

Full wwPDB NMR Structure Validation Report (i)

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PDB ID : 2KZG

Title: A Transient and Low Populated Protein Folding Intermediate at Atomic Res-

olution

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This is a Full wwPDB NMR 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/NMRValidationReportHelp
with specific help available everywhere you see the (i) 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 (i)) were used in the production of this report:

MolProbity: 4.02b-467

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

wwPDB-RCI : v 1n 11 5 13 A (Berjanski et al., 2005)

PANAV : Wang et al. (2010)

wwPDB-ShiftChecker : v1.2

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

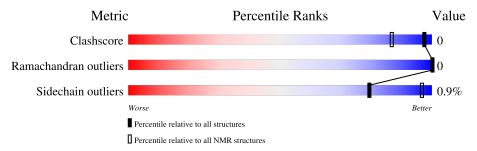
Validation Pipeline (wwPDB-VP) : 2.36.2

1 Overall quality at a glance (i)

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	NMR archive	
Metric	$(\# ext{Entries})$	$(\# ext{Entries})$	
Clashscore	158937	12864	
Ramachandran outliers	154571	11451	
Sidechain outliers	154315	11428	

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 <=5%

Mol	Chain	Length	Quality of chain				
1	Α.	7 1					
1	A	[71	52%	27%	21%		



2 Ensemble composition and analysis (i)

This entry contains 10 models. Model 2 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *lowest energy*.

The following residues are included in the computation of the global validation metrics.

Well-defined (core) protein residues							
Well-defined core	Well-defined core Residue range (total) Backbone RMSD (Å) Medoid model						
1	A:13-A:49 (37)	0.73	2				

Ill-defined regions of proteins are excluded from the global statistics.

Ligands and non-protein polymers are included in the analysis.

The models can be grouped into 2 clusters and 1 single-model cluster was found.

Cluster number	Models
1	1, 2, 4, 8, 9, 10
2	3, 5, 6
Single-model clusters	7



3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 937 atoms, of which 474 are hydrogens and 0 are deuteriums.

• Molecule 1 is a protein called Pre-mRNA-processing factor 40 homolog A.

Mol	Chain	Residues	Atoms					Trace	
1	Λ	E.G.	Total	С	Н	N	О	S	0
1	A	56	937	296	474	81	84	2	U

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	expression tag	UNP O75400



4 Residue-property plots (i)

4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-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. Stretches of 2 or more consecutive residues without any outliers are shown as green connectors. Residues which are classified as ill-defined in the NMR ensemble, are shown in cyan with an underline colour-coded according to the previous scheme. Residues which were present in the experimental sample, but not modelled in the final structure are shown in grey.

• Molecule 1: Pre-mRNA-processing factor 40 homolog A

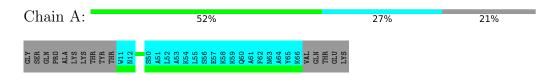


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

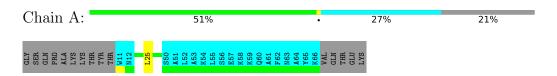
4.2.1 Score per residue for model 1

• Molecule 1: Pre-mRNA-processing factor 40 homolog A



4.2.2 Score per residue for model 2 (medoid)

• Molecule 1: Pre-mRNA-processing factor 40 homolog A





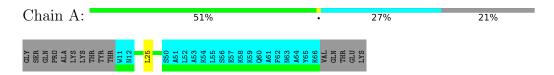
4.2.3 Score per residue for model 3

• Molecule 1: Pre-mRNA-processing factor 40 homolog A



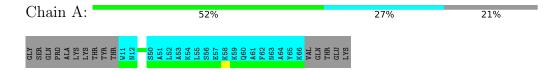
4.2.4 Score per residue for model 4

• Molecule 1: Pre-mRNA-processing factor 40 homolog A



4.2.5 Score per residue for model 5

• Molecule 1: Pre-mRNA-processing factor 40 homolog A



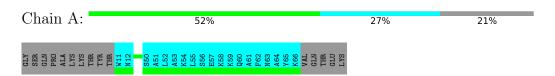
4.2.6 Score per residue for model 6

• Molecule 1: Pre-mRNA-processing factor 40 homolog A



4.2.7 Score per residue for model 7

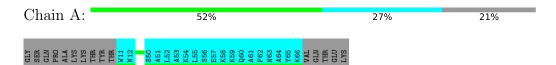
• Molecule 1: Pre-mRNA-processing factor 40 homolog A





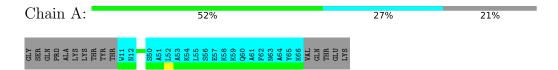
4.2.8 Score per residue for model 8

• Molecule 1: Pre-mRNA-processing factor 40 homolog A



4.2.9 Score per residue for model 9

• Molecule 1: Pre-mRNA-processing factor 40 homolog A



4.2.10 Score per residue for model 10

• Molecule 1: Pre-mRNA-processing factor 40 homolog A





Refinement protocol and experimental data overview (i) 5



The models were refined using the following method: *Monte Carlo*.

Of the 10000 calculated structures, 10 were deposited, based on the following criterion: structureswith the lowest energy.

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

Software name	Classification	Version
CS-ROSETTA	refinement	

No chemical shift data was provided.



6 Model quality (i)

6.1 Standard geometry (i)

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		В	Sond lengths	Bond angles		
		RMSZ	#Z>5	RMSZ	#Z>5	
1	A	0.86 ± 0.02	$0\pm0/314~(~0.0\pm~0.1\%)$	0.52 ± 0.02	$0\pm0/420~(~0.0\pm~0.0\%)$	
All	All	0.86	1/3140 (0.0%)	0.52	0/4200 (0.0%)	

All unique bond outliers are listed below.

Mol	Chain	Res	Type	Atoms	7.	Observed(Å)	Ideal(Å)	Mod	
IVIOI	Cham	ICCS	Type	$\mathbf{Z}_{\mathbf{ype}} \mid \mathbf{Atoms} \mid \mathbf{Z} \mid \mathbf{Observed}(A)$	Observed(11)	Ideal(11)	Worst	Total	
1	A	47	PRO	CG-CD	5.09	1.67	1.50	6	1

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	308	316	316	0±1
All	All	3080	3160	3160	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 0.

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

Atom 1	Atom-2	Clack(Å)	$\operatorname{Distance}(\mathring{\mathrm{A}})$	Models		
Atom-1	Atom-2	Clash(A)	Distance(A)	Worst	Total	
1:A:21:PHE:O	1:A:21:PHE:CD1	0.44	2.70	3	1	

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Atom-1	Atom-2	Clock(Å)	$Distance(\mathring{A})$	Models	
Atom-1	Atom-2	Clash(A)	Distance(A)	Worst	Total
1:A:21:PHE:CD1	1:A:21:PHE:C	0.42	2.91	3	1
1:A:21:PHE:O	1:A:21:PHE:HD1	0.41	1.97	3	1

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	Percer	ntiles
1	A	37/71 (52%)	37±0 (100±0%)	0±0 (0±0%)	0±0 (0±0%)	100	100
All	All	370/710 (52%)	370 (100%)	0 (0%)	0 (0%)	100	100

There are no Ramachandran outliers.

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 Percenti		ntiles
1	A	33/61 (54%)	33±0 (99±1%)	0±0 (1±1%)	79	97
All	All	330/610 (54%)	327 (99%)	3 (1%)	79	97

All 2 unique residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	25	LEU	2
1	A	21	PHE	1



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 monosaccharides in this entry.

6.6 Ligand geometry (i)

There are no ligands in this entry.

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 (i)

No chemical shift data were provided

