



# wwPDB NMR Structure Validation Summary Report ⓘ

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PDB ID : 1Q5L  
Title : NMR structure of the substrate binding domain of DnaK bound to the peptide  
NRLLLTG  
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Deposited on : 2003-08-08

This is a wwPDB NMR Structure Validation Summary 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

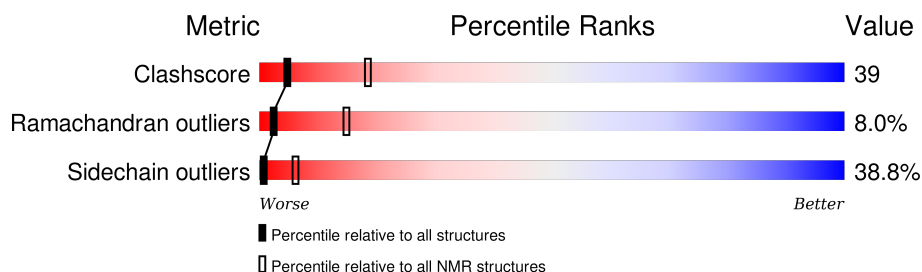
# 1 Overall quality at a glance

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	135	
2	B	7	

## 2 Ensemble composition and analysis

This entry contains 15 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: *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:394-A:503, B:902-B:907 (116)	0.72	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 3 clusters and 1 single-model cluster was found.

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

### 3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 1707 atoms, of which 795 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Chaperone protein dnaK.

Mol	Chain	Residues	Atoms						Trace
1	A	115	Total	C	H	N	O	S	0
			1595	529	738	151	174	3	

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	373	MET	-	CLONING ARTIFACT	UNP P0A6Y8
A	374	GLY	-	CLONING ARTIFACT	UNP P0A6Y8
A	375	SER	-	CLONING ARTIFACT	UNP P0A6Y8
A	376	SER	-	CLONING ARTIFACT	UNP P0A6Y8
A	377	HIS	-	CLONING ARTIFACT	UNP P0A6Y8
A	378	HIS	-	CLONING ARTIFACT	UNP P0A6Y8
A	379	HIS	-	CLONING ARTIFACT	UNP P0A6Y8
A	380	HIS	-	CLONING ARTIFACT	UNP P0A6Y8
A	381	HIS	-	CLONING ARTIFACT	UNP P0A6Y8
A	382	HIS	-	CLONING ARTIFACT	UNP P0A6Y8
A	383	GLY	-	CLONING ARTIFACT	UNP P0A6Y8
A	384	LEU	-	CLONING ARTIFACT	UNP P0A6Y8
A	385	VAL	-	CLONING ARTIFACT	UNP P0A6Y8
A	386	PRO	-	CLONING ARTIFACT	UNP P0A6Y8
A	387	ARG	-	CLONING ARTIFACT	UNP P0A6Y8
A	388	GLY	-	CLONING ARTIFACT	UNP P0A6Y8
A	389	SER	-	CLONING ARTIFACT	UNP P0A6Y8
A	390	HIS	-	CLONING ARTIFACT	UNP P0A6Y8
A	391	MET	-	CLONING ARTIFACT	UNP P0A6Y8
A	392	VAL	-	CLONING ARTIFACT	UNP P0A6Y8

- Molecule 2 is a protein called peptide NRLLLTG.

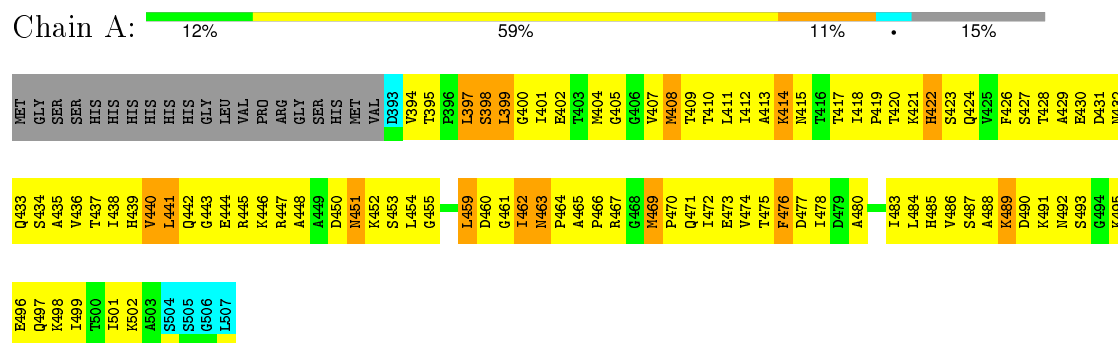
Mol	Chain	Residues	Atoms						Trace
2	B	7	Total	C	H	N	O		0
			112	34	57	11	10		

## 4 Residue-property plots

### 4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA and DNA 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: Chaperone protein dnaK



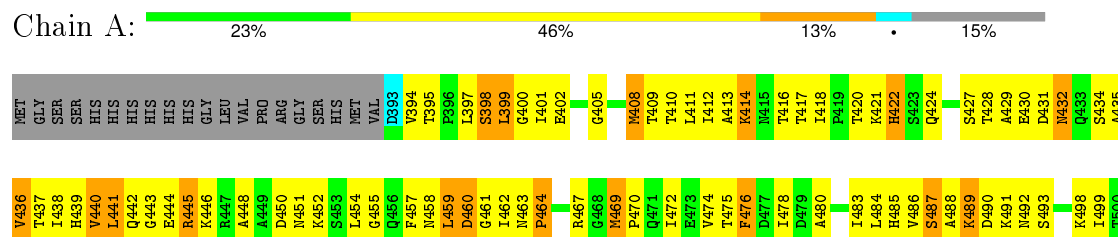
- Molecule 2: peptide NRRLLTG



### 4.2 Residue scores for the representative (medoid) model from the NMR ensemble

The representative model is number 2. Colouring as in section 4.1 above.

- Molecule 1: Chaperone protein dnaK





- Molecule 2: peptide NRLLLTG

Chain B:   
29% 43% 14% 14%

A horizontal color scale bar for Chain B. The bar is divided into four segments with the following percentages: 29% (green), 43% (yellow), 14% (orange), and 14% (cyan).



## 5 Refinement protocol and experimental data overview ⓘ

The models were refined using the following method: *torsion angle dynamics*.

Of the 60 calculated structures, 15 were deposited, based on the following criterion: *structures with acceptable covalent geometry, 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
ARIA/(CNS)	structure solution	1.0
ARIA/(CNS)	refinement	1.0

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](#)

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	824	714	842	68±16
2	B	47	50	56	6±3
All	All	13065	11460	13470	1026

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 39.

5 of 580 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:489:LYS:HB3	1:A:496:GLU:HA	0.93	1.40	12	1
1:A:416:THR:HG21	1:A:478:ILE:HD12	0.83	1.50	15	1
1:A:440:VAL:HB	1:A:454:LEU:HB2	0.82	1.48	10	4
1:A:440:VAL:HG11	1:A:486:VAL:HG21	0.81	1.52	15	7
1:A:463:ASN:HB3	1:A:464:PRO:HD3	0.81	1.51	14	2

### 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	110/135 (81%)	81±4 (74±4%)	20±4 (18±3%)	9±2 (8±2%)	2	14
2	B	5/7 (71%)	3±1 (67±21%)	1±1 (28±18%)	0±1 (5±11%)	4	25
All	All	1725/2130 (81%)	1272 (74%)	315 (18%)	138 (8%)	2	15

5 of 47 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	405	GLY	11
1	A	492	ASN	10
1	A	461	GLY	9
1	A	467	ARG	8
1	A	450	ASP	7

### 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	92/113 (81%)	56±3 (61±4%)	36±3 (39±4%)	1	6
2	B	5/6 (83%)	3±1 (59±26%)	2±1 (41±26%)	0	4
All	All	1455/1785 (82%)	891 (61%)	564 (39%)	1	6

5 of 86 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	395	THR	15
1	A	440	VAL	15
1	A	491	LYS	14
1	A	498	LYS	14
1	A	410	THR	13

### 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](#)

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

No chemical shift data were provided