



wwPDB NMR Structure Validation Summary Report ⓘ

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PDB ID : 1CXX
Title : MUTANT R122A OF QUAIL CYSTEINE AND GLYCINE-RICH PROTEIN,
NMR, MINIMIZED STRUCTURE
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Deposited on : 1999-08-31

This is a wwPDB NMR 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/NMRValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
ShiftChecker : trunk30686
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk30686

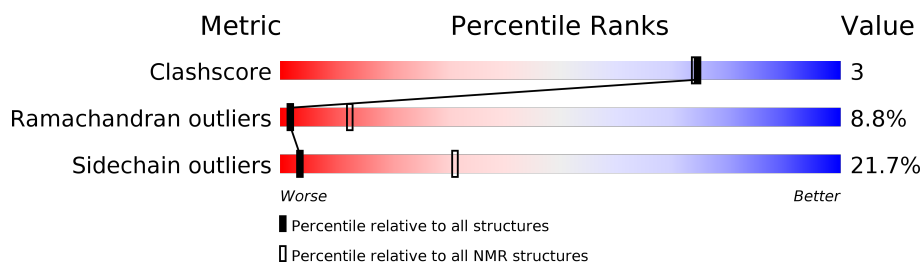
1 Overall quality at a glance

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	136279	12091
Ramachandran outliers	132675	10835
Sidechain outliers	132484	10811

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 ≥ 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	113	<div> <div style="width: 34%; background-color: green;"></div> <div style="width: 17%; background-color: yellow;"></div> <div style="width: 1%; background-color: orange;"></div> <div style="width: 48%; background-color: grey;"></div> </div> <div> <div>34%</div> <div>17%</div> <div>.</div> <div>48%</div> </div>

2 Ensemble composition and analysis ⓘ

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

3 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 868 atoms, of which 426 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called CYSTEINE AND GLYCINE-RICH PROTEIN CRP2.

Mol	Chain	Residues	Atoms						Trace
1	A	59	Total	C	H	N	O	S	0
			866	272	426	76	85	7	

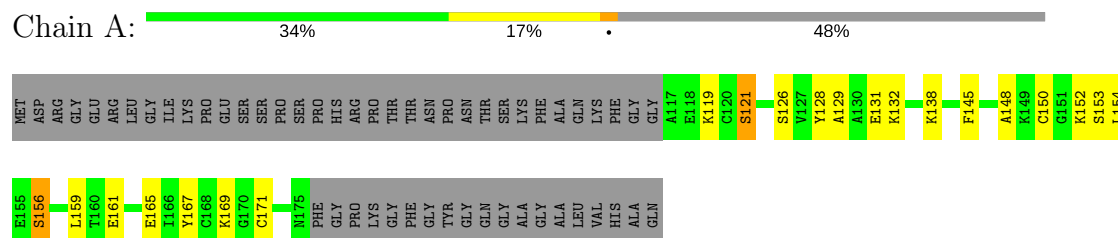
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	122	ALA	ARG	ENGINEERED	UNP Q05158

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	
2	A	2	Total	Zn
			2	2

- Molecule 1: CYSTEINE AND GLYCINE-RICH PROTEIN CRP2



5 Refinement protocol and experimental data overview

The models were refined using the following method: *SIMULATED ANNEALING, MOLECULAR DYNAMICS REFINEMENT, ENERGY MINIMIZATION*.

Of the 11 calculated structures, 1 were deposited, based on the following criterion: *STRUCTURES WITH THE LEAST RESTRAINT VIOLATIONS, STRUCTURES WITH THE LOWEST ENERGY*.

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

Software name	Classification	Version
X-PLOR	structure solution	3.1
X-PLOR	refinement	3.1

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 [i](#)

6.1 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 (average) 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	0.94	4/447 (0.9%)	1.24	0/596 (0.0%)
All	All	0.94	4/447 (0.9%)	1.24	0/596 (0.0%)

All bond outliers are listed below. They are sorted according to the Z-score.

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	126	SER	CB-OG	5.49	1.49	1.42
1	A	121	SER	CB-OG	5.33	1.49	1.42
1	A	156	SER	CB-OG	5.27	1.49	1.42
1	A	153	SER	CB-OG	5.15	1.49	1.42

There are no bond-angle outliers.

There are no chirality outliers.

There are no planarity outliers.

6.2 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 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	440	426	425	3
All	All	442	426	425	3

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 3.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)
1:A:167:TYR:CD1	1:A:167:TYR:N	0.49	2.80
1:A:148:ALA:HB3	1:A:167:TYR:CE2	0.46	2.45
1:A:150:CYS:SG	1:A:152:LYS:HG2	0.41	2.55

6.3 Torsion angles [i](#)

6.3.1 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 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	57/113 (50%)	42 (74%)	10 (18%)	5 (9%)	2	12
All	All	57/113 (50%)	42 (74%)	10 (18%)	5 (9%)	2	12

All 5 Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type
1	A	128	TYR
1	A	129	ALA
1	A	159	LEU
1	A	165	GLU
1	A	131	GLU

6.3.2 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 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	46/86 (53%)	36 (78%)	10 (22%)	3	31
All	All	46/86 (53%)	36 (78%)	10 (22%)	3	31

5 of 10 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	145	PHE
1	A	132	LYS
1	A	171	CYS
1	A	161	GLU
1	A	169	LYS

6.3.3 RNA [i](#)

There are no RNA molecules in this entry.

6.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.6 Ligand geometry [i](#)

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

6.7 Other polymers [i](#)

There are no such molecules in this entry.

6.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

7 Chemical shift validation

No chemical shift data were provided