Full wwPDB NMR Structure Validation Report (i)

Feb 12, 2022 – 05:40 PM EST

PDB ID	:	1FVL
Title	:	THE NUCLEAR MAGNETIC RESONANCE SOLUTION STRUCTURE OF FLAVORIDIN, AN ANTAGONIST OF THE PLATELET GP IIB-IIIA RECEPTOR
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Deposited on	:	1995-09-06

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

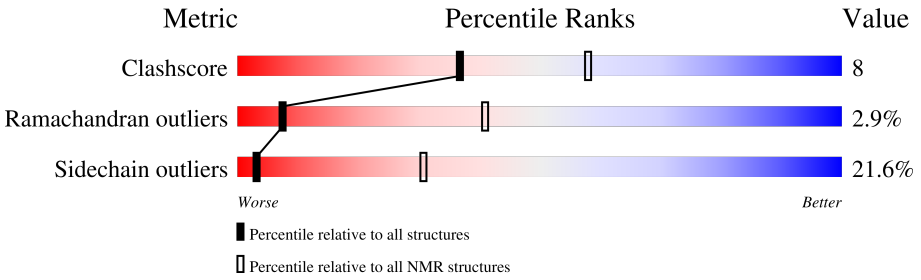
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	2.26
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.26

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	Whole archive (#Entries)	NMR archive (#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	A	70	60% 30% • 9%

2 Ensemble composition and analysis (i)

This entry contains 18 models. Model 9 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 model**
1	A:4-A:67 (64)	0.85	9

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, 3, 4, 6, 7, 8, 9, 10, 12, 14, 15, 16
2	5, 13, 17
3	11, 18

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 525 atoms, of which 0 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called FLAVORIDIN.

Mol	Chain	Residues	Atoms					Trace
			Total	C	N	O	S	
1	A	70	525	308	101	104	12	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: FLAVORIDIN

Chain A: 60% 30% • 9%

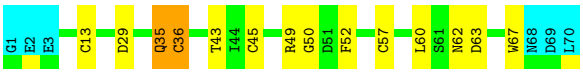
4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

• Molecule 1: FLAVORIDIN

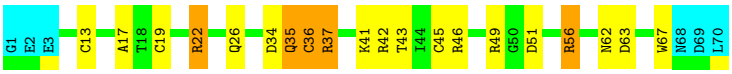
Chain A: 71% 17% • 9%



4.2.2 Score per residue for model 2

• Molecule 1: FLAVORIDIN

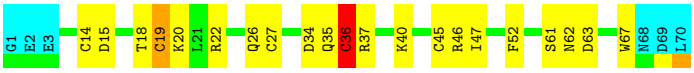
Chain A: 63% 21% 7% 9%



4.2.3 Score per residue for model 3

- Molecule 1: FLAVORIDIN

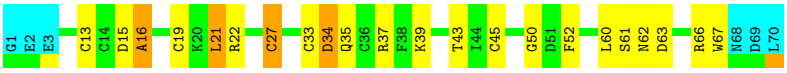
Chain A: 61% 27% •• 9%



4.2.4 Score per residue for model 4

- Molecule 1: FLAVORIDIN

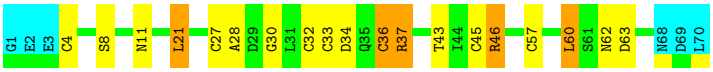
Chain A: 60% 26% 6% 9%



4.2.5 Score per residue for model 5

- Molecule 1: FLAVORIDIN

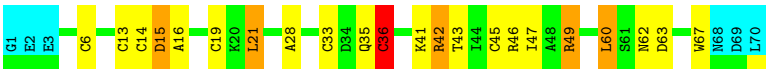
Chain A: 64% 20% 7% 9%



4.2.6 Score per residue for model 6

- Molecule 1: FLAVORIDIN

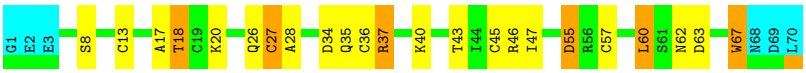
Chain A: 60% 23% 7% • 9%



4.2.7 Score per residue for model 7

- Molecule 1: FLAVORIDIN

Chain A: 59% 24% 9% 9%



4.2.8 Score per residue for model 8

- Molecule 1: FLAVORIDIN

Chain A: 61% 26% • 9%

G1 E2 E3 S8 D15 A16 A17 Q26 D29 D34 Q35 C36 R37 F38 K39 K40 K41 R42 T43 I44 C45 R56 C57 L60 S61 N62 D63 W67 N68 D69 L70

4.2.9 Score per residue for model 9 (medoid)

- Molecule 1: FLAVORIDIN

Chain A: 66% 21% • 9%

G1 E2 E3 C6 C13 L21 C27 D34 Q35 C36 R37 K41 R42 T43 R46 I47 A48 R49 C57 L60 D63 W67 N68 D69 L70

4.2.10 Score per residue for model 10

- Molecule 1: FLAVORIDIN

Chain A: 63% 27% • 9%

G1 E2 E3 D15 A16 A17 T18 C19 Q26 Q35 C36 K41 R42 C45 R46 I47 G50 D51 F52 R56 L60 S61 N62 D63 W67 N68 D69 L70

4.2.11 Score per residue for model 11

- Molecule 1: FLAVORIDIN

Chain A: 60% 27% • 9%

G1 E2 E3 C4 C14 C27 C33 D34 Q35 K41 R42 T43 I44 C45 R46 I47 G50 D51 F52 R56 C57 T58 S61 N62 D63 R66 W67 N68 D69 L70

4.2.12 Score per residue for model 12

- Molecule 1: FLAVORIDIN

Chain A: 66% 21% • 9%

G1 E2 E3 C4 D15 A16 A17 Q26 D34 Q35 C36 R37 K41 R42 T43 I44 I47 F52 C57 N62 W67 N68 D69 L70

4.2.13 Score per residue for model 13

- Molecule 1: FLAVORIDIN

Chain A: 76% 16% 9%

G1 E2 E3 C6 R22 D34 Q35 C36 R37 K40 C45 R49 S61 N62 D63 N68 D69 L70

4.2.14 Score per residue for model 14

- Molecule 1: FLAVORIDIN

Chain A: 56% 26% 9% • 9%

G1 E2 E3 C4 D5 C6 C13 C14 D15 A16 C19 K20 L21 Q26 C27 D34 Q35 C36 R37 F38 K39 K40 K41 R42 T43 I44 C45 R46 I47 A48 R49 C57 N62 D63 W67 N68 D69 L70

4.2.15 Score per residue for model 15

- Molecule 1: FLAVORIDIN

Chain A: 57% 26% 9% 9%

G1 E2 E3 C13 K20 L21 R22 C27 A28 D29 G30 L31 C32 C33 D34 Q35 C36 R37 T43 I44 C45 R46 R49 G50 D51 F52 D55 R56 C57 S61 N62 D63 N68 D69 L70

4.2.16 Score per residue for model 16

- Molecule 1: FLAVORIDIN

Chain A: 53% 34% • 9%

G1 E2 E3 C6 C14 D15 A16 A17 T18 C19 K20 L21 R22 A28 Q35 C36 K41 R42 T43 I44 C45 R46 I47 G50 D51 F52 P53 D54 C57 T58 G59 L60 S61 N62 D63 R66 W67 N68 D69 L70

4.2.17 Score per residue for model 17

- Molecule 1: FLAVORIDIN

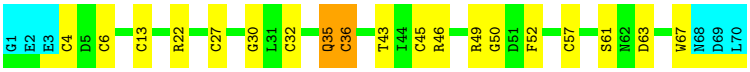
Chain A: 67% 23% • 9%

G1 E2 E3 C4 D5 C6 T18 C19 K20 L21 R22 D29 Q35 C36 R37 T43 I44 I47 C57 L60 S61 N62 D63 W67 N68 D69 L70

4.2.18 Score per residue for model 18

- Molecule 1: FLAVORIDIN

Chain A: 64% 24% • 9%



5 Refinement protocol and experimental data overview (i)

Of the ? calculated structures, 18 were deposited, based on the following criterion: *?*.

The authors did not provide any information on software used for structure solution, optimization or refinement.

No chemical shift data was provided.

6 Model quality (i)

6.1 Standard geometry (i)

There are no covalent bond-length or bond-angle outliers.

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
1	A	0.0±0.0	1.2±0.8
All	All	0	21

There are no bond-length outliers.

There are no bond-angle outliers.

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)
1	A	22	ARG	Sidechain	6
1	A	49	ARG	Sidechain	4
1	A	46	ARG	Sidechain	4
1	A	37	ARG	Sidechain	3
1	A	56	ARG	Sidechain	3
1	A	42	ARG	Sidechain	1

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	478	0	445	8±3
All	All	8604	0	8010	138

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.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:60:LEU:O	1:A:60:LEU:HD22	0.67	1.89	5	2
1:A:35:GLN:O	1:A:36:CYS:CB	0.62	2.47	14	12
1:A:15:ASP:O	1:A:16:ALA:C	0.60	2.40	4	4
1:A:44:ILE:HD12	1:A:44:ILE:N	0.59	2.12	12	2
1:A:21:LEU:HB3	1:A:28:ALA:HB2	0.59	1.75	5	1
1:A:60:LEU:HD13	1:A:60:LEU:N	0.59	2.13	7	2
1:A:21:LEU:C	1:A:21:LEU:HD22	0.58	2.18	17	3
1:A:41:LYS:O	1:A:42:ARG:CB	0.57	2.53	2	8
1:A:15:ASP:CG	1:A:16:ALA:N	0.56	2.59	16	3
1:A:60:LEU:HD13	1:A:60:LEU:H	0.55	1.61	8	2
1:A:13:CYS:SG	1:A:35:GLN:O	0.54	2.66	6	7
1:A:50:GLY:O	1:A:52:PHE:CD2	0.54	2.61	16	7
1:A:60:LEU:HD22	1:A:60:LEU:C	0.54	2.22	6	2
1:A:35:GLN:O	1:A:36:CYS:SG	0.53	2.66	16	10
1:A:18:THR:O	1:A:20:LYS:N	0.53	2.42	3	1
1:A:14:CYS:SG	1:A:28:ALA:HB1	0.51	2.46	16	1
1:A:58:THR:O	1:A:61:SER:N	0.51	2.44	11	2
1:A:34:ASP:N	1:A:37:ARG:O	0.50	2.45	9	7
1:A:34:ASP:O	1:A:35:GLN:C	0.50	2.49	3	7
1:A:21:LEU:CD2	1:A:21:LEU:N	0.49	2.76	6	2
1:A:15:ASP:O	1:A:16:ALA:HB3	0.49	2.08	6	1
1:A:18:THR:C	1:A:20:LYS:N	0.49	2.64	3	3
1:A:44:ILE:HG21	1:A:47:ILE:HD13	0.49	1.85	17	1
1:A:35:GLN:O	1:A:36:CYS:HB2	0.48	2.06	14	9
1:A:18:THR:O	1:A:19:CYS:C	0.48	2.51	3	1
1:A:51:ASP:O	1:A:52:PHE:CD1	0.48	2.67	16	2
1:A:5:ASP:HB2	1:A:21:LEU:HD21	0.47	1.85	14	1
1:A:44:ILE:N	1:A:44:ILE:CD1	0.47	2.77	11	2
1:A:21:LEU:H	1:A:21:LEU:HD22	0.46	1.71	14	2
1:A:62:ASN:O	1:A:62:ASN:CG	0.45	2.54	15	1
1:A:14:CYS:HB2	1:A:28:ALA:HB2	0.45	1.87	6	1
1:A:30:GLY:C	1:A:32:CYS:N	0.45	2.70	5	3
1:A:58:THR:O	1:A:59:GLY:C	0.44	2.54	16	1
1:A:50:GLY:O	1:A:52:PHE:CE2	0.44	2.71	16	5
1:A:33:CYS:HB2	1:A:62:ASN:ND2	0.44	2.28	5	1
1:A:27:CYS:SG	1:A:28:ALA:N	0.43	2.90	15	2
1:A:17:ALA:C	1:A:18:THR:OG1	0.43	2.56	7	1
1:A:55:ASP:HA	1:A:67:TRP:CD1	0.43	2.49	7	1
1:A:39:LYS:CD	1:A:43:THR:HG21	0.42	2.44	4	1
1:A:60:LEU:N	1:A:60:LEU:CD1	0.42	2.83	7	1
1:A:30:GLY:HA3	1:A:62:ASN:ND2	0.42	2.29	15	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:19:CYS:SG	1:A:19:CYS:O	0.42	2.78	2	1
1:A:21:LEU:N	1:A:21:LEU:CD1	0.42	2.82	9	1
1:A:43:THR:O	1:A:57:CYS:N	0.42	2.53	11	1
1:A:34:ASP:O	1:A:36:CYS:N	0.42	2.52	15	1
1:A:27:CYS:SG	1:A:37:ARG:O	0.41	2.79	5	1
1:A:13:CYS:SG	1:A:27:CYS:O	0.41	2.78	4	1
1:A:21:LEU:CD1	1:A:21:LEU:N	0.41	2.84	5	1
1:A:33:CYS:CB	1:A:62:ASN:ND2	0.41	2.84	5	1
1:A:30:GLY:C	1:A:32:CYS:H	0.41	2.18	15	1
1:A:34:ASP:O	1:A:37:ARG:N	0.41	2.54	4	1
1:A:19:CYS:O	1:A:19:CYS:SG	0.40	2.79	4	1
1:A:43:THR:HG22	1:A:57:CYS:HB2	0.40	1.94	17	1

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	64/70 (91%)	52±2 (81±3%)	10±2 (16±3%)	2±1 (3±1%)	7	41
All	All	1152/1260 (91%)	930 (81%)	189 (16%)	33 (3%)	7	41

All 8 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	36	CYS	13
1	A	35	GLN	6
1	A	17	ALA	5
1	A	4	CYS	5
1	A	19	CYS	1
1	A	16	ALA	1
1	A	42	ARG	1
1	A	41	LYS	1

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	A	54/59 (92%)	42±3 (78±6%)	12±3 (22±6%)	3 31
All	All	972/1062 (92%)	762 (78%)	210 (22%)	3 31

All 40 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	63	ASP	17
1	A	45	CYS	15
1	A	62	ASN	15
1	A	67	TRP	14
1	A	43	THR	13
1	A	57	CYS	11
1	A	60	LEU	9
1	A	47	ILE	9
1	A	27	CYS	8
1	A	26	GLN	7
1	A	46	ARG	7
1	A	21	LEU	7
1	A	6	CYS	7
1	A	35	GLN	6
1	A	61	SER	6
1	A	49	ARG	5
1	A	22	ARG	4
1	A	15	ASP	4
1	A	36	CYS	4
1	A	40	LYS	4
1	A	33	CYS	4
1	A	19	CYS	4
1	A	29	ASP	3
1	A	56	ARG	3
1	A	8	SER	3
1	A	37	ARG	3
1	A	14	CYS	2
1	A	66	ARG	2
1	A	55	ASP	2

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Mol	Chain	Res	Type	Models (Total)
1	A	20	LYS	2
1	A	51	ASP	1
1	A	34	ASP	1
1	A	11	ASN	1
1	A	13	CYS	1
1	A	18	THR	1
1	A	38	PHE	1
1	A	52	PHE	1
1	A	4	CYS	1
1	A	39	LYS	1
1	A	54	ASP	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)

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)

No chemical shift data were provided