



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 10:00 AM UTC

PDB ID : 9IYG / pdb_00009iyg
Title : Structure of Phosphopantetheine adenylyltransferase (PPAT) from *Enterobacter* spp. with the 17-mer expression tag bound in the substrate binding site of a neighbouring molecule at 2.60 Å resolution.
Authors : Ahmad, N.; Sharma, P.; Sharma, S.; Singh, T.P.
Deposited on : 2024-07-30
Resolution : 2.60 Å (reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

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

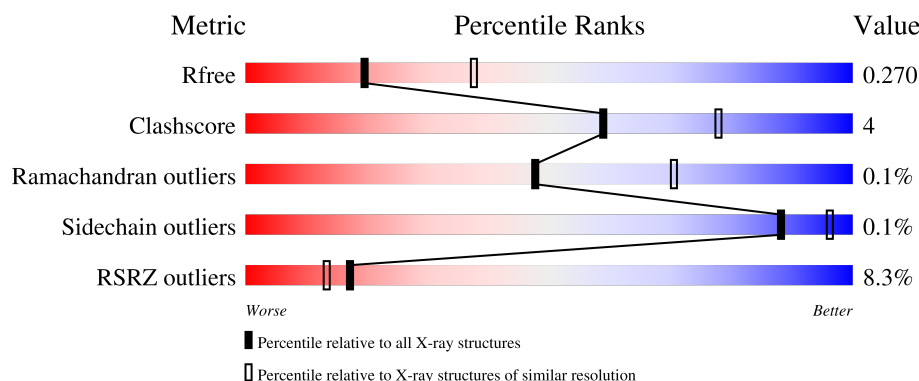
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

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	176	6% 80% 10% 10%
1	B	176	5% 91% 9%
1	C	176	4% 82% 8% 10%
1	D	176	3% 91% 8%
1	E	176	9% 81% 9% 10%

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Mol	Chain	Length	Quality of chain
1	F	176	21% 82% 9% 10%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 8271 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 Phosphopantetheine adenylyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	159	Total	C	N	O	S	0	0	0
			1246	796	216	224	10			
1	B	176	Total	C	N	O	S	0	1	0
			1367	864	241	248	14			
1	C	159	Total	C	N	O	S	0	0	0
			1246	796	216	224	10			
1	D	176	Total	C	N	O	S	0	0	0
			1359	859	240	247	13			
1	E	159	Total	C	N	O	S	0	2	0
			1256	804	216	224	12			
1	F	159	Total	C	N	O	S	0	1	0
			1257	802	220	225	10			

There are 102 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-16	GLY	-	expression tag	UNP A4W515
A	-15	SER	-	expression tag	UNP A4W515
A	-14	HIS	-	expression tag	UNP A4W515
A	-13	MET	-	expression tag	UNP A4W515
A	-12	ALA	-	expression tag	UNP A4W515
A	-11	SER	-	expression tag	UNP A4W515
A	-10	MET	-	expression tag	UNP A4W515
A	-9	THR	-	expression tag	UNP A4W515
A	-8	GLY	-	expression tag	UNP A4W515
A	-7	GLY	-	expression tag	UNP A4W515
A	-6	GLN	-	expression tag	UNP A4W515
A	-5	GLN	-	expression tag	UNP A4W515
A	-4	MET	-	expression tag	UNP A4W515
A	-3	GLY	-	expression tag	UNP A4W515
A	-2	ARG	-	expression tag	UNP A4W515
A	-1	GLY	-	expression tag	UNP A4W515
A	0	SER	-	expression tag	UNP A4W515

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-16	GLY	-	expression tag	UNP A4W515
B	-15	SER	-	expression tag	UNP A4W515
B	-14	HIS	-	expression tag	UNP A4W515
B	-13	MET	-	expression tag	UNP A4W515
B	-12	ALA	-	expression tag	UNP A4W515
B	-11	SER	-	expression tag	UNP A4W515
B	-10	MET	-	expression tag	UNP A4W515
B	-9	THR	-	expression tag	UNP A4W515
B	-8	GLY	-	expression tag	UNP A4W515
B	-7	GLY	-	expression tag	UNP A4W515
B	-6	GLN	-	expression tag	UNP A4W515
B	-5	GLN	-	expression tag	UNP A4W515
B	-4	MET	-	expression tag	UNP A4W515
B	-3	GLY	-	expression tag	UNP A4W515
B	-2	ARG	-	expression tag	UNP A4W515
B	-1	GLY	-	expression tag	UNP A4W515
B	0	SER	-	expression tag	UNP A4W515
C	-16	GLY	-	expression tag	UNP A4W515
C	-15	SER	-	expression tag	UNP A4W515
C	-14	HIS	-	expression tag	UNP A4W515
C	-13	MET	-	expression tag	UNP A4W515
C	-12	ALA	-	expression tag	UNP A4W515
C	-11	SER	-	expression tag	UNP A4W515
C	-10	MET	-	expression tag	UNP A4W515
C	-9	THR	-	expression tag	UNP A4W515
C	-8	GLY	-	expression tag	UNP A4W515
C	-7	GLY	-	expression tag	UNP A4W515
C	-6	GLN	-	expression tag	UNP A4W515
C	-5	GLN	-	expression tag	UNP A4W515
C	-4	MET	-	expression tag	UNP A4W515
C	-3	GLY	-	expression tag	UNP A4W515
C	-2	ARG	-	expression tag	UNP A4W515
C	-1	GLY	-	expression tag	UNP A4W515
C	0	SER	-	expression tag	UNP A4W515
D	-16	GLY	-	expression tag	UNP A4W515
D	-15	SER	-	expression tag	UNP A4W515
D	-14	HIS	-	expression tag	UNP A4W515
D	-13	MET	-	expression tag	UNP A4W515
D	-12	ALA	-	expression tag	UNP A4W515
D	-11	SER	-	expression tag	UNP A4W515
D	-10	MET	-	expression tag	UNP A4W515
D	-9	THR	-	expression tag	UNP A4W515

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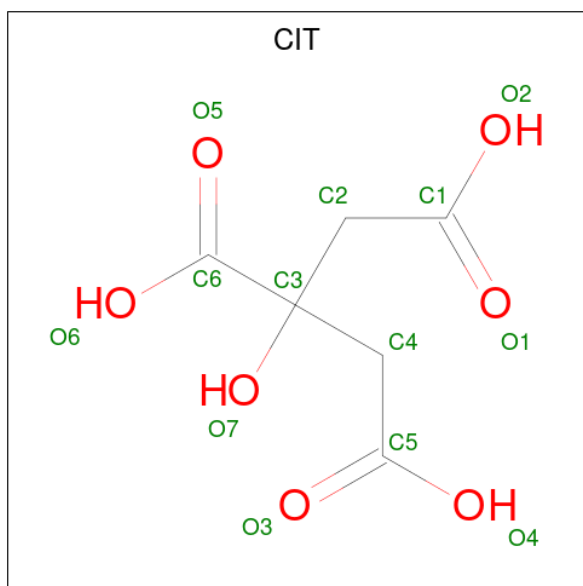
Chain	Residue	Modelled	Actual	Comment	Reference
D	-8	GLY	-	expression tag	UNP A4W515
D	-7	GLY	-	expression tag	UNP A4W515
D	-6	GLN	-	expression tag	UNP A4W515
D	-5	GLN	-	expression tag	UNP A4W515
D	-4	MET	-	expression tag	UNP A4W515
D	-3	GLY	-	expression tag	UNP A4W515
D	-2	ARG	-	expression tag	UNP A4W515
D	-1	GLY	-	expression tag	UNP A4W515
D	0	SER	-	expression tag	UNP A4W515
E	-16	GLY	-	expression tag	UNP A4W515
E	-15	SER	-	expression tag	UNP A4W515
E	-14	HIS	-	expression tag	UNP A4W515
E	-13	MET	-	expression tag	UNP A4W515
E	-12	ALA	-	expression tag	UNP A4W515
E	-11	SER	-	expression tag	UNP A4W515
E	-10	MET	-	expression tag	UNP A4W515
E	-9	THR	-	expression tag	UNP A4W515
E	-8	GLY	-	expression tag	UNP A4W515
E	-7	GLY	-	expression tag	UNP A4W515
E	-6	GLN	-	expression tag	UNP A4W515
E	-5	GLN	-	expression tag	UNP A4W515
E	-4	MET	-	expression tag	UNP A4W515
E	-3	GLY	-	expression tag	UNP A4W515
E	-2	ARG	-	expression tag	UNP A4W515
E	-1	GLY	-	expression tag	UNP A4W515
E	0	SER	-	expression tag	UNP A4W515
F	-16	GLY	-	expression tag	UNP A4W515
F	-15	SER	-	expression tag	UNP A4W515
F	-14	HIS	-	expression tag	UNP A4W515
F	-13	MET	-	expression tag	UNP A4W515
F	-12	ALA	-	expression tag	UNP A4W515
F	-11	SER	-	expression tag	UNP A4W515
F	-10	MET	-	expression tag	UNP A4W515
F	-9	THR	-	expression tag	UNP A4W515
F	-8	GLY	-	expression tag	UNP A4W515
F	-7	GLY	-	expression tag	UNP A4W515
F	-6	GLN	-	expression tag	UNP A4W515
F	-5	GLN	-	expression tag	UNP A4W515
F	-4	MET	-	expression tag	UNP A4W515
F	-3	GLY	-	expression tag	UNP A4W515
F	-2	ARG	-	expression tag	UNP A4W515
F	-1	GLY	-	expression tag	UNP A4W515

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Chain	Residue	Modelled	Actual	Comment	Reference
F	0	SER	-	expression tag	UNP A4W515

- Molecule 2 is CITRIC ACID (CCD ID: CIT) (formula: $C_6H_8O_7$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			13	6	7		
2	B	1	Total	C	O	0	0
			13	6	7		
2	C	1	Total	C	O	0	0
			13	6	7		
2	D	1	Total	C	O	0	0
			13	6	7		
2	E	1	Total	C	O	0	0
			13	6	7		
2	F	1	Total	C	O	0	0
			13	6	7		

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



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

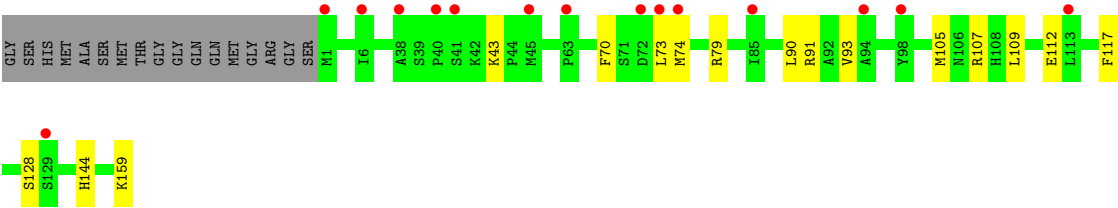
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	88	Total	O	0	0
			88	88		
4	B	119	Total	O	0	0
			119	119		
4	C	74	Total	O	0	0
			74	74		
4	D	115	Total	O	0	0
			115	115		
4	E	33	Total	O	0	0
			33	33		
4	F	27	Total	O	0	0
			27	27		

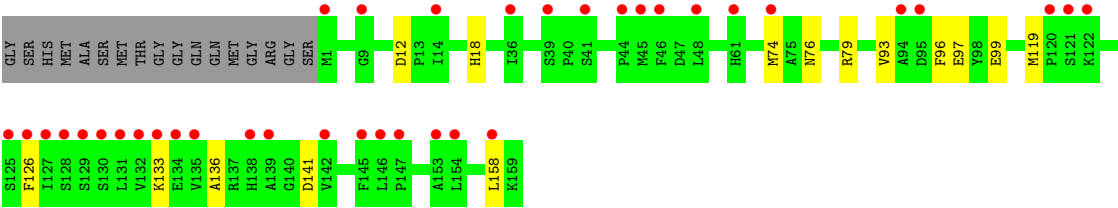
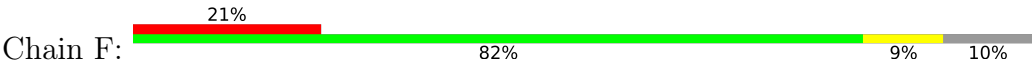
i

- Molecule 1: Phosphopantetheine adenylyltransferase





● Molecule 1: Phosphopantetheine adenylyltransferase



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	138.27Å 79.85Å 107.54Å 90.00° 93.35° 90.00°	Depositor
Resolution (Å)	59.74 – 2.60 59.74 – 2.60	Depositor EDS
% Data completeness (in resolution range)	97.8 (59.74-2.60) 97.8 (59.74-2.60)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.29 (at 2.61Å)	Xtriage
Refinement program	REFMAC 5.8.0425	Depositor
R, R_{free}	0.227 , 0.270 0.234 , 0.270	Depositor DCC
R_{free} test set	699 reflections (1.93%)	wwPDB-VP
Wilson B-factor (Å ²)	46.4	Xtriage
Anisotropy	0.110	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 35.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.005 for 1/2*h+3/2*k,1/2*h-1/2*k,-l 0.008 for 1/2*h-3/2*k,-1/2*h-1/2*k,-l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	8271	wwPDB-VP
Average B, all atoms (Å ²)	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.95% 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: CIT, GOL

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	0.58	0/1273	1.04	2/1722 (0.1%)
1	B	0.59	0/1395	1.04	2/1881 (0.1%)
1	C	0.58	0/1273	1.04	2/1722 (0.1%)
1	D	0.60	0/1387	1.04	1/1871 (0.1%)
1	E	0.55	0/1289	1.02	2/1743 (0.1%)
1	F	0.57	0/1284	1.10	1/1736 (0.1%)
All	All	0.58	0/7901	1.05	10/10675 (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	A	0	1
1	C	0	2
1	E	0	3
All	All	0	6

There are no bond length outliers.

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	47	ASP	CA-CB-CG	6.35	118.95	112.60
1	B	47	ASP	CA-CB-CG	6.04	118.64	112.60
1	A	72	ASP	CA-CB-CG	5.87	118.47	112.60
1	A	47	ASP	CA-CB-CG	5.85	118.45	112.60
1	C	47	ASP	CA-CB-CG	5.81	118.41	112.60

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	79	ARG	Sidechain
1	C	79	ARG	Sidechain
1	C	88	ARG	Sidechain
1	E	79	ARG	Sidechain
1	E	91	ARG	Sidechain

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	1246	0	1260	16	0
1	B	1367	0	1373	15	0
1	C	1246	0	1260	14	0
1	D	1359	0	1365	16	0
1	E	1256	0	1278	16	0
1	F	1257	0	1272	16	0
2	A	13	0	5	0	0
2	B	13	0	5	2	0
2	C	13	0	5	1	0
2	D	13	0	5	0	0
2	E	13	0	5	1	0
2	F	13	0	5	2	0
3	D	6	0	8	0	0
4	A	88	0	0	1	0
4	B	119	0	0	4	0
4	C	74	0	0	3	0
4	D	115	0	0	4	0
4	E	33	0	0	2	0
4	F	27	0	0	3	0
All	All	8271	0	7846	69	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.

The worst 5 of 69 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:F:79[B]:ARG:NH1	4:F:301:HOH:O	2.12	0.81
1:F:12:ASP:O	1:F:133:LYS:NZ	2.19	0.76
1:C:18:HIS:HE2	2:C:201:CIT:H21	1.53	0.73
1:B:18:HIS:HE2	2:B:201:CIT:H41	1.56	0.70
1:E:93:VAL:HG13	1:F:93:VAL:HG13	1.72	0.70

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	157/176 (89%)	156 (99%)	1 (1%)	0	100	100
1	B	175/176 (99%)	173 (99%)	2 (1%)	0	100	100
1	C	157/176 (89%)	156 (99%)	1 (1%)	0	100	100
1	D	174/176 (99%)	169 (97%)	4 (2%)	1 (1%)	21	42
1	E	159/176 (90%)	158 (99%)	1 (1%)	0	100	100
1	F	158/176 (90%)	154 (98%)	4 (2%)	0	100	100
All	All	980/1056 (93%)	966 (99%)	13 (1%)	1 (0%)	48	70

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	-15	SER

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	134/145 (92%)	134 (100%)	0	100	100
1	B	146/145 (101%)	145 (99%)	1 (1%)	76	89
1	C	134/145 (92%)	134 (100%)	0	100	100
1	D	145/145 (100%)	145 (100%)	0	100	100
1	E	136/145 (94%)	136 (100%)	0	100	100
1	F	135/145 (93%)	135 (100%)	0	100	100
All	All	830/870 (95%)	829 (100%)	1 (0%)	88	96

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	-13	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	138	HIS
1	F	101	GLN
1	F	104	HIS
1	B	138	HIS
1	B	-6	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

7 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	CIT	B	201	-	12,12,12	1.18	1 (8%)	17,17,17	1.13	2 (11%)
2	CIT	F	201	-	12,12,12	1.16	1 (8%)	17,17,17	1.24	3 (17%)
2	CIT	C	201	-	12,12,12	1.17	0	17,17,17	1.11	2 (11%)
3	GOL	D	202	-	5,5,5	0.11	0	5,5,5	0.30	0
2	CIT	E	201	-	12,12,12	1.19	0	17,17,17	1.06	2 (11%)
2	CIT	A	201	-	12,12,12	1.08	0	17,17,17	1.14	2 (11%)
2	CIT	D	201	-	12,12,12	1.13	0	17,17,17	1.20	3 (17%)

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	CIT	B	201	-	-	11/16/16/16	-
2	CIT	F	201	-	-	5/16/16/16	-
2	CIT	C	201	-	-	3/16/16/16	-
3	GOL	D	202	-	-	2/4/4/4	-
2	CIT	E	201	-	-	6/16/16/16	-
2	CIT	A	201	-	-	9/16/16/16	-
2	CIT	D	201	-	-	8/16/16/16	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	201	CIT	C3-C6	2.04	1.55	1.53
2	B	201	CIT	O2-C1	-2.04	1.24	1.30

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	201	CIT	O5-C6-C3	-2.66	116.94	122.09
2	F	201	CIT	O5-C6-C3	-2.63	116.99	122.09
2	B	201	CIT	O5-C6-C3	-2.58	117.09	122.09
2	F	201	CIT	O6-C6-C3	2.41	117.77	113.14
2	A	201	CIT	O6-C6-C3	2.38	117.71	113.14

There are no chirality outliers.

5 of 44 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	201	CIT	C2-C3-C4-C5
2	A	201	CIT	O7-C3-C4-C5
2	A	201	CIT	C6-C3-C4-C5
2	A	201	CIT	O7-C3-C6-O5
2	A	201	CIT	O7-C3-C6-O6

There are no ring outliers.

4 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	201	CIT	2	0
2	F	201	CIT	2	0
2	C	201	CIT	1	0
2	E	201	CIT	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 [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	159/176 (90%)	0.52	10 (6%) 26 20	30, 47, 89, 116	0
1	B	176/176 (100%)	0.39	8 (4%) 38 32	25, 46, 85, 116	1 (0%)
1	C	159/176 (90%)	0.47	7 (4%) 39 33	30, 48, 85, 112	0
1	D	176/176 (100%)	0.31	5 (2%) 55 49	27, 44, 83, 126	0
1	E	159/176 (90%)	1.01	15 (9%) 14 11	37, 74, 110, 139	2 (1%)
1	F	159/176 (90%)	1.49	37 (23%) 2 1	32, 91, 134, 146	1 (0%)
All	All	988/1056 (93%)	0.69	82 (8%) 17 13	25, 58, 115, 146	4 (0%)

The worst 5 of 82 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	130	SER	4.6
1	F	131	LEU	4.1
1	F	127	ILE	4.1
1	F	146	LEU	3.8
1	E	74	MET	3.7

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(Å ²)	Q<0.9
2	CIT	E	201	13/13	0.61	0.14	86,96,107,108	0
2	CIT	F	201	13/13	0.61	0.13	98,113,121,129	0
2	CIT	B	201	13/13	0.72	0.17	57,73,77,83	0
2	CIT	C	201	13/13	0.72	0.12	68,81,92,94	0
2	CIT	D	201	13/13	0.84	0.12	45,63,77,79	0
2	CIT	A	201	13/13	0.86	0.11	57,67,82,86	0
3	GOL	D	202	6/6	0.86	0.18	69,76,77,78	0

6.5 Other polymers [i](#)

There are no such residues in this entry.