



Full wwPDB NMR Structure Validation Report ⓘ

Mar 9, 2026 – 02:42 AM UTC

PDB ID : 2KW8 / pdb_00002kw8
BMRB ID : 16811
Title : Solution Structure of Bacillus anthracis Sortase A (SrtA) Transpeptidase
Authors : Weiner, E.M.; Robson, S.A.; Marohn, M.; Clubb, R.T.
Deposited on : 2010-03-31

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
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

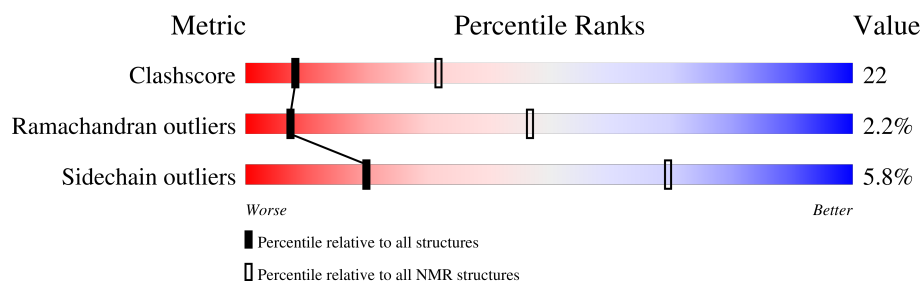
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 88%.

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	158	56% 29% • 13%

2 Ensemble composition and analysis

This entry contains 40 models. Model 8 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:64-A:186, A:196-A:210 (138)	0.50	8

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 5 clusters and 9 single-model clusters were found.

Cluster number	Models
1	1, 3, 6, 7, 8, 13, 14, 15, 19, 23, 25, 27, 29, 31, 36, 38, 39, 40
2	11, 16, 22, 35
3	18, 26, 34, 37
4	20, 21, 30
5	17, 24
Single-model clusters	2; 4; 5; 9; 10; 12; 28; 32; 33

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 2418 atoms, of which 1219 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called LPXTG-site transpeptidase family protein.

Mol	Chain	Residues	Atoms						Trace
1	A	158	Total	C	H	N	O	S	0
			2418	750	1219	201	244	4	

There are 4 discrepancies between the modelled and reference sequences:

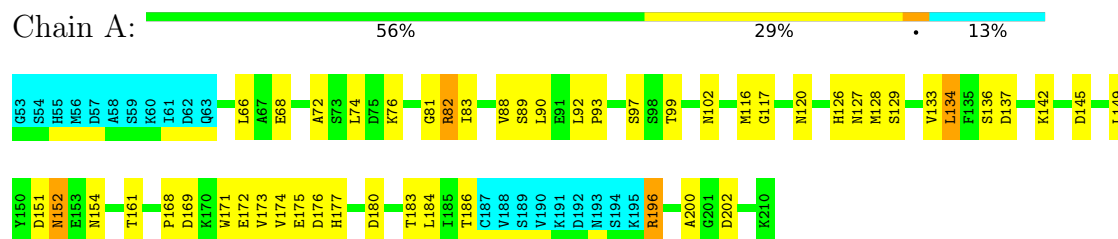
Chain	Residue	Modelled	Actual	Comment	Reference
A	53	GLY	-	expression tag	UNP Q81V16
A	54	SER	-	expression tag	UNP Q81V16
A	55	HIS	-	expression tag	UNP Q81V16
A	56	MET	-	expression tag	UNP Q81V16

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: LPXTG-site transpeptidase family protein

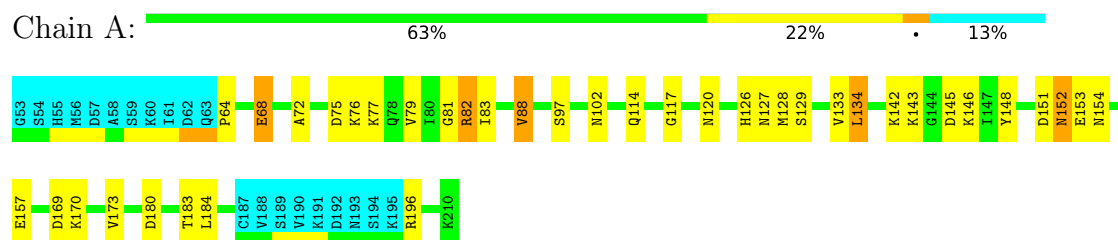


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

- Molecule 1: LPXTG-site transpeptidase family protein



4.2.2 Score per residue for model 2

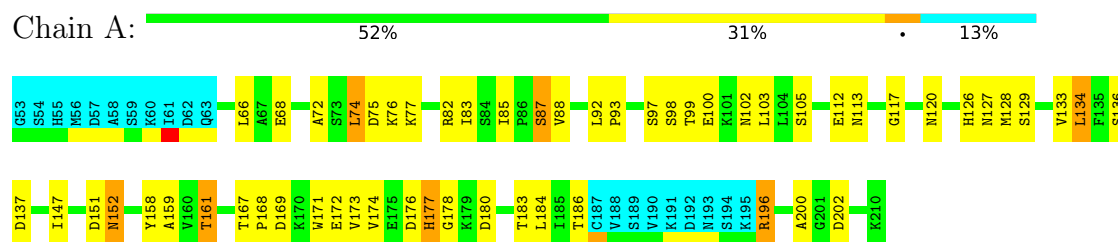
- Molecule 1: LPXTG-site transpeptidase family protein





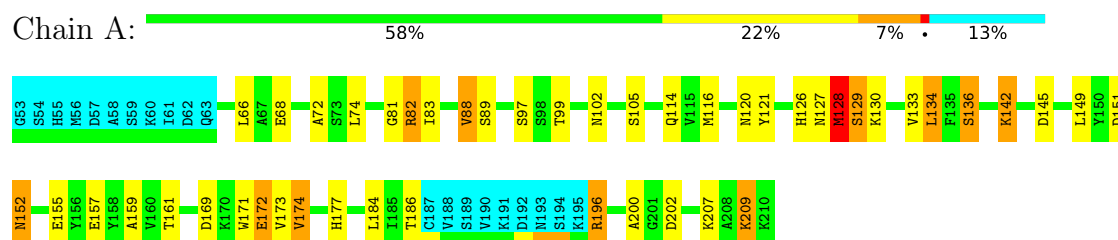
4.2.3 Score per residue for model 3

- Molecule 1: LPXTG-site transpeptidase family protein



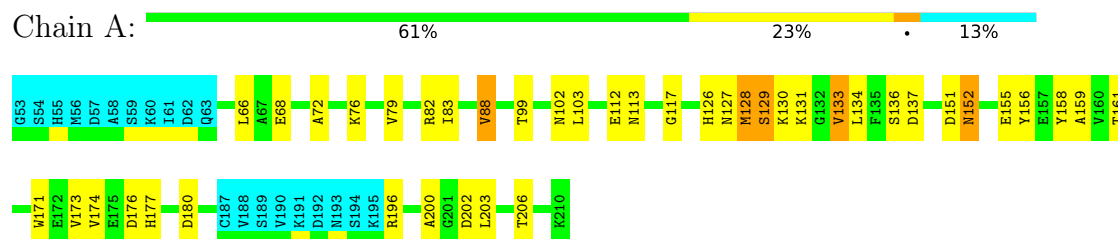
4.2.4 Score per residue for model 4

- Molecule 1: LPXTG-site transpeptidase family protein



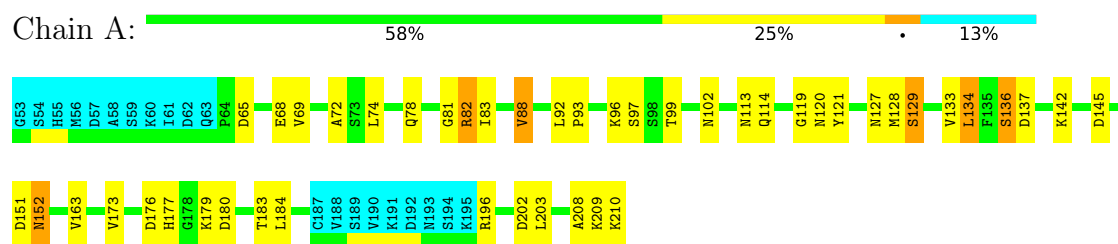
4.2.5 Score per residue for model 5

- Molecule 1: LPXTG-site transpeptidase family protein



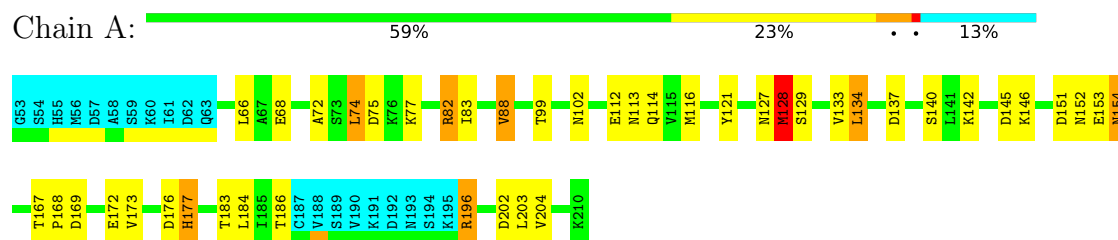
4.2.6 Score per residue for model 6

- Molecule 1: LPXTG-site transpeptidase family protein



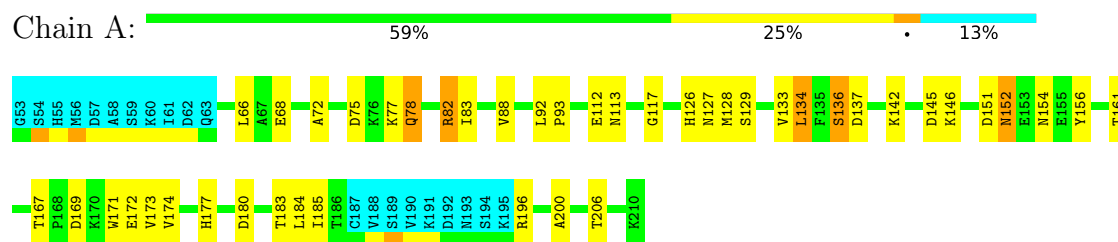
4.2.7 Score per residue for model 7

- Molecule 1: LPXTG-site transpeptidase family protein



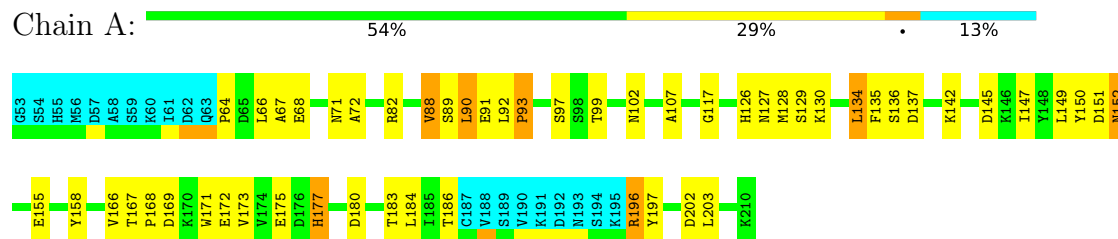
4.2.8 Score per residue for model 8 (medoid)

- Molecule 1: LPXTG-site transpeptidase family protein



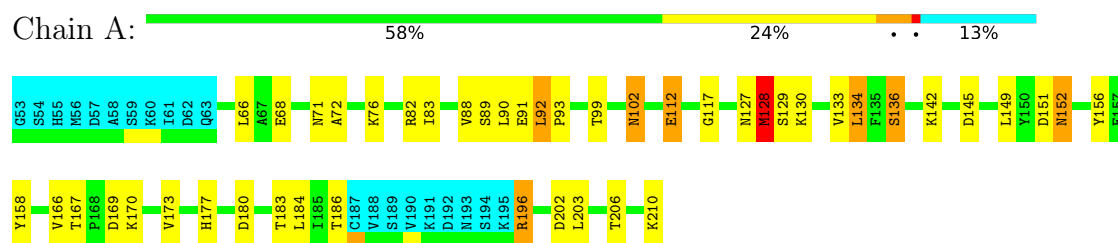
4.2.9 Score per residue for model 9

- Molecule 1: LPXTG-site transpeptidase family protein



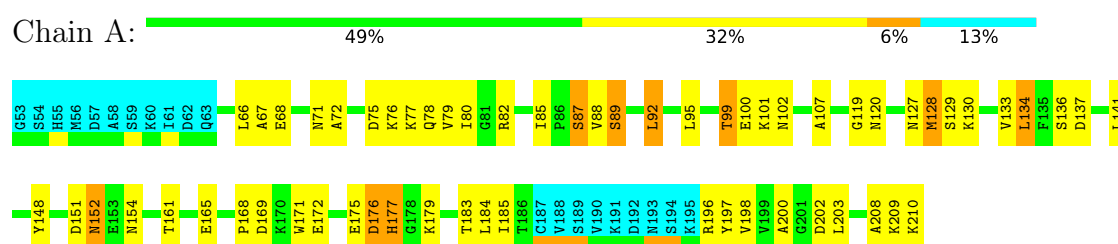
4.2.10 Score per residue for model 10

- Molecule 1: LPXTG-site transpeptidase family protein



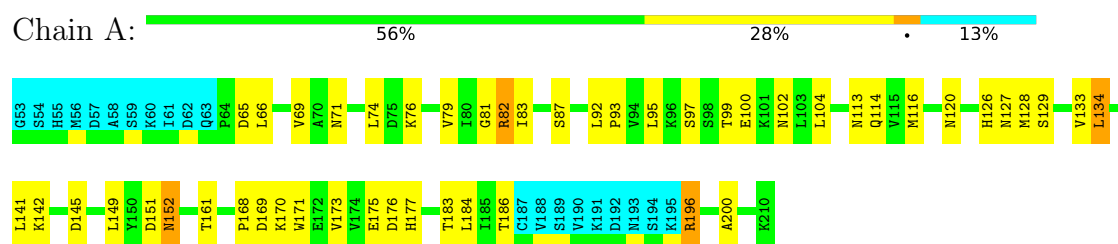
4.2.11 Score per residue for model 11

- Molecule 1: LPXTG-site transpeptidase family protein



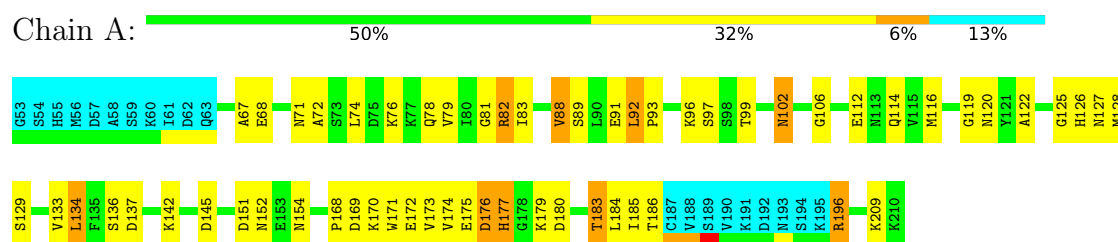
4.2.12 Score per residue for model 12

- Molecule 1: LPXTG-site transpeptidase family protein



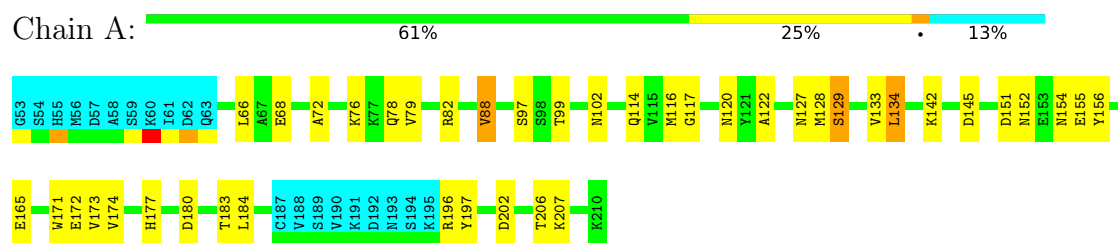
4.2.13 Score per residue for model 13

- Molecule 1: LPXTG-site transpeptidase family protein



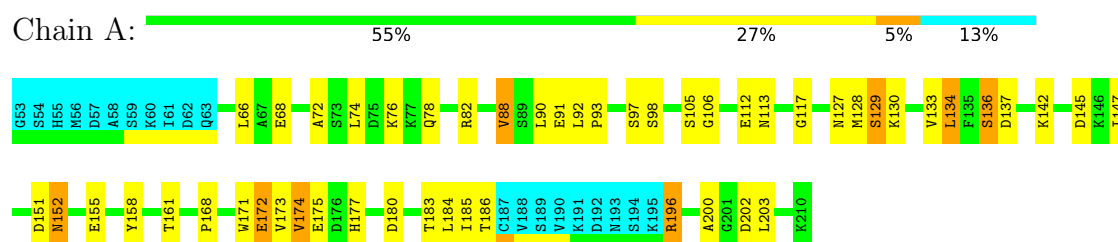
4.2.14 Score per residue for model 14

- Molecule 1: LPXTG-site transpeptidase family protein



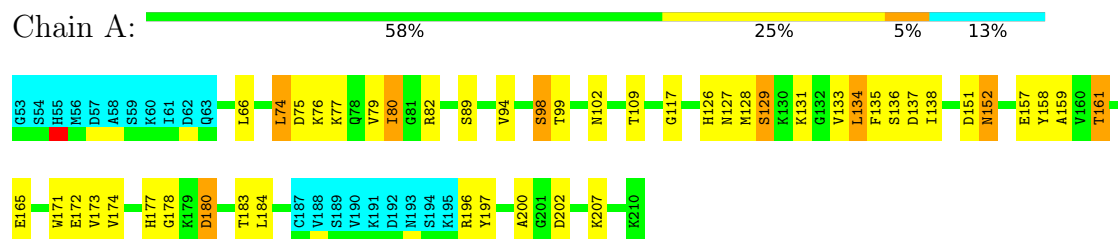
4.2.15 Score per residue for model 15

- Molecule 1: LPXTG-site transpeptidase family protein



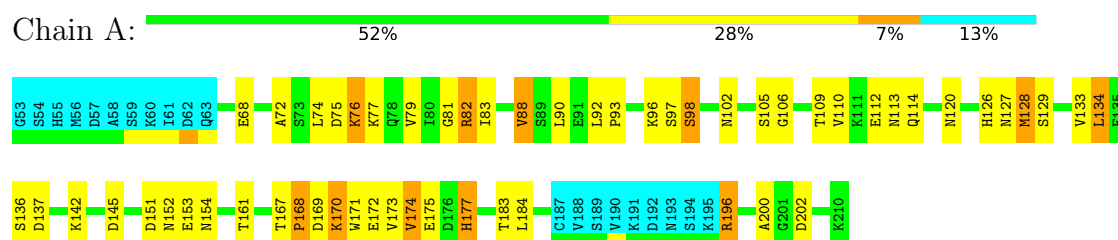
4.2.16 Score per residue for model 16

- Molecule 1: LPXTG-site transpeptidase family protein



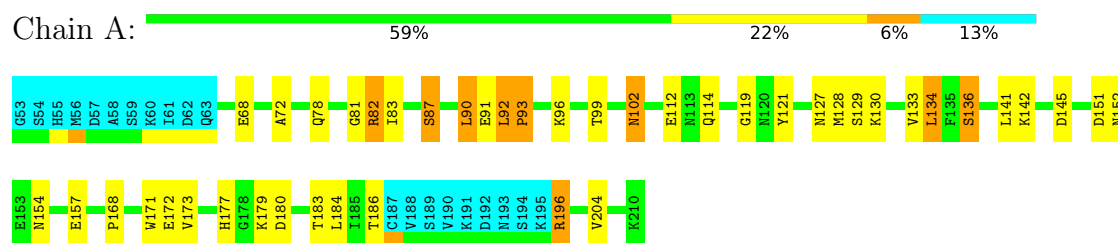
4.2.17 Score per residue for model 17

- Molecule 1: LPXTG-site transpeptidase family protein



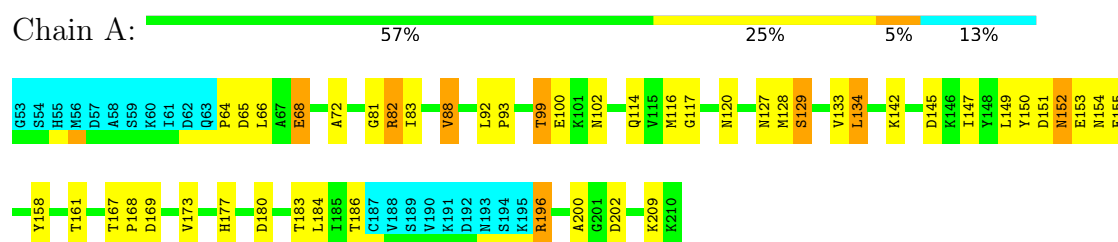
4.2.18 Score per residue for model 18

- Molecule 1: LPXTG-site transpeptidase family protein



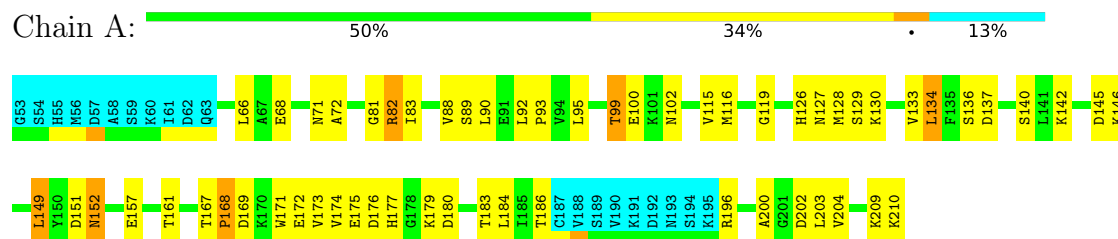
4.2.19 Score per residue for model 19

- Molecule 1: LPXTG-site transpeptidase family protein



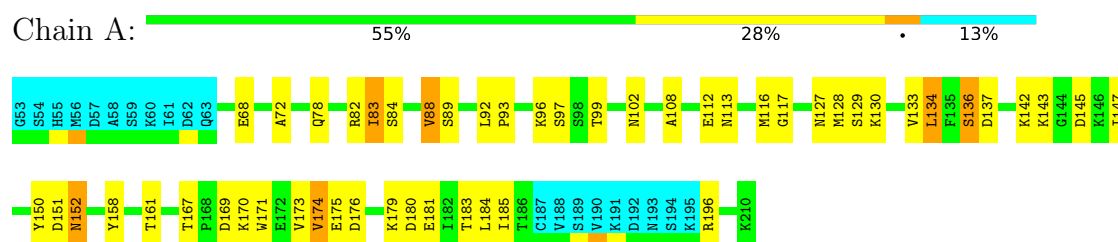
4.2.20 Score per residue for model 20

- Molecule 1: LPXTG-site transpeptidase family protein



4.2.21 Score per residue for model 21

- Molecule 1: LPXTG-site transpeptidase family protein



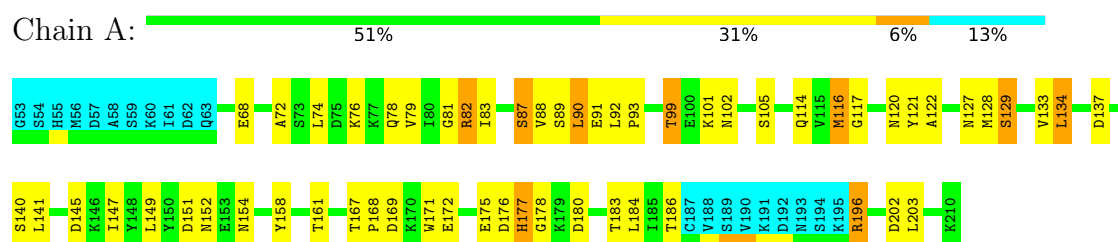
4.2.22 Score per residue for model 22

- Molecule 1: LPXTG-site transpeptidase family protein



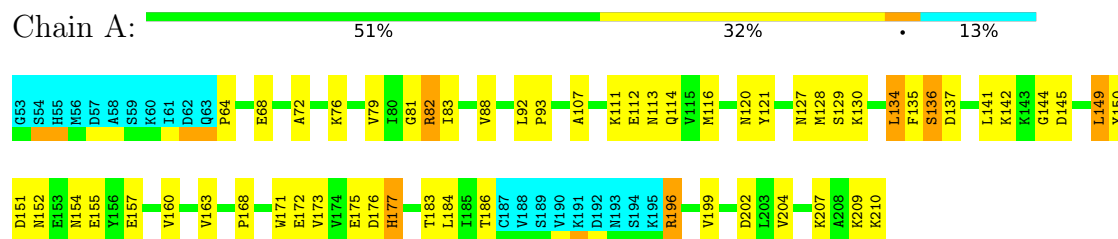
4.2.23 Score per residue for model 23

- Molecule 1: LPXTG-site transpeptidase family protein



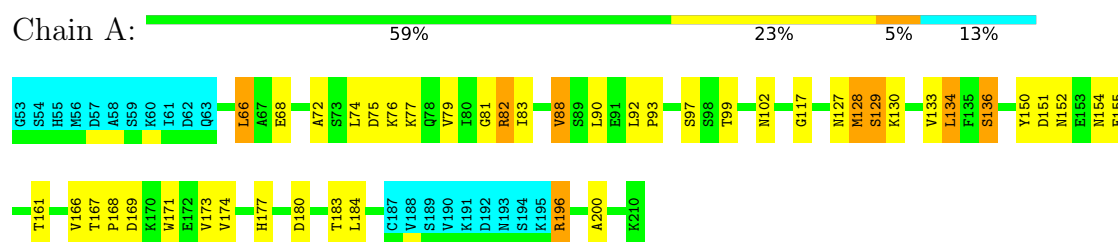
4.2.24 Score per residue for model 24

- Molecule 1: LPXTG-site transpeptidase family protein



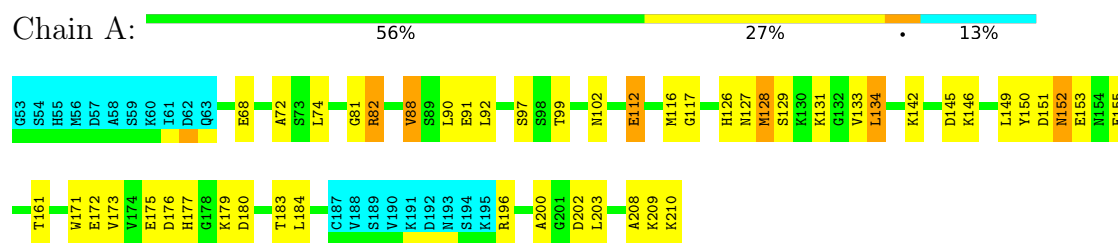
4.2.25 Score per residue for model 25

- Molecule 1: LPXTG-site transpeptidase family protein

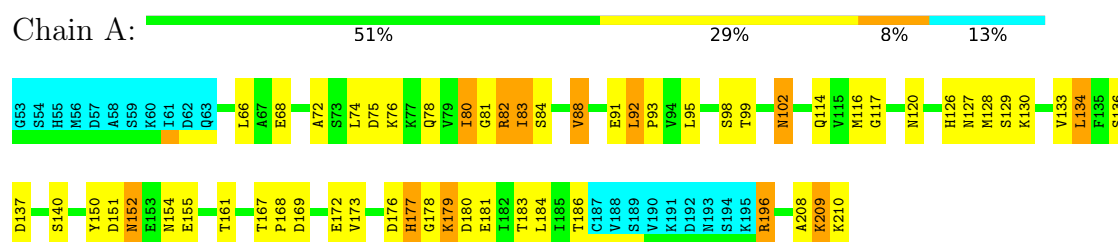


4.2.26 Score per residue for model 26

- Molecule 1: LPXTG-site transpeptidase family protein



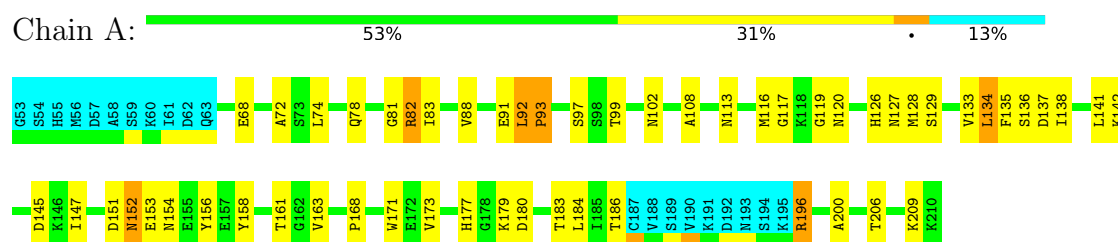
- Molecule 1: LPXTG-site transpeptidase family protein



- Molecule 1: LPXTG-site transpeptidase family protein

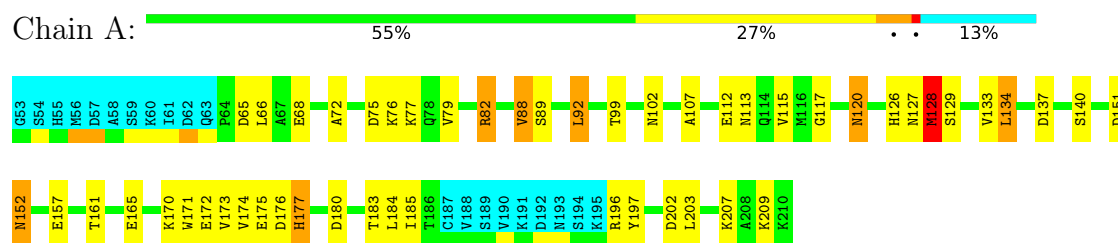


- Molecule 1: LPXTG-site transpeptidase family protein



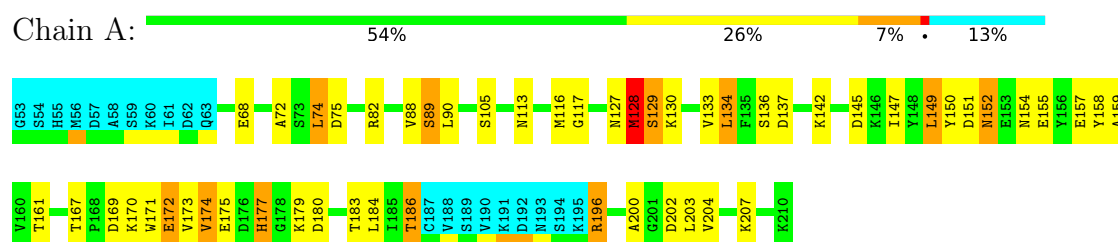
4.2.30 Score per residue for model 30

- Molecule 1: LPXTG-site transpeptidase family protein



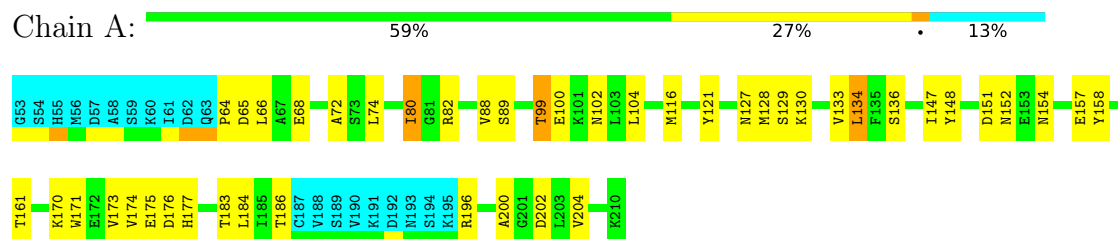
4.2.31 Score per residue for model 31

- Molecule 1: LPXTG-site transpeptidase family protein



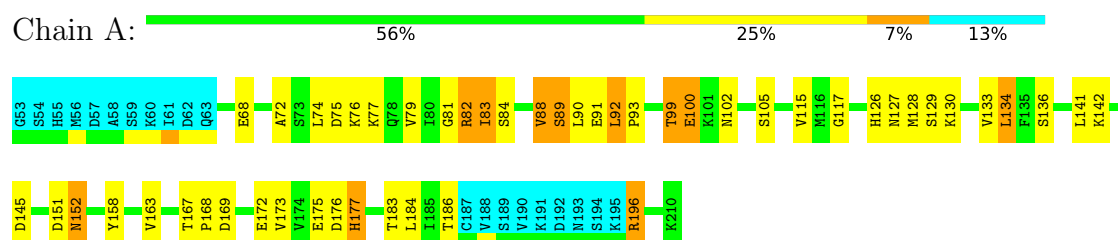
4.2.32 Score per residue for model 32

- Molecule 1: LPXTG-site transpeptidase family protein



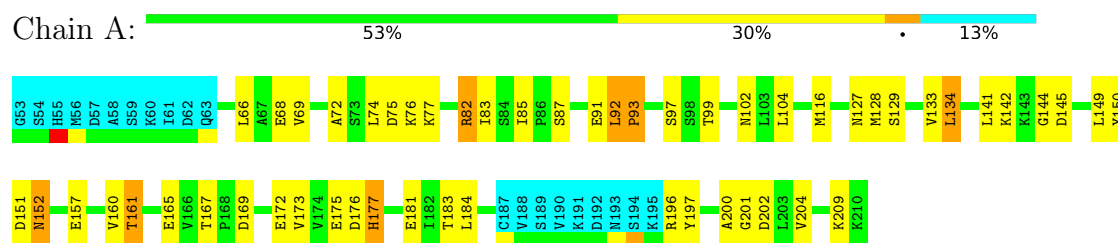
4.2.33 Score per residue for model 33

- Molecule 1: LPXTG-site transpeptidase family protein

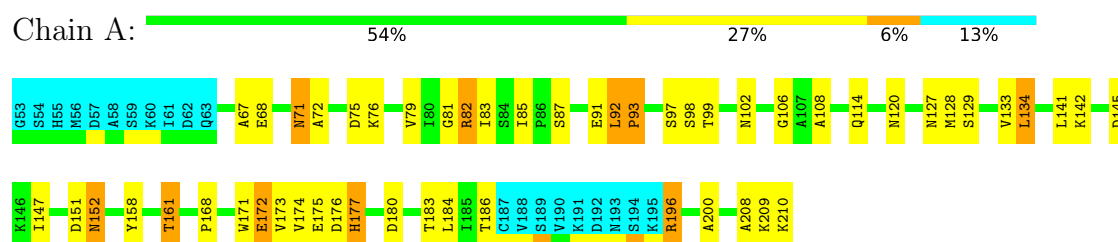


4.2.34 Score per residue for model 34

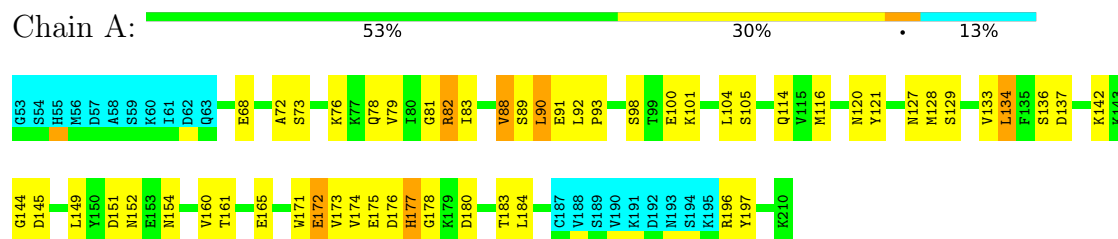
- Molecule 1: LPXTG-site transpeptidase family protein



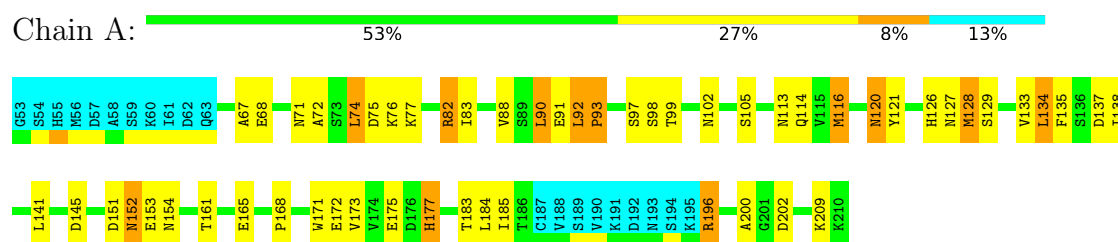
- Molecule 1: LPXTG-site transpeptidase family protein



- Molecule 1: LPXTG-site transpeptidase family protein

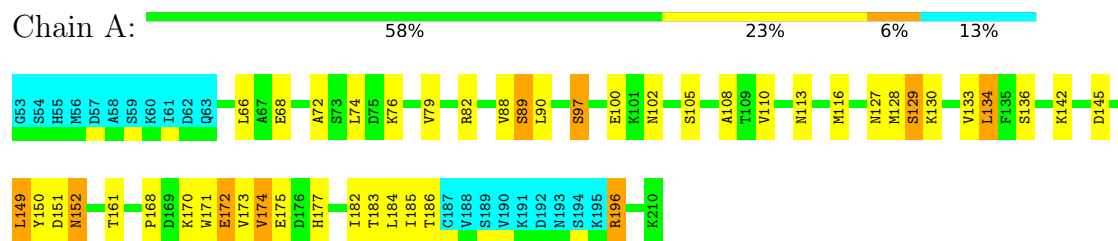


- Molecule 1: LPXTG-site transpeptidase family protein



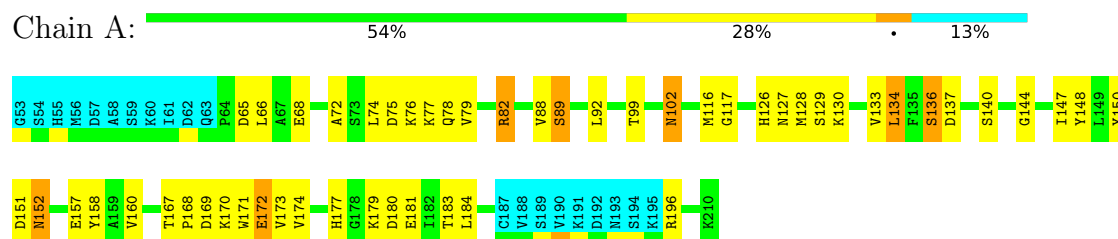
4.2.38 Score per residue for model 38

- Molecule 1: LPXTG-site transpeptidase family protein



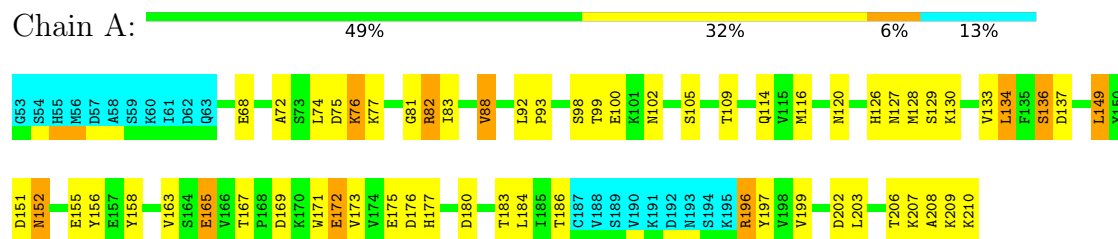
4.2.39 Score per residue for model 39

- Molecule 1: LPXTG-site transpeptidase family protein



4.2.40 Score per residue for model 40

- Molecule 1: LPXTG-site transpeptidase family protein



5 Refinement protocol and experimental data overview

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

Of the 100 calculated structures, 40 were deposited, based on the following criterion: *structures with the least restraint violations*.

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

Software name	Classification	Version
X-PLOR NIH	refinement	
ProcheckNMR	geometry optimization	
TALOS	geometry optimization	

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	1700
Number of shifts mapped to atoms	1700
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	88%

6 Model quality [i](#)

6.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#Z>5	RMSZ	#Z>5
1	A	0.64±0.01	0±0/1066 (0.0± 0.0%)	1.03±0.02	1±0/1437 (0.1± 0.0%)
All	All	0.64	0/42640 (0.0%)	1.03	33/57480 (0.1%)

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

Mol	Chain	Chirality	Planarity
1	A	0.0±0.0	2.0±0.0
All	All	0	80

There are no bond-length outliers.

All unique angle outliers are listed below.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	177	HIS	CA-CB-CG	-5.77	108.03	113.80	36	33

There are no chirality outliers.

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

Mol	Chain	Res	Type	Group	Models (Total)
1	A	82	ARG	Sidechain	40
1	A	196	ARG	Sidechain	40

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	1052	1074	1074	46±6
All	All	42080	42960	42960	1859

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 22.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:173:VAL:O	1:A:183:THR:HG21	0.77	1.80	27	15
1:A:134:LEU:HD23	1:A:134:LEU:N	0.74	1.97	23	14
1:A:91:GLU:O	1:A:92:LEU:HD22	0.71	1.85	13	4
1:A:133:VAL:HG12	1:A:134:LEU:H	0.70	1.46	17	38
1:A:133:VAL:HG12	1:A:134:LEU:N	0.70	2.01	4	36
1:A:146:LYS:HZ1	1:A:204:VAL:HG11	0.69	1.46	20	1
1:A:69:VAL:HG22	1:A:104:LEU:HD22	0.68	1.63	34	1
1:A:82:ARG:O	1:A:149:LEU:HD23	0.68	1.88	19	2
1:A:134:LEU:HD23	1:A:134:LEU:H	0.67	1.48	9	2
1:A:134:LEU:N	1:A:134:LEU:HD23	0.66	2.05	18	25
1:A:137:ASP:CG	1:A:140:SER:HG	0.66	1.99	7	4
1:A:116:MET:HE3	1:A:121:TYR:OH	0.65	1.91	24	6
1:A:87:SER:OG	1:A:141:LEU:HD23	0.64	1.93	11	4
1:A:82:ARG:HH22	1:A:209:LYS:HZ1	0.64	1.36	34	1
1:A:82:ARG:NH1	1:A:209:LYS:NZ	0.64	2.45	13	3
1:A:82:ARG:NH1	1:A:209:LYS:HZ1	0.63	1.91	13	1
1:A:68:GLU:O	1:A:72:ALA:HB2	0.63	1.93	13	38
1:A:99:THR:OG1	1:A:102:ASN:ND2	0.63	2.32	33	23
1:A:173:VAL:HG23	1:A:174:VAL:HG13	0.63	1.71	13	3
1:A:151:ASP:O	1:A:152:ASN:C	0.63	2.40	9	40
1:A:66:LEU:HD23	1:A:66:LEU:N	0.63	2.09	9	2
1:A:71:ASN:ND2	1:A:72:ALA:N	0.62	2.46	35	1
1:A:91:GLU:O	1:A:92:LEU:HD12	0.62	1.94	27	6
1:A:97:SER:O	1:A:102:ASN:ND2	0.62	2.33	35	7
1:A:66:LEU:HD23	1:A:66:LEU:O	0.61	1.94	7	2
1:A:149:LEU:HD13	1:A:150:TYR:N	0.61	2.10	2	2
1:A:82:ARG:HH12	1:A:209:LYS:NZ	0.61	1.91	13	1
1:A:82:ARG:HH22	1:A:209:LYS:NZ	0.61	1.93	34	2
1:A:92:LEU:CD1	1:A:107:ALA:H	0.61	2.08	11	2
1:A:104:LEU:HD12	1:A:104:LEU:N	0.61	2.10	32	3
1:A:82:ARG:NH2	1:A:209:LYS:HZ1	0.61	1.92	34	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:170:LYS:O	1:A:173:VAL:HG22	0.61	1.95	39	7
1:A:170:LYS:O	1:A:171:TRP:CD1	0.60	2.55	32	4
1:A:74:LEU:HD13	1:A:75:ASP:N	0.60	2.12	16	5
1:A:82:ARG:NH1	1:A:209:LYS:HZ3	0.60	1.94	30	1
1:A:74:LEU:HD23	1:A:105:SER:OG	0.60	1.96	31	3
1:A:186:THR:O	1:A:196:ARG:NH1	0.59	2.34	15	14
1:A:102:ASN:HD22	1:A:102:ASN:N	0.59	1.95	10	6
1:A:174:VAL:HG11	1:A:185:ILE:HD13	0.59	1.73	21	5
1:A:151:ASP:OD2	1:A:156:TYR:CE1	0.59	2.55	29	1
1:A:168:PRO:O	1:A:171:TRP:NE1	0.58	2.36	9	15
1:A:74:LEU:H	1:A:74:LEU:HD23	0.58	1.56	4	4
1:A:172:GLU:O	1:A:177:HIS:NE2	0.58	2.37	37	19
1:A:82:ARG:NH2	1:A:209:LYS:NZ	0.58	2.51	13	2
1:A:83:ILE:HG22	1:A:92:LEU:O	0.57	1.98	36	19
1:A:100:GLU:CD	1:A:100:GLU:N	0.57	2.62	3	1
1:A:78:GLN:NE2	1:A:102:ASN:OD1	0.57	2.37	39	3
1:A:127:ASN:O	1:A:129:SER:N	0.57	2.37	5	40
1:A:202:ASP:OD1	1:A:203:LEU:N	0.57	2.38	10	14
1:A:90:LEU:HD13	1:A:91:GLU:N	0.57	2.15	36	5
1:A:97:SER:OG	1:A:102:ASN:ND2	0.57	2.38	34	7
1:A:180:ASP:OD2	1:A:203:LEU:HD22	0.57	2.00	23	1
1:A:120:ASN:ND2	1:A:183:THR:OG1	0.56	2.38	22	13
1:A:114:GLN:NE2	1:A:122:ALA:N	0.56	2.53	14	3
1:A:172:GLU:H	1:A:172:GLU:CD	0.56	2.08	4	5
1:A:104:LEU:N	1:A:104:LEU:CD1	0.56	2.69	32	3
1:A:74:LEU:HD11	1:A:78:GLN:NE2	0.56	2.15	13	2
1:A:80:ILE:H	1:A:80:ILE:HD13	0.56	1.61	32	4
1:A:65:ASP:OD1	1:A:66:LEU:N	0.56	2.39	30	5
1:A:183:THR:C	1:A:184:LEU:HD12	0.56	2.26	12	38
1:A:155:GLU:CD	1:A:207:LYS:HZ1	0.56	2.10	24	1
1:A:133:VAL:CG1	1:A:134:LEU:N	0.55	2.70	21	36
1:A:134:LEU:H	1:A:134:LEU:CD2	0.55	2.12	24	2
1:A:91:GLU:N	1:A:91:GLU:OE1	0.55	2.39	15	1
1:A:96:LYS:NZ	1:A:112:GLU:O	0.55	2.38	13	3
1:A:173:VAL:O	1:A:173:VAL:HG12	0.55	1.99	34	4
1:A:171:TRP:C	1:A:173:VAL:H	0.55	2.10	31	20
1:A:148:TYR:CE2	1:A:157:GLU:OE1	0.55	2.60	1	4
1:A:179:LYS:NZ	1:A:181:GLU:CD	0.55	2.65	39	2
1:A:167:THR:O	1:A:196:ARG:NH2	0.55	2.40	2	1
1:A:78:GLN:N	1:A:78:GLN:OE1	0.55	2.39	18	4
1:A:151:ASP:OD1	1:A:151:ASP:N	0.54	2.39	29	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:155:GLU:OE1	1:A:207:LYS:NZ	0.54	2.39	14	4
1:A:166:VAL:O	1:A:196:ARG:NH1	0.54	2.41	10	1
1:A:74:LEU:N	1:A:74:LEU:HD23	0.54	2.17	32	3
1:A:73:SER:O	1:A:101:LYS:NZ	0.54	2.39	36	1
1:A:68:GLU:C	1:A:71:ASN:ND2	0.54	2.65	35	1
1:A:88:VAL:HG12	1:A:88:VAL:O	0.54	2.02	37	1
1:A:134:LEU:N	1:A:134:LEU:CD2	0.54	2.65	23	28
1:A:142:LYS:N	1:A:145:ASP:OD2	0.54	2.41	8	22
1:A:116:MET:SD	1:A:150:TYR:O	0.54	2.66	34	7
1:A:155:GLU:CD	1:A:207:LYS:NZ	0.54	2.66	24	1
1:A:114:GLN:OE1	1:A:121:TYR:CE1	0.54	2.61	37	1
1:A:170:LYS:O	1:A:171:TRP:CG	0.54	2.61	2	4
1:A:165:GLU:OE2	1:A:197:TYR:CZ	0.54	2.60	30	5
1:A:82:ARG:CZ	1:A:209:LYS:HZ1	0.54	2.14	13	1
1:A:150:TYR:CE2	1:A:155:GLU:OE2	0.54	2.61	25	1
1:A:133:VAL:CG1	1:A:134:LEU:H	0.54	2.15	4	33
1:A:165:GLU:N	1:A:165:GLU:OE1	0.54	2.41	16	2
1:A:68:GLU:O	1:A:71:ASN:ND2	0.54	2.41	35	1
1:A:171:TRP:C	1:A:173:VAL:N	0.53	2.66	21	22
1:A:114:GLN:OE1	1:A:121:TYR:CG	0.53	2.61	18	1
1:A:76:LYS:O	1:A:79:VAL:HG12	0.53	2.04	24	13
1:A:126:HIS:O	1:A:134:LEU:O	0.53	2.26	16	18
1:A:112:GLU:N	1:A:112:GLU:CD	0.53	2.66	15	2
1:A:175:GLU:O	1:A:177:HIS:CE1	0.53	2.61	38	5
1:A:83:ILE:HD13	1:A:84:SER:N	0.53	2.18	33	3
1:A:152:ASN:N	1:A:152:ASN:OD1	0.53	2.41	37	5
1:A:88:VAL:HG22	1:A:88:VAL:O	0.53	2.03	1	16
1:A:175:GLU:O	1:A:176:ASP:C	0.53	2.51	13	14
1:A:165:GLU:OE2	1:A:197:TYR:CE1	0.53	2.61	30	2
1:A:90:LEU:HD11	1:A:92:LEU:HD12	0.53	1.79	36	2
1:A:186:THR:OG1	1:A:196:ARG:NH1	0.53	2.41	18	3
1:A:74:LEU:HD23	1:A:74:LEU:N	0.53	2.19	4	4
1:A:74:LEU:HD22	1:A:105:SER:HB3	0.53	1.80	17	3
1:A:91:GLU:C	1:A:92:LEU:HD22	0.53	2.29	26	1
1:A:68:GLU:N	1:A:68:GLU:OE1	0.53	2.41	1	2
1:A:167:THR:O	1:A:169:ASP:N	0.53	2.42	7	16
1:A:99:THR:O	1:A:102:ASN:OD1	0.53	2.27	21	6
1:A:185:ILE:HG22	1:A:198:VAL:HG22	0.53	1.80	11	1
1:A:78:GLN:NE2	1:A:97:SER:OG	0.53	2.42	15	1
1:A:175:GLU:O	1:A:176:ASP:O	0.53	2.27	2	3
1:A:127:ASN:C	1:A:129:SER:N	0.52	2.67	28	40

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:66:LEU:N	1:A:66:LEU:HD12	0.52	2.19	28	7
1:A:117:GLY:N	1:A:158:TYR:OH	0.52	2.42	5	7
1:A:146:LYS:NZ	1:A:157:GLU:OE2	0.52	2.40	1	2
1:A:136:SER:OG	1:A:137:ASP:N	0.52	2.43	36	2
1:A:75:ASP:C	1:A:77:LYS:N	0.52	2.66	34	14
1:A:112:GLU:H	1:A:112:GLU:CD	0.52	2.11	10	1
1:A:114:GLN:OE1	1:A:121:TYR:CZ	0.52	2.63	22	1
1:A:74:LEU:HD22	1:A:105:SER:OG	0.52	2.05	4	2
1:A:179:LYS:NZ	1:A:181:GLU:OE1	0.52	2.40	27	2
1:A:120:ASN:CB	1:A:175:GLU:O	0.52	2.57	23	3
1:A:150:TYR:CZ	1:A:155:GLU:OE2	0.52	2.63	25	1
1:A:151:ASP:N	1:A:154:ASN:O	0.52	2.39	7	1
1:A:148:TYR:CD2	1:A:157:GLU:OE1	0.52	2.63	22	2
1:A:74:LEU:HD13	1:A:74:LEU:C	0.52	2.30	16	3
1:A:71:ASN:OD1	1:A:72:ALA:N	0.51	2.43	9	2
1:A:76:LYS:O	1:A:79:VAL:HG23	0.51	2.06	33	1
1:A:119:GLY:C	1:A:179:LYS:O	0.51	2.53	28	3
1:A:175:GLU:O	1:A:177:HIS:NE2	0.51	2.43	17	1
1:A:150:TYR:CD2	1:A:155:GLU:OE2	0.51	2.63	25	1
1:A:150:TYR:CE2	1:A:155:GLU:OE1	0.51	2.63	27	1
1:A:114:GLN:OE1	1:A:121:TYR:CD1	0.51	2.63	18	1
1:A:141:LEU:HD22	1:A:145:ASP:OD2	0.51	2.06	23	1
1:A:82:ARG:NH1	1:A:92:LEU:C	0.51	2.68	39	1
1:A:100:GLU:CD	1:A:100:GLU:H	0.51	2.14	3	1
1:A:133:VAL:C	1:A:136:SER:OG	0.51	2.54	8	2
1:A:147:ILE:N	1:A:158:TYR:O	0.51	2.43	15	12
1:A:89:SER:OG	1:A:89:SER:O	0.51	2.29	23	4
1:A:83:ILE:HG23	1:A:83:ILE:O	0.50	2.05	35	7
1:A:171:TRP:O	1:A:173:VAL:N	0.50	2.44	20	20
1:A:166:VAL:CG2	1:A:196:ARG:HH21	0.50	2.19	25	1
1:A:149:LEU:HD21	1:A:182:ILE:CD1	0.50	2.36	38	1
1:A:116:MET:HE2	1:A:149:LEU:HD21	0.50	1.82	4	1
1:A:116:MET:HE2	1:A:149:LEU:CD2	0.50	2.37	4	1
1:A:208:ALA:O	1:A:210:LYS:N	0.50	2.44	11	6
1:A:79:VAL:HG13	1:A:79:VAL:O	0.50	2.07	25	5
1:A:170:LYS:NZ	1:A:196:ARG:NH2	0.50	2.59	17	1
1:A:150:TYR:CE2	1:A:155:GLU:CD	0.50	2.89	25	1
1:A:66:LEU:N	1:A:66:LEU:CD2	0.50	2.74	12	9
1:A:157:GLU:OE1	1:A:157:GLU:N	0.50	2.45	4	1
1:A:172:GLU:O	1:A:177:HIS:CE1	0.50	2.65	17	5
1:A:66:LEU:HD23	1:A:66:LEU:H	0.50	1.66	9	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:114:GLN:NE2	1:A:122:ALA:H	0.50	2.05	23	1
1:A:71:ASN:ND2	1:A:72:ALA:H	0.50	2.04	35	1
1:A:161:THR:HG22	1:A:200:ALA:O	0.50	2.06	15	9
1:A:76:LYS:O	1:A:79:VAL:CG1	0.49	2.60	25	4
1:A:165:GLU:OE2	1:A:197:TYR:CE2	0.49	2.65	30	1
1:A:156:TYR:CD2	1:A:206:THR:OG1	0.49	2.59	14	5
1:A:165:GLU:N	1:A:165:GLU:CD	0.49	2.71	40	1
1:A:152:ASN:CG	1:A:153:GLU:N	0.49	2.71	7	1
1:A:85:ILE:CG2	1:A:141:LEU:HD21	0.49	2.36	11	1
1:A:100:GLU:CG	1:A:101:LYS:N	0.49	2.75	11	1
1:A:82:ARG:HH12	1:A:209:LYS:HZ3	0.49	1.48	13	1
1:A:167:THR:C	1:A:169:ASP:H	0.49	2.16	17	9
1:A:150:TYR:CG	1:A:155:GLU:OE2	0.49	2.66	25	1
1:A:89:SER:O	1:A:89:SER:OG	0.49	2.31	20	3
1:A:180:ASP:OD1	1:A:180:ASP:O	0.49	2.31	9	9
1:A:150:TYR:CE1	1:A:155:GLU:OE2	0.49	2.66	25	1
1:A:186:THR:O	1:A:196:ARG:CZ	0.49	2.61	38	2
1:A:167:THR:C	1:A:169:ASP:N	0.49	2.71	3	17
1:A:116:MET:SD	1:A:149:LEU:HD22	0.49	2.48	20	3
1:A:169:ASP:OD1	1:A:170:LYS:N	0.49	2.46	10	3
1:A:99:THR:N	1:A:102:ASN:OD1	0.49	2.43	28	1
1:A:186:THR:HG23	1:A:196:ARG:HE	0.49	1.67	40	1
1:A:90:LEU:CD2	1:A:92:LEU:HD23	0.49	2.38	26	1
1:A:150:TYR:CD2	1:A:155:GLU:OE1	0.49	2.66	27	1
1:A:165:GLU:OE2	1:A:197:TYR:CD1	0.49	2.66	30	1
1:A:101:LYS:CG	1:A:102:ASN:N	0.48	2.76	22	2
1:A:88:VAL:O	1:A:88:VAL:CG2	0.48	2.61	21	20
1:A:126:HIS:O	1:A:135:PHE:O	0.48	2.30	9	1
1:A:176:ASP:OD1	1:A:176:ASP:O	0.48	2.32	23	10
1:A:66:LEU:N	1:A:66:LEU:HD22	0.48	2.23	14	7
1:A:82:ARG:CZ	1:A:209:LYS:NZ	0.48	2.76	13	1
1:A:68:GLU:C	1:A:71:ASN:HD21	0.48	2.16	35	1
1:A:112:GLU:CG	1:A:113:ASN:N	0.48	2.76	30	4
1:A:80:ILE:CD1	1:A:80:ILE:N	0.48	2.76	32	4
1:A:74:LEU:H	1:A:74:LEU:CD2	0.48	2.21	32	4
1:A:173:VAL:O	1:A:173:VAL:CG1	0.48	2.62	34	1
1:A:75:ASP:C	1:A:77:LYS:H	0.48	2.16	1	14
1:A:151:ASP:CG	1:A:152:ASN:H	0.48	2.16	2	18
1:A:65:ASP:O	1:A:69:VAL:HG23	0.48	2.08	6	2
1:A:68:GLU:O	1:A:71:ASN:OD1	0.48	2.30	9	2
1:A:170:LYS:HZ2	1:A:196:ARG:NH2	0.48	2.06	17	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:130:LYS:O	1:A:136:SER:CB	0.48	2.61	9	17
1:A:152:ASN:ND2	1:A:154:ASN:OD1	0.48	2.46	37	1
1:A:88:VAL:HG23	1:A:90:LEU:HD23	0.48	1.85	10	1
1:A:112:GLU:CD	1:A:112:GLU:H	0.48	2.17	15	1
1:A:87:SER:CB	1:A:141:LEU:HD23	0.48	2.39	23	1
1:A:130:LYS:N	1:A:136:SER:OG	0.48	2.44	10	4
1:A:130:LYS:O	1:A:136:SER:OG	0.48	2.31	40	12
1:A:157:GLU:OE2	1:A:207:LYS:CE	0.48	2.62	16	2
1:A:92:LEU:O	1:A:93:PRO:C	0.48	2.57	29	25
1:A:120:ASN:HD21	1:A:183:THR:CB	0.48	2.21	40	1
1:A:152:ASN:CG	1:A:153:GLU:H	0.47	2.16	37	7
1:A:66:LEU:H	1:A:66:LEU:CD2	0.47	2.21	9	1
1:A:67:ALA:O	1:A:71:ASN:ND2	0.47	2.47	35	1
1:A:68:GLU:N	1:A:68:GLU:CD	0.47	2.71	19	2
1:A:102:ASN:OD1	1:A:102:ASN:C	0.47	2.56	38	1
1:A:169:ASP:O	1:A:169:ASP:OD1	0.47	2.31	9	9
1:A:174:VAL:HG11	1:A:185:ILE:HG21	0.47	1.84	13	1
1:A:180:ASP:OD1	1:A:180:ASP:N	0.47	2.46	28	2
1:A:74:LEU:N	1:A:74:LEU:CD2	0.47	2.77	4	7
1:A:168:PRO:O	1:A:171:TRP:CD1	0.47	2.67	28	3
1:A:107:ALA:HB2	1:A:135:PHE:CE1	0.47	2.44	24	1
1:A:119:GLY:CA	1:A:179:LYS:O	0.47	2.63	20	6
1:A:71:ASN:O	1:A:71:ASN:OD1	0.47	2.33	12	3
1:A:75:ASP:OD1	1:A:76:LYS:N	0.47	2.47	35	2
1:A:82:ARG:HH12	1:A:209:LYS:HZ1	0.47	1.52	37	1
1:A:185:ILE:CG2	1:A:196:ARG:NH1	0.47	2.78	37	1
1:A:66:LEU:N	1:A:66:LEU:CD1	0.47	2.78	28	7
1:A:151:ASP:OD1	1:A:152:ASN:N	0.47	2.46	11	11
1:A:100:GLU:O	1:A:104:LEU:CD1	0.47	2.63	28	3
1:A:74:LEU:HD11	1:A:78:GLN:HE22	0.47	1.70	13	1
1:A:75:ASP:O	1:A:77:LYS:N	0.47	2.48	37	9
1:A:88:VAL:CG2	1:A:88:VAL:O	0.47	2.63	25	3
1:A:150:TYR:CZ	1:A:155:GLU:OE1	0.47	2.67	27	1
1:A:186:THR:CG2	1:A:196:ARG:HE	0.47	2.22	40	1
1:A:97:SER:OG	1:A:102:ASN:OD1	0.47	2.33	13	1
1:A:102:ASN:ND2	1:A:102:ASN:N	0.47	2.63	39	3
1:A:150:TYR:CD1	1:A:155:GLU:OE2	0.47	2.67	25	1
1:A:117:GLY:O	1:A:180:ASP:CG	0.46	2.59	8	18
1:A:96:LYS:CG	1:A:97:SER:N	0.46	2.78	6	1
1:A:99:THR:OG1	1:A:102:ASN:OD1	0.46	2.32	22	1
1:A:129:SER:OG	1:A:129:SER:O	0.46	2.34	20	4

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:80:ILE:CD1	1:A:94:VAL:O	0.46	2.63	16	1
1:A:116:MET:N	1:A:121:TYR:CE1	0.46	2.83	37	2
1:A:99:THR:OG1	1:A:102:ASN:CG	0.46	2.58	6	11
1:A:157:GLU:O	1:A:204:VAL:HG12	0.46	2.11	31	5
1:A:155:GLU:CD	1:A:155:GLU:C	0.46	2.84	9	5
1:A:142:LYS:O	1:A:145:ASP:OD2	0.46	2.32	8	2
1:A:76:LYS:N	1:A:76:LYS:CD	0.46	2.78	38	4
1:A:80:ILE:H	1:A:80:ILE:CD1	0.46	2.23	32	4
1:A:168:PRO:CB	1:A:196:ARG:HH21	0.46	2.23	19	1
1:A:127:ASN:C	1:A:129:SER:H	0.46	2.19	28	27
1:A:142:LYS:O	1:A:145:ASP:CG	0.46	2.59	14	8
1:A:136:SER:O	1:A:137:ASP:OD1	0.46	2.34	16	16
1:A:169:ASP:N	1:A:169:ASP:OD1	0.46	2.46	34	1
1:A:77:LYS:N	1:A:77:LYS:CD	0.46	2.79	11	1
1:A:88:VAL:O	1:A:89:SER:CB	0.46	2.64	11	9
1:A:174:VAL:HG12	1:A:183:THR:CG2	0.46	2.41	30	1
1:A:88:VAL:O	1:A:88:VAL:HG22	0.46	2.10	26	6
1:A:209:LYS:O	1:A:209:LYS:CG	0.46	2.64	4	2
1:A:113:ASN:OD1	1:A:113:ASN:C	0.46	2.59	29	7
1:A:120:ASN:ND2	1:A:173:VAL:O	0.46	2.45	17	1
1:A:82:ARG:HH11	1:A:209:LYS:NZ	0.46	2.09	24	1
1:A:74:LEU:HD11	1:A:78:GLN:OE1	0.46	2.10	29	2
1:A:137:ASP:OD1	1:A:140:SER:OG	0.46	2.34	30	6
1:A:92:LEU:HD22	1:A:106:GLY:HA2	0.46	1.87	2	3
1:A:78:GLN:OE1	1:A:102:ASN:OD1	0.46	2.34	23	2
1:A:127:ASN:O	1:A:127:ASN:CG	0.46	2.59	33	3
1:A:82:ARG:HH11	1:A:150:TYR:CB	0.46	2.24	34	1
1:A:88:VAL:O	1:A:88:VAL:CG1	0.46	2.64	37	1
1:A:202:ASP:OD1	1:A:202:ASP:O	0.45	2.34	23	9
1:A:161:THR:OG1	1:A:200:ALA:O	0.45	2.34	37	12
1:A:71:ASN:N	1:A:71:ASN:HD22	0.45	2.07	35	1
1:A:127:ASN:O	1:A:128:MET:C	0.45	2.60	2	4
1:A:170:LYS:C	1:A:171:TRP:CD1	0.45	2.94	2	4
1:A:67:ALA:O	1:A:71:ASN:CG	0.45	2.59	37	4
1:A:165:GLU:OE1	1:A:197:TYR:CE1	0.45	2.69	40	1
1:A:152:ASN:OD1	1:A:153:GLU:N	0.45	2.47	29	3
1:A:76:LYS:C	1:A:78:GLN:N	0.45	2.73	15	2
1:A:144:GLY:N	1:A:160:VAL:O	0.45	2.44	24	5
1:A:184:LEU:HD12	1:A:184:LEU:N	0.45	2.27	4	3
1:A:114:GLN:NE2	1:A:121:TYR:CG	0.45	2.85	6	1
1:A:158:TYR:CZ	1:A:203:LEU:HD13	0.45	2.46	40	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:127:ASN:O	1:A:127:ASN:OD1	0.45	2.34	14	1
1:A:98:SER:OG	1:A:109:THR:O	0.45	2.28	17	3
1:A:172:GLU:CD	1:A:172:GLU:N	0.45	2.75	4	2
1:A:167:THR:C	1:A:196:ARG:HH12	0.45	2.20	10	1
1:A:88:VAL:HG21	1:A:137:ASP:O	0.45	2.11	28	3
1:A:172:GLU:CG	1:A:173:VAL:N	0.45	2.79	37	1
1:A:74:LEU:C	1:A:74:LEU:CD1	0.45	2.89	16	5
1:A:112:GLU:O	1:A:113:ASN:ND2	0.45	2.50	3	2
1:A:176:ASP:OD1	1:A:176:ASP:N	0.45	2.49	32	8
1:A:149:LEU:C	1:A:150:TYR:CD1	0.45	2.94	9	2
1:A:100:GLU:C	1:A:100:GLU:CD	0.45	2.85	36	5
1:A:102:ASN:HD21	1:A:108:ALA:HB2	0.45	1.72	29	3
1:A:79:VAL:O	1:A:79:VAL:CG1	0.45	2.65	24	4
1:A:78:GLN:N	1:A:78:GLN:CD	0.45	2.75	8	2
1:A:141:LEU:O	1:A:163:VAL:HG21	0.45	2.12	33	2
1:A:181:GLU:CD	1:A:201:GLY:O	0.45	2.60	34	1
1:A:152:ASN:OD1	1:A:152:ASN:N	0.45	2.48	26	2
1:A:76:LYS:O	1:A:79:VAL:HG22	0.45	2.12	16	3
1:A:74:LEU:HD13	1:A:102:ASN:OD1	0.45	2.11	12	1
1:A:135:PHE:CD2	1:A:138:ILE:HD13	0.45	2.47	28	4
1:A:158:TYR:OH	1:A:180:ASP:OD2	0.45	2.35	23	1
1:A:97:SER:O	1:A:102:ASN:CG	0.45	2.60	35	2
1:A:165:GLU:OE2	1:A:197:TYR:CD2	0.45	2.70	30	1
1:A:81:GLY:C	1:A:82:ARG:CG	0.44	2.90	29	20
1:A:137:ASP:CG	1:A:140:SER:OG	0.44	2.60	23	3
1:A:102:ASN:OD1	1:A:102:ASN:N	0.44	2.48	11	1
1:A:80:ILE:HD13	1:A:80:ILE:N	0.44	2.26	32	2
1:A:127:ASN:O	1:A:129:SER:OG	0.44	2.35	37	1
1:A:102:ASN:OD1	1:A:102:ASN:O	0.44	2.35	38	1
1:A:167:THR:OG1	1:A:169:ASP:OD1	0.44	2.36	10	2
1:A:165:GLU:OE2	1:A:197:TYR:CG	0.44	2.71	30	1
1:A:110:VAL:HG21	1:A:185:ILE:HD11	0.44	1.89	38	1
1:A:69:VAL:HG22	1:A:104:LEU:CD2	0.44	2.37	34	1
1:A:106:GLY:CA	1:A:134:LEU:HD13	0.44	2.43	35	1
1:A:143:LYS:CD	1:A:143:LYS:C	0.44	2.90	1	1
1:A:83:ILE:O	1:A:83:ILE:CG2	0.44	2.65	24	11
1:A:98:SER:O	1:A:98:SER:OG	0.44	2.34	3	4
1:A:74:LEU:HD13	1:A:105:SER:CB	0.44	2.42	15	1
1:A:129:SER:O	1:A:129:SER:OG	0.44	2.36	33	7
1:A:116:MET:HE3	1:A:121:TYR:CZ	0.44	2.47	36	3
1:A:117:GLY:C	1:A:180:ASP:CG	0.44	2.86	23	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:103:LEU:O	1:A:126:HIS:CD2	0.44	2.71	5	1
1:A:158:TYR:OH	1:A:180:ASP:CG	0.44	2.61	23	1
1:A:149:LEU:HD13	1:A:150:TYR:H	0.44	1.73	24	1
1:A:113:ASN:O	1:A:113:ASN:OD1	0.44	2.35	37	3
1:A:156:TYR:CE2	1:A:206:THR:HG21	0.43	2.48	8	2
1:A:130:LYS:C	1:A:136:SER:HG	0.43	2.21	10	2
1:A:92:LEU:HD22	1:A:105:SER:O	0.43	2.13	23	1
1:A:116:MET:SD	1:A:151:ASP:OD1	0.43	2.75	29	1
1:A:159:ALA:O	1:A:202:ASP:OD1	0.43	2.36	16	3
1:A:117:GLY:O	1:A:180:ASP:OD2	0.43	2.36	5	3
1:A:133:VAL:HG12	1:A:134:LEU:CD2	0.43	2.43	5	1
1:A:163:VAL:HG13	1:A:199:VAL:HG22	0.43	1.89	40	2
1:A:116:MET:SD	1:A:121:TYR:OH	0.43	2.71	37	1
1:A:92:LEU:HD23	1:A:93:PRO:HD2	0.43	1.89	9	1
1:A:66:LEU:CD2	1:A:66:LEU:H	0.43	2.26	10	1
1:A:92:LEU:O	1:A:93:PRO:O	0.43	2.36	35	2
1:A:74:LEU:CD2	1:A:105:SER:OG	0.43	2.67	31	2
1:A:127:ASN:C	1:A:127:ASN:OD1	0.43	2.61	24	3
1:A:74:LEU:HD22	1:A:105:SER:CB	0.43	2.43	40	2
1:A:150:TYR:CD1	1:A:150:TYR:N	0.43	2.86	31	1
1:A:102:ASN:ND2	1:A:108:ALA:HB2	0.43	2.29	38	1
1:A:75:ASP:H	1:A:78:GLN:NE2	0.43	2.11	11	1
1:A:120:ASN:HD22	1:A:120:ASN:C	0.43	2.22	37	1
1:A:71:ASN:HD22	1:A:72:ALA:H	0.43	1.54	35	1
1:A:184:LEU:CD1	1:A:184:LEU:N	0.43	2.82	36	1
1:A:102:ASN:N	1:A:102:ASN:ND2	0.43	2.64	10	2
1:A:100:GLU:CD	1:A:100:GLU:C	0.43	2.87	19	1
1:A:85:ILE:HG21	1:A:141:LEU:HD21	0.43	1.91	35	2
1:A:180:ASP:O	1:A:180:ASP:CG	0.43	2.61	20	1
1:A:150:TYR:CG	1:A:155:GLU:OE1	0.43	2.72	27	1
1:A:171:TRP:O	1:A:174:VAL:HG22	0.43	2.14	32	1
1:A:175:GLU:O	1:A:177:HIS:CD2	0.42	2.72	17	2
1:A:181:GLU:OE1	1:A:202:ASP:OD1	0.42	2.37	34	1
1:A:116:MET:SD	1:A:149:LEU:HD12	0.42	2.55	38	1
1:A:67:ALA:O	1:A:71:ASN:OD1	0.42	2.37	11	2
1:A:112:GLU:O	1:A:113:ASN:OD1	0.42	2.37	21	1
1:A:184:LEU:N	1:A:184:LEU:CD1	0.42	2.82	8	5
1:A:71:ASN:OD1	1:A:71:ASN:C	0.42	2.61	9	1
1:A:133:VAL:C	1:A:136:SER:HG	0.42	2.23	6	2
1:A:172:GLU:CD	1:A:175:GLU:OE1	0.42	2.62	15	2
1:A:102:ASN:HD21	1:A:108:ALA:CB	0.42	2.27	29	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:111:LYS:NZ	1:A:175:GLU:OE1	0.42	2.50	24	1
1:A:186:THR:O	1:A:196:ARG:NH2	0.42	2.51	33	1
1:A:79:VAL:CG1	1:A:79:VAL:O	0.42	2.67	23	1
1:A:176:ASP:OD1	1:A:177:HIS:N	0.42	2.52	6	2
1:A:184:LEU:N	1:A:184:LEU:HD12	0.42	2.28	36	1
1:A:179:LYS:HZ3	1:A:181:GLU:CD	0.42	2.22	39	1
1:A:151:ASP:CG	1:A:152:ASN:N	0.42	2.78	32	7
1:A:85:ILE:CG2	1:A:87:SER:OG	0.42	2.68	3	1
1:A:163:VAL:O	1:A:163:VAL:HG13	0.42	2.15	6	1
1:A:92:LEU:HD12	1:A:106:GLY:CA	0.42	2.45	13	1
1:A:102:ASN:HD22	1:A:102:ASN:H	0.42	1.57	13	1
1:A:96:LYS:NZ	1:A:112:GLU:OE2	0.42	2.52	21	1
1:A:74:LEU:HD23	1:A:74:LEU:H	0.42	1.74	26	2
1:A:181:GLU:OE2	1:A:202:ASP:CG	0.42	2.63	34	1
1:A:159:ALA:O	1:A:202:ASP:N	0.42	2.51	5	2
1:A:180:ASP:OD2	1:A:203:LEU:HD23	0.42	2.15	31	1
1:A:88:VAL:O	1:A:89:SER:OG	0.42	2.37	32	1
1:A:103:LEU:O	1:A:134:LEU:HD12	0.42	2.15	3	1
1:A:120:ASN:CG	1:A:174:VAL:O	0.42	2.63	4	1
1:A:131:LYS:N	1:A:131:LYS:HD3	0.42	2.30	5	1
1:A:150:TYR:CZ	1:A:155:GLU:CD	0.42	2.98	25	1
1:A:172:GLU:OE1	1:A:172:GLU:N	0.42	2.45	26	1
1:A:127:ASN:ND2	1:A:186:THR:OG1	0.41	2.53	32	1
1:A:141:LEU:CD2	1:A:145:ASP:OD2	0.41	2.68	37	1
1:A:74:LEU:HD23	1:A:105:SER:HG	0.41	1.75	3	1
1:A:146:LYS:NZ	1:A:204:VAL:HG11	0.41	2.30	7	1
1:A:85:ILE:HG22	1:A:141:LEU:HD21	0.41	1.90	11	1
1:A:74:LEU:CD2	1:A:95:LEU:HD13	0.41	2.45	12	2
1:A:68:GLU:OE1	1:A:68:GLU:CA	0.41	2.68	1	1
1:A:158:TYR:OH	1:A:180:ASP:OD1	0.41	2.39	23	1
1:A:165:GLU:OE2	1:A:197:TYR:OH	0.41	2.35	36	1
1:A:75:ASP:CB	1:A:78:GLN:NE2	0.41	2.84	8	1
1:A:107:ALA:HB2	1:A:135:PHE:CZ	0.41	2.50	9	1
1:A:131:LYS:O	1:A:131:LYS:CG	0.41	2.68	16	1
1:A:152:ASN:OD1	1:A:154:ASN:OD1	0.41	2.38	29	1
1:A:176:ASP:OD1	1:A:176:ASP:C	0.41	2.64	6	1
1:A:148:TYR:CD1	1:A:148:TYR:N	0.41	2.88	11	1
1:A:209:LYS:O	1:A:210:LYS:OXT	0.41	2.39	20	1
1:A:88:VAL:HG11	1:A:90:LEU:HD12	0.41	1.91	38	1
1:A:79:VAL:O	1:A:79:VAL:HG13	0.41	2.14	23	2
1:A:150:TYR:CE1	1:A:155:GLU:OE1	0.41	2.74	27	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:114:GLN:NE2	1:A:121:TYR:CE1	0.41	2.88	7	1
1:A:166:VAL:O	1:A:196:ARG:N	0.41	2.51	9	1
1:A:95:LEU:CD1	1:A:102:ASN:O	0.41	2.69	11	2
1:A:117:GLY:C	1:A:180:ASP:OD1	0.41	2.63	23	1
1:A:92:LEU:HD12	1:A:106:GLY:HA2	0.41	1.92	13	1
1:A:102:ASN:N	1:A:102:ASN:OD1	0.41	2.52	19	1
1:A:143:LYS:NZ	1:A:161:THR:O	0.41	2.43	21	1
1:A:90:LEU:HD13	1:A:90:LEU:C	0.41	2.41	23	1
1:A:74:LEU:HD13	1:A:105:SER:OG	0.41	2.16	38	1
1:A:120:ASN:OD1	1:A:120:ASN:C	0.41	2.64	35	1
1:A:113:ASN:CG	1:A:113:ASN:O	0.41	2.64	38	1
1:A:157:GLU:N	1:A:157:GLU:CD	0.40	2.79	4	1
1:A:87:SER:OG	1:A:145:ASP:OD1	0.40	2.34	23	1
1:A:83:ILE:O	1:A:83:ILE:HG23	0.40	2.15	29	1
1:A:141:LEU:O	1:A:163:VAL:CG2	0.40	2.69	29	1
1:A:120:ASN:C	1:A:120:ASN:ND2	0.40	2.79	37	1
1:A:88:VAL:CG2	1:A:90:LEU:HD23	0.40	2.47	10	1
1:A:179:LYS:HZ2	1:A:181:GLU:CD	0.40	2.23	21	1
1:A:76:LYS:O	1:A:79:VAL:HG13	0.40	2.15	39	1
1:A:120:ASN:HD22	1:A:177:HIS:CE1	0.40	2.33	13	1
1:A:88:VAL:O	1:A:88:VAL:HG12	0.40	2.16	28	1
1:A:100:GLU:O	1:A:104:LEU:HD21	0.40	2.15	36	1
1:A:82:ARG:CG	1:A:83:ILE:N	0.40	2.84	7	1
1:A:171:TRP:O	1:A:174:VAL:HG23	0.40	2.16	17	1
1:A:82:ARG:O	1:A:149:LEU:HD12	0.40	2.17	23	1
1:A:148:TYR:CD2	1:A:157:GLU:OE2	0.40	2.74	32	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	137/158 (87%)	123±2 (90±2%)	11±3 (8±2%)	3±1 (2±1%)	7	47
All	All	5480/6320 (87%)	4905 (90%)	456 (8%)	119 (2%)	7	47

All 10 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	128	MET	40
1	A	152	ASN	29
1	A	172	GLU	12
1	A	209	LYS	9
1	A	168	PRO	8
1	A	93	PRO	6
1	A	178	GLY	5
1	A	76	LYS	4
1	A	176	ASP	3
1	A	97	SER	3

6.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all NMR entries. The Analysed column shows the number of residues for which the sidechain conformation was analysed and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	116/134 (87%)	109±2 (94±2%)	7±2 (6±2%)	20	69
All	All	4640/5360 (87%)	4370 (94%)	270 (6%)	20	69

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	134	LEU	39
1	A	88	VAL	20
1	A	154	ASN	17
1	A	174	VAL	16
1	A	90	LEU	12
1	A	129	SER	12
1	A	161	THR	12
1	A	136	SER	12
1	A	149	LEU	11
1	A	89	SER	11
1	A	92	LEU	11
1	A	114	GLN	10
1	A	128	MET	10
1	A	99	THR	7

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Mol	Chain	Res	Type	Models (Total)
1	A	74	LEU	5
1	A	87	SER	5
1	A	102	ASN	5
1	A	80	ILE	5
1	A	116	MET	5
1	A	98	SER	4
1	A	115	VAL	3
1	A	83	ILE	3
1	A	179	LYS	3
1	A	68	GLU	2
1	A	66	LEU	2
1	A	146	LYS	2
1	A	112	GLU	2
1	A	210	LYS	2
1	A	180	ASP	2
1	A	120	ASN	2
1	A	142	LYS	1
1	A	133	VAL	1
1	A	78	GLN	1
1	A	82	ARG	1
1	A	185	ILE	1
1	A	197	TYR	1
1	A	183	THR	1
1	A	76	LYS	1
1	A	110	VAL	1
1	A	170	LYS	1
1	A	84	SER	1
1	A	131	LYS	1
1	A	196	ARG	1
1	A	186	THR	1
1	A	100	GLU	1
1	A	71	ASN	1
1	A	105	SER	1
1	A	165	GLU	1

6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

6.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.6 Ligand geometry [i](#)

There are no ligands in this entry.

6.7 Other polymers [i](#)

There are no such molecules in this entry.

6.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

7 Chemical shift validation

The completeness of assignment taking into account all chemical shift lists is 88% for the well-defined parts and 82% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *assigned_chem_shift_list_1*

7.1.1 Bookkeeping

The following table shows the results of parsing the chemical shift list and reports the number of nuclei with statistically unusual chemical shifts.

Total number of shifts	1700
Number of shifts mapped to atoms	1700
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

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	147	0.18 ± 0.11	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	135	-0.05 ± 0.10	None needed (< 0.5 ppm)
$^{13}\text{C}'$	135	0.34 ± 0.11	None needed (< 0.5 ppm)
^{15}N	140	0.29 ± 0.13	None needed (< 0.5 ppm)

7.1.3 Completeness of resonance assignments

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 88%, i.e. 1605 atoms were assigned a chemical shift out of a possible 1824. 0 out of 28 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	677/693 (98%)	280/283 (99%)	266/276 (96%)	131/134 (98%)
Sidechain	874/1041 (84%)	603/678 (89%)	266/332 (80%)	5/31 (16%)

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	Total	¹H	¹³C	¹⁵N
Aromatic	54/90 (60%)	27/43 (63%)	26/44 (59%)	1/3 (33%)
Overall	1605/1824 (88%)	910/1004 (91%)	558/652 (86%)	137/168 (82%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 82%, i.e. 1699 atoms were assigned a chemical shift out of a possible 2065. 0 out of 30 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Backbone	720/794 (91%)	298/324 (92%)	282/316 (89%)	140/154 (91%)
Sidechain	925/1174 (79%)	636/763 (83%)	284/375 (76%)	5/36 (14%)
Aromatic	54/97 (56%)	27/47 (57%)	26/46 (57%)	1/4 (25%)
Overall	1699/2065 (82%)	961/1134 (85%)	592/737 (80%)	146/194 (75%)

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	182	ILE	HB	0.04	0.35 – 3.22	-6.1
1	A	116	MET	HB2	0.30	0.42 – 3.63	-5.4

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:

