



# wwPDB X-ray Structure Validation Summary Report ⓘ

May 15, 2020 – 10:02 pm BST

PDB ID : 1RYZ  
Title : Uridine Phosphorylase from Salmonella typhimurium. Crystal Structure at 2.9 Å Resolution  
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Deposited on : 2003-12-23  
Resolution : 2.90 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](mailto: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.

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

MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

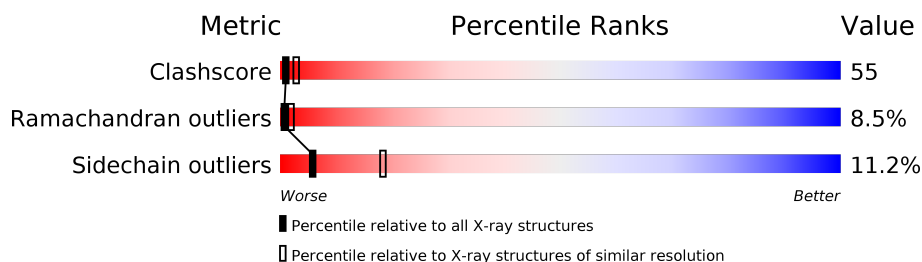
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.90 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))
Clashscore	141614	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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  $\leq 5\%$ .

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	253	
1	B	253	
1	C	253	
1	D	253	
1	E	253	
1	F	253	

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
2	ACY	B	254	-	-	X	-

## 2 Entry composition [i](#)

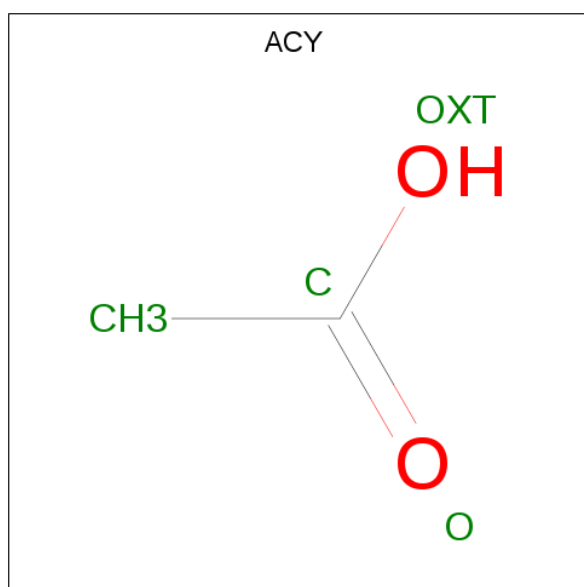
There are 2 unique types of molecules in this entry. The entry contains 11270 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Uridine phosphorylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	250	Total	C	N	O	S	0	0	0
			1877	1174	330	361	12			
1	B	250	Total	C	N	O	S	0	0	0
			1877	1174	330	361	12			
1	C	250	Total	C	N	O	S	0	0	0
			1877	1174	330	361	12			
1	D	250	Total	C	N	O	S	0	0	0
			1877	1174	330	361	12			
1	E	250	Total	C	N	O	S	0	0	0
			1877	1174	330	361	12			
1	F	250	Total	C	N	O	S	0	0	0
			1877	1174	330	361	12			

- Molecule 2 is ACETIC ACID (three-letter code: ACY) (formula: C<sub>2</sub>H<sub>4</sub>O<sub>2</sub>).



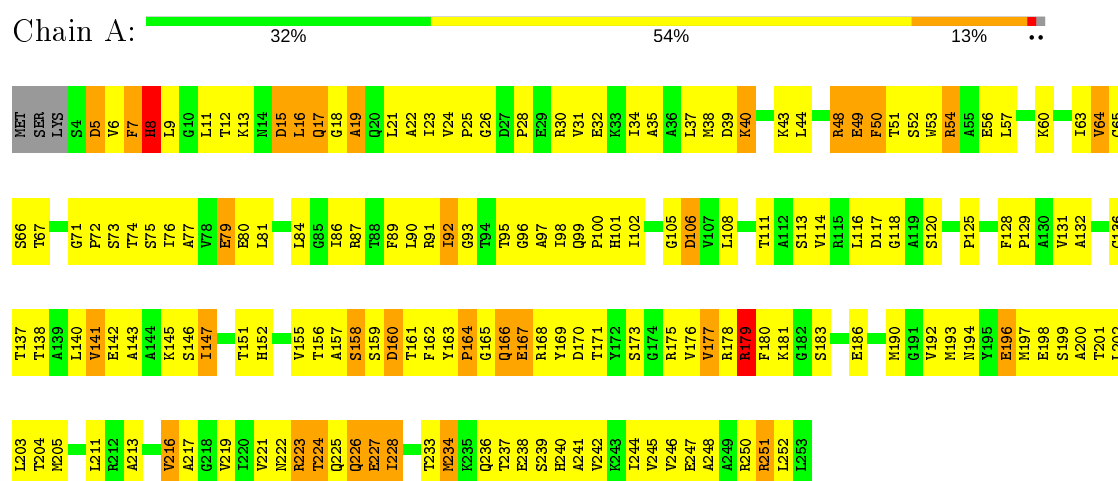
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total	C	O	0	0
			4	2	2		
2	B	1	Total	C	O	0	0
			4	2	2		

### 3 Residue-property plots

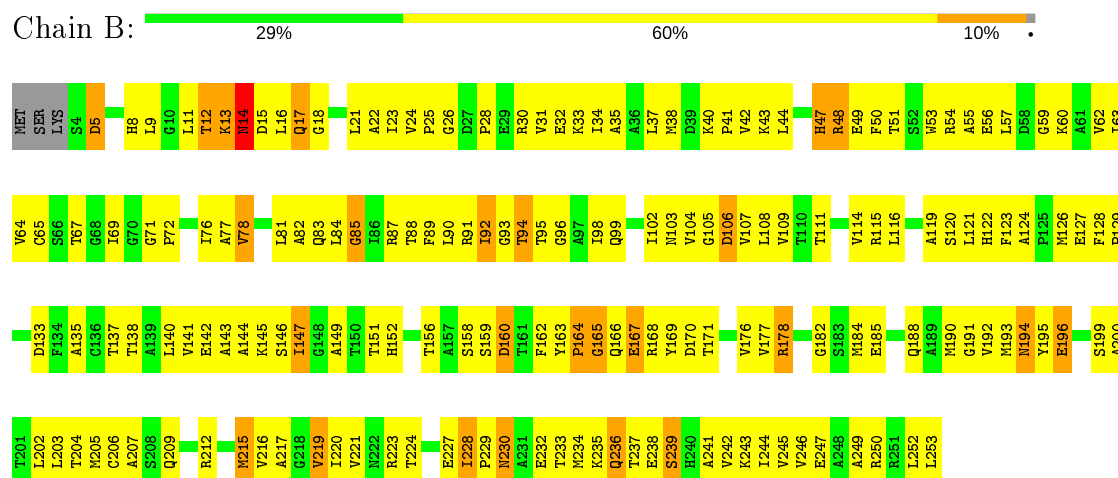
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

Note EDS was not executed.

- Molecule 1: Uridine phosphorylase

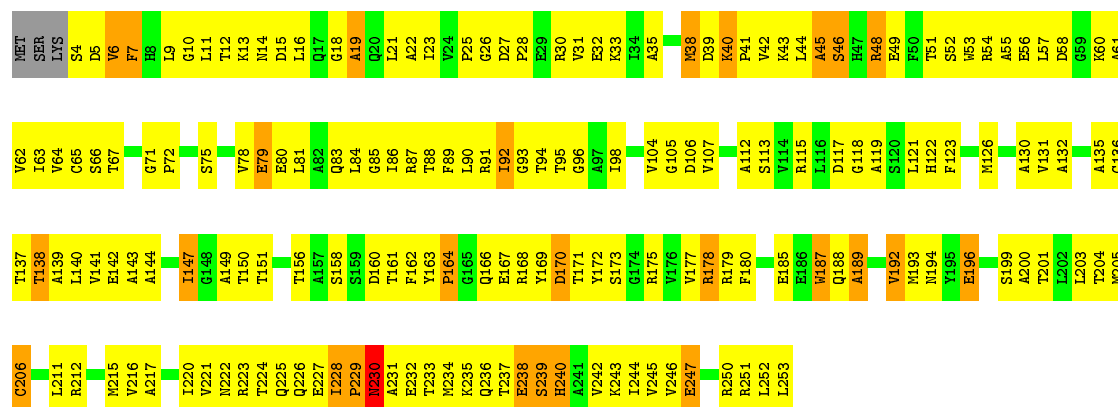


- Molecule 1: Uridine phosphorylase

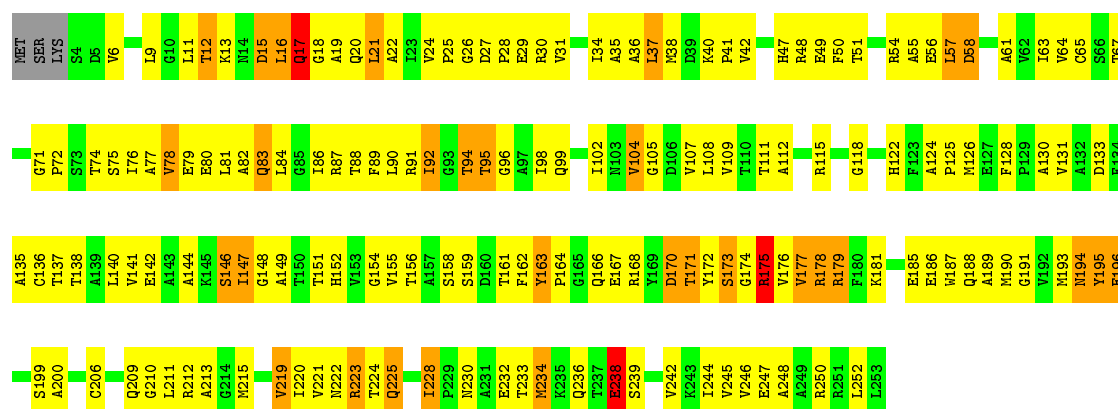


- Molecule 1: Uridine phosphorylase

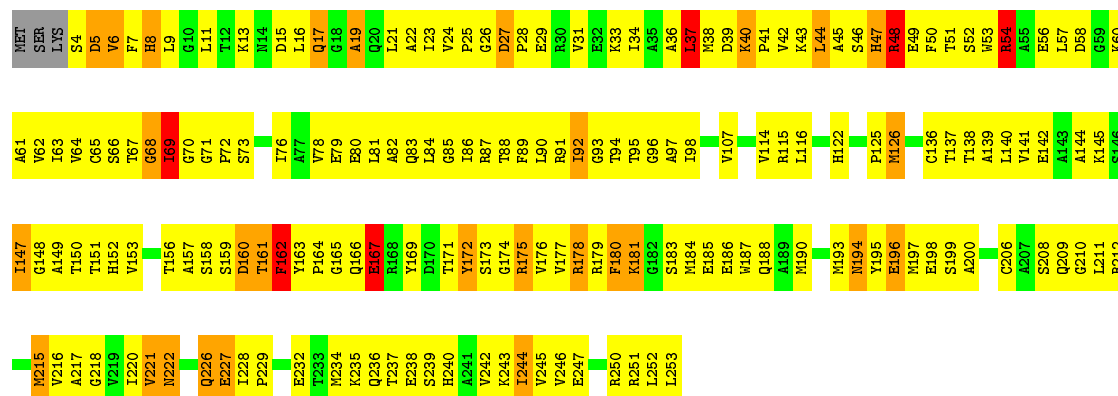




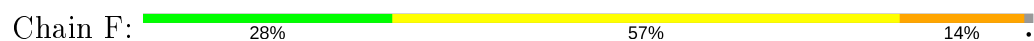
• Molecule 1: Uridine phosphorylase



• Molecule 1: Uridine phosphorylase



• Molecule 1: Uridine phosphorylase



A200	T201	L202	L203	T204	M205	Q209	R212	M215	V216	A217	I220	V221	N222	R223	E227	I228	P229	N230	A231	E232	T233	M234	K235	Q236	T237	E238	S239	H240	A241	V242	K243	I244	E247	A248	A249	R250	R251	L252	L253																	
Met	Ser	Lys	S4	D6	V6	F7	H8	L9	G10	L11	T12	D15	L16	Q17	L21	A22	I23	V24	P25	G26	D27	P28	E29	R30	V31	E32	K33	I34	A35	A36	L37	M38	D39	L44	R48	E49	F50	T51	S52	N53	R54	A55	E56	L57	D58	G59	K60	A61	V62	I63	V64	G65	S66	G71		
P72	T138	A139	L140	V141	A143	A144	K145	S146	G148	A149	T150	T151	H152	V153	G154	V155	T156	A157	S158	S159	D160	T161	F162	Y163	P164	G165	Q166	E167	R168	Y169	D170	T171	Y172	S173	G174	R175	V176	V177	R178	R179	F180	S183	M184	E185	E186	K187	Q188	V192	M193	N194	Y195	E196	M197	E198	S199	
S75	I76	A77	V78	E79	E80	L81	A82	Q83	L84	G85	I86	R87	T88	F89	L90	R91	I92	G93	T94	T95	G96	A97	I98	Q99	P100	H101	I102	N103	V104	G105	D106	V107	L108	V109	T110	T111	A112	S113	V114	R115	L116	D117	G118	A119	S120	F123	A124	P125	M126	E127	F128	P129	A130	V131	A132	D133



## 4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 61	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	92.26 Å 92.26 Å 267.46 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	29.46 – 2.90	Depositor
% Data completeness (in resolution range)	93.9 (29.46-2.90)	Depositor
$R_{merge}$	0.15	Depositor
$R_{sym}$	0.18	Depositor
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.212 , 0.284	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	11270	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	18.0	wwPDB-VP

## 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: ACY

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	0.42	0/1907	0.74	0/2584
1	B	0.40	0/1907	0.72	0/2584
1	C	0.41	0/1907	0.70	0/2584
1	D	0.40	0/1907	0.67	0/2584
1	E	0.41	0/1907	0.74	2/2584 (0.1%)
1	F	0.40	0/1907	0.73	0/2584
All	All	0.41	0/11442	0.72	2/15504 (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	6	VAL	N-CA-C	-6.19	94.29	111.00
1	E	47	HIS	N-CA-C	5.18	124.98	111.00

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	1877	0	1887	184	0
1	B	1877	0	1887	230	0
1	C	1877	0	1887	195	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	1877	0	1887	202	0
1	E	1877	0	1887	251	0
1	F	1877	0	1887	239	0
2	B	8	0	6	5	0
All	All	11270	0	11328	1237	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 55.

The worst 5 of 1237 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:232:GLU:HG2	1:B:236:GLN:HB2	1.27	1.16
1:E:167:GLU:HG3	1:E:183:SER:H	1.15	1.10
1:C:228:ILE:HB	1:C:229:PRO:HD2	1.37	1.06
1:C:104:VAL:HG11	1:C:229:PRO:HB3	1.34	1.06
1:E:22:ALA:HB2	1:E:86:ILE:HD13	1.36	1.05

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	248/253 (98%)	172 (69%)	53 (21%)	23 (9%)	0	1
1	B	248/253 (98%)	174 (70%)	55 (22%)	19 (8%)	1	2
1	C	248/253 (98%)	186 (75%)	40 (16%)	22 (9%)	1	1
1	D	248/253 (98%)	174 (70%)	58 (23%)	16 (6%)	1	3
1	E	248/253 (98%)	166 (67%)	57 (23%)	25 (10%)	0	1
1	F	248/253 (98%)	168 (68%)	59 (24%)	21 (8%)	1	2

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	1488/1518 (98%)	1040 (70%)	322 (22%)	126 (8%)	1	2

5 of 126 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	7	PHE
1	A	17	GLN
1	A	26	GLY
1	A	167	GLU
1	A	223	ARG

### 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	199/202 (98%)	176 (88%)	23 (12%)	5	16
1	B	199/202 (98%)	183 (92%)	16 (8%)	12	33
1	C	199/202 (98%)	181 (91%)	18 (9%)	9	29
1	D	199/202 (98%)	170 (85%)	29 (15%)	3	9
1	E	199/202 (98%)	174 (87%)	25 (13%)	4	13
1	F	199/202 (98%)	176 (88%)	23 (12%)	5	16
All	All	1194/1212 (98%)	1060 (89%)	134 (11%)	6	18

5 of 134 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	17	GLN
1	D	185	GLU
1	F	162	PHE
1	D	29	GLU
1	D	95	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 40 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	225	GLN
1	D	194	ASN
1	F	194	ASN
1	D	17	GLN
1	D	209	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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

2 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	ACY	B	255	-	1,3,3	3.09	1 (100%)	0,3,3	0.00	-
2	ACY	B	254	-	1,3,3	1.72	0	0,3,3	0.00	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	255	ACY	CH3-C	3.09	1.52	1.48

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	254	ACY	5	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 ⓘ

EDS was not executed - this section is therefore empty.

### 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

EDS was not executed - this section is therefore empty.

### 6.3 Carbohydrates ⓘ

EDS was not executed - this section is therefore empty.

### 6.4 Ligands ⓘ

EDS was not executed - this section is therefore empty.

### 6.5 Other polymers ⓘ

EDS was not executed - this section is therefore empty.