



Full wwPDB NMR Structure Validation Report ⓘ

Jan 22, 2018 – 03:18 AM EST

PDB ID : 2HGL
Title : NMR structure of the first qRRM domain of human hnRNP F
Authors : Dominguez, C.; Allain, F.H.-T.
Deposited on : 2006-06-27

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

<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 : rb-20030736
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20030736

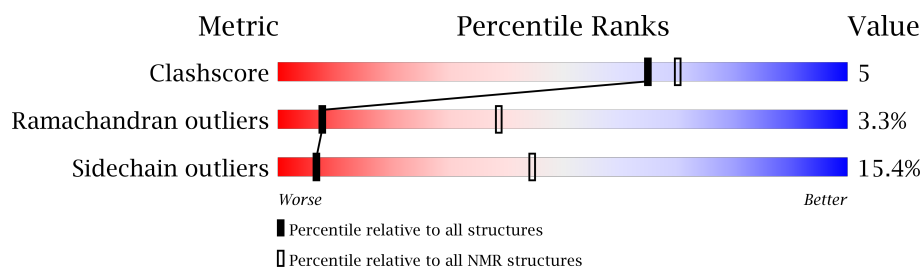
1 Overall quality at a glance

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	136	

2 Ensemble composition and analysis

This entry contains 15 models. Model 2 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:11-A:47, A:54-A:77, A:81-A:97 (78)	0.28	2

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	1, 2, 5, 11, 14
2	4, 7, 10, 12, 15
3	3, 8, 13
Single-model clusters	6; 9

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 1571 atoms, of which 768 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Heterogeneous nuclear ribonucleoprotein F.

Mol	Chain	Residues	Atoms						Trace
1	A	102	Total	C	H	N	O	S	0
			1571	502	768	141	153	7	

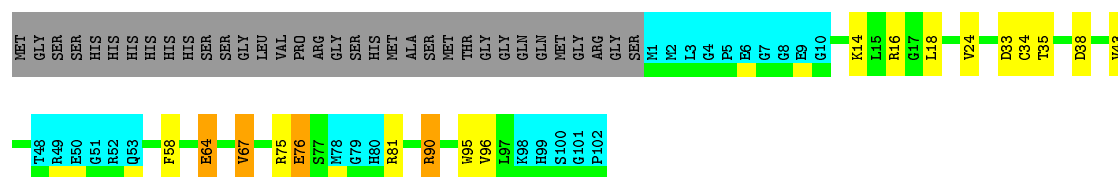
There are 34 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-33	MET	-	CLONING ARTIFACT	UNP Q5T0N2
A	-32	GLY	-	CLONING ARTIFACT	UNP Q5T0N2
A	-31	SER	-	CLONING ARTIFACT	UNP Q5T0N2
A	-30	SER	-	CLONING ARTIFACT	UNP Q5T0N2
A	-29	HIS	-	EXPRESSION TAG	UNP Q5T0N2
A	-28	HIS	-	EXPRESSION TAG	UNP Q5T0N2
A	-27	HIS	-	EXPRESSION TAG	UNP Q5T0N2
A	-26	HIS	-	EXPRESSION TAG	UNP Q5T0N2
A	-25	HIS	-	EXPRESSION TAG	UNP Q5T0N2
A	-24	HIS	-	EXPRESSION TAG	UNP Q5T0N2
A	-23	SER	-	CLONING ARTIFACT	UNP Q5T0N2
A	-22	SER	-	CLONING ARTIFACT	UNP Q5T0N2
A	-21	GLY	-	CLONING ARTIFACT	UNP Q5T0N2
A	-20	LEU	-	CLONING ARTIFACT	UNP Q5T0N2
A	-19	VAL	-	CLONING ARTIFACT	UNP Q5T0N2
A	-18	PRO	-	CLONING ARTIFACT	UNP Q5T0N2
A	-17	ARG	-	CLONING ARTIFACT	UNP Q5T0N2
A	-16	GLY	-	CLONING ARTIFACT	UNP Q5T0N2
A	-15	SER	-	CLONING ARTIFACT	UNP Q5T0N2
A	-14	HIS	-	CLONING ARTIFACT	UNP Q5T0N2
A	-13	MET	-	CLONING ARTIFACT	UNP Q5T0N2
A	-12	ALA	-	CLONING ARTIFACT	UNP Q5T0N2
A	-11	SER	-	CLONING ARTIFACT	UNP Q5T0N2
A	-10	MET	-	CLONING ARTIFACT	UNP Q5T0N2
A	-9	THR	-	CLONING ARTIFACT	UNP Q5T0N2
A	-8	GLY	-	CLONING ARTIFACT	UNP Q5T0N2
A	-7	GLY	-	CLONING ARTIFACT	UNP Q5T0N2
A	-6	GLN	-	CLONING ARTIFACT	UNP Q5T0N2
A	-5	GLN	-	CLONING ARTIFACT	UNP Q5T0N2
A	-4	MET	-	CLONING ARTIFACT	UNP Q5T0N2
A	-3	GLY	-	CLONING ARTIFACT	UNP Q5T0N2

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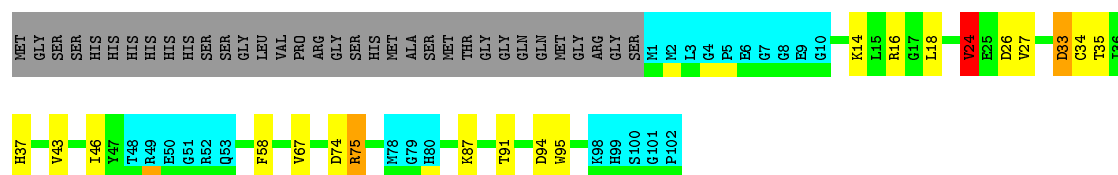
Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	ARG	-	CLONING ARTIFACT	UNP Q5T0N2
A	-1	GLY	-	CLONING ARTIFACT	UNP Q5T0N2
A	0	SER	-	CLONING ARTIFACT	UNP Q5T0N2



4.2.3 Score per residue for model 3

- Molecule 1: Heterogeneous nuclear ribonucleoprotein F

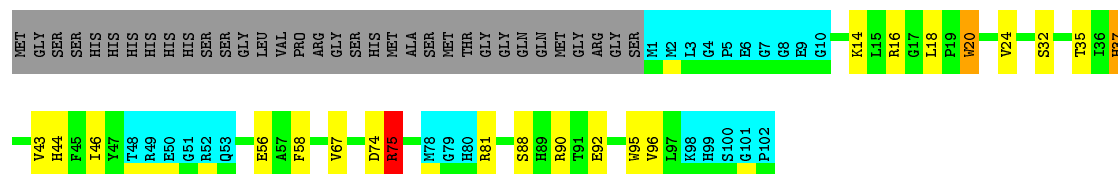
Chain A: 43% 13% 18% 25%



4.2.4 Score per residue for model 4

- Molecule 1: Heterogeneous nuclear ribonucleoprotein F

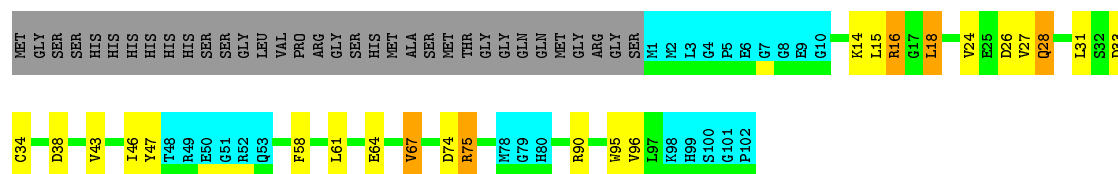
Chain A: 41% 14% 18% 25%



4.2.5 Score per residue for model 5

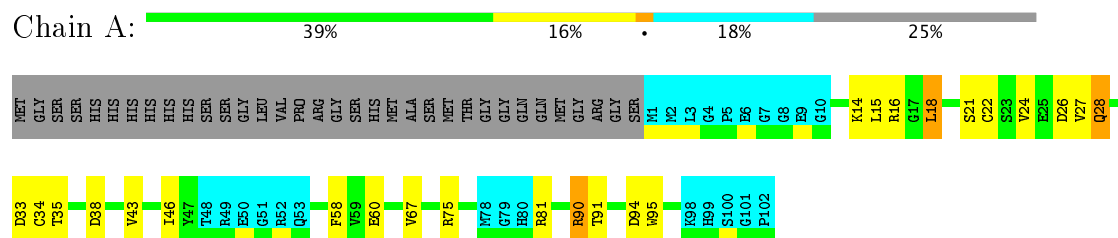
- Molecule 1: Heterogeneous nuclear ribonucleoprotein F

Chain A: 40% 14% 18% 25%



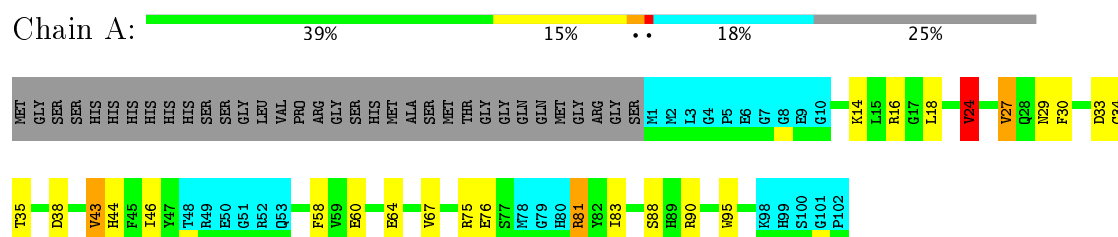
4.2.6 Score per residue for model 6

- Molecule 1: Heterogeneous nuclear ribonucleoprotein F



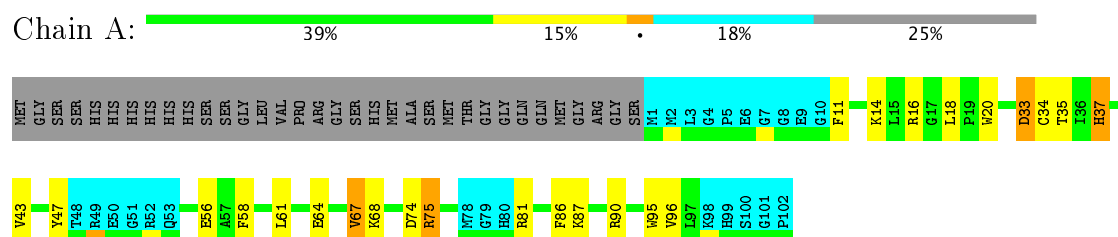
4.2.7 Score per residue for model 7

- Molecule 1: Heterogeneous nuclear ribonucleoprotein F



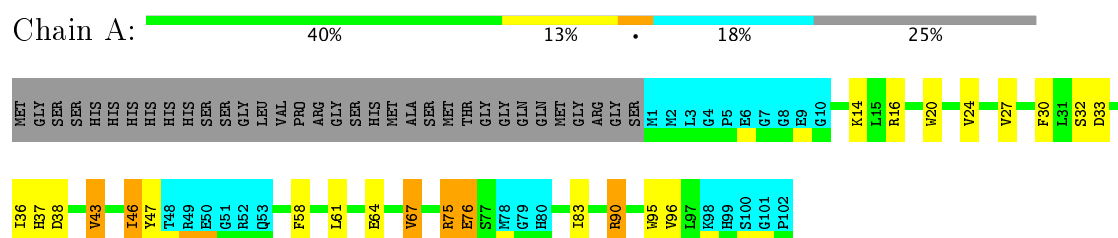
4.2.8 Score per residue for model 8

- Molecule 1: Heterogeneous nuclear ribonucleoprotein F



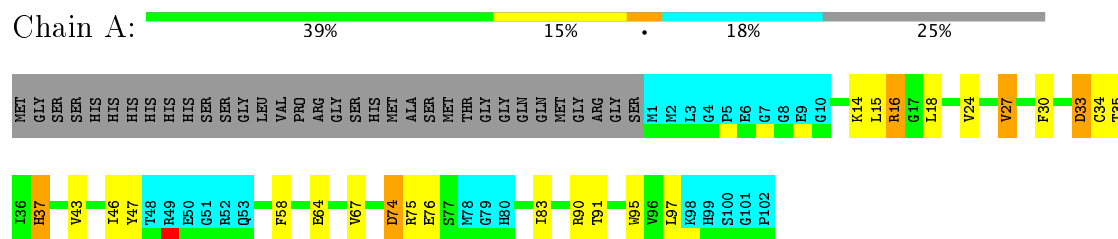
4.2.9 Score per residue for model 9

- Molecule 1: Heterogeneous nuclear ribonucleoprotein F



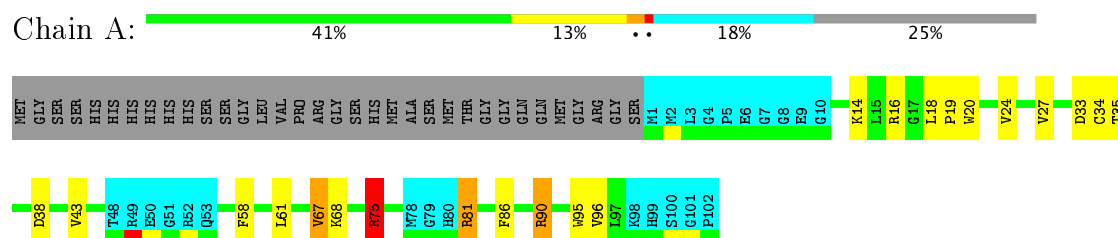
4.2.10 Score per residue for model 10

- Molecule 1: Heterogeneous nuclear ribonucleoprotein F



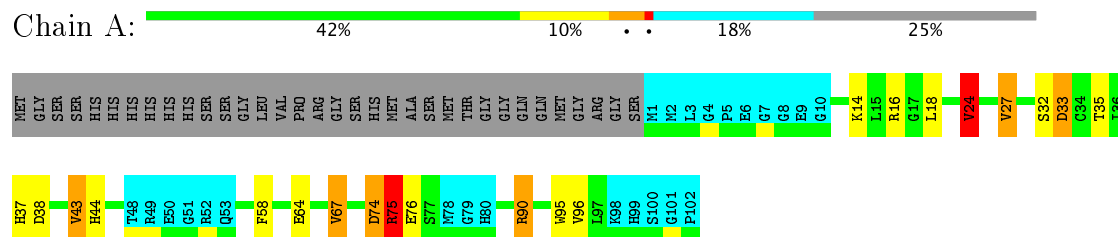
4.2.11 Score per residue for model 11

- Molecule 1: Heterogeneous nuclear ribonucleoprotein F



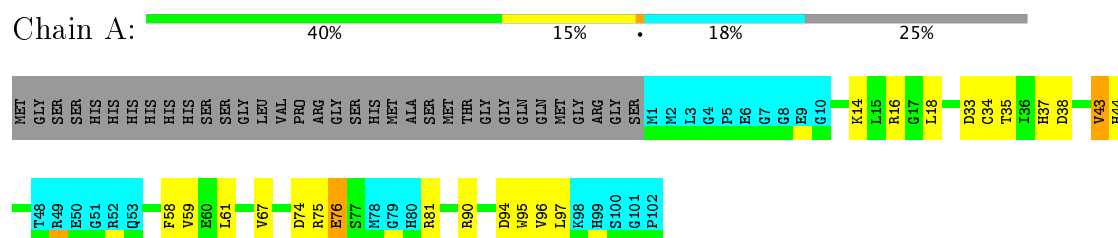
4.2.12 Score per residue for model 12

- Molecule 1: Heterogeneous nuclear ribonucleoprotein F



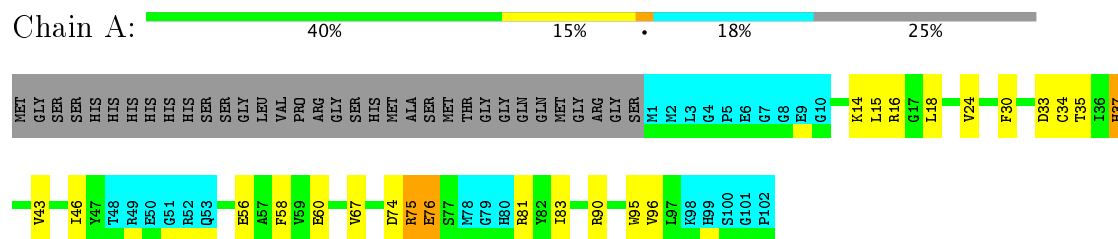
4.2.13 Score per residue for model 13

- Molecule 1: Heterogeneous nuclear ribonucleoprotein F



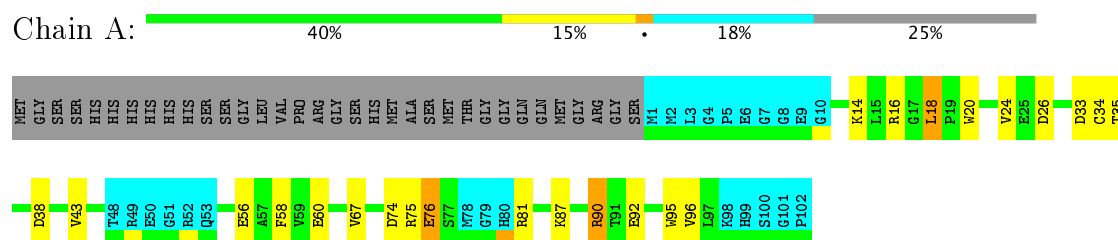
4.2.14 Score per residue for model 14

- Molecule 1: Heterogeneous nuclear ribonucleoprotein F



4.2.15 Score per residue for model 15

- Molecule 1: Heterogeneous nuclear ribonucleoprotein F



5 Refinement protocol and experimental data overview ⓘ

The models were refined using the following method: *simulated annealing*.

Of the 100 calculated structures, 15 were deposited, based on the following criterion: *target function*.

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

Software name	Classification	Version
Cyana	structure solution	2.1
AMBER	refinement	7.0

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

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	0.73±0.01	0±0/643 (0.0±0.0%)	1.37±0.03	7±1/868 (0.8±0.1%)
All	All	0.73	0/9645 (0.0%)	1.37	108/13020 (0.8%)

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	1.8±0.7
All	All	0	27

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	90	ARG	NE-CZ-NH1	10.09	125.34	120.30	1	14
1	A	75	ARG	NE-CZ-NH1	8.51	124.55	120.30	13	13
1	A	67	VAL	CA-CB-CG2	7.64	122.37	110.90	5	14
1	A	27	VAL	CA-CB-CG2	7.49	122.13	110.90	1	3
1	A	24	VAL	CA-CB-CG1	7.05	121.48	110.90	1	4
1	A	37	HIS	CA-CB-CG	7.03	125.55	113.60	8	4
1	A	81	ARG	NE-CZ-NH1	6.93	123.77	120.30	13	8
1	A	16	ARG	NE-CZ-NH2	-6.83	116.89	120.30	10	4
1	A	67	VAL	CG1-CB-CG2	6.80	121.78	110.90	9	13
1	A	90	ARG	NE-CZ-NH2	-6.72	116.94	120.30	4	1
1	A	16	ARG	NE-CZ-NH1	6.70	123.65	120.30	10	15
1	A	43	VAL	CG1-CB-CG2	-6.42	100.62	110.90	8	3
1	A	76	GLU	CB-CA-C	5.97	122.34	110.40	13	4
1	A	27	VAL	CA-CB-CG1	5.67	119.40	110.90	10	1
1	A	11	PHE	CB-CG-CD1	-5.61	116.87	120.80	8	1

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	28	GLN	CA-CB-CG	5.51	125.52	113.40	5	2
1	A	20	TRP	CB-CG-CD2	5.41	133.63	126.60	4	1
1	A	16	ARG	CD-NE-CZ	5.22	130.91	123.60	10	1
1	A	43	VAL	CA-CB-CG1	5.20	118.70	110.90	9	1
1	A	31	LEU	CA-CB-CG	-5.04	103.70	115.30	5	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)
1	A	33	ASP	Peptide	13
1	A	75	ARG	Sidechain	4
1	A	46	ILE	Peptide	2
1	A	28	GLN	Peptide	2
1	A	90	ARG	Peptide,Sidechain	2
1	A	97	LEU	Peptide	1
1	A	21	SER	Peptide	1
1	A	47	TYR	Peptide	1
1	A	76	GLU	Peptide	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	628	604	604	6±2
All	All	9420	9060	9060	89

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 5.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:24:VAL:HG22	1:A:43:VAL:CG2	0.64	2.22	9	8
1:A:24:VAL:HG22	1:A:43:VAL:HG21	0.62	1.70	6	8

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:58:PHE:CZ	1:A:96:VAL:HG21	0.60	2.31	12	9
1:A:58:PHE:CE1	1:A:96:VAL:HG21	0.60	2.32	8	8
1:A:61:LEU:HD13	1:A:67:VAL:HA	0.58	1.75	9	6
1:A:43:VAL:HG12	1:A:59:VAL:HG22	0.57	1.75	13	1
1:A:24:VAL:HG22	1:A:43:VAL:HG11	0.57	1.75	5	1
1:A:24:VAL:HB	1:A:43:VAL:HG21	0.55	1.77	1	4
1:A:14:LYS:HB2	1:A:58:PHE:CE2	0.53	2.39	15	15
1:A:24:VAL:HG22	1:A:43:VAL:CG1	0.52	2.34	5	1
1:A:24:VAL:HG13	1:A:43:VAL:HG21	0.49	1.83	14	6
1:A:24:VAL:HG13	1:A:43:VAL:HG11	0.49	1.84	5	1
1:A:24:VAL:HA	1:A:27:VAL:HG13	0.48	1.86	12	3
1:A:30:PHE:CE2	1:A:83:ILE:HG21	0.48	2.43	9	3
1:A:64:GLU:HA	1:A:67:VAL:HG13	0.47	1.86	5	3
1:A:24:VAL:CG2	1:A:43:VAL:HG11	0.45	2.42	12	3
1:A:24:VAL:HA	1:A:27:VAL:HG12	0.43	1.89	11	2
1:A:46:ILE:HG22	1:A:47:TYR:H	0.43	1.74	9	1
1:A:30:PHE:CD2	1:A:83:ILE:HG21	0.42	2.48	14	1
1:A:24:VAL:CB	1:A:43:VAL:HG21	0.41	2.45	3	1
1:A:14:LYS:HB3	1:A:86:PHE:HB2	0.41	1.93	8	2
1:A:24:VAL:HB	1:A:43:VAL:HG11	0.41	1.93	1	1
1:A:44:HIS:HB3	1:A:97:LEU:HD21	0.40	1.93	13	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	78/136 (57%)	63±2 (81±3%)	13±2 (16±3%)	3±1 (3±2%)	8	39
All	All	1170/2040 (57%)	943 (81%)	188 (16%)	39 (3%)	8	39

All 11 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	38	ASP	9

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Mol	Chain	Res	Type	Models (Total)
1	A	74	ASP	9
1	A	60	GLU	5
1	A	76	GLU	3
1	A	18	LEU	3
1	A	32	SER	3
1	A	36	ILE	2
1	A	37	HIS	2
1	A	90	ARG	1
1	A	19	PRO	1
1	A	20	TRP	1

6.3.2 Protein sidechains ⓘ

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	69/112 (62%)	58±2 (85±3%)	11±2 (15±3%)	7	44
All	All	1035/1680 (62%)	876 (85%)	159 (15%)	7	44

All 32 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	95	TRP	15
1	A	18	LEU	14
1	A	34	CYS	12
1	A	35	THR	12
1	A	75	ARG	11
1	A	64	GLU	6
1	A	46	ILE	6
1	A	37	HIS	6
1	A	76	GLU	6
1	A	33	ASP	6
1	A	20	TRP	5
1	A	87	LYS	4
1	A	81	ARG	4
1	A	15	LEU	4
1	A	26	ASP	4

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Mol	Chain	Res	Type	Models (Total)
1	A	27	VAL	4
1	A	56	GLU	4
1	A	24	VAL	4
1	A	91	THR	4
1	A	44	HIS	3
1	A	90	ARG	3
1	A	74	ASP	3
1	A	94	ASP	3
1	A	43	VAL	3
1	A	88	SER	2
1	A	47	TYR	2
1	A	16	ARG	2
1	A	68	LYS	2
1	A	92	GLU	2
1	A	22	CYS	1
1	A	29	ASN	1
1	A	38	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](#)

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 ⓘ

There are no chain breaks in this entry.

7 Chemical shift validation

No chemical shift data were provided