



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 11:53 AM UTC

PDB ID : 7UQ0 / pdb_00007uq0
Title : Putative periplasmic iron siderophore binding protein FecB (Rv3044) from Mycobacterium tuberculosis
Authors : Chao, A.; Cuthbert, B.J.; Gouling, C.W.
Deposited on : 2022-04-18
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

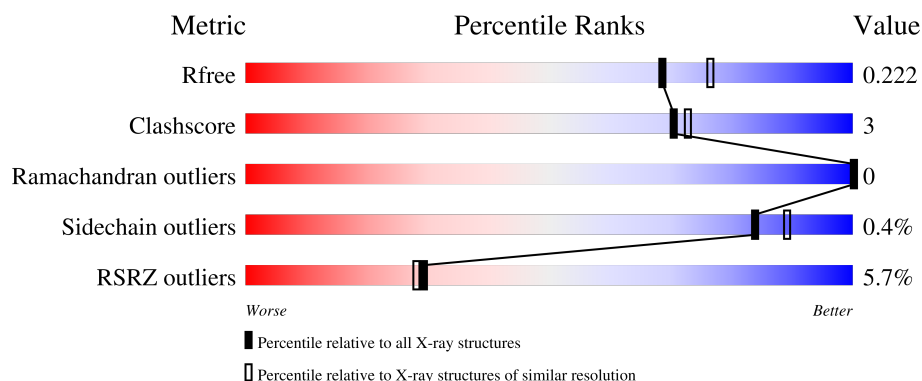
1 Overall quality at a glance

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	351	 4% 81% 6% 13%
1	B	351	 6% 81% 6% 13%

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
2	GOL	A	406	-	-	X	-

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 5018 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 Probable FEIII-dicitrate-binding periplasmic lipoprotein FecB.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	305	Total	C	N	O	S	0	5	0
			2239	1397	403	434	5			
1	B	307	Total	C	N	O	S	0	3	0
			2245	1400	401	439	5			

There are 40 discrepancies between the modelled and reference sequences:

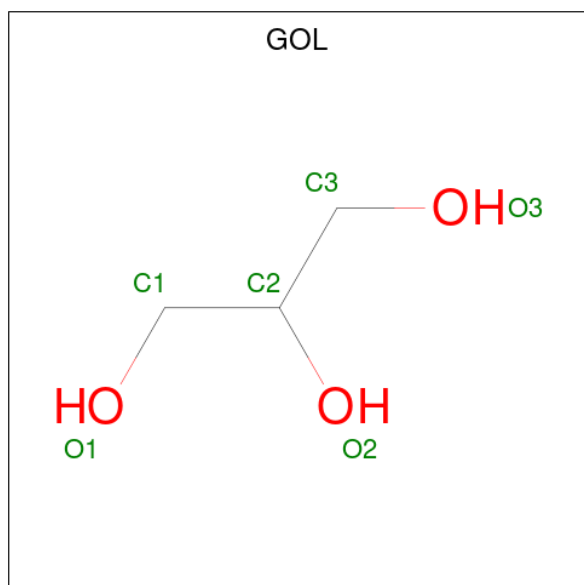
Chain	Residue	Modelled	Actual	Comment	Reference
A	9	MET	-	expression tag	UNP O53291
A	10	GLY	-	expression tag	UNP O53291
A	11	SER	-	expression tag	UNP O53291
A	12	SER	-	expression tag	UNP O53291
A	13	HIS	-	expression tag	UNP O53291
A	14	HIS	-	expression tag	UNP O53291
A	15	HIS	-	expression tag	UNP O53291
A	16	HIS	-	expression tag	UNP O53291
A	17	HIS	-	expression tag	UNP O53291
A	18	HIS	-	expression tag	UNP O53291
A	19	SER	-	expression tag	UNP O53291
A	20	SER	-	expression tag	UNP O53291
A	21	LEU	-	expression tag	UNP O53291
A	22	VAL	-	expression tag	UNP O53291
A	23	PRO	-	expression tag	UNP O53291
A	24	ARG	-	expression tag	UNP O53291
A	25	GLY	-	expression tag	UNP O53291
A	26	SER	-	expression tag	UNP O53291
A	27	HIS	-	expression tag	UNP O53291
A	28	MET	-	expression tag	UNP O53291
B	9	MET	-	expression tag	UNP O53291
B	10	GLY	-	expression tag	UNP O53291
B	11	SER	-	expression tag	UNP O53291
B	12	SER	-	expression tag	UNP O53291
B	13	HIS	-	expression tag	UNP O53291

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Chain	Residue	Modelled	Actual	Comment	Reference
B	14	HIS	-	expression tag	UNP O53291
B	15	HIS	-	expression tag	UNP O53291
B	16	HIS	-	expression tag	UNP O53291
B	17	HIS	-	expression tag	UNP O53291
B	18	HIS	-	expression tag	UNP O53291
B	19	SER	-	expression tag	UNP O53291
B	20	SER	-	expression tag	UNP O53291
B	21	LEU	-	expression tag	UNP O53291
B	22	VAL	-	expression tag	UNP O53291
B	23	PRO	-	expression tag	UNP O53291
B	24	ARG	-	expression tag	UNP O53291
B	25	GLY	-	expression tag	UNP O53291
B	26	SER	-	expression tag	UNP O53291
B	27	HIS	-	expression tag	UNP O53291
B	28	MET	-	expression tag	UNP O53291

- Molecule 2 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



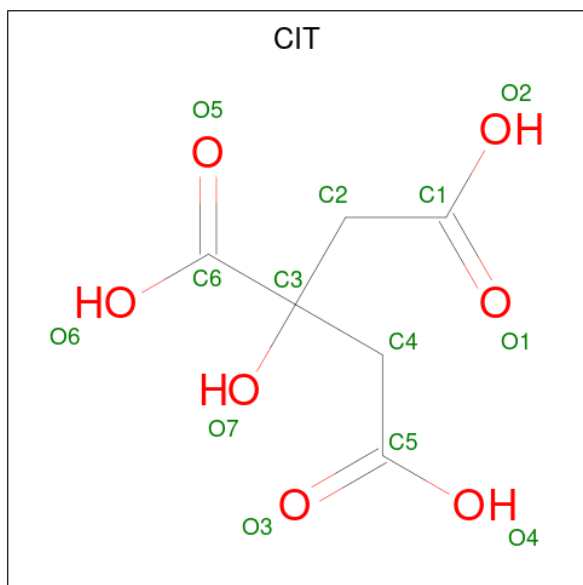
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			6	3	3		
2	A	1	Total	C	O	0	0
			6	3	3		
2	A	1	Total	C	O	0	0
			6	3	3		
2	A	1	Total	C	O	0	0
			6	3	3		

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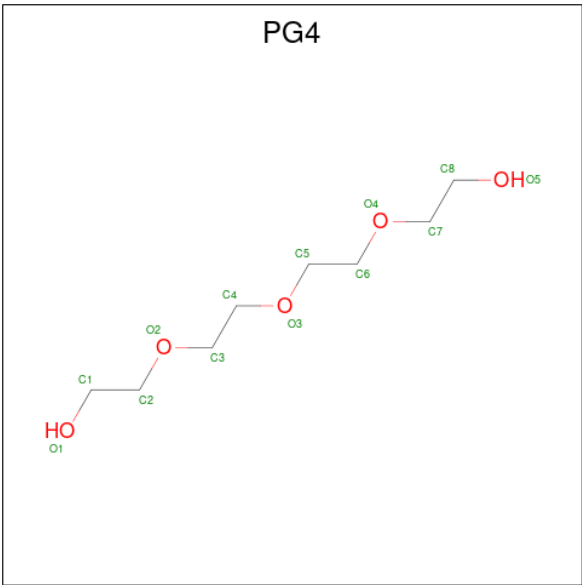
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total	C	O	0	0
			6	3	3		
2	B	1	Total	C	O	0	0
			6	3	3		
2	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 3 is CITRIC ACID (CCD ID: CIT) (formula: $C_6H_8O_7$).



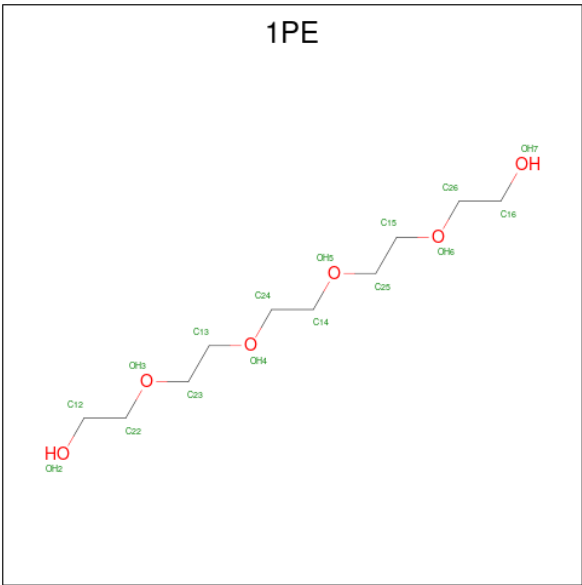
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			13	6	7		
3	B	1	Total	C	O	0	0
			13	6	7		

- Molecule 4 is TETRAETHYLENE GLYCOL (CCD ID: PG4) (formula: $C_8H_{18}O_5$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			7	4	3		
4	B	1	Total	C	O	0	0
			13	8	5		

- Molecule 5 is PENTAETHYLENE GLYCOL (CCD ID: 1PE) (formula: C₁₀H₂₂O₆).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			16	10	6		
5	A	1	Total	C	O	0	0
			16	10	6		

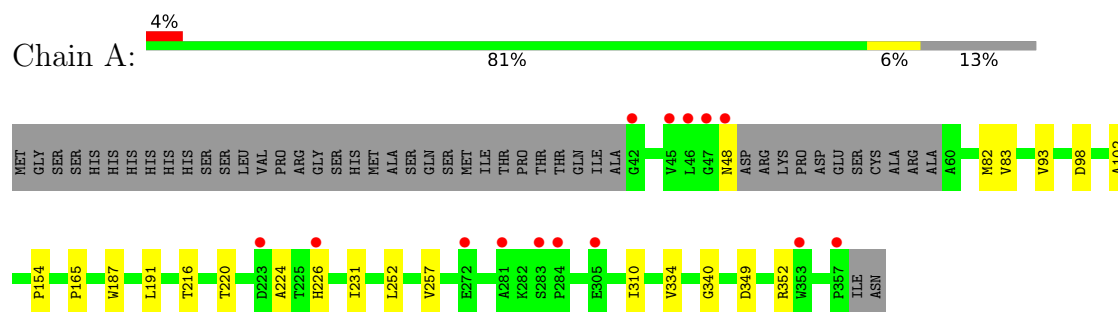
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	205	Total 205	O 205	0	0
6	B	209	Total 209	O 209	0	0

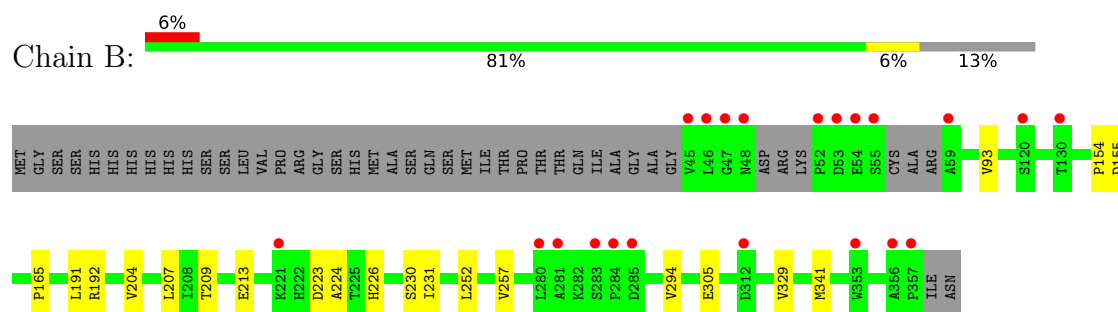
3 Residue-property plots [i](#)

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: Probable FEIII-dictrate-binding periplasmic lipoprotein FecB



- Molecule 1: Probable FEIII-dictrate-binding periplasmic lipoprotein FecB



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	138.65Å 87.07Å 71.73Å 90.00° 104.15° 90.00°	Depositor
Resolution (Å)	43.54 – 2.00 43.54 – 2.00	Depositor EDS
% Data completeness (in resolution range)	95.8 (43.54-2.00) 88.8 (43.54-2.00)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.89 (at 2.00Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.189 , 0.222 0.189 , 0.222	Depositor DCC
R_{free} test set	5376 reflections (9.62%)	wwPDB-VP
Wilson B-factor (Å ²)	22.0	Xtriage
Anisotropy	0.638	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 58.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5018	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.76% 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: CIT, GOL, PG4, 1PE

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	0.14	0/2300	0.33	0/3153
1	B	0.15	0/2300	0.32	0/3155
All	All	0.15	0/4600	0.33	0/6308

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	2239	0	2203	15	0
1	B	2245	0	2187	14	0
2	A	24	0	32	6	0
2	B	18	0	24	2	0
3	A	13	0	5	0	0
3	B	13	0	5	1	0
4	A	7	0	9	0	0
4	B	13	0	18	1	0
5	A	32	0	44	2	0
6	A	205	0	0	0	0
6	B	209	0	0	1	0
All	All	5018	0	4527	31	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 (31) 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:223:ASP:HB3	1:B:226:HIS:HD2	1.58	0.68
1:A:191:LEU:HB2	2:A:406:GOL:H2	1.74	0.67
1:A:165:PRO:HG3	2:B:401:GOL:H2	1.75	0.67
1:B:207:LEU:HB3	1:B:341:MET:HE3	1.80	0.63
1:A:349[B]:ASP:OD1	1:A:352:ARG:NH2	2.32	0.61
1:B:305:GLU:HG2	4:B:402:PG4:H31	1.83	0.60
1:A:102:ALA:HB2	2:A:406:GOL:H11	1.86	0.58
1:A:340:GLY:HA3	2:A:406:GOL:H12	1.86	0.57
1:B:224:ALA:HB1	1:B:257[A]:VAL:HG22	1.86	0.57
1:A:93:VAL:HG23	1:A:154:PRO:HB3	1.91	0.51
1:A:224:ALA:HB1	1:A:257:VAL:HG22	1.93	0.50
1:B:209:THR:O	1:B:213:GLU:HG3	2.13	0.48
1:B:191:LEU:HG	1:B:204:VAL:HG13	1.95	0.48
1:A:187:TRP:HE3	2:A:406:GOL:O2	1.96	0.47
1:A:98:ASP:HB2	2:A:406:GOL:C3	2.45	0.47
1:B:223:ASP:HB3	1:B:226:HIS:CD2	2.46	0.46
1:B:230:SER:HB3	1:B:294:VAL:HG22	1.97	0.46
1:A:340:GLY:CA	2:A:406:GOL:H12	2.45	0.46
1:A:48:ASN:CB	1:A:334:VAL:HG11	2.46	0.45
5:A:408:1PE:H131	1:B:165:PRO:HG3	1.98	0.45
1:B:155:ASP:OD1	1:B:155:ASP:N	2.38	0.44
1:B:93:VAL:HG23	1:B:154:PRO:HB3	1.99	0.44
1:B:329:VAL:HG21	3:B:404:CIT:H42	2.00	0.44
1:B:231:ILE:HD11	1:B:252:LEU:HD22	2.00	0.43
1:A:82:MET:HE3	1:A:82:MET:HB3	1.85	0.42
5:A:408:1PE:H141	5:A:408:1PE:H152	1.65	0.42
1:A:216:THR:O	1:A:220:THR:HG23	2.20	0.42
1:B:192:ARG:HA	1:B:204:VAL:HG11	2.03	0.41
1:A:231:ILE:HD11	1:A:252:LEU:HD22	2.02	0.40
1:A:226:HIS:CD2	1:A:226:HIS:N	2.89	0.40
2:B:401:GOL:H32	6:B:611:HOH:O	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	306/351 (87%)	300 (98%)	6 (2%)	0	100	100
1	B	304/351 (87%)	297 (98%)	7 (2%)	0	100	100
All	All	610/702 (87%)	597 (98%)	13 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	228/265 (86%)	226 (99%)	2 (1%)	70	78
1	B	228/265 (86%)	228 (100%)	0	100	100
All	All	456/530 (86%)	454 (100%)	2 (0%)	84	89

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	83	VAL
1	A	310	ILE

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	133	HIS

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Mol	Chain	Res	Type
1	A	226	HIS
1	B	226	HIS

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 ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

13 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	$\# Z > 2$
3	CIT	A	402	-	12,12,12	1.10	0	17,17,17	1.52	2 (11%)
2	GOL	A	401	-	5,5,5	0.95	0	5,5,5	1.08	0
5	1PE	A	408	-	15,15,15	0.13	0	14,14,14	0.08	0
2	GOL	A	406	-	5,5,5	1.56	1 (20%)	5,5,5	1.73	1 (20%)
2	GOL	A	405	-	5,5,5	0.95	0	5,5,5	0.99	0
4	PG4	B	402	-	12,12,12	0.13	0	11,11,11	0.12	0
3	CIT	B	404	-	12,12,12	1.02	0	17,17,17	1.57	4 (23%)
2	GOL	A	404	-	5,5,5	0.95	0	5,5,5	1.04	0
4	PG4	A	403	-	6,6,12	0.12	0	5,5,11	0.16	0
5	1PE	A	407	-	15,15,15	0.20	0	14,14,14	0.25	0
2	GOL	B	401	-	5,5,5	1.02	0	5,5,5	1.04	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	GOL	B	405	-	5,5,5	1.26	0	5,5,5	1.50	1 (20%)
2	GOL	B	403	-	5,5,5	0.90	0	5,5,5	0.97	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	CIT	A	402	-	-	7/16/16/16	-
2	GOL	A	401	-	-	0/4/4/4	-
5	1PE	A	408	-	-	9/13/13/13	-
2	GOL	A	406	-	-	0/4/4/4	-
2	GOL	A	405	-	-	2/4/4/4	-
4	PG4	B	402	-	-	4/10/10/10	-
3	CIT	B	404	-	-	5/16/16/16	-
2	GOL	A	404	-	-	2/4/4/4	-
4	PG4	A	403	-	-	0/4/4/10	-
5	1PE	A	407	-	-	1/13/13/13	-
2	GOL	B	401	-	-	0/4/4/4	-
2	GOL	B	405	-	-	0/4/4/4	-
2	GOL	B	403	-	-	0/4/4/4	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	406	GOL	C1-C2	-2.47	1.42	1.51

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	402	CIT	O6-C6-C3	4.23	121.25	113.14
2	A	406	GOL	C3-C2-C1	-3.62	98.54	111.80
3	B	404	CIT	O6-C6-C3	3.00	118.90	113.14
3	B	404	CIT	C4-C3-C2	2.75	116.38	109.31
3	A	402	CIT	O4-C5-C4	2.24	121.43	114.35
2	B	405	GOL	C3-C2-C1	-2.16	103.86	111.80
3	B	404	CIT	O2-C1-O1	-2.09	117.94	123.33
3	B	404	CIT	O7-C3-C6	-2.01	106.11	108.96

There are no chirality outliers.

All (30) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	402	CIT	C2-C3-C6-O5
3	A	402	CIT	C2-C3-C6-O6
3	A	402	CIT	O7-C3-C6-O5
3	A	402	CIT	O7-C3-C6-O6
3	B	404	CIT	O7-C3-C6-O5
3	B	404	CIT	O7-C3-C6-O6
3	B	404	CIT	C4-C3-C6-O5
3	B	404	CIT	C4-C3-C6-O6
4	B	402	PG4	C3-C4-O3-C5
5	A	408	1PE	OH4-C13-C23-OH3
5	A	408	1PE	C15-C25-OH5-C14
2	A	404	GOL	O1-C1-C2-C3
2	A	405	GOL	C1-C2-C3-O3
4	B	402	PG4	O3-C5-C6-O4
3	A	402	CIT	O7-C3-C4-C5
3	A	402	CIT	C6-C3-C4-C5
5	A	408	1PE	C16-C26-OH6-C15
5	A	408	1PE	OH7-C16-C26-OH6
3	A	402	CIT	C2-C3-C4-C5
3	B	404	CIT	O7-C3-C4-C5
4	B	402	PG4	C1-C2-O2-C3
5	A	408	1PE	C13-C23-OH3-C22
5	A	408	1PE	C14-C24-OH4-C13
5	A	408	1PE	C24-C14-OH5-C25
4	B	402	PG4	C5-C6-O4-C7
2	A	404	GOL	O1-C1-C2-O2
5	A	408	1PE	C12-C22-OH3-C23
2	A	405	GOL	O2-C2-C3-O3
5	A	407	1PE	C13-C23-OH3-C22
5	A	408	1PE	OH5-C14-C24-OH4

There are no ring outliers.

5 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	408	1PE	2	0
2	A	406	GOL	6	0
4	B	402	PG4	1	0
3	B	404	CIT	1	0
2	B	401	GOL	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	305/351 (86%)	0.24	14 (4%) 37 36	16, 30, 52, 77	5 (1%)
1	B	307/351 (87%)	0.44	21 (6%) 23 22	16, 33, 58, 76	3 (0%)
All	All	612/702 (87%)	0.34	35 (5%) 29 28	16, 31, 56, 77	8 (1%)

All (35) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	46	LEU	5.3
1	A	48	ASN	4.9
1	B	53	ASP	4.8
1	A	47	GLY	4.7
1	B	52	PRO	4.1
1	B	59	ALA	4.1
1	B	45	VAL	4.1
1	B	357	PRO	3.6
1	B	55	SER	3.4
1	A	46	LEU	3.4
1	B	281	ALA	3.3
1	B	54	GLU	3.2
1	B	353	TRP	3.0
1	A	284	PRO	3.0
1	B	48	ASN	2.9
1	B	283	SER	2.9
1	B	120	SER	2.8
1	A	42	GLY	2.8
1	B	356	ALA	2.8
1	B	312	ASP	2.8
1	A	45	VAL	2.6
1	B	284	PRO	2.6
1	A	353	TRP	2.5
1	A	357	PRO	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	223	ASP	2.4
1	A	226	HIS	2.2
1	B	130	THR	2.2
1	B	280	LEU	2.1
1	B	221	LYS	2.1
1	A	272	GLU	2.1
1	B	285	ASP	2.1
1	A	281	ALA	2.1
1	A	305	GLU	2.0
1	A	283	SER	2.0
1	B	47	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
2	GOL	A	405	6/6	0.68	0.21	60,66,69,72	0
3	CIT	B	404	13/13	0.71	0.24	55,71,78,82	13
5	1PE	A	407	16/16	0.76	0.22	49,69,86,87	0
2	GOL	A	401	6/6	0.78	0.20	46,52,65,65	0
4	PG4	A	403	7/13	0.79	0.22	32,39,45,49	7
2	GOL	A	404	6/6	0.79	0.19	51,56,62,65	0
2	GOL	B	403	6/6	0.80	0.17	58,63,70,79	0
4	PG4	B	402	13/13	0.81	0.19	48,61,65,66	13
2	GOL	B	401	6/6	0.81	0.19	48,53,57,63	0
3	CIT	A	402	13/13	0.83	0.22	34,36,41,42	13
5	1PE	A	408	16/16	0.84	0.20	38,53,60,71	16
2	GOL	B	405	6/6	0.87	0.22	39,49,56,62	6

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	GOL	A	406	6/6	0.90	0.27	27,30,43,70	6

6.5 Other polymers [i](#)

There are no such residues in this entry.