

Full wwPDB NMR Structure Validation Report (i)

Jun 14, 2020 – 06:03 pm BST

PDB ID : 2RQF

Title : Solution structure of juvenile hormone binding protein from silkworm in com-

plex with JH III

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Deposited on : 2009-04-27

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

Cyrange: Kirchner and Güntert (2011)

NmrClust : Kelley et al. (1996)

MolProbity: 4.02b-467

Mogul : 1.8.5 (274361), CSD as541be (2020)

buster-report : 1.1.7 (2018)

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 : 2.11

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

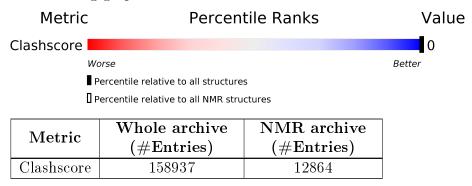
Validation Pipeline (wwPDB-VP) : 2.11

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.



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	A	227	97%	•



2 Ensemble composition and analysis (i)

This entry contains 20 models. Model 1 is the overall representative, medoid model (most similar to other models).

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:5-A:225 (221)	0.22	1					

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 3 single-model clusters were found.

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



3 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 3521 atoms, of which 1766 are hydrogens and 0 are deuteriums.

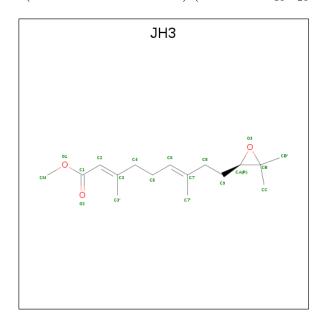
• Molecule 1 is a protein called Hemolymph juvenile hormone binding protein.

Mol	Chain	Residues		${f Atoms}$					Trace
1	Λ	227	Total	С	Н	N	О	S	0
	A	221	3476	1094	1740	285	349	8	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Α	-2	GLY	-	EXPRESSION TAG	UNP Q9U556
Α	-1	SER	-	EXPRESSION TAG	UNP Q9U556

• Molecule 2 is methyl (2E,6E)-9-[(2R)-3,3-dimethyloxiran-2-yl]-3,7-dimethylnona-2,6-dienoat e (three-letter code: JH3) (formula: $C_{16}H_{26}O_3$).



Mol	Chain	Residues	A	A ton	ns	
9	Λ	1	Total	С	Н	О
	A	1	45	16	26	3

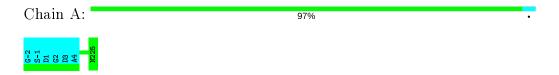


4 Residue-property plots (i)

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: Hemolymph juvenile hormone binding protein

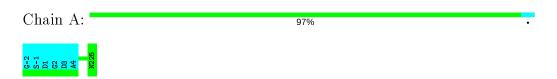


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

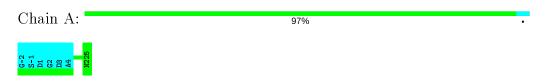
4.2.1 Score per residue for model 1 (medoid)

• Molecule 1: Hemolymph juvenile hormone binding protein



4.2.2 Score per residue for model 2

• Molecule 1: Hemolymph juvenile hormone binding protein





4.2.3 Score per residue for model 3

• Molecule 1: Hemolymph juvenile hormone binding protein

Chain A: 97%



4.2.4 Score per residue for model 4

• Molecule 1: Hemolymph juvenile hormone binding protein

Chain A: 97%



4.2.5 Score per residue for model 5

• Molecule 1: Hemolymph juvenile hormone binding protein

Chain A: 97%



4.2.6 Score per residue for model 6

• Molecule 1: Hemolymph juvenile hormone binding protein

Chain A: 97%



4.2.7 Score per residue for model 7

• Molecule 1: Hemolymph juvenile hormone binding protein

Chain A: 97%





4.2.8 Score per residue for model 8

• Molecule 1: Hemolymph juvenile hormone binding protein

Chain A: 97%



4.2.9 Score per residue for model 9

• Molecule 1: Hemolymph juvenile hormone binding protein

Chain A: 97% .



4.2.10 Score per residue for model 10

• Molecule 1: Hemolymph juvenile hormone binding protein

Chain A: 97%



4.2.11 Score per residue for model 11

• Molecule 1: Hemolymph juvenile hormone binding protein

Chain A: 97%



4.2.12 Score per residue for model 12

• Molecule 1: Hemolymph juvenile hormone binding protein

Chain A: 97%





4.2.13 Score per residue for model 13

• Molecule 1: Hemolymph juvenile hormone binding protein

Chain A: 97%



4.2.14 Score per residue for model 14

• Molecule 1: Hemolymph juvenile hormone binding protein

Chain A: 97% .



4.2.15 Score per residue for model 15

• Molecule 1: Hemolymph juvenile hormone binding protein

Chain A: 97%



4.2.16 Score per residue for model 16

• Molecule 1: Hemolymph juvenile hormone binding protein

Chain A:



4.2.17 Score per residue for model 17

• Molecule 1: Hemolymph juvenile hormone binding protein

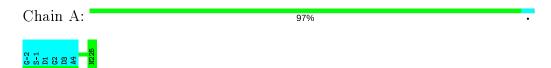
Chain A: 97%





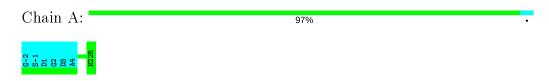
4.2.18 Score per residue for model 18

• Molecule 1: Hemolymph juvenile hormone binding protein



4.2.19 Score per residue for model 19

• Molecule 1: Hemolymph juvenile hormone binding protein



4.2.20 Score per residue for model 20

• Molecule 1: Hemolymph juvenile hormone binding protein





5 Refinement protocol and experimental data overview (i)



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

Of the 100 calculated structures, 20 were deposited, based on the following criterion: structures with the least restraint violations.

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

Software name	Classification	Version
CYANA	structure solution	2.1
CYANA	refinement	2.1

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: JH3

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	$\mathbf{H}(\mathbf{model})$	$\mathbf{H}(\mathbf{added})$	Clashes
All	All	34400	34840	0	-

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.

\mathbf{Mol}	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	0	-	-	-	-
All	All	0	-	-	-	-

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.

\mathbf{Mol}	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	0	-	-	-
All	All	0	-	-	-

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 carbohydrates in this entry.

6.6 Ligand geometry (i)

1 ligand 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	Типо	Chain	Pos	Link	Bond leng		ths
MIOI	туре	Chain	nes	Link	Counts	RMSZ	#Z>2
2	JH3	A	300	-	19,19,19	1.07 ± 0.00	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	Type	Chain	Dog	Tinle		Bond ang	les
MIOI	туре	Chain	nes	LIIIK	Counts	RMSZ	#Z>2
2	JH3	A	300	-	26,26,26	1.06 ± 0.00	0±0 (0±0%)

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
2	JH3	A	300	-	_	$0\pm0,17,25,25$	$0\pm0,1,1,1$

There are no bond-length outliers.

There are no bond-angle outliers.

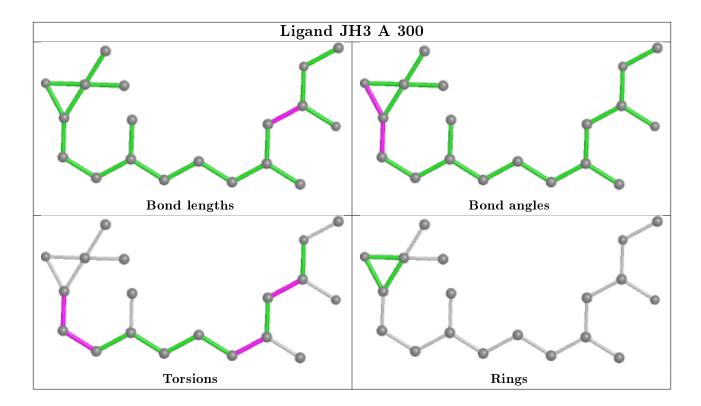
There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





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

