



# Full wwPDB X-ray Structure Validation Report ⓘ

Jul 10, 2025 – 12:08 PM EDT

PDB ID : 9PFI / pdb\_00009pfi  
Title : Crystal structure of SARS-CoV-2 Mpro Mutant P132H  
Authors : Kenward, C.; Mosimann, W.A.; Worrall, L.J.; Strynadka, N.C.J.  
Deposited on : 2025-07-04  
Resolution : 1.81 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](mailto: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>.

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

MolProbity : 4-5-2 with Phenix2.0rc1  
Xtriage (Phenix) : 2.0rc1  
EDS : 3.0  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
CCP4 : 9.0.006 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.44

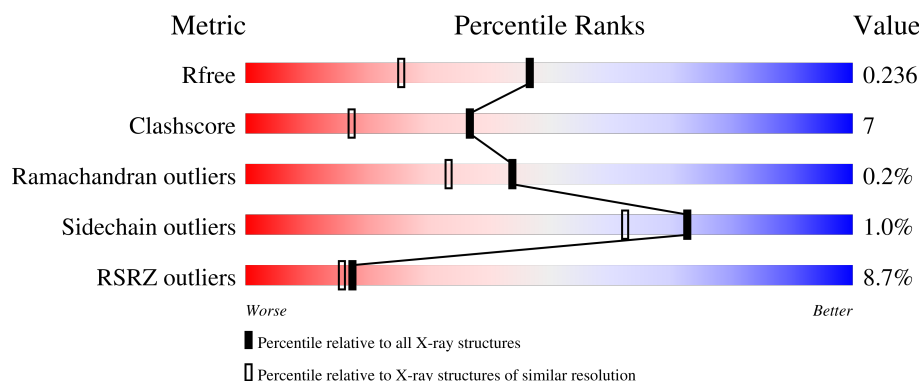
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.81 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))
$R_{free}$	164625	9242 (1.84-1.80)
Clashscore	180529	1080 (1.82-1.82)
Ramachandran outliers	177936	1073 (1.82-1.82)
Sidechain outliers	177891	1073 (1.82-1.82)
RSRZ outliers	164620	9241 (1.84-1.80)

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  $\geq 3$ , 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	
1	B	306	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4875 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	305	Total	C	N	O	S	0	0	0
			2357	1493	402	440	22			
1	B	306	Total	C	N	O	S	0	1	0
			2332	1482	391	437	22			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	132	HIS	PRO	engineered mutation	UNP P0DTC1
B	132	HIS	PRO	engineered mutation	UNP P0DTC1

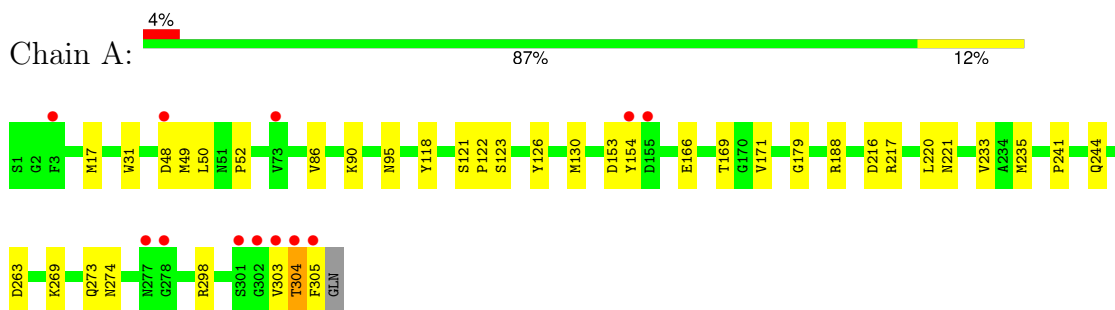
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	130	Total	O	0	0
			130	130		
2	B	56	Total	O	0	0
			56	56		

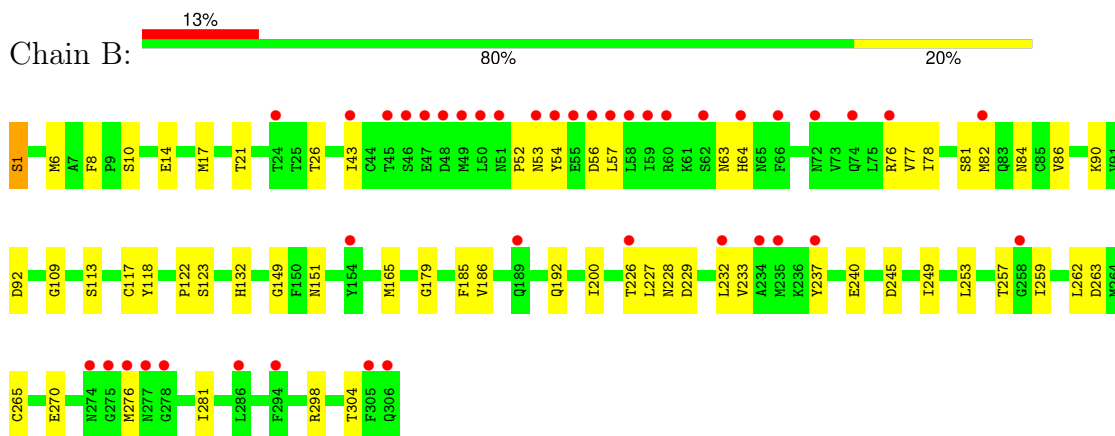
### 3 Residue-property plots [i](#)

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 nsp5



#### • Molecule 1: 3C-like proteinase nsp5



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	67.69Å 98.90Å 103.17Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	71.39 – 1.81 71.39 – 1.81	Depositor EDS
% Data completeness (in resolution range)	57.2 (71.39-1.81) 57.4 (71.39-1.81)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.65 (at 1.81Å)	Xtriage
Refinement program	PHENIX (1.20.1_4487: ???)	Depositor
R, $R_{free}$	0.187 , 0.237 0.188 , 0.236	Depositor DCC
$R_{free}$ test set	61846 reflections (5.42%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	27.1	Xtriage
Anisotropy	0.045	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 50.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.018 for -h,l,k	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	4875	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.95% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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

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	0.38	0/2410	0.61	0/3275
1	B	0.41	1/2388 (0.0%)	0.70	3/3249 (0.1%)
All	All	0.40	1/4798 (0.0%)	0.65	3/6524 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	52	PRO	CG-CD	-10.56	1.14	1.50

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	52	PRO	N-CD-CG	-15.42	80.07	103.20
1	B	52	PRO	CA-CB-CG	-9.82	85.85	104.50
1	B	52	PRO	CA-N-CD	-9.05	99.33	112.00

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	2357	0	2302	28	0
1	B	2332	0	2249	43	0
2	A	130	0	0	3	0
2	B	56	0	0	2	0
All	All	4875	0	4551	65	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 7.

All (65) 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:298:ARG:NH1	2:B:401:HOH:O	2.00	0.93
1:B:21:THR:HG23	1:B:26:THR:HG22	1.62	0.81
1:B:226:THR:HG22	1:B:227:LEU:N	2.00	0.77
1:B:263:ASP:OD1	2:B:402:HOH:O	2.07	0.70
1:A:221:ASN:OD1	2:A:401:HOH:O	2.12	0.68
1:B:82:MET:HE3	1:B:84:ASN:O	1.97	0.65
1:B:86[A]:VAL:HG13	1:B:179:GLY:HA2	1.78	0.65
1:B:186:VAL:H	1:B:192:GLN:HE22	1.43	0.64
1:A:86:VAL:HG23	1:A:179:GLY:HA2	1.80	0.64
1:A:304:THR:HA	1:B:118:TYR:HB2	1.80	0.63
1:A:273:GLN:HG2	1:A:274:ASN:OD1	1.99	0.62
1:B:226:THR:CG2	1:B:227:LEU:N	2.63	0.62
1:B:8:PHE:HE2	1:B:151:ASN:HD22	1.48	0.61
1:B:76:ARG:HB3	1:B:92:ASP:OD1	2.01	0.60
1:B:78:ILE:HG13	1:B:90:LYS:HE3	1.83	0.59
1:A:263:ASP:OD1	2:A:401:HOH:O	2.17	0.59
1:B:228:ASN:O	1:B:232:LEU:HG	2.03	0.59
1:B:186:VAL:H	1:B:192:GLN:NE2	2.01	0.58
1:B:276:MET:CE	1:B:281:ILE:HG13	2.34	0.57
1:B:245:ASP:O	1:B:249:ILE:HD12	2.05	0.57
1:A:169:THR:HG22	1:A:171:VAL:HG22	1.88	0.55
1:B:14:GLU:HB3	1:B:122:PRO:HG2	1.89	0.54
1:B:17:MET:HG3	1:B:117:CYS:SG	2.47	0.54
1:B:226:THR:HG22	1:B:227:LEU:H	1.72	0.53
1:A:126:TYR:CD1	1:B:6:MET:HE2	2.44	0.53
1:A:235:MET:SD	1:A:241:PRO:HG3	2.49	0.52
1:B:276:MET:HE3	1:B:281:ILE:HG13	1.90	0.52
1:B:226:THR:CG2	1:B:227:LEU:H	2.22	0.52
1:A:48:ASP:O	1:A:52:PRO:HB3	2.11	0.51
1:A:298:ARG:O	1:A:303:VAL:HB	2.10	0.51
1:B:53:ASN:HB3	1:B:56:ASP:HB3	1.93	0.49
1:A:233:VAL:HG11	1:A:269:LYS:HG3	1.93	0.49
1:B:226:THR:HB	1:B:229:ASP:OD2	2.15	0.47
1:A:123:SER:HB2	1:B:304:THR:HG22	1.96	0.46
1:B:10:SER:O	1:B:14:GLU:HG3	2.17	0.46
1:A:17:MET:HE3	1:A:17:MET:HB3	1.71	0.45
1:B:132:HIS:NE2	1:B:240:GLU:OE1	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:169:THR:CG2	1:A:171:VAL:HG22	2.47	0.44
1:A:304:THR:O	1:B:123:SER:HB2	2.17	0.44
1:A:52:PRO:HD2	1:A:188:ARG:HG2	2.00	0.44
1:B:165:MET:HE1	1:B:185:PHE:HB3	2.00	0.44
1:B:276:MET:HE1	1:B:281:ILE:HG13	2.00	0.44
1:A:244:GLN:NE2	2:A:405:HOH:O	2.50	0.44
1:B:262:LEU:HA	1:B:265:CYS:HB2	2.00	0.44
1:A:31:TRP:CE2	1:A:95:ASN:HB2	2.54	0.43
1:B:270:GLU:OE1	1:B:270:GLU:HA	2.18	0.43
1:A:130:MET:HE2	1:A:130:MET:HB2	1.93	0.43
1:B:43:ILE:HD13	1:B:57:LEU:HB2	2.01	0.43
1:A:49:MET:HE2	1:A:49:MET:HB3	1.73	0.42
1:B:63:ASN:O	1:B:77:VAL:HB	2.19	0.42
1:B:233:VAL:O	1:B:237:TYR:HD2	2.02	0.42
1:B:113:SER:O	1:B:149:GLY:HA2	2.20	0.42
1:A:303:VAL:O	1:A:305:PHE:N	2.53	0.42
1:B:259:ILE:N	1:B:259:ILE:HD12	2.35	0.42
1:B:43:ILE:HD11	1:B:54:TYR:HD1	1.84	0.41
1:A:50:LEU:HD13	1:A:50:LEU:HA	1.90	0.41
1:B:109:GLY:HA2	1:B:200:ILE:HD13	2.01	0.41
1:A:153:ASP:C	1:A:154:TYR:CD1	2.98	0.41
1:A:118:TYR:HB2	1:B:304:THR:HG21	2.03	0.41
1:B:249:ILE:HD12	1:B:249:ILE:H	1.85	0.41
1:B:253:LEU:O	1:B:257:THR:HG23	2.21	0.41
1:A:166:GLU:OE2	1:B:1:SER:HB2	2.21	0.40
1:A:217:ARG:HG2	1:A:220:LEU:HD12	2.03	0.40
1:A:121:SER:HA	1:A:122:PRO:HD3	1.95	0.40
1:A:31:TRP:CD2	1:A:95:ASN:HB2	2.56	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	303/306 (99%)	294 (97%)	8 (3%)	1 (0%)	37	26
1	B	305/306 (100%)	295 (97%)	10 (3%)	0	100	100
All	All	608/612 (99%)	589 (97%)	18 (3%)	1 (0%)	44	33

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	304	THR

### 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	261/263 (99%)	259 (99%)	2 (1%)	79	72
1	B	253/263 (96%)	250 (99%)	3 (1%)	67	56
All	All	514/526 (98%)	509 (99%)	5 (1%)	73	62

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

Mol	Chain	Res	Type
1	A	90	LYS
1	A	216	ASP
1	B	1	SER
1	B	64	HIS
1	B	81	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	19	GLN
1	A	41	HIS
1	A	64	HIS
1	A	69	GLN
1	A	119	ASN

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Mol	Chain	Res	Type
1	A	189	GLN
1	A	228	ASN
1	A	244	GLN
1	B	53	ASN
1	B	63	ASN
1	B	151	ASN
1	B	192	GLN
1	B	273	GLN

### 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](#)

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](#)

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	305/306 (99%)	-0.07	12 (3%) 44 43	14, 29, 56, 123	0
1	B	306/306 (100%)	0.52	41 (13%) 8 7	16, 38, 81, 137	1 (0%)
All	All	611/612 (99%)	0.22	53 (8%) 17 16	14, 32, 70, 137	1 (0%)

All (53) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	304	THR	7.3
1	A	305	PHE	6.0
1	A	303	VAL	5.6
1	B	306	GLN	5.4
1	B	47	GLU	4.2
1	B	59	ILE	4.1
1	A	154	TYR	4.0
1	B	50	LEU	3.8
1	B	235	MET	3.6
1	B	60	ARG	3.6
1	B	64	HIS	3.6
1	B	57	LEU	3.5
1	B	154	TYR	3.4
1	A	277	ASN	3.4
1	B	274	ASN	3.4
1	B	226	THR	3.3
1	A	301	SER	3.3
1	B	232	LEU	3.3
1	B	48	ASP	3.0
1	B	51	ASN	2.9
1	A	278	GLY	2.9
1	B	49	MET	2.8
1	A	302	GLY	2.8
1	B	277	ASN	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	286	LEU	2.7
1	B	66	PHE	2.7
1	B	58	LEU	2.7
1	B	276	MET	2.7
1	B	45	THR	2.6
1	B	24	THR	2.5
1	B	234	ALA	2.5
1	B	294	PHE	2.5
1	A	48	ASP	2.4
1	A	3	PHE	2.4
1	B	46	SER	2.4
1	B	56	ASP	2.4
1	B	305	PHE	2.4
1	B	43	ILE	2.4
1	B	275	GLY	2.4
1	B	278	GLY	2.3
1	B	76	ARG	2.3
1	B	62	SER	2.3
1	B	53	ASN	2.2
1	B	237	TYR	2.2
1	B	189	GLN	2.2
1	A	73	VAL	2.1
1	A	155	ASP	2.1
1	B	54	TYR	2.1
1	B	55	GLU	2.1
1	B	74	GLN	2.1
1	B	82	MET	2.0
1	B	258	GLY	2.0
1	B	72	ASN	2.0

## 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 ⓘ

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.