



Full wwPDB NMR Structure Validation Report ⓘ

Mar 25, 2026 – 08:32 AM UTC

PDB ID : 2JM5 / pdb_00002jm5
BMRB ID : 7106
Title : Solution Structure of the RGS domain from human RGS18
Authors : Higman, V.A.; Leidert, M.; Bray, J.; Elkins, J.; Soundararajan, M.; Doyle, D.A.; Gileadi, C.; Phillips, C.; Schoch, G.; Yang, X.; Brockmann, C.; Schmieder, P.; Diehl, A.; Sundstrom, M.; Arrowsmith, C.; Weigelt, J.; Edwards, A.; Oshkinat, H.; Ball, L.J.; Structural Genomics Consortium (SGC)
Deposited on : 2006-10-11

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

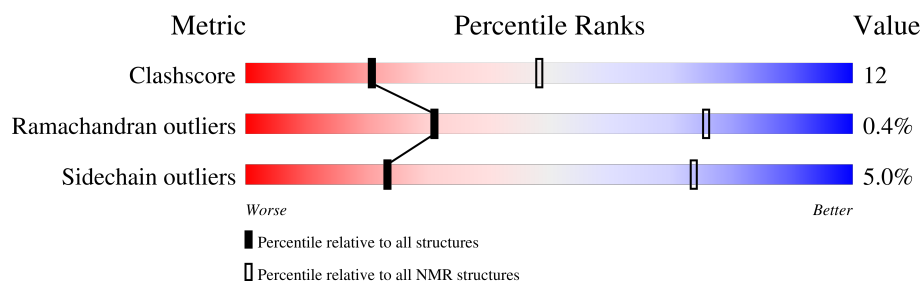
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 90%.

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	151	

2 Ensemble composition and analysis

This entry contains 20 models. Model 3 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:3-A:130 (128)	0.76	3

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 4 clusters and 1 single-model cluster was found.

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

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 2183 atoms, of which 1079 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Regulator of G-protein signaling 18.

Mol	Chain	Residues	Atoms						Trace
1	A	134	Total	C	H	N	O	S	0
			2183	706	1079	181	213	4	

There are 2 discrepancies between the modelled and reference sequences:

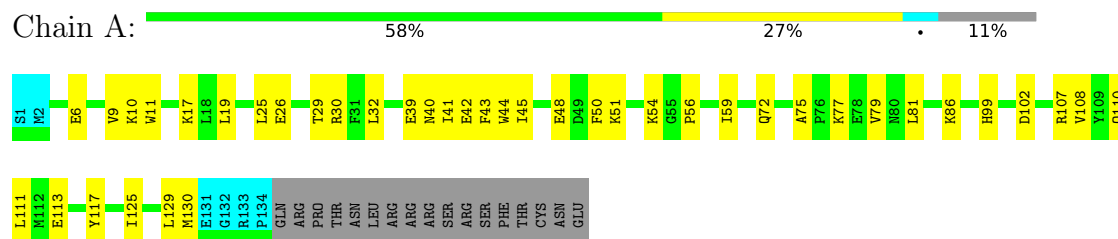
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	SER	-	cloning artifact	UNP Q9NS28
A	2	MET	-	cloning artifact	UNP Q9NS28

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: Regulator of G-protein signaling 18

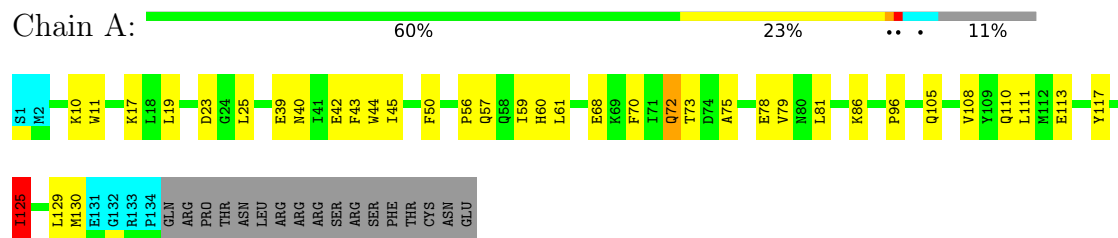


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

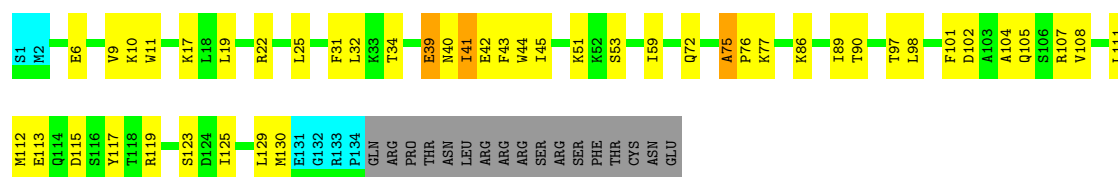
- Molecule 1: Regulator of G-protein signaling 18



4.2.2 Score per residue for model 2

- Molecule 1: Regulator of G-protein signaling 18

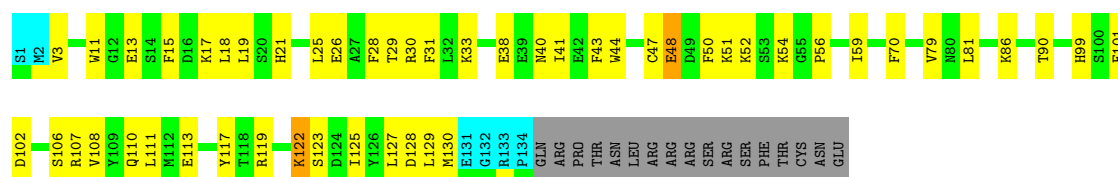




4.2.3 Score per residue for model 3 (medoid)

- Molecule 1: Regulator of G-protein signaling 18

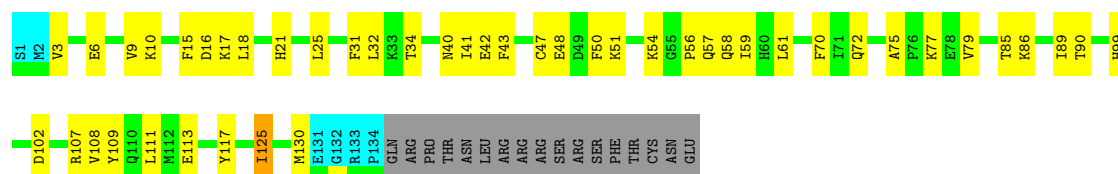
Chain A: 51% 32% 11%



4.2.4 Score per residue for model 4

- Molecule 1: Regulator of G-protein signaling 18

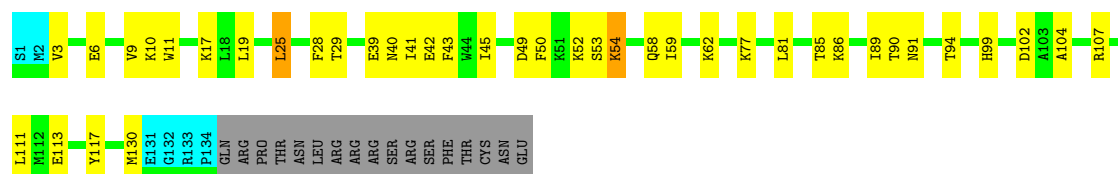
Chain A: 54% 30% 11%



4.2.5 Score per residue for model 5

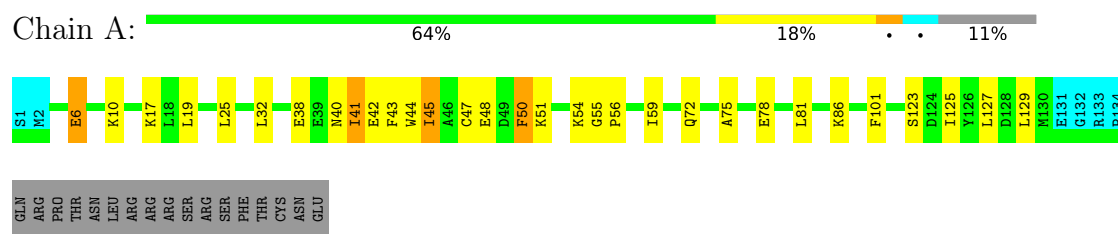
- Molecule 1: Regulator of G-protein signaling 18

Chain A: 58% 25% 11%



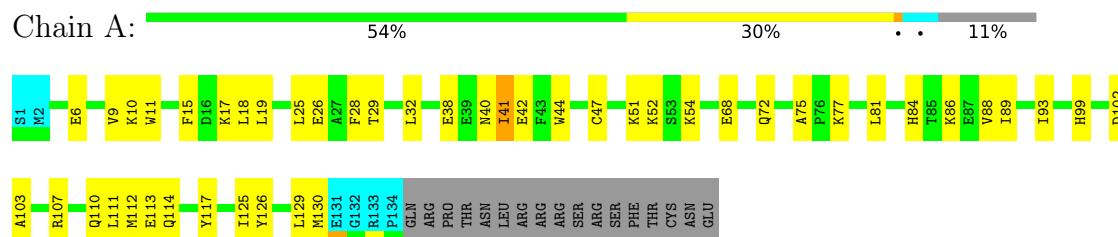
4.2.6 Score per residue for model 6

- Molecule 1: Regulator of G-protein signaling 18



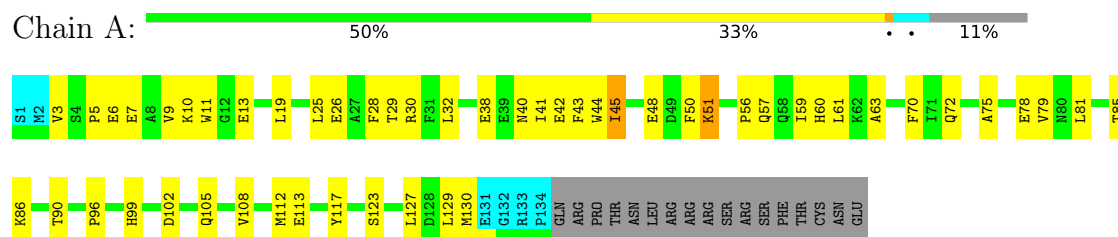
4.2.7 Score per residue for model 7

- Molecule 1: Regulator of G-protein signaling 18



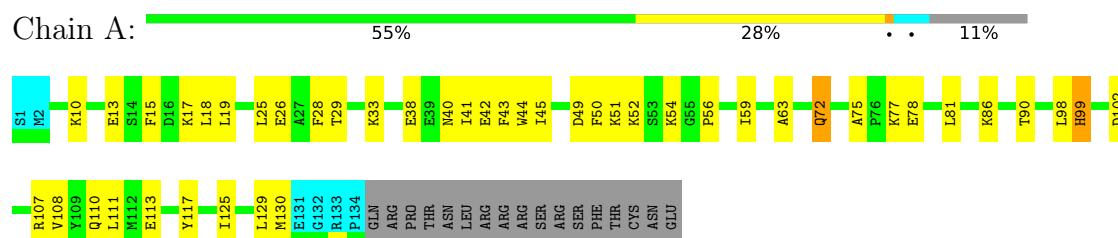
4.2.8 Score per residue for model 8

- Molecule 1: Regulator of G-protein signaling 18



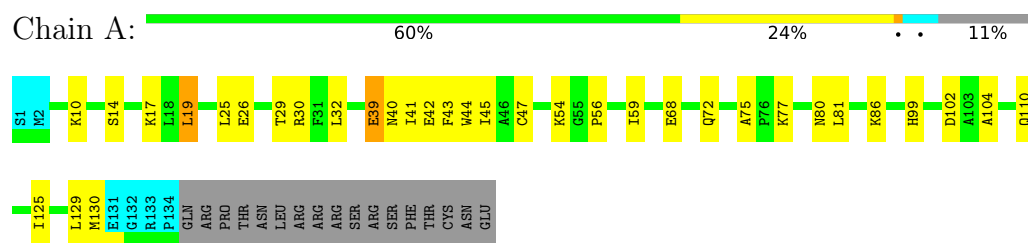
4.2.9 Score per residue for model 9

- Molecule 1: Regulator of G-protein signaling 18



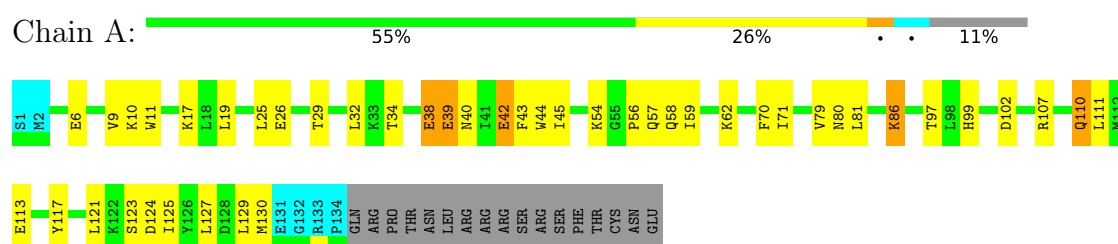
4.2.10 Score per residue for model 10

- Molecule 1: Regulator of G-protein signaling 18



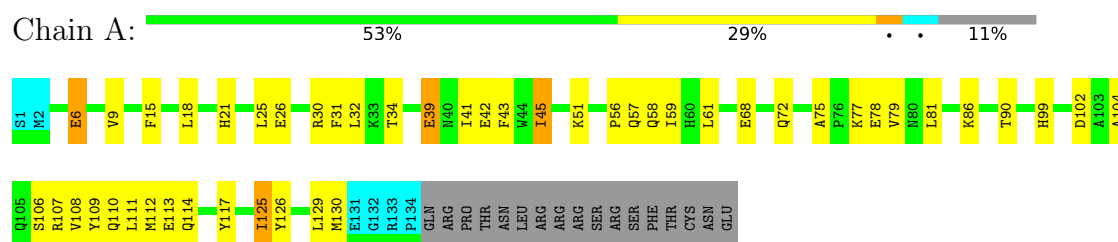
4.2.11 Score per residue for model 11

- Molecule 1: Regulator of G-protein signaling 18



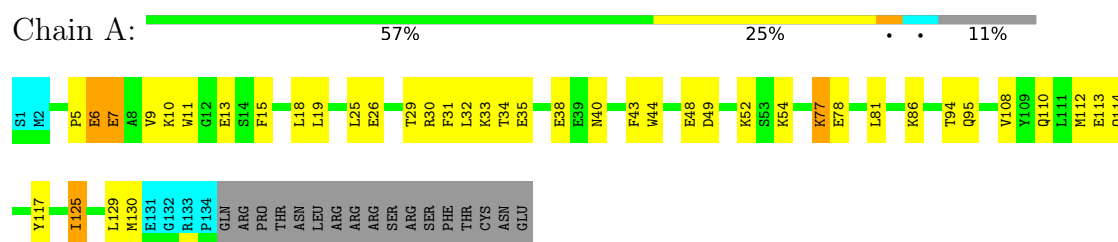
4.2.12 Score per residue for model 12

- Molecule 1: Regulator of G-protein signaling 18



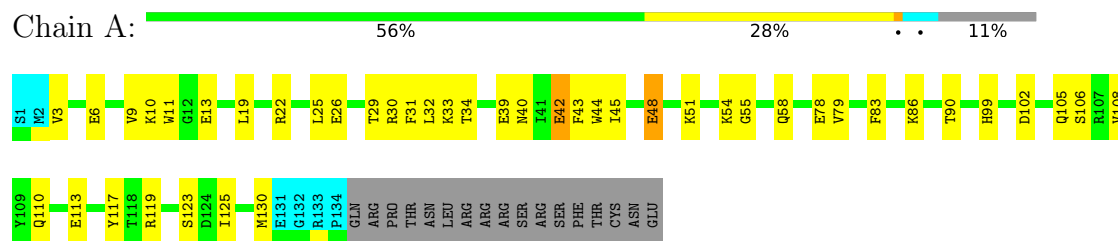
4.2.13 Score per residue for model 13

- Molecule 1: Regulator of G-protein signaling 18



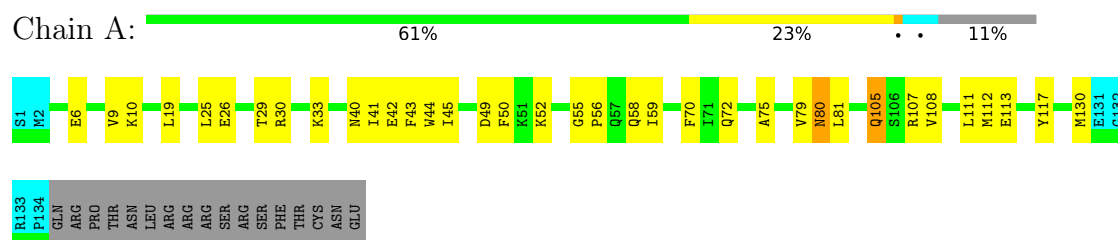
4.2.14 Score per residue for model 14

- Molecule 1: Regulator of G-protein signaling 18



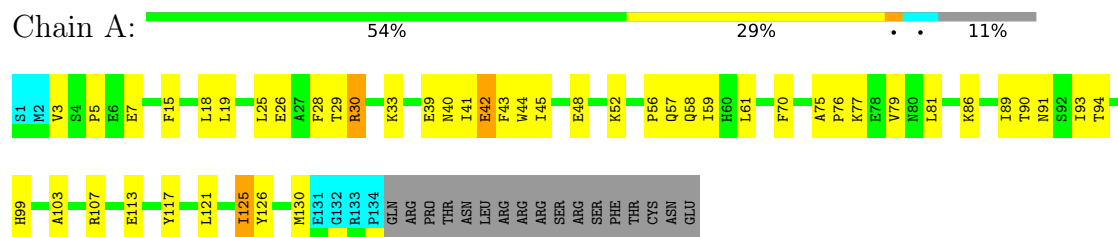
4.2.15 Score per residue for model 15

- Molecule 1: Regulator of G-protein signaling 18



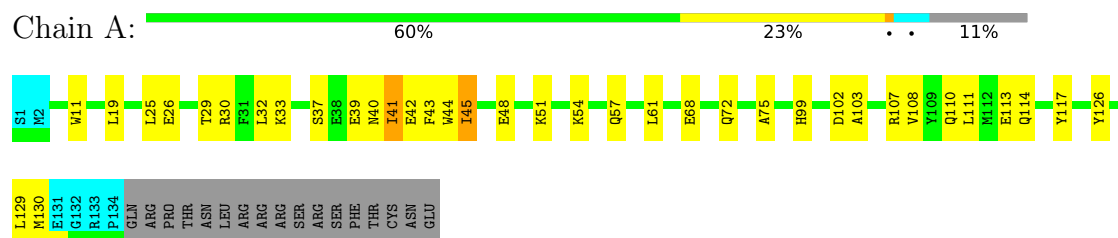
4.2.16 Score per residue for model 16

- Molecule 1: Regulator of G-protein signaling 18



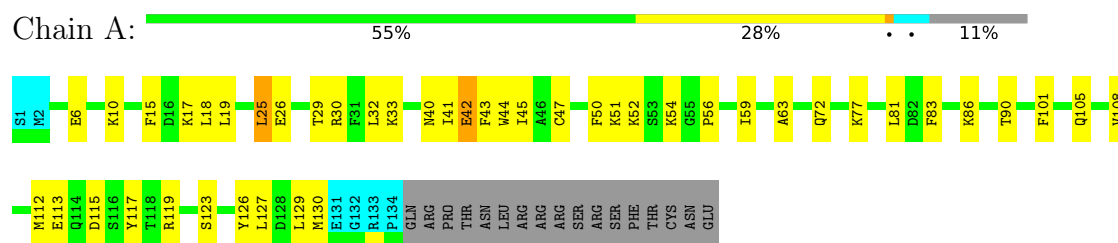
4.2.17 Score per residue for model 17

- Molecule 1: Regulator of G-protein signaling 18



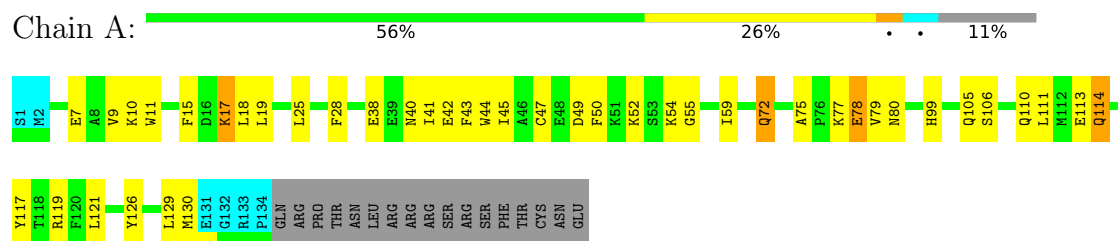
4.2.18 Score per residue for model 18

- Molecule 1: Regulator of G-protein signaling 18



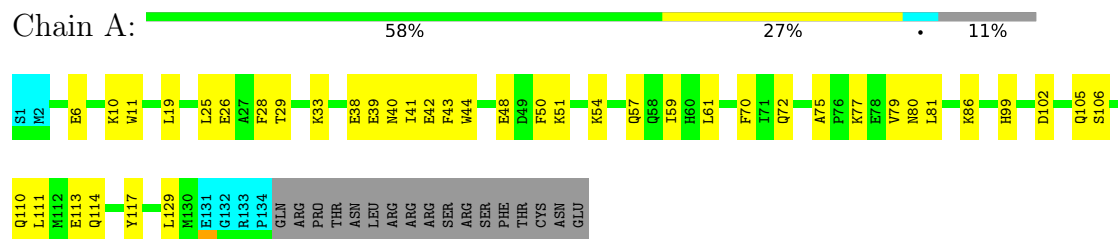
4.2.19 Score per residue for model 19

- Molecule 1: Regulator of G-protein signaling 18



4.2.20 Score per residue for model 20

- Molecule 1: Regulator of G-protein signaling 18



5 Refinement protocol and experimental data overview

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

Of the 200 calculated structures, 20 were deposited, based on the following criterion: *lowest energy*.

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

Software name	Classification	Version
CYANA	structure solution	2.0
X-PLOR NIH	structure solution	2.14
X-PLOR NIH	refinement	2.14

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	1659
Number of shifts mapped to atoms	1659
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	90%

6 Model quality [i](#)

6.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#Z>5	RMSZ	#Z>5
1	A	0.96±0.03	0±1/1085 (0.0± 0.1%)	1.02±0.02	0±0/1464 (0.0± 0.0%)
All	All	0.96	10/21700 (0.0%)	1.02	3/29280 (0.0%)

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

Mol	Chain	Chirality	Planarity
1	A	0.0±0.0	0.1±0.2
All	All	0	1

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
1	A	39	GLU	C-O	-6.75	1.16	1.24	11	1
1	A	125	ILE	CA-CB	5.55	1.61	1.54	4	3
1	A	72	GLN	C-N	-5.53	1.26	1.33	18	4
1	A	54	LYS	N-CA	-5.09	1.39	1.46	7	1
1	A	41	ILE	CA-CB	5.07	1.60	1.54	7	1

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	80	ASN	CA-CB-CG	7.35	119.95	112.60	15	1
1	A	7	GLU	N-CA-C	-5.65	105.20	111.36	8	1
1	A	73	THR	N-CA-C	-5.19	105.07	111.40	1	1

There are no chirality outliers.

All unique planar outliers are listed below.

Mol	Chain	Res	Type	Group	Models (Total)
1	A	119	ARG	Sidechain	1

6.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	1059	1034	1030	25±4
All	All	21180	20680	20600	502

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 12.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:32:LEU:HD13	1:A:38:GLU:HA	0.91	1.42	11	1
1:A:99:HIS:HB3	1:A:102:ASP:HB2	0.83	1.47	12	10
1:A:39:GLU:HG2	1:A:77:LYS:HD3	0.79	1.55	5	2
1:A:77:LYS:HA	1:A:77:LYS:HE2	0.79	1.55	9	7
1:A:81:LEU:HD23	1:A:86:LYS:HG2	0.77	1.55	10	4
1:A:130:MET:HA	1:A:130:MET:HE2	0.77	1.56	3	16
1:A:49:ASP:HA	1:A:52:LYS:HE2	0.76	1.58	9	2
1:A:80:ASN:HB2	1:A:111:LEU:HD21	0.75	1.56	10	4
1:A:99:HIS:HB3	1:A:102:ASP:HB3	0.71	1.59	14	2
1:A:72:GLN:HB2	1:A:75:ALA:HB2	0.69	1.64	12	6
1:A:40:ASN:HB2	1:A:108:VAL:HG13	0.69	1.65	14	2
1:A:26:GLU:HA	1:A:29:THR:HG22	0.68	1.63	9	10
1:A:68:GLU:HA	1:A:72:GLN:HG3	0.65	1.69	10	4
1:A:113:GLU:O	1:A:117:TYR:HB3	0.65	1.92	17	19
1:A:72:GLN:HB3	1:A:75:ALA:HB2	0.65	1.66	8	7
1:A:58:GLN:HA	1:A:61:LEU:HD12	0.64	1.70	12	3
1:A:32:LEU:HD23	1:A:41:ILE:HB	0.62	1.70	7	2
1:A:19:LEU:HD21	1:A:44:TRP:CZ2	0.62	2.30	11	14
1:A:81:LEU:HD23	1:A:86:LYS:HB3	0.61	1.72	7	8
1:A:44:TRP:HB2	1:A:105:GLN:HG2	0.61	1.73	20	2
1:A:107:ARG:O	1:A:111:LEU:HG	0.60	1.96	17	9

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:15:PHE:HD1	1:A:18:LEU:HD23	0.60	1.57	13	8
1:A:42:GLU:HA	1:A:45:ILE:HB	0.60	1.74	10	11
1:A:47:CYS:SG	1:A:101:PHE:HB2	0.59	2.37	6	2
1:A:3:VAL:HG11	1:A:11:TRP:CH2	0.58	2.34	3	2
1:A:108:VAL:HA	1:A:111:LEU:HD12	0.58	1.75	3	7
1:A:39:GLU:HA	1:A:77:LYS:HE3	0.58	1.75	12	1
1:A:40:ASN:O	1:A:43:PHE:HB3	0.57	1.98	19	18
1:A:70:PHE:HB3	1:A:79:VAL:CG2	0.57	2.30	3	8
1:A:31:PHE:CZ	1:A:119:ARG:HG3	0.57	2.35	3	1
1:A:29:THR:O	1:A:33:LYS:HG3	0.56	2.00	13	7
1:A:126:TYR:HE1	1:A:130:MET:HE3	0.56	1.59	16	1
1:A:28:PHE:HD2	1:A:41:ILE:HD12	0.56	1.60	20	7
1:A:26:GLU:O	1:A:30:ARG:HG2	0.56	2.01	14	1
1:A:44:TRP:HB2	1:A:105:GLN:HG3	0.56	1.78	19	1
1:A:26:GLU:O	1:A:30:ARG:HG3	0.55	2.00	13	8
1:A:40:ASN:HB3	1:A:112:MET:SD	0.55	2.42	7	1
1:A:50:PHE:HD1	1:A:62:LYS:HG2	0.55	1.62	5	1
1:A:44:TRP:CB	1:A:105:GLN:HG3	0.54	2.33	19	1
1:A:41:ILE:HG23	1:A:45:ILE:HD12	0.54	1.78	17	2
1:A:56:PRO:HA	1:A:59:ILE:HD12	0.54	1.80	8	1
1:A:50:PHE:CZ	1:A:59:ILE:HG23	0.54	2.38	3	4
1:A:25:LEU:O	1:A:29:THR:HG23	0.53	2.03	5	1
1:A:11:TRP:CZ3	1:A:129:LEU:HD13	0.53	2.38	13	9
1:A:48:GLU:HG2	1:A:51:LYS:HE3	0.53	1.81	4	1
1:A:19:LEU:HG	1:A:44:TRP:CH2	0.53	2.39	10	1
1:A:10:LYS:HB3	1:A:17:LYS:HE2	0.52	1.81	1	2
1:A:60:HIS:HA	1:A:96:PRO:HG3	0.52	1.82	1	2
1:A:10:LYS:O	1:A:13:GLU:HG2	0.52	2.04	9	2
1:A:10:LYS:O	1:A:17:LYS:HD2	0.51	2.05	6	6
1:A:102:ASP:HA	1:A:105:GLN:HE21	0.51	1.64	2	1
1:A:33:LYS:HA	1:A:38:GLU:HB3	0.51	1.82	3	1
1:A:57:GLN:O	1:A:61:LEU:HG	0.51	2.05	8	7
1:A:48:GLU:HA	1:A:51:LYS:HB3	0.51	1.82	6	1
1:A:43:PHE:CD1	1:A:79:VAL:HG21	0.51	2.41	19	2
1:A:125:ILE:O	1:A:129:LEU:HG	0.51	2.06	3	6
1:A:32:LEU:HD21	1:A:40:ASN:OD1	0.51	2.06	18	3
1:A:31:PHE:CZ	1:A:119:ARG:HB2	0.51	2.40	14	1
1:A:10:LYS:HB3	1:A:17:LYS:HD2	0.51	1.82	19	1
1:A:44:TRP:HB2	1:A:105:GLN:HE21	0.50	1.66	8	1
1:A:49:ASP:HA	1:A:52:LYS:HD3	0.50	1.82	19	1
1:A:31:PHE:HZ	1:A:119:ARG:HG3	0.50	1.64	3	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:48:GLU:O	1:A:52:LYS:HG3	0.50	2.06	13	3
1:A:10:LYS:HB3	1:A:17:LYS:HD3	0.50	1.82	11	1
1:A:58:GLN:HE21	1:A:62:LYS:HB2	0.50	1.67	5	1
1:A:6:GLU:O	1:A:9:VAL:HG22	0.50	2.07	8	9
1:A:40:ASN:HB2	1:A:108:VAL:CG1	0.49	2.37	18	3
1:A:6:GLU:HA	1:A:9:VAL:HG22	0.49	1.84	12	1
1:A:79:VAL:HG12	1:A:81:LEU:HB2	0.49	1.84	15	1
1:A:6:GLU:O	1:A:10:LYS:HG2	0.49	2.08	20	8
1:A:86:LYS:O	1:A:90:THR:HG23	0.49	2.07	8	10
1:A:44:TRP:HA	1:A:47:CYS:SG	0.49	2.48	10	1
1:A:94:THR:HG23	1:A:95:GLN:HG3	0.49	1.83	13	1
1:A:106:SER:O	1:A:110:GLN:HG2	0.49	2.05	14	5
1:A:32:LEU:CD2	1:A:41:ILE:HB	0.49	2.38	18	6
1:A:101:PHE:O	1:A:105:GLN:HG3	0.49	2.07	2	2
1:A:48:GLU:HA	1:A:51:LYS:HG3	0.49	1.82	8	1
1:A:14:SER:O	1:A:17:LYS:HG2	0.49	2.08	10	1
1:A:81:LEU:HD11	1:A:85:THR:HG21	0.49	1.85	8	1
1:A:123:SER:O	1:A:127:LEU:HG	0.49	2.07	8	5
1:A:51:LYS:HG2	1:A:98:LEU:HG	0.49	1.85	9	1
1:A:9:VAL:HG12	1:A:130:MET:SD	0.49	2.48	8	2
1:A:9:VAL:HA	1:A:126:TYR:OH	0.49	2.07	19	1
1:A:19:LEU:HD21	1:A:44:TRP:HZ2	0.48	1.68	13	8
1:A:15:PHE:CD1	1:A:18:LEU:HD23	0.48	2.43	12	7
1:A:31:PHE:O	1:A:34:THR:HG22	0.48	2.08	2	3
1:A:32:LEU:HD23	1:A:38:GLU:HA	0.48	1.84	6	1
1:A:126:TYR:HD1	1:A:129:LEU:HD12	0.48	1.69	18	3
1:A:48:GLU:HG3	1:A:51:LYS:HE3	0.48	1.85	17	1
1:A:48:GLU:O	1:A:51:LYS:HG2	0.48	2.09	20	1
1:A:44:TRP:HA	1:A:105:GLN:OE1	0.48	2.09	14	1
1:A:56:PRO:HA	1:A:59:ILE:HG12	0.47	1.86	16	11
1:A:81:LEU:HD11	1:A:104:ALA:HA	0.47	1.86	12	2
1:A:42:GLU:OE1	1:A:45:ILE:HD12	0.47	2.08	11	3
1:A:43:PHE:CE1	1:A:79:VAL:HG21	0.47	2.43	14	6
1:A:38:GLU:O	1:A:41:ILE:HG22	0.47	2.09	7	1
1:A:55:GLY:O	1:A:58:GLN:HB3	0.47	2.10	14	2
1:A:91:ASN:O	1:A:94:THR:HG22	0.47	2.09	5	2
1:A:48:GLU:HA	1:A:51:LYS:HG2	0.47	1.85	3	2
1:A:3:VAL:HG23	1:A:7:GLU:HB3	0.47	1.87	16	1
1:A:108:VAL:O	1:A:112:MET:HG2	0.47	2.09	8	2
1:A:110:GLN:O	1:A:114:GLN:HG3	0.46	2.10	19	1
1:A:51:LYS:HA	1:A:98:LEU:HG	0.46	1.87	2	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:68:GLU:HA	1:A:72:GLN:CG	0.46	2.40	12	3
1:A:10:LYS:O	1:A:17:LYS:HD3	0.46	2.10	10	1
1:A:32:LEU:HG	1:A:38:GLU:H	0.46	1.71	13	1
1:A:6:GLU:O	1:A:10:LYS:HD3	0.46	2.11	7	2
1:A:28:PHE:CZ	1:A:112:MET:HB3	0.46	2.45	7	1
1:A:77:LYS:HA	1:A:77:LYS:CE	0.46	2.39	7	1
1:A:68:GLU:HA	1:A:72:GLN:HB2	0.46	1.87	17	1
1:A:75:ALA:HB1	1:A:76:PRO:HD2	0.46	1.87	16	2
1:A:89:ILE:O	1:A:93:ILE:HB	0.46	2.11	16	2
1:A:11:TRP:HZ3	1:A:129:LEU:HD13	0.45	1.72	2	1
1:A:19:LEU:HG	1:A:44:TRP:HH2	0.45	1.71	10	1
1:A:83:PHE:HA	1:A:86:LYS:HG2	0.45	1.88	18	2
1:A:28:PHE:CD2	1:A:41:ILE:HD12	0.45	2.46	5	2
1:A:115:ASP:O	1:A:119:ARG:HG2	0.45	2.11	18	1
1:A:89:ILE:HD11	1:A:104:ALA:HB2	0.45	1.89	2	2
1:A:43:PHE:CZ	1:A:71:ILE:HD11	0.45	2.47	11	1
1:A:110:GLN:O	1:A:114:GLN:HG2	0.45	2.12	7	4
1:A:50:PHE:CZ	1:A:63:ALA:HB2	0.45	2.46	8	1
1:A:7:GLU:O	1:A:10:LYS:HB2	0.45	2.12	13	2
1:A:10:LYS:HA	1:A:13:GLU:HG3	0.44	1.88	8	1
1:A:32:LEU:HB3	1:A:38:GLU:HA	0.44	1.88	8	1
1:A:122:LYS:HE3	1:A:122:LYS:HA	0.44	1.90	3	1
1:A:47:CYS:O	1:A:50:PHE:HB3	0.44	2.12	4	2
1:A:53:SER:HB3	1:A:58:GLN:HG2	0.44	1.90	5	1
1:A:126:TYR:CD1	1:A:129:LEU:HD12	0.44	2.48	12	4
1:A:3:VAL:HG21	1:A:11:TRP:CZ2	0.44	2.47	8	2
1:A:9:VAL:N	1:A:130:MET:HE1	0.44	2.27	4	1
1:A:117:TYR:O	1:A:121:LEU:HG	0.44	2.13	16	3
1:A:123:SER:OG	1:A:125:ILE:HB	0.44	2.13	14	3
1:A:77:LYS:O	1:A:78:GLU:HB2	0.44	2.12	19	1
1:A:55:GLY:O	1:A:59:ILE:HG12	0.44	2.12	15	3
1:A:103:ALA:O	1:A:107:ARG:HG2	0.43	2.14	16	3
1:A:58:GLN:O	1:A:62:LYS:HB2	0.43	2.14	11	1
1:A:10:LYS:HB3	1:A:17:LYS:CD	0.43	2.44	11	1
1:A:49:ASP:O	1:A:52:LYS:HB3	0.43	2.13	5	1
1:A:31:PHE:HA	1:A:34:THR:HG22	0.43	1.90	12	2
1:A:77:LYS:HE2	1:A:77:LYS:CA	0.43	2.42	18	1
1:A:50:PHE:CE1	1:A:59:ILE:HG23	0.43	2.49	6	2
1:A:33:LYS:HG3	1:A:38:GLU:OE1	0.43	2.14	9	1
1:A:39:GLU:CD	1:A:79:VAL:HA	0.43	2.39	12	1
1:A:33:LYS:HG2	1:A:38:GLU:HB3	0.43	1.90	20	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:115:ASP:O	1:A:119:ARG:HD3	0.42	2.14	2	1
1:A:77:LYS:O	1:A:78:GLU:HG2	0.42	2.14	13	1
1:A:41:ILE:O	1:A:45:ILE:HB	0.42	2.13	6	1
1:A:39:GLU:HG3	1:A:77:LYS:HD3	0.42	1.90	2	1
1:A:51:LYS:HG3	1:A:98:LEU:HD23	0.42	1.90	2	1
1:A:39:GLU:HB3	1:A:77:LYS:HE2	0.42	1.90	10	1
1:A:25:LEU:HD11	1:A:45:ILE:HD11	0.42	1.91	18	1
1:A:5:PRO:O	1:A:9:VAL:HG13	0.42	2.14	8	2
1:A:50:PHE:CE1	1:A:63:ALA:HB2	0.42	2.49	9	1
1:A:41:ILE:HG12	1:A:44:TRP:CH2	0.42	2.50	6	1
1:A:109:TYR:O	1:A:113:GLU:HB2	0.42	2.15	12	1
1:A:53:SER:HB2	1:A:59:ILE:HD13	0.41	1.92	2	1
1:A:107:ARG:O	1:A:110:GLN:HG3	0.41	2.15	9	2
1:A:39:GLU:HG3	1:A:77:LYS:HG2	0.41	1.93	16	1
1:A:102:ASP:HA	1:A:105:GLN:NE2	0.41	2.28	2	1
1:A:44:TRP:O	1:A:48:GLU:HG2	0.41	2.15	20	1
1:A:32:LEU:HG	1:A:37:SER:C	0.41	2.41	17	1
1:A:85:THR:O	1:A:89:ILE:HG13	0.41	2.16	5	2
1:A:49:ASP:HA	1:A:52:LYS:HE3	0.41	1.91	15	1
1:A:63:ALA:HA	1:A:101:PHE:CE2	0.41	2.51	18	1
1:A:43:PHE:CE2	1:A:79:VAL:HG21	0.41	2.51	4	1
1:A:47:CYS:O	1:A:51:LYS:HG3	0.41	2.16	7	1
1:A:84:HIS:O	1:A:88:VAL:HG23	0.41	2.15	7	1
1:A:31:PHE:HZ	1:A:119:ARG:HB2	0.40	1.76	14	1
1:A:51:LYS:HE3	1:A:105:GLN:OE1	0.40	2.16	18	1
1:A:45:ILE:HA	1:A:48:GLU:HG3	0.40	1.93	14	1
1:A:30:ARG:HD2	1:A:125:ILE:HG21	0.40	1.93	16	1
1:A:29:THR:OG1	1:A:33:LYS:HE3	0.40	2.16	18	1
1:A:42:GLU:OE2	1:A:45:ILE:HD12	0.40	2.17	16	1
1:A:56:PRO:HA	1:A:59:ILE:CG1	0.40	2.46	6	1
1:A:47:CYS:HA	1:A:50:PHE:HB3	0.40	1.94	19	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	128/151 (85%)	119±2 (93±1%)	8±2 (6±1%)	1±1 (0±1%)	31 76
All	All	2560/3020 (85%)	2384 (93%)	165 (6%)	11 (0%)	31 76

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	78	GLU	6
1	A	54	LYS	3
1	A	75	ALA	1
1	A	130	MET	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	117/139 (84%)	111±2 (95±2%)	6±2 (5±2%)	23 74
All	All	2340/2780 (84%)	2224 (95%)	116 (5%)	23 74

All 38 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	25	LEU	20
1	A	54	LYS	11
1	A	39	GLU	7
1	A	42	GLU	7
1	A	125	ILE	6
1	A	112	MET	5
1	A	41	ILE	4
1	A	19	LEU	4
1	A	45	ILE	4
1	A	110	GLN	3
1	A	21	HIS	3
1	A	6	GLU	3
1	A	99	HIS	3
1	A	105	GLN	2

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Mol	Chain	Res	Type	Models (Total)
1	A	22	ARG	2
1	A	97	THR	2
1	A	13	GLU	2
1	A	17	LYS	2
1	A	48	GLU	2
1	A	77	LYS	2
1	A	52	LYS	2
1	A	51	LYS	2
1	A	38	GLU	2
1	A	114	GLN	2
1	A	122	LYS	1
1	A	3	VAL	1
1	A	16	ASP	1
1	A	109	TYR	1
1	A	50	PHE	1
1	A	34	THR	1
1	A	57	GLN	1
1	A	86	LYS	1
1	A	124	ASP	1
1	A	78	GLU	1
1	A	7	GLU	1
1	A	35	GLU	1
1	A	80	ASN	1
1	A	30	ARG	1

6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

6.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.6 Ligand geometry ⓘ

There are no ligands in this entry.

6.7 Other polymers [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 90% for the well-defined parts and 88% 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	1659
Number of shifts mapped to atoms	1659
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	7

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	131	0.21 ± 0.15	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	127	0.90 ± 0.06	Should be checked
$^{13}\text{C}'$	132	-0.09 ± 0.09	None needed (< 0.5 ppm)
^{15}N	128	0.63 ± 0.23	Should be applied

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 90%, i.e. 1617 atoms were assigned a chemical shift out of a possible 1799. 0 out of 16 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	633/635 (100%)	255/255 (100%)	254/256 (99%)	124/124 (100%)
Sidechain	840/972 (86%)	571/626 (91%)	265/312 (85%)	4/34 (12%)

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	Total	¹H	¹³C	¹⁵N
Aromatic	144/192 (75%)	76/94 (81%)	66/88 (75%)	2/10 (20%)
Overall	1617/1799 (90%)	902/975 (93%)	585/656 (89%)	130/168 (77%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 88%, i.e. 1659 atoms were assigned a chemical shift out of a possible 1875. 0 out of 16 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Backbone	655/664 (99%)	264/267 (99%)	263/268 (98%)	128/129 (99%)
Sidechain	860/1019 (84%)	584/656 (89%)	272/326 (83%)	4/37 (11%)
Aromatic	144/192 (75%)	76/94 (81%)	66/88 (75%)	2/10 (20%)
Overall	1659/1875 (88%)	924/1017 (91%)	601/682 (88%)	134/176 (76%)

7.1.4 Statistically unusual chemical shifts ⓘ

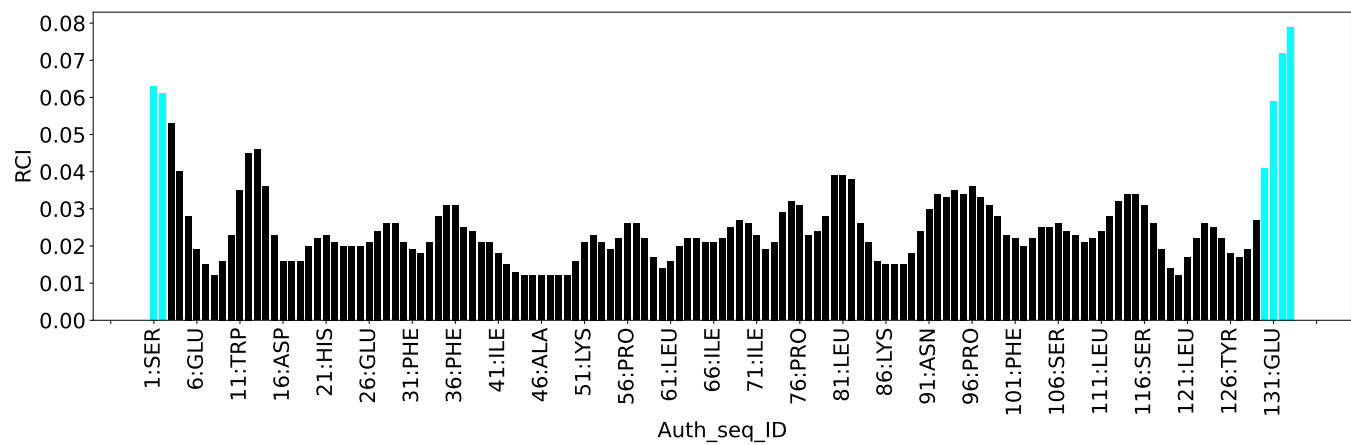
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	54	LYS	HG3	4.18	0.04 – 2.67	10.7
1	A	19	LEU	HD21	-0.98	-0.65 – 2.13	-6.2
1	A	19	LEU	HD22	-0.98	-0.65 – 2.13	-6.2
1	A	19	LEU	HD23	-0.98	-0.65 – 2.13	-6.2
1	A	25	LEU	CG	32.91	21.37 – 32.19	5.7
1	A	8	ALA	HA	1.91	2.13 – 6.34	-5.5
1	A	24	GLY	HA3	2.01	2.08 – 5.71	-5.2

7.1.5 Random Coil Index (RCI) plots ⓘ

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

Random coil index (RCI) for chain A:



8 NMR restraints analysis

8.1 Conformationally restricting restraints

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

Description	Value
Total distance restraints	2755
Intra-residue ($ i-j =0$)	62
Sequential ($ i-j =1$)	835
Medium range ($ i-j >1$ and $ i-j <5$)	867
Long range ($ i-j \geq 5$)	867
Inter-chain	0
Hydrogen bond restraints	124
Disulfide bond restraints	0
Total dihedral-angle restraints	0
Number of unmapped restraints	0
Number of restraints per residue	18.2
Number of long range restraints per residue ¹	5.7

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)	12.3	0.2
0.2-0.5 (Medium)	10.5	0.5
>0.5 (Large)	2.2	1.3

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

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

9 Distance violation analysis ⓘ

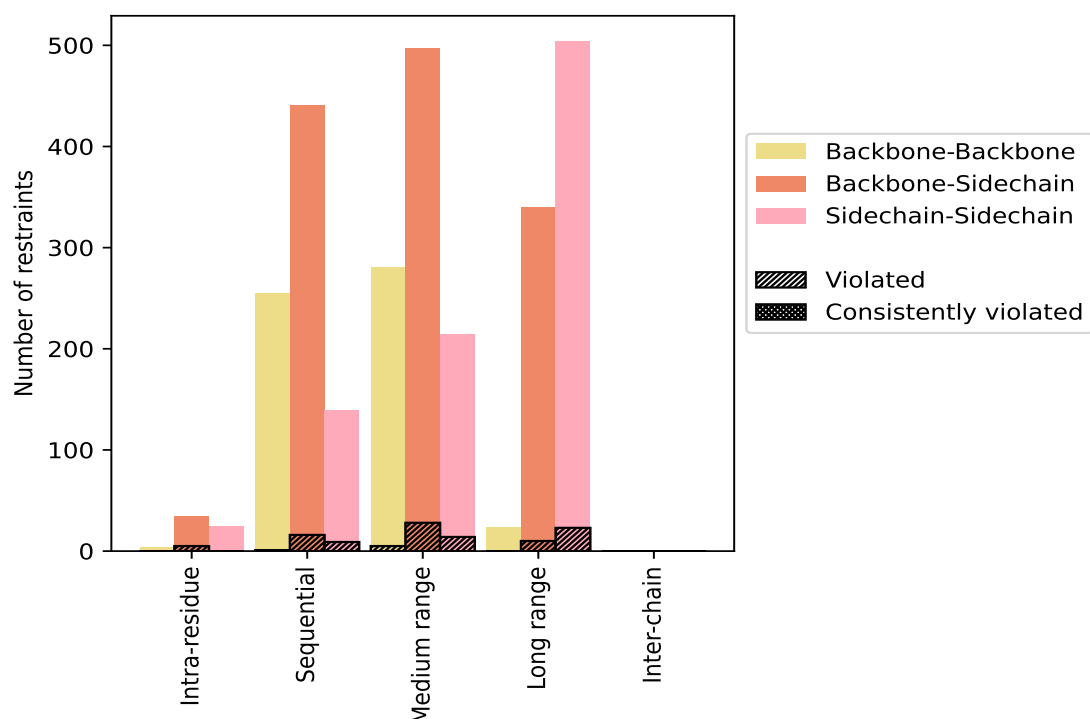
9.1 Summary of distance violations ⓘ

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

Restrains type	Count	% ¹	Violated ³			Consistently Violated ⁴		
			Count	% ²	% ¹	Count	% ²	% ¹
Intra-residue ($i-j =0$)	62	2.3	5	8.1	0.2	0	0.0	0.0
Backbone-Backbone	4	0.1	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	34	1.2	5	14.7	0.2	0	0.0	0.0
Sidechain-Sidechain	24	0.9	0	0.0	0.0	0	0.0	0.0
Sequential ($i-j =1$)	835	30.3	26	3.1	0.9	0	0.0	0.0
Backbone-Backbone	255	9.3	1	0.4	0.0	0	0.0	0.0
Backbone-Sidechain	441	16.0	16	3.6	0.6	0	0.0	0.0
Sidechain-Sidechain	139	5.0	9	6.5	0.3	0	0.0	0.0
Medium range ($i-j >1$ & $i-j <5$)	867	31.5	40	4.6	1.5	0	0.0	0.0
Backbone-Backbone	280	10.2	5	1.8	0.2	0	0.0	0.0
Backbone-Sidechain	373	13.5	21	5.6	0.8	0	0.0	0.0
Sidechain-Sidechain	214	7.8	14	6.5	0.5	0	0.0	0.0
Long range ($i-j \geq 5$)	867	31.5	33	3.8	1.2	0	0.0	0.0
Backbone-Backbone	23	0.8	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	340	12.3	10	2.9	0.4	0	0.0	0.0
Sidechain-Sidechain	504	18.3	23	4.6	0.8	0	0.0	0.0
Inter-chain	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Hydrogen bond	124	4.5	7	5.6	0.3	0	0.0	0.0
Disulfide bond	0	0.0	0	0.0	0.0	0	0.0	0.0
Total	2755	100.0	111	4.0	4.0	0	0.0	0.0
Backbone-Backbone	562	20.4	6	1.1	0.2	0	0.0	0.0
Backbone-Sidechain	1312	47.6	59	4.5	2.1	0	0.0	0.0
Sidechain-Sidechain	881	32.0	46	5.2	1.7	0	0.0	0.0

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

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



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

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

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

Model ID	Number of violations						Mean (Å)	Max (Å)	SD ⁶ (Å)	Median (Å)
	IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total				
1	2	6	15	6	0	29	0.22	0.56	0.13	0.17
2	2	5	10	6	0	23	0.31	0.76	0.17	0.22
3	2	1	16	6	0	25	0.25	0.54	0.13	0.21
4	2	3	8	7	0	20	0.24	0.76	0.17	0.16
5	1	5	9	6	0	21	0.29	0.49	0.12	0.29
6	3	3	9	10	0	25	0.24	0.56	0.14	0.18
7	3	7	12	10	0	32	0.27	0.8	0.19	0.2
8	3	3	11	4	0	21	0.25	0.84	0.17	0.21
9	3	4	13	8	0	28	0.29	0.67	0.15	0.27
10	2	7	12	7	0	28	0.23	0.55	0.14	0.18

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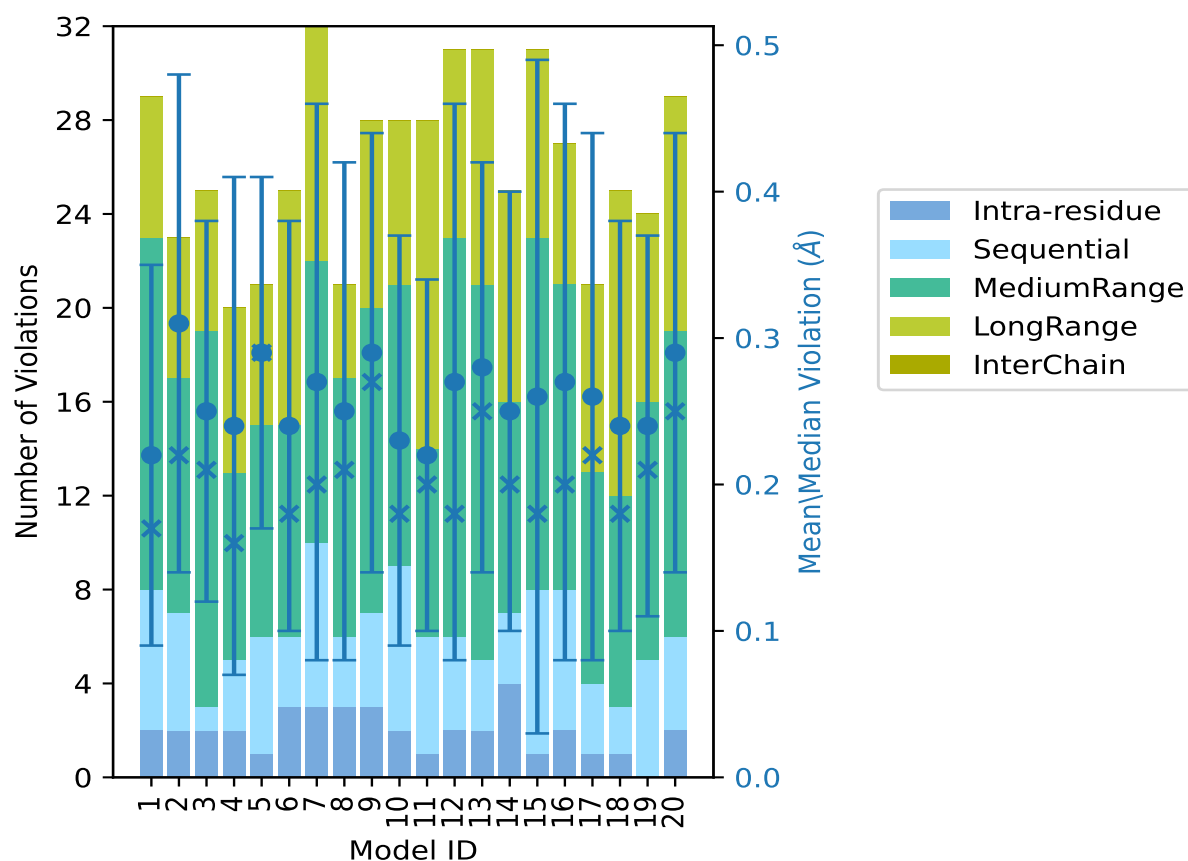
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Model ID	Number of violations						Mean (Å)	Max (Å)	SD ⁶ (Å)	Median (Å)
	IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total				
11	1	5	8	14	0	28	0.22	0.56	0.12	0.2
12	2	4	17	8	0	31	0.27	0.95	0.19	0.18
13	2	3	16	10	0	31	0.28	0.65	0.14	0.25
14	4	3	9	9	0	25	0.25	0.71	0.15	0.2
15	1	7	15	8	0	31	0.26	1.3	0.23	0.18
16	2	6	13	6	0	27	0.27	0.95	0.19	0.2
17	1	3	9	8	0	21	0.26	0.93	0.18	0.22
18	1	2	9	13	0	25	0.24	0.6	0.14	0.18
19	0	5	11	8	0	24	0.24	0.63	0.13	0.21
20	2	4	13	10	0	29	0.29	0.56	0.15	0.25

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

⁵Inter-chain restraints, ⁶Standard deviation

9.2.1 Bar graph : Distance Violation statistics for each model ⓘ



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

9.3 Distance violation statistics for the ensemble

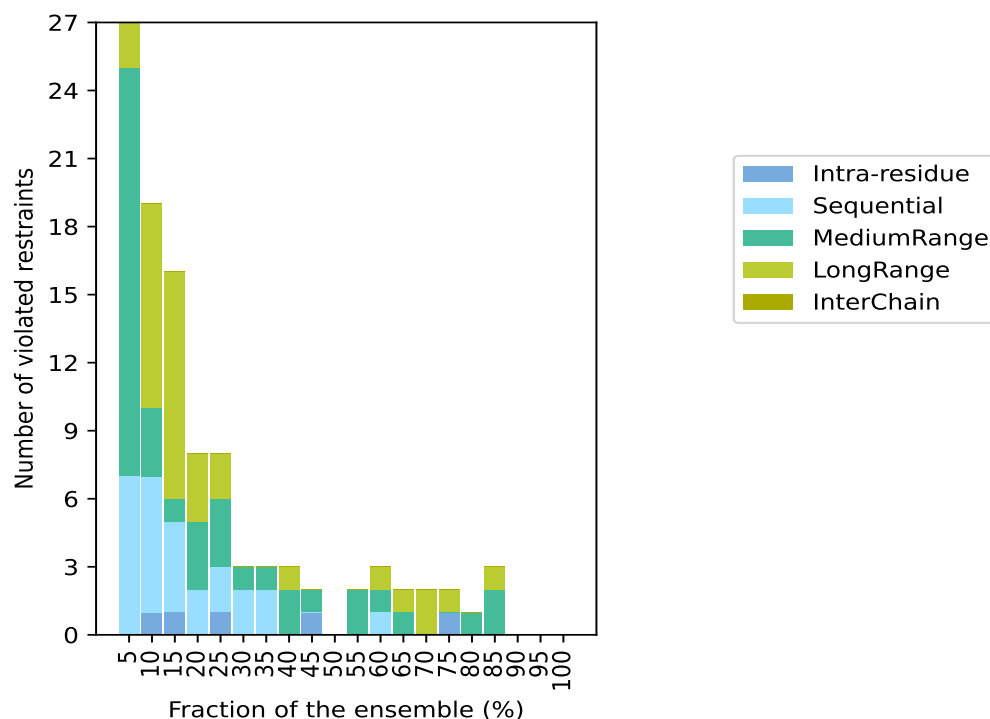
Violation analysis may find that some restraints are violated in few models and some are violated in most of models. The following table provides this information as number of violated restraints for a given fraction of the ensemble. In total, 2527(IR:57, SQ:809, MR:827, LR:834, IC:0) restraints are not violated in the ensemble.

Number of violated restraints						Fraction of the ensemble	
IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total	Count ⁶	%
0	7	18	2	0	27	1	5.0
1	6	3	9	0	19	2	10.0
1	4	1	10	0	16	3	15.0
0	2	3	3	0	8	4	20.0
1	2	3	2	0	8	5	25.0
0	2	1	0	0	3	6	30.0
0	2	1	0	0	3	7	35.0
0	0	2	1	0	3	8	40.0
1	0	1	0	0	2	9	45.0
0	0	0	0	0	0	10	50.0
0	0	2	0	0	2	11	55.0
0	1	1	1	0	3	12	60.0
0	0	1	1	0	2	13	65.0
0	0	0	2	0	2	14	70.0
1	0	0	1	0	2	15	75.0
0	0	1	0	0	1	16	80.0
0	0	2	1	0	3	17	85.0
0	0	0	0	0	0	18	90.0
0	0	0	0	0	0	19	95.0
0	0	0	0	0	0	20	100.0

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

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

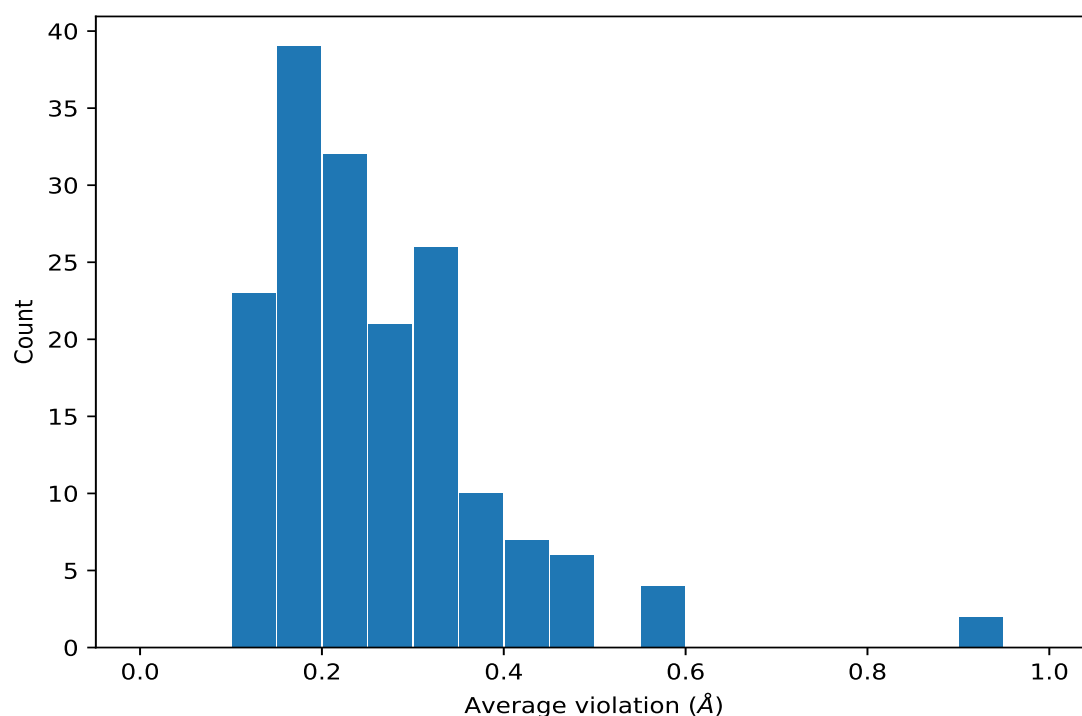
9.3.1 Bar graph : Distance violation statistics for the ensemble [i](#)



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

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

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



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

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

Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(2,36)	1:40:A:ASN:O	1:44:A:TRP:H	19	0.14	0.02	0.14
(1,824)	1:122:A:LYS:HE2	1:127:A:LEU:HB2	17	0.59	0.14	0.55
(1,824)	1:122:A:LYS:HE3	1:127:A:LEU:HB2	17	0.59	0.14	0.55
(1,1752)	1:27:A:ALA:H	1:24:A:GLY:HA3	17	0.12	0.01	0.12
(1,2451)	1:70:A:PHE:H	1:72:A:GLN:H	17	0.12	0.01	0.11
(1,965)	1:10:A:LYS:HE2	1:7:A:GLU:HA	16	0.3	0.14	0.2
(1,965)	1:10:A:LYS:HE3	1:7:A:GLU:HA	16	0.3	0.14	0.2
(1,2262)	1:11:A:TRP:H	1:17:A:LYS:HD3	15	0.26	0.11	0.25
(1,2262)	1:11:A:TRP:H	1:17:A:LYS:HD2	15	0.26	0.11	0.25
(1,469)	1:16:A:ASP:HA	1:16:A:ASP:HB3	15	0.21	0.03	0.22
(1,469)	1:28:A:PHE:HA	1:28:A:PHE:HB3	15	0.21	0.03	0.22
(1,1381)	1:41:A:ILE:HD11	1:28:A:PHE:HD1	14	0.28	0.09	0.29
(1,1381)	1:41:A:ILE:HD11	1:28:A:PHE:HD2	14	0.28	0.09	0.29
(1,1381)	1:41:A:ILE:HD12	1:28:A:PHE:HD1	14	0.28	0.09	0.29
(1,1381)	1:41:A:ILE:HD12	1:28:A:PHE:HD2	14	0.28	0.09	0.29
(1,1381)	1:41:A:ILE:HD13	1:28:A:PHE:HD1	14	0.28	0.09	0.29

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,1381)	1:41:A:ILE:HD13	1:28:A:PHE:HD2	14	0.28	0.09	0.29
(1,1429)	1:19:A:LEU:HD21	1:44:A:TRP:HZ2	14	0.23	0.08	0.29
(1,1429)	1:19:A:LEU:HD22	1:44:A:TRP:HZ2	14	0.23	0.08	0.29
(1,1429)	1:19:A:LEU:HD23	1:44:A:TRP:HZ2	14	0.23	0.08	0.29
(1,2533)	1:15:A:PHE:H	1:17:A:LYS:HG2	13	0.4	0.09	0.41
(1,455)	1:93:A:ILE:HG13	1:64:A:LYS:HE3	13	0.24	0.1	0.22
(1,455)	1:93:A:ILE:HG13	1:64:A:LYS:HE2	13	0.24	0.1	0.22
(1,1533)	1:6:A:GLU:HG2	1:7:A:GLU:H	12	0.31	0.1	0.34
(1,1533)	1:7:A:GLU:HG3	1:7:A:GLU:H	12	0.31	0.1	0.34
(1,1533)	1:7:A:GLU:HG2	1:7:A:GLU:H	12	0.31	0.1	0.34
(1,1533)	1:6:A:GLU:HG3	1:7:A:GLU:H	12	0.31	0.1	0.34
(1,49)	1:15:A:PHE:HD1	1:18:A:LEU:HD21	12	0.31	0.11	0.34
(1,49)	1:15:A:PHE:HD1	1:18:A:LEU:HD22	12	0.31	0.11	0.34
(1,49)	1:15:A:PHE:HD1	1:18:A:LEU:HD23	12	0.31	0.11	0.34
(1,49)	1:15:A:PHE:HD2	1:18:A:LEU:HD21	12	0.31	0.11	0.34
(1,49)	1:15:A:PHE:HD2	1:18:A:LEU:HD22	12	0.31	0.11	0.34
(1,49)	1:15:A:PHE:HD2	1:18:A:LEU:HD23	12	0.31	0.11	0.34
(1,213)	1:69:A:LYS:H	1:79:A:VAL:HG23	12	0.21	0.11	0.14
(1,213)	1:69:A:LYS:H	1:79:A:VAL:HG21	12	0.21	0.11	0.14
(1,213)	1:69:A:LYS:H	1:79:A:VAL:HG22	12	0.21	0.11	0.14
(1,213)	1:80:A:ASN:HD22	1:79:A:VAL:HG21	12	0.21	0.11	0.14
(1,1111)	1:72:A:GLN:HG3	1:70:A:PHE:HA	11	0.37	0.09	0.34
(1,1198)	1:129:A:LEU:HD11	1:126:A:TYR:HD1	11	0.22	0.06	0.2
(1,1198)	1:129:A:LEU:HD11	1:126:A:TYR:HD2	11	0.22	0.06	0.2
(1,1198)	1:129:A:LEU:HD12	1:126:A:TYR:HD1	11	0.22	0.06	0.2
(1,1198)	1:129:A:LEU:HD12	1:126:A:TYR:HD2	11	0.22	0.06	0.2
(1,1198)	1:129:A:LEU:HD13	1:126:A:TYR:HD1	11	0.22	0.06	0.2
(1,1198)	1:129:A:LEU:HD13	1:126:A:TYR:HD2	11	0.22	0.06	0.2
(2,112)	1:118:A:THR:O	1:122:A:LYS:H	10	0.13	0.03	0.13
(1,696)	1:62:A:LYS:HB2	1:62:A:LYS:HA	9	0.19	0.02	0.19
(1,696)	1:112:A:MET:HB2	1:112:A:MET:HA	9	0.19	0.02	0.19
(1,2346)	1:6:A:GLU:H	1:4:A:SER:HA	9	0.13	0.03	0.13
(2,114)	1:119:A:ARG:O	1:123:A:SER:H	9	0.12	0.01	0.11
(1,844)	1:17:A:LYS:HG2	1:13:A:GLU:HG2	8	0.46	0.13	0.52
(1,1148)	1:52:A:LYS:HE2	1:50:A:PHE:HA	8	0.44	0.28	0.38
(1,1148)	1:52:A:LYS:HE3	1:50:A:PHE:HA	8	0.44	0.28	0.38
(1,1408)	1:129:A:LEU:HD11	1:11:A:TRP:HZ3	8	0.15	0.04	0.14
(1,1408)	1:129:A:LEU:HD12	1:11:A:TRP:HZ3	8	0.15	0.04	0.14
(1,1408)	1:129:A:LEU:HD13	1:11:A:TRP:HZ3	8	0.15	0.04	0.14
(1,762)	1:53:A:SER:HB3	1:54:A:LYS:HG2	7	0.47	0.18	0.49
(1,762)	1:53:A:SER:HB2	1:54:A:LYS:HG2	7	0.47	0.18	0.49
(1,1134)	1:42:A:GLU:HA	1:45:A:ILE:HB	7	0.18	0.0	0.18

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,2110)	1:73:A:THR:H	1:72:A:GLN:HG2	7	0.18	0.02	0.17
(2,106)	1:113:A:GLU:O	1:117:A:TYR:H	7	0.12	0.02	0.11
(1,311)	1:72:A:GLN:HB2	1:75:A:ALA:HB1	6	0.29	0.03	0.29
(1,311)	1:72:A:GLN:HB2	1:75:A:ALA:HB2	6	0.29	0.03	0.29
(1,311)	1:72:A:GLN:HB2	1:75:A:ALA:HB3	6	0.29	0.03	0.29
(1,502)	1:25:A:LEU:HB3	1:26:A:GLU:HG2	6	0.23	0.17	0.16
(1,503)	1:25:A:LEU:HB3	1:26:A:GLU:HG2	6	0.23	0.17	0.16
(1,517)	1:62:A:LYS:HG3	1:58:A:GLN:HG3	5	0.4	0.1	0.42
(1,517)	1:62:A:LYS:HG2	1:58:A:GLN:HG3	5	0.4	0.1	0.42
(1,565)	1:69:A:LYS:HD2	1:76:A:PRO:HB3	5	0.37	0.13	0.38
(1,565)	1:69:A:LYS:HD3	1:76:A:PRO:HB3	5	0.37	0.13	0.38
(1,834)	1:51:A:LYS:HE2	1:98:A:LEU:HB3	5	0.37	0.07	0.39
(1,2491)	1:132:A:GLY:H	1:130:A:MET:HB2	5	0.37	0.11	0.4
(1,2491)	1:132:A:GLY:H	1:130:A:MET:HB3	5	0.37	0.11	0.4
(1,1579)	1:14:A:SER:HB2	1:15:A:PHE:H	5	0.35	0.1	0.37
(1,1579)	1:14:A:SER:HB3	1:15:A:PHE:H	5	0.35	0.1	0.37
(1,1728)	1:15:A:PHE:H	1:14:A:SER:HB2	5	0.35	0.1	0.37
(1,1728)	1:15:A:PHE:H	1:14:A:SER:HB3	5	0.35	0.1	0.37
(1,683)	1:105:A:GLN:HB2	1:105:A:GLN:HA	5	0.22	0.0	0.22
(1,2513)	1:13:A:GLU:H	1:14:A:SER:HB3	5	0.18	0.06	0.17
(1,2513)	1:13:A:GLU:H	1:10:A:LYS:HA	5	0.18	0.06	0.17
(1,2513)	1:13:A:GLU:H	1:14:A:SER:HB2	5	0.18	0.06	0.17
(1,1439)	1:10:A:LYS:HB2	1:21:A:HIS:HD2	4	0.48	0.12	0.44
(1,1439)	1:10:A:LYS:HB3	1:21:A:HIS:HD2	4	0.48	0.12	0.44
(1,463)	1:52:A:LYS:HE2	1:49:A:ASP:HB2	4	0.31	0.17	0.22
(1,463)	1:52:A:LYS:HE3	1:49:A:ASP:HB2	4	0.31	0.17	0.22
(1,2379)	1:16:A:ASP:H	1:14:A:SER:HB3	4	0.31	0.03	0.31
(1,870)	1:111:A:LEU:HD11	1:80:A:ASN:HB2	4	0.28	0.11	0.26
(1,870)	1:111:A:LEU:HD12	1:80:A:ASN:HB2	4	0.28	0.11	0.26
(1,870)	1:111:A:LEU:HD13	1:80:A:ASN:HB2	4	0.28	0.11	0.26
(1,870)	1:111:A:LEU:HD21	1:80:A:ASN:HB2	4	0.28	0.11	0.26
(1,870)	1:111:A:LEU:HD22	1:80:A:ASN:HB2	4	0.28	0.11	0.26
(1,870)	1:111:A:LEU:HD23	1:80:A:ASN:HB2	4	0.28	0.11	0.26
(1,558)	1:131:A:GLU:HG2	1:130:A:MET:HB2	4	0.24	0.13	0.22
(1,1541)	1:62:A:LYS:HB3	1:50:A:PHE:HD1	4	0.18	0.02	0.2
(1,1541)	1:62:A:LYS:HB3	1:50:A:PHE:HD2	4	0.18	0.02	0.2
(1,934)	1:111:A:LEU:HD11	1:108:A:VAL:HA	4	0.18	0.04	0.19
(1,934)	1:111:A:LEU:HD12	1:108:A:VAL:HA	4	0.18	0.04	0.19
(1,934)	1:111:A:LEU:HD13	1:108:A:VAL:HA	4	0.18	0.04	0.19
(1,934)	1:111:A:LEU:HD21	1:108:A:VAL:HA	4	0.18	0.04	0.19
(1,934)	1:111:A:LEU:HD22	1:108:A:VAL:HA	4	0.18	0.04	0.19
(1,934)	1:111:A:LEU:HD23	1:108:A:VAL:HA	4	0.18	0.04	0.19

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,1995)	1:65:A:ALA:H	1:64:A:LYS:HB3	4	0.14	0.02	0.14
(1,1995)	1:65:A:ALA:H	1:64:A:LYS:HB2	4	0.14	0.02	0.14
(1,1822)	1:50:A:PHE:H	1:62:A:LYS:HE2	3	0.44	0.18	0.56
(1,2417)	1:37:A:SER:H	1:38:A:GLU:HG3	3	0.4	0.18	0.33
(1,1674)	1:44:A:TRP:HE1	1:105:A:GLN:HG2	3	0.38	0.17	0.43
(1,1674)	1:44:A:TRP:HE1	1:112:A:MET:HB3	3	0.38	0.17	0.43
(1,580)	1:105:A:GLN:HB2	1:44:A:TRP:HB3	3	0.28	0.15	0.21
(1,1795)	1:54:A:LYS:H	1:53:A:SER:HB3	3	0.23	0.07	0.25
(1,1795)	1:54:A:LYS:H	1:53:A:SER:HB2	3	0.23	0.07	0.25
(1,1048)	1:129:A:LEU:HB3	1:126:A:TYR:HB3	3	0.19	0.07	0.21
(1,617)	1:50:A:PHE:HE1	1:59:A:ILE:HA	3	0.18	0.02	0.2
(1,617)	1:50:A:PHE:HE2	1:59:A:ILE:HA	3	0.18	0.02	0.2
(1,1087)	1:33:A:LYS:HG2	1:38:A:GLU:HB3	3	0.17	0.05	0.18
(1,568)	1:56:A:PRO:HA	1:56:A:PRO:HB2	3	0.17	0.01	0.16
(1,421)	1:43:A:PHE:HZ	1:71:A:ILE:HD11	3	0.16	0.04	0.14
(1,421)	1:43:A:PHE:HZ	1:71:A:ILE:HD12	3	0.16	0.04	0.14
(1,421)	1:43:A:PHE:HZ	1:71:A:ILE:HD13	3	0.16	0.04	0.14
(1,1374)	1:71:A:ILE:HD11	1:43:A:PHE:HZ	3	0.16	0.04	0.14
(1,1374)	1:71:A:ILE:HD12	1:43:A:PHE:HZ	3	0.16	0.04	0.14
(1,1374)	1:71:A:ILE:HD13	1:43:A:PHE:HZ	3	0.16	0.04	0.14
(1,1450)	1:48:A:GLU:HB3	1:99:A:HIS:HE1	3	0.14	0.01	0.14
(1,1539)	1:35:A:GLU:HG3	1:36:A:PHE:H	3	0.14	0.02	0.13
(1,2555)	1:36:A:PHE:H	1:35:A:GLU:HG3	3	0.14	0.02	0.13
(1,1672)	1:44:A:TRP:HE1	1:109:A:TYR:HB3	3	0.12	0.02	0.11
(1,705)	1:81:A:LEU:HB2	1:107:A:ARG:HA	3	0.11	0.01	0.11
(1,628)	1:62:A:LYS:HE2	1:53:A:SER:HB2	2	0.93	0.37	0.93
(1,628)	1:62:A:LYS:HE3	1:53:A:SER:HB3	2	0.93	0.37	0.93
(1,2329)	1:116:A:SER:H	1:119:A:ARG:HD2	2	0.55	0.01	0.55
(1,2329)	1:116:A:SER:H	1:119:A:ARG:HD3	2	0.55	0.01	0.55
(1,519)	1:62:A:LYS:HD2	1:58:A:GLN:HG3	2	0.46	0.04	0.46
(1,2060)	1:57:A:GLN:H	1:57:A:GLN:HG2	2	0.37	0.09	0.37
(1,2060)	1:57:A:GLN:H	1:57:A:GLN:HG3	2	0.37	0.09	0.37
(1,636)	1:32:A:LEU:HA	1:37:A:SER:HB2	2	0.34	0.01	0.34
(1,1734)	1:81:A:LEU:H	1:86:A:LYS:HE2	2	0.33	0.07	0.33
(1,1734)	1:81:A:LEU:H	1:86:A:LYS:HE3	2	0.33	0.07	0.33
(1,23)	1:38:A:GLU:HA	1:32:A:LEU:HD11	2	0.31	0.17	0.31
(1,23)	1:38:A:GLU:HA	1:32:A:LEU:HD12	2	0.31	0.17	0.31
(1,23)	1:38:A:GLU:HA	1:32:A:LEU:HD13	2	0.31	0.17	0.31
(1,23)	1:38:A:GLU:HA	1:32:A:LEU:HD21	2	0.31	0.17	0.31
(1,23)	1:38:A:GLU:HA	1:32:A:LEU:HD22	2	0.31	0.17	0.31
(1,23)	1:38:A:GLU:HA	1:32:A:LEU:HD23	2	0.31	0.17	0.31
(1,2419)	1:37:A:SER:H	1:35:A:GLU:HG3	2	0.26	0.04	0.26

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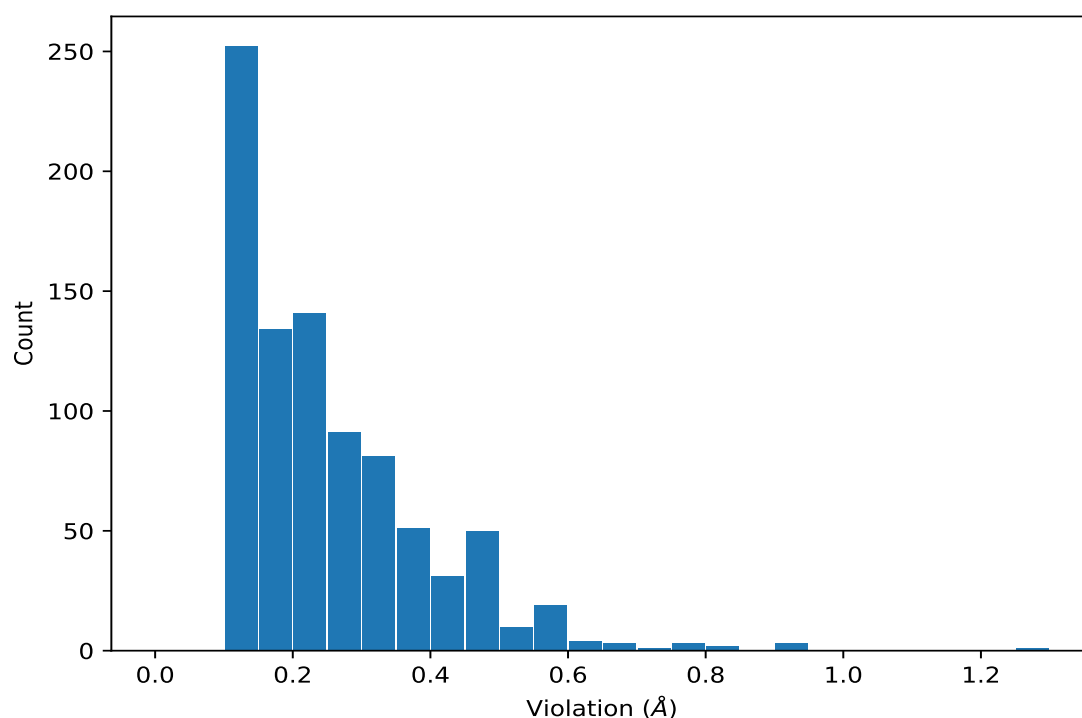
Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,26)	1:41:A:ILE:HB	1:32:A:LEU:HD11	2	0.22	0.06	0.22
(1,26)	1:41:A:ILE:HB	1:32:A:LEU:HD12	2	0.22	0.06	0.22
(1,26)	1:41:A:ILE:HB	1:32:A:LEU:HD13	2	0.22	0.06	0.22
(1,26)	1:41:A:ILE:HB	1:32:A:LEU:HD21	2	0.22	0.06	0.22
(1,26)	1:41:A:ILE:HB	1:32:A:LEU:HD22	2	0.22	0.06	0.22
(1,26)	1:41:A:ILE:HB	1:32:A:LEU:HD23	2	0.22	0.06	0.22
(1,336)	1:50:A:PHE:HZ	1:59:A:ILE:HG21	2	0.2	0.02	0.2
(1,336)	1:50:A:PHE:HZ	1:59:A:ILE:HG22	2	0.2	0.02	0.2
(1,336)	1:50:A:PHE:HZ	1:59:A:ILE:HG23	2	0.2	0.02	0.2
(1,365)	1:101:A:PHE:HD1	1:89:A:ILE:HD11	2	0.18	0.04	0.18
(1,365)	1:101:A:PHE:HD1	1:89:A:ILE:HD12	2	0.18	0.04	0.18
(1,365)	1:101:A:PHE:HD1	1:89:A:ILE:HD13	2	0.18	0.04	0.18
(1,365)	1:101:A:PHE:HD2	1:89:A:ILE:HD11	2	0.18	0.04	0.18
(1,365)	1:101:A:PHE:HD2	1:89:A:ILE:HD12	2	0.18	0.04	0.18
(1,365)	1:101:A:PHE:HD2	1:89:A:ILE:HD13	2	0.18	0.04	0.18
(1,1482)	1:97:A:THR:HG21	1:98:A:LEU:H	2	0.18	0.02	0.18
(1,1482)	1:97:A:THR:HG22	1:98:A:LEU:H	2	0.18	0.02	0.18
(1,1482)	1:97:A:THR:HG23	1:98:A:LEU:H	2	0.18	0.02	0.18
(1,101)	1:76:A:PRO:HD3	1:69:A:LYS:HG3	2	0.17	0.04	0.17
(1,593)	1:55:A:GLY:HA2	1:54:A:LYS:HD3	2	0.16	0.04	0.16
(1,593)	1:55:A:GLY:HA2	1:54:A:LYS:HD2	2	0.16	0.04	0.16
(1,446)	1:112:A:MET:HB3	1:111:A:LEU:HB2	2	0.16	0.05	0.16
(1,943)	1:58:A:GLN:HB3	1:53:A:SER:HB3	2	0.14	0.03	0.14
(1,2204)	1:125:A:ILE:H	1:124:A:ASP:HB3	2	0.13	0.02	0.13
(1,527)	1:111:A:LEU:HG	1:110:A:GLN:HG3	2	0.12	0.02	0.12
(1,1635)	1:78:A:GLU:HG2	1:79:A:VAL:H	2	0.12	0.0	0.12
(1,1635)	1:78:A:GLU:HG3	1:79:A:VAL:H	2	0.12	0.0	0.12
(2,35)	1:40:A:ASN:O	1:44:A:TRP:N	2	0.11	0.01	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)
(1,628)	1:62:A:LYS:HE3	1:53:A:SER:HB3	15	1.3
(1,1148)	1:52:A:LYS:HE3	1:50:A:PHE:HA	12	0.95
(1,868)	1:77:A:LYS:HG3	1:76:A:PRO:HG2	16	0.95
(1,646)	1:17:A:LYS:HE3	1:14:A:SER:HB2	17	0.93
(1,824)	1:122:A:LYS:HE3	1:127:A:LEU:HB2	8	0.84
(1,824)	1:122:A:LYS:HE2	1:127:A:LEU:HB2	7	0.8
(1,824)	1:122:A:LYS:HE3	1:127:A:LEU:HB2	16	0.78
(1,1148)	1:52:A:LYS:HE2	1:50:A:PHE:HA	2	0.76
(1,824)	1:122:A:LYS:HE2	1:127:A:LEU:HB2	4	0.76
(1,824)	1:122:A:LYS:HE2	1:127:A:LEU:HB2	14	0.71
(1,1439)	1:10:A:LYS:HB2	1:21:A:HIS:HD2	7	0.69
(1,762)	1:53:A:SER:HB2	1:54:A:LYS:HG2	9	0.67
(1,2417)	1:37:A:SER:H	1:38:A:GLU:HG3	13	0.65
(1,824)	1:122:A:LYS:HE2	1:127:A:LEU:HB2	9	0.64
(1,824)	1:122:A:LYS:HE2	1:127:A:LEU:HB2	2	0.63
(1,762)	1:53:A:SER:HB3	1:54:A:LYS:HG2	7	0.63

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,762)	1:53:A:SER:HB2	1:54:A:LYS:HG2	19	0.63
(1,844)	1:17:A:LYS:HG2	1:13:A:GLU:HG2	15	0.6
(1,824)	1:122:A:LYS:HE2	1:127:A:LEU:HB2	18	0.6
(1,463)	1:52:A:LYS:HE3	1:49:A:ASP:HB2	7	0.6
(1,503)	1:25:A:LEU:HB3	1:26:A:GLU:HG2	12	0.59
(1,502)	1:25:A:LEU:HB3	1:26:A:GLU:HG2	12	0.59
(1,1822)	1:50:A:PHE:H	1:62:A:LYS:HE2	7	0.57
(1,1822)	1:50:A:PHE:H	1:62:A:LYS:HE2	4	0.56
(1,1674)	1:44:A:TRP:HE1	1:105:A:GLN:HG2	2	0.56
(1,1148)	1:52:A:LYS:HE2	1:50:A:PHE:HA	20	0.56
(1,1111)	1:72:A:GLN:HG3	1:70:A:PHE:HA	11	0.56
(1,965)	1:10:A:LYS:HE2	1:7:A:GLU:HA	1	0.56
(1,844)	1:17:A:LYS:HG2	1:13:A:GLU:HG2	2	0.56
(1,628)	1:62:A:LYS:HE2	1:53:A:SER:HB2	20	0.56
(1,565)	1:69:A:LYS:HD2	1:76:A:PRO:HB3	6	0.56
(1,2329)	1:116:A:SER:H	1:119:A:ARG:HD2	10	0.55
(1,844)	1:17:A:LYS:HG2	1:13:A:GLU:HG2	18	0.55
(1,824)	1:122:A:LYS:HE2	1:127:A:LEU:HB2	15	0.55
(1,824)	1:122:A:LYS:HE2	1:127:A:LEU:HB2	20	0.55
(1,517)	1:62:A:LYS:HG3	1:58:A:GLN:HG3	10	0.55
(1,2533)	1:15:A:PHE:H	1:17:A:LYS:HG2	14	0.54
(1,2329)	1:116:A:SER:H	1:119:A:ARG:HD3	3	0.54
(1,2491)	1:132:A:GLY:H	1:130:A:MET:HB2	6	0.53
(1,824)	1:122:A:LYS:HE2	1:127:A:LEU:HB2	10	0.53
(1,2533)	1:15:A:PHE:H	1:17:A:LYS:HG2	3	0.52
(1,844)	1:17:A:LYS:HG2	1:13:A:GLU:HG2	20	0.52
(1,2533)	1:15:A:PHE:H	1:17:A:LYS:HG2	1	0.51
(1,844)	1:17:A:LYS:HG2	1:13:A:GLU:HG2	8	0.51
(1,824)	1:122:A:LYS:HE2	1:127:A:LEU:HB2	6	0.51
(1,519)	1:62:A:LYS:HD2	1:58:A:GLN:HG3	13	0.5
(1,965)	1:10:A:LYS:HE2	1:7:A:GLU:HA	8	0.49
(1,965)	1:10:A:LYS:HE2	1:7:A:GLU:HA	9	0.49
(1,762)	1:53:A:SER:HB2	1:54:A:LYS:HG2	5	0.49
(1,2262)	1:11:A:TRP:H	1:17:A:LYS:HD2	14	0.48
(1,1533)	1:7:A:GLU:HG3	1:7:A:GLU:H	14	0.48
(1,965)	1:10:A:LYS:HE2	1:7:A:GLU:HA	4	0.48
(1,580)	1:105:A:GLN:HB2	1:44:A:TRP:HB3	19	0.48
(1,23)	1:38:A:GLU:HA	1:32:A:LEU:HD11	11	0.48
(1,23)	1:38:A:GLU:HA	1:32:A:LEU:HD12	11	0.48
(1,23)	1:38:A:GLU:HA	1:32:A:LEU:HD13	11	0.48
(1,23)	1:38:A:GLU:HA	1:32:A:LEU:HD21	11	0.48
(1,23)	1:38:A:GLU:HA	1:32:A:LEU:HD22	11	0.48

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,23)	1:38:A:GLU:HA	1:32:A:LEU:HD23	11	0.48
(1,2533)	1:15:A:PHE:H	1:17:A:LYS:HG2	5	0.47
(1,2533)	1:15:A:PHE:H	1:17:A:LYS:HG2	18	0.47
(1,965)	1:10:A:LYS:HE2	1:7:A:GLU:HA	20	0.47
(1,824)	1:122:A:LYS:HE2	1:127:A:LEU:HB2	12	0.47
(1,49)	1:15:A:PHE:HD1	1:18:A:LEU:HD21	13	0.47
(1,49)	1:15:A:PHE:HD1	1:18:A:LEU:HD22	13	0.47
(1,49)	1:15:A:PHE:HD1	1:18:A:LEU:HD23	13	0.47
(1,49)	1:15:A:PHE:HD2	1:18:A:LEU:HD21	13	0.47
(1,49)	1:15:A:PHE:HD2	1:18:A:LEU:HD22	13	0.47
(1,49)	1:15:A:PHE:HD2	1:18:A:LEU:HD23	13	0.47
(1,2060)	1:57:A:GLN:H	1:57:A:GLN:HG3	12	0.46
(1,1148)	1:52:A:LYS:HE2	1:50:A:PHE:HA	3	0.46
(1,834)	1:51:A:LYS:HE2	1:98:A:LEU:HB3	5	0.46
(1,565)	1:69:A:LYS:HD3	1:76:A:PRO:HB3	20	0.46
(1,49)	1:15:A:PHE:HD1	1:18:A:LEU:HD21	7	0.46
(1,49)	1:15:A:PHE:HD1	1:18:A:LEU:HD22	7	0.46
(1,49)	1:15:A:PHE:HD1	1:18:A:LEU:HD23	7	0.46
(1,49)	1:15:A:PHE:HD2	1:18:A:LEU:HD21	7	0.46
(1,49)	1:15:A:PHE:HD2	1:18:A:LEU:HD22	7	0.46
(1,49)	1:15:A:PHE:HD2	1:18:A:LEU:HD23	7	0.46
(1,1728)	1:15:A:PHE:H	1:14:A:SER:HB2	13	0.45
(1,1579)	1:14:A:SER:HB2	1:15:A:PHE:H	13	0.45
(1,1111)	1:72:A:GLN:HG3	1:70:A:PHE:HA	6	0.45
(1,1111)	1:72:A:GLN:HG3	1:70:A:PHE:HA	13	0.45
(1,870)	1:111:A:LEU:HD11	1:80:A:ASN:HB2	10	0.45
(1,870)	1:111:A:LEU:HD12	1:80:A:ASN:HB2	10	0.45
(1,870)	1:111:A:LEU:HD13	1:80:A:ASN:HB2	10	0.45
(1,870)	1:111:A:LEU:HD21	1:80:A:ASN:HB2	10	0.45
(1,870)	1:111:A:LEU:HD22	1:80:A:ASN:HB2	10	0.45
(1,870)	1:111:A:LEU:HD23	1:80:A:ASN:HB2	10	0.45
(1,762)	1:53:A:SER:HB3	1:54:A:LYS:HG2	1	0.45
(1,312)	1:126:A:TYR:HE1	1:130:A:MET:HE1	16	0.45
(1,312)	1:126:A:TYR:HE1	1:130:A:MET:HE2	16	0.45
(1,312)	1:126:A:TYR:HE1	1:130:A:MET:HE3	16	0.45
(1,312)	1:126:A:TYR:HE2	1:130:A:MET:HE1	16	0.45
(1,312)	1:126:A:TYR:HE2	1:130:A:MET:HE2	16	0.45
(1,312)	1:126:A:TYR:HE2	1:130:A:MET:HE3	16	0.45
(1,1439)	1:10:A:LYS:HB2	1:21:A:HIS:HD2	13	0.44
(1,897)	1:51:A:LYS:HE3	1:48:A:GLU:HA	9	0.44
(1,824)	1:122:A:LYS:HE2	1:127:A:LEU:HB2	1	0.44
(1,824)	1:122:A:LYS:HE2	1:127:A:LEU:HB2	5	0.44

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,517)	1:62:A:LYS:HG3	1:58:A:GLN:HG3	9	0.44
(1,1674)	1:44:A:TRP:HE1	1:112:A:MET:HB3	7	0.43
(1,1439)	1:10:A:LYS:HB2	1:21:A:HIS:HD2	1	0.43
(1,844)	1:17:A:LYS:HG2	1:13:A:GLU:HG2	3	0.43
(1,213)	1:69:A:LYS:H	1:79:A:VAL:HG21	18	0.43
(1,2533)	1:15:A:PHE:H	1:17:A:LYS:HG2	12	0.42
(1,2491)	1:132:A:GLY:H	1:130:A:MET:HB2	3	0.42
(1,1111)	1:72:A:GLN:HG3	1:70:A:PHE:HA	20	0.42
(1,519)	1:62:A:LYS:HD2	1:58:A:GLN:HG3	9	0.42
(1,517)	1:62:A:LYS:HG2	1:58:A:GLN:HG3	5	0.42
(1,455)	1:93:A:ILE:HG13	1:64:A:LYS:HE2	12	0.42
(1,2533)	1:15:A:PHE:H	1:17:A:LYS:HG2	2	0.41
(1,1381)	1:41:A:ILE:HD11	1:28:A:PHE:HD1	20	0.41
(1,1381)	1:41:A:ILE:HD11	1:28:A:PHE:HD2	20	0.41
(1,1381)	1:41:A:ILE:HD12	1:28:A:PHE:HD1	20	0.41
(1,1381)	1:41:A:ILE:HD12	1:28:A:PHE:HD2	20	0.41
(1,1381)	1:41:A:ILE:HD13	1:28:A:PHE:HD1	20	0.41
(1,1381)	1:41:A:ILE:HD13	1:28:A:PHE:HD2	20	0.41
(1,824)	1:122:A:LYS:HE2	1:127:A:LEU:HB2	17	0.41
(1,558)	1:131:A:GLU:HG2	1:130:A:MET:HB2	9	0.41
(1,2491)	1:132:A:GLY:H	1:130:A:MET:HB3	19	0.4
(1,1734)	1:81:A:LEU:H	1:86:A:LYS:HE2	17	0.4
(1,1728)	1:15:A:PHE:H	1:14:A:SER:HB3	15	0.4
(1,1579)	1:14:A:SER:HB3	1:15:A:PHE:H	15	0.4
(1,1533)	1:6:A:GLU:HG2	1:7:A:GLU:H	2	0.4
(1,1533)	1:7:A:GLU:HG2	1:7:A:GLU:H	13	0.4
(1,455)	1:93:A:ILE:HG13	1:64:A:LYS:HE2	20	0.4
(1,1381)	1:41:A:ILE:HD11	1:28:A:PHE:HD1	5	0.39
(1,1381)	1:41:A:ILE:HD11	1:28:A:PHE:HD2	5	0.39
(1,1381)	1:41:A:ILE:HD12	1:28:A:PHE:HD1	5	0.39
(1,1381)	1:41:A:ILE:HD12	1:28:A:PHE:HD2	5	0.39
(1,1381)	1:41:A:ILE:HD13	1:28:A:PHE:HD1	5	0.39
(1,1381)	1:41:A:ILE:HD13	1:28:A:PHE:HD2	5	0.39
(1,1381)	1:41:A:ILE:HD11	1:28:A:PHE:HD1	8	0.39
(1,1381)	1:41:A:ILE:HD11	1:28:A:PHE:HD2	8	0.39
(1,1381)	1:41:A:ILE:HD12	1:28:A:PHE:HD1	8	0.39
(1,1381)	1:41:A:ILE:HD12	1:28:A:PHE:HD2	8	0.39
(1,1381)	1:41:A:ILE:HD13	1:28:A:PHE:HD1	8	0.39
(1,1381)	1:41:A:ILE:HD13	1:28:A:PHE:HD2	8	0.39
(1,844)	1:17:A:LYS:HG2	1:13:A:GLU:HG2	12	0.39
(1,834)	1:51:A:LYS:HE2	1:98:A:LEU:HB3	10	0.39
(1,834)	1:51:A:LYS:HE2	1:98:A:LEU:HB3	16	0.39

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,824)	1:122:A:LYS:HE3	1:127:A:LEU:HB2	19	0.39
(1,49)	1:15:A:PHE:HD1	1:18:A:LEU:HD21	9	0.39
(1,49)	1:15:A:PHE:HD1	1:18:A:LEU:HD22	9	0.39
(1,49)	1:15:A:PHE:HD1	1:18:A:LEU:HD23	9	0.39
(1,49)	1:15:A:PHE:HD2	1:18:A:LEU:HD21	9	0.39
(1,49)	1:15:A:PHE:HD2	1:18:A:LEU:HD22	9	0.39
(1,49)	1:15:A:PHE:HD2	1:18:A:LEU:HD23	9	0.39
(1,2262)	1:11:A:TRP:H	1:17:A:LYS:HD2	9	0.38
(1,1439)	1:10:A:LYS:HB3	1:21:A:HIS:HD2	12	0.38
(1,565)	1:69:A:LYS:HD2	1:76:A:PRO:HB3	13	0.38
(1,2262)	1:11:A:TRP:H	1:17:A:LYS:HD2	11	0.37
(1,1728)	1:15:A:PHE:H	1:14:A:SER:HB3	5	0.37
(1,1728)	1:15:A:PHE:H	1:14:A:SER:HB2	20	0.37
(1,1579)	1:14:A:SER:HB3	1:15:A:PHE:H	5	0.37
(1,1579)	1:14:A:SER:HB2	1:15:A:PHE:H	20	0.37
(1,1533)	1:7:A:GLU:HG3	1:7:A:GLU:H	6	0.37
(1,1533)	1:6:A:GLU:HG3	1:7:A:GLU:H	15	0.37
(1,639)	1:35:A:GLU:HG3	1:37:A:SER:HB2	13	0.37
(1,513)	1:37:A:SER:HB2	1:35:A:GLU:HG3	13	0.37
(1,213)	1:69:A:LYS:H	1:79:A:VAL:HG23	2	0.37
(1,1533)	1:7:A:GLU:HG3	1:7:A:GLU:H	9	0.36
(1,1381)	1:41:A:ILE:HD11	1:28:A:PHE:HD1	9	0.36
(1,1381)	1:41:A:ILE:HD11	1:28:A:PHE:HD2	9	0.36
(1,1381)	1:41:A:ILE:HD12	1:28:A:PHE:HD1	9	0.36
(1,1381)	1:41:A:ILE:HD12	1:28:A:PHE:HD2	9	0.36
(1,1381)	1:41:A:ILE:HD13	1:28:A:PHE:HD1	9	0.36
(1,1381)	1:41:A:ILE:HD13	1:28:A:PHE:HD2	9	0.36
(1,965)	1:10:A:LYS:HE2	1:7:A:GLU:HA	2	0.36
(1,834)	1:51:A:LYS:HE2	1:98:A:LEU:HB3	11	0.36
(1,517)	1:62:A:LYS:HG3	1:58:A:GLN:HG3	13	0.36
(1,49)	1:15:A:PHE:HD1	1:18:A:LEU:HD21	12	0.36
(1,49)	1:15:A:PHE:HD1	1:18:A:LEU:HD22	12	0.36
(1,49)	1:15:A:PHE:HD1	1:18:A:LEU:HD23	12	0.36
(1,49)	1:15:A:PHE:HD2	1:18:A:LEU:HD21	12	0.36
(1,49)	1:15:A:PHE:HD2	1:18:A:LEU:HD22	12	0.36
(1,49)	1:15:A:PHE:HD2	1:18:A:LEU:HD23	12	0.36
(1,2533)	1:15:A:PHE:H	1:17:A:LYS:HG2	11	0.35
(1,2533)	1:15:A:PHE:H	1:17:A:LYS:HG2	16	0.35
(1,2262)	1:11:A:TRP:H	1:17:A:LYS:HD2	2	0.35
(1,1111)	1:72:A:GLN:HG3	1:70:A:PHE:HA	4	0.35
(1,49)	1:15:A:PHE:HD1	1:18:A:LEU:HD21	4	0.35
(1,49)	1:15:A:PHE:HD1	1:18:A:LEU:HD22	4	0.35

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,49)	1:15:A:PHE:HD1	1:18:A:LEU:HD23	4	0.35
(1,49)	1:15:A:PHE:HD2	1:18:A:LEU:HD21	4	0.35
(1,49)	1:15:A:PHE:HD2	1:18:A:LEU:HD22	4	0.35
(1,49)	1:15:A:PHE:HD2	1:18:A:LEU:HD23	4	0.35
(1,2379)	1:16:A:ASP:H	1:14:A:SER:HB3	15	0.34
(1,1111)	1:72:A:GLN:HG3	1:70:A:PHE:HA	3	0.34
(1,1111)	1:72:A:GLN:HG3	1:70:A:PHE:HA	5	0.34
(1,1111)	1:72:A:GLN:HG3	1:70:A:PHE:HA	15	0.34
(1,636)	1:32:A:LEU:HA	1:37:A:SER:HB2	6	0.34
(1,213)	1:69:A:LYS:H	1:79:A:VAL:HG21	14	0.34
(1,49)	1:15:A:PHE:HD1	1:18:A:LEU:HD21	3	0.34
(1,49)	1:15:A:PHE:HD1	1:18:A:LEU:HD22	3	0.34
(1,49)	1:15:A:PHE:HD1	1:18:A:LEU:HD23	3	0.34
(1,49)	1:15:A:PHE:HD2	1:18:A:LEU:HD21	3	0.34
(1,49)	1:15:A:PHE:HD2	1:18:A:LEU:HD22	3	0.34
(1,49)	1:15:A:PHE:HD2	1:18:A:LEU:HD23	3	0.34
(1,2533)	1:15:A:PHE:H	1:17:A:LYS:HG2	15	0.33
(1,2417)	1:37:A:SER:H	1:38:A:GLU:HG3	6	0.33
(1,1198)	1:129:A:LEU:HD11	1:126:A:TYR:HD1	18	0.33
(1,1198)	1:129:A:LEU:HD11	1:126:A:TYR:HD2	18	0.33
(1,1198)	1:129:A:LEU:HD12	1:126:A:TYR:HD1	18	0.33
(1,1198)	1:129:A:LEU:HD12	1:126:A:TYR:HD2	18	0.33
(1,1198)	1:129:A:LEU:HD13	1:126:A:TYR:HD1	18	0.33
(1,1198)	1:129:A:LEU:HD13	1:126:A:TYR:HD2	18	0.33
(1,1111)	1:72:A:GLN:HG3	1:70:A:PHE:HA	17	0.33
(1,636)	1:32:A:LEU:HA	1:37:A:SER:HB2	14	0.33
(1,558)	1:131:A:GLU:HG2	1:130:A:MET:HB2	19	0.33
(1,455)	1:93:A:ILE:HG13	1:64:A:LYS:HE2	17	0.33
(1,49)	1:15:A:PHE:HD1	1:18:A:LEU:HD21	18	0.33
(1,49)	1:15:A:PHE:HD1	1:18:A:LEU:HD22	18	0.33
(1,49)	1:15:A:PHE:HD1	1:18:A:LEU:HD23	18	0.33
(1,49)	1:15:A:PHE:HD2	1:18:A:LEU:HD21	18	0.33
(1,49)	1:15:A:PHE:HD2	1:18:A:LEU:HD22	18	0.33
(1,49)	1:15:A:PHE:HD2	1:18:A:LEU:HD23	18	0.33
(1,2379)	1:16:A:ASP:H	1:14:A:SER:HB3	5	0.32
(1,2262)	1:11:A:TRP:H	1:17:A:LYS:HD2	18	0.32
(1,311)	1:72:A:GLN:HB2	1:75:A:ALA:HB1	9	0.32
(1,311)	1:72:A:GLN:HB2	1:75:A:ALA:HB2	9	0.32
(1,311)	1:72:A:GLN:HB2	1:75:A:ALA:HB3	9	0.32
(1,311)	1:72:A:GLN:HB2	1:75:A:ALA:HB1	12	0.32
(1,311)	1:72:A:GLN:HB2	1:75:A:ALA:HB2	12	0.32
(1,311)	1:72:A:GLN:HB2	1:75:A:ALA:HB3	12	0.32

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,2262)	1:11:A:TRP:H	1:17:A:LYS:HD2	15	0.31
(1,1795)	1:54:A:LYS:H	1:53:A:SER:HB3	9	0.31
(1,1533)	1:6:A:GLU:HG2	1:7:A:GLU:H	16	0.31
(1,1429)	1:19:A:LEU:HD21	1:44:A:TRP:HZ2	1	0.31
(1,1429)	1:19:A:LEU:HD22	1:44:A:TRP:HZ2	1	0.31
(1,1429)	1:19:A:LEU:HD23	1:44:A:TRP:HZ2	1	0.31
(1,1429)	1:19:A:LEU:HD21	1:44:A:TRP:HZ2	9	0.31
(1,1429)	1:19:A:LEU:HD22	1:44:A:TRP:HZ2	9	0.31
(1,1429)	1:19:A:LEU:HD23	1:44:A:TRP:HZ2	9	0.31
(1,1429)	1:19:A:LEU:HD21	1:44:A:TRP:HZ2	13	0.31
(1,1429)	1:19:A:LEU:HD22	1:44:A:TRP:HZ2	13	0.31
(1,1429)	1:19:A:LEU:HD23	1:44:A:TRP:HZ2	13	0.31
(1,1429)	1:19:A:LEU:HD21	1:44:A:TRP:HZ2	16	0.31
(1,1429)	1:19:A:LEU:HD22	1:44:A:TRP:HZ2	16	0.31
(1,1429)	1:19:A:LEU:HD23	1:44:A:TRP:HZ2	16	0.31
(1,1429)	1:19:A:LEU:HD21	1:44:A:TRP:HZ2	17	0.31
(1,1429)	1:19:A:LEU:HD22	1:44:A:TRP:HZ2	17	0.31
(1,1429)	1:19:A:LEU:HD23	1:44:A:TRP:HZ2	17	0.31
(1,1429)	1:19:A:LEU:HD21	1:44:A:TRP:HZ2	19	0.31
(1,1429)	1:19:A:LEU:HD22	1:44:A:TRP:HZ2	19	0.31
(1,1429)	1:19:A:LEU:HD23	1:44:A:TRP:HZ2	19	0.31
(1,1381)	1:41:A:ILE:HD11	1:28:A:PHE:HD1	16	0.31
(1,1381)	1:41:A:ILE:HD11	1:28:A:PHE:HD2	16	0.31
(1,1381)	1:41:A:ILE:HD12	1:28:A:PHE:HD1	16	0.31
(1,1381)	1:41:A:ILE:HD12	1:28:A:PHE:HD2	16	0.31
(1,1381)	1:41:A:ILE:HD13	1:28:A:PHE:HD1	16	0.31
(1,1381)	1:41:A:ILE:HD13	1:28:A:PHE:HD2	16	0.31
(1,49)	1:15:A:PHE:HD1	1:18:A:LEU:HD21	16	0.31
(1,49)	1:15:A:PHE:HD1	1:18:A:LEU:HD22	16	0.31
(1,49)	1:15:A:PHE:HD1	1:18:A:LEU:HD23	16	0.31
(1,49)	1:15:A:PHE:HD2	1:18:A:LEU:HD21	16	0.31
(1,49)	1:15:A:PHE:HD2	1:18:A:LEU:HD22	16	0.31
(1,49)	1:15:A:PHE:HD2	1:18:A:LEU:HD23	16	0.31
(1,2533)	1:15:A:PHE:H	1:17:A:LYS:HG2	20	0.3
(1,2419)	1:37:A:SER:H	1:35:A:GLU:HG3	14	0.3
(1,2379)	1:16:A:ASP:H	1:14:A:SER:HB3	20	0.3
(1,1381)	1:41:A:ILE:HD11	1:28:A:PHE:HD1	3	0.3
(1,1381)	1:41:A:ILE:HD11	1:28:A:PHE:HD2	3	0.3
(1,1381)	1:41:A:ILE:HD12	1:28:A:PHE:HD1	3	0.3
(1,1381)	1:41:A:ILE:HD12	1:28:A:PHE:HD2	3	0.3
(1,1381)	1:41:A:ILE:HD13	1:28:A:PHE:HD1	3	0.3
(1,1381)	1:41:A:ILE:HD13	1:28:A:PHE:HD2	3	0.3

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1381)	1:41:A:ILE:HD11	1:28:A:PHE:HD1	19	0.3
(1,1381)	1:41:A:ILE:HD11	1:28:A:PHE:HD2	19	0.3
(1,1381)	1:41:A:ILE:HD12	1:28:A:PHE:HD1	19	0.3
(1,1381)	1:41:A:ILE:HD12	1:28:A:PHE:HD2	19	0.3
(1,1381)	1:41:A:ILE:HD13	1:28:A:PHE:HD1	19	0.3
(1,1381)	1:41:A:ILE:HD13	1:28:A:PHE:HD2	19	0.3
(1,311)	1:72:A:GLN:HB2	1:75:A:ALA:HB1	1	0.3
(1,311)	1:72:A:GLN:HB2	1:75:A:ALA:HB2	1	0.3
(1,311)	1:72:A:GLN:HB2	1:75:A:ALA:HB3	1	0.3
(1,2533)	1:15:A:PHE:H	1:17:A:LYS:HG2	17	0.29
(1,2513)	1:13:A:GLU:H	1:14:A:SER:HB2	10	0.29
(1,1429)	1:19:A:LEU:HD21	1:44:A:TRP:HZ2	2	0.29
(1,1429)	1:19:A:LEU:HD22	1:44:A:TRP:HZ2	2	0.29
(1,1429)	1:19:A:LEU:HD23	1:44:A:TRP:HZ2	2	0.29
(1,1429)	1:19:A:LEU:HD21	1:44:A:TRP:HZ2	11	0.29
(1,1429)	1:19:A:LEU:HD22	1:44:A:TRP:HZ2	11	0.29
(1,1429)	1:19:A:LEU:HD23	1:44:A:TRP:HZ2	11	0.29
(1,1198)	1:129:A:LEU:HD11	1:126:A:TYR:HD1	12	0.29
(1,1198)	1:129:A:LEU:HD11	1:126:A:TYR:HD2	12	0.29
(1,1198)	1:129:A:LEU:HD12	1:126:A:TYR:HD1	12	0.29
(1,1198)	1:129:A:LEU:HD12	1:126:A:TYR:HD2	12	0.29
(1,1198)	1:129:A:LEU:HD13	1:126:A:TYR:HD1	12	0.29
(1,1198)	1:129:A:LEU:HD13	1:126:A:TYR:HD2	12	0.29
(1,1148)	1:52:A:LYS:HE2	1:50:A:PHE:HA	18	0.29
(1,1111)	1:72:A:GLN:HG3	1:70:A:PHE:HA	8	0.29
(1,965)	1:10:A:LYS:HE3	1:7:A:GLU:HA	19	0.29
(1,870)	1:111:A:LEU:HD11	1:80:A:ASN:HB2	20	0.29
(1,870)	1:111:A:LEU:HD12	1:80:A:ASN:HB2	20	0.29
(1,870)	1:111:A:LEU:HD13	1:80:A:ASN:HB2	20	0.29
(1,870)	1:111:A:LEU:HD21	1:80:A:ASN:HB2	20	0.29
(1,870)	1:111:A:LEU:HD22	1:80:A:ASN:HB2	20	0.29
(1,870)	1:111:A:LEU:HD23	1:80:A:ASN:HB2	20	0.29
(1,667)	1:86:A:LYS:HD3	1:83:A:PHE:HA	6	0.29
(1,496)	1:64:A:LYS:HG3	1:68:A:GLU:HG3	15	0.29
(1,455)	1:93:A:ILE:HG13	1:64:A:LYS:HE2	5	0.29
(1,26)	1:41:A:ILE:HB	1:32:A:LEU:HD11	7	0.29
(1,26)	1:41:A:ILE:HB	1:32:A:LEU:HD12	7	0.29
(1,26)	1:41:A:ILE:HB	1:32:A:LEU:HD13	7	0.29
(1,26)	1:41:A:ILE:HB	1:32:A:LEU:HD21	7	0.29
(1,26)	1:41:A:ILE:HB	1:32:A:LEU:HD22	7	0.29
(1,26)	1:41:A:ILE:HB	1:32:A:LEU:HD23	7	0.29
(1,2312)	1:131:A:GLU:H	1:130:A:MET:HB2	16	0.28

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,2262)	1:11:A:TRP:H	1:17:A:LYS:HD2	4	0.28
(1,2060)	1:57:A:GLN:H	1:57:A:GLN:HG2	16	0.28
(1,213)	1:69:A:LYS:H	1:79:A:VAL:HG23	5	0.28
(1,1533)	1:6:A:GLU:HG3	1:7:A:GLU:H	11	0.27
(1,1381)	1:41:A:ILE:HD11	1:28:A:PHE:HD1	10	0.27
(1,1381)	1:41:A:ILE:HD11	1:28:A:PHE:HD2	10	0.27
(1,1381)	1:41:A:ILE:HD12	1:28:A:PHE:HD1	10	0.27
(1,1381)	1:41:A:ILE:HD12	1:28:A:PHE:HD2	10	0.27
(1,1381)	1:41:A:ILE:HD13	1:28:A:PHE:HD1	10	0.27
(1,1381)	1:41:A:ILE:HD13	1:28:A:PHE:HD2	10	0.27
(1,1198)	1:129:A:LEU:HD11	1:126:A:TYR:HD1	7	0.27
(1,1198)	1:129:A:LEU:HD11	1:126:A:TYR:HD2	7	0.27
(1,1198)	1:129:A:LEU:HD12	1:126:A:TYR:HD1	7	0.27
(1,1198)	1:129:A:LEU:HD12	1:126:A:TYR:HD2	7	0.27
(1,1198)	1:129:A:LEU:HD13	1:126:A:TYR:HD1	7	0.27
(1,1198)	1:129:A:LEU:HD13	1:126:A:TYR:HD2	7	0.27
(1,1148)	1:52:A:LYS:HE2	1:50:A:PHE:HA	16	0.27
(1,762)	1:53:A:SER:HB3	1:54:A:LYS:HG2	16	0.27
(1,311)	1:72:A:GLN:HB2	1:75:A:ALA:HB1	7	0.27
(1,311)	1:72:A:GLN:HB2	1:75:A:ALA:HB2	7	0.27
(1,311)	1:72:A:GLN:HB2	1:75:A:ALA:HB3	7	0.27
(1,2491)	1:132:A:GLY:H	1:130:A:MET:HB2	1	0.26
(1,2379)	1:16:A:ASP:H	1:14:A:SER:HB3	13	0.26
(1,1734)	1:81:A:LEU:H	1:86:A:LYS:HE3	11	0.26
(1,1048)	1:129:A:LEU:HB3	1:126:A:TYR:HB3	13	0.26
(1,311)	1:72:A:GLN:HB2	1:75:A:ALA:HB1	19	0.26
(1,311)	1:72:A:GLN:HB2	1:75:A:ALA:HB2	19	0.26
(1,311)	1:72:A:GLN:HB2	1:75:A:ALA:HB3	19	0.26
(1,2262)	1:11:A:TRP:H	1:17:A:LYS:HD2	13	0.25
(1,1795)	1:54:A:LYS:H	1:53:A:SER:HB2	19	0.25
(1,1381)	1:41:A:ILE:HD11	1:28:A:PHE:HD1	11	0.25
(1,1381)	1:41:A:ILE:HD11	1:28:A:PHE:HD2	11	0.25
(1,1381)	1:41:A:ILE:HD12	1:28:A:PHE:HD1	11	0.25
(1,1381)	1:41:A:ILE:HD12	1:28:A:PHE:HD2	11	0.25
(1,1381)	1:41:A:ILE:HD13	1:28:A:PHE:HD1	11	0.25
(1,1381)	1:41:A:ILE:HD13	1:28:A:PHE:HD2	11	0.25
(1,517)	1:62:A:LYS:HG3	1:58:A:GLN:HG3	3	0.25
(1,463)	1:52:A:LYS:HE2	1:49:A:ASP:HB2	20	0.25
(1,455)	1:93:A:ILE:HG13	1:64:A:LYS:HE2	18	0.25
(1,455)	1:93:A:ILE:HG13	1:64:A:LYS:HE2	19	0.25
(1,2533)	1:15:A:PHE:H	1:17:A:LYS:HG2	8	0.24
(1,2262)	1:11:A:TRP:H	1:17:A:LYS:HD2	6	0.24

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1533)	1:7:A:GLU:HG2	1:7:A:GLU:H	8	0.24
(1,1408)	1:129:A:LEU:HD11	1:11:A:TRP:HZ3	2	0.24
(1,1408)	1:129:A:LEU:HD12	1:11:A:TRP:HZ3	2	0.24
(1,1408)	1:129:A:LEU:HD13	1:11:A:TRP:HZ3	2	0.24
(1,870)	1:111:A:LEU:HD11	1:80:A:ASN:HB2	19	0.24
(1,870)	1:111:A:LEU:HD12	1:80:A:ASN:HB2	19	0.24
(1,870)	1:111:A:LEU:HD13	1:80:A:ASN:HB2	19	0.24
(1,870)	1:111:A:LEU:HD21	1:80:A:ASN:HB2	19	0.24
(1,870)	1:111:A:LEU:HD22	1:80:A:ASN:HB2	19	0.24
(1,870)	1:111:A:LEU:HD23	1:80:A:ASN:HB2	19	0.24
(1,834)	1:51:A:LYS:HE2	1:98:A:LEU:HB3	17	0.24
(1,565)	1:69:A:LYS:HD2	1:76:A:PRO:HB3	3	0.24
(1,311)	1:72:A:GLN:HB2	1:75:A:ALA:HB1	10	0.24
(1,311)	1:72:A:GLN:HB2	1:75:A:ALA:HB2	10	0.24
(1,311)	1:72:A:GLN:HB2	1:75:A:ALA:HB3	10	0.24
(1,49)	1:15:A:PHE:HD1	1:18:A:LEU:HD21	17	0.24
(1,49)	1:15:A:PHE:HD1	1:18:A:LEU:HD22	17	0.24
(1,49)	1:15:A:PHE:HD1	1:18:A:LEU:HD23	17	0.24
(1,49)	1:15:A:PHE:HD2	1:18:A:LEU:HD21	17	0.24
(1,49)	1:15:A:PHE:HD2	1:18:A:LEU:HD22	17	0.24
(1,49)	1:15:A:PHE:HD2	1:18:A:LEU:HD23	17	0.24
(1,2491)	1:132:A:GLY:H	1:130:A:MET:HB3	7	0.23
(1,2262)	1:11:A:TRP:H	1:17:A:LYS:HD2	7	0.23
(1,2110)	1:73:A:THR:H	1:72:A:GLN:HG2	18	0.23
(1,1198)	1:129:A:LEU:HD11	1:126:A:TYR:HD1	9	0.23
(1,1198)	1:129:A:LEU:HD11	1:126:A:TYR:HD2	9	0.23
(1,1198)	1:129:A:LEU:HD12	1:126:A:TYR:HD1	9	0.23
(1,1198)	1:129:A:LEU:HD12	1:126:A:TYR:HD2	9	0.23
(1,1198)	1:129:A:LEU:HD13	1:126:A:TYR:HD1	9	0.23
(1,1198)	1:129:A:LEU:HD13	1:126:A:TYR:HD2	9	0.23
(1,1087)	1:33:A:LYS:HG2	1:38:A:GLU:HB3	6	0.23
(1,683)	1:105:A:GLN:HB2	1:105:A:GLN:HA	7	0.23
(1,683)	1:105:A:GLN:HB2	1:105:A:GLN:HA	14	0.23
(1,649)	1:13:A:GLU:HG3	1:14:A:SER:HB3	7	0.23
(1,469)	1:16:A:ASP:HA	1:16:A:ASP:HB3	20	0.23
(1,410)	1:56:A:PRO:HA	1:59:A:ILE:HD11	8	0.23
(1,410)	1:56:A:PRO:HA	1:59:A:ILE:HD12	8	0.23
(1,410)	1:56:A:PRO:HA	1:59:A:ILE:HD13	8	0.23
(1,2427)	1:55:A:GLY:H	1:58:A:GLN:HB3	20	0.22
(1,2419)	1:37:A:SER:H	1:35:A:GLU:HG3	10	0.22
(1,2417)	1:37:A:SER:H	1:38:A:GLU:HG3	17	0.22
(1,934)	1:111:A:LEU:HD11	1:108:A:VAL:HA	3	0.22

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,934)	1:111:A:LEU:HD12	1:108:A:VAL:HA	3	0.22
(1,934)	1:111:A:LEU:HD13	1:108:A:VAL:HA	3	0.22
(1,934)	1:111:A:LEU:HD21	1:108:A:VAL:HA	3	0.22
(1,934)	1:111:A:LEU:HD22	1:108:A:VAL:HA	3	0.22
(1,934)	1:111:A:LEU:HD23	1:108:A:VAL:HA	3	0.22
(1,696)	1:112:A:MET:HB2	1:112:A:MET:HA	7	0.22
(1,683)	1:105:A:GLN:HB2	1:105:A:GLN:HA	2	0.22
(1,683)	1:105:A:GLN:HB2	1:105:A:GLN:HA	4	0.22
(1,683)	1:105:A:GLN:HB2	1:105:A:GLN:HA	18	0.22
(1,565)	1:69:A:LYS:HD2	1:76:A:PRO:HB3	11	0.22
(1,469)	1:16:A:ASP:HA	1:16:A:ASP:HB3	1	0.22
(1,469)	1:28:A:PHE:HA	1:28:A:PHE:HB3	2	0.22
(1,469)	1:16:A:ASP:HA	1:16:A:ASP:HB3	5	0.22
(1,469)	1:28:A:PHE:HA	1:28:A:PHE:HB3	10	0.22
(1,469)	1:28:A:PHE:HA	1:28:A:PHE:HB3	11	0.22
(1,469)	1:16:A:ASP:HA	1:16:A:ASP:HB3	13	0.22
(1,469)	1:16:A:ASP:HA	1:16:A:ASP:HB3	14	0.22
(1,469)	1:28:A:PHE:HA	1:28:A:PHE:HB3	17	0.22
(1,455)	1:93:A:ILE:HG13	1:64:A:LYS:HE3	14	0.22
(1,365)	1:101:A:PHE:HD1	1:89:A:ILE:HD11	14	0.22
(1,365)	1:101:A:PHE:HD1	1:89:A:ILE:HD12	14	0.22
(1,365)	1:101:A:PHE:HD1	1:89:A:ILE:HD13	14	0.22
(1,365)	1:101:A:PHE:HD2	1:89:A:ILE:HD11	14	0.22
(1,365)	1:101:A:PHE:HD2	1:89:A:ILE:HD12	14	0.22
(1,365)	1:101:A:PHE:HD2	1:89:A:ILE:HD13	14	0.22
(1,336)	1:50:A:PHE:HZ	1:59:A:ILE:HG21	3	0.22
(1,336)	1:50:A:PHE:HZ	1:59:A:ILE:HG22	3	0.22
(1,336)	1:50:A:PHE:HZ	1:59:A:ILE:HG23	3	0.22
(1,213)	1:69:A:LYS:H	1:79:A:VAL:HG21	17	0.22
(1,1381)	1:41:A:ILE:HD11	1:28:A:PHE:HD1	13	0.21
(1,1381)	1:41:A:ILE:HD11	1:28:A:PHE:HD2	13	0.21
(1,1381)	1:41:A:ILE:HD12	1:28:A:PHE:HD1	13	0.21
(1,1381)	1:41:A:ILE:HD12	1:28:A:PHE:HD2	13	0.21
(1,1381)	1:41:A:ILE:HD13	1:28:A:PHE:HD1	13	0.21
(1,1381)	1:41:A:ILE:HD13	1:28:A:PHE:HD2	13	0.21
(1,1374)	1:71:A:ILE:HD11	1:43:A:PHE:HZ	11	0.21
(1,1374)	1:71:A:ILE:HD12	1:43:A:PHE:HZ	11	0.21
(1,1374)	1:71:A:ILE:HD13	1:43:A:PHE:HZ	11	0.21
(1,1048)	1:129:A:LEU:HB3	1:126:A:TYR:HB3	2	0.21
(1,696)	1:112:A:MET:HB2	1:112:A:MET:HA	3	0.21
(1,593)	1:55:A:GLY:HA2	1:54:A:LYS:HD2	20	0.21
(1,580)	1:105:A:GLN:HB2	1:44:A:TRP:HB3	4	0.21

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,514)	1:32:A:LEU:HA	1:35:A:GLU:HG2	12	0.21
(1,503)	1:25:A:LEU:HB3	1:26:A:GLU:HG2	8	0.21
(1,502)	1:25:A:LEU:HB3	1:26:A:GLU:HG2	8	0.21
(1,469)	1:16:A:ASP:HA	1:16:A:ASP:HB3	3	0.21
(1,469)	1:28:A:PHE:HA	1:28:A:PHE:HB3	7	0.21
(1,469)	1:16:A:ASP:HA	1:16:A:ASP:HB3	8	0.21
(1,469)	1:16:A:ASP:HA	1:16:A:ASP:HB3	9	0.21
(1,469)	1:28:A:PHE:HA	1:28:A:PHE:HB3	15	0.21
(1,421)	1:43:A:PHE:HZ	1:71:A:ILE:HD11	11	0.21
(1,421)	1:43:A:PHE:HZ	1:71:A:ILE:HD12	11	0.21
(1,421)	1:43:A:PHE:HZ	1:71:A:ILE:HD13	11	0.21
(1,101)	1:76:A:PRO:HD3	1:69:A:LYS:HG3	9	0.21
(1,2513)	1:13:A:GLU:H	1:14:A:SER:HB3	5	0.2
(1,2346)	1:6:A:GLU:H	1:4:A:SER:HA	12	0.2
(1,1541)	1:62:A:LYS:HB3	1:50:A:PHE:HD1	7	0.2
(1,1541)	1:62:A:LYS:HB3	1:50:A:PHE:HD2	7	0.2
(1,1541)	1:62:A:LYS:HB3	1:50:A:PHE:HD1	18	0.2
(1,1541)	1:62:A:LYS:HB3	1:50:A:PHE:HD2	18	0.2
(1,1482)	1:97:A:THR:HG21	1:98:A:LEU:H	10	0.2
(1,1482)	1:97:A:THR:HG22	1:98:A:LEU:H	10	0.2
(1,1482)	1:97:A:THR:HG23	1:98:A:LEU:H	10	0.2
(1,1198)	1:129:A:LEU:HD11	1:126:A:TYR:HD1	11	0.2
(1,1198)	1:129:A:LEU:HD11	1:126:A:TYR:HD2	11	0.2
(1,1198)	1:129:A:LEU:HD12	1:126:A:TYR:HD1	11	0.2
(1,1198)	1:129:A:LEU:HD12	1:126:A:TYR:HD2	11	0.2
(1,1198)	1:129:A:LEU:HD13	1:126:A:TYR:HD1	11	0.2
(1,1198)	1:129:A:LEU:HD13	1:126:A:TYR:HD2	11	0.2
(1,1198)	1:129:A:LEU:HD11	1:126:A:TYR:HD1	14	0.2
(1,1198)	1:129:A:LEU:HD11	1:126:A:TYR:HD2	14	0.2
(1,1198)	1:129:A:LEU:HD12	1:126:A:TYR:HD1	14	0.2
(1,1198)	1:129:A:LEU:HD12	1:126:A:TYR:HD2	14	0.2
(1,1198)	1:129:A:LEU:HD13	1:126:A:TYR:HD1	14	0.2
(1,1198)	1:129:A:LEU:HD13	1:126:A:TYR:HD2	14	0.2
(1,1198)	1:129:A:LEU:HD11	1:126:A:TYR:HD1	15	0.2
(1,1198)	1:129:A:LEU:HD11	1:126:A:TYR:HD2	15	0.2
(1,1198)	1:129:A:LEU:HD12	1:126:A:TYR:HD1	15	0.2
(1,1198)	1:129:A:LEU:HD12	1:126:A:TYR:HD2	15	0.2
(1,1198)	1:129:A:LEU:HD13	1:126:A:TYR:HD1	15	0.2
(1,1198)	1:129:A:LEU:HD13	1:126:A:TYR:HD2	15	0.2
(1,965)	1:10:A:LYS:HE2	1:7:A:GLU:HA	6	0.2
(1,934)	1:111:A:LEU:HD11	1:108:A:VAL:HA	12	0.2
(1,934)	1:111:A:LEU:HD12	1:108:A:VAL:HA	12	0.2

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,934)	1:111:A:LEU:HD13	1:108:A:VAL:HA	12	0.2
(1,934)	1:111:A:LEU:HD21	1:108:A:VAL:HA	12	0.2
(1,934)	1:111:A:LEU:HD22	1:108:A:VAL:HA	12	0.2
(1,934)	1:111:A:LEU:HD23	1:108:A:VAL:HA	12	0.2
(1,696)	1:112:A:MET:HB2	1:112:A:MET:HA	9	0.2
(1,696)	1:112:A:MET:HB2	1:112:A:MET:HA	14	0.2
(1,617)	1:50:A:PHE:HE1	1:59:A:ILE:HA	1	0.2
(1,617)	1:50:A:PHE:HE2	1:59:A:ILE:HA	1	0.2
(1,617)	1:50:A:PHE:HE1	1:59:A:ILE:HA	6	0.2
(1,617)	1:50:A:PHE:HE2	1:59:A:ILE:HA	6	0.2
(1,463)	1:52:A:LYS:HE2	1:49:A:ASP:HB2	1	0.2
(1,463)	1:52:A:LYS:HE2	1:49:A:ASP:HB2	16	0.2
(1,446)	1:112:A:MET:HB3	1:111:A:LEU:HB2	11	0.2
(1,1848)	1:124:A:ASP:H	1:127:A:LEU:HG	13	0.19
(1,1541)	1:62:A:LYS:HB3	1:50:A:PHE:HD1	16	0.19
(1,1541)	1:62:A:LYS:HB3	1:50:A:PHE:HD2	16	0.19
(1,1429)	1:19:A:LEU:HD21	1:44:A:TRP:HZ2	14	0.19
(1,1429)	1:19:A:LEU:HD22	1:44:A:TRP:HZ2	14	0.19
(1,1429)	1:19:A:LEU:HD23	1:44:A:TRP:HZ2	14	0.19
(1,1381)	1:41:A:ILE:HD11	1:28:A:PHE:HD1	14	0.19
(1,1381)	1:41:A:ILE:HD11	1:28:A:PHE:HD2	14	0.19
(1,1381)	1:41:A:ILE:HD12	1:28:A:PHE:HD1	14	0.19
(1,1381)	1:41:A:ILE:HD12	1:28:A:PHE:HD2	14	0.19
(1,1381)	1:41:A:ILE:HD13	1:28:A:PHE:HD1	14	0.19
(1,1381)	1:41:A:ILE:HD13	1:28:A:PHE:HD2	14	0.19
(1,1111)	1:72:A:GLN:HG3	1:70:A:PHE:HA	14	0.19
(1,965)	1:10:A:LYS:HE2	1:7:A:GLU:HA	13	0.19
(1,965)	1:10:A:LYS:HE2	1:7:A:GLU:HA	14	0.19
(1,965)	1:10:A:LYS:HE2	1:7:A:GLU:HA	15	0.19
(1,965)	1:10:A:LYS:HE2	1:7:A:GLU:HA	16	0.19
(1,696)	1:62:A:LYS:HB2	1:62:A:LYS:HA	1	0.19
(1,696)	1:112:A:MET:HB2	1:112:A:MET:HA	4	0.19
(1,503)	1:25:A:LEU:HB3	1:26:A:GLU:HG2	2	0.19
(1,502)	1:25:A:LEU:HB3	1:26:A:GLU:HG2	2	0.19
(1,455)	1:93:A:ILE:HG13	1:64:A:LYS:HE2	10	0.19
(2,112)	1:118:A:THR:O	1:122:A:LYS:H	6	0.18
(2,36)	1:40:A:ASN:O	1:44:A:TRP:H	19	0.18
(1,2110)	1:73:A:THR:H	1:72:A:GLN:HG2	9	0.18
(1,2110)	1:73:A:THR:H	1:72:A:GLN:HG2	19	0.18
(1,1995)	1:65:A:ALA:H	1:64:A:LYS:HB2	1	0.18
(1,1822)	1:50:A:PHE:H	1:62:A:LYS:HE2	14	0.18
(1,1647)	1:79:A:VAL:HA	1:80:A:ASN:H	15	0.18

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1533)	1:6:A:GLU:HG2	1:7:A:GLU:H	7	0.18
(1,1408)	1:129:A:LEU:HD11	1:11:A:TRP:HZ3	17	0.18
(1,1408)	1:129:A:LEU:HD12	1:11:A:TRP:HZ3	17	0.18
(1,1408)	1:129:A:LEU:HD13	1:11:A:TRP:HZ3	17	0.18
(1,1381)	1:41:A:ILE:HD11	1:28:A:PHE:HD1	18	0.18
(1,1381)	1:41:A:ILE:HD11	1:28:A:PHE:HD2	18	0.18
(1,1381)	1:41:A:ILE:HD12	1:28:A:PHE:HD1	18	0.18
(1,1381)	1:41:A:ILE:HD12	1:28:A:PHE:HD2	18	0.18
(1,1381)	1:41:A:ILE:HD13	1:28:A:PHE:HD1	18	0.18
(1,1381)	1:41:A:ILE:HD13	1:28:A:PHE:HD2	18	0.18
(1,1198)	1:129:A:LEU:HD11	1:126:A:TYR:HD1	4	0.18
(1,1198)	1:129:A:LEU:HD11	1:126:A:TYR:HD2	4	0.18
(1,1198)	1:129:A:LEU:HD12	1:126:A:TYR:HD1	4	0.18
(1,1198)	1:129:A:LEU:HD12	1:126:A:TYR:HD2	4	0.18
(1,1198)	1:129:A:LEU:HD13	1:126:A:TYR:HD1	4	0.18
(1,1198)	1:129:A:LEU:HD13	1:126:A:TYR:HD2	4	0.18
(1,1198)	1:129:A:LEU:HD11	1:126:A:TYR:HD1	8	0.18
(1,1198)	1:129:A:LEU:HD11	1:126:A:TYR:HD2	8	0.18
(1,1198)	1:129:A:LEU:HD12	1:126:A:TYR:HD1	8	0.18
(1,1198)	1:129:A:LEU:HD12	1:126:A:TYR:HD2	8	0.18
(1,1198)	1:129:A:LEU:HD13	1:126:A:TYR:HD1	8	0.18
(1,1198)	1:129:A:LEU:HD13	1:126:A:TYR:HD2	8	0.18
(1,1134)	1:42:A:GLU:HA	1:45:A:ILE:HB	2	0.18
(1,1134)	1:42:A:GLU:HA	1:45:A:ILE:HB	5	0.18
(1,1134)	1:42:A:GLU:HA	1:45:A:ILE:HB	9	0.18
(1,1134)	1:42:A:GLU:HA	1:45:A:ILE:HB	10	0.18
(1,1134)	1:42:A:GLU:HA	1:45:A:ILE:HB	15	0.18
(1,1087)	1:33:A:LYS:HG2	1:38:A:GLU:HB3	17	0.18
(1,965)	1:10:A:LYS:HE2	1:7:A:GLU:HA	7	0.18
(1,965)	1:10:A:LYS:HE2	1:7:A:GLU:HA	12	0.18
(1,965)	1:10:A:LYS:HE2	1:7:A:GLU:HA	18	0.18
(1,943)	1:58:A:GLN:HB3	1:53:A:SER:HB3	20	0.18
(1,934)	1:111:A:LEU:HD11	1:108:A:VAL:HA	2	0.18
(1,934)	1:111:A:LEU:HD12	1:108:A:VAL:HA	2	0.18
(1,934)	1:111:A:LEU:HD13	1:108:A:VAL:HA	2	0.18
(1,934)	1:111:A:LEU:HD21	1:108:A:VAL:HA	2	0.18
(1,934)	1:111:A:LEU:HD22	1:108:A:VAL:HA	2	0.18
(1,934)	1:111:A:LEU:HD23	1:108:A:VAL:HA	2	0.18
(1,891)	1:116:A:SER:HB3	1:120:A:PHE:HA	19	0.18
(1,568)	1:56:A:PRO:HA	1:56:A:PRO:HB2	10	0.18
(1,336)	1:50:A:PHE:HZ	1:59:A:ILE:HG21	5	0.18
(1,336)	1:50:A:PHE:HZ	1:59:A:ILE:HG22	5	0.18

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,336)	1:50:A:PHE:HZ	1:59:A:ILE:HG23	5	0.18
(2,112)	1:118:A:THR:O	1:122:A:LYS:H	1	0.17
(1,2555)	1:36:A:PHE:H	1:35:A:GLU:HG3	10	0.17
(1,2513)	1:13:A:GLU:H	1:14:A:SER:HB3	15	0.17
(1,2110)	1:73:A:THR:H	1:72:A:GLN:HG2	1	0.17
(1,1539)	1:35:A:GLU:HG3	1:36:A:PHE:H	10	0.17
(1,1533)	1:6:A:GLU:HG3	1:7:A:GLU:H	20	0.17
(1,1429)	1:19:A:LEU:HD21	1:44:A:TRP:HZ2	3	0.17
(1,1429)	1:19:A:LEU:HD22	1:44:A:TRP:HZ2	3	0.17
(1,1429)	1:19:A:LEU:HD23	1:44:A:TRP:HZ2	3	0.17
(1,1408)	1:129:A:LEU:HD11	1:11:A:TRP:HZ3	19	0.17
(1,1408)	1:129:A:LEU:HD12	1:11:A:TRP:HZ3	19	0.17
(1,1408)	1:129:A:LEU:HD13	1:11:A:TRP:HZ3	19	0.17
(1,1134)	1:42:A:GLU:HA	1:45:A:ILE:HB	1	0.17
(1,1134)	1:42:A:GLU:HA	1:45:A:ILE:HB	19	0.17
(1,965)	1:10:A:LYS:HE2	1:7:A:GLU:HA	3	0.17
(1,907)	1:101:A:PHE:HE1	1:63:A:ALA:HA	18	0.17
(1,907)	1:101:A:PHE:HE2	1:63:A:ALA:HA	18	0.17
(1,762)	1:53:A:SER:HB3	1:54:A:LYS:HG2	3	0.17
(1,696)	1:62:A:LYS:HB2	1:62:A:LYS:HA	16	0.17
(1,49)	1:15:A:PHE:HD1	1:18:A:LEU:HD21	2	0.17
(1,49)	1:15:A:PHE:HD1	1:18:A:LEU:HD22	2	0.17
(1,49)	1:15:A:PHE:HD1	1:18:A:LEU:HD23	2	0.17
(1,49)	1:15:A:PHE:HD2	1:18:A:LEU:HD21	2	0.17
(1,49)	1:15:A:PHE:HD2	1:18:A:LEU:HD22	2	0.17
(1,49)	1:15:A:PHE:HD2	1:18:A:LEU:HD23	2	0.17
(2,106)	1:113:A:GLU:O	1:117:A:TYR:H	17	0.16
(2,36)	1:40:A:ASN:O	1:44:A:TRP:H	1	0.16
(2,36)	1:40:A:ASN:O	1:44:A:TRP:H	5	0.16
(2,36)	1:40:A:ASN:O	1:44:A:TRP:H	9	0.16
(1,2305)	1:29:A:THR:H	1:30:A:ARG:HG2	11	0.16
(1,2110)	1:73:A:THR:H	1:72:A:GLN:HG2	10	0.16
(1,2110)	1:73:A:THR:H	1:72:A:GLN:HG2	12	0.16
(1,1855)	1:102:A:ASP:H	1:99:A:HIS:HA	1	0.16
(1,1728)	1:15:A:PHE:H	1:14:A:SER:HB2	2	0.16
(1,1674)	1:44:A:TRP:HE1	1:105:A:GLN:HG2	18	0.16
(1,1579)	1:14:A:SER:HB2	1:15:A:PHE:H	2	0.16
(1,1533)	1:6:A:GLU:HG3	1:7:A:GLU:H	18	0.16
(1,1482)	1:97:A:THR:HG21	1:98:A:LEU:H	15	0.16
(1,1482)	1:97:A:THR:HG22	1:98:A:LEU:H	15	0.16
(1,1482)	1:97:A:THR:HG23	1:98:A:LEU:H	15	0.16
(1,1381)	1:41:A:ILE:HD11	1:28:A:PHE:HD1	12	0.16

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1381)	1:41:A:ILE:HD11	1:28:A:PHE:HD2	12	0.16
(1,1381)	1:41:A:ILE:HD12	1:28:A:PHE:HD1	12	0.16
(1,1381)	1:41:A:ILE:HD12	1:28:A:PHE:HD2	12	0.16
(1,1381)	1:41:A:ILE:HD13	1:28:A:PHE:HD1	12	0.16
(1,1381)	1:41:A:ILE:HD13	1:28:A:PHE:HD2	12	0.16
(1,867)	1:49:A:ASP:HA	1:52:A:LYS:HD3	13	0.16
(1,844)	1:17:A:LYS:HG2	1:13:A:GLU:HG2	16	0.16
(1,696)	1:62:A:LYS:HB2	1:62:A:LYS:HA	6	0.16
(1,696)	1:62:A:LYS:HB2	1:62:A:LYS:HA	20	0.16
(1,587)	1:3:A:VAL:HG21	1:7:A:GLU:HB3	16	0.16
(1,587)	1:3:A:VAL:HG22	1:7:A:GLU:HB3	16	0.16
(1,587)	1:3:A:VAL:HG23	1:7:A:GLU:HB3	16	0.16
(1,568)	1:56:A:PRO:HA	1:56:A:PRO:HB2	8	0.16
(1,568)	1:56:A:PRO:HA	1:56:A:PRO:HB2	12	0.16
(1,455)	1:93:A:ILE:HG13	1:64:A:LYS:HE3	8	0.16
(1,26)	1:41:A:ILE:HB	1:32:A:LEU:HD11	12	0.16
(1,26)	1:41:A:ILE:HB	1:32:A:LEU:HD12	12	0.16
(1,26)	1:41:A:ILE:HB	1:32:A:LEU:HD13	12	0.16
(1,26)	1:41:A:ILE:HB	1:32:A:LEU:HD21	12	0.16
(1,26)	1:41:A:ILE:HB	1:32:A:LEU:HD22	12	0.16
(1,26)	1:41:A:ILE:HB	1:32:A:LEU:HD23	12	0.16
(1,2451)	1:70:A:PHE:H	1:72:A:GLN:H	9	0.15
(1,2346)	1:6:A:GLU:H	1:4:A:SER:HA	15	0.15
(1,2262)	1:11:A:TRP:H	1:17:A:LYS:HD3	10	0.15
(1,2204)	1:125:A:ILE:H	1:124:A:ASP:HB3	1	0.15
(1,2110)	1:73:A:THR:H	1:72:A:GLN:HG2	7	0.15
(1,1541)	1:62:A:LYS:HB3	1:50:A:PHE:HD1	9	0.15
(1,1541)	1:62:A:LYS:HB3	1:50:A:PHE:HD2	9	0.15
(1,1450)	1:48:A:GLU:HB3	1:99:A:HIS:HE1	15	0.15
(1,1198)	1:129:A:LEU:HD11	1:126:A:TYR:HD1	1	0.15
(1,1198)	1:129:A:LEU:HD11	1:126:A:TYR:HD2	1	0.15
(1,1198)	1:129:A:LEU:HD12	1:126:A:TYR:HD1	1	0.15
(1,1198)	1:129:A:LEU:HD12	1:126:A:TYR:HD2	1	0.15
(1,1198)	1:129:A:LEU:HD13	1:126:A:TYR:HD1	1	0.15
(1,1198)	1:129:A:LEU:HD13	1:126:A:TYR:HD2	1	0.15
(1,617)	1:50:A:PHE:HE1	1:59:A:ILE:HA	8	0.15
(1,617)	1:50:A:PHE:HE2	1:59:A:ILE:HA	8	0.15
(1,557)	1:127:A:LEU:HA	1:130:A:MET:HB2	20	0.15
(1,455)	1:93:A:ILE:HG13	1:64:A:LYS:HE3	13	0.15
(1,455)	1:93:A:ILE:HG13	1:64:A:LYS:HE2	16	0.15
(1,365)	1:101:A:PHE:HD1	1:89:A:ILE:HD11	10	0.15
(1,365)	1:101:A:PHE:HD1	1:89:A:ILE:HD12	10	0.15

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,365)	1:101:A:PHE:HD1	1:89:A:ILE:HD13	10	0.15
(1,365)	1:101:A:PHE:HD2	1:89:A:ILE:HD11	10	0.15
(1,365)	1:101:A:PHE:HD2	1:89:A:ILE:HD12	10	0.15
(1,365)	1:101:A:PHE:HD2	1:89:A:ILE:HD13	10	0.15
(1,213)	1:69:A:LYS:H	1:79:A:VAL:HG23	12	0.15
(2,114)	1:119:A:ARG:O	1:123:A:SER:H	5	0.14
(2,114)	1:119:A:ARG:O	1:123:A:SER:H	20	0.14
(2,112)	1:118:A:THR:O	1:122:A:LYS:H	13	0.14
(2,106)	1:113:A:GLU:O	1:117:A:TYR:H	19	0.14
(2,36)	1:40:A:ASN:O	1:44:A:TRP:H	4	0.14
(2,36)	1:40:A:ASN:O	1:44:A:TRP:H	8	0.14
(2,36)	1:40:A:ASN:O	1:44:A:TRP:H	10	0.14
(2,36)	1:40:A:ASN:O	1:44:A:TRP:H	11	0.14
(2,36)	1:40:A:ASN:O	1:44:A:TRP:H	12	0.14
(2,36)	1:40:A:ASN:O	1:44:A:TRP:H	15	0.14
(2,36)	1:40:A:ASN:O	1:44:A:TRP:H	16	0.14
(2,36)	1:40:A:ASN:O	1:44:A:TRP:H	17	0.14
(1,2513)	1:13:A:GLU:H	1:10:A:LYS:HA	14	0.14
(1,2451)	1:70:A:PHE:H	1:72:A:GLN:H	10	0.14
(1,2451)	1:70:A:PHE:H	1:72:A:GLN:H	12	0.14
(1,2346)	1:6:A:GLU:H	1:4:A:SER:HA	9	0.14
(1,2262)	1:11:A:TRP:H	1:17:A:LYS:HD2	20	0.14
(1,1995)	1:65:A:ALA:H	1:64:A:LYS:HB3	8	0.14
(1,1752)	1:27:A:ALA:H	1:24:A:GLY:HA3	1	0.14
(1,1752)	1:27:A:ALA:H	1:24:A:GLY:HA3	16	0.14
(1,1672)	1:44:A:TRP:HE1	1:109:A:TYR:HB3	7	0.14
(1,1450)	1:48:A:GLU:HB3	1:99:A:HIS:HE1	13	0.14
(1,1408)	1:129:A:LEU:HD11	1:11:A:TRP:HZ3	11	0.14
(1,1408)	1:129:A:LEU:HD12	1:11:A:TRP:HZ3	11	0.14
(1,1408)	1:129:A:LEU:HD13	1:11:A:TRP:HZ3	11	0.14
(1,1381)	1:41:A:ILE:HD11	1:28:A:PHE:HD1	1	0.14
(1,1381)	1:41:A:ILE:HD11	1:28:A:PHE:HD2	1	0.14
(1,1381)	1:41:A:ILE:HD12	1:28:A:PHE:HD1	1	0.14
(1,1381)	1:41:A:ILE:HD12	1:28:A:PHE:HD2	1	0.14
(1,1381)	1:41:A:ILE:HD13	1:28:A:PHE:HD1	1	0.14
(1,1381)	1:41:A:ILE:HD13	1:28:A:PHE:HD2	1	0.14
(1,1374)	1:71:A:ILE:HD11	1:43:A:PHE:HZ	13	0.14
(1,1374)	1:71:A:ILE:HD12	1:43:A:PHE:HZ	13	0.14
(1,1374)	1:71:A:ILE:HD13	1:43:A:PHE:HZ	13	0.14
(1,1207)	1:68:A:GLU:HG3	1:67:A:TYR:HD1	6	0.14
(1,1207)	1:68:A:GLU:HG3	1:67:A:TYR:HD2	6	0.14
(1,1198)	1:129:A:LEU:HD11	1:126:A:TYR:HD1	13	0.14

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1198)	1:129:A:LEU:HD11	1:126:A:TYR:HD2	13	0.14
(1,1198)	1:129:A:LEU:HD12	1:126:A:TYR:HD1	13	0.14
(1,1198)	1:129:A:LEU:HD12	1:126:A:TYR:HD2	13	0.14
(1,1198)	1:129:A:LEU:HD13	1:126:A:TYR:HD1	13	0.14
(1,1198)	1:129:A:LEU:HD13	1:126:A:TYR:HD2	13	0.14
(1,870)	1:111:A:LEU:HD11	1:80:A:ASN:HB2	11	0.14
(1,870)	1:111:A:LEU:HD12	1:80:A:ASN:HB2	11	0.14
(1,870)	1:111:A:LEU:HD13	1:80:A:ASN:HB2	11	0.14
(1,870)	1:111:A:LEU:HD21	1:80:A:ASN:HB2	11	0.14
(1,870)	1:111:A:LEU:HD22	1:80:A:ASN:HB2	11	0.14
(1,870)	1:111:A:LEU:HD23	1:80:A:ASN:HB2	11	0.14
(1,685)	1:33:A:LYS:HD2	1:30:A:ARG:HA	7	0.14
(1,580)	1:105:A:GLN:HB2	1:44:A:TRP:HB3	18	0.14
(1,527)	1:111:A:LEU:HG	1:110:A:GLN:HG3	11	0.14
(1,455)	1:93:A:ILE:HG13	1:64:A:LYS:HE3	4	0.14
(1,421)	1:43:A:PHE:HZ	1:71:A:ILE:HD11	13	0.14
(1,421)	1:43:A:PHE:HZ	1:71:A:ILE:HD12	13	0.14
(1,421)	1:43:A:PHE:HZ	1:71:A:ILE:HD13	13	0.14
(1,49)	1:15:A:PHE:HD1	1:18:A:LEU:HD21	14	0.14
(1,49)	1:15:A:PHE:HD1	1:18:A:LEU:HD22	14	0.14
(1,49)	1:15:A:PHE:HD1	1:18:A:LEU:HD23	14	0.14
(1,49)	1:15:A:PHE:HD2	1:18:A:LEU:HD21	14	0.14
(1,49)	1:15:A:PHE:HD2	1:18:A:LEU:HD22	14	0.14
(1,49)	1:15:A:PHE:HD2	1:18:A:LEU:HD23	14	0.14
(1,49)	1:15:A:PHE:HD1	1:18:A:LEU:HD21	15	0.14
(1,49)	1:15:A:PHE:HD1	1:18:A:LEU:HD22	15	0.14
(1,49)	1:15:A:PHE:HD1	1:18:A:LEU:HD23	15	0.14
(1,49)	1:15:A:PHE:HD2	1:18:A:LEU:HD21	15	0.14
(1,49)	1:15:A:PHE:HD2	1:18:A:LEU:HD22	15	0.14
(1,49)	1:15:A:PHE:HD2	1:18:A:LEU:HD23	15	0.14
(1,23)	1:38:A:GLU:HA	1:32:A:LEU:HD11	6	0.14
(1,23)	1:38:A:GLU:HA	1:32:A:LEU:HD12	6	0.14
(1,23)	1:38:A:GLU:HA	1:32:A:LEU:HD13	6	0.14
(1,23)	1:38:A:GLU:HA	1:32:A:LEU:HD21	6	0.14
(1,23)	1:38:A:GLU:HA	1:32:A:LEU:HD22	6	0.14
(1,23)	1:38:A:GLU:HA	1:32:A:LEU:HD23	6	0.14
(2,112)	1:118:A:THR:O	1:122:A:LYS:H	4	0.13
(2,112)	1:118:A:THR:O	1:122:A:LYS:H	7	0.13
(2,112)	1:118:A:THR:O	1:122:A:LYS:H	12	0.13
(2,112)	1:118:A:THR:O	1:122:A:LYS:H	18	0.13
(2,36)	1:40:A:ASN:O	1:44:A:TRP:H	2	0.13
(2,36)	1:40:A:ASN:O	1:44:A:TRP:H	3	0.13

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,36)	1:40:A:ASN:O	1:44:A:TRP:H	7	0.13
(2,36)	1:40:A:ASN:O	1:44:A:TRP:H	13	0.13
(1,2555)	1:36:A:PHE:H	1:35:A:GLU:HG3	7	0.13
(1,2451)	1:70:A:PHE:H	1:72:A:GLN:H	18	0.13
(1,2346)	1:6:A:GLU:H	1:4:A:SER:HA	3	0.13
(1,2346)	1:6:A:GLU:H	1:4:A:SER:HA	10	0.13
(1,2262)	1:11:A:TRP:H	1:17:A:LYS:HD2	3	0.13
(1,2262)	1:11:A:TRP:H	1:17:A:LYS:HD2	19	0.13
(1,1995)	1:65:A:ALA:H	1:64:A:LYS:HB3	6	0.13
(1,1795)	1:54:A:LYS:H	1:53:A:SER:HB2	5	0.13
(1,1752)	1:27:A:ALA:H	1:24:A:GLY:HA3	3	0.13
(1,1752)	1:27:A:ALA:H	1:24:A:GLY:HA3	4	0.13
(1,1752)	1:27:A:ALA:H	1:24:A:GLY:HA3	5	0.13
(1,1752)	1:27:A:ALA:H	1:24:A:GLY:HA3	6	0.13
(1,1752)	1:27:A:ALA:H	1:24:A:GLY:HA3	15	0.13
(1,1752)	1:27:A:ALA:H	1:24:A:GLY:HA3	19	0.13
(1,1539)	1:35:A:GLU:HG3	1:36:A:PHE:H	7	0.13
(1,1450)	1:48:A:GLU:HB3	1:99:A:HIS:HE1	18	0.13
(1,1429)	1:19:A:LEU:HD21	1:44:A:TRP:HZ2	6	0.13
(1,1429)	1:19:A:LEU:HD22	1:44:A:TRP:HZ2	6	0.13
(1,1429)	1:19:A:LEU:HD23	1:44:A:TRP:HZ2	6	0.13
(1,1429)	1:19:A:LEU:HD21	1:44:A:TRP:HZ2	18	0.13
(1,1429)	1:19:A:LEU:HD22	1:44:A:TRP:HZ2	18	0.13
(1,1429)	1:19:A:LEU:HD23	1:44:A:TRP:HZ2	18	0.13
(1,1408)	1:129:A:LEU:HD11	1:11:A:TRP:HZ3	9	0.13
(1,1408)	1:129:A:LEU:HD12	1:11:A:TRP:HZ3	9	0.13
(1,1408)	1:129:A:LEU:HD13	1:11:A:TRP:HZ3	9	0.13
(1,1374)	1:71:A:ILE:HD11	1:43:A:PHE:HZ	4	0.13
(1,1374)	1:71:A:ILE:HD12	1:43:A:PHE:HZ	4	0.13
(1,1374)	1:71:A:ILE:HD13	1:43:A:PHE:HZ	4	0.13
(1,503)	1:25:A:LEU:HB3	1:26:A:GLU:HG2	17	0.13
(1,502)	1:25:A:LEU:HB3	1:26:A:GLU:HG2	17	0.13
(1,421)	1:43:A:PHE:HZ	1:71:A:ILE:HD11	4	0.13
(1,421)	1:43:A:PHE:HZ	1:71:A:ILE:HD12	4	0.13
(1,421)	1:43:A:PHE:HZ	1:71:A:ILE:HD13	4	0.13
(1,213)	1:69:A:LYS:H	1:79:A:VAL:HG23	3	0.13
(1,213)	1:69:A:LYS:H	1:79:A:VAL:HG21	13	0.13
(1,166)	1:31:A:PHE:HA	1:34:A:THR:HG21	12	0.13
(1,166)	1:31:A:PHE:HA	1:34:A:THR:HG22	12	0.13
(1,166)	1:31:A:PHE:HA	1:34:A:THR:HG23	12	0.13
(1,101)	1:76:A:PRO:HD3	1:69:A:LYS:HG3	12	0.13
(2,114)	1:119:A:ARG:O	1:123:A:SER:H	6	0.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,114)	1:119:A:ARG:O	1:123:A:SER:H	12	0.12
(2,36)	1:40:A:ASN:O	1:44:A:TRP:H	6	0.12
(2,36)	1:40:A:ASN:O	1:44:A:TRP:H	20	0.12
(2,35)	1:40:A:ASN:O	1:44:A:TRP:N	19	0.12
(2,32)	1:38:A:GLU:O	1:42:A:GLU:H	11	0.12
(1,2513)	1:13:A:GLU:H	1:10:A:LYS:HA	9	0.12
(1,2451)	1:70:A:PHE:H	1:72:A:GLN:H	1	0.12
(1,2451)	1:70:A:PHE:H	1:72:A:GLN:H	15	0.12
(1,2346)	1:6:A:GLU:H	1:4:A:SER:HA	14	0.12
(1,2346)	1:6:A:GLU:H	1:4:A:SER:HA	16	0.12
(1,2346)	1:6:A:GLU:H	1:4:A:SER:HA	17	0.12
(1,1995)	1:65:A:ALA:H	1:64:A:LYS:HB2	11	0.12
(1,1753)	1:27:A:ALA:H	1:26:A:GLU:HB3	10	0.12
(1,1752)	1:27:A:ALA:H	1:24:A:GLY:HA3	2	0.12
(1,1635)	1:78:A:GLU:HG2	1:79:A:VAL:H	14	0.12
(1,1635)	1:78:A:GLU:HG3	1:79:A:VAL:H	14	0.12
(1,1635)	1:78:A:GLU:HG2	1:79:A:VAL:H	19	0.12
(1,1635)	1:78:A:GLU:HG3	1:79:A:VAL:H	19	0.12
(1,1429)	1:19:A:LEU:HD21	1:44:A:TRP:HZ2	7	0.12
(1,1429)	1:19:A:LEU:HD22	1:44:A:TRP:HZ2	7	0.12
(1,1429)	1:19:A:LEU:HD23	1:44:A:TRP:HZ2	7	0.12
(1,1408)	1:129:A:LEU:HD11	1:11:A:TRP:HZ3	20	0.12
(1,1408)	1:129:A:LEU:HD12	1:11:A:TRP:HZ3	20	0.12
(1,1408)	1:129:A:LEU:HD13	1:11:A:TRP:HZ3	20	0.12
(1,1148)	1:52:A:LYS:HE2	1:50:A:PHE:HA	1	0.12
(1,705)	1:81:A:LEU:HB2	1:107:A:ARG:HA	11	0.12
(1,593)	1:55:A:GLY:HA2	1:54:A:LYS:HD3	12	0.12
(1,558)	1:131:A:GLU:HG2	1:130:A:MET:HB2	7	0.12
(1,503)	1:25:A:LEU:HB3	1:26:A:GLU:HG2	1	0.12
(1,503)	1:25:A:LEU:HB3	1:26:A:GLU:HG2	4	0.12
(1,502)	1:25:A:LEU:HB3	1:26:A:GLU:HG2	1	0.12
(1,502)	1:25:A:LEU:HB3	1:26:A:GLU:HG2	4	0.12
(2,114)	1:119:A:ARG:O	1:123:A:SER:H	3	0.11
(2,114)	1:119:A:ARG:O	1:123:A:SER:H	15	0.11
(2,112)	1:118:A:THR:O	1:122:A:LYS:H	3	0.11
(2,106)	1:113:A:GLU:O	1:117:A:TYR:H	7	0.11
(2,106)	1:113:A:GLU:O	1:117:A:TYR:H	8	0.11
(1,2555)	1:36:A:PHE:H	1:35:A:GLU:HG3	14	0.11
(1,2451)	1:70:A:PHE:H	1:72:A:GLN:H	3	0.11
(1,2451)	1:70:A:PHE:H	1:72:A:GLN:H	4	0.11
(1,2451)	1:70:A:PHE:H	1:72:A:GLN:H	5	0.11
(1,2451)	1:70:A:PHE:H	1:72:A:GLN:H	6	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,2451)	1:70:A:PHE:H	1:72:A:GLN:H	7	0.11
(1,2451)	1:70:A:PHE:H	1:72:A:GLN:H	8	0.11
(1,2451)	1:70:A:PHE:H	1:72:A:GLN:H	11	0.11
(1,2451)	1:70:A:PHE:H	1:72:A:GLN:H	13	0.11
(1,2451)	1:70:A:PHE:H	1:72:A:GLN:H	16	0.11
(1,2451)	1:70:A:PHE:H	1:72:A:GLN:H	19	0.11
(1,2451)	1:70:A:PHE:H	1:72:A:GLN:H	20	0.11
(1,2262)	1:11:A:TRP:H	1:17:A:LYS:HD3	1	0.11
(1,2204)	1:125:A:ILE:H	1:124:A:ASP:HB3	4	0.11
(1,1752)	1:27:A:ALA:H	1:24:A:GLY:HA3	7	0.11
(1,1752)	1:27:A:ALA:H	1:24:A:GLY:HA3	8	0.11
(1,1752)	1:27:A:ALA:H	1:24:A:GLY:HA3	9	0.11
(1,1752)	1:27:A:ALA:H	1:24:A:GLY:HA3	10	0.11
(1,1752)	1:27:A:ALA:H	1:24:A:GLY:HA3	12	0.11
(1,1672)	1:44:A:TRP:HE1	1:109:A:TYR:HB3	18	0.11
(1,1539)	1:35:A:GLU:HG3	1:36:A:PHE:H	14	0.11
(1,1408)	1:129:A:LEU:HD11	1:11:A:TRP:HZ3	15	0.11
(1,1408)	1:129:A:LEU:HD12	1:11:A:TRP:HZ3	15	0.11
(1,1408)	1:129:A:LEU:HD13	1:11:A:TRP:HZ3	15	0.11
(1,1148)	1:52:A:LYS:HE3	1:50:A:PHE:HA	10	0.11
(1,1087)	1:33:A:LYS:HG2	1:38:A:GLU:HB3	15	0.11
(1,943)	1:58:A:GLN:HB3	1:53:A:SER:HB3	15	0.11
(1,934)	1:111:A:LEU:HD11	1:108:A:VAL:HA	15	0.11
(1,934)	1:111:A:LEU:HD12	1:108:A:VAL:HA	15	0.11
(1,934)	1:111:A:LEU:HD13	1:108:A:VAL:HA	15	0.11
(1,934)	1:111:A:LEU:HD21	1:108:A:VAL:HA	15	0.11
(1,934)	1:111:A:LEU:HD22	1:108:A:VAL:HA	15	0.11
(1,934)	1:111:A:LEU:HD23	1:108:A:VAL:HA	15	0.11
(1,705)	1:81:A:LEU:HB2	1:107:A:ARG:HA	18	0.11
(1,527)	1:111:A:LEU:HG	1:110:A:GLN:HG3	10	0.11
(1,455)	1:93:A:ILE:HG13	1:64:A:LYS:HE2	6	0.11
(1,446)	1:112:A:MET:HB3	1:111:A:LEU:HB2	16	0.11
(1,213)	1:69:A:LYS:H	1:79:A:VAL:HG21	6	0.11
(1,213)	1:69:A:LYS:H	1:79:A:VAL:HG22	11	0.11
(1,213)	1:80:A:ASN:HD22	1:79:A:VAL:HG21	16	0.11
(1,213)	1:69:A:LYS:H	1:79:A:VAL:HG21	20	0.11
(2,114)	1:119:A:ARG:O	1:123:A:SER:H	1	0.1
(2,114)	1:119:A:ARG:O	1:123:A:SER:H	14	0.1
(2,114)	1:119:A:ARG:O	1:123:A:SER:H	19	0.1
(2,112)	1:118:A:THR:O	1:122:A:LYS:H	10	0.1
(2,112)	1:118:A:THR:O	1:122:A:LYS:H	16	0.1
(2,106)	1:113:A:GLU:O	1:117:A:TYR:H	10	0.1

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,106)	1:113:A:GLU:O	1:117:A:TYR:H	11	0.1
(2,106)	1:113:A:GLU:O	1:117:A:TYR:H	12	0.1
(2,36)	1:40:A:ASN:O	1:44:A:TRP:H	18	0.1
(2,35)	1:40:A:ASN:O	1:44:A:TRP:N	1	0.1
(2,4)	1:6:A:GLU:O	1:10:A:LYS:H	17	0.1
(1,2346)	1:6:A:GLU:H	1:4:A:SER:HA	20	0.1
(1,1752)	1:27:A:ALA:H	1:24:A:GLY:HA3	11	0.1
(1,1752)	1:27:A:ALA:H	1:24:A:GLY:HA3	13	0.1
(1,1752)	1:27:A:ALA:H	1:24:A:GLY:HA3	17	0.1
(1,1672)	1:44:A:TRP:HE1	1:109:A:TYR:HB3	9	0.1
(1,1429)	1:19:A:LEU:HD21	1:44:A:TRP:HZ2	15	0.1
(1,1429)	1:19:A:LEU:HD22	1:44:A:TRP:HZ2	15	0.1
(1,1429)	1:19:A:LEU:HD23	1:44:A:TRP:HZ2	15	0.1
(1,1408)	1:129:A:LEU:HD11	1:11:A:TRP:HZ3	7	0.1
(1,1408)	1:129:A:LEU:HD12	1:11:A:TRP:HZ3	7	0.1
(1,1408)	1:129:A:LEU:HD13	1:11:A:TRP:HZ3	7	0.1
(1,1140)	1:38:A:GLU:HA	1:32:A:LEU:HB3	11	0.1
(1,1048)	1:129:A:LEU:HB3	1:126:A:TYR:HB3	8	0.1
(1,705)	1:81:A:LEU:HB2	1:107:A:ARG:HA	12	0.1
(1,558)	1:131:A:GLU:HG2	1:130:A:MET:HB2	15	0.1
(1,469)	1:28:A:PHE:HA	1:28:A:PHE:HB3	6	0.1

10 Dihedral-angle violation analysis ⓘ

No dihedral-angle restraints found