



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 06:12 AM UTC

PDB ID : 1SVA / pdb_00001sva
Title : SIMIAN VIRUS 40
Authors : Stehle, T.; Gamblin, S.J.; Harrison, S.C.
Deposited on : 1995-11-27
Resolution : 3.10 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

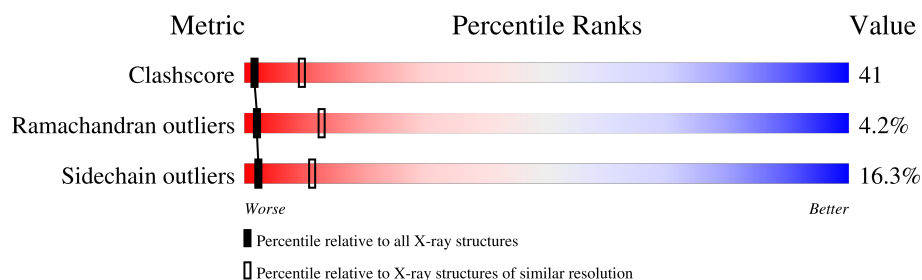
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 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	190562	1539 (3.10-3.10)
Ramachandran outliers	187476	1467 (3.10-3.10)
Sidechain outliers	187428	1467 (3.10-3.10)

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	1	361	27% 45% 19% 5% .
1	2	361	28% 50% 16% . .
1	3	361	33% 42% 17% . 5%
1	4	361	29% 46% 14% . 8%
1	5	361	29% 46% 18% . .
1	6	361	38% 43% 13% . 6%

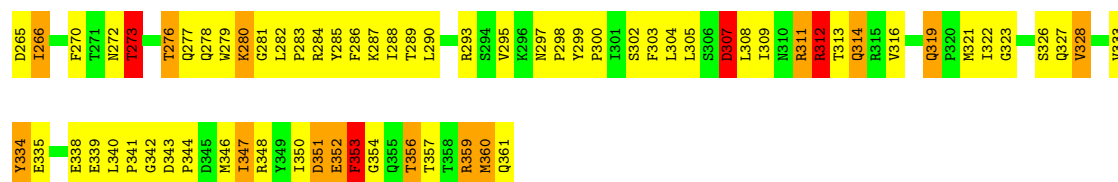
2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 15983 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.

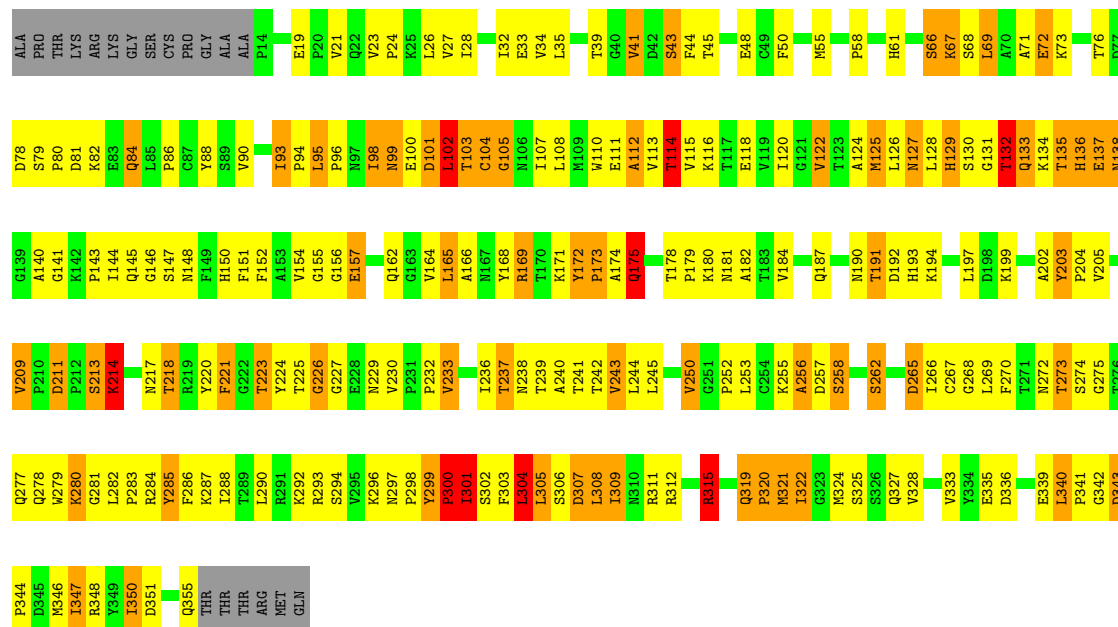
- Molecule 1 is a protein called SIMIAN VIRUS 40.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	1	348	Total	C	N	O	S	0	0	0
			2707	1703	460	530	14			
1	2	348	Total	C	N	O	S	0	0	0
			2707	1703	460	530	14			
1	3	342	Total	C	N	O	S	0	0	0
			2658	1675	450	520	13			
1	4	331	Total	C	N	O	S	0	0	0
			2560	1612	435	501	12			
1	5	347	Total	C	N	O	S	0	0	0
			2700	1698	459	529	14			
1	6	341	Total	C	N	O	S	0	0	0
			2651	1670	449	519	13			



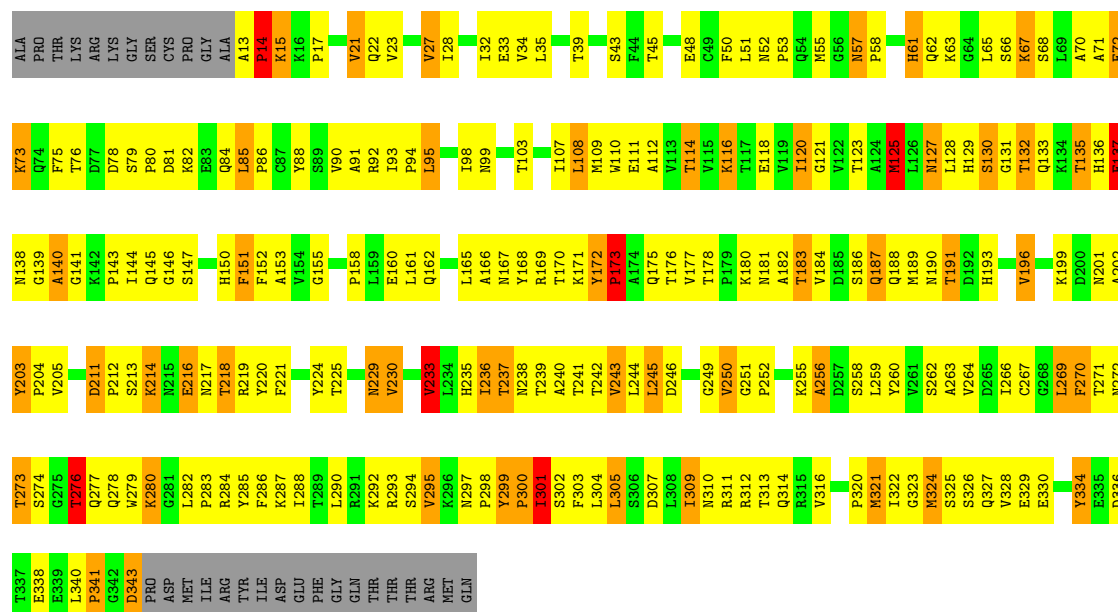
• Molecule 1: SIMIAN VIRUS 40

Chain 3: 33% 42% 17% 5%



• Molecule 1: SIMIAN VIRUS 40

Chain 4: 29% 46% 14% 8%



Chain 5: 29% 46% 18% . .



4 Data and refinement statistics

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

Property	Value	Source
Space group	I 2 3	Depositor
Cell constants a, b, c, α , β , γ	558.00Å 558.00Å 558.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	12.00 – 3.10	Depositor
% Data completeness (in resolution range)	80.2 (12.00-3.10)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.257 , 0.268	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	15983	wwPDB-VP
Average B, all atoms (Å ²)	56.0	wwPDB-VP

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	1	1.13	6/2766 (0.2%)	1.60	72/3761 (1.9%)
1	2	1.18	12/2766 (0.4%)	1.48	41/3761 (1.1%)
1	3	1.19	10/2717 (0.4%)	1.65	65/3695 (1.8%)
1	4	1.23	7/2616 (0.3%)	1.55	46/3560 (1.3%)
1	5	1.18	8/2758 (0.3%)	1.57	55/3750 (1.5%)
1	6	1.30	18/2709 (0.7%)	1.55	41/3684 (1.1%)
All	All	1.20	61/16332 (0.4%)	1.57	320/22211 (1.4%)

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	2	0	1
1	6	0	1
All	All	0	2

The worst 5 of 61 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	4	138	ASN	N-CA	11.49	1.58	1.46
1	6	125	MET	SD-CE	-9.79	1.55	1.79
1	6	27	VAL	CA-CB	-8.36	1.45	1.54
1	4	288	ILE	CA-CB	-8.19	1.44	1.54
1	3	243	VAL	CA-CB	-7.62	1.44	1.54

The worst 5 of 320 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	256	ALA	N-CA-C	-13.37	89.94	109.59
1	4	256	ALA	N-CA-C	-13.09	91.11	110.48
1	3	256	ALA	N-CA-C	-12.21	90.34	109.76

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	5	93	ILE	CA-C-N	11.62	134.37	119.84
1	5	93	ILE	C-N-CA	11.62	134.37	119.84

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	2	88	TYR	Sidechain
1	6	285	TYR	Sidechain

5.2 Too-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 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	1	2707	0	2676	268	0
1	2	2707	0	2676	259	0
1	3	2658	0	2625	228	0
1	4	2560	0	2535	250	0
1	5	2700	0	2668	273	0
1	6	2651	0	2617	193	0
All	All	15983	0	15797	1318	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 41.

The worst 5 of 1318 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)
1:2:121:GLY:HA2	1:3:209:VAL:HG11	1.28	1.12
1:4:27:VAL:HG12	1:4:28:ILE:HG22	1.31	1.12
1:1:27:VAL:HG12	1:1:28:ILE:HG22	1.26	1.10
1:6:237:THR:HG22	1:6:239:THR:H	1.14	1.09
1:5:165:LEU:HD11	1:5:168:TYR:HA	1.39	1.05

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	1	346/361 (96%)	276 (80%)	48 (14%)	22 (6%)	1	6
1	2	346/361 (96%)	292 (84%)	40 (12%)	14 (4%)	2	13
1	3	340/361 (94%)	287 (84%)	39 (12%)	14 (4%)	2	13
1	4	329/361 (91%)	267 (81%)	49 (15%)	13 (4%)	2	13
1	5	345/361 (96%)	279 (81%)	54 (16%)	12 (4%)	3	16
1	6	339/361 (94%)	288 (85%)	41 (12%)	10 (3%)	3	19
All	All	2045/2166 (94%)	1689 (83%)	271 (13%)	85 (4%)	2	13

5 of 85 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	1	137	GLU
1	1	174	ALA
1	1	191	THR
1	1	257	ASP
1	1	300	PRO

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	1	306/314 (98%)	242 (79%)	64 (21%)	1	5
1	2	306/314 (98%)	265 (87%)	41 (13%)	4	17
1	3	300/314 (96%)	251 (84%)	49 (16%)	2	11

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	4	289/314 (92%)	247 (86%)	42 (14%)	3	14
1	5	305/314 (97%)	246 (81%)	59 (19%)	1	7
1	6	299/314 (95%)	260 (87%)	39 (13%)	4	18
All	All	1805/1884 (96%)	1511 (84%)	294 (16%)	2	11

5 of 294 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	5	245	LEU
1	6	298	PRO
1	5	280	LYS
1	6	76	THR
1	2	289	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 102 such sidechains are listed below:

Mol	Chain	Res	Type
1	4	99	ASN
1	5	62	GLN
1	6	229	ASN
1	4	129	HIS
1	4	201	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 ⓘ

There are no oligosaccharides 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.