



Full wwPDB NMR Structure Validation Report ⓘ

Mar 26, 2026 – 07:21 AM UTC

PDB ID : 2MES / pdb_00002mes
BMRB ID : 19238
Title : Backbone ¹H, ¹³C, ¹⁵N resonance assignments of calcium-bound calmodulin
in complex with PSD95 N-terminal peptide
Authors : Zhang, Y.; Ames, J.B.
Deposited on : 2013-09-26

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

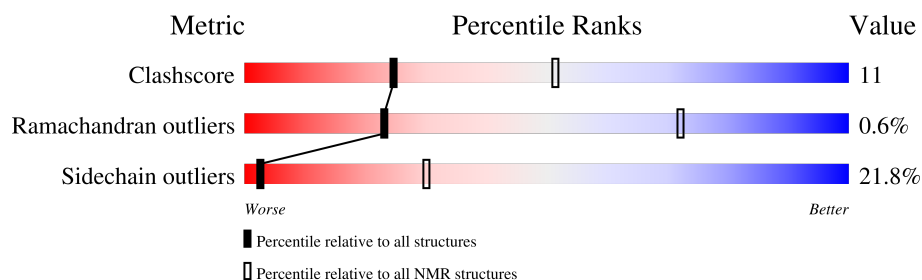
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 53%.

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	148	 72% 24% ..
2	B	71	 11% 11% . 73%

2 Ensemble composition and analysis

This entry contains 10 models. Model 9 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:147, B:1-B:19 (162)	0.69	9

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. No single-model clusters were found.

Cluster number	Models
1	1, 2, 3, 4, 5, 6, 7, 9
2	8, 10

3 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 2517 atoms, of which 1220 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Calmodulin.

Mol	Chain	Residues	Atoms						Trace
1	A	144	Total	C	H	N	O	S	0
			2198	696	1064	182	247	9	

- Molecule 2 is a protein called Disks large homolog 4.

Mol	Chain	Residues	Atoms						Trace
2	B	19	Total	C	H	N	O	S	0
			315	98	156	25	33	3	

- Molecule 3 is CALCIUM ION (CCD ID: CA) (formula: Ca).

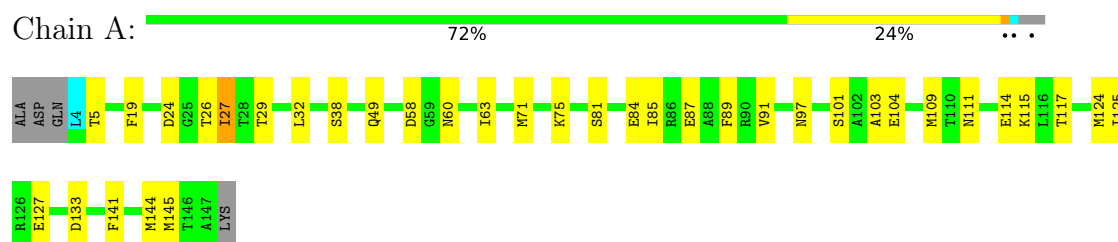
Mol	Chain	Residues	Atoms	
3	A	4	Total	Ca
			4	4

4 Residue-property plots [i](#)

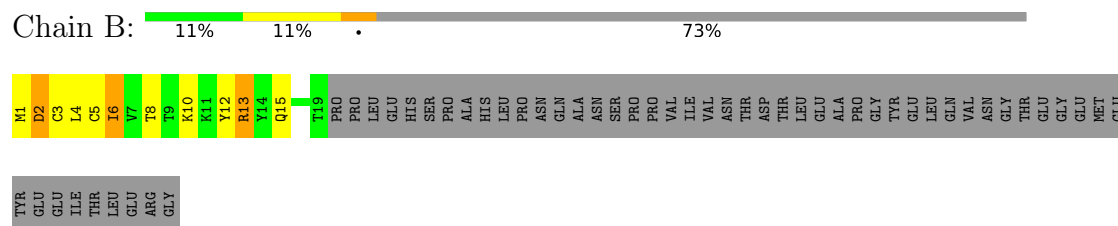
4.1 Average score per residue in the NMR ensemble

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: Calmodulin



- Molecule 2: Disks large homolog 4

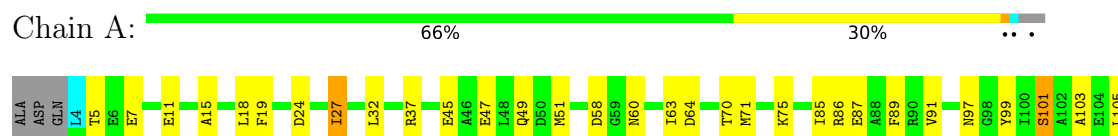


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

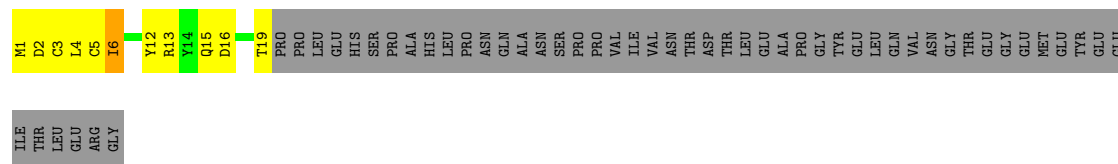
4.2.1 Score per residue for model 1

- Molecule 1: Calmodulin



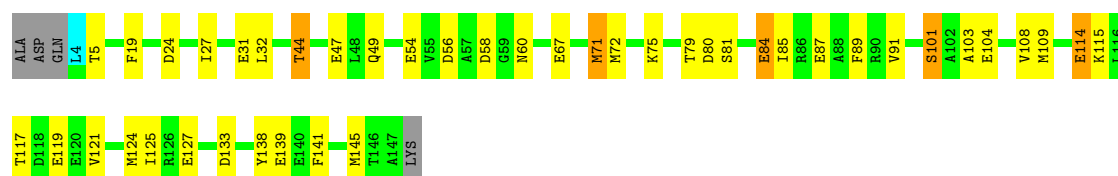


- Molecule 2: Disks large homolog 4

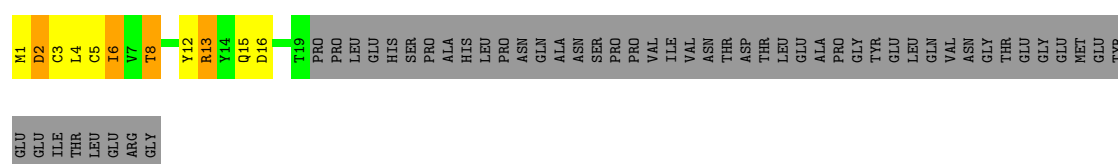


4.2.2 Score per residue for model 2

- Molecule 1: Calmodulin

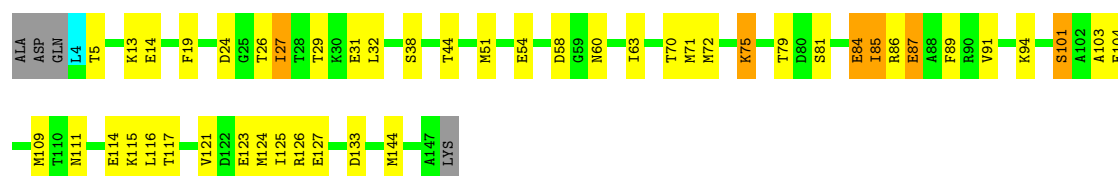


- Molecule 2: Disks large homolog 4

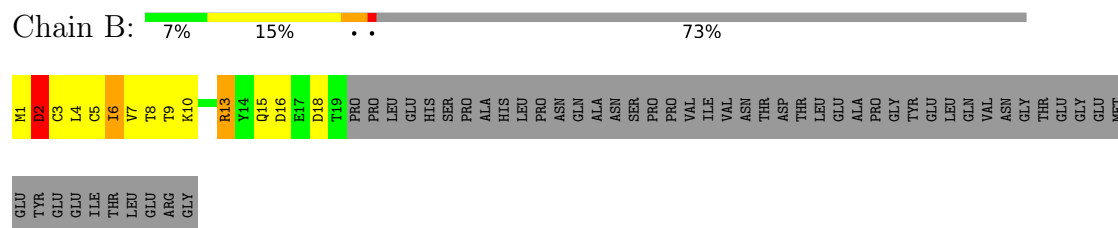


4.2.3 Score per residue for model 3

- Molecule 1: Calmodulin



- Molecule 2: Disks large homolog 4

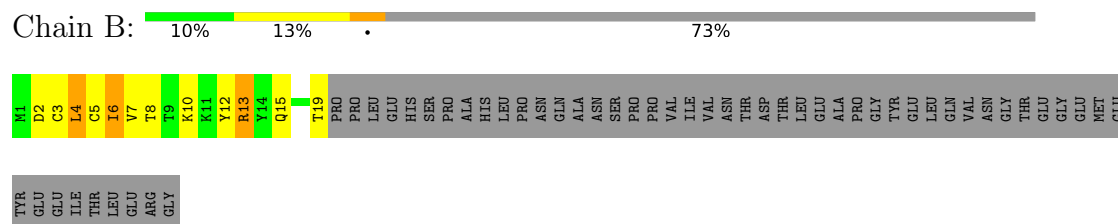


4.2.4 Score per residue for model 4

- Molecule 1: Calmodulin

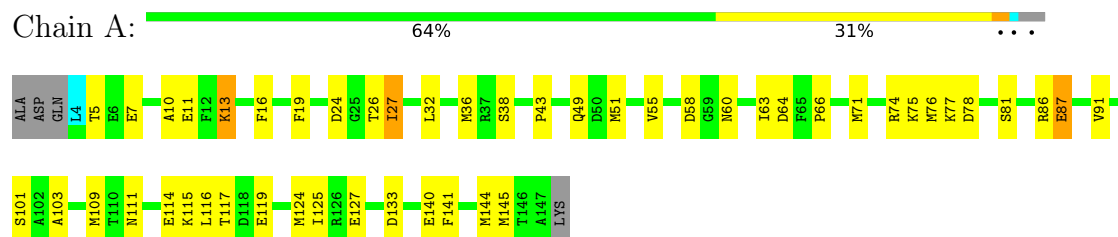


- Molecule 2: Disks large homolog 4

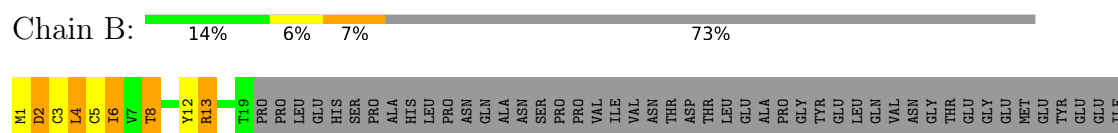


4.2.5 Score per residue for model 5

- Molecule 1: Calmodulin



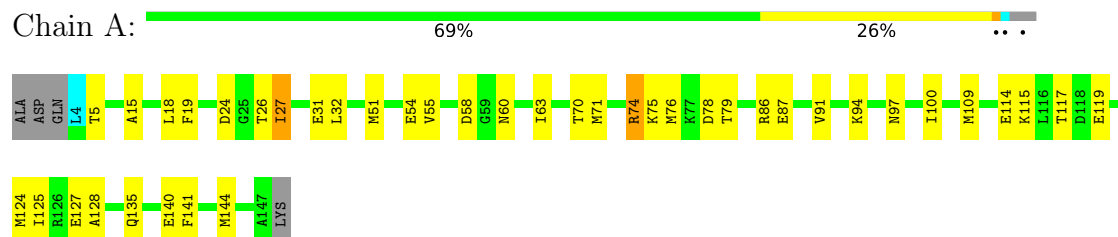
- Molecule 2: Disks large homolog 4



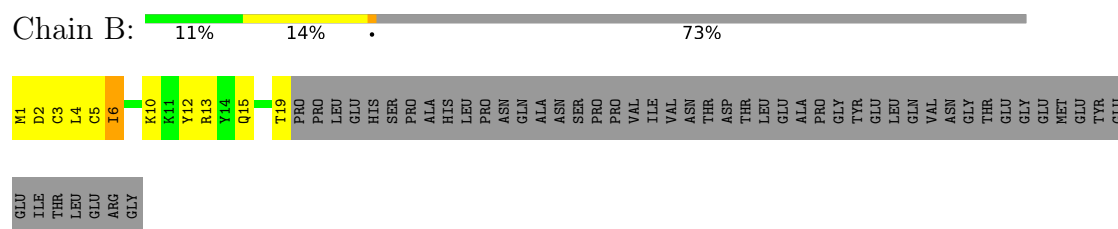
THR
LEU
GLU
ARG
GLY

4.2.6 Score per residue for model 6

- Molecule 1: Calmodulin

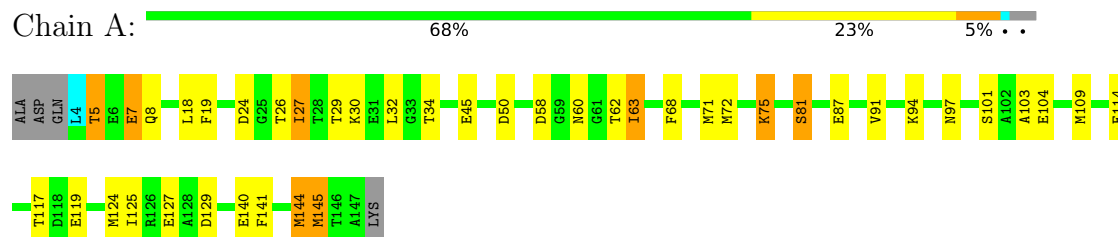


- Molecule 2: Disks large homolog 4

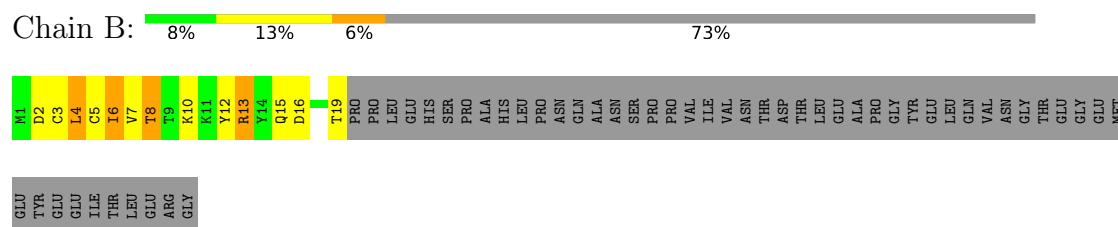


4.2.7 Score per residue for model 7

- Molecule 1: Calmodulin



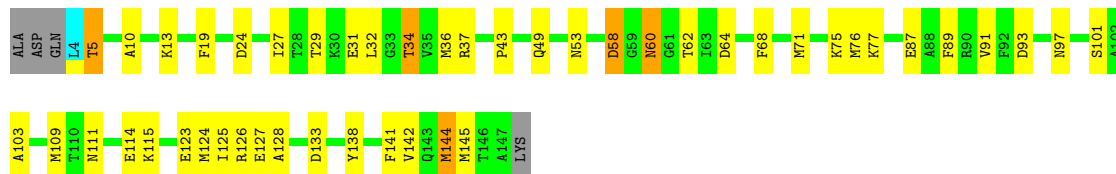
- Molecule 2: Disks large homolog 4



4.2.8 Score per residue for model 8

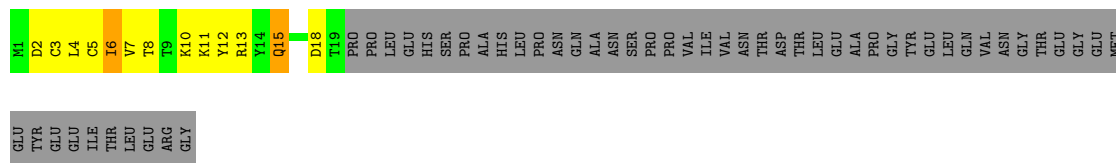
• Molecule 1: Calmodulin

Chain A:  65% 28% . . .



• Molecule 2: Disks large homolog 4

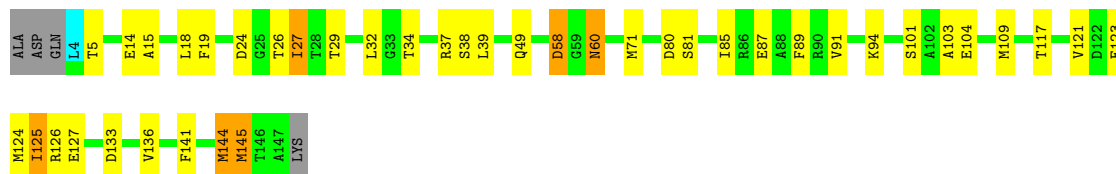
Chain B:  8% 15% . 73%



4.2.9 Score per residue for model 9 (medoid)

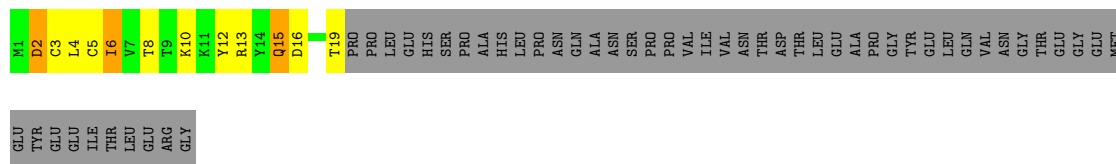
• Molecule 1: Calmodulin

Chain A:  69% 24% . . .



• Molecule 2: Disks large homolog 4

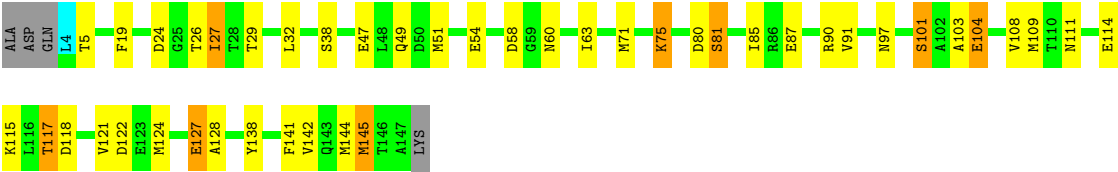
Chain B:  10% 13% . 73%



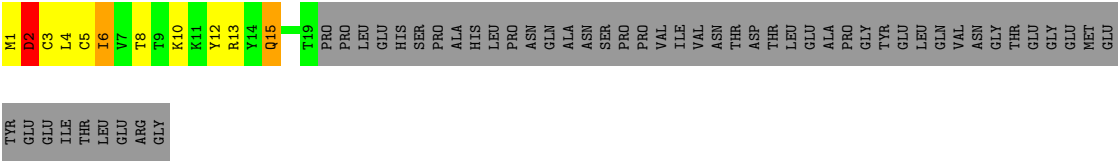
4.2.10 Score per residue for model 10

• Molecule 1: Calmodulin

Chain A:  67% 24% 5% . .



● Molecule 2: Disks large homolog 4



5 Refinement protocol and experimental data overview

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

Of the 200 calculated structures, 10 were deposited, based on the following criterion: *structures with the lowest energy*.

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

Software name	Classification	Version
CNS	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	1167
Number of shifts mapped to atoms	1149
Number of unparsed shifts	0
Number of shifts with mapping errors	18
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	53%

6 Model quality

6.1 Standard geometry

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

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

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no planarity outliers.

6.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	1126	1053	1053	26±4
2	B	159	156	156	16±2
All	All	12890	12090	12090	264

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 11.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:71:MET:HG2	2:B:4:LEU:HD21	0.82	1.48	3	1
1:A:91:VAL:HG21	2:B:5:CYS:SG	0.72	2.24	9	10
1:A:75:LYS:HE3	2:B:4:LEU:HD22	0.72	1.60	3	1
1:A:32:LEU:HD21	2:B:3:CYS:SG	0.70	2.27	9	10
1:A:124:MET:SD	2:B:13:ARG:HG2	0.69	2.26	2	3
1:A:124:MET:SD	2:B:13:ARG:HG3	0.68	2.29	1	7
1:A:19:PHE:CE2	2:B:6:ILE:HD12	0.68	2.23	5	10
1:A:71:MET:HG3	2:B:4:LEU:HD22	0.67	1.64	5	6
1:A:5:THR:HB	1:A:7:GLU:OE1	0.66	1.90	7	1
1:A:19:PHE:CZ	2:B:3:CYS:HA	0.65	2.27	9	9
1:A:71:MET:CG	2:B:4:LEU:HD22	0.65	2.21	7	8

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:27:ILE:HG21	1:A:63:ILE:HG13	0.64	1.70	4	2
1:A:84:GLU:H	1:A:84:GLU:CD	0.63	2.01	3	3
1:A:75:LYS:HB2	2:B:4:LEU:HD11	0.62	1.69	1	3
1:A:71:MET:HG2	2:B:4:LEU:CD2	0.62	2.24	3	1
1:A:74:ARG:O	1:A:78:ASP:HB2	0.62	1.94	4	3
1:A:71:MET:HG2	2:B:4:LEU:HD13	0.60	1.72	6	7
1:A:15:ALA:O	1:A:18:LEU:HG	0.59	1.96	6	3
1:A:91:VAL:HG11	2:B:5:CYS:SG	0.59	2.38	8	3
1:A:19:PHE:CE2	2:B:3:CYS:HA	0.58	2.32	7	10
1:A:145:MET:SD	2:B:8:THR:HG22	0.58	2.38	7	4
1:A:100:ILE:O	1:A:135:GLN:HA	0.57	2.00	6	1
1:A:99:TYR:CE2	1:A:137:ASN:HB3	0.57	2.35	1	1
1:A:87:GLU:OE2	2:B:4:LEU:HB3	0.56	2.01	2	3
1:A:55:VAL:HG13	2:B:1:MET:SD	0.56	2.41	6	1
1:A:141:PHE:CE1	2:B:12:TYR:CD1	0.55	2.93	10	8
1:A:71:MET:HG3	2:B:4:LEU:CD2	0.55	2.32	5	1
1:A:128:ALA:HB2	1:A:144:MET:HG3	0.55	1.78	10	2
1:A:85:ILE:O	1:A:89:PHE:HB2	0.55	2.00	9	5
1:A:55:VAL:HG11	1:A:63:ILE:HD13	0.55	1.79	4	1
1:A:55:VAL:HG22	2:B:4:LEU:HD23	0.54	1.79	5	1
1:A:51:MET:SD	2:B:1:MET:HB2	0.53	2.42	3	2
1:A:124:MET:HG3	1:A:127:GLU:OE2	0.53	2.03	5	1
1:A:141:PHE:CE2	2:B:12:TYR:CD1	0.53	2.97	5	1
1:A:145:MET:SD	2:B:8:THR:HG23	0.52	2.44	8	2
1:A:27:ILE:O	1:A:62:THR:HG23	0.52	2.05	7	1
1:A:85:ILE:CD1	1:A:142:VAL:HA	0.52	2.34	10	1
1:A:101:SER:C	1:A:103:ALA:H	0.51	2.13	9	8
1:A:140:GLU:O	1:A:144:MET:HB2	0.51	2.05	5	3
1:A:124:MET:HG3	1:A:127:GLU:OE1	0.51	2.05	6	1
1:A:7:GLU:O	1:A:11:GLU:HG3	0.50	2.05	1	2
1:A:76:MET:SD	1:A:77:LYS:HE2	0.50	2.46	5	2
2:B:9:THR:O	2:B:13:ARG:HB2	0.50	2.07	3	1
1:A:68:PHE:O	1:A:72:MET:HB2	0.50	2.06	4	2
1:A:27:ILE:CG2	1:A:63:ILE:HB	0.49	2.38	10	4
1:A:71:MET:HG2	1:A:72:MET:N	0.49	2.22	2	1
1:A:141:PHE:HE1	2:B:12:TYR:CD1	0.49	2.25	1	2
1:A:124:MET:O	1:A:127:GLU:HG2	0.49	2.08	5	2
1:A:123:GLU:HA	1:A:126:ARG:NH2	0.49	2.21	3	3
1:A:117:THR:O	1:A:121:VAL:HG23	0.49	2.07	3	3
1:A:144:MET:HE1	2:B:15:GLN:HB3	0.49	1.83	10	1
1:A:19:PHE:O	1:A:31:GLU:HB3	0.49	2.08	3	4

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:72:MET:SD	1:A:76:MET:HB2	0.49	2.48	4	1
1:A:54:GLU:HB3	2:B:1:MET:SD	0.48	2.48	6	1
1:A:27:ILE:HG23	1:A:32:LEU:HD13	0.48	1.86	7	3
1:A:114:GLU:HA	1:A:114:GLU:OE1	0.48	2.09	2	1
1:A:51:MET:HA	2:B:1:MET:SD	0.48	2.48	10	1
1:A:121:VAL:O	1:A:125:ILE:HB	0.48	2.08	9	1
1:A:144:MET:SD	2:B:15:GLN:HB3	0.48	2.48	9	1
1:A:36:MET:SD	1:A:43:PRO:HG3	0.47	2.49	8	3
1:A:116:LEU:HD11	2:B:13:ARG:HD2	0.47	1.87	3	1
2:B:1:MET:O	2:B:5:CYS:HB3	0.47	2.10	1	1
1:A:19:PHE:CD1	1:A:32:LEU:HG	0.47	2.45	3	1
1:A:84:GLU:CD	1:A:84:GLU:N	0.47	2.72	3	2
1:A:75:LYS:NZ	2:B:4:LEU:HG	0.47	2.24	6	2
1:A:32:LEU:HD23	2:B:2:ASP:CG	0.46	2.35	10	2
1:A:58:ASP:OD2	1:A:60:ASN:HB3	0.46	2.10	8	2
1:A:34:THR:O	1:A:37:ARG:HB3	0.46	2.10	8	1
2:B:3:CYS:O	2:B:7:VAL:HG23	0.46	2.10	7	3
1:A:47:GLU:O	1:A:51:MET:HG2	0.46	2.11	1	1
1:A:138:TYR:O	1:A:142:VAL:HG23	0.46	2.10	1	3
1:A:75:LYS:CE	2:B:4:LEU:HD12	0.46	2.41	5	1
1:A:75:LYS:CE	2:B:4:LEU:HG	0.44	2.42	8	1
1:A:91:VAL:HG21	2:B:5:CYS:CB	0.44	2.41	1	5
1:A:44:THR:H	1:A:47:GLU:CD	0.44	2.20	2	1
1:A:141:PHE:CD1	2:B:12:TYR:CE1	0.44	3.05	2	1
1:A:27:ILE:HB	1:A:63:ILE:O	0.44	2.13	4	1
1:A:27:ILE:HG23	1:A:32:LEU:CD1	0.43	2.43	4	2
1:A:75:LYS:HE3	2:B:4:LEU:HD11	0.43	1.90	10	1
1:A:104:GLU:O	1:A:108:VAL:HG23	0.43	2.13	10	2
1:A:37:ARG:HA	1:A:41:GLN:O	0.43	2.13	4	1
1:A:141:PHE:CE1	2:B:12:TYR:CE1	0.43	3.06	10	1
1:A:64:ASP:OD1	1:A:66:PRO:HD2	0.43	2.13	5	1
1:A:75:LYS:HZ2	2:B:4:LEU:HG	0.43	1.74	6	1
1:A:27:ILE:HG21	1:A:63:ILE:HD12	0.43	1.91	3	1
1:A:75:LYS:HG2	2:B:8:THR:OG1	0.43	2.13	4	1
1:A:145:MET:SD	2:B:8:THR:CG2	0.43	3.07	8	1
1:A:67:GLU:O	1:A:71:MET:HB3	0.42	2.14	2	1
1:A:56:ASP:HA	1:A:67:GLU:CD	0.42	2.39	2	1
1:A:124:MET:HE3	2:B:12:TYR:CD2	0.42	2.49	2	1
1:A:127:GLU:HG2	1:A:128:ALA:N	0.42	2.28	10	1
1:A:72:MET:SD	2:B:7:VAL:HG13	0.42	2.54	4	2
1:A:19:PHE:CZ	2:B:6:ILE:HD12	0.42	2.49	7	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:71:MET:SD	2:B:4:LEU:HB2	0.42	2.55	1	2
2:B:15:GLN:O	2:B:18:ASP:HB2	0.42	2.14	8	1
1:A:39:LEU:O	1:A:94:LYS:HE2	0.42	2.15	9	1
1:A:125:ILE:HD13	1:A:136:VAL:HG23	0.42	1.92	9	1
1:A:54:GLU:OE1	2:B:1:MET:HA	0.42	2.14	2	1
2:B:2:ASP:OD1	2:B:2:ASP:N	0.42	2.51	2	2
1:A:87:GLU:OE2	2:B:5:CYS:HA	0.42	2.13	3	1
1:A:51:MET:SD	2:B:1:MET:HG2	0.42	2.54	5	1
1:A:38:SER:HB2	1:A:111:ASN:OD1	0.42	2.14	4	1
1:A:10:ALA:O	1:A:13:LYS:HB3	0.42	2.14	8	2
1:A:143:GLN:O	1:A:147:ALA:HB3	0.42	2.15	4	1
1:A:127:GLU:HG3	1:A:128:ALA:N	0.41	2.30	6	1
1:A:71:MET:SD	2:B:4:LEU:HG	0.41	2.55	3	1
1:A:64:ASP:O	1:A:68:PHE:HB2	0.41	2.15	8	1
1:A:71:MET:SD	2:B:4:LEU:HD13	0.41	2.55	10	1
1:A:101:SER:C	1:A:103:ALA:N	0.41	2.78	10	1
1:A:99:TYR:CE1	1:A:137:ASN:HB3	0.41	2.51	4	1
1:A:15:ALA:HA	1:A:18:LEU:HD23	0.40	1.92	6	1
1:A:75:LYS:O	2:B:11:LYS:HG3	0.40	2.16	8	1
1:A:58:ASP:OD1	1:A:60:ASN:HB3	0.40	2.17	4	1
1:A:105:LEU:HD23	1:A:121:VAL:HG13	0.40	1.93	1	1
1:A:115:LYS:HD2	1:A:115:LYS:H	0.40	1.77	2	1
1:A:75:LYS:HE3	2:B:4:LEU:CD1	0.40	2.47	7	1
1:A:75:LYS:CE	1:A:84:GLU:HB3	0.40	2.45	4	1
1:A:60:ASN:HD21	1:A:62:THR:HB	0.40	1.76	8	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	142/148 (96%)	134±1 (95±1%)	7±1 (5±1%)	0±0 (0±0%)	31	76
2	B	17/71 (24%)	15±1 (89±4%)	1±1 (8±4%)	0±1 (2±4%)	7	44
All	All	1590/2190 (73%)	1497 (94%)	84 (5%)	9 (1%)	23	72

All 4 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	81	SER	4
2	B	2	ASP	3
2	B	18	ASP	1
1	A	103	ALA	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	122/126 (97%)	97±4 (80±3%)	25±4 (20±3%)	3	32
2	B	19/64 (30%)	13±1 (69±8%)	6±1 (31±8%)	1	16
All	All	1410/1900 (74%)	1102 (78%)	308 (22%)	2	30

All 74 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	5	THR	10
1	A	24	ASP	10
1	A	27	ILE	10
1	A	58	ASP	10
1	A	60	ASN	10
1	A	109	MET	10
2	B	2	ASP	10
2	B	6	ILE	10
1	A	114	GLU	9
2	B	15	GLN	9
1	A	125	ILE	8
1	A	127	GLU	8
1	A	49	GLN	7
1	A	115	LYS	7
1	A	26	THR	7
1	A	87	GLU	7
2	B	10	LYS	7
1	A	97	ASN	6

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Mol	Chain	Res	Type	Models (Total)
1	A	111	ASN	6
1	A	133	ASP	6
1	A	29	THR	6
1	A	117	THR	6
1	A	101	SER	5
1	A	144	MET	5
1	A	145	MET	5
2	B	16	ASP	5
2	B	19	THR	5
1	A	81	SER	5
2	B	13	ARG	5
1	A	38	SER	5
1	A	104	GLU	5
1	A	70	THR	4
1	A	86	ARG	4
1	A	75	LYS	4
1	A	79	THR	4
1	A	119	GLU	4
2	B	8	THR	4
1	A	37	ARG	3
1	A	45	GLU	3
1	A	80	ASP	3
1	A	84	GLU	3
1	A	94	LYS	3
2	B	4	LEU	3
1	A	34	THR	3
1	A	44	THR	2
1	A	138	TYR	2
1	A	13	LYS	2
1	A	14	GLU	2
1	A	54	GLU	2
1	A	16	PHE	2
1	A	63	ILE	2
1	A	74	ARG	2
1	A	89	PHE	2
1	A	64	ASP	1
1	A	131	ASP	1
1	A	71	MET	1
1	A	139	GLU	1
1	A	85	ILE	1
1	A	105	LEU	1
1	A	116	LEU	1

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Mol	Chain	Res	Type	Models (Total)
1	A	51	MET	1
1	A	76	MET	1
1	A	7	GLU	1
1	A	8	GLN	1
1	A	18	LEU	1
1	A	30	LYS	1
1	A	50	ASP	1
1	A	129	ASP	1
1	A	53	ASN	1
1	A	93	ASP	1
1	A	47	GLU	1
1	A	90	ARG	1
1	A	118	ASP	1
1	A	122	ASP	1

6.3.3 RNA [i](#)

There are no RNA molecules in this entry.

6.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.5 Carbohydrates [i](#)

There are no 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 53% for the well-defined parts and 53% 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	1167
Number of shifts mapped to atoms	1149
Number of unparsed shifts	0
Number of shifts with mapping errors	18
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	2

The following assigned chemical shifts were not mapped to the molecules present in the coordinate file.

- No matching atom found in the structure. All 18 occurrences are reported below.

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	2	ASP	HA	4.47	0.040	1
1	A	2	ASP	HB2	2.403	0.040	2
1	A	2	ASP	HB3	2.503	0.040	2
1	A	2	ASP	C	175.63	0.200	1
1	A	2	ASP	CA	54.745	0.200	1
1	A	2	ASP	CB	41.5	0.200	1
1	A	3	GLN	H	8.287	0.001	1
1	A	3	GLN	HA	4.225	0.040	1
1	A	3	GLN	HB2	1.872	0.040	2
1	A	3	GLN	HB3	1.92	0.040	2
1	A	3	GLN	C	175.599	0.200	1
1	A	3	GLN	CA	55.603	0.079	1
1	A	3	GLN	CB	29.852	0.020	1
1	A	3	GLN	N	120.104	0.023	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	148	LYS	H	7.731	0.001	1
1	A	148	LYS	CA	57.499	0.200	1
1	A	148	LYS	CB	33.741	0.200	1
1	A	148	LYS	N	126.158	0.007	1

7.1.2 Chemical shift referencing ⓘ

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	147	-0.25 ± 0.06	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	136	0.14 ± 0.06	None needed (< 0.5 ppm)
$^{13}\text{C}'$	138	-0.47 ± 0.10	None needed (< 0.5 ppm)
^{15}N	143	-0.32 ± 0.26	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 53%, i.e. 1141 atoms were assigned a chemical shift out of a possible 2134. 0 out of 17 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	707/817 (87%)	289/333 (87%)	278/324 (86%)	140/160 (88%)
Sidechain	434/1194 (36%)	283/763 (37%)	151/389 (39%)	0/42 (0%)
Aromatic	0/123 (0%)	0/60 (0%)	0/62 (0%)	0/1 (0%)
Overall	1141/2134 (53%)	572/1156 (49%)	429/775 (55%)	140/203 (69%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 53%, i.e. 1149 atoms were assigned a chemical shift out of a possible 2152. 0 out of 18 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	712/822 (87%)	291/335 (87%)	280/326 (86%)	141/161 (88%)
Sidechain	437/1207 (36%)	285/772 (37%)	152/393 (39%)	0/42 (0%)
Aromatic	0/123 (0%)	0/60 (0%)	0/62 (0%)	0/1 (0%)
Overall	1149/2152 (53%)	576/1167 (49%)	432/781 (55%)	141/204 (69%)

7.1.4 Statistically unusual chemical shifts [i](#)

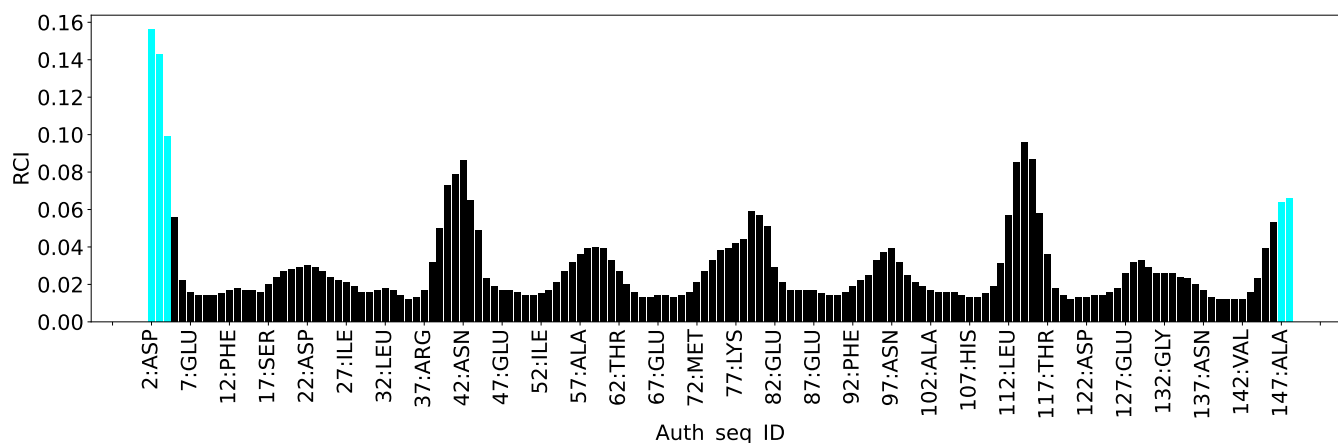
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	93	ASP	HB2	1.21	1.41 – 4.01	-5.8
1	A	20	ASP	HB2	1.35	1.41 – 4.01	-5.2

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

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

Random coil index (RCI) for chain A:



8 NMR restraints analysis

8.1 Conformationally restricting restraints

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

Description	Value
Total distance restraints	175
Intra-residue ($ i-j =0$)	0
Sequential ($ i-j =1$)	0
Medium range ($ i-j >1$ and $ i-j <5$)	12
Long range ($ i-j \geq 5$)	0
Inter-chain	128
Hydrogen bond restraints	35
Disulfide bond restraints	0
Total dihedral-angle restraints	47
Number of unmapped restraints	0
Number of restraints per residue	1.0
Number of long range restraints per residue ¹	0.0

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

8.2 Residual restraint violations

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

8.2.1 Average number of distance violations per model

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

Bins (Å)	Average number of violations per model	Max (Å)
0.1-0.2 (Small)	15.1	0.2
0.2-0.5 (Medium)	12.4	0.5
>0.5 (Large)	72.0	9.71

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)	2.1	8.69
10.0-20.0 (Medium)	0.3	13.77
>20.0 (Large)	None	None

9 Distance violation analysis ⓘ

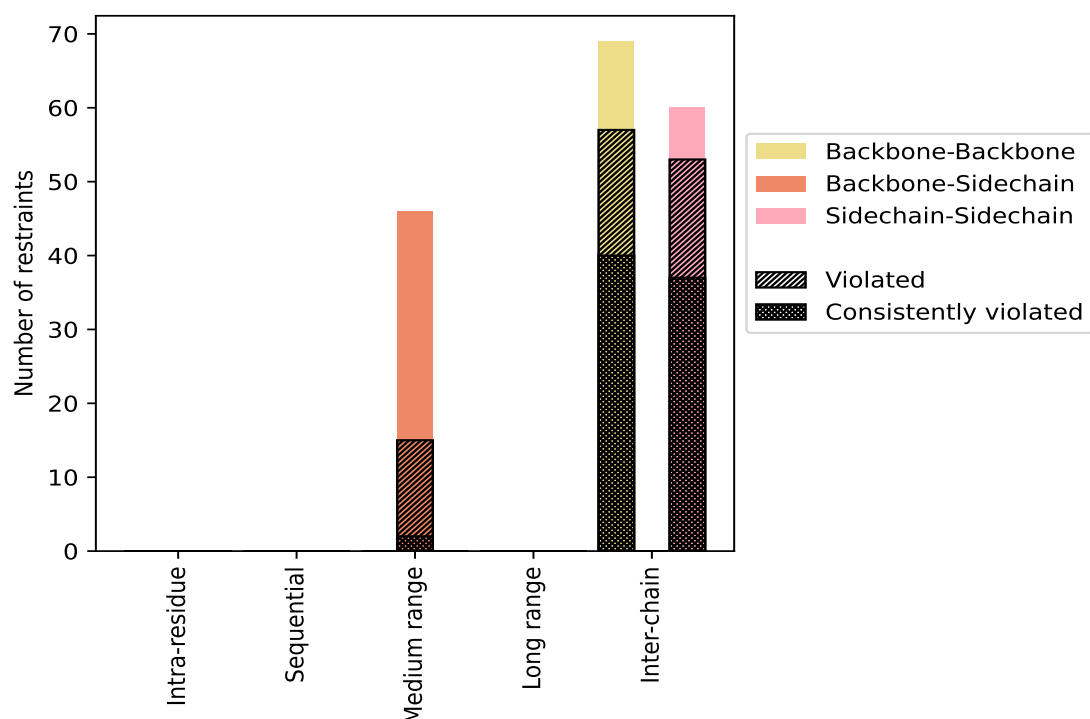
9.1 Summary of distance violations ⓘ

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

Restrains type	Count	% ¹	Violated ³			Consistently Violated ⁴		
			Count	% ²	% ¹	Count	% ²	% ¹
Intra-residue ($ i-j =0$)	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Sequential ($ i-j =1$)	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Medium range ($ i-j >1$ & $ i-j <5$)	12	6.9	11	91.7	6.3	2	16.7	1.1
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	12	6.9	11	91.7	6.3	2	16.7	1.1
Sidechain-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Long range ($ i-j \geq 5$)	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Inter-chain	128	73.1	109	85.2	62.3	77	60.2	44.0
Backbone-Backbone	69	39.4	57	82.6	32.6	40	58.0	22.9
Backbone-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	59	33.7	52	88.1	29.7	37	62.7	21.1
Hydrogen bond	35	20.0	5	14.3	2.9	0	0.0	0.0
Disulfide bond	0	0.0	0	0.0	0.0	0	0.0	0.0
Total	175	100.0	125	71.4	71.4	79	45.1	45.1
Backbone-Backbone	69	39.4	57	82.6	32.6	40	58.0	22.9
Backbone-Sidechain	46	26.3	15	32.6	8.6	2	4.3	1.1
Sidechain-Sidechain	60	34.3	53	88.3	30.3	37	61.7	21.1

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

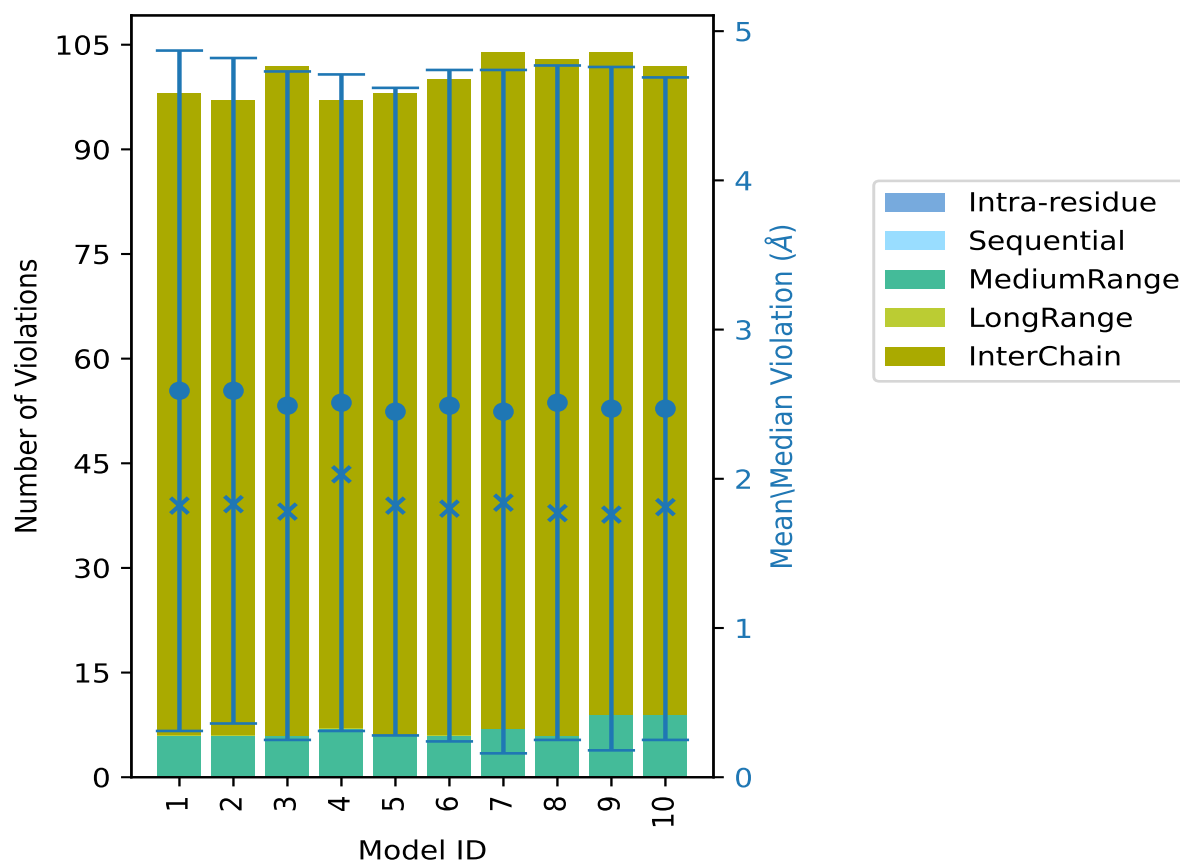
9.2 Distance violation statistics for each model [i](#)

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	0	0	6	0	92	98	2.59	9.71	2.28	1.82
2	0	0	6	0	91	97	2.59	8.39	2.23	1.83
3	0	0	6	0	96	102	2.49	8.69	2.24	1.78
4	0	0	7	0	90	97	2.51	8.9	2.2	2.03
5	0	0	6	0	92	98	2.45	8.91	2.17	1.82
6	0	0	6	0	94	100	2.49	8.72	2.25	1.8
7	0	0	7	0	97	104	2.45	9.29	2.29	1.84
8	0	0	6	0	97	103	2.51	9.04	2.26	1.77
9	0	0	9	0	95	104	2.47	9.34	2.29	1.76
10	0	0	9	0	93	102	2.47	8.89	2.22	1.81

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, 20(IR:0, SQ:0, MR:1, LR:0, IC:19) restraints are not violated in the ensemble.

Number of violated restraints						Fraction of the ensemble	
IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total	Count ⁶	%
0	0	1	0	6	7	1	10.0
0	0	2	0	6	8	2	20.0
0	0	0	0	3	3	3	30.0

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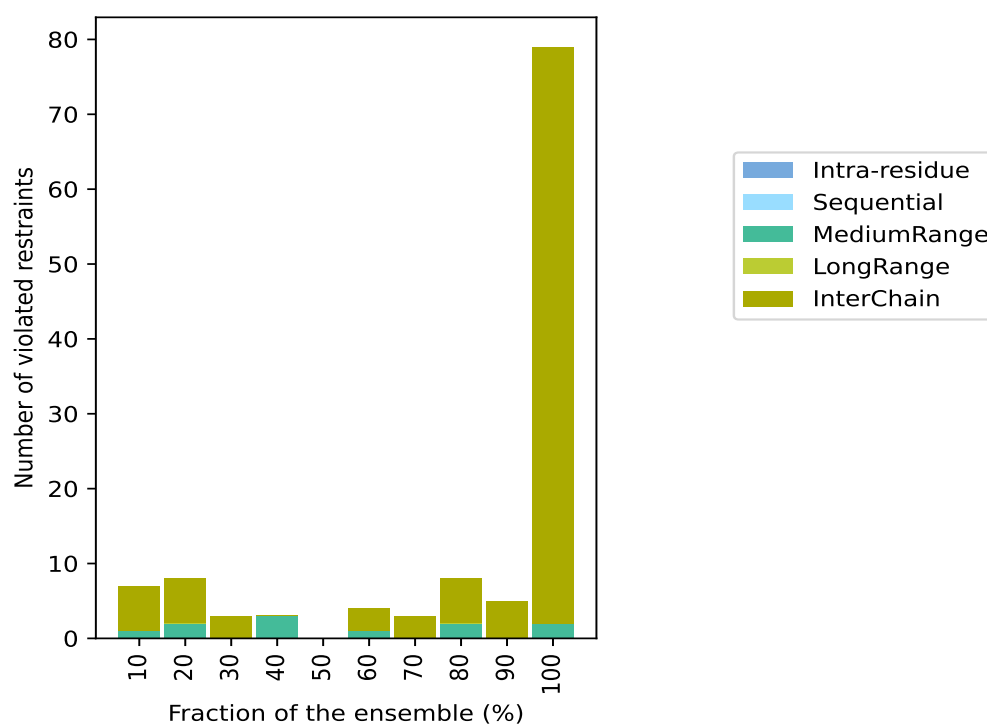
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Number of violated restraints						Fraction of the ensemble	
IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total	Count ⁶	%
0	0	3	0	0	3	4	40.0
0	0	0	0	0	0	5	50.0
0	0	1	0	3	4	6	60.0
0	0	0	0	3	3	7	70.0
0	0	2	0	6	8	8	80.0
0	0	0	0	5	5	9	90.0
0	0	2	0	77	79	10	100.0

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](#)

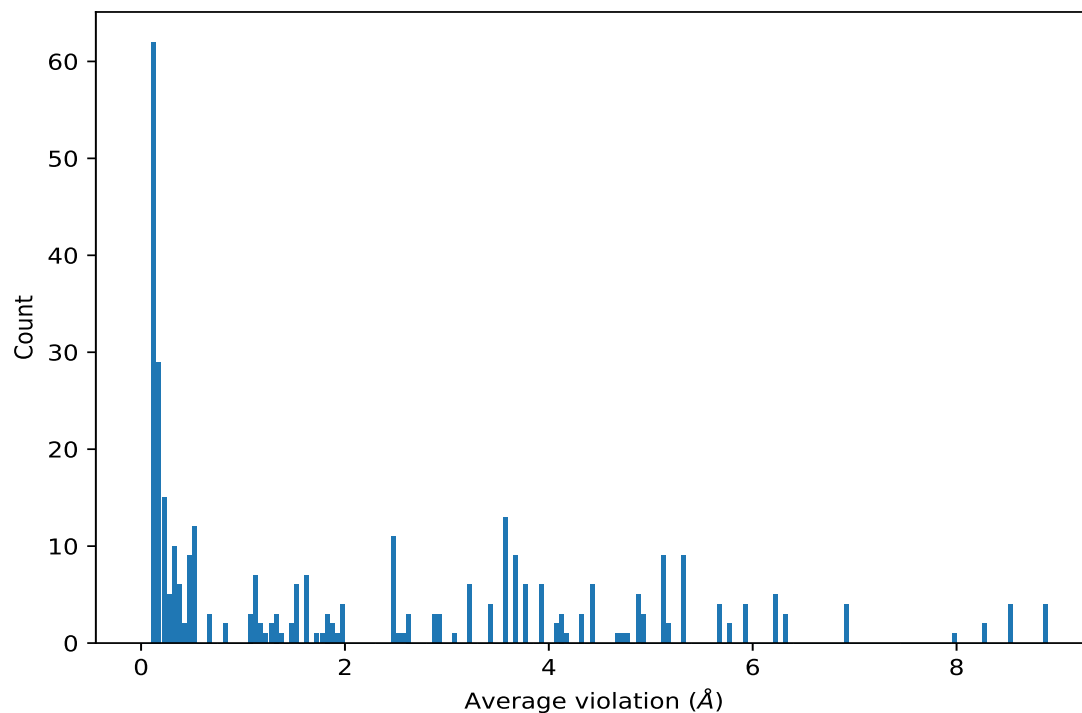


9.4 Most violated distance restraints in the ensemble [i](#)

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)
(1,35)	1:58:A:ASP:H	2:4:B:LEU:HD21	10	8.85	0.49	8.9
(1,35)	1:58:A:ASP:H	2:4:B:LEU:HD12	10	8.85	0.49	8.9
(1,35)	1:58:A:ASP:H	2:4:B:LEU:HD23	10	8.85	0.49	8.9
(1,35)	1:58:A:ASP:H	2:4:B:LEU:HD22	10	8.85	0.49	8.9
(1,56)	1:118:A:ASP:HA	2:13:B:ARG:HD2	10	8.53	0.4	8.44
(1,56)	1:118:A:ASP:O	2:13:B:ARG:HD2	10	8.53	0.4	8.44
(1,56)	1:118:A:ASP:N	2:13:B:ARG:HE	10	8.53	0.4	8.44
(1,56)	1:118:A:ASP:N	2:13:B:ARG:HH21	10	8.53	0.4	8.44
(1,17)	1:24:A:ASP:OD1	2:3:B:CYS:HG	10	8.25	0.09	8.24
(1,17)	1:24:A:ASP:OD2	2:3:B:CYS:HG	10	8.25	0.09	8.24
(1,62)	1:131:A:ASP:H	2:12:B:TYR:HH	10	7.96	0.19	8.04
(1,50)	1:106:A:ARG:HA	2:13:B:ARG:HD2	10	6.93	0.26	7.0
(1,50)	1:106:A:ARG:N	2:9:B:THR:HG22	10	6.93	0.26	7.0
(1,50)	1:106:A:ARG:N	2:9:B:THR:HG21	10	6.93	0.26	7.0
(1,50)	1:106:A:ARG:N	2:9:B:THR:HG23	10	6.93	0.26	7.0

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,52)	1:110:A:THR:N	2:9:B:THR:HG23	10	6.33	0.19	6.32
(1,52)	1:110:A:THR:N	2:9:B:THR:HG21	10	6.33	0.19	6.32
(1,52)	1:110:A:THR:N	2:9:B:THR:HG22	10	6.33	0.19	6.32
(1,34)	1:57:A:ALA:HB2	2:4:B:LEU:HD21	10	6.2	0.48	6.36
(1,34)	1:57:A:ALA:HB2	2:4:B:LEU:HD13	10	6.2	0.48	6.36
(1,34)	1:57:A:ALA:HB2	2:4:B:LEU:HD23	10	6.2	0.48	6.36
(1,34)	1:57:A:ALA:HB2	2:1:B:MET:HE1	10	6.2	0.48	6.36
(1,34)	1:57:A:ALA:HB2	2:4:B:LEU:HD22	10	6.2	0.48	6.36
(1,61)	1:130:A:ILE:H	2:12:B:TYR:HH	10	5.9	0.17	5.86
(1,61)	1:130:A:ILE:HG12	2:12:B:TYR:HH	10	5.9	0.17	5.86
(1,61)	1:130:A:ILE:HD11	2:12:B:TYR:HH	10	5.9	0.17	5.86
(1,61)	1:130:A:ILE:HD13	2:12:B:TYR:HE1	10	5.9	0.17	5.86
(1,28)	1:37:A:ARG:H	2:2:B:ASP:HB3	10	5.76	0.4	5.87
(1,28)	1:37:A:ARG:H	2:2:B:ASP:OD2	10	5.76	0.4	5.87
(1,25)	1:34:A:THR:N	2:2:B:ASP:HB3	10	5.69	0.44	5.78
(1,25)	1:34:A:THR:H	2:2:B:ASP:OD2	10	5.69	0.44	5.78
(1,25)	1:34:A:THR:H	2:2:B:ASP:HB3	10	5.69	0.44	5.78
(1,25)	1:34:A:THR:N	2:2:B:ASP:OD2	10	5.69	0.44	5.78
(1,121)	1:79:A:THR:HG21	2:8:B:THR:HG21	10	5.34	0.4	5.24
(1,121)	1:79:A:THR:HG21	2:8:B:THR:HG22	10	5.34	0.4	5.24
(1,121)	1:79:A:THR:HG21	2:8:B:THR:HG23	10	5.34	0.4	5.24
(1,121)	1:79:A:THR:HG22	2:8:B:THR:HG21	10	5.34	0.4	5.24
(1,121)	1:79:A:THR:HG22	2:8:B:THR:HG22	10	5.34	0.4	5.24
(1,121)	1:79:A:THR:HG22	2:8:B:THR:HG23	10	5.34	0.4	5.24
(1,121)	1:79:A:THR:HG23	2:8:B:THR:HG21	10	5.34	0.4	5.24
(1,121)	1:79:A:THR:HG23	2:8:B:THR:HG22	10	5.34	0.4	5.24
(1,121)	1:79:A:THR:HG23	2:8:B:THR:HG23	10	5.34	0.4	5.24
(1,15)	1:17:A:SER:H	2:6:B:ILE:HD11	10	5.19	0.18	5.18
(1,15)	1:17:A:SER:H	2:6:B:ILE:HD12	10	5.19	0.18	5.18
(1,30)	1:49:A:GLN:O	2:1:B:MET:HG2	10	5.13	0.21	5.11
(1,30)	1:49:A:GLN:O	2:1:B:MET:HG3	10	5.13	0.21	5.11
(1,30)	1:49:A:GLN:O	2:1:B:MET:N	10	5.13	0.21	5.11
(1,30)	1:49:A:GLN:HA	2:2:B:ASP:OD2	10	5.13	0.21	5.11
(1,30)	1:49:A:GLN:O	2:2:B:ASP:OD1	10	5.13	0.21	5.11
(1,30)	1:49:A:GLN:O	2:1:B:MET:HE1	10	5.13	0.21	5.11
(1,22)	1:31:A:GLU:HB2	2:3:B:CYS:HG	10	5.13	0.11	5.12
(1,22)	1:31:A:GLU:C	2:2:B:ASP:OD2	10	5.13	0.11	5.12
(1,22)	1:31:A:GLU:C	2:2:B:ASP:HB2	10	5.13	0.11	5.12
(1,53)	1:111:A:ASN:O	2:6:B:ILE:HD13	10	4.9	0.27	4.86
(1,53)	1:111:A:ASN:C	2:6:B:ILE:HD13	10	4.9	0.27	4.86
(1,53)	1:111:A:ASN:O	2:6:B:ILE:HD11	10	4.9	0.27	4.86
(1,18)	1:26:A:THR:C	2:3:B:CYS:HG	10	4.88	0.07	4.88

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,39)	1:69:A:LEU:O	2:7:B:VAL:HG12	10	4.86	0.3	4.9
(1,39)	1:69:A:LEU:O	2:7:B:VAL:HG11	10	4.86	0.3	4.9
(1,39)	1:69:A:LEU:O	2:7:B:VAL:HG23	10	4.86	0.3	4.9
(1,39)	1:69:A:LEU:O	2:4:B:LEU:HD11	10	4.86	0.3	4.9
(1,137)	1:141:A:PHE:CD2	2:12:B:TYR:CE2	10	4.75	0.74	5.04
(1,136)	1:141:A:PHE:CD2	2:12:B:TYR:CD2	10	4.73	0.72	4.94
(1,37)	1:64:A:ASP:N	2:3:B:CYS:HG	10	4.69	0.31	4.77
(1,138)	1:141:A:PHE:CE2	2:12:B:TYR:CE2	10	4.43	0.76	4.68
(1,57)	1:121:A:VAL:HA	2:13:B:ARG:HD2	10	4.4	0.34	4.42
(1,57)	1:121:A:VAL:O	2:12:B:TYR:HE2	10	4.4	0.34	4.42
(1,57)	1:121:A:VAL:HG21	2:13:B:ARG:HD2	10	4.4	0.34	4.42
(1,57)	1:121:A:VAL:HG13	2:12:B:TYR:HE2	10	4.4	0.34	4.42
(1,57)	1:121:A:VAL:HA	2:13:B:ARG:HG3	10	4.4	0.34	4.42
(1,21)	1:29:A:THR:HA	2:2:B:ASP:OD2	10	4.3	0.37	4.31
(1,21)	1:29:A:THR:HA	2:2:B:ASP:OD1	10	4.3	0.37	4.31
(1,21)	1:29:A:THR:HG22	2:2:B:ASP:OD1	10	4.3	0.37	4.31
(1,135)	1:141:A:PHE:CE2	2:12:B:TYR:CD2	10	4.16	0.78	4.41
(1,64)	1:142:A:VAL:N	2:12:B:TYR:HE1	10	4.14	0.34	4.26
(1,64)	1:142:A:VAL:O	2:11:B:LYS:HZ3	10	4.14	0.34	4.26
(1,65)	1:143:A:GLN:O	2:15:B:GLN:HG2	10	4.11	0.33	4.18
(1,20)	1:28:A:THR:O	2:3:B:CYS:HG	10	4.07	0.1	4.07
(1,20)	1:28:A:THR:H	2:3:B:CYS:HG	10	4.07	0.1	4.07
(1,31)	1:53:A:ASN:N	2:1:B:MET:HB2	10	3.91	0.75	4.23
(1,31)	1:53:A:ASN:C	2:1:B:MET:HG2	10	3.91	0.75	4.23
(1,31)	1:53:A:ASN:HD21	2:1:B:MET:HE3	10	3.91	0.75	4.23
(1,31)	1:53:A:ASN:H	2:1:B:MET:N	10	3.91	0.75	4.23
(1,31)	1:53:A:ASN:N	2:1:B:MET:N	10	3.91	0.75	4.23
(1,31)	1:53:A:ASN:HD21	2:1:B:MET:HE1	10	3.91	0.75	4.23
(1,129)	1:79:A:THR:HG21	2:11:B:LYS:HG2	10	3.78	0.47	3.55
(1,129)	1:79:A:THR:HG21	2:11:B:LYS:HG3	10	3.78	0.47	3.55
(1,129)	1:79:A:THR:HG22	2:11:B:LYS:HG2	10	3.78	0.47	3.55
(1,129)	1:79:A:THR:HG22	2:11:B:LYS:HG3	10	3.78	0.47	3.55
(1,129)	1:79:A:THR:HG23	2:11:B:LYS:HG2	10	3.78	0.47	3.55
(1,129)	1:79:A:THR:HG23	2:11:B:LYS:HG3	10	3.78	0.47	3.55
(1,46)	1:86:A:ARG:HB3	2:1:B:MET:HE1	10	3.67	0.51	3.84
(1,46)	1:86:A:ARG:O	2:1:B:MET:HG2	10	3.67	0.51	3.84
(1,46)	1:86:A:ARG:HG2	2:1:B:MET:HE1	10	3.67	0.51	3.84
(1,46)	1:86:A:ARG:C	2:1:B:MET:HG2	10	3.67	0.51	3.84
(1,46)	1:86:A:ARG:HB3	2:1:B:MET:HE3	10	3.67	0.51	3.84
(1,46)	1:86:A:ARG:N	2:8:B:THR:HG21	10	3.67	0.51	3.84
(1,40)	1:70:A:THR:O	2:4:B:LEU:HD13	10	3.66	0.18	3.64
(1,40)	1:70:A:THR:O	2:4:B:LEU:HD11	10	3.66	0.18	3.64

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,40)	1:70:A:THR:O	2:4:B:LEU:HD21	10	3.66	0.18	3.64
(1,45)	1:81:A:SER:HG	2:11:B:LYS:HZ1	10	3.59	0.81	3.72
(1,45)	1:81:A:SER:HG	2:11:B:LYS:HZ2	10	3.59	0.81	3.72
(1,45)	1:81:A:SER:HG	2:11:B:LYS:HE3	10	3.59	0.81	3.72
(1,45)	1:81:A:SER:HG	2:8:B:THR:HG22	10	3.59	0.81	3.72
(1,45)	1:81:A:SER:HG	2:8:B:THR:HG21	10	3.59	0.81	3.72
(1,24)	1:33:A:GLY:HA2	2:2:B:ASP:HB3	10	3.58	0.53	3.66
(1,24)	1:33:A:GLY:HA2	2:2:B:ASP:OD2	10	3.58	0.53	3.66
(1,24)	1:33:A:GLY:N	2:2:B:ASP:HB3	10	3.58	0.53	3.66
(1,24)	1:33:A:GLY:N	2:2:B:ASP:OD2	10	3.58	0.53	3.66
(1,29)	1:48:A:LEU:O	2:2:B:ASP:OD2	10	3.57	0.22	3.62
(1,29)	1:48:A:LEU:HD21	2:2:B:ASP:OD2	10	3.57	0.22	3.62
(1,29)	1:48:A:LEU:HD22	2:2:B:ASP:OD2	10	3.57	0.22	3.62
(1,29)	1:48:A:LEU:O	2:2:B:ASP:OD1	10	3.57	0.22	3.62
(1,14)	1:16:A:PHE:N	2:6:B:ILE:HG22	10	3.44	0.12	3.49
(1,14)	1:16:A:PHE:H	2:6:B:ILE:HG22	10	3.44	0.12	3.49
(1,14)	1:16:A:PHE:N	2:6:B:ILE:HD11	10	3.44	0.12	3.49
(1,14)	1:16:A:PHE:N	2:6:B:ILE:HD12	10	3.44	0.12	3.49
(1,130)	1:79:A:THR:HG21	2:11:B:LYS:HD2	10	3.21	0.62	3.16
(1,130)	1:79:A:THR:HG21	2:11:B:LYS:HD3	10	3.21	0.62	3.16
(1,130)	1:79:A:THR:HG22	2:11:B:LYS:HD2	10	3.21	0.62	3.16
(1,130)	1:79:A:THR:HG22	2:11:B:LYS:HD3	10	3.21	0.62	3.16
(1,130)	1:79:A:THR:HG23	2:11:B:LYS:HD2	10	3.21	0.62	3.16
(1,130)	1:79:A:THR:HG23	2:11:B:LYS:HD3	10	3.21	0.62	3.16
(1,131)	1:124:A:MET:CG	2:12:B:TYR:HH	10	3.08	0.32	3.14
(1,26)	1:35:A:VAL:HG12	2:6:B:ILE:HD13	10	2.94	0.45	3.09
(1,26)	1:35:A:VAL:HB	2:2:B:ASP:HB3	10	2.94	0.45	3.09
(1,26)	1:35:A:VAL:HG12	2:6:B:ILE:HD11	10	2.94	0.45	3.09
(1,43)	1:73:A:ALA:N	2:7:B:VAL:HG12	10	2.89	0.31	2.96
(1,43)	1:73:A:ALA:N	2:7:B:VAL:HG11	10	2.89	0.31	2.96
(1,43)	1:73:A:ALA:N	2:7:B:VAL:HG13	10	2.89	0.31	2.96
(1,94)	1:55:A:VAL:HG21	2:3:B:CYS:HG	10	2.65	0.19	2.7
(1,94)	1:55:A:VAL:HG22	2:3:B:CYS:HG	10	2.65	0.19	2.7
(1,94)	1:55:A:VAL:HG23	2:3:B:CYS:HG	10	2.65	0.19	2.7
(1,60)	1:129:A:ASP:H	2:12:B:TYR:HH	10	2.56	0.18	2.58
(1,102)	1:19:A:PHE:CZ	2:5:B:CYS:HG	10	2.52	0.15	2.47
(1,47)	1:90:A:ARG:HE	2:1:B:MET:SD	10	2.48	1.62	2.9
(1,47)	1:90:A:ARG:HH12	2:1:B:MET:SD	10	2.48	1.62	2.9
(1,47)	1:90:A:ARG:HH12	2:1:B:MET:HE2	10	2.48	1.62	2.9
(1,47)	1:90:A:ARG:HD3	2:1:B:MET:HB3	10	2.48	1.62	2.9
(1,47)	1:90:A:ARG:HD2	2:1:B:MET:HE1	10	2.48	1.62	2.9
(1,47)	1:90:A:ARG:H	2:5:B:CYS:HB2	10	2.48	1.62	2.9

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,47)	1:90:A:ARG:HH12	2:1:B:MET:HE1	10	2.48	1.62	2.9
(1,47)	1:90:A:ARG:HB2	2:1:B:MET:HG2	10	2.48	1.62	2.9
(1,81)	2:14:B:TYR:HD1	1:11:A:GLU:OE2	10	2.45	0.37	2.44
(1,81)	2:14:B:TYR:HD1	1:11:A:GLU:OE1	10	2.45	0.37	2.44
(1,81)	2:14:B:TYR:H	1:144:A:MET:HE2	10	2.45	0.37	2.44
(1,67)	1:146:A:THR:HA	2:11:B:LYS:HZ1	10	1.96	0.34	1.91
(1,67)	1:146:A:THR:N	2:11:B:LYS:HZ3	10	1.96	0.34	1.91
(1,67)	1:146:A:THR:HA	2:11:B:LYS:HZ2	10	1.96	0.34	1.91
(1,67)	1:146:A:THR:N	2:11:B:LYS:HZ1	10	1.96	0.34	1.91
(1,86)	1:19:A:PHE:CE1	2:3:B:CYS:SG	10	1.94	0.13	1.91
(1,132)	1:127:A:GLU:CD	2:12:B:TYR:CE1	10	1.9	0.19	1.85
(1,84)	1:19:A:PHE:CD1	2:3:B:CYS:SG	10	1.89	0.14	1.86
(1,82)	1:19:A:PHE:HB2	2:3:B:CYS:SG	10	1.8	0.14	1.79
(1,82)	1:19:A:PHE:HB3	2:3:B:CYS:SG	10	1.8	0.14	1.79
(1,106)	1:91:A:VAL:CB	2:5:B:CYS:SG	10	1.8	0.09	1.79
(1,99)	1:71:A:MET:SD	2:4:B:LEU:CD2	10	1.79	0.28	1.85
(1,93)	1:32:A:LEU:HG	2:3:B:CYS:SG	10	1.71	0.1	1.68
(1,49)	1:105:A:LEU:HD21	2:12:B:TYR:HE2	10	1.64	0.21	1.57
(1,49)	1:105:A:LEU:HD22	2:12:B:TYR:HE2	10	1.64	0.21	1.57
(1,49)	1:105:A:LEU:HD13	2:12:B:TYR:HE2	10	1.64	0.21	1.57
(1,101)	1:71:A:MET:CG	2:4:B:LEU:CG	10	1.62	0.2	1.64
(1,97)	1:63:A:ILE:HG12	2:3:B:CYS:HG	10	1.62	0.67	1.89
(1,97)	1:63:A:ILE:HG13	2:3:B:CYS:HG	10	1.62	0.67	1.89
(1,83)	1:19:A:PHE:CG	2:3:B:CYS:SG	10	1.61	0.15	1.56
(1,54)	1:115:A:LYS:HD2	2:13:B:ARG:HH22	10	1.5	0.5	1.42
(1,54)	1:115:A:LYS:HZ1	2:10:B:LYS:HZ2	10	1.5	0.5	1.42
(1,54)	1:115:A:LYS:HD2	2:13:B:ARG:HH12	10	1.5	0.5	1.42
(1,54)	1:115:A:LYS:HD2	2:13:B:ARG:HH21	10	1.5	0.5	1.42
(1,54)	1:115:A:LYS:HZ1	2:13:B:ARG:HH21	10	1.5	0.5	1.42
(1,54)	1:115:A:LYS:H	2:13:B:ARG:HH12	10	1.5	0.5	1.42
(1,128)	1:11:A:GLU:CD	2:10:B:LYS:CE	10	1.46	0.14	1.46
(1,104)	1:91:A:VAL:CG1	2:5:B:CYS:SG	10	1.46	0.11	1.46
(1,87)	1:19:A:PHE:CE2	2:3:B:CYS:SG	10	1.38	0.13	1.36
(1,85)	1:19:A:PHE:CD2	2:3:B:CYS:SG	10	1.33	0.14	1.27
(1,2)	2:2:B:ASP:HA	2:5:B:CYS:HB2	10	1.31	0.39	1.36
(1,2)	2:2:B:ASP:HA	2:5:B:CYS:HB3	10	1.31	0.39	1.36
(1,134)	1:127:A:GLU:CG	2:12:B:TYR:HH	10	1.28	0.54	1.48
(1,133)	1:127:A:GLU:CD	2:12:B:TYR:CZ	10	1.27	0.07	1.27
(1,105)	1:91:A:VAL:CG2	2:5:B:CYS:SG	10	1.23	0.06	1.21
(1,100)	1:71:A:MET:CG	2:4:B:LEU:CD2	10	1.18	0.08	1.17
(1,98)	1:63:A:ILE:HB	2:3:B:CYS:HG	10	1.16	0.41	1.27
(1,118)	1:72:A:MET:SD	2:7:B:VAL:HG11	10	1.12	0.9	1.08

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,118)	1:72:A:MET:SD	2:7:B:VAL:HG12	10	1.12	0.9	1.08
(1,118)	1:72:A:MET:SD	2:7:B:VAL:HG13	10	1.12	0.9	1.08
(1,111)	1:19:A:PHE:CE1	2:6:B:ILE:HD11	10	1.06	0.08	1.09
(1,111)	1:19:A:PHE:CE1	2:6:B:ILE:HD12	10	1.06	0.08	1.09
(1,111)	1:19:A:PHE:CE1	2:6:B:ILE:HD13	10	1.06	0.08	1.09
(1,27)	1:36:A:MET:HE1	2:2:B:ASP:HB3	10	0.67	0.49	0.6
(1,27)	1:36:A:MET:HE1	2:2:B:ASP:OD2	10	0.67	0.49	0.6
(1,27)	1:36:A:MET:HE3	2:2:B:ASP:OD2	10	0.67	0.49	0.6
(1,4)	2:4:B:LEU:HA	2:7:B:VAL:HB	10	0.54	0.34	0.39
(1,59)	1:128:A:ALA:HB2	2:12:B:TYR:HE1	10	0.52	0.21	0.5
(1,59)	1:128:A:ALA:HB2	2:12:B:TYR:HH	10	0.52	0.21	0.5
(1,59)	1:128:A:ALA:HB3	2:12:B:TYR:HE1	10	0.52	0.21	0.5
(1,113)	1:19:A:PHE:CZ	2:6:B:ILE:HG12	10	0.5	0.07	0.46
(1,113)	1:19:A:PHE:CZ	2:6:B:ILE:HG13	10	0.5	0.07	0.46
(1,120)	1:75:A:LYS:HB2	2:7:B:VAL:HB	10	0.4	0.19	0.36
(1,120)	1:75:A:LYS:HB3	2:7:B:VAL:HB	10	0.4	0.19	0.36
(1,124)	1:145:A:MET:SD	2:8:B:THR:HG21	10	0.38	0.31	0.29
(1,124)	1:145:A:MET:SD	2:8:B:THR:HG22	10	0.38	0.31	0.29
(1,124)	1:145:A:MET:SD	2:8:B:THR:HG23	10	0.38	0.31	0.29
(1,51)	1:109:A:MET:HE2	2:9:B:THR:HG21	10	0.37	0.1	0.36
(1,51)	1:109:A:MET:HE2	2:9:B:THR:HG22	10	0.37	0.1	0.36
(1,51)	1:109:A:MET:HE2	2:9:B:THR:HG23	10	0.37	0.1	0.36
(1,112)	1:19:A:PHE:CZ	2:6:B:ILE:HD11	10	0.24	0.04	0.24
(1,112)	1:19:A:PHE:CZ	2:6:B:ILE:HD12	10	0.24	0.04	0.24
(1,112)	1:19:A:PHE:CZ	2:6:B:ILE:HD13	10	0.24	0.04	0.24
(1,96)	1:63:A:ILE:HG21	2:3:B:CYS:HG	10	0.21	0.07	0.2
(1,96)	1:63:A:ILE:HG22	2:3:B:CYS:HG	10	0.21	0.07	0.2
(1,96)	1:63:A:ILE:HG23	2:3:B:CYS:HG	10	0.21	0.07	0.2
(1,140)	1:124:A:MET:SD	2:13:B:ARG:HG2	10	0.2	0.05	0.19
(1,140)	1:124:A:MET:SD	2:13:B:ARG:HG3	10	0.2	0.05	0.19
(1,38)	1:68:A:PHE:HE1	2:3:B:CYS:HB3	9	0.84	0.62	0.66
(1,38)	1:68:A:PHE:HE2	2:3:B:CYS:HB3	9	0.84	0.62	0.66
(1,63)	1:141:A:PHE:HD1	2:12:B:TYR:HE1	9	0.32	0.13	0.31
(1,63)	1:141:A:PHE:HE1	2:12:B:TYR:CE1	9	0.32	0.13	0.31
(1,63)	1:141:A:PHE:HE2	2:12:B:TYR:CD1	9	0.32	0.13	0.31
(1,63)	1:141:A:PHE:HE1	2:12:B:TYR:CD1	9	0.32	0.13	0.31
(1,63)	1:141:A:PHE:HZ	2:8:B:THR:HG23	9	0.32	0.13	0.31
(1,69)	2:2:B:ASP:CG	1:32:A:LEU:HD23	9	0.25	0.08	0.26
(1,69)	2:2:B:ASP:OD1	1:32:A:LEU:HD23	9	0.25	0.08	0.26
(1,69)	2:2:B:ASP:OD2	1:51:A:MET:HB3	9	0.25	0.08	0.26
(1,69)	2:2:B:ASP:OD2	1:36:A:MET:HE1	9	0.25	0.08	0.26
(1,69)	2:2:B:ASP:HB2	1:32:A:LEU:HD21	9	0.25	0.08	0.26

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,48)	1:91:A:VAL:HG23	2:5:B:CYS:SG	9	0.17	0.05	0.15
(1,48)	1:91:A:VAL:HG23	2:5:B:CYS:HB2	9	0.17	0.05	0.15
(1,48)	1:91:A:VAL:HG23	2:5:B:CYS:HB3	9	0.17	0.05	0.15
(1,23)	1:32:A:LEU:HD22	2:3:B:CYS:HG	9	0.16	0.03	0.16
(1,23)	1:32:A:LEU:HD21	2:3:B:CYS:HG	9	0.16	0.03	0.16
(1,23)	1:32:A:LEU:HD22	2:3:B:CYS:SG	9	0.16	0.03	0.16
(1,23)	1:32:A:LEU:HD23	2:2:B:ASP:OD1	9	0.16	0.03	0.16
(1,23)	1:32:A:LEU:HD23	2:3:B:CYS:HG	9	0.16	0.03	0.16
(1,33)	1:55:A:VAL:HG23	2:4:B:LEU:HB2	8	0.53	0.32	0.48
(1,33)	1:55:A:VAL:HG23	2:4:B:LEU:HD21	8	0.53	0.32	0.48
(1,33)	1:55:A:VAL:HG23	2:4:B:LEU:HG	8	0.53	0.32	0.48
(1,33)	1:55:A:VAL:HG23	2:4:B:LEU:HD23	8	0.53	0.32	0.48
(1,33)	1:55:A:VAL:HG23	2:4:B:LEU:HD22	8	0.53	0.32	0.48
(1,33)	1:55:A:VAL:HG22	2:1:B:MET:HA	8	0.53	0.32	0.48
(1,32)	1:54:A:GLU:OE2	2:4:B:LEU:HD11	8	0.47	0.09	0.49
(1,32)	1:54:A:GLU:HB3	2:1:B:MET:HE2	8	0.47	0.09	0.49
(1,32)	1:54:A:GLU:OE1	2:4:B:LEU:HD22	8	0.47	0.09	0.49
(1,32)	1:54:A:GLU:HB3	2:1:B:MET:SD	8	0.47	0.09	0.49
(1,32)	1:54:A:GLU:HB3	2:1:B:MET:HE3	8	0.47	0.09	0.49
(1,32)	1:54:A:GLU:HG3	2:1:B:MET:HE2	8	0.47	0.09	0.49
(1,32)	1:54:A:GLU:HG3	2:1:B:MET:HG3	8	0.47	0.09	0.49
(1,1)	2:1:B:MET:HA	2:4:B:LEU:HB2	8	0.47	0.29	0.38
(1,1)	2:1:B:MET:HA	2:4:B:LEU:HB3	8	0.47	0.29	0.38
(1,55)	1:116:A:LEU:HD13	2:13:B:ARG:HD2	8	0.34	0.14	0.34
(1,55)	1:116:A:LEU:HD23	2:13:B:ARG:HD2	8	0.34	0.14	0.34
(1,55)	1:116:A:LEU:HD11	2:13:B:ARG:HE	8	0.34	0.14	0.34
(1,55)	1:116:A:LEU:HD13	2:13:B:ARG:CZ	8	0.34	0.14	0.34
(1,55)	1:116:A:LEU:HD21	2:13:B:ARG:HD2	8	0.34	0.14	0.34
(2,35)	1:136:A:VAL:HG11	2:12:B:TYR:OH	8	0.18	0.07	0.16
(2,35)	1:136:A:VAL:HG12	2:12:B:TYR:OH	8	0.18	0.07	0.16
(2,35)	1:136:A:VAL:HG13	2:12:B:TYR:OH	8	0.18	0.07	0.16
(2,35)	1:136:A:VAL:HG21	2:12:B:TYR:OH	8	0.18	0.07	0.16
(2,35)	1:136:A:VAL:HG22	2:12:B:TYR:OH	8	0.18	0.07	0.16
(2,35)	1:136:A:VAL:HG23	2:12:B:TYR:OH	8	0.18	0.07	0.16
(1,90)	1:27:A:ILE:HG12	2:3:B:CYS:HG	8	0.18	0.05	0.18
(1,90)	1:27:A:ILE:HG13	2:3:B:CYS:HG	8	0.18	0.05	0.18
(1,72)	2:5:B:CYS:SG	1:91:A:VAL:HG23	8	0.17	0.06	0.15
(1,72)	2:5:B:CYS:HB2	1:91:A:VAL:HG23	8	0.17	0.06	0.15
(1,72)	2:5:B:CYS:HB3	1:91:A:VAL:HG23	8	0.17	0.06	0.15
(1,5)	2:5:B:CYS:HA	2:8:B:THR:HB	8	0.16	0.04	0.15
(1,92)	1:32:A:LEU:HD11	2:3:B:CYS:SG	8	0.16	0.03	0.16
(1,92)	1:32:A:LEU:HD12	2:3:B:CYS:SG	8	0.16	0.03	0.16

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,92)	1:32:A:LEU:HD13	2:3:B:CYS:SG	8	0.16	0.03	0.16
(1,92)	1:32:A:LEU:HD21	2:3:B:CYS:SG	8	0.16	0.03	0.16
(1,92)	1:32:A:LEU:HD22	2:3:B:CYS:SG	8	0.16	0.03	0.16
(1,92)	1:32:A:LEU:HD23	2:3:B:CYS:SG	8	0.16	0.03	0.16
(1,42)	1:72:A:MET:HG2	2:7:B:VAL:HG11	7	0.2	0.08	0.16
(1,42)	1:72:A:MET:HA	2:7:B:VAL:HG23	7	0.2	0.08	0.16
(1,42)	1:72:A:MET:HG2	2:7:B:VAL:HG12	7	0.2	0.08	0.16
(1,42)	1:72:A:MET:HA	2:7:B:VAL:HG11	7	0.2	0.08	0.16
(1,88)	1:27:A:ILE:HD11	2:3:B:CYS:HG	7	0.13	0.02	0.14
(1,88)	1:27:A:ILE:HD12	2:3:B:CYS:HG	7	0.13	0.02	0.14
(1,88)	1:27:A:ILE:HD13	2:3:B:CYS:HG	7	0.13	0.02	0.14
(1,103)	1:87:A:GLU:HG2	2:5:B:CYS:HB2	7	0.11	0.01	0.11
(1,103)	1:87:A:GLU:HG2	2:5:B:CYS:HB3	7	0.11	0.01	0.11
(1,103)	1:87:A:GLU:HG3	2:5:B:CYS:HB2	7	0.11	0.01	0.11
(1,103)	1:87:A:GLU:HG3	2:5:B:CYS:HB3	7	0.11	0.01	0.11
(1,44)	1:78:A:ASP:O	2:11:B:LYS:HE3	6	1.11	0.6	1.1
(1,44)	1:78:A:ASP:H	2:11:B:LYS:HG3	6	1.11	0.6	1.1
(1,44)	1:78:A:ASP:O	2:11:B:LYS:HZ2	6	1.11	0.6	1.1
(1,44)	1:78:A:ASP:H	2:11:B:LYS:HE3	6	1.11	0.6	1.1
(1,10)	2:10:B:LYS:HA	2:13:B:ARG:HB2	6	0.15	0.05	0.12
(1,10)	2:10:B:LYS:HA	2:13:B:ARG:HB3	6	0.15	0.05	0.12
(1,91)	1:32:A:LEU:HD11	2:3:B:CYS:HG	6	0.13	0.02	0.12
(1,91)	1:32:A:LEU:HD12	2:3:B:CYS:HG	6	0.13	0.02	0.12
(1,91)	1:32:A:LEU:HD13	2:3:B:CYS:HG	6	0.13	0.02	0.12
(1,91)	1:32:A:LEU:HD21	2:3:B:CYS:HG	6	0.13	0.02	0.12
(1,91)	1:32:A:LEU:HD22	2:3:B:CYS:HG	6	0.13	0.02	0.12
(1,91)	1:32:A:LEU:HD23	2:3:B:CYS:HG	6	0.13	0.02	0.12
(1,115)	1:112:A:LEU:HD21	2:6:B:ILE:HG12	6	0.13	0.02	0.12
(1,115)	1:112:A:LEU:HD21	2:6:B:ILE:HG13	6	0.13	0.02	0.12
(1,115)	1:112:A:LEU:HD22	2:6:B:ILE:HG12	6	0.13	0.02	0.12
(1,115)	1:112:A:LEU:HD22	2:6:B:ILE:HG13	6	0.13	0.02	0.12
(1,115)	1:112:A:LEU:HD23	2:6:B:ILE:HG12	6	0.13	0.02	0.12
(1,115)	1:112:A:LEU:HD23	2:6:B:ILE:HG13	6	0.13	0.02	0.12
(2,6)	2:3:B:CYS:O	2:7:B:VAL:H	5	0.13	0.02	0.11
(1,8)	2:8:B:THR:HA	2:11:B:LYS:HB2	4	0.14	0.02	0.13
(1,8)	2:8:B:THR:HA	2:11:B:LYS:HB3	4	0.14	0.02	0.13
(1,12)	2:12:B:TYR:HA	2:15:B:GLN:HB2	4	0.14	0.02	0.14
(1,12)	2:12:B:TYR:HA	2:15:B:GLN:HB3	4	0.14	0.02	0.14
(1,3)	2:3:B:CYS:HA	2:6:B:ILE:HB	4	0.13	0.01	0.12
(1,66)	1:144:A:MET:O	2:15:B:GLN:HG2	3	0.19	0.02	0.2
(1,66)	1:144:A:MET:HE1	2:15:B:GLN:HB3	3	0.19	0.02	0.2
(1,66)	1:144:A:MET:HE1	2:12:B:TYR:HD1	3	0.19	0.02	0.2

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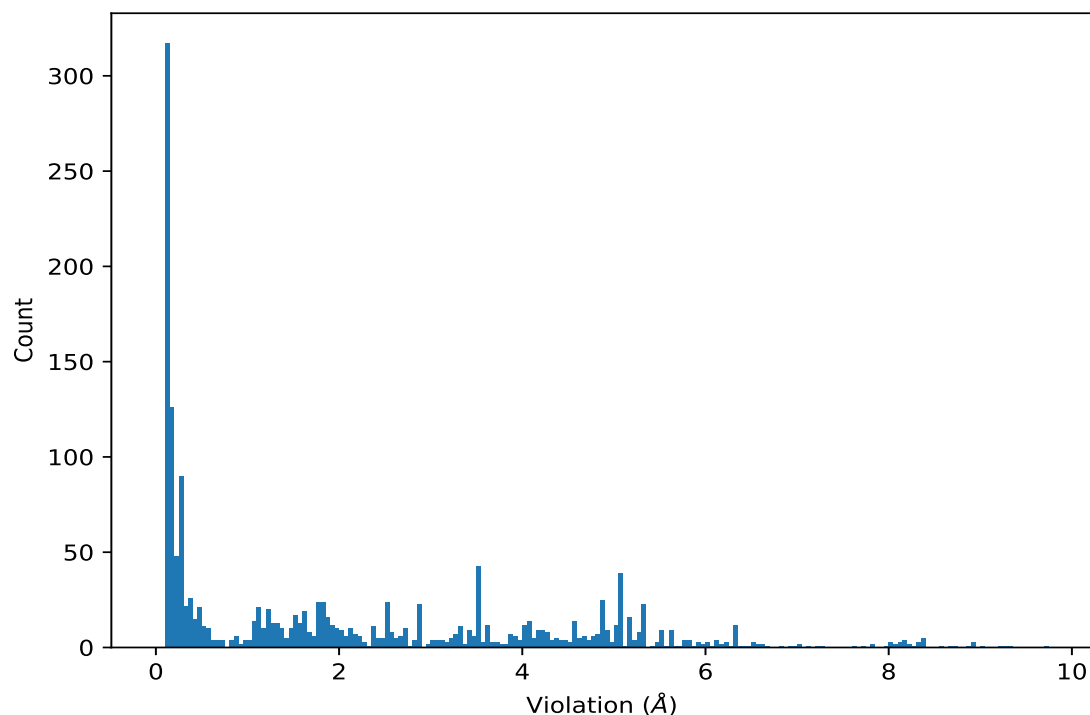
Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,126)	1:92:A:PHE:HE1	2:9:B:THR:HG21	3	0.13	0.0	0.13
(1,126)	1:92:A:PHE:HE1	2:9:B:THR:HG22	3	0.13	0.0	0.13
(1,126)	1:92:A:PHE:HE1	2:9:B:THR:HG23	3	0.13	0.0	0.13
(1,139)	1:124:A:MET:HE1	2:13:B:ARG:HG2	3	0.12	0.0	0.12
(1,139)	1:124:A:MET:HE1	2:13:B:ARG:HG3	3	0.12	0.0	0.12
(1,139)	1:124:A:MET:HE2	2:13:B:ARG:HG2	3	0.12	0.0	0.12
(1,139)	1:124:A:MET:HE2	2:13:B:ARG:HG3	3	0.12	0.0	0.12
(1,139)	1:124:A:MET:HE3	2:13:B:ARG:HG2	3	0.12	0.0	0.12
(1,139)	1:124:A:MET:HE3	2:13:B:ARG:HG3	3	0.12	0.0	0.12
(1,13)	1:15:A:ALA:HB1	2:6:B:ILE:HG22	2	0.24	0.05	0.24
(1,68)	2:1:B:MET:HB2	1:51:A:MET:SD	2	0.23	0.09	0.23
(1,68)	2:1:B:MET:HG2	1:87:A:GLU:OE2	2	0.23	0.09	0.23
(1,9)	2:9:B:THR:HA	2:12:B:TYR:HB2	2	0.14	0.02	0.14
(1,9)	2:9:B:THR:HA	2:12:B:TYR:HB3	2	0.14	0.02	0.14
(1,127)	1:109:A:MET:HE1	2:9:B:THR:HG21	2	0.14	0.02	0.14
(1,127)	1:109:A:MET:HE1	2:9:B:THR:HG22	2	0.14	0.02	0.14
(1,127)	1:109:A:MET:HE1	2:9:B:THR:HG23	2	0.14	0.02	0.14
(1,127)	1:109:A:MET:HE2	2:9:B:THR:HG21	2	0.14	0.02	0.14
(1,127)	1:109:A:MET:HE2	2:9:B:THR:HG22	2	0.14	0.02	0.14
(1,127)	1:109:A:MET:HE2	2:9:B:THR:HG23	2	0.14	0.02	0.14
(1,127)	1:109:A:MET:HE3	2:9:B:THR:HG21	2	0.14	0.02	0.14
(1,127)	1:109:A:MET:HE3	2:9:B:THR:HG22	2	0.14	0.02	0.14
(1,127)	1:109:A:MET:HE3	2:9:B:THR:HG23	2	0.14	0.02	0.14
(1,36)	1:63:A:ILE:HD13	2:3:B:CYS:HG	2	0.12	0.02	0.12
(1,36)	1:63:A:ILE:HD12	2:3:B:CYS:HG	2	0.12	0.02	0.12
(1,7)	2:7:B:VAL:HA	2:10:B:LYS:HB2	2	0.11	0.0	0.11
(1,7)	2:7:B:VAL:HA	2:10:B:LYS:HB3	2	0.11	0.0	0.11
(1,19)	1:27:A:ILE:HG22	2:3:B:CYS:HG	2	0.11	0.0	0.11
(1,109)	1:15:A:ALA:HB1	2:6:B:ILE:HD11	2	0.11	0.01	0.11
(1,109)	1:15:A:ALA:HB1	2:6:B:ILE:HD12	2	0.11	0.01	0.11
(1,109)	1:15:A:ALA:HB1	2:6:B:ILE:HD13	2	0.11	0.01	0.11
(1,109)	1:15:A:ALA:HB2	2:6:B:ILE:HD11	2	0.11	0.01	0.11
(1,109)	1:15:A:ALA:HB2	2:6:B:ILE:HD12	2	0.11	0.01	0.11
(1,109)	1:15:A:ALA:HB2	2:6:B:ILE:HD13	2	0.11	0.01	0.11
(1,109)	1:15:A:ALA:HB3	2:6:B:ILE:HD11	2	0.11	0.01	0.11
(1,109)	1:15:A:ALA:HB3	2:6:B:ILE:HD12	2	0.11	0.01	0.11
(1,109)	1:15:A:ALA:HB3	2:6:B:ILE:HD13	2	0.11	0.01	0.11
(2,28)	1:85:A:ILE:O	1:89:A:PHE: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)
(1,35)	1:58:A:ASP:H	2:4:B:LEU:HD21	1	9.71
(1,35)	1:58:A:ASP:H	2:4:B:LEU:HD21	9	9.34
(1,56)	1:118:A:ASP:O	2:13:B:ARG:HD2	7	9.29
(1,35)	1:58:A:ASP:H	2:4:B:LEU:HD22	7	9.22
(1,35)	1:58:A:ASP:H	2:4:B:LEU:HD23	8	9.04
(1,56)	1:118:A:ASP:N	2:13:B:ARG:HH21	9	8.92
(1,56)	1:118:A:ASP:N	2:13:B:ARG:HE	5	8.91
(1,35)	1:58:A:ASP:H	2:4:B:LEU:HD23	4	8.9
(1,35)	1:58:A:ASP:H	2:4:B:LEU:HD23	10	8.89
(1,35)	1:58:A:ASP:H	2:4:B:LEU:HD22	6	8.72

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,56)	1:118:A:ASP:O	2:13:B:ARG:HD2	3	8.69
(1,56)	1:118:A:ASP:O	2:13:B:ARG:HD2	10	8.56
(1,35)	1:58:A:ASP:H	2:4:B:LEU:HD21	2	8.39
(1,17)	1:24:A:ASP:OD1	2:3:B:CYS:HG	5	8.37
(1,17)	1:24:A:ASP:OD1	2:3:B:CYS:HG	10	8.37
(1,35)	1:58:A:ASP:H	2:4:B:LEU:HD12	3	8.36
(1,17)	1:24:A:ASP:OD2	2:3:B:CYS:HG	8	8.36
(1,56)	1:118:A:ASP:HA	2:13:B:ARG:HD2	1	8.33
(1,56)	1:118:A:ASP:HA	2:13:B:ARG:HD2	2	8.33
(1,17)	1:24:A:ASP:OD1	2:3:B:CYS:HG	4	8.3
(1,56)	1:118:A:ASP:HA	2:13:B:ARG:HD2	6	8.27
(1,17)	1:24:A:ASP:OD1	2:3:B:CYS:HG	7	8.24
(1,17)	1:24:A:ASP:OD1	2:3:B:CYS:HG	2	8.23
(1,17)	1:24:A:ASP:OD1	2:3:B:CYS:HG	3	8.2
(1,17)	1:24:A:ASP:OD1	2:3:B:CYS:HG	9	8.19
(1,62)	1:131:A:ASP:H	2:12:B:TYR:HH	1	8.18
(1,17)	1:24:A:ASP:OD1	2:3:B:CYS:HG	1	8.18
(1,62)	1:131:A:ASP:H	2:12:B:TYR:HH	9	8.14
(1,62)	1:131:A:ASP:H	2:12:B:TYR:HH	10	8.14
(1,17)	1:24:A:ASP:OD1	2:3:B:CYS:HG	6	8.11
(1,62)	1:131:A:ASP:H	2:12:B:TYR:HH	2	8.09
(1,62)	1:131:A:ASP:H	2:12:B:TYR:HH	5	8.05
(1,56)	1:118:A:ASP:O	2:13:B:ARG:HD2	8	8.04
(1,62)	1:131:A:ASP:H	2:12:B:TYR:HH	6	8.03
(1,56)	1:118:A:ASP:O	2:13:B:ARG:HD2	4	8.0
(1,35)	1:58:A:ASP:H	2:4:B:LEU:HD22	5	7.96
(1,62)	1:131:A:ASP:H	2:12:B:TYR:HH	3	7.84
(1,62)	1:131:A:ASP:H	2:12:B:TYR:HH	7	7.83
(1,62)	1:131:A:ASP:H	2:12:B:TYR:HH	8	7.72
(1,62)	1:131:A:ASP:H	2:12:B:TYR:HH	4	7.62
(1,50)	1:106:A:ARG:HA	2:13:B:ARG:HD2	2	7.29
(1,50)	1:106:A:ARG:N	2:9:B:THR:HG21	5	7.2
(1,50)	1:106:A:ARG:N	2:9:B:THR:HG21	7	7.11
(1,50)	1:106:A:ARG:N	2:9:B:THR:HG22	3	7.05
(1,50)	1:106:A:ARG:N	2:9:B:THR:HG21	9	7.05
(1,50)	1:106:A:ARG:N	2:9:B:THR:HG23	8	6.96
(1,50)	1:106:A:ARG:HA	2:13:B:ARG:HD2	6	6.91
(1,34)	1:57:A:ALA:HB2	2:4:B:LEU:HD21	1	6.82
(1,50)	1:106:A:ARG:HA	2:13:B:ARG:HD2	10	6.68
(1,34)	1:57:A:ALA:HB2	2:4:B:LEU:HD22	7	6.62
(1,52)	1:110:A:THR:N	2:9:B:THR:HG23	5	6.61
(1,34)	1:57:A:ALA:HB2	2:4:B:LEU:HD21	9	6.57

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,52)	1:110:A:THR:N	2:9:B:THR:HG21	3	6.56
(1,50)	1:106:A:ARG:HA	2:13:B:ARG:HD2	4	6.54
(1,52)	1:110:A:THR:N	2:9:B:THR:HG23	7	6.52
(1,50)	1:106:A:ARG:HA	2:13:B:ARG:HD2	1	6.51
(1,34)	1:57:A:ALA:HB2	2:4:B:LEU:HD23	8	6.47
(1,52)	1:110:A:THR:N	2:9:B:THR:HG23	4	6.4
(1,34)	1:57:A:ALA:HB2	2:4:B:LEU:HD21	2	6.39
(1,121)	1:79:A:THR:HG21	2:8:B:THR:HG21	8	6.33
(1,121)	1:79:A:THR:HG21	2:8:B:THR:HG22	8	6.33
(1,121)	1:79:A:THR:HG21	2:8:B:THR:HG23	8	6.33
(1,121)	1:79:A:THR:HG22	2:8:B:THR:HG21	8	6.33
(1,121)	1:79:A:THR:HG22	2:8:B:THR:HG22	8	6.33
(1,121)	1:79:A:THR:HG22	2:8:B:THR:HG23	8	6.33
(1,121)	1:79:A:THR:HG23	2:8:B:THR:HG21	8	6.33
(1,121)	1:79:A:THR:HG23	2:8:B:THR:HG22	8	6.33
(1,121)	1:79:A:THR:HG23	2:8:B:THR:HG23	8	6.33
(1,52)	1:110:A:THR:N	2:9:B:THR:HG23	8	6.33
(1,34)	1:57:A:ALA:HB2	2:4:B:LEU:HD23	4	6.33
(1,52)	1:110:A:THR:N	2:9:B:THR:HG21	6	6.32
(1,52)	1:110:A:THR:N	2:9:B:THR:HG23	2	6.28
(1,28)	1:37:A:ARG:H	2:2:B:ASP:HB3	5	6.24
(1,61)	1:130:A:ILE:H	2:12:B:TYR:HH	9	6.21
(1,25)	1:34:A:THR:N	2:2:B:ASP:HB3	1	6.21
(1,28)	1:37:A:ARG:H	2:2:B:ASP:HB3	3	6.16
(1,25)	1:34:A:THR:N	2:2:B:ASP:HB3	5	6.16
(1,34)	1:57:A:ALA:HB2	2:4:B:LEU:HD23	10	6.14
(1,52)	1:110:A:THR:N	2:9:B:THR:HG23	9	6.12
(1,52)	1:110:A:THR:N	2:9:B:THR:HG22	10	6.12
(1,25)	1:34:A:THR:N	2:2:B:ASP:HB3	9	6.12
(1,61)	1:130:A:ILE:H	2:12:B:TYR:HH	2	6.08
(1,28)	1:37:A:ARG:H	2:2:B:ASP:HB3	9	6.05
(1,52)	1:110:A:THR:N	2:9:B:THR:HG23	1	6.04
(1,28)	1:37:A:ARG:H	2:2:B:ASP:HB3	2	6.0
(1,61)	1:130:A:ILE:H	2:12:B:TYR:HH	1	5.99
(1,61)	1:130:A:ILE:HG12	2:12:B:TYR:HH	3	5.98
(1,34)	1:57:A:ALA:HB2	2:1:B:MET:HE1	6	5.94
(1,28)	1:37:A:ARG:H	2:2:B:ASP:HB3	1	5.92
(1,25)	1:34:A:THR:H	2:2:B:ASP:HB3	3	5.9
(1,61)	1:130:A:ILE:HD11	2:12:B:TYR:HH	10	5.86
(1,61)	1:130:A:ILE:HD11	2:12:B:TYR:HH	5	5.85
(1,61)	1:130:A:ILE:H	2:12:B:TYR:HH	4	5.83
(1,28)	1:37:A:ARG:H	2:2:B:ASP:HB3	10	5.82

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,61)	1:130:A:ILE:HD13	2:12:B:TYR:HE1	7	5.81
(1,28)	1:37:A:ARG:H	2:2:B:ASP:OD2	6	5.8
(1,61)	1:130:A:ILE:H	2:12:B:TYR:HH	8	5.79
(1,25)	1:34:A:THR:N	2:2:B:ASP:OD2	6	5.78
(1,25)	1:34:A:THR:H	2:2:B:ASP:HB3	10	5.77
(1,25)	1:34:A:THR:H	2:2:B:ASP:OD2	2	5.74
(1,30)	1:49:A:GLN:O	2:2:B:ASP:OD1	9	5.66
(1,121)	1:79:A:THR:HG21	2:8:B:THR:HG21	10	5.62
(1,121)	1:79:A:THR:HG21	2:8:B:THR:HG22	10	5.62
(1,121)	1:79:A:THR:HG21	2:8:B:THR:HG23	10	5.62
(1,121)	1:79:A:THR:HG22	2:8:B:THR:HG21	10	5.62
(1,121)	1:79:A:THR:HG22	2:8:B:THR:HG22	10	5.62
(1,121)	1:79:A:THR:HG22	2:8:B:THR:HG23	10	5.62
(1,121)	1:79:A:THR:HG23	2:8:B:THR:HG21	10	5.62
(1,121)	1:79:A:THR:HG23	2:8:B:THR:HG22	10	5.62
(1,121)	1:79:A:THR:HG23	2:8:B:THR:HG23	10	5.62
(1,61)	1:130:A:ILE:HD13	2:12:B:TYR:HE1	6	5.57
(1,121)	1:79:A:THR:HG21	2:8:B:THR:HG21	7	5.52
(1,121)	1:79:A:THR:HG21	2:8:B:THR:HG22	7	5.52
(1,121)	1:79:A:THR:HG21	2:8:B:THR:HG23	7	5.52
(1,121)	1:79:A:THR:HG22	2:8:B:THR:HG21	7	5.52
(1,121)	1:79:A:THR:HG22	2:8:B:THR:HG22	7	5.52
(1,121)	1:79:A:THR:HG22	2:8:B:THR:HG23	7	5.52
(1,121)	1:79:A:THR:HG23	2:8:B:THR:HG21	7	5.52
(1,121)	1:79:A:THR:HG23	2:8:B:THR:HG22	7	5.52
(1,121)	1:79:A:THR:HG23	2:8:B:THR:HG23	7	5.52
(1,28)	1:37:A:ARG:H	2:2:B:ASP:OD2	8	5.49
(1,15)	1:17:A:SER:H	2:6:B:ILE:HD11	2	5.46
(1,34)	1:57:A:ALA:HB2	2:4:B:LEU:HD13	3	5.45
(1,15)	1:17:A:SER:H	2:6:B:ILE:HD11	3	5.43
(1,121)	1:79:A:THR:HG21	2:8:B:THR:HG21	2	5.35
(1,121)	1:79:A:THR:HG21	2:8:B:THR:HG22	2	5.35
(1,121)	1:79:A:THR:HG21	2:8:B:THR:HG23	2	5.35
(1,121)	1:79:A:THR:HG22	2:8:B:THR:HG21	2	5.35
(1,121)	1:79:A:THR:HG22	2:8:B:THR:HG22	2	5.35
(1,121)	1:79:A:THR:HG22	2:8:B:THR:HG23	2	5.35
(1,121)	1:79:A:THR:HG23	2:8:B:THR:HG21	2	5.35
(1,121)	1:79:A:THR:HG23	2:8:B:THR:HG22	2	5.35
(1,121)	1:79:A:THR:HG23	2:8:B:THR:HG23	2	5.35
(1,121)	1:79:A:THR:HG21	2:8:B:THR:HG21	9	5.33
(1,121)	1:79:A:THR:HG21	2:8:B:THR:HG22	9	5.33
(1,121)	1:79:A:THR:HG21	2:8:B:THR:HG23	9	5.33

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,121)	1:79:A:THR:HG22	2:8:B:THR:HG21	9	5.33
(1,121)	1:79:A:THR:HG22	2:8:B:THR:HG22	9	5.33
(1,121)	1:79:A:THR:HG22	2:8:B:THR:HG23	9	5.33
(1,121)	1:79:A:THR:HG23	2:8:B:THR:HG21	9	5.33
(1,121)	1:79:A:THR:HG23	2:8:B:THR:HG22	9	5.33
(1,121)	1:79:A:THR:HG23	2:8:B:THR:HG23	9	5.33
(1,53)	1:111:A:ASN:O	2:6:B:ILE:HD13	7	5.33
(1,53)	1:111:A:ASN:C	2:6:B:ILE:HD13	4	5.32
(1,15)	1:17:A:SER:H	2:6:B:ILE:HD12	10	5.32
(1,136)	1:141:A:PHE:CD2	2:12:B:TYR:CD2	3	5.31
(1,15)	1:17:A:SER:H	2:6:B:ILE:HD11	8	5.31
(1,39)	1:69:A:LEU:O	2:7:B:VAL:HG11	3	5.29
(1,34)	1:57:A:ALA:HB2	2:4:B:LEU:HD21	5	5.29
(1,22)	1:31:A:GLU:C	2:2:B:ASP:HB2	10	5.29
(1,22)	1:31:A:GLU:HB2	2:3:B:CYS:HG	3	5.27
(1,137)	1:141:A:PHE:CD2	2:12:B:TYR:CE2	3	5.26
(1,30)	1:49:A:GLN:O	2:1:B:MET:N	7	5.26
(1,25)	1:34:A:THR:N	2:2:B:ASP:OD2	8	5.26
(1,15)	1:17:A:SER:H	2:6:B:ILE:HD12	9	5.26
(1,137)	1:141:A:PHE:CD2	2:12:B:TYR:CE2	1	5.24
(1,136)	1:141:A:PHE:CD2	2:12:B:TYR:CD2	1	5.23
(1,22)	1:31:A:GLU:HB2	2:3:B:CYS:HG	5	5.21
(1,22)	1:31:A:GLU:HB2	2:3:B:CYS:HG	6	5.2
(1,39)	1:69:A:LEU:O	2:4:B:LEU:HD11	9	5.19
(1,137)	1:141:A:PHE:CD2	2:12:B:TYR:CE2	4	5.17
(1,30)	1:49:A:GLN:O	2:1:B:MET:N	8	5.17
(1,39)	1:69:A:LEU:O	2:7:B:VAL:HG12	6	5.16
(1,30)	1:49:A:GLN:O	2:1:B:MET:HG2	1	5.16
(1,22)	1:31:A:GLU:HB2	2:3:B:CYS:HG	8	5.16
(1,136)	1:141:A:PHE:CD2	2:12:B:TYR:CD2	4	5.15
(1,121)	1:79:A:THR:HG21	2:8:B:THR:HG21	3	5.15
(1,121)	1:79:A:THR:HG21	2:8:B:THR:HG22	3	5.15
(1,121)	1:79:A:THR:HG21	2:8:B:THR:HG23	3	5.15
(1,121)	1:79:A:THR:HG22	2:8:B:THR:HG21	3	5.15
(1,121)	1:79:A:THR:HG22	2:8:B:THR:HG22	3	5.15
(1,121)	1:79:A:THR:HG22	2:8:B:THR:HG23	3	5.15
(1,121)	1:79:A:THR:HG23	2:8:B:THR:HG21	3	5.15
(1,121)	1:79:A:THR:HG23	2:8:B:THR:HG22	3	5.15
(1,121)	1:79:A:THR:HG23	2:8:B:THR:HG23	3	5.15
(1,30)	1:49:A:GLN:O	2:1:B:MET:N	6	5.14
(1,121)	1:79:A:THR:HG21	2:8:B:THR:HG21	1	5.1
(1,121)	1:79:A:THR:HG21	2:8:B:THR:HG22	1	5.1

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,121)	1:79:A:THR:HG21	2:8:B:THR:HG23	1	5.1
(1,121)	1:79:A:THR:HG22	2:8:B:THR:HG21	1	5.1
(1,121)	1:79:A:THR:HG22	2:8:B:THR:HG22	1	5.1
(1,121)	1:79:A:THR:HG22	2:8:B:THR:HG23	1	5.1
(1,121)	1:79:A:THR:HG23	2:8:B:THR:HG21	1	5.1
(1,121)	1:79:A:THR:HG23	2:8:B:THR:HG22	1	5.1
(1,121)	1:79:A:THR:HG23	2:8:B:THR:HG23	1	5.1
(1,15)	1:17:A:SER:H	2:6:B:ILE:HD11	1	5.1
(1,28)	1:37:A:ARG:H	2:2:B:ASP:OD2	4	5.09
(1,121)	1:79:A:THR:HG21	2:8:B:THR:HG21	4	5.08
(1,121)	1:79:A:THR:HG21	2:8:B:THR:HG22	4	5.08
(1,121)	1:79:A:THR:HG21	2:8:B:THR:HG23	4	5.08
(1,121)	1:79:A:THR:HG22	2:8:B:THR:HG21	4	5.08
(1,121)	1:79:A:THR:HG22	2:8:B:THR:HG22	4	5.08
(1,121)	1:79:A:THR:HG22	2:8:B:THR:HG23	4	5.08
(1,121)	1:79:A:THR:HG23	2:8:B:THR:HG21	4	5.08
(1,121)	1:79:A:THR:HG23	2:8:B:THR:HG22	4	5.08
(1,121)	1:79:A:THR:HG23	2:8:B:THR:HG23	4	5.08
(1,53)	1:111:A:ASN:O	2:6:B:ILE:HD13	2	5.08
(1,30)	1:49:A:GLN:O	2:1:B:MET:HG3	2	5.08
(1,22)	1:31:A:GLU:HB2	2:3:B:CYS:HG	1	5.08
(1,137)	1:141:A:PHE:CD2	2:12:B:TYR:CE2	6	5.07
(1,137)	1:141:A:PHE:CD2	2:12:B:TYR:CE2	8	5.07
(1,30)	1:49:A:GLN:O	2:1:B:MET:N	4	5.07
(1,15)	1:17:A:SER:H	2:6:B:ILE:HD11	4	5.07
(1,121)	1:79:A:THR:HG21	2:8:B:THR:HG21	5	5.06
(1,121)	1:79:A:THR:HG21	2:8:B:THR:HG22	5	5.06
(1,121)	1:79:A:THR:HG21	2:8:B:THR:HG23	5	5.06
(1,121)	1:79:A:THR:HG22	2:8:B:THR:HG21	5	5.06
(1,121)	1:79:A:THR:HG22	2:8:B:THR:HG22	5	5.06
(1,121)	1:79:A:THR:HG22	2:8:B:THR:HG23	5	5.06
(1,121)	1:79:A:THR:HG23	2:8:B:THR:HG21	5	5.06
(1,121)	1:79:A:THR:HG23	2:8:B:THR:HG22	5	5.06
(1,121)	1:79:A:THR:HG23	2:8:B:THR:HG23	5	5.06
(1,57)	1:121:A:VAL:HA	2:13:B:ARG:HG3	9	5.06
(1,39)	1:69:A:LEU:O	2:7:B:VAL:HG11	2	5.06
(1,30)	1:49:A:GLN:O	2:1:B:MET:N	3	5.06
(1,22)	1:31:A:GLU:HB2	2:3:B:CYS:HG	2	5.05
(1,28)	1:37:A:ARG:H	2:2:B:ASP:OD2	7	5.04
(1,22)	1:31:A:GLU:HB2	2:3:B:CYS:HG	9	5.04
(1,15)	1:17:A:SER:H	2:6:B:ILE:HD11	7	5.03
(1,137)	1:141:A:PHE:CD2	2:12:B:TYR:CE2	7	5.02

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,37)	1:64:A:ASP:N	2:3:B:CYS:HG	2	5.02
(1,37)	1:64:A:ASP:N	2:3:B:CYS:HG	3	5.02
(1,53)	1:111:A:ASN:O	2:6:B:ILE:HD13	5	5.01
(1,18)	1:26:A:THR:C	2:3:B:CYS:HG	10	5.01
(1,136)	1:141:A:PHE:CD2	2:12:B:TYR:CD2	8	5.0
(1,25)	1:34:A:THR:N	2:2:B:ASP:OD2	7	5.0
(1,22)	1:31:A:GLU:C	2:2:B:ASP:OD2	7	5.0
(1,136)	1:141:A:PHE:CD2	2:12:B:TYR:CD2	6	4.97
(1,15)	1:17:A:SER:H	2:6:B:ILE:HD11	6	4.97
(1,22)	1:31:A:GLU:C	2:2:B:ASP:OD2	4	4.96
(1,25)	1:34:A:THR:N	2:2:B:ASP:OD2	4	4.94
(1,21)	1:29:A:THR:HA	2:2:B:ASP:OD1	7	4.93
(1,18)	1:26:A:THR:C	2:3:B:CYS:HG	4	4.93
(1,138)	1:141:A:PHE:CE2	2:12:B:TYR:CE2	1	4.92
(1,136)	1:141:A:PHE:CD2	2:12:B:TYR:CD2	7	4.91
(1,39)	1:69:A:LEU:O	2:7:B:VAL:HG12	1	4.91
(1,30)	1:49:A:GLN:HA	2:2:B:ASP:OD2	5	4.91
(1,18)	1:26:A:THR:C	2:3:B:CYS:HG	5	4.91
(1,15)	1:17:A:SER:H	2:6:B:ILE:HD11	5	4.91
(1,136)	1:141:A:PHE:CD2	2:12:B:TYR:CD2	9	4.89
(1,45)	1:81:A:SER:HG	2:11:B:LYS:HZ1	8	4.89
(1,39)	1:69:A:LEU:O	2:7:B:VAL:HG11	8	4.89
(1,37)	1:64:A:ASP:N	2:3:B:CYS:HG	9	4.89
(1,18)	1:26:A:THR:C	2:3:B:CYS:HG	1	4.89
(1,18)	1:26:A:THR:C	2:3:B:CYS:HG	7	4.89
(1,129)	1:79:A:THR:HG21	2:11:B:LYS:HG2	8	4.88
(1,129)	1:79:A:THR:HG21	2:11:B:LYS:HG3	8	4.88
(1,129)	1:79:A:THR:HG22	2:11:B:LYS:HG2	8	4.88
(1,129)	1:79:A:THR:HG22	2:11:B:LYS:HG3	8	4.88
(1,129)	1:79:A:THR:HG23	2:11:B:LYS:HG2	8	4.88
(1,129)	1:79:A:THR:HG23	2:11:B:LYS:HG3	8	4.88
(1,53)	1:111:A:ASN:O	2:6:B:ILE:HD11	10	4.87
(1,18)	1:26:A:THR:C	2:3:B:CYS:HG	3	4.87
(1,121)	1:79:A:THR:HG21	2:8:B:THR:HG21	6	4.86
(1,121)	1:79:A:THR:HG21	2:8:B:THR:HG22	6	4.86
(1,121)	1:79:A:THR:HG21	2:8:B:THR:HG23	6	4.86
(1,121)	1:79:A:THR:HG22	2:8:B:THR:HG21	6	4.86
(1,121)	1:79:A:THR:HG22	2:8:B:THR:HG22	6	4.86
(1,121)	1:79:A:THR:HG22	2:8:B:THR:HG23	6	4.86
(1,121)	1:79:A:THR:HG23	2:8:B:THR:HG21	6	4.86
(1,121)	1:79:A:THR:HG23	2:8:B:THR:HG22	6	4.86
(1,121)	1:79:A:THR:HG23	2:8:B:THR:HG23	6	4.86

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,37)	1:64:A:ASP:N	2:3:B:CYS:HG	8	4.86
(1,18)	1:26:A:THR:C	2:3:B:CYS:HG	8	4.86
(1,138)	1:141:A:PHE:CE2	2:12:B:TYR:CE2	8	4.85
(1,37)	1:64:A:ASP:N	2:3:B:CYS:HG	1	4.85
(1,18)	1:26:A:THR:C	2:3:B:CYS:HG	2	4.85
(1,53)	1:111:A:ASN:O	2:6:B:ILE:HD13	6	4.84
(1,138)	1:141:A:PHE:CE2	2:12:B:TYR:CE2	4	4.82
(1,30)	1:49:A:GLN:O	2:1:B:MET:HE1	10	4.82
(1,137)	1:141:A:PHE:CD2	2:12:B:TYR:CE2	9	4.81
(1,138)	1:141:A:PHE:CE2	2:12:B:TYR:CE2	3	4.8
(1,53)	1:111:A:ASN:O	2:6:B:ILE:HD13	1	4.8
(1,18)	1:26:A:THR:C	2:3:B:CYS:HG	6	4.78
(1,45)	1:81:A:SER:HG	2:8:B:THR:HG22	10	4.77
(1,18)	1:26:A:THR:C	2:3:B:CYS:HG	9	4.77
(1,21)	1:29:A:THR:HG22	2:2:B:ASP:OD1	6	4.75
(1,65)	1:143:A:GLN:O	2:15:B:GLN:HG2	6	4.74
(1,138)	1:141:A:PHE:CE2	2:12:B:TYR:CE2	6	4.73
(1,57)	1:121:A:VAL:HG13	2:12:B:TYR:HE2	7	4.73
(1,53)	1:111:A:ASN:O	2:6:B:ILE:HD13	9	4.72
(1,136)	1:141:A:PHE:CD2	2:12:B:TYR:CD2	2	4.69
(1,135)	1:141:A:PHE:CE2	2:12:B:TYR:CD2	1	4.69
(1,37)	1:64:A:ASP:N	2:3:B:CYS:HG	5	4.69
(1,37)	1:64:A:ASP:N	2:3:B:CYS:HG	10	4.69
(1,137)	1:141:A:PHE:CD2	2:12:B:TYR:CE2	2	4.66
(1,39)	1:69:A:LEU:O	2:7:B:VAL:HG11	10	4.65
(1,135)	1:141:A:PHE:CE2	2:12:B:TYR:CD2	3	4.64
(1,31)	1:53:A:ASN:N	2:1:B:MET:N	9	4.64
(1,138)	1:141:A:PHE:CE2	2:12:B:TYR:CE2	7	4.63
(1,138)	1:141:A:PHE:CE2	2:12:B:TYR:CE2	9	4.62
(1,37)	1:64:A:ASP:N	2:3:B:CYS:HG	6	4.61
(1,137)	1:141:A:PHE:CD2	2:12:B:TYR:CE2	10	4.6
(1,64)	1:142:A:VAL:N	2:12:B:TYR:HE1	6	4.58
(1,57)	1:121:A:VAL:HA	2:13:B:ARG:HD2	10	4.58
(1,135)	1:141:A:PHE:CE2	2:12:B:TYR:CD2	4	4.57
(1,130)	1:79:A:THR:HG21	2:11:B:LYS:HD2	8	4.57
(1,130)	1:79:A:THR:HG21	2:11:B:LYS:HD3	8	4.57
(1,130)	1:79:A:THR:HG22	2:11:B:LYS:HD2	8	4.57
(1,130)	1:79:A:THR:HG22	2:11:B:LYS:HD3	8	4.57
(1,130)	1:79:A:THR:HG23	2:11:B:LYS:HD2	8	4.57
(1,130)	1:79:A:THR:HG23	2:11:B:LYS:HD3	8	4.57
(1,39)	1:69:A:LEU:O	2:7:B:VAL:HG11	7	4.57
(1,57)	1:121:A:VAL:HG21	2:13:B:ARG:HD2	5	4.56

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,21)	1:29:A:THR:HA	2:2:B:ASP:OD2	2	4.56
(1,53)	1:111:A:ASN:O	2:6:B:ILE:HD13	8	4.55
(1,135)	1:141:A:PHE:CE2	2:12:B:TYR:CD2	8	4.54
(1,57)	1:121:A:VAL:O	2:12:B:TYR:HE2	3	4.5
(1,39)	1:69:A:LEU:O	2:7:B:VAL:HG23	4	4.5
(1,138)	1:141:A:PHE:CE2	2:12:B:TYR:CE2	2	4.49
(1,53)	1:111:A:ASN:O	2:6:B:ILE:HD13	3	4.49
(1,136)	1:141:A:PHE:CD2	2:12:B:TYR:CD2	10	4.48
(1,135)	1:141:A:PHE:CE2	2:12:B:TYR:CD2	9	4.45
(1,64)	1:142:A:VAL:O	2:11:B:LYS:HZ3	3	4.44
(1,31)	1:53:A:ASN:N	2:1:B:MET:N	5	4.43
(1,31)	1:53:A:ASN:N	2:1:B:MET:N	7	4.4
(1,21)	1:29:A:THR:HA	2:2:B:ASP:OD1	8	4.4
(1,64)	1:142:A:VAL:N	2:12:B:TYR:HE1	1	4.38
(1,39)	1:69:A:LEU:O	2:7:B:VAL:HG23	5	4.38
(1,135)	1:141:A:PHE:CE2	2:12:B:TYR:CD2	6	4.37
(1,64)	1:142:A:VAL:N	2:12:B:TYR:HE1	5	4.36
(1,21)	1:29:A:THR:HG22	2:2:B:ASP:OD1	9	4.36
(1,57)	1:121:A:VAL:HA	2:13:B:ARG:HD2	1	4.33
(1,135)	1:141:A:PHE:CE2	2:12:B:TYR:CD2	7	4.32
(1,65)	1:143:A:GLN:O	2:15:B:GLN:HG2	1	4.32
(1,64)	1:142:A:VAL:O	2:11:B:LYS:HZ3	4	4.3
(1,31)	1:53:A:ASN:C	2:1:B:MET:HG2	2	4.27
(1,20)	1:28:A:THR:O	2:3:B:CYS:HG	7	4.27
(1,65)	1:143:A:GLN:O	2:15:B:GLN:HG2	3	4.26
(1,46)	1:86:A:ARG:C	2:1:B:MET:HG2	6	4.26
(1,21)	1:29:A:THR:HA	2:2:B:ASP:OD1	4	4.26
(1,138)	1:141:A:PHE:CE2	2:12:B:TYR:CE2	10	4.25
(1,135)	1:141:A:PHE:CE2	2:12:B:TYR:CD2	2	4.25
(1,31)	1:53:A:ASN:N	2:1:B:MET:N	8	4.25
(1,47)	1:90:A:ARG:H	2:5:B:CYS:HB2	7	4.23
(1,65)	1:143:A:GLN:O	2:15:B:GLN:HG2	2	4.22
(1,57)	1:121:A:VAL:HA	2:13:B:ARG:HD2	2	4.22
(1,65)	1:143:A:GLN:O	2:15:B:GLN:HG2	5	4.21
(1,64)	1:142:A:VAL:N	2:12:B:TYR:HE1	7	4.21
(1,47)	1:90:A:ARG:H	2:5:B:CYS:HB2	6	4.21
(1,37)	1:64:A:ASP:N	2:3:B:CYS:HG	7	4.21
(1,31)	1:53:A:ASN:N	2:1:B:MET:HB2	1	4.21
(1,24)	1:33:A:GLY:HA2	2:2:B:ASP:HB3	1	4.21
(1,20)	1:28:A:THR:O	2:3:B:CYS:HG	10	4.17
(1,129)	1:79:A:THR:HG21	2:11:B:LYS:HG2	10	4.16
(1,129)	1:79:A:THR:HG21	2:11:B:LYS:HG3	10	4.16

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,129)	1:79:A:THR:HG22	2:11:B:LYS:HG2	10	4.16
(1,129)	1:79:A:THR:HG22	2:11:B:LYS:HG3	10	4.16
(1,129)	1:79:A:THR:HG23	2:11:B:LYS:HG2	10	4.16
(1,129)	1:79:A:THR:HG23	2:11:B:LYS:HG3	10	4.16
(1,47)	1:90:A:ARG:H	2:5:B:CYS:HB2	8	4.16
(1,24)	1:33:A:GLY:N	2:2:B:ASP:HB3	9	4.16
(1,65)	1:143:A:GLN:O	2:15:B:GLN:HG2	4	4.14
(1,46)	1:86:A:ARG:N	2:8:B:THR:HG21	8	4.14
(1,57)	1:121:A:VAL:HA	2:13:B:ARG:HD2	8	4.13
(1,20)	1:28:A:THR:O	2:3:B:CYS:HG	2	4.13
(1,64)	1:142:A:VAL:N	2:12:B:TYR:HE1	10	4.11
(1,21)	1:29:A:THR:HA	2:2:B:ASP:OD2	10	4.09
(1,20)	1:28:A:THR:H	2:3:B:CYS:HG	6	4.09
(1,20)	1:28:A:THR:O	2:3:B:CYS:HG	8	4.09
(1,65)	1:143:A:GLN:O	2:15:B:GLN:HG2	9	4.07
(1,129)	1:79:A:THR:HG21	2:11:B:LYS:HG2	2	4.06
(1,129)	1:79:A:THR:HG21	2:11:B:LYS:HG3	2	4.06
(1,129)	1:79:A:THR:HG22	2:11:B:LYS:HG2	2	4.06
(1,129)	1:79:A:THR:HG22	2:11:B:LYS:HG3	2	4.06
(1,129)	1:79:A:THR:HG23	2:11:B:LYS:HG2	2	4.06
(1,129)	1:79:A:THR:HG23	2:11:B:LYS:HG3	2	4.06
(1,47)	1:90:A:ARG:HD3	2:1:B:MET:HB3	4	4.06
(1,37)	1:64:A:ASP:N	2:3:B:CYS:HG	4	4.06
(1,24)	1:33:A:GLY:N	2:2:B:ASP:HB3	3	4.06
(1,20)	1:28:A:THR:O	2:3:B:CYS:HG	9	4.05
(1,57)	1:121:A:VAL:HA	2:13:B:ARG:HD2	6	4.04
(1,20)	1:28:A:THR:O	2:3:B:CYS:HG	1	4.04
(1,46)	1:86:A:ARG:O	2:1:B:MET:HG2	3	4.02
(1,129)	1:79:A:THR:HG21	2:11:B:LYS:HG2	7	4.01
(1,129)	1:79:A:THR:HG21	2:11:B:LYS:HG3	7	4.01
(1,129)	1:79:A:THR:HG22	2:11:B:LYS:HG2	7	4.01
(1,129)	1:79:A:THR:HG22	2:11:B:LYS:HG3	7	4.01
(1,129)	1:79:A:THR:HG23	2:11:B:LYS:HG2	7	4.01
(1,129)	1:79:A:THR:HG23	2:11:B:LYS:HG3	7	4.01
(1,20)	1:28:A:THR:H	2:3:B:CYS:HG	3	4.01
(1,20)	1:28:A:THR:H	2:3:B:CYS:HG	5	4.01
(1,21)	1:29:A:THR:HA	2:2:B:ASP:OD2	3	4.0
(1,31)	1:53:A:ASN:H	2:1:B:MET:N	4	3.99
(1,31)	1:53:A:ASN:N	2:1:B:MET:N	6	3.99
(1,21)	1:29:A:THR:HA	2:2:B:ASP:OD2	1	3.97
(1,40)	1:70:A:THR:O	2:4:B:LEU:HD11	7	3.95
(1,64)	1:142:A:VAL:N	2:12:B:TYR:HE1	8	3.94

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,46)	1:86:A:ARG:HB3	2:1:B:MET:HE3	7	3.94
(1,40)	1:70:A:THR:O	2:4:B:LEU:HD11	4	3.93
(1,24)	1:33:A:GLY:N	2:2:B:ASP:OD2	5	3.93
(1,46)	1:86:A:ARG:HB3	2:1:B:MET:HE1	1	3.92
(1,45)	1:81:A:SER:HG	2:8:B:THR:HG22	5	3.91
(1,65)	1:143:A:GLN:O	2:15:B:GLN:HG2	7	3.9
(1,29)	1:48:A:LEU:O	2:2:B:ASP:OD1	9	3.88
(1,135)	1:141:A:PHE:CE2	2:12:B:TYR:CD2	10	3.87
(1,24)	1:33:A:GLY:HA2	2:2:B:ASP:HB3	10	3.87
(1,20)	1:28:A:THR:H	2:3:B:CYS:HG	4	3.87
(1,57)	1:121:A:VAL:HA	2:13:B:ARG:HD2	4	3.86
(1,45)	1:81:A:SER:HG	2:11:B:LYS:HZ1	7	3.85
(1,65)	1:143:A:GLN:O	2:15:B:GLN:HG2	8	3.82
(1,29)	1:48:A:LEU:HD21	2:2:B:ASP:OD2	7	3.82
(1,46)	1:86:A:ARG:C	2:1:B:MET:HG2	10	3.77
(1,40)	1:70:A:THR:O	2:4:B:LEU:HD13	10	3.76
(1,45)	1:81:A:SER:HG	2:8:B:THR:HG21	6	3.74
(1,40)	1:70:A:THR:O	2:4:B:LEU:HD11	8	3.74
(1,45)	1:81:A:SER:HG	2:11:B:LYS:HE3	3	3.71
(1,40)	1:70:A:THR:O	2:4:B:LEU:HD11	6	3.68
(1,29)	1:48:A:LEU:O	2:2:B:ASP:OD2	1	3.68
(1,29)	1:48:A:LEU:HD22	2:2:B:ASP:OD2	6	3.66
(1,130)	1:79:A:THR:HG21	2:11:B:LYS:HD2	10	3.64
(1,130)	1:79:A:THR:HG21	2:11:B:LYS:HD3	10	3.64
(1,130)	1:79:A:THR:HG22	2:11:B:LYS:HD2	10	3.64
(1,130)	1:79:A:THR:HG22	2:11:B:LYS:HD3	10	3.64
(1,130)	1:79:A:THR:HG23	2:11:B:LYS:HD2	10	3.64
(1,130)	1:79:A:THR:HG23	2:11:B:LYS:HD3	10	3.64
(1,46)	1:86:A:ARG:HG2	2:1:B:MET:HE1	5	3.64
(1,21)	1:29:A:THR:HA	2:2:B:ASP:OD2	5	3.63
(1,64)	1:142:A:VAL:N	2:12:B:TYR:HE1	2	3.62
(1,29)	1:48:A:LEU:HD21	2:2:B:ASP:OD2	2	3.62
(1,29)	1:48:A:LEU:HD21	2:2:B:ASP:OD2	10	3.61
(1,40)	1:70:A:THR:O	2:4:B:LEU:HD13	1	3.6
(1,14)	1:16:A:PHE:H	2:6:B:ILE:HG22	2	3.58
(1,40)	1:70:A:THR:O	2:4:B:LEU:HD11	2	3.57
(1,29)	1:48:A:LEU:HD22	2:2:B:ASP:OD2	8	3.56
(1,129)	1:79:A:THR:HG21	2:11:B:LYS:HG2	3	3.55
(1,129)	1:79:A:THR:HG21	2:11:B:LYS:HG3	3	3.55
(1,129)	1:79:A:THR:HG22	2:11:B:LYS:HG2	3	3.55
(1,129)	1:79:A:THR:HG22	2:11:B:LYS:HG3	3	3.55
(1,129)	1:79:A:THR:HG23	2:11:B:LYS:HG2	3	3.55

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,129)	1:79:A:THR:HG23	2:11:B:LYS:HG3	3	3.55
(1,129)	1:79:A:THR:HG21	2:11:B:LYS:HG2	9	3.55
(1,129)	1:79:A:THR:HG21	2:11:B:LYS:HG3	9	3.55
(1,129)	1:79:A:THR:HG22	2:11:B:LYS:HG2	9	3.55
(1,129)	1:79:A:THR:HG22	2:11:B:LYS:HG3	9	3.55
(1,129)	1:79:A:THR:HG23	2:11:B:LYS:HG2	9	3.55
(1,129)	1:79:A:THR:HG23	2:11:B:LYS:HG3	9	3.55
(1,26)	1:35:A:VAL:HB	2:2:B:ASP:HB3	5	3.55
(1,14)	1:16:A:PHE:N	2:6:B:ILE:HD11	8	3.55
(1,130)	1:79:A:THR:HG21	2:11:B:LYS:HD2	7	3.54
(1,130)	1:79:A:THR:HG21	2:11:B:LYS:HD3	7	3.54
(1,130)	1:79:A:THR:HG22	2:11:B:LYS:HD2	7	3.54
(1,130)	1:79:A:THR:HG22	2:11:B:LYS:HD3	7	3.54
(1,130)	1:79:A:THR:HG23	2:11:B:LYS:HD2	7	3.54
(1,130)	1:79:A:THR:HG23	2:11:B:LYS:HD3	7	3.54
(1,46)	1:86:A:ARG:HB3	2:1:B:MET:HE1	4	3.54
(1,129)	1:79:A:THR:HG21	2:11:B:LYS:HG2	6	3.52
(1,129)	1:79:A:THR:HG21	2:11:B:LYS:HG3	6	3.52
(1,129)	1:79:A:THR:HG22	2:11:B:LYS:HG2	6	3.52
(1,129)	1:79:A:THR:HG22	2:11:B:LYS:HG3	6	3.52
(1,129)	1:79:A:THR:HG23	2:11:B:LYS:HG2	6	3.52
(1,129)	1:79:A:THR:HG23	2:11:B:LYS:HG3	6	3.52
(1,14)	1:16:A:PHE:N	2:6:B:ILE:HD12	10	3.52
(1,131)	1:124:A:MET:CG	2:12:B:TYR:HH	4	3.51
(1,130)	1:79:A:THR:HG21	2:11:B:LYS:HD2	3	3.51
(1,130)	1:79:A:THR:HG21	2:11:B:LYS:HD3	3	3.51
(1,130)	1:79:A:THR:HG22	2:11:B:LYS:HD2	3	3.51
(1,130)	1:79:A:THR:HG22	2:11:B:LYS:HD3	3	3.51
(1,130)	1:79:A:THR:HG23	2:11:B:LYS:HD2	3	3.51
(1,130)	1:79:A:THR:HG23	2:11:B:LYS:HD3	3	3.51
(1,14)	1:16:A:PHE:N	2:6:B:ILE:HD11	7	3.51
(1,14)	1:16:A:PHE:H	2:6:B:ILE:HG22	9	3.51
(1,129)	1:79:A:THR:HG21	2:11:B:LYS:HG2	1	3.5
(1,129)	1:79:A:THR:HG21	2:11:B:LYS:HG3	1	3.5
(1,129)	1:79:A:THR:HG22	2:11:B:LYS:HG2	1	3.5
(1,129)	1:79:A:THR:HG22	2:11:B:LYS:HG3	1	3.5
(1,129)	1:79:A:THR:HG23	2:11:B:LYS:HG2	1	3.5
(1,129)	1:79:A:THR:HG23	2:11:B:LYS:HG3	1	3.5
(1,64)	1:142:A:VAL:N	2:12:B:TYR:HE1	9	3.49
(1,40)	1:70:A:THR:O	2:4:B:LEU:HD21	3	3.48
(1,40)	1:70:A:THR:O	2:4:B:LEU:HD11	9	3.48
(1,14)	1:16:A:PHE:H	2:6:B:ILE:HG22	5	3.47

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,14)	1:16:A:PHE:H	2:6:B:ILE:HG22	3	3.46
(1,24)	1:33:A:GLY:HA2	2:2:B:ASP:OD2	2	3.45
(1,24)	1:33:A:GLY:HA2	2:2:B:ASP:OD2	6	3.44
(1,130)	1:79:A:THR:HG21	2:11:B:LYS:HD2	2	3.42
(1,130)	1:79:A:THR:HG21	2:11:B:LYS:HD3	2	3.42
(1,130)	1:79:A:THR:HG22	2:11:B:LYS:HD2	2	3.42
(1,130)	1:79:A:THR:HG22	2:11:B:LYS:HD3	2	3.42
(1,130)	1:79:A:THR:HG23	2:11:B:LYS:HD2	2	3.42
(1,130)	1:79:A:THR:HG23	2:11:B:LYS:HD3	2	3.42
(1,40)	1:70:A:THR:O	2:4:B:LEU:HD13	5	3.42
(1,29)	1:48:A:LEU:O	2:2:B:ASP:OD2	3	3.41
(1,65)	1:143:A:GLN:O	2:15:B:GLN:HG2	10	3.4
(1,131)	1:124:A:MET:CG	2:12:B:TYR:HH	9	3.37
(1,26)	1:35:A:VAL:HB	2:2:B:ASP:HB3	9	3.34
(1,14)	1:16:A:PHE:H	2:6:B:ILE:HG22	6	3.34
(1,43)	1:73:A:ALA:N	2:7:B:VAL:HG11	2	3.33
(1,29)	1:48:A:LEU:HD21	2:2:B:ASP:OD2	4	3.33
(1,14)	1:16:A:PHE:N	2:6:B:ILE:HG22	4	3.32
(1,129)	1:79:A:THR:HG21	2:11:B:LYS:HG2	5	3.31
(1,129)	1:79:A:THR:HG21	2:11:B:LYS:HG3	5	3.31
(1,129)	1:79:A:THR:HG22	2:11:B:LYS:HG2	5	3.31
(1,129)	1:79:A:THR:HG22	2:11:B:LYS:HG3	5	3.31
(1,129)	1:79:A:THR:HG23	2:11:B:LYS:HG2	5	3.31
(1,129)	1:79:A:THR:HG23	2:11:B:LYS:HG3	5	3.31
(1,129)	1:79:A:THR:HG21	2:11:B:LYS:HG2	4	3.3
(1,129)	1:79:A:THR:HG21	2:11:B:LYS:HG3	4	3.3
(1,129)	1:79:A:THR:HG22	2:11:B:LYS:HG2	4	3.3
(1,129)	1:79:A:THR:HG22	2:11:B:LYS:HG3	4	3.3
(1,129)	1:79:A:THR:HG23	2:11:B:LYS:HG2	4	3.3
(1,129)	1:79:A:THR:HG23	2:11:B:LYS:HG3	4	3.3
(1,131)	1:124:A:MET:CG	2:12:B:TYR:HH	8	3.27
(1,26)	1:35:A:VAL:HG12	2:6:B:ILE:HD13	1	3.23
(1,131)	1:124:A:MET:CG	2:12:B:TYR:HH	1	3.22
(1,45)	1:81:A:SER:HG	2:11:B:LYS:HZ2	9	3.21
(1,131)	1:124:A:MET:CG	2:12:B:TYR:HH	3	3.2
(1,43)	1:73:A:ALA:N	2:7:B:VAL:HG11	9	3.2
(1,47)	1:90:A:ARG:HB2	2:1:B:MET:HG2	10	3.18
(1,14)	1:16:A:PHE:N	2:6:B:ILE:HG22	1	3.17
(1,43)	1:73:A:ALA:N	2:7:B:VAL:HG13	3	3.16
(1,43)	1:73:A:ALA:N	2:7:B:VAL:HG12	6	3.15
(1,26)	1:35:A:VAL:HB	2:2:B:ASP:HB3	6	3.13
(1,24)	1:33:A:GLY:HA2	2:2:B:ASP:OD2	8	3.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,29)	1:48:A:LEU:O	2:2:B:ASP:OD2	5	3.11
(1,26)	1:35:A:VAL:HB	2:2:B:ASP:HB3	2	3.09
(1,26)	1:35:A:VAL:HG12	2:6:B:ILE:HD11	10	3.09
(1,26)	1:35:A:VAL:HB	2:2:B:ASP:HB3	3	3.08
(1,131)	1:124:A:MET:CG	2:12:B:TYR:HH	7	3.07
(1,45)	1:81:A:SER:HG	2:11:B:LYS:HZ1	1	3.03
(1,131)	1:124:A:MET:CG	2:12:B:TYR:HH	2	3.02
(1,43)	1:73:A:ALA:N	2:7:B:VAL:HG12	1	3.02
(1,81)	2:14:B:TYR:H	1:144:A:MET:HE2	8	3.01
(1,131)	1:124:A:MET:CG	2:12:B:TYR:HH	10	2.98
(1,24)	1:33:A:GLY:HA2	2:2:B:ASP:OD2	7	2.95
(1,130)	1:79:A:THR:HG21	2:11:B:LYS:HD2	9	2.9
(1,130)	1:79:A:THR:HG21	2:11:B:LYS:HD3	9	2.9
(1,130)	1:79:A:THR:HG22	2:11:B:LYS:HD2	9	2.9
(1,130)	1:79:A:THR:HG22	2:11:B:LYS:HD3	9	2.9
(1,130)	1:79:A:THR:HG23	2:11:B:LYS:HD2	9	2.9
(1,130)	1:79:A:THR:HG23	2:11:B:LYS:HD3	9	2.9
(1,81)	2:14:B:TYR:HD1	1:11:A:GLU:OE1	3	2.9
(1,43)	1:73:A:ALA:N	2:7:B:VAL:HG11	10	2.89
(1,130)	1:79:A:THR:HG21	2:11:B:LYS:HD2	5	2.88
(1,130)	1:79:A:THR:HG21	2:11:B:LYS:HD3	5	2.88
(1,130)	1:79:A:THR:HG22	2:11:B:LYS:HD2	5	2.88
(1,130)	1:79:A:THR:HG22	2:11:B:LYS:HD3	5	2.88
(1,130)	1:79:A:THR:HG23	2:11:B:LYS:HD2	5	2.88
(1,130)	1:79:A:THR:HG23	2:11:B:LYS:HD3	5	2.88
(1,94)	1:55:A:VAL:HG21	2:3:B:CYS:HG	4	2.88
(1,94)	1:55:A:VAL:HG22	2:3:B:CYS:HG	4	2.88
(1,94)	1:55:A:VAL:HG23	2:3:B:CYS:HG	4	2.88
(1,94)	1:55:A:VAL:HG21	2:3:B:CYS:HG	8	2.88
(1,94)	1:55:A:VAL:HG22	2:3:B:CYS:HG	8	2.88
(1,94)	1:55:A:VAL:HG23	2:3:B:CYS:HG	8	2.88
(1,94)	1:55:A:VAL:HG21	2:3:B:CYS:HG	1	2.87
(1,94)	1:55:A:VAL:HG22	2:3:B:CYS:HG	1	2.87
(1,94)	1:55:A:VAL:HG23	2:3:B:CYS:HG	1	2.87
(1,102)	1:19:A:PHE:CZ	2:5:B:CYS:HG	2	2.84
(1,81)	2:14:B:TYR:HD1	1:11:A:GLU:OE2	5	2.83
(1,46)	1:86:A:ARG:HB3	2:1:B:MET:HE1	2	2.83
(1,131)	1:124:A:MET:CG	2:12:B:TYR:HH	6	2.82
(1,60)	1:129:A:ASP:H	2:12:B:TYR:HH	9	2.77
(1,102)	1:19:A:PHE:CZ	2:5:B:CYS:HG	3	2.73
(1,94)	1:55:A:VAL:HG21	2:3:B:CYS:HG	7	2.73
(1,94)	1:55:A:VAL:HG22	2:3:B:CYS:HG	7	2.73

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,94)	1:55:A:VAL:HG23	2:3:B:CYS:HG	7	2.73
(1,60)	1:129:A:ASP:H	2:12:B:TYR:HH	7	2.73
(1,94)	1:55:A:VAL:HG21	2:3:B:CYS:HG	9	2.72
(1,94)	1:55:A:VAL:HG22	2:3:B:CYS:HG	9	2.72
(1,94)	1:55:A:VAL:HG23	2:3:B:CYS:HG	9	2.72
(1,60)	1:129:A:ASP:H	2:12:B:TYR:HH	2	2.71
(1,136)	1:141:A:PHE:CD2	2:12:B:TYR:CD2	5	2.7
(1,60)	1:129:A:ASP:H	2:12:B:TYR:HH	5	2.69
(1,31)	1:53:A:ASN:HD21	2:1:B:MET:HE1	10	2.69
(1,43)	1:73:A:ALA:N	2:7:B:VAL:HG11	8	2.68
(1,94)	1:55:A:VAL:HG21	2:3:B:CYS:HG	2	2.67
(1,94)	1:55:A:VAL:HG22	2:3:B:CYS:HG	2	2.67
(1,94)	1:55:A:VAL:HG23	2:3:B:CYS:HG	2	2.67
(1,46)	1:86:A:ARG:HB3	2:1:B:MET:HE1	9	2.63
(1,137)	1:141:A:PHE:CD2	2:12:B:TYR:CE2	5	2.62
(1,60)	1:129:A:ASP:H	2:12:B:TYR:HH	6	2.62
(1,81)	2:14:B:TYR:HD1	1:11:A:GLU:OE1	2	2.61
(1,47)	1:90:A:ARG:HE	2:1:B:MET:SD	1	2.61
(1,24)	1:33:A:GLY:HA2	2:2:B:ASP:OD2	4	2.59
(1,130)	1:79:A:THR:HG21	2:11:B:LYS:HD2	4	2.58
(1,130)	1:79:A:THR:HG21	2:11:B:LYS:HD3	4	2.58
(1,130)	1:79:A:THR:HG22	2:11:B:LYS:HD2	4	2.58
(1,130)	1:79:A:THR:HG22	2:11:B:LYS:HD3	4	2.58
(1,130)	1:79:A:THR:HG23	2:11:B:LYS:HD2	4	2.58
(1,130)	1:79:A:THR:HG23	2:11:B:LYS:HD3	4	2.58
(1,102)	1:19:A:PHE:CZ	2:5:B:CYS:HG	10	2.56
(1,130)	1:79:A:THR:HG21	2:11:B:LYS:HD2	6	2.54
(1,130)	1:79:A:THR:HG21	2:11:B:LYS:HD3	6	2.54
(1,130)	1:79:A:THR:HG22	2:11:B:LYS:HD2	6	2.54
(1,130)	1:79:A:THR:HG22	2:11:B:LYS:HD3	6	2.54
(1,130)	1:79:A:THR:HG23	2:11:B:LYS:HD2	6	2.54
(1,130)	1:79:A:THR:HG23	2:11:B:LYS:HD3	6	2.54
(1,94)	1:55:A:VAL:HG21	2:3:B:CYS:HG	10	2.54
(1,94)	1:55:A:VAL:HG22	2:3:B:CYS:HG	10	2.54
(1,94)	1:55:A:VAL:HG23	2:3:B:CYS:HG	10	2.54
(1,60)	1:129:A:ASP:H	2:12:B:TYR:HH	1	2.54
(1,43)	1:73:A:ALA:N	2:7:B:VAL:HG11	7	2.53
(1,102)	1:19:A:PHE:CZ	2:5:B:CYS:HG	6	2.52
(1,81)	2:14:B:TYR:HD1	1:11:A:GLU:OE2	6	2.52
(1,130)	1:79:A:THR:HG21	2:11:B:LYS:HD2	1	2.51
(1,130)	1:79:A:THR:HG21	2:11:B:LYS:HD3	1	2.51
(1,130)	1:79:A:THR:HG22	2:11:B:LYS:HD2	1	2.51

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,130)	1:79:A:THR:HG22	2:11:B:LYS:HD3	1	2.51
(1,130)	1:79:A:THR:HG23	2:11:B:LYS:HD2	1	2.51
(1,130)	1:79:A:THR:HG23	2:11:B:LYS:HD3	1	2.51
(1,60)	1:129:A:ASP:H	2:12:B:TYR:HH	8	2.51
(1,45)	1:81:A:SER:HG	2:11:B:LYS:HZ1	4	2.51
(1,94)	1:55:A:VAL:HG21	2:3:B:CYS:HG	6	2.5
(1,94)	1:55:A:VAL:HG22	2:3:B:CYS:HG	6	2.5
(1,94)	1:55:A:VAL:HG23	2:3:B:CYS:HG	6	2.5
(1,102)	1:19:A:PHE:CZ	2:5:B:CYS:HG	7	2.49
(1,43)	1:73:A:ALA:N	2:7:B:VAL:HG11	5	2.49
(1,60)	1:129:A:ASP:H	2:12:B:TYR:HH	3	2.48
(1,43)	1:73:A:ALA:N	2:7:B:VAL:HG12	4	2.46
(1,102)	1:19:A:PHE:CZ	2:5:B:CYS:HG	4	2.45
(1,102)	1:19:A:PHE:CZ	2:5:B:CYS:HG	1	2.44
(1,102)	1:19:A:PHE:CZ	2:5:B:CYS:HG	5	2.44
(1,102)	1:19:A:PHE:CZ	2:5:B:CYS:HG	9	2.42
(1,67)	1:146:A:THR:HA	2:11:B:LYS:HZ1	1	2.42
(1,67)	1:146:A:THR:HA	2:11:B:LYS:HZ2	6	2.41
(1,67)	1:146:A:THR:N	2:11:B:LYS:HZ3	4	2.4
(1,26)	1:35:A:VAL:HB	2:2:B:ASP:HB3	8	2.4
(1,60)	1:129:A:ASP:H	2:12:B:TYR:HH	10	2.39
(1,94)	1:55:A:VAL:HG21	2:3:B:CYS:HG	5	2.38
(1,94)	1:55:A:VAL:HG22	2:3:B:CYS:HG	5	2.38
(1,94)	1:55:A:VAL:HG23	2:3:B:CYS:HG	5	2.38
(1,26)	1:35:A:VAL:HB	2:2:B:ASP:HB3	4	2.38
(1,81)	2:14:B:TYR:HD1	1:11:A:GLU:OE2	10	2.36
(1,94)	1:55:A:VAL:HG21	2:3:B:CYS:HG	3	2.35
(1,94)	1:55:A:VAL:HG22	2:3:B:CYS:HG	3	2.35
(1,94)	1:55:A:VAL:HG23	2:3:B:CYS:HG	3	2.35
(1,131)	1:124:A:MET:CG	2:12:B:TYR:HH	5	2.32
(1,102)	1:19:A:PHE:CZ	2:5:B:CYS:HG	8	2.29
(1,45)	1:81:A:SER:HG	2:11:B:LYS:HZ2	2	2.29
(1,31)	1:53:A:ASN:HD21	2:1:B:MET:HE3	3	2.25
(1,81)	2:14:B:TYR:HD1	1:11:A:GLU:OE2	9	2.24
(1,138)	1:141:A:PHE:CE2	2:12:B:TYR:CE2	5	2.23
(1,86)	1:19:A:PHE:CE1	2:3:B:CYS:SG	4	2.22
(1,132)	1:127:A:GLU:CD	2:12:B:TYR:CE1	8	2.21
(1,132)	1:127:A:GLU:CD	2:12:B:TYR:CE1	9	2.2
(1,84)	1:19:A:PHE:CD1	2:3:B:CYS:SG	4	2.2
(1,54)	1:115:A:LYS:HD2	2:13:B:ARG:HH12	4	2.18
(1,118)	1:72:A:MET:SD	2:7:B:VAL:HG11	5	2.17
(1,118)	1:72:A:MET:SD	2:7:B:VAL:HG12	5	2.17

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,118)	1:72:A:MET:SD	2:7:B:VAL:HG13	5	2.17
(1,97)	1:63:A:ILE:HG12	2:3:B:CYS:HG	1	2.17
(1,97)	1:63:A:ILE:HG13	2:3:B:CYS:HG	1	2.17
(1,60)	1:129:A:ASP:H	2:12:B:TYR:HH	4	2.17
(1,118)	1:72:A:MET:SD	2:7:B:VAL:HG11	2	2.14
(1,118)	1:72:A:MET:SD	2:7:B:VAL:HG12	2	2.14
(1,118)	1:72:A:MET:SD	2:7:B:VAL:HG13	2	2.14
(1,99)	1:71:A:MET:SD	2:4:B:LEU:CD2	1	2.14
(1,54)	1:115:A:LYS:HZ1	2:13:B:ARG:HH21	7	2.13
(1,81)	2:14:B:TYR:HD1	1:11:A:GLU:OE2	1	2.12
(1,99)	1:71:A:MET:SD	2:4:B:LEU:CD2	6	2.1
(1,84)	1:19:A:PHE:CD1	2:3:B:CYS:SG	7	2.1
(1,81)	2:14:B:TYR:HD1	1:11:A:GLU:OE1	4	2.1
(1,49)	1:105:A:LEU:HD22	2:12:B:TYR:HE2	2	2.1
(1,86)	1:19:A:PHE:CE1	2:3:B:CYS:SG	7	2.08
(1,26)	1:35:A:VAL:HB	2:2:B:ASP:HB3	7	2.08
(1,97)	1:63:A:ILE:HG12	2:3:B:CYS:HG	9	2.07
(1,97)	1:63:A:ILE:HG13	2:3:B:CYS:HG	9	2.07
(1,54)	1:115:A:LYS:HD2	2:13:B:ARG:HH12	3	2.07
(1,132)	1:127:A:GLU:CD	2:12:B:TYR:CE1	2	2.06
(1,82)	1:19:A:PHE:HB2	2:3:B:CYS:SG	7	2.05
(1,82)	1:19:A:PHE:HB3	2:3:B:CYS:SG	7	2.05
(1,82)	1:19:A:PHE:HB2	2:3:B:CYS:SG	4	2.03
(1,82)	1:19:A:PHE:HB3	2:3:B:CYS:SG	4	2.03
(1,86)	1:19:A:PHE:CE1	2:3:B:CYS:SG	3	2.01
(1,99)	1:71:A:MET:SD	2:4:B:LEU:CD2	9	2.0
(1,97)	1:63:A:ILE:HG12	2:3:B:CYS:HG	3	2.0
(1,97)	1:63:A:ILE:HG13	2:3:B:CYS:HG	3	2.0
(1,67)	1:146:A:THR:N	2:11:B:LYS:HZ1	8	2.0
(1,118)	1:72:A:MET:SD	2:7:B:VAL:HG11	10	1.99
(1,118)	1:72:A:MET:SD	2:7:B:VAL:HG12	10	1.99
(1,118)	1:72:A:MET:SD	2:7:B:VAL:HG13	10	1.99
(1,101)	1:71:A:MET:CG	2:4:B:LEU:CG	2	1.99
(1,67)	1:146:A:THR:N	2:11:B:LYS:HZ3	3	1.99
(1,2)	2:2:B:ASP:HA	2:5:B:CYS:HB2	3	1.99
(1,2)	2:2:B:ASP:HA	2:5:B:CYS:HB3	3	1.99
(1,97)	1:63:A:ILE:HG12	2:3:B:CYS:HG	2	1.98
(1,97)	1:63:A:ILE:HG13	2:3:B:CYS:HG	2	1.98
(1,106)	1:91:A:VAL:CB	2:5:B:CYS:SG	4	1.96
(1,97)	1:63:A:ILE:HG12	2:3:B:CYS:HG	8	1.95
(1,97)	1:63:A:ILE:HG13	2:3:B:CYS:HG	8	1.95
(1,27)	1:36:A:MET:HE1	2:2:B:ASP:HB3	5	1.95

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,135)	1:141:A:PHE:CE2	2:12:B:TYR:CD2	5	1.93
(1,132)	1:127:A:GLU:CD	2:12:B:TYR:CE1	7	1.93
(1,84)	1:19:A:PHE:CD1	2:3:B:CYS:SG	3	1.93
(1,106)	1:91:A:VAL:CB	2:5:B:CYS:SG	7	1.92
(1,83)	1:19:A:PHE:CG	2:3:B:CYS:SG	4	1.92
(1,86)	1:19:A:PHE:CE1	2:3:B:CYS:SG	1	1.91
(1,86)	1:19:A:PHE:CE1	2:3:B:CYS:SG	5	1.91
(1,86)	1:19:A:PHE:CE1	2:3:B:CYS:SG	9	1.91
(1,86)	1:19:A:PHE:CE1	2:3:B:CYS:SG	10	1.91
(1,99)	1:71:A:MET:SD	2:4:B:LEU:CD2	10	1.9
(1,93)	1:32:A:LEU:HG	2:3:B:CYS:SG	6	1.9
(1,84)	1:19:A:PHE:CD1	2:3:B:CYS:SG	5	1.9
(1,118)	1:72:A:MET:SD	2:7:B:VAL:HG11	7	1.89
(1,118)	1:72:A:MET:SD	2:7:B:VAL:HG12	7	1.89
(1,118)	1:72:A:MET:SD	2:7:B:VAL:HG13	7	1.89
(1,84)	1:19:A:PHE:CD1	2:3:B:CYS:SG	10	1.89
(1,99)	1:71:A:MET:SD	2:4:B:LEU:CD2	8	1.88
(1,83)	1:19:A:PHE:CG	2:3:B:CYS:SG	7	1.88
(1,44)	1:78:A:ASP:H	2:11:B:LYS:HG3	10	1.88
(1,118)	1:72:A:MET:SD	2:7:B:VAL:HG11	8	1.86
(1,118)	1:72:A:MET:SD	2:7:B:VAL:HG12	8	1.86
(1,118)	1:72:A:MET:SD	2:7:B:VAL:HG13	8	1.86
(1,132)	1:127:A:GLU:CD	2:12:B:TYR:CE1	3	1.85
(1,86)	1:19:A:PHE:CE1	2:3:B:CYS:SG	8	1.85
(1,81)	2:14:B:TYR:HD1	1:11:A:GLU:OE1	7	1.85
(1,132)	1:127:A:GLU:CD	2:12:B:TYR:CE1	10	1.84
(1,38)	1:68:A:PHE:HE1	2:3:B:CYS:HB3	9	1.84
(1,106)	1:91:A:VAL:CB	2:5:B:CYS:SG	2	1.83
(1,97)	1:63:A:ILE:HG12	2:3:B:CYS:HG	6	1.83
(1,97)	1:63:A:ILE:HG13	2:3:B:CYS:HG	6	1.83
(1,84)	1:19:A:PHE:CD1	2:3:B:CYS:SG	1	1.83
(1,67)	1:146:A:THR:HA	2:11:B:LYS:HZ1	5	1.83
(1,132)	1:127:A:GLU:CD	2:12:B:TYR:CE1	4	1.82
(1,99)	1:71:A:MET:SD	2:4:B:LEU:CD2	4	1.82
(1,93)	1:32:A:LEU:HG	2:3:B:CYS:SG	7	1.82
(1,93)	1:32:A:LEU:HG	2:3:B:CYS:SG	9	1.82
(1,82)	1:19:A:PHE:HB2	2:3:B:CYS:SG	6	1.82
(1,82)	1:19:A:PHE:HB3	2:3:B:CYS:SG	6	1.82
(1,82)	1:19:A:PHE:HB2	2:3:B:CYS:SG	10	1.82
(1,82)	1:19:A:PHE:HB3	2:3:B:CYS:SG	10	1.82
(1,67)	1:146:A:THR:HA	2:11:B:LYS:HZ1	7	1.82
(1,44)	1:78:A:ASP:H	2:11:B:LYS:HG3	5	1.82

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,82)	1:19:A:PHE:HB2	2:3:B:CYS:SG	5	1.81
(1,82)	1:19:A:PHE:HB3	2:3:B:CYS:SG	5	1.81
(1,49)	1:105:A:LEU:HD22	2:12:B:TYR:HE2	6	1.81
(1,106)	1:91:A:VAL:CB	2:5:B:CYS:SG	1	1.8
(1,106)	1:91:A:VAL:CB	2:5:B:CYS:SG	3	1.8
(1,97)	1:63:A:ILE:HG12	2:3:B:CYS:HG	10	1.8
(1,97)	1:63:A:ILE:HG13	2:3:B:CYS:HG	10	1.8
(1,86)	1:19:A:PHE:CE1	2:3:B:CYS:SG	2	1.79
(1,86)	1:19:A:PHE:CE1	2:3:B:CYS:SG	6	1.79
(1,84)	1:19:A:PHE:CD1	2:3:B:CYS:SG	6	1.79
(1,132)	1:127:A:GLU:CD	2:12:B:TYR:CE1	1	1.78
(1,106)	1:91:A:VAL:CB	2:5:B:CYS:SG	6	1.78
(1,99)	1:71:A:MET:SD	2:4:B:LEU:CD2	7	1.78
(1,49)	1:105:A:LEU:HD22	2:12:B:TYR:HE2	8	1.78
(1,106)	1:91:A:VAL:CB	2:5:B:CYS:SG	9	1.77
(1,93)	1:32:A:LEU:HG	2:3:B:CYS:SG	8	1.77
(1,84)	1:19:A:PHE:CD1	2:3:B:CYS:SG	8	1.77
(1,84)	1:19:A:PHE:CD1	2:3:B:CYS:SG	9	1.77
(1,82)	1:19:A:PHE:HB2	2:3:B:CYS:SG	3	1.77
(1,82)	1:19:A:PHE:HB3	2:3:B:CYS:SG	3	1.77
(1,49)	1:105:A:LEU:HD13	2:12:B:TYR:HE2	9	1.77
(1,134)	1:127:A:GLU:CG	2:12:B:TYR:HH	3	1.76
(1,82)	1:19:A:PHE:HB2	2:3:B:CYS:SG	2	1.76
(1,82)	1:19:A:PHE:HB3	2:3:B:CYS:SG	2	1.76
(1,134)	1:127:A:GLU:CG	2:12:B:TYR:HH	4	1.75
(1,128)	1:11:A:GLU:CD	2:10:B:LYS:CE	7	1.75
(1,101)	1:71:A:MET:CG	2:4:B:LEU:CG	5	1.75
(1,97)	1:63:A:ILE:HG12	2:3:B:CYS:HG	5	1.75
(1,97)	1:63:A:ILE:HG13	2:3:B:CYS:HG	5	1.75
(1,84)	1:19:A:PHE:CD1	2:3:B:CYS:SG	2	1.75
(1,54)	1:115:A:LYS:H	2:13:B:ARG:HH12	9	1.75
(1,132)	1:127:A:GLU:CD	2:12:B:TYR:CE1	5	1.74
(1,106)	1:91:A:VAL:CB	2:5:B:CYS:SG	10	1.73
(1,67)	1:146:A:THR:HA	2:11:B:LYS:HZ1	2	1.73
(1,82)	1:19:A:PHE:HB2	2:3:B:CYS:SG	8	1.71
(1,82)	1:19:A:PHE:HB3	2:3:B:CYS:SG	8	1.71
(1,38)	1:68:A:PHE:HE1	2:3:B:CYS:HB3	2	1.71
(1,106)	1:91:A:VAL:CB	2:5:B:CYS:SG	5	1.7
(1,82)	1:19:A:PHE:HB2	2:3:B:CYS:SG	1	1.7
(1,82)	1:19:A:PHE:HB3	2:3:B:CYS:SG	1	1.7
(1,104)	1:91:A:VAL:CG1	2:5:B:CYS:SG	4	1.69
(1,93)	1:32:A:LEU:HG	2:3:B:CYS:SG	1	1.69

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,93)	1:32:A:LEU:HG	2:3:B:CYS:SG	5	1.68
(1,134)	1:127:A:GLU:CG	2:12:B:TYR:HH	1	1.66
(1,106)	1:91:A:VAL:CB	2:5:B:CYS:SG	8	1.66
(1,101)	1:71:A:MET:CG	2:4:B:LEU:CG	9	1.65
(1,101)	1:71:A:MET:CG	2:4:B:LEU:CG	1	1.64
(1,101)	1:71:A:MET:CG	2:4:B:LEU:CG	7	1.64
(1,101)	1:71:A:MET:CG	2:4:B:LEU:CG	8	1.64
(1,93)	1:32:A:LEU:HG	2:3:B:CYS:SG	4	1.64
(1,87)	1:19:A:PHE:CE2	2:3:B:CYS:SG	4	1.64
(1,99)	1:71:A:MET:SD	2:4:B:LEU:CD2	3	1.63
(1,98)	1:63:A:ILE:HB	2:3:B:CYS:HG	2	1.62
(1,93)	1:32:A:LEU:HG	2:3:B:CYS:SG	10	1.62
(1,85)	1:19:A:PHE:CD2	2:3:B:CYS:SG	4	1.62
(1,134)	1:127:A:GLU:CG	2:12:B:TYR:HH	10	1.61
(1,101)	1:71:A:MET:CG	2:4:B:LEU:CG	4	1.61
(1,132)	1:127:A:GLU:CD	2:12:B:TYR:CE1	6	1.6
(1,128)	1:11:A:GLU:CD	2:10:B:LYS:CE	9	1.6
(1,101)	1:71:A:MET:CG	2:4:B:LEU:CG	6	1.6
(1,93)	1:32:A:LEU:HG	2:3:B:CYS:SG	2	1.6
(1,93)	1:32:A:LEU:HG	2:3:B:CYS:SG	3	1.6
(1,67)	1:146:A:THR:N	2:11:B:LYS:HZ1	10	1.6
(1,49)	1:105:A:LEU:HD21	2:12:B:TYR:HE2	10	1.6
(1,85)	1:19:A:PHE:CD2	2:3:B:CYS:SG	7	1.59
(1,2)	2:2:B:ASP:HA	2:5:B:CYS:HB2	10	1.59
(1,2)	2:2:B:ASP:HA	2:5:B:CYS:HB3	10	1.59
(1,101)	1:71:A:MET:CG	2:4:B:LEU:CG	10	1.58
(1,82)	1:19:A:PHE:HB2	2:3:B:CYS:SG	9	1.58
(1,82)	1:19:A:PHE:HB3	2:3:B:CYS:SG	9	1.58
(1,2)	2:2:B:ASP:HA	2:5:B:CYS:HB2	9	1.58
(1,2)	2:2:B:ASP:HA	2:5:B:CYS:HB3	9	1.58
(1,83)	1:19:A:PHE:CG	2:3:B:CYS:SG	3	1.57
(1,83)	1:19:A:PHE:CG	2:3:B:CYS:SG	5	1.57
(1,83)	1:19:A:PHE:CG	2:3:B:CYS:SG	10	1.57
(1,87)	1:19:A:PHE:CE2	2:3:B:CYS:SG	7	1.56
(1,83)	1:19:A:PHE:CG	2:3:B:CYS:SG	6	1.56
(1,99)	1:71:A:MET:SD	2:4:B:LEU:CD2	5	1.54
(1,83)	1:19:A:PHE:CG	2:3:B:CYS:SG	2	1.54
(1,49)	1:105:A:LEU:HD21	2:12:B:TYR:HE2	1	1.54
(1,128)	1:11:A:GLU:CD	2:10:B:LYS:CE	4	1.53
(1,104)	1:91:A:VAL:CG1	2:5:B:CYS:SG	2	1.53
(1,104)	1:91:A:VAL:CG1	2:5:B:CYS:SG	7	1.53
(1,83)	1:19:A:PHE:CG	2:3:B:CYS:SG	8	1.52

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,2)	2:2:B:ASP:HA	2:5:B:CYS:HB2	2	1.52
(1,2)	2:2:B:ASP:HA	2:5:B:CYS:HB3	2	1.52
(1,104)	1:91:A:VAL:CG1	2:5:B:CYS:SG	9	1.51
(1,83)	1:19:A:PHE:CG	2:3:B:CYS:SG	1	1.51
(1,2)	2:2:B:ASP:HA	2:5:B:CYS:HB2	5	1.51
(1,2)	2:2:B:ASP:HA	2:5:B:CYS:HB3	5	1.51
(1,134)	1:127:A:GLU:CG	2:12:B:TYR:HH	7	1.5
(1,128)	1:11:A:GLU:CD	2:10:B:LYS:CE	10	1.5
(1,98)	1:63:A:ILE:HB	2:3:B:CYS:HG	3	1.5
(1,98)	1:63:A:ILE:HB	2:3:B:CYS:HG	9	1.5
(1,54)	1:115:A:LYS:HD2	2:13:B:ARG:HH22	1	1.49
(1,49)	1:105:A:LEU:HD13	2:12:B:TYR:HE2	4	1.48
(1,49)	1:105:A:LEU:HD22	2:12:B:TYR:HE2	5	1.48
(1,134)	1:127:A:GLU:CG	2:12:B:TYR:HH	8	1.47
(1,128)	1:11:A:GLU:CD	2:10:B:LYS:CE	8	1.47
(1,104)	1:91:A:VAL:CG1	2:5:B:CYS:SG	3	1.47
(1,49)	1:105:A:LEU:HD22	2:12:B:TYR:HE2	3	1.47
(1,128)	1:11:A:GLU:CD	2:10:B:LYS:CE	1	1.46
(1,104)	1:91:A:VAL:CG1	2:5:B:CYS:SG	6	1.46
(1,83)	1:19:A:PHE:CG	2:3:B:CYS:SG	9	1.46
(1,128)	1:11:A:GLU:CD	2:10:B:LYS:CE	3	1.43
(1,87)	1:19:A:PHE:CE2	2:3:B:CYS:SG	8	1.42
(1,87)	1:19:A:PHE:CE2	2:3:B:CYS:SG	9	1.42
(1,104)	1:91:A:VAL:CG1	2:5:B:CYS:SG	1	1.41
(1,49)	1:105:A:LEU:HD22	2:12:B:TYR:HE2	7	1.41
(1,133)	1:127:A:GLU:CD	2:12:B:TYR:CZ	9	1.39
(1,128)	1:11:A:GLU:CD	2:10:B:LYS:CE	2	1.38
(1,104)	1:91:A:VAL:CG1	2:5:B:CYS:SG	5	1.38
(1,98)	1:63:A:ILE:HB	2:3:B:CYS:HG	1	1.38
(1,87)	1:19:A:PHE:CE2	2:3:B:CYS:SG	2	1.38
(1,67)	1:146:A:THR:HA	2:11:B:LYS:HZ1	9	1.37
(1,105)	1:91:A:VAL:CG2	2:5:B:CYS:SG	7	1.36
(1,98)	1:63:A:ILE:HB	2:3:B:CYS:HG	8	1.36
(1,54)	1:115:A:LYS:HD2	2:13:B:ARG:HH21	5	1.36
(1,104)	1:91:A:VAL:CG1	2:5:B:CYS:SG	10	1.35
(1,85)	1:19:A:PHE:CD2	2:3:B:CYS:SG	2	1.34
(1,85)	1:19:A:PHE:CD2	2:3:B:CYS:SG	8	1.34
(1,133)	1:127:A:GLU:CD	2:12:B:TYR:CZ	8	1.33
(1,87)	1:19:A:PHE:CE2	2:3:B:CYS:SG	1	1.33
(1,134)	1:127:A:GLU:CG	2:12:B:TYR:HH	9	1.32
(1,87)	1:19:A:PHE:CE2	2:3:B:CYS:SG	3	1.32
(1,38)	1:68:A:PHE:HE2	2:3:B:CYS:HB3	3	1.31

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,133)	1:127:A:GLU:CD	2:12:B:TYR:CZ	2	1.3
(1,133)	1:127:A:GLU:CD	2:12:B:TYR:CZ	3	1.3
(1,128)	1:11:A:GLU:CD	2:10:B:LYS:CE	6	1.3
(1,124)	1:145:A:MET:SD	2:8:B:THR:HG21	3	1.3
(1,124)	1:145:A:MET:SD	2:8:B:THR:HG22	3	1.3
(1,124)	1:145:A:MET:SD	2:8:B:THR:HG23	3	1.3
(1,133)	1:127:A:GLU:CD	2:12:B:TYR:CZ	10	1.29
(1,4)	2:4:B:LEU:HA	2:7:B:VAL:HB	5	1.29
(1,100)	1:71:A:MET:CG	2:4:B:LEU:CD2	9	1.28
(1,85)	1:19:A:PHE:CD2	2:3:B:CYS:SG	6	1.28
(1,105)	1:91:A:VAL:CG2	2:5:B:CYS:SG	1	1.27
(1,105)	1:91:A:VAL:CG2	2:5:B:CYS:SG	8	1.27
(1,100)	1:71:A:MET:CG	2:4:B:LEU:CD2	1	1.27
(1,100)	1:71:A:MET:CG	2:4:B:LEU:CD2	2	1.27
(1,87)	1:19:A:PHE:CE2	2:3:B:CYS:SG	6	1.27
(1,133)	1:127:A:GLU:CD	2:12:B:TYR:CZ	5	1.26
(1,85)	1:19:A:PHE:CD2	2:3:B:CYS:SG	9	1.26
(1,134)	1:127:A:GLU:CG	2:12:B:TYR:HH	2	1.25
(1,104)	1:91:A:VAL:CG1	2:5:B:CYS:SG	8	1.25
(1,133)	1:127:A:GLU:CD	2:12:B:TYR:CZ	4	1.24
(1,133)	1:127:A:GLU:CD	2:12:B:TYR:CZ	7	1.24
(1,105)	1:91:A:VAL:CG2	2:5:B:CYS:SG	3	1.24
(1,85)	1:19:A:PHE:CD2	2:3:B:CYS:SG	1	1.24
(1,85)	1:19:A:PHE:CD2	2:3:B:CYS:SG	3	1.24
(1,54)	1:115:A:LYS:HD2	2:13:B:ARG:HH21	8	1.24
(1,100)	1:71:A:MET:CG	2:4:B:LEU:CD2	6	1.23
(1,87)	1:19:A:PHE:CE2	2:3:B:CYS:SG	10	1.23
(1,133)	1:127:A:GLU:CD	2:12:B:TYR:CZ	1	1.22
(1,105)	1:91:A:VAL:CG2	2:5:B:CYS:SG	5	1.22
(1,87)	1:19:A:PHE:CE2	2:3:B:CYS:SG	5	1.22
(1,85)	1:19:A:PHE:CD2	2:3:B:CYS:SG	10	1.22
(1,2)	2:2:B:ASP:HA	2:5:B:CYS:HB2	7	1.22
(1,2)	2:2:B:ASP:HA	2:5:B:CYS:HB3	7	1.22
(1,128)	1:11:A:GLU:CD	2:10:B:LYS:CE	5	1.21
(1,105)	1:91:A:VAL:CG2	2:5:B:CYS:SG	2	1.21
(1,105)	1:91:A:VAL:CG2	2:5:B:CYS:SG	4	1.21
(1,85)	1:19:A:PHE:CD2	2:3:B:CYS:SG	5	1.21
(1,2)	2:2:B:ASP:HA	2:5:B:CYS:HB2	4	1.21
(1,2)	2:2:B:ASP:HA	2:5:B:CYS:HB3	4	1.21
(1,105)	1:91:A:VAL:CG2	2:5:B:CYS:SG	10	1.19
(1,100)	1:71:A:MET:CG	2:4:B:LEU:CD2	10	1.18
(1,98)	1:63:A:ILE:HB	2:3:B:CYS:HG	5	1.18

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,100)	1:71:A:MET:CG	2:4:B:LEU:CD2	8	1.17
(1,54)	1:115:A:LYS:HD2	2:13:B:ARG:HH21	10	1.17
(1,1)	2:1:B:MET:HA	2:4:B:LEU:HB2	1	1.17
(1,1)	2:1:B:MET:HA	2:4:B:LEU:HB3	1	1.17
(1,105)	1:91:A:VAL:CG2	2:5:B:CYS:SG	6	1.16
(1,105)	1:91:A:VAL:CG2	2:5:B:CYS:SG	9	1.16
(1,4)	2:4:B:LEU:HA	2:7:B:VAL:HB	2	1.16
(1,99)	1:71:A:MET:SD	2:4:B:LEU:CD2	2	1.15
(1,98)	1:63:A:ILE:HB	2:3:B:CYS:HG	6	1.14
(1,44)	1:78:A:ASP:H	2:11:B:LYS:HE3	8	1.14
(1,111)	1:19:A:PHE:CE1	2:6:B:ILE:HD11	2	1.13
(1,111)	1:19:A:PHE:CE1	2:6:B:ILE:HD12	2	1.13
(1,111)	1:19:A:PHE:CE1	2:6:B:ILE:HD13	2	1.13
(1,111)	1:19:A:PHE:CE1	2:6:B:ILE:HD11	4	1.13
(1,111)	1:19:A:PHE:CE1	2:6:B:ILE:HD12	4	1.13
(1,111)	1:19:A:PHE:CE1	2:6:B:ILE:HD13	4	1.13
(1,111)	1:19:A:PHE:CE1	2:6:B:ILE:HD11	3	1.12
(1,111)	1:19:A:PHE:CE1	2:6:B:ILE:HD12	3	1.12
(1,111)	1:19:A:PHE:CE1	2:6:B:ILE:HD13	3	1.12
(1,100)	1:71:A:MET:CG	2:4:B:LEU:CD2	4	1.12
(1,100)	1:71:A:MET:CG	2:4:B:LEU:CD2	5	1.12
(1,111)	1:19:A:PHE:CE1	2:6:B:ILE:HD11	6	1.11
(1,111)	1:19:A:PHE:CE1	2:6:B:ILE:HD12	6	1.11
(1,111)	1:19:A:PHE:CE1	2:6:B:ILE:HD13	6	1.11
(1,101)	1:71:A:MET:CG	2:4:B:LEU:CG	3	1.11
(1,98)	1:63:A:ILE:HB	2:3:B:CYS:HG	10	1.11
(1,133)	1:127:A:GLU:CD	2:12:B:TYR:CZ	6	1.1
(1,100)	1:71:A:MET:CG	2:4:B:LEU:CD2	7	1.1
(1,111)	1:19:A:PHE:CE1	2:6:B:ILE:HD11	8	1.09
(1,111)	1:19:A:PHE:CE1	2:6:B:ILE:HD12	8	1.09
(1,111)	1:19:A:PHE:CE1	2:6:B:ILE:HD13	8	1.09
(1,111)	1:19:A:PHE:CE1	2:6:B:ILE:HD11	9	1.09
(1,111)	1:19:A:PHE:CE1	2:6:B:ILE:HD12	9	1.09
(1,111)	1:19:A:PHE:CE1	2:6:B:ILE:HD13	9	1.09
(1,33)	1:55:A:VAL:HG23	2:4:B:LEU:HB2	1	1.07
(1,2)	2:2:B:ASP:HA	2:5:B:CYS:HB2	1	1.07
(1,2)	2:2:B:ASP:HA	2:5:B:CYS:HB3	1	1.07
(1,111)	1:19:A:PHE:CE1	2:6:B:ILE:HD11	1	1.06
(1,111)	1:19:A:PHE:CE1	2:6:B:ILE:HD12	1	1.06
(1,111)	1:19:A:PHE:CE1	2:6:B:ILE:HD13	1	1.06
(1,100)	1:71:A:MET:CG	2:4:B:LEU:CD2	3	1.06
(1,44)	1:78:A:ASP:O	2:11:B:LYS:HE3	3	1.05

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,111)	1:19:A:PHE:CE1	2:6:B:ILE:HD11	10	1.02
(1,111)	1:19:A:PHE:CE1	2:6:B:ILE:HD12	10	1.02
(1,111)	1:19:A:PHE:CE1	2:6:B:ILE:HD13	10	1.02
(1,27)	1:36:A:MET:HE1	2:2:B:ASP:HB3	3	1.02
(1,111)	1:19:A:PHE:CE1	2:6:B:ILE:HD11	5	0.99
(1,111)	1:19:A:PHE:CE1	2:6:B:ILE:HD12	5	0.99
(1,111)	1:19:A:PHE:CE1	2:6:B:ILE:HD13	5	0.99
(1,38)	1:68:A:PHE:HE1	2:3:B:CYS:HB3	5	0.99
(1,120)	1:75:A:LYS:HB2	2:7:B:VAL:HB	9	0.91
(1,120)	1:75:A:LYS:HB3	2:7:B:VAL:HB	9	0.91
(1,2)	2:2:B:ASP:HA	2:5:B:CYS:HB2	6	0.88
(1,2)	2:2:B:ASP:HA	2:5:B:CYS:HB3	6	0.88
(1,111)	1:19:A:PHE:CE1	2:6:B:ILE:HD11	7	0.86
(1,111)	1:19:A:PHE:CE1	2:6:B:ILE:HD12	7	0.86
(1,111)	1:19:A:PHE:CE1	2:6:B:ILE:HD13	7	0.86
(1,33)	1:55:A:VAL:HG23	2:4:B:LEU:HB2	9	0.86
(1,59)	1:128:A:ALA:HB2	2:12:B:TYR:HH	9	0.85
(1,54)	1:115:A:LYS:HZ1	2:10:B:LYS:HZ2	2	0.85
(1,59)	1:128:A:ALA:HB2	2:12:B:TYR:HH	2	0.8
(1,47)	1:90:A:ARG:HH12	2:1:B:MET:SD	2	0.8
(1,54)	1:115:A:LYS:HD2	2:13:B:ARG:HH22	6	0.73
(1,59)	1:128:A:ALA:HB2	2:12:B:TYR:HH	8	0.72
(1,33)	1:55:A:VAL:HG23	2:4:B:LEU:HB2	10	0.72
(1,27)	1:36:A:MET:HE1	2:2:B:ASP:HB3	9	0.72
(1,113)	1:19:A:PHE:CZ	2:6:B:ILE:HG12	3	0.66
(1,113)	1:19:A:PHE:CZ	2:6:B:ILE:HG13	3	0.66
(1,38)	1:68:A:PHE:HE1	2:3:B:CYS:HB3	6	0.66
(1,33)	1:55:A:VAL:HG23	2:4:B:LEU:HD22	7	0.65
(1,113)	1:19:A:PHE:CZ	2:6:B:ILE:HG12	8	0.62
(1,113)	1:19:A:PHE:CZ	2:6:B:ILE:HG13	8	0.62
(1,27)	1:36:A:MET:HE1	2:2:B:ASP:HB3	1	0.62
(1,27)	1:36:A:MET:HE3	2:2:B:ASP:OD2	8	0.61
(1,32)	1:54:A:GLU:OE1	2:4:B:LEU:HD22	5	0.6
(1,32)	1:54:A:GLU:HB3	2:1:B:MET:SD	7	0.59
(1,59)	1:128:A:ALA:HB2	2:12:B:TYR:HE1	3	0.58
(1,27)	1:36:A:MET:HE1	2:2:B:ASP:HB3	10	0.58
(1,2)	2:2:B:ASP:HA	2:5:B:CYS:HB2	8	0.57
(1,2)	2:2:B:ASP:HA	2:5:B:CYS:HB3	8	0.57
(1,63)	1:141:A:PHE:HE2	2:12:B:TYR:CD1	5	0.56
(1,55)	1:116:A:LEU:HD11	2:13:B:ARG:HE	7	0.56
(1,1)	2:1:B:MET:HA	2:4:B:LEU:HB2	9	0.55
(1,1)	2:1:B:MET:HA	2:4:B:LEU:HB3	9	0.55

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,51)	1:109:A:MET:HE2	2:9:B:THR:HG23	8	0.54
(1,55)	1:116:A:LEU:HD13	2:13:B:ARG:CZ	9	0.53
(1,47)	1:90:A:ARG:HD2	2:1:B:MET:HE1	5	0.53
(1,59)	1:128:A:ALA:HB2	2:12:B:TYR:HE1	1	0.52
(1,51)	1:109:A:MET:HE2	2:9:B:THR:HG22	3	0.52
(1,47)	1:90:A:ARG:HH12	2:1:B:MET:HE2	3	0.52
(1,38)	1:68:A:PHE:HE1	2:3:B:CYS:HB3	4	0.51
(1,32)	1:54:A:GLU:HB3	2:1:B:MET:HE3	8	0.51
(1,32)	1:54:A:GLU:HG3	2:1:B:MET:HE2	9	0.51
(1,113)	1:19:A:PHE:CZ	2:6:B:ILE:HG12	10	0.5
(1,113)	1:19:A:PHE:CZ	2:6:B:ILE:HG13	10	0.5
(1,120)	1:75:A:LYS:HB2	2:7:B:VAL:HB	8	0.48
(1,120)	1:75:A:LYS:HB3	2:7:B:VAL:HB	8	0.48
(1,113)	1:19:A:PHE:CZ	2:6:B:ILE:HG12	2	0.48
(1,113)	1:19:A:PHE:CZ	2:6:B:ILE:HG13	2	0.48
(1,47)	1:90:A:ARG:HH12	2:1:B:MET:HE1	9	0.48
(1,113)	1:19:A:PHE:CZ	2:6:B:ILE:HG12	9	0.47
(1,113)	1:19:A:PHE:CZ	2:6:B:ILE:HG13	9	0.47
(1,59)	1:128:A:ALA:HB3	2:12:B:TYR:HE1	10	0.47
(1,32)	1:54:A:GLU:HB3	2:1:B:MET:HE2	4	0.47
(1,120)	1:75:A:LYS:HB2	2:7:B:VAL:HB	6	0.45
(1,120)	1:75:A:LYS:HB3	2:7:B:VAL:HB	6	0.45
(1,113)	1:19:A:PHE:CZ	2:6:B:ILE:HG12	1	0.45
(1,113)	1:19:A:PHE:CZ	2:6:B:ILE:HG13	1	0.45
(1,113)	1:19:A:PHE:CZ	2:6:B:ILE:HG12	5	0.45
(1,113)	1:19:A:PHE:CZ	2:6:B:ILE:HG13	5	0.45
(1,113)	1:19:A:PHE:CZ	2:6:B:ILE:HG12	6	0.45
(1,113)	1:19:A:PHE:CZ	2:6:B:ILE:HG13	6	0.45
(1,113)	1:19:A:PHE:CZ	2:6:B:ILE:HG12	7	0.45
(1,113)	1:19:A:PHE:CZ	2:6:B:ILE:HG13	7	0.45
(1,1)	2:1:B:MET:HA	2:4:B:LEU:HB2	6	0.45
(1,1)	2:1:B:MET:HA	2:4:B:LEU:HB3	6	0.45
(1,113)	1:19:A:PHE:CZ	2:6:B:ILE:HG12	4	0.44
(1,113)	1:19:A:PHE:CZ	2:6:B:ILE:HG13	4	0.44
(1,51)	1:109:A:MET:HE2	2:9:B:THR:HG21	9	0.44
(1,63)	1:141:A:PHE:HD1	2:12:B:TYR:HE1	2	0.43
(1,27)	1:36:A:MET:HE1	2:2:B:ASP:OD2	4	0.43
(1,4)	2:4:B:LEU:HA	2:7:B:VAL:HB	6	0.43
(1,51)	1:109:A:MET:HE2	2:9:B:THR:HG22	6	0.42
(1,98)	1:63:A:ILE:HB	2:3:B:CYS:HG	7	0.41
(1,63)	1:141:A:PHE:HZ	2:8:B:THR:HG23	8	0.41
(1,32)	1:54:A:GLU:HB3	2:1:B:MET:SD	6	0.41

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,4)	2:4:B:LEU:HA	2:7:B:VAL:HB	1	0.41
(1,120)	1:75:A:LYS:HB2	2:7:B:VAL:HB	10	0.4
(1,120)	1:75:A:LYS:HB3	2:7:B:VAL:HB	10	0.4
(1,98)	1:63:A:ILE:HB	2:3:B:CYS:HG	4	0.4
(1,4)	2:4:B:LEU:HA	2:7:B:VAL:HB	4	0.4
(1,69)	2:2:B:ASP:CG	1:32:A:LEU:HD23	1	0.39
(1,59)	1:128:A:ALA:HB2	2:12:B:TYR:HE1	6	0.39
(1,44)	1:78:A:ASP:O	2:11:B:LYS:HZ2	6	0.39
(1,1)	2:1:B:MET:HA	2:4:B:LEU:HB2	8	0.39
(1,1)	2:1:B:MET:HA	2:4:B:LEU:HB3	8	0.39
(1,55)	1:116:A:LEU:HD23	2:13:B:ARG:HD2	4	0.38
(1,4)	2:4:B:LEU:HA	2:7:B:VAL:HB	10	0.38
(1,1)	2:1:B:MET:HA	2:4:B:LEU:HB2	4	0.38
(1,1)	2:1:B:MET:HA	2:4:B:LEU:HB3	4	0.38
(1,69)	2:2:B:ASP:CG	1:32:A:LEU:HD23	5	0.37
(1,51)	1:109:A:MET:HE2	2:9:B:THR:HG21	5	0.37
(1,32)	1:54:A:GLU:HG3	2:1:B:MET:HG3	10	0.37
(1,4)	2:4:B:LEU:HA	2:7:B:VAL:HB	7	0.37
(1,4)	2:4:B:LEU:HA	2:7:B:VAL:HB	8	0.37
(1,1)	2:1:B:MET:HA	2:4:B:LEU:HB2	7	0.37
(1,1)	2:1:B:MET:HA	2:4:B:LEU:HB3	7	0.37
(1,124)	1:145:A:MET:SD	2:8:B:THR:HG21	4	0.36
(1,124)	1:145:A:MET:SD	2:8:B:THR:HG22	4	0.36
(1,124)	1:145:A:MET:SD	2:8:B:THR:HG23	4	0.36
(1,120)	1:75:A:LYS:HB2	2:7:B:VAL:HB	2	0.36
(1,120)	1:75:A:LYS:HB3	2:7:B:VAL:HB	2	0.36
(1,120)	1:75:A:LYS:HB2	2:7:B:VAL:HB	7	0.36
(1,120)	1:75:A:LYS:HB3	2:7:B:VAL:HB	7	0.36
(1,78)	2:11:B:LYS:HG3	1:75:A:LYS:O	6	0.36
(1,59)	1:128:A:ALA:HB2	2:12:B:TYR:HE1	4	0.36
(1,44)	1:78:A:ASP:H	2:11:B:LYS:HE3	7	0.36
(1,59)	1:128:A:ALA:HB2	2:12:B:TYR:HE1	7	0.35
(1,55)	1:116:A:LEU:HD11	2:13:B:ARG:HE	5	0.35
(1,51)	1:109:A:MET:HE2	2:9:B:THR:HG21	7	0.35
(1,97)	1:63:A:ILE:HG12	2:3:B:CYS:HG	7	0.34
(1,97)	1:63:A:ILE:HG13	2:3:B:CYS:HG	7	0.34
(1,63)	1:141:A:PHE:HZ	2:8:B:THR:HG23	10	0.34
(1,42)	1:72:A:MET:HA	2:7:B:VAL:HG11	10	0.34
(1,120)	1:75:A:LYS:HB2	2:7:B:VAL:HB	4	0.33
(1,120)	1:75:A:LYS:HB3	2:7:B:VAL:HB	4	0.33
(1,96)	1:63:A:ILE:HG21	2:3:B:CYS:HG	2	0.33
(1,96)	1:63:A:ILE:HG22	2:3:B:CYS:HG	2	0.33

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,96)	1:63:A:ILE:HG23	2:3:B:CYS:HG	2	0.33
(1,55)	1:116:A:LEU:HD23	2:13:B:ARG:HD2	6	0.33
(1,32)	1:54:A:GLU:OE2	2:4:B:LEU:HD11	3	0.33
(1,124)	1:145:A:MET:SD	2:8:B:THR:HG21	1	0.32
(1,124)	1:145:A:MET:SD	2:8:B:THR:HG22	1	0.32
(1,124)	1:145:A:MET:SD	2:8:B:THR:HG23	1	0.32
(1,68)	2:1:B:MET:HB2	1:51:A:MET:SD	3	0.32
(1,33)	1:55:A:VAL:HG22	2:1:B:MET:HA	8	0.32
(1,63)	1:141:A:PHE:HD1	2:12:B:TYR:HE1	9	0.31
(1,4)	2:4:B:LEU:HA	2:7:B:VAL:HB	3	0.31
(1,4)	2:4:B:LEU:HA	2:7:B:VAL:HB	9	0.31
(2,35)	1:136:A:VAL:HG11	2:12:B:TYR:OH	5	0.3
(2,35)	1:136:A:VAL:HG12	2:12:B:TYR:OH	5	0.3
(2,35)	1:136:A:VAL:HG13	2:12:B:TYR:OH	5	0.3
(2,35)	1:136:A:VAL:HG21	2:12:B:TYR:OH	5	0.3
(2,35)	1:136:A:VAL:HG22	2:12:B:TYR:OH	5	0.3
(2,35)	1:136:A:VAL:HG23	2:12:B:TYR:OH	5	0.3
(1,140)	1:124:A:MET:SD	2:13:B:ARG:HG2	5	0.3
(1,140)	1:124:A:MET:SD	2:13:B:ARG:HG3	5	0.3
(1,124)	1:145:A:MET:SD	2:8:B:THR:HG21	10	0.3
(1,124)	1:145:A:MET:SD	2:8:B:THR:HG22	10	0.3
(1,124)	1:145:A:MET:SD	2:8:B:THR:HG23	10	0.3
(1,96)	1:63:A:ILE:HG21	2:3:B:CYS:HG	3	0.3
(1,96)	1:63:A:ILE:HG22	2:3:B:CYS:HG	3	0.3
(1,96)	1:63:A:ILE:HG23	2:3:B:CYS:HG	3	0.3
(1,51)	1:109:A:MET:HE2	2:9:B:THR:HG23	10	0.3
(1,124)	1:145:A:MET:SD	2:8:B:THR:HG21	6	0.29
(1,124)	1:145:A:MET:SD	2:8:B:THR:HG22	6	0.29
(1,124)	1:145:A:MET:SD	2:8:B:THR:HG23	6	0.29
(1,120)	1:75:A:LYS:HB2	2:7:B:VAL:HB	1	0.29
(1,120)	1:75:A:LYS:HB3	2:7:B:VAL:HB	1	0.29
(1,118)	1:72:A:MET:SD	2:7:B:VAL:HG11	9	0.29
(1,118)	1:72:A:MET:SD	2:7:B:VAL:HG12	9	0.29
(1,118)	1:72:A:MET:SD	2:7:B:VAL:HG13	9	0.29
(1,72)	2:5:B:CYS:SG	1:91:A:VAL:HG23	8	0.29
(1,63)	1:141:A:PHE:HE1	2:12:B:TYR:CD1	6	0.29
(1,48)	1:91:A:VAL:HG23	2:5:B:CYS:SG	8	0.29
(1,33)	1:55:A:VAL:HG23	2:4:B:LEU:HD23	4	0.29
(1,124)	1:145:A:MET:SD	2:8:B:THR:HG21	9	0.28
(1,124)	1:145:A:MET:SD	2:8:B:THR:HG22	9	0.28
(1,124)	1:145:A:MET:SD	2:8:B:THR:HG23	9	0.28
(1,112)	1:19:A:PHE:CZ	2:6:B:ILE:HD11	1	0.28

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,112)	1:19:A:PHE:CZ	2:6:B:ILE:HD12	1	0.28
(1,112)	1:19:A:PHE:CZ	2:6:B:ILE:HD13	1	0.28
(1,112)	1:19:A:PHE:CZ	2:6:B:ILE:HD11	4	0.28
(1,112)	1:19:A:PHE:CZ	2:6:B:ILE:HD12	4	0.28
(1,112)	1:19:A:PHE:CZ	2:6:B:ILE:HD13	4	0.28
(1,112)	1:19:A:PHE:CZ	2:6:B:ILE:HD11	6	0.28
(1,112)	1:19:A:PHE:CZ	2:6:B:ILE:HD12	6	0.28
(1,112)	1:19:A:PHE:CZ	2:6:B:ILE:HD13	6	0.28
(1,112)	1:19:A:PHE:CZ	2:6:B:ILE:HD11	9	0.28
(1,112)	1:19:A:PHE:CZ	2:6:B:ILE:HD12	9	0.28
(1,112)	1:19:A:PHE:CZ	2:6:B:ILE:HD13	9	0.28
(1,42)	1:72:A:MET:HG2	2:7:B:VAL:HG11	2	0.28
(1,13)	1:15:A:ALA:HB1	2:6:B:ILE:HG22	10	0.28
(2,35)	1:136:A:VAL:HG11	2:12:B:TYR:OH	6	0.27
(2,35)	1:136:A:VAL:HG12	2:12:B:TYR:OH	6	0.27
(2,35)	1:136:A:VAL:HG13	2:12:B:TYR:OH	6	0.27
(2,35)	1:136:A:VAL:HG21	2:12:B:TYR:OH	6	0.27
(2,35)	1:136:A:VAL:HG22	2:12:B:TYR:OH	6	0.27
(2,35)	1:136:A:VAL:HG23	2:12:B:TYR:OH	6	0.27
(1,69)	2:2:B:ASP:OD1	1:32:A:LEU:HD23	2	0.27
(1,69)	2:2:B:ASP:OD2	1:36:A:MET:HE1	7	0.27
(1,63)	1:141:A:PHE:HE1	2:12:B:TYR:CE1	3	0.27
(1,27)	1:36:A:MET:HE1	2:2:B:ASP:OD2	2	0.27
(1,27)	1:36:A:MET:HE1	2:2:B:ASP:OD2	7	0.27
(1,140)	1:124:A:MET:SD	2:13:B:ARG:HG2	7	0.26
(1,140)	1:124:A:MET:SD	2:13:B:ARG:HG3	7	0.26
(1,134)	1:127:A:GLU:CG	2:12:B:TYR:HH	5	0.26
(1,134)	1:127:A:GLU:CG	2:12:B:TYR:HH	6	0.26
(1,124)	1:145:A:MET:SD	2:8:B:THR:HG21	2	0.26
(1,124)	1:145:A:MET:SD	2:8:B:THR:HG22	2	0.26
(1,124)	1:145:A:MET:SD	2:8:B:THR:HG23	2	0.26
(1,118)	1:72:A:MET:SD	2:7:B:VAL:HG11	1	0.26
(1,118)	1:72:A:MET:SD	2:7:B:VAL:HG12	1	0.26
(1,118)	1:72:A:MET:SD	2:7:B:VAL:HG13	1	0.26
(1,97)	1:63:A:ILE:HG12	2:3:B:CYS:HG	4	0.26
(1,97)	1:63:A:ILE:HG13	2:3:B:CYS:HG	4	0.26
(1,90)	1:27:A:ILE:HG12	2:3:B:CYS:HG	4	0.26
(1,90)	1:27:A:ILE:HG13	2:3:B:CYS:HG	4	0.26
(1,69)	2:2:B:ASP:CG	1:32:A:LEU:HD23	10	0.26
(1,51)	1:109:A:MET:HE2	2:9:B:THR:HG21	1	0.26
(1,140)	1:124:A:MET:SD	2:13:B:ARG:HG2	9	0.25
(1,140)	1:124:A:MET:SD	2:13:B:ARG:HG3	9	0.25

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,124)	1:145:A:MET:SD	2:8:B:THR:HG21	5	0.25
(1,124)	1:145:A:MET:SD	2:8:B:THR:HG22	5	0.25
(1,124)	1:145:A:MET:SD	2:8:B:THR:HG23	5	0.25
(1,124)	1:145:A:MET:SD	2:8:B:THR:HG21	8	0.25
(1,124)	1:145:A:MET:SD	2:8:B:THR:HG22	8	0.25
(1,124)	1:145:A:MET:SD	2:8:B:THR:HG23	8	0.25
(1,120)	1:75:A:LYS:HB2	2:7:B:VAL:HB	3	0.25
(1,120)	1:75:A:LYS:HB3	2:7:B:VAL:HB	3	0.25
(1,112)	1:19:A:PHE:CZ	2:6:B:ILE:HD11	2	0.25
(1,112)	1:19:A:PHE:CZ	2:6:B:ILE:HD12	2	0.25
(1,112)	1:19:A:PHE:CZ	2:6:B:ILE:HD13	2	0.25
(1,96)	1:63:A:ILE:HG21	2:3:B:CYS:HG	1	0.25
(1,96)	1:63:A:ILE:HG22	2:3:B:CYS:HG	1	0.25
(1,96)	1:63:A:ILE:HG23	2:3:B:CYS:HG	1	0.25
(1,51)	1:109:A:MET:HE2	2:9:B:THR:HG21	2	0.25
(1,10)	2:10:B:LYS:HA	2:13:B:ARG:HB2	10	0.25
(1,10)	2:10:B:LYS:HA	2:13:B:ARG:HB3	10	0.25
(1,51)	1:109:A:MET:HE2	2:9:B:THR:HG21	4	0.24
(1,42)	1:72:A:MET:HG2	2:7:B:VAL:HG12	7	0.24
(1,1)	2:1:B:MET:HA	2:4:B:LEU:HB2	10	0.24
(1,1)	2:1:B:MET:HA	2:4:B:LEU:HB3	10	0.24
(1,55)	1:116:A:LEU:HD23	2:13:B:ARG:HD2	8	0.23
(1,124)	1:145:A:MET:SD	2:8:B:THR:HG21	7	0.22
(1,124)	1:145:A:MET:SD	2:8:B:THR:HG22	7	0.22
(1,124)	1:145:A:MET:SD	2:8:B:THR:HG23	7	0.22
(1,112)	1:19:A:PHE:CZ	2:6:B:ILE:HD11	5	0.22
(1,112)	1:19:A:PHE:CZ	2:6:B:ILE:HD12	5	0.22
(1,112)	1:19:A:PHE:CZ	2:6:B:ILE:HD13	5	0.22
(1,112)	1:19:A:PHE:CZ	2:6:B:ILE:HD11	10	0.22
(1,112)	1:19:A:PHE:CZ	2:6:B:ILE:HD12	10	0.22
(1,112)	1:19:A:PHE:CZ	2:6:B:ILE:HD13	10	0.22
(1,96)	1:63:A:ILE:HG21	2:3:B:CYS:HG	5	0.22
(1,96)	1:63:A:ILE:HG22	2:3:B:CYS:HG	5	0.22
(1,96)	1:63:A:ILE:HG23	2:3:B:CYS:HG	5	0.22
(1,96)	1:63:A:ILE:HG21	2:3:B:CYS:HG	9	0.22
(1,96)	1:63:A:ILE:HG22	2:3:B:CYS:HG	9	0.22
(1,96)	1:63:A:ILE:HG23	2:3:B:CYS:HG	9	0.22
(1,90)	1:27:A:ILE:HG12	2:3:B:CYS:HG	1	0.22
(1,90)	1:27:A:ILE:HG13	2:3:B:CYS:HG	1	0.22
(1,72)	2:5:B:CYS:SG	1:91:A:VAL:HG23	1	0.22
(1,48)	1:91:A:VAL:HG23	2:5:B:CYS:SG	1	0.22
(1,140)	1:124:A:MET:SD	2:13:B:ARG:HG2	4	0.21

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,140)	1:124:A:MET:SD	2:13:B:ARG:HG3	4	0.21
(1,120)	1:75:A:LYS:HB2	2:7:B:VAL:HB	5	0.21
(1,120)	1:75:A:LYS:HB3	2:7:B:VAL:HB	5	0.21
(1,118)	1:72:A:MET:SD	2:7:B:VAL:HG11	4	0.21
(1,118)	1:72:A:MET:SD	2:7:B:VAL:HG12	4	0.21
(1,118)	1:72:A:MET:SD	2:7:B:VAL:HG13	4	0.21
(1,90)	1:27:A:ILE:HG12	2:3:B:CYS:HG	7	0.21
(1,90)	1:27:A:ILE:HG13	2:3:B:CYS:HG	7	0.21
(1,69)	2:2:B:ASP:OD2	1:51:A:MET:HB3	3	0.21
(1,66)	1:144:A:MET:O	2:15:B:GLN:HG2	9	0.21
(1,55)	1:116:A:LEU:HD13	2:13:B:ARG:HD2	1	0.21
(1,5)	2:5:B:CYS:HA	2:8:B:THR:HB	5	0.21
(1,5)	2:5:B:CYS:HA	2:8:B:THR:HB	9	0.21
(1,118)	1:72:A:MET:SD	2:7:B:VAL:HG11	6	0.2
(1,118)	1:72:A:MET:SD	2:7:B:VAL:HG12	6	0.2
(1,118)	1:72:A:MET:SD	2:7:B:VAL:HG13	6	0.2
(1,112)	1:19:A:PHE:CZ	2:6:B:ILE:HD11	8	0.2
(1,112)	1:19:A:PHE:CZ	2:6:B:ILE:HD12	8	0.2
(1,112)	1:19:A:PHE:CZ	2:6:B:ILE:HD13	8	0.2
(1,66)	1:144:A:MET:HE1	2:15:B:GLN:HB3	2	0.2
(1,23)	1:32:A:LEU:HD21	2:3:B:CYS:HG	3	0.2
(1,23)	1:32:A:LEU:HD22	2:3:B:CYS:HG	6	0.2
(1,5)	2:5:B:CYS:HA	2:8:B:THR:HB	7	0.2
(1,140)	1:124:A:MET:SD	2:13:B:ARG:HG2	3	0.19
(1,140)	1:124:A:MET:SD	2:13:B:ARG:HG3	3	0.19
(1,140)	1:124:A:MET:SD	2:13:B:ARG:HG2	6	0.19
(1,140)	1:124:A:MET:SD	2:13:B:ARG:HG3	6	0.19
(1,112)	1:19:A:PHE:CZ	2:6:B:ILE:HD11	3	0.19
(1,112)	1:19:A:PHE:CZ	2:6:B:ILE:HD12	3	0.19
(1,112)	1:19:A:PHE:CZ	2:6:B:ILE:HD13	3	0.19
(1,112)	1:19:A:PHE:CZ	2:6:B:ILE:HD11	7	0.19
(1,112)	1:19:A:PHE:CZ	2:6:B:ILE:HD12	7	0.19
(1,112)	1:19:A:PHE:CZ	2:6:B:ILE:HD13	7	0.19
(1,90)	1:27:A:ILE:HG12	2:3:B:CYS:HG	2	0.19
(1,90)	1:27:A:ILE:HG13	2:3:B:CYS:HG	2	0.19
(1,69)	2:2:B:ASP:OD2	1:36:A:MET:HE1	6	0.19
(1,38)	1:68:A:PHE:HE1	2:3:B:CYS:HB3	1	0.19
(1,27)	1:36:A:MET:HE1	2:2:B:ASP:OD2	6	0.19
(1,23)	1:32:A:LEU:HD22	2:3:B:CYS:SG	7	0.19
(1,13)	1:15:A:ALA:HB1	2:6:B:ILE:HG22	8	0.19
(1,10)	2:10:B:LYS:HA	2:13:B:ARG:HB2	9	0.19
(1,10)	2:10:B:LYS:HA	2:13:B:ARG:HB3	9	0.19

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1)	2:1:B:MET:HA	2:4:B:LEU:HB2	3	0.19
(1,1)	2:1:B:MET:HA	2:4:B:LEU:HB3	3	0.19
(2,35)	1:136:A:VAL:HG11	2:12:B:TYR:OH	2	0.18
(2,35)	1:136:A:VAL:HG12	2:12:B:TYR:OH	2	0.18
(2,35)	1:136:A:VAL:HG13	2:12:B:TYR:OH	2	0.18
(2,35)	1:136:A:VAL:HG21	2:12:B:TYR:OH	2	0.18
(2,35)	1:136:A:VAL:HG22	2:12:B:TYR:OH	2	0.18
(2,35)	1:136:A:VAL:HG23	2:12:B:TYR:OH	2	0.18
(2,35)	1:136:A:VAL:HG11	2:12:B:TYR:OH	9	0.18
(2,35)	1:136:A:VAL:HG12	2:12:B:TYR:OH	9	0.18
(2,35)	1:136:A:VAL:HG13	2:12:B:TYR:OH	9	0.18
(2,35)	1:136:A:VAL:HG21	2:12:B:TYR:OH	9	0.18
(2,35)	1:136:A:VAL:HG22	2:12:B:TYR:OH	9	0.18
(2,35)	1:136:A:VAL:HG23	2:12:B:TYR:OH	9	0.18
(1,118)	1:72:A:MET:SD	2:7:B:VAL:HG11	3	0.18
(1,118)	1:72:A:MET:SD	2:7:B:VAL:HG12	3	0.18
(1,118)	1:72:A:MET:SD	2:7:B:VAL:HG13	3	0.18
(1,96)	1:63:A:ILE:HG21	2:3:B:CYS:HG	6	0.18
(1,96)	1:63:A:ILE:HG22	2:3:B:CYS:HG	6	0.18
(1,96)	1:63:A:ILE:HG23	2:3:B:CYS:HG	6	0.18
(1,96)	1:63:A:ILE:HG21	2:3:B:CYS:HG	8	0.18
(1,96)	1:63:A:ILE:HG22	2:3:B:CYS:HG	8	0.18
(1,96)	1:63:A:ILE:HG23	2:3:B:CYS:HG	8	0.18
(1,92)	1:32:A:LEU:HD11	2:3:B:CYS:SG	3	0.18
(1,92)	1:32:A:LEU:HD12	2:3:B:CYS:SG	3	0.18
(1,92)	1:32:A:LEU:HD13	2:3:B:CYS:SG	3	0.18
(1,92)	1:32:A:LEU:HD21	2:3:B:CYS:SG	3	0.18
(1,92)	1:32:A:LEU:HD22	2:3:B:CYS:SG	3	0.18
(1,92)	1:32:A:LEU:HD23	2:3:B:CYS:SG	3	0.18
(1,92)	1:32:A:LEU:HD11	2:3:B:CYS:SG	6	0.18
(1,92)	1:32:A:LEU:HD12	2:3:B:CYS:SG	6	0.18
(1,92)	1:32:A:LEU:HD13	2:3:B:CYS:SG	6	0.18
(1,92)	1:32:A:LEU:HD21	2:3:B:CYS:SG	6	0.18
(1,92)	1:32:A:LEU:HD22	2:3:B:CYS:SG	6	0.18
(1,92)	1:32:A:LEU:HD23	2:3:B:CYS:SG	6	0.18
(1,92)	1:32:A:LEU:HD11	2:3:B:CYS:SG	8	0.18
(1,92)	1:32:A:LEU:HD12	2:3:B:CYS:SG	8	0.18
(1,92)	1:32:A:LEU:HD13	2:3:B:CYS:SG	8	0.18
(1,92)	1:32:A:LEU:HD21	2:3:B:CYS:SG	8	0.18
(1,92)	1:32:A:LEU:HD22	2:3:B:CYS:SG	8	0.18
(1,92)	1:32:A:LEU:HD23	2:3:B:CYS:SG	8	0.18
(1,33)	1:55:A:VAL:HG23	2:4:B:LEU:HD21	2	0.18

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,23)	1:32:A:LEU:HD22	2:3:B:CYS:HG	1	0.18
(1,8)	2:8:B:THR:HA	2:11:B:LYS:HB2	7	0.18
(1,8)	2:8:B:THR:HA	2:11:B:LYS:HB3	7	0.18
(1,140)	1:124:A:MET:SD	2:13:B:ARG:HG2	10	0.17
(1,140)	1:124:A:MET:SD	2:13:B:ARG:HG3	10	0.17
(1,115)	1:112:A:LEU:HD21	2:6:B:ILE:HG12	7	0.17
(1,115)	1:112:A:LEU:HD21	2:6:B:ILE:HG13	7	0.17
(1,115)	1:112:A:LEU:HD22	2:6:B:ILE:HG12	7	0.17
(1,115)	1:112:A:LEU:HD22	2:6:B:ILE:HG13	7	0.17
(1,115)	1:112:A:LEU:HD23	2:6:B:ILE:HG12	7	0.17
(1,115)	1:112:A:LEU:HD23	2:6:B:ILE:HG13	7	0.17
(1,92)	1:32:A:LEU:HD11	2:3:B:CYS:SG	10	0.17
(1,92)	1:32:A:LEU:HD12	2:3:B:CYS:SG	10	0.17
(1,92)	1:32:A:LEU:HD13	2:3:B:CYS:SG	10	0.17
(1,92)	1:32:A:LEU:HD21	2:3:B:CYS:SG	10	0.17
(1,92)	1:32:A:LEU:HD22	2:3:B:CYS:SG	10	0.17
(1,92)	1:32:A:LEU:HD23	2:3:B:CYS:SG	10	0.17
(1,72)	2:5:B:CYS:SG	1:91:A:VAL:HG23	10	0.17
(1,59)	1:128:A:ALA:HB2	2:12:B:TYR:HE1	5	0.17
(1,48)	1:91:A:VAL:HG23	2:5:B:CYS:HB3	3	0.17
(1,48)	1:91:A:VAL:HG23	2:5:B:CYS:SG	10	0.17
(1,38)	1:68:A:PHE:HE1	2:3:B:CYS:HB3	7	0.17
(2,6)	2:3:B:CYS:O	2:7:B:VAL:H	5	0.16
(2,6)	2:3:B:CYS:O	2:7:B:VAL:H	6	0.16
(1,140)	1:124:A:MET:SD	2:13:B:ARG:HG2	1	0.16
(1,140)	1:124:A:MET:SD	2:13:B:ARG:HG3	1	0.16
(1,140)	1:124:A:MET:SD	2:13:B:ARG:HG2	8	0.16
(1,140)	1:124:A:MET:SD	2:13:B:ARG:HG3	8	0.16
(1,127)	1:109:A:MET:HE1	2:9:B:THR:HG21	3	0.16
(1,127)	1:109:A:MET:HE1	2:9:B:THR:HG22	3	0.16
(1,127)	1:109:A:MET:HE1	2:9:B:THR:HG23	3	0.16
(1,127)	1:109:A:MET:HE2	2:9:B:THR:HG21	3	0.16
(1,127)	1:109:A:MET:HE2	2:9:B:THR:HG22	3	0.16
(1,127)	1:109:A:MET:HE2	2:9:B:THR:HG23	3	0.16
(1,127)	1:109:A:MET:HE3	2:9:B:THR:HG21	3	0.16
(1,127)	1:109:A:MET:HE3	2:9:B:THR:HG22	3	0.16
(1,127)	1:109:A:MET:HE3	2:9:B:THR:HG23	3	0.16
(1,92)	1:32:A:LEU:HD11	2:3:B:CYS:SG	2	0.16
(1,92)	1:32:A:LEU:HD12	2:3:B:CYS:SG	2	0.16
(1,92)	1:32:A:LEU:HD13	2:3:B:CYS:SG	2	0.16
(1,92)	1:32:A:LEU:HD21	2:3:B:CYS:SG	2	0.16
(1,92)	1:32:A:LEU:HD22	2:3:B:CYS:SG	2	0.16

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,92)	1:32:A:LEU:HD23	2:3:B:CYS:SG	2	0.16
(1,91)	1:32:A:LEU:HD11	2:3:B:CYS:HG	8	0.16
(1,91)	1:32:A:LEU:HD12	2:3:B:CYS:HG	8	0.16
(1,91)	1:32:A:LEU:HD13	2:3:B:CYS:HG	8	0.16
(1,91)	1:32:A:LEU:HD21	2:3:B:CYS:HG	8	0.16
(1,91)	1:32:A:LEU:HD22	2:3:B:CYS:HG	8	0.16
(1,91)	1:32:A:LEU:HD23	2:3:B:CYS:HG	8	0.16
(1,90)	1:27:A:ILE:HG12	2:3:B:CYS:HG	9	0.16
(1,90)	1:27:A:ILE:HG13	2:3:B:CYS:HG	9	0.16
(1,90)	1:27:A:ILE:HG12	2:3:B:CYS:HG	10	0.16
(1,90)	1:27:A:ILE:HG13	2:3:B:CYS:HG	10	0.16
(1,88)	1:27:A:ILE:HD11	2:3:B:CYS:HG	10	0.16
(1,88)	1:27:A:ILE:HD12	2:3:B:CYS:HG	10	0.16
(1,88)	1:27:A:ILE:HD13	2:3:B:CYS:HG	10	0.16
(1,66)	1:144:A:MET:HE1	2:12:B:TYR:HD1	4	0.16
(1,55)	1:116:A:LEU:HD21	2:13:B:ARG:HD2	10	0.16
(1,42)	1:72:A:MET:HA	2:7:B:VAL:HG11	8	0.16
(1,38)	1:68:A:PHE:HE1	2:3:B:CYS:HB3	8	0.16
(1,23)	1:32:A:LEU:HD22	2:3:B:CYS:HG	2	0.16
(1,12)	2:12:B:TYR:HA	2:15:B:GLN:HB2	4	0.16
(1,12)	2:12:B:TYR:HA	2:15:B:GLN:HB3	4	0.16
(1,9)	2:9:B:THR:HA	2:12:B:TYR:HB2	2	0.16
(1,9)	2:9:B:THR:HA	2:12:B:TYR:HB3	2	0.16
(2,35)	1:136:A:VAL:HG11	2:12:B:TYR:OH	3	0.15
(2,35)	1:136:A:VAL:HG12	2:12:B:TYR:OH	3	0.15
(2,35)	1:136:A:VAL:HG13	2:12:B:TYR:OH	3	0.15
(2,35)	1:136:A:VAL:HG21	2:12:B:TYR:OH	3	0.15
(2,35)	1:136:A:VAL:HG22	2:12:B:TYR:OH	3	0.15
(2,35)	1:136:A:VAL:HG23	2:12:B:TYR:OH	3	0.15
(1,96)	1:63:A:ILE:HG21	2:3:B:CYS:HG	10	0.15
(1,96)	1:63:A:ILE:HG22	2:3:B:CYS:HG	10	0.15
(1,96)	1:63:A:ILE:HG23	2:3:B:CYS:HG	10	0.15
(1,95)	1:63:A:ILE:HD11	2:3:B:CYS:HG	4	0.15
(1,95)	1:63:A:ILE:HD12	2:3:B:CYS:HG	4	0.15
(1,95)	1:63:A:ILE:HD13	2:3:B:CYS:HG	4	0.15
(1,92)	1:32:A:LEU:HD11	2:3:B:CYS:SG	1	0.15
(1,92)	1:32:A:LEU:HD12	2:3:B:CYS:SG	1	0.15
(1,92)	1:32:A:LEU:HD13	2:3:B:CYS:SG	1	0.15
(1,92)	1:32:A:LEU:HD21	2:3:B:CYS:SG	1	0.15
(1,92)	1:32:A:LEU:HD22	2:3:B:CYS:SG	1	0.15
(1,92)	1:32:A:LEU:HD23	2:3:B:CYS:SG	1	0.15
(1,88)	1:27:A:ILE:HD11	2:3:B:CYS:HG	3	0.15

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,88)	1:27:A:ILE:HD12	2:3:B:CYS:HG	3	0.15
(1,88)	1:27:A:ILE:HD13	2:3:B:CYS:HG	3	0.15
(1,72)	2:5:B:CYS:HB3	1:91:A:VAL:HG23	5	0.15
(1,72)	2:5:B:CYS:SG	1:91:A:VAL:HG23	9	0.15
(1,69)	2:2:B:ASP:OD1	1:32:A:LEU:HD23	8	0.15
(1,69)	2:2:B:ASP:HB2	1:32:A:LEU:HD21	9	0.15
(1,63)	1:141:A:PHE:HD1	2:12:B:TYR:HE1	7	0.15
(1,48)	1:91:A:VAL:HG23	2:5:B:CYS:HB3	5	0.15
(1,48)	1:91:A:VAL:HG23	2:5:B:CYS:SG	9	0.15
(1,42)	1:72:A:MET:HG2	2:7:B:VAL:HG11	3	0.15
(1,33)	1:55:A:VAL:HG23	2:4:B:LEU:HG	3	0.15
(1,23)	1:32:A:LEU:HD23	2:2:B:ASP:OD1	8	0.15
(1,12)	2:12:B:TYR:HA	2:15:B:GLN:HB2	10	0.15
(1,12)	2:12:B:TYR:HA	2:15:B:GLN:HB3	10	0.15
(1,5)	2:5:B:CYS:HA	2:8:B:THR:HB	3	0.15
(1,5)	2:5:B:CYS:HA	2:8:B:THR:HB	4	0.15
(2,35)	1:136:A:VAL:HG11	2:12:B:TYR:OH	8	0.14
(2,35)	1:136:A:VAL:HG12	2:12:B:TYR:OH	8	0.14
(2,35)	1:136:A:VAL:HG13	2:12:B:TYR:OH	8	0.14
(2,35)	1:136:A:VAL:HG21	2:12:B:TYR:OH	8	0.14
(2,35)	1:136:A:VAL:HG22	2:12:B:TYR:OH	8	0.14
(2,35)	1:136:A:VAL:HG23	2:12:B:TYR:OH	8	0.14
(1,140)	1:124:A:MET:SD	2:13:B:ARG:HG2	2	0.14
(1,140)	1:124:A:MET:SD	2:13:B:ARG:HG3	2	0.14
(1,117)	1:72:A:MET:HG2	2:7:B:VAL:HG11	2	0.14
(1,117)	1:72:A:MET:HG2	2:7:B:VAL:HG12	2	0.14
(1,117)	1:72:A:MET:HG2	2:7:B:VAL:HG13	2	0.14
(1,117)	1:72:A:MET:HG3	2:7:B:VAL:HG11	2	0.14
(1,117)	1:72:A:MET:HG3	2:7:B:VAL:HG12	2	0.14
(1,117)	1:72:A:MET:HG3	2:7:B:VAL:HG13	2	0.14
(1,91)	1:32:A:LEU:HD11	2:3:B:CYS:HG	3	0.14
(1,91)	1:32:A:LEU:HD12	2:3:B:CYS:HG	3	0.14
(1,91)	1:32:A:LEU:HD13	2:3:B:CYS:HG	3	0.14
(1,91)	1:32:A:LEU:HD21	2:3:B:CYS:HG	3	0.14
(1,91)	1:32:A:LEU:HD22	2:3:B:CYS:HG	3	0.14
(1,91)	1:32:A:LEU:HD23	2:3:B:CYS:HG	3	0.14
(1,88)	1:27:A:ILE:HD11	2:3:B:CYS:HG	7	0.14
(1,88)	1:27:A:ILE:HD12	2:3:B:CYS:HG	7	0.14
(1,88)	1:27:A:ILE:HD13	2:3:B:CYS:HG	7	0.14
(1,88)	1:27:A:ILE:HD11	2:3:B:CYS:HG	8	0.14
(1,88)	1:27:A:ILE:HD12	2:3:B:CYS:HG	8	0.14
(1,88)	1:27:A:ILE:HD13	2:3:B:CYS:HG	8	0.14

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,68)	2:1:B:MET:HG2	1:87:A:GLU:OE2	4	0.14
(1,63)	1:141:A:PHE:HD1	2:12:B:TYR:HE1	4	0.14
(1,36)	1:63:A:ILE:HD13	2:3:B:CYS:HG	3	0.14
(1,23)	1:32:A:LEU:HD23	2:3:B:CYS:HG	9	0.14
(1,23)	1:32:A:LEU:HD22	2:3:B:CYS:HG	10	0.14
(1,8)	2:8:B:THR:HA	2:11:B:LYS:HB2	4	0.14
(1,8)	2:8:B:THR:HA	2:11:B:LYS:HB3	4	0.14
(1,6)	2:6:B:ILE:HA	2:9:B:THR:HB	10	0.14
(1,3)	2:3:B:CYS:HA	2:6:B:ILE:HB	7	0.14
(2,35)	1:136:A:VAL:HG11	2:12:B:TYR:OH	7	0.13
(2,35)	1:136:A:VAL:HG12	2:12:B:TYR:OH	7	0.13
(2,35)	1:136:A:VAL:HG13	2:12:B:TYR:OH	7	0.13
(2,35)	1:136:A:VAL:HG21	2:12:B:TYR:OH	7	0.13
(2,35)	1:136:A:VAL:HG22	2:12:B:TYR:OH	7	0.13
(2,35)	1:136:A:VAL:HG23	2:12:B:TYR:OH	7	0.13
(1,126)	1:92:A:PHE:HE1	2:9:B:THR:HG21	3	0.13
(1,126)	1:92:A:PHE:HE1	2:9:B:THR:HG22	3	0.13
(1,126)	1:92:A:PHE:HE1	2:9:B:THR:HG23	3	0.13
(1,126)	1:92:A:PHE:HE1	2:9:B:THR:HG21	7	0.13
(1,126)	1:92:A:PHE:HE1	2:9:B:THR:HG22	7	0.13
(1,126)	1:92:A:PHE:HE1	2:9:B:THR:HG23	7	0.13
(1,115)	1:112:A:LEU:HD21	2:6:B:ILE:HG12	9	0.13
(1,115)	1:112:A:LEU:HD21	2:6:B:ILE:HG13	9	0.13
(1,115)	1:112:A:LEU:HD22	2:6:B:ILE:HG12	9	0.13
(1,115)	1:112:A:LEU:HD22	2:6:B:ILE:HG13	9	0.13
(1,115)	1:112:A:LEU:HD23	2:6:B:ILE:HG12	9	0.13
(1,115)	1:112:A:LEU:HD23	2:6:B:ILE:HG13	9	0.13
(1,115)	1:112:A:LEU:HD21	2:6:B:ILE:HG12	10	0.13
(1,115)	1:112:A:LEU:HD21	2:6:B:ILE:HG13	10	0.13
(1,115)	1:112:A:LEU:HD22	2:6:B:ILE:HG12	10	0.13
(1,115)	1:112:A:LEU:HD22	2:6:B:ILE:HG13	10	0.13
(1,115)	1:112:A:LEU:HD23	2:6:B:ILE:HG12	10	0.13
(1,115)	1:112:A:LEU:HD23	2:6:B:ILE:HG13	10	0.13
(1,103)	1:87:A:GLU:HG2	2:5:B:CYS:HB2	4	0.13
(1,103)	1:87:A:GLU:HG2	2:5:B:CYS:HB3	4	0.13
(1,103)	1:87:A:GLU:HG3	2:5:B:CYS:HB2	4	0.13
(1,103)	1:87:A:GLU:HG3	2:5:B:CYS:HB3	4	0.13
(1,96)	1:63:A:ILE:HG21	2:3:B:CYS:HG	4	0.13
(1,96)	1:63:A:ILE:HG22	2:3:B:CYS:HG	4	0.13
(1,96)	1:63:A:ILE:HG23	2:3:B:CYS:HG	4	0.13
(1,91)	1:32:A:LEU:HD11	2:3:B:CYS:HG	6	0.13
(1,91)	1:32:A:LEU:HD12	2:3:B:CYS:HG	6	0.13

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,91)	1:32:A:LEU:HD13	2:3:B:CYS:HG	6	0.13
(1,91)	1:32:A:LEU:HD21	2:3:B:CYS:HG	6	0.13
(1,91)	1:32:A:LEU:HD22	2:3:B:CYS:HG	6	0.13
(1,91)	1:32:A:LEU:HD23	2:3:B:CYS:HG	6	0.13
(1,90)	1:27:A:ILE:HG12	2:3:B:CYS:HG	3	0.13
(1,90)	1:27:A:ILE:HG13	2:3:B:CYS:HG	3	0.13
(1,88)	1:27:A:ILE:HD11	2:3:B:CYS:HG	1	0.13
(1,88)	1:27:A:ILE:HD12	2:3:B:CYS:HG	1	0.13
(1,88)	1:27:A:ILE:HD13	2:3:B:CYS:HG	1	0.13
(1,72)	2:5:B:CYS:HB2	1:91:A:VAL:HG23	7	0.13
(1,48)	1:91:A:VAL:HG23	2:5:B:CYS:HB2	7	0.13
(1,12)	2:12:B:TYR:HA	2:15:B:GLN:HB2	8	0.13
(1,12)	2:12:B:TYR:HA	2:15:B:GLN:HB3	8	0.13
(1,5)	2:5:B:CYS:HA	2:8:B:THR:HB	2	0.13
(1,3)	2:3:B:CYS:HA	2:6:B:ILE:HB	10	0.13
(2,2)	2:1:B:MET:O	2:5:B:CYS:H	1	0.12
(1,139)	1:124:A:MET:HE1	2:13:B:ARG:HG2	1	0.12
(1,139)	1:124:A:MET:HE1	2:13:B:ARG:HG3	1	0.12
(1,139)	1:124:A:MET:HE2	2:13:B:ARG:HG2	1	0.12
(1,139)	1:124:A:MET:HE2	2:13:B:ARG:HG3	1	0.12
(1,139)	1:124:A:MET:HE3	2:13:B:ARG:HG2	1	0.12
(1,139)	1:124:A:MET:HE3	2:13:B:ARG:HG3	1	0.12
(1,139)	1:124:A:MET:HE1	2:13:B:ARG:HG2	8	0.12
(1,139)	1:124:A:MET:HE1	2:13:B:ARG:HG3	8	0.12
(1,139)	1:124:A:MET:HE2	2:13:B:ARG:HG2	8	0.12
(1,139)	1:124:A:MET:HE2	2:13:B:ARG:HG3	8	0.12
(1,139)	1:124:A:MET:HE3	2:13:B:ARG:HG2	8	0.12
(1,139)	1:124:A:MET:HE3	2:13:B:ARG:HG3	8	0.12
(1,139)	1:124:A:MET:HE1	2:13:B:ARG:HG2	9	0.12
(1,139)	1:124:A:MET:HE1	2:13:B:ARG:HG3	9	0.12
(1,139)	1:124:A:MET:HE2	2:13:B:ARG:HG2	9	0.12
(1,139)	1:124:A:MET:HE2	2:13:B:ARG:HG3	9	0.12
(1,139)	1:124:A:MET:HE3	2:13:B:ARG:HG2	9	0.12
(1,139)	1:124:A:MET:HE3	2:13:B:ARG:HG3	9	0.12
(1,126)	1:92:A:PHE:HE1	2:9:B:THR:HG21	9	0.12
(1,126)	1:92:A:PHE:HE1	2:9:B:THR:HG22	9	0.12
(1,126)	1:92:A:PHE:HE1	2:9:B:THR:HG23	9	0.12
(1,123)	1:88:A:ALA:HB1	2:8:B:THR:HB	8	0.12
(1,123)	1:88:A:ALA:HB2	2:8:B:THR:HB	8	0.12
(1,123)	1:88:A:ALA:HB3	2:8:B:THR:HB	8	0.12
(1,115)	1:112:A:LEU:HD21	2:6:B:ILE:HG12	5	0.12
(1,115)	1:112:A:LEU:HD21	2:6:B:ILE:HG13	5	0.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,115)	1:112:A:LEU:HD22	2:6:B:ILE:HG12	5	0.12
(1,115)	1:112:A:LEU:HD22	2:6:B:ILE:HG13	5	0.12
(1,115)	1:112:A:LEU:HD23	2:6:B:ILE:HG12	5	0.12
(1,115)	1:112:A:LEU:HD23	2:6:B:ILE:HG13	5	0.12
(1,109)	1:15:A:ALA:HB1	2:6:B:ILE:HD11	1	0.12
(1,109)	1:15:A:ALA:HB1	2:6:B:ILE:HD12	1	0.12
(1,109)	1:15:A:ALA:HB1	2:6:B:ILE:HD13	1	0.12
(1,109)	1:15:A:ALA:HB2	2:6:B:ILE:HD11	1	0.12
(1,109)	1:15:A:ALA:HB2	2:6:B:ILE:HD12	1	0.12
(1,109)	1:15:A:ALA:HB2	2:6:B:ILE:HD13	1	0.12
(1,109)	1:15:A:ALA:HB3	2:6:B:ILE:HD11	1	0.12
(1,109)	1:15:A:ALA:HB3	2:6:B:ILE:HD12	1	0.12
(1,109)	1:15:A:ALA:HB3	2:6:B:ILE:HD13	1	0.12
(1,103)	1:87:A:GLU:HG2	2:5:B:CYS:HB2	2	0.12
(1,103)	1:87:A:GLU:HG2	2:5:B:CYS:HB3	2	0.12
(1,103)	1:87:A:GLU:HG3	2:5:B:CYS:HB2	2	0.12
(1,103)	1:87:A:GLU:HG3	2:5:B:CYS:HB3	2	0.12
(1,92)	1:32:A:LEU:HD11	2:3:B:CYS:SG	5	0.12
(1,92)	1:32:A:LEU:HD12	2:3:B:CYS:SG	5	0.12
(1,92)	1:32:A:LEU:HD13	2:3:B:CYS:SG	5	0.12
(1,92)	1:32:A:LEU:HD21	2:3:B:CYS:SG	5	0.12
(1,92)	1:32:A:LEU:HD22	2:3:B:CYS:SG	5	0.12
(1,92)	1:32:A:LEU:HD23	2:3:B:CYS:SG	5	0.12
(1,91)	1:32:A:LEU:HD11	2:3:B:CYS:HG	4	0.12
(1,91)	1:32:A:LEU:HD12	2:3:B:CYS:HG	4	0.12
(1,91)	1:32:A:LEU:HD13	2:3:B:CYS:HG	4	0.12
(1,91)	1:32:A:LEU:HD21	2:3:B:CYS:HG	4	0.12
(1,91)	1:32:A:LEU:HD22	2:3:B:CYS:HG	4	0.12
(1,91)	1:32:A:LEU:HD23	2:3:B:CYS:HG	4	0.12
(1,91)	1:32:A:LEU:HD11	2:3:B:CYS:HG	7	0.12
(1,91)	1:32:A:LEU:HD12	2:3:B:CYS:HG	7	0.12
(1,91)	1:32:A:LEU:HD13	2:3:B:CYS:HG	7	0.12
(1,91)	1:32:A:LEU:HD21	2:3:B:CYS:HG	7	0.12
(1,91)	1:32:A:LEU:HD22	2:3:B:CYS:HG	7	0.12
(1,91)	1:32:A:LEU:HD23	2:3:B:CYS:HG	7	0.12
(1,72)	2:5:B:CYS:HB2	1:91:A:VAL:HG23	2	0.12
(1,72)	2:5:B:CYS:SG	1:91:A:VAL:HG23	6	0.12
(1,48)	1:91:A:VAL:HG23	2:5:B:CYS:HB2	2	0.12
(1,48)	1:91:A:VAL:HG23	2:5:B:CYS:SG	6	0.12
(1,42)	1:72:A:MET:HA	2:7:B:VAL:HG23	4	0.12
(1,23)	1:32:A:LEU:HD22	2:3:B:CYS:HG	5	0.12
(1,12)	2:12:B:TYR:HA	2:15:B:GLN:HB2	9	0.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,12)	2:12:B:TYR:HA	2:15:B:GLN:HB3	9	0.12
(1,10)	2:10:B:LYS:HA	2:13:B:ARG:HB2	5	0.12
(1,10)	2:10:B:LYS:HA	2:13:B:ARG:HB3	5	0.12
(1,10)	2:10:B:LYS:HA	2:13:B:ARG:HB2	6	0.12
(1,10)	2:10:B:LYS:HA	2:13:B:ARG:HB3	6	0.12
(1,8)	2:8:B:THR:HA	2:11:B:LYS:HB2	5	0.12
(1,8)	2:8:B:THR:HA	2:11:B:LYS:HB3	5	0.12
(1,8)	2:8:B:THR:HA	2:11:B:LYS:HB2	10	0.12
(1,8)	2:8:B:THR:HA	2:11:B:LYS:HB3	10	0.12
(1,3)	2:3:B:CYS:HA	2:6:B:ILE:HB	3	0.12
(1,3)	2:3:B:CYS:HA	2:6:B:ILE:HB	8	0.12
(2,32)	1:87:A:GLU:O	1:91:A:VAL:H	9	0.11
(2,28)	1:85:A:ILE:O	1:89:A:PHE:H	3	0.11
(2,28)	1:85:A:ILE:O	1:89:A:PHE:H	6	0.11
(2,6)	2:3:B:CYS:O	2:7:B:VAL:H	1	0.11
(2,6)	2:3:B:CYS:O	2:7:B:VAL:H	2	0.11
(2,6)	2:3:B:CYS:O	2:7:B:VAL:H	4	0.11
(1,127)	1:109:A:MET:HE1	2:9:B:THR:HG21	9	0.11
(1,127)	1:109:A:MET:HE1	2:9:B:THR:HG22	9	0.11
(1,127)	1:109:A:MET:HE1	2:9:B:THR:HG23	9	0.11
(1,127)	1:109:A:MET:HE2	2:9:B:THR:HG21	9	0.11
(1,127)	1:109:A:MET:HE2	2:9:B:THR:HG22	9	0.11
(1,127)	1:109:A:MET:HE2	2:9:B:THR:HG23	9	0.11
(1,127)	1:109:A:MET:HE3	2:9:B:THR:HG21	9	0.11
(1,127)	1:109:A:MET:HE3	2:9:B:THR:HG22	9	0.11
(1,127)	1:109:A:MET:HE3	2:9:B:THR:HG23	9	0.11
(1,115)	1:112:A:LEU:HD21	2:6:B:ILE:HG12	8	0.11
(1,115)	1:112:A:LEU:HD21	2:6:B:ILE:HG13	8	0.11
(1,115)	1:112:A:LEU:HD22	2:6:B:ILE:HG12	8	0.11
(1,115)	1:112:A:LEU:HD22	2:6:B:ILE:HG13	8	0.11
(1,115)	1:112:A:LEU:HD23	2:6:B:ILE:HG12	8	0.11
(1,115)	1:112:A:LEU:HD23	2:6:B:ILE:HG13	8	0.11
(1,114)	1:112:A:LEU:HD21	2:6:B:ILE:HD11	7	0.11
(1,114)	1:112:A:LEU:HD21	2:6:B:ILE:HD12	7	0.11
(1,114)	1:112:A:LEU:HD21	2:6:B:ILE:HD13	7	0.11
(1,114)	1:112:A:LEU:HD22	2:6:B:ILE:HD11	7	0.11
(1,114)	1:112:A:LEU:HD22	2:6:B:ILE:HD12	7	0.11
(1,114)	1:112:A:LEU:HD22	2:6:B:ILE:HD13	7	0.11
(1,114)	1:112:A:LEU:HD23	2:6:B:ILE:HD11	7	0.11
(1,114)	1:112:A:LEU:HD23	2:6:B:ILE:HD12	7	0.11
(1,114)	1:112:A:LEU:HD23	2:6:B:ILE:HD13	7	0.11
(1,103)	1:87:A:GLU:HG2	2:5:B:CYS:HB2	1	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,103)	1:87:A:GLU:HG2	2:5:B:CYS:HB3	1	0.11
(1,103)	1:87:A:GLU:HG3	2:5:B:CYS:HB2	1	0.11
(1,103)	1:87:A:GLU:HG3	2:5:B:CYS:HB3	1	0.11
(1,103)	1:87:A:GLU:HG2	2:5:B:CYS:HB2	6	0.11
(1,103)	1:87:A:GLU:HG2	2:5:B:CYS:HB3	6	0.11
(1,103)	1:87:A:GLU:HG3	2:5:B:CYS:HB2	6	0.11
(1,103)	1:87:A:GLU:HG3	2:5:B:CYS:HB3	6	0.11
(1,103)	1:87:A:GLU:HG2	2:5:B:CYS:HB2	8	0.11
(1,103)	1:87:A:GLU:HG2	2:5:B:CYS:HB3	8	0.11
(1,103)	1:87:A:GLU:HG3	2:5:B:CYS:HB2	8	0.11
(1,103)	1:87:A:GLU:HG3	2:5:B:CYS:HB3	8	0.11
(1,103)	1:87:A:GLU:HG2	2:5:B:CYS:HB2	10	0.11
(1,103)	1:87:A:GLU:HG2	2:5:B:CYS:HB3	10	0.11
(1,103)	1:87:A:GLU:HG3	2:5:B:CYS:HB2	10	0.11
(1,103)	1:87:A:GLU:HG3	2:5:B:CYS:HB3	10	0.11
(1,91)	1:32:A:LEU:HD11	2:3:B:CYS:HG	1	0.11
(1,91)	1:32:A:LEU:HD12	2:3:B:CYS:HG	1	0.11
(1,91)	1:32:A:LEU:HD13	2:3:B:CYS:HG	1	0.11
(1,91)	1:32:A:LEU:HD21	2:3:B:CYS:HG	1	0.11
(1,91)	1:32:A:LEU:HD22	2:3:B:CYS:HG	1	0.11
(1,91)	1:32:A:LEU:HD23	2:3:B:CYS:HG	1	0.11
(1,88)	1:27:A:ILE:HD11	2:3:B:CYS:HG	5	0.11
(1,88)	1:27:A:ILE:HD12	2:3:B:CYS:HG	5	0.11
(1,88)	1:27:A:ILE:HD13	2:3:B:CYS:HG	5	0.11
(1,42)	1:72:A:MET:HG2	2:7:B:VAL:HG12	9	0.11
(1,19)	1:27:A:ILE:HG22	2:3:B:CYS:HG	5	0.11
(1,19)	1:27:A:ILE:HG22	2:3:B:CYS:HG	7	0.11
(1,10)	2:10:B:LYS:HA	2:13:B:ARG:HB2	1	0.11
(1,10)	2:10:B:LYS:HA	2:13:B:ARG:HB3	1	0.11
(1,10)	2:10:B:LYS:HA	2:13:B:ARG:HB2	7	0.11
(1,10)	2:10:B:LYS:HA	2:13:B:ARG:HB3	7	0.11
(1,9)	2:9:B:THR:HA	2:12:B:TYR:HB2	9	0.11
(1,9)	2:9:B:THR:HA	2:12:B:TYR:HB3	9	0.11
(1,7)	2:7:B:VAL:HA	2:10:B:LYS:HB2	2	0.11
(1,7)	2:7:B:VAL:HA	2:10:B:LYS:HB3	2	0.11
(1,7)	2:7:B:VAL:HA	2:10:B:LYS:HB2	9	0.11
(1,7)	2:7:B:VAL:HA	2:10:B:LYS:HB3	9	0.11
(1,5)	2:5:B:CYS:HA	2:8:B:THR:HB	8	0.11
(1,5)	2:5:B:CYS:HA	2:8:B:THR:HB	10	0.11
(2,35)	1:136:A:VAL:HG11	2:12:B:TYR:OH	1	0.1
(2,35)	1:136:A:VAL:HG12	2:12:B:TYR:OH	1	0.1
(2,35)	1:136:A:VAL:HG13	2:12:B:TYR:OH	1	0.1

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,35)	1:136:A:VAL:HG21	2:12:B:TYR:OH	1	0.1
(2,35)	1:136:A:VAL:HG22	2:12:B:TYR:OH	1	0.1
(2,35)	1:136:A:VAL:HG23	2:12:B:TYR:OH	1	0.1
(1,122)	1:88:A:ALA:HB1	2:8:B:THR:HG21	3	0.1
(1,122)	1:88:A:ALA:HB1	2:8:B:THR:HG22	3	0.1
(1,122)	1:88:A:ALA:HB1	2:8:B:THR:HG23	3	0.1
(1,122)	1:88:A:ALA:HB2	2:8:B:THR:HG21	3	0.1
(1,122)	1:88:A:ALA:HB2	2:8:B:THR:HG22	3	0.1
(1,122)	1:88:A:ALA:HB2	2:8:B:THR:HG23	3	0.1
(1,122)	1:88:A:ALA:HB3	2:8:B:THR:HG21	3	0.1
(1,122)	1:88:A:ALA:HB3	2:8:B:THR:HG22	3	0.1
(1,122)	1:88:A:ALA:HB3	2:8:B:THR:HG23	3	0.1
(1,115)	1:112:A:LEU:HD21	2:6:B:ILE:HG12	4	0.1
(1,115)	1:112:A:LEU:HD21	2:6:B:ILE:HG13	4	0.1
(1,115)	1:112:A:LEU:HD22	2:6:B:ILE:HG12	4	0.1
(1,115)	1:112:A:LEU:HD22	2:6:B:ILE:HG13	4	0.1
(1,115)	1:112:A:LEU:HD23	2:6:B:ILE:HG12	4	0.1
(1,115)	1:112:A:LEU:HD23	2:6:B:ILE:HG13	4	0.1
(1,109)	1:15:A:ALA:HB1	2:6:B:ILE:HD11	6	0.1
(1,109)	1:15:A:ALA:HB1	2:6:B:ILE:HD12	6	0.1
(1,109)	1:15:A:ALA:HB1	2:6:B:ILE:HD13	6	0.1
(1,109)	1:15:A:ALA:HB2	2:6:B:ILE:HD11	6	0.1
(1,109)	1:15:A:ALA:HB2	2:6:B:ILE:HD12	6	0.1
(1,109)	1:15:A:ALA:HB2	2:6:B:ILE:HD13	6	0.1
(1,109)	1:15:A:ALA:HB3	2:6:B:ILE:HD11	6	0.1
(1,109)	1:15:A:ALA:HB3	2:6:B:ILE:HD12	6	0.1
(1,109)	1:15:A:ALA:HB3	2:6:B:ILE:HD13	6	0.1
(1,103)	1:87:A:GLU:HG2	2:5:B:CYS:HB2	9	0.1
(1,103)	1:87:A:GLU:HG2	2:5:B:CYS:HB3	9	0.1
(1,103)	1:87:A:GLU:HG3	2:5:B:CYS:HB2	9	0.1
(1,103)	1:87:A:GLU:HG3	2:5:B:CYS:HB3	9	0.1
(1,96)	1:63:A:ILE:HG21	2:3:B:CYS:HG	7	0.1
(1,96)	1:63:A:ILE:HG22	2:3:B:CYS:HG	7	0.1
(1,96)	1:63:A:ILE:HG23	2:3:B:CYS:HG	7	0.1
(1,92)	1:32:A:LEU:HD11	2:3:B:CYS:SG	7	0.1
(1,92)	1:32:A:LEU:HD12	2:3:B:CYS:SG	7	0.1
(1,92)	1:32:A:LEU:HD13	2:3:B:CYS:SG	7	0.1
(1,92)	1:32:A:LEU:HD21	2:3:B:CYS:SG	7	0.1
(1,92)	1:32:A:LEU:HD22	2:3:B:CYS:SG	7	0.1
(1,92)	1:32:A:LEU:HD23	2:3:B:CYS:SG	7	0.1
(1,90)	1:27:A:ILE:HG12	2:3:B:CYS:HG	5	0.1
(1,90)	1:27:A:ILE:HG13	2:3:B:CYS:HG	5	0.1

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,88)	1:27:A:ILE:HD11	2:3:B:CYS:HG	6	0.1
(1,88)	1:27:A:ILE:HD12	2:3:B:CYS:HG	6	0.1
(1,88)	1:27:A:ILE:HD13	2:3:B:CYS:HG	6	0.1
(1,36)	1:63:A:ILE:HD12	2:3:B:CYS:HG	6	0.1

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

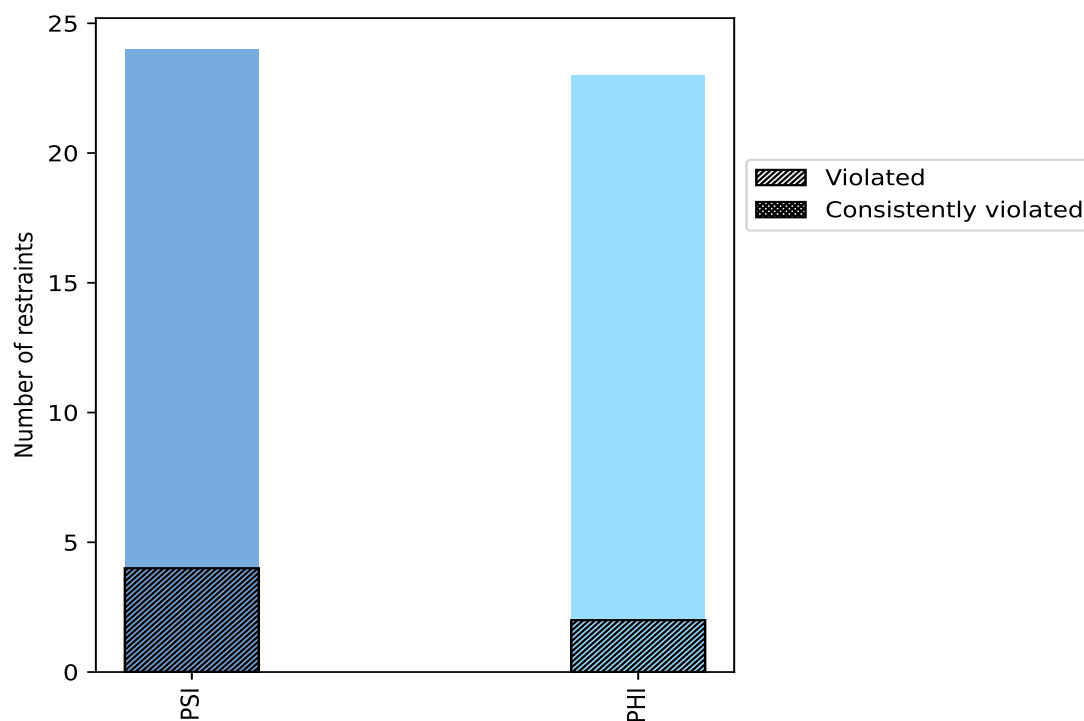
10.1 Summary of dihedral-angle violations [i](#)

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
PSI	24	51.1	4	16.7	8.5	0	0.0	0.0
PHI	23	48.9	2	8.7	4.3	0	0.0	0.0
Total	47	100.0	6	12.8	12.8	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](#)



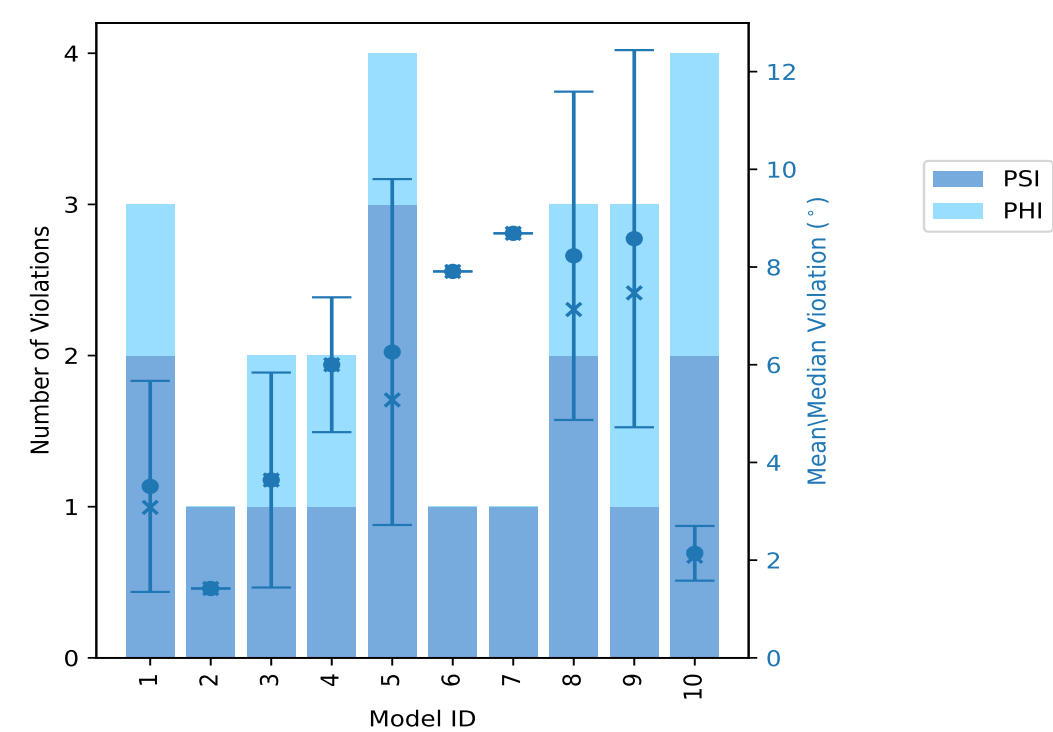
Violated and consistently violated restraints are shown using different hatch patterns in their respective categories

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 (°)
	PSI	PHI	Total				
1	2	1	3	3.51	6.35	2.16	3.08
2	1	0	1	1.42	1.42	0.0	1.42
3	1	1	2	3.64	5.84	2.2	3.64
4	1	1	2	6.0	7.37	1.38	6.0
5	3	1	4	6.26	12.04	3.54	5.28
6	1	0	1	7.91	7.91	0.0	7.91
7	1	0	1	8.69	8.69	0.0	8.69
8	2	1	3	8.23	12.78	3.36	7.13
9	1	2	3	8.58	13.77	3.86	7.47
10	2	2	4	2.14	2.96	0.56	2.08

10.2.1 Bar graph : Dihedral violation statistics for each model ⓘ



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

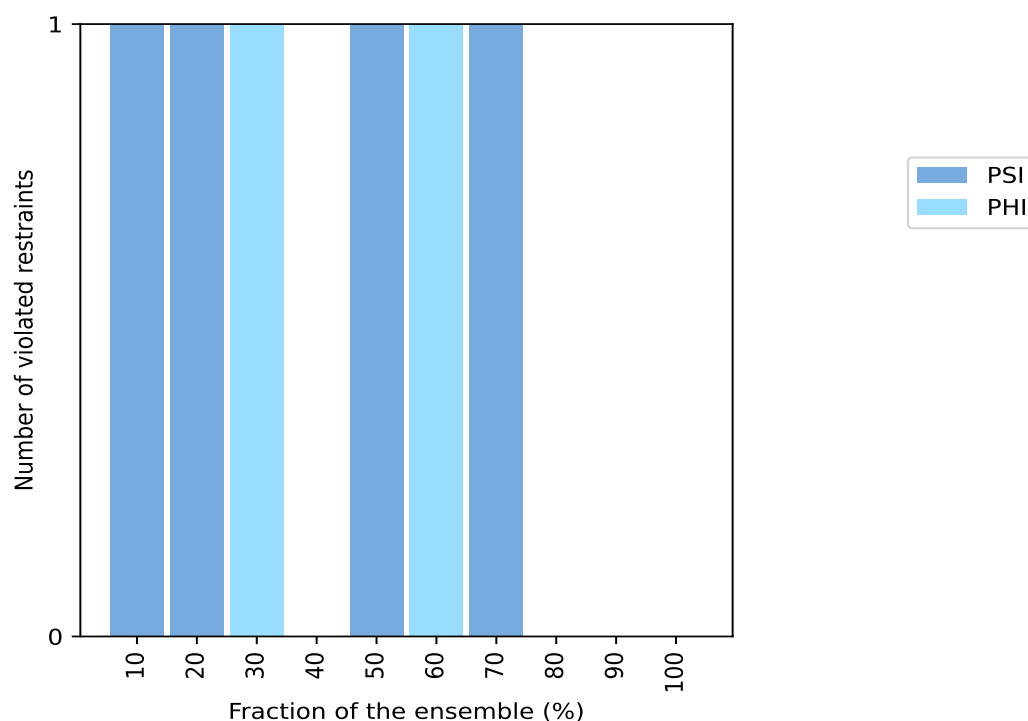
10.3 Dihedral-angle violation statistics for the ensemble [i](#)

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	
PSI	PHI	Total	Count ¹	%
1	0	1	1	10.0
1	0	1	2	20.0
0	1	1	3	30.0
0	0	0	4	40.0
1	0	1	5	50.0
0	1	1	6	60.0
1	0	1	7	70.0
0	0	0	8	80.0
0	0	0	9	90.0
0	0	0	10	100.0

¹ Number of models with violations

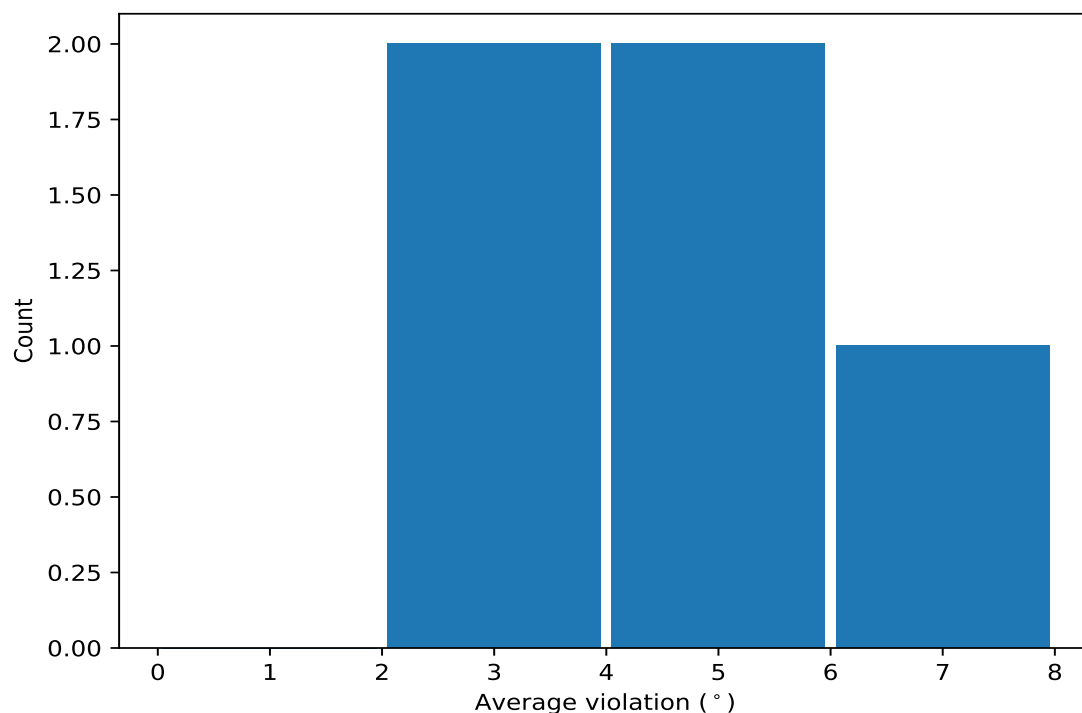
10.3.1 Bar graph : Dihedral-angle Violation statistics for the ensemble [i](#)



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.

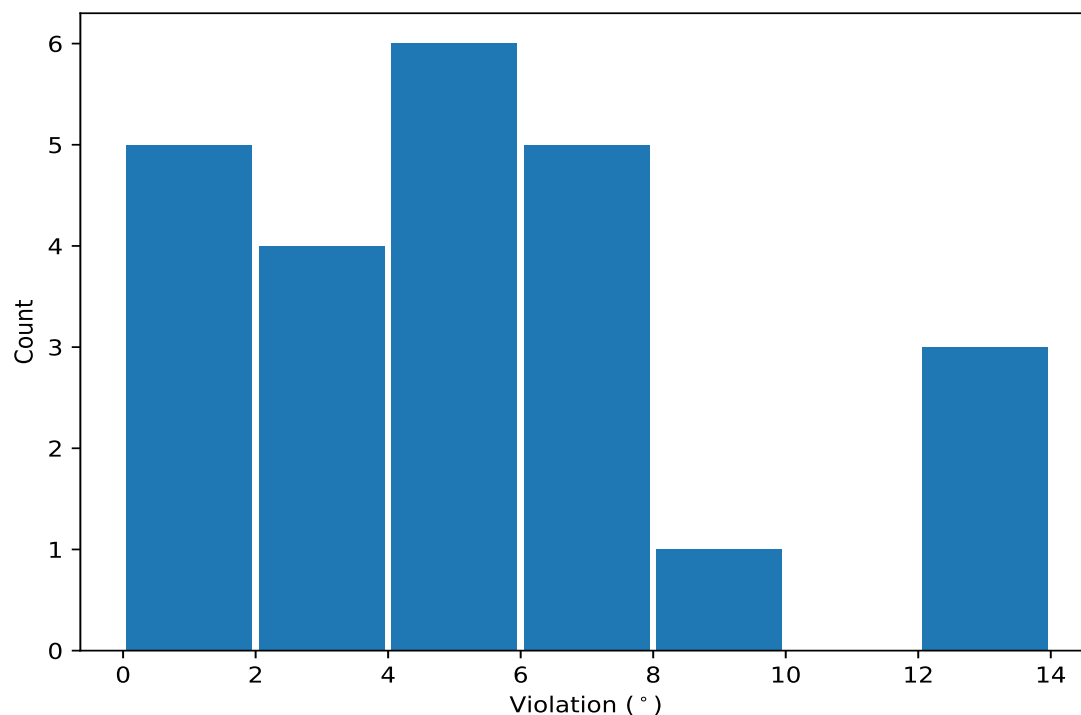
Key	Atom-1	Atom-2	Atom-3	Atom-4	Models ¹	Mean	SD ²	Median
(1,16)	2:1:B:MET:N	2:1:B:MET:CA	2:1:B:MET:C	2:2:B:ASP:N	7	5.57	2.47	5.76
(1,13)	2:13:B:ARG:C	2:14:B:TYR:N	2:14:B:TYR:CA	2:14:B:TYR:C	6	6.96	4.12	5.48
(1,17)	2:2:B:ASP:N	2:2:B:ASP:CA	2:2:B:ASP:C	2:3:B:CYS:N	5	3.84	2.4	2.46
(1,1)	2:1:B:MET:C	2:2:B:ASP:N	2:2:B:ASP:CA	2:2:B:ASP:C	3	5.68	5.72	1.84
(1,39)	1:83:A:GLU:N	1:83:A:GLU:CA	1:83:A:GLU:C	1:84:A:GLU:N	2	3.88	0.92	3.88

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 (°)
(1,1)	2:1:B:MET:C	2:2:B:ASP:N	2:2:B:ASP:CA	2:2:B:ASP:C	9	13.77
(1,13)	2:13:B:ARG:C	2:14:B:TYR:N	2:14:B:TYR:CA	2:14:B:TYR:C	8	12.78
(1,13)	2:13:B:ARG:C	2:14:B:TYR:N	2:14:B:TYR:CA	2:14:B:TYR:C	5	12.04
(1,16)	2:1:B:MET:N	2:1:B:MET:CA	2:1:B:MET:C	2:2:B:ASP:N	7	8.69
(1,16)	2:1:B:MET:N	2:1:B:MET:CA	2:1:B:MET:C	2:2:B:ASP:N	6	7.91
(1,17)	2:2:B:ASP:N	2:2:B:ASP:CA	2:2:B:ASP:C	2:3:B:CYS:N	9	7.47
(1,16)	2:1:B:MET:N	2:1:B:MET:CA	2:1:B:MET:C	2:2:B:ASP:N	4	7.37
(1,28)	2:13:B:ARG:N	2:13:B:ARG:CA	2:13:B:ARG:C	2:14:B:TYR:N	8	7.13
(1,13)	2:13:B:ARG:C	2:14:B:TYR:N	2:14:B:TYR:CA	2:14:B:TYR:C	1	6.35
(1,17)	2:2:B:ASP:N	2:2:B:ASP:CA	2:2:B:ASP:C	2:3:B:CYS:N	3	5.84
(1,16)	2:1:B:MET:N	2:1:B:MET:CA	2:1:B:MET:C	2:2:B:ASP:N	5	5.76
(1,39)	1:83:A:GLU:N	1:83:A:GLU:CA	1:83:A:GLU:C	1:84:A:GLU:N	5	4.79
(1,16)	2:1:B:MET:N	2:1:B:MET:CA	2:1:B:MET:C	2:2:B:ASP:N	8	4.77
(1,13)	2:13:B:ARG:C	2:14:B:TYR:N	2:14:B:TYR:CA	2:14:B:TYR:C	4	4.62

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,13)	2:13:B:ARG:C	2:14:B:TYR:N	2:14:B:TYR:CA	2:14:B:TYR:C	9	4.5
(1,16)	2:1:B:MET:N	2:1:B:MET:CA	2:1:B:MET:C	2:2:B:ASP:N	1	3.08
(1,39)	1:83:A:GLU:N	1:83:A:GLU:CA	1:83:A:GLU:C	1:84:A:GLU:N	10	2.96
(1,17)	2:2:B:ASP:N	2:2:B:ASP:CA	2:2:B:ASP:C	2:3:B:CYS:N	5	2.46
(1,17)	2:2:B:ASP:N	2:2:B:ASP:CA	2:2:B:ASP:C	2:3:B:CYS:N	10	2.31
(1,1)	2:1:B:MET:C	2:2:B:ASP:N	2:2:B:ASP:CA	2:2:B:ASP:C	10	1.84
(1,13)	2:13:B:ARG:C	2:14:B:TYR:N	2:14:B:TYR:CA	2:14:B:TYR:C	10	1.47
(1,1)	2:1:B:MET:C	2:2:B:ASP:N	2:2:B:ASP:CA	2:2:B:ASP:C	3	1.44
(1,16)	2:1:B:MET:N	2:1:B:MET:CA	2:1:B:MET:C	2:2:B:ASP:N	2	1.42
(1,17)	2:2:B:ASP:N	2:2:B:ASP:CA	2:2:B:ASP:C	2:3:B:CYS:N	1	1.11