



Full wwPDB NMR Structure Validation Report ⓘ

Apr 15, 2026 – 12:27 AM UTC

PDB ID : 9RB5 / pdb_00009rb5
BMRB ID : 34996
Title : Staphylokinase SY155
Authors : Legrand, A.; Kaderavek, P.; Zidek, L.; Marek, M.; Prokop, Z.; Damborsky, J.
Deposited on : 2025-05-21

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

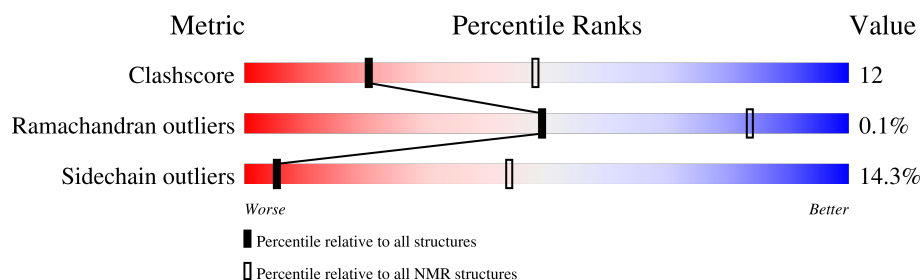
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 94%.

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	136	<div> <div>57%</div> <div>24%</div> <div>•</div> <div>16%</div> </div>

2 Ensemble composition and analysis

This entry contains 20 models. Model 12 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *target function*.

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:23-A:136 (114)	0.59	12

Ill-defined regions of proteins are excluded from the global statistics.

Ligands and non-protein polymers are included in the analysis.

The models can be grouped into 3 clusters and 6 single-model clusters were found.

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

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 2148 atoms, of which 1070 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Staphylokinase.

Mol	Chain	Residues	Atoms						Trace
1	A	136	Total	C	H	N	O	S	0
			2148	699	1070	171	207	1	

There are 12 discrepancies between the modelled and reference sequences:

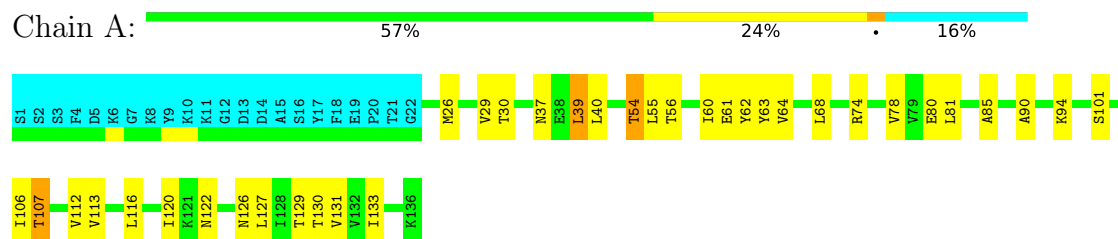
Chain	Residue	Modelled	Actual	Comment	Reference
A	35	ALA	LYS	conflict	UNP Q99SU7
A	65	GLN	GLU	conflict	UNP Q99SU7
A	74	ARG	LYS	conflict	UNP Q99SU7
A	82	ALA	ASP	conflict	UNP Q99SU7
A	84	ALA	SER	conflict	UNP Q99SU7
A	90	ALA	THR	conflict	UNP Q99SU7
A	99	ASP	GLU	conflict	UNP Q99SU7
A	101	SER	THR	conflict	UNP Q99SU7
A	108	ALA	GLU	conflict	UNP Q99SU7
A	109	ALA	LYS	conflict	UNP Q99SU7
A	130	THR	LYS	conflict	UNP Q99SU7
A	135	ARG	LYS	conflict	UNP Q99SU7

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: Staphylokinase

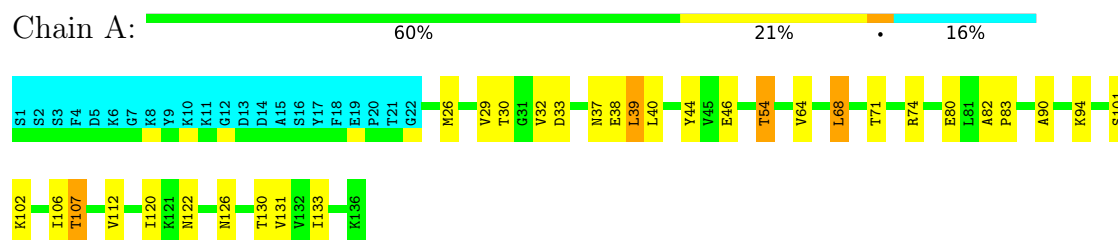


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

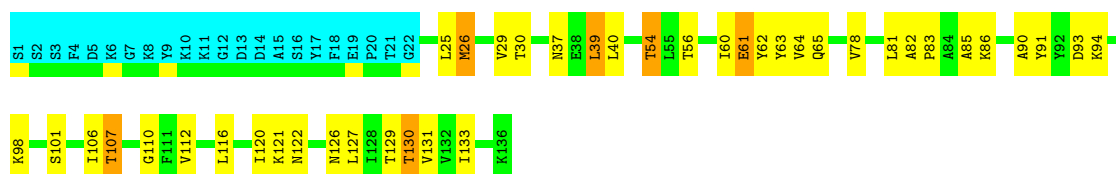
- Molecule 1: Staphylokinase



4.2.2 Score per residue for model 2

- Molecule 1: Staphylokinase

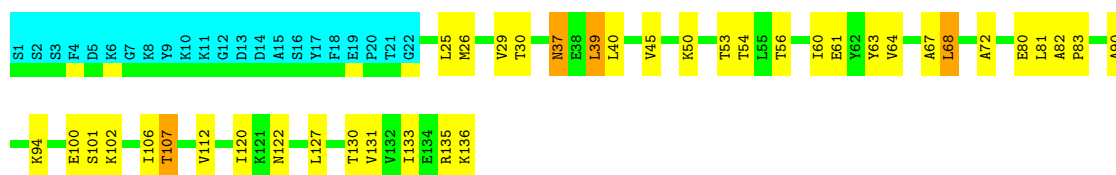




4.2.3 Score per residue for model 3

- Molecule 1: Staphylokinase

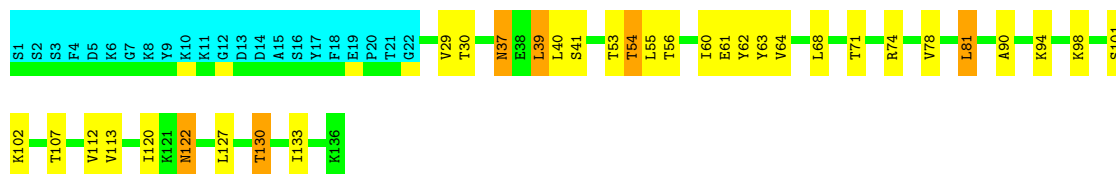
Chain A: 55% 26% 16%



4.2.4 Score per residue for model 4

- Molecule 1: Staphylokinase

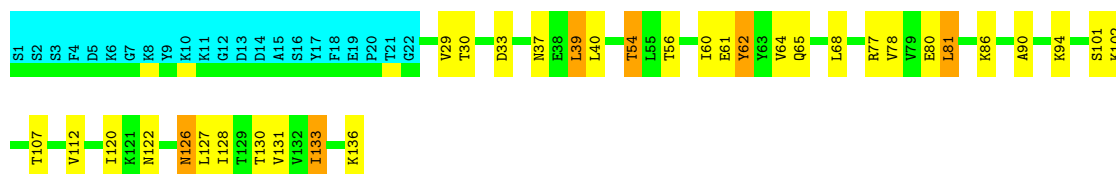
Chain A: 60% 20% 16%



4.2.5 Score per residue for model 5

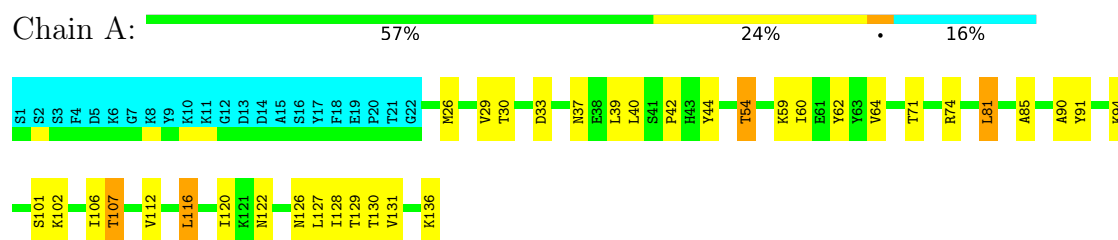
- Molecule 1: Staphylokinase

Chain A: 59% 21% 16%



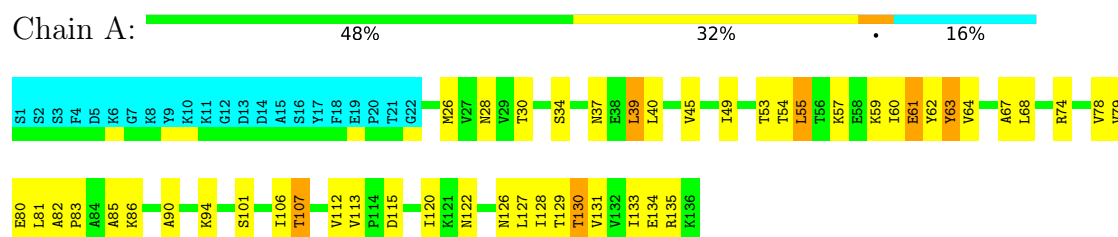
4.2.6 Score per residue for model 6

- Molecule 1: Staphylokinase



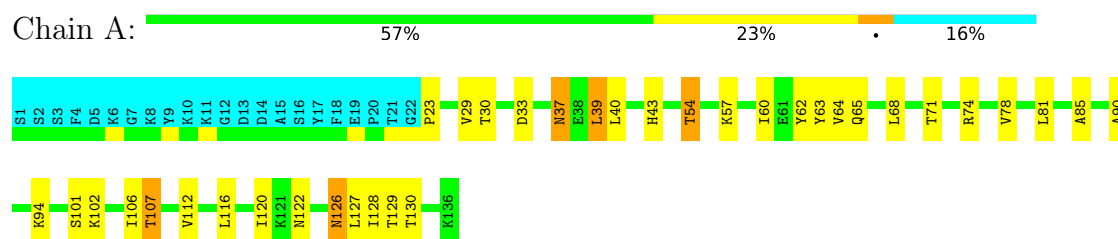
4.2.7 Score per residue for model 7

- Molecule 1: Staphylokinase



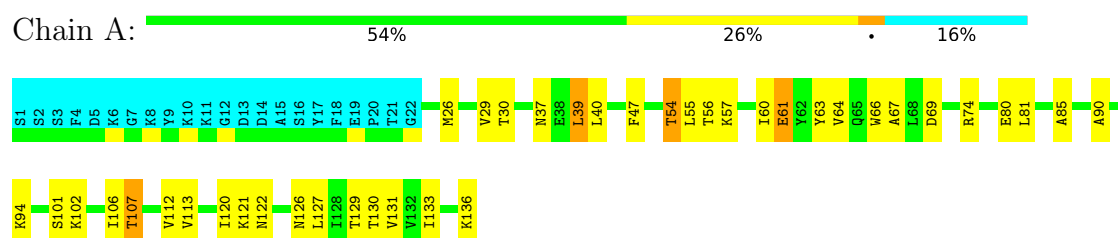
4.2.8 Score per residue for model 8

- Molecule 1: Staphylokinase



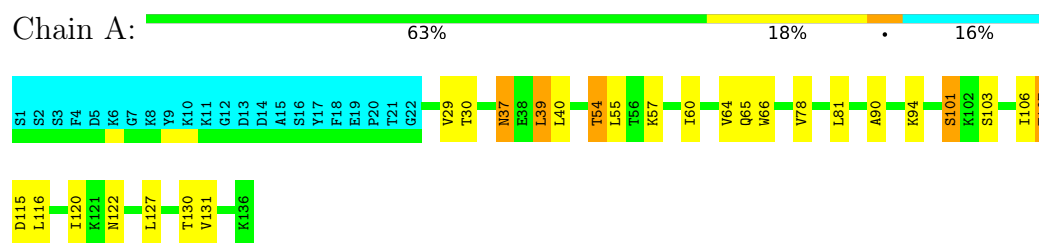
4.2.9 Score per residue for model 9

- Molecule 1: Staphylokinase



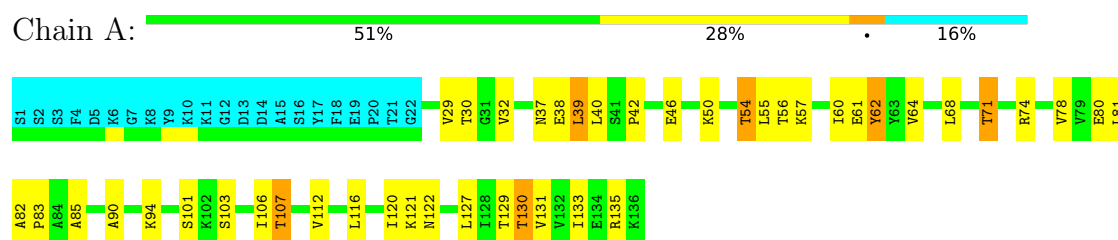
4.2.10 Score per residue for model 10

- Molecule 1: Staphylokinase



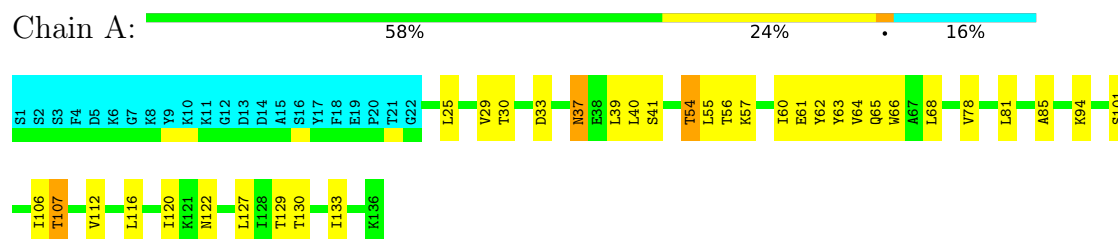
4.2.11 Score per residue for model 11

- Molecule 1: Staphylokinase



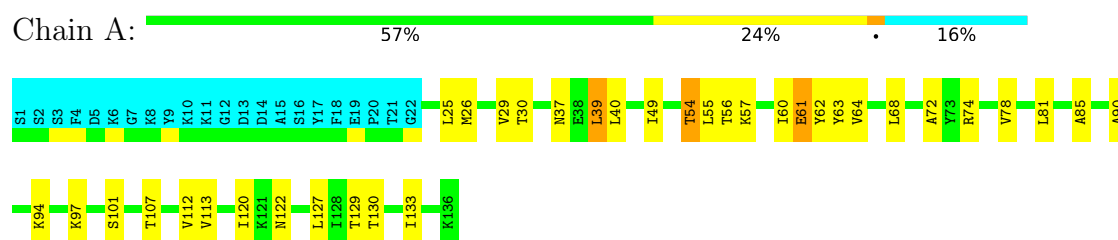
4.2.12 Score per residue for model 12 (medoid)

- Molecule 1: Staphylokinase



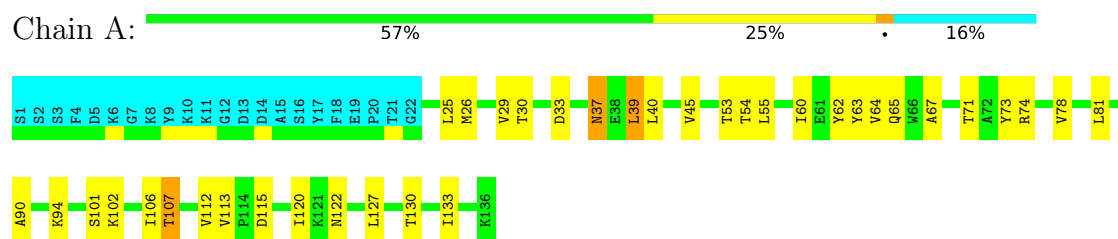
4.2.13 Score per residue for model 13

- Molecule 1: Staphylokinase



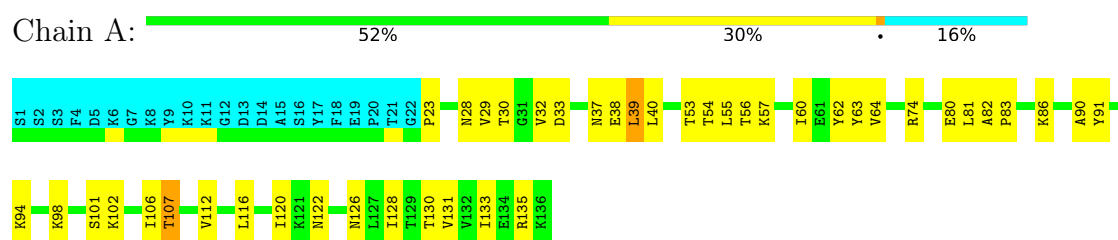
4.2.14 Score per residue for model 14

- Molecule 1: Staphylokinase



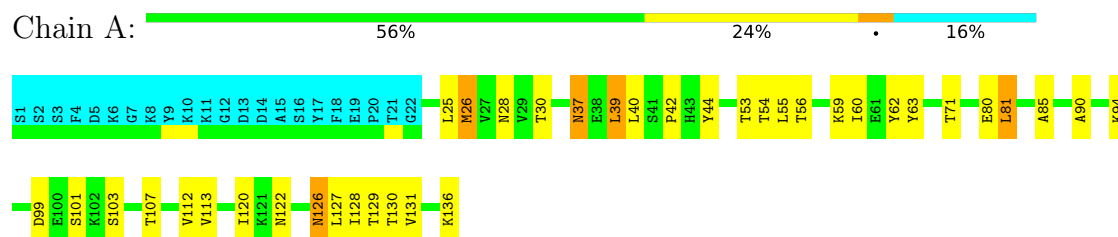
4.2.15 Score per residue for model 15

- Molecule 1: Staphylokinase



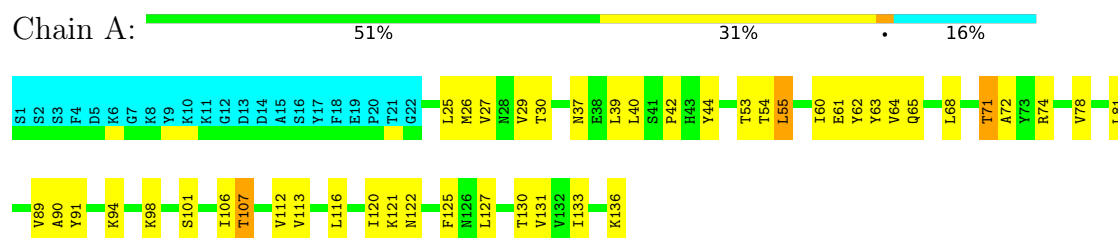
4.2.16 Score per residue for model 16

- Molecule 1: Staphylokinase



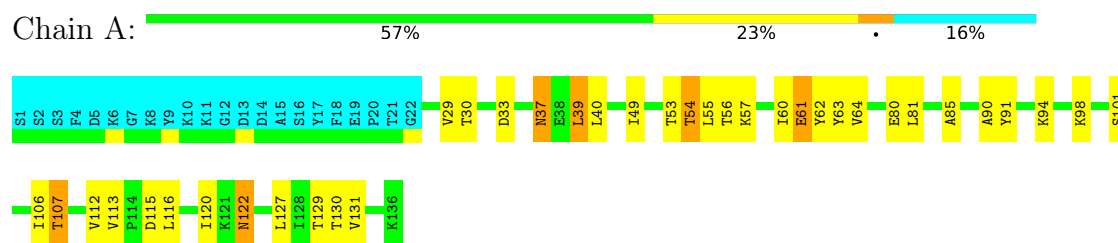
4.2.17 Score per residue for model 17

- Molecule 1: Staphylokinase



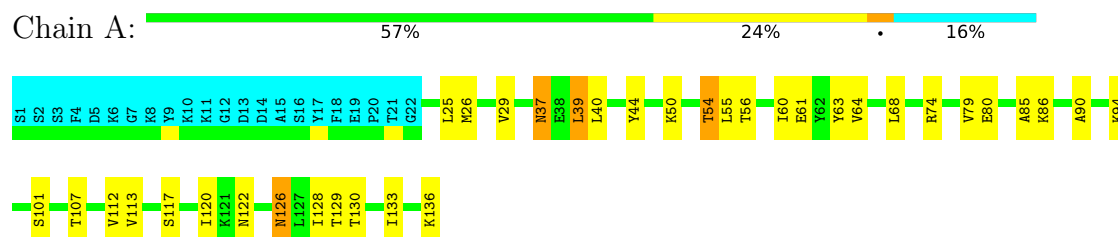
4.2.18 Score per residue for model 18

- Molecule 1: Staphylokinase



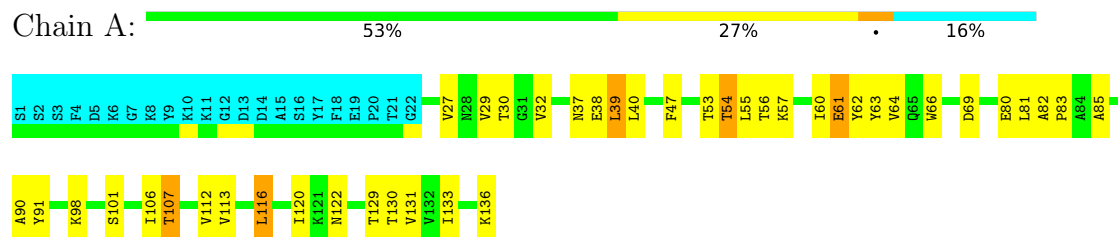
4.2.19 Score per residue for model 19

- Molecule 1: Staphylokinase



4.2.20 Score per residue for model 20

- Molecule 1: Staphylokinase



5 Refinement protocol and experimental data overview

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

Of the 20 calculated structures, 20 were deposited, based on the following criterion: *all calculated structures submitted*.

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

Software name	Classification	Version
ARTINA	structure calculation	
CYANA	structure calculation	

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

Chemical shift file(s)	working_cs.cif
Number of chemical shift lists	1
Total number of shifts	1715
Number of shifts mapped to atoms	1715
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	94%

6 Model quality ⓘ

6.1 Standard geometry ⓘ

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

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no planarity outliers.

6.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	908	916	916	22±4
All	All	18160	18320	18320	440

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:39:LEU:HD11	1:A:133:ILE:HD11	0.91	1.42	7	15
1:A:55:LEU:HD21	1:A:113:VAL:HG23	0.82	1.49	17	2
1:A:54:THR:HG23	1:A:112:VAL:HG22	0.81	1.53	13	14
1:A:29:VAL:HG11	1:A:64:VAL:HG21	0.71	1.63	9	9
1:A:29:VAL:HG11	1:A:64:VAL:HG11	0.69	1.64	20	3
1:A:60:ILE:HD11	1:A:81:LEU:HD22	0.69	1.65	18	5
1:A:45:VAL:HG21	1:A:67:ALA:HB1	0.69	1.65	3	2
1:A:91:TYR:CD2	1:A:116:LEU:HD22	0.69	2.23	17	3
1:A:120:ILE:HD12	1:A:122:ASN:O	0.68	1.89	20	20
1:A:53:THR:C	1:A:112:VAL:HG23	0.67	2.15	3	6
1:A:55:LEU:HD23	1:A:113:VAL:HG23	0.67	1.66	20	7
1:A:60:ILE:HD12	1:A:81:LEU:HD13	0.66	1.66	8	1
1:A:53:THR:HG23	1:A:55:LEU:HD21	0.66	1.68	20	1
1:A:55:LEU:CD2	1:A:113:VAL:HG23	0.65	2.21	7	7

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:60:ILE:HD12	1:A:81:LEU:HD22	0.65	1.66	14	2
1:A:64:VAL:HG21	1:A:81:LEU:HD21	0.65	1.68	8	1
1:A:68:LEU:HD22	1:A:78:VAL:HG12	0.64	1.69	12	1
1:A:57:LYS:HD3	1:A:81:LEU:HD21	0.64	1.70	9	1
1:A:54:THR:HG23	1:A:112:VAL:CG2	0.62	2.25	5	9
1:A:29:VAL:HG21	1:A:68:LEU:HD11	0.62	1.70	12	1
1:A:49:ILE:HG21	1:A:63:TYR:OH	0.61	1.95	13	2
1:A:26:MET:HE3	1:A:44:TYR:HB3	0.61	1.72	1	1
1:A:91:TYR:CE2	1:A:116:LEU:HD22	0.61	2.30	18	2
1:A:115:ASP:O	1:A:116:LEU:HD23	0.61	1.95	18	1
1:A:65:GLN:OE1	1:A:78:VAL:HG12	0.60	1.96	17	4
1:A:60:ILE:HD13	1:A:81:LEU:HD23	0.60	1.73	7	1
1:A:25:LEU:HD13	1:A:26:MET:N	0.60	2.12	13	6
1:A:30:THR:HB	1:A:130:THR:HG22	0.60	1.73	6	19
1:A:29:VAL:HG21	1:A:68:LEU:HD22	0.59	1.74	17	1
1:A:27:VAL:HG22	1:A:63:TYR:OH	0.59	1.98	17	1
1:A:90:ALA:HB2	1:A:101:SER:CB	0.58	2.29	1	19
1:A:57:LYS:CD	1:A:81:LEU:HD21	0.58	2.29	9	1
1:A:39:LEU:HD11	1:A:133:ILE:CD1	0.57	2.29	13	12
1:A:60:ILE:HD13	1:A:81:LEU:HD13	0.57	1.76	17	1
1:A:60:ILE:O	1:A:64:VAL:HG12	0.57	1.99	7	12
1:A:126:ASN:OD1	1:A:128:ILE:HD11	0.57	1.99	6	5
1:A:57:LYS:HG3	1:A:81:LEU:HD21	0.57	1.76	12	4
1:A:29:VAL:HG11	1:A:64:VAL:CG2	0.57	2.29	5	2
1:A:89:VAL:HG11	1:A:125:PHE:CE2	0.57	2.34	17	1
1:A:45:VAL:HG11	1:A:67:ALA:HB1	0.56	1.78	14	1
1:A:65:GLN:OE1	1:A:78:VAL:HG22	0.55	2.00	5	3
1:A:56:THR:O	1:A:60:ILE:HG23	0.54	2.02	16	12
1:A:81:LEU:HA	1:A:131:VAL:HG22	0.54	1.78	16	6
1:A:29:VAL:HG21	1:A:64:VAL:CG2	0.54	2.32	14	6
1:A:80:GLU:C	1:A:131:VAL:HG13	0.54	2.28	3	10
1:A:26:MET:HE3	1:A:44:TYR:CB	0.53	2.33	1	3
1:A:37:ASN:O	1:A:39:LEU:HD23	0.53	2.04	8	9
1:A:29:VAL:HG11	1:A:64:VAL:HG13	0.53	1.79	17	2
1:A:115:ASP:C	1:A:116:LEU:HD23	0.52	2.29	18	1
1:A:81:LEU:HD11	1:A:106:ILE:HD11	0.52	1.80	15	1
1:A:53:THR:HG23	1:A:55:LEU:CD2	0.52	2.34	20	3
1:A:42:PRO:CB	1:A:71:THR:HG21	0.52	2.35	16	3
1:A:33:ASP:OD2	1:A:39:LEU:HD22	0.52	2.05	6	1
1:A:28:ASN:OD1	1:A:128:ILE:HG23	0.52	2.05	15	2
1:A:29:VAL:HG21	1:A:68:LEU:CD2	0.51	2.35	8	2

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:68:LEU:HD22	1:A:78:VAL:CG1	0.51	2.35	12	3
1:A:64:VAL:HG12	1:A:68:LEU:HD23	0.51	1.83	1	3
1:A:25:LEU:HD12	1:A:26:MET:N	0.50	2.21	17	1
1:A:42:PRO:HB3	1:A:71:THR:HG21	0.50	1.83	17	3
1:A:57:LYS:HE3	1:A:107:THR:HG22	0.50	1.84	9	5
1:A:79:VAL:HG12	1:A:80:GLU:OE2	0.50	2.06	19	1
1:A:55:LEU:HD12	1:A:113:VAL:CG2	0.49	2.37	16	2
1:A:90:ALA:HB2	1:A:101:SER:HB2	0.49	1.83	3	8
1:A:32:VAL:HG12	1:A:38:GLU:HA	0.49	1.83	20	4
1:A:57:LYS:CG	1:A:81:LEU:HD21	0.49	2.38	12	1
1:A:29:VAL:HG21	1:A:64:VAL:HG21	0.49	1.83	14	1
1:A:85:ALA:HB2	1:A:129:THR:OG1	0.49	2.08	7	12
1:A:90:ALA:HB2	1:A:101:SER:HB3	0.48	1.83	1	3
1:A:79:VAL:HG22	1:A:134:GLU:CD	0.48	2.32	7	1
1:A:60:ILE:CD1	1:A:81:LEU:HD22	0.48	2.38	13	2
1:A:29:VAL:HG21	1:A:64:VAL:CG1	0.48	2.38	1	2
1:A:56:THR:HG22	1:A:110:GLY:HA3	0.48	1.86	2	1
1:A:60:ILE:HD13	1:A:106:ILE:HD11	0.48	1.86	8	1
1:A:26:MET:HE3	1:A:44:TYR:HB2	0.48	1.84	19	2
1:A:29:VAL:HG11	1:A:64:VAL:CG1	0.48	2.39	8	2
1:A:57:LYS:HE2	1:A:107:THR:HG22	0.47	1.85	8	1
1:A:60:ILE:O	1:A:64:VAL:HG23	0.47	2.09	20	3
1:A:26:MET:HE3	1:A:44:TYR:CD1	0.47	2.45	17	2
1:A:127:LEU:C	1:A:127:LEU:HD13	0.47	2.34	18	3
1:A:106:ILE:O	1:A:107:THR:HG23	0.46	2.10	12	15
1:A:39:LEU:CD1	1:A:133:ILE:HD11	0.46	2.30	17	3
1:A:29:VAL:CG1	1:A:64:VAL:HG21	0.46	2.38	9	1
1:A:25:LEU:HD13	1:A:25:LEU:C	0.46	2.36	2	6
1:A:91:TYR:HB3	1:A:116:LEU:HD23	0.46	1.87	6	2
1:A:80:GLU:O	1:A:131:VAL:HG13	0.46	2.10	9	4
1:A:60:ILE:HD13	1:A:81:LEU:CD1	0.45	2.40	17	1
1:A:62:TYR:CD1	1:A:62:TYR:C	0.45	2.95	17	12
1:A:62:TYR:C	1:A:62:TYR:CD1	0.45	2.92	5	1
1:A:47:PHE:CZ	1:A:67:ALA:HB2	0.45	2.47	9	1
1:A:33:ASP:CG	1:A:39:LEU:HD22	0.45	2.37	6	1
1:A:60:ILE:HD13	1:A:81:LEU:CD2	0.45	2.41	7	1
1:A:29:VAL:CG1	1:A:64:VAL:HG11	0.45	2.40	20	1
1:A:127:LEU:HD13	1:A:127:LEU:C	0.44	2.37	4	1
1:A:68:LEU:CD1	1:A:78:VAL:HG12	0.44	2.42	7	3
1:A:81:LEU:HD21	1:A:106:ILE:HD11	0.44	1.90	7	1
1:A:26:MET:HE1	1:A:126:ASN:ND2	0.44	2.28	7	1

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:81:LEU:HA	1:A:131:VAL:HG13	0.43	1.89	11	3
1:A:89:VAL:HG11	1:A:125:PHE:CD2	0.43	2.48	17	1
1:A:60:ILE:HD11	1:A:81:LEU:CD2	0.43	2.41	18	1
1:A:60:ILE:HD12	1:A:61:GLU:N	0.43	2.29	20	8
1:A:65:GLN:NE2	1:A:78:VAL:HG13	0.43	2.28	12	2
1:A:81:LEU:CD1	1:A:106:ILE:HD11	0.43	2.43	15	1
1:A:82:ALA:HB1	1:A:83:PRO:HD2	0.43	1.90	7	7
1:A:81:LEU:H	1:A:81:LEU:HD22	0.43	1.74	4	1
1:A:90:ALA:HB2	1:A:101:SER:OG	0.43	2.14	10	1
1:A:81:LEU:CB	1:A:131:VAL:HG22	0.43	2.44	11	1
1:A:68:LEU:HD22	1:A:78:VAL:HG13	0.42	1.90	11	1
1:A:127:LEU:HD13	1:A:127:LEU:O	0.42	2.14	4	1
1:A:55:LEU:HD22	1:A:55:LEU:N	0.42	2.30	20	4
1:A:29:VAL:HG21	1:A:68:LEU:HD21	0.42	1.90	19	1
1:A:53:THR:HG23	1:A:55:LEU:HD11	0.42	1.91	7	1
1:A:68:LEU:O	1:A:72:ALA:HB3	0.41	2.15	17	2
1:A:64:VAL:HG22	1:A:68:LEU:HD13	0.41	1.92	12	1
1:A:60:ILE:HG12	1:A:106:ILE:HD13	0.41	1.91	17	1
1:A:55:LEU:N	1:A:55:LEU:HD22	0.41	2.30	19	3
1:A:27:VAL:HG21	1:A:47:PHE:CE1	0.41	2.50	20	1
1:A:78:VAL:CG2	1:A:131:VAL:HG11	0.41	2.45	10	1
1:A:29:VAL:CG2	1:A:68:LEU:HD11	0.41	2.42	12	1
1:A:86:LYS:O	1:A:127:LEU:HD13	0.41	2.16	2	1
1:A:68:LEU:CD2	1:A:78:VAL:HG12	0.41	2.42	12	1
1:A:25:LEU:CD1	1:A:55:LEU:HD11	0.41	2.46	12	1
1:A:91:TYR:CD2	1:A:116:LEU:HD23	0.40	2.51	15	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	113/136 (83%)	104±1 (92±1%)	9±1 (8±1%)	0±0 (0±0%)	49	83
All	All	2260/2720 (83%)	2077 (92%)	180 (8%)	3 (0%)	49	83

All 3 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	43	HIS	1
1	A	72	ALA	1
1	A	73	TYR	1

6.3.2 Protein sidechains [i](#)

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	99/117 (85%)	85±2 (86±2%)	14±2 (14±2%)	5	44
All	All	1980/2340 (85%)	1696 (86%)	284 (14%)	5	44

All 48 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	37	ASN	20
1	A	40	LEU	20
1	A	54	THR	20
1	A	107	THR	20
1	A	94	LYS	19
1	A	39	LEU	17
1	A	63	TYR	13
1	A	74	ARG	12
1	A	61	GLU	11
1	A	127	LEU	11
1	A	102	LYS	9
1	A	126	ASN	8
1	A	136	LYS	8
1	A	33	ASP	7
1	A	71	THR	6
1	A	98	LYS	6
1	A	116	LEU	6
1	A	130	THR	5
1	A	121	LYS	4
1	A	135	ARG	4
1	A	81	LEU	4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Models (Total)
1	A	62	TYR	4
1	A	86	LYS	4
1	A	66	TRP	4
1	A	26	MET	3
1	A	50	LYS	3
1	A	59	LYS	3
1	A	115	ASP	3
1	A	103	SER	3
1	A	46	GLU	2
1	A	68	LEU	2
1	A	41	SER	2
1	A	122	ASN	2
1	A	55	LEU	2
1	A	57	LYS	2
1	A	69	ASP	2
1	A	101	SER	2
1	A	93	ASP	1
1	A	100	GLU	1
1	A	77	ARG	1
1	A	133	ILE	1
1	A	34	SER	1
1	A	97	LYS	1
1	A	28	ASN	1
1	A	99	ASP	1
1	A	49	ILE	1
1	A	53	THR	1
1	A	117	SER	1

6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

6.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.6 Ligand geometry

There are no ligands in this entry.

6.7 Other polymers

There are no such molecules in this entry.

6.8 Polymer linkage issues

There are no chain breaks in this entry.

7 Chemical shift validation [i](#)

The completeness of assignment taking into account all chemical shift lists is 94% for the well-defined parts and 93% for the entire structure.

7.1 Chemical shift list 1

File name: `working_cs.cif`

Chemical shift list name: `starch_output`

7.1.1 Bookkeeping [i](#)

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	1715
Number of shifts mapped to atoms	1715
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	2

7.1.2 Chemical shift referencing [i](#)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	136	2.80 ± 0.16	Should be applied
$^{13}\text{C}_\beta$	128	2.70 ± 0.19	Should be applied
$^{13}\text{C}'$	126	3.02 ± 0.14	Should be applied
^{15}N	126	-0.59 ± 0.29	Should be applied

7.1.3 Completeness of resonance assignments [i](#)

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 94%, i.e. 1474 atoms were assigned a chemical shift out of a possible 1575. 0 out of 20 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	551/559 (99%)	225/225 (100%)	220/228 (96%)	106/106 (100%)
Sidechain	821/877 (94%)	561/573 (98%)	254/278 (91%)	6/26 (23%)

Continued on next page...

Continued from previous page...

	Total	¹H	¹³C	¹⁵N
Aromatic	102/139 (73%)	63/67 (94%)	38/69 (55%)	1/3 (33%)
Overall	1474/1575 (94%)	849/865 (98%)	512/575 (89%)	113/135 (84%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 93%, i.e. 1715 atoms were assigned a chemical shift out of a possible 1838. 0 out of 20 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Backbone	658/670 (98%)	270/271 (100%)	262/272 (96%)	126/127 (99%)
Sidechain	927/991 (94%)	632/644 (98%)	289/317 (91%)	6/30 (20%)
Aromatic	130/177 (73%)	81/85 (95%)	48/89 (54%)	1/3 (33%)
Overall	1715/1838 (93%)	983/1000 (98%)	599/678 (88%)	133/160 (83%)

7.1.4 Statistically unusual chemical shifts ⓘ

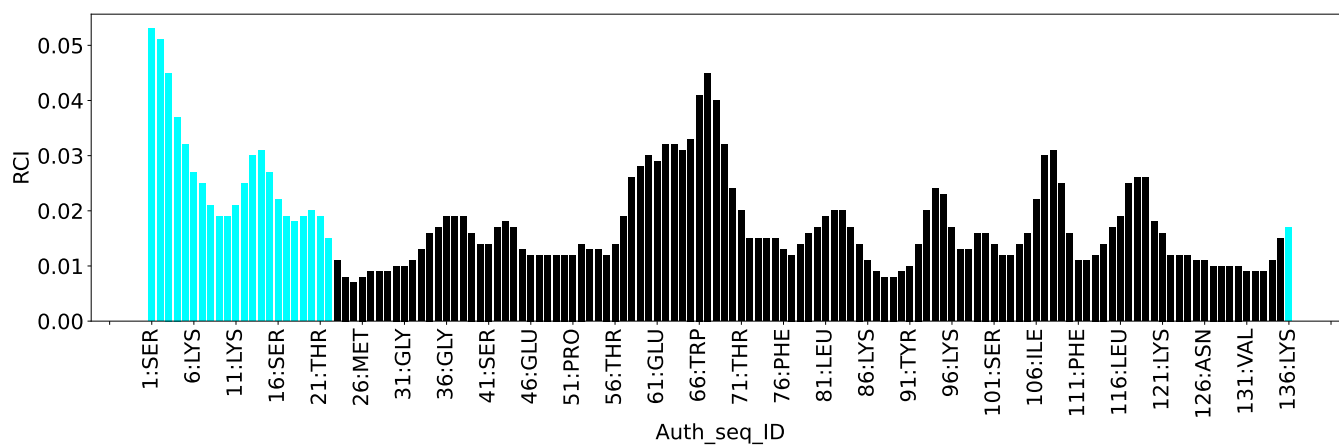
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	102	LYS	HE2	1.55	1.95 – 3.88	-7.1
1	A	129	THR	CG2	15.50	16.06 – 27.03	-5.5

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	1716
Intra-residue ($ i-j =0$)	432
Sequential ($ i-j =1$)	582
Medium range ($ i-j >1$ and $ i-j <5$)	232
Long range ($ i-j \geq 5$)	470
Inter-chain	0
Hydrogen bond restraints	0
Disulfide bond restraints	0
Total dihedral-angle restraints	0
Number of unmapped restraints	0
Number of restraints per residue	12.6
Number of long range restraints per residue ¹	3.5

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)	5.0	0.2
0.2-0.5 (Medium)	3.0	0.46
>0.5 (Large)	3.8	3.05

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 ⓘ

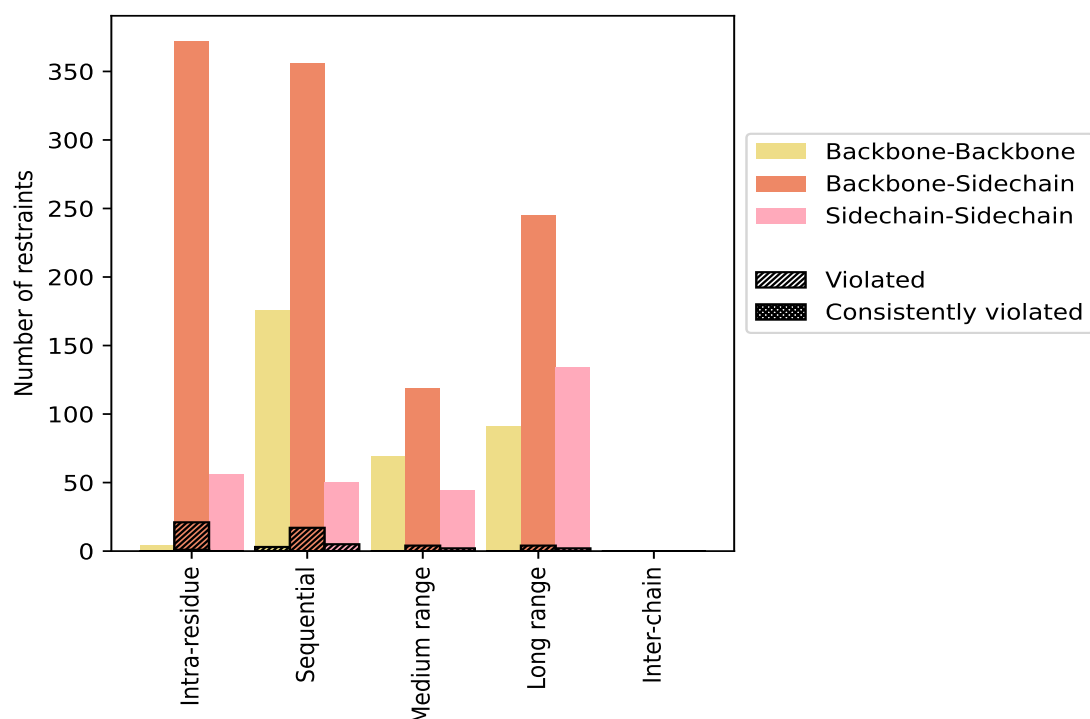
9.1 Summary of distance violations ⓘ

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)	432	25.2	21	4.9	1.2	1	0.2	0.1
Backbone-Backbone	4	0.2	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	372	21.7	21	5.6	1.2	1	0.3	0.1
Sidechain-Sidechain	56	3.3	0	0.0	0.0	0	0.0	0.0
Sequential (i-j =1)	582	33.9	25	4.3	1.5	0	0.0	0.0
Backbone-Backbone	176	10.3	3	1.7	0.2	0	0.0	0.0
Backbone-Sidechain	356	20.7	17	4.8	1.0	0	0.0	0.0
Sidechain-Sidechain	50	2.9	5	10.0	0.3	0	0.0	0.0
Medium range (i-j >1 & i-j <5)	232	13.5	6	2.6	0.3	0	0.0	0.0
Backbone-Backbone	69	4.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	119	6.9	4	3.4	0.2	0	0.0	0.0
Sidechain-Sidechain	44	2.6	2	4.5	0.1	0	0.0	0.0
Long range (i-j ≥5)	470	27.4	6	1.3	0.3	0	0.0	0.0
Backbone-Backbone	91	5.3	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	245	14.3	4	1.6	0.2	0	0.0	0.0
Sidechain-Sidechain	134	7.8	2	1.5	0.1	0	0.0	0.0
Inter-chain	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Hydrogen bond	0	0.0	0	0.0	0.0	0	0.0	0.0
Disulfide bond	0	0.0	0	0.0	0.0	0	0.0	0.0
Total	1716	100.0	58	3.4	3.4	1	0.1	0.1
Backbone-Backbone	340	19.8	3	0.9	0.2	0	0.0	0.0
Backbone-Sidechain	1092	63.6	46	4.2	2.7	1	0.1	0.1
Sidechain-Sidechain	284	16.6	9	3.2	0.5	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	1	2	1	0	0	4	0.16	0.21	0.05	0.16
2	8	7	1	0	0	16	0.32	1.28	0.34	0.16
3	4	2	1	3	0	10	0.86	2.7	0.79	0.59
4	3	2	1	2	0	8	0.43	1.18	0.41	0.24
5	2	2	0	5	0	9	0.89	2.94	0.86	0.69
6	3	2	0	1	0	6	0.42	1.41	0.45	0.26
7	9	2	1	3	0	15	0.74	3.01	0.76	0.41
8	6	2	0	2	0	10	0.9	2.35	0.67	0.74
9	6	4	0	0	0	10	0.41	1.34	0.47	0.14
10	8	2	0	0	0	10	0.43	1.09	0.34	0.28

Continued on next page...

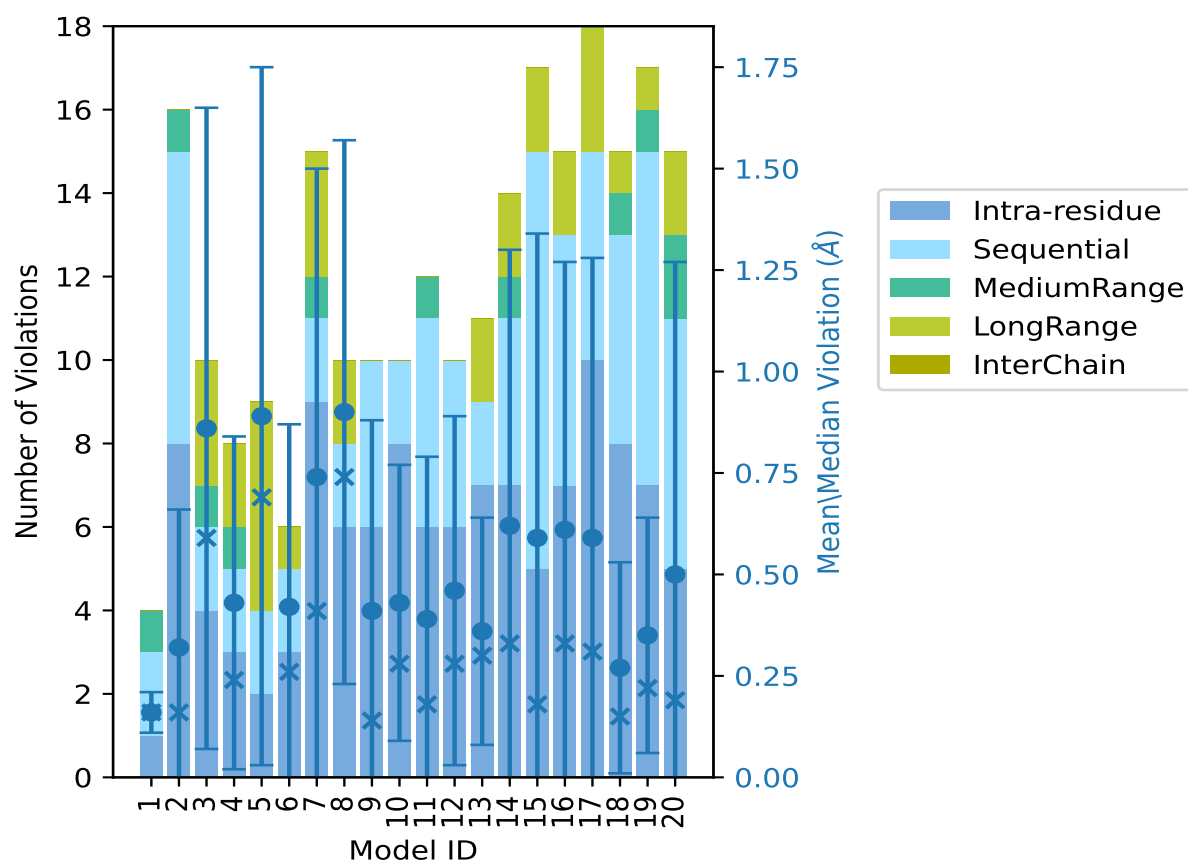
Continued from previous page...

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	6	5	1	0	0	12	0.39	1.44	0.4	0.18
12	6	4	0	0	0	10	0.46	1.43	0.43	0.28
13	7	2	0	2	0	11	0.36	1.11	0.28	0.3
14	7	4	1	2	0	14	0.62	2.62	0.68	0.33
15	5	10	0	2	0	17	0.59	2.88	0.75	0.18
16	7	6	0	2	0	15	0.61	2.59	0.66	0.33
17	10	5	0	3	0	18	0.59	2.96	0.69	0.31
18	8	5	1	1	0	15	0.27	1.1	0.26	0.15
19	7	8	1	1	0	17	0.35	1.08	0.29	0.22
20	5	6	2	2	0	15	0.5	3.05	0.77	0.19

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

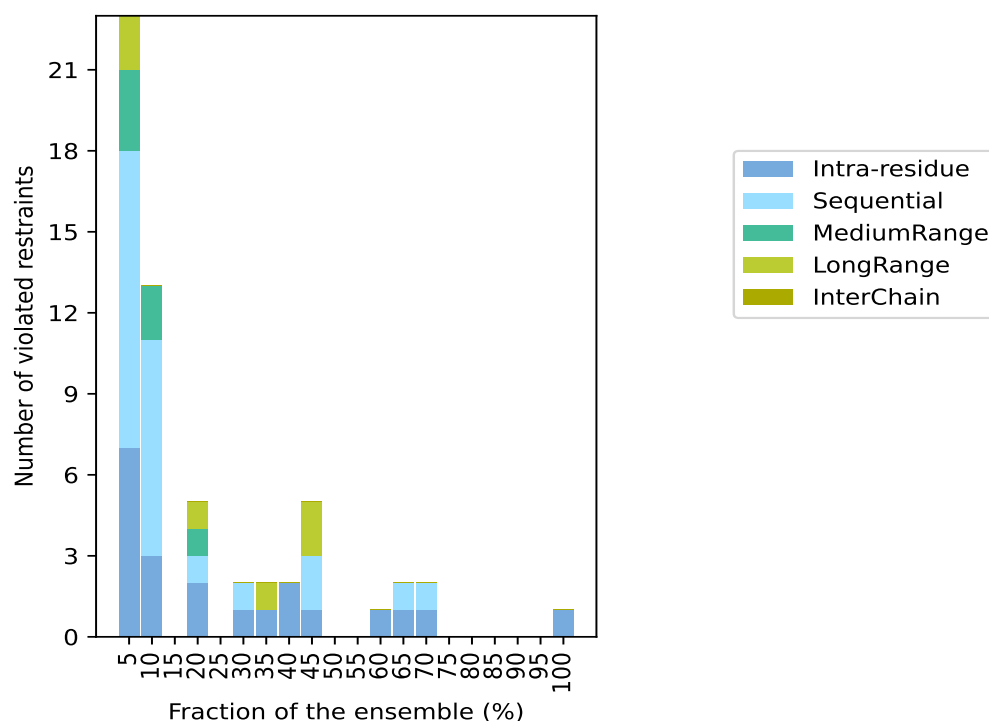
Violation analysis may find that some restraints are violated in few models and some are violated in most of models. The following table provides this information as number of violated restraints for a given fraction of the ensemble. In total, 1658(IR:411, SQ:557, MR:226, LR:464, IC:0) restraints are 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	%
7	11	3	2	0	23	1	5.0
3	8	2	0	0	13	2	10.0
0	0	0	0	0	0	3	15.0
2	1	1	1	0	5	4	20.0
0	0	0	0	0	0	5	25.0
1	1	0	0	0	2	6	30.0
1	0	0	1	0	2	7	35.0
2	0	0	0	0	2	8	40.0
1	2	0	2	0	5	9	45.0
0	0	0	0	0	0	10	50.0
0	0	0	0	0	0	11	55.0
1	0	0	0	0	1	12	60.0
1	1	0	0	0	2	13	65.0
1	1	0	0	0	2	14	70.0
0	0	0	0	0	0	15	75.0
0	0	0	0	0	0	16	80.0
0	0	0	0	0	0	17	85.0
0	0	0	0	0	0	18	90.0
0	0	0	0	0	0	19	95.0
1	0	0	0	0	1	20	100.0

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

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

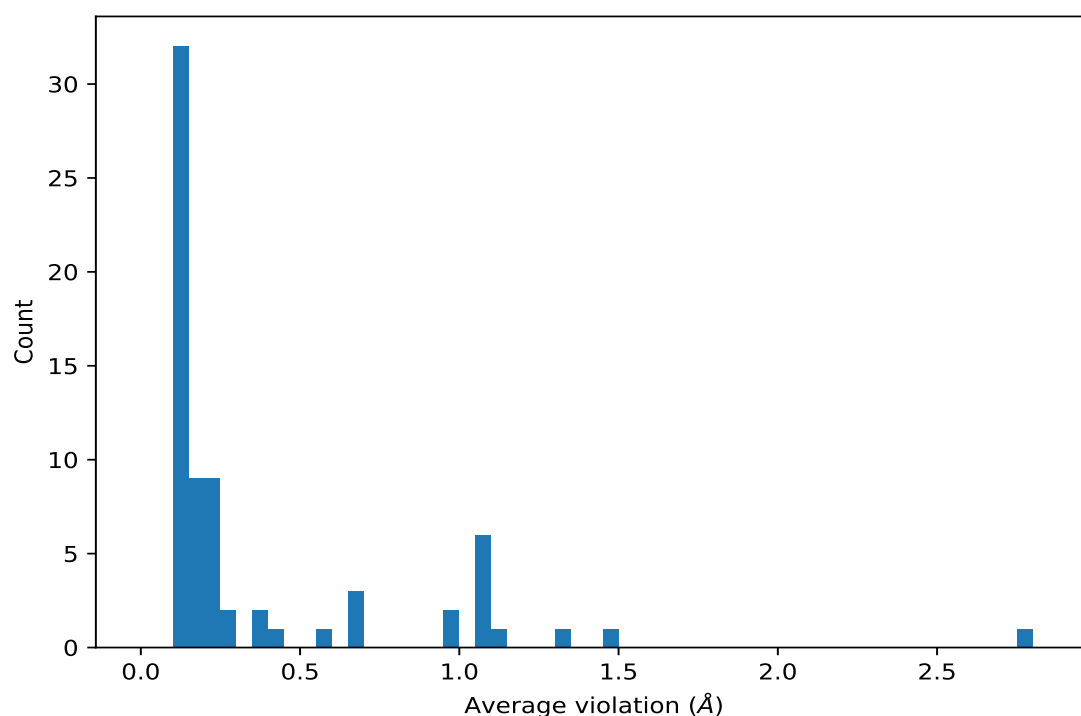
9.3.1 Bar graph : Distance violation statistics for the ensemble [i](#)



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

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

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



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

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

Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,225)	1:74:A:ARG:HA	1:74:A:ARG:HE	20	0.2	0.04	0.2
(1,1126)	1:9:A:TYR:HD2	1:10:A:LYS:H	14	1.1	0.21	1.01
(1,159)	1:9:A:TYR:HA	1:9:A:TYR:HD2	14	0.6	0.02	0.61
(1,1001)	1:9:A:TYR:H	1:9:A:TYR:HD2	13	0.39	0.08	0.41
(1,377)	1:119:A:HIS:H	1:120:A:ILE:HB	13	0.12	0.01	0.11
(1,998)	1:9:A:TYR:H	1:9:A:TYR:HE2	12	0.3	0.0	0.3
(1,1149)	1:27:A:VAL:H	1:44:A:TYR:HD2	9	2.79	0.22	2.88
(1,1169)	1:44:A:TYR:HD2	1:45:A:VAL:H	9	1.47	0.08	1.46
(1,1219)	1:18:A:PHE:H	1:18:A:PHE:HE1	9	1.3	0.16	1.34
(1,1411)	1:26:A:MET:HG2	1:44:A:TYR:HD2	9	0.97	0.19	0.94
(1,1411)	1:26:A:MET:HG3	1:44:A:TYR:HD2	9	0.97	0.19	0.94
(1,1537)	1:61:A:GLU:HG2	1:62:A:TYR:H	9	0.11	0.01	0.12
(1,1537)	1:61:A:GLU:HG3	1:62:A:TYR:H	9	0.11	0.01	0.12
(1,806)	1:44:A:TYR:H	1:44:A:TYR:HD1	8	0.42	0.16	0.39
(1,669)	1:21:A:THR:H	1:21:A:THR:HB	8	0.19	0.05	0.2
(1,284)	1:47:A:PHE:HE2	1:67:A:ALA:HB1	7	0.69	0.23	0.65

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,284)	1:47:A:PHE:HE2	1:67:A:ALA:HB2	7	0.69	0.23	0.65
(1,284)	1:47:A:PHE:HE2	1:67:A:ALA:HB3	7	0.69	0.23	0.65
(1,614)	1:55:A:LEU:H	1:55:A:LEU:HG	7	0.12	0.03	0.11
(1,1109)	1:25:A:LEU:H	1:25:A:LEU:HG	6	0.13	0.01	0.14
(1,1258)	1:115:A:ASP:H	1:116:A:LEU:HB2	6	0.13	0.02	0.13
(1,1258)	1:115:A:ASP:H	1:116:A:LEU:HB3	6	0.13	0.02	0.13
(1,1484)	1:45:A:VAL:HG11	1:47:A:PHE:HE2	4	1.05	0.56	1.27
(1,1484)	1:45:A:VAL:HG12	1:47:A:PHE:HE2	4	1.05	0.56	1.27
(1,1484)	1:45:A:VAL:HG13	1:47:A:PHE:HE2	4	1.05	0.56	1.27
(1,1484)	1:45:A:VAL:HG21	1:47:A:PHE:HE2	4	1.05	0.56	1.27
(1,1484)	1:45:A:VAL:HG22	1:47:A:PHE:HE2	4	1.05	0.56	1.27
(1,1484)	1:45:A:VAL:HG23	1:47:A:PHE:HE2	4	1.05	0.56	1.27
(1,920)	1:47:A:PHE:HE2	1:67:A:ALA:H	4	0.39	0.19	0.34
(1,559)	1:78:A:VAL:H	1:78:A:VAL:HG21	4	0.2	0.01	0.2
(1,559)	1:78:A:VAL:H	1:78:A:VAL:HG22	4	0.2	0.01	0.2
(1,559)	1:78:A:VAL:H	1:78:A:VAL:HG23	4	0.2	0.01	0.2
(1,805)	1:66:A:TRP:HB2	1:67:A:ALA:H	4	0.17	0.06	0.15
(1,909)	1:66:A:TRP:H	1:66:A:TRP:HD1	4	0.16	0.03	0.16
(1,656)	1:72:A:ALA:HA	1:73:A:TYR:H	2	0.29	0.0	0.29
(1,902)	1:8:A:LYS:HB2	1:9:A:TYR:H	2	0.22	0.08	0.22
(1,902)	1:8:A:LYS:HB3	1:9:A:TYR:H	2	0.22	0.08	0.22
(1,674)	1:108:A:ALA:HB1	1:110:A:GLY:H	2	0.2	0.0	0.2
(1,674)	1:108:A:ALA:HB2	1:110:A:GLY:H	2	0.2	0.0	0.2
(1,674)	1:108:A:ALA:HB3	1:110:A:GLY:H	2	0.2	0.0	0.2
(1,1237)	1:8:A:LYS:H	1:9:A:TYR:HA	2	0.18	0.08	0.18
(1,932)	1:11:A:LYS:HB2	1:12:A:GLY:H	2	0.18	0.0	0.18
(1,1524)	1:58:A:GLU:H	1:58:A:GLU:HG2	2	0.17	0.0	0.17
(1,1524)	1:58:A:GLU:H	1:58:A:GLU:HG3	2	0.17	0.0	0.17
(1,1579)	1:74:A:ARG:HG2	1:76:A:PHE:H	2	0.16	0.02	0.16
(1,1579)	1:74:A:ARG:HG3	1:76:A:PHE:H	2	0.16	0.02	0.16
(1,1642)	1:98:A:LYS:HA	1:98:A:LYS:HD2	2	0.15	0.02	0.15
(1,1642)	1:98:A:LYS:HA	1:98:A:LYS:HD3	2	0.15	0.02	0.15
(1,627)	1:115:A:ASP:H	1:115:A:ASP:HB2	2	0.13	0.03	0.13
(1,1640)	1:97:A:LYS:HB2	1:98:A:LYS:HG2	2	0.13	0.01	0.13
(1,1640)	1:97:A:LYS:HB3	1:98:A:LYS:HG2	2	0.13	0.01	0.13
(1,809)	1:98:A:LYS:HD2	1:99:A:ASP:H	2	0.12	0.02	0.12
(1,1670)	1:112:A:VAL:HG11	1:113:A:VAL:HG11	2	0.12	0.0	0.12
(1,1670)	1:112:A:VAL:HG11	1:113:A:VAL:HG12	2	0.12	0.0	0.12
(1,1670)	1:112:A:VAL:HG11	1:113:A:VAL:HG13	2	0.12	0.0	0.12
(1,1670)	1:112:A:VAL:HG12	1:113:A:VAL:HG11	2	0.12	0.0	0.12
(1,1670)	1:112:A:VAL:HG12	1:113:A:VAL:HG12	2	0.12	0.0	0.12
(1,1670)	1:112:A:VAL:HG12	1:113:A:VAL:HG13	2	0.12	0.0	0.12

Continued on next page...

Continued from previous page...

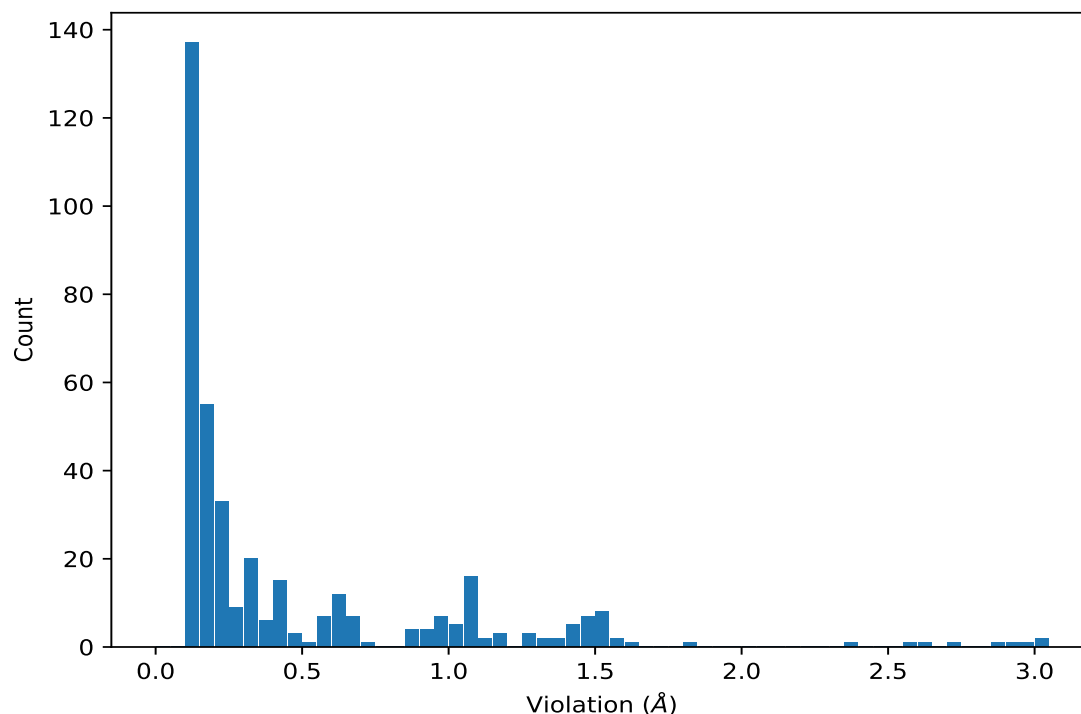
Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,1670)	1:112:A:VAL:HG13	1:113:A:VAL:HG11	2	0.12	0.0	0.12
(1,1670)	1:112:A:VAL:HG13	1:113:A:VAL:HG12	2	0.12	0.0	0.12
(1,1670)	1:112:A:VAL:HG13	1:113:A:VAL:HG13	2	0.12	0.0	0.12
(1,1670)	1:112:A:VAL:HG21	1:113:A:VAL:HG11	2	0.12	0.0	0.12
(1,1670)	1:112:A:VAL:HG21	1:113:A:VAL:HG12	2	0.12	0.0	0.12
(1,1670)	1:112:A:VAL:HG21	1:113:A:VAL:HG13	2	0.12	0.0	0.12
(1,1670)	1:112:A:VAL:HG22	1:113:A:VAL:HG11	2	0.12	0.0	0.12
(1,1670)	1:112:A:VAL:HG22	1:113:A:VAL:HG12	2	0.12	0.0	0.12
(1,1670)	1:112:A:VAL:HG22	1:113:A:VAL:HG13	2	0.12	0.0	0.12
(1,1670)	1:112:A:VAL:HG23	1:113:A:VAL:HG11	2	0.12	0.0	0.12
(1,1670)	1:112:A:VAL:HG23	1:113:A:VAL:HG12	2	0.12	0.0	0.12
(1,1670)	1:112:A:VAL:HG23	1:113:A:VAL:HG13	2	0.12	0.0	0.12
(1,906)	1:102:A:LYS:HG2	1:103:A:SER: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

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)
(1,1149)	1:27:A:VAL:H	1:44:A:TYR:HD2	20	3.05
(1,1149)	1:27:A:VAL:H	1:44:A:TYR:HD2	7	3.01
(1,1149)	1:27:A:VAL:H	1:44:A:TYR:HD2	17	2.96
(1,1149)	1:27:A:VAL:H	1:44:A:TYR:HD2	5	2.94
(1,1149)	1:27:A:VAL:H	1:44:A:TYR:HD2	15	2.88
(1,1149)	1:27:A:VAL:H	1:44:A:TYR:HD2	3	2.7
(1,1149)	1:27:A:VAL:H	1:44:A:TYR:HD2	14	2.62
(1,1149)	1:27:A:VAL:H	1:44:A:TYR:HD2	16	2.59
(1,1149)	1:27:A:VAL:H	1:44:A:TYR:HD2	8	2.35
(1,1126)	1:9:A:TYR:HD2	1:10:A:LYS:H	15	1.8
(1,1169)	1:44:A:TYR:HD2	1:45:A:VAL:H	5	1.6
(1,1169)	1:44:A:TYR:HD2	1:45:A:VAL:H	7	1.57
(1,1169)	1:44:A:TYR:HD2	1:45:A:VAL:H	17	1.55
(1,1484)	1:45:A:VAL:HG11	1:47:A:PHE:HE2	7	1.52
(1,1484)	1:45:A:VAL:HG12	1:47:A:PHE:HE2	7	1.52
(1,1484)	1:45:A:VAL:HG13	1:47:A:PHE:HE2	7	1.52
(1,1484)	1:45:A:VAL:HG21	1:47:A:PHE:HE2	7	1.52
(1,1484)	1:45:A:VAL:HG22	1:47:A:PHE:HE2	7	1.52
(1,1484)	1:45:A:VAL:HG23	1:47:A:PHE:HE2	7	1.52
(1,1219)	1:18:A:PHE:H	1:18:A:PHE:HE1	8	1.52
(1,1169)	1:44:A:TYR:HD2	1:45:A:VAL:H	8	1.5
(1,1484)	1:45:A:VAL:HG11	1:47:A:PHE:HE2	3	1.46
(1,1484)	1:45:A:VAL:HG12	1:47:A:PHE:HE2	3	1.46
(1,1484)	1:45:A:VAL:HG13	1:47:A:PHE:HE2	3	1.46
(1,1484)	1:45:A:VAL:HG21	1:47:A:PHE:HE2	3	1.46
(1,1484)	1:45:A:VAL:HG22	1:47:A:PHE:HE2	3	1.46
(1,1484)	1:45:A:VAL:HG23	1:47:A:PHE:HE2	3	1.46
(1,1169)	1:44:A:TYR:HD2	1:45:A:VAL:H	16	1.46
(1,1219)	1:18:A:PHE:H	1:18:A:PHE:HE1	11	1.44
(1,1169)	1:44:A:TYR:HD2	1:45:A:VAL:H	20	1.44
(1,1219)	1:18:A:PHE:H	1:18:A:PHE:HE1	12	1.43
(1,1219)	1:18:A:PHE:H	1:18:A:PHE:HE1	6	1.41
(1,1169)	1:44:A:TYR:HD2	1:45:A:VAL:H	15	1.41
(1,1169)	1:44:A:TYR:HD2	1:45:A:VAL:H	3	1.36
(1,1169)	1:44:A:TYR:HD2	1:45:A:VAL:H	14	1.36
(1,1219)	1:18:A:PHE:H	1:18:A:PHE:HE1	9	1.34
(1,1126)	1:9:A:TYR:HD2	1:10:A:LYS:H	9	1.31

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1219)	1:18:A:PHE:H	1:18:A:PHE:HE1	2	1.28
(1,1411)	1:26:A:MET:HG2	1:44:A:TYR:HD2	3	1.26
(1,1411)	1:26:A:MET:HG3	1:44:A:TYR:HD2	3	1.26
(1,1219)	1:18:A:PHE:H	1:18:A:PHE:HE1	4	1.18
(1,1411)	1:26:A:MET:HG2	1:44:A:TYR:HD2	16	1.17
(1,1411)	1:26:A:MET:HG3	1:44:A:TYR:HD2	16	1.17
(1,1126)	1:9:A:TYR:HD2	1:10:A:LYS:H	13	1.11
(1,1126)	1:9:A:TYR:HD2	1:10:A:LYS:H	18	1.1
(1,1219)	1:18:A:PHE:H	1:18:A:PHE:HE1	10	1.09
(1,1484)	1:45:A:VAL:HG11	1:47:A:PHE:HE2	19	1.08
(1,1484)	1:45:A:VAL:HG12	1:47:A:PHE:HE2	19	1.08
(1,1484)	1:45:A:VAL:HG13	1:47:A:PHE:HE2	19	1.08
(1,1484)	1:45:A:VAL:HG21	1:47:A:PHE:HE2	19	1.08
(1,1484)	1:45:A:VAL:HG22	1:47:A:PHE:HE2	19	1.08
(1,1484)	1:45:A:VAL:HG23	1:47:A:PHE:HE2	19	1.08
(1,1411)	1:26:A:MET:HG2	1:44:A:TYR:HD2	14	1.08
(1,1411)	1:26:A:MET:HG3	1:44:A:TYR:HD2	14	1.08
(1,1126)	1:9:A:TYR:HD2	1:10:A:LYS:H	17	1.08
(1,284)	1:47:A:PHE:HE2	1:67:A:ALA:HB1	4	1.08
(1,284)	1:47:A:PHE:HE2	1:67:A:ALA:HB2	4	1.08
(1,284)	1:47:A:PHE:HE2	1:67:A:ALA:HB3	4	1.08
(1,1126)	1:9:A:TYR:HD2	1:10:A:LYS:H	12	1.07
(1,1411)	1:26:A:MET:HG2	1:44:A:TYR:HD2	15	1.06
(1,1411)	1:26:A:MET:HG3	1:44:A:TYR:HD2	15	1.06
(1,1219)	1:18:A:PHE:H	1:18:A:PHE:HE1	17	1.01
(1,1126)	1:9:A:TYR:HD2	1:10:A:LYS:H	2	1.01
(1,1126)	1:9:A:TYR:HD2	1:10:A:LYS:H	8	1.01
(1,1126)	1:9:A:TYR:HD2	1:10:A:LYS:H	10	1.01
(1,1126)	1:9:A:TYR:HD2	1:10:A:LYS:H	16	1.0
(1,1126)	1:9:A:TYR:HD2	1:10:A:LYS:H	7	0.98
(1,1126)	1:9:A:TYR:HD2	1:10:A:LYS:H	11	0.98
(1,1126)	1:9:A:TYR:HD2	1:10:A:LYS:H	19	0.98
(1,1126)	1:9:A:TYR:HD2	1:10:A:LYS:H	14	0.97
(1,284)	1:47:A:PHE:HE2	1:67:A:ALA:HB1	5	0.97
(1,284)	1:47:A:PHE:HE2	1:67:A:ALA:HB2	5	0.97
(1,284)	1:47:A:PHE:HE2	1:67:A:ALA:HB3	5	0.97
(1,1411)	1:26:A:MET:HG2	1:44:A:TYR:HD2	5	0.94
(1,1411)	1:26:A:MET:HG3	1:44:A:TYR:HD2	5	0.94
(1,1411)	1:26:A:MET:HG2	1:44:A:TYR:HD2	7	0.9
(1,1411)	1:26:A:MET:HG3	1:44:A:TYR:HD2	7	0.9
(1,1411)	1:26:A:MET:HG2	1:44:A:TYR:HD2	20	0.88
(1,1411)	1:26:A:MET:HG3	1:44:A:TYR:HD2	20	0.88

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1411)	1:26:A:MET:HG2	1:44:A:TYR:HD2	8	0.86
(1,1411)	1:26:A:MET:HG3	1:44:A:TYR:HD2	8	0.86
(1,806)	1:44:A:TYR:H	1:44:A:TYR:HD1	3	0.72
(1,920)	1:47:A:PHE:HE2	1:67:A:ALA:H	5	0.69
(1,284)	1:47:A:PHE:HE2	1:67:A:ALA:HB1	7	0.69
(1,284)	1:47:A:PHE:HE2	1:67:A:ALA:HB2	7	0.69
(1,284)	1:47:A:PHE:HE2	1:67:A:ALA:HB3	7	0.69
(1,284)	1:47:A:PHE:HE2	1:67:A:ALA:HB1	19	0.65
(1,284)	1:47:A:PHE:HE2	1:67:A:ALA:HB2	19	0.65
(1,284)	1:47:A:PHE:HE2	1:67:A:ALA:HB3	19	0.65
(1,159)	1:9:A:TYR:HA	1:9:A:TYR:HD2	2	0.61
(1,159)	1:9:A:TYR:HA	1:9:A:TYR:HD2	7	0.61
(1,159)	1:9:A:TYR:HA	1:9:A:TYR:HD2	8	0.61
(1,159)	1:9:A:TYR:HA	1:9:A:TYR:HD2	10	0.61
(1,159)	1:9:A:TYR:HA	1:9:A:TYR:HD2	11	0.61
(1,159)	1:9:A:TYR:HA	1:9:A:TYR:HD2	13	0.61
(1,159)	1:9:A:TYR:HA	1:9:A:TYR:HD2	14	0.61
(1,159)	1:9:A:TYR:HA	1:9:A:TYR:HD2	16	0.61
(1,159)	1:9:A:TYR:HA	1:9:A:TYR:HD2	17	0.61
(1,159)	1:9:A:TYR:HA	1:9:A:TYR:HD2	18	0.61
(1,159)	1:9:A:TYR:HA	1:9:A:TYR:HD2	19	0.61
(1,159)	1:9:A:TYR:HA	1:9:A:TYR:HD2	12	0.6
(1,1411)	1:26:A:MET:HG2	1:44:A:TYR:HD2	17	0.59
(1,1411)	1:26:A:MET:HG3	1:44:A:TYR:HD2	17	0.59
(1,806)	1:44:A:TYR:H	1:44:A:TYR:HD1	15	0.57
(1,159)	1:9:A:TYR:HA	1:9:A:TYR:HD2	9	0.57
(1,284)	1:47:A:PHE:HE2	1:67:A:ALA:HB1	17	0.56
(1,284)	1:47:A:PHE:HE2	1:67:A:ALA:HB2	17	0.56
(1,284)	1:47:A:PHE:HE2	1:67:A:ALA:HB3	17	0.56
(1,159)	1:9:A:TYR:HA	1:9:A:TYR:HD2	15	0.53
(1,284)	1:47:A:PHE:HE2	1:67:A:ALA:HB1	3	0.46
(1,284)	1:47:A:PHE:HE2	1:67:A:ALA:HB2	3	0.46
(1,284)	1:47:A:PHE:HE2	1:67:A:ALA:HB3	3	0.46
(1,806)	1:44:A:TYR:H	1:44:A:TYR:HD1	20	0.43
(1,1001)	1:9:A:TYR:H	1:9:A:TYR:HD2	11	0.42
(1,284)	1:47:A:PHE:HE2	1:67:A:ALA:HB1	13	0.42
(1,284)	1:47:A:PHE:HE2	1:67:A:ALA:HB2	13	0.42
(1,284)	1:47:A:PHE:HE2	1:67:A:ALA:HB3	13	0.42
(1,1001)	1:9:A:TYR:H	1:9:A:TYR:HD2	2	0.41
(1,1001)	1:9:A:TYR:H	1:9:A:TYR:HD2	7	0.41
(1,1001)	1:9:A:TYR:H	1:9:A:TYR:HD2	8	0.41
(1,1001)	1:9:A:TYR:H	1:9:A:TYR:HD2	10	0.41

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1001)	1:9:A:TYR:H	1:9:A:TYR:HD2	13	0.41
(1,1001)	1:9:A:TYR:H	1:9:A:TYR:HD2	14	0.41
(1,1001)	1:9:A:TYR:H	1:9:A:TYR:HD2	16	0.41
(1,1001)	1:9:A:TYR:H	1:9:A:TYR:HD2	17	0.41
(1,1001)	1:9:A:TYR:H	1:9:A:TYR:HD2	18	0.41
(1,1001)	1:9:A:TYR:H	1:9:A:TYR:HD2	19	0.41
(1,1001)	1:9:A:TYR:H	1:9:A:TYR:HD2	12	0.39
(1,806)	1:44:A:TYR:H	1:44:A:TYR:HD1	5	0.39
(1,806)	1:44:A:TYR:H	1:44:A:TYR:HD1	7	0.39
(1,1528)	1:59:A:LYS:H	1:59:A:LYS:HD2	16	0.38
(1,1528)	1:59:A:LYS:H	1:59:A:LYS:HD3	16	0.38
(1,806)	1:44:A:TYR:H	1:44:A:TYR:HD1	14	0.36
(1,920)	1:47:A:PHE:HE2	1:67:A:ALA:H	4	0.34
(1,920)	1:47:A:PHE:HE2	1:67:A:ALA:H	13	0.34
(1,806)	1:44:A:TYR:H	1:44:A:TYR:HD1	16	0.33
(1,1578)	1:74:A:ARG:HG2	1:75:A:GLU:HB2	17	0.32
(1,1578)	1:74:A:ARG:HG2	1:75:A:GLU:HB3	17	0.32
(1,1578)	1:74:A:ARG:HG3	1:75:A:GLU:HB2	17	0.32
(1,1578)	1:74:A:ARG:HG3	1:75:A:GLU:HB3	17	0.32
(1,998)	1:9:A:TYR:H	1:9:A:TYR:HE2	11	0.31
(1,998)	1:9:A:TYR:H	1:9:A:TYR:HE2	2	0.3
(1,998)	1:9:A:TYR:H	1:9:A:TYR:HE2	7	0.3
(1,998)	1:9:A:TYR:H	1:9:A:TYR:HE2	8	0.3
(1,998)	1:9:A:TYR:H	1:9:A:TYR:HE2	10	0.3
(1,998)	1:9:A:TYR:H	1:9:A:TYR:HE2	13	0.3
(1,998)	1:9:A:TYR:H	1:9:A:TYR:HE2	14	0.3
(1,998)	1:9:A:TYR:H	1:9:A:TYR:HE2	16	0.3
(1,998)	1:9:A:TYR:H	1:9:A:TYR:HE2	17	0.3
(1,998)	1:9:A:TYR:H	1:9:A:TYR:HE2	18	0.3
(1,998)	1:9:A:TYR:H	1:9:A:TYR:HE2	19	0.3
(1,902)	1:8:A:LYS:HB2	1:9:A:TYR:H	6	0.3
(1,902)	1:8:A:LYS:HB3	1:9:A:TYR:H	6	0.3
(1,998)	1:9:A:TYR:H	1:9:A:TYR:HE2	12	0.29
(1,656)	1:72:A:ALA:HA	1:73:A:TYR:H	16	0.29
(1,805)	1:66:A:TRP:HB2	1:67:A:ALA:H	20	0.28
(1,656)	1:72:A:ALA:HA	1:73:A:TYR:H	6	0.28
(1,1237)	1:8:A:LYS:H	1:9:A:TYR:HA	15	0.26
(1,225)	1:74:A:ARG:HA	1:74:A:ARG:HE	5	0.26
(1,225)	1:74:A:ARG:HA	1:74:A:ARG:HE	10	0.26
(1,225)	1:74:A:ARG:HA	1:74:A:ARG:HE	12	0.26
(1,225)	1:74:A:ARG:HA	1:74:A:ARG:HE	8	0.25
(1,669)	1:21:A:THR:H	1:21:A:THR:HB	4	0.24

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,225)	1:74:A:ARG:HA	1:74:A:ARG:HE	6	0.24
(1,1369)	1:18:A:PHE:HB2	1:19:A:GLU:H	19	0.23
(1,1369)	1:18:A:PHE:HB3	1:19:A:GLU:H	19	0.23
(1,669)	1:21:A:THR:H	1:21:A:THR:HB	3	0.23
(1,669)	1:21:A:THR:H	1:21:A:THR:HB	7	0.23
(1,363)	1:3:A:SER:HB2	1:4:A:PHE:HA	19	0.23
(1,363)	1:3:A:SER:HB3	1:4:A:PHE:HA	19	0.23
(1,225)	1:74:A:ARG:HA	1:74:A:ARG:HE	4	0.23
(1,225)	1:74:A:ARG:HA	1:74:A:ARG:HE	15	0.23
(1,773)	1:78:A:VAL:H	1:78:A:VAL:HG11	19	0.22
(1,773)	1:78:A:VAL:H	1:78:A:VAL:HG12	19	0.22
(1,773)	1:78:A:VAL:H	1:78:A:VAL:HG13	19	0.22
(1,225)	1:74:A:ARG:HA	1:74:A:ARG:HE	19	0.22
(1,1575)	1:74:A:ARG:HA	1:74:A:ARG:HD2	17	0.21
(1,1575)	1:74:A:ARG:HA	1:74:A:ARG:HD3	17	0.21
(1,1066)	1:65:A:GLN:HE21	1:66:A:TRP:H	20	0.21
(1,1066)	1:65:A:GLN:HE22	1:66:A:TRP:H	20	0.21
(1,674)	1:108:A:ALA:HB1	1:110:A:GLY:H	2	0.21
(1,674)	1:108:A:ALA:HB2	1:110:A:GLY:H	2	0.21
(1,674)	1:108:A:ALA:HB3	1:110:A:GLY:H	2	0.21
(1,669)	1:21:A:THR:H	1:21:A:THR:HB	18	0.21
(1,225)	1:74:A:ARG:HA	1:74:A:ARG:HE	1	0.21
(1,225)	1:74:A:ARG:HA	1:74:A:ARG:HE	13	0.21
(1,674)	1:108:A:ALA:HB1	1:110:A:GLY:H	1	0.2
(1,674)	1:108:A:ALA:HB2	1:110:A:GLY:H	1	0.2
(1,674)	1:108:A:ALA:HB3	1:110:A:GLY:H	1	0.2
(1,559)	1:78:A:VAL:H	1:78:A:VAL:HG21	10	0.2
(1,559)	1:78:A:VAL:H	1:78:A:VAL:HG22	10	0.2
(1,559)	1:78:A:VAL:H	1:78:A:VAL:HG23	10	0.2
(1,559)	1:78:A:VAL:H	1:78:A:VAL:HG21	14	0.2
(1,559)	1:78:A:VAL:H	1:78:A:VAL:HG22	14	0.2
(1,559)	1:78:A:VAL:H	1:78:A:VAL:HG23	14	0.2
(1,1579)	1:74:A:ARG:HG2	1:76:A:PHE:H	11	0.19
(1,1579)	1:74:A:ARG:HG3	1:76:A:PHE:H	11	0.19
(1,1293)	1:18:A:PHE:HD1	1:19:A:GLU:H	19	0.19
(1,1293)	1:18:A:PHE:HD2	1:19:A:GLU:H	19	0.19
(1,669)	1:21:A:THR:H	1:21:A:THR:HB	20	0.19
(1,559)	1:78:A:VAL:H	1:78:A:VAL:HG21	8	0.19
(1,559)	1:78:A:VAL:H	1:78:A:VAL:HG22	8	0.19
(1,559)	1:78:A:VAL:H	1:78:A:VAL:HG23	8	0.19
(1,559)	1:78:A:VAL:H	1:78:A:VAL:HG21	17	0.19
(1,559)	1:78:A:VAL:H	1:78:A:VAL:HG22	17	0.19

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,559)	1:78:A:VAL:H	1:78:A:VAL:HG23	17	0.19
(1,225)	1:74:A:ARG:HA	1:74:A:ARG:HE	2	0.19
(1,225)	1:74:A:ARG:HA	1:74:A:ARG:HE	16	0.19
(1,225)	1:74:A:ARG:HA	1:74:A:ARG:HE	18	0.19
(1,225)	1:74:A:ARG:HA	1:74:A:ARG:HE	20	0.19
(1,1331)	1:2:A:SER:HB2	1:3:A:SER:HB2	19	0.18
(1,1331)	1:2:A:SER:HB2	1:3:A:SER:HB3	19	0.18
(1,1331)	1:2:A:SER:HB3	1:3:A:SER:HB2	19	0.18
(1,1331)	1:2:A:SER:HB3	1:3:A:SER:HB3	19	0.18
(1,932)	1:11:A:LYS:HB2	1:12:A:GLY:H	11	0.18
(1,920)	1:47:A:PHE:HE2	1:67:A:ALA:H	6	0.18
(1,909)	1:66:A:TRP:H	1:66:A:TRP:HD1	10	0.18
(1,909)	1:66:A:TRP:H	1:66:A:TRP:HD1	12	0.18
(1,614)	1:55:A:LEU:H	1:55:A:LEU:HG	15	0.18
(1,225)	1:74:A:ARG:HA	1:74:A:ARG:HE	3	0.18
(1,225)	1:74:A:ARG:HA	1:74:A:ARG:HE	9	0.18
(1,225)	1:74:A:ARG:HA	1:74:A:ARG:HE	14	0.18
(1,1524)	1:58:A:GLU:H	1:58:A:GLU:HG2	13	0.17
(1,1524)	1:58:A:GLU:H	1:58:A:GLU:HG3	13	0.17
(1,1524)	1:58:A:GLU:H	1:58:A:GLU:HG2	17	0.17
(1,1524)	1:58:A:GLU:H	1:58:A:GLU:HG3	17	0.17
(1,932)	1:11:A:LYS:HB2	1:12:A:GLY:H	15	0.17
(1,1642)	1:98:A:LYS:HA	1:98:A:LYS:HD2	2	0.16
(1,1642)	1:98:A:LYS:HA	1:98:A:LYS:HD3	2	0.16
(1,1547)	1:64:A:VAL:HG11	1:66:A:TRP:H	20	0.16
(1,1547)	1:64:A:VAL:HG12	1:66:A:TRP:H	20	0.16
(1,1547)	1:64:A:VAL:HG13	1:66:A:TRP:H	20	0.16
(1,1547)	1:64:A:VAL:HG21	1:66:A:TRP:H	20	0.16
(1,1547)	1:64:A:VAL:HG22	1:66:A:TRP:H	20	0.16
(1,1547)	1:64:A:VAL:HG23	1:66:A:TRP:H	20	0.16
(1,806)	1:44:A:TYR:H	1:44:A:TYR:HD1	17	0.16
(1,805)	1:66:A:TRP:HB2	1:67:A:ALA:H	12	0.16
(1,669)	1:21:A:THR:H	1:21:A:THR:HB	19	0.16
(1,627)	1:115:A:ASP:H	1:115:A:ASP:HB2	2	0.16
(1,556)	1:8:A:LYS:H	1:8:A:LYS:HB2	9	0.16
(1,556)	1:8:A:LYS:H	1:8:A:LYS:HB3	9	0.16
(1,1258)	1:115:A:ASP:H	1:116:A:LEU:HB2	18	0.15
(1,1258)	1:115:A:ASP:H	1:116:A:LEU:HB3	18	0.15
(1,1150)	1:65:A:GLN:HE21	1:67:A:ALA:H	20	0.15
(1,1150)	1:65:A:GLN:HE22	1:67:A:ALA:H	20	0.15
(1,1109)	1:25:A:LEU:H	1:25:A:LEU:HG	14	0.15
(1,873)	1:27:A:VAL:HB	1:45:A:VAL:H	18	0.15

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,431)	1:9:A:TYR:HA	1:10:A:LYS:H	15	0.15
(1,377)	1:119:A:HIS:H	1:120:A:ILE:HB	2	0.15
(1,225)	1:74:A:ARG:HA	1:74:A:ARG:HE	7	0.15
(1,1640)	1:97:A:LYS:HB2	1:98:A:LYS:HG2	18	0.14
(1,1640)	1:97:A:LYS:HB3	1:98:A:LYS:HG2	18	0.14
(1,1579)	1:74:A:ARG:HG2	1:76:A:PHE:H	14	0.14
(1,1579)	1:74:A:ARG:HG3	1:76:A:PHE:H	14	0.14
(1,1374)	1:19:A:GLU:HB2	1:23:A:PRO:HG2	18	0.14
(1,1374)	1:19:A:GLU:HB2	1:23:A:PRO:HG3	18	0.14
(1,1374)	1:19:A:GLU:HB3	1:23:A:PRO:HG2	18	0.14
(1,1374)	1:19:A:GLU:HB3	1:23:A:PRO:HG3	18	0.14
(1,1258)	1:115:A:ASP:H	1:116:A:LEU:HB2	15	0.14
(1,1258)	1:115:A:ASP:H	1:116:A:LEU:HB3	15	0.14
(1,1109)	1:25:A:LEU:H	1:25:A:LEU:HG	13	0.14
(1,1109)	1:25:A:LEU:H	1:25:A:LEU:HG	19	0.14
(1,909)	1:66:A:TRP:H	1:66:A:TRP:HD1	20	0.14
(1,902)	1:8:A:LYS:HB2	1:9:A:TYR:H	15	0.14
(1,902)	1:8:A:LYS:HB3	1:9:A:TYR:H	15	0.14
(1,809)	1:98:A:LYS:HD2	1:99:A:ASP:H	18	0.14
(1,614)	1:55:A:LEU:H	1:55:A:LEU:HG	17	0.14
(1,377)	1:119:A:HIS:H	1:120:A:ILE:HB	15	0.14
(1,225)	1:74:A:ARG:HA	1:74:A:ARG:HE	11	0.14
(1,158)	1:136:A:LYS:HA	1:136:A:LYS:HD2	7	0.14
(1,158)	1:136:A:LYS:HA	1:136:A:LYS:HD3	7	0.14
(1,1642)	1:98:A:LYS:HA	1:98:A:LYS:HD2	18	0.13
(1,1642)	1:98:A:LYS:HA	1:98:A:LYS:HD3	18	0.13
(1,1484)	1:45:A:VAL:HG11	1:47:A:PHE:HE2	4	0.13
(1,1484)	1:45:A:VAL:HG12	1:47:A:PHE:HE2	4	0.13
(1,1484)	1:45:A:VAL:HG13	1:47:A:PHE:HE2	4	0.13
(1,1484)	1:45:A:VAL:HG21	1:47:A:PHE:HE2	4	0.13
(1,1484)	1:45:A:VAL:HG22	1:47:A:PHE:HE2	4	0.13
(1,1484)	1:45:A:VAL:HG23	1:47:A:PHE:HE2	4	0.13
(1,1258)	1:115:A:ASP:H	1:116:A:LEU:HB2	16	0.13
(1,1258)	1:115:A:ASP:H	1:116:A:LEU:HB3	16	0.13
(1,1258)	1:115:A:ASP:H	1:116:A:LEU:HB2	17	0.13
(1,1258)	1:115:A:ASP:H	1:116:A:LEU:HB3	17	0.13
(1,1109)	1:25:A:LEU:H	1:25:A:LEU:HG	16	0.13
(1,805)	1:66:A:TRP:HB2	1:67:A:ALA:H	10	0.13
(1,377)	1:119:A:HIS:H	1:120:A:ILE:HB	17	0.13
(1,1670)	1:112:A:VAL:HG11	1:113:A:VAL:HG11	2	0.12
(1,1670)	1:112:A:VAL:HG11	1:113:A:VAL:HG12	2	0.12
(1,1670)	1:112:A:VAL:HG11	1:113:A:VAL:HG13	2	0.12

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1670)	1:112:A:VAL:HG12	1:113:A:VAL:HG11	2	0.12
(1,1670)	1:112:A:VAL:HG12	1:113:A:VAL:HG12	2	0.12
(1,1670)	1:112:A:VAL:HG12	1:113:A:VAL:HG13	2	0.12
(1,1670)	1:112:A:VAL:HG13	1:113:A:VAL:HG11	2	0.12
(1,1670)	1:112:A:VAL:HG13	1:113:A:VAL:HG12	2	0.12
(1,1670)	1:112:A:VAL:HG13	1:113:A:VAL:HG13	2	0.12
(1,1670)	1:112:A:VAL:HG21	1:113:A:VAL:HG11	2	0.12
(1,1670)	1:112:A:VAL:HG21	1:113:A:VAL:HG12	2	0.12
(1,1670)	1:112:A:VAL:HG21	1:113:A:VAL:HG13	2	0.12
(1,1670)	1:112:A:VAL:HG22	1:113:A:VAL:HG11	2	0.12
(1,1670)	1:112:A:VAL:HG22	1:113:A:VAL:HG12	2	0.12
(1,1670)	1:112:A:VAL:HG22	1:113:A:VAL:HG13	2	0.12
(1,1670)	1:112:A:VAL:HG23	1:113:A:VAL:HG11	2	0.12
(1,1670)	1:112:A:VAL:HG23	1:113:A:VAL:HG12	2	0.12
(1,1670)	1:112:A:VAL:HG23	1:113:A:VAL:HG13	2	0.12
(1,1640)	1:97:A:LYS:HB2	1:98:A:LYS:HG2	2	0.12
(1,1640)	1:97:A:LYS:HB3	1:98:A:LYS:HG2	2	0.12
(1,1537)	1:61:A:GLU:HG2	1:62:A:TYR:H	4	0.12
(1,1537)	1:61:A:GLU:HG3	1:62:A:TYR:H	4	0.12
(1,1537)	1:61:A:GLU:HG2	1:62:A:TYR:H	9	0.12
(1,1537)	1:61:A:GLU:HG3	1:62:A:TYR:H	9	0.12
(1,1537)	1:61:A:GLU:HG2	1:62:A:TYR:H	15	0.12
(1,1537)	1:61:A:GLU:HG3	1:62:A:TYR:H	15	0.12
(1,1537)	1:61:A:GLU:HG2	1:62:A:TYR:H	19	0.12
(1,1537)	1:61:A:GLU:HG3	1:62:A:TYR:H	19	0.12
(1,1537)	1:61:A:GLU:HG2	1:62:A:TYR:H	20	0.12
(1,1537)	1:61:A:GLU:HG3	1:62:A:TYR:H	20	0.12
(1,1258)	1:115:A:ASP:H	1:116:A:LEU:HB2	14	0.12
(1,1258)	1:115:A:ASP:H	1:116:A:LEU:HB3	14	0.12
(1,1245)	1:77:A:ARG:HE	1:134:A:GLU:H	5	0.12
(1,1109)	1:25:A:LEU:H	1:25:A:LEU:HG	2	0.12
(1,909)	1:66:A:TRP:H	1:66:A:TRP:HD1	9	0.12
(1,805)	1:66:A:TRP:HB2	1:67:A:ALA:H	9	0.12
(1,669)	1:21:A:THR:H	1:21:A:THR:HB	11	0.12
(1,614)	1:55:A:LEU:H	1:55:A:LEU:HG	13	0.12
(1,377)	1:119:A:HIS:H	1:120:A:ILE:HB	1	0.12
(1,377)	1:119:A:HIS:H	1:120:A:ILE:HB	16	0.12
(1,225)	1:74:A:ARG:HA	1:74:A:ARG:HE	17	0.12
(1,1670)	1:112:A:VAL:HG11	1:113:A:VAL:HG11	1	0.11
(1,1670)	1:112:A:VAL:HG11	1:113:A:VAL:HG12	1	0.11
(1,1670)	1:112:A:VAL:HG11	1:113:A:VAL:HG13	1	0.11
(1,1670)	1:112:A:VAL:HG12	1:113:A:VAL:HG11	1	0.11

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1670)	1:112:A:VAL:HG12	1:113:A:VAL:HG12	1	0.11
(1,1670)	1:112:A:VAL:HG12	1:113:A:VAL:HG13	1	0.11
(1,1670)	1:112:A:VAL:HG13	1:113:A:VAL:HG11	1	0.11
(1,1670)	1:112:A:VAL:HG13	1:113:A:VAL:HG12	1	0.11
(1,1670)	1:112:A:VAL:HG13	1:113:A:VAL:HG13	1	0.11
(1,1670)	1:112:A:VAL:HG21	1:113:A:VAL:HG11	1	0.11
(1,1670)	1:112:A:VAL:HG21	1:113:A:VAL:HG12	1	0.11
(1,1670)	1:112:A:VAL:HG21	1:113:A:VAL:HG13	1	0.11
(1,1670)	1:112:A:VAL:HG22	1:113:A:VAL:HG11	1	0.11
(1,1670)	1:112:A:VAL:HG22	1:113:A:VAL:HG12	1	0.11
(1,1670)	1:112:A:VAL:HG22	1:113:A:VAL:HG13	1	0.11
(1,1670)	1:112:A:VAL:HG23	1:113:A:VAL:HG11	1	0.11
(1,1670)	1:112:A:VAL:HG23	1:113:A:VAL:HG12	1	0.11
(1,1670)	1:112:A:VAL:HG23	1:113:A:VAL:HG13	1	0.11
(1,1643)	1:98:A:LYS:HA	1:98:A:LYS:HE2	18	0.11
(1,1643)	1:98:A:LYS:HA	1:98:A:LYS:HE3	18	0.11
(1,1537)	1:61:A:GLU:HG2	1:62:A:TYR:H	2	0.11
(1,1537)	1:61:A:GLU:HG3	1:62:A:TYR:H	2	0.11
(1,1537)	1:61:A:GLU:HG2	1:62:A:TYR:H	11	0.11
(1,1537)	1:61:A:GLU:HG3	1:62:A:TYR:H	11	0.11
(1,1537)	1:61:A:GLU:HG2	1:62:A:TYR:H	12	0.11
(1,1537)	1:61:A:GLU:HG3	1:62:A:TYR:H	12	0.11
(1,1237)	1:8:A:LYS:H	1:9:A:TYR:HA	9	0.11
(1,1109)	1:25:A:LEU:H	1:25:A:LEU:HG	3	0.11
(1,1001)	1:9:A:TYR:H	1:9:A:TYR:HD2	15	0.11
(1,906)	1:102:A:LYS:HG2	1:103:A:SER:H	11	0.11
(1,906)	1:102:A:LYS:HG2	1:103:A:SER:H	20	0.11
(1,809)	1:98:A:LYS:HD2	1:99:A:ASP:H	2	0.11
(1,669)	1:21:A:THR:H	1:21:A:THR:HB	6	0.11
(1,614)	1:55:A:LEU:H	1:55:A:LEU:HG	7	0.11
(1,614)	1:55:A:LEU:H	1:55:A:LEU:HG	20	0.11
(1,377)	1:119:A:HIS:H	1:120:A:ILE:HB	3	0.11
(1,377)	1:119:A:HIS:H	1:120:A:ILE:HB	5	0.11
(1,377)	1:119:A:HIS:H	1:120:A:ILE:HB	11	0.11
(1,377)	1:119:A:HIS:H	1:120:A:ILE:HB	12	0.11
(1,377)	1:119:A:HIS:H	1:120:A:ILE:HB	13	0.11
(1,377)	1:119:A:HIS:H	1:120:A:ILE:HB	14	0.11
(1,377)	1:119:A:HIS:H	1:120:A:ILE:HB	19	0.11
(1,377)	1:119:A:HIS:H	1:120:A:ILE:HB	20	0.11
(1,214)	1:2:A:SER:HA	1:3:A:SER:HB2	19	0.11
(1,214)	1:2:A:SER:HA	1:3:A:SER:HB3	19	0.11
(1,155)	1:60:A:ILE:HD11	1:61:A:GLU:HG3	16	0.11

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,155)	1:60:A:ILE:HD12	1:61:A:GLU:HG3	16	0.11
(1,155)	1:60:A:ILE:HD13	1:61:A:GLU:HG3	16	0.11
(1,1537)	1:61:A:GLU:HG2	1:62:A:TYR:H	18	0.1
(1,1537)	1:61:A:GLU:HG3	1:62:A:TYR:H	18	0.1
(1,1258)	1:115:A:ASP:H	1:116:A:LEU:HB2	2	0.1
(1,1258)	1:115:A:ASP:H	1:116:A:LEU:HB3	2	0.1
(1,634)	1:87:A:ILE:HG21	1:88:A:GLU:H	4	0.1
(1,634)	1:87:A:ILE:HG22	1:88:A:GLU:H	4	0.1
(1,634)	1:87:A:ILE:HG23	1:88:A:GLU:H	4	0.1
(1,627)	1:115:A:ASP:H	1:115:A:ASP:HB2	18	0.1
(1,614)	1:55:A:LEU:H	1:55:A:LEU:HG	9	0.1
(1,614)	1:55:A:LEU:H	1:55:A:LEU:HG	10	0.1
(1,569)	1:115:A:ASP:H	1:115:A:ASP:HB3	7	0.1
(1,318)	1:112:A:VAL:HA	1:113:A:VAL:HB	15	0.1

10 Dihedral-angle violation analysis ⓘ

No dihedral-angle restraints found