



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 10:54 PM UTC

PDB ID : 4M19 / pdb_00004m19
Title : dihydrodipicolinate synthase from *C. jejuni* with pyruvate bound to the active site and Lysine bound to allosteric site
Authors : Conly, C.J.T.
Deposited on : 2013-08-02
Resolution : 2.00 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

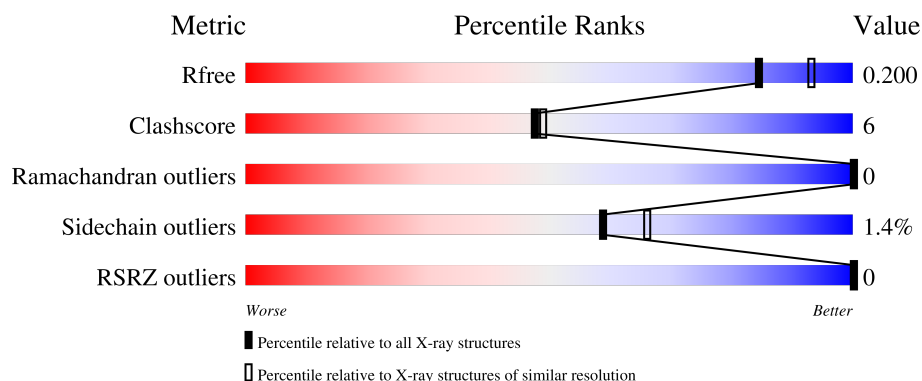
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	306	
1	B	306	
1	C	306	
1	D	306	

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 9740 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 4-hydroxy-tetrahydrodipicolinate synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	296	Total	C	N	O	S	0	5	0
			2299	1465	379	441	14			
1	B	295	Total	C	N	O	S	0	4	0
			2292	1458	383	438	13			
1	C	295	Total	C	N	O	S	0	0	0
			2270	1444	377	436	13			
1	D	295	Total	C	N	O	S	0	3	0
			2288	1458	380	436	14			

There are 32 discrepancies between the modelled and reference sequences:

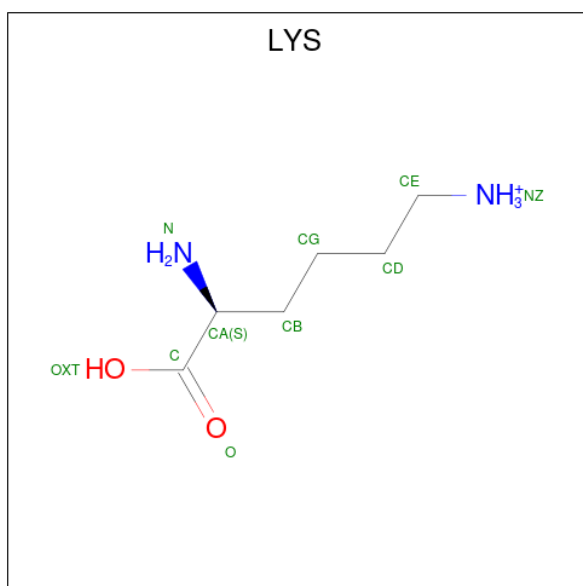
Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	HIS	-	expression tag	UNP Q9PPB4
A	-6	HIS	-	expression tag	UNP Q9PPB4
A	-5	HIS	-	expression tag	UNP Q9PPB4
A	-4	HIS	-	expression tag	UNP Q9PPB4
A	-3	HIS	-	expression tag	UNP Q9PPB4
A	-2	HIS	-	expression tag	UNP Q9PPB4
A	-1	ALA	-	expression tag	UNP Q9PPB4
A	0	SER	-	expression tag	UNP Q9PPB4
B	-7	HIS	-	expression tag	UNP Q9PPB4
B	-6	HIS	-	expression tag	UNP Q9PPB4
B	-5	HIS	-	expression tag	UNP Q9PPB4
B	-4	HIS	-	expression tag	UNP Q9PPB4
B	-3	HIS	-	expression tag	UNP Q9PPB4
B	-2	HIS	-	expression tag	UNP Q9PPB4
B	-1	ALA	-	expression tag	UNP Q9PPB4
B	0	SER	-	expression tag	UNP Q9PPB4
C	-7	HIS	-	expression tag	UNP Q9PPB4
C	-6	HIS	-	expression tag	UNP Q9PPB4
C	-5	HIS	-	expression tag	UNP Q9PPB4
C	-4	HIS	-	expression tag	UNP Q9PPB4
C	-3	HIS	-	expression tag	UNP Q9PPB4

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-2	HIS	-	expression tag	UNP Q9PPB4
C	-1	ALA	-	expression tag	UNP Q9PPB4
C	0	SER	-	expression tag	UNP Q9PPB4
D	-7	HIS	-	expression tag	UNP Q9PPB4
D	-6	HIS	-	expression tag	UNP Q9PPB4
D	-5	HIS	-	expression tag	UNP Q9PPB4
D	-4	HIS	-	expression tag	UNP Q9PPB4
D	-3	HIS	-	expression tag	UNP Q9PPB4
D	-2	HIS	-	expression tag	UNP Q9PPB4
D	-1	ALA	-	expression tag	UNP Q9PPB4
D	0	SER	-	expression tag	UNP Q9PPB4

- Molecule 2 is LYSINE (CCD ID: LYS) (formula: $C_6H_{15}N_2O_2$).



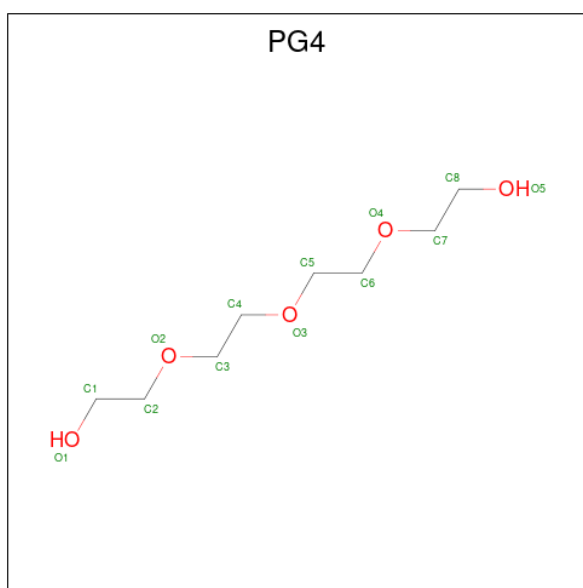
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			10	6	2	2		
2	B	1	Total	C	N	O	0	0
			10	6	2	2		
2	C	1	Total	C	N	O	0	0
			10	6	2	2		
2	D	1	Total	C	N	O	0	0
			10	6	2	2		

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



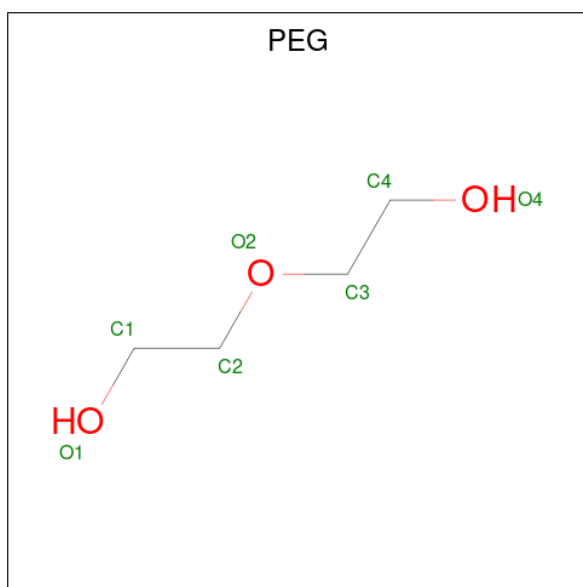
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	2	2		
3	C	1	Total	C	O	0	0
			4	2	2		

- Molecule 4 is TETRAETHYLENE GLYCOL (CCD ID: PG4) (formula: $C_8H_{18}O_5$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			13	8	5		

- Molecule 5 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



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

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	142	Total	O	0	0
			142	142		
6	B	136	Total	O	0	0
			136	136		
6	C	143	Total	O	0	0
			143	143		
6	D	102	Total	O	0	0
			102	102		

- Molecule 1: 4-hydroxy-tetrahydrodipicolinate synthase



I194	N195	Y196	P197
K204	L221	I246	N252
P253	I254	P255	M260
Y251	L262	K280	F283
K296	G297	F298	

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	78.64Å 96.99Å 79.56Å 90.00° 111.53° 90.00°	Depositor
Resolution (Å)	48.49 – 2.00 48.49 – 2.00	Depositor EDS
% Data completeness (in resolution range)	97.7 (48.49-2.00) 97.7 (48.49-2.00)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.29 (at 2.00Å)	Xtriage
Refinement program	PHENIX 1.7.1_743	Depositor
R, R_{free}	0.165 , 0.204 0.164 , 0.200	Depositor DCC
R_{free} test set	3668 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	21.2	Xtriage
Anisotropy	0.473	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 43.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.027 for l,-k,h	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	9740	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 4.64% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: PG4, EDO, PEG, KPI

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	0.43	0/2338	0.73	0/3160
1	B	0.46	1/2328 (0.0%)	0.75	3/3146 (0.1%)
1	C	0.43	0/2294	0.72	0/3102
1	D	0.41	0/2321	0.73	0/3137
All	All	0.43	1/9281 (0.0%)	0.73	3/12545 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	75	VAL	C-O	-5.51	1.18	1.24

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	73	THR	CA-C-N	-5.58	112.97	122.56
1	B	73	THR	C-N-CA	-5.58	112.97	122.56
1	B	73	THR	N-CA-C	-5.02	102.63	110.42

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	2299	0	2351	25	0
1	B	2292	0	2342	26	0
1	C	2270	0	2306	31	0
1	D	2288	0	2339	29	0
2	A	10	0	12	0	0
2	B	10	0	12	0	0
2	C	10	0	12	1	0
2	D	10	0	12	0	0
3	A	4	0	6	0	0
3	C	4	0	6	0	0
4	A	13	0	18	0	0
5	C	7	0	10	2	0
6	A	142	0	0	2	0
6	B	136	0	0	0	0
6	C	143	0	0	0	0
6	D	102	0	0	2	0
All	All	9740	0	9426	104	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 6.

All (104) 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:C:24:GLU:HG2	1:C:65:ILE:HD11	1.66	0.78
1:D:107:VAL:HA	1:D:137:TYR:HB3	1.66	0.78
1:A:172[A]:ILE:HG23	1:C:194:ILE:HG21	1.70	0.72
1:A:248:PHE:HZ	6:A:539:HOH:O	1.72	0.72
1:C:97:LYS:HE2	1:C:131:ASP:OD1	1.94	0.68
1:A:231:LYS:HE2	1:C:228:GLU:OE2	1.95	0.67
1:B:6:ILE:HG23	1:B:76:LYS:HD2	1.74	0.67
1:B:194:ILE:HG21	1:D:172[A]:ILE:HG23	1.74	0.67
1:C:107:VAL:HA	1:C:137:TYR:HB3	1.78	0.65
1:C:154:LYS:HD2	5:C:303:PEG:H21	1.78	0.64
1:B:29:ARG:HG2	1:B:298:PHE:CE1	2.34	0.62
1:D:149:THR:HG23	1:D:178:LEU:HD23	1.82	0.61
1:A:221:LEU:C	1:A:221:LEU:HD23	2.25	0.61
1:B:107:VAL:HA	1:B:137:TYR:HB3	1.83	0.61
1:C:246:ILE:HG12	1:C:289:VAL:HG21	1.84	0.60
1:D:182:GLU:O	1:D:185[A]:MET:HG2	2.03	0.59
1:B:57:GLU:OE1	1:B:60[B]:ARG:NH1	2.21	0.58
1:B:241:TYR:OH	1:B:245:LYS:HE3	2.03	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:248:PHE:CZ	6:A:539:HOH:O	2.52	0.57
1:A:107:VAL:HA	1:A:137:TYR:HB3	1.86	0.57
1:D:165:VAL:HG12	1:D:185[A]:MET:HE1	1.87	0.57
1:B:221:LEU:C	1:B:221:LEU:HD23	2.30	0.57
1:C:94:LYS:O	1:C:98:GLU:HG2	2.05	0.56
1:C:24:GLU:HG2	1:C:65:ILE:CD1	2.33	0.56
1:D:37:ASN:OD1	1:D:296:LYS:HD3	2.05	0.56
1:C:29:ARG:HG2	1:C:298:PHE:CE1	2.41	0.55
1:C:154:LYS:HZ3	5:C:303:PEG:H22	1.72	0.54
1:A:262:LEU:HD21	1:A:283:PHE:CZ	2.43	0.54
1:D:196:TYR:HB3	1:D:197:PRO:HD3	1.91	0.51
1:A:221:LEU:HD23	1:A:221:LEU:O	2.11	0.51
1:C:161:ASN:OD1	1:C:161:ASN:N	2.37	0.51
1:C:54:LEU:O	2:C:301:LYS:HE3	2.11	0.51
1:A:196:TYR:HB3	1:A:197:PRO:HD3	1.92	0.51
1:B:160:GLU:HG3	1:B:161:ASN:N	2.25	0.50
1:B:196:TYR:HB3	1:B:197:PRO:HD3	1.93	0.50
1:C:113:LYS:HE2	1:D:141:GLY:O	2.12	0.50
1:C:32:LYS:O	1:C:36:GLU:HG3	2.11	0.50
1:D:254:ILE:HB	1:D:255:PRO:HD3	1.93	0.49
1:A:142:ARG:HG2	1:B:113:LYS:HD2	1.94	0.49
1:C:221:LEU:HD23	1:C:221:LEU:C	2.37	0.49
1:C:254:ILE:HB	1:C:255:PRO:HD3	1.96	0.48
1:B:137:TYR:CD1	1:B:166:KPI:HD	2.49	0.48
1:C:290:MET:HG2	1:C:295:ILE:HD11	1.95	0.47
1:B:97:LYS:C	1:B:97:LYS:HD3	2.39	0.47
1:B:139:VAL:O	1:B:139:VAL:HG13	2.14	0.47
1:D:51:SER:HB2	6:D:501:HOH:O	2.14	0.47
1:A:95:PHE:CE1	1:A:99:HIS:CE1	3.02	0.47
1:C:294:LYS:HA	1:C:294:LYS:HD3	1.71	0.47
1:A:117:GLN:O	1:A:121:GLU:HG2	2.15	0.47
1:A:256:ILE:O	1:A:260:MET:HG2	2.15	0.47
1:A:34:GLN:OE1	1:A:39:ILE:HG13	2.15	0.47
1:A:40:ASP:OD2	1:A:223:HIS:CE1	2.67	0.47
1:D:13:LEU:HD11	1:D:42:VAL:HB	1.96	0.47
1:A:194:ILE:C	1:A:197:PRO:HD2	2.39	0.47
1:C:289:VAL:O	1:C:292:LYS:HG2	2.15	0.46
1:D:221:LEU:C	1:D:221:LEU:HD23	2.40	0.46
1:D:262:LEU:HD21	1:D:283:PHE:CZ	2.51	0.46
1:C:290:MET:HE3	1:C:290:MET:HB2	1.71	0.46
1:D:43:VAL:HG22	1:D:78:LEU:HB3	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:194:ILE:C	1:D:197:PRO:HD2	2.41	0.45
1:C:97:LYS:HD3	1:C:132:ILE:HG23	1.96	0.45
1:B:60[B]:ARG:HB3	1:B:95:PHE:CZ	2.51	0.45
1:D:67:VAL:HA	1:D:77:VAL:HG21	1.97	0.45
1:D:61:THR:O	1:D:65:ILE:HG13	2.17	0.45
1:B:10:MET:HG2	1:B:41:ALA:HB3	1.98	0.45
1:B:110:TYR:O	1:B:111:TYR:HB3	2.16	0.45
1:B:254:ILE:HB	1:B:255:PRO:HD3	1.98	0.45
1:D:296:LYS:HE2	1:D:296:LYS:HB3	1.70	0.45
1:B:60[B]:ARG:HD2	1:B:95:PHE:CD1	2.52	0.44
1:B:196:TYR:OH	1:B:230:TYR:HB3	2.17	0.44
1:A:29:ARG:HG2	1:A:298:PHE:CE1	2.53	0.43
1:B:102:ASP:O	1:B:133:PRO:HD2	2.18	0.43
1:D:252:ASN:OD1	1:D:253:PRO:HA	2.18	0.43
1:A:172[A]:ILE:HG23	1:C:194:ILE:CG2	2.46	0.43
1:A:221:LEU:C	1:A:221:LEU:CD2	2.91	0.43
1:B:60[A]:ARG:HB3	1:B:95:PHE:CZ	2.54	0.43
1:C:45:VAL:HG12	1:C:51:SER:HB3	2.01	0.43
1:D:186:MET:SD	1:D:204:LYS:HG3	2.58	0.43
1:A:139:VAL:O	1:A:139:VAL:HG13	2.19	0.43
1:C:252:ASN:OD1	1:C:253:PRO:HA	2.19	0.43
1:A:213:LEU:HD11	1:A:295:ILE:HD13	2.00	0.42
1:A:254:ILE:HB	1:A:255:PRO:HD3	2.00	0.42
1:D:14:ILE:HD13	1:D:260:MET:HG3	2.01	0.42
1:B:216:ASP:OD1	1:B:216:ASP:N	2.51	0.42
1:B:246:ILE:HD12	1:B:246:ILE:HA	1.93	0.42
1:B:294:LYS:HA	1:B:294:LYS:HD3	1.73	0.42
1:D:68:GLU:O	1:D:71:LYS:HB2	2.19	0.42
1:A:60:ARG:HB3	1:A:95:PHE:CZ	2.55	0.42
1:C:268:SER:OG	1:C:270:GLU:HG3	2.20	0.42
1:D:71:LYS:HD2	6:D:447:HOH:O	2.20	0.41
1:D:280:LYS:HD3	1:D:280:LYS:HA	1.79	0.41
1:C:246:ILE:CG1	1:C:289:VAL:HG21	2.48	0.41
1:D:139:VAL:HG13	1:D:139:VAL:O	2.20	0.41
1:A:141:GLY:O	1:B:113:LYS:HE2	2.21	0.41
1:B:149:THR:HG23	1:B:178:LEU:HD23	2.02	0.41
1:C:12:ALA:HA	1:C:43:VAL:HB	2.02	0.41
1:D:165:VAL:HG12	1:D:185[A]:MET:CE	2.49	0.41
1:D:262:LEU:HD21	1:D:283:PHE:CE2	2.56	0.41
1:C:102:ASP:O	1:C:133:PRO:HD2	2.20	0.41
1:D:107:VAL:HB	1:D:137:TYR:CD2	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:110:TYR:O	1:A:111:TYR:HB3	2.22	0.40
1:C:256:ILE:O	1:C:260:MET:HG2	2.21	0.40
1:C:110:TYR:O	1:C:111:TYR:HB3	2.21	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	298/306 (97%)	294 (99%)	4 (1%)	0	100	100
1	B	296/306 (97%)	293 (99%)	3 (1%)	0	100	100
1	C	292/306 (95%)	288 (99%)	4 (1%)	0	100	100
1	D	295/306 (96%)	290 (98%)	5 (2%)	0	100	100
All	All	1181/1224 (96%)	1165 (99%)	16 (1%)	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	253/257 (98%)	247 (98%)	6 (2%)	43	47
1	B	251/257 (98%)	250 (100%)	1 (0%)	84	89

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	247/257 (96%)	243 (98%)	4 (2%)	55	62
1	D	250/257 (97%)	247 (99%)	3 (1%)	63	70
All	All	1001/1028 (97%)	987 (99%)	14 (1%)	59	66

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	18	LYS
1	A	64	GLU
1	A	146	GLU
1	A	219	SER
1	A	234	LYS
1	A	280	LYS
1	B	146	GLU
1	C	161	ASN
1	C	227	ASP
1	C	246	ILE
1	C	280	LYS
1	D	21	LYS
1	D	74	LYS
1	D	246	ILE

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	4	ASN
1	A	237	ASN
1	B	99	HIS
1	C	25	GLN
1	C	99	HIS
1	D	99	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

4 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	KPI	B	166	1	11,13,14	1.45	1 (9%)	9,15,17	2.11	3 (33%)
1	KPI	C	166	1	11,13,14	1.56	1 (9%)	9,15,17	2.64	3 (33%)
1	KPI	A	166	1	11,13,14	1.40	1 (9%)	9,15,17	1.90	3 (33%)
1	KPI	D	166	1	11,13,14	1.35	1 (9%)	9,15,17	2.12	2 (22%)

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	KPI	B	166	1	-	2/13/14/16	-
1	KPI	C	166	1	-	4/13/14/16	-
1	KPI	A	166	1	-	3/13/14/16	-
1	KPI	D	166	1	-	2/13/14/16	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	166	KPI	CX2-CX1	3.97	1.54	1.49
1	B	166	KPI	CX2-CX1	3.69	1.54	1.49
1	A	166	KPI	CX2-CX1	3.20	1.53	1.49
1	D	166	KPI	CX2-CX1	2.97	1.53	1.49

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	166	KPI	C1-CX1-CX2	-5.89	112.56	118.11
1	D	166	KPI	C1-CX1-CX2	-5.24	113.17	118.11
1	B	166	KPI	C1-CX1-CX2	-4.38	113.98	118.11
1	A	166	KPI	C1-CX1-CX2	-4.13	114.22	118.11
1	C	166	KPI	CX2-CX1-NZ	3.37	122.83	114.88

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	166	KPI	CX2-CX1-NZ	3.07	122.12	114.88
1	A	166	KPI	CX2-CX1-NZ	2.80	121.48	114.88
1	D	166	KPI	CX2-CX1-NZ	2.50	120.76	114.88
1	B	166	KPI	CG-CD-CE	2.25	121.22	113.38
1	C	166	KPI	CG-CD-CE	2.24	121.19	113.38
1	A	166	KPI	CG-CD-CE	2.05	120.51	113.38

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	166	KPI	C1-CX1-NZ-CE
1	B	166	KPI	C1-CX1-NZ-CE
1	C	166	KPI	C1-CX1-NZ-CE
1	C	166	KPI	CX2-CX1-NZ-CE
1	C	166	KPI	NZ-CX1-CX2-O1
1	C	166	KPI	NZ-CX1-CX2-O2
1	D	166	KPI	C1-CX1-NZ-CE
1	D	166	KPI	CX2-CX1-NZ-CE
1	B	166	KPI	CX2-CX1-NZ-CE
1	A	166	KPI	NZ-CX1-CX2-O1
1	A	166	KPI	NZ-CX1-CX2-O2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	166	KPI	1	0

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

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	LYS	B	301	-	8,9,9	0.85	1 (12%)	7,10,10	1.00	1 (14%)
2	LYS	A	301	-	8,9,9	0.87	1 (12%)	7,10,10	1.10	1 (14%)
2	LYS	C	301	-	8,9,9	0.76	0	7,10,10	0.89	1 (14%)
3	EDO	A	302	-	3,3,3	0.46	0	2,2,2	0.35	0
5	PEG	C	303	-	6,6,6	0.63	0	5,5,5	1.44	1 (20%)
3	EDO	C	302	-	3,3,3	0.46	0	2,2,2	0.38	0
4	PG4	A	303	-	12,12,12	0.64	0	11,11,11	1.52	0
2	LYS	D	301	-	8,9,9	0.75	0	7,10,10	0.98	1 (14%)

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	LYS	B	301	-	-	0/9/9/9	-
2	LYS	A	301	-	-	1/9/9/9	-
2	LYS	C	301	-	-	0/9/9/9	-
3	EDO	A	302	-	-	1/1/1/1	-
5	PEG	C	303	-	-	2/4/4/4	-
3	EDO	C	302	-	-	1/1/1/1	-
4	PG4	A	303	-	-	5/10/10/10	-
2	LYS	D	301	-	-	1/9/9/9	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	301	LYS	OXT-C	-2.20	1.23	1.30
2	B	301	LYS	OXT-C	-2.17	1.23	1.30

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	301	LYS	OXT-C-O	-2.68	118.00	124.08
2	D	301	LYS	OXT-C-O	-2.35	118.74	124.08
2	B	301	LYS	OXT-C-O	-2.30	118.87	124.08

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	303	PEG	O2-C2-C1	2.22	119.88	110.11
2	C	301	LYS	OXT-C-O	-2.03	119.48	124.08

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	303	PG4	O3-C5-C6-O4
5	C	303	PEG	O2-C3-C4-O4
4	A	303	PG4	O2-C3-C4-O3
4	A	303	PG4	C5-C6-O4-C7
2	D	301	LYS	C-CA-CB-CG
4	A	303	PG4	C1-C2-O2-C3
5	C	303	PEG	C4-C3-O2-C2
3	A	302	EDO	O1-C1-C2-O2
3	C	302	EDO	O1-C1-C2-O2
4	A	303	PG4	C8-C7-O4-C6
2	A	301	LYS	CG-CD-CE-NZ

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	301	LYS	1	0
5	C	303	PEG	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 [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	295/306 (96%)	-0.51	0 100 100	9, 21, 40, 50	5 (1%)
1	B	294/306 (96%)	-0.46	0 100 100	9, 21, 37, 51	6 (2%)
1	C	294/306 (96%)	-0.55	0 100 100	13, 20, 35, 49	0
1	D	294/306 (96%)	-0.28	0 100 100	13, 24, 43, 53	4 (1%)
All	All	1177/1224 (96%)	-0.45	0 100 100	9, 21, 39, 53	15 (1%)

There are no RSRZ outliers to report.

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	KPI	C	166	14/15	0.93	0.08	13,21,30,31	0
1	KPI	B	166	14/15	0.94	0.07	15,23,27,28	0
1	KPI	D	166	14/15	0.96	0.06	15,22,26,27	0
1	KPI	A	166	14/15	0.97	0.05	13,16,20,22	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
4	PG4	A	303	13/13	0.86	0.12	31,40,53,53	0
3	EDO	C	302	4/4	0.88	0.10	35,38,45,49	0
3	EDO	A	302	4/4	0.88	0.13	33,40,46,49	0
5	PEG	C	303	7/7	0.94	0.09	30,38,40,49	0
2	LYS	C	301	10/10	0.95	0.07	11,15,19,20	0
2	LYS	D	301	10/10	0.95	0.07	14,18,22,25	0
2	LYS	A	301	10/10	0.95	0.06	10,14,17,18	0
2	LYS	B	301	10/10	0.96	0.06	12,16,19,20	0

6.5 Other polymers [i](#)

There are no such residues in this entry.