



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 05:52 AM UTC

PDB ID : 3BY0 / pdb_00003by0
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 : 4-5-2 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

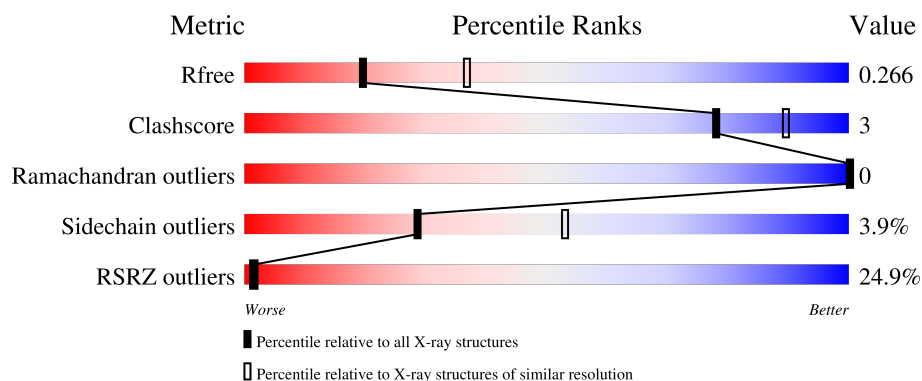
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.57 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}	180053	4770 (2.60-2.56)
Clashscore	190562	5124 (2.60-2.56)
Ramachandran outliers	187476	5046 (2.60-2.56)
Sidechain outliers	187428	5046 (2.60-2.56)
RSRZ outliers	180081	4770 (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 $\leq 5\%$. 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	198	3% 81% 6% 12%
1	B	198	59% 77% 10% 14%
1	C	198	4% 74% 13% 12%

2 Entry composition

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 (CCD ID: FE) (formula: Fe).

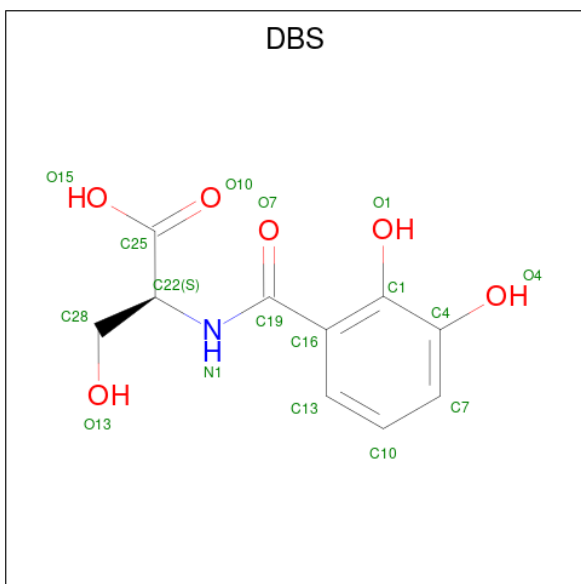
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Fe	0	0
			1	1		
2	B	1	Total	Fe	0	0
			1	1		
2	C	1	Total	Fe	0	0
			1	1		

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

- Molecule 4 is 2-(2,3-DIHYDROXY-BENZOYLAMINO)-3-HYDROXY-PROPIONIC ACID (CCD ID: DBS) (formula: C₁₀H₁₁NO₆).



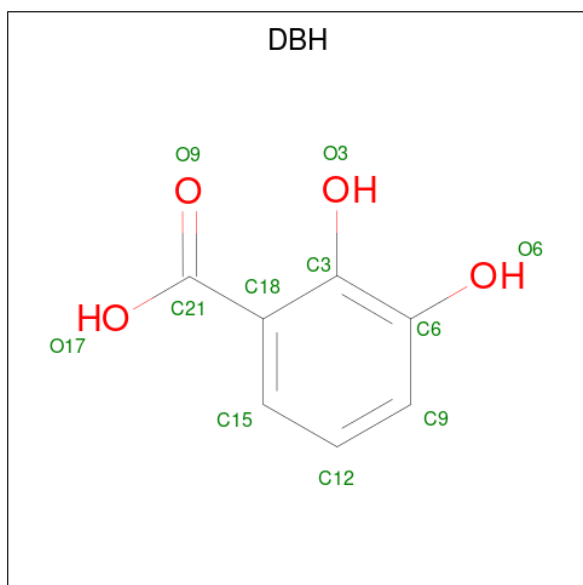
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			17	10	1	6		

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

- Molecule 5 is 2,3-DIHYDROXY-BENZOIC ACID (CCD ID: DBH) (formula: $C_7H_6O_4$).



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

- Molecule 6 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



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

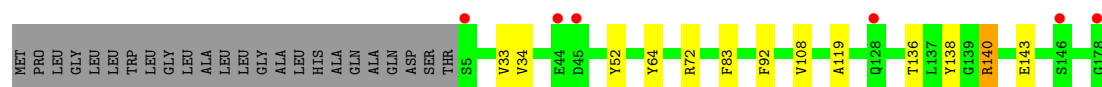
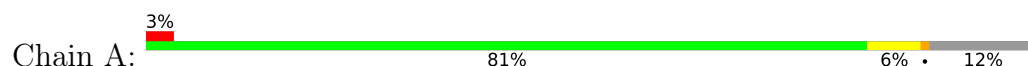
- Molecule 7 is water.

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

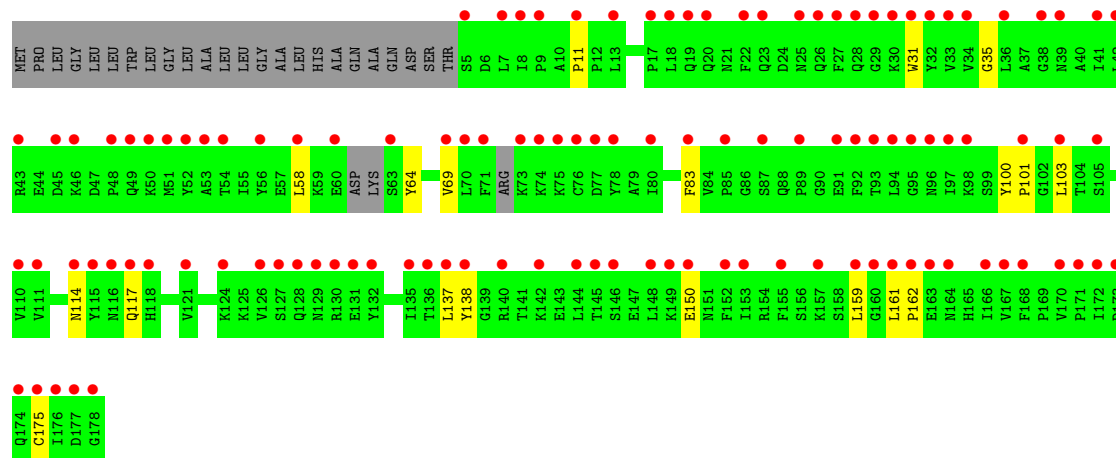
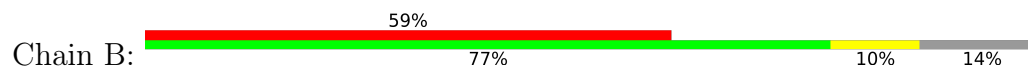
3 Residue-property plots [i](#)

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.

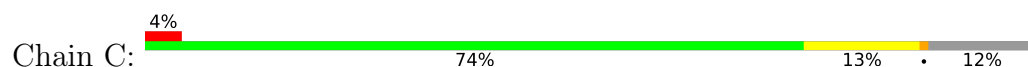
- Molecule 1: Neutrophil gelatinase-associated lipocalin



- Molecule 1: Neutrophil gelatinase-associated lipocalin



- Molecule 1: Neutrophil gelatinase-associated lipocalin



4 Data and refinement statistics

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) 99.6 (28.59-2.57)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ 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 (9.39%)	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 , 33.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	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.*

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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, FE, DBH, DBS, SO4

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	0.44	0/1446	0.67	0/1958
1	B	0.47	0/1398	0.74	0/1895
1	C	0.46	0/1485	0.67	0/2010
All	All	0.45	0/4329	0.69	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 [i](#)

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%)	42	67
1	B	150/174 (86%)	147 (98%)	3 (2%)	48	72
1	C	162/174 (93%)	151 (93%)	11 (7%)	14	31
All	All	469/522 (90%)	451 (96%)	18 (4%)	28	54

All (18) 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	103	LEU
1	B	150	GLU
1	C	13	LEU
1	C	14	SER
1	C	34	VAL
1	C	42	LEU
1	C	46	LYS
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. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	49	GLN
1	B	88	GLN
1	C	117	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides 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	$\# Z > 2$
5	DBH	B	201	2	11,11,11	0.76	0	15,15,15	0.64	0
5	DBH	A	193	2	11,11,11	0.84	0	15,15,15	0.78	0
6	GOL	C	602	-	5,5,5	0.40	0	5,5,5	0.20	0
4	DBS	C	301	2	17,17,17	0.70	0	23,23,23	0.72	0
6	GOL	A	601	-	5,5,5	0.39	0	5,5,5	0.41	0
3	SO4	A	531	-	4,4,4	0.23	0	6,6,6	0.11	0
4	DBS	C	302	2	17,17,17	0.67	0	23,23,23	0.83	1 (4%)
6	GOL	C	603	-	5,5,5	0.42	0	5,5,5	0.22	0
3	SO4	C	532	-	4,4,4	0.22	0	6,6,6	0.10	0
5	DBH	A	192	2	11,11,11	0.76	0	15,15,15	0.67	0
4	DBS	A	191	2	17,17,17	0.65	0	23,23,23	0.82	1 (4%)
5	DBH	C	303	2	11,11,11	0.73	0	15,15,15	0.66	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
5	DBH	B	201	2	-	2/4/4/4	0/1/1/1
5	DBH	A	193	2	-	4/4/4/4	0/1/1/1
6	GOL	C	602	-	-	2/4/4/4	-
4	DBS	C	301	2	-	4/14/14/14	0/1/1/1
6	GOL	A	601	-	-	2/4/4/4	-
4	DBS	C	302	2	-	0/14/14/14	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	A	191	2	-	2/14/14/14	0/1/1/1
5	DBH	C	303	2	-	4/4/4/4	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(°)	Ideal(°)
4	C	302	DBS	C28-C22-N1	-2.34	104.98	110.78
4	A	191	DBS	C28-C22-N1	-2.19	105.35	110.78

There are no chirality outliers.

All (28) 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
6	A	601	GOL	O1-C1-C2-C3
6	A	601	GOL	C1-C2-C3-O3
6	C	602	GOL	C1-C2-C3-O3
5	B	201	DBH	C3-C18-C21-O17
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
4	A	191	DBS	C28-C22-C25-O10
4	A	191	DBS	C28-C22-C25-O15
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
5	A	193	DBH	C15-C18-C21-O17
5	A	193	DBH	C15-C18-C21-O9
4	C	301	DBS	N1-C22-C28-O13
4	C	301	DBS	C28-C22-C25-O10

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	174/198 (87%)	0.35	6 (3%)	48 43	28, 43, 50, 56	2 (1%)
1	B	171/198 (86%)	2.48	116 (67%)	0 0	49, 90, 97, 99	2 (1%)
1	C	174/198 (87%)	0.11	7 (4%)	42 38	19, 35, 47, 54	5 (2%)
All	All	519/594 (87%)	0.97	129 (24%)	2 1	19, 44, 95, 99	9 (1%)

All (129) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	8	ILE	5.3
1	B	60	GLU	4.7
1	B	144	LEU	4.7
1	B	34	VAL	4.6
1	B	42	LEU	4.6
1	B	7	LEU	4.5
1	B	167	VAL	4.3
1	B	172	ILE	4.3
1	B	126	VAL	4.3
1	B	170	VAL	4.2
1	B	168	PHE	4.0
1	B	52	TYR	4.0
1	B	48	PRO	4.0
1	B	159	LEU	4.0
1	B	45	ASP	3.9
1	B	31	TRP	3.8
1	B	140	ARG	3.8
1	B	33	VAL	3.8
1	B	5	SER	3.7
1	B	53	ALA	3.7
1	B	13	LEU	3.6
1	B	166	ILE	3.5
1	B	175	CYS	3.4

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Mol	Chain	Res	Type	RSRZ
1	B	136	THR	3.4
1	B	71	PHE	3.4
1	B	63	SER	3.3
1	B	138	TYR	3.3
1	B	36	LEU	3.3
1	B	176	ILE	3.2
1	B	32	TYR	3.2
1	B	150	GLU	3.2
1	B	178	GLY	3.2
1	B	17	PRO	3.2
1	B	23	GLN	3.1
1	B	56	TYR	3.1
1	B	116	ASN	3.1
1	B	103	LEU	3.1
1	B	148	LEU	3.0
1	B	75	LYS	3.0
1	B	25	ASN	3.0
1	B	121	VAL	3.0
1	B	27	PHE	3.0
1	B	146	SER	3.0
1	B	163	GLU	3.0
1	B	77	ASP	3.0
1	B	89	PRO	2.9
1	B	115	TYR	2.9
1	B	161	LEU	2.9
1	B	149	LYS	2.9
1	B	69	VAL	2.9
1	B	137	LEU	2.9
1	B	152	PHE	2.9
1	B	29	GLY	2.9
1	B	97	ILE	2.8
1	B	135	ILE	2.8
1	B	145	THR	2.8
1	B	30	LYS	2.8
1	B	46	LYS	2.8
1	B	153	ILE	2.8
1	B	105[A]	SER	2.8
1	B	58	LEU	2.8
1	C	44	GLU	2.8
1	B	9	PRO	2.8
1	B	131	GLU	2.8
1	B	142	LYS	2.8

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Mol	Chain	Res	Type	RSRZ
1	C	45	ASP	2.8
1	B	28	GLN	2.7
1	B	132	TYR	2.7
1	B	177	ASP	2.7
1	B	39	ASN	2.7
1	B	98	LYS	2.7
1	B	94	LEU	2.6
1	B	164	ASN	2.6
1	A	5	SER	2.6
1	B	87	SER	2.6
1	B	174	GLN	2.6
1	B	124	LYS	2.6
1	B	157	LYS	2.6
1	B	51	MET	2.6
1	B	76	CYS	2.6
1	B	127	SER	2.6
1	B	50	LYS	2.6
1	B	155	PHE	2.5
1	B	49	GLN	2.5
1	B	111	VAL	2.5
1	B	117	GLN	2.5
1	B	110	VAL	2.5
1	B	114	ASN	2.5
1	B	101	PRO	2.5
1	B	171	PRO	2.4
1	B	38	GLY	2.4
1	A	128	GLN	2.4
1	A	178	GLY	2.4
1	B	11	PRO	2.4
1	B	41	ILE	2.4
1	A	146	SER	2.4
1	A	44	GLU	2.3
1	B	130	ARG	2.3
1	B	20	GLN	2.3
1	B	73	LYS	2.3
1	B	93	THR	2.3
1	B	160	GLY	2.3
1	B	80	ILE	2.3
1	C	47	ASP	2.2
1	B	19	GLN	2.2
1	C	4	THR	2.2
1	B	70	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	22	PHE	2.2
1	B	162	PRO	2.2
1	C	128	GLN	2.2
1	B	43	ARG	2.2
1	B	74	LYS	2.2
1	B	18	LEU	2.1
1	B	96	ASN	2.1
1	B	54	THR	2.1
1	B	78	TYR	2.1
1	B	85	PRO	2.1
1	B	83	PHE	2.1
1	B	128	GLN	2.1
1	B	129	ASN	2.1
1	B	173	ASP	2.1
1	B	118	HIS	2.1
1	A	45	ASP	2.1
1	B	26	GLN	2.0
1	B	92	PHE	2.0
1	C	72	ARG	2.0
1	B	91	GLU	2.0
1	C	143	GLU	2.0
1	B	95	GLY	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
6	GOL	A	601	6/6	0.69	0.23	79,79,80,80	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
6	GOL	C	603	6/6	0.72	0.17	65,66,66,66	0
3	SO4	A	531	5/5	0.75	0.16	98,98,98,98	0
5	DBH	B	201	11/11	0.77	0.16	84,84,85,85	0
3	SO4	C	532	5/5	0.80	0.22	94,94,94,94	0
2	FE	B	402	1/1	0.80	0.21	108,108,108,108	0
5	DBH	C	303	11/11	0.83	0.17	85,85,86,86	0
5	DBH	A	193	11/11	0.84	0.19	85,85,85,86	0
4	DBS	C	302	17/17	0.87	0.16	68,69,70,70	0
4	DBS	C	301	17/17	0.90	0.11	46,47,50,51	0
6	GOL	C	602	6/6	0.91	0.12	64,64,64,64	0
5	DBH	A	192	11/11	0.91	0.15	105,105,105,106	0
4	DBS	A	191	17/17	0.93	0.11	52,54,59,59	0
2	FE	A	401	1/1	0.99	0.03	57,57,57,57	0
2	FE	C	403	1/1	0.99	0.03	54,54,54,54	0

6.5 Other polymers [i](#)

There are no such residues in this entry.