



Full wwPDB NMR Structure Validation Report ⓘ

Feb 12, 2017 – 07:33 pm GMT

PDB ID : 1QHK
Title : N-TERMINAL DOMAIN OF SACCHAROMYCES CEREVISIAE RNASE
HI REVEALS A FOLD WITH A RESEMBLANCE TO THE N-TERMINAL
DOMAIN OF RIBOSOMAL PROTEIN L9
Authors : Evans, S.P.; Bycroft, M.
Deposited on : 1999-05-17

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

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

with specific help available everywhere you see the ⓘ symbol.

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
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
ShiftChecker : trunk28760
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : recalc28949

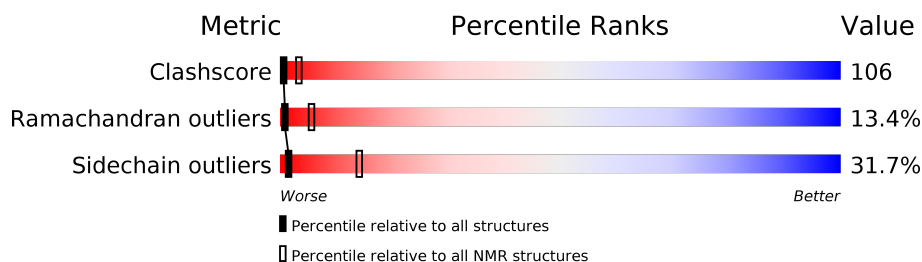
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

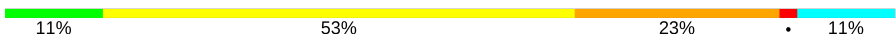
The overall completeness of chemical shifts assignment is 78%.

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	125131	11601
Ramachandran outliers	121729	10391
Sidechain outliers	121581	10367

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	47	

2 Ensemble composition and analysis

This entry contains 20 models. Model 13 is the overall representative, medoid model (most similar to other models). The authors have identified model 14 as representative.

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:6-A:12, A:18-A:52 (42)	0.38	13

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

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

The models can be grouped into 4 clusters and 2 single-model clusters were found.

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

3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 737 atoms, of which 357 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called PROTEIN (RIBONUCLEASE HI).

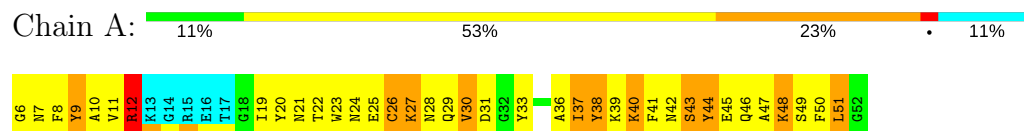
Mol	Chain	Residues	Atoms						Trace
1	A	47	Total	C	H	N	O	S	0
			737	242	357	66	71	1	

4 Residue-property plots

4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA and DNA 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: PROTEIN (RIBONUCLEASE HI)

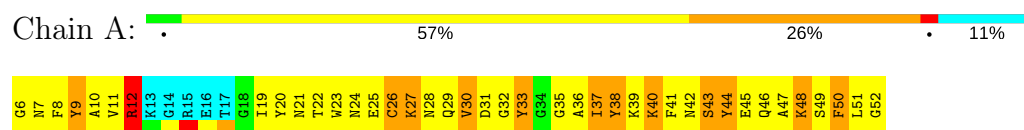


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

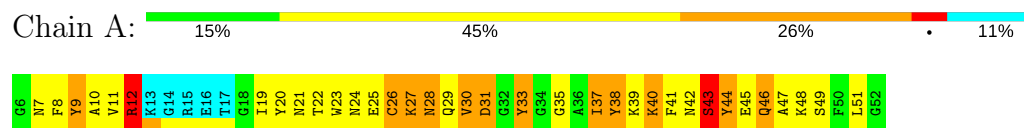
4.2.1 Score per residue for model 1

- Molecule 1: PROTEIN (RIBONUCLEASE HI)



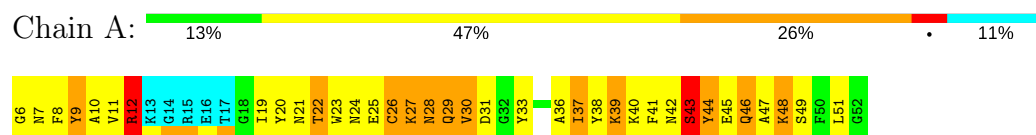
4.2.2 Score per residue for model 2

- Molecule 1: PROTEIN (RIBONUCLEASE HI)



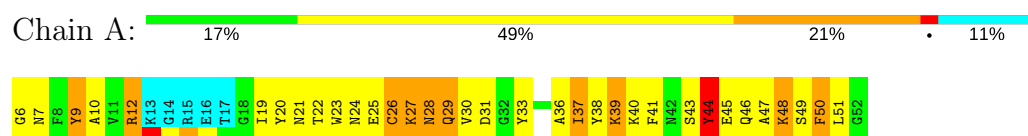
4.2.3 Score per residue for model 3

- Molecule 1: PROTEIN (RIBONUCLEASE HI)



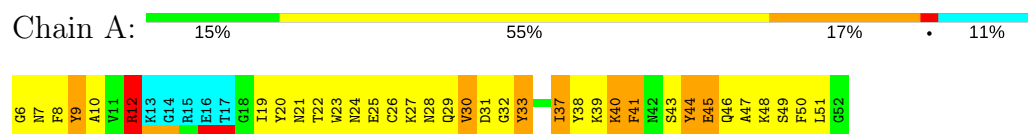
4.2.4 Score per residue for model 4

- Molecule 1: PROTEIN (RIBONUCLEASE HI)



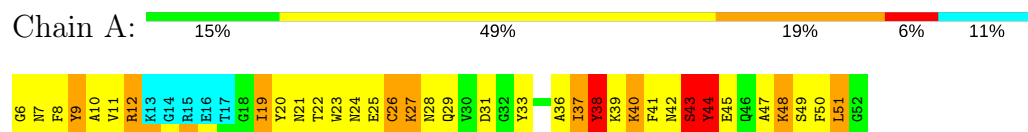
4.2.5 Score per residue for model 5

- Molecule 1: PROTEIN (RIBONUCLEASE HI)



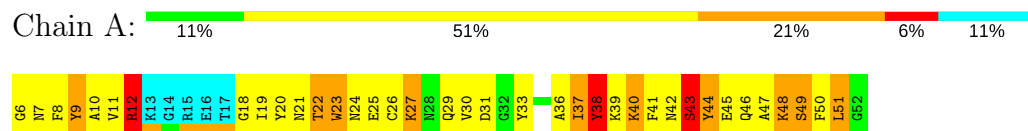
4.2.6 Score per residue for model 6

- Molecule 1: PROTEIN (RIBONUCLEASE HI)



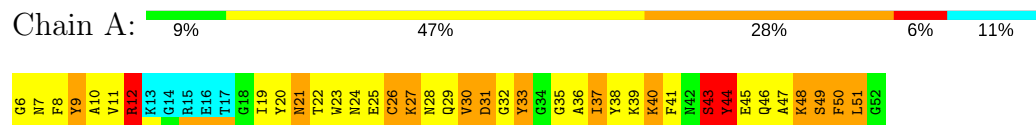
4.2.7 Score per residue for model 7

- Molecule 1: PROTEIN (RIBONUCLEASE HI)



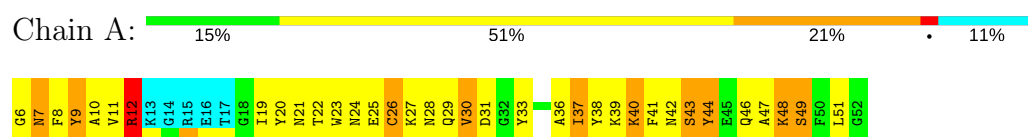
4.2.8 Score per residue for model 8

- Molecule 1: PROTEIN (RIBONUCLEASE HI)



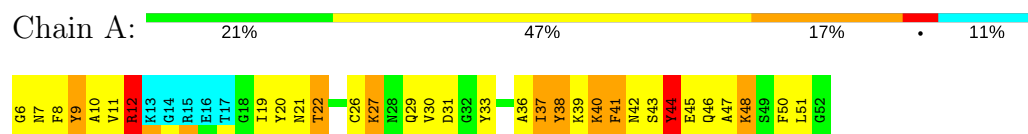
4.2.9 Score per residue for model 9

- Molecule 1: PROTEIN (RIBONUCLEASE HI)



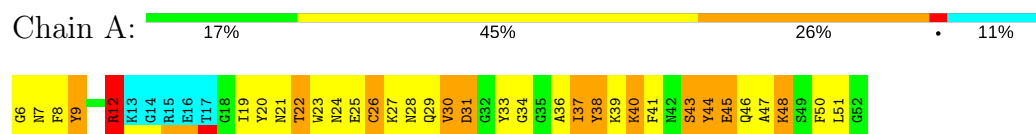
4.2.10 Score per residue for model 10

- Molecule 1: PROTEIN (RIBONUCLEASE HI)



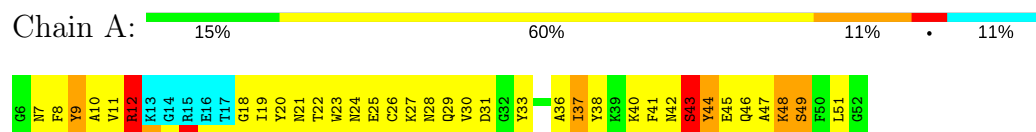
4.2.11 Score per residue for model 11

- Molecule 1: PROTEIN (RIBONUCLEASE HI)



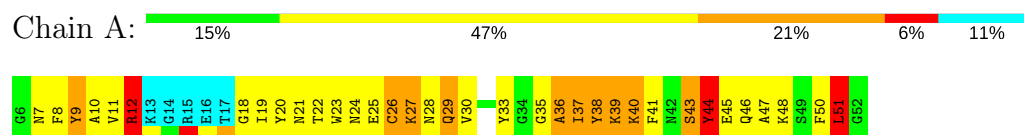
4.2.12 Score per residue for model 12

- Molecule 1: PROTEIN (RIBONUCLEASE HI)



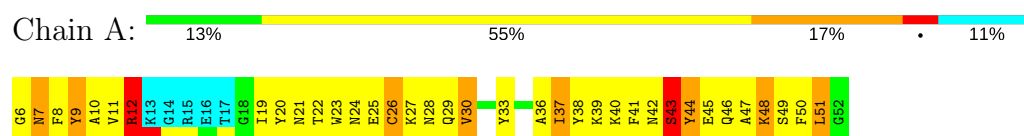
4.2.13 Score per residue for model 13 (medoid)

- Molecule 1: PROTEIN (RIBONUCLEASE HI)



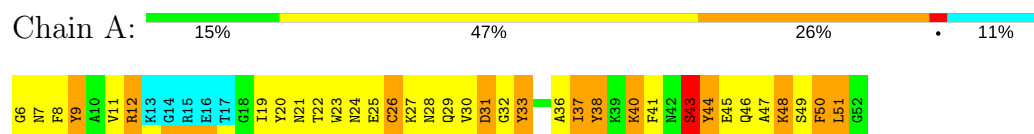
4.2.14 Score per residue for model 14

- Molecule 1: PROTEIN (RIBONUCLEASE HI)



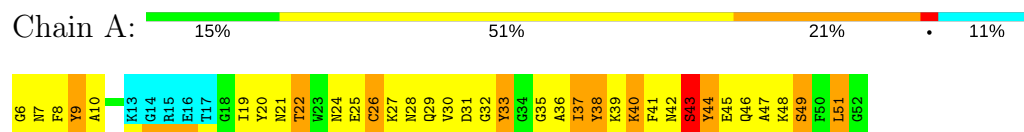
4.2.15 Score per residue for model 15

- Molecule 1: PROTEIN (RIBONUCLEASE HI)



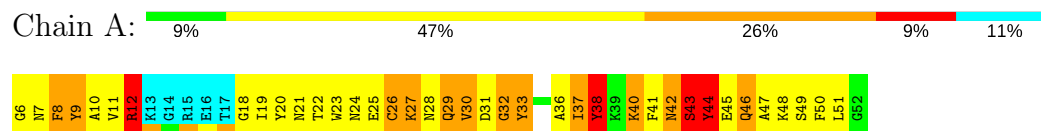
4.2.16 Score per residue for model 16

- Molecule 1: PROTEIN (RIBONUCLEASE HI)



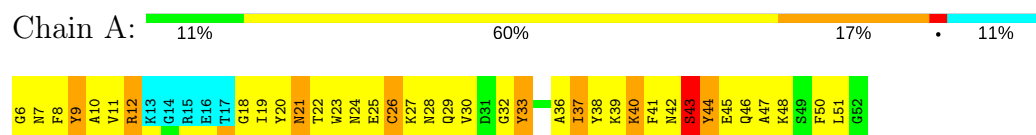
4.2.17 Score per residue for model 17

- Molecule 1: PROTEIN (RIBONUCLEASE HI)



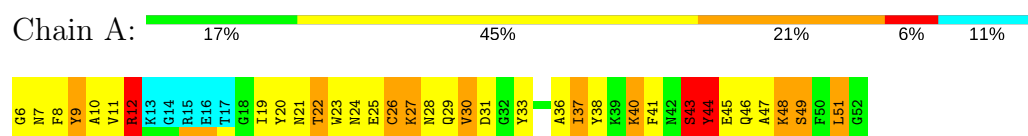
4.2.18 Score per residue for model 18

- Molecule 1: PROTEIN (RIBONUCLEASE HI)



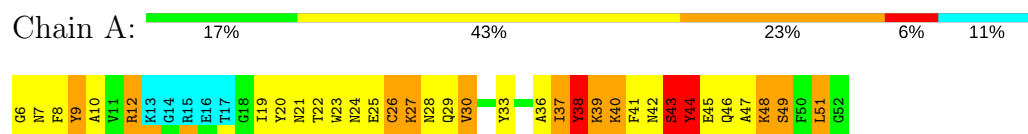
4.2.19 Score per residue for model 19

- Molecule 1: PROTEIN (RIBONUCLEASE HI)



4.2.20 Score per residue for model 20

- Molecule 1: PROTEIN (RIBONUCLEASE HI)



5 Refinement protocol and experimental data overview

The models were refined using the following method: *DISTANCE GEOMETRY AND SIMULATED ANNEALING*.

Of the 200 calculated structures, 20 were deposited, based on the following criterion: *LEAST RESTRAINT VIOLATION*.

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

Software name	Classification	Version
X-PLOR	refinement	3.1
X-PLOR	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)	BMRB entry 4424
Number of chemical shift lists	1
Total number of shifts	593
Number of shifts mapped to atoms	455
Number of unparsed shifts	0
Number of shifts with mapping errors	138
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	78%

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

6 Model quality [i](#)

6.1 Standard geometry [i](#)

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

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

Mol	Chain	Chirality	Planarity
1	A	0.0±0.0	0.8±0.4
All	All	0	17

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

All unique planar outliers are listed below.

Mol	Chain	Res	Type	Group	Models (Total)
1	A	12	ARG	Sidechain	17

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	340	315	314	69±8
All	All	6800	6300	6280	1383

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 106.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:19:ILE:CG1	1:A:51:LEU:HD11	1.00	1.86	10	11
1:A:10:ALA:HB1	1:A:51:LEU:HD21	0.95	1.34	2	8

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:19:ILE:HD13	1:A:47:ALA:HB1	0.94	1.39	9	12
1:A:19:ILE:HD13	1:A:47:ALA:CB	0.91	1.95	9	18
1:A:19:ILE:HG13	1:A:51:LEU:HD11	0.91	1.43	19	10
1:A:19:ILE:HD12	1:A:44:TYR:CE1	0.89	2.02	11	11
1:A:19:ILE:CD1	1:A:47:ALA:HB1	0.89	1.97	6	2
1:A:19:ILE:HD12	1:A:51:LEU:HD11	0.88	1.45	6	1
1:A:37:ILE:O	1:A:37:ILE:HD13	0.87	1.69	6	4
1:A:33:TYR:HB3	1:A:36:ALA:HB2	0.86	1.47	6	11
1:A:19:ILE:HD12	1:A:44:TYR:CD1	0.86	2.06	20	10
1:A:19:ILE:HD13	1:A:47:ALA:HB3	0.84	1.47	19	16
1:A:36:ALA:HB3	1:A:38:TYR:CD2	0.82	2.10	11	2
1:A:10:ALA:HB2	1:A:47:ALA:HB1	0.81	1.50	1	4
1:A:19:ILE:HD11	1:A:51:LEU:HD13	0.81	1.53	17	3
1:A:29:GLN:OE1	1:A:30:VAL:HG13	0.80	1.76	7	1
1:A:19:ILE:CG1	1:A:47:ALA:HB1	0.80	2.06	6	1
1:A:19:ILE:CG1	1:A:51:LEU:HD22	0.78	2.08	9	2
1:A:33:TYR:HB2	1:A:36:ALA:HB2	0.78	1.53	17	6
1:A:19:ILE:HG12	1:A:47:ALA:HB1	0.76	1.54	6	1
1:A:37:ILE:HD13	1:A:37:ILE:O	0.76	1.81	20	5
1:A:37:ILE:HD13	1:A:37:ILE:C	0.73	2.04	13	6
1:A:37:ILE:C	1:A:37:ILE:HD13	0.73	2.04	6	3
1:A:33:TYR:CB	1:A:36:ALA:HB2	0.72	2.15	17	15
1:A:9:TYR:CE1	1:A:38:TYR:CD2	0.71	2.78	20	4
1:A:20:TYR:CD2	1:A:29:GLN:NE2	0.71	2.59	10	3
1:A:10:ALA:HB1	1:A:51:LEU:CD2	0.69	2.16	4	7
1:A:9:TYR:CZ	1:A:38:TYR:CD2	0.69	2.80	7	4
1:A:10:ALA:HB3	1:A:39:LYS:HB2	0.69	1.65	16	4
1:A:30:VAL:HG21	1:A:38:TYR:CD2	0.68	2.24	20	2
1:A:33:TYR:CD1	1:A:33:TYR:N	0.68	2.62	2	6
1:A:11:VAL:HG21	1:A:29:GLN:OE1	0.68	1.90	12	3
1:A:9:TYR:CE2	1:A:40:LYS:CG	0.67	2.78	7	12
1:A:9:TYR:CZ	1:A:40:LYS:CG	0.67	2.77	2	14
1:A:10:ALA:HB2	1:A:19:ILE:HD11	0.66	1.67	6	1
1:A:48:LYS:HE3	1:A:51:LEU:HD12	0.66	1.68	5	1
1:A:37:ILE:HD13	1:A:38:TYR:N	0.66	2.06	10	11
1:A:36:ALA:HB3	1:A:38:TYR:CE2	0.65	2.27	10	2
1:A:41:PHE:CB	1:A:47:ALA:HB2	0.65	2.22	6	13
1:A:19:ILE:HG12	1:A:51:LEU:HD11	0.65	1.66	2	7
1:A:26:CYS:O	1:A:30:VAL:HG22	0.65	1.91	2	7
1:A:9:TYR:CE1	1:A:40:LYS:N	0.64	2.65	20	11
1:A:30:VAL:HG21	1:A:38:TYR:HD2	0.64	1.52	20	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:10:ALA:CB	1:A:51:LEU:HD21	0.63	2.23	4	4
1:A:9:TYR:CD1	1:A:11:VAL:CG2	0.63	2.82	12	5
1:A:19:ILE:HD11	1:A:51:LEU:HG	0.62	1.69	8	3
1:A:48:LYS:CE	1:A:51:LEU:HD12	0.62	2.24	5	1
1:A:9:TYR:CE2	1:A:40:LYS:CE	0.62	2.82	4	1
1:A:9:TYR:CZ	1:A:40:LYS:HB3	0.62	2.30	19	1
1:A:9:TYR:OH	1:A:38:TYR:CE2	0.62	2.53	7	4
1:A:30:VAL:HG11	1:A:38:TYR:HB3	0.62	1.71	13	3
1:A:38:TYR:CD1	1:A:38:TYR:O	0.62	2.52	11	10
1:A:9:TYR:CE1	1:A:40:LYS:CA	0.62	2.83	2	9
1:A:19:ILE:CD1	1:A:48:LYS:N	0.62	2.63	5	4
1:A:29:GLN:HG3	1:A:30:VAL:HG22	0.61	1.72	17	2
1:A:30:VAL:HG11	1:A:38:TYR:CD2	0.61	2.30	11	3
1:A:33:TYR:N	1:A:33:TYR:CD1	0.61	2.67	20	14
1:A:19:ILE:CD1	1:A:47:ALA:CB	0.61	2.78	6	3
1:A:10:ALA:HB3	1:A:39:LYS:HB3	0.61	1.70	2	1
1:A:11:VAL:HG13	1:A:37:ILE:O	0.61	1.95	7	2
1:A:19:ILE:CD1	1:A:51:LEU:HD11	0.61	2.25	10	8
1:A:36:ALA:HB3	1:A:38:TYR:CD1	0.60	2.30	13	3
1:A:9:TYR:CE1	1:A:29:GLN:NE2	0.60	2.68	3	1
1:A:23:TRP:CZ3	1:A:27:LYS:CD	0.60	2.85	20	2
1:A:19:ILE:HG13	1:A:51:LEU:HD22	0.60	1.71	9	2
1:A:19:ILE:HD12	1:A:51:LEU:CD1	0.60	2.23	6	1
1:A:9:TYR:CG	1:A:29:GLN:NE2	0.59	2.71	7	1
1:A:38:TYR:O	1:A:38:TYR:CD1	0.59	2.55	4	6
1:A:20:TYR:CZ	1:A:29:GLN:NE2	0.59	2.71	16	1
1:A:8:PHE:CD1	1:A:20:TYR:O	0.59	2.56	17	1
1:A:41:PHE:CE1	1:A:46:GLN:HB3	0.59	2.33	1	14
1:A:11:VAL:HG13	1:A:38:TYR:CA	0.59	2.28	17	1
1:A:37:ILE:HG23	1:A:38:TYR:N	0.59	2.12	11	5
1:A:12:ARG:O	1:A:12:ARG:CG	0.59	2.51	12	1
1:A:20:TYR:CD2	1:A:29:GLN:CD	0.59	2.76	4	3
1:A:38:TYR:C	1:A:38:TYR:CD1	0.58	2.75	14	7
1:A:9:TYR:O	1:A:19:ILE:HA	0.58	1.99	15	20
1:A:48:LYS:CD	1:A:49:SER:N	0.58	2.67	1	1
1:A:8:PHE:CZ	1:A:21:ASN:OD1	0.58	2.57	9	1
1:A:36:ALA:HB3	1:A:38:TYR:HE2	0.58	1.57	10	1
1:A:11:VAL:HG22	1:A:38:TYR:HA	0.58	1.75	13	2
1:A:23:TRP:CZ3	1:A:27:LYS:HD3	0.58	2.34	20	1
1:A:25:GLU:O	1:A:29:GLN:CG	0.58	2.52	19	18
1:A:32:GLY:O	1:A:33:TYR:C	0.58	2.42	1	7

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:11:VAL:O	1:A:12:ARG:HB2	0.58	1.98	12	4
1:A:19:ILE:HD12	1:A:51:LEU:HD21	0.57	1.74	6	1
1:A:9:TYR:CE2	1:A:40:LYS:HG3	0.57	2.34	6	10
1:A:19:ILE:CG1	1:A:51:LEU:CD2	0.57	2.81	9	3
1:A:20:TYR:CD2	1:A:29:GLN:OE1	0.57	2.57	17	1
1:A:19:ILE:HD11	1:A:51:LEU:CD1	0.57	2.30	3	6
1:A:9:TYR:CZ	1:A:40:LYS:HG3	0.57	2.34	1	9
1:A:19:ILE:HD11	1:A:51:LEU:HD11	0.57	1.74	3	5
1:A:9:TYR:HB3	1:A:11:VAL:HG23	0.57	1.76	15	3
1:A:9:TYR:CE2	1:A:40:LYS:HB2	0.57	2.35	19	1
1:A:9:TYR:CG	1:A:29:GLN:OE1	0.57	2.57	10	1
1:A:9:TYR:CE1	1:A:40:LYS:HA	0.57	2.35	13	6
1:A:9:TYR:CE2	1:A:40:LYS:HG2	0.57	2.35	16	11
1:A:32:GLY:C	1:A:33:TYR:CD1	0.56	2.78	15	5
1:A:10:ALA:HB2	1:A:47:ALA:CB	0.56	2.28	1	1
1:A:8:PHE:CE1	1:A:21:ASN:OD1	0.56	2.58	10	2
1:A:19:ILE:HB	1:A:44:TYR:CE1	0.56	2.36	17	6
1:A:19:ILE:HD11	1:A:48:LYS:CA	0.56	2.31	1	3
1:A:26:CYS:O	1:A:29:GLN:HG2	0.56	2.00	10	2
1:A:8:PHE:CZ	1:A:21:ASN:ND2	0.56	2.73	6	1
1:A:41:PHE:CD2	1:A:47:ALA:HA	0.56	2.36	17	19
1:A:8:PHE:CE1	1:A:21:ASN:ND2	0.56	2.74	20	1
1:A:20:TYR:CG	1:A:29:GLN:NE2	0.56	2.74	4	1
1:A:19:ILE:HD13	1:A:47:ALA:C	0.55	2.21	6	1
1:A:19:ILE:CD1	1:A:51:LEU:HD21	0.55	2.31	6	1
1:A:20:TYR:CZ	1:A:29:GLN:CD	0.55	2.80	16	3
1:A:44:TYR:CD1	1:A:44:TYR:O	0.55	2.60	16	1
1:A:24:ASN:O	1:A:28:ASN:CB	0.55	2.55	20	14
1:A:27:LYS:O	1:A:31:ASP:CB	0.55	2.55	12	3
1:A:44:TYR:O	1:A:48:LYS:CB	0.55	2.55	16	6
1:A:9:TYR:CE1	1:A:38:TYR:HB2	0.55	2.37	11	8
1:A:38:TYR:O	1:A:38:TYR:CD2	0.55	2.58	2	2
1:A:9:TYR:CD1	1:A:29:GLN:NE2	0.55	2.75	3	1
1:A:6:GLY:HA3	1:A:23:TRP:N	0.55	2.17	18	8
1:A:43:SER:O	1:A:45:GLU:N	0.55	2.40	19	19
1:A:37:ILE:O	1:A:38:TYR:C	0.55	2.45	13	9
1:A:41:PHE:CG	1:A:47:ALA:HB2	0.55	2.36	6	3
1:A:41:PHE:CE1	1:A:46:GLN:CB	0.54	2.90	1	3
1:A:44:TYR:CE1	1:A:48:LYS:HB3	0.54	2.37	1	1
1:A:37:ILE:CD1	1:A:37:ILE:C	0.54	2.76	13	5
1:A:11:VAL:HG22	1:A:38:TYR:HB2	0.54	1.78	7	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:44:TYR:O	1:A:48:LYS:CG	0.54	2.55	1	2
1:A:19:ILE:CD1	1:A:44:TYR:CE1	0.54	2.90	20	2
1:A:24:ASN:O	1:A:28:ASN:N	0.54	2.41	2	12
1:A:9:TYR:HB3	1:A:20:TYR:CD2	0.54	2.37	14	5
1:A:11:VAL:O	1:A:12:ARG:CB	0.54	2.54	12	3
1:A:23:TRP:CH2	1:A:27:LYS:HD3	0.54	2.38	2	1
1:A:27:LYS:O	1:A:31:ASP:N	0.54	2.40	12	8
1:A:19:ILE:CD1	1:A:51:LEU:HD22	0.54	2.32	9	3
1:A:11:VAL:CG2	1:A:29:GLN:OE1	0.54	2.56	17	2
1:A:7:ASN:O	1:A:21:ASN:HA	0.53	2.03	10	20
1:A:6:GLY:HA2	1:A:23:TRP:CA	0.53	2.33	14	5
1:A:30:VAL:O	1:A:33:TYR:CE1	0.53	2.61	1	5
1:A:20:TYR:CE2	1:A:29:GLN:CD	0.53	2.82	17	1
1:A:19:ILE:HD11	1:A:48:LYS:N	0.53	2.18	5	2
1:A:44:TYR:CD1	1:A:48:LYS:HB3	0.53	2.37	6	1
1:A:30:VAL:C	1:A:33:TYR:CE1	0.53	2.81	16	4
1:A:30:VAL:HG23	1:A:30:VAL:O	0.53	2.03	5	5
1:A:38:TYR:CD1	1:A:38:TYR:C	0.53	2.81	8	4
1:A:30:VAL:O	1:A:31:ASP:C	0.53	2.46	15	2
1:A:10:ALA:CA	1:A:19:ILE:HG13	0.53	2.34	6	1
1:A:19:ILE:HG13	1:A:51:LEU:CD2	0.53	2.34	9	7
1:A:44:TYR:CD1	1:A:48:LYS:HG2	0.53	2.39	10	2
1:A:9:TYR:CE2	1:A:40:LYS:HD2	0.53	2.38	3	2
1:A:9:TYR:CE2	1:A:40:LYS:NZ	0.53	2.76	4	1
1:A:43:SER:O	1:A:46:GLN:N	0.53	2.42	18	16
1:A:19:ILE:HD11	1:A:51:LEU:CG	0.53	2.34	8	3
1:A:36:ALA:O	1:A:38:TYR:CE1	0.53	2.62	1	2
1:A:45:GLU:O	1:A:49:SER:CB	0.53	2.57	6	1
1:A:23:TRP:CH2	1:A:27:LYS:HG3	0.53	2.39	15	7
1:A:20:TYR:CZ	1:A:29:GLN:HG3	0.53	2.38	13	3
1:A:44:TYR:CZ	1:A:48:LYS:HG3	0.53	2.39	15	2
1:A:37:ILE:C	1:A:37:ILE:CD1	0.52	2.78	15	4
1:A:48:LYS:O	1:A:51:LEU:N	0.52	2.43	4	11
1:A:19:ILE:HG21	1:A:47:ALA:CB	0.52	2.35	9	2
1:A:26:CYS:SG	1:A:27:LYS:N	0.52	2.82	14	15
1:A:20:TYR:CE2	1:A:29:GLN:HG3	0.52	2.40	9	13
1:A:37:ILE:HD13	1:A:38:TYR:H	0.52	1.64	9	9
1:A:23:TRP:CE3	1:A:24:ASN:N	0.52	2.77	7	1
1:A:6:GLY:HA3	1:A:23:TRP:CA	0.52	2.34	1	3
1:A:10:ALA:HB2	1:A:19:ILE:CD1	0.52	2.35	6	1
1:A:10:ALA:HA	1:A:18:GLY:O	0.52	2.05	17	4

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:10:ALA:HB1	1:A:51:LEU:CD1	0.52	2.33	18	2
1:A:9:TYR:CD1	1:A:40:LYS:HA	0.52	2.39	15	8
1:A:37:ILE:CG2	1:A:38:TYR:N	0.52	2.72	11	5
1:A:9:TYR:HE1	1:A:38:TYR:CD1	0.52	2.22	14	4
1:A:9:TYR:CZ	1:A:40:LYS:CB	0.52	2.92	19	4
1:A:30:VAL:HG23	1:A:31:ASP:H	0.52	1.65	15	2
1:A:19:ILE:HD11	1:A:47:ALA:HB1	0.52	1.81	6	1
1:A:30:VAL:HB	1:A:33:TYR:CD1	0.52	2.40	15	1
1:A:30:VAL:O	1:A:30:VAL:HG23	0.51	2.05	4	4
1:A:9:TYR:CD2	1:A:40:LYS:HD3	0.51	2.40	4	1
1:A:37:ILE:O	1:A:38:TYR:O	0.51	2.29	2	8
1:A:42:ASN:O	1:A:43:SER:CB	0.51	2.58	20	5
1:A:12:ARG:CG	1:A:12:ARG:O	0.51	2.58	19	1
1:A:8:PHE:CE1	1:A:21:ASN:HB2	0.51	2.41	6	3
1:A:11:VAL:HG22	1:A:38:TYR:CB	0.51	2.35	7	1
1:A:9:TYR:CE2	1:A:40:LYS:HD3	0.51	2.40	4	1
1:A:43:SER:O	1:A:44:TYR:C	0.51	2.48	4	20
1:A:30:VAL:HA	1:A:33:TYR:CD1	0.51	2.40	11	3
1:A:26:CYS:SG	1:A:27:LYS:CE	0.51	2.99	2	1
1:A:48:LYS:HD2	1:A:49:SER:N	0.51	2.21	1	1
1:A:20:TYR:CE2	1:A:29:GLN:HG2	0.51	2.41	4	1
1:A:8:PHE:CE2	1:A:21:ASN:HB2	0.50	2.40	20	4
1:A:11:VAL:CG2	1:A:38:TYR:HB2	0.50	2.36	7	2
1:A:11:VAL:HG12	1:A:12:ARG:N	0.50	2.21	9	4
1:A:33:TYR:HB3	1:A:36:ALA:CB	0.50	2.37	9	2
1:A:25:GLU:O	1:A:29:GLN:HG2	0.50	2.06	13	10
1:A:41:PHE:CE2	1:A:47:ALA:HA	0.50	2.41	10	8
1:A:38:TYR:O	1:A:38:TYR:CG	0.50	2.64	2	3
1:A:33:TYR:HB2	1:A:36:ALA:CB	0.50	2.33	17	4
1:A:30:VAL:O	1:A:31:ASP:O	0.50	2.30	2	2
1:A:8:PHE:CE1	1:A:21:ASN:CG	0.50	2.85	1	1
1:A:23:TRP:CZ2	1:A:27:LYS:HD2	0.50	2.41	4	2
1:A:27:LYS:CD	1:A:31:ASP:OD1	0.50	2.59	5	1
1:A:32:GLY:N	1:A:33:TYR:CD1	0.50	2.80	18	4
1:A:19:ILE:HD11	1:A:48:LYS:HA	0.50	1.82	1	3
1:A:26:CYS:O	1:A:29:GLN:HG3	0.50	2.07	7	2
1:A:38:TYR:CD2	1:A:38:TYR:O	0.50	2.65	1	1
1:A:10:ALA:HA	1:A:19:ILE:CG1	0.50	2.37	18	1
1:A:32:GLY:N	1:A:33:TYR:CE1	0.49	2.80	18	3
1:A:32:GLY:O	1:A:33:TYR:O	0.49	2.30	8	7
1:A:19:ILE:HB	1:A:44:TYR:CZ	0.49	2.42	19	4

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:8:PHE:CE1	1:A:44:TYR:HB2	0.49	2.42	12	2
1:A:9:TYR:CE1	1:A:40:LYS:HB3	0.49	2.42	15	1
1:A:37:ILE:O	1:A:38:TYR:HB3	0.49	2.07	7	8
1:A:20:TYR:OH	1:A:29:GLN:NE2	0.49	2.45	20	1
1:A:20:TYR:CE2	1:A:29:GLN:CG	0.49	2.95	16	7
1:A:19:ILE:CD1	1:A:51:LEU:HD13	0.49	2.34	17	2
1:A:19:ILE:HG21	1:A:44:TYR:HD1	0.49	1.65	18	1
1:A:19:ILE:HD11	1:A:51:LEU:HD22	0.49	1.85	9	2
1:A:9:TYR:CG	1:A:11:VAL:CG2	0.49	2.96	15	1
1:A:25:GLU:O	1:A:29:GLN:CD	0.49	2.51	4	1
1:A:11:VAL:HB	1:A:20:TYR:CZ	0.49	2.43	14	1
1:A:44:TYR:CD1	1:A:48:LYS:CG	0.49	2.95	8	2
1:A:6:GLY:O	1:A:7:ASN:ND2	0.49	2.45	3	2
1:A:44:TYR:CE1	1:A:48:LYS:HD2	0.49	2.43	4	1
1:A:44:TYR:CE1	1:A:48:LYS:HB2	0.48	2.43	16	1
1:A:25:GLU:O	1:A:29:GLN:HG3	0.48	2.08	4	1
1:A:29:GLN:HG3	1:A:30:VAL:HG13	0.48	1.84	12	2
1:A:19:ILE:HG12	1:A:47:ALA:CB	0.48	2.34	6	1
1:A:20:TYR:CE2	1:A:29:GLN:CB	0.48	2.97	7	2
1:A:44:TYR:O	1:A:48:LYS:HB2	0.48	2.08	5	15
1:A:30:VAL:HG11	1:A:38:TYR:CB	0.48	2.38	13	2
1:A:27:LYS:O	1:A:31:ASP:HB2	0.48	2.09	7	6
1:A:6:GLY:O	1:A:7:ASN:OD1	0.48	2.32	20	2
1:A:8:PHE:HA	1:A:20:TYR:O	0.48	2.08	8	13
1:A:48:LYS:C	1:A:48:LYS:CD	0.48	2.81	1	1
1:A:9:TYR:HE2	1:A:26:CYS:HG	0.48	1.43	11	3
1:A:11:VAL:HG13	1:A:38:TYR:HB3	0.48	1.83	9	1
1:A:23:TRP:CZ2	1:A:27:LYS:HG3	0.48	2.44	14	1
1:A:24:ASN:O	1:A:28:ASN:HB3	0.48	2.08	17	7
1:A:44:TYR:CE1	1:A:48:LYS:CB	0.48	2.97	1	1
1:A:50:PHE:O	1:A:51:LEU:O	0.48	2.32	15	3
1:A:19:ILE:HD11	1:A:47:ALA:C	0.48	2.29	18	1
1:A:37:ILE:O	1:A:39:LYS:HD3	0.47	2.09	20	1
1:A:6:GLY:HA2	1:A:23:TRP:N	0.47	2.24	17	7
1:A:21:ASN:OD1	1:A:21:ASN:O	0.47	2.32	14	2
1:A:44:TYR:CD1	1:A:44:TYR:C	0.47	2.87	1	1
1:A:9:TYR:CE1	1:A:38:TYR:CD1	0.47	3.02	11	5
1:A:9:TYR:CB	1:A:29:GLN:OE1	0.47	2.62	10	1
1:A:8:PHE:CZ	1:A:21:ASN:CG	0.47	2.88	20	3
1:A:29:GLN:CD	1:A:30:VAL:HG13	0.47	2.29	3	1
1:A:37:ILE:CG2	1:A:37:ILE:O	0.47	2.63	7	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:11:VAL:HB	1:A:20:TYR:CE2	0.47	2.45	2	4
1:A:42:ASN:OD1	1:A:42:ASN:O	0.47	2.33	6	2
1:A:31:ASP:OD1	1:A:31:ASP:O	0.47	2.33	17	2
1:A:10:ALA:HA	1:A:19:ILE:HG12	0.47	1.87	18	1
1:A:8:PHE:O	1:A:41:PHE:O	0.47	2.33	2	4
1:A:51:LEU:HD23	1:A:51:LEU:N	0.47	2.24	1	2
1:A:11:VAL:CG2	1:A:20:TYR:CE2	0.47	2.98	14	1
1:A:8:PHE:CE2	1:A:21:ASN:ND2	0.47	2.83	12	1
1:A:29:GLN:O	1:A:30:VAL:CG1	0.47	2.63	5	2
1:A:11:VAL:HG11	1:A:29:GLN:OE1	0.47	2.10	3	1
1:A:29:GLN:O	1:A:30:VAL:HG13	0.46	2.10	5	3
1:A:37:ILE:CD1	1:A:39:LYS:HG2	0.46	2.40	16	1
1:A:23:TRP:CH2	1:A:27:LYS:HD2	0.46	2.46	4	1
1:A:19:ILE:CD1	1:A:47:ALA:C	0.46	2.84	6	1
1:A:26:CYS:O	1:A:30:VAL:CG2	0.46	2.62	12	4
1:A:11:VAL:HG21	1:A:29:GLN:NE2	0.46	2.25	7	1
1:A:48:LYS:O	1:A:49:SER:C	0.46	2.54	4	14
1:A:7:ASN:OD1	1:A:42:ASN:OD1	0.46	2.33	14	1
1:A:37:ILE:O	1:A:39:LYS:CD	0.46	2.64	20	1
1:A:44:TYR:OH	1:A:48:LYS:NZ	0.46	2.43	18	1
1:A:44:TYR:CZ	1:A:48:LYS:HD3	0.46	2.46	2	2
1:A:40:LYS:HD2	1:A:41:PHE:N	0.46	2.25	19	1
1:A:33:TYR:CB	1:A:36:ALA:CB	0.46	2.94	9	1
1:A:25:GLU:C	1:A:29:GLN:NE2	0.46	2.69	4	1
1:A:27:LYS:O	1:A:30:VAL:N	0.46	2.49	11	2
1:A:12:ARG:NE	1:A:12:ARG:O	0.46	2.49	17	1
1:A:25:GLU:O	1:A:29:GLN:CB	0.46	2.64	15	6
1:A:9:TYR:CE2	1:A:40:LYS:CB	0.46	2.99	19	1
1:A:20:TYR:CZ	1:A:29:GLN:CG	0.46	2.99	5	1
1:A:31:ASP:O	1:A:31:ASP:CG	0.46	2.54	7	2
1:A:38:TYR:CD1	1:A:38:TYR:N	0.46	2.84	7	2
1:A:24:ASN:O	1:A:28:ASN:HB2	0.45	2.12	3	6
1:A:41:PHE:CD1	1:A:46:GLN:HB2	0.45	2.45	19	2
1:A:45:GLU:O	1:A:48:LYS:HG3	0.45	2.11	1	1
1:A:40:LYS:HG3	1:A:41:PHE:N	0.45	2.25	3	2
1:A:44:TYR:CE2	1:A:48:LYS:HG3	0.45	2.47	3	2
1:A:26:CYS:HA	1:A:29:GLN:NE2	0.45	2.26	10	3
1:A:21:ASN:O	1:A:21:ASN:CG	0.45	2.54	18	9
1:A:21:ASN:CG	1:A:21:ASN:O	0.45	2.54	15	7
1:A:11:VAL:HG21	1:A:20:TYR:CE2	0.45	2.46	14	4
1:A:9:TYR:CZ	1:A:30:VAL:HG21	0.45	2.46	14	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:37:ILE:O	1:A:37:ILE:CG2	0.45	2.64	19	7
1:A:21:ASN:O	1:A:21:ASN:ND2	0.45	2.49	9	2
1:A:29:GLN:HG3	1:A:30:VAL:N	0.45	2.27	3	2
1:A:6:GLY:CA	1:A:23:TRP:N	0.45	2.80	14	4
1:A:26:CYS:HA	1:A:29:GLN:OE1	0.45	2.12	4	1
1:A:23:TRP:CD1	1:A:27:LYS:HD3	0.45	2.46	11	1
1:A:19:ILE:CG2	1:A:47:ALA:HB1	0.45	2.41	9	1
1:A:8:PHE:CE2	1:A:44:TYR:HB2	0.45	2.47	11	2
1:A:29:GLN:CG	1:A:30:VAL:HG22	0.45	2.42	10	1
1:A:24:ASN:O	1:A:25:GLU:C	0.45	2.52	2	17
1:A:12:ARG:HB3	1:A:18:GLY:N	0.45	2.26	12	1
1:A:43:SER:O	1:A:43:SER:OG	0.45	2.35	12	1
1:A:33:TYR:HE2	1:A:38:TYR:HH	0.44	1.54	17	1
1:A:19:ILE:HG21	1:A:44:TYR:CD1	0.44	2.46	17	2
1:A:19:ILE:HG21	1:A:47:ALA:HB3	0.44	1.89	3	1
1:A:12:ARG:HG2	1:A:12:ARG:O	0.44	2.12	4	2
1:A:44:TYR:O	1:A:48:LYS:HD3	0.44	2.13	6	1
1:A:29:GLN:CG	1:A:30:VAL:N	0.44	2.79	10	2
1:A:26:CYS:O	1:A:27:LYS:C	0.44	2.54	15	4
1:A:42:ASN:CG	1:A:42:ASN:O	0.44	2.56	20	4
1:A:25:GLU:O	1:A:29:GLN:HB3	0.44	2.12	17	1
1:A:31:ASP:O	1:A:31:ASP:OD1	0.44	2.34	6	1
1:A:19:ILE:CG1	1:A:51:LEU:CD1	0.44	2.81	4	3
1:A:9:TYR:CE2	1:A:26:CYS:SG	0.44	3.07	6	1
1:A:48:LYS:HA	1:A:51:LEU:HG	0.44	1.88	3	3
1:A:26:CYS:O	1:A:29:GLN:N	0.44	2.51	15	2
1:A:37:ILE:C	1:A:38:TYR:CD2	0.44	2.90	10	1
1:A:9:TYR:CD1	1:A:40:LYS:CA	0.44	3.00	15	1
1:A:23:TRP:CZ3	1:A:27:LYS:HD2	0.44	2.47	20	1
1:A:6:GLY:HA2	1:A:22:THR:HA	0.44	1.90	16	5
1:A:9:TYR:OH	1:A:38:TYR:CD1	0.44	2.56	9	2
1:A:38:TYR:CG	1:A:38:TYR:O	0.44	2.69	7	2
1:A:9:TYR:CE2	1:A:40:LYS:CD	0.44	3.01	4	1
1:A:9:TYR:CE2	1:A:40:LYS:HE3	0.44	2.47	4	1
1:A:30:VAL:CG1	1:A:38:TYR:CD2	0.44	3.00	11	1
1:A:44:TYR:O	1:A:48:LYS:CD	0.44	2.65	6	1
1:A:33:TYR:CD2	1:A:36:ALA:CB	0.43	3.01	20	1
1:A:44:TYR:CD1	1:A:48:LYS:CD	0.43	3.01	9	1
1:A:19:ILE:HD12	1:A:51:LEU:CD2	0.43	2.43	6	1
1:A:19:ILE:CB	1:A:44:TYR:CE1	0.43	3.01	17	1
1:A:6:GLY:C	1:A:7:ASN:OD1	0.43	2.57	19	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:44:TYR:O	1:A:48:LYS:HG3	0.43	2.14	1	1
1:A:27:LYS:CA	1:A:31:ASP:HB2	0.43	2.43	2	1
1:A:11:VAL:HG13	1:A:38:TYR:HA	0.43	1.88	17	1
1:A:25:GLU:O	1:A:29:GLN:HB2	0.43	2.13	15	4
1:A:8:PHE:CE1	1:A:44:TYR:CD2	0.43	3.06	17	1
1:A:8:PHE:HB2	1:A:41:PHE:O	0.43	2.13	12	4
1:A:19:ILE:CD1	1:A:51:LEU:HG	0.43	2.43	16	1
1:A:8:PHE:CZ	1:A:44:TYR:HB2	0.43	2.49	17	1
1:A:27:LYS:HD3	1:A:31:ASP:OD1	0.43	2.14	5	1
1:A:41:PHE:HB3	1:A:47:ALA:HB2	0.43	1.90	6	1
1:A:21:ASN:C	1:A:21:ASN:ND2	0.42	2.72	18	1
1:A:8:PHE:CD2	1:A:43:SER:N	0.42	2.87	16	1
1:A:43:SER:C	1:A:45:GLU:N	0.42	2.72	5	13
1:A:44:TYR:CE2	1:A:48:LYS:HD3	0.42	2.49	2	1
1:A:31:ASP:N	1:A:33:TYR:CD1	0.42	2.87	5	1
1:A:45:GLU:O	1:A:48:LYS:HD3	0.42	2.15	6	1
1:A:29:GLN:HA	1:A:29:GLN:NE2	0.42	2.29	1	1
1:A:20:TYR:CE2	1:A:29:GLN:OE1	0.42	2.73	17	1
1:A:19:ILE:CG2	1:A:47:ALA:CB	0.42	2.98	9	1
1:A:50:PHE:O	1:A:51:LEU:C	0.42	2.56	1	1
1:A:10:ALA:N	1:A:19:ILE:HG13	0.42	2.29	6	1
1:A:26:CYS:SG	1:A:27:LYS:HD2	0.42	2.55	2	1
1:A:27:LYS:O	1:A:30:VAL:C	0.42	2.58	18	1
1:A:7:ASN:O	1:A:22:THR:N	0.42	2.52	3	1
1:A:10:ALA:HA	1:A:19:ILE:HG13	0.42	1.91	6	1
1:A:39:LYS:HG2	1:A:50:PHE:CD1	0.42	2.49	4	1
1:A:33:TYR:O	1:A:34:GLY:C	0.42	2.58	11	1
1:A:37:ILE:CD1	1:A:38:TYR:N	0.42	2.82	5	3
1:A:20:TYR:OH	1:A:29:GLN:OE1	0.42	2.33	6	1
1:A:32:GLY:C	1:A:33:TYR:CG	0.42	2.94	18	2
1:A:47:ALA:O	1:A:51:LEU:HG	0.42	2.15	6	4
1:A:6:GLY:HA2	1:A:23:TRP:HA	0.42	1.92	14	1
1:A:19:ILE:HB	1:A:44:TYR:CD1	0.41	2.50	3	1
1:A:23:TRP:CH2	1:A:27:LYS:CD	0.41	3.04	12	1
1:A:18:GLY:O	1:A:19:ILE:HG12	0.41	2.14	12	2
1:A:9:TYR:HB3	1:A:29:GLN:OE1	0.41	2.16	17	1
1:A:46:GLN:O	1:A:47:ALA:C	0.41	2.57	5	1
1:A:6:GLY:CA	1:A:23:TRP:HB2	0.41	2.46	5	1
1:A:44:TYR:O	1:A:48:LYS:N	0.41	2.38	9	1
1:A:6:GLY:HA3	1:A:23:TRP:HA	0.41	1.91	1	1
1:A:9:TYR:HH	1:A:38:TYR:HD2	0.41	1.55	13	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:48:LYS:HD3	1:A:49:SER:N	0.41	2.30	6	1
1:A:19:ILE:HD12	1:A:44:TYR:HE1	0.41	1.74	17	1
1:A:36:ALA:CB	1:A:38:TYR:CD1	0.41	3.04	1	1
1:A:19:ILE:HD12	1:A:44:TYR:CD2	0.41	2.50	1	1
1:A:9:TYR:CD2	1:A:40:LYS:HE3	0.41	2.51	4	1
1:A:12:ARG:O	1:A:12:ARG:HG3	0.41	2.15	10	1
1:A:9:TYR:HB3	1:A:11:VAL:CG2	0.41	2.45	15	1
1:A:33:TYR:CE2	1:A:38:TYR:CE1	0.41	3.09	2	1
1:A:19:ILE:O	1:A:19:ILE:HG22	0.41	2.16	6	1
1:A:25:GLU:OE1	1:A:25:GLU:HA	0.41	2.15	12	1
1:A:6:GLY:CA	1:A:23:TRP:CA	0.40	2.98	18	1
1:A:12:ARG:HB2	1:A:18:GLY:N	0.40	2.31	13	1
1:A:50:PHE:O	1:A:52:GLY:N	0.40	2.54	1	1
1:A:35:GLY:O	1:A:36:ALA:O	0.40	2.40	13	1
1:A:44:TYR:OH	1:A:48:LYS:HE2	0.40	2.16	12	1
1:A:44:TYR:O	1:A:48:LYS:HB3	0.40	2.17	6	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	40/47 (85%)	28±1 (70±3%)	7±2 (17±4%)	5±2 (13±5%)	1	5
All	All	800/940 (85%)	556 (70%)	137 (17%)	107 (13%)	1	5

All 12 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	44	TYR	19
1	A	26	CYS	17
1	A	43	SER	16
1	A	30	VAL	11
1	A	38	TYR	11
1	A	12	ARG	10

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Mol	Chain	Res	Type	Models (Total)
1	A	51	LEU	8
1	A	33	TYR	7
1	A	35	GLY	4
1	A	31	ASP	2
1	A	32	GLY	1
1	A	36	ALA	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	33/37 (89%)	23±2 (68±7%)	10±2 (32±7%)	1	14
All	All	660/740 (89%)	451 (68%)	209 (32%)	1	14

All 27 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	9	TYR	20
1	A	22	THR	20
1	A	37	ILE	20
1	A	40	LYS	17
1	A	48	LYS	14
1	A	43	SER	14
1	A	12	ARG	14
1	A	39	LYS	13
1	A	50	PHE	12
1	A	27	LYS	12
1	A	44	TYR	9
1	A	49	SER	7
1	A	42	ASN	6
1	A	46	GLN	4
1	A	29	GLN	4
1	A	38	TYR	4
1	A	28	ASN	3
1	A	21	ASN	2
1	A	51	LEU	2

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Mol	Chain	Res	Type	Models (Total)
1	A	41	PHE	2
1	A	31	ASP	2
1	A	45	GLU	2
1	A	7	ASN	2
1	A	8	PHE	1
1	A	19	ILE	1
1	A	33	TYR	1
1	A	23	TRP	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 78% for the well-defined parts and 72% for the entire structure.

7.1 Chemical shift list 1

File name: BMRB entry 4424

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	593
Number of shifts mapped to atoms	455
Number of unparsed shifts	0
Number of shifts with mapping errors	138
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	5

The following assigned chemical shifts were not mapped to the molecules present in the coordinate file.

- Residue not found in structure. All 138 occurrences are reported below.

Chain	Res	Type	Atom	Shift Data		
				Value	Uncertainty	Ambiguity
A	63	SER	HA	4.4	-1.0	1
A	60	TYR	HB3	2.84	-1.0	2
A	57	THR	HG22	1.04	-1.0	1
A	4	ARG	HA	4.25	-1.0	1
A	62	SER	CA	56.28	-1.0	1
A	4	ARG	CD	41.34	-1.0	1
A	54	PRO	HB2	2.1	-1.0	2
A	60	TYR	HE1	6.8	-1.0	1
A	57	THR	N	116.78	-1.0	1
A	54	PRO	HD3	3.53	-1.0	2
A	59	ASN	HA	4.62	-1.0	1
A	55	ASN	HB3	2.68	-1.0	2
A	58	SER	CB	61.35	-1.0	1
A	60	TYR	HD2	7.1	-1.0	1

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Chain	Res	Type	Atom	Shift Data		
				Value	Uncertainty	Ambiguity
A	58	SER	N	119.92	-1.0	1
A	60	TYR	CD1	131.19	-1.0	1
A	3	ALA	CB	17.05	-1.0	1
A	3	ALA	N	128.53	-1.0	1
A	55	ASN	H	8.55	-1.0	1
A	1	GLY	HA2	3.58	-1.0	1
A	60	TYR	CE2	116.07	-1.0	1
A	3	ALA	HB1	1.27	-1.0	1
A	60	TYR	HB2	3.0	-1.0	2
A	61	GLY	HA2	3.82	-1.0	1
A	57	THR	HG23	1.04	-1.0	1
A	54	PRO	CG	25.03	-1.0	1
A	4	ARG	HG2	1.48	-1.0	1
A	62	SER	CB	62.43	-1.0	1
A	61	GLY	CA	42.9	-1.0	1
A	62	SER	HA	4.43	-1.0	1
A	4	ARG	CA	53.57	-1.0	1
A	56	THR	H	8.13	-1.0	1
A	4	ARG	CG	24.67	-1.0	1
A	1	GLY	CA	41.46	-1.0	1
A	3	ALA	H	8.53	-1.0	1
A	63	SER	H	8.12	-1.0	1
A	55	ASN	CB	36.5	-1.0	1
A	55	ASN	N	120.67	-1.0	1
A	56	THR	HA	4.36	-1.0	1
A	5	GLN	CB	27.78	-1.0	1
A	58	SER	CA	55.64	-1.0	1
A	3	ALA	HA	4.27	-1.0	1
A	62	SER	N	117.9	-1.0	1
A	56	THR	CA	59.03	-1.0	1
A	3	ALA	HB2	1.27	-1.0	1
A	4	ARG	HB3	1.71	-1.0	2
A	62	SER	H	8.14	-1.0	1
A	53	GLN	HB2	1.92	-1.0	1
A	2	SER	N	117.89	-1.0	1
A	61	GLY	HA3	3.82	-1.0	1
A	2	SER	CB	61.7	-1.0	1
A	59	ASN	CA	51.03	-1.0	1
A	63	SER	HB3	2.91	-1.0	1
A	63	SER	N	124.09	-1.0	1
A	4	ARG	HG3	1.48	-1.0	1

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Chain	Res	Type	Atom	Shift Data		
				Value	Uncertainty	Ambiguity
A	4	ARG	N	123.0	-1.0	1
A	58	SER	HB3	3.69	-1.0	1
A	59	ASN	CB	36.29	-1.0	1
A	1	GLY	N	121.52	-1.0	1
A	5	GLN	H	8.47	-1.0	1
A	62	SER	HB3	3.78	-1.0	1
A	61	GLY	H	8.31	-1.0	1
A	56	THR	HB	4.23	-1.0	1
A	53	GLN	CB	26.34	-1.0	1
A	56	THR	HG23	1.24	-1.0	1
A	53	GLN	N	122.66	-1.0	1
A	5	GLN	HA	4.5	-1.0	1
A	60	TYR	N	122.9	-1.0	1
A	2	SER	H	8.65	-1.0	1
A	62	SER	HB2	3.78	-1.0	1
A	60	TYR	CB	36.29	-1.0	1
A	3	ALA	HB3	1.27	-1.0	1
A	4	ARG	HB2	1.65	-1.0	2
A	57	THR	HG21	1.04	-1.0	1
A	63	SER	HB2	2.91	-1.0	1
A	57	THR	CA	60.25	-1.0	1
A	54	PRO	CA	60.93	-1.0	1
A	57	THR	CB	68.25	-1.0	1
A	53	GLN	HG2	2.31	-1.0	1
A	2	SER	HB3	3.76	-1.0	1
A	2	SER	HB2	3.76	-1.0	1
A	61	GLY	N	112.94	-1.0	1
A	56	THR	CG2	19.37	-1.0	1
A	58	SER	HB2	3.69	-1.0	1
A	54	PRO	HD2	3.65	-1.0	2
A	60	TYR	HE2	6.8	-1.0	1
A	53	GLN	H	7.7	-1.0	1
A	4	ARG	H	8.45	-1.0	1
A	1	GLY	H	8.72	-1.0	1
A	60	TYR	HD1	7.1	-1.0	1
A	5	GLN	N	124.48	-1.0	1
A	60	TYR	H	8.2	-1.0	1
A	60	TYR	CD2	131.19	-1.0	1
A	3	ALA	CA	50.16	-1.0	1
A	53	GLN	CA	51.28	-1.0	1
A	56	THR	HG22	1.24	-1.0	1

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Chain	Res	Type	Atom	Shift Data		
				Value	Uncertainty	Ambiguity
A	59	ASN	HB3	2.59	-1.0	2
A	60	TYR	CE1	116.07	-1.0	1
A	54	PRO	HA	4.53	-1.0	1
A	54	PRO	HB3	1.8	-1.0	2
A	54	PRO	CD	48.32	-1.0	1
A	54	PRO	CB	30.05	-1.0	1
A	4	ARG	HD3	3.06	-1.0	1
A	53	GLN	HG3	2.31	-1.0	1
A	53	GLN	HB3	1.73	-1.0	1
A	4	ARG	CB	28.59	-1.0	1
A	53	GLN	HA	4.45	-1.0	1
A	2	SER	HA	4.41	-1.0	1
A	59	ASN	H	8.41	-1.0	1
A	54	PRO	HG3	1.89	-1.0	1
A	55	ASN	HA	4.62	-1.0	1
A	5	GLN	HG2	2.28	-1.0	1
A	55	ASN	CA	51.01	-1.0	1
A	5	GLN	CA	53.49	-1.0	1
A	5	GLN	CG	31.56	-1.0	1
A	5	GLN	HB3	1.92	-1.0	1
A	57	THR	HB	4.18	-1.0	1
A	56	THR	HG21	1.24	-1.0	1
A	56	THR	N	115.82	-1.0	1
A	2	SER	CA	55.63	-1.0	1
A	63	SER	CA	57.48	-1.0	1
A	57	THR	H	8.22	-1.0	1
A	59	ASN	HB2	2.65	-1.0	2
A	4	ARG	HD2	3.06	-1.0	1
A	59	ASN	N	122.75	-1.0	1
A	54	PRO	HG2	1.89	-1.0	1
A	60	TYR	HA	4.44	-1.0	1
A	5	GLN	HG3	2.28	-1.0	1
A	55	ASN	HB2	2.73	-1.0	2
A	5	GLN	HB2	2.03	-1.0	1
A	57	THR	HA	4.31	-1.0	1
A	53	GLN	CG	31.14	-1.0	1
A	58	SER	HA	4.32	-1.0	1
A	56	THR	CB	67.28	-1.0	1
A	1	GLY	HA3	3.58	-1.0	1
A	58	SER	H	8.3	-1.0	1
A	57	THR	CG2	19.48	-1.0	1

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Chain	Res	Type	Atom	Shift Data		
				Value	Uncertainty	Ambiguity
A	60	TYR	CA	56.0	-1.0	1

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
$^{13}\text{C}_\alpha$	61	2.17 ± 0.16	Should be applied
$^{13}\text{C}_\beta$	52	2.17 ± 0.15	Should be applied
$^{13}\text{C}'$	0	—	None (insufficient data)
^{15}N	58	-1.68 ± 0.20	Should be applied

7.1.3 Completeness of resonance assignments [i](#)

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 78%, i.e. 405 atoms were assigned a chemical shift out of a possible 517. 3 out of 3 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	168/210 (80%)	84/84 (100%)	42/84 (50%)	42/42 (100%)
Sidechain	168/228 (74%)	103/135 (76%)	65/79 (82%)	0/14 (0%)
Aromatic	69/79 (87%)	35/41 (85%)	34/37 (92%)	0/1 (0%)
Overall	405/517 (78%)	222/260 (85%)	141/200 (70%)	42/57 (74%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 72%, i.e. 418 atoms were assigned a chemical shift out of a possible 584. 3 out of 3 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	174/235 (74%)	86/94 (91%)	45/94 (48%)	43/47 (91%)
Sidechain	175/270 (65%)	107/160 (67%)	68/92 (74%)	0/18 (0%)
Aromatic	69/79 (87%)	35/41 (85%)	34/37 (92%)	0/1 (0%)
Overall	418/584 (72%)	228/295 (77%)	147/223 (66%)	43/66 (65%)

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.

Mol	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	48	LYS	CE	36.36	46.00 – 37.80	-6.8
1	A	27	LYS	HB2	0.15	3.03 – 0.53	-6.5
1	A	48	LYS	HD2	0.32	2.76 – 0.46	-5.6
1	A	48	LYS	HD3	0.32	2.75 – 0.45	-5.6
1	A	29	GLN	CG	28.00	39.38 – 28.18	-5.2

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.

Random coil index (RCI) for chain A:

