



Full wwPDB NMR Structure Validation Report ⓘ

Mar 19, 2026 – 11:27 AM UTC

PDB ID : 2F2D / pdb_00002f2d
Title : Solution structure of the FK506-binding domain of human FKBP38
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Deposited on : 2005-11-16

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with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
wwPDB-RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
wwPDB-ShiftChecker : v1.2
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

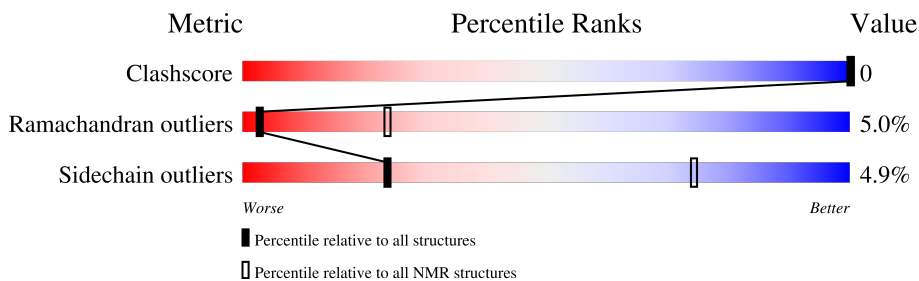
1 Overall quality at a glance

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	229148	14424
Ramachandran outliers	224038	12848
Sidechain outliers	223484	12823

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	121	

2 Ensemble composition and analysis

This entry contains 20 models. Model 6 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *fewest violations*.

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:35-A:149 (115)	1.44	6

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 2 clusters and 3 single-model clusters were found.

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

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 1836 atoms, of which 923 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called 38 kDa FK-506 binding protein homolog, FKBP38.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	121	1836	576	923	153	178	6	0

There are 2 discrepancies between the modelled and reference sequences:

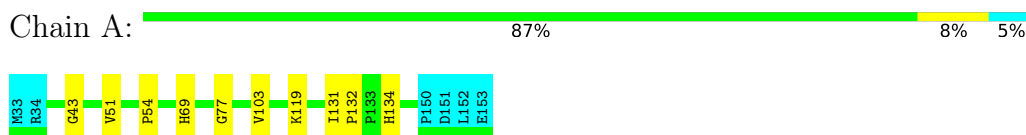
Chain	Residue	Modelled	Actual	Comment	Reference
A	33	MET	-	cloning artifact	UNP Q14318
A	34	ARG	-	cloning artifact	UNP Q14318

4 Residue-property plots

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: 38 kDa FK-506 binding protein homolog, FKBP38

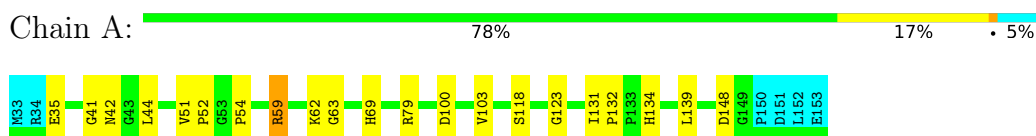


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

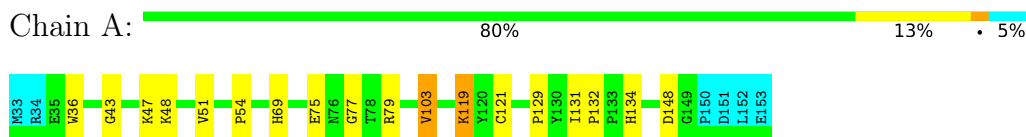
4.2.1 Score per residue for model 1

- Molecule 1: 38 kDa FK-506 binding protein homolog, FKBP38



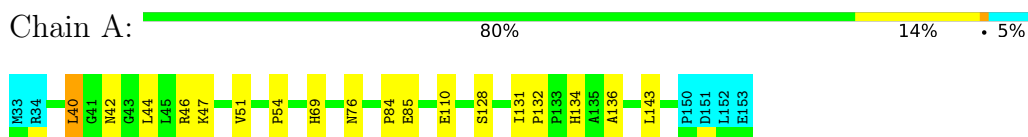
4.2.2 Score per residue for model 2

- Molecule 1: 38 kDa FK-506 binding protein homolog, FKBP38



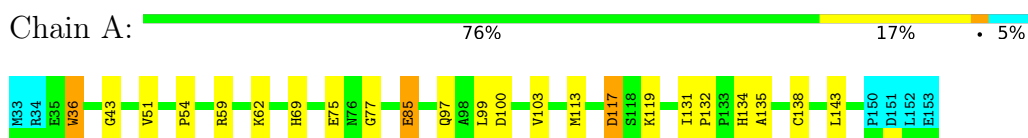
4.2.3 Score per residue for model 3

- Molecule 1: 38 kDa FK-506 binding protein homolog, FKBP38



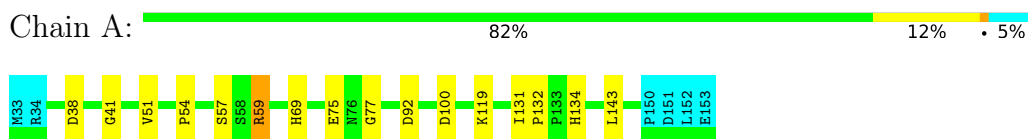
4.2.4 Score per residue for model 4

- Molecule 1: 38 kDa FK-506 binding protein homolog, FKBP38



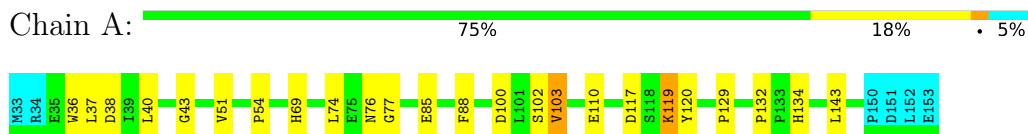
4.2.5 Score per residue for model 5

- Molecule 1: 38 kDa FK-506 binding protein homolog, FKBP38



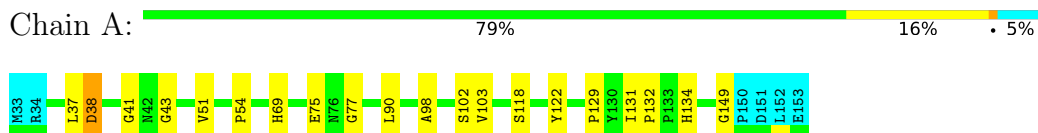
4.2.6 Score per residue for model 6 (medoid)

- Molecule 1: 38 kDa FK-506 binding protein homolog, FKBP38



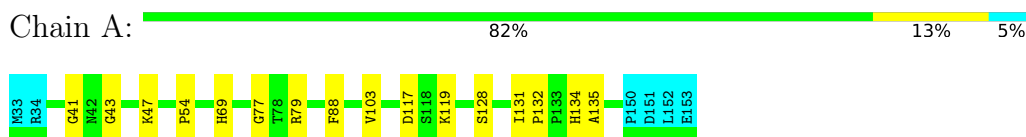
4.2.7 Score per residue for model 7

- Molecule 1: 38 kDa FK-506 binding protein homolog, FKBP38



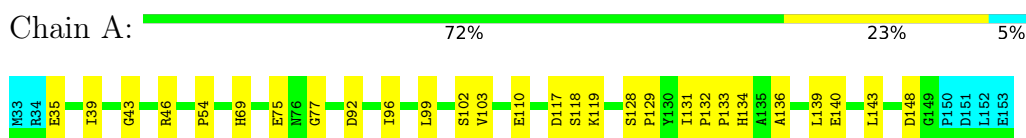
4.2.8 Score per residue for model 8

- Molecule 1: 38 kDa FK-506 binding protein homolog, FKBP38



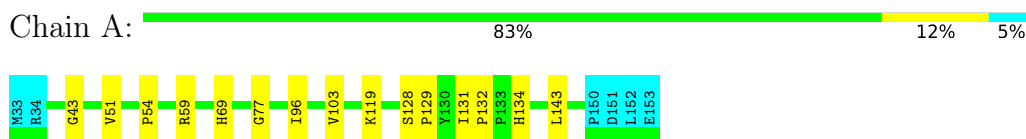
4.2.9 Score per residue for model 9

- Molecule 1: 38 kDa FK-506 binding protein homolog, FKBP38



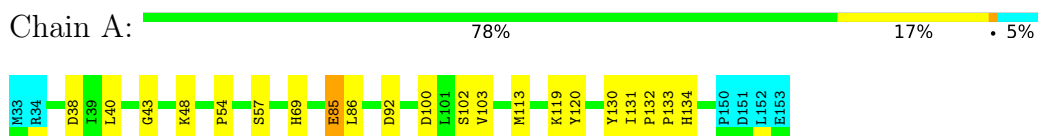
4.2.10 Score per residue for model 10

- Molecule 1: 38 kDa FK-506 binding protein homolog, FKBP38



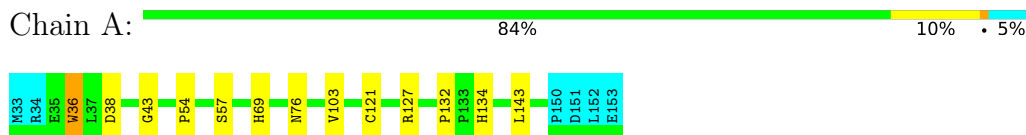
4.2.11 Score per residue for model 11

- Molecule 1: 38 kDa FK-506 binding protein homolog, FKBP38



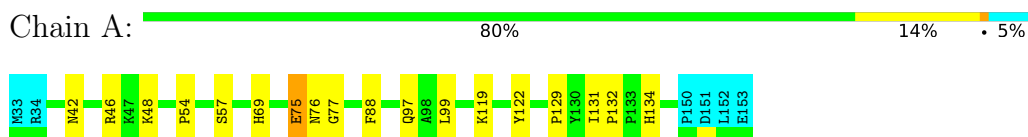
4.2.12 Score per residue for model 12

- Molecule 1: 38 kDa FK-506 binding protein homolog, FKBP38



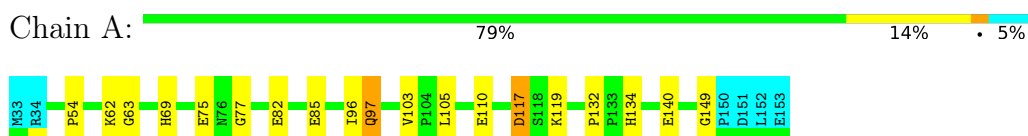
4.2.13 Score per residue for model 13

- Molecule 1: 38 kDa FK-506 binding protein homolog, FKBP38



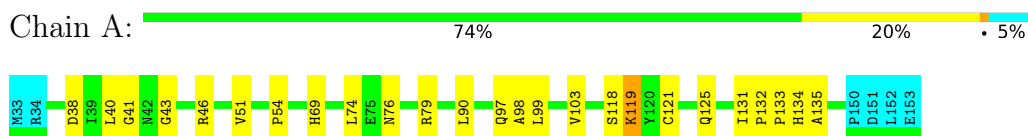
4.2.14 Score per residue for model 14

- Molecule 1: 38 kDa FK-506 binding protein homolog, FKBP38



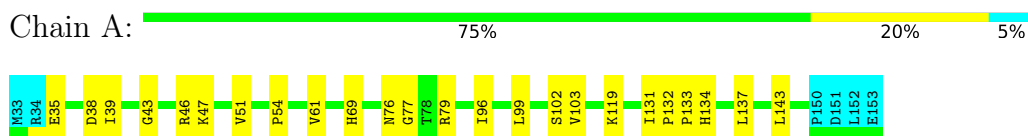
4.2.15 Score per residue for model 15

- Molecule 1: 38 kDa FK-506 binding protein homolog, FKBP38



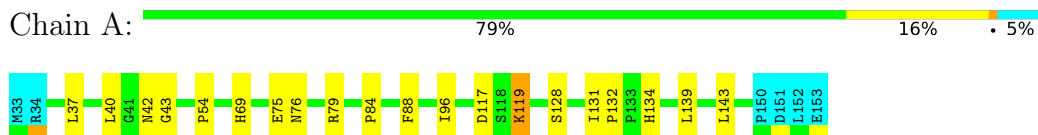
4.2.16 Score per residue for model 16

- Molecule 1: 38 kDa FK-506 binding protein homolog, FKBP38



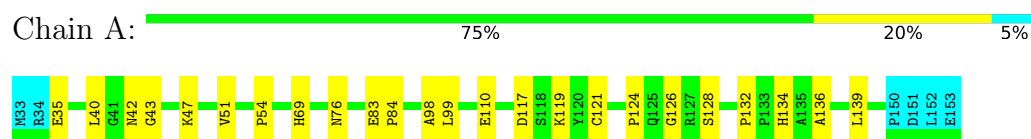
4.2.17 Score per residue for model 17

- Molecule 1: 38 kDa FK-506 binding protein homolog, FKBP38



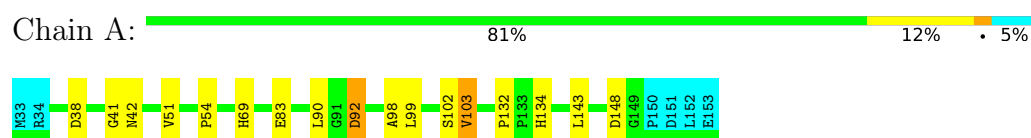
4.2.18 Score per residue for model 18

- Molecule 1: 38 kDa FK-506 binding protein homolog, FKBP38



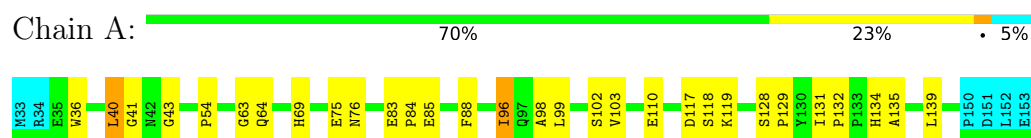
4.2.19 Score per residue for model 19

- Molecule 1: 38 kDa FK-506 binding protein homolog, FKBP38



4.2.20 Score per residue for model 20

- Molecule 1: 38 kDa FK-506 binding protein homolog, FKBP38



5 Refinement protocol and experimental data overview

The models were refined using the following method: *simulated annealing combined with torsion angle dynamics followed by energy minimization.*

Of the 100 calculated structures, 20 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
DYANA	structure solution	1.5
Discover	refinement	2000

No chemical shift data was provided.

6 Model quality i

6.1 Standard geometry i

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	1.79±0.02	7±1/880 (0.8± 0.2%)	1.60±0.03	12±2/1205 (1.0± 0.2%)
All	All	1.79	143/17600 (0.8%)	1.60	236/24100 (1.0%)

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	0.6±0.7
All	All	0	12

All unique bond 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(Å)	Ideal(Å)	Models	
								Worst	Total
1	A	103	VAL	CA-CB	8.65	1.58	1.54	6	13
1	A	132	PRO	CA-C	8.17	1.57	1.52	4	20
1	A	121	CYS	CA-C	6.86	1.55	1.52	15	1
1	A	103	VAL	CA-C	6.53	1.58	1.52	11	9
1	A	131	ILE	CA-C	6.42	1.58	1.53	8	13
1	A	54	PRO	CA-C	6.35	1.58	1.52	13	20
1	A	51	VAL	CA-C	6.32	1.58	1.52	4	12
1	A	69	HIS	CG-CD2	5.73	1.42	1.35	1	17
1	A	134	HIS	CG-CD2	5.49	1.41	1.35	20	5
1	A	134	HIS	CE1-NE2	5.41	1.38	1.32	2	19
1	A	69	HIS	CE1-NE2	5.37	1.38	1.32	20	12
1	A	83	GLU	CA-C	5.28	1.58	1.53	20	1
1	A	61	VAL	CA-C	5.05	1.57	1.52	16	1

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	69	HIS	ND1-CE1-NE2	12.10	120.50	108.40	7	20
1	A	134	HIS	ND1-CE1-NE2	12.05	120.45	108.40	5	20
1	A	69	HIS	CE1-NE2-CD2	-10.50	98.50	109.00	14	20
1	A	134	HIS	CE1-NE2-CD2	-10.40	98.60	109.00	9	20
1	A	38	ASP	CA-CB-CG	9.46	122.06	112.60	16	7
1	A	103	VAL	N-CA-CB	8.50	117.08	110.45	2	2
1	A	69	HIS	CA-CB-CG	7.89	121.69	113.80	8	12
1	A	117	ASP	CA-CB-CG	7.39	119.99	112.60	18	6
1	A	148	ASP	CA-CB-CG	7.27	119.87	112.60	9	4
1	A	59	ARG	N-CA-C	7.25	118.48	109.57	1	2
1	A	35	GLU	N-CA-CB	-6.81	101.03	110.29	16	1
1	A	85	GLU	N-CA-CB	6.74	121.89	110.49	4	2
1	A	92	ASP	CA-CB-CG	6.74	119.34	112.60	19	1
1	A	102	SER	CA-C-N	6.63	124.42	120.24	11	7
1	A	102	SER	C-N-CA	6.63	124.42	120.24	11	7
1	A	76	ASN	CA-CB-CG	6.52	119.12	112.60	3	7
1	A	131	ILE	CB-CA-C	6.36	117.52	110.71	1	1
1	A	90	LEU	N-CA-C	6.35	119.02	111.33	19	1
1	A	40	LEU	N-CA-C	6.19	118.03	111.28	17	1
1	A	42	ASN	CA-CB-CG	6.13	118.73	112.60	1	4
1	A	75	GLU	N-CA-C	6.06	119.50	111.75	13	7
1	A	51	VAL	CB-CA-C	6.04	116.26	110.16	10	1
1	A	134	HIS	CA-CB-CG	6.03	119.83	113.80	13	4
1	A	59	ARG	CB-CA-C	5.99	116.96	108.76	5	1
1	A	100	ASP	N-CA-C	5.94	118.51	111.33	1	4
1	A	88	PHE	CA-CB-CG	5.93	119.73	113.80	20	5
1	A	136	ALA	N-CA-C	5.86	117.62	110.41	18	1
1	A	103	VAL	CA-C-O	-5.70	114.87	118.69	9	3
1	A	98	ALA	N-CA-C	5.63	117.42	111.28	19	5
1	A	69	HIS	CG-ND1-CE1	-5.62	99.74	109.30	20	20
1	A	134	HIS	CG-ND1-CE1	-5.60	99.77	109.30	5	20
1	A	100	ASP	CA-CB-CG	5.58	118.17	112.60	11	1
1	A	117	ASP	N-CA-CB	-5.55	103.45	110.45	4	1
1	A	119	LYS	N-CA-C	5.48	117.26	111.28	20	1
1	A	97	GLN	N-CA-C	5.41	117.93	111.71	13	3
1	A	79	ARG	N-CA-C	5.39	118.63	111.30	15	1
1	A	102	SER	N-CA-C	5.31	116.87	111.14	11	1
1	A	131	ILE	N-CA-C	-5.24	102.96	108.15	11	1
1	A	83	GLU	CB-CA-C	5.23	115.35	110.17	18	1
1	A	36	TRP	N-CA-CB	5.23	119.32	110.49	4	2
1	A	96	ILE	CA-CB-CG1	5.13	119.12	110.40	20	1
1	A	118	SER	N-CA-C	5.12	116.86	111.28	1	3

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	130	TYR	N-CA-C	5.12	116.86	111.28	11	1
1	A	131	ILE	CA-C-O	-5.10	117.41	120.88	4	1
1	A	121	CYS	N-CA-C	5.04	117.17	111.02	2	1
1	A	124	PRO	N-CA-CB	-5.02	99.45	102.81	18	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	46	ARG	Sidechain	5
1	A	120	TYR	Sidechain	2
1	A	118	SER	Peptide	2
1	A	37	LEU	Peptide	1
1	A	122	TYR	Sidechain	1
1	A	79	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	862	873	873	0±0
All	All	17240	17460	17460	1

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 0.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:113:MET:SD	1:A:138:CYS:SG	0.44	3.16	4	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	115/121 (95%)	87±4 (76±4%)	22±4 (19±4%)	6±2 (5±2%)	3	24
All	All	2300/2420 (95%)	1737 (76%)	447 (19%)	116 (5%)	3	24

All 33 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	43	GLY	14
1	A	119	LYS	14
1	A	77	GLY	11
1	A	41	GLY	7
1	A	129	PRO	7
1	A	128	SER	7
1	A	40	LEU	6
1	A	36	TRP	5
1	A	84	PRO	4
1	A	135	ALA	4
1	A	57	SER	4
1	A	133	PRO	4
1	A	63	GLY	3
1	A	44	LEU	2
1	A	136	ALA	2
1	A	149	GLY	2
1	A	121	CYS	2
1	A	76	ASN	2
1	A	42	ASN	2
1	A	52	PRO	1
1	A	123	GLY	1
1	A	85	GLU	1
1	A	74	LEU	1
1	A	38	ASP	1
1	A	90	LEU	1
1	A	122	TYR	1
1	A	103	VAL	1

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Mol	Chain	Res	Type	Models (Total)
1	A	105	LEU	1
1	A	125	GLN	1
1	A	126	GLY	1
1	A	83	GLU	1
1	A	75	GLU	1
1	A	110	GLU	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	98/104 (94%)	93±2 (95±2%)	5±2 (5±2%)	24	74
All	All	1960/2080 (94%)	1864 (95%)	96 (5%)	24	74

All 31 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	143	LEU	10
1	A	99	LEU	8
1	A	96	ILE	6
1	A	139	LEU	5
1	A	47	LYS	5
1	A	85	GLU	5
1	A	110	GLU	5
1	A	79	ARG	4
1	A	103	VAL	4
1	A	119	LYS	4
1	A	92	ASP	4
1	A	35	GLU	3
1	A	59	ARG	3
1	A	62	LYS	3
1	A	48	LYS	3
1	A	117	ASP	3
1	A	40	LEU	2
1	A	37	LEU	2
1	A	39	ILE	2

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Mol	Chain	Res	Type	Models (Total)
1	A	140	GLU	2
1	A	75	GLU	2
1	A	97	GLN	2
1	A	86	LEU	1
1	A	113	MET	1
1	A	127	ARG	1
1	A	82	GLU	1
1	A	38	ASP	1
1	A	74	LEU	1
1	A	90	LEU	1
1	A	137	LEU	1
1	A	64	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 oligosaccharides 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

No chemical shift data were provided