



Full wwPDB NMR Structure Validation Report ⓘ

Mar 9, 2026 – 09:35 AM UTC

PDB ID : 5N5A / pdb_00005n5a
BMRB ID : 34098
Title : Structure of Tau(254-290) bound to F-actin
Authors : Fontela, Y.C.; Kadavath, H.; Zweckstetter, M.
Deposited on : 2017-02-13

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 ⓘ 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
BMRB Restraints Analysis : v1.2
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

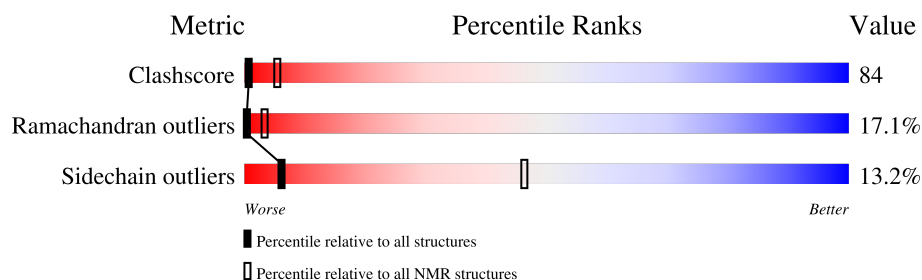
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 7%.

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	37	 16% 73% 11%

2 Ensemble composition and analysis

This entry contains 20 models. Model 10 is the overall representative, medoid model (most similar to other models). The authors have identified model 4 as representative, based on the following criterion: *closest to the average*.

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:254-A:290 (37)	2.44	10

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 14 single-model clusters were found.

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

3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 591 atoms, of which 309 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Microtubule-associated protein tau.

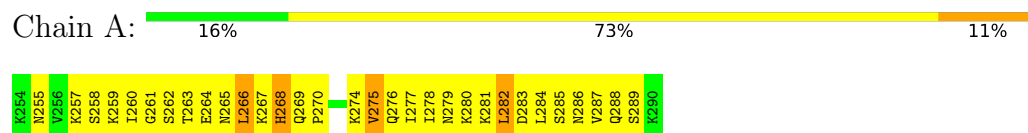
Mol	Chain	Residues	Atoms					Trace
1	A	37	Total	C	H	N	O	0
			591	174	309	54	54	

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: Microtubule-associated protein tau

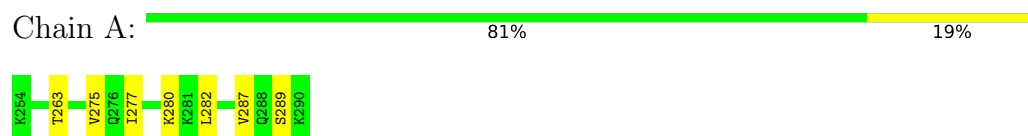


4.2 Scores per residue for each member of the ensemble

Colouring as in section [4.1](#) above.

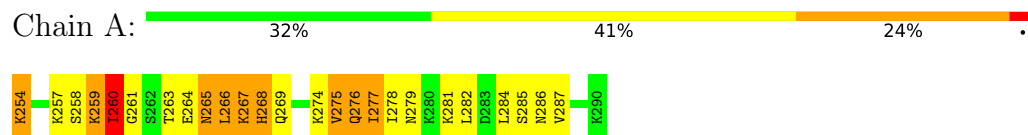
4.2.1 Score per residue for model 1

- Molecule 1: Microtubule-associated protein tau



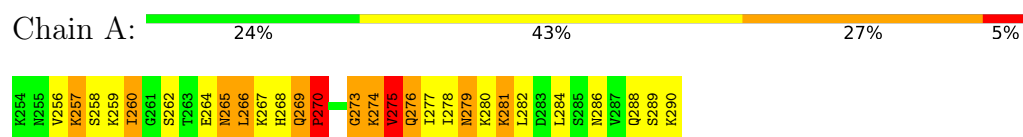
4.2.2 Score per residue for model 2

- Molecule 1: Microtubule-associated protein tau



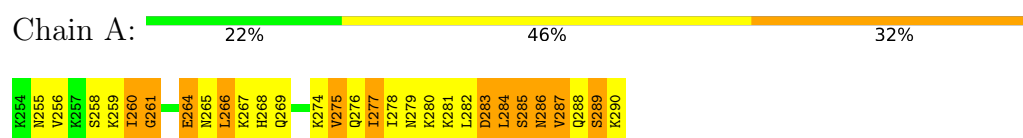
4.2.3 Score per residue for model 3

- Molecule 1: Microtubule-associated protein tau



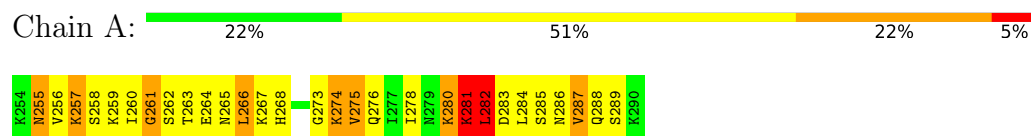
4.2.4 Score per residue for model 4

- Molecule 1: Microtubule-associated protein tau



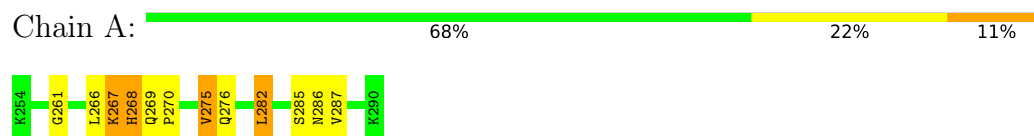
4.2.5 Score per residue for model 5

- Molecule 1: Microtubule-associated protein tau



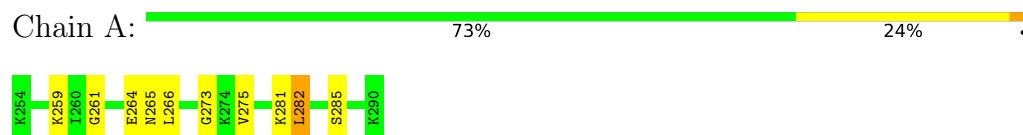
4.2.6 Score per residue for model 6

- Molecule 1: Microtubule-associated protein tau



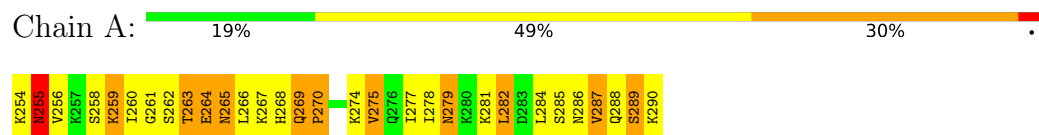
4.2.7 Score per residue for model 7

- Molecule 1: Microtubule-associated protein tau



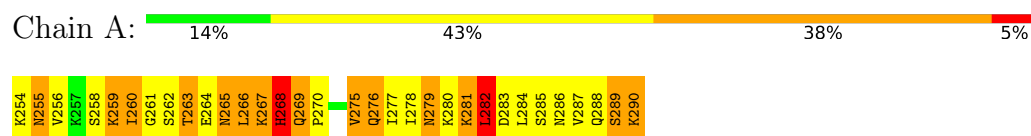
4.2.8 Score per residue for model 8

- Molecule 1: Microtubule-associated protein tau



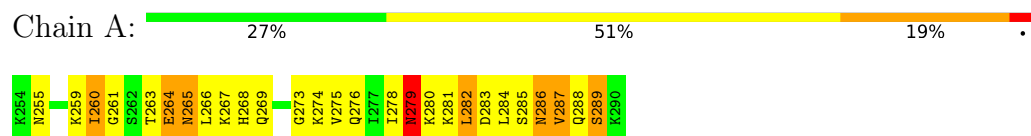
4.2.9 Score per residue for model 9

- Molecule 1: Microtubule-associated protein tau



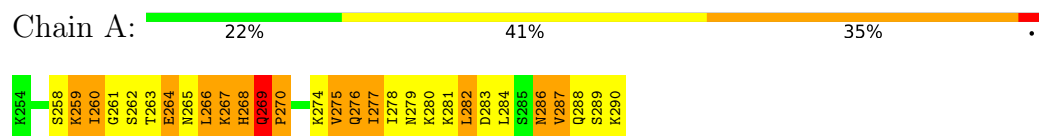
4.2.10 Score per residue for model 10 (medoid)

- Molecule 1: Microtubule-associated protein tau



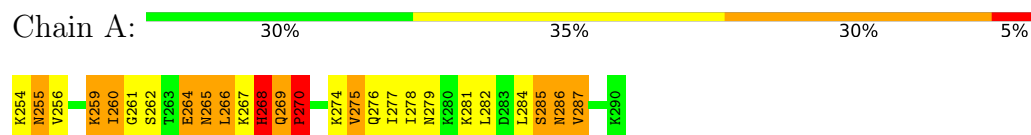
4.2.11 Score per residue for model 11

- Molecule 1: Microtubule-associated protein tau



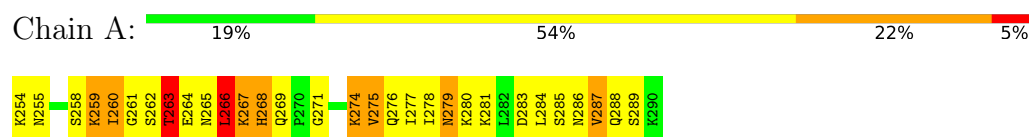
4.2.12 Score per residue for model 12

- Molecule 1: Microtubule-associated protein tau



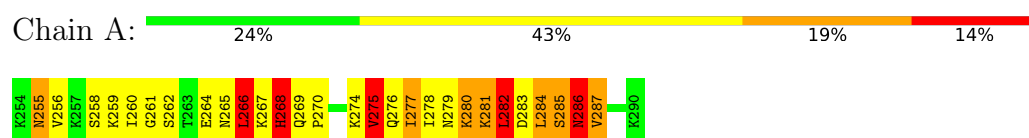
4.2.13 Score per residue for model 13

- Molecule 1: Microtubule-associated protein tau



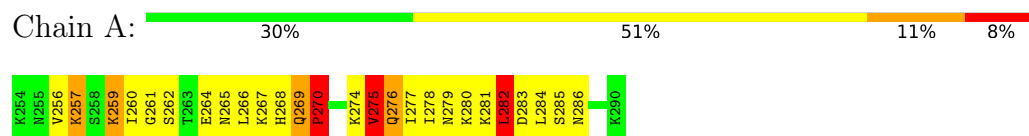
4.2.14 Score per residue for model 14

- Molecule 1: Microtubule-associated protein tau



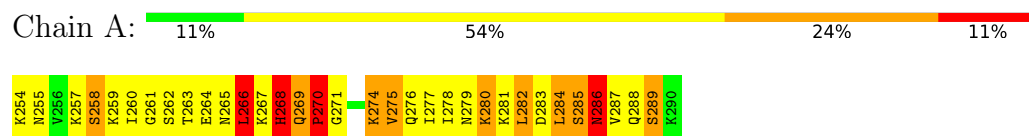
4.2.15 Score per residue for model 15

- Molecule 1: Microtubule-associated protein tau



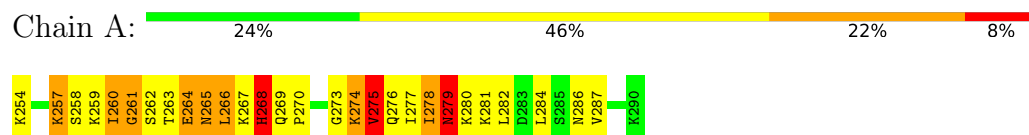
4.2.16 Score per residue for model 16

- Molecule 1: Microtubule-associated protein tau



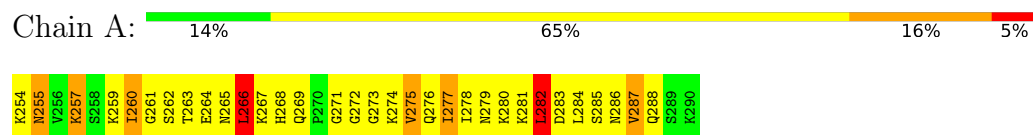
4.2.17 Score per residue for model 17

- Molecule 1: Microtubule-associated protein tau



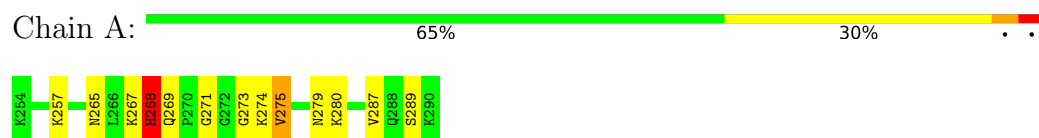
4.2.18 Score per residue for model 18

- Molecule 1: Microtubule-associated protein tau



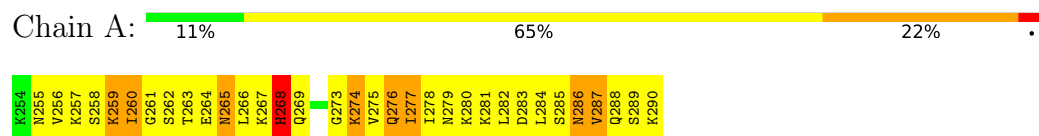
4.2.19 Score per residue for model 19

- Molecule 1: Microtubule-associated protein tau



4.2.20 Score per residue for model 20

- Molecule 1: Microtubule-associated protein tau



5 Refinement protocol and experimental data overview

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

Of the 200 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
Xplor-NIH	refinement	
CYANA	structure calculation	

The following table shows chemical shift validation statistics as aggregates over all chemical shift files. Detailed validation can be found in section 7 of this report.

Chemical shift file(s)	working_cs.cif
Number of chemical shift lists	1
Total number of shifts	36
Number of shifts mapped to atoms	36
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	7%

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	1.00±0.12	1±1/230 (0.2± 0.4%)	1.59±0.13	4±2/302 (1.4± 0.7%)
All	All	1.01	11/5574 (0.2%)	1.60	84/7346 (1.1%)

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	0.1±0.2
All	All	0	1

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	264	GLU	CA-C	-7.47	1.42	1.52	10	3
1	A	265	ASN	N-CA	-6.38	1.38	1.46	10	1
1	A	266	LEU	CA-C	6.30	1.60	1.52	14	1
1	A	268	HIS	ND1-CE1	6.27	1.38	1.32	9	1
1	A	267	LYS	CA-CB	-6.21	1.43	1.53	11	1
1	A	266	LEU	C-N	-6.21	1.25	1.34	11	1
1	A	265	ASN	C-N	-6.06	1.25	1.34	10	1
1	A	274	LYS	N-CA	-5.27	1.39	1.45	13	1
1	A	264	GLU	C-N	-5.00	1.27	1.33	10	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	268	HIS	CA-CB-CG	-16.69	97.11	113.80	19	8

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	267	LYS	N-CA-C	12.45	124.85	111.28	19	5
1	A	265	ASN	N-CA-C	-11.96	96.12	111.90	20	4
1	A	269	GLN	C-N-CD	-9.79	84.87	125.00	11	1
1	A	270	PRO	CA-N-CD	-8.59	99.97	112.00	3	4
1	A	261	GLY	N-CA-C	-8.42	102.08	113.27	5	5
1	A	286	ASN	CA-CB-CG	-8.04	104.56	112.60	10	8
1	A	274	LYS	N-CA-C	-7.88	103.67	113.20	5	4
1	A	267	LYS	CB-CA-C	-7.83	97.79	110.79	19	1
1	A	279	ASN	CA-CB-CG	-7.57	105.03	112.60	9	2
1	A	276	GLN	N-CA-C	-7.56	104.52	113.21	15	4
1	A	264	GLU	CB-CA-C	-7.39	96.95	110.63	11	2
1	A	279	ASN	N-CA-C	-6.70	103.23	111.33	10	1
1	A	281	LYS	N-CA-C	-6.69	102.00	111.56	3	1
1	A	273	GLY	N-CA-C	-6.63	106.08	115.30	3	2
1	A	255	ASN	N-CA-C	-6.49	104.21	111.28	18	5
1	A	285	SER	N-CA-C	-6.46	105.12	112.87	9	6
1	A	269	GLN	N-CA-C	-6.33	99.66	109.79	2	1
1	A	277	ILE	N-CA-C	-6.08	103.45	111.05	13	3
1	A	268	HIS	CG-CD2-NE2	6.03	113.23	107.20	9	1
1	A	265	ASN	CA-CB-CG	-5.92	106.69	112.60	9	1
1	A	266	LEU	N-CA-CB	5.89	119.29	110.22	9	1
1	A	278	ILE	N-CA-C	-5.58	105.74	113.00	17	1
1	A	280	LYS	N-CA-C	-5.58	106.47	113.28	17	4
1	A	268	HIS	N-CA-C	5.56	119.78	112.89	13	1
1	A	269	GLN	CA-C-N	5.47	125.29	119.28	8	2
1	A	269	GLN	C-N-CA	5.47	125.29	119.28	8	2
1	A	268	HIS	CB-CG-CD2	5.38	138.19	131.20	17	1
1	A	268	HIS	ND1-CE1-NE2	5.25	113.65	108.40	17	1
1	A	268	HIS	CE1-NE2-CD2	-5.23	103.77	109.00	17	1
1	A	286	ASN	N-CA-C	-5.22	104.69	111.74	20	1

There are no chirality outliers.

All unique planar outliers are listed below.

Mol	Chain	Res	Type	Group	Models (Total)
1	A	268	HIS	Sidechain	1

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	282	309	307	44±24
All	All	5640	6180	4912	884

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 84.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:265:ASN:O	1:A:268:HIS:CE1	1.22	1.92	10	7
1:A:264:GLU:O	1:A:266:LEU:N	1.19	1.72	8	5
1:A:266:LEU:O	1:A:269:GLN:NE2	1.18	1.75	11	2
1:A:276:GLN:O	1:A:279:ASN:N	1.08	1.84	11	11
1:A:265:ASN:O	1:A:268:HIS:ND1	1.07	1.88	8	3
1:A:279:ASN:HD22	1:A:279:ASN:N	1.05	1.48	17	2
1:A:266:LEU:HD13	1:A:267:LYS:N	1.05	1.66	18	2
1:A:276:GLN:C	1:A:279:ASN:ND2	1.01	2.18	17	2
1:A:266:LEU:HA	1:A:268:HIS:CE1	0.99	1.92	20	4
1:A:265:ASN:C	1:A:268:HIS:CE1	0.95	2.45	11	6
1:A:259:LYS:O	1:A:262:SER:N	0.95	1.98	20	5
1:A:259:LYS:HG2	1:A:260:ILE:H	0.94	1.22	5	2
1:A:276:GLN:O	1:A:278:ILE:N	0.94	2.01	2	4
1:A:268:HIS:ND1	1:A:269:GLN:N	0.93	2.16	12	5
1:A:274:LYS:O	1:A:276:GLN:N	0.93	2.01	4	8
1:A:276:GLN:C	1:A:279:ASN:HD21	0.91	1.70	17	1
1:A:266:LEU:HD22	1:A:267:LYS:H	0.91	1.25	13	1
1:A:279:ASN:ND2	1:A:279:ASN:H	0.90	1.46	17	1
1:A:279:ASN:ND2	1:A:280:LYS:H	0.90	1.62	3	1
1:A:281:LYS:O	1:A:283:ASP:N	0.89	2.05	5	8
1:A:286:ASN:O	1:A:288:GLN:N	0.88	2.05	8	8
1:A:266:LEU:HD23	1:A:267:LYS:N	0.87	1.83	3	3
1:A:280:LYS:O	1:A:281:LYS:HG2	0.87	1.69	14	3
1:A:257:LYS:HG3	1:A:258:SER:H	0.86	1.31	17	2
1:A:280:LYS:C	1:A:282:LEU:H	0.85	1.79	14	5
1:A:265:ASN:O	1:A:268:HIS:NE2	0.84	2.08	14	4
1:A:259:LYS:C	1:A:261:GLY:H	0.84	1.78	4	7

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:286:ASN:N	1:A:286:ASN:ND2	0.83	2.24	16	8
1:A:259:LYS:O	1:A:261:GLY:N	0.82	2.12	11	7
1:A:266:LEU:HD13	1:A:267:LYS:H	0.81	1.32	18	1
1:A:266:LEU:CA	1:A:268:HIS:CE1	0.81	2.64	17	4
1:A:274:LYS:C	1:A:276:GLN:H	0.80	1.84	18	11
1:A:262:SER:O	1:A:265:ASN:ND2	0.80	2.15	9	3
1:A:266:LEU:HD22	1:A:266:LEU:C	0.79	2.03	18	1
1:A:266:LEU:O	1:A:266:LEU:HD23	0.79	1.77	9	3
1:A:264:GLU:C	1:A:266:LEU:N	0.78	2.37	17	9
1:A:259:LYS:O	1:A:262:SER:CB	0.77	2.31	20	3
1:A:266:LEU:CD2	1:A:267:LYS:H	0.77	1.93	13	2
1:A:287:VAL:HG13	1:A:287:VAL:O	0.77	1.79	5	11
1:A:268:HIS:ND1	1:A:268:HIS:N	0.77	2.25	12	3
1:A:266:LEU:C	1:A:266:LEU:HD23	0.77	2.03	15	4
1:A:265:ASN:C	1:A:268:HIS:ND1	0.77	2.42	8	1
1:A:268:HIS:N	1:A:268:HIS:ND1	0.76	2.28	14	1
1:A:264:GLU:O	1:A:268:HIS:CE1	0.76	2.39	13	2
1:A:264:GLU:O	1:A:268:HIS:CG	0.75	2.40	3	2
1:A:259:LYS:O	1:A:262:SER:OG	0.74	2.05	16	2
1:A:266:LEU:CD1	1:A:266:LEU:N	0.74	2.51	13	1
1:A:286:ASN:N	1:A:286:ASN:HD22	0.74	1.78	16	4
1:A:261:GLY:C	1:A:263:THR:H	0.74	1.87	18	1
1:A:266:LEU:N	1:A:266:LEU:CD2	0.74	2.50	16	1
1:A:279:ASN:OD1	1:A:280:LYS:N	0.74	2.21	11	4
1:A:268:HIS:HD2	1:A:269:GLN:N	0.73	1.81	15	3
1:A:278:ILE:C	1:A:281:LYS:H	0.73	1.90	14	7
1:A:266:LEU:O	1:A:266:LEU:HD13	0.73	1.82	14	2
1:A:264:GLU:O	1:A:268:HIS:ND1	0.73	2.22	3	4
1:A:279:ASN:HD22	1:A:280:LYS:N	0.73	1.81	13	1
1:A:276:GLN:HB2	1:A:279:ASN:OD1	0.73	1.84	2	2
1:A:276:GLN:O	1:A:279:ASN:HB3	0.73	1.84	4	7
1:A:266:LEU:N	1:A:266:LEU:HD12	0.73	1.99	13	1
1:A:279:ASN:O	1:A:279:ASN:ND2	0.72	2.23	9	1
1:A:265:ASN:O	1:A:268:HIS:CG	0.72	2.42	9	3
1:A:284:LEU:C	1:A:286:ASN:H	0.72	1.92	8	15
1:A:286:ASN:HD22	1:A:286:ASN:N	0.72	1.83	12	5
1:A:278:ILE:O	1:A:281:LYS:N	0.72	2.22	18	16
1:A:268:HIS:CG	1:A:270:PRO:HD2	0.71	2.20	12	2
1:A:267:LYS:O	1:A:269:GLN:N	0.71	2.22	16	1
1:A:277:ILE:N	1:A:279:ASN:ND2	0.71	2.38	17	2
1:A:274:LYS:O	1:A:276:GLN:HG3	0.71	1.86	17	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:260:ILE:HD11	1:A:265:ASN:ND2	0.71	2.01	18	1
1:A:259:LYS:HG2	1:A:260:ILE:N	0.70	2.01	5	2
1:A:284:LEU:O	1:A:286:ASN:N	0.70	2.25	14	8
1:A:279:ASN:N	1:A:279:ASN:ND2	0.70	2.17	17	1
1:A:284:LEU:C	1:A:286:ASN:N	0.70	2.49	10	14
1:A:256:VAL:O	1:A:257:LYS:O	0.69	2.10	15	3
1:A:260:ILE:O	1:A:263:THR:N	0.69	2.24	5	4
1:A:260:ILE:C	1:A:262:SER:N	0.69	2.46	16	8
1:A:267:LYS:O	1:A:270:PRO:CD	0.69	2.40	11	1
1:A:268:HIS:NE2	1:A:269:GLN:NE2	0.69	2.39	11	1
1:A:257:LYS:O	1:A:259:LYS:N	0.69	2.25	16	1
1:A:268:HIS:CD2	1:A:269:GLN:CD	0.69	2.71	11	1
1:A:264:GLU:O	1:A:268:HIS:CD2	0.69	2.46	16	1
1:A:276:GLN:O	1:A:279:ASN:CB	0.69	2.41	15	7
1:A:264:GLU:O	1:A:265:ASN:C	0.68	2.33	14	10
1:A:268:HIS:CD2	1:A:269:GLN:N	0.68	2.61	15	3
1:A:266:LEU:C	1:A:268:HIS:CE1	0.68	2.71	12	3
1:A:279:ASN:ND2	1:A:280:LYS:N	0.67	2.42	3	2
1:A:268:HIS:CD2	1:A:269:GLN:H	0.67	2.08	11	3
1:A:266:LEU:O	1:A:268:HIS:N	0.67	2.28	2	1
1:A:284:LEU:O	1:A:286:ASN:ND2	0.67	2.28	8	4
1:A:267:LYS:O	1:A:270:PRO:CG	0.67	2.43	11	1
1:A:268:HIS:C	1:A:270:PRO:HD2	0.67	2.15	3	3
1:A:264:GLU:C	1:A:266:LEU:H	0.67	1.97	12	6
1:A:276:GLN:CB	1:A:279:ASN:HD21	0.67	2.02	17	1
1:A:277:ILE:C	1:A:279:ASN:H	0.67	1.96	2	5
1:A:276:GLN:O	1:A:279:ASN:CG	0.66	2.38	17	4
1:A:277:ILE:C	1:A:279:ASN:N	0.66	2.53	2	6
1:A:267:LYS:O	1:A:269:GLN:NE2	0.66	2.29	3	6
1:A:266:LEU:O	1:A:268:HIS:CE1	0.66	2.49	17	4
1:A:274:LYS:C	1:A:276:GLN:N	0.66	2.52	4	11
1:A:266:LEU:HD23	1:A:267:LYS:H	0.65	1.51	16	2
1:A:282:LEU:O	1:A:283:ASP:C	0.65	2.39	4	1
1:A:269:GLN:N	1:A:270:PRO:HD2	0.65	2.06	16	2
1:A:259:LYS:C	1:A:261:GLY:N	0.65	2.49	4	7
1:A:268:HIS:CD2	1:A:270:PRO:CD	0.65	2.80	15	2
1:A:268:HIS:NE2	1:A:270:PRO:HG3	0.65	2.07	8	1
1:A:266:LEU:C	1:A:268:HIS:ND1	0.65	2.55	20	4
1:A:268:HIS:NE2	1:A:269:GLN:CD	0.64	2.55	11	1
1:A:288:GLN:CD	1:A:288:GLN:H	0.64	2.00	11	2
1:A:280:LYS:C	1:A:282:LEU:N	0.64	2.55	5	4

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:268:HIS:CD2	1:A:270:PRO:N	0.64	2.66	15	2
1:A:266:LEU:N	1:A:266:LEU:HD22	0.64	2.08	16	1
1:A:264:GLU:O	1:A:267:LYS:N	0.63	2.30	14	2
1:A:273:GLY:O	1:A:274:LYS:CB	0.63	2.46	20	1
1:A:277:ILE:O	1:A:279:ASN:ND2	0.63	2.31	3	1
1:A:266:LEU:C	1:A:269:GLN:NE2	0.63	2.54	11	1
1:A:281:LYS:C	1:A:283:ASP:N	0.63	2.55	9	6
1:A:260:ILE:CD1	1:A:265:ASN:ND2	0.63	2.62	18	1
1:A:259:LYS:O	1:A:262:SER:HB3	0.63	1.93	20	1
1:A:284:LEU:HG	1:A:285:SER:H	0.63	1.53	20	2
1:A:288:GLN:N	1:A:288:GLN:CD	0.63	2.56	11	1
1:A:260:ILE:O	1:A:263:THR:HG22	0.62	1.94	9	1
1:A:276:GLN:C	1:A:278:ILE:N	0.62	2.56	2	7
1:A:267:LYS:O	1:A:270:PRO:N	0.62	2.31	11	1
1:A:260:ILE:C	1:A:262:SER:H	0.62	2.01	16	3
1:A:264:GLU:O	1:A:268:HIS:NE2	0.62	2.32	16	1
1:A:279:ASN:C	1:A:279:ASN:HD22	0.62	2.02	9	1
1:A:261:GLY:O	1:A:263:THR:N	0.62	2.33	18	1
1:A:276:GLN:HB2	1:A:279:ASN:CG	0.62	2.20	17	2
1:A:276:GLN:C	1:A:279:ASN:CG	0.62	2.68	17	1
1:A:281:LYS:CG	1:A:282:LEU:N	0.61	2.63	10	1
1:A:261:GLY:C	1:A:263:THR:N	0.61	2.56	18	1
1:A:276:GLN:CA	1:A:279:ASN:HD21	0.61	2.07	17	1
1:A:282:LEU:O	1:A:282:LEU:HD23	0.61	1.96	17	1
1:A:288:GLN:O	1:A:289:SER:CB	0.61	2.48	8	1
1:A:288:GLN:O	1:A:289:SER:C	0.60	2.44	9	2
1:A:255:ASN:C	1:A:255:ASN:HD22	0.60	2.04	8	2
1:A:255:ASN:C	1:A:255:ASN:ND2	0.60	2.59	8	2
1:A:269:GLN:N	1:A:270:PRO:CD	0.60	2.64	16	4
1:A:287:VAL:O	1:A:288:GLN:C	0.60	2.43	16	2
1:A:258:SER:O	1:A:259:LYS:C	0.60	2.43	13	5
1:A:265:ASN:O	1:A:266:LEU:O	0.60	2.19	2	2
1:A:288:GLN:O	1:A:289:SER:O	0.60	2.20	4	3
1:A:266:LEU:HD22	1:A:267:LYS:N	0.60	2.06	13	1
1:A:266:LEU:C	1:A:268:HIS:N	0.60	2.56	9	3
1:A:283:ASP:OD2	1:A:284:LEU:N	0.60	2.35	13	2
1:A:279:ASN:CG	1:A:280:LYS:N	0.59	2.60	16	7
1:A:275:VAL:HG22	1:A:275:VAL:O	0.59	1.96	5	1
1:A:266:LEU:HD22	1:A:266:LEU:O	0.59	1.96	18	1
1:A:259:LYS:O	1:A:262:SER:CA	0.59	2.50	20	1
1:A:279:ASN:HD22	1:A:279:ASN:H	0.59	0.71	17	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:287:VAL:O	1:A:287:VAL:CG1	0.59	2.50	18	10
1:A:259:LYS:O	1:A:260:ILE:C	0.59	2.44	20	4
1:A:259:LYS:HB2	1:A:261:GLY:H	0.59	1.57	10	1
1:A:288:GLN:CD	1:A:288:GLN:N	0.59	2.61	18	1
1:A:257:LYS:CG	1:A:258:SER:H	0.59	2.09	17	1
1:A:276:GLN:HB2	1:A:279:ASN:ND2	0.59	2.11	17	1
1:A:262:SER:O	1:A:265:ASN:CG	0.58	2.46	8	7
1:A:286:ASN:O	1:A:287:VAL:C	0.58	2.45	8	5
1:A:264:GLU:OE1	1:A:267:LYS:CE	0.58	2.52	8	1
1:A:275:VAL:HG12	1:A:276:GLN:NE2	0.58	2.14	13	2
1:A:266:LEU:CG	1:A:267:LYS:H	0.58	2.12	16	2
1:A:260:ILE:O	1:A:262:SER:N	0.58	2.37	16	2
1:A:276:GLN:CB	1:A:279:ASN:ND2	0.58	2.67	17	1
1:A:254:LYS:O	1:A:257:LYS:NZ	0.57	2.37	2	1
1:A:263:THR:O	1:A:266:LEU:N	0.57	2.37	2	1
1:A:283:ASP:OD2	1:A:286:ASN:ND2	0.57	2.38	4	1
1:A:267:LYS:O	1:A:270:PRO:CB	0.57	2.52	11	1
1:A:288:GLN:HG3	1:A:289:SER:H	0.57	1.60	3	1
1:A:268:HIS:C	1:A:270:PRO:N	0.57	2.61	16	1
1:A:276:GLN:NE2	1:A:279:ASN:CG	0.57	2.63	9	1
1:A:282:LEU:O	1:A:282:LEU:CD1	0.57	2.53	8	2
1:A:274:LYS:O	1:A:276:GLN:CG	0.57	2.53	17	1
1:A:266:LEU:C	1:A:266:LEU:CD1	0.56	2.78	14	2
1:A:281:LYS:C	1:A:283:ASP:H	0.56	2.07	14	4
1:A:266:LEU:HA	1:A:269:GLN:HE22	0.56	1.60	11	1
1:A:279:ASN:CG	1:A:280:LYS:H	0.56	2.08	3	1
1:A:266:LEU:HD23	1:A:266:LEU:C	0.56	2.25	12	3
1:A:266:LEU:HD21	1:A:268:HIS:CD2	0.56	2.35	2	1
1:A:266:LEU:O	1:A:267:LYS:C	0.56	2.49	2	2
1:A:266:LEU:C	1:A:266:LEU:CD2	0.56	2.75	18	5
1:A:268:HIS:CE1	1:A:270:PRO:HD3	0.56	2.35	17	3
1:A:266:LEU:HD23	1:A:266:LEU:O	0.56	1.99	10	2
1:A:276:GLN:O	1:A:279:ASN:OD1	0.56	2.24	17	2
1:A:273:GLY:O	1:A:279:ASN:OD1	0.56	2.24	17	1
1:A:274:LYS:HG2	1:A:275:VAL:H	0.56	1.59	20	1
1:A:289:SER:O	1:A:290:LYS:C	0.56	2.49	11	4
1:A:276:GLN:O	1:A:279:ASN:CA	0.55	2.54	11	3
1:A:286:ASN:H	1:A:286:ASN:HD22	0.55	1.44	10	1
1:A:255:ASN:O	1:A:258:SER:O	0.55	2.24	14	1
1:A:266:LEU:O	1:A:266:LEU:CD1	0.55	2.54	14	1
1:A:276:GLN:O	1:A:279:ASN:ND2	0.55	2.38	12	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:278:ILE:O	1:A:279:ASN:C	0.55	2.49	10	8
1:A:276:GLN:O	1:A:279:ASN:HB2	0.55	2.00	9	1
1:A:266:LEU:CD1	1:A:266:LEU:O	0.55	2.55	4	1
1:A:268:HIS:NE2	1:A:269:GLN:OE1	0.55	2.40	11	1
1:A:268:HIS:CE1	1:A:269:GLN:H	0.55	2.19	12	1
1:A:274:LYS:O	1:A:276:GLN:NE2	0.55	2.39	5	3
1:A:278:ILE:N	1:A:279:ASN:HD22	0.55	2.00	17	1
1:A:254:LYS:HG2	1:A:255:ASN:H	0.55	1.62	18	1
1:A:268:HIS:C	1:A:270:PRO:CD	0.55	2.80	12	1
1:A:279:ASN:ND2	1:A:279:ASN:C	0.54	2.56	9	2
1:A:286:ASN:O	1:A:288:GLN:OE1	0.54	2.25	18	2
1:A:289:SER:O	1:A:290:LYS:CB	0.54	2.55	3	1
1:A:266:LEU:O	1:A:269:GLN:N	0.54	2.35	9	2
1:A:259:LYS:CG	1:A:260:ILE:H	0.54	2.04	5	1
1:A:266:LEU:CD1	1:A:267:LYS:N	0.54	2.58	18	1
1:A:280:LYS:O	1:A:282:LEU:N	0.54	2.38	14	2
1:A:271:GLY:O	1:A:272:GLY:C	0.54	2.48	18	1
1:A:257:LYS:HG3	1:A:258:SER:N	0.54	2.12	17	3
1:A:288:GLN:NE2	1:A:289:SER:H	0.54	2.01	11	1
1:A:282:LEU:HD23	1:A:282:LEU:C	0.53	2.28	17	4
1:A:284:LEU:HG	1:A:286:ASN:H	0.53	1.64	9	3
1:A:263:THR:O	1:A:266:LEU:HD13	0.53	2.03	16	1
1:A:286:ASN:C	1:A:288:GLN:N	0.53	2.65	8	1
1:A:276:GLN:NE2	1:A:279:ASN:OD1	0.53	2.41	9	1
1:A:276:GLN:C	1:A:279:ASN:H	0.53	2.11	12	6
1:A:255:ASN:HD22	1:A:256:VAL:N	0.53	2.01	14	2
1:A:281:LYS:O	1:A:282:LEU:C	0.53	2.52	10	6
1:A:268:HIS:CD2	1:A:268:HIS:N	0.53	2.72	11	1
1:A:265:ASN:C	1:A:268:HIS:HD1	0.53	2.08	8	1
1:A:283:ASP:O	1:A:286:ASN:ND2	0.53	2.43	20	1
1:A:263:THR:HG23	1:A:267:LYS:HE3	0.52	1.79	18	1
1:A:275:VAL:CG1	1:A:275:VAL:O	0.52	2.57	17	1
1:A:275:VAL:CG1	1:A:276:GLN:NE2	0.52	2.72	13	2
1:A:266:LEU:HD13	1:A:266:LEU:C	0.52	2.28	14	2
1:A:265:ASN:O	1:A:266:LEU:C	0.52	2.51	2	3
1:A:257:LYS:O	1:A:258:SER:C	0.52	2.52	16	1
1:A:273:GLY:O	1:A:276:GLN:O	0.52	2.27	10	2
1:A:264:GLU:O	1:A:266:LEU:CB	0.52	2.57	8	2
1:A:262:SER:O	1:A:265:ASN:OD1	0.51	2.27	16	2
1:A:286:ASN:ND2	1:A:286:ASN:N	0.51	2.58	8	1
1:A:254:LYS:HB3	1:A:256:VAL:HG12	0.51	1.82	12	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:258:SER:O	1:A:259:LYS:O	0.51	2.28	13	3
1:A:260:ILE:O	1:A:261:GLY:C	0.51	2.53	5	4
1:A:275:VAL:CG1	1:A:276:GLN:HE22	0.51	2.18	13	2
1:A:275:VAL:C	1:A:277:ILE:H	0.51	2.13	15	1
1:A:268:HIS:HD2	1:A:269:GLN:H	0.51	1.39	11	2
1:A:258:SER:C	1:A:260:ILE:N	0.51	2.67	4	1
1:A:258:SER:O	1:A:259:LYS:HB3	0.51	2.06	17	1
1:A:267:LYS:O	1:A:269:GLN:CG	0.51	2.59	9	1
1:A:265:ASN:HA	1:A:268:HIS:NE2	0.51	2.21	13	1
1:A:264:GLU:O	1:A:266:LEU:CA	0.51	2.57	8	1
1:A:277:ILE:N	1:A:279:ASN:HD21	0.51	2.00	17	1
1:A:289:SER:O	1:A:290:LYS:O	0.51	2.29	9	1
1:A:266:LEU:HD12	1:A:266:LEU:H	0.50	1.65	13	1
1:A:259:LYS:O	1:A:260:ILE:HG12	0.50	2.06	10	1
1:A:268:HIS:CD2	1:A:270:PRO:HD2	0.50	2.42	3	2
1:A:273:GLY:C	1:A:275:VAL:H	0.50	2.15	5	1
1:A:278:ILE:O	1:A:281:LYS:CA	0.50	2.60	14	6
1:A:267:LYS:O	1:A:269:GLN:CD	0.50	2.54	14	3
1:A:263:THR:CG2	1:A:264:GLU:N	0.50	2.74	9	2
1:A:267:LYS:C	1:A:269:GLN:N	0.49	2.69	8	3
1:A:268:HIS:CD2	1:A:269:GLN:OE1	0.49	2.65	11	1
1:A:266:LEU:CA	1:A:269:GLN:HE22	0.49	2.19	11	1
1:A:274:LYS:C	1:A:275:VAL:HG23	0.49	2.32	15	3
1:A:276:GLN:O	1:A:277:ILE:C	0.49	2.54	2	8
1:A:279:ASN:OD1	1:A:279:ASN:C	0.49	2.55	8	3
1:A:264:GLU:HB3	1:A:268:HIS:N	0.49	2.21	12	1
1:A:255:ASN:OD1	1:A:256:VAL:HG23	0.49	2.08	20	1
1:A:265:ASN:O	1:A:268:HIS:CD2	0.49	2.66	4	3
1:A:260:ILE:HG13	1:A:261:GLY:H	0.49	1.67	9	1
1:A:261:GLY:O	1:A:265:ASN:N	0.49	2.45	20	1
1:A:266:LEU:CD2	1:A:268:HIS:CD2	0.49	2.96	2	1
1:A:259:LYS:O	1:A:260:ILE:HG13	0.49	2.07	3	1
1:A:259:LYS:HD2	1:A:261:GLY:H	0.49	1.68	15	1
1:A:274:LYS:O	1:A:275:VAL:HG12	0.49	2.08	5	1
1:A:282:LEU:O	1:A:282:LEU:HD13	0.48	2.07	8	1
1:A:265:ASN:C	1:A:268:HIS:CD2	0.48	2.91	17	1
1:A:279:ASN:HD22	1:A:279:ASN:C	0.48	2.15	13	1
1:A:266:LEU:HD22	1:A:266:LEU:H	0.48	1.65	16	1
1:A:260:ILE:HG23	1:A:263:THR:OG1	0.48	2.08	17	1
1:A:266:LEU:O	1:A:268:HIS:ND1	0.48	2.46	9	2
1:A:269:GLN:N	1:A:270:PRO:HD3	0.48	2.24	8	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:278:ILE:C	1:A:280:LYS:N	0.48	2.67	10	1
1:A:263:THR:O	1:A:266:LEU:HB3	0.47	2.09	2	1
1:A:259:LYS:O	1:A:262:SER:HB2	0.47	2.09	5	2
1:A:282:LEU:CD1	1:A:282:LEU:C	0.47	2.86	8	1
1:A:279:ASN:ND2	1:A:279:ASN:N	0.47	2.61	3	1
1:A:261:GLY:O	1:A:264:GLU:HB2	0.47	2.09	8	2
1:A:263:THR:HG22	1:A:267:LYS:HB2	0.47	1.86	5	1
1:A:286:ASN:HD22	1:A:286:ASN:H	0.47	1.47	16	4
1:A:289:SER:O	1:A:290:LYS:HB3	0.47	2.08	3	1
1:A:255:ASN:OD1	1:A:255:ASN:C	0.47	2.58	5	4
1:A:266:LEU:O	1:A:270:PRO:CD	0.47	2.62	8	1
1:A:254:LYS:HG2	1:A:255:ASN:N	0.47	2.25	16	1
1:A:262:SER:C	1:A:264:GLU:H	0.47	2.17	13	1
1:A:282:LEU:HD23	1:A:282:LEU:O	0.47	2.09	2	2
1:A:284:LEU:HG	1:A:285:SER:N	0.47	2.23	20	4
1:A:268:HIS:NE2	1:A:270:PRO:CG	0.47	2.75	8	1
1:A:265:ASN:C	1:A:267:LYS:N	0.47	2.72	11	1
1:A:288:GLN:CG	1:A:289:SER:N	0.47	2.77	13	1
1:A:278:ILE:C	1:A:281:LYS:N	0.47	2.69	14	1
1:A:255:ASN:C	1:A:255:ASN:OD1	0.47	2.58	9	2
1:A:257:LYS:HD3	1:A:257:LYS:H	0.46	1.70	18	1
1:A:276:GLN:C	1:A:278:ILE:H	0.46	2.15	5	4
1:A:268:HIS:CD2	1:A:270:PRO:HD3	0.46	2.45	8	1
1:A:279:ASN:C	1:A:281:LYS:N	0.46	2.68	9	1
1:A:266:LEU:HA	1:A:268:HIS:NE2	0.46	2.25	11	1
1:A:275:VAL:O	1:A:275:VAL:CG1	0.46	2.63	14	1
1:A:273:GLY:O	1:A:274:LYS:C	0.46	2.58	18	1
1:A:265:ASN:N	1:A:265:ASN:HD22	0.46	2.07	4	1
1:A:287:VAL:O	1:A:289:SER:O	0.46	2.33	16	1
1:A:266:LEU:N	1:A:268:HIS:CD2	0.46	2.84	17	1
1:A:268:HIS:CD2	1:A:270:PRO:HG3	0.46	2.46	8	1
1:A:265:ASN:O	1:A:267:LYS:N	0.46	2.49	11	1
1:A:265:ASN:O	1:A:268:HIS:CB	0.45	2.63	9	1
1:A:261:GLY:O	1:A:264:GLU:N	0.45	2.50	20	2
1:A:268:HIS:ND1	1:A:268:HIS:C	0.45	2.62	17	1
1:A:259:LYS:O	1:A:260:ILE:CB	0.45	2.65	10	2
1:A:274:LYS:C	1:A:275:VAL:HG12	0.45	2.37	5	2
1:A:267:LYS:O	1:A:269:GLN:HG2	0.45	2.12	9	1
1:A:278:ILE:HG23	1:A:281:LYS:CB	0.45	2.42	12	1
1:A:275:VAL:HG12	1:A:276:GLN:HE22	0.45	1.69	13	1
1:A:274:LYS:HB3	1:A:276:GLN:HG2	0.45	1.87	18	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:266:LEU:N	1:A:268:HIS:CE1	0.45	2.85	8	2
1:A:278:ILE:O	1:A:281:LYS:HA	0.45	2.11	14	1
1:A:259:LYS:O	1:A:260:ILE:CG1	0.45	2.65	3	1
1:A:288:GLN:HG3	1:A:289:SER:N	0.45	2.25	3	2
1:A:274:LYS:O	1:A:275:VAL:CG1	0.45	2.65	5	2
1:A:284:LEU:CG	1:A:285:SER:H	0.45	2.25	4	1
1:A:269:GLN:O	1:A:270:PRO:C	0.45	2.60	11	1
1:A:273:GLY:O	1:A:274:LYS:HB2	0.45	2.11	20	1
1:A:281:LYS:O	1:A:283:ASP:O	0.44	2.34	11	1
1:A:261:GLY:O	1:A:264:GLU:HG3	0.44	2.11	17	1
1:A:281:LYS:HG3	1:A:282:LEU:N	0.44	2.24	10	1
1:A:258:SER:O	1:A:259:LYS:CB	0.44	2.65	17	1
1:A:262:SER:C	1:A:264:GLU:N	0.44	2.75	13	1
1:A:254:LYS:CG	1:A:255:ASN:H	0.44	2.25	13	1
1:A:266:LEU:CG	1:A:267:LYS:N	0.44	2.81	16	2
1:A:267:LYS:C	1:A:269:GLN:H	0.44	2.19	8	1
1:A:268:HIS:O	1:A:269:GLN:OE1	0.43	2.36	13	1
1:A:276:GLN:HB2	1:A:279:ASN:HB3	0.43	1.90	13	1
1:A:274:LYS:O	1:A:275:VAL:HB	0.43	2.13	8	1
1:A:266:LEU:C	1:A:268:HIS:H	0.43	2.21	9	1
1:A:269:GLN:O	1:A:271:GLY:O	0.43	2.36	13	1
1:A:277:ILE:CD1	1:A:277:ILE:H	0.43	2.26	4	1
1:A:282:LEU:O	1:A:283:ASP:O	0.43	2.36	4	1
1:A:258:SER:C	1:A:259:LYS:O	0.43	2.62	8	1
1:A:260:ILE:HD11	1:A:265:ASN:HD21	0.43	1.70	18	1
1:A:276:GLN:O	1:A:278:ILE:C	0.43	2.56	2	1
1:A:260:ILE:HG22	1:A:260:ILE:O	0.43	2.13	3	1
1:A:256:VAL:C	1:A:257:LYS:O	0.43	2.62	15	1
1:A:266:LEU:HD21	1:A:268:HIS:NE2	0.43	2.29	2	1
1:A:275:VAL:O	1:A:275:VAL:CG2	0.43	2.66	5	1
1:A:281:LYS:O	1:A:283:ASP:CB	0.43	2.66	10	1
1:A:265:ASN:OD1	1:A:265:ASN:C	0.43	2.61	16	1
1:A:268:HIS:O	1:A:269:GLN:C	0.43	2.62	16	1
1:A:257:LYS:HG3	1:A:259:LYS:H	0.43	1.74	20	1
1:A:277:ILE:HA	1:A:279:ASN:HD22	0.42	1.73	2	1
1:A:287:VAL:CG1	1:A:288:GLN:N	0.42	2.83	16	2
1:A:267:LYS:CD	1:A:269:GLN:HE21	0.42	2.27	16	1
1:A:266:LEU:CA	1:A:268:HIS:NE2	0.42	2.81	11	1
1:A:259:LYS:O	1:A:259:LYS:HG2	0.42	2.14	17	1
1:A:256:VAL:O	1:A:259:LYS:CG	0.42	2.67	4	1
1:A:266:LEU:HA	1:A:268:HIS:ND1	0.42	2.28	9	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:288:GLN:C	1:A:289:SER:O	0.42	2.60	16	2
1:A:274:LYS:O	1:A:275:VAL:C	0.42	2.63	11	1
1:A:287:VAL:HG13	1:A:288:GLN:N	0.42	2.28	16	1
1:A:274:LYS:O	1:A:276:GLN:HG2	0.42	2.14	3	1
1:A:280:LYS:HE3	1:A:282:LEU:HD23	0.42	1.91	9	1
1:A:263:THR:O	1:A:263:THR:CG2	0.42	2.66	13	1
1:A:259:LYS:HG3	1:A:260:ILE:N	0.41	2.30	2	1
1:A:265:ASN:C	1:A:266:LEU:O	0.41	2.63	2	1
1:A:273:GLY:C	1:A:275:VAL:N	0.41	2.74	5	2
1:A:268:HIS:O	1:A:269:GLN:HB2	0.41	2.15	15	1
1:A:266:LEU:CD2	1:A:267:LYS:N	0.41	2.77	16	1
1:A:283:ASP:HB3	1:A:286:ASN:HD21	0.41	1.76	20	1
1:A:289:SER:OG	1:A:290:LYS:N	0.41	2.54	4	1
1:A:257:LYS:O	1:A:257:LYS:HG3	0.41	2.15	16	1
1:A:275:VAL:HG13	1:A:276:GLN:HG2	0.41	1.91	9	1
1:A:274:LYS:HG2	1:A:275:VAL:N	0.41	2.28	20	1
1:A:282:LEU:O	1:A:282:LEU:HD12	0.41	2.16	5	1
1:A:257:LYS:CG	1:A:258:SER:N	0.41	2.78	17	1
1:A:266:LEU:O	1:A:270:PRO:HD2	0.40	2.15	8	1
1:A:286:ASN:O	1:A:288:GLN:HG3	0.40	2.14	8	1
1:A:254:LYS:HD2	1:A:256:VAL:HG12	0.40	1.92	9	1
1:A:268:HIS:CD2	1:A:270:PRO:CG	0.40	3.04	15	1
1:A:277:ILE:CA	1:A:279:ASN:HD22	0.40	2.30	2	1
1:A:265:ASN:N	1:A:265:ASN:ND2	0.40	2.68	4	1
1:A:254:LYS:O	1:A:257:LYS:CG	0.40	2.68	17	1
1:A:258:SER:O	1:A:260:ILE:HG12	0.40	2.16	9	1
1:A:275:VAL:C	1:A:277:ILE:N	0.40	2.75	15	1
1:A:268:HIS:CE1	1:A:269:GLN:N	0.40	2.86	12	1
1:A:282:LEU:C	1:A:282:LEU:HD23	0.40	2.42	20	1

6.3 Torsion angles ⓘ

6.3.1 Protein backbone ⓘ

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	35/37 (95%)	24±2 (70±7%)	4±2 (12±5%)	6±1 (17±4%)	0 3

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	689/740 (93%)	488 (71%)	83 (12%)	118 (17%)	0 3

All 25 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	275	VAL	19
1	A	287	VAL	13
1	A	260	ILE	12
1	A	282	LEU	10
1	A	285	SER	8
1	A	289	SER	7
1	A	259	LYS	6
1	A	266	LEU	6
1	A	257	LYS	5
1	A	269	GLN	5
1	A	277	ILE	4
1	A	265	ASN	4
1	A	281	LYS	3
1	A	267	LYS	2
1	A	264	GLU	2
1	A	268	HIS	2
1	A	271	GLY	2
1	A	283	ASP	1
1	A	284	LEU	1
1	A	270	PRO	1
1	A	263	THR	1
1	A	258	SER	1
1	A	273	GLY	1
1	A	274	LYS	1
1	A	276	GLN	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	33/33 (100%)	27±4 (83±12%)	4±2 (13±7%)	6 48

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	630/660 (95%)	547 (87%)	83 (13%)	6 46

All 24 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	282	LEU	9
1	A	268	HIS	9
1	A	266	LEU	9
1	A	275	VAL	9
1	A	270	PRO	6
1	A	279	ASN	6
1	A	263	THR	5
1	A	259	LYS	3
1	A	269	GLN	3
1	A	260	ILE	2
1	A	276	GLN	2
1	A	277	ILE	2
1	A	281	LYS	2
1	A	267	LYS	2
1	A	255	ASN	2
1	A	284	LEU	2
1	A	286	ASN	2
1	A	280	LYS	2
1	A	254	LYS	1
1	A	290	LYS	1
1	A	285	SER	1
1	A	274	LYS	1
1	A	257	LYS	1
1	A	265	ASN	1

6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

6.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

The completeness of assignment taking into account all chemical shift lists is 7% for the well-defined parts and 7% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *Tau254-290_Factin_shift.tab*

7.1.1 Bookkeeping

The following table shows the results of parsing the chemical shift list and reports the number of nuclei with statistically unusual chemical shifts.

Total number of shifts	36
Number of shifts mapped to atoms	36
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

7.1.2 Chemical shift referencing

No chemical shift referencing corrections were calculated (not enough data).

7.1.3 Completeness of resonance assignments

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 7%, i.e. 35 atoms were assigned a chemical shift out of a possible 506. 0 out of 6 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	35/187 (19%)	35/77 (45%)	0/74 (0%)	0/36 (0%)
Sidechain	0/311 (0%)	0/199 (0%)	0/97 (0%)	0/15 (0%)
Aromatic	0/8 (0%)	0/4 (0%)	0/2 (0%)	0/2 (0%)
Overall	35/506 (7%)	35/280 (12%)	0/173 (0%)	0/53 (0%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 7%, i.e. 35 atoms were assigned a chemical shift out of a possible 506. 0 out of 6 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	35/187 (19%)	35/77 (45%)	0/74 (0%)	0/36 (0%)
Sidechain	0/311 (0%)	0/199 (0%)	0/97 (0%)	0/15 (0%)
Aromatic	0/8 (0%)	0/4 (0%)	0/2 (0%)	0/2 (0%)
Overall	35/506 (7%)	35/280 (12%)	0/173 (0%)	0/53 (0%)

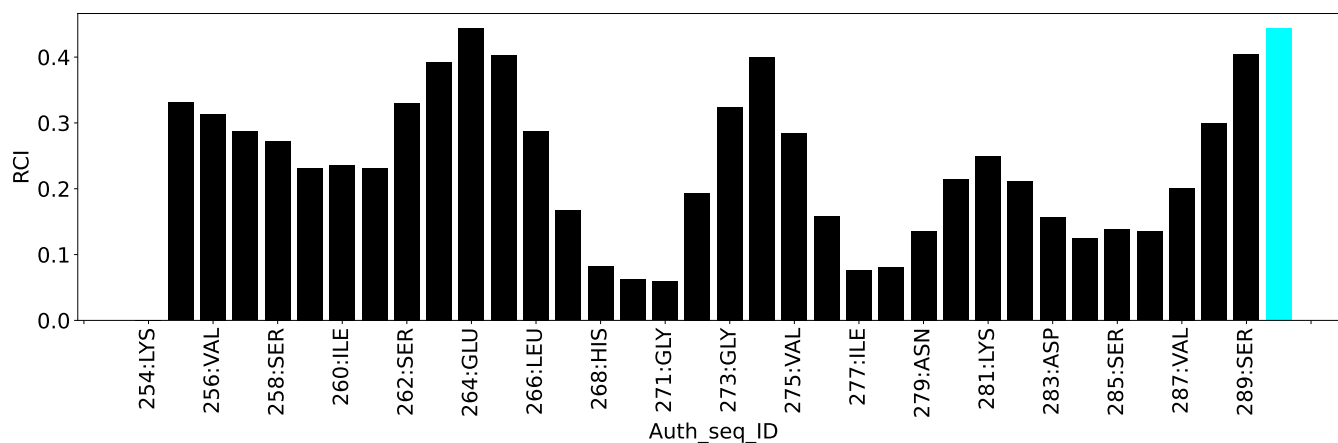
7.1.4 Statistically unusual chemical shifts [i](#)

There are no statistically unusual chemical shifts.

7.1.5 Random Coil Index (RCI) plots [i](#)

The image below reports *random coil index* values for the protein chains in the structure. The height of each bar gives a probability of a given residue to be disordered, as predicted from the available chemical shifts and the amino acid sequence. A value above 0.2 is an indication of significant predicted disorder. The colour of the bar shows whether the residue is in the well-defined core (black) or in the ill-defined residue ranges (cyan), as described in section 2 on ensemble composition. If well-defined core and ill-defined regions are not identified then it is shown as gray bars.

Random coil index (RCI) for chain A:



8 NMR restraints analysis

8.1 Conformationally restricting restraints

The following table provides the summary of experimentally observed NMR restraints in different categories. Restraints are classified into different categories based on the sequence separation of the atoms involved.

Description	Value
Total distance restraints	182
Intra-residue ($ i-j =0$)	0
Sequential ($ i-j =1$)	0
Medium range ($ i-j >1$ and $ i-j <5$)	182
Long range ($ i-j \geq 5$)	0
Inter-chain	0
Hydrogen bond restraints	0
Disulfide bond restraints	0
Total dihedral-angle restraints	0
Number of unmapped restraints	0
Number of restraints per residue	4.9
Number of long range restraints per residue ¹	0.0

¹Long range hydrogen bonds and disulfide bonds are counted as long range restraints while calculating the number of long range restraints per residue

8.2 Residual restraint violations

This section provides the overview of the restraint violations analysis. The violations are binned as small, medium and large violations based on its absolute value. Average number of violations per model is calculated by dividing the total number of violations in each bin by the size of the ensemble.

8.2.1 Average number of distance violations per model

Distance violations less than 0.1 Å are not included in the calculation.

Bins (Å)	Average number of violations per model	Max (Å)
0.1-0.2 (Small)	3.8	0.2
0.2-0.5 (Medium)	0.3	0.27
>0.5 (Large)	None	None

8.2.2 Average number of dihedral-angle violations per model [i](#)

Dihedral-angle violations less than 1° are not included in the calculation. There are no dihedral-angle violations

9 Distance violation analysis

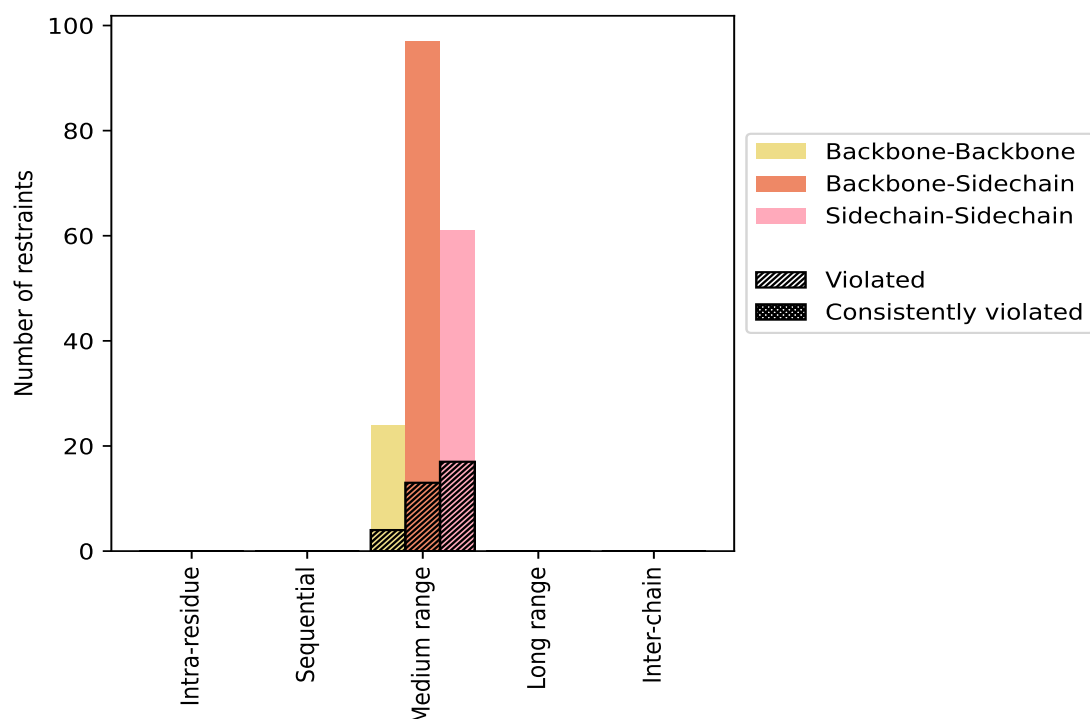
9.1 Summary of distance violations

The following table shows the summary of distance violations in different restraint categories based on the sequence separation of the atoms involved. Each category is further sub-divided into three sub-categories based on the atoms involved. Violations less than 0.1 Å are not included in the statistics.

Restrains type	Count	% ¹	Violated ³			Consistently Violated ⁴		
			Count	% ²	% ¹	Count	% ²	% ¹
Intra-residue (i-j =0)	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Sequential (i-j =1)	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Medium range (i-j >1 & i-j <5)	182	100.0	34	18.7	18.7	0	0.0	0.0
Backbone-Backbone	24	13.2	4	16.7	2.2	0	0.0	0.0
Backbone-Sidechain	97	53.3	13	13.4	7.1	0	0.0	0.0
Sidechain-Sidechain	61	33.5	17	27.9	9.3	0	0.0	0.0
Long range (i-j ≥5)	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Inter-chain	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Hydrogen bond	0	0.0	0	0.0	0.0	0	0.0	0.0
Disulfide bond	0	0.0	0	0.0	0.0	0	0.0	0.0
Total	182	100.0	34	18.7	18.7	0	0.0	0.0
Backbone-Backbone	24	13.2	4	16.7	2.2	0	0.0	0.0
Backbone-Sidechain	97	53.3	13	13.4	7.1	0	0.0	0.0
Sidechain-Sidechain	61	33.5	17	27.9	9.3	0	0.0	0.0

¹ percentage calculated with respect to the total number of distance restraints, ² percentage calculated with respect to the number of restraints in a particular restraint category, ³ violated in at least one model, ⁴ violated in all the models

9.1.1 Bar chart : Distribution of distance restraints and violations [i](#)



Violated and consistently violated restraints are shown using different hatch patterns in their respective categories. The hydrogen bonds and disulfied bonds are counted in their appropriate category on the x-axis

9.2 Distance violation statistics for each model [i](#)

The following table provides the distance violation statistics for each model in the ensemble. Violations less than 0.1 Å are not included in the statistics.

Model ID	Number of violations						Mean (Å)	Max (Å)	SD ⁶ (Å)	Median (Å)
	IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total				
1	0	0	2	0	0	2	0.14	0.15	0.02	0.14
2	0	0	2	0	0	2	0.16	0.19	0.03	0.16
3	0	0	4	0	0	4	0.14	0.17	0.03	0.14
4	0	0	4	0	0	4	0.14	0.18	0.03	0.14
5	0	0	4	0	0	4	0.14	0.16	0.02	0.14
6	0	0	4	0	0	4	0.12	0.13	0.01	0.12
7	0	0	4	0	0	4	0.14	0.18	0.02	0.13
8	0	0	5	0	0	5	0.12	0.15	0.02	0.12
9	0	0	5	0	0	5	0.14	0.18	0.02	0.14
10	0	0	2	0	0	2	0.15	0.17	0.02	0.15

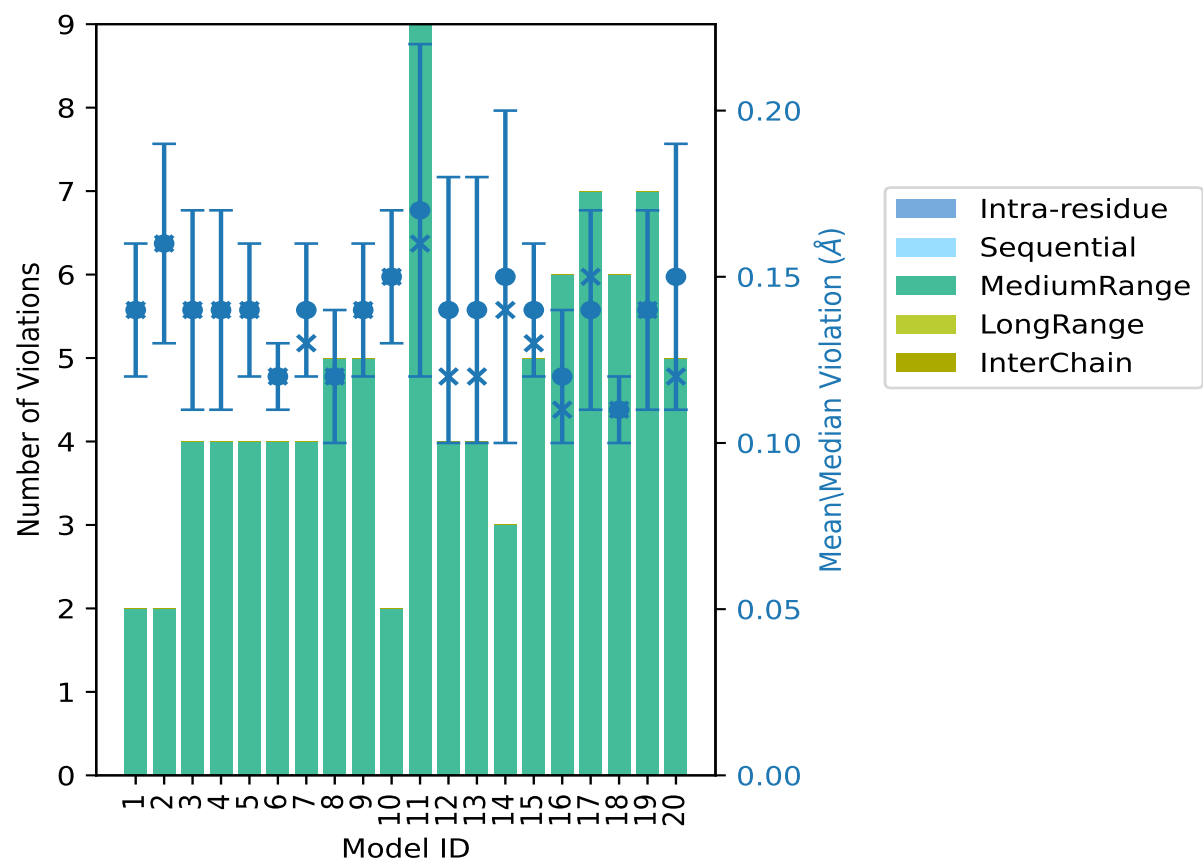
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Model ID	Number of violations						Mean (Å)	Max (Å)	SD ⁶ (Å)	Median (Å)
	IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total				
11	0	0	9	0	0	9	0.17	0.27	0.05	0.16
12	0	0	4	0	0	4	0.14	0.22	0.04	0.12
13	0	0	4	0	0	4	0.14	0.2	0.04	0.12
14	0	0	3	0	0	3	0.15	0.22	0.05	0.14
15	0	0	5	0	0	5	0.14	0.18	0.02	0.13
16	0	0	6	0	0	6	0.12	0.16	0.02	0.11
17	0	0	7	0	0	7	0.14	0.19	0.03	0.15
18	0	0	6	0	0	6	0.11	0.14	0.01	0.11
19	0	0	7	0	0	7	0.14	0.21	0.03	0.14
20	0	0	5	0	0	5	0.15	0.21	0.04	0.12

¹Intra-residue restraints, ²Sequential restraints, ³Medium range restraints, ⁴Long range restraints, ⁵Inter-chain restraints, ⁶Standard deviation

9.2.1 Bar graph : Distance Violation statistics for each model ⓘ



The mean(dot),median(x) and the standard deviation are shown in blue with respect to the y axis on the right

9.3 Distance violation statistics for the ensemble

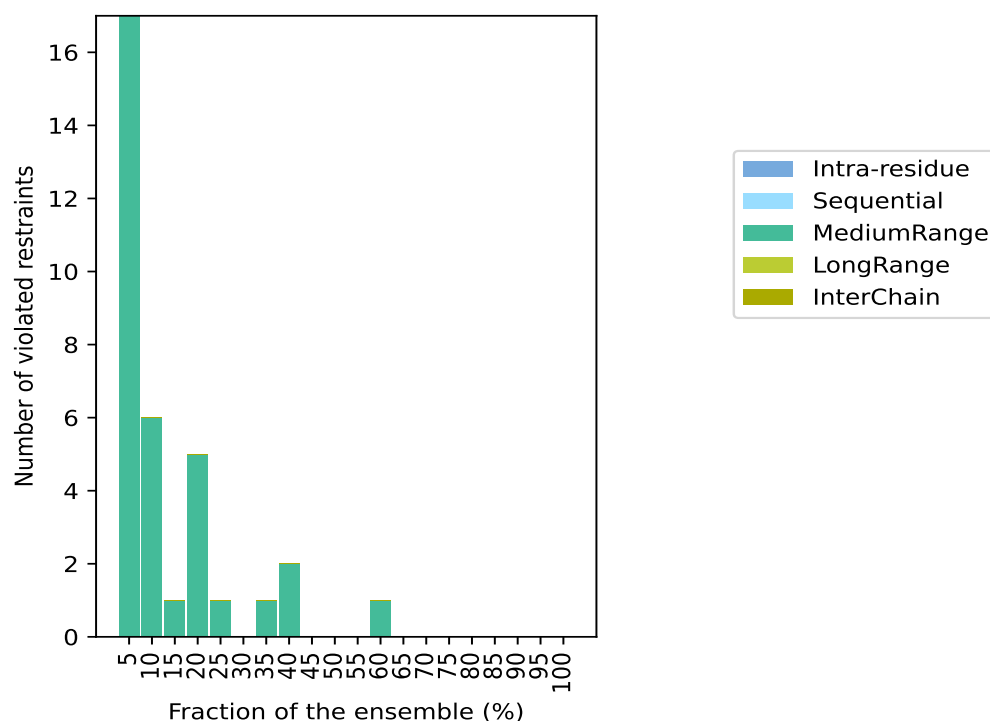
Violation analysis may find that some restraints are violated in few models and some are violated in most of models. The following table provides this information as number of violated restraints for a given fraction of the ensemble. In total, 148(IR:0, SQ:0, MR:148, LR:0, IC:0) restraints are not violated in the ensemble.

Number of violated restraints						Fraction of the ensemble	
IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total	Count ⁶	%
0	0	17	0	0	17	1	5.0
0	0	6	0	0	6	2	10.0
0	0	1	0	0	1	3	15.0
0	0	5	0	0	5	4	20.0
0	0	1	0	0	1	5	25.0
0	0	0	0	0	0	6	30.0
0	0	1	0	0	1	7	35.0
0	0	2	0	0	2	8	40.0
0	0	0	0	0	0	9	45.0
0	0	0	0	0	0	10	50.0
0	0	0	0	0	0	11	55.0
0	0	1	0	0	1	12	60.0
0	0	0	0	0	0	13	65.0
0	0	0	0	0	0	14	70.0
0	0	0	0	0	0	15	75.0
0	0	0	0	0	0	16	80.0
0	0	0	0	0	0	17	85.0
0	0	0	0	0	0	18	90.0
0	0	0	0	0	0	19	95.0
0	0	0	0	0	0	20	100.0

¹Intra-residue restraints, ²Sequential restraints, ³Medium range restraints, ⁴Long range restraints,

⁵Inter-chain restraints, ⁶ Number of models with violations

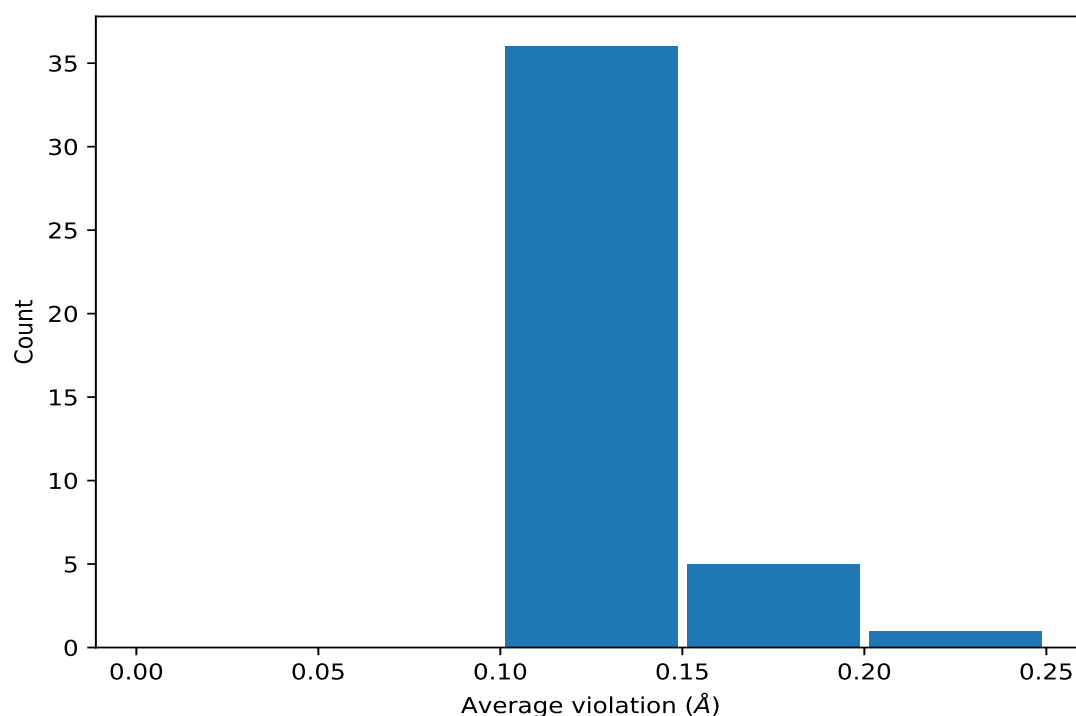
9.3.1 Bar graph : Distance violation statistics for the ensemble [i](#)



9.4 Most violated distance restraints in the ensemble [i](#)

9.4.1 Histogram : Distribution of mean distance violations [i](#)

The following histogram shows the distribution of the average value of the violation. The average is calculated for each restraint that is violated in more than one model over all the violated models in the ensemble



9.4.2 Table: Most violated distance restraints [i](#)

The following table provides the mean and the standard deviation of the violation for each restraint sorted by number of violated models and the mean value. The Key (restraint list ID, restraint ID) is the unique identifier for a given restraint. Rows with same key represent combinatorial or ambiguous restraints and are counted as a single restraint.

Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,16)	1:276:A:GLN:H	1:279:A:ASN:HA	12	0.13	0.03	0.12
(1,93)	1:260:A:ILE:H	1:262:A:SER:HA	8	0.15	0.04	0.16
(1,51)	1:265:A:ASN:HB3	1:268:A:HIS:H	8	0.13	0.02	0.12
(1,3)	1:264:A:GLU:HA	1:268:A:HIS:HE1	7	0.16	0.04	0.16
(1,96)	1:266:A:LEU:HD11	1:268:A:HIS:HE1	5	0.12	0.01	0.13
(1,96)	1:266:A:LEU:HD12	1:268:A:HIS:HE1	5	0.12	0.01	0.13
(1,96)	1:266:A:LEU:HD13	1:268:A:HIS:HE1	5	0.12	0.01	0.13
(1,7)	1:264:A:GLU:HB2	1:268:A:HIS:HE1	4	0.16	0.04	0.15
(1,137)	1:268:A:HIS:HE1	1:270:A:PRO:HA	4	0.14	0.05	0.11
(1,136)	1:255:A:ASN:H	1:257:A:LYS:H	4	0.12	0.02	0.12
(1,148)	1:260:A:ILE:HD11	1:262:A:SER:HB2	4	0.12	0.02	0.12
(1,148)	1:260:A:ILE:HD11	1:262:A:SER:HB3	4	0.12	0.02	0.12
(1,148)	1:260:A:ILE:HD12	1:262:A:SER:HB2	4	0.12	0.02	0.12
(1,148)	1:260:A:ILE:HD12	1:262:A:SER:HB3	4	0.12	0.02	0.12
(1,148)	1:260:A:ILE:HD13	1:262:A:SER:HB2	4	0.12	0.02	0.12
(1,148)	1:260:A:ILE:HD13	1:262:A:SER:HB3	4	0.12	0.02	0.12

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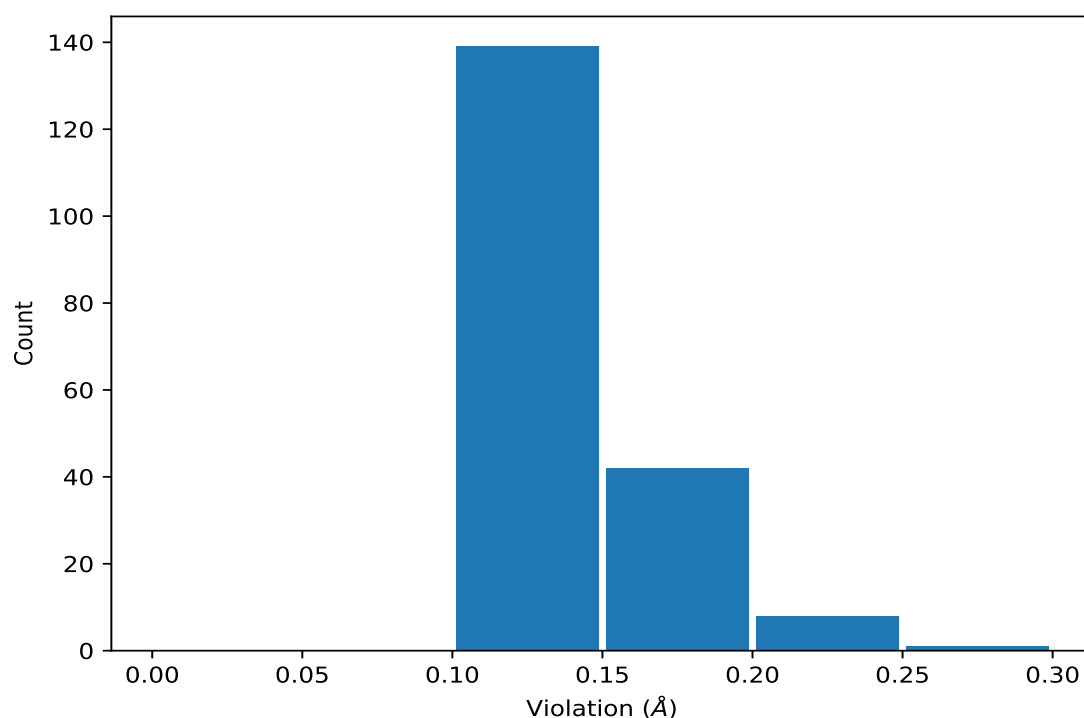
Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,74)	1:273:A:GLY:HA2	1:276:A:GLN:HE21	4	0.12	0.01	0.12
(1,74)	1:273:A:GLY:HA2	1:276:A:GLN:HE22	4	0.12	0.01	0.12
(1,74)	1:273:A:GLY:HA3	1:276:A:GLN:HE21	4	0.12	0.01	0.12
(1,74)	1:273:A:GLY:HA3	1:276:A:GLN:HE22	4	0.12	0.01	0.12
(1,115)	1:266:A:LEU:HD11	1:268:A:HIS:HD2	3	0.14	0.01	0.14
(1,115)	1:266:A:LEU:HD12	1:268:A:HIS:HD2	3	0.14	0.01	0.14
(1,115)	1:266:A:LEU:HD13	1:268:A:HIS:HD2	3	0.14	0.01	0.14
(1,113)	1:268:A:HIS:HD2	1:270:A:PRO:HG2	2	0.2	0.01	0.2
(1,6)	1:264:A:GLU:HB3	1:268:A:HIS:HE1	2	0.18	0.08	0.18
(1,41)	1:276:A:GLN:HA	1:279:A:ASN:HB3	2	0.17	0.02	0.17
(1,118)	1:267:A:LYS:HB3	1:269:A:GLN:HE22	2	0.16	0.0	0.16
(1,152)	1:264:A:GLU:HG2	1:266:A:LEU:HD11	2	0.12	0.0	0.12
(1,152)	1:264:A:GLU:HG2	1:266:A:LEU:HD12	2	0.12	0.0	0.12
(1,152)	1:264:A:GLU:HG2	1:266:A:LEU:HD13	2	0.12	0.0	0.12
(1,152)	1:264:A:GLU:HG2	1:266:A:LEU:HD21	2	0.12	0.0	0.12
(1,152)	1:264:A:GLU:HG2	1:266:A:LEU:HD22	2	0.12	0.0	0.12
(1,152)	1:264:A:GLU:HG2	1:266:A:LEU:HD23	2	0.12	0.0	0.12
(1,152)	1:264:A:GLU:HG3	1:266:A:LEU:HD11	2	0.12	0.0	0.12
(1,152)	1:264:A:GLU:HG3	1:266:A:LEU:HD12	2	0.12	0.0	0.12
(1,152)	1:264:A:GLU:HG3	1:266:A:LEU:HD13	2	0.12	0.0	0.12
(1,152)	1:264:A:GLU:HG3	1:266:A:LEU:HD21	2	0.12	0.0	0.12
(1,152)	1:264:A:GLU:HG3	1:266:A:LEU:HD22	2	0.12	0.0	0.12
(1,152)	1:264:A:GLU:HG3	1:266:A:LEU:HD23	2	0.12	0.0	0.12
(1,97)	1:266:A:LEU:HD21	1:268:A:HIS:HE1	2	0.11	0.0	0.11
(1,97)	1:266:A:LEU:HD22	1:268:A:HIS:HE1	2	0.11	0.0	0.11
(1,97)	1:266:A:LEU:HD23	1:268:A:HIS:HE1	2	0.11	0.0	0.11

¹Number of violated models, ²Standard deviation

9.5 All violated distance restraints [i](#)

9.5.1 Histogram : Distribution of distance violations [i](#)

The following histogram shows the distribution of the absolute value of the violation for all violated restraints in the ensemble.



9.5.2 Table : All distance violations [i](#)

The following table lists the absolute value of the violation for each restraint in the ensemble sorted by its value. The Key (restraint list ID, restraint ID) is the unique identifier for a given restraint. Rows with same key represent combinatorial or ambiguous restraints and are counted as a single restraint.

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,6)	1:264:A:GLU:HB3	1:268:A:HIS:HE1	11	0.27
(1,137)	1:268:A:HIS:HE1	1:270:A:PRO:HA	11	0.22
(1,7)	1:264:A:GLU:HB2	1:268:A:HIS:HE1	14	0.22
(1,3)	1:264:A:GLU:HA	1:268:A:HIS:HE1	12	0.22
(1,113)	1:268:A:HIS:HD2	1:270:A:PRO:HG2	19	0.21
(1,93)	1:260:A:ILE:H	1:262:A:SER:HA	20	0.21
(1,126)	1:267:A:LYS:HB2	1:269:A:GLN:HG2	11	0.2
(1,126)	1:267:A:LYS:HB2	1:269:A:GLN:HG3	11	0.2
(1,16)	1:276:A:GLN:H	1:279:A:ASN:HA	13	0.2
(1,113)	1:268:A:HIS:HD2	1:270:A:PRO:HG2	11	0.19
(1,41)	1:276:A:GLN:HA	1:279:A:ASN:HB3	2	0.19
(1,3)	1:264:A:GLU:HA	1:268:A:HIS:HE1	17	0.19
(1,170)	1:274:A:LYS:HE2	1:276:A:GLN:H	4	0.18
(1,170)	1:274:A:LYS:HE3	1:276:A:GLN:H	4	0.18
(1,93)	1:260:A:ILE:H	1:262:A:SER:HA	7	0.18
(1,93)	1:260:A:ILE:H	1:262:A:SER:HA	15	0.18

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,89)	1:279:A:ASN:HD21	1:282:A:LEU:HB2	9	0.18
(1,89)	1:279:A:ASN:HD21	1:282:A:LEU:HB3	9	0.18
(1,89)	1:279:A:ASN:HD22	1:282:A:LEU:HB2	9	0.18
(1,89)	1:279:A:ASN:HD22	1:282:A:LEU:HB3	9	0.18
(1,102)	1:264:A:GLU:HG3	1:266:A:LEU:H	3	0.17
(1,7)	1:264:A:GLU:HB2	1:268:A:HIS:HE1	20	0.17
(1,3)	1:264:A:GLU:HA	1:268:A:HIS:HE1	10	0.17
(1,118)	1:267:A:LYS:HB3	1:269:A:GLN:HE22	11	0.16
(1,118)	1:267:A:LYS:HB3	1:269:A:GLN:HE22	19	0.16
(1,93)	1:260:A:ILE:H	1:262:A:SER:HA	5	0.16
(1,93)	1:260:A:ILE:H	1:262:A:SER:HA	16	0.16
(1,51)	1:265:A:ASN:HB3	1:268:A:HIS:H	3	0.16
(1,51)	1:265:A:ASN:HB3	1:268:A:HIS:H	5	0.16
(1,3)	1:264:A:GLU:HA	1:268:A:HIS:HE1	4	0.16
(1,182)	1:286:A:ASN:HD21	1:288:A:GLN:HB2	8	0.15
(1,182)	1:286:A:ASN:HD21	1:288:A:GLN:HB3	8	0.15
(1,182)	1:286:A:ASN:HD22	1:288:A:GLN:HB2	8	0.15
(1,182)	1:286:A:ASN:HD22	1:288:A:GLN:HB3	8	0.15
(1,148)	1:260:A:ILE:HD11	1:262:A:SER:HB2	19	0.15
(1,148)	1:260:A:ILE:HD11	1:262:A:SER:HB3	19	0.15
(1,148)	1:260:A:ILE:HD12	1:262:A:SER:HB2	19	0.15
(1,148)	1:260:A:ILE:HD12	1:262:A:SER:HB3	19	0.15
(1,148)	1:260:A:ILE:HD13	1:262:A:SER:HB2	19	0.15
(1,148)	1:260:A:ILE:HD13	1:262:A:SER:HB3	19	0.15
(1,136)	1:255:A:ASN:H	1:257:A:LYS:H	11	0.15
(1,116)	1:266:A:LEU:HD21	1:268:A:HIS:HD2	9	0.15
(1,116)	1:266:A:LEU:HD22	1:268:A:HIS:HD2	9	0.15
(1,116)	1:266:A:LEU:HD23	1:268:A:HIS:HD2	9	0.15
(1,115)	1:266:A:LEU:HD11	1:268:A:HIS:HD2	17	0.15
(1,115)	1:266:A:LEU:HD12	1:268:A:HIS:HD2	17	0.15
(1,115)	1:266:A:LEU:HD13	1:268:A:HIS:HD2	17	0.15
(1,41)	1:276:A:GLN:HA	1:279:A:ASN:HB3	17	0.15
(1,26)	1:276:A:GLN:H	1:279:A:ASN:HB3	1	0.15
(1,16)	1:276:A:GLN:H	1:279:A:ASN:HA	15	0.15
(1,16)	1:276:A:GLN:H	1:279:A:ASN:HA	17	0.15
(1,115)	1:266:A:LEU:HD11	1:268:A:HIS:HD2	9	0.14
(1,115)	1:266:A:LEU:HD12	1:268:A:HIS:HD2	9	0.14
(1,115)	1:266:A:LEU:HD13	1:268:A:HIS:HD2	9	0.14
(1,96)	1:266:A:LEU:HD11	1:268:A:HIS:HE1	19	0.14
(1,96)	1:266:A:LEU:HD12	1:268:A:HIS:HE1	19	0.14
(1,96)	1:266:A:LEU:HD13	1:268:A:HIS:HE1	19	0.14
(1,51)	1:265:A:ASN:HB3	1:268:A:HIS:H	19	0.14

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,18)	1:273:A:GLY:HA3	1:276:A:GLN:H	18	0.14
(1,16)	1:276:A:GLN:H	1:279:A:ASN:HA	7	0.14
(1,16)	1:276:A:GLN:H	1:279:A:ASN:HA	14	0.14
(1,136)	1:255:A:ASN:H	1:257:A:LYS:H	2	0.13
(1,115)	1:266:A:LEU:HD11	1:268:A:HIS:HD2	12	0.13
(1,115)	1:266:A:LEU:HD12	1:268:A:HIS:HD2	12	0.13
(1,115)	1:266:A:LEU:HD13	1:268:A:HIS:HD2	12	0.13
(1,96)	1:266:A:LEU:HD11	1:268:A:HIS:HE1	10	0.13
(1,96)	1:266:A:LEU:HD12	1:268:A:HIS:HE1	10	0.13
(1,96)	1:266:A:LEU:HD13	1:268:A:HIS:HE1	10	0.13
(1,96)	1:266:A:LEU:HD11	1:268:A:HIS:HE1	15	0.13
(1,96)	1:266:A:LEU:HD12	1:268:A:HIS:HE1	15	0.13
(1,96)	1:266:A:LEU:HD13	1:268:A:HIS:HE1	15	0.13
(1,74)	1:273:A:GLY:HA2	1:276:A:GLN:HE21	11	0.13
(1,74)	1:273:A:GLY:HA2	1:276:A:GLN:HE22	11	0.13
(1,74)	1:273:A:GLY:HA3	1:276:A:GLN:HE21	11	0.13
(1,74)	1:273:A:GLY:HA3	1:276:A:GLN:HE22	11	0.13
(1,51)	1:265:A:ASN:HB3	1:268:A:HIS:H	13	0.13
(1,16)	1:276:A:GLN:H	1:279:A:ASN:HA	6	0.13
(1,7)	1:264:A:GLU:HB2	1:268:A:HIS:HE1	8	0.13
(1,160)	1:268:A:HIS:H	1:270:A:PRO:HB2	8	0.12
(1,160)	1:268:A:HIS:H	1:270:A:PRO:HB3	8	0.12
(1,152)	1:264:A:GLU:HG2	1:266:A:LEU:HD11	15	0.12
(1,152)	1:264:A:GLU:HG2	1:266:A:LEU:HD12	15	0.12
(1,152)	1:264:A:GLU:HG2	1:266:A:LEU:HD13	15	0.12
(1,152)	1:264:A:GLU:HG2	1:266:A:LEU:HD21	15	0.12
(1,152)	1:264:A:GLU:HG2	1:266:A:LEU:HD22	15	0.12
(1,152)	1:264:A:GLU:HG2	1:266:A:LEU:HD23	15	0.12
(1,152)	1:264:A:GLU:HG3	1:266:A:LEU:HD11	15	0.12
(1,152)	1:264:A:GLU:HG3	1:266:A:LEU:HD12	15	0.12
(1,152)	1:264:A:GLU:HG3	1:266:A:LEU:HD13	15	0.12
(1,152)	1:264:A:GLU:HG3	1:266:A:LEU:HD21	15	0.12
(1,152)	1:264:A:GLU:HG3	1:266:A:LEU:HD22	15	0.12
(1,152)	1:264:A:GLU:HG3	1:266:A:LEU:HD23	15	0.12
(1,149)	1:262:A:SER:HB2	1:264:A:GLU:HB2	6	0.12
(1,149)	1:262:A:SER:HB2	1:264:A:GLU:HB3	6	0.12
(1,149)	1:262:A:SER:HB3	1:264:A:GLU:HB2	6	0.12
(1,149)	1:262:A:SER:HB3	1:264:A:GLU:HB3	6	0.12
(1,148)	1:260:A:ILE:HD11	1:262:A:SER:HB2	7	0.12
(1,148)	1:260:A:ILE:HD11	1:262:A:SER:HB3	7	0.12
(1,148)	1:260:A:ILE:HD12	1:262:A:SER:HB2	7	0.12
(1,148)	1:260:A:ILE:HD12	1:262:A:SER:HB3	7	0.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,148)	1:260:A:ILE:HD13	1:262:A:SER:HB2	7	0.12
(1,148)	1:260:A:ILE:HD13	1:262:A:SER:HB3	7	0.12
(1,96)	1:266:A:LEU:HD11	1:268:A:HIS:HE1	16	0.12
(1,96)	1:266:A:LEU:HD12	1:268:A:HIS:HE1	16	0.12
(1,96)	1:266:A:LEU:HD13	1:268:A:HIS:HE1	16	0.12
(1,93)	1:260:A:ILE:H	1:262:A:SER:HA	6	0.12
(1,74)	1:273:A:GLY:HA2	1:276:A:GLN:HE21	13	0.12
(1,74)	1:273:A:GLY:HA2	1:276:A:GLN:HE22	13	0.12
(1,74)	1:273:A:GLY:HA3	1:276:A:GLN:HE21	13	0.12
(1,74)	1:273:A:GLY:HA3	1:276:A:GLN:HE22	13	0.12
(1,51)	1:265:A:ASN:HB3	1:268:A:HIS:H	15	0.12
(1,51)	1:265:A:ASN:HB3	1:268:A:HIS:H	17	0.12
(1,16)	1:276:A:GLN:H	1:279:A:ASN:HA	12	0.12
(1,16)	1:276:A:GLN:H	1:279:A:ASN:HA	18	0.12
(1,16)	1:276:A:GLN:H	1:279:A:ASN:HA	20	0.12
(1,11)	1:263:A:THR:HG21	1:267:A:LYS:HD2	9	0.12
(1,11)	1:263:A:THR:HG21	1:267:A:LYS:HD3	9	0.12
(1,11)	1:263:A:THR:HG22	1:267:A:LYS:HD2	9	0.12
(1,11)	1:263:A:THR:HG22	1:267:A:LYS:HD3	9	0.12
(1,11)	1:263:A:THR:HG23	1:267:A:LYS:HD2	9	0.12
(1,11)	1:263:A:THR:HG23	1:267:A:LYS:HD3	9	0.12
(1,3)	1:264:A:GLU:HA	1:268:A:HIS:HE1	1	0.12
(1,3)	1:264:A:GLU:HA	1:268:A:HIS:HE1	7	0.12
(1,3)	1:264:A:GLU:HA	1:268:A:HIS:HE1	20	0.12
(1,152)	1:264:A:GLU:HG2	1:266:A:LEU:HD11	18	0.11
(1,152)	1:264:A:GLU:HG2	1:266:A:LEU:HD12	18	0.11
(1,152)	1:264:A:GLU:HG2	1:266:A:LEU:HD13	18	0.11
(1,152)	1:264:A:GLU:HG2	1:266:A:LEU:HD21	18	0.11
(1,152)	1:264:A:GLU:HG2	1:266:A:LEU:HD22	18	0.11
(1,152)	1:264:A:GLU:HG2	1:266:A:LEU:HD23	18	0.11
(1,152)	1:264:A:GLU:HG3	1:266:A:LEU:HD11	18	0.11
(1,152)	1:264:A:GLU:HG3	1:266:A:LEU:HD12	18	0.11
(1,152)	1:264:A:GLU:HG3	1:266:A:LEU:HD13	18	0.11
(1,152)	1:264:A:GLU:HG3	1:266:A:LEU:HD21	18	0.11
(1,152)	1:264:A:GLU:HG3	1:266:A:LEU:HD22	18	0.11
(1,152)	1:264:A:GLU:HG3	1:266:A:LEU:HD23	18	0.11
(1,148)	1:260:A:ILE:HD11	1:262:A:SER:HB2	20	0.11
(1,148)	1:260:A:ILE:HD11	1:262:A:SER:HB3	20	0.11
(1,148)	1:260:A:ILE:HD12	1:262:A:SER:HB2	20	0.11
(1,148)	1:260:A:ILE:HD12	1:262:A:SER:HB3	20	0.11
(1,148)	1:260:A:ILE:HD13	1:262:A:SER:HB2	20	0.11
(1,148)	1:260:A:ILE:HD13	1:262:A:SER:HB3	20	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,137)	1:268:A:HIS:HE1	1:270:A:PRO:HA	3	0.11
(1,137)	1:268:A:HIS:HE1	1:270:A:PRO:HA	19	0.11
(1,136)	1:255:A:ASN:H	1:257:A:LYS:H	6	0.11
(1,135)	1:274:A:LYS:H	1:276:A:GLN:HG2	17	0.11
(1,109)	1:268:A:HIS:HD2	1:270:A:PRO:HA	16	0.11
(1,97)	1:266:A:LEU:HD21	1:268:A:HIS:HE1	5	0.11
(1,97)	1:266:A:LEU:HD22	1:268:A:HIS:HE1	5	0.11
(1,97)	1:266:A:LEU:HD23	1:268:A:HIS:HE1	5	0.11
(1,97)	1:266:A:LEU:HD21	1:268:A:HIS:HE1	13	0.11
(1,97)	1:266:A:LEU:HD22	1:268:A:HIS:HE1	13	0.11
(1,97)	1:266:A:LEU:HD23	1:268:A:HIS:HE1	13	0.11
(1,93)	1:260:A:ILE:H	1:262:A:SER:HA	9	0.11
(1,74)	1:273:A:GLY:HA2	1:276:A:GLN:HE21	16	0.11
(1,74)	1:273:A:GLY:HA2	1:276:A:GLN:HE22	16	0.11
(1,74)	1:273:A:GLY:HA3	1:276:A:GLN:HE21	16	0.11
(1,74)	1:273:A:GLY:HA3	1:276:A:GLN:HE22	16	0.11
(1,74)	1:273:A:GLY:HA2	1:276:A:GLN:HE21	18	0.11
(1,74)	1:273:A:GLY:HA2	1:276:A:GLN:HE22	18	0.11
(1,74)	1:273:A:GLY:HA3	1:276:A:GLN:HE21	18	0.11
(1,74)	1:273:A:GLY:HA3	1:276:A:GLN:HE22	18	0.11
(1,67)	1:259:A:LYS:HE2	1:262:A:SER:H	5	0.11
(1,67)	1:259:A:LYS:HE3	1:262:A:SER:H	5	0.11
(1,51)	1:265:A:ASN:HB3	1:268:A:HIS:H	12	0.11
(1,16)	1:276:A:GLN:H	1:279:A:ASN:HA	4	0.11
(1,16)	1:276:A:GLN:H	1:279:A:ASN:HA	11	0.11
(1,7)	1:264:A:GLU:HB2	1:268:A:HIS:HE1	17	0.11
(1,148)	1:260:A:ILE:HD11	1:262:A:SER:HB2	4	0.1
(1,148)	1:260:A:ILE:HD11	1:262:A:SER:HB3	4	0.1
(1,148)	1:260:A:ILE:HD12	1:262:A:SER:HB2	4	0.1
(1,148)	1:260:A:ILE:HD12	1:262:A:SER:HB3	4	0.1
(1,148)	1:260:A:ILE:HD13	1:262:A:SER:HB2	4	0.1
(1,148)	1:260:A:ILE:HD13	1:262:A:SER:HB3	4	0.1
(1,137)	1:268:A:HIS:HE1	1:270:A:PRO:HA	8	0.1
(1,136)	1:255:A:ASN:H	1:257:A:LYS:H	18	0.1
(1,127)	1:267:A:LYS:HB3	1:269:A:GLN:HG2	19	0.1
(1,127)	1:267:A:LYS:HB3	1:269:A:GLN:HG3	19	0.1
(1,119)	1:284:A:LEU:HD21	1:286:A:ASN:HD22	16	0.1
(1,119)	1:284:A:LEU:HD22	1:286:A:ASN:HD22	16	0.1
(1,119)	1:284:A:LEU:HD23	1:286:A:ASN:HD22	16	0.1
(1,96)	1:266:A:LEU:HD11	1:268:A:HIS:HE1	3	0.1
(1,96)	1:266:A:LEU:HD12	1:268:A:HIS:HE1	3	0.1
(1,96)	1:266:A:LEU:HD13	1:268:A:HIS:HE1	3	0.1

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,93)	1:260:A:ILE:H	1:262:A:SER:HA	11	0.1
(1,85)	1:278:A:ILE:HA	1:281:A:LYS:HD2	14	0.1
(1,85)	1:278:A:ILE:HA	1:281:A:LYS:HD3	14	0.1
(1,51)	1:265:A:ASN:HB3	1:268:A:HIS:H	18	0.1
(1,16)	1:276:A:GLN:H	1:279:A:ASN:HA	16	0.1
(1,6)	1:264:A:GLU:HB3	1:268:A:HIS:HE1	8	0.1

10 Dihedral-angle violation analysis ⓘ

No dihedral-angle restraints found