

# Full wwPDB NMR Structure Validation Report (i)

#### Nov 21, 2022 – 03:29 PM EST

PDB ID	:	7LSP
BMRB ID	:	30864
Title	:	D-Phenylseptin - The second residue of PHE of the peptide is a D-amino acid
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Deposited on	:	2021-02-18

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 (1)) were used in the production of this report:

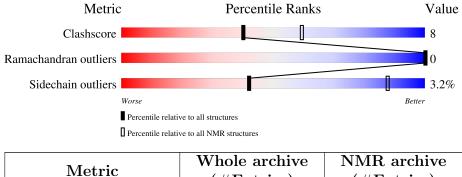
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. $(2010)$
ShiftChecker	:	2.31.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

# 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 is 48%.

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	(# Entries)	(#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	А	18	83%	17%



# 2 Ensemble composition and analysis (i)

This entry contains 20 models. Model 12 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 Residue range (total) Backbone RMSD (Å) Medoid model				
1	A:4-A:18 (15)	0.20	12	

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 4 clusters and 1 single-model cluster was found.

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



# 3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 286 atoms, of which 148 are hydrogens and 0 are deuteriums.

• Molecule 1 is a protein called D-Phenylseptin.

Mol	Chain	Residues		At	toms			Trace
1	٨	19	Total	С	Η	Ν	0	0
	1 A	10	286	94	148	21	23	0

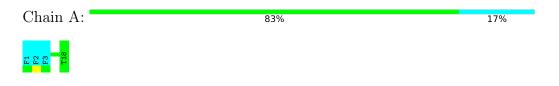


# 4 Residue-property plots (i)

# 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: D-Phenylseptin

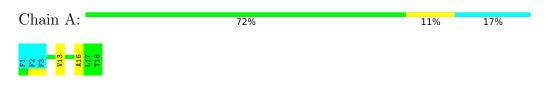


### 4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

#### 4.2.1 Score per residue for model 1

• Molecule 1: D-Phenylseptin



#### 4.2.2 Score per residue for model 2

• Molecule 1: D-Phenylseptin

Chain A: 56% 28% 17%



#### 4.2.3 Score per residue for model 3

• Molecule 1: D-Phenylseptin

Chain A:	61%	22%	17%
F1 F2 F3 F15 F16 F117 F118			

#### 4.2.4 Score per residue for model 4

• Molecule 1: D-Phenylseptin

Chain A:	72%	11%	17%
12 22 23 23 2 18 18			

#### 4.2.5 Score per residue for model 5

• Molecule 1: D-Phenylseptin

Chain A:	67%	17%	17%

#### F1 F3 V13 A16 E17 T18

#### 4.2.6 Score per residue for model 6

Molecule 1: D-Phenylseptin
Chain A: 72% 11% 17%

### 4.2.7 Score per residue for model 7

• Molecule 1: D-Phenylseptin Chain A:





17%

#### 4.2.8 Score per residue for model 8

• Molecule 1: D-Phenylseptin

Chain A:	61%	17%	6%	17%
F1 F2 F3 F3 F3 F3 F3 F3 F1 F1 F1 F1 F1 F1 F1 F1 F1 F1 F1 F1 F1				

#### 4.2.9 Score per residue for model 9

• Molecule 1: D-Phenylseptin

Chain A: 83% 17%

#### 4.2.10 Score per residue for model 10

• Molecule 1: D-Phenylseptin

Chain A: 67% 11% 6% 17%

- 4.2.11 Score per residue for model 11
- Molecule 1: D-Phenylseptin

Chain A: 67% 6% 11% 17%

- 4.2.12 Score per residue for model 12 (medoid)
- Molecule 1: D-Phenylseptin

Chain A:	83%	17%



#### 4.2.13 Score per residue for model 13

• Molecule 1: D-Phenylseptin



#### 4.2.14 Score per residue for model 14

• Molecule 1: D-Phenylseptin

Chain A:	61%	22%	17%
F1 52 75 15 11 11 11 11 11 11 11 11 11 11 11 11			

#### 4.2.15 Score per residue for model 15

• Molecule 1: D-Phenylseptin

Chain A:	50%	33%	17%

#### 

#### 4.2.16 Score per residue for model 16

Molecule 1: D-Phenylseptin
Chain A: 72% 11% 17%

#### 4.2.17 Score per residue for model 17

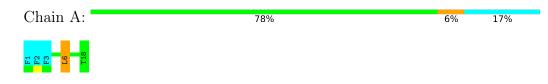
• Molecule 1: D-Phenylseptin

Chain A:	83%	17%
F1 F2 T18 T18		



#### 4.2.18 Score per residue for model 18

• Molecule 1: D-Phenylseptin



#### 4.2.19 Score per residue for model 19

• Molecule 1: D-Phenylseptin

Chain A:	56%	28%	17%
F1 F2 F3 F14 F14 F14 F15 F15 F15 T18 T18			

#### 4.2.20 Score per residue for model 20

• Molecule 1: D-Phenylseptin

Chain A:	72%	11%	17%
118 118 118			



# 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
X-PLOR NIH	refinement	
X-PLOR NIH	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	124
Number of shifts mapped to atoms	124
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	48%



# 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: DPN

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	А	105	119	119	$2{\pm}1$
All	All	2100	2380	2380	34

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 8.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Mod	dels
Atom-1	Atom-2	Clash(A)	Distance(A)	Worst	Total
1:A:9:LEU:O	1:A:9:LEU:HD23	0.56	2.00	2	1
1:A:4:ASP:OD1	1:A:5:THR:N	0.55	2.40	2	5
1:A:4:ASP:OD2	1:A:5:THR:N	0.53	2.42	16	1
1:A:13:VAL:O	1:A:16:ALA:HB3	0.53	2.04	5	9
1:A:8:ASN:C	1:A:8:ASN:ND2	0.51	2.63	13	2
1:A:9:LEU:HD13	1:A:9:LEU:O	0.51	2.05	10	1
1:A:5:THR:O	1:A:8:ASN:OD1	0.49	2.30	13	2
1:A:6:LEU:O	1:A:6:LEU:HD13	0.49	2.08	18	2
1:A:17:LEU:O	1:A:17:LEU:HD13	0.47	2.10	11	1
1:A:14:ILE:N	1:A:14:ILE:CD1	0.44	2.79	19	1
1:A:4:ASP:OD2	1:A:4:ASP:O	0.44	2.36	11	1
1:A:17:LEU:CD2	1:A:17:LEU:N	0.43	2.81	20	1

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

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
Atom-1	Atom-2	Clash(A)	Distance(A)	Worst	Total
1:A:17:LEU:O	1:A:18:THR:O	0.43	2.36	6	2
1:A:9:LEU:HD23	1:A:9:LEU:C	0.43	2.34	2	1
1:A:14:ILE:N	1:A:14:ILE:HD12	0.42	2.29	19	1
1:A:17:LEU:O	1:A:18:THR:C	0.42	2.57	3	2
1:A:17:LEU:O	1:A:18:THR:OG1	0.42	2.37	15	1

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# 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	А	14/18~(78%)	$14\pm0~(100\pm0\%)$	0±0 (0±0%)	0±0 (0±0%)	100	100
All	All	280/360~(78%)	280 (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 side chain 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 side chain conformation was analysed and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	А	11/13~(85%)	$11 \pm 1 (97 \pm 5\%)$	$0\pm1~(3\pm5\%)$	42 88
All	All	220/260~(85%)	213 (97%)	7 (3%)	42 88

All 5 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	А	8	ASN	2
1	А	6	LEU	2
1	А	18	THR	1

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Mol	Chain	Res	Type	Models (Total)
1	А	9	LEU	1
1	А	17	LEU	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)

1 non-standard protein/DNA/RNA residue is modelled in this entry.

In the following table, the Counts columns list the number of bonds for which Mogul statistics could be retrieved, the number of bonds that are observed in the model and the number of bonds that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length is the number of standard deviations the observed value is removed from the expected value. A bond length with |Z| > 2 is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond lengths.

Mal	Tuno	Chain	Dog	Link		Bond leng	ths
	туре	Ullain	nes		Counts	RMSZ	#Z>2
1	DPN	А	2	1	10,11,12	$0.70{\pm}0.03$	0±0 (0±0%)

In the following table, the Counts columns list the number of angles for which Mogul statistics could be retrieved, the number of angles that are observed in the model and the number of angles that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond angle is the number of standard deviations the observed value is removed from the expected value. A bond angle with |Z| > 2 is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond angles.

Mal	Turne	Chain	Dec	Tink		Bond ang	gles
	туре	Chain	nes	LINK	Counts	RMSZ	#Z>2
1	DPN	А	2	1	10,13,15	$0.74{\pm}0.04$	0±0 (0±2%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	DPN	А	2	1	-	$0\pm 0,5,6,8$	$0\pm 0,1,1,1$



There are no bond-length outliers.

All unique angle outliers are listed below.

Mol	Chain	Res	Type	Atoms	Ζ	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$	Moo Worst	<b>iels</b> Total
1	А	2	DPN	CG-CB-CA	2.01	110.02	114.10	13	1

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

### 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 48% for the well-defined parts and 48% 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	124
Number of shifts mapped to atoms	124
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)

No chemical shift referencing corrections were calculated (not enough data).

#### 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 48%, i.e. 80 atoms were assigned a chemical shift out of a possible 166. 0 out of 4 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^{1}\mathbf{H}$	$^{13}\mathbf{C}$	$^{15}\mathbf{N}$
Backbone	42/75~(56%)	28/30~(93%)	14/30~(47%)	0/15~(0%)
Sidechain	38/91~(42%)	28/51~(55%)	10/37~(27%)	0/3~(0%)
Aromatic	0/0 (%)	0/0 (%)	0/0 (%)	0/0 (%)
Overall	80/166~(48%)	56/81~(69%)	24/67~(36%)	0/18~(0%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 48%, i.e. 95 atoms were assigned a chemical shift out of a possible 200. 0 out of 4 assigned methyl groups (LEU and VAL) were assigned stereospecifically.



	Total	$^{1}\mathbf{H}$	$^{13}\mathrm{C}$	$^{15}\mathbf{N}$
Backbone	47/85~(55%)	31/34~(91%)	16/34~(47%)	0/17~(0%)
Sidechain	44/97~(45%)	32/55~(58%)	12/39~(31%)	0/3~(0%)
Aromatic	4/18 (22%)	4/10~(40%)	0/8~(0%)	$0/0 \ (\%)$
Overall	95/200~(48%)	67/99~(68%)	28/81~(35%)	0/20~(0%)

#### 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:



