



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 12:28 pm GMT

PDB ID : 3TZX
Title : Crystal structure of a fragment containing the acyltransferase domain of Pks13 from Mycobacterium tuberculosis in tetragonal apo form at 2.3 Å
Authors : Bergeret, F.; Pedelacq, J.D.; Mourey, L.; Bon, C.
Deposited on : 2011-09-28
Resolution : 2.30 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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : recalc28949

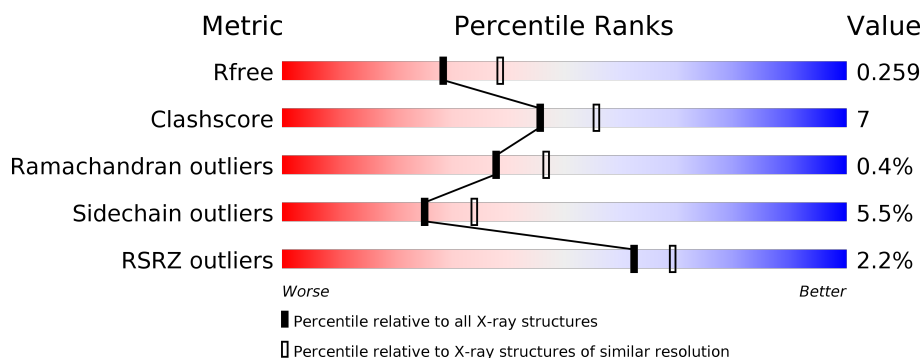
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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}	100719	4130 (2.30-2.30)
Clashscore	112137	4751 (2.30-2.30)
Ramachandran outliers	110173	4705 (2.30-2.30)
Sidechain outliers	110143	4704 (2.30-2.30)
RSRZ outliers	101464	4156 (2.30-2.30)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	491	<div> <div>2%</div> <div> <div></div> <div>79%</div> <div>14%</div> <div>•• 5%</div> </div> </div>
1	B	491	<div> <div>2%</div> <div> <div></div> <div>79%</div> <div>14%</div> <div>• 5%</div> </div> </div>
2	C	12	<div> <div>8%</div> <div> <div></div> <div>67%</div> <div>17%</div> <div>8%</div> <div>8%</div> </div> </div>
2	D	12	<div> <div>8%</div> <div> <div></div> <div>33%</div> <div>17%</div> <div>8%</div> <div>17%</div> <div>25%</div> </div> </div>

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	GOL	A	6	-	-	X	-
3	GOL	B	2	-	-	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7524 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 Polyketide synthase PKS13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	465	Total	C	N	O	S	0	0	0
			3479	2199	600	668	12			
1	B	467	Total	C	N	O	S	0	1	0
			3489	2210	610	657	12			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	572	GLY	-	EXPRESSION TAG	UNP O53579
A	573	SER	-	EXPRESSION TAG	UNP O53579
A	574	HIS	-	EXPRESSION TAG	UNP O53579
A	575	MET	-	EXPRESSION TAG	UNP O53579
B	572	GLY	-	EXPRESSION TAG	UNP O53579
B	573	SER	-	EXPRESSION TAG	UNP O53579
B	574	HIS	-	EXPRESSION TAG	UNP O53579
B	575	MET	-	EXPRESSION TAG	UNP O53579

- Molecule 2 is a protein called 12-mer peptide.

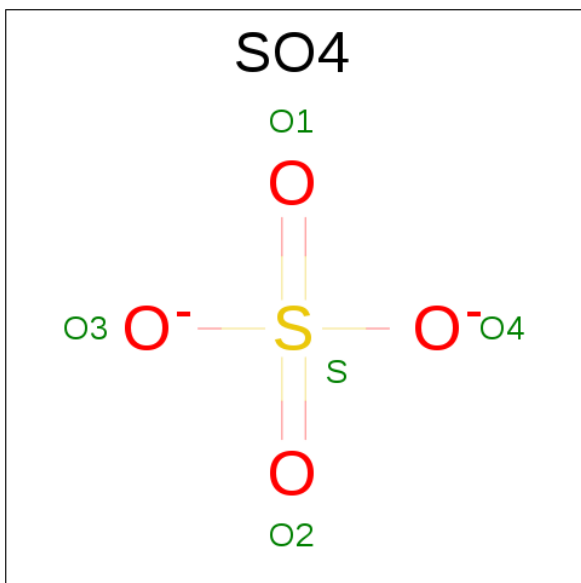
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	12	Total	C	N	O	S	0	0	0
			94	60	15	18	1			
2	D	9	Total	C	N	O	S	0	0	0
			67	45	11	10	1			

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



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

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

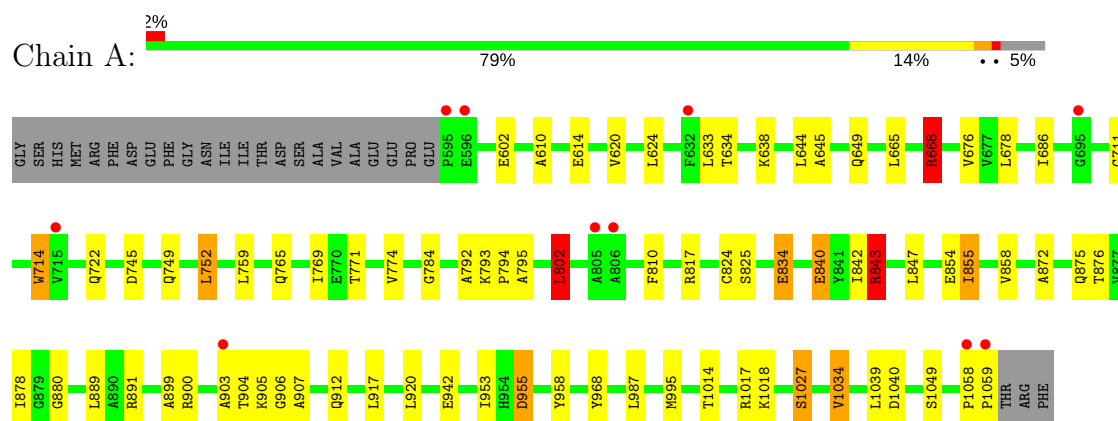
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	169	Total	O	0	0
			169	169		
5	B	180	Total	O	0	0
			180	180		
5	D	2	Total	O	0	0
			2	2		

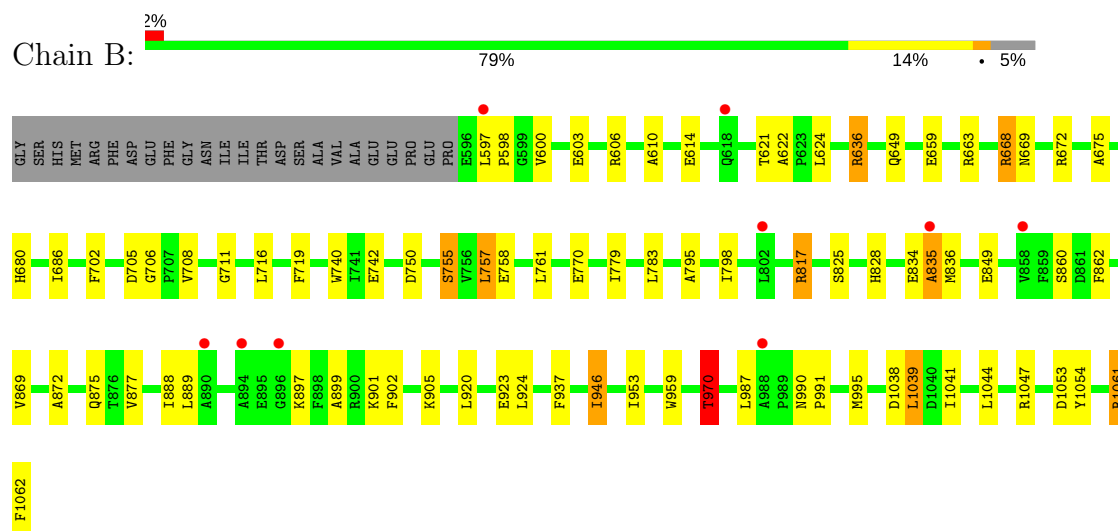
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

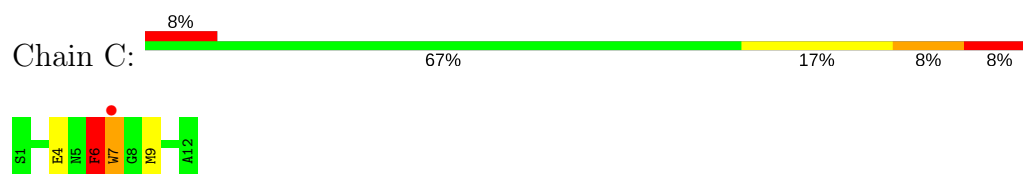
• Molecule 1: Polyketide synthase PKS13



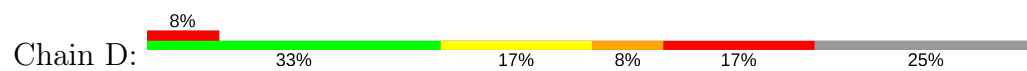
• Molecule 1: Polyketide synthase PKS13



• Molecule 2: 12-mer peptide



- Molecule 2: 12-mer peptide



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	106.56Å 106.56Å 258.61Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	41.12 – 2.30 39.96 – 2.30	Depositor EDS
% Data completeness (in resolution range)	96.9 (41.12-2.30) 97.0 (39.96-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.62 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.200 , 0.260 0.201 , 0.259	Depositor DCC
R_{free} test set	3291 reflections (5.33%)	DCC
Wilson B-factor (Å ²)	38.5	Xtriage
Anisotropy	0.127	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 37.2	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	0.95	EDS
Total number of atoms	7524	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.59% 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, 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	0.94	2/3552 (0.1%)	0.97	8/4834 (0.2%)
1	B	1.00	3/3562 (0.1%)	0.99	4/4846 (0.1%)
2	C	1.27	1/96 (1.0%)	1.41	1/128 (0.8%)
2	D	1.33	1/69 (1.4%)	1.04	0/93
All	All	0.98	7/7279 (0.1%)	0.99	13/9901 (0.1%)

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	959	TRP	CD2-CE2	5.62	1.48	1.41
1	B	740	TRP	CD2-CE2	5.53	1.48	1.41
2	D	7	TRP	CD2-CE2	5.43	1.47	1.41
2	C	7	TRP	CD2-CE2	5.24	1.47	1.41
1	A	714	TRP	CD2-CE2	5.22	1.47	1.41
1	A	955	ASP	CB-CG	-5.09	1.41	1.51
1	B	659	GLU	CD-OE1	-5.05	1.20	1.25

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	955	ASP	N-CA-CB	-9.32	93.82	110.60
1	A	953	ILE	CB-CA-C	-8.03	95.53	111.60
1	B	668	ARG	NE-CZ-NH1	5.88	123.24	120.30
1	A	802	LEU	CA-CB-CG	5.80	128.63	115.30
1	B	636	ARG	NE-CZ-NH1	5.76	123.18	120.30
1	A	1040	ASP	CB-CG-OD1	5.52	123.27	118.30
1	A	802	LEU	CB-CG-CD1	-5.30	101.99	111.00
1	B	705	ASP	CB-CG-OD2	5.29	123.06	118.30
2	C	6	PHE	N-CA-CB	5.20	119.95	110.60
1	A	668	ARG	NE-CZ-NH1	5.19	122.90	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1014	THR	N-CA-CB	5.18	120.14	110.30
1	A	843	ARG	CG-CD-NE	-5.17	100.94	111.80
1	B	970	THR	CB-CA-C	-5.06	97.93	111.60

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	3479	0	3405	50	0
1	B	3489	0	3424	50	0
2	C	94	0	86	6	0
2	D	67	0	54	5	0
3	A	12	0	16	5	0
3	B	12	0	16	0	0
4	B	15	0	0	1	0
4	C	5	0	0	0	0
5	A	169	0	0	2	0
5	B	180	0	0	3	0
5	D	2	0	0	0	0
All	All	7524	0	7001	103	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 7.

All (103) 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:903:ALA:H	3:A:6:GOL:H12	1.23	0.98
1:A:840:GLU:HG3	1:A:840:GLU:O	1.61	0.97
1:B:680:HIS:HE1	2:C:6:PHE:HE2	1.26	0.80
1:A:842:ILE:HG21	1:A:905:LYS:HG2	1.66	0.78
1:A:987:LEU:HD12	1:A:987:LEU:N	1.98	0.78
1:A:676:VAL:HG23	1:A:1034:VAL:HG23	1.69	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:719:PHE:CE2	1:B:902:PHE:CE2	2.76	0.73
1:B:716:LEU:HD11	1:B:987:LEU:HD12	1.69	0.72
1:A:903:ALA:N	3:A:6:GOL:H12	2.02	0.70
1:A:610:ALA:O	1:A:614:GLU:HG3	1.92	0.69
1:A:878:ILE:C	1:A:878:ILE:HD12	2.15	0.67
1:A:878:ILE:O	1:A:878:ILE:HD12	1.95	0.67
1:A:842:ILE:HG21	1:A:905:LYS:CG	2.26	0.65
1:A:906:GLY:HA3	5:A:230:HOH:O	1.96	0.64
1:B:624:LEU:HD11	2:C:7:TRP:HZ3	1.61	0.64
1:B:834:GLU:HG3	1:B:905:LYS:HB2	1.79	0.64
1:B:649:GLN:HG3	1:B:686:ILE:HD13	1.81	0.63
2:D:5:ASN:OD1	2:D:9:MET:HG3	1.99	0.63
1:B:610:ALA:O	1:B:614:GLU:HG3	1.98	0.63
1:A:711:GLY:HA3	1:A:795:ALA:HB2	1.79	0.63
1:B:889:LEU:HD22	1:B:899:ALA:HB1	1.81	0.62
1:A:872:ALA:HB3	1:A:875:GLN:HB2	1.80	0.62
2:D:4:GLU:HA	2:D:9:MET:O	2.00	0.61
1:B:680:HIS:CE1	2:C:6:PHE:HE2	2.14	0.61
1:A:634:THR:HG22	1:A:638:LYS:HE3	1.82	0.61
1:B:603:GLU:OE1	1:B:606:ARG:NH1	2.34	0.60
1:A:784:GLY:HA3	1:A:810:PHE:CZ	2.37	0.59
1:A:889:LEU:HD23	1:A:899:ALA:HB1	1.85	0.59
1:B:663:ARG:HD2	1:B:1053:ASP:O	2.03	0.59
1:B:849:GLU:HB3	1:B:897:LYS:HB3	1.84	0.59
1:A:903:ALA:H	3:A:6:GOL:C1	2.07	0.58
1:B:680:HIS:HE1	2:C:6:PHE:CE2	2.15	0.58
1:B:600:VAL:HG21	1:B:742:GLU:HG2	1.85	0.58
1:B:1038:ASP:O	1:B:1039:LEU:HB2	2.02	0.58
1:B:719:PHE:CE2	1:B:902:PHE:HE2	2.20	0.58
1:B:1061:ARG:HG2	5:B:340:HOH:O	2.04	0.58
1:B:600:VAL:CG2	1:B:742:GLU:HG2	2.34	0.57
1:B:719:PHE:HE2	1:B:902:PHE:HE2	1.52	0.56
1:B:872:ALA:HA	1:B:970:THR:HG23	1.86	0.55
1:B:889:LEU:HD11	1:B:901:LYS:HB3	1.88	0.55
2:D:6:PHE:HD1	2:D:6:PHE:O	1.90	0.54
1:B:860:SER:C	1:B:862:PHE:H	2.11	0.53
1:A:987:LEU:HD12	1:A:987:LEU:H	1.74	0.53
1:B:755:SER:OG	1:B:758:GLU:HG3	2.09	0.52
1:B:711:GLY:HA3	1:B:795:ALA:HB2	1.90	0.52
1:B:624:LEU:CD1	2:C:7:TRP:HZ3	2.22	0.52
1:A:878:ILE:C	1:A:878:ILE:CD1	2.80	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:597:LEU:HB3	1:B:598:PRO:HD2	1.94	0.49
1:A:668:ARG:NH1	5:A:213:HOH:O	2.27	0.49
1:A:752:LEU:HD22	1:A:824:CYS:SG	2.53	0.49
1:A:1017:ARG:O	1:A:1018:LYS:CB	2.61	0.49
1:A:722:GLN:HE22	3:A:6:GOL:H31	1.79	0.48
1:B:1047:ARG:NH2	4:B:11:SO4:S	2.87	0.48
1:B:872:ALA:HB3	1:B:875:GLN:HB2	1.95	0.48
1:B:672:ARG:O	1:B:706:GLY:HA2	2.15	0.47
1:A:987:LEU:N	1:A:987:LEU:CD1	2.71	0.47
1:B:622:ALA:O	1:B:680:HIS:HD2	1.97	0.47
1:B:825:SER:HB3	1:B:920:LEU:HD12	1.96	0.47
1:B:624:LEU:HD11	2:C:7:TRP:CZ3	2.46	0.46
1:A:825:SER:HB3	1:A:920:LEU:HD12	1.97	0.46
1:B:757:LEU:HD22	1:B:761:LEU:CD1	2.46	0.46
1:A:634:THR:O	1:A:638:LYS:HG3	2.16	0.46
1:A:745:ASP:O	1:A:749:GLN:HG3	2.16	0.45
1:A:792:ALA:O	1:A:793:LYS:HG3	2.16	0.45
1:A:714:TRP:CD2	1:A:794:PRO:HB3	2.51	0.45
1:A:955:ASP:HB3	1:A:958:TYR:H	1.82	0.45
1:A:942:GLU:HA	1:A:968:TYR:CG	2.52	0.44
1:A:843:ARG:HG2	1:A:880:GLY:C	2.37	0.44
1:A:759:LEU:HD22	1:A:765:GLN:HG2	1.99	0.44
1:B:675:ALA:HA	1:B:702:PHE:O	2.18	0.44
1:A:678:LEU:HD13	1:A:1027:SER:HB2	1.99	0.43
1:A:722:GLN:HE22	3:A:6:GOL:C3	2.30	0.43
1:B:750:ASP:HB3	1:B:817:ARG:HH22	1.84	0.43
1:A:644:LEU:HD21	1:A:665:LEU:HD11	2.00	0.43
1:A:771:THR:HA	1:A:774:VAL:HG22	1.99	0.43
1:B:834:GLU:O	1:B:835:ALA:C	2.55	0.43
1:B:869:VAL:HB	1:B:877:VAL:HB	1.99	0.43
1:B:783:LEU:HD23	1:B:783:LEU:HA	1.83	0.43
1:B:946:ILE:HD12	1:B:953:ILE:HD13	2.01	0.43
1:A:854:GLU:O	1:A:858:VAL:HG23	2.19	0.43
1:A:855:ILE:HD13	1:A:876:THR:HG21	2.01	0.42
1:A:769:ILE:CD1	1:A:834:GLU:HG3	2.49	0.42
1:B:798:ILE:HG13	1:B:937:PHE:O	2.18	0.42
1:A:649:GLN:NE2	1:A:686:ILE:HD13	2.35	0.42
1:B:668:ARG:NE	5:B:197:HOH:O	2.30	0.42
1:B:924:LEU:HA	1:B:924:LEU:HD23	1.88	0.42
1:B:779:ILE:O	1:B:783:LEU:HG	2.20	0.42
1:B:1041:ILE:HG13	1:B:1044:LEU:HD22	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:770:GLU:OE2	1:B:828:HIS:HA	2.20	0.41
1:B:990:ASN:HA	1:B:991:PRO:HD3	1.81	0.41
1:B:663:ARG:HG2	1:B:1054:TYR:CE1	2.54	0.41
1:B:849:GLU:O	1:B:849:GLU:HG2	2.20	0.41
1:A:847:LEU:HD11	1:A:875:GLN:HB3	2.02	0.41
1:A:645:ALA:O	1:A:649:GLN:HG2	2.20	0.41
1:A:1058:PRO:HA	1:A:1059:PRO:HD3	1.83	0.41
1:A:624:LEU:CD1	2:D:7:TRP:HZ3	2.34	0.41
1:B:902:PHE:HB3	5:B:162:HOH:O	2.20	0.41
1:A:802:LEU:HD23	1:A:802:LEU:C	2.41	0.41
1:B:716:LEU:HD13	1:B:987:LEU:HB2	2.03	0.41
1:A:711:GLY:HA3	1:A:795:ALA:CB	2.48	0.40
1:A:907:ALA:HB3	1:A:912:GLN:HB3	2.04	0.40
1:A:917:LEU:HD23	1:A:917:LEU:HA	1.87	0.40
1:A:624:LEU:HD11	2:D:7:TRP:HZ3	1.86	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	463/491 (94%)	447 (96%)	15 (3%)	1 (0%)	51	63
1	B	466/491 (95%)	447 (96%)	17 (4%)	2 (0%)	38	47
2	C	10/12 (83%)	10 (100%)	0	0	100	100
2	D	7/12 (58%)	6 (86%)	0	1 (14%)	0	0
All	All	946/1006 (94%)	910 (96%)	32 (3%)	4 (0%)	38	47

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	6	PHE
1	B	835	ALA
1	B	1039	LEU
1	A	1039	LEU

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	352/387 (91%)	334 (95%)	18 (5%)	28	37
1	B	348/387 (90%)	333 (96%)	15 (4%)	33	45
2	C	9/9 (100%)	6 (67%)	3 (33%)	0	0
2	D	5/9 (56%)	2 (40%)	3 (60%)	0	0
All	All	714/792 (90%)	675 (94%)	39 (6%)	25	34

All (39) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	602	GLU
1	A	620	VAL
1	A	633	LEU
1	A	668	ARG
1	A	752	LEU
1	A	802	LEU
1	A	817	ARG
1	A	834	GLU
1	A	840	GLU
1	A	843	ARG
1	A	855	ILE
1	A	891	ARG
1	A	900	ARG
1	A	904	THR
1	A	995	MET
1	A	1027	SER
1	A	1034	VAL
1	A	1049	SER

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Mol	Chain	Res	Type
1	B	621	THR
1	B	636	ARG
1	B	669	ASN
1	B	708	VAL
1	B	755	SER
1	B	757	LEU
1	B	817	ARG
1	B	836	MET
1	B	888	ILE
1	B	923	GLU
1	B	946	ILE
1	B	970	THR
1	B	995	MET
1	B	1061	ARG
1	B	1062	PHE
2	C	4	GLU
2	C	6	PHE
2	C	9	MET
2	D	6	PHE
2	D	7	TRP
2	D	9	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	654	GLN
1	A	971	HIS
1	B	680	HIS
1	B	697	GLN
1	B	975	ASN
1	B	1010	GLN

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 [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

8 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	A	4	-	5,5,5	0.37	0	5,5,5	1.14	0
3	GOL	A	6	-	5,5,5	0.45	0	5,5,5	0.50	0
4	SO4	B	11	-	4,4,4	0.64	0	6,6,6	0.79	0
4	SO4	B	12	-	4,4,4	0.58	0	6,6,6	0.41	0
3	GOL	B	2	-	5,5,5	1.04	0	5,5,5	1.00	0
3	GOL	B	3	-	5,5,5	0.51	0	5,5,5	1.21	0
4	SO4	B	9	-	4,4,4	0.59	0	6,6,6	0.37	0
4	SO4	C	13	-	4,4,4	0.58	0	6,6,6	0.42	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	A	4	-	-	0/4/4/4	0/0/0/0
3	GOL	A	6	-	-	0/4/4/4	0/0/0/0
4	SO4	B	11	-	-	0/0/0/0	0/0/0/0
4	SO4	B	12	-	-	0/0/0/0	0/0/0/0
3	GOL	B	2	-	-	0/4/4/4	0/0/0/0
3	GOL	B	3	-	-	0/4/4/4	0/0/0/0
4	SO4	B	9	-	-	0/0/0/0	0/0/0/0
4	SO4	C	13	-	-	0/0/0/0	0/0/0/0

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.

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	6	GOL	5	0
4	B	11	SO4	1	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	465/491 (94%)	-0.17	10 (2%) 62 69	24, 36, 58, 100	0
1	B	467/491 (95%)	-0.19	9 (1%) 67 73	20, 34, 57, 83	0
2	C	12/12 (100%)	0.03	1 (8%) 12 16	41, 48, 74, 75	0
2	D	9/12 (75%)	1.23	1 (11%) 6 8	72, 86, 94, 99	0
All	All	953/1006 (94%)	-0.16	21 (2%) 62 69	20, 36, 60, 100	0

All (21) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	595	PRO	5.0
2	D	7	TRP	4.1
1	B	894	ALA	3.8
1	B	890	ALA	3.2
1	B	858	VAL	3.1
1	A	1059	PRO	3.0
2	C	7	TRP	3.0
1	B	896	GLY	2.9
1	A	596	GLU	2.8
1	A	806	ALA	2.7
1	B	802	LEU	2.7
1	B	835	ALA	2.6
1	A	715	VAL	2.5
1	A	695	GLY	2.4
1	B	618	GLN	2.4
1	B	597	LEU	2.4
1	A	632	PHE	2.3
1	A	1058	PRO	2.2
1	B	988	ALA	2.2
1	A	805	ALA	2.2
1	A	903	ALA	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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
3	GOL	B	2	6/6	0.75	0.19	3.17	54,57,67,71	0
3	GOL	A	6	6/6	0.72	0.17	0.28	62,67,69,70	0
4	SO4	B	9	5/5	0.97	0.13	-	73,73,77,79	0
3	GOL	A	4	6/6	0.82	0.16	-	39,50,51,56	0
4	SO4	B	11	5/5	0.91	0.15	-	88,91,100,102	0
4	SO4	C	13	5/5	0.98	0.11	-	52,52,57,58	0
3	GOL	B	3	6/6	0.82	0.15	-	45,48,52,59	0
4	SO4	B	12	5/5	0.92	0.19	-	83,84,87,101	0

6.5 Other polymers [i](#)

There are no such residues in this entry.