



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 04:12 AM UTC

PDB ID : 6D6K / pdb_00006d6k
Title : Structure of polynucleotide nucleotidyltransferase from *Acinetobacter baumannii*
Authors : Seattle Structural Genomics Center for Infectious Disease (SSGCID)
Deposited on : 2018-04-21
Resolution : 2.50 Å (reported)

This is a Full wwPDB X-ray Structure Validation 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
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

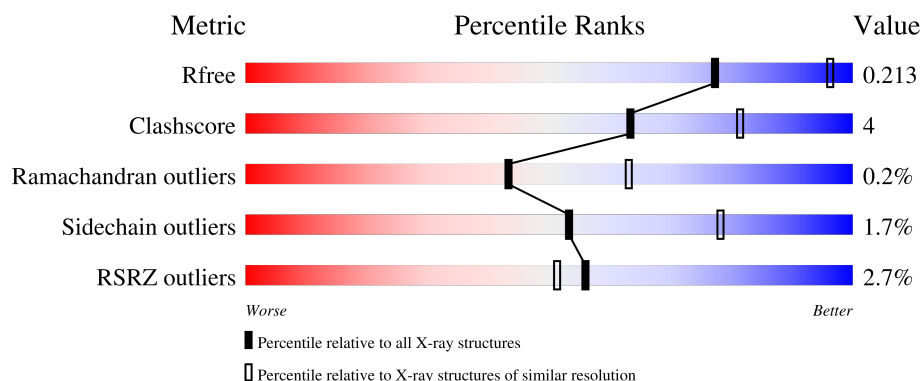
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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}	180053	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (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 $\leq 5\%$. 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	705	
1	B	705	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 8614 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 Polyribonucleotide nucleotidyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	543	Total	C	N	O	S	0	2	0
			4004	2510	698	776	20			
1	B	552	Total	C	N	O	S	0	2	0
			4105	2577	715	793	20			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	MET	-	initiating methionine	UNP V5VH92
A	-6	ALA	-	expression tag	UNP V5VH92
A	-5	HIS	-	expression tag	UNP V5VH92
A	-4	HIS	-	expression tag	UNP V5VH92
A	-3	HIS	-	expression tag	UNP V5VH92
A	-2	HIS	-	expression tag	UNP V5VH92
A	-1	HIS	-	expression tag	UNP V5VH92
A	0	HIS	-	expression tag	UNP V5VH92
B	-7	MET	-	initiating methionine	UNP V5VH92
B	-6	ALA	-	expression tag	UNP V5VH92
B	-5	HIS	-	expression tag	UNP V5VH92
B	-4	HIS	-	expression tag	UNP V5VH92
B	-3	HIS	-	expression tag	UNP V5VH92
B	-2	HIS	-	expression tag	UNP V5VH92
B	-1	HIS	-	expression tag	UNP V5VH92
B	0	HIS	-	expression tag	UNP V5VH92

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	254	Total	O	0	1
			255	255		
2	B	250	Total	O	0	0
			250	250		

ARG
ILE
LYS
LEU
THR
MET
LYS
ASP
ILE
GLU
GLN
ALA

4 Data and refinement statistics

Property	Value	Source
Space group	P 63	Depositor
Cell constants a, b, c, α , β , γ	93.69Å 93.69Å 266.61Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	44.44 – 2.50 44.44 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.7 (44.44-2.50) 99.8 (44.44-2.50)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.14 (at 2.51Å)	Xtriage
Refinement program	PHENIX (dev_3092)	Depositor
R, R_{free}	0.157 , 0.207 0.164 , 0.213	Depositor DCC
R_{free} test set	2020 reflections (4.43%)	wwPDB-VP
Wilson B-factor (Å ²)	37.0	Xtriage
Anisotropy	0.596	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 55.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.129 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	8614	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.44% 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

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	0.27	0/4071	0.48	0/5525
1	B	0.25	0/4175	0.48	0/5661
All	All	0.26	0/8246	0.48	0/11186

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

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	4004	0	3911	36	0
1	B	4105	0	4047	28	0
2	A	255	0	0	4	0
2	B	250	0	0	6	0
All	All	8614	0	7958	64	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.

All (64) 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:A:507:LEU:HD21	1:A:509:MET:HE2	1.62	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:401:ARG:NH1	2:A:701:HOH:O	2.13	0.80
1:A:500:SER:O	1:A:532:ARG:NH2	2.17	0.77
1:A:347:ARG:NH1	2:A:704:HOH:O	2.18	0.77
1:B:507:LEU:HD21	1:B:509:MET:HE2	1.68	0.74
1:A:486:ASP:O	1:A:489:HIS:ND1	2.21	0.73
1:B:329:LEU:HD12	1:B:538:GLU:HG3	1.73	0.71
1:B:8[B]:ARG:NH1	1:B:10:GLU:OE2	2.23	0.70
1:A:190:VAL:HG21	1:A:509:MET:HE3	1.75	0.68
1:B:190:VAL:HG21	1:B:509:MET:HE3	1.75	0.68
1:A:10:GLU:HG2	1:A:19:VAL:HG22	1.75	0.68
1:B:500:SER:O	1:B:532:ARG:NH2	2.30	0.64
1:B:494:ASP:OD2	2:B:701:HOH:O	2.15	0.63
1:A:329:LEU:HD12	1:A:538:GLU:HG3	1.81	0.62
1:A:470:LEU:HB3	1:A:493:MET:HB3	1.83	0.61
1:B:158:ILE:HD12	1:B:163:VAL:HG21	1.82	0.61
1:A:76:GLY:O	2:A:702:HOH:O	2.16	0.60
1:A:175:ASP:HA	1:A:195:LYS:HD2	1.83	0.60
1:B:175:ASP:HA	1:B:195:LYS:HD2	1.83	0.59
1:B:147:ARG:NH1	2:B:703:HOH:O	2.35	0.59
1:B:10:GLU:HG2	1:B:19:VAL:HG22	1.85	0.58
1:A:158:ILE:HD12	1:A:163:VAL:HG21	1.86	0.57
1:A:26:ALA:HB3	1:A:31:THR:HG21	1.86	0.57
1:A:401:ARG:NH1	1:A:401:ARG:HB3	2.21	0.56
1:A:94:ARG:HH11	1:A:404:GLY:HA3	1.69	0.55
1:A:304:TYR:CD2	1:A:490:LEU:HD22	2.42	0.55
1:A:94:ARG:NH1	1:A:404:GLY:HA3	2.22	0.54
1:B:347:ARG:NH1	2:B:707:HOH:O	2.38	0.52
1:A:307:VAL:HB	1:A:490:LEU:CD1	2.40	0.51
1:B:26:ALA:HB3	1:B:31:THR:HG21	1.93	0.51
1:B:15:GLN:HG2	2:B:831:HOH:O	2.11	0.51
1:B:433:ILE:HD12	1:B:440:SER:HB2	1.93	0.50
1:A:495:PHE:CZ	1:A:524:ALA:HB1	2.48	0.49
1:A:232:SER:OG	2:A:703:HOH:O	2.18	0.49
1:A:183:THR:HG23	1:A:188:LEU:HD11	1.94	0.49
1:B:401:ARG:HB3	1:B:401:ARG:NH2	2.28	0.49
1:A:433:ILE:HD12	1:A:440:SER:HB2	1.95	0.48
1:A:433:ILE:CD1	1:A:440:SER:HB2	2.44	0.48
1:B:185:SER:OG	1:B:514:GLU:OE2	2.14	0.47
1:B:492:ASP:HB3	1:B:513:ILE:HG12	1.97	0.47
1:B:433:ILE:CD1	1:B:440:SER:HB2	2.44	0.46
1:B:66:GLU:HG2	1:B:118:VAL:HG21	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:429:ILE:HD13	1:A:448:ALA:HB1	1.98	0.45
1:B:378:PHE:CE2	1:B:410:ARG:HG3	2.52	0.44
1:A:486:ASP:HA	1:A:489:HIS:HD1	1.83	0.44
1:B:102:PRO:HG3	2:B:879:HOH:O	2.18	0.44
1:B:338:ARG:HD3	1:B:338:ARG:HA	1.78	0.44
1:A:8[A]:ARG:HH22	1:A:10:GLU:CD	2.25	0.43
1:A:312:LEU:HD23	1:A:312:LEU:HA	1.80	0.43
1:B:167:ASN:OD1	1:B:169:GLU:HG3	2.18	0.43
1:B:347:ARG:NH2	1:B:438:GLY:O	2.52	0.43
1:B:283:VAL:HA	1:B:284:PRO:HD2	1.84	0.42
1:A:268:TYR:OH	1:A:486:ASP:OD1	2.17	0.42
1:A:511:ILE:HG23	1:A:516:ILE:HD12	2.02	0.42
1:B:493:MET:HE2	1:B:495:PHE:CD2	2.54	0.42
1:A:486:ASP:C	1:A:489:HIS:HD1	2.27	0.41
1:A:468:MET:HE3	1:A:468:MET:HB3	1.90	0.41
1:A:489:HIS:CE1	1:A:490:LEU:HG	2.55	0.41
1:A:338:ARG:HD3	1:A:338:ARG:HA	1.76	0.41
1:B:514:GLU:HG3	2:B:836:HOH:O	2.20	0.41
1:A:145:PRO:HG3	1:A:234:TRP:HB3	2.02	0.41
1:A:378:PHE:CE1	1:A:410:ARG:HG3	2.56	0.41
1:B:401:ARG:HB3	1:B:401:ARG:CZ	2.51	0.40
1:A:185:SER:OG	1:A:514:GLU:OE1	2.21	0.40

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	539/705 (76%)	529 (98%)	9 (2%)	1 (0%)	43	63
1	B	550/705 (78%)	536 (98%)	13 (2%)	1 (0%)	43	63
All	All	1089/1410 (77%)	1065 (98%)	22 (2%)	2 (0%)	43	63

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	439	SER
1	B	439	SER

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	402/558 (72%)	392 (98%)	10 (2%)	42	69
1	B	415/558 (74%)	410 (99%)	5 (1%)	63	83
All	All	817/1116 (73%)	802 (98%)	15 (2%)	53	77

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8[A]	ARG
1	A	8[B]	ARG
1	A	39	VAL
1	A	173	GLN
1	A	337	GLU
1	A	361	THR
1	A	475	GLU
1	A	476	ARG
1	A	494	ASP
1	A	557	PHE
1	B	294	GLU
1	B	337	GLU
1	B	361	THR
1	B	475	GLU
1	B	494	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	351	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 [i](#)

There are no ligands in this entry.

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

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	543/705 (77%)	-0.24	19 (3%)	47 42	18, 39, 88, 129	2 (0%)
1	B	552/705 (78%)	-0.36	11 (1%)	65 61	21, 41, 80, 127	2 (0%)
All	All	1095/1410 (77%)	-0.30	30 (2%)	56 51	18, 40, 87, 129	4 (0%)

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	77	GLY	4.1
1	A	489	HIS	3.9
1	A	557	PHE	3.9
1	B	290	GLY	3.8
1	A	77	GLY	3.3
1	B	557	PHE	3.3
1	B	284	PRO	3.3
1	A	255	ILE	3.1
1	B	233	ASP	3.0
1	A	564	PRO	2.7
1	B	367	VAL	2.6
1	A	78	TYR	2.6
1	A	562	ILE	2.6
1	A	269	ALA	2.5
1	A	298	LEU	2.5
1	A	490	LEU	2.5
1	A	263	VAL	2.4
1	B	395	GLU	2.4
1	B	78	TYR	2.4
1	A	556	THR	2.3
1	A	559	VAL	2.3
1	A	297	TYR	2.3
1	A	563	ASN	2.2
1	B	556	THR	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	265	GLN	2.1
1	A	256	SER	2.1
1	A	561	THR	2.0
1	A	279	VAL	2.0
1	B	558	GLU	2.0
1	B	397	GLY	2.0

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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.