



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 04:12 AM UTC

PDB ID : 7O1J / pdb_00007o1j
Title : Structure of Mycobacterium tuberculosis beta-oxidation trifunctional enzyme
beta-C92A mutant
Authors : Dalwani, S.; Wierenga, R.K.; Venkatesan, R.
Deposited on : 2021-03-29
Resolution : 2.36 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

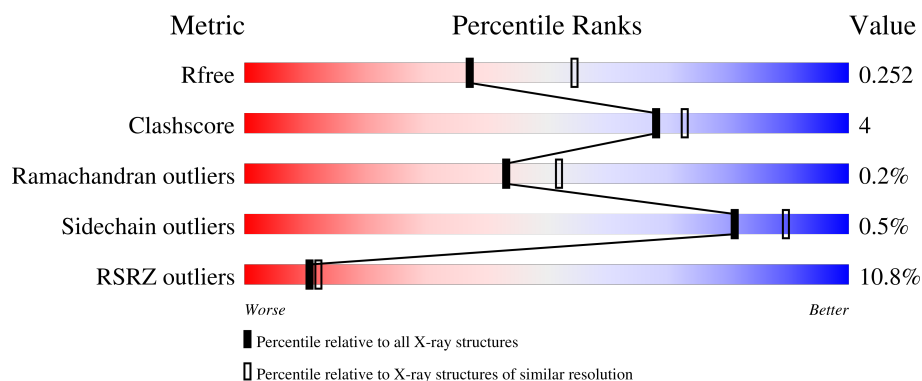
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.36 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	1596 (2.36-2.36)
Clashscore	190562	1663 (2.36-2.36)
Ramachandran outliers	187476	1646 (2.36-2.36)
Sidechain outliers	187428	1646 (2.36-2.36)
RSRZ outliers	180081	1598 (2.36-2.36)

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	D	403	
2	A	736	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 8399 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 Putative acyltransferase Rv0859.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	D	402	Total	C	N	O	S	0	2	0
			2960	1848	525	573	14			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	92	ALA	CYS	engineered mutation	UNP O53871

- Molecule 2 is a protein called 3-hydroxyacyl-CoA dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	723	Total	C	N	O	S	0	2	0
			5213	3301	895	996	21			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-15	MET	-	initiating methionine	UNP O53872
A	-14	GLY	-	expression tag	UNP O53872
A	-13	SER	-	expression tag	UNP O53872
A	-12	SER	-	expression tag	UNP O53872
A	-11	HIS	-	expression tag	UNP O53872
A	-10	HIS	-	expression tag	UNP O53872
A	-9	HIS	-	expression tag	UNP O53872
A	-8	HIS	-	expression tag	UNP O53872
A	-7	HIS	-	expression tag	UNP O53872
A	-6	HIS	-	expression tag	UNP O53872
A	-5	SER	-	expression tag	UNP O53872
A	-4	GLN	-	expression tag	UNP O53872
A	-3	ASP	-	expression tag	UNP O53872
A	-2	PRO	-	expression tag	UNP O53872
A	-1	ASN	-	expression tag	UNP O53872

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	SER	-	expression tag	UNP O53872

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 4 is SULFATE ION (CCD ID: SO4) (formula: O_4S).



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

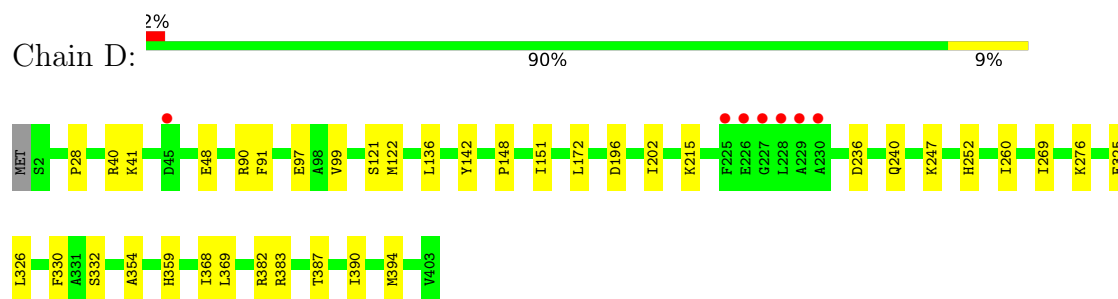
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	D	84	Total 84	O 84	0	0
5	A	59	Total 59	O 59	0	0

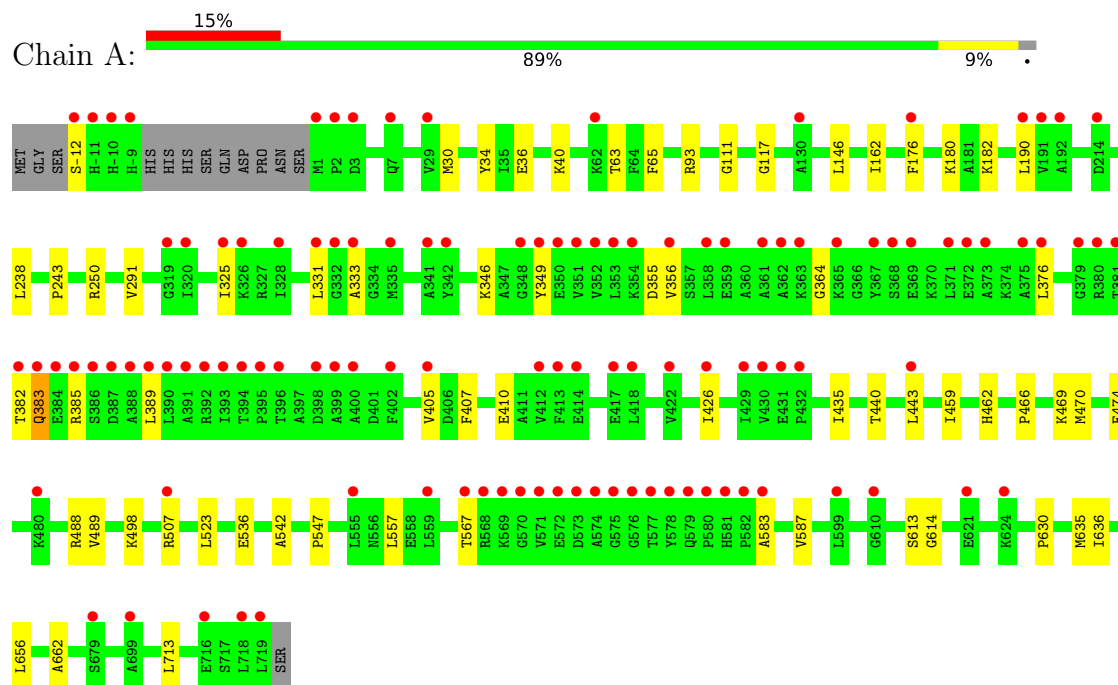
3 Residue-property plots

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: Putative acyltransferase Rv0859



• Molecule 2: 3-hydroxyacyl-CoA dehydrogenase



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	101.33Å 209.28Å 133.45Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	66.73 – 2.36 66.73 – 2.36	Depositor EDS
% Data completeness (in resolution range)	99.4 (66.73-2.36) 99.4 (66.73-2.36)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.52 (at 2.37Å)	Xtriage
Refinement program	PHENIX 1.18.2_3874	Depositor
R, R_{free}	0.211 , 0.250 0.215 , 0.252	Depositor DCC
R_{free} test set	2832 reflections (4.84%)	wwPDB-VP
Wilson B-factor (Å ²)	45.4	Xtriage
Anisotropy	0.596	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 55.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	8399	wwPDB-VP
Average B, all atoms (Å ²)	66.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.31% 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: CSO, SO4, GOL

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	D	0.11	0/3002	0.33	0/4065
2	A	0.09	0/5316	0.26	0/7221
All	All	0.10	0/8318	0.29	0/11286

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	D	2960	0	2980	26	0
2	A	5213	0	5123	35	0
3	A	6	0	8	0	0
3	D	12	0	16	2	0
4	A	20	0	0	0	0
4	D	45	0	0	0	0
5	A	59	0	0	0	0
5	D	84	0	0	0	0
All	All	8399	0	8127	59	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 4.

All (59) 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:90:ARG:HH11	1:D:394:MET:HE1	1.51	0.76
2:A:507:ARG:HD2	2:A:567:THR:HG22	1.74	0.69
2:A:-12:SER:O	2:A:93:ARG:NH1	2.28	0.66
1:D:252:HIS:HE1	1:D:332:SER:H	1.48	0.61
2:A:36:GLU:HG3	2:A:40:LYS:HE3	1.87	0.56
1:D:99:VAL:HG13	1:D:269:ILE:HD11	1.88	0.56
2:A:182:LYS:HD2	2:A:190:LEU:HG	1.86	0.55
1:D:252:HIS:CE1	1:D:332:SER:H	2.25	0.54
2:A:176:PHE:HD1	2:A:180:LYS:HE3	1.75	0.52
1:D:148:PRO:HG2	1:D:151:ILE:HD12	1.92	0.52
1:D:172:LEU:HD22	1:D:215:LYS:HG2	1.92	0.51
2:A:630:PRO:HG2	2:A:635:MET:HE2	1.92	0.51
1:D:354:ALA:HB1	1:D:359:HIS:HB2	1.93	0.51
2:A:440:THR:HG21	2:A:443:LEU:HB2	1.91	0.51
2:A:557:LEU:HG	2:A:587:VAL:HG13	1.94	0.49
1:D:90:ARG:HH21	1:D:97:GLU:CD	2.20	0.49
2:A:146:LEU:HD22	2:A:291:VAL:HG22	1.95	0.49
1:D:91:PHE:HB2	1:D:390:ILE:HG23	1.95	0.49
2:A:462:HIS:HB3	2:A:474:GLU:HB3	1.93	0.48
2:A:63:THR:HA	2:A:111:GLY:HA3	1.94	0.48
2:A:65:PHE:HB3	2:A:117:GLY:HA2	1.96	0.48
1:D:136:LEU:HD12	2:A:243:PRO:HG3	1.95	0.48
1:D:326:LEU:HD13	1:D:387:THR:HG23	1.96	0.47
2:A:405:VAL:HG12	2:A:407:PHE:H	1.79	0.47
1:D:28:PRO:HG3	1:D:121[B]:SER:HB3	1.97	0.47
2:A:459:ILE:HG21	2:A:489:VAL:HG21	1.96	0.47
1:D:142:TYR:O	2:A:250:ARG:NH1	2.48	0.47
2:A:162:ILE:HD12	2:A:238:LEU:HD21	1.97	0.46
1:D:382:ARG:HG3	1:D:383:ARG:HG3	1.98	0.46
1:D:28:PRO:HG3	1:D:121[A]:SER:HB3	1.97	0.45
1:D:48:GLU:HG2	3:D:501:GOL:H32	1.98	0.45
1:D:40:ARG:HG2	3:D:501:GOL:H31	1.97	0.45
2:A:435:ILE:HD11	2:A:488:ARG:HD3	1.99	0.45
2:A:613:SER:OG	2:A:614:GLY:N	2.50	0.45
2:A:470:MET:O	2:A:498:LYS:NZ	2.41	0.45
2:A:346:LYS:HA	2:A:389:LEU:HD13	1.99	0.44
1:D:122:MET:HE2	1:D:260:ILE:HG23	1.98	0.44
2:A:65:PHE:HB3	2:A:117:GLY:CA	2.47	0.44
2:A:466:PRO:HG2	2:A:469:LYS:HB2	1.99	0.44
1:D:252:HIS:CE1	1:D:330:PHE:HB3	2.52	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:333:ALA:HB1	2:A:364:GLY:HA3	1.99	0.44
1:D:236:ASP:O	1:D:240:GLN:HG3	2.18	0.43
1:D:390:ILE:HB	1:D:394:MET:HB2	1.98	0.43
2:A:325:ILE:HB	2:A:349:TYR:CE1	2.54	0.43
2:A:536:GLU:CD	2:A:547:PRO:HB2	2.44	0.43
2:A:355:ASP:OD1	2:A:356:VAL:HG22	2.19	0.42
2:A:542:ALA:HB2	2:A:636:ILE:HG23	2.00	0.42
1:D:276:LYS:HE2	1:D:276:LYS:HB3	1.86	0.42
1:D:394:MET:HE2	1:D:394:MET:HB3	1.84	0.41
2:A:355:ASP:OD1	2:A:356:VAL:N	2.50	0.41
2:A:331:LEU:HB2	2:A:410:GLU:HA	2.03	0.41
2:A:523:LEU:HB2	2:A:583:ALA:HB1	2.02	0.41
1:D:325:GLU:HG2	1:D:368:ILE:HB	2.03	0.41
2:A:656:LEU:HD13	2:A:662:ALA:HB2	2.03	0.41
2:A:30:MET:HG3	2:A:34:TYR:CD2	2.56	0.40
1:D:196:ASP:HB3	1:D:202:ILE:HD11	2.03	0.40
2:A:383:GLN:C	2:A:385:ARG:H	2.29	0.40
1:D:99:VAL:HG11	1:D:369:LEU:HD22	2.04	0.40
2:A:713:LEU:HD23	2:A:713:LEU:HA	1.88	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	D	401/403 (100%)	387 (96%)	14 (4%)	0	100	100
2	A	721/736 (98%)	690 (96%)	29 (4%)	2 (0%)	36	43
All	All	1122/1139 (98%)	1077 (96%)	43 (4%)	2 (0%)	43	52

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	382	THR
2	A	383	GLN

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	D	306/308 (99%)	304 (99%)	2 (1%)	76	86
2	A	512/566 (90%)	510 (100%)	2 (0%)	84	91
All	All	818/874 (94%)	814 (100%)	4 (0%)	81	89

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	41	LYS
1	D	247	LYS
2	A	376	LEU
2	A	426	ILE

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

Mol	Chain	Res	Type
1	D	104	GLN
1	D	380	ASN
2	A	28	ASN
2	A	294	GLN
2	A	311	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](#)

1 non-standard protein/DNA/RNA residue is 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	$\# Z > 2$
1	CSO	D	389	1	3,6,7	0.64	0	1,6,8	0.02	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
1	CSO	D	389	1	-	0/1/5/7	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

16 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	GOL	D	511	-	5,5,5	0.97	0	5,5,5	1.05	0
4	SO4	D	507	-	4,4,4	0.24	0	6,6,6	0.07	0
4	SO4	D	504	-	4,4,4	0.23	0	6,6,6	0.08	0
4	SO4	D	505	-	4,4,4	0.24	0	6,6,6	0.06	0
3	GOL	D	501	-	5,5,5	0.95	0	5,5,5	1.03	0
4	SO4	D	508	-	4,4,4	0.24	0	6,6,6	0.06	0
4	SO4	D	510	-	4,4,4	0.23	0	6,6,6	0.08	0
4	SO4	A	802	-	4,4,4	0.23	0	6,6,6	0.10	0
3	GOL	A	801	-	5,5,5	0.93	0	5,5,5	1.07	0
4	SO4	A	804	-	4,4,4	0.24	0	6,6,6	0.08	0
4	SO4	A	805	-	4,4,4	0.23	0	6,6,6	0.08	0
4	SO4	D	502	-	4,4,4	0.23	0	6,6,6	0.09	0
4	SO4	A	803	-	4,4,4	0.24	0	6,6,6	0.07	0
4	SO4	D	509	-	4,4,4	0.24	0	6,6,6	0.07	0
4	SO4	D	503	-	4,4,4	0.24	0	6,6,6	0.08	0
4	SO4	D	506	-	4,4,4	0.23	0	6,6,6	0.07	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	D	511	-	-	2/4/4/4	-
3	GOL	A	801	-	-	2/4/4/4	-
3	GOL	D	501	-	-	0/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	801	GOL	C1-C2-C3-O3
3	D	511	GOL	C1-C2-C3-O3
3	A	801	GOL	O2-C2-C3-O3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
3	D	511	GOL	O2-C2-C3-O3

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	501	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

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	D	401/403 (99%)	0.07	7 (1%) 69 74	24, 47, 70, 118	2 (0%)
2	A	723/736 (98%)	0.96	114 (15%) 5 5	35, 73, 127, 195	2 (0%)
All	All	1124/1139 (98%)	0.64	121 (10%) 11 12	24, 60, 122, 195	4 (0%)

All (121) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	A	386	SER	6.3
2	A	402	PHE	5.9
2	A	571	VAL	5.7
2	A	393	ILE	5.7
2	A	574	ALA	5.5
1	D	228	LEU	5.2
2	A	389	LEU	4.9
2	A	575	GLY	4.7
2	A	388	ALA	4.5
2	A	-9	HIS	4.5
2	A	578	TYR	4.4
2	A	352	VAL	4.4
2	A	576	GLY	4.3
2	A	577	THR	4.3
2	A	382	THR	4.2
2	A	353	LEU	4.1
2	A	570	GLY	4.0
2	A	381	THR	4.0
2	A	356	VAL	3.9
2	A	400	ALA	3.9
2	A	555	LEU	3.9
2	A	387	ASP	3.9
2	A	351	VAL	3.9
2	A	385	ARG	3.8

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
2	A	567	THR	3.8
2	A	367	TYR	3.8
2	A	599	LEU	3.6
2	A	380	ARG	3.6
2	A	573	ASP	3.6
2	A	358	LEU	3.5
2	A	414	GLU	3.5
1	D	225	PHE	3.5
2	A	-11	HIS	3.4
2	A	333	ALA	3.4
2	A	398	ASP	3.4
1	D	230	ALA	3.4
2	A	399	ALA	3.4
2	A	362	ALA	3.3
1	D	229	ALA	3.3
2	A	1	MET	3.3
2	A	371	LEU	3.3
2	A	350	GLU	3.3
2	A	412	VAL	3.3
2	A	328	ILE	3.1
2	A	361	ALA	3.1
2	A	579	GLN	3.1
2	A	326	LYS	3.1
2	A	390	LEU	3.1
2	A	396	THR	3.0
2	A	335	MET	3.0
2	A	559	LEU	3.0
2	A	373	ALA	3.0
2	A	384	GLU	3.0
2	A	621	GLU	3.0
2	A	349	TYR	3.0
2	A	413	PHE	2.9
2	A	395	PRO	2.9
2	A	320	ILE	2.9
2	A	426	ILE	2.9
2	A	572	GLU	2.9
1	D	45	ASP	2.9
2	A	365	LYS	2.8
2	A	582	PRO	2.8
2	A	581	HIS	2.8
2	A	342	TYR	2.8
1	D	226	GLU	2.8

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
2	A	417	GLU	2.8
2	A	130	ALA	2.8
2	A	507	ARG	2.8
2	A	391	ALA	2.8
2	A	418	LEU	2.7
2	A	610	GLY	2.7
2	A	332	GLY	2.6
2	A	583	ALA	2.6
2	A	405	VAL	2.6
2	A	348	GLY	2.6
2	A	2	PRO	2.6
2	A	-12	SER	2.6
2	A	719	LEU	2.6
2	A	372	GLU	2.6
2	A	359	GLU	2.6
2	A	431	GLU	2.6
2	A	214	ASP	2.5
2	A	354	LYS	2.5
2	A	376	LEU	2.5
2	A	192	ALA	2.5
2	A	190	LEU	2.4
2	A	331	LEU	2.4
2	A	7	GLN	2.4
2	A	392	ARG	2.4
2	A	368	SER	2.4
2	A	569	LYS	2.4
2	A	443	LEU	2.4
2	A	325	ILE	2.4
2	A	29	VAL	2.3
2	A	176	PHE	2.3
2	A	716	GLU	2.3
2	A	580	PRO	2.3
2	A	375	ALA	2.2
2	A	62	LYS	2.2
2	A	568	ARG	2.2
2	A	341	ALA	2.2
2	A	699	ALA	2.2
2	A	718	LEU	2.1
2	A	191	VAL	2.1
2	A	624	LYS	2.1
1	D	227	GLY	2.1
2	A	363	LYS	2.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
2	A	369	GLU	2.1
2	A	383	GLN	2.1
2	A	422	VAL	2.1
2	A	394	THR	2.1
2	A	-10	HIS	2.1
2	A	3	ASP	2.1
2	A	319	GLY	2.1
2	A	379	GLY	2.1
2	A	679[A]	SER	2.0
2	A	430	VAL	2.0
2	A	480	LYS	2.0
2	A	429	ILE	2.0
2	A	432	PRO	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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
1	CSO	D	389	7/8	0.93	0.11	41,49,53,69	0

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	D	511	6/6	0.59	0.20	77,88,94,95	0
4	SO4	D	510	5/5	0.66	0.12	85,104,116,138	0
4	SO4	A	804	5/5	0.76	0.10	104,118,125,129	0
4	SO4	A	805	5/5	0.76	0.09	108,109,133,155	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	SO4	D	506	5/5	0.77	0.11	102,106,118,125	0
4	SO4	D	505	5/5	0.82	0.09	76,86,113,114	0
4	SO4	D	507	5/5	0.82	0.15	69,71,76,77	5
4	SO4	D	509	5/5	0.82	0.13	97,115,131,146	0
3	GOL	A	801	6/6	0.83	0.18	69,73,80,80	0
4	SO4	D	504	5/5	0.85	0.10	84,95,107,123	0
3	GOL	D	501	6/6	0.86	0.20	50,56,69,73	0
4	SO4	A	803	5/5	0.86	0.08	82,96,113,118	0
4	SO4	D	508	5/5	0.87	0.08	83,88,111,115	0
4	SO4	D	503	5/5	0.88	0.10	62,80,87,113	0
4	SO4	A	802	5/5	0.92	0.10	71,75,83,92	0
4	SO4	D	502	5/5	0.95	0.12	63,64,67,69	0

6.5 Other polymers [i](#)

There are no such residues in this entry.