wwPDB X-ray Structure Validation Summary Report (i)

May 12, 2020 – 11:43 pm BST

PDB ID	:	4ANE
Title	:	R80N MUTANT OF NUCLEOSIDE DIPHOSPHATE KINASE FROM MYCOBACTERIUM TUBERCULOSIS
Authors	:	Georgescauld, F.; Moynie, L.; Habersetzer, J.; Lascu, I.; Dautant, A.
Deposited on	:	2012-03-16
Resolution	:	1.90 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*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

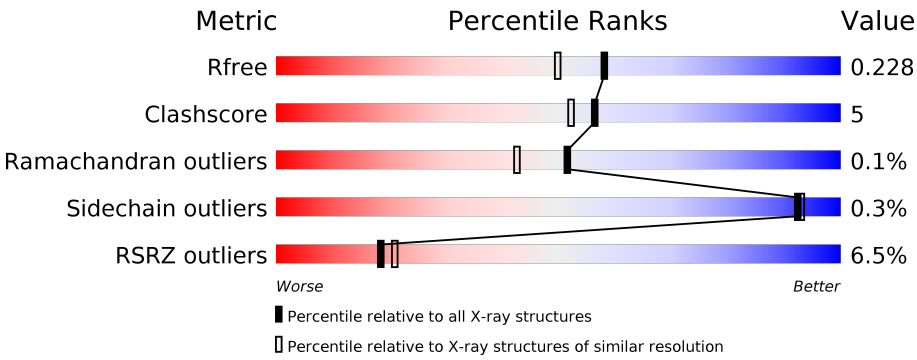
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 1.90 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))
R_{free}	130704	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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 >=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% 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	136	% 89% 10% •
1	B	136	9% 82% 14% • •
1	C	136	4% 89% 10% •
1	D	136	8% 84% 13% •
1	E	136	6% 86% 13% •
1	F	136	11% 78% 15% 7%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 6518 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.

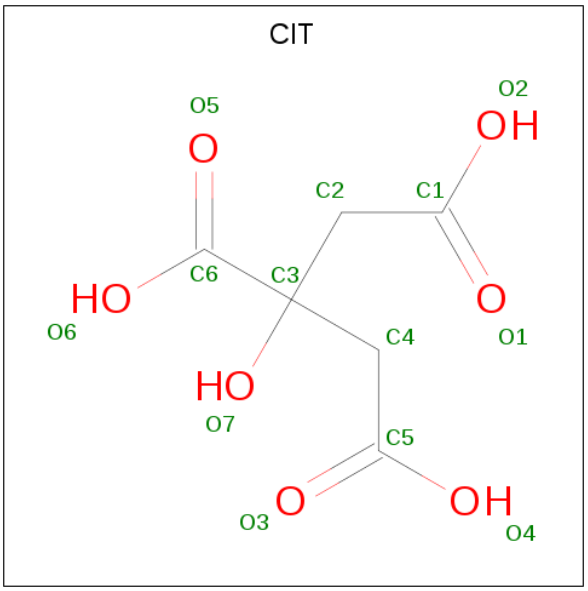
- Molecule 1 is a protein called NUCLEOSIDE DIPHOSPHATE KINASE.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
1	A	135	1042	660	187	195	0	4	0
1	B	132	999	632	177	190	0	3	0
1	C	135	1040	659	184	197	0	4	0
1	D	131	978	620	171	187	0	2	0
1	E	135	1021	645	181	195	0	1	0
1	F	127	951	599	170	182	0	1	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	80	ASN	ARG	engineered mutation	UNP P84284
B	80	ASN	ARG	engineered mutation	UNP P84284
C	80	ASN	ARG	engineered mutation	UNP P84284
D	80	ASN	ARG	engineered mutation	UNP P84284
E	80	ASN	ARG	engineered mutation	UNP P84284
F	80	ASN	ARG	engineered mutation	UNP P84284

- Molecule 2 is CITRIC ACID (three-letter code: CIT) (formula: $C_6H_8O_7$).



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

- Molecule 3 is water.

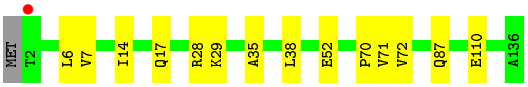
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	109	109	109	0	0
			Total	O		
3	B	69	69	69	0	0
			Total	O		
3	C	76	76	76	0	0
			Total	O		
3	D	74	74	74	0	0
			Total	O		
3	E	50	50	50	0	0
			Total	O		
3	F	70	70	70	0	0

3 Residue-property plots (i)

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 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.

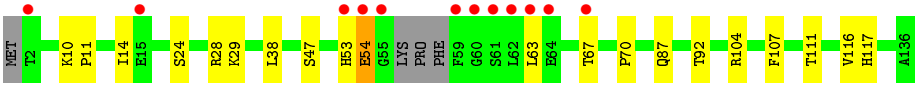
- Molecule 1: NUCLEOSIDE DIPHOSPHATE KINASE

Chain A:



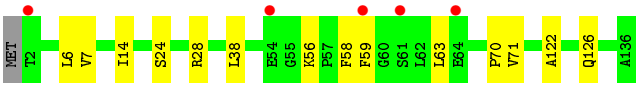
- Molecule 1: NUCLEOSIDE DIPHOSPHATE KINASE

Chain B:



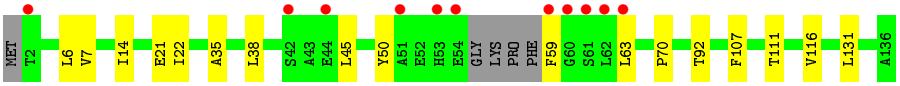
- Molecule 1: NUCLEOSIDE DIPHOSPHATE KINASE

Chain C:



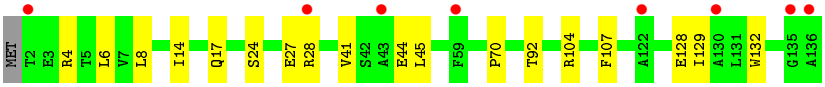
- Molecule 1: NUCLEOSIDE DIPHOSPHATE KINASE

Chain D:



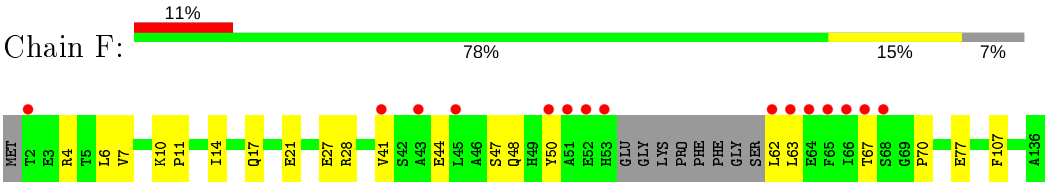
- Molecule 1: NUCLEOSIDE DIPHOSPHATE KINASE

Chain E:



- Molecule 1: NUCLEOSIDE DIPHOSPHATE KINASE

Chain F:


11%
78%
15%
7%
MET
T2
E3
R4
T5
L6
V7
K10
P11
I14
Q17
E21
E27
R28
V41
S42
A43
E44
L45
A46
S47
Q48
H49
Y50
A51
E52
H53
GLU
GLY
LYS
PRO
PHE
PHE
GLY
SER
L62
L63
E64
F65
I66
T67
S68
G69
P70
E77
F107
A136

4 Data and refinement statistics (i)

Property	Value	Source
Space group	I 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	68.82Å 113.34Å 107.56Å 90.00° 106.40° 90.00°	Depositor
Resolution (Å)	29.65 – 1.90 32.90 – 1.90	Depositor EDS
% Data completeness (in resolution range)	92.6 (29.65-1.90) 92.5 (32.90-1.90)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.44 (at 1.89Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.184 , 0.235 0.180 , 0.228	Depositor DCC
R_{free} test set	2926 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å^2)	21.1	Xtriage
Anisotropy	0.192	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 63.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	6518	wwPDB-VP
Average B, all atoms (Å^2)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.72% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: CIT

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	0.40	0/1071	0.58	0/1450
1	B	0.36	0/1022	0.56	0/1385
1	C	0.37	0/1069	0.55	0/1448
1	D	0.37	0/997	0.55	0/1353
1	E	0.35	0/1041	0.53	0/1411
1	F	0.36	0/966	0.54	0/1310
All	All	0.37	0/6166	0.55	0/8357

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	1042	0	1068	10	0
1	B	999	0	1017	14	0
1	C	1040	0	1061	9	0
1	D	978	0	992	10	0
1	E	1021	0	1031	10	0
1	F	951	0	966	14	0
2	A	13	0	5	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	13	0	4	0	0
2	F	13	0	6	0	0
3	A	109	0	0	2	0
3	B	69	0	0	0	0
3	C	76	0	0	0	0
3	D	74	0	0	0	0
3	E	50	0	0	0	0
3	F	70	0	0	0	0
All	All	6518	0	6150	61	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 61 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:122:ALA:O	1:C:126:GLN:HG2	1.84	0.78
1:A:38[A]:LEU:HD11	1:A:70:PRO:HB2	1.78	0.65
1:B:47:SER:HA	1:B:63:LEU:HD21	1.80	0.64
1:E:4:ARG:HH21	1:E:129:ILE:HG21	1.66	0.59
1:E:6:LEU:HD22	1:E:128:GLU:HB3	1.84	0.59

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	137/136 (101%)	132 (96%)	5 (4%)	0	100 100
1	B	131/136 (96%)	127 (97%)	3 (2%)	1 (1%)	19 9
1	C	137/136 (101%)	133 (97%)	4 (3%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	129/136 (95%)	126 (98%)	3 (2%)	0	100	100
1	E	134/136 (98%)	132 (98%)	2 (2%)	0	100	100
1	F	124/136 (91%)	121 (98%)	3 (2%)	0	100	100
All	All	792/816 (97%)	771 (97%)	20 (2%)	1 (0%)	51	43

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	54	GLU

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	107/104 (103%)	106 (99%)	1 (1%)	78	79
1	B	102/104 (98%)	102 (100%)	0	100	100
1	C	107/104 (103%)	107 (100%)	0	100	100
1	D	99/104 (95%)	99 (100%)	0	100	100
1	E	104/104 (100%)	103 (99%)	1 (1%)	76	76
1	F	96/104 (92%)	96 (100%)	0	100	100
All	All	615/624 (99%)	613 (100%)	2 (0%)	92	93

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	110	GLU
1	E	44	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	37	GLN
1	D	112	GLN
1	E	112	GLN
1	C	37	GLN
1	E	37	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)

3 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	A	200	-	3,12,12	9.56	3 (100%)	3,17,17	2.40	2 (66%)
2	CIT	D	200	-	3,12,12	6.54	3 (100%)	3,17,17	2.73	2 (66%)
2	CIT	F	200	-	3,12,12	4.98	1 (33%)	3,17,17	2.57	2 (66%)

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	A	200	-	-	3/6/16/16	-
2	CIT	D	200	-	-	3/6/16/16	-
2	CIT	F	200	-	-	3/6/16/16	-

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	200	CIT	C4-C3	-14.60	1.34	1.54
2	D	200	CIT	O7-C3	-9.27	1.28	1.43
2	F	200	CIT	C4-C3	-8.54	1.42	1.54
2	A	200	CIT	C2-C3	-6.04	1.46	1.54
2	D	200	CIT	C2-C3	-5.96	1.46	1.54

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	D	200	CIT	C3-C4-C5	3.57	120.69	114.98
2	F	200	CIT	C3-C2-C1	3.19	120.09	114.98
2	D	200	CIT	C3-C2-C1	3.11	119.96	114.98
2	F	200	CIT	C3-C4-C5	3.10	119.95	114.98
2	A	200	CIT	C3-C2-C1	3.10	119.94	114.98

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	200	CIT	C6-C3-C4-C5
2	D	200	CIT	C1-C2-C3-C6
2	F	200	CIT	C6-C3-C4-C5
2	A	200	CIT	O7-C3-C4-C5
2	D	200	CIT	C1-C2-C3-O7

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	135/136 (99%)	-0.11	1 (0%) 87 88	11, 22, 46, 57	0
1	B	132/136 (97%)	0.33	12 (9%) 9 10	12, 24, 70, 102	0
1	C	135/136 (99%)	0.10	5 (3%) 41 44	14, 28, 64, 85	0
1	D	131/136 (96%)	0.09	11 (8%) 11 12	12, 24, 60, 90	0
1	E	135/136 (99%)	0.33	8 (5%) 22 25	15, 31, 71, 80	0
1	F	127/136 (93%)	0.45	15 (11%) 4 5	13, 26, 78, 103	0
All	All	795/816 (97%)	0.20	52 (6%) 18 21	11, 26, 67, 103	0

The worst 5 of 52 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	62	LEU	6.9
1	B	59	PHE	6.3
1	F	53	HIS	5.9
1	D	2	THR	5.5
1	B	60	GLY	5.4

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(Å^2)	Q<0.9
2	CIT	A	200	13/13	0.83	0.21	29,42,80,86	0
2	CIT	F	200	13/13	0.86	0.17	37,51,64,68	0
2	CIT	D	200	13/13	0.91	0.11	33,51,60,71	0

6.5 Other polymers (i)

There are no such residues in this entry.