wwPDB X-ray Structure Validation Summary Report (i)

May 17, 2020 – 08:24 pm BST

PDB ID	:	1CWP
Title	:	STRUCTURES OF THE NATIVE AND SWOLLEN FORMS OF COWPEA CHLOROTIC MOTTLE VIRUS DETERMINED BY X-RAY CRYSTALLOGRAPHY AND CRYO-ELECTRON MICROSCOPY
Authors	:	Speir, J.A.; Johnson, J.E.; Munshi, S.; Wang, G.; Timothy, S.; Baker, T.S.
Deposited on	:	1995-05-22
Resolution	:	3.20 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 (i) symbol.

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

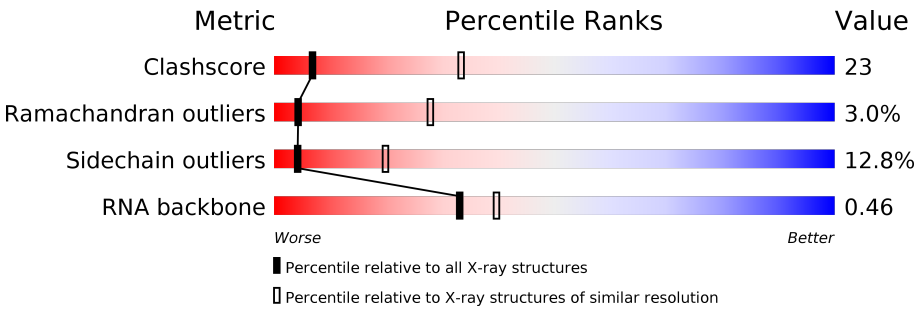
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 3.20 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	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)
RNA backbone	3102	1010 (3.50-2.90)

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 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 <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	D	4	25% 25% 50%
1	F	4	100%
2	E	2	50% 50%
3	A	190	47% 27% • • 22%
3	B	190	52% 27% 7% • 14%
3	C	190	47% 33% 5% • 14%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 3784 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(*AP*UP*AP*U)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
1	D	4	84	38	14	28	4	0	0	0
1	F	4	84	38	14	28	4	0	0	0

- Molecule 2 is a RNA chain called RNA (5'-R(*AP*U)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
2	E	2	42	19	7	14	2	0	0	0

- Molecule 3 is a protein called Coat protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	A	149	1122	717	181	221	3	0	0	0
3	B	164	1226	784	198	241	3	0	0	0
3	C	164	1226	784	198	241	3	0	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 the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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. 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(*AP*UP*AP*U)-3')

Chain D:

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

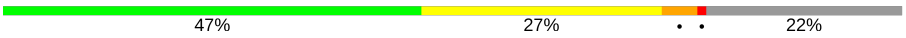
Chain F:

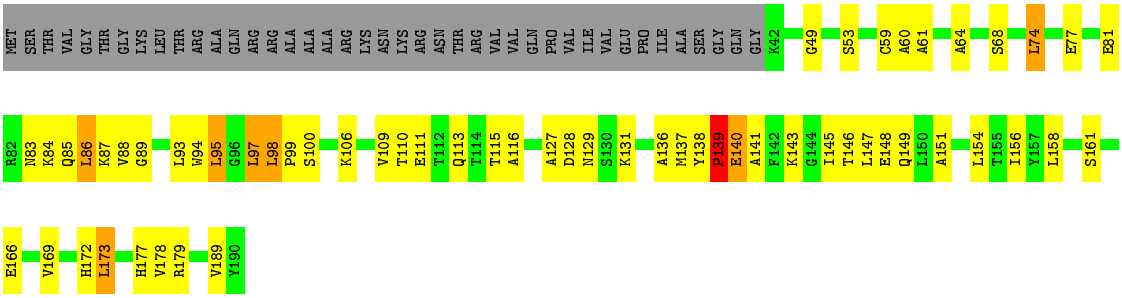
- Molecule 2: RNA (5'-R(*AP*U)-3')

Chain E:

- Molecule 3: Coat protein

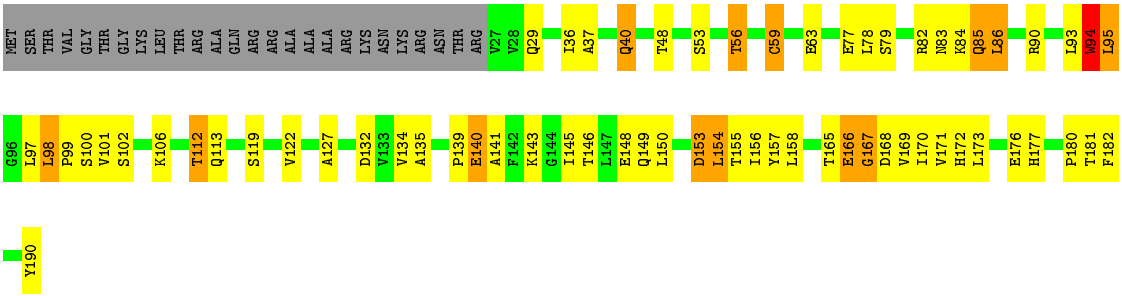
Chain A:





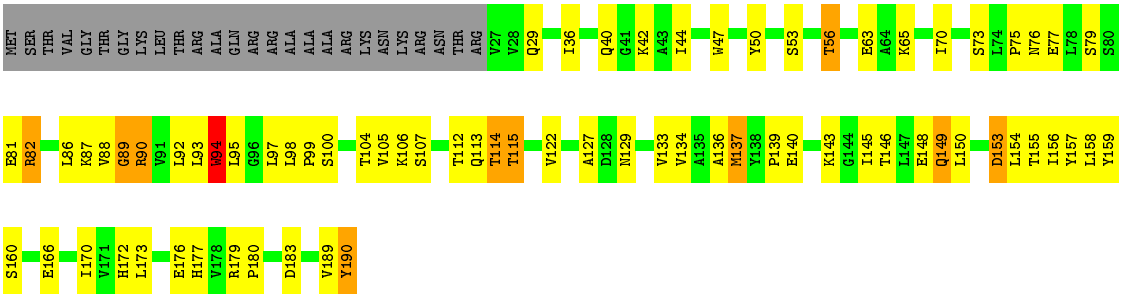
- Molecule 3: Coat protein

Chain B:



- Molecule 3: Coat protein

Chain C:



4 Data and refinement statistics (i)

Xtriage (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	381.30Å 381.30Å 408.60Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	7.00 – 3.20	Depositor
% Data completeness (in resolution range)	57.0 (7.00-3.20)	Depositor
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.310 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3784	wwPDB-VP
Average B, all atoms ($Å^2$)	19.0	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	D	4.32	4/93 (4.3%)	4.63	10/142 (7.0%)
1	F	1.03	0/93	1.70	1/142 (0.7%)
2	E	1.80	1/46 (2.2%)	1.44	0/69
3	A	0.55	0/1143	0.88	2/1560 (0.1%)
3	B	0.56	1/1249 (0.1%)	0.96	3/1707 (0.2%)
3	C	0.58	1/1249 (0.1%)	0.96	2/1707 (0.1%)
All	All	0.90	7/3873 (0.2%)	1.22	18/5327 (0.3%)

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
3	A	0	1
3	C	0	1
All	All	0	2

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	203	A	O3'-P	28.80	1.95	1.61
1	D	202	U	O3'-P	-24.04	1.32	1.61
1	D	203	A	N9-C4	-10.58	1.31	1.37
3	B	94	TRP	CB-CG	-6.57	1.38	1.50
3	C	94	TRP	CB-CG	-6.20	1.39	1.50

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	203	A	O3'-P-O5'	-24.17	58.08	104.00
1	D	203	A	OP2-P-O3'	24.04	158.08	105.20
1	D	202	U	OP2-P-O3'	-22.53	55.64	105.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	203	A	OP1-P-O3'	-20.73	59.59	105.20
1	D	203	A	P-O3'-C3'	14.89	137.57	119.70

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	A	139	PRO	Mainchain
3	C	190	TYR	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	D	84	0	42	12	0
1	F	84	0	41	28	0
2	E	42	0	22	2	0
3	A	1122	0	1133	40	0
3	B	1226	0	1243	45	0
3	C	1226	0	1243	60	0
All	All	3784	0	3724	174	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 23.

The worst 5 of 174 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:D:202:U:H2'	1:D:203:A:C8	1.58	1.37
1:F:203:A:O2'	1:F:204:U:O4'	1.54	1.24
1:F:203:A:H2'	1:F:204:U:C6	1.75	1.20
1:F:203:A:O2'	1:F:204:U:H5'	1.55	1.07
1:D:202:U:C2'	1:D:203:A:H8	1.71	1.03

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
3	A	147/190 (77%)	136 (92%)	8 (5%)	3 (2%)	7 38
3	B	162/190 (85%)	145 (90%)	12 (7%)	5 (3%)	4 26
3	C	162/190 (85%)	139 (86%)	17 (10%)	6 (4%)	3 22
All	All	471/570 (83%)	420 (89%)	37 (8%)	14 (3%)	4 28

5 of 14 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	116	ALA
3	A	140	GLU
3	B	140	GLU
3	C	90	ARG
3	A	139	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
3	A	122/154 (79%)	106 (87%)	16 (13%)	4 19
3	B	134/154 (87%)	117 (87%)	17 (13%)	4 20
3	C	134/154 (87%)	117 (87%)	17 (13%)	4 20
All	All	390/462 (84%)	340 (87%)	50 (13%)	4 20

5 of 50 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	B	79	SER
3	B	97	LEU
3	C	153	ASP
3	B	85	GLN
3	B	94	TRP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
3	B	83	ASN
3	C	177	HIS
3	B	149	GLN
3	A	113	GLN
3	B	177	HIS

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	D	3/4 (75%)	2 (66%)	2 (66%)
1	F	3/4 (75%)	2 (66%)	1 (33%)
2	E	1/2 (50%)	0	0
All	All	7/10 (70%)	4 (57%)	3 (42%)

All (4) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	D	203	A
1	D	204	U
1	F	203	A
1	F	204	U

All (3) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	D	202	U
1	D	203	A
1	F	202	U

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)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	D	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	D	203:A	O3'	204:U	P	1.95
1	D	202:U	O3'	203:A	P	1.32

6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.