



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 28, 2021 – 12:12 PM JST

PDB ID : 7E6M
Title : Crystal structure of Human coronavirus NL63 3C-like protease
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Deposited on : 2021-02-22
Resolution : 1.83 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 ⓘ symbol.

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

MolProbity : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.23.2
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.23.2

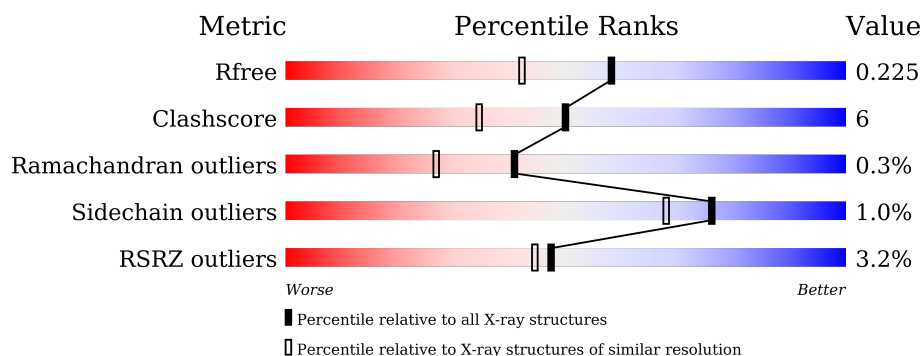
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.83 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))
R_{free}	130704	4003 (1.86-1.82)
Clashscore	141614	4233 (1.86-1.82)
Ramachandran outliers	138981	4185 (1.86-1.82)
Sidechain outliers	138945	4186 (1.86-1.82)
RSRZ outliers	127900	3957 (1.86-1.82)

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	303	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 0%, red 1%, orange 1%, orange 90%, yellow 90%, yellow 98%, grey 98%, grey 100%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> % 90% 8% . </div> </div>
1	B	303	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 0%, red 5%, orange 5%, orange 83%, yellow 83%, yellow 99%, grey 99%, grey 100%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 5% 83% 16% . </div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4685 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 3C-like proteinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	299	Total	C	N	O	S	0	0	0
			2236	1416	379	424	17			
1	B	299	Total	C	N	O	S	0	0	0
			2237	1420	380	421	16			

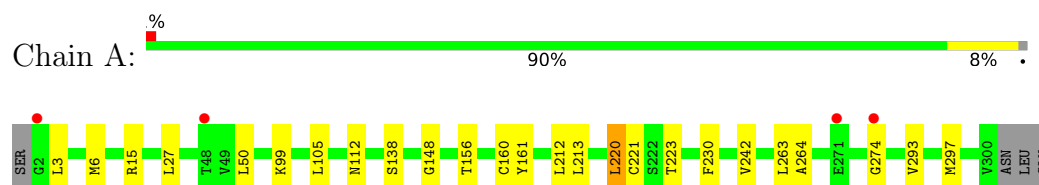
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	124	Total	O	0	0
			124	124		
2	B	88	Total	O	0	0
			88	88		

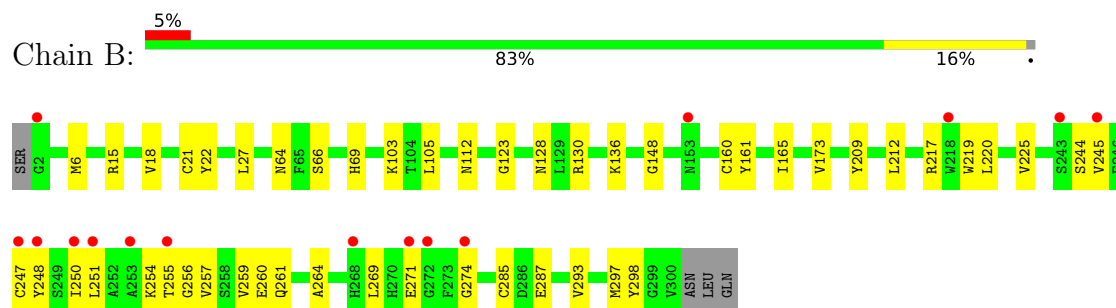
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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: 3C-like proteinase



- Molecule 1: 3C-like proteinase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	62.51Å 80.69Å 63.29Å 90.00° 108.21° 90.00°	Depositor
Resolution (Å)	60.12 – 1.83 60.12 – 1.83	Depositor EDS
% Data completeness (in resolution range)	99.8 (60.12-1.83) 99.8 (60.12-1.83)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.51 (at 1.83Å)	Xtriage
Refinement program	PHENIX 1.11.1_2575	Depositor
R, R_{free}	0.191 , 0.225 0.191 , 0.225	Depositor DCC
R_{free} test set	2585 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	27.1	Xtriage
Anisotropy	0.700	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 44.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.033 for l,-k,h	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	4685	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.81% 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](#)

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	0.37	0/2287	0.57	0/3114
1	B	0.37	0/2288	0.58	0/3114
All	All	0.37	0/4575	0.57	0/6228

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	A	2236	0	2140	18	0
1	B	2237	0	2156	36	0
2	A	124	0	0	0	0
2	B	88	0	0	0	0
All	All	4685	0	4296	51	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 6.

All (51) 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:212:LEU:HD13	1:B:255:THR:HG21	1.49	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:250:ILE:HG23	1:B:251:LEU:HG	1.76	0.68
1:B:244:SER:OG	1:B:247:CYS:SG	2.53	0.67
1:B:255:THR:HB	1:B:257:VAL:H	1.58	0.65
1:A:15:ARG:HH21	1:B:15:ARG:HE	1.43	0.65
1:B:165:ILE:HG13	1:B:173:VAL:HB	1.82	0.61
1:B:255:THR:H	1:B:256:GLY:HA2	1.66	0.60
1:A:223:THR:HG23	1:A:264:ALA:HB1	1.82	0.59
1:A:212:LEU:HD21	1:A:220:LEU:HG	1.86	0.58
1:B:130:ARG:HH12	1:B:136:LYS:HE2	1.70	0.56
1:B:130:ARG:NH1	1:B:136:LYS:HE2	2.22	0.55
1:B:219:TRP:HB2	1:B:269:LEU:HD11	1.87	0.55
1:B:285:CYS:SG	1:B:287:GLU:HB3	2.48	0.53
1:B:271:GLU:N	1:B:271:GLU:OE2	2.43	0.51
1:B:128:ASN:ND2	1:B:287:GLU:O	2.35	0.50
1:B:209:TYR:HB3	1:B:251:LEU:HD13	1.94	0.49
1:B:112:ASN:O	1:B:148:GLY:HA2	2.12	0.49
1:B:293:VAL:O	1:B:297:MET:HG2	2.11	0.49
1:A:242:VAL:HG11	1:A:263:LEU:HD21	1.94	0.49
1:B:225:VAL:HG13	1:B:264:ALA:HB2	1.95	0.48
1:B:255:THR:HB	1:B:257:VAL:N	2.25	0.48
1:A:221:CYS:HB3	1:A:223:THR:HG22	1.95	0.48
1:A:105:LEU:HG	1:A:160:CYS:HB2	1.95	0.48
1:B:250:ILE:HG23	1:B:251:LEU:H	1.80	0.47
1:B:255:THR:N	1:B:256:GLY:HA2	2.29	0.47
1:A:112:ASN:O	1:A:148:GLY:HA2	2.15	0.46
1:B:225:VAL:O	1:B:260:GLU:HB3	2.16	0.46
1:A:230:PHE:CE2	1:A:242:VAL:HG13	2.51	0.46
1:B:209:TYR:CE2	1:B:248:TYR:HB3	2.51	0.46
1:B:212:LEU:HB3	1:B:255:THR:HG23	1.99	0.45
1:B:245:VAL:HG22	1:B:259:VAL:HG11	1.97	0.45
1:A:148:GLY:HA3	1:A:161:TYR:HB3	1.98	0.45
1:A:99:LYS:HB3	1:A:99:LYS:HE2	1.73	0.44
1:A:99:LYS:HE3	1:A:156:THR:OG1	2.17	0.44
1:B:148:GLY:HA3	1:B:161:TYR:HB3	1.99	0.44
1:A:223:THR:HG23	1:A:264:ALA:CB	2.47	0.44
1:A:50:LEU:H	1:A:50:LEU:HD22	1.82	0.43
1:B:18:VAL:HG12	1:B:69:HIS:HB2	2.00	0.43
1:A:213:LEU:HD12	1:A:297:MET:HE1	2.01	0.42
1:A:221:CYS:HB3	1:A:223:THR:CG2	2.50	0.42
1:A:6:MET:HE3	1:B:123:GLY:HA3	2.01	0.42
1:B:22:TYR:CE1	1:B:64:ASN:HB2	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:257:VAL:HG13	1:B:261:GLN:HB3	2.01	0.42
1:A:3:LEU:HD21	1:A:293:VAL:HG22	2.01	0.42
1:B:250:ILE:HG23	1:B:251:LEU:N	2.35	0.41
1:B:105:LEU:HG	1:B:160:CYS:HB2	2.02	0.41
1:B:254:LYS:HD3	1:B:298:TYR:OH	2.21	0.41
1:B:251:LEU:O	1:B:255:THR:OG1	2.30	0.41
1:B:21:CYS:HB3	1:B:66:SER:HB3	2.02	0.40
1:B:220:LEU:HD23	1:B:220:LEU:HA	1.86	0.40
1:A:138:SER:HB3	1:B:6:MET:HE1	2.04	0.40

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	297/303 (98%)	290 (98%)	6 (2%)	1 (0%)	41	27
1	B	297/303 (98%)	291 (98%)	5 (2%)	1 (0%)	41	27
All	All	594/606 (98%)	581 (98%)	11 (2%)	2 (0%)	41	27

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	274	GLY
1	B	274	GLY

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	A	243/254 (96%)	241 (99%)	2 (1%)	81	75
1	B	243/254 (96%)	240 (99%)	3 (1%)	71	61
All	All	486/508 (96%)	481 (99%)	5 (1%)	76	68

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	27	LEU
1	A	220	LEU
1	B	27	LEU
1	B	103	LYS
1	B	217	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 monosaccharides 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 ⓘ

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, 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	299/303 (98%)	-0.20	4 (1%) 77 77	21, 32, 47, 56	0
1	B	299/303 (98%)	0.13	15 (5%) 28 26	21, 34, 62, 73	0
All	All	598/606 (98%)	-0.03	19 (3%) 47 44	21, 33, 56, 73	0

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	2	GLY	7.0
1	B	255	THR	6.2
1	B	272	GLY	6.1
1	A	2	GLY	6.0
1	B	250	ILE	6.0
1	B	245	VAL	5.8
1	B	251	LEU	4.2
1	B	274	GLY	4.0
1	B	271	GLU	3.9
1	B	268	HIS	3.3
1	B	247	CYS	3.3
1	B	248	TYR	3.1
1	A	48	THR	3.0
1	B	243	SER	2.9
1	B	253	ALA	2.5
1	A	274	GLY	2.3
1	B	218	TRP	2.3
1	A	271	GLU	2.3
1	B	153	ASN	2.2

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 monosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.