



wwPDB X-ray Structure Validation Summary Report i

Mar 1, 2014 – 04:22 AM GMT

PDB ID : 1N1L
Title : CRYSTAL STRUCTURE OF HCV NS3 PROTEASE DOMAIN:NS4A PEPTIDE COMPLEX WITH COVALENTLY BOUND INHIBITOR (GW472467X)
Authors : Andrews, D.M.; Chaignot, H.; Coomber, B.A.; Good, A.C.; Hind, S.L.; Jones, P.S.; Mill, G.; Robinson, J.E.; Skarzynski, T.; Slater, M.J.; Somers, D.O.N.
Deposited on : 2002-10-18
Resolution : 2.60 Å(reported)

This is a wwPDB validation summary report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

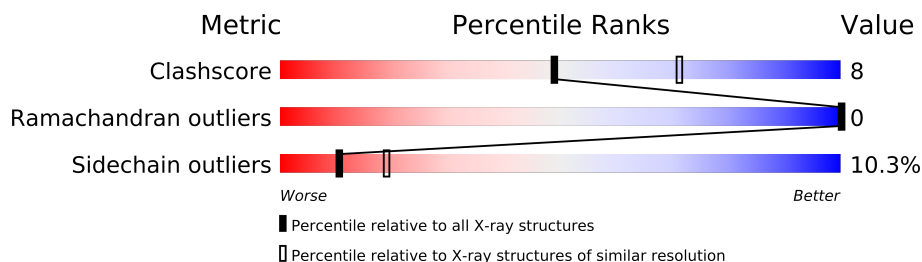
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	21963
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.60 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))
Clashscore	79885	2154 (2.60-2.60)
Ramachandran outliers	78287	2113 (2.60-2.60)
Sidechain outliers	78261	2113 (2.60-2.60)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	198	
1	B	198	
2	C	23	
2	D	23	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 2870 atoms, of which 0 are hydrogen and 0 are deuterium.

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 HCV NS3 SERINE PROTEASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	180	Total	C	N	O	S	0	0	0
			1337	834	243	251	9			
1	B	153	Total	C	N	O	S	0	0	0
			1138	711	206	213	8			

There are 38 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-9	ALA	-	CLONING ARTIFACT	UNP P27958
A	-8	SER	-	CLONING ARTIFACT	UNP P27958
A	-7	MET	-	CLONING ARTIFACT	UNP P27958
A	-6	THR	-	CLONING ARTIFACT	UNP P27958
A	-5	GLY	-	CLONING ARTIFACT	UNP P27958
A	-4	GLY	-	CLONING ARTIFACT	UNP P27958
A	-3	GLN	-	CLONING ARTIFACT	UNP P27958
A	-2	GLN	-	CLONING ARTIFACT	UNP P27958
A	-1	MET	-	CLONING ARTIFACT	UNP P27958
A	0	GLY	-	CLONING ARTIFACT	UNP P27958
A	164	THR	ALA	ENGINEERED	UNP P27958
A	181	GLY	-	EXPRESSION TAG	UNP P27958
A	182	SER	-	EXPRESSION TAG	UNP P27958
A	183	HIS	-	EXPRESSION TAG	UNP P27958
A	184	HIS	-	EXPRESSION TAG	UNP P27958
A	185	HIS	-	EXPRESSION TAG	UNP P27958
A	186	HIS	-	EXPRESSION TAG	UNP P27958
A	187	HIS	-	EXPRESSION TAG	UNP P27958
A	188	HIS	-	EXPRESSION TAG	UNP P27958
B	-9	ALA	-	CLONING ARTIFACT	UNP P27958
B	-8	SER	-	CLONING ARTIFACT	UNP P27958
B	-7	MET	-	CLONING ARTIFACT	UNP P27958
B	-6	THR	-	CLONING ARTIFACT	UNP P27958
B	-5	GLY	-	CLONING ARTIFACT	UNP P27958
B	-4	GLY	-	CLONING ARTIFACT	UNP P27958

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-3	GLN	-	CLONING ARTIFACT	UNP P27958
B	-2	GLN	-	CLONING ARTIFACT	UNP P27958
B	-1	MET	-	CLONING ARTIFACT	UNP P27958
B	0	GLY	-	CLONING ARTIFACT	UNP P27958
B	164	THR	ALA	ENGINEERED	UNP P27958
B	181	GLY	-	EXPRESSION TAG	UNP P27958
B	182	SER	-	EXPRESSION TAG	UNP P27958
B	183	HIS	-	EXPRESSION TAG	UNP P27958
B	184	HIS	-	EXPRESSION TAG	UNP P27958
B	185	HIS	-	EXPRESSION TAG	UNP P27958
B	186	HIS	-	EXPRESSION TAG	UNP P27958
B	187	HIS	-	EXPRESSION TAG	UNP P27958
B	188	HIS	-	EXPRESSION TAG	UNP P27958

- Molecule 2 is a protein called NS4A COFACTOR.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	21	Total	C	N	O	0	0	0
			149	99	27	23			
2	D	16	Total	C	N	O	0	0	0
			108	70	20	18			

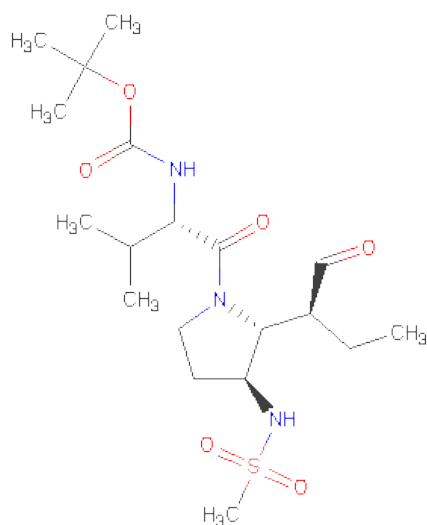
There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	19	LYS	-	CLONING ARTIFACT	GB 5748511
C	20	LYS	-	CLONING ARTIFACT	GB 5748511
C	40	LYS	-	CLONING ARTIFACT	GB 5748511
C	41	LYS	-	CLONING ARTIFACT	GB 5748511
D	19	LYS	-	CLONING ARTIFACT	GB 5748511
D	20	LYS	-	CLONING ARTIFACT	GB 5748511
D	40	LYS	-	CLONING ARTIFACT	GB 5748511
D	41	LYS	-	CLONING ARTIFACT	GB 5748511

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

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

- Molecule 4 is {1-[2-(1-FORMYL-PROPYL)-3-METHANESULFONYLAMINO-PYRROLIDINE-1-CARBONYL]-2-METHYL-PROPYL}-CARBAMICACID TERT-BUTYL ESTER (three-letter code: TRL) (formula: C₁₉H₃₅N₃O₆S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	S	0	0
			29	19	3	6	1		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	46	Total	O	0	0
			46	46		
5	B	43	Total	O	0	0
			43	43		
5	C	5	Total	O	0	0
			5	5		
5	D	13	Total	O	0	0
			13	13		

4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, α , β , γ	225.45Å 225.45Å 75.89Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 2.60	Depositor
% Data completeness (in resolution range)	100.0 (20.00-2.60)	Depositor
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	REFMAC	Depositor
R, R_{free}	0.183 , 0.220	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2870	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

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

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	0.70	0/1363	0.93	1/1859 (0.1%)
1	B	0.75	0/1162	0.93	4/1586 (0.3%)
2	C	0.88	0/150	0.83	0/201
2	D	0.88	0/108	0.79	0/145
All	All	0.74	0/2783	0.92	5/3791 (0.1%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	79	ASP	CB-CG-OD2	5.89	123.60	118.30
1	B	81	ASP	CB-CG-OD2	5.75	123.48	118.30
1	B	121	ASP	CB-CG-OD2	5.75	123.48	118.30
1	B	92	ARG	NE-CZ-NH1	5.56	123.08	120.30
1	A	108	THR	N-CA-CB	-5.15	100.51	110.30

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1337	0	1353	26	0
1	B	1138	0	1142	17	0
2	C	149	0	180	2	0
2	D	108	0	125	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	29	0	34	5	0
5	A	46	0	0	1	0
5	B	43	0	0	0	0
5	C	5	0	0	1	0
5	D	13	0	0	0	0
All	All	2870	0	2834	43	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 8.

The worst 5 of 43 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1:ALA:HB1	1:A:2:PRO:HD2	1.55	0.89
1:A:1:ALA:HB1	1:A:2:PRO:CD	2.02	0.89
1:A:14:LEU:O	1:A:18:ILE:HD12	1.77	0.83
1:A:1:ALA:CB	1:A:2:PRO:HD2	2.10	0.82
1:A:1:ALA:CB	1:A:2:PRO:CD	2.65	0.75

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	178/198 (90%)	175 (98%)	3 (2%)	0	100	100
1	B	151/198 (76%)	144 (95%)	7 (5%)	0	100	100
2	C	19/23 (83%)	19 (100%)	0	0	100	100
2	D	14/23 (61%)	14 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	362/442 (82%)	352 (97%)	10 (3%)	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	147/160 (92%)	128 (87%)	19 (13%)	6	11
1	B	126/160 (79%)	117 (93%)	9 (7%)	21	40
2	C	17/19 (90%)	15 (88%)	2 (12%)	8	14
2	D	12/19 (63%)	11 (92%)	1 (8%)	16	30
All	All	302/358 (84%)	271 (90%)	31 (10%)	10	19

5 of 31 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	133	SER
1	A	165	LYS
2	C	22	SER
1	A	159	CYS
1	A	172	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	49	ASN
1	B	89	GLN
1	B	174	ASN

5.3.3 RNA ⓘ

There are no RNA chains 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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 3 ligands modelled in this entry, 2 are monoatomic - leaving 1 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	$\# Z > 2$
4	TRL	A	200	1	29,29,29	0.95	1 (3%)	43,43,43	2.55	14 (32%)

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
4	TRL	A	200	1	-	0/34/47/47	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	200	TRL	C27-C28	2.28	1.54	1.50

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	200	TRL	C15-O6-C11	8.11	134.68	121.11
4	A	200	TRL	C27-C8-N10	7.36	122.51	112.84
4	A	200	TRL	C5-N1-C11	6.17	135.39	120.77

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	200	TRL	C6-C5-N1	-5.91	96.34	111.37
4	A	200	TRL	O4-S1-N3	-2.99	101.84	107.41

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers ⓘ

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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.