



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 07:47 AM UTC

PDB ID : 6TZU / pdb_00006tzu
Title : Dihydrodipicolinate synthase (DHDPS) from C.jejuni, N84A mutant with pyruvate bound in the active site
Authors : Saran, S.; Majdi Yazdi, M.; Lehnert, C.; Palmer, D.R.J.; Sanders, D.A.R.
Deposited on : 2019-08-13
Resolution : 1.80 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:

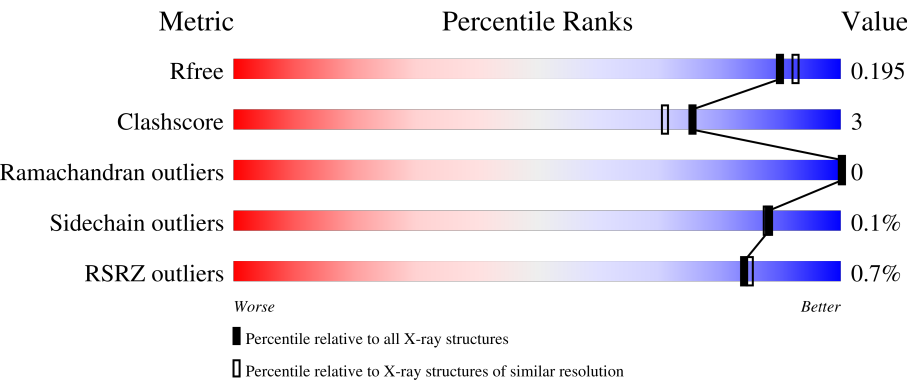
MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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	7662 (1.80-1.80)
Clashscore	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)
RSRZ outliers	180081	7663 (1.80-1.80)

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	310	90%6%5%
1	B	310	% 92%5%
1	C	310	% 90%6%5%
1	D	310	% 92%6%
1	E	310	% 91%. .

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Mol	Chain	Length	Quality of chain
2	F	310	 92% 5%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	EDO	E	305	-	-	X	-
7	PEG	C	307	-	-	X	-

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 15399 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	3	0
			2282	1450	378	441	13			
1	B	304	Total	C	N	O	S	0	1	0
			2341	1485	394	448	14			
1	C	296	Total	C	N	O	S	0	1	0
			2273	1446	378	436	13			
1	D	306	Total	C	N	O	S	0	2	0
			2364	1499	402	449	14			
1	E	297	Total	C	N	O	S	0	2	0
			2284	1451	379	441	13			

There are 65 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-11	MET	-	expression tag	UNP Q9PPB4
A	-10	ARG	-	expression tag	UNP Q9PPB4
A	-9	GLY	-	expression tag	UNP Q9PPB4
A	-8	SER	-	expression tag	UNP Q9PPB4
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
A	84	ALA	ASN	engineered mutation	UNP Q9PPB4
B	-11	MET	-	expression tag	UNP Q9PPB4
B	-10	ARG	-	expression tag	UNP Q9PPB4
B	-9	GLY	-	expression tag	UNP Q9PPB4
B	-8	SER	-	expression tag	UNP Q9PPB4
B	-7	HIS	-	expression tag	UNP Q9PPB4
B	-6	HIS	-	expression tag	UNP Q9PPB4

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Chain	Residue	Modelled	Actual	Comment	Reference
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
B	84	ALA	ASN	engineered mutation	UNP Q9PPB4
C	-11	MET	-	expression tag	UNP Q9PPB4
C	-10	ARG	-	expression tag	UNP Q9PPB4
C	-9	GLY	-	expression tag	UNP Q9PPB4
C	-8	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
C	-2	HIS	-	expression tag	UNP Q9PPB4
C	-1	GLY	-	expression tag	UNP Q9PPB4
C	0	SER	-	expression tag	UNP Q9PPB4
C	84	ALA	ASN	engineered mutation	UNP Q9PPB4
D	-11	MET	-	expression tag	UNP Q9PPB4
D	-10	ARG	-	expression tag	UNP Q9PPB4
D	-9	GLY	-	expression tag	UNP Q9PPB4
D	-8	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
D	84	ALA	ASN	engineered mutation	UNP Q9PPB4
E	-11	MET	-	expression tag	UNP Q9PPB4
E	-10	ARG	-	expression tag	UNP Q9PPB4
E	-9	GLY	-	expression tag	UNP Q9PPB4
E	-8	SER	-	expression tag	UNP Q9PPB4
E	-7	HIS	-	expression tag	UNP Q9PPB4
E	-6	HIS	-	expression tag	UNP Q9PPB4
E	-5	HIS	-	expression tag	UNP Q9PPB4
E	-4	HIS	-	expression tag	UNP Q9PPB4
E	-3	HIS	-	expression tag	UNP Q9PPB4

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-2	HIS	-	expression tag	UNP Q9PPB4
E	-1	GLY	-	expression tag	UNP Q9PPB4
E	0	SER	-	expression tag	UNP Q9PPB4
E	84	ALA	ASN	engineered mutation	UNP Q9PPB4

- Molecule 2 is a protein called 4-hydroxy-tetrahydrodipicolinate synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	F	296	Total	C	N	O	S	0	2	0
			2289	1458	379	439	13			

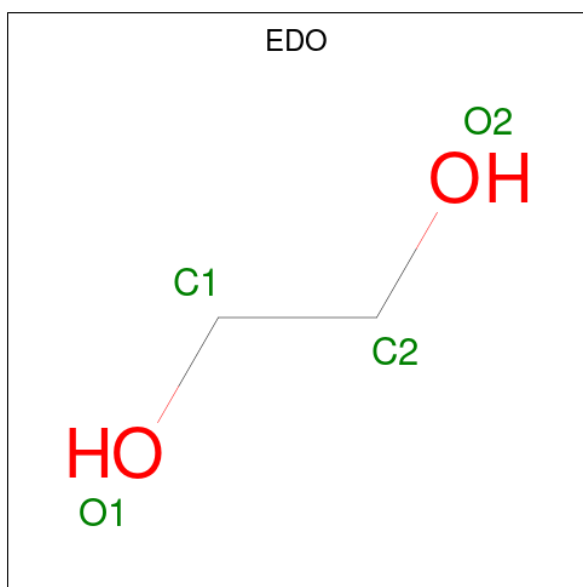
There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	-11	MET	-	expression tag	UNP Q9PPB4
F	-10	ARG	-	expression tag	UNP Q9PPB4
F	-9	GLY	-	expression tag	UNP Q9PPB4
F	-8	SER	-	expression tag	UNP Q9PPB4
F	-7	HIS	-	expression tag	UNP Q9PPB4
F	-6	HIS	-	expression tag	UNP Q9PPB4
F	-5	HIS	-	expression tag	UNP Q9PPB4
F	-4	HIS	-	expression tag	UNP Q9PPB4
F	-3	HIS	-	expression tag	UNP Q9PPB4
F	-2	HIS	-	expression tag	UNP Q9PPB4
F	-1	GLY	-	expression tag	UNP Q9PPB4
F	0	SER	-	expression tag	UNP Q9PPB4
F	84	ALA	ASN	engineered mutation	UNP Q9PPB4

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	2	Total	Mg	0	0
			2	2		
3	B	1	Total	Mg	0	0
			1	1		
3	E	1	Total	Mg	0	0
			1	1		
3	F	1	Total	Mg	0	0
			1	1		

- Molecule 4 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



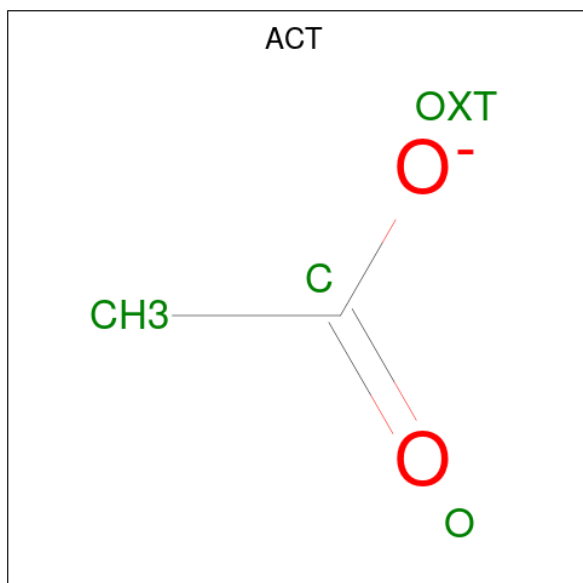
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total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

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

- Molecule 5 is ACETATE ION (CCD ID: ACT) (formula: $C_2H_3O_2$).



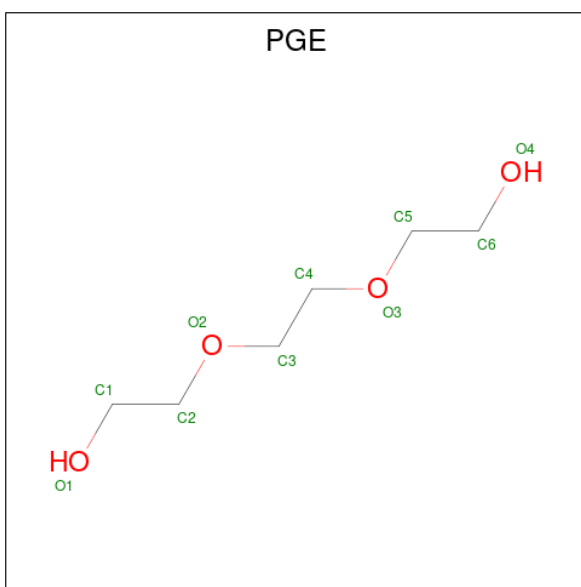
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			4	2	2		

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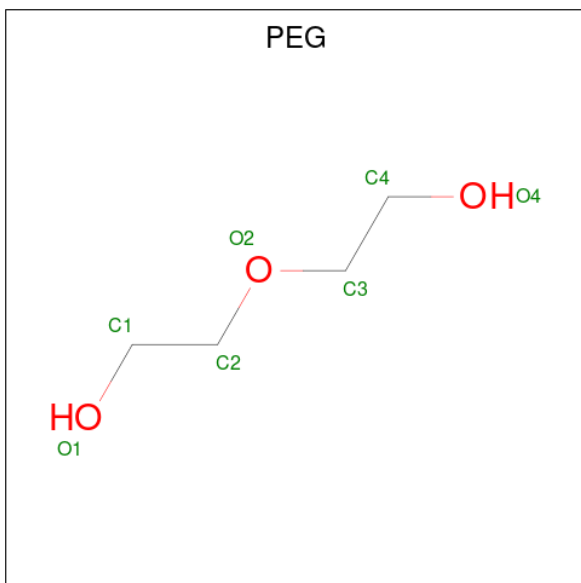
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total 4	C 2	O 2	0	0
5	B	1	Total 4	C 2	O 2	0	0
5	C	1	Total 4	C 2	O 2	0	0
5	C	1	Total 4	C 2	O 2	0	0
5	C	1	Total 4	C 2	O 2	0	0
5	C	1	Total 4	C 2	O 2	0	0
5	C	1	Total 4	C 2	O 2	0	0
5	E	1	Total 4	C 2	O 2	0	0
5	E	1	Total 4	C 2	O 2	0	0
5	E	1	Total 4	C 2	O 2	0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

- Molecule 6 is TRIETHYLENE GLYCOL (CCD ID: PGE) (formula: C₆H₁₄O₄).



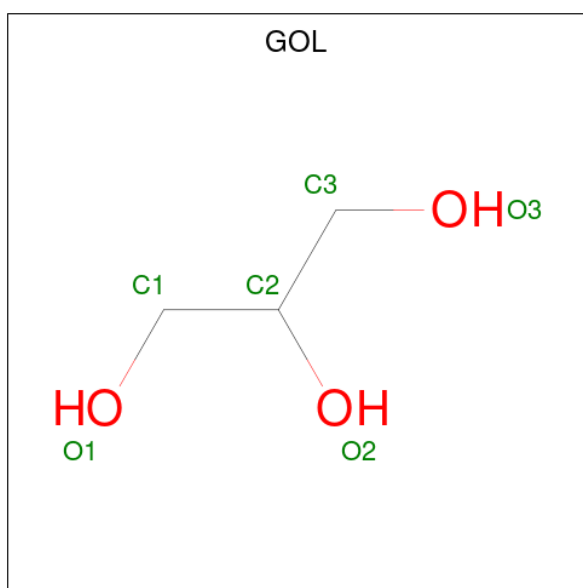
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			10	6	4		
6	B	1	Total	C	O	0	0
			10	6	4		
6	D	1	Total	C	O	0	0
			10	6	4		
6	F	1	Total	C	O	0	0
			10	6	4		

- Molecule 7 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



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

- Molecule 8 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	D	1	Total C O 6 3 3	0	0
8	E	1	Total C O 6 3 3	0	0

- Molecule 9 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	A	209	Total O 209 209	0	0
9	B	227	Total O 227 227	0	0
9	C	214	Total O 214 214	0	0
9	D	236	Total O 236 236	0	0

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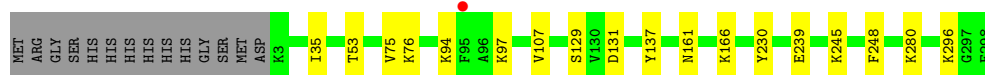
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	E	247	Total 247	O 247	0	0
9	F	188	Total 188	O 188	0	0

3 Residue-property plots

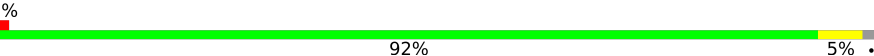
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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.

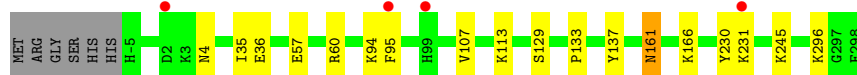
- Molecule 1: 4-hydroxy-tetrahydrodipicolinate synthase

Chain A: 



- Molecule 1: 4-hydroxy-tetrahydrodipicolinate synthase

Chain B: 

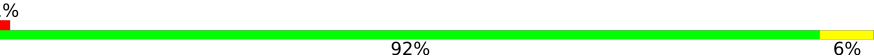


- Molecule 1: 4-hydroxy-tetrahydrodipicolinate synthase

Chain C: 

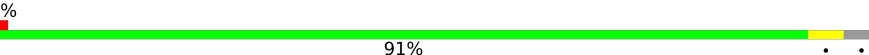


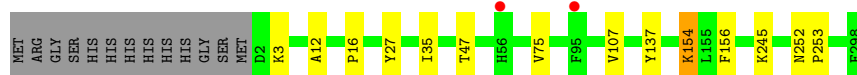
- Molecule 1: 4-hydroxy-tetrahydrodipicolinate synthase

Chain D: 



- Molecule 1: 4-hydroxy-tetrahydrodipicolinate synthase

Chain E: 



- Molecule 2: 4-hydroxy-tetrahydrodipicolinate synthase

Chain F:  92% 5%

MET	ARG	GLY	SER	HIS	HIS	HIS	HIS	HIS	GLY	SER	MET	ASP	R3	L13	V42	A81	H87	F36	Y107	Y137	K166	K245	I254	P255	A263	F271	F298
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4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	84.93Å 225.81Å 200.74Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.20 – 1.80 49.20 – 1.80	Depositor EDS
% Data completeness (in resolution range)	99.9 (49.20-1.80) 99.9 (49.20-1.80)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.70 (at 1.79Å)	Xtriage
Refinement program	PHENIX dev_2398	Depositor
R, R_{free}	0.172 , 0.201 (Not available) , 0.195	Depositor DCC
R_{free} test set	8882 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	21.3	Xtriage
Anisotropy	0.346	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 36.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	15399	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.02% 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: ACT, PEG, PGE, MG, GOL, EDO, 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	0.19	0/2338	0.42	0/3159
1	B	0.21	0/2390	0.45	0/3229
1	C	0.18	0/2317	0.42	0/3131
1	D	0.19	0/2420	0.44	0/3270
1	E	0.23	0/2333	0.47	2/3153 (0.1%)
2	F	0.18	0/2319	0.42	0/3133
All	All	0.20	0/14117	0.44	2/19075 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	154	LYS	CA-CB-CG	7.77	129.64	114.10
1	E	154	LYS	CG-CD-CE	5.58	124.13	111.30

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	2282	0	2316	16	0
1	B	2341	0	2368	17	0
1	C	2273	0	2319	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	2364	0	2388	17	0
1	E	2284	0	2323	12	0
2	F	2289	0	2327	8	0
3	A	2	0	0	0	0
3	B	1	0	0	0	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0
4	A	16	0	24	3	0
4	B	24	0	36	2	0
4	D	28	0	42	6	0
4	E	16	0	24	4	0
4	F	12	0	18	1	0
5	A	4	0	3	0	0
5	B	8	0	6	0	0
5	C	20	0	15	1	0
5	E	16	0	12	0	0
5	F	16	0	12	0	0
6	A	10	0	14	0	0
6	B	10	0	14	0	0
6	D	10	0	14	0	0
6	F	10	0	14	0	0
7	B	7	0	10	2	0
7	C	14	0	20	6	0
7	E	7	0	10	1	0
8	D	6	0	8	1	0
8	E	6	0	8	0	0
9	A	209	0	0	3	0
9	B	227	0	0	2	0
9	C	214	0	0	1	0
9	D	236	0	0	3	0
9	E	247	0	0	1	0
9	F	188	0	0	1	0
All	All	15399	0	14345	84	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 3.

All (84) 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:E:47:THR:H	4:E:305:EDO:H12	1.44	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:81:ALA:O	9:F:401:HOH:O	2.10	0.70
1:D:47:THR:H	4:D:301:EDO:H12	1.55	0.69
1:D:298:PHE:HD1	4:D:305:EDO:H22	1.58	0.67
1:B:113:LYS:NZ	9:B:401:HOH:O	2.28	0.65
1:A:166:LYS:NZ	4:A:306:EDO:H12	2.13	0.63
1:A:166:LYS:HZ1	4:A:306:EDO:H12	1.63	0.63
1:C:60:ARG:HB2	1:C:95:PHE:HZ	1.62	0.63
1:A:94:LYS:HE2	1:A:129:SER:HB2	1.78	0.63
1:E:154:LYS:HD2	7:E:310:PEG:H11	1.82	0.61
1:A:76:LYS:NZ	9:A:403:HOH:O	2.35	0.59
1:A:107:VAL:HA	1:A:137:TYR:HB3	1.83	0.59
1:D:107:VAL:HA	1:D:137:TYR:HB3	1.86	0.58
2:F:263:ALA:HA	4:F:303:EDO:H11	1.85	0.58
1:E:47:THR:N	4:E:305:EDO:H12	2.17	0.57
1:D:47:THR:HB	4:D:301:EDO:H21	1.86	0.57
1:C:60:ARG:HB2	1:C:95:PHE:CZ	2.39	0.56
1:D:97:LYS:NZ	1:D:131:ASP:OD1	2.36	0.56
1:E:107:VAL:HA	1:E:137:TYR:HB3	1.88	0.56
2:F:107:VAL:HA	2:F:137:TYR:HB3	1.87	0.56
1:D:142:ARG:HE	8:D:309:GOL:H31	1.72	0.55
1:C:107:VAL:HA	1:C:137:TYR:HB3	1.89	0.55
1:B:161:ASN:OD1	1:B:161:ASN:N	2.38	0.54
1:B:36:GLU:HA	7:B:310:PEG:H21	1.90	0.54
1:B:107:VAL:HA	1:B:137:TYR:HB3	1.89	0.54
1:E:47:THR:HB	4:E:305:EDO:H21	1.89	0.54
1:B:94:LYS:HE2	1:B:129:SER:HB2	1.92	0.51
1:B:35:ILE:HG22	7:B:310:PEG:H12	1.92	0.51
1:B:296:LYS:NZ	9:B:405:HOH:O	2.43	0.50
1:B:166:LYS:NZ	4:B:302:EDO:H12	2.27	0.50
1:A:239:GLU:HG3	9:A:421:HOH:O	2.11	0.49
1:C:47:THR:HB	7:C:307:PEG:H32	1.92	0.49
1:B:60:ARG:HG3	1:B:95:PHE:HZ	1.78	0.48
1:B:231:LYS:O	1:B:231:LYS:HD3	2.14	0.47
1:C:97:LYS:HE2	1:C:131:ASP:OD1	2.13	0.47
1:B:4:ASN:HB2	1:B:133:PRO:HG3	1.97	0.47
1:C:202:GLY:HA2	5:C:304:ACT:H1	1.96	0.47
1:D:81:ALA:O	9:D:401:HOH:O	2.19	0.47
1:E:245:LYS:HD2	9:E:505:HOH:O	2.14	0.46
1:E:252:ASN:ND2	1:E:253:PRO:HA	2.30	0.46
1:C:47:THR:N	7:C:307:PEG:H21	2.31	0.46
1:D:128:GLN:NE2	9:D:403:HOH:O	2.27	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:248:PHE:HE2	4:A:305:EDO:H11	1.81	0.45
1:B:57:GLU:H	1:B:57:GLU:CD	2.24	0.45
1:B:95:PHE:C	1:B:95:PHE:CD2	2.95	0.45
1:D:102:ASP:O	1:D:133:PRO:HD2	2.17	0.45
1:A:245:LYS:HA	1:A:245:LYS:HD2	1.83	0.44
1:C:13:LEU:HD11	1:C:42:VAL:HB	1.99	0.44
1:B:231:LYS:HD3	1:B:231:LYS:C	2.43	0.44
1:C:166:LYS:HZ1	7:C:307:PEG:H31	1.82	0.44
1:C:245:LYS:HA	1:C:245:LYS:HD2	1.79	0.44
1:D:168:ALA:HA	1:D:191:GLU:HG3	2.00	0.43
1:C:12:ALA:HB1	7:C:307:PEG:H22	2.00	0.43
1:A:97:LYS:HE2	1:A:131:ASP:OD1	2.18	0.43
1:C:168:ALA:HA	1:C:191:GLU:HG3	1.99	0.43
2:F:13:LEU:HD11	2:F:42:VAL:HB	2.00	0.43
1:D:124:LYS:HE3	1:D:124:LYS:HB3	1.85	0.43
7:C:307:PEG:H31	7:C:307:PEG:H12	1.40	0.42
1:E:16:PRO:HD2	1:E:27:TYR:HD1	1.84	0.42
1:C:280:LYS:HE3	1:C:281:GLU:OE2	2.19	0.42
1:D:241:TYR:OH	1:D:245:LYS:HE3	2.19	0.42
1:A:280:LYS:HB3	1:A:280:LYS:HE2	1.80	0.42
2:F:254:ILE:HA	2:F:271:PHE:CE2	2.55	0.42
1:D:-2:HIS:HE1	9:D:612:HOH:O	2.02	0.42
1:D:32:LYS:NZ	4:D:304:EDO:H21	2.35	0.42
1:E:3:LYS:HE3	1:E:156:PHE:CZ	2.54	0.42
2:F:245:LYS:HA	2:F:245:LYS:HD2	1.84	0.42
1:C:294:LYS:HD3	9:C:576:HOH:O	2.19	0.42
1:A:245:LYS:HD2	9:A:451:HOH:O	2.20	0.41
1:A:35:ILE:HG12	1:A:75:VAL:HG21	2.01	0.41
1:A:161:ASN:OD1	1:A:161:ASN:N	2.42	0.41
1:D:48:THR:H	4:D:301:EDO:C2	2.34	0.41
1:D:161:ASN:OD1	1:D:161:ASN:N	2.42	0.41
1:E:35:ILE:HG12	1:E:75:VAL:HG21	2.03	0.41
1:A:296:LYS:HB3	1:A:296:LYS:HE2	1.84	0.41
2:F:254:ILE:HB	2:F:255:PRO:HD3	2.02	0.41
1:A:230:TYR:HD2	1:B:230:TYR:CD2	2.39	0.41
1:B:230:TYR:OH	4:B:307:EDO:H21	2.20	0.41
1:B:245:LYS:HA	1:B:245:LYS:HD2	1.78	0.41
1:E:245:LYS:HD2	1:E:245:LYS:HA	1.80	0.41
1:E:12:ALA:HB1	4:E:305:EDO:H22	2.03	0.40
1:D:298:PHE:CD1	4:D:305:EDO:H22	2.46	0.40
1:A:53:THR:O	2:F:87:HIS:HE1	2.05	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:166:LYS:NZ	7:C:307:PEG:H31	2.36	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	297/310 (96%)	291 (98%)	6 (2%)	0	100	100
1	B	303/310 (98%)	297 (98%)	6 (2%)	0	100	100
1	C	295/310 (95%)	289 (98%)	6 (2%)	0	100	100
1	D	306/310 (99%)	299 (98%)	7 (2%)	0	100	100
1	E	297/310 (96%)	290 (98%)	7 (2%)	0	100	100
2	F	295/310 (95%)	287 (97%)	8 (3%)	0	100	100
All	All	1793/1860 (96%)	1753 (98%)	40 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains

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	251/260 (96%)	251 (100%)	0	100	100
1	B	256/260 (98%)	255 (100%)	1 (0%)	84	83

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	249/260 (96%)	249 (100%)	0	100	100
1	D	259/260 (100%)	258 (100%)	1 (0%)	84	83
1	E	251/260 (96%)	251 (100%)	0	100	100
2	F	249/259 (96%)	249 (100%)	0	100	100
All	All	1515/1559 (97%)	1513 (100%)	2 (0%)	88	88

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	161	ASN
1	D	161	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	19	ASN
1	B	19	ASN
1	B	37	ASN
1	B	56	HIS
1	B	117	GLN
1	C	59	HIS
1	D	-2	HIS
1	D	37	ASN
1	D	201	ASN
1	E	56	HIS
1	E	201	ASN
2	F	56	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is 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	KPI	F	166	2	11,13,14	0.98	1 (9%)	9,15,17	3.97	5 (55%)

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	KPI	F	166	2	-	2/13/14/16	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	166	KPI	O1-CX2	2.14	1.36	1.30

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	166	KPI	C1-CX1-CX2	-9.55	109.11	118.11
2	F	166	KPI	O2-CX2-CX1	5.50	128.07	121.35
2	F	166	KPI	O1-CX2-O2	-2.59	117.74	123.90
2	F	166	KPI	CE-NZ-CX1	2.39	128.13	121.58
2	F	166	KPI	CD-CE-NZ	2.08	114.35	110.67

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	F	166	KPI	C1-CX1-CX2-O1
2	F	166	KPI	C1-CX1-CX2-O2

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 55 ligands modelled in this entry, 5 are monoatomic - leaving 50 for Mogul analysis.

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	$\# Z > 2$
7	PEG	E	310	-	6,6,6	0.48	0	5,5,5	0.29	0
5	ACT	C	302	-	3,3,3	0.82	0	3,3,3	1.31	0
5	ACT	B	309	-	3,3,3	0.82	0	3,3,3	1.37	0
8	GOL	D	309	-	5,5,5	0.39	0	5,5,5	0.16	0
4	EDO	B	302	-	3,3,3	0.39	0	2,2,2	0.51	0
4	EDO	B	304	-	3,3,3	0.43	0	2,2,2	0.40	0
4	EDO	B	306	-	3,3,3	0.41	0	2,2,2	0.48	0
4	EDO	D	303	-	3,3,3	0.47	0	2,2,2	0.31	0
4	EDO	D	306	-	3,3,3	0.43	0	2,2,2	0.37	0
5	ACT	C	303	-	3,3,3	0.78	0	3,3,3	1.38	0
5	ACT	F	308	-	3,3,3	0.81	0	3,3,3	1.36	0
6	PGE	F	309	-	9,9,9	0.31	0	8,8,8	0.29	0
5	ACT	A	307	-	3,3,3	0.83	0	3,3,3	1.39	0
4	EDO	D	305	-	3,3,3	0.45	0	2,2,2	0.26	0
6	PGE	A	308	-	9,9,9	0.32	0	8,8,8	0.28	0
4	EDO	E	303	-	3,3,3	0.44	0	2,2,2	0.38	0
5	ACT	E	308	-	3,3,3	0.81	0	3,3,3	1.36	0
4	EDO	A	304	-	3,3,3	0.45	0	2,2,2	0.35	0
5	ACT	F	306	-	3,3,3	0.79	0	3,3,3	1.30	0
4	EDO	B	305	-	3,3,3	0.42	0	2,2,2	0.47	0
7	PEG	C	306	-	6,6,6	0.49	0	5,5,5	0.21	0
4	EDO	E	305	-	3,3,3	0.42	0	2,2,2	0.39	0
5	ACT	C	304	-	3,3,3	0.85	0	3,3,3	1.31	0
5	ACT	C	305	-	3,3,3	0.81	0	3,3,3	1.33	0
5	ACT	E	306	-	3,3,3	0.79	0	3,3,3	1.33	0
6	PGE	D	308	-	9,9,9	0.31	0	8,8,8	0.26	0
5	ACT	E	307	-	3,3,3	0.82	0	3,3,3	1.32	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	ACT	F	307	-	3,3,3	0.81	0	3,3,3	1.35	0
7	PEG	B	310	-	6,6,6	0.47	0	5,5,5	0.29	0
7	PEG	C	307	-	6,6,6	0.47	0	5,5,5	0.61	0
4	EDO	A	305	-	3,3,3	0.39	0	2,2,2	0.50	0
4	EDO	D	304	-	3,3,3	0.43	0	2,2,2	0.38	0
5	ACT	B	308	-	3,3,3	0.80	0	3,3,3	1.33	0
4	EDO	D	307	-	3,3,3	0.46	0	2,2,2	0.32	0
4	EDO	F	304	-	3,3,3	0.43	0	2,2,2	0.44	0
4	EDO	F	303	-	3,3,3	0.43	0	2,2,2	0.37	0
4	EDO	B	307	-	3,3,3	0.42	0	2,2,2	0.27	0
5	ACT	F	305	-	3,3,3	0.82	0	3,3,3	1.36	0
8	GOL	E	311	-	5,5,5	0.33	0	5,5,5	0.63	0
4	EDO	D	301	-	3,3,3	0.42	0	2,2,2	0.42	0
5	ACT	C	301	-	3,3,3	0.86	0	3,3,3	1.32	0
4	EDO	A	306	-	3,3,3	0.40	0	2,2,2	0.48	0
4	EDO	F	302	-	3,3,3	0.37	0	2,2,2	0.62	0
6	PGE	B	311	-	9,9,9	0.31	0	8,8,8	0.23	0
4	EDO	A	303	-	3,3,3	0.46	0	2,2,2	0.25	0
4	EDO	E	302	-	3,3,3	0.41	0	2,2,2	0.46	0
5	ACT	E	309	-	3,3,3	0.82	0	3,3,3	1.35	0
4	EDO	B	303	-	3,3,3	0.42	0	2,2,2	0.39	0
4	EDO	D	302	-	3,3,3	0.45	0	2,2,2	0.37	0
4	EDO	E	304	-	3,3,3	0.45	0	2,2,2	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
7	PEG	E	310	-	-	2/4/4/4	-
8	GOL	D	309	-	-	2/4/4/4	-
4	EDO	B	302	-	-	1/1/1/1	-
4	EDO	B	304	-	-	0/1/1/1	-
4	EDO	B	306	-	-	1/1/1/1	-
4	EDO	D	303	-	-	1/1/1/1	-
4	EDO	D	306	-	-	1/1/1/1	-
6	PGE	F	309	-	-	0/7/7/7	-
4	EDO	D	305	-	-	0/1/1/1	-
6	PGE	A	308	-	-	2/7/7/7	-
4	EDO	E	303	-	-	0/1/1/1	-
4	EDO	A	304	-	-	0/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	EDO	B	305	-	-	0/1/1/1	-
7	PEG	C	306	-	-	3/4/4/4	-
4	EDO	E	305	-	-	0/1/1/1	-
6	PGE	D	308	-	-	0/7/7/7	-
7	PEG	C	307	-	-	4/4/4/4	-
7	PEG	B	310	-	-	3/4/4/4	-
4	EDO	A	305	-	-	0/1/1/1	-
4	EDO	D	304	-	-	0/1/1/1	-
4	EDO	D	307	-	-	0/1/1/1	-
4	EDO	F	304	-	-	0/1/1/1	-
4	EDO	F	303	-	-	0/1/1/1	-
4	EDO	B	307	-	-	0/1/1/1	-
8	GOL	E	311	-	-	2/4/4/4	-
4	EDO	D	301	-	-	0/1/1/1	-
4	EDO	A	306	-	-	1/1/1/1	-
4	EDO	F	302	-	-	1/1/1/1	-
6	PGE	B	311	-	-	1/7/7/7	-
4	EDO	A	303	-	-	0/1/1/1	-
4	EDO	E	302	-	-	0/1/1/1	-
4	EDO	B	303	-	-	0/1/1/1	-
4	EDO	D	302	-	-	0/1/1/1	-
4	EDO	E	304	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (25) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	C	307	PEG	C1-C2-O2-C3
8	D	309	GOL	O1-C1-C2-O2
7	C	307	PEG	O1-C1-C2-O2
8	D	309	GOL	O1-C1-C2-C3
8	E	311	GOL	O1-C1-C2-C3
7	B	310	PEG	C1-C2-O2-C3
6	B	311	PGE	O3-C5-C6-O4
7	B	310	PEG	O1-C1-C2-O2
7	E	310	PEG	O1-C1-C2-O2
4	B	302	EDO	O1-C1-C2-O2
4	A	306	EDO	O1-C1-C2-O2

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Mol	Chain	Res	Type	Atoms
4	D	306	EDO	O1-C1-C2-O2
7	B	310	PEG	C4-C3-O2-C2
7	C	306	PEG	C4-C3-O2-C2
7	C	307	PEG	O2-C3-C4-O4
7	C	307	PEG	C4-C3-O2-C2
8	E	311	GOL	O1-C1-C2-O2
6	A	308	PGE	C4-C3-O2-C2
7	C	306	PEG	C1-C2-O2-C3
4	D	303	EDO	O1-C1-C2-O2
7	E	310	PEG	C1-C2-O2-C3
7	C	306	PEG	O2-C3-C4-O4
6	A	308	PGE	C1-C2-O2-C3
4	B	306	EDO	O1-C1-C2-O2
4	F	302	EDO	O1-C1-C2-O2

There are no ring outliers.

14 monomers are involved in 27 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	E	310	PEG	1	0
8	D	309	GOL	1	0
4	B	302	EDO	1	0
4	D	305	EDO	2	0
4	E	305	EDO	4	0
5	C	304	ACT	1	0
7	B	310	PEG	2	0
7	C	307	PEG	6	0
4	A	305	EDO	1	0
4	D	304	EDO	1	0
4	F	303	EDO	1	0
4	B	307	EDO	1	0
4	D	301	EDO	3	0
4	A	306	EDO	2	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [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	296/310 (95%)	-0.30	1 (0%) 90 90	11, 18, 33, 46	3 (1%)
1	B	304/310 (98%)	-0.25	4 (1%) 75 75	13, 19, 35, 47	1 (0%)
1	C	296/310 (95%)	-0.22	2 (0%) 84 85	15, 20, 35, 47	1 (0%)
1	D	306/310 (98%)	-0.22	3 (0%) 79 80	14, 19, 34, 45	2 (0%)
1	E	297/310 (95%)	-0.25	2 (0%) 84 85	14, 18, 32, 46	2 (0%)
2	F	295/310 (95%)	-0.13	1 (0%) 90 90	8, 20, 36, 46	2 (0%)
All	All	1794/1860 (96%)	-0.23	13 (0%) 84 85	8, 19, 35, 47	11 (0%)

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	95	PHE	3.8
1	D	230	TYR	3.5
1	B	95	PHE	3.4
1	E	95	PHE	3.3
2	F	95[A]	PHE	3.1
1	D	95	PHE	3.0
1	B	99	HIS	2.8
1	B	231	LYS	2.6
1	E	56	HIS	2.5
1	B	2	ASP	2.5
1	D	74	LYS	2.4
1	A	95	PHE	2.4
1	C	56	HIS	2.3

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
2	KPI	F	166	14/15	0.90	0.11	14,20,31,33	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
5	ACT	C	301	4/4	0.70	0.17	36,39,45,45	0
5	ACT	F	308	4/4	0.70	0.17	40,49,49,55	0
4	EDO	F	302	4/4	0.73	0.24	40,41,45,46	0
7	PEG	E	310	7/7	0.73	0.17	31,36,42,44	0
5	ACT	C	302	4/4	0.77	0.22	40,48,49,63	0
5	ACT	E	309	4/4	0.77	0.20	33,36,41,42	0
4	EDO	F	304	4/4	0.79	0.18	27,39,42,47	0
5	ACT	F	305	4/4	0.80	0.15	46,47,50,50	0
5	ACT	F	307	4/4	0.80	0.14	41,43,51,57	0
5	ACT	E	306	4/4	0.80	0.14	36,37,39,46	0
4	EDO	B	306	4/4	0.80	0.16	28,32,37,39	0
5	ACT	E	307	4/4	0.81	0.15	37,39,44,47	0
4	EDO	B	305	4/4	0.81	0.14	31,34,36,51	0
5	ACT	B	309	4/4	0.82	0.20	30,34,43,57	0
4	EDO	D	304	4/4	0.82	0.13	36,39,40,45	0
5	ACT	E	308	4/4	0.82	0.17	47,50,50,61	0
7	PEG	B	310	7/7	0.82	0.14	35,37,41,42	0
4	EDO	D	306	4/4	0.82	0.21	32,35,39,45	0
6	PGE	F	309	10/10	0.83	0.13	33,38,53,55	0
5	ACT	C	304	4/4	0.83	0.17	25,38,50,51	0
4	EDO	F	303	4/4	0.83	0.15	35,45,46,54	0
5	ACT	F	306	4/4	0.84	0.24	24,43,48,59	0
5	ACT	C	305	4/4	0.84	0.17	40,48,53,53	0
8	GOL	D	309	6/6	0.84	0.18	22,35,46,56	0
4	EDO	D	301	4/4	0.85	0.19	19,24,29,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	MG	E	301	1/1	0.85	0.16	53,53,53,53	0
5	ACT	A	307	4/4	0.85	0.10	26,33,36,41	0
5	ACT	B	308	4/4	0.85	0.12	33,43,43,46	0
4	EDO	D	305	4/4	0.85	0.14	32,34,35,36	0
7	PEG	C	307	7/7	0.85	0.15	23,36,41,42	0
4	EDO	B	304	4/4	0.85	0.15	38,39,40,50	0
4	EDO	B	307	4/4	0.85	0.14	25,28,31,47	0
5	ACT	C	303	4/4	0.86	0.17	29,33,45,51	0
4	EDO	B	303	4/4	0.86	0.13	33,41,45,46	0
4	EDO	B	302	4/4	0.87	0.19	21,25,33,53	0
4	EDO	E	303	4/4	0.87	0.11	27,40,43,43	0
8	GOL	E	311	6/6	0.87	0.15	16,40,45,49	0
6	PGE	A	308	10/10	0.88	0.12	33,39,44,46	0
6	PGE	B	311	10/10	0.88	0.11	28,34,40,50	0
4	EDO	E	305	4/4	0.88	0.15	10,22,30,49	0
4	EDO	A	305	4/4	0.88	0.13	30,35,39,46	0
4	EDO	E	302	4/4	0.89	0.13	41,41,44,48	0
4	EDO	A	306	4/4	0.89	0.15	17,20,29,44	0
4	EDO	D	303	4/4	0.90	0.16	21,31,38,44	0
4	EDO	A	303	4/4	0.90	0.12	24,33,34,36	0
4	EDO	D	302	4/4	0.90	0.10	32,40,42,44	0
7	PEG	C	306	7/7	0.90	0.11	26,33,42,46	0
6	PGE	D	308	10/10	0.91	0.09	28,34,41,44	0
4	EDO	D	307	4/4	0.92	0.12	19,25,28,35	0
3	MG	A	302	1/1	0.93	0.10	44,44,44,44	0
4	EDO	A	304	4/4	0.95	0.09	20,25,28,34	0
3	MG	F	301	1/1	0.96	0.13	32,32,32,32	0
3	MG	A	301	1/1	0.96	0.04	20,20,20,20	0
4	EDO	E	304	4/4	0.97	0.06	19,20,21,22	0
3	MG	B	301	1/1	0.98	0.10	23,23,23,23	0

6.5 Other polymers ⓘ

There are no such residues in this entry.