



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 17, 2026 – 06:11 PM UTC

PDB ID : 9JLO / pdb_00009jlo
Title : Crystal structure L-lactate dehydrogenase from *Lactobacillus reuteri* in its apoform
Authors : Matyuta, I.O.; Minyaev, M.E.; Shirokova, A.A.; Pometun, A.A.; Tishkov, V.I.; Popov, V.O.; Boyko, K.M.
Deposited on : 2024-09-19
Resolution : 2.15 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

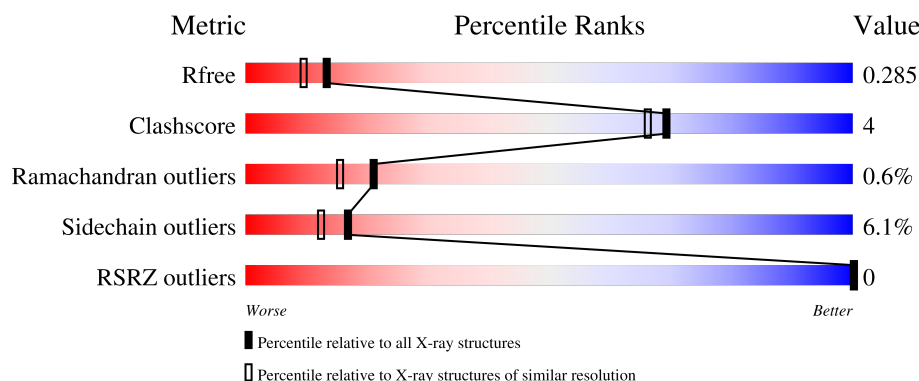
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.15 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	2057 (2.16-2.16)
Clashscore	190562	2159 (2.16-2.16)
Ramachandran outliers	187476	2134 (2.16-2.16)
Sidechain outliers	187428	2133 (2.16-2.16)
RSRZ outliers	180081	2059 (2.16-2.16)

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	319	76% 21% ..
1	B	319	76% 22% ..

2 Entry composition [i](#)

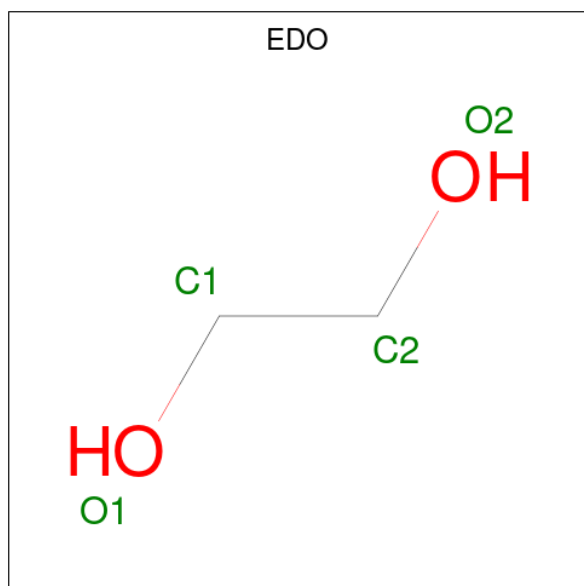
There are 3 unique types of molecules in this entry. The entry contains 4794 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 L-lactate dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	315	Total	C	N	O	S	0	4	0
			2350	1480	395	467	8			
1	B	314	Total	C	N	O	S	0	1	0
			2319	1461	390	460	8			

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



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

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

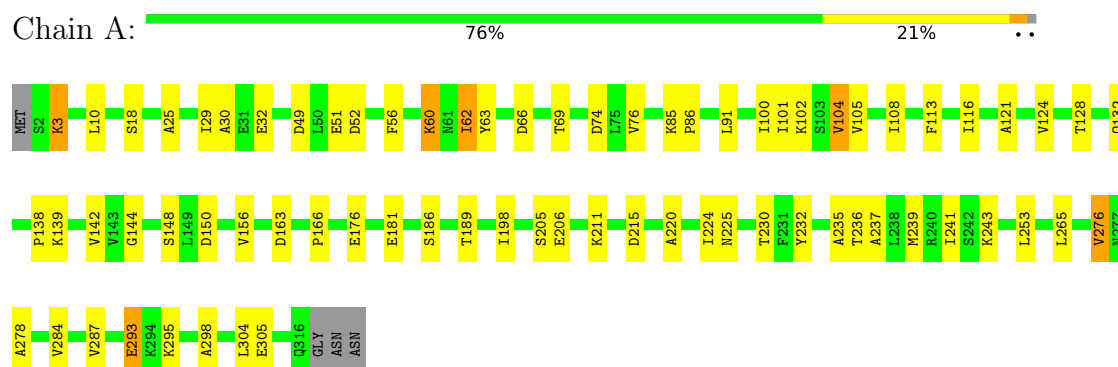
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	50	Total	O	0	0
			50	50		
3	B	43	Total	O	0	0
			43	43		

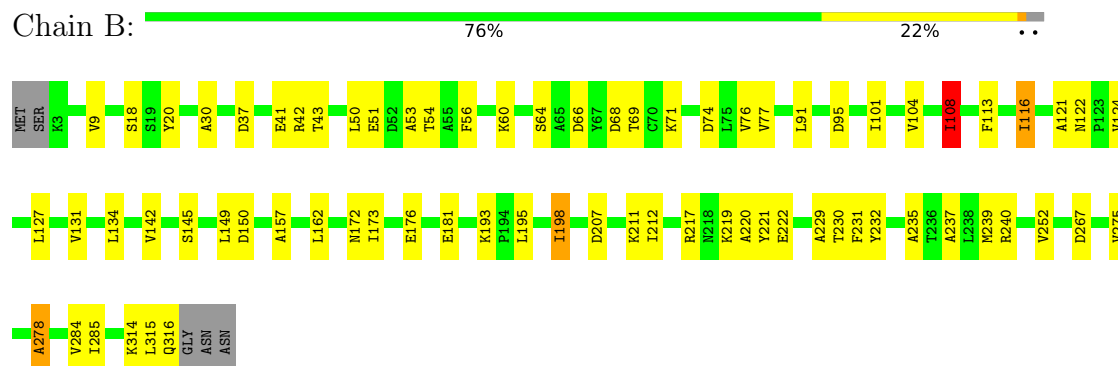
3 Residue-property plots

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: L-lactate dehydrogenase



• Molecule 1: L-lactate dehydrogenase



4 Data and refinement statistics

Property	Value	Source
Space group	P 2 21 21	Depositor
Cell constants a, b, c, α , β , γ	76.52Å 93.12Å 101.52Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	22.26 – 2.15 22.26 – 2.15	Depositor EDS
% Data completeness (in resolution range)	78.1 (22.26-2.15) 78.1 (22.26-2.15)	Depositor EDS
R_{merge}	0.27	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.99 (at 2.15Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.244 , 0.283 0.248 , 0.285	Depositor DCC
R_{free} test set	1909 reflections (4.77%)	wwPDB-VP
Wilson B-factor (Å ²)	19.0	Xtriage
Anisotropy	1.161	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 6.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.40$, $\langle L^2 \rangle = 0.23$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	4794	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 6.89% 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

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	1.45	13/2391 (0.5%)	1.84	36/3239 (1.1%)
1	B	1.44	12/2352 (0.5%)	1.85	35/3186 (1.1%)
All	All	1.44	25/4743 (0.5%)	1.85	71/6425 (1.1%)

All (25) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	148	SER	C-O	8.52	1.33	1.24
1	B	237	ALA	C-O	7.91	1.33	1.24
1	A	105	VAL	C-O	7.10	1.32	1.24
1	A	62	ILE	C-O	-6.94	1.16	1.24
1	A	132	GLN	C-O	6.88	1.32	1.24
1	B	42	ARG	C-O	6.39	1.31	1.24
1	B	142	VAL	C-O	6.37	1.31	1.24
1	B	240	ARG	C-O	6.34	1.31	1.24
1	A	224	ILE	C-O	-6.32	1.16	1.24
1	A	25	ALA	C-O	-6.30	1.16	1.24
1	A	235	ALA	C-O	6.29	1.31	1.24
1	A	32	GLU	C-O	-6.14	1.17	1.23
1	B	173	ILE	C-O	6.11	1.31	1.24
1	B	235	ALA	C-O	6.09	1.31	1.24
1	A	18	SER	C-O	-6.08	1.17	1.24
1	B	9	VAL	C-O	6.03	1.30	1.24
1	B	108	ILE	C-O	-5.95	1.17	1.24
1	A	237	ALA	C-O	5.88	1.31	1.24
1	B	229	ALA	C-O	5.61	1.30	1.23
1	B	278	ALA	C-O	5.48	1.31	1.24
1	A	206	GLU	C-O	5.47	1.30	1.24
1	A	100	ILE	C-O	-5.29	1.17	1.24
1	B	267	ASP	C-O	5.12	1.30	1.23
1	B	53	ALA	C-O	5.12	1.30	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	29	ILE	C-O	5.09	1.29	1.24

All (71) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	166	PRO	N-CA-CB	-9.78	92.98	103.25
1	B	54	THR	CA-CB-OG1	-9.37	95.54	109.60
1	B	66	ASP	CA-C-N	6.74	129.61	120.38
1	B	66	ASP	C-N-CA	6.74	129.61	120.38
1	A	293	GLU	CB-CA-C	6.67	123.99	110.38
1	B	51	GLU	CB-CA-C	-6.64	99.40	110.68
1	B	20	TYR	CA-C-O	-6.57	113.87	120.90
1	B	41	GLU	CB-CG-CD	6.49	123.64	112.60
1	A	232	TYR	CA-C-O	-6.48	113.55	120.42
1	A	60	LYS	CB-CA-C	6.42	120.74	109.89
1	A	74	ASP	N-CA-C	-6.37	105.66	113.50
1	A	66	ASP	CA-C-N	6.27	129.53	120.38
1	A	66	ASP	C-N-CA	6.27	129.53	120.38
1	A	18	SER	CA-C-N	6.25	128.66	120.28
1	A	18	SER	C-N-CA	6.25	128.66	120.28
1	A	56	PHE	CB-CA-C	6.21	120.20	109.15
1	B	220	ALA	CA-C-N	6.21	128.51	120.44
1	B	220	ALA	C-N-CA	6.21	128.51	120.44
1	B	18	SER	O-C-N	6.20	128.46	122.07
1	B	18	SER	CA-C-N	6.08	128.75	120.54
1	B	18	SER	C-N-CA	6.08	128.75	120.54
1	A	156	VAL	CA-C-O	-6.00	114.49	120.85
1	A	104	VAL	CA-C-N	6.00	128.68	120.46
1	A	104	VAL	C-N-CA	6.00	128.68	120.46
1	B	315	LEU	O-C-N	5.93	128.25	122.09
1	A	205	SER	CA-C-N	5.91	128.52	120.54
1	A	205	SER	C-N-CA	5.91	128.52	120.54
1	A	232	TYR	O-C-N	5.88	128.85	122.15
1	A	243	LYS	CA-C-O	-5.75	114.78	120.82
1	A	52	ASP	CA-C-N	5.74	128.25	120.38
1	A	52	ASP	C-N-CA	5.74	128.25	120.38
1	B	232	TYR	CA-C-O	-5.71	114.37	120.42
1	B	315	LEU	CA-C-N	5.65	131.87	121.70
1	B	315	LEU	C-N-CA	5.65	131.87	121.70
1	A	230	THR	CA-C-O	-5.64	114.06	120.32
1	A	284	VAL	CA-C-O	-5.61	114.38	120.71
1	A	10	LEU	CA-C-O	-5.56	114.25	120.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	56	PHE	CB-CA-C	5.52	118.29	109.02
1	A	265	LEU	CA-C-O	-5.46	114.99	121.16
1	B	221	TYR	CA-C-N	5.43	127.56	120.28
1	B	221	TYR	C-N-CA	5.43	127.56	120.28
1	B	275	VAL	CA-C-O	-5.38	114.63	120.71
1	B	176	GLU	CB-CG-CD	5.35	121.69	112.60
1	A	236	THR	CA-C-O	-5.32	115.23	120.82
1	A	49	ASP	CA-CB-CG	5.32	117.92	112.60
1	B	219	LYS	CA-C-O	-5.28	114.95	120.55
1	B	42	ARG	CG-CD-NE	-5.27	100.40	112.00
1	B	37	ASP	CA-C-N	5.27	127.29	120.70
1	B	37	ASP	C-N-CA	5.27	127.29	120.70
1	B	74	ASP	N-CA-C	-5.26	106.71	113.23
1	A	215	ASP	CA-CB-CG	5.25	117.85	112.60
1	B	232	TYR	CA-C-N	5.25	125.76	119.94
1	B	232	TYR	C-N-CA	5.25	125.76	119.94
1	B	231	PHE	CA-C-O	-5.23	113.03	120.51
1	B	122	ASN	CB-CA-C	5.23	116.39	108.86
1	A	225	ASN	CA-CB-CG	5.19	117.79	112.60
1	B	198	ILE	CA-C-N	5.19	127.54	120.54
1	B	198	ILE	C-N-CA	5.19	127.54	120.54
1	A	198	ILE	CA-C-N	5.16	127.51	120.54
1	A	198	ILE	C-N-CA	5.16	127.51	120.54
1	B	50	LEU	CA-C-O	-5.14	114.97	120.42
1	B	284	VAL	CA-C-O	-5.13	115.01	121.11
1	B	145	SER	N-CA-C	-5.11	105.79	111.36
1	A	63	TYR	CA-C-N	5.10	128.09	120.95
1	A	63	TYR	C-N-CA	5.10	128.09	120.95
1	A	239	MET	CA-C-O	-5.08	115.14	120.63
1	B	134	LEU	CA-C-O	-5.08	114.61	120.24
1	A	241	ILE	O-C-N	5.05	127.03	121.83
1	A	144	GLY	CA-C-O	-5.03	116.34	120.92
1	A	220	ALA	CA-C-N	5.00	126.94	120.44
1	A	220	ALA	C-N-CA	5.00	126.94	120.44

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	2350	0	2346	12	0
1	B	2319	0	2310	21	0
2	A	8	0	12	1	0
2	B	24	0	36	4	0
3	A	50	0	0	1	0
3	B	43	0	0	4	0
All	All	4794	0	4704	33	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 4.

All (33) 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:253:LEU:HD12	1:A:276:VAL:HG11	1.66	0.78
1:B:239:MET:SD	3:B:536:HOH:O	2.46	0.72
1:B:77:VAL:HG13	3:B:535:HOH:O	1.88	0.72
1:B:172:ASN:N	3:B:501:HOH:O	2.29	0.62
1:B:104:VAL:O	1:B:108:ILE:HG13	2.02	0.59
1:A:76:VAL:HG23	1:A:113:PHE:CE1	2.40	0.57
1:B:76:VAL:HG23	1:B:113:PHE:CE1	2.41	0.56
1:A:104:VAL:O	1:A:108:ILE:HG12	2.07	0.55
1:A:298:ALA:HA	2:A:402:EDO:H11	1.89	0.55
1:B:43:THR:OG1	1:B:64:SER:OG	2.28	0.52
1:B:157:ALA:HB2	2:B:404:EDO:H22	1.93	0.51
1:A:176:GLU:OE2	1:A:304:LEU:HD13	2.12	0.50
1:B:149:LEU:HD22	2:B:405:EDO:H12	1.95	0.48
1:B:76:VAL:HG11	1:B:108:ILE:HD12	1.97	0.47
1:B:60:LYS:NZ	3:B:507:HOH:O	2.48	0.46
1:A:276:VAL:HB	3:A:530:HOH:O	2.15	0.46
1:B:127:LEU:O	1:B:131:VAL:HG23	2.16	0.45
1:B:95:ASP:OD2	1:B:314:LYS:NZ	2.42	0.45
1:A:128:THR:HG23	1:A:142:VAL:HG12	1.99	0.45
1:B:91:LEU:HD22	1:B:91:LEU:H	1.81	0.45
1:B:116:ILE:CD1	1:B:278:ALA:O	2.66	0.44
1:A:51[A]:GLU:OE2	1:A:62:ILE:O	2.36	0.44
1:B:222:GLU:OE2	1:B:222:GLU:HA	2.18	0.44
1:A:186:SER:OG	1:A:293:GLU:OE1	2.34	0.43
1:A:116:ILE:CD1	1:A:278:ALA:O	2.66	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:230:THR:HG23	2:B:405:EDO:C1	2.50	0.42
1:B:162:LEU:HD13	1:B:198:ILE:HG21	2.02	0.41
1:A:150:ASP:OD2	1:A:181:GLU:OE2	2.39	0.41
1:B:252:VAL:HG13	1:B:285:ILE:CD1	2.51	0.41
1:B:149:LEU:CD2	2:B:405:EDO:H12	2.51	0.41
1:A:121:ALA:O	1:A:124:VAL:HA	2.21	0.40
1:B:121:ALA:O	1:B:124:VAL:HA	2.21	0.40
1:B:150:ASP:OD2	1:B:181:GLU:OE2	2.40	0.40

There are no symmetry-related clashes.

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	317/319 (99%)	302 (95%)	12 (4%)	3 (1%)	14	9
1	B	313/319 (98%)	297 (95%)	15 (5%)	1 (0%)	36	34
All	All	630/638 (99%)	599 (95%)	27 (4%)	4 (1%)	21	15

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	3	LYS
1	A	30	ALA
1	B	30	ALA
1	A	138	PRO

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	243/254 (96%)	227 (93%)	16 (7%)	15	10
1	B	239/254 (94%)	226 (95%)	13 (5%)	20	16
All	All	482/508 (95%)	453 (94%)	29 (6%)	17	13

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	LYS
1	A	60	LYS
1	A	69	THR
1	A	85	LYS
1	A	86	PRO
1	A	91	LEU
1	A	101	ILE
1	A	102	LYS
1	A	139	LYS
1	A	163	ASP
1	A	189	THR
1	A	211	LYS
1	A	276	VAL
1	A	287	VAL
1	A	295	LYS
1	A	305	GLU
1	B	68	ASP
1	B	69	THR
1	B	71	LYS
1	B	101	ILE
1	B	108	ILE
1	B	116	ILE
1	B	193	LYS
1	B	195	LEU
1	B	207	ASP
1	B	211	LYS
1	B	212	ILE
1	B	217	ARG
1	B	316	GLN

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

Mol	Chain	Res	Type
1	A	84	GLN
1	A	122	ASN
1	A	172	ASN
1	A	177	HIS
1	A	225	ASN
1	B	92	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](#)

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](#)

8 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	EDO	B	401	-	3,3,3	0.25	0	2,2,2	0.06	0
2	EDO	B	406	-	3,3,3	0.69	0	2,2,2	0.58	0
2	EDO	B	404	-	3,3,3	0.12	0	2,2,2	0.96	0
2	EDO	B	403	-	3,3,3	0.18	0	2,2,2	0.19	0
2	EDO	A	401	-	3,3,3	1.09	0	2,2,2	1.03	0
2	EDO	B	402	-	3,3,3	0.30	0	2,2,2	0.54	0
2	EDO	B	405	-	3,3,3	0.49	0	2,2,2	0.82	0
2	EDO	A	402	-	3,3,3	0.34	0	2,2,2	0.55	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	B	401	-	-	1/1/1/1	-
2	EDO	B	406	-	-	1/1/1/1	-
2	EDO	B	404	-	-	1/1/1/1	-
2	EDO	B	403	-	-	1/1/1/1	-
2	EDO	A	401	-	-	1/1/1/1	-
2	EDO	B	402	-	-	1/1/1/1	-
2	EDO	B	405	-	-	1/1/1/1	-
2	EDO	A	402	-	-	1/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	402	EDO	O1-C1-C2-O2
2	A	401	EDO	O1-C1-C2-O2
2	B	406	EDO	O1-C1-C2-O2
2	B	403	EDO	O1-C1-C2-O2
2	B	404	EDO	O1-C1-C2-O2
2	B	405	EDO	O1-C1-C2-O2
2	B	402	EDO	O1-C1-C2-O2
2	B	401	EDO	O1-C1-C2-O2

There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	404	EDO	1	0
2	B	405	EDO	3	0
2	A	402	EDO	1	0

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	315/319 (98%)	-1.28	0 100 100	10, 22, 34, 41	4 (1%)
1	B	314/319 (98%)	-1.23	0 100 100	11, 23, 40, 50	1 (0%)
All	All	629/638 (98%)	-1.25	0 100 100	10, 22, 36, 50	5 (0%)

There are no RSRZ outliers to report.

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 [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(Å ²)	Q<0.9
2	EDO	A	402	4/4	0.98	0.05	23,24,25,26	0
2	EDO	B	402	4/4	0.98	0.04	29,32,33,36	0
2	EDO	B	403	4/4	0.98	0.07	29,31,35,35	0
2	EDO	A	401	4/4	0.99	0.03	27,31,32,32	0
2	EDO	B	401	4/4	0.99	0.03	25,28,29,32	0
2	EDO	B	404	4/4	0.99	0.04	13,18,21,25	0
2	EDO	B	405	4/4	0.99	0.04	18,19,21,21	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	EDO	B	406	4/4	0.99	0.04	24,26,28,29	0

6.5 Other polymers [i](#)

There are no such residues in this entry.