



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 08:17 PM UTC

PDB ID : 5GUL / pdb_00005gul
Title : Crystal structure of Tris/PPix2/Mg2+ bound form of cyclolavandulyl diphosphate synthase (CLDS) from Streptomyces sp. CL190
Authors : Tomita, T.; Kobayashi, M.; Nishiyama, M.; Kuzuyama, T.
Deposited on : 2016-08-29
Resolution : 1.73 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

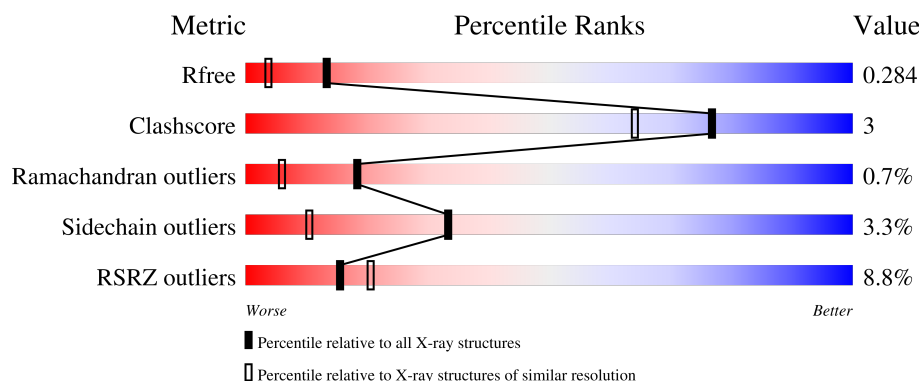
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.73 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	1187 (1.74-1.74)
Clashscore	190562	1207 (1.74-1.74)
Ramachandran outliers	187476	1200 (1.74-1.74)
Sidechain outliers	187428	1200 (1.74-1.74)
RSRZ outliers	180081	1188 (1.74-1.74)

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	238	2% 86% 5% 9%
1	B	238	5% 84% 6% 9%
1	C	238	10% 82% 8% 9%
1	D	238	16% 78% 12% 9%

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	TRS	D	304	-	X	-	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7196 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 Cyclolavandulyl diphosphate synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	216	Total	C	N	O	S	0	0	0
			1703	1082	284	327	10			
1	B	216	Total	C	N	O	S	0	0	0
			1703	1082	284	327	10			
1	C	216	Total	C	N	O	S	0	0	0
			1703	1082	284	327	10			
1	D	216	Total	C	N	O	S	0	0	0
			1703	1082	284	327	10			

There are 88 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-20	MET	-	initiating methionine	UNP X5IYJ5
A	-19	LYS	-	expression tag	UNP X5IYJ5
A	-18	HIS	-	expression tag	UNP X5IYJ5
A	-17	HIS	-	expression tag	UNP X5IYJ5
A	-16	HIS	-	expression tag	UNP X5IYJ5
A	-15	HIS	-	expression tag	UNP X5IYJ5
A	-14	HIS	-	expression tag	UNP X5IYJ5
A	-13	HIS	-	expression tag	UNP X5IYJ5
A	-12	HIS	-	expression tag	UNP X5IYJ5
A	-11	HIS	-	expression tag	UNP X5IYJ5
A	-10	GLY	-	expression tag	UNP X5IYJ5
A	-9	GLY	-	expression tag	UNP X5IYJ5
A	-8	LEU	-	expression tag	UNP X5IYJ5
A	-7	VAL	-	expression tag	UNP X5IYJ5
A	-6	PRO	-	expression tag	UNP X5IYJ5
A	-5	ARG	-	expression tag	UNP X5IYJ5
A	-4	GLY	-	expression tag	UNP X5IYJ5
A	-3	SER	-	expression tag	UNP X5IYJ5
A	-2	HIS	-	expression tag	UNP X5IYJ5
A	-1	GLY	-	expression tag	UNP X5IYJ5
A	0	GLY	-	expression tag	UNP X5IYJ5

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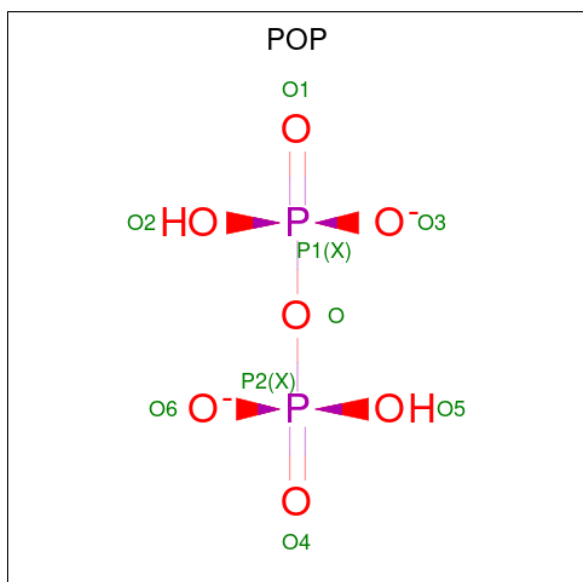
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	SER	-	expression tag	UNP X5IYJ5
B	-20	MET	-	initiating methionine	UNP X5IYJ5
B	-19	LYS	-	expression tag	UNP X5IYJ5
B	-18	HIS	-	expression tag	UNP X5IYJ5
B	-17	HIS	-	expression tag	UNP X5IYJ5
B	-16	HIS	-	expression tag	UNP X5IYJ5
B	-15	HIS	-	expression tag	UNP X5IYJ5
B	-14	HIS	-	expression tag	UNP X5IYJ5
B	-13	HIS	-	expression tag	UNP X5IYJ5
B	-12	HIS	-	expression tag	UNP X5IYJ5
B	-11	HIS	-	expression tag	UNP X5IYJ5
B	-10	GLY	-	expression tag	UNP X5IYJ5
B	-9	GLY	-	expression tag	UNP X5IYJ5
B	-8	LEU	-	expression tag	UNP X5IYJ5
B	-7	VAL	-	expression tag	UNP X5IYJ5
B	-6	PRO	-	expression tag	UNP X5IYJ5
B	-5	ARG	-	expression tag	UNP X5IYJ5
B	-4	GLY	-	expression tag	UNP X5IYJ5
B	-3	SER	-	expression tag	UNP X5IYJ5
B	-2	HIS	-	expression tag	UNP X5IYJ5
B	-1	GLY	-	expression tag	UNP X5IYJ5
B	0	GLY	-	expression tag	UNP X5IYJ5
B	1	SER	-	expression tag	UNP X5IYJ5
C	-20	MET	-	initiating methionine	UNP X5IYJ5
C	-19	LYS	-	expression tag	UNP X5IYJ5
C	-18	HIS	-	expression tag	UNP X5IYJ5
C	-17	HIS	-	expression tag	UNP X5IYJ5
C	-16	HIS	-	expression tag	UNP X5IYJ5
C	-15	HIS	-	expression tag	UNP X5IYJ5
C	-14	HIS	-	expression tag	UNP X5IYJ5
C	-13	HIS	-	expression tag	UNP X5IYJ5
C	-12	HIS	-	expression tag	UNP X5IYJ5
C	-11	HIS	-	expression tag	UNP X5IYJ5
C	-10	GLY	-	expression tag	UNP X5IYJ5
C	-9	GLY	-	expression tag	UNP X5IYJ5
C	-8	LEU	-	expression tag	UNP X5IYJ5
C	-7	VAL	-	expression tag	UNP X5IYJ5
C	-6	PRO	-	expression tag	UNP X5IYJ5
C	-5	ARG	-	expression tag	UNP X5IYJ5
C	-4	GLY	-	expression tag	UNP X5IYJ5
C	-3	SER	-	expression tag	UNP X5IYJ5
C	-2	HIS	-	expression tag	UNP X5IYJ5

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-1	GLY	-	expression tag	UNP X5IYJ5
C	0	GLY	-	expression tag	UNP X5IYJ5
C	1	SER	-	expression tag	UNP X5IYJ5
D	-20	MET	-	initiating methionine	UNP X5IYJ5
D	-19	LYS	-	expression tag	UNP X5IYJ5
D	-18	HIS	-	expression tag	UNP X5IYJ5
D	-17	HIS	-	expression tag	UNP X5IYJ5
D	-16	HIS	-	expression tag	UNP X5IYJ5
D	-15	HIS	-	expression tag	UNP X5IYJ5
D	-14	HIS	-	expression tag	UNP X5IYJ5
D	-13	HIS	-	expression tag	UNP X5IYJ5
D	-12	HIS	-	expression tag	UNP X5IYJ5
D	-11	HIS	-	expression tag	UNP X5IYJ5
D	-10	GLY	-	expression tag	UNP X5IYJ5
D	-9	GLY	-	expression tag	UNP X5IYJ5
D	-8	LEU	-	expression tag	UNP X5IYJ5
D	-7	VAL	-	expression tag	UNP X5IYJ5
D	-6	PRO	-	expression tag	UNP X5IYJ5
D	-5	ARG	-	expression tag	UNP X5IYJ5
D	-4	GLY	-	expression tag	UNP X5IYJ5
D	-3	SER	-	expression tag	UNP X5IYJ5
D	-2	HIS	-	expression tag	UNP X5IYJ5
D	-1	GLY	-	expression tag	UNP X5IYJ5
D	0	GLY	-	expression tag	UNP X5IYJ5
D	1	SER	-	expression tag	UNP X5IYJ5

- Molecule 2 is PYROPHOSPHATE 2- (CCD ID: POP) (formula: $\text{H}_2\text{O}_7\text{P}_2$).

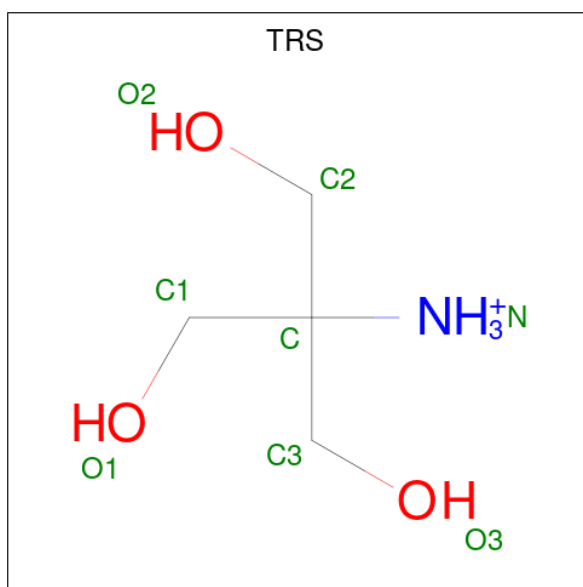


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total O P 9 7 2	0	0
2	A	1	Total O P 9 7 2	0	0
2	B	1	Total O P 9 7 2	0	0
2	B	1	Total O P 9 7 2	0	0
2	C	1	Total O P 9 7 2	0	0
2	C	1	Total O P 9 7 2	0	0
2	D	1	Total O P 9 7 2	0	0
2	D	1	Total O P 9 7 2	0	0

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

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Mg 1 1	0	0
3	B	1	Total Mg 1 1	0	0
3	C	1	Total Mg 1 1	0	0
3	D	1	Total Mg 1 1	0	0

- Molecule 4 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (CCD ID: TRS) (formula: C₄H₁₂NO₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			8	4	1	3		
4	B	1	Total	C	N	O	0	0
			8	4	1	3		
4	C	1	Total	C	N	O	0	0
			8	4	1	3		
4	D	1	Total	C	N	O	0	0
			8	4	1	3		

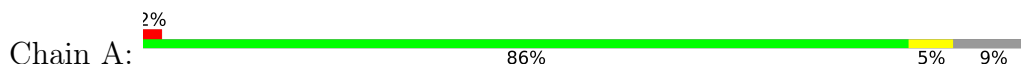
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	114	Total	O	0	0
			114	114		
5	B	73	Total	O	0	0
			73	73		
5	C	39	Total	O	0	0
			39	39		
5	D	50	Total	O	0	0
			50	50		

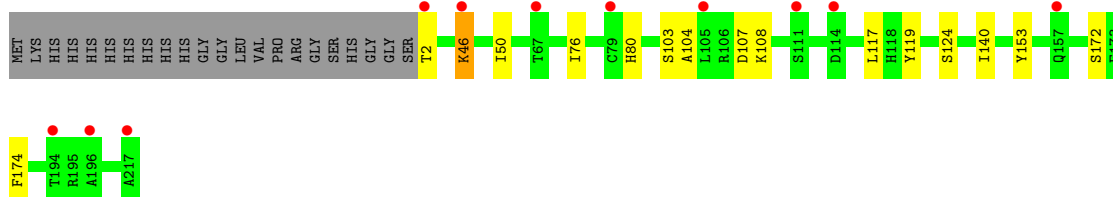
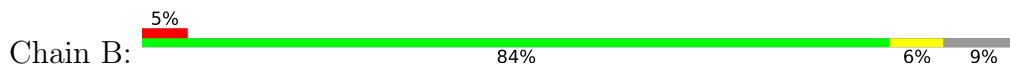
3 Residue-property plots [i](#)

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.

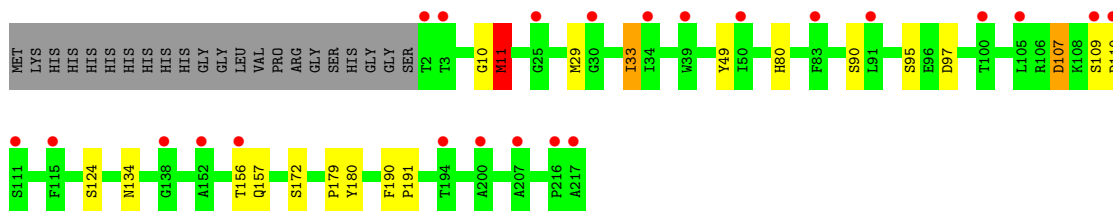
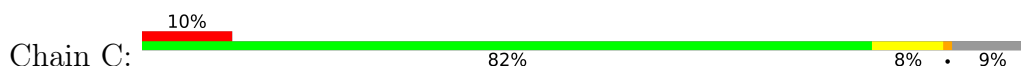
- Molecule 1: Cyclolavandulyl diphosphate synthase



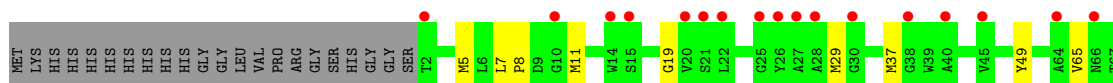
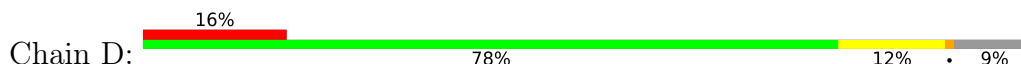
- Molecule 1: Cyclolavandulyl diphosphate synthase

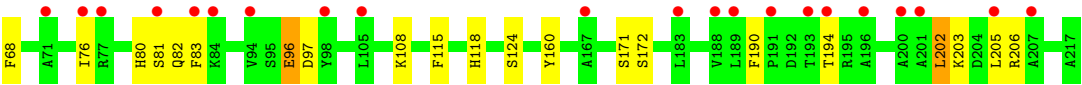


- Molecule 1: Cyclolavandulyl diphosphate synthase



- Molecule 1: Cyclolavandulyl diphosphate synthase





4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	46.85Å 61.66Å 82.24Å 74.00° 84.54° 86.04°	Depositor
Resolution (Å)	55.04 – 1.73 55.04 – 1.73	Depositor EDS
% Data completeness (in resolution range)	85.6 (55.04-1.73) 85.8 (55.04-1.73)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.78 (at 1.73Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.216 , 0.278 0.223 , 0.284	Depositor DCC
R_{free} test set	3967 reflections (4.29%)	wwPDB-VP
Wilson B-factor (Å ²)	31.5	Xtriage
Anisotropy	0.020	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 29.9	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	0.95	EDS
Total number of atoms	7196	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.57% 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: MG, POP, TRS

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	1.24	3/1742 (0.2%)	1.12	1/2354 (0.0%)
1	B	1.17	2/1742 (0.1%)	1.09	1/2354 (0.0%)
1	C	1.04	2/1742 (0.1%)	1.09	4/2354 (0.2%)
1	D	1.02	0/1742	1.07	0/2354
All	All	1.12	7/6968 (0.1%)	1.09	6/9416 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	D	0	1

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	175	PRO	C-O	7.88	1.31	1.23
1	A	50	ILE	C-O	-7.10	1.16	1.24
1	B	174	PHE	C-O	-6.60	1.15	1.24
1	B	153	TYR	C-N	-5.71	1.28	1.33
1	C	90	SER	C-O	5.36	1.29	1.23
1	A	154	VAL	N-CA	5.28	1.50	1.46
1	C	179	PRO	CA-C	5.09	1.60	1.52

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	11	MET	CG-SD-CE	5.54	113.09	100.90
1	C	33	ILE	N-CA-C	-5.40	105.24	110.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	80	HIS	N-CA-C	5.34	118.58	111.75
1	C	134	ASN	CA-C-N	5.22	127.28	120.28
1	C	134	ASN	C-N-CA	5.22	127.28	120.28
1	A	168	ILE	CB-CA-C	5.03	119.55	111.29

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	19	GLY	Peptide

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	1703	0	1651	2	0
1	B	1703	0	1651	6	0
1	C	1703	0	1651	15	0
1	D	1703	0	1651	19	0
2	A	18	0	0	0	0
2	B	18	0	0	0	0
2	C	18	0	0	0	0
2	D	18	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	8	0	12	0	0
4	B	8	0	12	0	0
4	C	8	0	12	0	0
4	D	8	0	12	0	0
5	A	114	0	0	0	0
5	B	73	0	0	0	0
5	C	39	0	0	1	0
5	D	50	0	0	0	0
All	All	7196	0	6652	39	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 (39) 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:11:MET:N	1:C:11:MET:HE3	1.87	0.90
1:D:11:MET:HE2	1:D:29:MET:HB2	1.63	0.80
1:C:11:MET:HE1	1:C:190:PHE:HB3	1.74	0.68
1:C:11:MET:N	1:C:11:MET:CE	2.60	0.65
1:C:11:MET:HE2	1:C:191:PRO:HD3	1.78	0.65
1:D:11:MET:HE2	1:D:29:MET:CB	2.27	0.63
1:D:11:MET:HE2	1:D:29:MET:CG	2.31	0.60
1:D:11:MET:HE1	1:D:190:PHE:HB3	1.85	0.59
1:D:37:MET:HE1	1:D:83:PHE:CD2	2.39	0.58
1:C:29:MET:HE3	1:C:33:ILE:HD12	1.86	0.57
1:D:65:VAL:HA	1:D:68:PHE:CE2	2.39	0.57
1:C:11:MET:CE	1:C:191:PRO:HD3	2.34	0.56
1:C:10:GLY:C	1:C:11:MET:HE3	2.31	0.55
1:B:2:THR:CG2	1:B:46:LYS:HG2	2.38	0.54
1:D:11:MET:CE	1:D:29:MET:HB2	2.36	0.53
1:D:37:MET:HE3	1:D:115:PHE:CE2	2.44	0.52
1:D:202:LEU:HD23	1:D:206:ARG:CZ	2.40	0.51
1:B:50:ILE:HD12	1:B:117:LEU:HD11	1.92	0.51
1:D:37:MET:HE1	1:D:83:PHE:HD2	1.79	0.48
1:D:11:MET:HE2	1:D:29:MET:HG3	1.96	0.48
1:A:166:GLY:HA2	1:A:187:PRO:HA	1.95	0.48
1:C:29:MET:HE3	1:C:33:ILE:CD1	2.45	0.47
1:A:50:ILE:HD12	1:A:117:LEU:HD11	1.96	0.47
1:D:76:ILE:O	1:D:80:HIS:HB3	2.14	0.47
1:D:202:LEU:HD23	1:D:206:ARG:NH1	2.30	0.47
1:B:140:ILE:HG22	1:D:96:GLU:HG2	1.97	0.46
1:C:107:ASP:HB2	5:C:438:HOH:O	2.16	0.45
1:B:104:ALA:O	1:B:107:ASP:HB2	2.17	0.45
1:B:2:THR:HG23	1:B:46:LYS:HG2	2.00	0.44
1:D:160:TYR:HB3	1:D:205:LEU:HD13	2.00	0.43
1:C:180:TYR:CD1	1:D:171:SER:HA	2.53	0.43
1:B:76:ILE:HD11	1:B:119:TYR:CZ	2.53	0.43
1:C:10:GLY:C	1:C:11:MET:CE	2.92	0.42
1:C:80:HIS:O	1:C:109:SER:HA	2.20	0.42
1:D:49:TYR:CD1	1:D:118:HIS:HB3	2.55	0.41
1:C:11:MET:CE	1:C:11:MET:CA	2.98	0.41
1:C:180:TYR:CE1	1:D:171:SER:HA	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:49:TYR:HH	1:C:156:THR:HG1	1.55	0.41
1:D:5:MET:HA	1:D:49:TYR:O	2.22	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	214/238 (90%)	209 (98%)	4 (2%)	1 (0%)	24	12
1	B	214/238 (90%)	210 (98%)	3 (1%)	1 (0%)	24	12
1	C	214/238 (90%)	208 (97%)	4 (2%)	2 (1%)	14	3
1	D	214/238 (90%)	205 (96%)	7 (3%)	2 (1%)	14	3
All	All	856/952 (90%)	832 (97%)	18 (2%)	6 (1%)	18	6

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	124	SER
1	C	110	ASP
1	D	124	SER
1	A	124	SER
1	B	124	SER
1	D	8	PRO

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	182/199 (92%)	178 (98%)	4 (2%)	45	22
1	B	182/199 (92%)	178 (98%)	4 (2%)	45	22
1	C	182/199 (92%)	176 (97%)	6 (3%)	33	10
1	D	182/199 (92%)	172 (94%)	10 (6%)	19	3
All	All	728/796 (92%)	704 (97%)	24 (3%)	33	10

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	THR
1	A	96	GLU
1	A	142	GLU
1	A	172	SER
1	B	46	LYS
1	B	103	SER
1	B	108	LYS
1	B	172	SER
1	C	11	MET
1	C	95	SER
1	C	97	ASP
1	C	107	ASP
1	C	157	GLN
1	C	172	SER
1	D	7	LEU
1	D	81	SER
1	D	82	GLN
1	D	96	GLU
1	D	97	ASP
1	D	108	LYS
1	D	172	SER
1	D	194	THR
1	D	202	LEU
1	D	203	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	82	GLN

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Mol	Chain	Res	Type
1	C	82	GLN
1	D	80	HIS
1	D	157	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 16 ligands modelled in this entry, 4 are monoatomic - leaving 12 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	$\# Z > 2$
4	TRS	C	304	-	7,7,7	1.05	1 (14%)	9,9,9	1.30	2 (22%)
2	POP	D	301	3	6,8,8	0.76	0	12,13,13	1.10	1 (8%)
4	TRS	B	304	-	7,7,7	0.51	0	9,9,9	1.20	1 (11%)
2	POP	D	302	3	6,8,8	0.93	0	12,13,13	1.54	1 (8%)
2	POP	A	302	3	6,8,8	0.94	0	12,13,13	1.60	3 (25%)
2	POP	B	301	3	6,8,8	1.24	1 (16%)	12,13,13	1.58	2 (16%)
2	POP	A	301	3	6,8,8	1.18	0	12,13,13	1.15	0
4	TRS	A	304	-	7,7,7	0.53	0	9,9,9	1.52	2 (22%)
4	TRS	D	304	-	7,7,7	1.22	0	9,9,9	4.15	6 (66%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	POP	B	302	3	6,8,8	0.89	0	12,13,13	1.12	1 (8%)
2	POP	C	302	3	6,8,8	1.06	0	12,13,13	1.52	3 (25%)
2	POP	C	301	3	6,8,8	0.81	0	12,13,13	1.27	1 (8%)

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
4	TRS	C	304	-	-	5/9/9/9	-
2	POP	D	301	3	-	3/6/6/6	-
4	TRS	B	304	-	-	3/9/9/9	-
2	POP	D	302	3	-	0/6/6/6	-
2	POP	A	302	3	-	0/6/6/6	-
2	POP	B	301	3	-	0/6/6/6	-
2	POP	A	301	3	-	0/6/6/6	-
4	TRS	A	304	-	-	1/9/9/9	-
4	TRS	D	304	-	-	4/9/9/9	-
2	POP	B	302	3	-	1/6/6/6	-
2	POP	C	302	3	-	0/6/6/6	-
2	POP	C	301	3	-	2/6/6/6	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	301	POP	P1-O2	-2.29	1.46	1.54
4	C	304	TRS	C2-C	-2.24	1.47	1.53

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	304	TRS	C3-C-C1	-5.82	95.15	110.66
4	D	304	TRS	C2-C-N	5.52	122.24	108.17
4	D	304	TRS	C3-C-C2	-5.38	96.32	110.66
4	D	304	TRS	C3-C-N	-5.29	94.67	108.17
4	D	304	TRS	C1-C-N	4.53	119.72	108.17
2	D	302	POP	O2-P1-O	4.48	119.67	104.64
2	B	301	POP	O2-P1-O1	4.33	127.71	110.83
2	A	302	POP	O3-P1-O2	2.94	118.82	107.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	302	POP	O6-P2-O5	2.94	118.81	107.80
2	A	302	POP	O6-P2-O5	2.76	118.15	107.80
4	A	304	TRS	C3-C-C2	-2.74	103.35	110.66
4	D	304	TRS	O1-C1-C	-2.48	103.96	110.88
2	B	301	POP	O6-P2-O4	2.44	120.34	110.83
2	D	301	POP	O6-P2-O4	2.42	120.25	110.83
2	B	302	POP	O3-P1-O1	2.36	120.03	110.83
4	B	304	TRS	C2-C-N	2.29	114.00	108.17
4	C	304	TRS	C2-C-C1	-2.18	104.86	110.66
2	C	302	POP	O3-P1-O2	2.17	115.95	107.80
2	C	302	POP	O-P1-O1	-2.15	99.75	111.04
4	C	304	TRS	C2-C-N	2.08	113.46	108.17
2	C	301	POP	O-P2-O4	-2.04	100.33	111.04
4	A	304	TRS	C2-C-N	2.02	113.32	108.17
2	A	302	POP	O5-P2-O4	2.01	118.65	110.83

There are no chirality outliers.

All (19) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	301	POP	P1-O-P2-O6
4	D	304	TRS	N-C-C1-O1
4	D	304	TRS	N-C-C2-O2
4	B	304	TRS	C1-C-C2-O2
2	C	301	POP	P2-O-P1-O1
2	C	301	POP	P1-O-P2-O4
4	B	304	TRS	C3-C-C2-O2
2	D	301	POP	P1-O-P2-O5
4	A	304	TRS	C1-C-C2-O2
4	C	304	TRS	C3-C-C2-O2
4	C	304	TRS	C2-C-C3-O3
4	D	304	TRS	C2-C-C1-O1
4	D	304	TRS	C3-C-C2-O2
4	B	304	TRS	N-C-C2-O2
2	D	301	POP	P1-O-P2-O4
2	B	302	POP	P2-O-P1-O3
4	C	304	TRS	C1-C-C2-O2
4	C	304	TRS	C1-C-C3-O3
4	C	304	TRS	N-C-C3-O3

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	216/238 (90%)	0.47	4 (1%) 66 73	23, 31, 45, 64	0
1	B	216/238 (90%)	0.69	11 (5%) 33 41	24, 35, 51, 73	0
1	C	216/238 (90%)	0.96	23 (10%) 11 15	27, 41, 59, 80	0
1	D	216/238 (90%)	1.20	38 (17%) 4 5	26, 44, 69, 81	0
All	All	864/952 (90%)	0.83	76 (8%) 15 20	23, 37, 62, 81	0

All (76) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	217	ALA	4.1
1	D	21	SER	4.0
1	D	10	GLY	4.0
1	D	14	TRP	3.8
1	D	207	ALA	3.6
1	D	66	ASN	3.5
1	D	2	THR	3.5
1	D	188	VAL	3.4
1	D	25	GLY	3.4
1	D	194	THR	3.4
1	D	38	GLY	3.2
1	D	26	TYR	3.1
1	D	200	ALA	3.1
1	B	111	SER	3.1
1	B	105	LEU	3.0
1	C	3	THR	3.0
1	A	10	GLY	3.0
1	D	22	LEU	3.0
1	D	191	PRO	3.0
1	C	105	LEU	2.9
1	D	30	GLY	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	2	THR	2.8
1	C	138	GLY	2.8
1	C	115	PHE	2.8
1	D	105	LEU	2.8
1	C	217	ALA	2.7
1	C	156	THR	2.6
1	D	45	VAL	2.6
1	D	196	ALA	2.6
1	B	2	THR	2.5
1	C	207	ALA	2.5
1	D	205	LEU	2.5
1	D	28	ALA	2.5
1	D	167	ALA	2.4
1	C	2	THR	2.4
1	D	83	PHE	2.4
1	D	98	TYR	2.4
1	D	193	THR	2.4
1	C	110	ASP	2.4
1	D	20	VAL	2.3
1	D	201	ALA	2.3
1	D	76	ILE	2.3
1	C	39	TRP	2.3
1	C	111	SER	2.3
1	B	46	LYS	2.3
1	B	114	ASP	2.3
1	C	34	ILE	2.3
1	C	194	THR	2.2
1	C	200	ALA	2.2
1	D	27	ALA	2.2
1	D	189	LEU	2.2
1	B	196	ALA	2.2
1	C	152	ALA	2.2
1	D	71	ALA	2.2
1	C	30	GLY	2.2
1	C	216	PRO	2.2
1	C	25	GLY	2.1
1	A	64	ALA	2.1
1	D	94	VAL	2.1
1	D	81	SER	2.1
1	C	100	THR	2.1
1	C	50	ILE	2.1
1	D	40	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	79	CYS	2.1
1	C	109	SER	2.1
1	D	15	SER	2.1
1	D	183	LEU	2.1
1	B	67	THR	2.1
1	B	194	THR	2.1
1	B	157	GLN	2.0
1	D	77	ARG	2.0
1	C	91	LEU	2.0
1	D	84	LYS	2.0
1	A	98	TYR	2.0
1	C	83	PHE	2.0
1	D	64	ALA	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 [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($\text{\AA}^2$)	Q<0.9
2	POP	D	301	9/9	0.90	0.10	36,43,51,61	0
4	TRS	D	304	8/8	0.91	0.10	38,42,45,45	0
2	POP	D	302	9/9	0.94	0.08	35,42,47,50	0
4	TRS	C	304	8/8	0.96	0.07	31,33,34,35	0
4	TRS	B	304	8/8	0.96	0.07	28,30,32,32	0
3	MG	D	303	1/1	0.97	0.07	42,42,42,42	0
4	TRS	A	304	8/8	0.97	0.06	24,25,26,28	0
2	POP	C	301	9/9	0.97	0.06	27,31,36,39	0
2	POP	A	302	9/9	0.97	0.07	25,26,31,33	0
2	POP	B	302	9/9	0.97	0.07	26,27,32,34	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	POP	B	301	9/9	0.98	0.06	25,28,29,30	0
2	POP	C	302	9/9	0.98	0.04	29,31,32,35	0
2	POP	A	301	9/9	0.98	0.04	25,27,30,32	0
3	MG	C	303	1/1	0.99	0.02	32,32,32,32	0
3	MG	A	303	1/1	1.00	0.04	30,30,30,30	0
3	MG	B	303	1/1	1.00	0.02	28,28,28,28	0

6.5 Other polymers [i](#)

There are no such residues in this entry.