



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 03:01 PM UTC

PDB ID : 2OIN / pdb_00002oin
Title : crystal structure of HCV NS3-4A R155K mutant
Authors : Wei, Y.
Deposited on : 2007-01-11
Resolution : 2.50 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 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
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

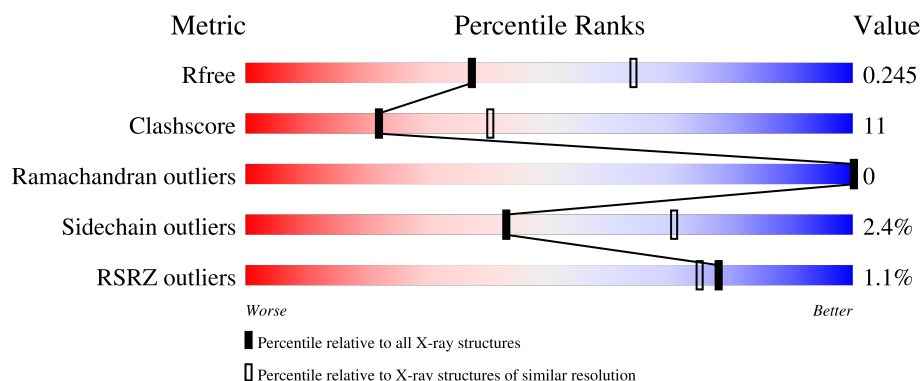
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	200	
1	B	200	
2	C	21	
2	D	21	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 2891 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 Polyprotein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	151	Total	C	N	O	S	0	0	0
			1110	696	197	209	8			
1	B	181	Total	C	N	O	S	0	0	0
			1323	826	239	249	9			

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	16	MET	-	cloning artifact	UNP Q9ELS8
A	17	ALA	-	cloning artifact	UNP Q9ELS8
A	18	SER	-	cloning artifact	UNP Q9ELS8
A	19	MET	-	cloning artifact	UNP Q9ELS8
A	20	THR	-	cloning artifact	UNP Q9ELS8
A	21	GLY	-	cloning artifact	UNP Q9ELS8
A	22	GLY	-	cloning artifact	UNP Q9ELS8
A	23	GLN	-	cloning artifact	UNP Q9ELS8
A	24	GLN	-	cloning artifact	UNP Q9ELS8
A	25	MET	-	cloning artifact	UNP Q9ELS8
A	26	GLY	-	cloning artifact	UNP Q9ELS8
A	145	ARG	GLN	conflict	UNP Q9ELS8
A	181	LYS	ARG	engineered mutation	UNP Q9ELS8
A	208	GLY	-	cloning artifact	UNP Q9ELS8
A	209	SER	-	cloning artifact	UNP Q9ELS8
A	210	HIS	-	expression tag	UNP Q9ELS8
A	211	HIS	-	expression tag	UNP Q9ELS8
A	212	HIS	-	expression tag	UNP Q9ELS8
A	213	HIS	-	expression tag	UNP Q9ELS8
A	214	HIS	-	expression tag	UNP Q9ELS8
A	215	HIS	-	expression tag	UNP Q9ELS8
B	1016	MET	-	cloning artifact	UNP Q9ELS8
B	1017	ALA	-	cloning artifact	UNP Q9ELS8
B	1018	SER	-	cloning artifact	UNP Q9ELS8
B	1019	MET	-	cloning artifact	UNP Q9ELS8

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1020	THR	-	cloning artifact	UNP Q9ELS8
B	1021	GLY	-	cloning artifact	UNP Q9ELS8
B	1022	GLY	-	cloning artifact	UNP Q9ELS8
B	1023	GLN	-	cloning artifact	UNP Q9ELS8
B	1024	GLN	-	cloning artifact	UNP Q9ELS8
B	1025	MET	-	cloning artifact	UNP Q9ELS8
B	1026	GLY	-	cloning artifact	UNP Q9ELS8
B	1145	ARG	GLN	conflict	UNP Q9ELS8
B	1181	LYS	ARG	engineered mutation	UNP Q9ELS8
B	1208	GLY	-	cloning artifact	UNP Q9ELS8
B	1209	SER	-	cloning artifact	UNP Q9ELS8
B	1210	HIS	-	expression tag	UNP Q9ELS8
B	1211	HIS	-	expression tag	UNP Q9ELS8
B	1212	HIS	-	expression tag	UNP Q9ELS8
B	1213	HIS	-	expression tag	UNP Q9ELS8
B	1214	HIS	-	expression tag	UNP Q9ELS8
B	1215	HIS	-	expression tag	UNP Q9ELS8

- Molecule 2 is a protein called NS4A peptide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	16	Total	C	N	O	0	0	0
			108	70	20	18			
2	D	21	Total	C	N	O	0	0	0
			142	93	25	24			

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Zn	0	0
			1	1		
3	B	1	Total	Zn	0	0
			1	1		

- Molecule 4 is water.

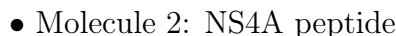
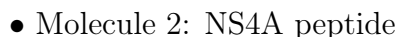
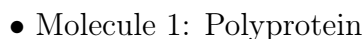
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	105	Total	O	0	0
			105	105		
4	B	83	Total	O	0	0
			83	83		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	C	11	Total 11	O 11	0	0
4	D	7	Total 7	O 7	0	0

- Molecule 1: Polyprotein



There are no outlier residues recorded for this chain.

4 Data and refinement statistics

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, α , β , γ	225.31Å 225.31Å 75.66Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	19.93 – 2.50 19.93 – 2.50	Depositor EDS
% Data completeness (in resolution range)	86.2 (19.93-2.50) 86.9 (19.93-2.50)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.50 (at 2.50Å)	Xtriage
Refinement program	CNS, CNX 2005	Depositor
R, R_{free}	0.200 , 0.246 0.202 , 0.245	Depositor DCC
R_{free} test set	1132 reflections (5.12%)	wwPDB-VP
Wilson B-factor (Å ²)	42.2	Xtriage
Anisotropy	0.187	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 47.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	2891	wwPDB-VP
Average B, all atoms (Å ²)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.65% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ZN

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	0/1134	0.76	0/1550
1	B	0.38	0/1349	0.78	0/1843
2	C	0.54	0/108	1.04	2/145 (1.4%)
2	D	0.50	0/143	0.83	0/193
All	All	0.39	0/2734	0.79	2/3731 (0.1%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	34	LYS	CA-C-N	5.05	125.49	120.14
2	C	34	LYS	C-N-CA	5.05	125.49	120.14

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	1110	0	1108	30	0
1	B	1323	0	1322	27	0
2	C	108	0	125	5	0
2	D	142	0	161	0	0
3	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	1	0	0	0	0
4	A	105	0	0	7	0
4	B	83	0	0	1	0
4	C	11	0	0	0	0
4	D	7	0	0	0	0
All	All	2891	0	2716	58	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 11.

All (58) 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:1156:ARG:HH11	1:B:1156:ARG:HG3	1.48	0.78
1:B:1158:ILE:HD12	1:B:1190:ALA:HB2	1.66	0.78
1:A:169:LEU:HG	4:A:939:HOH:O	1.83	0.77
1:A:75:ASN:HD22	1:A:205:MET:HE1	1.51	0.75
1:A:64:THR:HG22	1:A:65:ALA:N	2.04	0.72
1:A:158:ILE:HD13	1:A:158:ILE:O	1.91	0.71
1:A:193:VAL:HG21	4:A:946:HOH:O	1.92	0.70
1:B:1186:THR:O	1:B:1187:ARG:HB2	1.92	0.67
1:A:169:LEU:HD21	4:A:946:HOH:O	1.94	0.66
1:A:64:THR:CG2	1:A:65:ALA:N	2.60	0.65
1:B:1122:PRO:HB3	1:B:1198:VAL:HG11	1.80	0.63
1:B:1156:ARG:HH11	1:B:1156:ARG:CG	2.13	0.61
1:B:1108:LEU:HD11	1:B:1201:LEU:HD12	1.82	0.60
1:A:64:THR:HG22	1:A:66:THR:H	1.66	0.60
1:A:88:ARG:HG2	2:C:21:GLY:O	2.02	0.59
2:C:30:VAL:O	2:C:30:VAL:HG13	2.02	0.59
1:B:1177:VAL:O	1:B:1198:VAL:HG23	2.04	0.58
1:A:132:LEU:HD23	1:A:133:VAL:N	2.18	0.58
1:B:1103:ASN:ND2	1:B:1106:GLN:HG2	2.20	0.57
1:B:1177:VAL:C	1:B:1198:VAL:HG23	2.29	0.57
1:B:1132:LEU:HD23	1:B:1140:ILE:HD11	1.87	0.57
1:B:1176:ALA:O	1:B:1198:VAL:HG21	2.05	0.57
1:A:64:THR:CG2	1:A:65:ALA:H	2.19	0.55
1:A:115:GLN:HG2	4:A:944:HOH:O	2.09	0.52
1:A:120:LEU:HD13	1:A:176:ALA:HB2	1.91	0.52
1:A:199:GLU:HG2	4:A:993:HOH:O	2.09	0.52
1:B:1143:ARG:HB2	1:B:1153:LEU:HD21	1.93	0.51
1:B:1158:ILE:CD1	1:B:1190:ALA:HB2	2.40	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:61:ILE:O	2:C:26:VAL:HG22	2.11	0.51
1:A:89:THR:HG22	1:A:98:ILE:HA	1.93	0.50
1:B:1156:ARG:HG2	1:B:1160:TYR:CD1	2.47	0.49
1:A:136:HIS:O	1:A:137:ALA:HB3	2.12	0.49
1:A:132:LEU:HD12	4:A:946:HOH:O	2.11	0.49
1:B:1198:VAL:O	1:B:1201:LEU:HB2	2.12	0.48
1:A:60:GLN:HG2	1:A:71:ALA:HB3	1.96	0.48
1:A:128:SER:HB2	1:A:143:ARG:NH2	2.31	0.46
1:B:1156:ARG:CG	1:B:1156:ARG:NH1	2.74	0.46
1:A:158:ILE:HG12	1:A:185:CYS:SG	2.56	0.46
1:A:60:GLN:NE2	1:A:73:CYS:SG	2.87	0.45
1:B:1100:MET:HG3	1:B:1112:PRO:HD3	1.99	0.45
1:B:1156:ARG:NH1	1:B:1160:TYR:CE1	2.85	0.45
1:A:132:LEU:HD23	1:A:132:LEU:C	2.43	0.44
1:B:1070:LEU:HD21	1:B:1135:ARG:HG3	2.00	0.44
1:B:1142:VAL:HG22	1:B:1152:LEU:HD23	2.00	0.44
1:B:1069:PHE:N	1:B:1069:PHE:CD2	2.86	0.43
1:B:1156:ARG:NH1	1:B:1160:TYR:HE1	2.16	0.43
1:B:1158:ILE:HD13	1:B:1185:CYS:HB2	1.99	0.43
1:A:55:VAL:HG21	2:C:36:ALA:HA	2.02	0.42
1:B:1099:GLN:HG3	4:B:43:HOH:O	2.18	0.42
1:A:55:VAL:CG2	2:C:36:ALA:HA	2.50	0.41
1:A:116:GLY:HA2	4:A:974:HOH:O	2.19	0.41
1:A:100:MET:HE2	1:A:101:TYR:CE1	2.55	0.41
1:B:1058:GLU:HA	1:B:1118:ARG:O	2.19	0.41
1:B:1186:THR:O	1:B:1187:ARG:CB	2.64	0.41
1:A:101:TYR:CE2	1:A:205:MET:HA	2.56	0.41
1:A:73:CYS:HA	1:A:77:VAL:O	2.21	0.41
1:B:1037:ARG:HH12	1:B:1051:ASP:CG	2.29	0.40
1:A:130:LEU:HD22	1:A:177:VAL:HG21	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	149/200 (74%)	146 (98%)	3 (2%)	0	100	100
1	B	179/200 (90%)	169 (94%)	10 (6%)	0	100	100
2	C	14/21 (67%)	14 (100%)	0	0	100	100
2	D	19/21 (90%)	19 (100%)	0	0	100	100
All	All	361/442 (82%)	348 (96%)	13 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	122/161 (76%)	119 (98%)	3 (2%)	42	69
1	B	143/161 (89%)	140 (98%)	3 (2%)	47	74
2	C	12/16 (75%)	11 (92%)	1 (8%)	10	22
2	D	15/16 (94%)	15 (100%)	0	100	100
All	All	292/354 (82%)	285 (98%)	7 (2%)	43	70

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

Mol	Chain	Res	Type
1	A	60	GLN
1	A	88	ARG
1	A	158	ILE
1	B	1039	LEU
1	B	1068	THR
1	B	1156	ARG
2	C	22	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	60	GLN
1	A	67	GLN
1	A	75	ASN
1	A	136	HIS
1	A	200	ASN
1	B	1075	ASN

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](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	151/200 (75%)	-0.38	1 (0%) 84 81	26, 41, 57, 64	0
1	B	181/200 (90%)	-0.21	2 (1%) 78 75	26, 44, 65, 79	0
2	C	16/21 (76%)	-0.45	1 (6%) 26 23	26, 32, 44, 53	0
2	D	21/21 (100%)	-0.36	0 100 100	29, 33, 50, 60	0
All	All	369/442 (83%)	-0.30	4 (1%) 78 75	26, 41, 63, 79	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	1185	CYS	2.9
2	C	36	ALA	2.8
1	B	1207	SER	2.3
1	A	118	ARG	2.3

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($\text{\AA}^2$)	Q<0.9
3	ZN	B	902	1/1	0.98	0.04	42,42,42,42	0
3	ZN	A	901	1/1	1.00	0.05	41,41,41,41	0

6.5 Other polymers [i](#)

There are no such residues in this entry.