



Full wwPDB NMR Structure Validation Report ⓘ

Mar 28, 2026 – 03:40 PM UTC

PDB ID : 6TVM / pdb_00006tvm
BMRB ID : 34475
Title : LEDGF/p75 dimer (residues 345-467)
Authors : Lux, V.; Veverka, V.
Deposited on : 2020-01-10

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

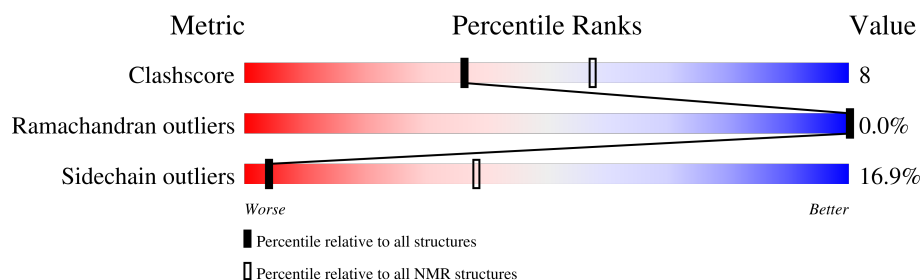
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 45%.

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	128	47% 16% 37%
1	B	128	46% 17% 37%

2 Ensemble composition and analysis

This entry contains 30 models. Model 22 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *lowest energy*.

The following residues are included in the computation of the global validation metrics.

Well-defined (core) protein residues			
Well-defined core	Residue range (total)	Backbone RMSD (Å)	Medoid model
1	A:347-A:427, B:347-B:427 (162)	0.27	22

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 2 single-model clusters were found.

Cluster number	Models
1	1, 3, 4, 5, 7, 8, 9, 10, 12, 14, 15, 16, 17, 18, 20, 21, 22, 23, 26, 27, 28
2	2, 6, 11, 13, 24, 25, 30
Single-model clusters	19; 29

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 4152 atoms, of which 2114 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called PC4 and SFRS1-interacting protein.

Mol	Chain	Residues	Atoms						Trace
1	A	128	Total	C	H	N	O	S	0
			2076	627	1057	187	198	7	
1	B	128	Total	C	H	N	O	S	0
			2076	627	1057	187	198	7	

There are 10 discrepancies between the modelled and reference sequences:

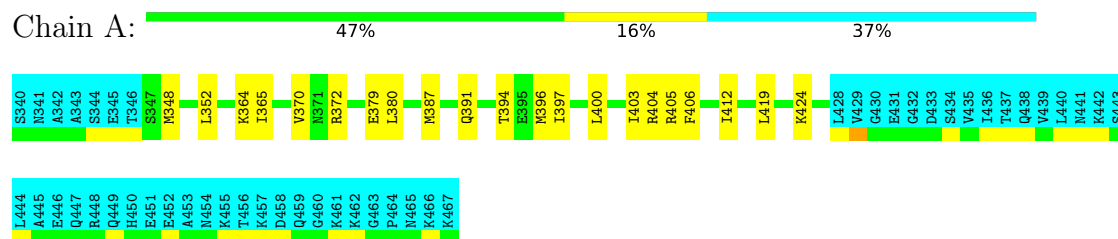
Chain	Residue	Modelled	Actual	Comment	Reference
A	340	SER	-	expression tag	UNP O75475
A	341	ASN	-	expression tag	UNP O75475
A	342	ALA	-	expression tag	UNP O75475
A	343	ALA	-	expression tag	UNP O75475
A	344	SER	-	expression tag	UNP O75475
B	340	SER	-	expression tag	UNP O75475
B	341	ASN	-	expression tag	UNP O75475
B	342	ALA	-	expression tag	UNP O75475
B	343	ALA	-	expression tag	UNP O75475
B	344	SER	-	expression tag	UNP O75475

4 Residue-property plots

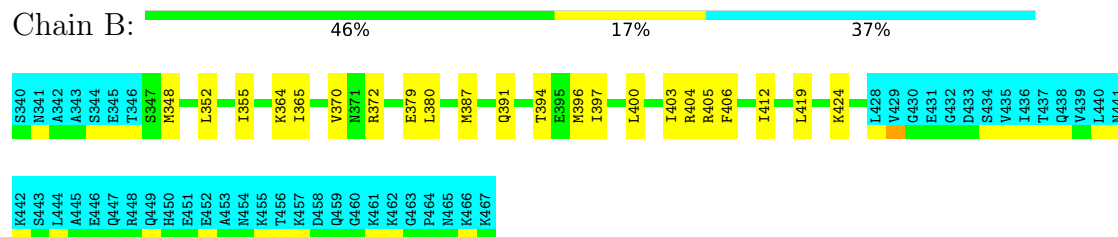
4.1 Average score per residue in the NMR ensemble

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: PC4 and SFRS1-interacting protein



- Molecule 1: PC4 and SFRS1-interacting protein

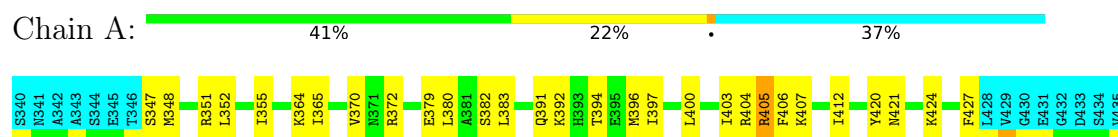


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

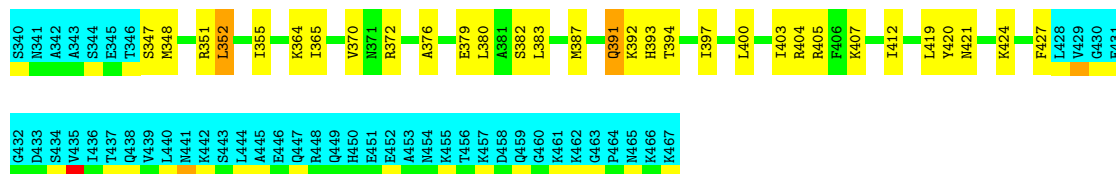
- Molecule 1: PC4 and SFRS1-interacting protein





- Molecule 1: PC4 and SFRS1-interacting protein

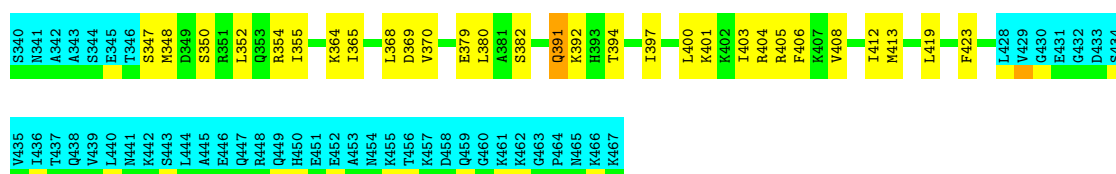
Chain B: 39% 23% 37%



4.2.2 Score per residue for model 2

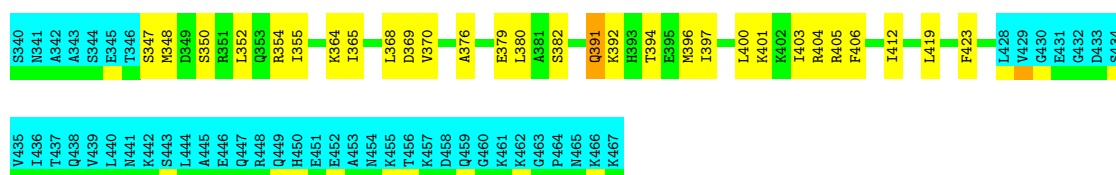
- Molecule 1: PC4 and SFRS1-interacting protein

Chain A: 41% 22% 37%



- Molecule 1: PC4 and SFRS1-interacting protein

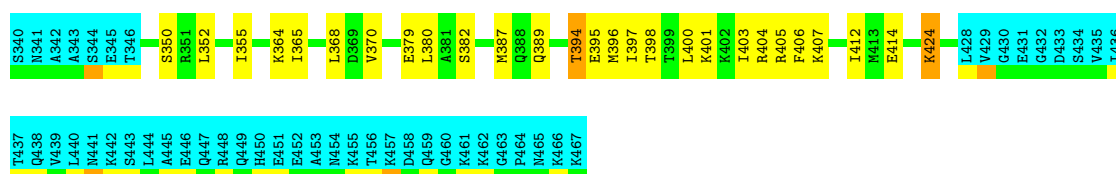
Chain B: 41% 22% 37%



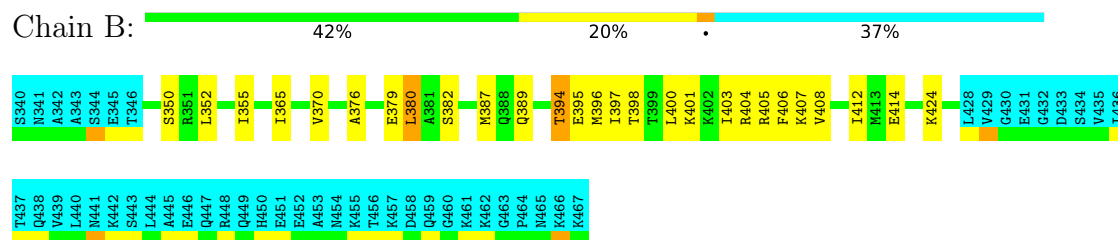
4.2.3 Score per residue for model 3

- Molecule 1: PC4 and SFRS1-interacting protein

Chain A: 42% 20% 37%

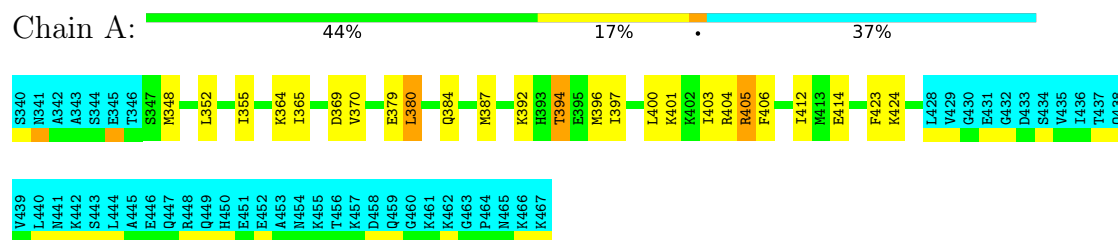


- Molecule 1: PC4 and SFRS1-interacting protein

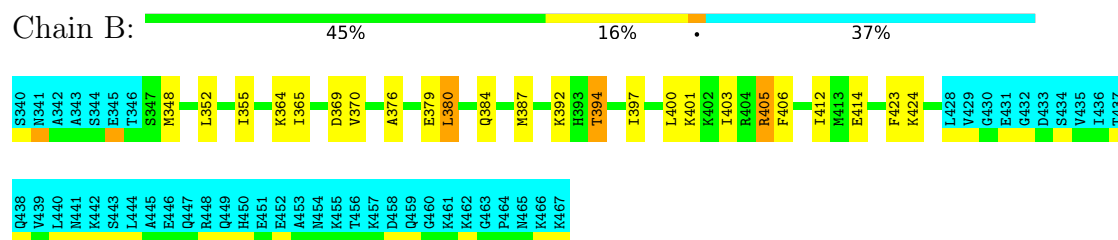


4.2.4 Score per residue for model 4

- Molecule 1: PC4 and SFRS1-interacting protein

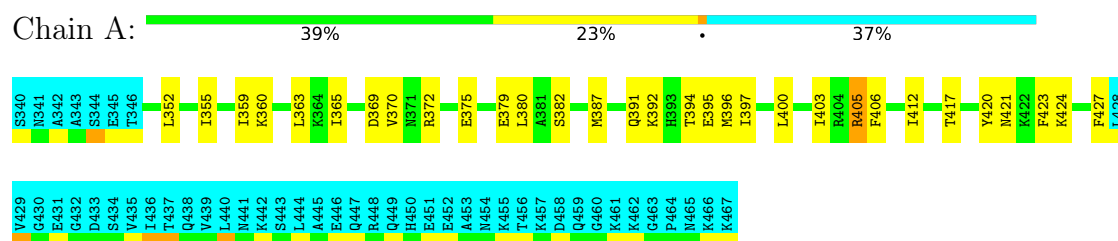


- Molecule 1: PC4 and SFRS1-interacting protein

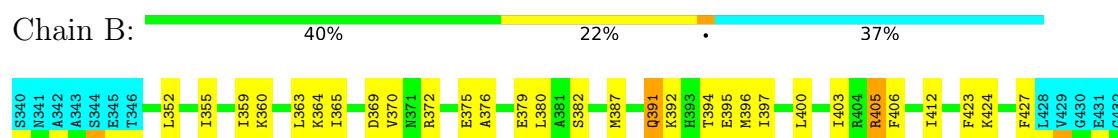


4.2.5 Score per residue for model 5

- Molecule 1: PC4 and SFRS1-interacting protein



- Molecule 1: PC4 and SFRS1-interacting protein



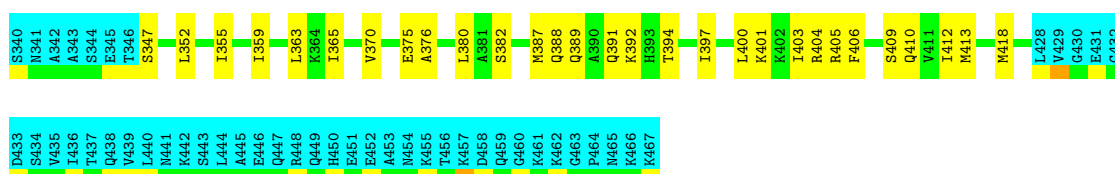


4.2.6 Score per residue for model 6

- Molecule 1: PC4 and SFRS1-interacting protein

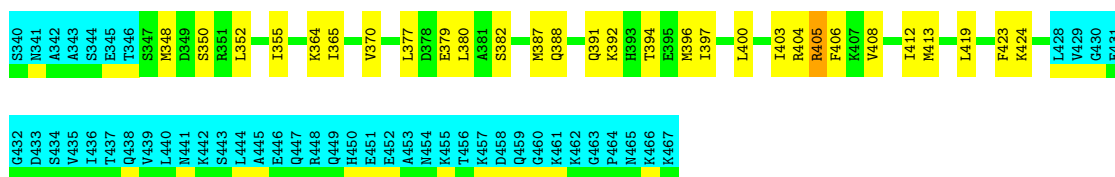


- Molecule 1: PC4 and SFRS1-interacting protein

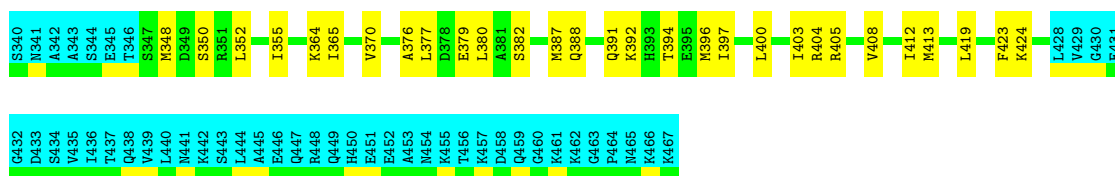


4.2.7 Score per residue for model 7

- Molecule 1: PC4 and SFRS1-interacting protein

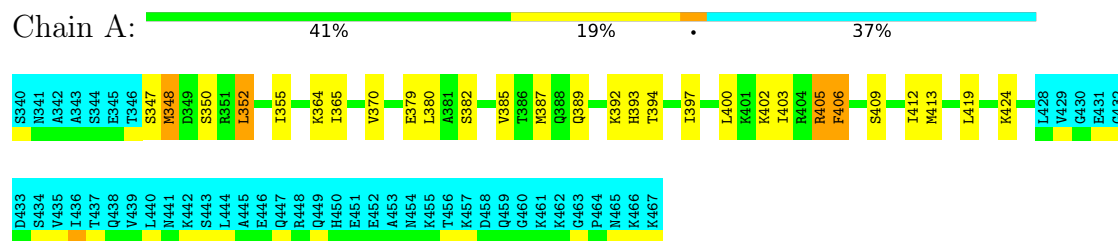


- Molecule 1: PC4 and SFRS1-interacting protein

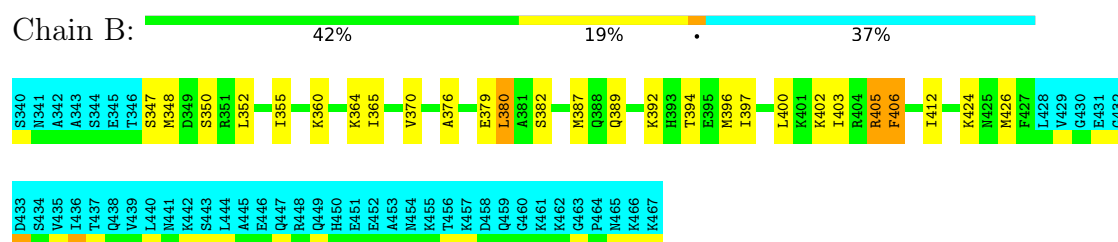


4.2.8 Score per residue for model 8

- Molecule 1: PC4 and SFRS1-interacting protein

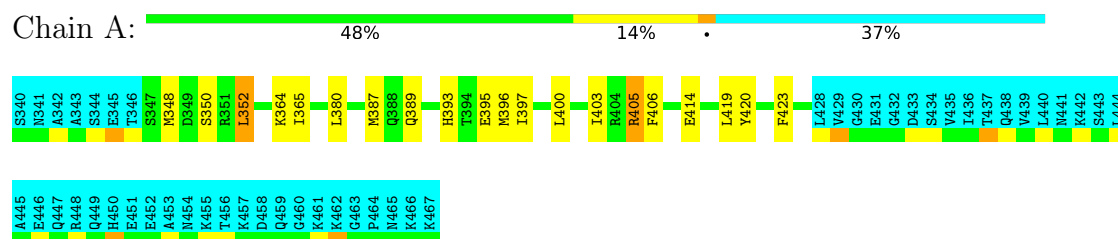


- Molecule 1: PC4 and SFRS1-interacting protein

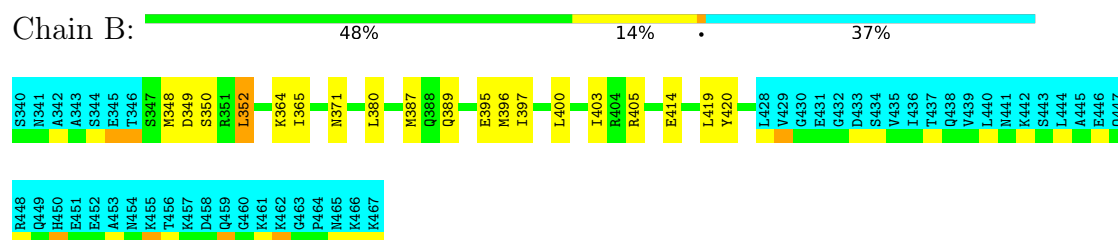


4.2.9 Score per residue for model 9

- Molecule 1: PC4 and SFRS1-interacting protein

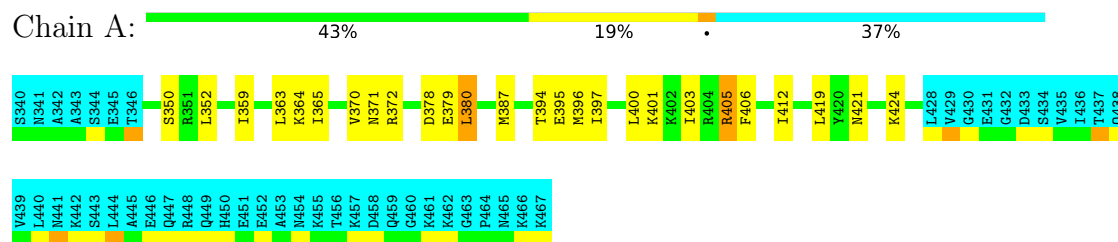


- Molecule 1: PC4 and SFRS1-interacting protein

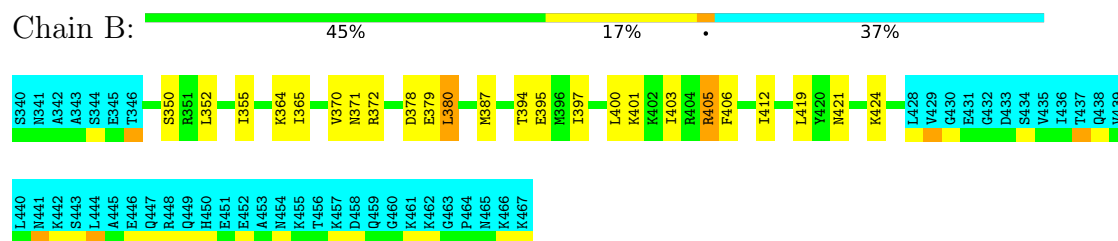


4.2.10 Score per residue for model 10

- Molecule 1: PC4 and SFRS1-interacting protein

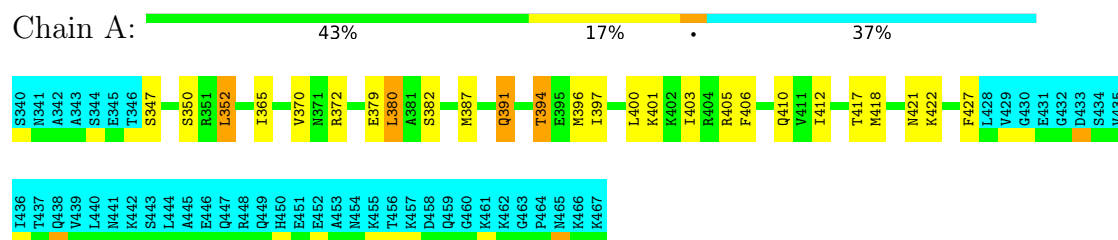


- Molecule 1: PC4 and SFRS1-interacting protein

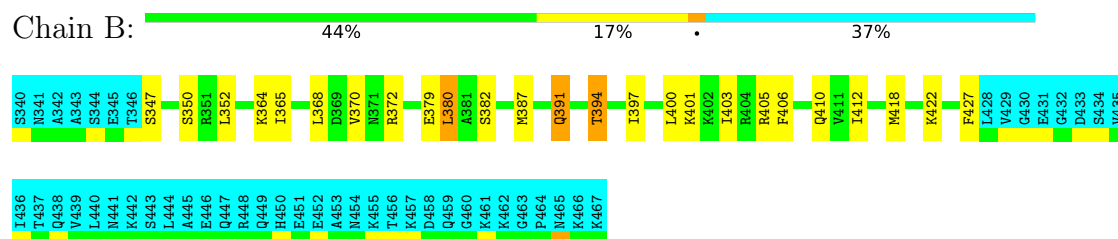


4.2.11 Score per residue for model 11

- Molecule 1: PC4 and SFRS1-interacting protein

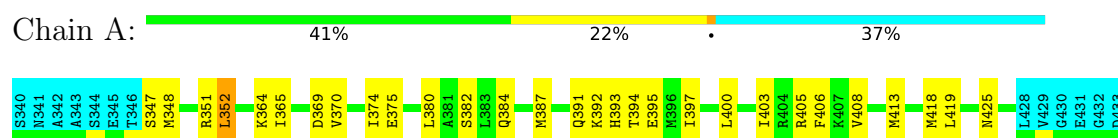


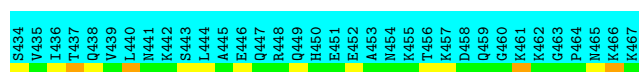
- Molecule 1: PC4 and SFRS1-interacting protein



4.2.12 Score per residue for model 12

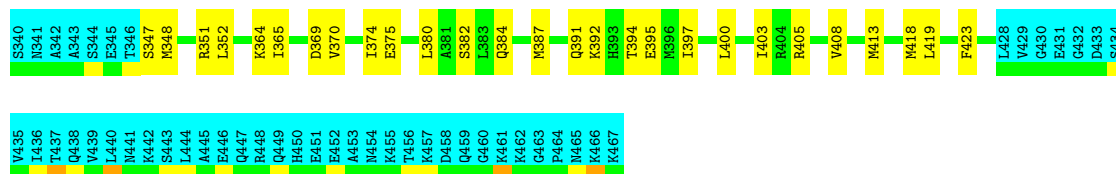
- Molecule 1: PC4 and SFRS1-interacting protein





- Molecule 1: PC4 and SFRS1-interacting protein

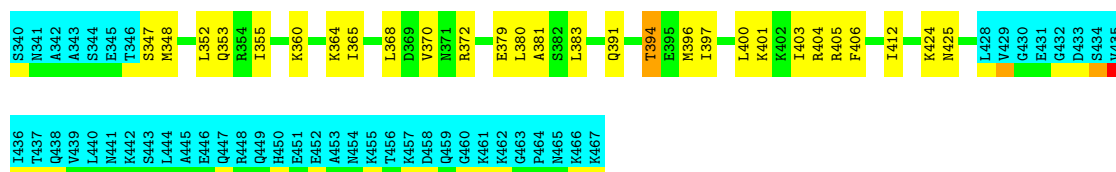
Chain B: 42% 21% 37%



4.2.13 Score per residue for model 13

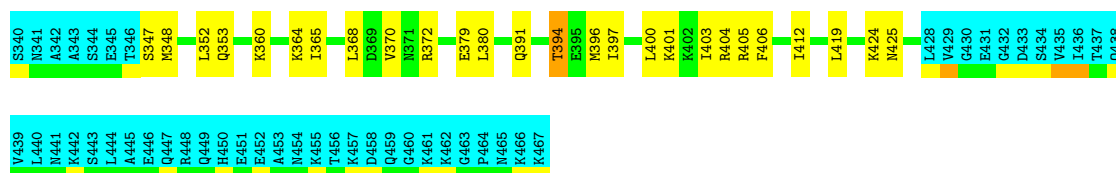
- Molecule 1: PC4 and SFRS1-interacting protein

Chain A: 41% 21% 37%



- Molecule 1: PC4 and SFRS1-interacting protein

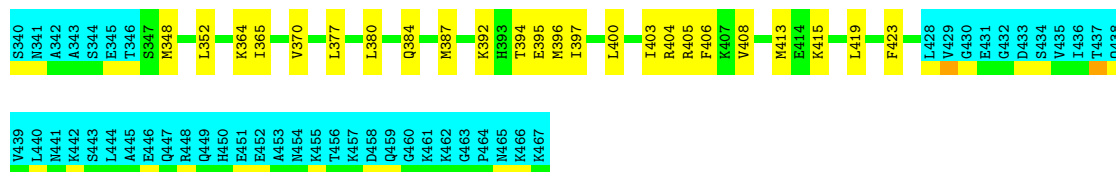
Chain B: 43% 20% 37%



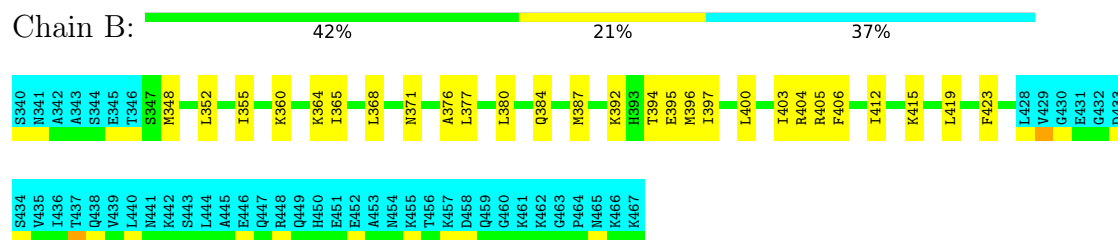
4.2.14 Score per residue for model 14

- Molecule 1: PC4 and SFRS1-interacting protein

Chain A: 45% 19% 37%

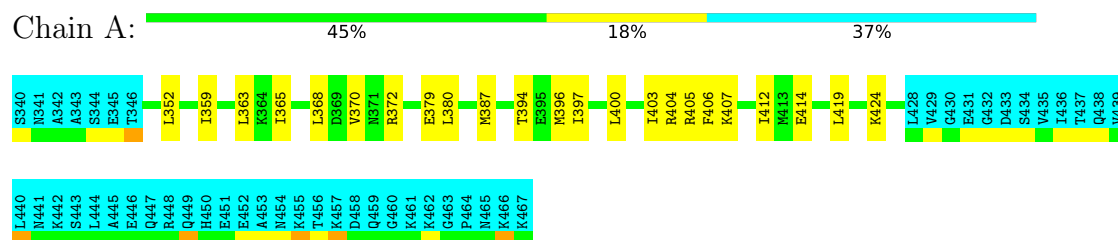


- Molecule 1: PC4 and SFRS1-interacting protein

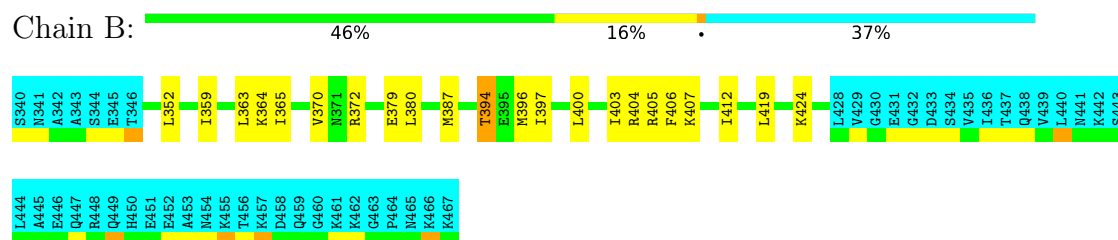


4.2.15 Score per residue for model 15

- Molecule 1: PC4 and SFRS1-interacting protein

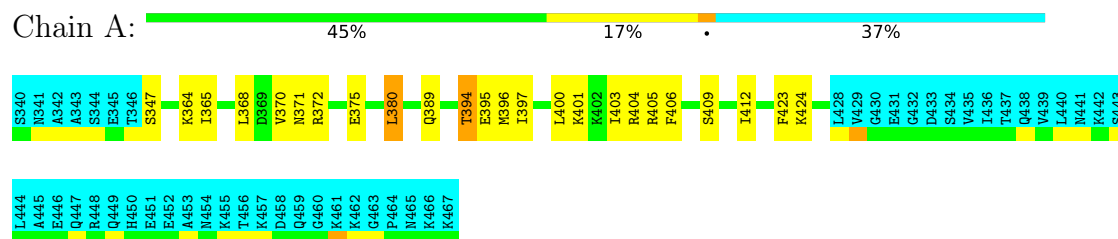


- Molecule 1: PC4 and SFRS1-interacting protein

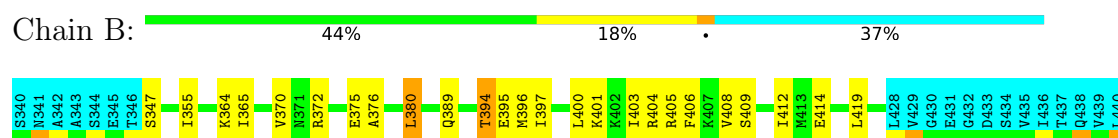


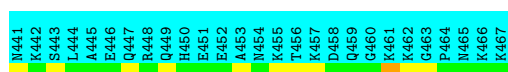
4.2.16 Score per residue for model 16

- Molecule 1: PC4 and SFRS1-interacting protein



- Molecule 1: PC4 and SFRS1-interacting protein

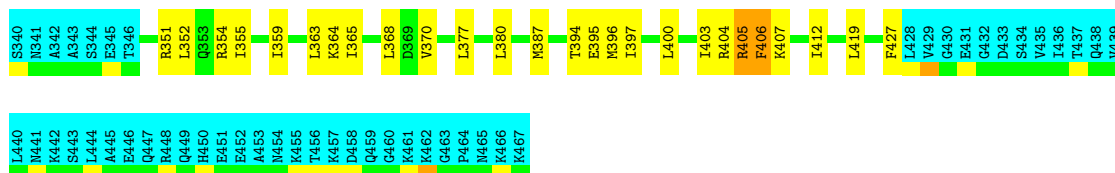




4.2.17 Score per residue for model 17

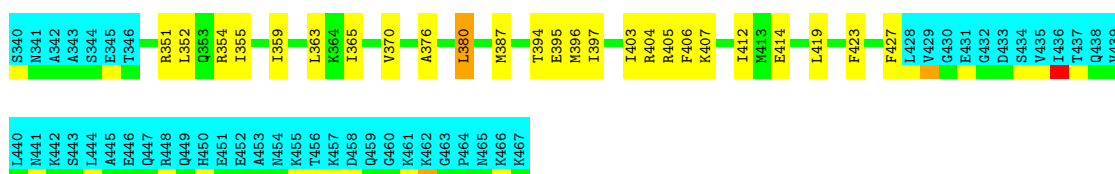
- Molecule 1: PC4 and SFRS1-interacting protein

Chain A: 43% 19% 0% 37%



- Molecule 1: PC4 and SFRS1-interacting protein

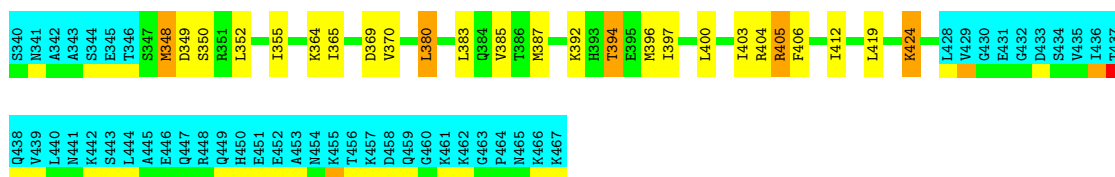
Chain B: 44% 19% 0% 37%



4.2.18 Score per residue for model 18

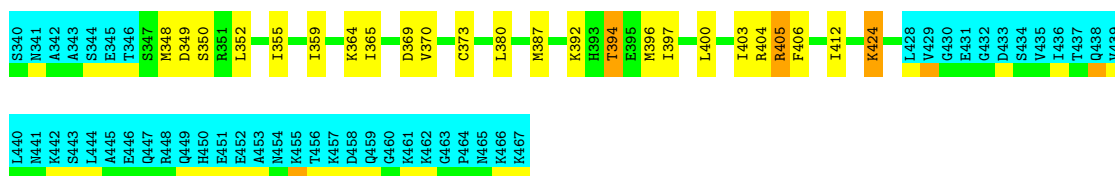
- Molecule 1: PC4 and SFRS1-interacting protein

Chain A: 44% 16% 0% 37%



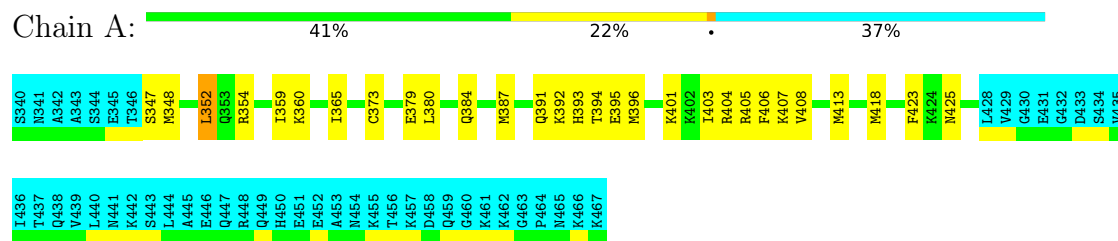
- Molecule 1: PC4 and SFRS1-interacting protein

Chain B: 45% 16% 0% 37%

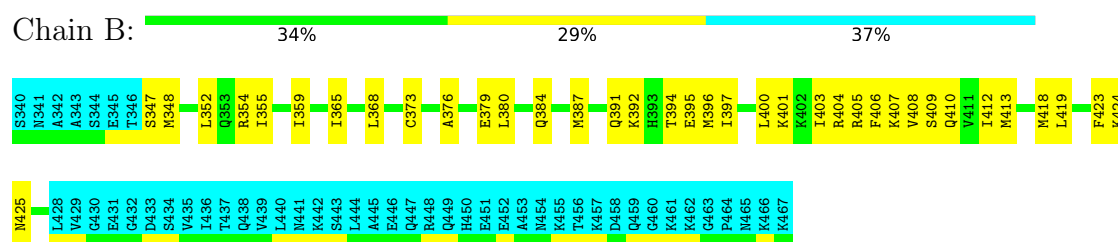


4.2.19 Score per residue for model 19

- Molecule 1: PC4 and SFRS1-interacting protein

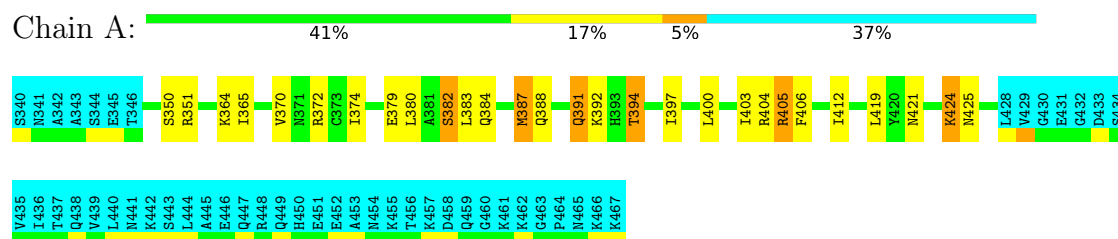


- Molecule 1: PC4 and SFRS1-interacting protein

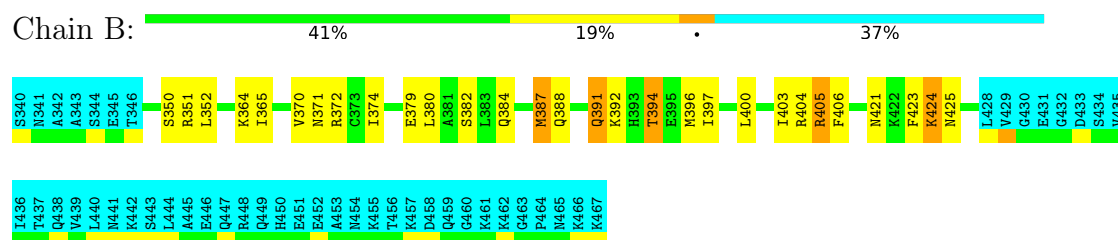


4.2.20 Score per residue for model 20

- Molecule 1: PC4 and SFRS1-interacting protein

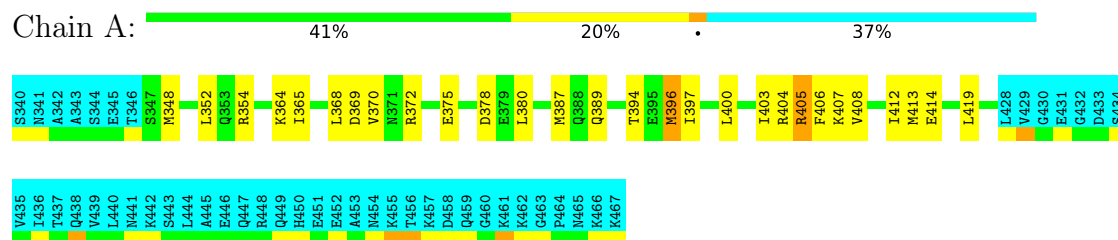


- Molecule 1: PC4 and SFRS1-interacting protein

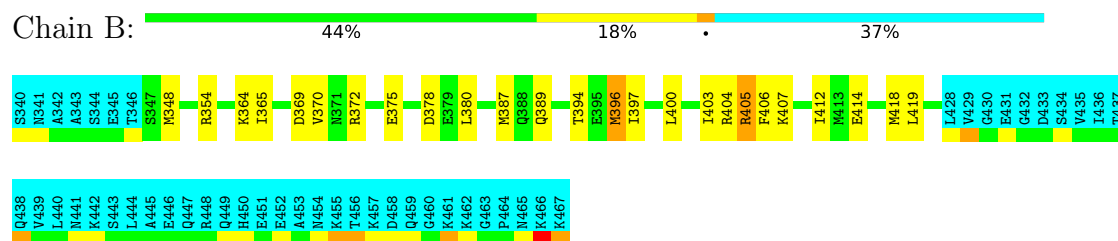


4.2.21 Score per residue for model 21

- Molecule 1: PC4 and SFRS1-interacting protein

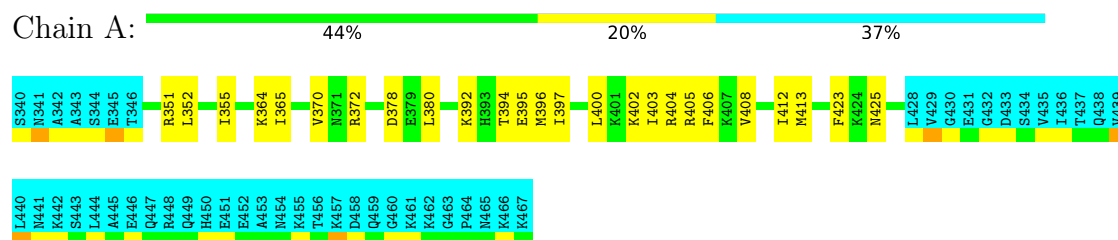


- Molecule 1: PC4 and SFRS1-interacting protein

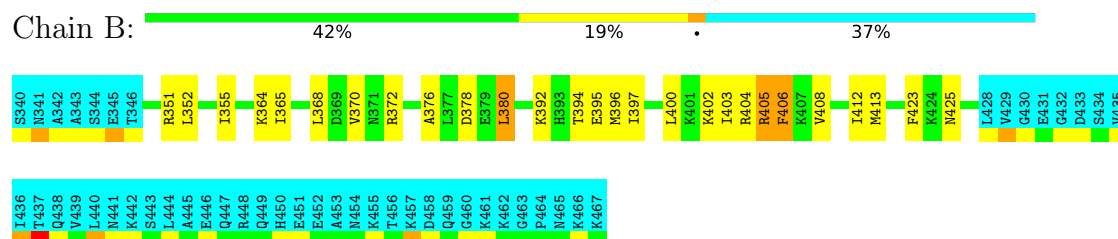


4.2.22 Score per residue for model 22 (medoid)

- Molecule 1: PC4 and SFRS1-interacting protein

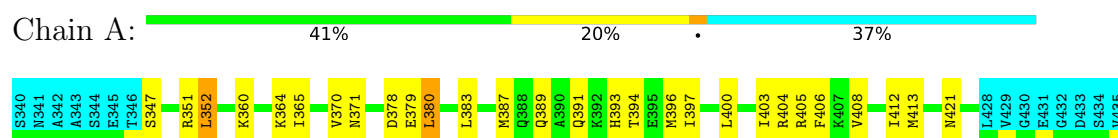


- Molecule 1: PC4 and SFRS1-interacting protein



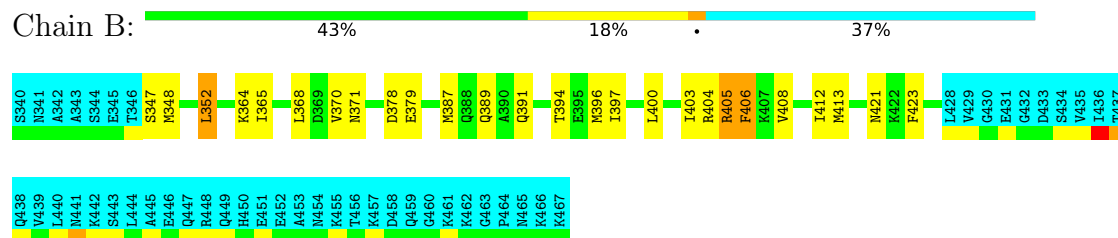
4.2.23 Score per residue for model 23

- Molecule 1: PC4 and SFRS1-interacting protein



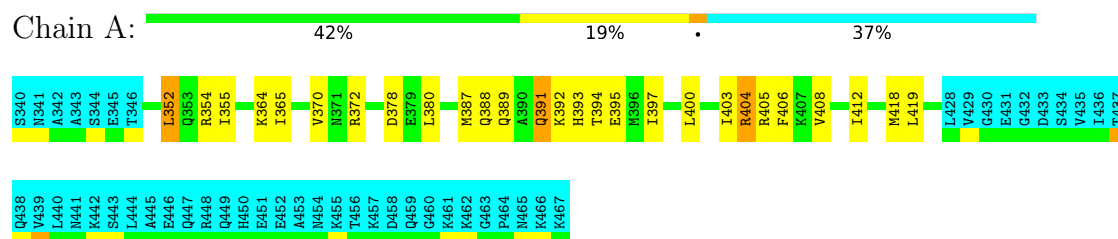


- Molecule 1: PC4 and SFRS1-interacting protein

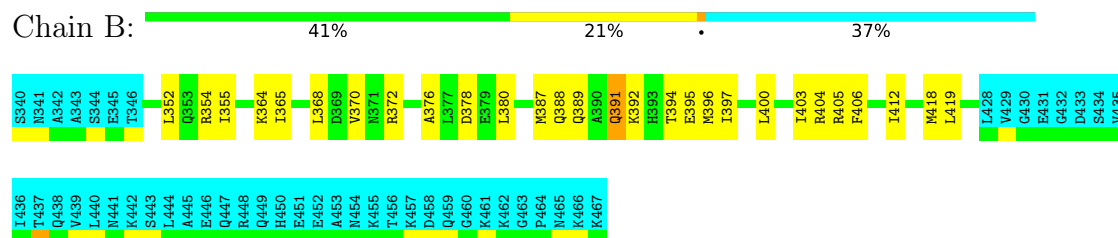


4.2.24 Score per residue for model 24

- Molecule 1: PC4 and SFRS1-interacting protein

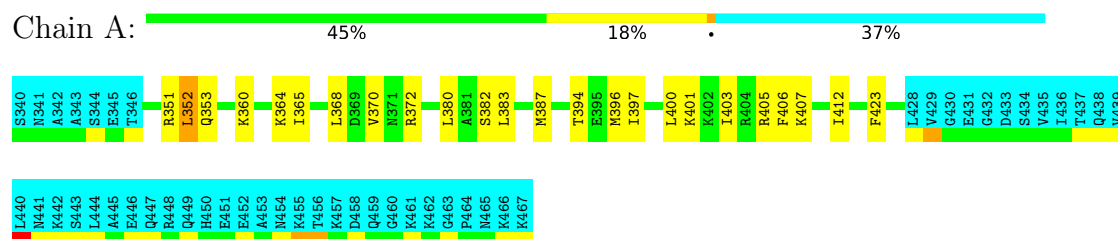


- Molecule 1: PC4 and SFRS1-interacting protein

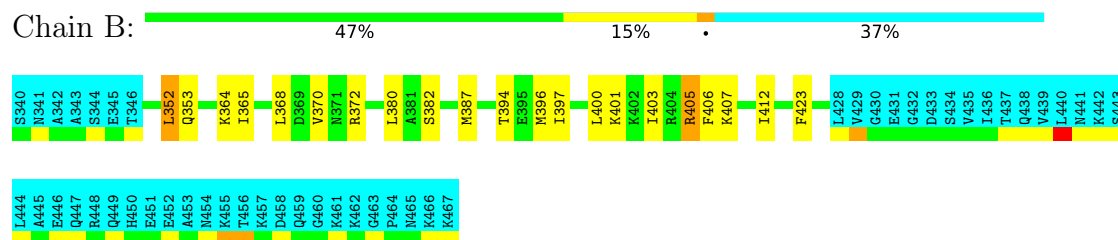


4.2.25 Score per residue for model 25

- Molecule 1: PC4 and SFRS1-interacting protein

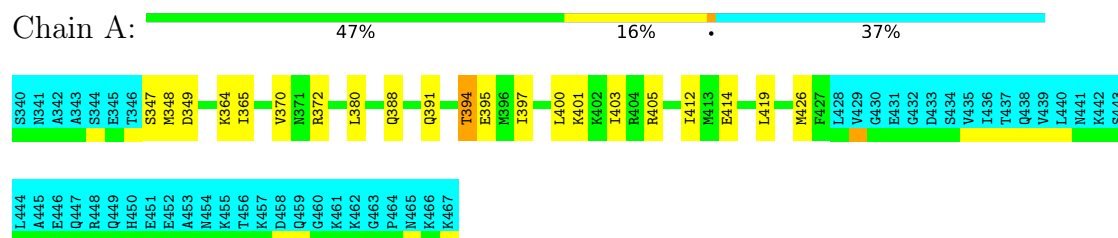


- Molecule 1: PC4 and SFRS1-interacting protein

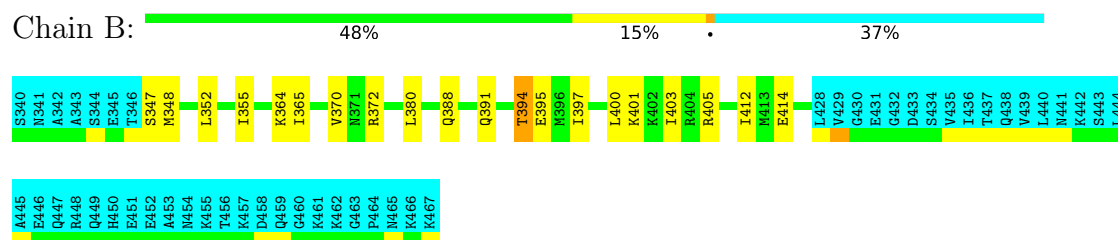


4.2.26 Score per residue for model 26

- Molecule 1: PC4 and SFRS1-interacting protein

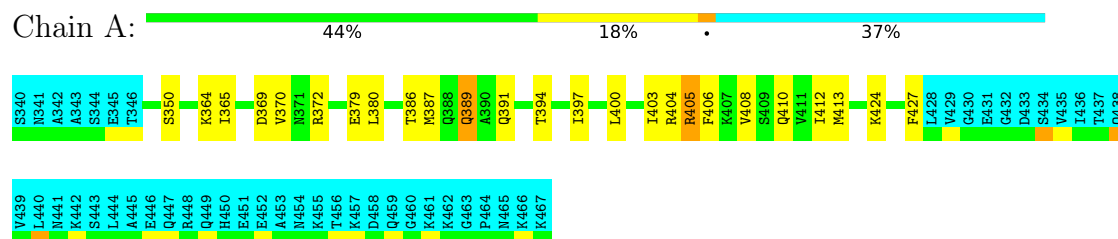


- Molecule 1: PC4 and SFRS1-interacting protein

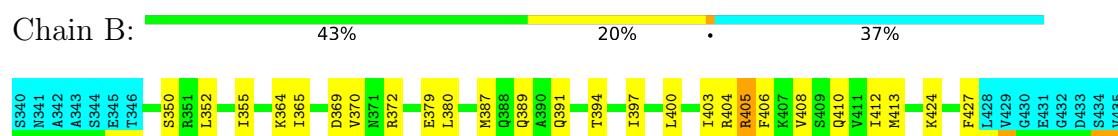


4.2.27 Score per residue for model 27

- Molecule 1: PC4 and SFRS1-interacting protein



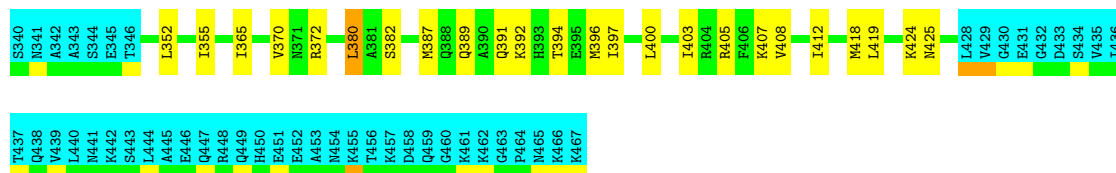
- Molecule 1: PC4 and SFRS1-interacting protein





4.2.28 Score per residue for model 28

- Molecule 1: PC4 and SFRS1-interacting protein

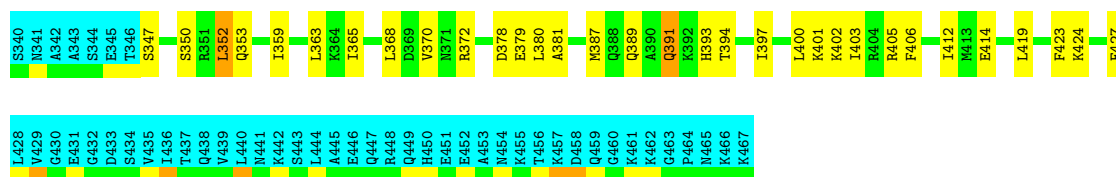


- Molecule 1: PC4 and SFRS1-interacting protein

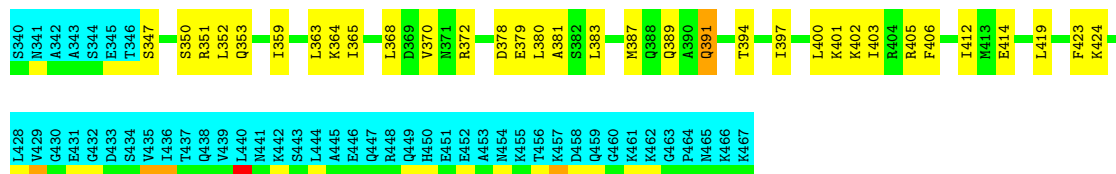
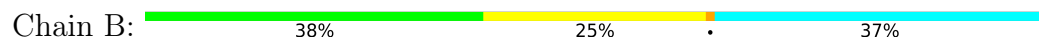


4.2.29 Score per residue for model 29

- Molecule 1: PC4 and SFRS1-interacting protein

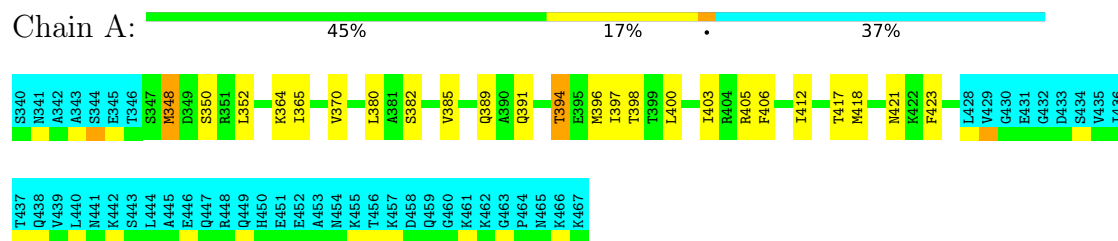


- Molecule 1: PC4 and SFRS1-interacting protein

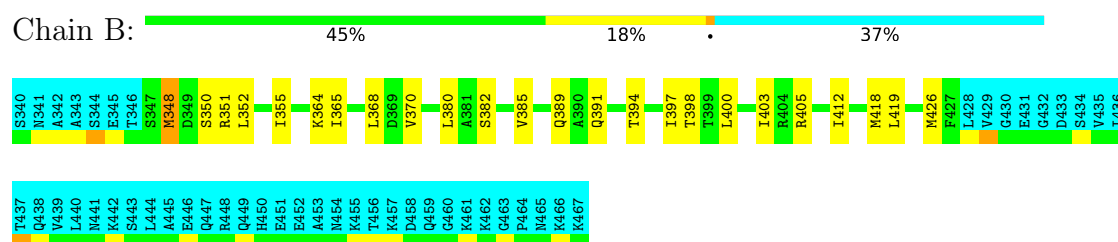


4.2.30 Score per residue for model 30

- Molecule 1: PC4 and SFRS1-interacting protein



- Molecule 1: PC4 and SFRS1-interacting protein



5 Refinement protocol and experimental data overview

The models were refined using the following method: *torsion angle dynamics*.

Of the 100 calculated structures, 30 were deposited, based on the following criterion: *structures with the least restraint violations*.

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

Software name	Classification	Version
CYANA	refinement	

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	1561
Number of shifts mapped to atoms	1561
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	45%

6 Model quality

6.1 Standard geometry

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

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no planarity outliers.

6.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in each chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes averaged over the ensemble.

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	665	701	701	16±2
1	B	665	701	701	15±2
All	All	39900	42060	42060	633

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:403:ILE:HG22	1:B:365:ILE:HD11	0.94	1.39	3	30
1:A:365:ILE:HD11	1:B:403:ILE:HG22	0.94	1.39	13	30
1:A:380:LEU:HD23	1:B:419:LEU:HD13	0.82	1.50	21	1
1:A:419:LEU:HD13	1:B:380:LEU:HD23	0.82	1.50	18	2
1:A:352:LEU:HD22	1:A:396:MET:HE1	0.78	1.55	1	12
1:B:352:LEU:HD22	1:B:396:MET:HE1	0.78	1.53	20	12
1:A:419:LEU:HD12	1:B:380:LEU:HD12	0.66	1.66	17	4
1:A:419:LEU:HD13	1:B:380:LEU:CD2	0.65	2.21	18	2
1:A:352:LEU:HD22	1:A:396:MET:HE2	0.65	1.66	18	1
1:A:406:PHE:CD2	1:B:368:LEU:HD13	0.63	2.28	19	8
1:A:380:LEU:HD12	1:B:419:LEU:HD12	0.63	1.70	28	3
1:A:412:ILE:HD11	1:B:370:VAL:HB	0.62	1.71	17	26
1:A:380:LEU:CD2	1:B:419:LEU:HD13	0.62	2.24	21	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:368:LEU:HD13	1:B:406:PHE:CE1	0.61	2.31	15	5
1:A:380:LEU:HD12	1:B:419:LEU:HD22	0.61	1.72	12	4
1:A:397:ILE:HD13	1:B:427:PHE:CE2	0.60	2.32	27	3
1:A:348:MET:HE2	1:A:385:VAL:HG22	0.60	1.72	8	1
1:A:406:PHE:CE2	1:B:368:LEU:HD13	0.60	2.32	19	5
1:A:408:VAL:O	1:A:413:MET:HE2	0.60	1.96	19	7
1:A:370:VAL:HB	1:B:412:ILE:HD11	0.59	1.72	11	26
1:A:397:ILE:HA	1:A:400:LEU:HD12	0.59	1.74	20	29
1:B:397:ILE:HA	1:B:400:LEU:HD12	0.59	1.74	20	29
1:B:352:LEU:HA	1:B:355:ILE:HD12	0.59	1.74	8	17
1:A:427:PHE:CE2	1:B:397:ILE:HD13	0.59	2.33	27	3
1:B:394:THR:HA	1:B:397:ILE:HD12	0.58	1.74	12	12
1:A:380:LEU:O	1:A:380:LEU:HD13	0.58	1.99	20	10
1:A:394:THR:HA	1:A:397:ILE:HD12	0.57	1.74	12	12
1:A:427:PHE:CD1	1:B:387:MET:HE1	0.57	2.35	29	2
1:A:408:VAL:HG13	1:A:413:MET:HE2	0.57	1.75	12	5
1:B:380:LEU:O	1:B:380:LEU:HD13	0.57	2.00	1	10
1:A:365:ILE:CD1	1:B:403:ILE:HG22	0.57	2.26	11	29
1:A:415:LYS:CB	1:B:377:LEU:HD23	0.57	2.30	14	1
1:A:351:ARG:CZ	1:A:383:LEU:HD21	0.56	2.30	23	2
1:B:351:ARG:CZ	1:B:383:LEU:HD21	0.56	2.31	29	2
1:A:381:ALA:HB2	1:B:419:LEU:HD21	0.56	1.78	29	2
1:A:419:LEU:HG	1:B:380:LEU:HD12	0.56	1.77	20	1
1:A:348:MET:HE2	1:A:385:VAL:HB	0.56	1.78	30	2
1:B:408:VAL:HG13	1:B:413:MET:HE2	0.56	1.76	12	3
1:A:377:LEU:HD23	1:B:419:LEU:HD12	0.56	1.77	17	1
1:B:387:MET:HE3	1:B:391:GLN:HG3	0.55	1.77	29	1
1:A:403:ILE:HG22	1:B:365:ILE:CD1	0.55	2.28	6	29
1:A:352:LEU:HD23	1:A:393:HIS:CG	0.55	2.37	8	7
1:A:352:LEU:HG	1:A:396:MET:HE1	0.54	1.79	11	5
1:B:355:ILE:HG23	1:B:376:ALA:HB1	0.53	1.80	16	15
1:A:419:LEU:HD13	1:B:380:LEU:HD12	0.53	1.78	24	4
1:A:387:MET:HE3	1:A:391:GLN:HG3	0.52	1.79	29	1
1:A:423:PHE:CZ	1:B:380:LEU:HD11	0.52	2.39	2	12
1:A:377:LEU:HD22	1:B:419:LEU:HD12	0.52	1.80	7	1
1:A:419:LEU:HD22	1:B:380:LEU:HD12	0.52	1.82	12	3
1:A:377:LEU:HD23	1:B:415:LYS:CB	0.52	2.34	14	1
1:A:380:LEU:HD11	1:B:423:PHE:CZ	0.52	2.39	29	13
1:A:391:GLN:O	1:A:394:THR:HG23	0.52	2.05	20	10
1:A:406:PHE:CD1	1:B:368:LEU:HD13	0.52	2.40	14	3
1:A:380:LEU:HD12	1:B:419:LEU:HD13	0.51	1.82	19	5

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:B:352:LEU:HG	1:B:396:MET:HE1	0.51	1.82	9	3
1:A:352:LEU:HA	1:A:355:ILE:HD12	0.51	1.83	28	11
1:B:408:VAL:O	1:B:413:MET:HE2	0.51	2.06	27	5
1:B:348:MET:HE2	1:B:385:VAL:HB	0.50	1.80	30	1
1:B:409:SER:O	1:B:413:MET:HE3	0.50	2.06	6	1
1:A:417:THR:HG22	1:A:421:ASN:OD1	0.50	2.06	11	2
1:B:391:GLN:O	1:B:394:THR:HG23	0.50	2.07	6	12
1:A:394:THR:HG22	1:B:427:PHE:CZ	0.49	2.42	1	1
1:A:419:LEU:CD1	1:B:380:LEU:HD12	0.49	2.36	17	4
1:A:419:LEU:HD21	1:B:381:ALA:HB2	0.49	1.83	29	1
1:A:427:PHE:CZ	1:B:394:THR:HG22	0.49	2.42	1	1
1:A:397:ILE:HD13	1:B:427:PHE:CZ	0.48	2.42	11	2
1:A:355:ILE:CD1	1:A:383:LEU:HD11	0.48	2.39	13	2
1:A:368:LEU:HD13	1:B:406:PHE:CD1	0.48	2.43	6	6
1:A:368:LEU:HD13	1:B:406:PHE:CD2	0.47	2.44	25	4
1:A:406:PHE:CE1	1:B:368:LEU:HD13	0.47	2.45	22	2
1:A:380:LEU:HD23	1:A:383:LEU:HD12	0.47	1.85	18	1
1:A:380:LEU:C	1:A:380:LEU:HD13	0.47	2.35	29	5
1:A:380:LEU:HD13	1:A:380:LEU:C	0.47	2.35	1	7
1:B:380:LEU:HD11	1:B:396:MET:HE1	0.47	1.86	21	1
1:A:427:PHE:CZ	1:B:397:ILE:HD13	0.47	2.44	27	2
1:B:410:GLN:HA	1:B:413:MET:HE3	0.46	1.87	19	1
1:A:380:LEU:HD13	1:A:380:LEU:O	0.46	2.10	29	3
1:A:406:PHE:CE1	1:B:408:VAL:HG13	0.46	2.45	3	2
1:B:370:VAL:O	1:B:374:ILE:HD12	0.46	2.11	20	2
1:B:380:LEU:HD13	1:B:380:LEU:C	0.46	2.35	29	9
1:A:415:LYS:HB2	1:B:377:LEU:HD23	0.45	1.87	14	1
1:B:359:ILE:HG22	1:B:363:LEU:HD12	0.45	1.89	6	5
1:B:352:LEU:CD2	1:B:380:LEU:HD23	0.45	2.42	20	1
1:A:406:PHE:CD2	1:B:365:ILE:HD13	0.45	2.47	14	1
1:A:380:LEU:HD12	1:B:419:LEU:CD1	0.44	2.42	10	2
1:A:370:VAL:O	1:A:374:ILE:HD12	0.44	2.13	12	2
1:A:359:ILE:HG22	1:A:363:LEU:HD12	0.44	1.88	15	5
1:A:359:ILE:HG23	1:A:373:CYS:SG	0.44	2.52	19	1
1:A:387:MET:HE2	1:A:391:GLN:CG	0.43	2.43	20	1
1:A:419:LEU:HD12	1:B:377:LEU:HD22	0.43	1.89	7	1
1:A:386:THR:HG22	1:A:389:GLN:CD	0.43	2.38	27	1
1:A:408:VAL:O	1:A:408:VAL:HG13	0.43	2.13	19	1
1:A:380:LEU:HD11	1:A:396:MET:HE1	0.43	1.90	21	1
1:A:409:SER:O	1:A:413:MET:HE3	0.43	2.13	8	1
1:A:423:PHE:HZ	1:B:380:LEU:HD11	0.43	1.74	9	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:408:VAL:HG13	1:B:406:PHE:CE2	0.43	2.48	24	1
1:A:365:ILE:HD11	1:B:403:ILE:CG2	0.42	2.29	30	1
1:A:405:ARG:O	1:A:406:PHE:C	0.42	2.62	27	14
1:B:387:MET:HE3	1:B:391:GLN:CG	0.42	2.44	1	2
1:A:368:LEU:HD13	1:B:406:PHE:CE2	0.42	2.50	25	1
1:A:352:LEU:HD23	1:A:355:ILE:HD12	0.42	1.92	13	1
1:A:382:SER:O	1:A:383:LEU:HD23	0.42	2.14	20	1
1:B:405:ARG:O	1:B:406:PHE:C	0.41	2.63	8	11
1:A:351:ARG:NH2	1:A:383:LEU:HD22	0.41	2.30	20	1
1:B:387:MET:HE2	1:B:391:GLN:CG	0.41	2.45	20	1
1:B:408:VAL:HG22	1:B:412:ILE:HB	0.41	1.92	19	2
1:A:351:ARG:HH11	1:A:383:LEU:HD22	0.41	1.75	25	1
1:A:417:THR:HG22	1:A:421:ASN:ND2	0.41	2.30	5	1
1:A:427:PHE:HD1	1:B:387:MET:HE1	0.41	1.74	1	1
1:A:380:LEU:HD11	1:B:423:PHE:HZ	0.41	1.76	17	2
1:A:408:VAL:HG23	1:A:413:MET:HE2	0.41	1.93	2	1
1:A:408:VAL:HG22	1:A:412:ILE:HB	0.41	1.92	28	1
1:B:352:LEU:HD23	1:B:393:HIS:CG	0.41	2.51	1	1
1:A:382:SER:C	1:A:383:LEU:HD23	0.41	2.41	20	1
1:A:370:VAL:CB	1:B:412:ILE:HD11	0.40	2.45	11	1
1:A:412:ILE:HD11	1:B:370:VAL:CB	0.40	2.45	17	1
1:B:359:ILE:HG23	1:B:373:CYS:SG	0.40	2.56	19	2
1:A:403:ILE:CG2	1:B:365:ILE:HD11	0.40	2.28	3	1
1:A:415:LYS:HB3	1:B:377:LEU:HD23	0.40	1.93	14	1
1:B:380:LEU:HD21	1:B:396:MET:CE	0.40	2.47	3	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	81/128 (63%)	76±1 (93±1%)	5±1 (7±1%)	0±0 (0±0%)	100	100
1	B	81/128 (63%)	76±1 (93±1%)	5±1 (7±1%)	0±0 (0±0%)	100	100
All	All	4860/7680 (63%)	4538 (93%)	321 (7%)	1 (0%)	100	100

All 1 unique Ramachandran outliers are listed below.

Mol	Chain	Res	Type	Models (Total)
1	B	409	SER	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	77/116 (66%)	64±2 (83±3%)	13±2 (17±3%)	4	38
1	B	77/116 (66%)	64±2 (83±3%)	13±2 (17±3%)	4	38
All	All	4620/6960 (66%)	3839 (83%)	781 (17%)	4	38

All 83 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	B	405	ARG	30
1	A	405	ARG	29
1	B	364	LYS	26
1	A	364	LYS	24
1	A	387	MET	22
1	B	387	MET	21
1	A	404	ARG	19
1	A	394	THR	19
1	B	394	THR	19
1	B	404	ARG	18
1	A	372	ARG	16
1	A	379	GLU	16
1	B	372	ARG	16
1	B	379	GLU	16
1	A	392	LYS	15
1	B	348	MET	15
1	B	392	LYS	15
1	A	348	MET	14
1	A	382	SER	13
1	B	382	SER	13
1	A	347	SER	12
1	A	424	LYS	12

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Mol	Chain	Res	Type	Models (Total)
1	B	347	SER	12
1	A	350	SER	12
1	A	401	LYS	12
1	B	350	SER	12
1	B	401	LYS	12
1	A	389	GLN	12
1	A	395	GLU	12
1	B	389	GLN	12
1	B	395	GLU	12
1	A	391	GLN	11
1	B	391	GLN	11
1	B	424	LYS	11
1	B	380	LEU	11
1	A	380	LEU	10
1	A	352	LEU	10
1	A	407	LYS	8
1	B	352	LEU	8
1	B	407	LYS	8
1	B	414	GLU	8
1	B	418	MET	8
1	A	369	ASP	7
1	B	369	ASP	7
1	A	414	GLU	7
1	A	418	MET	7
1	A	360	LYS	6
1	B	406	PHE	6
1	A	378	ASP	6
1	B	378	ASP	6
1	A	354	ARG	5
1	B	354	ARG	5
1	A	384	GLN	5
1	B	384	GLN	5
1	A	375	GLU	5
1	B	375	GLU	5
1	B	396	MET	5
1	A	388	GLN	5
1	B	388	GLN	5
1	B	371	ASN	5
1	A	425	ASN	5
1	B	425	ASN	5
1	A	421	ASN	4
1	B	421	ASN	4

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Mol	Chain	Res	Type	Models (Total)
1	A	396	MET	4
1	B	360	LYS	4
1	A	406	PHE	4
1	B	351	ARG	4
1	A	410	GLN	3
1	B	410	GLN	3
1	A	402	LYS	3
1	B	402	LYS	3
1	A	371	ASN	3
1	A	351	ARG	3
1	A	353	GLN	3
1	B	353	GLN	3
1	A	398	THR	2
1	B	398	THR	2
1	A	422	LYS	1
1	B	422	LYS	1
1	A	409	SER	1
1	B	409	SER	1
1	A	349	ASP	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 ⓘ

There are no oligosaccharides in this entry.

6.6 Ligand geometry ⓘ

There are no ligands in this entry.

6.7 Other polymers ⓘ

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

The completeness of assignment taking into account all chemical shift lists is 45% for the well-defined parts and 43% for the entire structure.

7.1 Chemical shift list 1

File name: `working_cs.cif`

Chemical shift list name: *starch_output*

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	1561
Number of shifts mapped to atoms	1561
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	2

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	126	-0.67 ± 0.13	Should be checked
$^{13}\text{C}_\beta$	121	0.27 ± 0.04	None needed (< 0.5 ppm)
$^{13}\text{C}'$	126	-0.47 ± 0.08	None needed (< 0.5 ppm)
^{15}N	122	-0.41 ± 0.19	None needed (< 0.5 ppm)

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 45%, i.e. 1064 atoms were assigned a chemical shift out of a possible 2382. 0 out of 24 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	396/810 (49%)	158/324 (49%)	160/324 (49%)	78/162 (48%)
Sidechain	638/1466 (44%)	435/948 (46%)	195/448 (44%)	8/70 (11%)

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	Total	¹H	¹³C	¹⁵N
Aromatic	30/106 (28%)	20/54 (37%)	10/48 (21%)	0/4 (0%)
Overall	1064/2382 (45%)	613/1326 (46%)	365/820 (45%)	86/236 (36%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 43%, i.e. 1559 atoms were assigned a chemical shift out of a possible 3590. 0 out of 36 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Backbone	626/1284 (49%)	252/518 (49%)	252/512 (49%)	122/254 (48%)
Sidechain	903/2186 (41%)	608/1404 (43%)	287/676 (42%)	8/106 (8%)
Aromatic	30/120 (25%)	20/62 (32%)	10/52 (19%)	0/6 (0%)
Overall	1559/3590 (43%)	880/1984 (44%)	549/1240 (44%)	130/366 (36%)

7.1.4 Statistically unusual chemical shifts ⓘ

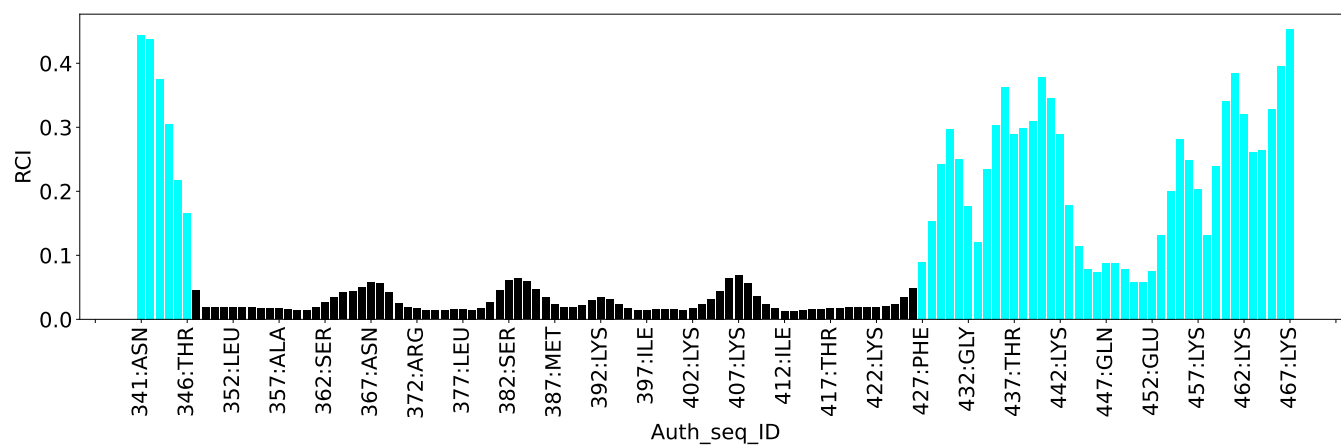
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	417	THR	HG1	5.62	0.08 – 2.19	21.2
1	A	386	THR	HG1	5.57	0.08 – 2.19	21.0

7.1.5 Random Coil Index (RCI) plots ⓘ

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	4091
Intra-residue ($ i-j =0$)	1140
Sequential ($ i-j =1$)	925
Medium range ($ i-j >1$ and $ i-j <5$)	985
Long range ($ i-j \geq 5$)	346
Inter-chain	695
Hydrogen bond restraints	0
Disulfide bond restraints	0
Total dihedral-angle restraints	348
Number of unmapped restraints	0
Number of restraints per residue	17.3
Number of long range restraints per residue ¹	1.4

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)	16.7	0.2
0.2-0.5 (Medium)	6.9	0.41
>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.

Bins (°)	Average number of violations per model	Max (°)
1.0-10.0 (Small)	15.8	5.66
10.0-20.0 (Medium)	None	None
>20.0 (Large)	None	None

9 Distance violation analysis ⓘ

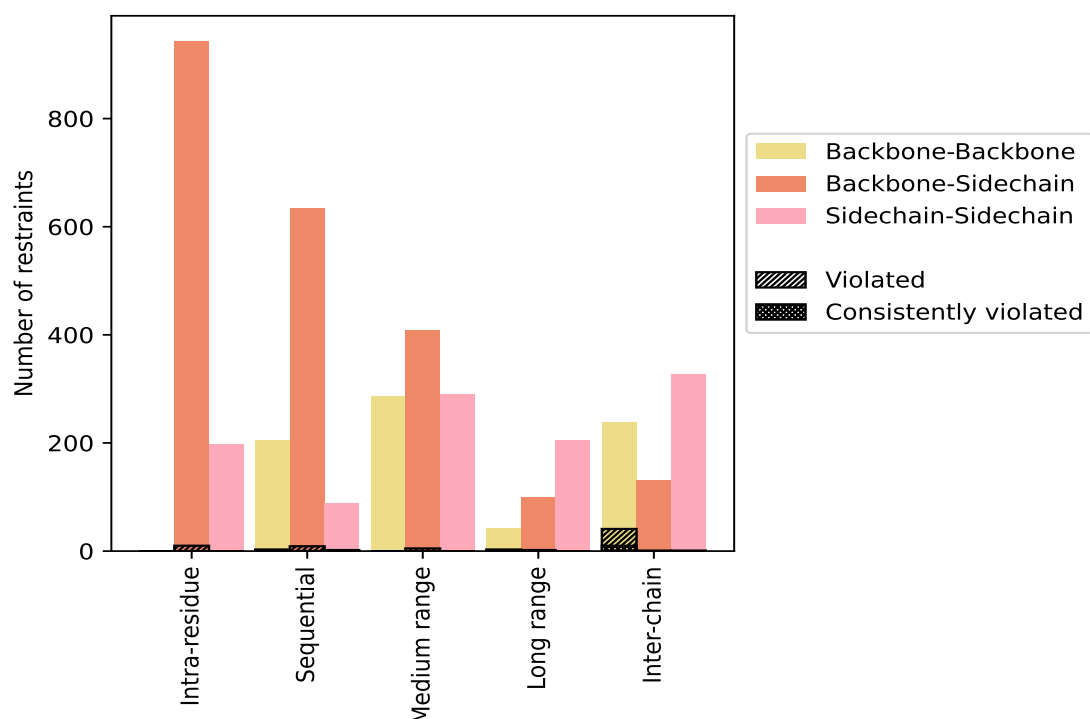
9.1 Summary of distance violations ⓘ

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 ($i-j =0$)	1140	27.9	10	0.9	0.2	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	943	23.1	10	1.1	0.2	0	0.0	0.0
Sidechain-Sidechain	197	4.8	0	0.0	0.0	0	0.0	0.0
Sequential ($i-j =1$)	925	22.6	14	1.5	0.3	0	0.0	0.0
Backbone-Backbone	204	5.0	3	1.5	0.1	0	0.0	0.0
Backbone-Sidechain	633	15.5	9	1.4	0.2	0	0.0	0.0
Sidechain-Sidechain	88	2.2	2	2.3	0.0	0	0.0	0.0
Medium range ($i-j >1$ & $i-j <5$)	985	24.1	5	0.5	0.1	0	0.0	0.0
Backbone-Backbone	286	7.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	409	10.0	5	1.2	0.1	0	0.0	0.0
Sidechain-Sidechain	290	7.1	0	0.0	0.0	0	0.0	0.0
Long range ($i-j \geq 5$)	346	8.5	5	1.4	0.1	0	0.0	0.0
Backbone-Backbone	42	1.0	3	7.1	0.1	0	0.0	0.0
Backbone-Sidechain	100	2.4	2	2.0	0.0	0	0.0	0.0
Sidechain-Sidechain	204	5.0	0	0.0	0.0	0	0.0	0.0
Inter-chain	695	17.0	43	6.2	1.1	10	1.4	0.2
Backbone-Backbone	238	5.8	41	17.2	1.0	10	4.2	0.2
Backbone-Sidechain	130	3.2	1	0.8	0.0	0	0.0	0.0
Sidechain-Sidechain	327	8.0	1	0.3	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	4091	100.0	77	1.9	1.9	10	0.2	0.2
Backbone-Backbone	770	18.8	47	6.1	1.1	10	1.3	0.2
Backbone-Sidechain	2215	54.1	27	1.2	0.7	0	0.0	0.0
Sidechain-Sidechain	1106	27.0	3	0.3	0.1	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 disulfid 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	0	0	22	22	0.17	0.32	0.07	0.16
2	0	0	2	1	26	29	0.16	0.41	0.08	0.12
3	0	0	1	0	23	24	0.18	0.38	0.07	0.15
4	0	1	1	1	18	21	0.18	0.31	0.07	0.16
5	0	1	0	0	18	19	0.19	0.32	0.07	0.16
6	0	1	1	1	23	26	0.19	0.33	0.07	0.18
7	0	1	0	0	21	22	0.18	0.32	0.07	0.16
8	0	0	2	0	24	26	0.17	0.31	0.07	0.14
9	0	0	2	1	21	24	0.17	0.31	0.07	0.12
10	0	0	0	2	19	21	0.18	0.32	0.07	0.16

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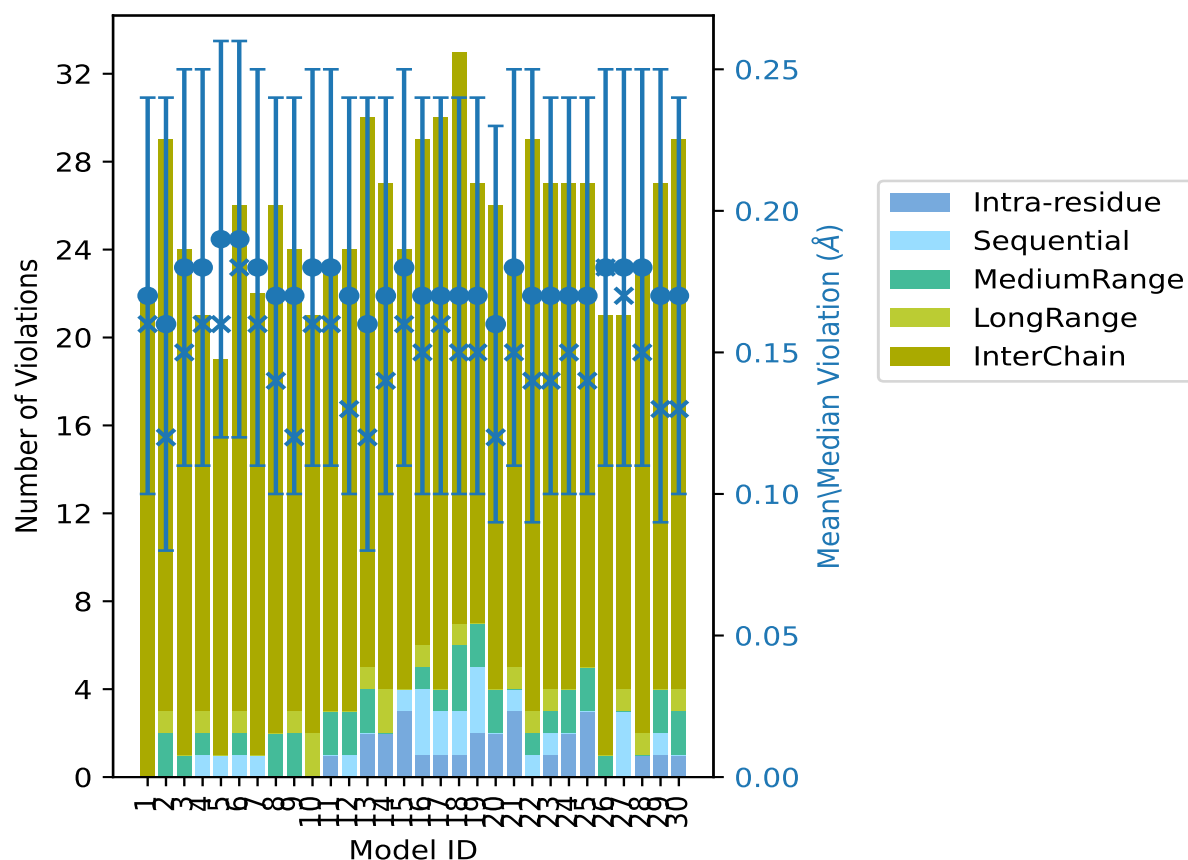
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Model ID	Number of violations						Mean (Å)	Max (Å)	SD ⁶ (Å)	Median (Å)
	IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total				
11	1	0	2	0	20	23	0.18	0.32	0.07	0.16
12	0	1	2	0	21	24	0.17	0.31	0.07	0.13
13	2	0	2	1	25	30	0.16	0.41	0.08	0.12
14	2	0	0	2	23	27	0.17	0.33	0.07	0.14
15	3	1	0	0	20	24	0.18	0.33	0.07	0.16
16	1	3	1	1	23	29	0.17	0.38	0.07	0.15
17	1	2	1	0	26	30	0.17	0.31	0.07	0.16
18	1	2	3	1	26	33	0.17	0.32	0.07	0.15
19	2	3	2	0	20	27	0.17	0.4	0.07	0.15
20	2	0	2	0	22	26	0.16	0.3	0.07	0.12
21	3	1	0	1	18	23	0.18	0.31	0.07	0.15
22	0	1	1	1	26	29	0.17	0.33	0.08	0.14
23	1	1	1	1	23	27	0.17	0.34	0.07	0.14
24	2	0	2	0	23	27	0.17	0.37	0.07	0.15
25	3	0	2	0	22	27	0.17	0.37	0.07	0.14
26	0	0	1	0	20	21	0.18	0.3	0.07	0.18
27	0	3	0	1	17	21	0.18	0.31	0.07	0.17
28	1	0	0	1	21	23	0.18	0.31	0.07	0.15
29	1	1	2	0	23	27	0.17	0.41	0.08	0.13
30	1	0	2	1	25	29	0.17	0.4	0.07	0.13

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 [i](#)



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 [i](#)

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, 4014(IR:1130, SQ:911, MR:980, LR:341, IC:652) 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	%
4	9	3	2	7	25	1	3.3
2	3	0	0	2	7	2	6.7
1	0	0	1	2	4	3	10.0
1	2	0	0	0	3	4	13.3
0	0	0	1	3	4	5	16.7
2	0	0	0	5	7	6	20.0

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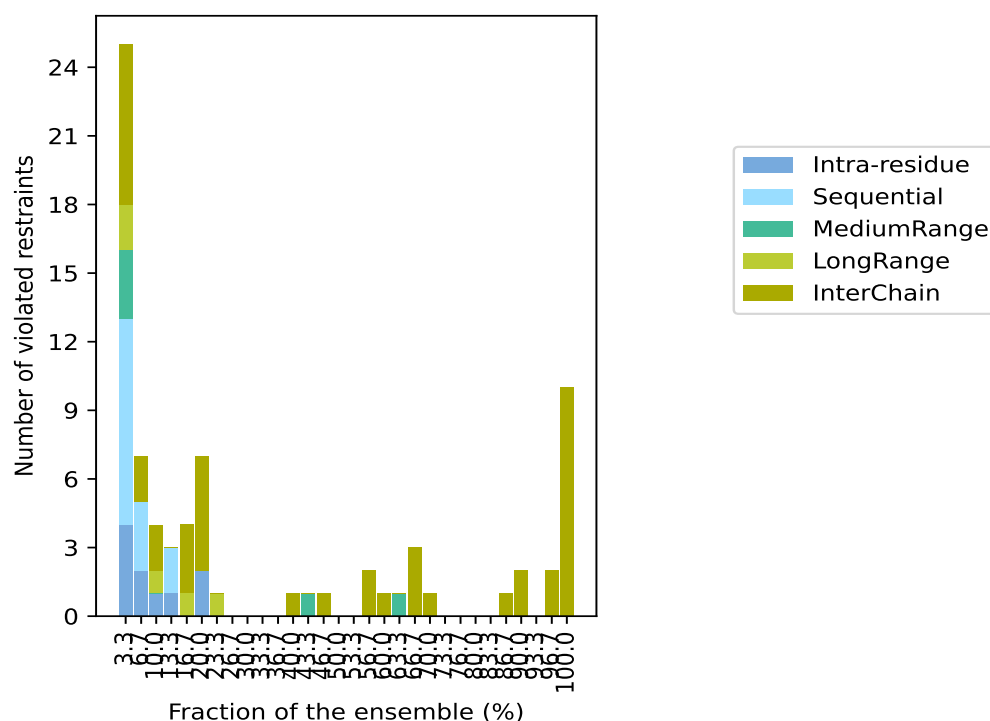
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Number of violated restraints						Fraction of the ensemble	
IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total	Count ⁶	%
0	0	0	1	0	1	7	23.3
0	0	0	0	0	0	8	26.7
0	0	0	0	0	0	9	30.0
0	0	0	0	0	0	10	33.3
0	0	0	0	0	0	11	36.7
0	0	0	0	1	1	12	40.0
0	0	1	0	0	1	13	43.3
0	0	0	0	1	1	14	46.7
0	0	0	0	0	0	15	50.0
0	0	0	0	0	0	16	53.3
0	0	0	0	2	2	17	56.7
0	0	0	0	1	1	18	60.0
0	0	1	0	0	1	19	63.3
0	0	0	0	3	3	20	66.7
0	0	0	0	1	1	21	70.0
0	0	0	0	0	0	22	73.3
0	0	0	0	0	0	23	76.7
0	0	0	0	0	0	24	80.0
0	0	0	0	0	0	25	83.3
0	0	0	0	1	1	26	86.7
0	0	0	0	2	2	27	90.0
0	0	0	0	0	0	28	93.3
0	0	0	0	2	2	29	96.7
0	0	0	0	10	10	30	100.0

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

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

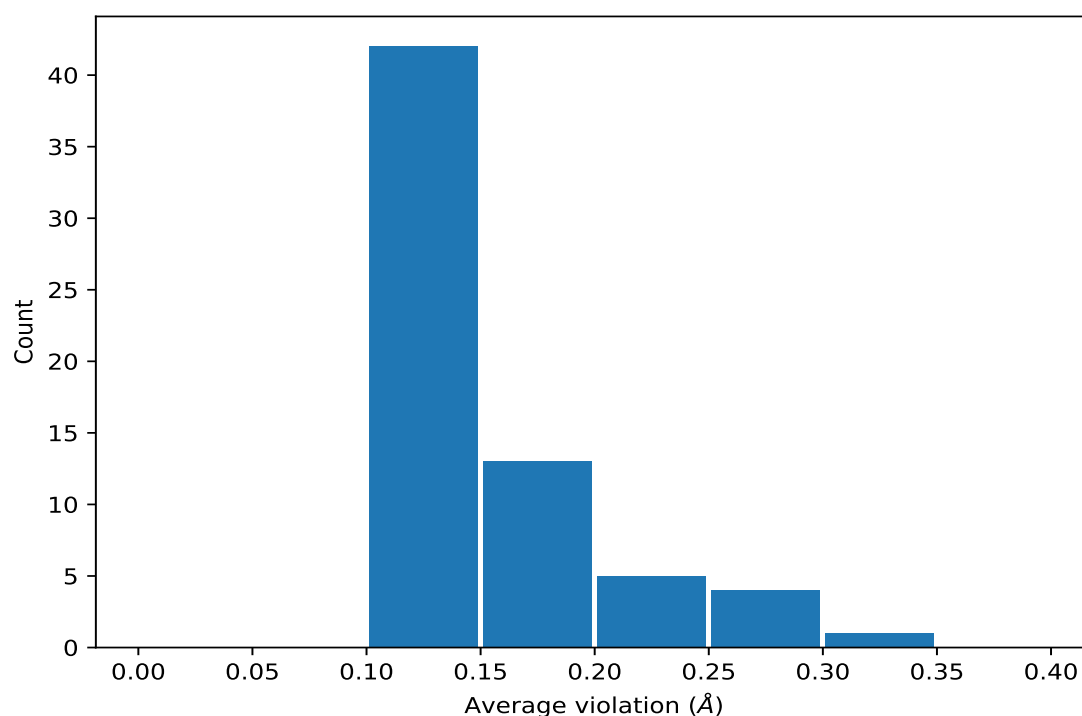
9.3.1 Bar graph : Distance violation statistics for the ensemble [i](#)



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)
(5,80)	1:407:A:LYS:CA	1:407:B:LYS:CA	30	0.33	0.05	0.31
(5,108)	1:404:A:ARG:CA	1:416:B:SER:CA	30	0.3	0.02	0.3
(5,107)	1:416:A:SER:CA	1:404:B:ARG:CA	30	0.3	0.01	0.3
(3,97)	1:416:A:SER:CA	1:403:B:ILE:CA	30	0.28	0.02	0.28
(3,98)	1:403:A:ILE:CA	1:416:B:SER:CA	30	0.28	0.02	0.28
(5,100)	1:404:A:ARG:CA	1:413:B:MET:CA	30	0.18	0.02	0.18
(5,99)	1:413:A:MET:CA	1:404:B:ARG:CA	30	0.18	0.02	0.18
(5,76)	1:406:A:PHE:CA	1:365:B:ILE:CA	30	0.17	0.02	0.17
(3,66)	1:404:A:ARG:CA	1:412:B:ILE:CA	30	0.14	0.02	0.13
(3,67)	1:412:A:ILE:CA	1:404:B:ARG:CA	30	0.14	0.02	0.14
(5,77)	1:365:A:ILE:CA	1:406:B:PHE:CA	29	0.18	0.02	0.17
(3,73)	1:407:A:LYS:CA	1:406:B:PHE:CA	29	0.18	0.04	0.19
(3,68)	1:405:A:ARG:CA	1:413:B:MET:CA	27	0.13	0.02	0.12
(3,69)	1:413:A:MET:CA	1:405:B:ARG:CA	27	0.13	0.02	0.12
(3,72)	1:406:A:PHE:CA	1:407:B:LYS:CA	26	0.17	0.04	0.18
(3,91)	1:413:A:MET:CA	1:403:B:ILE:CA	21	0.13	0.03	0.11

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(3,81)	1:408:A:VAL:CA	1:406:B:PHE:CA	20	0.16	0.05	0.15
(3,92)	1:403:A:ILE:CA	1:413:B:MET:CA	20	0.12	0.02	0.12
(3,77)	1:408:A:VAL:CA	1:363:B:LEU:CA	20	0.12	0.01	0.12
(1,386)	1:365:A:ILE:HD11	1:367:A:ASN:H	19	0.11	0.01	0.11
(1,386)	1:365:A:ILE:HD12	1:367:A:ASN:H	19	0.11	0.01	0.11
(1,386)	1:365:A:ILE:HD13	1:367:A:ASN:H	19	0.11	0.01	0.11
(5,12)	1:365:A:ILE:CA	1:360:B:LYS:CA	18	0.12	0.01	0.12
(5,13)	1:360:A:LYS:CA	1:365:B:ILE:CA	17	0.12	0.02	0.12
(3,78)	1:363:A:LEU:CA	1:408:B:VAL:CA	17	0.12	0.02	0.11
(3,82)	1:406:A:PHE:CA	1:408:B:VAL:CA	14	0.17	0.05	0.18
(1,387)	1:365:B:ILE:HD11	1:367:B:ASN:H	13	0.11	0.01	0.11
(1,387)	1:365:B:ILE:HD12	1:367:B:ASN:H	13	0.11	0.01	0.11
(1,387)	1:365:B:ILE:HD13	1:367:B:ASN:H	13	0.11	0.01	0.11
(3,11)	1:364:A:LYS:CA	1:364:B:LYS:CA	12	0.12	0.01	0.12
(3,106)	1:352:A:LEU:CA	1:393:A:HIS:CA	7	0.11	0.01	0.11
(3,56)	1:401:A:LYS:CA	1:420:B:TYR:CA	6	0.12	0.03	0.11
(1,1529)	1:353:A:GLN:HA	1:353:A:GLN:HG2	6	0.12	0.0	0.12
(5,81)	1:407:A:LYS:CA	1:408:B:VAL:CA	6	0.12	0.02	0.12
(5,89)	1:409:A:SER:CA	1:370:B:VAL:CA	6	0.12	0.02	0.12
(3,57)	1:420:A:TYR:CA	1:401:B:LYS:CA	6	0.12	0.01	0.11
(1,1530)	1:353:B:GLN:HA	1:353:B:GLN:HG2	6	0.12	0.01	0.12
(5,82)	1:408:A:VAL:CA	1:407:B:LYS:CA	6	0.1	0.0	0.11
(3,21)	1:406:A:PHE:CA	1:368:B:LEU:CA	5	0.12	0.02	0.12
(5,90)	1:370:A:VAL:CA	1:409:B:SER:CA	5	0.12	0.01	0.12
(5,101)	1:414:A:GLU:CA	1:404:B:ARG:CA	5	0.11	0.01	0.11
(5,4)	1:352:A:LEU:CA	1:380:A:LEU:CA	5	0.11	0.01	0.11
(1,3713)	1:414:B:GLU:H	1:414:B:GLU:HG2	4	0.21	0.04	0.23
(1,3713)	1:414:B:GLU:H	1:414:B:GLU:HG3	4	0.21	0.04	0.23
(1,1228)	1:421:B:ASN:HB3	1:422:B:LYS:H	4	0.14	0.01	0.14
(1,1227)	1:421:A:ASN:HB3	1:422:A:LYS:H	4	0.13	0.01	0.12
(1,3153)	1:414:A:GLU:H	1:414:A:GLU:HG2	3	0.22	0.04	0.24
(1,3153)	1:414:A:GLU:H	1:414:A:GLU:HG3	3	0.22	0.04	0.24
(3,80)	1:403:A:ILE:CA	1:408:B:VAL:CA	3	0.15	0.04	0.13
(3,109)	1:355:A:ILE:CA	1:380:A:LEU:CA	3	0.12	0.02	0.11
(5,58)	1:400:A:LEU:CA	1:420:B:TYR:CA	3	0.11	0.0	0.11
(1,363)	1:437:B:THR:HA	1:438:B:GLN:H	2	0.23	0.02	0.23
(1,362)	1:437:A:THR:HA	1:438:A:GLN:H	2	0.18	0.03	0.18
(1,2760)	1:361:A:ASN:HB2	1:362:A:SER:HB2	2	0.17	0.01	0.17
(1,2760)	1:361:A:ASN:HB2	1:362:A:SER:HB3	2	0.17	0.01	0.17
(1,2760)	1:361:A:ASN:HB3	1:362:A:SER:HB2	2	0.17	0.01	0.17
(1,2760)	1:361:A:ASN:HB3	1:362:A:SER:HB3	2	0.17	0.01	0.17
(1,2446)	1:436:A:ILE:HA	1:436:A:ILE:HD11	2	0.13	0.0	0.13

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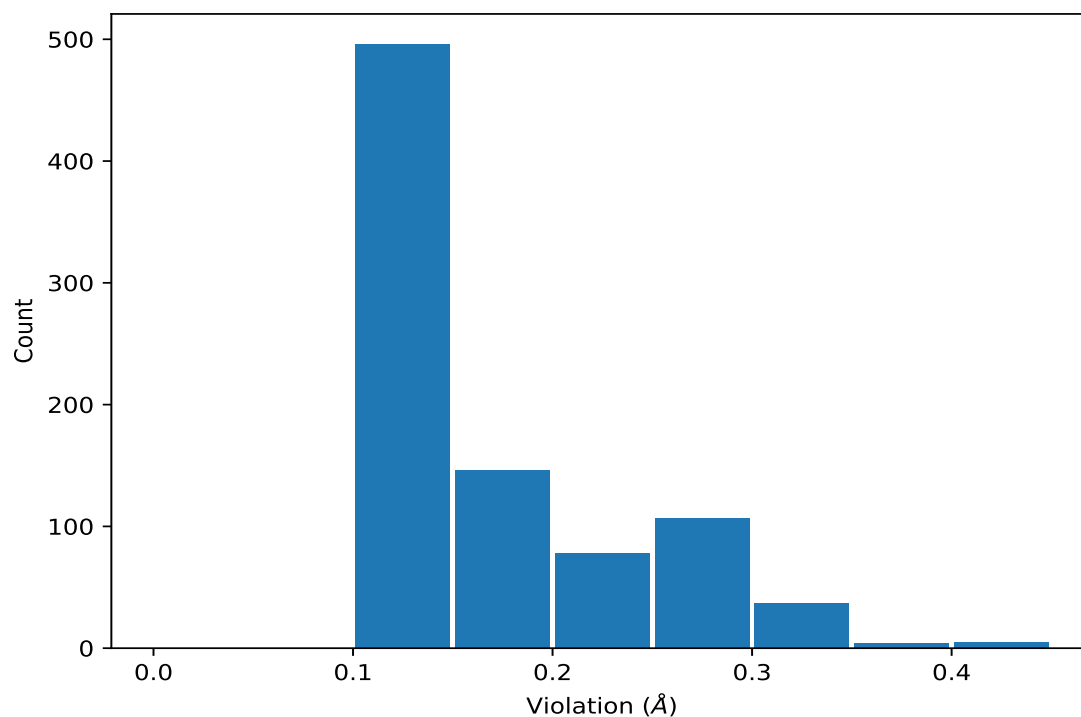
Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,2446)	1:436:A:ILE:HA	1:436:A:ILE:HD12	2	0.13	0.0	0.13
(1,2446)	1:436:A:ILE:HA	1:436:A:ILE:HD13	2	0.13	0.0	0.13
(1,2447)	1:436:B:ILE:HA	1:436:B:ILE:HD11	2	0.12	0.01	0.12
(1,2447)	1:436:B:ILE:HA	1:436:B:ILE:HD12	2	0.12	0.01	0.12
(1,2447)	1:436:B:ILE:HA	1:436:B:ILE:HD13	2	0.12	0.01	0.12
(5,95)	1:412:A:ILE:CA	1:403:B:ILE:CA	2	0.12	0.01	0.12
(5,102)	1:404:A:ARG:CA	1:414:B:GLU:CA	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)
(5,80)	1:407:A:LYS:CA	1:407:B:LYS:CA	2	0.41
(5,80)	1:407:A:LYS:CA	1:407:B:LYS:CA	13	0.41
(5,80)	1:407:A:LYS:CA	1:407:B:LYS:CA	29	0.41
(5,80)	1:407:A:LYS:CA	1:407:B:LYS:CA	30	0.4
(1,1040)	1:409:B:SER:H	1:412:B:ILE:HB	19	0.4
(5,80)	1:407:A:LYS:CA	1:407:B:LYS:CA	3	0.38
(5,80)	1:407:A:LYS:CA	1:407:B:LYS:CA	16	0.38
(5,80)	1:407:A:LYS:CA	1:407:B:LYS:CA	24	0.37
(5,80)	1:407:A:LYS:CA	1:407:B:LYS:CA	25	0.37
(5,108)	1:404:A:ARG:CA	1:416:B:SER:CA	23	0.34
(5,108)	1:404:A:ARG:CA	1:416:B:SER:CA	13	0.33
(5,107)	1:416:A:SER:CA	1:404:B:ARG:CA	13	0.33
(5,80)	1:407:A:LYS:CA	1:407:B:LYS:CA	14	0.33
(5,80)	1:407:A:LYS:CA	1:407:B:LYS:CA	15	0.33
(3,98)	1:403:A:ILE:CA	1:416:B:SER:CA	6	0.33
(1,1409)	1:439:A:VAL:HB	1:440:A:LEU:H	22	0.33
(5,108)	1:404:A:ARG:CA	1:416:B:SER:CA	5	0.32
(5,108)	1:404:A:ARG:CA	1:416:B:SER:CA	10	0.32
(5,108)	1:404:A:ARG:CA	1:416:B:SER:CA	18	0.32
(5,108)	1:404:A:ARG:CA	1:416:B:SER:CA	19	0.32
(5,108)	1:404:A:ARG:CA	1:416:B:SER:CA	22	0.32
(5,107)	1:416:A:SER:CA	1:404:B:ARG:CA	10	0.32
(5,107)	1:416:A:SER:CA	1:404:B:ARG:CA	11	0.32
(5,107)	1:416:A:SER:CA	1:404:B:ARG:CA	18	0.32
(5,107)	1:416:A:SER:CA	1:404:B:ARG:CA	23	0.32
(5,107)	1:416:A:SER:CA	1:404:B:ARG:CA	29	0.32
(5,107)	1:416:A:SER:CA	1:404:B:ARG:CA	30	0.32
(5,80)	1:407:A:LYS:CA	1:407:B:LYS:CA	1	0.32
(5,80)	1:407:A:LYS:CA	1:407:B:LYS:CA	5	0.32
(5,80)	1:407:A:LYS:CA	1:407:B:LYS:CA	6	0.32
(5,80)	1:407:A:LYS:CA	1:407:B:LYS:CA	7	0.32
(5,108)	1:404:A:ARG:CA	1:416:B:SER:CA	4	0.31
(5,108)	1:404:A:ARG:CA	1:416:B:SER:CA	17	0.31
(5,108)	1:404:A:ARG:CA	1:416:B:SER:CA	29	0.31
(5,107)	1:416:A:SER:CA	1:404:B:ARG:CA	4	0.31
(5,107)	1:416:A:SER:CA	1:404:B:ARG:CA	8	0.31
(5,107)	1:416:A:SER:CA	1:404:B:ARG:CA	21	0.31
(5,107)	1:416:A:SER:CA	1:404:B:ARG:CA	27	0.31
(5,80)	1:407:A:LYS:CA	1:407:B:LYS:CA	4	0.31
(5,80)	1:407:A:LYS:CA	1:407:B:LYS:CA	8	0.31
(5,80)	1:407:A:LYS:CA	1:407:B:LYS:CA	9	0.31
(5,80)	1:407:A:LYS:CA	1:407:B:LYS:CA	12	0.31
(5,80)	1:407:A:LYS:CA	1:407:B:LYS:CA	21	0.31

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(5,80)	1:407:A:LYS:CA	1:407:B:LYS:CA	28	0.31
(3,97)	1:416:A:SER:CA	1:403:B:ILE:CA	6	0.31
(3,97)	1:416:A:SER:CA	1:403:B:ILE:CA	22	0.31
(5,108)	1:404:A:ARG:CA	1:416:B:SER:CA	2	0.3
(5,108)	1:404:A:ARG:CA	1:416:B:SER:CA	3	0.3
(5,108)	1:404:A:ARG:CA	1:416:B:SER:CA	8	0.3
(5,108)	1:404:A:ARG:CA	1:416:B:SER:CA	11	0.3
(5,108)	1:404:A:ARG:CA	1:416:B:SER:CA	14	0.3
(5,108)	1:404:A:ARG:CA	1:416:B:SER:CA	16	0.3
(5,108)	1:404:A:ARG:CA	1:416:B:SER:CA	21	0.3
(5,108)	1:404:A:ARG:CA	1:416:B:SER:CA	27	0.3
(5,108)	1:404:A:ARG:CA	1:416:B:SER:CA	28	0.3
(5,108)	1:404:A:ARG:CA	1:416:B:SER:CA	30	0.3
(5,107)	1:416:A:SER:CA	1:404:B:ARG:CA	2	0.3
(5,107)	1:416:A:SER:CA	1:404:B:ARG:CA	5	0.3
(5,107)	1:416:A:SER:CA	1:404:B:ARG:CA	15	0.3
(5,107)	1:416:A:SER:CA	1:404:B:ARG:CA	19	0.3
(5,107)	1:416:A:SER:CA	1:404:B:ARG:CA	22	0.3
(5,107)	1:416:A:SER:CA	1:404:B:ARG:CA	24	0.3
(5,107)	1:416:A:SER:CA	1:404:B:ARG:CA	25	0.3
(5,107)	1:416:A:SER:CA	1:404:B:ARG:CA	28	0.3
(5,80)	1:407:A:LYS:CA	1:407:B:LYS:CA	10	0.3
(5,80)	1:407:A:LYS:CA	1:407:B:LYS:CA	20	0.3
(5,80)	1:407:A:LYS:CA	1:407:B:LYS:CA	22	0.3
(5,80)	1:407:A:LYS:CA	1:407:B:LYS:CA	23	0.3
(5,80)	1:407:A:LYS:CA	1:407:B:LYS:CA	26	0.3
(5,80)	1:407:A:LYS:CA	1:407:B:LYS:CA	27	0.3
(3,98)	1:403:A:ILE:CA	1:416:B:SER:CA	20	0.3
(3,98)	1:403:A:ILE:CA	1:416:B:SER:CA	28	0.3
(3,97)	1:416:A:SER:CA	1:403:B:ILE:CA	7	0.3
(3,97)	1:416:A:SER:CA	1:403:B:ILE:CA	14	0.3
(3,97)	1:416:A:SER:CA	1:403:B:ILE:CA	28	0.3
(5,108)	1:404:A:ARG:CA	1:416:B:SER:CA	6	0.29
(5,108)	1:404:A:ARG:CA	1:416:B:SER:CA	12	0.29
(5,108)	1:404:A:ARG:CA	1:416:B:SER:CA	15	0.29
(5,108)	1:404:A:ARG:CA	1:416:B:SER:CA	20	0.29
(5,108)	1:404:A:ARG:CA	1:416:B:SER:CA	25	0.29
(5,107)	1:416:A:SER:CA	1:404:B:ARG:CA	3	0.29
(5,107)	1:416:A:SER:CA	1:404:B:ARG:CA	6	0.29
(5,107)	1:416:A:SER:CA	1:404:B:ARG:CA	14	0.29
(5,107)	1:416:A:SER:CA	1:404:B:ARG:CA	17	0.29
(5,107)	1:416:A:SER:CA	1:404:B:ARG:CA	20	0.29

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(5,107)	1:416:A:SER:CA	1:404:B:ARG:CA	26	0.29
(5,80)	1:407:A:LYS:CA	1:407:B:LYS:CA	17	0.29
(5,80)	1:407:A:LYS:CA	1:407:B:LYS:CA	18	0.29
(3,98)	1:403:A:ILE:CA	1:416:B:SER:CA	1	0.29
(3,98)	1:403:A:ILE:CA	1:416:B:SER:CA	7	0.29
(3,98)	1:403:A:ILE:CA	1:416:B:SER:CA	8	0.29
(3,98)	1:403:A:ILE:CA	1:416:B:SER:CA	9	0.29
(3,98)	1:403:A:ILE:CA	1:416:B:SER:CA	14	0.29
(3,98)	1:403:A:ILE:CA	1:416:B:SER:CA	22	0.29
(3,97)	1:416:A:SER:CA	1:403:B:ILE:CA	1	0.29
(3,97)	1:416:A:SER:CA	1:403:B:ILE:CA	9	0.29
(3,97)	1:416:A:SER:CA	1:403:B:ILE:CA	11	0.29
(3,97)	1:416:A:SER:CA	1:403:B:ILE:CA	12	0.29
(3,97)	1:416:A:SER:CA	1:403:B:ILE:CA	19	0.29
(3,97)	1:416:A:SER:CA	1:403:B:ILE:CA	20	0.29
(5,108)	1:404:A:ARG:CA	1:416:B:SER:CA	1	0.28
(5,108)	1:404:A:ARG:CA	1:416:B:SER:CA	7	0.28
(5,108)	1:404:A:ARG:CA	1:416:B:SER:CA	9	0.28
(5,108)	1:404:A:ARG:CA	1:416:B:SER:CA	24	0.28
(5,108)	1:404:A:ARG:CA	1:416:B:SER:CA	26	0.28
(5,107)	1:416:A:SER:CA	1:404:B:ARG:CA	1	0.28
(5,107)	1:416:A:SER:CA	1:404:B:ARG:CA	7	0.28
(5,107)	1:416:A:SER:CA	1:404:B:ARG:CA	9	0.28
(5,107)	1:416:A:SER:CA	1:404:B:ARG:CA	12	0.28
(5,107)	1:416:A:SER:CA	1:404:B:ARG:CA	16	0.28
(3,98)	1:403:A:ILE:CA	1:416:B:SER:CA	10	0.28
(3,98)	1:403:A:ILE:CA	1:416:B:SER:CA	11	0.28
(3,98)	1:403:A:ILE:CA	1:416:B:SER:CA	12	0.28
(3,98)	1:403:A:ILE:CA	1:416:B:SER:CA	15	0.28
(3,98)	1:403:A:ILE:CA	1:416:B:SER:CA	17	0.28
(3,98)	1:403:A:ILE:CA	1:416:B:SER:CA	24	0.28
(3,98)	1:403:A:ILE:CA	1:416:B:SER:CA	26	0.28
(3,97)	1:416:A:SER:CA	1:403:B:ILE:CA	8	0.28
(3,97)	1:416:A:SER:CA	1:403:B:ILE:CA	10	0.28
(3,97)	1:416:A:SER:CA	1:403:B:ILE:CA	17	0.28
(3,97)	1:416:A:SER:CA	1:403:B:ILE:CA	18	0.28
(3,98)	1:403:A:ILE:CA	1:416:B:SER:CA	2	0.27
(3,98)	1:403:A:ILE:CA	1:416:B:SER:CA	4	0.27
(3,98)	1:403:A:ILE:CA	1:416:B:SER:CA	18	0.27
(3,98)	1:403:A:ILE:CA	1:416:B:SER:CA	21	0.27
(3,98)	1:403:A:ILE:CA	1:416:B:SER:CA	25	0.27
(3,97)	1:416:A:SER:CA	1:403:B:ILE:CA	2	0.27

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,97)	1:416:A:SER:CA	1:403:B:ILE:CA	5	0.27
(3,97)	1:416:A:SER:CA	1:403:B:ILE:CA	21	0.27
(3,97)	1:416:A:SER:CA	1:403:B:ILE:CA	24	0.27
(3,97)	1:416:A:SER:CA	1:403:B:ILE:CA	26	0.27
(3,97)	1:416:A:SER:CA	1:403:B:ILE:CA	27	0.27
(3,98)	1:403:A:ILE:CA	1:416:B:SER:CA	3	0.26
(3,98)	1:403:A:ILE:CA	1:416:B:SER:CA	5	0.26
(3,98)	1:403:A:ILE:CA	1:416:B:SER:CA	23	0.26
(3,98)	1:403:A:ILE:CA	1:416:B:SER:CA	27	0.26
(3,98)	1:403:A:ILE:CA	1:416:B:SER:CA	29	0.26
(3,97)	1:416:A:SER:CA	1:403:B:ILE:CA	3	0.26
(3,97)	1:416:A:SER:CA	1:403:B:ILE:CA	4	0.26
(3,97)	1:416:A:SER:CA	1:403:B:ILE:CA	16	0.26
(3,97)	1:416:A:SER:CA	1:403:B:ILE:CA	23	0.26
(3,97)	1:416:A:SER:CA	1:403:B:ILE:CA	25	0.26
(3,97)	1:416:A:SER:CA	1:403:B:ILE:CA	29	0.26
(1,3153)	1:414:A:GLU:H	1:414:A:GLU:HG2	17	0.26
(1,3153)	1:414:A:GLU:H	1:414:A:GLU:HG3	17	0.26
(5,80)	1:407:A:LYS:CA	1:407:B:LYS:CA	11	0.25
(3,98)	1:403:A:ILE:CA	1:416:B:SER:CA	19	0.25
(3,98)	1:403:A:ILE:CA	1:416:B:SER:CA	30	0.25
(3,97)	1:416:A:SER:CA	1:403:B:ILE:CA	15	0.25
(1,675)	1:380:A:LEU:HD11	1:382:A:SER:H	18	0.25
(1,675)	1:380:A:LEU:HD12	1:382:A:SER:H	18	0.25
(1,675)	1:380:A:LEU:HD13	1:382:A:SER:H	18	0.25
(1,363)	1:437:B:THR:HA	1:438:B:GLN:H	23	0.25
(3,98)	1:403:A:ILE:CA	1:416:B:SER:CA	13	0.24
(3,98)	1:403:A:ILE:CA	1:416:B:SER:CA	16	0.24
(3,97)	1:416:A:SER:CA	1:403:B:ILE:CA	13	0.24
(3,97)	1:416:A:SER:CA	1:403:B:ILE:CA	30	0.24
(3,82)	1:406:A:PHE:CA	1:408:B:VAL:CA	25	0.24
(1,3153)	1:414:A:GLU:H	1:414:A:GLU:HG2	16	0.24
(1,3153)	1:414:A:GLU:H	1:414:A:GLU:HG3	16	0.24
(5,77)	1:365:A:ILE:CA	1:406:B:PHE:CA	3	0.23
(5,77)	1:365:A:ILE:CA	1:406:B:PHE:CA	17	0.23
(5,76)	1:406:A:PHE:CA	1:365:B:ILE:CA	11	0.23
(3,82)	1:406:A:PHE:CA	1:408:B:VAL:CA	24	0.23
(3,81)	1:408:A:VAL:CA	1:406:B:PHE:CA	3	0.23
(3,81)	1:408:A:VAL:CA	1:406:B:PHE:CA	16	0.23
(3,81)	1:408:A:VAL:CA	1:406:B:PHE:CA	25	0.23
(3,73)	1:407:A:LYS:CA	1:406:B:PHE:CA	4	0.23
(3,73)	1:407:A:LYS:CA	1:406:B:PHE:CA	5	0.23

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,73)	1:407:A:LYS:CA	1:406:B:PHE:CA	21	0.23
(3,72)	1:406:A:PHE:CA	1:407:B:LYS:CA	19	0.23
(1,3713)	1:414:B:GLU:H	1:414:B:GLU:HG2	15	0.23
(1,3713)	1:414:B:GLU:H	1:414:B:GLU:HG3	15	0.23
(1,3713)	1:414:B:GLU:H	1:414:B:GLU:HG2	25	0.23
(1,3713)	1:414:B:GLU:H	1:414:B:GLU:HG3	25	0.23
(1,3713)	1:414:B:GLU:H	1:414:B:GLU:HG2	30	0.23
(1,3713)	1:414:B:GLU:H	1:414:B:GLU:HG3	30	0.23
(5,100)	1:404:A:ARG:CA	1:413:B:MET:CA	8	0.22
(5,100)	1:404:A:ARG:CA	1:413:B:MET:CA	17	0.22
(5,77)	1:365:A:ILE:CA	1:406:B:PHE:CA	16	0.22
(3,82)	1:406:A:PHE:CA	1:408:B:VAL:CA	2	0.22
(3,82)	1:406:A:PHE:CA	1:408:B:VAL:CA	13	0.22
(3,82)	1:406:A:PHE:CA	1:408:B:VAL:CA	29	0.22
(3,82)	1:406:A:PHE:CA	1:408:B:VAL:CA	30	0.22
(3,81)	1:408:A:VAL:CA	1:406:B:PHE:CA	2	0.22
(3,81)	1:408:A:VAL:CA	1:406:B:PHE:CA	13	0.22
(3,81)	1:408:A:VAL:CA	1:406:B:PHE:CA	24	0.22
(3,81)	1:408:A:VAL:CA	1:406:B:PHE:CA	29	0.22
(3,73)	1:407:A:LYS:CA	1:406:B:PHE:CA	18	0.22
(3,73)	1:407:A:LYS:CA	1:406:B:PHE:CA	20	0.22
(3,72)	1:406:A:PHE:CA	1:407:B:LYS:CA	9	0.22
(3,72)	1:406:A:PHE:CA	1:407:B:LYS:CA	20	0.22
(5,100)	1:404:A:ARG:CA	1:413:B:MET:CA	11	0.21
(5,100)	1:404:A:ARG:CA	1:413:B:MET:CA	18	0.21
(5,100)	1:404:A:ARG:CA	1:413:B:MET:CA	28	0.21
(5,99)	1:413:A:MET:CA	1:404:B:ARG:CA	6	0.21
(5,99)	1:413:A:MET:CA	1:404:B:ARG:CA	8	0.21
(5,99)	1:413:A:MET:CA	1:404:B:ARG:CA	11	0.21
(5,99)	1:413:A:MET:CA	1:404:B:ARG:CA	17	0.21
(5,99)	1:413:A:MET:CA	1:404:B:ARG:CA	18	0.21
(5,99)	1:413:A:MET:CA	1:404:B:ARG:CA	28	0.21
(5,76)	1:406:A:PHE:CA	1:365:B:ILE:CA	24	0.21
(3,73)	1:407:A:LYS:CA	1:406:B:PHE:CA	8	0.21
(3,73)	1:407:A:LYS:CA	1:406:B:PHE:CA	10	0.21
(3,73)	1:407:A:LYS:CA	1:406:B:PHE:CA	22	0.21
(3,73)	1:407:A:LYS:CA	1:406:B:PHE:CA	27	0.21
(3,73)	1:407:A:LYS:CA	1:406:B:PHE:CA	28	0.21
(3,72)	1:406:A:PHE:CA	1:407:B:LYS:CA	6	0.21
(3,72)	1:406:A:PHE:CA	1:407:B:LYS:CA	8	0.21
(3,72)	1:406:A:PHE:CA	1:407:B:LYS:CA	28	0.21
(3,68)	1:405:A:ARG:CA	1:413:B:MET:CA	17	0.21

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,363)	1:437:B:THR:HA	1:438:B:GLN:H	17	0.21
(1,362)	1:437:A:THR:HA	1:438:A:GLN:H	27	0.21
(5,100)	1:404:A:ARG:CA	1:413:B:MET:CA	6	0.2
(5,100)	1:404:A:ARG:CA	1:413:B:MET:CA	7	0.2
(5,100)	1:404:A:ARG:CA	1:413:B:MET:CA	15	0.2
(5,80)	1:407:A:LYS:CA	1:407:B:LYS:CA	19	0.2
(5,77)	1:365:A:ILE:CA	1:406:B:PHE:CA	6	0.2
(5,77)	1:365:A:ILE:CA	1:406:B:PHE:CA	25	0.2
(5,77)	1:365:A:ILE:CA	1:406:B:PHE:CA	26	0.2
(5,77)	1:365:A:ILE:CA	1:406:B:PHE:CA	29	0.2
(5,76)	1:406:A:PHE:CA	1:365:B:ILE:CA	6	0.2
(5,76)	1:406:A:PHE:CA	1:365:B:ILE:CA	30	0.2
(3,80)	1:403:A:ILE:CA	1:408:B:VAL:CA	14	0.2
(3,78)	1:363:A:LEU:CA	1:408:B:VAL:CA	6	0.2
(3,73)	1:407:A:LYS:CA	1:406:B:PHE:CA	1	0.2
(3,72)	1:406:A:PHE:CA	1:407:B:LYS:CA	10	0.2
(3,72)	1:406:A:PHE:CA	1:407:B:LYS:CA	18	0.2
(3,72)	1:406:A:PHE:CA	1:407:B:LYS:CA	27	0.2
(3,69)	1:413:A:MET:CA	1:405:B:ARG:CA	14	0.2
(3,66)	1:404:A:ARG:CA	1:412:B:ILE:CA	6	0.2
(5,100)	1:404:A:ARG:CA	1:413:B:MET:CA	1	0.19
(5,100)	1:404:A:ARG:CA	1:413:B:MET:CA	9	0.19
(5,100)	1:404:A:ARG:CA	1:413:B:MET:CA	12	0.19
(5,99)	1:413:A:MET:CA	1:404:B:ARG:CA	7	0.19
(5,99)	1:413:A:MET:CA	1:404:B:ARG:CA	9	0.19
(5,99)	1:413:A:MET:CA	1:404:B:ARG:CA	12	0.19
(5,99)	1:413:A:MET:CA	1:404:B:ARG:CA	14	0.19
(5,99)	1:413:A:MET:CA	1:404:B:ARG:CA	15	0.19
(5,77)	1:365:A:ILE:CA	1:406:B:PHE:CA	2	0.19
(5,77)	1:365:A:ILE:CA	1:406:B:PHE:CA	15	0.19
(5,77)	1:365:A:ILE:CA	1:406:B:PHE:CA	18	0.19
(5,77)	1:365:A:ILE:CA	1:406:B:PHE:CA	22	0.19
(5,76)	1:406:A:PHE:CA	1:365:B:ILE:CA	2	0.19
(5,76)	1:406:A:PHE:CA	1:365:B:ILE:CA	25	0.19
(5,76)	1:406:A:PHE:CA	1:365:B:ILE:CA	26	0.19
(5,76)	1:406:A:PHE:CA	1:365:B:ILE:CA	29	0.19
(3,82)	1:406:A:PHE:CA	1:408:B:VAL:CA	3	0.19
(3,81)	1:408:A:VAL:CA	1:406:B:PHE:CA	30	0.19
(3,73)	1:407:A:LYS:CA	1:406:B:PHE:CA	3	0.19
(3,73)	1:407:A:LYS:CA	1:406:B:PHE:CA	7	0.19
(3,73)	1:407:A:LYS:CA	1:406:B:PHE:CA	9	0.19
(3,73)	1:407:A:LYS:CA	1:406:B:PHE:CA	12	0.19

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,73)	1:407:A:LYS:CA	1:406:B:PHE:CA	23	0.19
(3,72)	1:406:A:PHE:CA	1:407:B:LYS:CA	1	0.19
(3,72)	1:406:A:PHE:CA	1:407:B:LYS:CA	12	0.19
(1,3427)	1:361:B:ASN:HB2	1:362:B:SER:HB2	18	0.19
(1,3427)	1:361:B:ASN:HB2	1:362:B:SER:HB3	18	0.19
(1,3427)	1:361:B:ASN:HB3	1:362:B:SER:HB2	18	0.19
(1,3427)	1:361:B:ASN:HB3	1:362:B:SER:HB3	18	0.19
(5,100)	1:404:A:ARG:CA	1:413:B:MET:CA	2	0.18
(5,100)	1:404:A:ARG:CA	1:413:B:MET:CA	3	0.18
(5,100)	1:404:A:ARG:CA	1:413:B:MET:CA	5	0.18
(5,100)	1:404:A:ARG:CA	1:413:B:MET:CA	14	0.18
(5,100)	1:404:A:ARG:CA	1:413:B:MET:CA	21	0.18
(5,100)	1:404:A:ARG:CA	1:413:B:MET:CA	26	0.18
(5,100)	1:404:A:ARG:CA	1:413:B:MET:CA	27	0.18
(5,100)	1:404:A:ARG:CA	1:413:B:MET:CA	29	0.18
(5,99)	1:413:A:MET:CA	1:404:B:ARG:CA	1	0.18
(5,99)	1:413:A:MET:CA	1:404:B:ARG:CA	5	0.18
(5,99)	1:413:A:MET:CA	1:404:B:ARG:CA	26	0.18
(5,99)	1:413:A:MET:CA	1:404:B:ARG:CA	29	0.18
(5,77)	1:365:A:ILE:CA	1:406:B:PHE:CA	13	0.18
(5,77)	1:365:A:ILE:CA	1:406:B:PHE:CA	23	0.18
(5,77)	1:365:A:ILE:CA	1:406:B:PHE:CA	28	0.18
(5,76)	1:406:A:PHE:CA	1:365:B:ILE:CA	13	0.18
(5,76)	1:406:A:PHE:CA	1:365:B:ILE:CA	18	0.18
(5,76)	1:406:A:PHE:CA	1:365:B:ILE:CA	28	0.18
(3,91)	1:413:A:MET:CA	1:403:B:ILE:CA	23	0.18
(3,73)	1:407:A:LYS:CA	1:406:B:PHE:CA	11	0.18
(3,73)	1:407:A:LYS:CA	1:406:B:PHE:CA	26	0.18
(3,72)	1:406:A:PHE:CA	1:407:B:LYS:CA	5	0.18
(3,72)	1:406:A:PHE:CA	1:407:B:LYS:CA	26	0.18
(3,69)	1:413:A:MET:CA	1:405:B:ARG:CA	11	0.18
(3,56)	1:401:A:LYS:CA	1:420:B:TYR:CA	7	0.18
(1,2760)	1:361:A:ASN:HB2	1:362:A:SER:HB2	6	0.18
(1,2760)	1:361:A:ASN:HB2	1:362:A:SER:HB3	6	0.18
(1,2760)	1:361:A:ASN:HB3	1:362:A:SER:HB2	6	0.18
(1,2760)	1:361:A:ASN:HB3	1:362:A:SER:HB3	6	0.18
(1,1029)	1:408:A:VAL:HG11	1:409:A:SER:H	19	0.18
(1,1029)	1:408:A:VAL:HG12	1:409:A:SER:H	19	0.18
(1,1029)	1:408:A:VAL:HG13	1:409:A:SER:H	19	0.18
(5,100)	1:404:A:ARG:CA	1:413:B:MET:CA	4	0.17
(5,100)	1:404:A:ARG:CA	1:413:B:MET:CA	13	0.17
(5,100)	1:404:A:ARG:CA	1:413:B:MET:CA	22	0.17

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(5,100)	1:404:A:ARG:CA	1:413:B:MET:CA	23	0.17
(5,99)	1:413:A:MET:CA	1:404:B:ARG:CA	2	0.17
(5,99)	1:413:A:MET:CA	1:404:B:ARG:CA	4	0.17
(5,99)	1:413:A:MET:CA	1:404:B:ARG:CA	13	0.17
(5,99)	1:413:A:MET:CA	1:404:B:ARG:CA	21	0.17
(5,99)	1:413:A:MET:CA	1:404:B:ARG:CA	24	0.17
(5,99)	1:413:A:MET:CA	1:404:B:ARG:CA	27	0.17
(5,77)	1:365:A:ILE:CA	1:406:B:PHE:CA	1	0.17
(5,77)	1:365:A:ILE:CA	1:406:B:PHE:CA	4	0.17
(5,77)	1:365:A:ILE:CA	1:406:B:PHE:CA	9	0.17
(5,77)	1:365:A:ILE:CA	1:406:B:PHE:CA	10	0.17
(5,77)	1:365:A:ILE:CA	1:406:B:PHE:CA	12	0.17
(5,77)	1:365:A:ILE:CA	1:406:B:PHE:CA	27	0.17
(5,77)	1:365:A:ILE:CA	1:406:B:PHE:CA	30	0.17
(5,76)	1:406:A:PHE:CA	1:365:B:ILE:CA	1	0.17
(5,76)	1:406:A:PHE:CA	1:365:B:ILE:CA	10	0.17
(5,76)	1:406:A:PHE:CA	1:365:B:ILE:CA	12	0.17
(5,76)	1:406:A:PHE:CA	1:365:B:ILE:CA	22	0.17
(5,76)	1:406:A:PHE:CA	1:365:B:ILE:CA	23	0.17
(5,13)	1:360:A:LYS:CA	1:365:B:ILE:CA	16	0.17
(3,91)	1:413:A:MET:CA	1:403:B:ILE:CA	30	0.17
(3,82)	1:406:A:PHE:CA	1:408:B:VAL:CA	16	0.17
(3,81)	1:408:A:VAL:CA	1:406:B:PHE:CA	6	0.17
(3,73)	1:407:A:LYS:CA	1:406:B:PHE:CA	15	0.17
(3,72)	1:406:A:PHE:CA	1:407:B:LYS:CA	4	0.17
(3,72)	1:406:A:PHE:CA	1:407:B:LYS:CA	17	0.17
(3,72)	1:406:A:PHE:CA	1:407:B:LYS:CA	21	0.17
(3,72)	1:406:A:PHE:CA	1:407:B:LYS:CA	24	0.17
(3,69)	1:413:A:MET:CA	1:405:B:ARG:CA	19	0.17
(3,68)	1:405:A:ARG:CA	1:413:B:MET:CA	15	0.17
(3,67)	1:412:A:ILE:CA	1:404:B:ARG:CA	11	0.17
(3,67)	1:412:A:ILE:CA	1:404:B:ARG:CA	18	0.17
(1,3153)	1:414:A:GLU:H	1:414:A:GLU:HG2	24	0.17
(1,3153)	1:414:A:GLU:H	1:414:A:GLU:HG3	24	0.17
(1,2621)	1:418:B:MET:HE1	1:419:B:LEU:H	21	0.17
(1,2621)	1:418:B:MET:HE2	1:419:B:LEU:H	21	0.17
(1,2621)	1:418:B:MET:HE3	1:419:B:LEU:H	21	0.17
(5,100)	1:404:A:ARG:CA	1:413:B:MET:CA	10	0.16
(5,100)	1:404:A:ARG:CA	1:413:B:MET:CA	24	0.16
(5,100)	1:404:A:ARG:CA	1:413:B:MET:CA	25	0.16
(5,100)	1:404:A:ARG:CA	1:413:B:MET:CA	30	0.16
(5,99)	1:413:A:MET:CA	1:404:B:ARG:CA	3	0.16

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(5,99)	1:413:A:MET:CA	1:404:B:ARG:CA	10	0.16
(5,99)	1:413:A:MET:CA	1:404:B:ARG:CA	16	0.16
(5,99)	1:413:A:MET:CA	1:404:B:ARG:CA	25	0.16
(5,99)	1:413:A:MET:CA	1:404:B:ARG:CA	30	0.16
(5,77)	1:365:A:ILE:CA	1:406:B:PHE:CA	5	0.16
(5,77)	1:365:A:ILE:CA	1:406:B:PHE:CA	7	0.16
(5,77)	1:365:A:ILE:CA	1:406:B:PHE:CA	8	0.16
(5,77)	1:365:A:ILE:CA	1:406:B:PHE:CA	11	0.16
(5,77)	1:365:A:ILE:CA	1:406:B:PHE:CA	20	0.16
(5,77)	1:365:A:ILE:CA	1:406:B:PHE:CA	21	0.16
(5,76)	1:406:A:PHE:CA	1:365:B:ILE:CA	4	0.16
(5,76)	1:406:A:PHE:CA	1:365:B:ILE:CA	7	0.16
(5,76)	1:406:A:PHE:CA	1:365:B:ILE:CA	8	0.16
(5,76)	1:406:A:PHE:CA	1:365:B:ILE:CA	9	0.16
(5,76)	1:406:A:PHE:CA	1:365:B:ILE:CA	20	0.16
(5,76)	1:406:A:PHE:CA	1:365:B:ILE:CA	27	0.16
(3,92)	1:403:A:ILE:CA	1:413:B:MET:CA	16	0.16
(3,92)	1:403:A:ILE:CA	1:413:B:MET:CA	20	0.16
(3,91)	1:413:A:MET:CA	1:403:B:ILE:CA	19	0.16
(3,91)	1:413:A:MET:CA	1:403:B:ILE:CA	20	0.16
(3,81)	1:408:A:VAL:CA	1:406:B:PHE:CA	15	0.16
(3,78)	1:363:A:LEU:CA	1:408:B:VAL:CA	17	0.16
(3,73)	1:407:A:LYS:CA	1:406:B:PHE:CA	14	0.16
(3,73)	1:407:A:LYS:CA	1:406:B:PHE:CA	16	0.16
(3,73)	1:407:A:LYS:CA	1:406:B:PHE:CA	17	0.16
(3,72)	1:406:A:PHE:CA	1:407:B:LYS:CA	7	0.16
(3,72)	1:406:A:PHE:CA	1:407:B:LYS:CA	11	0.16
(3,72)	1:406:A:PHE:CA	1:407:B:LYS:CA	15	0.16
(3,68)	1:405:A:ARG:CA	1:413:B:MET:CA	6	0.16
(3,67)	1:412:A:ILE:CA	1:404:B:ARG:CA	4	0.16
(3,66)	1:404:A:ARG:CA	1:412:B:ILE:CA	4	0.16
(3,66)	1:404:A:ARG:CA	1:412:B:ILE:CA	17	0.16
(3,66)	1:404:A:ARG:CA	1:412:B:ILE:CA	18	0.16
(3,21)	1:406:A:PHE:CA	1:368:B:LEU:CA	14	0.16
(1,2760)	1:361:A:ASN:HB2	1:362:A:SER:HB2	4	0.16
(1,2760)	1:361:A:ASN:HB2	1:362:A:SER:HB3	4	0.16
(1,2760)	1:361:A:ASN:HB3	1:362:A:SER:HB2	4	0.16
(1,2760)	1:361:A:ASN:HB3	1:362:A:SER:HB3	4	0.16
(1,890)	1:401:B:LYS:H	1:401:B:LYS:HB2	19	0.16
(1,889)	1:401:A:LYS:H	1:401:A:LYS:HB2	19	0.16
(5,100)	1:404:A:ARG:CA	1:413:B:MET:CA	16	0.15
(5,99)	1:413:A:MET:CA	1:404:B:ARG:CA	22	0.15

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(5,89)	1:409:A:SER:CA	1:370:B:VAL:CA	18	0.15
(5,77)	1:365:A:ILE:CA	1:406:B:PHE:CA	24	0.15
(5,76)	1:406:A:PHE:CA	1:365:B:ILE:CA	3	0.15
(5,76)	1:406:A:PHE:CA	1:365:B:ILE:CA	5	0.15
(5,76)	1:406:A:PHE:CA	1:365:B:ILE:CA	16	0.15
(5,76)	1:406:A:PHE:CA	1:365:B:ILE:CA	17	0.15
(5,76)	1:406:A:PHE:CA	1:365:B:ILE:CA	21	0.15
(5,13)	1:360:A:LYS:CA	1:365:B:ILE:CA	3	0.15
(5,12)	1:365:A:ILE:CA	1:360:B:LYS:CA	24	0.15
(5,12)	1:365:A:ILE:CA	1:360:B:LYS:CA	29	0.15
(3,92)	1:403:A:ILE:CA	1:413:B:MET:CA	19	0.15
(3,92)	1:403:A:ILE:CA	1:413:B:MET:CA	22	0.15
(3,91)	1:413:A:MET:CA	1:403:B:ILE:CA	22	0.15
(3,91)	1:413:A:MET:CA	1:403:B:ILE:CA	25	0.15
(3,77)	1:408:A:VAL:CA	1:363:B:LEU:CA	18	0.15
(3,69)	1:413:A:MET:CA	1:405:B:ARG:CA	28	0.15
(3,68)	1:405:A:ARG:CA	1:413:B:MET:CA	14	0.15
(3,68)	1:405:A:ARG:CA	1:413:B:MET:CA	28	0.15
(3,67)	1:412:A:ILE:CA	1:404:B:ARG:CA	6	0.15
(3,67)	1:412:A:ILE:CA	1:404:B:ARG:CA	8	0.15
(3,67)	1:412:A:ILE:CA	1:404:B:ARG:CA	19	0.15
(3,67)	1:412:A:ILE:CA	1:404:B:ARG:CA	21	0.15
(3,67)	1:412:A:ILE:CA	1:404:B:ARG:CA	23	0.15
(3,67)	1:412:A:ILE:CA	1:404:B:ARG:CA	27	0.15
(3,67)	1:412:A:ILE:CA	1:404:B:ARG:CA	28	0.15
(3,66)	1:404:A:ARG:CA	1:412:B:ILE:CA	8	0.15
(3,66)	1:404:A:ARG:CA	1:412:B:ILE:CA	27	0.15
(3,66)	1:404:A:ARG:CA	1:412:B:ILE:CA	28	0.15
(3,57)	1:420:A:TYR:CA	1:401:B:LYS:CA	30	0.15
(1,1227)	1:421:A:ASN:HB3	1:422:A:LYS:H	5	0.15
(5,101)	1:414:A:GLU:CA	1:404:B:ARG:CA	19	0.14
(5,100)	1:404:A:ARG:CA	1:413:B:MET:CA	20	0.14
(5,99)	1:413:A:MET:CA	1:404:B:ARG:CA	19	0.14
(5,90)	1:370:A:VAL:CA	1:409:B:SER:CA	18	0.14
(5,81)	1:407:A:LYS:CA	1:408:B:VAL:CA	6	0.14
(5,81)	1:407:A:LYS:CA	1:408:B:VAL:CA	19	0.14
(5,76)	1:406:A:PHE:CA	1:365:B:ILE:CA	14	0.14
(5,13)	1:360:A:LYS:CA	1:365:B:ILE:CA	29	0.14
(3,109)	1:355:A:ILE:CA	1:380:A:LEU:CA	14	0.14
(3,92)	1:403:A:ILE:CA	1:413:B:MET:CA	10	0.14
(3,92)	1:403:A:ILE:CA	1:413:B:MET:CA	23	0.14
(3,91)	1:413:A:MET:CA	1:403:B:ILE:CA	10	0.14

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,81)	1:408:A:VAL:CA	1:406:B:PHE:CA	17	0.14
(3,78)	1:363:A:LEU:CA	1:408:B:VAL:CA	18	0.14
(3,77)	1:408:A:VAL:CA	1:363:B:LEU:CA	19	0.14
(3,73)	1:407:A:LYS:CA	1:406:B:PHE:CA	6	0.14
(3,69)	1:413:A:MET:CA	1:405:B:ARG:CA	22	0.14
(3,69)	1:413:A:MET:CA	1:405:B:ARG:CA	23	0.14
(3,68)	1:405:A:ARG:CA	1:413:B:MET:CA	5	0.14
(3,68)	1:405:A:ARG:CA	1:413:B:MET:CA	21	0.14
(3,68)	1:405:A:ARG:CA	1:413:B:MET:CA	22	0.14
(3,67)	1:412:A:ILE:CA	1:404:B:ARG:CA	1	0.14
(3,67)	1:412:A:ILE:CA	1:404:B:ARG:CA	3	0.14
(3,67)	1:412:A:ILE:CA	1:404:B:ARG:CA	5	0.14
(3,67)	1:412:A:ILE:CA	1:404:B:ARG:CA	13	0.14
(3,67)	1:412:A:ILE:CA	1:404:B:ARG:CA	14	0.14
(3,67)	1:412:A:ILE:CA	1:404:B:ARG:CA	22	0.14
(3,66)	1:404:A:ARG:CA	1:412:B:ILE:CA	5	0.14
(3,66)	1:404:A:ARG:CA	1:412:B:ILE:CA	11	0.14
(3,66)	1:404:A:ARG:CA	1:412:B:ILE:CA	13	0.14
(3,66)	1:404:A:ARG:CA	1:412:B:ILE:CA	19	0.14
(3,66)	1:404:A:ARG:CA	1:412:B:ILE:CA	21	0.14
(3,66)	1:404:A:ARG:CA	1:412:B:ILE:CA	24	0.14
(3,66)	1:404:A:ARG:CA	1:412:B:ILE:CA	25	0.14
(3,11)	1:364:A:LYS:CA	1:364:B:LYS:CA	25	0.14
(1,3713)	1:414:B:GLU:H	1:414:B:GLU:HG2	24	0.14
(1,3713)	1:414:B:GLU:H	1:414:B:GLU:HG3	24	0.14
(1,1228)	1:421:B:ASN:HB3	1:422:B:LYS:H	18	0.14
(1,1228)	1:421:B:ASN:HB3	1:422:B:LYS:H	27	0.14
(1,362)	1:437:A:THR:HA	1:438:A:GLN:H	17	0.14
(5,99)	1:413:A:MET:CA	1:404:B:ARG:CA	20	0.13
(5,99)	1:413:A:MET:CA	1:404:B:ARG:CA	23	0.13
(5,95)	1:412:A:ILE:CA	1:403:B:ILE:CA	15	0.13
(5,90)	1:370:A:VAL:CA	1:409:B:SER:CA	6	0.13
(5,13)	1:360:A:LYS:CA	1:365:B:ILE:CA	14	0.13
(3,106)	1:352:A:LEU:CA	1:393:A:HIS:CA	13	0.13
(3,106)	1:352:A:LEU:CA	1:393:A:HIS:CA	21	0.13
(3,92)	1:403:A:ILE:CA	1:413:B:MET:CA	15	0.13
(3,92)	1:403:A:ILE:CA	1:413:B:MET:CA	25	0.13
(3,91)	1:413:A:MET:CA	1:403:B:ILE:CA	12	0.13
(3,91)	1:413:A:MET:CA	1:403:B:ILE:CA	24	0.13
(3,81)	1:408:A:VAL:CA	1:406:B:PHE:CA	5	0.13
(3,81)	1:408:A:VAL:CA	1:406:B:PHE:CA	21	0.13
(3,80)	1:403:A:ILE:CA	1:408:B:VAL:CA	23	0.13

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,78)	1:363:A:LEU:CA	1:408:B:VAL:CA	3	0.13
(3,78)	1:363:A:LEU:CA	1:408:B:VAL:CA	8	0.13
(3,77)	1:408:A:VAL:CA	1:363:B:LEU:CA	8	0.13
(3,77)	1:408:A:VAL:CA	1:363:B:LEU:CA	11	0.13
(3,77)	1:408:A:VAL:CA	1:363:B:LEU:CA	14	0.13
(3,77)	1:408:A:VAL:CA	1:363:B:LEU:CA	23	0.13
(3,77)	1:408:A:VAL:CA	1:363:B:LEU:CA	24	0.13
(3,77)	1:408:A:VAL:CA	1:363:B:LEU:CA	28	0.13
(3,77)	1:408:A:VAL:CA	1:363:B:LEU:CA	29	0.13
(3,73)	1:407:A:LYS:CA	1:406:B:PHE:CA	24	0.13
(3,69)	1:413:A:MET:CA	1:405:B:ARG:CA	6	0.13
(3,69)	1:413:A:MET:CA	1:405:B:ARG:CA	7	0.13
(3,69)	1:413:A:MET:CA	1:405:B:ARG:CA	10	0.13
(3,69)	1:413:A:MET:CA	1:405:B:ARG:CA	24	0.13
(3,69)	1:413:A:MET:CA	1:405:B:ARG:CA	26	0.13
(3,68)	1:405:A:ARG:CA	1:413:B:MET:CA	3	0.13
(3,68)	1:405:A:ARG:CA	1:413:B:MET:CA	4	0.13
(3,68)	1:405:A:ARG:CA	1:413:B:MET:CA	7	0.13
(3,68)	1:405:A:ARG:CA	1:413:B:MET:CA	10	0.13
(3,67)	1:412:A:ILE:CA	1:404:B:ARG:CA	2	0.13
(3,67)	1:412:A:ILE:CA	1:404:B:ARG:CA	9	0.13
(3,67)	1:412:A:ILE:CA	1:404:B:ARG:CA	10	0.13
(3,67)	1:412:A:ILE:CA	1:404:B:ARG:CA	16	0.13
(3,67)	1:412:A:ILE:CA	1:404:B:ARG:CA	17	0.13
(3,67)	1:412:A:ILE:CA	1:404:B:ARG:CA	25	0.13
(3,67)	1:412:A:ILE:CA	1:404:B:ARG:CA	29	0.13
(3,66)	1:404:A:ARG:CA	1:412:B:ILE:CA	1	0.13
(3,66)	1:404:A:ARG:CA	1:412:B:ILE:CA	2	0.13
(3,66)	1:404:A:ARG:CA	1:412:B:ILE:CA	3	0.13
(3,66)	1:404:A:ARG:CA	1:412:B:ILE:CA	7	0.13
(3,66)	1:404:A:ARG:CA	1:412:B:ILE:CA	10	0.13
(3,66)	1:404:A:ARG:CA	1:412:B:ILE:CA	12	0.13
(3,66)	1:404:A:ARG:CA	1:412:B:ILE:CA	15	0.13
(3,66)	1:404:A:ARG:CA	1:412:B:ILE:CA	26	0.13
(3,66)	1:404:A:ARG:CA	1:412:B:ILE:CA	29	0.13
(3,66)	1:404:A:ARG:CA	1:412:B:ILE:CA	30	0.13
(1,2615)	1:418:B:MET:HA	1:418:B:MET:HE1	21	0.13
(1,2615)	1:418:B:MET:HA	1:418:B:MET:HE2	21	0.13
(1,2615)	1:418:B:MET:HA	1:418:B:MET:HE3	21	0.13
(1,2447)	1:436:B:ILE:HA	1:436:B:ILE:HD11	28	0.13
(1,2447)	1:436:B:ILE:HA	1:436:B:ILE:HD12	28	0.13
(1,2447)	1:436:B:ILE:HA	1:436:B:ILE:HD13	28	0.13

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,2446)	1:436:A:ILE:HA	1:436:A:ILE:HD11	11	0.13
(1,2446)	1:436:A:ILE:HA	1:436:A:ILE:HD12	11	0.13
(1,2446)	1:436:A:ILE:HA	1:436:A:ILE:HD13	11	0.13
(1,2446)	1:436:A:ILE:HA	1:436:A:ILE:HD11	29	0.13
(1,2446)	1:436:A:ILE:HA	1:436:A:ILE:HD12	29	0.13
(1,2446)	1:436:A:ILE:HA	1:436:A:ILE:HD13	29	0.13
(1,1503)	1:352:A:LEU:HD21	1:380:A:LEU:HA	30	0.13
(1,1503)	1:352:A:LEU:HD22	1:380:A:LEU:HA	30	0.13
(1,1503)	1:352:A:LEU:HD23	1:380:A:LEU:HA	30	0.13
(1,1406)	1:440:B:LEU:H	1:441:B:ASN:H	27	0.13
(1,1228)	1:421:B:ASN:HB3	1:422:B:LYS:H	15	0.13
(1,1228)	1:421:B:ASN:HB3	1:422:B:LYS:H	29	0.13
(1,1227)	1:421:A:ASN:HB3	1:422:A:LYS:H	12	0.13
(1,387)	1:365:B:ILE:HD11	1:367:B:ASN:H	24	0.13
(1,387)	1:365:B:ILE:HD12	1:367:B:ASN:H	24	0.13
(1,387)	1:365:B:ILE:HD13	1:367:B:ASN:H	24	0.13
(5,101)	1:414:A:GLU:CA	1:404:B:ARG:CA	23	0.12
(5,100)	1:404:A:ARG:CA	1:413:B:MET:CA	19	0.12
(5,90)	1:370:A:VAL:CA	1:409:B:SER:CA	8	0.12
(5,89)	1:409:A:SER:CA	1:370:B:VAL:CA	8	0.12
(5,89)	1:409:A:SER:CA	1:370:B:VAL:CA	19	0.12
(5,89)	1:409:A:SER:CA	1:370:B:VAL:CA	28	0.12
(5,81)	1:407:A:LYS:CA	1:408:B:VAL:CA	17	0.12
(5,77)	1:365:A:ILE:CA	1:406:B:PHE:CA	14	0.12
(5,76)	1:406:A:PHE:CA	1:365:B:ILE:CA	15	0.12
(5,76)	1:406:A:PHE:CA	1:365:B:ILE:CA	19	0.12
(5,13)	1:360:A:LYS:CA	1:365:B:ILE:CA	2	0.12
(5,13)	1:360:A:LYS:CA	1:365:B:ILE:CA	6	0.12
(5,13)	1:360:A:LYS:CA	1:365:B:ILE:CA	13	0.12
(5,13)	1:360:A:LYS:CA	1:365:B:ILE:CA	15	0.12
(5,13)	1:360:A:LYS:CA	1:365:B:ILE:CA	17	0.12
(5,13)	1:360:A:LYS:CA	1:365:B:ILE:CA	22	0.12
(5,13)	1:360:A:LYS:CA	1:365:B:ILE:CA	23	0.12
(5,13)	1:360:A:LYS:CA	1:365:B:ILE:CA	26	0.12
(5,12)	1:365:A:ILE:CA	1:360:B:LYS:CA	2	0.12
(5,12)	1:365:A:ILE:CA	1:360:B:LYS:CA	13	0.12
(5,12)	1:365:A:ILE:CA	1:360:B:LYS:CA	15	0.12
(5,12)	1:365:A:ILE:CA	1:360:B:LYS:CA	16	0.12
(5,12)	1:365:A:ILE:CA	1:360:B:LYS:CA	17	0.12
(5,12)	1:365:A:ILE:CA	1:360:B:LYS:CA	23	0.12
(5,12)	1:365:A:ILE:CA	1:360:B:LYS:CA	25	0.12
(5,12)	1:365:A:ILE:CA	1:360:B:LYS:CA	30	0.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(5,4)	1:352:A:LEU:CA	1:380:A:LEU:CA	14	0.12
(3,92)	1:403:A:ILE:CA	1:413:B:MET:CA	9	0.12
(3,92)	1:403:A:ILE:CA	1:413:B:MET:CA	30	0.12
(3,91)	1:413:A:MET:CA	1:403:B:ILE:CA	26	0.12
(3,82)	1:406:A:PHE:CA	1:408:B:VAL:CA	9	0.12
(3,80)	1:403:A:ILE:CA	1:408:B:VAL:CA	22	0.12
(3,78)	1:363:A:LEU:CA	1:408:B:VAL:CA	13	0.12
(3,78)	1:363:A:LEU:CA	1:408:B:VAL:CA	15	0.12
(3,78)	1:363:A:LEU:CA	1:408:B:VAL:CA	29	0.12
(3,77)	1:408:A:VAL:CA	1:363:B:LEU:CA	3	0.12
(3,77)	1:408:A:VAL:CA	1:363:B:LEU:CA	6	0.12
(3,73)	1:407:A:LYS:CA	1:406:B:PHE:CA	2	0.12
(3,73)	1:407:A:LYS:CA	1:406:B:PHE:CA	13	0.12
(3,72)	1:406:A:PHE:CA	1:407:B:LYS:CA	13	0.12
(3,72)	1:406:A:PHE:CA	1:407:B:LYS:CA	25	0.12
(3,72)	1:406:A:PHE:CA	1:407:B:LYS:CA	29	0.12
(3,72)	1:406:A:PHE:CA	1:407:B:LYS:CA	30	0.12
(3,69)	1:413:A:MET:CA	1:405:B:ARG:CA	1	0.12
(3,69)	1:413:A:MET:CA	1:405:B:ARG:CA	8	0.12
(3,69)	1:413:A:MET:CA	1:405:B:ARG:CA	9	0.12
(3,69)	1:413:A:MET:CA	1:405:B:ARG:CA	12	0.12
(3,69)	1:413:A:MET:CA	1:405:B:ARG:CA	20	0.12
(3,69)	1:413:A:MET:CA	1:405:B:ARG:CA	21	0.12
(3,69)	1:413:A:MET:CA	1:405:B:ARG:CA	27	0.12
(3,68)	1:405:A:ARG:CA	1:413:B:MET:CA	1	0.12
(3,68)	1:405:A:ARG:CA	1:413:B:MET:CA	8	0.12
(3,68)	1:405:A:ARG:CA	1:413:B:MET:CA	9	0.12
(3,68)	1:405:A:ARG:CA	1:413:B:MET:CA	12	0.12
(3,68)	1:405:A:ARG:CA	1:413:B:MET:CA	16	0.12
(3,68)	1:405:A:ARG:CA	1:413:B:MET:CA	18	0.12
(3,68)	1:405:A:ARG:CA	1:413:B:MET:CA	20	0.12
(3,68)	1:405:A:ARG:CA	1:413:B:MET:CA	26	0.12
(3,68)	1:405:A:ARG:CA	1:413:B:MET:CA	27	0.12
(3,67)	1:412:A:ILE:CA	1:404:B:ARG:CA	7	0.12
(3,67)	1:412:A:ILE:CA	1:404:B:ARG:CA	12	0.12
(3,67)	1:412:A:ILE:CA	1:404:B:ARG:CA	20	0.12
(3,67)	1:412:A:ILE:CA	1:404:B:ARG:CA	24	0.12
(3,67)	1:412:A:ILE:CA	1:404:B:ARG:CA	26	0.12
(3,66)	1:404:A:ARG:CA	1:412:B:ILE:CA	9	0.12
(3,66)	1:404:A:ARG:CA	1:412:B:ILE:CA	14	0.12
(3,66)	1:404:A:ARG:CA	1:412:B:ILE:CA	20	0.12
(3,66)	1:404:A:ARG:CA	1:412:B:ILE:CA	23	0.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,56)	1:401:A:LYS:CA	1:420:B:TYR:CA	22	0.12
(3,21)	1:406:A:PHE:CA	1:368:B:LEU:CA	18	0.12
(3,21)	1:406:A:PHE:CA	1:368:B:LEU:CA	23	0.12
(3,11)	1:364:A:LYS:CA	1:364:B:LYS:CA	2	0.12
(3,11)	1:364:A:LYS:CA	1:364:B:LYS:CA	3	0.12
(3,11)	1:364:A:LYS:CA	1:364:B:LYS:CA	8	0.12
(3,11)	1:364:A:LYS:CA	1:364:B:LYS:CA	13	0.12
(3,11)	1:364:A:LYS:CA	1:364:B:LYS:CA	14	0.12
(3,11)	1:364:A:LYS:CA	1:364:B:LYS:CA	16	0.12
(3,11)	1:364:A:LYS:CA	1:364:B:LYS:CA	18	0.12
(3,11)	1:364:A:LYS:CA	1:364:B:LYS:CA	30	0.12
(1,2447)	1:436:B:ILE:HA	1:436:B:ILE:HD11	23	0.12
(1,2447)	1:436:B:ILE:HA	1:436:B:ILE:HD12	23	0.12
(1,2447)	1:436:B:ILE:HA	1:436:B:ILE:HD13	23	0.12
(1,1530)	1:353:B:GLN:HA	1:353:B:GLN:HG2	14	0.12
(1,1530)	1:353:B:GLN:HA	1:353:B:GLN:HG2	15	0.12
(1,1530)	1:353:B:GLN:HA	1:353:B:GLN:HG2	20	0.12
(1,1530)	1:353:B:GLN:HA	1:353:B:GLN:HG2	21	0.12
(1,1530)	1:353:B:GLN:HA	1:353:B:GLN:HG2	25	0.12
(1,1529)	1:353:A:GLN:HA	1:353:A:GLN:HG2	14	0.12
(1,1529)	1:353:A:GLN:HA	1:353:A:GLN:HG2	15	0.12
(1,1529)	1:353:A:GLN:HA	1:353:A:GLN:HG2	20	0.12
(1,1529)	1:353:A:GLN:HA	1:353:A:GLN:HG2	21	0.12
(1,1529)	1:353:A:GLN:HA	1:353:A:GLN:HG2	25	0.12
(1,1227)	1:421:A:ASN:HB3	1:422:A:LYS:H	7	0.12
(1,644)	1:379:B:GLU:HG3	1:380:B:LEU:H	16	0.12
(1,637)	1:379:A:GLU:HG2	1:380:A:LEU:H	16	0.12
(1,387)	1:365:B:ILE:HD11	1:367:B:ASN:H	2	0.12
(1,387)	1:365:B:ILE:HD12	1:367:B:ASN:H	2	0.12
(1,387)	1:365:B:ILE:HD13	1:367:B:ASN:H	2	0.12
(1,387)	1:365:B:ILE:HD11	1:367:B:ASN:H	13	0.12
(1,387)	1:365:B:ILE:HD12	1:367:B:ASN:H	13	0.12
(1,387)	1:365:B:ILE:HD13	1:367:B:ASN:H	13	0.12
(1,387)	1:365:B:ILE:HD11	1:367:B:ASN:H	30	0.12
(1,387)	1:365:B:ILE:HD12	1:367:B:ASN:H	30	0.12
(1,387)	1:365:B:ILE:HD13	1:367:B:ASN:H	30	0.12
(1,386)	1:365:A:ILE:HD11	1:367:A:ASN:H	2	0.12
(1,386)	1:365:A:ILE:HD12	1:367:A:ASN:H	2	0.12
(1,386)	1:365:A:ILE:HD13	1:367:A:ASN:H	2	0.12
(1,386)	1:365:A:ILE:HD11	1:367:A:ASN:H	13	0.12
(1,386)	1:365:A:ILE:HD12	1:367:A:ASN:H	13	0.12
(1,386)	1:365:A:ILE:HD13	1:367:A:ASN:H	13	0.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,386)	1:365:A:ILE:HD11	1:367:A:ASN:H	16	0.12
(1,386)	1:365:A:ILE:HD12	1:367:A:ASN:H	16	0.12
(1,386)	1:365:A:ILE:HD13	1:367:A:ASN:H	16	0.12
(1,386)	1:365:A:ILE:HD11	1:367:A:ASN:H	25	0.12
(1,386)	1:365:A:ILE:HD12	1:367:A:ASN:H	25	0.12
(1,386)	1:365:A:ILE:HD13	1:367:A:ASN:H	25	0.12
(5,102)	1:404:A:ARG:CA	1:414:B:GLU:CA	6	0.11
(5,101)	1:414:A:GLU:CA	1:404:B:ARG:CA	22	0.11
(5,95)	1:412:A:ILE:CA	1:403:B:ILE:CA	17	0.11
(5,90)	1:370:A:VAL:CA	1:409:B:SER:CA	17	0.11
(5,90)	1:370:A:VAL:CA	1:409:B:SER:CA	28	0.11
(5,82)	1:408:A:VAL:CA	1:407:B:LYS:CA	4	0.11
(5,82)	1:408:A:VAL:CA	1:407:B:LYS:CA	8	0.11
(5,82)	1:408:A:VAL:CA	1:407:B:LYS:CA	18	0.11
(5,81)	1:407:A:LYS:CA	1:408:B:VAL:CA	8	0.11
(5,58)	1:400:A:LEU:CA	1:420:B:TYR:CA	18	0.11
(5,58)	1:400:A:LEU:CA	1:420:B:TYR:CA	30	0.11
(5,13)	1:360:A:LYS:CA	1:365:B:ILE:CA	9	0.11
(5,13)	1:360:A:LYS:CA	1:365:B:ILE:CA	11	0.11
(5,13)	1:360:A:LYS:CA	1:365:B:ILE:CA	12	0.11
(5,13)	1:360:A:LYS:CA	1:365:B:ILE:CA	18	0.11
(5,13)	1:360:A:LYS:CA	1:365:B:ILE:CA	30	0.11
(5,12)	1:365:A:ILE:CA	1:360:B:LYS:CA	1	0.11
(5,12)	1:365:A:ILE:CA	1:360:B:LYS:CA	6	0.11
(5,12)	1:365:A:ILE:CA	1:360:B:LYS:CA	12	0.11
(5,12)	1:365:A:ILE:CA	1:360:B:LYS:CA	22	0.11
(5,12)	1:365:A:ILE:CA	1:360:B:LYS:CA	26	0.11
(5,4)	1:352:A:LEU:CA	1:380:A:LEU:CA	2	0.11
(5,4)	1:352:A:LEU:CA	1:380:A:LEU:CA	6	0.11
(5,4)	1:352:A:LEU:CA	1:380:A:LEU:CA	9	0.11
(3,109)	1:355:A:ILE:CA	1:380:A:LEU:CA	27	0.11
(3,106)	1:352:A:LEU:CA	1:393:A:HIS:CA	4	0.11
(3,106)	1:352:A:LEU:CA	1:393:A:HIS:CA	18	0.11
(3,106)	1:352:A:LEU:CA	1:393:A:HIS:CA	22	0.11
(3,106)	1:352:A:LEU:CA	1:393:A:HIS:CA	28	0.11
(3,92)	1:403:A:ILE:CA	1:413:B:MET:CA	1	0.11
(3,92)	1:403:A:ILE:CA	1:413:B:MET:CA	2	0.11
(3,92)	1:403:A:ILE:CA	1:413:B:MET:CA	3	0.11
(3,92)	1:403:A:ILE:CA	1:413:B:MET:CA	12	0.11
(3,92)	1:403:A:ILE:CA	1:413:B:MET:CA	13	0.11
(3,92)	1:403:A:ILE:CA	1:413:B:MET:CA	26	0.11
(3,92)	1:403:A:ILE:CA	1:413:B:MET:CA	27	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,92)	1:403:A:ILE:CA	1:413:B:MET:CA	29	0.11
(3,91)	1:413:A:MET:CA	1:403:B:ILE:CA	1	0.11
(3,91)	1:413:A:MET:CA	1:403:B:ILE:CA	2	0.11
(3,91)	1:413:A:MET:CA	1:403:B:ILE:CA	7	0.11
(3,91)	1:413:A:MET:CA	1:403:B:ILE:CA	9	0.11
(3,91)	1:413:A:MET:CA	1:403:B:ILE:CA	13	0.11
(3,91)	1:413:A:MET:CA	1:403:B:ILE:CA	16	0.11
(3,82)	1:406:A:PHE:CA	1:408:B:VAL:CA	1	0.11
(3,82)	1:406:A:PHE:CA	1:408:B:VAL:CA	8	0.11
(3,82)	1:406:A:PHE:CA	1:408:B:VAL:CA	11	0.11
(3,82)	1:406:A:PHE:CA	1:408:B:VAL:CA	28	0.11
(3,81)	1:408:A:VAL:CA	1:406:B:PHE:CA	1	0.11
(3,81)	1:408:A:VAL:CA	1:406:B:PHE:CA	4	0.11
(3,81)	1:408:A:VAL:CA	1:406:B:PHE:CA	7	0.11
(3,81)	1:408:A:VAL:CA	1:406:B:PHE:CA	8	0.11
(3,81)	1:408:A:VAL:CA	1:406:B:PHE:CA	22	0.11
(3,78)	1:363:A:LEU:CA	1:408:B:VAL:CA	1	0.11
(3,78)	1:363:A:LEU:CA	1:408:B:VAL:CA	2	0.11
(3,78)	1:363:A:LEU:CA	1:408:B:VAL:CA	9	0.11
(3,78)	1:363:A:LEU:CA	1:408:B:VAL:CA	12	0.11
(3,78)	1:363:A:LEU:CA	1:408:B:VAL:CA	14	0.11
(3,78)	1:363:A:LEU:CA	1:408:B:VAL:CA	16	0.11
(3,78)	1:363:A:LEU:CA	1:408:B:VAL:CA	30	0.11
(3,77)	1:408:A:VAL:CA	1:363:B:LEU:CA	1	0.11
(3,77)	1:408:A:VAL:CA	1:363:B:LEU:CA	2	0.11
(3,77)	1:408:A:VAL:CA	1:363:B:LEU:CA	4	0.11
(3,77)	1:408:A:VAL:CA	1:363:B:LEU:CA	12	0.11
(3,77)	1:408:A:VAL:CA	1:363:B:LEU:CA	13	0.11
(3,77)	1:408:A:VAL:CA	1:363:B:LEU:CA	16	0.11
(3,77)	1:408:A:VAL:CA	1:363:B:LEU:CA	17	0.11
(3,77)	1:408:A:VAL:CA	1:363:B:LEU:CA	22	0.11
(3,73)	1:407:A:LYS:CA	1:406:B:PHE:CA	29	0.11
(3,73)	1:407:A:LYS:CA	1:406:B:PHE:CA	30	0.11
(3,72)	1:406:A:PHE:CA	1:407:B:LYS:CA	2	0.11
(3,69)	1:413:A:MET:CA	1:405:B:ARG:CA	4	0.11
(3,69)	1:413:A:MET:CA	1:405:B:ARG:CA	5	0.11
(3,69)	1:413:A:MET:CA	1:405:B:ARG:CA	18	0.11
(3,69)	1:413:A:MET:CA	1:405:B:ARG:CA	25	0.11
(3,69)	1:413:A:MET:CA	1:405:B:ARG:CA	29	0.11
(3,69)	1:413:A:MET:CA	1:405:B:ARG:CA	30	0.11
(3,68)	1:405:A:ARG:CA	1:413:B:MET:CA	2	0.11
(3,68)	1:405:A:ARG:CA	1:413:B:MET:CA	23	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,68)	1:405:A:ARG:CA	1:413:B:MET:CA	29	0.11
(3,66)	1:404:A:ARG:CA	1:412:B:ILE:CA	22	0.11
(3,62)	1:403:A:ILE:CA	1:365:B:ILE:CA	16	0.11
(3,57)	1:420:A:TYR:CA	1:401:B:LYS:CA	7	0.11
(3,57)	1:420:A:TYR:CA	1:401:B:LYS:CA	13	0.11
(3,57)	1:420:A:TYR:CA	1:401:B:LYS:CA	17	0.11
(3,57)	1:420:A:TYR:CA	1:401:B:LYS:CA	19	0.11
(3,57)	1:420:A:TYR:CA	1:401:B:LYS:CA	21	0.11
(3,56)	1:401:A:LYS:CA	1:420:B:TYR:CA	3	0.11
(3,56)	1:401:A:LYS:CA	1:420:B:TYR:CA	17	0.11
(3,56)	1:401:A:LYS:CA	1:420:B:TYR:CA	25	0.11
(3,21)	1:406:A:PHE:CA	1:368:B:LEU:CA	11	0.11
(3,21)	1:406:A:PHE:CA	1:368:B:LEU:CA	22	0.11
(3,20)	1:368:A:LEU:CA	1:406:B:PHE:CA	18	0.11
(3,11)	1:364:A:LYS:CA	1:364:B:LYS:CA	22	0.11
(3,11)	1:364:A:LYS:CA	1:364:B:LYS:CA	26	0.11
(1,3686)	1:409:B:SER:H	1:412:B:ILE:HG12	19	0.11
(1,3686)	1:409:B:SER:H	1:412:B:ILE:HG13	19	0.11
(1,3656)	1:401:B:LYS:HB2	1:402:B:LYS:H	19	0.11
(1,3656)	1:401:B:LYS:HB3	1:402:B:LYS:H	19	0.11
(1,3069)	1:401:A:LYS:HB2	1:402:A:LYS:H	19	0.11
(1,3069)	1:401:A:LYS:HB3	1:402:A:LYS:H	19	0.11
(1,2255)	1:408:A:VAL:HG21	1:406:B:PHE:HE1	17	0.11
(1,2255)	1:408:A:VAL:HG21	1:406:B:PHE:HE2	17	0.11
(1,2255)	1:408:A:VAL:HG22	1:406:B:PHE:HE1	17	0.11
(1,2255)	1:408:A:VAL:HG22	1:406:B:PHE:HE2	17	0.11
(1,2255)	1:408:A:VAL:HG23	1:406:B:PHE:HE1	17	0.11
(1,2255)	1:408:A:VAL:HG23	1:406:B:PHE:HE2	17	0.11
(1,1529)	1:353:A:GLN:HA	1:353:A:GLN:HG2	13	0.11
(1,1521)	1:352:A:LEU:HD11	1:380:A:LEU:HA	10	0.11
(1,1521)	1:352:A:LEU:HD12	1:380:A:LEU:HA	10	0.11
(1,1521)	1:352:A:LEU:HD13	1:380:A:LEU:HA	10	0.11
(1,1227)	1:421:A:ASN:HB3	1:422:A:LYS:H	16	0.11
(1,387)	1:365:B:ILE:HD11	1:367:B:ASN:H	8	0.11
(1,387)	1:365:B:ILE:HD12	1:367:B:ASN:H	8	0.11
(1,387)	1:365:B:ILE:HD13	1:367:B:ASN:H	8	0.11
(1,387)	1:365:B:ILE:HD11	1:367:B:ASN:H	9	0.11
(1,387)	1:365:B:ILE:HD12	1:367:B:ASN:H	9	0.11
(1,387)	1:365:B:ILE:HD13	1:367:B:ASN:H	9	0.11
(1,387)	1:365:B:ILE:HD11	1:367:B:ASN:H	11	0.11
(1,387)	1:365:B:ILE:HD12	1:367:B:ASN:H	11	0.11
(1,387)	1:365:B:ILE:HD13	1:367:B:ASN:H	11	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,387)	1:365:B:ILE:HD11	1:367:B:ASN:H	18	0.11
(1,387)	1:365:B:ILE:HD12	1:367:B:ASN:H	18	0.11
(1,387)	1:365:B:ILE:HD13	1:367:B:ASN:H	18	0.11
(1,387)	1:365:B:ILE:HD11	1:367:B:ASN:H	20	0.11
(1,387)	1:365:B:ILE:HD12	1:367:B:ASN:H	20	0.11
(1,387)	1:365:B:ILE:HD13	1:367:B:ASN:H	20	0.11
(1,387)	1:365:B:ILE:HD11	1:367:B:ASN:H	25	0.11
(1,387)	1:365:B:ILE:HD12	1:367:B:ASN:H	25	0.11
(1,387)	1:365:B:ILE:HD13	1:367:B:ASN:H	25	0.11
(1,387)	1:365:B:ILE:HD11	1:367:B:ASN:H	29	0.11
(1,387)	1:365:B:ILE:HD12	1:367:B:ASN:H	29	0.11
(1,387)	1:365:B:ILE:HD13	1:367:B:ASN:H	29	0.11
(1,386)	1:365:A:ILE:HD11	1:367:A:ASN:H	3	0.11
(1,386)	1:365:A:ILE:HD12	1:367:A:ASN:H	3	0.11
(1,386)	1:365:A:ILE:HD13	1:367:A:ASN:H	3	0.11
(1,386)	1:365:A:ILE:HD11	1:367:A:ASN:H	8	0.11
(1,386)	1:365:A:ILE:HD12	1:367:A:ASN:H	8	0.11
(1,386)	1:365:A:ILE:HD13	1:367:A:ASN:H	8	0.11
(1,386)	1:365:A:ILE:HD11	1:367:A:ASN:H	9	0.11
(1,386)	1:365:A:ILE:HD12	1:367:A:ASN:H	9	0.11
(1,386)	1:365:A:ILE:HD13	1:367:A:ASN:H	9	0.11
(1,386)	1:365:A:ILE:HD11	1:367:A:ASN:H	11	0.11
(1,386)	1:365:A:ILE:HD12	1:367:A:ASN:H	11	0.11
(1,386)	1:365:A:ILE:HD13	1:367:A:ASN:H	11	0.11
(1,386)	1:365:A:ILE:HD11	1:367:A:ASN:H	12	0.11
(1,386)	1:365:A:ILE:HD12	1:367:A:ASN:H	12	0.11
(1,386)	1:365:A:ILE:HD13	1:367:A:ASN:H	12	0.11
(1,386)	1:365:A:ILE:HD11	1:367:A:ASN:H	18	0.11
(1,386)	1:365:A:ILE:HD12	1:367:A:ASN:H	18	0.11
(1,386)	1:365:A:ILE:HD13	1:367:A:ASN:H	18	0.11
(1,386)	1:365:A:ILE:HD11	1:367:A:ASN:H	20	0.11
(1,386)	1:365:A:ILE:HD12	1:367:A:ASN:H	20	0.11
(1,386)	1:365:A:ILE:HD13	1:367:A:ASN:H	20	0.11
(1,386)	1:365:A:ILE:HD11	1:367:A:ASN:H	22	0.11
(1,386)	1:365:A:ILE:HD12	1:367:A:ASN:H	22	0.11
(1,386)	1:365:A:ILE:HD13	1:367:A:ASN:H	22	0.11
(1,386)	1:365:A:ILE:HD11	1:367:A:ASN:H	23	0.11
(1,386)	1:365:A:ILE:HD12	1:367:A:ASN:H	23	0.11
(1,386)	1:365:A:ILE:HD13	1:367:A:ASN:H	23	0.11
(1,386)	1:365:A:ILE:HD11	1:367:A:ASN:H	24	0.11
(1,386)	1:365:A:ILE:HD12	1:367:A:ASN:H	24	0.11
(1,386)	1:365:A:ILE:HD13	1:367:A:ASN:H	24	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,386)	1:365:A:ILE:HD11	1:367:A:ASN:H	29	0.11
(1,386)	1:365:A:ILE:HD12	1:367:A:ASN:H	29	0.11
(1,386)	1:365:A:ILE:HD13	1:367:A:ASN:H	29	0.11
(1,386)	1:365:A:ILE:HD11	1:367:A:ASN:H	30	0.11
(1,386)	1:365:A:ILE:HD12	1:367:A:ASN:H	30	0.11
(1,386)	1:365:A:ILE:HD13	1:367:A:ASN:H	30	0.11
(5,102)	1:404:A:ARG:CA	1:414:B:GLU:CA	20	0.1
(5,101)	1:414:A:GLU:CA	1:404:B:ARG:CA	14	0.1
(5,101)	1:414:A:GLU:CA	1:404:B:ARG:CA	20	0.1
(5,92)	1:374:A:ILE:CA	1:411:B:VAL:CA	20	0.1
(5,89)	1:409:A:SER:CA	1:370:B:VAL:CA	11	0.1
(5,89)	1:409:A:SER:CA	1:370:B:VAL:CA	14	0.1
(5,82)	1:408:A:VAL:CA	1:407:B:LYS:CA	5	0.1
(5,82)	1:408:A:VAL:CA	1:407:B:LYS:CA	20	0.1
(5,82)	1:408:A:VAL:CA	1:407:B:LYS:CA	21	0.1
(5,81)	1:407:A:LYS:CA	1:408:B:VAL:CA	18	0.1
(5,81)	1:407:A:LYS:CA	1:408:B:VAL:CA	20	0.1
(5,58)	1:400:A:LEU:CA	1:420:B:TYR:CA	2	0.1
(5,12)	1:365:A:ILE:CA	1:360:B:LYS:CA	3	0.1
(5,12)	1:365:A:ILE:CA	1:360:B:LYS:CA	9	0.1
(5,12)	1:365:A:ILE:CA	1:360:B:LYS:CA	11	0.1
(5,4)	1:352:A:LEU:CA	1:380:A:LEU:CA	10	0.1
(3,109)	1:355:A:ILE:CA	1:380:A:LEU:CA	23	0.1
(3,106)	1:352:A:LEU:CA	1:393:A:HIS:CA	16	0.1
(3,92)	1:403:A:ILE:CA	1:413:B:MET:CA	7	0.1
(3,92)	1:403:A:ILE:CA	1:413:B:MET:CA	24	0.1
(3,91)	1:413:A:MET:CA	1:403:B:ILE:CA	3	0.1
(3,91)	1:413:A:MET:CA	1:403:B:ILE:CA	5	0.1
(3,91)	1:413:A:MET:CA	1:403:B:ILE:CA	14	0.1
(3,91)	1:413:A:MET:CA	1:403:B:ILE:CA	27	0.1
(3,91)	1:413:A:MET:CA	1:403:B:ILE:CA	29	0.1
(3,82)	1:406:A:PHE:CA	1:408:B:VAL:CA	10	0.1
(3,81)	1:408:A:VAL:CA	1:406:B:PHE:CA	10	0.1
(3,81)	1:408:A:VAL:CA	1:406:B:PHE:CA	28	0.1
(3,78)	1:363:A:LEU:CA	1:408:B:VAL:CA	24	0.1
(3,78)	1:363:A:LEU:CA	1:408:B:VAL:CA	28	0.1
(3,77)	1:408:A:VAL:CA	1:363:B:LEU:CA	7	0.1
(3,73)	1:407:A:LYS:CA	1:406:B:PHE:CA	25	0.1
(3,72)	1:406:A:PHE:CA	1:407:B:LYS:CA	23	0.1
(3,69)	1:413:A:MET:CA	1:405:B:ARG:CA	2	0.1
(3,69)	1:413:A:MET:CA	1:405:B:ARG:CA	13	0.1
(3,69)	1:413:A:MET:CA	1:405:B:ARG:CA	17	0.1

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,68)	1:405:A:ARG:CA	1:413:B:MET:CA	13	0.1
(3,68)	1:405:A:ARG:CA	1:413:B:MET:CA	24	0.1
(3,68)	1:405:A:ARG:CA	1:413:B:MET:CA	25	0.1
(3,67)	1:412:A:ILE:CA	1:404:B:ARG:CA	15	0.1
(3,67)	1:412:A:ILE:CA	1:404:B:ARG:CA	30	0.1
(3,66)	1:404:A:ARG:CA	1:412:B:ILE:CA	16	0.1
(3,64)	1:403:A:ILE:CA	1:366:B:ASP:CA	22	0.1
(3,63)	1:365:A:ILE:CA	1:403:B:ILE:CA	30	0.1
(3,56)	1:401:A:LYS:CA	1:420:B:TYR:CA	2	0.1
(3,11)	1:364:A:LYS:CA	1:364:B:LYS:CA	24	0.1
(1,1888)	1:380:A:LEU:H	1:380:A:LEU:HD11	18	0.1
(1,1888)	1:380:A:LEU:H	1:380:A:LEU:HD12	18	0.1
(1,1888)	1:380:A:LEU:H	1:380:A:LEU:HD13	18	0.1
(1,1530)	1:353:B:GLN:HA	1:353:B:GLN:HG2	13	0.1
(1,1031)	1:370:A:VAL:HG21	1:409:B:SER:H	19	0.1
(1,1031)	1:370:A:VAL:HG22	1:409:B:SER:H	19	0.1
(1,1031)	1:370:A:VAL:HG23	1:409:B:SER:H	19	0.1
(1,387)	1:365:B:ILE:HD11	1:367:B:ASN:H	12	0.1
(1,387)	1:365:B:ILE:HD12	1:367:B:ASN:H	12	0.1
(1,387)	1:365:B:ILE:HD13	1:367:B:ASN:H	12	0.1
(1,387)	1:365:B:ILE:HD11	1:367:B:ASN:H	26	0.1
(1,387)	1:365:B:ILE:HD12	1:367:B:ASN:H	26	0.1
(1,387)	1:365:B:ILE:HD13	1:367:B:ASN:H	26	0.1
(1,386)	1:365:A:ILE:HD11	1:367:A:ASN:H	4	0.1
(1,386)	1:365:A:ILE:HD12	1:367:A:ASN:H	4	0.1
(1,386)	1:365:A:ILE:HD13	1:367:A:ASN:H	4	0.1
(1,386)	1:365:A:ILE:HD11	1:367:A:ASN:H	6	0.1
(1,386)	1:365:A:ILE:HD12	1:367:A:ASN:H	6	0.1
(1,386)	1:365:A:ILE:HD13	1:367:A:ASN:H	6	0.1
(1,386)	1:365:A:ILE:HD11	1:367:A:ASN:H	17	0.1
(1,386)	1:365:A:ILE:HD12	1:367:A:ASN:H	17	0.1
(1,386)	1:365:A:ILE:HD13	1:367:A:ASN:H	17	0.1

10 Dihedral-angle violation analysis [i](#)

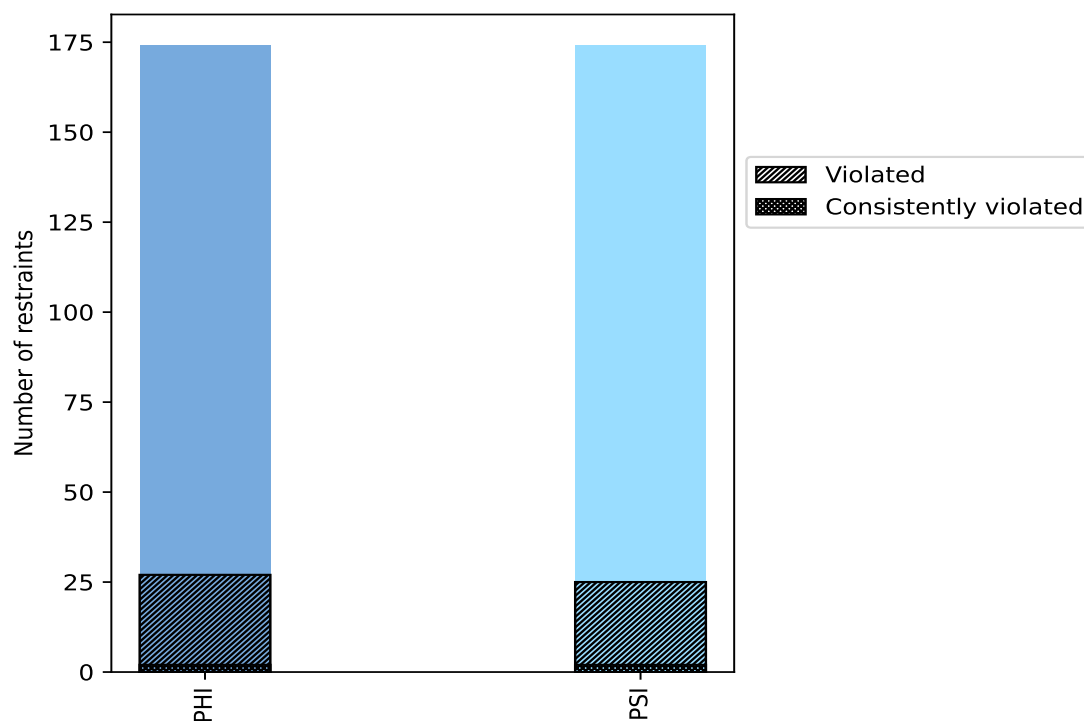
10.1 Summary of dihedral-angle violations [i](#)

The following table provides the summary of dihedral-angle violations in different dihedral-angle types. Violations less than 1° are not included in the calculation.

Angle type	Count	% ¹	Violated ³			Consistently Violated ⁴		
			Count	% ²	% ¹	Count	% ²	% ¹
PHI	174	50.0	27	15.5	7.8	2	1.1	0.6
PSI	174	50.0	25	14.4	7.2	2	1.1	0.6
Total	348	100.0	52	14.9	14.9	4	1.1	1.1

¹ percentage calculated with respect to total number of dihedral-angle restraints, ² percentage calculated with respect to number of restraints in a particular dihedral-angle type, ³ violated in at least one model, ⁴ violated in all the models

10.1.1 Bar chart : Distribution of dihedral-angles and violations [i](#)



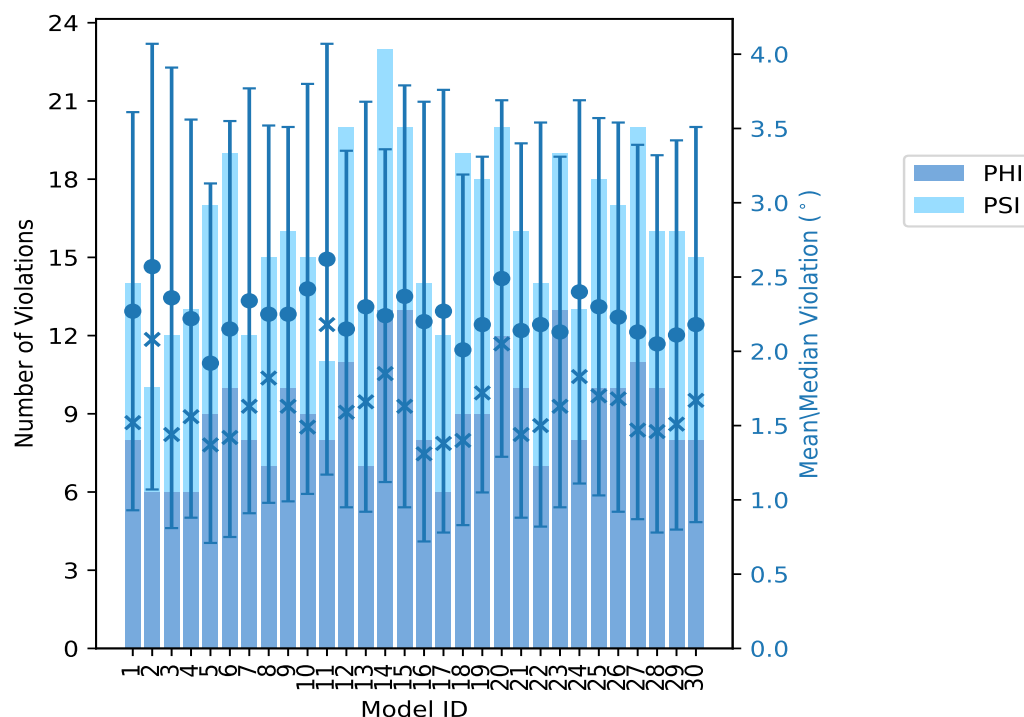
Violated and consistently violated restraints are shown using different hatch patterns in their respective categories

10.2 Dihedral-angle violation statistics for each model

The following table provides the dihedral-angle violation statistics for each model in the ensemble. Violations less than 1° are not included in the statistics.

Model ID	Number of violations			Mean (°)	Max (°)	SD (°)	Median (°)
	PHI	PSI	Total				
1	8	6	14	2.27	4.92	1.34	1.52
2	6	4	10	2.57	4.77	1.5	2.08
3	6	6	12	2.36	4.8	1.55	1.44
4	6	7	13	2.22	4.81	1.34	1.56
5	9	8	17	1.92	4.71	1.21	1.37
6	10	9	19	2.15	5.52	1.4	1.42
7	8	4	12	2.34	5.16	1.43	1.63
8	7	8	15	2.25	4.94	1.27	1.82
9	10	6	16	2.25	4.97	1.26	1.63
10	9	6	15	2.42	4.92	1.38	1.49
11	8	3	11	2.62	5.28	1.45	2.18
12	11	9	20	2.15	5.06	1.2	1.59
13	7	6	13	2.3	4.67	1.38	1.66
14	13	10	23	2.24	4.77	1.12	1.85
15	13	7	20	2.37	5.26	1.42	1.63
16	8	6	14	2.2	4.9	1.48	1.31
17	6	6	12	2.27	5.15	1.49	1.38
18	9	10	19	2.01	4.97	1.18	1.4
19	9	9	18	2.18	4.62	1.13	1.72
20	12	8	20	2.49	5.1	1.2	2.05
21	10	6	16	2.14	4.72	1.26	1.44
22	7	7	14	2.18	5.66	1.36	1.5
23	13	6	19	2.13	5.53	1.18	1.63
24	8	5	13	2.4	4.59	1.29	1.83
25	10	8	18	2.3	4.89	1.27	1.7
26	10	7	17	2.23	5.23	1.31	1.68
27	11	9	20	2.13	4.78	1.26	1.47
28	10	6	16	2.05	4.91	1.27	1.46
29	8	8	16	2.11	4.94	1.31	1.51
30	8	7	15	2.18	4.76	1.33	1.67

10.2.1 Bar graph : Dihedral violation statistics for each model [i](#)



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

10.3 Dihedral-angle violation statistics for the ensemble [i](#)

Violation analysis may find that some restraints are violated in very 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 ensemble.

Number of violated restraints			Fraction of the ensemble	
PHI	PSI	Total	Count ¹	%
3	5	8	1	3.3
7	5	12	2	6.7
5	4	9	3	10.0
0	2	2	4	13.3
2	2	4	5	16.7
1	1	2	6	20.0
0	0	0	7	23.3
0	0	0	8	26.7
1	0	1	9	30.0
0	0	0	10	33.3
0	0	0	11	36.7

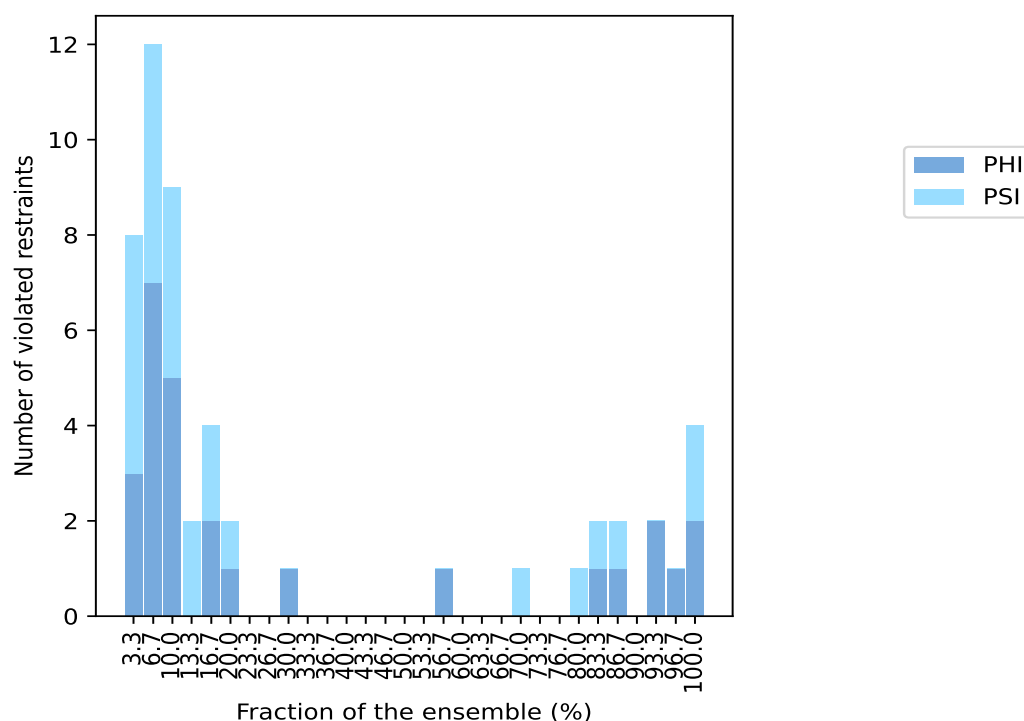
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Number of violated restraints			Fraction of the ensemble	
PHI	PSI	Total	Count ¹	%
0	0	0	12	40.0
0	0	0	13	43.3
0	0	0	14	46.7
0	0	0	15	50.0
0	0	0	16	53.3
1	0	1	17	56.7
0	0	0	18	60.0
0	0	0	19	63.3
0	0	0	20	66.7
0	1	1	21	70.0
0	0	0	22	73.3
0	0	0	23	76.7
0	1	1	24	80.0
1	1	2	25	83.3
1	1	2	26	86.7
0	0	0	27	90.0
2	0	2	28	93.3
1	0	1	29	96.7
2	2	4	30	100.0

¹ Number of models with violations

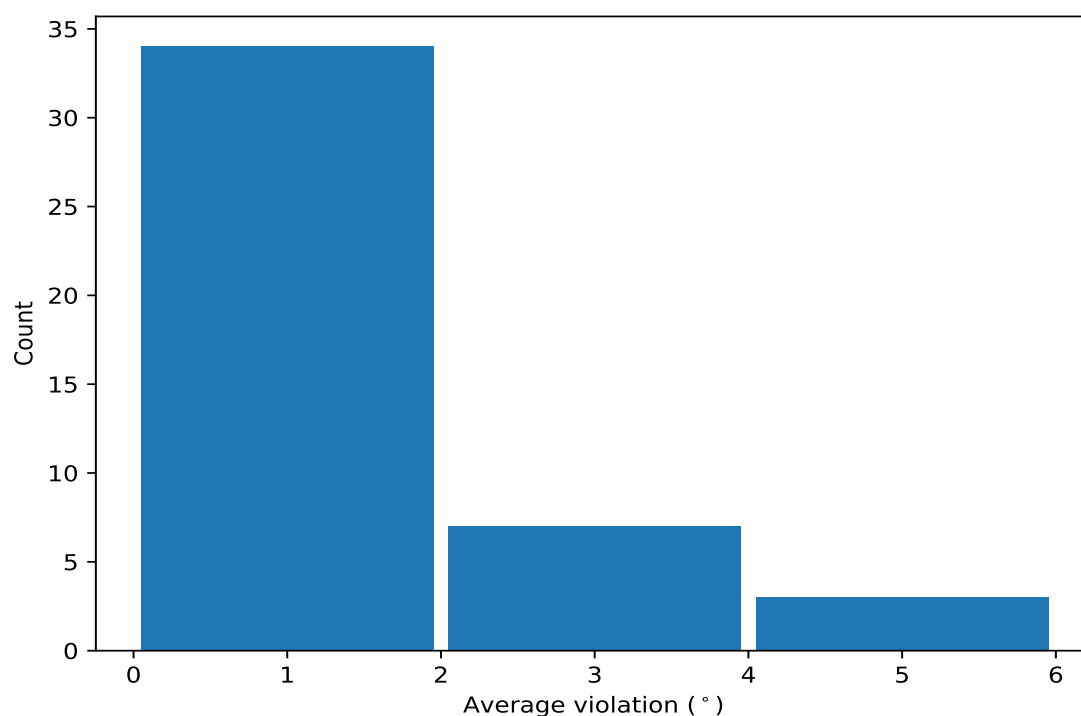
10.3.1 Bar graph : Dihedral-angle Violation statistics for the ensemble [i](#)



10.4 Most violated dihedral-angle restraints in the ensemble [i](#)

10.4.1 Histogram : Distribution of mean dihedral-angle 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



10.4.2 Table: Most violated dihedral-angle 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.

Key	Atom-1	Atom-2	Atom-3	Atom-4	Models ¹	Mean	SD ²	Median
(1,282)	1:403:B:ILE:N	1:403:B:ILE:CA	1:403:B:ILE:C	1:404:B:ARG:N	30	4.85	0.32	4.8
(1,108)	1:403:A:ILE:N	1:403:A:ILE:CA	1:403:A:ILE:C	1:404:A:ARG:N	30	4.63	0.67	4.81
(1,103)	1:400:A:LEU:C	1:401:A:LYS:N	1:401:A:LYS:CA	1:401:A:LYS:C	30	3.71	0.33	3.68
(1,277)	1:400:B:LEU:C	1:401:B:LYS:N	1:401:B:LYS:CA	1:401:B:LYS:C	30	3.66	0.34	3.68
(1,209)	1:364:B:LYS:C	1:365:B:ILE:N	1:365:B:ILE:CA	1:365:B:ILE:C	29	1.72	0.25	1.68
(1,35)	1:364:A:LYS:C	1:365:A:ILE:N	1:365:A:ILE:CA	1:365:A:ILE:C	28	1.7	0.23	1.68
(1,221)	1:370:B:VAL:C	1:371:B:ASN:N	1:371:B:ASN:CA	1:371:B:ASN:C	28	1.37	0.24	1.37
(1,47)	1:370:A:VAL:C	1:371:A:ASN:N	1:371:A:ASN:CA	1:371:A:ASN:C	26	1.37	0.24	1.34
(1,278)	1:401:B:LYS:N	1:401:B:LYS:CA	1:401:B:LYS:C	1:402:B:LYS:N	26	1.27	0.21	1.21
(1,9)	1:350:A:SER:C	1:351:A:ARG:N	1:351:A:ARG:CA	1:351:A:ARG:C	25	1.85	0.89	1.51
(1,104)	1:401:A:LYS:N	1:401:A:LYS:CA	1:401:A:LYS:C	1:402:A:LYS:N	25	1.31	0.23	1.25
(1,208)	1:363:B:LEU:N	1:363:B:LEU:CA	1:363:B:LEU:C	1:364:B:LYS:N	24	1.34	0.21	1.32
(1,34)	1:363:A:LEU:N	1:363:A:LEU:CA	1:363:A:LEU:C	1:364:A:LYS:N	21	1.36	0.22	1.34
(1,183)	1:350:B:SER:C	1:351:B:ARG:N	1:351:B:ARG:CA	1:351:B:ARG:C	17	1.89	0.85	1.5
(1,11)	1:351:A:ARG:C	1:352:A:LEU:N	1:352:A:LEU:CA	1:352:A:LEU:C	9	3.55	0.76	3.63
(1,5)	1:348:A:MET:C	1:349:A:ASP:N	1:349:A:ASP:CA	1:349:A:ASP:C	6	1.3	0.3	1.13
(1,10)	1:351:A:ARG:N	1:351:A:ARG:CA	1:351:A:ARG:C	1:352:A:LEU:N	6	1.2	0.15	1.21
(1,185)	1:351:B:ARG:C	1:352:B:LEU:N	1:352:B:LEU:CA	1:352:B:LEU:C	5	3.21	0.55	3.04
(1,15)	1:353:A:GLN:C	1:354:A:ARG:N	1:354:A:ARG:CA	1:354:A:ARG:C	5	2.0	0.6	2.05
(1,150)	1:442:A:LYS:N	1:442:A:LYS:CA	1:442:A:LYS:C	1:443:A:SER:N	5	1.46	0.15	1.43
(1,324)	1:442:B:LYS:N	1:442:B:LYS:CA	1:442:B:LYS:C	1:443:B:SER:N	5	1.37	0.12	1.35

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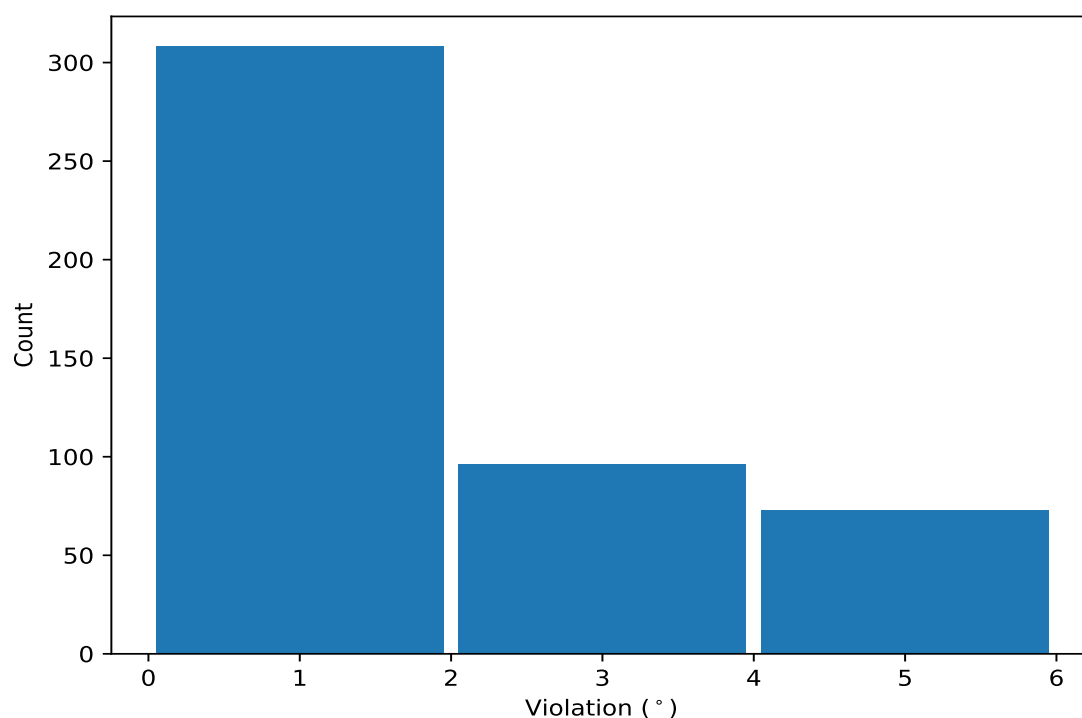
Key	Atom-1	Atom-2	Atom-3	Atom-4	Models ¹	Mean	SD ²	Median
(1,214)	1:367:B:ASN:N	1:367:B:ASN:CA	1:367:B:ASN:C	1:368:B:LEU:N	4	1.26	0.18	1.23
(1,306)	1:419:B:LEU:N	1:419:B:LEU:CA	1:419:B:LEU:C	1:420:B:TYR:N	4	1.22	0.1	1.22
(1,184)	1:351:B:ARG:N	1:351:B:ARG:CA	1:351:B:ARG:C	1:352:B:LEU:N	3	1.62	0.35	1.81
(1,70)	1:382:A:SER:N	1:382:A:SER:CA	1:382:A:SER:C	1:383:A:LEU:N	3	1.41	0.23	1.29
(1,117)	1:411:A:VAL:C	1:412:A:ILE:N	1:412:A:ILE:CA	1:412:A:ILE:C	3	1.34	0.21	1.4
(1,291)	1:411:B:VAL:C	1:412:B:ILE:N	1:412:B:ILE:CA	1:412:B:ILE:C	3	1.32	0.17	1.42
(1,40)	1:367:A:ASN:N	1:367:A:ASN:CA	1:367:A:ASN:C	1:368:A:LEU:N	3	1.3	0.17	1.41
(1,215)	1:367:B:ASN:C	1:368:B:LEU:N	1:368:B:LEU:CA	1:368:B:LEU:C	3	1.28	0.12	1.27
(1,305)	1:418:B:MET:C	1:419:B:LEU:N	1:419:B:LEU:CA	1:419:B:LEU:C	3	1.28	0.22	1.25
(1,179)	1:348:B:MET:C	1:349:B:ASP:N	1:349:B:ASP:CA	1:349:B:ASP:C	3	1.21	0.13	1.19
(1,42)	1:368:A:LEU:N	1:368:A:LEU:CA	1:368:A:LEU:C	1:369:A:ASP:N	3	1.17	0.06	1.18
(1,285)	1:404:B:ARG:C	1:405:B:ARG:N	1:405:B:ARG:CA	1:405:B:ARG:C	2	4.24	0.45	4.24
(1,111)	1:404:A:ARG:C	1:405:A:ARG:N	1:405:A:ARG:CA	1:405:A:ARG:C	2	2.28	0.07	2.28
(1,286)	1:405:B:ARG:N	1:405:B:ARG:CA	1:405:B:ARG:C	1:406:B:PHE:N	2	2.1	0.17	2.1
(1,189)	1:353:B:GLN:C	1:354:B:ARG:N	1:354:B:ARG:CA	1:354:B:ARG:C	2	1.6	0.15	1.6
(1,41)	1:367:A:ASN:C	1:368:A:LEU:N	1:368:A:LEU:CA	1:368:A:LEU:C	2	1.36	0.09	1.36
(1,308)	1:420:B:TYR:N	1:420:B:TYR:CA	1:420:B:TYR:C	1:421:B:ASN:N	2	1.34	0.09	1.34
(1,132)	1:419:A:LEU:N	1:419:A:LEU:CA	1:419:A:LEU:C	1:420:A:TYR:N	2	1.27	0.04	1.27
(1,303)	1:417:B:THR:C	1:418:B:MET:N	1:418:B:MET:CA	1:418:B:MET:C	2	1.19	0.03	1.19
(1,131)	1:418:A:MET:C	1:419:A:LEU:N	1:419:A:LEU:CA	1:419:A:LEU:C	2	1.16	0.11	1.16
(1,216)	1:368:B:LEU:N	1:368:B:LEU:CA	1:368:B:LEU:C	1:369:B:ASP:N	2	1.14	0.05	1.14
(1,129)	1:417:A:THR:C	1:418:A:MET:N	1:418:A:MET:CA	1:418:A:MET:C	2	1.1	0.06	1.1
(1,28)	1:360:A:LYS:N	1:360:A:LYS:CA	1:360:A:LYS:C	1:361:A:ASN:N	2	1.08	0.04	1.08

¹ Number of violated models, ²Standard deviation, All angle values are in degree (°)

10.5 All violated dihedral-angle restraints ⓘ

10.5.1 Histogram : Distribution of violations ⓘ

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



10.5.2 Table: All violated dihedral-angle restraints ⓘ

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.

Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,282)	1:403:B:ILE:N	1:403:B:ILE:CA	1:403:B:ILE:C	1:404:B:ARG:N	22	5.66
(1,282)	1:403:B:ILE:N	1:403:B:ILE:CA	1:403:B:ILE:C	1:404:B:ARG:N	23	5.53
(1,108)	1:403:A:ILE:N	1:403:A:ILE:CA	1:403:A:ILE:C	1:404:A:ARG:N	6	5.52
(1,282)	1:403:B:ILE:N	1:403:B:ILE:CA	1:403:B:ILE:C	1:404:B:ARG:N	11	5.28
(1,108)	1:403:A:ILE:N	1:403:A:ILE:CA	1:403:A:ILE:C	1:404:A:ARG:N	15	5.26
(1,282)	1:403:B:ILE:N	1:403:B:ILE:CA	1:403:B:ILE:C	1:404:B:ARG:N	26	5.23
(1,282)	1:403:B:ILE:N	1:403:B:ILE:CA	1:403:B:ILE:C	1:404:B:ARG:N	7	5.16
(1,108)	1:403:A:ILE:N	1:403:A:ILE:CA	1:403:A:ILE:C	1:404:A:ARG:N	17	5.15
(1,108)	1:403:A:ILE:N	1:403:A:ILE:CA	1:403:A:ILE:C	1:404:A:ARG:N	26	5.14
(1,282)	1:403:B:ILE:N	1:403:B:ILE:CA	1:403:B:ILE:C	1:404:B:ARG:N	20	5.1
(1,282)	1:403:B:ILE:N	1:403:B:ILE:CA	1:403:B:ILE:C	1:404:B:ARG:N	12	5.06
(1,108)	1:403:A:ILE:N	1:403:A:ILE:CA	1:403:A:ILE:C	1:404:A:ARG:N	20	5.01
(1,108)	1:403:A:ILE:N	1:403:A:ILE:CA	1:403:A:ILE:C	1:404:A:ARG:N	9	4.97
(1,108)	1:403:A:ILE:N	1:403:A:ILE:CA	1:403:A:ILE:C	1:404:A:ARG:N	18	4.97
(1,108)	1:403:A:ILE:N	1:403:A:ILE:CA	1:403:A:ILE:C	1:404:A:ARG:N	7	4.95
(1,108)	1:403:A:ILE:N	1:403:A:ILE:CA	1:403:A:ILE:C	1:404:A:ARG:N	12	4.95
(1,108)	1:403:A:ILE:N	1:403:A:ILE:CA	1:403:A:ILE:C	1:404:A:ARG:N	8	4.94
(1,108)	1:403:A:ILE:N	1:403:A:ILE:CA	1:403:A:ILE:C	1:404:A:ARG:N	29	4.94
(1,282)	1:403:B:ILE:N	1:403:B:ILE:CA	1:403:B:ILE:C	1:404:B:ARG:N	1	4.92
(1,282)	1:403:B:ILE:N	1:403:B:ILE:CA	1:403:B:ILE:C	1:404:B:ARG:N	9	4.92
(1,108)	1:403:A:ILE:N	1:403:A:ILE:CA	1:403:A:ILE:C	1:404:A:ARG:N	10	4.92

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,108)	1:403:A:ILE:N	1:403:A:ILE:CA	1:403:A:ILE:C	1:404:A:ARG:N	28	4.91
(1,282)	1:403:B:ILE:N	1:403:B:ILE:CA	1:403:B:ILE:C	1:404:B:ARG:N	16	4.9
(1,282)	1:403:B:ILE:N	1:403:B:ILE:CA	1:403:B:ILE:C	1:404:B:ARG:N	25	4.89
(1,282)	1:403:B:ILE:N	1:403:B:ILE:CA	1:403:B:ILE:C	1:404:B:ARG:N	8	4.88
(1,108)	1:403:A:ILE:N	1:403:A:ILE:CA	1:403:A:ILE:C	1:404:A:ARG:N	1	4.85
(1,282)	1:403:B:ILE:N	1:403:B:ILE:CA	1:403:B:ILE:C	1:404:B:ARG:N	10	4.84
(1,282)	1:403:B:ILE:N	1:403:B:ILE:CA	1:403:B:ILE:C	1:404:B:ARG:N	18	4.84
(1,108)	1:403:A:ILE:N	1:403:A:ILE:CA	1:403:A:ILE:C	1:404:A:ARG:N	16	4.82
(1,282)	1:403:B:ILE:N	1:403:B:ILE:CA	1:403:B:ILE:C	1:404:B:ARG:N	4	4.81
(1,282)	1:403:B:ILE:N	1:403:B:ILE:CA	1:403:B:ILE:C	1:404:B:ARG:N	29	4.8
(1,108)	1:403:A:ILE:N	1:403:A:ILE:CA	1:403:A:ILE:C	1:404:A:ARG:N	3	4.8
(1,108)	1:403:A:ILE:N	1:403:A:ILE:CA	1:403:A:ILE:C	1:404:A:ARG:N	27	4.78
(1,282)	1:403:B:ILE:N	1:403:B:ILE:CA	1:403:B:ILE:C	1:404:B:ARG:N	15	4.77
(1,108)	1:403:A:ILE:N	1:403:A:ILE:CA	1:403:A:ILE:C	1:404:A:ARG:N	2	4.77
(1,11)	1:351:A:ARG:C	1:352:A:LEU:N	1:352:A:LEU:CA	1:352:A:LEU:C	14	4.77
(1,282)	1:403:B:ILE:N	1:403:B:ILE:CA	1:403:B:ILE:C	1:404:B:ARG:N	30	4.76
(1,282)	1:403:B:ILE:N	1:403:B:ILE:CA	1:403:B:ILE:C	1:404:B:ARG:N	2	4.74
(1,282)	1:403:B:ILE:N	1:403:B:ILE:CA	1:403:B:ILE:C	1:404:B:ARG:N	27	4.73
(1,108)	1:403:A:ILE:N	1:403:A:ILE:CA	1:403:A:ILE:C	1:404:A:ARG:N	21	4.72
(1,282)	1:403:B:ILE:N	1:403:B:ILE:CA	1:403:B:ILE:C	1:404:B:ARG:N	5	4.71
(1,108)	1:403:A:ILE:N	1:403:A:ILE:CA	1:403:A:ILE:C	1:404:A:ARG:N	25	4.71
(1,285)	1:404:B:ARG:C	1:405:B:ARG:N	1:405:B:ARG:CA	1:405:B:ARG:C	14	4.69
(1,282)	1:403:B:ILE:N	1:403:B:ILE:CA	1:403:B:ILE:C	1:404:B:ARG:N	21	4.68
(1,282)	1:403:B:ILE:N	1:403:B:ILE:CA	1:403:B:ILE:C	1:404:B:ARG:N	3	4.67
(1,282)	1:403:B:ILE:N	1:403:B:ILE:CA	1:403:B:ILE:C	1:404:B:ARG:N	6	4.67
(1,282)	1:403:B:ILE:N	1:403:B:ILE:CA	1:403:B:ILE:C	1:404:B:ARG:N	13	4.67
(1,282)	1:403:B:ILE:N	1:403:B:ILE:CA	1:403:B:ILE:C	1:404:B:ARG:N	28	4.66
(1,282)	1:403:B:ILE:N	1:403:B:ILE:CA	1:403:B:ILE:C	1:404:B:ARG:N	19	4.62
(1,108)	1:403:A:ILE:N	1:403:A:ILE:CA	1:403:A:ILE:C	1:404:A:ARG:N	13	4.62
(1,282)	1:403:B:ILE:N	1:403:B:ILE:CA	1:403:B:ILE:C	1:404:B:ARG:N	24	4.59
(1,103)	1:400:A:LEU:C	1:401:A:LYS:N	1:401:A:LYS:CA	1:401:A:LYS:C	3	4.57
(1,108)	1:403:A:ILE:N	1:403:A:ILE:CA	1:403:A:ILE:C	1:404:A:ARG:N	5	4.48
(1,108)	1:403:A:ILE:N	1:403:A:ILE:CA	1:403:A:ILE:C	1:404:A:ARG:N	30	4.48
(1,103)	1:400:A:LEU:C	1:401:A:LYS:N	1:401:A:LYS:CA	1:401:A:LYS:C	16	4.48
(1,108)	1:403:A:ILE:N	1:403:A:ILE:CA	1:403:A:ILE:C	1:404:A:ARG:N	4	4.47
(1,282)	1:403:B:ILE:N	1:403:B:ILE:CA	1:403:B:ILE:C	1:404:B:ARG:N	17	4.33
(1,108)	1:403:A:ILE:N	1:403:A:ILE:CA	1:403:A:ILE:C	1:404:A:ARG:N	24	4.32
(1,277)	1:400:B:LEU:C	1:401:B:LYS:N	1:401:B:LYS:CA	1:401:B:LYS:C	30	4.29
(1,108)	1:403:A:ILE:N	1:403:A:ILE:CA	1:403:A:ILE:C	1:404:A:ARG:N	22	4.28
(1,108)	1:403:A:ILE:N	1:403:A:ILE:CA	1:403:A:ILE:C	1:404:A:ARG:N	11	4.23
(1,103)	1:400:A:LEU:C	1:401:A:LYS:N	1:401:A:LYS:CA	1:401:A:LYS:C	14	4.21
(1,277)	1:400:B:LEU:C	1:401:B:LYS:N	1:401:B:LYS:CA	1:401:B:LYS:C	13	4.2
(1,185)	1:351:B:ARG:C	1:352:B:LEU:N	1:352:B:LEU:CA	1:352:B:LEU:C	15	4.2
(1,277)	1:400:B:LEU:C	1:401:B:LYS:N	1:401:B:LYS:CA	1:401:B:LYS:C	17	4.17
(1,277)	1:400:B:LEU:C	1:401:B:LYS:N	1:401:B:LYS:CA	1:401:B:LYS:C	24	4.15
(1,11)	1:351:A:ARG:C	1:352:A:LEU:N	1:352:A:LEU:CA	1:352:A:LEU:C	15	4.14
(1,11)	1:351:A:ARG:C	1:352:A:LEU:N	1:352:A:LEU:CA	1:352:A:LEU:C	25	4.14
(1,277)	1:400:B:LEU:C	1:401:B:LYS:N	1:401:B:LYS:CA	1:401:B:LYS:C	15	4.1
(1,277)	1:400:B:LEU:C	1:401:B:LYS:N	1:401:B:LYS:CA	1:401:B:LYS:C	2	4.08
(1,103)	1:400:A:LEU:C	1:401:A:LYS:N	1:401:A:LYS:CA	1:401:A:LYS:C	11	4.04
(1,183)	1:350:B:SER:C	1:351:B:ARG:N	1:351:B:ARG:CA	1:351:B:ARG:C	20	4.03

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,282)	1:403:B:ILE:N	1:403:B:ILE:CA	1:403:B:ILE:C	1:404:B:ARG:N	14	4.01
(1,277)	1:400:B:LEU:C	1:401:B:LYS:N	1:401:B:LYS:CA	1:401:B:LYS:C	3	3.98
(1,103)	1:400:A:LEU:C	1:401:A:LYS:N	1:401:A:LYS:CA	1:401:A:LYS:C	24	3.98
(1,277)	1:400:B:LEU:C	1:401:B:LYS:N	1:401:B:LYS:CA	1:401:B:LYS:C	11	3.93
(1,103)	1:400:A:LEU:C	1:401:A:LYS:N	1:401:A:LYS:CA	1:401:A:LYS:C	19	3.93
(1,103)	1:400:A:LEU:C	1:401:A:LYS:N	1:401:A:LYS:CA	1:401:A:LYS:C	4	3.89
(1,103)	1:400:A:LEU:C	1:401:A:LYS:N	1:401:A:LYS:CA	1:401:A:LYS:C	23	3.88
(1,9)	1:350:A:SER:C	1:351:A:ARG:N	1:351:A:ARG:CA	1:351:A:ARG:C	10	3.87
(1,11)	1:351:A:ARG:C	1:352:A:LEU:N	1:352:A:LEU:CA	1:352:A:LEU:C	10	3.83
(1,277)	1:400:B:LEU:C	1:401:B:LYS:N	1:401:B:LYS:CA	1:401:B:LYS:C	25	3.81
(1,285)	1:404:B:ARG:C	1:405:B:ARG:N	1:405:B:ARG:CA	1:405:B:ARG:C	19	3.8
(1,103)	1:400:A:LEU:C	1:401:A:LYS:N	1:401:A:LYS:CA	1:401:A:LYS:C	1	3.8
(1,103)	1:400:A:LEU:C	1:401:A:LYS:N	1:401:A:LYS:CA	1:401:A:LYS:C	29	3.78
(1,103)	1:400:A:LEU:C	1:401:A:LYS:N	1:401:A:LYS:CA	1:401:A:LYS:C	13	3.76
(1,277)	1:400:B:LEU:C	1:401:B:LYS:N	1:401:B:LYS:CA	1:401:B:LYS:C	16	3.75
(1,108)	1:403:A:ILE:N	1:403:A:ILE:CA	1:403:A:ILE:C	1:404:A:ARG:N	23	3.74
(1,103)	1:400:A:LEU:C	1:401:A:LYS:N	1:401:A:LYS:CA	1:401:A:LYS:C	26	3.73
(1,103)	1:400:A:LEU:C	1:401:A:LYS:N	1:401:A:LYS:CA	1:401:A:LYS:C	30	3.73
(1,9)	1:350:A:SER:C	1:351:A:ARG:N	1:351:A:ARG:CA	1:351:A:ARG:C	6	3.73
(1,277)	1:400:B:LEU:C	1:401:B:LYS:N	1:401:B:LYS:CA	1:401:B:LYS:C	1	3.72
(1,277)	1:400:B:LEU:C	1:401:B:LYS:N	1:401:B:LYS:CA	1:401:B:LYS:C	18	3.72
(1,277)	1:400:B:LEU:C	1:401:B:LYS:N	1:401:B:LYS:CA	1:401:B:LYS:C	19	3.71
(1,277)	1:400:B:LEU:C	1:401:B:LYS:N	1:401:B:LYS:CA	1:401:B:LYS:C	27	3.7
(1,103)	1:400:A:LEU:C	1:401:A:LYS:N	1:401:A:LYS:CA	1:401:A:LYS:C	2	3.7
(1,103)	1:400:A:LEU:C	1:401:A:LYS:N	1:401:A:LYS:CA	1:401:A:LYS:C	21	3.7
(1,9)	1:350:A:SER:C	1:351:A:ARG:N	1:351:A:ARG:CA	1:351:A:ARG:C	27	3.7
(1,277)	1:400:B:LEU:C	1:401:B:LYS:N	1:401:B:LYS:CA	1:401:B:LYS:C	9	3.69
(1,277)	1:400:B:LEU:C	1:401:B:LYS:N	1:401:B:LYS:CA	1:401:B:LYS:C	6	3.67
(1,103)	1:400:A:LEU:C	1:401:A:LYS:N	1:401:A:LYS:CA	1:401:A:LYS:C	25	3.67
(1,103)	1:400:A:LEU:C	1:401:A:LYS:N	1:401:A:LYS:CA	1:401:A:LYS:C	7	3.65
(1,103)	1:400:A:LEU:C	1:401:A:LYS:N	1:401:A:LYS:CA	1:401:A:LYS:C	22	3.63
(1,11)	1:351:A:ARG:C	1:352:A:LEU:N	1:352:A:LEU:CA	1:352:A:LEU:C	6	3.63
(1,277)	1:400:B:LEU:C	1:401:B:LYS:N	1:401:B:LYS:CA	1:401:B:LYS:C	21	3.62
(1,103)	1:400:A:LEU:C	1:401:A:LYS:N	1:401:A:LYS:CA	1:401:A:LYS:C	5	3.6
(1,277)	1:400:B:LEU:C	1:401:B:LYS:N	1:401:B:LYS:CA	1:401:B:LYS:C	29	3.59
(1,277)	1:400:B:LEU:C	1:401:B:LYS:N	1:401:B:LYS:CA	1:401:B:LYS:C	28	3.58
(1,103)	1:400:A:LEU:C	1:401:A:LYS:N	1:401:A:LYS:CA	1:401:A:LYS:C	8	3.56
(1,103)	1:400:A:LEU:C	1:401:A:LYS:N	1:401:A:LYS:CA	1:401:A:LYS:C	28	3.56
(1,277)	1:400:B:LEU:C	1:401:B:LYS:N	1:401:B:LYS:CA	1:401:B:LYS:C	26	3.55
(1,103)	1:400:A:LEU:C	1:401:A:LYS:N	1:401:A:LYS:CA	1:401:A:LYS:C	17	3.54
(1,103)	1:400:A:LEU:C	1:401:A:LYS:N	1:401:A:LYS:CA	1:401:A:LYS:C	27	3.51
(1,11)	1:351:A:ARG:C	1:352:A:LEU:N	1:352:A:LEU:CA	1:352:A:LEU:C	27	3.51
(1,103)	1:400:A:LEU:C	1:401:A:LYS:N	1:401:A:LYS:CA	1:401:A:LYS:C	12	3.49
(1,277)	1:400:B:LEU:C	1:401:B:LYS:N	1:401:B:LYS:CA	1:401:B:LYS:C	4	3.43
(1,277)	1:400:B:LEU:C	1:401:B:LYS:N	1:401:B:LYS:CA	1:401:B:LYS:C	8	3.43
(1,277)	1:400:B:LEU:C	1:401:B:LYS:N	1:401:B:LYS:CA	1:401:B:LYS:C	14	3.42
(1,103)	1:400:A:LEU:C	1:401:A:LYS:N	1:401:A:LYS:CA	1:401:A:LYS:C	6	3.41
(1,103)	1:400:A:LEU:C	1:401:A:LYS:N	1:401:A:LYS:CA	1:401:A:LYS:C	20	3.4
(1,277)	1:400:B:LEU:C	1:401:B:LYS:N	1:401:B:LYS:CA	1:401:B:LYS:C	20	3.39
(1,103)	1:400:A:LEU:C	1:401:A:LYS:N	1:401:A:LYS:CA	1:401:A:LYS:C	10	3.39
(1,103)	1:400:A:LEU:C	1:401:A:LYS:N	1:401:A:LYS:CA	1:401:A:LYS:C	15	3.37

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,277)	1:400:B:LEU:C	1:401:B:LYS:N	1:401:B:LYS:CA	1:401:B:LYS:C	12	3.35
(1,277)	1:400:B:LEU:C	1:401:B:LYS:N	1:401:B:LYS:CA	1:401:B:LYS:C	5	3.3
(1,103)	1:400:A:LEU:C	1:401:A:LYS:N	1:401:A:LYS:CA	1:401:A:LYS:C	9	3.3
(1,277)	1:400:B:LEU:C	1:401:B:LYS:N	1:401:B:LYS:CA	1:401:B:LYS:C	10	3.29
(1,108)	1:403:A:ILE:N	1:403:A:ILE:CA	1:403:A:ILE:C	1:404:A:ARG:N	19	3.28
(1,185)	1:351:B:ARG:C	1:352:B:LEU:N	1:352:B:LEU:CA	1:352:B:LEU:C	20	3.26
(1,277)	1:400:B:LEU:C	1:401:B:LYS:N	1:401:B:LYS:CA	1:401:B:LYS:C	23	3.15
(1,277)	1:400:B:LEU:C	1:401:B:LYS:N	1:401:B:LYS:CA	1:401:B:LYS:C	22	3.05
(1,185)	1:351:B:ARG:C	1:352:B:LEU:N	1:352:B:LEU:CA	1:352:B:LEU:C	12	3.04
(1,183)	1:350:B:SER:C	1:351:B:ARG:N	1:351:B:ARG:CA	1:351:B:ARG:C	15	3.04
(1,183)	1:350:B:SER:C	1:351:B:ARG:N	1:351:B:ARG:CA	1:351:B:ARG:C	12	3.0
(1,185)	1:351:B:ARG:C	1:352:B:LEU:N	1:352:B:LEU:CA	1:352:B:LEU:C	9	2.98
(1,15)	1:353:A:GLN:C	1:354:A:ARG:N	1:354:A:ARG:CA	1:354:A:ARG:C	20	2.98
(1,277)	1:400:B:LEU:C	1:401:B:LYS:N	1:401:B:LYS:CA	1:401:B:LYS:C	7	2.97
(1,183)	1:350:B:SER:C	1:351:B:ARG:N	1:351:B:ARG:CA	1:351:B:ARG:C	23	2.93
(1,11)	1:351:A:ARG:C	1:352:A:LEU:N	1:352:A:LEU:CA	1:352:A:LEU:C	11	2.92
(1,103)	1:400:A:LEU:C	1:401:A:LYS:N	1:401:A:LYS:CA	1:401:A:LYS:C	18	2.89
(1,11)	1:351:A:ARG:C	1:352:A:LEU:N	1:352:A:LEU:CA	1:352:A:LEU:C	20	2.89
(1,304)	1:418:B:MET:N	1:418:B:MET:CA	1:418:B:MET:C	1:419:B:LEU:N	21	2.81
(1,9)	1:350:A:SER:C	1:351:A:ARG:N	1:351:A:ARG:CA	1:351:A:ARG:C	15	2.79
(1,9)	1:350:A:SER:C	1:351:A:ARG:N	1:351:A:ARG:CA	1:351:A:ARG:C	14	2.64
(1,9)	1:350:A:SER:C	1:351:A:ARG:N	1:351:A:ARG:CA	1:351:A:ARG:C	20	2.57
(1,185)	1:351:B:ARG:C	1:352:B:LEU:N	1:352:B:LEU:CA	1:352:B:LEU:C	23	2.56
(1,9)	1:350:A:SER:C	1:351:A:ARG:N	1:351:A:ARG:CA	1:351:A:ARG:C	25	2.44
(1,111)	1:404:A:ARG:C	1:405:A:ARG:N	1:405:A:ARG:CA	1:405:A:ARG:C	14	2.35
(1,286)	1:405:B:ARG:N	1:405:B:ARG:CA	1:405:B:ARG:C	1:406:B:PHE:N	19	2.27
(1,9)	1:350:A:SER:C	1:351:A:ARG:N	1:351:A:ARG:CA	1:351:A:ARG:C	24	2.24
(1,111)	1:404:A:ARG:C	1:405:A:ARG:N	1:405:A:ARG:CA	1:405:A:ARG:C	19	2.21
(1,183)	1:350:B:SER:C	1:351:B:ARG:N	1:351:B:ARG:CA	1:351:B:ARG:C	26	2.2
(1,209)	1:364:B:LYS:C	1:365:B:ILE:N	1:365:B:ILE:CA	1:365:B:ILE:C	11	2.18
(1,15)	1:353:A:GLN:C	1:354:A:ARG:N	1:354:A:ARG:CA	1:354:A:ARG:C	15	2.17
(1,183)	1:350:B:SER:C	1:351:B:ARG:N	1:351:B:ARG:CA	1:351:B:ARG:C	24	2.16
(1,209)	1:364:B:LYS:C	1:365:B:ILE:N	1:365:B:ILE:CA	1:365:B:ILE:C	2	2.14
(1,11)	1:351:A:ARG:C	1:352:A:LEU:N	1:352:A:LEU:CA	1:352:A:LEU:C	26	2.12
(1,209)	1:364:B:LYS:C	1:365:B:ILE:N	1:365:B:ILE:CA	1:365:B:ILE:C	8	2.11
(1,209)	1:364:B:LYS:C	1:365:B:ILE:N	1:365:B:ILE:CA	1:365:B:ILE:C	20	2.11
(1,35)	1:364:A:LYS:C	1:365:A:ILE:N	1:365:A:ILE:CA	1:365:A:ILE:C	8	2.1
(1,47)	1:370:A:VAL:C	1:371:A:ASN:N	1:371:A:ASN:CA	1:371:A:ASN:C	18	2.09
(1,15)	1:353:A:GLN:C	1:354:A:ARG:N	1:354:A:ARG:CA	1:354:A:ARG:C	25	2.05
(1,278)	1:401:B:LYS:N	1:401:B:LYS:CA	1:401:B:LYS:C	1:402:B:LYS:N	19	2.04
(1,221)	1:370:B:VAL:C	1:371:B:ASN:N	1:371:B:ASN:CA	1:371:B:ASN:C	18	2.04
(1,209)	1:364:B:LYS:C	1:365:B:ILE:N	1:365:B:ILE:CA	1:365:B:ILE:C	26	2.03
(1,35)	1:364:A:LYS:C	1:365:A:ILE:N	1:365:A:ILE:CA	1:365:A:ILE:C	2	2.01
(1,35)	1:364:A:LYS:C	1:365:A:ILE:N	1:365:A:ILE:CA	1:365:A:ILE:C	26	2.01
(1,209)	1:364:B:LYS:C	1:365:B:ILE:N	1:365:B:ILE:CA	1:365:B:ILE:C	14	2.0
(1,35)	1:364:A:LYS:C	1:365:A:ILE:N	1:365:A:ILE:CA	1:365:A:ILE:C	20	2.0
(1,104)	1:401:A:LYS:N	1:401:A:LYS:CA	1:401:A:LYS:C	1:402:A:LYS:N	19	1.98
(1,9)	1:350:A:SER:C	1:351:A:ARG:N	1:351:A:ARG:CA	1:351:A:ARG:C	7	1.96
(1,286)	1:405:B:ARG:N	1:405:B:ARG:CA	1:405:B:ARG:C	1:406:B:PHE:N	14	1.94
(1,35)	1:364:A:LYS:C	1:365:A:ILE:N	1:365:A:ILE:CA	1:365:A:ILE:C	30	1.94
(1,209)	1:364:B:LYS:C	1:365:B:ILE:N	1:365:B:ILE:CA	1:365:B:ILE:C	30	1.93

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,184)	1:351:B:ARG:N	1:351:B:ARG:CA	1:351:B:ARG:C	1:352:B:LEU:N	23	1.92
(1,209)	1:364:B:LYS:C	1:365:B:ILE:N	1:365:B:ILE:CA	1:365:B:ILE:C	29	1.91
(1,47)	1:370:A:VAL:C	1:371:A:ASN:N	1:371:A:ASN:CA	1:371:A:ASN:C	8	1.91
(1,35)	1:364:A:LYS:C	1:365:A:ILE:N	1:365:A:ILE:CA	1:365:A:ILE:C	3	1.91
(1,35)	1:364:A:LYS:C	1:365:A:ILE:N	1:365:A:ILE:CA	1:365:A:ILE:C	25	1.91
(1,209)	1:364:B:LYS:C	1:365:B:ILE:N	1:365:B:ILE:CA	1:365:B:ILE:C	13	1.89
(1,35)	1:364:A:LYS:C	1:365:A:ILE:N	1:365:A:ILE:CA	1:365:A:ILE:C	17	1.89
(1,209)	1:364:B:LYS:C	1:365:B:ILE:N	1:365:B:ILE:CA	1:365:B:ILE:C	18	1.87
(1,183)	1:350:B:SER:C	1:351:B:ARG:N	1:351:B:ARG:CA	1:351:B:ARG:C	14	1.86
(1,35)	1:364:A:LYS:C	1:365:A:ILE:N	1:365:A:ILE:CA	1:365:A:ILE:C	14	1.86
(1,108)	1:403:A:ILE:N	1:403:A:ILE:CA	1:403:A:ILE:C	1:404:A:ARG:N	14	1.85
(1,35)	1:364:A:LYS:C	1:365:A:ILE:N	1:365:A:ILE:CA	1:365:A:ILE:C	18	1.85
(1,209)	1:364:B:LYS:C	1:365:B:ILE:N	1:365:B:ILE:CA	1:365:B:ILE:C	24	1.83
(1,221)	1:370:B:VAL:C	1:371:B:ASN:N	1:371:B:ASN:CA	1:371:B:ASN:C	8	1.82
(1,35)	1:364:A:LYS:C	1:365:A:ILE:N	1:365:A:ILE:CA	1:365:A:ILE:C	16	1.82
(1,208)	1:363:B:LEU:N	1:363:B:LEU:CA	1:363:B:LEU:C	1:364:B:LYS:N	20	1.81
(1,184)	1:351:B:ARG:N	1:351:B:ARG:CA	1:351:B:ARG:C	1:352:B:LEU:N	12	1.81
(1,9)	1:350:A:SER:C	1:351:A:ARG:N	1:351:A:ARG:CA	1:351:A:ARG:C	29	1.8
(1,209)	1:364:B:LYS:C	1:365:B:ILE:N	1:365:B:ILE:CA	1:365:B:ILE:C	9	1.77
(1,104)	1:401:A:LYS:N	1:401:A:LYS:CA	1:401:A:LYS:C	1:402:A:LYS:N	14	1.77
(1,5)	1:348:A:MET:C	1:349:A:ASP:N	1:349:A:ASP:CA	1:349:A:ASP:C	23	1.76
(1,209)	1:364:B:LYS:C	1:365:B:ILE:N	1:365:B:ILE:CA	1:365:B:ILE:C	25	1.74
(1,189)	1:353:B:GLN:C	1:354:B:ARG:N	1:354:B:ARG:CA	1:354:B:ARG:C	15	1.74
(1,34)	1:363:A:LEU:N	1:363:A:LEU:CA	1:363:A:LEU:C	1:364:A:LYS:N	1	1.74
(1,70)	1:382:A:SER:N	1:382:A:SER:CA	1:382:A:SER:C	1:383:A:LEU:N	30	1.73
(1,150)	1:442:A:LYS:N	1:442:A:LYS:CA	1:442:A:LYS:C	1:443:A:SER:N	22	1.72
(1,35)	1:364:A:LYS:C	1:365:A:ILE:N	1:365:A:ILE:CA	1:365:A:ILE:C	13	1.72
(1,35)	1:364:A:LYS:C	1:365:A:ILE:N	1:365:A:ILE:CA	1:365:A:ILE:C	4	1.71
(1,35)	1:364:A:LYS:C	1:365:A:ILE:N	1:365:A:ILE:CA	1:365:A:ILE:C	6	1.71
(1,209)	1:364:B:LYS:C	1:365:B:ILE:N	1:365:B:ILE:CA	1:365:B:ILE:C	4	1.7
(1,208)	1:363:B:LEU:N	1:363:B:LEU:CA	1:363:B:LEU:C	1:364:B:LYS:N	1	1.7
(1,209)	1:364:B:LYS:C	1:365:B:ILE:N	1:365:B:ILE:CA	1:365:B:ILE:C	23	1.68
(1,34)	1:363:A:LEU:N	1:363:A:LEU:CA	1:363:A:LEU:C	1:364:A:LYS:N	26	1.68
(1,9)	1:350:A:SER:C	1:351:A:ARG:N	1:351:A:ARG:CA	1:351:A:ARG:C	21	1.68
(1,5)	1:348:A:MET:C	1:349:A:ASP:N	1:349:A:ASP:CA	1:349:A:ASP:C	30	1.67
(1,183)	1:350:B:SER:C	1:351:B:ARG:N	1:351:B:ARG:CA	1:351:B:ARG:C	13	1.66
(1,174)	1:454:A:ASN:N	1:454:A:ASN:CA	1:454:A:ASN:C	1:455:A:LYS:N	25	1.66
(1,35)	1:364:A:LYS:C	1:365:A:ILE:N	1:365:A:ILE:CA	1:365:A:ILE:C	9	1.66
(1,35)	1:364:A:LYS:C	1:365:A:ILE:N	1:365:A:ILE:CA	1:365:A:ILE:C	22	1.66
(1,34)	1:363:A:LEU:N	1:363:A:LEU:CA	1:363:A:LEU:C	1:364:A:LYS:N	20	1.65
(1,35)	1:364:A:LYS:C	1:365:A:ILE:N	1:365:A:ILE:CA	1:365:A:ILE:C	24	1.64
(1,34)	1:363:A:LEU:N	1:363:A:LEU:CA	1:363:A:LEU:C	1:364:A:LYS:N	9	1.64
(1,209)	1:364:B:LYS:C	1:365:B:ILE:N	1:365:B:ILE:CA	1:365:B:ILE:C	7	1.63
(1,209)	1:364:B:LYS:C	1:365:B:ILE:N	1:365:B:ILE:CA	1:365:B:ILE:C	16	1.63
(1,35)	1:364:A:LYS:C	1:365:A:ILE:N	1:365:A:ILE:CA	1:365:A:ILE:C	7	1.63
(1,35)	1:364:A:LYS:C	1:365:A:ILE:N	1:365:A:ILE:CA	1:365:A:ILE:C	12	1.63
(1,35)	1:364:A:LYS:C	1:365:A:ILE:N	1:365:A:ILE:CA	1:365:A:ILE:C	23	1.63
(1,221)	1:370:B:VAL:C	1:371:B:ASN:N	1:371:B:ASN:CA	1:371:B:ASN:C	20	1.62
(1,208)	1:363:B:LEU:N	1:363:B:LEU:CA	1:363:B:LEU:C	1:364:B:LYS:N	9	1.62
(1,47)	1:370:A:VAL:C	1:371:A:ASN:N	1:371:A:ASN:CA	1:371:A:ASN:C	28	1.62
(1,209)	1:364:B:LYS:C	1:365:B:ILE:N	1:365:B:ILE:CA	1:365:B:ILE:C	12	1.61

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,209)	1:364:B:LYS:C	1:365:B:ILE:N	1:365:B:ILE:CA	1:365:B:ILE:C	27	1.61
(1,47)	1:370:A:VAL:C	1:371:A:ASN:N	1:371:A:ASN:CA	1:371:A:ASN:C	6	1.61
(1,34)	1:363:A:LEU:N	1:363:A:LEU:CA	1:363:A:LEU:C	1:364:A:LYS:N	12	1.61
(1,209)	1:364:B:LYS:C	1:365:B:ILE:N	1:365:B:ILE:CA	1:365:B:ILE:C	3	1.6
(1,209)	1:364:B:LYS:C	1:365:B:ILE:N	1:365:B:ILE:CA	1:365:B:ILE:C	22	1.6
(1,221)	1:370:B:VAL:C	1:371:B:ASN:N	1:371:B:ASN:CA	1:371:B:ASN:C	9	1.59
(1,348)	1:454:B:ASN:N	1:454:B:ASN:CA	1:454:B:ASN:C	1:455:B:LYS:N	25	1.58
(1,15)	1:353:A:GLN:C	1:354:A:ARG:N	1:354:A:ARG:CA	1:354:A:ARG:C	14	1.58
(1,221)	1:370:B:VAL:C	1:371:B:ASN:N	1:371:B:ASN:CA	1:371:B:ASN:C	12	1.57
(1,221)	1:370:B:VAL:C	1:371:B:ASN:N	1:371:B:ASN:CA	1:371:B:ASN:C	28	1.57
(1,208)	1:363:B:LEU:N	1:363:B:LEU:CA	1:363:B:LEU:C	1:364:B:LYS:N	12	1.57
(1,34)	1:363:A:LEU:N	1:363:A:LEU:CA	1:363:A:LEU:C	1:364:A:LYS:N	14	1.57
(1,324)	1:442:B:LYS:N	1:442:B:LYS:CA	1:442:B:LYS:C	1:443:B:SER:N	29	1.56
(1,305)	1:418:B:MET:C	1:419:B:LEU:N	1:419:B:LEU:CA	1:419:B:LEU:C	27	1.56
(1,221)	1:370:B:VAL:C	1:371:B:ASN:N	1:371:B:ASN:CA	1:371:B:ASN:C	4	1.56
(1,208)	1:363:B:LEU:N	1:363:B:LEU:CA	1:363:B:LEU:C	1:364:B:LYS:N	26	1.56
(1,117)	1:411:A:VAL:C	1:412:A:ILE:N	1:412:A:ILE:CA	1:412:A:ILE:C	23	1.56
(1,9)	1:350:A:SER:C	1:351:A:ARG:N	1:351:A:ARG:CA	1:351:A:ARG:C	13	1.56
(1,35)	1:364:A:LYS:C	1:365:A:ILE:N	1:365:A:ILE:CA	1:365:A:ILE:C	29	1.54
(1,209)	1:364:B:LYS:C	1:365:B:ILE:N	1:365:B:ILE:CA	1:365:B:ILE:C	10	1.53
(1,104)	1:401:A:LYS:N	1:401:A:LYS:CA	1:401:A:LYS:C	1:402:A:LYS:N	1	1.53
(1,35)	1:364:A:LYS:C	1:365:A:ILE:N	1:365:A:ILE:CA	1:365:A:ILE:C	27	1.53
(1,278)	1:401:B:LYS:N	1:401:B:LYS:CA	1:401:B:LYS:C	1:402:B:LYS:N	8	1.52
(1,209)	1:364:B:LYS:C	1:365:B:ILE:N	1:365:B:ILE:CA	1:365:B:ILE:C	15	1.52
(1,208)	1:363:B:LEU:N	1:363:B:LEU:CA	1:363:B:LEU:C	1:364:B:LYS:N	4	1.52
(1,35)	1:364:A:LYS:C	1:365:A:ILE:N	1:365:A:ILE:CA	1:365:A:ILE:C	11	1.52
(1,278)	1:401:B:LYS:N	1:401:B:LYS:CA	1:401:B:LYS:C	1:402:B:LYS:N	1	1.51
(1,221)	1:370:B:VAL:C	1:371:B:ASN:N	1:371:B:ASN:CA	1:371:B:ASN:C	14	1.51
(1,214)	1:367:B:ASN:N	1:367:B:ASN:CA	1:367:B:ASN:C	1:368:B:LEU:N	28	1.51
(1,9)	1:350:A:SER:C	1:351:A:ARG:N	1:351:A:ARG:CA	1:351:A:ARG:C	9	1.51
(1,183)	1:350:B:SER:C	1:351:B:ARG:N	1:351:B:ARG:CA	1:351:B:ARG:C	25	1.5
(1,104)	1:401:A:LYS:N	1:401:A:LYS:CA	1:401:A:LYS:C	1:402:A:LYS:N	27	1.5
(1,47)	1:370:A:VAL:C	1:371:A:ASN:N	1:371:A:ASN:CA	1:371:A:ASN:C	14	1.5
(1,209)	1:364:B:LYS:C	1:365:B:ILE:N	1:365:B:ILE:CA	1:365:B:ILE:C	21	1.49
(1,47)	1:370:A:VAL:C	1:371:A:ASN:N	1:371:A:ASN:CA	1:371:A:ASN:C	1	1.49
(1,47)	1:370:A:VAL:C	1:371:A:ASN:N	1:371:A:ASN:CA	1:371:A:ASN:C	9	1.49
(1,35)	1:364:A:LYS:C	1:365:A:ILE:N	1:365:A:ILE:CA	1:365:A:ILE:C	1	1.49
(1,35)	1:364:A:LYS:C	1:365:A:ILE:N	1:365:A:ILE:CA	1:365:A:ILE:C	10	1.49
(1,278)	1:401:B:LYS:N	1:401:B:LYS:CA	1:401:B:LYS:C	1:402:B:LYS:N	14	1.48
(1,221)	1:370:B:VAL:C	1:371:B:ASN:N	1:371:B:ASN:CA	1:371:B:ASN:C	10	1.48
(1,208)	1:363:B:LEU:N	1:363:B:LEU:CA	1:363:B:LEU:C	1:364:B:LYS:N	29	1.48
(1,47)	1:370:A:VAL:C	1:371:A:ASN:N	1:371:A:ASN:CA	1:371:A:ASN:C	10	1.48
(1,104)	1:401:A:LYS:N	1:401:A:LYS:CA	1:401:A:LYS:C	1:402:A:LYS:N	24	1.47
(1,34)	1:363:A:LEU:N	1:363:A:LEU:CA	1:363:A:LEU:C	1:364:A:LYS:N	8	1.47
(1,291)	1:411:B:VAL:C	1:412:B:ILE:N	1:412:B:ILE:CA	1:412:B:ILE:C	19	1.46
(1,209)	1:364:B:LYS:C	1:365:B:ILE:N	1:365:B:ILE:CA	1:365:B:ILE:C	1	1.46
(1,183)	1:350:B:SER:C	1:351:B:ARG:N	1:351:B:ARG:CA	1:351:B:ARG:C	29	1.46
(1,150)	1:442:A:LYS:N	1:442:A:LYS:CA	1:442:A:LYS:C	1:443:A:SER:N	29	1.46
(1,41)	1:367:A:ASN:C	1:368:A:LEU:N	1:368:A:LEU:CA	1:368:A:LEU:C	28	1.46
(1,35)	1:364:A:LYS:C	1:365:A:ILE:N	1:365:A:ILE:CA	1:365:A:ILE:C	21	1.46
(1,278)	1:401:B:LYS:N	1:401:B:LYS:CA	1:401:B:LYS:C	1:402:B:LYS:N	6	1.45

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,209)	1:364:B:LYS:C	1:365:B:ILE:N	1:365:B:ILE:CA	1:365:B:ILE:C	5	1.45
(1,209)	1:364:B:LYS:C	1:365:B:ILE:N	1:365:B:ILE:CA	1:365:B:ILE:C	28	1.45
(1,189)	1:353:B:GLN:C	1:354:B:ARG:N	1:354:B:ARG:CA	1:354:B:ARG:C	20	1.45
(1,104)	1:401:A:LYS:N	1:401:A:LYS:CA	1:401:A:LYS:C	1:402:A:LYS:N	23	1.45
(1,47)	1:370:A:VAL:C	1:371:A:ASN:N	1:371:A:ASN:CA	1:371:A:ASN:C	12	1.45
(1,47)	1:370:A:VAL:C	1:371:A:ASN:N	1:371:A:ASN:CA	1:371:A:ASN:C	17	1.45
(1,34)	1:363:A:LEU:N	1:363:A:LEU:CA	1:363:A:LEU:C	1:364:A:LYS:N	18	1.45
(1,34)	1:363:A:LEU:N	1:363:A:LEU:CA	1:363:A:LEU:C	1:364:A:LYS:N	19	1.45
(1,308)	1:420:B:TYR:N	1:420:B:TYR:CA	1:420:B:TYR:C	1:421:B:ASN:N	27	1.44
(1,215)	1:367:B:ASN:C	1:368:B:LEU:N	1:368:B:LEU:CA	1:368:B:LEU:C	28	1.44
(1,104)	1:401:A:LYS:N	1:401:A:LYS:CA	1:401:A:LYS:C	1:402:A:LYS:N	20	1.44
(1,324)	1:442:B:LYS:N	1:442:B:LYS:CA	1:442:B:LYS:C	1:443:B:SER:N	12	1.43
(1,208)	1:363:B:LEU:N	1:363:B:LEU:CA	1:363:B:LEU:C	1:364:B:LYS:N	14	1.43
(1,150)	1:442:A:LYS:N	1:442:A:LYS:CA	1:442:A:LYS:C	1:443:A:SER:N	12	1.43
(1,40)	1:367:A:ASN:N	1:367:A:ASN:CA	1:367:A:ASN:C	1:368:A:LEU:N	19	1.43
(1,291)	1:411:B:VAL:C	1:412:B:ILE:N	1:412:B:ILE:CA	1:412:B:ILE:C	6	1.42
(1,150)	1:442:A:LYS:N	1:442:A:LYS:CA	1:442:A:LYS:C	1:443:A:SER:N	14	1.42
(1,221)	1:370:B:VAL:C	1:371:B:ASN:N	1:371:B:ASN:CA	1:371:B:ASN:C	5	1.41
(1,183)	1:350:B:SER:C	1:351:B:ARG:N	1:351:B:ARG:CA	1:351:B:ARG:C	21	1.41
(1,104)	1:401:A:LYS:N	1:401:A:LYS:CA	1:401:A:LYS:C	1:402:A:LYS:N	12	1.41
(1,40)	1:367:A:ASN:N	1:367:A:ASN:CA	1:367:A:ASN:C	1:368:A:LEU:N	28	1.41
(1,34)	1:363:A:LEU:N	1:363:A:LEU:CA	1:363:A:LEU:C	1:364:A:LYS:N	5	1.41
(1,221)	1:370:B:VAL:C	1:371:B:ASN:N	1:371:B:ASN:CA	1:371:B:ASN:C	1	1.4
(1,208)	1:363:B:LEU:N	1:363:B:LEU:CA	1:363:B:LEU:C	1:364:B:LYS:N	18	1.4
(1,117)	1:411:A:VAL:C	1:412:A:ILE:N	1:412:A:ILE:CA	1:412:A:ILE:C	22	1.4
(1,278)	1:401:B:LYS:N	1:401:B:LYS:CA	1:401:B:LYS:C	1:402:B:LYS:N	22	1.39
(1,221)	1:370:B:VAL:C	1:371:B:ASN:N	1:371:B:ASN:CA	1:371:B:ASN:C	7	1.39
(1,221)	1:370:B:VAL:C	1:371:B:ASN:N	1:371:B:ASN:CA	1:371:B:ASN:C	24	1.39
(1,208)	1:363:B:LEU:N	1:363:B:LEU:CA	1:363:B:LEU:C	1:364:B:LYS:N	16	1.39
(1,104)	1:401:A:LYS:N	1:401:A:LYS:CA	1:401:A:LYS:C	1:402:A:LYS:N	8	1.39
(1,47)	1:370:A:VAL:C	1:371:A:ASN:N	1:371:A:ASN:CA	1:371:A:ASN:C	20	1.39
(1,278)	1:401:B:LYS:N	1:401:B:LYS:CA	1:401:B:LYS:C	1:402:B:LYS:N	27	1.38
(1,179)	1:348:B:MET:C	1:349:B:ASP:N	1:349:B:ASP:CA	1:349:B:ASP:C	23	1.38
(1,47)	1:370:A:VAL:C	1:371:A:ASN:N	1:371:A:ASN:CA	1:371:A:ASN:C	5	1.38
(1,10)	1:351:A:ARG:N	1:351:A:ARG:CA	1:351:A:ARG:C	1:352:A:LEU:N	25	1.38
(1,10)	1:351:A:ARG:N	1:351:A:ARG:CA	1:351:A:ARG:C	1:352:A:LEU:N	26	1.38
(1,306)	1:419:B:LEU:N	1:419:B:LEU:CA	1:419:B:LEU:C	1:420:B:TYR:N	18	1.37
(1,221)	1:370:B:VAL:C	1:371:B:ASN:N	1:371:B:ASN:CA	1:371:B:ASN:C	27	1.37
(1,208)	1:363:B:LEU:N	1:363:B:LEU:CA	1:363:B:LEU:C	1:364:B:LYS:N	5	1.37
(1,104)	1:401:A:LYS:N	1:401:A:LYS:CA	1:401:A:LYS:C	1:402:A:LYS:N	21	1.37
(1,241)	1:380:B:LEU:C	1:381:B:ALA:N	1:381:B:ALA:CA	1:381:B:ALA:C	21	1.36
(1,221)	1:370:B:VAL:C	1:371:B:ASN:N	1:371:B:ASN:CA	1:371:B:ASN:C	23	1.36
(1,324)	1:442:B:LYS:N	1:442:B:LYS:CA	1:442:B:LYS:C	1:443:B:SER:N	22	1.35
(1,104)	1:401:A:LYS:N	1:401:A:LYS:CA	1:401:A:LYS:C	1:402:A:LYS:N	5	1.35
(1,47)	1:370:A:VAL:C	1:371:A:ASN:N	1:371:A:ASN:CA	1:371:A:ASN:C	27	1.35
(1,214)	1:367:B:ASN:N	1:367:B:ASN:CA	1:367:B:ASN:C	1:368:B:LEU:N	19	1.34
(1,208)	1:363:B:LEU:N	1:363:B:LEU:CA	1:363:B:LEU:C	1:364:B:LYS:N	25	1.34
(1,34)	1:363:A:LEU:N	1:363:A:LEU:CA	1:363:A:LEU:C	1:364:A:LYS:N	10	1.34
(1,324)	1:442:B:LYS:N	1:442:B:LYS:CA	1:442:B:LYS:C	1:443:B:SER:N	14	1.33
(1,221)	1:370:B:VAL:C	1:371:B:ASN:N	1:371:B:ASN:CA	1:371:B:ASN:C	11	1.33
(1,47)	1:370:A:VAL:C	1:371:A:ASN:N	1:371:A:ASN:CA	1:371:A:ASN:C	4	1.33

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,47)	1:370:A:VAL:C	1:371:A:ASN:N	1:371:A:ASN:CA	1:371:A:ASN:C	26	1.33
(1,221)	1:370:B:VAL:C	1:371:B:ASN:N	1:371:B:ASN:CA	1:371:B:ASN:C	21	1.32
(1,278)	1:401:B:LYS:N	1:401:B:LYS:CA	1:401:B:LYS:C	1:402:B:LYS:N	9	1.31
(1,209)	1:364:B:LYS:C	1:365:B:ILE:N	1:365:B:ILE:CA	1:365:B:ILE:C	17	1.31
(1,132)	1:419:A:LEU:N	1:419:A:LEU:CA	1:419:A:LEU:C	1:420:A:TYR:N	5	1.31
(1,278)	1:401:B:LYS:N	1:401:B:LYS:CA	1:401:B:LYS:C	1:402:B:LYS:N	20	1.3
(1,208)	1:363:B:LEU:N	1:363:B:LEU:CA	1:363:B:LEU:C	1:364:B:LYS:N	27	1.3
(1,9)	1:350:A:SER:C	1:351:A:ARG:N	1:351:A:ARG:CA	1:351:A:ARG:C	23	1.3
(1,221)	1:370:B:VAL:C	1:371:B:ASN:N	1:371:B:ASN:CA	1:371:B:ASN:C	3	1.29
(1,221)	1:370:B:VAL:C	1:371:B:ASN:N	1:371:B:ASN:CA	1:371:B:ASN:C	26	1.29
(1,208)	1:363:B:LEU:N	1:363:B:LEU:CA	1:363:B:LEU:C	1:364:B:LYS:N	22	1.29
(1,70)	1:382:A:SER:N	1:382:A:SER:CA	1:382:A:SER:C	1:383:A:LEU:N	13	1.29
(1,47)	1:370:A:VAL:C	1:371:A:ASN:N	1:371:A:ASN:CA	1:371:A:ASN:C	21	1.29
(1,9)	1:350:A:SER:C	1:351:A:ARG:N	1:351:A:ARG:CA	1:351:A:ARG:C	30	1.29
(1,215)	1:367:B:ASN:C	1:368:B:LEU:N	1:368:B:LEU:CA	1:368:B:LEU:C	19	1.27
(1,131)	1:418:A:MET:C	1:419:A:LEU:N	1:419:A:LEU:CA	1:419:A:LEU:C	5	1.27
(1,47)	1:370:A:VAL:C	1:371:A:ASN:N	1:371:A:ASN:CA	1:371:A:ASN:C	7	1.27
(1,41)	1:367:A:ASN:C	1:368:A:LEU:N	1:368:A:LEU:CA	1:368:A:LEU:C	19	1.27
(1,306)	1:419:B:LEU:N	1:419:B:LEU:CA	1:419:B:LEU:C	1:420:B:TYR:N	15	1.26
(1,150)	1:442:A:LYS:N	1:442:A:LYS:CA	1:442:A:LYS:C	1:443:A:SER:N	30	1.26
(1,104)	1:401:A:LYS:N	1:401:A:LYS:CA	1:401:A:LYS:C	1:402:A:LYS:N	11	1.26
(1,9)	1:350:A:SER:C	1:351:A:ARG:N	1:351:A:ARG:CA	1:351:A:ARG:C	12	1.26
(1,308)	1:420:B:TYR:N	1:420:B:TYR:CA	1:420:B:TYR:C	1:421:B:ASN:N	18	1.25
(1,305)	1:418:B:MET:C	1:419:B:LEU:N	1:419:B:LEU:CA	1:419:B:LEU:C	18	1.25
(1,278)	1:401:B:LYS:N	1:401:B:LYS:CA	1:401:B:LYS:C	1:402:B:LYS:N	15	1.25
(1,208)	1:363:B:LEU:N	1:363:B:LEU:CA	1:363:B:LEU:C	1:364:B:LYS:N	28	1.25
(1,104)	1:401:A:LYS:N	1:401:A:LYS:CA	1:401:A:LYS:C	1:402:A:LYS:N	9	1.25
(1,278)	1:401:B:LYS:N	1:401:B:LYS:CA	1:401:B:LYS:C	1:402:B:LYS:N	5	1.24
(1,278)	1:401:B:LYS:N	1:401:B:LYS:CA	1:401:B:LYS:C	1:402:B:LYS:N	25	1.24
(1,221)	1:370:B:VAL:C	1:371:B:ASN:N	1:371:B:ASN:CA	1:371:B:ASN:C	22	1.24
(1,208)	1:363:B:LEU:N	1:363:B:LEU:CA	1:363:B:LEU:C	1:364:B:LYS:N	10	1.24
(1,183)	1:350:B:SER:C	1:351:B:ARG:N	1:351:B:ARG:CA	1:351:B:ARG:C	10	1.24
(1,104)	1:401:A:LYS:N	1:401:A:LYS:CA	1:401:A:LYS:C	1:402:A:LYS:N	22	1.24
(1,42)	1:368:A:LEU:N	1:368:A:LEU:CA	1:368:A:LEU:C	1:369:A:ASP:N	18	1.24
(1,34)	1:363:A:LEU:N	1:363:A:LEU:CA	1:363:A:LEU:C	1:364:A:LYS:N	27	1.24
(1,278)	1:401:B:LYS:N	1:401:B:LYS:CA	1:401:B:LYS:C	1:402:B:LYS:N	18	1.23
(1,132)	1:419:A:LEU:N	1:419:A:LEU:CA	1:419:A:LEU:C	1:420:A:TYR:N	16	1.23
(1,47)	1:370:A:VAL:C	1:371:A:ASN:N	1:371:A:ASN:CA	1:371:A:ASN:C	23	1.23
(1,34)	1:363:A:LEU:N	1:363:A:LEU:CA	1:363:A:LEU:C	1:364:A:LYS:N	28	1.23
(1,10)	1:351:A:ARG:N	1:351:A:ARG:CA	1:351:A:ARG:C	1:352:A:LEU:N	6	1.23
(1,303)	1:417:B:THR:C	1:418:B:MET:N	1:418:B:MET:CA	1:418:B:MET:C	29	1.22
(1,209)	1:364:B:LYS:C	1:365:B:ILE:N	1:365:B:ILE:CA	1:365:B:ILE:C	6	1.22
(1,104)	1:401:A:LYS:N	1:401:A:LYS:CA	1:401:A:LYS:C	1:402:A:LYS:N	13	1.22
(1,34)	1:363:A:LEU:N	1:363:A:LEU:CA	1:363:A:LEU:C	1:364:A:LYS:N	15	1.22
(1,9)	1:350:A:SER:C	1:351:A:ARG:N	1:351:A:ARG:CA	1:351:A:ARG:C	8	1.22
(1,104)	1:401:A:LYS:N	1:401:A:LYS:CA	1:401:A:LYS:C	1:402:A:LYS:N	26	1.21
(1,70)	1:382:A:SER:N	1:382:A:SER:CA	1:382:A:SER:C	1:383:A:LEU:N	18	1.21
(1,15)	1:353:A:GLN:C	1:354:A:ARG:N	1:354:A:ARG:CA	1:354:A:ARG:C	26	1.21
(1,9)	1:350:A:SER:C	1:351:A:ARG:N	1:351:A:ARG:CA	1:351:A:ARG:C	18	1.21
(1,324)	1:442:B:LYS:N	1:442:B:LYS:CA	1:442:B:LYS:C	1:443:B:SER:N	30	1.2
(1,278)	1:401:B:LYS:N	1:401:B:LYS:CA	1:401:B:LYS:C	1:402:B:LYS:N	21	1.2

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,208)	1:363:B:LEU:N	1:363:B:LEU:CA	1:363:B:LEU:C	1:364:B:LYS:N	8	1.2
(1,35)	1:364:A:LYS:C	1:365:A:ILE:N	1:365:A:ILE:CA	1:365:A:ILE:C	15	1.2
(1,216)	1:368:B:LEU:N	1:368:B:LEU:CA	1:368:B:LEU:C	1:369:B:ASP:N	18	1.19
(1,179)	1:348:B:MET:C	1:349:B:ASP:N	1:349:B:ASP:CA	1:349:B:ASP:C	12	1.19
(1,10)	1:351:A:ARG:N	1:351:A:ARG:CA	1:351:A:ARG:C	1:352:A:LEU:N	20	1.19
(1,306)	1:419:B:LEU:N	1:419:B:LEU:CA	1:419:B:LEU:C	1:420:B:TYR:N	27	1.18
(1,278)	1:401:B:LYS:N	1:401:B:LYS:CA	1:401:B:LYS:C	1:402:B:LYS:N	12	1.18
(1,208)	1:363:B:LEU:N	1:363:B:LEU:CA	1:363:B:LEU:C	1:364:B:LYS:N	23	1.18
(1,104)	1:401:A:LYS:N	1:401:A:LYS:CA	1:401:A:LYS:C	1:402:A:LYS:N	4	1.18
(1,47)	1:370:A:VAL:C	1:371:A:ASN:N	1:371:A:ASN:CA	1:371:A:ASN:C	24	1.18
(1,42)	1:368:A:LEU:N	1:368:A:LEU:CA	1:368:A:LEU:C	1:369:A:ASP:N	8	1.18
(1,9)	1:350:A:SER:C	1:351:A:ARG:N	1:351:A:ARG:CA	1:351:A:ARG:C	26	1.18
(1,303)	1:417:B:THR:C	1:418:B:MET:N	1:418:B:MET:CA	1:418:B:MET:C	27	1.17
(1,221)	1:370:B:VAL:C	1:371:B:ASN:N	1:371:B:ASN:CA	1:371:B:ASN:C	25	1.17
(1,183)	1:350:B:SER:C	1:351:B:ARG:N	1:351:B:ARG:CA	1:351:B:ARG:C	7	1.17
(1,183)	1:350:B:SER:C	1:351:B:ARG:N	1:351:B:ARG:CA	1:351:B:ARG:C	9	1.17
(1,129)	1:417:A:THR:C	1:418:A:MET:N	1:418:A:MET:CA	1:418:A:MET:C	16	1.17
(1,47)	1:370:A:VAL:C	1:371:A:ASN:N	1:371:A:ASN:CA	1:371:A:ASN:C	3	1.17
(1,278)	1:401:B:LYS:N	1:401:B:LYS:CA	1:401:B:LYS:C	1:402:B:LYS:N	2	1.16
(1,278)	1:401:B:LYS:N	1:401:B:LYS:CA	1:401:B:LYS:C	1:402:B:LYS:N	16	1.16
(1,104)	1:401:A:LYS:N	1:401:A:LYS:CA	1:401:A:LYS:C	1:402:A:LYS:N	10	1.16
(1,104)	1:401:A:LYS:N	1:401:A:LYS:CA	1:401:A:LYS:C	1:402:A:LYS:N	30	1.16
(1,34)	1:363:A:LEU:N	1:363:A:LEU:CA	1:363:A:LEU:C	1:364:A:LYS:N	17	1.16
(1,19)	1:355:A:ILE:C	1:356:A:HIS:N	1:356:A:HIS:CA	1:356:A:HIS:C	14	1.16
(1,221)	1:370:B:VAL:C	1:371:B:ASN:N	1:371:B:ASN:CA	1:371:B:ASN:C	17	1.15
(1,183)	1:350:B:SER:C	1:351:B:ARG:N	1:351:B:ARG:CA	1:351:B:ARG:C	18	1.15
(1,34)	1:363:A:LEU:N	1:363:A:LEU:CA	1:363:A:LEU:C	1:364:A:LYS:N	24	1.15
(1,278)	1:401:B:LYS:N	1:401:B:LYS:CA	1:401:B:LYS:C	1:402:B:LYS:N	3	1.14
(1,221)	1:370:B:VAL:C	1:371:B:ASN:N	1:371:B:ASN:CA	1:371:B:ASN:C	15	1.14
(1,215)	1:367:B:ASN:C	1:368:B:LEU:N	1:368:B:LEU:CA	1:368:B:LEU:C	5	1.14
(1,104)	1:401:A:LYS:N	1:401:A:LYS:CA	1:401:A:LYS:C	1:402:A:LYS:N	16	1.14
(1,47)	1:370:A:VAL:C	1:371:A:ASN:N	1:371:A:ASN:CA	1:371:A:ASN:C	16	1.14
(1,47)	1:370:A:VAL:C	1:371:A:ASN:N	1:371:A:ASN:CA	1:371:A:ASN:C	25	1.14
(1,278)	1:401:B:LYS:N	1:401:B:LYS:CA	1:401:B:LYS:C	1:402:B:LYS:N	10	1.13
(1,208)	1:363:B:LEU:N	1:363:B:LEU:CA	1:363:B:LEU:C	1:364:B:LYS:N	6	1.13
(1,35)	1:364:A:LYS:C	1:365:A:ILE:N	1:365:A:ILE:CA	1:365:A:ILE:C	28	1.13
(1,9)	1:350:A:SER:C	1:351:A:ARG:N	1:351:A:ARG:CA	1:351:A:ARG:C	1	1.13
(1,5)	1:348:A:MET:C	1:349:A:ASP:N	1:349:A:ASP:CA	1:349:A:ASP:C	9	1.13
(1,5)	1:348:A:MET:C	1:349:A:ASP:N	1:349:A:ASP:CA	1:349:A:ASP:C	21	1.13
(1,278)	1:401:B:LYS:N	1:401:B:LYS:CA	1:401:B:LYS:C	1:402:B:LYS:N	24	1.12
(1,214)	1:367:B:ASN:N	1:367:B:ASN:CA	1:367:B:ASN:C	1:368:B:LEU:N	5	1.12
(1,208)	1:363:B:LEU:N	1:363:B:LEU:CA	1:363:B:LEU:C	1:364:B:LYS:N	7	1.12
(1,184)	1:351:B:ARG:N	1:351:B:ARG:CA	1:351:B:ARG:C	1:352:B:LEU:N	20	1.12
(1,112)	1:405:A:ARG:N	1:405:A:ARG:CA	1:405:A:ARG:C	1:406:A:PHE:N	19	1.12
(1,47)	1:370:A:VAL:C	1:371:A:ASN:N	1:371:A:ASN:CA	1:371:A:ASN:C	30	1.12
(1,34)	1:363:A:LEU:N	1:363:A:LEU:CA	1:363:A:LEU:C	1:364:A:LYS:N	7	1.12
(1,278)	1:401:B:LYS:N	1:401:B:LYS:CA	1:401:B:LYS:C	1:402:B:LYS:N	13	1.11
(1,278)	1:401:B:LYS:N	1:401:B:LYS:CA	1:401:B:LYS:C	1:402:B:LYS:N	26	1.11
(1,221)	1:370:B:VAL:C	1:371:B:ASN:N	1:371:B:ASN:CA	1:371:B:ASN:C	16	1.11
(1,208)	1:363:B:LEU:N	1:363:B:LEU:CA	1:363:B:LEU:C	1:364:B:LYS:N	3	1.11
(1,65)	1:379:A:GLU:C	1:380:A:LEU:N	1:380:A:LEU:CA	1:380:A:LEU:C	13	1.11

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,47)	1:370:A:VAL:C	1:371:A:ASN:N	1:371:A:ASN:CA	1:371:A:ASN:C	11	1.11
(1,34)	1:363:A:LEU:N	1:363:A:LEU:CA	1:363:A:LEU:C	1:364:A:LYS:N	30	1.11
(1,28)	1:360:A:LYS:N	1:360:A:LYS:CA	1:360:A:LYS:C	1:361:A:ASN:N	6	1.11
(1,183)	1:350:B:SER:C	1:351:B:ARG:N	1:351:B:ARG:CA	1:351:B:ARG:C	27	1.1
(1,42)	1:368:A:LEU:N	1:368:A:LEU:CA	1:368:A:LEU:C	1:369:A:ASP:N	6	1.1
(1,306)	1:419:B:LEU:N	1:419:B:LEU:CA	1:419:B:LEU:C	1:420:B:TYR:N	29	1.09
(1,278)	1:401:B:LYS:N	1:401:B:LYS:CA	1:401:B:LYS:C	1:402:B:LYS:N	29	1.09
(1,216)	1:368:B:LEU:N	1:368:B:LEU:CA	1:368:B:LEU:C	1:369:B:ASP:N	8	1.09
(1,183)	1:350:B:SER:C	1:351:B:ARG:N	1:351:B:ARG:CA	1:351:B:ARG:C	6	1.09
(1,104)	1:401:A:LYS:N	1:401:A:LYS:CA	1:401:A:LYS:C	1:402:A:LYS:N	6	1.09
(1,34)	1:363:A:LEU:N	1:363:A:LEU:CA	1:363:A:LEU:C	1:364:A:LYS:N	29	1.09
(1,291)	1:411:B:VAL:C	1:412:B:ILE:N	1:412:B:ILE:CA	1:412:B:ILE:C	23	1.08
(1,278)	1:401:B:LYS:N	1:401:B:LYS:CA	1:401:B:LYS:C	1:402:B:LYS:N	4	1.08
(1,208)	1:363:B:LEU:N	1:363:B:LEU:CA	1:363:B:LEU:C	1:364:B:LYS:N	21	1.08
(1,186)	1:352:B:LEU:N	1:352:B:LEU:CA	1:352:B:LEU:C	1:353:B:GLN:N	13	1.08
(1,104)	1:401:A:LYS:N	1:401:A:LYS:CA	1:401:A:LYS:C	1:402:A:LYS:N	25	1.08
(1,34)	1:363:A:LEU:N	1:363:A:LEU:CA	1:363:A:LEU:C	1:364:A:LYS:N	4	1.08
(1,278)	1:401:B:LYS:N	1:401:B:LYS:CA	1:401:B:LYS:C	1:402:B:LYS:N	23	1.07
(1,208)	1:363:B:LEU:N	1:363:B:LEU:CA	1:363:B:LEU:C	1:364:B:LYS:N	17	1.07
(1,9)	1:350:A:SER:C	1:351:A:ARG:N	1:351:A:ARG:CA	1:351:A:ARG:C	5	1.07
(1,221)	1:370:B:VAL:C	1:371:B:ASN:N	1:371:B:ASN:CA	1:371:B:ASN:C	19	1.06
(1,221)	1:370:B:VAL:C	1:371:B:ASN:N	1:371:B:ASN:CA	1:371:B:ASN:C	30	1.06
(1,214)	1:367:B:ASN:N	1:367:B:ASN:CA	1:367:B:ASN:C	1:368:B:LEU:N	14	1.06
(1,208)	1:363:B:LEU:N	1:363:B:LEU:CA	1:363:B:LEU:C	1:364:B:LYS:N	15	1.06
(1,179)	1:348:B:MET:C	1:349:B:ASP:N	1:349:B:ASP:CA	1:349:B:ASP:C	1	1.06
(1,47)	1:370:A:VAL:C	1:371:A:ASN:N	1:371:A:ASN:CA	1:371:A:ASN:C	22	1.06
(1,34)	1:363:A:LEU:N	1:363:A:LEU:CA	1:363:A:LEU:C	1:364:A:LYS:N	3	1.06
(1,221)	1:370:B:VAL:C	1:371:B:ASN:N	1:371:B:ASN:CA	1:371:B:ASN:C	6	1.05
(1,131)	1:418:A:MET:C	1:419:A:LEU:N	1:419:A:LEU:CA	1:419:A:LEU:C	12	1.05
(1,117)	1:411:A:VAL:C	1:412:A:ILE:N	1:412:A:ILE:CA	1:412:A:ILE:C	19	1.05
(1,40)	1:367:A:ASN:N	1:367:A:ASN:CA	1:367:A:ASN:C	1:368:A:LEU:N	6	1.05
(1,9)	1:350:A:SER:C	1:351:A:ARG:N	1:351:A:ARG:CA	1:351:A:ARG:C	28	1.05
(1,5)	1:348:A:MET:C	1:349:A:ASP:N	1:349:A:ASP:CA	1:349:A:ASP:C	2	1.05
(1,278)	1:401:B:LYS:N	1:401:B:LYS:CA	1:401:B:LYS:C	1:402:B:LYS:N	17	1.04
(1,129)	1:417:A:THR:C	1:418:A:MET:N	1:418:A:MET:CA	1:418:A:MET:C	5	1.04
(1,104)	1:401:A:LYS:N	1:401:A:LYS:CA	1:401:A:LYS:C	1:402:A:LYS:N	2	1.04
(1,47)	1:370:A:VAL:C	1:371:A:ASN:N	1:371:A:ASN:CA	1:371:A:ASN:C	15	1.04
(1,28)	1:360:A:LYS:N	1:360:A:LYS:CA	1:360:A:LYS:C	1:361:A:ASN:N	4	1.04
(1,305)	1:418:B:MET:C	1:419:B:LEU:N	1:419:B:LEU:CA	1:419:B:LEU:C	15	1.03
(1,104)	1:401:A:LYS:N	1:401:A:LYS:CA	1:401:A:LYS:C	1:402:A:LYS:N	3	1.03
(1,104)	1:401:A:LYS:N	1:401:A:LYS:CA	1:401:A:LYS:C	1:402:A:LYS:N	15	1.03
(1,5)	1:348:A:MET:C	1:349:A:ASP:N	1:349:A:ASP:CA	1:349:A:ASP:C	28	1.03
(1,9)	1:350:A:SER:C	1:351:A:ARG:N	1:351:A:ARG:CA	1:351:A:ARG:C	2	1.02
(1,221)	1:370:B:VAL:C	1:371:B:ASN:N	1:371:B:ASN:CA	1:371:B:ASN:C	29	1.01
(1,10)	1:351:A:ARG:N	1:351:A:ARG:CA	1:351:A:ARG:C	1:352:A:LEU:N	17	1.01
(1,9)	1:350:A:SER:C	1:351:A:ARG:N	1:351:A:ARG:CA	1:351:A:ARG:C	11	1.01
(1,10)	1:351:A:ARG:N	1:351:A:ARG:CA	1:351:A:ARG:C	1:352:A:LEU:N	27	1.0
(1,9)	1:350:A:SER:C	1:351:A:ARG:N	1:351:A:ARG:CA	1:351:A:ARG:C	16	1.0