



Full wwPDB NMR Structure Validation Report ⓘ

Feb 12, 2017 – 06:02 pm GMT

PDB ID : 1F5Y
Title : NMR STRUCTURE OF A CONCATEMER OF THE FIRST AND SECOND
LIGAND-BINDING MODULES OF THE HUMAN LDL RECEPTOR
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Deposited on : 2000-06-18

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A user guide is available at

<http://wwpdb.org/validation/2016/NMRValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

Cyrange	:	Kirchner and Güntert (2011)
NmrClust	:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	trunk28760
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	recalc28949

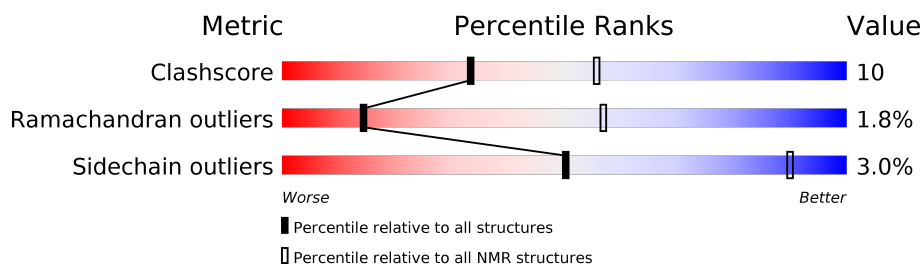
1 Overall quality at a glance

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	125131	11601
Ramachandran outliers	121729	10391
Sidechain outliers	121581	10367

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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	85	

2 Ensemble composition and analysis

This entry contains 20 models. Model 4 is the overall representative, medoid model (most similar to other models). The authors have identified model 2 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:12-A:40 (29)	0.13	7
2	A:52-A:85 (34)	0.43	4

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 4 single-model clusters were found.

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

3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 1183 atoms, of which 545 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called LOW-DENSITY LIPOPROTEIN RECEPTOR.

Mol	Chain	Residues	Atoms						Trace
1	A	85	Total	C	H	N	O	S	0
			1181	370	545	115	139	12	

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	CLONING ARTIFACT	UNP P01130
A	2	SER	-	CLONING ARTIFACT	UNP P01130

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

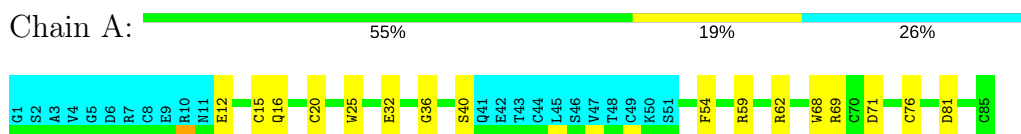
Mol	Chain	Residues	Atoms	
2	A	2	Total	Ca
			2	2

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: LOW-DENSITY LIPOPROTEIN RECEPTOR

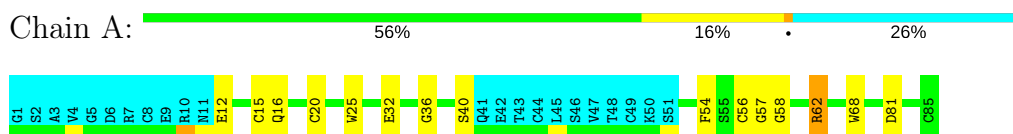


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

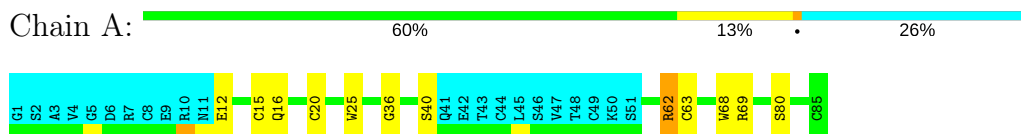
4.2.1 Score per residue for model 1

- Molecule 1: LOW-DENSITY LIPOPROTEIN RECEPTOR



4.2.2 Score per residue for model 2

- Molecule 1: LOW-DENSITY LIPOPROTEIN RECEPTOR



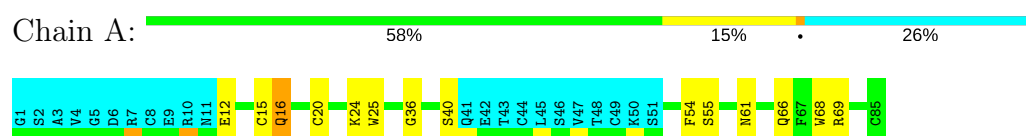
4.2.3 Score per residue for model 3

- Molecule 1: LOW-DENSITY LIPOPROTEIN RECEPTOR



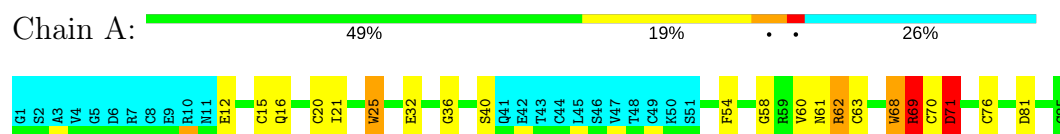
4.2.4 Score per residue for model 4 (medoid)

- Molecule 1: LOW-DENSITY LIPOPROTEIN RECEPTOR



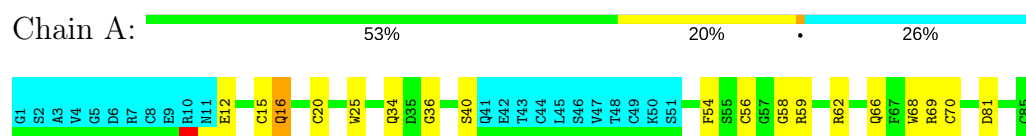
4.2.5 Score per residue for model 5

- Molecule 1: LOW-DENSITY LIPOPROTEIN RECEPTOR



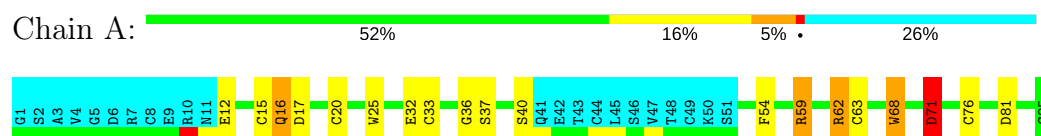
4.2.6 Score per residue for model 6

- Molecule 1: LOW-DENSITY LIPOPROTEIN RECEPTOR



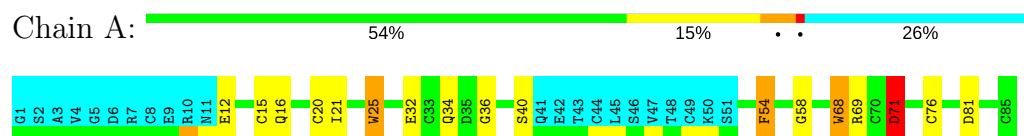
4.2.7 Score per residue for model 7

- Molecule 1: LOW-DENSITY LIPOPROTEIN RECEPTOR



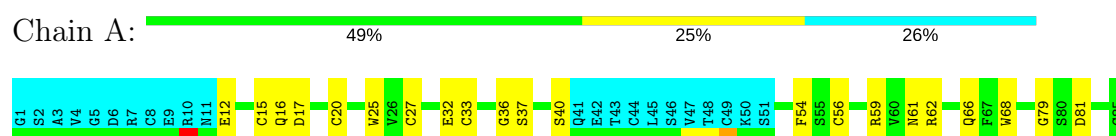
4.2.8 Score per residue for model 8

- Molecule 1: LOW-DENSITY LIPOPROTEIN RECEPTOR



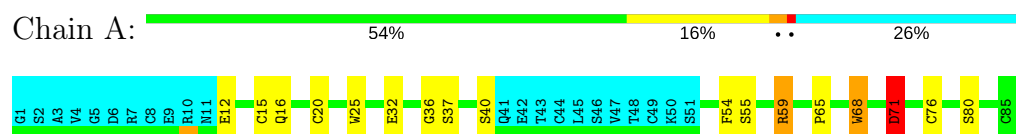
4.2.9 Score per residue for model 9

- Molecule 1: LOW-DENSITY LIPOPROTEIN RECEPTOR



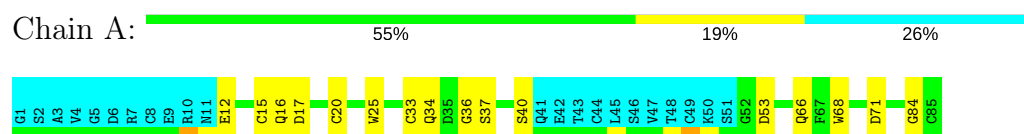
4.2.10 Score per residue for model 10

- Molecule 1: LOW-DENSITY LIPOPROTEIN RECEPTOR



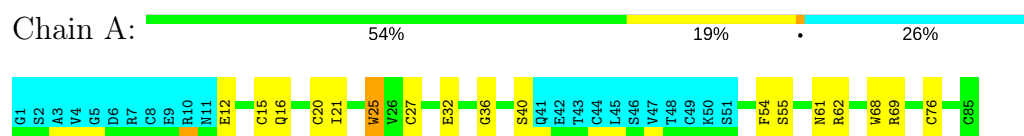
4.2.11 Score per residue for model 11

- Molecule 1: LOW-DENSITY LIPOPROTEIN RECEPTOR



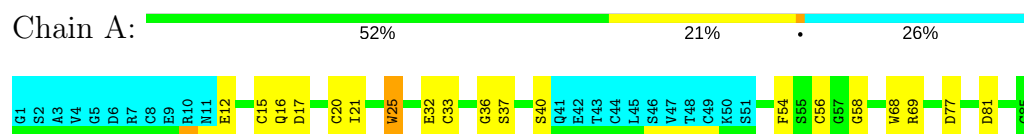
4.2.12 Score per residue for model 12

- Molecule 1: LOW-DENSITY LIPOPROTEIN RECEPTOR



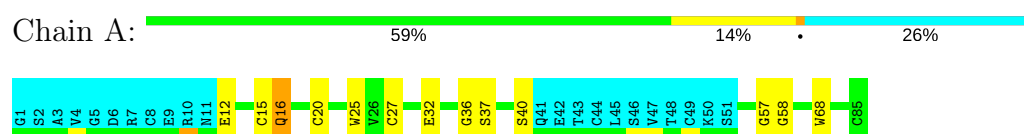
4.2.13 Score per residue for model 13

- Molecule 1: LOW-DENSITY LIPOPROTEIN RECEPTOR



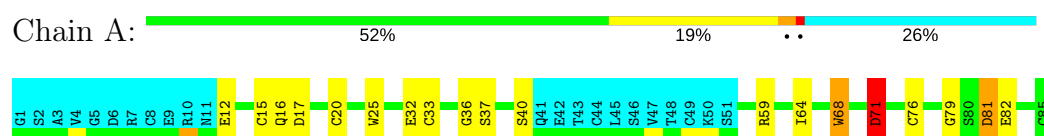
4.2.14 Score per residue for model 14

- Molecule 1: LOW-DENSITY LIPOPROTEIN RECEPTOR



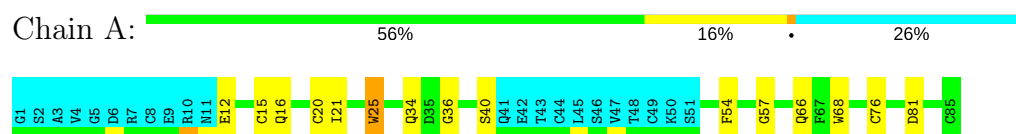
4.2.15 Score per residue for model 15

- Molecule 1: LOW-DENSITY LIPOPROTEIN RECEPTOR



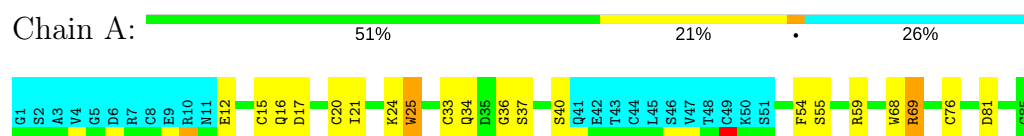
4.2.16 Score per residue for model 16

- Molecule 1: LOW-DENSITY LIPOPROTEIN RECEPTOR



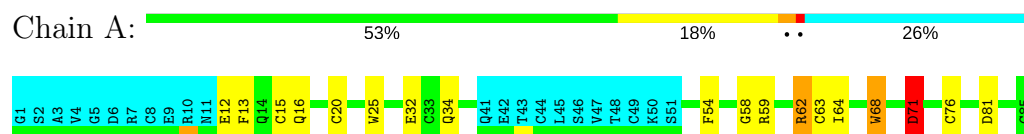
4.2.17 Score per residue for model 17

- Molecule 1: LOW-DENSITY LIPOPROTEIN RECEPTOR



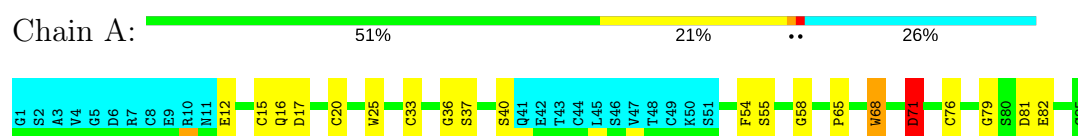
4.2.18 Score per residue for model 18

• Molecule 1: LOW-DENSITY LIPOPROTEIN RECEPTOR



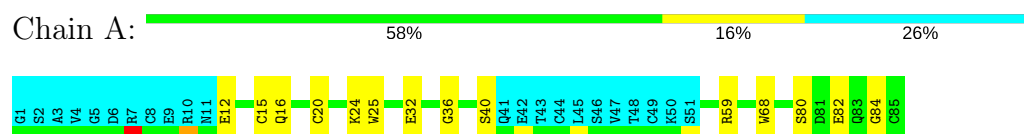
4.2.19 Score per residue for model 19

• Molecule 1: LOW-DENSITY LIPOPROTEIN RECEPTOR



4.2.20 Score per residue for model 20

• Molecule 1: LOW-DENSITY LIPOPROTEIN RECEPTOR



5 Refinement protocol and experimental data overview

The models were refined using the following method: *Torsion angle dynamics (DYANA) followed by simulated annealing and molecular dynamics (X-PLOR) for calcium coordination.*

Of the 50 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
DYANA	structure solution	1.5
X-PLOR	refinement	3.85

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

6.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CA

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	Bond lengths		Bond angles	
		RMSZ	#Z>5	RMSZ	#Z>5
1	A	1.24±0.01	0±0/485 (0.0±0.0%)	1.50±0.03	9±1/650 (1.4±0.1%)
All	All	1.24	0/9700 (0.0%)	1.50	176/13000 (1.4%)

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	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	71	ASP	CB-CG-OD1	-10.96	108.43	118.30	18	5
1	A	71	ASP	CB-CG-OD2	-10.66	108.71	118.30	10	3
1	A	68	TRP	CD1-NE1-CE2	8.49	116.64	109.00	10	20
1	A	25	TRP	CD1-NE1-CE2	8.20	116.38	109.00	6	20
1	A	27	CYS	CA-CB-SG	7.79	128.02	114.00	12	3
1	A	25	TRP	NE1-CE2-CZ2	7.53	138.68	130.40	13	20
1	A	68	TRP	NE1-CE2-CZ2	6.97	138.07	130.40	18	20
1	A	76	CYS	CA-CB-SG	6.78	126.20	114.00	8	1
1	A	59	ARG	NE-CZ-NH2	-6.32	117.14	120.30	9	8
1	A	68	TRP	CG-CD1-NE1	-6.17	103.93	110.10	10	20
1	A	69	ARG	NE-CZ-NH2	-6.06	117.27	120.30	3	6
1	A	62	ARG	NE-CZ-NH2	-5.82	117.39	120.30	3	8
1	A	25	TRP	CG-CD1-NE1	-5.79	104.31	110.10	6	20
1	A	71	ASP	N-CA-CB	-5.47	100.75	110.60	11	1
1	A	25	TRP	NE1-CE2-CD2	-5.47	101.83	107.30	13	20
1	A	27	CYS	N-CA-CB	-5.12	101.39	110.60	12	1

There are no chirality outliers.

There are no planarity outliers.

6.2 Too-close contacts ⓘ

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	477	395	395	9±3
All	All	9580	7900	7900	181

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 10.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:54:PHE:CE2	1:A:76:CYS:SG	0.70	2.85	16	6
1:A:54:PHE:CE2	1:A:56:CYS:SG	0.69	2.85	13	4
1:A:54:PHE:CE2	1:A:81:ASP:HB3	0.58	2.33	5	11
1:A:12:GLU:CB	1:A:20:CYS:SG	0.58	2.92	5	20
1:A:54:PHE:CD1	1:A:55:SER:N	0.57	2.73	12	4
1:A:15:CYS:SG	1:A:16:GLN:N	0.54	2.81	7	20
1:A:54:PHE:CE1	1:A:76:CYS:SG	0.54	3.01	12	2
1:A:62:ARG:NE	1:A:62:ARG:HA	0.52	2.20	3	4
1:A:15:CYS:SG	1:A:37:SER:CB	0.51	2.99	9	5
1:A:12:GLU:HB2	1:A:20:CYS:SG	0.51	2.46	17	4
1:A:12:GLU:HB3	1:A:20:CYS:SG	0.50	2.47	9	12
1:A:15:CYS:SG	1:A:37:SER:HB3	0.50	2.45	9	9
1:A:17:ASP:HB3	1:A:33:CYS:SG	0.50	2.46	17	7
1:A:62:ARG:HE	1:A:63:CYS:N	0.48	2.06	7	4
1:A:59:ARG:H	1:A:59:ARG:HD3	0.48	1.68	10	1
1:A:36:GLY:O	1:A:40:SER:N	0.48	2.47	11	19
1:A:32:GLU:CD	1:A:32:GLU:N	0.47	2.67	8	8
1:A:64:ILE:HG13	1:A:76:CYS:SG	0.47	2.50	15	2
1:A:32:GLU:N	1:A:32:GLU:CD	0.46	2.68	9	5
1:A:59:ARG:NH2	1:A:80:SER:HB2	0.45	2.26	10	1
1:A:62:ARG:HA	1:A:62:ARG:NE	0.45	2.27	7	3
1:A:68:TRP:C	1:A:71:ASP:OD1	0.45	2.56	18	5
1:A:65:PRO:HG2	1:A:68:TRP:CD2	0.44	2.47	10	2
1:A:69:ARG:HD3	1:A:70:CYS:N	0.43	2.28	5	1
1:A:80:SER:O	1:A:84:GLY:HA3	0.43	2.13	20	1
1:A:21:ILE:HD13	1:A:25:TRP:HB2	0.43	1.91	5	6
1:A:79:GLY:C	1:A:81:ASP:H	0.43	2.16	19	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:24:LYS:H	1:A:24:LYS:CD	0.43	2.26	17	1
1:A:68:TRP:C	1:A:71:ASP:OD2	0.42	2.57	10	2
1:A:59:ARG:HD3	1:A:59:ARG:N	0.42	2.28	10	1
1:A:54:PHE:CZ	1:A:56:CYS:SG	0.42	3.13	9	1
1:A:24:LYS:N	1:A:24:LYS:HD2	0.41	2.30	20	2
1:A:60:VAL:HG22	1:A:61:ASN:N	0.41	2.31	5	1
1:A:54:PHE:HE1	1:A:76:CYS:SG	0.40	2.39	10	2
1:A:54:PHE:CG	1:A:55:SER:N	0.40	2.90	10	1
1:A:24:LYS:HD2	1:A:24:LYS:H	0.40	1.76	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	62/85 (73%)	51±3 (83±4%)	10±2 (15±4%)	1±1 (2±1%)	14	57
All	All	1240/1700 (73%)	1026 (83%)	192 (15%)	22 (2%)	14	57

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	58	GLY	8
1	A	66	GLN	6
1	A	57	GLY	3
1	A	54	PHE	1
1	A	84	GLY	1
1	A	70	CYS	1
1	A	77	ASP	1
1	A	80	SER	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	53/72 (74%)	51±1 (97±2%)	2±1 (3±2%)	50	90
All	All	1060/1440 (74%)	1028 (97%)	32 (3%)	50	90

All 8 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	71	ASP	7
1	A	34	GLN	6
1	A	16	GLN	5
1	A	69	ARG	5
1	A	82	GLU	3
1	A	61	ASN	3
1	A	59	ARG	2
1	A	81	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 carbohydrates in this entry.

6.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

6.7 Other polymers [i](#)

There are no such molecules in this entry.

6.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

7 Chemical shift validation

No chemical shift data were provided