



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 17, 2026 – 11:21 PM UTC

PDB ID : 8DRZ / pdb_00008drz
Title : Product structure of SARS-CoV-2 Mpro C145A mutant in complex with nsp13-nsp14 (C13) cut site sequence
Authors : Lee, J.; Kenward, C.; Worrall, L.J.; Vuckovic, M.; Paetzel, M.; Strynadka, N.C.J.
Deposited on : 2022-07-21
Resolution : 1.98 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
Mogul : 2022.3.0, CSD as543be (2022)
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

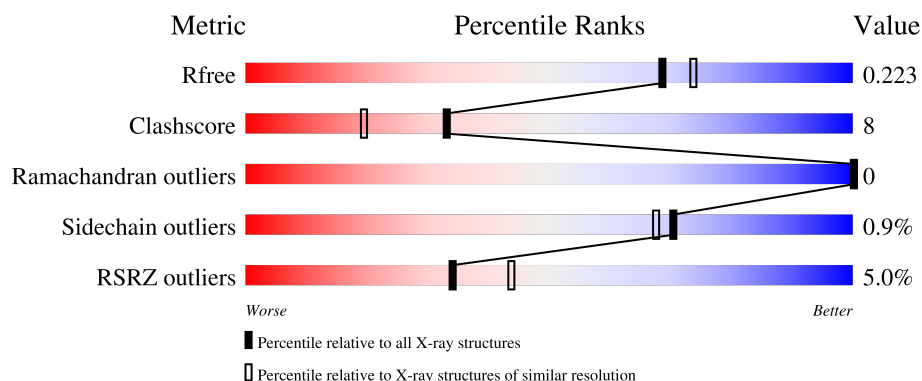
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.98 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}	180053	1506 (1.98-1.98)
Clashscore	190562	1534 (1.98-1.98)
Ramachandran outliers	187476	1518 (1.98-1.98)
Sidechain outliers	187428	1518 (1.98-1.98)
RSRZ outliers	180081	1506 (1.98-1.98)

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	306	6% 85% 15%
1	B	306	6% 88% 11%
1	C	306	6% 84% 15%
1	D	306	7% 82% 18%
1	E	306	12% 83% 14%

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Mol	Chain	Length	Quality of chain
1	F	306	 3% 76% 23%
1	G	306	 6% 86% 13%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	PEG	A	403	-	-	X	-
2	PEG	C	404	-	-	X	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 18081 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 nsp5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	306	Total	C	N	O	S	0	1	0
			2367	1496	403	447	21			
1	B	306	Total	C	N	O	S	0	1	0
			2372	1501	404	446	21			
1	C	306	Total	C	N	O	S	0	0	0
			2364	1497	402	444	21			
1	D	306	Total	C	N	O	S	0	1	0
			2365	1497	401	445	22			
1	E	301	Total	C	N	O	S	0	0	0
			2305	1458	391	436	20			
1	F	305	Total	C	N	O	S	0	1	0
			2372	1501	403	447	21			
1	G	306	Total	C	N	O	S	0	0	0
			2354	1489	399	445	21			

There are 49 discrepancies between the modelled and reference sequences:

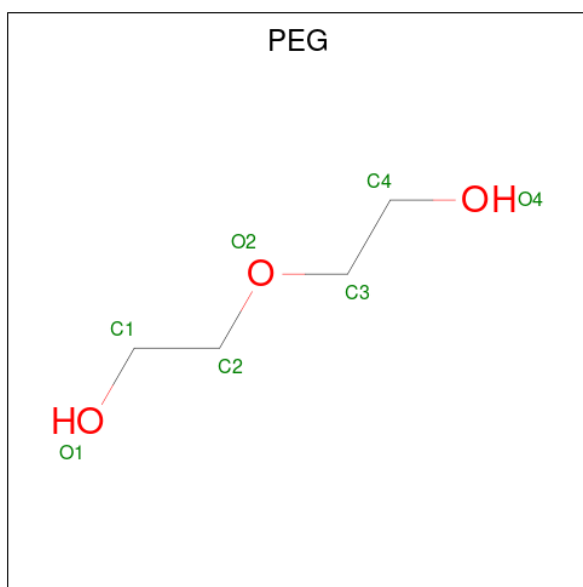
Chain	Residue	Modelled	Actual	Comment	Reference
A	145	ALA	CYS	engineered mutation	UNP P0DTD1
A	301	ASN	-	expression tag	UNP P0DTD1
A	302	VAL	-	expression tag	UNP P0DTD1
A	303	ALA	-	expression tag	UNP P0DTD1
A	304	THR	-	expression tag	UNP P0DTD1
A	305	LEU	-	expression tag	UNP P0DTD1
A	306	GLN	-	expression tag	UNP P0DTD1
B	145	ALA	CYS	engineered mutation	UNP P0DTD1
B	301	ASN	-	expression tag	UNP P0DTD1
B	302	VAL	-	expression tag	UNP P0DTD1
B	303	ALA	-	expression tag	UNP P0DTD1
B	304	THR	-	expression tag	UNP P0DTD1
B	305	LEU	-	expression tag	UNP P0DTD1
B	306	GLN	-	expression tag	UNP P0DTD1
C	145	ALA	CYS	engineered mutation	UNP P0DTD1

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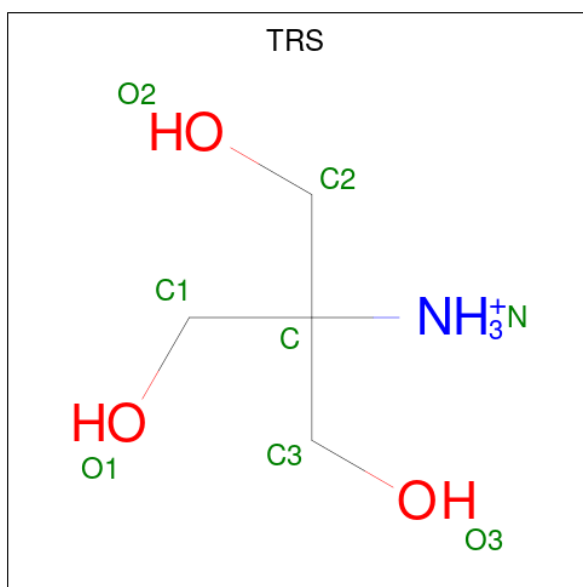
Chain	Residue	Modelled	Actual	Comment	Reference
C	301	ASN	-	expression tag	UNP P0DTD1
C	302	VAL	-	expression tag	UNP P0DTD1
C	303	ALA	-	expression tag	UNP P0DTD1
C	304	THR	-	expression tag	UNP P0DTD1
C	305	LEU	-	expression tag	UNP P0DTD1
C	306	GLN	-	expression tag	UNP P0DTD1
D	145	ALA	CYS	engineered mutation	UNP P0DTD1
D	301	ASN	-	expression tag	UNP P0DTD1
D	302	VAL	-	expression tag	UNP P0DTD1
D	303	ALA	-	expression tag	UNP P0DTD1
D	304	THR	-	expression tag	UNP P0DTD1
D	305	LEU	-	expression tag	UNP P0DTD1
D	306	GLN	-	expression tag	UNP P0DTD1
E	145	ALA	CYS	engineered mutation	UNP P0DTD1
E	301	ASN	-	expression tag	UNP P0DTD1
E	302	VAL	-	expression tag	UNP P0DTD1
E	303	ALA	-	expression tag	UNP P0DTD1
E	304	THR	-	expression tag	UNP P0DTD1
E	305	LEU	-	expression tag	UNP P0DTD1
E	306	GLN	-	expression tag	UNP P0DTD1
F	145	ALA	CYS	engineered mutation	UNP P0DTD1
F	301	ASN	-	expression tag	UNP P0DTD1
F	302	VAL	-	expression tag	UNP P0DTD1
F	303	ALA	-	expression tag	UNP P0DTD1
F	304	THR	-	expression tag	UNP P0DTD1
F	305	LEU	-	expression tag	UNP P0DTD1
F	306	GLN	-	expression tag	UNP P0DTD1
G	145	ALA	CYS	engineered mutation	UNP P0DTD1
G	301	ASN	-	expression tag	UNP P0DTD1
G	302	VAL	-	expression tag	UNP P0DTD1
G	303	ALA	-	expression tag	UNP P0DTD1
G	304	THR	-	expression tag	UNP P0DTD1
G	305	LEU	-	expression tag	UNP P0DTD1
G	306	GLN	-	expression tag	UNP P0DTD1

- Molecule 2 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: C₄H₁₀O₃).



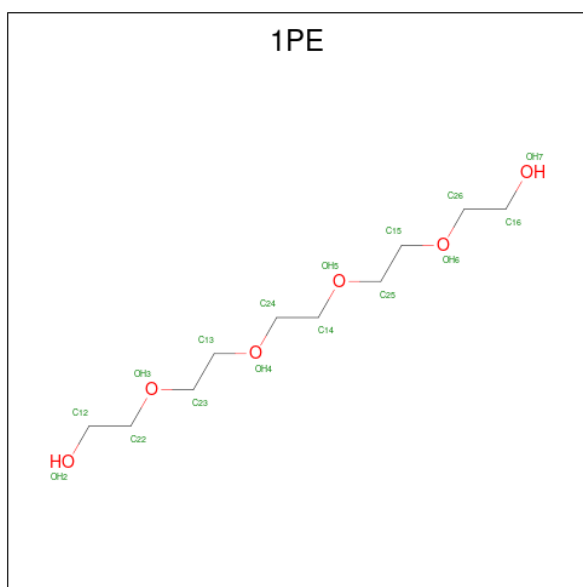
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			7	4	3		
2	A	1	Total	C	O	0	0
			7	4	3		
2	A	1	Total	C	O	0	0
			7	4	3		
2	C	1	Total	C	O	0	0
			7	4	3		
2	D	1	Total	C	O	0	0
			7	4	3		
2	D	1	Total	C	O	0	0
			7	4	3		
2	D	1	Total	C	O	0	0
			7	4	3		
2	F	1	Total	C	O	0	0
			7	4	3		
2	F	1	Total	C	O	0	0
			7	4	3		
2	F	1	Total	C	O	0	0
			7	4	3		

- Molecule 3 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (CCD ID: TRS) (formula: $C_4H_{12}NO_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			8	4	1	3		
3	A	1	Total	C	N	O	0	0
			8	4	1	3		
3	A	1	Total	C	N	O	0	0
			8	4	1	3		
3	B	1	Total	C	N	O	0	0
			8	4	1	3		
3	B	1	Total	C	N	O	0	0
			8	4	1	3		
3	C	1	Total	C	N	O	0	0
			8	4	1	3		
3	C	1	Total	C	N	O	0	0
			8	4	1	3		
3	E	1	Total	C	N	O	0	0
			8	4	1	3		
3	F	1	Total	C	N	O	0	0
			8	4	1	3		
3	G	1	Total	C	N	O	0	0
			8	4	1	3		

- Molecule 4 is PENTAETHYLENE GLYCOL (CCD ID: 1PE) (formula: C₁₀H₂₂O₆).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			13	8	5		
4	B	1	Total	C	O	0	0
			10	6	4		
4	D	1	Total	C	O	0	0
			10	6	4		

- Molecule 5 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	1	Total	Na	0	0
			1	1		
5	C	1	Total	Na	0	0
			1	1		
5	F	1	Total	Na	0	0
			1	1		
5	G	1	Total	Na	0	0
			1	1		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	215	Total	O	0	0
			215	215		
6	B	280	Total	O	0	0
			280	280		

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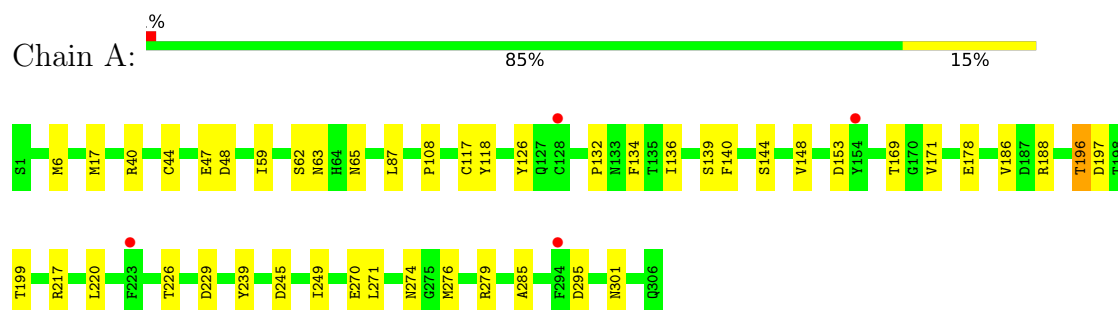
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	C	255	Total 255	O 255	0	0
6	D	195	Total 195	O 195	0	0
6	E	164	Total 164	O 164	0	0
6	F	164	Total 164	O 164	0	0
6	G	122	Total 122	O 122	0	0

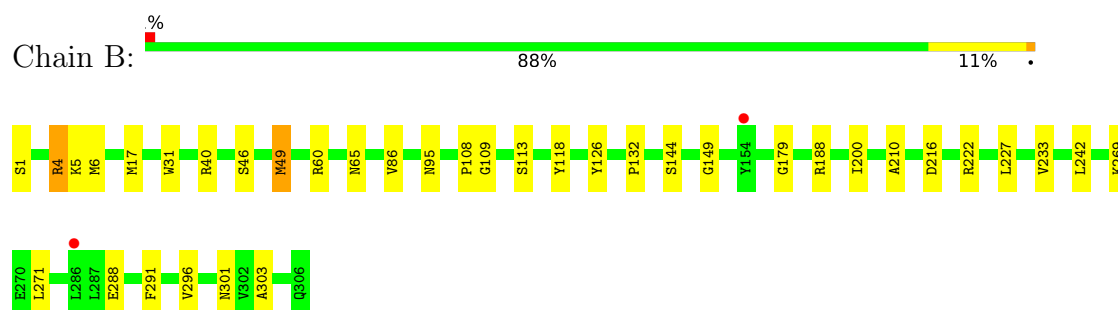
3 Residue-property plots

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.

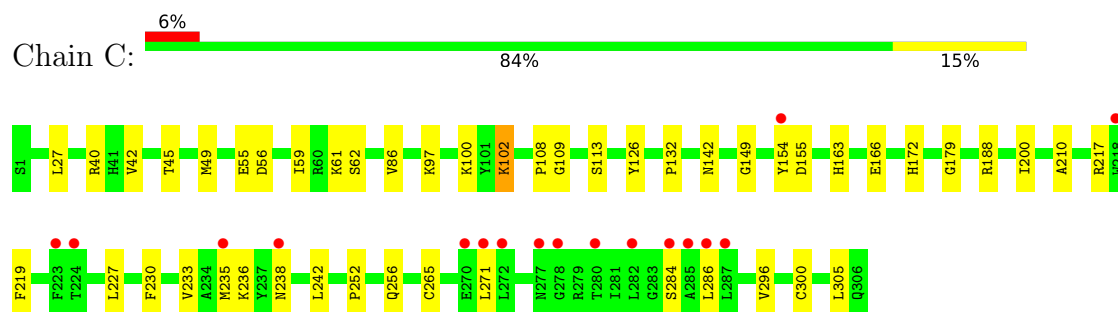
- Molecule 1: 3C-like proteinase nsp5



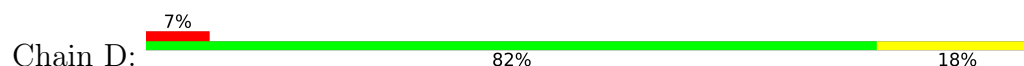
- Molecule 1: 3C-like proteinase nsp5

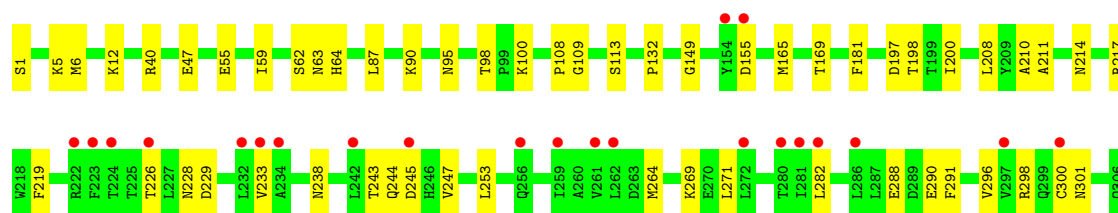


- Molecule 1: 3C-like proteinase nsp5

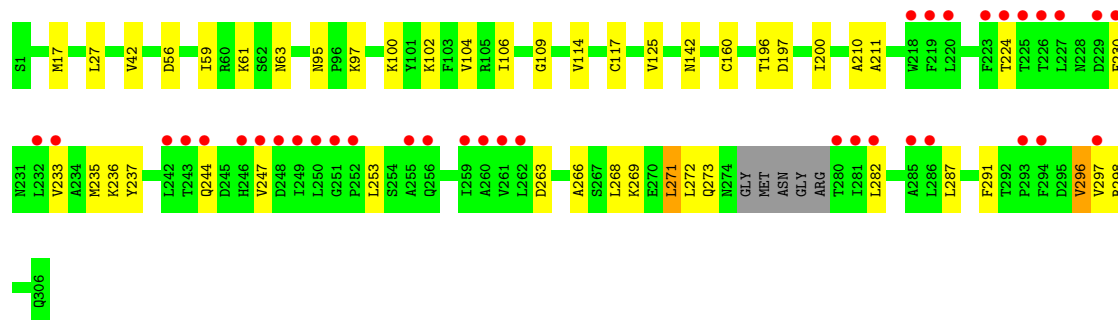
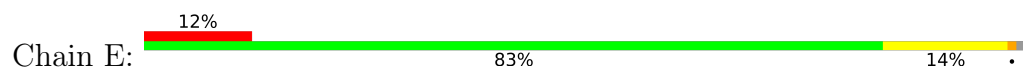


- Molecule 1: 3C-like proteinase nsp5

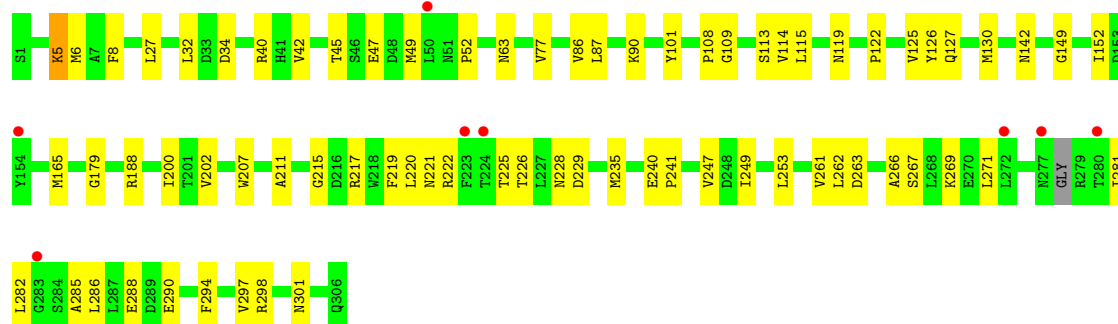
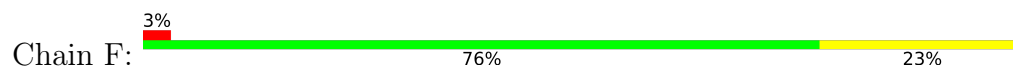




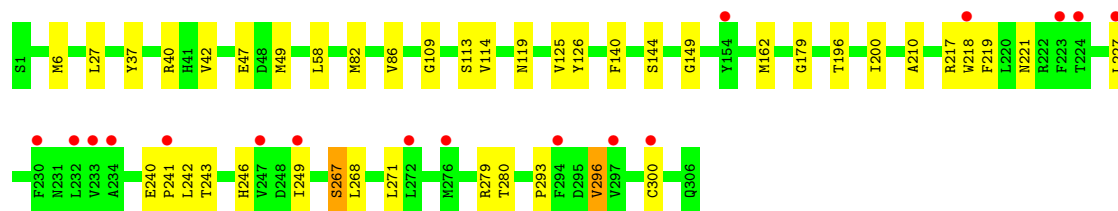
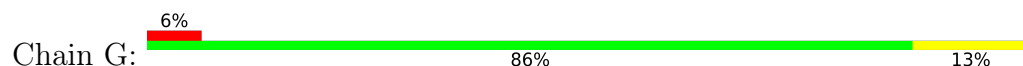
• Molecule 1: 3C-like proteinase nsp5



• Molecule 1: 3C-like proteinase nsp5



• Molecule 1: 3C-like proteinase nsp5



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	105.94Å 216.82Å 121.25Å 90.00° 94.01° 90.00°	Depositor
Resolution (Å)	47.50 – 1.98 47.50 – 1.98	Depositor EDS
% Data completeness (in resolution range)	99.9 (47.50-1.98) 99.9 (47.50-1.98)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.38 (at 1.98Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.177 , 0.223 0.177 , 0.223	Depositor DCC
R_{free} test set	9532 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	31.7	Xtriage
Anisotropy	0.247	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 48.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	18081	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.21% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NA, PEG, TRS, 1PE

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	0.65	0/2421	0.86	1/3291 (0.0%)
1	B	0.65	0/2427	0.79	1/3299 (0.0%)
1	C	0.63	0/2416	0.80	1/3284 (0.0%)
1	D	0.57	0/2417	0.71	1/3286 (0.0%)
1	E	0.52	0/2354	0.70	0/3203
1	F	0.56	0/2423	0.77	1/3292 (0.0%)
1	G	0.52	0/2406	0.76	0/3273
All	All	0.59	0/16864	0.77	5/22928 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	295	ASP	CB-CA-C	-5.97	100.88	110.79
1	F	263	ASP	N-CA-C	-5.39	105.32	111.14
1	C	100	LYS	N-CA-C	-5.19	102.17	109.96
1	D	245	ASP	N-CA-C	-5.06	105.95	111.82
1	B	49	MET	N-CA-CB	-5.03	102.04	110.39

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	2367	0	2317	43	0
1	B	2372	0	2324	33	0
1	C	2364	0	2314	35	0
1	D	2365	0	2307	47	0
1	E	2305	0	2241	33	0
1	F	2372	0	2319	53	0
1	G	2354	0	2287	30	0
2	A	21	0	30	9	0
2	C	7	0	10	7	0
2	D	21	0	30	3	0
2	F	21	0	30	3	0
3	A	24	0	36	5	0
3	B	16	0	24	2	0
3	C	16	0	24	1	0
3	E	8	0	12	1	0
3	F	8	0	12	2	0
3	G	8	0	12	0	0
4	A	13	0	17	0	0
4	B	10	0	12	3	0
4	D	10	0	12	4	0
5	B	1	0	0	0	0
5	C	1	0	0	0	0
5	F	1	0	0	0	0
5	G	1	0	0	0	0
6	A	215	0	0	8	0
6	B	280	0	0	0	0
6	C	255	0	0	5	0
6	D	195	0	0	4	0
6	E	164	0	0	6	0
6	F	164	0	0	3	0
6	G	122	0	0	1	0
All	All	18081	0	16370	258	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 8.

The worst 5 of 258 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:F:247:VAL:HG13	1:F:261:VAL:HG21	1.40	0.98
1:E:211:ALA:HA	1:E:282:LEU:HD11	1.55	0.89
1:A:217:ARG:HD3	1:A:220:LEU:HD12	1.57	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:211:ALA:HA	1:D:282:LEU:HD21	1.58	0.83
1:F:52:PRO:HD2	1:F:188:ARG:HG2	1.60	0.82

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	305/306 (100%)	296 (97%)	9 (3%)	0	100	100
1	B	305/306 (100%)	300 (98%)	5 (2%)	0	100	100
1	C	304/306 (99%)	298 (98%)	6 (2%)	0	100	100
1	D	305/306 (100%)	297 (97%)	8 (3%)	0	100	100
1	E	297/306 (97%)	293 (99%)	4 (1%)	0	100	100
1	F	302/306 (99%)	292 (97%)	10 (3%)	0	100	100
1	G	304/306 (99%)	294 (97%)	10 (3%)	0	100	100
All	All	2122/2142 (99%)	2070 (98%)	52 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	262/262 (100%)	261 (100%)	1 (0%)	84	82
1	B	263/262 (100%)	261 (99%)	2 (1%)	73	71
1	C	261/262 (100%)	259 (99%)	2 (1%)	73	71
1	D	261/262 (100%)	260 (100%)	1 (0%)	84	82
1	E	253/262 (97%)	250 (99%)	3 (1%)	63	58
1	F	263/262 (100%)	258 (98%)	5 (2%)	50	44
1	G	259/262 (99%)	256 (99%)	3 (1%)	63	58
All	All	1822/1834 (99%)	1805 (99%)	17 (1%)	70	67

5 of 17 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	267	SER
1	G	300	CYS
1	E	271	LEU
1	E	296	VAL
1	F	5	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 37 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	119	ASN
1	G	244	GLN
1	F	127	GLN
1	G	51	ASN
1	C	214	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 27 ligands modelled in this entry, 4 are monoatomic - leaving 23 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	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	TRS	B	402	-	7,7,7	0.28	0	9,9,9	0.47	0
3	TRS	E	401	-	7,7,7	0.36	0	9,9,9	1.13	1 (11%)
3	TRS	F	405	-	7,7,7	0.53	0	9,9,9	1.23	2 (22%)
2	PEG	F	403	-	6,6,6	0.25	0	5,5,5	0.12	0
4	1PE	B	404	-	9,9,15	0.19	0	8,8,14	0.45	0
2	PEG	D	402	-	6,6,6	0.30	0	5,5,5	0.29	0
2	PEG	C	404	-	6,6,6	0.11	0	5,5,5	0.47	0
3	TRS	A	402	-	7,7,7	0.41	0	9,9,9	1.06	0
4	1PE	A	404	-	12,12,15	0.13	0	11,11,14	0.16	0
4	1PE	D	404	-	9,9,15	0.23	0	8,8,14	0.26	0
2	PEG	A	401	-	6,6,6	0.36	0	5,5,5	0.29	0
3	TRS	A	405	-	7,7,7	0.22	0	9,9,9	0.34	0
2	PEG	A	407	-	6,6,6	0.19	0	5,5,5	0.21	0
3	TRS	A	406	-	7,7,7	0.35	0	9,9,9	0.61	0
2	PEG	D	401	-	6,6,6	0.37	0	5,5,5	0.19	0
3	TRS	C	403	-	7,7,7	0.47	0	9,9,9	0.79	0
3	TRS	B	403	-	7,7,7	0.44	0	9,9,9	0.75	0
3	TRS	C	402	-	7,7,7	0.43	0	9,9,9	0.90	0
2	PEG	D	403	-	6,6,6	0.18	0	5,5,5	0.15	0
2	PEG	F	404	-	6,6,6	0.32	0	5,5,5	0.19	0
2	PEG	F	402	-	6,6,6	0.28	0	5,5,5	0.13	0
3	TRS	G	402	-	7,7,7	0.30	0	9,9,9	0.76	0
2	PEG	A	403	-	6,6,6	0.70	0	5,5,5	0.50	0

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
3	TRS	B	402	-	-	6/9/9/9	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	TRS	E	401	-	-	6/9/9/9	-
3	TRS	F	405	-	-	0/9/9/9	-
2	PEG	F	403	-	-	3/4/4/4	-
4	1PE	B	404	-	-	6/7/7/13	-
2	PEG	D	402	-	-	1/4/4/4	-
2	PEG	C	404	-	-	3/4/4/4	-
3	TRS	A	402	-	-	3/9/9/9	-
4	1PE	A	404	-	-	5/10/10/13	-
4	1PE	D	404	-	-	6/7/7/13	-
2	PEG	A	401	-	-	2/4/4/4	-
3	TRS	A	405	-	-	3/9/9/9	-
2	PEG	A	407	-	-	2/4/4/4	-
3	TRS	A	406	-	-	9/9/9/9	-
2	PEG	D	401	-	-	3/4/4/4	-
3	TRS	C	403	-	-	5/9/9/9	-
3	TRS	B	403	-	-	3/9/9/9	-
3	TRS	C	402	-	-	8/9/9/9	-
2	PEG	D	403	-	-	3/4/4/4	-
2	PEG	F	404	-	-	3/4/4/4	-
2	PEG	F	402	-	-	0/4/4/4	-
3	TRS	G	402	-	-	3/9/9/9	-
2	PEG	A	403	-	-	3/4/4/4	-

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	401	TRS	O2-C2-C	2.25	117.14	110.88
3	F	405	TRS	O2-C2-C	2.22	117.06	110.88
3	F	405	TRS	O3-C3-C	2.11	116.75	110.88

There are no chirality outliers.

5 of 86 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	402	TRS	C1-C-C3-O3
3	A	402	TRS	C2-C-C3-O3

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Mol	Chain	Res	Type	Atoms
3	A	402	TRS	N-C-C3-O3
3	A	405	TRS	C2-C-C1-O1
3	A	406	TRS	N-C-C1-O1

There are no ring outliers.

16 monomers are involved in 40 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	402	TRS	2	0
3	E	401	TRS	1	0
3	F	405	TRS	2	0
4	B	404	1PE	3	0
2	C	404	PEG	7	0
3	A	402	TRS	1	0
4	D	404	1PE	4	0
2	A	401	PEG	3	0
3	A	405	TRS	3	0
2	A	407	PEG	1	0
3	A	406	TRS	1	0
2	D	401	PEG	2	0
3	C	402	TRS	1	0
2	D	403	PEG	1	0
2	F	404	PEG	3	0
2	A	403	PEG	5	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, 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	306/306 (100%)	-0.03	4 (1%) 75 82	23, 36, 67, 91	1 (0%)
1	B	306/306 (100%)	-0.28	2 (0%) 84 89	21, 32, 58, 94	1 (0%)
1	C	306/306 (100%)	0.14	17 (5%) 30 38	22, 36, 76, 106	0
1	D	306/306 (100%)	0.27	22 (7%) 21 28	14, 39, 85, 122	1 (0%)
1	E	301/306 (98%)	0.46	36 (11%) 9 12	26, 43, 109, 133	0
1	F	305/306 (99%)	0.18	8 (2%) 57 67	24, 43, 84, 113	1 (0%)
1	G	306/306 (100%)	0.37	17 (5%) 30 38	31, 49, 90, 114	0
All	All	2136/2142 (99%)	0.16	106 (4%) 34 44	14, 40, 87, 133	4 (0%)

The worst 5 of 106 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	230	PHE	5.1
1	E	225	THR	4.9
1	E	260	ALA	4.5
1	E	249	ILE	4.4
1	C	277	ASN	4.4

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 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
3	TRS	B	402	8/8	0.64	0.17	59,77,85,88	0
3	TRS	A	405	8/8	0.67	0.18	45,60,62,62	0
3	TRS	G	402	8/8	0.67	0.13	73,85,87,91	0
3	TRS	C	403	8/8	0.68	0.14	58,72,75,77	0
3	TRS	F	405	8/8	0.69	0.15	58,61,70,70	0
3	TRS	A	406	8/8	0.70	0.15	65,74,85,86	0
2	PEG	C	404	7/7	0.71	0.19	57,61,72,77	0
2	PEG	D	403	7/7	0.71	0.15	60,65,72,75	0
4	1PE	D	404	10/16	0.71	0.19	47,63,75,78	0
2	PEG	D	402	7/7	0.72	0.19	60,63,70,71	0
3	TRS	A	402	8/8	0.73	0.13	57,65,72,77	0
2	PEG	F	402	7/7	0.73	0.14	65,72,75,75	0
3	TRS	E	401	8/8	0.76	0.14	53,63,71,71	0
2	PEG	A	403	7/7	0.76	0.17	38,46,56,64	0
2	PEG	F	403	7/7	0.78	0.14	59,59,69,71	0
2	PEG	D	401	7/7	0.78	0.16	41,60,65,71	0
3	TRS	B	403	8/8	0.80	0.14	43,58,65,69	0
4	1PE	B	404	10/16	0.81	0.16	46,58,65,65	0
2	PEG	A	401	7/7	0.82	0.17	38,51,61,65	0
3	TRS	C	402	8/8	0.83	0.12	42,60,61,65	0
2	PEG	A	407	7/7	0.84	0.15	44,57,62,69	0
4	1PE	A	404	13/16	0.85	0.14	46,53,64,69	0
2	PEG	F	404	7/7	0.87	0.14	56,62,63,67	0
5	NA	C	401	1/1	0.96	0.09	37,37,37,37	0
5	NA	B	401	1/1	0.97	0.04	31,31,31,31	1
5	NA	F	401	1/1	0.97	0.06	46,46,46,46	0
5	NA	G	401	1/1	0.98	0.08	47,47,47,47	0

6.5 Other polymers [i](#)

There are no such residues in this entry.