

Full wwPDB NMR Structure Validation Report (i)

Mar 1, 2022 – 12:36 PM EST

PDB ID	:	2H3S
Title	:	cis-Azobenzene-avian pancreatic polypeptide bound to DPC micelles
Authors	:	Jurt, S.; Aemissegger, A.; Guentert, P.; Zerbe, O.; Hilvert, D.
Deposited on	:	2006-05-23

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:

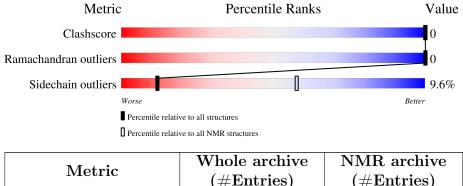
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	2.27
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.27

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	(# 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	9	100%	
2	В	25	88%	8%



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 Residue range (total) Backbone RMSD (Å) Medoid mode				
1	B:12-B:34 (23)	0.45	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 3 clusters. No single-model clusters were found.

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



3 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 579 atoms, of which 280 are hydrogens and 0 are deuteriums.

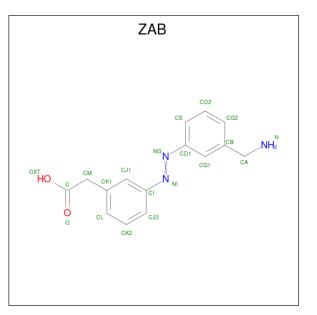
• Molecule 1 is a protein called Pancreatic hormone.

Mol	Chain	Residues	Atoms			Trace		
1	٨	0	Total	С	Η	Ν	0	0
	A	9	119	40	56	10	13	0

• Molecule 2 is a protein called Pancreatic hormone.

Mol	Chain	Residues	Atoms				Trace	
0	р	25	Total	С	Н	Ν	0	1
	D	23	428	139	211	40	38	1

• Molecule 3 is (3-{(Z)-[3-(AMINOMETHYL)PHENYL]DIAZENYL}PHENYL)ACETIC ACID (three-letter code: ZAB) (formula: C₁₅H₁₅N₃O₂).



Mol	Chain	Residues		Ate	oms		
9	٨	1	Total	С	Η	Ν	0
0	A	1	32	15	13	3	1



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: Pancreatic hormone

Chain A:	100%		
8 2 2 3 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5			
• Molecule 2: Pancreatic hormone			
Chain B:	88%	·	8%

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: Pancreatic hormone

Chain A: 100%



4.2.2 Score per residue for model 2

Chain A:	100%		
61 72 74 73 74 75 75 75 69 69			
• Molecule 2	: Pancreatic hormone		
Chain B:	84%	8%	8%
P11 N27 130 NH235			
4.2.3 Scor	e per residue for model 3		
• Molecule 1	: Pancreatic hormone		
Chain A:	100%		
60 7 4 7 6 7 8 2 7 4 7 6 9 7 4 6 9 7 4 7 4 6 9 8 7 4 7 4 7 4 7 6 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8			
• Molecule 2	: Pancreatic hormone		
Chain B:	80%	12%	8%
P11 D21 T30 R33 R33 V34 NH235			
4.2.4 Scor	e per residue for model 4		
• Molecule 1	: Pancreatic hormone		
Chain A:	100%		
G1 P2 P2 P5 P5 P8 P8 P8 C9			
• Molecule 2	: Pancreatic hormone		
Chain B:	84%	8%	8%
P11 Y19 T30 NH235			



4.2.5 Score per residue for model 5

• Molecule 1: Pancreatic hormone

Chain A:	100%	
G1 23 76 75 77 77 88 69		
• Molecule 2: Pancr	eatic hormone	
Chain B:	80%	12% 8%
P11 L15 T30 M1235 M1235		
4.2.6 Score per	residue for model 6	
• Molecule 1: Pancr	eatic hormone	
Chain A:	100%	
G 7 4 4 9 7 7 6 7 7 7 6 7 7 7 6 7 7 7 7 8 7 7 7 7		
• Molecule 2: Pancr	eatic hormone	
Chain B:	76%	12% • 8%
P111 M27 M27 M21 M22 M33 M34 M1235		
4.2.7 Score per	residue for model 7	
• Molecule 1: Pancr	eatic hormone	
Chain A:	100%	
С 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		
• Molecule 2: Pancr	eatic hormone	
Chain B:	80%	8% • 8%



P11

Chain B:

P11

4.2.8 Score per residue for model 8

• Molecule 1: Pancreatic hormone

Chain A:	100%	
8 2 2 8 2 2 5 6 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5		
• Molecule 2: Pancreatic hormone		
Chain B:	8%	• 8%
P11 D21 MH235		
4.2.9 Score per residue for mod	el 9	
• Molecule 1: Pancreatic hormone		
Chain A:	100%	
0 2 2 2 3 2 7 1 1 2 4 2 3 2 7 1 1 2 4 2 4 2 1 1 2 4 2 1 2 1 2 1 2 1 2		
• Molecule 2: Pancreatic hormone		
Chain B: 72%		20% 8%
P11 17 17 126 126 130 133 144 1833 1444 1833		
4.2.10 Score per residue for mo	del 10	
• Molecule 1: Pancreatic hormone		
Chain A:	100%	
9 8 4 4 4 4 5 8 7 7 8 9 8 4 4 9 8 4 7 8 9 8 4 4 8 9 7 8 6		
• Molecule 2: Pancreatic hormone		

88%

DB ATA BANK • 8%

P11 L15 Y19 NH23

4.2.11 Score per residue for model 11

Chain A:	100%		
61 P2 75 77 98 98 98			
• Molecule 2: Pancreatic	hormone		
Chain B:	80%	12%	8%
P11 R17 T30 Y34 MH235			
4.2.12 Score per resi	due for model 12		
• Molecule 1: Pancreatic	hormone		
Chain A:	100%		
0 11 0 2 2 0 4 4 0 9 8 0 9 8 0 9 8 0 9 8			
• Molecule 2: Pancreatic	hormone		
Chain B:	84%	8%	8%
P11 130 1130			
4.2.13 Score per resi	due for model 13		
• Molecule 1: Pancreatic	hormone		
Chain A:	100%		
01 73 75 75 77 78 78 78 78			
• Molecule 2: Pancreatic	hormone		
Chain B:	84%	8%	8%



P11

4.2.14 Score per residue for model 14

Chain A:	100%		
61 833 94 74 74 79 89 89 89 89			
• Molecule 2: Pancrea	atic hormone		
Chain B:	72%	16% ·	8%
P11 V12 E13 E14 D14 D14 D14 D21 D21 D21 D21 D21 D21 D21 D21 D21 D21			
4.2.15 Score per 1	residue for model 15		
• Molecule 1: Pancrea	atic hormone		
Chain A:	100%		
G1 23 75 75 75 75 75 75 76 76 76 76 76 76 76 76 76 76 76 76 76			
• Molecule 2: Pancrea	atic hormone		
Chain B:	80%	12%	8%
P11 V12 E13 E13 H32 H32 Y34 NH235			
4.2.16 Score per u	residue for model 16		
• Molecule 1: Pancrea	atic hormone		
Chain A:	100%		
0 7 2 7 4 7 5 7 4 7 7 6 9 8 7 4 7 6 9 8 7 4 7 6 9 8 7 4 7 6 7 7 7 6 7 7 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8			
• Molecule 2: Pancrea	atic hormone		
Chain B:	84%	8%	8%



4.2.17 Score per residue for model 17

Chain A:	100%		
61 P2 P5 P5 P5 P8 P8 P8 P8			
• Molecule 2: Pan	acreatic hormone		
Chain B:	80%	8% •	8%
P11 D14 P17 F18 V19 MH235			
4.2.18 Score p	er residue for model 18		
• Molecule 1: Pan	creatic hormone		
Chain A:	100%		
61 72 76 76 77 77 798 698 698			
• Molecule 2: Pan	acreatic hormone		
Chain B:	88%	•	8%
P11 T30 MH235			
4.2.19 Score p	er residue for model 19		
• Molecule 1: Pan	acreatic hormone		
Chain A:	100%		
С С С С С С С С С С С С С С С С С С С			
• Molecule 2: Pan	acreatic hormone		
Chain B:	72%	20%	8%
P11 D14 L15 D21 D21 T30 T30			



4.2.20 Score per residue for model 20

Chain A:	100%		
13 23 23 24 24 24 24 24 24 24 24 24 24 24 24 24			
• Molecule 2: Pancreatic hormone			
Chain B:	84%	8%	8%
P11 1094 11235			



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 acceptable covalent geometry, structures with favorable non-bond energy, 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
CYANA	refinement	2.2.2
CYANA	structure solution	2.2.2

No chemical shift data was provided.



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: ZAB, NH2

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		E	Sond lengths	Bond angles		
	Chain	RMSZ	$\#Z{>}5$	RMSZ	$\#Z{>}5$	
2	В	$0.69 {\pm} 0.01$	$0{\pm}0/213~(~0.0{\pm}~0.0\%)$	$0.97 {\pm} 0.04$	$0{\pm}0/288~(~0.1{\pm}~0.1\%)$	
All	All	0.69	0/4260 ($0.0%$)	0.97	3/5760~(~0.1%)	

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	Chirality	Planarity
2	В	$0.0{\pm}0.0$	$0.8 {\pm} 0.9$
All	All	0	16

There are no bond-length outliers.

All unique angle outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Z Observed(°)		Moo	
IVIOI	Unam	Ites	турс	Atoms		Observed()	$Ideal(^{o})$	Worst	Total
2	В	17	ARG	NE-CZ-NH2	-5.50	117.55	120.30	12	2
2	В	33	ARG	NE-CZ-NH1	5.37	122.99	120.30	6	1

There are no chirality outliers.

All unique planar outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Group	Models (Total)
2	В	21	ASP	Sidechain	4
2	В	19	TYR	Sidechain	2
2	В	33	ARG	Sidechain	2
2	В	14	ASP	Sidechain	2

Continued on next page...



Contre	Continued from previous page								
Mol	Chain	\mathbf{Res}	Type	Group	Models (Total)				
2	В	34	TYR	Sidechain	2				
2	В	13	GLU	Sidechain	2				
2	В	25	TYR	Sidechain	1				
2	В	26	LEU	Mainchain	1				

Continued from previous page...

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.

Ι	Mol	Chain	Non-H	H(model)	H(added)	Clashes
	All	All	4560	4300	4286	-

The all-atom clash score is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clash score 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	Percentiles
1	А	0	-	-	-	-
2	В	23/25~(92%)	$22 \pm 1 (94 \pm 4\%)$	$1\pm1~(6\pm4\%)$	0±0 (0±0%)	100 100
All	All	460/680~(68%)	433 (94%)	27~(6%)	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



Mol	Chain	Analysed Rotameric Outliers		Percentiles		
1	А	0	-	-	-	
2	В	23/24~(96%)	$21 \pm 1 (90 \pm 5\%)$	$2\pm1 (10\pm5\%)$	12 58	
All	All	460/620~(74%)	416 (90%)	44 (10%)	12 58	

entries. The Analysed column shows the number of residues for which the sidechain conformation was analysed and the total number of residues.

All 11 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)
2	В	30	THR	14
2	В	15	LEU	6
2	В	19	TYR	5
2	В	32	HIS	3
2	В	27	ASN	3
2	В	21	ASP	3
2	В	33	ARG	3
2	В	25	TYR	2
2	В	14	ASP	2
2	В	17	ARG	2
2	В	24	GLN	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)

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	Turne	Chain Res Link		Bond leng	gths		
NIOI	туре		nes		Counts	RMSZ	#Z>2
3	ZAB	А	10	2,1	20,20,21	$1.17 {\pm} 0.01$	$1\pm0~(5\pm0\%)$

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.

Mol	Turne	Chain	Dec	Tink		Bond an	gles
	туре	Unam	nes		Counts	RMSZ	#Z>2
3	ZAB	А	10	2,1	$25,\!25,\!27$	$1.31 {\pm} 0.06$	3 ± 0 (12±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
3	ZAB	А	10	2,1	-	$0\pm0,10,10,11$	$0\pm 0,2,2,2$

All unique bond outliers are listed below.

Mol	Chain	Ros	Type	Atoms	Z Observed(Å)		Ideal(Å)	Moo	
	Ullalli	nes	s Type	Atoms	2	Observed(A)	Iueai(A)	Worst	Total
3	А	10	ZAB	NI-NG	3.16	1.10	1.24	17	20

All unique angle outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$	Models	
	Unain	nes	туре	Atoms				Worst	Total
3	А	10	ZAB	CD1-NG-NI	4.60	135.81	112.99	19	20
3	А	10	ZAB	CI-NI-NG	4.24	134.03	112.99	12	20
3	А	10	ZAB	O-C-CM	3.07	118.06	126.64	14	19

Continued on next page...



Continued from previous page...

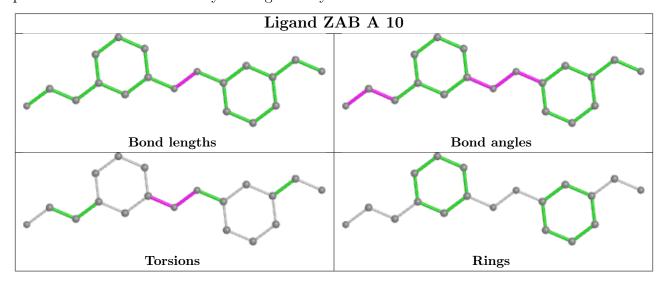
Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$\operatorname{Ideal}(^{o})$	Moo Worst	dels Total
3	А	10	ZAB	CK1-CM-C	2.09	118.93	114.17	18	1

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

