

Full wwPDB NMR Structure Validation Report (i)

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PDB ID	:	1BYV
Title	:	GLYCOSYLATED EEL CALCITONIN
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Deposited on	:	1998-10-16

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)
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)
${ m ShiftChecker}$:	2.13.1
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.13.1

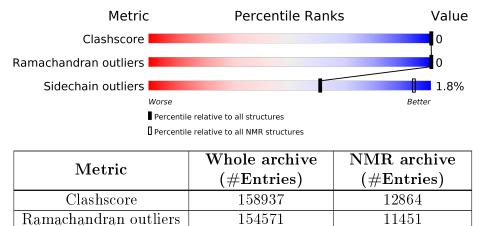
Sidechain outliers

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.



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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%

11428

Mol	Chain	Length	Quality of chain		
1	Δ	33	2606	6404	
1	A	33	36%	64%	



2 Ensemble composition and analysis (i)

This entry contains 10 models. Model 5 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 me					
1	A:7-A:18 (12)	0.07	5		

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 2 single-model clusters were found.

Cluster number	Models
1	2, 4, 5, 7
2	3, 9
3	1, 10
Single-model clusters	6; 8



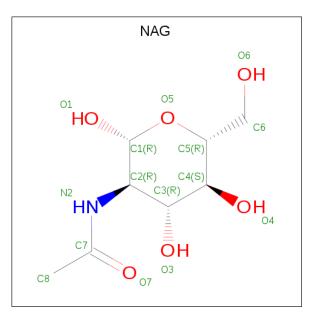
3 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 508 atoms, of which 256 are hydrogens and 0 are deuteriums.

• Molecule 1 is a protein called PROTEIN (CALCITONIN).

Mol	Chain	Residues		ŀ	Atoms	5			Trace
1	Λ	22	Total	С	Η	Ν	Ο	S	1
	A		480	146	242	43	47	2	

• Molecule 2 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues		At	\mathbf{oms}		
0	Λ	1	Total	С	Η	Ν	0
	A	1	28	8	14	1	5



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: PROTEIN (CALCITONIN)

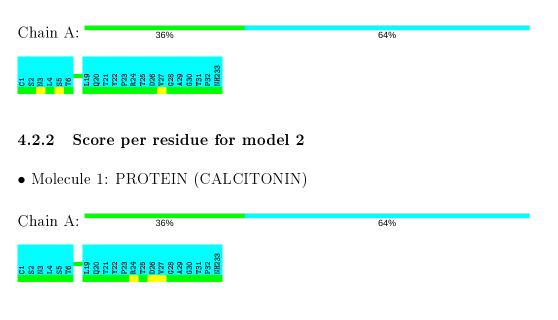
Chain A:	36%	64%
C1 N3 N3 N3 N3 N3 N3 N3 N3 N3 N3 N3 N3 N3	L19 L19 Q20 Y22 Y22 R24 R24 C23 Q26 C30 C30 C30 C30 C30 C30 C30 C30 C30 C30	

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: PROTEIN (CALCITONIN)





4.2.3 Score per residue for model 3

• Molecule 1: PROTEIN (CALCITONIN)

Chain A:	36%	64%
C1 S2 S5 S5 S5	119 120 121 121 125 125 125 125 125 125 125 125	

4.2.4 Score per residue for model 4

• Molecule 1: PROTEIN (CALCITONIN)

Chain A:		33%	•	64%
C 1 S 2 1 4 7 5 7 5 7 6 7 6 7 7 7 6 7 7 7 6 7 7 7 7 7 7 7 7	K11	L119 Q20 Y22 P23 P23 R24 T25 U26 Q28 G28 A29	G30 T31 P32 NH233	

- 4.2.5 Score per residue for model 5 (medoid)
- Molecule 1: PROTEIN (CALCITONIN)

Chain A:	36%	64%
2 2 2 2 1 0 0 2 2 2 2 2 1 0 0 2 2 2 2 2 1 0 0 2 2 2 2 2 1 0 0 0 2 2 2 2 2 1 0 0 0 2 2 2 2 2 1 0 0 0 0 2 2 2 2 2 1 0 0 0 0 0 0 2 2 2 2 2 2 2 1 0 0 0 0 0 0 0 0 0 0 0 0	V27 028 134 133 133 133 133	
4.2.6 Score per	residue for model 6	
• Molecule 1: PRO	TEIN (CALCITONIN)	

Chain A:	36%	64%
C1 S2 S5 76 76	L19 121 121 125 125 125 125 125 125 125 125	

4.2.7 Score per residue for model 7

• Molecule 1: PROTEIN (CALCITONIN)

Chain A:	36%	64%
C 22 25 25 25 25 25 25 25 25 25 25 25 25	L19 T21 T21 T22 T25 T25 T25 T25 G30 G30 G30 G30 F33 F33 F33 F33	

4.2.8 Score per residue for model 8

• Molecule 1: PROTEIN (CALCITONIN)

Chain A:	33%	•	64%
5 8 7 8 8 8 8 8 9 8 9	H17 K18 L19 L19 L21 P22 P25 P25 C28 V27 V27 V27 V27 V27 V27 V27 V27 V27 V27	P32 NH233	

4.2.9 Score per residue for model 9

• Molecule 1: PROTEIN (CALCITONIN)

Chain A:	36%	64%
12 22 22 23 23 24 25 25 25 24 25 25 25	119 129 121 121 122 123 125 125 125 125 125 125 125 125 125 125	

- 4.2.10 Score per residue for model 10
- Molecule 1: PROTEIN (CALCITONIN)

Chain A:	36%	64%
CC 12 25 2 2 2 13 2 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	L19 120 121 122 123 125 125 125 125 125 125 125 125 125 125	



5 Refinement protocol and experimental data overview (i)

The models were refined using the following method: distance geometry.

Of the 20 calculated structures, 10 were deposited, based on the following criterion: VIOLA-TION.

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

Software name	Classification	Version
DGII	refinement	
Felix	structure solution	

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: NAG, NH2

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
All	All	1070	1150	1140	-

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	Percenti	les
1	А	12/33~(36%)	$12\pm0~(100\pm0\%)$	0±0 (0±0%)	0±0 (0±0%)	100 10)0
All	All	120/330~(36%)	120~(100%)	0 (0%)	0 (0%)	100 10)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.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	А	11/28~(39%)	11 ± 0 (98 $\pm4\%$)	0±0 (2±4%)	61	94
All	All	110/280~(39%)	108 (98%)	2 (2%)	61	94

All 2 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	17	HIS	1
1	А	11	LYS	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.



Mol	Tree	Chain	Dec	Tink	Bond lengths			
10101	Type	Chain	nes	LINK	Counts	RMSZ	#Z>2	
2	NAG	А	300	1	14,14,15	$0.49 {\pm} 0.00$	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	Tree	Chain	Dec	Tink	Bond angles			
IVIOI	Type	Unam	nes		Counts	RMSZ	#Z>2	
2	NAG	А	300	1	17,19,21	$0.94{\pm}0.00$	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	\mathbf{Res}	Link	Chirals	Torsions	Rings
2	NAG	А	300	1	-	$0\pm0,\!6,\!23,\!26$	$0{\pm}0{,}1{,}1{,}1$

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.

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

