



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 1, 2014 – 03:00 AM GMT

PDB ID : 1VAS
Title : ATOMIC MODEL OF A PYRIMIDINE DIMER SPECIFIC EXCISION REPAIR ENZYME COMPLEXED WITH A DNA SUBSTRATE: STRUCTURAL BASIS FOR DAMAGED DNA RECOGNITION
Authors : Vassylyev, D.G.; Kashiwagi, T.; Mikami, Y.; Ariyoshi, M.; Iwai, S.; Ohtsuka, E.; Morikawa, K.
Deposited on : 1995-09-08
Resolution : 2.75 Å(reported)

This is a full wwPDB validation 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>

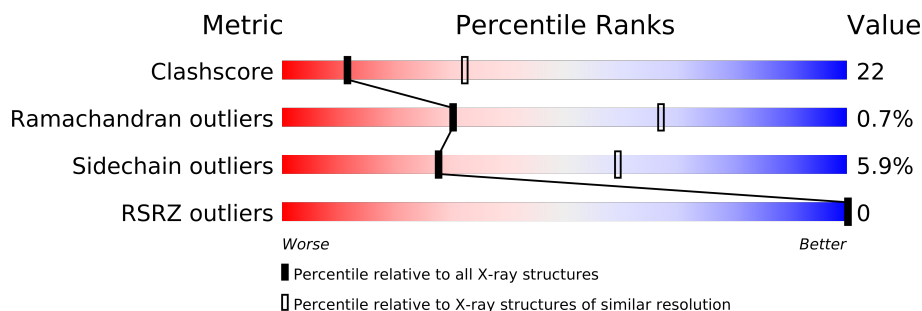
The following versions of software and data (see [references](#)) were used in the production of this report:

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 2.75 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	79885	2995 (2.80-2.72)
Ramachandran outliers	78287	2941 (2.80-2.72)
Sidechain outliers	78261	2944 (2.80-2.72)
RSRZ outliers	66119	2409 (2.80-2.72)

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	B	13	
2	C	13	
3	A	137	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 1799 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 DNA chain called DNA (5'-D(*AP*TP*CP*GP*CP*GP*TP*TP*GP*CP*GP*CP*T)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	13	Total	C	N	O	P	0	0	0
			262	126	45	79	12			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	13	Total	C	N	O	P	0	0	0
			265	126	54	73	12			

- Molecule 3 is a protein called PROTEIN (T4 ENDONUCLEASE V (E.C.3.1.25.1)).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	A	137	Total	C	N	O	S	0	0	0
			1129	726	202	199	2			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	23	GLN	GLU	ENGINEERED	UNP P04418

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	90	Total	O	0	0
			90	90		
4	B	24	Total	O	0	0
			24	24		
4	C	29	Total	O	0	0
			29	29		

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: DNA (5'-D(*AP*TP*CP*GP*CP*GP*TP*TP*GP*CP*GP*CP*T)-3')

Chain B: 



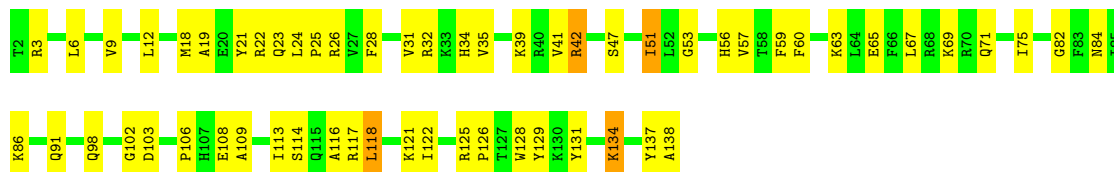
- Molecule 2: DNA (5'-D(*TP*AP*GP*CP*GP*CP*AP*AP*CP*GP*CP*GP*A)-3')

Chain C: 



- Molecule 3: PROTEIN (T4 ENDONUCLEASE V (E.C.3.1.25.1))

Chain A: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, α , β , γ	118.82Å 118.82Å 36.28Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	10.00 – 2.75 38.89 – 2.75	Depositor EDS
% Data completeness (in resolution range)	72.0 (10.00-2.75) 71.6 (38.89-2.75)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$	-	Xtriage
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.152 , 0.240 0.150 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	23.4	Xtriage
Anisotropy	0.263	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 105.0	EDS
Estimated twinning fraction	0.108 for h,-h-k,-l	Xtriage
L-test for twinning	$\langle L \rangle = 0.37$, $\langle L^2 \rangle = 0.20$	Xtriage
Outliers	0 of 5622 reflections	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	1799	wwPDB-VP
Average B, all atoms (Å ²)	16.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.33% of the height of the origin peak. No significant pseudotranslation is detected.*

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	B	3.51	13/292 (4.5%)	2.73	23/449 (5.1%)
2	C	1.68	4/298 (1.3%)	1.80	6/458 (1.3%)
3	A	0.51	0/1154	0.70	0/1554
All	All	1.65	17/1744 (1.0%)	1.51	29/2461 (1.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	2

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	208	DT	C5-C6	32.90	1.57	1.34
1	B	207	DT	C5-C6	30.51	1.55	1.34
1	B	208	DT	N1-C6	13.76	1.47	1.38
1	B	207	DT	N1-C6	11.72	1.46	1.38
1	B	207	DT	C4-C5	11.07	1.54	1.45
1	B	208	DT	C4-C5	8.64	1.52	1.45
1	B	207	DT	C5-C7	7.17	1.54	1.50
2	C	214	DT	N1-C2	7.09	1.43	1.38
1	B	206	DG	C3'-C2'	-6.40	1.44	1.52
1	B	209	DG	O3'-P	-6.25	1.53	1.61
1	B	208	DT	O3'-P	-6.16	1.53	1.61
1	B	208	DT	P-O5'	-6.07	1.53	1.59
1	B	206	DG	C5'-C4'	-5.73	1.45	1.51
2	C	214	DT	C5-C7	5.31	1.53	1.50
2	C	222	DC	C2'-C1'	-5.29	1.47	1.52
1	B	208	DT	C5-C7	5.27	1.53	1.50
2	C	222	DC	O3'-P	-5.05	1.55	1.61

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	207	DT	C4-C5-C7	-17.27	108.64	119.00
1	B	208	DT	C4-C5-C7	-16.82	108.91	119.00
1	B	207	DT	C6-C5-C7	-15.88	113.37	122.90
1	B	208	DT	C6-C5-C7	-15.61	113.53	122.90
1	B	208	DT	C5-C6-N1	-14.24	115.15	123.70
1	B	207	DT	C5-C6-N1	-12.52	116.19	123.70
2	C	221	DA	O4'-C4'-C3'	11.85	113.11	106.00
1	B	207	DT	O4'-C1'-N1	9.42	114.59	108.00
1	B	207	DT	C6-N1-C2	8.56	125.58	121.30
2	C	220	DA	P-O3'-C3'	-7.86	110.27	119.70
1	B	208	DT	C6-N1-C2	7.55	125.08	121.30
1	B	208	DT	P-O3'-C3'	7.08	128.20	119.70
2	C	221	DA	C4'-C3'-C2'	-6.68	97.09	103.10
2	C	214	DT	C6-C5-C7	-6.47	119.02	122.90
1	B	213	DT	C6-C5-C7	-6.06	119.26	122.90
1	B	208	DT	O4'-C4'-C3'	6.02	109.61	106.00
1	B	208	DT	N3-C4-C5	5.89	118.74	115.20
1	B	208	DT	N1-C2-N3	5.84	118.11	114.60
1	B	207	DT	N3-C4-C5	5.66	118.60	115.20
1	B	206	DG	P-O3'-C3'	-5.50	113.10	119.70
1	B	208	DT	O3'-P-O5'	-5.45	93.64	104.00
1	B	202	DT	C6-C5-C7	-5.35	119.69	122.90
1	B	206	DG	C5'-C4'-C3'	-5.34	104.49	114.10
2	C	221	DA	P-O3'-C3'	5.31	126.07	119.70
1	B	206	DG	O4'-C1'-N9	5.27	111.69	108.00
2	C	214	DT	C4-C5-C6	5.21	121.13	118.00
1	B	207	DT	C5'-C4'-O4'	5.11	119.01	109.30
1	B	207	DT	C6-N1-C1'	-5.03	112.86	120.40
1	B	213	DT	C4-C5-C6	5.01	121.01	118.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	207	DT	Sidechain
1	B	208	DT	Sidechain

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	B	262	0	149	17	0
2	C	265	0	146	13	0
3	A	1129	0	1143	57	0
4	A	90	0	0	6	0
4	B	24	0	0	4	0
4	C	29	0	0	3	0
All	All	1799	0	1438	68	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 22.

All (68) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:C:221:DA:H2''	2:C:222:DC:H5'	1.68	0.76
3:A:109:ALA:O	3:A:113:ILE:HD13	1.85	0.76
3:A:126:PRO:HB2	3:A:138:ALA:HB2	1.67	0.75
1:B:213:DT:H71	4:B:335:HOH:O	1.90	0.70
1:B:209:DG:OP1	3:A:53:GLY:HA2	1.94	0.67
1:B:206:DG:H5'	3:A:128:TRP:CH2	2.34	0.63
1:B:207:DT:OP2	3:A:121:LYS:HE2	1.99	0.61
3:A:31:VAL:O	3:A:35:VAL:HG23	2.01	0.60
1:B:206:DG:H5'	3:A:128:TRP:CZ3	2.37	0.59
2:C:221:DA:H8	3:A:22:ARG:HA	1.68	0.59
3:A:59:PHE:CZ	3:A:63:LYS:HE2	2.38	0.57
3:A:56:HIS:O	3:A:59:PHE:HB3	2.03	0.57
3:A:6:LEU:HD13	3:A:106:PRO:HB3	1.86	0.57
4:B:419:HOH:O	3:A:18:MET:HB3	2.04	0.56
2:C:221:DA:N6	3:A:75:ILE:HD11	2.22	0.55
1:B:209:DG:H5''	3:A:53:GLY:O	2.06	0.55
3:A:122:ILE:HA	3:A:129:TYR:CE2	2.41	0.55
3:A:51:ILE:HD13	3:A:51:ILE:N	2.21	0.55
3:A:19:ALA:HA	3:A:22:ARG:NH1	2.22	0.55
2:C:226:DA:H1'	4:C:423:HOH:O	2.07	0.54
4:C:355:HOH:O	3:A:86:LYS:HE2	2.07	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:210:DC:C5'	3:A:57:VAL:HG22	2.37	0.54
3:A:98:GLN:H	3:A:98:GLN:NE2	2.07	0.53
3:A:125:ARG:HG3	3:A:129:TYR:CE2	2.43	0.53
3:A:137:TYR:O	3:A:138:ALA:HB3	2.10	0.52
1:B:210:DC:H5'	3:A:57:VAL:HG22	1.92	0.52
2:C:221:DA:C8	3:A:25:PRO:HG2	2.45	0.51
3:A:60:PHE:CD2	3:A:67:LEU:HD21	2.45	0.50
3:A:69:LYS:HB3	4:A:317:HOH:O	2.11	0.50
1:B:210:DC:H2''	1:B:211:DG:C8	2.46	0.50
3:A:9:VAL:HA	3:A:12:LEU:HD12	1.94	0.50
3:A:9:VAL:HA	3:A:12:LEU:CD1	2.42	0.50
3:A:24:LEU:HB3	3:A:25:PRO:HD3	1.93	0.49
3:A:34:HIS:HD2	3:A:39:LYS:NZ	2.12	0.48
1:B:208:DT:OP1	3:A:117:ARG:NH1	2.46	0.48
4:B:419:HOH:O	3:A:18:MET:HE2	2.15	0.47
3:A:116:ALA:HB3	4:A:313:HOH:O	2.15	0.47
1:B:207:DT:H1'	1:B:208:DT:O4'	2.15	0.46
3:A:125:ARG:HG3	3:A:129:TYR:HE2	1.80	0.46
3:A:28:PHE:O	3:A:32:ARG:HG3	2.16	0.45
2:C:220:DA:H1'	3:A:26:ARG:CD	2.46	0.45
2:C:221:DA:C8	3:A:21:TYR:O	2.70	0.45
2:C:221:DA:N6	3:A:71:GLN:NE2	2.66	0.44
1:B:206:DG:N2	4:B:419:HOH:O	2.50	0.44
1:B:212:DC:C2'	1:B:213:DT:H72	2.48	0.44
3:A:34:HIS:HB3	3:A:39:LYS:HB2	1.99	0.44
1:B:203:DC:H2''	1:B:204:DG:C8	2.53	0.44
3:A:131:TYR:O	3:A:134:LYS:HD3	2.18	0.44
3:A:3:ARG:HH12	3:A:121:LYS:HD3	1.83	0.44
3:A:23:GLN:HG2	3:A:26:ARG:NH1	2.32	0.44
3:A:82:GLY:HA2	4:A:444:HOH:O	2.16	0.43
3:A:24:LEU:HD21	3:A:67:LEU:HB3	2.00	0.43
3:A:137:TYR:O	3:A:138:ALA:CB	2.66	0.43
2:C:221:DA:C2'	2:C:222:DC:H5'	2.44	0.42
2:C:221:DA:C5	3:A:25:PRO:HG2	2.55	0.42
3:A:3:ARG:HD2	4:A:357:HOH:O	2.20	0.42
3:A:108:GLU:HG2	4:A:418:HOH:O	2.20	0.42
1:B:210:DC:C5'	3:A:57:VAL:CG2	2.98	0.41
1:B:210:DC:H5''	3:A:57:VAL:HG22	2.01	0.41
2:C:223:DG:H4'	3:A:18:MET:HE1	2.01	0.41
3:A:65:GLU:HB2	3:A:102:GLY:O	2.20	0.41
3:A:114:SER:O	3:A:118:LEU:HD22	2.21	0.41
1:B:205:DC:H2'	1:B:205:DC:H6	1.71	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:C:218:DG:H4'	4:C:305:HOH:O	2.21	0.41
2:C:220:DA:H1'	3:A:26:ARG:HD3	2.03	0.40
3:A:118:LEU:O	3:A:122:ILE:HG13	2.21	0.40
3:A:47:SER:N	4:A:378:HOH:O	2.50	0.40
3:A:42:ARG:HH11	3:A:42:ARG:HG2	1.85	0.40

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
3	A	135/137 (98%)	128 (95%)	6 (4%)	1 (1%)	30 67

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	84	ASN

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	118/118 (100%)	111 (94%)	7 (6%)	28 59

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	A	41	VAL
3	A	42	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	A	51	ILE
3	A	91	GLN
3	A	103	ASP
3	A	118	LEU
3	A	134	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
3	A	34	HIS
3	A	98	GLN

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 ⓘ

There are no ligands in this entry.

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	B	13/13 (100%)	-0.51	0 100 100	6, 30, 55, 61	0
2	C	13/13 (100%)	-0.40	0 100 100	15, 34, 58, 60	0
3	A	137/137 (100%)	-0.92	0 100 100	2, 6, 22, 29	0
All	All	163/163 (100%)	-0.85	0 100 100	2, 8, 35, 61	0

There are no RSRZ outliers to report.

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 ⓘ

There are no ligands in this entry.

6.5 Other polymers ⓘ

There are no such residues in this entry.