



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 12, 2026 – 09:34 PM UTC

PDB ID : 3S6P / pdb_00003s6p
Title : Crystal Structure of Helicoverpa Armigera Stunt Virus
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Deposited on : 2011-05-25
Resolution : 2.50 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)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

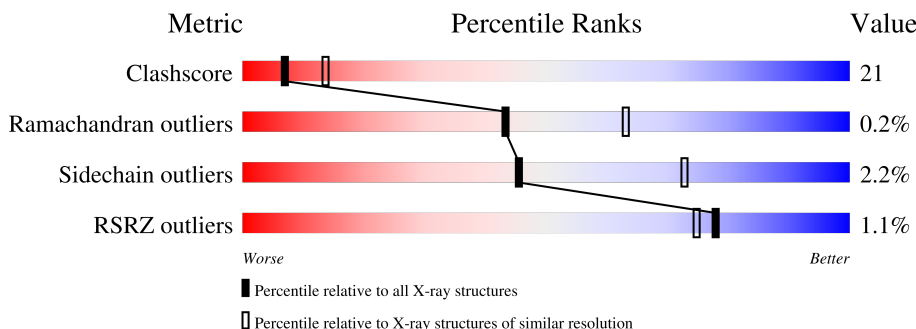
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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 $\leq 5\%$. 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.

Mol	Chain	Length	Quality of chain
1	A	575	% 61% 28% • 8%
1	B	575	% 62% 28% • 8%
1	C	575	% 60% 31% • 7%
1	D	575	% 65% 25% • 7%
2	E	72	31% 15% 54%
2	F	72	% 22% 11% 67%

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Mol	Chain	Length	Quality of chain
2	G	72	6% 61% 25% 12%
2	H	72	51% 33% 12%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 19383 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 Capsid protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	529	Total	C	N	O	S	0	4	0
			4145	2629	695	809	12			
1	B	530	Total	C	N	O	S	0	3	0
			4143	2628	694	809	12			
1	C	536	Total	C	N	O	S	0	2	0
			4182	2652	704	814	12			
1	D	532	Total	C	N	O	S	0	6	0
			4177	2652	701	811	13			

- Molecule 2 is a protein called Capsid protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	33	Total	C	N	O	S	0	0	0
			227	143	36	47	1			
2	F	24	Total	C	N	O	S	0	0	0
			164	103	26	34	1			
2	G	72	Total	C	N	O	S	0	5	0
			547	339	112	93	3			
2	H	63	Total	C	N	O	S	0	5	0
			485	300	99	83	3			

- Molecule 3 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Ca	0	0
			1	1		
3	C	1	Total	Ca	0	0
			1	1		

- Molecule 4 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

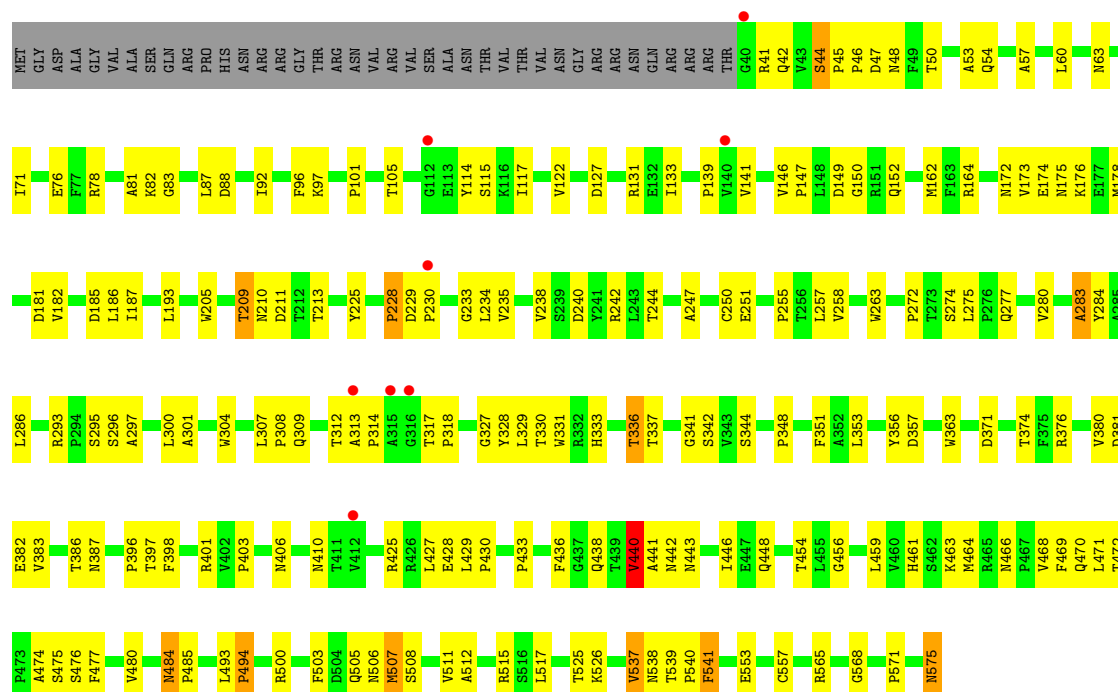
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	C	1	Total Cl 1 1	0	0
4	D	1	Total Cl 1 1	0	0

- Molecule 5 is water.

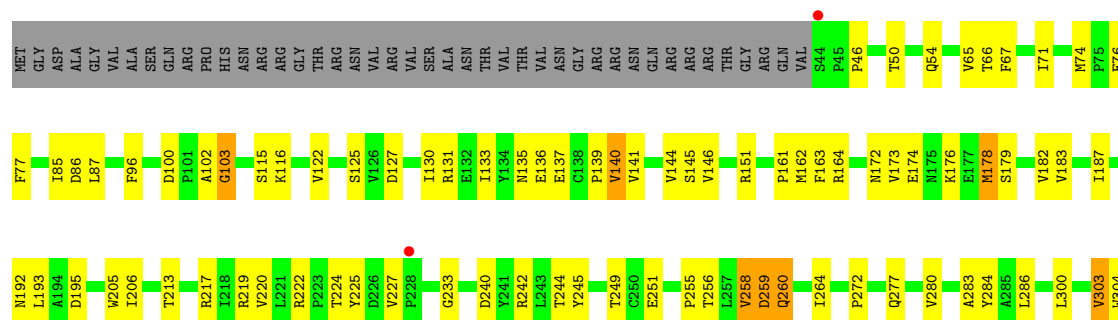
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	330	Total O 330 330	0	0
5	E	7	Total O 7 7	0	0
5	B	313	Total O 313 313	0	0
5	F	4	Total O 4 4	0	0
5	C	290	Total O 290 290	0	0
5	G	43	Total O 43 43	0	0
5	D	287	Total O 287 287	0	0
5	H	35	Total O 35 35	0	0

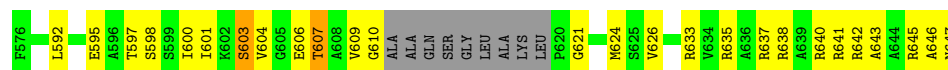


• Molecule 1: Capsid protein



• Molecule 1: Capsid protein





4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	404.12Å 405.57Å 406.04Å 119.20° 114.44° 94.79°	Depositor
Resolution (Å)	40.00 – 2.50 40.00 – 2.50	Depositor EDS
% Data completeness (in resolution range)	27.3 (40.00-2.50) 22.2 (40.00-2.50)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.64 (at 2.51Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.237 , (Not available) 0.240 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	32.9	Xtriage
Anisotropy	0.132	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 189.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.002 for k,h,-h-k-l 0.002 for l,-h-k-l,h 0.002 for -h-k-l,l,k	Xtriage
F_o, F_c correlation	0.49	EDS
Total number of atoms	19383	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.55% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.66	0/4270	1.08	31/5846 (0.5%)
1	B	0.66	0/4266	1.05	19/5842 (0.3%)
1	C	0.64	0/4303	1.07	23/5892 (0.4%)
1	D	0.65	0/4311	1.05	25/5902 (0.4%)
2	E	0.70	0/228	0.99	1/307 (0.3%)
2	F	0.79	0/165	0.92	0/222
2	G	0.73	1/565 (0.2%)	1.11	6/753 (0.8%)
2	H	0.67	0/502	1.08	3/664 (0.5%)
All	All	0.66	1/18610 (0.0%)	1.06	108/25428 (0.4%)

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
2	G	0	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	G	601	ILE	CA-CB	5.70	1.62	1.54

The worst 5 of 108 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	336	THR	N-CA-C	-8.53	102.32	112.89
1	D	280	VAL	N-CA-C	8.48	118.56	110.42
1	A	149	ASP	N-CA-C	8.23	121.14	110.53
1	C	280	VAL	N-CA-C	8.16	118.21	110.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	603	SER	N-CA-C	8.16	119.95	111.14

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	G	645[A]	ARG	Sidechain
2	G	645[B]	ARG	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	A	4145	0	3962	175	0
1	B	4143	0	3957	176	0
1	C	4182	0	4002	176	0
1	D	4177	0	4004	140	0
2	E	227	0	233	25	0
2	F	164	0	163	12	0
2	G	547	0	608	65	0
2	H	485	0	535	43	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
5	A	330	0	0	18	0
5	B	313	0	0	5	0
5	C	290	0	0	13	0
5	D	287	0	0	8	0
5	E	7	0	0	0	0
5	F	4	0	0	0	0
5	G	43	0	0	9	0
5	H	35	0	0	8	0
All	All	19383	0	17464	748	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 21.

The worst 5 of 748 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:181:ASP:CB	1:D:334:ASN:HD22	1.44	1.28
1:C:44:SER:OG	1:C:45:PRO:HA	1.36	1.23
1:A:575:ASN:C	1:A:575:ASN:HD22	1.46	1.20
1:B:575:ASN:C	1:B:575:ASN:HD22	1.49	1.17
1:B:160:PHE:HB2	1:B:162:MET:HE2	1.25	1.16

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	531/575 (92%)	509 (96%)	21 (4%)	1 (0%)	43	63
1	B	531/575 (92%)	509 (96%)	21 (4%)	1 (0%)	43	63
1	C	536/575 (93%)	512 (96%)	23 (4%)	1 (0%)	43	63
1	D	536/575 (93%)	517 (96%)	19 (4%)	0	100	100
2	E	31/72 (43%)	31 (100%)	0	0	100	100
2	F	22/72 (31%)	22 (100%)	0	0	100	100
2	G	75/72 (104%)	71 (95%)	3 (4%)	1 (1%)	9	18
2	H	63/72 (88%)	62 (98%)	1 (2%)	0	100	100
All	All	2325/2588 (90%)	2233 (96%)	88 (4%)	4 (0%)	43	63

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	296	SER
2	G	609	VAL
1	A	229	ASP

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Mol	Chain	Res	Type
1	B	230	PRO

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	449/483 (93%)	441 (98%)	8 (2%)	51	77
1	B	449/483 (93%)	440 (98%)	9 (2%)	48	75
1	C	453/483 (94%)	441 (97%)	12 (3%)	40	68
1	D	454/483 (94%)	444 (98%)	10 (2%)	45	73
2	E	24/49 (49%)	24 (100%)	0	100	100
2	F	17/49 (35%)	17 (100%)	0	100	100
2	G	54/49 (110%)	50 (93%)	4 (7%)	13	27
2	H	49/49 (100%)	48 (98%)	1 (2%)	48	75
All	All	1949/2128 (92%)	1905 (98%)	44 (2%)	45	72

5 of 44 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	575	ASN
1	D	141	VAL
2	G	600	ILE
2	G	624[B]	MET
1	D	178[B]	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 49 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	470	GLN
2	G	613	GLN
1	C	484	ASN
1	C	529	GLN

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Mol	Chain	Res	Type
1	D	135	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 4 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 ⓘ

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	A	529/575 (92%)	0.03	6 (1%) 78 75	19, 33, 84, 133	4 (0%)
1	B	530/575 (92%)	0.06	4 (0%) 82 80	18, 30, 85, 125	3 (0%)
1	C	536/575 (93%)	0.01	8 (1%) 72 68	15, 31, 73, 139	2 (0%)
1	D	532/575 (92%)	-0.09	3 (0%) 85 83	13, 30, 68, 124	7 (1%)
2	E	33/72 (45%)	0.12	0 100 100	24, 42, 133, 140	0
2	F	24/72 (33%)	0.31	1 (4%) 40 36	21, 30, 119, 131	0
2	G	72/72 (100%)	0.40	4 (5%) 30 26	25, 47, 123, 126	5 (6%)
2	H	63/72 (87%)	0.46	0 100 100	23, 46, 125, 130	5 (7%)
All	All	2319/2588 (89%)	0.03	26 (1%) 78 75	13, 32, 86, 140	26 (1%)

The worst 5 of 26 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	361	GLY	3.3
1	C	412	VAL	2.9
2	F	599	SER	2.7
1	A	122	VAL	2.7
1	C	315	ALA	2.7

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 oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	CL	C	577	1/1	0.95	0.23	64,64,64,64	0
3	CA	B	576	1/1	0.97	0.11	62,62,62,62	0
4	CL	D	576	1/1	0.97	0.13	56,56,56,56	0
3	CA	C	576	1/1	0.98	0.12	95,95,95,95	0

6.5 Other polymers [i](#)

There are no such residues in this entry.