



Full wwPDB NMR Structure Validation Report ⓘ

Mar 25, 2026 – 11:56 PM UTC

PDB ID : 2L51 / pdb_00002l51
BMRB ID : 17262
Title : Solution structure of calcium bound S100A16
Authors : Babini, E.; Bertini, I.; Borsi, V.; Calderone, V.; Hu, X.; Luchinat, C.; Parigi, G.
Deposited on : 2010-10-22

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

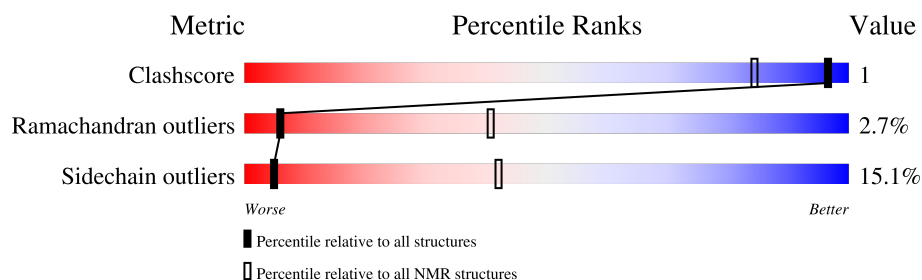
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 69%.

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	102	74% 14% 13%
1	B	102	74% 14% 13%

2 Ensemble composition and analysis

This entry contains 30 models. Model 25 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:5-A:24, A:33-A:101, B:108-B:127, B:136-B:204 (178)	0.94	25

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, 10, 14, 17, 18, 19, 20, 23, 25, 28
2	2, 6, 9, 11, 12, 13, 16, 21, 22, 24, 26, 29, 30
Single-model clusters	15; 27

3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3282 atoms, of which 1636 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Protein S100-A16.

Mol	Chain	Residues	Atoms						Trace
1	A	102	Total	C	H	N	O	S	0
			1639	517	818	139	162	3	
1	B	102	Total	C	H	N	O	S	0
			1639	517	818	139	162	3	

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

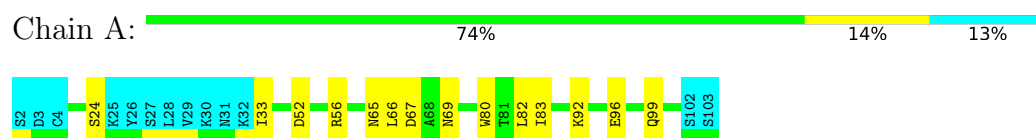
Mol	Chain	Residues	Atoms	
2	A	2	Total	Ca
			2	2
2	B	2	Total	Ca
			2	2

4 Residue-property plots [i](#)

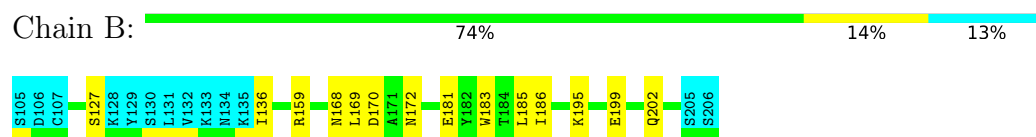
4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA, 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: Protein S100-A16



• Molecule 1: Protein S100-A16

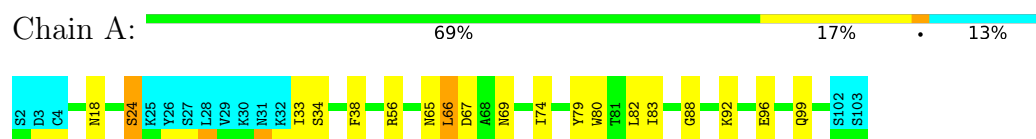


4.2 Scores per residue for each member of the ensemble

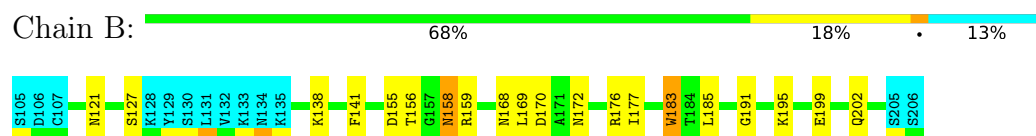
Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

• Molecule 1: Protein S100-A16

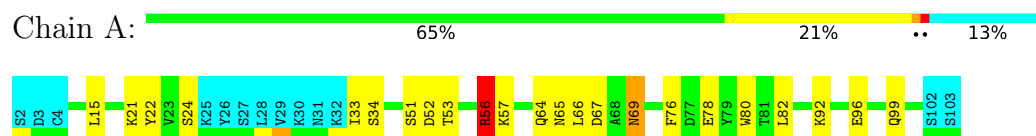


• Molecule 1: Protein S100-A16

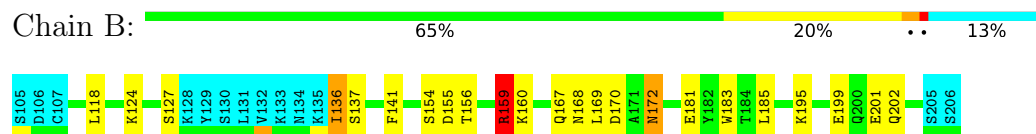


4.2.2 Score per residue for model 2

- Molecule 1: Protein S100-A16

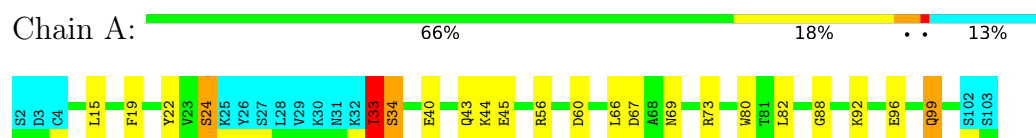


- Molecule 1: Protein S100-A16

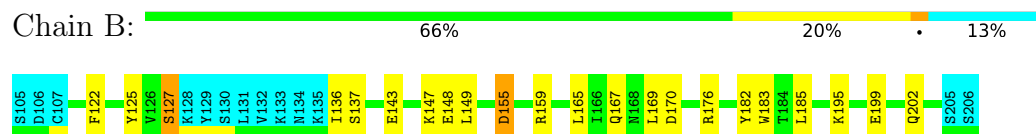


4.2.3 Score per residue for model 3

- Molecule 1: Protein S100-A16

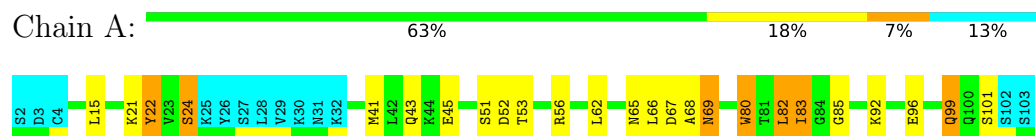


- Molecule 1: Protein S100-A16

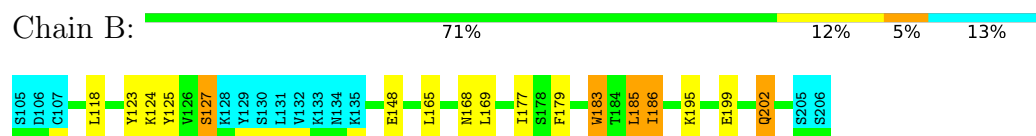


4.2.4 Score per residue for model 4

- Molecule 1: Protein S100-A16

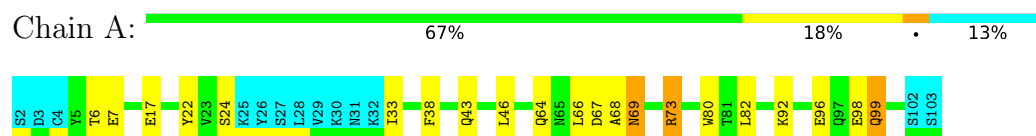


- Molecule 1: Protein S100-A16

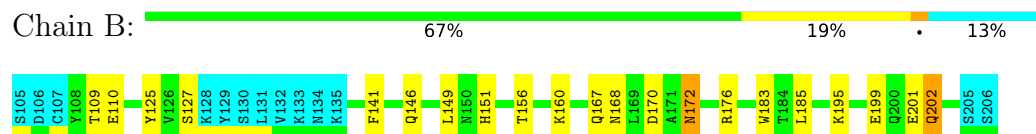


4.2.5 Score per residue for model 5

- Molecule 1: Protein S100-A16

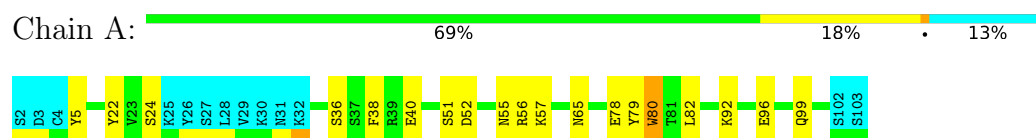


- Molecule 1: Protein S100-A16

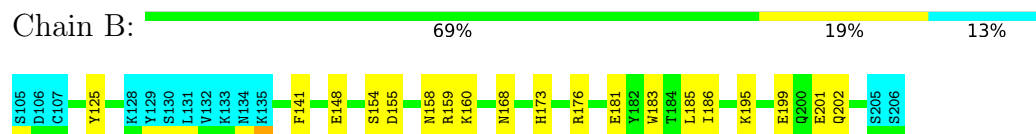


4.2.6 Score per residue for model 6

- Molecule 1: Protein S100-A16

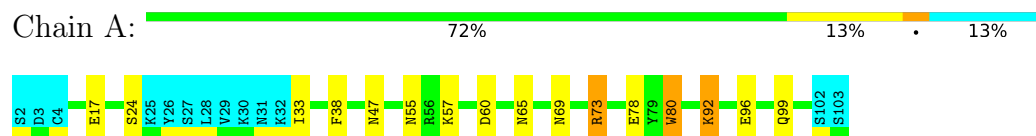


- Molecule 1: Protein S100-A16

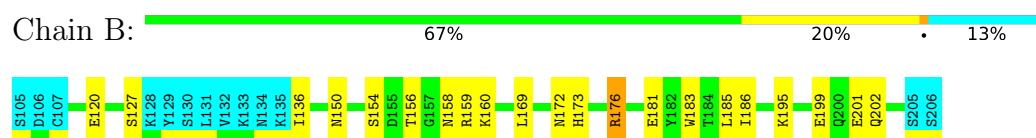


4.2.7 Score per residue for model 7

- Molecule 1: Protein S100-A16

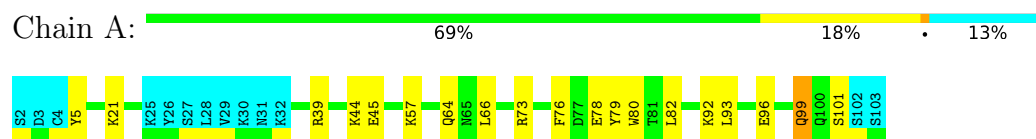


- Molecule 1: Protein S100-A16

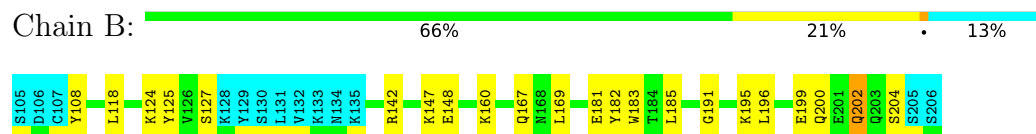


4.2.8 Score per residue for model 8

- Molecule 1: Protein S100-A16

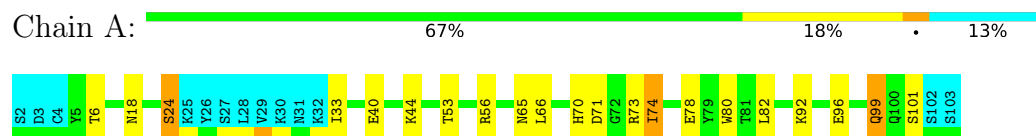


- Molecule 1: Protein S100-A16

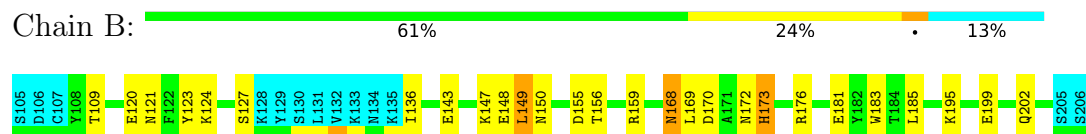


4.2.9 Score per residue for model 9

- Molecule 1: Protein S100-A16

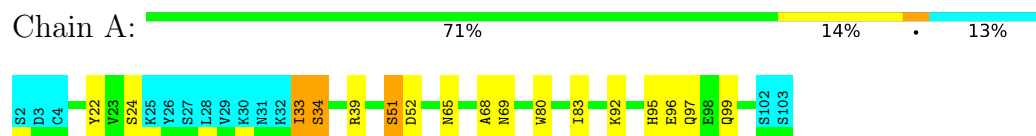


- Molecule 1: Protein S100-A16

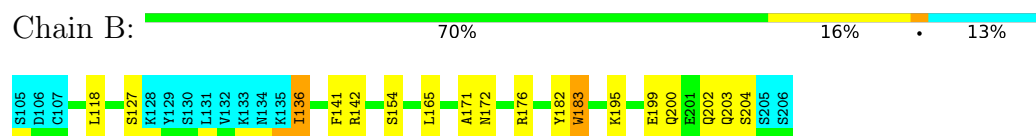


4.2.10 Score per residue for model 10

- Molecule 1: Protein S100-A16

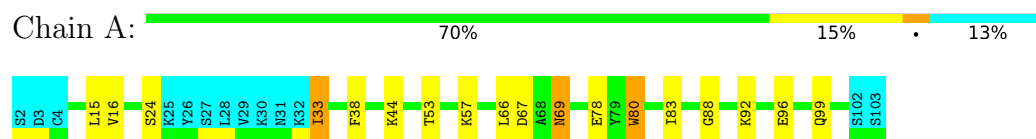


- Molecule 1: Protein S100-A16

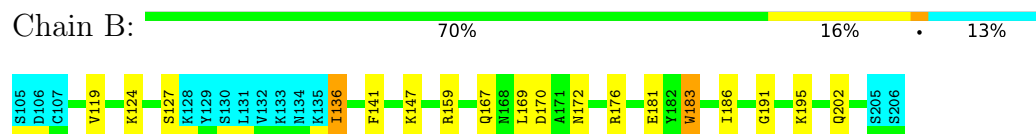


4.2.11 Score per residue for model 11

- Molecule 1: Protein S100-A16

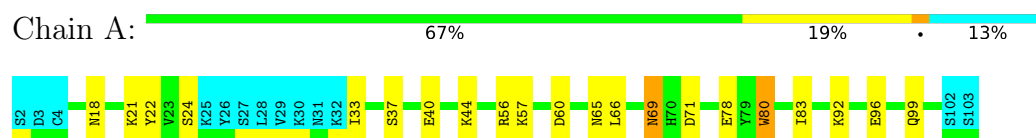


- Molecule 1: Protein S100-A16

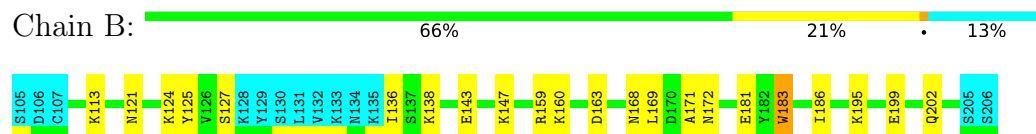


4.2.12 Score per residue for model 12

- Molecule 1: Protein S100-A16

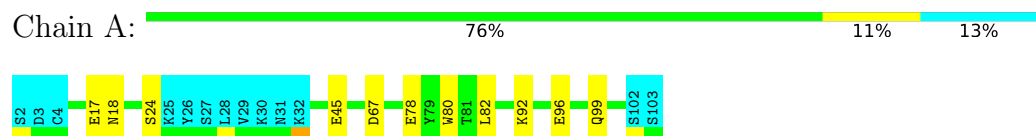


- Molecule 1: Protein S100-A16

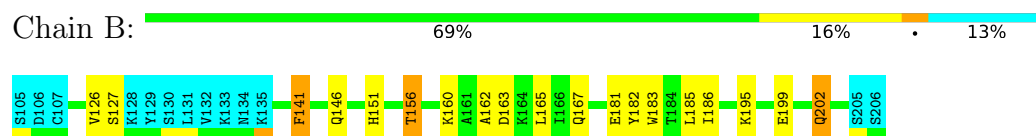


4.2.13 Score per residue for model 13

- Molecule 1: Protein S100-A16

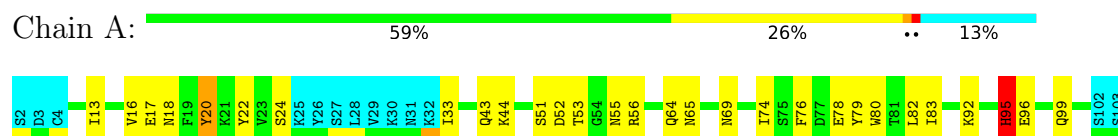


- Molecule 1: Protein S100-A16

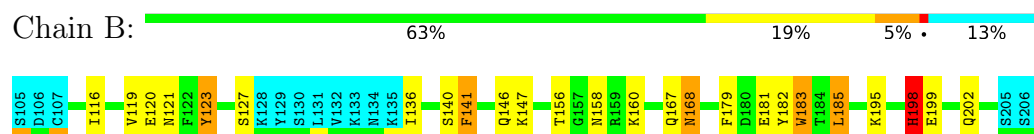


4.2.14 Score per residue for model 14

- Molecule 1: Protein S100-A16

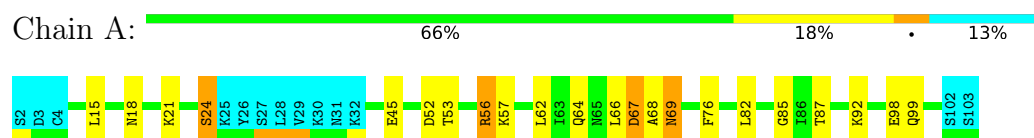


- Molecule 1: Protein S100-A16

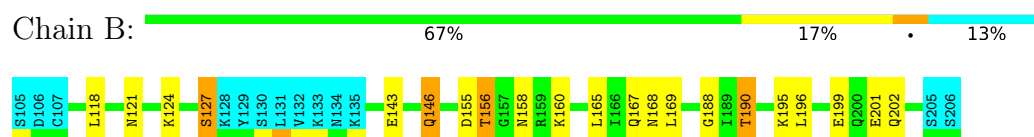


4.2.15 Score per residue for model 15

- Molecule 1: Protein S100-A16

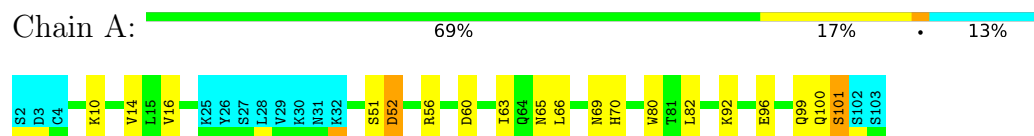


- Molecule 1: Protein S100-A16

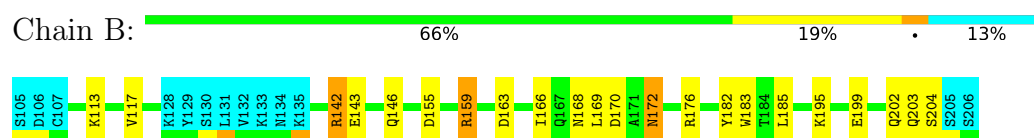


4.2.16 Score per residue for model 16

- Molecule 1: Protein S100-A16

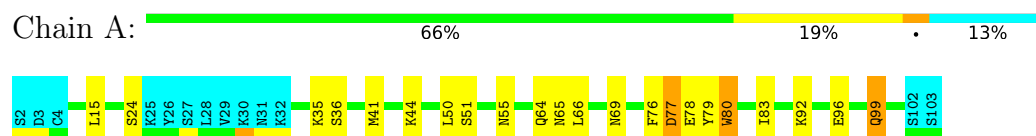


- Molecule 1: Protein S100-A16

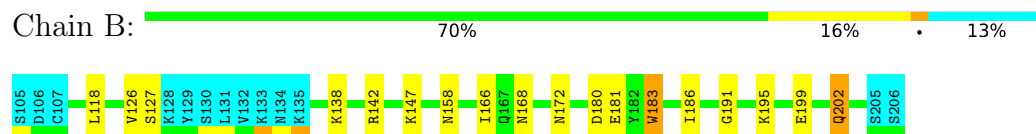


4.2.17 Score per residue for model 17

- Molecule 1: Protein S100-A16

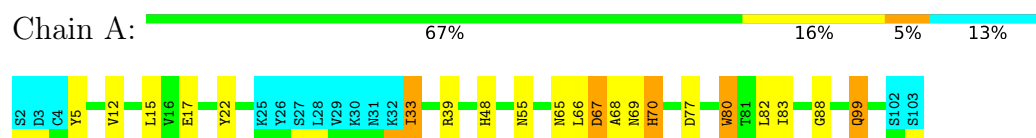


- Molecule 1: Protein S100-A16

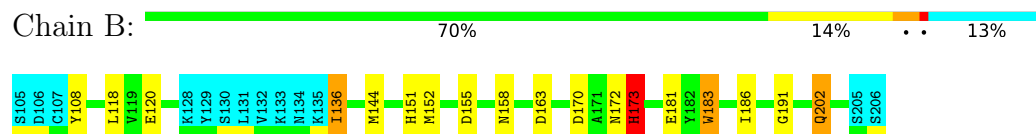


4.2.18 Score per residue for model 18

- Molecule 1: Protein S100-A16

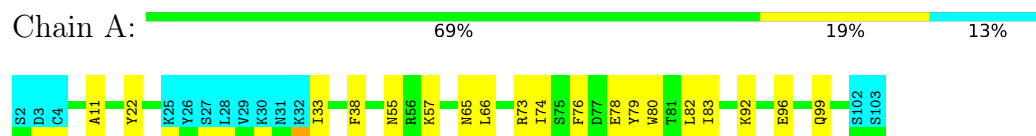


- Molecule 1: Protein S100-A16

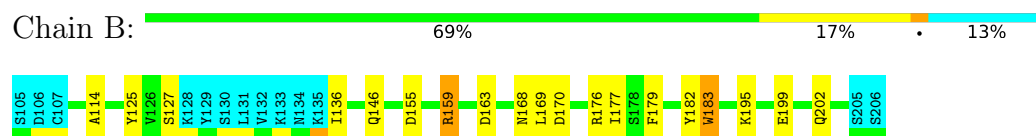


4.2.19 Score per residue for model 19

- Molecule 1: Protein S100-A16

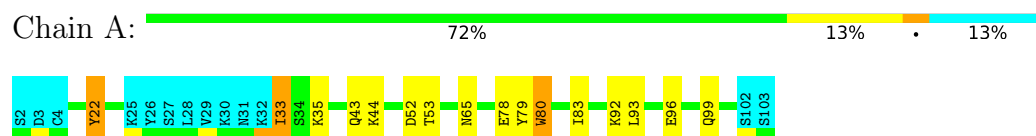


- Molecule 1: Protein S100-A16

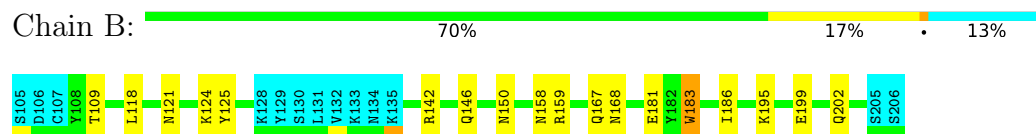


4.2.20 Score per residue for model 20

- Molecule 1: Protein S100-A16

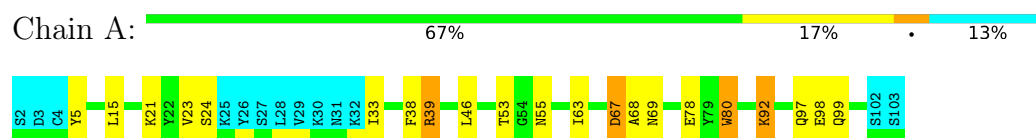


- Molecule 1: Protein S100-A16

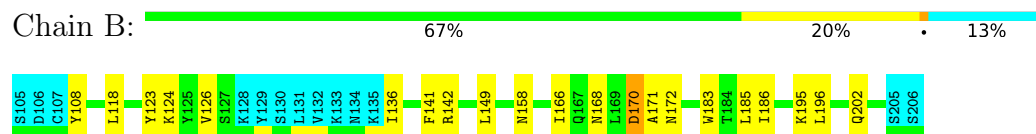


4.2.21 Score per residue for model 21

- Molecule 1: Protein S100-A16

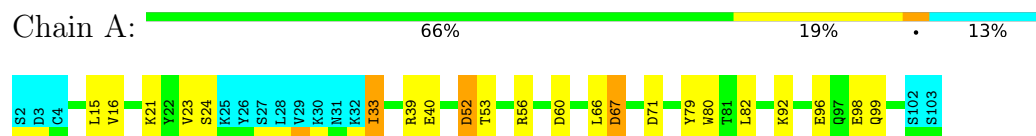


- Molecule 1: Protein S100-A16

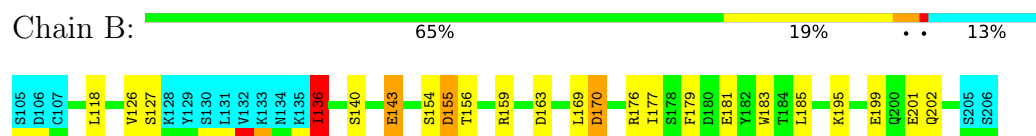


4.2.22 Score per residue for model 22

- Molecule 1: Protein S100-A16

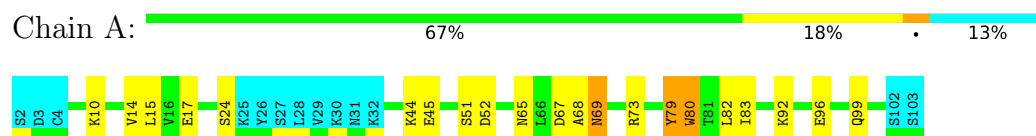


- Molecule 1: Protein S100-A16

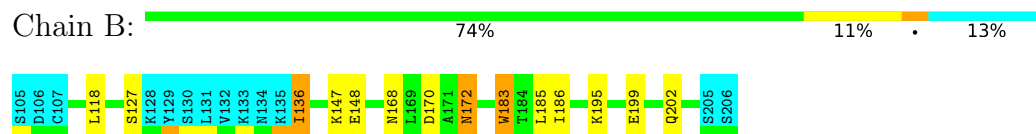


4.2.23 Score per residue for model 23

- Molecule 1: Protein S100-A16

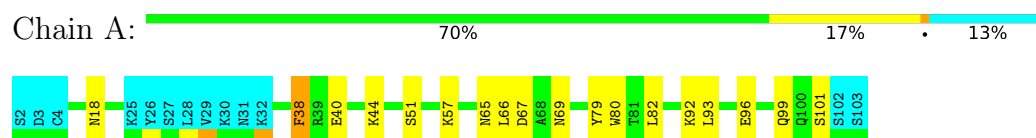


- Molecule 1: Protein S100-A16

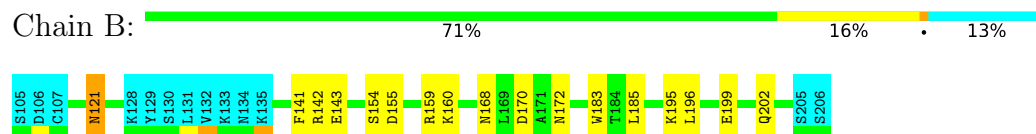


4.2.24 Score per residue for model 24

- Molecule 1: Protein S100-A16

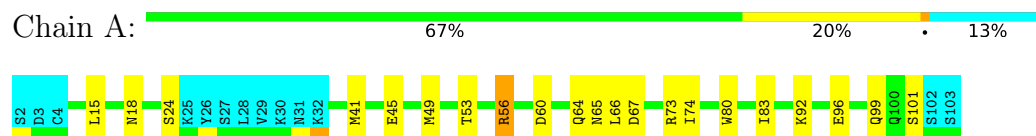


- Molecule 1: Protein S100-A16

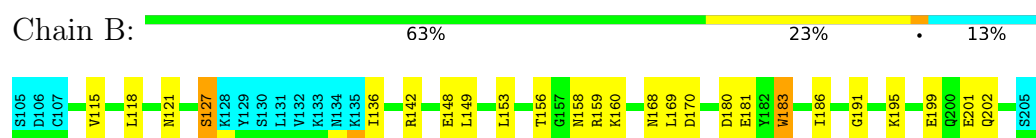


4.2.25 Score per residue for model 25 (medoid)

- Molecule 1: Protein S100-A16

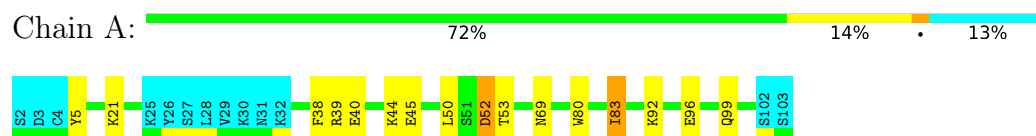


- Molecule 1: Protein S100-A16

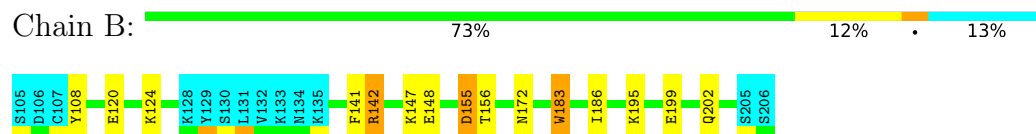


4.2.26 Score per residue for model 26

- Molecule 1: Protein S100-A16

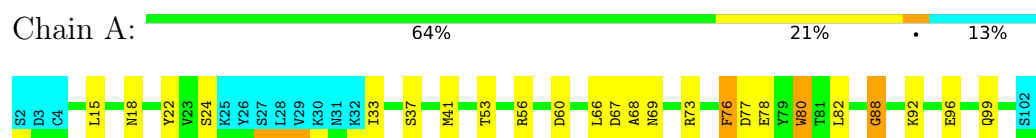


- Molecule 1: Protein S100-A16

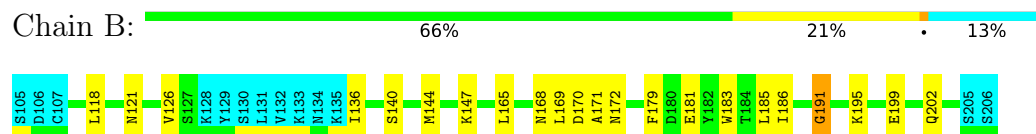


4.2.27 Score per residue for model 27

- Molecule 1: Protein S100-A16

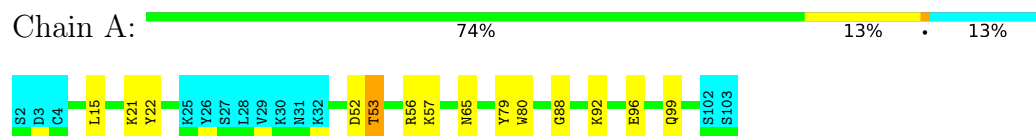


- Molecule 1: Protein S100-A16

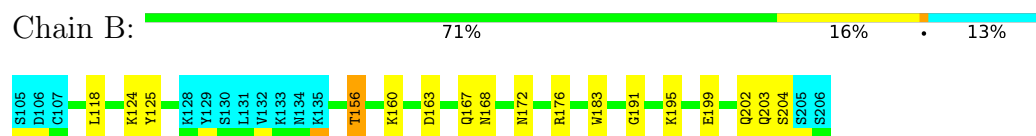


4.2.28 Score per residue for model 28

- Molecule 1: Protein S100-A16

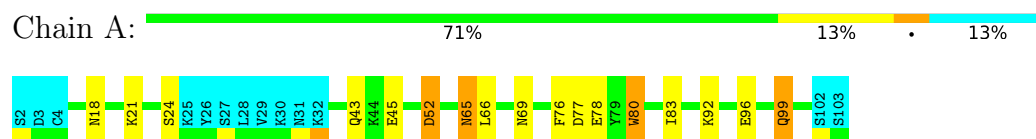


- Molecule 1: Protein S100-A16

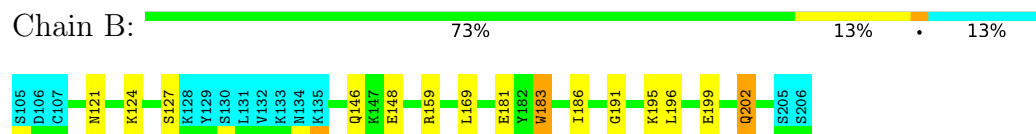


4.2.29 Score per residue for model 29

- Molecule 1: Protein S100-A16

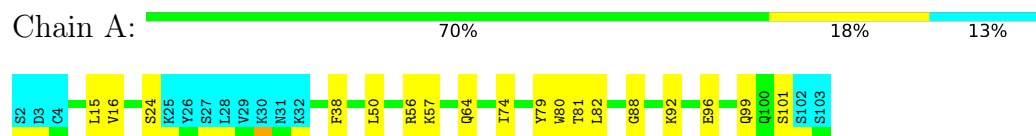


- Molecule 1: Protein S100-A16

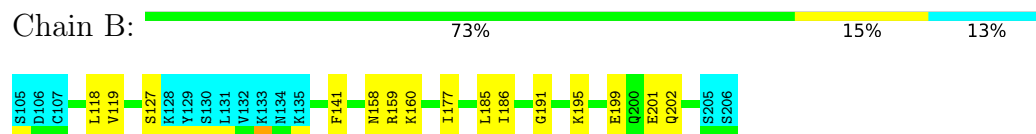


4.2.30 Score per residue for model 30

- Molecule 1: Protein S100-A16



- Molecule 1: Protein S100-A16



5 Refinement protocol and experimental data overview

The models were refined using the following method: *distance geometry*.

Of the 350 calculated structures, 30 were deposited, based on the following criterion: *target function*.

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

Software name	Classification	Version
Amber	structure solution	10.0
CYANA	structure solution	2.1
ProcheckNMR	structure solution	
TALOS	structure solution	
WHAT IF	structure solution	
WHAT IF	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	1932
Number of shifts mapped to atoms	1932
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	69%

6 Model quality (i)

6.1 Standard geometry (i)

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

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the (average) root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#Z>5	RMSZ	#Z>5
1	A	0.82±0.01	0±0/733 (0.0± 0.0%)	1.57±0.04	5±3/988 (0.5± 0.3%)
1	B	0.82±0.02	0±0/733 (0.0± 0.0%)	1.57±0.04	5±2/988 (0.5± 0.2%)
All	All	0.82	0/43980 (0.0%)	1.57	281/59280 (0.5%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	Chirality	Planarity
1	A	0.0±0.0	2.2±1.5
1	B	0.0±0.0	2.1±1.5
All	All	0	131

There are no bond-length outliers.

All unique angle outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	39	ARG	CD-NE-CZ	8.17	135.84	124.40	21	1
1	A	24	SER	CA-C-N	8.15	133.75	120.63	3	5
1	A	24	SER	C-N-CA	8.15	133.75	120.63	3	5
1	A	69	ASN	CA-CB-CG	7.68	120.28	112.60	29	13
1	B	168	ASN	CA-CB-CG	7.50	120.10	112.60	27	12
1	B	127	SER	CA-C-N	7.50	131.33	120.38	3	3
1	B	127	SER	C-N-CA	7.50	131.33	120.38	3	3
1	A	65	ASN	CA-CB-CG	7.42	120.03	112.60	25	13
1	B	123	TYR	CA-C-N	7.09	130.65	120.79	9	2
1	B	123	TYR	C-N-CA	7.09	130.65	120.79	9	2

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	B	142	ARG	CD-NE-CZ	6.95	134.13	124.40	21	1
1	B	141	PHE	CA-CB-CG	6.78	120.58	113.80	5	10
1	A	20	TYR	CA-C-N	6.74	129.61	120.38	14	1
1	A	20	TYR	C-N-CA	6.74	129.61	120.38	14	1
1	B	126	VAL	CA-C-N	6.68	134.30	121.54	21	2
1	B	126	VAL	C-N-CA	6.68	134.30	121.54	21	2
1	A	101	SER	CA-C-N	6.55	134.05	121.54	8	2
1	A	101	SER	C-N-CA	6.55	134.05	121.54	8	2
1	B	163	ASP	CA-CB-CG	6.54	119.14	112.60	12	3
1	B	159	ARG	CD-NE-CZ	6.46	133.44	124.40	2	2
1	B	204	SER	CA-C-N	6.27	133.52	121.54	8	2
1	B	204	SER	C-N-CA	6.27	133.52	121.54	8	2
1	B	173	HIS	CA-C-N	6.23	128.92	120.44	9	1
1	B	173	HIS	C-N-CA	6.23	128.92	120.44	9	1
1	A	38	PHE	CA-CB-CG	6.20	120.00	113.80	19	9
1	B	179	PHE	CA-C-N	6.20	129.06	120.63	22	4
1	B	179	PHE	C-N-CA	6.20	129.06	120.63	22	4
1	A	56	ARG	CD-NE-CZ	6.16	133.02	124.40	2	4
1	B	181	GLU	OE1-CD-OE2	-6.07	108.33	122.90	8	16
1	A	76	PHE	CA-C-N	6.07	128.69	120.44	19	6
1	A	76	PHE	C-N-CA	6.07	128.69	120.44	19	6
1	A	60	ASP	CA-CB-CG	6.05	118.65	112.60	12	3
1	A	43	GLN	OE1-CD-NE2	-6.03	116.57	122.60	29	2
1	B	172	ASN	CA-CB-CG	6.02	118.62	112.60	23	8
1	A	78	GLU	OE1-CD-OE2	-5.98	108.55	122.90	9	15
1	B	156	THR	CA-C-N	5.97	126.57	119.94	25	4
1	B	156	THR	C-N-CA	5.97	126.57	119.94	25	4
1	A	71	ASP	CA-CB-CG	5.93	118.53	112.60	12	3
1	B	198	HIS	CB-CG-CD2	-5.91	123.52	131.20	14	1
1	B	180	ASP	CA-CB-CG	5.87	118.47	112.60	25	1
1	A	99	GLN	OE1-CD-NE2	-5.87	116.73	122.60	18	8
1	A	52	ASP	CA-C-N	5.81	128.34	120.38	20	1
1	A	52	ASP	C-N-CA	5.81	128.34	120.38	20	1
1	A	52	ASP	N-CA-C	5.80	115.89	108.24	26	1
1	B	143	GLU	CA-C-N	5.79	128.31	120.38	3	2
1	B	143	GLU	C-N-CA	5.79	128.31	120.38	3	2
1	B	202	GLN	OE1-CD-NE2	-5.77	116.83	122.60	18	7
1	A	37	SER	CA-C-N	5.77	128.27	120.65	12	1
1	A	37	SER	C-N-CA	5.77	128.27	120.65	12	1
1	B	124	LYS	CG-CD-CE	-5.76	98.05	111.30	15	1
1	B	122	PHE	CA-CB-CG	5.75	119.55	113.80	3	1

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	B	155	ASP	N-CA-C	5.75	115.82	108.24	26	1
1	B	151	HIS	CA-C-N	5.73	128.53	120.28	13	1
1	B	151	HIS	C-N-CA	5.73	128.53	120.28	13	1
1	A	23	VAL	CA-C-N	5.68	132.38	121.54	21	1
1	A	23	VAL	C-N-CA	5.68	132.38	121.54	21	1
1	A	53	THR	CA-C-N	5.58	126.30	119.99	21	3
1	A	53	THR	C-N-CA	5.58	126.30	119.99	21	3
1	B	146	GLN	OE1-CD-NE2	-5.58	117.02	122.60	15	2
1	A	100	GLN	OE1-CD-NE2	-5.58	117.02	122.60	16	1
1	A	33	ILE	CA-C-N	5.55	132.15	121.54	2	2
1	A	33	ILE	C-N-CA	5.55	132.15	121.54	2	2
1	A	83	ILE	CA-CB-CG2	5.53	119.91	110.50	4	2
1	B	186	ILE	CA-CB-CG2	5.53	119.90	110.50	4	3
1	B	165	LEU	CA-C-N	5.50	127.49	120.56	27	3
1	B	165	LEU	C-N-CA	5.50	127.49	120.56	27	3
1	B	121	ASN	CA-CB-CG	5.48	118.08	112.60	24	1
1	B	203	GLN	OE1-CD-NE2	-5.38	117.22	122.60	16	3
1	A	13	ILE	CA-C-O	-5.37	115.48	121.17	14	1
1	B	154	SER	N-CA-C	5.36	119.31	112.34	7	1
1	B	155	ASP	CA-C-N	5.35	128.18	120.38	18	1
1	B	155	ASP	C-N-CA	5.35	128.18	120.38	18	1
1	A	100	GLN	CA-C-N	5.34	131.74	121.54	16	1
1	A	100	GLN	C-N-CA	5.34	131.74	121.54	16	1
1	A	95	HIS	CB-CG-CD2	-5.31	124.30	131.20	14	2
1	B	173	HIS	CA-CB-CG	-5.30	108.50	113.80	18	1
1	A	43	GLN	N-CA-C	5.28	117.03	111.28	4	1
1	A	69	ASN	OD1-CG-ND2	-5.22	117.38	122.60	4	2
1	A	92	LYS	CA-C-N	5.21	127.27	120.28	21	1
1	A	92	LYS	C-N-CA	5.21	127.27	120.28	21	1
1	B	136	ILE	CA-C-N	5.21	131.50	121.54	2	1
1	B	136	ILE	C-N-CA	5.21	131.50	121.54	2	1
1	B	116	ILE	CA-C-O	-5.20	115.66	121.17	14	1
1	B	170	ASP	CA-CB-CG	-5.18	107.42	112.60	22	1
1	B	138	LYS	N-CA-C	5.18	117.33	111.11	12	1
1	A	51	SER	CA-C-N	5.14	131.36	121.54	10	2
1	A	51	SER	C-N-CA	5.14	131.36	121.54	10	2
1	B	203	GLN	CA-C-N	5.13	131.34	121.54	16	1
1	B	203	GLN	C-N-CA	5.13	131.34	121.54	16	1
1	B	158	ASN	CA-CB-CG	5.11	117.71	112.60	1	1
1	A	19	PHE	CA-CB-CG	5.11	118.91	113.80	3	1
1	A	21	LYS	CG-CD-CE	-5.11	99.55	111.30	15	1

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	18	ASN	CA-CB-CG	5.09	117.69	112.60	24	1
1	B	154	SER	CA-C-N	5.08	131.24	121.54	24	1
1	B	154	SER	C-N-CA	5.08	131.24	121.54	24	1
1	A	64	GLN	CA-C-N	5.07	128.02	120.31	25	2
1	A	64	GLN	C-N-CA	5.07	128.02	120.31	25	2
1	A	40	GLU	CA-C-N	5.04	127.74	120.38	3	1
1	A	40	GLU	C-N-CA	5.04	127.74	120.38	3	1
1	A	77	ASP	CA-C-N	5.02	127.01	120.28	18	1
1	A	77	ASP	C-N-CA	5.02	127.01	120.28	18	1
1	B	149	LEU	CA-C-N	5.01	131.11	121.54	9	1
1	B	149	LEU	C-N-CA	5.01	131.11	121.54	9	1

There are no chirality outliers.

All unique planar outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Group	Models (Total)
1	A	67	ASP	Peptide	15
1	B	170	ASP	Peptide	14
1	B	159	ARG	Sidechain	10
1	A	22	TYR	Sidechain	10
1	B	125	TYR	Sidechain	8
1	A	56	ARG	Sidechain	7
1	A	68	ALA	Peptide	7
1	A	79	TYR	Sidechain	6
1	B	176	ARG	Peptide	5
1	A	39	ARG	Sidechain	5
1	B	142	ARG	Sidechain	5
1	A	52	ASP	Peptide	5
1	B	155	ASP	Peptide	4
1	A	51	SER	Peptide	3
1	A	73	ARG	Peptide	3
1	B	171	ALA	Peptide	3
1	B	182	TYR	Sidechain	2
1	B	123	TYR	Sidechain	2
1	A	5	TYR	Sidechain	2
1	B	154	SER	Peptide	2
1	B	136	ILE	Peptide	2
1	A	45	GLU	Peptide	1
1	B	148	GLU	Peptide	1
1	B	126	VAL	Peptide	1

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Mol	Chain	Res	Type	Group	Models (Total)
1	A	69	ASN	Peptide	1
1	A	70	HIS	Sidechain,Peptide	1
1	B	108	TYR	Sidechain	1
1	B	172	ASN	Peptide	1
1	B	173	HIS	Sidechain,Peptide	1
1	B	127	SER	Peptide	1

6.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	720	713	713	2±2
1	B	720	713	713	2±1
All	All	43320	42780	42779	66

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 1.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:33:ILE:HG23	1:A:34:SER:H	0.65	1.49	10	1
1:A:11:ALA:HB1	1:B:114:ALA:HB1	0.53	1.79	19	1
1:A:18:ASN:OD1	1:A:41:MET:HE2	0.48	2.09	25	1
1:A:73:ARG:C	1:A:74:ILE:HD12	0.47	2.35	9	1
1:A:83:ILE:HG23	1:B:183:TRP:CZ3	0.47	2.45	18	14
1:B:141:PHE:CE1	1:B:182:TYR:CE1	0.47	3.02	14	1
1:A:62:LEU:HD11	1:A:85:GLY:C	0.47	2.35	15	2
1:A:22:TYR:CB	1:A:41:MET:HE2	0.46	2.41	4	1
1:A:80:TRP:CZ3	1:B:186:ILE:HG23	0.46	2.45	18	13
1:B:165:LEU:HD13	1:B:185:LEU:O	0.46	2.11	4	1
1:A:18:ASN:HA	1:A:21:LYS:HE2	0.46	1.88	12	1
1:A:22:TYR:CD1	1:A:22:TYR:C	0.45	2.94	20	1
1:A:20:TYR:CD2	1:B:198:HIS:CG	0.45	3.05	14	1
1:A:10:LYS:O	1:A:14:VAL:HG23	0.45	2.12	23	2
1:B:146:GLN:HE22	1:B:159:ARG:NH1	0.45	2.10	16	1
1:A:12:VAL:HG11	1:B:152:MET:HE1	0.45	1.88	18	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:B:120:GLU:CD	1:B:124:LYS:HZ3	0.45	2.20	9	1
1:B:165:LEU:HD11	1:B:188:GLY:C	0.45	2.36	15	1
1:A:38:PHE:CE1	1:A:79:TYR:CE1	0.44	3.06	24	1
1:A:62:LEU:HD13	1:A:82:LEU:O	0.44	2.13	4	1
1:B:121:ASN:HA	1:B:124:LYS:HE2	0.44	1.88	12	1
1:B:162:ALA:HA	1:B:165:LEU:HD12	0.44	1.89	13	1
1:B:113:LYS:O	1:B:117:VAL:HG23	0.43	2.13	16	1
1:B:149:LEU:HD11	1:B:186:ILE:CD1	0.43	2.42	25	1
1:A:76:PHE:CD2	1:B:191:GLY:HA2	0.43	2.48	27	2
1:A:83:ILE:HG23	1:B:183:TRP:HZ3	0.43	1.74	4	1
1:A:95:HIS:CG	1:B:123:TYR:CD2	0.43	3.06	14	1
1:B:142:ARG:HE	1:B:166:ILE:CD1	0.43	2.27	17	1
1:A:22:TYR:CZ	1:A:33:ILE:HD12	0.42	2.49	12	1
1:A:88:GLY:HA2	1:B:179:PHE:CD2	0.42	2.49	27	1
1:B:125:TYR:CZ	1:B:136:ILE:HD12	0.42	2.50	12	1
1:B:126:VAL:HG23	1:B:136:ILE:HG23	0.41	1.90	22	1
1:A:80:TRP:HZ3	1:B:186:ILE:HG23	0.41	1.75	4	1
1:B:155:ASP:CG	1:B:156:THR:N	0.41	2.79	15	1
1:A:49:MET:HE1	1:B:115:VAL:HG11	0.41	1.92	25	1
1:A:92:LYS:HE2	1:A:92:LYS:HA	0.40	1.93	7	1
1:B:141:PHE:CE1	1:B:182:TYR:CE2	0.40	3.10	13	1
1:A:22:TYR:HB3	1:A:41:MET:HE3	0.40	1.92	27	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	89/102 (87%)	77±2 (87±2%)	9±2 (10±2%)	2±1 (3±1%)	6	40
1	B	89/102 (87%)	78±3 (88±3%)	8±2 (9±3%)	2±1 (3±1%)	6	41
All	All	5340/6120 (87%)	4673 (88%)	521 (10%)	146 (3%)	6	41

All 33 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	24	SER	20
1	B	127	SER	20
1	B	136	ILE	13
1	A	33	ILE	12
1	B	191	GLY	9
1	A	52	ASP	8
1	A	88	GLY	7
1	B	155	ASP	6
1	A	69	ASN	6
1	B	172	ASN	5
1	A	34	SER	4
1	B	156	THR	4
1	A	66	LEU	3
1	B	169	LEU	3
1	B	137	SER	2
1	A	101	SER	2
1	A	5	TYR	2
1	B	108	TYR	2
1	B	204	SER	2
1	A	67	ASP	2
1	A	51	SER	2
1	B	173	HIS	1
1	B	150	ASN	1
1	B	171	ALA	1
1	B	185	LEU	1
1	A	87	THR	1
1	B	190	THR	1
1	A	70	HIS	1
1	A	77	ASP	1
1	A	68	ALA	1
1	B	124	LYS	1
1	A	45	GLU	1
1	A	53	THR	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	79/92 (86%)	67±2 (85±3%)	12±2 (15±3%)	5	42

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	79/92 (86%)	67±3 (85±3%)	12±3 (15±3%)	5	42
All	All	4740/5520 (86%)	4024 (85%)	716 (15%)	5	42

All 110 unique residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	99	GLN	30
1	B	202	GLN	30
1	A	92	LYS	29
1	B	195	LYS	29
1	A	80	TRP	28
1	B	183	TRP	28
1	A	96	GLU	27
1	B	199	GLU	27
1	A	82	LEU	19
1	B	185	LEU	18
1	A	66	LEU	17
1	B	118	LEU	15
1	A	15	LEU	14
1	B	160	LYS	13
1	B	169	LEU	13
1	B	158	ASN	11
1	A	57	LYS	11
1	A	44	LYS	11
1	A	53	THR	10
1	B	167	GLN	10
1	B	147	LYS	10
1	B	121	ASN	9
1	B	168	ASN	9
1	A	21	LYS	8
1	A	56	ARG	8
1	B	124	LYS	8
1	B	201	GLU	8
1	B	148	GLU	8
1	B	176	ARG	8
1	A	18	ASN	7
1	A	69	ASN	7
1	B	159	ARG	7
1	B	172	ASN	7
1	A	45	GLU	7
1	A	73	ARG	7

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Mol	Chain	Res	Type	Models (Total)
1	A	65	ASN	7
1	A	55	ASN	7
1	A	74	ILE	6
1	A	79	TYR	6
1	A	64	GLN	6
1	B	156	THR	6
1	A	33	ILE	6
1	A	17	GLU	6
1	B	146	GLN	6
1	A	40	GLU	6
1	B	143	GLU	6
1	B	177	ILE	5
1	B	196	LEU	5
1	A	16	VAL	5
1	B	149	LEU	4
1	A	98	GLU	4
1	A	60	ASP	4
1	B	120	GLU	4
1	A	101	SER	4
1	B	136	ILE	4
1	B	163	ASP	4
1	B	142	ARG	4
1	A	51	SER	3
1	A	43	GLN	3
1	B	109	THR	3
1	B	173	HIS	3
1	A	93	LEU	3
1	B	182	TYR	3
1	B	119	VAL	3
1	B	140	SER	3
1	A	50	LEU	3
1	A	77	ASP	3
1	B	138	LYS	2
1	B	154	SER	2
1	A	6	THR	2
1	A	46	LEU	2
1	B	151	HIS	2
1	A	24	SER	2
1	A	36	SER	2
1	B	150	ASN	2
1	B	200	GLN	2
1	A	70	HIS	2

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Mol	Chain	Res	Type	Models (Total)
1	B	155	ASP	2
1	B	170	ASP	2
1	A	97	GLN	2
1	B	141	PHE	2
1	A	63	ILE	2
1	B	166	ILE	2
1	A	35	LYS	2
1	A	67	ASP	2
1	B	144	MET	2
1	A	52	ASP	2
1	A	34	SER	1
1	A	7	GLU	1
1	B	110	GLU	1
1	A	47	ASN	1
1	A	38	PHE	1
1	B	113	LYS	1
1	A	95	HIS	1
1	B	198	HIS	1
1	B	190	THR	1
1	A	41	MET	1
1	B	180	ASP	1
1	A	48	HIS	1
1	A	22	TYR	1
1	A	5	TYR	1
1	A	39	ARG	1
1	B	108	TYR	1
1	A	23	VAL	1
1	B	153	LEU	1
1	A	37	SER	1
1	A	76	PHE	1
1	B	126	VAL	1
1	B	127	SER	1
1	A	81	THR	1

6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

6.7 Other polymers [i](#)

There are no such molecules in this entry.

6.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

7 Chemical shift validation

The completeness of assignment taking into account all chemical shift lists is 69% for the well-defined parts and 69% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *assigned_chem_shift_list_1*

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	1932
Number of shifts mapped to atoms	1932
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	10

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	202	2.04 ± 0.19	Should be checked
$^{13}\text{C}_\beta$	192	2.96 ± 0.11	Should be checked
$^{13}\text{C}'$	188	2.33 ± 0.15	Should be applied
^{15}N	196	0.26 ± 0.18	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 69%, i.e. 1712 atoms were assigned a chemical shift out of a possible 2482. 0 out of 26 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	870/896 (97%)	356/364 (98%)	342/356 (96%)	172/176 (98%)
Sidechain	842/1388 (61%)	442/898 (49%)	374/438 (85%)	26/52 (50%)

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	Total	¹H	¹³C	¹⁵N
Aromatic	0/198 (0%)	0/98 (0%)	0/92 (0%)	0/8 (0%)
Overall	1712/2482 (69%)	798/1360 (59%)	716/886 (81%)	198/236 (84%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 69%, i.e. 1932 atoms were assigned a chemical shift out of a possible 2812. 0 out of 30 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Backbone	992/1026 (97%)	406/416 (98%)	390/408 (96%)	196/202 (97%)
Sidechain	940/1570 (60%)	486/1014 (48%)	426/496 (86%)	28/60 (47%)
Aromatic	0/216 (0%)	0/106 (0%)	0/102 (0%)	0/8 (0%)
Overall	1932/2812 (69%)	892/1536 (58%)	816/1006 (81%)	224/270 (83%)

7.1.4 Statistically unusual chemical shifts ⓘ

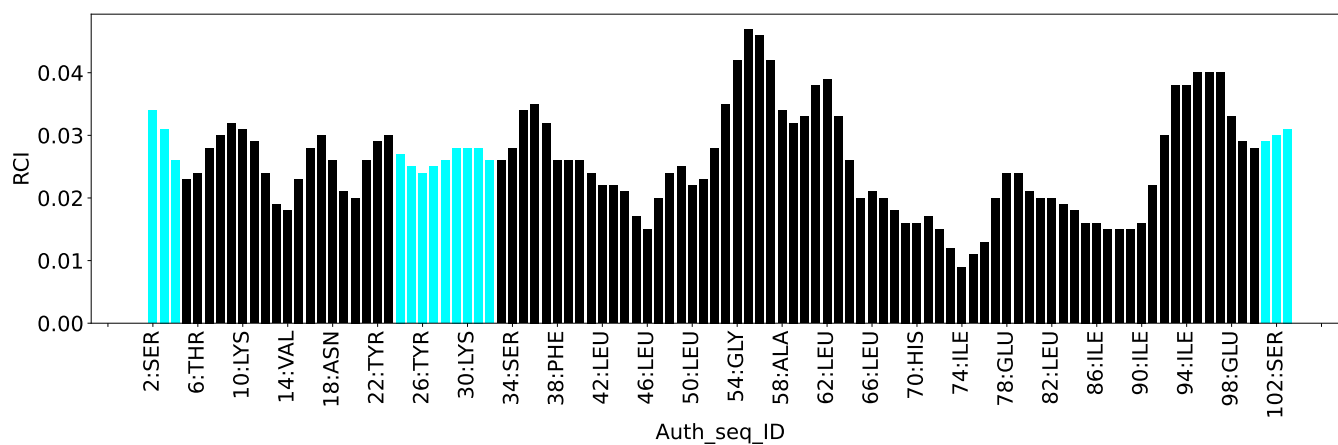
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	73	ARG	NE	125.00	76.53 – 92.65	25.1
1	B	176	ARG	NE	125.00	76.53 – 92.65	25.1
1	A	56	ARG	NE	124.90	76.53 – 92.65	25.0
1	B	159	ARG	NE	124.90	76.53 – 92.65	25.0
1	A	39	ARG	NE	124.80	76.53 – 92.65	24.9
1	B	142	ARG	NE	124.80	76.53 – 92.65	24.9
1	A	32	LYS	CD	39.20	23.50 – 34.42	9.4
1	B	135	LYS	CD	39.20	23.50 – 34.42	9.4
1	A	84	GLY	HA3	1.77	2.08 – 5.71	-5.8
1	B	187	GLY	HA3	1.77	2.08 – 5.71	-5.8

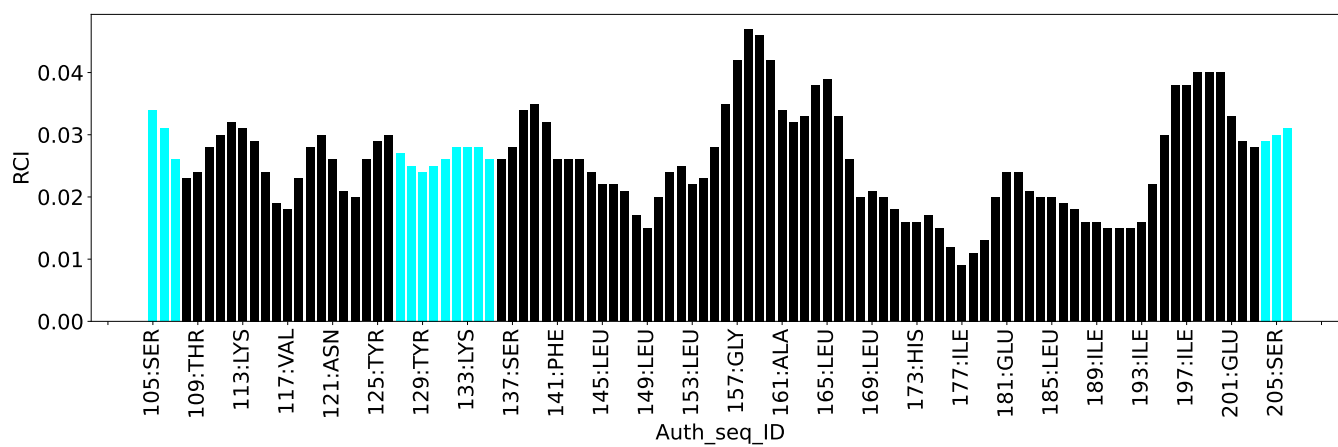
7.1.5 Random Coil Index (RCI) plots ⓘ

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:



Random coil index (RCI) for chain B:



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	2442
Intra-residue ($ i-j =0$)	1072
Sequential ($ i-j =1$)	566
Medium range ($ i-j >1$ and $ i-j <5$)	440
Long range ($ i-j \geq 5$)	168
Inter-chain	178
Hydrogen bond restraints	0
Disulfide bond restraints	0
Total dihedral-angle restraints	248
Number of unmapped restraints	0
Number of restraints per residue	12.9
Number of long range restraints per residue ¹	0.8

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)	6.6	0.2
0.2-0.5 (Medium)	2.9	0.49
>0.5 (Large)	3.2	1.85

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)	9.5	10.0
10.0-20.0 (Medium)	2.4	19.82
>20.0 (Large)	2.9	57.4

9 Distance violation analysis ⓘ

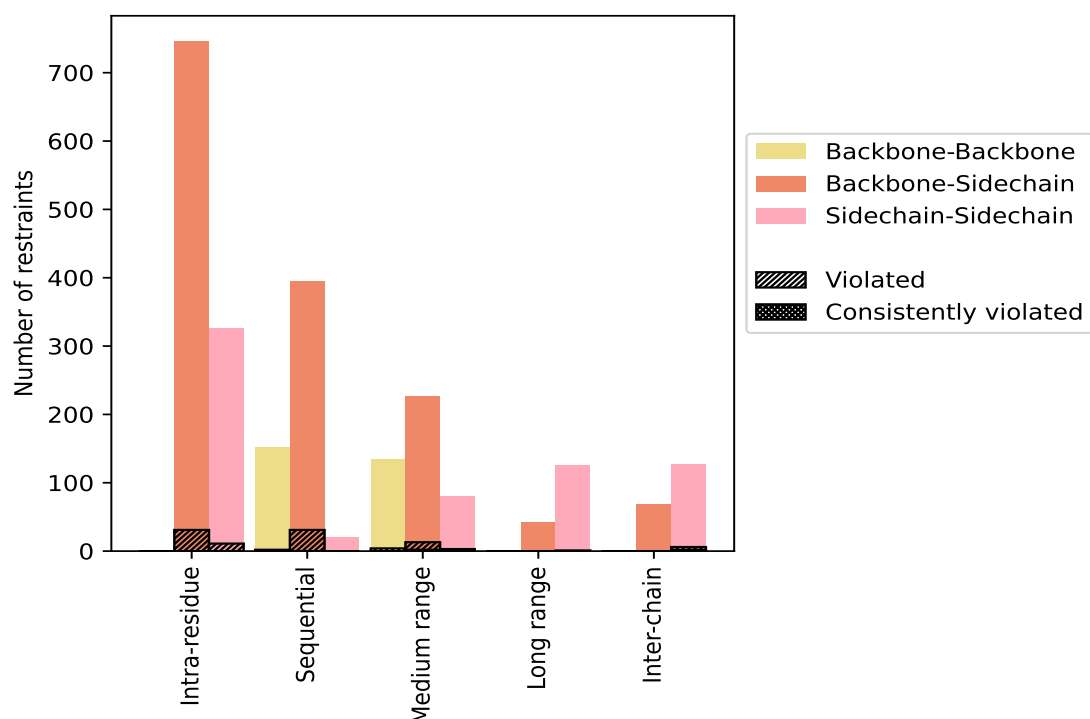
9.1 Summary of distance violations ⓘ

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 ($i-j =0$)	1072	43.9	42	3.9	1.7	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	746	30.5	31	4.2	1.3	0	0.0	0.0
Sidechain-Sidechain	326	13.3	11	3.4	0.5	0	0.0	0.0
Sequential ($i-j =1$)	566	23.2	33	5.8	1.4	0	0.0	0.0
Backbone-Backbone	152	6.2	2	1.3	0.1	0	0.0	0.0
Backbone-Sidechain	394	16.1	31	7.9	1.3	0	0.0	0.0
Sidechain-Sidechain	20	0.8	0	0.0	0.0	0	0.0	0.0
Medium range ($i-j >1$ & $i-j <5$)	440	18.0	20	4.5	0.8	2	0.5	0.1
Backbone-Backbone	134	5.5	4	3.0	0.2	0	0.0	0.0
Backbone-Sidechain	226	9.3	13	5.8	0.5	2	0.9	0.1
Sidechain-Sidechain	80	3.3	3	3.8	0.1	0	0.0	0.0
Long range ($i-j \geq 5$)	168	6.9	1	0.6	0.0	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	42	1.7	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	126	5.2	1	0.8	0.0	0	0.0	0.0
Inter-chain	178	7.3	2	1.1	0.1	2	1.1	0.1
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	69	2.8	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	109	4.5	2	1.8	0.1	2	1.8	0.1
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	2442	100.0	102	4.2	4.2	4	0.2	0.2
Backbone-Backbone	286	11.7	6	2.1	0.2	0	0.0	0.0
Backbone-Sidechain	1477	60.5	75	5.1	3.1	2	0.1	0.1
Sidechain-Sidechain	679	27.8	21	3.1	0.9	2	0.3	0.1

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

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



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

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

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

Model ID	Number of violations						Mean (Å)	Max (Å)	SD ⁶ (Å)	Median (Å)
	IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total				
1	1	3	6	0	2	12	0.46	1.57	0.51	0.22
2	2	3	5	0	2	12	0.52	1.84	0.61	0.22
3	4	3	3	0	2	12	0.4	1.6	0.51	0.16
4	7	1	4	0	2	14	0.32	1.42	0.42	0.12
5	4	4	5	0	4	17	0.38	1.51	0.46	0.13
6	1	5	5	0	2	13	0.46	1.62	0.5	0.29
7	3	2	7	1	2	15	0.34	1.27	0.34	0.17
8	2	0	6	0	2	10	0.38	1.02	0.31	0.32
9	8	2	5	0	2	17	0.37	1.55	0.45	0.12
10	3	1	5	0	4	13	0.44	1.57	0.44	0.29

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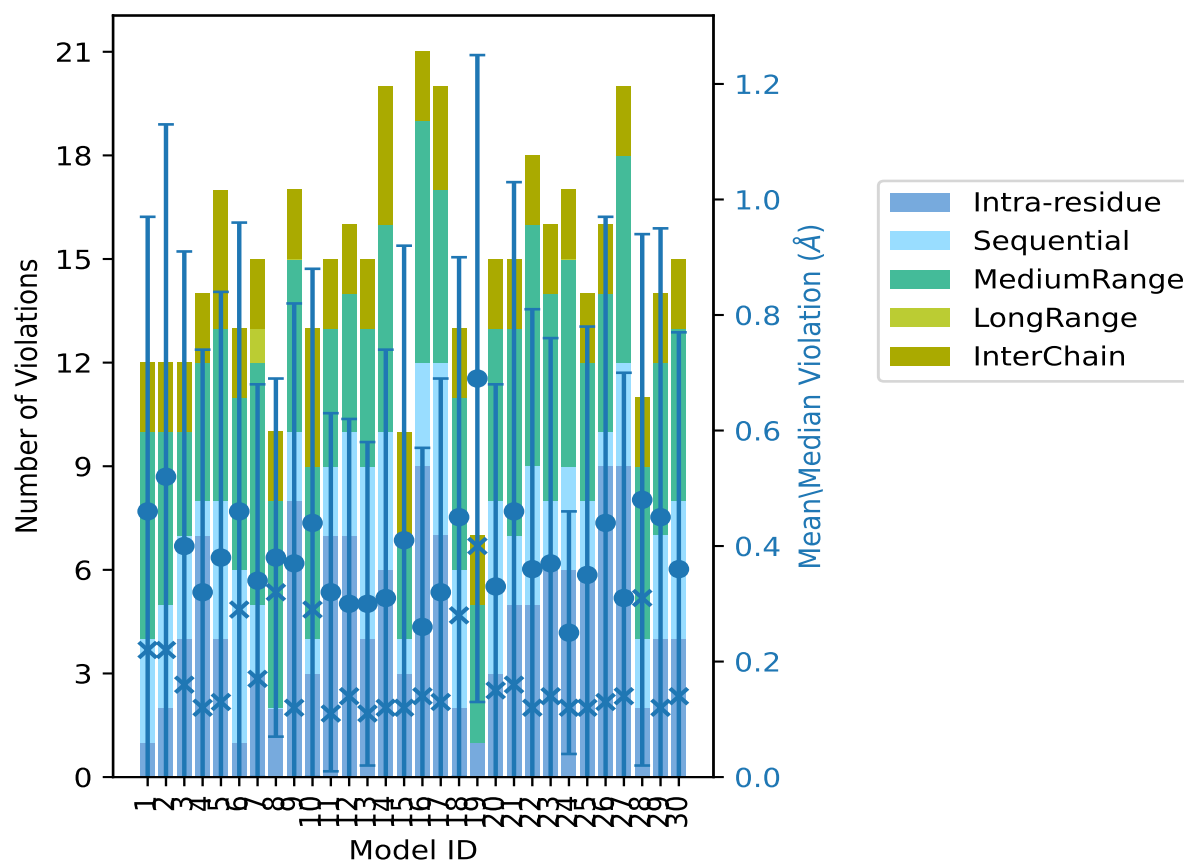
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Model ID	Number of violations						Mean (Å)	Max (Å)	SD ⁶ (Å)	Median (Å)
	IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total				
11	7	2	4	0	2	15	0.32	1.05	0.31	0.11
12	7	3	4	0	2	16	0.3	1.18	0.32	0.14
13	4	5	4	0	2	15	0.3	1.02	0.28	0.11
14	6	4	6	0	4	20	0.31	1.62	0.43	0.12
15	3	1	3	0	3	10	0.41	1.43	0.51	0.12
16	9	3	7	0	2	21	0.26	1.4	0.31	0.14
17	7	5	5	0	3	20	0.32	1.38	0.37	0.13
18	2	4	5	0	2	13	0.45	1.46	0.45	0.28
19	1	0	4	0	2	7	0.69	1.54	0.56	0.4
20	3	5	5	0	2	15	0.33	1.4	0.35	0.15
21	5	2	6	0	2	15	0.46	1.85	0.57	0.16
22	5	4	7	0	2	18	0.36	1.65	0.45	0.12
23	6	2	6	0	2	16	0.37	1.26	0.39	0.14
24	6	3	6	0	2	17	0.25	0.75	0.21	0.12
25	6	2	4	0	2	14	0.35	1.4	0.43	0.12
26	9	1	4	0	2	16	0.44	1.69	0.53	0.13
27	9	3	6	0	2	20	0.31	1.58	0.39	0.14
28	2	2	5	0	2	11	0.48	1.39	0.46	0.31
29	4	3	5	0	2	14	0.45	1.6	0.5	0.12
30	4	4	5	0	2	15	0.36	1.35	0.41	0.14

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, 2326(IR:1030, SQ:533, MR:420, LR:167, IC:176) 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	%
16	21	11	1	0	49	1	3.3
10	3	2	0	0	15	2	6.7
2	3	1	0	0	6	3	10.0
6	2	0	0	0	8	4	13.3
2	2	0	0	0	4	5	16.7
0	0	0	0	0	0	6	20.0

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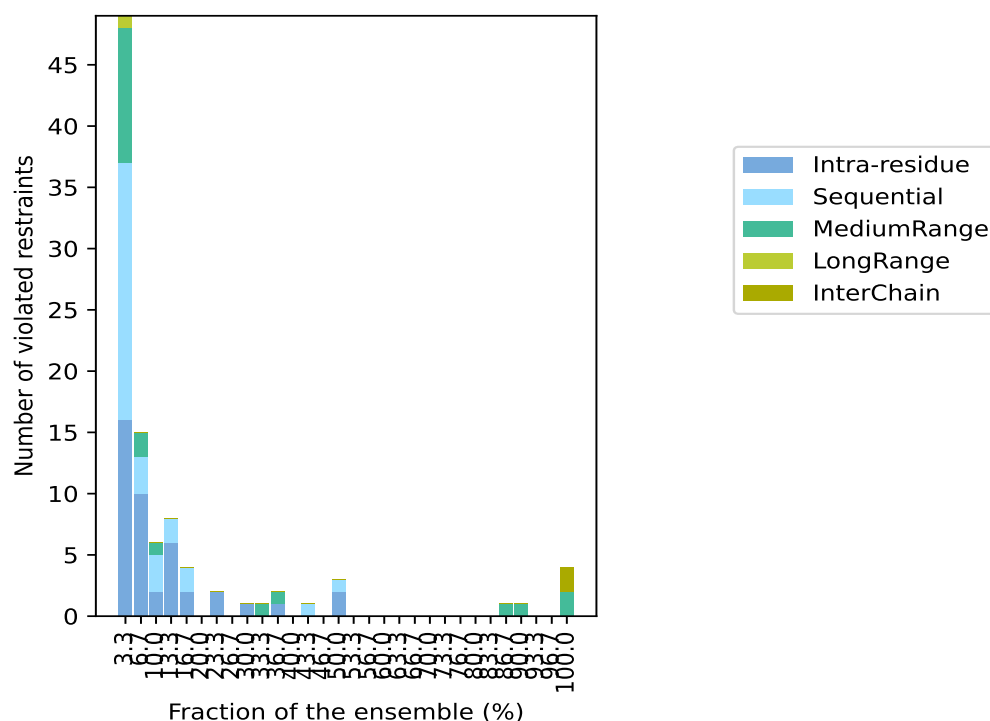
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Number of violated restraints						Fraction of the ensemble	
IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total	Count ⁶	%
2	0	0	0	0	2	7	23.3
0	0	0	0	0	0	8	26.7
1	0	0	0	0	1	9	30.0
0	0	1	0	0	1	10	33.3
1	0	1	0	0	2	11	36.7
0	0	0	0	0	0	12	40.0
0	1	0	0	0	1	13	43.3
0	0	0	0	0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

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

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

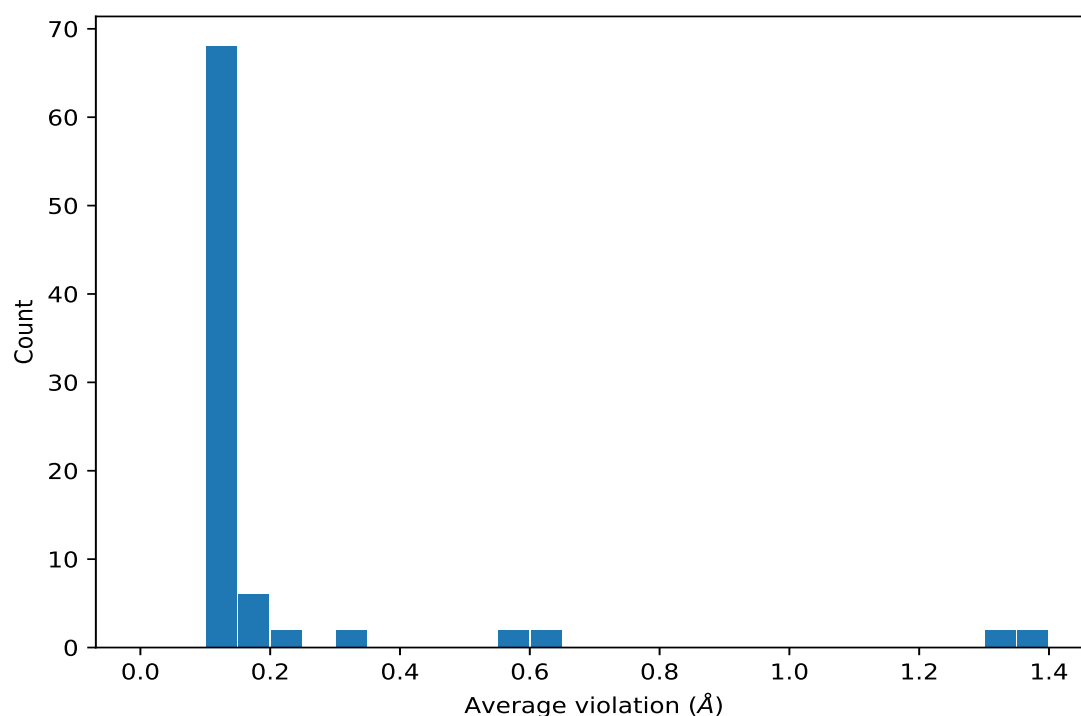
9.3.1 Bar graph : Distance violation statistics for the ensemble [i](#)



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)
(1,2355)	1:122:B:PHE:HD1	1:125:B:TYR:H	30	1.35	0.27	1.4
(1,2355)	1:122:B:PHE:HD2	1:125:B:TYR:H	30	1.35	0.27	1.4
(1,1153)	1:19:A:PHE:HD1	1:22:A:TYR:H	30	1.33	0.29	1.38
(1,1153)	1:19:A:PHE:HD2	1:22:A:TYR:H	30	1.33	0.29	1.38
(1,1199)	1:80:A:TRP:HZ2	1:183:B:TRP:HD1	30	0.32	0.02	0.32
(1,1200)	1:80:A:TRP:HD1	1:183:B:TRP:HZ2	30	0.32	0.01	0.32
(1,2399)	1:182:B:TYR:HE1	1:185:B:LEU:HB2	27	0.61	0.23	0.64
(1,2399)	1:182:B:TYR:HE2	1:185:B:LEU:HB2	27	0.61	0.23	0.64
(1,1225)	1:79:A:TYR:HE1	1:82:A:LEU:HB2	26	0.59	0.21	0.6
(1,1225)	1:79:A:TYR:HE2	1:82:A:LEU:HB2	26	0.59	0.21	0.6
(1,552)	1:96:A:GLU:HG2	1:97:A:GLN:H	15	0.13	0.02	0.12
(1,701)	1:90:A:ILE:HA	1:90:A:ILE:HD11	15	0.12	0.01	0.12
(1,701)	1:90:A:ILE:HA	1:90:A:ILE:HD12	15	0.12	0.01	0.12
(1,701)	1:90:A:ILE:HA	1:90:A:ILE:HD13	15	0.12	0.01	0.12
(1,1989)	1:193:B:ILE:HA	1:193:B:ILE:HD11	15	0.11	0.01	0.11
(1,1989)	1:193:B:ILE:HA	1:193:B:ILE:HD12	15	0.11	0.01	0.11

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,1989)	1:193:B:ILE:HA	1:193:B:ILE:HD13	15	0.11	0.01	0.11
(1,1844)	1:199:B:GLU:HG2	1:200:B:GLN:H	13	0.13	0.02	0.12
(1,1853)	1:139:B:SER:HA	1:142:B:ARG:H	11	0.2	0.07	0.2
(1,912)	1:97:A:GLN:HG3	1:97:A:GLN:HE21	11	0.12	0.02	0.12
(1,561)	1:36:A:SER:HA	1:39:A:ARG:H	10	0.2	0.07	0.2
(1,451)	1:43:A:GLN:HB3	1:43:A:GLN:HG2	9	0.11	0.01	0.11
(1,683)	1:21:A:LYS:HA	1:21:A:LYS:HD2	7	0.12	0.02	0.12
(1,683)	1:21:A:LYS:HA	1:21:A:LYS:HD3	7	0.12	0.02	0.12
(1,1971)	1:124:B:LYS:HA	1:124:B:LYS:HD2	7	0.11	0.01	0.11
(1,1971)	1:124:B:LYS:HA	1:124:B:LYS:HD3	7	0.11	0.01	0.11
(1,1977)	1:160:B:LYS:HB2	1:160:B:LYS:HE2	5	0.17	0.03	0.16
(1,1977)	1:160:B:LYS:HB2	1:160:B:LYS:HE3	5	0.17	0.03	0.16
(1,1977)	1:160:B:LYS:HB3	1:160:B:LYS:HE2	5	0.17	0.03	0.16
(1,1977)	1:160:B:LYS:HB3	1:160:B:LYS:HE3	5	0.17	0.03	0.16
(1,2174)	1:200:B:GLN:HG3	1:200:B:GLN:HE21	5	0.12	0.01	0.13
(1,455)	1:57:A:LYS:HD2	1:58:A:ALA:H	5	0.11	0.01	0.11
(1,455)	1:57:A:LYS:HD3	1:58:A:ALA:H	5	0.11	0.01	0.11
(1,1711)	1:145:B:LEU:HD11	1:146:B:GLN:H	5	0.11	0.01	0.1
(1,1711)	1:145:B:LEU:HD12	1:146:B:GLN:H	5	0.11	0.01	0.1
(1,1711)	1:145:B:LEU:HD13	1:146:B:GLN:H	5	0.11	0.01	0.1
(1,1833)	1:147:B:LYS:HA	1:147:B:LYS:HD2	4	0.12	0.01	0.12
(1,453)	1:43:A:GLN:HG2	1:43:A:GLN:HE22	4	0.12	0.01	0.12
(1,1748)	1:160:B:LYS:HD2	1:161:B:ALA:H	4	0.12	0.01	0.12
(1,1748)	1:160:B:LYS:HD3	1:161:B:ALA:H	4	0.12	0.01	0.12
(1,937)	1:97:A:GLN:HG2	1:98:A:GLU:H	4	0.12	0.02	0.11
(1,232)	1:93:A:LEU:H	1:93:A:LEU:HG	4	0.11	0.0	0.11
(1,1533)	1:196:B:LEU:H	1:196:B:LEU:HG	4	0.11	0.01	0.1
(1,1615)	1:166:B:ILE:HA	1:166:B:ILE:HD11	4	0.1	0.0	0.1
(1,1615)	1:166:B:ILE:HA	1:166:B:ILE:HD12	4	0.1	0.0	0.1
(1,1615)	1:166:B:ILE:HA	1:166:B:ILE:HD13	4	0.1	0.0	0.1
(1,1746)	1:146:B:GLN:HG2	1:146:B:GLN:HE22	4	0.1	0.0	0.1
(2,4)	2:207:A:CA:CA	1:32:A:LYS:O	3	0.16	0.04	0.15
(2,13)	2:209:B:CA:CA	1:135:B:LYS:O	3	0.15	0.06	0.12
(1,416)	1:42:A:LEU:HD11	1:43:A:GLN:H	3	0.14	0.03	0.12
(1,416)	1:42:A:LEU:HD12	1:43:A:GLN:H	3	0.14	0.03	0.12
(1,416)	1:42:A:LEU:HD13	1:43:A:GLN:H	3	0.14	0.03	0.12
(1,689)	1:57:A:LYS:HB2	1:57:A:LYS:HE2	3	0.13	0.0	0.13
(1,689)	1:57:A:LYS:HB2	1:57:A:LYS:HE3	3	0.13	0.0	0.13
(1,689)	1:57:A:LYS:HB3	1:57:A:LYS:HE2	3	0.13	0.0	0.13
(1,689)	1:57:A:LYS:HB3	1:57:A:LYS:HE3	3	0.13	0.0	0.13
(1,541)	1:44:A:LYS:HA	1:44:A:LYS:HD2	3	0.13	0.01	0.14
(1,2116)	1:165:B:LEU:HD21	1:166:B:ILE:H	3	0.11	0.0	0.11

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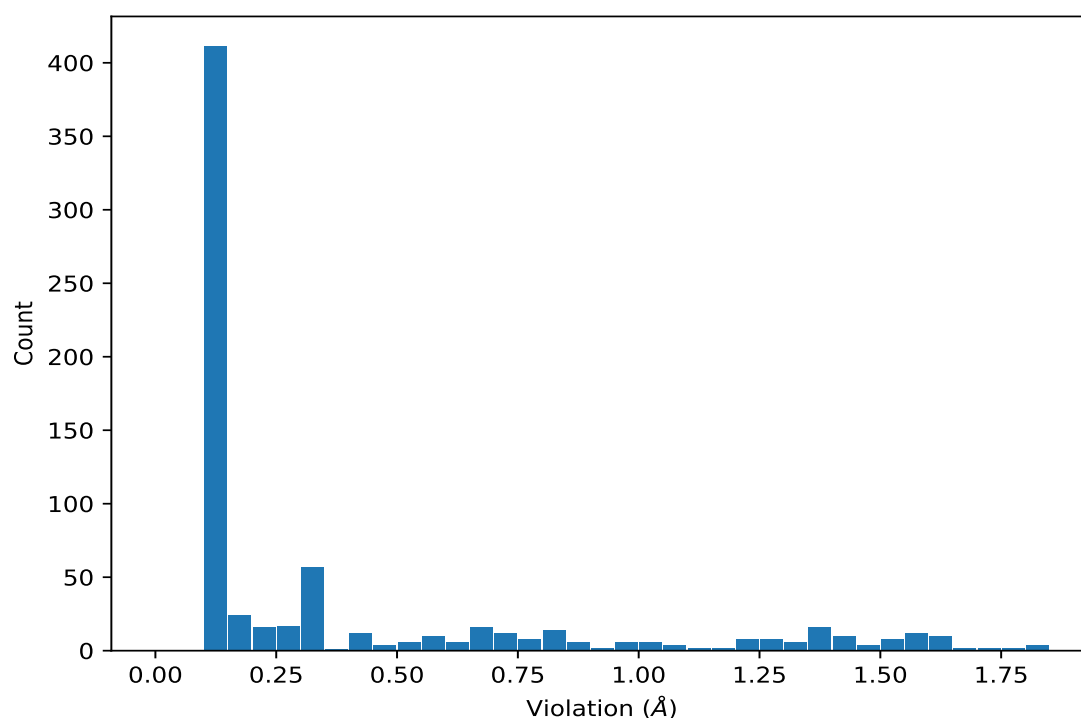
Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,2116)	1:165:B:LEU:HD22	1:166:B:ILE:H	3	0.11	0.0	0.11
(1,2116)	1:165:B:LEU:HD23	1:166:B:ILE:H	3	0.11	0.0	0.11
(1,846)	1:62:A:LEU:HD21	1:63:A:ILE:H	3	0.1	0.0	0.1
(1,846)	1:62:A:LEU:HD22	1:63:A:ILE:H	3	0.1	0.0	0.1
(1,846)	1:62:A:LEU:HD23	1:63:A:ILE:H	3	0.1	0.0	0.1
(1,1595)	1:114:B:ALA:HB1	1:117:B:VAL:H	3	0.1	0.0	0.1
(1,1595)	1:114:B:ALA:HB2	1:117:B:VAL:H	3	0.1	0.0	0.1
(1,1595)	1:114:B:ALA:HB3	1:117:B:VAL:H	3	0.1	0.0	0.1
(1,2245)	1:143:B:GLU:H	1:143:B:GLU:HG2	2	0.14	0.02	0.14
(1,492)	1:44:A:LYS:H	1:44:A:LYS:HD3	2	0.13	0.02	0.13
(1,305)	1:40:A:GLU:HG3	1:41:A:MET:H	2	0.12	0.02	0.12
(1,987)	1:40:A:GLU:H	1:40:A:GLU:HG2	2	0.12	0.02	0.12
(1,2071)	1:195:B:LYS:H	1:195:B:LYS:HG2	2	0.12	0.02	0.12
(1,2199)	1:200:B:GLN:HG2	1:201:B:GLU:H	2	0.12	0.02	0.12
(1,785)	1:92:A:LYS:H	1:92:A:LYS:HG2	2	0.12	0.0	0.12
(1,1784)	1:147:B:LYS:H	1:147:B:LYS:HD3	2	0.12	0.0	0.12
(1,1926)	1:204:B:SER:H	1:204:B:SER:HB2	2	0.11	0.01	0.11
(1,1926)	1:204:B:SER:H	1:204:B:SER:HB3	2	0.11	0.01	0.11
(1,1943)	1:143:B:GLU:HA	1:146:B:GLN:HB3	2	0.11	0.01	0.11
(1,318)	1:63:A:ILE:HA	1:63:A:ILE:HD11	2	0.11	0.0	0.11
(1,318)	1:63:A:ILE:HA	1:63:A:ILE:HD12	2	0.11	0.0	0.11
(1,318)	1:63:A:ILE:HA	1:63:A:ILE:HD13	2	0.11	0.0	0.11
(1,342)	1:43:A:GLN:HB2	1:43:A:GLN:HE21	2	0.11	0.0	0.11
(1,1288)	1:95:A:HIS:HD2	1:98:A:GLU:H	2	0.11	0.0	0.11
(1,1744)	1:146:B:GLN:HB3	1:146:B:GLN:HG2	2	0.11	0.0	0.11
(1,1938)	1:109:B:THR:HG21	1:110:B:GLU:H	2	0.11	0.0	0.11
(1,1938)	1:109:B:THR:HG22	1:110:B:GLU:H	2	0.11	0.0	0.11
(1,1938)	1:109:B:THR:HG23	1:110:B:GLU:H	2	0.11	0.0	0.11

¹Number of violated models, ²Standard deviation

9.5 All violated distance restraints [i](#)

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

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



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

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

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,2355)	1:122:B:PHE:HD1	1:125:B:TYR:H	21	1.85
(1,2355)	1:122:B:PHE:HD2	1:125:B:TYR:H	21	1.85
(1,2355)	1:122:B:PHE:HD1	1:125:B:TYR:H	2	1.84
(1,2355)	1:122:B:PHE:HD2	1:125:B:TYR:H	2	1.84
(1,1153)	1:19:A:PHE:HD1	1:22:A:TYR:H	2	1.78
(1,1153)	1:19:A:PHE:HD2	1:22:A:TYR:H	2	1.78
(1,1153)	1:19:A:PHE:HD1	1:22:A:TYR:H	21	1.74
(1,1153)	1:19:A:PHE:HD2	1:22:A:TYR:H	21	1.74
(1,1153)	1:19:A:PHE:HD1	1:22:A:TYR:H	26	1.69
(1,1153)	1:19:A:PHE:HD2	1:22:A:TYR:H	26	1.69
(1,2355)	1:122:B:PHE:HD1	1:125:B:TYR:H	22	1.65
(1,2355)	1:122:B:PHE:HD2	1:125:B:TYR:H	22	1.65
(1,2355)	1:122:B:PHE:HD1	1:125:B:TYR:H	14	1.62
(1,2355)	1:122:B:PHE:HD2	1:125:B:TYR:H	14	1.62
(1,1153)	1:19:A:PHE:HD1	1:22:A:TYR:H	6	1.62
(1,1153)	1:19:A:PHE:HD2	1:22:A:TYR:H	6	1.62

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,2355)	1:122:B:PHE:HD1	1:125:B:TYR:H	3	1.6
(1,2355)	1:122:B:PHE:HD2	1:125:B:TYR:H	3	1.6
(1,2355)	1:122:B:PHE:HD1	1:125:B:TYR:H	29	1.6
(1,2355)	1:122:B:PHE:HD2	1:125:B:TYR:H	29	1.6
(1,1153)	1:19:A:PHE:HD1	1:22:A:TYR:H	27	1.58
(1,1153)	1:19:A:PHE:HD2	1:22:A:TYR:H	27	1.58
(1,1153)	1:19:A:PHE:HD1	1:22:A:TYR:H	1	1.57
(1,1153)	1:19:A:PHE:HD2	1:22:A:TYR:H	1	1.57
(1,1153)	1:19:A:PHE:HD1	1:22:A:TYR:H	10	1.57
(1,1153)	1:19:A:PHE:HD2	1:22:A:TYR:H	10	1.57
(1,2355)	1:122:B:PHE:HD1	1:125:B:TYR:H	26	1.56
(1,2355)	1:122:B:PHE:HD2	1:125:B:TYR:H	26	1.56
(1,1153)	1:19:A:PHE:HD1	1:22:A:TYR:H	9	1.55
(1,1153)	1:19:A:PHE:HD2	1:22:A:TYR:H	9	1.55
(1,1153)	1:19:A:PHE:HD1	1:22:A:TYR:H	14	1.55
(1,1153)	1:19:A:PHE:HD2	1:22:A:TYR:H	14	1.55
(1,2355)	1:122:B:PHE:HD1	1:125:B:TYR:H	19	1.54
(1,2355)	1:122:B:PHE:HD2	1:125:B:TYR:H	19	1.54
(1,1153)	1:19:A:PHE:HD1	1:22:A:TYR:H	19	1.54
(1,1153)	1:19:A:PHE:HD2	1:22:A:TYR:H	19	1.54
(1,1153)	1:19:A:PHE:HD1	1:22:A:TYR:H	5	1.51
(1,1153)	1:19:A:PHE:HD2	1:22:A:TYR:H	5	1.51
(1,2355)	1:122:B:PHE:HD1	1:125:B:TYR:H	6	1.5
(1,2355)	1:122:B:PHE:HD2	1:125:B:TYR:H	6	1.5
(1,1153)	1:19:A:PHE:HD1	1:22:A:TYR:H	3	1.48
(1,1153)	1:19:A:PHE:HD2	1:22:A:TYR:H	3	1.48
(1,2355)	1:122:B:PHE:HD1	1:125:B:TYR:H	18	1.46
(1,2355)	1:122:B:PHE:HD2	1:125:B:TYR:H	18	1.46
(1,2355)	1:122:B:PHE:HD1	1:125:B:TYR:H	1	1.44
(1,2355)	1:122:B:PHE:HD2	1:125:B:TYR:H	1	1.44
(1,2355)	1:122:B:PHE:HD1	1:125:B:TYR:H	5	1.43
(1,2355)	1:122:B:PHE:HD2	1:125:B:TYR:H	5	1.43
(1,2355)	1:122:B:PHE:HD1	1:125:B:TYR:H	15	1.43
(1,2355)	1:122:B:PHE:HD2	1:125:B:TYR:H	15	1.43
(1,1153)	1:19:A:PHE:HD1	1:22:A:TYR:H	4	1.42
(1,1153)	1:19:A:PHE:HD2	1:22:A:TYR:H	4	1.42
(1,1153)	1:19:A:PHE:HD1	1:22:A:TYR:H	15	1.42
(1,1153)	1:19:A:PHE:HD2	1:22:A:TYR:H	15	1.42
(1,2355)	1:122:B:PHE:HD1	1:125:B:TYR:H	20	1.4
(1,2355)	1:122:B:PHE:HD2	1:125:B:TYR:H	20	1.4
(1,2355)	1:122:B:PHE:HD1	1:125:B:TYR:H	25	1.4
(1,2355)	1:122:B:PHE:HD2	1:125:B:TYR:H	25	1.4

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1153)	1:19:A:PHE:HD1	1:22:A:TYR:H	16	1.4
(1,1153)	1:19:A:PHE:HD2	1:22:A:TYR:H	16	1.4
(1,2355)	1:122:B:PHE:HD1	1:125:B:TYR:H	9	1.39
(1,2355)	1:122:B:PHE:HD2	1:125:B:TYR:H	9	1.39
(1,2355)	1:122:B:PHE:HD1	1:125:B:TYR:H	28	1.39
(1,2355)	1:122:B:PHE:HD2	1:125:B:TYR:H	28	1.39
(1,2355)	1:122:B:PHE:HD1	1:125:B:TYR:H	17	1.38
(1,2355)	1:122:B:PHE:HD2	1:125:B:TYR:H	17	1.38
(1,1153)	1:19:A:PHE:HD1	1:22:A:TYR:H	25	1.35
(1,1153)	1:19:A:PHE:HD2	1:22:A:TYR:H	25	1.35
(1,1153)	1:19:A:PHE:HD1	1:22:A:TYR:H	30	1.35
(1,1153)	1:19:A:PHE:HD2	1:22:A:TYR:H	30	1.35
(1,2355)	1:122:B:PHE:HD1	1:125:B:TYR:H	30	1.34
(1,2355)	1:122:B:PHE:HD2	1:125:B:TYR:H	30	1.34
(1,1153)	1:19:A:PHE:HD1	1:22:A:TYR:H	22	1.33
(1,1153)	1:19:A:PHE:HD2	1:22:A:TYR:H	22	1.33
(1,2355)	1:122:B:PHE:HD1	1:125:B:TYR:H	27	1.32
(1,2355)	1:122:B:PHE:HD2	1:125:B:TYR:H	27	1.32
(1,1153)	1:19:A:PHE:HD1	1:22:A:TYR:H	29	1.28
(1,1153)	1:19:A:PHE:HD2	1:22:A:TYR:H	29	1.28
(1,2355)	1:122:B:PHE:HD1	1:125:B:TYR:H	7	1.27
(1,2355)	1:122:B:PHE:HD2	1:125:B:TYR:H	7	1.27
(1,2355)	1:122:B:PHE:HD1	1:125:B:TYR:H	23	1.26
(1,2355)	1:122:B:PHE:HD2	1:125:B:TYR:H	23	1.26
(1,1153)	1:19:A:PHE:HD1	1:22:A:TYR:H	28	1.25
(1,1153)	1:19:A:PHE:HD2	1:22:A:TYR:H	28	1.25
(1,1153)	1:19:A:PHE:HD1	1:22:A:TYR:H	18	1.24
(1,1153)	1:19:A:PHE:HD2	1:22:A:TYR:H	18	1.24
(1,2355)	1:122:B:PHE:HD1	1:125:B:TYR:H	4	1.22
(1,2355)	1:122:B:PHE:HD2	1:125:B:TYR:H	4	1.22
(1,2355)	1:122:B:PHE:HD1	1:125:B:TYR:H	10	1.22
(1,2355)	1:122:B:PHE:HD2	1:125:B:TYR:H	10	1.22
(1,1153)	1:19:A:PHE:HD1	1:22:A:TYR:H	23	1.22
(1,1153)	1:19:A:PHE:HD2	1:22:A:TYR:H	23	1.22
(1,1153)	1:19:A:PHE:HD1	1:22:A:TYR:H	12	1.18
(1,1153)	1:19:A:PHE:HD2	1:22:A:TYR:H	12	1.18
(1,1153)	1:19:A:PHE:HD1	1:22:A:TYR:H	17	1.12
(1,1153)	1:19:A:PHE:HD2	1:22:A:TYR:H	17	1.12
(1,2355)	1:122:B:PHE:HD1	1:125:B:TYR:H	12	1.08
(1,2355)	1:122:B:PHE:HD2	1:125:B:TYR:H	12	1.08
(1,1153)	1:19:A:PHE:HD1	1:22:A:TYR:H	11	1.05
(1,1153)	1:19:A:PHE:HD2	1:22:A:TYR:H	11	1.05

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,2355)	1:122:B:PHE:HD1	1:125:B:TYR:H	8	1.02
(1,2355)	1:122:B:PHE:HD2	1:125:B:TYR:H	8	1.02
(1,2355)	1:122:B:PHE:HD1	1:125:B:TYR:H	13	1.02
(1,2355)	1:122:B:PHE:HD2	1:125:B:TYR:H	13	1.02
(1,1225)	1:79:A:TYR:HE1	1:82:A:LEU:HB2	26	1.0
(1,1225)	1:79:A:TYR:HE2	1:82:A:LEU:HB2	26	1.0
(1,2399)	1:182:B:TYR:HE1	1:185:B:LEU:HB2	29	0.99
(1,2399)	1:182:B:TYR:HE2	1:185:B:LEU:HB2	29	0.99
(1,2399)	1:182:B:TYR:HE1	1:185:B:LEU:HB2	26	0.98
(1,2399)	1:182:B:TYR:HE2	1:185:B:LEU:HB2	26	0.98
(1,1225)	1:79:A:TYR:HE1	1:82:A:LEU:HB2	29	0.96
(1,1225)	1:79:A:TYR:HE2	1:82:A:LEU:HB2	29	0.96
(1,2355)	1:122:B:PHE:HD1	1:125:B:TYR:H	16	0.92
(1,2355)	1:122:B:PHE:HD2	1:125:B:TYR:H	16	0.92
(1,1153)	1:19:A:PHE:HD1	1:22:A:TYR:H	7	0.88
(1,1153)	1:19:A:PHE:HD2	1:22:A:TYR:H	7	0.88
(1,2399)	1:182:B:TYR:HE1	1:185:B:LEU:HB2	22	0.87
(1,2399)	1:182:B:TYR:HE2	1:185:B:LEU:HB2	22	0.87
(1,1153)	1:19:A:PHE:HD1	1:22:A:TYR:H	8	0.86
(1,1153)	1:19:A:PHE:HD2	1:22:A:TYR:H	8	0.86
(1,1225)	1:79:A:TYR:HE1	1:82:A:LEU:HB2	21	0.84
(1,1225)	1:79:A:TYR:HE2	1:82:A:LEU:HB2	21	0.84
(1,2399)	1:182:B:TYR:HE1	1:185:B:LEU:HB2	5	0.83
(1,2399)	1:182:B:TYR:HE2	1:185:B:LEU:HB2	5	0.83
(1,2399)	1:182:B:TYR:HE1	1:185:B:LEU:HB2	9	0.83
(1,2399)	1:182:B:TYR:HE2	1:185:B:LEU:HB2	9	0.83
(1,2399)	1:182:B:TYR:HE1	1:185:B:LEU:HB2	17	0.83
(1,2399)	1:182:B:TYR:HE2	1:185:B:LEU:HB2	17	0.83
(1,1225)	1:79:A:TYR:HE1	1:82:A:LEU:HB2	18	0.83
(1,1225)	1:79:A:TYR:HE2	1:82:A:LEU:HB2	18	0.83
(1,1225)	1:79:A:TYR:HE1	1:82:A:LEU:HB2	5	0.82
(1,1225)	1:79:A:TYR:HE2	1:82:A:LEU:HB2	5	0.82
(1,1153)	1:19:A:PHE:HD1	1:22:A:TYR:H	20	0.81
(1,1153)	1:19:A:PHE:HD2	1:22:A:TYR:H	20	0.81
(1,2399)	1:182:B:TYR:HE1	1:185:B:LEU:HB2	23	0.78
(1,2399)	1:182:B:TYR:HE2	1:185:B:LEU:HB2	23	0.78
(1,1153)	1:19:A:PHE:HD1	1:22:A:TYR:H	13	0.77
(1,1153)	1:19:A:PHE:HD2	1:22:A:TYR:H	13	0.77
(1,1225)	1:79:A:TYR:HE1	1:82:A:LEU:HB2	28	0.75
(1,1225)	1:79:A:TYR:HE2	1:82:A:LEU:HB2	28	0.75
(1,1153)	1:19:A:PHE:HD1	1:22:A:TYR:H	24	0.75
(1,1153)	1:19:A:PHE:HD2	1:22:A:TYR:H	24	0.75

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,2399)	1:182:B:TYR:HE1	1:185:B:LEU:HB2	11	0.74
(1,2399)	1:182:B:TYR:HE2	1:185:B:LEU:HB2	11	0.74
(1,2355)	1:122:B:PHE:HD1	1:125:B:TYR:H	11	0.74
(1,2355)	1:122:B:PHE:HD2	1:125:B:TYR:H	11	0.74
(1,2399)	1:182:B:TYR:HE1	1:185:B:LEU:HB2	18	0.73
(1,2399)	1:182:B:TYR:HE2	1:185:B:LEU:HB2	18	0.73
(1,2399)	1:182:B:TYR:HE1	1:185:B:LEU:HB2	1	0.72
(1,2399)	1:182:B:TYR:HE2	1:185:B:LEU:HB2	1	0.72
(1,2399)	1:182:B:TYR:HE1	1:185:B:LEU:HB2	28	0.72
(1,2399)	1:182:B:TYR:HE2	1:185:B:LEU:HB2	28	0.72
(1,2355)	1:122:B:PHE:HD1	1:125:B:TYR:H	24	0.71
(1,2355)	1:122:B:PHE:HD2	1:125:B:TYR:H	24	0.71
(1,2399)	1:182:B:TYR:HE1	1:185:B:LEU:HB2	6	0.7
(1,2399)	1:182:B:TYR:HE2	1:185:B:LEU:HB2	6	0.7
(1,2399)	1:182:B:TYR:HE1	1:185:B:LEU:HB2	21	0.69
(1,2399)	1:182:B:TYR:HE2	1:185:B:LEU:HB2	21	0.69
(1,1225)	1:79:A:TYR:HE1	1:82:A:LEU:HB2	22	0.69
(1,1225)	1:79:A:TYR:HE2	1:82:A:LEU:HB2	22	0.69
(1,1225)	1:79:A:TYR:HE1	1:82:A:LEU:HB2	23	0.69
(1,1225)	1:79:A:TYR:HE2	1:82:A:LEU:HB2	23	0.69
(1,1225)	1:79:A:TYR:HE1	1:82:A:LEU:HB2	11	0.68
(1,1225)	1:79:A:TYR:HE2	1:82:A:LEU:HB2	11	0.68
(1,1225)	1:79:A:TYR:HE1	1:82:A:LEU:HB2	9	0.67
(1,1225)	1:79:A:TYR:HE2	1:82:A:LEU:HB2	9	0.67
(1,1225)	1:79:A:TYR:HE1	1:82:A:LEU:HB2	13	0.67
(1,1225)	1:79:A:TYR:HE2	1:82:A:LEU:HB2	13	0.67
(1,1225)	1:79:A:TYR:HE1	1:82:A:LEU:HB2	17	0.67
(1,1225)	1:79:A:TYR:HE2	1:82:A:LEU:HB2	17	0.67
(1,2399)	1:182:B:TYR:HE1	1:185:B:LEU:HB2	2	0.64
(1,2399)	1:182:B:TYR:HE2	1:185:B:LEU:HB2	2	0.64
(1,2399)	1:182:B:TYR:HE1	1:185:B:LEU:HB2	7	0.63
(1,2399)	1:182:B:TYR:HE2	1:185:B:LEU:HB2	7	0.63
(1,1225)	1:79:A:TYR:HE1	1:82:A:LEU:HB2	6	0.61
(1,1225)	1:79:A:TYR:HE2	1:82:A:LEU:HB2	6	0.61
(1,2399)	1:182:B:TYR:HE1	1:185:B:LEU:HB2	19	0.6
(1,2399)	1:182:B:TYR:HE2	1:185:B:LEU:HB2	19	0.6
(1,1225)	1:79:A:TYR:HE1	1:82:A:LEU:HB2	2	0.6
(1,1225)	1:79:A:TYR:HE2	1:82:A:LEU:HB2	2	0.6
(1,1225)	1:79:A:TYR:HE1	1:82:A:LEU:HB2	1	0.58
(1,1225)	1:79:A:TYR:HE2	1:82:A:LEU:HB2	1	0.58
(1,1225)	1:79:A:TYR:HE1	1:82:A:LEU:HB2	10	0.58
(1,1225)	1:79:A:TYR:HE2	1:82:A:LEU:HB2	10	0.58

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,2399)	1:182:B:TYR:HE1	1:185:B:LEU:HB2	20	0.57
(1,2399)	1:182:B:TYR:HE2	1:185:B:LEU:HB2	20	0.57
(1,2399)	1:182:B:TYR:HE1	1:185:B:LEU:HB2	10	0.54
(1,2399)	1:182:B:TYR:HE2	1:185:B:LEU:HB2	10	0.54
(1,1225)	1:79:A:TYR:HE1	1:82:A:LEU:HB2	7	0.54
(1,1225)	1:79:A:TYR:HE2	1:82:A:LEU:HB2	7	0.54
(1,2399)	1:182:B:TYR:HE1	1:185:B:LEU:HB2	24	0.51
(1,2399)	1:182:B:TYR:HE2	1:185:B:LEU:HB2	24	0.51
(1,2399)	1:182:B:TYR:HE1	1:185:B:LEU:HB2	30	0.49
(1,2399)	1:182:B:TYR:HE2	1:185:B:LEU:HB2	30	0.49
(1,1225)	1:79:A:TYR:HE1	1:82:A:LEU:HB2	8	0.48
(1,1225)	1:79:A:TYR:HE2	1:82:A:LEU:HB2	8	0.48
(1,2399)	1:182:B:TYR:HE1	1:185:B:LEU:HB2	13	0.44
(1,2399)	1:182:B:TYR:HE2	1:185:B:LEU:HB2	13	0.44
(1,2399)	1:182:B:TYR:HE1	1:185:B:LEU:HB2	27	0.44
(1,2399)	1:182:B:TYR:HE2	1:185:B:LEU:HB2	27	0.44
(1,1225)	1:79:A:TYR:HE1	1:82:A:LEU:HB2	30	0.43
(1,1225)	1:79:A:TYR:HE2	1:82:A:LEU:HB2	30	0.43
(1,2399)	1:182:B:TYR:HE1	1:185:B:LEU:HB2	8	0.41
(1,2399)	1:182:B:TYR:HE2	1:185:B:LEU:HB2	8	0.41
(1,1225)	1:79:A:TYR:HE1	1:82:A:LEU:HB2	19	0.4
(1,1225)	1:79:A:TYR:HE2	1:82:A:LEU:HB2	19	0.4
(1,1225)	1:79:A:TYR:HE1	1:82:A:LEU:HB2	20	0.4
(1,1225)	1:79:A:TYR:HE2	1:82:A:LEU:HB2	20	0.4
(1,1199)	1:80:A:TRP:HZ2	1:183:B:TRP:HD1	27	0.36
(1,1200)	1:80:A:TRP:HD1	1:183:B:TRP:HZ2	12	0.35
(1,1200)	1:80:A:TRP:HD1	1:183:B:TRP:HZ2	14	0.35
(1,1200)	1:80:A:TRP:HD1	1:183:B:TRP:HZ2	3	0.34
(1,1199)	1:80:A:TRP:HZ2	1:183:B:TRP:HD1	3	0.34
(1,1199)	1:80:A:TRP:HZ2	1:183:B:TRP:HD1	12	0.34
(1,1199)	1:80:A:TRP:HZ2	1:183:B:TRP:HD1	14	0.34
(1,1199)	1:80:A:TRP:HZ2	1:183:B:TRP:HD1	22	0.34
(1,1199)	1:80:A:TRP:HZ2	1:183:B:TRP:HD1	24	0.34
(1,1200)	1:80:A:TRP:HD1	1:183:B:TRP:HZ2	2	0.33
(1,1200)	1:80:A:TRP:HD1	1:183:B:TRP:HZ2	18	0.33
(1,1200)	1:80:A:TRP:HD1	1:183:B:TRP:HZ2	22	0.33
(1,1200)	1:80:A:TRP:HD1	1:183:B:TRP:HZ2	23	0.33
(1,1200)	1:80:A:TRP:HD1	1:183:B:TRP:HZ2	24	0.33
(1,1200)	1:80:A:TRP:HD1	1:183:B:TRP:HZ2	25	0.33
(1,1200)	1:80:A:TRP:HD1	1:183:B:TRP:HZ2	27	0.33
(1,1200)	1:80:A:TRP:HD1	1:183:B:TRP:HZ2	29	0.33
(1,1199)	1:80:A:TRP:HZ2	1:183:B:TRP:HD1	6	0.33

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1199)	1:80:A:TRP:HZ2	1:183:B:TRP:HD1	23	0.33
(1,1199)	1:80:A:TRP:HZ2	1:183:B:TRP:HD1	29	0.33
(1,1225)	1:79:A:TYR:HE1	1:82:A:LEU:HB2	25	0.32
(1,1225)	1:79:A:TYR:HE2	1:82:A:LEU:HB2	25	0.32
(1,1200)	1:80:A:TRP:HD1	1:183:B:TRP:HZ2	1	0.32
(1,1200)	1:80:A:TRP:HD1	1:183:B:TRP:HZ2	7	0.32
(1,1200)	1:80:A:TRP:HD1	1:183:B:TRP:HZ2	10	0.32
(1,1200)	1:80:A:TRP:HD1	1:183:B:TRP:HZ2	11	0.32
(1,1200)	1:80:A:TRP:HD1	1:183:B:TRP:HZ2	16	0.32
(1,1200)	1:80:A:TRP:HD1	1:183:B:TRP:HZ2	17	0.32
(1,1200)	1:80:A:TRP:HD1	1:183:B:TRP:HZ2	19	0.32
(1,1200)	1:80:A:TRP:HD1	1:183:B:TRP:HZ2	21	0.32
(1,1200)	1:80:A:TRP:HD1	1:183:B:TRP:HZ2	30	0.32
(1,1199)	1:80:A:TRP:HZ2	1:183:B:TRP:HD1	1	0.32
(1,1199)	1:80:A:TRP:HZ2	1:183:B:TRP:HD1	2	0.32
(1,1199)	1:80:A:TRP:HZ2	1:183:B:TRP:HD1	8	0.32
(1,1199)	1:80:A:TRP:HZ2	1:183:B:TRP:HD1	10	0.32
(1,1199)	1:80:A:TRP:HZ2	1:183:B:TRP:HD1	13	0.32
(1,1199)	1:80:A:TRP:HZ2	1:183:B:TRP:HD1	16	0.32
(1,1199)	1:80:A:TRP:HZ2	1:183:B:TRP:HD1	17	0.32
(1,1199)	1:80:A:TRP:HZ2	1:183:B:TRP:HD1	19	0.32
(1,1199)	1:80:A:TRP:HZ2	1:183:B:TRP:HD1	20	0.32
(1,1199)	1:80:A:TRP:HZ2	1:183:B:TRP:HD1	21	0.32
(1,1199)	1:80:A:TRP:HZ2	1:183:B:TRP:HD1	25	0.32
(1,1199)	1:80:A:TRP:HZ2	1:183:B:TRP:HD1	30	0.32
(1,2399)	1:182:B:TYR:HE1	1:185:B:LEU:HB2	14	0.31
(1,2399)	1:182:B:TYR:HE2	1:185:B:LEU:HB2	14	0.31
(1,1225)	1:79:A:TYR:HE1	1:82:A:LEU:HB2	24	0.31
(1,1225)	1:79:A:TYR:HE2	1:82:A:LEU:HB2	24	0.31
(1,1200)	1:80:A:TRP:HD1	1:183:B:TRP:HZ2	5	0.31
(1,1200)	1:80:A:TRP:HD1	1:183:B:TRP:HZ2	6	0.31
(1,1200)	1:80:A:TRP:HD1	1:183:B:TRP:HZ2	8	0.31
(1,1200)	1:80:A:TRP:HD1	1:183:B:TRP:HZ2	9	0.31
(1,1200)	1:80:A:TRP:HD1	1:183:B:TRP:HZ2	20	0.31
(1,1200)	1:80:A:TRP:HD1	1:183:B:TRP:HZ2	28	0.31
(1,1199)	1:80:A:TRP:HZ2	1:183:B:TRP:HD1	5	0.31
(1,1199)	1:80:A:TRP:HZ2	1:183:B:TRP:HD1	7	0.31
(1,1199)	1:80:A:TRP:HZ2	1:183:B:TRP:HD1	11	0.31
(1,1199)	1:80:A:TRP:HZ2	1:183:B:TRP:HD1	18	0.31
(1,1199)	1:80:A:TRP:HZ2	1:183:B:TRP:HD1	28	0.31
(1,1853)	1:139:B:SER:HA	1:142:B:ARG:H	16	0.3
(1,1853)	1:139:B:SER:HA	1:142:B:ARG:H	23	0.3

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1200)	1:80:A:TRP:HD1	1:183:B:TRP:HZ2	13	0.3
(1,1199)	1:80:A:TRP:HZ2	1:183:B:TRP:HD1	4	0.3
(1,1199)	1:80:A:TRP:HZ2	1:183:B:TRP:HD1	9	0.3
(1,1853)	1:139:B:SER:HA	1:142:B:ARG:H	10	0.29
(1,1200)	1:80:A:TRP:HD1	1:183:B:TRP:HZ2	4	0.29
(1,1200)	1:80:A:TRP:HD1	1:183:B:TRP:HZ2	15	0.29
(1,1200)	1:80:A:TRP:HD1	1:183:B:TRP:HZ2	26	0.29
(1,1199)	1:80:A:TRP:HZ2	1:183:B:TRP:HD1	15	0.29
(1,1199)	1:80:A:TRP:HZ2	1:183:B:TRP:HD1	26	0.29
(1,561)	1:36:A:SER:HA	1:39:A:ARG:H	6	0.29
(1,561)	1:36:A:SER:HA	1:39:A:ARG:H	16	0.29
(1,1225)	1:79:A:TYR:HE1	1:82:A:LEU:HB2	14	0.28
(1,1225)	1:79:A:TYR:HE2	1:82:A:LEU:HB2	14	0.28
(1,561)	1:36:A:SER:HA	1:39:A:ARG:H	18	0.28
(1,1853)	1:139:B:SER:HA	1:142:B:ARG:H	12	0.26
(2,13)	2:209:B:CA:CA	1:135:B:LYS:O	10	0.24
(1,2399)	1:182:B:TYR:HE1	1:185:B:LEU:HB2	25	0.24
(1,2399)	1:182:B:TYR:HE2	1:185:B:LEU:HB2	25	0.24
(2,4)	2:207:A:CA:CA	1:32:A:LYS:O	10	0.22
(1,1977)	1:160:B:LYS:HB2	1:160:B:LYS:HE2	20	0.22
(1,1977)	1:160:B:LYS:HB2	1:160:B:LYS:HE3	20	0.22
(1,1977)	1:160:B:LYS:HB3	1:160:B:LYS:HE2	20	0.22
(1,1977)	1:160:B:LYS:HB3	1:160:B:LYS:HE3	20	0.22
(1,1225)	1:79:A:TYR:HE1	1:82:A:LEU:HB2	16	0.22
(1,1225)	1:79:A:TYR:HE2	1:82:A:LEU:HB2	16	0.22
(1,561)	1:36:A:SER:HA	1:39:A:ARG:H	4	0.22
(1,561)	1:36:A:SER:HA	1:39:A:ARG:H	12	0.22
(1,1853)	1:139:B:SER:HA	1:142:B:ARG:H	7	0.2
(1,1853)	1:139:B:SER:HA	1:142:B:ARG:H	27	0.2
(1,1225)	1:79:A:TYR:HE1	1:82:A:LEU:HB2	27	0.2
(1,1225)	1:79:A:TYR:HE2	1:82:A:LEU:HB2	27	0.2
(1,1977)	1:160:B:LYS:HB2	1:160:B:LYS:HE2	3	0.19
(1,1977)	1:160:B:LYS:HB2	1:160:B:LYS:HE3	3	0.19
(1,1977)	1:160:B:LYS:HB3	1:160:B:LYS:HE2	3	0.19
(1,1977)	1:160:B:LYS:HB3	1:160:B:LYS:HE3	3	0.19
(1,561)	1:36:A:SER:HA	1:39:A:ARG:H	27	0.19
(1,416)	1:42:A:LEU:HD11	1:43:A:GLN:H	27	0.18
(1,416)	1:42:A:LEU:HD12	1:43:A:GLN:H	27	0.18
(1,416)	1:42:A:LEU:HD13	1:43:A:GLN:H	27	0.18
(1,2399)	1:182:B:TYR:HE1	1:185:B:LEU:HB2	16	0.17
(1,2399)	1:182:B:TYR:HE2	1:185:B:LEU:HB2	16	0.17
(1,1853)	1:139:B:SER:HA	1:142:B:ARG:H	3	0.17

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1853)	1:139:B:SER:HA	1:142:B:ARG:H	4	0.17
(1,1844)	1:199:B:GLU:HG2	1:200:B:GLN:H	7	0.17
(1,2245)	1:143:B:GLU:H	1:143:B:GLU:HG2	26	0.16
(1,1977)	1:160:B:LYS:HB2	1:160:B:LYS:HE2	16	0.16
(1,1977)	1:160:B:LYS:HB2	1:160:B:LYS:HE3	16	0.16
(1,1977)	1:160:B:LYS:HB3	1:160:B:LYS:HE2	16	0.16
(1,1977)	1:160:B:LYS:HB3	1:160:B:LYS:HE3	16	0.16
(1,1844)	1:199:B:GLU:HG2	1:200:B:GLN:H	17	0.16
(1,683)	1:21:A:LYS:HA	1:21:A:LYS:HD2	21	0.16
(1,683)	1:21:A:LYS:HA	1:21:A:LYS:HD3	21	0.16
(1,552)	1:96:A:GLU:HG2	1:97:A:GLN:H	17	0.16
(1,552)	1:96:A:GLU:HG2	1:97:A:GLN:H	21	0.16
(1,219)	1:73:A:ARG:H	1:73:A:ARG:HD3	30	0.16
(2,4)	2:207:A:CA:CA	1:32:A:LYS:O	17	0.15
(1,1844)	1:199:B:GLU:HG2	1:200:B:GLN:H	20	0.15
(1,1602)	1:143:B:GLU:HG3	1:144:B:MET:H	12	0.15
(1,1486)	1:145:B:LEU:HG	1:146:B:GLN:H	14	0.15
(1,912)	1:97:A:GLN:HG3	1:97:A:GLN:HE21	14	0.15
(1,552)	1:96:A:GLU:HG2	1:97:A:GLN:H	5	0.15
(1,552)	1:96:A:GLU:HG2	1:97:A:GLN:H	20	0.15
(1,492)	1:44:A:LYS:H	1:44:A:LYS:HD3	3	0.15
(1,2071)	1:195:B:LYS:H	1:195:B:LYS:HG2	16	0.14
(1,1971)	1:124:B:LYS:HA	1:124:B:LYS:HD2	12	0.14
(1,1971)	1:124:B:LYS:HA	1:124:B:LYS:HD3	12	0.14
(1,1853)	1:139:B:SER:HA	1:142:B:ARG:H	21	0.14
(1,1844)	1:199:B:GLU:HG2	1:200:B:GLN:H	5	0.14
(1,1844)	1:199:B:GLU:HG2	1:200:B:GLN:H	21	0.14
(1,1833)	1:147:B:LYS:HA	1:147:B:LYS:HD2	13	0.14
(1,987)	1:40:A:GLU:H	1:40:A:GLU:HG2	26	0.14
(1,937)	1:97:A:GLN:HG2	1:98:A:GLU:H	23	0.14
(1,912)	1:97:A:GLN:HG3	1:97:A:GLN:HE21	12	0.14
(1,912)	1:97:A:GLN:HG3	1:97:A:GLN:HE21	30	0.14
(1,701)	1:90:A:ILE:HA	1:90:A:ILE:HD11	27	0.14
(1,701)	1:90:A:ILE:HA	1:90:A:ILE:HD12	27	0.14
(1,701)	1:90:A:ILE:HA	1:90:A:ILE:HD13	27	0.14
(1,689)	1:57:A:LYS:HB2	1:57:A:LYS:HE2	16	0.14
(1,689)	1:57:A:LYS:HB2	1:57:A:LYS:HE3	16	0.14
(1,689)	1:57:A:LYS:HB3	1:57:A:LYS:HE2	16	0.14
(1,689)	1:57:A:LYS:HB3	1:57:A:LYS:HE3	16	0.14
(1,683)	1:21:A:LYS:HA	1:21:A:LYS:HD2	12	0.14
(1,683)	1:21:A:LYS:HA	1:21:A:LYS:HD3	12	0.14
(1,552)	1:96:A:GLU:HG2	1:97:A:GLN:H	6	0.14

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,541)	1:44:A:LYS:HA	1:44:A:LYS:HD2	24	0.14
(1,541)	1:44:A:LYS:HA	1:44:A:LYS:HD2	27	0.14
(1,305)	1:40:A:GLU:HG3	1:41:A:MET:H	12	0.14
(1,2199)	1:200:B:GLN:HG2	1:201:B:GLU:H	2	0.13
(1,2174)	1:200:B:GLN:HG3	1:200:B:GLN:HE21	5	0.13
(1,2174)	1:200:B:GLN:HG3	1:200:B:GLN:HE21	25	0.13
(1,2174)	1:200:B:GLN:HG3	1:200:B:GLN:HE21	27	0.13
(1,1989)	1:193:B:ILE:HA	1:193:B:ILE:HD11	27	0.13
(1,1989)	1:193:B:ILE:HA	1:193:B:ILE:HD12	27	0.13
(1,1989)	1:193:B:ILE:HA	1:193:B:ILE:HD13	27	0.13
(1,1977)	1:160:B:LYS:HB2	1:160:B:LYS:HE2	17	0.13
(1,1977)	1:160:B:LYS:HB2	1:160:B:LYS:HE3	17	0.13
(1,1977)	1:160:B:LYS:HB3	1:160:B:LYS:HE2	17	0.13
(1,1977)	1:160:B:LYS:HB3	1:160:B:LYS:HE3	17	0.13
(1,1977)	1:160:B:LYS:HB2	1:160:B:LYS:HE2	18	0.13
(1,1977)	1:160:B:LYS:HB2	1:160:B:LYS:HE3	18	0.13
(1,1977)	1:160:B:LYS:HB3	1:160:B:LYS:HE2	18	0.13
(1,1977)	1:160:B:LYS:HB3	1:160:B:LYS:HE3	18	0.13
(1,1833)	1:147:B:LYS:HA	1:147:B:LYS:HD2	8	0.13
(1,1748)	1:160:B:LYS:HD2	1:161:B:ALA:H	17	0.13
(1,1748)	1:160:B:LYS:HD3	1:161:B:ALA:H	17	0.13
(1,1711)	1:145:B:LEU:HD11	1:146:B:GLN:H	20	0.13
(1,1711)	1:145:B:LEU:HD12	1:146:B:GLN:H	20	0.13
(1,1711)	1:145:B:LEU:HD13	1:146:B:GLN:H	20	0.13
(1,1520)	1:176:B:ARG:H	1:176:B:ARG:HD3	30	0.13
(1,1480)	1:204:B:SER:H	1:205:B:SER:H	16	0.13
(1,912)	1:97:A:GLN:HG3	1:97:A:GLN:HE21	27	0.13
(1,711)	1:30:A:LYS:HG2	1:31:A:ASN:H	27	0.13
(1,689)	1:57:A:LYS:HB2	1:57:A:LYS:HE2	3	0.13
(1,689)	1:57:A:LYS:HB2	1:57:A:LYS:HE3	3	0.13
(1,689)	1:57:A:LYS:HB3	1:57:A:LYS:HE2	3	0.13
(1,689)	1:57:A:LYS:HB3	1:57:A:LYS:HE3	3	0.13
(1,689)	1:57:A:LYS:HB2	1:57:A:LYS:HE2	23	0.13
(1,689)	1:57:A:LYS:HB2	1:57:A:LYS:HE3	23	0.13
(1,689)	1:57:A:LYS:HB3	1:57:A:LYS:HE2	23	0.13
(1,689)	1:57:A:LYS:HB3	1:57:A:LYS:HE3	23	0.13
(1,683)	1:21:A:LYS:HA	1:21:A:LYS:HD2	9	0.13
(1,683)	1:21:A:LYS:HA	1:21:A:LYS:HD3	9	0.13
(1,561)	1:36:A:SER:HA	1:39:A:ARG:H	17	0.13
(1,453)	1:43:A:GLN:HG2	1:43:A:GLN:HE22	4	0.13
(1,452)	1:43:A:GLN:H	1:43:A:GLN:HG2	24	0.13
(1,403)	1:50:A:LEU:HG	1:51:A:SER:H	3	0.13

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,13)	2:209:B:CA:CA	1:135:B:LYS:O	14	0.12
(2,12)	2:209:B:CA:CA	1:131:B:LEU:O	5	0.12
(2,4)	2:207:A:CA:CA	1:32:A:LYS:O	14	0.12
(2,3)	2:207:A:CA:CA	1:28:A:LEU:O	5	0.12
(1,2399)	1:182:B:TYR:HE1	1:185:B:LEU:HB2	15	0.12
(1,2399)	1:182:B:TYR:HE2	1:185:B:LEU:HB2	15	0.12
(1,2007)	1:123:B:TYR:HA	1:126:B:VAL:HG21	22	0.12
(1,2007)	1:123:B:TYR:HA	1:126:B:VAL:HG22	22	0.12
(1,2007)	1:123:B:TYR:HA	1:126:B:VAL:HG23	22	0.12
(1,1989)	1:193:B:ILE:HA	1:193:B:ILE:HD11	2	0.12
(1,1989)	1:193:B:ILE:HA	1:193:B:ILE:HD12	2	0.12
(1,1989)	1:193:B:ILE:HA	1:193:B:ILE:HD13	2	0.12
(1,1989)	1:193:B:ILE:HA	1:193:B:ILE:HD11	12	0.12
(1,1989)	1:193:B:ILE:HA	1:193:B:ILE:HD12	12	0.12
(1,1989)	1:193:B:ILE:HA	1:193:B:ILE:HD13	12	0.12
(1,1989)	1:193:B:ILE:HA	1:193:B:ILE:HD11	16	0.12
(1,1989)	1:193:B:ILE:HA	1:193:B:ILE:HD12	16	0.12
(1,1989)	1:193:B:ILE:HA	1:193:B:ILE:HD13	16	0.12
(1,1989)	1:193:B:ILE:HA	1:193:B:ILE:HD11	22	0.12
(1,1989)	1:193:B:ILE:HA	1:193:B:ILE:HD12	22	0.12
(1,1989)	1:193:B:ILE:HA	1:193:B:ILE:HD13	22	0.12
(1,1989)	1:193:B:ILE:HA	1:193:B:ILE:HD11	25	0.12
(1,1989)	1:193:B:ILE:HA	1:193:B:ILE:HD12	25	0.12
(1,1989)	1:193:B:ILE:HA	1:193:B:ILE:HD13	25	0.12
(1,1989)	1:193:B:ILE:HA	1:193:B:ILE:HD11	26	0.12
(1,1989)	1:193:B:ILE:HA	1:193:B:ILE:HD12	26	0.12
(1,1989)	1:193:B:ILE:HA	1:193:B:ILE:HD13	26	0.12
(1,1971)	1:124:B:LYS:HA	1:124:B:LYS:HD2	17	0.12
(1,1971)	1:124:B:LYS:HA	1:124:B:LYS:HD3	17	0.12
(1,1969)	1:147:B:LYS:HG2	1:148:B:GLU:H	18	0.12
(1,1943)	1:143:B:GLU:HA	1:146:B:GLN:HB3	23	0.12
(1,1926)	1:204:B:SER:H	1:204:B:SER:HB2	14	0.12
(1,1926)	1:204:B:SER:H	1:204:B:SER:HB3	14	0.12
(1,1886)	1:161:B:ALA:HA	1:163:B:ASP:H	14	0.12
(1,1844)	1:199:B:GLU:HG2	1:200:B:GLN:H	15	0.12
(1,1844)	1:199:B:GLU:HG2	1:200:B:GLN:H	25	0.12
(1,1833)	1:147:B:LYS:HA	1:147:B:LYS:HD2	9	0.12
(1,1801)	1:186:B:ILE:H	1:186:B:ILE:HD11	12	0.12
(1,1801)	1:186:B:ILE:H	1:186:B:ILE:HD12	12	0.12
(1,1801)	1:186:B:ILE:H	1:186:B:ILE:HD13	12	0.12
(1,1784)	1:147:B:LYS:H	1:147:B:LYS:HD3	15	0.12
(1,1748)	1:160:B:LYS:HD2	1:161:B:ALA:H	18	0.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1748)	1:160:B:LYS:HD3	1:161:B:ALA:H	18	0.12
(1,1748)	1:160:B:LYS:HD2	1:161:B:ALA:H	24	0.12
(1,1748)	1:160:B:LYS:HD3	1:161:B:ALA:H	24	0.12
(1,1564)	1:133:B:LYS:H	1:133:B:LYS:HG3	22	0.12
(1,1533)	1:196:B:LEU:H	1:196:B:LEU:HG	26	0.12
(1,912)	1:97:A:GLN:HG3	1:97:A:GLN:HE21	5	0.12
(1,912)	1:97:A:GLN:HG3	1:97:A:GLN:HE21	6	0.12
(1,785)	1:92:A:LYS:H	1:92:A:LYS:HG2	16	0.12
(1,777)	1:53:A:THR:HA	1:56:A:ARG:HD2	30	0.12
(1,701)	1:90:A:ILE:HA	1:90:A:ILE:HD11	2	0.12
(1,701)	1:90:A:ILE:HA	1:90:A:ILE:HD12	2	0.12
(1,701)	1:90:A:ILE:HA	1:90:A:ILE:HD13	2	0.12
(1,701)	1:90:A:ILE:HA	1:90:A:ILE:HD11	9	0.12
(1,701)	1:90:A:ILE:HA	1:90:A:ILE:HD12	9	0.12
(1,701)	1:90:A:ILE:HA	1:90:A:ILE:HD13	9	0.12
(1,701)	1:90:A:ILE:HA	1:90:A:ILE:HD11	12	0.12
(1,701)	1:90:A:ILE:HA	1:90:A:ILE:HD12	12	0.12
(1,701)	1:90:A:ILE:HA	1:90:A:ILE:HD13	12	0.12
(1,701)	1:90:A:ILE:HA	1:90:A:ILE:HD11	16	0.12
(1,701)	1:90:A:ILE:HA	1:90:A:ILE:HD12	16	0.12
(1,701)	1:90:A:ILE:HA	1:90:A:ILE:HD13	16	0.12
(1,701)	1:90:A:ILE:HA	1:90:A:ILE:HD11	22	0.12
(1,701)	1:90:A:ILE:HA	1:90:A:ILE:HD12	22	0.12
(1,701)	1:90:A:ILE:HA	1:90:A:ILE:HD13	22	0.12
(1,701)	1:90:A:ILE:HA	1:90:A:ILE:HD11	25	0.12
(1,701)	1:90:A:ILE:HA	1:90:A:ILE:HD12	25	0.12
(1,701)	1:90:A:ILE:HA	1:90:A:ILE:HD13	25	0.12
(1,701)	1:90:A:ILE:HA	1:90:A:ILE:HD11	26	0.12
(1,701)	1:90:A:ILE:HA	1:90:A:ILE:HD12	26	0.12
(1,701)	1:90:A:ILE:HA	1:90:A:ILE:HD13	26	0.12
(1,683)	1:21:A:LYS:HA	1:21:A:LYS:HD2	16	0.12
(1,683)	1:21:A:LYS:HA	1:21:A:LYS:HD3	16	0.12
(1,683)	1:21:A:LYS:HA	1:21:A:LYS:HD2	24	0.12
(1,683)	1:21:A:LYS:HA	1:21:A:LYS:HD3	24	0.12
(1,637)	1:101:A:SER:H	1:101:A:SER:HB2	14	0.12
(1,637)	1:101:A:SER:H	1:101:A:SER:HB3	14	0.12
(1,561)	1:36:A:SER:HA	1:39:A:ARG:H	5	0.12
(1,552)	1:96:A:GLU:HG2	1:97:A:GLN:H	7	0.12
(1,552)	1:96:A:GLU:HG2	1:97:A:GLN:H	9	0.12
(1,552)	1:96:A:GLU:HG2	1:97:A:GLN:H	22	0.12
(1,552)	1:96:A:GLU:HG2	1:97:A:GLN:H	30	0.12
(1,509)	1:83:A:ILE:H	1:83:A:ILE:HD11	12	0.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,509)	1:83:A:ILE:H	1:83:A:ILE:HD12	12	0.12
(1,509)	1:83:A:ILE:H	1:83:A:ILE:HD13	12	0.12
(1,455)	1:57:A:LYS:HD2	1:58:A:ALA:H	24	0.12
(1,455)	1:57:A:LYS:HD3	1:58:A:ALA:H	24	0.12
(1,453)	1:43:A:GLN:HG2	1:43:A:GLN:HE22	29	0.12
(1,451)	1:43:A:GLN:HB3	1:43:A:GLN:HG2	17	0.12
(1,416)	1:42:A:LEU:HD11	1:43:A:GLN:H	5	0.12
(1,416)	1:42:A:LEU:HD12	1:43:A:GLN:H	5	0.12
(1,416)	1:42:A:LEU:HD13	1:43:A:GLN:H	5	0.12
(1,407)	1:53:A:THR:HB	1:54:A:GLY:H	29	0.12
(1,188)	1:94:A:ILE:HA	1:97:A:GLN:HE21	24	0.12
(1,2245)	1:143:B:GLU:H	1:143:B:GLU:HG2	27	0.11
(1,2174)	1:200:B:GLN:HG3	1:200:B:GLN:HE21	7	0.11
(1,2174)	1:200:B:GLN:HG3	1:200:B:GLN:HE21	18	0.11
(1,2116)	1:165:B:LEU:HD21	1:166:B:ILE:H	13	0.11
(1,2116)	1:165:B:LEU:HD22	1:166:B:ILE:H	13	0.11
(1,2116)	1:165:B:LEU:HD23	1:166:B:ILE:H	13	0.11
(1,2116)	1:165:B:LEU:HD21	1:166:B:ILE:H	14	0.11
(1,2116)	1:165:B:LEU:HD22	1:166:B:ILE:H	14	0.11
(1,2116)	1:165:B:LEU:HD23	1:166:B:ILE:H	14	0.11
(1,1989)	1:193:B:ILE:HA	1:193:B:ILE:HD11	9	0.11
(1,1989)	1:193:B:ILE:HA	1:193:B:ILE:HD12	9	0.11
(1,1989)	1:193:B:ILE:HA	1:193:B:ILE:HD13	9	0.11
(1,1989)	1:193:B:ILE:HA	1:193:B:ILE:HD11	13	0.11
(1,1989)	1:193:B:ILE:HA	1:193:B:ILE:HD12	13	0.11
(1,1989)	1:193:B:ILE:HA	1:193:B:ILE:HD13	13	0.11
(1,1989)	1:193:B:ILE:HA	1:193:B:ILE:HD11	14	0.11
(1,1989)	1:193:B:ILE:HA	1:193:B:ILE:HD12	14	0.11
(1,1989)	1:193:B:ILE:HA	1:193:B:ILE:HD13	14	0.11
(1,1989)	1:193:B:ILE:HA	1:193:B:ILE:HD11	17	0.11
(1,1989)	1:193:B:ILE:HA	1:193:B:ILE:HD12	17	0.11
(1,1989)	1:193:B:ILE:HA	1:193:B:ILE:HD13	17	0.11
(1,1989)	1:193:B:ILE:HA	1:193:B:ILE:HD11	24	0.11
(1,1989)	1:193:B:ILE:HA	1:193:B:ILE:HD12	24	0.11
(1,1989)	1:193:B:ILE:HA	1:193:B:ILE:HD13	24	0.11
(1,1989)	1:193:B:ILE:HA	1:193:B:ILE:HD11	28	0.11
(1,1989)	1:193:B:ILE:HA	1:193:B:ILE:HD12	28	0.11
(1,1989)	1:193:B:ILE:HA	1:193:B:ILE:HD13	28	0.11
(1,1971)	1:124:B:LYS:HA	1:124:B:LYS:HD2	25	0.11
(1,1971)	1:124:B:LYS:HA	1:124:B:LYS:HD3	25	0.11
(1,1971)	1:124:B:LYS:HA	1:124:B:LYS:HD2	29	0.11
(1,1971)	1:124:B:LYS:HA	1:124:B:LYS:HD3	29	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1938)	1:109:B:THR:HG21	1:110:B:GLU:H	4	0.11
(1,1938)	1:109:B:THR:HG22	1:110:B:GLU:H	4	0.11
(1,1938)	1:109:B:THR:HG23	1:110:B:GLU:H	4	0.11
(1,1853)	1:139:B:SER:HA	1:142:B:ARG:H	22	0.11
(1,1844)	1:199:B:GLU:HG2	1:200:B:GLN:H	6	0.11
(1,1844)	1:199:B:GLU:HG2	1:200:B:GLN:H	13	0.11
(1,1844)	1:199:B:GLU:HG2	1:200:B:GLN:H	22	0.11
(1,1844)	1:199:B:GLU:HG2	1:200:B:GLN:H	30	0.11
(1,1833)	1:147:B:LYS:HA	1:147:B:LYS:HD2	20	0.11
(1,1784)	1:147:B:LYS:H	1:147:B:LYS:HD3	11	0.11
(1,1746)	1:146:B:GLN:HG2	1:146:B:GLN:HE22	10	0.11
(1,1744)	1:146:B:GLN:HB3	1:146:B:GLN:HG2	17	0.11
(1,1711)	1:145:B:LEU:HD11	1:146:B:GLN:H	10	0.11
(1,1711)	1:145:B:LEU:HD12	1:146:B:GLN:H	10	0.11
(1,1711)	1:145:B:LEU:HD13	1:146:B:GLN:H	10	0.11
(1,1698)	1:153:B:LEU:HG	1:154:B:SER:H	22	0.11
(1,1615)	1:166:B:ILE:HA	1:166:B:ILE:HD11	25	0.11
(1,1615)	1:166:B:ILE:HA	1:166:B:ILE:HD12	25	0.11
(1,1615)	1:166:B:ILE:HA	1:166:B:ILE:HD13	25	0.11
(1,1527)	1:111:B:LEU:HD21	1:112:B:GLU:H	17	0.11
(1,1527)	1:111:B:LEU:HD22	1:112:B:GLU:H	17	0.11
(1,1527)	1:111:B:LEU:HD23	1:112:B:GLU:H	17	0.11
(1,1435)	1:113:B:LYS:H	1:113:B:LYS:HD3	29	0.11
(1,1288)	1:95:A:HIS:HD2	1:98:A:GLU:H	20	0.11
(1,962)	1:30:A:LYS:HG3	1:31:A:ASN:H	14	0.11
(1,937)	1:97:A:GLN:HG2	1:98:A:GLU:H	2	0.11
(1,937)	1:97:A:GLN:HG2	1:98:A:GLU:H	3	0.11
(1,912)	1:97:A:GLN:HG3	1:97:A:GLN:HE21	9	0.11
(1,912)	1:97:A:GLN:HG3	1:97:A:GLN:HE21	11	0.11
(1,912)	1:97:A:GLN:HG3	1:97:A:GLN:HE21	25	0.11
(1,899)	1:64:A:GLN:HA	1:64:A:GLN:HE22	9	0.11
(1,846)	1:62:A:LEU:HD21	1:63:A:ILE:H	13	0.11
(1,846)	1:62:A:LEU:HD22	1:63:A:ILE:H	13	0.11
(1,846)	1:62:A:LEU:HD23	1:63:A:ILE:H	13	0.11
(1,818)	1:30:A:LYS:HB2	1:31:A:ASN:H	11	0.11
(1,815)	1:43:A:GLN:H	1:43:A:GLN:HG3	21	0.11
(1,785)	1:92:A:LYS:H	1:92:A:LYS:HG2	10	0.11
(1,778)	1:53:A:THR:HA	1:56:A:ARG:HB3	24	0.11
(1,757)	1:96:A:GLU:HG3	1:97:A:GLN:H	20	0.11
(1,701)	1:90:A:ILE:HA	1:90:A:ILE:HD11	4	0.11
(1,701)	1:90:A:ILE:HA	1:90:A:ILE:HD12	4	0.11
(1,701)	1:90:A:ILE:HA	1:90:A:ILE:HD13	4	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,701)	1:90:A:ILE:HA	1:90:A:ILE:HD11	13	0.11
(1,701)	1:90:A:ILE:HA	1:90:A:ILE:HD12	13	0.11
(1,701)	1:90:A:ILE:HA	1:90:A:ILE:HD13	13	0.11
(1,701)	1:90:A:ILE:HA	1:90:A:ILE:HD11	14	0.11
(1,701)	1:90:A:ILE:HA	1:90:A:ILE:HD12	14	0.11
(1,701)	1:90:A:ILE:HA	1:90:A:ILE:HD13	14	0.11
(1,701)	1:90:A:ILE:HA	1:90:A:ILE:HD11	17	0.11
(1,701)	1:90:A:ILE:HA	1:90:A:ILE:HD12	17	0.11
(1,701)	1:90:A:ILE:HA	1:90:A:ILE:HD13	17	0.11
(1,701)	1:90:A:ILE:HA	1:90:A:ILE:HD11	24	0.11
(1,701)	1:90:A:ILE:HA	1:90:A:ILE:HD12	24	0.11
(1,701)	1:90:A:ILE:HA	1:90:A:ILE:HD13	24	0.11
(1,701)	1:90:A:ILE:HA	1:90:A:ILE:HD11	28	0.11
(1,701)	1:90:A:ILE:HA	1:90:A:ILE:HD12	28	0.11
(1,701)	1:90:A:ILE:HA	1:90:A:ILE:HD13	28	0.11
(1,681)	1:44:A:LYS:HG2	1:45:A:GLU:H	18	0.11
(1,595)	1:58:A:ALA:HA	1:60:A:ASP:H	14	0.11
(1,561)	1:36:A:SER:HA	1:39:A:ARG:H	1	0.11
(1,561)	1:36:A:SER:HA	1:39:A:ARG:H	22	0.11
(1,552)	1:96:A:GLU:HG2	1:97:A:GLN:H	1	0.11
(1,552)	1:96:A:GLU:HG2	1:97:A:GLN:H	2	0.11
(1,552)	1:96:A:GLU:HG2	1:97:A:GLN:H	13	0.11
(1,552)	1:96:A:GLU:HG2	1:97:A:GLN:H	25	0.11
(1,552)	1:96:A:GLU:HG2	1:97:A:GLN:H	28	0.11
(1,552)	1:96:A:GLU:HG2	1:97:A:GLN:H	29	0.11
(1,541)	1:44:A:LYS:HA	1:44:A:LYS:HD2	9	0.11
(1,492)	1:44:A:LYS:H	1:44:A:LYS:HD3	11	0.11
(1,455)	1:57:A:LYS:HD2	1:58:A:ALA:H	3	0.11
(1,455)	1:57:A:LYS:HD3	1:58:A:ALA:H	3	0.11
(1,455)	1:57:A:LYS:HD2	1:58:A:ALA:H	12	0.11
(1,455)	1:57:A:LYS:HD3	1:58:A:ALA:H	12	0.11
(1,455)	1:57:A:LYS:HD2	1:58:A:ALA:H	30	0.11
(1,455)	1:57:A:LYS:HD3	1:58:A:ALA:H	30	0.11
(1,453)	1:43:A:GLN:HG2	1:43:A:GLN:HE22	11	0.11
(1,453)	1:43:A:GLN:HG2	1:43:A:GLN:HE22	26	0.11
(1,451)	1:43:A:GLN:HB3	1:43:A:GLN:HG2	10	0.11
(1,451)	1:43:A:GLN:HB3	1:43:A:GLN:HG2	13	0.11
(1,451)	1:43:A:GLN:HB3	1:43:A:GLN:HG2	15	0.11
(1,451)	1:43:A:GLN:HB3	1:43:A:GLN:HG2	21	0.11
(1,451)	1:43:A:GLN:HB3	1:43:A:GLN:HG2	23	0.11
(1,416)	1:42:A:LEU:HD11	1:43:A:GLN:H	30	0.11
(1,416)	1:42:A:LEU:HD12	1:43:A:GLN:H	30	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,416)	1:42:A:LEU:HD13	1:43:A:GLN:H	30	0.11
(1,342)	1:43:A:GLN:HB2	1:43:A:GLN:HE21	24	0.11
(1,328)	1:21:A:LYS:HB3	1:21:A:LYS:HE2	5	0.11
(1,328)	1:21:A:LYS:HB3	1:21:A:LYS:HE3	5	0.11
(1,318)	1:63:A:ILE:HA	1:63:A:ILE:HD11	27	0.11
(1,318)	1:63:A:ILE:HA	1:63:A:ILE:HD12	27	0.11
(1,318)	1:63:A:ILE:HA	1:63:A:ILE:HD13	27	0.11
(1,314)	1:21:A:LYS:HB3	1:21:A:LYS:HD2	26	0.11
(1,314)	1:21:A:LYS:HB3	1:21:A:LYS:HD3	26	0.11
(1,298)	1:11:A:ALA:HB1	1:14:A:VAL:H	28	0.11
(1,298)	1:11:A:ALA:HB2	1:14:A:VAL:H	28	0.11
(1,298)	1:11:A:ALA:HB3	1:14:A:VAL:H	28	0.11
(1,232)	1:93:A:LEU:H	1:93:A:LEU:HG	11	0.11
(1,232)	1:93:A:LEU:H	1:93:A:LEU:HG	14	0.11
(1,232)	1:93:A:LEU:H	1:93:A:LEU:HG	16	0.11
(1,232)	1:93:A:LEU:H	1:93:A:LEU:HG	26	0.11
(1,226)	1:8:A:LEU:HD21	1:9:A:GLU:H	17	0.11
(1,226)	1:8:A:LEU:HD22	1:9:A:GLU:H	17	0.11
(1,226)	1:8:A:LEU:HD23	1:9:A:GLU:H	17	0.11
(1,185)	1:42:A:LEU:HG	1:43:A:GLN:H	14	0.11
(1,179)	1:101:A:SER:H	1:102:A:SER:H	16	0.11
(2,13)	2:209:B:CA:CA	1:135:B:LYS:O	15	0.1
(1,2417)	1:198:B:HIS:HD2	1:201:B:GLU:H	2	0.1
(1,2270)	1:149:B:LEU:HB2	1:186:B:ILE:HD11	7	0.1
(1,2270)	1:149:B:LEU:HB2	1:186:B:ILE:HD12	7	0.1
(1,2270)	1:149:B:LEU:HB2	1:186:B:ILE:HD13	7	0.1
(1,2199)	1:200:B:GLN:HG2	1:201:B:GLU:H	23	0.1
(1,2196)	1:164:B:LYS:HG2	1:165:B:LEU:H	20	0.1
(1,2116)	1:165:B:LEU:HD21	1:166:B:ILE:H	24	0.1
(1,2116)	1:165:B:LEU:HD22	1:166:B:ILE:H	24	0.1
(1,2116)	1:165:B:LEU:HD23	1:166:B:ILE:H	24	0.1
(1,2103)	1:133:B:LYS:HB2	1:134:B:ASN:H	11	0.1
(1,2071)	1:195:B:LYS:H	1:195:B:LYS:HG2	26	0.1
(1,2044)	1:199:B:GLU:HG3	1:200:B:GLN:H	6	0.1
(1,1989)	1:193:B:ILE:HA	1:193:B:ILE:HD11	4	0.1
(1,1989)	1:193:B:ILE:HA	1:193:B:ILE:HD12	4	0.1
(1,1989)	1:193:B:ILE:HA	1:193:B:ILE:HD13	4	0.1
(1,1989)	1:193:B:ILE:HA	1:193:B:ILE:HD11	7	0.1
(1,1989)	1:193:B:ILE:HA	1:193:B:ILE:HD12	7	0.1
(1,1989)	1:193:B:ILE:HA	1:193:B:ILE:HD13	7	0.1
(1,1971)	1:124:B:LYS:HA	1:124:B:LYS:HD2	5	0.1
(1,1971)	1:124:B:LYS:HA	1:124:B:LYS:HD3	5	0.1

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1971)	1:124:B:LYS:HA	1:124:B:LYS:HD2	19	0.1
(1,1971)	1:124:B:LYS:HA	1:124:B:LYS:HD3	19	0.1
(1,1971)	1:124:B:LYS:HA	1:124:B:LYS:HD2	23	0.1
(1,1971)	1:124:B:LYS:HA	1:124:B:LYS:HD3	23	0.1
(1,1947)	1:158:B:ASN:HB3	1:161:B:ALA:HB1	7	0.1
(1,1947)	1:158:B:ASN:HB3	1:161:B:ALA:HB2	7	0.1
(1,1947)	1:158:B:ASN:HB3	1:161:B:ALA:HB3	7	0.1
(1,1943)	1:143:B:GLU:HA	1:146:B:GLN:HB3	1	0.1
(1,1938)	1:109:B:THR:HG21	1:110:B:GLU:H	22	0.1
(1,1938)	1:109:B:THR:HG22	1:110:B:GLU:H	22	0.1
(1,1938)	1:109:B:THR:HG23	1:110:B:GLU:H	22	0.1
(1,1926)	1:204:B:SER:H	1:204:B:SER:HB2	21	0.1
(1,1926)	1:204:B:SER:H	1:204:B:SER:HB3	21	0.1
(1,1853)	1:139:B:SER:HA	1:142:B:ARG:H	29	0.1
(1,1844)	1:199:B:GLU:HG2	1:200:B:GLN:H	1	0.1
(1,1844)	1:199:B:GLU:HG2	1:200:B:GLN:H	9	0.1
(1,1748)	1:160:B:LYS:HD2	1:161:B:ALA:H	16	0.1
(1,1748)	1:160:B:LYS:HD3	1:161:B:ALA:H	16	0.1
(1,1746)	1:146:B:GLN:HG2	1:146:B:GLN:HE22	4	0.1
(1,1746)	1:146:B:GLN:HG2	1:146:B:GLN:HE22	11	0.1
(1,1746)	1:146:B:GLN:HG2	1:146:B:GLN:HE22	23	0.1
(1,1744)	1:146:B:GLN:HB3	1:146:B:GLN:HG2	4	0.1
(1,1711)	1:145:B:LEU:HD11	1:146:B:GLN:H	6	0.1
(1,1711)	1:145:B:LEU:HD12	1:146:B:GLN:H	6	0.1
(1,1711)	1:145:B:LEU:HD13	1:146:B:GLN:H	6	0.1
(1,1711)	1:145:B:LEU:HD11	1:146:B:GLN:H	13	0.1
(1,1711)	1:145:B:LEU:HD12	1:146:B:GLN:H	13	0.1
(1,1711)	1:145:B:LEU:HD13	1:146:B:GLN:H	13	0.1
(1,1711)	1:145:B:LEU:HD11	1:146:B:GLN:H	27	0.1
(1,1711)	1:145:B:LEU:HD12	1:146:B:GLN:H	27	0.1
(1,1711)	1:145:B:LEU:HD13	1:146:B:GLN:H	27	0.1
(1,1702)	1:156:B:THR:HB	1:157:B:GLY:H	29	0.1
(1,1615)	1:166:B:ILE:HA	1:166:B:ILE:HD11	3	0.1
(1,1615)	1:166:B:ILE:HA	1:166:B:ILE:HD12	3	0.1
(1,1615)	1:166:B:ILE:HA	1:166:B:ILE:HD13	3	0.1
(1,1615)	1:166:B:ILE:HA	1:166:B:ILE:HD11	8	0.1
(1,1615)	1:166:B:ILE:HA	1:166:B:ILE:HD12	8	0.1
(1,1615)	1:166:B:ILE:HA	1:166:B:ILE:HD13	8	0.1
(1,1615)	1:166:B:ILE:HA	1:166:B:ILE:HD11	27	0.1
(1,1615)	1:166:B:ILE:HA	1:166:B:ILE:HD12	27	0.1
(1,1615)	1:166:B:ILE:HA	1:166:B:ILE:HD13	27	0.1
(1,1595)	1:114:B:ALA:HB1	1:117:B:VAL:H	7	0.1

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1595)	1:114:B:ALA:HB2	1:117:B:VAL:H	7	0.1
(1,1595)	1:114:B:ALA:HB3	1:117:B:VAL:H	7	0.1
(1,1595)	1:114:B:ALA:HB1	1:117:B:VAL:H	8	0.1
(1,1595)	1:114:B:ALA:HB2	1:117:B:VAL:H	8	0.1
(1,1595)	1:114:B:ALA:HB3	1:117:B:VAL:H	8	0.1
(1,1595)	1:114:B:ALA:HB1	1:117:B:VAL:H	16	0.1
(1,1595)	1:114:B:ALA:HB2	1:117:B:VAL:H	16	0.1
(1,1595)	1:114:B:ALA:HB3	1:117:B:VAL:H	16	0.1
(1,1533)	1:196:B:LEU:H	1:196:B:LEU:HG	4	0.1
(1,1533)	1:196:B:LEU:H	1:196:B:LEU:HG	16	0.1
(1,1533)	1:196:B:LEU:H	1:196:B:LEU:HG	23	0.1
(1,1489)	1:197:B:ILE:HA	1:200:B:GLN:HE21	21	0.1
(1,1288)	1:95:A:HIS:HD2	1:98:A:GLU:H	9	0.1
(1,987)	1:40:A:GLU:H	1:40:A:GLU:HG2	27	0.1
(1,937)	1:97:A:GLN:HG2	1:98:A:GLU:H	6	0.1
(1,912)	1:97:A:GLN:HG3	1:97:A:GLN:HE21	7	0.1
(1,912)	1:97:A:GLN:HG3	1:97:A:GLN:HE21	29	0.1
(1,846)	1:62:A:LEU:HD21	1:63:A:ILE:H	5	0.1
(1,846)	1:62:A:LEU:HD22	1:63:A:ILE:H	5	0.1
(1,846)	1:62:A:LEU:HD23	1:63:A:ILE:H	5	0.1
(1,846)	1:62:A:LEU:HD21	1:63:A:ILE:H	18	0.1
(1,846)	1:62:A:LEU:HD22	1:63:A:ILE:H	18	0.1
(1,846)	1:62:A:LEU:HD23	1:63:A:ILE:H	18	0.1
(1,806)	1:99:A:GLN:HB2	1:100:A:GLN:H	28	0.1
(1,721)	1:56:A:ARG:HA	1:56:A:ARG:HD3	15	0.1
(1,701)	1:90:A:ILE:HA	1:90:A:ILE:HD11	11	0.1
(1,701)	1:90:A:ILE:HA	1:90:A:ILE:HD12	11	0.1
(1,701)	1:90:A:ILE:HA	1:90:A:ILE:HD13	11	0.1
(1,683)	1:21:A:LYS:HA	1:21:A:LYS:HD2	17	0.1
(1,683)	1:21:A:LYS:HA	1:21:A:LYS:HD3	17	0.1
(1,683)	1:21:A:LYS:HA	1:21:A:LYS:HD2	23	0.1
(1,683)	1:21:A:LYS:HA	1:21:A:LYS:HD3	23	0.1
(1,677)	1:10:A:LYS:HA	1:10:A:LYS:HD2	20	0.1
(1,655)	1:40:A:GLU:HA	1:43:A:GLN:HB3	8	0.1
(1,582)	1:64:A:GLN:HA	1:64:A:GLN:HG3	22	0.1
(1,455)	1:57:A:LYS:HD2	1:58:A:ALA:H	1	0.1
(1,455)	1:57:A:LYS:HD3	1:58:A:ALA:H	1	0.1
(1,451)	1:43:A:GLN:HB3	1:43:A:GLN:HG2	9	0.1
(1,451)	1:43:A:GLN:HB3	1:43:A:GLN:HG2	22	0.1
(1,451)	1:43:A:GLN:HB3	1:43:A:GLN:HG2	30	0.1
(1,342)	1:43:A:GLN:HB2	1:43:A:GLN:HE21	21	0.1
(1,318)	1:63:A:ILE:HA	1:63:A:ILE:HD11	1	0.1

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,318)	1:63:A:ILE:HA	1:63:A:ILE:HD12	1	0.1
(1,318)	1:63:A:ILE:HA	1:63:A:ILE:HD13	1	0.1
(1,305)	1:40:A:GLU:HG3	1:41:A:MET:H	26	0.1
(1,134)	1:10:A:LYS:H	1:10:A:LYS:HD3	4	0.1

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

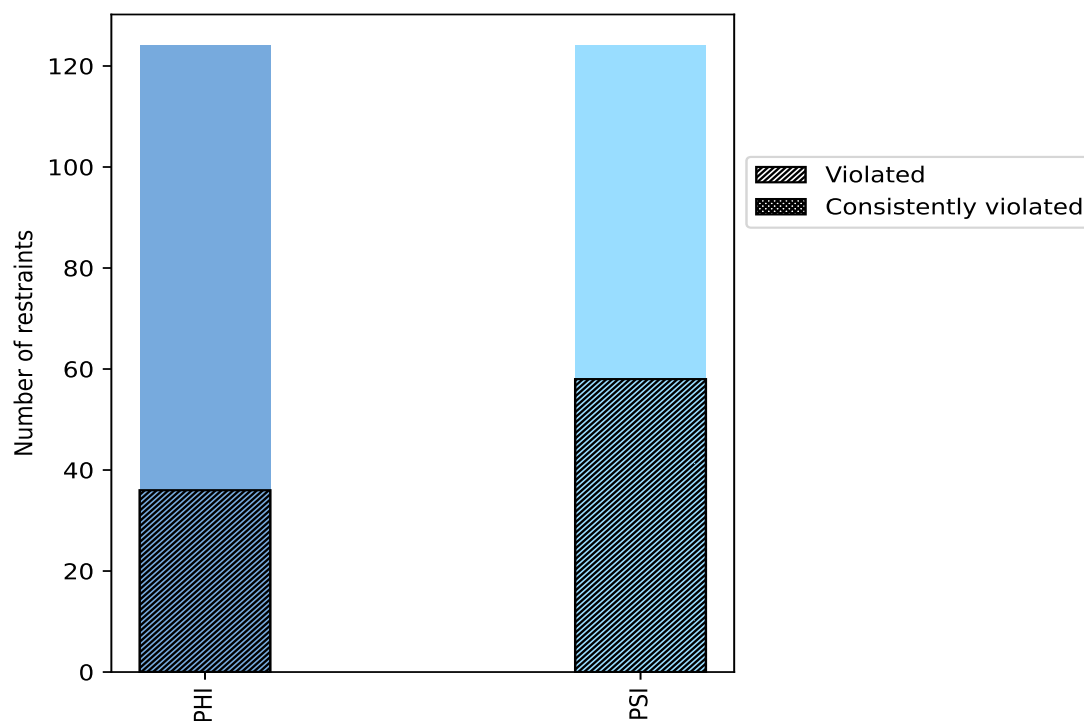
10.1 Summary of dihedral-angle violations [i](#)

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	124	50.0	36	29.0	14.5	0	0.0	0.0
PSI	124	50.0	58	46.8	23.4	0	0.0	0.0
Total	248	100.0	94	37.9	37.9	0	0.0	0.0

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](#)



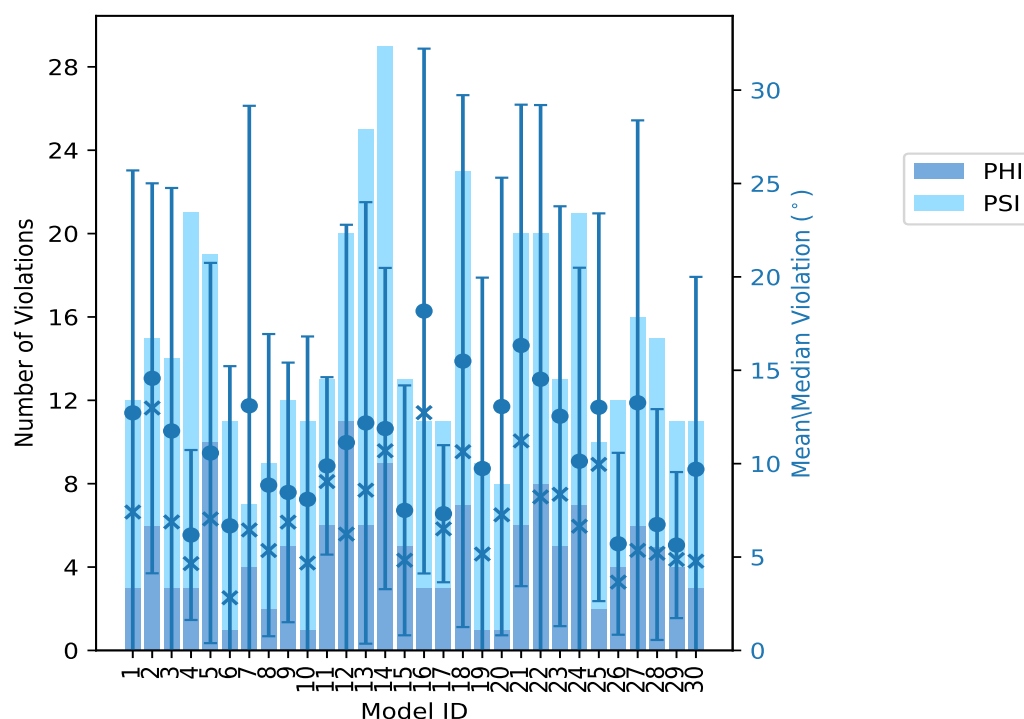
Violated and consistently violated restraints are shown using different hatch patterns in their respective categories

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	3	9	12	12.72	49.8	12.98	7.41
2	6	9	15	14.57	30.27	10.44	12.98
3	3	11	14	11.75	41.67	13.01	6.88
4	3	18	21	6.18	18.56	4.55	4.65
5	10	9	19	10.57	36.7	10.18	7.04
6	1	10	11	6.67	24.83	8.55	2.82
7	4	3	7	13.1	51.67	16.06	6.45
8	2	7	9	8.85	25.26	8.09	5.35
9	5	7	12	8.46	21.94	6.95	6.87
10	1	10	11	8.09	28.72	8.72	4.68
11	6	7	13	9.88	16.72	4.75	9.04
12	11	9	20	11.13	35.14	11.66	6.23
13	6	19	25	12.18	48.85	11.82	8.58
14	9	20	29	11.88	31.19	8.6	10.69
15	5	8	13	7.5	20.19	6.69	4.83
16	3	8	11	18.17	53.14	14.05	12.73
17	3	8	11	7.32	15.73	3.67	6.51
18	7	16	23	15.49	57.4	14.24	10.64
19	1	8	9	9.74	33.75	10.22	5.16
20	1	7	8	13.06	37.98	12.25	7.26
21	6	14	20	16.33	46.0	12.89	11.22
22	8	12	20	14.52	53.94	14.68	8.22
23	5	8	13	12.54	34.7	11.24	8.36
24	7	14	21	10.13	39.44	10.36	6.65
25	2	8	10	13.02	28.89	10.38	9.96
26	4	8	12	5.71	17.29	4.87	3.66
27	6	10	16	13.26	47.47	15.12	5.36
28	5	10	15	6.74	23.16	6.18	5.2
29	4	7	11	5.64	14.54	3.91	4.87
30	3	8	11	9.7	37.48	10.3	4.78

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	%
16	16	32	1	3.3
2	10	12	2	6.7
3	7	10	3	10.0
3	4	7	4	13.3
1	3	4	5	16.7
4	2	6	6	20.0
2	0	2	7	23.3
1	2	3	8	26.7
0	4	4	9	30.0
0	1	1	10	33.3
2	1	3	11	36.7

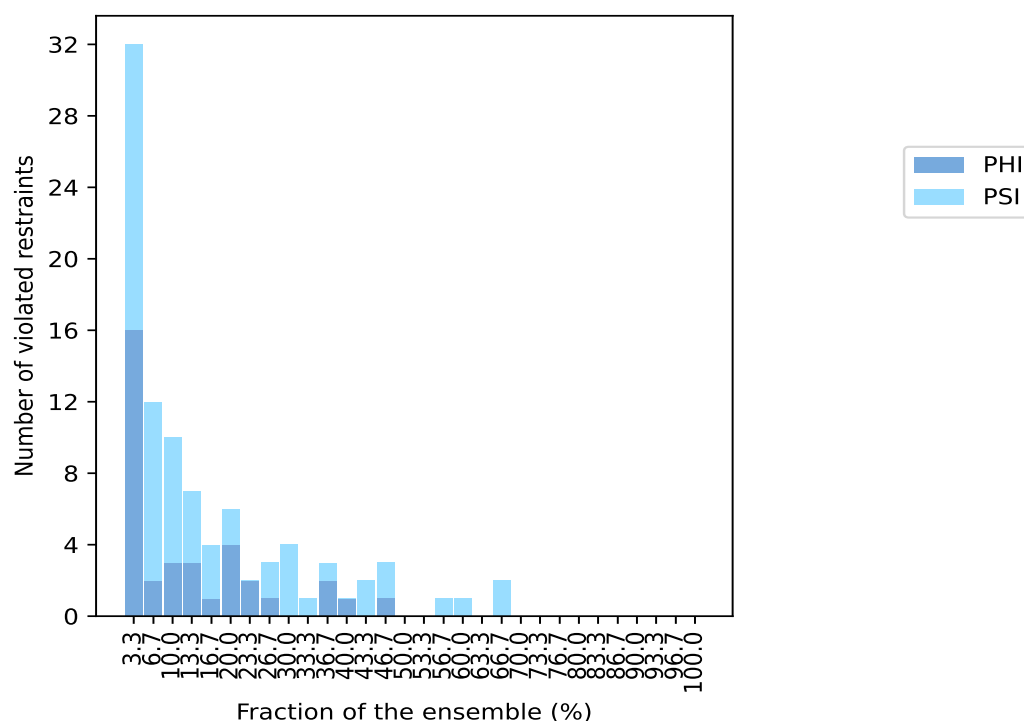
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Number of violated restraints			Fraction of the ensemble	
PHI	PSI	Total	Count ¹	%
1	0	1	12	40.0
0	2	2	13	43.3
1	2	3	14	46.7
0	0	0	15	50.0
0	0	0	16	53.3
0	1	1	17	56.7
0	1	1	18	60.0
0	0	0	19	63.3
0	2	2	20	66.7
0	0	0	21	70.0
0	0	0	22	73.3
0	0	0	23	76.7
0	0	0	24	80.0
0	0	0	25	83.3
0	0	0	26	86.7
0	0	0	27	90.0
0	0	0	28	93.3
0	0	0	29	96.7
0	0	0	30	100.0

¹ Number of models with violations

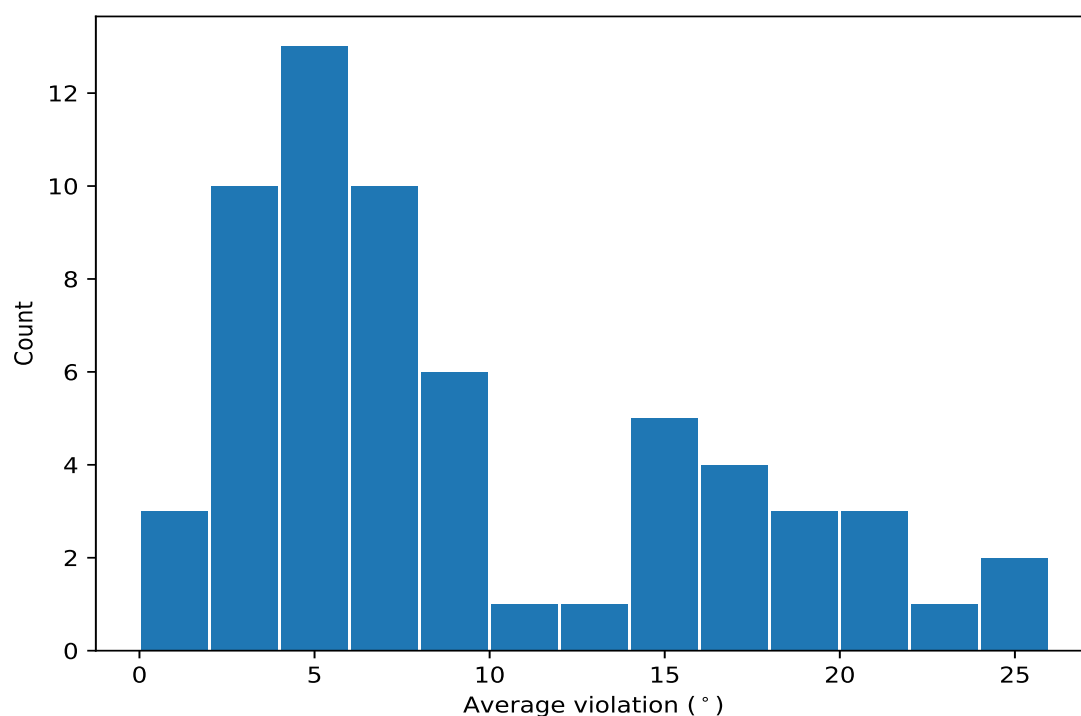
10.3.1 Bar graph : Dihedral-angle Violation statistics for the ensemble [i](#)



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
(1,76)	1:66:A:LEU:N	1:66:A:LEU:CA	1:66:A:LEU:C	1:67:A:ASP:N	20	20.32	16.56	15.16
(1,228)	1:188:B:GLY:N	1:188:B:GLY:CA	1:188:B:GLY:C	1:189:B:ILE:N	20	6.81	5.29	4.26
(1,200)	1:169:B:LEU:N	1:169:B:LEU:CA	1:169:B:LEU:C	1:170:B:ASP:N	18	21.95	15.7	13.12
(1,104)	1:85:A:GLY:N	1:85:A:GLY:CA	1:85:A:GLY:C	1:86:A:ILE:N	17	7.14	4.92	5.35
(1,170)	1:145:B:LEU:N	1:145:B:LEU:CA	1:145:B:LEU:C	1:146:B:GLN:N	14	24.11	8.0	24.42
(1,199)	1:168:B:ASN:C	1:169:B:LEU:N	1:169:B:LEU:CA	1:169:B:LEU:C	14	14.02	13.46	7.98
(1,220)	1:184:B:THR:N	1:184:B:THR:CA	1:184:B:THR:C	1:185:B:LEU:N	14	5.91	3.72	4.6
(1,46)	1:42:A:LEU:N	1:42:A:LEU:CA	1:42:A:LEU:C	1:43:A:GLN:N	13	21.03	13.61	21.94
(1,96)	1:81:A:THR:N	1:81:A:THR:CA	1:81:A:THR:C	1:82:A:LEU:N	13	7.83	3.22	8.57
(1,47)	1:42:A:LEU:C	1:43:A:GLN:N	1:43:A:GLN:CA	1:43:A:GLN:C	12	12.12	8.39	9.34
(1,75)	1:65:A:ASN:C	1:66:A:LEU:N	1:66:A:LEU:CA	1:66:A:LEU:C	11	17.74	16.7	7.62
(1,196)	1:167:B:GLN:N	1:167:B:GLN:CA	1:167:B:GLN:C	1:168:B:ASN:N	11	16.38	9.34	20.37
(1,171)	1:145:B:LEU:C	1:146:B:GLN:N	1:146:B:GLN:CA	1:146:B:GLN:C	11	15.25	10.53	12.36
(1,72)	1:64:A:GLN:N	1:64:A:GLN:CA	1:64:A:GLN:C	1:65:A:ASN:N	10	15.0	8.29	16.62
(1,162)	1:140:B:SER:N	1:140:B:SER:CA	1:140:B:SER:C	1:141:B:PHE:N	9	9.67	4.16	8.37
(1,38)	1:37:A:SER:N	1:37:A:SER:CA	1:37:A:SER:C	1:38:A:PHE:N	9	6.03	5.85	4.6
(1,98)	1:82:A:LEU:N	1:82:A:LEU:CA	1:82:A:LEU:C	1:83:A:ILE:N	9	5.64	2.67	6.48
(1,22)	1:17:A:GLU:N	1:17:A:GLU:CA	1:17:A:GLU:C	1:18:A:ASN:N	9	3.59	3.39	1.69
(1,197)	1:167:B:GLN:C	1:168:B:ASN:N	1:168:B:ASN:CA	1:168:B:ASN:C	8	18.34	11.06	23.68
(1,222)	1:185:B:LEU:N	1:185:B:LEU:CA	1:185:B:LEU:C	1:186:B:ILE:N	8	7.17	4.77	7.1
(1,146)	1:120:B:GLU:N	1:120:B:GLU:CA	1:120:B:GLU:C	1:121:B:ASN:N	8	4.04	3.0	3.0

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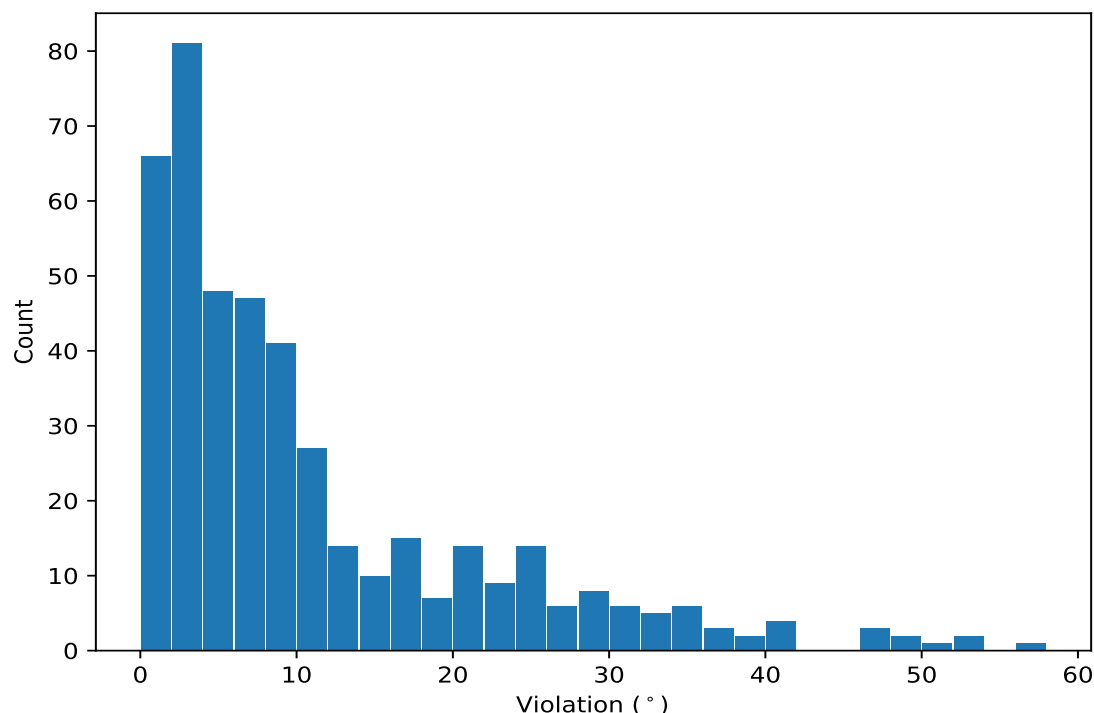
Key	Atom-1	Atom-2	Atom-3	Atom-4	Models ¹	Mean	SD ²	Median
(1,73)	1:64:A:GLN:C	1:65:A:ASN:N	1:65:A:ASN:CA	1:65:A:ASN:C	7	15.43	8.77	16.58
(1,99)	1:82:A:LEU:C	1:83:A:ILE:N	1:83:A:ILE:CA	1:83:A:ILE:C	7	8.24	6.08	8.36
(1,41)	1:39:A:ARG:C	1:40:A:GLU:N	1:40:A:GLU:CA	1:40:A:GLU:C	6	19.1	13.39	19.3
(1,223)	1:185:B:LEU:C	1:186:B:ILE:N	1:186:B:ILE:CA	1:186:B:ILE:C	6	11.84	6.53	12.18
(1,71)	1:63:A:ILE:C	1:64:A:GLN:N	1:64:A:GLN:CA	1:64:A:GLN:C	6	7.6	5.74	7.04
(1,195)	1:166:B:ILE:C	1:167:B:GLN:N	1:167:B:GLN:CA	1:167:B:GLN:C	6	5.03	3.11	3.88
(1,158)	1:138:B:LYS:N	1:138:B:LYS:CA	1:138:B:LYS:C	1:139:B:SER:N	6	4.82	4.95	2.73
(1,2)	1:7:A:GLU:N	1:7:A:GLU:CA	1:7:A:GLU:C	1:8:A:LEU:N	6	3.34	2.4	2.35
(1,165)	1:142:B:ARG:C	1:143:B:GLU:N	1:143:B:GLU:CA	1:143:B:GLU:C	5	19.87	18.14	16.7
(1,154)	1:124:B:LYS:N	1:124:B:LYS:CA	1:124:B:LYS:C	1:125:B:TYR:N	5	5.89	5.87	3.98
(1,172)	1:146:B:GLN:N	1:146:B:GLN:CA	1:146:B:GLN:C	1:147:B:LYS:N	5	3.21	1.31	3.29
(1,148)	1:121:B:ASN:N	1:121:B:ASN:CA	1:121:B:ASN:C	1:122:B:PHE:N	5	1.84	0.97	1.39
(1,155)	1:124:B:LYS:C	1:125:B:TYR:N	1:125:B:TYR:CA	1:125:B:TYR:C	4	17.65	14.96	13.96
(1,238)	1:198:B:HIS:N	1:198:B:HIS:CA	1:198:B:HIS:C	1:199:B:GLU:N	4	14.04	12.84	11.18
(1,157)	1:137:B:SER:C	1:138:B:LYS:N	1:138:B:LYS:CA	1:138:B:LYS:C	4	9.76	7.08	10.07
(1,19)	1:15:A:LEU:C	1:16:A:VAL:N	1:16:A:VAL:CA	1:16:A:VAL:C	4	6.44	5.99	3.52
(1,30)	1:21:A:LYS:N	1:21:A:LYS:CA	1:21:A:LYS:C	1:22:A:TYR:N	4	6.2	2.18	5.14
(1,142)	1:118:B:LEU:N	1:118:B:LEU:CA	1:118:B:LEU:C	1:119:B:VAL:N	4	5.84	4.55	3.7
(1,126)	1:110:B:GLU:N	1:110:B:GLU:CA	1:110:B:GLU:C	1:111:B:LEU:N	4	3.35	2.02	2.86
(1,31)	1:21:A:LYS:C	1:22:A:TYR:N	1:22:A:TYR:CA	1:22:A:TYR:C	3	22.82	14.73	26.58
(1,83)	1:74:A:ILE:C	1:75:A:SER:N	1:75:A:SER:CA	1:75:A:SER:C	3	17.46	12.03	11.73
(1,88)	1:77:A:ASP:N	1:77:A:ASP:CA	1:77:A:ASP:C	1:78:A:GLU:N	3	9.4	5.77	10.69
(1,18)	1:15:A:LEU:N	1:15:A:LEU:CA	1:15:A:LEU:C	1:16:A:VAL:N	3	9.08	4.63	6.0
(1,52)	1:54:A:GLY:N	1:54:A:GLY:CA	1:54:A:GLY:C	1:55:A:ASN:N	3	8.24	4.77	7.19
(1,143)	1:118:B:LEU:C	1:119:B:VAL:N	1:119:B:VAL:CA	1:119:B:VAL:C	3	6.79	1.6	5.94
(1,212)	1:180:B:ASP:N	1:180:B:ASP:CA	1:180:B:ASP:C	1:181:B:GLU:N	3	5.86	4.24	3.97
(1,150)	1:122:B:PHE:N	1:122:B:PHE:CA	1:122:B:PHE:C	1:123:B:TYR:N	3	3.75	2.18	2.94
(1,218)	1:183:B:TRP:N	1:183:B:TRP:CA	1:183:B:TRP:C	1:184:B:THR:N	3	3.72	1.63	3.47
(1,156)	1:125:B:TYR:N	1:125:B:TYR:CA	1:125:B:TYR:C	1:126:B:VAL:N	3	2.11	0.51	2.44
(1,114)	1:95:A:HIS:N	1:95:A:HIS:CA	1:95:A:HIS:C	1:96:A:GLU:N	2	24.74	7.32	24.74
(1,34)	1:35:A:LYS:N	1:35:A:LYS:CA	1:35:A:LYS:C	1:36:A:SER:N	2	7.68	1.65	7.68
(1,160)	1:139:B:SER:N	1:139:B:SER:CA	1:139:B:SER:C	1:140:B:SER:N	2	5.99	0.58	5.99
(1,36)	1:36:A:SER:N	1:36:A:SER:CA	1:36:A:SER:C	1:37:A:SER:N	2	5.22	3.57	5.22
(1,244)	1:201:B:GLU:N	1:201:B:GLU:CA	1:201:B:GLU:C	1:202:B:GLN:N	2	5.0	3.3	5.0
(1,94)	1:80:A:TRP:N	1:80:A:TRP:CA	1:80:A:TRP:C	1:81:A:THR:N	2	4.94	1.52	4.94
(1,20)	1:16:A:VAL:N	1:16:A:VAL:CA	1:16:A:VAL:C	1:17:A:GLU:N	2	4.09	0.76	4.09
(1,185)	1:161:B:ALA:C	1:162:B:ALA:N	1:162:B:ALA:CA	1:162:B:ALA:C	2	3.5	1.1	3.5
(1,144)	1:119:B:VAL:N	1:119:B:VAL:CA	1:119:B:VAL:C	1:120:B:GLU:N	2	2.74	0.93	2.74
(1,24)	1:18:A:ASN:N	1:18:A:ASN:CA	1:18:A:ASN:C	1:19:A:PHE:N	2	2.68	1.2	2.68
(1,173)	1:146:B:GLN:C	1:147:B:LYS:N	1:147:B:LYS:CA	1:147:B:LYS:C	2	1.96	0.64	1.96
(1,48)	1:43:A:GLN:N	1:43:A:GLN:CA	1:43:A:GLN:C	1:44:A:LYS:N	2	1.76	0.45	1.76

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

10.5 All violated dihedral-angle restraints [i](#)

10.5.1 Histogram : Distribution of violations [i](#)

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 [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.

Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,75)	1:65:A:ASN:C	1:66:A:LEU:N	1:66:A:LEU:CA	1:66:A:LEU:C	18	57.4
(1,76)	1:66:A:LEU:N	1:66:A:LEU:CA	1:66:A:LEU:C	1:67:A:ASP:N	22	53.94
(1,199)	1:168:B:ASN:C	1:169:B:LEU:N	1:169:B:LEU:CA	1:169:B:LEU:C	16	53.14
(1,165)	1:142:B:ARG:C	1:143:B:GLU:N	1:143:B:GLU:CA	1:143:B:GLU:C	7	51.67
(1,200)	1:169:B:LEU:N	1:169:B:LEU:CA	1:169:B:LEU:C	1:170:B:ASP:N	1	49.8
(1,76)	1:66:A:LEU:N	1:66:A:LEU:CA	1:66:A:LEU:C	1:67:A:ASP:N	13	48.85
(1,46)	1:42:A:LEU:N	1:42:A:LEU:CA	1:42:A:LEU:C	1:43:A:GLN:N	27	47.47
(1,200)	1:169:B:LEU:N	1:169:B:LEU:CA	1:169:B:LEU:C	1:170:B:ASP:N	22	47.44
(1,76)	1:66:A:LEU:N	1:66:A:LEU:CA	1:66:A:LEU:C	1:67:A:ASP:N	21	46.0
(1,155)	1:124:B:LYS:C	1:125:B:TYR:N	1:125:B:TYR:CA	1:125:B:TYR:C	3	41.67
(1,200)	1:169:B:LEU:N	1:169:B:LEU:CA	1:169:B:LEU:C	1:170:B:ASP:N	18	40.79
(1,200)	1:169:B:LEU:N	1:169:B:LEU:CA	1:169:B:LEU:C	1:170:B:ASP:N	21	40.57
(1,171)	1:145:B:LEU:C	1:146:B:GLN:N	1:146:B:GLN:CA	1:146:B:GLN:C	27	40.13
(1,76)	1:66:A:LEU:N	1:66:A:LEU:CA	1:66:A:LEU:C	1:67:A:ASP:N	24	39.44

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,31)	1:21:A:LYS:C	1:22:A:TYR:N	1:22:A:TYR:CA	1:22:A:TYR:C	3	38.69
(1,170)	1:145:B:LEU:N	1:145:B:LEU:CA	1:145:B:LEU:C	1:146:B:GLN:N	20	37.98
(1,46)	1:42:A:LEU:N	1:42:A:LEU:CA	1:42:A:LEU:C	1:43:A:GLN:N	30	37.48
(1,200)	1:169:B:LEU:N	1:169:B:LEU:CA	1:169:B:LEU:C	1:170:B:ASP:N	5	36.7
(1,41)	1:39:A:ARG:C	1:40:A:GLU:N	1:40:A:GLU:CA	1:40:A:GLU:C	13	35.17
(1,207)	1:177:B:ILE:C	1:178:B:SER:N	1:178:B:SER:CA	1:178:B:SER:C	12	35.14
(1,170)	1:145:B:LEU:N	1:145:B:LEU:CA	1:145:B:LEU:C	1:146:B:GLN:N	27	35.01
(1,75)	1:65:A:ASN:C	1:66:A:LEU:N	1:66:A:LEU:CA	1:66:A:LEU:C	16	34.88
(1,41)	1:39:A:ARG:C	1:40:A:GLU:N	1:40:A:GLU:CA	1:40:A:GLU:C	23	34.7
(1,83)	1:74:A:ILE:C	1:75:A:SER:N	1:75:A:SER:CA	1:75:A:SER:C	12	34.19
(1,46)	1:42:A:LEU:N	1:42:A:LEU:CA	1:42:A:LEU:C	1:43:A:GLN:N	19	33.75
(1,200)	1:169:B:LEU:N	1:169:B:LEU:CA	1:169:B:LEU:C	1:170:B:ASP:N	24	33.6
(1,238)	1:198:B:HIS:N	1:198:B:HIS:CA	1:198:B:HIS:C	1:199:B:GLU:N	21	32.58
(1,76)	1:66:A:LEU:N	1:66:A:LEU:CA	1:66:A:LEU:C	1:67:A:ASP:N	18	32.54
(1,114)	1:95:A:HIS:N	1:95:A:HIS:CA	1:95:A:HIS:C	1:96:A:GLU:N	21	32.06
(1,47)	1:42:A:LEU:C	1:43:A:GLN:N	1:43:A:GLN:CA	1:43:A:GLN:C	27	31.96
(1,197)	1:167:B:GLN:C	1:168:B:ASN:N	1:168:B:ASN:CA	1:168:B:ASN:C	14	31.19
(1,76)	1:66:A:LEU:N	1:66:A:LEU:CA	1:66:A:LEU:C	1:67:A:ASP:N	23	31.05
(1,75)	1:65:A:ASN:C	1:66:A:LEU:N	1:66:A:LEU:CA	1:66:A:LEU:C	12	30.34
(1,199)	1:168:B:ASN:C	1:169:B:LEU:N	1:169:B:LEU:CA	1:169:B:LEU:C	18	30.32
(1,76)	1:66:A:LEU:N	1:66:A:LEU:CA	1:66:A:LEU:C	1:67:A:ASP:N	2	30.27
(1,199)	1:168:B:ASN:C	1:169:B:LEU:N	1:169:B:LEU:CA	1:169:B:LEU:C	12	29.71
(1,170)	1:145:B:LEU:N	1:145:B:LEU:CA	1:145:B:LEU:C	1:146:B:GLN:N	13	29.34
(1,200)	1:169:B:LEU:N	1:169:B:LEU:CA	1:169:B:LEU:C	1:170:B:ASP:N	23	29.18
(1,200)	1:169:B:LEU:N	1:169:B:LEU:CA	1:169:B:LEU:C	1:170:B:ASP:N	25	28.89
(1,170)	1:145:B:LEU:N	1:145:B:LEU:CA	1:145:B:LEU:C	1:146:B:GLN:N	10	28.72
(1,46)	1:42:A:LEU:N	1:42:A:LEU:CA	1:42:A:LEU:C	1:43:A:GLN:N	5	28.5
(1,196)	1:167:B:GLN:N	1:167:B:GLN:CA	1:167:B:GLN:C	1:168:B:ASN:N	22	28.18
(1,170)	1:145:B:LEU:N	1:145:B:LEU:CA	1:145:B:LEU:C	1:146:B:GLN:N	25	28.18
(1,197)	1:167:B:GLN:C	1:168:B:ASN:N	1:168:B:ASN:CA	1:168:B:ASN:C	13	27.81
(1,196)	1:167:B:GLN:N	1:167:B:GLN:CA	1:167:B:GLN:C	1:168:B:ASN:N	2	26.71
(1,31)	1:21:A:LYS:C	1:22:A:TYR:N	1:22:A:TYR:CA	1:22:A:TYR:C	14	26.58
(1,171)	1:145:B:LEU:C	1:146:B:GLN:N	1:146:B:GLN:CA	1:146:B:GLN:C	20	26.5
(1,73)	1:64:A:GLN:C	1:65:A:ASN:N	1:65:A:ASN:CA	1:65:A:ASN:C	14	26.13
(1,115)	1:95:A:HIS:C	1:96:A:GLU:N	1:96:A:GLU:CA	1:96:A:GLU:C	21	26.06
(1,196)	1:167:B:GLN:N	1:167:B:GLN:CA	1:167:B:GLN:C	1:168:B:ASN:N	14	25.69
(1,197)	1:167:B:GLN:C	1:168:B:ASN:N	1:168:B:ASN:CA	1:168:B:ASN:C	2	25.61
(1,165)	1:142:B:ARG:C	1:143:B:GLU:N	1:143:B:GLU:CA	1:143:B:GLU:C	2	25.52
(1,72)	1:64:A:GLN:N	1:64:A:GLN:CA	1:64:A:GLN:C	1:65:A:ASN:N	14	25.34
(1,46)	1:42:A:LEU:N	1:42:A:LEU:CA	1:42:A:LEU:C	1:43:A:GLN:N	8	25.26
(1,75)	1:65:A:ASN:C	1:66:A:LEU:N	1:66:A:LEU:CA	1:66:A:LEU:C	2	25.13
(1,170)	1:145:B:LEU:N	1:145:B:LEU:CA	1:145:B:LEU:C	1:146:B:GLN:N	24	24.99
(1,73)	1:64:A:GLN:C	1:65:A:ASN:N	1:65:A:ASN:CA	1:65:A:ASN:C	22	24.97
(1,170)	1:145:B:LEU:N	1:145:B:LEU:CA	1:145:B:LEU:C	1:146:B:GLN:N	6	24.83
(1,41)	1:39:A:ARG:C	1:40:A:GLU:N	1:40:A:GLU:CA	1:40:A:GLU:C	25	24.52
(1,46)	1:42:A:LEU:N	1:42:A:LEU:CA	1:42:A:LEU:C	1:43:A:GLN:N	6	24.4
(1,72)	1:64:A:GLN:N	1:64:A:GLN:CA	1:64:A:GLN:C	1:65:A:ASN:N	22	24.3
(1,197)	1:167:B:GLN:C	1:168:B:ASN:N	1:168:B:ASN:CA	1:168:B:ASN:C	22	24.2
(1,170)	1:145:B:LEU:N	1:145:B:LEU:CA	1:145:B:LEU:C	1:146:B:GLN:N	5	24.02
(1,196)	1:167:B:GLN:N	1:167:B:GLN:CA	1:167:B:GLN:C	1:168:B:ASN:N	13	23.85
(1,72)	1:64:A:GLN:N	1:64:A:GLN:CA	1:64:A:GLN:C	1:65:A:ASN:N	18	23.58

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,76)	1:66:A:LEU:N	1:66:A:LEU:CA	1:66:A:LEU:C	1:67:A:ASP:N	5	23.48
(1,49)	1:43:A:GLN:C	1:44:A:LYS:N	1:44:A:LYS:CA	1:44:A:LYS:C	3	23.47
(1,197)	1:167:B:GLN:C	1:168:B:ASN:N	1:168:B:ASN:CA	1:168:B:ASN:C	28	23.16
(1,33)	1:34:A:SER:C	1:35:A:LYS:N	1:35:A:LYS:CA	1:35:A:LYS:C	18	23.16
(1,171)	1:145:B:LEU:C	1:146:B:GLN:N	1:146:B:GLN:CA	1:146:B:GLN:C	10	22.75
(1,73)	1:64:A:GLN:C	1:65:A:ASN:N	1:65:A:ASN:CA	1:65:A:ASN:C	2	22.52
(1,196)	1:167:B:GLN:N	1:167:B:GLN:CA	1:167:B:GLN:C	1:168:B:ASN:N	18	22.34
(1,46)	1:42:A:LEU:N	1:42:A:LEU:CA	1:42:A:LEU:C	1:43:A:GLN:N	9	21.94
(1,239)	1:198:B:HIS:C	1:199:B:GLU:N	1:199:B:GLU:CA	1:199:B:GLU:C	21	21.79
(1,170)	1:145:B:LEU:N	1:145:B:LEU:CA	1:145:B:LEU:C	1:146:B:GLN:N	9	21.65
(1,170)	1:145:B:LEU:N	1:145:B:LEU:CA	1:145:B:LEU:C	1:146:B:GLN:N	21	21.55
(1,170)	1:145:B:LEU:N	1:145:B:LEU:CA	1:145:B:LEU:C	1:146:B:GLN:N	8	21.53
(1,38)	1:37:A:SER:N	1:37:A:SER:CA	1:37:A:SER:C	1:38:A:PHE:N	18	21.45
(1,47)	1:42:A:LEU:C	1:43:A:GLN:N	1:43:A:GLN:CA	1:43:A:GLN:C	19	21.38
(1,46)	1:42:A:LEU:N	1:42:A:LEU:CA	1:42:A:LEU:C	1:43:A:GLN:N	21	21.1
(1,76)	1:66:A:LEU:N	1:66:A:LEU:CA	1:66:A:LEU:C	1:67:A:ASP:N	1	21.02
(1,47)	1:42:A:LEU:C	1:43:A:GLN:N	1:43:A:GLN:CA	1:43:A:GLN:C	30	20.52
(1,196)	1:167:B:GLN:N	1:167:B:GLN:CA	1:167:B:GLN:C	1:168:B:ASN:N	16	20.37
(1,72)	1:64:A:GLN:N	1:64:A:GLN:CA	1:64:A:GLN:C	1:65:A:ASN:N	16	20.21
(1,170)	1:145:B:LEU:N	1:145:B:LEU:CA	1:145:B:LEU:C	1:146:B:GLN:N	15	20.19
(1,72)	1:64:A:GLN:N	1:64:A:GLN:CA	1:64:A:GLN:C	1:65:A:ASN:N	2	20.14
(1,171)	1:145:B:LEU:C	1:146:B:GLN:N	1:146:B:GLN:CA	1:146:B:GLN:C	13	19.82
(1,223)	1:185:B:LEU:C	1:186:B:ILE:N	1:186:B:ILE:CA	1:186:B:ILE:C	1	19.61
(1,238)	1:198:B:HIS:N	1:198:B:HIS:CA	1:198:B:HIS:C	1:199:B:GLU:N	14	19.41
(1,223)	1:185:B:LEU:C	1:186:B:ILE:N	1:186:B:ILE:CA	1:186:B:ILE:C	12	19.25
(1,104)	1:85:A:GLY:N	1:85:A:GLY:CA	1:85:A:GLY:C	1:86:A:ILE:N	15	18.84
(1,228)	1:188:B:GLY:N	1:188:B:GLY:CA	1:188:B:GLY:C	1:189:B:ILE:N	4	18.56
(1,162)	1:140:B:SER:N	1:140:B:SER:CA	1:140:B:SER:C	1:141:B:PHE:N	18	18.42
(1,71)	1:63:A:ILE:C	1:64:A:GLN:N	1:64:A:GLN:CA	1:64:A:GLN:C	16	17.78
(1,228)	1:188:B:GLY:N	1:188:B:GLY:CA	1:188:B:GLY:C	1:189:B:ILE:N	15	17.56
(1,99)	1:82:A:LEU:C	1:83:A:ILE:N	1:83:A:ILE:CA	1:83:A:ILE:C	12	17.45
(1,114)	1:95:A:HIS:N	1:95:A:HIS:CA	1:95:A:HIS:C	1:96:A:GLU:N	14	17.42
(1,157)	1:137:B:SER:C	1:138:B:LYS:N	1:138:B:LYS:CA	1:138:B:LYS:C	26	17.29
(1,104)	1:85:A:GLY:N	1:85:A:GLY:CA	1:85:A:GLY:C	1:86:A:ILE:N	4	17.13
(1,75)	1:65:A:ASN:C	1:66:A:LEU:N	1:66:A:LEU:CA	1:66:A:LEU:C	23	17.08
(1,154)	1:124:B:LYS:N	1:124:B:LYS:CA	1:124:B:LYS:C	1:125:B:TYR:N	20	17.07
(1,76)	1:66:A:LEU:N	1:66:A:LEU:CA	1:66:A:LEU:C	1:67:A:ASP:N	25	16.97
(1,19)	1:15:A:LEU:C	1:16:A:VAL:N	1:16:A:VAL:CA	1:16:A:VAL:C	11	16.72
(1,165)	1:142:B:ARG:C	1:143:B:GLU:N	1:143:B:GLU:CA	1:143:B:GLU:C	11	16.7
(1,155)	1:124:B:LYS:C	1:125:B:TYR:N	1:125:B:TYR:CA	1:125:B:TYR:C	14	16.59
(1,46)	1:42:A:LEU:N	1:42:A:LEU:CA	1:42:A:LEU:C	1:43:A:GLN:N	22	16.59
(1,73)	1:64:A:GLN:C	1:65:A:ASN:N	1:65:A:ASN:CA	1:65:A:ASN:C	28	16.58
(1,157)	1:137:B:SER:C	1:138:B:LYS:N	1:138:B:LYS:CA	1:138:B:LYS:C	18	16.28
(1,222)	1:185:B:LEU:N	1:185:B:LEU:CA	1:185:B:LEU:C	1:186:B:ILE:N	14	15.88
(1,170)	1:145:B:LEU:N	1:145:B:LEU:CA	1:145:B:LEU:C	1:146:B:GLN:N	14	15.75
(1,88)	1:77:A:ASP:N	1:77:A:ASP:CA	1:77:A:ASP:C	1:78:A:GLU:N	17	15.73
(1,99)	1:82:A:LEU:C	1:83:A:ILE:N	1:83:A:ILE:CA	1:83:A:ILE:C	1	15.67
(1,18)	1:15:A:LEU:N	1:15:A:LEU:CA	1:15:A:LEU:C	1:16:A:VAL:N	11	15.63
(1,47)	1:42:A:LEU:C	1:43:A:GLN:N	1:43:A:GLN:CA	1:43:A:GLN:C	5	15.36
(1,158)	1:138:B:LYS:N	1:138:B:LYS:CA	1:138:B:LYS:C	1:139:B:SER:N	1	15.23
(1,223)	1:185:B:LEU:C	1:186:B:ILE:N	1:186:B:ILE:CA	1:186:B:ILE:C	9	14.85

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,52)	1:54:A:GLY:N	1:54:A:GLY:CA	1:54:A:GLY:C	1:55:A:ASN:N	29	14.54
(1,41)	1:39:A:ARG:C	1:40:A:GLU:N	1:40:A:GLU:CA	1:40:A:GLU:C	11	14.08
(1,178)	1:158:B:ASN:N	1:158:B:ASN:CA	1:158:B:ASN:C	1:159:B:ARG:N	24	13.69
(1,142)	1:118:B:LEU:N	1:118:B:LEU:CA	1:118:B:LEU:C	1:119:B:VAL:N	11	13.64
(1,96)	1:81:A:THR:N	1:81:A:THR:CA	1:81:A:THR:C	1:82:A:LEU:N	24	13.64
(1,162)	1:140:B:SER:N	1:140:B:SER:CA	1:140:B:SER:C	1:141:B:PHE:N	7	13.55
(1,76)	1:66:A:LEU:N	1:66:A:LEU:CA	1:66:A:LEU:C	1:67:A:ASP:N	3	13.35
(1,200)	1:169:B:LEU:N	1:169:B:LEU:CA	1:169:B:LEU:C	1:170:B:ASP:N	26	13.25
(1,72)	1:64:A:GLN:N	1:64:A:GLN:CA	1:64:A:GLN:C	1:65:A:ASN:N	24	13.1
(1,228)	1:188:B:GLY:N	1:188:B:GLY:CA	1:188:B:GLY:C	1:189:B:ILE:N	13	12.98
(1,200)	1:169:B:LEU:N	1:169:B:LEU:CA	1:169:B:LEU:C	1:170:B:ASP:N	2	12.98
(1,104)	1:85:A:GLY:N	1:85:A:GLY:CA	1:85:A:GLY:C	1:86:A:ILE:N	16	12.73
(1,76)	1:66:A:LEU:N	1:66:A:LEU:CA	1:66:A:LEU:C	1:67:A:ASP:N	16	12.65
(1,171)	1:145:B:LEU:C	1:146:B:GLN:N	1:146:B:GLN:CA	1:146:B:GLN:C	25	12.64
(1,171)	1:145:B:LEU:C	1:146:B:GLN:N	1:146:B:GLN:CA	1:146:B:GLN:C	5	12.36
(1,200)	1:169:B:LEU:N	1:169:B:LEU:CA	1:169:B:LEU:C	1:170:B:ASP:N	16	12.21
(1,220)	1:184:B:THR:N	1:184:B:THR:CA	1:184:B:THR:C	1:185:B:LEU:N	24	11.99
(1,222)	1:185:B:LEU:N	1:185:B:LEU:CA	1:185:B:LEU:C	1:186:B:ILE:N	30	11.92
(1,197)	1:167:B:GLN:C	1:168:B:ASN:N	1:168:B:ASN:CA	1:168:B:ASN:C	18	11.91
(1,47)	1:42:A:LEU:C	1:43:A:GLN:N	1:43:A:GLN:CA	1:43:A:GLN:C	21	11.84
(1,228)	1:188:B:GLY:N	1:188:B:GLY:CA	1:188:B:GLY:C	1:189:B:ILE:N	16	11.83
(1,228)	1:188:B:GLY:N	1:188:B:GLY:CA	1:188:B:GLY:C	1:189:B:ILE:N	28	11.81
(1,220)	1:184:B:THR:N	1:184:B:THR:CA	1:184:B:THR:C	1:185:B:LEU:N	21	11.76
(1,212)	1:180:B:ASP:N	1:180:B:ASP:CA	1:180:B:ASP:C	1:181:B:GLU:N	17	11.74
(1,83)	1:74:A:ILE:C	1:75:A:SER:N	1:75:A:SER:CA	1:75:A:SER:C	14	11.73
(1,155)	1:124:B:LYS:C	1:125:B:TYR:N	1:125:B:TYR:CA	1:125:B:TYR:C	5	11.33
(1,220)	1:184:B:THR:N	1:184:B:THR:CA	1:184:B:THR:C	1:185:B:LEU:N	14	11.23
(1,200)	1:169:B:LEU:N	1:169:B:LEU:CA	1:169:B:LEU:C	1:170:B:ASP:N	14	11.23
(1,162)	1:140:B:SER:N	1:140:B:SER:CA	1:140:B:SER:C	1:141:B:PHE:N	14	11.15
(1,71)	1:63:A:ILE:C	1:64:A:GLN:N	1:64:A:GLN:CA	1:64:A:GLN:C	13	11.1
(1,195)	1:166:B:ILE:C	1:167:B:GLN:N	1:167:B:GLN:CA	1:167:B:GLN:C	22	10.84
(1,199)	1:168:B:ASN:C	1:169:B:LEU:N	1:169:B:LEU:CA	1:169:B:LEU:C	27	10.79
(1,104)	1:85:A:GLY:N	1:85:A:GLY:CA	1:85:A:GLY:C	1:86:A:ILE:N	21	10.69
(1,88)	1:77:A:ASP:N	1:77:A:ASP:CA	1:77:A:ASP:C	1:78:A:GLU:N	14	10.69
(1,22)	1:17:A:GLU:N	1:17:A:GLU:CA	1:17:A:GLU:C	1:18:A:ASN:N	18	10.64
(1,96)	1:81:A:THR:N	1:81:A:THR:CA	1:81:A:THR:C	1:82:A:LEU:N	13	10.6
(1,96)	1:81:A:THR:N	1:81:A:THR:CA	1:81:A:THR:C	1:82:A:LEU:N	4	10.59
(1,220)	1:184:B:THR:N	1:184:B:THR:CA	1:184:B:THR:C	1:185:B:LEU:N	30	10.48
(1,146)	1:120:B:GLU:N	1:120:B:GLU:CA	1:120:B:GLU:C	1:121:B:ASN:N	18	10.43
(1,199)	1:168:B:ASN:C	1:169:B:LEU:N	1:169:B:LEU:CA	1:169:B:LEU:C	23	10.4
(1,72)	1:64:A:GLN:N	1:64:A:GLN:CA	1:64:A:GLN:C	1:65:A:ASN:N	5	10.18
(1,99)	1:82:A:LEU:C	1:83:A:ILE:N	1:83:A:ILE:CA	1:83:A:ILE:C	29	10.09
(1,200)	1:169:B:LEU:N	1:169:B:LEU:CA	1:169:B:LEU:C	1:170:B:ASP:N	3	10.0
(1,196)	1:167:B:GLN:N	1:167:B:GLN:CA	1:167:B:GLN:C	1:168:B:ASN:N	24	9.97
(1,30)	1:21:A:LYS:N	1:21:A:LYS:CA	1:21:A:LYS:C	1:22:A:TYR:N	28	9.92
(1,162)	1:140:B:SER:N	1:140:B:SER:CA	1:140:B:SER:C	1:141:B:PHE:N	4	9.91
(1,152)	1:123:B:TYR:N	1:123:B:TYR:CA	1:123:B:TYR:C	1:124:B:LYS:N	3	9.9
(1,96)	1:81:A:THR:N	1:81:A:THR:CA	1:81:A:THR:C	1:82:A:LEU:N	11	9.8
(1,96)	1:81:A:THR:N	1:81:A:THR:CA	1:81:A:THR:C	1:82:A:LEU:N	14	9.79
(1,200)	1:169:B:LEU:N	1:169:B:LEU:CA	1:169:B:LEU:C	1:170:B:ASP:N	19	9.73
(1,228)	1:188:B:GLY:N	1:188:B:GLY:CA	1:188:B:GLY:C	1:189:B:ILE:N	14	9.57

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,223)	1:185:B:LEU:C	1:186:B:ILE:N	1:186:B:ILE:CA	1:186:B:ILE:C	23	9.52
(1,176)	1:157:B:GLY:N	1:157:B:GLY:CA	1:157:B:GLY:C	1:158:B:ASN:N	29	9.5
(1,171)	1:145:B:LEU:C	1:146:B:GLN:N	1:146:B:GLN:CA	1:146:B:GLN:C	15	9.42
(1,47)	1:42:A:LEU:C	1:43:A:GLN:N	1:43:A:GLN:CA	1:43:A:GLN:C	24	9.37
(1,96)	1:81:A:THR:N	1:81:A:THR:CA	1:81:A:THR:C	1:82:A:LEU:N	22	9.35
(1,46)	1:42:A:LEU:N	1:42:A:LEU:CA	1:42:A:LEU:C	1:43:A:GLN:N	13	9.35
(1,34)	1:35:A:LYS:N	1:35:A:LYS:CA	1:35:A:LYS:C	1:36:A:SER:N	13	9.33
(1,47)	1:42:A:LEU:C	1:43:A:GLN:N	1:43:A:GLN:CA	1:43:A:GLN:C	8	9.32
(1,228)	1:188:B:GLY:N	1:188:B:GLY:CA	1:188:B:GLY:C	1:189:B:ILE:N	21	9.26
(1,98)	1:82:A:LEU:N	1:82:A:LEU:CA	1:82:A:LEU:C	1:83:A:ILE:N	14	9.05
(1,143)	1:118:B:LEU:C	1:119:B:VAL:N	1:119:B:VAL:CA	1:119:B:VAL:C	11	9.04
(1,104)	1:85:A:GLY:N	1:85:A:GLY:CA	1:85:A:GLY:C	1:86:A:ILE:N	3	9.01
(1,76)	1:66:A:LEU:N	1:66:A:LEU:CA	1:66:A:LEU:C	1:67:A:ASP:N	14	8.91
(1,81)	1:73:A:ARG:C	1:74:A:ILE:N	1:74:A:ILE:CA	1:74:A:ILE:C	17	8.87
(1,222)	1:185:B:LEU:N	1:185:B:LEU:CA	1:185:B:LEU:C	1:186:B:ILE:N	24	8.8
(1,36)	1:36:A:SER:N	1:36:A:SER:CA	1:36:A:SER:C	1:37:A:SER:N	1	8.79
(1,174)	1:147:B:LYS:N	1:147:B:LYS:CA	1:147:B:LYS:C	1:148:B:GLU:N	27	8.7
(1,77)	1:71:A:ASP:C	1:72:A:GLY:N	1:72:A:GLY:CA	1:72:A:GLY:C	9	8.66
(1,38)	1:37:A:SER:N	1:37:A:SER:CA	1:37:A:SER:C	1:38:A:PHE:N	13	8.66
(1,120)	1:98:A:GLU:N	1:98:A:GLU:CA	1:98:A:GLU:C	1:99:A:GLN:N	18	8.58
(1,47)	1:42:A:LEU:C	1:43:A:GLN:N	1:43:A:GLN:CA	1:43:A:GLN:C	13	8.58
(1,96)	1:81:A:THR:N	1:81:A:THR:CA	1:81:A:THR:C	1:82:A:LEU:N	17	8.57
(1,22)	1:17:A:GLU:N	1:17:A:GLU:CA	1:17:A:GLU:C	1:18:A:ASN:N	22	8.47
(1,2)	1:7:A:GLU:N	1:7:A:GLU:CA	1:7:A:GLU:C	1:8:A:LEU:N	12	8.44
(1,162)	1:140:B:SER:N	1:140:B:SER:CA	1:140:B:SER:C	1:141:B:PHE:N	10	8.37
(1,222)	1:185:B:LEU:N	1:185:B:LEU:CA	1:185:B:LEU:C	1:186:B:ILE:N	2	8.36
(1,99)	1:82:A:LEU:C	1:83:A:ILE:N	1:83:A:ILE:CA	1:83:A:ILE:C	23	8.36
(1,76)	1:66:A:LEU:N	1:66:A:LEU:CA	1:66:A:LEU:C	1:67:A:ASP:N	26	8.34
(1,244)	1:201:B:GLU:N	1:201:B:GLU:CA	1:201:B:GLU:C	1:202:B:GLN:N	18	8.31
(1,196)	1:167:B:GLN:N	1:167:B:GLN:CA	1:167:B:GLN:C	1:168:B:ASN:N	4	8.23
(1,199)	1:168:B:ASN:C	1:169:B:LEU:N	1:169:B:LEU:CA	1:169:B:LEU:C	21	8.13
(1,71)	1:63:A:ILE:C	1:64:A:GLN:N	1:64:A:GLN:CA	1:64:A:GLN:C	28	8.04
(1,199)	1:168:B:ASN:C	1:169:B:LEU:N	1:169:B:LEU:CA	1:169:B:LEU:C	15	8.03
(1,228)	1:188:B:GLY:N	1:188:B:GLY:CA	1:188:B:GLY:C	1:189:B:ILE:N	11	7.97
(1,98)	1:82:A:LEU:N	1:82:A:LEU:CA	1:82:A:LEU:C	1:83:A:ILE:N	22	7.97
(1,199)	1:168:B:ASN:C	1:169:B:LEU:N	1:169:B:LEU:CA	1:169:B:LEU:C	5	7.92
(1,98)	1:82:A:LEU:N	1:82:A:LEU:CA	1:82:A:LEU:C	1:83:A:ILE:N	30	7.91
(1,162)	1:140:B:SER:N	1:140:B:SER:CA	1:140:B:SER:C	1:141:B:PHE:N	20	7.79
(1,73)	1:64:A:GLN:C	1:65:A:ASN:N	1:65:A:ASN:CA	1:65:A:ASN:C	18	7.78
(1,98)	1:82:A:LEU:N	1:82:A:LEU:CA	1:82:A:LEU:C	1:83:A:ILE:N	13	7.73
(1,228)	1:188:B:GLY:N	1:188:B:GLY:CA	1:188:B:GLY:C	1:189:B:ILE:N	17	7.65
(1,75)	1:65:A:ASN:C	1:66:A:LEU:N	1:66:A:LEU:CA	1:66:A:LEU:C	21	7.62
(1,162)	1:140:B:SER:N	1:140:B:SER:CA	1:140:B:SER:C	1:141:B:PHE:N	13	7.59
(1,162)	1:140:B:SER:N	1:140:B:SER:CA	1:140:B:SER:C	1:141:B:PHE:N	23	7.47
(1,199)	1:168:B:ASN:C	1:169:B:LEU:N	1:169:B:LEU:CA	1:169:B:LEU:C	7	7.36
(1,171)	1:145:B:LEU:C	1:146:B:GLN:N	1:146:B:GLN:CA	1:146:B:GLN:C	9	7.35
(1,104)	1:85:A:GLY:N	1:85:A:GLY:CA	1:85:A:GLY:C	1:86:A:ILE:N	14	7.33
(1,96)	1:81:A:THR:N	1:81:A:THR:CA	1:81:A:THR:C	1:82:A:LEU:N	25	7.29
(1,199)	1:168:B:ASN:C	1:169:B:LEU:N	1:169:B:LEU:CA	1:169:B:LEU:C	2	7.21
(1,75)	1:65:A:ASN:C	1:66:A:LEU:N	1:66:A:LEU:CA	1:66:A:LEU:C	13	7.2
(1,52)	1:54:A:GLY:N	1:54:A:GLY:CA	1:54:A:GLY:C	1:55:A:ASN:N	4	7.19

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,220)	1:184:B:THR:N	1:184:B:THR:CA	1:184:B:THR:C	1:185:B:LEU:N	10	7.18
(1,195)	1:166:B:ILE:C	1:167:B:GLN:N	1:167:B:GLN:CA	1:167:B:GLN:C	28	7.11
(1,196)	1:167:B:GLN:N	1:167:B:GLN:CA	1:167:B:GLN:C	1:168:B:ASN:N	5	7.04
(1,104)	1:85:A:GLY:N	1:85:A:GLY:CA	1:85:A:GLY:C	1:86:A:ILE:N	11	6.95
(1,171)	1:145:B:LEU:C	1:146:B:GLN:N	1:146:B:GLN:CA	1:146:B:GLN:C	26	6.91
(1,202)	1:175:B:GLY:N	1:175:B:GLY:CA	1:175:B:GLY:C	1:176:B:ARG:N	9	6.88
(1,118)	1:97:A:GLN:N	1:97:A:GLN:CA	1:97:A:GLN:C	1:98:A:GLU:N	21	6.88
(1,47)	1:42:A:LEU:C	1:43:A:GLN:N	1:43:A:GLN:CA	1:43:A:GLN:C	9	6.86
(1,150)	1:122:B:PHE:N	1:122:B:PHE:CA	1:122:B:PHE:C	1:123:B:TYR:N	20	6.73
(1,146)	1:120:B:GLU:N	1:120:B:GLU:CA	1:120:B:GLU:C	1:121:B:ASN:N	22	6.71
(1,73)	1:64:A:GLN:C	1:65:A:ASN:N	1:65:A:ASN:CA	1:65:A:ASN:C	12	6.66
(1,199)	1:168:B:ASN:C	1:169:B:LEU:N	1:169:B:LEU:CA	1:169:B:LEU:C	24	6.65
(1,160)	1:139:B:SER:N	1:139:B:SER:CA	1:139:B:SER:C	1:140:B:SER:N	4	6.57
(1,126)	1:110:B:GLU:N	1:110:B:GLU:CA	1:110:B:GLU:C	1:111:B:LEU:N	12	6.54
(1,205)	1:176:B:ARG:C	1:177:B:ILE:N	1:177:B:ILE:CA	1:177:B:ILE:C	17	6.51
(1,96)	1:81:A:THR:N	1:81:A:THR:CA	1:81:A:THR:C	1:82:A:LEU:N	21	6.5
(1,98)	1:82:A:LEU:N	1:82:A:LEU:CA	1:82:A:LEU:C	1:83:A:ILE:N	11	6.48
(1,94)	1:80:A:TRP:N	1:80:A:TRP:CA	1:80:A:TRP:C	1:81:A:THR:N	12	6.46
(1,83)	1:74:A:ILE:C	1:75:A:SER:N	1:75:A:SER:CA	1:75:A:SER:C	7	6.45
(1,196)	1:167:B:GLN:N	1:167:B:GLN:CA	1:167:B:GLN:C	1:168:B:ASN:N	10	6.44
(1,26)	1:19:A:PHE:N	1:19:A:PHE:CA	1:19:A:PHE:C	1:20:A:TYR:N	4	6.38
(1,45)	1:41:A:MET:C	1:42:A:LEU:N	1:42:A:LEU:CA	1:42:A:LEU:C	27	6.2
(1,199)	1:168:B:ASN:C	1:169:B:LEU:N	1:169:B:LEU:CA	1:169:B:LEU:C	14	6.09
(1,200)	1:169:B:LEU:N	1:169:B:LEU:CA	1:169:B:LEU:C	1:170:B:ASP:N	7	6.08
(1,96)	1:81:A:THR:N	1:81:A:THR:CA	1:81:A:THR:C	1:82:A:LEU:N	8	6.07
(1,71)	1:63:A:ILE:C	1:64:A:GLN:N	1:64:A:GLN:CA	1:64:A:GLN:C	22	6.05
(1,34)	1:35:A:LYS:N	1:35:A:LYS:CA	1:35:A:LYS:C	1:36:A:SER:N	1	6.03
(1,171)	1:145:B:LEU:C	1:146:B:GLN:N	1:146:B:GLN:CA	1:146:B:GLN:C	24	6.02
(1,18)	1:15:A:LEU:N	1:15:A:LEU:CA	1:15:A:LEU:C	1:16:A:VAL:N	12	6.0
(1,154)	1:124:B:LYS:N	1:124:B:LYS:CA	1:124:B:LYS:C	1:125:B:TYR:N	28	5.98
(1,143)	1:118:B:LEU:C	1:119:B:VAL:N	1:119:B:VAL:CA	1:119:B:VAL:C	4	5.94
(1,222)	1:185:B:LEU:N	1:185:B:LEU:CA	1:185:B:LEU:C	1:186:B:ILE:N	17	5.84
(1,218)	1:183:B:TRP:N	1:183:B:TRP:CA	1:183:B:TRP:C	1:184:B:THR:N	12	5.83
(1,158)	1:138:B:LYS:N	1:138:B:LYS:CA	1:138:B:LYS:C	1:139:B:SER:N	26	5.81
(1,75)	1:65:A:ASN:C	1:66:A:LEU:N	1:66:A:LEU:CA	1:66:A:LEU:C	27	5.77
(1,72)	1:64:A:GLN:N	1:64:A:GLN:CA	1:64:A:GLN:C	1:65:A:ASN:N	4	5.74
(1,18)	1:15:A:LEU:N	1:15:A:LEU:CA	1:15:A:LEU:C	1:16:A:VAL:N	24	5.62
(1,30)	1:21:A:LYS:N	1:21:A:LYS:CA	1:21:A:LYS:C	1:22:A:TYR:N	6	5.6
(1,199)	1:168:B:ASN:C	1:169:B:LEU:N	1:169:B:LEU:CA	1:169:B:LEU:C	22	5.54
(1,160)	1:139:B:SER:N	1:139:B:SER:CA	1:139:B:SER:C	1:140:B:SER:N	1	5.41
(1,104)	1:85:A:GLY:N	1:85:A:GLY:CA	1:85:A:GLY:C	1:86:A:ILE:N	19	5.41
(1,143)	1:118:B:LEU:C	1:119:B:VAL:N	1:119:B:VAL:CA	1:119:B:VAL:C	15	5.4
(1,104)	1:85:A:GLY:N	1:85:A:GLY:CA	1:85:A:GLY:C	1:86:A:ILE:N	8	5.35
(1,38)	1:37:A:SER:N	1:37:A:SER:CA	1:37:A:SER:C	1:38:A:PHE:N	25	5.22
(1,228)	1:188:B:GLY:N	1:188:B:GLY:CA	1:188:B:GLY:C	1:189:B:ILE:N	29	5.21
(1,104)	1:85:A:GLY:N	1:85:A:GLY:CA	1:85:A:GLY:C	1:86:A:ILE:N	28	5.2
(1,172)	1:146:B:GLN:N	1:146:B:GLN:CA	1:146:B:GLN:C	1:147:B:LYS:N	19	5.16
(1,220)	1:184:B:THR:N	1:184:B:THR:CA	1:184:B:THR:C	1:185:B:LEU:N	17	5.13
(1,38)	1:37:A:SER:N	1:37:A:SER:CA	1:37:A:SER:C	1:38:A:PHE:N	19	5.11
(1,199)	1:168:B:ASN:C	1:169:B:LEU:N	1:169:B:LEU:CA	1:169:B:LEU:C	1	4.99
(1,220)	1:184:B:THR:N	1:184:B:THR:CA	1:184:B:THR:C	1:185:B:LEU:N	27	4.96

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,200)	1:169:B:LEU:N	1:169:B:LEU:CA	1:169:B:LEU:C	1:170:B:ASP:N	29	4.88
(1,41)	1:39:A:ARG:C	1:40:A:GLU:N	1:40:A:GLU:CA	1:40:A:GLU:C	29	4.87
(1,20)	1:16:A:VAL:N	1:16:A:VAL:CA	1:16:A:VAL:C	1:17:A:GLU:N	21	4.85
(1,146)	1:120:B:GLU:N	1:120:B:GLU:CA	1:120:B:GLU:C	1:121:B:ASN:N	15	4.83
(1,76)	1:66:A:LEU:N	1:66:A:LEU:CA	1:66:A:LEU:C	1:67:A:ASP:N	30	4.78
(1,195)	1:166:B:ILE:C	1:167:B:GLN:N	1:167:B:GLN:CA	1:167:B:GLN:C	12	4.75
(1,96)	1:81:A:THR:N	1:81:A:THR:CA	1:81:A:THR:C	1:82:A:LEU:N	3	4.74
(1,98)	1:82:A:LEU:N	1:82:A:LEU:CA	1:82:A:LEU:C	1:83:A:ILE:N	2	4.71
(1,30)	1:21:A:LYS:N	1:21:A:LYS:CA	1:21:A:LYS:C	1:22:A:TYR:N	10	4.68
(1,46)	1:42:A:LEU:N	1:42:A:LEU:CA	1:42:A:LEU:C	1:43:A:GLN:N	14	4.67
(1,22)	1:17:A:GLU:N	1:17:A:GLU:CA	1:17:A:GLU:C	1:18:A:ASN:N	4	4.65
(1,185)	1:161:B:ALA:C	1:162:B:ALA:N	1:162:B:ALA:CA	1:162:B:ALA:C	4	4.6
(1,38)	1:37:A:SER:N	1:37:A:SER:CA	1:37:A:SER:C	1:38:A:PHE:N	23	4.6
(1,30)	1:21:A:LYS:N	1:21:A:LYS:CA	1:21:A:LYS:C	1:22:A:TYR:N	9	4.6
(1,200)	1:169:B:LEU:N	1:169:B:LEU:CA	1:169:B:LEU:C	1:170:B:ASP:N	13	4.55
(1,104)	1:85:A:GLY:N	1:85:A:GLY:CA	1:85:A:GLY:C	1:86:A:ILE:N	17	4.52
(1,104)	1:85:A:GLY:N	1:85:A:GLY:CA	1:85:A:GLY:C	1:86:A:ILE:N	27	4.51
(1,165)	1:142:B:ARG:C	1:143:B:GLU:N	1:143:B:GLU:CA	1:143:B:GLU:C	21	4.43
(1,104)	1:85:A:GLY:N	1:85:A:GLY:CA	1:85:A:GLY:C	1:86:A:ILE:N	5	4.41
(1,19)	1:15:A:LEU:C	1:16:A:VAL:N	1:16:A:VAL:CA	1:16:A:VAL:C	15	4.35
(1,220)	1:184:B:THR:N	1:184:B:THR:CA	1:184:B:THR:C	1:185:B:LEU:N	11	4.24
(1,38)	1:37:A:SER:N	1:37:A:SER:CA	1:37:A:SER:C	1:38:A:PHE:N	4	4.15
(1,142)	1:118:B:LEU:N	1:118:B:LEU:CA	1:118:B:LEU:C	1:119:B:VAL:N	4	4.12
(1,47)	1:42:A:LEU:C	1:43:A:GLN:N	1:43:A:GLN:CA	1:43:A:GLN:C	6	4.07
(1,223)	1:185:B:LEU:C	1:186:B:ILE:N	1:186:B:ILE:CA	1:186:B:ILE:C	5	4.01
(1,172)	1:146:B:GLN:N	1:146:B:GLN:CA	1:146:B:GLN:C	1:147:B:LYS:N	29	4.01
(1,76)	1:66:A:LEU:N	1:66:A:LEU:CA	1:66:A:LEU:C	1:67:A:ASP:N	27	3.99
(1,72)	1:64:A:GLN:N	1:64:A:GLN:CA	1:64:A:GLN:C	1:65:A:ASN:N	10	3.99
(1,154)	1:124:B:LYS:N	1:124:B:LYS:CA	1:124:B:LYS:C	1:125:B:TYR:N	9	3.98
(1,212)	1:180:B:ASP:N	1:180:B:ASP:CA	1:180:B:ASP:C	1:181:B:GLU:N	22	3.97
(1,158)	1:138:B:LYS:N	1:138:B:LYS:CA	1:138:B:LYS:C	1:139:B:SER:N	3	3.96
(1,24)	1:18:A:ASN:N	1:18:A:ASN:CA	1:18:A:ASN:C	1:19:A:PHE:N	30	3.88
(1,161)	1:139:B:SER:C	1:140:B:SER:N	1:140:B:SER:CA	1:140:B:SER:C	26	3.87
(1,171)	1:145:B:LEU:C	1:146:B:GLN:N	1:146:B:GLN:CA	1:146:B:GLN:C	8	3.86
(1,157)	1:137:B:SER:C	1:138:B:LYS:N	1:138:B:LYS:CA	1:138:B:LYS:C	11	3.86
(1,75)	1:65:A:ASN:C	1:66:A:LEU:N	1:66:A:LEU:CA	1:66:A:LEU:C	7	3.82
(1,223)	1:185:B:LEU:C	1:186:B:ILE:N	1:186:B:ILE:CA	1:186:B:ILE:C	29	3.81
(1,47)	1:42:A:LEU:C	1:43:A:GLN:N	1:43:A:GLN:CA	1:43:A:GLN:C	22	3.8
(1,170)	1:145:B:LEU:N	1:145:B:LEU:CA	1:145:B:LEU:C	1:146:B:GLN:N	19	3.79
(1,148)	1:121:B:ASN:N	1:121:B:ASN:CA	1:121:B:ASN:C	1:122:B:PHE:N	13	3.76
(1,220)	1:184:B:THR:N	1:184:B:THR:CA	1:184:B:THR:C	1:185:B:LEU:N	8	3.68
(1,144)	1:119:B:VAL:N	1:119:B:VAL:CA	1:119:B:VAL:C	1:120:B:GLU:N	2	3.67
(1,76)	1:66:A:LEU:N	1:66:A:LEU:CA	1:66:A:LEU:C	1:67:A:ASP:N	6	3.64
(1,2)	1:7:A:GLU:N	1:7:A:GLU:CA	1:7:A:GLU:C	1:8:A:LEU:N	23	3.58
(1,222)	1:185:B:LEU:N	1:185:B:LEU:CA	1:185:B:LEU:C	1:186:B:ILE:N	13	3.55
(1,98)	1:82:A:LEU:N	1:82:A:LEU:CA	1:82:A:LEU:C	1:83:A:ILE:N	17	3.53
(1,126)	1:110:B:GLU:N	1:110:B:GLU:CA	1:110:B:GLU:C	1:111:B:LEU:N	23	3.48
(1,218)	1:183:B:TRP:N	1:183:B:TRP:CA	1:183:B:TRP:C	1:184:B:THR:N	13	3.47
(1,72)	1:64:A:GLN:N	1:64:A:GLN:CA	1:64:A:GLN:C	1:65:A:ASN:N	20	3.46
(1,104)	1:85:A:GLY:N	1:85:A:GLY:CA	1:85:A:GLY:C	1:86:A:ILE:N	26	3.44
(1,94)	1:80:A:TRP:N	1:80:A:TRP:CA	1:80:A:TRP:C	1:81:A:THR:N	26	3.42

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,146)	1:120:B:GLU:N	1:120:B:GLU:CA	1:120:B:GLU:C	1:121:B:ASN:N	4	3.34
(1,73)	1:64:A:GLN:C	1:65:A:ASN:N	1:65:A:ASN:CA	1:65:A:ASN:C	11	3.34
(1,20)	1:16:A:VAL:N	1:16:A:VAL:CA	1:16:A:VAL:C	1:17:A:GLU:N	2	3.33
(1,228)	1:188:B:GLY:N	1:188:B:GLY:CA	1:188:B:GLY:C	1:189:B:ILE:N	27	3.31
(1,220)	1:184:B:THR:N	1:184:B:THR:CA	1:184:B:THR:C	1:185:B:LEU:N	25	3.31
(1,172)	1:146:B:GLN:N	1:146:B:GLN:CA	1:146:B:GLN:C	1:147:B:LYS:N	18	3.29
(1,142)	1:118:B:LEU:N	1:118:B:LEU:CA	1:118:B:LEU:C	1:119:B:VAL:N	12	3.28
(1,200)	1:169:B:LEU:N	1:169:B:LEU:CA	1:169:B:LEU:C	1:170:B:ASP:N	27	3.23
(1,104)	1:85:A:GLY:N	1:85:A:GLY:CA	1:85:A:GLY:C	1:86:A:ILE:N	13	3.21
(1,96)	1:81:A:THR:N	1:81:A:THR:CA	1:81:A:THR:C	1:82:A:LEU:N	27	3.2
(1,31)	1:21:A:LYS:C	1:22:A:TYR:N	1:22:A:TYR:CA	1:22:A:TYR:C	5	3.19
(1,75)	1:65:A:ASN:C	1:66:A:LEU:N	1:66:A:LEU:CA	1:66:A:LEU:C	22	3.17
(1,195)	1:166:B:ILE:C	1:167:B:GLN:N	1:167:B:GLN:CA	1:167:B:GLN:C	24	3.0
(1,52)	1:54:A:GLY:N	1:54:A:GLY:CA	1:54:A:GLY:C	1:55:A:ASN:N	14	2.99
(1,238)	1:198:B:HIS:N	1:198:B:HIS:CA	1:198:B:HIS:C	1:199:B:GLU:N	16	2.96
(1,150)	1:122:B:PHE:N	1:122:B:PHE:CA	1:122:B:PHE:C	1:123:B:TYR:N	4	2.94
(1,228)	1:188:B:GLY:N	1:188:B:GLY:CA	1:188:B:GLY:C	1:189:B:ILE:N	6	2.82
(1,108)	1:92:A:LYS:N	1:92:A:LYS:CA	1:92:A:LYS:C	1:93:A:LEU:N	7	2.8
(1,76)	1:66:A:LEU:N	1:66:A:LEU:CA	1:66:A:LEU:C	1:67:A:ASP:N	20	2.79
(1,162)	1:140:B:SER:N	1:140:B:SER:CA	1:140:B:SER:C	1:141:B:PHE:N	28	2.78
(1,75)	1:65:A:ASN:C	1:66:A:LEU:N	1:66:A:LEU:CA	1:66:A:LEU:C	24	2.73
(1,220)	1:184:B:THR:N	1:184:B:THR:CA	1:184:B:THR:C	1:185:B:LEU:N	13	2.71
(1,228)	1:188:B:GLY:N	1:188:B:GLY:CA	1:188:B:GLY:C	1:189:B:ILE:N	30	2.7
(1,19)	1:15:A:LEU:C	1:16:A:VAL:N	1:16:A:VAL:CA	1:16:A:VAL:C	28	2.7
(1,228)	1:188:B:GLY:N	1:188:B:GLY:CA	1:188:B:GLY:C	1:189:B:ILE:N	26	2.67
(1,146)	1:120:B:GLU:N	1:120:B:GLU:CA	1:120:B:GLU:C	1:121:B:ASN:N	8	2.67
(1,228)	1:188:B:GLY:N	1:188:B:GLY:CA	1:188:B:GLY:C	1:189:B:ILE:N	3	2.65
(1,228)	1:188:B:GLY:N	1:188:B:GLY:CA	1:188:B:GLY:C	1:189:B:ILE:N	5	2.65
(1,173)	1:146:B:GLN:C	1:147:B:LYS:N	1:147:B:LYS:CA	1:147:B:LYS:C	18	2.6
(1,201)	1:174:B:ASP:C	1:175:B:GLY:N	1:175:B:GLY:CA	1:175:B:GLY:C	30	2.53
(1,156)	1:125:B:TYR:N	1:125:B:TYR:CA	1:125:B:TYR:C	1:126:B:VAL:N	4	2.49
(1,156)	1:125:B:TYR:N	1:125:B:TYR:CA	1:125:B:TYR:C	1:126:B:VAL:N	13	2.44
(1,47)	1:42:A:LEU:C	1:43:A:GLN:N	1:43:A:GLN:CA	1:43:A:GLN:C	17	2.42
(1,228)	1:188:B:GLY:N	1:188:B:GLY:CA	1:188:B:GLY:C	1:189:B:ILE:N	10	2.41
(1,2)	1:7:A:GLU:N	1:7:A:GLU:CA	1:7:A:GLU:C	1:8:A:LEU:N	24	2.41
(1,185)	1:161:B:ALA:C	1:162:B:ALA:N	1:162:B:ALA:CA	1:162:B:ALA:C	15	2.39
(1,195)	1:166:B:ILE:C	1:167:B:GLN:N	1:167:B:GLN:CA	1:167:B:GLN:C	5	2.36
(1,76)	1:66:A:LEU:N	1:66:A:LEU:CA	1:66:A:LEU:C	1:67:A:ASP:N	4	2.33
(1,142)	1:118:B:LEU:N	1:118:B:LEU:CA	1:118:B:LEU:C	1:119:B:VAL:N	3	2.31
(1,2)	1:7:A:GLU:N	1:7:A:GLU:CA	1:7:A:GLU:C	1:8:A:LEU:N	1	2.29
(1,126)	1:110:B:GLU:N	1:110:B:GLU:CA	1:110:B:GLU:C	1:111:B:LEU:N	1	2.25
(1,2)	1:7:A:GLU:N	1:7:A:GLU:CA	1:7:A:GLU:C	1:8:A:LEU:N	30	2.25
(1,99)	1:82:A:LEU:C	1:83:A:ILE:N	1:83:A:ILE:CA	1:83:A:ILE:C	30	2.21
(1,48)	1:43:A:GLN:N	1:43:A:GLN:CA	1:43:A:GLN:C	1:44:A:LYS:N	29	2.21
(1,146)	1:120:B:GLU:N	1:120:B:GLU:CA	1:120:B:GLU:C	1:121:B:ASN:N	20	2.2
(1,119)	1:97:A:GLN:C	1:98:A:GLU:N	1:98:A:GLU:CA	1:98:A:GLU:C	14	2.16
(1,195)	1:166:B:ILE:C	1:167:B:GLN:N	1:167:B:GLN:CA	1:167:B:GLN:C	14	2.11
(1,172)	1:146:B:GLN:N	1:146:B:GLN:CA	1:146:B:GLN:C	1:147:B:LYS:N	3	2.09
(1,220)	1:184:B:THR:N	1:184:B:THR:CA	1:184:B:THR:C	1:185:B:LEU:N	15	2.07
(1,76)	1:66:A:LEU:N	1:66:A:LEU:CA	1:66:A:LEU:C	1:67:A:ASP:N	19	2.07
(1,50)	1:44:A:LYS:N	1:44:A:LYS:CA	1:44:A:LYS:C	1:45:A:GLU:N	28	2.05

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,220)	1:184:B:THR:N	1:184:B:THR:CA	1:184:B:THR:C	1:185:B:LEU:N	6	2.02
(1,220)	1:184:B:THR:N	1:184:B:THR:CA	1:184:B:THR:C	1:185:B:LEU:N	22	2.02
(1,19)	1:15:A:LEU:C	1:16:A:VAL:N	1:16:A:VAL:CA	1:16:A:VAL:C	12	2.01
(1,61)	1:58:A:ALA:C	1:59:A:ALA:N	1:59:A:ALA:CA	1:59:A:ALA:C	4	2.0
(1,22)	1:17:A:GLU:N	1:17:A:GLU:CA	1:17:A:GLU:C	1:18:A:ASN:N	15	2.0
(1,8)	1:10:A:LYS:N	1:10:A:LYS:CA	1:10:A:LYS:C	1:11:A:ALA:N	5	1.98
(1,99)	1:82:A:LEU:C	1:83:A:ILE:N	1:83:A:ILE:CA	1:83:A:ILE:C	5	1.97
(1,5)	1:8:A:LEU:C	1:9:A:GLU:N	1:9:A:GLU:CA	1:9:A:GLU:C	5	1.95
(1,99)	1:82:A:LEU:C	1:83:A:ILE:N	1:83:A:ILE:CA	1:83:A:ILE:C	9	1.94
(1,38)	1:37:A:SER:N	1:37:A:SER:CA	1:37:A:SER:C	1:38:A:PHE:N	8	1.89
(1,212)	1:180:B:ASP:N	1:180:B:ASP:CA	1:180:B:ASP:C	1:181:B:GLU:N	23	1.88
(1,98)	1:82:A:LEU:N	1:82:A:LEU:CA	1:82:A:LEU:C	1:83:A:ILE:N	6	1.87
(1,218)	1:183:B:TRP:N	1:183:B:TRP:CA	1:183:B:TRP:C	1:184:B:THR:N	29	1.86
(1,144)	1:119:B:VAL:N	1:119:B:VAL:CA	1:119:B:VAL:C	1:120:B:GLU:N	21	1.81
(1,46)	1:42:A:LEU:N	1:42:A:LEU:CA	1:42:A:LEU:C	1:43:A:GLN:N	24	1.81
(1,88)	1:77:A:ASP:N	1:77:A:ASP:CA	1:77:A:ASP:C	1:78:A:GLU:N	23	1.78
(1,153)	1:123:B:TYR:C	1:124:B:LYS:N	1:124:B:LYS:CA	1:124:B:LYS:C	27	1.77
(1,228)	1:188:B:GLY:N	1:188:B:GLY:CA	1:188:B:GLY:C	1:189:B:ILE:N	25	1.75
(1,32)	1:22:A:TYR:N	1:22:A:TYR:CA	1:22:A:TYR:C	1:23:A:VAL:N	12	1.72
(1,244)	1:201:B:GLU:N	1:201:B:GLU:CA	1:201:B:GLU:C	1:202:B:GLN:N	14	1.7
(1,22)	1:17:A:GLU:N	1:17:A:GLU:CA	1:17:A:GLU:C	1:18:A:ASN:N	10	1.69
(1,197)	1:167:B:GLN:C	1:168:B:ASN:N	1:168:B:ASN:CA	1:168:B:ASN:C	24	1.65
(1,36)	1:36:A:SER:N	1:36:A:SER:CA	1:36:A:SER:C	1:37:A:SER:N	4	1.65
(1,38)	1:37:A:SER:N	1:37:A:SER:CA	1:37:A:SER:C	1:38:A:PHE:N	28	1.62
(1,157)	1:137:B:SER:C	1:138:B:LYS:N	1:138:B:LYS:CA	1:138:B:LYS:C	24	1.61
(1,96)	1:81:A:THR:N	1:81:A:THR:CA	1:81:A:THR:C	1:82:A:LEU:N	10	1.61
(1,222)	1:185:B:LEU:N	1:185:B:LEU:CA	1:185:B:LEU:C	1:186:B:ILE:N	22	1.6
(1,150)	1:122:B:PHE:N	1:122:B:PHE:CA	1:122:B:PHE:C	1:123:B:TYR:N	18	1.59
(1,38)	1:37:A:SER:N	1:37:A:SER:CA	1:37:A:SER:C	1:38:A:PHE:N	1	1.57
(1,104)	1:85:A:GLY:N	1:85:A:GLY:CA	1:85:A:GLY:C	1:86:A:ILE:N	6	1.55
(1,148)	1:121:B:ASN:N	1:121:B:ASN:CA	1:121:B:ASN:C	1:122:B:PHE:N	24	1.54
(1,172)	1:146:B:GLN:N	1:146:B:GLN:CA	1:146:B:GLN:C	1:147:B:LYS:N	26	1.5
(1,158)	1:138:B:LYS:N	1:138:B:LYS:CA	1:138:B:LYS:C	1:139:B:SER:N	13	1.5
(1,71)	1:63:A:ILE:C	1:64:A:GLN:N	1:64:A:GLN:CA	1:64:A:GLN:C	14	1.49
(1,98)	1:82:A:LEU:N	1:82:A:LEU:CA	1:82:A:LEU:C	1:83:A:ILE:N	25	1.48
(1,24)	1:18:A:ASN:N	1:18:A:ASN:CA	1:18:A:ASN:C	1:19:A:PHE:N	28	1.48
(1,228)	1:188:B:GLY:N	1:188:B:GLY:CA	1:188:B:GLY:C	1:189:B:ILE:N	9	1.46
(1,222)	1:185:B:LEU:N	1:185:B:LEU:CA	1:185:B:LEU:C	1:186:B:ILE:N	6	1.39
(1,156)	1:125:B:TYR:N	1:125:B:TYR:CA	1:125:B:TYR:C	1:126:B:VAL:N	12	1.39
(1,148)	1:121:B:ASN:N	1:121:B:ASN:CA	1:121:B:ASN:C	1:122:B:PHE:N	9	1.39
(1,22)	1:17:A:GLU:N	1:17:A:GLU:CA	1:17:A:GLU:C	1:18:A:ASN:N	13	1.39
(1,228)	1:188:B:GLY:N	1:188:B:GLY:CA	1:188:B:GLY:C	1:189:B:ILE:N	18	1.37
(1,129)	1:111:B:LEU:C	1:112:B:GLU:N	1:112:B:GLU:CA	1:112:B:GLU:C	5	1.37
(1,28)	1:20:A:TYR:N	1:20:A:TYR:CA	1:20:A:TYR:C	1:21:A:LYS:N	3	1.37
(1,196)	1:167:B:GLN:N	1:167:B:GLN:CA	1:167:B:GLN:C	1:168:B:ASN:N	28	1.35
(1,166)	1:143:B:GLU:N	1:143:B:GLU:CA	1:143:B:GLU:C	1:144:B:MET:N	14	1.35
(1,148)	1:121:B:ASN:N	1:121:B:ASN:CA	1:121:B:ASN:C	1:122:B:PHE:N	28	1.33
(1,173)	1:146:B:GLN:C	1:147:B:LYS:N	1:147:B:LYS:CA	1:147:B:LYS:C	22	1.31
(1,48)	1:43:A:GLN:N	1:43:A:GLN:CA	1:43:A:GLN:C	1:44:A:LYS:N	18	1.31
(1,41)	1:39:A:ARG:C	1:40:A:GLU:N	1:40:A:GLU:CA	1:40:A:GLU:C	2	1.29
(1,158)	1:138:B:LYS:N	1:138:B:LYS:CA	1:138:B:LYS:C	1:139:B:SER:N	19	1.25

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,42)	1:40:A:GLU:N	1:40:A:GLU:CA	1:40:A:GLU:C	1:41:A:MET:N	3	1.24
(1,238)	1:198:B:HIS:N	1:198:B:HIS:CA	1:198:B:HIS:C	1:199:B:GLU:N	15	1.23
(1,154)	1:124:B:LYS:N	1:124:B:LYS:CA	1:124:B:LYS:C	1:125:B:TYR:N	6	1.23
(1,22)	1:17:A:GLU:N	1:17:A:GLU:CA	1:17:A:GLU:C	1:18:A:ASN:N	12	1.21
(1,154)	1:124:B:LYS:N	1:124:B:LYS:CA	1:124:B:LYS:C	1:125:B:TYR:N	27	1.2
(1,197)	1:167:B:GLN:C	1:168:B:ASN:N	1:168:B:ASN:CA	1:168:B:ASN:C	12	1.19
(1,116)	1:96:A:GLU:N	1:96:A:GLU:CA	1:96:A:GLU:C	1:97:A:GLN:N	15	1.18
(1,104)	1:85:A:GLY:N	1:85:A:GLY:CA	1:85:A:GLY:C	1:86:A:ILE:N	10	1.18
(1,158)	1:138:B:LYS:N	1:138:B:LYS:CA	1:138:B:LYS:C	1:139:B:SER:N	14	1.17
(1,148)	1:121:B:ASN:N	1:121:B:ASN:CA	1:121:B:ASN:C	1:122:B:PHE:N	4	1.17
(1,22)	1:17:A:GLU:N	1:17:A:GLU:CA	1:17:A:GLU:C	1:18:A:ASN:N	2	1.14
(1,22)	1:17:A:GLU:N	1:17:A:GLU:CA	1:17:A:GLU:C	1:18:A:ASN:N	21	1.14
(1,126)	1:110:B:GLU:N	1:110:B:GLU:CA	1:110:B:GLU:C	1:111:B:LEU:N	18	1.12
(1,71)	1:63:A:ILE:C	1:64:A:GLN:N	1:64:A:GLN:CA	1:64:A:GLN:C	12	1.12
(1,146)	1:120:B:GLU:N	1:120:B:GLU:CA	1:120:B:GLU:C	1:121:B:ASN:N	24	1.09
(1,46)	1:42:A:LEU:N	1:42:A:LEU:CA	1:42:A:LEU:C	1:43:A:GLN:N	18	1.06
(1,2)	1:7:A:GLU:N	1:7:A:GLU:CA	1:7:A:GLU:C	1:8:A:LEU:N	16	1.06
(1,165)	1:142:B:ARG:C	1:143:B:GLU:N	1:143:B:GLU:CA	1:143:B:GLU:C	29	1.05
(1,155)	1:124:B:LYS:C	1:125:B:TYR:N	1:125:B:TYR:CA	1:125:B:TYR:C	26	1.01
(1,146)	1:120:B:GLU:N	1:120:B:GLU:CA	1:120:B:GLU:C	1:121:B:ASN:N	26	1.01