wwPDB X-ray Structure Validation Summary Report (i)

Feb 1, 2016 – 12:41 AM GMT

PDB ID	:	2BBV
Title	:	THE REFINED THREE-DIMENSIONAL STRUCTURE OF AN INSECT VIRUS AT 2.8 ANGSTROMS RESOLUTION
Authors	:	Wery, J.-P.; Reddy, V.S.; Hosur, M.V.; Johnson, J.E.
Deposited on	:	1994-06-06
Resolution	:	2.80 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
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

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

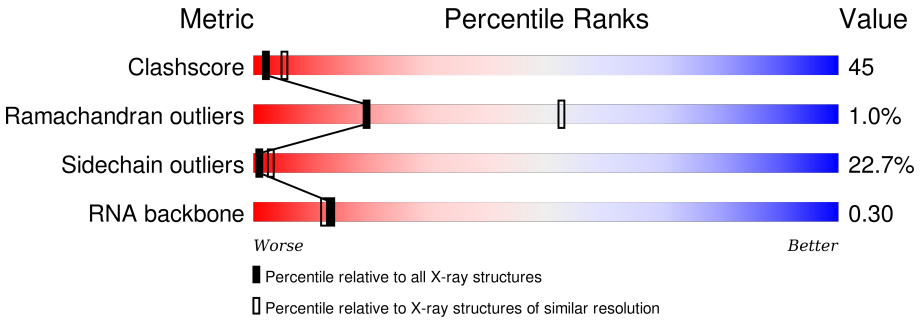
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.80 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	102246	2827 (2.80-2.80)
Ramachandran outliers	100387	2782 (2.80-2.80)
Sidechain outliers	100360	2784 (2.80-2.80)
RNA backbone	2183	1091 (3.20-2.40)

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. 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	N	10	50% 40% 10%
2	A	363	39% 34% 11% • 15%
2	B	363	40% 34% 9% • 15%
2	C	363	36% 38% 13% • 12%
3	D	44	7% 16% 9% 5% 64%
3	E	44	11% 16% 5% 5% 64%

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Mol	Chain	Length	Quality of chain
3	F	44	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7817 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 RNA chain called RNA (5'-R(*UP*CP*UP*UP*AP*UP*AP*UP*CP*U)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	N	10	Total	C	N	O	P	0	0	0
			201	92	28	72	9			

- Molecule 2 is a protein called PROTEIN (BLACK BEETLE VIRUS CAPSID PROTEIN).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	308	Total	C	N	O	S	0	0	0
			2311	1478	385	438	10			
2	B	308	Total	C	N	O	S	0	0	0
			2311	1478	385	438	10			
2	C	321	Total	C	N	O	S	0	0	0
			2406	1536	402	458	10			

- Molecule 3 is a protein called PROTEIN (BLACK BEETLE VIRUS CAPSID PROTEIN).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	16	Total	C	N	O	S	0	0	0
			125	80	22	22	1			
3	E	16	Total	C	N	O	S	0	0	0
			125	80	22	22	1			
3	F	16	Total	C	N	O	S	0	0	0
			125	80	22	22	1			

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Ca	0	0
			1	1		
4	A	2	Total	Ca	0	0
			2	2		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	C	2	Total Ca 2 2	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	68	Total O 68 68	0	0
5	B	70	Total O 70 70	0	0
5	C	65	Total O 65 65	0	0
5	D	1	Total O 1 1	0	0
5	F	4	Total O 4 4	0	0

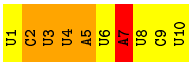
3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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.

Note EDS was not executed.

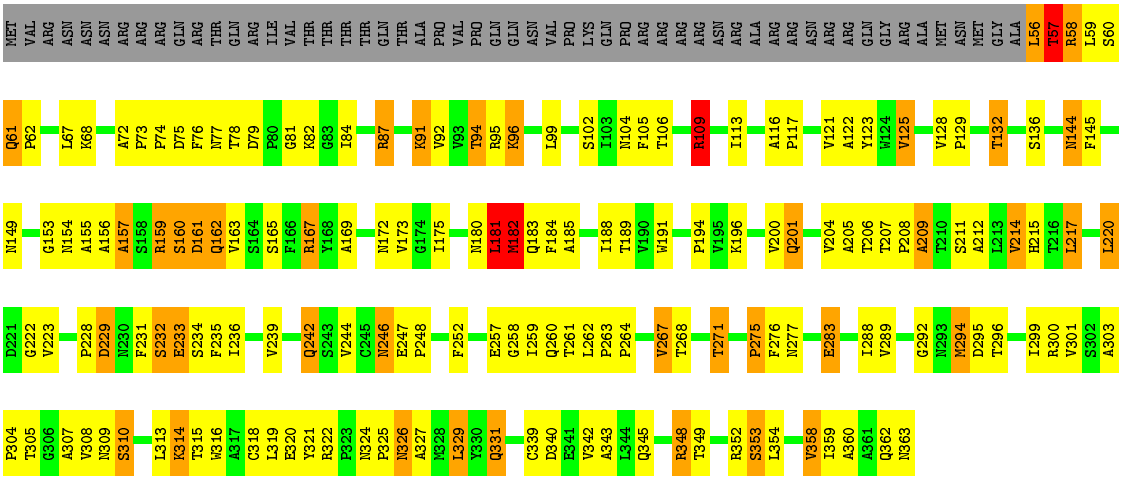
- Molecule 1: RNA (5'-R(*UP*CP*UP*UP*AP*UP*AP*UP*CP*U)-3')

Chain N:



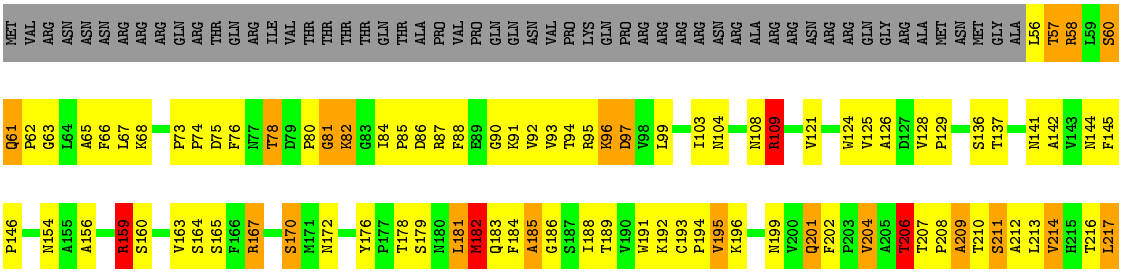
- Molecule 2: PROTEIN (BLACK BEETLE VIRUS CAPSID PROTEIN)

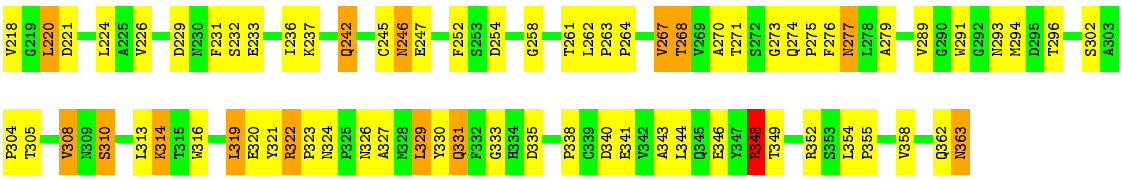
Chain A:

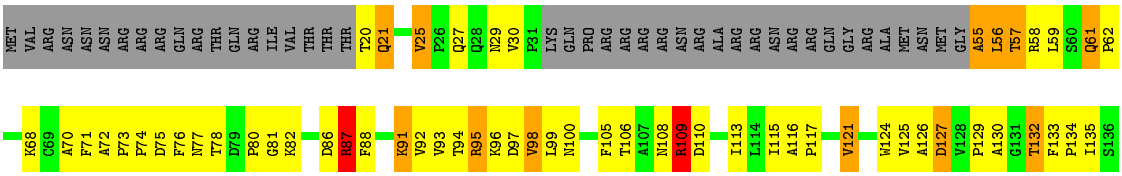


- Molecule 2: PROTEIN (BLACK BEETLE VIRUS CAPSID PROTEIN)

Chain B:

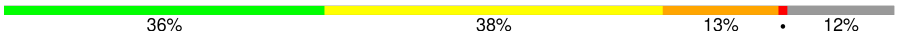






• Molecule 2: PROTEIN (BLACK BEETLE VIRUS CAPSID PROTEIN)

Chain C:



• Molecule 3: PROTEIN (BLACK BEETLE VIRUS CAPSID PROTEIN)

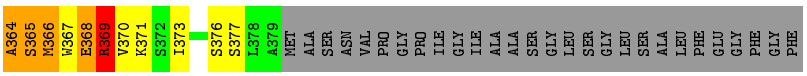
Chain D:

• Molecule 3: PROTEIN (BLACK BEETLE VIRUS CAPSID PROTEIN)

Chain E:

• Molecule 3: PROTEIN (BLACK BEETLE VIRUS CAPSID PROTEIN)

Chain F:



4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 42 3 2	Depositor
Cell constants a, b, c, α, β, γ	362.00Å 362.00Å 362.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	6.00 – 2.80	Depositor
% Data completeness (in resolution range)	67.5 (6.00-2.80)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR, PROLSQ	Depositor
R, R_{free}	0.221 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	7817	wwPDB-VP
Average B, all atoms (Å^2)	12.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

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

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	N	1.31	1/222 (0.5%)	1.59	3/342 (0.9%)
2	A	0.89	0/2372	1.41	15/3249 (0.5%)
2	B	0.88	0/2372	1.43	15/3249 (0.5%)
2	C	0.88	1/2469 (0.0%)	1.41	22/3384 (0.7%)
3	D	1.01	0/126	1.57	5/167 (3.0%)
3	E	1.02	0/126	1.43	2/167 (1.2%)
3	F	1.48	1/126 (0.8%)	1.75	3/167 (1.8%)
All	All	0.92	3/7813 (0.0%)	1.43	65/10725 (0.6%)

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
2	B	0	1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	F	364	ALA	CA-CB	12.65	1.79	1.52
1	N	7	A	N9-C4	-10.46	1.31	1.37
2	C	363	ASN	CA-C	-8.50	1.30	1.52

The worst 5 of 65 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	F	364	ALA	N-CA-CB	-13.14	91.71	110.10
2	A	352	ARG	NE-CZ-NH1	11.89	126.24	120.30
2	C	348	ARG	NE-CZ-NH2	10.31	125.45	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	87	ARG	NE-CZ-NH1	9.61	125.11	120.30
2	C	55	ALA	O-C-N	8.82	136.81	122.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	58	ARG	Sidechain

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	N	201	0	106	34	0
2	A	2311	0	2262	209	0
2	B	2311	0	2262	190	0
2	C	2406	0	2357	242	0
3	D	125	0	135	18	0
3	E	125	0	135	22	0
3	F	125	0	135	12	0
4	A	2	0	0	0	0
4	B	1	0	0	0	0
4	C	2	0	0	0	0
5	A	68	0	0	7	0
5	B	70	0	0	12	0
5	C	65	0	0	13	0
5	D	1	0	0	0	0
5	F	4	0	0	0	0
All	All	7817	0	7392	674	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 45.

The worst 5 of 674 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:F:364:ALA:CA	3:F:364:ALA:CB	1.79	1.58
2:B:207:THR:CG2	2:B:208:PRO:HD3	1.36	1.52
2:C:21:GLN:HG3	2:C:181:LEU:CD1	1.40	1.48
2:C:21:GLN:CG	2:C:181:LEU:HD11	1.54	1.36
2:C:264:PRO:O	2:C:267:VAL:HG13	1.22	1.32

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
2	A	306/363 (84%)	280 (92%)	23 (8%)	3 (1%)	19 52
2	B	306/363 (84%)	278 (91%)	25 (8%)	3 (1%)	19 52
2	C	317/363 (87%)	296 (93%)	18 (6%)	3 (1%)	21 55
3	D	14/44 (32%)	12 (86%)	2 (14%)	0	100 100
3	E	14/44 (32%)	13 (93%)	1 (7%)	0	100 100
3	F	14/44 (32%)	13 (93%)	0	1 (7%)	1 3
All	All	971/1221 (80%)	892 (92%)	69 (7%)	10 (1%)	19 52

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	57	THR
2	A	209	ALA
2	B	81	GLY
2	B	206	THR
2	C	236	ILE

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
2	A	251/301 (83%)	196 (78%)	55 (22%)	1 3
2	B	251/301 (83%)	202 (80%)	49 (20%)	2 5
2	C	263/301 (87%)	202 (77%)	61 (23%)	1 3
3	D	14/32 (44%)	5 (36%)	9 (64%)	0 0
3	E	14/32 (44%)	9 (64%)	5 (36%)	0 0
3	F	14/32 (44%)	10 (71%)	4 (29%)	0 1
All	All	807/999 (81%)	624 (77%)	183 (23%)	1 3

5 of 183 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	181	LEU
2	B	310	SER
2	C	319	LEU
2	B	195	VAL
2	B	220	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 34 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	242	GLN
2	B	326	ASN
2	C	331	GLN
2	B	293	ASN
2	A	246	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	N	9/10 (90%)	5 (55%)	0

All (5) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	N	2	C
1	N	3	U
1	N	4	U
1	N	5	A
1	N	7	A

There are no RNA pucker outliers to report.

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)

Of 5 ligands modelled in this entry, 5 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

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 (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

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates

EDS was not executed - this section will therefore be empty.

6.4 Ligands

EDS was not executed - this section will therefore be empty.

6.5 Other polymers

EDS was not executed - this section will therefore be empty.