



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 23, 2024 – 04:17 PM EDT

PDB ID : 4LY8
Title : dihydrodipicolinate synthase from *C. jejuni* with pyruvate bound to the active site
Authors : Conly, C.J.T.
Deposited on : 2013-07-30
Resolution : 1.70 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36.1
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) : 2.36.1

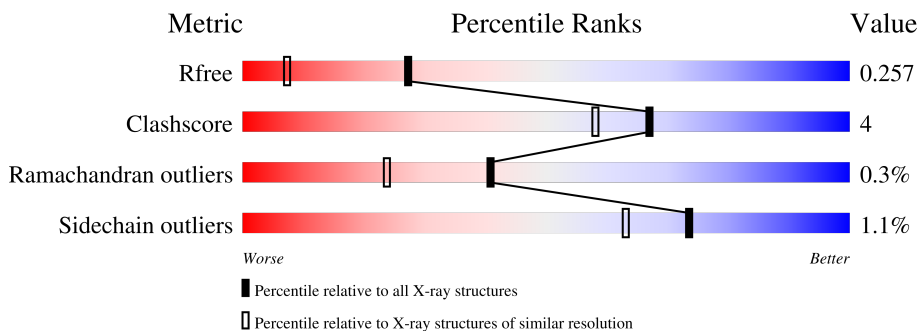
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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	4298 (1.70-1.70)
Clashscore	141614	4695 (1.70-1.70)
Ramachandran outliers	138981	4610 (1.70-1.70)
Sidechain outliers	138945	4610 (1.70-1.70)

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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	306	86% 10% ..
1	B	306	89% 8% ..
1	C	306	87% 9% ..
1	D	306	88% 8% .

2 Entry composition i

There are 7 unique types of molecules in this entry. The entry contains 10073 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
			Total	C	N	O	S			
1	A	298	2316	1472	384	446	14	0	4	0
1	B	297	2296	1459	383	441	13	0	1	0
1	C	298	2301	1463	381	443	14	0	1	0
1	D	297	2288	1454	380	441	13	2	0	0

There are 32 discrepancies between the modelled and reference sequences:

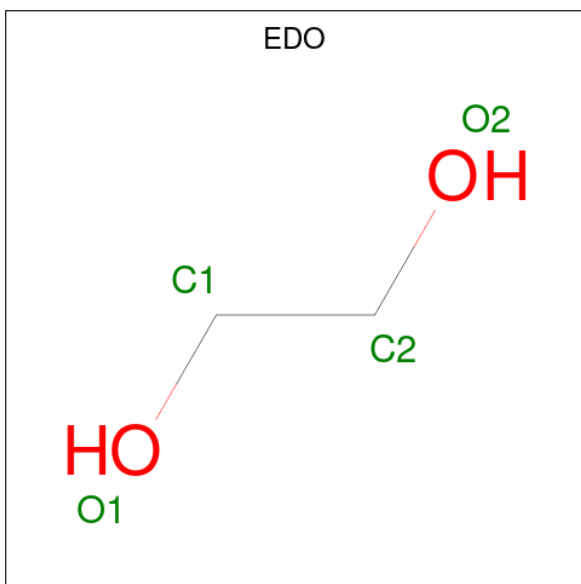
Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	HIS	-	expression tag	UNP Q9PPB4
A	-6	HIS	-	expression tag	UNP Q9PPB4
A	-5	HIS	-	expression tag	UNP Q9PPB4
A	-4	HIS	-	expression tag	UNP Q9PPB4
A	-3	HIS	-	expression tag	UNP Q9PPB4
A	-2	HIS	-	expression tag	UNP Q9PPB4
A	-1	GLY	-	expression tag	UNP Q9PPB4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

- Molecule 2 is 1,2-ETHANEDIOL (three-letter code: 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	A	1	Total	C O	0	0
			4	2 2		
2	A	1	Total	C O	0	0
			4	2 2		

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

- Molecule 3 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula: C₆H₁₄O₄).



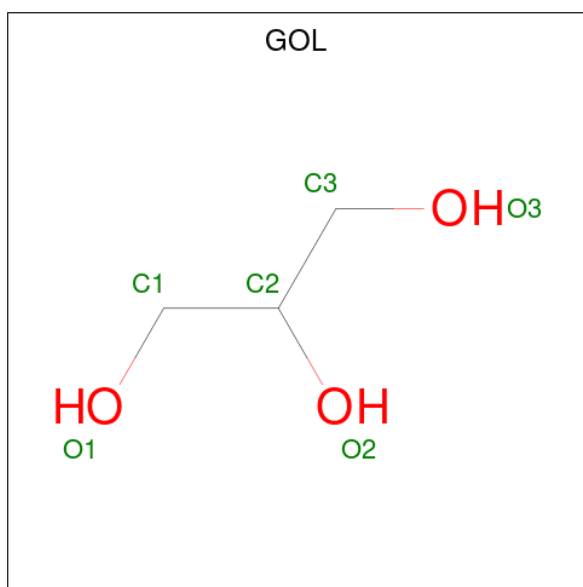
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 10 6 4	0	0
3	A	1	Total C O 10 6 4	0	0
3	A	1	Total C O 10 6 4	0	0
3	A	1	Total C O 10 6 4	0	0
3	B	1	Total C O 10 6 4	0	0
3	B	1	Total C O 10 6 4	0	0
3	B	1	Total C O 10 6 4	0	0
3	B	1	Total C O 10 6 4	0	0
3	C	1	Total C O 10 6 4	0	0
3	C	1	Total C O 10 6 4	0	0
3	D	1	Total C O 10 6 4	0	0

- Molecule 4 is ACETATE ION (three-letter code: ACT) (formula: C₂H₃O₂).



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

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



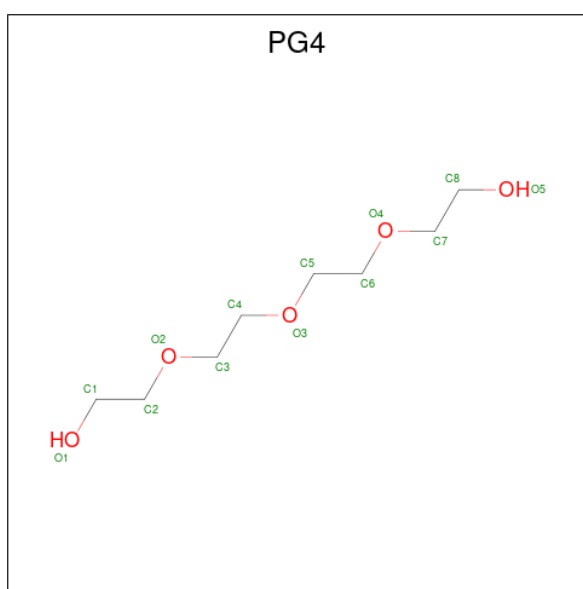
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			6	3	3		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			6	3	3		
5	B	1	Total	C	O	0	0
			6	3	3		
5	B	1	Total	C	O	0	0
			6	3	3		
5	D	1	Total	C	O	0	0
			6	3	3		

- Molecule 6 is TETRAETHYLENE GLYCOL (three-letter code: PG4) (formula: C₈H₁₈O₅).



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

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	163	Total	O	0	0
			163	163		
7	B	156	Total	O	0	0
			156	156		
7	C	145	Total	O	0	0
			145	145		

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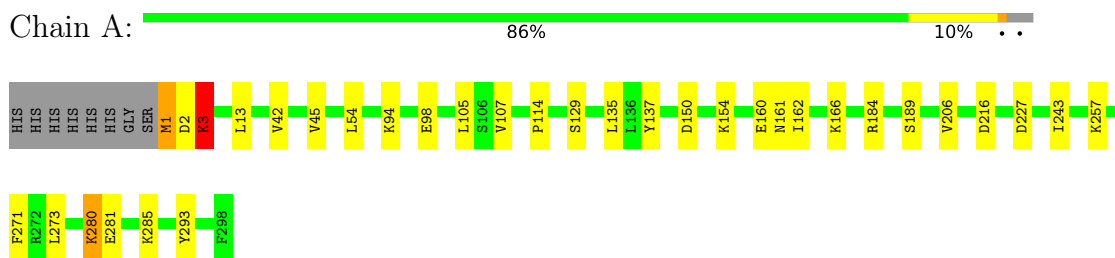
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	D	146	Total 146	O 146	0	0

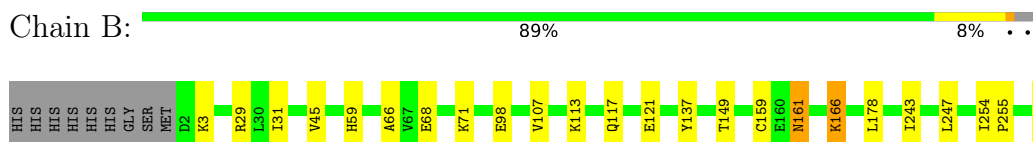
3 Residue-property plots [i](#)

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. 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. 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.

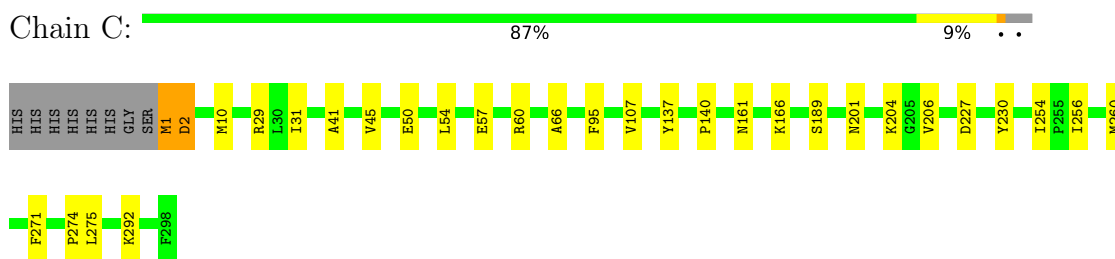
- Molecule 1: 4-hydroxy-tetrahydrodipicolinate synthase



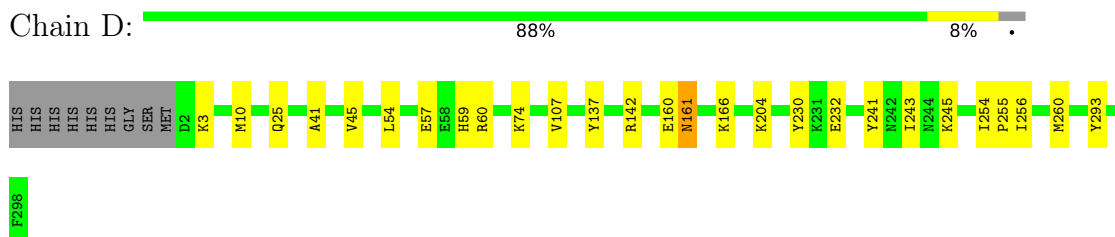
- Molecule 1: 4-hydroxy-tetrahydrodipicolinate synthase



- Molecule 1: 4-hydroxy-tetrahydrodipicolinate synthase



- Molecule 1: 4-hydroxy-tetrahydrodipicolinate synthase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	81.25Å 101.40Å 147.96Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.01 – 1.70 43.01 – 1.60	Depositor EDS
% Data completeness (in resolution range)	99.7 (43.01-1.70) 98.2 (43.01-1.60)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.04 (at 1.60Å)	Xtrriage
Refinement program	PHENIX dev_1327	Depositor
R, R_{free}	0.209 , 0.256 0.213 , 0.257	Depositor DCC
R_{free} test set	7948 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	13.6	Xtrriage
Anisotropy	0.194	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 53.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.41$, $\langle L^2 \rangle = 0.24$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	10073	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.81% 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, KPI, ACT, EDO, GOL, PGE

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	0.36	0/2352	0.53	0/3176
1	B	0.34	0/2323	0.52	0/3138
1	C	0.32	0/2328	0.51	0/3146
1	D	0.34	0/2312	0.50	0/3124
All	All	0.34	0/9315	0.52	0/12584

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 [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	2316	0	2364	25	0
1	B	2296	0	2335	14	0
1	C	2301	0	2341	23	0
1	D	2288	0	2323	16	0
2	A	24	0	36	0	0
2	B	12	0	18	0	0
2	C	20	0	30	0	0
2	D	28	0	42	0	0
3	A	40	0	56	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	40	0	56	0	0
3	C	20	0	28	3	0
3	D	10	0	14	0	0
4	A	8	0	6	0	0
4	C	4	0	3	0	0
5	A	12	0	16	0	0
5	B	12	0	16	1	0
5	D	6	0	8	0	0
6	A	13	0	18	2	0
6	C	13	0	18	0	0
7	A	163	0	0	1	0
7	B	156	0	0	0	0
7	C	145	0	0	3	0
7	D	146	0	0	0	0
All	All	10073	0	9728	74	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 (74) 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:150:ASP:HB3	6:A:313:PG4:H71	1.61	0.82
1:C:1:MET:O	1:C:2:ASP:CB	2.32	0.78
1:A:280:LYS:HE3	1:A:280:LYS:H	1.49	0.75
1:C:1:MET:O	1:C:2:ASP:HB2	1.93	0.68
1:C:1:MET:O	1:C:2:ASP:CG	2.32	0.68
1:A:2:ASP:N	1:A:2:ASP:OD1	2.28	0.66
1:A:1:MET:H3	1:A:184:ARG:HD2	1.62	0.65
1:D:45:VAL:HG11	1:D:59:HIS:CD2	2.31	0.64
1:A:1:MET:HE2	1:A:160:GLU:HA	1.80	0.64
1:C:292:LYS:NZ	7:C:543:HOH:O	2.29	0.61
1:D:10:MET:HG2	1:D:41:ALA:HB3	1.84	0.60
1:C:10:MET:HG2	1:C:41:ALA:HB3	1.84	0.60
1:A:273:LEU:H	3:A:304:PGE:C2	2.15	0.59
1:D:160:GLU:H	1:D:160:GLU:CD	2.04	0.59
1:C:107:VAL:HA	1:C:137:TYR:HB3	1.84	0.59
1:C:230:TYR:HD2	1:D:230:TYR:HD2	1.50	0.59
1:B:68:GLU:OE1	1:B:71:LYS:NZ	2.35	0.58
1:B:45:VAL:HG21	1:B:59:HIS:CD2	2.38	0.58
1:C:189:SER:HB3	1:C:206:VAL:HG12	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:57:GLU:OE1	1:D:60:ARG:NH2	2.37	0.57
1:D:107:VAL:HA	1:D:137:TYR:HB3	1.88	0.56
1:A:107:VAL:HA	1:A:137:TYR:HB3	1.88	0.55
1:A:273:LEU:H	3:A:304:PGE:H22	1.70	0.55
1:B:107:VAL:HA	1:B:137:TYR:HB3	1.89	0.55
1:A:98:GLU:HB2	7:A:555:HOH:O	2.07	0.54
1:D:25:GLN:H	1:D:25:GLN:CD	2.11	0.53
1:A:3:LYS:NZ	1:A:162:ILE:O	2.34	0.53
1:A:1:MET:N	1:A:184:ARG:HD2	2.23	0.52
1:B:166:KPI:H1B	5:B:302:GOL:O3	2.09	0.52
1:D:45:VAL:HG23	1:D:54:LEU:HD12	1.91	0.51
1:B:161:ASN:OD1	1:B:161:ASN:N	2.38	0.50
1:C:204:LYS:NZ	3:C:304:PGE:H52	2.28	0.49
1:C:140:PRO:HB2	3:C:308:PGE:H22	1.94	0.48
1:C:230:TYR:HD2	1:D:230:TYR:CD2	2.30	0.48
1:D:161:ASN:OD1	1:D:161:ASN:N	2.35	0.48
1:A:94:LYS:HE3	1:A:129[A]:SER:HB3	1.96	0.47
1:C:57:GLU:OE2	1:C:57:GLU:N	2.45	0.47
1:A:154:LYS:NZ	6:A:313:PG4:H61	2.30	0.46
1:A:243:ILE:HB	1:A:293:TYR:CE2	2.50	0.46
1:A:114:PRO:HB3	1:C:274:PRO:HB2	1.98	0.45
1:B:29:ARG:HG2	1:B:298:PHE:CE1	2.52	0.45
1:C:256:ILE:O	1:C:260:MET:HG2	2.17	0.45
1:C:140:PRO:HG2	3:C:308:PGE:H6	1.99	0.45
1:A:105:LEU:HD13	1:A:135:LEU:HD23	1.99	0.44
1:C:161:ASN:OD1	1:C:161:ASN:N	2.38	0.44
1:B:254:ILE:HB	1:B:255:PRO:HD3	2.00	0.44
1:C:50:GLU:HG2	1:C:275:LEU:HD12	2.00	0.44
1:D:254:ILE:HB	1:D:255:PRO:HD3	1.99	0.44
1:C:45:VAL:HG13	1:C:54:LEU:HD12	1.99	0.43
1:C:29:ARG:NH1	7:C:477:HOH:O	2.51	0.43
1:D:241:TYR:CZ	1:D:245:LYS:HD2	2.54	0.43
1:A:257:LYS:HD3	1:A:271:PHE:CE1	2.54	0.43
1:B:113:LYS:HD2	1:D:142:ARG:HG2	2.00	0.43
1:B:247:LEU:HD23	1:B:247:LEU:HA	1.90	0.42
1:C:31:ILE:HD13	1:C:66:ALA:HA	2.00	0.42
1:A:189:SER:HB3	1:A:206:VAL:HG12	2.01	0.42
1:D:256:ILE:O	1:D:260:MET:HG2	2.20	0.42
1:A:161:ASN:OD1	1:A:161:ASN:N	2.48	0.42
1:B:243:ILE:HB	1:B:293:TYR:CE2	2.54	0.42
1:C:201:ASN:HB2	7:C:517:HOH:O	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:254:ILE:HA	1:C:271:PHE:CE1	2.55	0.42
1:D:204:LYS:HD3	1:D:204:LYS:HA	1.89	0.41
1:B:117:GLN:O	1:B:121:GLU:HG3	2.20	0.41
1:D:243:ILE:HB	1:D:293:TYR:CE2	2.55	0.41
1:A:1:MET:HB3	1:A:3:LYS:HE3	2.03	0.41
1:A:45:VAL:HG13	1:A:54:LEU:HD12	2.02	0.41
1:A:280:LYS:HE3	1:A:280:LYS:N	2.27	0.41
1:B:31:ILE:HD13	1:B:66:ALA:HA	2.02	0.41
1:C:60:ARG:HB2	1:C:95:PHE:HZ	1.85	0.41
1:B:3:LYS:NZ	1:B:159:CYS:O	2.54	0.40
1:A:216:ASP:N	1:A:216:ASP:OD1	2.55	0.40
1:A:281:GLU:O	1:A:285:LYS:HG3	2.22	0.40
1:A:13:LEU:HD11	1:A:42:VAL:HB	2.03	0.40
1:B:149:THR:HG23	1:B:178:LEU:HD23	2.03	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	299/306 (98%)	292 (98%)	6 (2%)	1 (0%)	41	24
1	B	295/306 (96%)	289 (98%)	6 (2%)	0	100	100
1	C	296/306 (97%)	289 (98%)	6 (2%)	1 (0%)	41	24
1	D	294/306 (96%)	286 (97%)	7 (2%)	1 (0%)	41	24
All	All	1184/1224 (97%)	1156 (98%)	25 (2%)	3 (0%)	41	24

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	3	LYS

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Mol	Chain	Res	Type
1	C	2	ASP
1	D	3	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	254/257 (99%)	250 (98%)	4 (2%)	62	48
1	B	250/257 (97%)	248 (99%)	2 (1%)	81	74
1	C	251/257 (98%)	249 (99%)	2 (1%)	81	74
1	D	249/257 (97%)	246 (99%)	3 (1%)	71	59
All	All	1004/1028 (98%)	993 (99%)	11 (1%)	73	63

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	3	LYS
1	A	227	ASP
1	A	280	LYS
1	B	98	GLU
1	B	161	ASN
1	C	1	MET
1	C	227	ASP
1	D	74	LYS
1	D	161	ASN
1	D	232	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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	A	166	1	11,13,14	2.23	3 (27%)	10,15,17	2.58	3 (30%)
1	KPI	C	166	1	11,13,14	2.01	2 (18%)	10,15,17	3.34	1 (10%)
1	KPI	B	166	1	11,13,14	2.12	4 (36%)	10,15,17	2.81	1 (10%)
1	KPI	D	166	1	11,13,14	2.15	4 (36%)	10,15,17	3.11	2 (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	KPI	A	166	1	-	3/13/14/16	-
1	KPI	C	166	1	-	3/13/14/16	-
1	KPI	B	166	1	-	2/13/14/16	-
1	KPI	D	166	1	-	2/13/14/16	-

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	166	KPI	C1-CX1	-5.20	1.39	1.49
1	D	166	KPI	C1-CX1	-5.07	1.40	1.49
1	C	166	KPI	C1-CX1	-5.05	1.40	1.49
1	B	166	KPI	C1-CX1	-5.02	1.40	1.49
1	A	166	KPI	CX2-CX1	3.83	1.54	1.49
1	B	166	KPI	CX2-CX1	3.17	1.53	1.49
1	D	166	KPI	CX2-CX1	2.85	1.53	1.49
1	C	166	KPI	CB-CA	-2.79	1.49	1.53
1	D	166	KPI	CB-CA	-2.74	1.49	1.53
1	A	166	KPI	CB-CA	-2.18	1.50	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	166	KPI	O2-CX2	2.16	1.28	1.22
1	B	166	KPI	CB-CA	-2.14	1.50	1.53
1	D	166	KPI	O2-CX2	2.00	1.28	1.22

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	166	KPI	C1-CX1-CX2	-9.86	108.59	118.17
1	D	166	KPI	C1-CX1-CX2	-9.13	109.29	118.17
1	B	166	KPI	C1-CX1-CX2	-8.10	110.29	118.17
1	A	166	KPI	C1-CX1-CX2	-6.59	111.76	118.17
1	A	166	KPI	CX2-CX1-NZ	3.00	122.29	114.98
1	D	166	KPI	CX2-CX1-NZ	2.56	121.23	114.98
1	A	166	KPI	O1-CX2-O2	-2.52	117.84	123.61

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	166	KPI	C1-CX1-NZ-CE
1	A	166	KPI	NZ-CX1-CX2-O1
1	A	166	KPI	NZ-CX1-CX2-O2
1	B	166	KPI	C1-CX1-NZ-CE
1	C	166	KPI	C1-CX1-NZ-CE
1	C	166	KPI	C1-CX1-CX2-O1
1	D	166	KPI	C1-CX1-NZ-CE
1	C	166	KPI	C1-CX1-CX2-O2
1	D	166	KPI	CG-CD-CE-NZ
1	B	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 [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry

42 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	C	303	-	3,3,3	0.46	0	2,2,2	0.36	0
3	PGE	A	304	-	9,9,9	0.65	0	8,8,8	0.67	0
2	EDO	D	306	-	3,3,3	0.46	0	2,2,2	0.38	0
2	EDO	D	305	-	3,3,3	0.48	0	2,2,2	0.41	0
3	PGE	A	302	-	9,9,9	0.65	0	8,8,8	0.79	0
3	PGE	B	306	-	9,9,9	0.67	0	8,8,8	0.75	0
2	EDO	C	306	-	3,3,3	0.51	0	2,2,2	0.24	0
2	EDO	A	306	-	3,3,3	0.53	0	2,2,2	0.15	0
4	ACT	A	308	-	3,3,3	0.79	0	3,3,3	1.28	0
5	GOL	D	302	-	5,5,5	0.33	0	5,5,5	0.20	0
5	GOL	A	314	-	5,5,5	0.35	0	5,5,5	0.37	0
2	EDO	B	309	-	3,3,3	0.49	0	2,2,2	0.25	0
5	GOL	A	310	-	5,5,5	0.36	0	5,5,5	0.13	0
2	EDO	D	308	-	3,3,3	0.43	0	2,2,2	0.36	0
2	EDO	D	303	-	3,3,3	0.40	0	2,2,2	0.43	0
2	EDO	A	315	-	3,3,3	0.44	0	2,2,2	0.38	0
2	EDO	B	308	-	3,3,3	0.43	0	2,2,2	0.44	0
2	EDO	A	303	-	3,3,3	0.45	0	2,2,2	0.23	0
2	EDO	A	301	-	3,3,3	0.46	0	2,2,2	0.24	0
6	PG4	C	301	-	12,12,12	0.69	0	11,11,11	1.46	0
2	EDO	D	307	-	3,3,3	0.50	0	2,2,2	0.24	0
3	PGE	C	308	-	9,9,9	0.63	0	8,8,8	0.76	0
5	GOL	B	302	-	5,5,5	0.34	0	5,5,5	0.35	0
2	EDO	D	309	-	3,3,3	0.48	0	2,2,2	0.29	0
3	PGE	B	303	-	9,9,9	0.66	0	8,8,8	0.71	0
4	ACT	C	309	-	3,3,3	0.87	0	3,3,3	1.46	0
3	PGE	A	307	-	9,9,9	0.65	0	8,8,8	0.70	0
2	EDO	C	307	-	3,3,3	0.50	0	2,2,2	0.32	0
2	EDO	A	309	-	3,3,3	0.41	0	2,2,2	0.45	0
5	GOL	B	307	-	5,5,5	0.36	0	5,5,5	0.33	0
3	PGE	D	301	-	9,9,9	0.68	0	8,8,8	0.72	0
3	PGE	A	305	-	9,9,9	0.63	0	8,8,8	0.78	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	PGE	B	305	-	9,9,9	0.65	0	8,8,8	0.79	0
2	EDO	C	305	-	3,3,3	0.48	0	2,2,2	0.31	0
4	ACT	A	312	-	3,3,3	0.75	0	3,3,3	1.28	0
3	PGE	C	304	-	9,9,9	0.67	0	8,8,8	0.82	0
2	EDO	B	304	-	3,3,3	0.43	0	2,2,2	0.40	0
6	PG4	A	313	-	12,12,12	0.64	0	11,11,11	1.60	2 (18%)
2	EDO	C	302	-	3,3,3	0.47	0	2,2,2	0.37	0
2	EDO	A	311	-	3,3,3	0.44	0	2,2,2	0.38	0
3	PGE	B	301	-	9,9,9	0.61	0	8,8,8	0.76	0
2	EDO	D	304	-	3,3,3	0.45	0	2,2,2	0.40	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	C	303	-	-	0/1/1/1	-
3	PGE	A	304	-	-	4/7/7/7	-
2	EDO	D	306	-	-	1/1/1/1	-
2	EDO	D	305	-	-	1/1/1/1	-
3	PGE	A	302	-	-	4/7/7/7	-
3	PGE	B	306	-	-	5/7/7/7	-
2	EDO	C	306	-	-	1/1/1/1	-
2	EDO	A	306	-	-	0/1/1/1	-
5	GOL	D	302	-	-	4/4/4/4	-
5	GOL	A	314	-	-	4/4/4/4	-
2	EDO	B	309	-	-	0/1/1/1	-
5	GOL	A	310	-	-	2/4/4/4	-
2	EDO	D	308	-	-	1/1/1/1	-
2	EDO	D	303	-	-	1/1/1/1	-
2	EDO	A	315	-	-	0/1/1/1	-
2	EDO	B	308	-	-	1/1/1/1	-
2	EDO	A	303	-	-	0/1/1/1	-
2	EDO	A	301	-	-	1/1/1/1	-
6	PG4	C	301	-	-	6/10/10/10	-
2	EDO	D	307	-	-	0/1/1/1	-
3	PGE	C	308	-	-	4/7/7/7	-
5	GOL	B	302	-	-	4/4/4/4	-
2	EDO	D	309	-	-	0/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	PGE	B	303	-	-	5/7/7/7	-
3	PGE	A	307	-	-	2/7/7/7	-
2	EDO	C	307	-	-	1/1/1/1	-
2	EDO	A	309	-	-	1/1/1/1	-
5	GOL	B	307	-	-	4/4/4/4	-
3	PGE	D	301	-	-	1/7/7/7	-
3	PGE	A	305	-	-	2/7/7/7	-
3	PGE	B	305	-	-	3/7/7/7	-
2	EDO	C	305	-	-	0/1/1/1	-
3	PGE	C	304	-	-	4/7/7/7	-
2	EDO	B	304	-	-	0/1/1/1	-
6	PG4	A	313	-	-	5/10/10/10	-
2	EDO	C	302	-	-	0/1/1/1	-
2	EDO	A	311	-	-	0/1/1/1	-
3	PGE	B	301	-	-	1/7/7/7	-
2	EDO	D	304	-	-	0/1/1/1	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	313	PG4	O4-C7-C8	2.24	119.89	110.07
6	A	313	PG4	O4-C6-C5	2.13	119.99	110.39

There are no chirality outliers.

All (73) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	310	GOL	C1-C2-C3-O3
5	A	314	GOL	O1-C1-C2-C3
5	A	314	GOL	C1-C2-C3-O3
5	B	302	GOL	O1-C1-C2-C3
5	B	302	GOL	C1-C2-C3-O3
5	B	307	GOL	O1-C1-C2-C3
5	B	307	GOL	C1-C2-C3-O3
5	D	302	GOL	O1-C1-C2-C3
5	D	302	GOL	C1-C2-C3-O3
3	B	303	PGE	O2-C3-C4-O3
6	A	313	PG4	O3-C5-C6-O4

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Mol	Chain	Res	Type	Atoms
3	C	308	PGE	O2-C3-C4-O3
6	C	301	PG4	O2-C3-C4-O3
6	C	301	PG4	O3-C5-C6-O4
3	A	307	PGE	O1-C1-C2-O2
5	A	310	GOL	O2-C2-C3-O3
3	C	304	PGE	C1-C2-O2-C3
3	B	305	PGE	O3-C5-C6-O4
3	B	303	PGE	O1-C1-C2-O2
3	C	304	PGE	O3-C5-C6-O4
3	A	302	PGE	O1-C1-C2-O2
3	B	306	PGE	O2-C3-C4-O3
5	A	314	GOL	O1-C1-C2-O2
5	B	302	GOL	O1-C1-C2-O2
5	B	307	GOL	O2-C2-C3-O3
5	D	302	GOL	O1-C1-C2-O2
5	D	302	GOL	O2-C2-C3-O3
6	A	313	PG4	O1-C1-C2-O2
2	A	309	EDO	O1-C1-C2-O2
2	B	308	EDO	O1-C1-C2-O2
2	C	306	EDO	O1-C1-C2-O2
3	A	302	PGE	O2-C3-C4-O3
3	A	304	PGE	O1-C1-C2-O2
3	B	306	PGE	O1-C1-C2-O2
6	A	313	PG4	O4-C7-C8-O5
5	A	314	GOL	O2-C2-C3-O3
5	B	302	GOL	O2-C2-C3-O3
5	B	307	GOL	O1-C1-C2-O2
2	C	307	EDO	O1-C1-C2-O2
2	D	306	EDO	O1-C1-C2-O2
3	C	308	PGE	O3-C5-C6-O4
3	A	305	PGE	O3-C5-C6-O4
3	B	303	PGE	C4-C3-O2-C2
6	C	301	PG4	C3-C4-O3-C5
3	B	303	PGE	C3-C4-O3-C5
3	C	304	PGE	C3-C4-O3-C5
6	A	313	PG4	C5-C6-O4-C7
3	B	305	PGE	C6-C5-O3-C4
6	C	301	PG4	C1-C2-O2-C3
3	A	302	PGE	C1-C2-O2-C3
3	B	306	PGE	C1-C2-O2-C3
3	C	308	PGE	C1-C2-O2-C3
3	B	306	PGE	C6-C5-O3-C4

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Mol	Chain	Res	Type	Atoms
3	A	304	PGE	C6-C5-O3-C4
3	A	304	PGE	O3-C5-C6-O4
3	C	308	PGE	C3-C4-O3-C5
3	A	304	PGE	C3-C4-O3-C5
6	A	313	PG4	C4-C3-O2-C2
3	A	305	PGE	O1-C1-C2-O2
3	A	302	PGE	C6-C5-O3-C4
6	C	301	PG4	C6-C5-O3-C4
3	A	307	PGE	C1-C2-O2-C3
3	D	301	PGE	O1-C1-C2-O2
2	D	303	EDO	O1-C1-C2-O2
6	C	301	PG4	O1-C1-C2-O2
3	B	303	PGE	C1-C2-O2-C3
3	B	305	PGE	O2-C3-C4-O3
2	A	301	EDO	O1-C1-C2-O2
2	D	305	EDO	O1-C1-C2-O2
3	C	304	PGE	O2-C3-C4-O3
3	B	301	PGE	O3-C5-C6-O4
2	D	308	EDO	O1-C1-C2-O2
3	B	306	PGE	C4-C3-O2-C2

There are no ring outliers.

5 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	304	PGE	2	0
3	C	308	PGE	2	0
5	B	302	GOL	1	0
3	C	304	PGE	1	0
6	A	313	PG4	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](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.