



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 04:00 PM UTC

PDB ID : 6KI9 / pdb_00006ki9
Title : Apo structure of FabMG, novel types of Enoyl-acyl carrier protein reductase
Authors : Kim, S.; Rhee, S.
Deposited on : 2019-07-17
Resolution : 1.64 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

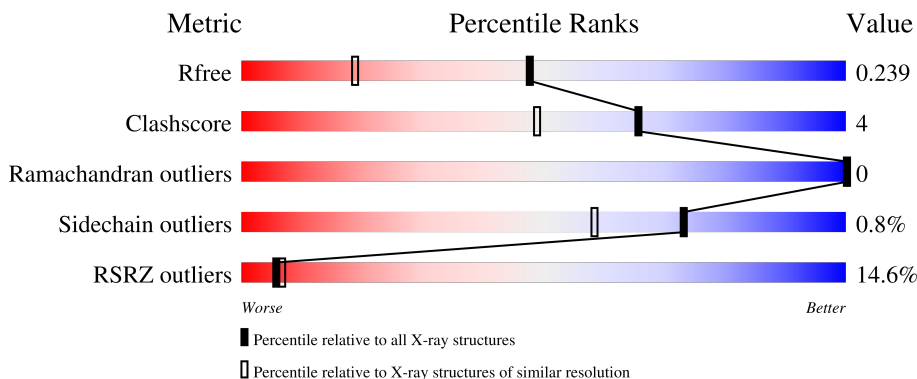
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.64 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	1141 (1.64-1.64)
Clashscore	190562	1171 (1.64-1.64)
Ramachandran outliers	187476	1151 (1.64-1.64)
Sidechain outliers	187428	1150 (1.64-1.64)
RSRZ outliers	180081	1141 (1.64-1.64)

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	446	4% 91% 8%
1	B	446	12% 91% 9%
1	C	446	24% 70% 8% 22%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 10603 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 FabMG, novel types of Enoyl-acyl carrier protein reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	440	Total	C	N	O	S	0	0	0
			3412	2161	592	641	18			
1	B	442	Total	C	N	O	S	0	0	0
			3437	2178	603	638	18			
1	C	349	Total	C	N	O	S	0	0	0
			2738	1750	465	510	13			

There are 24 discrepancies between the modelled and reference sequences:

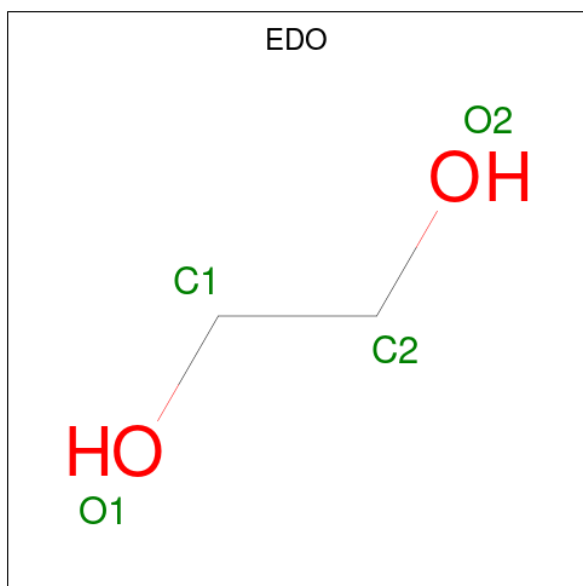
Chain	Residue	Modelled	Actual	Comment	Reference
A	439	LEU	-	expression tag	UNP A0A1C9HA64
A	440	GLU	-	expression tag	UNP A0A1C9HA64
A	441	HIS	-	expression tag	UNP A0A1C9HA64
A	442	HIS	-	expression tag	UNP A0A1C9HA64
A	443	HIS	-	expression tag	UNP A0A1C9HA64
A	444	HIS	-	expression tag	UNP A0A1C9HA64
A	445	HIS	-	expression tag	UNP A0A1C9HA64
A	446	HIS	-	expression tag	UNP A0A1C9HA64
B	439	LEU	-	expression tag	UNP A0A1C9HA64
B	440	GLU	-	expression tag	UNP A0A1C9HA64
B	441	HIS	-	expression tag	UNP A0A1C9HA64
B	442	HIS	-	expression tag	UNP A0A1C9HA64
B	443	HIS	-	expression tag	UNP A0A1C9HA64
B	444	HIS	-	expression tag	UNP A0A1C9HA64
B	445	HIS	-	expression tag	UNP A0A1C9HA64
B	446	HIS	-	expression tag	UNP A0A1C9HA64
C	439	LEU	-	expression tag	UNP A0A1C9HA64
C	440	GLU	-	expression tag	UNP A0A1C9HA64
C	441	HIS	-	expression tag	UNP A0A1C9HA64
C	442	HIS	-	expression tag	UNP A0A1C9HA64
C	443	HIS	-	expression tag	UNP A0A1C9HA64
C	444	HIS	-	expression tag	UNP A0A1C9HA64
C	445	HIS	-	expression tag	UNP A0A1C9HA64

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Chain	Residue	Modelled	Actual	Comment	Reference
C	446	HIS	-	expression tag	UNP A0A1C9HA64

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



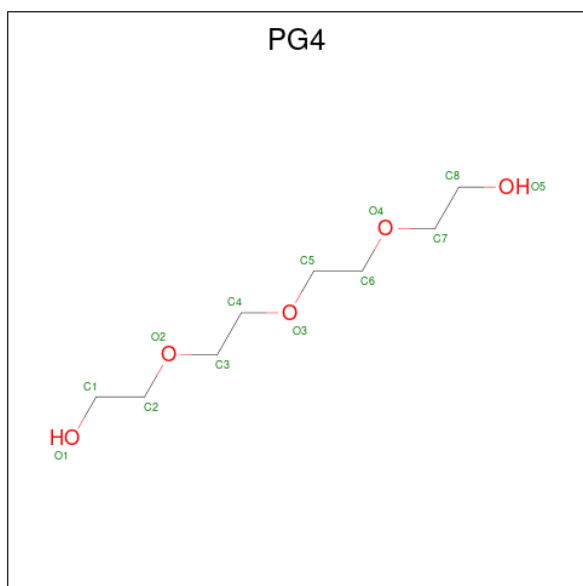
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			4	2	2		
2	A	1	Total	C	O	0	0
			4	2	2		
2	A	1	Total	C	O	0	0
			4	2	2		
2	A	1	Total	C	O	0	0
			4	2	2		
2	A	1	Total	C	O	0	0
			4	2	2		
2	A	1	Total	C	O	0	0
			4	2	2		
2	B	1	Total	C	O	0	0
			4	2	2		
2	B	1	Total	C	O	0	0
			4	2	2		
2	B	1	Total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

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

- Molecule 3 is TETRAETHYLENE GLYCOL (CCD ID: PG4) (formula: $C_8H_{18}O_5$).



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

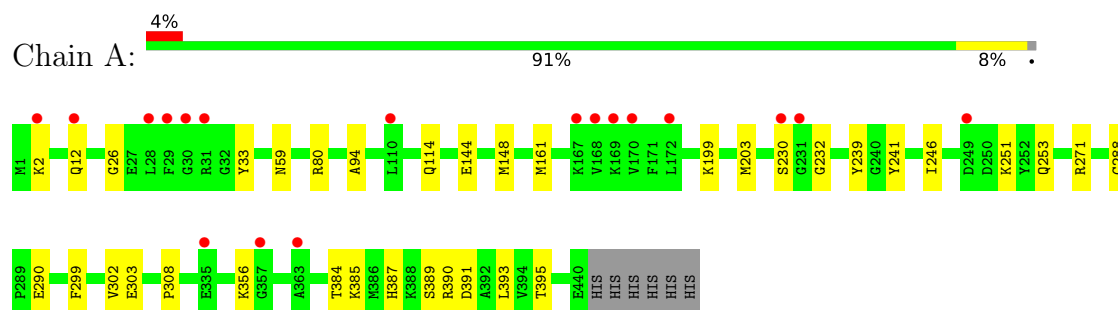
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	376	Total 376	O 376	0	0
4	B	383	Total 383	O 383	0	0
4	C	159	Total 159	O 159	0	0

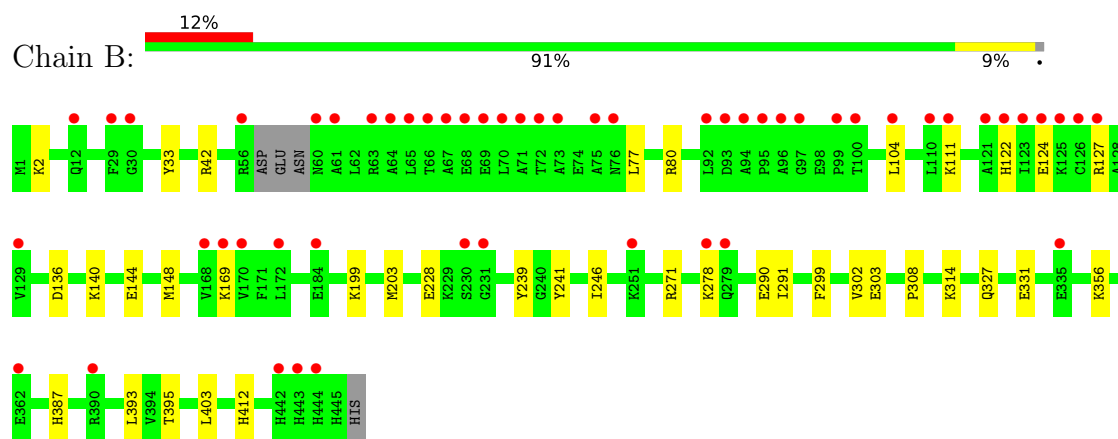
3 Residue-property plots [i](#)

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 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.

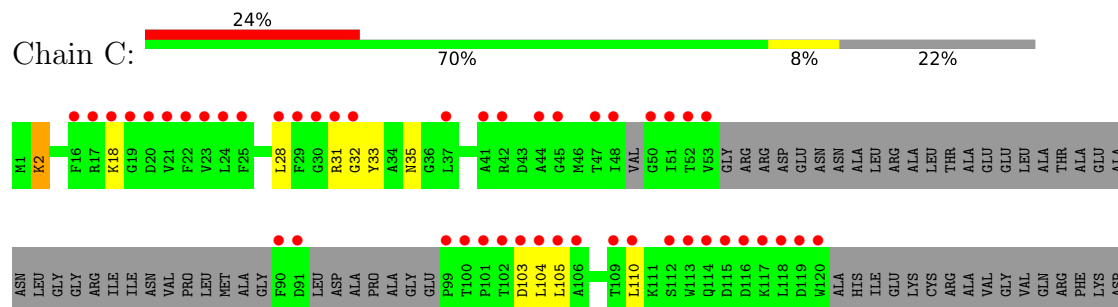
- Molecule 1: FabMG, novel types of Enoyl-acyl carrier protein reductase

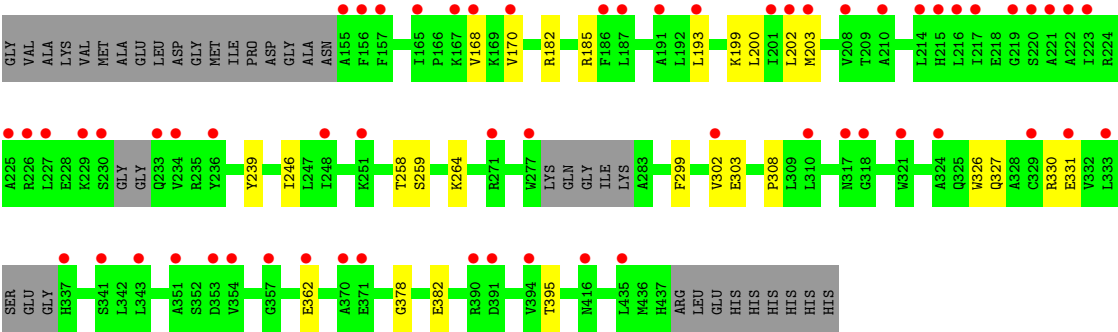


- Molecule 1: FabMG, novel types of Enoyl-acyl carrier protein reductase



- Molecule 1: FabMG, novel types of Enoyl-acyl carrier protein reductase





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	63.86Å 137.00Å 156.86Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	26.73 – 1.64 26.73 – 1.64	Depositor EDS
% Data completeness (in resolution range)	99.9 (26.73-1.64) 95.1 (26.73-1.64)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.25 (at 1.64Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.217 , 0.242 0.223 , 0.239	Depositor DCC
R_{free} test set	2000 reflections (1.19%)	wwPDB-VP
Wilson B-factor (Å ²)	20.9	Xtriage
Anisotropy	0.421	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 43.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	10603	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.94% 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: EDO, PG4

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	0.35	0/3479	0.68	2/4705 (0.0%)
1	B	0.36	0/3508	0.68	0/4743
1	C	0.31	0/2793	0.69	0/3774
All	All	0.34	0/9780	0.68	2/13222 (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	A	232	GLY	N-CA-C	5.76	122.17	113.02
1	A	26	GLY	N-CA-C	-5.12	104.76	111.37

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	3412	0	3405	23	0
1	B	3437	0	3423	29	1
1	C	2738	0	2700	21	1
2	A	32	0	48	2	0
2	B	24	0	36	1	0
2	C	16	0	24	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	13	0	18	6	0
3	B	13	0	18	6	0
4	A	376	0	0	2	0
4	B	383	0	0	3	0
4	C	159	0	0	3	0
All	All	10603	0	9672	73	1

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 (73) 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:291:ILE:H	3:B:507:PG4:H42	1.53	0.72
1:A:290:GLU:HA	3:A:509:PG4:H62	1.74	0.70
1:A:94:ALA:H	2:A:506:EDO:H22	1.56	0.70
1:B:42:ARG:NH2	1:B:77:LEU:O	2.31	0.64
1:A:12:GLN:NE2	4:A:602:HOH:O	2.29	0.63
1:C:327:GLN:NE2	1:C:331:GLU:OE2	2.33	0.62
1:A:80:ARG:HG2	1:A:80:ARG:HH11	1.65	0.61
1:B:124:GLU:OE1	1:B:127:ARG:NH2	2.33	0.61
1:C:110:LEU:HD12	1:C:170:VAL:HG23	1.85	0.58
1:A:161:MET:HA	2:A:503:EDO:H12	1.86	0.58
1:B:144:GLU:HG2	1:B:148:MET:HE3	1.86	0.57
1:B:290:GLU:HA	3:B:507:PG4:H42	1.87	0.57
1:A:144:GLU:HG2	1:A:148:MET:HE3	1.87	0.56
1:B:314:LYS:NZ	4:B:609:HOH:O	2.36	0.56
1:B:271:ARG:NH2	4:B:606:HOH:O	2.32	0.55
1:C:199:LYS:NZ	4:C:604:HOH:O	2.39	0.55
1:A:271:ARG:NH2	4:A:601:HOH:O	2.26	0.55
1:B:80:ARG:NH2	1:B:144:GLU:OE2	2.41	0.54
1:B:136:ASP:O	1:B:140:LYS:HG3	2.09	0.53
1:A:385:LYS:HA	1:A:390:ARG:HH12	1.76	0.51
1:C:246:ILE:HD12	1:C:308:PRO:HG2	1.92	0.50
1:C:28:LEU:HD11	1:C:35:ASN:ND2	2.26	0.50
1:C:182:ARG:NH2	4:C:601:HOH:O	2.33	0.50
1:B:327:GLN:O	1:B:331:GLU:HG2	2.13	0.49
1:A:59:ASN:OD1	1:C:185:ARG:NH1	2.44	0.49
1:B:299:PHE:O	1:B:302:VAL:HG12	2.13	0.48
1:A:251:LYS:HE3	1:A:253:GLN:HG2	1.95	0.48
1:A:288:CYS:HB2	3:A:509:PG4:H31	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:246:ILE:HD12	1:A:308:PRO:HG2	1.95	0.47
1:C:33:TYR:HB3	1:C:239:TYR:CE1	2.50	0.47
1:A:33:TYR:HB3	1:A:239:TYR:CE1	2.50	0.47
1:B:80:ARG:HE	1:B:148:MET:HE1	1.80	0.46
1:C:299:PHE:O	1:C:302:VAL:HG12	2.15	0.46
1:B:104:LEU:HD11	1:B:122:HIS:HD2	1.80	0.46
1:B:302:VAL:HG21	3:B:507:PG4:H71	1.97	0.46
1:A:114:GLN:O	1:B:2:LYS:NZ	2.48	0.46
1:C:31:ARG:NH2	4:C:609:HOH:O	2.49	0.46
1:A:199:LYS:O	1:A:203:MET:HG3	2.16	0.45
1:C:32:GLY:H	1:C:35:ASN:ND2	2.14	0.45
1:B:356:LYS:HE3	1:B:356:LYS:HB2	1.45	0.45
1:A:303:GLU:HG3	1:A:395:THR:HG21	1.99	0.44
1:C:105:LEU:HD11	1:C:200:LEU:HD23	2.00	0.44
1:C:2:LYS:HB3	1:C:2:LYS:HE3	1.60	0.43
1:B:33:TYR:HB3	1:B:239:TYR:CE1	2.53	0.43
1:C:199:LYS:O	1:C:203:MET:HG3	2.19	0.43
1:B:241:TYR:HB2	3:B:507:PG4:H21	2.01	0.43
1:B:246:ILE:HD12	1:B:308:PRO:HG2	2.00	0.42
1:B:199:LYS:O	1:B:203:MET:HG3	2.19	0.42
1:C:326:TRP:O	1:C:330:ARG:HG3	2.20	0.42
1:C:378:GLY:O	1:C:382:GLU:HG3	2.19	0.42
1:A:384:THR:HG22	1:A:390:ARG:HH11	1.85	0.42
1:C:168:VAL:HG12	1:C:170:VAL:HG12	2.01	0.42
1:A:387:HIS:CD2	1:A:393:LEU:HA	2.55	0.41
1:B:228:GLU:OE2	4:B:601:HOH:O	2.21	0.41
1:A:389:SER:OG	1:A:391:ASP:OD1	2.32	0.41
3:A:509:PG4:H42	3:A:509:PG4:H72	2.02	0.41
1:B:291:ILE:HG12	3:B:507:PG4:H32	2.01	0.41
1:C:193:LEU:HD22	1:C:202:LEU:HD11	2.02	0.41
1:B:412:HIS:HE1	2:B:502:EDO:H21	1.85	0.41
1:B:291:ILE:N	3:B:507:PG4:H42	2.29	0.41
1:C:258:THR:HA	1:C:259:SER:HA	1.78	0.41
1:B:278:LYS:HD2	1:B:278:LYS:HA	1.78	0.41
1:C:303:GLU:HG3	1:C:395:THR:HG21	2.03	0.41
1:C:104:LEU:HD12	1:C:104:LEU:HA	1.95	0.40
3:A:509:PG4:H72	3:A:509:PG4:H51	1.70	0.40
1:A:299:PHE:O	1:A:302:VAL:HG12	2.22	0.40
1:B:2:LYS:HE2	1:B:2:LYS:HB3	1.91	0.40
1:B:33:TYR:HA	1:B:403:LEU:HD22	2.02	0.40
1:B:303:GLU:HB2	1:B:395:THR:HG21	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:241:TYR:CD1	3:A:509:PG4:H41	2.57	0.40
1:B:387:HIS:CD2	1:B:393:LEU:HA	2.56	0.40
1:A:241:TYR:HB2	3:A:509:PG4:H22	2.04	0.40
1:A:384:THR:HG22	1:A:390:ARG:NH1	2.37	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:169:LYS:NZ	1:C:103:ASP:OD2[3_445]	2.08	0.12

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	438/446 (98%)	430 (98%)	8 (2%)	0	100	100
1	B	438/446 (98%)	432 (99%)	6 (1%)	0	100	100
1	C	333/446 (75%)	327 (98%)	6 (2%)	0	100	100
All	All	1209/1338 (90%)	1189 (98%)	20 (2%)	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	357/363 (98%)	354 (99%)	3 (1%)	73	58
1	B	359/363 (99%)	358 (100%)	1 (0%)	86	79
1	C	289/363 (80%)	285 (99%)	4 (1%)	59	35
All	All	1005/1089 (92%)	997 (99%)	8 (1%)	73	58

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	LYS
1	A	230	SER
1	A	356	LYS
1	B	111	LYS
1	C	2	LYS
1	C	18	LYS
1	C	264	LYS
1	C	362	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	35	ASN
1	C	253	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

20 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	A	505	-	3,3,3	0.42	0	2,2,2	0.42	0
3	PG4	A	509	-	12,12,12	0.58	0	11,11,11	0.46	0
2	EDO	A	507	-	3,3,3	0.42	0	2,2,2	0.38	0
2	EDO	B	504	-	3,3,3	0.43	0	2,2,2	0.32	0
2	EDO	A	508	-	3,3,3	0.41	0	2,2,2	0.41	0
2	EDO	A	501	-	3,3,3	0.44	0	2,2,2	0.35	0
3	PG4	B	507	-	12,12,12	0.59	0	11,11,11	0.34	0
2	EDO	B	505	-	3,3,3	0.42	0	2,2,2	0.35	0
2	EDO	C	501	-	3,3,3	0.43	0	2,2,2	0.36	0
2	EDO	B	501	-	3,3,3	0.42	0	2,2,2	0.34	0
2	EDO	A	503	-	3,3,3	0.44	0	2,2,2	0.26	0
2	EDO	A	504	-	3,3,3	0.42	0	2,2,2	0.47	0
2	EDO	C	503	-	3,3,3	0.41	0	2,2,2	0.40	0
2	EDO	A	506	-	3,3,3	0.40	0	2,2,2	0.38	0
2	EDO	A	502	-	3,3,3	0.42	0	2,2,2	0.41	0
2	EDO	B	503	-	3,3,3	0.43	0	2,2,2	0.33	0
2	EDO	C	504	-	3,3,3	0.41	0	2,2,2	0.42	0
2	EDO	B	502	-	3,3,3	0.41	0	2,2,2	0.34	0
2	EDO	B	506	-	3,3,3	0.43	0	2,2,2	0.37	0
2	EDO	C	502	-	3,3,3	0.43	0	2,2,2	0.36	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	A	505	-	-	0/1/1/1	-
3	PG4	A	509	-	-	4/10/10/10	-
2	EDO	A	507	-	-	1/1/1/1	-
2	EDO	B	504	-	-	0/1/1/1	-
2	EDO	A	508	-	-	0/1/1/1	-
2	EDO	A	501	-	-	0/1/1/1	-
3	PG4	B	507	-	-	6/10/10/10	-
2	EDO	B	505	-	-	0/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	EDO	C	501	-	-	1/1/1/1	-
2	EDO	B	501	-	-	0/1/1/1	-
2	EDO	A	503	-	-	1/1/1/1	-
2	EDO	A	504	-	-	0/1/1/1	-
2	EDO	C	503	-	-	0/1/1/1	-
2	EDO	A	506	-	-	0/1/1/1	-
2	EDO	A	502	-	-	0/1/1/1	-
2	EDO	B	503	-	-	0/1/1/1	-
2	EDO	C	504	-	-	0/1/1/1	-
2	EDO	B	502	-	-	0/1/1/1	-
2	EDO	B	506	-	-	0/1/1/1	-
2	EDO	C	502	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	509	PG4	C5-C6-O4-C7
3	B	507	PG4	O1-C1-C2-O2
3	B	507	PG4	O3-C5-C6-O4
2	C	501	EDO	O1-C1-C2-O2
3	A	509	PG4	C1-C2-O2-C3
3	B	507	PG4	C3-C4-O3-C5
3	B	507	PG4	C4-C3-O2-C2
3	A	509	PG4	C4-C3-O2-C2
2	A	503	EDO	O1-C1-C2-O2
3	B	507	PG4	C5-C6-O4-C7
2	A	507	EDO	O1-C1-C2-O2
3	A	509	PG4	C3-C4-O3-C5
3	B	507	PG4	C6-C5-O3-C4

There are no ring outliers.

5 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	509	PG4	6	0
3	B	507	PG4	6	0
2	A	503	EDO	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	506	EDO	1	0
2	B	502	EDO	1	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

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	440/446 (98%)	0.40	18 (4%) 41 46	15, 26, 40, 58	0
1	B	442/446 (99%)	0.61	54 (12%) 8 10	16, 25, 50, 87	0
1	C	349/446 (78%)	1.66	108 (30%) 1 1	25, 41, 64, 94	0
All	All	1231/1338 (92%)	0.83	180 (14%) 6 7	15, 29, 54, 94	0

All (180) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	99	PRO	8.5
1	A	231	GLY	6.3
1	B	66	THR	5.6
1	B	60	ASN	5.6
1	B	71	ALA	5.5
1	B	67	ALA	5.3
1	C	48	ILE	5.1
1	C	222	ALA	5.1
1	C	120	TRP	5.0
1	C	118	LEU	4.7
1	C	230	SER	4.7
1	C	221	ALA	4.5
1	A	29	PHE	4.4
1	C	21	VAL	4.4
1	C	234	VAL	4.3
1	C	233	GLN	4.2
1	C	168	VAL	4.1
1	C	223	ILE	4.1
1	C	105	LEU	4.1
1	B	94	ALA	4.0
1	B	69	GLU	4.0
1	C	220	SER	4.0
1	A	31	ARG	3.9

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Mol	Chain	Res	Type	RSRZ
1	B	61	ALA	3.9
1	C	217	ILE	3.9
1	C	119	ASP	3.9
1	B	72	THR	3.8
1	B	168	VAL	3.8
1	C	225	ALA	3.7
1	B	70	LEU	3.7
1	C	116	ASP	3.7
1	B	96	ALA	3.7
1	C	102	THR	3.7
1	B	97	GLY	3.7
1	C	53	VAL	3.6
1	C	100	THR	3.6
1	C	112	SER	3.6
1	A	12	GLN	3.6
1	C	30	GLY	3.6
1	C	47	THR	3.5
1	B	390	ARG	3.5
1	C	29	PHE	3.5
1	B	65	LEU	3.4
1	C	227	LEU	3.4
1	C	370	ALA	3.4
1	B	75	ALA	3.3
1	C	51	ILE	3.3
1	C	104	LEU	3.3
1	B	442	HIS	3.3
1	B	110	LEU	3.3
1	C	90	PHE	3.3
1	A	230	SER	3.2
1	C	156	PHE	3.2
1	B	73	ALA	3.2
1	C	155	ALA	3.2
1	A	30	GLY	3.2
1	C	226	ARG	3.2
1	C	19	GLY	3.2
1	C	310	LEU	3.1
1	C	28	LEU	3.1
1	C	106	ALA	3.1
1	C	44	ALA	3.1
1	C	91	ASP	3.1
1	C	50	GLY	3.0
1	C	219	GLY	3.0

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Mol	Chain	Res	Type	RSRZ
1	C	390	ARG	3.0
1	C	353	ASP	3.0
1	C	23	VAL	3.0
1	C	435	LEU	3.0
1	B	443	HIS	2.9
1	C	113	TRP	2.9
1	B	12	GLN	2.9
1	C	20	ASP	2.9
1	C	354	VAL	2.9
1	B	121	ALA	2.9
1	B	172	LEU	2.9
1	C	229	LYS	2.9
1	C	52	THR	2.9
1	A	110	LEU	2.9
1	B	93	ASP	2.9
1	B	123	ILE	2.9
1	A	167	LYS	2.9
1	C	186	PHE	2.8
1	C	45	GLY	2.8
1	C	110	LEU	2.8
1	B	126	CYS	2.8
1	B	76	ASN	2.8
1	C	109	THR	2.8
1	B	68	GLU	2.8
1	B	111	LYS	2.8
1	B	251	LYS	2.8
1	C	157	PHE	2.8
1	B	169	LYS	2.8
1	C	117	LYS	2.8
1	C	302	VAL	2.8
1	C	22	PHE	2.7
1	C	103	ASP	2.7
1	C	31	ARG	2.7
1	C	357	GLY	2.7
1	B	99	PRO	2.7
1	C	341	SER	2.7
1	C	191	ALA	2.7
1	A	2	LYS	2.7
1	C	101	PRO	2.6
1	C	271	ARG	2.6
1	C	187	LEU	2.6
1	C	193	LEU	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	230	SER	2.5
1	C	333	LEU	2.5
1	B	56	ARG	2.5
1	B	63	ARG	2.5
1	B	279	GLN	2.5
1	C	210	ALA	2.5
1	B	231	GLY	2.5
1	A	335	GLU	2.5
1	B	335	GLU	2.5
1	B	362	GLU	2.5
1	B	124	GLU	2.5
1	C	277	TRP	2.4
1	C	331	GLU	2.4
1	B	170	VAL	2.4
1	C	165	ILE	2.4
1	C	416	ASN	2.4
1	B	127	ARG	2.4
1	B	64	ALA	2.4
1	B	100	THR	2.4
1	A	170	VAL	2.4
1	B	129	VAL	2.4
1	C	42	ARG	2.4
1	B	30	GLY	2.4
1	C	202	LEU	2.4
1	C	214	LEU	2.4
1	B	184	GLU	2.3
1	A	363	ALA	2.3
1	C	24	LEU	2.3
1	C	25	PHE	2.3
1	C	362	GLU	2.3
1	A	172	LEU	2.3
1	C	16	PHE	2.3
1	C	321	TRP	2.3
1	C	18	LYS	2.3
1	C	215	HIS	2.3
1	C	114	GLN	2.3
1	C	203	MET	2.3
1	C	208	VAL	2.3
1	C	371	GLU	2.2
1	C	317	ASN	2.2
1	C	337	HIS	2.2
1	A	168	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
1	C	41	ALA	2.2
1	B	125	LYS	2.2
1	C	391	ASP	2.2
1	C	216	LEU	2.2
1	A	249	ASP	2.2
1	A	357	GLY	2.2
1	B	104	LEU	2.2
1	B	444	HIS	2.2
1	B	95	PRO	2.2
1	C	201	ILE	2.2
1	C	115	ASP	2.1
1	C	394	VAL	2.1
1	C	248	ILE	2.1
1	C	324	ALA	2.1
1	C	351	ALA	2.1
1	C	329	CYS	2.1
1	C	343	LEU	2.1
1	B	278	LYS	2.1
1	C	32	GLY	2.1
1	C	251	LYS	2.1
1	B	92	LEU	2.1
1	B	29	PHE	2.1
1	C	236	TYR	2.1
1	C	17	ARG	2.0
1	C	170	VAL	2.0
1	A	28	LEU	2.0
1	C	37	LEU	2.0
1	C	318	GLY	2.0
1	A	169	LYS	2.0
1	B	122	HIS	2.0
1	C	167	LYS	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	EDO	B	504	4/4	0.60	0.20	51,54,57,59	0
2	EDO	C	504	4/4	0.73	0.17	54,54,54,55	0
2	EDO	A	504	4/4	0.74	0.17	45,47,47,48	0
2	EDO	B	502	4/4	0.74	0.20	54,55,56,58	0
2	EDO	A	508	4/4	0.75	0.18	59,60,61,61	0
2	EDO	A	507	4/4	0.76	0.15	52,53,53,53	0
3	PG4	B	507	13/13	0.76	0.20	29,38,52,52	0
2	EDO	A	501	4/4	0.77	0.20	56,56,57,57	0
2	EDO	B	505	4/4	0.78	0.20	61,61,61,62	0
3	PG4	A	509	13/13	0.78	0.18	32,38,46,46	0
2	EDO	B	506	4/4	0.78	0.16	66,66,66,66	0
2	EDO	A	505	4/4	0.84	0.18	48,48,48,49	0
2	EDO	A	506	4/4	0.84	0.16	45,48,50,50	0
2	EDO	C	503	4/4	0.84	0.23	58,59,59,59	0
2	EDO	C	501	4/4	0.86	0.13	50,50,50,51	0
2	EDO	C	502	4/4	0.86	0.16	52,53,53,53	0
2	EDO	A	503	4/4	0.87	0.13	35,39,43,47	0
2	EDO	B	501	4/4	0.88	0.14	37,41,42,43	0
2	EDO	A	502	4/4	0.92	0.10	29,29,32,33	0
2	EDO	B	503	4/4	0.95	0.08	24,28,28,29	0

6.5 Other polymers

There are no such residues in this entry.