Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 04:20 PM GMT

PDB ID	:	4EF6
Title	:	Crystal Structure of Mycobacterium tuberculosis Pantothenate synthetase in complex with fragment 1
Authors	:	Silvestre, H.L.; Ciulli, A.; Abell, C.; Blundell, T.
Deposited on	:	2012-03-29
Resolution	:	1.94 Å(reported)

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

|		
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
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)	:	trunk26865

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 1.94 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.
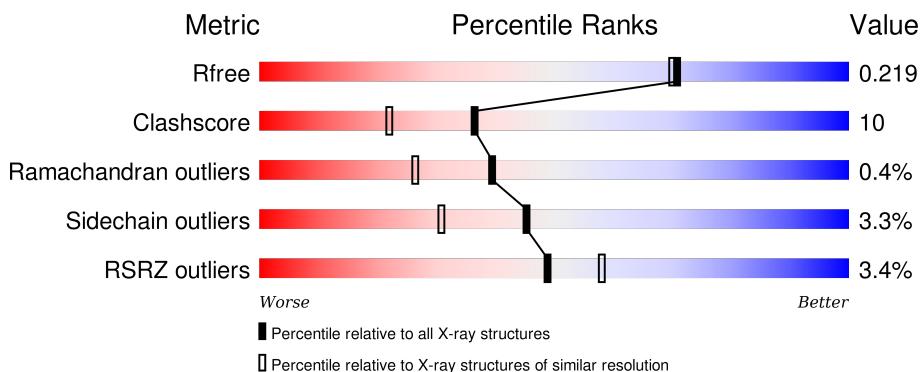
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	2910 (1.96-1.92)
Clashscore	102246	3095 (1.96-1.92)
Ramachandran outliers	100387	3062 (1.96-1.92)
Sidechain outliers	100360	3062 (1.96-1.92)
RSRZ outliers	91569	2915 (1.96-1.92)

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 <=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	300	2% 81% — 13% · ·
1	B	300	4% 79% — 11% · 8%
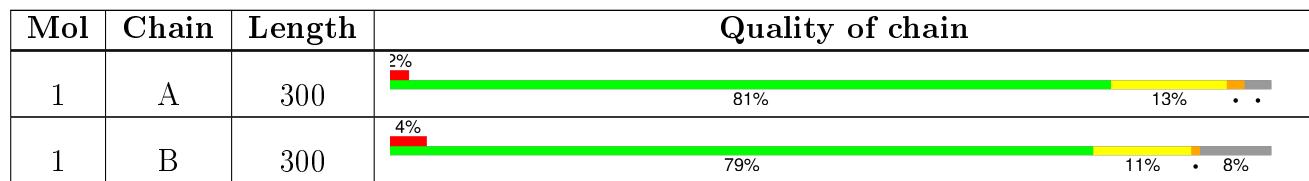
The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	EOH	A	401	-	-	X	X
2	EOH	A	402	-	-	X	X
3	I2E	B	406	-	-	-	X
4	EDO	A	405	-	-	-	X
5	GOL	A	407	-	-	-	X
5	GOL	B	402	-	-	-	X
5	GOL	B	403	-	-	-	X
5	GOL	B	404	-	-	-	X
5	GOL	B	405	-	-	-	X

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 4834 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 Pantothenate synthetase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	290	Total 2158	C 1366	N 385	O 401	S 6	0	6	0
1	B	276	Total 2102	C 1328	N 381	O 387	S 6	0	9	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	2	ALA	THR	ENGINEERED MUTATION	UNP P0A5R0
A	77	GLY	GLU	ENGINEERED MUTATION	UNP P0A5R0
B	2	ALA	THR	ENGINEERED MUTATION	UNP P0A5R0
B	77	GLY	GLU	ENGINEERED MUTATION	UNP P0A5R0

- Molecule 2 is ETHANOL (three-letter code: EOH) (formula: C_2H_6O).
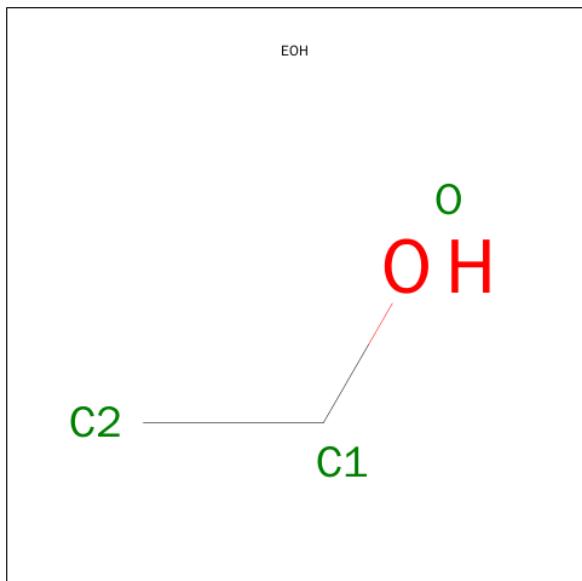
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total 3	C 2	O 1	0	0
2	A	1	Total 3	C 2	O 1	0	0
2	A	1	Total 3	C 2	O 1	0	0
2	A	1	Total 3	C 2	O 1	0	0
2	A	1	Total 3	C 2	O 1	0	0

- Molecule 3 is 3-(1,3-BENZODIOXOL-5-YL)PROPANOIC ACID (three-letter code: I2E) (formula: $C_{10}H_{10}O_4$).
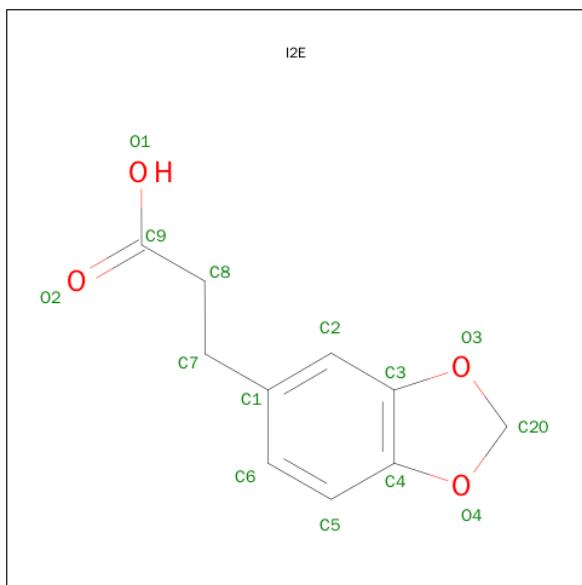
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total 14	C 10	O 4	0	0
3	B	1	Total 14	C 10	O 4	0	0

- Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).
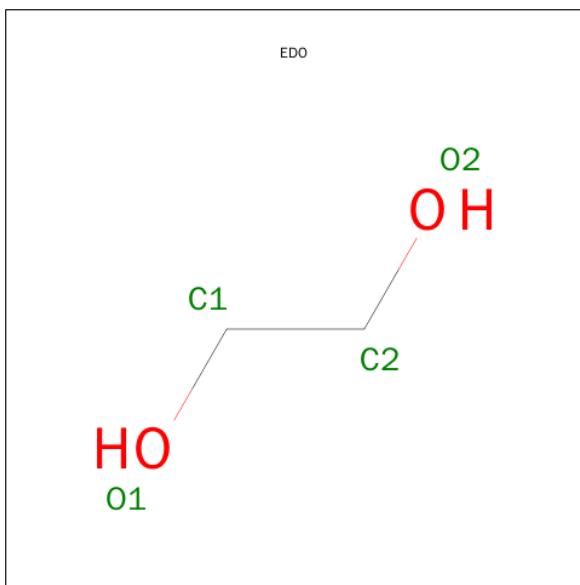
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total 4	C 2	O 2	0	0
4	A	1	Total 4	C 2	O 2	0	0
4	B	1	Total 4	C 2	O 2	0	0

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).
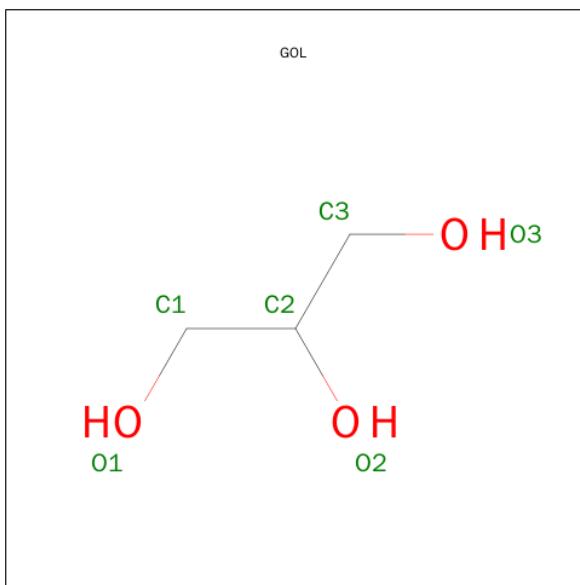
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total 6	C 3	O 3	0	0

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

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	258	Total 258	O 258	0	0
6	B	231	Total 231	O 231	0	0

3 Residue-property plots ⓘ

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: Pantothenate synthetase
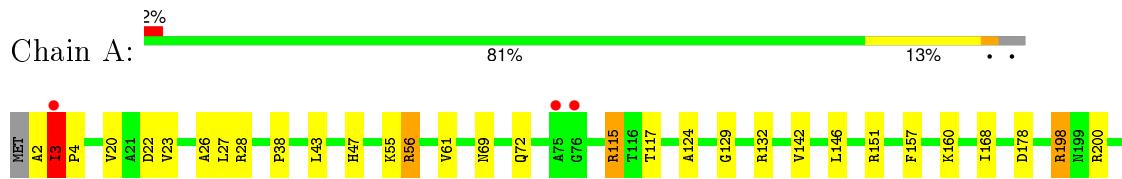
• Molecule 1: Pantothenate synthetase
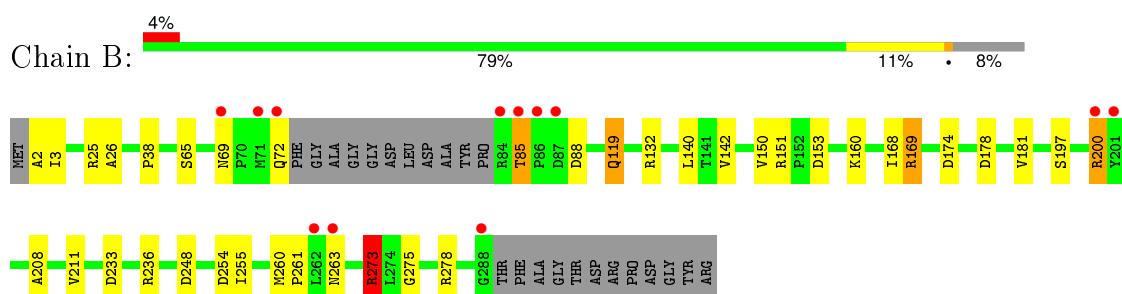
4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	48.12Å 70.70Å 82.11Å 90.00° 99.48° 90.00°	Depositor
Resolution (Å)	38.29 – 1.94 38.29 – 1.94	Depositor EDS
% Data completeness (in resolution range)	99.4 (38.29-1.94) 99.4 (38.29-1.94)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.77 (at 1.94Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, R_{free}	0.164 , 0.218 0.164 , 0.219	Depositor DCC
R_{free} test set	2019 reflections (5.30%)	DCC
Wilson B-factor (Å^2)	21.4	Xtriage
Anisotropy	0.066	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 51.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< |L| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Outliers	0 of 40092 reflections	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	4834	wwPDB-VP
Average B, all atoms (Å^2)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.99% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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, EOH, I2E, EDO

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	1.04	1/2197 (0.0%)	0.92	4/3002 (0.1%)
1	B	1.03	2/2139 (0.1%)	0.96	7/2920 (0.2%)
All	All	1.04	3/4336 (0.1%)	0.94	11/5922 (0.2%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	181	VAL	CB-CG2	5.70	1.64	1.52
1	A	142	VAL	CB-CG1	5.60	1.64	1.52
1	B	150	VAL	CB-CG1	5.54	1.64	1.52

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	28	ARG	NE-CZ-NH1	-7.29	116.66	120.30
1	B	169[A]	ARG	NE-CZ-NH1	5.88	123.24	120.30
1	B	169[B]	ARG	NE-CZ-NH1	5.88	123.24	120.30
1	A	56	ARG	NE-CZ-NH1	5.68	123.14	120.30
1	B	278	ARG	NE-CZ-NH2	-5.29	117.66	120.30
1	A	115	ARG	NE-CZ-NH1	-5.20	117.70	120.30
1	B	153	ASP	CB-CG-OD2	5.17	122.95	118.30
1	B	273[A]	ARG	NE-CZ-NH1	-5.07	117.77	120.30
1	B	273[B]	ARG	NE-CZ-NH1	-5.07	117.77	120.30
1	A	28	ARG	NE-CZ-NH2	5.03	122.81	120.30
1	B	233	ASP	CB-CG-OD1	5.00	122.80	118.30

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	2158	0	2191	44	0
1	B	2102	0	2157	41	0
2	A	15	0	30	7	0
3	A	14	0	9	0	0
3	B	14	0	9	2	0
4	A	8	0	12	2	0
4	B	4	0	6	0	0
5	A	6	0	8	0	0
5	B	24	0	32	5	0
6	A	258	0	0	10	1
6	B	231	0	0	10	1
All	All	4834	0	4454	84	1

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 10.

All (84) 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:273[A]:ARG:HG2	1:B:273[A]:ARG:HH11	1.06	1.13
1:B:169[B]:ARG:NH1	6:B:628:HOH:O	1.79	1.05
1:A:263:ASN:CG	1:A:264:GLY:H	1.58	1.03
1:A:285[B]:ILE:HD11	1:A:287:ILE:HG12	1.41	1.00
1:B:273[A]:ARG:CG	1:B:273[A]:ARG:HH11	1.72	0.99
2:A:409:EOH:H21	1:B:178[A]:ASP:OD2	1.66	0.94
1:B:273[A]:ARG:NH1	1:B:275:GLY:O	2.02	0.91
1:B:132:ARG:NH1	6:B:591:HOH:O	2.09	0.86
1:A:69:ASN:HD22	1:A:72:GLN:HE21	1.23	0.86
1:A:263:ASN:CG	1:A:264:GLY:N	2.28	0.83
1:B:273[A]:ARG:HG2	1:B:273[A]:ARG:NH1	1.90	0.81
1:B:273[A]:ARG:CG	1:B:273[A]:ARG:NH1	2.39	0.78
1:A:2:ALA:HB1	1:A:26:ALA:CB	2.15	0.75
1:B:273[A]:ARG:HB3	1:B:273[A]:ARG:NH1	2.06	0.71
1:B:25:ARG:HB2	5:B:405:GOL:H11	1.73	0.70
1:B:140:LEU:HD22	1:B:168[A]:ILE:HD13	1.74	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:132:ARG:NE	6:A:718:HOH:O	2.21	0.69
1:A:285[B]:ILE:CD1	1:A:287:ILE:HG12	2.22	0.69
3:B:406:I2E:C20	6:B:721:HOH:O	2.42	0.68
1:B:151:ARG:CZ	5:B:405:GOL:H32	2.26	0.66
1:A:151:ARG:HH22	1:B:151:ARG:CZ	2.09	0.65
1:A:285[B]:ILE:HD11	1:A:287:ILE:CG1	2.22	0.65
1:B:69:ASN:CG	1:B:142[B]:VAL:HG21	2.17	0.64
1:A:117:THR:OG1	2:A:401:EOH:H21	1.99	0.63
1:A:286:GLU:HB3	1:A:290:PHE:HB3	1.80	0.62
1:B:254:ASP:HB3	1:B:261:PRO:HD3	1.82	0.62
1:B:3:ILE:HD13	1:B:26:ALA:HB2	1.82	0.62
1:B:254:ASP:HB2	6:B:568:HOH:O	2.01	0.61
1:A:2:ALA:HB1	1:A:26:ALA:HB3	1.82	0.60
1:B:2:ALA:N	6:B:729:HOH:O	2.34	0.60
1:A:221:ALA:HA	1:A:285[A]:ILE:HD13	1.84	0.60
1:B:273[A]:ARG:CB	1:B:273[A]:ARG:NH1	2.64	0.60
1:A:178[A]:ASP:OD1	1:B:151:ARG:NH1	2.31	0.60
2:A:401:EOH:H21	1:B:119:GLN:HG2	1.84	0.59
1:A:200:ARG:NH2	6:A:587:HOH:O	2.35	0.59
2:A:401:EOH:C2	1:B:119:GLN:HG2	2.33	0.57
1:B:69:ASN:HB3	1:B:72:GLN:HG2	1.86	0.57
1:B:248:ASP:HB3	6:B:531:HOH:O	2.04	0.57
1:A:115:ARG:O	2:A:401:EOH:H22	2.04	0.57
1:A:214:SER:O	1:A:218:THR:HG23	2.05	0.56
2:A:402:EOH:C2	6:A:731:HOH:O	2.53	0.56
1:A:263:ASN:OD1	1:A:264:GLY:N	2.22	0.56
1:B:208:ALA:O	1:B:211[A]:VAL:HG12	2.06	0.55
1:B:273[A]:ARG:HB3	1:B:273[A]:ARG:CZ	2.36	0.54
1:A:290:PHE:HD1	6:A:757:HOH:O	1.90	0.53
2:A:402:EOH:H22	6:A:731:HOH:O	2.10	0.52
1:A:3:ILE:HG21	1:A:22:ASP:OD2	2.10	0.51
1:B:255:ILE:HD11	6:B:551:HOH:O	2.10	0.51
1:A:55:LYS:NZ	6:A:645:HOH:O	2.45	0.50
3:B:406:I2E:H201	6:B:721:HOH:O	2.08	0.50
1:B:85:THR:HB	1:B:88:ASP:HB3	1.92	0.50
1:B:260:MET:SD	1:B:261:PRO:HD2	2.52	0.50
1:A:132:ARG:NH2	6:A:718:HOH:O	2.43	0.50
1:A:268:LEU:HB2	1:A:285[A]:ILE:HG13	1.94	0.49
1:A:255:ILE:HD11	6:A:574:HOH:O	2.11	0.49
1:A:27:LEU:HD13	1:A:61:VAL:HG11	1.95	0.49
1:A:263:ASN:HB3	6:A:691:HOH:O	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2:ALA:HB3	1:A:23:VAL:HA	1.94	0.49
1:B:151:ARG:NH2	5:B:405:GOL:H32	2.28	0.48
1:B:273[A]:ARG:CB	1:B:273[A]:ARG:CZ	2.90	0.47
1:A:274:LEU:HD13	1:A:279:LEU:HD12	1.96	0.47
1:B:72:GLN:HE22	5:B:404:GOL:H12	1.79	0.47
1:A:218:THR:O	1:A:222:HIS:HD2	1.98	0.47
1:A:157:PHE:CZ	1:A:168:ILE:HD13	2.50	0.47
1:B:236:ARG:HD2	6:B:681:HOH:O	2.14	0.46
1:B:197:SER:O	1:B:200:ARG:HG2	2.16	0.46
1:A:132:ARG:CZ	6:A:718:HOH:O	2.59	0.46
1:A:2:ALA:CB	1:A:26:ALA:HB3	2.45	0.45
1:A:38:PRO:HB2	4:A:405:EDO:H21	1.99	0.45
4:A:406:EDO:H12	1:B:174:ASP:HB3	1.98	0.45
1:A:151:ARG:NH1	1:B:151:ARG:HD2	2.32	0.44
1:A:55:LYS:HE3	1:A:55:LYS:HB3	1.72	0.44
1:A:2:ALA:N	1:A:4:PRO:O	2.51	0.44
1:A:259:PRO:HD2	1:A:260:MET:HE2	2.00	0.44
1:B:211[B]:VAL:HG21	6:B:659:HOH:O	2.18	0.43
1:B:38:PRO:HA	1:B:65:SER:OG	2.18	0.43
1:A:285[B]:ILE:O	1:A:285[B]:ILE:HG13	2.10	0.43
1:A:151:ARG:NH1	1:B:151:ARG:CD	2.83	0.41
1:A:43:LEU:HA	1:A:47:HIS:ND1	2.35	0.41
1:A:146:LEU:HD23	1:A:146:LEU:HA	1.93	0.41
1:A:198:ARG:HA	1:A:198:ARG:HD2	1.94	0.41
1:A:151:ARG:CZ	1:B:151:ARG:HD2	2.51	0.41
1:A:124:ALA:O	1:A:129:GLY:HA3	2.22	0.40
1:B:273[A]:ARG:HH22	5:B:402:GOL:H2	1.85	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:724:HOH:O	6:B:730:HOH:O[2_656]	2.09	0.11

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	292/300 (97%)	280 (96%)	10 (3%)	2 (1%)	26	13
1	B	281/300 (94%)	277 (99%)	4 (1%)	0	100	100
All	All	573/600 (96%)	557 (97%)	14 (2%)	2 (0%)	39	35

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	3	ILE
1	A	290	PHE

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	218/223 (98%)	210 (96%)	8 (4%)	41	26
1	B	215/223 (96%)	208 (97%)	7 (3%)	45	31
All	All	433/446 (97%)	418 (96%)	15 (4%)	45	28

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	ILE
1	A	20	VAL
1	A	56	ARG
1	A	160[A]	LYS
1	A	198	ARG
1	A	260	MET
1	A	263	ASN
1	A	274	LEU
1	B	85	THR
1	B	119	GLN

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Mol	Chain	Res	Type
1	B	160	LYS
1	B	200	ARG
1	B	263	ASN
1	B	273[A]	ARG
1	B	273[B]	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	72	GLN
1	A	148	GLN
1	A	222	HIS

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 carbohydrates in this entry.

5.6   Ligand geometry (i)

15 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	#$|Z| > 2$
2	EOH	A	401	-	2,2,2	0.52	0	1,1,1	0.31	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	#|Z| > 2	Counts	RMSZ	#|Z| > 2
2	EOH	A	402	-	2,2,2	0.55	0	1,1,1	0.29	0
2	EOH	A	403	-	2,2,2	0.47	0	1,1,1	0.33	0
3	I2E	A	404	-	12,15,15	1.59	3 (25%)	17,20,20	0.51	0
4	EDO	A	405	-	3,3,3	0.40	0	2,2,2	0.57	0
4	EDO	A	406	-	3,3,3	0.25	0	2,2,2	0.52	0
5	GOL	A	407	-	5,5,5	0.22	0	5,5,5	1.18	1 (20%)
2	EOH	A	408	-	2,2,2	0.43	0	1,1,1	0.05	0
2	EOH	A	409	-	2,2,2	0.44	0	1,1,1	0.46	0
4	EDO	B	401	-	3,3,3	0.46	0	2,2,2	0.80	0
5	GOL	B	402	-	5,5,5	0.73	0	5,5,5	0.66	0
5	GOL	B	403	-	5,5,5	0.21	0	5,5,5	0.85	0
5	GOL	B	404	-	5,5,5	0.35	0	5,5,5	1.04	0
5	GOL	B	405	-	5,5,5	0.43	0	5,5,5	0.74	0
3	I2E	B	406	-	12,15,15	1.74	2 (16%)	17,20,20	1.02	1 (5%)

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
2	EOH	A	401	-	-	0/0/0/0	0/0/0/0
2	EOH	A	402	-	-	0/0/0/0	0/0/0/0
2	EOH	A	403	-	-	0/0/0/0	0/0/0/0
3	I2E	A	404	-	-	0/3/11/11	0/2/2/2
4	EDO	A	405	-	-	0/1/1/1	0/0/0/0
4	EDO	A	406	-	-	0/1/1/1	0/0/0/0
5	GOL	A	407	-	-	0/4/4/4	0/0/0/0
2	EOH	A	408	-	-	0/0/0/0	0/0/0/0
2	EOH	A	409	-	-	0/0/0/0	0/0/0/0
4	EDO	B	401	-	-	0/1/1/1	0/0/0/0
5	GOL	B	402	-	-	0/4/4/4	0/0/0/0
5	GOL	B	403	-	-	0/4/4/4	0/0/0/0
5	GOL	B	404	-	-	0/4/4/4	0/0/0/0
5	GOL	B	405	-	-	0/4/4/4	0/0/0/0
3	I2E	B	406	-	-	0/3/11/11	0/2/2/2

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	406	I2E	C7-C1	-3.68	1.41	1.51
3	A	404	I2E	C7-C1	-3.39	1.42	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	404	I2E	O4-C20	2.18	1.47	1.43
3	A	404	I2E	C6-C1	2.21	1.43	1.38
3	B	406	I2E	O4-C20	2.86	1.48	1.43

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	B	406	I2E	C7-C8-C9	2.36	117.08	112.75
5	A	407	GOL	O3-C3-C2	2.41	121.85	110.18

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

9 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	401	EOH	4	0
2	A	402	EOH	2	0
4	A	405	EDO	1	0
4	A	406	EDO	1	0
2	A	409	EOH	1	0
5	B	402	GOL	1	0
5	B	404	GOL	1	0
5	B	405	GOL	3	0
3	B	406	I2E	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(Å²)	Q<0.9
1	A	290/300 (96%)	-0.26	7 (2%)	62	70	9, 19, 36, 60	3 (1%)
1	B	276/300 (92%)	-0.26	12 (4%)	39	48	11, 21, 39, 60	1 (0%)
All	All	566/600 (94%)	-0.26	19 (3%)	49	58	9, 20, 39, 60	4 (0%)

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	3	ILE	7.0
1	B	84	ARG	5.3
1	B	262	LEU	4.4
1	A	75	ALA	3.9
1	A	76	GLY	3.7
1	B	71	MET	3.5
1	B	85	THR	3.4
1	A	291	ALA	3.0
1	A	290	PHE	2.9
1	B	86	PRO	2.9
1	B	288	GLY	2.8
1	B	72	GLN	2.7
1	A	243	PRO	2.6
1	A	289	THR	2.6
1	B	200	ARG	2.4
1	B	201	TYR	2.4
1	B	87	ASP	2.3
1	B	69	ASN	2.1
1	B	263	ASN	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
5	GOL	A	407	6/6	0.83	0.32	33.06	30,40,45,45	0
2	EOH	A	402	3/3	0.80	0.19	12.27	28,28,29,30	0
3	I2E	B	406	14/14	0.79	0.19	3.93	20,27,31,32	14
2	EOH	A	401	3/3	0.88	0.14	3.89	41,41,42,43	0
5	GOL	B	402	6/6	0.90	0.17	3.53	35,41,44,46	0
4	EDO	A	405	4/4	0.95	0.16	3.19	33,35,36,38	0
5	GOL	B	405	6/6	0.92	0.22	2.69	43,46,47,50	0
5	GOL	B	403	6/6	0.86	0.13	2.47	46,47,48,50	0
5	GOL	B	404	6/6	0.77	0.25	2.14	50,52,53,53	0
4	EDO	A	406	4/4	0.98	0.12	1.62	18,19,21,22	0
3	I2E	A	404	14/14	0.93	0.09	0.93	17,23,27,28	0
4	EDO	B	401	4/4	0.97	0.10	0.49	25,26,27,28	0
2	EOH	A	409	3/3	0.92	0.11	0.42	34,34,35,36	0
2	EOH	A	408	3/3	0.97	0.10	-	39,39,39,40	0
2	EOH	A	403	3/3	0.90	0.19	-	43,43,43,45	0

6.5 Other polymers (i)

There are no such residues in this entry.