



# Full wwPDB NMR Structure Validation Report ⓘ

Apr 26, 2016 – 04:10 PM BST

PDB ID : 1OVQ  
Title : Solution structure of the hypothetical protein YqgF from Escherichia coli  
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Deposited on : 2003-03-27

This is a Full wwPDB NMR Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<http://wwpdb.org/validation/2016/NMRValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

Cyrange	:	Kirchner and Güntert (2011)
NmrClust	:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Mogul	:	unknown
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	rb-20027457
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20027457

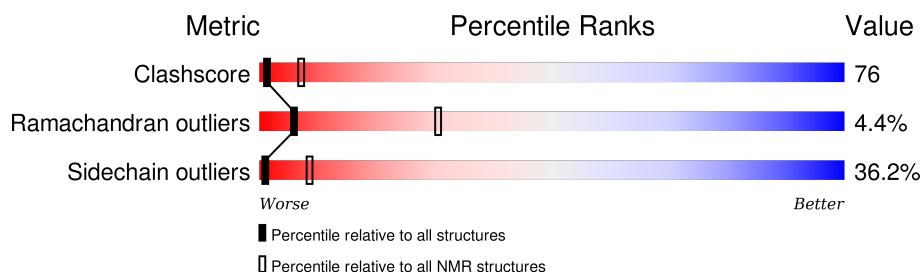
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*SOLUTION NMR*


The overall completeness of chemical shifts assignment is 83%.

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	114402	11133
Ramachandran outliers	111179	9975
Sidechain outliers	111093	9958

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  $\geq 3$ , 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	138	

## 2 Ensemble composition and analysis

This entry contains 25 models. Model 14 is the overall representative, medoid model (most similar to other models).

The following residues are included in the computation of the global validation metrics.

Well-defined (core) protein residues			
Well-defined core	Residue range (total)	Backbone RMSD (Å)	Medoid model
1	A:3-A:61, A:76-A:94, A:123-A:135 (91)	0.35	14

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 2 single-model clusters were found.

Cluster number	Models
1	3, 7, 10, 12, 14, 15, 16, 18, 23
2	4, 5, 9, 11
3	6, 13, 17
4	21, 22, 24, 25
5	2, 19, 20
Single-model clusters	1; 8

### 3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 2151 atoms, of which 1079 are hydrogens and 0 are deuteriums.

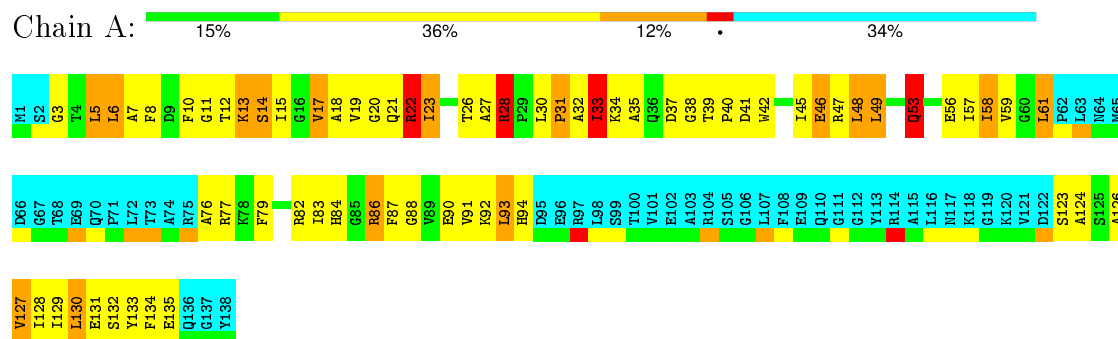
- Molecule 1 is a protein called Hypothetical protein yqgF.

Mol	Chain	Residues	Atoms						Trace
1	A	138	Total	C	H	N	O	S	0
			2151	678	1079	191	201	2	



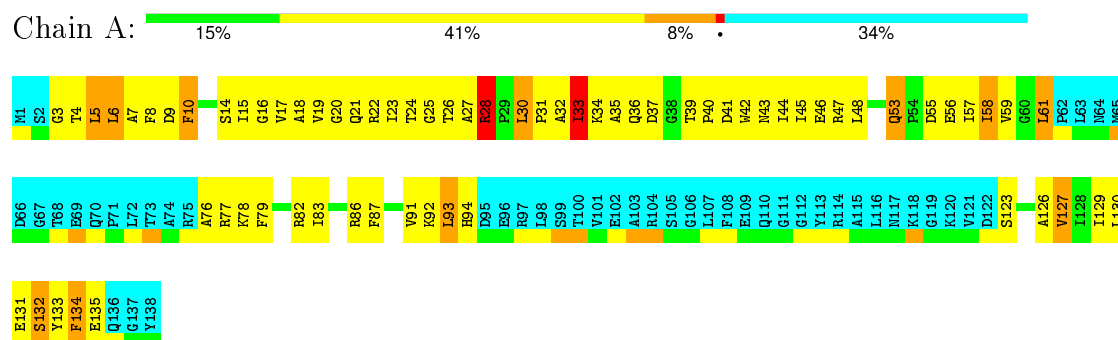
## 4.2.2 Score per residue for model 2

- Molecule 1: Hypothetical protein yqqF



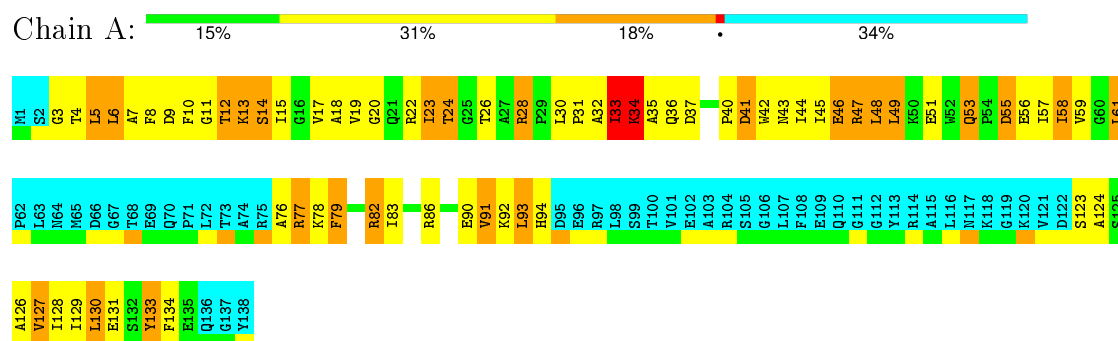
## 4.2.3 Score per residue for model 3

- Molecule 1: Hypothetical protein yqqF



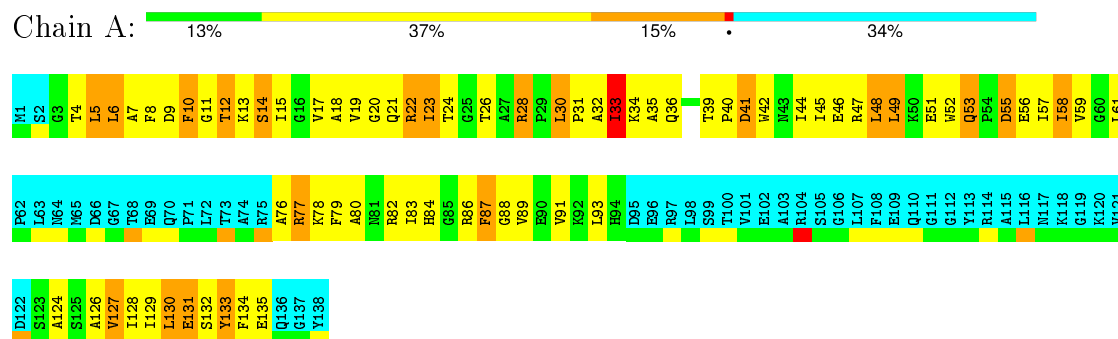
## 4.2.4 Score per residue for model 4

- Molecule 1: Hypothetical protein yqqF



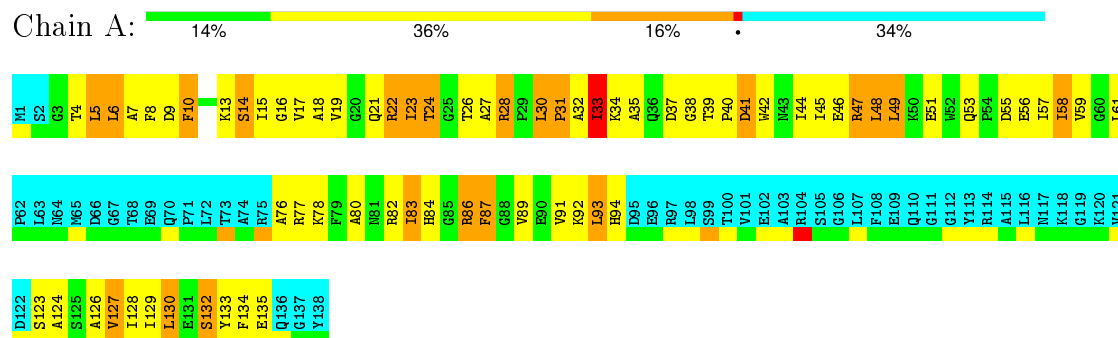
### 4.2.5 Score per residue for model 5

- Molecule 1: Hypothetical protein yqqF



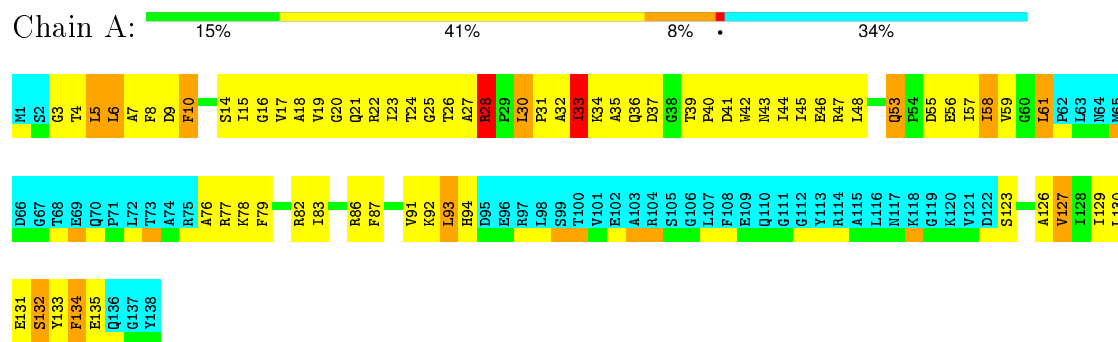
### 4.2.6 Score per residue for model 6

- Molecule 1: Hypothetical protein yqqF



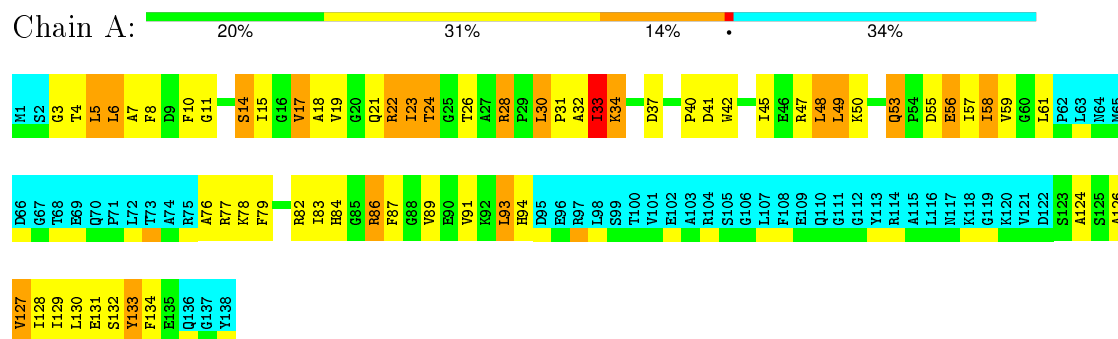
### 4.2.7 Score per residue for model 7

- Molecule 1: Hypothetical protein yqqF



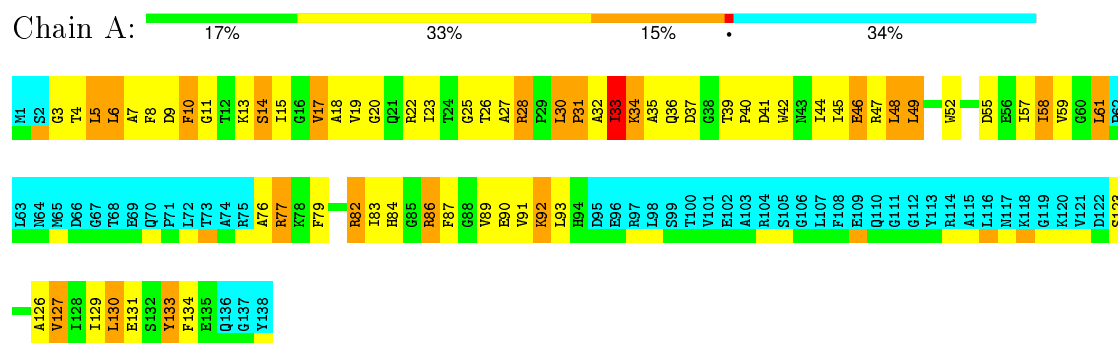
### 4.2.8 Score per residue for model 8

- Molecule 1: Hypothetical protein yqqF



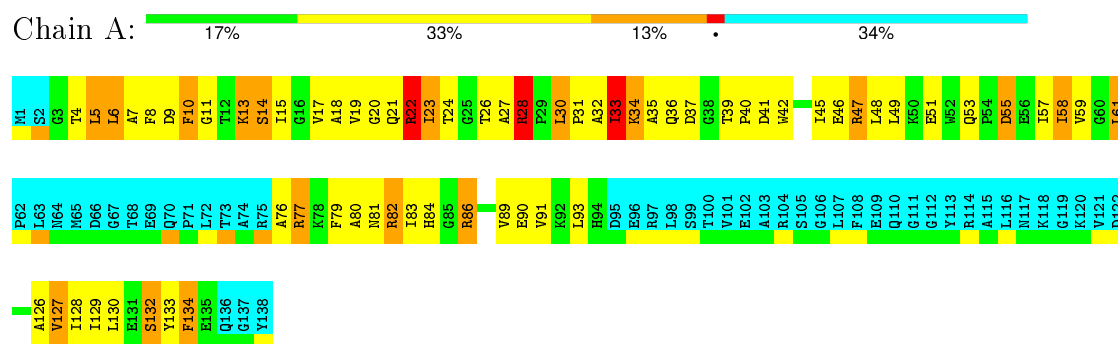
### 4.2.9 Score per residue for model 9

- Molecule 1: Hypothetical protein yqqF



### 4.2.10 Score per residue for model 10

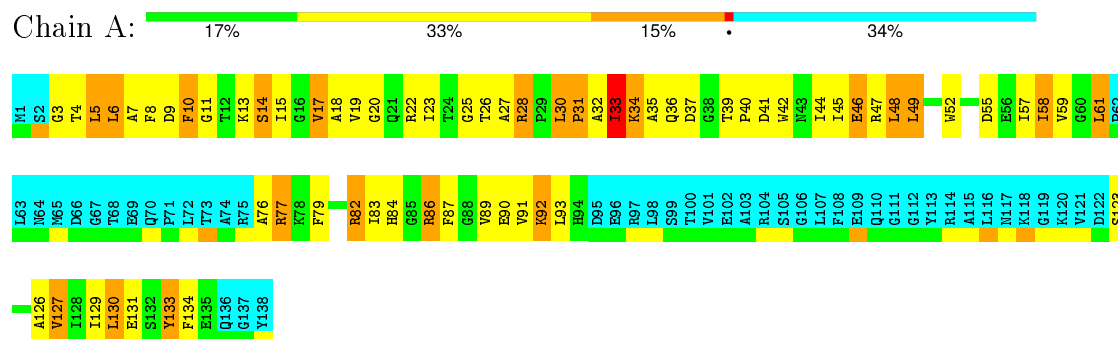
- Molecule 1: Hypothetical protein yqqF





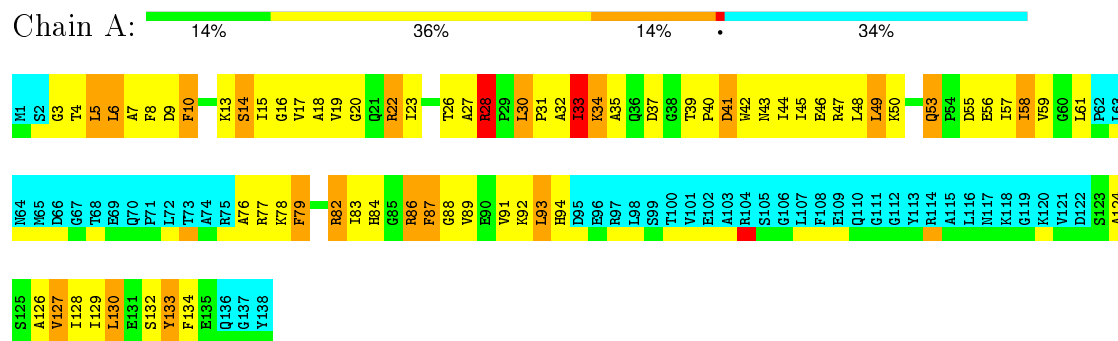
### 4.2.11 Score per residue for model 11

- Molecule 1: Hypothetical protein yqgF



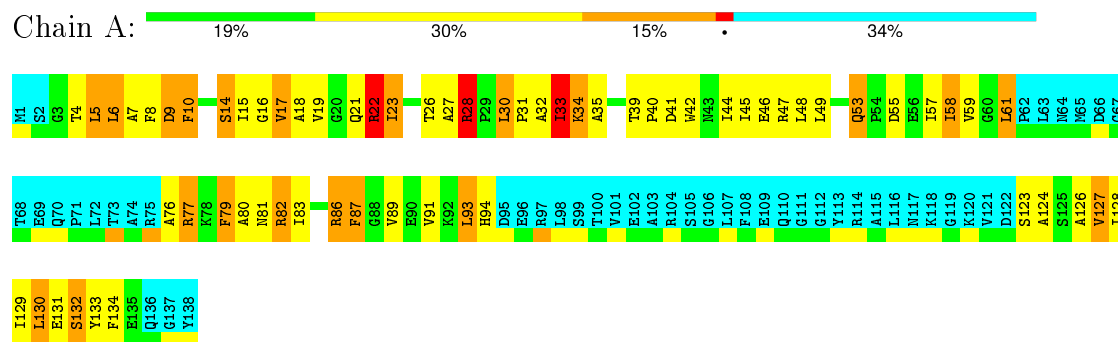
### 4.2.12 Score per residue for model 12

- Molecule 1: Hypothetical protein yqgF



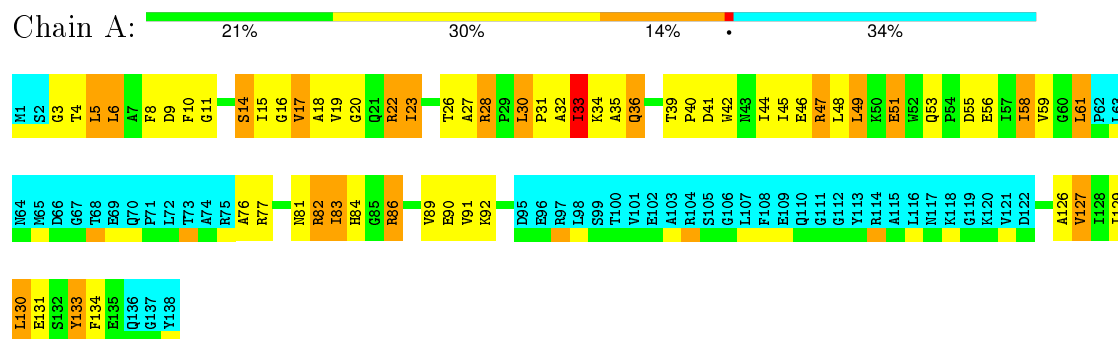
### 4.2.13 Score per residue for model 13

- Molecule 1: Hypothetical protein yqgF



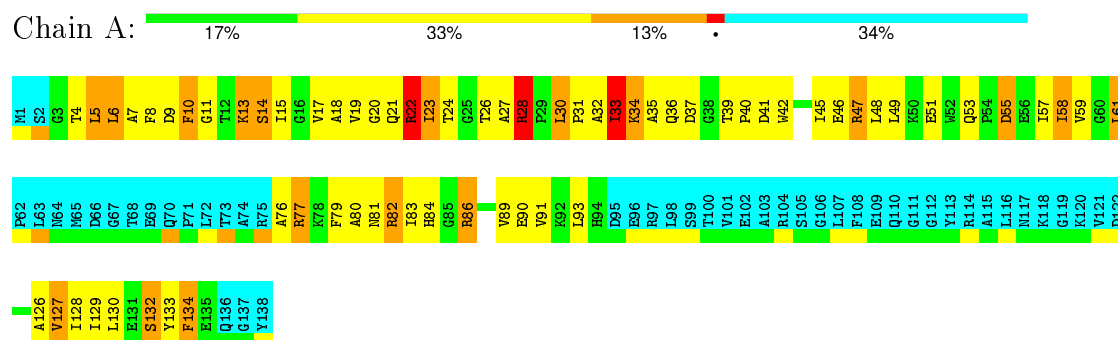
#### 4.2.14 Score per residue for model 14 (medoid)

- Molecule 1: Hypothetical protein yqgF



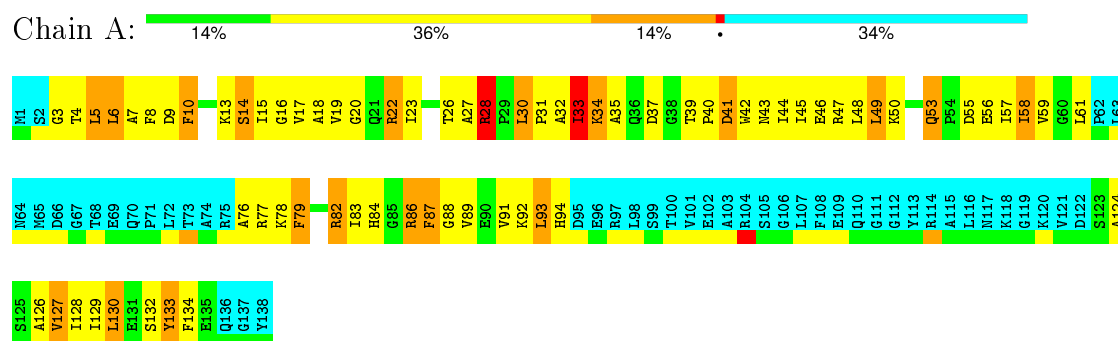
#### 4.2.15 Score per residue for model 15

- Molecule 1: Hypothetical protein yqgF



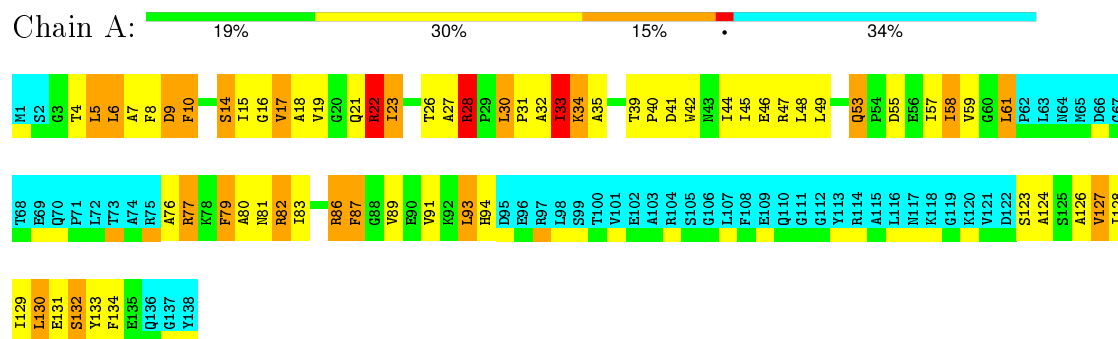
#### 4.2.16 Score per residue for model 16

- Molecule 1: Hypothetical protein yqgF



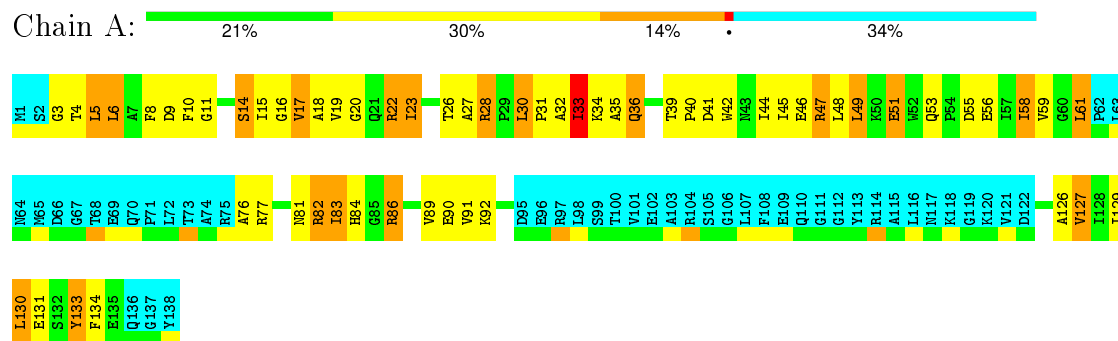
#### 4.2.17 Score per residue for model 17

- Molecule 1: Hypothetical protein yggF



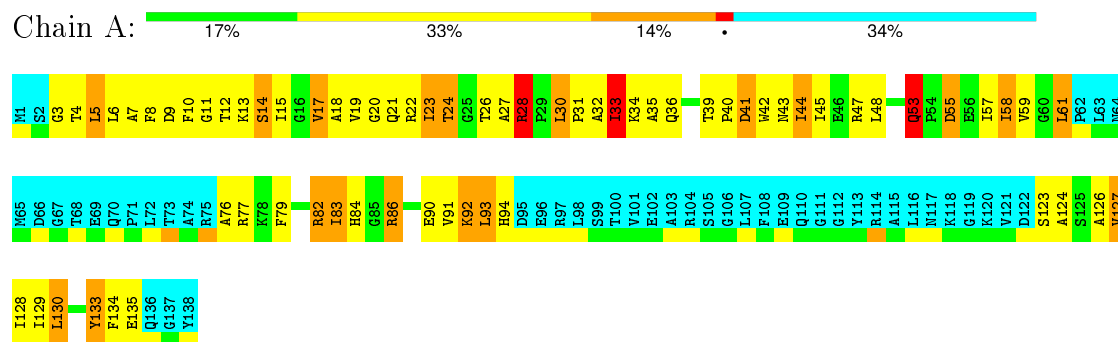
#### 4.2.18 Score per residue for model 18

- Molecule 1: Hypothetical protein yqgF



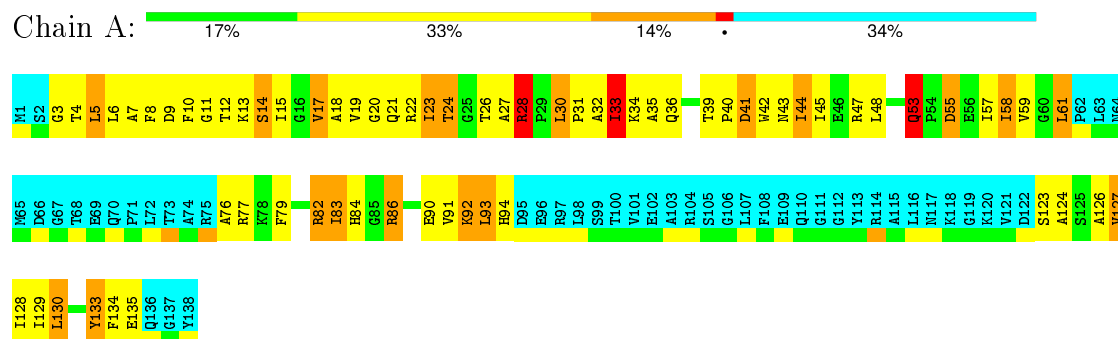
#### 4.2.19 Score per residue for model 19

- Molecule 1: Hypothetical protein yqgF



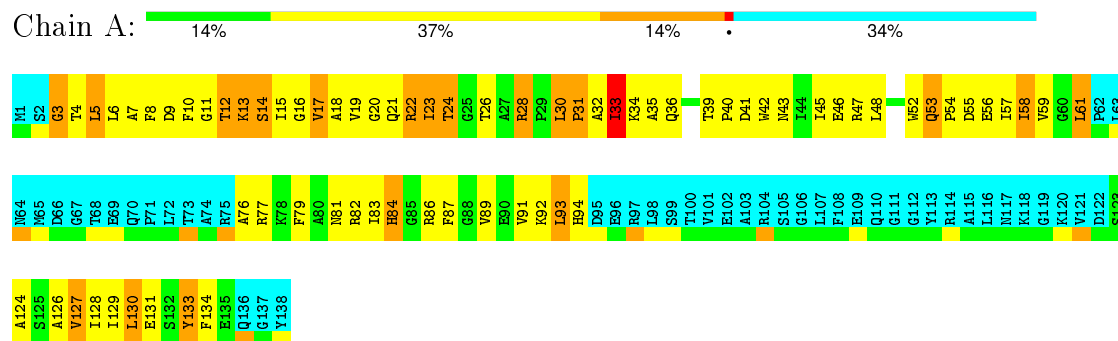
## 4.2.20 Score per residue for model 20

- Molecule 1: Hypothetical protein yqqF



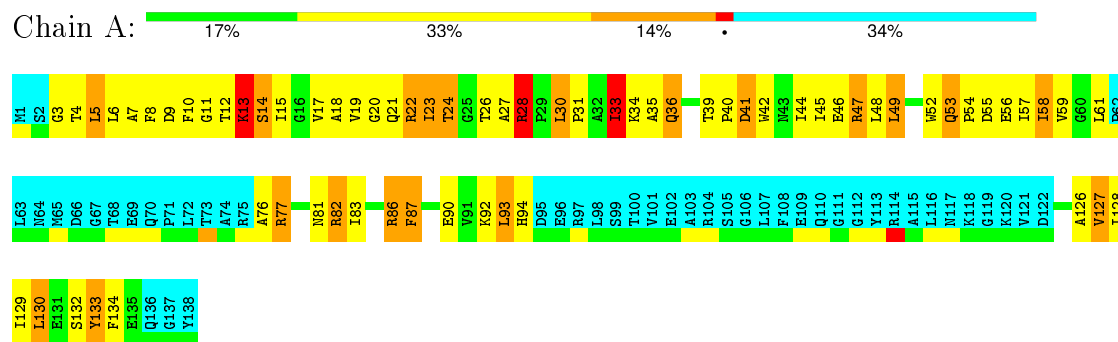
## 4.2.21 Score per residue for model 21

- Molecule 1: Hypothetical protein yqqF



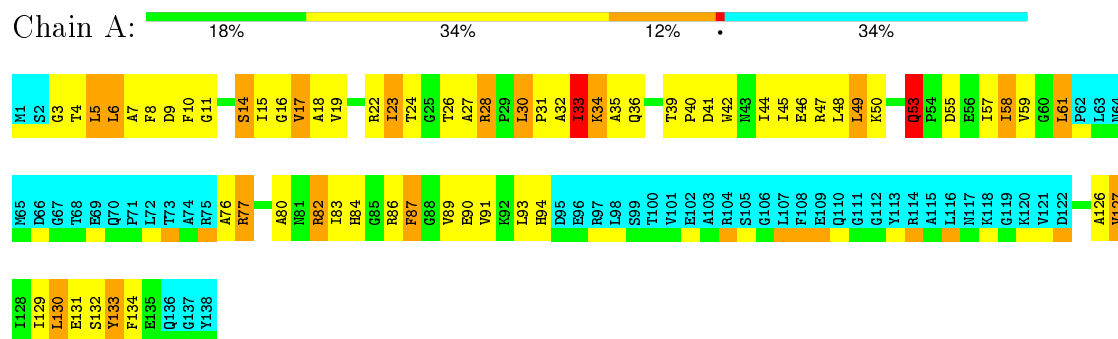
## 4.2.22 Score per residue for model 22

- Molecule 1: Hypothetical protein yqqF



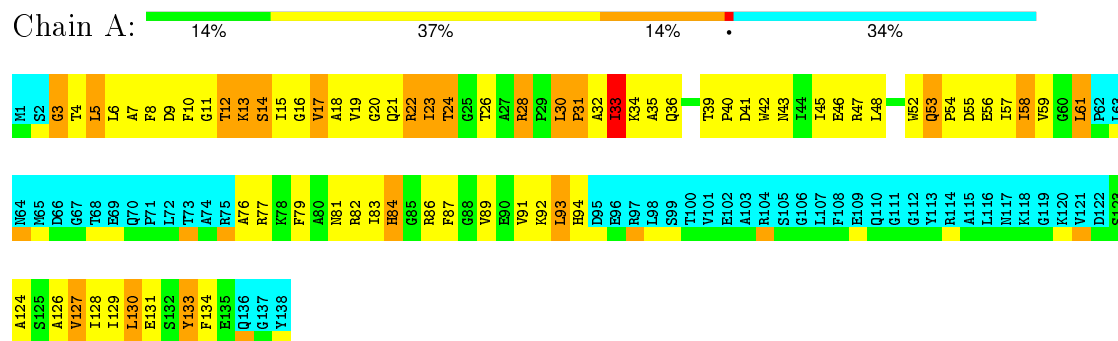
### 4.2.23 Score per residue for model 23

- Molecule 1: Hypothetical protein yqgF



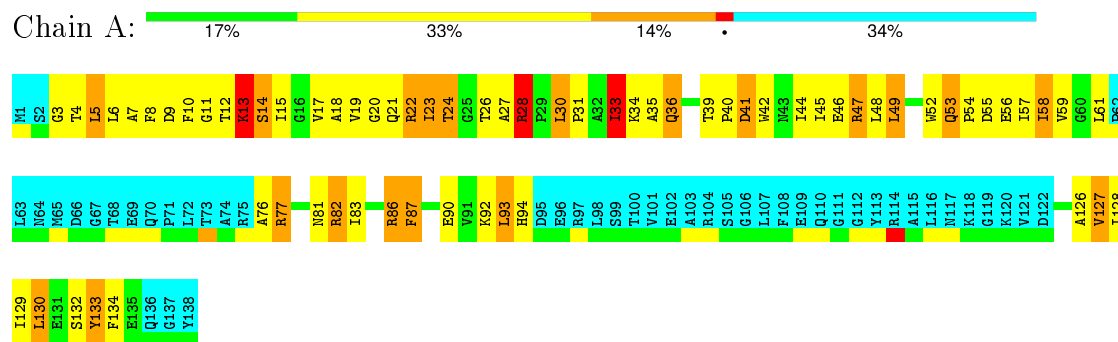
### 4.2.24 Score per residue for model 24

- Molecule 1: Hypothetical protein yqgF



### 4.2.25 Score per residue for model 25

- Molecule 1: Hypothetical protein yqgF



## 5 Refinement protocol and experimental data overview

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

Of the 100 calculated structures, 25 were deposited, based on the following criterion: *back calculated data agree with experimental NOESY spectrum*.

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

Software name	Classification	Version
X-PLOR	structure solution	98
X-PLOR	refinement	98

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)	BMRB entry 5758
Number of chemical shift lists	1
Total number of shifts	1370
Number of shifts mapped to atoms	1370
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	83%

No validations of the models with respect to experimental NMR restraints is performed at this time.

## 6 Model quality

### 6.1 Standard geometry

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	1.05±0.00	0±0/725 (0.0±0.0%)	1.28±0.01	0±0/984 (0.0±0.0%)
All	All	1.05	0/18125 (0.0%)	1.28	2/24600 (0.0%)

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

Mol	Chain	Chirality	Planarity
1	A	0.0±0.0	6.0±0.0
All	All	0	150

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	14	SER	N-CA-CB	-5.47	102.29	110.50	22	2

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	22	ARG	Sidechain	25
1	A	77	ARG	Sidechain	25
1	A	47	ARG	Sidechain	25
1	A	86	ARG	Sidechain	25
1	A	82	ARG	Sidechain	25
1	A	28	ARG	Sidechain	25

## 6.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	709	726	726	109±8
All	All	17725	18150	18150	2717

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 76.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:6:LEU:HD21	1:A:48:LEU:HD13	1.12	1.20	20	15
1:A:6:LEU:HD11	1:A:19:VAL:HG13	1.07	1.25	14	16
1:A:5:LEU:HD21	1:A:58:ILE:HD11	1.04	1.20	22	16
1:A:5:LEU:HD22	1:A:133:TYR:CE2	0.97	1.95	13	7
1:A:83:ILE:HD11	1:A:91:VAL:HG21	0.96	1.33	24	15
1:A:6:LEU:HD21	1:A:48:LEU:HD11	0.91	1.38	6	4
1:A:5:LEU:HD22	1:A:6:LEU:N	0.91	1.80	23	18
1:A:5:LEU:HD13	1:A:133:TYR:CE1	0.90	2.01	13	7
1:A:17:VAL:HG13	1:A:30:LEU:HD22	0.90	1.42	11	14
1:A:93:LEU:HD22	1:A:94:HIS:N	0.89	1.82	2	14
1:A:48:LEU:O	1:A:48:LEU:HD22	0.88	1.68	8	4
1:A:48:LEU:HD22	1:A:48:LEU:O	0.88	1.68	1	4
1:A:5:LEU:HD22	1:A:133:TYR:CZ	0.88	2.04	3	7
1:A:61:LEU:O	1:A:61:LEU:HD13	0.87	1.69	2	6
1:A:56:GLU:O	1:A:57:ILE:HD13	0.87	1.69	22	4
1:A:41:ASP:O	1:A:45:ILE:HD12	0.86	1.70	6	25
1:A:6:LEU:HD11	1:A:19:VAL:CG1	0.86	2.00	20	12
1:A:130:LEU:HD12	1:A:134:PHE:CE2	0.86	2.05	2	13
1:A:5:LEU:CD2	1:A:58:ILE:HD11	0.85	2.01	22	18
1:A:17:VAL:CG1	1:A:30:LEU:HD13	0.85	2.02	12	11
1:A:61:LEU:HD13	1:A:61:LEU:O	0.85	1.72	10	5
1:A:48:LEU:HD13	1:A:49:LEU:N	0.85	1.86	5	8
1:A:15:ILE:HD11	1:A:40:PRO:HB3	0.84	1.49	1	25
1:A:5:LEU:HD21	1:A:58:ILE:CD1	0.82	2.04	22	15
1:A:5:LEU:O	1:A:5:LEU:HD13	0.82	1.74	1	9
1:A:5:LEU:HD13	1:A:5:LEU:O	0.82	1.74	8	6
1:A:8:PHE:CE2	1:A:17:VAL:HG11	0.82	2.09	13	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:6:LEU:CD2	1:A:48:LEU:HD13	0.82	2.05	3	8
1:A:23:ILE:HD13	1:A:23:ILE:C	0.82	1.95	14	9
1:A:93:LEU:O	1:A:93:LEU:HD13	0.81	1.76	3	5
1:A:59:VAL:HG11	1:A:83:ILE:CD1	0.81	2.06	4	13
1:A:23:ILE:C	1:A:23:ILE:HD13	0.81	1.96	4	7
1:A:93:LEU:HD13	1:A:93:LEU:O	0.81	1.76	13	9
1:A:17:VAL:CG1	1:A:30:LEU:HD22	0.81	2.06	11	14
1:A:19:VAL:HG13	1:A:48:LEU:HD21	0.80	1.53	13	2
1:A:59:VAL:HG21	1:A:83:ILE:CD1	0.79	2.07	11	14
1:A:10:PHE:CD2	1:A:15:ILE:HD13	0.79	2.11	5	3
1:A:35:ALA:HB1	1:A:39:THR:O	0.79	1.77	22	22
1:A:23:ILE:CD1	1:A:24:THR:HG23	0.79	2.07	20	7
1:A:6:LEU:CD2	1:A:48:LEU:HD11	0.79	2.07	6	6
1:A:19:VAL:CG1	1:A:48:LEU:HD22	0.78	2.09	10	4
1:A:19:VAL:CG1	1:A:48:LEU:HD21	0.78	2.08	13	3
1:A:83:ILE:HD11	1:A:91:VAL:CG2	0.78	2.07	24	3
1:A:59:VAL:HG11	1:A:83:ILE:HD13	0.77	1.56	22	16
1:A:59:VAL:HG21	1:A:83:ILE:HD12	0.77	1.56	5	12
1:A:15:ILE:HD11	1:A:40:PRO:CB	0.77	2.09	24	25
1:A:17:VAL:HG11	1:A:30:LEU:HD13	0.76	1.58	5	11
1:A:8:PHE:HB2	1:A:59:VAL:HG23	0.76	1.56	14	6
1:A:14:SER:OG	1:A:33:ILE:HD11	0.75	1.81	3	7
1:A:19:VAL:HG11	1:A:48:LEU:HD22	0.75	1.58	10	4
1:A:57:ILE:HG22	1:A:91:VAL:HG23	0.75	1.59	2	3
1:A:10:PHE:O	1:A:61:LEU:HD23	0.75	1.80	1	2
1:A:8:PHE:HB2	1:A:59:VAL:HG22	0.74	1.58	23	12
1:A:93:LEU:HD13	1:A:93:LEU:N	0.74	1.97	20	3
1:A:5:LEU:HD11	1:A:130:LEU:HD21	0.74	1.59	2	1
1:A:83:ILE:HD13	1:A:84:HIS:N	0.74	1.98	6	5
1:A:8:PHE:CD2	1:A:17:VAL:HG21	0.73	2.18	1	10
1:A:18:ALA:HB2	1:A:127:VAL:N	0.73	1.99	2	25
1:A:54:PRO:HB2	1:A:57:ILE:HD11	0.73	1.59	24	2
1:A:17:VAL:CG2	1:A:30:LEU:HD13	0.72	2.14	13	14
1:A:5:LEU:C	1:A:5:LEU:HD13	0.72	2.05	1	8
1:A:15:ILE:HG21	1:A:41:ASP:OD2	0.72	1.85	14	8
1:A:5:LEU:HD13	1:A:5:LEU:C	0.72	2.05	8	9
1:A:83:ILE:CD1	1:A:91:VAL:HG21	0.72	2.15	3	15
1:A:5:LEU:HD13	1:A:133:TYR:CZ	0.70	2.20	13	7
1:A:124:ALA:O	1:A:128:ILE:HD13	0.70	1.86	24	13
1:A:6:LEU:CD2	1:A:19:VAL:HG22	0.70	2.16	24	3
1:A:61:LEU:C	1:A:61:LEU:HD22	0.70	2.07	17	6

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:61:LEU:HD22	1:A:61:LEU:C	0.70	2.07	13	5
1:A:57:ILE:C	1:A:58:ILE:HD13	0.69	2.07	1	12
1:A:8:PHE:CE1	1:A:57:ILE:HG23	0.69	2.21	3	6
1:A:49:LEU:HD22	1:A:87:PHE:CD2	0.69	2.22	22	2
1:A:30:LEU:HD11	1:A:44:ILE:HD11	0.69	1.63	20	2
1:A:9:ASP:HB2	1:A:129:ILE:HD12	0.68	1.65	23	5
1:A:23:ILE:C	1:A:23:ILE:HD12	0.68	2.09	1	2
1:A:61:LEU:HD21	1:A:76:ALA:HB2	0.67	1.65	22	2
1:A:5:LEU:HD11	1:A:133:TYR:CE2	0.67	2.25	1	2
1:A:8:PHE:CD1	1:A:59:VAL:HG22	0.67	2.25	1	4
1:A:48:LEU:HD13	1:A:48:LEU:C	0.67	2.10	4	5
1:A:10:PHE:HD2	1:A:15:ILE:HD13	0.66	1.47	11	3
1:A:5:LEU:HD12	1:A:133:TYR:CE2	0.66	2.24	20	15
1:A:23:ILE:HD12	1:A:23:ILE:C	0.66	2.10	6	1
1:A:17:VAL:HG13	1:A:30:LEU:CD2	0.66	2.19	11	14
1:A:17:VAL:HG13	1:A:30:LEU:HB3	0.66	1.66	24	14
1:A:14:SER:HB2	1:A:33:ILE:HD11	0.66	1.65	2	12
1:A:83:ILE:HD12	1:A:91:VAL:HG21	0.66	1.68	20	2
1:A:5:LEU:HD22	1:A:6:LEU:H	0.65	1.49	5	10
1:A:30:LEU:HD21	1:A:44:ILE:HG21	0.65	1.68	3	4
1:A:61:LEU:HD22	1:A:61:LEU:O	0.65	1.92	13	2
1:A:8:PHE:CG	1:A:59:VAL:HG22	0.64	2.27	10	2
1:A:48:LEU:HD23	1:A:52:TRP:CE3	0.64	2.27	5	1
1:A:4:THR:O	1:A:55:ASP:N	0.64	2.31	22	24
1:A:15:ILE:C	1:A:33:ILE:HA	0.64	2.13	1	25
1:A:19:VAL:HG11	1:A:48:LEU:CD2	0.64	2.22	10	4
1:A:14:SER:HB3	1:A:33:ILE:HD11	0.64	1.69	12	6
1:A:48:LEU:C	1:A:48:LEU:HD13	0.64	2.13	11	3
1:A:58:ILE:HD13	1:A:58:ILE:N	0.64	2.08	10	7
1:A:17:VAL:HA	1:A:126:ALA:CB	0.63	2.23	1	25
1:A:58:ILE:N	1:A:58:ILE:HD13	0.63	2.07	6	6
1:A:61:LEU:CD2	1:A:76:ALA:HB2	0.63	2.24	22	2
1:A:9:ASP:HB3	1:A:126:ALA:HB2	0.63	1.68	11	6
1:A:61:LEU:HD23	1:A:61:LEU:O	0.62	1.93	24	3
1:A:8:PHE:HB3	1:A:59:VAL:HG23	0.62	1.71	13	2
1:A:8:PHE:HE1	1:A:57:ILE:HG23	0.62	1.54	3	6
1:A:44:ILE:HD12	1:A:44:ILE:C	0.62	2.15	20	2
1:A:5:LEU:CD1	1:A:133:TYR:CE2	0.62	2.83	23	17
1:A:6:LEU:CG	1:A:19:VAL:HG13	0.62	2.25	24	3
1:A:93:LEU:C	1:A:93:LEU:HD13	0.62	2.15	8	7
1:A:9:ASP:CB	1:A:126:ALA:HB2	0.62	2.25	11	6

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:93:LEU:HD13	1:A:93:LEU:C	0.62	2.15	1	7
1:A:61:LEU:HD12	1:A:76:ALA:HB2	0.62	1.72	4	1
1:A:130:LEU:HD12	1:A:134:PHE:CZ	0.62	2.29	2	1
1:A:56:GLU:C	1:A:57:ILE:HD13	0.61	2.16	22	4
1:A:93:LEU:HD22	1:A:93:LEU:O	0.61	1.95	20	3
1:A:8:PHE:HA	1:A:17:VAL:HG22	0.61	1.71	5	4
1:A:6:LEU:HD12	1:A:8:PHE:CZ	0.61	2.31	2	3
1:A:19:VAL:HG13	1:A:48:LEU:CD2	0.61	2.26	13	2
1:A:30:LEU:HD11	1:A:45:ILE:CG1	0.61	2.26	6	4
1:A:48:LEU:C	1:A:48:LEU:HD22	0.61	2.16	5	4
1:A:48:LEU:HD22	1:A:48:LEU:C	0.61	2.16	4	4
1:A:6:LEU:HG	1:A:19:VAL:HG13	0.61	1.71	24	3
1:A:80:ALA:HB3	1:A:93:LEU:CD2	0.60	2.26	10	3
1:A:6:LEU:HD21	1:A:48:LEU:CD1	0.60	2.23	12	4
1:A:7:ALA:HB3	1:A:130:LEU:CD2	0.60	2.27	2	2
1:A:93:LEU:HD22	1:A:93:LEU:C	0.60	2.17	12	6
1:A:93:LEU:C	1:A:93:LEU:HD22	0.60	2.17	16	8
1:A:15:ILE:HG21	1:A:41:ASP:CG	0.59	2.18	13	6
1:A:8:PHE:O	1:A:129:ILE:HD13	0.59	1.97	10	2
1:A:10:PHE:O	1:A:61:LEU:HD12	0.59	1.97	13	2
1:A:23:ILE:HD13	1:A:24:THR:HG23	0.59	1.74	20	6
1:A:17:VAL:HG22	1:A:30:LEU:HD13	0.59	1.74	20	14
1:A:133:TYR:CE2	1:A:134:PHE:CE1	0.59	2.91	11	15
1:A:8:PHE:CB	1:A:59:VAL:HG22	0.59	2.27	10	2
1:A:6:LEU:HD12	1:A:8:PHE:CE1	0.59	2.33	6	2
1:A:45:ILE:HA	1:A:48:LEU:HD12	0.59	1.73	10	2
1:A:35:ALA:HB1	1:A:39:THR:C	0.59	2.17	21	18
1:A:61:LEU:CD1	1:A:76:ALA:HB2	0.59	2.27	20	3
1:A:61:LEU:HD22	1:A:76:ALA:HB2	0.59	1.74	24	3
1:A:10:PHE:CD1	1:A:79:PHE:CE1	0.59	2.90	3	6
1:A:6:LEU:HD23	1:A:8:PHE:CZ	0.58	2.33	3	4
1:A:5:LEU:HD12	1:A:22:ARG:HB2	0.58	1.74	10	5
1:A:10:PHE:CG	1:A:79:PHE:CE1	0.58	2.92	12	6
1:A:130:LEU:CD1	1:A:134:PHE:CE2	0.58	2.87	11	16
1:A:44:ILE:HD12	1:A:44:ILE:N	0.58	2.14	6	6
1:A:30:LEU:HD11	1:A:45:ILE:HG12	0.58	1.76	6	3
1:A:10:PHE:CD1	1:A:79:PHE:CZ	0.58	2.91	13	4
1:A:15:ILE:HG21	1:A:41:ASP:HB2	0.58	1.76	12	2
1:A:61:LEU:HD13	1:A:61:LEU:C	0.57	2.20	2	2
1:A:6:LEU:HD21	1:A:19:VAL:HG13	0.57	1.77	1	2
1:A:15:ILE:N	1:A:33:ILE:HA	0.57	2.15	6	25

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:23:ILE:C	1:A:23:ILE:CD1	0.57	2.73	4	6
1:A:8:PHE:CB	1:A:59:VAL:HG23	0.57	2.30	6	3
1:A:23:ILE:CD1	1:A:23:ILE:C	0.57	2.72	24	12
1:A:45:ILE:HG22	1:A:49:LEU:HD13	0.56	1.77	2	8
1:A:5:LEU:HD22	1:A:133:TYR:CD2	0.56	2.35	13	5
1:A:133:TYR:CD1	1:A:134:PHE:N	0.56	2.73	3	8
1:A:8:PHE:CD2	1:A:17:VAL:HG11	0.56	2.35	3	6
1:A:61:LEU:HD11	1:A:76:ALA:HB2	0.56	1.77	20	2
1:A:8:PHE:N	1:A:8:PHE:CD1	0.56	2.73	12	9
1:A:8:PHE:CD1	1:A:8:PHE:N	0.56	2.73	16	9
1:A:23:ILE:O	1:A:23:ILE:HD13	0.56	2.00	2	5
1:A:93:LEU:H	1:A:93:LEU:HD13	0.56	1.58	6	2
1:A:30:LEU:CD2	1:A:44:ILE:HG21	0.56	2.31	13	4
1:A:10:PHE:HB2	1:A:14:SER:O	0.56	2.01	22	18
1:A:14:SER:CB	1:A:33:ILE:HG13	0.56	2.31	22	14
1:A:5:LEU:HD12	1:A:20:GLY:HA3	0.55	1.77	2	1
1:A:27:ALA:CB	1:A:127:VAL:CG1	0.55	2.85	3	13
1:A:130:LEU:O	1:A:130:LEU:HD13	0.55	2.00	24	6
1:A:6:LEU:HB3	1:A:57:ILE:HG23	0.55	1.77	13	2
1:A:11:GLY:CA	1:A:79:PHE:CE2	0.55	2.90	2	1
1:A:23:ILE:HD13	1:A:23:ILE:O	0.55	2.02	14	5
1:A:17:VAL:HG21	1:A:30:LEU:HD13	0.55	1.79	2	14
1:A:14:SER:CB	1:A:33:ILE:HD11	0.55	2.30	2	8
1:A:7:ALA:CB	1:A:130:LEU:HD23	0.55	2.32	13	8
1:A:13:LYS:O	1:A:35:ALA:HB3	0.55	2.02	4	1
1:A:61:LEU:O	1:A:61:LEU:HD12	0.54	2.02	1	3
1:A:61:LEU:HD12	1:A:61:LEU:O	0.54	2.02	8	1
1:A:10:PHE:CD2	1:A:11:GLY:N	0.54	2.75	2	11
1:A:5:LEU:HG	1:A:133:TYR:CZ	0.54	2.38	12	18
1:A:20:GLY:HA3	1:A:130:LEU:HD21	0.54	1.77	10	2
1:A:130:LEU:HD22	1:A:133:TYR:HE2	0.54	1.62	3	7
1:A:7:ALA:CB	1:A:130:LEU:CD2	0.54	2.85	2	10
1:A:61:LEU:C	1:A:61:LEU:HD12	0.54	2.23	5	3
1:A:58:ILE:HB	1:A:129:ILE:HG22	0.54	1.80	3	14
1:A:83:ILE:CD1	1:A:91:VAL:HG11	0.54	2.32	6	1
1:A:57:ILE:HG22	1:A:59:VAL:HG23	0.54	1.78	4	3
1:A:15:ILE:H	1:A:33:ILE:HA	0.54	1.63	4	25
1:A:58:ILE:CD1	1:A:58:ILE:N	0.54	2.71	6	7
1:A:6:LEU:CD2	1:A:19:VAL:HG13	0.54	2.33	1	3
1:A:57:ILE:HD12	1:A:57:ILE:N	0.53	2.18	20	2
1:A:7:ALA:HB2	1:A:130:LEU:CD2	0.53	2.34	13	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:8:PHE:CD2	1:A:17:VAL:CG2	0.53	2.91	1	3
1:A:7:ALA:HB2	1:A:58:ILE:HG12	0.53	1.80	2	2
1:A:19:VAL:O	1:A:28:ARG:N	0.53	2.42	4	22
1:A:6:LEU:HD12	1:A:7:ALA:N	0.53	2.17	13	4
1:A:93:LEU:HD13	1:A:93:LEU:H	0.53	1.63	19	1
1:A:17:VAL:CB	1:A:30:LEU:HD13	0.53	2.32	3	9
1:A:61:LEU:C	1:A:61:LEU:HD13	0.53	2.24	3	4
1:A:44:ILE:N	1:A:44:ILE:HD12	0.53	2.18	12	6
1:A:18:ALA:CB	1:A:127:VAL:N	0.53	2.72	5	11
1:A:8:PHE:CA	1:A:17:VAL:HG22	0.53	2.34	5	2
1:A:57:ILE:HG22	1:A:91:VAL:CG2	0.53	2.31	2	1
1:A:130:LEU:HD13	1:A:130:LEU:C	0.53	2.24	10	7
1:A:130:LEU:C	1:A:130:LEU:HD13	0.53	2.24	15	2
1:A:80:ALA:HA	1:A:83:ILE:HD12	0.53	1.81	13	2
1:A:16:GLY:N	1:A:33:ILE:HD12	0.53	2.19	3	2
1:A:7:ALA:HB2	1:A:58:ILE:CG1	0.53	2.34	23	2
1:A:80:ALA:CB	1:A:93:LEU:HD23	0.53	2.34	10	2
1:A:5:LEU:O	1:A:6:LEU:HD12	0.53	2.04	11	6
1:A:133:TYR:OH	1:A:134:PHE:CE1	0.52	2.61	22	14
1:A:6:LEU:CD1	1:A:8:PHE:CZ	0.52	2.91	2	1
1:A:6:LEU:CD1	1:A:19:VAL:HG13	0.52	2.35	24	8
1:A:5:LEU:HD22	1:A:5:LEU:C	0.52	2.22	23	4
1:A:87:PHE:HB3	1:A:89:VAL:HG13	0.52	1.80	1	9
1:A:10:PHE:CD1	1:A:11:GLY:N	0.52	2.78	20	2
1:A:49:LEU:CD2	1:A:87:PHE:CG	0.52	2.93	22	2
1:A:58:ILE:N	1:A:58:ILE:CD1	0.52	2.72	13	3
1:A:18:ALA:CB	1:A:127:VAL:CA	0.51	2.89	5	14
1:A:33:ILE:HG23	1:A:34:LYS:N	0.51	2.19	4	1
1:A:133:TYR:CZ	1:A:134:PHE:CE1	0.51	2.98	24	14
1:A:17:VAL:HB	1:A:30:LEU:HB3	0.51	1.82	5	11
1:A:5:LEU:CD1	1:A:133:TYR:CE1	0.51	2.89	6	7
1:A:126:ALA:HA	1:A:129:ILE:HD12	0.51	1.81	3	4
1:A:9:ASP:HB2	1:A:126:ALA:HB2	0.51	1.80	3	4
1:A:27:ALA:HB1	1:A:127:VAL:HG13	0.51	1.80	12	13
1:A:10:PHE:HB2	1:A:59:VAL:HG22	0.51	1.83	6	1
1:A:27:ALA:HB3	1:A:127:VAL:CG1	0.51	2.35	3	13
1:A:83:ILE:HD13	1:A:83:ILE:C	0.51	2.26	18	2
1:A:61:LEU:HD12	1:A:76:ALA:CB	0.51	2.35	4	1
1:A:83:ILE:C	1:A:83:ILE:HD13	0.51	2.26	14	1
1:A:133:TYR:C	1:A:133:TYR:CD1	0.51	2.84	13	5
1:A:130:LEU:CD1	1:A:134:PHE:CZ	0.51	2.94	5	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:79:PHE:CD1	1:A:79:PHE:N	0.51	2.78	2	1
1:A:83:ILE:HD12	1:A:84:HIS:N	0.51	2.20	24	2
1:A:17:VAL:HG22	1:A:30:LEU:CD1	0.50	2.36	13	14
1:A:27:ALA:HB2	1:A:134:PHE:CZ	0.50	2.40	2	1
1:A:61:LEU:HD22	1:A:76:ALA:CB	0.50	2.36	24	3
1:A:10:PHE:CD2	1:A:14:SER:O	0.50	2.64	2	5
1:A:10:PHE:CE2	1:A:79:PHE:CE1	0.50	2.99	1	2
1:A:5:LEU:HG	1:A:133:TYR:CE2	0.50	2.40	12	13
1:A:133:TYR:CD1	1:A:133:TYR:C	0.50	2.85	10	4
1:A:32:ALA:O	1:A:34:LYS:N	0.50	2.44	23	22
1:A:17:VAL:HA	1:A:126:ALA:HB1	0.50	1.84	10	9
1:A:12:THR:HG23	1:A:79:PHE:CE1	0.50	2.42	5	1
1:A:93:LEU:O	1:A:93:LEU:CD2	0.50	2.60	20	1
1:A:93:LEU:CD2	1:A:93:LEU:O	0.50	2.60	19	2
1:A:8:PHE:CD2	1:A:17:VAL:CG1	0.49	2.95	3	4
1:A:7:ALA:O	1:A:17:VAL:HG13	0.49	2.08	10	9
1:A:5:LEU:CD1	1:A:130:LEU:CD2	0.49	2.90	11	15
1:A:15:ILE:O	1:A:33:ILE:HA	0.49	2.07	5	25
1:A:12:THR:HG23	1:A:12:THR:O	0.49	2.06	22	2
1:A:19:VAL:HG11	1:A:48:LEU:HD21	0.49	1.84	23	1
1:A:49:LEU:CD2	1:A:87:PHE:CD2	0.49	2.96	22	2
1:A:59:VAL:CG1	1:A:79:PHE:CE2	0.49	2.95	24	3
1:A:7:ALA:HB3	1:A:130:LEU:HD23	0.49	1.84	1	4
1:A:5:LEU:HD11	1:A:130:LEU:HD22	0.49	1.83	24	12
1:A:6:LEU:CD1	1:A:8:PHE:CE1	0.49	2.95	6	2
1:A:15:ILE:HG21	1:A:41:ASP:OD1	0.49	2.07	11	2
1:A:59:VAL:CG1	1:A:91:VAL:CG2	0.49	2.91	13	4
1:A:83:ILE:HD11	1:A:91:VAL:HG11	0.49	1.83	2	1
1:A:6:LEU:HG	1:A:8:PHE:CE1	0.49	2.43	15	3
1:A:10:PHE:O	1:A:79:PHE:CE2	0.49	2.66	4	3
1:A:17:VAL:CG2	1:A:18:ALA:N	0.49	2.76	23	11
1:A:59:VAL:HG12	1:A:79:PHE:CE2	0.49	2.43	4	1
1:A:10:PHE:O	1:A:61:LEU:CB	0.48	2.61	24	8
1:A:124:ALA:HA	1:A:127:VAL:HG13	0.48	1.84	2	10
1:A:76:ALA:HA	1:A:79:PHE:CD2	0.48	2.43	2	1
1:A:5:LEU:CD1	1:A:133:TYR:CD2	0.48	2.95	5	4
1:A:10:PHE:CZ	1:A:79:PHE:CE1	0.48	3.01	11	2
1:A:10:PHE:CE1	1:A:79:PHE:CZ	0.48	3.01	3	2
1:A:17:VAL:HB	1:A:30:LEU:HD13	0.48	1.84	3	7
1:A:8:PHE:N	1:A:58:ILE:O	0.48	2.43	11	9
1:A:59:VAL:HG12	1:A:91:VAL:HG22	0.48	1.85	13	4

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:11:GLY:O	1:A:13:LYS:N	0.48	2.46	4	5
1:A:130:LEU:HD13	1:A:130:LEU:O	0.48	2.08	11	2
1:A:57:ILE:CG2	1:A:91:VAL:HG23	0.48	2.37	12	3
1:A:59:VAL:CG1	1:A:80:ALA:CB	0.48	2.92	6	1
1:A:57:ILE:N	1:A:57:ILE:HD12	0.48	2.24	1	3
1:A:45:ILE:HG22	1:A:49:LEU:CD1	0.48	2.39	2	11
1:A:44:ILE:CD1	1:A:44:ILE:N	0.48	2.77	22	3
1:A:5:LEU:CD2	1:A:133:TYR:CZ	0.48	2.91	3	3
1:A:44:ILE:N	1:A:44:ILE:CD1	0.48	2.77	25	4
1:A:17:VAL:HB	1:A:30:LEU:CB	0.48	2.39	3	11
1:A:23:ILE:HD13	1:A:24:THR:N	0.48	2.23	22	6
1:A:48:LEU:O	1:A:53:GLN:N	0.48	2.46	23	9
1:A:84:HIS:CE1	1:A:89:VAL:O	0.48	2.67	6	1
1:A:61:LEU:CG	1:A:61:LEU:O	0.48	2.62	1	1
1:A:61:LEU:O	1:A:61:LEU:CG	0.48	2.62	8	1
1:A:5:LEU:CD1	1:A:130:LEU:HD21	0.47	2.39	12	13
1:A:5:LEU:HG	1:A:133:TYR:CE1	0.47	2.44	12	16
1:A:84:HIS:CD2	1:A:89:VAL:O	0.47	2.67	10	7
1:A:12:THR:N	1:A:79:PHE:CE1	0.47	2.82	5	1
1:A:3:GLY:O	1:A:22:ARG:CG	0.47	2.62	22	6
1:A:10:PHE:HB2	1:A:59:VAL:HG13	0.47	1.84	3	4
1:A:61:LEU:CD1	1:A:76:ALA:CB	0.47	2.92	20	2
1:A:93:LEU:CD1	1:A:93:LEU:N	0.47	2.69	20	2
1:A:93:LEU:N	1:A:93:LEU:CD1	0.47	2.69	19	1
1:A:14:SER:CB	1:A:33:ILE:CG1	0.47	2.92	22	11
1:A:57:ILE:HB	1:A:91:VAL:HG23	0.47	1.87	20	2
1:A:30:LEU:HD23	1:A:31:PRO:CD	0.47	2.39	6	6
1:A:130:LEU:O	1:A:133:TYR:CD2	0.47	2.68	6	7
1:A:8:PHE:CE2	1:A:17:VAL:HG21	0.47	2.43	24	2
1:A:8:PHE:CE1	1:A:17:VAL:HG21	0.47	2.45	20	2
1:A:83:ILE:HD11	1:A:91:VAL:CB	0.47	2.39	24	2
1:A:5:LEU:O	1:A:20:GLY:N	0.46	2.47	3	12
1:A:17:VAL:N	1:A:123:SER:CB	0.46	2.78	20	2
1:A:17:VAL:CG1	1:A:18:ALA:N	0.46	2.77	4	7
1:A:18:ALA:CB	1:A:127:VAL:HA	0.46	2.40	12	8
1:A:6:LEU:HD23	1:A:19:VAL:HG22	0.46	1.84	24	2
1:A:17:VAL:HG13	1:A:30:LEU:CB	0.46	2.40	23	8
1:A:7:ALA:CB	1:A:58:ILE:CG1	0.46	2.93	23	1
1:A:6:LEU:HD21	1:A:48:LEU:HD12	0.46	1.88	24	2
1:A:19:VAL:CG1	1:A:48:LEU:CD2	0.46	2.94	23	1
1:A:80:ALA:HB3	1:A:93:LEU:HD23	0.46	1.88	10	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:15:ILE:HD11	1:A:40:PRO:CA	0.46	2.40	3	10
1:A:7:ALA:HB1	1:A:129:ILE:HG22	0.46	1.86	20	2
1:A:12:THR:O	1:A:13:LYS:CB	0.46	2.62	4	3
1:A:17:VAL:HB	1:A:30:LEU:HD22	0.46	1.88	12	3
1:A:130:LEU:CD1	1:A:130:LEU:C	0.46	2.84	10	4
1:A:130:LEU:C	1:A:130:LEU:CD1	0.46	2.84	15	2
1:A:9:ASP:CB	1:A:16:GLY:O	0.46	2.64	13	7
1:A:30:LEU:CG	1:A:44:ILE:HG21	0.46	2.41	13	2
1:A:17:VAL:O	1:A:30:LEU:CB	0.46	2.64	12	12
1:A:33:ILE:O	1:A:33:ILE:CG1	0.46	2.64	15	7
1:A:33:ILE:CG1	1:A:33:ILE:O	0.46	2.64	10	10
1:A:5:LEU:C	1:A:5:LEU:CD1	0.45	2.85	21	4
1:A:5:LEU:CD1	1:A:5:LEU:C	0.45	2.85	24	4
1:A:130:LEU:CD1	1:A:133:TYR:CD1	0.45	2.99	2	1
1:A:126:ALA:O	1:A:129:ILE:N	0.45	2.49	20	19
1:A:10:PHE:CD1	1:A:14:SER:O	0.45	2.69	20	2
1:A:10:PHE:O	1:A:61:LEU:HB3	0.45	2.12	12	9
1:A:9:ASP:CB	1:A:129:ILE:HD12	0.45	2.39	23	1
1:A:22:ARG:CG	1:A:133:TYR:OH	0.45	2.65	22	4
1:A:42:TRP:O	1:A:46:GLU:CB	0.45	2.64	23	19
1:A:27:ALA:CB	1:A:127:VAL:HG13	0.45	2.42	3	4
1:A:93:LEU:HD22	1:A:94:HIS:H	0.45	1.68	2	1
1:A:15:ILE:O	1:A:33:ILE:CA	0.45	2.65	5	25
1:A:5:LEU:CG	1:A:133:TYR:CE2	0.45	3.00	20	10
1:A:15:ILE:O	1:A:33:ILE:N	0.45	2.50	4	18
1:A:5:LEU:O	1:A:20:GLY:O	0.45	2.35	4	10
1:A:8:PHE:HB3	1:A:10:PHE:CD1	0.45	2.47	1	4
1:A:12:THR:HG23	1:A:79:PHE:HE1	0.45	1.72	5	1
1:A:11:GLY:HA3	1:A:79:PHE:CE2	0.45	2.46	2	1
1:A:6:LEU:HG	1:A:8:PHE:CZ	0.45	2.47	10	4
1:A:8:PHE:HA	1:A:17:VAL:HB	0.45	1.89	2	3
1:A:11:GLY:HA2	1:A:79:PHE:CE2	0.45	2.46	2	2
1:A:5:LEU:C	1:A:5:LEU:HD22	0.45	2.33	18	4
1:A:10:PHE:O	1:A:61:LEU:CA	0.45	2.65	12	5
1:A:15:ILE:HG21	1:A:41:ASP:CB	0.45	2.42	12	2
1:A:14:SER:OG	1:A:33:ILE:CD1	0.45	2.65	22	2
1:A:9:ASP:O	1:A:10:PHE:HB3	0.45	2.12	10	12
1:A:6:LEU:O	1:A:57:ILE:HA	0.45	2.12	1	4
1:A:5:LEU:HB2	1:A:133:TYR:CZ	0.45	2.47	2	1
1:A:3:GLY:O	1:A:22:ARG:HB2	0.44	2.12	22	4
1:A:129:ILE:O	1:A:132:SER:CB	0.44	2.65	3	7

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:61:LEU:CD1	1:A:61:LEU:N	0.44	2.80	20	1
1:A:77:ARG:HA	1:A:93:LEU:HD22	0.44	1.90	5	3
1:A:42:TRP:CD1	1:A:46:GLU:HG3	0.44	2.48	10	2
1:A:9:ASP:O	1:A:16:GLY:O	0.44	2.36	14	5
1:A:61:LEU:N	1:A:61:LEU:CD1	0.44	2.80	19	1
1:A:6:LEU:HB3	1:A:8:PHE:CE1	0.44	2.48	4	12
1:A:5:LEU:HG	1:A:133:TYR:CD2	0.44	2.48	20	8
1:A:7:ALA:CB	1:A:58:ILE:HG12	0.44	2.42	2	2
1:A:14:SER:OG	1:A:33:ILE:CG1	0.44	2.64	12	8
1:A:14:SER:HB3	1:A:33:ILE:CG1	0.44	2.42	13	12
1:A:52:TRP:O	1:A:53:GLN:O	0.44	2.35	24	2
1:A:87:PHE:CD1	1:A:87:PHE:O	0.44	2.71	24	2
1:A:6:LEU:CG	1:A:8:PHE:CE1	0.44	3.00	6	1
1:A:11:GLY:C	1:A:79:PHE:CE2	0.44	2.91	11	4
1:A:7:ALA:CB	1:A:130:LEU:HD22	0.44	2.42	2	2
1:A:61:LEU:CD1	1:A:61:LEU:O	0.44	2.59	13	3
1:A:59:VAL:HG11	1:A:91:VAL:CG2	0.44	2.43	13	2
1:A:17:VAL:CG1	1:A:30:LEU:CD1	0.44	2.89	4	5
1:A:5:LEU:HD11	1:A:130:LEU:CD2	0.44	2.43	12	8
1:A:7:ALA:O	1:A:17:VAL:HG23	0.44	2.13	24	3
1:A:61:LEU:O	1:A:61:LEU:HD23	0.44	2.12	18	1
1:A:6:LEU:HG	1:A:19:VAL:HA	0.43	1.88	25	4
1:A:14:SER:CB	1:A:33:ILE:CD1	0.43	2.97	2	1
1:A:83:ILE:CG1	1:A:84:HIS:N	0.43	2.80	2	1
1:A:84:HIS:CG	1:A:91:VAL:HG12	0.43	2.47	6	1
1:A:14:SER:HB2	1:A:33:ILE:CG1	0.43	2.44	3	7
1:A:6:LEU:N	1:A:56:GLU:O	0.43	2.50	1	2
1:A:61:LEU:O	1:A:61:LEU:CD1	0.43	2.66	1	1
1:A:130:LEU:O	1:A:133:TYR:N	0.43	2.51	2	1
1:A:19:VAL:O	1:A:27:ALA:HA	0.43	2.14	22	7
1:A:124:ALA:O	1:A:128:ILE:CD1	0.43	2.65	20	6
1:A:61:LEU:O	1:A:61:LEU:HD22	0.43	2.12	20	2
1:A:42:TRP:O	1:A:46:GLU:CG	0.43	2.67	10	2
1:A:49:LEU:HD21	1:A:89:VAL:HG11	0.43	1.88	6	3
1:A:25:GLY:HA2	1:A:134:PHE:CZ	0.43	2.49	3	2
1:A:40:PRO:O	1:A:42:TRP:N	0.43	2.51	1	12
1:A:44:ILE:CD1	1:A:44:ILE:C	0.43	2.85	20	1
1:A:59:VAL:HG12	1:A:92:LYS:O	0.43	2.14	20	2
1:A:8:PHE:CD1	1:A:59:VAL:CG2	0.43	3.00	10	2
1:A:47:ARG:O	1:A:51:GLU:CB	0.43	2.66	6	5
1:A:10:PHE:O	1:A:61:LEU:HB2	0.43	2.14	11	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:22:ARG:CD	1:A:133:TYR:OH	0.43	2.66	2	2
1:A:83:ILE:HG13	1:A:84:HIS:N	0.43	2.29	2	1
1:A:44:ILE:C	1:A:44:ILE:CD1	0.43	2.85	19	1
1:A:36:GLN:O	1:A:39:THR:CB	0.43	2.66	22	4
1:A:84:HIS:O	1:A:88:GLY:N	0.43	2.51	2	4
1:A:14:SER:HB2	1:A:33:ILE:CD1	0.43	2.43	24	6
1:A:79:PHE:CD1	1:A:79:PHE:C	0.43	2.92	11	1
1:A:79:PHE:C	1:A:79:PHE:CD1	0.43	2.92	9	1
1:A:127:VAL:O	1:A:130:LEU:CB	0.43	2.67	2	1
1:A:34:LYS:CG	1:A:34:LYS:O	0.43	2.66	23	1
1:A:8:PHE:HA	1:A:17:VAL:HG13	0.43	1.91	22	2
1:A:133:TYR:CE2	1:A:134:PHE:CZ	0.43	3.07	5	3
1:A:7:ALA:HB2	1:A:58:ILE:HG13	0.43	1.89	12	2
1:A:58:ILE:HB	1:A:129:ILE:CG2	0.43	2.44	13	6
1:A:33:ILE:O	1:A:34:LYS:C	0.43	2.57	4	1
1:A:10:PHE:CE1	1:A:79:PHE:CE1	0.43	3.07	3	2
1:A:11:GLY:HA2	1:A:79:PHE:CZ	0.43	2.49	5	1
1:A:42:TRP:CD1	1:A:42:TRP:O	0.43	2.71	2	1
1:A:49:LEU:O	1:A:53:GLN:N	0.42	2.52	2	3
1:A:6:LEU:HD21	1:A:19:VAL:HG22	0.42	1.90	5	1
1:A:19:VAL:HG11	1:A:48:LEU:HG	0.42	1.90	2	1
1:A:133:TYR:OH	1:A:134:PHE:CE2	0.42	2.67	13	4
1:A:59:VAL:HG21	1:A:83:ILE:HD11	0.42	1.87	10	2
1:A:18:ALA:HB2	1:A:126:ALA:C	0.42	2.35	23	3
1:A:23:ILE:CD1	1:A:24:THR:OG1	0.42	2.67	10	2
1:A:48:LEU:C	1:A:48:LEU:CD2	0.42	2.87	6	1
1:A:5:LEU:CB	1:A:133:TYR:OH	0.42	2.67	6	1
1:A:49:LEU:HD23	1:A:87:PHE:CE2	0.42	2.49	11	2
1:A:87:PHE:N	1:A:87:PHE:CD1	0.42	2.87	3	1
1:A:80:ALA:HB3	1:A:93:LEU:HD21	0.42	1.90	5	1
1:A:87:PHE:CD1	1:A:87:PHE:N	0.42	2.87	7	1
1:A:61:LEU:CD2	1:A:61:LEU:C	0.42	2.82	13	1
1:A:61:LEU:C	1:A:61:LEU:CD2	0.42	2.82	17	1
1:A:22:ARG:HG2	1:A:133:TYR:OH	0.42	2.15	21	4
1:A:48:LEU:HD22	1:A:52:TRP:HB2	0.42	1.91	11	2
1:A:57:ILE:HD13	1:A:89:VAL:HB	0.42	1.91	12	2
1:A:8:PHE:O	1:A:59:VAL:HA	0.42	2.15	2	1
1:A:28:ARG:CD	1:A:28:ARG:N	0.42	2.81	2	1
1:A:84:HIS:ND1	1:A:89:VAL:O	0.42	2.53	24	5
1:A:93:LEU:C	1:A:93:LEU:CD1	0.42	2.88	21	2
1:A:93:LEU:CD1	1:A:93:LEU:C	0.42	2.88	24	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:9:ASP:HB2	1:A:126:ALA:CA	0.42	2.45	11	2
1:A:18:ALA:HB2	1:A:127:VAL:HG22	0.42	1.91	11	4
1:A:17:VAL:HG12	1:A:18:ALA:N	0.42	2.29	6	1
1:A:18:ALA:HB2	1:A:127:VAL:CA	0.42	2.44	2	5
1:A:17:VAL:N	1:A:123:SER:OG	0.42	2.53	13	2
1:A:10:PHE:CG	1:A:11:GLY:N	0.42	2.87	23	1
1:A:7:ALA:HB2	1:A:130:LEU:HD22	0.42	1.89	22	6
1:A:128:ILE:O	1:A:132:SER:N	0.42	2.53	10	2
1:A:93:LEU:C	1:A:93:LEU:CD2	0.42	2.89	24	1
1:A:5:LEU:O	1:A:20:GLY:CA	0.42	2.68	3	2
1:A:4:THR:HG21	1:A:52:TRP:HB3	0.41	1.92	22	2
1:A:127:VAL:O	1:A:131:GLU:N	0.41	2.53	14	2
1:A:89:VAL:O	1:A:91:VAL:N	0.41	2.52	13	2
1:A:36:GLN:O	1:A:39:THR:N	0.41	2.53	3	10
1:A:7:ALA:HA	1:A:58:ILE:O	0.41	2.15	1	3
1:A:11:GLY:HA2	1:A:79:PHE:CD2	0.41	2.50	2	1
1:A:5:LEU:HD12	1:A:22:ARG:CD	0.41	2.45	13	2
1:A:18:ALA:N	1:A:126:ALA:HB1	0.41	2.30	23	1
1:A:45:ILE:O	1:A:49:LEU:HD13	0.41	2.15	10	2
1:A:32:ALA:O	1:A:33:ILE:O	0.41	2.39	4	1
1:A:5:LEU:CB	1:A:22:ARG:CG	0.41	2.98	5	1
1:A:5:LEU:CB	1:A:22:ARG:HG3	0.41	2.45	5	1
1:A:41:ASP:N	1:A:41:ASP:OD1	0.41	2.54	23	1
1:A:19:VAL:HB	1:A:28:ARG:HB3	0.41	1.92	22	2
1:A:77:ARG:CA	1:A:93:LEU:HD22	0.41	2.45	10	2
1:A:6:LEU:HB3	1:A:8:PHE:CZ	0.41	2.50	12	2
1:A:21:GLN:CG	1:A:21:GLN:O	0.41	2.69	2	1
1:A:132:SER:OG	1:A:133:TYR:N	0.41	2.53	22	4
1:A:10:PHE:CE2	1:A:79:PHE:CZ	0.41	3.09	10	2
1:A:23:ILE:HD12	1:A:24:THR:N	0.41	2.30	1	3
1:A:25:GLY:HA2	1:A:134:PHE:CE1	0.41	2.50	11	2
1:A:14:SER:HB3	1:A:33:ILE:HG13	0.41	1.92	24	3
1:A:19:VAL:HG12	1:A:21:GLN:HE21	0.41	1.75	24	2
1:A:83:ILE:CD1	1:A:91:VAL:CG2	0.41	2.91	24	2
1:A:8:PHE:HD1	1:A:59:VAL:HG22	0.41	1.73	1	2
1:A:131:GLU:HA	1:A:134:PHE:CD2	0.41	2.50	5	1
1:A:8:PHE:CD1	1:A:17:VAL:HG21	0.41	2.50	20	2
1:A:130:LEU:HD13	1:A:133:TYR:CE2	0.41	2.51	6	1
1:A:61:LEU:CD2	1:A:61:LEU:O	0.41	2.66	13	2
1:A:77:ARG:O	1:A:80:ALA:HB3	0.41	2.15	23	1
1:A:43:ASN:O	1:A:47:ARG:CD	0.41	2.68	4	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:10:PHE:CD1	1:A:10:PHE:C	0.41	2.91	11	2
1:A:57:ILE:O	1:A:92:LYS:N	0.41	2.53	11	4
1:A:133:TYR:OH	1:A:134:PHE:CZ	0.41	2.65	1	2
1:A:5:LEU:CD1	1:A:22:ARG:HD3	0.41	2.46	6	1
1:A:14:SER:CA	1:A:33:ILE:HG13	0.41	2.46	3	6
1:A:17:VAL:HG23	1:A:18:ALA:N	0.41	2.31	14	2
1:A:8:PHE:CZ	1:A:17:VAL:HG11	0.41	2.48	13	2
1:A:83:ILE:CG1	1:A:91:VAL:HG21	0.41	2.45	4	1
1:A:13:LYS:CG	1:A:38:GLY:HA2	0.41	2.46	2	1
1:A:84:HIS:C	1:A:84:HIS:CD2	0.40	2.95	10	2
1:A:84:HIS:HB2	1:A:91:VAL:HG11	0.40	1.93	14	2
1:A:9:ASP:HB2	1:A:126:ALA:CB	0.40	2.47	14	2
1:A:17:VAL:HG22	1:A:30:LEU:CB	0.40	2.45	2	1
1:A:6:LEU:HD22	1:A:48:LEU:HD22	0.40	1.92	13	2
1:A:45:ILE:O	1:A:49:LEU:CD1	0.40	2.69	10	2
1:A:5:LEU:HB2	1:A:22:ARG:CG	0.40	2.47	5	1
1:A:7:ALA:CB	1:A:130:LEU:HB2	0.40	2.45	13	2
1:A:59:VAL:CG1	1:A:91:VAL:HG22	0.40	2.46	13	2
1:A:4:THR:O	1:A:54:PRO:HA	0.40	2.15	22	2
1:A:11:GLY:C	1:A:79:PHE:CZ	0.40	2.95	20	2
1:A:5:LEU:HG	1:A:133:TYR:CD1	0.40	2.51	20	2
1:A:124:ALA:O	1:A:128:ILE:CG1	0.40	2.70	6	1
1:A:19:VAL:CG1	1:A:48:LEU:HG	0.40	2.46	6	1
1:A:30:LEU:HD11	1:A:44:ILE:HG22	0.40	1.93	13	2
1:A:94:HIS:CG	1:A:129:ILE:HG12	0.40	2.51	23	1
1:A:13:LYS:CG	1:A:13:LYS:O	0.40	2.69	10	1
1:A:13:LYS:O	1:A:13:LYS:CG	0.40	2.69	15	1
1:A:13:LYS:CD	1:A:38:GLY:CA	0.40	2.99	6	1
1:A:19:VAL:N	1:A:28:ARG:O	0.40	2.47	24	2
1:A:15:ILE:CA	1:A:33:ILE:HA	0.40	2.47	1	2
1:A:8:PHE:CB	1:A:10:PHE:CD1	0.40	3.05	2	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	91/138 (66%)	80±2 (88±2%)	7±1 (8±1%)	4±1 (4±1%)	6	30
All	All	2275/3450 (66%)	1996 (88%)	180 (8%)	99 (4%)	6	30

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	33	ILE	25
1	A	31	PRO	25
1	A	53	GLN	17
1	A	3	GLY	15
1	A	13	LYS	6
1	A	12	THR	6
1	A	10	PHE	2
1	A	123	SER	2
1	A	34	LYS	1

### 6.3.2 Protein sidechains ⓘ

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	73/111 (66%)	47±3 (64±4%)	26±3 (36±4%)	1	8
All	All	1825/2775 (66%)	1165 (64%)	660 (36%)	1	8

All 56 unique residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	5	LEU	25
1	A	33	ILE	25
1	A	23	ILE	25
1	A	58	ILE	25
1	A	127	VAL	25
1	A	26	THR	25
1	A	30	LEU	23
1	A	14	SER	21
1	A	6	LEU	19

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Mol	Chain	Res	Type	Models (Total)
1	A	130	LEU	19
1	A	93	LEU	19
1	A	86	ARG	18
1	A	133	TYR	17
1	A	61	LEU	17
1	A	82	ARG	16
1	A	28	ARG	15
1	A	49	LEU	15
1	A	92	LYS	15
1	A	24	THR	14
1	A	21	GLN	14
1	A	17	VAL	14
1	A	53	GLN	14
1	A	131	GLU	14
1	A	34	LYS	14
1	A	90	GLU	13
1	A	37	ASP	13
1	A	132	SER	12
1	A	56	GLU	12
1	A	13	LYS	11
1	A	36	GLN	11
1	A	87	PHE	10
1	A	81	ASN	10
1	A	10	PHE	10
1	A	22	ARG	9
1	A	41	ASP	9
1	A	78	LYS	9
1	A	48	LEU	8
1	A	43	ASN	8
1	A	135	GLU	7
1	A	77	ARG	7
1	A	55	ASP	6
1	A	83	ILE	5
1	A	50	LYS	5
1	A	79	PHE	5
1	A	123	SER	5
1	A	134	PHE	4
1	A	51	GLU	4
1	A	46	GLU	4
1	A	94	HIS	3
1	A	9	ASP	2
1	A	47	ARG	2

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Mol	Chain	Res	Type	Models (Total)
1	A	128	ILE	2
1	A	44	ILE	2
1	A	84	HIS	2
1	A	12	THR	1
1	A	91	VAL	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 carbohydrates 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 83% for the well-defined parts and 73% for the entire structure.

### 7.1 Chemical shift list 1

File name: BMRB entry 5758

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	1370
Number of shifts mapped to atoms	1370
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
$^{13}\text{C}_\alpha$	124	$0.21 \pm 0.19$	None needed ( $< 0.5$ ppm)
$^{13}\text{C}_\beta$	111	$0.19 \pm 0.12$	None needed ( $< 0.5$ ppm)
$^{13}\text{C}'$	110	$-0.01 \pm 0.12$	None needed ( $< 0.5$ ppm)
$^{15}\text{N}$	113	$0.24 \pm 0.19$	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 83%, i.e. 934 atoms were assigned a chemical shift out of a possible 1127. 4 out of 14 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^1\text{H}$	$^{13}\text{C}$	$^{15}\text{N}$
Backbone	430/447 (96%)	171/178 (96%)	175/182 (96%)	84/87 (97%)
Sidechain	445/589 (76%)	274/343 (80%)	167/218 (77%)	4/28 (14%)

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	<b>Total</b>	<b><sup>1</sup>H</b>	<b><sup>13</sup>C</b>	<b><sup>15</sup>N</b>
Aromatic	59/91 (65%)	43/49 (88%)	14/38 (37%)	2/4 (50%)
Overall	934/1127 (83%)	488/570 (86%)	356/438 (81%)	90/119 (76%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 73%, i.e. 1233 atoms were assigned a chemical shift out of a possible 1692. 6 out of 21 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	<b>Total</b>	<b><sup>1</sup>H</b>	<b><sup>13</sup>C</b>	<b><sup>15</sup>N</b>
Backbone	578/678 (85%)	231/270 (86%)	234/276 (85%)	113/132 (86%)
Sidechain	588/898 (65%)	369/525 (70%)	212/326 (65%)	7/47 (15%)
Aromatic	67/116 (58%)	49/62 (79%)	16/50 (32%)	2/4 (50%)
Overall	1233/1692 (73%)	649/857 (76%)	462/652 (71%)	122/183 (67%)

#### 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.

Mol	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	86	ARG	HD2	1.66	4.27 – 1.97	-6.3
1	A	86	ARG	HB2	0.43	3.15 – 0.45	-5.1

#### 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.

Random coil index (RCI) for chain A:

