



wwPDB X-ray Structure Validation Summary Report

Feb 27, 2014 – 02:03 AM GMT

PDB ID : 2Y1T
Title : BACILLUS SUBTILIS PROPHAGE DUTPASE IN COMPLEX WITH DUDP
Authors : Garcia-Nafria, J.; Harkiolaki, M.; Persson, R.; Fogg, M.J.; Wilson, K.S.
Deposited on : 2010-12-10
Resolution : 1.89 Å(reported)

This is a wwPDB validation summary report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

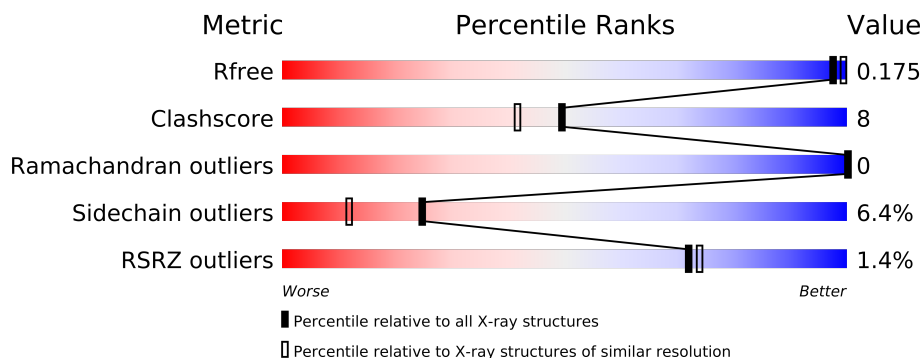
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	stable22639
Percentile statistics	:	21963
Refmac	:	5.8.0049
CCP4	:	6.3.0 (Settle)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

1 Overall quality at a glance

The reported resolution of this entry is 1.89 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}	66092	3684 (1.90-1.90)
Clashscore	79885	4465 (1.90-1.90)
Ramachandran outliers	78287	4413 (1.90-1.90)
Sidechain outliers	78261	4414 (1.90-1.90)
RSRZ outliers	66119	3686 (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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	142	
1	B	142	
1	C	142	
1	D	142	
1	E	142	
1	F	142	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
2	DUD	C	143	-	X

2 Entry composition i

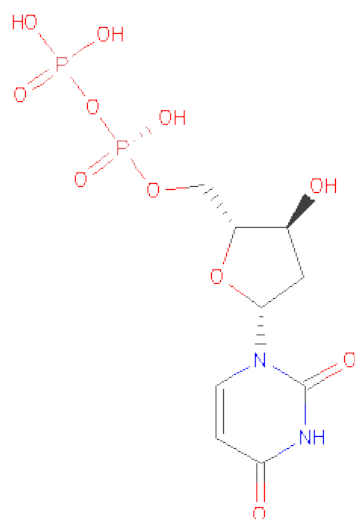
There are 3 unique types of molecules in this entry. The entry contains 6896 atoms, of which 0 are hydrogen and 0 are deuterium.

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 SPBC2 PROPHAGE-DERIVED DEOXYURIDINE 5'-TRIPHOSPHATE NUCLEOTIDOHYDROLASE YOSS.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	128	Total	C	N	O	S	12	3	0
			1058	678	179	194	7			
1	B	128	Total	C	N	O	S	26	2	0
			1051	672	178	194	7			
1	C	125	Total	C	N	O	S	6	2	0
			1028	659	174	189	6			
1	D	128	Total	C	N	O	S	12	1	0
			1049	671	178	193	7			
1	E	127	Total	C	N	O	S	25	1	0
			1037	665	174	191	7			
1	F	127	Total	C	N	O	S	22	2	0
			1046	670	177	193	6			

- Molecule 2 is DEOXYURIDINE-5'-DIPHOSPHATE (three-letter code: DUD) (formula: $C_9H_{14}N_2O_{11}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	B	1	Total	C	N	O	P	0	0
			24	9	2	11	2		
2	C	1	Total	C	N	O	P	0	0
			24	9	2	11	2		
2	D	1	Total	C	N	O	P	0	0
			24	9	2	11	2		
2	E	1	Total	C	N	O	P	0	0
			24	9	2	11	2		
2	E	1	Total	C	N	O	P	0	0
			24	9	2	11	2		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	86	Total	O	0	0
			86	86		
3	B	92	Total	O	0	0
			92	92		
3	C	80	Total	O	0	0
			80	80		
3	D	75	Total	O	0	0
			75	75		
3	E	97	Total	O	0	0
			97	97		
3	F	77	Total	O	0	0
			77	77		

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: SPBC2 PROPHAGE-DERIVED DEOXYURIDINE 5'-TRIPHOSPHATE NUCLEOTIDOHYDROLASE YOSS

Chain A: 



- Molecule 1: SPBC2 PROPHAGE-DERIVED DEOXYURIDINE 5'-TRIPHOSPHATE NUCLEOTIDOHYDROLASE YOSS

Chain B: 



- Molecule 1: SPBC2 PROPHAGE-DERIVED DEOXYURIDINE 5'-TRIPHOSPHATE NUCLEOTIDOHYDROLASE YOSS

Chain C: 



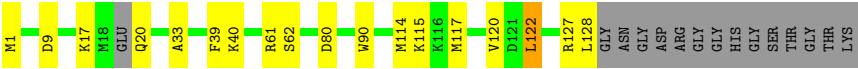
- Molecule 1: SPBC2 PROPHAGE-DERIVED DEOXYURIDINE 5'-TRIPHOSPHATE NUCLEOTIDOHYDROLASE YOSS

Chain D: 



- Molecule 1: SPBC2 PROPHAGE-DERIVED DEOXYURIDINE 5'-TRIPHOSPHATE NUCLEOTIDOHYDROLASE YOSS

Chain E: 



● Molecule 1: SPBC2 PROPHAGE-DERIVED DEOXYURIDINE 5'-TRIPHOSPHATE NUCLEOTIDOHYDROLASE YOSS

Chain F:



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	99.52Å 99.34Å 99.31Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	70.31 – 1.89 19.89 – 1.89	Depositor EDS
% Data completeness (in resolution range)	98.9 (70.31-1.89) 99.1 (19.89-1.89)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.21 (at 1.89Å)	Xtriage
Refinement program	REFMAC 5.6.0086	Depositor
R, R_{free}	0.140 , 0.166 0.150 , 0.175	Depositor DCC
R_{free} test set	3934 reflections (5.29%)	DCC
Wilson B-factor (Å ²)	28.2	Xtriage
Anisotropy	0.108	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 25.1	EDS
Estimated twinning fraction	0.555 for H, K, L 0.408 for -L, -H, K 0.037 for K, -L, -H 0.078 for k,h,l 0.077 for -l,-k,-h 0.077 for -h,l,k 0.279 for l,h,k 0.279 for k,l,h	Xtriage
Reported twinning fraction	0.555 for H, K, L 0.408 for -L, -H, K 0.037 for K, -L, -H	Depositor
L-test for twinning	$\langle L \rangle = 0.41$, $\langle L^2 \rangle = 0.24$	Xtriage
Outliers	0 of 78442 reflections	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	6896	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.02% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: DUD

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	1.32	3/1089 (0.3%)	1.05	4/1462 (0.3%)
1	B	1.23	1/1080 (0.1%)	1.00	1/1451 (0.1%)
1	C	1.31	2/1053 (0.2%)	1.09	3/1415 (0.2%)
1	D	1.29	1/1074 (0.1%)	1.10	3/1443 (0.2%)
1	E	1.38	3/1059 (0.3%)	1.11	4/1422 (0.3%)
1	F	1.23	0/1071	1.05	1/1438 (0.1%)
All	All	1.29	10/6426 (0.2%)	1.07	16/8631 (0.2%)

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	30	GLU	CD-OE1	-5.98	1.19	1.25
1	E	39	PHE	CD2-CE2	5.62	1.50	1.39
1	A	33	ALA	CA-CB	5.29	1.63	1.52
1	E	90	TRP	CB-CG	5.26	1.59	1.50
1	E	33	ALA	CA-CB	5.24	1.63	1.52

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	25	ASP	CB-CG-OD2	-5.86	113.03	118.30
1	C	112	ARG	NE-CZ-NH1	5.78	123.19	120.30
1	D	107	ARG	NE-CZ-NH1	5.76	123.18	120.30
1	F	99	ASP	CB-CG-OD1	5.74	123.47	118.30
1	A	61	ARG	NE-CZ-NH1	5.66	123.13	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1058	0	1081	40	0
1	B	1051	0	1064	28	0
1	C	1028	0	1043	19	0
1	D	1049	0	1063	13	0
1	E	1037	0	1052	6	0
1	F	1046	0	1062	21	0
2	B	24	0	11	0	0
2	C	24	0	11	1	0
2	D	24	0	11	0	0
2	E	48	0	22	3	0
3	A	86	0	0	0	0
3	B	92	0	0	1	0
3	C	80	0	0	1	0
3	D	75	0	0	2	0
3	E	97	0	0	2	0
3	F	77	0	0	0	0
All	All	6896	0	6420	96	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 8.

The worst 5 of 96 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:65:TYR:CE2	1:C:39:PHE:CD1	2.40	1.09
1:B:65:TYR:HE2	1:C:39:PHE:CG	1.75	1.04
1:B:65:TYR:CE2	1:C:39:PHE:CG	2.57	0.93
1:A:126:ASP:C	1:A:127:ARG:HG3	1.89	0.91
1:B:65:TYR:OH	1:C:95:TYR:HD2	1.58	0.84

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

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	129/142 (91%)	124 (96%)	5 (4%)	0	100	100
1	B	128/142 (90%)	127 (99%)	1 (1%)	0	100	100
1	C	123/142 (87%)	120 (98%)	3 (2%)	0	100	100
1	D	127/142 (89%)	125 (98%)	2 (2%)	0	100	100
1	E	124/142 (87%)	121 (98%)	3 (2%)	0	100	100
1	F	125/142 (88%)	123 (98%)	2 (2%)	0	100	100
All	All	756/852 (89%)	740 (98%)	16 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	116/121 (96%)	110 (95%)	6 (5%)	32	19
1	B	115/121 (95%)	105 (91%)	10 (9%)	15	6
1	C	112/121 (93%)	106 (95%)	6 (5%)	31	17
1	D	114/121 (94%)	106 (93%)	8 (7%)	21	10
1	E	113/121 (93%)	106 (94%)	7 (6%)	26	12
1	F	114/121 (94%)	108 (95%)	6 (5%)	32	18
All	All	684/726 (94%)	641 (94%)	43 (6%)	25	12

5 of 43 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	122	LEU
1	D	20	GLN
1	F	17	LYS
1	C	126	ASP
1	C	127	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	2	GLN
1	C	16	ASN
1	D	87	ASN
1	F	16	ASN

5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

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	DUD	B	143	-	25,25,25	1.65	4 (16%)	33,38,38	1.44	5 (15%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	DUD	C	143	-	25,25,25	2.10	6 (24%)	33,38,38	1.76	6 (18%)
2	DUD	D	143	-	25,25,25	1.52	5 (20%)	33,38,38	1.38	6 (18%)
2	DUD	E	143	-	25,25,25	1.79	6 (24%)	33,38,38	1.35	4 (12%)
2	DUD	E	144	-	25,25,25	1.45	3 (12%)	33,38,38	1.63	7 (21%)

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	DUD	B	143	-	-	0/13/28/28	0/2/2/2
2	DUD	C	143	-	-	0/13/28/28	0/2/2/2
2	DUD	D	143	-	-	0/13/28/28	0/2/2/2
2	DUD	E	143	-	-	0/13/28/28	0/2/2/2
2	DUD	E	144	-	-	0/13/28/28	0/2/2/2

The worst 5 of 24 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	143	DUD	C2-N1	5.36	1.44	1.38
2	C	143	DUD	C6-C5	5.04	1.44	1.36
2	C	143	DUD	PB-O1B	4.74	1.67	1.51
2	C	143	DUD	PA-O3A	4.73	1.68	1.59
2	E	143	DUD	C4-N3	-4.14	1.30	1.37

The worst 5 of 28 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	143	DUD	N3-C2-N1	6.21	121.15	115.97
2	E	144	DUD	N3-C2-N1	5.39	120.47	115.97
2	E	143	DUD	N3-C2-N1	5.39	120.47	115.97
2	B	143	DUD	O5'-PA-O1A	-4.09	93.34	109.37
2	D	143	DUD	O3A-PA-O5'	3.35	118.39	103.41

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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 ⓘ

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	128/142 (90%)	-0.01	3 (2%) 57 59	15, 23, 40, 51	3 (2%)
1	B	128/142 (90%)	-0.06	2 (1%) 68 70	16, 23, 40, 58	7 (5%)
1	C	125/142 (88%)	-0.13	2 (1%) 68 70	16, 23, 38, 54	2 (1%)
1	D	128/142 (90%)	-0.06	2 (1%) 68 70	15, 23, 40, 58	3 (2%)
1	E	127/142 (89%)	-0.13	0 100 100	14, 21, 36, 49	7 (5%)
1	F	127/142 (89%)	-0.00	2 (1%) 68 70	15, 24, 39, 58	6 (4%)
All	All	763/852 (89%)	-0.07	11 (1%) 72 74	14, 23, 40, 58	28 (3%)

The worst 5 of 11 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	65	TYR	4.2
1	A	18	MET	4.1
1	F	19	GLU	2.4
1	B	15	ILE	2.3
1	A	17	LYS	2.3

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands

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, 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	RSR	LLDF	B-factors(Å ²)	Q<0.9
2	DUD	C	143	24/24	0.14	2.15	19,31,63,68	0
2	DUD	E	143	24/24	0.12	0.46	22,34,54,56	0
2	DUD	D	143	24/24	0.10	0.15	20,25,32,38	0
2	DUD	E	144	24/24	0.10	0.03	22,28,49,49	0
2	DUD	B	143	24/24	0.09	-0.10	20,23,30,32	0

6.5 Other polymers

There are no such residues in this entry.