



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 01:01 PM GMT

PDB ID : 3SI6  
Title : RB69 DNA Polymerase Triple Mutant (L561A/S565G/Y567A) Ternary Complex with dUpNpp and a Deoxy-terminated Primer in the presence of Mg<sup>2+</sup>  
Authors : Wang, M.; Wang, J.; Konigsberg, W.H.  
Deposited on : 2011-06-17  
Resolution : 1.85 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  
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

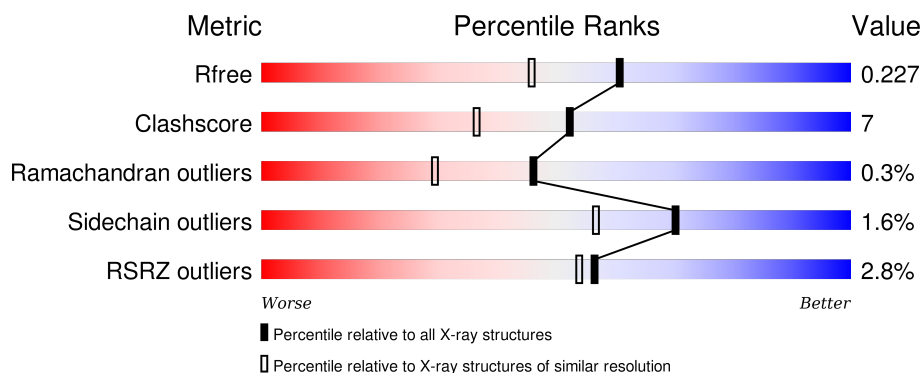
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.85 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))
$R_{free}$	91344	1745 (1.86-1.86)
Clashscore	102246	1898 (1.86-1.86)
Ramachandran outliers	100387	1875 (1.86-1.86)
Sidechain outliers	100360	1875 (1.86-1.86)
RSRZ outliers	91569	1747 (1.86-1.86)

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. 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	T	18	<div> <div></div> <div>72%28%</div> </div>
2	P	13	<div> <div></div> <div>54%38%8%</div> </div>
3	A	903	<div> <div>3%</div> <div>88%11%.</div> </div>

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 9145 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 DNA chain called 5'-D(\*TP\*CP\*AP\*AP\*GP\*TP\*AP\*AP\*GP\*CP\*AP\*GP\*TP\*CP\*CP\*GP\*CP\*G)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	T	18	Total	C	N	O	P	0	0	0
			367	175	71	104	17			

- Molecule 2 is a DNA chain called 5'-D(\*GP\*CP\*GP\*GP\*AP\*CP\*TP\*GP\*CP\*TP\*TP\*AP\*C)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	P	13	Total	C	N	O	P	0	0	0
			263	126	48	77	12			

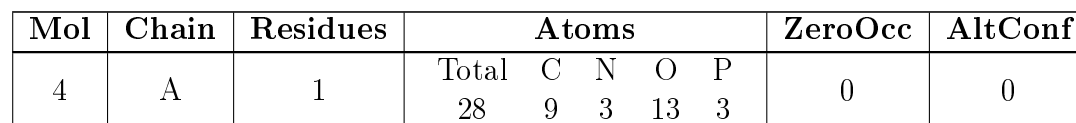
- Molecule 3 is a protein called DNA polymerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	A	903	Total	C	N	O	S	0	2	0
			7372	4734	1229	1376	33			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	222	ALA	ASP	ENGINEERED MUTATION	UNP Q38087
A	327	ALA	ASP	ENGINEERED MUTATION	UNP Q38087
A	561	ALA	LEU	ENGINEERED MUTATION	UNP Q38087
A	565	GLY	SER	ENGINEERED MUTATION	UNP Q38087
A	567	ALA	TYR	ENGINEERED MUTATION	UNP Q38087
A	902	ALA	ASP	CONFLICT	UNP Q38087

- Molecule 4 is 2'-DEOXYURIDINE 5'-ALPHA,BETA-IMIDO-TRIPHOSPHATE (three-letter code: DUP) (formula: C<sub>9</sub>H<sub>16</sub>N<sub>3</sub>O<sub>13</sub>P<sub>3</sub>).



- | Mol | Chain | Residues | Atoms           | ZeroOcc | AltConf |
|-----|-------|----------|-----------------|---------|---------|
| 5   | A     | 1        | Total Mg<br>1 1 | 0       | 0       |

- | Mol | Chain | Residues | Atoms              | ZeroOcc | AltConf |
|-----|-------|----------|--------------------|---------|---------|
| 6   | T     | 106      | Total O<br>106 106 | 0       | 0       |
| 6   | P     | 41       | Total O<br>41 41   | 0       | 0       |
| 6   | A     | 967      | Total O<br>967 967 | 0       | 0       |



● Molecule 1: 5'-D(\*TP\*CP\*AP\*AP\*GP\*TP\*AP\*AP\*GP\*CP\*AP\*GP\*TP\*CP\*CP\*GP\*CP\*G)-3'



- |      |      |      |      |      |      |
|------|------|------|------|------|------|
| G103 | C104 | G105 | T113 | A114 | C115 |
|------|------|------|------|------|------|

- |      |      |      |      |
|------|------|------|------|
| H864 | G609 | I309 | K1   |
| V870 | T611 | Y323 | K2   |
| L871 | E612 | I326 | E3   |
| E873 | D623 | R330 | R27  |
| K874 | K631 | V331 | E43  |
| K878 | K635 | L332 | S44  |
| P879 | D652 | Q333 | Q45  |
| K894 | K640 | L343 | A46  |
| A895 | D656 | M347 | R66  |
| S896 | H679 | Y350 | A82  |
| L897 | D684 | Q354 | L90  |
| R898 | L693 | K363 | F113 |
| D899 | E716 | Q382 | Q128 |
| F901 | A721 | Y391 | H131 |
| A902 | E731 | P392 | M153 |
| F903 | K734 | D411 | Y156 |
|      | P738 | L412 | D192 |
|      | K739 | T413 | K195 |
|      | E758 | A414 | E196 |
|      | E762 | L415 | N203 |
|      | M786 | K435 | P204 |
|      | V793 | V436 | K208 |
|      | G794 | A437 | M216 |
|      | F795 | P472 | N217 |
|      | F796 | K477 | F234 |
|      | K800 | K483 | R241 |
|      | L809 | M505 | K251 |
|      | G817 | P606 | K256 |
|      | M818 | M507 | P257 |
|      | L819 | L508 | D275 |
|      | D820 | L514 | P286 |
|      | G827 | L533 | Y292 |
|      | P834 | I580 | E295 |
|      |      | L605 | K302 |
|      |      | M606 | L303 |
|      |      | E607 |      |

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	75.46Å 120.19Å 131.21Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.31 – 1.85 38.32 – 1.85	Depositor EDS
% Data completeness (in resolution range)	97.9 (44.31-1.85) 97.9 (38.32-1.85)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	0.68 (at 1.84Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, $R_{free}$	0.183 , 0.217 0.194 , 0.227	Depositor DCC
$R_{free}$ test set	5009 reflections (5.25%)	DCC
Wilson B-factor (Å <sup>2</sup> )	20.6	Xtriage
Anisotropy	0.147	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 39.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	2 of 100436 reflections (0.002%)	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	9145	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.33% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: DUP, MG

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	T	0.50	0/412	1.12	1/634 (0.2%)
2	P	0.53	0/294	1.27	5/452 (1.1%)
3	A	0.26	0/7558	0.41	0/10212
All	All	0.29	0/8264	0.54	6/11298 (0.1%)

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	T	8	DA	O4'-C1'-N9	7.78	113.45	108.00
2	P	115	DC	C1'-O4'-C4'	-6.49	103.61	110.10
2	P	103	DG	O4'-C1'-N9	5.55	111.89	108.00
2	P	115	DC	O4'-C1'-N1	5.19	111.64	108.00
2	P	105	DG	O4'-C1'-N9	5.15	111.61	108.00

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	T	367	0	203	6	0
2	P	263	0	148	4	0
3	A	7372	0	7273	99	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	28	0	12	0	0
5	A	1	0	0	0	0
6	A	967	0	0	24	0
6	P	41	0	0	2	0
6	T	106	0	0	3	0
All	All	9145	0	7636	105	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 7.

The worst 5 of 105 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)
3:A:896:SER:HB2	3:A:897:LEU:HA	1.11	1.09
3:A:871:LEU:HD11	6:A:1266:HOH:O	1.54	1.03
3:A:896:SER:HB2	3:A:897:LEU:CA	1.92	1.00
6:T:916:HOH:O	3:A:251:LYS:HE2	1.61	0.99
1:T:16:DG:H5'	6:T:1009:HOH:O	1.63	0.99

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
3	A	903/903 (100%)	881 (98%)	19 (2%)	3 (0%)	46 29

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	896	SER
3	A	414	SER

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Mol	Chain	Res	Type
3	A	902	ALA

### 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
3	A	798/796 (100%)	785 (98%)	13 (2%)	70 57

5 of 13 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	A	411	ASP
3	A	580	LEU
3	A	835	LEU
3	A	332	LEU
3	A	693	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
3	A	444	ASN
3	A	546	GLN
3	A	773	GLN
3	A	354	GLN
3	A	786	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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](#)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 for Mogul analysis.

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	$\# Z  > 2$
4	DUP	A	904	5	23,29,29	1.96	4 (17%)	32,45,45	1.79	6 (18%)

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
4	DUP	A	904	5	-	0/13/34/34	0/2/2/2

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	904	DUP	PB-O3B	2.15	1.61	1.59
4	A	904	DUP	PB-O1B	4.54	1.51	1.46
4	A	904	DUP	PA-O1A	4.71	1.51	1.46
4	A	904	DUP	O4-C4	4.77	1.36	1.24

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	904	DUP	PG-O3B-PB	-2.91	122.90	132.67
4	A	904	DUP	C2'-C1'-N1	-2.41	108.31	114.16
4	A	904	DUP	O1A-PA-N3A	-2.28	108.40	111.90
4	A	904	DUP	O2A-PA-O1A	3.32	116.94	110.00
4	A	904	DUP	O2B-PB-O1B	3.74	117.80	110.00

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

There are no such residues in this entry.

## 5.8 Polymer linkage issues

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	T	18/18 (100%)	-0.35	0	100	100	14, 22, 33, 34	0
2	P	13/13 (100%)	-0.03	0	100	100	14, 22, 43, 48	0
3	A	903/903 (100%)	0.11	26 (2%)	55	52	11, 21, 42, 112	0
All	All	934/934 (100%)	0.09	26 (2%)	56	54	11, 21, 42, 112	0

The worst 5 of 26 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	A	901	PHE	15.7
3	A	902	ALA	10.8
3	A	903	PHE	8.7
3	A	897	LEU	6.8
3	A	819	ILE	5.6

### 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
4	DUP	A	904	28/28	0.97	0.13	0.19	13,16,21,26	0
5	MG	A	905	1/1	0.95	0.03	-4.69	25,25,25,25	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.