



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2018 – 01:11 PM EST

PDB ID : 1C6V
Title : SIV INTEGRASE (CATALYTIC DOMAIN + DNA BINDING DOMAIN COMPRISING RESIDUES 50-293) MUTANT WITH PHE 185 REPLACED BY HIS (F185H)
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Deposited on : 1999-12-21
Resolution : 3.00 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 ⓘ symbol.

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

MolProbity : 4.02b-467
Xtrriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20030736

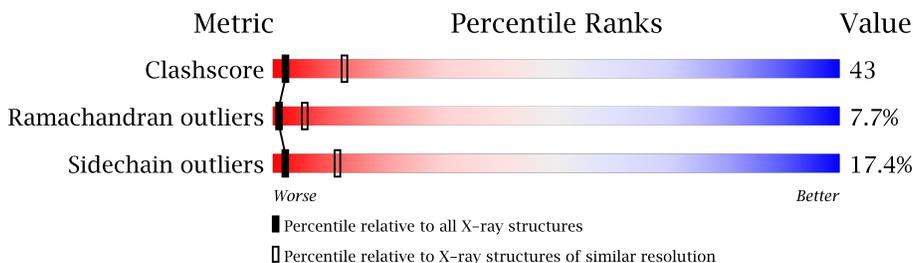
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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	112137	2037 (3.00-3.00)
Ramachandran outliers	110173	1973 (3.00-3.00)
Sidechain outliers	110143	1976 (3.00-3.00)

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 $\leq 5\%$. 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	164	
1	B	164	
1	C	164	
1	D	164	
2	X	81	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5030 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 PROTEIN (SIV INTEGRASE).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
			Total	C	N	O				S
1	A	148	1169	733	213	214	9	0	0	0
1	B	142	1111	697	203	202	9	0	0	0
1	C	143	1118	702	204	203	9	0	0	0
1	D	142	1111	697	203	202	9	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	185	HIS	PHE	ENGINEERED MUTATION	UNP Q88016
B	185	HIS	PHE	ENGINEERED MUTATION	UNP Q88016
C	185	HIS	PHE	ENGINEERED MUTATION	UNP Q88016
D	185	HIS	PHE	ENGINEERED MUTATION	UNP Q88016

- Molecule 2 is a protein called PROTEIN (SIU89134).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	X	55	455	296	85	74	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
X	250	LEU	ILE	CONFLICT	UNP Q87706

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	16	Total 16	O 16	0	0
3	B	10	Total 10	O 10	0	0
3	C	24	Total 24	O 24	0	0
3	D	12	Total 12	O 12	0	0
3	X	4	Total 4	O 4	0	0



- Molecule 1: PROTEIN (SIV INTEGRASE)

Chain D: 40% 37% 9% 13%



- Molecule 2: PROTEIN (SIU89134)

Chain X: 22% 33% 12% 32%



4 Data and refinement statistics

Xtrriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	79.57Å 100.00Å 150.50Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	6.00 – 3.00	Depositor
% Data completeness (in resolution range)	(Not available) (6.00-3.00)	Depositor
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.203 , 0.362	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	5030	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.52	0/1192	0.81	0/1612
1	B	0.48	0/1133	0.84	2/1533 (0.1%)
1	C	0.51	0/1140	0.85	4/1543 (0.3%)
1	D	0.46	0/1133	0.74	0/1533
2	X	0.49	0/464	0.77	0/618
All	All	0.49	0/5062	0.80	6/6839 (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	C	190	GLY	N-CA-C	-6.53	96.76	113.10
1	C	121	PHE	N-CA-C	5.49	125.81	111.00
1	B	101	LEU	CA-CB-CG	5.47	127.88	115.30
1	B	187	ARG	N-CA-C	5.41	125.59	111.00
1	C	104	LEU	CA-CB-CG	5.24	127.36	115.30

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	A	1169	0	1146	118	0
1	B	1111	0	1092	104	0
1	C	1118	0	1101	115	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	1111	0	1092	78	0
2	X	455	0	487	44	0
3	A	16	0	0	2	0
3	B	10	0	0	0	0
3	C	24	0	0	1	0
3	D	12	0	0	0	0
3	X	4	0	0	0	0
All	All	5030	0	4918	423	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 43.

The worst 5 of 423 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:B:119:ALA:HA	1:B:122:ALA:HB3	1.22	1.11
1:B:71:LYS:HG3	1:B:172:VAL:HG21	1.44	1.00
1:A:165:ILE:HD11	1:A:182:CYS:SG	2.03	0.98
1:B:158:LEU:HA	1:B:183:MET:HE1	1.46	0.95
1:B:81:SER:HA	1:B:199:ARG:HD2	1.46	0.94

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	144/164 (88%)	107 (74%)	25 (17%)	12 (8%)	1 4
1	B	138/164 (84%)	109 (79%)	18 (13%)	11 (8%)	1 5
1	C	139/164 (85%)	105 (76%)	25 (18%)	9 (6%)	1 8
1	D	138/164 (84%)	115 (83%)	15 (11%)	8 (6%)	2 11

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	X	53/81 (65%)	33 (62%)	13 (24%)	7 (13%)	0	1
All	All	612/737 (83%)	469 (77%)	96 (16%)	47 (8%)	1	5

5 of 47 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	79	VAL
1	A	117	ASN
1	A	153	ALA
1	A	166	ARG
1	B	139	PHE

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	
1	A	124/138 (90%)	104 (84%)	20 (16%)	3	14
1	B	117/138 (85%)	98 (84%)	19 (16%)	3	14
1	C	118/138 (86%)	96 (81%)	22 (19%)	2	10
1	D	117/138 (85%)	96 (82%)	21 (18%)	2	11
2	X	47/67 (70%)	38 (81%)	9 (19%)	2	9
All	All	523/619 (84%)	432 (83%)	91 (17%)	2	11

5 of 91 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	71	LYS
1	C	128	MET
2	X	227	TYR
1	C	72	ILE
1	C	96	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 27 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	67	HIS
1	C	124	GLN
1	D	160	ASN
1	C	114	HIS
1	A	184	ASN

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 carbohydrates 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

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.