



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 02:26 PM UTC

PDB ID : 3JZL / pdb_00003jzl
Title : CRYSTAL STRUCTURE OF A PUTATIVE CYSTATHIONINE BETA-LYASE INVOLVED IN ALUMINUM RESISTANCE (LMOF2365_1314) FROM LISTERIA MONOCYTOGENES STR. 4B F2365 AT 1.91 Å RESOLUTION
Authors : Joint Center for Structural Genomics (JCSG)
Deposited on : 2009-09-23
Resolution : 1.91 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

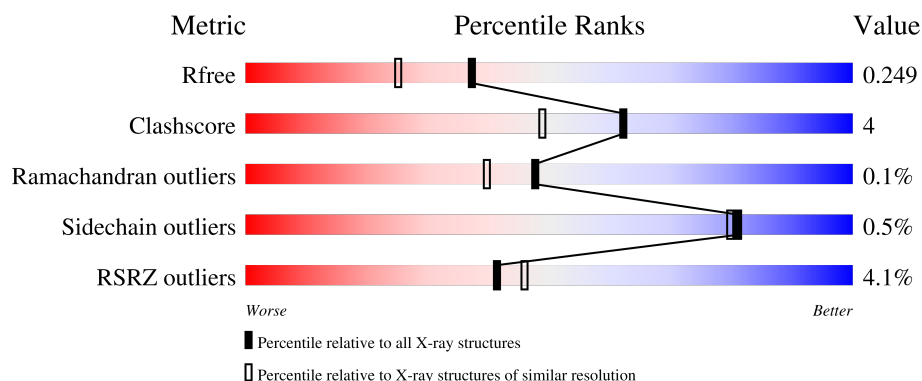
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

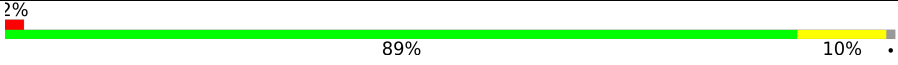
The reported resolution of this entry is 1.91 Å.

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	1188 (1.92-1.92)
Clashscore	190562	1209 (1.92-1.92)
Ramachandran outliers	187476	1195 (1.92-1.92)
Sidechain outliers	187428	1195 (1.92-1.92)
RSRZ outliers	180081	1188 (1.92-1.92)

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 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	409	
1	B	409	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 6397 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.

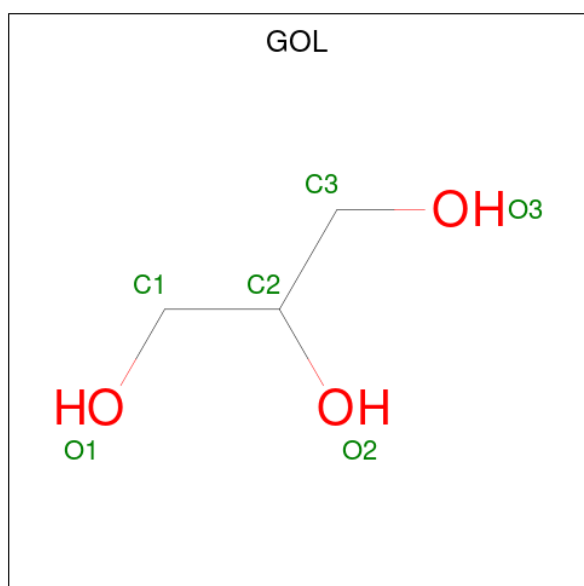
- Molecule 1 is a protein called Putative cystathionine beta-lyase involved in aluminum resistance.

Mol	Chain	Residues	Atoms							ZeroOcc	AltConf	Trace
1	A	405	Total	C	N	O	P	S	Se	0	6	0
			3109	1997	509	592	1	2	8			
1	B	394	Total	C	N	O	P	S	Se	0	10	0
			2990	1916	494	571	1	2	6			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	expression tag	UNP Q720C5
B	0	GLY	-	expression tag	UNP Q720C5

- Molecule 2 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



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

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

- Molecule 3 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	4	2		

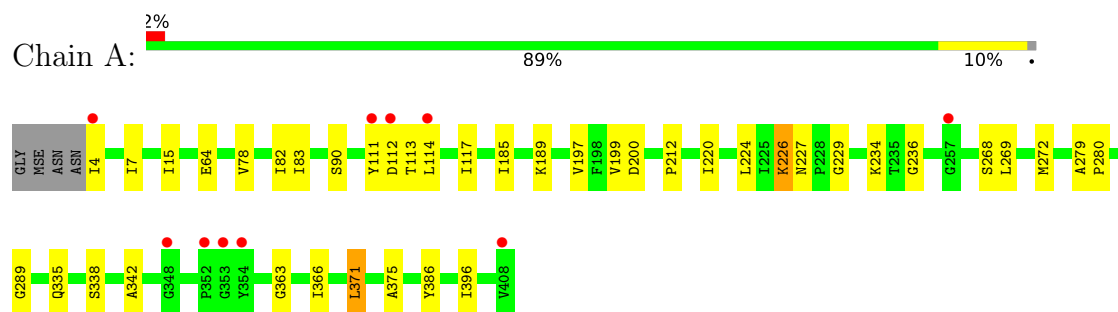
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	154	Total	O	0	0
			154	154		
4	B	120	Total	O	0	0
			120	120		

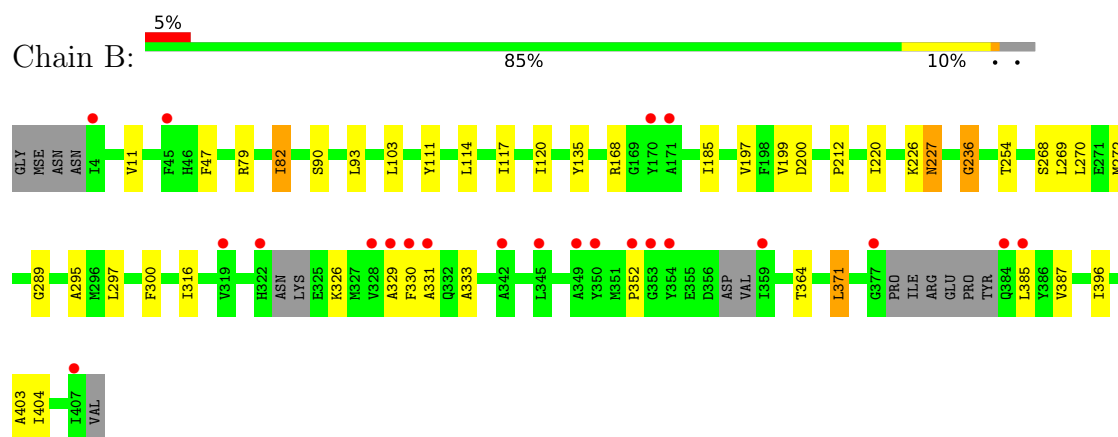
3 Residue-property plots

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: Putative cystathionine beta-lyase involved in aluminum resistance



- Molecule 1: Putative cystathionine beta-lyase involved in aluminum resistance



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	54.41Å 153.17Å 183.99Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.44 – 1.91 39.44 – 1.91	Depositor EDS
% Data completeness (in resolution range)	97.9 (39.44-1.91) 97.9 (39.44-1.91)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.89 (at 1.91Å)	Xtriage
Refinement program	REFMAC 5.5.0072, PHENIX	Depositor
R, R_{free}	0.210 , 0.241 0.221 , 0.249	Depositor DCC
R_{free} test set	2967 reflections (4.93%)	wwPDB-VP
Wilson B-factor (Å ²)	23.3	Xtriage
Anisotropy	0.927	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 50.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6397	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.89% 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: LLP, GOL, PEG

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	0.87	0/3160	1.02	7/4284 (0.2%)
1	B	0.89	1/3044 (0.0%)	1.08	10/4123 (0.2%)
All	All	0.88	1/6204 (0.0%)	1.05	17/8407 (0.2%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	254	THR	CA-C	6.58	1.55	1.52

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	371	LEU	N-CA-C	-8.45	102.41	112.89
1	B	236	GLY	N-CA-C	7.84	121.26	111.85
1	B	212	PRO	N-CA-C	7.67	120.06	110.70
1	A	212	PRO	N-CA-C	7.31	119.61	110.70
1	A	371	LEU	N-CA-C	-6.82	104.22	112.54
1	B	269	LEU	N-CA-C	6.62	118.15	111.07
1	B	316	ILE	N-CA-C	6.18	117.02	109.30
1	A	112	ASP	N-CA-C	6.17	120.36	112.34
1	B	82	ILE	N-CA-C	-5.91	99.19	108.23
1	A	200	ASP	N-CA-C	-5.83	100.75	109.15
1	A	269	LEU	N-CA-C	5.80	117.27	111.07
1	B	200	ASP	N-CA-C	-5.65	101.02	109.15
1	B	79	ARG	N-CA-C	5.62	117.33	108.23
1	A	236	GLY	N-CA-C	5.35	117.48	112.08
1	A	82	ILE	N-CA-C	-5.17	100.17	107.98
1	B	168	ARG	N-CA-C	5.04	117.50	111.71
1	B	364	THR	N-CA-C	5.03	117.32	109.52

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	3109	0	3029	21	0
1	B	2990	0	2890	28	0
2	A	6	0	8	0	0
2	B	12	0	16	0	0
3	A	6	0	7	0	0
4	A	154	0	0	1	0
4	B	120	0	0	1	0
All	All	6397	0	5950	49	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 (49) 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:331:ALA:HB3	4:B:447:HOH:O	1.78	0.82
1:B:114[B]:LEU:HD23	1:B:117:ILE:HD12	1.68	0.74
1:B:331:ALA:HB2	1:B:385:LEU:CD1	2.19	0.72
1:B:331:ALA:HB2	1:B:385:LEU:HD11	1.73	0.71
1:B:329:ALA:O	1:B:333:ALA:HB2	1.99	0.61
1:B:268:SER:HB3	1:B:272:MSE:HE2	1.86	0.57
1:A:189[A]:LYS:NZ	1:A:197:VAL:HG23	2.23	0.53
1:B:93:LEU:HD22	1:B:103:LEU:HD22	1.92	0.52
1:B:82:ILE:O	1:B:236:GLY:HA2	2.10	0.52
1:B:331:ALA:CB	1:B:385:LEU:HD11	2.39	0.52
1:B:111:TYR:CE1	1:B:114[B]:LEU:HG	2.46	0.51
1:B:90:SER:HB2	1:B:117:ILE:HD13	1.93	0.50
1:B:330:PHE:HE1	1:B:387:VAL:HG21	1.76	0.50
1:A:114:LEU:HD23	1:A:117:ILE:HD12	1.93	0.49
1:A:234:LYS:HA	1:A:366[A]:ILE:HD13	1.95	0.49
1:A:227:ASN:HA	1:A:371:LEU:HD22	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:268:SER:HB3	1:A:272:MSE:HE2	1.95	0.49
1:B:227:ASN:HA	1:B:371:LEU:HD22	1.94	0.49
1:B:11:VAL:HG13	1:B:295:ALA:HB1	1.95	0.49
1:B:331:ALA:HB2	1:B:385:LEU:HD13	1.96	0.48
1:B:297[A]:LEU:HD22	1:B:404:ILE:HD11	1.95	0.48
1:A:4:ILE:HG23	1:A:7:ILE:H	1.79	0.47
1:A:83:ILE:HG22	4:A:491:HOH:O	2.14	0.47
1:A:189[A]:LYS:HZ2	1:A:197:VAL:HG23	1.79	0.47
1:B:47:PHE:CD2	1:B:270:LEU:HD13	2.49	0.47
1:A:64:GLU:HG2	1:A:78:VAL:HG23	1.97	0.47
1:A:338:SER:O	1:A:342:ALA:HB2	2.15	0.46
1:B:120:ILE:HD11	1:B:135:TYR:HE2	1.81	0.46
1:A:90:SER:HB2	1:A:117:ILE:HD13	1.99	0.45
1:A:224:LEU:O	1:A:229:GLY:HA3	2.16	0.45
1:B:289:GLY:HA3	1:B:396:ILE:HG21	1.98	0.45
1:B:199:VAL:HB	1:B:220:ILE:HG22	1.98	0.44
1:B:114[B]:LEU:HD23	1:B:114[B]:LEU:HA	1.74	0.44
1:A:268:SER:CB	1:A:272:MSE:HE2	2.47	0.43
1:B:330:PHE:CD2	1:B:403:ALA:HB1	2.53	0.43
1:A:375:ALA:HA	1:A:386:TYR:O	2.19	0.43
1:A:199:VAL:HB	1:A:220:ILE:HG22	2.01	0.43
1:A:185:ILE:HG12	1:A:197:VAL:HG11	2.01	0.42
1:A:111:TYR:CZ	1:A:226:LLP:H6	2.55	0.42
1:B:114[B]:LEU:CD2	1:B:117:ILE:HD12	2.43	0.42
1:B:185:ILE:HG12	1:B:197:VAL:HG11	2.02	0.41
1:B:289:GLY:HA3	1:B:396:ILE:HD13	2.03	0.41
1:A:279:ALA:HB3	1:A:280:PRO:HD3	2.01	0.41
1:A:111:TYR:CE2	1:A:113:THR:OG1	2.70	0.41
1:A:289:GLY:HA3	1:A:396:ILE:HD13	2.02	0.41
1:A:335[B]:GLN:OE1	1:A:363:GLY:N	2.54	0.41
1:B:385:LEU:HD23	1:B:387:VAL:CG2	2.51	0.41
1:B:300:PHE:CE1	1:B:404:ILE:HG21	2.57	0.40
1:B:114[A]:LEU:HD12	1:B:117:ILE:HB	2.04	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	408/409 (100%)	395 (97%)	13 (3%)	0	100	100
1	B	395/409 (97%)	374 (95%)	20 (5%)	1 (0%)	36	26
All	All	803/818 (98%)	769 (96%)	33 (4%)	1 (0%)	48	40

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	326	LYS

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	314/323 (97%)	313 (100%)	1 (0%)	86	86
1	B	296/323 (92%)	294 (99%)	2 (1%)	76	73
All	All	610/646 (94%)	607 (100%)	3 (0%)	81	80

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	15	ILE
1	B	227	ASN
1	B	352	PRO

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such

sidechains are listed below:

Mol	Chain	Res	Type
1	A	38	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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	226	1	23,24,25	1.74	3 (13%)	25,32,34	1.57	5 (20%)
1	LLP	B	226	1	23,24,25	1.77	4 (17%)	25,32,34	1.64	4 (16%)

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	226	1	-	1/16/17/19	0/1/1/1
1	LLP	B	226	1	-	2/16/17/19	0/1/1/1

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	226	LLP	O3-C3	-6.03	1.23	1.36
1	A	226	LLP	O3-C3	-5.84	1.23	1.36
1	A	226	LLP	C4-C4'	2.59	1.52	1.46
1	B	226	LLP	C4-C4'	2.50	1.52	1.46
1	B	226	LLP	P-OP3	-2.18	1.46	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	226	LLP	C4'-NZ	2.18	1.34	1.27
1	A	226	LLP	C2-N1	2.12	1.37	1.33

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	226	LLP	OP4-C5'-C5	4.69	118.15	109.36
1	A	226	LLP	C5-C4-C4'	-3.28	116.42	121.47
1	B	226	LLP	C5-C4-C4'	-3.03	116.79	121.47
1	A	226	LLP	OP4-P-OP1	-2.84	98.77	106.44
1	A	226	LLP	OP4-C5'-C5	2.73	114.46	109.36
1	A	226	LLP	CE-NZ-C4'	-2.70	110.09	118.72
1	A	226	LLP	C3-C4-C4'	2.59	125.07	120.40
1	B	226	LLP	C3-C4-C4'	2.56	125.02	120.40
1	B	226	LLP	C4-C3-C2	2.01	121.28	120.14

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	B	226	LLP	C4-C4'-NZ-CE
1	A	226	LLP	C4-C4'-NZ-CE
1	B	226	LLP	C5'-OP4-P-OP3

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	226	LLP	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

4 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	PEG	A	410	-	5,5,6	0.53	0	4,4,5	0.43	0
2	GOL	B	410	-	5,5,5	0.52	0	5,5,5	0.46	0
2	GOL	A	409	-	5,5,5	0.45	0	5,5,5	0.32	0
2	GOL	B	409	-	5,5,5	0.48	0	5,5,5	0.32	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	PEG	A	410	-	-	1/3/3/4	-
2	GOL	B	410	-	-	4/4/4/4	-
2	GOL	A	409	-	-	0/4/4/4	-
2	GOL	B	409	-	-	1/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	410	GOL	O1-C1-C2-C3
2	B	410	GOL	C1-C2-C3-O3
2	B	409	GOL	C1-C2-C3-O3
2	B	410	GOL	O2-C2-C3-O3
3	A	410	PEG	O1-C1-C2-O2
2	B	410	GOL	O1-C1-C2-O2

There are no ring outliers.

No monomer is involved in short contacts.

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	396/409 (96%)	0.21	10 (2%) 58 64	10, 22, 35, 48	6 (1%)
1	B	385/409 (94%)	0.36	22 (5%) 29 34	11, 22, 35, 49	10 (2%)
All	All	781/818 (95%)	0.29	32 (4%) 41 46	10, 22, 35, 49	16 (2%)

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	352	PRO	4.9
1	B	359	ILE	4.8
1	B	377	GLY	3.7
1	B	352	PRO	3.6
1	A	408	VAL	3.6
1	B	385	LEU	3.5
1	B	354	TYR	3.5
1	A	4	ILE	3.4
1	B	330	PHE	3.3
1	B	329	ALA	3.2
1	B	4	ILE	3.1
1	A	348	GLY	3.0
1	B	322	HIS	3.0
1	B	350	TYR	3.0
1	B	328	VAL	2.9
1	B	353	GLY	2.9
1	B	407	ILE	2.9
1	B	170	TYR	2.9
1	B	319	VAL	2.8
1	B	331	ALA	2.3
1	B	345	LEU	2.3
1	A	353	GLY	2.2
1	B	171	ALA	2.2
1	A	111	TYR	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	114	LEU	2.1
1	B	45	PHE	2.1
1	A	257	GLY	2.1
1	B	342	ALA	2.1
1	B	349	ALA	2.1
1	A	354	TYR	2.0
1	B	384	GLN	2.0
1	A	112	ASP	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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
1	LLP	A	226	24/25	0.93	0.08	16,27,31,32	0
1	LLP	B	226	24/25	0.94	0.07	17,26,30,31	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(Å ²)	Q<0.9
2	GOL	B	410	6/6	0.78	0.16	67,68,69,69	0
2	GOL	A	409	6/6	0.85	0.13	26,32,34,34	0
3	PEG	A	410	6/7	0.86	0.16	55,56,57,59	0
2	GOL	B	409	6/6	0.88	0.10	40,47,48,53	0

6.5 Other polymers [i](#)

There are no such residues in this entry.