

# Full wwPDB NMR Structure Validation Report (i)

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PDB ID : 7QAO

Title: Three-dimensional structure of the PGAM5 C12S mutant TMD

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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 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)

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

PANAV : Wang et al. (2010)

ShiftChecker : 2.28

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

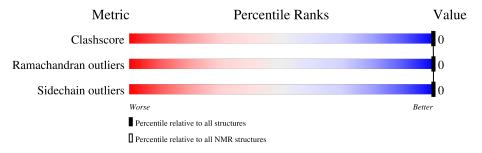
Validation Pipeline (wwPDB-VP) : 2.28

## 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 is 71%.

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 $(\# \text{Entries})$	$egin{array}{c} { m NMR \ archive} \ (\#{ m Entries}) \end{array}$
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 o	chain
1	A	35	57%	43%



## 2 Ensemble composition and analysis (i)

This entry contains 20 models. Model 4 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: closest to the average.

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

Well-defined (core) protein residues					
Well-defined core Residue range (total) Backbone RMSD (Å) Medoid model					
1	A:3-A:13 (11)	0.33	4		
2	A:18-A:26 (9)	0.17	3		

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 6 clusters and 1 single-model cluster was found.

Cluster number	Models
1	2, 6, 9, 18, 19
2	5, 7, 11, 15
3	8, 16, 17
4	3, 12, 13
5	4, 20
6	1, 14
Single-model clusters	10



## 3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 472 atoms, of which 240 are hydrogens and 0 are deuteriums.

• Molecule 1 is a protein called Serine/threonine-protein phosphatase PGAM5, mitochondrial.

$\mathbf{M}$	ol	Chain	Residues	Atoms				Trace	
1		Λ	35	Total	С	Н	N	О	0
1		A	39	472	145	240	44	43	U

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	12	SER	CYS	engineered mutation	UNP Q96HS1



## 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: Serine/threonine-protein phosphatase PGAM5, mitochondrial



### 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: Serine/threonine-protein phosphatase PGAM5, mitochondrial

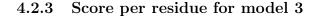


#### 4.2.2 Score per residue for model 2

• Molecule 1: Serine/threonine-protein phosphatase PGAM5, mitochondrial







• Molecule 1: Serine/threonine-protein phosphatase PGAM5, mitochondrial

Chain A: 57% 43%

A2 L114 L114 A15 G16 G17 A27 R30 R30 R30 R32 R33 G34 G35 D36

### 4.2.4 Score per residue for model 4 (medoid)

• Molecule 1: Serine/threonine-protein phosphatase PGAM5, mitochondrial

Chain A: 57% 43%

A2 L14 A15 G16 G17 V28 K30 K30 K30 R32 G34 G35

### 4.2.5 Score per residue for model 5

• Molecule 1: Serine/threonine-protein phosphatase PGAM5, mitochondrial

Chain A: 57% 43%

A27 V28 G17 V28 G29 K30 P31 R33 G34 G36 G36

#### 4.2.6 Score per residue for model 6

• Molecule 1: Serine/threonine-protein phosphatase PGAM5, mitochondrial

Chain A: 57% 43%

A27 A15 G16 G16 G17 A27 V28 G29 K30 P31 R32 A33 A33 A33 B34 G35 G36

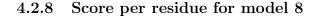
#### 4.2.7 Score per residue for model 7

• Molecule 1: Serine/threonine-protein phosphatase PGAM5, mitochondrial

Chain A: 57% 43%

A2 L114 A15 G16 G17 A27 V28 K30 K30 K30 A33 G34 G35 D36





• Molecule 1: Serine/threonine-protein phosphatase PGAM5, mitochondrial

Chain A: 57% 43%

A2 L114 L114 A15 G16 G17 A27 K30 K30 K30 K30 G29 K30 G39 G39 G35

### 4.2.9 Score per residue for model 9

• Molecule 1: Serine/threonine-protein phosphatase PGAM5, mitochondrial

Chain A: 57% 43%

A2 L114 A15 G17 A27 V28 K30 K30 K30 R32 G34 G35

### 4.2.10 Score per residue for model 10

• Molecule 1: Serine/threonine-protein phosphatase PGAM5, mitochondrial

Chain A: 57% 43%

A2 L14 A15 G16 G17 A27 A29 K30 P31 R32 A33 G34 G35 G35 G36

#### 4.2.11 Score per residue for model 11

• Molecule 1: Serine/threonine-protein phosphatase PGAM5, mitochondrial

Chain A: 57% 43%

A2 L114 A15 G16 G17 V28 G29 G29 K30 F31 R32 A33 G34 G34

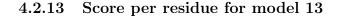
#### 4.2.12 Score per residue for model 12

• Molecule 1: Serine/threonine-protein phosphatase PGAM5, mitochondrial

Chain A: 57% 43%

A2 L114 A15 G16 G17 A27 V28 K30 K30 K30 R33 G29 K33 G35 D36





• Molecule 1: Serine/threonine-protein phosphatase PGAM5, mitochondrial

Chain A: 57% 43%

A2 L114 L114 A15 G17 A27 A27 R30 K30 K30 R33 G34 G35 G35

## 4.2.14 Score per residue for model 14

• Molecule 1: Serine/threonine-protein phosphatase PGAM5, mitochondrial

Chain A: 57% 43%

A2 L114 A15 G16 G17 V28 K30 K30 K30 R32 G35 G35

### 4.2.15 Score per residue for model 15

• Molecule 1: Serine/threonine-protein phosphatase PGAM5, mitochondrial

Chain A: 57% 43%

A27 A15 A16 G16 G17 A27 V28 G29 K30 P31 R32 A33 G34 G34 G35 G36

#### 4.2.16 Score per residue for model 16

• Molecule 1: Serine/threonine-protein phosphatase PGAM5, mitochondrial

Chain A: 57% 43%

A2 L114 A15 G16 G17 A27 V28 G29 K30 P31 R32 A33 G34 G34

#### 4.2.17 Score per residue for model 17

• Molecule 1: Serine/threonine-protein phosphatase PGAM5, mitochondrial

Chain A: 57% 43%

A2 L114 A15 G16 G17 A27 V28 K30 K30 F31 R32 A33 G34 G35



### 4.2.18 Score per residue for model 18

• Molecule 1: Serine/threonine-protein phosphatase PGAM5, mitochondrial

Chain A: 57% 43%

A2 L114 A15 G16 G17 A27 V28 K30 K30 K30 A33 G34 G35 D36

### 4.2.19 Score per residue for model 19

• Molecule 1: Serine/threonine-protein phosphatase PGAM5, mitochondrial

Chain A: 57% 43%

A2 L114 A15 G16 G17 A27 V28 K30 K30 K30 R31 G34 G35

### 4.2.20 Score per residue for model 20

• Molecule 1: Serine/threonine-protein phosphatase PGAM5, mitochondrial

Chain A: 57% 43%

A2 A15 A15 A16 G16 G17 A27 V28 G29 K30 P31 R32 A33 G34 G35 D36



## 5 Refinement protocol and experimental data overview (i)

The models were refined using the following method: *simulated annealing*.

Of the 200 calculated structures, 20 were deposited, based on the following criterion: *structures* with the lowest energy.

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

Software name	Classification	Version
CNS	refinement	
ARIA	structure calculation	

The following table shows chemical shift validation statistics as aggregates over all chemical shift files. Detailed validation can be found in section 7 of this report.

Chemical shift file(s)	working_cs.cif
Number of chemical shift lists	1
Total number of shifts	305
Number of shifts mapped to atoms	305
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	71%



## 6 Model quality (i)

## 6.1 Standard geometry (i)

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 (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	141	146	146	0±0
All	All	2820	2920	2920	-

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 -.

There are no clashes.

## 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	Perce	ntiles
1	A	20/35~(57%)	20±0 (100±1%)	0±0 (0±1%)	0±0 (0±0%)	100	100
All	All	400/700 (57%)	399 (100%)	1 (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	Chain Analysed Rotameric Outliers		Outliers	Perce	ntiles
1	A	13/19 (68%)	13±0 (100±0%)	0±0 (0±0%)	100	100
All	All	260/380 (68%)	260 (100%)	0 (0%)	100	100

There are no protein residues with a non-rotameric sidechain to report.

### 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)

The completeness of assignment taking into account all chemical shift lists is 71% for the well-defined parts and 74% for the entire structure.

### 7.1 Chemical shift list 1

File name: working\_cs.cif

Chemical shift list name: starch\_output

### 7.1.1 Bookkeeping (i)

The following table shows the results of parsing the chemical shift list and reports the number of nuclei with statistically unusual chemical shifts.

Total number of shifts	305
Number of shifts mapped to atoms	305
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

## 7.1.2 Chemical shift referencing (i)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, $ppm$	Suggested action
$^{13}\mathrm{C}_{\alpha}$	35	$1.11 \pm 0.10$	Should be applied
$^{13}C_{\beta}$	29	$1.73 \pm 0.10$	Should be applied
<sup>13</sup> C′	0		None (insufficient data)
$^{15}N$	34	$0.77 \pm 0.24$	Should be applied

## 7.1.3 Completeness of resonance assignments (i)

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 71%, i.e. 158 atoms were assigned a chemical shift out of a possible 222. 2 out of 5 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^{1}\mathbf{H}$	$^{13}\mathbf{C}$	$^{15}{ m N}$
Backbone	80/100 (80%)	40/40 (100%)	20/40 (50%)	20/20 (100%)
Sidechain	70/104 (67%)	42/60 (70%)	28/39 (72%)	0/5 (0%)

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	Total	$^{1}\mathbf{H}$	$^{13}\mathbf{C}$	$^{15}\mathbf{N}$
Aromatic	8/18 (44%)	8/10 (80%)	0/8 (0%)	0/0 (%)
Overall	158/222 (71%)	90/110 (82%)	48/87 (55%)	20/25 (80%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 74%, i.e. 267 atoms were assigned a chemical shift out of a possible 362. 3 out of 7 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^{1}\mathrm{H}$	$^{13}\mathbf{C}$	$^{15}{ m N}$
Backbone	137/173 (79%)	68/69~(99%)	35/70~(50%)	34/34 (100%)
Sidechain	122/171 (71%)	74/99 (75%)	48/63 (76%)	0/9 (0%)
Aromatic	8/18 (44%)	8/10 (80%)	0/8 (0%)	0/0 (%)
Overall	267/362 (74%)	150/178 (84%)	83/141 (59%)	34/43 (79%)

### 7.1.4 Statistically unusual chemical shifts (i)

There are no statistically unusual chemical shifts.

### 7.1.5 Random Coil Index (RCI) plots (i)

The image below reports random coil index values for the protein chains in the structure. The height of each bar gives a probability of a given residue to be disordered, as predicted from the available chemical shifts and the amino acid sequence. A value above 0.2 is an indication of significant predicted disorder. The colour of the bar shows whether the residue is in the well-defined core (black) or in the ill-defined residue ranges (cyan), as described in section 2 on ensemble composition.

Random coil index (RCI) for chain A:

