



# Full wwPDB NMR Structure Validation Report ⓘ

Apr 26, 2016 – 06:00 PM BST

PDB ID : 1XNA  
Title : NMR SOLUTION STRUCTURE OF THE SINGLE-STRAND BREAK REPAIR PROTEIN XRCC1-N-TERMINAL DOMAIN  
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Deposited on : 1999-02-27

This is a Full wwPDB NMR 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  
<http://wwpdb.org/validation/2016/NMRValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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

Cyrange : Kirchner and Güntert (2011)  
NmrClust : Kelley et al. (1996)  
MolProbity : 4.02b-467  
Mogul : unknown  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
RCI : v\_1n\_11\_5\_13\_A (Berjanski et al., 2005)  
PANAV : Wang et al. (2010)  
ShiftChecker : rb-20027457  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20027457

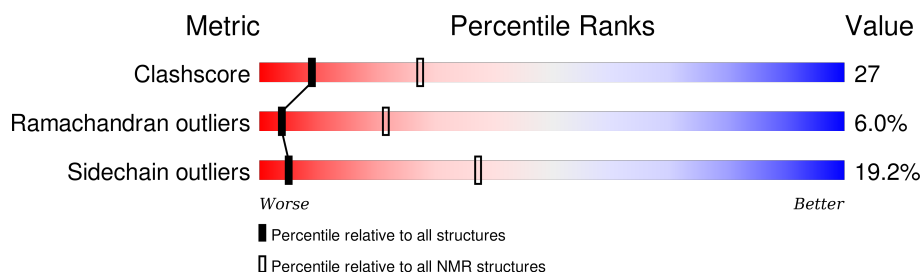
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*SOLUTION NMR*

The overall completeness of chemical shifts assignment was not calculated.

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)	NMR archive (#Entries)
Clashscore	114402	11133
Ramachandran outliers	111179	9975
Sidechain outliers	111093	9958

The table below summarises the geometric issues observed across the polymeric chains and their fit to the experimental data. The red, orange, yellow and green segments indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A cyan segment indicates the fraction of residues that are not part of the well-defined cores, and 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  $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	183	

## 2 Ensemble composition and analysis ⓘ

This entry contains 1 models. Identification of well-defined residues and clustering analysis are not possible.

### 3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 2323 atoms, of which 1153 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called PROTEIN (DNA-REPAIR PROTEIN XRCC1).

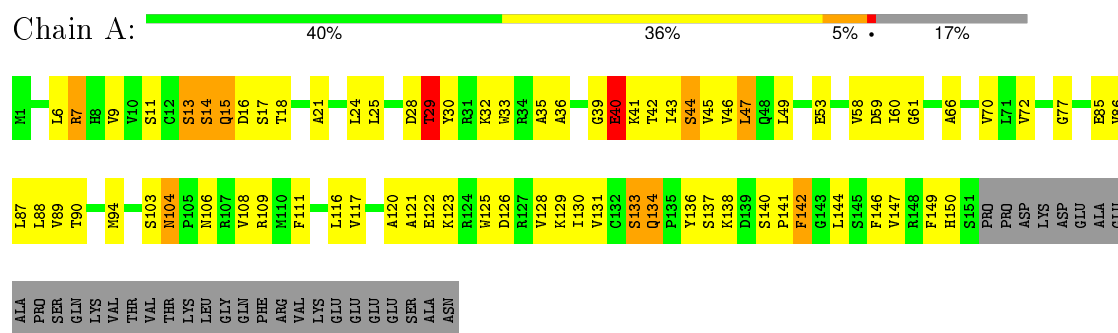
Mol	Chain	Residues	Atoms						Trace
1	A	151	Total	C	H	N	O	S	
			2323	726	1153	212	226	6	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	179	GLU	ASP	CLONING ARTIFACT	UNP P18887



- Molecule 1: PROTEIN (DNA-REPAIR PROTEIN XRCC1)



## 5 Refinement protocol and experimental data overview

The models were refined using the following method: *TORSION ANGLE DYNAMICS*.

Of the ? calculated structures, 1 were deposited, based on the following criterion: *MINIMIZED AVERAGE STRUCTURE OF 23 CONFORMERS*.

The following table shows the software used for structure solution, optimisation and refinement.

Software name	Classification	Version
X-PLOR	refinement	3.851
DYANA	structure solution	1.5

No chemical shift data was provided. No validations of the models with respect to experimental NMR restraints is performed at this time.

## 6 Model quality

### 6.1 Standard geometry

There are no covalent bond-length or bond-angle outliers.

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 6.2 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 each 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 averaged over the ensemble.

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	1170	1153	1155	63
All	All	1170	1153	1155	63

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 27.

All clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)
1:A:116:LEU:HD13	1:A:121:ALA:CB	0.85	2.02
1:A:117:VAL:CG1	1:A:120:ALA:HB3	0.81	2.06
1:A:21:ALA:HB1	1:A:45:VAL:HG21	0.66	1.66
1:A:66:ALA:HB3	1:A:134:GLN:HB2	0.65	1.67
1:A:117:VAL:HG13	1:A:120:ALA:HB3	0.65	1.68
1:A:59:ASP:C	1:A:60:ILE:HD12	0.64	2.13
1:A:59:ASP:O	1:A:60:ILE:HD12	0.62	1.94
1:A:24:LEU:HD21	1:A:33:TRP:HB2	0.62	1.71
1:A:116:LEU:HD12	1:A:116:LEU:O	0.60	1.95
1:A:33:TRP:CH2	1:A:43:ILE:HD12	0.60	2.30
1:A:42:THR:HG22	1:A:133:SER:OG	0.60	1.96
1:A:70:VAL:HG13	1:A:130:ILE:CD1	0.60	2.26
1:A:128:VAL:HG11	1:A:149:PHE:CE2	0.60	2.31
1:A:24:LEU:HB3	1:A:147:VAL:HG22	0.59	1.73
1:A:6:LEU:CD2	1:A:47:LEU:HD22	0.58	2.28

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Atom-1	Atom-2	Clash(Å)	Distance(Å)
1:A:70:VAL:HG13	1:A:130:ILE:HD13	0.57	1.77
1:A:14:SER:OG	1:A:43:ILE:HG22	0.56	2.00
1:A:9:VAL:O	1:A:9:VAL:HG13	0.56	1.99
1:A:70:VAL:HG22	1:A:130:ILE:CD1	0.56	2.31
1:A:88:LEU:HD13	1:A:111:PHE:CD2	0.55	2.37
1:A:88:LEU:HD13	1:A:111:PHE:CE2	0.55	2.36
1:A:45:VAL:O	1:A:45:VAL:HG13	0.54	2.03
1:A:33:TRP:CZ3	1:A:43:ILE:HD12	0.53	2.38
1:A:58:VAL:HG13	1:A:149:PHE:CD1	0.53	2.37
1:A:15:GLN:O	1:A:36:ALA:HB2	0.53	2.02
1:A:66:ALA:HB3	1:A:134:GLN:CB	0.53	2.33
1:A:111:PHE:N	1:A:111:PHE:CD1	0.53	2.76
1:A:6:LEU:HD21	1:A:47:LEU:HD22	0.52	1.79
1:A:41:LYS:O	1:A:42:THR:HG23	0.51	2.05
1:A:21:ALA:O	1:A:24:LEU:HD12	0.51	2.06
1:A:116:LEU:HD13	1:A:121:ALA:HB1	0.51	1.81
1:A:7:ARG:C	1:A:25:LEU:HD11	0.50	2.26
1:A:94:MET:HE3	1:A:104:ASN:O	0.50	2.06
1:A:35:ALA:HB2	1:A:43:ILE:HG21	0.50	1.83
1:A:117:VAL:HG11	1:A:120:ALA:HB3	0.49	1.81
1:A:72:VAL:HG13	1:A:87:LEU:HB2	0.48	1.85
1:A:44:SER:HB3	1:A:131:VAL:HG22	0.48	1.86
1:A:133:SER:O	1:A:134:GLN:HB2	0.48	2.08
1:A:72:VAL:CG1	1:A:87:LEU:HD22	0.47	2.39
1:A:21:ALA:HB1	1:A:45:VAL:CG2	0.46	2.38
1:A:14:SER:CB	1:A:43:ILE:HG22	0.46	2.40
1:A:13:SER:O	1:A:14:SER:CB	0.45	2.64
1:A:40:GLU:CB	1:A:136:TYR:CE1	0.45	2.99
1:A:33:TRP:CH2	1:A:43:ILE:CD1	0.45	2.99
1:A:33:TRP:CH2	1:A:43:ILE:CG1	0.45	2.99
1:A:128:VAL:HG11	1:A:149:PHE:CZ	0.45	2.47
1:A:60:ILE:HG23	1:A:144:LEU:CD2	0.45	2.42
1:A:33:TRP:CZ3	1:A:43:ILE:CD1	0.44	3.01
1:A:49:LEU:HD12	1:A:126:ASP:HA	0.44	1.89
1:A:46:VAL:HG22	1:A:129:LYS:HG3	0.43	1.89
1:A:6:LEU:HD21	1:A:47:LEU:CB	0.43	2.43
1:A:123:LYS:O	1:A:125:TRP:CD1	0.43	2.72
1:A:72:VAL:HG11	1:A:87:LEU:HD13	0.42	1.91
1:A:24:LEU:HD22	1:A:147:VAL:HG13	0.42	1.92
1:A:39:GLY:O	1:A:41:LYS:N	0.41	2.53
1:A:60:ILE:HG23	1:A:144:LEU:HD23	0.41	1.91
1:A:70:VAL:HG22	1:A:130:ILE:HD12	0.41	1.91

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Atom-1	Atom-2	Clash(Å)	Distance(Å)
1:A:133:SER:O	1:A:134:GLN:CB	0.41	2.68
1:A:141:PRO:O	1:A:142:PHE:CD2	0.41	2.74
1:A:61:GLY:HA2	1:A:108:VAL:HA	0.41	1.92
1:A:61:GLY:HA3	1:A:146:PHE:CE2	0.41	2.51
1:A:28:ASP:O	1:A:29:THR:HG23	0.40	2.16
1:A:15:GLN:O	1:A:15:GLN:NE2	0.40	2.54

## 6.3 Torsion angles

### 6.3.1 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 PDB entries followed by that with respect to all NMR entries. 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	149/183 (81%)	117 (79%)	23 (15%)	9 (6%)	4	21
All	All	149/183 (81%)	117 (79%)	23 (15%)	9 (6%)	4	21

All 9 Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type
1	A	134	GLN
1	A	77	GLY
1	A	29	THR
1	A	14	SER
1	A	138	LYS
1	A	40	GLU
1	A	86	VAL
1	A	89	VAL
1	A	30	TYR

### 6.3.2 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 PDB entries followed by that with respect to all NMR entries. 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	130/158 (82%)	105 (81%)	25 (19%)	5	37
All	All	130/158 (82%)	105 (81%)	25 (19%)	5	37

All 25 residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type
1	A	16	ASP
1	A	90	THR
1	A	122	GLU
1	A	109	ARG
1	A	44	SER
1	A	104	ASN
1	A	103	SER
1	A	40	GLU
1	A	32	LYS
1	A	7	ARG
1	A	142	PHE
1	A	13	SER
1	A	137	SER
1	A	140	SER
1	A	85	GLU
1	A	29	THR
1	A	106	ASN
1	A	18	THR
1	A	133	SER
1	A	15	GLN
1	A	150	HIS
1	A	11	SER
1	A	47	LEU
1	A	53	GLU
1	A	17	SER

### 6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 6.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

## 6.5 Carbohydrates

There are no carbohydrates in this entry.

## 6.6 Ligand geometry

There are no ligands in this entry.

## 6.7 Other polymers

There are no such molecules in this entry.

## 6.8 Polymer linkage issues

There are no chain breaks in this entry.

## 7 Chemical shift validation

No chemical shift data were provided