



wwPDB X-ray Structure Validation Summary Report ⓘ

May 25, 2020 – 10:25 am BST

PDB ID : 3DDO
Title : X-RAY Structure of the Uridine Phosphorylase from Salmonella Typhimurium
in Complex with by Phosphate Ion at 1.5A Resolution
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Deposited on : 2008-06-06
Resolution : 1.50 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 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) : 1.13
EDS : 2.11
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

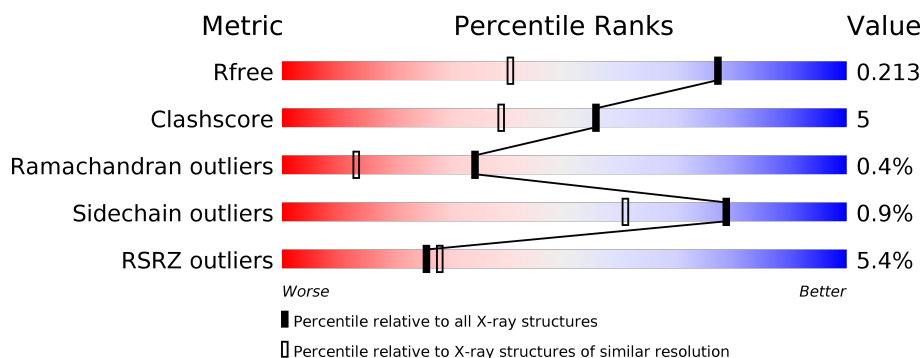
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.50 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}	130704	2936 (1.50-1.50)
Clashscore	141614	3144 (1.50-1.50)
Ramachandran outliers	138981	3066 (1.50-1.50)
Sidechain outliers	138945	3064 (1.50-1.50)
RSRZ outliers	127900	2884 (1.50-1.50)

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 ≥ 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	253	
1	B	253	
1	C	253	
1	D	253	
1	E	253	
1	F	253	

2 Entry composition [i](#)

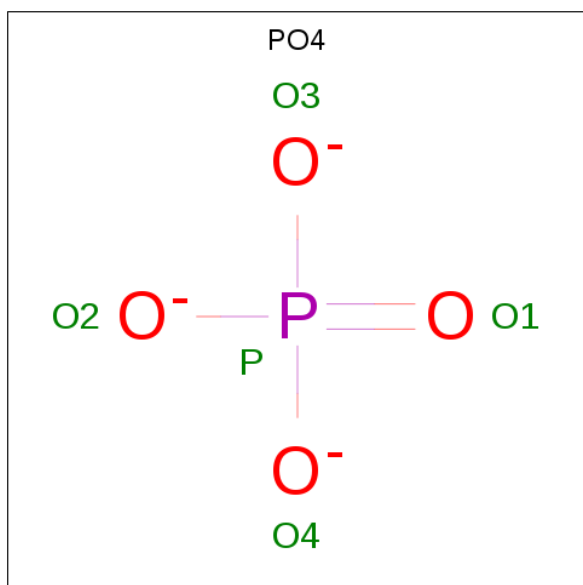
There are 3 unique types of molecules in this entry. The entry contains 12812 atoms, of which 0 are hydrogens and 0 are deuteriums.

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	240	Total	C	N	O	S	0	7	0
			1825	1150	320	344	11			
1	B	244	Total	C	N	O	S	0	3	0
			1848	1162	326	349	11			
1	C	249	Total	C	N	O	S	0	6	0
			1912	1195	343	362	12			
1	D	251	Total	C	N	O	S	0	2	0
			1895	1187	334	362	12			
1	E	242	Total	C	N	O	S	0	3	0
			1832	1151	321	349	11			
1	F	243	Total	C	N	O	S	0	2	0
			1831	1150	324	346	11			

- Molecule 2 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).

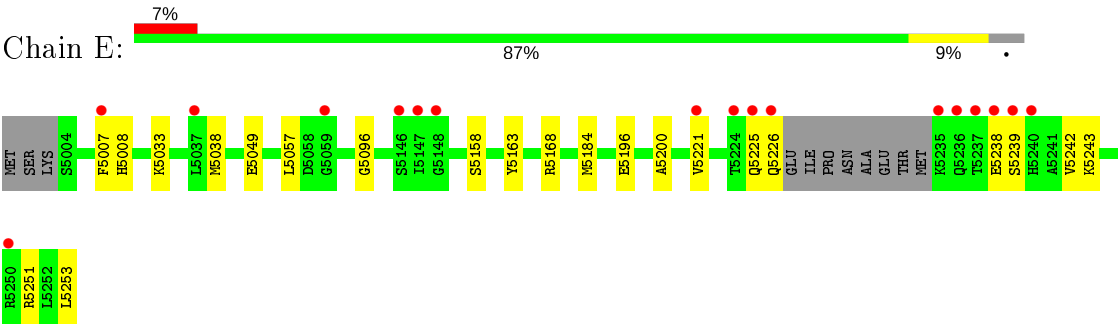


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total O P 5 4 1	0	0
2	B	1	Total O P 5 4 1	0	0
2	C	1	Total O P 5 4 1	0	0
2	D	1	Total O P 5 4 1	0	0
2	F	1	Total O P 5 4 1	0	0

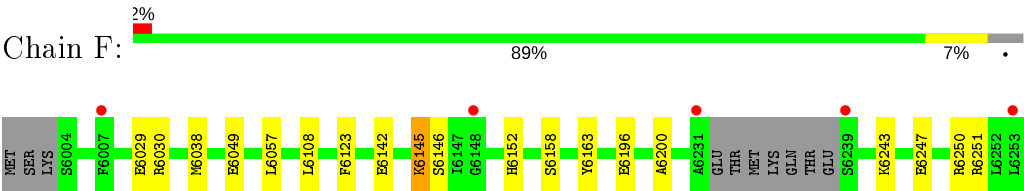
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	263	Total O 263 263	0	0
3	B	251	Total O 251 251	0	0
3	C	277	Total O 277 277	0	0
3	D	305	Total O 305 305	0	0
3	E	250	Total O 250 250	0	0
3	F	298	Total O 298 298	0	0

● Molecule 1: Uridine phosphorylase



● Molecule 1: Uridine phosphorylase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	89.60Å 124.92Å 134.93Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.91 – 1.50 42.17 – 1.50	Depositor EDS
% Data completeness (in resolution range)	98.1 (19.91-1.50) 98.2 (42.17-1.50)	Depositor EDS
R_{merge}	0.21	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.45 (at 1.50Å)	Xtriage
Refinement program	PHENIX (phenix.refine)	Depositor
R, R_{free}	0.166 , 0.212 0.167 , 0.213	Depositor DCC
R_{free} test set	11848 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	13.7	Xtriage
Anisotropy	0.228	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 52.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	12812	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 4.03% 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: PO4

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	0.34	0/1874	0.54	0/2539
1	B	0.35	0/1886	0.54	0/2554
1	C	0.35	0/1952	0.55	0/2638
1	D	0.36	0/1932	0.54	0/2618
1	E	0.34	0/1870	0.51	0/2532
1	F	0.36	0/1866	0.53	0/2530
All	All	0.35	0/11380	0.53	0/15411

There are no bond length outliers.

There are no bond angle outliers.

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	1825	0	1857	22	0
1	B	1848	0	1880	15	0
1	C	1912	0	1943	36	0
1	D	1895	0	1912	14	0
1	E	1832	0	1849	14	0
1	F	1831	0	1854	17	0
2	A	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	5	0	0	0	0
2	C	5	0	0	0	0
2	D	5	0	0	0	0
2	F	5	0	0	0	0
3	A	263	0	0	4	0
3	B	251	0	0	2	0
3	C	277	0	0	9	0
3	D	305	0	0	5	0
3	E	250	0	0	4	0
3	F	298	0	0	5	0
All	All	12812	0	11295	114	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 5.

The worst 5 of 114 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:6247:GLU:HG3	1:F:6251:ARG:HH12	1.30	0.96
1:B:2060[A]:LYS:HD2	1:B:2253:LEU:HD22	1.53	0.89
1:F:6247:GLU:HG3	1:F:6251:ARG:NH1	1.87	0.89
1:D:4039:ASP:HB3	3:D:1119:HOH:O	1.71	0.88
1:C:3003:LYS:H	1:C:3003:LYS:HD3	1.41	0.84

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	241/253 (95%)	238 (99%)	2 (1%)	1 (0%)	34 13
1	B	243/253 (96%)	239 (98%)	3 (1%)	1 (0%)	34 13

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	251/253 (99%)	247 (98%)	3 (1%)	1 (0%)	34	13
1	D	251/253 (99%)	246 (98%)	4 (2%)	1 (0%)	34	13
1	E	241/253 (95%)	238 (99%)	2 (1%)	1 (0%)	34	13
1	F	241/253 (95%)	239 (99%)	1 (0%)	1 (0%)	34	13
All	All	1468/1518 (97%)	1447 (99%)	15 (1%)	6 (0%)	34	13

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	4163	TYR
1	A	1163	TYR
1	B	2163	TYR
1	C	3163	TYR
1	E	5163	TYR

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	196/202 (97%)	194 (99%)	2 (1%)	76	57
1	B	197/202 (98%)	195 (99%)	2 (1%)	76	57
1	C	204/202 (101%)	202 (99%)	2 (1%)	76	57
1	D	202/202 (100%)	200 (99%)	2 (1%)	76	57
1	E	195/202 (96%)	194 (100%)	1 (0%)	88	78
1	F	194/202 (96%)	192 (99%)	2 (1%)	76	57
All	All	1188/1212 (98%)	1177 (99%)	11 (1%)	78	61

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	3003	LYS
1	C	3196	GLU

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Mol	Chain	Res	Type
1	E	5196	GLU
1	B	2237	THR
1	D	4215	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	2209	GLN
1	C	3230	ASN
1	C	3236	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](#)

5 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	PO4	C	5	-	4,4,4	0.85	0	6,6,6	0.38	0
2	PO4	A	4	-	4,4,4	0.89	0	6,6,6	0.32	0
2	PO4	B	2	-	4,4,4	0.89	0	6,6,6	0.46	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	PO4	D	3	-	4,4,4	1.01	0	6,6,6	0.70	0
2	PO4	F	1	-	4,4,4	0.97	0	6,6,6	0.28	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

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 [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	240/253 (94%)	0.34	19 (7%) 12 13	10, 17, 45, 69	0
1	B	244/253 (96%)	0.10	5 (2%) 65 70	8, 15, 35, 70	0
1	C	249/253 (98%)	0.26	17 (6%) 17 18	8, 14, 44, 65	0
1	D	251/253 (99%)	0.14	16 (6%) 19 20	8, 13, 44, 75	0
1	E	242/253 (95%)	0.32	17 (7%) 16 17	10, 19, 43, 71	0
1	F	243/253 (96%)	0.00	5 (2%) 63 68	8, 14, 34, 51	0
All	All	1469/1518 (96%)	0.19	79 (5%) 25 28	8, 15, 41, 75	0

The worst 5 of 79 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	5226	GLN	12.5
1	A	1237	THR	9.5
1	B	2237	THR	8.7
1	C	3233	THR	8.7
1	A	1236	GLN	8.7

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 carbohydrates 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(\AA^2)	Q<0.9
2	PO4	C	5	5/5	0.92	0.18	54,55,57,58	0
2	PO4	A	4	5/5	0.98	0.09	29,29,31,32	0
2	PO4	B	2	5/5	0.99	0.05	16,16,17,19	0
2	PO4	D	3	5/5	0.99	0.07	18,18,20,22	0
2	PO4	F	1	5/5	0.99	0.06	15,15,15,16	0

6.5 Other polymers [i](#)

There are no such residues in this entry.