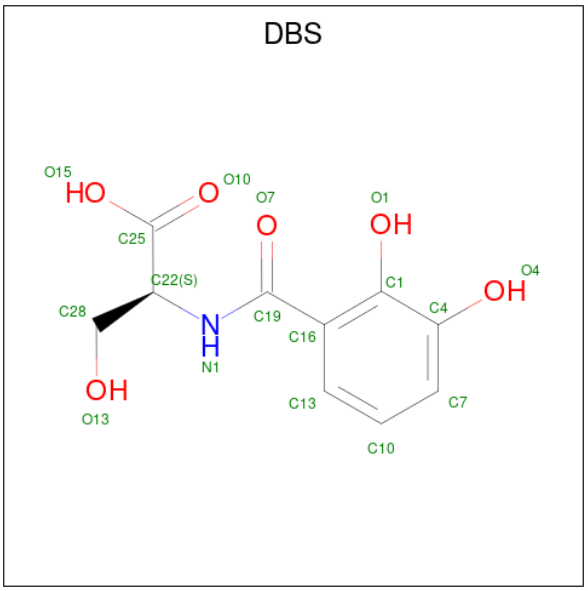
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Fe	0	0
			1	1		
2	B	1	Total	Fe	0	0
			1	1		
2	C	1	Total	Fe	0	0
			1	1		

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total O S 5 4 1	0	0
3	C	1	Total O S 5 4 1	0	0

- Molecule 4 is 2-(2,3-DIHYDROXY-BENZOYLAMINO)-3-HYDROXY-PROPIONIC ACID (three-letter code: DBS) (formula: $C_{10}H_{11}NO_6$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C N O 17 10 1 6	0	0

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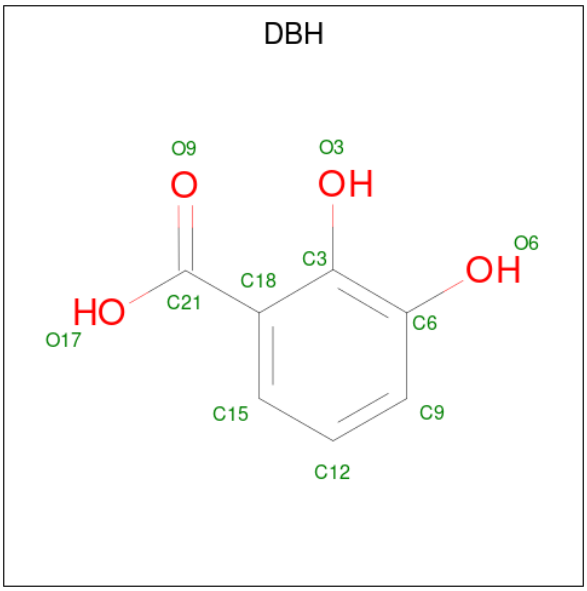
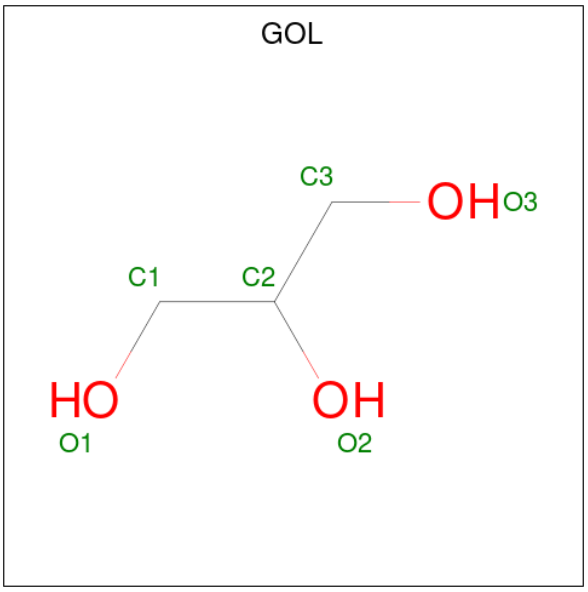
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	C	1	Total C N O 17 10 1 6	0	0
4	C	1	Total C N O 17 10 1 6	0	0

- Molecule 5 is 2,3-DIHYDROXY-BENZOIC ACID (three-letter code: DBH) (formula: $C_7H_6O_4$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 11 7 4	0	0
5	A	1	Total C O 11 7 4	0	0
5	B	1	Total C O 11 7 4	0	0
5	C	1	Total C O 11 7 4	0	0

- Molecule 6 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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

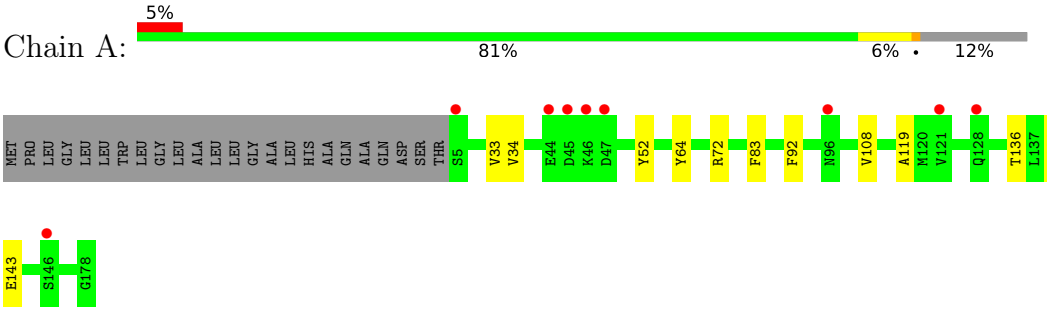
- Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	31	Total O 31 31	0	0
7	B	1	Total O 1 1	0	0
7	C	46	Total O 46 46	0	0

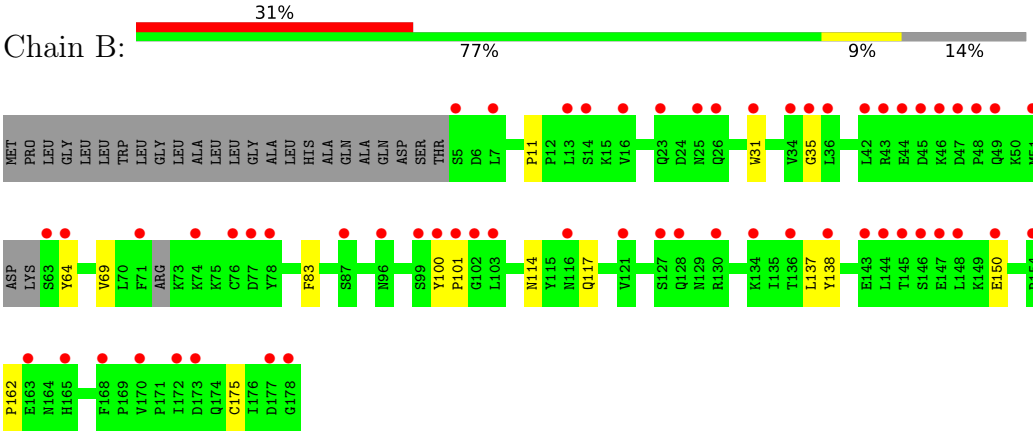
3 Residue-property plots (i)

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.

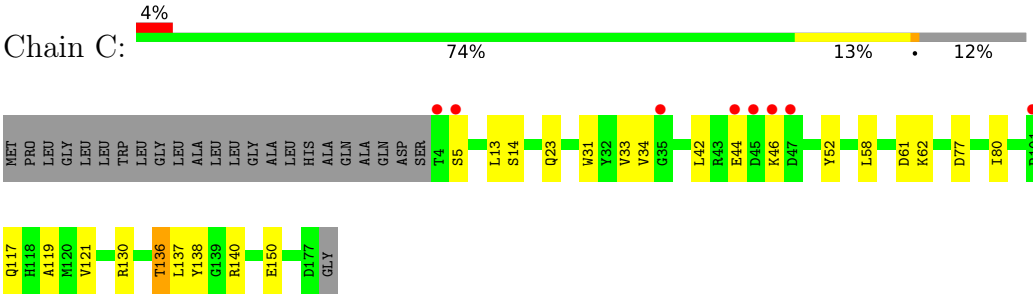
• Molecule 1: Neutrophil gelatinase-associated lipocalin



• Molecule 1: Neutrophil gelatinase-associated lipocalin



• Molecule 1: Neutrophil gelatinase-associated lipocalin



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α, β, γ	114.36Å 114.36Å 119.04Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	28.59 – 2.57 28.59 – 2.57	Depositor EDS
% Data completeness (in resolution range)	99.7 (28.59-2.57) 99.7 (28.59-2.57)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	6.35 (at 2.57Å)	Xtriage
Refinement program	REFMAC 5.2	Depositor
R, R_{free}	0.248 , 0.262 0.247 , 0.266	Depositor DCC
R_{free} test set	2410 reflections (9.41%)	wwPDB-VP
Wilson B-factor (Å^2)	49.9	Xtriage
Anisotropy	0.003	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 40.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.014 for -h,l,k 0.010 for -l,-k,-h	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	4403	wwPDB-VP
Average B, all atoms (Å^2)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.17% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 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: FE, DBH, GOL, SO4, DBS

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	0.32	0/1446	0.47	0/1958
1	B	0.34	0/1398	0.45	0/1895
1	C	0.35	0/1485	0.49	0/2010
All	All	0.34	0/4329	0.47	0/5863

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	1405	0	1400	7	0
1	B	1362	0	1335	8	0
1	C	1432	0	1436	10	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
3	A	5	0	0	0	0
3	C	5	0	0	0	0
4	A	17	0	8	0	0
4	C	34	0	16	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	22	0	6	0	0
5	B	11	0	3	0	0
5	C	11	0	3	0	0
6	A	6	0	8	0	0
6	C	12	0	16	0	0
7	A	31	0	0	0	0
7	B	1	0	0	0	0
7	C	46	0	0	0	0
All	All	4403	0	4231	24	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 (24) 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:A:140:ARG:HG2	1:C:23:GLN:NE2	2.11	0.65
1:C:5:SER:O	1:C:130:ARG:NH1	2.39	0.54
1:B:64:TYR:HB2	1:B:83:PHE:HB2	1.90	0.54
1:A:92:PHE:HB2	1:A:108:VAL:HB	1.89	0.54
1:C:31:TRP:CE3	1:C:138:TYR:HB3	2.43	0.52
1:B:31:TRP:CE3	1:B:138:TYR:HB3	2.46	0.49
1:C:119:ALA:HB3	1:C:138:TYR:HB2	1.93	0.49
1:B:35:GLY:HA3	1:B:137:LEU:HB3	1.94	0.48
1:A:119:ALA:HB3	1:A:138:TYR:HB2	1.97	0.47
1:C:33:VAL:HG21	1:C:52:TYR:CE2	2.50	0.47
1:C:121:VAL:HB	1:C:136:THR:HG22	1.97	0.46
1:B:69:VAL:HG22	1:B:175:CYS:HB3	1.99	0.45
1:A:33:VAL:HG21	1:A:52:TYR:CE2	2.52	0.45
1:A:136:THR:HG21	1:A:138:TYR:CE1	2.52	0.44
1:B:161:LEU:HA	1:B:162:PRO:HD3	1.85	0.44
1:C:114:ASN:HD21	1:C:117:GLN:HB2	1.82	0.44
1:C:61:ASP:O	1:C:62:LYS:HB2	2.17	0.43
1:B:100:TYR:HA	1:B:101:PRO:HD3	1.87	0.43
1:A:33:VAL:HG13	1:A:136:THR:HG23	1.99	0.43
1:C:44:GLU:HG3	1:C:46:LYS:HD2	2.01	0.43
1:A:64:TYR:HB2	1:A:83:PHE:HB2	2.01	0.42
1:B:114:ASN:HD21	1:B:117:GLN:HB2	1.85	0.42
1:C:115:TYR:O	1:C:140:ARG:HD2	2.20	0.42
1:B:11:PRO:HG3	1:B:159:LEU:HB3	2.01	0.41

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	174/198 (88%)	171 (98%)	3 (2%)	0	100	100
1	B	166/198 (84%)	158 (95%)	8 (5%)	0	100	100
1	C	177/198 (89%)	173 (98%)	4 (2%)	0	100	100
All	All	517/594 (87%)	502 (97%)	15 (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	157/174 (90%)	153 (98%)	4 (2%)	47	70
1	B	150/174 (86%)	148 (99%)	2 (1%)	69	85
1	C	162/174 (93%)	152 (94%)	10 (6%)	18	35
All	All	469/522 (90%)	453 (97%)	16 (3%)	36	60

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	34	VAL
1	A	72	ARG

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Mol	Chain	Res	Type
1	A	140	ARG
1	A	143	GLU
1	B	58	LEU
1	B	150	GLU
1	C	13	LEU
1	C	14	SER
1	C	34	VAL
1	C	42	LEU
1	C	58	LEU
1	C	77	ASP
1	C	80	ILE
1	C	136	THR
1	C	137	LEU
1	C	150	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 15 ligands modelled in this entry, 3 are monoatomic - leaving 12 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	$\#\|Z\|>2$
4	DBS	C	301	2	17,17,17	0.68	0	22,23,23	0.71	0
3	SO4	C	532	-	4,4,4	0.13	0	6,6,6	0.09	0
6	GOL	A	601	-	5,5,5	0.38	0	5,5,5	0.40	0
5	DBH	B	201	2	11,11,11	0.74	0	15,15,15	0.64	0
5	DBH	C	303	2	11,11,11	0.72	0	15,15,15	0.65	0
3	SO4	A	531	-	4,4,4	0.13	0	6,6,6	0.09	0
6	GOL	C	602	-	5,5,5	0.40	0	5,5,5	0.19	0
4	DBS	A	191	2	17,17,17	0.63	0	22,23,23	0.84	1 (4%)
5	DBH	A	193	2	11,11,11	0.82	0	15,15,15	0.77	0
6	GOL	C	603	-	5,5,5	0.40	0	5,5,5	0.22	0
5	DBH	A	192	2	11,11,11	0.75	0	15,15,15	0.66	0
4	DBS	C	302	2	17,17,17	0.65	0	22,23,23	0.86	1 (4%)

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	DBS	C	301	2	-	6/14/14/14	0/1/1/1
6	GOL	A	601	-	-	2/4/4/4	-
6	GOL	C	602	-	-	2/4/4/4	-
5	DBH	B	201	2	-	2/4/4/4	0/1/1/1
5	DBH	C	303	2	-	4/4/4/4	0/1/1/1
4	DBS	A	191	2	-	2/14/14/14	0/1/1/1
5	DBH	A	193	2	-	4/4/4/4	0/1/1/1
6	GOL	C	603	-	-	4/4/4/4	-
5	DBH	A	192	2	-	4/4/4/4	0/1/1/1
4	DBS	C	302	2	-	0/14/14/14	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	C	302	DBS	C28-C22-N1	-2.47	104.98	110.56
4	A	191	DBS	C28-C22-N1	-2.31	105.35	110.56

There are no chirality outliers.

All (30) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	C	303	DBH	C3-C18-C21-O9
6	C	603	GOL	O1-C1-C2-C3
6	C	603	GOL	C1-C2-C3-O3
5	A	193	DBH	C3-C18-C21-O17
5	A	193	DBH	C3-C18-C21-O9
5	C	303	DBH	C3-C18-C21-O17
5	A	192	DBH	C3-C18-C21-O17
5	A	192	DBH	C3-C18-C21-O9
6	C	602	GOL	O2-C2-C3-O3
6	C	603	GOL	O1-C1-C2-O2
5	B	201	DBH	C3-C18-C21-O17
6	A	601	GOL	O1-C1-C2-C3
6	A	601	GOL	C1-C2-C3-O3
6	C	602	GOL	C1-C2-C3-O3
6	C	603	GOL	O2-C2-C3-O3
5	B	201	DBH	C3-C18-C21-O9
4	C	301	DBS	N1-C22-C25-O15
4	C	301	DBS	N1-C22-C25-O10
5	C	303	DBH	C15-C18-C21-O9
5	C	303	DBH	C15-C18-C21-O17
5	A	192	DBH	C15-C18-C21-O9
5	A	192	DBH	C15-C18-C21-O17
4	A	191	DBS	C28-C22-C25-O10
4	A	191	DBS	C28-C22-C25-O15
4	C	301	DBS	C28-C22-C25-O10
4	C	301	DBS	N1-C22-C28-O13
5	A	193	DBH	C15-C18-C21-O17
5	A	193	DBH	C15-C18-C21-O9
4	C	301	DBS	C28-C22-C25-O15
4	C	301	DBS	C1-C16-C19-O7

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	A	174/198 (87%)	0.39	9 (5%) 27 23	33, 43, 50, 56	0
1	B	171/198 (86%)	1.93	62 (36%) 0 0	58, 90, 97, 99	1 (0%)
1	C	174/198 (87%)	0.31	8 (4%) 32 28	26, 35, 48, 54	0
All	All	519/594 (87%)	0.87	79 (15%) 2 1	26, 44, 95, 99	1 (0%)

All (79) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	42	LEU	7.4
1	B	145	THR	7.0
1	B	46	LYS	6.7
1	B	45	ASP	6.7
1	B	170	VAL	5.8
1	B	34	VAL	5.0
1	B	48	PRO	5.0
1	B	58	LEU	4.9
1	A	46	LYS	4.8
1	B	47	ASP	4.8
1	B	146	SER	4.7
1	B	159	LEU	4.7
1	B	71	PHE	4.6
1	B	101	PRO	4.5
1	B	128	GLN	4.2
1	B	25	ASN	4.1
1	B	148	LEU	4.0
1	B	136	THR	4.0
1	B	7	LEU	3.7
1	B	165	HIS	3.6
1	B	13	LEU	3.6
1	B	5	SER	3.5
1	B	103	LEU	3.4

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Mol	Chain	Res	Type	RSRZ
1	B	87	SER	3.4
1	B	130	ARG	3.4
1	A	5	SER	3.4
1	B	144	LEU	3.4
1	B	49	GLN	3.3
1	C	4	THR	3.3
1	B	116	ASN	3.3
1	B	31	TRP	3.3
1	B	147	GLU	3.2
1	B	44	GLU	3.1
1	B	78	TYR	3.1
1	B	168	PHE	3.0
1	B	74	LYS	3.0
1	B	178	GLY	3.0
1	A	45	ASP	2.9
1	B	59	LYS	2.9
1	B	99	SER	2.9
1	B	43	ARG	2.8
1	B	172	ILE	2.8
1	B	100	TYR	2.8
1	B	102	GLY	2.8
1	B	177	ASP	2.7
1	A	146	SER	2.7
1	C	44	GLU	2.6
1	B	63	SER	2.6
1	C	46	LYS	2.6
1	B	173	ASP	2.6
1	B	51	MET	2.5
1	A	44	GLU	2.5
1	B	143	GLU	2.5
1	B	77	ASP	2.5
1	A	47	ASP	2.4
1	B	14	SER	2.4
1	B	76	CYS	2.4
1	B	154	ARG	2.4
1	B	163	GLU	2.4
1	B	23	GLN	2.4
1	B	127	SER	2.3
1	B	150	GLU	2.3
1	C	47	ASP	2.3
1	B	35	GLY	2.2
1	B	64	TYR	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	121	VAL	2.2
1	B	36	LEU	2.2
1	C	45	ASP	2.2
1	B	138	TYR	2.2
1	B	26	GLN	2.2
1	A	96	ASN	2.1
1	C	5	SER	2.1
1	A	128	GLN	2.1
1	B	134	LYS	2.1
1	B	16	VAL	2.1
1	C	35	GLY	2.1
1	B	121	VAL	2.0
1	B	96	ASN	2.0
1	C	101	PRO	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 monosaccharides 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, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
6	GOL	A	601	6/6	0.67	0.26	79,79,80,80	0
5	DBH	A	192	11/11	0.76	0.34	105,105,105,106	0
5	DBH	B	201	11/11	0.77	0.23	84,84,85,85	0
5	DBH	C	303	11/11	0.78	0.31	85,85,86,86	0
6	GOL	C	603	6/6	0.78	0.28	65,66,66,66	0
2	FE	B	402	1/1	0.84	0.30	108,108,108,108	0
3	SO4	C	532	5/5	0.87	0.34	94,94,94,94	0
3	SO4	A	531	5/5	0.90	0.27	98,98,98,98	0
4	DBS	C	302	17/17	0.91	0.22	68,69,70,70	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	DBS	C	301	17/17	0.91	0.20	46,47,50,51	0
6	GOL	C	602	6/6	0.93	0.19	64,64,64,64	0
5	DBH	A	193	11/11	0.93	0.23	85,85,85,86	0
4	DBS	A	191	17/17	0.94	0.19	52,54,59,59	0
2	FE	C	403	1/1	0.97	0.14	54,54,54,54	0
2	FE	A	401	1/1	0.99	0.15	57,57,57,57	0

6.5 Other polymers (i)

There are no such residues in this entry.