wwPDB X-ray Structure Validation Summary Report (i)

Dec 6, 2023 – 04:04 am GMT

PDB ID	:	2VA1
Title	:	Crystal structure of UMP kinase from Ureaplasma parvum
Authors	:	Egeblad-Welin, L.; Welin, M.; Wang, L.; Eriksson, S.
Deposited on	:	2007-08-28
Resolution	:	2.50 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 (i) 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 (i)) were used in the production of this report:

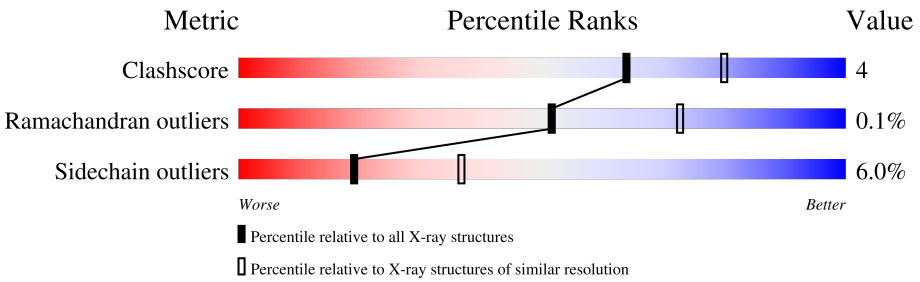
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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))
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)

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 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 <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	256	75% 11% • 12%
1	B	256	82% 9% • 8%
1	C	256	77% 11% • 11%
1	D	256	80% 7% • 11%
1	E	256	78% 12% • 8%
1	F	256	77% 8% • 12%

2 Entry composition (i)

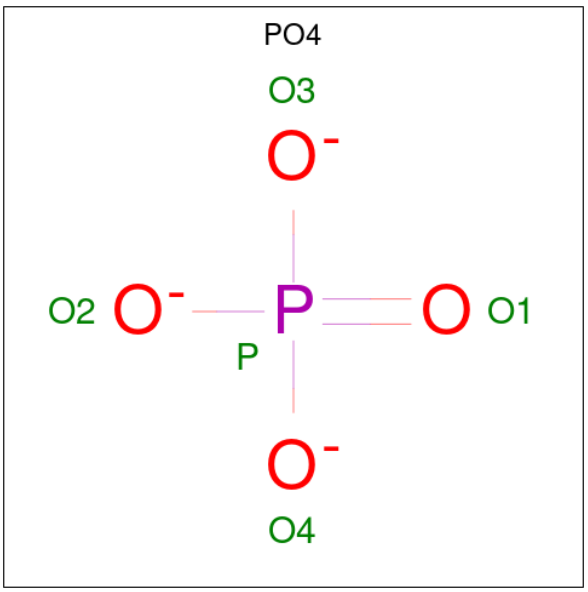
There are 3 unique types of molecules in this entry. The entry contains 10788 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 URIDYLATE KINASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	226	1743	1102	295	334	12	0	0	0
1	B	235	1798	1136	306	342	14	0	0	0
1	C	227	1746	1104	294	336	12	0	0	0
1	D	228	1757	1111	298	335	13	0	0	0
1	E	235	1812	1145	308	346	13	0	0	0
1	F	226	1744	1103	296	333	12	0	0	0

- Molecule 2 is PHOSPHATE ION (three-letter code: PO4) (formula: O_4P).



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

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	33	33	33	0	0
3	B	27	27	27	0	0
3	C	27	27	27	0	0
3	D	23	23	23	0	0
3	E	31	31	31	0	0
3	F	17	17	17	0	0

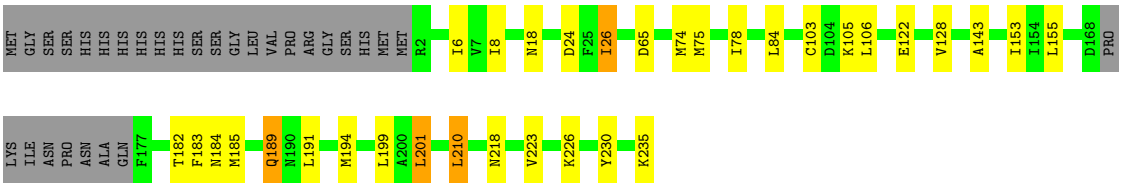
3 Residue-property plots (i)

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. 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.

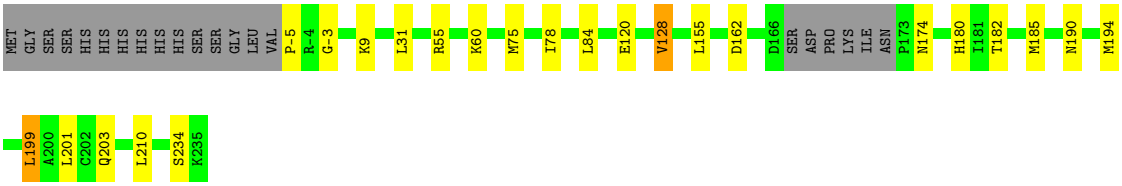
• Molecule 1: URIDYLATE KINASE

Chain A:



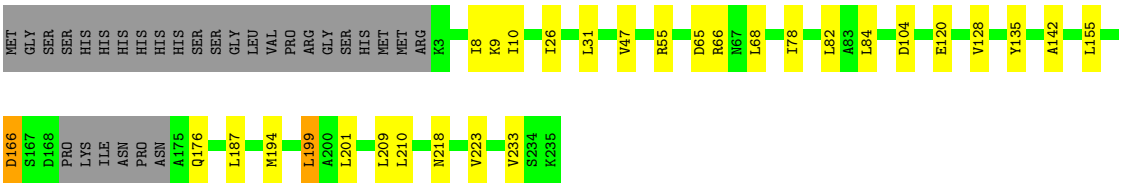
• Molecule 1: URIDYLATE KINASE

Chain B:



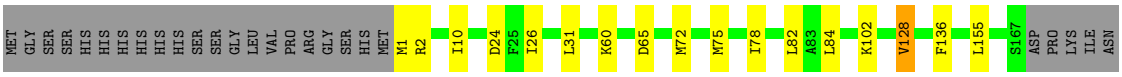
• Molecule 1: URIDYLATE KINASE

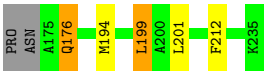
Chain C:



• Molecule 1: URIDYLATE KINASE

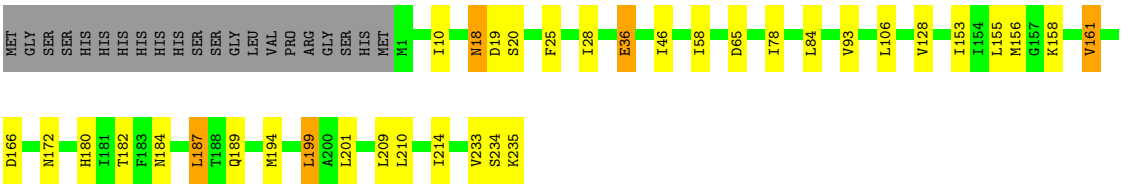
Chain D:





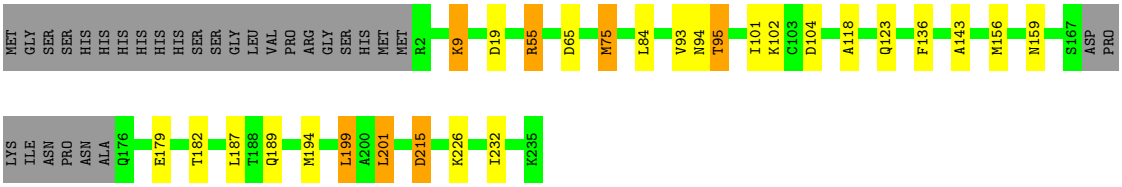
• Molecule 1: URIDYLATE KINASE

Chain E:



• Molecule 1: URIDYLATE KINASE

Chain F:



4 Data and refinement statistics (i)

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

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	79.75Å 96.55Å 96.27Å 90.00° 105.75° 90.00°	Depositor
Resolution (Å)	20.00 – 2.50	Depositor
% Data completeness (in resolution range)	99.9 (20.00-2.50)	Depositor
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.232 , 0.285	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	10788	wwPDB-VP
Average B, all atoms (Å^2)	34.0	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: 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	0.37	0/1760	0.52	0/2370
1	B	0.36	0/1816	0.56	1/2445 (0.0%)
1	C	0.36	0/1763	0.54	0/2375
1	D	0.37	0/1774	0.52	0/2388
1	E	0.36	0/1832	0.54	0/2470
1	F	0.37	0/1761	0.54	0/2371
All	All	0.37	0/10706	0.54	1/14419 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	-5	PRO	N-CA-CB	5.96	110.45	103.30

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	1743	0	1798	24	0
1	B	1798	0	1845	12	0
1	C	1746	0	1798	14	0
1	D	1757	0	1819	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	1812	0	1874	18	0
1	F	1744	0	1802	20	0
2	A	5	0	0	0	0
2	B	5	0	0	0	0
2	C	5	0	0	0	0
2	D	5	0	0	0	0
2	E	5	0	0	0	0
2	F	5	0	0	0	0
3	A	33	0	0	0	0
3	B	27	0	0	0	0
3	C	27	0	0	1	0
3	D	23	0	0	0	0
3	E	31	0	0	2	0
3	F	17	0	0	0	0
All	All	10788	0	10936	90	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 90 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:55:ARG:HH11	1:F:55:ARG:HG3	1.29	0.94
1:F:55:ARG:HH11	1:F:55:ARG:CG	2.03	0.72
1:B:194:MET:HE2	1:B:199:LEU:HD12	1.73	0.71
1:C:223:VAL:HG12	3:C:2026:HOH:O	1.94	0.68
1:D:194:MET:HB2	1:D:199:LEU:HD13	1.77	0.66

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	222/256 (87%)	213 (96%)	9 (4%)	0	100	100
1	B	231/256 (90%)	223 (96%)	7 (3%)	1 (0%)	34	54
1	C	223/256 (87%)	218 (98%)	5 (2%)	0	100	100
1	D	224/256 (88%)	218 (97%)	6 (3%)	0	100	100
1	E	233/256 (91%)	225 (97%)	8 (3%)	0	100	100
1	F	222/256 (87%)	218 (98%)	4 (2%)	0	100	100
All	All	1355/1536 (88%)	1315 (97%)	39 (3%)	1 (0%)	51	73

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	-3	GLY

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	194/220 (88%)	185 (95%)	9 (5%)	27	50
1	B	197/220 (90%)	184 (93%)	13 (7%)	16	32
1	C	194/220 (88%)	182 (94%)	12 (6%)	18	35
1	D	195/220 (89%)	185 (95%)	10 (5%)	24	45
1	E	202/220 (92%)	191 (95%)	11 (5%)	22	42
1	F	194/220 (88%)	178 (92%)	16 (8%)	11	22
All	All	1176/1320 (89%)	1105 (94%)	71 (6%)	19	37

5 of 71 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	75	MET
1	F	94	ASN
1	F	189	GLN
1	C	55	ARG

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Mol	Chain	Res	Type
1	C	26	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 37 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	176	GLN
1	F	123	GLN
1	E	180	HIS
1	F	86	ASN
1	B	174	ASN

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

6 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	E	1236	-	4,4,4	0.89	0	6,6,6	0.40	0
2	PO4	C	1236	-	4,4,4	0.94	0	6,6,6	0.54	0
2	PO4	D	1236	-	4,4,4	0.89	0	6,6,6	0.49	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	PO4	A	1236	-	4,4,4	0.95	0	6,6,6	0.48	0
2	PO4	B	1236	-	4,4,4	0.92	0	6,6,6	0.55	0
2	PO4	F	1236	-	4,4,4	0.95	0	6,6,6	0.40	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)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.