

Full wwPDB X-ray Structure Validation Report (i)

May 16, 2020 - 10:31 am BST

PDB ID	:	4M0W
Title	:	Crystal Structure of SARS-CoV papain-like protease C112S mutant in complex
		with ubiquitin
Authors	:	Chou, CY.; Chen, HY.; Lai, HY.; Cheng, SC.; Chou, YW.
Deposited on		
Resolution	:	1.40 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 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 (1)) were used in the production of this report:

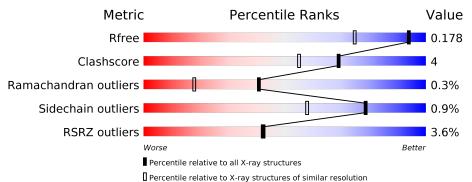
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
$\rm CCP4$:	$7.0.044 (\mathrm{Gargrove})$
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal 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 1.40 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries},{ m resolution\ range}({ m \AA}))$
R _{free}	130704	1714 (1.40-1.40)
Clashscore	141614	1812 (1.40-1.40)
Ramachandran outliers	138981	1763(1.40-1.40)
Sidechain outliers	138945	1762(1.40-1.40)
RSRZ outliers	127900	1674(1.40-1.40)

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% 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	А	327	90%	6% •
2	В	76	92%	7% •



2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 3535 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 Replicase polyprotein 1a.

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
1	А	317	Total 2548	C 1626	N 419	O 482	S 21	0	9	0

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	EXPRESSION TAG	UNP P0C6U8
А	112	SER	CYS	ENGINEERED MUTATION	UNP P0C6U8
А	320	LEU	-	EXPRESSION TAG	UNP P0C6U8
A	321	GLU	-	EXPRESSION TAG	UNP P0C6U8
А	322	HIS	-	EXPRESSION TAG	UNP P0C6U8
A	323	HIS	-	EXPRESSION TAG	UNP P0C6U8
А	324	HIS	-	EXPRESSION TAG	UNP P0C6U8
А	325	HIS	-	EXPRESSION TAG	UNP P0C6U8
А	326	HIS	-	EXPRESSION TAG	UNP P0C6U8
А	327	HIS	-	EXPRESSION TAG	UNP P0C6U8

• Molecule 2 is a protein called Ubiquitin.

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
2	В	76	Total 628	C 393	N 110	0 124	S 1	0	3	0

• Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

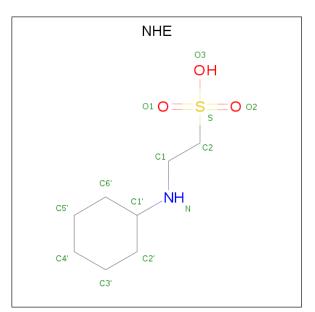
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total Z	ín 1	0	0

• Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).



Mo	l Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	1	Total Na 1 1	0	0

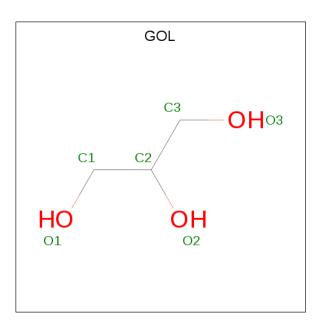
• Molecule 5 is 2-[N-CYCLOHEXYLAMINO]ETHANE SULFONIC ACID (three-letter code: NHE) (formula: C₈H₁₇NO₃S).



Mol	Chain	Residues		Ato	oms			ZeroOcc	AltConf
5	Λ	1	Total	С	Ν	Ο	S	0	0
0	А	L	13	8	1	3	1	0	0
Б	Δ	1	Total	С	Ν	Ο	S	0	0
			13	8	1	3	1		U

• Molecule 6 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	А	1	$\begin{array}{ccc} {\rm Total} & {\rm C} & {\rm O} \\ 6 & 3 & 3 \end{array}$	0	0
6	А	1	$\begin{array}{ccc} {\rm Total} & {\rm C} & {\rm O} \\ 6 & 3 & 3 \end{array}$	0	0
6	В	1	$\begin{array}{ccc} \text{Total} \text{C} \text{O} \\ 6 3 3 \end{array}$	0	0

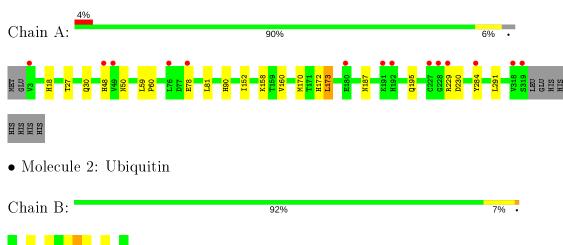
• Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	А	242	Total O 242 242	0	0
7	В	71	Total O 71 71	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 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.



• Molecule 1: Replicase polyprotein 1a



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	47.46Å 68.31 Å 68.42 Å	Depositor
a, b, c, α , β , γ	90.00° 95.66° 90.00°	Depositor
Resolution (Å)	30.00 - 1.40	Depositor
Resolution (A)	24.11 - 1.40	EDS
% Data completeness	99.5 (30.00-1.40)	Depositor
(in resolution range)	99.6 (24.11-1.40)	EDS
R _{merge}	(Not available)	Depositor
R _{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$2.72 (at 1.40 \text{\AA})$	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
D D.	0.156 , 0.180	Depositor
R, R_{free}	0.154 , 0.178	DCC
R_{free} test set	4248 reflections (5.00%)	wwPDB-VP
Wilson B-factor $(Å^2)$	14.8	Xtriage
Anisotropy	0.304	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.42 , 46.3	EDS
L-test for twinning ²	$ \langle L \rangle = 0.50, \langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	3535	wwPDB-VP
Average B, all atoms $(Å^2)$	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 6.11% of the height of the origin peak. No significant pseudotranslation is detected.

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.



¹Intensities estimated from amplitudes.

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: NHE, GOL, ZN, NA

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		
	Unam	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	0.45	0/2638	0.56	0/3576	
2	В	0.37	0/634	0.59	0/850	
All	All	0.44	0/3272	0.57	0/4426	

There are no bond length outliers.

There are no bond angle outliers.

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	А	2548	0	2535	18	0
2	В	628	0	653	6	0
3	А	1	0	0	0	0
4	А	1	0	0	0	0
5	А	26	0	34	0	0
6	А	12	0	16	1	0
6	В	6	0	8	1	0
7	А	242	0	0	3	0
7	В	71	0	0	1	0
All	All	3535	0	3246	24	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 4.

All (24) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic	Clash
Atom-1	At0111-2	distance (Å)	overlap (Å)
1:A:59:LEU:HD12	1:A:60:PRO:HD2	1.42	0.99
1:A:48:HIS:HD2	1:A:50:ASN:H	1.37	0.71
1:A:59:LEU:HD12	1:A:60:PRO:CD	2.23	0.68
1:A:78:GLU:H	1:A:78:GLU:CD	2.02	0.63
1:A:27:THR:H	1:A:30:GLN:HE21	1.48	0.62
1:A:152:ILE:HG12	1:A:173[A]:LEU:HD21	1.82	0.61
1:A:172:HIS:HE1	7:A:635:HOH:O	1.84	0.60
1:A:229:ARG:HG3	1:A:230:ASP:N	2.20	0.57
2:B:24:GLU:HG2	6:B:101:GOL:H31	1.88	0.56
1:A:48:HIS:CD2	1:A:50:ASN:H	2.22	0.56
1:A:284:TYR:CD2	1:A:291:LEU:HD11	2.42	0.55
2:B:68:HIS:HD2	7:B:203:HOH:O	1.91	0.53
1:A:229:ARG:HG3	1:A:230:ASP:H	1.75	0.51
1:A:187[A]:ASN:ND2	7:A:650:HOH:O	2.42	0.51
1:A:187[A]:ASN:OD1	1:A:195:GLN:HG2	2.10	0.51
1:A:18:HIS:HB3	6:A:405:GOL:H32	1.93	0.51
2:B:31[B]:GLN:C	2:B:33[B]:LYS:H	2.14	0.50
2:B:31[B]:GLN:O	2:B:33[B]:LYS:N	2.46	0.48
1:A:187[A]:ASN:OD1	1:A:195:GLN:CG	2.61	0.48
2:B:29:LYS:HA	2:B:32[B]:ASP:HB2	1.96	0.48
1:A:27:THR:H	1:A:30:GLN:NE2	2.11	0.46
1:A:158:LYS:HD3	7:A:624:HOH:O	2.14	0.46
2:B:31[B]:GLN:C	2:B:33[B]:LYS:N	2.70	0.45
1:A:90:HIS:HB2	1:A:160:VAL:HG21	2.03	0.41

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	Perce	ntiles
1	А	326/327~(100%)	320~(98%)	6(2%)	0	100	100
2	В	77/76~(101%)	71 (92%)	4(5%)	2(3%)	5	0
All	All	403/403~(100%)	391~(97%)	10~(2%)	2~(0%)	41	9

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	В	32[A]	ASP
2	В	32[B]	ASP

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	Analysed Rotameric Outliers		Percentiles		
1	А	285/284~(100%)	278~(98%)	7~(2%)	47 14		
2	В	71/68~(104%)	71~(100%)	0	100 100		
All	All	356/352~(101%)	349~(98%)	7~(2%)	78 23		

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	81	LEU
1	А	170[A]	MET
1	А	170[B]	MET
1	А	170[C]	MET
1	А	170[D]	MET
1	А	173[A]	LEU
1	А	173[B]	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	\mathbf{Res}	Type
1	А	30	GLN
1	А	48	HIS

Continued on next page...



Mol	Chain	Res	Type
1	А	50	ASN
1	А	172	HIS
1	А	195	GLN
1	А	256	GLN
1	А	263	ASN
2	В	2	GLN
2	В	25	ASN
2	В	68	HIS

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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)

Of 7 ligands modelled in this entry, 2 are monoatomic - leaving 5 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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| > 2 is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	True	Chain	Res Link		Chain Bog Link Bond lengths			$_{\rm ths}$	Bond angles		
	Type	Chain	nes		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2	
6	GOL	А	406	-	$5,\!5,\!5$	0.26	0	5, 5, 5	0.30	0	
6	GOL	А	405	-	$5,\!5,\!5$	0.30	0	5, 5, 5	0.63	0	
6	GOL	В	101	-	$5,\!5,\!5$	0.35	0	5, 5, 5	0.25	0	
5	NHE	А	403	-	$13,\!13,\!13$	2.67	2 (15%)	16,17,17	3.45	10 (62%)	
5	NHE	А	404	-	13, 13, 13	2.43	2 (15%)	16,17,17	<mark>6.31</mark>	<mark>6 (37%)</mark>	



In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	GOL	А	406	-	-	0/4/4/4	-
6	GOL	А	405	-	-	2/4/4/4	-
6	GOL	В	101	-	-	0/4/4/4	-
5	NHE	А	403	-	-	2/7/15/15	0/1/1/1
5	NHE	А	404	-	-	3/7/15/15	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\operatorname{\AA})$	Ideal(Å)
5	А	403	NHE	C2-S	-8.44	1.65	1.77
5	А	404	NHE	C2-S	-7.20	1.67	1.77
5	А	404	NHE	O3-S	4.62	1.63	1.47
5	А	403	NHE	O3-S	3.91	1.61	1.47

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
5	А	404	NHE	O3-S-C2	-12.69	85.24	105.77
5	А	404	NHE	O2-S-C2	10.96	120.11	106.92
5	А	404	NHE	O3-S-O2	-10.82	84.84	111.27
5	А	404	NHE	O3-S-O1	-10.15	86.47	111.27
5	А	404	NHE	O1-S-C2	9.71	118.61	106.92
5	А	403	NHE	O1-S-C2	7.50	115.95	106.92
5	А	404	NHE	C1-N-C1'	5.61	125.16	114.14
5	А	403	NHE	O3-S-O1	-4.69	99.81	111.27
5	А	403	NHE	O2-S-C2	4.47	112.30	106.92
5	А	403	NHE	C1-N-C1'	4.23	122.45	114.14
5	А	403	NHE	O3-S-C2	-3.97	99.35	105.77
5	А	403	NHE	O3-S-O2	-3.65	102.36	111.27
5	А	403	NHE	C3'-C2'-C1'	3.46	117.63	111.11
5	А	403	NHE	C5'-C6'-C1'	3.34	117.40	111.11
5	А	403	NHE	C6'-C1'-C2'	3.30	116.54	110.82
5	А	403	NHE	O2-S-O1	2.30	121.92	113.95

There are no chirality outliers.

All (7) torsion outliers are listed below:



Mol	Chain	Res	Type	Atoms
5	А	404	NHE	C2'-C1'-N-C1
5	А	404	NHE	C1-C2-S-O2
5	А	404	NHE	C1-C2-S-O3
5	А	403	NHE	C2'-C1'-N-C1
6	А	405	GOL	C1-C2-C3-O3
6	А	405	GOL	O2-C2-C3-O3
5	А	403	NHE	C1-C2-S-O1

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	А	405	GOL	1	0
6	В	101	GOL	1	0

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)

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, 95^{th} 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	А	317/327~(96%)	-0.10	14 (4%) 34 34	10, 16, 27, 44	0
2	В	76/76~(100%)	-0.39	0 100 100	11, 16, 27, 32	0
All	All	393/403~(97%)	-0.16	14 (3%) 42 42	10, 16, 27, 44	0

All (14) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	А	229	ARG	5.8
1	А	192	HIS	5.5
1	А	318	VAL	4.4
1	А	3	VAL	3.7
1	А	49	VAL	3.3
1	А	228	GLY	2.8
1	А	191	LYS	2.6
1	А	227	CYS	2.4
1	А	78	GLU	2.2
1	А	284	TYR	2.2
1	А	319	SER	2.2
1	А	180	GLU	2.0
1	А	76	LEU	2.0
1	А	48	HIS	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates (i)

There are no carbohydrates 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, 95^{th} 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	$\mathbf{B} ext{-factors}(\mathbf{A}^2)$	Q < 0.9
6	GOL	В	101	6/6	0.83	0.14	$25,\!28,\!29,\!32$	0
5	NHE	А	404	13/13	0.86	0.23	$27,\!29,\!41,\!43$	0
6	GOL	А	405	6/6	0.89	0.17	$26,\!34,\!36,\!38$	0
6	GOL	А	406	6/6	0.97	0.08	$19,\!20,\!22,\!23$	0
5	NHE	А	403	13/13	0.97	0.09	$15,\!16,\!18,\!22$	0
3	ZN	А	401	1/1	1.00	0.07	$26,\!26,\!26,\!26$	0
4	NA	А	402	1/1	1.00	0.02	$17,\!17,\!17,\!17$	0

6.5 Other polymers (i)

There are no such residues in this entry.

