



Full wwPDB X-ray Structure Validation Report ⓘ

May 26, 2020 – 11:36 am BST

PDB ID : 5XLW
Title : Mycobacterium tuberculosis Pantothenate kinase mutant F247A/F254A
Authors : Paul, A.; Kumar, P.; Surolia, A.; Vijayan, M.
Deposited on : 2017-05-11
Resolution : 2.26 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

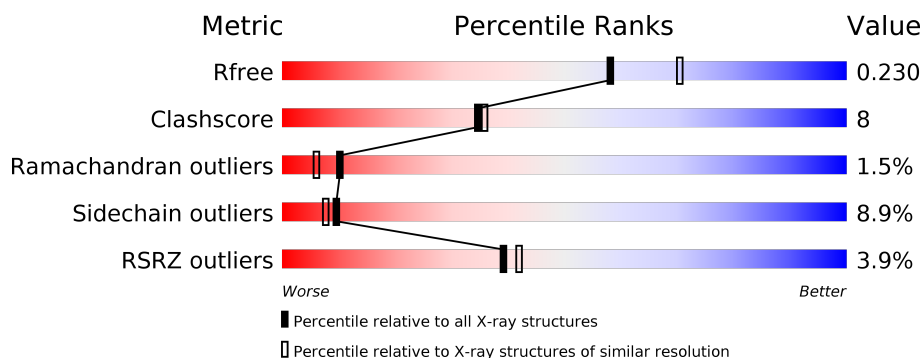
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.26 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}	130704	1377 (2.26-2.26)
Clashscore	141614	1487 (2.26-2.26)
Ramachandran outliers	138981	1449 (2.26-2.26)
Sidechain outliers	138945	1450 (2.26-2.26)
RSRZ outliers	127900	1356 (2.26-2.26)

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 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	312	<div> <div>4%</div> <div> <div></div> <div>80%</div> <div>14%</div> <div>• • •</div> </div> </div>
1	B	312	<div> <div>3%</div> <div> <div></div> <div>72%</div> <div>16%</div> <div>• 8%</div> </div> </div>

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 4963 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 kinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	287	Total	C	N	O	S	0	0	0
			2245	1438	401	401	5			
1	A	306	Total	C	N	O	S	0	2	0
			2417	1541	437	433	6			

There are 4 discrepancies between the modelled and reference sequences:

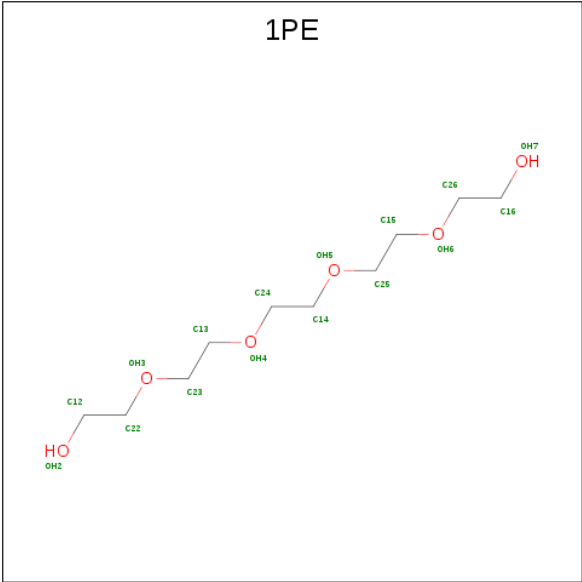
Chain	Residue	Modelled	Actual	Comment	Reference
B	247	ALA	PHE	engineered mutation	UNP P9WPA7
B	254	ALA	PHE	engineered mutation	UNP P9WPA7
A	247	ALA	PHE	engineered mutation	UNP P9WPA7
A	254	ALA	PHE	engineered mutation	UNP P9WPA7

- Molecule 2 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



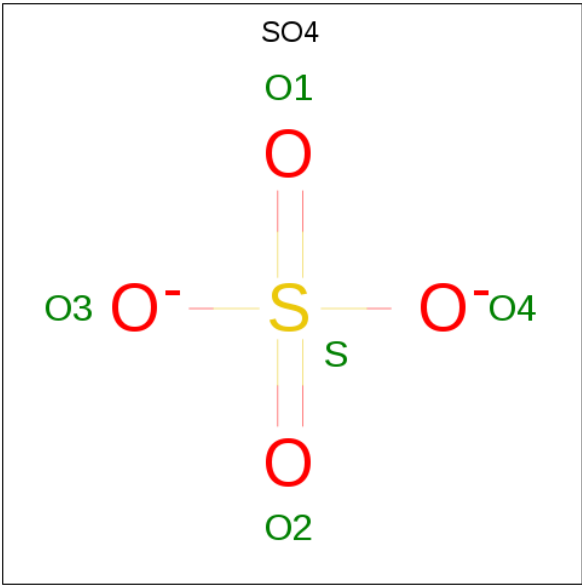
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total C O 4 2 2	0	0
2	B	1	Total C O 4 2 2	0	0
2	B	1	Total C O 4 2 2	0	0
2	B	1	Total C O 4 2 2	0	0
2	B	1	Total C O 4 2 2	0	0
2	B	1	Total C O 4 2 2	0	0
2	B	1	Total C O 4 2 2	0	0
2	B	1	Total C O 4 2 2	0	0
2	B	1	Total C O 4 2 2	0	0
2	B	1	Total C O 4 2 2	0	0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

- Molecule 3 is PENTAETHYLENE GLYCOL (three-letter code: 1PE) (formula: C₁₀H₂₂O₆).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	C	O	0	0
			16	10	6		

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



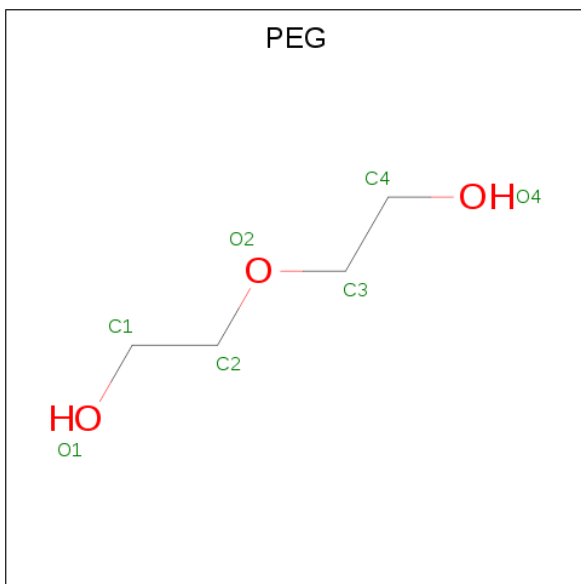
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		

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

- Molecule 5 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$).



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

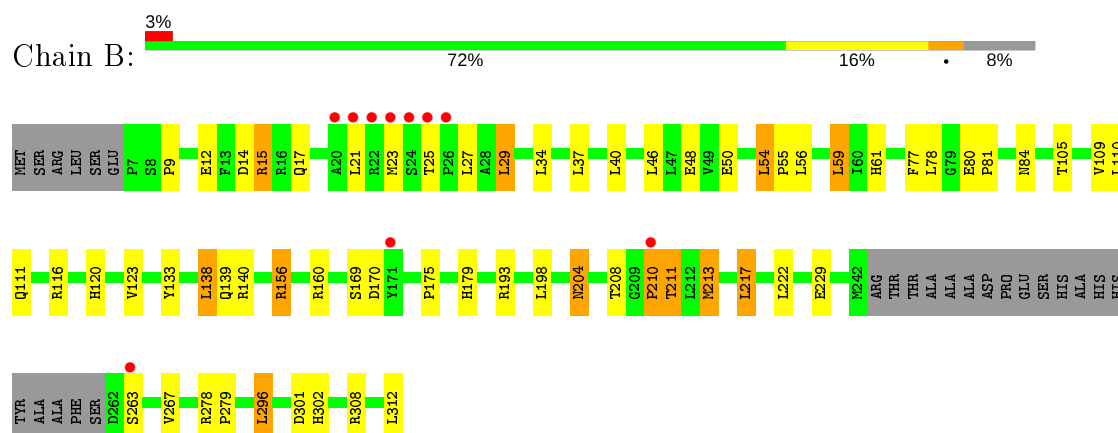
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	96	Total	O	0	0
			96	96		
6	A	82	Total	O	0	0
			82	82		

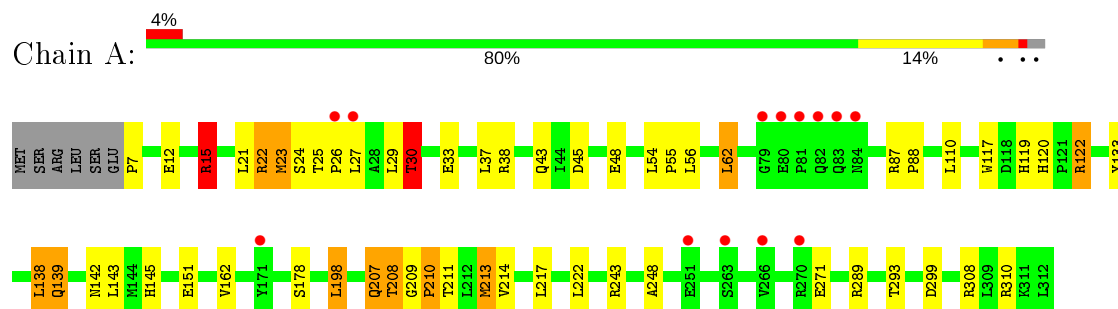
3 Residue-property plots [i](#)

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: Pantothenate kinase



• Molecule 1: Pantothenate kinase



4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	119.33Å 119.33Å 127.44Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	43.55 – 2.26 43.55 – 2.26	Depositor EDS
% Data completeness (in resolution range)	99.5 (43.55-2.26) 99.5 (43.55-2.26)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.09 (at 2.27Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.191 , 0.228 0.197 , 0.230	Depositor DCC
R_{free} test set	2500 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	37.0	Xtriage
Anisotropy	0.345	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 43.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.028 for -h,-k,l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4963	wwPDB-VP
Average B, all atoms (Å ²)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.27% 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: PEG, 1PE, EDO, 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	0.92	0/2482	1.03	8/3385 (0.2%)
1	B	0.97	0/2296	1.04	5/3129 (0.2%)
All	All	0.94	0/4778	1.03	13/6514 (0.2%)

There are no bond length outliers.

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	15	ARG	NE-CZ-NH2	-7.92	116.34	120.30
1	A	299	ASP	CB-CA-C	-7.59	95.23	110.40
1	A	15	ARG	NE-CZ-NH1	7.42	124.01	120.30
1	B	14	ASP	CB-CG-OD2	-7.10	111.91	118.30
1	A	222	LEU	CA-CB-CG	6.03	129.16	115.30
1	A	222	LEU	CB-CA-C	-5.94	98.92	110.20
1	B	217	LEU	CB-CG-CD1	5.75	120.77	111.00
1	B	15	ARG	NE-CZ-NH2	-5.62	117.49	120.30
1	B	156	ARG	NE-CZ-NH1	5.59	123.09	120.30
1	B	14	ASP	CB-CG-OD1	5.14	122.92	118.30
1	A	122	ARG	NE-CZ-NH2	5.08	122.84	120.30
1	A	198	LEU	CB-CG-CD2	5.06	119.61	111.00
1	A	62	LEU	CB-CG-CD1	5.02	119.53	111.00

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	2417	0	2390	43	0
1	B	2245	0	2216	37	0
2	A	32	0	48	4	0
2	B	48	0	72	7	0
3	B	16	0	22	0	0
4	A	10	0	0	0	0
4	B	10	0	0	0	0
5	A	7	0	10	0	0
6	A	82	0	0	3	0
6	B	96	0	0	4	0
All	All	4963	0	4758	79	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 8.

All (79) 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:208:THR:HA	1:A:213:MET:CE	2.00	0.92
1:A:139:GLN:HE21	1:A:139:GLN:HA	1.35	0.90
1:B:210:PRO:HA	1:A:208:THR:CG2	2.02	0.89
1:A:208:THR:HA	1:A:213:MET:HE2	1.54	0.88
1:A:139:GLN:NE2	1:A:139:GLN:HA	1.90	0.86
1:B:210:PRO:HA	1:A:208:THR:HG21	1.59	0.84
1:A:133:TYR:HB2	1:A:138:LEU:HD13	1.59	0.82
1:A:310:ARG:NH1	6:A:501:HOH:O	2.11	0.82
1:B:204:ASN:H	1:B:204:ASN:HD22	1.29	0.78
1:A:30:THR:HG22	1:A:33:GLU:H	1.47	0.78
1:B:133:TYR:HB2	1:B:138:LEU:HD13	1.68	0.73
1:A:30:THR:HB	1:A:33:GLU:OE1	1.88	0.73
1:A:38:ARG:HD3	6:A:561:HOH:O	1.93	0.69
1:A:208:THR:HA	1:A:213:MET:HE1	1.74	0.67
1:A:209:GLY:H	1:A:213:MET:CE	2.09	0.65
1:B:160:ARG:CD	2:B:411:EDO:H21	2.28	0.64
1:A:207:GLN:HB3	2:A:407:EDO:H11	1.79	0.63
1:B:29:LEU:HD22	1:B:29:LEU:N	2.13	0.63
1:A:23:MET:HB2	6:A:532:HOH:O	1.99	0.63
1:B:208:THR:HA	1:B:213:MET:CE	2.29	0.63
2:B:405:EDO:H21	6:B:510:HOH:O	2.00	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:7:PRO:HA	2:A:408:EDO:H22	1.84	0.59
1:A:29:LEU:CD2	1:A:33:GLU:HB3	2.33	0.58
1:B:204:ASN:H	1:B:204:ASN:ND2	2.00	0.58
1:B:15:ARG:NH2	1:B:48:GLU:OE2	2.38	0.57
1:A:15:ARG:NH2	1:A:48:GLU:OE2	2.38	0.56
1:B:61:HIS:HD2	1:B:120:HIS:NE2	2.03	0.56
1:B:12:GLU:HG2	1:B:308:ARG:HG2	1.87	0.55
1:B:160:ARG:CD	2:B:411:EDO:C2	2.86	0.54
1:B:204:ASN:N	1:B:204:ASN:HD22	1.98	0.54
1:B:29:LEU:HD13	1:B:50:GLU:HG3	1.91	0.53
1:B:263:SER:O	1:B:267:VAL:HG23	2.09	0.53
1:B:170:ASP:O	1:B:193:ARG:HA	2.09	0.51
1:A:22:ARG:O	1:A:23:MET:HB2	2.11	0.51
1:A:12:GLU:OE2	1:A:308:ARG:NE	2.38	0.51
1:B:278:ARG:HB3	1:B:279:PRO:HD3	1.93	0.50
1:A:208:THR:HG22	1:A:208:THR:O	2.12	0.50
1:A:209:GLY:N	1:A:213:MET:CE	2.74	0.50
1:B:301:ASP:O	1:B:302:HIS:HB2	2.12	0.49
1:B:111:GLN:HG3	1:B:123:VAL:HG22	1.95	0.49
1:B:208:THR:HA	1:B:213:MET:HE3	1.94	0.48
1:B:179:HIS:HB2	2:B:409:EDO:H22	1.95	0.48
1:A:43:GLN:OE1	1:A:43:GLN:N	2.28	0.47
1:A:54:LEU:HB3	1:A:55:PRO:CD	2.45	0.47
1:B:81:PRO:HG2	1:B:84:ASN:HB2	1.96	0.47
1:B:77:PHE:O	1:A:23:MET:HA	2.14	0.47
1:B:29:LEU:CD1	1:B:50:GLU:HG3	2.44	0.47
1:A:289:ARG:HE	2:A:406:EDO:H22	1.80	0.47
1:A:54:LEU:HB3	1:A:55:PRO:HD3	1.96	0.47
1:A:119[B]:HIS:H	1:A:119[B]:HIS:CD2	2.33	0.47
1:A:29:LEU:HD22	1:A:33:GLU:HB3	1.98	0.46
1:A:45:ASP:C	1:A:45:ASP:OD1	2.52	0.45
1:A:122:ARG:HH21	1:A:122:ARG:HG2	1.82	0.45
1:B:54:LEU:CB	1:B:55:PRO:HD3	2.47	0.45
1:A:209:GLY:O	1:A:210:PRO:O	2.35	0.44
1:B:211:THR:H	1:A:208:THR:HG21	1.81	0.44
1:B:222:LEU:HD23	1:B:296:LEU:HD22	1.98	0.44
1:B:27:LEU:HD23	6:B:577:HOH:O	2.18	0.43
2:B:411:EDO:O2	2:B:412:EDO:H22	2.17	0.43
1:B:59:LEU:HD12	1:B:59:LEU:HA	1.85	0.43
1:A:117:TRP:HB2	1:A:120:HIS:CE1	2.54	0.43
1:A:22:ARG:O	1:A:23:MET:CB	2.65	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:271:GLU:OE2	1:A:271:GLU:HA	2.19	0.42
1:B:139:GLN:O	1:B:140:ARG:C	2.57	0.42
1:A:243:ARG:C	1:A:243:ARG:HD2	2.40	0.42
1:B:213:MET:HG2	1:B:213:MET:H	1.78	0.42
1:B:105:THR:O	1:B:109:VAL:HG13	2.20	0.42
1:B:56:LEU:HD11	1:B:296:LEU:HD11	2.02	0.42
2:B:405:EDO:C2	6:B:510:HOH:O	2.63	0.42
1:A:209:GLY:H	1:A:213:MET:HE3	1.85	0.41
1:A:151:GLU:OE1	1:A:151:GLU:N	2.35	0.41
1:B:17:GLN:O	1:B:21:LEU:HG	2.20	0.41
1:A:87:ARG:HB2	1:A:88:PRO:HD2	2.02	0.41
1:B:23:MET:HE2	6:B:563:HOH:O	2.19	0.41
1:B:229:GLU:CD	1:B:229:GLU:H	2.24	0.41
1:A:289:ARG:HE	2:A:406:EDO:C2	2.33	0.40
1:A:145:HIS:CD2	1:A:145:HIS:H	2.40	0.40
1:B:175:PRO:O	2:B:405:EDO:H22	2.22	0.40
1:A:162:VAL:HG21	1:A:214:VAL:CG2	2.52	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	306/312 (98%)	290 (95%)	9 (3%)	7 (2%)	6	3
1	B	283/312 (91%)	272 (96%)	9 (3%)	2 (1%)	22	21
All	All	589/624 (94%)	562 (95%)	18 (3%)	9 (2%)	10	6

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	211	THR

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Mol	Chain	Res	Type
1	A	22	ARG
1	A	23	MET
1	A	26	PRO
1	A	211	THR
1	A	248	ALA
1	A	30	THR
1	A	210	PRO
1	B	25	THR

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	253/268 (94%)	232 (92%)	21 (8%)	11	9
1	B	231/268 (86%)	209 (90%)	22 (10%)	8	6
All	All	484/536 (90%)	441 (91%)	43 (9%)	9	8

All (43) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	9	PRO
1	B	29	LEU
1	B	34	LEU
1	B	37	LEU
1	B	40	LEU
1	B	46	LEU
1	B	54	LEU
1	B	59	LEU
1	B	78	LEU
1	B	80	GLU
1	B	110	LEU
1	B	116	ARG
1	B	138	LEU
1	B	156	ARG
1	B	169	SER

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Mol	Chain	Res	Type
1	B	198	LEU
1	B	204	ASN
1	B	210	PRO
1	B	213	MET
1	B	217	LEU
1	B	296	LEU
1	B	312	LEU
1	A	15	ARG
1	A	21	LEU
1	A	24	SER
1	A	25	THR
1	A	27	LEU
1	A	30	THR
1	A	37	LEU
1	A	56	LEU
1	A	62	LEU
1	A	110	LEU
1	A	138	LEU
1	A	139	GLN
1	A	142	ASN
1	A	143	LEU
1	A	178	SER
1	A	198	LEU
1	A	207	GLN
1	A	208	THR
1	A	213	MET
1	A	217	LEU
1	A	293	THR

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

Mol	Chain	Res	Type
1	B	61	HIS
1	B	179	HIS
1	B	204	ASN
1	A	139	GLN
1	A	145	HIS

5.3.3 RNA ⓘ

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](#)

26 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	EDO	A	408	-	3,3,3	0.54	0	2,2,2	0.27	0
4	SO4	A	410	-	4,4,4	0.49	0	6,6,6	0.82	0
2	EDO	B	410	-	3,3,3	0.52	0	2,2,2	0.22	0
2	EDO	B	406	-	3,3,3	0.71	0	2,2,2	0.36	0
2	EDO	A	403	-	3,3,3	0.67	0	2,2,2	0.21	0
4	SO4	B	414	-	4,4,4	0.73	0	6,6,6	0.63	0
2	EDO	B	402	-	3,3,3	0.47	0	2,2,2	0.12	0
2	EDO	B	401	-	3,3,3	0.68	0	2,2,2	0.20	0
2	EDO	A	407	-	3,3,3	0.58	0	2,2,2	0.81	0
5	PEG	A	401	-	6,6,6	0.56	0	5,5,5	0.70	0
4	SO4	B	415	-	4,4,4	0.55	0	6,6,6	0.43	0
2	EDO	B	403	-	3,3,3	0.58	0	2,2,2	0.20	0
2	EDO	B	407	-	3,3,3	0.59	0	2,2,2	0.57	0
2	EDO	A	402	-	3,3,3	0.48	0	2,2,2	0.46	0
2	EDO	A	406	-	3,3,3	0.63	0	2,2,2	0.20	0
2	EDO	B	405	-	3,3,3	0.45	0	2,2,2	0.31	0
2	EDO	A	409	-	3,3,3	0.40	0	2,2,2	0.46	0
2	EDO	B	409	-	3,3,3	0.55	0	2,2,2	0.08	0
2	EDO	A	404	-	3,3,3	0.69	0	2,2,2	0.18	0
2	EDO	B	404	-	3,3,3	0.65	0	2,2,2	0.21	0
2	EDO	A	405	-	3,3,3	0.48	0	2,2,2	0.39	0
2	EDO	B	408	-	3,3,3	0.70	0	2,2,2	0.10	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	EDO	B	411	-	3,3,3	0.44	0	2,2,2	0.22	0
4	SO4	A	411	-	4,4,4	0.63	0	6,6,6	0.95	0
3	1PE	B	413	-	15,15,15	0.69	0	14,14,14	0.61	0
2	EDO	B	412	-	3,3,3	0.42	0	2,2,2	0.61	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
2	EDO	A	408	-	-	1/1/1/1	-
2	EDO	B	410	-	-	0/1/1/1	-
2	EDO	B	406	-	-	1/1/1/1	-
2	EDO	A	403	-	-	1/1/1/1	-
2	EDO	B	402	-	-	1/1/1/1	-
2	EDO	B	401	-	-	1/1/1/1	-
2	EDO	A	407	-	-	1/1/1/1	-
5	PEG	A	401	-	-	2/4/4/4	-
2	EDO	B	403	-	-	0/1/1/1	-
2	EDO	B	407	-	-	1/1/1/1	-
2	EDO	A	402	-	-	0/1/1/1	-
2	EDO	A	406	-	-	0/1/1/1	-
2	EDO	B	405	-	-	1/1/1/1	-
2	EDO	A	409	-	-	0/1/1/1	-
2	EDO	B	409	-	-	0/1/1/1	-
2	EDO	A	404	-	-	1/1/1/1	-
2	EDO	B	404	-	-	1/1/1/1	-
2	EDO	A	405	-	-	0/1/1/1	-
2	EDO	B	408	-	-	1/1/1/1	-
2	EDO	B	411	-	-	0/1/1/1	-
3	1PE	B	413	-	-	8/13/13/13	-
2	EDO	B	412	-	-	1/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (22) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	413	1PE	OH6-C15-C25-OH5

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Mol	Chain	Res	Type	Atoms
3	B	413	1PE	OH4-C13-C23-OH3
5	A	401	PEG	O1-C1-C2-O2
5	A	401	PEG	O2-C3-C4-O4
3	B	413	1PE	OH2-C12-C22-OH3
2	A	403	EDO	O1-C1-C2-O2
2	B	407	EDO	O1-C1-C2-O2
2	B	405	EDO	O1-C1-C2-O2
2	B	404	EDO	O1-C1-C2-O2
2	B	408	EDO	O1-C1-C2-O2
2	A	407	EDO	O1-C1-C2-O2
2	B	406	EDO	O1-C1-C2-O2
2	A	404	EDO	O1-C1-C2-O2
3	B	413	1PE	C15-C25-OH5-C14
3	B	413	1PE	C16-C26-OH6-C15
2	B	402	EDO	O1-C1-C2-O2
2	B	401	EDO	O1-C1-C2-O2
3	B	413	1PE	C25-C15-OH6-C26
2	B	412	EDO	O1-C1-C2-O2
3	B	413	1PE	OH7-C16-C26-OH6
2	A	408	EDO	O1-C1-C2-O2
3	B	413	1PE	C13-C23-OH3-C22

There are no ring outliers.

7 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	408	EDO	1	0
2	A	407	EDO	1	0
2	A	406	EDO	2	0
2	B	405	EDO	3	0
2	B	409	EDO	1	0
2	B	411	EDO	3	0
2	B	412	EDO	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	306/312 (98%)	-0.04	13 (4%) 36 38	19, 40, 76, 122	0
1	B	287/312 (91%)	-0.15	10 (3%) 44 46	20, 35, 70, 101	0
All	All	593/624 (95%)	-0.09	23 (3%) 39 42	19, 38, 75, 122	0

All (23) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	26	PRO	5.4
1	B	26	PRO	5.3
1	B	24	SER	5.0
1	B	20	ALA	4.3
1	B	23	MET	3.9
1	B	22	ARG	3.9
1	A	79	GLY	3.6
1	B	25	THR	3.3
1	A	81	PRO	3.2
1	B	210	PRO	3.1
1	A	171	TYR	2.9
1	A	270	ARG	2.8
1	A	82	GLN	2.6
1	A	84	ASN	2.4
1	A	83	GLN	2.4
1	A	251	GLU	2.4
1	B	171	TYR	2.3
1	A	27	LEU	2.3
1	B	21	LEU	2.2
1	A	263[A]	SER	2.2
1	A	266	VAL	2.1
1	B	263	SER	2.1
1	A	80	GLU	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. 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(\AA^2)	Q<0.9
2	EDO	A	403	4/4	0.63	0.20	70,72,73,75	0
2	EDO	B	401	4/4	0.71	0.24	60,65,65,73	0
2	EDO	B	408	4/4	0.73	0.21	74,82,85,86	0
2	EDO	B	409	4/4	0.84	0.20	69,76,82,84	0
2	EDO	B	410	4/4	0.85	0.23	57,59,60,61	0
2	EDO	A	404	4/4	0.86	0.16	52,60,62,63	0
2	EDO	A	405	4/4	0.88	0.19	65,65,66,68	0
2	EDO	A	406	4/4	0.88	0.17	60,60,69,73	0
2	EDO	A	408	4/4	0.89	0.18	71,76,84,84	0
2	EDO	B	404	4/4	0.90	0.29	59,66,71,73	0
2	EDO	A	409	4/4	0.91	0.19	71,74,74,75	0
2	EDO	B	412	4/4	0.91	0.11	62,64,70,71	0
2	EDO	A	402	4/4	0.92	0.39	46,55,61,62	0
2	EDO	A	407	4/4	0.92	0.20	58,67,68,72	0
2	EDO	B	407	4/4	0.92	0.20	44,50,53,54	0
5	PEG	A	401	7/7	0.93	0.14	52,55,65,70	0
2	EDO	B	403	4/4	0.93	0.40	66,72,76,82	0
2	EDO	B	406	4/4	0.93	0.39	50,52,54,55	0
3	1PE	B	413	16/16	0.93	0.14	41,51,66,69	0
2	EDO	B	402	4/4	0.93	0.24	50,52,52,56	0
2	EDO	B	405	4/4	0.94	0.37	37,57,65,68	0
2	EDO	B	411	4/4	0.94	0.16	56,57,57,64	0
4	SO4	A	410	5/5	0.95	0.26	64,66,72,73	0
4	SO4	B	415	5/5	0.98	0.21	50,54,56,58	0
4	SO4	A	411	5/5	0.99	0.11	21,27,31,32	0
4	SO4	B	414	5/5	1.00	0.12	21,22,25,29	0

6.5 Other polymers

There are no such residues in this entry.