



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 09:15 PM UTC

PDB ID : 4EF6 / pdb_00004ef6
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)

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

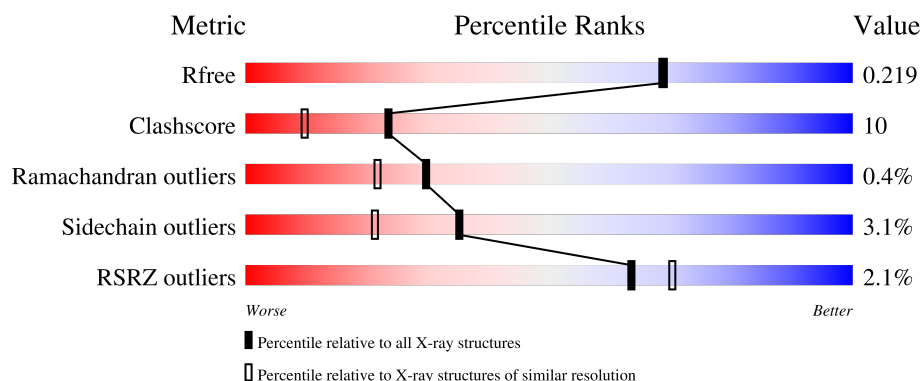
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

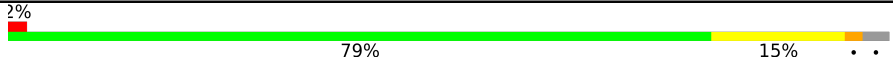
The reported resolution of this entry is 1.94 Å.

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}	180053	1452 (1.94-1.94)
Clashscore	190562	1494 (1.94-1.94)
Ramachandran outliers	187476	1479 (1.94-1.94)
Sidechain outliers	187428	1479 (1.94-1.94)
RSRZ outliers	180081	1453 (1.94-1.94)

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	300	
1	B	300	

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	-
2	EOH	A	402	-	-	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.

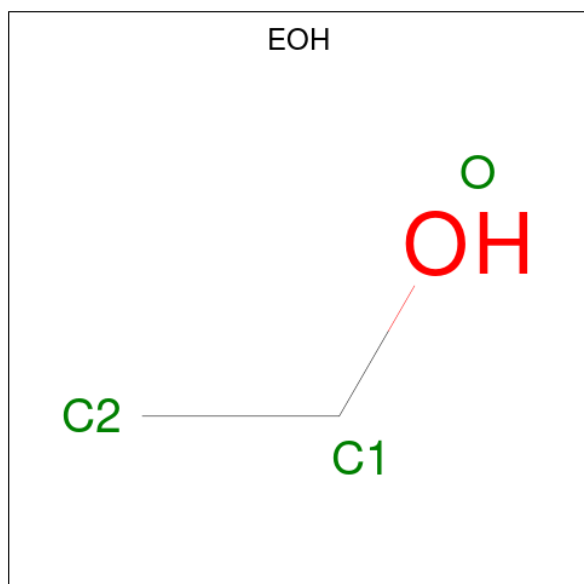
- Molecule 1 is a protein called Pantothenate synthetase.

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

There are 4 discrepancies between the modelled and reference sequences:

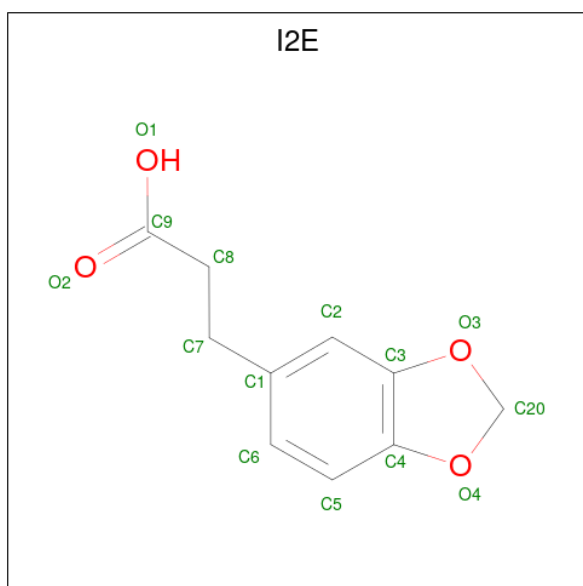
Chain	Residue	Modelled	Actual	Comment	Reference
A	2	ALA	THR	engineered mutation	UNP P0A5R0
A	77	GLY	GLU	engineered mutation	UNP P0A5R0
B	2	ALA	THR	engineered mutation	UNP P0A5R0
B	77	GLY	GLU	engineered mutation	UNP P0A5R0

- Molecule 2 is ETHANOL (CCD ID: EOH) (formula: C₂H₆O).



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

- Molecule 3 is 3-(1,3-benzodioxol-5-yl)propanoic acid (CCD ID: I2E) (formula: C₁₀H₁₀O₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			14	10	4		
3	B	1	Total	C	O	0	0
			14	10	4		

- Molecule 4 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 5 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



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

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

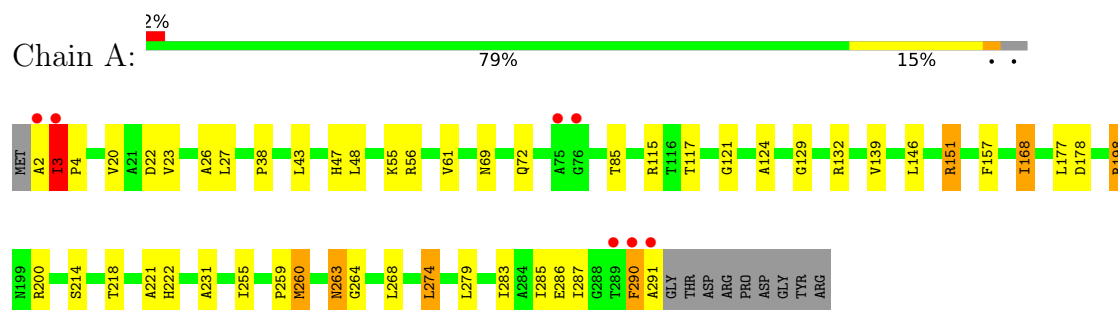
- Molecule 6 is water.

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

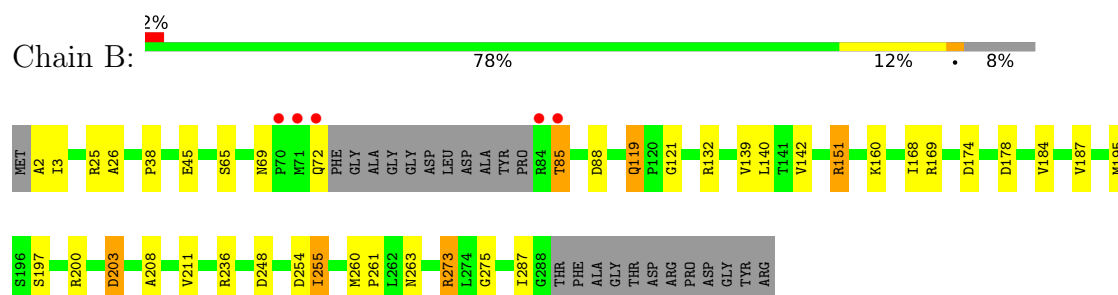
3 Residue-property plots [i](#)

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: Pantothenate synthetase



• Molecule 1: Pantothenate synthetase



4 Data and refinement statistics

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
$\langle I/\sigma(I) \rangle$ 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 (5.01%)	wwPDB-VP
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 , 45.1	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	0.96	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.*

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: EOH, GOL, EDO, I2E

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	1.32	7/2197 (0.3%)	1.19	9/3002 (0.3%)
1	B	1.28	4/2139 (0.2%)	1.15	5/2920 (0.2%)
All	All	1.30	11/4336 (0.3%)	1.17	14/5922 (0.2%)

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	283	ILE	CA-CB	6.71	1.65	1.55
1	A	151	ARG	C-O	6.22	1.26	1.23
1	B	151	ARG	C-O	6.12	1.26	1.23
1	B	139	VAL	CA-CB	6.04	1.61	1.54
1	A	231	ALA	CA-CB	5.86	1.62	1.53
1	B	151	ARG	CA-C	5.78	1.57	1.53
1	B	184	VAL	CA-C	5.65	1.57	1.52
1	A	48	LEU	N-CA	5.63	1.53	1.46
1	A	3	ILE	CA-C	5.55	1.58	1.52
1	A	3	ILE	CA-CB	5.31	1.61	1.54
1	A	139	VAL	CA-CB	5.07	1.60	1.54

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	121	GLY	CA-C-N	6.87	127.44	119.47
1	A	121	GLY	C-N-CA	6.87	127.44	119.47
1	A	85	THR	CA-C-N	-6.69	112.82	120.04
1	A	85	THR	C-N-CA	-6.69	112.82	120.04
1	B	121	GLY	CA-C-N	6.27	125.95	119.56
1	B	121	GLY	C-N-CA	6.27	125.95	119.56
1	B	203	ASP	CA-C-N	-6.24	112.57	119.19
1	B	203	ASP	C-N-CA	-6.24	112.57	119.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	168	ILE	N-CA-C	5.54	116.27	110.62
1	A	151	ARG	CA-C-N	-5.38	115.03	120.31
1	A	151	ARG	C-N-CA	-5.38	115.03	120.31
1	A	177	LEU	CA-C-N	-5.29	113.45	122.56
1	A	177	LEU	C-N-CA	-5.29	113.45	122.56
1	B	187	VAL	N-CA-C	-5.16	101.03	108.87

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	2158	0	2191	46	0
1	B	2102	0	2157	45	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	11	1
6	B	231	0	0	10	1
All	All	4834	0	4454	90	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 (90) 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:HH11	1:B:273[A]:ARG:HG2	1.06	1.13
1:A:263:ASN:CG	1:A:264:GLY:H	1.58	1.07
1:B:169[B]:ARG:NH1	6:B:628:HOH:O	1.79	1.05

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:285[B]:ILE:HD11	1:A:287:ILE:HG12	1.41	1.00
1:B:273[A]:ARG:HH11	1:B:273[A]:ARG:CG	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:A:263:ASN:CG	1:A:264:GLY:N	2.28	0.87
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:B:273[A]:ARG:HG2	1:B:273[A]:ARG:NH1	1.90	0.81
1:A:259:PRO:HD2	1:A:260:MET:HE2	1.64	0.79
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:NH1	1:B:273[A]:ARG:HB3	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
1:A:132:ARG:NE	6:A:718:HOH:O	2.21	0.69
1:B:69:ASN:CG	1:B:142[B]:VAL:HG21	2.17	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: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:A:178[A]:ASP:OD1	1:B:151:ARG:NH1	2.31	0.60
1:B:273[A]:ARG:NH1	1:B:273[A]:ARG:CB	2.64	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:B:260:MET:HE2	1:B:287:ILE:CG1	2.43	0.49
1:A:27:LEU:HD13	1:A:61:VAL:HG11	1.95	0.49
1:A:2:ALA:HB3	1:A:23:VAL:HA	1.94	0.49
1:A:263:ASN:HB3	6:A:691:HOH:O	2.13	0.49
1:B:151:ARG:NH2	5:B:405:GOL:H32	2.28	0.48
1:A:274:LEU:HD13	1:A:279:LEU:HD12	1.96	0.47
1:B:273[A]:ARG:CB	1:B:273[A]:ARG:CZ	2.90	0.47
1:B:72:GLN:HE22	5:B:404:GOL:H12	1.79	0.47
1:A:157:PHE:CZ	1:A:168:ILE:HD13	2.50	0.47
1:A:218:THR:O	1:A:222:HIS:HD2	1.98	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:B:260:MET:HE2	1:B:287:ILE:HG13	1.98	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:B:45:GLU:HB2	1:B:195:MET:HE3	1.98	0.44
1:A:2:ALA:N	1:A:4:PRO:O	2.51	0.44
1:B:211[B]:VAL:HG21	6:B:659:HOH:O	2.18	0.43
1:A:178[A]:ASP:C	1:A:178[A]:ASP:OD2	2.61	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:291:ALA:C	6:A:667:HOH:O	2.64	0.41
1:A:43:LEU:HA	1:A:47:HIS:ND1	2.35	0.41
1:A:151:ARG:NH1	1:B:151:ARG:CD	2.83	0.41
1:A:146:LEU:HD23	1:A:146:LEU:HA	1.93	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:198:ARG:HA	1:A:198:ARG:HD2	1.94	0.41
1:B:203:ASP:OD1	1:B:203:ASP:C	2.64	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 [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	292/300 (97%)	280 (96%)	10 (3%)	2 (1%)	18	9
1	B	281/300 (94%)	277 (99%)	4 (1%)	0	100	100
All	All	573/600 (96%)	557 (97%)	14 (2%)	2 (0%)	30	30

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%)	211 (97%)	7 (3%)	34	20
1	B	215/223 (96%)	208 (97%)	7 (3%)	33	20
All	All	433/446 (97%)	419 (97%)	14 (3%)	35	20

All (14) 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	198	ARG
1	A	260	MET
1	A	263	ASN
1	A	274	LEU
1	B	85	THR
1	B	119	GLN
1	B	160	LYS
1	B	255	ILE
1	B	263	ASN
1	B	273[A]	ARG
1	B	273[B]	ARG

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	72	GLN
1	A	148	GLN
1	A	222	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 [i](#)

There are no oligosaccharides 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	$\# Z > 2$
4	EDO	A	405	-	3,3,3	0.35	0	2,2,2	0.52	0
4	EDO	B	401	-	3,3,3	0.40	0	2,2,2	0.73	0
2	EOH	A	403	-	2,2,2	0.47	0	1,1,1	0.33	0
4	EDO	A	406	-	3,3,3	0.21	0	2,2,2	0.47	0
2	EOH	A	409	-	2,2,2	0.44	0	1,1,1	0.47	0
2	EOH	A	402	-	2,2,2	0.57	0	1,1,1	0.36	0
5	GOL	B	405	-	5,5,5	0.41	0	5,5,5	0.83	0
5	GOL	A	407	-	5,5,5	0.28	0	5,5,5	1.23	1 (20%)
3	I2E	A	404	-	15,15,15	1.70	4 (26%)	20,20,20	0.91	2 (10%)
3	I2E	B	406	-	15,15,15	1.97	4 (26%)	20,20,20	0.96	1 (5%)
5	GOL	B	404	-	5,5,5	0.36	0	5,5,5	1.08	0
5	GOL	B	403	-	5,5,5	0.23	0	5,5,5	0.90	0
2	EOH	A	401	-	2,2,2	0.53	0	1,1,1	0.30	0
5	GOL	B	402	-	5,5,5	0.72	0	5,5,5	0.73	0
2	EOH	A	408	-	2,2,2	0.43	0	1,1,1	0.03	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
4	EDO	A	405	-	-	0/1/1/1	-
4	EDO	B	401	-	-	0/1/1/1	-
4	EDO	A	406	-	-	1/1/1/1	-
5	GOL	B	405	-	-	0/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	GOL	A	407	-	-	4/4/4/4	-
3	I2E	A	404	-	-	4/5/11/11	0/2/2/2
3	I2E	B	406	-	-	0/5/11/11	0/2/2/2
5	GOL	B	404	-	-	2/4/4/4	-
5	GOL	B	403	-	-	2/4/4/4	-
5	GOL	B	402	-	-	1/4/4/4	-

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	406	I2E	C7-C1	-3.72	1.41	1.51
3	A	404	I2E	C7-C1	-3.43	1.42	1.51
3	B	406	I2E	C8-C9	3.22	1.58	1.50
3	B	406	I2E	O2-C9	3.16	1.32	1.22
3	A	404	I2E	C8-C9	2.87	1.57	1.50
3	B	406	I2E	O4-C20	2.75	1.48	1.43
3	A	404	I2E	C6-C1	2.32	1.43	1.38
3	A	404	I2E	O4-C20	2.09	1.47	1.43

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	404	I2E	O2-C9-C8	-2.56	114.97	123.09
5	A	407	GOL	O3-C3-C2	2.55	121.85	110.38
3	A	404	I2E	O1-C9-C8	2.39	121.55	114.00
3	B	406	I2E	O3-C20-O4	-2.05	104.88	108.09

There are no chirality outliers.

All (14) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	407	GOL	O1-C1-C2-C3
5	B	403	GOL	O1-C1-C2-C3
5	B	404	GOL	C1-C2-C3-O3
5	B	404	GOL	O2-C2-C3-O3
5	A	407	GOL	C1-C2-C3-O3
5	A	407	GOL	O1-C1-C2-O2
5	A	407	GOL	O2-C2-C3-O3
5	B	403	GOL	O1-C1-C2-O2
5	B	402	GOL	C1-C2-C3-O3

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Mol	Chain	Res	Type	Atoms
4	A	406	EDO	O1-C1-C2-O2
3	A	404	I2E	C1-C7-C8-C9
3	A	404	I2E	C2-C1-C7-C8
3	A	404	I2E	C7-C8-C9-O1
3	A	404	I2E	C6-C1-C7-C8

There are no ring outliers.

9 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	405	EDO	1	0
4	A	406	EDO	1	0
2	A	409	EOH	1	0
2	A	402	EOH	2	0
5	B	405	GOL	3	0
3	B	406	I2E	2	0
5	B	404	GOL	1	0
2	A	401	EOH	4	0
5	B	402	GOL	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 [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	290/300 (96%)	-0.41	7 (2%) 59 67	9, 19, 36, 60	7 (2%)
1	B	276/300 (92%)	-0.40	5 (1%) 67 74	6, 20, 39, 60	10 (3%)
All	All	566/600 (94%)	-0.41	12 (2%) 63 70	6, 19, 39, 60	17 (3%)

All (12) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	76	GLY	4.9
1	A	75	ALA	3.9
1	A	291	ALA	3.3
1	A	3	ILE	3.1
1	A	289	THR	3.1
1	A	2	ALA	2.8
1	B	71	MET	2.7
1	A	290	PHE	2.7
1	B	70	PRO	2.6
1	B	72	GLN	2.6
1	B	85	THR	2.5
1	B	84	ARG	2.3

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

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	I2E	B	406	14/14	0.79	0.15	20,27,31,32	14
5	GOL	B	404	6/6	0.79	0.16	50,52,53,53	0
2	EOH	A	409	3/3	0.86	0.15	34,34,35,36	0
5	GOL	B	402	6/6	0.87	0.13	35,41,44,46	0
5	GOL	B	403	6/6	0.87	0.12	46,47,48,50	0
2	EOH	A	402	3/3	0.87	0.14	28,28,29,30	0
2	EOH	A	401	3/3	0.89	0.10	41,41,42,43	0
5	GOL	A	407	6/6	0.90	0.10	30,40,45,45	0
2	EOH	A	403	3/3	0.90	0.12	43,43,43,45	0
5	GOL	B	405	6/6	0.90	0.11	43,46,47,50	0
4	EDO	A	405	4/4	0.92	0.10	33,35,36,38	0
2	EOH	A	408	3/3	0.93	0.13	39,39,39,40	0
3	I2E	A	404	14/14	0.95	0.06	17,23,27,28	0
4	EDO	B	401	4/4	0.96	0.10	25,26,27,28	0
4	EDO	A	406	4/4	0.98	0.04	18,19,21,22	0

6.5 Other polymers

There are no such residues in this entry.