



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 05:45 AM GMT

PDB ID : 2SNV
Title : THE REFINED STRUCTURE OF SINDBIS VIRUS CORE PROTEIN IN
COMPARISON WITH OTHER CHYMOTRYPSIN-LIKE SERINE PRO-
TEINASE STRUCTURES
Authors : Tong, L.; Rossmann, M.G.
Deposited on : 1992-07-17
Resolution : 2.80 Å(reported)

This is a Full wwPDB X-ray Structure 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/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
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

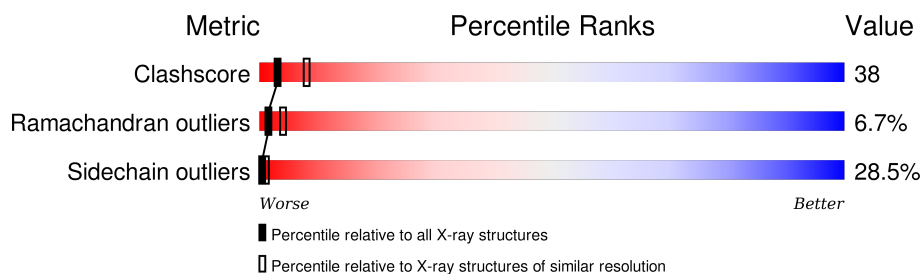
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 Å.

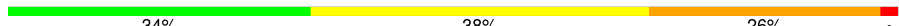
Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



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)

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	151	 34% 38% 26% •

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 1164 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 SINDBIS VIRUS COAT PROTEIN.

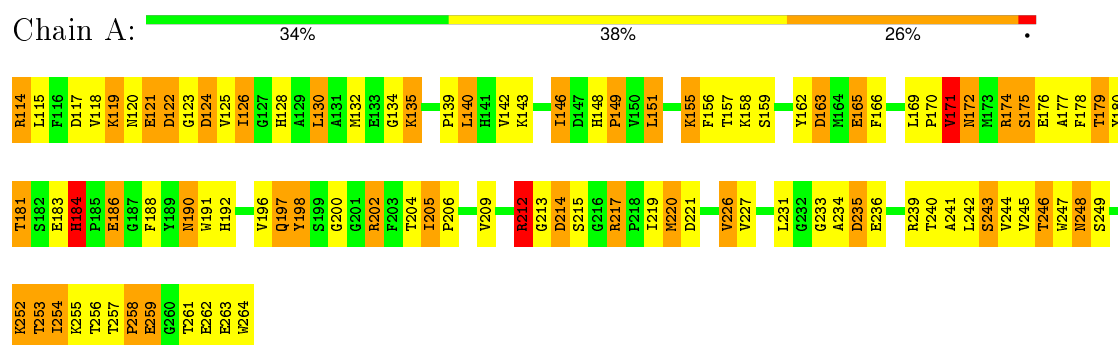
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	151	1164	731	207	221	5	0	0	0

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.

Note EDS was not executed.

• Molecule 1: SINDBIS VIRUS COAT PROTEIN



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	57.00 Å 57.00 Å 109.80 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	(Not available) – 2.80	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-2.80)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.200 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	1164	wwPDB-VP
Average B, all atoms (Å ²)	27.0	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	A	1.40	9/1192 (0.8%)	1.67	22/1609 (1.4%)

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	186	GLU	CD-OE1	8.71	1.35	1.25
1	A	176	GLU	CD-OE1	8.56	1.35	1.25
1	A	121	GLU	CD-OE1	8.02	1.34	1.25
1	A	165	GLU	CD-OE1	7.26	1.33	1.25
1	A	259	GLU	CD-OE1	6.39	1.32	1.25
1	A	236	GLU	CD-OE1	6.15	1.32	1.25
1	A	262	GLU	CD-OE1	6.03	1.32	1.25
1	A	263	GLU	CD-OE2	5.78	1.32	1.25
1	A	254	ILE	N-CA	-5.64	1.35	1.46

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	122	ASP	CB-CG-OD1	8.29	125.76	118.30
1	A	117	ASP	CB-CG-OD2	-8.20	110.92	118.30
1	A	257	THR	C-N-CD	-8.05	102.89	120.60
1	A	214	ASP	CB-CG-OD2	-7.52	111.53	118.30
1	A	248	ASN	C-N-CA	7.21	139.72	121.70
1	A	212	ARG	NE-CZ-NH2	-6.80	116.90	120.30
1	A	202	ARG	NE-CZ-NH1	6.79	123.69	120.30
1	A	212	ARG	NE-CZ-NH1	6.74	123.67	120.30
1	A	214	ASP	CB-CG-OD1	6.68	124.31	118.30
1	A	221	ASP	CB-CG-OD2	6.64	124.27	118.30
1	A	239	ARG	NE-CZ-NH1	6.31	123.46	120.30
1	A	117	ASP	CB-CG-OD1	6.24	123.92	118.30
1	A	235	ASP	CB-CG-OD1	6.09	123.78	118.30
1	A	248	ASN	N-CA-CB	5.74	120.94	110.60
1	A	123	GLY	N-CA-C	-5.73	98.77	113.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	163	ASP	CB-CG-OD2	5.59	123.33	118.30
1	A	124	ASP	CB-CG-OD2	5.59	123.33	118.30
1	A	248	ASN	CA-C-N	-5.57	104.95	117.20
1	A	254	ILE	N-CA-CB	-5.53	98.08	110.80
1	A	124	ASP	CB-CG-OD1	-5.50	113.35	118.30
1	A	163	ASP	CB-CG-OD1	-5.47	113.38	118.30
1	A	184	HIS	CA-CB-CG	5.18	122.41	113.60

There are no chirality outliers.

There are no planarity outliers.

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	A	1164	0	1134	88	0
All	All	1164	0	1134	88	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 38.

All (88) 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:A:212:ARG:HG2	1:A:212:ARG:HH11	1.26	1.00
1:A:248:ASN:HB3	1:A:255:LYS:HZ2	1.31	0.94
1:A:231:LEU:HD11	1:A:245:VAL:HG23	1.50	0.93
1:A:169:LEU:HD13	1:A:174:ARG:HA	1.51	0.92
1:A:248:ASN:HB3	1:A:255:LYS:NZ	1.84	0.92
1:A:120:ASN:ND2	1:A:124:ASP:HB2	1.85	0.91
1:A:202:ARG:HE	1:A:241:ALA:HB2	1.48	0.79
1:A:206:PRO:HG2	1:A:209:VAL:HG21	1.65	0.78
1:A:202:ARG:NE	1:A:241:ALA:HB2	2.02	0.75
1:A:254:ILE:O	1:A:255:LYS:HG3	1.88	0.73
1:A:132:MET:SD	1:A:226:VAL:HG11	2.32	0.69
1:A:247:TRP:HA	1:A:253:THR:O	1.93	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:248:ASN:CB	1:A:255:LYS:HZ2	2.08	0.65
1:A:245:VAL:HA	1:A:255:LYS:O	1.97	0.65
1:A:135:LYS:HB3	1:A:135:LYS:NZ	2.12	0.65
1:A:119:LYS:HA	1:A:124:ASP:O	1.95	0.64
1:A:114:ARG:HG2	1:A:178:PHE:CD2	2.33	0.63
1:A:134:GLY:HA2	1:A:174:ARG:HD3	1.81	0.62
1:A:184:HIS:HD2	1:A:227:VAL:HG22	1.66	0.60
1:A:130:LEU:HD13	1:A:130:LEU:O	2.02	0.60
1:A:240:THR:HG21	1:A:264:TRP:HH2	1.65	0.59
1:A:169:LEU:CD1	1:A:174:ARG:HA	2.27	0.59
1:A:212:ARG:HG2	1:A:212:ARG:NH1	2.01	0.59
1:A:202:ARG:HE	1:A:241:ALA:CB	2.16	0.58
1:A:139:PRO:HB3	1:A:231:LEU:HD23	1.85	0.58
1:A:162:TYR:HA	1:A:256:THR:OG1	2.04	0.57
1:A:140:LEU:CD2	1:A:165:GLU:HB2	2.35	0.56
1:A:120:ASN:HD21	1:A:124:ASP:HB2	1.66	0.56
1:A:214:ASP:O	1:A:217:ARG:HG3	2.05	0.56
1:A:146:ILE:HD11	1:A:151:LEU:HB3	1.87	0.56
1:A:148:HIS:CD2	1:A:149:PRO:HD2	2.40	0.56
1:A:135:LYS:HB3	1:A:135:LYS:HZ2	1.70	0.56
1:A:148:HIS:HB3	1:A:151:LEU:HB2	1.87	0.55
1:A:159:SER:HG	1:A:162:TYR:HD2	1.53	0.55
1:A:186:GLU:HA	1:A:198:TYR:HB3	1.90	0.54
1:A:235:ASP:HA	1:A:240:THR:HA	1.90	0.54
1:A:171:VAL:O	1:A:171:VAL:HG13	2.08	0.54
1:A:114:ARG:HG2	1:A:178:PHE:CE2	2.44	0.53
1:A:205:ILE:HD12	1:A:242:LEU:HD11	1.90	0.53
1:A:126:ILE:HG13	1:A:142:VAL:HG13	1.91	0.52
1:A:205:ILE:CD1	1:A:242:LEU:HD11	2.40	0.52
1:A:140:LEU:HD22	1:A:165:GLU:HB2	1.91	0.51
1:A:246:THR:CG2	1:A:247:TRP:N	2.74	0.51
1:A:146:ILE:HD11	1:A:151:LEU:CB	2.40	0.51
1:A:252:LYS:HG3	1:A:252:LYS:O	2.12	0.50
1:A:233:GLY:HA3	1:A:264:TRP:CH2	2.47	0.50
1:A:234:ALA:HB3	1:A:259:GLU:HB2	1.94	0.49
1:A:132:MET:HB2	1:A:178:PHE:HB2	1.93	0.49
1:A:119:LYS:HD3	1:A:125:VAL:HG22	1.94	0.49
1:A:157:THR:HB	1:A:166:PHE:CZ	2.48	0.49
1:A:214:ASP:HA	1:A:217:ARG:HG3	1.94	0.49
1:A:188:PHE:HA	1:A:196:VAL:O	2.13	0.49
1:A:155:LYS:NZ	1:A:155:LYS:HA	2.28	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:114:ARG:HB3	1:A:178:PHE:CE2	2.47	0.49
1:A:170:PRO:O	1:A:172:ASN:N	2.43	0.48
1:A:197:GLN:HG3	1:A:198:TYR:N	2.29	0.48
1:A:214:ASP:OD1	1:A:217:ARG:NH1	2.44	0.48
1:A:198:TYR:HD1	1:A:198:TYR:HA	1.58	0.48
1:A:132:MET:SD	1:A:226:VAL:CG1	3.02	0.47
1:A:247:TRP:CD1	1:A:252:LYS:HB2	2.50	0.47
1:A:162:TYR:CE1	1:A:254:ILE:HG23	2.50	0.46
1:A:243:SER:OG	1:A:261:THR:HG21	2.16	0.46
1:A:196:VAL:HG11	1:A:219:ILE:HD13	1.98	0.46
1:A:256:THR:O	1:A:258:PRO:HD3	2.17	0.45
1:A:159:SER:OG	1:A:162:TYR:HD2	1.98	0.45
1:A:134:GLY:O	1:A:169:LEU:HB2	2.17	0.45
1:A:139:PRO:HB3	1:A:231:LEU:CD2	2.46	0.44
1:A:120:ASN:HD22	1:A:126:ILE:HG23	1.82	0.44
1:A:179:THR:O	1:A:226:VAL:HG12	2.16	0.44
1:A:120:ASN:CG	1:A:124:ASP:HB2	2.36	0.44
1:A:118:VAL:HG11	1:A:142:VAL:HG12	1.99	0.44
1:A:126:ILE:HG12	1:A:126:ILE:H	1.68	0.44
1:A:180:TYR:CG	1:A:181:THR:N	2.86	0.44
1:A:174:ARG:O	1:A:177:ALA:HB2	2.18	0.43
1:A:202:ARG:NE	1:A:241:ALA:CB	2.77	0.42
1:A:190:ASN:OD1	1:A:190:ASN:N	2.52	0.42
1:A:256:THR:C	1:A:258:PRO:HD3	2.40	0.42
1:A:155:LYS:HZ2	1:A:155:LYS:HA	1.84	0.42
1:A:162:TYR:O	1:A:163:ASP:HB3	2.20	0.41
1:A:202:ARG:CZ	1:A:241:ALA:HB2	2.50	0.41
1:A:220:MET:H	1:A:220:MET:HG2	1.69	0.41
1:A:156:PHE:HB3	1:A:165:GLU:CG	2.50	0.41
1:A:134:GLY:HA2	1:A:169:LEU:HD12	2.01	0.41
1:A:206:PRO:CG	1:A:209:VAL:HG21	2.44	0.41
1:A:254:ILE:C	1:A:255:LYS:HG3	2.42	0.40
1:A:135:LYS:CB	1:A:135:LYS:NZ	2.81	0.40
1:A:240:THR:HG21	1:A:264:TRP:CH2	2.52	0.40
1:A:128:HIS:ND1	1:A:213:GLY:O	2.54	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
1	A	149/151 (99%)	123 (83%)	16 (11%)	10 (7%)	1 4

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	121	GLU
1	A	172	ASN
1	A	249	SER
1	A	258	PRO
1	A	171	VAL
1	A	192	HIS
1	A	175	SER
1	A	200	GLY
1	A	149	PRO
1	A	174	ARG

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	123/123 (100%)	88 (72%)	35 (28%)	0 1

All (35) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	114	ARG

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Mol	Chain	Res	Type
1	A	115	LEU
1	A	119	LYS
1	A	122	ASP
1	A	126	ILE
1	A	130	LEU
1	A	135	LYS
1	A	140	LEU
1	A	143	LYS
1	A	146	ILE
1	A	151	LEU
1	A	155	LYS
1	A	158	LYS
1	A	171	VAL
1	A	175	SER
1	A	179	THR
1	A	181	THR
1	A	183	GLU
1	A	184	HIS
1	A	190	ASN
1	A	191	TRP
1	A	197	GLN
1	A	198	TYR
1	A	204	THR
1	A	205	ILE
1	A	212	ARG
1	A	215	SER
1	A	217	ARG
1	A	220	MET
1	A	226	VAL
1	A	243	SER
1	A	244	VAL
1	A	246	THR
1	A	252	LYS
1	A	253	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	168	GLN
1	A	184	HIS
1	A	222	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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

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

6.4 Ligands [i](#)

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

6.5 Other polymers [i](#)

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