



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 08:19 PM UTC

PDB ID : 8AHW / pdb_00008ahw
Title : Structure of DCS-resistant variant D322N of alanine racemase from *Mycobacterium tuberculosis*
Authors : de Chiara, C.; Prosser, G.; Ogrodowicz, R.W.; de Carvalho, L.P.S.
Deposited on : 2022-07-22
Resolution : 1.58 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

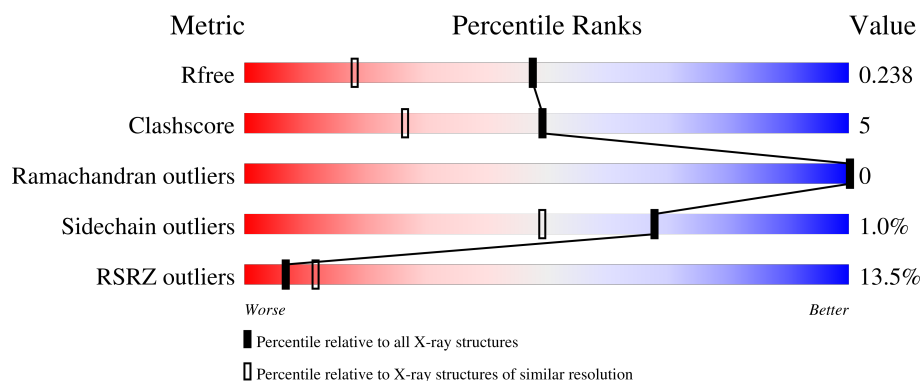
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.58 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	1094 (1.58-1.58)
Clashscore	190562	1105 (1.58-1.58)
Ramachandran outliers	187476	1082 (1.58-1.58)
Sidechain outliers	187428	1081 (1.58-1.58)
RSRZ outliers	180081	1094 (1.58-1.58)

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	387	10% 87% 7% 5%
1	B	387	15% 78% 12% 10%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 10746 atoms, of which 5198 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 Alanine racemase.

Mol	Chain	Residues	Atoms								ZeroOcc	AltConf	Trace
1	A	366	Total	C	H	N	O	P	S		0	2	0
			5338	1689	2648	482	503	1	15				
1	B	348	Total	C	H	N	O	P	S		0	0	0
			5064	1597	2513	459	481	1	13				

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	expression tag	UNP P9WQA9
A	1	SER	-	expression tag	UNP P9WQA9
A	2	HIS	-	expression tag	UNP P9WQA9
A	322	ASN	ASP	engineered mutation	UNP P9WQA9
B	0	GLY	-	expression tag	UNP P9WQA9
B	1	SER	-	expression tag	UNP P9WQA9
B	2	HIS	-	expression tag	UNP P9WQA9
B	322	ASN	ASP	engineered mutation	UNP P9WQA9

- Molecule 2 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	H	O	0	0
			13	3	7	3		

- Molecule 3 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	H	O	0	0
			10	2	6	2		
3	A	1	Total	C	H	O	0	0
			10	2	6	2		
3	B	1	Total	C	H	O	0	0
			10	2	6	2		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	B	1	Total	C	H	O	0	0
			10	2	6	2		
3	B	1	Total	C	H	O	0	0
			10	2	6	2		

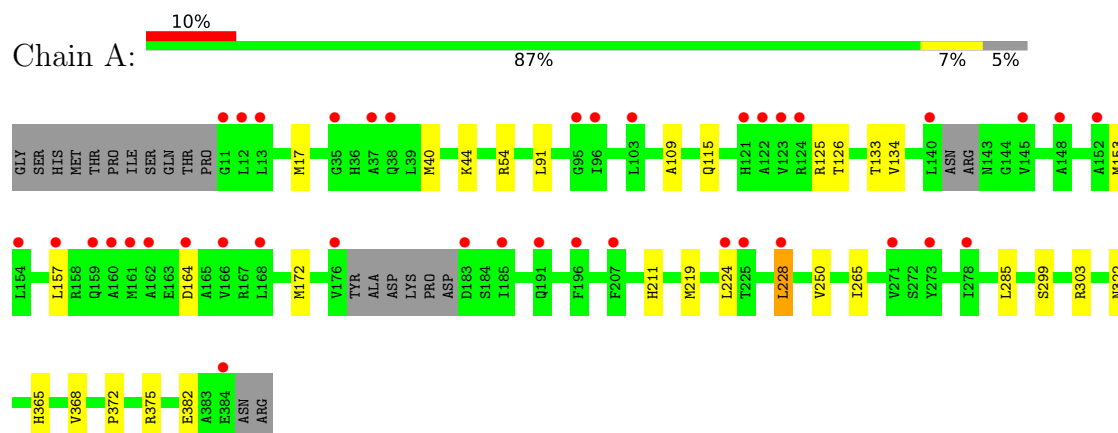
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	158	Total	O	0	0
			158	158		
4	B	123	Total	O	0	0
			123	123		

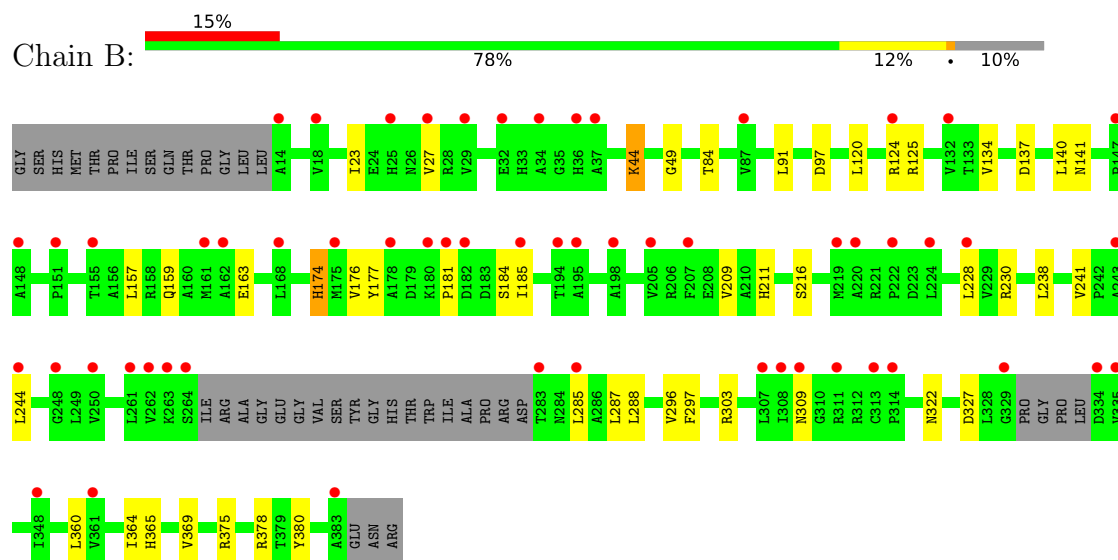
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Alanine racemase



• Molecule 1: Alanine racemase



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	165.32Å 165.32Å 57.76Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.35 – 1.58 47.35 – 1.58	Depositor EDS
% Data completeness (in resolution range)	100.0 (47.35-1.58) 100.0 (47.35-1.58)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.49 (at 1.58Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.227 , 0.234 (Not available) , 0.238	Depositor DCC
R_{free} test set	5503 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	29.7	Xtriage
Anisotropy	0.189	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.41 , 43.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	10746	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.18% 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: EDO, LLP, GOL

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.41	0/2717	0.61	0/3699
1	B	0.35	0/2566	0.56	0/3493
All	All	0.38	0/5283	0.59	0/7192

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2690	2648	2661	22	1
1	B	2551	2513	2516	33	1
2	A	6	7	8	0	0
3	A	8	12	12	2	0
3	B	12	18	18	5	0
4	A	158	0	0	4	0
4	B	123	0	0	4	0
All	All	5548	5198	5215	57	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 5.

All (57) 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:40:MET:HE3	1:A:228:LEU:HD21	1.55	0.88
1:A:17:MET:HE1	4:A:621:HOH:O	1.76	0.86
1:B:84:THR:O	4:B:501:HOH:O	2.12	0.68
1:B:44:LLP:H2'2	1:B:174:HIS:CD2	2.35	0.61
1:B:91:LEU:HB2	3:B:402:EDO:H21	1.83	0.59
1:B:211:HIS:CD2	1:B:230:ARG:HH11	2.20	0.59
1:B:211:HIS:HD2	1:B:230:ARG:HD3	1.68	0.58
1:B:91:LEU:HD22	4:B:591:HOH:O	2.02	0.58
1:B:309:ASN:O	1:B:309:ASN:OD1	2.23	0.57
1:A:91:LEU:HD22	4:B:595:HOH:O	2.05	0.57
1:B:97:ASP:OD1	1:B:125:ARG:NH2	2.38	0.56
1:B:44:LLP:H2'2	1:B:174:HIS:NE2	2.22	0.55
1:B:364:ILE:HG22	3:B:403:EDO:H11	1.88	0.55
1:A:17:MET:CE	4:A:621:HOH:O	2.45	0.54
1:A:299:SER:O	1:A:303:ARG:NH1	2.42	0.53
1:B:49:GLY:HA2	3:B:401:EDO:H12	1.90	0.53
1:B:181:PRO:HG3	1:B:216:SER:OG	2.09	0.52
1:B:211:HIS:HD2	1:B:230:ARG:HH11	1.57	0.52
1:A:211:HIS:HB3	1:A:228:LEU:HB3	1.92	0.51
1:B:209:VAL:HG21	1:B:228:LEU:HD11	1.92	0.51
1:A:40:MET:HE3	1:A:228:LEU:CD2	2.34	0.50
1:B:285:LEU:HD23	1:B:327:ASP:HA	1.94	0.49
1:B:303:ARG:NH1	1:B:360:LEU:O	2.46	0.49
1:B:120:LEU:O	1:B:124:ARG:HG2	2.14	0.47
3:A:403:EDO:C2	4:A:545:HOH:O	2.62	0.47
1:B:134:VAL:HG21	1:B:157:LEU:HD11	1.97	0.47
1:A:109:ALA:HA	1:A:133:THR:O	2.14	0.47
1:B:159:GLN:NE2	1:B:163:GLU:OE2	2.48	0.47
1:A:153:MET:O	1:A:157:LEU:HG	2.15	0.46
1:B:322:ASN:HB3	1:B:375:ARG:CZ	2.46	0.46
1:A:54[A]:ARG:NH2	1:A:382:GLU:OE1	2.47	0.45
1:B:23:ILE:O	1:B:27:VAL:HG23	2.16	0.45
1:B:241:VAL:HB	1:B:244:LEU:HD12	1.99	0.45
3:B:401:EDO:H11	4:B:535:HOH:O	2.17	0.45
1:A:368:VAL:O	1:A:372:PRO:HD3	2.17	0.45
1:B:378:ARG:HD3	1:B:380:TYR:OH	2.17	0.44
1:A:250:VAL:HG22	3:A:403:EDO:H21	2.00	0.44
1:A:125:ARG:NH1	1:A:125:ARG:HG3	2.33	0.43
1:B:137:ASP:OD2	1:B:141:ASN:HA	2.17	0.43
1:A:17:MET:HE2	1:A:17:MET:HB3	1.89	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:134:VAL:HG21	1:A:157:LEU:HD11	2.00	0.43
1:B:287:LEU:C	1:B:288:LEU:HD23	2.44	0.42
1:A:125:ARG:HG3	1:A:125:ARG:HH11	1.84	0.42
1:A:265:ILE:HD13	1:A:285:LEU:HD11	2.01	0.42
1:B:238:LEU:HD11	1:B:369:VAL:HG11	2.01	0.42
1:A:115:GLN:HG2	4:A:531:HOH:O	2.19	0.42
1:B:211:HIS:ND1	1:B:228:LEU:HD12	2.35	0.42
1:B:309:ASN:O	1:B:309:ASN:CG	2.62	0.42
1:B:174:HIS:CE1	3:B:402:EDO:H12	2.55	0.41
1:B:177:TYR:CE2	1:B:185:ILE:HG21	2.56	0.41
1:B:140:LEU:HA	1:B:176:VAL:HG22	2.02	0.41
1:A:172:MET:HB3	1:A:211:HIS:CE1	2.56	0.41
1:A:164:ASP:N	1:A:164:ASP:OD1	2.54	0.41
1:B:296:VAL:O	1:B:297:PHE:C	2.64	0.41
1:A:322:ASN:HB3	1:A:375:ARG:CZ	2.51	0.41
1:B:159:GLN:O	1:B:163:GLU:HG2	2.21	0.40
1:A:219[A]:MET:HE2	1:A:219[A]:MET:HB3	2.01	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)
1:A:126:THR:O	1:B:184:SER:OG[3_545]	2.19	0.01

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	361/387 (93%)	353 (98%)	8 (2%)	0	100	100
1	B	341/387 (88%)	332 (97%)	9 (3%)	0	100	100
All	All	702/774 (91%)	685 (98%)	17 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	264/293 (90%)	261 (99%)	3 (1%)	65	43
1	B	250/293 (85%)	248 (99%)	2 (1%)	73	57
All	All	514/586 (88%)	509 (99%)	5 (1%)	68	49

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	224	LEU
1	A	228	LEU
1	A	365	HIS
1	B	174	HIS
1	B	365	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	275	HIS
1	B	203	GLN
1	B	211	HIS
1	B	323	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

2 non-standard protein/DNA/RNA residues 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$
1	LLP	A	44	1	23,24,25	2.39	5 (21%)	25,32,34	1.11	2 (8%)
1	LLP	B	44	1	23,24,25	2.42	7 (30%)	25,32,34	1.49	5 (20%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	LLP	A	44	1	-	2/16/17/19	0/1/1/1
1	LLP	B	44	1	-	1/16/17/19	0/1/1/1

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	44	LLP	C4-C4'	7.39	1.62	1.46
1	B	44	LLP	C4-C4'	7.13	1.61	1.46
1	A	44	LLP	C4'-NZ	5.07	1.44	1.27
1	B	44	LLP	C4'-NZ	4.88	1.43	1.27
1	B	44	LLP	C2'-C2	3.80	1.56	1.50
1	A	44	LLP	C2'-C2	3.68	1.56	1.50
1	B	44	LLP	C6-N1	2.86	1.40	1.34
1	A	44	LLP	C4-C5	-2.72	1.38	1.42
1	B	44	LLP	C4-C5	-2.48	1.38	1.42
1	A	44	LLP	C6-N1	2.47	1.39	1.34
1	B	44	LLP	C5'-C5	2.37	1.57	1.50
1	B	44	LLP	C3-C2	2.06	1.43	1.41

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	44	LLP	CE-NZ-C4'	-3.19	108.52	118.72
1	A	44	LLP	C5-C6-N1	-2.95	119.03	123.83
1	B	44	LLP	C4-C4'-NZ	-2.78	111.21	124.04
1	B	44	LLP	C5-C4-C4'	-2.76	117.22	121.47

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	44	LLP	C5-C6-N1	-2.67	119.49	123.83
1	A	44	LLP	C4-C4'-NZ	-2.58	112.16	124.04
1	B	44	LLP	C3-C4-C5	2.56	120.33	118.28

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	44	LLP	C4-C4'-NZ-CE
1	B	44	LLP	C4-C4'-NZ-CE
1	A	44	LLP	CG-CD-CE-NZ

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	44	LLP	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

6 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	EDO	A	402	-	3,3,3	0.43	0	2,2,2	0.41	0
3	EDO	A	403	-	3,3,3	0.39	0	2,2,2	0.50	0
3	EDO	B	401	-	3,3,3	0.47	0	2,2,2	0.27	0
3	EDO	B	403	-	3,3,3	0.51	0	2,2,2	0.21	0
3	EDO	B	402	-	3,3,3	0.49	0	2,2,2	0.49	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	GOL	A	401	-	5,5,5	0.57	0	5,5,5	0.74	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	EDO	A	402	-	-	0/1/1/1	-
3	EDO	A	403	-	-	0/1/1/1	-
3	EDO	B	401	-	-	1/1/1/1	-
3	EDO	B	403	-	-	0/1/1/1	-
3	EDO	B	402	-	-	0/1/1/1	-
2	GOL	A	401	-	-	0/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	401	EDO	O1-C1-C2-O2

There are no ring outliers.

4 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	403	EDO	2	0
3	B	401	EDO	2	0
3	B	403	EDO	1	0
3	B	402	EDO	2	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å ²)	Q<0.9
1	A	365/387 (94%)	0.76	39 (10%)	11 17	19, 42, 68, 83	2 (0%)
1	B	347/387 (89%)	1.08	57 (16%)	4 8	33, 54, 74, 89	0
All	All	712/774 (91%)	0.92	96 (13%)	7 12	19, 49, 71, 89	2 (0%)

All (96) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	140	LEU	8.4
1	A	12	LEU	6.7
1	A	176	VAL	6.5
1	A	11	GLY	5.0
1	A	185	ILE	4.9
1	B	228	LEU	4.5
1	A	273	TYR	4.2
1	B	348	ILE	4.2
1	A	168	LEU	4.1
1	B	36	HIS	3.7
1	A	162	ALA	3.6
1	A	207	PHE	3.4
1	B	329	GLY	3.4
1	A	225	THR	3.4
1	B	168	LEU	3.4
1	B	335	VAL	3.3
1	B	224	LEU	3.2
1	B	314	PRO	3.2
1	A	121	HIS	3.2
1	B	243	ALA	3.2
1	B	182	ASP	3.1
1	B	383	ALA	3.1
1	B	309	ASN	3.1
1	A	384	GLU	3.0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	124	ARG	3.0
1	A	161	MET	2.9
1	B	14	ALA	2.9
1	A	164	ASP	2.8
1	B	222	PRO	2.8
1	A	160	ALA	2.7
1	A	103	LEU	2.7
1	A	154	LEU	2.7
1	A	224	LEU	2.7
1	B	162	ALA	2.7
1	A	148	ALA	2.7
1	A	159	GLN	2.6
1	B	124	ARG	2.6
1	A	95	GLY	2.6
1	B	244	LEU	2.6
1	A	157	LEU	2.5
1	B	262	VAL	2.5
1	B	263	LYS	2.5
1	B	285	LEU	2.5
1	B	205	VAL	2.5
1	A	122	ALA	2.4
1	A	152	ALA	2.4
1	B	311	ARG	2.4
1	B	250	VAL	2.4
1	B	198	ALA	2.4
1	B	194	THR	2.4
1	B	307	LEU	2.4
1	B	248	GLY	2.4
1	B	178	ALA	2.3
1	B	313	CYS	2.3
1	B	334	ASP	2.3
1	A	145	VAL	2.3
1	B	147	PRO	2.3
1	B	264	SER	2.3
1	A	228	LEU	2.3
1	B	308	ILE	2.3
1	A	37	ALA	2.3
1	B	151	PRO	2.3
1	A	38	GLN	2.3
1	B	148	ALA	2.2
1	B	220	ALA	2.2
1	A	191	GLN	2.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	161	MET	2.2
1	A	123	VAL	2.2
1	A	271	VAL	2.2
1	B	18	VAL	2.2
1	B	207	PHE	2.2
1	B	361	VAL	2.2
1	B	37	ALA	2.1
1	B	181	PRO	2.1
1	B	195	ALA	2.1
1	A	278	ILE	2.1
1	B	185	ILE	2.1
1	B	27	VAL	2.1
1	B	29	VAL	2.1
1	A	13	LEU	2.1
1	B	261	LEU	2.1
1	A	96	ILE	2.1
1	B	25	HIS	2.1
1	A	35	GLY	2.1
1	A	196	PHE	2.1
1	A	166	VAL	2.1
1	B	34	ALA	2.1
1	B	155	THR	2.1
1	B	283	THR	2.1
1	B	32	GLU	2.1
1	B	175	MET	2.1
1	B	180	LYS	2.0
1	B	87	VAL	2.0
1	B	132	VAL	2.0
1	B	219	MET	2.0
1	A	183	ASP	2.0

6.2 Non-standard residues in protein, DNA, RNA chains

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
1	LLP	B	44	24/25	0.96	0.08	34,42,51,57	0
1	LLP	A	44	24/25	0.98	0.07	29,38,46,48	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	EDO	A	402	4/4	0.79	0.17	50,60,69,71	0
3	EDO	A	403	4/4	0.80	0.19	42,54,64,67	10
2	GOL	A	401	6/6	0.86	0.17	30,39,52,52	13
3	EDO	B	401	4/4	0.90	0.11	37,46,56,56	0
3	EDO	B	403	4/4	0.90	0.12	40,50,54,65	0
3	EDO	B	402	4/4	0.94	0.12	28,46,67,67	0

6.5 Other polymers [i](#)

There are no such residues in this entry.