



Full wwPDB NMR Structure Validation Report ⓘ

Jun 5, 2023 – 04:50 PM EDT

PDB ID : 2M5D
BMRB ID : 19048
Title : Solution Structure of the Bacillus cereus Metallo-Beta-Lactamase BcII in Complex with R-Thiomandelic Acid
Authors : Karsisiotis, A.I.; Damblon, C.F.; Roberts, G.C.K.
Deposited on : 2013-02-20

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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
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) : 2.33

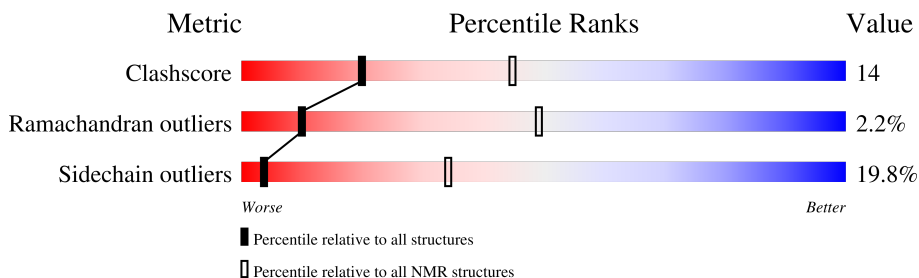
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 85%.

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	158937	12864
Ramachandran outliers	154571	11451
Sidechain outliers	154315	11428

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	227	

2 Ensemble composition and analysis i

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: *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:8-A:32, A:39-A:133, A:138-A:173, A:181-A:227 (203)	0.32	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 7 clusters and 3 single-model clusters were found.

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

3 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 3607 atoms, of which 1836 are hydrogens and 0 are deuteriums.

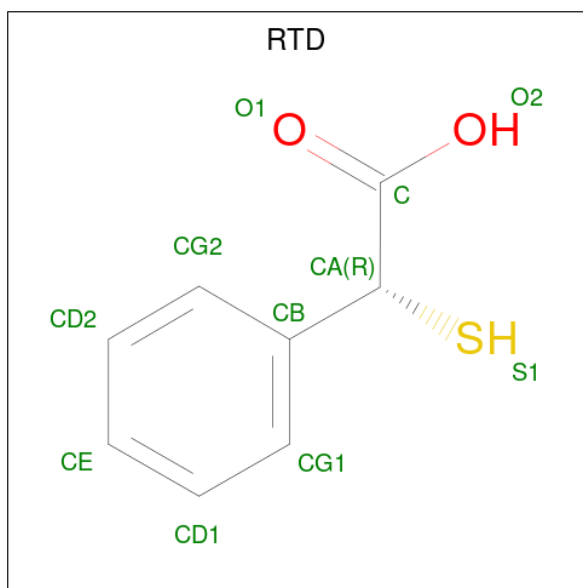
- Molecule 1 is a protein called Beta-lactamase 2.

Mol	Chain	Residues	Atoms					Trace	
			Total	C	H	N	O		S
1	A	227	3588	1113	1830	304	338	3	0

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	
			Total	Zn
2	A	2	2	2

- Molecule 3 is (2R)-phenyl(sulfanyl)ethanoic acid (three-letter code: RTD) (formula: C₈H₈O₂S).



Mol	Chain	Residues	Atoms				
			Total	C	H	O	S
3	A	1	17	8	6	2	1

4 Residue-property plots

4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outliers are shown as green connectors. Residues which are classified as ill-defined in the NMR ensemble, are shown in cyan with an underline colour-coded according to the previous scheme. Residues which were present in the experimental sample, but not modelled in the final structure are shown in grey.

- Molecule 1: Beta-lactamase 2

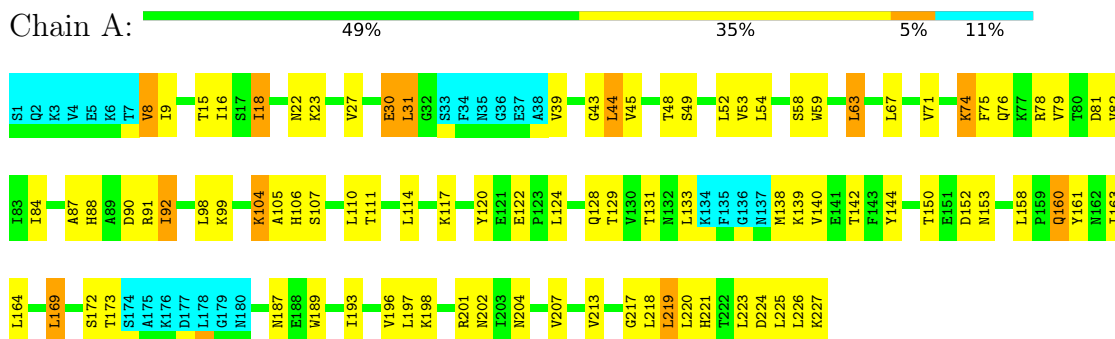


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

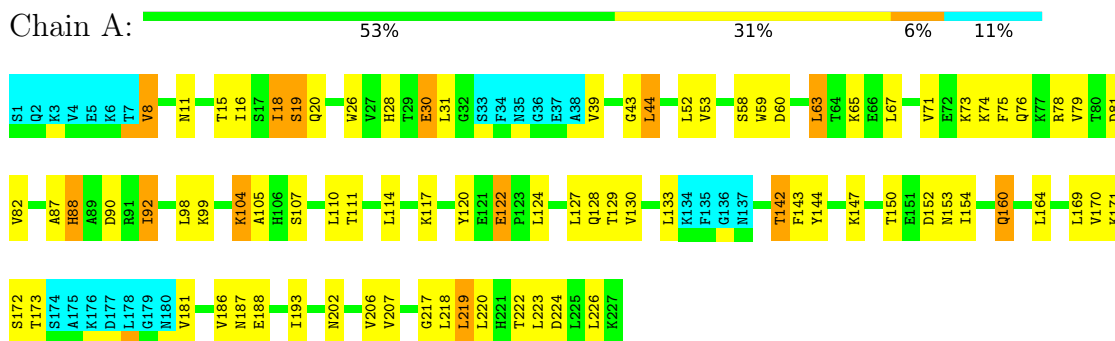
4.2.1 Score per residue for model 1

- Molecule 1: Beta-lactamase 2



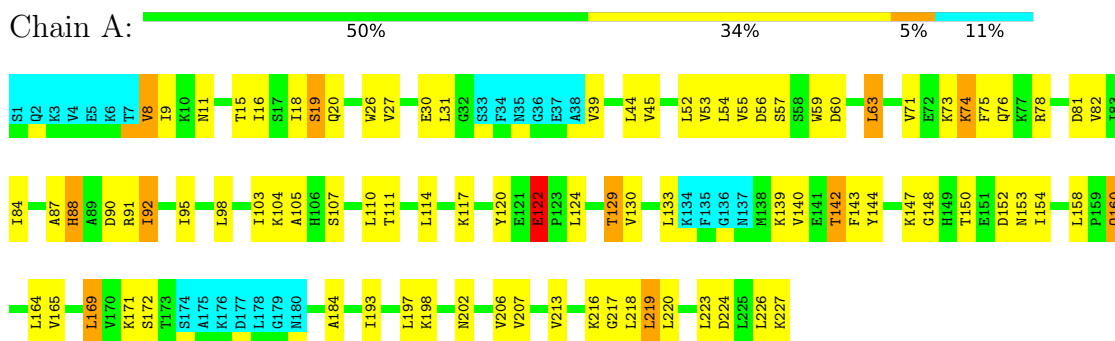
4.2.2 Score per residue for model 2

- Molecule 1: Beta-lactamase 2



4.2.3 Score per residue for model 3

- Molecule 1: Beta-lactamase 2



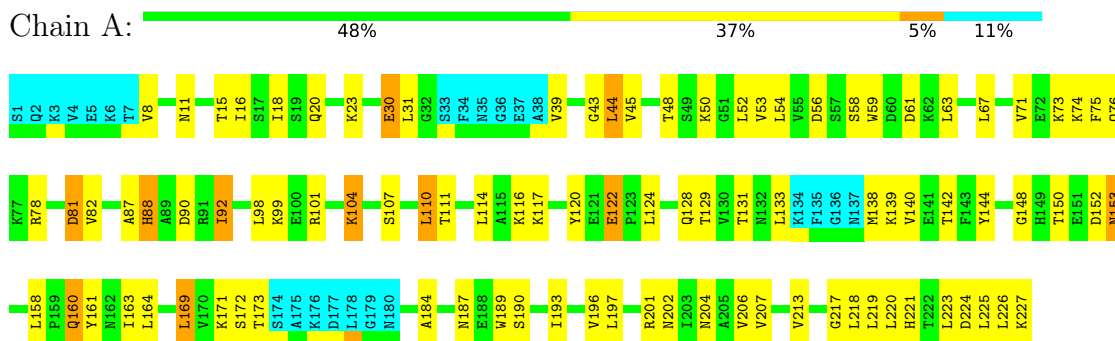
4.2.4 Score per residue for model 4

- Molecule 1: Beta-lactamase 2



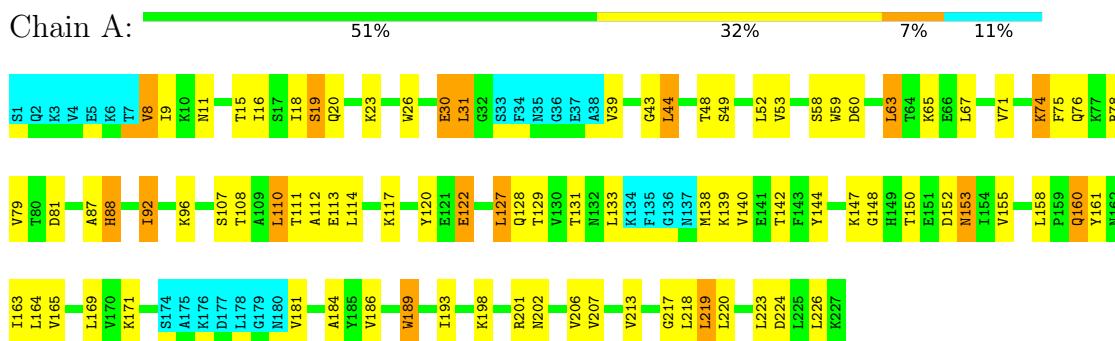
4.2.5 Score per residue for model 5

- Molecule 1: Beta-lactamase 2



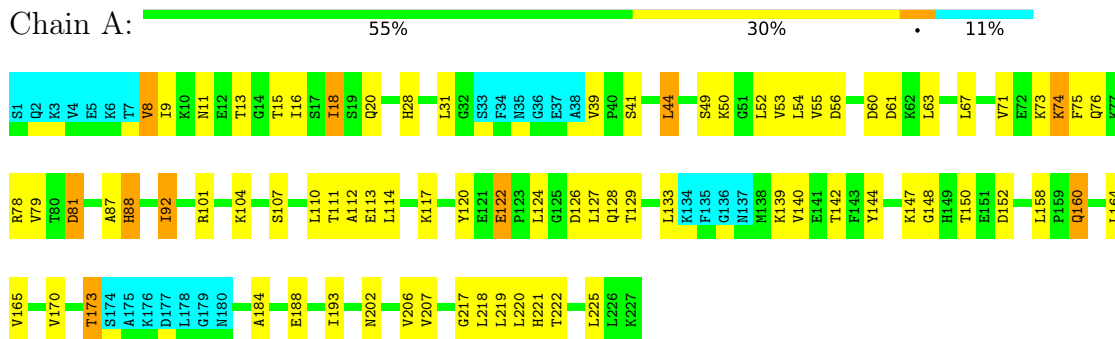
4.2.6 Score per residue for model 6

- Molecule 1: Beta-lactamase 2



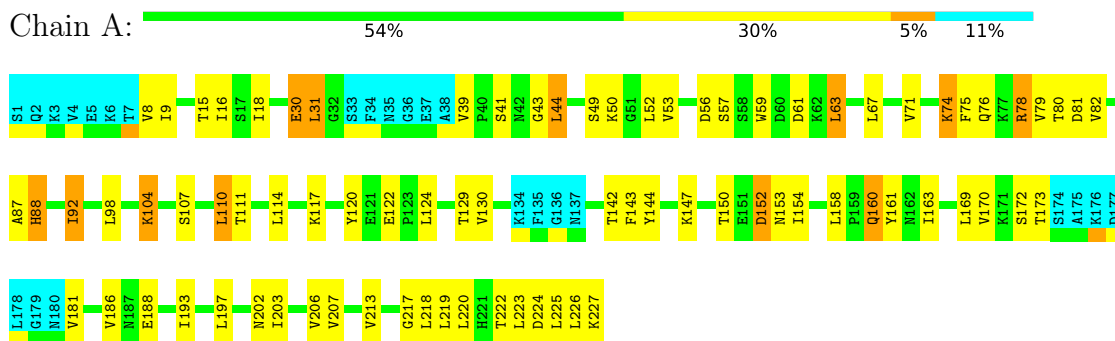
4.2.7 Score per residue for model 7

- Molecule 1: Beta-lactamase 2



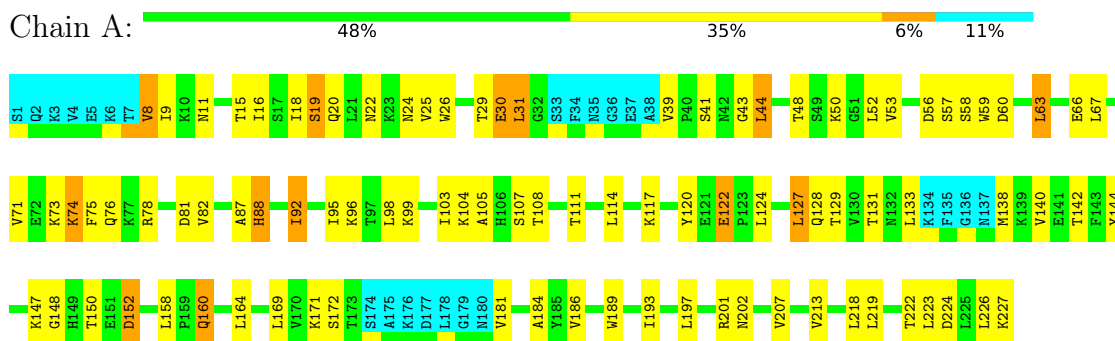
4.2.8 Score per residue for model 8

- Molecule 1: Beta-lactamase 2



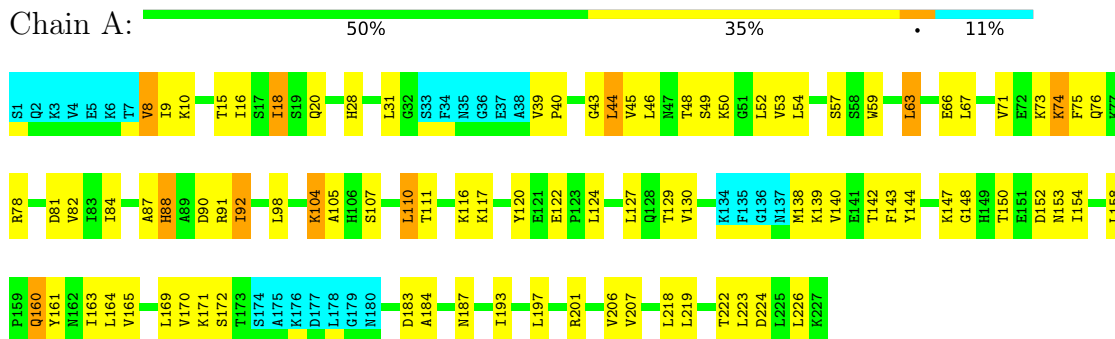
4.2.9 Score per residue for model 9

- Molecule 1: Beta-lactamase 2



4.2.10 Score per residue for model 10

- Molecule 1: Beta-lactamase 2



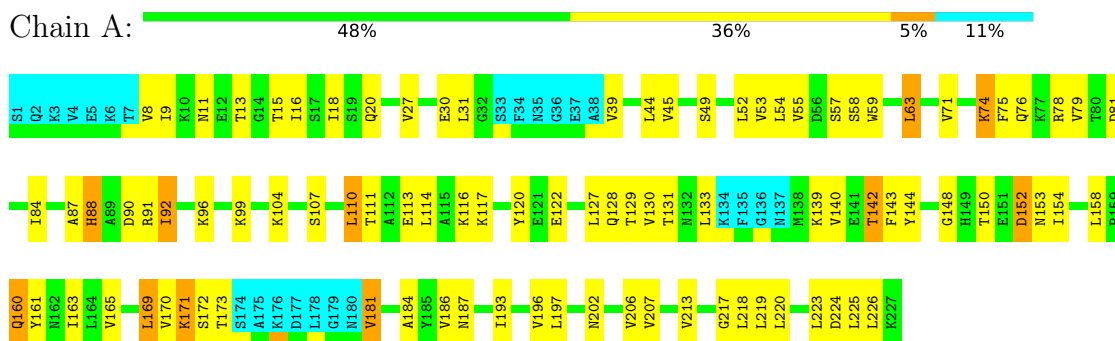
4.2.11 Score per residue for model 11

- Molecule 1: Beta-lactamase 2



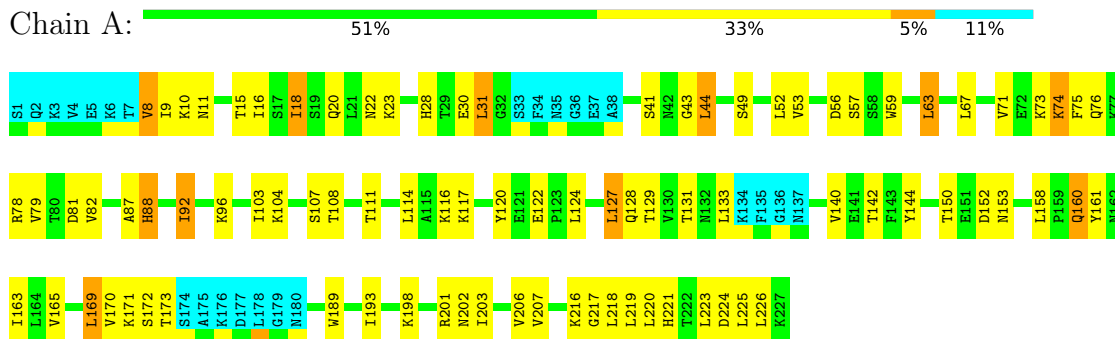
4.2.12 Score per residue for model 12 (medoid)

- Molecule 1: Beta-lactamase 2



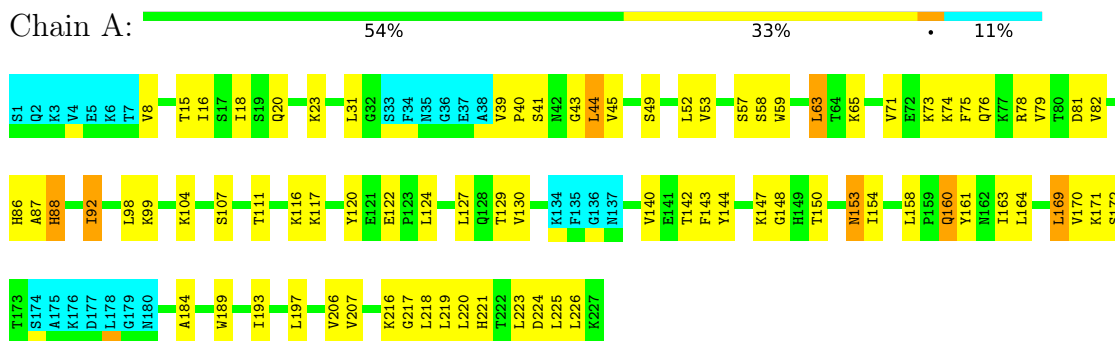
4.2.13 Score per residue for model 13

- Molecule 1: Beta-lactamase 2



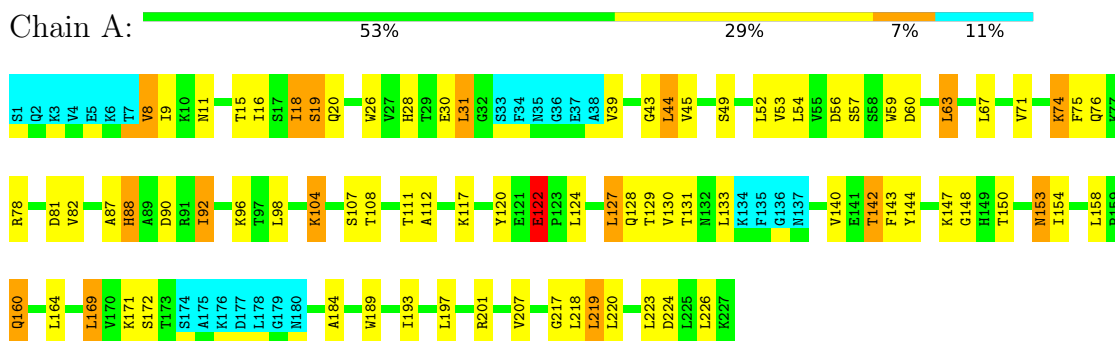
4.2.14 Score per residue for model 14

- Molecule 1: Beta-lactamase 2



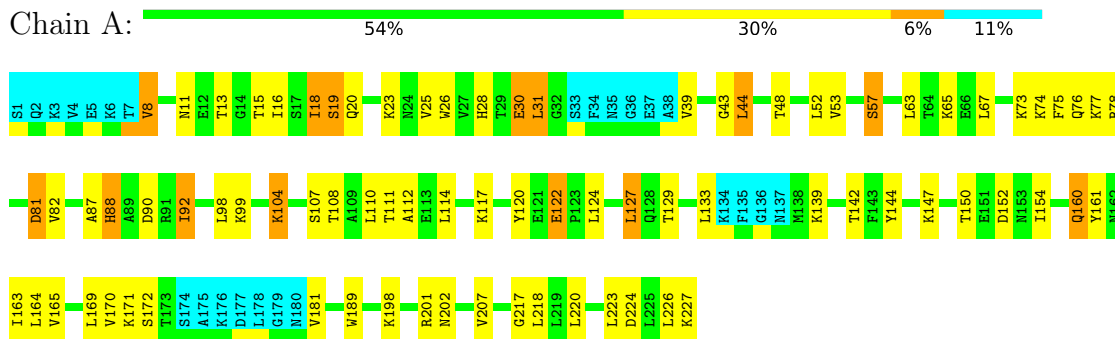
4.2.15 Score per residue for model 15

- Molecule 1: Beta-lactamase 2



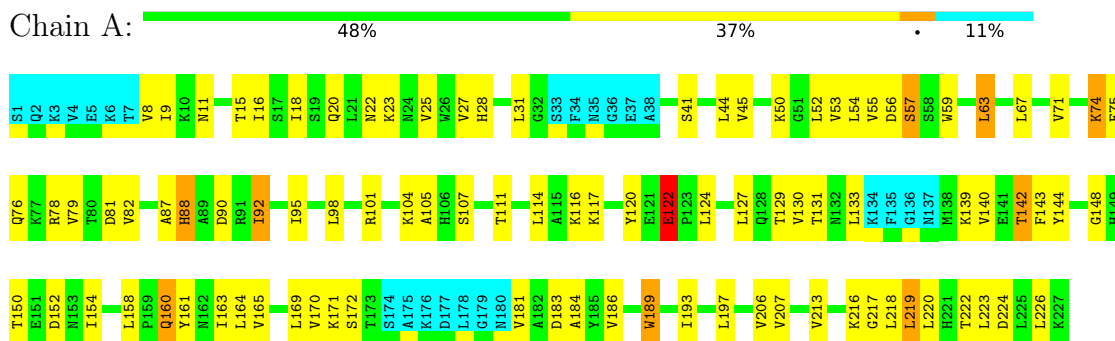
4.2.16 Score per residue for model 16

- Molecule 1: Beta-lactamase 2



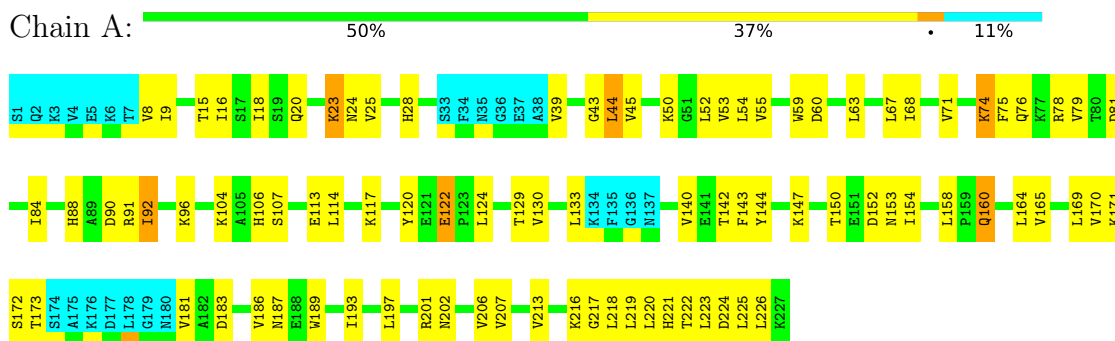
4.2.17 Score per residue for model 17

- Molecule 1: Beta-lactamase 2



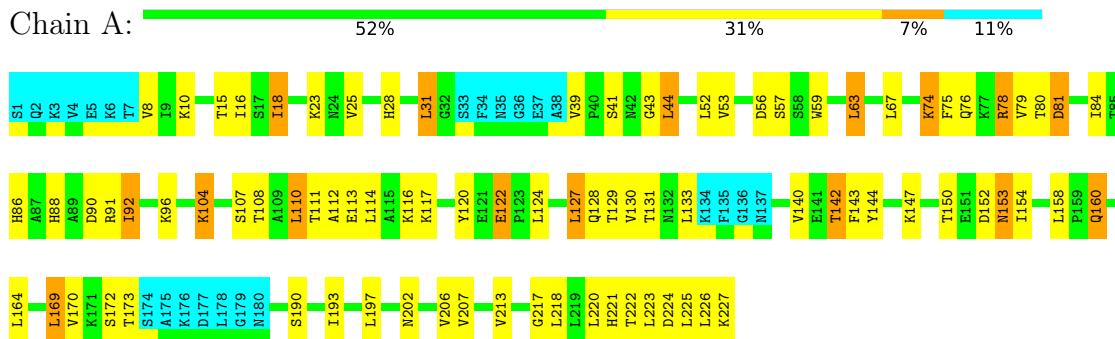
4.2.18 Score per residue for model 18

- Molecule 1: Beta-lactamase 2



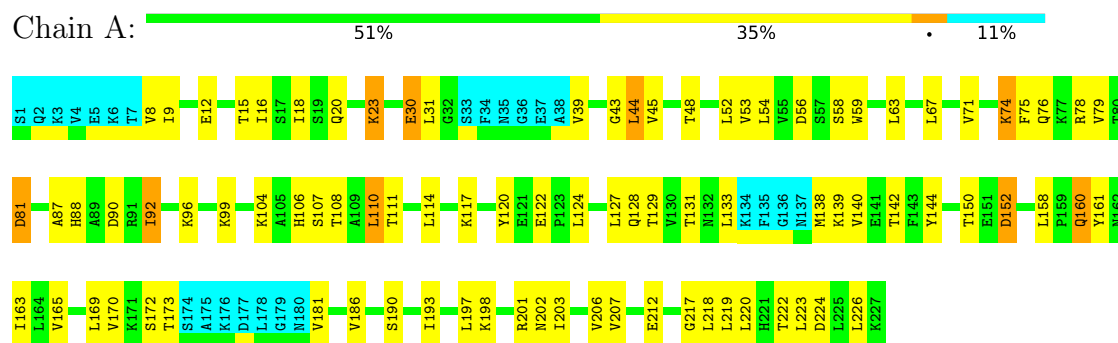
4.2.19 Score per residue for model 19

- Molecule 1: Beta-lactamase 2



4.2.20 Score per residue for model 20

• Molecule 1: Beta-lactamase 2



5 Refinement protocol and experimental data overview

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

Of the 100 calculated structures, 20 were deposited, based on the following criterion: *structures with the lowest energy*.

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

Software name	Classification	Version
CYANA	structure solution	
CYANA	refinement	
CANDID	structure solution	

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	2
Total number of shifts	4044
Number of shifts mapped to atoms	4044
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	85%

6 Model quality i

6.1 Standard geometry i

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

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 i

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	1579	1654	1625	44±5
3	A	11	6	6	1±0
All	All	31840	33200	32620	888

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 14.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:44:LEU:HD11	1:A:207:VAL:HG21	0.87	1.46	8	16
1:A:44:LEU:HD13	1:A:207:VAL:HG21	0.86	1.46	4	4
1:A:27:VAL:HG21	1:A:213:VAL:HG21	0.82	1.52	12	5
1:A:193:ILE:HG22	1:A:197:LEU:HD23	0.77	1.54	10	14
1:A:98:LEU:HD12	1:A:105:ALA:HB2	0.77	1.56	9	2
1:A:44:LEU:HD22	1:A:165:VAL:HG21	0.70	1.63	12	7
1:A:207:VAL:HG22	1:A:213:VAL:HG22	0.69	1.64	18	8
1:A:87:ALA:HB2	1:A:111:THR:O	0.64	1.92	13	18
1:A:52:LEU:HD21	1:A:75:PHE:HB3	0.64	1.70	6	16
1:A:9:ILE:HD11	1:A:74:LYS:CE	0.64	2.23	3	14
1:A:129:THR:HG23	1:A:144:TYR:HB3	0.64	1.70	3	20

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:206:VAL:CG1	1:A:218:LEU:HD12	0.63	2.24	10	11
1:A:44:LEU:HD13	1:A:165:VAL:HG22	0.63	1.68	18	1
1:A:53:VAL:HG22	1:A:81:ASP:HB2	0.62	1.69	10	18
1:A:52:LEU:HD13	1:A:71:VAL:HB	0.62	1.72	17	17
1:A:44:LEU:CD1	1:A:207:VAL:HG21	0.61	2.25	3	5
1:A:54:LEU:HD12	1:A:79:VAL:HG11	0.61	1.72	7	1
1:A:181:VAL:HG11	1:A:186:VAL:CG2	0.60	2.26	6	8
1:A:48:THR:HG22	1:A:138:MET:HB2	0.60	1.74	20	5
1:A:206:VAL:HG12	1:A:218:LEU:HD12	0.60	1.72	20	8
1:A:39:VAL:HG11	3:A:303:RTD:HD1	0.60	1.73	19	5
1:A:223:LEU:HA	1:A:226:LEU:HD12	0.60	1.73	19	19
1:A:27:VAL:HG22	1:A:44:LEU:HD12	0.60	1.74	3	4
1:A:193:ILE:HG23	1:A:219:LEU:HD12	0.59	1.74	9	3
1:A:130:VAL:HG13	1:A:142:THR:O	0.59	1.97	12	7
1:A:104:LYS:HB2	1:A:124:LEU:HD11	0.59	1.75	5	18
1:A:170:VAL:HG11	1:A:206:VAL:HG11	0.59	1.75	20	12
1:A:129:THR:HG22	1:A:130:VAL:HG23	0.59	1.75	3	11
1:A:39:VAL:HG11	3:A:303:RTD:HD2	0.59	1.74	1	4
1:A:114:LEU:HD13	1:A:152:ASP:OD2	0.58	1.97	7	3
1:A:44:LEU:HD13	1:A:165:VAL:CG2	0.58	2.28	18	5
1:A:173:THR:HG23	1:A:218:LEU:HD23	0.58	1.76	7	3
1:A:88:HIS:O	1:A:92:ILE:HD13	0.58	1.99	18	20
1:A:221:HIS:NE2	1:A:225:LEU:HD21	0.58	2.14	19	7
1:A:170:VAL:HG11	1:A:206:VAL:CG1	0.58	2.29	2	2
1:A:15:THR:HG23	1:A:16:ILE:HG13	0.57	1.76	2	20
1:A:126:ASP:O	1:A:127:LEU:HD23	0.57	1.99	7	1
1:A:59:TRP:HB2	1:A:63:LEU:HD13	0.57	1.75	1	17
1:A:114:LEU:HD12	1:A:152:ASP:OD2	0.57	2.00	6	8
1:A:39:VAL:HG13	1:A:59:TRP:CZ2	0.57	2.35	2	5
1:A:140:VAL:HG13	1:A:158:LEU:HD23	0.57	1.77	15	15
1:A:54:LEU:CD1	1:A:79:VAL:HG11	0.57	2.28	7	1
1:A:142:THR:HG22	1:A:154:ILE:HD12	0.56	1.77	11	8
1:A:9:ILE:HD11	1:A:74:LYS:HE3	0.56	1.77	12	11
1:A:148:GLY:O	1:A:184:ALA:HB1	0.56	2.01	4	12
1:A:114:LEU:HD13	1:A:152:ASP:OD1	0.56	2.00	11	3
1:A:169:LEU:HD12	1:A:189:TRP:NE1	0.55	2.15	18	3
1:A:30:GLU:OE2	1:A:67:LEU:HD22	0.55	2.01	9	8
1:A:45:VAL:HG22	1:A:54:LEU:HD13	0.55	1.78	4	11
1:A:43:GLY:O	1:A:44:LEU:HD12	0.55	2.01	20	15
1:A:114:LEU:HD12	1:A:152:ASP:OD1	0.55	2.02	1	3
1:A:82:VAL:HG23	1:A:103:ILE:HG21	0.54	1.79	9	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:18:ILE:HD12	1:A:74:LYS:NZ	0.54	2.18	19	1
1:A:44:LEU:HD22	1:A:165:VAL:CG2	0.54	2.31	12	4
1:A:130:VAL:HG22	1:A:143:PHE:HA	0.54	1.77	12	11
1:A:217:GLY:HA2	1:A:220:LEU:HD12	0.54	1.79	14	18
1:A:45:VAL:HG22	1:A:54:LEU:CD1	0.54	2.33	4	4
1:A:112:ALA:HB1	1:A:122:GLU:OE1	0.54	2.03	15	4
1:A:39:VAL:HG21	3:A:303:RTD:HD2	0.54	1.80	14	5
1:A:98:LEU:CD1	1:A:105:ALA:HB2	0.53	2.31	9	5
1:A:86:HIS:C	1:A:111:THR:HG23	0.53	2.24	14	1
1:A:186:VAL:HG13	1:A:226:LEU:CD2	0.53	2.34	17	2
1:A:30:GLU:OE1	1:A:67:LEU:HD22	0.53	2.03	8	1
1:A:52:LEU:HD21	1:A:75:PHE:CB	0.53	2.34	19	14
1:A:82:VAL:HG21	1:A:98:LEU:CD2	0.53	2.33	1	8
1:A:172:SER:HA	1:A:218:LEU:HD22	0.53	1.80	17	18
1:A:39:VAL:HG21	3:A:303:RTD:HD1	0.53	1.80	5	3
1:A:87:ALA:N	1:A:111:THR:HG23	0.53	2.18	7	1
1:A:29:THR:HG23	1:A:41:SER:O	0.53	2.04	9	1
1:A:44:LEU:HD12	1:A:207:VAL:HG11	0.52	1.79	8	13
1:A:193:ILE:HG21	1:A:219:LEU:O	0.52	2.03	7	13
1:A:9:ILE:HD11	1:A:74:LYS:HE2	0.52	1.79	6	6
1:A:161:TYR:CB	1:A:163:ILE:HD13	0.52	2.35	8	12
1:A:52:LEU:HB2	1:A:79:VAL:HG22	0.51	1.82	20	12
1:A:53:VAL:HG13	1:A:81:ASP:HB3	0.51	1.82	10	8
1:A:44:LEU:HD11	1:A:207:VAL:CG2	0.51	2.33	16	11
1:A:24:ASN:OD1	1:A:25:VAL:HG23	0.51	2.04	9	2
1:A:16:ILE:HG21	1:A:67:LEU:HD13	0.51	1.83	17	3
1:A:197:LEU:HD12	1:A:197:LEU:O	0.50	2.06	10	4
1:A:181:VAL:HG21	1:A:186:VAL:CG2	0.50	2.36	12	1
1:A:8:VAL:HG22	1:A:19:SER:OG	0.50	2.07	16	6
1:A:82:VAL:HG21	1:A:98:LEU:HD22	0.50	1.84	2	8
1:A:140:VAL:HG13	1:A:158:LEU:CD2	0.50	2.37	12	7
1:A:110:LEU:HD12	1:A:152:ASP:HB3	0.50	1.83	10	7
1:A:68:ILE:HG23	1:A:79:VAL:HG21	0.50	1.84	18	1
1:A:129:THR:HG22	1:A:130:VAL:HG13	0.50	1.83	18	1
1:A:181:VAL:HG11	1:A:186:VAL:HG23	0.49	1.83	6	2
1:A:131:THR:HG22	1:A:133:LEU:HD23	0.49	1.84	9	11
1:A:155:VAL:CG1	1:A:169:LEU:HD22	0.49	2.37	6	1
1:A:28:HIS:CE1	1:A:67:LEU:HD21	0.48	2.43	17	6
1:A:110:LEU:HD23	1:A:152:ASP:HA	0.48	1.86	16	2
1:A:75:PHE:O	1:A:76:GLN:C	0.48	2.52	16	20
1:A:8:VAL:HG13	1:A:18:ILE:O	0.48	2.09	11	5

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:153:ASN:OD1	1:A:169:LEU:HD13	0.48	2.09	6	9
1:A:144:TYR:CD1	1:A:154:ILE:HG22	0.48	2.44	10	8
1:A:45:VAL:HG11	1:A:71:VAL:HG11	0.47	1.86	18	3
1:A:112:ALA:HB1	1:A:122:GLU:OE2	0.47	2.10	19	2
1:A:158:LEU:HD12	1:A:163:ILE:HB	0.47	1.85	8	5
1:A:27:VAL:HG21	1:A:213:VAL:CG2	0.47	2.34	12	1
1:A:68:ILE:HG23	1:A:79:VAL:CG2	0.47	2.40	18	1
1:A:130:VAL:HG12	1:A:143:PHE:HA	0.47	1.87	18	1
1:A:44:LEU:CD1	1:A:207:VAL:HG11	0.47	2.39	8	4
1:A:142:THR:CG2	1:A:154:ILE:HD12	0.47	2.40	15	2
1:A:18:ILE:HG23	1:A:28:HIS:HB3	0.46	1.87	15	7
1:A:27:VAL:HG22	1:A:44:LEU:CD1	0.46	2.40	3	3
1:A:31:LEU:HD12	1:A:40:PRO:HA	0.46	1.86	14	2
1:A:31:LEU:HD12	1:A:40:PRO:CA	0.46	2.40	14	2
1:A:220:LEU:HA	1:A:223:LEU:HD12	0.46	1.85	2	1
1:A:78:ARG:HD3	1:A:80:THR:HG23	0.45	1.89	11	2
1:A:82:VAL:HG11	1:A:98:LEU:HD11	0.45	1.88	1	6
1:A:114:LEU:HD22	1:A:152:ASP:OD1	0.45	2.11	9	1
1:A:108:THR:HG22	1:A:127:LEU:HB3	0.45	1.88	20	7
1:A:181:VAL:HB	1:A:184:ALA:HB3	0.45	1.88	12	1
1:A:27:VAL:CG2	1:A:213:VAL:HG21	0.45	2.36	4	1
1:A:82:VAL:HG23	1:A:103:ILE:CG2	0.45	2.42	9	2
1:A:75:PHE:C	1:A:76:GLN:HG3	0.44	2.33	16	20
1:A:106:HIS:HA	1:A:124:LEU:HD12	0.44	1.87	11	4
1:A:197:LEU:HD12	1:A:198:LYS:HG2	0.44	1.90	20	1
1:A:84:ILE:HG23	1:A:91:ARG:HB3	0.44	1.89	1	1
1:A:207:VAL:HG22	1:A:213:VAL:CG2	0.44	2.41	18	1
1:A:110:LEU:HD23	1:A:152:ASP:HB3	0.44	1.89	11	5
1:A:48:THR:HG22	1:A:138:MET:CB	0.44	2.42	9	2
1:A:78:ARG:HD2	1:A:80:THR:HG23	0.44	1.90	19	1
1:A:203:ILE:HG21	1:A:206:VAL:CG2	0.44	2.43	8	3
1:A:42:ASN:HD21	1:A:212:GLU:N	0.43	2.11	4	1
1:A:16:ILE:CG2	1:A:67:LEU:HD13	0.43	2.43	17	1
1:A:82:VAL:HG21	1:A:98:LEU:HD13	0.43	1.90	15	2
1:A:55:VAL:O	1:A:55:VAL:HG12	0.43	2.13	17	5
1:A:52:LEU:HD13	1:A:71:VAL:CG2	0.43	2.44	18	1
1:A:84:ILE:HD12	1:A:91:ARG:O	0.43	2.13	1	7
1:A:196:VAL:CG1	1:A:219:LEU:HD21	0.43	2.44	12	3
1:A:95:ILE:HD11	1:A:122:GLU:C	0.42	2.34	9	3
1:A:31:LEU:O	1:A:63:LEU:HD21	0.42	2.14	9	3
1:A:186:VAL:HG13	1:A:226:LEU:HD23	0.42	1.91	12	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:86:HIS:HA	1:A:111:THR:HG23	0.42	1.90	19	1
1:A:53:VAL:HG22	1:A:81:ASP:CB	0.42	2.44	20	1
1:A:193:ILE:HG23	1:A:219:LEU:CD1	0.42	2.43	9	1
1:A:161:TYR:HB2	1:A:163:ILE:HD13	0.42	1.91	13	3
1:A:186:VAL:HG13	1:A:226:LEU:HD22	0.42	1.90	17	2
1:A:46:LEU:HB3	1:A:138:MET:HE3	0.41	1.92	10	1
1:A:16:ILE:HD13	1:A:67:LEU:HB2	0.41	1.92	13	1
1:A:23:LYS:O	1:A:25:VAL:HG23	0.41	2.14	16	3
1:A:196:VAL:HG12	1:A:219:LEU:HD21	0.41	1.90	4	1
1:A:53:VAL:HG13	1:A:81:ASP:HB2	0.41	1.91	8	4
1:A:55:VAL:HG12	1:A:55:VAL:O	0.41	2.16	4	1
1:A:170:VAL:HG12	1:A:218:LEU:HB3	0.41	1.92	16	1
1:A:18:ILE:HG23	1:A:28:HIS:CB	0.41	2.45	19	1
1:A:21:LEU:HD13	1:A:27:VAL:HG23	0.41	1.92	11	1
1:A:181:VAL:HG21	1:A:186:VAL:HG21	0.40	1.92	12	1
1:A:44:LEU:HD13	1:A:165:VAL:CG1	0.40	2.46	20	1

6.3 Torsion angles [i](#)

6.3.1 Protein backbone [i](#)

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	202/227 (89%)	167±4 (83±2%)	30±3 (15±2%)	4±1 (2±0%)	10	49
All	All	4040/4540 (89%)	3341 (83%)	610 (15%)	89 (2%)	10	49

All 9 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	120	TYR	20
1	A	122	GLU	20
1	A	160	GLN	20
1	A	8	VAL	19
1	A	57	SER	3
1	A	48	THR	2

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Mol	Chain	Res	Type	Models (Total)
1	A	181	VAL	2
1	A	23	LYS	2
1	A	129	THR	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	177/196 (90%)	142±3 (80±2%)	35±3 (20±2%)	4	34
All	All	3540/3920 (90%)	2838 (80%)	702 (20%)	4	34

All 72 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	18	ILE	20
1	A	74	LYS	20
1	A	78	ARG	20
1	A	92	ILE	20
1	A	107	SER	20
1	A	117	LYS	20
1	A	142	THR	20
1	A	150	THR	20
1	A	160	GLN	20
1	A	224	ASP	19
1	A	63	LEU	18
1	A	20	GLN	17
1	A	44	LEU	16
1	A	88	HIS	16
1	A	164	LEU	15
1	A	169	LEU	15
1	A	202	ASN	15
1	A	30	GLU	14
1	A	90	ASP	13
1	A	11	ASN	13
1	A	171	LYS	13
1	A	128	GLN	12

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Mol	Chain	Res	Type	Models (Total)
1	A	139	LYS	12
1	A	127	LEU	12
1	A	147	LYS	12
1	A	49	SER	11
1	A	73	LYS	11
1	A	222	THR	11
1	A	57	SER	11
1	A	58	SER	10
1	A	104	LYS	10
1	A	201	ARG	10
1	A	153	ASN	10
1	A	56	ASP	10
1	A	99	LYS	9
1	A	173	THR	9
1	A	96	LYS	9
1	A	23	LYS	8
1	A	31	LEU	8
1	A	227	LYS	8
1	A	60	ASP	8
1	A	122	GLU	8
1	A	116	LYS	8
1	A	187	ASN	7
1	A	19	SER	7
1	A	41	SER	7
1	A	50	LYS	7
1	A	110	LEU	7
1	A	22	ASN	6
1	A	219	LEU	6
1	A	133	LEU	6
1	A	216	LYS	6
1	A	198	LYS	5
1	A	65	LYS	5
1	A	81	ASP	5
1	A	113	GLU	5
1	A	188	GLU	4
1	A	190	SER	4
1	A	152	ASP	4
1	A	61	ASP	3
1	A	101	ARG	3
1	A	13	THR	3
1	A	66	GLU	3
1	A	10	LYS	3

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Mol	Chain	Res	Type	Models (Total)
1	A	183	ASP	3
1	A	204	ASN	2
1	A	212	GLU	2
1	A	189	TRP	2
1	A	12	GLU	2
1	A	77	LYS	2
1	A	194	GLU	1
1	A	154	ILE	1

6.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

6.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 2 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds for which Mogul statistics could be retrieved, the number of bonds that are observed in the model and the number of bonds that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length is the number of standard deviations the observed value is removed from the expected value. A bond length with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond lengths.

Mol	Type	Chain	Res	Link	Bond lengths		
					Counts	RMSZ	#Z>2
3	RTD	A	303	2	10,11,11	1.34±0.02	1±0 (10±0%)

In the following table, the Counts columns list the number of angles for which Mogul statistics could be retrieved, the number of angles that are observed in the model and the number of angles that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond angle is the number of standard

deviations the observed value is removed from the expected value. A bond angle with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond angles.

Mol	Type	Chain	Res	Link	Bond angles		
					Counts	RMSZ	#Z>2
3	RTD	A	303	2	10,14,14	0.60±0.06	0±0 (0±0%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	RTD	A	303	2	-	0±0,4,8,8	0±0,1,1,1

All unique bond outliers are listed below.

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
3	A	303	RTD	CA-C	3.13	1.60	1.52	12	20

There are no bond-angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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 (i)

The completeness of assignment taking into account all chemical shift lists is 85% for the well-defined parts and 83% 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 (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	2315
Number of shifts mapped to atoms	2315
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	14

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
$^{13}\text{C}_\alpha$	223	-0.40 ± 0.06	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	200	0.09 ± 0.09	None needed (< 0.5 ppm)
$^{13}\text{C}'$	0	—	None (insufficient data)
^{15}N	0	—	None (insufficient data)

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 76%, i.e. 2129 atoms were assigned a chemical shift out of a possible 2786. 0 out of 46 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	612/1022 (60%)	411/418 (98%)	201/406 (50%)	0/198 (0%)
Sidechain	1398/1597 (88%)	973/1043 (93%)	425/503 (84%)	0/51 (0%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	119/167 (71%)	70/82 (85%)	49/69 (71%)	0/16 (0%)
Overall	2129/2786 (76%)	1454/1543 (94%)	675/978 (69%)	0/265 (0%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 75%, i.e. 2309 atoms were assigned a chemical shift out of a possible 3082. 0 out of 48 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	678/1145 (59%)	455/469 (97%)	223/454 (49%)	0/222 (0%)
Sidechain	1498/1750 (86%)	1045/1139 (92%)	453/552 (82%)	0/59 (0%)
Aromatic	133/187 (71%)	79/92 (86%)	54/79 (68%)	0/16 (0%)
Overall	2309/3082 (75%)	1579/1700 (93%)	730/1085 (67%)	0/297 (0%)

7.1.4 Statistically unusual chemical shifts [i](#)

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

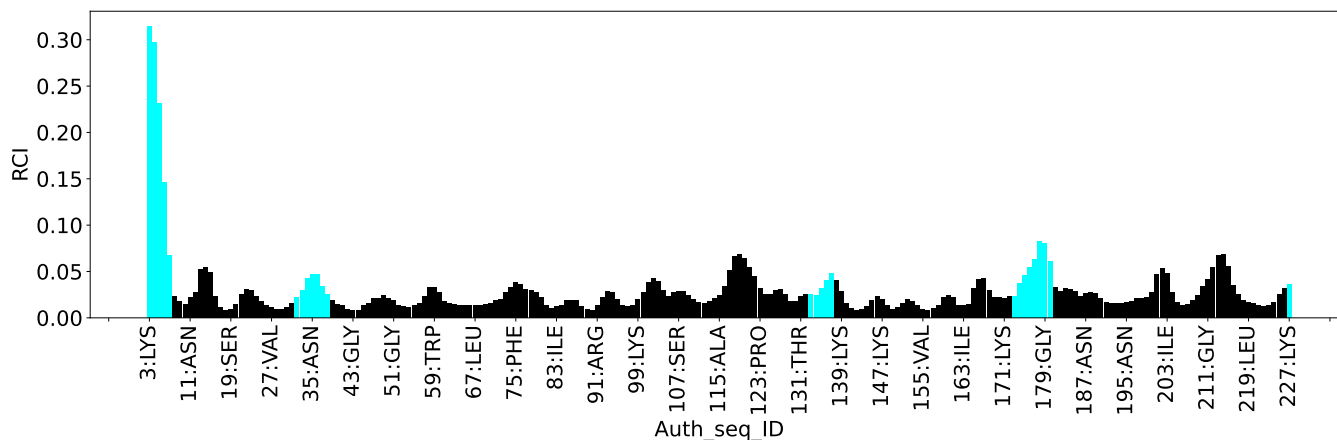
List Id	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	108	THR	HG1	6.78	0.08 – 2.19	26.7
1	A	80	THR	HG1	6.29	0.08 – 2.19	24.4
1	A	48	THR	HG1	5.69	0.08 – 2.19	21.6
1	A	142	THR	HG1	5.54	0.08 – 2.19	20.9
1	A	222	THR	HG1	5.28	0.08 – 2.19	19.6
1	A	90	ASP	HB3	0.51	1.32 – 4.00	-8.0
1	A	20	GLN	HB3	-0.02	0.71 – 3.33	-7.8
1	A	199	ARG	HD2	1.35	1.97 – 4.26	-7.7
1	A	199	ARG	HD3	1.22	1.81 – 4.39	-7.3
1	A	90	ASP	HA	2.40	3.04 – 6.12	-7.1
1	A	199	ARG	HG3	-0.24	0.15 – 2.94	-6.4
1	A	147	LYS	HD3	0.30	0.54 – 2.65	-6.2
1	A	32	GLY	HA3	1.74	2.08 – 5.71	-5.9
1	A	75	PHE	HZ	4.83	4.94 – 9.06	-5.3

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

The image below reports *random coil index* values for the protein chains in the structure. The height of each bar gives a probability of a given residue to be disordered, as predicted from the available chemical shifts and the amino acid sequence. A value above 0.2 is an indication of significant predicted disorder. The colour of the bar shows whether the residue is in the well-defined core (black) or in the ill-defined residue ranges (cyan), as described in section 2 on ensemble

composition. If well-defined core and ill-defined regions are not identified then it is shown as gray bars.

Random coil index (RCI) for chain A:



7.2 Chemical shift list 2

File name: working_cs.cif

Chemical shift list name: *assigned_chem_shift_list_2*

7.2.1 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	1729
Number of shifts mapped to atoms	1729
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	10

7.2.2 Chemical shift referencing [i](#)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	0	—	None (insufficient data)
$^{13}\text{C}_\beta$	0	—	None (insufficient data)
$^{13}\text{C}'$	0	—	None (insufficient data)
^{15}N	207	0.55 ± 0.18	Should be applied

7.2.3 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 57%, i.e. 1593 atoms were assigned a chemical shift out of a possible 2786. 0 out of 46 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Backbone	595/1022 (58%)	405/418 (97%)	0/406 (0%)	190/198 (96%)
Sidechain	959/1597 (60%)	943/1043 (90%)	0/503 (0%)	16/51 (31%)
Aromatic	39/167 (23%)	35/82 (43%)	0/69 (0%)	4/16 (25%)
Overall	1593/2786 (57%)	1383/1543 (90%)	0/978 (0%)	210/265 (79%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 56%, i.e. 1726 atoms were assigned a chemical shift out of a possible 3082. 0 out of 48 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Backbone	652/1145 (57%)	445/469 (95%)	0/454 (0%)	207/222 (93%)
Sidechain	1031/1750 (59%)	1011/1139 (89%)	0/552 (0%)	20/59 (34%)
Aromatic	43/187 (23%)	39/92 (42%)	0/79 (0%)	4/16 (25%)
Overall	1726/3082 (56%)	1495/1700 (88%)	0/1085 (0%)	231/297 (78%)

7.2.4 Statistically unusual chemical shifts [i](#)

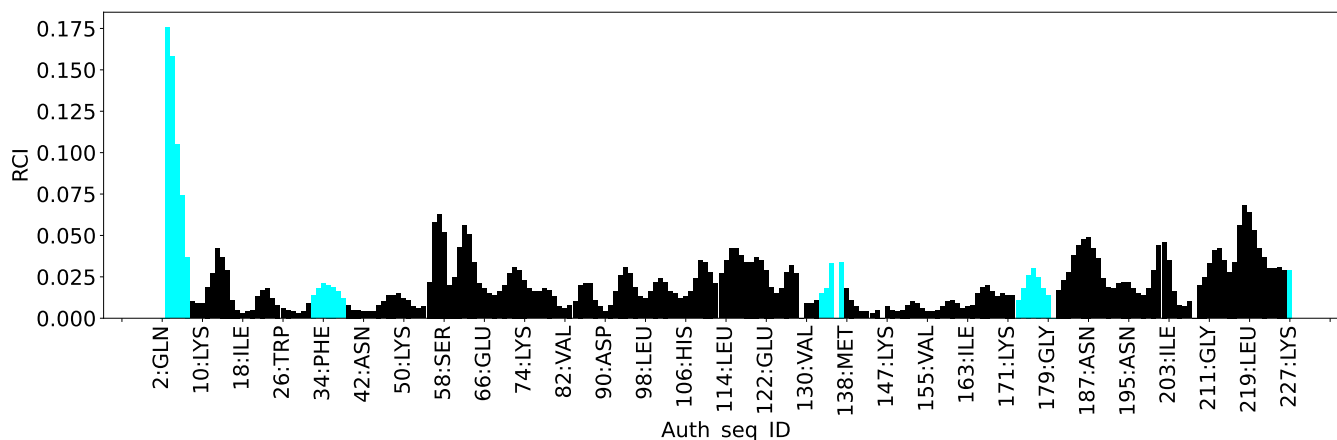
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
2	A	80	THR	HG1	6.27	0.08 – 2.19	24.3
2	A	48	THR	HG1	5.67	0.08 – 2.19	21.5
2	A	222	THR	HG1	5.28	0.08 – 2.19	19.6
2	A	90	ASP	HB3	0.53	1.32 – 4.00	-8.0
2	A	199	ARG	HD2	1.31	1.97 – 4.26	-7.9
2	A	20	GLN	HB3	0.01	0.71 – 3.33	-7.7
2	A	199	ARG	HD3	1.22	1.81 – 4.39	-7.3
2	A	90	ASP	HA	2.40	3.04 – 6.12	-7.1
2	A	199	ARG	HG3	-0.22	0.15 – 2.94	-6.3
2	A	32	GLY	HA3	1.78	2.08 – 5.71	-5.8

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

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

Random coil index (RCI) for chain A:



8 NMR restraints analysis

8.1 Conformationally restricting restraints

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

Description	Value
Total distance restraints	6241
Intra-residue ($ i-j =0$)	1193
Sequential ($ i-j =1$)	1444
Medium range ($ i-j >1$ and $ i-j <5$)	1011
Long range ($ i-j \geq 5$)	2591
Inter-chain	0
Hydrogen bond restraints	0
Disulfide bond restraints	2
Total dihedral-angle restraints	0
Number of unmapped restraints	0
Number of restraints per residue	27.5
Number of long range restraints per residue ¹	11.4

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

8.2 Residual restraint violations

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

8.2.1 Average number of distance violations per model

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

Bins (Å)	Average number of violations per model	Max (Å)
0.1-0.2 (Small)	6.2	0.2
0.2-0.5 (Medium)	1.1	0.24
>0.5 (Large)	None	None

8.2.2 Average number of dihedral-angle violations per model

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

9 Distance violation analysis [i](#)

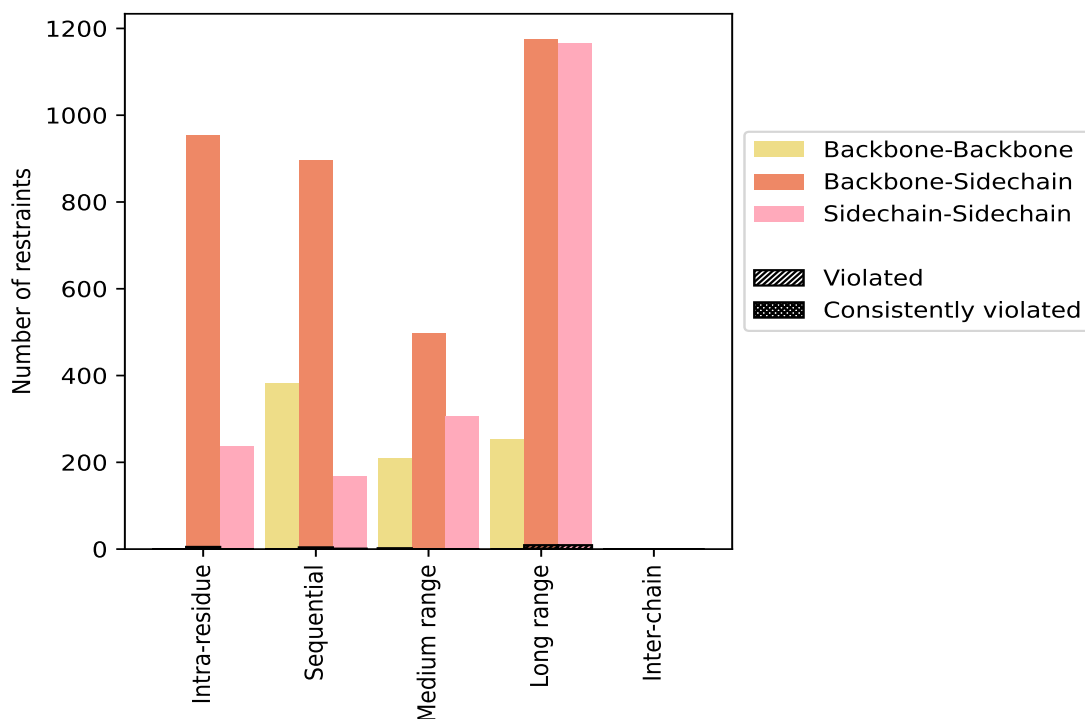
9.1 Summary of distance violations [i](#)

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 ($i-j =0$)	1193	19.1	5	0.4	0.1	0	0.0	0.0
Backbone-Backbone	2	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	954	15.3	5	0.5	0.1	0	0.0	0.0
Sidechain-Sidechain	237	3.8	0	0.0	0.0	0	0.0	0.0
Sequential ($i-j =1$)	1444	23.1	5	0.3	0.1	0	0.0	0.0
Backbone-Backbone	382	6.1	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	895	14.3	4	0.4	0.1	0	0.0	0.0
Sidechain-Sidechain	167	2.7	1	0.6	0.0	0	0.0	0.0
Medium range ($i-j >1$ & $i-j <5$)	1011	16.2	2	0.2	0.0	0	0.0	0.0
Backbone-Backbone	210	3.4	2	1.0	0.0	0	0.0	0.0
Backbone-Sidechain	496	7.9	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	305	4.9	0	0.0	0.0	0	0.0	0.0
Long range ($i-j \geq 5$)	2591	41.5	17	0.7	0.3	1	0.0	0.0
Backbone-Backbone	253	4.1	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	1175	18.8	9	0.8	0.1	1	0.1	0.0
Sidechain-Sidechain	1163	18.6	8	0.7	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	2	0.0	1	50.0	0.0	0	0.0	0.0
Total	6241	100.0	30	0.5	0.5	1	0.0	0.0
Backbone-Backbone	847	13.6	2	0.2	0.0	0	0.0	0.0
Backbone-Sidechain	3520	56.4	18	0.5	0.3	1	0.0	0.0
Sidechain-Sidechain	1874	30.0	10	0.5	0.2	0	0.0	0.0

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

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



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

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

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

Model ID	Number of violations						Mean (Å)	Max (Å)	SD ⁶ (Å)	Median (Å)
	IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total				
1	0	1	0	8	0	9	0.16	0.21	0.03	0.15
2	0	1	0	3	0	4	0.16	0.21	0.04	0.15
3	1	1	0	3	0	5	0.15	0.21	0.03	0.15
4	1	1	0	8	0	10	0.16	0.24	0.04	0.14
5	0	1	0	4	0	5	0.17	0.21	0.03	0.17
6	1	1	0	4	0	6	0.16	0.2	0.03	0.15
7	0	1	0	6	0	7	0.17	0.21	0.04	0.16
8	1	1	0	5	0	7	0.14	0.21	0.04	0.11
9	2	1	0	4	0	7	0.18	0.22	0.03	0.17
10	1	1	0	5	0	7	0.14	0.21	0.03	0.12
11	0	2	0	6	0	8	0.14	0.2	0.03	0.12

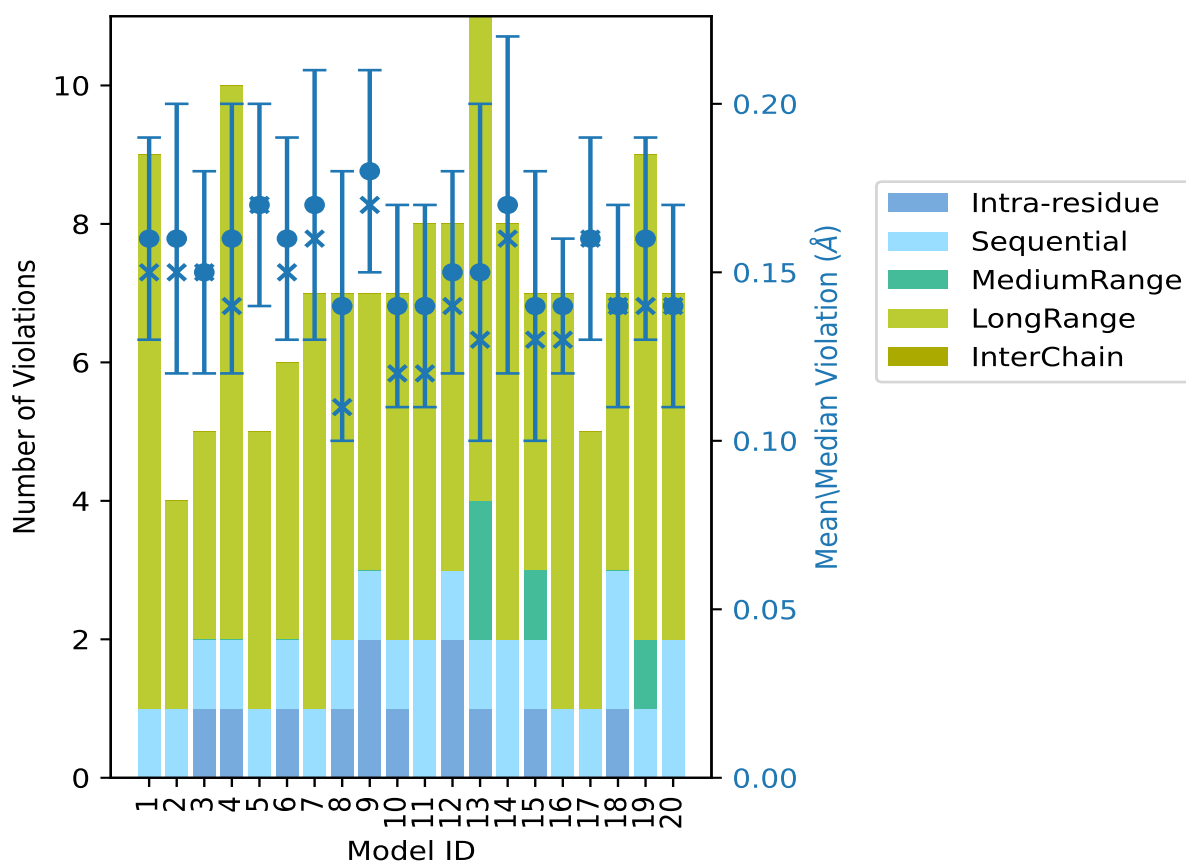
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Model ID	Number of violations					Total	Mean (Å)	Max (Å)	SD ⁶ (Å)	Median (Å)
	IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵					
12	2	1	0	5	0	8	0.15	0.21	0.03	0.14
13	1	1	2	7	0	11	0.15	0.23	0.05	0.13
14	0	2	0	6	0	8	0.17	0.23	0.05	0.16
15	1	1	1	4	0	7	0.14	0.21	0.04	0.13
16	0	1	0	6	0	7	0.14	0.17	0.02	0.13
17	0	1	0	4	0	5	0.16	0.2	0.03	0.16
18	1	2	0	4	0	7	0.14	0.2	0.03	0.14
19	0	1	1	7	0	9	0.16	0.2	0.03	0.14
20	0	2	0	5	0	7	0.14	0.21	0.03	0.14

¹Intra-residue restraints, ²Sequential restraints, ³Medium range restraints, ⁴Long range restraints, ⁵Inter-chain restraints, ⁶Standard deviation

9.2.1 Bar graph : Distance Violation statistics for each model [i](#)



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

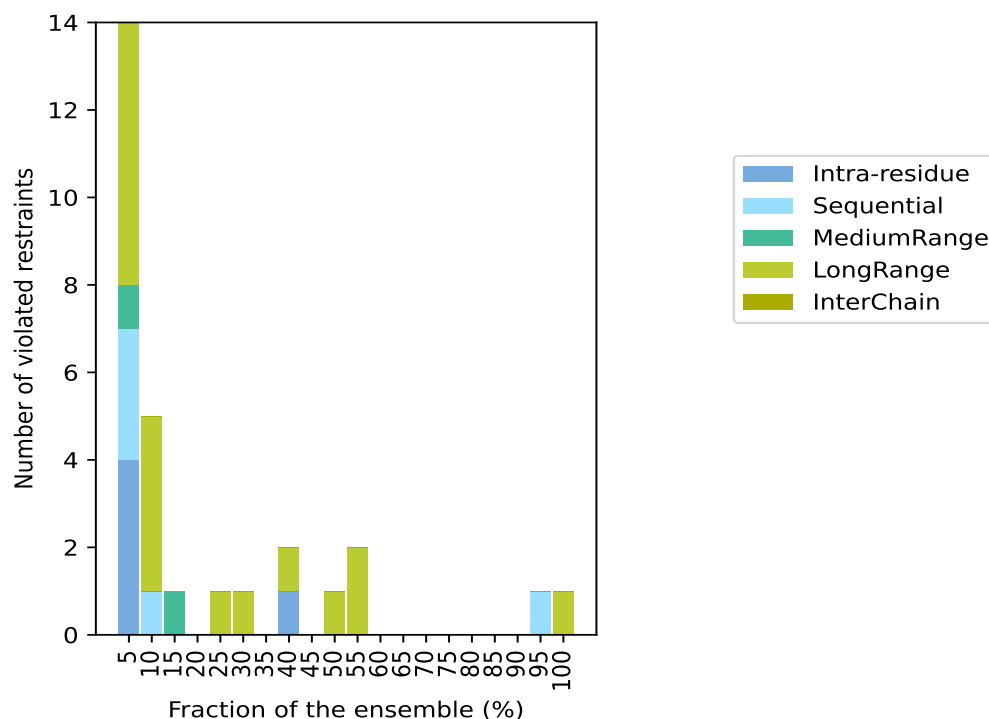
9.3 Distance violation statistics for the ensemble

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, 6210(IR:1188, SQ:1439, MR:1009, LR:2574, 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	%
4	3	1	6	0	14	1	5.0
0	1	0	4	0	5	2	10.0
0	0	1	0	0	1	3	15.0
0	0	0	0	0	0	4	20.0
0	0	0	1	0	1	5	25.0
0	0	0	1	0	1	6	30.0
0	0	0	0	0	0	7	35.0
1	0	0	1	0	2	8	40.0
0	0	0	0	0	0	9	45.0
0	0	0	1	0	1	10	50.0
0	0	0	2	0	2	11	55.0
0	0	0	0	0	0	12	60.0
0	0	0	0	0	0	13	65.0
0	0	0	0	0	0	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	1	0	0	0	1	19	95.0
0	0	0	1	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

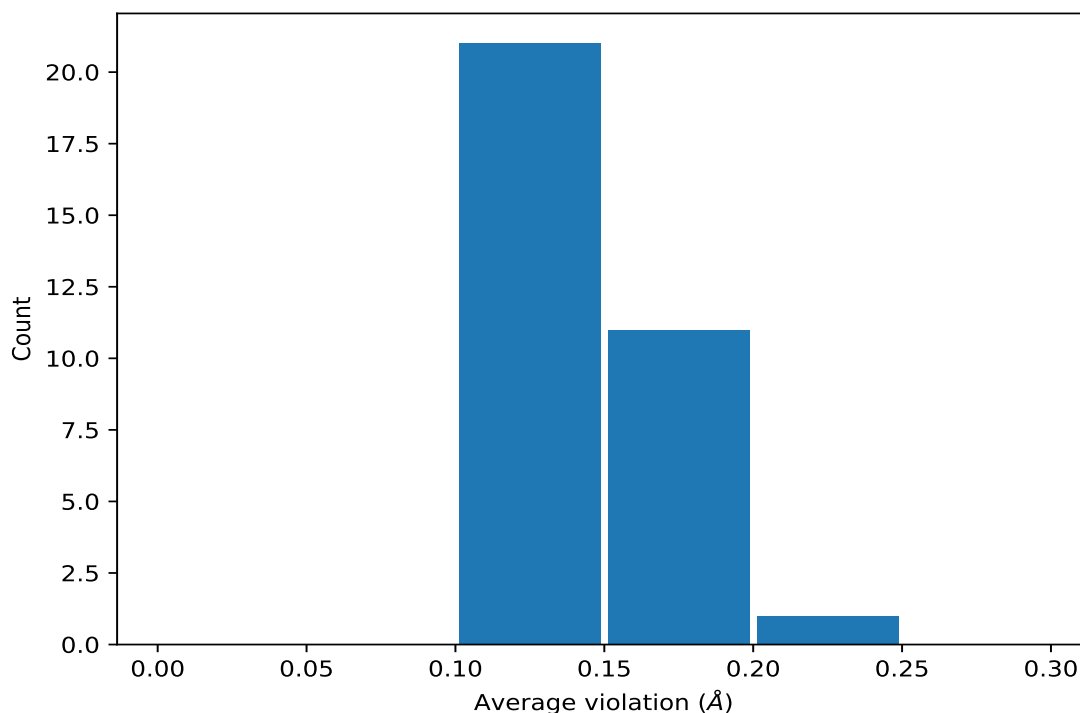
9.3.1 Bar graph : Distance violation statistics for the ensemble [i](#)



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)
(1,5315)	1:A:82:VAL:HG11	1:A:106:HIS:HA	20	0.17	0.01	0.17
(1,5315)	1:A:82:VAL:HG12	1:A:106:HIS:HA	20	0.17	0.01	0.17
(1,5315)	1:A:82:VAL:HG13	1:A:106:HIS:HA	20	0.17	0.01	0.17
(1,5315)	1:A:82:VAL:HG21	1:A:106:HIS:HA	20	0.17	0.01	0.17
(1,5315)	1:A:82:VAL:HG22	1:A:106:HIS:HA	20	0.17	0.01	0.17
(1,5315)	1:A:82:VAL:HG23	1:A:106:HIS:HA	20	0.17	0.01	0.17
(3,4)	1:A:168:CYS:SG	2:A:302:ZN:ZN	19	0.21	0.01	0.21
(1,1)	1:A:7:THR:HA	1:A:8:VAL:HG11	19	0.15	0.01	0.15
(1,1)	1:A:7:THR:HA	1:A:8:VAL:HG12	19	0.15	0.01	0.15
(1,1)	1:A:7:THR:HA	1:A:8:VAL:HG13	19	0.15	0.01	0.15
(3,6)	1:A:90:ASP:OD2	2:A:302:ZN:ZN	11	0.19	0.04	0.2
(1,2305)	1:A:143:PHE:HD1	1:A:155:VAL:HA	11	0.12	0.01	0.11
(1,2305)	1:A:143:PHE:HD2	1:A:155:VAL:HA	11	0.12	0.01	0.11
(1,4452)	1:A:7:THR:HG21	1:A:26:TRP:HZ3	10	0.13	0.01	0.13
(1,4452)	1:A:7:THR:HG22	1:A:26:TRP:HZ3	10	0.13	0.01	0.13
(1,4452)	1:A:7:THR:HG23	1:A:26:TRP:HZ3	10	0.13	0.01	0.13

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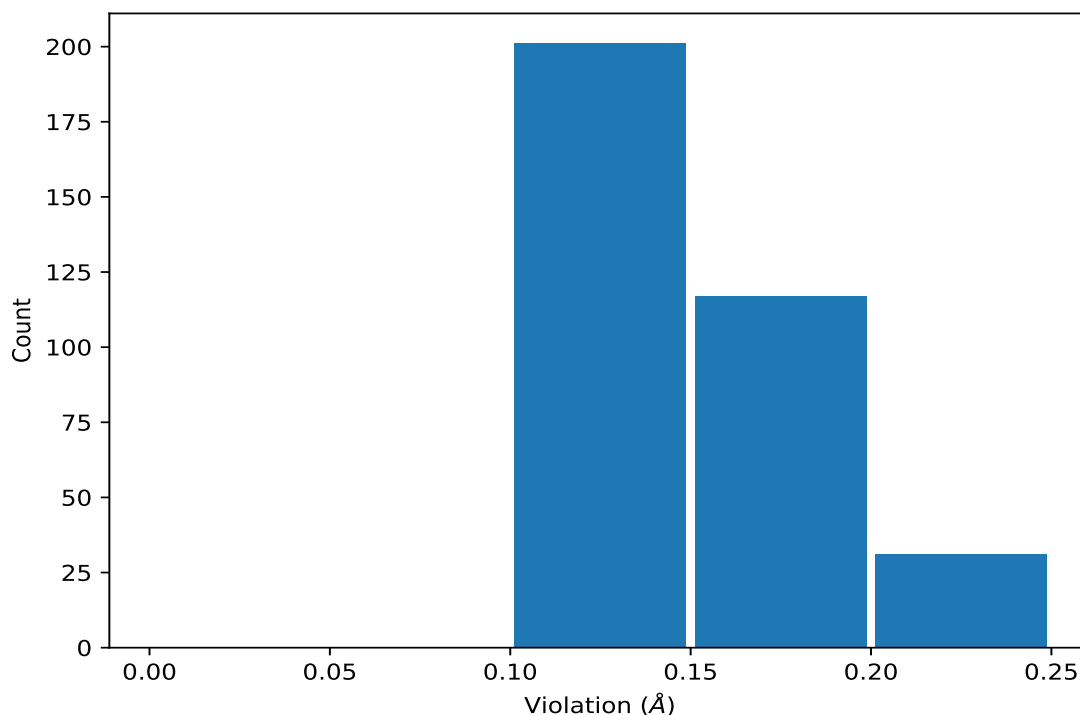
Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,3172)	1:A:47:ASN:H	1:A:47:ASN:HB3	8	0.12	0.01	0.12
(1,6216)	3:A:303:RTD:HA	1:A:210:HIS:HE1	8	0.12	0.01	0.12
(3,5)	1:A:210:HIS:NE2	2:A:302:ZN:ZN	6	0.19	0.02	0.2
(1,2665)	1:A:163:ILE:HB	1:A:204:ASN:H	5	0.12	0.01	0.12
(1,3654)	1:A:134:LYS:HA	1:A:138:MET:H	3	0.12	0.0	0.12
(1,6222)	1:A:34:PHE:HB2	3:A:303:RTD:HD1	2	0.14	0.0	0.14
(1,6222)	1:A:34:PHE:HB2	3:A:303:RTD:HD2	2	0.14	0.0	0.14
(1,6222)	1:A:34:PHE:HB2	3:A:303:RTD:HG1	2	0.14	0.0	0.14
(1,6222)	1:A:34:PHE:HB2	3:A:303:RTD:HG2	2	0.14	0.0	0.14
(1,3195)	1:A:52:LEU:H	1:A:77:LYS:HD2	2	0.12	0.01	0.12
(1,3195)	1:A:52:LEU:H	1:A:77:LYS:HD3	2	0.12	0.01	0.12
(1,423)	1:A:20:GLN:HA	1:A:75:PHE:HE1	2	0.12	0.0	0.12
(1,423)	1:A:20:GLN:HA	1:A:75:PHE:HE2	2	0.12	0.0	0.12
(1,42)	1:A:7:THR:HG21	1:A:8:VAL:HA	2	0.12	0.0	0.12
(1,42)	1:A:7:THR:HG22	1:A:8:VAL:HA	2	0.12	0.0	0.12
(1,42)	1:A:7:THR:HG23	1:A:8:VAL:HA	2	0.12	0.0	0.12
(1,3078)	1:A:21:LEU:HG	1:A:27:VAL:H	2	0.12	0.0	0.12

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)
(3,4)	1:A:168:CYS:SG	2:A:302:ZN:ZN	4	0.24
(3,6)	1:A:90:ASP:OD2	2:A:302:ZN:ZN	4	0.23
(3,6)	1:A:90:ASP:OD2	2:A:302:ZN:ZN	13	0.23
(3,6)	1:A:90:ASP:OD2	2:A:302:ZN:ZN	14	0.23
(3,4)	1:A:168:CYS:SG	2:A:302:ZN:ZN	13	0.23
(3,4)	1:A:168:CYS:SG	2:A:302:ZN:ZN	14	0.23
(3,6)	1:A:90:ASP:OD2	2:A:302:ZN:ZN	9	0.22
(3,4)	1:A:168:CYS:SG	2:A:302:ZN:ZN	9	0.22
(3,6)	1:A:90:ASP:OD2	2:A:302:ZN:ZN	7	0.21
(3,5)	1:A:210:HIS:NE2	2:A:302:ZN:ZN	13	0.21
(3,5)	1:A:210:HIS:NE2	2:A:302:ZN:ZN	14	0.21
(3,4)	1:A:168:CYS:SG	2:A:302:ZN:ZN	1	0.21
(3,4)	1:A:168:CYS:SG	2:A:302:ZN:ZN	2	0.21
(3,4)	1:A:168:CYS:SG	2:A:302:ZN:ZN	3	0.21
(3,4)	1:A:168:CYS:SG	2:A:302:ZN:ZN	5	0.21
(3,4)	1:A:168:CYS:SG	2:A:302:ZN:ZN	7	0.21

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,4)	1:A:168:CYS:SG	2:A:302:ZN:ZN	8	0.21
(3,4)	1:A:168:CYS:SG	2:A:302:ZN:ZN	10	0.21
(3,4)	1:A:168:CYS:SG	2:A:302:ZN:ZN	12	0.21
(3,4)	1:A:168:CYS:SG	2:A:302:ZN:ZN	15	0.21
(3,4)	1:A:168:CYS:SG	2:A:302:ZN:ZN	20	0.21
(3,6)	1:A:90:ASP:OD2	2:A:302:ZN:ZN	1	0.2
(3,6)	1:A:90:ASP:OD2	2:A:302:ZN:ZN	5	0.2
(3,5)	1:A:210:HIS:NE2	2:A:302:ZN:ZN	1	0.2
(3,5)	1:A:210:HIS:NE2	2:A:302:ZN:ZN	7	0.2
(3,5)	1:A:210:HIS:NE2	2:A:302:ZN:ZN	9	0.2
(3,4)	1:A:168:CYS:SG	2:A:302:ZN:ZN	6	0.2
(3,4)	1:A:168:CYS:SG	2:A:302:ZN:ZN	11	0.2
(3,4)	1:A:168:CYS:SG	2:A:302:ZN:ZN	17	0.2
(3,4)	1:A:168:CYS:SG	2:A:302:ZN:ZN	18	0.2
(3,4)	1:A:168:CYS:SG	2:A:302:ZN:ZN	19	0.2
(3,6)	1:A:90:ASP:OD2	2:A:302:ZN:ZN	19	0.19
(2,1)	1:A:9:ILE:HG21	1:A:75:PHE:HE1	19	0.19
(2,1)	1:A:9:ILE:HG21	1:A:75:PHE:HE2	19	0.19
(2,1)	1:A:9:ILE:HG22	1:A:75:PHE:HE1	19	0.19
(2,1)	1:A:9:ILE:HG22	1:A:75:PHE:HE2	19	0.19
(2,1)	1:A:9:ILE:HG23	1:A:75:PHE:HE1	19	0.19
(2,1)	1:A:9:ILE:HG23	1:A:75:PHE:HE2	19	0.19
(1,5315)	1:A:82:VAL:HG11	1:A:106:HIS:HA	4	0.19
(1,5315)	1:A:82:VAL:HG12	1:A:106:HIS:HA	4	0.19
(1,5315)	1:A:82:VAL:HG13	1:A:106:HIS:HA	4	0.19
(1,5315)	1:A:82:VAL:HG21	1:A:106:HIS:HA	4	0.19
(1,5315)	1:A:82:VAL:HG22	1:A:106:HIS:HA	4	0.19
(1,5315)	1:A:82:VAL:HG23	1:A:106:HIS:HA	4	0.19
(1,5315)	1:A:82:VAL:HG11	1:A:106:HIS:HA	6	0.18
(1,5315)	1:A:82:VAL:HG12	1:A:106:HIS:HA	6	0.18
(1,5315)	1:A:82:VAL:HG13	1:A:106:HIS:HA	6	0.18
(1,5315)	1:A:82:VAL:HG21	1:A:106:HIS:HA	6	0.18
(1,5315)	1:A:82:VAL:HG22	1:A:106:HIS:HA	6	0.18
(1,5315)	1:A:82:VAL:HG23	1:A:106:HIS:HA	6	0.18
(1,5315)	1:A:82:VAL:HG11	1:A:106:HIS:HA	8	0.18
(1,5315)	1:A:82:VAL:HG12	1:A:106:HIS:HA	8	0.18
(1,5315)	1:A:82:VAL:HG13	1:A:106:HIS:HA	8	0.18
(1,5315)	1:A:82:VAL:HG21	1:A:106:HIS:HA	8	0.18
(1,5315)	1:A:82:VAL:HG22	1:A:106:HIS:HA	8	0.18
(1,5315)	1:A:82:VAL:HG23	1:A:106:HIS:HA	8	0.18
(1,5315)	1:A:82:VAL:HG11	1:A:106:HIS:HA	12	0.18
(1,5315)	1:A:82:VAL:HG12	1:A:106:HIS:HA	12	0.18

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,5315)	1:A:82:VAL:HG13	1:A:106:HIS:HA	12	0.18
(1,5315)	1:A:82:VAL:HG21	1:A:106:HIS:HA	12	0.18
(1,5315)	1:A:82:VAL:HG22	1:A:106:HIS:HA	12	0.18
(1,5315)	1:A:82:VAL:HG23	1:A:106:HIS:HA	12	0.18
(1,5315)	1:A:82:VAL:HG11	1:A:106:HIS:HA	15	0.18
(1,5315)	1:A:82:VAL:HG12	1:A:106:HIS:HA	15	0.18
(1,5315)	1:A:82:VAL:HG13	1:A:106:HIS:HA	15	0.18
(1,5315)	1:A:82:VAL:HG21	1:A:106:HIS:HA	15	0.18
(1,5315)	1:A:82:VAL:HG22	1:A:106:HIS:HA	15	0.18
(1,5315)	1:A:82:VAL:HG23	1:A:106:HIS:HA	15	0.18
(1,5315)	1:A:82:VAL:HG11	1:A:106:HIS:HA	19	0.18
(1,5315)	1:A:82:VAL:HG12	1:A:106:HIS:HA	19	0.18
(1,5315)	1:A:82:VAL:HG13	1:A:106:HIS:HA	19	0.18
(1,5315)	1:A:82:VAL:HG21	1:A:106:HIS:HA	19	0.18
(1,5315)	1:A:82:VAL:HG22	1:A:106:HIS:HA	19	0.18
(1,5315)	1:A:82:VAL:HG23	1:A:106:HIS:HA	19	0.18
(1,627)	1:A:31:LEU:HG	1:A:39:VAL:HA	16	0.17
(1,5315)	1:A:82:VAL:HG11	1:A:106:HIS:HA	1	0.17
(1,5315)	1:A:82:VAL:HG12	1:A:106:HIS:HA	1	0.17
(1,5315)	1:A:82:VAL:HG13	1:A:106:HIS:HA	1	0.17
(1,5315)	1:A:82:VAL:HG21	1:A:106:HIS:HA	1	0.17
(1,5315)	1:A:82:VAL:HG22	1:A:106:HIS:HA	1	0.17
(1,5315)	1:A:82:VAL:HG23	1:A:106:HIS:HA	1	0.17
(1,5315)	1:A:82:VAL:HG11	1:A:106:HIS:HA	5	0.17
(1,5315)	1:A:82:VAL:HG12	1:A:106:HIS:HA	5	0.17
(1,5315)	1:A:82:VAL:HG13	1:A:106:HIS:HA	5	0.17
(1,5315)	1:A:82:VAL:HG21	1:A:106:HIS:HA	5	0.17
(1,5315)	1:A:82:VAL:HG22	1:A:106:HIS:HA	5	0.17
(1,5315)	1:A:82:VAL:HG23	1:A:106:HIS:HA	5	0.17
(1,5315)	1:A:82:VAL:HG11	1:A:106:HIS:HA	9	0.17
(1,5315)	1:A:82:VAL:HG12	1:A:106:HIS:HA	9	0.17
(1,5315)	1:A:82:VAL:HG13	1:A:106:HIS:HA	9	0.17
(1,5315)	1:A:82:VAL:HG21	1:A:106:HIS:HA	9	0.17
(1,5315)	1:A:82:VAL:HG22	1:A:106:HIS:HA	9	0.17
(1,5315)	1:A:82:VAL:HG23	1:A:106:HIS:HA	9	0.17
(1,5315)	1:A:82:VAL:HG11	1:A:106:HIS:HA	11	0.17
(1,5315)	1:A:82:VAL:HG12	1:A:106:HIS:HA	11	0.17
(1,5315)	1:A:82:VAL:HG13	1:A:106:HIS:HA	11	0.17
(1,5315)	1:A:82:VAL:HG21	1:A:106:HIS:HA	11	0.17
(1,5315)	1:A:82:VAL:HG22	1:A:106:HIS:HA	11	0.17
(1,5315)	1:A:82:VAL:HG23	1:A:106:HIS:HA	11	0.17
(1,5315)	1:A:82:VAL:HG11	1:A:106:HIS:HA	14	0.17

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,5315)	1:A:82:VAL:HG12	1:A:106:HIS:HA	14	0.17
(1,5315)	1:A:82:VAL:HG13	1:A:106:HIS:HA	14	0.17
(1,5315)	1:A:82:VAL:HG21	1:A:106:HIS:HA	14	0.17
(1,5315)	1:A:82:VAL:HG22	1:A:106:HIS:HA	14	0.17
(1,5315)	1:A:82:VAL:HG23	1:A:106:HIS:HA	14	0.17
(1,5315)	1:A:82:VAL:HG11	1:A:106:HIS:HA	18	0.17
(1,5315)	1:A:82:VAL:HG12	1:A:106:HIS:HA	18	0.17
(1,5315)	1:A:82:VAL:HG13	1:A:106:HIS:HA	18	0.17
(1,5315)	1:A:82:VAL:HG21	1:A:106:HIS:HA	18	0.17
(1,5315)	1:A:82:VAL:HG22	1:A:106:HIS:HA	18	0.17
(1,5315)	1:A:82:VAL:HG23	1:A:106:HIS:HA	18	0.17
(1,5315)	1:A:82:VAL:HG11	1:A:106:HIS:HA	7	0.16
(1,5315)	1:A:82:VAL:HG12	1:A:106:HIS:HA	7	0.16
(1,5315)	1:A:82:VAL:HG13	1:A:106:HIS:HA	7	0.16
(1,5315)	1:A:82:VAL:HG21	1:A:106:HIS:HA	7	0.16
(1,5315)	1:A:82:VAL:HG22	1:A:106:HIS:HA	7	0.16
(1,5315)	1:A:82:VAL:HG23	1:A:106:HIS:HA	7	0.16
(1,5315)	1:A:82:VAL:HG11	1:A:106:HIS:HA	13	0.16
(1,5315)	1:A:82:VAL:HG12	1:A:106:HIS:HA	13	0.16
(1,5315)	1:A:82:VAL:HG13	1:A:106:HIS:HA	13	0.16
(1,5315)	1:A:82:VAL:HG21	1:A:106:HIS:HA	13	0.16
(1,5315)	1:A:82:VAL:HG22	1:A:106:HIS:HA	13	0.16
(1,5315)	1:A:82:VAL:HG23	1:A:106:HIS:HA	13	0.16
(1,5315)	1:A:82:VAL:HG11	1:A:106:HIS:HA	16	0.16
(1,5315)	1:A:82:VAL:HG12	1:A:106:HIS:HA	16	0.16
(1,5315)	1:A:82:VAL:HG13	1:A:106:HIS:HA	16	0.16
(1,5315)	1:A:82:VAL:HG21	1:A:106:HIS:HA	16	0.16
(1,5315)	1:A:82:VAL:HG22	1:A:106:HIS:HA	16	0.16
(1,5315)	1:A:82:VAL:HG23	1:A:106:HIS:HA	16	0.16
(1,5315)	1:A:82:VAL:HG11	1:A:106:HIS:HA	17	0.16
(1,5315)	1:A:82:VAL:HG12	1:A:106:HIS:HA	17	0.16
(1,5315)	1:A:82:VAL:HG13	1:A:106:HIS:HA	17	0.16
(1,5315)	1:A:82:VAL:HG21	1:A:106:HIS:HA	17	0.16
(1,5315)	1:A:82:VAL:HG22	1:A:106:HIS:HA	17	0.16
(1,5315)	1:A:82:VAL:HG23	1:A:106:HIS:HA	17	0.16
(1,5315)	1:A:82:VAL:HG11	1:A:106:HIS:HA	20	0.16
(1,5315)	1:A:82:VAL:HG12	1:A:106:HIS:HA	20	0.16
(1,5315)	1:A:82:VAL:HG13	1:A:106:HIS:HA	20	0.16
(1,5315)	1:A:82:VAL:HG21	1:A:106:HIS:HA	20	0.16
(1,5315)	1:A:82:VAL:HG22	1:A:106:HIS:HA	20	0.16
(1,5315)	1:A:82:VAL:HG23	1:A:106:HIS:HA	20	0.16
(1,183)	1:A:96:LYS:HA	1:A:96:LYS:HD2	9	0.16

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,183)	1:A:96:LYS:HA	1:A:96:LYS:HD3	9	0.16
(1,1325)	1:A:78:ARG:HA	1:A:78:ARG:HD2	6	0.16
(1,1325)	1:A:78:ARG:HA	1:A:78:ARG:HD3	6	0.16
(1,1)	1:A:7:THR:HA	1:A:8:VAL:HG11	17	0.16
(1,1)	1:A:7:THR:HA	1:A:8:VAL:HG12	17	0.16
(1,1)	1:A:7:THR:HA	1:A:8:VAL:HG13	17	0.16
(1,5315)	1:A:82:VAL:HG11	1:A:106:HIS:HA	2	0.15
(1,5315)	1:A:82:VAL:HG12	1:A:106:HIS:HA	2	0.15
(1,5315)	1:A:82:VAL:HG13	1:A:106:HIS:HA	2	0.15
(1,5315)	1:A:82:VAL:HG21	1:A:106:HIS:HA	2	0.15
(1,5315)	1:A:82:VAL:HG22	1:A:106:HIS:HA	2	0.15
(1,5315)	1:A:82:VAL:HG23	1:A:106:HIS:HA	2	0.15
(1,5315)	1:A:82:VAL:HG11	1:A:106:HIS:HA	3	0.15
(1,5315)	1:A:82:VAL:HG12	1:A:106:HIS:HA	3	0.15
(1,5315)	1:A:82:VAL:HG13	1:A:106:HIS:HA	3	0.15
(1,5315)	1:A:82:VAL:HG21	1:A:106:HIS:HA	3	0.15
(1,5315)	1:A:82:VAL:HG22	1:A:106:HIS:HA	3	0.15
(1,5315)	1:A:82:VAL:HG23	1:A:106:HIS:HA	3	0.15
(1,5315)	1:A:82:VAL:HG11	1:A:106:HIS:HA	10	0.15
(1,5315)	1:A:82:VAL:HG12	1:A:106:HIS:HA	10	0.15
(1,5315)	1:A:82:VAL:HG13	1:A:106:HIS:HA	10	0.15
(1,5315)	1:A:82:VAL:HG21	1:A:106:HIS:HA	10	0.15
(1,5315)	1:A:82:VAL:HG22	1:A:106:HIS:HA	10	0.15
(1,5315)	1:A:82:VAL:HG23	1:A:106:HIS:HA	10	0.15
(1,1)	1:A:7:THR:HA	1:A:8:VAL:HG11	1	0.15
(1,1)	1:A:7:THR:HA	1:A:8:VAL:HG12	1	0.15
(1,1)	1:A:7:THR:HA	1:A:8:VAL:HG13	1	0.15
(1,1)	1:A:7:THR:HA	1:A:8:VAL:HG11	2	0.15
(1,1)	1:A:7:THR:HA	1:A:8:VAL:HG12	2	0.15
(1,1)	1:A:7:THR:HA	1:A:8:VAL:HG13	2	0.15
(1,1)	1:A:7:THR:HA	1:A:8:VAL:HG11	3	0.15
(1,1)	1:A:7:THR:HA	1:A:8:VAL:HG12	3	0.15
(1,1)	1:A:7:THR:HA	1:A:8:VAL:HG13	3	0.15
(1,1)	1:A:7:THR:HA	1:A:8:VAL:HG11	4	0.15
(1,1)	1:A:7:THR:HA	1:A:8:VAL:HG12	4	0.15
(1,1)	1:A:7:THR:HA	1:A:8:VAL:HG13	4	0.15
(1,1)	1:A:7:THR:HA	1:A:8:VAL:HG11	5	0.15
(1,1)	1:A:7:THR:HA	1:A:8:VAL:HG12	5	0.15
(1,1)	1:A:7:THR:HA	1:A:8:VAL:HG13	5	0.15
(1,1)	1:A:7:THR:HA	1:A:8:VAL:HG11	7	0.15
(1,1)	1:A:7:THR:HA	1:A:8:VAL:HG12	7	0.15
(1,1)	1:A:7:THR:HA	1:A:8:VAL:HG13	7	0.15

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1)	1:A:7:THR:HA	1:A:8:VAL:HG11	9	0.15
(1,1)	1:A:7:THR:HA	1:A:8:VAL:HG12	9	0.15
(1,1)	1:A:7:THR:HA	1:A:8:VAL:HG13	9	0.15
(1,1)	1:A:7:THR:HA	1:A:8:VAL:HG11	10	0.15
(1,1)	1:A:7:THR:HA	1:A:8:VAL:HG12	10	0.15
(1,1)	1:A:7:THR:HA	1:A:8:VAL:HG13	10	0.15
(1,1)	1:A:7:THR:HA	1:A:8:VAL:HG11	11	0.15
(1,1)	1:A:7:THR:HA	1:A:8:VAL:HG12	11	0.15
(1,1)	1:A:7:THR:HA	1:A:8:VAL:HG13	11	0.15
(1,1)	1:A:7:THR:HA	1:A:8:VAL:HG11	12	0.15
(1,1)	1:A:7:THR:HA	1:A:8:VAL:HG12	12	0.15
(1,1)	1:A:7:THR:HA	1:A:8:VAL:HG13	12	0.15
(1,1)	1:A:7:THR:HA	1:A:8:VAL:HG11	13	0.15
(1,1)	1:A:7:THR:HA	1:A:8:VAL:HG12	13	0.15
(1,1)	1:A:7:THR:HA	1:A:8:VAL:HG13	13	0.15
(1,1)	1:A:7:THR:HA	1:A:8:VAL:HG11	14	0.15
(1,1)	1:A:7:THR:HA	1:A:8:VAL:HG12	14	0.15
(1,1)	1:A:7:THR:HA	1:A:8:VAL:HG13	14	0.15
(1,1)	1:A:7:THR:HA	1:A:8:VAL:HG11	15	0.15
(1,1)	1:A:7:THR:HA	1:A:8:VAL:HG12	15	0.15
(1,1)	1:A:7:THR:HA	1:A:8:VAL:HG13	15	0.15
(1,1)	1:A:7:THR:HA	1:A:8:VAL:HG11	16	0.15
(1,1)	1:A:7:THR:HA	1:A:8:VAL:HG12	16	0.15
(1,1)	1:A:7:THR:HA	1:A:8:VAL:HG13	16	0.15
(1,1)	1:A:7:THR:HA	1:A:8:VAL:HG11	18	0.15
(1,1)	1:A:7:THR:HA	1:A:8:VAL:HG12	18	0.15
(1,1)	1:A:7:THR:HA	1:A:8:VAL:HG13	18	0.15
(1,1)	1:A:7:THR:HA	1:A:8:VAL:HG11	20	0.15
(1,1)	1:A:7:THR:HA	1:A:8:VAL:HG12	20	0.15
(1,1)	1:A:7:THR:HA	1:A:8:VAL:HG13	20	0.15
(3,6)	1:A:90:ASP:OD2	2:A:302:ZN:ZN	6	0.14
(3,5)	1:A:210:HIS:NE2	2:A:302:ZN:ZN	4	0.14
(1,6222)	1:A:34:PHE:HB2	3:A:303:RTD:HD1	1	0.14
(1,6222)	1:A:34:PHE:HB2	3:A:303:RTD:HD2	1	0.14
(1,6222)	1:A:34:PHE:HB2	3:A:303:RTD:HG1	1	0.14
(1,6222)	1:A:34:PHE:HB2	3:A:303:RTD:HG2	1	0.14
(1,6222)	1:A:34:PHE:HB2	3:A:303:RTD:HD1	19	0.14
(1,6222)	1:A:34:PHE:HB2	3:A:303:RTD:HD2	19	0.14
(1,6222)	1:A:34:PHE:HB2	3:A:303:RTD:HG1	19	0.14
(1,6222)	1:A:34:PHE:HB2	3:A:303:RTD:HG2	19	0.14
(1,4452)	1:A:7:THR:HG21	1:A:26:TRP:HZ3	1	0.14
(1,4452)	1:A:7:THR:HG22	1:A:26:TRP:HZ3	1	0.14

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,4452)	1:A:7:THR:HG23	1:A:26:TRP:HZ3	1	0.14
(1,4452)	1:A:7:THR:HG21	1:A:26:TRP:HZ3	4	0.14
(1,4452)	1:A:7:THR:HG22	1:A:26:TRP:HZ3	4	0.14
(1,4452)	1:A:7:THR:HG23	1:A:26:TRP:HZ3	4	0.14
(1,4452)	1:A:7:THR:HG21	1:A:26:TRP:HZ3	19	0.14
(1,4452)	1:A:7:THR:HG22	1:A:26:TRP:HZ3	19	0.14
(1,4452)	1:A:7:THR:HG23	1:A:26:TRP:HZ3	19	0.14
(1,4452)	1:A:7:THR:HG21	1:A:26:TRP:HZ3	20	0.14
(1,4452)	1:A:7:THR:HG22	1:A:26:TRP:HZ3	20	0.14
(1,4452)	1:A:7:THR:HG23	1:A:26:TRP:HZ3	20	0.14
(1,3172)	1:A:47:ASN:H	1:A:47:ASN:HB3	12	0.14
(1,3172)	1:A:47:ASN:H	1:A:47:ASN:HB3	18	0.14
(1,1)	1:A:7:THR:HA	1:A:8:VAL:HG11	6	0.14
(1,1)	1:A:7:THR:HA	1:A:8:VAL:HG12	6	0.14
(1,1)	1:A:7:THR:HA	1:A:8:VAL:HG13	6	0.14
(1,6216)	3:A:303:RTD:HA	1:A:210:HIS:HE1	1	0.13
(1,6216)	3:A:303:RTD:HA	1:A:210:HIS:HE1	16	0.13
(1,4452)	1:A:7:THR:HG21	1:A:26:TRP:HZ3	12	0.13
(1,4452)	1:A:7:THR:HG22	1:A:26:TRP:HZ3	12	0.13
(1,4452)	1:A:7:THR:HG23	1:A:26:TRP:HZ3	12	0.13
(1,4452)	1:A:7:THR:HG21	1:A:26:TRP:HZ3	13	0.13
(1,4452)	1:A:7:THR:HG22	1:A:26:TRP:HZ3	13	0.13
(1,4452)	1:A:7:THR:HG23	1:A:26:TRP:HZ3	13	0.13
(1,4452)	1:A:7:THR:HG21	1:A:26:TRP:HZ3	17	0.13
(1,4452)	1:A:7:THR:HG22	1:A:26:TRP:HZ3	17	0.13
(1,4452)	1:A:7:THR:HG23	1:A:26:TRP:HZ3	17	0.13
(1,3381)	1:A:32:GLY:H	1:A:39:VAL:HB	16	0.13
(1,3195)	1:A:52:LEU:H	1:A:77:LYS:HD2	16	0.13
(1,3195)	1:A:52:LEU:H	1:A:77:LYS:HD3	16	0.13
(1,3172)	1:A:47:ASN:H	1:A:47:ASN:HB3	4	0.13
(1,2665)	1:A:163:ILE:HB	1:A:204:ASN:H	4	0.13
(1,2305)	1:A:143:PHE:HD1	1:A:155:VAL:HA	11	0.13
(1,2305)	1:A:143:PHE:HD2	1:A:155:VAL:HA	11	0.13
(1,2305)	1:A:143:PHE:HD1	1:A:155:VAL:HA	15	0.13
(1,2305)	1:A:143:PHE:HD2	1:A:155:VAL:HA	15	0.13
(1,2305)	1:A:143:PHE:HD1	1:A:155:VAL:HA	17	0.13
(1,2305)	1:A:143:PHE:HD2	1:A:155:VAL:HA	17	0.13
(1,19)	1:A:7:THR:HB	1:A:8:VAL:HB	8	0.13
(1,1550)	1:A:96:LYS:HA	1:A:96:LYS:HG3	9	0.13
(1,1)	1:A:7:THR:HA	1:A:8:VAL:HG11	19	0.13
(1,1)	1:A:7:THR:HA	1:A:8:VAL:HG12	19	0.13
(1,1)	1:A:7:THR:HA	1:A:8:VAL:HG13	19	0.13

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,6)	1:A:90:ASP:OD2	2:A:302:ZN:ZN	18	0.12
(1,663)	1:A:34:PHE:HA	1:A:37:GLU:H	13	0.12
(1,653)	1:A:31:LEU:HD21	1:A:38:ALA:HB1	16	0.12
(1,653)	1:A:31:LEU:HD21	1:A:38:ALA:HB2	16	0.12
(1,653)	1:A:31:LEU:HD21	1:A:38:ALA:HB3	16	0.12
(1,653)	1:A:31:LEU:HD22	1:A:38:ALA:HB1	16	0.12
(1,653)	1:A:31:LEU:HD22	1:A:38:ALA:HB2	16	0.12
(1,653)	1:A:31:LEU:HD22	1:A:38:ALA:HB3	16	0.12
(1,653)	1:A:31:LEU:HD23	1:A:38:ALA:HB1	16	0.12
(1,653)	1:A:31:LEU:HD23	1:A:38:ALA:HB2	16	0.12
(1,653)	1:A:31:LEU:HD23	1:A:38:ALA:HB3	16	0.12
(1,6216)	3:A:303:RTD:HA	1:A:210:HIS:HE1	10	0.12
(1,6216)	3:A:303:RTD:HA	1:A:210:HIS:HE1	12	0.12
(1,6216)	3:A:303:RTD:HA	1:A:210:HIS:HE1	13	0.12
(1,4452)	1:A:7:THR:HG21	1:A:26:TRP:HZ3	7	0.12
(1,4452)	1:A:7:THR:HG22	1:A:26:TRP:HZ3	7	0.12
(1,4452)	1:A:7:THR:HG23	1:A:26:TRP:HZ3	7	0.12
(1,4452)	1:A:7:THR:HG21	1:A:26:TRP:HZ3	10	0.12
(1,4452)	1:A:7:THR:HG22	1:A:26:TRP:HZ3	10	0.12
(1,4452)	1:A:7:THR:HG23	1:A:26:TRP:HZ3	10	0.12
(1,423)	1:A:20:GLN:HA	1:A:75:PHE:HE1	5	0.12
(1,423)	1:A:20:GLN:HA	1:A:75:PHE:HE2	5	0.12
(1,423)	1:A:20:GLN:HA	1:A:75:PHE:HE1	14	0.12
(1,423)	1:A:20:GLN:HA	1:A:75:PHE:HE2	14	0.12
(1,42)	1:A:7:THR:HG21	1:A:8:VAL:HA	11	0.12
(1,42)	1:A:7:THR:HG22	1:A:8:VAL:HA	11	0.12
(1,42)	1:A:7:THR:HG23	1:A:8:VAL:HA	11	0.12
(1,3795)	1:A:160:GLN:H	1:A:160:GLN:HG2	12	0.12
(1,3654)	1:A:134:LYS:HA	1:A:138:MET:H	15	0.12
(1,3654)	1:A:134:LYS:HA	1:A:138:MET:H	19	0.12
(1,3195)	1:A:52:LEU:H	1:A:77:LYS:HD2	11	0.12
(1,3195)	1:A:52:LEU:H	1:A:77:LYS:HD3	11	0.12
(1,3172)	1:A:47:ASN:H	1:A:47:ASN:HB3	3	0.12
(1,3172)	1:A:47:ASN:H	1:A:47:ASN:HB3	10	0.12
(1,3078)	1:A:21:LEU:HG	1:A:27:VAL:H	11	0.12
(1,2665)	1:A:163:ILE:HB	1:A:204:ASN:H	12	0.12
(1,2665)	1:A:163:ILE:HB	1:A:204:ASN:H	13	0.12
(1,2665)	1:A:163:ILE:HB	1:A:204:ASN:H	20	0.12
(1,2305)	1:A:143:PHE:HD1	1:A:155:VAL:HA	10	0.12
(1,2305)	1:A:143:PHE:HD2	1:A:155:VAL:HA	10	0.12
(1,2305)	1:A:143:PHE:HD1	1:A:155:VAL:HA	14	0.12
(1,2305)	1:A:143:PHE:HD2	1:A:155:VAL:HA	14	0.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,6)	1:A:90:ASP:OD2	2:A:302:ZN:ZN	20	0.11
(1,6216)	3:A:303:RTD:HA	1:A:210:HIS:HE1	4	0.11
(1,6216)	3:A:303:RTD:HA	1:A:210:HIS:HE1	8	0.11
(1,6216)	3:A:303:RTD:HA	1:A:210:HIS:HE1	11	0.11
(1,6062)	1:A:206:VAL:HG11	1:A:218:LEU:HG	15	0.11
(1,6062)	1:A:206:VAL:HG12	1:A:218:LEU:HG	15	0.11
(1,6062)	1:A:206:VAL:HG13	1:A:218:LEU:HG	15	0.11
(1,6062)	1:A:206:VAL:HG21	1:A:218:LEU:HG	15	0.11
(1,6062)	1:A:206:VAL:HG22	1:A:218:LEU:HG	15	0.11
(1,6062)	1:A:206:VAL:HG23	1:A:218:LEU:HG	15	0.11
(1,551)	1:A:209:GLY:HA3	1:A:210:HIS:HB2	18	0.11
(1,4753)	1:A:26:TRP:HD1	1:A:47:ASN:HB2	8	0.11
(1,4753)	1:A:26:TRP:HD1	1:A:47:ASN:HB3	8	0.11
(1,4452)	1:A:7:THR:HG21	1:A:26:TRP:HZ3	18	0.11
(1,4452)	1:A:7:THR:HG22	1:A:26:TRP:HZ3	18	0.11
(1,4452)	1:A:7:THR:HG23	1:A:26:TRP:HZ3	18	0.11
(1,42)	1:A:7:THR:HG21	1:A:8:VAL:HA	14	0.11
(1,42)	1:A:7:THR:HG22	1:A:8:VAL:HA	14	0.11
(1,42)	1:A:7:THR:HG23	1:A:8:VAL:HA	14	0.11
(1,3654)	1:A:134:LYS:HA	1:A:138:MET:H	13	0.11
(1,3433)	1:A:96:LYS:HD2	1:A:97:THR:H	20	0.11
(1,3433)	1:A:96:LYS:HD3	1:A:97:THR:H	20	0.11
(1,3172)	1:A:47:ASN:H	1:A:47:ASN:HB3	8	0.11
(1,3172)	1:A:47:ASN:H	1:A:47:ASN:HB3	13	0.11
(1,3172)	1:A:47:ASN:H	1:A:47:ASN:HB3	15	0.11
(1,3078)	1:A:21:LEU:HG	1:A:27:VAL:H	7	0.11
(1,2665)	1:A:163:ILE:HB	1:A:204:ASN:H	8	0.11
(1,2305)	1:A:143:PHE:HD1	1:A:155:VAL:HA	1	0.11
(1,2305)	1:A:143:PHE:HD2	1:A:155:VAL:HA	1	0.11
(1,2305)	1:A:143:PHE:HD1	1:A:155:VAL:HA	2	0.11
(1,2305)	1:A:143:PHE:HD2	1:A:155:VAL:HA	2	0.11
(1,2305)	1:A:143:PHE:HD1	1:A:155:VAL:HA	3	0.11
(1,2305)	1:A:143:PHE:HD2	1:A:155:VAL:HA	3	0.11
(1,2305)	1:A:143:PHE:HD1	1:A:155:VAL:HA	4	0.11
(1,2305)	1:A:143:PHE:HD2	1:A:155:VAL:HA	4	0.11
(1,2305)	1:A:143:PHE:HD1	1:A:155:VAL:HA	6	0.11
(1,2305)	1:A:143:PHE:HD2	1:A:155:VAL:HA	6	0.11
(1,2305)	1:A:143:PHE:HD1	1:A:155:VAL:HA	19	0.11
(1,2305)	1:A:143:PHE:HD2	1:A:155:VAL:HA	19	0.11

10 Dihedral-angle violation analysis

No dihedral-angle restraints found