Full wwPDB NMR Structure Validation Report (i)

Jun 17, 2020 – 02:35 am BST

PDB ID	:	2JU4
Title	:	NMR structure of the gamma subunit of cGMP phosphodiesterase
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Deposited on	:	2007-08-14

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 (i) symbol.

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

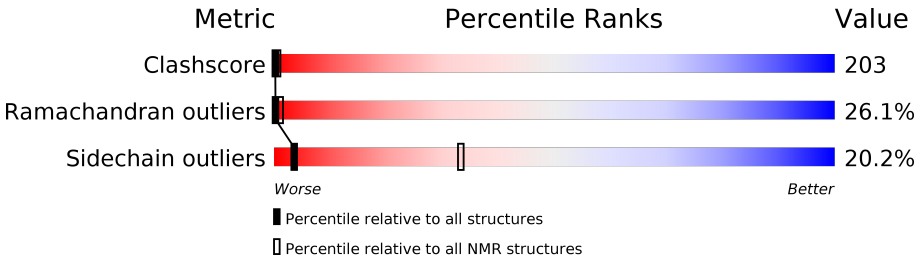
Cyrange	:	Kirchner and Güntert (2011)
NmrClust	:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	2.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 68%.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	NMR archive (#Entries)
Clashscore	158937	12864
Ramachandran outliers	154571	11451
Sidechain outliers	154315	11428

The table below summarises the geometric issues observed across the polymeric chains and their fit to the experimental data. The red, orange, yellow and green segments indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. A cyan segment indicates the fraction of residues that are not part of the well-defined cores, and a grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5%

Mol	Chain	Length	Quality of chain
1	A	87	21% · 77%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA and RNA chains that are outliers for geometric criteria:

Mol	Chain	Compound	Res	Total models with violations	
				Chirality	Geometry
2	A	RCY	110	47	-
2	A	RCY	121	45	-
2	A	RCY	130	61	1
2	A	RCY	138	52	-
2	A	RCY	150	53	-
2	A	RCY	160	70	-
2	A	RCY	168	69	-

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Mol	Chain	Compound	Res	Total models with violations	
				Chirality	Geometry
2	A	RCY	173	50	-
2	A	RCY	176	56	-
2	A	RCY	187	57	-

2 Ensemble composition and analysis

This entry contains 100 models. Model 6 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *fewest violations*.

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:59-A:78 (20)	1.97	6

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 6 clusters and 2 single-model clusters were found.

Cluster number	Models
1	11, 12, 16, 17, 19, 20, 21, 22, 26, 27, 28, 29, 32, 33, 36, 37, 38, 39, 40, 41, 44, 45, 48, 49, 52, 53, 56, 58, 67, 70, 71, 74, 82, 83, 84, 86, 88, 89, 91, 92, 93, 94, 96, 97, 99
2	1, 2, 3, 7, 8, 10, 13, 14, 23, 24, 25, 30, 31, 35, 42, 43, 46, 50, 55, 57, 59, 60, 61, 62, 64, 65, 66, 72, 73, 75, 79, 80, 87, 98, 100
3	4, 5, 6, 15, 18, 47, 54, 69, 77, 78, 85
4	51, 63, 68
5	34, 76
6	9, 95
Single-model clusters	81; 90

3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 1478 atoms, of which 659 are hydrogens and 0 are deuteriums.

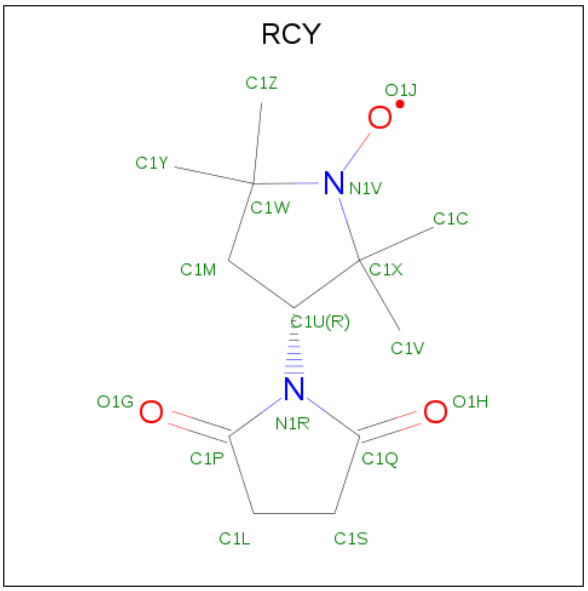
- Molecule 1 is a protein called Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	87	1288	395	639	122	119	13	0

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	10	CYS	PHE	engineered mutation	UNP P04972
A	21	CYS	VAL	engineered mutation	UNP P04972
A	30	CYS	PHE	engineered mutation	UNP P04972
A	38	CYS	PHE	engineered mutation	UNP P04972
A	50	CYS	PHE	engineered mutation	UNP P04972
A	60	CYS	LEU	engineered mutation	UNP P04972
A	73	CYS	PHE	engineered mutation	UNP P04972
A	76	CYS	LEU	engineered mutation	UNP P04972
A	87	CYS	ILE	engineered mutation	UNP P04972

- Molecule 2 is (3'R)-1'-oxyl-2',2',5',5'-tetramethyl-1,3'-bipyrrolidine-2,5-dione (three-letter code: RCY) (formula: $C_{12}H_{19}N_2O_3$).



Mol	Chain	Residues	Atoms				
2	A	1	Total 19	C 12	H 2	N 2	O 3
2	A	1	Total 19	C 12	H 2	N 2	O 3
2	A	1	Total 19	C 12	H 2	N 2	O 3
2	A	1	Total 19	C 12	H 2	N 2	O 3
2	A	1	Total 19	C 12	H 2	N 2	O 3
2	A	1	Total 19	C 12	H 2	N 2	O 3
2	A	1	Total 19	C 12	H 2	N 2	O 3
2	A	1	Total 19	C 12	H 2	N 2	O 3
2	A	1	Total 19	C 12	H 2	N 2	O 3
2	A	1	Total 19	C 12	H 2	N 2	O 3

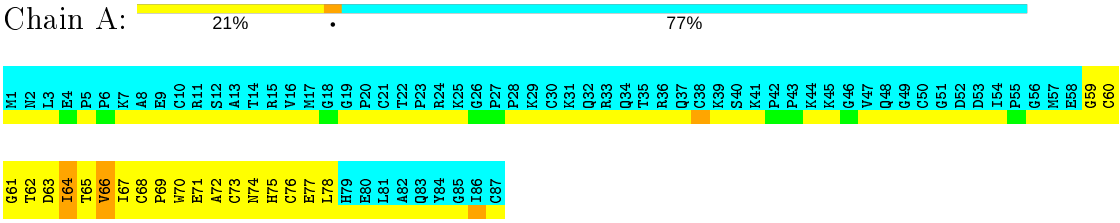
4 Residue-property plots

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: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

Chain A:



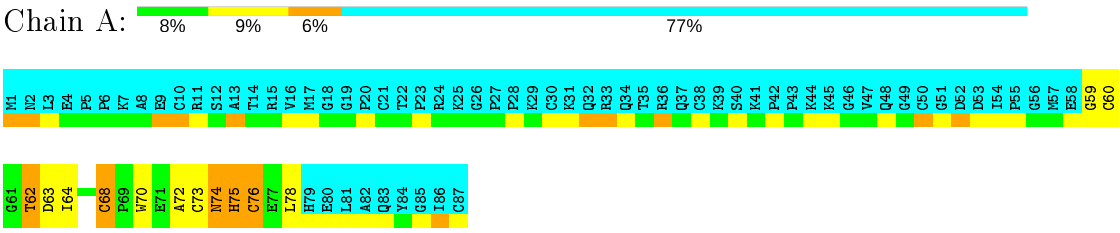
4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

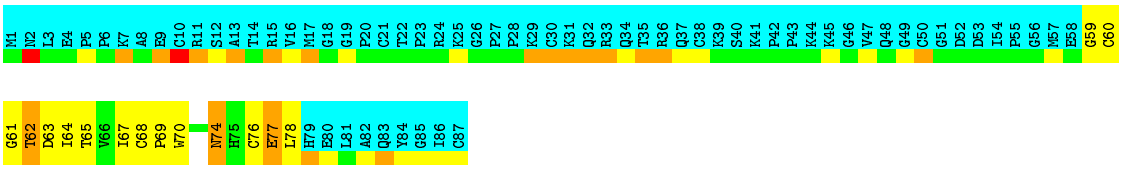
Chain A:



4.2.2 Score per residue for model 2

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

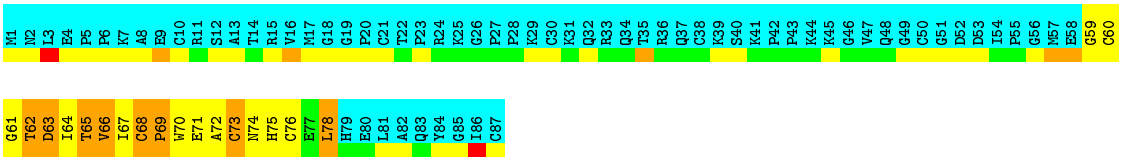
Chain A:



4.2.3 Score per residue for model 3

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

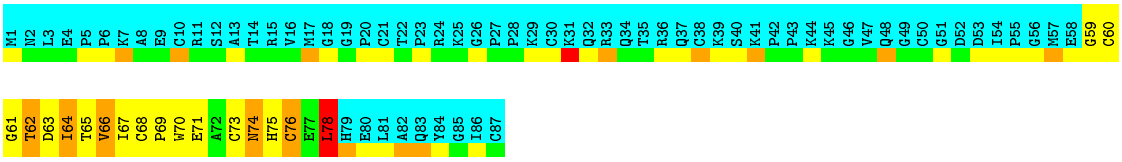
Chain A: • 13% 9% 77%



4.2.4 Score per residue for model 4

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

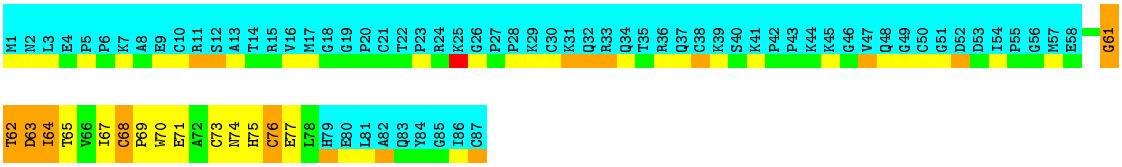
Chain A: • 14% 6% • 77%



4.2.5 Score per residue for model 5

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

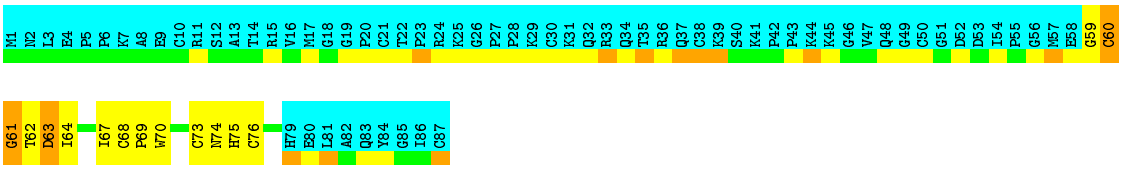
Chain A: 6% 10% 7% 77%



4.2.6 Score per residue for model 6 (medoid)

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

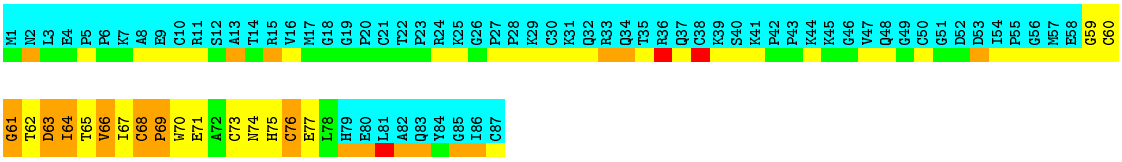
Chain A: 7% 13% • 77%



4.2.7 Score per residue for model 7

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

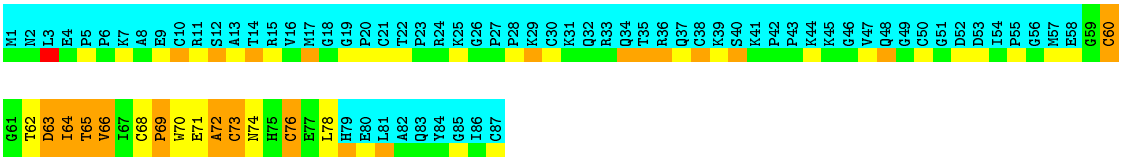
Chain A: • 13% 8% 77%



4.2.8 Score per residue for model 8

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

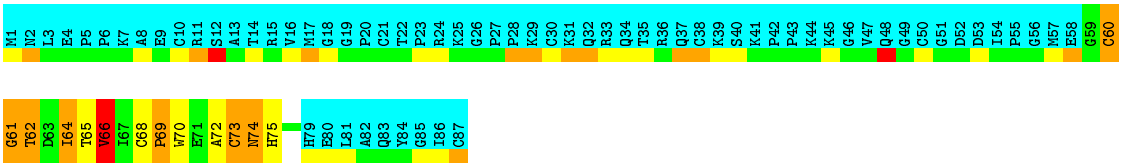
Chain A: 6% 7% 10% 77%



4.2.9 Score per residue for model 9

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

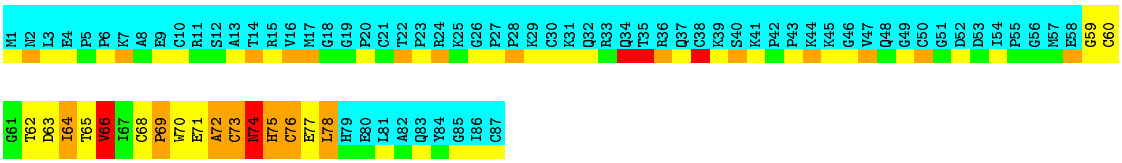
Chain A: 8% 6% 8% • 77%



4.2.10 Score per residue for model 10

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

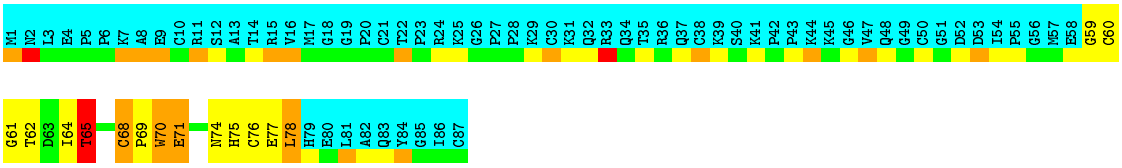
Chain A: • 10% 8% • 77%



4.2.11 Score per residue for model 11

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

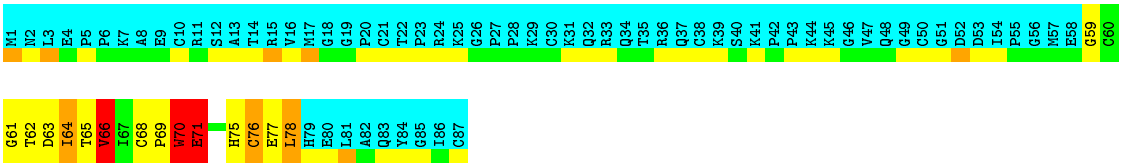
Chain A: 6% 11% 5% • 77%



4.2.12 Score per residue for model 12

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

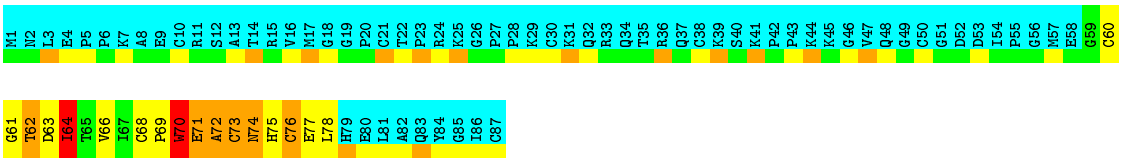
Chain A: 6% 10% • • 77%



4.2.13 Score per residue for model 13

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

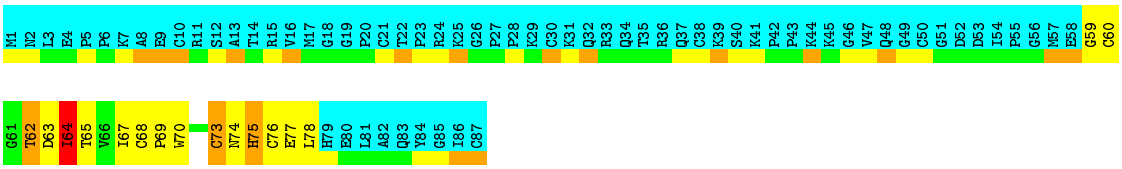
Chain A: • 10% 7% • 77%



4.2.14 Score per residue for model 14

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

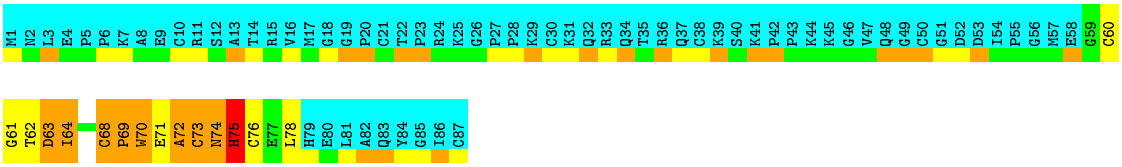
Chain A: 5% 14% • • 77%



4.2.15 Score per residue for model 15

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

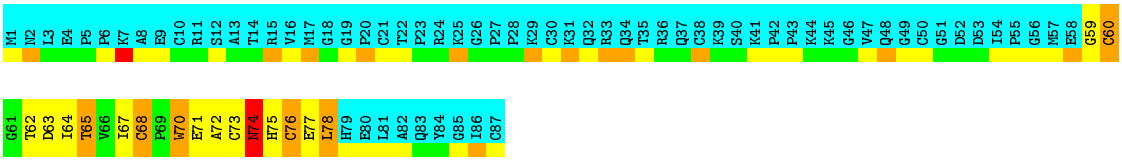
Chain A: 6% 7% 9% 77%



4.2.16 Score per residue for model 16

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

Chain A: 11% 7% 77%



4.2.17 Score per residue for model 17

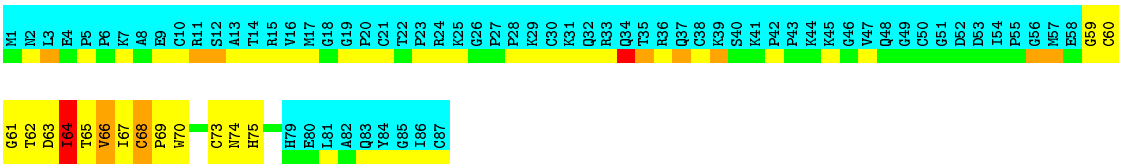
• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

Chain A: 8% 9% 77%

4.2.18 Score per residue for model 18

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

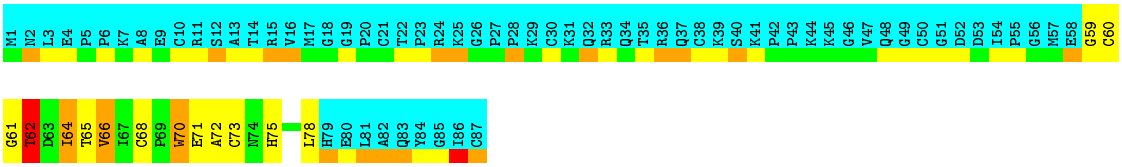
Chain A: 6% 14% 77%



4.2.19 Score per residue for model 19

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

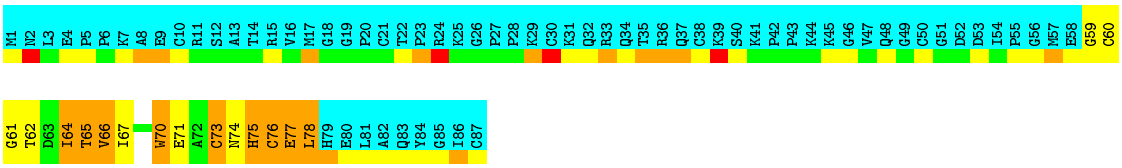
Chain A: 7% 11% 77%



4.2.20 Score per residue for model 20

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

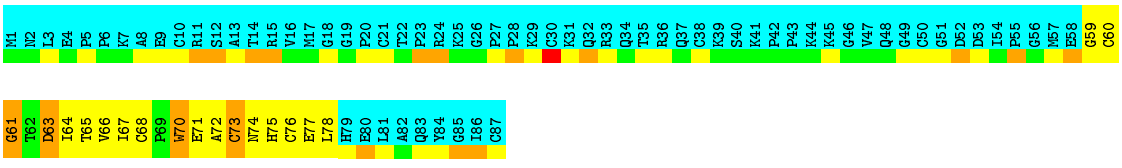
Chain A: 5% 8% 10% 77%



4.2.21 Score per residue for model 21

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

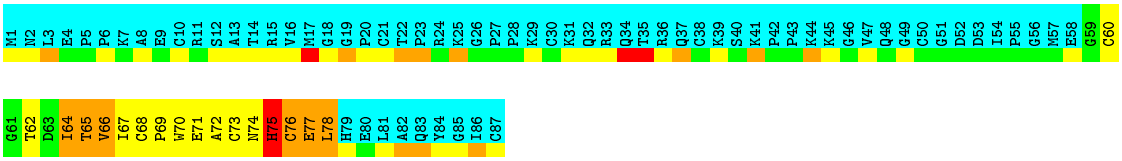
Chain A: 16% 5% 77%



4.2.22 Score per residue for model 22

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

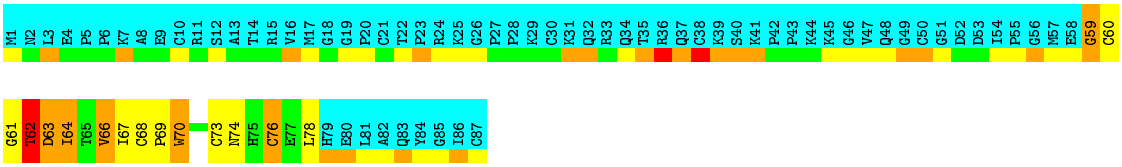
Chain A: • 11% 7% • 77%



4.2.23 Score per residue for model 23

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

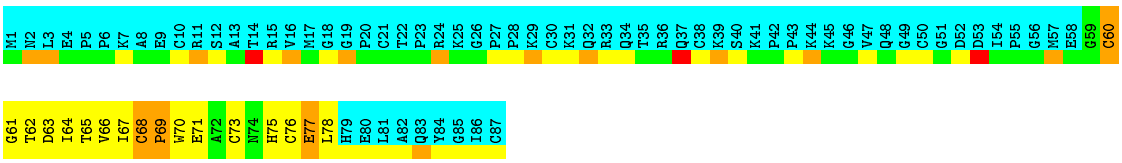
Chain A: 6% 9% 7% • 77%



4.2.24 Score per residue for model 24

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

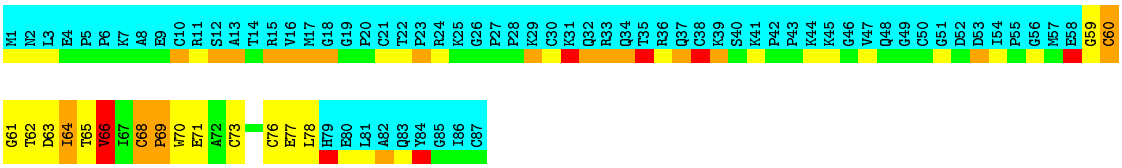
Chain A: • 15% 5% 77%



4.2.25 Score per residue for model 25

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

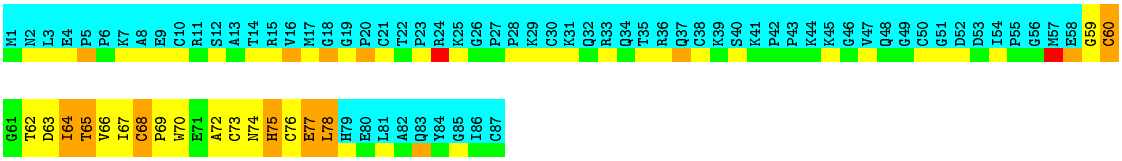
Chain A: 5% 13% 5% • 77%



4.2.26 Score per residue for model 26

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

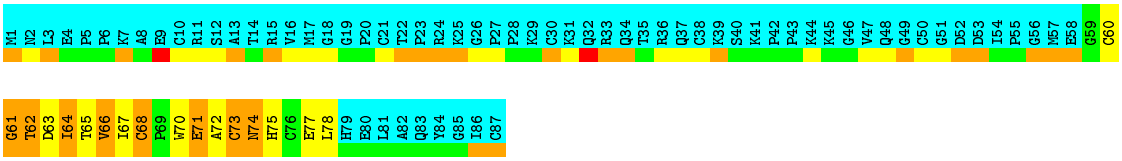
Chain A: • 13% 8% 77%



4.2.27 Score per residue for model 27

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

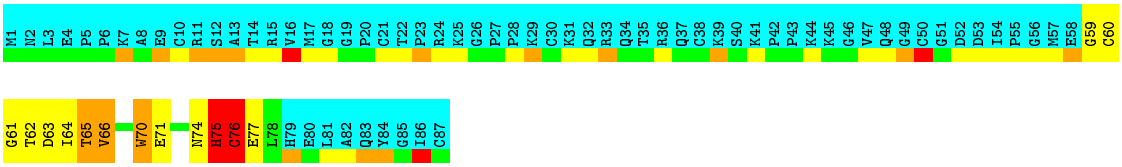
Chain A: • 10% 9% 77%



4.2.28 Score per residue for model 28

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

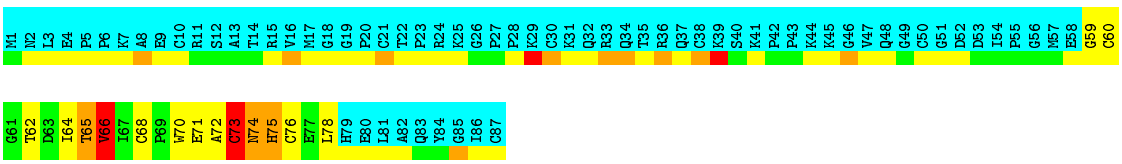
Chain A: 7% 10% • • 77%



4.2.29 Score per residue for model 29

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

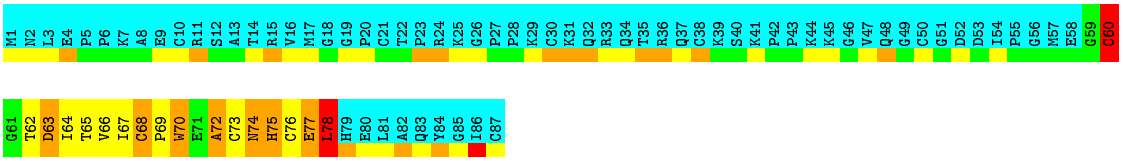
Chain A: 6% 11% • • 77%



4.2.30 Score per residue for model 30

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

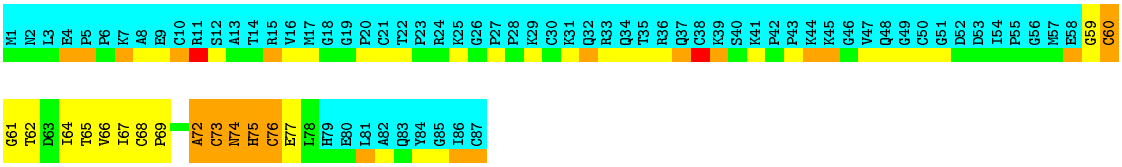
Chain A: • 9% 8% • 77%



4.2.31 Score per residue for model 31

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

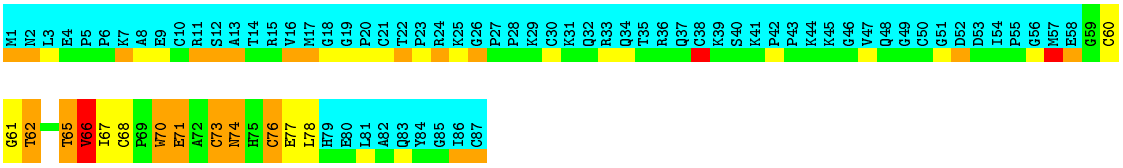
Chain A: 5% 11% 7% 77%



4.2.32 Score per residue for model 32

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

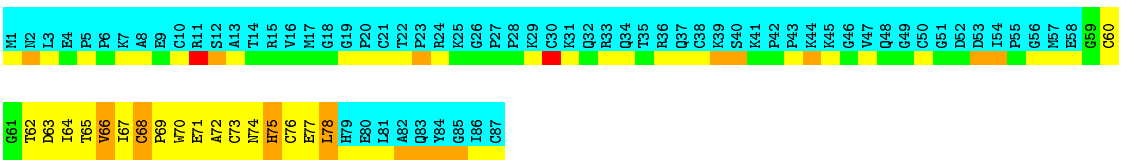
Chain A: 7% 7% 8% • 77%



4.2.33 Score per residue for model 33

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

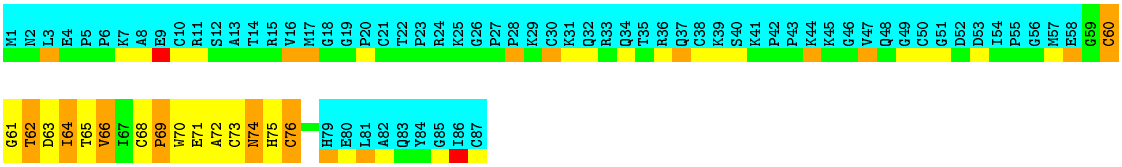
Chain A: • 16% 5% 77%



4.2.34 Score per residue for model 34

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

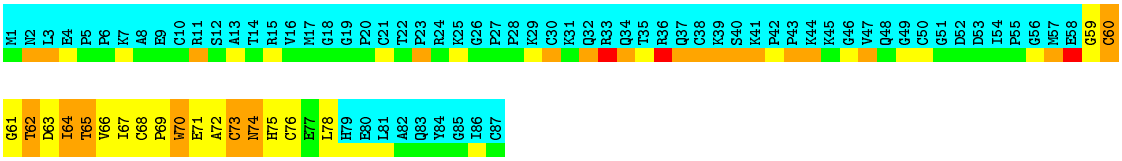
Chain A: 5% 10% 8% 77%



4.2.35 Score per residue for model 35

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

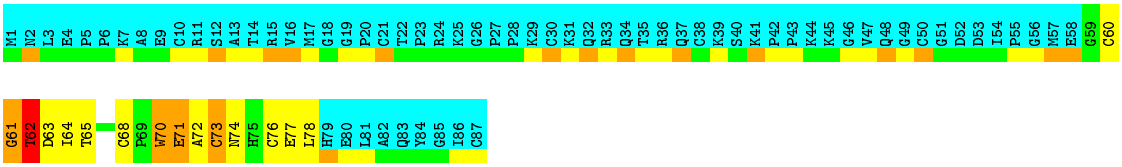
Chain A: 14% 8% 77%



4.2.36 Score per residue for model 36

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

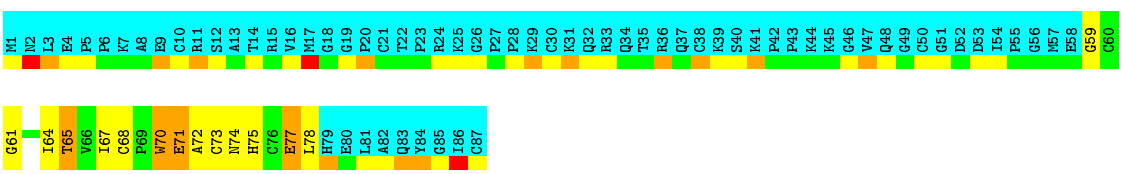
Chain A: 6% 11% 5% 77%



4.2.37 Score per residue for model 37

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

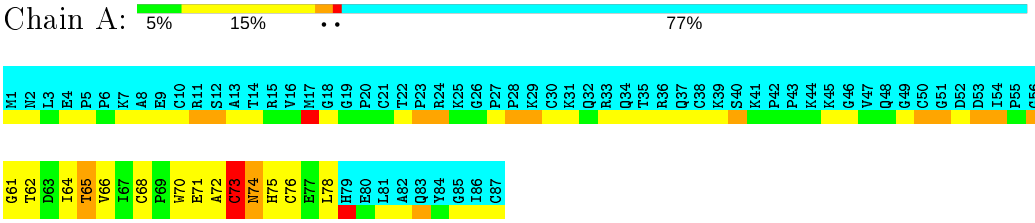
Chain A: 7% 11% 5% 77%



4.2.38 Score per residue for model 38

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

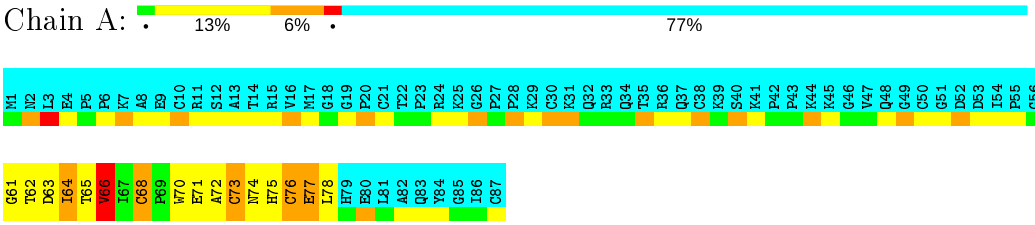
Chain A:



4.2.39 Score per residue for model 39

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

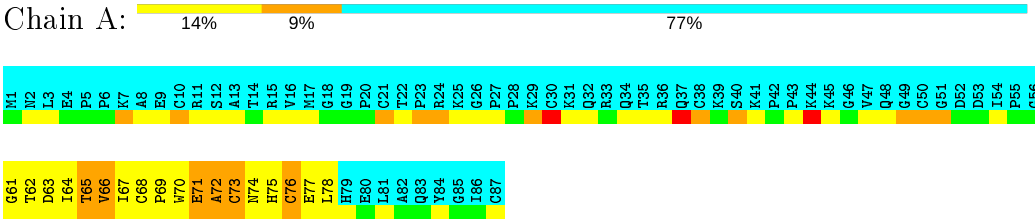
Chain A:



4.2.40 Score per residue for model 40

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

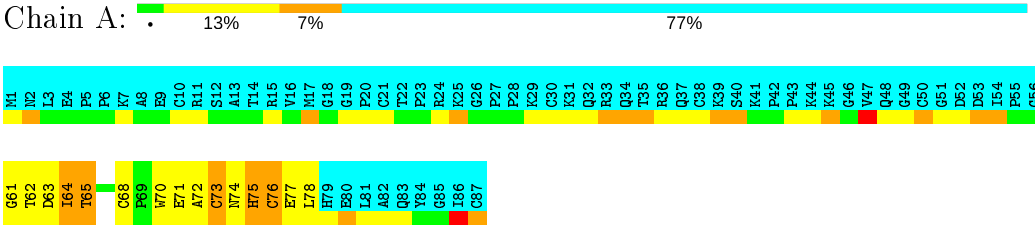
Chain A:



4.2.41 Score per residue for model 41

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

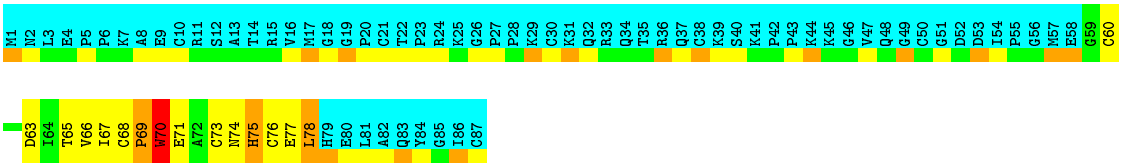
Chain A:



4.2.42 Score per residue for model 42

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

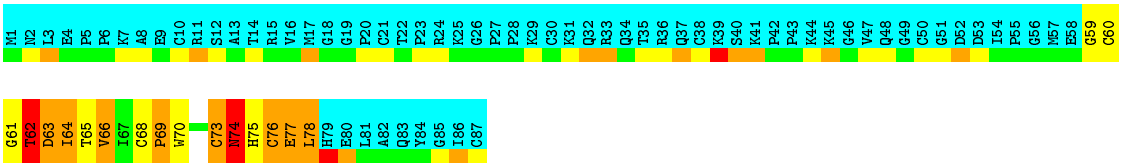
Chain A: 6% 13% 77%



4.2.43 Score per residue for model 43

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

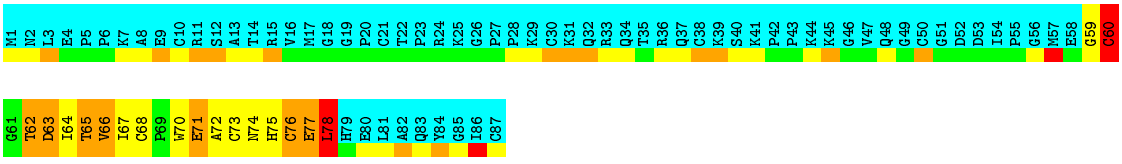
Chain A: 8% 9% 77%



4.2.44 Score per residue for model 44

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

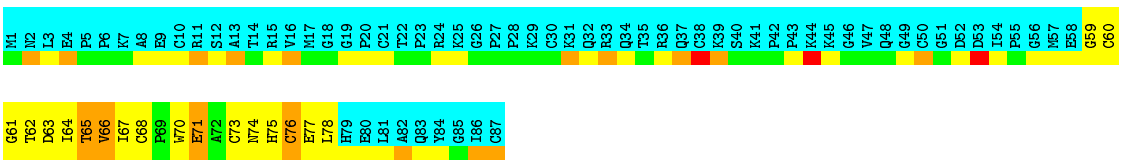
Chain A: 10% 8% 77%



4.2.45 Score per residue for model 45

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

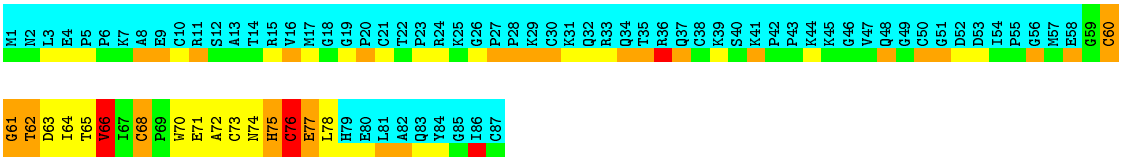
Chain A: 16% 5% 77%



4.2.46 Score per residue for model 46

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

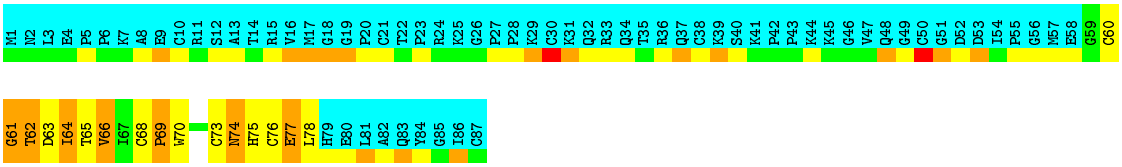
Chain A: 



4.2.47 Score per residue for model 47

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

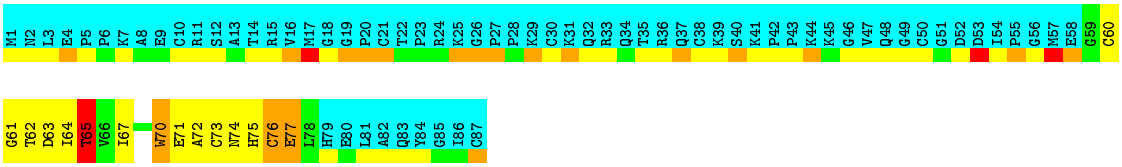
Chain A: 



4.2.48 Score per residue for model 48

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

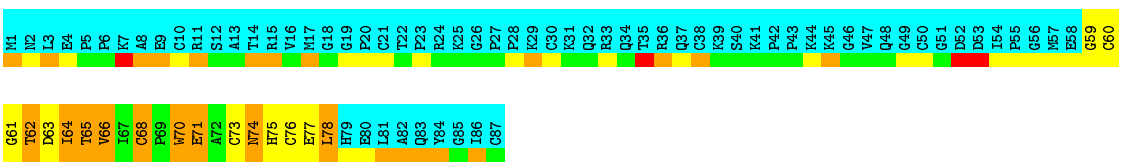
Chain A: 



4.2.49 Score per residue for model 49

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

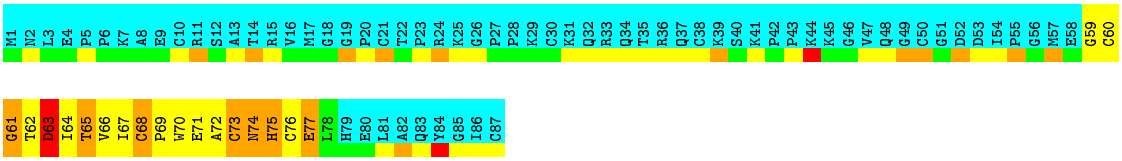
Chain A: 



4.2.50 Score per residue for model 50

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

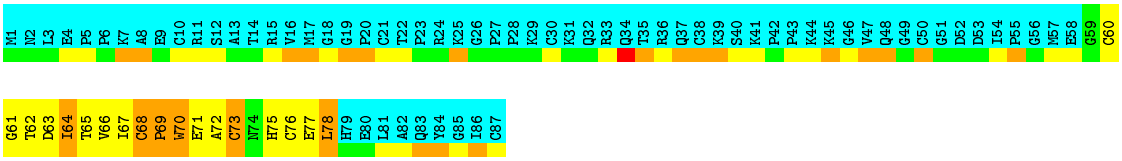
Chain A: 13% 8% 77%



4.2.51 Score per residue for model 51

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

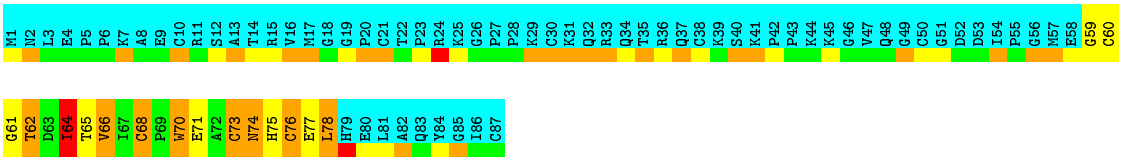
Chain A: 14% 7% 77%



4.2.52 Score per residue for model 52

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

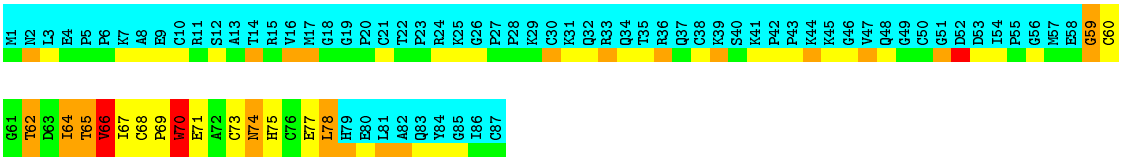
Chain A: 5% 8% 9% 77%



4.2.53 Score per residue for model 53

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

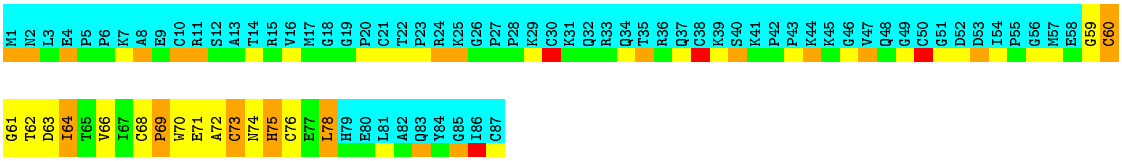
Chain A: 5% 9% 7% 77%



4.2.54 Score per residue for model 54

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

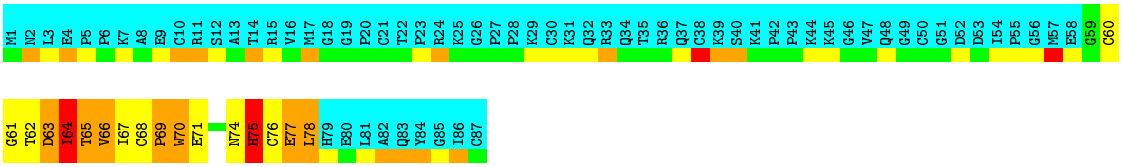
Chain A: • 13% 7% 77%



4.2.55 Score per residue for model 55

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

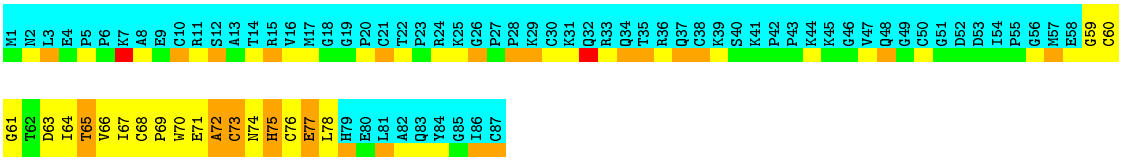
Chain A: • 9% 8% • 77%



4.2.56 Score per residue for model 56

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

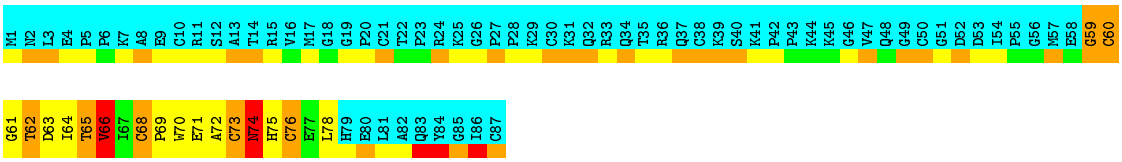
Chain A: • 16% 6% 77%



4.2.57 Score per residue for model 57

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

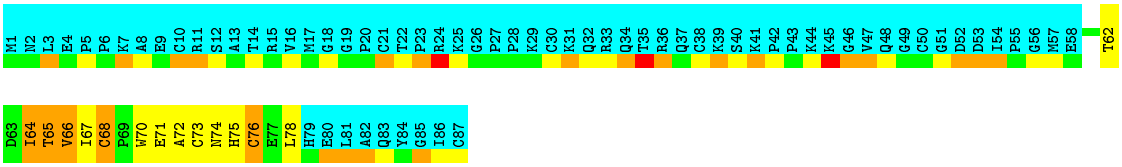
Chain A: • 10% 8% • 77%



4.2.58 Score per residue for model 58

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

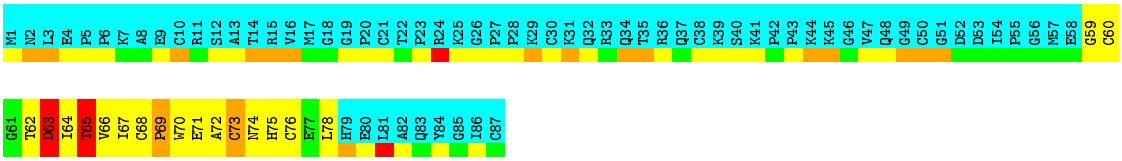
Chain A: 7% 10% 6% 77%



4.2.59 Score per residue for model 59

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

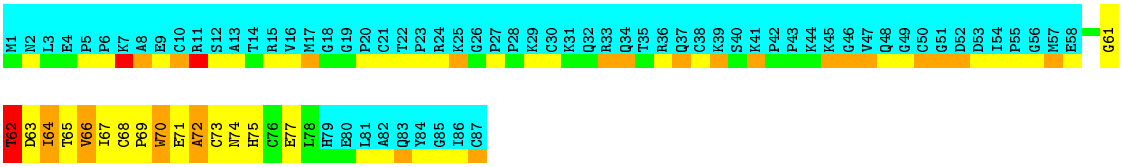
Chain A: 16% 77%



4.2.60 Score per residue for model 60

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

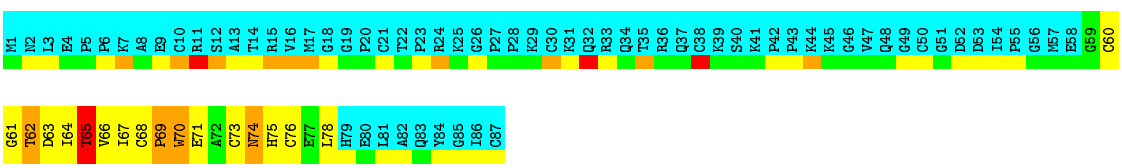
Chain A: 5% 13% 5% 77%



4.2.61 Score per residue for model 61

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

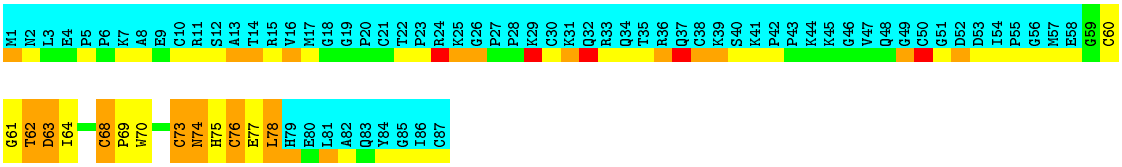
Chain A: 14% 5% 77%



4.2.62 Score per residue for model 62

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

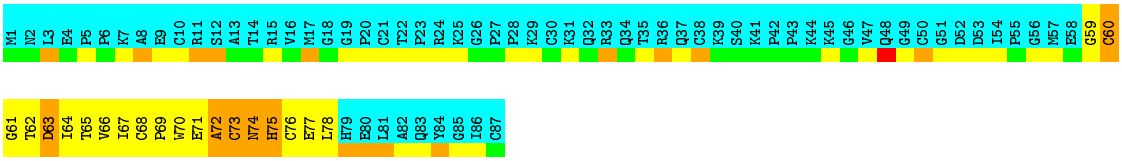
Chain A: 7% 8% 8% 77%



4.2.63 Score per residue for model 63

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

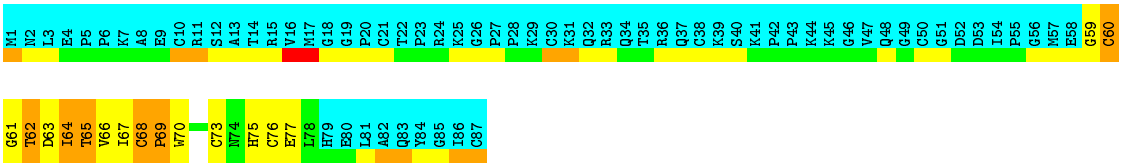
Chain A: 16% 7% 77%



4.2.64 Score per residue for model 64

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

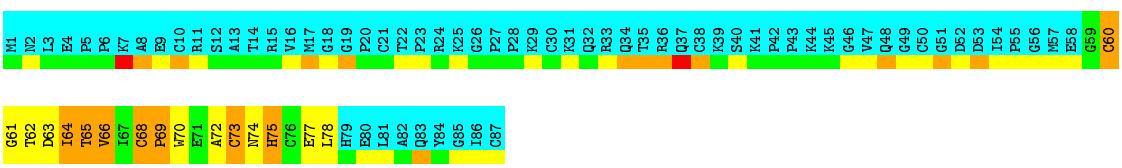
Chain A: 5% 11% 7% 77%



4.2.65 Score per residue for model 65

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

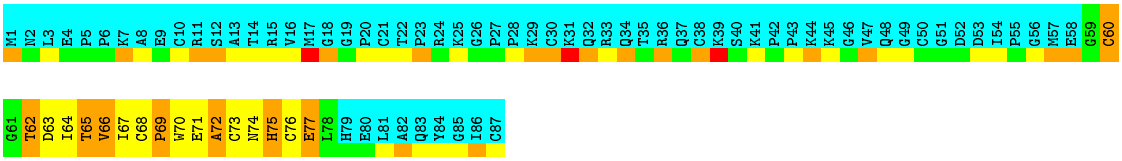
Chain A: 5% 9% 9% 77%



4.2.66 Score per residue for model 66

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

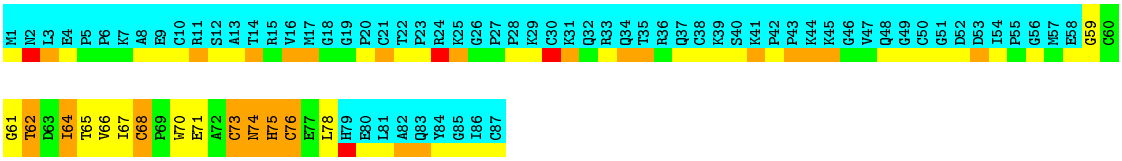
Chain A: 



4.2.67 Score per residue for model 67

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

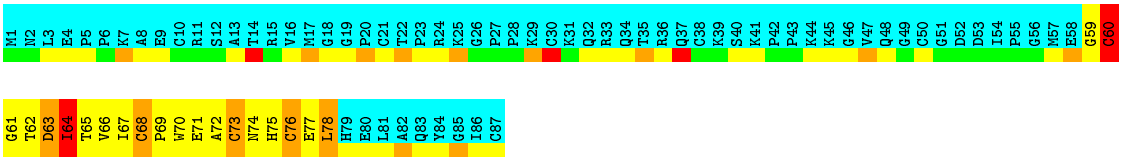
Chain A: 



4.2.68 Score per residue for model 68

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

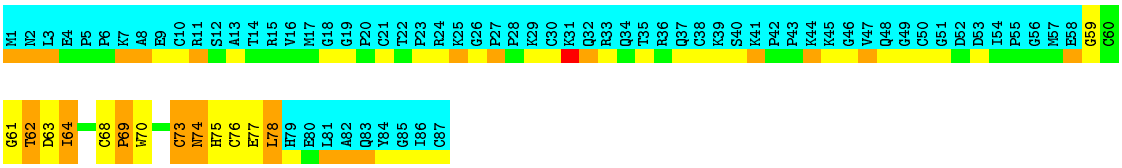
Chain A: 



4.2.69 Score per residue for model 69

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

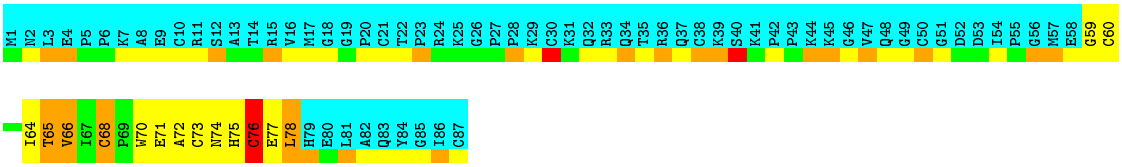
Chain A: 



4.2.70 Score per residue for model 70

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

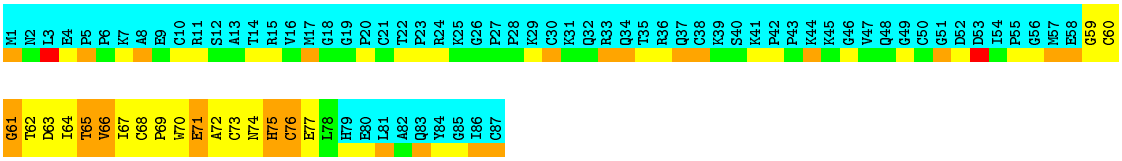
Chain A: 6% 11% 5% • 77%



4.2.71 Score per residue for model 71

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

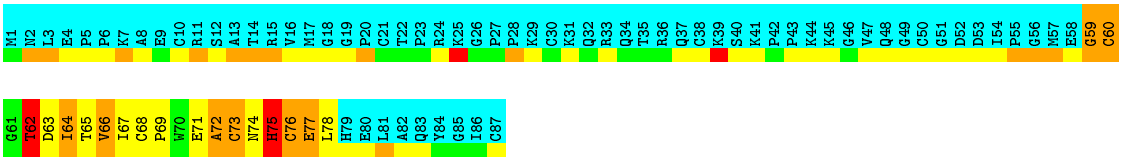
Chain A: • 15% 7% 77%



4.2.72 Score per residue for model 72

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

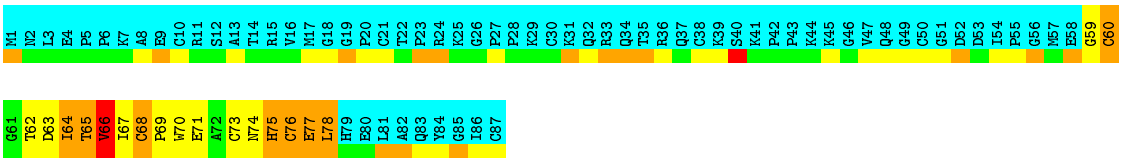
Chain A: • 9% 9% • 77%



4.2.73 Score per residue for model 73

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

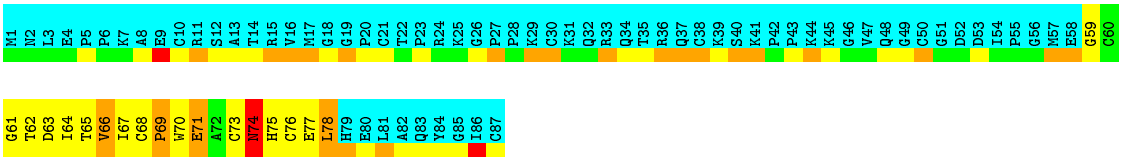
Chain A: • 10% 9% • 77%



4.2.74 Score per residue for model 74

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

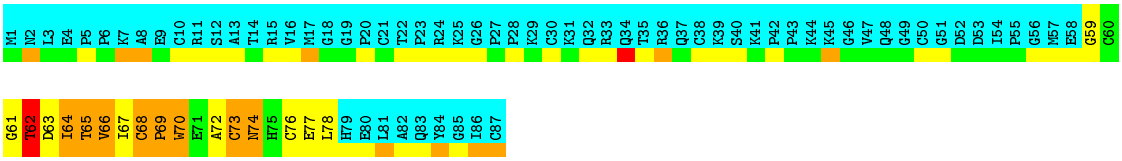
Chain A: 15% 5% 77%



4.2.75 Score per residue for model 75

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

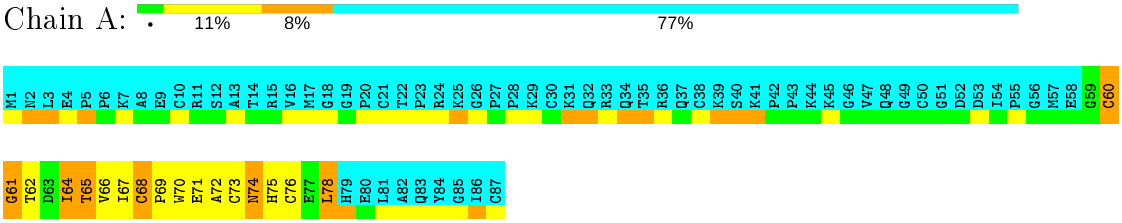
Chain A: 9% 9% 77%



4.2.76 Score per residue for model 76

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

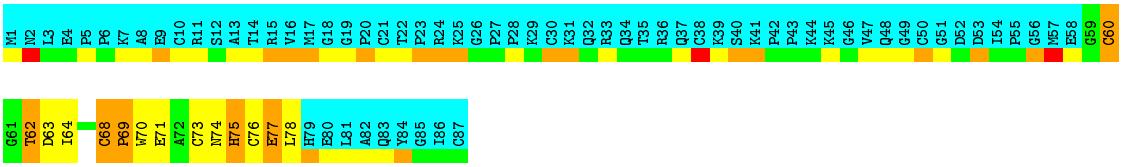
Chain A: 11% 8% 77%



4.2.77 Score per residue for model 77

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

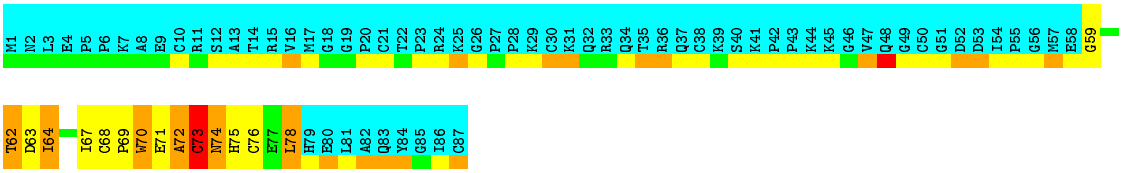
Chain A: 7% 9% 7% 77%



4.2.78 Score per residue for model 78

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

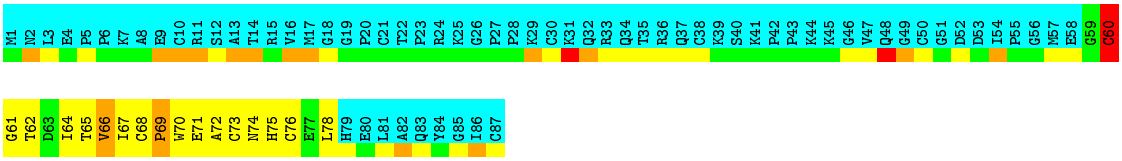
Chain A: 6% 9% 7% • 77%



4.2.79 Score per residue for model 79

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

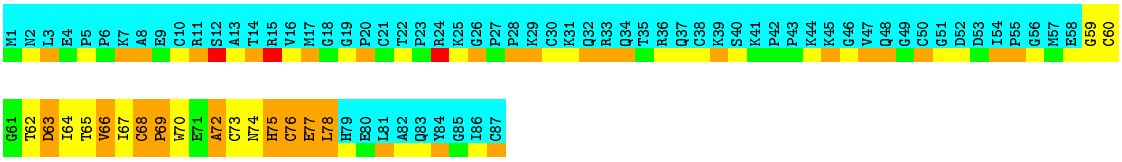
Chain A: • 16% •• 77%



4.2.80 Score per residue for model 80

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

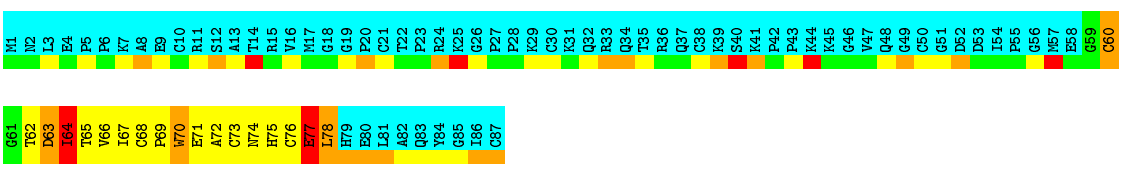
Chain A: • 10% 10% 77%



4.2.81 Score per residue for model 81

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

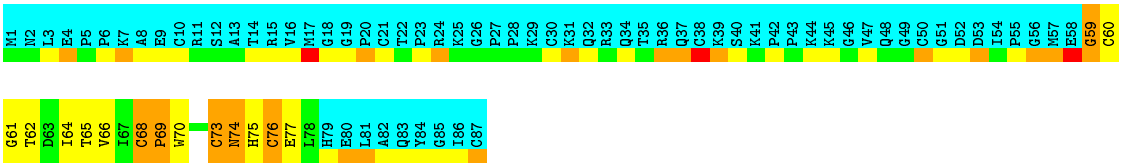
Chain A: • 14% 5% • 77%



4.2.82 Score per residue for model 82

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

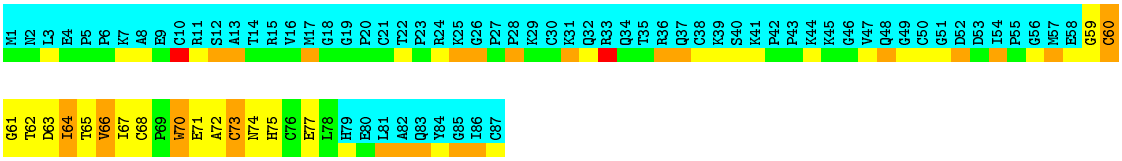
Chain A: 6% 10% 7% 77%



4.2.83 Score per residue for model 83

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

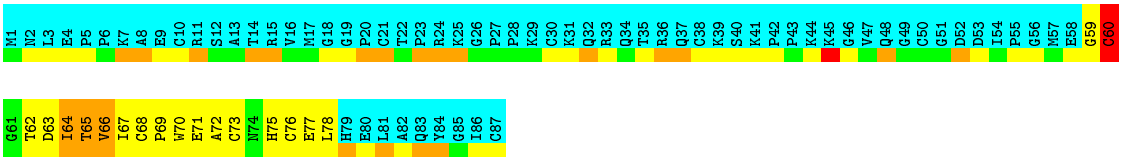
Chain A: 14% 6% 77%



4.2.84 Score per residue for model 84

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

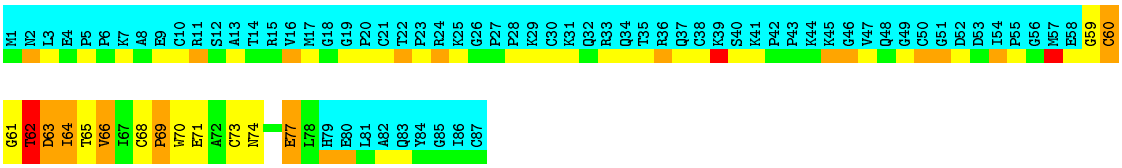
Chain A: 16% 77%



4.2.85 Score per residue for model 85

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

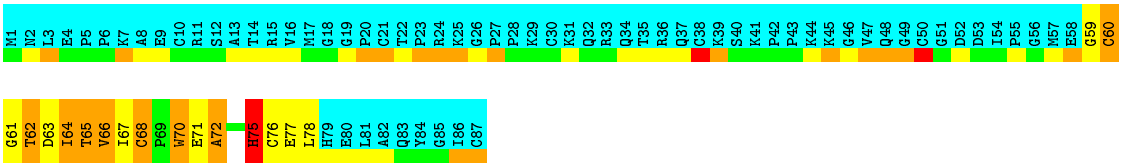
Chain A: 6% 9% 7% 77%



4.2.86 Score per residue for model 86

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

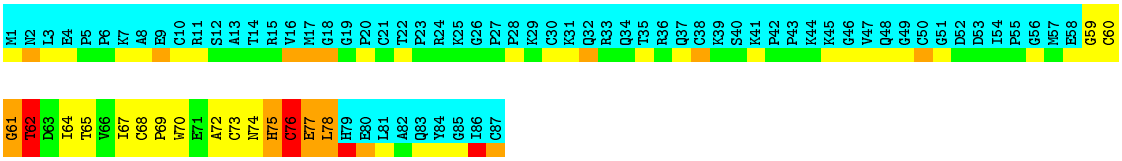
Chain A: 9% 9% 77%



4.2.87 Score per residue for model 87

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

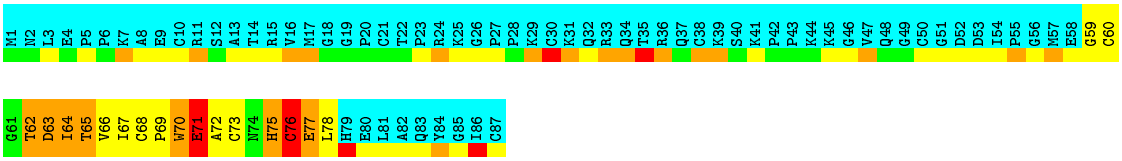
Chain A: 13% 5% 77%



4.2.88 Score per residue for model 88

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

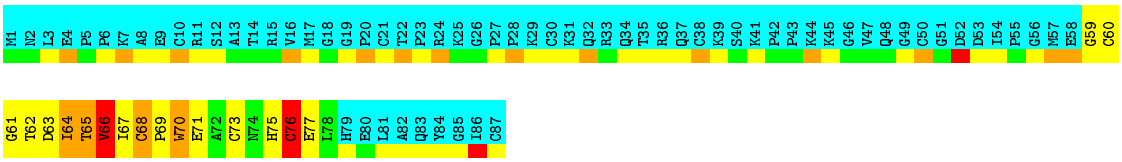
Chain A: 10% 8% 77%



4.2.89 Score per residue for model 89

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

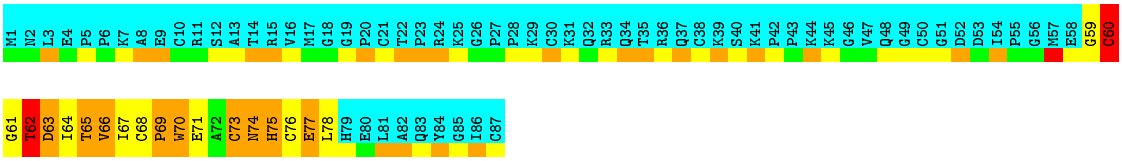
Chain A: 13% 5% 77%



4.2.90 Score per residue for model 90

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

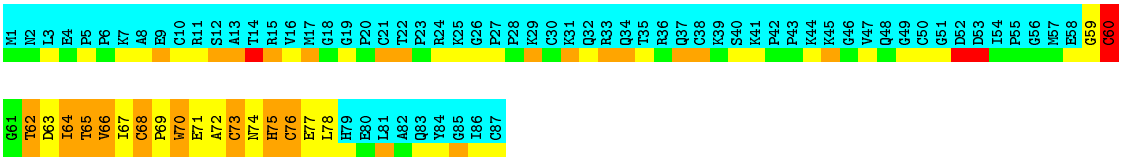
Chain A: • 9% 10% • 77%



4.2.91 Score per residue for model 91

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

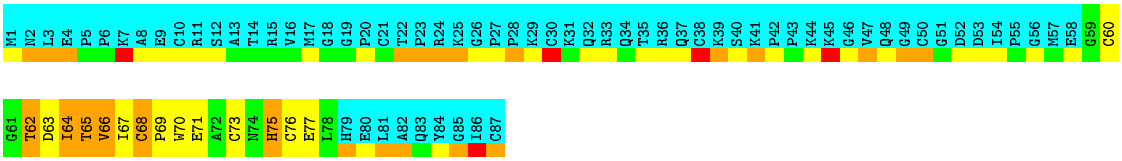
Chain A: • 10% 10% • 77%



4.2.92 Score per residue for model 92

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

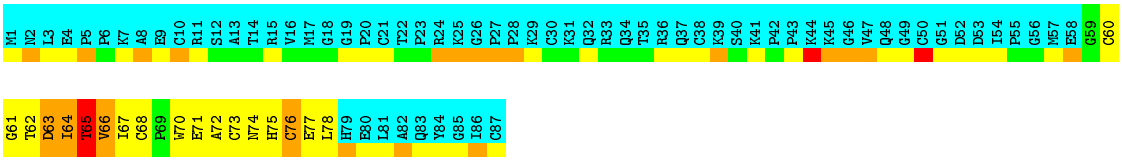
Chain A: 6% 10% 7% 77%



4.2.93 Score per residue for model 93

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

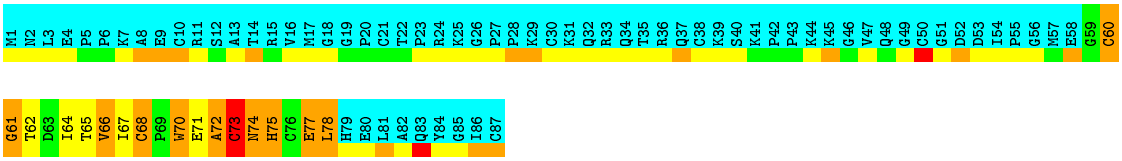
Chain A: • 15% 5% • 77%



4.2.94 Score per residue for model 94

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

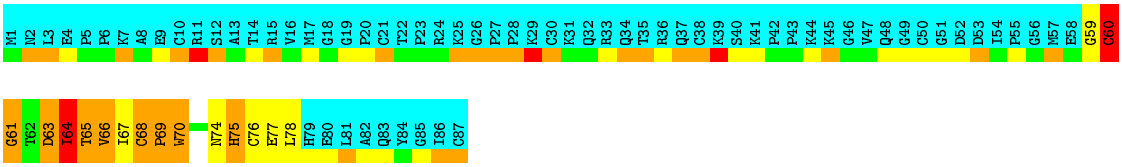
Chain A: 5% 6% 11% • 77%



4.2.95 Score per residue for model 95

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

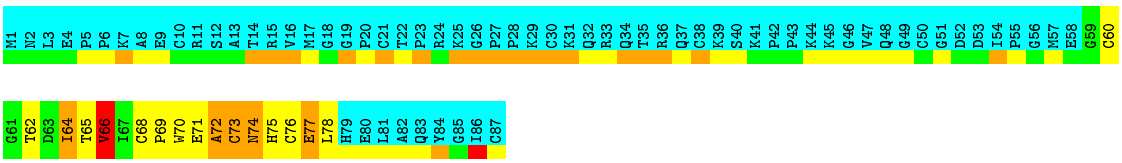
Chain A: 5% 7% 9% • 77%



4.2.96 Score per residue for model 96

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

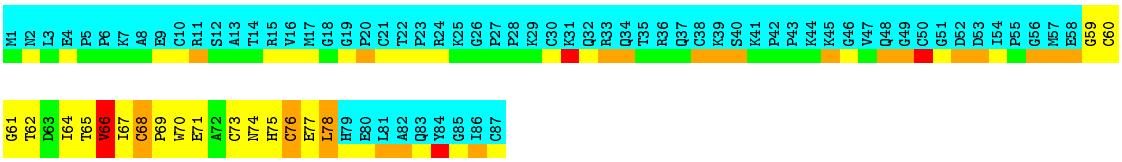
Chain A: 5% 11% 6% • 77%



4.2.97 Score per residue for model 97

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

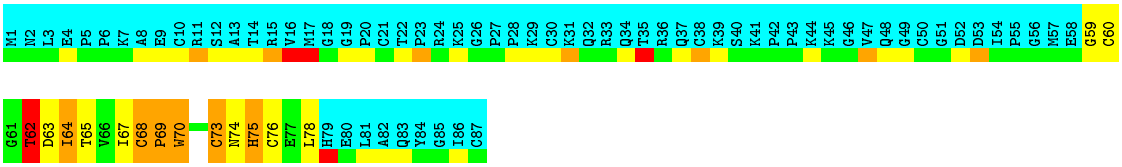
Chain A: • 16% • • 77%



4.2.98 Score per residue for model 98

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

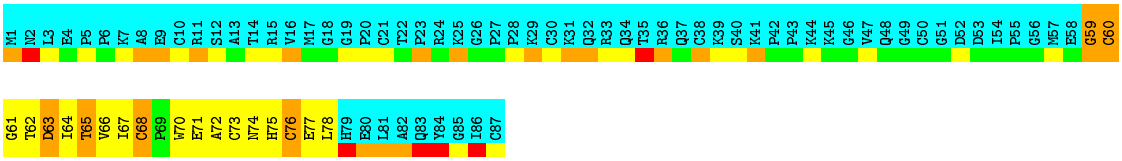
Chain A: 6% 9% 7% 77%



4.2.99 Score per residue for model 99

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

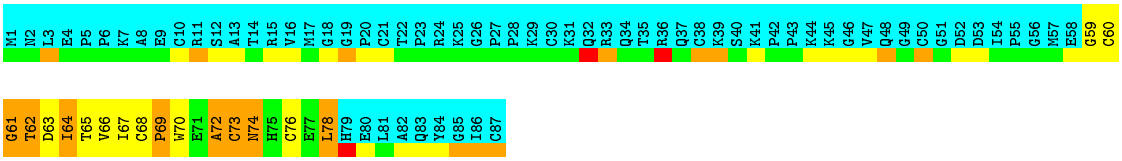
Chain A: 15% 7% 77%



4.2.100 Score per residue for model 100

• Molecule 1: Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma

Chain A: 10% 9% 77%



5 Refinement protocol and experimental data overview

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

Of the 200 calculated structures, 100 were deposited, based on the following criterion: *structures with the lowest energy.*

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

Software name	Classification	Version
XPLOR-NIH	refinement	2.11.2

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)	input_cs.cif
Number of chemical shift lists	1
Total number of shifts	845
Number of shifts mapped to atoms	727
Number of unparsed shifts	0
Number of shifts with mapping errors	118
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	68%

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

6 Model quality

6.1 Standard geometry

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

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

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no planarity outliers.

6.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	147	130	128	57±23
2	A	170	20	152	105±32
All	All	31700	15000	27846	12091

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 203.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:160:RCY:C1M	2:A:168:RCY:H1Z	1.67	1.18	9	1
1:A:70:TRP:CD1	2:A:176:RCY:H1CA	1.66	1.15	62	1
1:A:70:TRP:CZ2	2:A:168:RCY:H1MA	1.66	1.25	59	1
1:A:64:ILE:CD1	2:A:168:RCY:C1P	1.66	1.74	12	2
1:A:70:TRP:CB	2:A:121:RCY:H1V	1.65	1.17	30	1
2:A:168:RCY:C1W	2:A:173:RCY:H1VB	1.65	1.15	45	2
1:A:70:TRP:CD2	2:A:187:RCY:H1ZA	1.65	1.24	76	1
1:A:64:ILE:HD11	2:A:160:RCY:C1M	1.65	1.21	6	2
2:A:150:RCY:C1Y	2:A:160:RCY:C1Z	1.64	1.75	29	1
2:A:150:RCY:H1V	2:A:160:RCY:C1V	1.64	1.12	42	1
1:A:70:TRP:CZ2	2:A:176:RCY:H1MA	1.64	1.15	85	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:173:RCY:C1Z	2:A:176:RCY:H1M	1.64	1.12	37	1
2:A:173:RCY:C1Y	2:A:176:RCY:C1M	1.64	1.76	87	4
2:A:130:RCY:H1Y	2:A:160:RCY:C1P	1.64	1.18	50	1
2:A:173:RCY:C1P	2:A:176:RCY:H1VA	1.63	1.22	11	1
1:A:70:TRP:CD1	2:A:121:RCY:C1Y	1.63	1.76	49	1
1:A:70:TRP:CE2	2:A:176:RCY:H1YA	1.63	1.23	80	1
1:A:70:TRP:CD2	2:A:187:RCY:C1Z	1.63	1.81	76	2
2:A:173:RCY:C1C	2:A:187:RCY:C1P	1.63	1.74	88	1
2:A:173:RCY:C1Y	2:A:187:RCY:H1Z	1.63	1.16	89	3
2:A:168:RCY:H1Z	2:A:187:RCY:C1P	1.63	1.15	3	1
2:A:138:RCY:C1C	2:A:187:RCY:C1Y	1.62	1.76	100	2
2:A:168:RCY:H1L	2:A:173:RCY:C1V	1.62	1.24	4	1
2:A:130:RCY:C1Z	2:A:130:RCY:C1W	1.62	1.75	79	1
2:A:160:RCY:H1M	2:A:168:RCY:C1Z	1.62	1.20	9	1
1:A:62:THR:CG2	2:A:130:RCY:C1M	1.62	1.76	9	1
1:A:69:PRO:CG	2:A:173:RCY:C1Z	1.62	1.77	57	1
2:A:160:RCY:C1Y	2:A:168:RCY:H1S	1.61	1.10	100	2
2:A:160:RCY:C1M	2:A:168:RCY:H1V	1.61	1.24	48	1
2:A:168:RCY:H1C	2:A:173:RCY:C1Y	1.61	1.17	21	2
2:A:168:RCY:H1ZA	2:A:187:RCY:C1M	1.61	1.22	84	1
2:A:168:RCY:H1M	2:A:187:RCY:C1Z	1.61	1.21	31	3
1:A:67:ILE:CG2	2:A:173:RCY:H1C	1.61	1.15	31	1
1:A:68:CYS:H	2:A:168:RCY:C1S	1.61	1.02	27	6
2:A:160:RCY:H1M	2:A:168:RCY:C1V	1.61	1.25	48	2
2:A:173:RCY:H1C	2:A:176:RCY:C1C	1.61	1.17	8	1
1:A:66:VAL:HG11	2:A:121:RCY:C1V	1.61	1.17	83	1
2:A:150:RCY:H1VA	2:A:160:RCY:C1Y	1.60	1.24	42	1
2:A:173:RCY:H1Y	2:A:176:RCY:C1V	1.60	1.26	81	1
2:A:168:RCY:C1L	2:A:173:RCY:H1Y	1.60	1.11	62	1
1:A:64:ILE:HD12	2:A:168:RCY:C1S	1.60	1.26	12	1
1:A:70:TRP:CZ3	2:A:168:RCY:H1M	1.60	1.08	33	1
1:A:65:THR:CG2	2:A:160:RCY:H1MA	1.60	1.13	100	2
2:A:173:RCY:C1U	2:A:176:RCY:H1S	1.60	1.12	38	1
2:A:168:RCY:C1M	2:A:173:RCY:C1Y	1.59	1.74	31	2
2:A:173:RCY:C1Z	2:A:187:RCY:C1L	1.59	1.75	96	3
2:A:130:RCY:C1Y	2:A:160:RCY:C1M	1.59	1.78	50	1
1:A:70:TRP:CZ2	2:A:176:RCY:H1V	1.59	1.08	4	1
2:A:130:RCY:C1V	2:A:160:RCY:C1S	1.59	1.74	8	1
2:A:138:RCY:C1L	2:A:150:RCY:C1Q	1.59	1.80	23	1
2:A:176:RCY:C1X	2:A:176:RCY:C1U	1.59	1.79	25	1
2:A:138:RCY:C1Y	2:A:176:RCY:C1V	1.59	1.78	22	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:173:RCY:C1P	2:A:176:RCY:H1VB	1.59	1.23	19	2
1:A:62:THR:CG2	2:A:173:RCY:H1VA	1.59	1.22	18	1
1:A:70:TRP:CZ3	2:A:168:RCY:H1L	1.59	1.30	48	1
1:A:70:TRP:CZ3	2:A:168:RCY:H1ZA	1.59	1.32	98	2
2:A:168:RCY:H1C	2:A:173:RCY:C1M	1.59	1.23	99	1
2:A:168:RCY:H1ZA	2:A:187:RCY:C1P	1.58	1.21	100	1
1:A:71:GLU:CG	2:A:168:RCY:H1CB	1.58	1.07	93	3
1:A:70:TRP:CD1	2:A:176:RCY:C1C	1.58	1.79	62	1
2:A:110:RCY:H1C	2:A:121:RCY:C1Y	1.58	1.23	5	1
2:A:160:RCY:C1Z	2:A:168:RCY:H1YB	1.58	1.21	43	2
2:A:176:RCY:C1Y	2:A:187:RCY:C1Y	1.58	1.74	5	1
2:A:160:RCY:C1P	2:A:168:RCY:H1Y	1.58	1.29	9	1
2:A:150:RCY:H1MA	2:A:168:RCY:C1Y	1.58	1.22	74	1
2:A:168:RCY:C1S	2:A:176:RCY:C1Z	1.58	1.77	77	1
2:A:138:RCY:C1V	2:A:150:RCY:H1M	1.58	1.24	1	1
2:A:160:RCY:C1Z	2:A:173:RCY:C1C	1.57	1.76	86	2
2:A:176:RCY:C1U	2:A:187:RCY:H1Z	1.57	1.17	5	1
2:A:168:RCY:H1ZA	2:A:173:RCY:C1P	1.57	1.19	58	1
1:A:76:CYS:N	2:A:173:RCY:C1C	1.57	1.67	29	1
2:A:138:RCY:C1C	2:A:150:RCY:H1VA	1.57	1.24	10	2
2:A:160:RCY:H1YB	2:A:173:RCY:C1Z	1.57	1.06	4	2
2:A:173:RCY:C1Y	2:A:187:RCY:C1Q	1.57	1.76	92	2
1:A:73:CYS:SG	2:A:173:RCY:H1SA	1.57	1.39	79	1
1:A:78:LEU:HD21	2:A:176:RCY:C1W	1.57	1.23	91	1
1:A:70:TRP:CE3	2:A:173:RCY:H1ZA	1.57	1.03	92	2
2:A:138:RCY:C1M	2:A:173:RCY:C1V	1.57	1.77	92	1
1:A:69:PRO:HD3	2:A:173:RCY:C1Z	1.57	1.27	61	1
2:A:176:RCY:H1CB	2:A:187:RCY:C1Y	1.57	1.05	26	1
2:A:173:RCY:C1C	2:A:176:RCY:C1V	1.57	1.75	63	2
2:A:176:RCY:C1Y	2:A:187:RCY:C1L	1.57	1.76	92	1
2:A:150:RCY:H1Z	2:A:160:RCY:C1Y	1.56	1.08	88	1
1:A:69:PRO:HB2	2:A:173:RCY:C1Y	1.56	1.28	35	1
2:A:160:RCY:C1X	2:A:160:RCY:C1U	1.56	1.75	79	1
1:A:78:LEU:CG	2:A:176:RCY:H1MA	1.56	1.16	91	1
1:A:67:ILE:HB	2:A:150:RCY:C1V	1.56	1.27	31	1
2:A:168:RCY:C1V	2:A:176:RCY:H1M	1.56	1.13	20	3
2:A:138:RCY:H1C	2:A:150:RCY:C1Z	1.56	1.30	29	1
2:A:168:RCY:H1YA	2:A:173:RCY:C1X	1.56	1.22	45	1
2:A:168:RCY:C1M	2:A:187:RCY:H1Z	1.56	1.23	31	2
2:A:138:RCY:H1V	2:A:150:RCY:C1Z	1.56	1.20	87	1
1:A:66:VAL:CG1	2:A:121:RCY:H1V	1.56	1.09	83	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:168:RCY:C1Y	2:A:187:RCY:H1ZB	1.55	1.20	21	1
2:A:138:RCY:C1Y	2:A:187:RCY:H1YA	1.55	1.26	86	1
2:A:138:RCY:H1YA	2:A:187:RCY:C1Y	1.55	1.27	86	2
2:A:138:RCY:C1M	2:A:150:RCY:C1V	1.55	1.85	19	2
2:A:160:RCY:C1Z	2:A:168:RCY:C1V	1.55	1.80	55	3
1:A:73:CYS:H	2:A:173:RCY:C1L	1.55	1.09	10	5
1:A:64:ILE:CD1	2:A:160:RCY:C1Y	1.55	1.77	49	1
2:A:150:RCY:C1Z	2:A:176:RCY:C1C	1.55	1.83	3	1
2:A:173:RCY:C1W	2:A:176:RCY:C1C	1.55	1.76	38	1
2:A:173:RCY:H1Z	2:A:187:RCY:C1Z	1.55	1.29	84	1
2:A:173:RCY:H1M	2:A:187:RCY:C1Y	1.55	1.15	31	1
2:A:168:RCY:C1Z	2:A:173:RCY:C1U	1.55	1.75	70	3
2:A:168:RCY:C1V	2:A:173:RCY:H1MA	1.55	1.31	29	1
2:A:160:RCY:H1Z	2:A:168:RCY:C1C	1.55	1.28	69	1
2:A:138:RCY:H1C	2:A:187:RCY:C1M	1.55	1.22	11	1
2:A:173:RCY:C1Y	2:A:187:RCY:H1Y	1.55	1.29	31	1
2:A:168:RCY:C1M	2:A:173:RCY:H1V	1.55	1.09	27	1
1:A:72:ALA:HB1	2:A:173:RCY:C1P	1.54	1.08	30	3
2:A:168:RCY:C1Y	2:A:187:RCY:C1W	1.54	1.76	97	1
2:A:168:RCY:H1LA	2:A:173:RCY:C1Y	1.54	1.31	62	1
2:A:138:RCY:H1YB	2:A:150:RCY:C1Q	1.54	1.30	60	2
2:A:130:RCY:H1U	2:A:160:RCY:C1M	1.54	1.20	7	1
2:A:160:RCY:H1VA	2:A:168:RCY:C1Y	1.54	1.08	32	1
2:A:160:RCY:C1Z	2:A:168:RCY:H1V	1.54	1.04	55	2
1:A:71:GLU:CB	2:A:168:RCY:H1MA	1.54	1.27	37	1
2:A:160:RCY:C1Y	2:A:173:RCY:H1Z	1.54	1.03	4	1
2:A:173:RCY:C1Z	2:A:187:RCY:H1ZA	1.54	1.19	84	2
1:A:62:THR:HG21	2:A:173:RCY:C1V	1.54	1.29	18	1
1:A:59:GLY:CA	2:A:160:RCY:C1P	1.54	1.75	70	1
2:A:160:RCY:H1MA	2:A:168:RCY:C1S	1.54	1.33	34	1
1:A:67:ILE:HG22	2:A:173:RCY:C1M	1.54	1.04	80	1
2:A:168:RCY:H1YA	2:A:187:RCY:C1S	1.53	1.32	88	1
2:A:173:RCY:H1YA	2:A:187:RCY:C1Z	1.53	1.28	89	3
2:A:168:RCY:C1Q	2:A:168:RCY:N1R	1.53	1.67	79	1
2:A:176:RCY:C1C	2:A:187:RCY:C1W	1.53	1.82	4	1
1:A:70:TRP:CZ3	2:A:150:RCY:H1Y	1.53	1.33	47	1
1:A:62:THR:CG2	2:A:160:RCY:H1ZB	1.53	1.33	46	1
2:A:138:RCY:N1R	2:A:138:RCY:C1U	1.53	1.71	25	1
2:A:138:RCY:C1M	2:A:150:RCY:H1C	1.53	1.33	97	2
1:A:70:TRP:CZ3	2:A:168:RCY:H1Z	1.53	1.32	41	1
2:A:160:RCY:H1YB	2:A:168:RCY:C1P	1.53	1.21	58	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:110:RCY:C1Y	2:A:121:RCY:H1C	1.53	1.30	81	1
2:A:160:RCY:N1R	2:A:160:RCY:C1U	1.53	1.72	79	2
2:A:168:RCY:H1V	2:A:173:RCY:C1C	1.53	1.07	45	1
1:A:70:TRP:CB	2:A:121:RCY:C1V	1.53	1.87	30	1
2:A:176:RCY:C1C	2:A:187:RCY:C1Y	1.53	1.80	26	2
1:A:65:THR:HB	2:A:168:RCY:C1P	1.53	1.05	80	1
2:A:173:RCY:C1V	2:A:176:RCY:C1Y	1.53	1.87	2	6
2:A:110:RCY:C1C	2:A:121:RCY:H1YB	1.53	1.26	5	1
2:A:138:RCY:C1M	2:A:150:RCY:H1VB	1.52	1.32	19	1
2:A:168:RCY:C1C	2:A:173:RCY:H1M	1.52	1.27	99	1
2:A:138:RCY:H1U	2:A:187:RCY:C1C	1.52	1.06	5	1
2:A:168:RCY:C1W	2:A:187:RCY:C1Z	1.52	1.80	97	1
2:A:160:RCY:C1M	2:A:168:RCY:H1S	1.52	1.28	34	1
1:A:69:PRO:C	2:A:173:RCY:H1Z	1.52	1.22	85	1
2:A:150:RCY:H1VA	2:A:173:RCY:C1V	1.52	1.30	31	1
1:A:78:LEU:CD2	2:A:176:RCY:C1M	1.52	1.84	91	1
1:A:64:ILE:HD11	2:A:168:RCY:C1P	1.52	1.27	12	2
2:A:168:RCY:C1U	2:A:176:RCY:C1Y	1.52	1.87	59	3
1:A:67:ILE:HG13	2:A:176:RCY:C1V	1.52	1.34	16	1
2:A:168:RCY:C1M	2:A:187:RCY:C1Y	1.52	1.87	7	2
2:A:168:RCY:C1U	2:A:176:RCY:H1YB	1.52	1.30	98	1
2:A:130:RCY:C1Z	2:A:160:RCY:C1P	1.52	1.85	61	1
2:A:173:RCY:C1C	2:A:176:RCY:C1P	1.52	1.83	72	1
1:A:62:THR:HG21	2:A:160:RCY:C1Z	1.52	1.27	46	1
1:A:73:CYS:H	2:A:173:RCY:C1S	1.51	1.07	21	5
2:A:150:RCY:C1Z	2:A:160:RCY:C1Y	1.51	1.84	88	1
2:A:150:RCY:C1Y	2:A:187:RCY:H1YB	1.51	1.28	41	3
2:A:173:RCY:H1VB	2:A:187:RCY:C1C	1.51	1.31	55	1
1:A:76:CYS:C	2:A:176:RCY:H1LA	1.51	1.26	31	5
2:A:168:RCY:C1Z	2:A:187:RCY:C1P	1.51	1.85	100	2
2:A:168:RCY:H1MA	2:A:187:RCY:C1Z	1.51	0.99	84	1
1:A:69:PRO:HG3	2:A:187:RCY:C1Z	1.51	1.33	54	1
2:A:130:RCY:C1Z	2:A:160:RCY:C1L	1.51	1.89	61	1
2:A:160:RCY:C1Z	2:A:168:RCY:H1C	1.51	1.04	69	1
2:A:176:RCY:C1M	2:A:187:RCY:C1Y	1.51	1.84	5	1
2:A:173:RCY:C1S	2:A:176:RCY:H1LA	1.51	1.31	28	2
2:A:173:RCY:C1U	2:A:173:RCY:N1R	1.51	1.69	79	1
2:A:168:RCY:C1S	2:A:173:RCY:H1U	1.51	1.35	71	1
1:A:75:HIS:NE2	2:A:173:RCY:C1Z	1.51	1.74	42	1
2:A:168:RCY:C1Y	2:A:176:RCY:C1V	1.51	1.88	94	2
2:A:176:RCY:C1U	2:A:176:RCY:N1R	1.51	1.73	79	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:160:RCY:H1U	2:A:168:RCY:C1C	1.51	1.02	49	1
1:A:69:PRO:HG2	2:A:173:RCY:C1C	1.51	1.08	77	1
2:A:138:RCY:C1M	2:A:150:RCY:C1P	1.51	1.89	1	1
2:A:173:RCY:C1U	2:A:176:RCY:C1V	1.50	1.86	89	2
1:A:69:PRO:CG	2:A:187:RCY:H1ZB	1.50	1.26	54	1
1:A:64:ILE:HG13	2:A:160:RCY:C1Y	1.50	1.31	19	1
2:A:168:RCY:C1L	2:A:173:RCY:C1Y	1.50	1.85	62	1
2:A:173:RCY:C1V	2:A:176:RCY:H1YB	1.50	1.37	32	3
2:A:160:RCY:C1Y	2:A:168:RCY:H1CB	1.50	1.30	47	1
1:A:63:ASP:CB	2:A:130:RCY:H1YB	1.50	1.36	73	1
2:A:160:RCY:C1S	2:A:160:RCY:C1Q	1.50	1.85	25	1
1:A:60:CYS:C	2:A:138:RCY:H1VB	1.50	1.11	7	1
1:A:70:TRP:C	2:A:173:RCY:C1V	1.50	1.78	84	2
2:A:173:RCY:C1Y	2:A:176:RCY:H1CA	1.50	1.34	98	2
1:A:72:ALA:CB	2:A:173:RCY:H1L	1.50	1.34	10	1
2:A:176:RCY:H1M	2:A:187:RCY:C1Y	1.50	1.15	5	1
1:A:60:CYS:SG	2:A:160:RCY:H1SA	1.50	1.45	79	2
1:A:70:TRP:CZ3	2:A:168:RCY:H1V	1.50	1.38	56	1
1:A:66:VAL:HG12	2:A:121:RCY:C1Y	1.50	0.98	83	1
2:A:150:RCY:H1M	2:A:160:RCY:C1V	1.50	1.30	42	1
2:A:173:RCY:C1P	2:A:176:RCY:C1V	1.50	1.85	11	4
1:A:73:CYS:CB	2:A:176:RCY:C1C	1.50	1.83	52	1
2:A:138:RCY:H1L	2:A:150:RCY:C1Q	1.50	1.34	23	1
1:A:64:ILE:HB	2:A:168:RCY:C1Z	1.49	1.33	30	2
2:A:173:RCY:C1L	2:A:176:RCY:C1C	1.49	1.76	52	1
1:A:71:GLU:HA	2:A:173:RCY:C1P	1.49	1.28	17	2
2:A:176:RCY:C1Z	2:A:187:RCY:H1C	1.49	1.32	64	1
1:A:70:TRP:HZ3	2:A:168:RCY:C1M	1.49	1.18	33	1
1:A:77:GLU:N	2:A:176:RCY:C1L	1.49	1.71	87	3
1:A:62:THR:HG21	2:A:160:RCY:C1V	1.49	1.36	55	1
2:A:168:RCY:C1C	2:A:173:RCY:H1YA	1.49	1.01	21	2
2:A:168:RCY:C1V	2:A:173:RCY:H1CB	1.49	0.99	45	1
2:A:173:RCY:N1R	2:A:173:RCY:C1U	1.49	1.71	25	1
2:A:176:RCY:C1C	2:A:187:RCY:H1YB	1.49	1.24	26	1
2:A:150:RCY:C1U	2:A:150:RCY:N1R	1.49	1.76	79	2
2:A:160:RCY:H1U	2:A:168:RCY:C1M	1.49	1.01	96	1
1:A:70:TRP:CG	2:A:173:RCY:C1Y	1.49	1.95	84	2
1:A:70:TRP:CG	2:A:173:RCY:H1YA	1.49	1.40	84	1
2:A:110:RCY:C1Y	2:A:121:RCY:C1C	1.49	1.89	81	1
2:A:173:RCY:C1Y	2:A:187:RCY:H1ZB	1.49	1.36	92	1
1:A:73:CYS:N	2:A:173:RCY:H1LA	1.48	1.22	10	4

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:138:RCY:C1Y	2:A:150:RCY:C1Y	1.48	1.88	89	3
2:A:110:RCY:C1U	2:A:110:RCY:N1R	1.48	1.74	79	1
1:A:59:GLY:HA2	2:A:160:RCY:C1P	1.48	0.98	70	2
1:A:78:LEU:HD21	2:A:176:RCY:C1M	1.48	1.36	91	1
2:A:160:RCY:C1U	2:A:168:RCY:C1C	1.48	1.89	49	1
2:A:168:RCY:H1MA	2:A:173:RCY:C1V	1.48	0.97	27	1
1:A:70:TRP:CE3	2:A:176:RCY:C1Y	1.48	1.95	94	1
2:A:176:RCY:C1V	2:A:187:RCY:H1YA	1.48	1.32	54	2
1:A:64:ILE:CD1	2:A:160:RCY:C1M	1.48	1.87	6	2
1:A:70:TRP:CH2	2:A:168:RCY:C1P	1.48	1.91	48	2
1:A:70:TRP:CZ3	2:A:168:RCY:C1M	1.48	1.96	33	4
1:A:73:CYS:HA	2:A:173:RCY:C1L	1.48	1.23	38	7
2:A:150:RCY:C1V	2:A:160:RCY:H1YA	1.48	1.35	42	1
1:A:70:TRP:CB	2:A:173:RCY:H1YA	1.48	1.36	84	1
2:A:138:RCY:C1M	2:A:187:RCY:C1Y	1.48	1.87	68	1
2:A:168:RCY:C1C	2:A:176:RCY:H1Y	1.48	1.34	59	2
1:A:70:TRP:CH2	2:A:168:RCY:C1L	1.48	1.96	48	1
2:A:168:RCY:C1Q	2:A:173:RCY:H1U	1.48	1.32	71	2
2:A:173:RCY:C1V	2:A:187:RCY:H1C	1.48	1.34	55	1
2:A:138:RCY:C1Y	2:A:187:RCY:C1Y	1.48	1.84	86	3
2:A:168:RCY:C1M	2:A:187:RCY:C1Z	1.48	1.89	84	3
1:A:69:PRO:CB	2:A:150:RCY:H1ZB	1.48	1.34	92	1
2:A:168:RCY:H1ZA	2:A:187:RCY:C1S	1.48	1.35	100	1
2:A:173:RCY:H1VB	2:A:187:RCY:C1X	1.48	1.35	55	1
1:A:69:PRO:C	2:A:173:RCY:C1V	1.48	1.79	64	1
1:A:63:ASP:CG	2:A:160:RCY:H1ZA	1.48	1.23	73	1
2:A:130:RCY:C1U	2:A:130:RCY:N1R	1.48	1.76	25	1
1:A:67:ILE:HG21	2:A:130:RCY:C1M	1.48	1.35	30	1
1:A:69:PRO:HD2	2:A:168:RCY:C1L	1.47	1.38	78	9
2:A:187:RCY:C1U	2:A:187:RCY:N1R	1.47	1.74	79	2
2:A:110:RCY:N1R	2:A:110:RCY:C1U	1.47	1.72	25	1
1:A:64:ILE:HG21	2:A:168:RCY:C1Z	1.47	1.32	83	1
2:A:173:RCY:H1C	2:A:187:RCY:C1M	1.47	1.37	97	1
1:A:63:ASP:HB3	2:A:130:RCY:C1Y	1.47	1.35	73	1
2:A:173:RCY:H1CB	2:A:176:RCY:C1P	1.47	1.31	72	2
2:A:150:RCY:C1V	2:A:173:RCY:H1VA	1.47	1.34	31	1
1:A:70:TRP:HZ3	2:A:150:RCY:C1Y	1.47	1.18	47	1
1:A:70:TRP:CD2	2:A:176:RCY:H1YA	1.47	1.41	80	1
2:A:176:RCY:N1R	2:A:176:RCY:C1Q	1.47	1.77	25	1
1:A:70:TRP:CB	2:A:176:RCY:H1ZA	1.47	1.39	18	2
1:A:71:GLU:CA	2:A:168:RCY:H1MA	1.47	1.37	37	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:160:RCY:C1V	2:A:168:RCY:C1Y	1.47	1.89	32	1
2:A:168:RCY:H1VA	2:A:176:RCY:C1M	1.47	1.39	20	1
2:A:168:RCY:C1Q	2:A:173:RCY:H1ZA	1.46	1.38	39	2
1:A:69:PRO:CD	2:A:168:RCY:H1S	1.46	1.40	75	3
2:A:138:RCY:C1M	2:A:187:RCY:H1YB	1.46	0.96	68	1
1:A:70:TRP:HZ3	2:A:168:RCY:C1V	1.46	1.22	56	1
2:A:168:RCY:H1ZA	2:A:187:RCY:C1L	1.46	1.36	100	1
2:A:138:RCY:C1Y	2:A:150:RCY:N1R	1.46	1.74	60	1
1:A:70:TRP:HB2	2:A:173:RCY:C1V	1.46	1.39	4	2
2:A:138:RCY:C1U	2:A:138:RCY:N1R	1.46	1.76	79	1
1:A:65:THR:HG21	2:A:160:RCY:C1M	1.46	1.33	100	3
1:A:70:TRP:CB	2:A:173:RCY:H1VB	1.46	1.36	4	1
2:A:160:RCY:C1Y	2:A:168:RCY:C1S	1.46	1.89	100	2
2:A:121:RCY:C1U	2:A:121:RCY:N1R	1.46	1.74	25	2
2:A:138:RCY:C1C	2:A:150:RCY:H1ZA	1.46	1.39	29	1
1:A:62:THR:HG21	2:A:168:RCY:C1Z	1.46	1.35	72	1
2:A:138:RCY:C1U	2:A:187:RCY:C1C	1.46	1.92	5	1
1:A:70:TRP:N	2:A:173:RCY:H1Z	1.46	1.08	85	1
2:A:168:RCY:C1Q	2:A:173:RCY:C1U	1.46	1.83	71	1
2:A:173:RCY:C1C	2:A:176:RCY:H1M	1.45	1.30	52	2
1:A:66:VAL:CG1	2:A:121:RCY:H1YA	1.45	0.93	83	1
2:A:173:RCY:C1Q	2:A:173:RCY:C1S	1.45	1.76	79	1
1:A:62:THR:CB	2:A:160:RCY:H1CA	1.45	1.38	46	1
1:A:71:GLU:CG	2:A:168:RCY:C1C	1.45	1.92	93	1
1:A:69:PRO:CB	2:A:176:RCY:C1Z	1.45	1.93	66	1
2:A:173:RCY:C1C	2:A:187:RCY:H1M	1.45	1.41	97	1
2:A:173:RCY:H1V	2:A:176:RCY:C1U	1.45	1.36	38	2
2:A:138:RCY:O1J	2:A:160:RCY:C1Q	1.45	1.64	18	1
1:A:70:TRP:HE1	2:A:121:RCY:C1W	1.45	1.21	49	1
2:A:130:RCY:C1C	2:A:160:RCY:C1U	1.45	1.76	7	1
2:A:168:RCY:C1Y	2:A:176:RCY:O1G	1.45	1.63	20	1
2:A:168:RCY:C1Z	2:A:187:RCY:C1S	1.45	1.92	100	2
1:A:64:ILE:HD13	2:A:160:RCY:C1Y	1.45	0.93	49	1
1:A:69:PRO:HB2	2:A:176:RCY:C1Z	1.45	1.38	66	1
2:A:168:RCY:C1Y	2:A:187:RCY:H1S	1.44	1.41	88	3
2:A:138:RCY:C1V	2:A:150:RCY:H1VA	1.44	1.41	19	1
1:A:68:CYS:CB	2:A:160:RCY:H1Y	1.44	1.40	19	1
1:A:70:TRP:CD1	2:A:173:RCY:H1YB	1.44	1.46	84	1
1:A:68:CYS:O	2:A:173:RCY:C1V	1.44	1.64	100	2
1:A:70:TRP:CZ3	2:A:168:RCY:C1Z	1.44	2.00	41	3
2:A:173:RCY:C1Z	2:A:187:RCY:C1Z	1.44	1.88	84	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:160:RCY:C1V	2:A:168:RCY:H1VB	1.44	1.42	48	1
2:A:138:RCY:C1Z	2:A:187:RCY:C1C	1.44	1.75	71	3
1:A:71:GLU:HG2	2:A:168:RCY:C1C	1.44	1.42	93	2
2:A:168:RCY:O1J	2:A:187:RCY:C1M	1.44	1.66	70	1
2:A:160:RCY:H1CA	2:A:168:RCY:N1R	1.44	1.25	39	1
1:A:69:PRO:CB	2:A:173:RCY:C1Z	1.44	1.96	57	4
2:A:138:RCY:C1C	2:A:150:RCY:H1V	1.44	1.41	54	1
2:A:168:RCY:H1M	2:A:187:RCY:C1Y	1.43	1.39	7	2
1:A:75:HIS:CA	2:A:176:RCY:H1L	1.43	1.40	13	1
2:A:173:RCY:C1L	2:A:176:RCY:H1VB	1.43	1.43	11	1
2:A:168:RCY:H1LA	2:A:173:RCY:C1V	1.43	1.41	80	1
1:A:70:TRP:CD1	2:A:176:RCY:C1Y	1.43	1.99	80	1
2:A:160:RCY:H1Z	2:A:168:RCY:C1Z	1.43	0.92	78	1
2:A:160:RCY:C1Z	2:A:168:RCY:H1Z	1.43	0.94	78	1
2:A:110:RCY:O1J	2:A:121:RCY:C1V	1.43	1.66	5	1
1:A:69:PRO:CG	2:A:187:RCY:C1Z	1.43	1.90	54	1
1:A:76:CYS:CA	2:A:176:RCY:O1H	1.43	1.65	74	3
1:A:74:ASN:OD1	2:A:176:RCY:C1L	1.43	1.65	78	1
1:A:69:PRO:CD	2:A:173:RCY:H1ZA	1.43	1.41	61	1
2:A:138:RCY:C1Z	2:A:150:RCY:O1G	1.43	1.66	98	3
2:A:138:RCY:H1Z	2:A:187:RCY:C1C	1.43	1.42	74	2
1:A:70:TRP:CG	2:A:176:RCY:C1Y	1.43	2.00	80	1
1:A:72:ALA:N	2:A:173:RCY:H1M	1.43	1.24	78	1
2:A:130:RCY:H1ZA	2:A:160:RCY:C1L	1.43	1.39	61	1
2:A:173:RCY:H1U	2:A:176:RCY:C1S	1.43	0.90	38	1
2:A:150:RCY:C1M	2:A:160:RCY:C1V	1.43	1.96	42	1
1:A:63:ASP:CB	2:A:168:RCY:H1VA	1.43	1.41	5	1
2:A:168:RCY:H1U	2:A:176:RCY:C1Y	1.43	1.42	98	2
2:A:168:RCY:H1ZA	2:A:173:RCY:N1R	1.43	1.22	58	1
1:A:69:PRO:CB	2:A:173:RCY:C1C	1.43	1.89	7	1
2:A:168:RCY:C1Y	2:A:187:RCY:C1Z	1.43	1.97	21	3
1:A:70:TRP:HZ3	2:A:168:RCY:C1Z	1.42	1.24	98	3
2:A:138:RCY:C1Y	2:A:187:RCY:O1G	1.42	1.67	89	2
2:A:187:RCY:C1Q	2:A:187:RCY:N1R	1.42	1.74	25	1
2:A:176:RCY:C1Y	2:A:187:RCY:C1Q	1.42	1.74	19	1
1:A:76:CYS:CB	2:A:173:RCY:C1C	1.42	1.93	29	1
1:A:71:GLU:HA	2:A:168:RCY:C1C	1.42	1.44	29	1
1:A:72:ALA:HB3	2:A:173:RCY:C1L	1.42	1.42	10	1
1:A:70:TRP:N	2:A:176:RCY:H1C	1.42	1.05	13	1
1:A:70:TRP:CE2	2:A:176:RCY:C1M	1.42	1.83	4	2
2:A:168:RCY:C1L	2:A:173:RCY:H1V	1.42	1.43	4	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:173:RCY:C1M	2:A:176:RCY:C1V	1.42	1.83	89	4
1:A:73:CYS:CA	2:A:173:RCY:H1LA	1.42	1.19	71	8
2:A:150:RCY:C1Q	2:A:150:RCY:N1R	1.42	1.68	79	1
2:A:160:RCY:H1YA	2:A:168:RCY:C1C	1.42	1.39	47	1
1:A:64:ILE:CD1	2:A:168:RCY:C1L	1.42	1.95	12	2
2:A:173:RCY:H1VA	2:A:176:RCY:C1Y	1.42	1.44	32	3
2:A:168:RCY:C1M	2:A:173:RCY:O1H	1.42	1.65	36	1
1:A:64:ILE:CG2	2:A:160:RCY:H1YB	1.41	1.42	49	2
2:A:110:RCY:C1Z	2:A:121:RCY:O1J	1.41	1.66	33	1
2:A:173:RCY:C1U	2:A:187:RCY:C1Y	1.41	1.93	70	1
1:A:78:LEU:HD11	2:A:176:RCY:N1R	1.41	1.28	56	1
2:A:130:RCY:H1ZA	2:A:160:RCY:C1P	1.41	0.89	61	1
1:A:70:TRP:CH2	2:A:168:RCY:O1G	1.41	1.68	48	3
2:A:130:RCY:O1J	2:A:138:RCY:C1L	1.41	1.68	58	2
1:A:70:TRP:CE3	2:A:168:RCY:O1G	1.41	1.69	94	4
2:A:168:RCY:C1V	2:A:176:RCY:H1YA	1.41	1.41	76	2
2:A:130:RCY:N1V	2:A:130:RCY:C1M	1.41	1.83	79	1
2:A:138:RCY:C1Y	2:A:150:RCY:H1Y	1.41	1.34	9	1
1:A:72:ALA:H	2:A:173:RCY:C1M	1.41	1.27	78	1
1:A:75:HIS:CD2	2:A:173:RCY:H1Z	1.41	1.51	42	1
1:A:71:GLU:CB	2:A:168:RCY:C1L	1.41	1.89	57	5
1:A:69:PRO:CD	2:A:168:RCY:O1H	1.41	1.67	23	2
2:A:138:RCY:C1V	2:A:150:RCY:H1ZA	1.41	1.45	87	1
1:A:70:TRP:CG	2:A:176:RCY:H1CA	1.41	1.47	62	1
2:A:138:RCY:H1C	2:A:150:RCY:C1V	1.41	1.45	54	2
2:A:173:RCY:C1Q	2:A:176:RCY:C1V	1.41	1.98	76	1
2:A:168:RCY:N1V	2:A:173:RCY:H1VB	1.41	1.21	48	2
2:A:160:RCY:N1V	2:A:168:RCY:H1C	1.41	1.28	89	1
2:A:150:RCY:H1ZA	2:A:176:RCY:C1C	1.41	0.88	3	1
1:A:68:CYS:CB	2:A:160:RCY:C1Y	1.40	1.99	19	2
2:A:150:RCY:C1W	2:A:187:RCY:C1V	1.40	1.96	76	1
2:A:130:RCY:C1L	2:A:130:RCY:C1S	1.40	1.97	79	1
1:A:71:GLU:CB	2:A:168:RCY:H1L	1.40	1.03	57	3
1:A:64:ILE:HG12	2:A:160:RCY:C1C	1.40	1.42	48	1
2:A:173:RCY:C1Z	2:A:176:RCY:O1J	1.40	1.69	71	1
2:A:160:RCY:C1C	2:A:173:RCY:C1Z	1.40	1.84	11	1
1:A:64:ILE:CG2	2:A:168:RCY:C1Z	1.40	1.98	83	1
2:A:168:RCY:C1V	2:A:176:RCY:C1M	1.40	1.94	20	3
1:A:70:TRP:CB	2:A:150:RCY:C1U	1.40	1.76	34	1
1:A:71:GLU:HB2	2:A:168:RCY:C1M	1.40	1.45	37	1
2:A:138:RCY:C1Z	2:A:150:RCY:H1LA	1.40	1.47	1	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:73:CYS:N	2:A:173:RCY:C1S	1.40	1.85	76	6
1:A:65:THR:CB	2:A:160:RCY:H1ZA	1.40	1.45	100	1
1:A:73:CYS:C	2:A:173:RCY:H1LA	1.40	1.33	33	3
2:A:168:RCY:H1Z	2:A:173:RCY:C1V	1.40	1.45	58	2
2:A:168:RCY:C1Y	2:A:176:RCY:H1V	1.40	1.40	94	1
1:A:70:TRP:CZ3	2:A:168:RCY:C1L	1.40	2.02	48	1
2:A:173:RCY:C1W	2:A:176:RCY:C1V	1.40	1.98	31	2
2:A:130:RCY:C1U	2:A:160:RCY:H1M	1.40	0.88	7	1
1:A:70:TRP:NE1	2:A:176:RCY:H1M	1.40	1.30	4	1
1:A:77:GLU:OE2	2:A:176:RCY:C1Z	1.40	1.68	73	1
2:A:168:RCY:H1Y	2:A:173:RCY:C1Z	1.40	1.24	20	1
1:A:66:VAL:CG1	2:A:121:RCY:H1Z	1.40	1.47	89	1
1:A:70:TRP:CZ2	2:A:121:RCY:O1H	1.40	1.74	78	1
1:A:65:THR:CG2	2:A:160:RCY:C1M	1.40	1.89	100	3
2:A:138:RCY:C1C	2:A:150:RCY:O1H	1.40	1.67	62	1
1:A:72:ALA:O	2:A:168:RCY:C1Y	1.40	1.70	57	1
1:A:70:TRP:CZ2	2:A:176:RCY:C1V	1.40	2.05	4	1
2:A:173:RCY:C1Y	2:A:187:RCY:C1Z	1.39	1.98	92	4
1:A:60:CYS:HA	2:A:160:RCY:C1L	1.39	1.26	99	2
1:A:60:CYS:N	2:A:160:RCY:H1VB	1.39	1.30	83	2
2:A:150:RCY:C1Y	2:A:187:RCY:H1YA	1.39	1.45	18	1
1:A:60:CYS:O	2:A:130:RCY:C1Q	1.39	1.68	18	1
2:A:160:RCY:C1V	2:A:168:RCY:H1YA	1.39	1.38	32	1
1:A:76:CYS:HA	2:A:176:RCY:C1L	1.39	1.42	62	7
2:A:160:RCY:H1ZA	2:A:168:RCY:C1V	1.39	1.39	55	3
1:A:66:VAL:O	2:A:168:RCY:C1C	1.39	1.69	58	2
2:A:168:RCY:C1Z	2:A:173:RCY:C1P	1.39	1.98	58	1
1:A:59:GLY:O	2:A:160:RCY:C1L	1.39	1.65	53	2
1:A:70:TRP:CZ2	2:A:160:RCY:H1CB	1.39	1.50	34	1
2:A:138:RCY:H1MA	2:A:187:RCY:C1Y	1.39	1.43	68	1
2:A:138:RCY:C1Y	2:A:187:RCY:C1C	1.39	2.01	96	3
2:A:160:RCY:C1U	2:A:168:RCY:C1M	1.39	1.97	96	1
2:A:176:RCY:C1Y	2:A:187:RCY:H1V	1.39	1.46	72	2
2:A:160:RCY:C1Y	2:A:173:RCY:C1Z	1.39	2.01	41	2
1:A:67:ILE:CG2	2:A:173:RCY:C1M	1.39	2.00	80	1
2:A:138:RCY:H1C	2:A:160:RCY:C1Y	1.39	1.34	27	1
2:A:138:RCY:H1MA	2:A:150:RCY:C1P	1.39	1.46	1	1
1:A:64:ILE:CG1	2:A:168:RCY:H1L	1.39	1.37	96	3
1:A:71:GLU:OE2	2:A:176:RCY:C1C	1.39	1.69	37	2
1:A:71:GLU:CB	2:A:168:RCY:C1M	1.39	2.00	37	1
2:A:160:RCY:C1U	2:A:168:RCY:H1C	1.39	1.40	49	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:168:RCY:N1R	2:A:168:RCY:C1U	1.39	1.85	25	1
2:A:160:RCY:H1CA	2:A:168:RCY:C1Q	1.39	1.47	39	1
2:A:173:RCY:C1M	2:A:187:RCY:C1Y	1.39	2.00	31	1
1:A:75:HIS:ND1	2:A:176:RCY:H1C	1.38	1.33	84	1
2:A:168:RCY:C1Q	2:A:173:RCY:C1Z	1.38	1.98	39	2
1:A:64:ILE:HD12	2:A:168:RCY:C1L	1.38	1.47	12	1
2:A:168:RCY:O1J	2:A:187:RCY:C1U	1.38	1.69	70	1
2:A:138:RCY:H1Y	2:A:187:RCY:C1C	1.38	1.45	96	2
1:A:70:TRP:CD1	2:A:173:RCY:H1C	1.38	1.53	38	1
2:A:150:RCY:C1V	2:A:160:RCY:C1V	1.38	1.79	42	1
2:A:160:RCY:C1Z	2:A:168:RCY:C1U	1.38	1.99	52	3
2:A:160:RCY:H1Y	2:A:173:RCY:C1Z	1.38	1.48	41	1
1:A:70:TRP:CA	2:A:173:RCY:H1ZA	1.38	1.17	49	3
2:A:173:RCY:C1Z	2:A:176:RCY:C1Z	1.38	2.01	60	1
2:A:168:RCY:H1CB	2:A:176:RCY:C1W	1.38	1.46	59	1
2:A:168:RCY:C1Q	2:A:173:RCY:C1M	1.38	2.02	71	1
2:A:121:RCY:C1V	2:A:168:RCY:H1YB	1.38	1.47	49	1
1:A:65:THR:CB	2:A:168:RCY:C1P	1.38	1.98	80	1
1:A:63:ASP:OD2	2:A:160:RCY:C1Z	1.38	1.72	73	1
2:A:130:RCY:H1YA	2:A:160:RCY:C1Q	1.38	1.47	88	1
2:A:168:RCY:H1U	2:A:187:RCY:N1V	1.38	1.22	64	1
2:A:160:RCY:C1Z	2:A:168:RCY:O1G	1.38	1.69	1	2
2:A:110:RCY:H1VA	2:A:121:RCY:C1M	1.38	1.48	5	1
2:A:130:RCY:N1V	2:A:130:RCY:C1X	1.38	1.85	79	1
1:A:69:PRO:CG	2:A:173:RCY:C1C	1.38	1.99	77	1
1:A:68:CYS:C	2:A:173:RCY:C1V	1.38	1.89	100	1
2:A:150:RCY:C1Z	2:A:160:RCY:H1YB	1.38	1.42	88	1
2:A:150:RCY:C1V	2:A:160:RCY:H1V	1.38	0.87	42	1
1:A:69:PRO:CD	2:A:150:RCY:H1YA	1.38	1.44	85	1
2:A:173:RCY:H1CA	2:A:173:RCY:O1H	1.38	1.18	9	5
2:A:168:RCY:C1C	2:A:173:RCY:C1Y	1.38	1.86	21	1
1:A:67:ILE:CB	2:A:150:RCY:H1V	1.38	1.46	31	1
2:A:138:RCY:H1M	2:A:150:RCY:C1C	1.38	1.46	97	2
1:A:73:CYS:CA	2:A:173:RCY:C1L	1.38	1.79	32	8
1:A:65:THR:HG21	2:A:160:RCY:C1W	1.37	1.47	100	1
1:A:73:CYS:HB2	2:A:176:RCY:C1C	1.38	0.87	52	1
1:A:75:HIS:ND1	2:A:176:RCY:C1C	1.38	1.85	84	1
1:A:60:CYS:CA	2:A:160:RCY:H1LA	1.38	1.23	99	1
1:A:61:GLY:N	2:A:138:RCY:C1V	1.38	1.84	7	1
1:A:72:ALA:CB	2:A:173:RCY:C1P	1.38	1.99	30	2
2:A:176:RCY:C1V	2:A:187:RCY:O1J	1.37	1.72	91	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:64:ILE:HG12	2:A:168:RCY:C1L	1.37	1.37	96	2
2:A:173:RCY:H1C	2:A:187:RCY:C1Y	1.37	1.48	48	2
2:A:138:RCY:H1CB	2:A:160:RCY:C1V	1.37	1.26	27	1
2:A:138:RCY:C1V	2:A:187:RCY:O1J	1.37	1.70	96	2
1:A:73:CYS:CA	2:A:168:RCY:C1Z	1.37	1.99	99	1
2:A:173:RCY:C1P	2:A:187:RCY:H1CB	1.37	1.49	99	1
2:A:138:RCY:C1C	2:A:160:RCY:H1YA	1.37	1.33	27	2
2:A:150:RCY:C1Z	2:A:187:RCY:H1YA	1.37	1.47	49	3
1:A:71:GLU:HB2	2:A:168:RCY:C1U	1.37	1.49	37	1
1:A:78:LEU:CD2	2:A:187:RCY:C1X	1.37	2.03	91	1
2:A:160:RCY:H1MA	2:A:168:RCY:C1M	1.37	1.47	41	1
2:A:168:RCY:H1VB	2:A:173:RCY:C1M	1.37	1.47	29	1
2:A:121:RCY:C1Y	2:A:160:RCY:H1ZB	1.37	1.50	44	1
2:A:173:RCY:C1Y	2:A:187:RCY:O1G	1.37	1.70	93	2
1:A:69:PRO:HB3	2:A:150:RCY:C1Z	1.37	1.48	92	1
2:A:176:RCY:H1U	2:A:187:RCY:C1Z	1.36	1.50	5	1
2:A:168:RCY:C1U	2:A:168:RCY:N1R	1.36	1.84	79	1
1:A:70:TRP:CA	2:A:168:RCY:H1CA	1.36	1.28	57	1
2:A:160:RCY:C1C	2:A:168:RCY:C1Q	1.36	2.01	39	1
1:A:76:CYS:CA	2:A:176:RCY:H1LA	1.36	1.37	31	5
1:A:70:TRP:O	2:A:173:RCY:C1P	1.36	1.71	94	3
1:A:70:TRP:HZ2	2:A:160:RCY:C1C	1.36	1.30	34	1
2:A:173:RCY:H1ZA	2:A:176:RCY:C1M	1.36	1.48	37	1
2:A:173:RCY:C1M	2:A:176:RCY:C1M	1.36	2.01	89	2
1:A:65:THR:HG21	2:A:160:RCY:C1Z	1.36	1.47	100	1
2:A:138:RCY:H1CA	2:A:138:RCY:O1G	1.36	1.18	17	5
1:A:71:GLU:CA	2:A:173:RCY:O1G	1.36	1.72	83	2
2:A:160:RCY:C1V	2:A:168:RCY:H1M	1.36	1.16	92	3
2:A:173:RCY:C1L	2:A:176:RCY:O1G	1.36	1.71	71	2
2:A:138:RCY:H1V	2:A:150:RCY:C1V	1.36	1.48	19	2
2:A:168:RCY:H1ZB	2:A:173:RCY:O1J	1.36	1.16	55	1
1:A:64:ILE:CG2	2:A:150:RCY:H1VA	1.36	1.47	16	1
1:A:70:TRP:HA	2:A:173:RCY:C1Z	1.36	1.50	85	2
1:A:74:ASN:OD1	2:A:173:RCY:C1C	1.36	1.69	91	1
1:A:78:LEU:HD21	2:A:176:RCY:C1Y	1.36	1.51	91	1
1:A:69:PRO:HB3	2:A:173:RCY:N1V	1.36	1.33	9	1
2:A:173:RCY:C1C	2:A:187:RCY:O1H	1.36	1.74	56	1
2:A:176:RCY:H1VB	2:A:176:RCY:O1G	1.36	1.20	4	4
1:A:73:CYS:C	2:A:176:RCY:C1C	1.36	1.85	20	2
2:A:173:RCY:C1W	2:A:176:RCY:C1Y	1.36	2.02	81	2
2:A:173:RCY:C1V	2:A:187:RCY:H1VA	1.36	1.51	55	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:67:ILE:CA	2:A:176:RCY:H1VA	1.36	1.51	16	1
2:A:138:RCY:O1H	2:A:150:RCY:C1Z	1.36	1.70	82	2
2:A:173:RCY:H1L	2:A:176:RCY:C1P	1.36	1.48	71	1
2:A:168:RCY:H1ZA	2:A:176:RCY:N1V	1.36	1.35	11	1
2:A:173:RCY:H1MA	2:A:176:RCY:C1X	1.36	1.51	89	1
2:A:150:RCY:C1Y	2:A:187:RCY:C1Y	1.35	2.01	41	4
2:A:176:RCY:C1M	2:A:187:RCY:O1G	1.35	1.73	10	1
2:A:173:RCY:C1Z	2:A:187:RCY:C1Q	1.35	1.78	92	2
2:A:168:RCY:C1Z	2:A:176:RCY:O1J	1.35	1.70	11	1
1:A:71:GLU:OE2	2:A:168:RCY:C1V	1.35	1.74	93	3
2:A:130:RCY:O1J	2:A:160:RCY:H1CB	1.35	1.19	23	2
2:A:173:RCY:C1V	2:A:176:RCY:H1M	1.35	1.49	69	5
2:A:173:RCY:H1YB	2:A:187:RCY:C1V	1.35	1.31	64	1
2:A:150:RCY:C1Z	2:A:187:RCY:C1V	1.35	1.80	37	3
2:A:150:RCY:C1Y	2:A:173:RCY:N1V	1.35	1.69	3	1
2:A:138:RCY:C1C	2:A:160:RCY:C1V	1.35	2.00	27	1
2:A:173:RCY:C1C	2:A:176:RCY:C1C	1.35	2.05	8	1
1:A:71:GLU:HB3	2:A:173:RCY:O1H	1.35	1.21	89	1
2:A:110:RCY:O1J	2:A:121:RCY:H1YA	1.35	1.22	5	1
1:A:70:TRP:NE1	2:A:121:RCY:C1W	1.35	1.79	49	1
2:A:130:RCY:H1CA	2:A:130:RCY:O1G	1.35	1.21	100	5
1:A:65:THR:CG2	2:A:160:RCY:C1Z	1.35	2.05	100	1
2:A:173:RCY:H1VB	2:A:176:RCY:C1Q	1.35	1.49	38	3
1:A:70:TRP:CZ3	2:A:168:RCY:C1C	1.35	2.05	95	2
2:A:110:RCY:O1G	2:A:110:RCY:H1VB	1.35	1.20	3	3
1:A:70:TRP:CA	2:A:173:RCY:C1Z	1.35	2.04	85	2
1:A:70:TRP:CE2	2:A:121:RCY:C1Y	1.35	2.07	49	1
1:A:70:TRP:HB3	2:A:168:RCY:C1L	1.35	1.51	46	1
1:A:62:THR:HG21	2:A:160:RCY:C1W	1.35	1.49	46	1
2:A:173:RCY:C1Y	2:A:187:RCY:H1U	1.35	1.49	77	1
2:A:160:RCY:H1ZA	2:A:168:RCY:C1U	1.34	1.48	52	2
2:A:160:RCY:H1Y	2:A:168:RCY:C1P	1.34	1.52	3	3
2:A:168:RCY:C1W	2:A:173:RCY:C1V	1.34	1.84	45	3
2:A:150:RCY:H1Z	2:A:187:RCY:C1V	1.34	1.52	26	1
1:A:65:THR:O	2:A:173:RCY:C1C	1.34	1.72	71	1
2:A:168:RCY:C1Z	2:A:173:RCY:C1M	1.34	2.05	70	1
2:A:138:RCY:C1V	2:A:150:RCY:H1VB	1.34	1.51	67	1
1:A:69:PRO:CB	2:A:176:RCY:H1ZB	1.34	1.50	66	1
2:A:168:RCY:H1VB	2:A:168:RCY:O1G	1.34	1.22	18	7
1:A:69:PRO:O	2:A:173:RCY:C1M	1.34	1.67	76	1
1:A:70:TRP:CZ2	2:A:176:RCY:C1M	1.34	2.10	85	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:71:GLU:HA	2:A:173:RCY:O1G	1.34	1.19	83	2
2:A:121:RCY:H1CA	2:A:121:RCY:O1G	1.34	1.20	98	7
1:A:73:CYS:HB2	2:A:176:RCY:C1Z	1.34	1.48	58	2
2:A:176:RCY:C1U	2:A:187:RCY:C1Z	1.34	2.05	5	1
1:A:71:GLU:C	2:A:168:RCY:H1MA	1.34	1.16	91	1
2:A:168:RCY:C1S	2:A:173:RCY:C1Z	1.34	2.06	39	1
2:A:173:RCY:C1M	2:A:176:RCY:H1M	1.34	1.33	89	2
1:A:70:TRP:CZ3	2:A:168:RCY:C1V	1.34	1.99	56	2
2:A:176:RCY:C1V	2:A:187:RCY:H1V	1.34	1.52	26	1
1:A:63:ASP:O	2:A:168:RCY:C1V	1.34	1.76	5	1
2:A:168:RCY:C1P	2:A:168:RCY:C1Q	1.34	2.06	79	1
1:A:78:LEU:CG	2:A:176:RCY:C1M	1.34	1.99	91	1
2:A:150:RCY:C1U	2:A:187:RCY:H1V	1.34	1.50	89	1
1:A:65:THR:O	2:A:138:RCY:C1C	1.34	1.75	38	1
1:A:75:HIS:CD2	2:A:173:RCY:C1Z	1.34	2.08	42	1
1:A:75:HIS:O	2:A:176:RCY:C1Q	1.34	1.74	84	2
1:A:74:ASN:O	2:A:176:RCY:C1C	1.34	1.72	62	1
2:A:173:RCY:O1H	2:A:187:RCY:H1C	1.34	1.22	7	1
1:A:74:ASN:OD1	2:A:173:RCY:C1L	1.34	1.74	2	1
1:A:63:ASP:CB	2:A:130:RCY:C1Y	1.34	1.96	73	1
1:A:71:GLU:CG	2:A:176:RCY:H1YA	1.34	1.50	92	1
2:A:160:RCY:H1V	2:A:168:RCY:C1M	1.34	1.15	92	1
1:A:74:ASN:OD1	2:A:176:RCY:C1P	1.33	1.75	78	1
1:A:70:TRP:O	2:A:187:RCY:H1V	1.33	1.20	16	1
1:A:70:TRP:CD1	2:A:187:RCY:C1Z	1.33	1.95	92	4
2:A:121:RCY:H1YB	2:A:160:RCY:C1Z	1.33	1.50	44	1
2:A:121:RCY:O1H	2:A:121:RCY:H1CA	1.33	1.18	69	5
2:A:138:RCY:H1VB	2:A:150:RCY:C1C	1.33	1.41	10	1
2:A:121:RCY:H1VB	2:A:121:RCY:O1G	1.33	1.21	12	4
2:A:173:RCY:C1Z	2:A:176:RCY:C1M	1.33	2.02	37	2
1:A:70:TRP:NE1	2:A:176:RCY:H1YA	1.33	1.38	80	1
1:A:68:CYS:SG	2:A:176:RCY:C1Z	1.33	2.16	77	1
1:A:77:GLU:HA	2:A:176:RCY:C1P	1.33	1.47	55	1
1:A:64:ILE:HD11	2:A:168:RCY:C1V	1.33	1.51	27	2
2:A:160:RCY:O1J	2:A:168:RCY:C1Z	1.33	1.74	5	2
2:A:150:RCY:C1Y	2:A:187:RCY:H1Y	1.33	1.53	32	2
1:A:60:CYS:H	2:A:160:RCY:C1V	1.33	1.34	83	1
1:A:69:PRO:CA	2:A:173:RCY:O1J	1.33	1.76	9	1
1:A:68:CYS:SG	2:A:176:RCY:N1V	1.33	1.99	80	3
2:A:173:RCY:O1H	2:A:173:RCY:H1CA	1.33	1.22	63	4
2:A:160:RCY:H1CA	2:A:160:RCY:O1H	1.33	1.16	7	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:130:RCY:C1Y	2:A:160:RCY:O1G	1.33	1.77	50	1
1:A:73:CYS:N	2:A:173:RCY:O1H	1.33	1.60	56	4
1:A:71:GLU:HB3	2:A:168:RCY:C1Q	1.33	1.35	91	2
2:A:168:RCY:H1ZA	2:A:176:RCY:O1J	1.33	1.19	11	1
1:A:61:GLY:N	2:A:150:RCY:C1V	1.33	1.80	11	1
2:A:173:RCY:C1V	2:A:176:RCY:C1U	1.32	2.06	38	3
2:A:176:RCY:O1H	2:A:176:RCY:H1CA	1.32	1.21	51	4
1:A:67:ILE:HB	2:A:173:RCY:C1Y	1.32	1.52	80	1
2:A:138:RCY:H1M	2:A:150:RCY:N1R	1.32	1.20	1	1
1:A:63:ASP:O	2:A:168:RCY:C1Z	1.32	1.75	78	1
1:A:70:TRP:HB2	2:A:173:RCY:O1J	1.32	1.13	64	1
1:A:70:TRP:CD2	2:A:176:RCY:C1Y	1.32	2.09	80	2
1:A:70:TRP:CD1	2:A:187:RCY:H1ZA	1.32	1.59	16	2
1:A:71:GLU:C	2:A:176:RCY:C1V	1.32	1.98	76	1
2:A:168:RCY:O1H	2:A:173:RCY:H1ZA	1.32	1.16	17	2
2:A:176:RCY:H1VB	2:A:187:RCY:C1V	1.32	1.53	26	2
2:A:138:RCY:H1VA	2:A:176:RCY:C1C	1.32	1.54	9	1
1:A:75:HIS:O	2:A:176:RCY:C1Z	1.32	1.73	51	1
1:A:76:CYS:SG	2:A:160:RCY:H1YA	1.32	1.64	73	1
1:A:74:ASN:CA	2:A:176:RCY:O1G	1.32	1.74	78	1
2:A:130:RCY:O1G	2:A:130:RCY:H1ZB	1.32	1.25	38	6
2:A:173:RCY:H1U	2:A:176:RCY:C1V	1.32	1.44	89	2
2:A:160:RCY:H1VB	2:A:160:RCY:O1G	1.32	1.25	56	7
1:A:71:GLU:OE2	2:A:150:RCY:C1P	1.32	1.76	58	1
2:A:168:RCY:H1CA	2:A:168:RCY:O1H	1.32	1.22	54	3
1:A:68:CYS:C	2:A:173:RCY:O1G	1.32	1.68	10	2
2:A:150:RCY:C1S	2:A:160:RCY:H1YB	1.32	1.53	85	1
1:A:69:PRO:HB3	2:A:173:RCY:C1W	1.32	1.52	9	1
1:A:70:TRP:CD1	2:A:121:RCY:H1M	1.32	1.58	49	1
2:A:138:RCY:C1Z	2:A:187:RCY:H1YA	1.32	1.51	32	1
1:A:74:ASN:CA	2:A:173:RCY:O1G	1.32	1.71	15	2
2:A:173:RCY:C1P	2:A:176:RCY:H1L	1.32	1.55	28	1
1:A:64:ILE:CD1	2:A:168:RCY:O1H	1.31	1.78	58	2
1:A:67:ILE:CB	2:A:173:RCY:H1YB	1.31	1.52	80	1
2:A:121:RCY:H1ZB	2:A:121:RCY:O1G	1.31	1.24	86	1
2:A:168:RCY:C1M	2:A:187:RCY:H1ZA	1.31	1.48	84	1
2:A:138:RCY:H1ZA	2:A:187:RCY:C1Y	1.31	1.53	32	3
1:A:64:ILE:HG21	2:A:150:RCY:C1V	1.31	1.56	16	1
1:A:60:CYS:CB	2:A:130:RCY:O1H	1.31	1.76	18	1
2:A:176:RCY:C1V	2:A:187:RCY:C1Y	1.31	2.01	54	2
1:A:68:CYS:SG	2:A:168:RCY:H1SA	1.31	1.64	25	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:138:RCY:H1VA	2:A:173:RCY:O1J	1.31	1.23	15	1
1:A:63:ASP:O	2:A:160:RCY:C1V	1.31	1.79	3	1
2:A:176:RCY:C1Y	2:A:187:RCY:H1VA	1.31	1.56	27	1
1:A:68:CYS:SG	2:A:160:RCY:H1Z	1.31	1.65	19	1
2:A:168:RCY:O1G	2:A:168:RCY:H1VB	1.31	1.21	85	3
2:A:173:RCY:H1CB	2:A:176:RCY:C1L	1.31	1.54	36	2
2:A:138:RCY:C1Z	2:A:187:RCY:H1CB	1.31	1.51	44	1
2:A:160:RCY:O1J	2:A:168:RCY:C1C	1.31	1.78	89	1
2:A:160:RCY:O1J	2:A:187:RCY:C1Z	1.31	1.78	97	1
2:A:150:RCY:O1G	2:A:150:RCY:H1CA	1.31	1.23	60	8
1:A:71:GLU:CG	2:A:150:RCY:H1U	1.31	1.53	58	1
1:A:70:TRP:CB	2:A:173:RCY:H1ZA	1.31	1.55	94	1
1:A:71:GLU:OE2	2:A:176:RCY:H1CB	1.31	1.11	44	2
1:A:60:CYS:N	2:A:160:RCY:H1LA	1.31	1.38	70	1
2:A:138:RCY:H1VB	2:A:150:RCY:C1Y	1.31	1.54	1	1
2:A:176:RCY:C1C	2:A:187:RCY:O1G	1.31	1.79	61	2
2:A:173:RCY:H1V	2:A:176:RCY:C1M	1.31	1.54	17	3
2:A:121:RCY:H1ZB	2:A:121:RCY:O1H	1.31	1.24	50	6
2:A:160:RCY:C1Y	2:A:168:RCY:C1P	1.31	2.09	58	5
2:A:130:RCY:H1CA	2:A:160:RCY:O1J	1.31	1.21	16	1
2:A:138:RCY:C1P	2:A:150:RCY:H1M	1.31	1.55	23	2
2:A:176:RCY:C1C	2:A:187:RCY:H1V	1.31	1.56	93	2
1:A:62:THR:CG2	2:A:160:RCY:O1G	1.31	1.78	82	1
1:A:74:ASN:HA	2:A:173:RCY:O1G	1.31	1.11	27	2
2:A:138:RCY:O1J	2:A:150:RCY:C1M	1.30	1.73	88	1
2:A:168:RCY:C1C	2:A:176:RCY:C1Y	1.30	2.09	59	2
2:A:160:RCY:H1YB	2:A:168:RCY:C1M	1.30	1.56	34	1
2:A:173:RCY:H1VB	2:A:176:RCY:C1Y	1.30	1.45	76	3
2:A:173:RCY:C1Z	2:A:187:RCY:O1H	1.30	1.67	81	1
2:A:168:RCY:H1Y	2:A:173:RCY:C1P	1.30	1.54	91	2
1:A:61:GLY:N	2:A:138:RCY:H1VB	1.30	1.38	7	1
2:A:176:RCY:O1G	2:A:176:RCY:H1ZB	1.30	1.16	61	3
2:A:160:RCY:C1M	2:A:168:RCY:H1VB	1.30	1.53	55	1
2:A:173:RCY:C1Z	2:A:176:RCY:H1Z	1.30	1.52	60	1
2:A:176:RCY:H1ZA	2:A:187:RCY:C1V	1.30	1.56	10	1
1:A:70:TRP:N	2:A:176:RCY:C1C	1.30	1.92	13	1
1:A:70:TRP:NE1	2:A:187:RCY:H1ZA	1.30	1.37	92	2
2:A:168:RCY:C1S	2:A:173:RCY:H1ZA	1.30	1.53	39	1
2:A:173:RCY:H1YB	2:A:187:RCY:C1Z	1.30	1.55	92	2
1:A:70:TRP:HZ3	2:A:168:RCY:C1W	1.30	1.38	41	2
2:A:168:RCY:O1G	2:A:168:RCY:H1ZB	1.30	1.25	65	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:173:RCY:C1V	2:A:187:RCY:C1C	1.30	2.00	55	1
1:A:70:TRP:NE1	2:A:168:RCY:C1Y	1.30	1.92	37	1
1:A:77:GLU:CD	2:A:176:RCY:C1V	1.30	1.98	7	1
2:A:173:RCY:C1U	2:A:176:RCY:H1YB	1.30	1.56	41	2
1:A:68:CYS:HA	2:A:168:RCY:C1L	1.30	1.32	75	3
2:A:173:RCY:H1VB	2:A:187:RCY:C1V	1.30	1.57	55	1
2:A:173:RCY:O1G	2:A:173:RCY:H1CA	1.30	1.23	86	3
2:A:160:RCY:C1V	2:A:168:RCY:C1V	1.30	2.00	48	2
2:A:176:RCY:C1M	2:A:187:RCY:C1U	1.30	2.01	96	2
1:A:70:TRP:NE1	2:A:168:RCY:H1YA	1.30	1.36	37	1
2:A:160:RCY:C1Z	2:A:168:RCY:C1Y	1.30	2.08	43	4
2:A:173:RCY:H1VB	2:A:176:RCY:N1R	1.30	1.38	69	3
2:A:130:RCY:H1VB	2:A:130:RCY:O1G	1.30	1.24	71	4
1:A:69:PRO:C	2:A:173:RCY:C1Z	1.30	2.00	85	1
2:A:138:RCY:N1R	2:A:150:RCY:H1YA	1.30	1.10	23	1
1:A:67:ILE:O	2:A:173:RCY:C1V	1.30	1.78	80	1
2:A:130:RCY:O1G	2:A:130:RCY:H1CA	1.29	1.24	86	5
2:A:176:RCY:H1ZB	2:A:176:RCY:O1H	1.29	1.19	26	1
1:A:64:ILE:HG21	2:A:160:RCY:C1Y	1.29	1.54	49	1
1:A:71:GLU:CB	2:A:173:RCY:O1H	1.29	1.78	89	1
1:A:68:CYS:HB3	2:A:160:RCY:C1Z	1.29	1.57	19	1
2:A:173:RCY:C1V	2:A:187:RCY:C1V	1.29	2.08	55	1
2:A:168:RCY:C1Z	2:A:187:RCY:C1M	1.29	2.09	84	1
1:A:69:PRO:CA	2:A:168:RCY:H1MA	1.29	1.28	5	1
1:A:69:PRO:HD2	2:A:150:RCY:C1Y	1.29	1.57	85	1
2:A:173:RCY:O1G	2:A:176:RCY:C1C	1.29	1.79	11	3
2:A:130:RCY:C1Y	2:A:160:RCY:C1P	1.29	2.11	50	1
2:A:187:RCY:O1G	2:A:187:RCY:H1CA	1.29	1.20	4	4
2:A:160:RCY:C1Z	2:A:168:RCY:C1C	1.29	1.91	69	1
1:A:59:GLY:HA2	2:A:160:RCY:C1L	1.29	1.58	28	2
1:A:72:ALA:N	2:A:168:RCY:H1MA	1.29	1.37	91	1
1:A:74:ASN:OD1	2:A:176:RCY:H1V	1.29	1.20	44	1
1:A:71:GLU:HG3	2:A:168:RCY:N1R	1.29	1.39	93	1
1:A:59:GLY:N	2:A:160:RCY:C1P	1.29	1.91	78	2
2:A:160:RCY:C1Z	2:A:168:RCY:H1U	1.29	1.56	52	3
2:A:176:RCY:O1G	2:A:187:RCY:H1M	1.29	1.19	60	1
1:A:66:VAL:HG13	2:A:121:RCY:O1G	1.29	1.26	34	1
2:A:168:RCY:O1J	2:A:187:RCY:C1V	1.29	1.80	70	2
1:A:71:GLU:HG2	2:A:173:RCY:O1G	1.29	1.28	17	1
2:A:160:RCY:C1Z	2:A:168:RCY:C1L	1.29	2.03	73	2
2:A:187:RCY:O1G	2:A:187:RCY:H1VB	1.29	1.22	31	7

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:138:RCY:H1ZB	2:A:187:RCY:C1Z	1.29	1.55	77	2
1:A:70:TRP:HB2	2:A:173:RCY:C1Y	1.29	1.58	85	1
1:A:70:TRP:HB2	2:A:176:RCY:C1Z	1.29	1.57	18	1
2:A:130:RCY:C1M	2:A:130:RCY:C1W	1.29	2.08	79	1
1:A:70:TRP:CD1	2:A:173:RCY:O1G	1.29	1.86	44	1
1:A:70:TRP:O	2:A:173:RCY:C1L	1.29	1.81	82	2
2:A:173:RCY:C1C	2:A:176:RCY:H1L	1.29	1.56	36	1
2:A:168:RCY:C1Y	2:A:173:RCY:C1Z	1.29	1.94	20	1
2:A:173:RCY:H1MA	2:A:176:RCY:C1U	1.29	1.58	89	1
1:A:64:ILE:CG1	2:A:168:RCY:H1ZA	1.28	1.57	78	2
2:A:160:RCY:H1V	2:A:168:RCY:C1C	1.28	1.56	14	2
2:A:187:RCY:H1ZB	2:A:187:RCY:O1G	1.28	1.24	50	2
2:A:173:RCY:O1H	2:A:176:RCY:H1YA	1.28	1.11	68	2
1:A:64:ILE:HD13	2:A:160:RCY:C1M	1.28	1.57	1	2
2:A:187:RCY:O1H	2:A:187:RCY:H1VB	1.28	1.26	36	5
1:A:70:TRP:CZ2	2:A:168:RCY:C1M	1.28	2.16	59	1
1:A:66:VAL:HG12	2:A:121:RCY:C1Z	1.28	1.56	89	1
1:A:66:VAL:HG12	2:A:121:RCY:C1W	1.28	1.57	83	1
1:A:73:CYS:CB	2:A:176:RCY:C1Z	1.28	2.10	58	1
2:A:176:RCY:O1H	2:A:176:RCY:H1ZB	1.28	1.26	27	4
2:A:168:RCY:C1V	2:A:176:RCY:C1Y	1.28	1.94	76	3
1:A:60:CYS:N	2:A:160:RCY:H1L	1.28	1.40	28	2
1:A:70:TRP:CH2	2:A:168:RCY:H1L	1.28	1.51	48	1
1:A:64:ILE:HD11	2:A:168:RCY:O1J	1.28	1.23	4	1
2:A:173:RCY:C1Z	2:A:187:RCY:O1G	1.28	1.81	92	1
2:A:168:RCY:H1M	2:A:173:RCY:O1J	1.28	1.21	100	1
2:A:130:RCY:O1H	2:A:130:RCY:H1VB	1.28	1.26	39	6
2:A:168:RCY:O1G	2:A:187:RCY:H1Y	1.28	1.22	64	1
2:A:168:RCY:C1P	2:A:173:RCY:H1Y	1.28	1.58	62	2
2:A:168:RCY:H1MA	2:A:173:RCY:O1J	1.28	1.25	60	2
2:A:168:RCY:H1LA	2:A:173:RCY:C1Z	1.28	1.48	11	4
1:A:70:TRP:HB2	2:A:150:RCY:C1U	1.28	0.98	34	1
1:A:63:ASP:C	2:A:168:RCY:H1LA	1.28	1.49	59	1
2:A:130:RCY:C1S	2:A:130:RCY:C1Q	1.28	2.10	79	1
1:A:62:THR:HG22	2:A:130:RCY:C1M	1.28	1.38	9	1
2:A:160:RCY:H1VB	2:A:160:RCY:O1H	1.28	1.28	96	5
2:A:173:RCY:H1M	2:A:176:RCY:C1P	1.28	1.59	38	1
2:A:150:RCY:C1V	2:A:187:RCY:H1ZA	1.28	1.57	64	2
2:A:138:RCY:C1C	2:A:150:RCY:C1V	1.28	2.08	10	2
2:A:168:RCY:N1R	2:A:173:RCY:H1Z	1.28	1.42	10	1
1:A:69:PRO:CD	2:A:150:RCY:C1Y	1.28	2.11	85	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:130:RCY:C1U	2:A:160:RCY:C1M	1.28	1.85	7	1
1:A:70:TRP:CE2	2:A:176:RCY:H1M	1.28	1.00	4	1
2:A:168:RCY:H1Y	2:A:187:RCY:C1S	1.28	1.58	3	1
2:A:160:RCY:O1J	2:A:168:RCY:C1Y	1.28	1.82	78	5
1:A:71:GLU:CD	2:A:168:RCY:H1CB	1.28	1.48	93	2
2:A:110:RCY:H1VB	2:A:110:RCY:O1H	1.28	1.27	14	4
2:A:130:RCY:H1VA	2:A:160:RCY:C1Q	1.28	1.57	8	1
2:A:150:RCY:H1ZB	2:A:150:RCY:O1G	1.28	1.21	12	2
2:A:168:RCY:H1Y	2:A:187:RCY:C1Z	1.28	1.50	21	2
2:A:138:RCY:O1J	2:A:176:RCY:C1C	1.28	1.82	51	1
1:A:65:THR:CB	2:A:168:RCY:O1G	1.28	1.80	80	1
2:A:150:RCY:H1CA	2:A:150:RCY:O1G	1.27	1.19	61	2
2:A:173:RCY:H1CB	2:A:187:RCY:O1J	1.27	1.26	55	2
2:A:168:RCY:C1C	2:A:173:RCY:C1M	1.27	1.96	99	1
1:A:69:PRO:CG	2:A:150:RCY:H1Y	1.27	1.56	85	1
2:A:160:RCY:O1G	2:A:168:RCY:C1Y	1.27	1.82	9	1
2:A:121:RCY:H1VA	2:A:168:RCY:C1Y	1.27	1.56	49	1
1:A:69:PRO:C	2:A:187:RCY:H1CA	1.27	1.48	7	1
2:A:176:RCY:H1VB	2:A:176:RCY:O1H	1.27	1.28	45	5
2:A:168:RCY:C1L	2:A:173:RCY:H1M	1.27	1.59	49	2
2:A:121:RCY:O1G	2:A:121:RCY:H1VB	1.27	1.26	95	5
1:A:69:PRO:CD	2:A:168:RCY:H1L	1.27	1.59	60	2
2:A:173:RCY:H1CB	2:A:176:RCY:C1Q	1.27	1.57	34	1
1:A:69:PRO:HB2	2:A:173:RCY:C1W	1.27	1.48	35	1
1:A:59:GLY:CA	2:A:160:RCY:C1L	1.27	2.12	57	3
2:A:150:RCY:H1ZA	2:A:187:RCY:C1X	1.27	1.50	37	1
2:A:130:RCY:C1X	2:A:160:RCY:C1M	1.27	2.12	7	1
1:A:60:CYS:HA	2:A:168:RCY:O1G	1.27	1.23	95	1
1:A:68:CYS:HB3	2:A:176:RCY:C1Y	1.27	1.34	80	1
2:A:173:RCY:H1M	2:A:187:RCY:O1J	1.27	1.30	89	2
1:A:60:CYS:HB3	2:A:130:RCY:O1H	1.27	1.09	18	1
2:A:150:RCY:O1G	2:A:187:RCY:C1V	1.27	1.81	18	2
1:A:67:ILE:CG2	2:A:173:RCY:C1C	1.27	2.10	31	1
1:A:69:PRO:CD	2:A:168:RCY:H1LA	1.27	1.56	78	4
1:A:74:ASN:HA	2:A:176:RCY:C1P	1.27	1.59	78	1
2:A:176:RCY:O1H	2:A:176:RCY:H1VB	1.27	1.26	69	5
2:A:168:RCY:H1VB	2:A:168:RCY:O1H	1.27	1.28	49	10
2:A:176:RCY:C1U	2:A:187:RCY:H1M	1.27	1.58	26	1
2:A:138:RCY:C1V	2:A:150:RCY:C1M	1.27	2.11	1	3
1:A:70:TRP:HZ2	2:A:168:RCY:C1M	1.27	1.40	59	1
1:A:59:GLY:C	2:A:160:RCY:C1L	1.27	2.03	57	6

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:70:TRP:CE3	2:A:168:RCY:H1M	1.27	1.62	49	2
1:A:71:GLU:OE2	2:A:173:RCY:C1C	1.27	1.81	89	1
2:A:138:RCY:H1C	2:A:173:RCY:C1Z	1.27	1.59	15	2
1:A:66:VAL:CB	2:A:121:RCY:H1YA	1.27	1.59	83	1
1:A:73:CYS:N	2:A:173:RCY:H1S	1.27	1.07	76	6
1:A:70:TRP:CE2	2:A:187:RCY:C1Z	1.27	2.16	76	2
2:A:168:RCY:C1X	2:A:173:RCY:H1YA	1.27	1.49	21	1
1:A:63:ASP:CB	2:A:160:RCY:C1C	1.27	2.12	63	2
2:A:160:RCY:C1M	2:A:168:RCY:H1M	1.26	1.60	41	2
1:A:66:VAL:O	2:A:168:RCY:H1U	1.26	1.23	51	2
2:A:173:RCY:O1G	2:A:176:RCY:H1C	1.26	1.09	11	2
1:A:71:GLU:HA	2:A:168:RCY:C1V	1.26	1.36	76	1
1:A:72:ALA:C	2:A:168:RCY:C1Z	1.26	1.78	57	1
2:A:138:RCY:H1Z	2:A:187:RCY:O1G	1.26	1.28	71	1
2:A:130:RCY:C1C	2:A:160:RCY:C1L	1.26	2.13	66	2
1:A:63:ASP:OD2	2:A:160:RCY:H1ZA	1.26	1.17	73	1
1:A:65:THR:OG1	2:A:160:RCY:H1ZA	1.26	1.16	100	1
2:A:173:RCY:C1V	2:A:176:RCY:H1Y	1.26	1.47	2	3
2:A:150:RCY:H1YB	2:A:187:RCY:C1Y	1.26	1.53	41	2
2:A:187:RCY:H1VB	2:A:187:RCY:O1H	1.26	1.30	72	6
2:A:176:RCY:O1G	2:A:187:RCY:H1MA	1.26	1.19	26	1
1:A:69:PRO:HA	2:A:176:RCY:C1V	1.26	1.58	72	1
1:A:71:GLU:O	2:A:173:RCY:C1S	1.26	1.82	76	2
2:A:176:RCY:C1W	2:A:187:RCY:C1Y	1.26	2.13	5	1
1:A:66:VAL:HB	2:A:160:RCY:O1H	1.26	1.29	68	1
1:A:59:GLY:HA2	2:A:160:RCY:O1G	1.26	1.23	70	2
2:A:176:RCY:H1CA	2:A:176:RCY:O1G	1.26	1.25	46	3
2:A:173:RCY:H1Y	2:A:187:RCY:C1U	1.26	1.53	77	1
2:A:168:RCY:H1C	2:A:176:RCY:C1Z	1.26	1.54	3	1
2:A:110:RCY:O1G	2:A:110:RCY:H1ZB	1.26	1.23	56	4
1:A:68:CYS:HB2	2:A:160:RCY:C1Y	1.26	1.56	19	1
2:A:160:RCY:C1Z	2:A:168:RCY:C1M	1.26	2.13	52	1
2:A:138:RCY:C1Q	2:A:150:RCY:C1P	1.26	2.13	41	1
1:A:71:GLU:CD	2:A:130:RCY:H1MA	1.26	1.46	94	1
2:A:138:RCY:C1Y	2:A:150:RCY:C1Q	1.26	2.08	60	2
1:A:69:PRO:HB3	2:A:173:RCY:O1H	1.26	1.16	81	2
2:A:173:RCY:C1Y	2:A:176:RCY:C1V	1.26	2.13	81	1
1:A:64:ILE:CG1	2:A:160:RCY:H1CA	1.26	1.60	48	1
2:A:138:RCY:H1Z	2:A:187:RCY:C1P	1.26	1.60	71	1
2:A:138:RCY:C1L	2:A:150:RCY:O1H	1.26	1.76	23	1
1:A:70:TRP:CE2	2:A:176:RCY:C1Y	1.26	2.18	80	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:130:RCY:O1J	2:A:160:RCY:H1VA	1.26	1.21	67	2
2:A:110:RCY:H1ZB	2:A:110:RCY:O1H	1.26	1.21	37	2
1:A:63:ASP:O	2:A:168:RCY:H1LA	1.26	1.13	59	1
2:A:160:RCY:C1P	2:A:168:RCY:C1Y	1.26	2.13	9	1
2:A:130:RCY:O1H	2:A:130:RCY:H1ZB	1.26	1.29	66	2
2:A:176:RCY:H1YA	2:A:187:RCY:C1V	1.26	1.60	27	1
2:A:173:RCY:C1Y	2:A:187:RCY:N1V	1.26	1.93	92	1
2:A:150:RCY:H1ZB	2:A:150:RCY:O1H	1.26	1.31	43	7
2:A:150:RCY:H1CA	2:A:150:RCY:O1H	1.26	1.18	81	4
2:A:173:RCY:O1G	2:A:173:RCY:H1VB	1.26	1.31	60	2
2:A:138:RCY:H1ZB	2:A:150:RCY:C1P	1.26	1.60	81	1
2:A:138:RCY:C1Z	2:A:150:RCY:C1P	1.26	2.09	98	3
2:A:150:RCY:O1J	2:A:187:RCY:C1M	1.26	1.83	59	1
1:A:69:PRO:CB	2:A:173:RCY:O1J	1.26	1.84	9	3
2:A:130:RCY:C1C	2:A:130:RCY:C1M	1.26	2.12	79	1
1:A:62:THR:OG1	2:A:168:RCY:H1L	1.26	1.29	23	1
2:A:173:RCY:H1MA	2:A:176:RCY:C1Y	1.26	1.57	77	2
2:A:138:RCY:C1V	2:A:150:RCY:C1Z	1.26	2.09	87	1
2:A:150:RCY:C1Z	2:A:187:RCY:C1Y	1.25	2.13	9	6
2:A:160:RCY:C1Y	2:A:173:RCY:H1ZA	1.25	1.57	41	2
1:A:70:TRP:CZ3	2:A:168:RCY:O1J	1.25	1.88	41	1
2:A:160:RCY:O1G	2:A:160:RCY:H1VB	1.25	1.28	3	4
1:A:68:CYS:CA	2:A:168:RCY:O1H	1.25	1.76	66	4
1:A:70:TRP:CD1	2:A:173:RCY:C1Y	1.25	2.15	84	1
1:A:70:TRP:CE2	2:A:168:RCY:C1Z	1.25	2.18	24	1
1:A:64:ILE:CD1	2:A:187:RCY:H1M	1.25	1.58	85	1
1:A:71:GLU:CD	2:A:176:RCY:H1CB	1.25	1.49	37	2
2:A:176:RCY:C1X	2:A:187:RCY:H1VA	1.25	1.61	33	1
1:A:61:GLY:O	2:A:150:RCY:H1M	1.25	1.21	11	1
2:A:168:RCY:C1W	2:A:187:RCY:H1S	1.25	1.52	3	1
2:A:173:RCY:O1G	2:A:176:RCY:H1VB	1.25	1.29	19	2
2:A:150:RCY:H1YA	2:A:187:RCY:C1Z	1.25	1.61	41	1
2:A:173:RCY:H1VB	2:A:176:RCY:C1V	1.25	1.59	62	2
2:A:130:RCY:O1G	2:A:130:RCY:H1VB	1.25	1.29	12	6
1:A:69:PRO:CA	2:A:168:RCY:C1M	1.25	1.86	5	1
1:A:69:PRO:CB	2:A:173:RCY:H1YB	1.25	1.60	35	1
2:A:138:RCY:H1V	2:A:150:RCY:C1Y	1.25	1.59	51	1
2:A:121:RCY:O1G	2:A:121:RCY:H1ZB	1.25	1.28	48	4
1:A:68:CYS:SG	2:A:176:RCY:O1J	1.25	1.95	22	2
2:A:160:RCY:H1V	2:A:168:RCY:C1V	1.25	1.29	48	2
1:A:70:TRP:N	2:A:173:RCY:C1V	1.25	1.77	64	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:173:RCY:H1YA	2:A:176:RCY:C1M	1.25	1.61	99	2
2:A:168:RCY:H1CB	2:A:176:RCY:C1Y	1.25	1.62	59	1
1:A:70:TRP:CB	2:A:168:RCY:H1LA	1.25	1.60	46	2
2:A:110:RCY:C1V	2:A:121:RCY:H1M	1.25	1.60	5	1
1:A:60:CYS:N	2:A:160:RCY:O1H	1.25	1.68	91	4
2:A:150:RCY:H1CB	2:A:187:RCY:C1Y	1.25	1.62	81	2
1:A:71:GLU:OE2	2:A:173:RCY:H1CB	1.25	1.08	89	1
2:A:160:RCY:H1Z	2:A:168:RCY:C1W	1.25	1.60	78	1
2:A:187:RCY:O1H	2:A:187:RCY:H1CA	1.25	1.21	100	5
1:A:68:CYS:N	2:A:168:RCY:H1S	1.25	1.23	51	7
2:A:138:RCY:C1Q	2:A:150:RCY:H1V	1.25	1.61	19	1
2:A:130:RCY:C1V	2:A:160:RCY:O1J	1.25	1.84	64	1
1:A:70:TRP:CE3	2:A:168:RCY:C1V	1.25	2.20	94	2
2:A:168:RCY:C1P	2:A:173:RCY:C1Z	1.25	2.13	10	2
2:A:176:RCY:C1M	2:A:187:RCY:O1H	1.25	1.66	3	2
1:A:69:PRO:HB3	2:A:173:RCY:C1Q	1.25	1.60	81	1
2:A:168:RCY:C1U	2:A:176:RCY:H1YA	1.25	1.52	59	1
1:A:71:GLU:C	2:A:173:RCY:O1H	1.25	1.74	67	3
2:A:168:RCY:C1M	2:A:187:RCY:O1J	1.25	1.83	64	3
1:A:70:TRP:CD1	2:A:176:RCY:H1U	1.25	1.65	62	1
2:A:138:RCY:H1VB	2:A:138:RCY:O1H	1.25	1.27	94	3
2:A:138:RCY:H1YB	2:A:150:RCY:N1R	1.25	0.88	60	1
1:A:68:CYS:O	2:A:168:RCY:H1S	1.25	1.07	83	3
2:A:173:RCY:C1W	2:A:176:RCY:H1VA	1.25	1.54	31	2
1:A:70:TRP:C	2:A:173:RCY:H1V	1.24	1.36	78	1
2:A:130:RCY:O1J	2:A:160:RCY:H1C	1.24	1.20	64	2
2:A:110:RCY:O1H	2:A:110:RCY:H1VB	1.24	1.27	80	7
2:A:160:RCY:C1W	2:A:168:RCY:H1U	1.24	1.40	52	1
2:A:150:RCY:H1VB	2:A:150:RCY:O1H	1.24	1.29	1	8
1:A:65:THR:HG21	2:A:160:RCY:C1Y	1.24	1.60	55	1
1:A:76:CYS:CA	2:A:173:RCY:C1C	1.24	2.13	29	1
1:A:70:TRP:NE1	2:A:168:RCY:H1ZB	1.24	1.45	24	1
2:A:173:RCY:C1Z	2:A:176:RCY:C1W	1.24	2.15	81	4
1:A:77:GLU:OE2	2:A:173:RCY:H1L	1.24	1.32	33	1
1:A:60:CYS:C	2:A:138:RCY:C1V	1.24	2.03	7	1
1:A:64:ILE:CG1	2:A:160:RCY:H1VA	1.24	1.62	54	1
1:A:70:TRP:O	2:A:173:RCY:H1LA	1.24	1.06	82	2
1:A:74:ASN:O	2:A:173:RCY:H1VB	1.24	1.08	15	1
2:A:121:RCY:H1VB	2:A:121:RCY:O1H	1.24	1.31	51	7
2:A:130:RCY:C1Y	2:A:160:RCY:C1Q	1.24	2.08	88	1
2:A:187:RCY:O1G	2:A:187:RCY:H1ZB	1.24	1.26	22	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:70:TRP:N	2:A:168:RCY:H1L	1.24	1.45	28	2
2:A:168:RCY:C1Q	2:A:176:RCY:H1YB	1.24	1.62	59	1
2:A:160:RCY:C1M	2:A:168:RCY:C1Z	1.24	1.90	9	2
1:A:63:ASP:CB	2:A:160:RCY:H1C	1.24	1.58	63	1
2:A:173:RCY:C1P	2:A:176:RCY:C1L	1.24	2.11	28	1
1:A:70:TRP:CD1	2:A:173:RCY:C1C	1.24	2.20	38	2
2:A:150:RCY:C1X	2:A:160:RCY:H1V	1.24	1.60	42	1
2:A:173:RCY:C1P	2:A:176:RCY:C1C	1.24	2.16	64	2
2:A:121:RCY:H1CA	2:A:121:RCY:O1H	1.24	1.17	67	5
2:A:138:RCY:C1L	2:A:160:RCY:H1ZB	1.24	1.29	18	1
1:A:70:TRP:HA	2:A:168:RCY:C1C	1.24	1.60	57	1
2:A:121:RCY:O1G	2:A:121:RCY:H1CA	1.24	1.23	90	3
2:A:160:RCY:O1H	2:A:160:RCY:H1VB	1.24	1.27	59	11
1:A:77:GLU:HA	2:A:176:RCY:O1G	1.24	1.02	55	1
1:A:68:CYS:HA	2:A:168:RCY:O1H	1.24	1.05	87	3
2:A:160:RCY:C1M	2:A:168:RCY:C1S	1.24	2.01	34	2
2:A:173:RCY:H1YB	2:A:176:RCY:C1C	1.24	1.63	86	2
2:A:130:RCY:H1CA	2:A:130:RCY:O1H	1.24	1.30	29	2
2:A:138:RCY:C1V	2:A:150:RCY:C1C	1.24	2.13	10	2
1:A:63:ASP:CA	2:A:168:RCY:H1VA	1.24	1.61	5	1
2:A:150:RCY:O1H	2:A:150:RCY:H1VB	1.24	1.26	46	4
2:A:138:RCY:C1Y	2:A:176:RCY:O1J	1.24	1.84	9	1
2:A:130:RCY:C1Z	2:A:160:RCY:H1YA	1.24	1.59	7	1
2:A:138:RCY:C1Y	2:A:150:RCY:C1C	1.24	2.14	97	2
2:A:173:RCY:H1VA	2:A:187:RCY:O1J	1.24	1.24	67	1
1:A:66:VAL:O	2:A:168:RCY:C1V	1.24	1.86	27	3
2:A:173:RCY:N1R	2:A:176:RCY:C1V	1.24	2.01	76	2
2:A:138:RCY:O1H	2:A:138:RCY:H1VB	1.24	1.29	99	2
1:A:70:TRP:CE3	2:A:187:RCY:H1ZA	1.24	1.68	76	1
2:A:121:RCY:C1Y	2:A:176:RCY:H1LA	1.24	1.63	35	1
2:A:168:RCY:C1L	2:A:168:RCY:C1Q	1.24	2.16	79	1
2:A:176:RCY:C1X	2:A:187:RCY:C1V	1.24	2.13	33	1
2:A:168:RCY:H1V	2:A:173:RCY:C1X	1.24	1.61	45	1
2:A:168:RCY:O1H	2:A:168:RCY:H1CA	1.24	1.23	89	2
2:A:138:RCY:H1S	2:A:160:RCY:C1U	1.24	1.63	27	1
1:A:78:LEU:HD11	2:A:176:RCY:C1U	1.24	1.63	56	1
1:A:69:PRO:CG	2:A:150:RCY:H1ZB	1.24	1.62	92	1
2:A:173:RCY:H1VB	2:A:173:RCY:O1G	1.23	1.32	100	5
1:A:70:TRP:CE3	2:A:168:RCY:H1Z	1.23	1.65	41	1
2:A:110:RCY:C1Y	2:A:121:RCY:C1V	1.23	2.15	81	2
1:A:70:TRP:N	2:A:173:RCY:C1P	1.23	2.01	6	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:150:RCY:O1J	2:A:160:RCY:C1Z	1.23	1.85	87	2
1:A:62:THR:HG21	2:A:160:RCY:O1G	1.23	1.05	82	1
1:A:69:PRO:CB	2:A:168:RCY:H1YA	1.23	1.62	66	1
2:A:173:RCY:C1Z	2:A:187:RCY:C1S	1.23	2.17	92	1
2:A:150:RCY:C1Y	2:A:187:RCY:H1CB	1.23	1.63	78	1
1:A:70:TRP:HA	2:A:173:RCY:O1H	1.23	1.09	14	1
1:A:71:GLU:N	2:A:173:RCY:C1V	1.23	2.01	84	1
2:A:110:RCY:H1YB	2:A:121:RCY:C1C	1.23	1.55	81	1
2:A:138:RCY:C1L	2:A:160:RCY:C1Z	1.23	2.10	18	1
2:A:138:RCY:H1YB	2:A:150:RCY:C1Y	1.23	1.49	89	2
2:A:138:RCY:C1V	2:A:187:RCY:H1ZA	1.23	1.62	49	2
1:A:62:THR:HB	2:A:160:RCY:C1C	1.23	1.38	46	1
1:A:67:ILE:CB	2:A:150:RCY:C1V	1.23	2.08	31	1
1:A:70:TRP:CH2	2:A:121:RCY:O1H	1.23	1.85	78	1
2:A:138:RCY:C1Y	2:A:150:RCY:O1J	1.23	1.86	97	2
2:A:150:RCY:H1VB	2:A:150:RCY:O1G	1.23	1.28	68	6
2:A:138:RCY:C1Z	2:A:187:RCY:C1Y	1.23	2.11	32	3
2:A:176:RCY:C1Z	2:A:187:RCY:H1V	1.23	1.62	10	1
1:A:69:PRO:O	2:A:173:RCY:H1LA	1.23	1.01	6	1
2:A:176:RCY:C1M	2:A:187:RCY:H1U	1.23	1.60	96	2
1:A:71:GLU:HB3	2:A:168:RCY:O1H	1.23	1.04	37	2
1:A:70:TRP:HB2	2:A:168:RCY:C1Q	1.23	1.63	20	1
2:A:173:RCY:C1V	2:A:176:RCY:C1Q	1.23	2.15	38	3
2:A:150:RCY:O1G	2:A:150:RCY:C1Z	1.23	1.86	18	3
1:A:70:TRP:O	2:A:150:RCY:C1Z	1.23	1.85	58	1
2:A:176:RCY:O1G	2:A:176:RCY:H1VB	1.23	1.27	81	4
1:A:69:PRO:C	2:A:173:RCY:C1L	1.23	2.06	6	1
2:A:138:RCY:O1J	2:A:150:RCY:H1ZA	1.23	1.28	35	1
2:A:168:RCY:N1V	2:A:187:RCY:C1M	1.23	1.98	70	1
1:A:75:HIS:O	2:A:176:RCY:H1ZB	1.23	1.06	51	1
2:A:110:RCY:H1ZB	2:A:110:RCY:O1G	1.22	1.33	7	6
2:A:173:RCY:C1C	2:A:187:RCY:N1R	1.22	2.01	88	1
2:A:173:RCY:O1H	2:A:173:RCY:H1VB	1.22	1.34	26	5
2:A:138:RCY:O1H	2:A:138:RCY:H1ZB	1.22	1.26	40	5
2:A:173:RCY:H1VB	2:A:173:RCY:O1H	1.22	1.34	28	3
1:A:70:TRP:HE3	2:A:168:RCY:O1G	1.22	0.85	94	2
2:A:130:RCY:H1Y	2:A:160:RCY:N1R	1.22	1.47	50	1
1:A:67:ILE:CG1	2:A:176:RCY:H1V	1.22	1.64	16	1
1:A:67:ILE:HA	2:A:176:RCY:C1V	1.22	1.63	16	1
2:A:130:RCY:C1C	2:A:160:RCY:C1M	1.22	2.16	7	1
1:A:67:ILE:HG23	2:A:173:RCY:O1G	1.22	1.29	21	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:173:RCY:C1Y	2:A:187:RCY:C1Y	1.22	2.17	31	1
1:A:65:THR:CG2	2:A:160:RCY:H1ZA	1.22	1.59	100	1
1:A:76:CYS:HB2	2:A:173:RCY:O1G	1.22	1.24	38	2
2:A:160:RCY:O1G	2:A:160:RCY:H1CA	1.22	1.30	29	2
1:A:71:GLU:CA	2:A:173:RCY:O1H	1.22	1.87	67	3
1:A:68:CYS:CA	2:A:168:RCY:H1LA	1.22	1.55	30	4
1:A:74:ASN:OD1	2:A:173:RCY:H1L	1.22	1.03	2	1
1:A:72:ALA:HB1	2:A:173:RCY:N1R	1.22	1.48	30	2
2:A:138:RCY:H1C	2:A:160:RCY:C1L	1.22	1.60	73	1
2:A:138:RCY:O1G	2:A:150:RCY:H1MA	1.22	1.34	30	1
2:A:173:RCY:C1C	2:A:176:RCY:C1M	1.22	2.17	52	3
1:A:69:PRO:HA	2:A:168:RCY:C1M	1.22	1.49	5	1
1:A:69:PRO:HB2	2:A:173:RCY:O1J	1.22	1.34	85	2
2:A:138:RCY:H1L	2:A:160:RCY:C1Z	1.22	1.61	18	1
2:A:138:RCY:C1C	2:A:187:RCY:C1M	1.22	2.17	11	1
2:A:173:RCY:C1Q	2:A:176:RCY:H1M	1.22	1.63	67	1
2:A:168:RCY:C1L	2:A:173:RCY:H1ZA	1.22	1.49	11	2
2:A:150:RCY:H1S	2:A:160:RCY:C1Y	1.22	1.63	85	1
2:A:173:RCY:H1ZA	2:A:187:RCY:C1L	1.22	1.65	45	2
2:A:160:RCY:C1S	2:A:176:RCY:O1G	1.22	1.87	73	1
2:A:173:RCY:C1C	2:A:176:RCY:O1J	1.22	1.78	56	3
2:A:130:RCY:H1C	2:A:160:RCY:C1L	1.22	1.65	66	1
2:A:168:RCY:O1H	2:A:168:RCY:H1VB	1.22	1.28	61	4
2:A:173:RCY:C1V	2:A:176:RCY:N1R	1.22	2.02	17	4
2:A:138:RCY:N1R	2:A:150:RCY:O1H	1.22	1.73	62	1
1:A:69:PRO:N	2:A:173:RCY:C1P	1.22	2.03	10	1
2:A:138:RCY:H1ZB	2:A:150:RCY:O1G	1.22	1.31	81	1
2:A:168:RCY:N1R	2:A:176:RCY:C1Y	1.22	2.03	59	1
2:A:173:RCY:H1L	2:A:176:RCY:O1G	1.22	1.03	71	1
2:A:160:RCY:O1G	2:A:168:RCY:H1Y	1.22	1.01	9	1
1:A:76:CYS:C	2:A:176:RCY:O1H	1.22	1.78	73	1
1:A:64:ILE:CG2	2:A:168:RCY:O1J	1.22	1.66	30	1
2:A:176:RCY:H1C	2:A:187:RCY:C1P	1.21	1.65	61	1
2:A:150:RCY:C1V	2:A:160:RCY:C1Y	1.21	2.06	42	1
1:A:71:GLU:OE1	2:A:168:RCY:H1V	1.21	1.32	99	1
1:A:74:ASN:H	2:A:173:RCY:C1Q	1.21	1.48	82	2
1:A:60:CYS:N	2:A:160:RCY:C1L	1.21	2.02	28	3
2:A:173:RCY:C1W	2:A:187:RCY:H1Y	1.21	1.64	31	1
2:A:138:RCY:H1ZA	2:A:150:RCY:C1L	1.21	1.62	1	1
2:A:168:RCY:H1LA	2:A:173:RCY:C1M	1.21	1.65	49	2
2:A:160:RCY:N1R	2:A:168:RCY:H1M	1.21	1.44	52	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:173:RCY:C1Z	2:A:187:RCY:H1C	1.21	1.65	64	1
2:A:176:RCY:C1Y	2:A:187:RCY:H1YA	1.21	1.63	72	1
2:A:138:RCY:H1L	2:A:150:RCY:N1R	1.21	0.99	23	1
2:A:160:RCY:O1J	2:A:168:RCY:H1U	1.21	1.26	47	1
1:A:63:ASP:OD1	2:A:160:RCY:H1CA	1.21	1.35	14	2
2:A:130:RCY:C1V	2:A:160:RCY:C1Q	1.21	2.15	8	1
1:A:73:CYS:CB	2:A:176:RCY:H1ZA	1.21	1.59	58	1
1:A:71:GLU:CG	2:A:130:RCY:H1MA	1.21	1.64	94	1
2:A:168:RCY:H1ZA	2:A:173:RCY:C1Z	1.21	1.66	31	2
1:A:76:CYS:N	2:A:176:RCY:C1Q	1.21	2.04	10	2
1:A:63:ASP:O	2:A:168:RCY:H1VB	1.21	1.05	5	1
2:A:168:RCY:H1MA	2:A:187:RCY:O1G	1.21	0.99	100	2
1:A:70:TRP:HB2	2:A:168:RCY:C1L	1.21	1.64	33	4
2:A:130:RCY:H1VA	2:A:160:RCY:O1G	1.21	1.31	87	1
2:A:138:RCY:N1R	2:A:150:RCY:C1Y	1.21	2.03	23	2
2:A:168:RCY:O1J	2:A:176:RCY:H1Z	1.21	1.34	17	1
1:A:70:TRP:CE2	2:A:187:RCY:H1Z	1.21	1.69	76	1
1:A:69:PRO:HG3	2:A:173:RCY:C1Z	1.21	1.47	57	1
2:A:160:RCY:H1MA	2:A:168:RCY:C1Z	1.21	1.52	96	2
2:A:150:RCY:O1J	2:A:160:RCY:H1Z	1.21	1.31	32	1
2:A:130:RCY:O1H	2:A:130:RCY:H1CA	1.20	1.36	33	3
1:A:77:GLU:CA	2:A:176:RCY:O1G	1.20	1.89	55	1
2:A:150:RCY:H1VB	2:A:187:RCY:C1Z	1.20	1.65	64	1
2:A:173:RCY:H1U	2:A:176:RCY:C1Q	1.20	1.67	38	1
2:A:176:RCY:C1Y	2:A:187:RCY:N1R	1.20	2.02	19	1
1:A:69:PRO:HB3	2:A:173:RCY:C1P	1.20	1.66	75	1
2:A:160:RCY:H1Y	2:A:168:RCY:O1G	1.20	1.03	65	3
1:A:66:VAL:O	2:A:168:RCY:C1U	1.20	1.90	51	2
2:A:110:RCY:H1CA	2:A:110:RCY:O1G	1.20	1.30	77	5
2:A:176:RCY:C1P	2:A:187:RCY:C1M	1.20	2.17	60	2
2:A:176:RCY:O1G	2:A:187:RCY:C1M	1.20	1.88	60	2
1:A:69:PRO:HB3	2:A:173:RCY:C1Z	1.20	1.58	57	4
2:A:150:RCY:C1Y	2:A:173:RCY:C1X	1.20	2.18	3	1
2:A:138:RCY:O1J	2:A:187:RCY:O1J	1.20	1.60	47	2
2:A:173:RCY:C1V	2:A:176:RCY:H1U	1.20	1.60	38	1
1:A:70:TRP:CE2	2:A:160:RCY:H1VB	1.20	1.70	34	1
1:A:73:CYS:HB2	2:A:176:RCY:N1R	1.20	1.26	70	1
1:A:70:TRP:CB	2:A:168:RCY:H1CB	1.20	1.65	20	1
2:A:138:RCY:C1M	2:A:187:RCY:C1V	1.20	2.18	92	1
2:A:168:RCY:C1Z	2:A:173:RCY:C1V	1.20	2.17	70	3
2:A:168:RCY:C1Z	2:A:187:RCY:H1M	1.20	1.65	84	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:70:TRP:CE2	2:A:168:RCY:H1Z	1.20	1.72	24	1
2:A:173:RCY:C1Q	2:A:176:RCY:H1LA	1.20	1.65	28	2
2:A:176:RCY:H1M	2:A:187:RCY:C1W	1.20	1.66	5	1
2:A:138:RCY:C1Z	2:A:187:RCY:H1Z	1.20	1.64	77	2
2:A:176:RCY:C1M	2:A:187:RCY:C1C	1.20	2.17	87	2
2:A:138:RCY:C1Z	2:A:187:RCY:O1G	1.20	1.89	71	1
1:A:70:TRP:CE3	2:A:168:RCY:H1MA	1.20	1.72	44	2
2:A:130:RCY:C1X	2:A:160:RCY:H1M	1.20	1.56	7	1
2:A:150:RCY:C1Y	2:A:173:RCY:C1C	1.20	2.19	3	1
1:A:70:TRP:HH2	2:A:168:RCY:O1G	1.20	0.81	48	2
2:A:160:RCY:C1Y	2:A:168:RCY:O1G	1.20	1.90	32	4
2:A:160:RCY:C1Y	2:A:168:RCY:H1M	1.20	1.65	34	2
1:A:72:ALA:HB3	2:A:173:RCY:O1H	1.20	1.34	13	2
2:A:168:RCY:C1X	2:A:176:RCY:H1Y	1.20	1.64	59	1
1:A:70:TRP:CH2	2:A:168:RCY:H1YA	1.20	1.71	49	2
1:A:68:CYS:CB	2:A:176:RCY:H1Y	1.20	1.66	80	1
1:A:70:TRP:HD1	2:A:176:RCY:C1U	1.19	1.50	62	1
2:A:130:RCY:C1P	2:A:160:RCY:O1G	1.19	1.83	62	1
1:A:62:THR:OG1	2:A:168:RCY:C1P	1.19	1.90	72	2
1:A:71:GLU:C	2:A:168:RCY:C1M	1.19	1.94	91	1
1:A:73:CYS:C	2:A:173:RCY:H1L	1.19	1.55	32	1
2:A:176:RCY:C1C	2:A:187:RCY:C1U	1.19	2.19	4	1
2:A:138:RCY:H1V	2:A:150:RCY:O1J	1.19	1.36	36	1
2:A:150:RCY:C1M	2:A:168:RCY:C1Y	1.19	2.19	74	1
1:A:63:ASP:O	2:A:160:RCY:C1Z	1.19	1.89	78	2
1:A:68:CYS:CA	2:A:168:RCY:H1L	1.19	1.67	75	1
1:A:75:HIS:CA	2:A:176:RCY:C1L	1.19	2.20	13	1
2:A:173:RCY:H1ZB	2:A:176:RCY:O1J	1.19	1.14	71	1
2:A:168:RCY:N1R	2:A:176:RCY:H1M	1.19	1.24	71	1
2:A:176:RCY:C1V	2:A:187:RCY:C1X	1.19	2.19	33	1
1:A:77:GLU:OE1	2:A:176:RCY:C1V	1.19	1.89	7	1
1:A:62:THR:CB	2:A:160:RCY:C1C	1.19	2.02	46	1
1:A:70:TRP:CE3	2:A:176:RCY:C1C	1.19	2.24	77	1
2:A:150:RCY:C1Z	2:A:187:RCY:H1YB	1.19	1.67	9	2
2:A:168:RCY:H1VA	2:A:176:RCY:C1Y	1.19	1.45	76	1
1:A:69:PRO:CB	2:A:173:RCY:H1ZA	1.19	1.66	35	2
1:A:73:CYS:O	2:A:173:RCY:H1CA	1.19	1.35	35	1
1:A:77:GLU:CG	2:A:176:RCY:H1U	1.19	1.67	39	1
1:A:70:TRP:CD1	2:A:176:RCY:H1VB	1.19	1.71	77	1
2:A:168:RCY:H1ZA	2:A:176:RCY:C1V	1.19	1.66	31	1
2:A:150:RCY:H1VB	2:A:160:RCY:C1M	1.19	1.67	42	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:130:RCY:O1J	2:A:138:RCY:H1L	1.19	1.15	58	1
2:A:168:RCY:C1Q	2:A:173:RCY:C1Y	1.19	2.20	84	1
1:A:71:GLU:OE1	2:A:168:RCY:O1G	1.19	1.59	40	2
2:A:168:RCY:C1V	2:A:173:RCY:C1Q	1.19	2.20	76	1
2:A:150:RCY:H1ZA	2:A:187:RCY:C1Y	1.19	1.68	3	3
2:A:150:RCY:H1ZA	2:A:187:RCY:C1V	1.19	0.88	37	2
1:A:69:PRO:CB	2:A:173:RCY:H1Y	1.19	1.67	9	1
1:A:64:ILE:HD12	2:A:168:RCY:C1C	1.19	1.65	4	1
1:A:69:PRO:HG3	2:A:168:RCY:C1W	1.19	1.59	66	1
2:A:150:RCY:H1ZB	2:A:187:RCY:C1Y	1.19	1.68	49	2
1:A:75:HIS:CG	2:A:176:RCY:C1C	1.19	2.23	84	1
2:A:160:RCY:C1U	2:A:168:RCY:H1S	1.19	1.68	34	1
1:A:69:PRO:HB2	2:A:176:RCY:O1G	1.18	1.34	64	1
1:A:75:HIS:CB	2:A:176:RCY:H1L	1.18	1.68	13	1
1:A:69:PRO:O	2:A:173:RCY:C1L	1.18	1.91	6	1
2:A:150:RCY:H1YA	2:A:173:RCY:N1R	1.18	1.51	3	1
1:A:65:THR:O	2:A:150:RCY:H1YB	1.18	1.32	31	1
2:A:168:RCY:C1M	2:A:173:RCY:O1J	1.18	1.92	20	3
2:A:173:RCY:O1H	2:A:173:RCY:H1ZB	1.18	1.38	2	4
1:A:64:ILE:HG13	2:A:168:RCY:C1S	1.18	1.68	26	2
2:A:130:RCY:C1L	2:A:160:RCY:O1G	1.18	1.92	62	1
2:A:168:RCY:C1C	2:A:176:RCY:C1Z	1.18	2.07	3	2
2:A:138:RCY:H1VB	2:A:138:RCY:O1G	1.18	1.37	54	3
1:A:69:PRO:HA	2:A:173:RCY:O1J	1.18	1.29	9	1
1:A:63:ASP:HB3	2:A:160:RCY:C1C	1.18	1.67	63	1
2:A:160:RCY:H1U	2:A:168:RCY:C1W	1.18	1.60	96	1
1:A:69:PRO:CG	2:A:150:RCY:C1Y	1.18	2.21	85	1
2:A:168:RCY:H1VA	2:A:176:RCY:O1H	1.18	1.37	71	1
1:A:62:THR:CG2	2:A:160:RCY:C1Z	1.18	2.06	46	1
1:A:75:HIS:O	2:A:176:RCY:O1H	1.18	1.59	84	1
2:A:138:RCY:H1CA	2:A:150:RCY:C1Y	1.18	1.68	59	1
2:A:138:RCY:H1YA	2:A:176:RCY:O1J	1.18	0.96	9	1
2:A:160:RCY:O1J	2:A:168:RCY:C1U	1.18	1.91	47	1
1:A:67:ILE:O	2:A:173:RCY:H1V	1.18	1.00	80	1
1:A:72:ALA:CB	2:A:173:RCY:N1R	1.18	2.06	30	2
2:A:160:RCY:O1G	2:A:168:RCY:H1CB	1.18	1.35	89	1
2:A:138:RCY:C1S	2:A:160:RCY:H1U	1.18	1.63	27	1
2:A:130:RCY:C1Z	2:A:160:RCY:H1LA	1.18	1.52	61	1
2:A:168:RCY:C1Z	2:A:187:RCY:N1R	1.18	2.07	100	1
2:A:150:RCY:C1Y	2:A:173:RCY:O1J	1.18	1.89	3	3
1:A:76:CYS:SG	2:A:187:RCY:H1Z	1.18	1.79	80	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:160:RCY:H1YB	2:A:168:RCY:N1R	1.18	1.52	58	1
2:A:110:RCY:H1CA	2:A:110:RCY:O1H	1.18	1.38	50	4
2:A:110:RCY:C1C	2:A:121:RCY:C1Y	1.18	1.97	5	1
1:A:64:ILE:HD11	2:A:168:RCY:O1G	1.18	1.38	12	1
1:A:77:GLU:CD	2:A:176:RCY:H1VA	1.18	1.54	7	1
1:A:71:GLU:CD	2:A:173:RCY:H1CB	1.18	1.59	89	1
1:A:71:GLU:HA	2:A:173:RCY:C1L	1.17	1.69	17	1
1:A:71:GLU:CD	2:A:168:RCY:C1C	1.17	2.10	93	2
2:A:173:RCY:H1YA	2:A:187:RCY:C1W	1.17	1.69	92	3
2:A:173:RCY:H1ZB	2:A:173:RCY:O1H	1.17	1.35	21	4
1:A:70:TRP:CZ3	2:A:168:RCY:C1W	1.17	2.25	41	2
2:A:130:RCY:H1VB	2:A:130:RCY:O1H	1.17	1.39	72	7
1:A:69:PRO:HG3	2:A:187:RCY:C1Y	1.17	1.42	87	2
1:A:63:ASP:HB3	2:A:168:RCY:C1V	1.17	1.68	5	1
2:A:160:RCY:H1C	2:A:168:RCY:C1L	1.17	1.67	48	1
1:A:61:GLY:C	2:A:150:RCY:H1M	1.17	1.57	11	1
2:A:176:RCY:N1R	2:A:176:RCY:C1U	1.17	2.07	25	1
1:A:66:VAL:CG1	2:A:121:RCY:C1Z	1.17	2.20	89	1
1:A:61:GLY:N	2:A:160:RCY:H1LA	1.17	1.53	19	1
1:A:63:ASP:C	2:A:168:RCY:C1V	1.17	2.12	5	1
1:A:63:ASP:HB2	2:A:150:RCY:C1X	1.17	1.33	85	1
1:A:74:ASN:OD1	2:A:173:RCY:O1G	1.17	1.58	91	1
2:A:138:RCY:C1V	2:A:187:RCY:H1Y	1.17	1.69	66	1
1:A:70:TRP:O	2:A:173:RCY:H1V	1.17	1.36	78	1
2:A:173:RCY:O1H	2:A:173:RCY:C1Z	1.17	1.90	22	4
2:A:173:RCY:C1U	2:A:176:RCY:H1VA	1.17	1.69	19	1
2:A:150:RCY:H1Y	2:A:187:RCY:C1Y	1.17	1.67	18	2
2:A:173:RCY:C1L	2:A:176:RCY:C1V	1.17	2.14	11	3
1:A:74:ASN:HA	2:A:173:RCY:C1P	1.17	1.48	27	1
1:A:68:CYS:HA	2:A:168:RCY:C1Q	1.17	1.70	87	4
1:A:71:GLU:CG	2:A:173:RCY:O1G	1.17	1.91	17	1
1:A:68:CYS:H	2:A:168:RCY:C1L	1.17	1.51	21	3
1:A:70:TRP:CD1	2:A:176:RCY:C1U	1.17	2.25	62	1
2:A:138:RCY:C1P	2:A:150:RCY:H1C	1.17	1.69	94	2
1:A:67:ILE:CG1	2:A:176:RCY:C1V	1.17	2.19	16	1
1:A:70:TRP:CG	2:A:187:RCY:C1Z	1.17	2.27	76	2
1:A:70:TRP:CA	2:A:173:RCY:H1VB	1.17	1.32	6	1
2:A:173:RCY:C1S	2:A:176:RCY:C1L	1.17	2.22	28	2
1:A:75:HIS:CD2	2:A:168:RCY:C1Z	1.17	2.27	73	1
2:A:173:RCY:C1S	2:A:176:RCY:H1M	1.17	1.69	67	1
2:A:138:RCY:C1C	2:A:150:RCY:H1CB	1.17	1.65	66	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:160:RCY:H1Y	2:A:168:RCY:O1J	1.17	1.36	59	3
1:A:69:PRO:CB	2:A:173:RCY:C1Y	1.17	2.23	35	2
1:A:71:GLU:CB	2:A:168:RCY:O1H	1.17	1.93	37	3
1:A:77:GLU:N	2:A:176:RCY:H1LA	1.17	1.51	31	2
1:A:70:TRP:HB2	2:A:121:RCY:C1V	1.17	1.49	30	1
2:A:173:RCY:C1Y	2:A:176:RCY:C1W	1.16	2.21	87	2
2:A:138:RCY:C1U	2:A:187:RCY:H1C	1.16	1.56	5	1
1:A:68:CYS:SG	2:A:173:RCY:H1VB	1.16	1.79	71	1
2:A:138:RCY:O1G	2:A:150:RCY:C1M	1.16	1.93	30	1
1:A:71:GLU:CA	2:A:173:RCY:C1P	1.16	2.23	17	2
1:A:76:CYS:HB2	2:A:173:RCY:C1P	1.16	1.68	38	2
2:A:150:RCY:C1V	2:A:160:RCY:H1M	1.16	1.71	42	1
2:A:168:RCY:C1V	2:A:176:RCY:C1W	1.16	2.23	94	1
1:A:70:TRP:N	2:A:173:RCY:C1Z	1.16	2.00	85	2
1:A:76:CYS:SG	2:A:176:RCY:H1S	1.16	1.80	25	2
1:A:70:TRP:CH2	2:A:160:RCY:H1VB	1.16	1.45	37	1
2:A:138:RCY:C1Y	2:A:160:RCY:O1H	1.16	1.92	73	1
2:A:168:RCY:C1Y	2:A:187:RCY:N1V	1.16	2.07	97	1
1:A:70:TRP:CD2	2:A:173:RCY:H1ZA	1.16	1.71	92	1
2:A:130:RCY:O1J	2:A:138:RCY:C1P	1.16	1.92	58	2
2:A:173:RCY:O1H	2:A:176:RCY:C1V	1.16	1.93	62	2
2:A:168:RCY:H1Y	2:A:176:RCY:C1V	1.16	1.52	94	1
1:A:73:CYS:N	2:A:173:RCY:C1L	1.16	1.93	10	8
2:A:138:RCY:H1ZB	2:A:138:RCY:O1G	1.16	1.39	21	3
2:A:138:RCY:C1Y	2:A:187:RCY:H1CA	1.16	1.65	96	2
1:A:72:ALA:O	2:A:168:RCY:C1Z	1.16	1.85	57	1
2:A:138:RCY:C1P	2:A:150:RCY:C1M	1.16	2.22	23	2
2:A:138:RCY:C1C	2:A:187:RCY:H1M	1.16	1.70	11	1
2:A:173:RCY:C1Y	2:A:187:RCY:C1U	1.16	2.15	77	1
2:A:168:RCY:H1VA	2:A:176:RCY:O1J	1.16	1.41	43	1
2:A:173:RCY:H1ZB	2:A:176:RCY:C1Y	1.16	1.70	41	2
1:A:68:CYS:HB3	2:A:173:RCY:O1J	1.16	1.39	50	1
1:A:64:ILE:HD11	2:A:168:RCY:C1Y	1.16	1.70	6	1
2:A:168:RCY:O1G	2:A:173:RCY:O1J	1.16	1.64	53	2
1:A:69:PRO:CD	2:A:168:RCY:C1V	1.16	2.24	63	1
2:A:160:RCY:H1YA	2:A:168:RCY:C1Q	1.16	1.70	100	1
1:A:76:CYS:CB	2:A:173:RCY:C1P	1.16	2.23	38	1
2:A:138:RCY:C1V	2:A:150:RCY:C1V	1.16	2.24	67	2
1:A:62:THR:CG2	2:A:160:RCY:O1H	1.16	1.94	8	1
1:A:70:TRP:CD1	2:A:173:RCY:H1CA	1.16	1.52	64	1
2:A:138:RCY:C1C	2:A:150:RCY:C1Z	1.16	2.09	29	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:67:ILE:HG21	2:A:138:RCY:O1H	1.16	1.38	72	1
2:A:160:RCY:H1VA	2:A:176:RCY:C1V	1.16	1.69	57	1
2:A:150:RCY:O1J	2:A:160:RCY:H1ZA	1.16	0.94	87	1
2:A:173:RCY:C1M	2:A:176:RCY:H1V	1.15	1.72	17	1
1:A:68:CYS:N	2:A:168:RCY:C1S	1.15	2.09	51	7
2:A:150:RCY:O1G	2:A:150:RCY:H1VB	1.15	1.40	28	4
2:A:168:RCY:N1R	2:A:187:RCY:O1J	1.15	1.79	64	1
1:A:70:TRP:C	2:A:173:RCY:O1G	1.15	1.84	94	1
2:A:168:RCY:O1G	2:A:176:RCY:C1Z	1.15	1.94	13	1
2:A:160:RCY:C1V	2:A:168:RCY:H1L	1.15	1.69	24	1
2:A:187:RCY:H1CA	2:A:187:RCY:O1H	1.15	1.37	44	3
2:A:168:RCY:N1V	2:A:173:RCY:C1V	1.15	2.09	48	1
1:A:76:CYS:HA	2:A:176:RCY:O1H	1.15	0.93	74	3
1:A:59:GLY:O	2:A:160:RCY:H1L	1.15	1.37	89	2
2:A:138:RCY:O1H	2:A:150:RCY:H1Z	1.15	0.93	82	1
1:A:70:TRP:CE3	2:A:168:RCY:C1Z	1.15	2.28	41	2
2:A:173:RCY:C1Q	2:A:176:RCY:C1L	1.15	2.22	23	4
2:A:160:RCY:N1V	2:A:168:RCY:H1ZB	1.15	1.57	5	1
1:A:76:CYS:O	2:A:160:RCY:C1V	1.15	1.95	73	1
1:A:71:GLU:OE1	2:A:173:RCY:O1H	1.15	1.60	89	1
2:A:168:RCY:H1Z	2:A:187:RCY:C1L	1.15	1.71	3	1
2:A:138:RCY:C1M	2:A:150:RCY:N1R	1.15	2.02	1	1
1:A:64:ILE:HA	2:A:168:RCY:O1H	1.15	1.35	78	1
1:A:62:THR:CA	2:A:138:RCY:H1ZA	1.15	1.72	38	1
1:A:66:VAL:C	2:A:176:RCY:H1YB	1.15	1.36	22	1
1:A:70:TRP:CB	2:A:168:RCY:H1S	1.15	1.70	19	2
2:A:150:RCY:O1G	2:A:150:RCY:H1ZB	1.15	1.41	8	2
2:A:173:RCY:C1M	2:A:176:RCY:O1J	1.15	1.93	55	1
1:A:70:TRP:CZ2	2:A:160:RCY:O1H	1.15	1.98	58	1
1:A:70:TRP:HB2	2:A:150:RCY:N1R	1.15	1.55	34	1
2:A:176:RCY:H1M	2:A:187:RCY:O1J	1.15	1.35	91	2
2:A:168:RCY:H1S	2:A:173:RCY:H1U	1.15	1.16	71	1
2:A:168:RCY:H1MA	2:A:176:RCY:O1J	1.15	1.40	11	1
2:A:150:RCY:C1X	2:A:176:RCY:O1G	1.15	1.94	82	1
2:A:168:RCY:C1M	2:A:187:RCY:O1G	1.15	1.93	100	2
1:A:69:PRO:HA	2:A:173:RCY:H1ZB	1.15	1.16	75	1
1:A:76:CYS:SG	2:A:173:RCY:O1J	1.15	2.02	75	2
2:A:138:RCY:C1U	2:A:150:RCY:O1H	1.15	1.91	62	2
1:A:64:ILE:CG1	2:A:168:RCY:H1MA	1.15	1.70	6	1
1:A:66:VAL:HG12	2:A:160:RCY:O1J	1.15	1.36	68	1
1:A:70:TRP:CD1	2:A:121:RCY:C1M	1.15	2.29	49	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:71:GLU:HA	2:A:173:RCY:C1Q	1.15	1.72	49	4
1:A:64:ILE:CG2	2:A:168:RCY:H1M	1.15	1.72	95	1
2:A:173:RCY:O1G	2:A:176:RCY:O1H	1.15	1.65	96	1
1:A:66:VAL:CG1	2:A:121:RCY:C1V	1.15	1.90	83	1
2:A:130:RCY:O1J	2:A:160:RCY:C1C	1.15	1.95	43	3
2:A:168:RCY:N1V	2:A:176:RCY:H1Z	1.15	1.56	17	3
2:A:160:RCY:H1ZB	2:A:160:RCY:O1G	1.15	1.24	30	2
1:A:69:PRO:CB	2:A:173:RCY:C1W	1.15	2.23	35	2
2:A:138:RCY:C1V	2:A:176:RCY:H1CA	1.15	1.72	9	1
1:A:60:CYS:C	2:A:168:RCY:H1U	1.15	1.62	95	1
1:A:64:ILE:CG2	2:A:160:RCY:H1MA	1.15	1.71	47	1
1:A:68:CYS:CB	2:A:173:RCY:H1MA	1.15	1.64	73	1
2:A:138:RCY:H1YB	2:A:187:RCY:C1M	1.15	1.69	89	1
1:A:64:ILE:CD1	2:A:168:RCY:H1V	1.15	1.71	27	1
2:A:173:RCY:H1M	2:A:176:RCY:C1Q	1.14	1.71	88	1
2:A:150:RCY:C1V	2:A:160:RCY:C1M	1.14	2.25	42	1
2:A:176:RCY:C1M	2:A:187:RCY:O1J	1.14	1.89	91	2
2:A:168:RCY:C1Z	2:A:173:RCY:H1M	1.14	1.67	70	1
2:A:130:RCY:O1H	2:A:130:RCY:N1V	1.14	1.79	2	1
1:A:70:TRP:CG	2:A:176:RCY:H1VB	1.14	1.61	77	1
2:A:138:RCY:C1C	2:A:160:RCY:H1V	1.14	1.66	27	1
2:A:173:RCY:C1P	2:A:176:RCY:H1Y	1.14	1.62	97	1
2:A:168:RCY:C1Z	2:A:187:RCY:H1S	1.14	1.55	100	1
2:A:160:RCY:H1ZA	2:A:168:RCY:N1R	1.14	1.55	52	2
1:A:71:GLU:CG	2:A:150:RCY:C1U	1.14	2.19	58	1
2:A:168:RCY:H1Y	2:A:176:RCY:H1VB	1.14	1.17	94	1
1:A:69:PRO:CA	2:A:173:RCY:C1P	1.14	2.26	10	1
2:A:160:RCY:H1ZA	2:A:168:RCY:O1G	1.14	1.22	1	2
2:A:168:RCY:C1L	2:A:173:RCY:H1Z	1.14	1.70	5	1
1:A:70:TRP:CA	2:A:173:RCY:C1P	1.14	2.24	6	1
2:A:168:RCY:H1M	2:A:187:RCY:C1V	1.14	1.71	90	1
1:A:60:CYS:O	2:A:160:RCY:H1LA	1.14	1.41	30	1
2:A:176:RCY:C1C	2:A:187:RCY:H1CA	1.14	1.72	75	1
2:A:176:RCY:N1V	2:A:187:RCY:H1U	1.14	1.50	29	2
2:A:130:RCY:H1Y	2:A:138:RCY:C1Z	1.14	1.70	73	1
1:A:69:PRO:CG	2:A:176:RCY:C1Z	1.14	2.23	66	1
2:A:138:RCY:C1V	2:A:150:RCY:C1Y	1.14	2.26	1	4
1:A:68:CYS:CB	2:A:160:RCY:C1Z	1.14	2.25	19	1
2:A:138:RCY:O1G	2:A:138:RCY:H1ZB	1.14	1.40	62	8
2:A:150:RCY:C1C	2:A:187:RCY:O1J	1.14	1.95	84	1
2:A:168:RCY:C1Z	2:A:176:RCY:H1Z	1.14	1.72	11	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:138:RCY:O1G	2:A:150:RCY:H1M	1.14	1.37	23	2
2:A:160:RCY:O1J	2:A:168:RCY:N1V	1.14	1.81	78	3
1:A:65:THR:OG1	2:A:160:RCY:C1Z	1.14	1.96	100	1
2:A:160:RCY:H1YA	2:A:168:RCY:C1S	1.14	1.60	100	1
2:A:173:RCY:C1U	2:A:176:RCY:C1S	1.14	1.87	38	1
2:A:160:RCY:H1ZA	2:A:168:RCY:O1H	1.14	1.43	58	1
2:A:168:RCY:H1YA	2:A:176:RCY:C1V	1.14	1.56	94	2
1:A:70:TRP:HB3	2:A:173:RCY:C1Z	1.14	1.72	94	1
2:A:160:RCY:C1Z	2:A:168:RCY:C1P	1.14	2.26	1	2
1:A:62:THR:CG2	2:A:168:RCY:H1ZA	1.14	1.72	72	1
1:A:63:ASP:CB	2:A:150:RCY:H1CB	1.14	1.71	85	1
1:A:65:THR:O	2:A:173:RCY:H1C	1.14	0.92	71	1
2:A:150:RCY:C1Y	2:A:187:RCY:O1J	1.14	1.96	53	1
2:A:173:RCY:O1J	2:A:176:RCY:H1VB	1.13	1.06	23	4
1:A:62:THR:HA	2:A:138:RCY:C1Z	1.13	1.72	38	1
2:A:138:RCY:C1P	2:A:150:RCY:C1C	1.13	2.26	9	2
2:A:121:RCY:O1H	2:A:121:RCY:H1ZB	1.13	1.41	99	2
1:A:71:GLU:HA	2:A:176:RCY:C1V	1.13	1.46	67	3
2:A:138:RCY:C1Z	2:A:187:RCY:C1Z	1.13	2.25	77	2
2:A:173:RCY:H1MA	2:A:176:RCY:C1V	1.13	1.36	89	2
2:A:168:RCY:O1J	2:A:173:RCY:O1J	1.13	1.67	96	1
2:A:173:RCY:C1M	2:A:187:RCY:H1YA	1.13	1.62	31	1
1:A:78:LEU:CD1	2:A:176:RCY:N1R	1.13	2.11	56	1
1:A:70:TRP:HB3	2:A:121:RCY:C1V	1.13	1.53	30	1
2:A:150:RCY:H1YA	2:A:187:RCY:C1V	1.13	1.72	38	1
2:A:168:RCY:C1Z	2:A:173:RCY:N1R	1.13	2.09	58	1
1:A:68:CYS:N	2:A:168:RCY:C1L	1.13	2.12	91	4
1:A:71:GLU:OE2	2:A:130:RCY:C1Q	1.13	1.97	94	1
1:A:73:CYS:O	2:A:173:RCY:H1L	1.13	1.40	29	2
1:A:73:CYS:SG	2:A:176:RCY:O1G	1.13	2.06	40	2
1:A:73:CYS:CA	2:A:168:RCY:H1ZA	1.13	1.60	99	1
1:A:71:GLU:CD	2:A:168:RCY:H1VB	1.13	1.61	93	2
2:A:176:RCY:C1W	2:A:187:RCY:H1V	1.13	1.65	10	1
2:A:138:RCY:C1V	2:A:150:RCY:H1MA	1.13	1.73	26	2
1:A:70:TRP:N	2:A:173:RCY:H1ZA	1.13	1.49	5	1
1:A:69:PRO:C	2:A:173:RCY:H1LA	1.13	1.57	6	2
1:A:65:THR:HB	2:A:168:RCY:O1G	1.13	1.33	80	1
1:A:69:PRO:CG	2:A:168:RCY:C1M	1.13	2.17	66	1
2:A:168:RCY:C1Y	2:A:187:RCY:C1S	1.13	2.22	3	3
2:A:173:RCY:C1M	2:A:176:RCY:C1Y	1.13	2.15	77	4
1:A:69:PRO:HB3	2:A:173:RCY:O1G	1.13	1.39	75	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:70:TRP:HB3	2:A:173:RCY:C1M	1.13	1.69	84	1
2:A:176:RCY:H1YB	2:A:187:RCY:C1Y	1.13	1.73	72	1
1:A:64:ILE:HG12	2:A:168:RCY:C1P	1.13	1.73	18	1
1:A:75:HIS:N	2:A:173:RCY:O1G	1.13	1.81	91	1
2:A:176:RCY:O1H	2:A:187:RCY:H1V	1.13	1.42	93	1
2:A:173:RCY:C1V	2:A:176:RCY:H1C	1.13	1.70	67	1
2:A:176:RCY:C1Z	2:A:187:RCY:C1L	1.13	2.27	92	1
2:A:173:RCY:H1MA	2:A:176:RCY:N1V	1.13	1.28	55	1
2:A:168:RCY:H1C	2:A:173:RCY:C1U	1.13	1.70	99	1
2:A:173:RCY:N1R	2:A:187:RCY:H1CB	1.13	1.53	99	1
1:A:70:TRP:CA	2:A:168:RCY:C1C	1.13	2.24	57	1
1:A:78:LEU:CG	2:A:187:RCY:C1C	1.13	2.25	91	1
2:A:130:RCY:C1M	2:A:160:RCY:H1YA	1.13	1.72	7	1
2:A:168:RCY:C1V	2:A:173:RCY:C1C	1.13	1.85	45	1
2:A:138:RCY:C1X	2:A:150:RCY:H1ZA	1.13	1.66	87	1
2:A:138:RCY:C1C	2:A:173:RCY:H1ZA	1.13	1.74	66	1
2:A:130:RCY:C1Z	2:A:160:RCY:O1G	1.12	1.96	22	2
2:A:168:RCY:H1ZA	2:A:187:RCY:C1Q	1.13	1.73	100	1
2:A:173:RCY:C1V	2:A:176:RCY:C1C	1.12	2.18	72	4
2:A:138:RCY:C1C	2:A:150:RCY:O1J	1.12	1.96	59	2
2:A:173:RCY:H1C	2:A:176:RCY:H1CB	1.12	1.22	8	1
2:A:160:RCY:C1M	2:A:168:RCY:H1YA	1.12	1.73	41	1
2:A:168:RCY:C1X	2:A:176:RCY:C1Y	1.12	2.27	94	3
2:A:130:RCY:C1Y	2:A:160:RCY:C1U	1.12	2.26	50	1
1:A:62:THR:CG2	2:A:168:RCY:C1Z	1.12	2.26	72	1
1:A:60:CYS:CA	2:A:130:RCY:H1MA	1.12	1.36	18	1
1:A:59:GLY:CA	2:A:160:RCY:H1L	1.12	1.73	57	4
1:A:70:TRP:CH2	2:A:160:RCY:C1V	1.13	2.20	37	1
2:A:173:RCY:C1Z	2:A:176:RCY:N1V	1.13	2.11	71	2
2:A:168:RCY:C1Y	2:A:173:RCY:H1ZB	1.13	1.47	20	1
1:A:64:ILE:CD1	2:A:121:RCY:O1G	1.12	1.96	68	1
2:A:138:RCY:H1YB	2:A:150:RCY:C1V	1.12	1.71	81	1
2:A:173:RCY:H1YA	2:A:187:RCY:N1V	1.12	1.19	92	1
1:A:72:ALA:CB	2:A:173:RCY:C1S	1.12	2.26	78	1
2:A:138:RCY:O1H	2:A:160:RCY:H1L	1.12	1.43	38	1
2:A:150:RCY:C1M	2:A:160:RCY:H1VA	1.12	1.64	42	1
2:A:173:RCY:H1V	2:A:176:RCY:C1Y	1.12	1.56	2	2
1:A:76:CYS:HA	2:A:176:RCY:C1Q	1.12	1.74	74	3
1:A:69:PRO:N	2:A:168:RCY:C1V	1.12	2.11	63	1
2:A:176:RCY:C1W	2:A:187:RCY:C1L	1.12	2.08	92	1
2:A:173:RCY:O1J	2:A:187:RCY:H1V	1.12	1.42	8	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:160:RCY:O1H	2:A:160:RCY:H1ZB	1.12	1.44	91	2
1:A:70:TRP:O	2:A:150:RCY:H1ZB	1.12	0.91	58	1
2:A:150:RCY:N1V	2:A:187:RCY:C1C	1.12	2.11	50	1
1:A:69:PRO:O	2:A:173:RCY:C1Z	1.12	1.95	85	2
2:A:160:RCY:O1J	2:A:168:RCY:H1M	1.12	1.42	21	2
1:A:63:ASP:OD2	2:A:168:RCY:O1G	1.12	1.66	92	1
2:A:150:RCY:C1Y	2:A:187:RCY:C1X	1.12	2.28	76	2
2:A:138:RCY:O1J	2:A:150:RCY:H1MA	1.12	0.90	88	1
2:A:150:RCY:H1ZB	2:A:187:RCY:O1H	1.12	1.43	84	1
2:A:138:RCY:C1Y	2:A:150:RCY:C1U	1.12	2.27	60	1
2:A:176:RCY:H1Y	2:A:187:RCY:C1V	1.12	1.74	72	2
2:A:176:RCY:C1M	2:A:187:RCY:C1Z	1.12	2.28	5	1
2:A:168:RCY:H1S	2:A:173:RCY:C1Z	1.12	1.69	39	1
2:A:138:RCY:C1Y	2:A:187:RCY:H1C	1.12	1.73	96	1
2:A:173:RCY:C1Z	2:A:176:RCY:C1X	1.12	2.27	31	1
1:A:74:ASN:ND2	2:A:173:RCY:O1G	1.12	1.82	27	1
2:A:160:RCY:C1M	2:A:168:RCY:C1V	1.12	2.00	48	3
2:A:160:RCY:C1M	2:A:168:RCY:H1LA	1.12	1.73	58	1
2:A:130:RCY:H1VA	2:A:160:RCY:O1J	1.12	1.40	64	1
1:A:75:HIS:CE1	2:A:176:RCY:H1L	1.12	1.78	24	1
2:A:173:RCY:O1H	2:A:176:RCY:C1Y	1.12	1.97	68	1
2:A:160:RCY:C1C	2:A:168:RCY:H1LA	1.12	1.72	48	1
2:A:173:RCY:C1V	2:A:187:RCY:H1ZA	1.12	1.75	53	1
1:A:70:TRP:N	2:A:176:RCY:H1YB	1.12	1.59	80	1
2:A:168:RCY:H1C	2:A:176:RCY:O1J	1.11	1.40	43	3
2:A:130:RCY:H1MA	2:A:160:RCY:O1G	1.11	1.43	61	1
1:A:76:CYS:HB3	2:A:176:RCY:O1H	1.11	1.38	14	15
2:A:173:RCY:C1Y	2:A:176:RCY:C1X	1.11	2.28	38	1
2:A:150:RCY:H1M	2:A:160:RCY:H1VB	1.11	1.20	42	1
2:A:168:RCY:O1J	2:A:173:RCY:O1H	1.11	1.68	8	1
2:A:110:RCY:H1Y	2:A:121:RCY:C1V	1.11	1.68	81	2
2:A:110:RCY:H1YA	2:A:121:RCY:H1C	1.11	1.15	81	1
1:A:63:ASP:CB	2:A:150:RCY:C1C	1.11	2.28	85	1
2:A:138:RCY:O1J	2:A:160:RCY:N1R	1.11	1.83	18	1
1:A:72:ALA:CA	2:A:168:RCY:C1Z	1.11	2.20	57	1
2:A:173:RCY:H1VA	2:A:187:RCY:C1V	1.11	1.74	48	1
2:A:168:RCY:C1X	2:A:173:RCY:H1VB	1.11	1.67	48	2
1:A:74:ASN:O	2:A:187:RCY:N1V	1.11	1.70	56	1
2:A:168:RCY:H1MA	2:A:187:RCY:C1P	1.11	1.75	100	1
2:A:176:RCY:C1Z	2:A:187:RCY:C1C	1.11	2.27	64	5
1:A:64:ILE:CG1	2:A:160:RCY:C1Y	1.11	2.27	19	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:69:PRO:HA	2:A:173:RCY:C1Z	1.11	1.73	75	1
2:A:168:RCY:H1MA	2:A:173:RCY:C1Q	1.11	1.61	36	2
2:A:168:RCY:H1MA	2:A:187:RCY:C1W	1.11	1.59	84	2
2:A:173:RCY:O1G	2:A:187:RCY:C1V	1.11	1.99	16	3
2:A:160:RCY:H1ZA	2:A:168:RCY:H1VA	1.11	1.16	69	1
1:A:70:TRP:CE2	2:A:176:RCY:H1MA	1.11	1.80	85	1
1:A:62:THR:HG21	2:A:130:RCY:C1M	1.11	1.50	9	1
2:A:160:RCY:N1V	2:A:168:RCY:H1U	1.11	1.58	47	1
1:A:76:CYS:C	2:A:176:RCY:C1L	1.11	2.16	31	2
2:A:138:RCY:C1Y	2:A:187:RCY:C1P	1.11	2.27	89	1
2:A:138:RCY:C1C	2:A:173:RCY:C1Z	1.11	2.27	66	2
1:A:61:GLY:O	2:A:168:RCY:H1CA	1.11	1.45	61	1
2:A:150:RCY:C1Y	2:A:187:RCY:C1V	1.11	2.29	38	2
2:A:150:RCY:C1U	2:A:160:RCY:C1V	1.11	2.28	42	1
2:A:138:RCY:H1CB	2:A:150:RCY:O1J	1.11	1.36	59	2
2:A:168:RCY:C1Z	2:A:173:RCY:H1VB	1.11	1.76	58	3
2:A:138:RCY:H1VA	2:A:187:RCY:C1Z	1.11	1.74	11	1
1:A:71:GLU:OE2	2:A:150:RCY:N1R	1.11	1.82	58	1
2:A:173:RCY:C1P	2:A:176:RCY:H1CB	1.11	1.67	64	1
1:A:73:CYS:HA	2:A:173:RCY:H1L	1.11	1.17	94	3
2:A:130:RCY:H1Y	2:A:160:RCY:O1G	1.11	1.34	50	1
1:A:72:ALA:C	2:A:173:RCY:H1S	1.11	1.65	76	2
2:A:160:RCY:O1J	2:A:168:RCY:H1ZB	1.11	0.90	5	2
1:A:71:GLU:HA	2:A:173:RCY:C1Y	1.11	1.73	33	1
1:A:64:ILE:CB	2:A:168:RCY:H1ZA	1.11	1.76	78	1
1:A:64:ILE:CD1	2:A:168:RCY:H1ZA	1.11	1.74	6	2
1:A:76:CYS:HA	2:A:176:RCY:H1L	1.11	1.17	5	2
1:A:61:GLY:C	2:A:160:RCY:C1L	1.11	2.19	19	1
1:A:70:TRP:HB2	2:A:168:RCY:C1P	1.11	1.76	45	4
1:A:70:TRP:NE1	2:A:168:RCY:C1Z	1.11	2.13	24	1
1:A:70:TRP:H	2:A:173:RCY:C1Z	1.11	1.39	5	1
1:A:70:TRP:NE1	2:A:176:RCY:C1Y	1.11	2.07	80	1
2:A:160:RCY:C1Q	2:A:176:RCY:O1G	1.11	0.81	73	1
1:A:68:CYS:SG	2:A:160:RCY:H1VA	1.11	1.85	3	1
2:A:173:RCY:H1C	2:A:187:RCY:C1Z	1.11	1.74	93	1
2:A:138:RCY:H1VB	2:A:150:RCY:C1V	1.11	1.75	67	1
1:A:69:PRO:CB	2:A:150:RCY:C1Z	1.11	2.20	92	1
1:A:63:ASP:O	2:A:168:RCY:H1Z	1.10	1.37	78	1
2:A:187:RCY:O1H	2:A:187:RCY:C1Z	1.10	1.93	19	4
2:A:160:RCY:H1ZB	2:A:168:RCY:C1M	1.10	1.70	52	2
2:A:130:RCY:C1Z	2:A:160:RCY:C1Y	1.10	2.23	7	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:75:HIS:H	2:A:176:RCY:C1C	1.10	1.58	20	1
2:A:138:RCY:O1G	2:A:150:RCY:O1G	1.10	1.66	77	1
2:A:173:RCY:C1Y	2:A:187:RCY:C1W	1.10	2.17	92	2
1:A:68:CYS:N	2:A:176:RCY:H1Y	1.10	1.56	22	1
2:A:173:RCY:C1M	2:A:176:RCY:H1VA	1.10	1.75	31	2
2:A:173:RCY:C1M	2:A:176:RCY:N1V	1.10	1.90	55	1
2:A:138:RCY:H1VB	2:A:160:RCY:C1Z	1.10	1.74	64	1
1:A:70:TRP:HB3	2:A:173:RCY:H1ZA	1.10	1.12	94	1
2:A:176:RCY:C1C	2:A:187:RCY:H1YA	1.10	1.72	26	1
1:A:64:ILE:HG23	2:A:168:RCY:C1C	1.10	1.76	54	1
2:A:150:RCY:H1YA	2:A:187:RCY:O1J	1.10	1.44	53	1
2:A:168:RCY:C1L	2:A:173:RCY:C1V	1.10	2.17	4	2
2:A:187:RCY:O1G	2:A:187:RCY:C1C	1.10	1.99	71	6
2:A:138:RCY:O1H	2:A:150:RCY:C1P	1.10	1.99	41	1
2:A:110:RCY:H1VB	2:A:110:RCY:O1G	1.10	1.43	65	3
1:A:71:GLU:C	2:A:168:RCY:H1C	1.10	1.65	86	1
2:A:173:RCY:O1H	2:A:176:RCY:O1H	1.10	1.70	60	3
1:A:73:CYS:CA	2:A:168:RCY:H1ZB	1.10	1.68	99	1
2:A:138:RCY:C1C	2:A:187:RCY:H1YB	1.10	1.76	99	1
1:A:70:TRP:CZ2	2:A:168:RCY:H1Z	1.10	1.82	24	1
2:A:173:RCY:H1Z	2:A:176:RCY:C1Y	1.10	1.75	72	2
1:A:64:ILE:CD1	2:A:168:RCY:C1S	1.10	2.22	12	1
1:A:71:GLU:CB	2:A:168:RCY:C1Q	1.10	2.26	91	3
1:A:64:ILE:CD1	2:A:168:RCY:O1J	1.10	1.98	4	1
1:A:72:ALA:HB2	2:A:173:RCY:C1M	1.10	1.76	80	1
2:A:168:RCY:H1Z	2:A:187:RCY:H1S	1.10	1.13	100	1
2:A:160:RCY:C1V	2:A:168:RCY:C1C	1.10	2.25	14	2
1:A:70:TRP:CD1	2:A:176:RCY:C1X	1.10	2.33	62	1
2:A:176:RCY:H1M	2:A:187:RCY:O1G	1.10	0.89	10	1
2:A:173:RCY:C1L	2:A:187:RCY:C1Y	1.10	2.23	34	1
1:A:70:TRP:CG	2:A:187:RCY:H1ZA	1.10	1.80	76	1
1:A:63:ASP:C	2:A:168:RCY:H1VB	1.10	1.66	5	1
2:A:138:RCY:H1YB	2:A:150:RCY:H1V	1.10	1.22	81	1
2:A:173:RCY:H1V	2:A:176:RCY:H1ZA	1.10	1.15	59	1
1:A:78:LEU:HD11	2:A:176:RCY:C1Z	1.10	1.75	91	1
2:A:160:RCY:O1J	2:A:173:RCY:H1CA	1.10	1.42	11	1
1:A:60:CYS:HB2	2:A:168:RCY:C1C	1.10	1.76	95	1
2:A:176:RCY:C1Y	2:A:187:RCY:H1VB	1.10	1.58	2	1
2:A:160:RCY:C1M	2:A:168:RCY:H1ZA	1.10	1.77	96	1
1:A:59:GLY:CA	2:A:160:RCY:H1VA	1.10	1.75	83	1
1:A:60:CYS:HB3	2:A:160:RCY:O1H	1.10	1.35	44	22

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:176:RCY:O1G	2:A:176:RCY:C1Z	1.10	1.99	61	3
2:A:168:RCY:C1Z	2:A:187:RCY:C1Q	1.10	2.28	100	1
1:A:69:PRO:CB	2:A:173:RCY:O1H	1.10	1.99	81	4
2:A:138:RCY:C1C	2:A:150:RCY:C1Q	1.10	2.30	62	1
1:A:71:GLU:HG3	2:A:168:RCY:C1Q	1.10	1.77	93	3
2:A:110:RCY:H1YB	2:A:121:RCY:C1X	1.10	1.77	81	1
1:A:64:ILE:CG1	2:A:168:RCY:O1G	1.10	1.99	18	1
1:A:65:THR:CG2	2:A:130:RCY:H1C	1.10	1.76	9	1
2:A:168:RCY:C1M	2:A:187:RCY:H1Y	1.10	1.61	7	2
1:A:64:ILE:HB	2:A:168:RCY:O1H	1.10	1.44	95	1
2:A:173:RCY:H1C	2:A:176:RCY:C1Z	1.10	1.75	27	1
1:A:69:PRO:HB2	2:A:176:RCY:H1ZA	1.10	1.13	66	1
2:A:160:RCY:H1V	2:A:168:RCY:H1CB	1.10	1.16	30	1
2:A:173:RCY:C1V	2:A:176:RCY:H1VB	1.09	1.76	43	1
2:A:173:RCY:C1V	2:A:176:RCY:C1V	1.09	2.14	62	3
2:A:173:RCY:C1M	2:A:176:RCY:C1C	1.09	2.30	38	2
2:A:176:RCY:C1Y	2:A:187:RCY:C1V	1.09	2.30	72	4
2:A:173:RCY:H1V	2:A:187:RCY:H1VA	1.09	1.17	55	1
2:A:168:RCY:C1M	2:A:176:RCY:H1ZA	1.09	1.75	64	1
2:A:176:RCY:C1V	2:A:187:RCY:C1Z	1.09	2.25	34	2
1:A:74:ASN:ND2	2:A:168:RCY:H1YB	1.09	1.61	91	1
2:A:138:RCY:C1P	2:A:150:RCY:H1CA	1.09	1.74	9	1
1:A:61:GLY:HA2	2:A:160:RCY:C1L	1.09	1.76	2	1
1:A:74:ASN:O	2:A:173:RCY:C1V	1.09	2.00	15	1
1:A:65:THR:HG21	2:A:160:RCY:C1C	1.09	1.77	31	1
2:A:138:RCY:O1J	2:A:150:RCY:H1YA	1.09	1.46	77	4
2:A:168:RCY:C1X	2:A:187:RCY:O1J	1.09	1.99	64	1
1:A:66:VAL:CB	2:A:160:RCY:O1H	1.09	1.99	68	1
2:A:168:RCY:C1V	2:A:176:RCY:O1H	1.09	2.00	71	1
2:A:138:RCY:C1P	2:A:150:RCY:O1H	1.09	2.00	23	1
1:A:69:PRO:HB2	2:A:187:RCY:C1C	1.09	1.67	7	2
2:A:173:RCY:C1X	2:A:176:RCY:H1YB	1.09	1.77	2	1
1:A:65:THR:CG2	2:A:160:RCY:H1M	1.09	1.76	36	1
1:A:74:ASN:CA	2:A:173:RCY:C1P	1.09	2.30	27	1
2:A:160:RCY:O1G	2:A:168:RCY:O1G	1.09	1.70	92	1
2:A:130:RCY:O1J	2:A:160:RCY:C1V	1.09	2.01	67	3
2:A:130:RCY:H1YB	2:A:160:RCY:H1M	1.09	1.11	61	1
1:A:60:CYS:HB2	2:A:160:RCY:O1H	1.09	1.38	93	14
2:A:176:RCY:H1ZB	2:A:187:RCY:C1X	1.09	1.68	17	1
2:A:150:RCY:C1M	2:A:187:RCY:H1VB	1.09	1.77	38	1
2:A:173:RCY:H1ZB	2:A:176:RCY:C1Z	1.09	1.63	60	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:75:HIS:HA	2:A:176:RCY:C1L	1.09	1.77	13	1
2:A:138:RCY:H1YA	2:A:150:RCY:C1C	1.09	1.72	97	2
2:A:138:RCY:C1Y	2:A:150:RCY:O1G	1.09	1.99	37	1
1:A:69:PRO:HD2	2:A:168:RCY:O1H	1.09	0.87	23	1
1:A:70:TRP:O	2:A:173:RCY:C1U	1.09	2.00	11	1
1:A:70:TRP:CZ3	2:A:150:RCY:C1Y	1.09	2.11	47	1
2:A:173:RCY:C1M	2:A:187:RCY:H1Y	1.09	1.66	31	1
2:A:173:RCY:C1Y	2:A:176:RCY:C1C	1.09	2.30	98	4
2:A:138:RCY:C1V	2:A:150:RCY:O1J	1.09	1.99	36	4
1:A:71:GLU:HB2	2:A:168:RCY:H1CA	1.09	1.21	86	1
1:A:68:CYS:HB2	2:A:168:RCY:O1H	1.09	1.45	80	7
1:A:70:TRP:CZ3	2:A:168:RCY:H1C	1.09	1.36	95	2
1:A:69:PRO:HG3	2:A:173:RCY:C1Q	1.09	1.70	10	2
2:A:160:RCY:C1Y	2:A:168:RCY:O1J	1.09	2.00	59	3
2:A:173:RCY:C1V	2:A:176:RCY:H1YA	1.09	1.65	9	3
2:A:173:RCY:C1C	2:A:187:RCY:H1Y	1.09	1.76	48	2
2:A:168:RCY:H1MA	2:A:173:RCY:C1M	1.09	1.76	70	1
1:A:77:GLU:OE1	2:A:121:RCY:H1YA	1.09	1.43	11	1
2:A:173:RCY:C1U	2:A:176:RCY:H1VB	1.09	1.68	89	1
1:A:67:ILE:CG2	2:A:130:RCY:C1M	1.09	2.31	30	1
2:A:130:RCY:O1G	2:A:130:RCY:C1Z	1.09	1.99	82	5
2:A:173:RCY:O1J	2:A:187:RCY:C1V	1.09	2.00	8	3
1:A:73:CYS:HB3	2:A:173:RCY:O1H	1.09	1.46	62	14
2:A:173:RCY:C1V	2:A:176:RCY:C1M	1.09	2.29	69	5
1:A:68:CYS:O	2:A:168:RCY:H1L	1.09	1.47	38	3
2:A:138:RCY:C1W	2:A:150:RCY:H1VB	1.09	1.77	19	1
1:A:71:GLU:HG3	2:A:150:RCY:H1U	1.09	1.20	58	1
2:A:160:RCY:H1ZA	2:A:168:RCY:C1Q	1.09	1.77	58	1
1:A:70:TRP:CZ3	2:A:176:RCY:C1Y	1.09	2.35	94	1
1:A:71:GLU:HB3	2:A:168:RCY:C1L	1.09	1.70	57	5
2:A:173:RCY:H1ZA	2:A:176:RCY:H1YA	1.09	1.14	70	1
2:A:176:RCY:C1C	2:A:187:RCY:C1V	1.09	2.31	93	2
1:A:63:ASP:HB2	2:A:138:RCY:H1Z	1.09	1.09	73	1
2:A:138:RCY:C1V	2:A:173:RCY:O1J	1.09	2.00	15	1
1:A:63:ASP:HA	2:A:160:RCY:H1ZB	1.08	1.15	14	1
2:A:168:RCY:C1M	2:A:173:RCY:C1Q	1.08	2.27	36	2
1:A:70:TRP:CZ2	2:A:160:RCY:C1C	1.08	2.21	34	1
1:A:69:PRO:CB	2:A:176:RCY:H1YA	1.08	1.78	72	1
1:A:63:ASP:HB2	2:A:150:RCY:C1V	1.08	1.78	85	1
1:A:71:GLU:HA	2:A:173:RCY:H1YA	1.08	1.10	33	1
1:A:70:TRP:CD1	2:A:176:RCY:H1YA	1.08	1.69	80	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:70:TRP:CZ2	2:A:176:RCY:H1VA	1.08	1.83	82	1
2:A:138:RCY:H1C	2:A:160:RCY:H1LA	1.08	1.16	73	1
1:A:76:CYS:O	2:A:176:RCY:O1H	1.08	1.71	73	1
2:A:176:RCY:C1C	2:A:176:RCY:O1G	1.08	2.00	36	2
1:A:64:ILE:CB	2:A:168:RCY:C1Z	1.08	2.29	30	2
2:A:168:RCY:C1P	2:A:173:RCY:H1Z	1.08	1.70	10	1
2:A:110:RCY:C1Y	2:A:121:RCY:H1VA	1.08	1.73	81	1
1:A:70:TRP:CD1	2:A:168:RCY:H1YB	1.08	1.82	37	1
2:A:160:RCY:H1YA	2:A:168:RCY:H1U	1.08	1.15	44	1
2:A:138:RCY:C1V	2:A:187:RCY:H1MA	1.08	1.76	49	1
2:A:168:RCY:H1MA	2:A:187:RCY:C1Y	1.08	1.75	7	1
2:A:160:RCY:H1YB	2:A:168:RCY:H1YB	1.08	1.25	53	1
2:A:168:RCY:C1Q	2:A:176:RCY:C1Z	1.08	2.25	77	1
2:A:150:RCY:H1YB	2:A:187:RCY:H1CA	1.08	1.10	83	1
1:A:75:HIS:CG	2:A:176:RCY:H1C	1.08	1.82	84	1
1:A:69:PRO:HG3	2:A:176:RCY:C1Y	1.08	1.79	72	1
2:A:173:RCY:C1Z	2:A:176:RCY:H1YA	1.08	1.77	70	3
1:A:73:CYS:SG	2:A:130:RCY:H1VA	1.08	1.88	5	1
2:A:173:RCY:H1YA	2:A:187:RCY:O1G	1.08	0.86	93	2
1:A:69:PRO:HG2	2:A:176:RCY:H1Z	1.08	1.15	66	1
2:A:138:RCY:H1YA	2:A:150:RCY:N1V	1.08	1.62	97	1
1:A:74:ASN:HA	2:A:176:RCY:H1VA	1.08	1.26	100	1
2:A:173:RCY:O1G	2:A:176:RCY:C1V	1.08	1.99	19	3
2:A:168:RCY:C1L	2:A:173:RCY:C1M	1.08	2.27	49	2
2:A:176:RCY:O1G	2:A:176:RCY:C1C	1.08	2.01	71	5
1:A:76:CYS:HB3	2:A:187:RCY:H1CB	1.08	1.25	34	1
2:A:150:RCY:C1Z	2:A:187:RCY:H1VA	1.08	1.78	26	1
2:A:150:RCY:C1Z	2:A:150:RCY:O1G	1.08	2.01	12	1
1:A:66:VAL:HB	2:A:160:RCY:C1Q	1.08	1.79	68	1
2:A:168:RCY:H1CB	2:A:173:RCY:H1YA	1.08	1.17	85	1
1:A:70:TRP:CA	2:A:173:RCY:H1Z	1.08	1.69	85	1
1:A:70:TRP:N	2:A:187:RCY:H1CA	1.08	1.62	7	1
2:A:173:RCY:O1J	2:A:176:RCY:C1V	1.08	2.00	23	7
2:A:160:RCY:H1Y	2:A:168:RCY:H1S	1.08	1.11	100	2
2:A:160:RCY:C1Z	2:A:173:RCY:H1ZA	1.08	1.77	99	2
2:A:160:RCY:H1MA	2:A:168:RCY:C1P	1.08	1.79	34	1
2:A:138:RCY:O1H	2:A:160:RCY:C1P	1.08	2.02	69	1
2:A:176:RCY:H1Y	2:A:187:RCY:H1V	1.08	1.20	72	1
1:A:66:VAL:CG1	2:A:160:RCY:O1J	1.08	2.01	68	1
2:A:168:RCY:C1L	2:A:168:RCY:C1S	1.08	2.32	79	1
1:A:78:LEU:CD2	2:A:176:RCY:H1M	1.08	1.69	91	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:78:LEU:HD11	2:A:176:RCY:O1H	1.08	1.48	91	1
1:A:71:GLU:CB	2:A:168:RCY:H1LA	1.08	1.79	32	3
1:A:60:CYS:C	2:A:160:RCY:C1S	1.08	2.13	2	1
1:A:70:TRP:O	2:A:173:RCY:C1V	1.07	1.98	78	1
2:A:168:RCY:O1H	2:A:168:RCY:H1ZB	1.07	1.48	30	6
2:A:130:RCY:C1M	2:A:160:RCY:O1G	1.07	2.02	61	1
1:A:76:CYS:CA	2:A:176:RCY:C1L	1.07	2.18	31	7
2:A:173:RCY:O1G	2:A:173:RCY:C1C	1.07	2.02	86	7
1:A:70:TRP:CB	2:A:173:RCY:C1Y	1.07	2.31	85	2
2:A:130:RCY:C1L	2:A:160:RCY:C1P	1.07	2.23	62	1
2:A:121:RCY:O1G	2:A:121:RCY:C1C	1.07	2.02	90	4
1:A:69:PRO:HB3	2:A:176:RCY:C1Y	1.07	1.79	72	1
2:A:168:RCY:H1LA	2:A:173:RCY:H1Z	1.07	1.19	5	1
2:A:176:RCY:N1V	2:A:176:RCY:O1H	1.07	1.80	57	1
1:A:71:GLU:CA	2:A:168:RCY:C1M	1.07	2.30	37	2
1:A:78:LEU:CD1	2:A:176:RCY:H1MA	1.07	1.79	91	1
1:A:71:GLU:CA	2:A:173:RCY:H1YA	1.07	1.78	33	1
2:A:176:RCY:H1VA	2:A:187:RCY:C1X	1.07	1.76	33	1
1:A:70:TRP:CZ3	2:A:168:RCY:H1YA	1.07	1.84	49	2
2:A:138:RCY:C1Y	2:A:150:RCY:H1CA	1.07	1.75	97	2
2:A:150:RCY:O1G	2:A:150:RCY:C1C	1.07	2.01	61	9
2:A:150:RCY:C1Z	2:A:187:RCY:C1Z	1.07	2.31	88	1
1:A:63:ASP:CA	2:A:160:RCY:H1ZB	1.07	1.79	14	1
1:A:68:CYS:CB	2:A:160:RCY:H1Z	1.07	1.75	19	1
1:A:69:PRO:CD	2:A:168:RCY:C1S	1.07	2.31	75	2
1:A:62:THR:CG2	2:A:160:RCY:C1V	1.07	2.32	55	1
2:A:173:RCY:C1V	2:A:176:RCY:H1V	1.07	1.62	62	2
1:A:76:CYS:N	2:A:176:RCY:O1H	1.07	1.86	10	4
2:A:173:RCY:C1C	2:A:176:RCY:C1S	1.07	2.30	72	1
2:A:110:RCY:O1H	2:A:110:RCY:H1ZB	1.07	1.47	5	3
1:A:74:ASN:OD1	2:A:168:RCY:C1Y	1.07	2.02	91	1
1:A:69:PRO:N	2:A:168:RCY:H1VB	1.07	1.62	63	1
1:A:71:GLU:H	2:A:168:RCY:C1Q	1.07	1.57	22	1
2:A:173:RCY:H1U	2:A:176:RCY:C1Y	1.07	1.78	41	3
1:A:74:ASN:O	2:A:176:RCY:H1CB	1.07	1.34	62	1
1:A:78:LEU:HD11	2:A:176:RCY:H1S	1.07	1.24	69	1
1:A:62:THR:OG1	2:A:168:RCY:C1L	1.07	2.01	23	2
1:A:64:ILE:HD11	2:A:168:RCY:C1W	1.07	1.79	6	1
2:A:168:RCY:O1H	2:A:173:RCY:C1M	1.07	1.95	71	1
1:A:62:THR:CG2	2:A:160:RCY:N1V	1.07	2.17	46	1
2:A:168:RCY:C1Y	2:A:173:RCY:H1Z	1.07	1.76	20	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:160:RCY:H1Z	2:A:168:RCY:C1U	1.07	1.79	3	1
2:A:168:RCY:H1ZA	2:A:176:RCY:H1VB	1.07	1.08	31	1
1:A:69:PRO:CG	2:A:168:RCY:H1YA	1.07	1.79	66	1
1:A:73:CYS:C	2:A:173:RCY:C1L	1.07	2.21	33	5
2:A:121:RCY:C1Z	2:A:121:RCY:O1H	1.07	2.02	87	2
2:A:173:RCY:H1CB	2:A:176:RCY:C1M	1.07	1.75	52	1
2:A:173:RCY:C1C	2:A:176:RCY:H1CB	1.07	1.74	8	1
1:A:69:PRO:CG	2:A:168:RCY:H1CB	1.07	1.78	8	1
1:A:70:TRP:CZ3	2:A:168:RCY:N1V	1.07	2.23	41	1
2:A:160:RCY:H1ZB	2:A:168:RCY:H1V	1.07	1.12	55	1
2:A:130:RCY:O1G	2:A:130:RCY:C1C	1.07	2.02	86	2
2:A:150:RCY:H1Z	2:A:187:RCY:H1M	1.07	1.24	76	2
2:A:176:RCY:H1M	2:A:187:RCY:H1YB	1.07	1.17	5	2
2:A:168:RCY:C1V	2:A:187:RCY:H1ZB	1.07	1.79	85	1
2:A:176:RCY:H1V	2:A:187:RCY:O1J	1.07	0.91	91	1
2:A:150:RCY:H1YA	2:A:187:RCY:H1Y	1.07	1.19	32	2
1:A:60:CYS:HB2	2:A:168:RCY:H1CA	1.07	1.09	95	1
1:A:67:ILE:C	2:A:173:RCY:H1M	1.07	1.68	80	1
1:A:70:TRP:CG	2:A:176:RCY:H1YB	1.07	1.69	80	1
2:A:150:RCY:C1V	2:A:187:RCY:H1Y	1.07	1.79	66	1
2:A:138:RCY:O1J	2:A:160:RCY:H1VA	1.07	1.49	92	1
1:A:69:PRO:HD2	2:A:168:RCY:H1LA	1.07	1.08	100	5
2:A:173:RCY:H1VB	2:A:176:RCY:O1H	1.07	1.48	38	1
2:A:150:RCY:C1Y	2:A:187:RCY:H1ZA	1.07	1.78	41	1
2:A:176:RCY:C1Z	2:A:176:RCY:O1H	1.07	2.03	26	4
2:A:187:RCY:C1C	2:A:187:RCY:O1G	1.07	2.03	90	3
2:A:173:RCY:H1Z	2:A:176:RCY:H1YA	1.07	1.17	72	2
2:A:150:RCY:H1CB	2:A:187:RCY:H1Y	1.07	1.10	81	2
1:A:60:CYS:C	2:A:130:RCY:H1MA	1.07	1.68	18	1
1:A:70:TRP:CZ3	2:A:160:RCY:H1V	1.07	1.83	91	1
1:A:66:VAL:HG23	2:A:168:RCY:H1V	1.07	1.16	80	1
2:A:160:RCY:H1U	2:A:168:RCY:H1MA	1.07	1.23	96	1
1:A:64:ILE:CG2	2:A:168:RCY:H1Z	1.07	1.68	83	1
2:A:168:RCY:C1V	2:A:176:RCY:O1J	1.06	2.02	43	2
2:A:160:RCY:H1Z	2:A:168:RCY:H1YB	1.06	1.07	43	1
2:A:130:RCY:H1ZA	2:A:160:RCY:O1G	1.06	1.48	61	1
1:A:74:ASN:H	2:A:173:RCY:C1L	1.06	1.64	82	2
2:A:150:RCY:H1Y	2:A:187:RCY:H1YB	1.06	1.22	41	3
2:A:173:RCY:C1Z	2:A:176:RCY:H1Y	1.06	1.80	41	1
1:A:74:ASN:N	2:A:173:RCY:C1Q	1.06	2.17	82	3
2:A:160:RCY:H1L	2:A:168:RCY:O1G	1.06	1.44	26	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:173:RCY:C1V	2:A:176:RCY:H1ZA	1.06	1.80	59	2
2:A:138:RCY:H1YA	2:A:187:RCY:C1C	1.06	1.73	59	2
1:A:78:LEU:HG	2:A:176:RCY:C1M	1.06	1.69	91	1
1:A:73:CYS:C	2:A:176:RCY:O1G	1.06	1.94	70	1
1:A:68:CYS:O	2:A:168:RCY:C1S	1.06	2.02	83	2
2:A:173:RCY:H1CA	2:A:176:RCY:O1J	1.06	1.03	56	2
2:A:150:RCY:C1Z	2:A:160:RCY:H1Y	1.06	1.62	88	1
1:A:69:PRO:HG3	2:A:168:RCY:C1C	1.06	1.78	8	1
1:A:69:PRO:HD2	2:A:168:RCY:H1S	1.06	1.07	75	5
1:A:62:THR:CG2	2:A:160:RCY:H1VB	1.06	1.81	55	1
2:A:121:RCY:C1Z	2:A:121:RCY:O1G	1.06	2.03	86	4
1:A:64:ILE:CG1	2:A:168:RCY:C1P	1.06	2.31	18	2
2:A:176:RCY:H1YB	2:A:187:RCY:H1V	1.06	1.22	72	1
2:A:168:RCY:O1J	2:A:187:RCY:C1X	1.06	2.03	70	1
2:A:168:RCY:C1V	2:A:168:RCY:H1L	1.06	1.80	7	1
2:A:168:RCY:C1M	2:A:176:RCY:O1J	1.06	2.02	11	1
2:A:168:RCY:O1G	2:A:173:RCY:H1CB	1.06	1.50	21	1
1:A:77:GLU:HB2	2:A:173:RCY:H1CB	1.06	1.10	51	1
1:A:62:THR:HG21	2:A:160:RCY:N1V	1.06	1.66	46	1
2:A:150:RCY:C1M	2:A:168:RCY:H1YA	1.06	1.76	74	1
2:A:168:RCY:C1Z	2:A:173:RCY:H1U	1.06	1.62	89	1
1:A:69:PRO:CG	2:A:168:RCY:H1M	1.06	1.76	66	1
2:A:110:RCY:O1G	2:A:110:RCY:C1Z	1.06	2.03	56	7
1:A:76:CYS:HB2	2:A:176:RCY:O1H	1.06	1.36	44	6
2:A:168:RCY:H1S	2:A:173:RCY:C1Y	1.06	1.79	94	2
1:A:70:TRP:CH2	2:A:160:RCY:H1U	1.06	1.86	34	1
2:A:138:RCY:H1V	2:A:150:RCY:C1M	1.06	1.74	1	2
2:A:160:RCY:H1VB	2:A:168:RCY:H1L	1.06	1.28	24	1
2:A:173:RCY:H1VA	2:A:176:RCY:C1M	1.06	1.79	9	2
1:A:67:ILE:C	2:A:150:RCY:O1J	1.06	1.93	72	1
1:A:60:CYS:CA	2:A:130:RCY:C1M	1.06	2.27	18	1
1:A:71:GLU:HB3	2:A:168:RCY:H1L	1.06	1.07	11	4
1:A:77:GLU:HG3	2:A:173:RCY:H1VB	1.06	1.20	32	1
2:A:168:RCY:H1VB	2:A:173:RCY:H1CB	1.06	1.13	45	1
1:A:70:TRP:CG	2:A:176:RCY:H1YA	1.06	1.71	80	2
1:A:77:GLU:CG	2:A:176:RCY:C1U	1.06	2.32	39	1
2:A:138:RCY:H1C	2:A:173:RCY:H1Z	1.06	1.24	66	2
2:A:173:RCY:C1U	2:A:176:RCY:H1ZA	1.06	1.76	77	1
2:A:173:RCY:O1J	2:A:176:RCY:O1G	1.06	1.70	3	2
1:A:72:ALA:HB1	2:A:173:RCY:H1S	1.06	1.22	78	1
1:A:65:THR:CB	2:A:160:RCY:C1Z	1.06	2.31	100	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:168:RCY:C1C	2:A:187:RCY:C1M	1.06	2.09	88	2
2:A:150:RCY:O1H	2:A:150:RCY:H1CA	1.06	1.50	45	3
1:A:61:GLY:O	2:A:160:RCY:H1L	1.06	1.51	19	1
2:A:138:RCY:N1R	2:A:150:RCY:O1G	1.06	1.88	41	1
2:A:138:RCY:H1M	2:A:150:RCY:C1U	1.06	1.81	1	2
2:A:176:RCY:H1M	2:A:187:RCY:C1Z	1.06	1.80	5	1
1:A:59:GLY:C	2:A:160:RCY:H1L	1.06	1.67	28	5
1:A:70:TRP:NE1	2:A:121:RCY:H1Y	1.06	1.53	49	1
2:A:138:RCY:H1VB	2:A:187:RCY:C1M	1.06	1.79	49	1
1:A:77:GLU:OE1	2:A:176:RCY:H1VB	1.06	1.45	7	1
1:A:71:GLU:HG3	2:A:168:RCY:C1P	1.06	1.80	32	1
1:A:70:TRP:HB3	2:A:187:RCY:H1Z	1.06	1.20	51	1
1:A:69:PRO:HG2	2:A:187:RCY:C1Z	1.06	1.75	54	1
2:A:150:RCY:H1MA	2:A:168:RCY:H1Y	1.06	1.12	74	1
1:A:77:GLU:HG2	2:A:176:RCY:H1U	1.06	1.20	39	1
1:A:67:ILE:HG22	2:A:173:RCY:C1C	1.06	1.73	31	1
2:A:150:RCY:C1Y	2:A:187:RCY:O1H	1.06	2.00	27	1
1:A:71:GLU:N	2:A:187:RCY:O1G	1.06	1.88	92	1
1:A:75:HIS:CA	2:A:173:RCY:H1VA	1.06	1.65	22	1
2:A:168:RCY:C1S	2:A:173:RCY:H1YB	1.06	1.80	94	1
2:A:150:RCY:H1CA	2:A:187:RCY:H1CA	1.06	1.28	50	1
2:A:176:RCY:C1M	2:A:187:RCY:H1V	1.06	1.79	10	1
1:A:64:ILE:HD12	2:A:168:RCY:H1S	1.06	1.06	12	1
1:A:78:LEU:HD23	2:A:187:RCY:C1C	1.06	1.60	91	1
2:A:150:RCY:C1V	2:A:176:RCY:O1G	1.06	2.03	82	1
1:A:73:CYS:C	2:A:176:RCY:H1C	1.06	1.42	20	1
1:A:71:GLU:HA	2:A:168:RCY:O1H	1.06	1.50	93	1
2:A:168:RCY:H1ZA	2:A:187:RCY:C1Y	1.06	1.75	97	1
2:A:173:RCY:C1C	2:A:187:RCY:C1L	1.05	2.34	88	1
1:A:70:TRP:CA	2:A:173:RCY:O1H	1.05	2.04	14	1
1:A:70:TRP:HZ2	2:A:121:RCY:H1ZA	1.05	1.02	41	1
2:A:173:RCY:C1V	2:A:176:RCY:H1L	1.05	1.81	35	1
1:A:63:ASP:CB	2:A:150:RCY:C1X	1.05	2.22	85	1
1:A:64:ILE:CD1	2:A:187:RCY:C1M	1.05	2.23	85	1
2:A:138:RCY:C1P	2:A:160:RCY:H1U	1.05	1.74	18	1
2:A:173:RCY:C1C	2:A:187:RCY:C1Y	1.05	2.33	48	2
2:A:173:RCY:H1M	2:A:176:RCY:H1YA	1.05	1.06	2	1
2:A:168:RCY:C1Z	2:A:176:RCY:H1VB	1.05	1.81	31	1
2:A:138:RCY:H1V	2:A:150:RCY:H1ZB	1.05	1.11	87	1
1:A:59:GLY:HA3	2:A:160:RCY:H1VA	1.05	1.13	83	1
2:A:150:RCY:H1M	2:A:187:RCY:H1VB	1.05	1.08	38	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:173:RCY:N1R	2:A:176:RCY:H1S	1.05	1.66	38	1
2:A:173:RCY:C1V	2:A:176:RCY:O1G	1.05	2.05	36	2
1:A:70:TRP:CZ2	2:A:160:RCY:C1X	1.05	2.38	34	1
1:A:60:CYS:N	2:A:160:RCY:C1V	1.05	2.06	83	2
1:A:64:ILE:HD13	2:A:121:RCY:O1G	1.05	1.46	68	1
2:A:138:RCY:H1VA	2:A:187:RCY:O1J	1.05	1.34	96	1
1:A:71:GLU:C	2:A:173:RCY:O1G	1.05	1.87	83	1
2:A:176:RCY:O1G	2:A:187:RCY:O1G	1.05	1.72	88	1
2:A:173:RCY:C1M	2:A:176:RCY:C1P	1.05	2.34	38	1
2:A:173:RCY:H1V	2:A:176:RCY:C1X	1.05	1.80	38	1
2:A:168:RCY:C1Z	2:A:176:RCY:C1Z	1.05	2.35	11	3
1:A:78:LEU:CD2	2:A:176:RCY:C1Y	1.05	2.22	91	1
1:A:66:VAL:O	2:A:168:RCY:C1Q	1.05	2.03	51	1
2:A:168:RCY:C1M	2:A:173:RCY:C1V	1.05	1.91	27	2
1:A:71:GLU:OE2	2:A:121:RCY:H1V	1.05	1.51	78	1
2:A:160:RCY:H1ZA	2:A:168:RCY:H1Z	1.05	1.19	78	1
1:A:73:CYS:HB2	2:A:173:RCY:O1H	1.05	1.32	77	14
2:A:138:RCY:H1VA	2:A:168:RCY:H1CA	1.05	1.25	19	1
2:A:110:RCY:C1C	2:A:110:RCY:O1G	1.05	2.05	77	3
2:A:176:RCY:C1Q	2:A:187:RCY:H1ZA	1.05	1.67	60	1
2:A:173:RCY:H1LA	2:A:176:RCY:C1V	1.05	1.78	11	2
2:A:160:RCY:H1Z	2:A:173:RCY:C1V	1.05	1.80	37	1
1:A:69:PRO:CB	2:A:173:RCY:N1V	1.05	2.20	9	1
2:A:168:RCY:H1ZA	2:A:176:RCY:C1W	1.05	1.82	11	1
1:A:66:VAL:HA	2:A:160:RCY:H1VA	1.05	1.28	21	1
1:A:64:ILE:HG23	2:A:168:RCY:H1L	1.05	1.15	77	3
2:A:150:RCY:C1V	2:A:187:RCY:H1U	1.05	1.79	38	1
2:A:150:RCY:H1V	2:A:160:RCY:C1X	1.05	1.80	42	1
1:A:69:PRO:HD3	2:A:168:RCY:H1S	1.05	1.20	75	1
2:A:168:RCY:C1Z	2:A:173:RCY:C1X	1.05	2.35	70	2
2:A:138:RCY:H1CA	2:A:150:RCY:H1Y	1.05	1.18	59	1
1:A:63:ASP:HB3	2:A:150:RCY:H1CB	1.05	1.08	85	1
1:A:71:GLU:HA	2:A:168:RCY:H1MA	1.05	1.21	37	1
1:A:73:CYS:CA	2:A:176:RCY:O1G	1.05	2.03	70	1
1:A:70:TRP:CH2	2:A:176:RCY:H1V	1.05	1.86	4	1
2:A:168:RCY:H1VB	2:A:176:RCY:C1Y	1.05	1.81	98	2
2:A:150:RCY:O1J	2:A:173:RCY:H1YA	1.05	1.47	89	1
2:A:160:RCY:C1Z	2:A:160:RCY:O1G	1.05	2.04	30	1
2:A:150:RCY:H1Y	2:A:187:RCY:H1U	1.04	1.27	78	1
2:A:168:RCY:O1G	2:A:168:RCY:C1Z	1.04	2.04	65	6
2:A:168:RCY:H1MA	2:A:176:RCY:C1Z	1.04	1.80	64	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:168:RCY:C1V	2:A:173:RCY:C1M	1.04	2.20	29	1
2:A:173:RCY:H1VA	2:A:176:RCY:H1M	1.04	1.19	9	2
1:A:64:ILE:CD1	2:A:160:RCY:H1M	1.04	1.80	1	2
1:A:64:ILE:CG2	2:A:168:RCY:C1C	1.04	2.34	54	1
1:A:63:ASP:HB2	2:A:160:RCY:H1C	1.04	1.26	63	1
1:A:70:TRP:H	2:A:168:RCY:C1L	1.04	1.58	28	1
2:A:176:RCY:H1C	2:A:187:RCY:O1G	1.04	0.83	61	1
2:A:168:RCY:O1J	2:A:176:RCY:C1Z	1.04	2.03	17	1
1:A:61:GLY:O	2:A:160:RCY:C1L	1.04	2.05	19	1
2:A:173:RCY:C1Z	2:A:187:RCY:C1C	1.04	2.36	64	3
2:A:110:RCY:C1V	2:A:121:RCY:C1M	1.04	2.28	5	1
2:A:121:RCY:H1Y	2:A:176:RCY:C1L	1.04	1.82	35	1
1:A:70:TRP:HB2	2:A:173:RCY:H1Y	1.04	1.17	85	1
1:A:70:TRP:HZ3	2:A:160:RCY:H1V	1.04	0.91	91	1
1:A:70:TRP:CD1	2:A:176:RCY:H1Y	1.04	1.85	80	1
1:A:73:CYS:C	2:A:176:RCY:H1CB	1.04	1.67	20	1
2:A:173:RCY:O1J	2:A:187:RCY:H1MA	1.04	1.49	93	1
2:A:150:RCY:H1YB	2:A:187:RCY:C1C	1.04	1.83	83	1
1:A:59:GLY:CA	2:A:160:RCY:H1M	1.04	1.81	78	1
2:A:168:RCY:C1C	2:A:176:RCY:O1J	1.04	2.04	43	3
2:A:150:RCY:H1VB	2:A:187:RCY:H1U	1.04	1.30	38	1
1:A:69:PRO:HD2	2:A:168:RCY:C1S	1.04	1.81	75	6
2:A:168:RCY:H1LA	2:A:173:RCY:H1YA	1.04	1.13	62	1
1:A:72:ALA:N	2:A:173:RCY:O1H	1.04	1.89	50	1
2:A:168:RCY:N1R	2:A:173:RCY:C1Z	1.04	2.21	10	1
2:A:160:RCY:H1MA	2:A:168:RCY:C1L	1.04	1.81	34	1
1:A:66:VAL:CG1	2:A:121:RCY:O1G	1.04	2.06	34	1
2:A:176:RCY:H1CB	2:A:187:RCY:C1W	1.04	1.82	26	1
2:A:138:RCY:C1Y	2:A:150:RCY:H1YB	1.04	1.83	26	2
2:A:160:RCY:C1V	2:A:176:RCY:H1VA	1.04	1.81	57	1
2:A:138:RCY:C1Z	2:A:187:RCY:H1C	1.04	1.70	74	3
1:A:64:ILE:HD13	2:A:160:RCY:H1Y	1.04	1.22	49	1
2:A:168:RCY:H1Z	2:A:176:RCY:H1Z	1.04	1.22	11	1
2:A:138:RCY:O1J	2:A:176:RCY:H1C	1.04	1.46	51	1
1:A:76:CYS:SG	2:A:173:RCY:H1C	1.04	1.91	30	1
2:A:138:RCY:C1L	2:A:150:RCY:H1VB	1.04	1.81	98	1
2:A:173:RCY:C1Q	2:A:176:RCY:C1M	1.04	2.35	67	3
1:A:62:THR:CA	2:A:138:RCY:C1Z	1.04	2.34	38	1
2:A:150:RCY:H1YB	2:A:176:RCY:H1Z	1.04	1.24	42	1
2:A:138:RCY:C1M	2:A:150:RCY:H1V	1.04	1.71	19	3
1:A:62:THR:HG23	2:A:160:RCY:O1H	1.04	1.49	8	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:173:RCY:H1U	2:A:176:RCY:H1YB	1.04	1.26	2	2
2:A:173:RCY:C1U	2:A:176:RCY:C1Y	1.04	2.32	2	3
1:A:69:PRO:O	2:A:173:RCY:H1S	1.04	1.50	75	1
2:A:121:RCY:C1C	2:A:121:RCY:O1H	1.04	2.05	69	7
2:A:130:RCY:H1V	2:A:173:RCY:H1YA	1.04	1.29	94	1
2:A:173:RCY:H1Z	2:A:176:RCY:H1S	1.04	1.07	29	1
2:A:173:RCY:H1ZA	2:A:187:RCY:H1ZA	1.04	1.24	40	1
1:A:71:GLU:OE1	2:A:168:RCY:C1V	1.04	2.05	99	1
2:A:168:RCY:H1CB	2:A:173:RCY:H1Y	1.04	1.25	39	2
2:A:160:RCY:H1MA	2:A:168:RCY:C1Q	1.04	1.83	34	1
1:A:70:TRP:HE3	2:A:173:RCY:H1ZA	1.04	1.08	26	1
1:A:64:ILE:HD11	2:A:160:RCY:C1W	1.04	1.81	6	2
2:A:173:RCY:H1VA	2:A:176:RCY:C1L	1.04	1.83	35	1
2:A:150:RCY:C1C	2:A:150:RCY:O1H	1.04	2.06	81	2
1:A:64:ILE:HD12	2:A:187:RCY:H1M	1.04	1.27	85	1
2:A:130:RCY:C1Y	2:A:130:RCY:C1Z	1.04	2.35	79	1
1:A:61:GLY:O	2:A:168:RCY:O1H	1.04	1.73	11	1
2:A:168:RCY:H1MA	2:A:187:RCY:O1J	1.04	1.53	82	1
2:A:160:RCY:C1C	2:A:168:RCY:N1R	1.04	2.16	39	1
2:A:130:RCY:C1C	2:A:130:RCY:O1G	1.04	2.05	9	7
2:A:150:RCY:H1ZA	2:A:187:RCY:H1YB	1.04	1.19	9	2
1:A:68:CYS:N	2:A:176:RCY:C1Y	1.04	2.02	22	1
1:A:64:ILE:HG13	2:A:160:RCY:H1YA	1.04	1.17	19	1
2:A:138:RCY:C1Y	2:A:187:RCY:H1Y	1.04	1.82	2	2
1:A:69:PRO:O	2:A:173:RCY:O1H	1.04	1.73	64	3
2:A:173:RCY:O1H	2:A:176:RCY:H1V	1.04	1.53	62	2
1:A:71:GLU:CA	2:A:168:RCY:C1C	1.04	2.36	29	1
2:A:150:RCY:C1C	2:A:187:RCY:H1CA	1.04	1.82	50	1
2:A:138:RCY:H1YA	2:A:150:RCY:C1Y	1.04	1.66	89	2
1:A:69:PRO:HA	2:A:173:RCY:C1Y	1.04	1.79	72	1
1:A:64:ILE:HG23	1:A:65:THR:H	1.04	1.09	49	7
2:A:138:RCY:C1Y	2:A:150:RCY:H1V	1.04	1.80	81	1
2:A:168:RCY:O1J	2:A:187:RCY:H1V	1.04	1.45	70	2
1:A:67:ILE:O	2:A:173:RCY:H1M	1.04	1.51	80	1
2:A:168:RCY:C1Y	2:A:176:RCY:C1P	1.04	2.36	20	1
2:A:173:RCY:H1M	2:A:176:RCY:O1H	1.03	1.49	52	3
2:A:150:RCY:C1Y	2:A:187:RCY:C1Z	1.03	2.36	41	1
2:A:138:RCY:H1YA	2:A:187:RCY:H1Y	1.03	1.22	86	2
2:A:173:RCY:C1C	2:A:173:RCY:O1H	1.03	2.06	9	6
1:A:71:GLU:CD	2:A:168:RCY:C1V	1.03	2.23	93	2
1:A:69:PRO:CB	2:A:173:RCY:H1S	1.03	1.77	26	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:70:TRP:CB	2:A:173:RCY:H1Y	1.03	1.82	85	1
2:A:173:RCY:H1ZB	2:A:176:RCY:H1M	1.03	1.04	37	1
1:A:73:CYS:O	2:A:176:RCY:O1G	1.03	1.76	70	1
2:A:168:RCY:C1M	2:A:187:RCY:H1YB	1.03	1.77	7	1
1:A:69:PRO:HB2	2:A:173:RCY:C1C	1.03	1.08	7	2
1:A:67:ILE:HG13	2:A:176:RCY:C1C	1.03	1.82	53	2
1:A:67:ILE:CB	2:A:173:RCY:C1Y	1.03	2.24	80	1
1:A:67:ILE:CG2	2:A:173:RCY:H1YB	1.03	1.82	80	1
2:A:176:RCY:C1S	2:A:187:RCY:H1Z	1.03	1.82	80	1
1:A:64:ILE:HG23	2:A:168:RCY:C1L	1.03	1.82	1	2
2:A:173:RCY:C1P	2:A:176:RCY:O1H	1.03	2.05	96	1
2:A:176:RCY:H1VB	2:A:187:RCY:H1M	1.03	1.30	96	1
1:A:59:GLY:HA2	2:A:160:RCY:H1LA	1.03	1.22	28	1
1:A:70:TRP:HB2	2:A:121:RCY:H1VA	1.03	1.28	30	1
2:A:150:RCY:C1Y	2:A:187:RCY:C1C	1.03	2.36	78	2
2:A:138:RCY:O1G	2:A:138:RCY:H1CA	1.03	1.51	10	6
1:A:59:GLY:C	2:A:160:RCY:H1LA	1.03	1.66	57	3
2:A:138:RCY:H1YA	2:A:150:RCY:O1J	1.03	1.52	75	3
1:A:77:GLU:CA	2:A:176:RCY:C1P	1.03	2.30	55	1
1:A:66:VAL:O	2:A:168:RCY:H1CB	1.03	1.37	58	2
2:A:168:RCY:C1V	2:A:173:RCY:O1H	1.03	2.06	76	2
1:A:70:TRP:HA	2:A:173:RCY:H1ZA	1.03	1.04	49	2
2:A:160:RCY:C1W	2:A:168:RCY:H1V	1.03	1.81	48	1
2:A:168:RCY:N1R	2:A:176:RCY:C1M	1.03	2.17	71	1
1:A:69:PRO:CG	2:A:173:RCY:H1Y	1.03	1.83	9	1
1:A:59:GLY:HA2	2:A:160:RCY:C1Z	1.03	1.84	49	1
1:A:69:PRO:CD	2:A:168:RCY:H1VB	1.03	1.80	63	1
2:A:150:RCY:H1VB	2:A:176:RCY:O1G	1.03	1.51	82	1
2:A:138:RCY:O1J	2:A:173:RCY:H1ZB	1.03	1.52	15	1
1:A:71:GLU:HG2	2:A:176:RCY:C1Y	1.03	1.83	92	1
2:A:173:RCY:H1ZB	2:A:187:RCY:O1G	1.03	1.42	92	1
2:A:168:RCY:H1Z	2:A:187:RCY:C1Z	1.03	1.83	17	1
2:A:160:RCY:C1U	2:A:168:RCY:H1YA	1.03	1.82	41	1
2:A:150:RCY:H1YB	2:A:187:RCY:C1W	1.03	1.84	41	1
1:A:71:GLU:OE2	2:A:130:RCY:H1MA	1.03	1.52	94	1
2:A:121:RCY:H1ZA	2:A:168:RCY:H1L	1.03	1.24	94	1
1:A:69:PRO:CB	2:A:176:RCY:C1Y	1.03	2.37	72	1
1:A:74:ASN:C	2:A:173:RCY:O1G	1.03	1.84	91	2
1:A:70:TRP:CD2	2:A:121:RCY:H1V	1.03	1.87	49	1
2:A:168:RCY:H1CA	2:A:187:RCY:H1MA	1.03	1.12	70	1
2:A:173:RCY:C1Y	2:A:187:RCY:H1L	1.03	1.82	45	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:69:PRO:HD3	2:A:168:RCY:C1V	1.03	1.81	63	1
1:A:72:ALA:HB2	2:A:173:RCY:H1MA	1.03	1.24	80	1
1:A:69:PRO:CG	2:A:187:RCY:C1Y	1.03	2.36	87	1
2:A:138:RCY:H1V	2:A:150:RCY:H1CB	1.03	1.06	67	1
2:A:138:RCY:H1CA	2:A:150:RCY:H1CB	1.03	1.23	66	1
1:A:68:CYS:H	2:A:168:RCY:H1S	1.03	0.95	38	5
2:A:173:RCY:C1W	2:A:176:RCY:C1M	1.03	2.37	87	2
1:A:76:CYS:HB2	2:A:173:RCY:C1C	1.03	1.81	29	2
2:A:110:RCY:O1H	2:A:110:RCY:C1C	1.03	2.06	39	3
2:A:173:RCY:C1V	2:A:176:RCY:O1J	1.03	2.05	11	2
1:A:70:TRP:CE2	2:A:121:RCY:H1V	1.03	1.88	49	1
2:A:138:RCY:C1Y	2:A:187:RCY:H1YB	1.03	1.82	32	1
2:A:138:RCY:H1CB	2:A:187:RCY:H1YA	1.03	1.29	21	1
1:A:64:ILE:HG12	2:A:160:RCY:H1VA	1.03	1.03	54	1
1:A:70:TRP:CE3	2:A:176:RCY:H1M	1.03	1.89	80	1
1:A:71:GLU:CG	2:A:176:RCY:C1Y	1.03	2.35	92	1
1:A:63:ASP:O	2:A:160:RCY:C1Y	1.03	2.07	78	1
2:A:168:RCY:H1ZA	2:A:187:RCY:N1R	1.03	1.62	100	1
2:A:160:RCY:C1M	2:A:168:RCY:C1M	1.03	2.24	52	2
2:A:160:RCY:H1Y	2:A:173:RCY:H1Z	1.03	1.29	41	2
2:A:138:RCY:C1P	2:A:150:RCY:O1G	1.03	2.07	77	2
2:A:168:RCY:C1U	2:A:187:RCY:O1J	1.03	0.73	64	1
2:A:138:RCY:C1V	2:A:187:RCY:C1Z	1.03	2.37	49	1
1:A:64:ILE:CD1	2:A:168:RCY:C1C	1.03	2.36	4	1
2:A:160:RCY:H1YB	2:A:173:RCY:H1ZB	1.03	1.31	4	1
1:A:65:THR:CG2	2:A:168:RCY:O1G	1.03	2.06	80	1
1:A:71:GLU:CA	2:A:168:RCY:O1H	1.03	2.06	93	1
2:A:160:RCY:H1Z	2:A:168:RCY:C1P	1.03	1.82	1	1
2:A:173:RCY:H1S	2:A:176:RCY:H1M	1.03	1.31	67	1
1:A:66:VAL:CG1	2:A:121:RCY:C1Y	1.03	1.82	83	1
2:A:168:RCY:C1M	2:A:176:RCY:H1YB	1.03	1.82	98	1
2:A:150:RCY:H1M	2:A:187:RCY:C1V	1.02	1.82	38	1
2:A:187:RCY:O1G	2:A:187:RCY:C1Z	1.02	2.05	22	3
2:A:138:RCY:C1Z	2:A:138:RCY:O1H	1.02	2.07	40	4
2:A:176:RCY:O1G	2:A:176:RCY:H1CA	1.02	1.53	44	2
2:A:130:RCY:H1LA	2:A:160:RCY:O1G	1.02	1.52	62	1
2:A:160:RCY:C1Y	2:A:168:RCY:H1ZA	1.02	1.83	53	3
1:A:68:CYS:HB3	2:A:168:RCY:O1H	1.02	1.26	59	7
2:A:168:RCY:H1Y	2:A:173:RCY:O1G	1.02	1.54	91	1
2:A:138:RCY:H1YB	2:A:150:RCY:H1Y	1.02	1.03	9	1
2:A:138:RCY:C1L	2:A:150:RCY:H1CA	1.02	1.84	9	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:65:THR:CB	2:A:130:RCY:H1C	1.02	1.72	9	1
2:A:173:RCY:H1VB	2:A:187:RCY:H1ZA	1.02	1.03	53	1
1:A:64:ILE:HG21	2:A:168:RCY:H1M	1.02	1.31	95	1
2:A:138:RCY:H1VA	2:A:150:RCY:C1Y	1.02	1.84	97	2
1:A:73:CYS:N	2:A:173:RCY:H1L	1.02	1.69	83	1
1:A:74:ASN:HA	2:A:176:RCY:O1G	1.02	0.81	78	1
2:A:138:RCY:C1U	2:A:150:RCY:C1C	1.02	1.87	43	1
2:A:168:RCY:C1W	2:A:187:RCY:C1S	1.02	2.38	3	2
2:A:150:RCY:O1H	2:A:150:RCY:H1ZB	1.02	1.55	48	3
2:A:160:RCY:H1ZB	2:A:168:RCY:H1MA	1.02	1.30	52	1
2:A:176:RCY:H1CA	2:A:187:RCY:H1CA	1.02	1.31	75	1
2:A:160:RCY:N1R	2:A:168:RCY:H1C	1.02	1.68	49	3
2:A:160:RCY:H1Z	2:A:173:RCY:H1ZA	1.02	1.20	99	1
2:A:168:RCY:H1V	2:A:176:RCY:C1M	1.02	1.31	76	1
2:A:168:RCY:H1CB	2:A:176:RCY:N1V	1.02	1.69	59	1
2:A:173:RCY:H1V	2:A:176:RCY:H1YB	1.02	1.25	9	2
2:A:168:RCY:H1C	2:A:173:RCY:H1YB	1.02	1.29	21	1
2:A:160:RCY:C1Z	2:A:187:RCY:C1Z	1.02	2.38	31	2
2:A:168:RCY:H1L	2:A:173:RCY:C1X	1.02	1.82	4	1
1:A:75:HIS:O	2:A:173:RCY:H1C	1.02	1.51	73	1
2:A:176:RCY:C1V	2:A:187:RCY:C1L	1.02	2.38	15	1
2:A:173:RCY:C1Z	2:A:187:RCY:H1U	1.02	1.82	77	1
2:A:160:RCY:H1YB	2:A:168:RCY:C1S	1.02	1.79	100	1
2:A:168:RCY:C1Z	2:A:173:RCY:H1C	1.02	1.83	55	1
2:A:168:RCY:H1ZA	2:A:173:RCY:H1ZB	1.02	1.10	60	1
2:A:130:RCY:O1G	2:A:160:RCY:H1Y	1.02	1.54	40	1
2:A:173:RCY:H1VB	2:A:176:RCY:H1YA	1.02	1.14	9	2
1:A:70:TRP:CE2	2:A:121:RCY:C1V	1.02	2.42	49	1
2:A:160:RCY:H1U	2:A:168:RCY:H1CB	1.02	1.05	49	1
2:A:160:RCY:C1C	2:A:173:RCY:H1Z	1.02	1.54	11	1
2:A:168:RCY:C1Z	2:A:176:RCY:C1W	1.02	2.37	11	1
2:A:160:RCY:H1Z	2:A:187:RCY:H1Z	1.02	1.30	21	1
2:A:176:RCY:H1U	2:A:187:RCY:H1V	1.02	1.15	4	1
1:A:67:ILE:HG22	2:A:173:RCY:H1M	1.02	1.09	80	1
1:A:67:ILE:HG22	2:A:173:RCY:H1L	1.02	1.26	73	1
1:A:67:ILE:HG12	2:A:168:RCY:C1C	1.02	1.85	27	1
1:A:69:PRO:HG3	2:A:187:RCY:H1YB	1.02	1.17	87	1
1:A:67:ILE:CG2	2:A:130:RCY:H1MA	1.02	1.85	30	1
2:A:160:RCY:H1ZB	2:A:168:RCY:C1Y	1.02	1.83	43	3
2:A:173:RCY:C1U	2:A:176:RCY:C1Q	1.02	2.34	38	2
2:A:130:RCY:H1ZB	2:A:160:RCY:O1G	1.02	1.54	22	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:75:HIS:CA	2:A:173:RCY:C1V	1.02	2.21	22	1
1:A:71:GLU:HB2	2:A:168:RCY:C1C	1.02	1.84	86	1
1:A:69:PRO:CB	2:A:176:RCY:O1G	1.02	2.07	64	1
2:A:138:RCY:C1Q	2:A:160:RCY:C1C	1.02	2.38	69	1
1:A:66:VAL:H	2:A:150:RCY:C1Y	1.02	1.66	72	1
2:A:173:RCY:H1VA	2:A:176:RCY:C1S	1.02	1.85	35	1
2:A:168:RCY:O1G	2:A:173:RCY:C1C	1.02	2.07	21	2
2:A:138:RCY:H1Y	2:A:187:RCY:O1H	1.02	1.51	59	2
1:A:74:ASN:CG	2:A:168:RCY:C1Y	1.02	2.28	91	1
2:A:110:RCY:H1Z	2:A:121:RCY:O1J	1.02	1.53	33	1
2:A:173:RCY:C1C	2:A:176:RCY:C1L	1.02	2.27	36	1
1:A:72:ALA:HB3	2:A:168:RCY:O1J	1.02	1.52	36	1
2:A:130:RCY:H1C	2:A:160:RCY:C1S	1.02	1.85	66	1
1:A:64:ILE:HG21	2:A:168:RCY:H1ZA	1.02	1.07	83	1
1:A:67:ILE:HD13	2:A:130:RCY:C1Y	1.02	1.85	78	1
1:A:59:GLY:HA3	2:A:160:RCY:C1M	1.02	1.81	78	1
2:A:110:RCY:O1G	2:A:110:RCY:H1CA	1.02	1.54	11	3
2:A:168:RCY:H1YB	2:A:187:RCY:H1L	1.02	1.17	100	1
2:A:173:RCY:O1J	2:A:187:RCY:H1LA	1.02	1.52	76	2
2:A:173:RCY:H1V	2:A:176:RCY:N1R	1.02	1.61	38	2
1:A:70:TRP:HD1	2:A:173:RCY:C1C	1.02	1.57	38	2
2:A:138:RCY:H1YB	2:A:187:RCY:C1Y	1.02	1.84	86	3
1:A:70:TRP:CB	2:A:173:RCY:O1J	1.02	2.07	64	1
1:A:70:TRP:HB2	2:A:173:RCY:H1YA	1.02	1.25	84	1
2:A:176:RCY:C1C	2:A:176:RCY:O1H	1.02	2.08	93	3
2:A:176:RCY:H1U	2:A:187:RCY:C1M	1.02	1.84	26	2
2:A:150:RCY:C1P	2:A:187:RCY:C1V	1.02	2.37	18	2
2:A:150:RCY:C1Y	2:A:176:RCY:H1Y	1.02	1.82	37	1
2:A:138:RCY:H1VB	2:A:187:RCY:C1Z	1.02	1.85	49	1
1:A:71:GLU:CB	2:A:176:RCY:C1V	1.02	2.37	49	1
1:A:76:CYS:SG	2:A:187:RCY:C1Z	1.02	2.47	80	1
1:A:71:GLU:HG3	2:A:168:RCY:C1U	1.02	1.83	93	1
1:A:69:PRO:HB3	2:A:168:RCY:H1YA	1.02	1.20	66	1
1:A:69:PRO:HG2	2:A:176:RCY:C1Z	1.02	1.81	66	1
2:A:150:RCY:H1ZB	2:A:187:RCY:C1Z	1.01	1.83	88	1
2:A:160:RCY:H1Z	2:A:168:RCY:C1L	1.01	1.80	73	2
1:A:66:VAL:O	2:A:168:RCY:H1CA	1.01	1.55	58	1
1:A:67:ILE:HG12	2:A:160:RCY:H1C	1.01	1.28	86	1
2:A:138:RCY:O1G	2:A:150:RCY:H1C	1.01	1.53	94	1
2:A:173:RCY:C1Z	2:A:176:RCY:H1S	1.01	1.70	29	2
2:A:160:RCY:C1C	2:A:160:RCY:O1H	1.01	2.08	7	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:72:ALA:CA	2:A:168:RCY:O1G	1.01	2.03	91	1
2:A:160:RCY:H1V	2:A:168:RCY:H1YA	1.01	1.24	32	1
1:A:63:ASP:HB2	2:A:130:RCY:H1Y	1.01	1.26	73	1
2:A:168:RCY:H1S	2:A:173:RCY:H1ZB	1.01	1.29	39	1
1:A:74:ASN:N	2:A:176:RCY:H1C	1.01	1.68	20	1
2:A:160:RCY:C1Y	2:A:187:RCY:H1YB	1.01	1.85	27	1
2:A:138:RCY:H1VB	2:A:150:RCY:H1YB	1.01	1.21	1	1
1:A:69:PRO:HG2	2:A:168:RCY:H1M	1.01	1.07	66	1
1:A:76:CYS:HA	2:A:176:RCY:H1LA	1.01	1.24	68	5
2:A:173:RCY:H1V	2:A:176:RCY:C1C	1.01	1.83	38	1
1:A:75:HIS:HA	2:A:173:RCY:H1VA	1.01	1.19	22	1
2:A:173:RCY:N1R	2:A:176:RCY:H1VB	1.01	1.70	19	2
2:A:168:RCY:C1Y	2:A:176:RCY:H1VB	1.01	1.71	94	1
1:A:69:PRO:N	2:A:173:RCY:O1G	1.01	1.85	10	1
1:A:69:PRO:HA	2:A:173:RCY:C1P	1.01	1.83	10	1
1:A:63:ASP:CB	2:A:168:RCY:C1V	1.01	2.35	5	1
1:A:64:ILE:HD11	2:A:168:RCY:C1Z	1.01	1.86	6	1
1:A:63:ASP:O	2:A:168:RCY:C1L	1.01	2.07	59	1
2:A:168:RCY:C1V	2:A:187:RCY:C1Z	1.01	2.37	85	2
1:A:73:CYS:SG	2:A:121:RCY:O1J	1.01	2.17	91	1
1:A:74:ASN:N	2:A:168:RCY:H1Y	1.01	1.71	91	1
2:A:173:RCY:H1ZB	2:A:176:RCY:N1V	1.01	1.64	71	1
1:A:73:CYS:CA	2:A:173:RCY:H1L	1.01	1.80	23	2
1:A:67:ILE:CG2	2:A:173:RCY:C1W	1.01	2.37	80	1
1:A:71:GLU:OE2	2:A:168:RCY:H1VB	1.01	0.80	93	2
2:A:138:RCY:H1V	2:A:150:RCY:C1C	1.01	1.85	67	1
1:A:62:THR:HG21	2:A:160:RCY:H1V	1.01	1.28	55	1
1:A:64:ILE:HG12	2:A:168:RCY:H1MA	1.01	1.21	6	1
1:A:70:TRP:CH2	2:A:176:RCY:H1ZA	1.01	1.90	85	1
2:A:176:RCY:H1VA	2:A:187:RCY:H1Z	1.01	1.31	91	1
2:A:138:RCY:C1C	2:A:187:RCY:H1YA	1.01	1.84	21	2
2:A:176:RCY:H1VA	2:A:187:RCY:H1YA	1.01	1.07	54	1
1:A:76:CYS:SG	2:A:160:RCY:C1Y	1.01	2.47	73	1
2:A:150:RCY:H1U	2:A:187:RCY:C1V	1.01	1.85	89	1
2:A:150:RCY:H1YA	2:A:173:RCY:C1C	1.01	1.83	3	1
2:A:168:RCY:H1Y	2:A:187:RCY:C1L	1.01	1.85	3	1
2:A:173:RCY:H1YA	2:A:187:RCY:H1Y	1.01	1.27	31	1
1:A:72:ALA:HB1	2:A:173:RCY:C1S	1.01	1.80	78	1
2:A:168:RCY:C1C	2:A:187:RCY:H1MA	1.01	1.64	88	2
2:A:173:RCY:C1V	2:A:176:RCY:C1P	1.01	2.39	17	2
1:A:75:HIS:NE2	2:A:173:RCY:H1ZA	1.01	1.40	42	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:68:CYS:HB3	2:A:160:RCY:C1Y	1.01	1.71	19	2
2:A:138:RCY:H1Y	2:A:150:RCY:H1YB	1.01	1.25	26	2
2:A:138:RCY:C1Y	2:A:187:RCY:O1H	1.01	1.87	59	2
1:A:60:CYS:N	2:A:160:RCY:C1S	1.01	2.23	28	2
1:A:73:CYS:CB	2:A:168:RCY:C1V	1.01	2.38	57	1
2:A:138:RCY:H1YA	2:A:150:RCY:O1G	1.01	1.55	37	1
1:A:70:TRP:CZ3	2:A:168:RCY:H1MA	1.01	1.90	44	3
1:A:69:PRO:C	2:A:187:RCY:C1C	1.01	2.28	7	1
2:A:168:RCY:H1YA	2:A:187:RCY:C1U	1.01	1.84	90	1
1:A:64:ILE:HD12	2:A:168:RCY:H1CA	1.01	1.24	4	1
1:A:60:CYS:CA	2:A:168:RCY:O1G	1.01	2.07	95	1
2:A:176:RCY:H1Y	2:A:187:RCY:H1VB	1.01	1.12	2	1
1:A:59:GLY:CA	2:A:160:RCY:H1V	1.01	1.85	2	1
2:A:168:RCY:H1LA	2:A:173:RCY:H1VB	1.01	1.10	80	1
2:A:168:RCY:H1U	2:A:173:RCY:H1CA	1.01	1.30	20	1
2:A:168:RCY:H1U	2:A:187:RCY:C1Y	1.01	1.85	87	1
2:A:130:RCY:H1C	2:A:160:RCY:C1P	1.01	1.86	66	1
1:A:71:GLU:CD	2:A:176:RCY:H1C	1.01	1.74	97	1
1:A:70:TRP:HH2	2:A:130:RCY:H1YB	1.01	1.09	88	1
2:A:150:RCY:C1V	2:A:160:RCY:C1W	1.01	2.38	42	1
2:A:138:RCY:C1Y	2:A:150:RCY:H1VB	1.01	1.85	19	1
2:A:138:RCY:N1R	2:A:150:RCY:C1P	1.01	2.18	41	1
2:A:121:RCY:O1H	2:A:121:RCY:C1Z	1.01	2.07	29	6
2:A:176:RCY:H1U	2:A:187:RCY:H1M	1.01	1.11	26	1
1:A:75:HIS:C	2:A:176:RCY:H1L	1.01	1.76	13	1
1:A:70:TRP:N	2:A:173:RCY:O1G	1.01	1.92	6	1
2:A:110:RCY:C1Y	2:A:121:RCY:C1X	1.01	2.38	81	1
2:A:138:RCY:H1VA	2:A:150:RCY:H1CA	1.01	1.23	70	1
2:A:160:RCY:C1W	2:A:168:RCY:H1C	1.01	1.70	89	1
2:A:138:RCY:C1Z	2:A:150:RCY:H1ZA	1.01	1.86	30	1
2:A:173:RCY:H1YA	2:A:187:RCY:H1Z	1.00	1.04	42	2
2:A:138:RCY:C1U	2:A:150:RCY:C1V	1.00	2.38	19	1
2:A:168:RCY:C1Z	2:A:173:RCY:O1J	1.00	2.09	55	2
1:A:68:CYS:N	2:A:168:RCY:O1H	1.00	1.93	86	1
2:A:138:RCY:H1C	2:A:150:RCY:H1Z	1.00	1.22	29	1
2:A:110:RCY:O1J	2:A:121:RCY:C1Y	1.00	2.09	5	1
2:A:160:RCY:H1YA	2:A:168:RCY:C1U	1.00	1.60	44	1
2:A:173:RCY:H1M	2:A:176:RCY:C1Y	1.00	1.85	2	1
1:A:67:ILE:HG22	2:A:173:RCY:C1W	1.00	1.85	80	1
2:A:150:RCY:C1C	2:A:176:RCY:O1G	1.00	2.09	82	1
1:A:63:ASP:C	2:A:160:RCY:H1VB	1.00	1.77	3	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:168:RCY:H1U	2:A:173:RCY:H1M	1.00	1.33	27	1
2:A:176:RCY:H1CB	2:A:187:RCY:H1V	1.00	1.30	93	1
1:A:70:TRP:O	2:A:173:RCY:C1C	1.00	2.07	38	1
2:A:168:RCY:C1L	2:A:173:RCY:C1Z	1.00	2.39	10	4
2:A:138:RCY:H1V	2:A:150:RCY:H1MA	1.00	1.26	26	1
1:A:64:ILE:HG13	2:A:168:RCY:H1S	1.00	1.02	26	1
2:A:138:RCY:H1CA	2:A:150:RCY:C1W	1.00	1.86	59	1
2:A:160:RCY:C1M	2:A:168:RCY:O1J	1.00	2.10	9	1
2:A:168:RCY:H1MA	2:A:187:RCY:H1YB	1.00	1.25	7	1
2:A:168:RCY:H1YA	2:A:187:RCY:C1Z	1.00	1.77	21	2
2:A:138:RCY:H1V	2:A:150:RCY:H1YA	1.00	1.27	51	1
1:A:62:THR:CB	2:A:160:RCY:N1V	1.00	2.20	46	1
1:A:70:TRP:H	2:A:176:RCY:C1Y	1.00	1.70	80	1
2:A:168:RCY:C1Z	2:A:173:RCY:H1ZA	1.00	1.85	31	1
1:A:64:ILE:CD1	2:A:168:RCY:C1V	1.00	2.34	27	1
2:A:150:RCY:H1VA	2:A:187:RCY:H1Y	1.00	1.30	66	1
1:A:64:ILE:HG22	2:A:168:RCY:O1J	1.00	1.26	30	1
1:A:63:ASP:O	2:A:168:RCY:H1ZB	1.00	1.52	78	1
2:A:173:RCY:H1ZB	2:A:187:RCY:H1L	1.00	1.32	100	1
2:A:168:RCY:H1M	2:A:173:RCY:C1Y	1.00	1.85	31	3
2:A:160:RCY:C1P	2:A:168:RCY:H1M	1.00	1.87	52	2
2:A:173:RCY:C1C	2:A:187:RCY:O1J	1.00	2.10	55	2
2:A:173:RCY:H1VA	2:A:187:RCY:H1C	1.00	1.23	55	1
2:A:138:RCY:H1C	2:A:187:RCY:H1YB	1.00	1.32	99	2
2:A:168:RCY:C1C	2:A:173:RCY:H1Y	1.00	1.87	39	2
2:A:138:RCY:H1U	2:A:187:RCY:H1CA	1.00	1.08	5	2
1:A:69:PRO:HG2	2:A:150:RCY:H1Y	1.00	1.27	85	1
2:A:168:RCY:O1J	2:A:173:RCY:C1P	1.00	1.99	37	1
2:A:173:RCY:H1VA	2:A:176:RCY:O1J	1.00	1.54	11	1
1:A:64:ILE:CD1	2:A:168:RCY:H1C	1.00	1.85	4	1
1:A:70:TRP:CD1	2:A:176:RCY:C1M	1.00	2.45	4	1
1:A:60:CYS:CB	2:A:168:RCY:C1C	1.00	2.39	95	1
2:A:138:RCY:H1ZA	2:A:187:RCY:H1C	1.00	1.26	74	1
1:A:71:GLU:CD	2:A:173:RCY:O1H	1.00	1.98	89	1
2:A:160:RCY:O1J	2:A:168:RCY:H1CA	1.00	1.57	89	1
2:A:138:RCY:H1V	2:A:187:RCY:O1J	1.00	1.52	96	1
1:A:62:THR:CA	2:A:160:RCY:H1CA	1.00	1.87	46	1
2:A:168:RCY:C1U	2:A:173:RCY:H1CA	1.00	1.86	20	1
2:A:173:RCY:C1Y	2:A:176:RCY:C1Z	1.00	1.94	87	1
1:A:69:PRO:CD	2:A:168:RCY:C1L	1.00	2.37	31	5
2:A:160:RCY:O1J	2:A:168:RCY:H1C	1.00	1.35	89	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:69:PRO:CG	2:A:150:RCY:C1Z	1.00	2.38	92	1
2:A:160:RCY:H1ZA	2:A:168:RCY:C1P	1.00	1.85	34	3
2:A:173:RCY:H1ZB	2:A:187:RCY:C1C	1.00	1.86	81	2
2:A:160:RCY:C1Y	2:A:168:RCY:C1Z	1.00	2.40	9	3
1:A:69:PRO:CG	2:A:176:RCY:C1Y	1.00	2.39	72	1
1:A:76:CYS:SG	2:A:176:RCY:H1SA	1.00	1.93	79	1
2:A:168:RCY:C1P	2:A:173:RCY:H1M	1.00	1.85	49	1
2:A:130:RCY:H1MA	2:A:160:RCY:H1YA	1.00	1.25	7	1
1:A:71:GLU:HB2	2:A:168:RCY:H1LA	1.00	1.09	32	2
2:A:138:RCY:O1J	2:A:176:RCY:H1CB	1.00	1.57	51	1
2:A:176:RCY:C1U	2:A:187:RCY:H1V	1.00	1.85	4	1
1:A:61:GLY:CA	2:A:160:RCY:N1R	1.00	2.13	2	1
1:A:63:ASP:HB2	2:A:130:RCY:C1Y	1.00	1.83	73	1
1:A:71:GLU:CA	2:A:173:RCY:C1L	1.00	2.33	17	1
2:A:168:RCY:C1P	2:A:176:RCY:H1M	1.00	1.87	71	1
2:A:173:RCY:H1M	2:A:176:RCY:H1M	1.00	1.11	89	1
2:A:173:RCY:O1J	2:A:187:RCY:C1M	1.00	2.10	93	1
1:A:70:TRP:HB3	2:A:121:RCY:H1LA	1.00	1.27	30	1
2:A:138:RCY:H1CA	2:A:160:RCY:H1C	0.99	1.31	49	1
1:A:70:TRP:NE1	2:A:121:RCY:C1Y	0.99	0.85	49	1
1:A:64:ILE:HG21	2:A:160:RCY:C1M	0.99	1.86	47	2
2:A:173:RCY:H1CB	2:A:176:RCY:N1R	0.99	1.72	34	1
2:A:168:RCY:H1V	2:A:176:RCY:O1G	0.99	1.57	20	1
2:A:160:RCY:N1V	2:A:168:RCY:C1C	0.99	2.23	89	1
1:A:64:ILE:HD13	2:A:160:RCY:H1M	0.99	1.04	1	1
1:A:67:ILE:HG21	2:A:130:RCY:H1MA	0.99	1.01	30	1
1:A:65:THR:CG2	2:A:160:RCY:C1Y	0.99	2.39	55	1
2:A:168:RCY:H1YB	2:A:187:RCY:H1V	0.99	1.30	94	1
2:A:173:RCY:C1P	2:A:187:RCY:C1C	0.99	2.39	99	1
2:A:121:RCY:H1YB	2:A:176:RCY:H1LA	0.99	1.33	35	1
1:A:64:ILE:HG13	2:A:168:RCY:O1G	0.99	1.52	18	1
2:A:160:RCY:C1W	2:A:168:RCY:H1Z	0.99	1.88	9	1
2:A:168:RCY:C1L	2:A:173:RCY:C1U	0.99	2.40	49	1
2:A:173:RCY:C1V	2:A:187:RCY:C1Z	0.99	2.39	53	2
1:A:68:CYS:CB	2:A:176:RCY:C1Y	0.99	2.29	80	1
1:A:70:TRP:HB3	2:A:168:RCY:C1C	0.99	1.87	20	1
2:A:173:RCY:H1CA	2:A:173:RCY:O1G	0.99	1.57	67	3
1:A:64:ILE:HG13	2:A:160:RCY:H1YB	0.99	1.05	19	1
1:A:64:ILE:HD13	2:A:150:RCY:H1LA	0.99	1.06	75	1
1:A:73:CYS:O	2:A:173:RCY:C1L	0.99	2.10	29	1
2:A:150:RCY:H1CA	2:A:187:RCY:C1C	0.99	1.87	50	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:138:RCY:H1YA	2:A:150:RCY:H1M	0.99	1.30	26	1
2:A:160:RCY:H1ZB	2:A:168:RCY:H1C	0.99	1.32	69	1
2:A:138:RCY:H1C	2:A:187:RCY:H1M	0.99	1.01	11	2
2:A:138:RCY:H1Y	2:A:150:RCY:H1Y	0.99	1.33	9	1
2:A:138:RCY:H1VA	2:A:187:RCY:C1M	0.99	1.85	21	1
1:A:64:ILE:CG2	2:A:168:RCY:C1M	0.99	2.40	95	1
1:A:70:TRP:HB2	2:A:176:RCY:C1Y	0.99	1.86	64	1
2:A:160:RCY:H1M	2:A:168:RCY:C1W	0.99	1.87	9	1
2:A:173:RCY:C1Z	2:A:187:RCY:H1LA	0.99	1.87	45	1
1:A:67:ILE:HG21	2:A:173:RCY:H1C	0.99	1.06	31	1
2:A:168:RCY:C1Y	2:A:187:RCY:H1ZA	0.99	1.87	97	1
2:A:130:RCY:H1V	2:A:173:RCY:C1Y	0.99	1.85	94	1
2:A:176:RCY:H1U	2:A:187:RCY:C1V	0.99	1.86	4	2
1:A:68:CYS:O	2:A:168:RCY:H1LA	0.99	1.56	91	1
2:A:160:RCY:O1G	2:A:168:RCY:C1C	0.99	2.10	89	1
2:A:173:RCY:H1C	2:A:176:RCY:H1Z	0.99	1.27	27	1
2:A:138:RCY:N1R	2:A:150:RCY:H1V	0.99	1.72	19	1
2:A:173:RCY:C1M	2:A:176:RCY:H1YB	0.99	1.88	41	1
1:A:63:ASP:HB3	2:A:150:RCY:C1C	0.99	1.87	85	1
2:A:160:RCY:C1U	2:A:168:RCY:C1V	0.99	2.41	48	1
2:A:176:RCY:H1YA	2:A:187:RCY:H1VA	0.99	1.08	27	2
1:A:59:GLY:HA2	2:A:160:RCY:H1ZA	0.99	1.33	49	1
2:A:173:RCY:C1U	2:A:176:RCY:O1H	0.99	2.10	96	2
1:A:69:PRO:CG	2:A:187:RCY:H1YB	0.99	1.87	87	1
2:A:168:RCY:C1U	2:A:176:RCY:H1Y	0.99	1.64	59	2
1:A:69:PRO:CB	2:A:150:RCY:H1Y	0.99	1.86	85	1
2:A:173:RCY:H1C	2:A:187:RCY:H1YA	0.99	1.29	48	1
2:A:173:RCY:C1U	2:A:176:RCY:C1Z	0.99	2.41	77	1
2:A:173:RCY:H1C	2:A:187:RCY:H1ZB	0.99	1.07	93	1
1:A:64:ILE:HB	2:A:168:RCY:H1ZB	0.99	1.34	30	1
2:A:150:RCY:C1Y	2:A:187:RCY:C1W	0.99	2.41	41	1
2:A:173:RCY:H1YB	2:A:187:RCY:C1X	0.99	1.88	64	1
2:A:168:RCY:H1ZB	2:A:176:RCY:C1Z	0.99	1.86	6	1
2:A:168:RCY:H1M	2:A:187:RCY:H1Y	0.99	0.99	7	1
1:A:68:CYS:CB	2:A:173:RCY:C1M	0.99	2.40	73	1
1:A:64:ILE:CD1	2:A:168:RCY:H1L	0.99	1.86	88	2
1:A:62:THR:HG21	2:A:160:RCY:H1VB	0.99	1.00	55	1
1:A:71:GLU:OE1	2:A:130:RCY:H1ZA	0.99	1.56	94	1
1:A:64:ILE:CG1	2:A:168:RCY:H1S	0.99	1.86	26	1
1:A:64:ILE:HB	2:A:168:RCY:O1G	0.99	1.25	69	1
2:A:173:RCY:C1S	2:A:176:RCY:O1G	0.99	2.09	71	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:70:TRP:CH2	2:A:176:RCY:H1MA	0.99	1.92	85	1
1:A:62:THR:HG21	2:A:130:RCY:C1C	0.99	1.85	18	1
1:A:60:CYS:O	2:A:138:RCY:O1G	0.99	1.81	7	1
2:A:173:RCY:C1M	2:A:176:RCY:H1YA	0.99	1.88	2	2
2:A:138:RCY:H1YA	2:A:187:RCY:H1M	0.99	1.34	82	1
1:A:63:ASP:CB	2:A:130:RCY:H1Y	0.99	1.86	73	1
1:A:70:TRP:CG	2:A:168:RCY:H1S	0.99	1.76	20	1
2:A:176:RCY:C1V	2:A:187:RCY:H1LA	0.99	1.88	15	1
2:A:176:RCY:H1YA	2:A:187:RCY:C1X	0.99	1.87	27	1
1:A:69:PRO:HD2	2:A:168:RCY:H1L	0.98	1.05	15	4
1:A:71:GLU:HG2	2:A:130:RCY:C1M	0.98	1.87	94	1
1:A:74:ASN:CG	2:A:168:RCY:H1YB	0.98	1.79	91	1
2:A:138:RCY:C1C	2:A:160:RCY:H1VA	0.98	1.84	27	1
2:A:138:RCY:H1ZB	2:A:173:RCY:C1C	0.98	1.88	92	1
2:A:160:RCY:C1C	2:A:168:RCY:C1V	0.98	2.18	44	1
2:A:168:RCY:H1M	2:A:187:RCY:C1W	0.98	1.73	7	2
2:A:150:RCY:O1J	2:A:187:RCY:O1H	0.98	1.80	14	1
2:A:150:RCY:H1Y	2:A:173:RCY:O1J	0.98	1.56	85	2
2:A:168:RCY:O1G	2:A:187:RCY:C1Y	0.98	2.11	64	1
1:A:65:THR:OG1	2:A:168:RCY:H1C	0.98	1.58	24	1
2:A:160:RCY:H1M	2:A:176:RCY:H1Y	0.98	1.32	71	1
1:A:64:ILE:CG1	2:A:160:RCY:C1V	0.98	2.41	54	1
1:A:70:TRP:CG	2:A:176:RCY:H1MA	0.98	1.90	4	1
2:A:138:RCY:C1V	2:A:150:RCY:H1C	0.98	1.78	10	1
1:A:70:TRP:CZ2	2:A:160:RCY:C1U	0.98	2.47	34	1
1:A:70:TRP:O	2:A:187:RCY:C1V	0.98	2.11	16	1
1:A:65:THR:OG1	2:A:168:RCY:O1H	0.98	1.81	31	1
1:A:66:VAL:O	2:A:168:RCY:H1VB	0.98	1.56	27	1
2:A:173:RCY:O1J	2:A:176:RCY:H1LA	0.98	1.57	93	2
1:A:70:TRP:CH2	2:A:150:RCY:O1J	0.98	2.16	93	1
2:A:168:RCY:H1LA	2:A:173:RCY:H1M	0.98	1.29	14	2
1:A:68:CYS:SG	2:A:160:RCY:H1MA	0.98	1.99	58	1
1:A:60:CYS:CA	2:A:160:RCY:O1H	0.98	2.12	29	4
1:A:63:ASP:HB3	2:A:168:RCY:H1VA	0.98	0.99	5	1
1:A:59:GLY:N	2:A:160:RCY:O1G	0.98	1.95	78	2
1:A:70:TRP:CD1	2:A:150:RCY:C1L	0.98	1.90	34	1
1:A:70:TRP:HA	2:A:173:RCY:C1P	0.98	1.88	6	1
2:A:176:RCY:H1ZA	2:A:187:RCY:C1C	0.98	1.89	91	1
2:A:173:RCY:H1MA	2:A:176:RCY:C1W	0.98	1.55	77	1
1:A:64:ILE:CG1	2:A:160:RCY:H1YB	0.98	1.85	19	2
2:A:160:RCY:C1M	2:A:168:RCY:C1Y	0.98	2.40	41	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:138:RCY:C1Y	2:A:187:RCY:H1V	0.98	1.87	29	3
1:A:62:THR:OG1	2:A:168:RCY:O1G	0.98	1.80	72	2
1:A:63:ASP:CA	2:A:168:RCY:C1V	0.98	2.41	5	1
2:A:160:RCY:H1Z	2:A:173:RCY:H1VA	0.98	1.01	37	1
1:A:62:THR:HG23	2:A:160:RCY:H1ZB	0.98	1.33	46	1
1:A:72:ALA:HB1	2:A:173:RCY:C1L	0.98	1.86	30	1
2:A:160:RCY:O1J	2:A:168:RCY:H1YA	0.98	1.53	78	2
2:A:150:RCY:H1VB	2:A:160:RCY:H1V	0.98	1.35	42	1
2:A:168:RCY:H1MA	2:A:176:RCY:H1ZA	0.98	1.01	64	1
2:A:187:RCY:C1Z	2:A:187:RCY:O1G	0.98	2.11	50	1
1:A:70:TRP:CZ3	2:A:176:RCY:C1Z	0.98	2.47	85	1
2:A:138:RCY:C1P	2:A:150:RCY:H1YA	0.98	1.87	23	1
1:A:70:TRP:O	2:A:173:RCY:H1U	0.98	1.54	11	1
1:A:68:CYS:C	2:A:173:RCY:C1M	0.98	2.21	73	1
1:A:78:LEU:CD1	2:A:176:RCY:H1U	0.98	1.88	56	1
2:A:138:RCY:C1Z	2:A:173:RCY:C1C	0.98	2.10	92	1
2:A:150:RCY:O1H	2:A:150:RCY:C1Z	0.98	2.10	43	7
2:A:187:RCY:O1G	2:A:187:RCY:C1V	0.98	2.12	85	5
2:A:138:RCY:C1C	2:A:138:RCY:O1G	0.98	2.12	57	5
2:A:138:RCY:H1YA	2:A:150:RCY:C1U	0.98	1.88	60	2
1:A:66:VAL:HA	2:A:160:RCY:O1J	0.98	1.56	68	1
2:A:110:RCY:C1Z	2:A:110:RCY:O1H	0.98	2.11	37	1
2:A:138:RCY:H1C	2:A:187:RCY:H1MA	0.98	1.03	11	1
1:A:61:GLY:O	2:A:150:RCY:C1M	0.98	2.11	11	1
2:A:168:RCY:C1S	2:A:176:RCY:H1ZA	0.98	1.86	77	1
2:A:138:RCY:H1VA	2:A:168:RCY:C1C	0.98	1.88	19	1
1:A:70:TRP:CZ2	2:A:121:RCY:H1ZA	0.98	1.93	41	1
1:A:71:GLU:CA	2:A:168:RCY:H1CA	0.98	1.87	29	1
1:A:68:CYS:H	2:A:168:RCY:H1LA	0.98	1.19	93	2
1:A:68:CYS:SG	2:A:150:RCY:H1M	0.97	1.99	85	1
2:A:160:RCY:C1U	2:A:168:RCY:H1CB	0.97	1.71	49	1
1:A:67:ILE:HG23	2:A:173:RCY:C1P	0.97	1.87	21	1
1:A:64:ILE:O	2:A:168:RCY:O1H	0.97	1.81	54	1
2:A:176:RCY:C1X	2:A:187:RCY:C1M	0.97	2.42	4	1
1:A:70:TRP:CE2	2:A:173:RCY:O1G	0.97	2.16	93	1
1:A:64:ILE:HB	2:A:168:RCY:H1Z	0.97	1.00	30	2
2:A:173:RCY:O1H	2:A:176:RCY:H1VB	0.97	1.59	70	2
2:A:121:RCY:C1Z	2:A:168:RCY:H1L	0.97	1.89	94	1
2:A:168:RCY:O1J	2:A:187:RCY:H1CB	0.97	1.56	99	1
2:A:160:RCY:C1L	2:A:168:RCY:O1G	0.97	2.12	26	1
2:A:168:RCY:O1J	2:A:176:RCY:H1U	0.97	1.59	16	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:70:TRP:HB2	2:A:173:RCY:H1M	0.97	1.36	6	1
2:A:150:RCY:H1CB	2:A:176:RCY:O1G	0.97	1.60	82	1
2:A:173:RCY:C1M	2:A:176:RCY:C1W	0.97	2.21	77	1
2:A:160:RCY:H1U	2:A:168:RCY:H1M	0.97	1.00	96	1
2:A:173:RCY:H1Z	2:A:187:RCY:C1L	0.97	1.88	96	1
1:A:71:GLU:CG	2:A:168:RCY:N1R	0.97	2.26	93	1
1:A:70:TRP:HB2	2:A:168:RCY:H1M	0.97	1.35	28	1
1:A:70:TRP:H	2:A:176:RCY:C1C	0.97	1.61	13	1
1:A:71:GLU:O	2:A:173:RCY:H1S	0.97	1.57	68	3
2:A:150:RCY:C1C	2:A:187:RCY:H1Y	0.97	1.88	57	2
2:A:173:RCY:C1Y	2:A:187:RCY:O1H	0.97	2.12	92	2
1:A:70:TRP:CG	2:A:176:RCY:C1M	0.97	2.35	4	1
2:A:187:RCY:C1V	2:A:187:RCY:O1G	0.97	2.12	31	3
1:A:67:ILE:CG2	2:A:173:RCY:C1Y	0.97	2.41	80	1
1:A:77:GLU:HG2	2:A:176:RCY:C1U	0.97	1.84	39	1
2:A:173:RCY:C1V	2:A:187:RCY:O1J	0.97	2.11	67	1
1:A:68:CYS:C	2:A:173:RCY:C1Z	0.97	2.30	16	1
1:A:66:VAL:CA	2:A:160:RCY:O1J	0.97	2.12	68	1
2:A:160:RCY:H1M	2:A:168:RCY:H1VA	0.97	1.31	48	1
2:A:138:RCY:C1C	2:A:150:RCY:O1G	0.97	2.11	53	1
1:A:78:LEU:CD1	2:A:176:RCY:C1U	0.97	2.42	56	1
2:A:138:RCY:H1CB	2:A:173:RCY:H1ZA	0.97	1.35	66	1
2:A:168:RCY:O1H	2:A:173:RCY:C1Z	0.97	2.12	17	2
2:A:168:RCY:O1G	2:A:168:RCY:C1V	0.97	2.12	18	7
2:A:168:RCY:H1VB	2:A:187:RCY:C1Z	0.97	1.88	85	1
2:A:130:RCY:C1V	2:A:130:RCY:O1G	0.97	2.12	71	2
2:A:150:RCY:H1C	2:A:187:RCY:H1YA	0.97	1.35	53	1
2:A:138:RCY:C1C	2:A:160:RCY:C1L	0.97	2.39	73	1
2:A:138:RCY:C1Z	2:A:187:RCY:H1CA	0.97	1.72	74	1
1:A:77:GLU:H	2:A:176:RCY:C1P	0.97	1.71	31	1
2:A:168:RCY:C1V	2:A:168:RCY:O1G	0.97	2.12	8	7
2:A:160:RCY:H1M	2:A:168:RCY:H1LA	0.97	0.98	58	1
2:A:138:RCY:C1C	2:A:150:RCY:H1Y	0.97	1.88	59	1
2:A:160:RCY:O1H	2:A:173:RCY:H1YB	0.97	1.57	71	1
1:A:62:THR:HG22	2:A:130:RCY:C1U	0.97	1.88	9	1
2:A:168:RCY:H1CA	2:A:187:RCY:C1M	0.97	1.89	70	1
1:A:67:ILE:O	2:A:173:RCY:H1YB	0.97	1.58	63	1
2:A:150:RCY:C1Z	2:A:173:RCY:O1J	0.97	2.13	3	1
1:A:74:ASN:HA	2:A:176:RCY:H1U	0.97	1.34	67	1
1:A:60:CYS:O	2:A:168:RCY:H1YB	0.97	1.59	30	1
1:A:69:PRO:HD3	2:A:173:RCY:H1VB	0.97	1.33	30	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:71:GLU:OE1	2:A:176:RCY:C1V	0.97	2.11	92	1
2:A:160:RCY:O1J	2:A:168:RCY:C1V	0.97	2.13	70	3
2:A:173:RCY:C1Z	2:A:173:RCY:O1H	0.97	2.12	70	6
2:A:150:RCY:H1M	2:A:160:RCY:H1VA	0.97	0.98	42	1
1:A:68:CYS:N	2:A:168:RCY:H1L	0.97	1.74	21	3
1:A:63:ASP:C	2:A:168:RCY:C1L	0.97	2.32	59	1
2:A:160:RCY:O1J	2:A:168:RCY:O1G	0.97	1.81	48	4
2:A:160:RCY:C1Z	2:A:187:RCY:H1Z	0.97	1.88	31	2
1:A:63:ASP:OD1	2:A:160:RCY:H1ZA	0.97	1.59	73	1
2:A:168:RCY:C1W	2:A:173:RCY:O1J	0.97	1.88	20	1
2:A:168:RCY:C1Z	2:A:173:RCY:C1Z	0.97	2.42	31	1
2:A:121:RCY:O1G	2:A:121:RCY:C1V	0.97	2.13	95	5
2:A:160:RCY:C1V	2:A:160:RCY:O1G	0.97	2.13	3	7
2:A:168:RCY:H1L	2:A:173:RCY:H1Y	0.97	1.29	62	1
1:A:72:ALA:H	2:A:173:RCY:C1Z	0.97	1.72	50	1
2:A:138:RCY:H1CB	2:A:150:RCY:H1VA	0.97	0.98	10	2
1:A:70:TRP:CZ2	2:A:160:RCY:H1U	0.97	1.95	34	1
2:A:168:RCY:H1V	2:A:176:RCY:H1M	0.97	0.97	76	1
2:A:150:RCY:C1Z	2:A:150:RCY:O1H	0.97	2.13	96	2
1:A:76:CYS:H	2:A:176:RCY:H1S	0.97	1.17	24	2
1:A:71:GLU:OE2	2:A:130:RCY:C1Z	0.97	2.13	94	1
2:A:130:RCY:C1Y	2:A:160:RCY:H1VA	0.97	1.89	81	1
2:A:138:RCY:H1ZB	2:A:187:RCY:H1Z	0.97	0.99	77	2
1:A:70:TRP:O	2:A:173:RCY:N1R	0.97	1.97	82	2
1:A:60:CYS:CA	2:A:160:RCY:C1Q	0.97	2.43	83	2
1:A:64:ILE:HD11	2:A:168:RCY:H1L	0.97	1.36	88	1
2:A:160:RCY:C1Y	2:A:168:RCY:C1M	0.97	2.34	34	2
2:A:168:RCY:C1V	2:A:173:RCY:C1Z	0.97	2.43	29	1
2:A:173:RCY:H1YA	2:A:176:RCY:H1YB	0.97	1.33	59	1
1:A:77:GLU:OE2	2:A:176:RCY:C1V	0.97	2.11	7	1
1:A:70:TRP:CE2	2:A:176:RCY:H1VA	0.97	1.94	82	1
2:A:160:RCY:O1H	2:A:160:RCY:H1CB	0.96	1.56	74	9
2:A:168:RCY:C1Y	2:A:187:RCY:H1L	0.96	1.89	100	2
1:A:74:ASN:OD1	2:A:176:RCY:C1V	0.96	2.12	44	1
2:A:150:RCY:H1Z	2:A:187:RCY:C1Y	0.96	1.84	9	1
1:A:67:ILE:O	2:A:173:RCY:C1Y	0.96	2.12	63	1
2:A:130:RCY:H1YA	2:A:173:RCY:H1S	0.96	1.36	15	1
1:A:68:CYS:HA	2:A:160:RCY:H1VA	0.96	1.31	15	1
2:A:168:RCY:H1CA	2:A:187:RCY:H1YA	0.96	1.37	87	1
1:A:69:PRO:HG2	2:A:168:RCY:C1M	0.96	1.86	66	1
1:A:64:ILE:CB	2:A:168:RCY:H1Z	0.96	1.89	30	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:173:RCY:H1Y	2:A:187:RCY:C1Q	0.96	1.90	81	1
2:A:176:RCY:N1R	2:A:176:RCY:H1U	0.96	1.72	79	2
2:A:160:RCY:H1CB	2:A:173:RCY:C1Z	0.96	1.60	11	1
2:A:168:RCY:C1Z	2:A:176:RCY:N1V	0.96	2.17	11	1
2:A:138:RCY:H1VA	2:A:187:RCY:H1M	0.96	1.36	21	1
2:A:138:RCY:C1V	2:A:150:RCY:H1CB	0.96	1.90	67	1
2:A:150:RCY:H1YA	2:A:187:RCY:H1ZA	0.96	1.02	41	1
2:A:138:RCY:C1Q	2:A:150:RCY:O1G	0.96	2.12	41	1
2:A:168:RCY:H1V	2:A:187:RCY:H1YA	0.96	1.37	40	1
2:A:150:RCY:H1Z	2:A:187:RCY:H1VA	0.96	1.32	26	1
1:A:69:PRO:HB3	2:A:173:RCY:H1S	0.96	1.33	26	1
2:A:160:RCY:H1VB	2:A:168:RCY:H1VB	0.96	1.34	48	1
1:A:78:LEU:HG	2:A:176:RCY:H1MA	0.96	0.97	91	1
1:A:67:ILE:CG2	2:A:173:RCY:O1G	0.96	2.13	21	1
1:A:72:ALA:CB	2:A:173:RCY:H1MA	0.96	1.90	80	1
2:A:176:RCY:H1CB	2:A:187:RCY:C1V	0.96	1.89	93	1
2:A:160:RCY:H1ZB	2:A:168:RCY:H1YB	0.96	1.36	43	2
2:A:160:RCY:H1ZB	2:A:168:RCY:C1V	0.96	1.72	55	1
2:A:176:RCY:C1Z	2:A:187:RCY:C1V	0.96	2.32	10	1
1:A:64:ILE:HG12	2:A:160:RCY:C1V	0.96	1.90	54	1
1:A:64:ILE:CG1	2:A:168:RCY:O1H	0.96	2.13	58	2
2:A:138:RCY:C1V	2:A:168:RCY:H1CA	0.96	1.88	19	1
2:A:173:RCY:C1V	2:A:173:RCY:O1G	0.96	2.14	60	6
2:A:138:RCY:H1ZA	2:A:150:RCY:C1Q	0.96	1.90	60	1
2:A:138:RCY:H1YA	2:A:150:RCY:H1U	0.96	1.36	60	2
2:A:130:RCY:N1V	2:A:130:RCY:C1V	0.96	2.27	79	1
2:A:173:RCY:H1C	2:A:187:RCY:H1Y	0.96	1.25	48	1
2:A:138:RCY:H1VB	2:A:187:RCY:C1W	0.96	1.89	49	1
1:A:61:GLY:N	2:A:138:RCY:H1VA	0.96	1.70	7	1
1:A:68:CYS:H	2:A:168:RCY:H1L	0.96	1.15	21	1
1:A:68:CYS:SG	2:A:176:RCY:C1W	0.96	2.53	77	1
2:A:176:RCY:H1YB	2:A:187:RCY:C1V	0.96	1.65	38	2
1:A:76:CYS:N	2:A:176:RCY:H1S	0.96	1.74	13	4
2:A:138:RCY:C1X	2:A:150:RCY:O1H	0.96	2.12	62	1
1:A:69:PRO:CB	2:A:173:RCY:H1Z	0.96	1.90	69	2
1:A:69:PRO:HA	2:A:176:RCY:H1VA	0.96	1.35	72	1
1:A:70:TRP:HE1	2:A:168:RCY:C1Y	0.96	1.63	37	1
1:A:67:ILE:HG22	2:A:173:RCY:H1MA	0.96	0.98	80	1
2:A:130:RCY:C1Y	2:A:138:RCY:H1Z	0.96	1.91	73	1
1:A:59:GLY:HA3	2:A:160:RCY:H1M	0.96	0.98	78	1
1:A:71:GLU:CD	2:A:130:RCY:C1M	0.96	2.32	94	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:173:RCY:H1V	2:A:176:RCY:H1Y	0.96	0.97	2	1
2:A:110:RCY:C1V	2:A:110:RCY:O1G	0.96	2.13	3	4
1:A:64:ILE:HD11	2:A:168:RCY:O1H	0.96	1.60	58	1
2:A:160:RCY:C1Z	2:A:173:RCY:C1Z	0.96	2.44	99	2
2:A:121:RCY:C1Y	2:A:176:RCY:C1L	0.96	2.40	35	1
1:A:78:LEU:CD1	2:A:176:RCY:C1Z	0.96	2.44	91	1
1:A:72:ALA:CB	2:A:173:RCY:C1U	0.96	2.43	80	2
2:A:138:RCY:C1W	2:A:150:RCY:H1C	0.96	1.91	97	1
2:A:138:RCY:C1W	2:A:173:RCY:C1V	0.96	2.18	92	1
1:A:66:VAL:C	2:A:176:RCY:C1Y	0.96	2.33	22	1
2:A:160:RCY:H1Y	2:A:168:RCY:H1M	0.96	1.38	58	1
2:A:168:RCY:O1J	2:A:176:RCY:H1V	0.96	1.57	84	1
2:A:138:RCY:H1VB	2:A:187:RCY:H1ZA	0.96	1.36	49	1
2:A:168:RCY:C1V	2:A:176:RCY:O1G	0.96	2.14	20	1
2:A:138:RCY:H1M	2:A:173:RCY:C1V	0.96	1.87	92	1
2:A:138:RCY:O1G	2:A:138:RCY:C1C	0.96	2.14	17	4
2:A:160:RCY:H1C	2:A:168:RCY:O1G	0.96	1.60	19	2
1:A:73:CYS:H	2:A:173:RCY:C1Q	0.96	1.73	16	2
1:A:69:PRO:CG	2:A:176:RCY:H1YA	0.96	1.90	72	1
1:A:69:PRO:HB3	2:A:173:RCY:H1ZA	0.96	0.98	35	1
2:A:176:RCY:O1G	2:A:176:RCY:C1V	0.96	2.13	4	4
2:A:121:RCY:C1V	2:A:121:RCY:O1G	0.96	2.12	71	2
2:A:160:RCY:H1MA	2:A:168:RCY:O1J	0.96	1.60	9	1
2:A:168:RCY:C1W	2:A:176:RCY:O1J	0.96	2.14	11	1
1:A:69:PRO:CG	2:A:168:RCY:C1Y	0.96	2.43	66	1
1:A:69:PRO:CG	2:A:176:RCY:H1Z	0.96	1.84	66	1
2:A:150:RCY:C1C	2:A:168:RCY:O1J	0.95	2.14	19	1
1:A:65:THR:HG21	2:A:160:RCY:H1YA	0.95	1.36	55	1
1:A:70:TRP:NE1	2:A:176:RCY:H1CA	0.95	1.74	62	1
2:A:110:RCY:H1VA	2:A:121:RCY:H1MA	0.95	1.33	5	1
2:A:138:RCY:H1MA	2:A:187:RCY:H1YA	0.95	1.36	68	1
2:A:138:RCY:C1Z	2:A:187:RCY:H1VB	0.95	1.57	85	1
1:A:70:TRP:CE3	2:A:168:RCY:H1L	0.95	1.96	48	1
1:A:71:GLU:CA	2:A:173:RCY:C1Q	0.95	2.44	49	2
2:A:173:RCY:H1VA	2:A:187:RCY:C1Y	0.95	1.89	54	1
2:A:150:RCY:H1VA	2:A:173:RCY:H1YA	0.95	1.35	39	1
2:A:130:RCY:C1W	2:A:160:RCY:O1G	0.95	1.85	22	3
2:A:176:RCY:H1ZA	2:A:187:RCY:O1J	0.95	1.60	17	1
1:A:71:GLU:OE2	2:A:176:RCY:H1LA	0.95	1.61	40	1
1:A:70:TRP:HB2	2:A:173:RCY:H1V	0.95	1.34	26	1
2:A:168:RCY:C1C	2:A:176:RCY:C1W	0.95	2.41	59	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:63:ASP:HB2	2:A:150:RCY:C1C	0.95	1.88	85	1
2:A:150:RCY:H1Y	2:A:187:RCY:H1YA	0.95	0.99	18	1
2:A:150:RCY:H1Z	2:A:176:RCY:C1P	0.95	1.89	3	1
2:A:130:RCY:O1G	2:A:130:RCY:C1V	0.95	2.13	12	5
2:A:160:RCY:H1Y	2:A:168:RCY:C1Z	0.95	1.92	53	2
2:A:168:RCY:O1J	2:A:173:RCY:O1G	0.95	1.82	37	1
1:A:65:THR:HG21	2:A:160:RCY:H1CA	0.95	1.30	31	1
1:A:71:GLU:CD	2:A:187:RCY:O1H	0.95	2.05	88	1
2:A:168:RCY:H1Z	2:A:173:RCY:H1VB	0.95	0.96	58	1
2:A:168:RCY:O1G	2:A:168:RCY:H1CA	0.95	1.59	53	3
1:A:62:THR:OG1	2:A:150:RCY:C1C	0.95	2.08	11	1
2:A:168:RCY:C1Q	2:A:173:RCY:H1Z	0.95	1.89	39	1
1:A:67:ILE:HG21	2:A:173:RCY:C1C	0.95	1.77	31	1
2:A:173:RCY:O1G	2:A:173:RCY:C1V	0.95	2.14	100	3
2:A:150:RCY:H1VB	2:A:160:RCY:H1M	0.95	0.95	42	1
2:A:173:RCY:C1Z	2:A:176:RCY:C1Y	0.95	2.45	37	7
2:A:160:RCY:H1Y	2:A:168:RCY:H1ZA	0.95	0.98	53	2
2:A:138:RCY:C1W	2:A:187:RCY:H1YB	0.95	1.90	68	1
1:A:60:CYS:O	2:A:130:RCY:N1R	0.95	1.99	18	1
1:A:78:LEU:HD11	2:A:176:RCY:C1Q	0.95	1.90	91	1
2:A:160:RCY:O1J	2:A:168:RCY:N1R	0.95	1.99	47	1
1:A:60:CYS:HA	2:A:160:RCY:H1L	0.95	1.32	89	1
2:A:176:RCY:C1V	2:A:187:RCY:C1M	0.95	2.41	96	1
2:A:138:RCY:H1YA	2:A:187:RCY:C1Z	0.95	1.91	3	1
2:A:138:RCY:O1J	2:A:187:RCY:H1M	0.95	1.61	52	1
2:A:176:RCY:H1CA	2:A:176:RCY:C1Q	0.95	1.91	93	4
2:A:130:RCY:C1C	2:A:130:RCY:O1H	0.95	2.14	85	4
1:A:73:CYS:CA	2:A:173:RCY:O1H	0.95	2.13	56	2
2:A:130:RCY:H1M	2:A:173:RCY:H1YA	0.95	1.38	94	1
2:A:121:RCY:H1CA	2:A:121:RCY:C1Q	0.95	1.90	69	6
1:A:75:HIS:C	2:A:176:RCY:C1S	0.95	2.35	13	1
1:A:70:TRP:CB	2:A:173:RCY:C1V	0.95	2.19	4	2
2:A:150:RCY:C1V	2:A:150:RCY:O1G	0.95	2.13	68	4
2:A:173:RCY:N1V	2:A:176:RCY:H1VA	0.95	1.77	71	1
1:A:59:GLY:HA2	2:A:160:RCY:N1R	0.95	1.75	70	1
1:A:62:THR:HG1	2:A:168:RCY:H1L	0.95	1.13	23	1
2:A:130:RCY:H1MA	2:A:160:RCY:C1Y	0.95	1.90	7	1
2:A:138:RCY:H1CA	2:A:187:RCY:O1G	0.95	1.61	11	1
1:A:59:GLY:CA	2:A:160:RCY:C1V	0.95	2.44	83	2
2:A:160:RCY:C1Z	2:A:168:RCY:C1Z	0.95	1.81	78	1
2:A:160:RCY:C1U	2:A:168:RCY:H1M	0.95	1.71	96	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:72:ALA:HB3	2:A:173:RCY:C1P	0.95	1.91	10	1
2:A:173:RCY:H1S	2:A:176:RCY:C1L	0.95	1.83	28	3
1:A:62:THR:HG23	2:A:130:RCY:H1U	0.95	1.35	18	1
1:A:59:GLY:CA	2:A:160:RCY:O1G	0.95	1.95	70	2
1:A:68:CYS:HB3	2:A:173:RCY:C1M	0.95	1.90	73	1
2:A:150:RCY:C1Y	2:A:187:RCY:H1VB	0.95	1.89	38	1
2:A:150:RCY:H1YB	2:A:187:RCY:H1YB	0.95	0.95	41	2
1:A:66:VAL:CB	2:A:160:RCY:O1J	0.95	2.14	68	1
2:A:168:RCY:C1M	2:A:187:RCY:C1V	0.95	2.45	90	1
2:A:130:RCY:H1Y	2:A:138:RCY:H1Z	0.95	0.98	73	1
2:A:173:RCY:C1M	2:A:176:RCY:O1H	0.95	2.00	52	2
2:A:176:RCY:C1Z	2:A:187:RCY:N1V	0.95	2.29	17	1
2:A:176:RCY:H1ZB	2:A:187:RCY:N1V	0.95	1.74	17	1
1:A:70:TRP:HB2	2:A:168:RCY:H1S	0.95	1.37	19	2
1:A:68:CYS:HA	2:A:168:RCY:H1LA	0.95	1.02	30	3
2:A:150:RCY:H1ZB	2:A:160:RCY:C1Q	0.95	1.91	16	1
1:A:69:PRO:O	2:A:173:RCY:H1ZA	0.95	1.61	69	1
2:A:110:RCY:N1V	2:A:121:RCY:H1YA	0.95	1.77	5	1
2:A:176:RCY:C1X	2:A:187:RCY:H1Z	0.95	1.85	5	1
1:A:69:PRO:CB	2:A:187:RCY:C1C	0.95	2.35	7	1
1:A:62:THR:OG1	2:A:150:RCY:H1CB	0.95	1.62	11	1
2:A:138:RCY:H1VA	2:A:187:RCY:N1R	0.95	1.74	21	1
1:A:63:ASP:HB3	2:A:160:RCY:H1CB	0.95	1.39	54	2
2:A:173:RCY:H1VA	2:A:176:RCY:O1G	0.95	1.59	36	1
1:A:76:CYS:CB	2:A:173:RCY:O1G	0.95	2.14	38	2
2:A:173:RCY:H1Z	2:A:187:RCY:H1ZB	0.95	1.35	84	1
1:A:71:GLU:CG	2:A:130:RCY:C1M	0.95	2.42	94	1
2:A:160:RCY:C1P	2:A:168:RCY:H1VA	0.95	1.92	60	1
2:A:150:RCY:H1CA	2:A:150:RCY:C1Q	0.95	1.91	81	4
2:A:138:RCY:H1U	2:A:187:RCY:H1C	0.95	0.95	5	1
1:A:74:ASN:HA	2:A:173:RCY:H1CB	0.95	1.34	35	1
1:A:69:PRO:HA	2:A:173:RCY:H1CB	0.95	1.34	66	1
2:A:150:RCY:H1YA	2:A:187:RCY:C1C	0.94	1.91	78	1
1:A:71:GLU:HA	2:A:173:RCY:O1H	0.94	1.49	67	3
2:A:173:RCY:H1M	2:A:176:RCY:O1J	0.94	1.58	55	1
2:A:176:RCY:O1H	2:A:176:RCY:C1Z	0.94	2.14	5	2
2:A:121:RCY:O1H	2:A:121:RCY:C1C	0.94	2.14	67	6
2:A:176:RCY:C1M	2:A:187:RCY:H1Z	0.94	1.89	5	1
2:A:168:RCY:C1M	2:A:173:RCY:H1M	0.94	1.91	70	1
2:A:150:RCY:H1CB	2:A:176:RCY:H1U	0.94	1.39	82	1
2:A:138:RCY:H1VA	2:A:150:RCY:H1Y	0.94	1.37	36	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:70:TRP:CH2	2:A:130:RCY:H1YB	0.94	1.97	88	1
2:A:173:RCY:H1CA	2:A:173:RCY:C1Q	0.94	1.91	9	7
1:A:73:CYS:CB	2:A:173:RCY:O1H	0.94	2.15	59	23
2:A:176:RCY:O1H	2:A:187:RCY:C1V	0.94	2.09	42	2
1:A:68:CYS:HB3	2:A:160:RCY:C1W	0.94	1.92	19	1
2:A:176:RCY:C1Y	2:A:187:RCY:C1P	0.94	2.43	92	3
2:A:173:RCY:H1VA	2:A:176:RCY:H1Y	0.94	0.96	76	1
2:A:160:RCY:H1Y	2:A:168:RCY:H1V	0.94	1.37	70	1
2:A:173:RCY:C1Z	2:A:176:RCY:H1L	0.94	1.92	20	1
2:A:150:RCY:H1VB	2:A:187:RCY:H1L	0.94	1.38	87	1
1:A:74:ASN:O	2:A:173:RCY:O1J	0.94	1.77	22	1
1:A:69:PRO:HB3	2:A:173:RCY:O1J	0.94	1.52	9	2
1:A:71:GLU:OE2	2:A:150:RCY:C1U	0.94	2.14	58	1
2:A:130:RCY:C1W	2:A:160:RCY:H1YA	0.94	1.92	7	1
1:A:66:VAL:O	2:A:168:RCY:N1R	0.94	1.99	51	1
2:A:173:RCY:O1G	2:A:187:RCY:O1J	0.94	1.84	89	1
1:A:70:TRP:CE3	2:A:168:RCY:O1J	0.94	2.19	41	1
2:A:110:RCY:H1YA	2:A:121:RCY:C1C	0.94	1.78	81	1
2:A:168:RCY:C1Y	2:A:173:RCY:C1P	0.94	2.45	91	2
2:A:173:RCY:C1U	2:A:187:RCY:H1Y	0.94	1.89	70	1
2:A:138:RCY:C1V	2:A:150:RCY:H1YA	0.94	1.91	51	3
1:A:70:TRP:H	2:A:168:RCY:H1L	0.94	0.78	28	2
2:A:138:RCY:C1Y	2:A:187:RCY:H1M	0.94	1.92	82	1
1:A:64:ILE:HD11	2:A:160:RCY:H1YB	0.94	1.39	74	1
2:A:138:RCY:N1V	2:A:150:RCY:O1J	0.94	2.00	97	1
2:A:176:RCY:C1Z	2:A:187:RCY:H1CA	0.94	1.91	38	1
2:A:150:RCY:H1Z	2:A:187:RCY:H1VB	0.94	1.35	26	1
1:A:73:CYS:HA	2:A:173:RCY:H1LA	0.94	1.14	33	3
2:A:150:RCY:H1U	2:A:187:RCY:H1V	0.94	0.95	89	1
2:A:138:RCY:H1M	2:A:150:RCY:C1M	0.94	1.92	1	1
2:A:121:RCY:C1C	2:A:121:RCY:O1G	0.94	2.15	98	5
1:A:70:TRP:CD2	2:A:168:RCY:C1V	0.94	2.50	94	2
1:A:59:GLY:O	2:A:160:RCY:O1H	0.94	1.83	20	2
2:A:160:RCY:H1C	2:A:168:RCY:H1LA	0.94	0.96	48	1
2:A:173:RCY:H1S	2:A:176:RCY:H1LA	0.94	0.98	28	1
1:A:66:VAL:O	2:A:176:RCY:H1YB	0.94	1.63	22	1
1:A:63:ASP:OD2	2:A:121:RCY:C1V	0.94	2.16	42	1
1:A:71:GLU:HA	2:A:168:RCY:H1CA	0.94	0.97	29	1
2:A:173:RCY:H1ZA	2:A:187:RCY:H1LA	0.94	0.99	45	2
1:A:59:GLY:CA	2:A:160:RCY:H1LA	0.94	1.83	57	2
1:A:60:CYS:O	2:A:168:RCY:H1U	0.94	1.62	95	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:173:RCY:H1ZA	2:A:176:RCY:C1X	0.94	1.88	31	1
1:A:64:ILE:CG2	2:A:168:RCY:H1ZA	0.94	1.71	83	1
2:A:168:RCY:C1Z	2:A:187:RCY:C1L	0.94	2.17	100	2
1:A:70:TRP:HH2	2:A:130:RCY:C1Y	0.94	1.75	88	1
1:A:75:HIS:HD2	2:A:173:RCY:H1Z	0.94	1.21	42	1
1:A:68:CYS:CA	2:A:168:RCY:C1L	0.94	2.25	75	4
2:A:138:RCY:H1MA	2:A:150:RCY:C1V	0.94	1.93	75	1
1:A:67:ILE:C	2:A:168:RCY:H1S	0.94	1.82	58	3
1:A:70:TRP:O	2:A:173:RCY:O1G	0.94	1.84	16	3
1:A:70:TRP:CZ2	2:A:168:RCY:C1Z	0.94	2.49	24	1
2:A:138:RCY:N1R	2:A:187:RCY:H1CB	0.94	1.78	5	1
1:A:70:TRP:HA	2:A:173:RCY:N1R	0.94	1.77	6	1
2:A:138:RCY:C1P	2:A:160:RCY:C1U	0.94	2.21	18	1
2:A:138:RCY:C1M	2:A:138:RCY:N1R	0.94	2.31	79	1
2:A:168:RCY:H1YA	2:A:173:RCY:C1C	0.94	1.91	91	1
1:A:70:TRP:CE3	2:A:168:RCY:C1M	0.94	2.50	49	3
2:A:130:RCY:C1M	2:A:160:RCY:C1Y	0.94	2.45	7	1
2:A:138:RCY:H1C	2:A:150:RCY:O1G	0.94	1.60	53	1
2:A:150:RCY:C1U	2:A:176:RCY:O1G	0.94	2.15	82	1
2:A:130:RCY:H1Z	2:A:138:RCY:O1J	0.94	1.62	73	1
2:A:173:RCY:C1W	2:A:187:RCY:H1U	0.94	1.93	77	1
2:A:168:RCY:H1YA	2:A:176:RCY:H1ZB	0.94	1.38	66	1
1:A:71:GLU:HG2	2:A:176:RCY:H1YA	0.94	0.96	92	1
1:A:70:TRP:CZ2	2:A:121:RCY:C1Q	0.94	2.42	78	1
2:A:160:RCY:C1Y	2:A:168:RCY:C1Q	0.94	2.40	100	3
1:A:68:CYS:H	2:A:176:RCY:C1Y	0.94	1.56	22	1
1:A:69:PRO:HD3	2:A:173:RCY:O1G	0.94	1.62	24	2
2:A:138:RCY:O1G	2:A:138:RCY:C1Z	0.94	2.16	30	8
2:A:138:RCY:H1VB	2:A:150:RCY:H1S	0.94	1.39	62	1
2:A:138:RCY:O1G	2:A:150:RCY:C1Q	0.94	2.16	81	1
2:A:160:RCY:C1U	2:A:168:RCY:O1J	0.94	2.16	9	1
1:A:67:ILE:CG2	2:A:173:RCY:H1L	0.94	1.93	73	1
2:A:160:RCY:C1C	2:A:168:RCY:O1H	0.94	2.13	39	1
2:A:150:RCY:C1Y	2:A:176:RCY:H1Z	0.94	1.91	42	1
2:A:130:RCY:H1LA	2:A:160:RCY:C1P	0.94	1.90	62	1
2:A:176:RCY:C1Q	2:A:187:RCY:C1Z	0.94	2.42	60	1
2:A:176:RCY:H1C	2:A:187:RCY:C1Y	0.94	1.92	26	1
2:A:168:RCY:C1Q	2:A:176:RCY:C1Y	0.94	2.43	59	1
1:A:70:TRP:HH2	2:A:168:RCY:C1P	0.94	1.45	48	1
1:A:70:TRP:CD1	2:A:121:RCY:H1V	0.94	1.98	49	1
1:A:77:GLU:CB	2:A:173:RCY:H1CB	0.94	1.93	51	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:173:RCY:H1ZB	2:A:176:RCY:C1X	0.94	1.90	31	1
1:A:60:CYS:CB	2:A:160:RCY:O1H	0.93	2.15	85	32
2:A:121:RCY:C1Q	2:A:121:RCY:H1CA	0.93	1.93	35	5
2:A:176:RCY:H1YB	2:A:187:RCY:H1MA	0.93	1.34	69	1
2:A:173:RCY:C1Y	2:A:176:RCY:H1YB	0.93	1.93	59	1
2:A:168:RCY:C1W	2:A:173:RCY:H1M	0.93	1.92	70	1
1:A:74:ASN:H	2:A:173:RCY:H1LA	0.93	1.21	82	1
1:A:70:TRP:O	2:A:168:RCY:C1V	0.93	2.15	20	1
2:A:150:RCY:C1U	2:A:187:RCY:C1V	0.93	2.45	89	1
2:A:160:RCY:H1Z	2:A:168:RCY:C1V	0.93	1.92	18	2
1:A:78:LEU:CD1	2:A:176:RCY:H1ZA	0.93	1.92	91	1
2:A:138:RCY:H1V	2:A:187:RCY:H1ZA	0.93	1.38	49	1
2:A:173:RCY:O1H	2:A:176:RCY:C1L	0.93	2.14	23	1
1:A:64:ILE:HG21	2:A:168:RCY:C1M	0.93	1.93	95	1
2:A:150:RCY:H1ZA	2:A:173:RCY:O1J	0.93	1.60	3	1
2:A:168:RCY:H1YA	2:A:176:RCY:C1Z	0.93	1.92	66	1
1:A:67:ILE:HG21	2:A:130:RCY:H1M	0.93	1.38	30	1
1:A:76:CYS:CB	2:A:176:RCY:O1H	0.93	2.17	80	20
2:A:150:RCY:C1Z	2:A:187:RCY:O1H	0.93	2.16	84	1
1:A:71:GLU:OE2	2:A:110:RCY:H1VB	0.93	1.61	5	1
1:A:62:THR:CG2	2:A:130:RCY:H1U	0.93	1.93	18	1
2:A:138:RCY:H1V	2:A:150:RCY:H1YB	0.93	1.33	51	1
1:A:74:ASN:OD1	2:A:173:RCY:C1S	0.93	2.16	2	1
2:A:150:RCY:C1C	2:A:176:RCY:H1U	0.93	1.92	82	1
2:A:110:RCY:N1R	2:A:110:RCY:H1U	0.93	1.74	25	1
2:A:138:RCY:C1C	2:A:150:RCY:C1C	0.93	2.32	66	1
2:A:160:RCY:H1ZA	2:A:168:RCY:H1YB	0.93	1.39	43	1
2:A:168:RCY:C1M	2:A:187:RCY:C1P	0.93	2.44	100	1
2:A:168:RCY:H1CA	2:A:173:RCY:H1V	0.93	1.36	85	2
2:A:168:RCY:C1Q	2:A:173:RCY:H1ZB	0.93	1.94	10	1
1:A:76:CYS:HB2	2:A:187:RCY:C1V	0.93	1.92	34	1
1:A:71:GLU:CG	2:A:168:RCY:C1Q	0.93	2.47	93	2
1:A:67:ILE:HG13	2:A:176:RCY:H1C	0.93	1.40	53	2
2:A:138:RCY:H1M	2:A:150:RCY:C1Y	0.93	1.93	89	1
2:A:176:RCY:C1V	2:A:187:RCY:H1M	0.93	1.88	96	1
2:A:138:RCY:H1VB	2:A:150:RCY:C1M	0.93	1.87	1	1
2:A:160:RCY:H1YB	2:A:168:RCY:H1S	0.93	1.34	100	1
2:A:173:RCY:H1U	2:A:176:RCY:H1VA	0.93	1.34	19	1
1:A:69:PRO:O	2:A:173:RCY:C1V	0.93	2.17	64	1
2:A:138:RCY:H1CA	2:A:150:RCY:O1H	0.93	1.62	62	1
2:A:176:RCY:N1V	2:A:187:RCY:C1U	0.93	2.31	29	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:70:TRP:CG	2:A:121:RCY:H1V	0.93	1.96	49	2
1:A:59:GLY:CA	2:A:160:RCY:C1Z	0.93	2.47	49	1
2:A:160:RCY:O1J	2:A:168:RCY:C1M	0.93	2.16	21	2
2:A:168:RCY:H1Y	2:A:176:RCY:C1L	0.93	1.92	20	1
2:A:138:RCY:H1C	2:A:187:RCY:O1J	0.93	1.63	3	1
2:A:168:RCY:C1X	2:A:176:RCY:H1YB	0.93	1.92	98	1
2:A:160:RCY:C1Z	2:A:168:RCY:C1X	0.93	2.45	69	1
1:A:71:GLU:HA	2:A:168:RCY:C1M	0.93	1.89	37	2
1:A:70:TRP:HE1	2:A:121:RCY:C1Y	0.93	0.52	49	1
2:A:160:RCY:C1C	2:A:173:RCY:H1ZB	0.93	1.90	11	1
1:A:69:PRO:N	2:A:173:RCY:C1V	0.93	2.31	100	1
2:A:150:RCY:C1Y	2:A:160:RCY:H1VA	0.93	1.92	42	1
2:A:160:RCY:O1G	2:A:168:RCY:O1J	0.93	1.85	64	1
1:A:68:CYS:CB	2:A:168:RCY:O1H	0.93	2.17	59	11
2:A:173:RCY:H1YB	2:A:187:RCY:C1L	0.93	1.92	45	1
1:A:75:HIS:CG	2:A:168:RCY:C1Z	0.93	2.51	73	1
2:A:168:RCY:C1X	2:A:176:RCY:O1J	0.93	2.17	43	1
1:A:70:TRP:HZ2	2:A:121:RCY:C1Z	0.93	1.76	41	1
2:A:173:RCY:O1H	2:A:173:RCY:C1C	0.93	2.15	55	4
2:A:168:RCY:C1M	2:A:173:RCY:C1Z	0.93	2.47	84	1
2:A:160:RCY:H1YB	2:A:168:RCY:O1G	0.93	1.58	32	2
2:A:110:RCY:C1Q	2:A:110:RCY:H1CA	0.93	1.93	50	4
2:A:173:RCY:H1Y	2:A:187:RCY:C1S	0.93	1.93	81	1
2:A:176:RCY:H1CA	2:A:187:RCY:H1V	0.93	1.39	93	1
2:A:138:RCY:H1YB	2:A:150:RCY:C1P	0.93	1.94	60	1
1:A:71:GLU:CB	2:A:173:RCY:H1V	0.93	1.92	50	1
1:A:64:ILE:CG1	2:A:168:RCY:C1Z	0.93	2.46	78	2
2:A:130:RCY:H1ZB	2:A:160:RCY:C1L	0.93	1.91	61	1
1:A:64:ILE:CD1	2:A:150:RCY:H1LA	0.93	1.93	75	1
2:A:138:RCY:H1Y	2:A:187:RCY:H1YA	0.93	1.38	86	1
2:A:138:RCY:H1Y	2:A:150:RCY:C1Y	0.93	1.94	26	1
2:A:110:RCY:H1Y	2:A:121:RCY:H1VB	0.93	1.41	81	2
1:A:64:ILE:O	2:A:138:RCY:C1Y	0.93	2.17	85	1
1:A:68:CYS:N	2:A:168:RCY:H1LA	0.93	1.79	91	3
1:A:61:GLY:HA2	2:A:160:RCY:N1R	0.93	1.71	2	1
1:A:67:ILE:HG22	2:A:173:RCY:H1C	0.93	0.93	31	1
1:A:64:ILE:HG13	2:A:168:RCY:H1ZA	0.92	1.38	78	2
2:A:173:RCY:H1V	2:A:176:RCY:H1M	0.92	0.96	17	3
1:A:70:TRP:HB3	2:A:168:RCY:H1S	0.92	1.38	19	1
2:A:173:RCY:O1J	2:A:187:RCY:H1YA	0.92	1.54	99	2
2:A:160:RCY:C1Z	2:A:168:RCY:H1VB	0.92	1.93	58	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:160:RCY:H1M	2:A:168:RCY:C1L	0.92	1.93	58	1
2:A:168:RCY:C1S	2:A:173:RCY:C1U	0.92	2.28	71	1
2:A:173:RCY:C1Q	2:A:187:RCY:H1C	0.92	1.93	7	1
2:A:138:RCY:H1YB	2:A:173:RCY:H1ZA	0.92	1.40	32	1
2:A:150:RCY:H1MA	2:A:168:RCY:H1YA	0.92	0.95	74	1
2:A:176:RCY:H1U	2:A:187:RCY:H1MA	0.92	1.38	96	1
1:A:67:ILE:HG12	2:A:168:RCY:H1CB	0.92	1.40	27	1
2:A:110:RCY:O1G	2:A:110:RCY:C1C	0.92	2.17	11	7
2:A:173:RCY:C1Q	2:A:176:RCY:H1MA	0.92	1.92	61	1
1:A:67:ILE:HG12	2:A:176:RCY:H1MA	0.92	1.38	22	1
2:A:160:RCY:N1R	2:A:168:RCY:C1M	0.92	2.33	52	2
1:A:60:CYS:HB3	2:A:168:RCY:C1Z	0.92	1.93	52	1
2:A:176:RCY:C1C	2:A:187:RCY:C1M	0.92	0.93	4	3
1:A:67:ILE:O	2:A:150:RCY:O1J	0.92	1.87	72	1
1:A:71:GLU:OE2	2:A:173:RCY:H1V	0.92	1.64	68	1
2:A:110:RCY:C1Z	2:A:121:RCY:H1VA	0.92	1.95	81	1
2:A:160:RCY:O1H	2:A:176:RCY:O1G	0.92	1.85	73	1
1:A:60:CYS:H	2:A:160:RCY:H1L	0.92	1.10	28	1
2:A:138:RCY:H1L	2:A:150:RCY:H1VB	0.92	1.39	98	1
2:A:168:RCY:C1C	2:A:173:RCY:H1V	0.92	1.95	41	2
2:A:160:RCY:H1YB	2:A:168:RCY:C1L	0.92	1.95	58	3
1:A:70:TRP:HZ3	2:A:168:RCY:H1C	0.92	1.16	95	2
2:A:168:RCY:C1V	2:A:173:RCY:H1ZA	0.92	1.94	29	1
1:A:78:LEU:CD2	2:A:187:RCY:C1C	0.92	0.92	91	1
1:A:63:ASP:O	2:A:160:RCY:H1VB	0.92	1.55	3	1
2:A:173:RCY:O1J	2:A:176:RCY:C1L	0.92	2.16	93	2
2:A:173:RCY:H1S	2:A:176:RCY:C1M	0.92	1.92	67	1
1:A:62:THR:HA	2:A:138:RCY:H1ZA	0.92	0.96	38	1
1:A:65:THR:HG22	2:A:168:RCY:H1L	0.92	1.39	55	1
2:A:130:RCY:C1Q	2:A:130:RCY:H1CA	0.92	1.94	85	4
1:A:75:HIS:C	2:A:176:RCY:C1L	0.92	2.36	13	1
1:A:75:HIS:HA	2:A:176:RCY:C1P	0.92	1.94	13	1
1:A:73:CYS:SG	2:A:130:RCY:C1V	0.92	2.58	5	1
2:A:168:RCY:H1V	2:A:187:RCY:H1ZB	0.92	1.38	31	2
2:A:160:RCY:C1Y	2:A:168:RCY:C1U	0.92	2.47	44	1
1:A:63:ASP:OD1	2:A:150:RCY:H1Z	0.92	1.62	80	1
2:A:160:RCY:H1U	2:A:160:RCY:N1R	0.92	1.77	25	1
2:A:130:RCY:C1X	2:A:160:RCY:C1S	0.92	2.48	8	1
2:A:160:RCY:C1W	2:A:168:RCY:C1V	0.92	2.46	55	1
1:A:71:GLU:OE1	2:A:176:RCY:C1Z	0.92	2.17	84	1
2:A:138:RCY:C1C	2:A:173:RCY:H1Z	0.92	1.94	15	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:138:RCY:H1MA	2:A:150:RCY:O1G	0.92	1.65	1	1
2:A:150:RCY:C1Y	2:A:187:RCY:C1U	0.92	2.48	78	1
1:A:68:CYS:O	2:A:168:RCY:C1L	0.92	2.17	38	2
1:A:71:GLU:N	2:A:168:RCY:C1Q	0.92	2.13	22	1
1:A:67:ILE:HG21	2:A:138:RCY:C1Q	0.92	1.93	72	1
1:A:64:ILE:HG12	2:A:168:RCY:C1M	0.92	1.94	6	1
2:A:168:RCY:H1CB	2:A:176:RCY:C1Z	0.92	1.93	59	1
2:A:110:RCY:H1Z	2:A:121:RCY:C1C	0.92	1.94	33	1
2:A:173:RCY:N1V	2:A:187:RCY:H1MA	0.92	1.79	93	1
1:A:70:TRP:CD2	2:A:173:RCY:H1YB	0.92	1.98	92	1
1:A:72:ALA:N	2:A:173:RCY:C1M	0.92	2.05	78	1
2:A:150:RCY:O1H	2:A:150:RCY:C1C	0.92	2.18	93	4
2:A:173:RCY:H1VA	2:A:176:RCY:C1Z	0.92	1.94	4	1
1:A:60:CYS:C	2:A:160:RCY:N1R	0.92	2.12	2	1
2:A:173:RCY:C1C	2:A:187:RCY:H1ZB	0.92	1.94	93	1
2:A:130:RCY:C1Z	2:A:130:RCY:O1H	0.92	2.17	66	1
2:A:150:RCY:H1CA	2:A:150:RCY:C1P	0.92	1.95	61	7
2:A:130:RCY:H1Y	2:A:160:RCY:H1VB	0.92	1.37	43	1
2:A:173:RCY:C1C	2:A:187:RCY:O1G	0.92	2.18	100	2
2:A:187:RCY:O1H	2:A:187:RCY:C1V	0.92	2.18	72	4
2:A:160:RCY:N1V	2:A:173:RCY:C1C	0.92	2.24	11	1
2:A:187:RCY:C1C	2:A:187:RCY:O1H	0.92	2.18	18	2
1:A:67:ILE:HD11	2:A:160:RCY:H1VA	0.92	1.41	86	1
1:A:69:PRO:HG2	2:A:173:RCY:C1Z	0.92	1.92	57	1
1:A:62:THR:C	2:A:160:RCY:H1CA	0.92	1.84	46	1
1:A:68:CYS:SG	2:A:160:RCY:H1C	0.92	2.05	3	1
1:A:69:PRO:CB	2:A:173:RCY:O1G	0.92	2.17	75	1
2:A:173:RCY:C1Z	2:A:187:RCY:H1ZB	0.92	1.93	84	1
2:A:176:RCY:C1Y	2:A:187:RCY:O1G	0.92	2.13	10	2
2:A:168:RCY:H1MA	2:A:173:RCY:H1MA	0.92	1.40	70	1
1:A:60:CYS:O	2:A:160:RCY:C1L	0.92	2.16	30	2
2:A:150:RCY:H1YB	2:A:187:RCY:H1CB	0.91	1.39	78	1
2:A:173:RCY:H1ZB	2:A:187:RCY:C1L	0.91	1.94	100	1
1:A:71:GLU:HG2	2:A:150:RCY:N1V	0.91	1.59	58	2
1:A:71:GLU:OE1	2:A:160:RCY:H1VB	0.91	1.65	58	1
2:A:168:RCY:H1MA	2:A:173:RCY:C1Z	0.91	1.93	84	1
2:A:173:RCY:H1ZB	2:A:187:RCY:H1ZA	0.91	0.94	84	1
2:A:138:RCY:H1YA	2:A:187:RCY:H1C	0.91	1.39	59	2
2:A:168:RCY:C1Q	2:A:176:RCY:H1ZA	0.91	1.90	77	1
2:A:138:RCY:H1YB	2:A:150:RCY:H1CA	0.91	1.42	97	1
2:A:150:RCY:H1Y	2:A:187:RCY:C1U	0.91	1.94	78	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:74:ASN:O	2:A:176:RCY:C1V	0.91	2.19	62	2
2:A:176:RCY:H1ZB	2:A:187:RCY:C1U	0.91	1.95	17	1
2:A:168:RCY:O1J	2:A:187:RCY:H1U	0.91	1.65	70	2
2:A:138:RCY:H1YA	2:A:187:RCY:C1W	0.91	1.95	86	1
1:A:69:PRO:HG2	2:A:150:RCY:C1Y	0.91	1.87	85	1
1:A:70:TRP:CA	2:A:173:RCY:C1Y	0.91	2.48	85	1
2:A:138:RCY:H1L	2:A:160:RCY:H1ZB	0.91	1.17	18	1
2:A:176:RCY:H1YA	2:A:187:RCY:C1C	0.91	1.94	27	2
1:A:77:GLU:CD	2:A:176:RCY:H1VB	0.91	1.74	7	1
2:A:150:RCY:C1Y	2:A:173:RCY:N1R	0.91	2.32	3	1
2:A:150:RCY:C1V	2:A:173:RCY:C1V	0.91	2.16	31	1
2:A:130:RCY:C1Y	2:A:160:RCY:N1R	0.91	2.24	50	2
2:A:138:RCY:C1Q	2:A:150:RCY:O1H	0.91	2.18	62	1
1:A:70:TRP:HZ2	2:A:160:RCY:C1X	0.91	1.75	34	1
2:A:138:RCY:O1J	2:A:150:RCY:C1Y	0.91	2.18	6	2
1:A:71:GLU:CD	2:A:173:RCY:H1V	0.91	1.84	68	1
1:A:73:CYS:O	2:A:173:RCY:C1C	0.91	2.17	35	1
2:A:168:RCY:O1J	2:A:173:RCY:C1V	0.91	2.19	48	1
1:A:70:TRP:CD1	2:A:168:RCY:C1Y	0.91	2.50	37	1
2:A:160:RCY:N1V	2:A:168:RCY:C1U	0.91	2.33	47	1
1:A:71:GLU:OE2	2:A:168:RCY:C1P	0.91	2.18	93	1
1:A:69:PRO:HG3	2:A:168:RCY:C1M	0.91	1.76	66	1
2:A:160:RCY:H1ZA	2:A:168:RCY:H1VB	0.91	1.41	58	2
2:A:138:RCY:C1C	2:A:160:RCY:C1Y	0.91	1.97	27	2
1:A:72:ALA:O	2:A:168:RCY:C1W	0.91	2.03	57	1
2:A:160:RCY:H1CB	2:A:173:RCY:H1Z	0.91	0.94	11	1
2:A:168:RCY:C1C	2:A:168:RCY:O1G	0.91	2.17	80	3
2:A:138:RCY:H1MA	2:A:150:RCY:H1V	0.91	1.39	75	2
2:A:173:RCY:C1V	2:A:173:RCY:O1H	0.91	2.19	83	6
2:A:173:RCY:H1Z	2:A:176:RCY:C1S	0.91	1.93	29	1
2:A:138:RCY:N1R	2:A:160:RCY:C1C	0.91	2.21	69	1
2:A:168:RCY:H1ZB	2:A:176:RCY:H1Z	0.91	1.43	6	1
2:A:173:RCY:C1X	2:A:176:RCY:H1VA	0.91	1.55	71	1
1:A:63:ASP:CB	2:A:160:RCY:H1CB	0.91	1.93	63	2
1:A:64:ILE:HB	2:A:160:RCY:H1YB	0.91	1.40	47	1
2:A:176:RCY:C1U	2:A:187:RCY:C1C	0.91	2.48	87	1
1:A:65:THR:H	2:A:168:RCY:H1L	0.91	1.22	97	1
1:A:63:ASP:O	2:A:160:RCY:H1Z	0.91	1.63	78	2
1:A:65:THR:HG21	2:A:160:RCY:H1Y	0.91	1.37	55	1
2:A:168:RCY:H1ZB	2:A:173:RCY:N1V	0.91	1.80	55	1
1:A:69:PRO:HB2	2:A:173:RCY:H1YB	0.91	0.94	35	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:69:PRO:CB	2:A:173:RCY:C1Q	0.91	2.48	81	1
2:A:187:RCY:H1U	2:A:187:RCY:N1R	0.91	1.80	79	2
1:A:66:VAL:C	2:A:168:RCY:O1H	0.91	2.08	51	1
1:A:62:THR:O	2:A:160:RCY:C1C	0.91	2.19	46	1
1:A:66:VAL:HA	2:A:121:RCY:C1Y	0.91	1.96	83	1
2:A:173:RCY:H1C	2:A:176:RCY:N1R	0.91	1.73	78	1
1:A:74:ASN:HA	2:A:173:RCY:C1V	0.91	1.96	78	1
1:A:67:ILE:C	2:A:173:RCY:C1Y	0.91	2.16	100	2
2:A:168:RCY:C1U	2:A:187:RCY:H1ZA	0.91	1.96	84	1
1:A:71:GLU:CG	2:A:173:RCY:H1V	0.91	1.95	50	1
1:A:59:GLY:H	2:A:160:RCY:H1ZB	0.91	1.23	49	1
1:A:63:ASP:HB2	2:A:138:RCY:C1Z	0.91	1.96	73	1
2:A:173:RCY:H1CB	2:A:176:RCY:H1LA	0.91	1.39	36	1
1:A:64:ILE:O	1:A:66:VAL:N	0.91	2.04	73	41
1:A:71:GLU:O	2:A:173:RCY:C1L	0.91	2.18	88	2
2:A:176:RCY:C1P	2:A:187:RCY:H1MA	0.91	1.96	26	2
2:A:173:RCY:C1C	2:A:176:RCY:C1Q	0.91	2.48	34	2
1:A:64:ILE:N	2:A:138:RCY:C1V	0.91	2.17	85	1
2:A:168:RCY:H1Z	2:A:187:RCY:O1G	0.91	1.66	3	1
2:A:121:RCY:H1C	2:A:168:RCY:H1CA	0.91	1.42	27	1
1:A:65:THR:HB	2:A:160:RCY:H1YB	0.91	1.43	100	1
2:A:130:RCY:H1CA	2:A:130:RCY:C1P	0.91	1.96	86	5
1:A:64:ILE:O	2:A:168:RCY:H1LA	0.91	1.65	17	1
1:A:70:TRP:NE1	2:A:168:RCY:C1S	0.91	2.34	42	1
1:A:71:GLU:OE2	2:A:150:RCY:O1G	0.91	1.87	58	1
1:A:73:CYS:HB3	2:A:168:RCY:C1Z	0.91	1.44	99	1
1:A:70:TRP:CD2	2:A:173:RCY:C1Y	0.91	2.31	26	2
2:A:168:RCY:H1CA	2:A:176:RCY:H1Y	0.91	1.41	15	2
2:A:160:RCY:C1Z	2:A:173:RCY:H1VA	0.91	1.95	37	1
1:A:71:GLU:HB3	2:A:168:RCY:H1LA	0.91	1.35	27	2
2:A:160:RCY:O1J	2:A:168:RCY:H1VB	0.91	1.63	70	1
1:A:62:THR:CG2	2:A:160:RCY:C1P	0.91	2.49	82	1
2:A:138:RCY:C1C	2:A:160:RCY:H1LA	0.91	1.89	73	1
2:A:173:RCY:C1V	2:A:187:RCY:H1ZB	0.91	1.95	36	1
2:A:150:RCY:C1Y	2:A:187:RCY:H1CA	0.91	1.95	83	1
1:A:59:GLY:HA3	2:A:160:RCY:H1ZB	0.91	1.38	100	1
2:A:138:RCY:H1YB	2:A:150:RCY:C1U	0.91	1.92	60	1
2:A:138:RCY:C1Y	2:A:150:RCY:H1U	0.91	1.91	60	1
1:A:64:ILE:CG1	2:A:168:RCY:C1M	0.91	2.48	6	1
2:A:173:RCY:O1G	2:A:176:RCY:C1X	0.91	2.19	11	1
2:A:160:RCY:H1ZB	2:A:160:RCY:O1H	0.90	1.65	68	4

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:187:RCY:H1CA	2:A:187:RCY:C1P	0.90	1.95	4	6
2:A:168:RCY:H1Z	2:A:173:RCY:H1V	0.90	1.42	58	1
1:A:70:TRP:O	2:A:176:RCY:H1C	0.90	1.66	62	1
1:A:71:GLU:CD	2:A:130:RCY:H1ZA	0.90	1.84	94	1
1:A:64:ILE:HG13	2:A:168:RCY:N1R	0.90	1.80	69	1
2:A:160:RCY:C1V	2:A:160:RCY:O1H	0.90	2.18	98	7
2:A:138:RCY:C1W	2:A:187:RCY:H1CB	0.90	1.93	44	1
2:A:138:RCY:H1VA	2:A:176:RCY:H1CA	0.90	0.91	9	1
1:A:69:PRO:CG	2:A:173:RCY:C1Y	0.90	2.48	9	1
1:A:67:ILE:CG2	2:A:150:RCY:C1V	0.90	2.50	31	1
2:A:138:RCY:H1VB	2:A:150:RCY:H1VB	0.90	0.90	67	1
1:A:66:VAL:CB	2:A:121:RCY:C1Y	0.90	2.34	83	1
2:A:173:RCY:C1M	2:A:176:RCY:C1Q	0.90	2.37	88	2
2:A:160:RCY:C1Y	2:A:173:RCY:C1W	0.90	2.27	41	1
2:A:138:RCY:C1W	2:A:150:RCY:C1Q	0.90	2.50	60	1
2:A:173:RCY:N1R	2:A:187:RCY:C1C	0.90	2.32	99	1
2:A:150:RCY:H1M	2:A:187:RCY:H1Z	0.90	1.43	69	1
1:A:70:TRP:C	2:A:173:RCY:H1VB	0.90	1.87	6	1
1:A:63:ASP:O	2:A:150:RCY:C1V	0.90	2.19	85	1
2:A:173:RCY:H1YA	2:A:187:RCY:O1J	0.90	1.65	92	1
2:A:150:RCY:C1M	2:A:160:RCY:H1VB	0.90	1.79	42	1
2:A:138:RCY:C1Q	2:A:150:RCY:C1V	0.90	2.49	19	1
2:A:173:RCY:H1VB	2:A:176:RCY:H1V	0.90	0.91	62	2
2:A:173:RCY:H1VA	2:A:187:RCY:H1VA	0.90	0.90	48	1
1:A:62:THR:O	2:A:160:RCY:H1CA	0.90	1.67	46	1
2:A:160:RCY:O1J	2:A:168:RCY:C1W	0.90	2.18	78	2
2:A:121:RCY:C1P	2:A:121:RCY:H1CA	0.90	1.96	90	7
1:A:64:ILE:HD11	2:A:168:RCY:C1L	0.90	1.76	12	2
1:A:61:GLY:CA	2:A:160:RCY:H1LA	0.90	1.95	19	1
1:A:61:GLY:HA2	2:A:168:RCY:C1P	0.90	1.95	24	1
2:A:150:RCY:O1H	2:A:150:RCY:C1V	0.90	2.19	90	8
1:A:75:HIS:O	2:A:173:RCY:C1C	0.90	2.20	73	1
2:A:168:RCY:C1U	2:A:173:RCY:H1V	0.90	1.95	27	1
2:A:130:RCY:C1Y	2:A:160:RCY:H1VB	0.90	1.96	18	2
1:A:70:TRP:CH2	2:A:130:RCY:C1Y	0.90	2.53	88	1
1:A:78:LEU:HD22	2:A:138:RCY:H1V	0.90	1.43	40	2
2:A:176:RCY:H1CA	2:A:187:RCY:C1M	0.90	1.95	86	1
2:A:130:RCY:H1VA	2:A:187:RCY:H1VB	0.90	1.44	94	1
1:A:70:TRP:CG	2:A:187:RCY:H1ZB	0.90	2.00	76	1
1:A:73:CYS:CB	2:A:176:RCY:N1R	0.90	2.14	70	1
2:A:168:RCY:C1Y	2:A:187:RCY:H1Y	0.90	1.95	7	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:70:TRP:HB3	2:A:168:RCY:H1CB	0.90	0.92	20	1
2:A:138:RCY:H1M	2:A:150:RCY:H1C	0.90	1.43	56	2
2:A:150:RCY:C1U	2:A:160:RCY:H1VB	0.90	1.94	42	1
2:A:173:RCY:H1S	2:A:176:RCY:O1H	0.90	1.64	54	2
2:A:173:RCY:C1P	2:A:173:RCY:H1CA	0.90	1.96	86	4
2:A:173:RCY:C1Y	2:A:176:RCY:H1MA	0.90	1.95	62	1
2:A:110:RCY:H1YB	2:A:121:RCY:C1V	0.90	1.93	81	1
2:A:150:RCY:H1VA	2:A:187:RCY:C1Y	0.90	1.97	66	1
1:A:61:GLY:C	2:A:160:RCY:H1LA	0.90	1.85	19	1
1:A:61:GLY:CA	2:A:160:RCY:C1L	0.90	2.46	2	2
2:A:130:RCY:C1C	2:A:160:RCY:H1CB	0.90	1.97	8	1
1:A:75:HIS:C	2:A:173:RCY:C1C	0.90	2.39	29	1
2:A:150:RCY:O1J	2:A:187:RCY:C1C	0.90	2.19	50	1
2:A:121:RCY:H1CA	2:A:121:RCY:C1P	0.90	1.97	98	6
1:A:73:CYS:CB	2:A:176:RCY:H1C	0.90	1.66	52	1
1:A:71:GLU:OE2	2:A:110:RCY:H1CB	0.90	1.65	5	1
1:A:69:PRO:CD	2:A:160:RCY:C1C	0.90	2.50	35	1
1:A:71:GLU:OE2	2:A:168:RCY:H1CB	0.90	1.66	36	2
2:A:173:RCY:C1C	2:A:187:RCY:C1Z	0.90	2.50	93	1
1:A:73:CYS:O	2:A:173:RCY:H1S	0.90	1.67	41	2
2:A:168:RCY:C1Y	2:A:173:RCY:H1V	0.90	1.97	58	2
2:A:168:RCY:H1S	2:A:173:RCY:H1YB	0.90	0.92	94	1
1:A:71:GLU:HG3	2:A:173:RCY:H1V	0.90	1.43	50	1
2:A:187:RCY:H1ZB	2:A:187:RCY:O1H	0.90	1.67	68	3
2:A:138:RCY:H1Z	2:A:187:RCY:H1CB	0.90	0.91	44	1
2:A:168:RCY:H1VB	2:A:168:RCY:H1L	0.90	1.42	7	1
1:A:77:GLU:HG3	2:A:173:RCY:C1V	0.90	1.97	32	1
1:A:66:VAL:HG13	2:A:121:RCY:H1CB	0.90	1.44	4	1
1:A:72:ALA:CB	2:A:173:RCY:C1M	0.90	2.49	80	1
1:A:71:GLU:HB3	2:A:173:RCY:C1Q	0.90	1.97	89	1
1:A:68:CYS:CB	2:A:176:RCY:O1J	0.90	2.20	80	2
2:A:176:RCY:O1H	2:A:176:RCY:C1V	0.90	2.18	45	4
2:A:173:RCY:H1VA	2:A:176:RCY:H1S	0.90	1.41	35	1
1:A:70:TRP:CH2	2:A:176:RCY:C1Z	0.90	2.55	85	1
2:A:150:RCY:H1YA	2:A:187:RCY:C1Y	0.90	1.96	32	2
1:A:70:TRP:NE1	2:A:176:RCY:C1M	0.90	2.14	4	1
2:A:130:RCY:H1CA	2:A:160:RCY:H1CB	0.89	1.43	8	1
2:A:138:RCY:C1Z	2:A:150:RCY:C1Q	0.89	2.50	60	1
1:A:64:ILE:HD11	2:A:187:RCY:H1M	0.89	1.37	85	1
1:A:70:TRP:HE1	2:A:121:RCY:H1Y	0.89	1.04	49	1
1:A:63:ASP:O	2:A:160:RCY:H1V	0.89	1.68	3	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:173:RCY:C1S	2:A:176:RCY:C1M	0.89	2.47	67	1
2:A:173:RCY:H1U	2:A:176:RCY:C1L	0.89	1.97	38	1
1:A:70:TRP:HA	2:A:168:RCY:H1VB	0.89	1.41	22	1
2:A:187:RCY:O1H	2:A:187:RCY:H1ZB	0.89	1.66	42	4
1:A:74:ASN:OD1	2:A:173:RCY:H1C	0.89	1.67	91	1
1:A:70:TRP:NE1	2:A:176:RCY:C1V	0.89	2.35	82	1
1:A:65:THR:HG22	2:A:160:RCY:H1MA	0.89	0.91	100	1
2:A:168:RCY:C1Z	2:A:187:RCY:H1ZB	0.89	1.97	100	2
1:A:70:TRP:HE1	2:A:168:RCY:C1Q	0.89	1.80	42	2
2:A:160:RCY:O1H	2:A:160:RCY:C1Z	0.89	2.19	91	4
2:A:173:RCY:H1VA	2:A:176:RCY:H1V	0.89	1.44	69	1
1:A:70:TRP:HB2	2:A:173:RCY:C1M	0.89	1.74	6	1
2:A:150:RCY:O1J	2:A:187:RCY:C1Y	0.89	2.19	37	2
2:A:130:RCY:C1X	2:A:130:RCY:C1M	0.89	0.90	79	1
1:A:70:TRP:CH2	2:A:176:RCY:C1V	0.89	2.52	4	1
1:A:75:HIS:HA	2:A:168:RCY:H1ZB	0.89	1.43	73	1
1:A:66:VAL:CA	2:A:121:RCY:C1Y	0.89	2.50	83	1
1:A:68:CYS:N	2:A:176:RCY:N1V	0.89	1.85	22	1
2:A:173:RCY:H1C	2:A:176:RCY:H1C	0.89	0.91	8	1
1:A:64:ILE:HD13	2:A:150:RCY:C1L	0.89	1.97	75	1
1:A:60:CYS:O	2:A:130:RCY:O1H	0.89	1.91	18	1
2:A:150:RCY:C1W	2:A:187:RCY:O1J	0.89	2.08	53	1
1:A:70:TRP:CD2	2:A:168:RCY:H1VB	0.89	2.02	28	1
1:A:65:THR:N	2:A:168:RCY:O1J	0.89	2.05	30	1
2:A:168:RCY:O1H	2:A:168:RCY:C1V	0.89	2.19	42	8
2:A:187:RCY:H1CA	2:A:187:RCY:C1Q	0.89	1.96	18	2
2:A:173:RCY:H1YA	2:A:176:RCY:C1W	0.89	1.86	99	2
2:A:138:RCY:C1C	2:A:150:RCY:H1Z	0.89	1.96	59	2
2:A:168:RCY:O1G	2:A:176:RCY:O1H	0.89	1.82	76	1
1:A:74:ASN:HA	2:A:173:RCY:C1C	0.89	1.96	35	1
2:A:160:RCY:H1VA	2:A:176:RCY:H1VA	0.89	0.92	57	1
2:A:138:RCY:H1VA	2:A:187:RCY:H1ZA	0.89	0.91	11	1
1:A:70:TRP:CD1	2:A:176:RCY:H1M	0.89	2.03	4	1
2:A:173:RCY:H1Z	2:A:187:RCY:O1J	0.89	1.67	82	1
1:A:63:ASP:CG	2:A:160:RCY:C1Z	0.89	2.19	73	1
2:A:173:RCY:H1MA	2:A:176:RCY:H1YA	0.89	1.45	74	1
2:A:173:RCY:H1Z	2:A:176:RCY:H1VB	0.89	0.93	31	1
2:A:110:RCY:O1H	2:A:110:RCY:C1V	0.89	2.18	80	6
1:A:74:ASN:HB3	2:A:176:RCY:C1P	0.89	1.97	52	1
2:A:176:RCY:H1CA	2:A:176:RCY:C1P	0.89	1.96	46	5
2:A:168:RCY:C1Q	2:A:173:RCY:H1YA	0.89	1.90	84	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:138:RCY:H1MA	2:A:187:RCY:H1YB	0.89	1.00	68	1
2:A:130:RCY:H1YA	2:A:160:RCY:C1V	0.89	1.97	81	1
1:A:71:GLU:OE2	2:A:176:RCY:O1G	0.89	1.90	37	1
2:A:121:RCY:C1C	2:A:168:RCY:H1CA	0.89	1.97	27	1
2:A:138:RCY:H1YA	2:A:150:RCY:C1M	0.89	1.96	26	2
1:A:71:GLU:CG	2:A:176:RCY:C1C	0.89	2.51	44	1
1:A:69:PRO:HD2	2:A:168:RCY:C1Q	0.89	1.98	23	3
1:A:69:PRO:CG	2:A:173:RCY:H1YB	0.89	1.96	35	2
1:A:69:PRO:CD	2:A:160:RCY:H1CA	0.89	1.98	35	2
2:A:130:RCY:N1V	2:A:138:RCY:H1L	0.89	1.82	58	1
1:A:74:ASN:H	2:A:176:RCY:H1VA	0.89	1.23	62	1
2:A:168:RCY:H1CB	2:A:173:RCY:H1M	0.89	1.44	99	2
2:A:176:RCY:H1V	2:A:187:RCY:N1V	0.89	1.82	91	1
1:A:64:ILE:HB	2:A:160:RCY:C1Y	0.89	1.95	47	1
1:A:60:CYS:C	2:A:160:RCY:C1P	0.89	2.41	2	1
2:A:138:RCY:O1G	2:A:187:RCY:C1Y	0.89	2.20	63	1
2:A:150:RCY:C1M	2:A:187:RCY:H1V	0.89	1.95	89	1
1:A:59:GLY:HA3	2:A:160:RCY:C1V	0.89	1.96	83	1
1:A:70:TRP:CD2	2:A:187:RCY:H1ZB	0.89	2.02	92	1
2:A:130:RCY:O1H	2:A:130:RCY:C1V	0.89	2.21	72	7
1:A:64:ILE:HG23	2:A:168:RCY:O1H	0.89	1.66	62	2
1:A:69:PRO:CB	2:A:173:RCY:C1S	0.89	2.44	26	1
1:A:70:TRP:HE1	2:A:168:RCY:H1ZB	0.89	1.19	24	1
1:A:73:CYS:HB3	2:A:176:RCY:H1M	0.89	1.43	70	1
1:A:73:CYS:O	2:A:176:RCY:H1CB	0.89	1.66	20	1
1:A:62:THR:HB	2:A:130:RCY:H1V	0.89	1.44	9	1
2:A:168:RCY:C1Y	2:A:176:RCY:O1J	0.89	2.21	90	1
2:A:150:RCY:H1ZB	2:A:160:RCY:H1YB	0.88	1.38	88	1
2:A:168:RCY:H1ZA	2:A:187:RCY:C1W	0.88	1.91	84	1
2:A:150:RCY:H1CA	2:A:187:RCY:N1V	0.88	1.83	50	1
2:A:138:RCY:H1M	2:A:187:RCY:H1YB	0.88	0.90	68	1
1:A:71:GLU:HB2	2:A:176:RCY:C1V	0.88	1.95	49	1
1:A:70:TRP:HB3	2:A:187:RCY:C1Z	0.88	1.98	51	1
1:A:67:ILE:O	2:A:173:RCY:C1M	0.88	2.19	80	1
1:A:76:CYS:HB3	2:A:160:RCY:N1V	0.88	1.80	73	1
1:A:66:VAL:HG12	2:A:121:RCY:H1Z	0.88	0.91	89	1
2:A:176:RCY:H1VB	2:A:187:RCY:C1M	0.88	1.96	96	1
2:A:168:RCY:H1S	2:A:173:RCY:H1Y	0.88	1.44	84	1
2:A:138:RCY:H1VB	2:A:150:RCY:H1C	0.88	0.89	10	1
2:A:110:RCY:O1H	2:A:110:RCY:C1Z	0.88	2.21	5	2
2:A:150:RCY:H1Y	2:A:176:RCY:H1Y	0.88	1.44	37	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:70:TRP:O	2:A:168:RCY:H1VB	0.88	1.68	20	1
1:A:70:TRP:HB2	2:A:168:RCY:C1M	0.88	1.95	28	1
2:A:130:RCY:C1P	2:A:130:RCY:H1CA	0.88	1.98	9	6
2:A:173:RCY:C1U	2:A:176:RCY:O1J	0.88	2.21	51	2
2:A:130:RCY:H1VA	2:A:187:RCY:C1V	0.88	1.98	94	1
2:A:168:RCY:H1Z	2:A:176:RCY:C1Z	0.88	1.95	11	2
2:A:150:RCY:C1Z	2:A:187:RCY:C1W	0.88	2.39	49	2
1:A:74:ASN:H	2:A:173:RCY:H1L	0.88	1.25	52	1
1:A:75:HIS:HB2	2:A:176:RCY:H1L	0.88	1.45	13	1
1:A:60:CYS:CA	2:A:130:RCY:O1H	0.88	2.20	18	1
2:A:168:RCY:C1M	2:A:173:RCY:C1M	0.88	2.52	70	1
1:A:70:TRP:HB3	2:A:168:RCY:H1LA	0.88	0.90	46	1
2:A:150:RCY:H1YA	2:A:173:RCY:C1X	0.88	1.90	3	1
2:A:173:RCY:H1VB	2:A:187:RCY:H1Y	0.88	1.46	67	1
1:A:75:HIS:O	2:A:173:RCY:H1Z	0.88	1.68	88	1
2:A:173:RCY:H1CB	2:A:176:RCY:H1M	0.88	0.89	52	1
1:A:73:CYS:HB2	2:A:176:RCY:H1C	0.88	0.89	52	1
2:A:173:RCY:O1G	2:A:176:RCY:H1MA	0.88	1.68	41	1
2:A:173:RCY:C1P	2:A:176:RCY:H1C	0.88	1.95	64	1
2:A:121:RCY:H1ZB	2:A:121:RCY:C1Q	0.88	1.99	29	5
1:A:70:TRP:CZ2	2:A:160:RCY:H1VB	0.88	2.03	34	1
1:A:70:TRP:CB	2:A:176:RCY:C1Z	0.88	2.31	18	1
2:A:168:RCY:C1Q	2:A:168:RCY:C1S	0.88	2.51	79	1
2:A:168:RCY:O1H	2:A:168:RCY:C1C	0.88	2.18	54	2
2:A:173:RCY:H1ZB	2:A:176:RCY:C1L	0.88	1.99	20	1
2:A:168:RCY:H1U	2:A:176:RCY:C1W	0.88	1.99	98	1
1:A:64:ILE:CA	2:A:168:RCY:O1H	0.88	2.20	78	1
1:A:62:THR:O	2:A:168:RCY:C1C	0.88	2.21	61	2
2:A:173:RCY:H1YB	2:A:187:RCY:H1Z	0.88	0.90	42	1
1:A:74:ASN:ND2	2:A:121:RCY:O1J	0.88	2.06	35	1
1:A:64:ILE:HD12	2:A:187:RCY:C1Y	0.88	1.99	85	1
1:A:78:LEU:HD22	2:A:187:RCY:C1C	0.88	0.63	91	1
2:A:173:RCY:O1H	2:A:176:RCY:O1G	0.88	1.92	23	2
1:A:70:TRP:CE3	2:A:176:RCY:C1Z	0.88	2.34	4	1
1:A:75:HIS:N	2:A:176:RCY:C1C	0.88	2.36	20	1
1:A:65:THR:O	2:A:150:RCY:C1Y	0.88	2.22	31	1
1:A:78:LEU:HD11	2:A:176:RCY:H1U	0.88	1.37	56	1
1:A:69:PRO:HG3	2:A:173:RCY:H1YB	0.88	1.45	61	1
2:A:138:RCY:O1J	2:A:187:RCY:C1Y	0.88	2.21	88	3
2:A:130:RCY:H1C	2:A:160:RCY:H1CA	0.88	1.44	64	1
2:A:150:RCY:N1V	2:A:187:RCY:H1CB	0.88	1.78	50	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:67:ILE:CG2	2:A:173:RCY:H1MA	0.88	1.77	80	1
2:A:138:RCY:C1L	2:A:138:RCY:C1V	0.88	2.51	74	1
1:A:71:GLU:HG2	2:A:168:RCY:H1LA	0.88	1.44	74	1
2:A:138:RCY:O1J	2:A:160:RCY:C1V	0.88	2.20	92	1
2:A:110:RCY:C1P	2:A:110:RCY:H1CA	0.88	1.98	77	5
2:A:138:RCY:H1CA	2:A:138:RCY:C1P	0.88	1.97	17	5
2:A:173:RCY:C1Q	2:A:173:RCY:H1CA	0.88	1.99	63	6
1:A:70:TRP:O	2:A:173:RCY:C1M	0.88	2.21	11	2
2:A:168:RCY:H1CA	2:A:168:RCY:C1Q	0.88	1.99	98	5
1:A:70:TRP:HZ2	2:A:168:RCY:O1J	0.88	1.52	24	1
1:A:67:ILE:HD11	2:A:173:RCY:O1H	0.88	1.68	16	1
1:A:70:TRP:HB2	2:A:173:RCY:H1YB	0.88	1.46	85	2
2:A:173:RCY:H1ZA	2:A:176:RCY:O1J	0.88	1.66	71	1
2:A:176:RCY:C1Y	2:A:187:RCY:H1C	0.88	1.98	27	1
2:A:168:RCY:H1ZA	2:A:187:RCY:H1Y	0.88	1.43	97	1
1:A:70:TRP:CE2	2:A:187:RCY:H1ZA	0.88	2.02	92	1
2:A:187:RCY:C1Q	2:A:187:RCY:H1CA	0.88	1.98	100	6
2:A:138:RCY:C1U	2:A:150:RCY:H1V	0.88	1.94	19	2
2:A:138:RCY:H1YA	2:A:150:RCY:C1X	0.88	1.98	97	1
1:A:72:ALA:CB	2:A:173:RCY:H1S	0.88	1.95	78	2
1:A:70:TRP:O	2:A:173:RCY:H1C	0.88	1.68	38	1
2:A:130:RCY:O1J	2:A:138:RCY:O1G	0.88	1.90	58	1
1:A:64:ILE:HD12	2:A:168:RCY:O1H	0.88	1.68	58	2
1:A:75:HIS:ND1	2:A:176:RCY:H1CB	0.88	1.80	84	1
2:A:138:RCY:H1Y	2:A:176:RCY:C1P	0.88	1.98	48	1
2:A:173:RCY:H1LA	2:A:176:RCY:H1V	0.88	1.45	7	1
1:A:69:PRO:CG	2:A:187:RCY:H1ZA	0.88	1.99	54	1
1:A:64:ILE:HG21	2:A:160:RCY:H1MA	0.88	0.90	47	2
1:A:63:ASP:CB	2:A:150:RCY:H1Z	0.88	1.98	80	1
2:A:150:RCY:H1YA	2:A:173:RCY:C1U	0.88	1.97	3	1
1:A:74:ASN:N	2:A:173:RCY:H1L	0.87	1.84	52	2
1:A:67:ILE:CD1	2:A:160:RCY:H1VA	0.87	1.99	86	1
2:A:160:RCY:C1Q	2:A:160:RCY:C1C	0.87	2.38	7	2
2:A:173:RCY:O1H	2:A:187:RCY:C1C	0.87	2.17	7	1
2:A:168:RCY:H1YB	2:A:187:RCY:H1VA	0.87	1.44	82	1
2:A:160:RCY:H1ZA	2:A:168:RCY:C1L	0.87	1.79	73	1
1:A:69:PRO:HB3	2:A:176:RCY:H1ZB	0.87	1.42	66	1
2:A:121:RCY:C1V	2:A:121:RCY:O1H	0.87	2.22	27	6
1:A:75:HIS:NE2	2:A:173:RCY:H1ZB	0.87	1.84	42	1
2:A:160:RCY:H1Z	2:A:168:RCY:H1V	0.87	1.45	58	3
2:A:150:RCY:C1Y	2:A:160:RCY:H1ZA	0.87	1.97	29	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:65:THR:OG1	2:A:168:RCY:C1Q	0.87	2.15	60	1
1:A:71:GLU:OE1	2:A:110:RCY:O1G	0.87	1.91	5	1
2:A:176:RCY:C1U	2:A:187:RCY:H1VB	0.87	1.98	77	2
1:A:60:CYS:C	2:A:130:RCY:C1M	0.87	2.42	18	1
2:A:173:RCY:O1G	2:A:176:RCY:H1VA	0.87	1.66	11	1
1:A:69:PRO:HG3	2:A:187:RCY:H1Z	0.87	1.46	54	1
1:A:67:ILE:HB	2:A:173:RCY:H1YA	0.87	1.44	80	1
2:A:138:RCY:H1V	2:A:150:RCY:H1M	0.87	0.91	1	1
2:A:176:RCY:C1Q	2:A:176:RCY:H1CA	0.87	1.98	51	4
2:A:110:RCY:H1ZB	2:A:110:RCY:C1Q	0.87	1.99	37	4
1:A:60:CYS:HB3	2:A:130:RCY:C1Q	0.87	2.00	18	1
1:A:71:GLU:HG2	2:A:176:RCY:O1G	0.87	1.69	44	1
1:A:59:GLY:C	2:A:160:RCY:C1P	0.87	2.42	70	1
2:A:130:RCY:C1Y	2:A:160:RCY:C1V	0.87	2.52	81	4
2:A:130:RCY:H1YA	2:A:160:RCY:O1H	0.87	1.68	88	1
2:A:168:RCY:C1L	2:A:173:RCY:H1ZB	0.87	1.99	10	1
1:A:69:PRO:HB3	2:A:176:RCY:H1Y	0.87	1.42	72	1
2:A:138:RCY:H1Z	2:A:187:RCY:O1H	0.87	1.67	59	1
2:A:168:RCY:H1YA	2:A:176:RCY:N1V	0.87	1.83	90	1
2:A:173:RCY:H1MA	2:A:176:RCY:C1M	0.87	1.65	89	1
1:A:70:TRP:CD1	2:A:168:RCY:H1S	0.87	2.04	42	1
2:A:173:RCY:C1C	2:A:176:RCY:C1Z	0.87	2.52	27	3
2:A:187:RCY:C1V	2:A:187:RCY:O1H	0.87	2.21	36	5
1:A:76:CYS:CB	2:A:187:RCY:H1CB	0.87	1.94	34	1
1:A:64:ILE:HD12	2:A:187:RCY:H1YA	0.87	1.46	85	1
1:A:70:TRP:HZ2	2:A:176:RCY:H1V	0.87	1.06	4	1
2:A:160:RCY:H1C	2:A:168:RCY:C1Q	0.87	1.99	39	1
2:A:168:RCY:H1VB	2:A:176:RCY:C1M	0.87	2.00	20	1
1:A:67:ILE:O	2:A:150:RCY:H1YA	0.87	1.69	31	1
1:A:71:GLU:OE1	2:A:176:RCY:H1VA	0.87	1.67	92	1
2:A:187:RCY:O1H	2:A:187:RCY:C1C	0.87	2.22	70	3
2:A:168:RCY:C1M	2:A:173:RCY:H1ZB	0.87	1.97	84	1
1:A:70:TRP:CZ3	2:A:168:RCY:N1R	0.87	2.36	50	1
1:A:64:ILE:CD1	2:A:168:RCY:C1Z	0.87	2.49	6	1
1:A:70:TRP:CA	2:A:176:RCY:C1Z	0.87	2.51	18	1
1:A:60:CYS:H	2:A:160:RCY:H1LA	0.87	1.13	70	1
2:A:168:RCY:C1U	2:A:187:RCY:H1Z	0.87	1.99	31	1
1:A:71:GLU:C	2:A:173:RCY:H1M	0.87	1.85	78	1
2:A:150:RCY:H1V	2:A:187:RCY:C1V	0.87	2.00	38	1
1:A:70:TRP:HZ3	2:A:168:RCY:C1Y	0.87	1.81	41	2
2:A:160:RCY:C1W	2:A:168:RCY:H1VB	0.87	1.99	55	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:173:RCY:H1YB	2:A:176:RCY:H1CB	0.87	1.46	86	1
2:A:168:RCY:H1ZB	2:A:168:RCY:O1G	0.87	1.69	60	2
2:A:168:RCY:C1Q	2:A:168:RCY:H1CA	0.87	1.99	89	2
1:A:70:TRP:CD1	2:A:176:RCY:H1MA	0.87	2.03	4	1
1:A:62:THR:CG2	2:A:160:RCY:C1W	0.87	2.42	46	1
1:A:66:VAL:HG23	1:A:67:ILE:H	0.87	1.30	83	3
2:A:168:RCY:C1U	2:A:173:RCY:H1M	0.87	1.98	27	1
1:A:71:GLU:CD	2:A:168:RCY:C1X	0.87	2.43	93	1
1:A:64:ILE:HG13	2:A:168:RCY:O1H	0.87	1.68	6	3
2:A:173:RCY:C1X	2:A:176:RCY:C1Q	0.87	2.53	38	1
2:A:130:RCY:C1V	2:A:130:RCY:O1H	0.87	2.22	70	6
1:A:71:GLU:HB2	2:A:168:RCY:H1U	0.87	1.46	37	1
1:A:66:VAL:CG2	2:A:168:RCY:H1V	0.87	1.98	80	1
1:A:71:GLU:CG	2:A:168:RCY:C1X	0.87	2.52	93	1
2:A:150:RCY:H1YA	2:A:187:RCY:H1V	0.87	1.44	38	1
2:A:173:RCY:H1YA	2:A:187:RCY:C1Y	0.87	1.91	31	2
2:A:160:RCY:C1P	2:A:168:RCY:C1M	0.87	2.32	26	2
2:A:138:RCY:C1Z	2:A:138:RCY:O1G	0.87	2.23	62	2
1:A:70:TRP:CE2	2:A:168:RCY:H1ZB	0.87	1.93	24	1
2:A:138:RCY:N1R	2:A:187:RCY:C1C	0.87	2.35	5	1
2:A:110:RCY:H1YB	2:A:121:RCY:H1C	0.87	1.03	81	1
2:A:173:RCY:O1H	2:A:176:RCY:C1P	0.87	2.23	23	1
1:A:68:CYS:C	2:A:168:RCY:H1S	0.87	1.90	83	1
2:A:168:RCY:H1ZB	2:A:187:RCY:C1P	0.86	2.00	100	1
2:A:160:RCY:H1YB	2:A:168:RCY:C1Z	0.86	1.99	9	2
1:A:71:GLU:CD	2:A:130:RCY:C1Z	0.86	2.43	94	1
2:A:138:RCY:O1G	2:A:150:RCY:C1C	0.86	2.22	9	2
1:A:70:TRP:CE3	2:A:187:RCY:C1Z	0.86	2.44	76	1
1:A:69:PRO:CD	2:A:173:RCY:C1Z	0.86	2.24	61	1
2:A:173:RCY:C1P	2:A:176:RCY:C1Y	0.86	2.48	97	2
2:A:160:RCY:C1C	2:A:168:RCY:O1G	0.86	2.22	19	2
1:A:72:ALA:N	2:A:173:RCY:C1Z	0.86	2.35	50	1
2:A:173:RCY:H1C	2:A:176:RCY:H1S	0.86	1.45	72	1
2:A:168:RCY:H1S	2:A:173:RCY:C1M	0.86	1.63	18	1
1:A:69:PRO:CD	2:A:168:RCY:H1V	0.86	1.99	63	1
2:A:176:RCY:H1C	2:A:187:RCY:O1J	0.86	1.70	31	1
2:A:168:RCY:H1V	2:A:187:RCY:C1Z	0.86	1.99	31	1
2:A:160:RCY:H1ZA	2:A:168:RCY:C1X	0.86	1.98	69	3
2:A:130:RCY:N1V	2:A:160:RCY:O1J	0.86	2.08	64	1
1:A:71:GLU:OE1	2:A:176:RCY:H1ZA	0.86	1.69	84	1
2:A:138:RCY:C1L	2:A:150:RCY:H1C	0.86	1.99	94	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:150:RCY:C1Y	2:A:160:RCY:C1W	0.86	2.54	29	1
2:A:110:RCY:O1H	2:A:110:RCY:H1CA	0.86	1.69	32	2
1:A:70:TRP:CD1	2:A:187:RCY:H1ZB	0.86	2.05	76	2
2:A:173:RCY:H1YB	2:A:187:RCY:H1L	0.86	1.45	45	1
2:A:138:RCY:H1CB	2:A:160:RCY:H1YA	0.86	1.47	27	1
2:A:138:RCY:H1VB	2:A:150:RCY:C1W	0.86	1.99	1	1
2:A:150:RCY:C1Y	2:A:187:RCY:H1U	0.86	1.99	78	1
2:A:138:RCY:C1V	2:A:138:RCY:O1H	0.86	2.21	94	2
1:A:67:ILE:C	2:A:173:RCY:C1Z	0.86	2.43	63	1
2:A:168:RCY:H1ZA	2:A:173:RCY:H1ZA	0.86	0.93	31	1
1:A:74:ASN:HA	2:A:176:RCY:C1U	0.86	2.01	67	1
1:A:70:TRP:HD1	2:A:173:RCY:H1C	0.86	0.77	38	1
1:A:72:ALA:CB	2:A:173:RCY:O1H	0.86	2.22	13	1
1:A:71:GLU:CA	2:A:176:RCY:C1V	0.86	2.52	49	3
1:A:69:PRO:HG2	2:A:187:RCY:H1ZA	0.86	1.46	54	1
1:A:68:CYS:C	2:A:168:RCY:H1VB	0.86	1.91	63	1
2:A:150:RCY:C1M	2:A:168:RCY:H1Y	0.86	1.86	74	1
2:A:168:RCY:H1ZA	2:A:176:RCY:C1Z	0.86	1.97	11	2
2:A:173:RCY:H1C	2:A:176:RCY:C1S	0.86	1.98	72	1
1:A:71:GLU:HA	2:A:168:RCY:C1Z	0.86	2.00	37	1
1:A:77:GLU:HB2	2:A:173:RCY:C1C	0.86	1.98	51	1
2:A:176:RCY:C1U	2:A:187:RCY:C1U	0.86	2.53	96	1
1:A:69:PRO:CD	2:A:173:RCY:H1VB	0.86	1.99	30	2
2:A:130:RCY:C1C	2:A:160:RCY:C1S	0.86	2.46	66	1
1:A:68:CYS:CB	2:A:160:RCY:C1W	0.86	2.54	19	1
2:A:173:RCY:C1V	2:A:187:RCY:C1X	0.86	2.31	55	1
2:A:173:RCY:H1Y	2:A:187:RCY:O1G	0.86	1.69	44	1
2:A:173:RCY:O1H	2:A:176:RCY:C1Q	0.86	2.23	70	1
1:A:63:ASP:CG	2:A:150:RCY:H1Z	0.86	1.89	80	1
1:A:65:THR:HA	2:A:168:RCY:H1LA	0.86	1.45	82	1
1:A:70:TRP:CB	2:A:168:RCY:H1M	0.86	2.00	28	1
2:A:168:RCY:C1Z	2:A:187:RCY:C1Y	0.86	2.54	97	1
1:A:71:GLU:O	2:A:173:RCY:H1L	0.86	1.69	88	1
1:A:70:TRP:H	2:A:173:RCY:H1ZA	0.86	0.71	5	1
1:A:69:PRO:HG3	2:A:168:RCY:C1Y	0.86	1.98	66	1
2:A:150:RCY:H1Z	2:A:160:RCY:H1YB	0.86	0.96	88	1
1:A:76:CYS:HB3	2:A:173:RCY:C1P	0.86	1.98	38	1
2:A:173:RCY:C1S	2:A:176:RCY:C1V	0.86	2.53	76	1
1:A:68:CYS:HA	2:A:173:RCY:O1J	0.86	1.69	59	2
2:A:138:RCY:C1Z	2:A:187:RCY:C1V	0.86	2.48	85	1
1:A:63:ASP:O	2:A:150:RCY:H1VB	0.86	1.70	85	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:64:ILE:CG1	2:A:160:RCY:C1C	0.86	2.37	48	1
1:A:66:VAL:HG13	2:A:121:RCY:C1C	0.86	2.01	4	1
2:A:160:RCY:H1Z	2:A:168:RCY:N1R	0.86	1.84	3	1
2:A:176:RCY:C1V	2:A:176:RCY:O1H	0.86	2.21	17	4
2:A:160:RCY:H1YB	2:A:168:RCY:H1L	0.86	1.48	1	2
2:A:138:RCY:H1CB	2:A:150:RCY:C1V	0.86	2.01	54	2
2:A:160:RCY:C1Z	2:A:168:RCY:H1M	0.86	2.00	34	1
2:A:110:RCY:C1X	2:A:121:RCY:C1Y	0.86	2.53	5	1
2:A:138:RCY:C1Z	2:A:187:RCY:C1P	0.86	2.44	71	1
1:A:59:GLY:O	2:A:160:RCY:H1S	0.86	1.69	90	2
2:A:150:RCY:C1Z	2:A:187:RCY:H1LA	0.86	2.01	36	1
2:A:160:RCY:O1H	2:A:160:RCY:C1V	0.85	2.22	54	7
2:A:173:RCY:O1G	2:A:176:RCY:C1M	0.85	2.22	41	1
2:A:168:RCY:C1M	2:A:176:RCY:H1VA	0.85	2.00	40	1
1:A:69:PRO:HG3	2:A:187:RCY:H1YA	0.85	1.43	72	1
2:A:160:RCY:C1V	2:A:176:RCY:C1V	0.85	2.50	57	1
2:A:160:RCY:H1ZA	2:A:173:RCY:H1ZA	0.85	1.46	4	1
1:A:76:CYS:CB	2:A:160:RCY:H1YA	0.85	2.00	73	1
2:A:173:RCY:H1C	2:A:176:RCY:H1L	0.85	1.45	36	1
1:A:60:CYS:CB	2:A:160:RCY:H1SA	0.85	2.01	25	1
2:A:150:RCY:C1X	2:A:173:RCY:H1VA	0.85	2.00	31	1
1:A:66:VAL:HG13	2:A:121:RCY:C1V	0.85	2.01	83	1
1:A:72:ALA:HB3	2:A:168:RCY:H1ZB	0.85	1.46	22	1
2:A:173:RCY:H1MA	2:A:176:RCY:H1VA	0.85	1.45	31	2
2:A:160:RCY:C1V	2:A:168:RCY:C1L	0.85	2.54	24	1
2:A:138:RCY:O1H	2:A:160:RCY:C1C	0.85	2.24	69	1
2:A:138:RCY:O1J	2:A:150:RCY:C1Z	0.85	2.20	35	1
2:A:168:RCY:H1YA	2:A:176:RCY:H1V	0.85	0.87	94	1
2:A:168:RCY:H1VA	2:A:173:RCY:H1ZA	0.85	1.48	29	1
2:A:160:RCY:H1ZB	2:A:168:RCY:O1G	0.85	1.68	34	1
2:A:130:RCY:O1H	2:A:130:RCY:C1C	0.85	2.25	37	1
2:A:138:RCY:H1Y	2:A:168:RCY:C1Y	0.85	2.01	7	1
1:A:65:THR:HG22	2:A:160:RCY:H1M	0.85	1.47	36	1
2:A:160:RCY:H1YA	2:A:187:RCY:H1YB	0.85	1.48	27	1
2:A:138:RCY:C1P	2:A:150:RCY:O1J	0.85	2.24	81	2
1:A:65:THR:O	2:A:176:RCY:C1Y	0.85	2.25	22	1
2:A:173:RCY:O1H	2:A:173:RCY:C1V	0.85	2.25	41	3
1:A:73:CYS:HB3	2:A:176:RCY:C1Z	0.85	2.01	58	1
2:A:150:RCY:C1Y	2:A:160:RCY:C1Y	0.85	2.54	29	1
1:A:66:VAL:N	2:A:150:RCY:C1Y	0.85	2.39	72	1
2:A:138:RCY:H1Y	2:A:187:RCY:H1CA	0.85	1.31	96	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:73:CYS:N	2:A:168:RCY:O1G	0.85	2.10	91	1
1:A:71:GLU:HG3	2:A:168:RCY:C1S	0.85	2.00	28	1
2:A:168:RCY:H1VA	2:A:173:RCY:C1Z	0.85	2.00	29	1
2:A:138:RCY:H1ZA	2:A:150:RCY:O1H	0.85	1.71	60	1
1:A:60:CYS:CB	2:A:130:RCY:C1Q	0.85	2.54	18	1
2:A:176:RCY:O1J	2:A:176:RCY:O1H	0.85	1.94	57	1
1:A:70:TRP:CE2	2:A:176:RCY:C1V	0.85	2.58	82	1
1:A:70:TRP:HZ3	2:A:168:RCY:H1VA	0.85	1.32	56	1
2:A:130:RCY:H1CA	2:A:138:RCY:H1ZB	0.85	1.45	67	1
1:A:67:ILE:HD13	2:A:130:RCY:H1YB	0.85	1.47	78	1
2:A:121:RCY:H1ZA	2:A:168:RCY:C1L	0.85	2.02	94	1
1:A:71:GLU:O	2:A:173:RCY:C1Q	0.85	2.23	29	3
2:A:138:RCY:H1ZB	2:A:187:RCY:H1ZB	0.85	1.44	59	1
1:A:59:GLY:O	2:A:160:RCY:C1M	0.85	2.25	85	1
2:A:168:RCY:H1MA	2:A:173:RCY:H1M	0.85	1.45	70	1
2:A:138:RCY:C1V	2:A:187:RCY:C1Y	0.85	2.53	66	2
1:A:68:CYS:CA	2:A:173:RCY:H1MA	0.85	2.02	73	1
2:A:160:RCY:O1H	2:A:168:RCY:C1M	0.85	2.25	39	1
2:A:168:RCY:H1Y	2:A:187:RCY:N1V	0.85	1.86	97	1
2:A:168:RCY:H1ZB	2:A:187:RCY:N1R	0.85	1.85	100	1
2:A:168:RCY:H1VA	2:A:173:RCY:O1H	0.85	1.72	76	1
1:A:70:TRP:CB	2:A:176:RCY:O1J	0.85	2.24	76	1
2:A:150:RCY:H1L	2:A:160:RCY:H1M	0.85	1.48	85	1
1:A:70:TRP:HA	2:A:168:RCY:H1CA	0.85	0.86	57	1
2:A:160:RCY:H1M	2:A:176:RCY:C1Y	0.85	1.92	71	1
1:A:70:TRP:CD1	2:A:121:RCY:C1W	0.85	2.44	49	1
1:A:76:CYS:HB2	2:A:173:RCY:O1J	0.85	1.71	42	1
2:A:173:RCY:H1MA	2:A:176:RCY:H1C	0.85	1.48	19	1
1:A:71:GLU:HB2	2:A:168:RCY:C1L	0.85	1.99	32	4
2:A:173:RCY:C1C	2:A:176:RCY:H1C	0.85	1.85	8	1
2:A:160:RCY:H1U	2:A:168:RCY:H1YA	0.85	1.46	41	1
1:A:70:TRP:CE3	2:A:150:RCY:O1G	0.85	2.30	75	1
2:A:168:RCY:H1MA	2:A:173:RCY:C1S	0.85	1.99	58	1
2:A:150:RCY:C1Q	2:A:150:RCY:H1ZB	0.85	2.00	96	5
1:A:64:ILE:HD11	2:A:187:RCY:C1P	0.85	2.01	85	1
1:A:70:TRP:HE1	2:A:168:RCY:C1L	0.85	1.84	89	1
1:A:67:ILE:HG21	2:A:130:RCY:H1YB	0.85	1.45	78	1
2:A:168:RCY:H1M	2:A:173:RCY:H1YA	0.85	1.48	14	1
2:A:130:RCY:H1YB	2:A:176:RCY:C1Z	0.85	2.01	41	1
1:A:71:GLU:O	2:A:173:RCY:N1R	0.85	2.09	94	1
2:A:173:RCY:C1Q	2:A:176:RCY:O1H	0.85	2.25	60	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:72:ALA:CB	2:A:173:RCY:C1L	0.85	2.23	10	1
2:A:176:RCY:H1V	2:A:187:RCY:C1Z	0.85	2.01	34	1
1:A:63:ASP:HB3	2:A:168:RCY:C1X	0.85	2.02	5	1
2:A:150:RCY:C1C	2:A:187:RCY:C1Y	0.85	2.52	81	2
1:A:71:GLU:CG	2:A:168:RCY:H1LA	0.85	2.02	74	2
1:A:65:THR:HG21	2:A:160:RCY:O1H	0.85	1.71	36	1
2:A:160:RCY:H1CA	2:A:168:RCY:C1P	0.85	2.01	39	1
2:A:176:RCY:H1VB	2:A:187:RCY:C1P	0.85	2.01	15	1
2:A:168:RCY:H1YB	2:A:187:RCY:C1L	0.85	2.01	100	1
2:A:168:RCY:C1W	2:A:187:RCY:C1P	0.85	2.53	100	1
2:A:173:RCY:C1Q	2:A:173:RCY:H1ZB	0.85	2.02	21	4
2:A:138:RCY:C1L	2:A:150:RCY:C1C	0.85	2.55	9	2
1:A:70:TRP:CZ2	2:A:160:RCY:C1V	0.85	2.60	34	1
2:A:168:RCY:C1U	2:A:173:RCY:H1U	0.85	2.02	48	2
2:A:173:RCY:H1ZB	2:A:176:RCY:H1V	0.85	1.48	37	1
2:A:176:RCY:C1W	2:A:187:RCY:H1VA	0.85	1.93	27	2
1:A:73:CYS:CB	2:A:176:RCY:C1M	0.85	2.55	70	1
2:A:138:RCY:H1C	2:A:150:RCY:C1P	0.85	2.01	53	1
2:A:138:RCY:H1Z	2:A:187:RCY:H1CA	0.85	0.86	74	1
2:A:173:RCY:C1M	2:A:176:RCY:C1U	0.85	2.37	89	1
1:A:66:VAL:HB	2:A:150:RCY:C1M	0.85	2.02	31	1
1:A:70:TRP:CH2	2:A:160:RCY:O1H	0.84	2.29	58	2
1:A:70:TRP:CB	2:A:173:RCY:H1M	0.84	2.01	84	1
1:A:71:GLU:OE2	2:A:130:RCY:C1M	0.84	2.25	94	1
2:A:160:RCY:H1M	2:A:168:RCY:H1S	0.84	1.46	34	1
2:A:130:RCY:C1C	2:A:160:RCY:O1J	0.84	2.18	16	1
2:A:138:RCY:C1P	2:A:150:RCY:C1Y	0.84	2.52	23	1
2:A:168:RCY:C1S	2:A:173:RCY:H1V	0.84	2.01	4	1
2:A:173:RCY:H1S	2:A:176:RCY:H1L	0.84	1.48	3	1
2:A:130:RCY:C1Q	2:A:130:RCY:H1ZB	0.84	2.01	66	1
2:A:150:RCY:H1Z	2:A:160:RCY:H1YA	0.84	1.43	88	1
1:A:64:ILE:CG1	2:A:160:RCY:H1YA	0.84	1.94	19	1
2:A:160:RCY:H1CA	2:A:160:RCY:C1P	0.84	2.01	29	5
1:A:75:HIS:CG	2:A:176:RCY:H1CA	0.84	2.06	84	1
2:A:138:RCY:H1CB	2:A:150:RCY:H1ZA	0.84	1.48	29	1
1:A:73:CYS:CB	2:A:168:RCY:C1Z	0.84	0.85	99	1
1:A:78:LEU:HD11	2:A:176:RCY:C1S	0.84	2.01	69	1
2:A:173:RCY:H1VA	2:A:176:RCY:H1L	0.84	1.42	35	1
2:A:130:RCY:C1V	2:A:160:RCY:H1M	0.84	2.01	18	1
1:A:70:TRP:CD2	2:A:121:RCY:C1V	0.84	2.58	49	1
2:A:173:RCY:N1R	2:A:176:RCY:H1VA	0.84	1.86	11	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:150:RCY:H1C	2:A:187:RCY:C1Y	0.84	1.97	53	1
1:A:77:GLU:HG3	2:A:176:RCY:H1U	0.84	1.50	39	1
2:A:150:RCY:C1Q	2:A:150:RCY:H1CA	0.84	2.01	14	4
2:A:176:RCY:H1Y	2:A:187:RCY:O1H	0.84	1.72	76	1
2:A:138:RCY:H1L	2:A:160:RCY:H1ZA	0.84	1.46	18	1
1:A:70:TRP:HH2	2:A:160:RCY:H1VB	0.84	1.20	37	1
2:A:110:RCY:H1Z	2:A:121:RCY:H1C	0.84	1.49	33	1
2:A:160:RCY:C1Y	2:A:168:RCY:C1C	0.84	2.22	47	3
1:A:61:GLY:O	2:A:160:RCY:H1CB	0.84	1.72	11	1
2:A:173:RCY:H1U	2:A:176:RCY:O1J	0.84	1.71	51	1
1:A:59:GLY:HA3	2:A:160:RCY:C1Z	0.84	2.02	100	1
2:A:160:RCY:C1M	2:A:168:RCY:C1C	0.84	2.46	5	1
1:A:70:TRP:CE3	2:A:168:RCY:C1Q	0.84	2.61	33	1
2:A:160:RCY:H1CB	2:A:168:RCY:O1G	0.84	1.73	96	1
2:A:160:RCY:H1MA	2:A:168:RCY:H1ZA	0.84	0.85	96	1
2:A:173:RCY:O1G	2:A:176:RCY:C1Q	0.84	2.23	96	1
2:A:138:RCY:C1S	2:A:160:RCY:C1U	0.84	2.21	27	1
1:A:70:TRP:CZ3	2:A:150:RCY:O1J	0.84	2.30	93	1
1:A:70:TRP:O	2:A:168:RCY:H1LA	0.84	1.71	52	1
1:A:71:GLU:HB2	2:A:168:RCY:H1L	0.84	0.84	57	2
2:A:160:RCY:H1U	2:A:168:RCY:C1Y	0.84	2.01	41	1
2:A:173:RCY:C1V	2:A:176:RCY:C1L	0.84	2.51	35	1
2:A:130:RCY:C1V	2:A:130:RCY:C1M	0.84	2.55	79	1
2:A:168:RCY:C1C	2:A:168:RCY:O1H	0.84	2.24	98	1
2:A:168:RCY:C1S	2:A:173:RCY:H1Y	0.84	2.03	84	1
1:A:70:TRP:CA	2:A:176:RCY:H1C	0.84	2.01	13	1
1:A:71:GLU:CD	2:A:110:RCY:H1CB	0.84	1.91	5	1
1:A:70:TRP:CZ3	2:A:176:RCY:H1ZB	0.84	2.07	85	1
1:A:69:PRO:HG2	2:A:173:RCY:H1Y	0.84	1.49	9	1
2:A:173:RCY:C1Q	2:A:187:RCY:O1J	0.84	2.26	54	1
2:A:168:RCY:H1LA	2:A:173:RCY:H1VA	0.84	1.45	80	1
2:A:150:RCY:H1U	2:A:176:RCY:O1G	0.84	1.73	82	1
1:A:75:HIS:CD2	2:A:168:RCY:H1Z	0.84	2.07	73	1
2:A:168:RCY:O1J	2:A:187:RCY:H1ZB	0.84	1.73	17	1
2:A:168:RCY:C1Z	2:A:176:RCY:H1ZB	0.84	2.01	60	1
1:A:59:GLY:N	2:A:160:RCY:C1Z	0.84	2.40	49	1
2:A:173:RCY:O1G	2:A:187:RCY:N1V	0.84	2.11	89	1
1:A:68:CYS:SG	2:A:160:RCY:C1V	0.84	2.62	3	1
1:A:70:TRP:N	2:A:168:RCY:C1L	0.84	2.24	28	1
2:A:168:RCY:C1Y	2:A:176:RCY:C1Z	0.84	2.55	66	1
1:A:69:PRO:HA	2:A:173:RCY:C1C	0.84	2.03	66	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:70:TRP:HB3	2:A:121:RCY:H1V	0.84	0.84	30	1
1:A:60:CYS:H	2:A:160:RCY:H1VB	0.84	0.67	83	1
1:A:69:PRO:HD3	2:A:173:RCY:H1Z	0.84	1.48	31	2
2:A:110:RCY:C1V	2:A:110:RCY:O1H	0.84	2.22	9	2
2:A:176:RCY:O1H	2:A:176:RCY:C1C	0.84	2.17	51	3
1:A:64:ILE:HG23	1:A:65:THR:N	0.84	1.88	49	9
1:A:67:ILE:CG1	2:A:160:RCY:H1VA	0.84	2.02	86	1
1:A:70:TRP:CB	2:A:173:RCY:C1Z	0.84	2.41	94	1
1:A:60:CYS:HA	2:A:160:RCY:C1Q	0.84	2.00	83	3
2:A:138:RCY:C1V	2:A:150:RCY:H1CA	0.84	2.02	70	2
1:A:70:TRP:NE1	2:A:160:RCY:H1VB	0.84	1.87	34	1
2:A:173:RCY:H1ZA	2:A:176:RCY:H1M	0.84	0.90	37	1
2:A:138:RCY:C1C	2:A:187:RCY:O1G	0.84	2.24	11	1
1:A:72:ALA:C	2:A:173:RCY:H1L	0.84	1.93	83	1
2:A:173:RCY:H1ZB	2:A:173:RCY:C1Q	0.84	2.03	2	4
2:A:173:RCY:H1CA	2:A:176:RCY:H1M	0.84	1.48	52	1
2:A:138:RCY:H1C	2:A:150:RCY:C1X	0.84	2.01	54	2
2:A:173:RCY:O1G	2:A:187:RCY:H1V	0.84	1.72	16	1
1:A:70:TRP:CA	2:A:176:RCY:H1ZA	0.84	2.01	18	1
2:A:168:RCY:C1Y	2:A:173:RCY:C1C	0.84	2.55	91	1
1:A:72:ALA:O	2:A:110:RCY:H1Z	0.84	1.72	70	1
2:A:160:RCY:H1VA	2:A:168:RCY:H1Y	0.84	0.85	32	1
2:A:150:RCY:H1ZA	2:A:187:RCY:H1LA	0.84	1.49	36	1
2:A:173:RCY:H1VA	2:A:187:RCY:H1U	0.84	1.49	93	1
2:A:176:RCY:C1U	2:A:187:RCY:C1M	0.84	2.51	26	2
2:A:168:RCY:H1LA	2:A:176:RCY:O1J	0.84	1.71	13	1
1:A:70:TRP:CD1	2:A:187:RCY:C1W	0.84	2.50	16	1
2:A:173:RCY:C1L	2:A:176:RCY:C1P	0.84	2.32	71	2
1:A:64:ILE:HD12	2:A:160:RCY:C1Y	0.84	1.99	49	2
2:A:130:RCY:H1U	2:A:160:RCY:C1W	0.84	2.03	7	1
1:A:60:CYS:CB	2:A:168:RCY:H1CB	0.84	2.03	95	1
2:A:150:RCY:H1ZA	2:A:160:RCY:H1Y	0.83	1.50	88	1
1:A:67:ILE:CG1	2:A:176:RCY:H1MA	0.83	2.00	22	1
2:A:150:RCY:H1CB	2:A:168:RCY:O1J	0.83	1.73	19	1
2:A:176:RCY:C1V	2:A:176:RCY:O1G	0.83	2.22	81	3
2:A:121:RCY:H1CB	2:A:121:RCY:O1H	0.83	1.63	13	3
2:A:168:RCY:N1R	2:A:176:RCY:H1Y	0.83	1.74	59	1
1:A:63:ASP:OD2	2:A:121:RCY:H1VA	0.83	1.73	42	1
1:A:68:CYS:SG	2:A:160:RCY:C1Z	0.83	2.60	19	1
2:A:130:RCY:H1VA	2:A:160:RCY:O1H	0.83	1.73	8	1
1:A:70:TRP:C	2:A:173:RCY:H1ZA	0.83	1.92	94	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:70:TRP:CB	2:A:173:RCY:H1V	0.83	1.95	26	2
1:A:60:CYS:CA	2:A:138:RCY:H1VB	0.83	2.03	7	1
1:A:71:GLU:CB	2:A:173:RCY:C1M	0.83	2.56	11	1
2:A:130:RCY:C1Z	2:A:130:RCY:O1G	0.83	2.25	19	1
2:A:150:RCY:C1P	2:A:150:RCY:H1CA	0.83	2.03	91	4
1:A:71:GLU:OE2	2:A:130:RCY:O1H	0.83	1.94	94	1
1:A:70:TRP:HZ2	2:A:160:RCY:H1CB	0.83	0.74	34	1
2:A:176:RCY:C1Y	2:A:187:RCY:O1H	0.83	2.26	76	1
2:A:150:RCY:C1M	2:A:187:RCY:C1V	0.83	2.55	89	2
1:A:68:CYS:C	2:A:168:RCY:H1LA	0.83	1.94	91	1
1:A:74:ASN:CG	2:A:173:RCY:O1G	0.83	2.17	91	2
2:A:138:RCY:H1VA	2:A:187:RCY:N1V	0.83	1.86	96	1
2:A:160:RCY:H1YA	2:A:168:RCY:H1S	0.83	1.16	100	1
1:A:71:GLU:OE2	2:A:187:RCY:O1H	0.83	1.94	88	1
1:A:69:PRO:HB2	2:A:168:RCY:C1Y	0.83	2.02	22	1
2:A:160:RCY:C1Z	2:A:173:RCY:O1G	0.83	2.26	5	2
1:A:70:TRP:CE2	2:A:160:RCY:C1V	0.83	2.59	34	1
1:A:74:ASN:N	2:A:173:RCY:O1H	0.83	2.11	82	2
1:A:69:PRO:HA	2:A:168:RCY:H1MA	0.83	0.85	5	1
1:A:63:ASP:OD2	2:A:150:RCY:O1G	0.83	1.96	85	1
1:A:70:TRP:CZ3	2:A:176:RCY:H1ZA	0.83	2.06	85	1
1:A:70:TRP:HE3	2:A:168:RCY:H1MA	0.83	1.26	44	1
1:A:70:TRP:NE1	2:A:176:RCY:H1V	0.83	1.87	82	1
2:A:130:RCY:C1M	2:A:160:RCY:H1Y	0.83	2.03	67	1
2:A:138:RCY:C1C	2:A:150:RCY:C1P	0.83	2.57	53	2
2:A:173:RCY:H1ZB	2:A:176:RCY:H1Y	0.83	0.85	41	1
2:A:130:RCY:H1CA	2:A:130:RCY:C1Q	0.83	2.03	75	1
1:A:72:ALA:HB1	2:A:173:RCY:H1L	0.83	1.49	10	1
2:A:173:RCY:H1VB	2:A:176:RCY:C1U	0.83	2.04	69	1
1:A:73:CYS:HB2	2:A:168:RCY:C1V	0.83	2.03	57	1
1:A:70:TRP:CE3	2:A:168:RCY:H1V	0.83	2.08	56	1
2:A:168:RCY:C1Z	2:A:187:RCY:H1Y	0.83	2.02	97	1
1:A:69:PRO:HB3	2:A:150:RCY:H1Z	0.83	1.49	92	1
2:A:160:RCY:O1G	2:A:160:RCY:C1V	0.83	2.25	46	4
2:A:138:RCY:H1YB	2:A:187:RCY:H1YA	0.83	1.40	86	1
2:A:160:RCY:H1CA	2:A:160:RCY:C1Q	0.83	2.03	84	2
2:A:160:RCY:C1M	2:A:168:RCY:H1CA	0.83	1.66	94	1
2:A:160:RCY:C1M	2:A:168:RCY:C1Q	0.83	2.50	34	1
1:A:73:CYS:CB	2:A:176:RCY:H1M	0.83	2.02	70	1
1:A:77:GLU:OE1	2:A:121:RCY:C1Y	0.83	2.24	11	1
2:A:138:RCY:C1C	2:A:150:RCY:C1L	0.83	2.56	53	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:173:RCY:C1Z	2:A:187:RCY:H1VB	0.83	2.04	77	1
2:A:168:RCY:H1YB	2:A:176:RCY:O1J	0.83	1.72	66	1
1:A:64:ILE:O	1:A:65:THR:OG1	0.83	1.95	76	11
2:A:173:RCY:C1L	2:A:176:RCY:C1Q	0.83	2.53	55	1
2:A:160:RCY:O1J	2:A:187:RCY:O1J	0.83	1.95	26	1
2:A:110:RCY:H1CA	2:A:110:RCY:C1Q	0.83	2.02	32	4
1:A:70:TRP:HZ3	2:A:160:RCY:C1V	0.83	1.83	91	1
1:A:71:GLU:HG3	2:A:121:RCY:H1YB	0.83	1.50	4	1
2:A:173:RCY:H1VA	2:A:176:RCY:H1ZA	0.83	1.46	4	1
2:A:173:RCY:C1U	2:A:176:RCY:C1W	0.83	2.50	77	1
1:A:65:THR:CG2	2:A:160:RCY:C1C	0.83	2.56	31	1
2:A:168:RCY:C1W	2:A:187:RCY:C1L	0.83	2.57	100	1
1:A:74:ASN:N	2:A:173:RCY:N1V	0.83	2.23	22	1
1:A:66:VAL:O	2:A:168:RCY:C1X	0.83	2.26	27	2
1:A:74:ASN:O	2:A:176:RCY:H1C	0.83	1.72	62	1
1:A:71:GLU:HG2	2:A:176:RCY:C1C	0.83	2.02	44	1
1:A:67:ILE:CG2	2:A:173:RCY:H1M	0.83	1.84	80	1
1:A:76:CYS:C	2:A:160:RCY:C1V	0.83	2.35	73	1
2:A:176:RCY:C1Z	2:A:187:RCY:O1J	0.83	2.25	36	2
2:A:138:RCY:C1Q	2:A:150:RCY:N1R	0.83	2.42	41	1
2:A:160:RCY:C1U	2:A:168:RCY:C1Y	0.83	2.57	41	1
2:A:168:RCY:C1Z	2:A:173:RCY:H1V	0.83	2.02	70	2
1:A:68:CYS:CB	2:A:173:RCY:O1J	0.83	2.26	50	1
1:A:76:CYS:CB	2:A:187:RCY:C1V	0.83	2.53	34	1
2:A:173:RCY:H1VB	2:A:176:RCY:C1C	0.83	2.04	49	1
2:A:176:RCY:H1ZB	2:A:187:RCY:O1J	0.83	1.72	36	1
1:A:70:TRP:HA	2:A:168:RCY:C1V	0.83	2.00	22	1
2:A:168:RCY:C1S	2:A:173:RCY:C1Y	0.83	2.57	84	2
1:A:73:CYS:HB2	2:A:168:RCY:H1ZB	0.83	0.84	99	1
1:A:75:HIS:C	2:A:176:RCY:H1S	0.83	1.95	51	2
2:A:176:RCY:C1M	2:A:187:RCY:H1YB	0.83	1.86	5	1
2:A:173:RCY:H1V	2:A:176:RCY:C1Z	0.83	2.00	59	1
1:A:71:GLU:CB	2:A:168:RCY:C1U	0.83	2.41	37	1
1:A:71:GLU:CG	2:A:168:RCY:C1P	0.83	2.56	32	1
2:A:173:RCY:O1J	2:A:176:RCY:C1Y	0.83	2.26	82	1
2:A:173:RCY:H1Z	2:A:176:RCY:C1V	0.83	1.62	31	1
2:A:130:RCY:C1C	2:A:160:RCY:H1S	0.83	2.02	66	1
2:A:173:RCY:H1ZA	2:A:187:RCY:O1G	0.83	1.54	92	1
2:A:150:RCY:H1V	2:A:187:RCY:H1ZA	0.82	1.50	41	1
2:A:138:RCY:H1M	2:A:150:RCY:C1V	0.82	1.98	75	1
2:A:160:RCY:H1V	2:A:168:RCY:H1L	0.82	1.48	24	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:150:RCY:H1Z	2:A:187:RCY:C1M	0.82	1.98	18	2
1:A:60:CYS:N	2:A:130:RCY:C1M	0.82	2.42	18	1
1:A:77:GLU:OE2	2:A:176:RCY:H1ZB	0.82	1.74	73	1
2:A:173:RCY:O1G	2:A:176:RCY:H1Y	0.82	1.74	97	1
1:A:68:CYS:HB3	2:A:160:RCY:H1ZA	0.82	1.49	19	1
1:A:62:THR:HG21	2:A:160:RCY:O1H	0.82	1.71	8	1
2:A:176:RCY:C1X	2:A:187:RCY:H1U	0.82	2.03	29	1
1:A:76:CYS:N	2:A:173:RCY:H1CB	0.82	1.86	29	1
1:A:70:TRP:CB	2:A:173:RCY:H1YB	0.82	2.03	85	2
2:A:150:RCY:H1CA	2:A:187:RCY:H1C	0.82	1.47	18	1
2:A:130:RCY:H1VB	2:A:130:RCY:C1L	0.82	2.04	7	1
2:A:173:RCY:C1C	2:A:176:RCY:H1MA	0.82	2.04	96	1
2:A:176:RCY:H1U	2:A:187:RCY:C1C	0.82	2.04	87	1
2:A:168:RCY:H1YA	2:A:187:RCY:C1L	0.82	2.04	88	1
2:A:160:RCY:C1Y	2:A:168:RCY:H1U	0.82	2.04	52	2
2:A:150:RCY:H1ZB	2:A:187:RCY:H1YA	0.82	0.85	49	1
1:A:70:TRP:HE3	2:A:176:RCY:C1C	0.82	1.83	77	1
2:A:150:RCY:H1YA	2:A:173:RCY:C1Q	0.82	2.03	3	1
1:A:67:ILE:CB	2:A:150:RCY:H1VB	0.82	2.02	31	1
1:A:69:PRO:HG3	2:A:150:RCY:C1Z	0.82	2.02	92	1
2:A:168:RCY:C1Z	2:A:173:RCY:C1C	0.82	2.58	55	1
2:A:150:RCY:H1VB	2:A:187:RCY:H1ZA	0.82	0.86	64	1
2:A:138:RCY:H1U	2:A:150:RCY:C1P	0.82	2.02	81	2
1:A:65:THR:HG21	2:A:168:RCY:H1CB	0.82	1.51	60	1
2:A:150:RCY:N1V	2:A:187:RCY:H1CA	0.82	1.88	50	1
1:A:69:PRO:HB2	2:A:173:RCY:H1Z	0.82	1.51	69	2
2:A:138:RCY:C1U	2:A:187:RCY:H1CB	0.82	2.00	5	1
1:A:72:ALA:C	2:A:168:RCY:O1G	0.82	2.18	91	1
2:A:160:RCY:H1Z	2:A:168:RCY:O1G	0.82	1.61	1	1
2:A:150:RCY:C1X	2:A:160:RCY:C1V	0.82	2.39	42	1
1:A:70:TRP:CZ2	2:A:168:RCY:O1J	0.82	2.32	24	1
2:A:150:RCY:H1YB	2:A:173:RCY:O1J	0.82	1.72	85	1
1:A:74:ASN:OD1	2:A:176:RCY:H1M	0.82	1.74	44	1
1:A:76:CYS:O	2:A:176:RCY:C1Q	0.82	2.27	73	1
1:A:69:PRO:HG3	2:A:176:RCY:H1U	0.82	1.48	31	1
2:A:130:RCY:H1YB	2:A:160:RCY:C1M	0.82	2.02	61	1
2:A:160:RCY:H1CA	2:A:160:RCY:O1G	0.82	1.74	58	2
1:A:69:PRO:HB2	2:A:187:RCY:H1VB	0.82	1.50	14	1
2:A:173:RCY:H1LA	2:A:176:RCY:C1Q	0.82	2.03	55	1
1:A:71:GLU:C	2:A:168:RCY:C1C	0.82	2.47	86	1
1:A:70:TRP:CG	2:A:176:RCY:C1C	0.82	2.24	62	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:69:PRO:HG3	2:A:173:RCY:O1H	0.82	1.74	10	2
2:A:138:RCY:H1ZB	2:A:187:RCY:H1C	0.82	1.49	44	2
1:A:77:GLU:OE2	2:A:173:RCY:C1L	0.82	2.24	33	1
2:A:160:RCY:C1Y	2:A:168:RCY:H1Z	0.82	2.01	9	1
2:A:138:RCY:H1YB	2:A:187:RCY:O1J	0.82	1.74	98	1
1:A:63:ASP:O	2:A:160:RCY:H1ZA	0.82	1.73	78	1
2:A:130:RCY:H1Z	2:A:160:RCY:H1LA	0.82	1.48	61	1
2:A:168:RCY:H1Z	2:A:187:RCY:H1Z	0.82	1.51	17	1
1:A:66:VAL:O	2:A:168:RCY:H1V	0.82	1.75	38	2
1:A:76:CYS:HB2	2:A:173:RCY:H1CA	0.82	1.28	29	2
2:A:110:RCY:C1C	2:A:121:RCY:H1YA	0.82	2.03	5	1
1:A:59:GLY:N	2:A:160:RCY:H1ZB	0.82	1.88	49	1
2:A:138:RCY:C1Y	2:A:168:RCY:H1Y	0.82	2.03	7	1
2:A:150:RCY:C1Z	2:A:176:RCY:C1P	0.82	2.49	3	1
2:A:150:RCY:H1C	2:A:173:RCY:H1VB	0.82	1.50	31	1
1:A:64:ILE:HD13	2:A:160:RCY:H1MA	0.82	1.49	1	1
2:A:168:RCY:O1H	2:A:187:RCY:C1C	0.82	2.28	88	1
1:A:70:TRP:NE1	2:A:168:RCY:C1Q	0.82	2.42	42	1
2:A:168:RCY:C1X	2:A:173:RCY:C1V	0.82	2.51	48	1
2:A:176:RCY:C1X	2:A:187:RCY:O1J	0.82	2.27	91	1
1:A:63:ASP:OD2	2:A:160:RCY:H1VB	0.82	1.75	63	1
1:A:67:ILE:O	2:A:168:RCY:C1L	0.82	2.28	75	1
2:A:168:RCY:H1CB	2:A:173:RCY:C1Y	0.82	2.03	85	4
1:A:62:THR:HG21	2:A:168:RCY:H1ZA	0.82	0.84	72	1
1:A:66:VAL:O	2:A:168:RCY:O1G	0.82	1.98	21	1
1:A:67:ILE:C	2:A:173:RCY:H1ZA	0.82	1.94	63	1
2:A:173:RCY:C1Z	2:A:176:RCY:C1L	0.82	2.57	20	1
2:A:160:RCY:O1J	2:A:173:RCY:H1C	0.82	1.74	20	1
1:A:60:CYS:H	2:A:160:RCY:C1L	0.82	1.75	28	1
1:A:70:TRP:HD1	2:A:187:RCY:H1YB	0.82	1.35	92	1
1:A:59:GLY:O	2:A:160:RCY:H1LA	0.82	1.75	100	3
1:A:60:CYS:SG	2:A:130:RCY:C1V	0.82	2.68	8	1
2:A:130:RCY:O1J	2:A:176:RCY:H1C	0.82	1.75	41	1
2:A:168:RCY:C1Z	2:A:187:RCY:H1MA	0.82	2.04	84	1
1:A:71:GLU:CD	2:A:173:RCY:C1Y	0.82	2.21	50	1
2:A:176:RCY:C1W	2:A:187:RCY:C1V	0.82	2.54	10	1
1:A:70:TRP:HD1	2:A:121:RCY:H1M	0.82	1.31	49	1
2:A:130:RCY:C1S	2:A:130:RCY:H1VB	0.82	2.05	51	1
1:A:64:ILE:CD1	2:A:160:RCY:H1VA	0.82	2.04	54	1
1:A:59:GLY:HA2	2:A:160:RCY:H1V	0.82	1.48	2	1
2:A:173:RCY:C1X	2:A:176:RCY:C1V	0.82	2.57	63	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:66:VAL:O	2:A:150:RCY:C1C	0.82	2.27	96	1
2:A:160:RCY:C1Z	2:A:168:RCY:H1Y	0.81	2.04	78	1
2:A:150:RCY:C1V	2:A:160:RCY:C1X	0.81	2.51	42	1
2:A:138:RCY:O1G	2:A:150:RCY:H1CA	0.81	1.73	9	1
2:A:173:RCY:C1Y	2:A:187:RCY:C1L	0.81	2.55	45	1
1:A:70:TRP:CG	2:A:168:RCY:O1G	0.81	2.33	45	1
1:A:67:ILE:HD12	2:A:130:RCY:H1YB	0.81	1.50	30	1
1:A:63:ASP:C	2:A:160:RCY:H1ZA	0.81	1.95	78	1
1:A:74:ASN:CG	2:A:176:RCY:C1L	0.81	2.48	78	1
2:A:173:RCY:C1Y	2:A:176:RCY:C1Y	0.81	2.58	59	4
2:A:150:RCY:O1J	2:A:187:RCY:H1YB	0.81	1.74	59	1
2:A:173:RCY:H1LA	2:A:176:RCY:H1VB	0.81	0.84	11	1
1:A:68:CYS:HB3	2:A:176:RCY:H1Y	0.81	0.83	80	1
1:A:62:THR:HG21	2:A:160:RCY:C1P	0.81	2.03	82	1
2:A:173:RCY:H1LA	2:A:176:RCY:C1P	0.81	2.04	20	1
1:A:71:GLU:HG3	2:A:168:RCY:H1S	0.81	1.51	28	1
1:A:65:THR:HA	2:A:168:RCY:C1P	0.81	2.05	97	1
1:A:60:CYS:HA	2:A:130:RCY:C1Z	0.81	2.05	88	1
2:A:150:RCY:H1MA	2:A:187:RCY:H1YB	0.81	1.52	88	1
2:A:173:RCY:C1Z	2:A:176:RCY:C1S	0.81	2.57	54	2
1:A:65:THR:HG21	2:A:168:RCY:C1C	0.81	2.06	60	1
2:A:173:RCY:H1V	2:A:176:RCY:C1Q	0.81	2.06	69	1
2:A:173:RCY:C1C	2:A:176:RCY:H1S	0.81	2.03	72	2
2:A:173:RCY:H1U	2:A:173:RCY:N1R	0.81	1.86	79	1
1:A:62:THR:HG21	2:A:130:RCY:C1Y	0.81	2.04	9	1
2:A:168:RCY:C1P	2:A:173:RCY:C1M	0.81	2.54	49	1
2:A:160:RCY:C1X	2:A:168:RCY:H1CB	0.81	2.04	49	1
1:A:68:CYS:SG	2:A:176:RCY:C1U	0.81	2.68	77	1
2:A:138:RCY:C1P	2:A:138:RCY:H1CA	0.81	2.05	10	8
2:A:150:RCY:H1ZB	2:A:150:RCY:C1Q	0.81	2.05	82	5
1:A:65:THR:CG2	2:A:160:RCY:C1W	0.81	2.30	100	1
2:A:160:RCY:H1Y	2:A:173:RCY:C1Y	0.81	2.05	8	1
1:A:59:GLY:O	1:A:60:CYS:O	0.81	1.98	91	5
1:A:73:CYS:HA	2:A:168:RCY:H1ZA	0.81	1.52	99	1
2:A:168:RCY:H1ZB	2:A:168:RCY:C1Q	0.81	2.05	30	4
1:A:65:THR:HG21	2:A:130:RCY:H1C	0.81	1.48	9	1
1:A:71:GLU:HA	2:A:173:RCY:C1S	0.81	2.04	49	1
1:A:76:CYS:SG	2:A:173:RCY:H1L	0.81	2.15	54	1
2:A:168:RCY:H1Y	2:A:176:RCY:H1L	0.81	1.48	20	1
1:A:71:GLU:CG	2:A:173:RCY:O1H	0.81	2.29	89	1
1:A:66:VAL:O	2:A:150:RCY:H1C	0.81	1.76	96	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:150:RCY:C1W	2:A:173:RCY:O1J	0.81	2.22	3	1
2:A:176:RCY:H1V	2:A:187:RCY:C1X	0.81	1.93	33	1
1:A:70:TRP:CZ3	2:A:168:RCY:H1VA	0.81	2.09	56	1
2:A:160:RCY:C1Y	2:A:173:RCY:C1Y	0.81	2.58	8	1
2:A:176:RCY:H1C	2:A:187:RCY:H1CA	0.81	1.53	75	1
1:A:70:TRP:CD1	2:A:176:RCY:H1CB	0.81	2.05	62	1
1:A:70:TRP:HB2	2:A:168:RCY:C1S	0.81	2.01	16	2
1:A:64:ILE:HD11	2:A:187:RCY:N1R	0.81	1.88	85	1
2:A:130:RCY:C1X	2:A:130:RCY:C1W	0.81	2.58	79	1
2:A:138:RCY:C1C	2:A:187:RCY:H1MA	0.81	1.89	11	1
2:A:168:RCY:C1V	2:A:168:RCY:O1H	0.81	2.23	49	8
1:A:73:CYS:CB	2:A:168:RCY:H1ZB	0.81	0.74	99	1
2:A:110:RCY:C1C	2:A:110:RCY:O1H	0.81	2.28	32	2
1:A:62:THR:CG2	2:A:173:RCY:C1V	0.81	2.15	18	1
2:A:160:RCY:C1X	2:A:168:RCY:C1V	0.81	2.59	48	1
1:A:69:PRO:CB	2:A:187:RCY:H1C	0.81	2.05	7	1
1:A:61:GLY:C	2:A:150:RCY:C1M	0.81	2.47	11	1
1:A:67:ILE:HB	2:A:173:RCY:H1YB	0.81	1.04	80	1
1:A:70:TRP:CZ3	2:A:168:RCY:C1Y	0.81	2.60	41	3
1:A:69:PRO:HG3	2:A:173:RCY:H1ZB	0.81	1.46	57	1
1:A:71:GLU:CG	2:A:176:RCY:H1CB	0.81	2.03	44	2
2:A:138:RCY:C1V	2:A:187:RCY:C1M	0.81	2.51	49	1
1:A:63:ASP:OD1	2:A:150:RCY:H1Y	0.81	1.75	80	1
2:A:173:RCY:C1U	2:A:176:RCY:H1YA	0.81	2.03	74	1
1:A:72:ALA:N	2:A:173:RCY:O1G	0.81	2.01	100	1
1:A:70:TRP:HB3	2:A:173:RCY:C1W	0.81	2.05	84	2
2:A:168:RCY:H1CB	2:A:173:RCY:C1M	0.81	2.01	99	1
2:A:150:RCY:C1C	2:A:187:RCY:N1V	0.81	2.43	50	1
1:A:67:ILE:HD13	2:A:138:RCY:C1P	0.81	2.04	72	1
1:A:69:PRO:HB2	2:A:173:RCY:H1Y	0.81	1.49	9	1
2:A:138:RCY:H1VA	2:A:150:RCY:C1C	0.81	2.05	70	1
2:A:160:RCY:O1J	2:A:173:RCY:C1C	0.81	2.29	20	2
2:A:168:RCY:H1YA	2:A:176:RCY:O1J	0.81	1.75	90	1
2:A:138:RCY:H1M	2:A:150:RCY:C1P	0.81	1.70	1	1
2:A:130:RCY:C1Y	2:A:160:RCY:H1V	0.81	2.05	61	1
2:A:160:RCY:H1VA	2:A:168:RCY:O1J	0.81	1.75	94	1
2:A:138:RCY:C1Y	2:A:150:RCY:C1P	0.81	2.57	60	1
2:A:138:RCY:C1W	2:A:187:RCY:C1Y	0.81	2.57	68	2
2:A:121:RCY:H1U	2:A:121:RCY:N1R	0.81	1.89	79	2
2:A:160:RCY:C1Y	2:A:168:RCY:H1V	0.81	2.06	48	2
1:A:70:TRP:NE1	2:A:121:RCY:H1V	0.81	1.91	49	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:176:RCY:C1P	2:A:176:RCY:H1CA	0.80	2.06	65	2
2:A:176:RCY:C1V	2:A:187:RCY:H1U	0.80	2.05	29	2
1:A:69:PRO:C	2:A:173:RCY:C1P	0.80	2.43	6	1
2:A:173:RCY:H1VA	2:A:187:RCY:H1YA	0.80	1.44	54	1
1:A:75:HIS:N	2:A:176:RCY:H1CB	0.80	1.92	20	1
1:A:64:ILE:HG21	1:A:68:CYS:SG	0.80	2.16	89	1
1:A:70:TRP:CH2	2:A:138:RCY:C1U	0.80	2.38	27	1
1:A:69:PRO:O	2:A:173:RCY:C1S	0.80	2.28	82	2
1:A:70:TRP:CZ2	2:A:168:RCY:H1LA	0.80	2.11	71	1
1:A:71:GLU:O	2:A:173:RCY:C1V	0.80	2.28	33	1
2:A:160:RCY:N1R	2:A:168:RCY:O1J	0.80	2.13	9	1
1:A:65:THR:O	2:A:168:RCY:O1H	0.80	1.98	51	1
1:A:60:CYS:HB3	2:A:168:RCY:H1CB	0.80	1.53	95	1
2:A:130:RCY:H1YA	2:A:160:RCY:H1YA	0.80	1.54	67	1
1:A:70:TRP:CZ3	2:A:168:RCY:H1Y	0.80	2.12	41	1
2:A:173:RCY:H1VB	2:A:173:RCY:C1Q	0.80	2.06	83	5
2:A:187:RCY:H1VB	2:A:187:RCY:C1Q	0.80	2.06	72	6
2:A:176:RCY:C1V	2:A:187:RCY:H1Z	0.80	2.07	91	1
1:A:70:TRP:HD1	2:A:187:RCY:H1ZB	0.80	1.33	51	1
2:A:160:RCY:H1YB	2:A:168:RCY:C1Y	0.80	2.06	53	1
1:A:64:ILE:HD13	2:A:168:RCY:H1C	0.80	1.51	4	1
2:A:138:RCY:H1VA	2:A:150:RCY:C1V	0.80	2.04	67	1
2:A:168:RCY:H1U	2:A:176:RCY:C1Z	0.80	2.06	98	1
2:A:150:RCY:H1YA	2:A:187:RCY:H1VB	0.80	1.49	38	1
2:A:150:RCY:C1W	2:A:160:RCY:H1VA	0.80	2.06	42	1
2:A:138:RCY:H1M	2:A:187:RCY:C1Y	0.80	1.77	68	2
1:A:64:ILE:HG23	2:A:168:RCY:H1CA	0.80	1.51	54	1
1:A:67:ILE:HG13	2:A:168:RCY:C1Y	0.80	2.06	80	1
1:A:63:ASP:OD2	2:A:160:RCY:H1MA	0.80	1.76	73	1
2:A:110:RCY:H1CB	2:A:110:RCY:O1G	0.80	1.77	27	4
2:A:130:RCY:H1YB	2:A:176:RCY:H1ZB	0.80	1.53	41	1
1:A:71:GLU:HG2	2:A:173:RCY:H1VA	0.80	1.50	41	1
1:A:59:GLY:N	2:A:138:RCY:H1MA	0.80	1.90	64	1
2:A:150:RCY:N1V	2:A:187:RCY:H1MA	0.80	1.92	59	1
1:A:67:ILE:HG21	2:A:173:RCY:H1ZA	0.80	1.53	80	1
2:A:168:RCY:H1U	2:A:173:RCY:C1C	0.80	2.05	20	1
2:A:150:RCY:H1C	2:A:173:RCY:C1V	0.80	2.06	31	1
2:A:173:RCY:H1YA	2:A:187:RCY:C1P	0.80	2.01	93	1
2:A:130:RCY:C1P	2:A:130:RCY:H1ZB	0.80	2.07	38	4
2:A:168:RCY:H1VB	2:A:168:RCY:C1Q	0.80	2.07	20	10
2:A:168:RCY:H1YB	2:A:173:RCY:H1Z	0.80	1.53	20	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:168:RCY:C1C	2:A:173:RCY:H1MA	0.80	2.05	99	1
1:A:68:CYS:O	2:A:173:RCY:O1G	0.80	1.99	4	2
1:A:70:TRP:CA	2:A:173:RCY:C1V	0.80	2.59	26	1
1:A:62:THR:HG22	2:A:173:RCY:H1VA	0.80	1.48	18	1
1:A:78:LEU:O	1:A:78:LEU:HD22	0.80	1.77	51	1
1:A:77:GLU:HG3	2:A:176:RCY:C1U	0.80	2.01	39	1
2:A:168:RCY:C1U	2:A:173:RCY:C1Y	0.80	2.60	31	1
2:A:168:RCY:C1C	2:A:176:RCY:N1V	0.80	2.45	59	2
2:A:168:RCY:H1CB	2:A:168:RCY:O1G	0.80	1.77	45	7
1:A:70:TRP:NE1	2:A:168:RCY:H1S	0.80	1.89	42	1
2:A:187:RCY:H1ZB	2:A:187:RCY:C1P	0.80	2.06	50	1
2:A:176:RCY:C1M	2:A:187:RCY:C1V	0.80	2.60	10	1
1:A:75:HIS:CB	2:A:176:RCY:C1L	0.80	2.57	13	1
2:A:110:RCY:N1V	2:A:121:RCY:C1V	0.80	2.42	5	1
1:A:70:TRP:CE2	2:A:168:RCY:H1YA	0.80	2.12	37	1
1:A:70:TRP:CE2	2:A:176:RCY:H1V	0.80	2.04	4	1
2:A:150:RCY:H1Z	2:A:176:RCY:N1R	0.80	1.91	3	1
1:A:70:TRP:CD1	2:A:187:RCY:C1Y	0.80	2.50	92	1
1:A:64:ILE:HD13	1:A:65:THR:N	0.80	1.91	17	1
2:A:160:RCY:C1M	2:A:168:RCY:C1L	0.80	2.56	58	2
1:A:65:THR:O	1:A:66:VAL:HG13	0.80	1.77	32	5
2:A:130:RCY:H1VB	2:A:130:RCY:C1Q	0.80	2.07	72	6
2:A:160:RCY:N1V	2:A:168:RCY:C1Z	0.80	2.36	5	1
2:A:138:RCY:H1CA	2:A:150:RCY:N1V	0.80	1.92	59	1
2:A:130:RCY:H1Z	2:A:130:RCY:H1Y	0.80	1.54	79	1
2:A:176:RCY:H1YA	2:A:187:RCY:H1C	0.80	1.49	27	2
1:A:73:CYS:HB2	2:A:176:RCY:C1U	0.80	2.07	70	1
1:A:62:THR:HG1	2:A:150:RCY:H1CB	0.80	1.35	11	1
1:A:63:ASP:OD2	2:A:160:RCY:H1ZB	0.80	1.77	73	1
1:A:64:ILE:HG13	2:A:168:RCY:C1Z	0.80	2.04	78	2
1:A:69:PRO:HD2	2:A:168:RCY:C1P	0.80	2.07	78	3
2:A:168:RCY:H1MA	2:A:173:RCY:N1V	0.80	1.92	14	1
2:A:138:RCY:O1H	2:A:138:RCY:H1CA	0.80	1.77	93	2
1:A:69:PRO:CB	2:A:173:RCY:C1P	0.80	2.57	75	1
1:A:59:GLY:O	2:A:160:RCY:H1M	0.80	1.75	85	1
2:A:173:RCY:H1Z	2:A:176:RCY:H1YB	0.80	1.54	37	1
1:A:73:CYS:O	2:A:176:RCY:O1H	0.80	2.00	20	1
1:A:66:VAL:C	2:A:168:RCY:H1CB	0.80	1.95	58	1
2:A:160:RCY:C1Z	2:A:173:RCY:H1CA	0.80	2.00	86	1
1:A:70:TRP:C	2:A:173:RCY:C1Z	0.80	2.50	94	1
2:A:150:RCY:C1C	2:A:187:RCY:C1C	0.80	2.55	50	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:70:TRP:HB2	2:A:176:RCY:C1M	0.80	2.07	6	1
2:A:138:RCY:H1VB	2:A:187:RCY:H1YB	0.80	1.54	11	1
1:A:74:ASN:O	2:A:173:RCY:C1S	0.80	2.30	90	1
2:A:138:RCY:H1Z	2:A:150:RCY:H1ZA	0.80	1.50	30	1
2:A:176:RCY:H1VB	2:A:176:RCY:C1Q	0.79	2.06	45	6
2:A:168:RCY:O1G	2:A:168:RCY:H1CB	0.79	1.77	38	5
2:A:173:RCY:H1CB	2:A:176:RCY:C1Z	0.79	2.07	84	1
2:A:160:RCY:H1VB	2:A:160:RCY:C1Q	0.79	2.06	98	5
1:A:71:GLU:CG	2:A:121:RCY:H1YB	0.79	2.07	4	1
1:A:69:PRO:HD3	2:A:168:RCY:H1V	0.79	1.53	63	1
1:A:65:THR:CG2	2:A:160:RCY:O1H	0.79	2.29	36	1
2:A:130:RCY:C1Y	2:A:173:RCY:H1S	0.79	2.05	15	1
1:A:64:ILE:CG1	2:A:168:RCY:H1VB	0.79	2.07	27	1
2:A:121:RCY:C1P	2:A:121:RCY:H1ZB	0.79	2.08	48	4
2:A:138:RCY:O1G	2:A:138:RCY:H1CB	0.79	1.77	61	6
2:A:160:RCY:O1G	2:A:160:RCY:H1CB	0.79	1.78	20	6
2:A:173:RCY:H1MA	2:A:187:RCY:H1MA	0.79	1.52	40	1
1:A:76:CYS:HB2	2:A:187:RCY:H1VB	0.79	1.51	34	1
1:A:75:HIS:CE1	2:A:176:RCY:C1L	0.79	2.65	24	1
1:A:72:ALA:HA	2:A:168:RCY:O1G	0.79	1.75	91	1
1:A:72:ALA:N	2:A:168:RCY:C1M	0.79	2.33	91	1
1:A:74:ASN:OD1	2:A:176:RCY:C1M	0.79	2.30	44	1
1:A:70:TRP:CZ2	2:A:176:RCY:H1M	0.79	2.04	4	1
2:A:138:RCY:C1Z	2:A:150:RCY:C1L	0.79	2.40	1	1
2:A:130:RCY:H1C	2:A:160:RCY:H1S	0.79	1.54	66	1
2:A:173:RCY:H1M	2:A:176:RCY:C1C	0.79	2.03	38	1
1:A:60:CYS:C	2:A:160:RCY:H1LA	0.79	1.98	99	3
1:A:69:PRO:CA	2:A:173:RCY:H1ZB	0.79	2.05	75	1
1:A:70:TRP:CB	2:A:173:RCY:C1M	0.79	2.57	84	1
1:A:71:GLU:CB	2:A:168:RCY:C1P	0.79	2.54	57	2
2:A:138:RCY:H1YA	2:A:150:RCY:C1P	0.79	1.85	80	1
1:A:67:ILE:HG13	2:A:168:RCY:H1Y	0.79	1.54	80	1
1:A:71:GLU:CG	2:A:168:RCY:C1U	0.79	2.61	93	1
1:A:63:ASP:HA	2:A:160:RCY:C1Z	0.79	2.06	14	1
1:A:73:CYS:HB2	2:A:176:RCY:H1ZA	0.79	0.80	58	1
1:A:66:VAL:C	2:A:168:RCY:C1C	0.79	2.50	58	1
2:A:168:RCY:C1P	2:A:168:RCY:H1ZB	0.79	2.05	72	2
1:A:75:HIS:ND1	2:A:176:RCY:H1L	0.79	1.92	24	1
2:A:138:RCY:C1C	2:A:150:RCY:C1W	0.79	2.59	59	1
1:A:78:LEU:HD21	2:A:176:RCY:C1Z	0.79	2.06	91	1
1:A:63:ASP:HB3	2:A:160:RCY:H1C	0.79	1.32	63	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:73:CYS:HB2	2:A:176:RCY:H1LA	0.79	1.53	63	1
1:A:71:GLU:HG2	2:A:187:RCY:O1G	0.79	1.77	92	1
2:A:160:RCY:H1CB	2:A:160:RCY:O1G	0.79	1.78	15	8
2:A:150:RCY:C1Q	2:A:150:RCY:H1VB	0.79	2.06	1	7
2:A:176:RCY:H1ZA	2:A:187:RCY:C1X	0.79	2.02	10	1
1:A:64:ILE:CD1	2:A:168:RCY:H1S	0.79	1.91	12	2
1:A:63:ASP:HB3	2:A:160:RCY:C1V	0.79	2.07	5	1
2:A:176:RCY:C1P	2:A:176:RCY:H1ZB	0.79	2.08	61	3
2:A:150:RCY:O1G	2:A:150:RCY:H1CB	0.79	1.78	44	5
2:A:173:RCY:H1CA	2:A:173:RCY:C1P	0.79	2.07	67	5
2:A:110:RCY:C1Q	2:A:110:RCY:H1VB	0.79	2.07	80	7
2:A:150:RCY:H1VB	2:A:150:RCY:C1Q	0.79	2.06	90	9
2:A:138:RCY:O1H	2:A:138:RCY:C1V	0.79	2.24	99	5
1:A:78:LEU:HD22	2:A:138:RCY:C1V	0.79	2.07	40	1
2:A:173:RCY:O1G	2:A:187:RCY:H1VB	0.79	1.74	16	1
1:A:69:PRO:CA	2:A:168:RCY:H1M	0.79	1.83	5	1
2:A:138:RCY:H1YB	2:A:187:RCY:H1YB	0.79	1.53	32	1
1:A:67:ILE:CG1	2:A:176:RCY:H1C	0.79	2.07	53	1
1:A:63:ASP:CB	2:A:138:RCY:H1Z	0.79	2.02	73	1
1:A:70:TRP:CH2	2:A:138:RCY:H1U	0.79	2.12	27	1
1:A:69:PRO:HG3	2:A:168:RCY:H1CB	0.79	1.34	8	1
1:A:74:ASN:O	2:A:176:RCY:C1X	0.79	2.31	62	1
1:A:70:TRP:CZ2	2:A:187:RCY:H1Z	0.79	2.12	76	1
1:A:65:THR:HG21	2:A:168:RCY:O1G	0.79	1.75	80	1
2:A:173:RCY:H1V	2:A:176:RCY:H1C	0.79	1.52	67	1
2:A:160:RCY:N1V	2:A:168:RCY:H1Y	0.79	1.92	78	1
2:A:160:RCY:C1Y	2:A:168:RCY:N1R	0.79	2.35	58	2
2:A:176:RCY:H1CB	2:A:176:RCY:O1G	0.79	1.78	13	4
1:A:67:ILE:O	2:A:168:RCY:H1S	0.79	1.77	55	1
2:A:138:RCY:C1C	2:A:150:RCY:N1V	0.79	2.45	59	2
2:A:176:RCY:H1YB	2:A:187:RCY:H1YA	0.79	0.85	72	1
2:A:138:RCY:C1Z	2:A:187:RCY:H1ZB	0.79	2.04	59	1
1:A:68:CYS:CB	2:A:176:RCY:N1V	0.79	2.43	80	1
2:A:138:RCY:H1YB	2:A:187:RCY:O1G	0.79	1.74	89	2
2:A:138:RCY:H1C	2:A:150:RCY:C1C	0.79	2.07	66	1
1:A:71:GLU:OE1	2:A:168:RCY:H1CB	0.79	1.77	38	2
2:A:160:RCY:H1Y	2:A:168:RCY:C1L	0.79	2.07	3	2
1:A:70:TRP:HB2	2:A:168:RCY:O1G	0.79	1.77	3	3
2:A:150:RCY:H1V	2:A:160:RCY:H1ZA	0.79	1.53	29	1
1:A:64:ILE:CG1	2:A:168:RCY:C1L	0.79	2.16	96	3
2:A:173:RCY:O1G	2:A:173:RCY:H1CB	0.79	1.77	32	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:67:ILE:O	2:A:173:RCY:O1J	0.79	2.00	31	2
1:A:70:TRP:HE1	2:A:168:RCY:H1YA	0.79	1.00	37	1
1:A:73:CYS:HA	2:A:168:RCY:O1J	0.79	1.77	91	1
1:A:64:ILE:HB	2:A:168:RCY:C1Q	0.79	2.06	95	1
2:A:130:RCY:H1ZB	2:A:130:RCY:C1P	0.79	2.08	82	2
2:A:138:RCY:C1W	2:A:150:RCY:C1L	0.79	2.61	1	1
2:A:138:RCY:H1CB	2:A:138:RCY:O1G	0.79	1.77	100	13
2:A:121:RCY:C1Q	2:A:121:RCY:H1VB	0.79	2.08	27	4
2:A:160:RCY:C1P	2:A:168:RCY:H1C	0.79	2.06	64	2
2:A:110:RCY:H1CA	2:A:110:RCY:C1P	0.79	2.06	11	6
1:A:76:CYS:CA	2:A:176:RCY:C1Q	0.79	2.53	10	3
1:A:65:THR:HG23	2:A:168:RCY:O1J	0.79	1.77	24	1
2:A:168:RCY:C1Y	2:A:173:RCY:H1CA	0.79	1.91	91	1
2:A:138:RCY:C1V	2:A:187:RCY:N1R	0.79	2.44	21	1
1:A:70:TRP:CZ3	2:A:176:RCY:H1M	0.79	2.12	80	1
2:A:173:RCY:H1V	2:A:187:RCY:O1G	0.79	1.78	93	1
1:A:60:CYS:HA	2:A:130:RCY:H1ZA	0.78	1.52	88	1
2:A:173:RCY:H1VB	2:A:176:RCY:C1P	0.78	2.07	69	3
2:A:173:RCY:N1V	2:A:176:RCY:C1C	0.78	2.46	38	1
1:A:70:TRP:HB2	2:A:168:RCY:H1L	0.78	1.52	94	3
2:A:160:RCY:O1H	2:A:160:RCY:C1C	0.78	2.26	84	1
1:A:71:GLU:O	2:A:173:RCY:O1H	0.78	2.01	56	5
1:A:74:ASN:O	2:A:187:RCY:H1MA	0.78	1.78	34	1
2:A:160:RCY:C1W	2:A:173:RCY:H1Z	0.78	2.07	4	1
2:A:168:RCY:C1V	2:A:173:RCY:C1X	0.78	2.42	45	1
1:A:64:ILE:CD1	2:A:160:RCY:H1YB	0.78	2.07	74	1
2:A:150:RCY:H1VA	2:A:173:RCY:C1Y	0.78	2.08	39	2
2:A:168:RCY:H1C	2:A:176:RCY:H1ZB	0.78	1.53	3	1
1:A:72:ALA:HB3	2:A:173:RCY:C1Q	0.78	1.77	78	3
2:A:138:RCY:O1H	2:A:150:RCY:C1S	0.78	2.32	41	1
2:A:138:RCY:C1U	2:A:150:RCY:H1M	0.78	2.06	75	1
2:A:160:RCY:H1Y	2:A:173:RCY:H1Y	0.78	1.56	8	1
1:A:60:CYS:CA	2:A:160:RCY:C1L	0.78	2.14	99	2
2:A:138:RCY:C1S	2:A:138:RCY:H1CA	0.78	2.06	50	1
1:A:69:PRO:CA	2:A:176:RCY:C1V	0.78	2.54	72	1
1:A:70:TRP:CB	2:A:176:RCY:C1M	0.78	2.61	6	1
1:A:64:ILE:CD1	2:A:121:RCY:C1P	0.78	2.60	68	1
2:A:130:RCY:O1J	2:A:130:RCY:O1H	0.78	2.01	2	1
1:A:65:THR:HA	2:A:168:RCY:C1L	0.78	2.07	82	2
2:A:173:RCY:N1R	2:A:176:RCY:C1Y	0.78	2.39	56	2
2:A:176:RCY:C1Q	2:A:176:RCY:H1VB	0.78	2.08	69	5

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:150:RCY:H1V	2:A:187:RCY:H1VB	0.78	1.55	38	1
2:A:173:RCY:C1S	2:A:176:RCY:C1C	0.78	2.60	52	1
1:A:71:GLU:HG2	2:A:150:RCY:C1U	0.78	1.92	58	1
2:A:168:RCY:C1P	2:A:173:RCY:C1Y	0.78	2.39	62	2
2:A:160:RCY:N1V	2:A:168:RCY:O1J	0.78	2.14	94	1
2:A:150:RCY:C1Y	2:A:160:RCY:H1Y	0.78	2.09	29	1
2:A:160:RCY:H1M	2:A:168:RCY:C1C	0.78	2.09	5	1
2:A:173:RCY:C1Q	2:A:176:RCY:H1YA	0.78	2.06	68	1
2:A:168:RCY:O1J	2:A:173:RCY:H1VA	0.78	1.77	48	1
1:A:66:VAL:HG23	2:A:168:RCY:C1V	0.78	2.04	80	1
1:A:76:CYS:N	2:A:176:RCY:C1S	0.78	2.47	13	5
2:A:138:RCY:H1YB	2:A:187:RCY:C1V	0.78	2.09	84	1
2:A:121:RCY:O1H	2:A:121:RCY:H1CB	0.78	1.77	30	2
2:A:160:RCY:O1J	2:A:168:RCY:O1J	0.78	2.00	32	1
2:A:187:RCY:O1G	2:A:187:RCY:H1CB	0.78	1.78	74	2
1:A:67:ILE:CG1	2:A:168:RCY:H1CB	0.78	2.09	27	1
1:A:65:THR:HG1	2:A:160:RCY:H1ZA	0.78	1.34	100	1
1:A:73:CYS:O	2:A:173:RCY:H1LA	0.78	1.76	100	1
2:A:130:RCY:C1Q	2:A:130:RCY:H1VB	0.78	2.07	70	7
2:A:173:RCY:H1ZA	2:A:176:RCY:C1Y	0.78	1.33	81	2
1:A:70:TRP:CH2	2:A:160:RCY:C1U	0.78	2.67	34	1
1:A:71:GLU:OE2	2:A:110:RCY:C1C	0.78	2.32	5	1
2:A:160:RCY:O1J	2:A:168:RCY:H1YB	0.78	1.78	21	1
1:A:66:VAL:C	2:A:168:RCY:C1Q	0.78	2.52	51	1
1:A:66:VAL:CA	2:A:121:RCY:H1YA	0.78	2.06	83	1
2:A:168:RCY:C1Y	2:A:187:RCY:C1L	0.78	2.62	100	3
2:A:160:RCY:C1C	2:A:160:RCY:O1G	0.78	2.24	29	4
1:A:67:ILE:O	1:A:67:ILE:HG23	0.78	1.79	23	2
2:A:130:RCY:H1YA	2:A:160:RCY:C1Y	0.78	2.07	67	2
1:A:69:PRO:HA	2:A:173:RCY:H1VB	0.78	1.55	100	1
1:A:68:CYS:HA	2:A:168:RCY:H1L	0.78	0.79	75	2
2:A:160:RCY:C1P	2:A:160:RCY:H1VB	0.78	2.08	81	7
1:A:69:PRO:HD2	2:A:160:RCY:H1CA	0.78	1.55	65	1
2:A:176:RCY:H1MA	2:A:187:RCY:H1V	0.78	1.54	10	1
2:A:121:RCY:H1CB	2:A:121:RCY:O1G	0.78	1.79	24	7
2:A:138:RCY:C1U	2:A:150:RCY:C1Y	0.78	2.61	88	1
1:A:60:CYS:HB3	2:A:168:RCY:C1Y	0.78	2.09	52	1
2:A:130:RCY:C1V	2:A:173:RCY:H1YA	0.78	2.07	18	2
2:A:187:RCY:H1CB	2:A:187:RCY:O1G	0.78	1.77	73	4
2:A:150:RCY:H1CA	2:A:187:RCY:C1X	0.78	2.06	50	1
1:A:75:HIS:O	2:A:187:RCY:C1P	0.78	2.32	34	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:138:RCY:H1CA	2:A:160:RCY:C1Y	0.78	2.08	26	1
2:A:187:RCY:C1P	2:A:187:RCY:H1VB	0.78	2.08	85	5
1:A:71:GLU:OE2	2:A:110:RCY:C1V	0.78	2.31	5	1
1:A:60:CYS:O	2:A:121:RCY:C1Y	0.78	2.32	9	1
1:A:60:CYS:O	2:A:121:RCY:H1YA	0.78	1.78	9	1
1:A:62:THR:HG21	2:A:130:RCY:C1W	0.78	2.09	9	1
1:A:69:PRO:CG	2:A:168:RCY:C1L	0.78	2.61	7	1
2:A:173:RCY:C1L	2:A:176:RCY:H1V	0.78	2.07	20	2
2:A:160:RCY:C1V	2:A:168:RCY:H1Y	0.78	1.81	32	1
1:A:71:GLU:O	2:A:173:RCY:H1MA	0.78	1.79	21	1
2:A:130:RCY:C1S	2:A:130:RCY:C1V	0.78	2.62	51	1
1:A:64:ILE:HG22	1:A:65:THR:N	0.78	1.92	38	4
2:A:187:RCY:C1Q	2:A:187:RCY:H1VB	0.78	2.09	28	6
2:A:168:RCY:H1ZB	2:A:168:RCY:C1P	0.78	2.09	31	4
1:A:59:GLY:N	2:A:160:RCY:N1R	0.78	2.31	85	1
2:A:173:RCY:H1VB	2:A:187:RCY:C1Z	0.78	1.93	53	1
2:A:173:RCY:C1X	2:A:176:RCY:C1Y	0.78	2.53	2	1
2:A:173:RCY:N1R	2:A:176:RCY:O1H	0.78	2.16	96	1
2:A:138:RCY:H1S	2:A:160:RCY:H1U	0.78	0.81	27	1
2:A:138:RCY:C1W	2:A:150:RCY:H1LA	0.78	2.09	1	1
2:A:168:RCY:H1M	2:A:176:RCY:H1Z	0.78	1.56	66	1
2:A:168:RCY:C1V	2:A:176:RCY:H1YB	0.78	2.00	98	1
2:A:176:RCY:C1Y	2:A:187:RCY:H1LA	0.78	2.05	92	1
1:A:69:PRO:CA	2:A:173:RCY:C1V	0.77	2.62	100	2
2:A:168:RCY:C1Q	2:A:168:RCY:H1ZB	0.77	2.08	52	3
2:A:121:RCY:C1P	2:A:121:RCY:H1VB	0.77	2.09	8	4
2:A:168:RCY:H1VB	2:A:168:RCY:C1P	0.77	2.08	34	6
2:A:150:RCY:H1YB	2:A:187:RCY:C1M	0.77	2.09	41	1
2:A:168:RCY:C1P	2:A:168:RCY:H1VB	0.77	2.09	55	3
2:A:176:RCY:H1CA	2:A:187:RCY:H1M	0.77	1.56	86	1
2:A:110:RCY:H1VB	2:A:110:RCY:C1P	0.77	2.08	3	3
1:A:68:CYS:SG	2:A:173:RCY:H1ZA	0.77	2.18	39	1
2:A:168:RCY:H1ZA	2:A:173:RCY:H1VB	0.77	1.55	27	1
2:A:138:RCY:H1V	2:A:150:RCY:H1V	0.77	1.55	1	1
1:A:71:GLU:O	2:A:173:RCY:H1LA	0.77	1.01	76	2
2:A:160:RCY:C1M	2:A:168:RCY:C1W	0.77	2.62	41	2
2:A:168:RCY:H1VB	2:A:176:RCY:H1VA	0.77	1.55	59	1
2:A:168:RCY:C1C	2:A:176:RCY:H1Z	0.77	1.52	3	2
2:A:138:RCY:H1U	2:A:150:RCY:C1Q	0.77	1.67	33	1
1:A:65:THR:CG2	2:A:130:RCY:C1C	0.77	2.61	9	1
1:A:71:GLU:HA	2:A:173:RCY:N1R	0.77	1.93	11	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:69:PRO:HB3	2:A:173:RCY:C1C	0.77	2.06	7	1
2:A:138:RCY:H1Z	2:A:187:RCY:C1Y	0.77	2.09	32	1
2:A:176:RCY:C1Z	2:A:187:RCY:H1CB	0.77	2.10	2	1
2:A:138:RCY:C1M	2:A:150:RCY:C1Y	0.77	2.62	89	1
1:A:71:GLU:OE2	2:A:121:RCY:C1V	0.77	2.30	78	1
1:A:74:ASN:O	2:A:176:RCY:H1VB	0.77	1.79	100	2
2:A:130:RCY:C1P	2:A:130:RCY:H1VB	0.77	2.09	49	9
1:A:72:ALA:C	2:A:173:RCY:H1LA	0.77	1.96	30	2
2:A:160:RCY:H1Z	2:A:173:RCY:C1Z	0.77	2.04	99	1
2:A:121:RCY:H1VB	2:A:121:RCY:C1P	0.77	2.09	82	5
1:A:71:GLU:HB2	2:A:173:RCY:H1VA	0.77	1.54	33	1
2:A:130:RCY:C1M	2:A:160:RCY:H1M	0.77	2.00	7	1
2:A:160:RCY:C1W	2:A:173:RCY:C1Z	0.77	2.61	4	1
2:A:173:RCY:C1Z	2:A:176:RCY:C1V	0.77	0.78	31	1
2:A:173:RCY:H1VA	2:A:187:RCY:C1U	0.77	2.08	93	1
2:A:187:RCY:C1P	2:A:187:RCY:H1ZB	0.77	2.10	49	5
1:A:70:TRP:CD2	2:A:176:RCY:H1CA	0.77	2.12	62	1
1:A:76:CYS:H	2:A:176:RCY:C1S	0.77	1.90	24	1
2:A:138:RCY:H1VA	2:A:187:RCY:H1MA	0.77	1.55	49	1
1:A:59:GLY:H	2:A:160:RCY:C1Z	0.77	1.93	49	1
2:A:173:RCY:H1Z	2:A:187:RCY:C1V	0.77	2.10	32	1
2:A:138:RCY:C1V	2:A:187:RCY:H1M	0.77	2.09	21	1
1:A:69:PRO:HD3	2:A:168:RCY:H1VB	0.77	1.44	63	1
2:A:150:RCY:H1CB	2:A:176:RCY:C1P	0.77	2.09	82	1
2:A:138:RCY:C1Y	2:A:187:RCY:C1Z	0.77	2.61	3	2
2:A:160:RCY:O1H	2:A:168:RCY:O1J	0.77	2.02	56	1
2:A:168:RCY:H1ZB	2:A:187:RCY:H1ZB	0.77	1.55	100	1
2:A:150:RCY:C1P	2:A:150:RCY:H1ZB	0.77	2.09	12	3
1:A:70:TRP:CZ2	2:A:121:RCY:C1Z	0.77	2.63	41	1
2:A:173:RCY:C1W	2:A:176:RCY:H1YB	0.77	1.88	81	2
2:A:173:RCY:C1Y	2:A:176:RCY:H1M	0.77	2.10	99	2
2:A:150:RCY:O1J	2:A:187:RCY:H1Y	0.77	1.79	37	1
1:A:59:GLY:HA2	2:A:160:RCY:C1V	0.77	2.10	2	1
2:A:187:RCY:H1VB	2:A:187:RCY:C1P	0.77	2.08	31	3
1:A:64:ILE:HG21	2:A:168:RCY:H1ZB	0.77	1.50	83	1
2:A:168:RCY:H1MA	2:A:173:RCY:H1S	0.77	1.54	58	1
2:A:138:RCY:H1VB	2:A:138:RCY:C1Q	0.77	2.10	36	4
2:A:176:RCY:H1ZB	2:A:176:RCY:C1Q	0.77	2.08	84	5
1:A:70:TRP:CB	2:A:168:RCY:C1P	0.77	2.60	45	2
1:A:64:ILE:CG2	1:A:65:THR:H	0.77	1.92	49	4
2:A:160:RCY:C1C	2:A:168:RCY:C1L	0.77	2.50	48	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:121:RCY:O1H	2:A:121:RCY:C1V	0.77	2.26	51	2
2:A:187:RCY:C1P	2:A:187:RCY:H1CA	0.77	1.96	90	3
2:A:168:RCY:H1ZA	2:A:173:RCY:H1C	0.77	1.55	55	1
1:A:70:TRP:CD1	2:A:173:RCY:H1M	0.77	2.15	84	1
2:A:138:RCY:H1VB	2:A:150:RCY:C1S	0.77	2.09	62	1
2:A:173:RCY:H1ZB	2:A:176:RCY:H1ZB	0.77	1.55	60	1
1:A:61:GLY:CA	2:A:168:RCY:C1P	0.77	2.62	24	1
2:A:173:RCY:C1Z	2:A:187:RCY:C1Y	0.77	2.63	72	1
2:A:110:RCY:H1ZB	2:A:110:RCY:C1P	0.77	2.10	56	6
1:A:65:THR:O	1:A:66:VAL:HG23	0.77	1.80	86	1
1:A:74:ASN:H	2:A:176:RCY:C1V	0.77	1.92	62	1
2:A:173:RCY:O1J	2:A:176:RCY:O1H	0.77	2.03	70	2
2:A:150:RCY:C1Z	2:A:160:RCY:C1Q	0.77	2.63	16	1
2:A:150:RCY:H1VB	2:A:150:RCY:C1P	0.77	2.10	68	5
2:A:138:RCY:N1V	2:A:150:RCY:H1ZA	0.77	1.94	35	1
2:A:176:RCY:C1P	2:A:176:RCY:H1VB	0.77	2.08	4	4
1:A:64:ILE:CD1	2:A:187:RCY:O1G	0.77	2.28	85	1
2:A:176:RCY:H1M	2:A:187:RCY:H1U	0.77	1.57	48	1
2:A:130:RCY:H1VB	2:A:130:RCY:C1P	0.77	2.08	71	3
1:A:63:ASP:CG	2:A:160:RCY:H1CB	0.77	2.00	63	2
1:A:74:ASN:CA	2:A:176:RCY:C1P	0.77	2.31	78	1
1:A:73:CYS:C	2:A:173:RCY:C1Z	0.77	2.40	22	1
2:A:121:RCY:H1ZB	2:A:121:RCY:C1P	0.77	2.10	86	1
2:A:168:RCY:O1J	2:A:176:RCY:C1V	0.77	2.13	84	1
1:A:75:HIS:CE1	2:A:176:RCY:H1CB	0.77	2.15	84	1
2:A:168:RCY:H1L	2:A:176:RCY:H1C	0.77	1.56	49	1
1:A:70:TRP:CB	2:A:168:RCY:C1Q	0.77	2.56	20	1
2:A:168:RCY:H1U	2:A:187:RCY:H1YB	0.77	1.55	87	1
1:A:71:GLU:CD	2:A:176:RCY:C1V	0.77	2.53	92	1
1:A:76:CYS:N	2:A:176:RCY:C1L	0.77	2.48	10	2
2:A:160:RCY:C1V	2:A:168:RCY:O1J	0.77	2.33	94	3
1:A:77:GLU:CG	2:A:176:RCY:O1G	0.77	2.33	55	1
2:A:173:RCY:H1ZA	2:A:187:RCY:C1Z	0.77	2.08	40	1
2:A:160:RCY:C1M	2:A:168:RCY:C1P	0.77	2.63	34	1
1:A:60:CYS:O	1:A:62:THR:HG23	0.77	1.80	76	1
1:A:64:ILE:HD13	2:A:168:RCY:C1P	0.77	2.04	12	1
1:A:64:ILE:HD12	2:A:187:RCY:C1M	0.77	1.97	85	1
1:A:64:ILE:CG2	2:A:160:RCY:C1M	0.77	2.57	47	1
1:A:66:VAL:O	2:A:168:RCY:H1C	0.77	1.80	27	1
2:A:150:RCY:H1YA	2:A:160:RCY:H1VA	0.76	1.56	42	1
2:A:160:RCY:C1Y	2:A:168:RCY:C1L	0.76	2.61	58	5

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:160:RCY:C1Y	2:A:173:RCY:H1YA	0.76	2.10	8	1
2:A:160:RCY:H1ZB	2:A:160:RCY:C1Q	0.76	2.10	68	4
2:A:168:RCY:C1Z	2:A:173:RCY:O1G	0.76	2.31	58	1
1:A:67:ILE:HG12	2:A:160:RCY:C1C	0.76	2.07	86	1
2:A:168:RCY:H1CB	2:A:187:RCY:H1Z	0.76	1.54	64	1
2:A:130:RCY:C1M	2:A:160:RCY:C1L	0.76	2.62	18	1
1:A:66:VAL:HG13	2:A:121:RCY:C1X	0.76	2.10	4	1
2:A:138:RCY:H1YA	2:A:187:RCY:C1P	0.76	2.10	89	1
2:A:138:RCY:O1G	2:A:138:RCY:H1VB	0.76	1.80	88	2
1:A:76:CYS:H	2:A:176:RCY:C1L	0.76	1.94	10	1
2:A:160:RCY:H1MA	2:A:168:RCY:N1R	0.76	1.95	34	1
1:A:70:TRP:CH2	2:A:168:RCY:H1ZA	0.76	2.15	59	1
1:A:65:THR:HG23	1:A:65:THR:O	0.76	1.79	44	3
1:A:69:PRO:HB3	2:A:173:RCY:H1ZB	0.76	1.56	57	1
2:A:138:RCY:C1Y	2:A:173:RCY:H1ZA	0.76	2.10	32	1
2:A:173:RCY:C1W	2:A:187:RCY:C1L	0.76	2.63	96	2
2:A:130:RCY:C1Y	2:A:173:RCY:C1S	0.76	2.62	15	1
1:A:69:PRO:CD	2:A:168:RCY:C1P	0.76	2.63	13	4
1:A:62:THR:O	2:A:168:RCY:H1CB	0.76	1.78	61	1
2:A:160:RCY:C1Q	2:A:160:RCY:H1VB	0.76	2.09	54	9
2:A:173:RCY:C1S	2:A:176:RCY:O1H	0.76	2.32	54	3
2:A:173:RCY:H1V	2:A:187:RCY:C1V	0.76	1.87	55	1
2:A:130:RCY:C1Z	2:A:130:RCY:H1Y	0.76	2.08	79	1
1:A:70:TRP:CE3	2:A:168:RCY:C1P	0.76	2.68	46	1
2:A:110:RCY:C1Z	2:A:110:RCY:O1G	0.76	2.32	63	1
2:A:176:RCY:H1S	2:A:187:RCY:H1Z	0.76	1.55	80	1
2:A:160:RCY:H1Z	2:A:168:RCY:C1M	0.76	2.09	3	1
2:A:138:RCY:C1Y	2:A:150:RCY:H1C	0.76	1.92	97	1
2:A:168:RCY:C1W	2:A:187:RCY:C1W	0.76	2.31	97	1
2:A:173:RCY:H1VB	2:A:176:RCY:O1G	0.76	1.79	36	2
1:A:60:CYS:HA	2:A:160:RCY:O1H	0.76	1.78	29	3
2:A:176:RCY:C1W	2:A:187:RCY:O1G	0.76	2.33	10	1
1:A:70:TRP:CE3	2:A:173:RCY:C1Z	0.76	1.95	92	2
2:A:110:RCY:C1X	2:A:121:RCY:H1M	0.76	2.09	5	1
1:A:62:THR:CG2	2:A:130:RCY:C1U	0.76	2.64	18	1
2:A:168:RCY:H1LA	2:A:173:RCY:H1U	0.76	1.57	21	1
2:A:176:RCY:C1C	2:A:176:RCY:C1U	0.76	2.61	25	1
2:A:138:RCY:C1W	2:A:150:RCY:O1J	0.76	2.33	97	1
2:A:173:RCY:H1VB	2:A:173:RCY:C1P	0.76	2.10	46	4
2:A:176:RCY:H1VB	2:A:176:RCY:C1P	0.76	2.11	9	3
2:A:168:RCY:H1ZA	2:A:187:RCY:H1M	0.76	0.77	84	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:176:RCY:H1V	2:A:187:RCY:H1ZA	0.76	1.53	34	1
2:A:150:RCY:O1J	2:A:187:RCY:C1W	0.76	2.34	59	1
2:A:168:RCY:C1V	2:A:176:RCY:C1Q	0.76	2.64	71	1
2:A:173:RCY:H1CB	2:A:176:RCY:H1L	0.76	1.11	36	2
2:A:150:RCY:C1V	2:A:173:RCY:H1YA	0.76	2.10	39	1
2:A:176:RCY:N1V	2:A:187:RCY:C1S	0.76	2.31	96	1
2:A:138:RCY:C1V	2:A:138:RCY:O1G	0.76	2.30	54	3
2:A:160:RCY:H1VB	2:A:160:RCY:C1P	0.76	2.10	56	6
1:A:61:GLY:O	1:A:64:ILE:HG22	0.76	1.81	94	2
1:A:70:TRP:N	2:A:176:RCY:H1Z	0.76	1.94	18	1
2:A:150:RCY:C1W	2:A:187:RCY:H1YA	0.76	2.09	18	1
1:A:70:TRP:CE3	2:A:168:RCY:N1R	0.76	2.54	33	1
2:A:150:RCY:H1Y	2:A:187:RCY:H1Y	0.76	1.55	32	1
2:A:168:RCY:O1J	2:A:176:RCY:O1J	0.76	2.03	89	1
2:A:150:RCY:H1VA	2:A:173:RCY:C1X	0.76	2.10	31	1
1:A:64:ILE:CB	2:A:168:RCY:O1G	0.76	2.06	69	1
1:A:78:LEU:HD22	1:A:78:LEU:O	0.76	1.81	12	2
1:A:70:TRP:CZ3	2:A:168:RCY:H1CB	0.76	2.16	95	1
2:A:173:RCY:H1VA	2:A:176:RCY:H1CB	0.76	1.57	28	1
1:A:68:CYS:HB3	2:A:176:RCY:O1J	0.76	1.81	78	2
2:A:173:RCY:C1Z	2:A:187:RCY:H1L	0.76	2.10	45	2
1:A:76:CYS:O	1:A:76:CYS:SG	0.76	2.44	69	4
2:A:150:RCY:C1V	2:A:187:RCY:C1U	0.76	2.63	38	1
1:A:71:GLU:O	2:A:176:RCY:H1C	0.76	1.78	44	1
1:A:59:GLY:CA	2:A:160:RCY:N1R	0.76	2.45	70	1
1:A:78:LEU:HD11	2:A:176:RCY:C1P	0.76	2.11	56	1
1:A:64:ILE:HG23	2:A:168:RCY:C1Z	0.76	2.09	83	1
2:A:160:RCY:C1Z	2:A:168:RCY:H1MA	0.76	1.95	52	2
2:A:173:RCY:C1P	2:A:173:RCY:H1VB	0.76	2.10	60	3
1:A:69:PRO:HB3	2:A:173:RCY:H1Z	0.76	1.57	69	1
1:A:66:VAL:HB	2:A:138:RCY:H1V	0.76	1.58	72	1
1:A:70:TRP:CA	2:A:173:RCY:N1R	0.76	2.43	6	1
2:A:168:RCY:H1U	2:A:176:RCY:H1YA	0.76	0.77	59	1
1:A:70:TRP:HD1	2:A:187:RCY:C1Z	0.76	1.94	51	1
1:A:60:CYS:O	2:A:160:RCY:C1Q	0.76	2.33	2	1
2:A:173:RCY:C1C	2:A:176:RCY:H1Z	0.76	2.10	27	1
1:A:63:ASP:OD2	2:A:168:RCY:O1J	0.76	1.82	78	2
1:A:65:THR:HG22	1:A:65:THR:O	0.76	1.81	90	7
1:A:70:TRP:NE1	2:A:187:RCY:C1Z	0.76	2.28	92	2
2:A:160:RCY:N1R	2:A:160:RCY:H1U	0.76	1.91	79	1
1:A:73:CYS:HB2	2:A:168:RCY:C1U	0.76	2.10	57	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:160:RCY:H1Y	2:A:176:RCY:H1Y	0.76	1.58	89	1
1:A:70:TRP:CD1	2:A:168:RCY:H1L	0.76	2.16	89	1
2:A:138:RCY:C1L	2:A:150:RCY:H1M	0.76	2.10	30	1
1:A:70:TRP:N	2:A:173:RCY:C1C	0.76	2.48	92	1
2:A:138:RCY:O1H	2:A:160:RCY:C1L	0.75	2.29	38	1
1:A:69:PRO:CA	2:A:173:RCY:C1Z	0.75	2.59	75	1
2:A:173:RCY:H1Z	2:A:176:RCY:H1Z	0.75	1.57	60	1
2:A:150:RCY:O1J	2:A:187:RCY:H1CA	0.75	1.81	50	1
2:A:110:RCY:H1VB	2:A:110:RCY:C1Q	0.75	2.09	9	4
2:A:176:RCY:H1YB	2:A:187:RCY:C1M	0.75	2.11	69	1
1:A:69:PRO:HG3	2:A:176:RCY:H1YB	0.75	1.57	72	1
1:A:68:CYS:SG	2:A:176:RCY:C1Y	0.75	2.74	18	1
2:A:173:RCY:H1ZB	2:A:176:RCY:C1M	0.75	1.86	37	1
2:A:121:RCY:H1VA	2:A:168:RCY:H1YB	0.75	0.76	49	1
2:A:130:RCY:O1J	2:A:138:RCY:H1LA	0.75	1.81	73	1
1:A:74:ASN:OD1	2:A:176:RCY:C1Y	0.75	2.34	56	1
2:A:173:RCY:C1L	2:A:176:RCY:C1L	0.75	2.63	28	1
1:A:65:THR:H	2:A:168:RCY:C1L	0.75	1.94	97	1
1:A:70:TRP:CD1	1:A:70:TRP:O	0.75	2.39	86	7
2:A:130:RCY:O1G	2:A:130:RCY:H1CB	0.75	1.81	88	4
2:A:121:RCY:C1Q	2:A:121:RCY:H1ZB	0.75	2.10	14	2
1:A:73:CYS:HB2	2:A:168:RCY:C1Z	0.75	1.52	99	1
2:A:138:RCY:C1C	2:A:138:RCY:C1S	0.75	2.63	50	1
1:A:69:PRO:HB2	2:A:150:RCY:H1Y	0.75	1.59	85	1
2:A:160:RCY:H1U	2:A:168:RCY:H1C	0.75	0.81	49	1
1:A:64:ILE:CG2	2:A:168:RCY:H1C	0.75	2.10	54	1
2:A:130:RCY:H1ZB	2:A:130:RCY:O1H	0.75	1.81	2	1
2:A:138:RCY:C1Q	2:A:150:RCY:H1Z	0.75	2.04	82	1
2:A:176:RCY:H1VB	2:A:187:RCY:O1G	0.75	1.82	15	1
1:A:69:PRO:CD	2:A:173:RCY:C1C	0.75	2.64	77	1
1:A:70:TRP:C	2:A:168:RCY:H1S	0.75	2.02	28	1
1:A:60:CYS:O	2:A:168:RCY:C1Y	0.75	2.34	30	1
1:A:65:THR:HG22	2:A:160:RCY:C1M	0.75	1.78	100	2
1:A:65:THR:O	2:A:176:RCY:H1Y	0.75	1.81	22	1
1:A:70:TRP:HZ2	2:A:160:RCY:O1H	0.75	1.61	58	1
2:A:138:RCY:H1ZB	2:A:138:RCY:C1P	0.75	2.11	21	6
2:A:168:RCY:H1MA	2:A:173:RCY:H1ZB	0.75	1.48	84	1
1:A:71:GLU:N	2:A:176:RCY:C1V	0.75	2.01	76	1
2:A:150:RCY:H1Y	2:A:187:RCY:H1MA	0.75	1.37	59	1
2:A:110:RCY:C1Y	2:A:121:RCY:O1J	0.75	2.34	33	1
2:A:168:RCY:C1W	2:A:187:RCY:H1Y	0.75	2.11	7	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:168:RCY:C1U	2:A:187:RCY:C1V	0.75	2.63	90	1
2:A:168:RCY:H1L	2:A:173:RCY:H1V	0.75	0.76	4	1
2:A:138:RCY:C1M	2:A:150:RCY:C1L	0.75	2.64	1	1
2:A:121:RCY:H1VB	2:A:121:RCY:C1Q	0.75	2.12	51	4
1:A:73:CYS:HA	2:A:173:RCY:O1H	0.75	1.81	65	2
2:A:168:RCY:O1H	2:A:176:RCY:O1J	0.75	2.04	76	1
1:A:71:GLU:OE2	2:A:173:RCY:C1V	0.75	2.34	68	2
2:A:130:RCY:H1VA	2:A:173:RCY:H1YA	0.75	1.56	18	1
1:A:69:PRO:HG3	2:A:130:RCY:C1C	0.75	2.11	18	1
2:A:130:RCY:O1H	2:A:130:RCY:C1Z	0.75	2.33	2	2
2:A:168:RCY:H1Y	2:A:187:RCY:H1L	0.75	1.58	3	1
2:A:150:RCY:C1V	2:A:187:RCY:H1L	0.75	2.12	87	1
2:A:130:RCY:C1V	2:A:160:RCY:O1G	0.75	2.26	87	1
1:A:77:GLU:CG	2:A:173:RCY:O1G	0.75	2.34	28	1
2:A:138:RCY:H1C	2:A:150:RCY:H1CB	0.75	1.56	66	1
2:A:173:RCY:C1M	2:A:187:RCY:O1J	0.75	2.25	89	2
2:A:130:RCY:C1X	2:A:160:RCY:O1J	0.75	2.34	64	1
2:A:138:RCY:C1Q	2:A:138:RCY:H1VB	0.75	2.09	94	1
2:A:130:RCY:H1VA	2:A:130:RCY:O1J	0.75	1.82	79	1
2:A:168:RCY:H1CB	2:A:173:RCY:O1G	0.75	1.82	48	1
2:A:168:RCY:H1S	2:A:176:RCY:H1VB	0.75	1.56	71	1
1:A:77:GLU:CG	2:A:173:RCY:H1VB	0.75	2.09	32	1
1:A:63:ASP:OD1	2:A:150:RCY:C1Z	0.75	2.34	80	1
2:A:173:RCY:H1Y	2:A:187:RCY:C1M	0.75	2.11	77	1
2:A:150:RCY:C1W	2:A:176:RCY:C1C	0.75	2.64	3	1
2:A:138:RCY:C1X	2:A:150:RCY:C1Y	0.75	2.01	88	1
2:A:138:RCY:C1C	2:A:150:RCY:C1Y	0.75	2.57	59	1
1:A:70:TRP:HH2	2:A:168:RCY:H1ZA	0.75	1.42	59	1
1:A:60:CYS:CA	2:A:138:RCY:C1V	0.75	2.62	7	1
1:A:66:VAL:O	2:A:168:RCY:O1H	0.75	2.05	51	1
2:A:160:RCY:H1ZB	2:A:168:RCY:C1U	0.75	2.12	20	1
2:A:176:RCY:C1C	2:A:187:RCY:C1P	0.75	2.50	61	2
2:A:187:RCY:C1Q	2:A:187:RCY:H1ZB	0.75	2.12	23	4
2:A:168:RCY:O1J	2:A:187:RCY:C1C	0.75	2.34	99	1
1:A:76:CYS:CB	2:A:187:RCY:H1VB	0.75	2.10	34	1
1:A:60:CYS:O	2:A:138:RCY:H1VB	0.75	1.79	7	1
1:A:78:LEU:CD1	1:A:78:LEU:N	0.75	2.50	51	3
2:A:168:RCY:C1V	2:A:173:RCY:C1U	0.75	2.64	45	1
2:A:160:RCY:C1C	2:A:168:RCY:H1M	0.75	2.11	96	1
2:A:150:RCY:C1Y	2:A:173:RCY:C1U	0.75	2.61	3	1
2:A:138:RCY:C1P	2:A:138:RCY:H1ZB	0.75	2.11	62	6

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:71:GLU:CB	2:A:173:RCY:C1V	0.75	2.57	50	1
2:A:176:RCY:H1U	2:A:187:RCY:H1Z	0.75	0.75	5	1
1:A:78:LEU:C	1:A:78:LEU:HD22	0.75	2.02	12	2
2:A:110:RCY:C1Y	2:A:121:RCY:H1CB	0.75	2.08	81	1
2:A:160:RCY:C1C	2:A:160:RCY:C1U	0.75	2.63	79	1
2:A:138:RCY:H1YB	2:A:173:RCY:C1Z	0.75	2.10	32	1
2:A:168:RCY:O1G	2:A:173:RCY:N1V	0.75	2.19	4	1
1:A:71:GLU:OE1	2:A:173:RCY:C1Q	0.75	2.34	89	1
2:A:160:RCY:H1ZB	2:A:160:RCY:C1P	0.75	2.10	30	5
1:A:70:TRP:CH2	2:A:168:RCY:O1J	0.75	2.39	41	1
2:A:150:RCY:H1CB	2:A:150:RCY:O1G	0.75	1.82	13	4
1:A:70:TRP:CE2	2:A:168:RCY:H1LA	0.75	2.17	71	1
1:A:68:CYS:SG	2:A:173:RCY:C1V	0.75	2.70	71	1
1:A:63:ASP:O	2:A:168:RCY:H1S	0.75	1.82	80	1
1:A:70:TRP:CG	2:A:168:RCY:C1S	0.75	2.63	20	1
2:A:160:RCY:C1U	2:A:168:RCY:C1W	0.75	2.23	96	1
1:A:63:ASP:OD2	2:A:138:RCY:H1U	0.75	1.82	27	1
1:A:66:VAL:O	2:A:168:RCY:H1VA	0.75	1.81	27	1
2:A:168:RCY:H1CA	2:A:168:RCY:O1G	0.74	1.82	43	1
1:A:69:PRO:HG3	2:A:173:RCY:C1Y	0.74	2.12	61	1
1:A:76:CYS:CB	2:A:173:RCY:H1Y	0.74	2.12	42	1
1:A:70:TRP:CB	2:A:173:RCY:C1W	0.74	2.64	84	1
1:A:70:TRP:CB	2:A:168:RCY:O1J	0.74	2.36	76	1
1:A:66:VAL:CG1	2:A:160:RCY:O1H	0.74	2.34	68	1
2:A:168:RCY:H1CA	2:A:173:RCY:C1V	0.74	2.11	85	1
1:A:72:ALA:N	2:A:173:RCY:H1ZA	0.74	1.97	50	1
2:A:176:RCY:C1X	2:A:187:RCY:H1M	0.74	2.10	26	1
2:A:168:RCY:H1VA	2:A:173:RCY:H1U	0.74	1.57	45	1
2:A:160:RCY:O1H	2:A:168:RCY:H1M	0.74	1.82	39	1
1:A:60:CYS:CA	2:A:160:RCY:H1L	0.74	2.11	89	1
2:A:150:RCY:C1X	2:A:173:RCY:C1V	0.74	2.65	31	1
2:A:138:RCY:C1L	2:A:150:RCY:C1V	0.74	2.55	98	1
1:A:71:GLU:HG3	2:A:176:RCY:C1Y	0.74	2.12	92	1
2:A:138:RCY:H1ZA	2:A:176:RCY:C1L	0.74	2.12	22	1
1:A:71:GLU:HG2	2:A:130:RCY:H1M	0.74	1.58	94	1
2:A:176:RCY:H1CB	2:A:187:RCY:C1M	0.74	2.12	26	1
1:A:70:TRP:CZ2	2:A:168:RCY:C1P	0.74	2.69	48	2
2:A:173:RCY:H1CA	2:A:176:RCY:H1S	0.74	1.59	33	1
2:A:168:RCY:C1X	2:A:187:RCY:C1M	0.74	2.65	70	1
1:A:74:ASN:O	2:A:173:RCY:C1L	0.74	2.35	90	1
2:A:150:RCY:H1CB	2:A:176:RCY:C1U	0.74	2.12	82	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:160:RCY:C1U	2:A:168:RCY:H1MA	0.74	1.95	96	1
1:A:66:VAL:HG11	2:A:121:RCY:C1X	0.74	2.09	83	1
2:A:168:RCY:C1Q	2:A:168:RCY:H1VB	0.74	2.12	70	7
2:A:138:RCY:C1Y	2:A:150:RCY:C1S	0.74	2.66	60	1
1:A:70:TRP:HB3	2:A:168:RCY:O1J	0.74	1.81	76	1
1:A:69:PRO:O	2:A:173:RCY:H1ZB	0.74	1.80	85	2
2:A:121:RCY:H1ZB	2:A:121:RCY:C1S	0.74	2.11	59	1
1:A:75:HIS:HE1	2:A:173:RCY:H1YB	0.74	1.42	33	1
1:A:69:PRO:HG3	2:A:187:RCY:H1ZB	0.74	0.79	54	1
2:A:160:RCY:C1Y	2:A:168:RCY:H1YB	0.74	2.09	53	1
1:A:69:PRO:HB2	2:A:176:RCY:H1ZB	0.74	1.16	66	1
2:A:173:RCY:H1VA	2:A:176:RCY:C1P	0.74	2.11	17	1
2:A:130:RCY:H1CB	2:A:160:RCY:H1ZB	0.74	1.57	62	1
2:A:110:RCY:O1H	2:A:110:RCY:H1CB	0.74	1.83	18	4
2:A:173:RCY:H1C	2:A:176:RCY:H1ZB	0.74	1.60	27	2
2:A:138:RCY:H1Z	2:A:150:RCY:H1ZB	0.74	1.58	76	1
1:A:64:ILE:CD1	2:A:187:RCY:C1P	0.74	2.65	85	1
1:A:70:TRP:NE1	2:A:173:RCY:O1G	0.74	2.20	44	2
2:A:160:RCY:C1M	2:A:168:RCY:H1ZB	0.74	2.10	9	1
2:A:138:RCY:H1V	2:A:176:RCY:O1J	0.74	1.81	9	1
2:A:168:RCY:H1VA	2:A:173:RCY:C1U	0.74	2.12	45	1
2:A:168:RCY:C1L	2:A:173:RCY:H1VA	0.74	2.07	80	1
1:A:63:ASP:C	2:A:160:RCY:C1V	0.74	2.48	3	1
2:A:150:RCY:O1H	2:A:150:RCY:H1CB	0.74	1.83	88	3
2:A:176:RCY:C1V	2:A:187:RCY:C1V	0.74	2.36	26	2
1:A:65:THR:N	2:A:168:RCY:H1L	0.74	1.98	97	2
2:A:173:RCY:C1Z	2:A:176:RCY:H1VB	0.74	0.75	31	1
2:A:173:RCY:C1C	2:A:187:RCY:C1Q	0.74	2.66	88	1
1:A:63:ASP:OD2	2:A:121:RCY:H1YA	0.74	1.83	42	1
1:A:64:ILE:HG13	2:A:168:RCY:C1Q	0.74	2.12	58	2
2:A:150:RCY:H1CB	2:A:187:RCY:H1YB	0.74	1.56	81	1
1:A:70:TRP:HA	2:A:173:RCY:C1W	0.74	2.11	85	1
2:A:130:RCY:H1VA	2:A:160:RCY:H1V	0.74	1.59	18	1
1:A:64:ILE:HG23	2:A:160:RCY:H1CB	0.74	1.60	48	1
2:A:160:RCY:C1W	2:A:168:RCY:C1Z	0.74	2.58	9	1
1:A:62:THR:N	2:A:150:RCY:C1V	0.74	2.50	11	1
2:A:150:RCY:C1W	2:A:187:RCY:H1VB	0.74	2.13	38	1
2:A:187:RCY:C1Z	2:A:187:RCY:O1H	0.74	2.36	42	4
2:A:176:RCY:H1C	2:A:187:RCY:H1YB	0.74	1.44	26	1
2:A:150:RCY:C1Z	2:A:187:RCY:H1M	0.74	2.11	76	1
2:A:173:RCY:H1VB	2:A:176:RCY:N1V	0.74	1.96	11	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:168:RCY:H1YB	2:A:176:RCY:H1C	0.74	1.57	90	1
2:A:160:RCY:H1C	2:A:168:RCY:H1ZB	0.74	1.58	47	1
1:A:64:ILE:HD11	2:A:160:RCY:C1Y	0.74	2.12	74	1
1:A:64:ILE:HD13	2:A:160:RCY:H1VA	0.74	1.56	39	1
2:A:168:RCY:C1P	2:A:168:RCY:H1CA	0.74	2.12	53	3
2:A:138:RCY:H1V	2:A:150:RCY:H1VA	0.74	0.76	19	1
1:A:69:PRO:HG2	2:A:160:RCY:H1Y	0.74	1.57	57	1
1:A:61:GLY:CA	2:A:138:RCY:C1V	0.74	2.65	7	1
2:A:168:RCY:H1YB	2:A:173:RCY:H1VA	0.74	0.76	45	1
1:A:70:TRP:CB	2:A:168:RCY:O1G	0.74	2.35	45	2
2:A:130:RCY:O1H	2:A:130:RCY:H1CB	0.74	1.83	44	8
1:A:68:CYS:O	2:A:173:RCY:H1V	0.74	1.74	100	1
1:A:69:PRO:HB2	2:A:168:RCY:H1YB	0.74	1.56	22	1
1:A:65:THR:CG2	2:A:160:RCY:H1YA	0.74	2.03	55	1
1:A:75:HIS:CE1	2:A:176:RCY:C1C	0.74	2.70	84	1
2:A:138:RCY:O1J	2:A:160:RCY:O1H	0.74	2.04	18	1
2:A:173:RCY:H1ZA	2:A:176:RCY:H1MA	0.74	1.56	37	1
1:A:70:TRP:HZ3	2:A:160:RCY:C1Y	0.74	1.96	44	1
1:A:71:GLU:HG2	2:A:168:RCY:H1CB	0.74	0.77	93	2
2:A:168:RCY:C1Y	2:A:187:RCY:H1VA	0.74	2.12	82	1
2:A:138:RCY:C1Q	2:A:150:RCY:H1U	0.74	2.13	67	1
1:A:64:ILE:HB	2:A:160:RCY:C1Z	0.73	2.13	78	1
2:A:130:RCY:H1Y	2:A:160:RCY:C1V	0.73	2.12	43	2
2:A:168:RCY:C1Z	2:A:187:RCY:C1Z	0.73	2.64	17	1
1:A:70:TRP:HA	2:A:173:RCY:C1Q	0.73	2.12	6	2
2:A:168:RCY:C1C	2:A:173:RCY:C1Q	0.73	2.65	8	1
1:A:59:GLY:H	2:A:160:RCY:C1P	0.73	1.95	85	1
1:A:78:LEU:HD22	1:A:78:LEU:C	0.73	2.03	44	1
2:A:150:RCY:H1CB	2:A:150:RCY:O1H	0.73	1.83	9	2
1:A:71:GLU:HB3	2:A:160:RCY:H1VB	0.73	1.58	58	1
2:A:176:RCY:C1Y	2:A:187:RCY:O1J	0.73	2.32	29	1
2:A:168:RCY:O1G	2:A:173:RCY:H1CA	0.73	1.83	60	2
2:A:110:RCY:N1V	2:A:121:RCY:H1M	0.73	1.98	5	1
2:A:173:RCY:H1CB	2:A:173:RCY:O1H	0.73	1.83	81	2
2:A:138:RCY:H1CB	2:A:187:RCY:C1Y	0.73	2.09	21	1
2:A:176:RCY:H1V	2:A:187:RCY:C1L	0.73	2.13	15	1
2:A:138:RCY:H1CB	2:A:160:RCY:H1V	0.73	0.74	27	1
2:A:150:RCY:H1YB	2:A:187:RCY:O1H	0.73	1.17	27	1
1:A:70:TRP:CD1	2:A:173:RCY:H1CB	0.73	2.18	38	1
1:A:78:LEU:N	1:A:78:LEU:CD1	0.73	2.51	44	8
2:A:173:RCY:C1Z	2:A:187:RCY:C1U	0.73	2.65	77	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:70:TRP:HB2	2:A:173:RCY:N1V	0.73	1.96	64	1
1:A:68:CYS:SG	2:A:176:RCY:H1Y	0.73	2.24	18	1
1:A:70:TRP:CG	2:A:176:RCY:C1V	0.73	2.08	77	1
2:A:138:RCY:H1C	2:A:160:RCY:H1Y	0.73	1.49	27	1
2:A:173:RCY:C1Y	2:A:187:RCY:C1S	0.73	2.66	92	1
1:A:76:CYS:SG	2:A:173:RCY:C1Y	0.73	2.77	42	1
1:A:69:PRO:HA	2:A:173:RCY:C1L	0.73	2.12	10	2
2:A:160:RCY:O1H	2:A:173:RCY:C1Y	0.73	2.34	71	1
2:A:160:RCY:C1V	2:A:168:RCY:C1M	0.73	2.03	92	2
1:A:70:TRP:C	2:A:168:RCY:H1ZB	0.73	2.04	36	1
2:A:173:RCY:N1R	2:A:173:RCY:C1M	0.73	2.52	25	1
2:A:138:RCY:C1P	2:A:187:RCY:H1VA	0.73	2.13	39	1
2:A:168:RCY:C1W	2:A:176:RCY:O1G	0.73	2.34	20	1
1:A:75:HIS:C	2:A:173:RCY:H1Z	0.73	2.03	88	1
2:A:110:RCY:C1P	2:A:110:RCY:H1ZB	0.73	2.13	38	4
2:A:176:RCY:H1YB	2:A:187:RCY:H1VA	0.73	1.60	38	1
2:A:168:RCY:O1H	2:A:168:RCY:H1CB	0.73	1.84	67	3
1:A:69:PRO:HG3	2:A:173:RCY:C1V	0.73	2.12	10	2
2:A:176:RCY:H1CB	2:A:176:RCY:O1H	0.73	1.84	24	1
1:A:67:ILE:CB	2:A:176:RCY:C1V	0.73	2.65	16	1
1:A:69:PRO:HB3	2:A:168:RCY:C1Y	0.73	2.07	66	1
1:A:73:CYS:HB2	2:A:168:RCY:C1C	0.73	2.14	22	1
2:A:138:RCY:O1H	2:A:138:RCY:H1CB	0.73	1.84	60	3
2:A:138:RCY:H1CB	2:A:138:RCY:O1H	0.73	1.83	26	1
1:A:64:ILE:CB	2:A:150:RCY:H1VA	0.73	2.14	16	1
1:A:67:ILE:CG1	2:A:176:RCY:C1C	0.73	2.64	53	1
1:A:66:VAL:HG12	2:A:121:RCY:H1U	0.73	1.60	4	1
1:A:63:ASP:HA	2:A:150:RCY:H1ZA	0.73	1.59	80	1
2:A:173:RCY:O1J	2:A:176:RCY:C1P	0.73	2.36	93	3
2:A:173:RCY:H1M	2:A:176:RCY:N1R	0.73	1.98	38	1
1:A:71:GLU:HG2	2:A:173:RCY:C1V	0.73	2.13	41	1
2:A:138:RCY:C1Y	2:A:187:RCY:C1V	0.73	2.67	29	3
2:A:173:RCY:H1ZB	2:A:187:RCY:C1Z	0.73	1.81	84	1
2:A:138:RCY:C1M	2:A:187:RCY:H1U	0.73	1.92	13	1
1:A:67:ILE:CB	2:A:176:RCY:H1VA	0.73	2.14	16	1
2:A:138:RCY:C1P	2:A:187:RCY:H1CB	0.73	2.13	5	1
1:A:78:LEU:HD23	2:A:176:RCY:H1M	0.73	1.59	91	1
2:A:173:RCY:C1Z	2:A:187:RCY:H1V	0.73	2.13	32	1
1:A:75:HIS:O	2:A:176:RCY:H1ZA	0.73	1.84	67	1
2:A:173:RCY:C1Z	2:A:187:RCY:C1P	0.73	0.73	92	1
1:A:75:HIS:O	2:A:173:RCY:H1L	0.73	1.82	61	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:63:ASP:C	2:A:160:RCY:H1ZB	0.73	2.03	14	1
2:A:110:RCY:C1P	2:A:110:RCY:H1VB	0.73	2.14	12	3
1:A:72:ALA:HB3	2:A:173:RCY:H1S	0.73	1.61	65	1
2:A:110:RCY:H1CB	2:A:110:RCY:O1H	0.73	1.83	59	4
2:A:160:RCY:H1V	2:A:168:RCY:C1L	0.73	2.11	24	1
1:A:70:TRP:CE3	2:A:176:RCY:H1ZB	0.73	2.19	85	1
1:A:71:GLU:CB	2:A:173:RCY:O1G	0.73	2.37	17	1
2:A:168:RCY:C1M	2:A:173:RCY:N1V	0.73	2.51	14	1
2:A:138:RCY:H1MA	2:A:150:RCY:C1Q	0.73	2.14	41	1
1:A:73:CYS:HB3	2:A:168:RCY:C1V	0.73	2.12	57	1
2:A:160:RCY:C1U	2:A:168:RCY:H1V	0.73	2.01	48	1
2:A:168:RCY:C1U	2:A:173:RCY:H1VB	0.73	2.12	48	1
2:A:160:RCY:C1V	2:A:168:RCY:H1CB	0.73	2.05	30	2
2:A:176:RCY:H1VA	2:A:187:RCY:O1G	0.73	1.84	23	1
2:A:138:RCY:C1V	2:A:187:RCY:H1YB	0.73	2.14	11	1
1:A:59:GLY:H	2:A:138:RCY:H1S	0.73	1.42	73	1
2:A:168:RCY:H1C	2:A:176:RCY:N1V	0.73	1.99	43	1
1:A:61:GLY:O	2:A:168:RCY:C1C	0.73	2.34	61	2
2:A:160:RCY:H1Z	2:A:168:RCY:C1S	0.73	2.13	19	1
2:A:150:RCY:C1Y	2:A:187:RCY:C1P	0.73	2.67	74	3
1:A:69:PRO:CB	2:A:173:RCY:H1ZB	0.73	2.06	57	1
1:A:62:THR:CG2	2:A:130:RCY:H1MA	0.73	2.07	9	1
2:A:168:RCY:H1VB	2:A:168:RCY:C1L	0.73	2.13	7	1
2:A:138:RCY:H1C	2:A:150:RCY:C1L	0.73	2.11	53	1
1:A:66:VAL:CG1	2:A:121:RCY:C1X	0.73	2.67	83	2
1:A:70:TRP:CZ3	2:A:150:RCY:H1C	0.73	2.18	93	1
1:A:68:CYS:SG	2:A:160:RCY:H1YB	0.72	2.24	100	1
1:A:63:ASP:HB3	2:A:160:RCY:O1J	0.72	1.83	14	1
2:A:160:RCY:H1YB	2:A:168:RCY:H1ZA	0.72	1.60	62	1
1:A:70:TRP:O	2:A:176:RCY:C1C	0.72	2.37	62	1
2:A:150:RCY:O1G	2:A:150:RCY:C1V	0.72	2.36	27	5
1:A:70:TRP:HA	2:A:173:RCY:C1V	0.72	2.14	26	1
2:A:138:RCY:O1J	2:A:160:RCY:C1M	0.72	2.36	69	1
1:A:62:THR:HB	2:A:160:RCY:N1V	0.72	1.80	46	1
2:A:176:RCY:C1S	2:A:187:RCY:C1Z	0.72	2.67	80	1
2:A:150:RCY:H1VB	2:A:176:RCY:C1P	0.72	2.14	82	1
2:A:130:RCY:N1R	2:A:130:RCY:H1U	0.72	1.96	25	1
1:A:70:TRP:CZ2	2:A:173:RCY:O1G	0.72	2.42	93	1
1:A:75:HIS:N	2:A:176:RCY:H1MA	0.72	1.99	67	1
2:A:176:RCY:C1M	2:A:187:RCY:H1S	0.72	1.99	92	1
1:A:69:PRO:CA	2:A:173:RCY:H1VB	0.72	2.15	100	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:150:RCY:C1C	2:A:150:RCY:O1G	0.72	2.29	91	5
1:A:65:THR:O	1:A:65:THR:HG22	0.72	1.82	42	4
2:A:160:RCY:H1V	2:A:168:RCY:C1X	0.72	2.14	14	1
2:A:138:RCY:O1H	2:A:150:RCY:N1R	0.72	2.21	41	1
2:A:130:RCY:H1U	2:A:160:RCY:C1C	0.72	2.14	62	1
2:A:168:RCY:H1U	2:A:173:RCY:H1U	0.72	1.60	48	2
1:A:77:GLU:N	2:A:173:RCY:O1G	0.72	2.21	28	2
2:A:173:RCY:O1J	2:A:176:RCY:O1J	0.72	2.05	3	1
1:A:61:GLY:O	2:A:160:RCY:H1YA	0.72	1.83	97	1
1:A:70:TRP:N	2:A:173:RCY:H1CA	0.72	1.99	92	1
2:A:168:RCY:H1YB	2:A:173:RCY:H1ZB	0.72	1.60	100	1
1:A:76:CYS:O	2:A:176:RCY:H1LA	0.72	1.84	17	1
2:A:150:RCY:H1C	2:A:168:RCY:O1J	0.72	1.81	19	1
2:A:130:RCY:N1V	2:A:160:RCY:C1S	0.72	2.40	8	1
2:A:130:RCY:H1CB	2:A:130:RCY:O1H	0.72	1.84	63	5
1:A:70:TRP:HB3	2:A:173:RCY:H1M	0.72	1.29	84	1
2:A:138:RCY:C1X	2:A:187:RCY:H1C	0.72	2.13	5	1
1:A:60:CYS:C	2:A:130:RCY:O1H	0.72	2.27	18	1
1:A:64:ILE:CD1	2:A:160:RCY:C1V	0.72	2.67	54	1
2:A:150:RCY:O1G	2:A:187:RCY:H1Z	0.72	1.84	46	1
2:A:160:RCY:H1M	2:A:168:RCY:H1CA	0.72	1.58	94	2
1:A:72:ALA:HB3	2:A:173:RCY:H1L	0.72	0.81	10	2
2:A:138:RCY:O1J	2:A:160:RCY:H1M	0.72	1.85	69	1
1:A:68:CYS:SG	2:A:150:RCY:C1Y	0.72	2.78	85	1
2:A:173:RCY:C1C	2:A:176:RCY:H1VA	0.72	2.15	71	2
2:A:168:RCY:C1P	2:A:173:RCY:C1C	0.72	2.67	21	1
2:A:160:RCY:C1L	2:A:176:RCY:O1G	0.72	2.37	73	1
1:A:76:CYS:HA	2:A:187:RCY:H1CA	0.72	1.61	73	1
1:A:77:GLU:HG2	2:A:173:RCY:O1G	0.72	1.84	28	1
1:A:71:GLU:O	2:A:168:RCY:H1C	0.72	1.84	86	1
1:A:70:TRP:HD1	2:A:173:RCY:H1CA	0.72	0.91	64	1
2:A:168:RCY:H1ZB	2:A:176:RCY:H1Y	0.72	1.61	35	1
2:A:168:RCY:C1Z	2:A:187:RCY:O1G	0.72	2.33	3	2
1:A:66:VAL:HB	2:A:150:RCY:H1MA	0.72	1.61	31	1
1:A:72:ALA:CB	2:A:173:RCY:C1Q	0.72	2.66	80	3
1:A:69:PRO:HD2	2:A:160:RCY:C1C	0.72	2.15	35	2
2:A:138:RCY:C1Z	2:A:150:RCY:C1S	0.72	2.59	33	2
2:A:138:RCY:O1G	2:A:187:RCY:C1V	0.72	2.38	5	1
2:A:176:RCY:C1U	2:A:187:RCY:O1J	0.72	2.38	91	1
2:A:130:RCY:H1Z	2:A:173:RCY:H1U	0.72	1.60	15	1
1:A:67:ILE:H	2:A:150:RCY:C1Y	0.72	1.98	31	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:138:RCY:H1U	2:A:150:RCY:C1C	0.72	2.07	43	1
1:A:62:THR:CB	2:A:138:RCY:C1Z	0.72	2.68	38	1
2:A:138:RCY:H1M	2:A:150:RCY:H1U	0.72	1.61	60	1
2:A:173:RCY:H1Z	2:A:187:RCY:H1YA	0.72	1.60	72	1
2:A:150:RCY:H1Y	2:A:187:RCY:N1R	0.72	2.00	59	1
2:A:160:RCY:C1X	2:A:168:RCY:H1VB	0.72	2.13	48	1
2:A:130:RCY:C1V	2:A:130:RCY:C1L	0.72	2.66	7	1
2:A:168:RCY:C1W	2:A:187:RCY:C1Y	0.72	2.68	7	2
1:A:69:PRO:CA	2:A:187:RCY:H1CA	0.72	2.13	7	1
1:A:69:PRO:HB2	2:A:187:RCY:H1CA	0.72	1.59	7	1
2:A:176:RCY:H1VB	2:A:187:RCY:C1L	0.72	2.15	15	1
1:A:65:THR:N	2:A:168:RCY:C1L	0.72	2.52	97	1
2:A:138:RCY:O1J	2:A:187:RCY:C1M	0.72	2.38	52	1
2:A:160:RCY:H1ZA	2:A:168:RCY:H1V	0.72	0.72	55	1
2:A:138:RCY:H1C	2:A:187:RCY:C1Y	0.72	2.12	99	3
2:A:110:RCY:N1V	2:A:121:RCY:C1Y	0.72	2.52	5	1
2:A:138:RCY:H1ZB	2:A:150:RCY:C1S	0.72	2.13	33	1
2:A:160:RCY:O1J	2:A:168:RCY:O1H	0.72	2.06	70	2
1:A:74:ASN:CA	2:A:176:RCY:H1U	0.72	2.10	67	1
2:A:150:RCY:H1YA	2:A:187:RCY:N1R	0.72	2.00	78	1
2:A:173:RCY:O1J	2:A:187:RCY:H1CB	0.72	1.84	61	2
2:A:160:RCY:C1W	2:A:168:RCY:H1M	0.72	2.13	34	2
1:A:73:CYS:HA	2:A:173:RCY:C1Q	0.72	2.14	91	2
1:A:68:CYS:C	2:A:168:RCY:H1L	0.72	2.03	70	1
1:A:75:HIS:O	2:A:176:RCY:O1G	0.72	2.08	21	1
1:A:71:GLU:OE1	2:A:168:RCY:C1C	0.72	2.38	93	2
2:A:160:RCY:C1Z	2:A:168:RCY:C1Q	0.72	2.63	58	1
2:A:150:RCY:H1V	2:A:160:RCY:C1Z	0.72	2.15	29	1
2:A:173:RCY:H1YA	2:A:176:RCY:H1MA	0.72	1.56	99	1
1:A:61:GLY:CA	2:A:138:RCY:H1VA	0.72	2.15	7	1
2:A:173:RCY:H1VB	2:A:176:RCY:H1VA	0.72	1.60	11	1
1:A:67:ILE:HG23	2:A:130:RCY:H1YB	0.72	1.59	30	1
2:A:160:RCY:N1V	2:A:168:RCY:C1Y	0.71	2.53	78	1
2:A:168:RCY:H1ZA	2:A:173:RCY:C1Q	0.71	2.12	58	1
2:A:150:RCY:C1V	2:A:187:RCY:C1Z	0.71	2.46	64	2
1:A:64:ILE:CD1	2:A:168:RCY:N1R	0.71	2.53	12	1
2:A:138:RCY:O1G	2:A:150:RCY:O1H	0.71	2.08	23	2
1:A:70:TRP:CZ3	2:A:160:RCY:H1C	0.71	2.20	48	1
1:A:78:LEU:CD2	2:A:176:RCY:C1Z	0.71	2.67	91	1
1:A:78:LEU:HD11	2:A:176:RCY:C1L	0.71	2.13	91	1
2:A:168:RCY:C1M	2:A:173:RCY:H1VB	0.71	2.12	45	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:160:RCY:H1CA	2:A:168:RCY:H1V	0.71	1.62	96	1
1:A:67:ILE:HG23	2:A:168:RCY:C1U	0.71	2.14	83	1
1:A:71:GLU:CA	2:A:173:RCY:H1L	0.71	2.16	88	1
2:A:160:RCY:O1G	2:A:160:RCY:C1C	0.71	2.37	42	1
2:A:168:RCY:H1CB	2:A:168:RCY:O1H	0.71	1.85	47	2
2:A:130:RCY:H1ZB	2:A:130:RCY:C1Q	0.71	2.15	2	2
2:A:168:RCY:H1V	2:A:173:RCY:C1V	0.71	2.15	45	1
2:A:176:RCY:H1S	2:A:187:RCY:C1Z	0.71	2.14	80	1
2:A:168:RCY:C1Z	2:A:176:RCY:H1CB	0.71	2.15	31	1
2:A:130:RCY:H1Z	2:A:160:RCY:O1G	0.71	1.85	43	1
2:A:150:RCY:H1MA	2:A:187:RCY:C1Y	0.71	2.14	88	1
1:A:69:PRO:HD3	2:A:168:RCY:C1S	0.71	2.02	75	1
2:A:173:RCY:C1Z	2:A:176:RCY:H1YB	0.71	0.55	81	2
2:A:173:RCY:H1VA	2:A:176:RCY:H1YB	0.71	0.74	32	2
2:A:173:RCY:H1VB	2:A:176:RCY:H1C	0.71	1.62	67	2
2:A:138:RCY:C1P	2:A:150:RCY:C1W	0.71	2.69	23	1
2:A:168:RCY:H1M	2:A:176:RCY:C1V	0.71	2.15	90	1
2:A:138:RCY:H1VA	2:A:150:RCY:H1YA	0.71	1.61	97	2
2:A:138:RCY:H1L	2:A:150:RCY:H1M	0.71	1.62	30	1
2:A:173:RCY:O1H	2:A:187:RCY:C1M	0.71	2.38	40	1
2:A:168:RCY:H1CA	2:A:173:RCY:H1Y	0.71	1.61	10	1
1:A:78:LEU:CD1	2:A:176:RCY:C1Q	0.71	2.61	56	2
1:A:75:HIS:H	2:A:176:RCY:H1CA	0.71	1.39	20	1
1:A:76:CYS:SG	2:A:173:RCY:C1C	0.71	2.76	30	1
2:A:173:RCY:C1P	2:A:187:RCY:C1V	0.71	2.67	92	1
2:A:138:RCY:O1J	2:A:187:RCY:H1YB	0.71	1.85	88	3
1:A:71:GLU:HB3	2:A:173:RCY:C1M	0.71	2.14	11	1
1:A:66:VAL:O	2:A:176:RCY:C1Y	0.71	2.37	22	1
1:A:69:PRO:HB2	2:A:176:RCY:C1P	0.71	2.12	64	1
2:A:150:RCY:C1Z	2:A:187:RCY:H1CB	0.71	2.15	50	1
1:A:63:ASP:O	2:A:160:RCY:O1G	0.71	2.08	5	1
1:A:66:VAL:HG23	1:A:67:ILE:N	0.71	2.01	83	4
1:A:71:GLU:CD	2:A:173:RCY:C1C	0.71	2.44	89	1
2:A:130:RCY:H1ZB	2:A:160:RCY:H1LA	0.71	1.50	61	1
1:A:69:PRO:CG	2:A:173:RCY:C1V	0.71	2.63	10	1
2:A:150:RCY:C1V	2:A:168:RCY:C1Y	0.71	2.69	53	1
1:A:65:THR:OG1	2:A:168:RCY:H1S	0.71	1.85	87	1
2:A:138:RCY:C1V	2:A:150:RCY:C1W	0.71	2.65	1	1
1:A:64:ILE:CB	2:A:160:RCY:H1YB	0.71	2.15	49	2
2:A:150:RCY:C1P	2:A:187:RCY:H1ZA	0.71	2.15	8	1
2:A:138:RCY:H1MA	2:A:150:RCY:N1R	0.71	1.63	41	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:173:RCY:H1LA	2:A:187:RCY:H1Z	0.71	1.61	75	1
2:A:176:RCY:H1CA	2:A:187:RCY:C1C	0.71	2.14	75	1
1:A:70:TRP:CG	2:A:173:RCY:H1ZA	0.71	2.21	94	1
1:A:70:TRP:CD1	2:A:173:RCY:O1J	0.71	2.43	50	1
1:A:71:GLU:HB2	2:A:173:RCY:C1V	0.71	2.16	33	2
1:A:64:ILE:HG13	2:A:168:RCY:C1L	0.71	2.15	26	1
2:A:173:RCY:H1VB	2:A:176:RCY:H1L	0.71	1.62	35	1
1:A:69:PRO:HD2	2:A:150:RCY:H1V	0.71	1.61	85	1
1:A:64:ILE:HG23	1:A:64:ILE:O	0.71	1.84	18	1
2:A:138:RCY:C1P	2:A:138:RCY:H1VB	0.71	2.15	54	2
2:A:150:RCY:C1V	2:A:150:RCY:O1H	0.71	2.38	74	1
1:A:65:THR:CG2	2:A:160:RCY:H1CA	0.71	2.10	31	1
2:A:160:RCY:C1Z	2:A:168:RCY:C1W	0.71	2.43	78	1
2:A:173:RCY:O1J	2:A:187:RCY:H1M	0.71	1.85	43	1
2:A:138:RCY:C1X	2:A:150:RCY:C1V	0.71	2.68	19	1
2:A:138:RCY:C1C	2:A:150:RCY:C1X	0.71	2.69	10	1
2:A:138:RCY:N1R	2:A:150:RCY:O1J	0.71	2.24	81	1
1:A:70:TRP:HA	2:A:173:RCY:C1Y	0.71	2.12	85	1
2:A:160:RCY:C1M	2:A:168:RCY:N1V	0.71	2.54	9	1
1:A:70:TRP:NE1	2:A:121:RCY:N1V	0.71	2.39	49	1
1:A:70:TRP:CH2	2:A:168:RCY:H1S	0.71	2.21	54	1
1:A:64:ILE:HG22	2:A:168:RCY:C1M	0.71	2.16	95	1
1:A:66:VAL:H	2:A:168:RCY:H1C	0.71	1.43	30	1
1:A:69:PRO:HB2	2:A:173:RCY:H1CA	0.71	1.62	78	2
2:A:168:RCY:C1W	2:A:173:RCY:H1V	0.71	2.15	58	1
2:A:121:RCY:C1Q	2:A:121:RCY:C1C	0.71	2.68	35	5
2:A:168:RCY:O1H	2:A:168:RCY:C1Z	0.71	2.31	30	3
2:A:168:RCY:C1Y	2:A:173:RCY:O1G	0.71	2.34	91	1
2:A:168:RCY:H1S	2:A:173:RCY:C1U	0.71	2.00	71	1
2:A:150:RCY:H1Z	2:A:187:RCY:H1Y	0.71	1.61	9	1
1:A:70:TRP:NE1	2:A:168:RCY:H1L	0.71	2.00	89	2
1:A:68:CYS:HB3	2:A:173:RCY:H1M	0.71	1.63	73	1
2:A:173:RCY:C1C	2:A:187:RCY:H1LA	0.70	2.15	88	1
1:A:73:CYS:O	2:A:173:RCY:C1S	0.70	2.39	29	2
2:A:130:RCY:H1M	2:A:173:RCY:C1Y	0.70	2.16	94	1
2:A:168:RCY:C1P	2:A:173:RCY:H1CA	0.70	2.16	60	1
2:A:168:RCY:H1ZA	2:A:176:RCY:H1ZB	0.70	1.61	60	1
2:A:168:RCY:C1Z	2:A:173:RCY:H1ZB	0.70	2.06	60	1
1:A:73:CYS:C	2:A:173:RCY:H1CA	0.70	2.05	35	1
2:A:138:RCY:C1M	2:A:150:RCY:C1M	0.70	2.57	1	1
1:A:64:ILE:O	1:A:65:THR:CB	0.70	2.39	76	14

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:138:RCY:H1ZA	2:A:176:RCY:H1LA	0.70	1.60	22	1
1:A:75:HIS:CG	1:A:76:CYS:H	0.70	2.04	99	1
1:A:78:LEU:CD1	2:A:176:RCY:H1S	0.70	2.10	69	1
2:A:168:RCY:H1VB	2:A:176:RCY:C1V	0.70	2.14	59	1
1:A:70:TRP:HE3	2:A:168:RCY:N1R	0.70	1.84	33	2
2:A:173:RCY:C1X	2:A:187:RCY:C1Y	0.70	2.69	70	1
1:A:70:TRP:CD2	2:A:176:RCY:H1M	0.70	2.22	80	1
1:A:70:TRP:H	2:A:176:RCY:H1YB	0.70	0.85	80	1
2:A:168:RCY:H1VA	2:A:176:RCY:H1Z	0.70	1.62	3	1
1:A:67:ILE:H	2:A:168:RCY:C1C	0.70	1.99	30	1
2:A:173:RCY:H1M	2:A:176:RCY:O1G	0.70	1.87	38	1
2:A:138:RCY:H1ZA	2:A:150:RCY:C1S	0.70	2.16	60	1
2:A:160:RCY:C1U	2:A:168:RCY:C1S	0.70	2.55	34	1
2:A:150:RCY:H1ZA	2:A:187:RCY:H1VA	0.70	1.59	26	1
1:A:67:ILE:CG2	2:A:138:RCY:O1H	0.70	2.31	72	1
1:A:69:PRO:HB2	2:A:173:RCY:C1Z	0.70	1.96	35	2
2:A:130:RCY:N1V	2:A:130:RCY:C1Z	0.70	2.52	79	1
2:A:176:RCY:H1VA	2:A:187:RCY:C1Z	0.70	2.12	91	1
2:A:168:RCY:H1YB	2:A:173:RCY:C1V	0.70	1.37	45	1
2:A:138:RCY:C1P	2:A:187:RCY:C1Y	0.70	2.66	63	1
1:A:71:GLU:HG2	2:A:173:RCY:C1Y	0.70	2.16	73	1
1:A:71:GLU:CD	2:A:176:RCY:H1VA	0.70	2.06	92	1
1:A:77:GLU:HG2	2:A:176:RCY:O1G	0.70	1.84	55	1
2:A:130:RCY:H1C	2:A:160:RCY:C1C	0.70	2.16	64	1
2:A:168:RCY:C1U	2:A:176:RCY:H1C	0.70	2.17	40	1
1:A:73:CYS:HB3	2:A:168:RCY:H1Z	0.70	1.19	99	1
2:A:110:RCY:C1Q	2:A:110:RCY:C1C	0.70	2.68	50	3
2:A:138:RCY:H1C	2:A:150:RCY:H1V	0.70	0.74	54	2
1:A:70:TRP:CA	2:A:173:RCY:H1V	0.70	2.14	26	1
2:A:173:RCY:C1Q	2:A:176:RCY:C1P	0.70	2.69	59	1
1:A:68:CYS:CA	2:A:173:RCY:O1J	0.70	2.38	59	2
2:A:173:RCY:H1YB	2:A:187:RCY:C1S	0.70	2.16	45	1
1:A:72:ALA:HB2	2:A:173:RCY:C1U	0.70	2.09	80	2
2:A:150:RCY:H1ZA	2:A:187:RCY:C1L	0.70	2.15	36	1
2:A:168:RCY:C1V	2:A:176:RCY:H1MA	0.70	2.09	20	1
2:A:138:RCY:C1V	2:A:150:RCY:C1X	0.70	2.70	67	1
2:A:160:RCY:H1Z	2:A:168:RCY:C1Y	0.70	1.90	43	3
2:A:138:RCY:H1Y	2:A:187:RCY:C1V	0.70	2.17	86	1
2:A:173:RCY:H1VA	2:A:176:RCY:C1V	0.70	2.16	69	1
2:A:130:RCY:H1YA	2:A:160:RCY:H1V	0.70	1.63	81	1
1:A:71:GLU:OE1	2:A:176:RCY:H1U	0.70	1.87	37	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:64:ILE:CG2	2:A:168:RCY:H1CA	0.70	2.11	54	1
2:A:160:RCY:H1ZB	2:A:168:RCY:H1Y	0.70	1.63	78	1
2:A:187:RCY:C1P	2:A:187:RCY:C1C	0.70	2.70	71	5
1:A:70:TRP:CZ2	2:A:121:RCY:C1W	0.70	2.68	41	1
2:A:173:RCY:C1Q	2:A:173:RCY:H1VB	0.70	2.14	26	2
1:A:74:ASN:OD1	2:A:168:RCY:H1Y	0.70	1.86	91	1
2:A:138:RCY:H1Y	2:A:168:RCY:H1Y	0.70	1.61	7	1
2:A:138:RCY:H1Y	2:A:150:RCY:O1J	0.70	1.86	97	1
1:A:68:CYS:HB3	1:A:70:TRP:NE1	0.70	2.02	61	1
2:A:168:RCY:H1Z	2:A:187:RCY:H1ZB	0.70	1.64	17	2
1:A:67:ILE:CG1	2:A:168:RCY:C1C	0.70	2.65	27	1
1:A:64:ILE:O	1:A:65:THR:C	0.70	2.30	28	38
2:A:121:RCY:O1G	2:A:121:RCY:H1CB	0.70	1.86	94	4
1:A:71:GLU:CB	2:A:168:RCY:C1C	0.70	2.66	86	1
2:A:168:RCY:C1U	2:A:176:RCY:H1VA	0.70	2.16	40	1
2:A:168:RCY:C1P	2:A:173:RCY:H1ZA	0.70	2.13	10	1
2:A:138:RCY:O1J	2:A:187:RCY:H1C	0.70	1.86	26	1
2:A:138:RCY:O1G	2:A:150:RCY:C1S	0.70	2.40	81	1
2:A:138:RCY:N1R	2:A:138:RCY:H1MA	0.70	1.99	79	1
1:A:70:TRP:CZ3	2:A:160:RCY:C1Y	0.70	2.75	44	1
2:A:160:RCY:H1CB	2:A:168:RCY:C1Q	0.70	2.15	11	1
2:A:173:RCY:H1VB	2:A:187:RCY:C1Y	0.70	2.16	67	1
1:A:64:ILE:CG1	1:A:64:ILE:O	0.70	2.39	73	8
1:A:68:CYS:SG	1:A:70:TRP:CD1	0.70	2.85	17	4
1:A:70:TRP:O	1:A:70:TRP:CD1	0.70	2.45	37	8
1:A:70:TRP:HD1	2:A:187:RCY:C1M	0.70	1.99	16	1
1:A:64:ILE:HD12	2:A:168:RCY:C1Q	0.70	2.13	12	2
2:A:168:RCY:H1M	2:A:187:RCY:O1J	0.70	1.87	85	1
1:A:63:ASP:HB2	2:A:150:RCY:H1VB	0.70	1.62	85	1
1:A:71:GLU:OE2	2:A:150:RCY:O1J	0.70	2.10	32	1
2:A:168:RCY:C1P	2:A:173:RCY:H1CB	0.70	2.16	21	1
1:A:75:HIS:CG	2:A:168:RCY:H1ZB	0.70	2.21	73	1
2:A:176:RCY:C1C	2:A:176:RCY:C1P	0.70	2.69	36	2
1:A:74:ASN:CA	2:A:176:RCY:H1VA	0.70	2.10	100	1
1:A:61:GLY:C	2:A:160:RCY:H1L	0.70	1.95	19	1
2:A:176:RCY:C1C	2:A:176:RCY:C1Q	0.70	2.67	93	4
2:A:138:RCY:C1Q	2:A:176:RCY:H1V	0.70	2.17	29	1
2:A:138:RCY:H1LA	2:A:150:RCY:C1C	0.70	2.16	9	1
2:A:176:RCY:O1J	2:A:187:RCY:O1J	0.70	2.10	11	1
2:A:138:RCY:H1C	2:A:160:RCY:H1YA	0.70	0.73	27	1
2:A:160:RCY:H1Z	2:A:168:RCY:H1CB	0.70	1.63	1	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:67:ILE:CG1	2:A:168:RCY:C1U	0.70	2.48	83	1
2:A:138:RCY:O1J	2:A:187:RCY:H1YA	0.69	1.87	69	2
1:A:76:CYS:HA	2:A:173:RCY:H1CB	0.69	1.64	17	1
1:A:60:CYS:HB3	2:A:168:RCY:H1ZA	0.69	1.64	52	1
1:A:70:TRP:CH2	2:A:168:RCY:H1Y	0.69	2.22	41	1
1:A:70:TRP:CH2	2:A:176:RCY:C1Y	0.69	2.75	94	1
2:A:160:RCY:N1V	2:A:168:RCY:O1G	0.69	2.25	48	1
2:A:121:RCY:C1V	2:A:168:RCY:C1Y	0.69	2.40	49	1
1:A:66:VAL:HA	2:A:160:RCY:C1V	0.69	2.14	21	1
2:A:173:RCY:H1CA	2:A:176:RCY:C1V	0.69	2.09	63	1
1:A:68:CYS:SG	2:A:160:RCY:C1C	0.69	2.76	3	1
1:A:69:PRO:HB2	2:A:168:RCY:C1C	0.69	2.16	3	1
1:A:71:GLU:HG2	2:A:168:RCY:H1CA	0.69	1.55	93	1
2:A:173:RCY:C1V	2:A:176:RCY:H1CB	0.69	2.17	28	1
2:A:168:RCY:C1Y	2:A:176:RCY:H1Z	0.69	2.17	66	1
2:A:150:RCY:H1VB	2:A:187:RCY:C1W	0.69	2.17	64	1
2:A:138:RCY:H1YB	2:A:150:RCY:C1S	0.69	2.14	60	1
2:A:150:RCY:H1ZA	2:A:187:RCY:H1YA	0.69	1.59	9	2
2:A:150:RCY:C1S	2:A:160:RCY:C1Y	0.69	2.46	85	1
2:A:168:RCY:H1L	2:A:173:RCY:C1U	0.69	2.15	49	1
1:A:64:ILE:CG1	2:A:168:RCY:C1V	0.69	2.70	27	1
2:A:130:RCY:H1Y	2:A:176:RCY:C1C	0.69	2.17	41	1
1:A:71:GLU:O	2:A:173:RCY:C1P	0.69	2.40	94	1
2:A:168:RCY:H1ZB	2:A:176:RCY:H1ZA	0.69	1.64	6	1
2:A:130:RCY:H1M	2:A:160:RCY:C1L	0.69	2.17	18	1
1:A:75:HIS:HA	2:A:168:RCY:O1J	0.69	1.84	57	1
1:A:67:ILE:HG13	2:A:168:RCY:H1V	0.69	1.62	83	1
2:A:168:RCY:H1VB	2:A:176:RCY:H1Y	0.69	1.62	98	1
1:A:68:CYS:CB	2:A:160:RCY:H1YB	0.69	2.11	19	1
2:A:173:RCY:C1Y	2:A:176:RCY:H1YA	0.69	2.18	75	1
2:A:187:RCY:C1Q	2:A:187:RCY:C1C	0.69	2.70	70	3
2:A:150:RCY:O1J	2:A:187:RCY:H1CB	0.69	1.84	50	1
2:A:138:RCY:C1C	2:A:187:RCY:C1W	0.69	2.54	21	1
2:A:138:RCY:O1J	2:A:150:RCY:H1Z	0.69	1.87	36	1
2:A:130:RCY:H1YA	2:A:173:RCY:C1S	0.69	2.14	15	1
2:A:150:RCY:C1V	2:A:187:RCY:H1S	0.69	2.15	87	1
1:A:67:ILE:HG21	2:A:130:RCY:C1W	0.69	2.16	30	1
2:A:138:RCY:H1YB	2:A:150:RCY:C1C	0.69	2.04	97	1
1:A:74:ASN:CG	2:A:176:RCY:C1P	0.69	2.58	78	1
1:A:69:PRO:CB	2:A:187:RCY:H1VB	0.69	2.17	14	1
2:A:138:RCY:H1YA	2:A:150:RCY:H1VB	0.69	1.64	19	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:121:RCY:C1Y	2:A:187:RCY:O1G	0.69	2.41	62	1
1:A:60:CYS:C	2:A:160:RCY:C1L	0.69	2.61	2	2
2:A:173:RCY:H1CB	2:A:176:RCY:C1S	0.69	2.04	72	2
1:A:69:PRO:HD3	2:A:160:RCY:H1CA	0.69	1.63	35	1
1:A:70:TRP:CE2	2:A:121:RCY:H1VA	0.69	2.22	49	1
1:A:71:GLU:OE1	2:A:150:RCY:H1C	0.69	1.87	32	1
2:A:150:RCY:C1W	2:A:160:RCY:C1V	0.69	2.69	42	1
2:A:121:RCY:C1C	2:A:121:RCY:C1Q	0.69	2.68	3	6
2:A:138:RCY:H1Y	2:A:187:RCY:H1V	0.69	1.61	86	2
1:A:71:GLU:O	2:A:176:RCY:O1G	0.69	2.10	40	1
2:A:130:RCY:C1Z	2:A:168:RCY:H1VA	0.69	2.18	34	1
1:A:64:ILE:C	2:A:168:RCY:H1L	0.69	2.08	26	1
2:A:168:RCY:C1S	2:A:173:RCY:H1Z	0.69	2.14	5	1
1:A:66:VAL:O	2:A:168:RCY:H1SA	0.69	1.88	79	1
2:A:138:RCY:H1Y	2:A:187:RCY:H1CB	0.69	1.58	96	2
1:A:69:PRO:HB2	2:A:173:RCY:H1MA	0.69	1.64	4	1
2:A:160:RCY:H1Z	2:A:168:RCY:H1U	0.69	1.64	20	2
1:A:70:TRP:CE3	2:A:176:RCY:H1C	0.69	2.16	77	1
2:A:173:RCY:H1M	2:A:187:RCY:H1YA	0.69	0.69	31	1
1:A:71:GLU:HB2	2:A:168:RCY:C1Q	0.69	2.18	93	1
2:A:168:RCY:C1C	2:A:168:RCY:C1Q	0.69	2.70	98	1
1:A:63:ASP:O	2:A:160:RCY:C1W	0.69	2.40	78	1
2:A:138:RCY:C1U	2:A:150:RCY:C1M	0.69	2.32	75	1
2:A:138:RCY:C1V	2:A:160:RCY:C1Z	0.69	2.65	64	1
2:A:160:RCY:H1YA	2:A:168:RCY:C1Z	0.69	2.17	62	1
2:A:150:RCY:C1V	2:A:160:RCY:C1Z	0.69	2.70	29	1
2:A:150:RCY:C1Z	2:A:187:RCY:C1M	0.69	2.69	49	2
1:A:63:ASP:CB	2:A:150:RCY:C1V	0.69	2.65	85	1
1:A:77:GLU:OE2	2:A:176:RCY:H1VB	0.69	1.80	7	1
1:A:69:PRO:HG2	2:A:168:RCY:C1L	0.69	2.17	7	1
1:A:73:CYS:H	2:A:173:RCY:H1S	0.69	1.48	61	2
1:A:68:CYS:SG	1:A:69:PRO:HD2	0.69	2.28	30	5
2:A:187:RCY:C1C	2:A:187:RCY:C1Q	0.69	2.69	18	2
2:A:173:RCY:H1CB	2:A:173:RCY:O1G	0.69	1.85	47	2
1:A:76:CYS:SG	2:A:173:RCY:H1Y	0.69	2.27	42	1
2:A:160:RCY:H1V	2:A:168:RCY:O1J	0.69	1.88	14	1
2:A:176:RCY:O1H	2:A:176:RCY:H1CB	0.69	1.88	20	4
1:A:68:CYS:HB3	2:A:160:RCY:H1YB	0.69	1.65	19	2
2:A:130:RCY:C1C	2:A:130:RCY:C1Q	0.69	2.70	37	6
1:A:70:TRP:N	1:A:70:TRP:CD1	0.69	2.60	55	9
1:A:71:GLU:OE1	2:A:160:RCY:H1CB	0.69	1.88	58	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:168:RCY:C1M	2:A:176:RCY:C1Z	0.69	2.54	64	1
2:A:168:RCY:C1Z	2:A:187:RCY:C1W	0.69	2.57	84	1
1:A:75:HIS:CG	1:A:76:CYS:N	0.69	2.60	99	3
2:A:168:RCY:O1H	2:A:173:RCY:H1ZB	0.69	1.86	26	1
1:A:67:ILE:HD13	2:A:168:RCY:O1G	0.69	1.87	76	1
2:A:176:RCY:C1Q	2:A:176:RCY:H1ZB	0.69	2.15	27	3
1:A:76:CYS:HG	2:A:176:RCY:H1S	0.69	1.46	79	1
2:A:168:RCY:H1CB	2:A:173:RCY:C1P	0.69	2.17	48	1
1:A:71:GLU:CD	2:A:176:RCY:C1C	0.69	2.36	37	2
1:A:70:TRP:CH2	2:A:168:RCY:C1Y	0.69	2.66	49	1
1:A:69:PRO:CB	2:A:187:RCY:H1ZB	0.69	2.13	54	1
2:A:176:RCY:C1U	2:A:187:RCY:H1MA	0.69	2.16	96	1
1:A:70:TRP:CD1	2:A:187:RCY:H1YB	0.69	2.15	92	1
1:A:68:CYS:O	1:A:70:TRP:N	0.69	2.26	69	31
2:A:130:RCY:C1W	2:A:160:RCY:C1P	0.69	2.70	61	2
1:A:68:CYS:O	1:A:71:GLU:N	0.69	2.26	90	16
2:A:150:RCY:N1R	2:A:187:RCY:H1ZA	0.69	2.01	8	1
2:A:173:RCY:H1YB	2:A:176:RCY:H1CA	0.69	1.62	86	2
2:A:150:RCY:C1C	2:A:150:RCY:C1Q	0.69	2.69	93	4
2:A:138:RCY:C1V	2:A:176:RCY:C1C	0.69	2.49	9	1
2:A:138:RCY:O1J	2:A:150:RCY:C1U	0.69	2.41	88	1
2:A:150:RCY:H1ZB	2:A:187:RCY:C1W	0.69	2.18	88	1
2:A:168:RCY:C1C	2:A:173:RCY:O1H	0.69	2.41	8	1
2:A:138:RCY:H1L	2:A:150:RCY:C1C	0.69	2.18	94	1
1:A:70:TRP:O	2:A:173:RCY:O1H	0.69	2.10	68	1
2:A:173:RCY:C1C	2:A:173:RCY:C1Q	0.69	2.69	7	2
2:A:168:RCY:C1Y	2:A:176:RCY:C1L	0.69	2.67	20	1
2:A:138:RCY:C1W	2:A:150:RCY:C1P	0.69	2.71	1	1
1:A:68:CYS:CA	2:A:168:RCY:C1Q	0.68	2.57	87	4
1:A:67:ILE:CG1	2:A:160:RCY:H1C	0.68	2.14	86	1
1:A:75:HIS:CB	2:A:176:RCY:C1C	0.68	2.71	84	1
2:A:138:RCY:C1Q	2:A:150:RCY:C1Q	0.68	2.71	62	1
1:A:69:PRO:CG	2:A:173:RCY:H1V	0.68	2.18	10	1
2:A:138:RCY:H1VA	2:A:150:RCY:H1MA	0.68	1.64	26	1
2:A:173:RCY:C1C	2:A:176:RCY:H1ZB	0.68	2.15	27	2
2:A:150:RCY:N1V	2:A:187:RCY:C1M	0.68	2.53	59	1
2:A:173:RCY:C1V	2:A:176:RCY:C1W	0.68	2.66	32	2
1:A:70:TRP:CZ2	2:A:168:RCY:H1YA	0.68	2.22	49	1
2:A:176:RCY:C1C	2:A:187:RCY:O1J	0.68	2.42	31	1
1:A:64:ILE:CG2	2:A:160:RCY:H1ZA	0.68	2.17	1	1
2:A:168:RCY:H1Z	2:A:187:RCY:C1S	0.68	1.84	100	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:176:RCY:H1ZB	2:A:187:RCY:H1U	0.68	1.65	17	1
2:A:173:RCY:O1G	2:A:176:RCY:H1CB	0.68	1.73	64	1
1:A:64:ILE:CD1	1:A:64:ILE:N	0.68	2.56	76	2
2:A:168:RCY:H1S	2:A:176:RCY:C1V	0.68	2.17	71	1
2:A:150:RCY:H1Y	2:A:168:RCY:O1H	0.68	1.89	31	1
2:A:138:RCY:O1H	2:A:176:RCY:C1V	0.68	2.41	29	1
1:A:76:CYS:HB3	2:A:187:RCY:C1C	0.68	1.96	34	1
1:A:59:GLY:C	2:A:160:RCY:C1V	0.68	2.61	83	2
2:A:130:RCY:C1C	2:A:160:RCY:N1R	0.68	2.55	7	1
1:A:60:CYS:O	2:A:160:RCY:C1P	0.68	2.41	2	2
2:A:138:RCY:H1YB	2:A:187:RCY:C1Z	0.68	2.17	89	1
1:A:64:ILE:HD12	1:A:67:ILE:O	0.68	1.88	67	2
2:A:173:RCY:C1V	2:A:187:RCY:O1G	0.68	2.40	93	2
2:A:150:RCY:H1V	2:A:187:RCY:H1U	0.68	1.64	38	1
1:A:70:TRP:O	2:A:173:RCY:C1Z	0.68	2.42	94	1
1:A:68:CYS:O	2:A:173:RCY:O1J	0.68	2.07	50	1
2:A:138:RCY:H1ZB	2:A:187:RCY:H1ZA	0.68	1.58	77	1
1:A:60:CYS:N	2:A:160:RCY:C1Q	0.68	2.57	83	3
2:A:138:RCY:O1J	2:A:160:RCY:C1U	0.68	2.32	18	1
1:A:62:THR:HG23	2:A:130:RCY:C1U	0.68	2.18	18	1
1:A:73:CYS:CB	2:A:173:RCY:H1SA	0.68	2.18	79	1
2:A:150:RCY:H1YB	2:A:187:RCY:C1Z	0.68	2.19	21	1
1:A:64:ILE:HD11	2:A:160:RCY:C1V	0.68	2.18	54	1
1:A:74:ASN:O	2:A:187:RCY:O1J	0.68	2.11	56	1
1:A:72:ALA:H	2:A:173:RCY:H1MA	0.68	1.42	78	1
1:A:69:PRO:CG	2:A:168:RCY:C1C	0.68	2.53	8	1
1:A:70:TRP:CD2	2:A:168:RCY:O1G	0.68	2.43	94	2
2:A:176:RCY:H1MA	2:A:187:RCY:C1V	0.68	2.19	10	1
1:A:60:CYS:O	2:A:130:RCY:C1U	0.68	2.41	18	1
2:A:150:RCY:C1C	2:A:173:RCY:C1V	0.68	2.71	31	1
2:A:138:RCY:C1S	2:A:150:RCY:H1U	0.68	2.18	67	1
2:A:168:RCY:H1VB	2:A:176:RCY:H1YA	0.68	1.66	98	1
1:A:65:THR:HG21	2:A:160:RCY:H1ZB	0.68	1.61	100	1
2:A:138:RCY:H1YA	2:A:187:RCY:N1V	0.68	2.03	86	1
1:A:70:TRP:CD1	2:A:173:RCY:C1M	0.68	2.77	84	1
1:A:70:TRP:NE1	2:A:176:RCY:C1C	0.68	2.46	62	1
1:A:63:ASP:C	2:A:150:RCY:H1VB	0.68	2.09	85	1
2:A:160:RCY:N1V	2:A:168:RCY:H1YB	0.68	2.03	21	1
1:A:59:GLY:HA3	2:A:160:RCY:H1L	0.68	1.66	45	1
2:A:150:RCY:H1U	2:A:168:RCY:C1V	0.68	2.18	74	1
2:A:168:RCY:H1Y	2:A:173:RCY:H1ZB	0.68	0.69	20	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:70:TRP:NE1	2:A:168:RCY:C1L	0.68	2.56	89	1
2:A:121:RCY:H1C	2:A:168:RCY:C1C	0.68	2.19	27	1
1:A:61:GLY:O	2:A:160:RCY:H1LA	0.68	1.83	19	1
1:A:68:CYS:SG	1:A:70:TRP:NE1	0.68	2.67	40	1
1:A:70:TRP:CD1	2:A:173:RCY:H1Z	0.68	2.24	76	1
1:A:60:CYS:H	2:A:160:RCY:C1Z	0.68	2.02	91	1
2:A:160:RCY:H1C	2:A:168:RCY:C1V	0.68	2.16	44	1
1:A:76:CYS:N	2:A:173:RCY:O1G	0.68	2.26	33	1
1:A:65:THR:HG21	2:A:160:RCY:H1MA	0.68	1.66	36	2
1:A:59:GLY:N	2:A:138:RCY:C1Q	0.68	2.52	73	1
1:A:63:ASP:O	1:A:65:THR:N	0.68	2.27	88	9
2:A:173:RCY:H1ZB	2:A:187:RCY:C1Y	0.68	2.19	72	1
1:A:63:ASP:CG	2:A:150:RCY:C1P	0.68	2.51	85	1
2:A:168:RCY:H1U	2:A:176:RCY:H1VB	0.68	1.64	37	1
1:A:61:GLY:H	2:A:138:RCY:C1V	0.68	2.01	7	1
1:A:63:ASP:CB	2:A:150:RCY:C1Z	0.68	2.71	80	1
2:A:176:RCY:H1S	2:A:187:RCY:H1Y	0.68	1.65	80	1
1:A:66:VAL:CG1	2:A:121:RCY:C1M	0.68	2.71	83	1
1:A:74:ASN:HA	2:A:173:RCY:N1R	0.68	1.21	22	1
1:A:70:TRP:CB	2:A:176:RCY:C1Y	0.68	2.70	64	1
2:A:160:RCY:C1P	2:A:168:RCY:C1V	0.68	2.70	60	1
1:A:69:PRO:HG3	2:A:173:RCY:H1Z	0.68	1.65	72	1
2:A:173:RCY:H1VA	2:A:176:RCY:C1W	0.68	2.19	9	1
1:A:70:TRP:CZ2	2:A:168:RCY:H1S	0.68	2.23	54	1
2:A:138:RCY:O1J	2:A:168:RCY:O1J	0.68	2.12	82	1
1:A:76:CYS:CB	2:A:160:RCY:C1Y	0.68	2.70	73	1
1:A:74:ASN:CB	2:A:173:RCY:O1G	0.68	2.42	27	1
2:A:130:RCY:H1Z	2:A:160:RCY:C1P	0.67	2.19	43	1
2:A:168:RCY:C1Z	2:A:168:RCY:O1H	0.67	2.40	52	2
1:A:60:CYS:SG	1:A:60:CYS:O	0.67	2.52	94	3
1:A:68:CYS:C	2:A:173:RCY:O1J	0.67	2.32	50	2
1:A:63:ASP:CA	2:A:150:RCY:H1VB	0.67	2.19	85	1
1:A:64:ILE:HG12	2:A:160:RCY:H1CA	0.67	0.72	48	1
2:A:176:RCY:H1VB	2:A:187:RCY:H1VB	0.67	0.74	33	1
1:A:60:CYS:CB	2:A:168:RCY:H1CA	0.67	1.98	95	1
1:A:67:ILE:HG21	2:A:173:RCY:C1Z	0.67	2.18	80	1
2:A:130:RCY:C1Y	2:A:160:RCY:H1M	0.67	2.06	61	1
2:A:130:RCY:H1YA	2:A:160:RCY:N1R	0.67	2.04	88	1
1:A:71:GLU:CD	2:A:173:RCY:C1L	0.67	2.60	88	1
1:A:70:TRP:HE3	2:A:150:RCY:O1G	0.67	1.68	75	1
1:A:70:TRP:HB3	2:A:173:RCY:C1Y	0.67	2.20	94	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:168:RCY:H1VA	2:A:176:RCY:H1YA	0.67	0.70	76	1
2:A:138:RCY:H1V	2:A:187:RCY:C1Z	0.67	2.10	49	2
2:A:110:RCY:H1Z	2:A:121:RCY:N1V	0.67	2.04	33	1
2:A:168:RCY:H1C	2:A:173:RCY:H1Y	0.67	1.66	53	1
2:A:138:RCY:H1CB	2:A:150:RCY:O1H	0.67	1.89	82	1
2:A:168:RCY:H1ZA	2:A:176:RCY:C1C	0.67	2.18	31	1
1:A:76:CYS:CB	2:A:173:RCY:O1J	0.67	2.42	42	1
1:A:70:TRP:CH2	2:A:160:RCY:C1Q	0.67	2.76	58	1
1:A:66:VAL:HG12	2:A:121:RCY:C1U	0.67	2.19	4	1
1:A:60:CYS:C	2:A:160:RCY:C1Q	0.67	2.63	2	2
2:A:168:RCY:C1L	2:A:173:RCY:H1VB	0.67	2.04	80	1
2:A:160:RCY:H1ZA	2:A:168:RCY:O1J	0.67	1.90	39	1
2:A:173:RCY:N1R	2:A:176:RCY:C1M	0.67	2.47	67	1
2:A:138:RCY:C1Q	2:A:138:RCY:H1ZB	0.67	2.15	40	4
2:A:168:RCY:H1V	2:A:173:RCY:H1MA	0.67	1.54	29	1
1:A:64:ILE:CD1	2:A:187:RCY:H1YA	0.67	2.18	85	1
1:A:75:HIS:CA	2:A:168:RCY:O1J	0.67	2.42	57	1
1:A:63:ASP:OD2	2:A:160:RCY:C1M	0.67	2.43	73	1
2:A:173:RCY:C1X	2:A:187:RCY:H1C	0.67	2.19	55	1
1:A:71:GLU:OE1	2:A:110:RCY:C1P	0.67	2.42	5	1
2:A:110:RCY:C1C	2:A:110:RCY:C1Q	0.67	2.71	32	4
2:A:173:RCY:C1Z	2:A:187:RCY:C1V	0.67	2.72	77	2
1:A:64:ILE:HD12	1:A:68:CYS:SG	0.67	2.28	39	1
1:A:71:GLU:C	2:A:173:RCY:H1L	0.67	2.10	88	1
1:A:69:PRO:CD	2:A:168:RCY:H1CB	0.67	2.19	8	1
1:A:61:GLY:O	1:A:62:THR:HG23	0.67	1.89	60	2
1:A:74:ASN:N	2:A:173:RCY:H1S	0.67	2.04	90	2
1:A:66:VAL:O	2:A:168:RCY:C1S	0.67	2.42	79	1
2:A:150:RCY:H1VB	2:A:187:RCY:C1L	0.67	2.19	87	1
2:A:168:RCY:C1Y	2:A:176:RCY:H1ZB	0.67	2.14	66	1
1:A:69:PRO:CG	2:A:168:RCY:C1W	0.67	2.43	66	1
2:A:173:RCY:H1ZA	2:A:187:RCY:C1P	0.67	0.76	92	1
1:A:63:ASP:OD1	2:A:160:RCY:C1C	0.67	2.30	14	3
1:A:76:CYS:SG	1:A:77:GLU:N	0.67	2.68	72	7
1:A:75:HIS:HB3	2:A:176:RCY:O1J	0.67	1.89	84	1
1:A:76:CYS:CA	2:A:176:RCY:H1L	0.67	2.10	5	1
1:A:60:CYS:H	2:A:160:RCY:H1ZB	0.67	1.48	91	1
2:A:110:RCY:C1W	2:A:121:RCY:O1J	0.67	2.42	33	1
1:A:77:GLU:CB	2:A:173:RCY:O1G	0.67	2.43	28	1
1:A:70:TRP:HB3	2:A:168:RCY:C1S	0.67	2.17	19	1
2:A:176:RCY:O1G	2:A:176:RCY:H1CB	0.67	1.90	50	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:160:RCY:C1P	2:A:168:RCY:C1C	0.67	2.72	64	1
2:A:176:RCY:O1G	2:A:187:RCY:C1Z	0.67	2.41	36	2
1:A:60:CYS:C	2:A:130:RCY:C1Q	0.67	2.61	18	1
1:A:70:TRP:CZ2	2:A:168:RCY:C1L	0.67	2.77	71	2
2:A:168:RCY:H1Y	2:A:173:RCY:H1V	0.67	0.67	45	1
2:A:168:RCY:H1M	2:A:176:RCY:H1YB	0.67	1.67	98	1
1:A:70:TRP:CD1	1:A:70:TRP:N	0.67	2.62	42	6
2:A:168:RCY:H1MA	2:A:176:RCY:H1YA	0.67	1.67	14	1
2:A:173:RCY:C1Q	2:A:176:RCY:N1V	0.67	2.47	52	1
1:A:65:THR:OG1	2:A:150:RCY:H1LA	0.67	1.88	50	1
1:A:76:CYS:CB	2:A:187:RCY:C1C	0.67	2.43	34	1
1:A:64:ILE:N	1:A:64:ILE:HD12	0.67	2.03	72	2
2:A:173:RCY:H1YB	2:A:176:RCY:C1Y	0.67	2.19	59	1
1:A:78:LEU:CD2	2:A:187:RCY:N1V	0.67	2.58	91	1
1:A:64:ILE:O	2:A:168:RCY:C1L	0.67	2.42	26	2
2:A:130:RCY:H1Y	2:A:160:RCY:O1H	0.67	1.70	75	1
2:A:168:RCY:H1V	2:A:187:RCY:C1Y	0.67	2.17	40	1
1:A:73:CYS:SG	2:A:176:RCY:C1P	0.67	2.83	76	1
1:A:71:GLU:HB2	2:A:168:RCY:N1R	0.67	2.05	37	1
1:A:59:GLY:O	2:A:160:RCY:C1Q	0.67	2.43	20	2
1:A:61:GLY:O	2:A:160:RCY:C1C	0.67	2.43	11	1
2:A:168:RCY:H1YA	2:A:176:RCY:C1X	0.67	2.18	90	1
1:A:70:TRP:CE3	2:A:168:RCY:C1L	0.67	2.78	46	1
1:A:75:HIS:NE2	2:A:168:RCY:C1Z	0.67	2.58	73	1
2:A:160:RCY:N1V	2:A:168:RCY:N1V	0.66	2.40	78	1
1:A:75:HIS:O	2:A:176:RCY:H1LA	0.66	1.90	61	2
2:A:138:RCY:C1C	2:A:138:RCY:C1P	0.66	2.73	57	4
2:A:130:RCY:H1V	2:A:160:RCY:O1J	0.66	1.88	64	1
1:A:69:PRO:HB2	2:A:173:RCY:H1ZA	0.66	1.64	76	1
1:A:78:LEU:N	1:A:78:LEU:HD13	0.66	2.05	44	2
2:A:150:RCY:C1L	2:A:160:RCY:H1YB	0.66	2.21	85	1
2:A:168:RCY:H1VA	2:A:176:RCY:C1C	0.66	2.20	85	1
1:A:71:GLU:HB2	2:A:176:RCY:H1VB	0.66	1.66	49	1
1:A:73:CYS:H	2:A:173:RCY:C1P	0.66	2.03	82	1
2:A:150:RCY:C1V	2:A:173:RCY:C1Y	0.66	2.73	39	1
1:A:70:TRP:CB	2:A:168:RCY:C1C	0.66	2.61	20	1
2:A:168:RCY:O1J	2:A:187:RCY:O1G	0.66	2.13	96	1
1:A:64:ILE:HD11	2:A:168:RCY:H1V	0.66	0.74	27	1
1:A:66:VAL:HG12	2:A:121:RCY:N1V	0.66	2.06	83	1
2:A:130:RCY:N1V	2:A:160:RCY:O1G	0.66	2.25	22	2
2:A:160:RCY:C1P	2:A:160:RCY:H1CA	0.66	2.18	42	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:70:TRP:CE3	2:A:168:RCY:H1ZB	0.66	2.24	41	1
2:A:168:RCY:C1Y	2:A:173:RCY:C1V	0.66	0.66	45	2
1:A:69:PRO:CG	2:A:176:RCY:O1G	0.66	2.42	64	1
1:A:69:PRO:HD3	2:A:168:RCY:H1L	0.66	1.63	60	1
2:A:173:RCY:C1V	2:A:176:RCY:C1Z	0.66	2.67	59	2
1:A:66:VAL:CG1	2:A:121:RCY:H1U	0.66	2.21	4	1
1:A:68:CYS:N	2:A:173:RCY:H1ZA	0.66	2.03	63	1
1:A:69:PRO:CB	2:A:176:RCY:H1ZA	0.66	1.88	66	1
2:A:150:RCY:H1ZB	2:A:187:RCY:H1Y	0.66	1.67	88	1
2:A:168:RCY:C1Q	2:A:173:RCY:H1Y	0.66	2.14	84	1
1:A:70:TRP:CE3	2:A:168:RCY:C1C	0.66	2.78	94	1
2:A:138:RCY:H1ZB	2:A:138:RCY:C1Q	0.66	2.21	50	3
1:A:70:TRP:O	2:A:150:RCY:O1G	0.66	2.12	34	1
1:A:69:PRO:HG2	2:A:173:RCY:C1Y	0.66	2.13	9	1
1:A:71:GLU:N	2:A:173:RCY:C1Q	0.66	2.55	49	1
1:A:69:PRO:CA	2:A:168:RCY:C1V	0.66	2.73	63	1
1:A:65:THR:CA	2:A:168:RCY:C1L	0.66	2.73	97	1
2:A:138:RCY:O1H	2:A:150:RCY:H1V	0.66	1.72	19	1
1:A:67:ILE:O	1:A:67:ILE:CG2	0.66	2.44	23	2
1:A:71:GLU:OE2	2:A:110:RCY:C1X	0.66	2.43	5	1
1:A:70:TRP:N	2:A:173:RCY:C1L	0.66	2.48	6	1
2:A:168:RCY:C1Y	2:A:187:RCY:C1Y	0.66	2.74	7	1
2:A:168:RCY:C1V	2:A:176:RCY:H1Z	0.66	1.86	3	1
1:A:66:VAL:CG1	2:A:121:RCY:C1W	0.66	2.43	83	1
2:A:168:RCY:C1W	2:A:187:RCY:H1L	0.66	2.18	100	1
2:A:150:RCY:H1Z	2:A:160:RCY:H1Y	0.66	1.18	88	1
2:A:150:RCY:H1VA	2:A:160:RCY:H1YB	0.66	1.56	42	1
1:A:71:GLU:OE1	2:A:160:RCY:C1V	0.66	2.43	58	1
2:A:160:RCY:C1Q	2:A:168:RCY:H1LA	0.66	2.20	35	1
1:A:59:GLY:C	2:A:160:RCY:C1Q	0.66	2.64	70	2
1:A:68:CYS:HB2	2:A:173:RCY:H1ZA	0.66	1.67	11	1
2:A:173:RCY:H1VA	2:A:187:RCY:H1Y	0.66	1.67	54	1
2:A:138:RCY:N1V	2:A:187:RCY:H1CA	0.66	2.05	96	1
1:A:74:ASN:CB	2:A:176:RCY:O1G	0.66	2.44	52	2
1:A:62:THR:O	2:A:168:RCY:H1CA	0.66	1.91	61	1
2:A:160:RCY:H1M	2:A:168:RCY:O1G	0.66	1.90	24	1
1:A:59:GLY:C	2:A:160:RCY:H1VB	0.66	2.09	83	2
2:A:173:RCY:O1J	2:A:187:RCY:C1L	0.66	2.38	76	1
1:A:62:THR:HG21	2:A:130:RCY:C1X	0.66	2.19	18	1
2:A:138:RCY:H1VA	2:A:160:RCY:H1ZA	0.66	1.66	71	1
2:A:160:RCY:H1MA	2:A:168:RCY:N1V	0.66	2.06	9	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:72:ALA:O	2:A:110:RCY:C1Z	0.66	2.44	70	1
2:A:168:RCY:H1M	2:A:176:RCY:H1ZB	0.66	1.65	23	1
2:A:168:RCY:C1Y	2:A:176:RCY:H1C	0.66	2.20	90	1
2:A:168:RCY:C1Z	2:A:187:RCY:H1Z	0.66	2.18	17	1
1:A:76:CYS:O	1:A:78:LEU:N	0.66	2.28	96	8
2:A:176:RCY:C1X	2:A:187:RCY:H1YA	0.66	2.21	26	1
2:A:173:RCY:O1J	2:A:176:RCY:H1Y	0.66	1.91	82	1
1:A:64:ILE:HG13	1:A:65:THR:N	0.66	2.06	89	1
2:A:138:RCY:C1M	2:A:150:RCY:C1C	0.66	2.67	56	2
1:A:61:GLY:N	2:A:160:RCY:C1L	0.66	2.47	19	1
1:A:75:HIS:CB	2:A:176:RCY:H1C	0.66	2.20	84	1
1:A:70:TRP:NE1	2:A:160:RCY:C1V	0.66	2.59	34	1
1:A:64:ILE:CG1	2:A:168:RCY:N1R	0.66	2.59	69	1
2:A:138:RCY:O1G	2:A:187:RCY:H1VB	0.66	1.90	5	1
2:A:138:RCY:H1ZB	2:A:138:RCY:O1H	0.66	1.91	35	2
2:A:173:RCY:H1U	2:A:176:RCY:H1VB	0.66	1.31	89	1
1:A:71:GLU:HG2	2:A:150:RCY:C1Y	0.66	2.20	96	1
2:A:138:RCY:H1YA	2:A:168:RCY:O1J	0.66	1.90	19	2
1:A:64:ILE:HG12	1:A:64:ILE:O	0.66	1.89	73	4
2:A:168:RCY:H1Z	2:A:173:RCY:H1C	0.66	1.66	55	1
2:A:176:RCY:H1VA	2:A:187:RCY:C1U	0.66	2.21	29	1
2:A:176:RCY:C1C	2:A:187:RCY:H1M	0.66	2.21	26	1
1:A:69:PRO:CA	2:A:176:RCY:H1VA	0.66	2.14	72	1
2:A:173:RCY:H1S	2:A:176:RCY:O1G	0.66	1.91	71	2
1:A:78:LEU:HD21	2:A:187:RCY:C1C	0.66	1.11	91	1
1:A:71:GLU:C	2:A:173:RCY:H1V	0.66	2.11	33	1
2:A:130:RCY:C1U	2:A:160:RCY:C1Y	0.66	2.72	7	1
2:A:173:RCY:C1Q	2:A:187:RCY:C1C	0.66	2.70	7	1
1:A:63:ASP:OD1	2:A:150:RCY:C1Y	0.66	2.44	80	1
1:A:70:TRP:HA	2:A:130:RCY:O1G	0.66	1.91	27	1
2:A:138:RCY:O1H	2:A:150:RCY:H1S	0.66	1.90	41	1
2:A:168:RCY:H1CA	2:A:176:RCY:O1J	0.66	1.91	6	1
2:A:138:RCY:C1Z	2:A:187:RCY:O1H	0.66	2.00	59	1
2:A:138:RCY:C1W	2:A:187:RCY:H1CA	0.66	2.20	96	1
1:A:62:THR:O	1:A:64:ILE:N	0.65	2.30	43	32
2:A:160:RCY:C1W	2:A:168:RCY:C1M	0.65	2.63	52	1
2:A:150:RCY:C1Y	2:A:173:RCY:H1Z	0.65	2.20	8	1
2:A:187:RCY:H1CB	2:A:187:RCY:O1H	0.65	1.91	11	4
2:A:138:RCY:H1L	2:A:150:RCY:H1C	0.65	1.68	94	1
1:A:73:CYS:H	2:A:173:RCY:H1LA	0.65	1.49	80	3
2:A:150:RCY:H1U	2:A:150:RCY:N1R	0.65	1.98	25	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:71:GLU:HB3	2:A:168:RCY:C1P	0.65	2.21	11	2
2:A:168:RCY:C1Y	2:A:187:RCY:H1Z	0.65	2.16	21	1
2:A:160:RCY:C1P	2:A:176:RCY:O1G	0.65	1.84	73	1
1:A:69:PRO:CG	2:A:173:RCY:H1U	0.65	2.08	73	1
1:A:70:TRP:O	2:A:176:RCY:C1V	0.65	2.40	78	1
1:A:65:THR:C	1:A:66:VAL:HG23	0.65	2.11	73	19
1:A:74:ASN:N	2:A:173:RCY:C1L	0.65	2.58	52	4
1:A:68:CYS:SG	1:A:70:TRP:CZ2	0.65	2.90	42	1
2:A:168:RCY:C1M	2:A:173:RCY:H1YA	0.65	2.20	49	2
2:A:168:RCY:H1CA	2:A:173:RCY:C1Q	0.65	2.22	8	1
2:A:168:RCY:H1Z	2:A:173:RCY:H1VA	0.65	1.66	55	1
1:A:74:ASN:C	2:A:176:RCY:C1C	0.65	2.62	62	1
1:A:65:THR:HA	2:A:168:RCY:O1G	0.65	1.91	97	1
1:A:59:GLY:C	1:A:60:CYS:SG	0.65	2.75	91	9
1:A:69:PRO:O	2:A:173:RCY:C1Q	0.65	2.44	64	1
2:A:168:RCY:H1L	2:A:173:RCY:C1Y	0.65	2.01	62	1
1:A:68:CYS:SG	2:A:150:RCY:H1YA	0.65	2.32	85	1
2:A:173:RCY:H1ZB	2:A:176:RCY:C1V	0.65	0.79	31	2
2:A:138:RCY:C1U	2:A:150:RCY:C1Q	0.65	2.28	33	1
2:A:160:RCY:C1Y	2:A:176:RCY:C1Y	0.65	2.64	11	1
1:A:70:TRP:CG	2:A:168:RCY:H1LA	0.65	2.24	46	1
1:A:70:TRP:HB2	2:A:168:RCY:N1R	0.65	2.05	20	1
1:A:67:ILE:HD12	2:A:130:RCY:C1Y	0.65	2.20	30	1
1:A:72:ALA:HB1	2:A:173:RCY:C1Q	0.65	2.21	30	1
1:A:76:CYS:HB2	2:A:173:RCY:N1V	0.65	2.06	42	1
1:A:63:ASP:CB	2:A:150:RCY:H1VB	0.65	2.21	85	1
2:A:130:RCY:C1V	2:A:130:RCY:O1J	0.65	2.43	79	1
2:A:138:RCY:C1M	2:A:173:RCY:H1ZA	0.65	2.22	32	1
1:A:77:GLU:CA	2:A:176:RCY:H1LA	0.65	2.22	45	1
1:A:70:TRP:CZ2	1:A:71:GLU:CD	0.65	2.70	86	1
1:A:69:PRO:CG	2:A:173:RCY:C1Q	0.65	2.54	10	1
2:A:110:RCY:C1X	2:A:121:RCY:H1YB	0.65	2.09	5	1
2:A:176:RCY:O1J	2:A:187:RCY:H1ZA	0.65	1.91	71	1
1:A:69:PRO:HG2	2:A:168:RCY:H1L	0.65	1.65	7	1
2:A:160:RCY:C1X	2:A:168:RCY:H1U	0.65	2.21	47	1
2:A:168:RCY:H1YB	2:A:173:RCY:C1Z	0.65	2.21	100	1
1:A:68:CYS:SG	1:A:70:TRP:CE2	0.65	2.89	42	4
2:A:138:RCY:C1V	2:A:150:RCY:C1S	0.65	2.71	62	1
1:A:69:PRO:O	2:A:176:RCY:C1V	0.65	2.45	62	2
1:A:67:ILE:CD1	2:A:173:RCY:O1H	0.65	2.44	16	1
2:A:173:RCY:H1MA	2:A:176:RCY:O1J	0.65	1.91	68	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:60:CYS:O	2:A:138:RCY:C1Q	0.65	2.43	7	1
1:A:63:ASP:CG	2:A:160:RCY:C1C	0.65	2.62	63	2
2:A:168:RCY:C1Z	2:A:173:RCY:H1Z	0.65	2.21	31	1
2:A:150:RCY:C1V	2:A:187:RCY:C1L	0.65	2.75	87	1
2:A:173:RCY:O1G	2:A:187:RCY:C1Z	0.65	2.43	67	1
1:A:72:ALA:CB	2:A:168:RCY:H1ZB	0.65	2.21	22	1
2:A:150:RCY:H1VB	2:A:160:RCY:C1U	0.65	2.20	42	1
1:A:77:GLU:OE2	2:A:138:RCY:H1VA	0.65	1.91	52	1
1:A:71:GLU:OE1	2:A:110:RCY:H1U	0.65	1.91	5	1
1:A:64:ILE:HG13	2:A:168:RCY:H1MA	0.65	1.65	6	1
1:A:69:PRO:HG2	2:A:150:RCY:C1W	0.65	2.21	85	1
1:A:76:CYS:HG	2:A:176:RCY:C1S	0.65	2.00	79	1
2:A:160:RCY:O1H	2:A:176:RCY:C1Y	0.65	2.44	71	1
2:A:130:RCY:H1U	2:A:160:RCY:C1Y	0.65	2.22	7	1
1:A:69:PRO:CA	2:A:168:RCY:H1VA	0.65	2.21	63	1
1:A:67:ILE:CG1	2:A:168:RCY:H1U	0.65	2.21	83	1
2:A:150:RCY:C1M	2:A:187:RCY:H1YB	0.65	2.21	88	1
2:A:168:RCY:H1ZB	2:A:176:RCY:C1Y	0.65	2.22	35	2
1:A:71:GLU:CG	2:A:173:RCY:H1VA	0.65	2.21	41	1
1:A:64:ILE:HG23	1:A:66:VAL:H	0.65	1.52	83	3
2:A:168:RCY:O1G	2:A:173:RCY:C1Y	0.65	2.38	13	2
1:A:71:GLU:HB3	2:A:168:RCY:H1S	0.65	1.69	48	1
2:A:168:RCY:O1J	2:A:173:RCY:H1MA	0.65	1.92	91	1
1:A:71:GLU:HG3	2:A:121:RCY:C1Y	0.65	2.21	4	1
1:A:69:PRO:N	2:A:168:RCY:H1VA	0.65	2.05	63	1
1:A:68:CYS:SG	1:A:70:TRP:CD2	0.65	2.90	15	2
2:A:168:RCY:H1ZA	2:A:176:RCY:C1X	0.65	2.21	31	1
2:A:150:RCY:H1V	2:A:187:RCY:C1U	0.65	2.20	38	1
1:A:73:CYS:SG	2:A:176:RCY:C1C	0.65	2.84	52	1
2:A:160:RCY:H1MA	2:A:168:RCY:C1U	0.65	2.14	41	1
2:A:150:RCY:H1CB	2:A:187:RCY:O1J	0.65	1.88	84	1
2:A:110:RCY:C1W	2:A:121:RCY:H1VA	0.65	2.21	81	1
2:A:121:RCY:O1G	2:A:121:RCY:C1Z	0.65	2.40	59	1
1:A:63:ASP:CA	2:A:168:RCY:C1L	0.65	2.75	59	1
1:A:73:CYS:HB2	2:A:176:RCY:C1M	0.65	2.20	70	1
2:A:168:RCY:C1L	2:A:173:RCY:H1U	0.65	2.21	21	1
1:A:70:TRP:HE3	2:A:168:RCY:C1P	0.65	2.05	46	1
2:A:168:RCY:H1M	2:A:187:RCY:H1ZA	0.65	1.66	97	1
1:A:65:THR:CG2	1:A:65:THR:O	0.65	2.45	44	4
2:A:150:RCY:H1U	2:A:160:RCY:H1VB	0.65	1.66	42	1
1:A:63:ASP:CG	2:A:160:RCY:H1CA	0.65	2.13	14	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:168:RCY:H1C	2:A:173:RCY:H1M	0.65	0.80	99	1
1:A:64:ILE:O	1:A:64:ILE:HG22	0.65	1.92	46	3
1:A:70:TRP:N	2:A:187:RCY:C1C	0.65	2.51	7	1
2:A:173:RCY:C1L	2:A:176:RCY:H1M	0.65	2.22	20	1
2:A:130:RCY:O1J	2:A:160:RCY:C1X	0.64	2.45	64	4
2:A:130:RCY:C1C	2:A:160:RCY:C1C	0.64	2.75	8	2
1:A:74:ASN:CA	2:A:173:RCY:H1CB	0.64	2.17	35	1
2:A:176:RCY:H1CA	2:A:187:RCY:O1H	0.64	1.93	32	1
2:A:160:RCY:H1ZA	2:A:173:RCY:C1Z	0.64	2.22	4	1
2:A:138:RCY:H1C	2:A:187:RCY:H1V	0.64	1.68	63	1
2:A:176:RCY:H1S	2:A:187:RCY:C1Y	0.64	2.22	80	1
2:A:160:RCY:H1ZB	2:A:168:RCY:H1U	0.64	1.68	20	1
1:A:71:GLU:HG2	2:A:176:RCY:H1ZA	0.64	1.68	20	1
2:A:138:RCY:C1W	2:A:150:RCY:C1Y	0.64	2.73	89	1
1:A:70:TRP:CG	2:A:168:RCY:H1VB	0.64	2.26	28	1
1:A:75:HIS:O	1:A:76:CYS:O	0.64	2.15	48	10
1:A:63:ASP:HA	2:A:168:RCY:H1U	0.64	1.69	61	1
2:A:150:RCY:H1V	2:A:160:RCY:N1V	0.64	2.08	42	1
2:A:176:RCY:C1Z	2:A:176:RCY:O1G	0.64	2.45	89	2
1:A:65:THR:CG2	2:A:168:RCY:H1CB	0.64	2.22	60	1
2:A:138:RCY:C1S	2:A:160:RCY:H1ZB	0.64	2.17	18	1
2:A:168:RCY:C1M	2:A:187:RCY:C1W	0.64	2.30	7	2
2:A:130:RCY:C1W	2:A:130:RCY:O1H	0.64	2.43	2	1
2:A:150:RCY:C1V	2:A:187:RCY:C1S	0.64	2.76	87	1
1:A:67:ILE:C	2:A:168:RCY:H1ZA	0.64	2.10	83	1
1:A:70:TRP:HD1	2:A:187:RCY:C1Y	0.64	1.88	92	1
2:A:130:RCY:H1Y	2:A:176:RCY:C1X	0.64	1.88	41	1
2:A:160:RCY:H1ZA	2:A:168:RCY:H1M	0.64	1.67	34	2
2:A:130:RCY:O1J	2:A:160:RCY:H1S	0.64	1.92	86	1
2:A:130:RCY:C1V	2:A:173:RCY:C1Y	0.64	2.73	94	1
1:A:75:HIS:HB2	2:A:176:RCY:C1L	0.64	2.17	13	1
2:A:173:RCY:H1VB	2:A:176:RCY:C1M	0.64	2.06	69	1
1:A:69:PRO:O	2:A:173:RCY:C1U	0.64	2.42	76	1
2:A:168:RCY:H1U	2:A:187:RCY:H1Y	0.64	1.63	87	1
1:A:69:PRO:HG3	2:A:150:RCY:H1ZA	0.64	1.69	92	1
2:A:160:RCY:C1P	2:A:168:RCY:O1J	0.64	2.45	64	1
1:A:75:HIS:ND1	1:A:76:CYS:N	0.64	2.45	99	4
1:A:70:TRP:CG	1:A:70:TRP:O	0.64	2.49	34	4
2:A:176:RCY:H1VB	2:A:187:RCY:H1YA	0.64	1.69	26	1
1:A:63:ASP:HA	2:A:150:RCY:C1Z	0.64	2.22	80	1
2:A:160:RCY:H1Z	2:A:173:RCY:H1Y	0.64	1.68	39	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:168:RCY:H1ZB	2:A:187:RCY:C1Z	0.64	2.22	100	1
1:A:67:ILE:CD1	2:A:173:RCY:C1Y	0.64	2.68	100	1
1:A:64:ILE:O	1:A:68:CYS:SG	0.64	2.55	100	10
1:A:69:PRO:HD3	2:A:168:RCY:N1R	0.64	2.07	8	1
1:A:75:HIS:CB	2:A:187:RCY:C1Z	0.64	2.75	56	1
1:A:74:ASN:CA	2:A:176:RCY:C1U	0.64	2.73	67	1
1:A:69:PRO:HB2	2:A:176:RCY:H1M	0.64	1.69	43	1
2:A:130:RCY:C1P	2:A:130:RCY:C1C	0.64	2.71	9	5
1:A:64:ILE:HD13	1:A:64:ILE:C	0.64	2.12	17	2
1:A:74:ASN:N	2:A:173:RCY:H1LA	0.64	2.03	33	3
1:A:69:PRO:C	2:A:173:RCY:O1H	0.64	2.35	64	1
1:A:70:TRP:CE2	2:A:176:RCY:H1CA	0.64	2.27	62	1
2:A:176:RCY:C1Q	2:A:176:RCY:C1C	0.64	2.76	29	3
1:A:73:CYS:CB	2:A:168:RCY:H1Z	0.64	1.24	99	1
2:A:138:RCY:O1J	2:A:150:RCY:H1Y	0.64	1.93	6	2
1:A:70:TRP:CG	2:A:173:RCY:H1VB	0.64	2.24	4	1
1:A:70:TRP:HE3	2:A:168:RCY:C1L	0.64	2.05	46	2
2:A:173:RCY:H1C	2:A:187:RCY:C1W	0.64	2.19	97	1
2:A:173:RCY:C1P	2:A:173:RCY:C1C	0.64	2.74	69	6
1:A:63:ASP:OD2	2:A:121:RCY:C1Y	0.64	2.45	42	1
1:A:63:ASP:CA	2:A:160:RCY:C1Z	0.64	2.69	14	1
2:A:130:RCY:C1M	2:A:173:RCY:H1YA	0.64	2.18	94	1
1:A:73:CYS:HA	2:A:173:RCY:C1P	0.64	2.22	33	1
2:A:138:RCY:C1V	2:A:176:RCY:O1J	0.64	2.46	9	1
2:A:150:RCY:C1U	2:A:187:RCY:H1L	0.64	1.91	27	1
1:A:74:ASN:O	2:A:187:RCY:C1X	0.64	2.42	56	1
2:A:150:RCY:H1VA	2:A:160:RCY:H1YA	0.64	0.64	42	1
2:A:160:RCY:C1C	2:A:168:RCY:C1P	0.64	2.75	19	2
2:A:160:RCY:H1YB	2:A:168:RCY:C1Q	0.64	2.23	58	1
2:A:138:RCY:C1Z	2:A:187:RCY:H1Y	0.64	2.22	94	1
1:A:60:CYS:CA	2:A:160:RCY:H1VB	0.64	2.21	72	1
2:A:173:RCY:C1V	2:A:176:RCY:N1V	0.64	2.57	11	2
1:A:70:TRP:CA	2:A:173:RCY:H1Y	0.64	2.19	85	1
1:A:71:GLU:HA	2:A:168:RCY:C1W	0.64	2.22	37	1
1:A:70:TRP:HE3	2:A:168:RCY:C1M	0.64	2.02	44	1
1:A:70:TRP:NE1	2:A:121:RCY:C1M	0.64	2.48	49	1
2:A:168:RCY:N1R	2:A:168:RCY:H1U	0.64	1.97	25	1
2:A:160:RCY:C1Z	2:A:173:RCY:H1C	0.64	2.23	20	1
2:A:173:RCY:H1V	2:A:187:RCY:C1Y	0.64	2.22	31	1
1:A:77:GLU:N	2:A:176:RCY:C1S	0.64	2.59	87	1
2:A:110:RCY:C1M	2:A:121:RCY:C1Y	0.64	2.69	22	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:176:RCY:C1C	2:A:187:RCY:C1Z	0.64	2.76	99	1
2:A:187:RCY:O1H	2:A:187:RCY:H1CB	0.64	1.92	26	3
1:A:63:ASP:C	2:A:168:RCY:H1VA	0.64	1.88	5	1
2:A:130:RCY:C1V	2:A:173:RCY:C1S	0.64	2.76	5	1
1:A:69:PRO:HB3	2:A:173:RCY:C1Y	0.64	2.00	9	1
2:A:160:RCY:H1U	2:A:168:RCY:C1X	0.64	2.13	49	1
1:A:61:GLY:C	2:A:150:RCY:C1V	0.64	2.66	11	1
2:A:173:RCY:C1P	2:A:187:RCY:H1VA	0.64	2.23	89	1
1:A:74:ASN:O	2:A:176:RCY:O1H	0.64	2.16	44	2
1:A:70:TRP:CB	2:A:168:RCY:C1S	0.64	2.75	20	2
2:A:176:RCY:H1CA	2:A:176:RCY:O1H	0.64	1.91	29	1
2:A:168:RCY:H1M	2:A:187:RCY:H1YA	0.64	1.70	40	1
1:A:75:HIS:C	2:A:176:RCY:O1H	0.64	2.36	67	2
2:A:176:RCY:H1VB	2:A:187:RCY:H1V	0.64	0.73	26	1
1:A:67:ILE:HA	2:A:176:RCY:H1VA	0.64	0.72	16	1
2:A:130:RCY:H1VA	2:A:130:RCY:N1V	0.64	2.07	79	1
1:A:63:ASP:OD2	2:A:138:RCY:C1U	0.64	2.44	27	1
2:A:110:RCY:C1C	2:A:110:RCY:C1P	0.63	2.76	43	5
2:A:173:RCY:O1H	2:A:176:RCY:H1MA	0.63	1.94	61	1
2:A:130:RCY:C1Y	2:A:160:RCY:O1H	0.63	2.38	88	2
2:A:173:RCY:C1U	2:A:176:RCY:C1P	0.63	2.73	38	1
2:A:150:RCY:H1YB	2:A:187:RCY:C1V	0.63	2.22	38	1
1:A:60:CYS:CB	2:A:168:RCY:H1ZA	0.63	2.23	52	1
2:A:160:RCY:H1LA	2:A:168:RCY:H1CA	0.63	1.67	64	1
2:A:130:RCY:C1C	2:A:130:RCY:C1P	0.63	2.71	92	5
1:A:69:PRO:CA	2:A:176:RCY:H1YA	0.63	2.22	72	1
1:A:71:GLU:CG	2:A:168:RCY:C1L	0.63	2.76	32	1
1:A:69:PRO:CD	2:A:168:RCY:C1Q	0.63	2.75	90	2
2:A:130:RCY:C1P	2:A:160:RCY:H1Z	0.63	2.22	67	1
1:A:64:ILE:CB	2:A:168:RCY:H1ZB	0.63	2.09	30	1
1:A:65:THR:CB	2:A:160:RCY:C1W	0.63	2.72	100	1
1:A:74:ASN:ND2	1:A:75:HIS:CD2	0.63	2.66	38	1
1:A:77:GLU:CB	2:A:176:RCY:O1G	0.63	2.45	55	1
2:A:160:RCY:H1ZA	2:A:168:RCY:C1M	0.63	2.24	34	2
1:A:71:GLU:CG	2:A:168:RCY:O1G	0.63	2.21	99	2
1:A:73:CYS:N	2:A:168:RCY:C1M	0.63	2.61	99	1
1:A:62:THR:HB	2:A:160:RCY:H1CA	0.63	0.93	46	1
2:A:160:RCY:H1Y	2:A:168:RCY:H1CB	0.63	1.70	87	1
1:A:73:CYS:HB2	2:A:176:RCY:O1J	0.63	1.92	84	1
1:A:70:TRP:CZ2	2:A:176:RCY:O1J	0.63	2.51	94	1
2:A:168:RCY:C1S	2:A:173:RCY:H1ZB	0.63	2.23	10	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:168:RCY:N1V	2:A:173:RCY:C1P	0.63	2.60	37	1
2:A:173:RCY:H1VB	2:A:176:RCY:C1X	0.63	2.23	11	1
1:A:64:ILE:CD1	2:A:160:RCY:H1C	0.63	2.24	39	1
1:A:70:TRP:HH2	2:A:150:RCY:O1J	0.63	1.69	93	1
2:A:150:RCY:H1ZB	2:A:187:RCY:H1Z	0.63	1.69	88	1
2:A:150:RCY:H1V	2:A:187:RCY:C1Z	0.63	2.24	41	1
1:A:70:TRP:HE3	2:A:168:RCY:C1Z	0.63	2.01	41	1
2:A:121:RCY:H1YA	2:A:187:RCY:O1G	0.63	1.92	62	1
2:A:138:RCY:C1Z	2:A:150:RCY:O1H	0.63	2.45	60	1
1:A:78:LEU:HD13	2:A:138:RCY:H1VA	0.63	1.71	40	1
2:A:173:RCY:H1V	2:A:176:RCY:O1H	0.63	1.92	69	1
1:A:70:TRP:CA	2:A:173:RCY:C1W	0.63	2.75	85	1
1:A:70:TRP:CZ3	2:A:168:RCY:O1G	0.63	2.50	46	2
1:A:70:TRP:N	2:A:176:RCY:C1Y	0.63	2.46	80	1
2:A:168:RCY:H1C	2:A:176:RCY:H1YB	0.63	1.70	74	1
2:A:160:RCY:C1Z	2:A:168:RCY:O1J	0.63	2.43	39	1
2:A:173:RCY:C1Q	2:A:176:RCY:H1V	0.63	2.23	31	1
1:A:68:CYS:SG	1:A:69:PRO:CD	0.63	2.87	30	1
2:A:173:RCY:C1X	2:A:176:RCY:H1M	0.63	2.23	69	2
1:A:70:TRP:CB	2:A:168:RCY:H1L	0.63	2.23	94	3
2:A:168:RCY:H1LA	2:A:173:RCY:H1ZB	0.63	1.64	10	1
1:A:66:VAL:HB	2:A:138:RCY:C1V	0.63	2.23	72	1
2:A:173:RCY:H1YA	2:A:176:RCY:C1Y	0.63	2.15	59	1
1:A:64:ILE:CD1	1:A:64:ILE:O	0.63	2.47	73	2
1:A:70:TRP:CZ2	2:A:168:RCY:H1L	0.63	2.23	48	1
2:A:168:RCY:C1P	2:A:176:RCY:C1M	0.63	2.73	71	1
2:A:160:RCY:C1X	2:A:168:RCY:H1M	0.63	2.23	96	1
2:A:168:RCY:H1Z	2:A:176:RCY:H1CB	0.63	1.71	31	1
2:A:173:RCY:H1ZB	2:A:173:RCY:O1G	0.63	1.94	17	2
1:A:64:ILE:CG2	1:A:65:THR:N	0.63	2.62	53	9
2:A:187:RCY:C1C	2:A:187:RCY:C1P	0.63	2.70	90	4
1:A:74:ASN:N	2:A:168:RCY:C1Y	0.63	2.57	91	1
1:A:67:ILE:O	2:A:168:RCY:C1Q	0.63	2.46	63	2
2:A:160:RCY:H1Y	2:A:168:RCY:C1S	0.63	2.23	1	1
2:A:138:RCY:C1P	2:A:138:RCY:C1C	0.63	2.74	10	7
2:A:176:RCY:C1Z	2:A:187:RCY:C1Z	0.63	2.69	38	1
1:A:75:HIS:CD2	2:A:173:RCY:H1ZB	0.63	2.17	42	1
1:A:69:PRO:CG	2:A:187:RCY:H1V	0.63	2.24	14	1
1:A:71:GLU:HB3	2:A:160:RCY:C1V	0.63	2.24	58	1
2:A:168:RCY:H1VA	2:A:173:RCY:C1Q	0.63	2.19	76	1
2:A:160:RCY:O1J	2:A:168:RCY:H1VA	0.63	1.93	70	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:176:RCY:C1V	2:A:187:RCY:H1ZA	0.63	2.24	57	1
2:A:160:RCY:H1C	2:A:168:RCY:C1P	0.63	2.23	48	1
2:A:121:RCY:C1Y	2:A:160:RCY:C1Z	0.63	2.38	44	1
2:A:176:RCY:N1V	2:A:187:RCY:H1VA	0.63	2.07	33	1
1:A:70:TRP:CD2	2:A:168:RCY:H1M	0.63	2.27	49	1
1:A:64:ILE:O	1:A:65:THR:HG23	0.63	1.93	11	1
2:A:138:RCY:H1YB	2:A:173:RCY:H1MA	0.63	1.69	32	1
2:A:168:RCY:H1Y	2:A:187:RCY:C1V	0.63	2.24	74	1
1:A:71:GLU:CG	2:A:176:RCY:H1ZA	0.63	2.08	20	1
1:A:70:TRP:CB	2:A:121:RCY:H1VB	0.63	2.16	30	1
1:A:65:THR:O	2:A:168:RCY:C1V	0.63	2.47	17	1
1:A:72:ALA:N	2:A:173:RCY:C1Q	0.63	2.62	50	1
1:A:64:ILE:HG13	2:A:168:RCY:C1P	0.63	2.20	69	2
2:A:176:RCY:C1U	2:A:187:RCY:C1V	0.63	2.68	81	1
2:A:138:RCY:C1V	2:A:187:RCY:C1P	0.63	2.77	21	1
1:A:67:ILE:CB	2:A:173:RCY:H1M	0.63	2.23	80	1
2:A:138:RCY:H1CB	2:A:150:RCY:C1Q	0.63	2.22	82	1
1:A:70:TRP:CA	2:A:168:RCY:H1ZB	0.63	2.24	36	1
1:A:77:GLU:H	2:A:173:RCY:C1P	0.63	2.07	28	1
2:A:176:RCY:O1J	2:A:187:RCY:H1YA	0.63	1.94	55	1
2:A:176:RCY:N1R	2:A:187:RCY:H1M	0.63	2.09	26	1
1:A:62:THR:OG1	1:A:66:VAL:HG22	0.63	1.94	68	1
2:A:168:RCY:H1VB	2:A:173:RCY:O1H	0.63	1.94	57	1
2:A:150:RCY:H1YB	2:A:160:RCY:O1G	0.63	1.94	91	1
2:A:168:RCY:H1YB	2:A:187:RCY:H1ZA	0.63	1.70	47	1
2:A:130:RCY:C1Y	2:A:160:RCY:H1YA	0.63	2.23	67	1
1:A:63:ASP:C	2:A:160:RCY:C1Z	0.62	2.58	78	2
1:A:62:THR:HG23	2:A:130:RCY:C1Z	0.62	2.23	88	1
2:A:160:RCY:H1MA	2:A:168:RCY:H1M	0.62	0.69	41	1
1:A:72:ALA:N	2:A:168:RCY:C1C	0.62	2.61	86	1
1:A:67:ILE:HG13	2:A:176:RCY:H1V	0.62	0.68	16	1
2:A:130:RCY:C1V	2:A:160:RCY:H1V	0.62	2.23	18	1
2:A:160:RCY:C1Q	2:A:160:RCY:H1ZB	0.62	2.22	91	1
1:A:62:THR:N	2:A:150:RCY:H1VB	0.62	2.08	11	1
1:A:71:GLU:CA	2:A:173:RCY:C1M	0.62	2.76	11	1
1:A:78:LEU:HD13	1:A:78:LEU:N	0.62	2.07	51	1
1:A:68:CYS:SG	1:A:70:TRP:CG	0.62	2.92	15	1
2:A:173:RCY:C1Z	2:A:176:RCY:H1VA	0.62	1.19	31	1
2:A:168:RCY:C1Z	2:A:176:RCY:C1C	0.62	2.77	31	1
1:A:64:ILE:CG2	2:A:168:RCY:C1L	0.62	2.71	1	1
1:A:64:ILE:CG2	1:A:64:ILE:O	0.62	2.47	98	5

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:110:RCY:O1G	2:A:110:RCY:C1V	0.62	2.35	65	2
2:A:160:RCY:N1V	2:A:168:RCY:C1P	0.62	2.62	48	1
1:A:60:CYS:O	2:A:138:RCY:C1P	0.62	2.46	7	1
1:A:69:PRO:CG	2:A:187:RCY:O1G	0.62	2.47	95	1
2:A:176:RCY:H1VA	2:A:187:RCY:H1LA	0.62	1.68	15	1
2:A:173:RCY:H1VB	2:A:176:RCY:H1U	0.62	1.65	38	1
1:A:74:ASN:N	2:A:176:RCY:C1C	0.62	2.41	20	2
1:A:68:CYS:SG	2:A:160:RCY:C1M	0.62	2.85	58	1
2:A:168:RCY:C1V	2:A:173:RCY:C1W	0.62	2.77	29	1
2:A:173:RCY:H1Z	2:A:187:RCY:C1Y	0.62	2.23	72	1
2:A:168:RCY:H1YB	2:A:187:RCY:H1Y	0.62	1.69	7	1
1:A:71:GLU:HG3	2:A:168:RCY:C1L	0.62	2.24	32	1
2:A:176:RCY:H1YB	2:A:187:RCY:H1Z	0.62	1.71	47	1
1:A:71:GLU:N	2:A:173:RCY:H1V	0.62	2.06	78	1
1:A:67:ILE:HD13	2:A:130:RCY:H1Y	0.62	1.67	78	1
2:A:173:RCY:O1J	2:A:187:RCY:C1P	0.62	2.48	61	1
1:A:70:TRP:CH2	2:A:130:RCY:H1Y	0.62	2.29	88	1
2:A:160:RCY:O1G	2:A:168:RCY:H1VA	0.62	1.95	60	1
2:A:150:RCY:H1Y	2:A:187:RCY:C1P	0.62	2.23	59	1
1:A:69:PRO:HG2	2:A:150:RCY:N1V	0.62	2.09	85	1
1:A:61:GLY:O	2:A:168:RCY:C1Q	0.62	2.46	11	1
1:A:76:CYS:CB	2:A:160:RCY:N1V	0.62	2.57	73	1
2:A:150:RCY:C1U	2:A:168:RCY:H1YA	0.62	2.23	74	1
1:A:69:PRO:HD3	2:A:168:RCY:C1C	0.62	1.91	66	1
2:A:173:RCY:H1YA	2:A:176:RCY:O1H	0.62	1.95	61	2
1:A:62:THR:HG23	1:A:62:THR:O	0.62	1.93	14	1
2:A:176:RCY:C1P	2:A:176:RCY:C1C	0.62	2.69	71	4
1:A:67:ILE:HD11	2:A:160:RCY:C1V	0.62	2.21	86	1
1:A:70:TRP:CZ3	2:A:168:RCY:H1LA	0.62	2.16	48	1
2:A:168:RCY:H1Y	2:A:176:RCY:O1J	0.62	1.93	90	1
1:A:67:ILE:CG2	2:A:173:RCY:C1Z	0.62	2.78	80	1
1:A:71:GLU:HG3	2:A:168:RCY:C1C	0.62	2.24	36	1
1:A:66:VAL:CG1	2:A:121:RCY:H1ZA	0.62	2.23	89	1
2:A:130:RCY:C1C	2:A:160:RCY:C1P	0.62	2.66	66	1
1:A:70:TRP:CH2	2:A:138:RCY:H1C	0.62	2.30	19	1
2:A:173:RCY:H1Z	2:A:187:RCY:H1Z	0.62	1.57	84	1
2:A:160:RCY:C1Z	2:A:168:RCY:N1R	0.62	2.61	3	2
2:A:168:RCY:H1VA	2:A:176:RCY:H1CA	0.62	1.69	16	2
1:A:70:TRP:CH2	2:A:168:RCY:C1Z	0.62	2.83	59	1
2:A:150:RCY:H1S	2:A:160:RCY:H1YB	0.62	0.72	85	1
1:A:78:LEU:HD12	1:A:78:LEU:O	0.62	1.94	46	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:70:TRP:HE1	1:A:75:HIS:CE1	0.62	2.12	73	1
2:A:138:RCY:N1R	2:A:138:RCY:C1M	0.62	2.58	25	1
1:A:61:GLY:O	1:A:65:THR:N	0.62	2.32	39	1
1:A:77:GLU:HG3	2:A:176:RCY:C1M	0.62	2.23	39	1
2:A:160:RCY:H1Z	2:A:173:RCY:C1C	0.62	2.24	20	1
1:A:70:TRP:HE1	2:A:168:RCY:H1LA	0.62	1.52	89	1
2:A:150:RCY:C1V	2:A:187:RCY:C1Y	0.62	2.62	66	1
2:A:138:RCY:C1Y	2:A:173:RCY:H1YA	0.62	2.23	92	1
2:A:138:RCY:C1Q	2:A:138:RCY:H1CA	0.62	2.25	93	4
1:A:67:ILE:O	2:A:168:RCY:H1LA	0.62	1.94	75	2
1:A:69:PRO:HB2	2:A:173:RCY:H1CB	0.62	1.71	26	1
1:A:64:ILE:HG21	2:A:150:RCY:H1VA	0.62	0.69	16	1
2:A:160:RCY:H1Z	2:A:173:RCY:C1X	0.62	2.25	37	1
1:A:71:GLU:OE2	2:A:176:RCY:C1P	0.62	2.48	37	1
2:A:160:RCY:C1Q	2:A:168:RCY:O1J	0.62	2.48	9	1
1:A:74:ASN:C	1:A:75:HIS:CG	0.62	2.73	20	3
2:A:150:RCY:H1ZB	2:A:187:RCY:H1CB	0.62	1.70	50	1
2:A:176:RCY:C1X	2:A:187:RCY:H1V	0.62	2.23	4	3
2:A:160:RCY:H1YA	2:A:168:RCY:O1J	0.62	1.94	13	1
1:A:69:PRO:CB	2:A:173:RCY:H1L	0.62	2.25	6	2
2:A:150:RCY:C1M	2:A:187:RCY:H1Z	0.62	2.23	69	1
2:A:150:RCY:H1YB	2:A:176:RCY:H1Y	0.62	1.68	37	1
1:A:64:ILE:HD13	2:A:160:RCY:H1CB	0.62	1.70	96	1
1:A:71:GLU:N	1:A:74:ASN:HD21	0.62	1.93	3	1
2:A:150:RCY:H1VA	2:A:187:RCY:H1S	0.62	1.69	87	1
1:A:72:ALA:O	1:A:74:ASN:N	0.62	2.33	78	17
2:A:121:RCY:C1C	2:A:121:RCY:C1P	0.62	2.71	62	4
1:A:62:THR:HG21	2:A:168:RCY:H1VA	0.62	1.72	75	1
1:A:66:VAL:HA	2:A:160:RCY:N1V	0.62	2.04	68	1
2:A:130:RCY:H1Y	2:A:173:RCY:N1R	0.62	2.09	15	1
1:A:68:CYS:HB2	2:A:160:RCY:H1Y	0.62	0.65	19	1
1:A:64:ILE:CD1	2:A:168:RCY:C1W	0.62	2.66	6	1
1:A:59:GLY:H	2:A:160:RCY:C1S	0.62	2.08	85	1
1:A:61:GLY:C	2:A:138:RCY:H1VA	0.62	2.15	7	1
2:A:138:RCY:O1G	2:A:138:RCY:O1H	0.62	1.76	2	1
2:A:138:RCY:H1VA	2:A:150:RCY:H1ZA	0.61	1.71	26	1
1:A:62:THR:OG1	2:A:168:RCY:H1LA	0.61	1.91	72	1
1:A:67:ILE:HG23	2:A:168:RCY:O1G	0.61	1.95	76	1
2:A:160:RCY:C1W	2:A:168:RCY:C1C	0.61	2.70	47	2
1:A:63:ASP:O	2:A:168:RCY:C1S	0.61	2.48	80	1
1:A:69:PRO:HB3	2:A:173:RCY:H1M	0.61	1.72	15	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:150:RCY:C1C	2:A:173:RCY:H1VB	0.61	2.21	31	1
2:A:150:RCY:H1M	2:A:187:RCY:C1P	0.61	1.92	27	1
1:A:66:VAL:HG11	2:A:121:RCY:H1VA	0.61	1.70	93	1
1:A:65:THR:CB	2:A:168:RCY:H1S	0.61	2.25	87	1
1:A:64:ILE:CA	2:A:168:RCY:C1Z	0.61	2.78	78	1
2:A:130:RCY:H1Y	2:A:160:RCY:H1V	0.61	1.71	61	1
1:A:64:ILE:C	1:A:68:CYS:SG	0.61	2.79	87	11
1:A:70:TRP:CE3	2:A:168:RCY:O1H	0.61	2.53	41	1
2:A:130:RCY:C1Z	2:A:160:RCY:C1C	0.61	2.78	69	1
2:A:160:RCY:H1ZA	2:A:168:RCY:C1C	0.61	2.01	69	1
1:A:67:ILE:CG2	2:A:138:RCY:C1Q	0.61	2.73	72	1
1:A:70:TRP:CD2	2:A:187:RCY:H1Z	0.61	1.91	76	1
1:A:64:ILE:N	1:A:67:ILE:O	0.61	2.33	68	2
1:A:70:TRP:HB2	2:A:176:RCY:H1ZA	0.61	0.67	18	1
1:A:62:THR:CG2	2:A:130:RCY:C1X	0.61	2.78	18	1
1:A:71:GLU:CB	2:A:168:RCY:N1R	0.61	2.63	37	1
1:A:62:THR:CB	2:A:130:RCY:H1V	0.61	2.23	9	1
2:A:176:RCY:H1Y	2:A:187:RCY:O1G	0.61	1.55	90	1
1:A:66:VAL:HB	2:A:150:RCY:H1M	0.61	1.72	31	1
1:A:65:THR:O	2:A:168:RCY:C1L	0.61	2.47	93	1
2:A:138:RCY:H1C	2:A:168:RCY:C1Z	0.61	2.25	97	1
2:A:173:RCY:O1J	2:A:187:RCY:H1VA	0.61	1.94	8	1
2:A:160:RCY:H1ZA	2:A:168:RCY:H1U	0.61	1.73	41	1
1:A:71:GLU:C	2:A:173:RCY:C1P	0.61	2.68	94	1
2:A:138:RCY:C1M	2:A:150:RCY:O1H	0.61	2.48	60	1
2:A:168:RCY:C1U	2:A:173:RCY:H1Z	0.61	2.25	10	1
2:A:138:RCY:H1C	2:A:187:RCY:C1V	0.61	2.24	63	1
1:A:68:CYS:C	2:A:168:RCY:C1V	0.61	2.62	63	1
2:A:168:RCY:H1ZB	2:A:187:RCY:H1CB	0.61	1.71	3	1
1:A:71:GLU:H	2:A:168:RCY:C1S	0.61	2.07	83	1
2:A:150:RCY:H1YA	2:A:160:RCY:C1V	0.61	2.25	42	1
1:A:73:CYS:N	2:A:173:RCY:C1Q	0.61	2.58	16	3
2:A:168:RCY:H1U	2:A:173:RCY:C1U	0.61	2.24	48	1
2:A:160:RCY:C1V	2:A:168:RCY:C1U	0.61	1.90	44	1
1:A:70:TRP:CE3	2:A:168:RCY:H1VB	0.61	2.28	56	1
1:A:75:HIS:NE2	2:A:173:RCY:O1H	0.61	2.33	42	1
1:A:62:THR:CG2	2:A:160:RCY:H1V	0.61	2.11	55	1
1:A:71:GLU:O	2:A:187:RCY:H1VA	0.61	1.95	34	1
2:A:138:RCY:C1P	2:A:187:RCY:C1C	0.61	2.77	5	1
2:A:173:RCY:O1G	2:A:187:RCY:C1X	0.61	2.48	89	1
1:A:74:ASN:H	1:A:74:ASN:ND2	0.61	1.92	100	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:70:TRP:HB2	2:A:176:RCY:O1J	0.61	1.94	76	3
2:A:150:RCY:C1P	2:A:150:RCY:H1VB	0.61	2.25	27	5
2:A:176:RCY:H1Z	2:A:187:RCY:C1C	0.61	2.26	29	1
2:A:150:RCY:O1G	2:A:187:RCY:C1X	0.61	2.48	18	1
1:A:70:TRP:CD1	2:A:173:RCY:C1Z	0.61	2.84	94	2
2:A:176:RCY:C1Z	2:A:187:RCY:C1X	0.61	2.69	10	1
2:A:130:RCY:N1V	2:A:130:RCY:C1C	0.61	2.63	79	1
1:A:78:LEU:CD1	2:A:187:RCY:C1C	0.61	2.79	91	1
1:A:63:ASP:HB2	2:A:150:RCY:H1Z	0.61	1.73	80	1
2:A:168:RCY:C1M	2:A:173:RCY:H1CA	0.61	2.23	20	1
2:A:168:RCY:C1C	2:A:173:RCY:C1C	0.61	2.78	3	1
1:A:72:ALA:HB2	2:A:173:RCY:H1U	0.61	1.72	30	1
1:A:61:GLY:O	1:A:63:ASP:N	0.61	2.34	69	20
1:A:73:CYS:O	1:A:74:ASN:ND2	0.61	2.34	16	5
2:A:130:RCY:H1CA	2:A:160:RCY:C1C	0.61	2.20	8	1
2:A:173:RCY:O1H	2:A:187:RCY:O1J	0.61	2.19	54	1
2:A:176:RCY:H1Z	2:A:187:RCY:H1CB	0.61	1.71	2	1
1:A:60:CYS:N	2:A:160:RCY:H1S	0.61	2.08	28	1
1:A:64:ILE:HB	2:A:168:RCY:H1ZA	0.61	1.48	78	1
1:A:75:HIS:O	1:A:77:GLU:N	0.61	2.33	99	13
1:A:62:THR:OG1	1:A:63:ASP:N	0.61	2.32	99	9
1:A:70:TRP:CB	2:A:168:RCY:C1L	0.61	2.75	94	2
2:A:138:RCY:C1M	2:A:160:RCY:C1C	0.61	2.61	69	1
1:A:69:PRO:CA	2:A:173:RCY:O1H	0.61	2.47	81	2
1:A:70:TRP:CZ3	2:A:160:RCY:C1V	0.61	2.71	91	1
2:A:138:RCY:H1Y	2:A:187:RCY:H1YB	0.61	1.67	32	1
1:A:66:VAL:CG1	2:A:121:RCY:C1U	0.61	2.79	4	1
2:A:173:RCY:O1H	2:A:176:RCY:H1M	0.61	1.96	63	2
2:A:168:RCY:H1CA	2:A:168:RCY:C1P	0.61	2.24	36	1
1:A:71:GLU:OE1	1:A:71:GLU:N	0.61	2.34	74	1
1:A:65:THR:O	2:A:121:RCY:H1Y	0.61	1.96	83	1
2:A:138:RCY:C1Y	2:A:187:RCY:O1J	0.61	2.47	98	1
2:A:138:RCY:H1C	2:A:168:RCY:H1ZB	0.61	1.71	97	1
2:A:173:RCY:O1J	2:A:187:RCY:C1C	0.61	2.49	61	2
1:A:75:HIS:C	1:A:77:GLU:H	0.61	2.00	99	8
2:A:173:RCY:H1VB	2:A:176:RCY:C1L	0.61	2.25	17	1
1:A:67:ILE:HA	2:A:168:RCY:C1P	0.61	2.26	58	1
2:A:160:RCY:C1V	2:A:160:RCY:C1Q	0.61	2.79	35	7
2:A:176:RCY:H1M	2:A:187:RCY:C1U	0.61	2.15	48	1
2:A:168:RCY:H1YB	2:A:187:RCY:C1Y	0.61	2.26	7	1
1:A:77:GLU:HB2	2:A:173:RCY:C1P	0.61	2.26	32	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:64:ILE:CB	2:A:168:RCY:H1M	0.61	2.25	95	1
1:A:75:HIS:CA	2:A:168:RCY:H1ZB	0.61	2.24	73	1
1:A:64:ILE:CG2	2:A:168:RCY:H1L	0.61	2.08	77	2
1:A:65:THR:HB	2:A:160:RCY:C1Y	0.60	2.23	100	1
1:A:65:THR:O	1:A:67:ILE:N	0.60	2.34	93	27
2:A:168:RCY:H1C	2:A:173:RCY:C1Q	0.60	2.26	8	1
1:A:71:GLU:CD	2:A:173:RCY:C1V	0.60	2.69	94	1
2:A:138:RCY:H1YA	2:A:187:RCY:C1M	0.60	2.18	82	1
1:A:66:VAL:HG11	2:A:121:RCY:C1Z	0.60	2.21	89	1
1:A:74:ASN:C	2:A:173:RCY:C1P	0.60	2.65	15	1
1:A:62:THR:HB	2:A:160:RCY:H1M	0.60	1.73	97	1
1:A:73:CYS:SG	1:A:74:ASN:N	0.60	2.74	61	6
1:A:75:HIS:O	1:A:76:CYS:SG	0.60	2.59	17	12
1:A:65:THR:O	1:A:66:VAL:C	0.60	2.36	93	11
2:A:138:RCY:H1VB	2:A:150:RCY:O1J	0.60	1.96	53	2
1:A:64:ILE:O	1:A:64:ILE:CG1	0.60	2.47	85	7
1:A:74:ASN:HB3	2:A:176:RCY:O1G	0.60	1.94	52	1
1:A:71:GLU:OE2	2:A:150:RCY:H1U	0.60	1.88	58	1
1:A:63:ASP:N	1:A:63:ASP:OD1	0.60	2.34	40	6
2:A:110:RCY:C1P	2:A:110:RCY:C1C	0.60	2.75	11	5
1:A:70:TRP:HD1	2:A:173:RCY:O1G	0.60	1.65	44	1
1:A:63:ASP:OD2	2:A:160:RCY:C1W	0.60	2.47	73	1
1:A:66:VAL:HA	2:A:121:RCY:H1YB	0.60	1.73	83	1
2:A:173:RCY:C1U	2:A:176:RCY:C1L	0.60	2.70	38	1
1:A:59:GLY:O	1:A:60:CYS:SG	0.60	2.59	41	9
2:A:150:RCY:C1P	2:A:150:RCY:C1C	0.60	2.74	19	5
1:A:70:TRP:CG	2:A:173:RCY:H1M	0.60	2.30	84	1
1:A:73:CYS:C	2:A:173:RCY:H1S	0.60	2.17	90	2
1:A:73:CYS:N	2:A:168:RCY:H1ZB	0.60	2.11	99	1
2:A:130:RCY:H1CB	2:A:130:RCY:O1G	0.60	1.97	3	3
1:A:70:TRP:HD1	2:A:176:RCY:H1L	0.60	1.55	32	1
1:A:64:ILE:HG23	2:A:168:RCY:H1CB	0.60	1.67	54	1
2:A:138:RCY:N1V	2:A:173:RCY:H1ZB	0.60	2.10	15	1
2:A:150:RCY:O1J	2:A:176:RCY:H1L	0.60	1.95	3	1
1:A:72:ALA:N	2:A:121:RCY:O1J	0.60	2.35	94	1
2:A:168:RCY:H1Y	2:A:187:RCY:H1ZB	0.60	0.62	21	1
1:A:75:HIS:C	2:A:173:RCY:H1C	0.60	2.17	73	1
2:A:168:RCY:C1U	2:A:173:RCY:C1C	0.60	2.74	20	1
2:A:168:RCY:O1J	2:A:176:RCY:N1V	0.60	2.34	89	1
1:A:67:ILE:HG13	2:A:176:RCY:H1CA	0.60	1.72	89	1
1:A:66:VAL:CG1	2:A:121:RCY:N1V	0.60	2.65	83	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:121:RCY:C1V	2:A:121:RCY:C1L	0.60	2.79	88	1
2:A:150:RCY:C1V	2:A:160:RCY:C1U	0.60	2.79	42	1
1:A:70:TRP:O	2:A:150:RCY:C1P	0.60	2.50	34	1
2:A:173:RCY:H1ZA	2:A:187:RCY:O1H	0.60	1.58	81	1
1:A:71:GLU:CA	2:A:173:RCY:C1Y	0.60	2.57	33	1
1:A:64:ILE:HG21	2:A:160:RCY:C1W	0.60	2.25	49	1
1:A:72:ALA:HB1	2:A:110:RCY:H1ZB	0.60	1.72	70	1
1:A:59:GLY:HA3	2:A:160:RCY:H1V	0.60	1.72	2	1
1:A:70:TRP:HE1	2:A:176:RCY:C1V	0.60	2.10	82	1
2:A:138:RCY:H1Y	2:A:160:RCY:O1H	0.60	1.91	73	1
2:A:173:RCY:O1G	2:A:187:RCY:H1VA	0.60	1.96	89	1
2:A:138:RCY:H1VA	2:A:150:RCY:H1VB	0.60	1.57	67	1
1:A:67:ILE:HG23	2:A:168:RCY:H1U	0.60	1.71	83	1
1:A:67:ILE:HG23	1:A:71:GLU:O	0.60	1.97	61	1
2:A:173:RCY:O1G	2:A:173:RCY:H1ZB	0.60	1.97	14	2
1:A:60:CYS:CB	2:A:168:RCY:C1Y	0.60	2.80	52	1
2:A:138:RCY:O1H	2:A:150:RCY:C1L	0.60	2.48	41	1
2:A:173:RCY:C1V	2:A:173:RCY:C1Q	0.60	2.79	41	4
1:A:70:TRP:CH2	1:A:71:GLU:OE2	0.60	2.54	86	1
1:A:67:ILE:O	2:A:173:RCY:H1CB	0.60	1.96	24	1
1:A:69:PRO:CG	2:A:187:RCY:H1VA	0.60	2.26	72	2
2:A:187:RCY:H1ZB	2:A:187:RCY:C1Q	0.60	2.27	77	3
1:A:71:GLU:HA	2:A:173:RCY:H1S	0.60	1.72	49	1
1:A:63:ASP:OD2	2:A:160:RCY:C1V	0.60	2.49	63	1
1:A:76:CYS:SG	2:A:187:RCY:C1X	0.60	2.77	73	1
2:A:168:RCY:O1H	2:A:173:RCY:H1VA	0.60	1.95	3	1
1:A:74:ASN:HA	2:A:176:RCY:C1V	0.60	2.16	100	1
1:A:62:THR:CB	2:A:138:RCY:H1ZB	0.60	2.26	38	1
2:A:150:RCY:O1J	2:A:187:RCY:N1R	0.60	2.33	84	1
2:A:168:RCY:H1Z	2:A:176:RCY:H1ZB	0.60	1.73	60	1
1:A:59:GLY:O	2:A:168:RCY:C1C	0.60	2.50	80	1
1:A:62:THR:HG23	2:A:160:RCY:C1L	0.60	2.25	82	1
1:A:64:ILE:HD13	1:A:64:ILE:O	0.60	1.97	73	1
2:A:130:RCY:C1V	2:A:130:RCY:C1Q	0.60	2.80	90	6
1:A:61:GLY:C	1:A:62:THR:HG22	0.60	2.16	23	2
2:A:130:RCY:C1X	2:A:160:RCY:C1Q	0.60	2.72	8	1
2:A:138:RCY:H1YB	2:A:187:RCY:H1VA	0.60	1.74	84	1
1:A:65:THR:CB	2:A:160:RCY:H1L	0.60	2.26	35	1
1:A:69:PRO:HA	2:A:168:RCY:H1VA	0.60	1.72	63	1
1:A:67:ILE:HG13	2:A:168:RCY:C1V	0.60	2.27	83	1
2:A:173:RCY:C1Q	2:A:173:RCY:C1C	0.60	2.78	63	9

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:73:CYS:HB3	2:A:176:RCY:C1V	0.60	2.26	62	1
1:A:73:CYS:CB	2:A:168:RCY:H1ZA	0.60	1.18	99	1
1:A:70:TRP:O	2:A:187:RCY:C1Y	0.60	2.45	16	1
2:A:173:RCY:H1ZA	2:A:176:RCY:N1V	0.60	2.02	71	1
1:A:69:PRO:CB	2:A:173:RCY:H1MA	0.60	2.27	4	1
1:A:70:TRP:CE3	2:A:176:RCY:H1ZA	0.60	2.29	4	1
1:A:70:TRP:HA	2:A:168:RCY:H1ZB	0.60	1.73	36	1
1:A:67:ILE:CD1	2:A:130:RCY:C1Y	0.60	2.74	78	1
1:A:59:GLY:CA	2:A:160:RCY:C1M	0.60	2.43	78	1
2:A:130:RCY:C1Y	2:A:176:RCY:C1Z	0.60	2.77	41	1
2:A:173:RCY:C1C	2:A:176:RCY:O1G	0.60	2.46	3	2
1:A:70:TRP:N	2:A:176:RCY:C1Z	0.60	2.65	18	1
2:A:138:RCY:C1W	2:A:150:RCY:O1G	0.60	2.28	37	1
1:A:65:THR:HG21	2:A:130:RCY:C1C	0.60	2.25	9	1
2:A:173:RCY:N1R	2:A:187:RCY:C1Y	0.60	2.65	70	1
2:A:138:RCY:C1V	2:A:150:RCY:H1V	0.60	2.26	1	1
2:A:173:RCY:C1P	2:A:187:RCY:H1YA	0.60	2.26	92	1
2:A:173:RCY:C1U	2:A:176:RCY:N1R	0.59	2.65	38	1
1:A:74:ASN:O	1:A:75:HIS:CG	0.59	2.55	90	8
1:A:70:TRP:CE2	1:A:71:GLU:CG	0.59	2.85	86	1
2:A:168:RCY:H1VB	2:A:173:RCY:C1U	0.59	2.23	29	1
2:A:173:RCY:H1Y	2:A:176:RCY:H1L	0.59	1.73	26	1
2:A:138:RCY:H1ZB	2:A:187:RCY:C1C	0.59	2.09	44	1
2:A:160:RCY:H1S	2:A:168:RCY:H1VA	0.59	1.74	9	1
1:A:68:CYS:H	2:A:168:RCY:C1Q	0.59	2.10	53	1
1:A:64:ILE:CB	2:A:160:RCY:C1M	0.59	2.79	47	1
1:A:62:THR:HG23	1:A:63:ASP:N	0.59	2.12	74	2
2:A:138:RCY:H1VB	2:A:138:RCY:C1P	0.59	2.26	88	3
2:A:173:RCY:C1P	2:A:187:RCY:C1Z	0.59	2.79	75	1
2:A:130:RCY:O1G	2:A:160:RCY:C1Y	0.59	2.42	40	1
2:A:173:RCY:O1J	2:A:187:RCY:C1Y	0.59	2.43	99	1
1:A:69:PRO:CG	2:A:173:RCY:H1L	0.59	2.26	24	1
1:A:69:PRO:CD	2:A:150:RCY:C1V	0.59	2.81	85	1
1:A:70:TRP:NE1	2:A:121:RCY:C1V	0.59	2.61	49	1
2:A:173:RCY:H1Y	2:A:176:RCY:C1Y	0.59	2.15	23	1
2:A:173:RCY:C1X	2:A:187:RCY:H1MA	0.59	2.28	93	1
1:A:71:GLU:CG	2:A:187:RCY:O1G	0.59	2.49	92	1
1:A:78:LEU:C	1:A:78:LEU:HD12	0.59	2.18	38	4
2:A:138:RCY:C1U	2:A:150:RCY:C1P	0.59	2.73	64	3
2:A:138:RCY:H1M	2:A:150:RCY:C1X	0.59	1.86	75	1
1:A:73:CYS:CA	2:A:173:RCY:C1Q	0.59	2.80	56	5

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:173:RCY:C1U	2:A:187:RCY:H1VA	0.59	2.28	55	1
1:A:78:LEU:HD12	1:A:78:LEU:H	0.59	1.57	10	1
2:A:138:RCY:H1YB	2:A:187:RCY:H1Y	0.59	1.72	68	1
1:A:68:CYS:C	2:A:168:RCY:C1Q	0.59	2.03	57	1
1:A:64:ILE:HG22	1:A:67:ILE:H	0.59	1.57	71	1
2:A:138:RCY:H1VA	2:A:176:RCY:H1C	0.59	1.65	9	1
1:A:65:THR:HB	2:A:168:RCY:C1S	0.59	2.27	87	1
1:A:64:ILE:HG21	1:A:68:CYS:N	0.59	2.12	83	3
2:A:173:RCY:C1L	2:A:187:RCY:H1Z	0.59	2.26	75	1
2:A:110:RCY:O1G	2:A:110:RCY:H1CB	0.59	1.97	20	3
1:A:76:CYS:HA	2:A:187:RCY:O1G	0.59	1.96	34	1
2:A:160:RCY:C1X	2:A:168:RCY:C1C	0.59	2.70	49	1
2:A:168:RCY:C1Y	2:A:187:RCY:C1V	0.59	2.81	82	1
2:A:173:RCY:C1C	2:A:187:RCY:H1ZA	0.59	2.26	93	1
1:A:74:ASN:O	1:A:76:CYS:N	0.59	2.35	20	11
2:A:160:RCY:C1Q	2:A:160:RCY:C1V	0.59	2.81	21	6
1:A:71:GLU:CD	2:A:150:RCY:O1G	0.59	2.41	58	1
1:A:70:TRP:HB3	2:A:173:RCY:C1V	0.59	2.28	76	2
1:A:78:LEU:H	1:A:78:LEU:HD13	0.59	1.58	12	3
1:A:71:GLU:N	2:A:173:RCY:O1H	0.59	2.20	49	1
2:A:138:RCY:C1Z	2:A:187:RCY:H1YB	0.59	2.18	32	1
2:A:176:RCY:C1V	2:A:187:RCY:H1Y	0.59	2.18	54	1
1:A:62:THR:OG1	1:A:65:THR:N	0.59	2.35	53	4
1:A:61:GLY:HA2	2:A:168:RCY:H1MA	0.59	1.74	95	1
1:A:71:GLU:CG	2:A:150:RCY:N1V	0.59	2.65	96	1
2:A:168:RCY:C1C	2:A:173:RCY:C1V	0.59	2.77	41	1
1:A:60:CYS:SG	1:A:61:GLY:N	0.59	2.75	32	5
2:A:168:RCY:C1Q	2:A:168:RCY:C1C	0.59	2.78	54	3
2:A:173:RCY:H1YA	2:A:176:RCY:H1M	0.59	1.57	99	1
2:A:168:RCY:H1Y	2:A:173:RCY:C1V	0.59	1.35	45	1
1:A:62:THR:C	2:A:160:RCY:C1C	0.59	2.65	46	1
2:A:150:RCY:C1Y	2:A:176:RCY:C1Z	0.59	2.77	42	1
1:A:76:CYS:HB2	2:A:173:RCY:H1Y	0.59	1.74	42	1
2:A:173:RCY:O1G	2:A:176:RCY:H1M	0.59	1.97	41	1
1:A:64:ILE:HD11	2:A:168:RCY:H1VB	0.59	1.74	58	1
2:A:130:RCY:N1R	2:A:160:RCY:O1G	0.59	2.35	62	1
2:A:160:RCY:H1U	2:A:168:RCY:H1S	0.59	1.67	34	1
1:A:70:TRP:CA	2:A:176:RCY:C1C	0.59	2.74	13	1
2:A:110:RCY:C1Z	2:A:121:RCY:H1C	0.59	2.26	33	1
2:A:173:RCY:H1Z	2:A:187:RCY:H1V	0.59	1.70	32	1
1:A:70:TRP:CZ3	2:A:150:RCY:H1YB	0.59	2.21	47	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:138:RCY:N1R	2:A:138:RCY:H1U	0.59	2.02	25	1
2:A:138:RCY:C1W	2:A:187:RCY:C1Z	0.59	2.70	3	1
2:A:130:RCY:H1YB	2:A:160:RCY:H1V	0.59	1.74	61	1
2:A:121:RCY:C1L	2:A:121:RCY:H1VB	0.59	2.27	88	1
1:A:59:GLY:O	1:A:61:GLY:N	0.59	2.35	63	12
1:A:71:GLU:CD	2:A:176:RCY:H1LA	0.59	2.17	40	1
2:A:160:RCY:C1M	2:A:168:RCY:N1R	0.59	2.66	34	1
2:A:130:RCY:C1Q	2:A:130:RCY:C1V	0.59	2.79	70	8
1:A:65:THR:HG22	1:A:68:CYS:SG	0.59	2.38	59	1
1:A:68:CYS:HB2	2:A:173:RCY:H1YB	0.59	1.75	4	1
1:A:76:CYS:HA	2:A:173:RCY:H1L	0.59	1.72	28	1
1:A:64:ILE:HB	2:A:160:RCY:H1ZA	0.59	1.75	78	1
2:A:168:RCY:C1C	2:A:168:RCY:C1P	0.59	2.81	43	2
1:A:75:HIS:O	1:A:75:HIS:CD2	0.59	2.56	65	1
2:A:160:RCY:H1ZB	2:A:168:RCY:C1P	0.59	2.17	34	1
2:A:121:RCY:H1VB	2:A:168:RCY:H1YB	0.59	1.65	49	1
2:A:173:RCY:H1CB	2:A:187:RCY:H1Y	0.59	1.73	70	1
1:A:74:ASN:N	1:A:74:ASN:HD22	0.59	1.95	11	1
1:A:59:GLY:H	2:A:138:RCY:C1S	0.59	2.10	73	1
2:A:160:RCY:H1CA	2:A:168:RCY:H1M	0.59	1.73	96	1
2:A:138:RCY:H1VA	2:A:187:RCY:C1S	0.59	2.27	93	1
1:A:74:ASN:H	1:A:74:ASN:HD22	0.59	1.39	100	1
1:A:64:ILE:HG21	2:A:160:RCY:H1YB	0.59	0.66	49	2
2:A:173:RCY:H1MA	2:A:176:RCY:H1ZA	0.59	1.73	41	1
1:A:62:THR:HG1	2:A:168:RCY:C1L	0.59	1.98	23	2
1:A:74:ASN:O	2:A:173:RCY:C1P	0.59	2.51	15	1
2:A:138:RCY:H1YB	2:A:187:RCY:H1V	0.58	1.75	84	1
1:A:75:HIS:O	2:A:176:RCY:H1CB	0.58	1.97	62	1
2:A:173:RCY:O1H	2:A:187:RCY:H1M	0.58	1.98	40	1
1:A:59:GLY:C	2:A:160:RCY:C1S	0.58	2.54	85	2
2:A:110:RCY:C1M	2:A:110:RCY:N1R	0.58	2.61	79	1
2:A:160:RCY:H1U	2:A:160:RCY:C1X	0.58	2.10	79	1
2:A:138:RCY:H1M	2:A:187:RCY:H1Y	0.58	1.74	71	1
2:A:160:RCY:H1C	2:A:168:RCY:O1H	0.58	1.88	39	1
1:A:67:ILE:H	2:A:168:RCY:H1CB	0.58	1.58	30	1
2:A:130:RCY:C1V	2:A:187:RCY:H1VB	0.58	2.22	94	1
2:A:187:RCY:C1Q	2:A:187:RCY:C1V	0.58	2.81	95	5
2:A:176:RCY:H1U	2:A:187:RCY:H1VB	0.58	1.69	81	1
2:A:176:RCY:H1VB	2:A:187:RCY:H1ZA	0.58	1.73	57	1
1:A:78:LEU:CD2	2:A:176:RCY:H1ZA	0.58	2.27	91	1
1:A:76:CYS:SG	2:A:187:RCY:C1C	0.58	2.91	73	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:76:CYS:HA	2:A:176:RCY:C1P	0.58	2.27	31	1
2:A:150:RCY:H1C	2:A:187:RCY:O1J	0.58	1.98	66	1
1:A:70:TRP:HB3	2:A:121:RCY:H1VB	0.58	1.66	30	1
1:A:71:GLU:CD	2:A:173:RCY:H1L	0.58	2.17	88	1
2:A:176:RCY:C1C	2:A:187:RCY:H1VA	0.58	2.28	8	1
2:A:176:RCY:C1Z	2:A:187:RCY:C1S	0.58	2.81	58	1
1:A:63:ASP:HA	2:A:168:RCY:O1H	0.58	1.98	50	1
2:A:110:RCY:O1J	2:A:121:RCY:H1VA	0.58	1.84	5	1
1:A:64:ILE:O	1:A:64:ILE:CG2	0.58	2.51	35	1
2:A:168:RCY:O1G	2:A:173:RCY:H1C	0.58	1.96	81	1
1:A:63:ASP:O	2:A:150:RCY:H1V	0.58	1.96	85	1
1:A:76:CYS:CA	2:A:187:RCY:O1J	0.58	2.25	73	1
1:A:62:THR:O	2:A:168:RCY:H1C	0.58	1.98	30	1
1:A:67:ILE:CG2	2:A:130:RCY:C1W	0.58	2.81	30	1
1:A:65:THR:CG2	2:A:160:RCY:H1ZB	0.58	2.21	100	1
1:A:65:THR:O	1:A:66:VAL:CG2	0.58	2.50	86	2
1:A:63:ASP:HB3	2:A:168:RCY:C1C	0.58	2.28	5	1
1:A:64:ILE:CD1	2:A:168:RCY:C1M	0.58	2.81	6	1
2:A:168:RCY:C1X	2:A:173:RCY:C1Y	0.58	2.37	21	1
1:A:67:ILE:H	2:A:150:RCY:H1YB	0.58	1.57	31	1
1:A:63:ASP:N	2:A:168:RCY:C1Y	0.58	2.65	30	1
2:A:176:RCY:H1CB	2:A:187:RCY:O1G	0.58	1.99	88	1
1:A:73:CYS:N	2:A:168:RCY:C1Z	0.58	2.65	99	1
1:A:78:LEU:H	1:A:78:LEU:CD1	0.58	2.12	10	1
2:A:150:RCY:C1Y	2:A:160:RCY:O1G	0.58	2.51	91	1
1:A:67:ILE:HG21	2:A:173:RCY:H1YB	0.58	1.68	80	1
1:A:75:HIS:CG	1:A:75:HIS:O	0.58	2.57	65	3
1:A:74:ASN:ND2	1:A:75:HIS:H	0.58	1.97	29	3
2:A:150:RCY:C1V	2:A:150:RCY:C1Q	0.58	2.82	74	3
1:A:70:TRP:CA	2:A:173:RCY:C1L	0.58	2.81	6	1
2:A:138:RCY:H1CA	2:A:160:RCY:H1VA	0.58	1.69	27	1
2:A:176:RCY:C1W	2:A:187:RCY:C1C	0.58	2.53	87	1
2:A:138:RCY:H1VB	2:A:150:RCY:H1VA	0.58	1.60	19	1
1:A:65:THR:CB	2:A:150:RCY:H1LA	0.58	2.29	50	1
1:A:69:PRO:HG2	2:A:160:RCY:C1Y	0.58	2.28	73	2
1:A:64:ILE:HD12	2:A:160:RCY:H1V	0.58	1.75	49	1
1:A:69:PRO:HD3	2:A:168:RCY:O1H	0.58	1.86	23	1
2:A:121:RCY:C1P	2:A:121:RCY:C1C	0.58	2.70	90	5
1:A:74:ASN:O	2:A:173:RCY:H1S	0.58	1.99	90	1
1:A:69:PRO:CG	2:A:168:RCY:H1V	0.58	2.29	63	1
2:A:130:RCY:H1ZA	2:A:160:RCY:C1Z	0.58	2.29	73	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:71:GLU:OE2	2:A:173:RCY:H1VA	0.58	1.99	56	1
2:A:168:RCY:C1C	2:A:187:RCY:H1YA	0.58	2.22	87	1
2:A:150:RCY:C1Q	2:A:150:RCY:C1C	0.58	2.80	14	1
1:A:60:CYS:O	1:A:62:THR:HG22	0.58	1.98	14	2
1:A:65:THR:HA	2:A:168:RCY:O1J	0.58	1.98	24	1
1:A:70:TRP:CE2	2:A:187:RCY:H1ZB	0.58	2.27	76	1
2:A:168:RCY:C1W	2:A:176:RCY:N1V	0.58	2.57	11	1
2:A:168:RCY:C1C	2:A:176:RCY:H1YB	0.58	2.28	74	1
2:A:150:RCY:H1L	2:A:187:RCY:H1CA	0.58	1.74	98	1
1:A:69:PRO:CG	2:A:168:RCY:O1G	0.58	2.51	78	1
1:A:65:THR:CB	2:A:160:RCY:H1YB	0.58	2.26	100	1
1:A:64:ILE:O	1:A:67:ILE:N	0.58	2.37	91	8
2:A:173:RCY:C1Z	2:A:187:RCY:H1CB	0.58	2.29	58	1
2:A:121:RCY:H1Y	2:A:176:RCY:H1L	0.58	1.71	35	1
1:A:64:ILE:HG12	2:A:160:RCY:H1CB	0.58	1.61	48	1
2:A:173:RCY:H1Y	2:A:176:RCY:H1YA	0.58	1.76	23	1
2:A:130:RCY:H1U	2:A:160:RCY:H1M	0.58	0.60	7	1
2:A:150:RCY:H1U	2:A:168:RCY:H1V	0.58	1.76	74	1
1:A:69:PRO:HB2	2:A:173:RCY:C1V	0.58	2.28	64	1
1:A:71:GLU:OE1	2:A:173:RCY:H1U	0.58	1.99	94	1
2:A:150:RCY:C1W	2:A:160:RCY:C1Z	0.58	2.74	29	1
1:A:71:GLU:O	2:A:187:RCY:C1V	0.58	2.51	34	1
1:A:62:THR:OG1	2:A:168:RCY:H1ZB	0.58	1.99	72	1
1:A:72:ALA:C	2:A:173:RCY:C1S	0.58	2.49	76	1
1:A:71:GLU:OE2	2:A:168:RCY:H1S	0.58	1.98	70	1
2:A:138:RCY:H1YB	2:A:150:RCY:O1H	0.58	1.99	80	1
2:A:160:RCY:H1CA	2:A:168:RCY:C1U	0.58	2.26	39	1
2:A:176:RCY:C1M	2:A:187:RCY:N1V	0.58	2.52	87	1
2:A:138:RCY:H1MA	2:A:150:RCY:C1L	0.58	2.22	1	1
1:A:73:CYS:O	1:A:75:HIS:N	0.57	2.37	15	15
1:A:74:ASN:O	1:A:75:HIS:O	0.57	2.22	65	6
2:A:168:RCY:H1VB	2:A:173:RCY:H1MA	0.57	0.62	29	1
1:A:69:PRO:CA	2:A:173:RCY:N1R	0.57	2.55	10	1
2:A:110:RCY:C1X	2:A:121:RCY:H1YA	0.57	2.23	5	1
1:A:60:CYS:N	2:A:130:RCY:H1M	0.57	2.11	18	1
1:A:63:ASP:OD2	2:A:121:RCY:O1J	0.57	2.22	57	1
2:A:160:RCY:C1V	2:A:168:RCY:C1P	0.57	2.81	37	1
2:A:138:RCY:O1J	2:A:150:RCY:O1H	0.57	2.21	70	1
1:A:73:CYS:SG	1:A:75:HIS:CE1	0.57	2.96	90	1
2:A:138:RCY:C1V	2:A:176:RCY:H1U	0.57	2.26	82	1
2:A:168:RCY:C1Y	2:A:173:RCY:O1J	0.57	2.50	20	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:173:RCY:C1X	2:A:176:RCY:H1ZA	0.57	2.29	77	1
1:A:74:ASN:OD1	2:A:176:RCY:O1G	0.57	2.20	78	1
2:A:160:RCY:C1P	2:A:160:RCY:C1C	0.57	2.83	42	2
2:A:176:RCY:C1Q	2:A:176:RCY:C1V	0.57	2.82	59	4
2:A:168:RCY:C1Z	2:A:173:RCY:N1V	0.57	2.64	55	2
2:A:138:RCY:H1MA	2:A:150:RCY:O1H	0.57	1.98	60	1
1:A:69:PRO:HD2	2:A:150:RCY:C1V	0.57	2.29	85	1
1:A:64:ILE:O	1:A:65:THR:HG22	0.57	1.98	44	2
2:A:138:RCY:H1S	2:A:187:RCY:H1Z	0.57	1.76	49	1
1:A:61:GLY:C	2:A:160:RCY:C1C	0.57	2.68	11	1
1:A:77:GLU:N	2:A:176:RCY:H1L	0.57	2.03	31	1
1:A:64:ILE:O	1:A:64:ILE:HD12	0.57	1.98	52	1
1:A:70:TRP:C	2:A:168:RCY:H1LA	0.57	1.81	29	1
1:A:70:TRP:HA	2:A:173:RCY:H1V	0.57	1.70	26	1
2:A:138:RCY:H1M	2:A:160:RCY:C1C	0.57	2.28	69	1
1:A:62:THR:CB	2:A:168:RCY:H1ZB	0.57	2.29	72	1
1:A:59:GLY:N	2:A:160:RCY:C1Q	0.57	2.67	85	1
1:A:71:GLU:HG2	2:A:176:RCY:H1CA	0.57	1.75	45	2
2:A:168:RCY:H1CA	2:A:187:RCY:C1Y	0.57	2.21	87	1
1:A:70:TRP:CG	2:A:168:RCY:C1V	0.57	2.88	28	1
1:A:60:CYS:O	1:A:62:THR:N	0.57	2.37	94	5
1:A:61:GLY:C	2:A:160:RCY:H1CB	0.57	2.20	11	1
1:A:77:GLU:HB2	2:A:173:RCY:O1G	0.57	1.99	32	2
1:A:70:TRP:CG	2:A:176:RCY:C1P	0.57	2.70	77	1
2:A:173:RCY:H1VA	2:A:176:RCY:O1H	0.57	1.99	30	1
2:A:173:RCY:C1C	2:A:176:RCY:N1R	0.57	2.61	34	3
1:A:63:ASP:OD2	2:A:121:RCY:H1V	0.57	1.99	42	1
2:A:168:RCY:C1W	2:A:173:RCY:N1R	0.57	2.65	58	1
2:A:176:RCY:H1Z	2:A:187:RCY:C1S	0.57	2.29	58	1
1:A:71:GLU:OE2	2:A:176:RCY:C1L	0.57	2.48	40	1
1:A:66:VAL:CB	2:A:160:RCY:C1Q	0.57	2.66	68	1
1:A:69:PRO:CB	2:A:150:RCY:C1Y	0.57	2.73	85	1
1:A:78:LEU:HD11	2:A:176:RCY:H1MA	0.57	1.73	91	1
2:A:160:RCY:H1Y	2:A:168:RCY:H1YA	0.57	1.76	70	1
1:A:77:GLU:O	2:A:176:RCY:H1L	0.57	2.00	31	1
2:A:176:RCY:O1G	2:A:187:RCY:H1C	0.57	1.99	83	1
1:A:68:CYS:SG	1:A:71:GLU:HB3	0.57	2.40	88	1
1:A:60:CYS:CB	2:A:168:RCY:C1Z	0.57	2.77	52	1
2:A:168:RCY:H1CA	2:A:173:RCY:O1H	0.57	1.99	8	1
2:A:168:RCY:C1V	2:A:168:RCY:C1P	0.57	2.82	32	4
2:A:168:RCY:C1Z	2:A:176:RCY:H1V	0.57	2.29	84	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:70:TRP:CE3	2:A:176:RCY:H1CA	0.57	2.34	13	1
1:A:62:THR:CG2	2:A:168:RCY:H1ZB	0.57	2.22	72	1
1:A:69:PRO:HB2	2:A:173:RCY:C1M	0.57	2.28	4	1
1:A:68:CYS:CA	2:A:168:RCY:H1VB	0.57	2.27	63	1
1:A:62:THR:CG2	2:A:160:RCY:C1L	0.57	2.82	82	1
1:A:68:CYS:C	2:A:173:RCY:H1MA	0.57	2.01	73	1
2:A:138:RCY:C1X	2:A:150:RCY:O1J	0.57	2.45	36	2
2:A:173:RCY:O1H	2:A:176:RCY:H1LA	0.57	1.99	93	1
2:A:150:RCY:C1C	2:A:150:RCY:C1P	0.57	2.82	91	5
1:A:69:PRO:HG3	2:A:173:RCY:N1R	0.57	2.13	42	1
2:A:110:RCY:C1Q	2:A:110:RCY:H1ZB	0.57	2.29	41	2
2:A:168:RCY:C1P	2:A:168:RCY:C1V	0.57	2.83	92	6
1:A:64:ILE:O	2:A:168:RCY:C1Q	0.57	2.53	6	1
1:A:69:PRO:CG	2:A:160:RCY:H1CA	0.57	2.28	35	1
1:A:74:ASN:CA	2:A:173:RCY:C1C	0.57	2.77	35	1
2:A:150:RCY:H1VA	2:A:187:RCY:H1ZA	0.57	1.77	59	1
1:A:64:ILE:CD1	2:A:187:RCY:C1W	0.57	2.82	85	1
1:A:74:ASN:CG	2:A:168:RCY:H1Y	0.57	2.14	91	1
2:A:130:RCY:H1C	2:A:160:RCY:C1U	0.57	2.14	7	1
2:A:168:RCY:C1Q	2:A:168:RCY:C1V	0.57	2.79	13	9
1:A:76:CYS:O	2:A:176:RCY:C1L	0.57	2.53	17	1
1:A:60:CYS:O	1:A:60:CYS:SG	0.57	2.63	42	1
1:A:65:THR:O	1:A:65:THR:CG2	0.57	2.53	90	6
2:A:138:RCY:H1V	2:A:150:RCY:H1U	0.57	1.76	60	1
2:A:173:RCY:C1Z	2:A:187:RCY:H1YA	0.57	2.24	72	1
2:A:160:RCY:H1M	2:A:168:RCY:C1U	0.57	2.28	5	1
1:A:69:PRO:HD2	2:A:150:RCY:H1YA	0.57	0.68	85	1
2:A:160:RCY:C1Y	2:A:173:RCY:C1C	0.57	2.58	11	1
1:A:73:CYS:N	2:A:173:RCY:C1P	0.57	2.64	82	1
2:A:138:RCY:C1V	2:A:150:RCY:N1V	0.57	2.68	36	1
1:A:69:PRO:HD2	2:A:173:RCY:H1VB	0.57	1.75	3	1
2:A:173:RCY:C1M	2:A:176:RCY:N1R	0.57	2.65	38	2
2:A:160:RCY:H1Y	2:A:168:RCY:C1M	0.57	2.21	58	1
2:A:168:RCY:O1G	2:A:173:RCY:H1Y	0.57	1.95	62	1
2:A:138:RCY:H1CA	2:A:187:RCY:H1YB	0.57	1.70	99	1
1:A:69:PRO:HA	2:A:173:RCY:H1LA	0.57	1.76	10	1
2:A:138:RCY:O1H	2:A:138:RCY:C1Z	0.57	2.52	24	3
1:A:70:TRP:HA	2:A:173:RCY:C1L	0.57	2.29	6	1
1:A:69:PRO:CG	2:A:160:RCY:C1C	0.57	2.82	35	1
2:A:173:RCY:C1C	2:A:187:RCY:H1YA	0.57	2.16	48	2
1:A:74:ASN:OD1	2:A:168:RCY:H1YA	0.57	1.94	91	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:78:LEU:HD23	2:A:187:RCY:C1X	0.57	2.01	91	1
2:A:138:RCY:C1Y	2:A:187:RCY:H1MA	0.57	2.28	63	1
1:A:63:ASP:OD2	2:A:160:RCY:H1CB	0.57	1.97	15	1
2:A:138:RCY:H1Z	2:A:187:RCY:C1Z	0.57	2.26	77	1
2:A:173:RCY:H1ZA	2:A:176:RCY:C1V	0.57	0.87	31	1
1:A:64:ILE:O	1:A:64:ILE:HG23	0.57	1.98	27	1
1:A:62:THR:C	1:A:64:ILE:H	0.57	2.02	64	29
2:A:160:RCY:H1CB	2:A:160:RCY:O1H	0.57	2.00	65	1
2:A:138:RCY:C1V	2:A:138:RCY:C1Q	0.57	2.79	51	3
2:A:138:RCY:C1X	2:A:150:RCY:C1Q	0.57	2.60	62	1
1:A:70:TRP:N	2:A:168:RCY:H1LA	0.57	2.14	29	1
2:A:138:RCY:C1Z	2:A:150:RCY:H1S	0.57	2.29	60	1
2:A:176:RCY:O1J	2:A:187:RCY:C1Y	0.57	2.53	10	1
2:A:130:RCY:C1C	2:A:173:RCY:C1P	0.57	2.83	18	1
2:A:150:RCY:N1V	2:A:187:RCY:H1YA	0.57	2.15	18	1
1:A:78:LEU:HD13	2:A:176:RCY:H1ZA	0.57	1.72	91	1
2:A:168:RCY:H1L	2:A:176:RCY:C1C	0.57	2.29	49	1
1:A:59:GLY:C	2:A:160:RCY:N1R	0.57	2.58	70	1
1:A:61:GLY:N	2:A:160:RCY:O1H	0.57	2.38	46	1
2:A:150:RCY:C1Z	2:A:176:RCY:N1R	0.57	2.67	3	1
1:A:62:THR:HB	2:A:138:RCY:H1ZB	0.56	1.77	38	1
2:A:160:RCY:C1C	2:A:160:RCY:C1P	0.56	2.80	29	4
2:A:173:RCY:H1MA	2:A:187:RCY:C1M	0.56	2.30	40	1
2:A:138:RCY:H1CA	2:A:138:RCY:C1Q	0.56	2.30	89	3
2:A:130:RCY:H1VB	2:A:173:RCY:C1L	0.56	2.28	5	1
1:A:70:TRP:C	1:A:70:TRP:CD1	0.56	2.75	95	5
1:A:64:ILE:HD12	2:A:187:RCY:C1W	0.56	2.30	85	1
1:A:76:CYS:SG	2:A:160:RCY:C1W	0.56	2.85	73	1
1:A:73:CYS:HB3	2:A:176:RCY:N1R	0.56	2.13	20	1
2:A:160:RCY:N1V	2:A:168:RCY:H1L	0.56	2.15	15	1
1:A:66:VAL:CG1	2:A:121:RCY:H1VA	0.56	2.15	83	2
1:A:74:ASN:O	1:A:75:HIS:ND1	0.56	2.38	28	4
1:A:63:ASP:O	1:A:64:ILE:CB	0.56	2.52	55	2
2:A:173:RCY:H1YB	2:A:187:RCY:N1V	0.56	2.15	64	1
1:A:74:ASN:N	2:A:173:RCY:C1S	0.56	2.68	50	1
2:A:168:RCY:H1LA	2:A:173:RCY:H1ZA	0.56	1.77	10	2
2:A:160:RCY:H1Z	2:A:168:RCY:H1C	0.56	0.65	69	1
1:A:69:PRO:HG3	2:A:176:RCY:H1YA	0.56	1.48	72	1
1:A:70:TRP:CB	2:A:173:RCY:N1V	0.56	2.35	76	1
1:A:62:THR:CB	2:A:173:RCY:H1VA	0.56	2.19	18	1
2:A:168:RCY:H1L	2:A:176:RCY:C1V	0.56	2.30	49	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:71:GLU:CD	2:A:121:RCY:H1YB	0.56	2.19	4	1
1:A:67:ILE:CD1	2:A:150:RCY:C1Y	0.56	2.83	63	1
1:A:69:PRO:HG3	2:A:173:RCY:C1P	0.56	2.30	42	1
2:A:160:RCY:H1V	2:A:168:RCY:N1V	0.56	2.15	14	1
1:A:69:PRO:HG3	2:A:173:RCY:H1S	0.56	1.75	8	1
1:A:69:PRO:HG3	2:A:168:RCY:H1CA	0.56	1.71	8	1
1:A:70:TRP:CZ2	2:A:121:RCY:C1M	0.56	2.88	41	1
2:A:160:RCY:C1M	2:A:168:RCY:C1U	0.56	2.71	5	2
1:A:70:TRP:CG	2:A:173:RCY:C1Z	0.56	2.85	94	1
2:A:138:RCY:H1C	2:A:150:RCY:N1V	0.56	2.14	10	1
1:A:69:PRO:HG2	2:A:173:RCY:H1V	0.56	1.77	10	1
2:A:176:RCY:H1MA	2:A:187:RCY:C1L	0.56	2.25	26	1
1:A:61:GLY:O	1:A:62:THR:O	0.56	2.23	13	2
2:A:130:RCY:H1ZA	2:A:160:RCY:C1C	0.56	2.31	69	1
2:A:130:RCY:O1J	2:A:160:RCY:H1Z	0.56	2.00	81	1
2:A:168:RCY:C1W	2:A:173:RCY:C1P	0.56	2.72	37	1
1:A:70:TRP:CD1	2:A:176:RCY:H1L	0.56	2.35	32	1
2:A:138:RCY:C1V	2:A:150:RCY:H1YB	0.56	2.06	1	2
1:A:67:ILE:CG2	2:A:173:RCY:H1ZA	0.56	2.30	80	1
1:A:59:GLY:N	2:A:138:RCY:C1S	0.56	2.68	73	1
2:A:138:RCY:H1VA	2:A:173:RCY:N1V	0.56	2.14	15	1
1:A:67:ILE:CG2	2:A:150:RCY:H1VB	0.56	2.29	31	1
2:A:168:RCY:C1W	2:A:176:RCY:H1V	0.56	2.25	94	1
1:A:78:LEU:HD12	1:A:78:LEU:N	0.56	2.15	27	5
1:A:73:CYS:H	2:A:173:RCY:H1L	0.56	1.59	76	1
1:A:62:THR:O	1:A:65:THR:OG1	0.56	2.24	28	3
2:A:168:RCY:C1V	2:A:176:RCY:C1Z	0.56	2.75	3	1
1:A:76:CYS:HB2	2:A:173:RCY:C1Y	0.56	2.31	42	1
2:A:173:RCY:O1J	2:A:176:RCY:C1Q	0.56	2.53	62	2
2:A:160:RCY:H1Y	2:A:168:RCY:C1V	0.56	2.24	70	1
2:A:138:RCY:C1L	2:A:150:RCY:C1M	0.56	2.53	23	1
2:A:160:RCY:H1Z	2:A:168:RCY:H1MA	0.56	1.77	3	1
1:A:69:PRO:CG	2:A:173:RCY:H1Z	0.56	2.30	72	1
1:A:67:ILE:O	2:A:168:RCY:H1V	0.56	2.01	5	1
2:A:150:RCY:C1Q	2:A:150:RCY:C1V	0.56	2.83	89	7
2:A:138:RCY:H1CB	2:A:150:RCY:O1G	0.56	1.98	53	1
1:A:70:TRP:H	2:A:173:RCY:H1M	0.56	1.59	4	1
2:A:138:RCY:C1C	2:A:173:RCY:H1ZB	0.56	2.28	15	1
2:A:121:RCY:H1VA	2:A:168:RCY:O1J	0.56	2.01	27	1
2:A:173:RCY:H1YB	2:A:176:RCY:H1C	0.56	1.69	86	1
2:A:150:RCY:H1YB	2:A:160:RCY:H1Y	0.56	1.78	29	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:70:TRP:H	2:A:173:RCY:H1CA	0.56	1.58	92	1
1:A:71:GLU:HG3	2:A:173:RCY:C1Y	0.56	2.30	78	1
1:A:61:GLY:O	1:A:62:THR:C	0.56	2.44	36	15
1:A:73:CYS:O	1:A:73:CYS:SG	0.56	2.64	14	3
2:A:168:RCY:O1G	2:A:187:RCY:H1Z	0.56	2.00	84	1
1:A:65:THR:HB	2:A:160:RCY:H1L	0.56	1.76	35	1
1:A:64:ILE:CG2	1:A:67:ILE:O	0.56	2.53	93	3
2:A:110:RCY:H1Z	2:A:121:RCY:C1X	0.56	2.31	33	1
2:A:138:RCY:C1L	2:A:150:RCY:N1R	0.56	1.96	23	1
2:A:173:RCY:C1P	2:A:176:RCY:C1X	0.56	2.68	11	1
1:A:68:CYS:N	2:A:173:RCY:C1Y	0.56	2.68	100	1
2:A:150:RCY:H1C	2:A:168:RCY:N1V	0.56	2.16	19	1
1:A:70:TRP:CD1	1:A:70:TRP:C	0.56	2.77	23	3
1:A:69:PRO:CA	2:A:173:RCY:H1L	0.56	2.31	24	1
2:A:160:RCY:C1Z	2:A:173:RCY:C1V	0.56	2.73	37	1
1:A:67:ILE:O	2:A:173:RCY:C1U	0.56	2.54	80	1
2:A:160:RCY:C1C	2:A:168:RCY:C1U	0.56	2.84	39	1
2:A:138:RCY:O1G	2:A:160:RCY:C1C	0.56	2.54	67	1
2:A:138:RCY:O1J	2:A:150:RCY:O1G	0.56	2.21	88	1
1:A:60:CYS:CB	2:A:130:RCY:C1V	0.56	2.83	8	1
2:A:160:RCY:H1YA	2:A:168:RCY:H1VA	0.56	1.78	8	1
2:A:150:RCY:H1L	2:A:160:RCY:C1M	0.56	2.27	85	1
2:A:168:RCY:H1V	2:A:168:RCY:H1L	0.56	1.73	7	1
1:A:73:CYS:SG	1:A:73:CYS:O	0.56	2.64	90	1
1:A:70:TRP:HB3	2:A:168:RCY:H1L	0.56	1.63	46	1
2:A:150:RCY:H1U	2:A:187:RCY:H1L	0.56	1.77	27	1
1:A:69:PRO:CG	2:A:187:RCY:C1V	0.55	2.83	14	2
2:A:173:RCY:C1C	2:A:187:RCY:H1C	0.55	2.31	55	2
2:A:173:RCY:C1C	2:A:176:RCY:H1ZA	0.55	2.30	84	1
2:A:130:RCY:C1Y	2:A:160:RCY:C1Y	0.55	2.81	67	2
2:A:138:RCY:H1C	2:A:187:RCY:H1YA	0.55	1.74	44	1
1:A:62:THR:HG21	2:A:130:RCY:H1YB	0.55	1.78	9	1
1:A:75:HIS:C	2:A:176:RCY:H1ZB	0.55	2.07	51	1
1:A:67:ILE:CA	2:A:173:RCY:H1M	0.55	2.31	80	1
2:A:138:RCY:O1J	2:A:150:RCY:N1V	0.55	2.10	43	1
1:A:64:ILE:C	1:A:66:VAL:H	0.55	2.04	55	5
1:A:76:CYS:SG	1:A:76:CYS:O	0.55	2.63	48	5
1:A:63:ASP:OD1	1:A:63:ASP:N	0.55	2.39	92	11
2:A:110:RCY:C1Q	2:A:110:RCY:C1V	0.55	2.80	91	5
1:A:75:HIS:HB3	2:A:176:RCY:C1C	0.55	2.31	84	1
1:A:75:HIS:O	2:A:187:RCY:O1G	0.55	2.23	34	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:66:VAL:CB	2:A:160:RCY:N1V	0.55	2.68	68	1
2:A:150:RCY:H1Y	2:A:187:RCY:C1M	0.55	2.13	59	1
1:A:67:ILE:O	2:A:173:RCY:C1X	0.55	2.53	80	1
1:A:68:CYS:C	2:A:173:RCY:H1M	0.55	2.17	73	1
2:A:173:RCY:H1ZA	2:A:176:RCY:C1C	0.55	2.31	31	1
2:A:176:RCY:C1P	2:A:187:RCY:O1H	0.55	2.55	38	1
1:A:78:LEU:N	1:A:78:LEU:HD12	0.55	2.17	35	5
1:A:70:TRP:O	2:A:168:RCY:H1CA	0.55	2.01	29	1
2:A:160:RCY:H1ZA	2:A:173:RCY:C1Y	0.55	2.32	99	1
2:A:138:RCY:O1H	2:A:160:RCY:O1G	0.55	2.21	69	1
1:A:78:LEU:N	1:A:78:LEU:HD22	0.55	2.15	3	2
1:A:63:ASP:CA	2:A:150:RCY:C1Z	0.55	2.84	80	1
1:A:71:GLU:CD	2:A:176:RCY:H1V	0.55	2.20	92	1
2:A:150:RCY:H1Y	2:A:187:RCY:C1X	0.55	2.32	78	1
2:A:168:RCY:H1V	2:A:173:RCY:C1M	0.55	2.22	29	1
2:A:168:RCY:N1V	2:A:176:RCY:H1U	0.55	2.11	16	1
2:A:150:RCY:C1P	2:A:187:RCY:C1C	0.55	2.84	18	1
2:A:150:RCY:N1R	2:A:187:RCY:C1V	0.55	2.57	18	1
2:A:168:RCY:O1G	2:A:168:RCY:C1C	0.55	2.47	53	2
1:A:78:LEU:CD2	1:A:78:LEU:N	0.55	2.69	3	3
1:A:66:VAL:O	2:A:121:RCY:H1YA	0.55	2.02	4	1
1:A:69:PRO:HB2	2:A:187:RCY:H1C	0.55	1.76	73	1
2:A:138:RCY:H1ZA	2:A:150:RCY:H1LA	0.55	0.66	1	1
2:A:138:RCY:H1S	2:A:150:RCY:H1U	0.55	1.78	67	1
2:A:176:RCY:C1V	2:A:176:RCY:C1Q	0.55	2.84	100	2
1:A:60:CYS:HB3	2:A:130:RCY:O1G	0.55	2.00	8	1
2:A:121:RCY:C1P	2:A:121:RCY:C1V	0.55	2.81	82	5
2:A:130:RCY:C1Y	2:A:138:RCY:C1V	0.55	2.59	69	1
2:A:130:RCY:H1Y	2:A:160:RCY:H1VA	0.55	1.77	81	1
2:A:160:RCY:H1Z	2:A:187:RCY:C1Z	0.55	2.20	21	1
1:A:69:PRO:CB	2:A:168:RCY:C1Y	0.55	2.58	66	1
2:A:150:RCY:C1Y	2:A:187:RCY:N1R	0.55	2.66	78	2
1:A:65:THR:C	1:A:67:ILE:H	0.55	2.05	45	17
2:A:176:RCY:H1C	2:A:187:RCY:H1VA	0.55	1.78	8	1
2:A:168:RCY:H1Z	2:A:176:RCY:H1V	0.55	1.78	84	1
1:A:69:PRO:HD3	2:A:168:RCY:C1L	0.55	2.29	60	1
2:A:150:RCY:C1X	2:A:187:RCY:H1CA	0.55	2.18	50	1
1:A:76:CYS:SG	2:A:121:RCY:C1Y	0.55	2.95	35	1
1:A:73:CYS:SG	2:A:173:RCY:C1L	0.55	2.93	79	2
1:A:63:ASP:OD1	2:A:160:RCY:H1CB	0.55	2.02	15	2
1:A:67:ILE:HG12	2:A:168:RCY:H1U	0.55	1.77	83	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:168:RCY:H1U	2:A:176:RCY:H1ZA	0.55	1.78	98	1
2:A:173:RCY:C1P	2:A:173:RCY:H1ZB	0.55	2.32	14	3
2:A:168:RCY:C1Z	2:A:173:RCY:H1YA	0.55	2.31	42	1
1:A:60:CYS:HB2	2:A:130:RCY:C1V	0.55	2.32	8	1
1:A:73:CYS:CA	2:A:176:RCY:H1MA	0.55	2.31	58	1
1:A:69:PRO:HG2	2:A:176:RCY:O1G	0.55	2.01	64	1
1:A:70:TRP:O	2:A:168:RCY:H1YB	0.55	2.01	37	1
2:A:138:RCY:H1VA	2:A:187:RCY:C1W	0.55	2.31	11	1
1:A:64:ILE:HG22	2:A:168:RCY:H1MA	0.55	1.76	95	1
1:A:65:THR:CA	2:A:168:RCY:H1LA	0.55	2.28	82	2
2:A:138:RCY:C1L	2:A:138:RCY:H1VB	0.55	2.31	74	1
2:A:150:RCY:C1V	2:A:187:RCY:H1MA	0.55	2.31	64	1
1:A:60:CYS:O	2:A:138:RCY:H1Z	0.55	2.01	62	1
1:A:74:ASN:OD1	1:A:75:HIS:ND1	0.55	2.40	76	1
1:A:64:ILE:HD12	2:A:168:RCY:C1P	0.55	1.78	12	1
1:A:71:GLU:OE2	2:A:168:RCY:O1G	0.55	2.25	93	1
1:A:62:THR:O	1:A:68:CYS:SG	0.55	2.64	43	2
1:A:67:ILE:CA	2:A:168:RCY:H1S	0.55	2.30	58	3
2:A:138:RCY:C1S	2:A:138:RCY:C1X	0.55	2.61	50	1
2:A:160:RCY:N1R	2:A:168:RCY:C1C	0.55	2.50	49	2
2:A:138:RCY:H1V	2:A:187:RCY:C1P	0.55	2.31	21	1
2:A:173:RCY:C1V	2:A:187:RCY:C1Y	0.55	2.85	53	1
1:A:77:GLU:HA	2:A:176:RCY:H1LA	0.55	1.77	45	1
2:A:138:RCY:H1V	2:A:150:RCY:N1V	0.55	2.16	36	1
2:A:121:RCY:C1M	2:A:121:RCY:N1R	0.55	2.65	25	1
2:A:138:RCY:H1YB	2:A:187:RCY:C1W	0.55	2.32	89	1
1:A:71:GLU:HG2	2:A:150:RCY:H1YA	0.55	1.79	96	1
2:A:138:RCY:H1CA	2:A:150:RCY:C1C	0.55	2.08	66	1
1:A:67:ILE:CG2	2:A:130:RCY:H1YB	0.55	2.32	30	1
1:A:71:GLU:CD	1:A:71:GLU:O	0.55	2.45	88	3
1:A:78:LEU:O	1:A:78:LEU:HD12	0.55	2.01	38	1
1:A:69:PRO:CB	2:A:168:RCY:H1YB	0.55	2.31	22	1
1:A:73:CYS:HB2	2:A:168:RCY:H1CA	0.55	1.78	22	1
2:A:150:RCY:C1Y	2:A:160:RCY:C1V	0.55	2.78	42	1
1:A:72:ALA:C	1:A:74:ASN:H	0.55	2.05	63	8
2:A:160:RCY:C1U	2:A:168:RCY:H1VB	0.55	2.16	48	1
2:A:160:RCY:H1VB	2:A:168:RCY:H1CB	0.55	1.79	49	1
1:A:69:PRO:CA	2:A:187:RCY:C1C	0.55	2.81	7	1
1:A:65:THR:O	2:A:110:RCY:H1YA	0.55	2.01	63	1
1:A:71:GLU:OE1	2:A:168:RCY:C1Q	0.55	2.55	74	1
1:A:71:GLU:CA	1:A:74:ASN:HD21	0.55	2.15	3	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:67:ILE:C	2:A:150:RCY:H1YA	0.55	2.21	31	1
2:A:176:RCY:H1VA	2:A:187:RCY:O1J	0.54	1.98	8	1
2:A:138:RCY:C1Y	2:A:150:RCY:H1M	0.54	2.21	26	1
2:A:168:RCY:O1H	2:A:176:RCY:H1YB	0.54	1.97	59	1
1:A:70:TRP:O	1:A:75:HIS:CD2	0.54	2.60	57	1
2:A:160:RCY:C1P	2:A:160:RCY:C1V	0.54	2.85	46	1
2:A:168:RCY:H1ZA	2:A:187:RCY:O1G	0.54	2.01	77	1
2:A:150:RCY:C1Z	2:A:176:RCY:H1YB	0.54	2.32	83	1
1:A:66:VAL:CG1	2:A:121:RCY:H1M	0.54	2.32	83	1
2:A:121:RCY:C1Q	2:A:121:RCY:C1V	0.54	2.85	26	5
1:A:67:ILE:O	2:A:168:RCY:H1L	0.54	1.99	75	1
2:A:160:RCY:C1Z	2:A:168:RCY:H1YA	0.54	2.32	55	1
1:A:61:GLY:C	1:A:62:THR:HG23	0.54	2.22	12	3
2:A:168:RCY:C1Y	2:A:173:RCY:H1VA	0.54	0.93	45	1
1:A:68:CYS:SG	2:A:176:RCY:C1M	0.54	2.89	77	1
1:A:67:ILE:O	2:A:150:RCY:C1Y	0.54	2.52	31	1
1:A:64:ILE:HG22	2:A:168:RCY:H1Z	0.54	1.71	83	1
1:A:71:GLU:H	2:A:168:RCY:H1S	0.54	1.61	83	1
2:A:173:RCY:H1YB	2:A:187:RCY:H1ZB	0.54	0.62	92	1
2:A:138:RCY:N1R	2:A:150:RCY:C1V	0.54	2.54	19	1
2:A:168:RCY:H1YB	2:A:187:RCY:C1V	0.54	2.28	82	2
2:A:160:RCY:C1V	2:A:168:RCY:N1R	0.54	2.70	37	2
1:A:59:GLY:N	2:A:160:RCY:O1H	0.54	2.40	91	1
1:A:69:PRO:HG2	2:A:160:RCY:H1YB	0.54	1.79	73	1
2:A:160:RCY:H1YA	2:A:168:RCY:C1V	0.54	2.32	8	1
1:A:72:ALA:O	1:A:74:ASN:ND2	0.54	2.41	8	3
1:A:70:TRP:O	1:A:70:TRP:CG	0.54	2.61	41	3
2:A:173:RCY:C1V	2:A:173:RCY:C1P	0.54	2.81	46	4
2:A:160:RCY:C1C	2:A:160:RCY:C1Q	0.54	2.85	34	1
1:A:69:PRO:CA	2:A:173:RCY:C1Y	0.54	2.72	72	1
1:A:68:CYS:HA	2:A:173:RCY:H1VB	0.54	1.78	80	1
1:A:70:TRP:HE1	2:A:173:RCY:H1L	0.54	1.61	93	1
1:A:62:THR:HA	2:A:130:RCY:H1YB	0.54	1.80	98	1
1:A:69:PRO:HG2	2:A:187:RCY:H1V	0.54	1.79	14	1
2:A:173:RCY:C1W	2:A:176:RCY:O1H	0.54	2.55	52	1
2:A:130:RCY:O1J	2:A:176:RCY:C1C	0.54	2.55	41	1
2:A:176:RCY:H1CA	2:A:187:RCY:C1P	0.54	2.33	86	1
2:A:138:RCY:H1ZA	2:A:187:RCY:H1YA	0.54	0.65	32	2
1:A:78:LEU:N	1:A:78:LEU:CD2	0.54	2.71	21	2
1:A:62:THR:CB	2:A:168:RCY:C1Z	0.54	2.85	72	1
2:A:130:RCY:H1VB	2:A:173:RCY:H1L	0.54	1.78	5	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:71:GLU:CA	2:A:173:RCY:C1S	0.54	2.83	49	1
1:A:77:GLU:OE2	2:A:176:RCY:O1H	0.54	2.25	7	1
1:A:60:CYS:N	2:A:150:RCY:C1V	0.54	2.71	11	1
1:A:67:ILE:HG22	1:A:67:ILE:O	0.54	2.03	32	1
1:A:78:LEU:O	1:A:78:LEU:HD13	0.54	2.03	73	2
2:A:173:RCY:H1M	2:A:176:RCY:C1M	0.54	1.94	89	1
1:A:70:TRP:CD1	2:A:176:RCY:C1V	0.54	2.55	77	1
1:A:64:ILE:HG21	2:A:160:RCY:H1ZA	0.54	1.78	1	1
1:A:71:GLU:CA	2:A:187:RCY:O1G	0.54	2.56	92	1
2:A:173:RCY:C1P	2:A:173:RCY:C1V	0.54	2.81	100	3
2:A:138:RCY:O1J	2:A:187:RCY:H1Z	0.54	2.03	100	1
2:A:138:RCY:H1YA	2:A:150:RCY:C1V	0.54	2.27	19	1
2:A:160:RCY:O1G	2:A:160:RCY:H1ZB	0.54	2.01	34	3
1:A:70:TRP:HE3	2:A:168:RCY:H1ZB	0.54	1.60	41	1
1:A:73:CYS:O	1:A:75:HIS:ND1	0.54	2.41	65	3
1:A:66:VAL:CA	2:A:168:RCY:C1C	0.54	2.86	58	1
1:A:64:ILE:O	2:A:168:RCY:H1L	0.54	2.01	26	1
1:A:65:THR:CA	2:A:168:RCY:H1L	0.54	2.32	26	1
2:A:138:RCY:C1Q	2:A:138:RCY:H1MA	0.54	2.32	79	1
2:A:121:RCY:H1M	2:A:160:RCY:H1ZA	0.54	1.78	44	1
2:A:138:RCY:H1YB	2:A:168:RCY:H1Y	0.54	1.79	7	1
1:A:69:PRO:CG	2:A:173:RCY:H1VB	0.54	2.31	30	1
1:A:69:PRO:C	1:A:71:GLU:H	0.54	2.06	53	19
2:A:138:RCY:C1Z	2:A:176:RCY:H1LA	0.54	2.30	22	1
1:A:75:HIS:CA	2:A:176:RCY:C1S	0.54	2.83	13	1
1:A:78:LEU:C	1:A:78:LEU:CD2	0.54	2.76	12	2
1:A:78:LEU:CD2	2:A:187:RCY:C1V	0.54	2.83	91	1
1:A:69:PRO:CG	2:A:168:RCY:H1L	0.54	2.28	7	1
1:A:77:GLU:OE2	2:A:176:RCY:H1VA	0.54	1.79	7	1
2:A:138:RCY:H1C	2:A:150:RCY:H1L	0.54	1.79	53	1
1:A:67:ILE:HG21	2:A:173:RCY:C1W	0.54	2.26	80	1
1:A:71:GLU:CG	2:A:168:RCY:H1S	0.54	2.29	28	1
1:A:70:TRP:HZ3	2:A:168:RCY:H1ZA	0.54	0.42	98	1
1:A:73:CYS:O	1:A:74:ASN:O	0.54	2.25	34	5
2:A:173:RCY:H1U	2:A:187:RCY:H1LA	0.54	1.80	100	1
2:A:173:RCY:C1M	2:A:176:RCY:C1L	0.54	2.86	38	1
2:A:173:RCY:C1Y	2:A:187:RCY:C1V	0.54	2.10	64	1
1:A:74:ASN:N	2:A:176:RCY:H1VA	0.54	2.07	62	1
1:A:74:ASN:O	2:A:187:RCY:C1M	0.54	2.54	34	1
2:A:173:RCY:H1ZB	2:A:187:RCY:O1J	0.54	2.02	68	1
1:A:69:PRO:HG2	2:A:173:RCY:H1YB	0.54	1.77	35	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:168:RCY:C1U	2:A:173:RCY:C1V	0.54	2.83	48	1
1:A:71:GLU:CG	2:A:176:RCY:O1G	0.54	2.50	44	1
1:A:62:THR:OG1	2:A:168:RCY:C1S	0.54	2.56	23	1
1:A:67:ILE:O	2:A:173:RCY:H1Y	0.54	1.97	63	1
1:A:71:GLU:O	1:A:73:CYS:N	0.54	2.41	19	10
2:A:173:RCY:H1VA	2:A:187:RCY:C1C	0.54	2.01	55	1
2:A:176:RCY:H1CB	2:A:187:RCY:H1YB	0.54	0.75	26	1
2:A:150:RCY:H1C	2:A:187:RCY:H1Z	0.54	1.79	81	1
1:A:66:VAL:O	2:A:173:RCY:C1C	0.54	2.56	71	1
2:A:168:RCY:N1V	2:A:176:RCY:O1G	0.54	2.40	20	1
2:A:138:RCY:C1Y	2:A:160:RCY:H1MA	0.54	2.33	87	1
1:A:70:TRP:HD1	2:A:173:RCY:C1M	0.54	2.13	84	1
1:A:70:TRP:HB3	2:A:173:RCY:H1YB	0.54	1.79	94	1
1:A:70:TRP:CD1	1:A:74:ASN:O	0.54	2.61	26	1
2:A:150:RCY:C1Z	2:A:160:RCY:N1R	0.54	2.71	16	1
1:A:64:ILE:HG13	2:A:168:RCY:H1VB	0.54	1.79	18	1
1:A:71:GLU:O	1:A:75:HIS:CE1	0.54	2.61	57	1
1:A:71:GLU:CG	2:A:168:RCY:O1H	0.54	2.55	37	2
2:A:176:RCY:C1C	2:A:187:RCY:C1X	0.54	2.85	4	1
1:A:64:ILE:CB	2:A:168:RCY:O1H	0.54	2.37	95	1
2:A:150:RCY:C1Z	2:A:168:RCY:C1Y	0.54	2.86	74	1
2:A:160:RCY:N1R	2:A:168:RCY:H1MA	0.54	2.17	96	1
2:A:173:RCY:C1C	2:A:187:RCY:H1YB	0.54	2.33	97	1
2:A:173:RCY:O1G	2:A:173:RCY:C1Z	0.53	2.56	17	1
1:A:76:CYS:CB	2:A:173:RCY:C1Y	0.53	2.86	42	1
1:A:75:HIS:NE2	1:A:78:LEU:O	0.53	2.41	84	1
1:A:70:TRP:NE1	1:A:71:GLU:OE1	0.53	2.40	35	1
1:A:65:THR:CG2	2:A:160:RCY:C1Q	0.53	2.86	36	2
1:A:70:TRP:CE3	2:A:150:RCY:H1Y	0.53	2.21	47	1
2:A:187:RCY:C1V	2:A:187:RCY:C1P	0.53	2.81	31	3
1:A:75:HIS:H	2:A:176:RCY:H1MA	0.53	1.63	67	1
2:A:173:RCY:C1V	2:A:187:RCY:C1W	0.53	2.84	67	1
1:A:71:GLU:HA	2:A:173:RCY:H1L	0.53	1.80	88	1
2:A:168:RCY:H1M	2:A:187:RCY:C1C	0.53	2.32	64	1
1:A:64:ILE:CG2	1:A:67:ILE:H	0.53	2.16	37	1
1:A:62:THR:HG22	2:A:130:RCY:H1U	0.53	1.77	9	1
2:A:187:RCY:C1V	2:A:187:RCY:C1Q	0.53	2.86	51	3
2:A:138:RCY:C1W	2:A:173:RCY:H1ZA	0.53	2.33	32	1
1:A:70:TRP:CE2	2:A:176:RCY:C1W	0.53	2.87	80	1
1:A:61:GLY:O	2:A:160:RCY:H1V	0.53	2.03	97	1
2:A:160:RCY:O1G	2:A:168:RCY:C1P	0.53	2.53	92	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:138:RCY:C1Y	2:A:173:RCY:C1Y	0.53	2.86	92	1
1:A:63:ASP:C	1:A:64:ILE:HG22	0.53	2.22	55	3
2:A:176:RCY:O1H	2:A:187:RCY:C1X	0.53	2.56	42	1
2:A:176:RCY:C1Y	2:A:187:RCY:H1MA	0.53	2.23	69	2
1:A:62:THR:CG2	2:A:168:RCY:H1VA	0.53	2.33	75	1
1:A:71:GLU:CD	2:A:168:RCY:O1G	0.53	2.47	51	3
2:A:138:RCY:H1VB	2:A:150:RCY:H1CA	0.53	1.58	10	1
2:A:130:RCY:H1ZA	2:A:168:RCY:H1VA	0.53	1.78	34	1
1:A:62:THR:CB	2:A:168:RCY:O1G	0.53	2.56	72	1
1:A:70:TRP:NE1	2:A:187:RCY:H1ZB	0.53	2.19	76	1
1:A:67:ILE:O	2:A:168:RCY:O1H	0.53	2.27	87	2
1:A:70:TRP:CZ2	2:A:168:RCY:O1G	0.53	2.51	48	1
1:A:64:ILE:CG2	2:A:168:RCY:H1MA	0.53	2.28	95	1
2:A:168:RCY:C1V	2:A:173:RCY:H1U	0.53	2.28	45	1
2:A:138:RCY:H1VB	2:A:150:RCY:C1X	0.53	2.32	67	1
2:A:130:RCY:C1C	2:A:138:RCY:H1ZB	0.53	2.28	67	1
1:A:74:ASN:HA	2:A:176:RCY:N1R	0.53	2.18	67	1
1:A:67:ILE:C	2:A:168:RCY:H1LA	0.53	1.93	30	1
2:A:173:RCY:C1Y	2:A:176:RCY:C1Q	0.53	2.64	75	1
1:A:78:LEU:C	1:A:78:LEU:HD13	0.53	2.23	76	3
1:A:62:THR:CG2	2:A:130:RCY:C1C	0.53	2.77	18	1
2:A:173:RCY:C1C	2:A:187:RCY:C1M	0.53	2.32	97	1
1:A:71:GLU:HA	2:A:173:RCY:C1C	0.53	2.34	19	1
1:A:71:GLU:O	1:A:74:ASN:ND2	0.53	2.42	8	2
2:A:168:RCY:H1ZA	2:A:173:RCY:C1S	0.53	2.33	58	1
2:A:160:RCY:H1LA	2:A:168:RCY:H1VB	0.53	1.80	60	1
2:A:138:RCY:H1CA	2:A:160:RCY:H1YA	0.53	1.81	26	1
1:A:77:GLU:CD	1:A:77:GLU:H	0.53	2.06	93	6
1:A:69:PRO:HG2	2:A:187:RCY:H1VA	0.53	1.80	72	1
2:A:173:RCY:H1V	2:A:176:RCY:O1J	0.53	2.03	5	1
2:A:150:RCY:C1V	2:A:150:RCY:C1P	0.53	2.86	30	4
1:A:73:CYS:C	2:A:173:RCY:C1Q	0.53	2.77	82	1
1:A:74:ASN:ND2	2:A:173:RCY:C1P	0.53	2.68	27	1
1:A:68:CYS:SG	2:A:187:RCY:N1R	0.53	2.81	92	1
2:A:160:RCY:O1J	2:A:168:RCY:C1X	0.53	2.55	78	1
1:A:69:PRO:HG2	2:A:168:RCY:O1G	0.53	2.03	78	1
2:A:168:RCY:C1V	2:A:168:RCY:C1Q	0.53	2.87	40	6
2:A:176:RCY:C1Z	2:A:187:RCY:O1G	0.53	2.56	100	1
2:A:168:RCY:H1L	2:A:176:RCY:H1MA	0.53	1.81	62	1
1:A:77:GLU:OE2	1:A:78:LEU:N	0.53	2.41	26	1
1:A:70:TRP:H	2:A:176:RCY:H1C	0.53	0.70	13	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:75:HIS:O	1:A:75:HIS:CG	0.53	2.62	59	6
2:A:150:RCY:C1M	2:A:168:RCY:O1H	0.53	2.57	85	1
1:A:64:ILE:HG23	2:A:168:RCY:C1S	0.53	2.33	79	1
2:A:173:RCY:C1U	2:A:176:RCY:H1LA	0.53	2.34	91	1
1:A:71:GLU:HG3	2:A:173:RCY:H1CA	0.53	1.81	89	1
2:A:173:RCY:O1G	2:A:176:RCY:H1L	0.53	1.99	28	1
2:A:138:RCY:C1S	2:A:150:RCY:H1VB	0.53	2.33	98	1
2:A:138:RCY:O1G	2:A:176:RCY:O1J	0.53	2.26	88	1
1:A:73:CYS:HA	2:A:176:RCY:H1MA	0.53	1.80	58	2
2:A:173:RCY:H1S	2:A:176:RCY:C1P	0.53	2.34	59	1
2:A:130:RCY:C1M	2:A:130:RCY:C1U	0.53	2.86	79	1
2:A:160:RCY:C1X	2:A:168:RCY:H1V	0.53	2.24	48	1
1:A:60:CYS:HA	2:A:168:RCY:C1P	0.53	2.23	95	1
2:A:176:RCY:C1Y	2:A:187:RCY:C1X	0.53	2.75	27	1
2:A:173:RCY:H1ZB	2:A:187:RCY:C1P	0.53	0.96	92	1
1:A:63:ASP:C	1:A:65:THR:N	0.53	2.62	35	8
1:A:60:CYS:O	1:A:61:GLY:C	0.53	2.46	94	4
1:A:64:ILE:CD1	1:A:64:ILE:C	0.53	2.76	17	2
1:A:74:ASN:OD1	1:A:75:HIS:N	0.53	2.42	91	9
1:A:70:TRP:HE1	1:A:76:CYS:N	0.53	2.02	26	1
1:A:64:ILE:HD11	2:A:168:RCY:C1M	0.53	2.33	6	1
1:A:63:ASP:OD2	2:A:121:RCY:H1Z	0.53	2.04	57	1
2:A:168:RCY:C1Y	2:A:173:RCY:C1X	0.53	2.73	91	1
1:A:78:LEU:CD1	2:A:176:RCY:C1M	0.53	2.65	91	1
2:A:138:RCY:C1C	2:A:150:RCY:H1L	0.53	2.34	53	1
2:A:168:RCY:C1U	2:A:187:RCY:C1Y	0.53	2.75	87	1
1:A:64:ILE:HD12	2:A:168:RCY:H1ZA	0.53	1.74	6	2
1:A:63:ASP:C	1:A:65:THR:H	0.53	2.06	35	5
1:A:70:TRP:CD1	2:A:173:RCY:C1V	0.53	2.92	38	1
1:A:70:TRP:NE1	2:A:176:RCY:O1H	0.53	2.42	38	1
2:A:173:RCY:N1R	2:A:187:RCY:H1ZB	0.53	2.19	75	1
2:A:176:RCY:N1V	2:A:187:RCY:O1G	0.53	2.39	86	1
2:A:138:RCY:C1M	2:A:150:RCY:H1U	0.53	2.34	60	1
2:A:176:RCY:H1ZA	2:A:187:RCY:H1VA	0.53	1.70	10	1
1:A:75:HIS:CE1	2:A:173:RCY:H1YB	0.53	2.32	33	1
2:A:130:RCY:C1U	2:A:160:RCY:C1W	0.53	2.77	7	1
1:A:66:VAL:C	1:A:67:ILE:HD12	0.53	2.24	32	1
1:A:70:TRP:CB	2:A:187:RCY:C1Z	0.53	2.82	51	1
1:A:65:THR:HG21	2:A:160:RCY:C1Q	0.53	2.34	36	1
2:A:187:RCY:C1P	2:A:187:RCY:C1U	0.53	2.83	25	1
2:A:150:RCY:O1G	2:A:187:RCY:N1V	0.53	2.42	98	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:168:RCY:C1M	2:A:187:RCY:C1L	0.53	2.86	100	1
2:A:173:RCY:H1VA	2:A:176:RCY:H1U	0.53	1.72	38	1
1:A:73:CYS:CB	2:A:176:RCY:H1MA	0.53	2.34	58	1
1:A:70:TRP:O	2:A:173:RCY:H1ZB	0.53	2.04	94	1
1:A:71:GLU:O	2:A:176:RCY:C1P	0.53	2.57	40	1
1:A:64:ILE:HG12	1:A:68:CYS:HB3	0.53	1.81	76	1
2:A:138:RCY:C1V	2:A:150:RCY:H1ZB	0.53	2.03	87	1
2:A:176:RCY:H1U	2:A:187:RCY:O1G	0.53	2.03	97	1
1:A:67:ILE:CD1	2:A:130:RCY:H1Y	0.52	2.33	78	1
2:A:160:RCY:C1Y	2:A:168:RCY:H1LA	0.52	2.30	58	1
2:A:173:RCY:H1Z	2:A:176:RCY:H1MA	0.52	1.80	94	1
1:A:71:GLU:C	2:A:173:RCY:N1R	0.52	2.63	94	1
2:A:176:RCY:O1J	2:A:187:RCY:N1R	0.52	2.34	29	1
1:A:68:CYS:HA	2:A:173:RCY:H1U	0.52	1.80	10	1
1:A:70:TRP:CB	2:A:173:RCY:N1R	0.52	2.65	6	1
2:A:168:RCY:H1VB	2:A:176:RCY:N1V	0.52	2.18	59	1
2:A:176:RCY:H1V	2:A:187:RCY:C1C	0.52	2.33	33	1
1:A:71:GLU:OE2	2:A:168:RCY:C1C	0.52	2.56	32	2
2:A:173:RCY:H1U	2:A:187:RCY:C1L	0.52	2.33	56	1
2:A:130:RCY:C1W	2:A:160:RCY:H1Y	0.52	2.34	67	1
1:A:69:PRO:CG	2:A:168:RCY:C1P	0.52	2.86	78	1
1:A:71:GLU:OE1	2:A:110:RCY:C1U	0.52	2.57	5	1
1:A:66:VAL:CA	2:A:160:RCY:N1V	0.52	2.69	68	1
2:A:168:RCY:H1CA	2:A:187:RCY:O1G	0.52	2.04	70	1
1:A:67:ILE:HG13	2:A:176:RCY:H1CB	0.52	1.72	53	1
2:A:173:RCY:C1W	2:A:187:RCY:H1L	0.52	2.35	45	1
2:A:173:RCY:H1ZA	2:A:176:RCY:H1L	0.52	1.76	20	1
2:A:138:RCY:H1Z	2:A:187:RCY:H1Z	0.52	1.71	77	1
1:A:65:THR:CB	2:A:160:RCY:C1Y	0.52	2.87	100	1
1:A:77:GLU:N	1:A:77:GLU:OE1	0.52	2.42	50	2
2:A:176:RCY:C1P	2:A:176:RCY:C1V	0.52	2.81	9	4
2:A:168:RCY:H1M	2:A:176:RCY:C1Z	0.52	2.34	23	1
1:A:64:ILE:CG2	2:A:168:RCY:O1H	0.52	2.58	54	2
1:A:63:ASP:CG	2:A:160:RCY:H1VB	0.52	2.24	63	1
1:A:75:HIS:CE1	2:A:168:RCY:C1Z	0.52	2.91	73	1
1:A:66:VAL:O	2:A:150:RCY:H1CB	0.52	2.02	96	1
2:A:160:RCY:C1Z	2:A:168:RCY:H1CB	0.52	2.33	1	1
1:A:67:ILE:CG2	2:A:168:RCY:C1U	0.52	2.75	83	1
1:A:61:GLY:O	1:A:62:THR:OG1	0.52	2.26	47	10
2:A:150:RCY:C1M	2:A:187:RCY:C1Y	0.52	2.84	88	1
2:A:160:RCY:C1X	2:A:168:RCY:O1G	0.52	2.57	19	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:176:RCY:C1V	2:A:187:RCY:C1U	0.52	2.81	29	1
1:A:74:ASN:O	2:A:173:RCY:C1C	0.52	2.57	13	1
2:A:176:RCY:H1YB	2:A:187:RCY:O1H	0.52	2.04	76	1
2:A:168:RCY:H1MA	2:A:173:RCY:H1YA	0.52	1.81	49	1
2:A:138:RCY:C1Q	2:A:138:RCY:C1C	0.52	2.88	70	1
1:A:71:GLU:CG	2:A:121:RCY:C1Y	0.52	2.84	4	1
2:A:176:RCY:H1YB	2:A:187:RCY:C1Z	0.52	2.34	47	1
2:A:168:RCY:C1M	2:A:173:RCY:H1VA	0.52	2.29	45	2
1:A:64:ILE:HD12	2:A:160:RCY:H1C	0.52	1.79	39	1
2:A:176:RCY:C1Y	2:A:187:RCY:C1C	0.52	2.70	27	1
1:A:72:ALA:O	2:A:187:RCY:H1YB	0.52	2.04	56	1
1:A:63:ASP:O	1:A:64:ILE:C	0.52	2.48	23	7
1:A:71:GLU:CD	2:A:173:RCY:C1P	0.52	2.78	17	1
2:A:160:RCY:H1ZB	2:A:168:RCY:H1M	0.52	1.70	52	1
2:A:150:RCY:O1J	2:A:160:RCY:C1V	0.52	2.58	6	1
1:A:63:ASP:HA	2:A:168:RCY:C1L	0.52	2.32	59	1
1:A:69:PRO:HG2	2:A:150:RCY:O1J	0.52	2.04	85	1
2:A:150:RCY:H1VA	2:A:176:RCY:H1YA	0.52	1.81	57	1
1:A:67:ILE:CA	2:A:168:RCY:H1L	0.52	2.34	21	1
1:A:63:ASP:HB2	2:A:150:RCY:C1Z	0.52	2.32	80	1
2:A:168:RCY:C1M	2:A:173:RCY:C1C	0.52	2.87	20	1
2:A:168:RCY:O1H	2:A:173:RCY:C1V	0.52	2.58	3	1
2:A:138:RCY:C1V	2:A:173:RCY:H1YB	0.52	2.34	66	1
1:A:67:ILE:HA	2:A:168:RCY:N1R	0.52	2.20	58	1
1:A:70:TRP:CD1	2:A:173:RCY:C1W	0.52	2.92	84	1
2:A:138:RCY:H1VA	2:A:150:RCY:C1Z	0.52	2.35	26	1
2:A:168:RCY:C1V	2:A:176:RCY:H1CA	0.52	2.34	85	2
2:A:150:RCY:H1Z	2:A:160:RCY:O1G	0.52	2.05	6	1
2:A:130:RCY:H1CA	2:A:130:RCY:C1M	0.52	2.26	79	1
1:A:69:PRO:HB3	2:A:173:RCY:H1MA	0.52	1.81	57	1
1:A:78:LEU:HD21	2:A:187:RCY:N1V	0.52	2.05	91	1
1:A:61:GLY:N	1:A:65:THR:OG1	0.52	2.43	36	1
2:A:130:RCY:C1W	2:A:160:RCY:C1Y	0.52	2.88	67	1
1:A:74:ASN:C	1:A:76:CYS:N	0.52	2.63	78	5
1:A:74:ASN:N	1:A:74:ASN:ND2	0.52	2.56	11	2
2:A:173:RCY:O1G	2:A:176:RCY:H1V	0.52	1.99	19	1
1:A:61:GLY:C	1:A:63:ASP:H	0.52	2.08	6	11
2:A:176:RCY:H1ZB	2:A:187:RCY:O1G	0.52	2.05	86	1
1:A:64:ILE:HD12	1:A:68:CYS:HB3	0.52	1.81	86	1
1:A:61:GLY:O	1:A:64:ILE:N	0.52	2.40	94	4
1:A:74:ASN:OD1	1:A:74:ASN:N	0.52	2.43	50	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:77:GLU:CD	1:A:77:GLU:N	0.52	2.63	26	3
2:A:173:RCY:H1ZB	2:A:187:RCY:H1YB	0.52	1.80	72	1
2:A:173:RCY:H1ZB	2:A:176:RCY:H1YB	0.52	0.52	81	1
1:A:65:THR:HG23	1:A:66:VAL:N	0.52	2.20	85	1
1:A:68:CYS:SG	2:A:176:RCY:H1YB	0.52	2.43	18	1
1:A:62:THR:CG2	2:A:168:RCY:O1J	0.52	2.56	7	1
2:A:138:RCY:C1L	2:A:138:RCY:H1V	0.52	2.33	74	1
1:A:69:PRO:CD	2:A:173:RCY:H1Z	0.52	2.30	31	1
2:A:150:RCY:H1YA	2:A:187:RCY:C1U	0.52	2.23	78	1
1:A:71:GLU:CG	2:A:173:RCY:C1Y	0.52	2.87	78	1
1:A:64:ILE:C	1:A:66:VAL:N	0.52	2.61	43	19
1:A:71:GLU:OE2	2:A:176:RCY:H1V	0.52	1.99	17	1
2:A:176:RCY:H1ZB	2:A:176:RCY:O1G	0.52	2.05	8	1
2:A:130:RCY:C1Y	2:A:176:RCY:H1CA	0.52	2.35	41	1
1:A:70:TRP:O	1:A:73:CYS:SG	0.52	2.68	41	2
2:A:138:RCY:O1J	2:A:187:RCY:H1VA	0.52	2.04	86	2
2:A:168:RCY:H1ZB	2:A:187:RCY:H1Y	0.52	1.81	26	1
2:A:168:RCY:O1J	2:A:176:RCY:C1U	0.52	2.46	16	1
2:A:110:RCY:H1ZA	2:A:121:RCY:H1VA	0.52	1.79	81	1
2:A:173:RCY:C1X	2:A:187:RCY:H1Y	0.52	2.33	70	1
1:A:64:ILE:CG2	1:A:66:VAL:H	0.52	2.17	53	1
2:A:173:RCY:H1ZA	2:A:176:RCY:H1VA	0.52	1.00	31	1
2:A:173:RCY:C1W	2:A:176:RCY:H1V	0.52	1.95	31	1
2:A:130:RCY:N1R	2:A:160:RCY:H1Z	0.52	2.19	67	1
2:A:173:RCY:H1C	2:A:187:RCY:H1M	0.52	0.58	97	1
1:A:65:THR:HG23	1:A:66:VAL:HG22	0.52	1.82	38	1
2:A:138:RCY:C1Y	2:A:168:RCY:O1J	0.52	2.57	19	1
2:A:173:RCY:C1X	2:A:187:RCY:H1VA	0.52	2.27	55	1
1:A:71:GLU:OE1	2:A:160:RCY:C1C	0.52	2.56	58	1
1:A:64:ILE:CG1	1:A:65:THR:N	0.52	2.72	89	2
2:A:138:RCY:C1Y	2:A:187:RCY:N1R	0.52	2.69	71	1
2:A:150:RCY:O1G	2:A:187:RCY:C1Z	0.52	2.55	46	2
1:A:70:TRP:CD2	2:A:176:RCY:H1YB	0.52	2.10	80	1
2:A:160:RCY:N1V	2:A:173:RCY:H1C	0.52	2.19	20	1
2:A:173:RCY:C1X	2:A:176:RCY:C1C	0.52	2.88	38	1
1:A:70:TRP:CD1	2:A:168:RCY:C1S	0.52	2.83	42	1
1:A:69:PRO:HB2	2:A:173:RCY:H1V	0.52	1.81	64	1
1:A:77:GLU:OE2	2:A:176:RCY:C1C	0.52	2.58	7	1
2:A:176:RCY:H1Y	2:A:187:RCY:C1L	0.52	2.35	32	1
1:A:71:GLU:OE1	2:A:168:RCY:O1J	0.52	2.28	51	1
1:A:70:TRP:O	1:A:72:ALA:N	0.52	2.43	96	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:67:ILE:HB	2:A:150:RCY:H1V	0.52	0.55	31	1
2:A:160:RCY:H1VA	2:A:168:RCY:H1M	0.52	1.82	93	1
1:A:72:ALA:CB	2:A:173:RCY:O1G	0.52	2.51	30	1
2:A:173:RCY:H1U	2:A:176:RCY:C1P	0.51	2.33	38	1
1:A:76:CYS:SG	2:A:173:RCY:H1YA	0.51	2.43	42	1
1:A:74:ASN:OD1	1:A:75:HIS:CE1	0.51	2.64	76	1
1:A:72:ALA:HA	2:A:173:RCY:C1P	0.51	2.35	21	1
1:A:67:ILE:HG22	2:A:173:RCY:C1L	0.51	2.17	73	1
1:A:78:LEU:CD1	2:A:176:RCY:C1P	0.51	2.82	56	1
1:A:77:GLU:H	2:A:176:RCY:H1L	0.51	1.65	28	1
1:A:66:VAL:CG2	1:A:67:ILE:H	0.51	2.12	83	1
2:A:173:RCY:O1G	2:A:176:RCY:C1Y	0.51	2.52	97	1
1:A:71:GLU:CG	2:A:176:RCY:H1V	0.51	2.36	92	1
1:A:71:GLU:CG	2:A:173:RCY:C1P	0.51	2.80	17	1
1:A:65:THR:O	2:A:176:RCY:H1YB	0.51	2.03	22	1
1:A:68:CYS:SG	2:A:176:RCY:H1C	0.51	2.45	22	1
2:A:168:RCY:H1MA	2:A:176:RCY:C1Y	0.51	2.35	14	1
2:A:176:RCY:C1V	2:A:176:RCY:C1P	0.51	2.85	81	3
1:A:68:CYS:C	1:A:70:TRP:H	0.51	2.08	69	5
2:A:160:RCY:N1V	2:A:168:RCY:C1W	0.51	2.71	5	1
1:A:70:TRP:HE1	1:A:76:CYS:H	0.51	1.48	57	1
1:A:59:GLY:O	1:A:70:TRP:CZ2	0.51	2.62	71	1
2:A:160:RCY:H1CB	2:A:168:RCY:C1V	0.51	2.27	44	1
1:A:67:ILE:HG21	2:A:173:RCY:C1Y	0.51	2.29	80	1
1:A:67:ILE:HD13	2:A:173:RCY:C1Y	0.51	2.36	100	1
2:A:130:RCY:C1M	2:A:160:RCY:C1S	0.51	2.81	8	1
1:A:62:THR:C	1:A:64:ILE:N	0.51	2.64	64	14
2:A:150:RCY:H1YA	2:A:187:RCY:H1YA	0.51	1.63	18	1
1:A:71:GLU:CD	2:A:176:RCY:C1X	0.51	2.78	37	1
1:A:60:CYS:O	2:A:168:RCY:C1U	0.51	2.48	95	1
2:A:138:RCY:O1H	2:A:150:RCY:H1ZB	0.51	1.86	82	1
1:A:71:GLU:C	1:A:74:ASN:HD21	0.51	2.09	3	1
2:A:130:RCY:N1V	2:A:160:RCY:C1Y	0.51	2.51	67	1
1:A:64:ILE:HG22	1:A:64:ILE:O	0.51	2.05	28	4
1:A:63:ASP:O	1:A:64:ILE:CG2	0.51	2.59	88	2
1:A:69:PRO:CB	2:A:187:RCY:C1V	0.51	2.89	14	1
1:A:64:ILE:O	1:A:64:ILE:CD1	0.51	2.59	52	1
1:A:73:CYS:O	1:A:75:HIS:CE1	0.51	2.63	65	1
2:A:168:RCY:C1Z	2:A:173:RCY:C1S	0.51	2.88	58	1
2:A:168:RCY:H1ZA	2:A:176:RCY:H1Z	0.51	1.79	60	1
1:A:70:TRP:HB2	2:A:173:RCY:H1CA	0.51	1.82	40	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:110:RCY:C1V	2:A:110:RCY:C1Q	0.51	2.84	9	3
2:A:160:RCY:H1M	2:A:168:RCY:C1S	0.51	2.16	34	1
1:A:70:TRP:CD1	2:A:187:RCY:C1M	0.51	2.85	16	1
1:A:66:VAL:HB	2:A:160:RCY:N1V	0.51	2.20	68	1
1:A:69:PRO:HA	2:A:173:RCY:O1H	0.51	2.04	3	2
2:A:168:RCY:H1VA	2:A:176:RCY:H1C	0.51	1.81	85	1
1:A:78:LEU:CD2	1:A:78:LEU:C	0.51	2.77	44	1
2:A:173:RCY:C1V	2:A:187:RCY:H1YB	0.51	2.36	53	1
1:A:62:THR:CG2	2:A:160:RCY:O1J	0.51	2.57	46	1
2:A:150:RCY:C1X	2:A:187:RCY:H1V	0.51	2.28	89	1
1:A:75:HIS:CE1	1:A:77:GLU:CD	0.51	2.84	96	1
2:A:173:RCY:C1L	2:A:176:RCY:H1L	0.51	2.25	28	1
2:A:173:RCY:C1V	2:A:187:RCY:N1V	0.51	2.73	67	1
1:A:65:THR:O	1:A:66:VAL:CB	0.51	2.58	86	11
2:A:150:RCY:N1R	2:A:150:RCY:C1M	0.51	2.66	79	1
2:A:176:RCY:C1V	2:A:187:RCY:H1VB	0.51	1.04	33	1
1:A:78:LEU:CG	1:A:78:LEU:O	0.51	2.59	46	1
1:A:67:ILE:CD1	2:A:173:RCY:H1YB	0.51	2.35	80	1
2:A:168:RCY:C1U	2:A:176:RCY:H1ZA	0.51	2.35	98	1
1:A:74:ASN:CG	2:A:176:RCY:O1G	0.51	2.47	78	1
2:A:173:RCY:H1MA	2:A:176:RCY:C1C	0.51	2.30	19	1
2:A:168:RCY:H1LA	2:A:173:RCY:C1W	0.51	2.35	5	1
1:A:64:ILE:CG2	2:A:160:RCY:H1CB	0.51	2.32	48	1
1:A:67:ILE:HG13	2:A:168:RCY:H1CB	0.51	1.82	51	1
1:A:74:ASN:O	2:A:173:RCY:O1G	0.51	2.28	15	1
1:A:65:THR:OG1	2:A:150:RCY:C1Y	0.51	2.58	31	1
2:A:150:RCY:H1VA	2:A:173:RCY:H1VA	0.51	0.60	31	1
1:A:69:PRO:CG	2:A:176:RCY:H1U	0.51	2.30	31	1
2:A:110:RCY:H1M	2:A:121:RCY:C1Y	0.51	2.34	22	1
1:A:74:ASN:ND2	1:A:75:HIS:N	0.51	2.58	29	1
1:A:72:ALA:CA	2:A:173:RCY:H1L	0.51	2.24	10	1
2:A:160:RCY:H1VB	2:A:168:RCY:C1L	0.51	2.17	24	1
1:A:73:CYS:HA	2:A:168:RCY:N1V	0.51	2.17	91	1
2:A:168:RCY:C1L	2:A:176:RCY:H1C	0.51	2.33	49	1
2:A:150:RCY:C1Z	2:A:187:RCY:N1R	0.51	2.74	74	1
1:A:68:CYS:SG	2:A:176:RCY:C1X	0.51	2.98	77	1
2:A:168:RCY:H1VA	2:A:176:RCY:C1Z	0.51	2.35	3	1
1:A:66:VAL:HG12	1:A:67:ILE:N	0.51	2.20	86	1
1:A:70:TRP:C	1:A:72:ALA:N	0.51	2.65	96	2
1:A:77:GLU:CD	1:A:78:LEU:N	0.51	2.64	62	2
2:A:160:RCY:C1X	2:A:168:RCY:O1J	0.51	2.58	94	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:70:TRP:HE1	1:A:76:CYS:CB	0.51	2.19	47	2
1:A:64:ILE:CD1	2:A:187:RCY:C1Y	0.51	2.81	85	1
2:A:110:RCY:C1P	2:A:110:RCY:C1V	0.51	2.88	75	2
1:A:66:VAL:HA	2:A:168:RCY:C1C	0.51	2.35	58	1
1:A:74:ASN:C	2:A:176:RCY:H1C	0.51	2.25	62	1
1:A:63:ASP:O	1:A:64:ILE:HD13	0.51	2.06	24	1
2:A:130:RCY:H1U	2:A:160:RCY:H1MA	0.51	1.56	7	1
1:A:73:CYS:O	1:A:75:HIS:CD2	0.51	2.63	90	1
2:A:173:RCY:H1V	2:A:187:RCY:H1YB	0.51	1.83	31	1
2:A:130:RCY:H1M	2:A:160:RCY:H1Y	0.51	1.81	67	1
1:A:69:PRO:HD3	2:A:173:RCY:C1V	0.51	2.23	30	1
1:A:70:TRP:H	2:A:173:RCY:C1C	0.51	2.19	92	1
1:A:71:GLU:HG2	2:A:176:RCY:H1V	0.51	1.82	92	1
1:A:62:THR:C	2:A:138:RCY:C1Z	0.51	2.80	38	1
2:A:138:RCY:C1Q	2:A:176:RCY:C1V	0.51	2.87	29	1
2:A:150:RCY:C1P	2:A:187:RCY:H1CB	0.51	2.36	18	1
1:A:74:ASN:HD21	2:A:168:RCY:H1YB	0.51	1.56	91	1
2:A:173:RCY:H1VB	2:A:176:RCY:H1YB	0.51	1.43	2	1
1:A:69:PRO:HD3	2:A:173:RCY:H1ZA	0.50	0.54	61	1
2:A:176:RCY:O1G	2:A:187:RCY:O1H	0.50	2.28	38	2
2:A:160:RCY:H1V	2:A:168:RCY:H1V	0.50	1.83	8	2
1:A:69:PRO:CB	2:A:173:RCY:C1V	0.50	2.89	64	1
2:A:150:RCY:H1ZB	2:A:187:RCY:H1VB	0.50	1.83	50	1
2:A:130:RCY:H1Z	2:A:168:RCY:H1VA	0.50	1.84	34	1
1:A:66:VAL:CG2	1:A:67:ILE:N	0.50	2.74	21	2
2:A:138:RCY:H1CB	2:A:150:RCY:C1P	0.50	2.33	53	1
1:A:64:ILE:HD12	2:A:168:RCY:O1G	0.50	2.06	15	1
2:A:176:RCY:C1V	2:A:187:RCY:C1P	0.50	2.77	15	1
2:A:168:RCY:H1ZA	2:A:173:RCY:C1V	0.50	2.33	27	1
2:A:138:RCY:H1VB	2:A:150:RCY:H1MA	0.50	1.84	87	1
1:A:69:PRO:O	1:A:71:GLU:N	0.50	2.44	53	10
1:A:62:THR:C	2:A:138:RCY:H1ZA	0.50	2.23	38	1
2:A:138:RCY:C1V	2:A:168:RCY:C1C	0.50	2.69	19	1
2:A:173:RCY:H1CB	2:A:176:RCY:C1U	0.50	2.31	52	1
1:A:73:CYS:O	1:A:74:ASN:CB	0.50	2.60	62	7
1:A:64:ILE:CA	1:A:68:CYS:SG	0.50	2.99	60	3
1:A:64:ILE:HG21	1:A:67:ILE:O	0.50	2.06	40	2
2:A:173:RCY:O1H	2:A:176:RCY:C1W	0.50	2.59	68	1
2:A:173:RCY:C1Z	2:A:173:RCY:C1Q	0.50	2.88	70	1
2:A:173:RCY:C1Q	2:A:176:RCY:O1G	0.50	2.49	23	2
1:A:62:THR:H	2:A:150:RCY:H1VB	0.50	1.66	11	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:78:LEU:O	1:A:78:LEU:CD1	0.50	2.59	46	3
2:A:130:RCY:C1Y	2:A:138:RCY:C1Z	0.50	2.65	73	1
1:A:76:CYS:CB	2:A:168:RCY:O1G	0.50	2.60	73	1
2:A:150:RCY:H1ZA	2:A:187:RCY:C1P	0.50	2.36	36	1
1:A:74:ASN:O	1:A:75:HIS:CB	0.50	2.60	34	4
2:A:160:RCY:H1YA	2:A:168:RCY:C1P	0.50	2.16	65	1
1:A:75:HIS:C	1:A:76:CYS:SG	0.50	2.89	13	7
1:A:71:GLU:CB	2:A:176:RCY:H1C	0.50	2.37	44	1
1:A:78:LEU:HD22	1:A:78:LEU:N	0.50	2.20	23	2
2:A:138:RCY:O1J	2:A:150:RCY:C1V	0.50	2.58	51	1
2:A:160:RCY:H1YA	2:A:173:RCY:H1CA	0.50	1.80	73	1
2:A:160:RCY:O1J	2:A:173:RCY:C1V	0.50	2.60	20	1
2:A:121:RCY:C1C	2:A:168:RCY:C1C	0.50	2.81	27	1
2:A:187:RCY:C1P	2:A:187:RCY:C1V	0.50	2.89	61	5
1:A:74:ASN:ND2	1:A:75:HIS:NE2	0.50	2.60	38	1
2:A:138:RCY:O1H	2:A:150:RCY:C1Q	0.50	2.59	41	1
2:A:130:RCY:C1Y	2:A:160:RCY:O1J	0.50	2.59	64	1
2:A:130:RCY:H1YA	2:A:160:RCY:O1J	0.50	2.06	64	1
1:A:69:PRO:HA	2:A:173:RCY:H1S	0.50	1.83	24	1
1:A:78:LEU:HD12	1:A:78:LEU:C	0.50	2.27	69	1
2:A:138:RCY:C1U	2:A:187:RCY:H1CA	0.50	1.97	5	1
1:A:64:ILE:O	1:A:65:THR:CG2	0.50	2.60	98	4
2:A:121:RCY:C1S	2:A:121:RCY:C1Z	0.50	2.88	59	1
2:A:160:RCY:H1Z	2:A:168:RCY:H1VA	0.50	1.81	18	1
2:A:176:RCY:H1ZB	2:A:176:RCY:C1P	0.50	2.37	33	1
1:A:70:TRP:O	2:A:176:RCY:H1YB	0.50	2.07	70	1
2:A:168:RCY:H1U	2:A:187:RCY:H1VA	0.50	1.83	90	1
1:A:69:PRO:HG3	2:A:187:RCY:O1G	0.50	2.06	95	1
1:A:76:CYS:SG	2:A:187:RCY:H1C	0.50	2.47	73	1
2:A:150:RCY:C1P	2:A:150:RCY:C1V	0.50	2.89	27	3
2:A:138:RCY:C1C	2:A:168:RCY:C1Z	0.50	2.89	97	1
2:A:173:RCY:O1G	2:A:187:RCY:C1Q	0.50	2.59	88	1
1:A:63:ASP:O	1:A:66:VAL:N	0.50	2.45	17	1
1:A:71:GLU:CA	2:A:173:RCY:H1S	0.50	2.36	49	1
1:A:70:TRP:HZ3	2:A:150:RCY:H1C	0.50	1.65	93	1
2:A:173:RCY:C1Q	2:A:176:RCY:C1U	0.50	2.82	67	1
1:A:67:ILE:HG23	2:A:168:RCY:N1R	0.50	2.22	83	1
2:A:160:RCY:C1V	2:A:160:RCY:C1P	0.50	2.88	6	7
1:A:61:GLY:C	1:A:63:ASP:N	0.50	2.65	5	11
1:A:69:PRO:HG3	2:A:176:RCY:N1R	0.50	2.19	59	1
1:A:59:GLY:O	2:A:150:RCY:H1L	0.50	2.06	85	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:150:RCY:N1V	2:A:187:RCY:C1Y	0.50	2.73	18	1
1:A:76:CYS:SG	2:A:173:RCY:C1L	0.50	2.96	54	1
1:A:63:ASP:HB2	2:A:160:RCY:C1C	0.50	2.04	63	1
2:A:160:RCY:C1P	2:A:168:RCY:H1MA	0.50	2.37	96	1
2:A:176:RCY:C1V	2:A:187:RCY:H1S	0.50	2.37	98	1
2:A:168:RCY:H1ZB	2:A:187:RCY:C1M	0.50	2.36	100	1
2:A:168:RCY:H1YA	2:A:187:RCY:H1S	0.50	0.57	88	1
2:A:130:RCY:H1Y	2:A:176:RCY:H1CA	0.50	1.84	41	1
1:A:75:HIS:N	2:A:173:RCY:C1C	0.50	2.75	91	1
1:A:70:TRP:HB2	2:A:168:RCY:O1H	0.50	2.06	44	1
2:A:173:RCY:C1X	2:A:176:RCY:H1S	0.50	2.23	33	1
1:A:76:CYS:CB	2:A:173:RCY:H1CA	0.50	2.37	73	1
1:A:64:ILE:CA	2:A:168:RCY:H1ZB	0.50	2.35	78	1
2:A:138:RCY:O1H	2:A:150:RCY:C1V	0.50	2.42	19	1
1:A:75:HIS:C	1:A:75:HIS:ND1	0.50	2.65	33	2
1:A:75:HIS:C	2:A:176:RCY:H1CB	0.50	2.27	62	1
1:A:61:GLY:O	1:A:62:THR:CG2	0.50	2.57	60	2
2:A:150:RCY:H1YB	2:A:160:RCY:C1P	0.50	2.37	91	1
1:A:71:GLU:C	2:A:173:RCY:C1V	0.50	2.77	33	1
1:A:70:TRP:CZ2	2:A:168:RCY:C1Y	0.50	2.95	49	1
2:A:173:RCY:C1P	2:A:187:RCY:C1Y	0.50	2.90	70	1
2:A:138:RCY:C1Y	2:A:173:RCY:H1MA	0.50	2.36	32	1
2:A:168:RCY:O1H	2:A:173:RCY:H1MA	0.50	2.07	36	1
1:A:71:GLU:CG	2:A:173:RCY:C1C	0.50	2.90	89	1
1:A:71:GLU:N	1:A:74:ASN:ND2	0.50	2.59	3	1
2:A:138:RCY:C1S	2:A:150:RCY:C1V	0.50	2.90	98	1
1:A:71:GLU:O	1:A:71:GLU:CD	0.50	2.50	37	2
1:A:73:CYS:C	2:A:173:RCY:C1C	0.50	2.77	35	1
2:A:121:RCY:C1V	2:A:121:RCY:C1P	0.50	2.81	95	2
1:A:73:CYS:C	2:A:173:RCY:C1S	0.50	2.80	90	1
1:A:75:HIS:ND1	1:A:75:HIS:C	0.50	2.65	95	1
1:A:70:TRP:O	2:A:168:RCY:H1VA	0.50	1.90	20	1
1:A:71:GLU:O	2:A:176:RCY:C1U	0.50	2.59	20	1
2:A:150:RCY:H1ZB	2:A:150:RCY:C1P	0.50	2.37	56	1
1:A:61:GLY:O	1:A:62:THR:CB	0.49	2.59	60	2
1:A:75:HIS:O	1:A:76:CYS:C	0.49	2.50	13	5
1:A:63:ASP:O	1:A:64:ILE:HG22	0.49	2.07	55	1
2:A:173:RCY:C1Q	2:A:173:RCY:C1V	0.49	2.79	28	2
2:A:176:RCY:H1VA	2:A:187:RCY:C1M	0.49	2.36	29	1
2:A:138:RCY:C1M	2:A:150:RCY:C1Q	0.49	2.90	60	1
2:A:150:RCY:H1CA	2:A:187:RCY:O1J	0.49	2.06	50	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:138:RCY:C1C	2:A:138:RCY:C1Q	0.49	2.90	89	2
2:A:168:RCY:H1V	2:A:176:RCY:C1Y	0.49	1.85	76	1
2:A:168:RCY:C1P	2:A:173:RCY:H1YA	0.49	2.37	49	1
2:A:138:RCY:N1R	2:A:187:RCY:H1ZA	0.49	2.22	49	1
2:A:160:RCY:C1C	2:A:168:RCY:H1Y	0.49	2.36	17	1
1:A:64:ILE:CG2	2:A:168:RCY:C1S	0.49	2.90	79	1
2:A:160:RCY:H1Y	2:A:168:RCY:N1V	0.49	2.22	89	1
2:A:130:RCY:H1Z	2:A:173:RCY:C1U	0.49	2.34	15	1
1:A:71:GLU:C	1:A:73:CYS:H	0.49	2.08	96	4
2:A:160:RCY:H1CA	2:A:168:RCY:H1Y	0.49	1.82	17	1
1:A:64:ILE:HD12	1:A:68:CYS:CB	0.49	2.37	75	1
1:A:70:TRP:HD1	2:A:176:RCY:H1U	0.49	1.03	62	1
2:A:150:RCY:H1Z	2:A:176:RCY:C1V	0.49	2.37	26	1
1:A:65:THR:CG2	2:A:150:RCY:C1C	0.49	2.83	72	1
1:A:70:TRP:CD2	2:A:176:RCY:C1M	0.49	2.95	80	1
1:A:70:TRP:H	2:A:173:RCY:C1X	0.49	2.21	92	1
1:A:75:HIS:C	1:A:77:GLU:N	0.49	2.64	99	7
1:A:75:HIS:CA	2:A:176:RCY:H1CB	0.49	2.37	62	1
2:A:130:RCY:O1J	2:A:160:RCY:O1J	0.49	2.30	81	1
1:A:70:TRP:HZ3	2:A:160:RCY:H1C	0.49	1.67	48	1
2:A:168:RCY:C1V	2:A:173:RCY:C1V	0.49	2.87	45	1
1:A:68:CYS:CB	1:A:70:TRP:NE1	0.49	2.75	89	1
1:A:76:CYS:HA	2:A:173:RCY:C1L	0.49	2.37	28	1
1:A:74:ASN:C	1:A:76:CYS:H	0.49	2.10	32	6
1:A:67:ILE:O	2:A:168:RCY:H1M	0.49	2.03	100	1
1:A:74:ASN:C	1:A:75:HIS:ND1	0.49	2.66	20	3
2:A:130:RCY:C1V	2:A:130:RCY:C1P	0.49	2.85	1	4
1:A:66:VAL:C	2:A:168:RCY:H1SA	0.49	2.27	79	1
2:A:173:RCY:C1U	2:A:187:RCY:C1M	0.49	2.87	32	1
1:A:64:ILE:CD1	1:A:67:ILE:O	0.49	2.59	67	1
2:A:138:RCY:C1V	2:A:138:RCY:C1P	0.49	2.90	88	1
2:A:138:RCY:H1ZA	2:A:176:RCY:C1Q	0.49	2.37	22	1
2:A:150:RCY:C1C	2:A:168:RCY:C1Z	0.49	2.91	19	1
1:A:65:THR:CG2	2:A:168:RCY:H1L	0.49	2.26	55	1
1:A:60:CYS:O	2:A:130:RCY:H1MA	0.49	2.03	18	1
2:A:160:RCY:H1M	2:A:168:RCY:H1Z	0.49	0.52	9	1
1:A:70:TRP:CE2	1:A:71:GLU:OE2	0.49	2.65	7	1
2:A:168:RCY:H1VA	2:A:176:RCY:C1U	0.49	2.25	20	1
1:A:71:GLU:HG3	2:A:150:RCY:C1X	0.49	2.26	96	1
1:A:72:ALA:C	1:A:74:ASN:N	0.49	2.65	68	7
2:A:160:RCY:C1L	2:A:168:RCY:H1CA	0.49	2.37	64	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:69:PRO:O	2:A:176:RCY:H1VA	0.49	2.08	72	2
2:A:168:RCY:C1L	2:A:187:RCY:O1J	0.49	2.59	7	1
2:A:168:RCY:C1P	2:A:173:RCY:C1U	0.49	2.89	21	1
1:A:68:CYS:O	1:A:71:GLU:CG	0.49	2.60	27	2
2:A:138:RCY:H1ZA	2:A:150:RCY:H1VA	0.49	1.83	89	1
2:A:150:RCY:O1J	2:A:176:RCY:C1L	0.49	2.60	3	1
1:A:74:ASN:CB	2:A:176:RCY:C1P	0.49	2.82	52	2
2:A:160:RCY:H1ZB	2:A:168:RCY:H1VA	0.49	1.77	55	1
2:A:168:RCY:C1Z	2:A:173:RCY:C1L	0.49	2.88	58	1
2:A:168:RCY:O1G	2:A:176:RCY:H1VB	0.49	2.08	40	1
2:A:176:RCY:H1U	2:A:187:RCY:C1U	0.49	2.18	26	1
1:A:69:PRO:CG	2:A:173:RCY:O1J	0.49	2.55	9	1
1:A:68:CYS:O	2:A:173:RCY:H1M	0.49	2.06	73	1
1:A:73:CYS:O	1:A:74:ASN:C	0.49	2.51	34	8
2:A:130:RCY:H1VA	2:A:173:RCY:C1S	0.49	2.35	5	1
1:A:59:GLY:CA	2:A:160:RCY:H1S	0.49	2.38	85	1
1:A:59:GLY:N	2:A:160:RCY:C1S	0.49	2.75	85	1
1:A:63:ASP:O	1:A:68:CYS:SG	0.49	2.71	73	4
1:A:70:TRP:HA	2:A:176:RCY:C1Z	0.49	2.35	18	1
1:A:76:CYS:C	1:A:78:LEU:N	0.49	2.66	45	3
2:A:130:RCY:H1YB	2:A:160:RCY:C1Q	0.49	2.25	88	1
1:A:71:GLU:CD	2:A:130:RCY:C1W	0.49	2.80	94	1
1:A:70:TRP:CB	2:A:176:RCY:C1C	0.49	2.91	13	1
1:A:65:THR:HG22	2:A:150:RCY:C1C	0.49	2.38	72	1
1:A:73:CYS:HB2	2:A:168:RCY:H1U	0.49	1.84	57	1
1:A:67:ILE:N	2:A:150:RCY:H1M	0.49	2.23	31	1
1:A:69:PRO:CD	2:A:168:RCY:N1R	0.49	2.75	87	1
2:A:138:RCY:C1Z	2:A:150:RCY:C1Z	0.49	2.77	30	1
1:A:77:GLU:O	1:A:78:LEU:O	0.48	2.31	42	7
1:A:60:CYS:HB3	2:A:168:RCY:H1Z	0.48	1.78	52	1
1:A:70:TRP:CG	2:A:176:RCY:H1C	0.48	2.42	13	1
1:A:71:GLU:CB	2:A:168:RCY:O1G	0.48	2.44	76	1
2:A:110:RCY:H1Z	2:A:121:RCY:H1VA	0.48	1.81	81	1
2:A:168:RCY:H1U	2:A:168:RCY:N1R	0.48	2.05	79	1
2:A:150:RCY:H1Y	2:A:176:RCY:C1Y	0.48	2.27	37	1
1:A:71:GLU:O	2:A:173:RCY:H1VA	0.48	2.05	33	1
1:A:59:GLY:N	2:A:138:RCY:H1S	0.48	2.18	73	1
2:A:138:RCY:H1ZA	2:A:187:RCY:C1C	0.48	1.95	74	1
1:A:69:PRO:CD	2:A:187:RCY:H1YB	0.48	2.37	87	1
2:A:176:RCY:H1CB	2:A:187:RCY:H1M	0.48	1.84	88	1
2:A:173:RCY:O1G	2:A:187:RCY:N1R	0.48	2.45	88	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:71:GLU:HA	2:A:150:RCY:O1J	0.48	2.08	58	1
2:A:176:RCY:H1VA	2:A:187:RCY:C1V	0.48	0.72	33	2
1:A:70:TRP:CB	2:A:173:RCY:C1P	0.48	2.90	6	1
1:A:61:GLY:HA2	2:A:168:RCY:C1Z	0.48	2.38	95	1
1:A:64:ILE:HG22	1:A:66:VAL:H	0.48	1.68	74	1
1:A:61:GLY:C	2:A:160:RCY:C1P	0.48	2.81	19	1
1:A:69:PRO:O	2:A:176:RCY:H1V	0.48	2.08	62	1
1:A:70:TRP:CE3	2:A:168:RCY:H1CB	0.48	2.43	94	1
2:A:176:RCY:H1VA	2:A:187:RCY:H1U	0.48	1.73	29	1
1:A:64:ILE:O	1:A:66:VAL:HG23	0.48	2.09	40	2
1:A:76:CYS:CA	2:A:187:RCY:O1G	0.48	2.61	34	1
2:A:173:RCY:H1VB	2:A:176:RCY:H1ZA	0.48	1.77	4	2
1:A:59:GLY:HA3	2:A:160:RCY:O1G	0.48	2.06	18	1
1:A:76:CYS:O	2:A:176:RCY:C1P	0.48	2.61	57	1
1:A:78:LEU:CD2	2:A:176:RCY:C1W	0.48	2.18	91	1
1:A:78:LEU:HD11	2:A:176:RCY:C1M	0.48	2.35	91	1
1:A:71:GLU:HG3	2:A:168:RCY:H1CB	0.48	1.85	36	2
2:A:160:RCY:H1Z	2:A:168:RCY:C1Q	0.48	2.39	70	1
2:A:173:RCY:C1S	2:A:176:RCY:H1L	0.48	2.32	3	1
1:A:70:TRP:CG	2:A:173:RCY:H1VA	0.48	2.44	38	1
1:A:63:ASP:O	1:A:64:ILE:HB	0.48	2.08	93	2
2:A:168:RCY:C1Z	2:A:173:RCY:C1Q	0.48	2.87	58	1
1:A:70:TRP:CE2	1:A:71:GLU:HG2	0.48	2.43	86	1
2:A:176:RCY:C1M	2:A:187:RCY:C1L	0.48	2.86	26	1
2:A:173:RCY:C1S	2:A:176:RCY:C1P	0.48	2.92	59	1
1:A:68:CYS:SG	2:A:150:RCY:C1M	0.48	2.91	85	1
2:A:168:RCY:H1U	2:A:173:RCY:C1V	0.48	2.39	48	1
2:A:138:RCY:C1P	2:A:138:RCY:C1V	0.48	2.89	54	2
2:A:168:RCY:C1W	2:A:173:RCY:C1M	0.48	2.71	70	1
1:A:73:CYS:C	2:A:176:RCY:C1P	0.48	2.73	70	1
2:A:160:RCY:H1Y	2:A:168:RCY:C1C	0.48	2.36	87	2
1:A:72:ALA:HB3	2:A:173:RCY:N1R	0.48	2.11	80	1
1:A:68:CYS:CA	2:A:173:RCY:C1M	0.48	2.75	73	1
2:A:173:RCY:N1R	2:A:176:RCY:C1Q	0.48	2.73	96	1
1:A:66:VAL:CA	2:A:121:RCY:H1YB	0.48	2.36	83	1
2:A:173:RCY:H1C	2:A:176:RCY:C1P	0.48	2.38	78	1
2:A:130:RCY:C1Y	2:A:176:RCY:H1ZB	0.48	2.31	41	1
2:A:173:RCY:C1M	2:A:187:RCY:H1VA	0.48	2.38	55	1
2:A:130:RCY:N1V	2:A:160:RCY:H1C	0.48	2.21	64	1
2:A:168:RCY:O1G	2:A:173:RCY:H1Z	0.48	2.08	62	1
2:A:168:RCY:H1YA	2:A:176:RCY:H1M	0.48	1.83	94	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:76:CYS:O	1:A:78:LEU:HD12	0.48	2.09	91	1
1:A:75:HIS:HD1	1:A:76:CYS:N	0.48	2.07	33	1
1:A:61:GLY:N	2:A:150:RCY:H1VB	0.48	2.07	11	1
1:A:64:ILE:HD12	2:A:168:RCY:C1Y	0.48	2.39	95	1
2:A:130:RCY:C1Z	2:A:138:RCY:O1J	0.48	2.49	73	1
1:A:71:GLU:N	2:A:176:RCY:N1V	0.48	2.55	77	1
1:A:62:THR:H	2:A:160:RCY:C1S	0.48	2.11	27	1
1:A:73:CYS:C	1:A:75:HIS:H	0.48	2.12	84	7
1:A:69:PRO:HG3	2:A:173:RCY:C1U	0.48	2.21	42	1
2:A:130:RCY:C1P	2:A:130:RCY:C1V	0.48	2.91	14	3
1:A:75:HIS:N	1:A:75:HIS:CD2	0.48	2.81	86	1
1:A:60:CYS:O	2:A:138:RCY:H1L	0.48	2.08	64	1
1:A:71:GLU:CD	2:A:176:RCY:H1ZA	0.48	2.29	84	1
1:A:70:TRP:CE3	2:A:173:RCY:C1Y	0.48	2.94	26	2
2:A:176:RCY:C1X	2:A:187:RCY:C1Y	0.48	2.79	26	1
2:A:130:RCY:H1CA	2:A:160:RCY:N1V	0.48	2.18	16	1
2:A:176:RCY:H1Y	2:A:187:RCY:C1Q	0.48	2.39	76	1
1:A:71:GLU:HG2	2:A:110:RCY:H1ZA	0.48	1.84	57	1
1:A:62:THR:CG2	1:A:63:ASP:N	0.48	2.76	74	2
1:A:68:CYS:SG	2:A:173:RCY:C1Z	0.48	3.02	92	2
1:A:71:GLU:OE2	2:A:176:RCY:H1C	0.48	2.04	97	1
1:A:64:ILE:O	1:A:64:ILE:HG12	0.48	2.09	34	2
1:A:59:GLY:C	1:A:61:GLY:N	0.48	2.67	12	5
1:A:69:PRO:HD3	2:A:168:RCY:C1P	0.48	2.38	31	2
1:A:68:CYS:SG	1:A:68:CYS:O	0.48	2.71	88	1
1:A:63:ASP:HB3	2:A:168:RCY:H1ZB	0.48	1.85	59	1
1:A:64:ILE:HG12	2:A:168:RCY:O1G	0.48	1.76	18	1
2:A:138:RCY:H1Y	2:A:168:RCY:H1YA	0.48	1.80	7	1
1:A:70:TRP:C	2:A:173:RCY:C1M	0.48	2.82	11	1
1:A:71:GLU:N	2:A:168:RCY:C1S	0.48	2.69	83	1
1:A:62:THR:CA	2:A:138:RCY:H1ZB	0.48	2.32	38	1
2:A:160:RCY:C1Z	2:A:168:RCY:C1S	0.48	2.90	19	1
1:A:72:ALA:CB	2:A:173:RCY:O1J	0.48	2.62	75	1
1:A:77:GLU:CD	1:A:78:LEU:H	0.48	2.12	62	1
1:A:71:GLU:OE2	2:A:168:RCY:O1H	0.48	2.20	29	1
2:A:160:RCY:C1Z	2:A:173:RCY:C1Y	0.48	2.91	99	1
2:A:168:RCY:C1U	2:A:176:RCY:C1S	0.48	2.76	42	1
2:A:138:RCY:C1W	2:A:150:RCY:O1H	0.48	2.62	60	1
2:A:173:RCY:H1U	2:A:176:RCY:H1LA	0.48	1.86	69	2
1:A:76:CYS:SG	1:A:78:LEU:HD11	0.48	2.48	69	1
1:A:63:ASP:C	1:A:67:ILE:O	0.48	2.52	68	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:60:CYS:N	2:A:160:RCY:H1ZB	0.48	2.21	91	1
2:A:173:RCY:H1VB	2:A:187:RCY:H1ZB	0.48	1.79	36	1
1:A:64:ILE:HG23	2:A:160:RCY:H1YB	0.48	1.86	1	1
2:A:138:RCY:H1MA	2:A:150:RCY:H1VA	0.48	1.82	75	1
1:A:67:ILE:CG1	2:A:160:RCY:C1V	0.48	2.86	86	1
1:A:73:CYS:C	1:A:75:HIS:N	0.48	2.66	27	5
1:A:63:ASP:O	1:A:67:ILE:N	0.48	2.44	26	1
1:A:70:TRP:O	1:A:74:ASN:O	0.48	2.32	77	2
2:A:160:RCY:O1J	2:A:168:RCY:H1ZA	0.48	2.09	76	1
1:A:70:TRP:CZ3	2:A:168:RCY:H1S	0.48	2.43	37	1
2:A:176:RCY:C1C	2:A:187:RCY:O1H	0.48	2.62	32	1
2:A:168:RCY:C1Y	2:A:176:RCY:C1C	0.48	2.91	90	1
1:A:68:CYS:HB2	1:A:70:TRP:NE1	0.48	2.23	89	1
1:A:71:GLU:OE1	2:A:176:RCY:H1V	0.48	2.01	92	1
2:A:173:RCY:H1M	2:A:187:RCY:H1VA	0.47	1.86	55	1
1:A:75:HIS:O	2:A:176:RCY:H1CA	0.47	2.09	84	1
2:A:130:RCY:H1V	2:A:173:RCY:H1Y	0.47	1.78	94	1
1:A:68:CYS:CA	2:A:173:RCY:O1G	0.47	2.58	10	1
1:A:71:GLU:CB	2:A:176:RCY:O1H	0.47	2.59	76	1
1:A:71:GLU:C	2:A:173:RCY:H1S	0.47	2.29	11	3
1:A:69:PRO:O	1:A:73:CYS:SG	0.47	2.71	81	1
1:A:76:CYS:N	2:A:176:RCY:O1G	0.47	2.46	91	1
2:A:173:RCY:O1J	2:A:187:RCY:H1ZA	0.47	2.08	21	1
2:A:150:RCY:H1U	2:A:168:RCY:H1VA	0.47	1.86	74	1
1:A:65:THR:HG22	2:A:168:RCY:C1L	0.47	2.29	55	1
2:A:187:RCY:H1CA	2:A:187:RCY:O1G	0.47	2.07	5	2
1:A:78:LEU:CD2	1:A:78:LEU:O	0.47	2.57	51	3
1:A:64:ILE:CG1	1:A:66:VAL:H	0.47	2.21	81	2
2:A:173:RCY:C1V	2:A:176:RCY:H1CA	0.47	2.38	49	1
1:A:71:GLU:C	1:A:73:CYS:N	0.47	2.67	96	3
2:A:130:RCY:N1V	2:A:160:RCY:C1V	0.47	2.77	67	1
1:A:72:ALA:CA	2:A:173:RCY:C1P	0.47	2.85	30	1
2:A:168:RCY:C1P	2:A:176:RCY:C1Z	0.47	2.85	13	2
1:A:71:GLU:OE2	1:A:71:GLU:O	0.47	2.32	88	2
2:A:138:RCY:C1C	2:A:187:RCY:H1C	0.47	2.38	5	1
1:A:59:GLY:C	1:A:61:GLY:H	0.47	2.11	37	3
2:A:173:RCY:C1M	2:A:173:RCY:N1R	0.47	2.66	79	1
2:A:173:RCY:H1CA	2:A:187:RCY:H1Y	0.47	1.75	48	1
1:A:65:THR:C	1:A:67:ILE:N	0.47	2.67	51	8
1:A:70:TRP:CE2	2:A:168:RCY:H1L	0.47	2.44	9	1
1:A:63:ASP:OD1	2:A:160:RCY:C1V	0.47	2.62	15	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:63:ASP:N	2:A:160:RCY:H1L	0.47	2.21	3	1
2:A:168:RCY:H1ZB	2:A:187:RCY:H1MA	0.47	1.83	84	2
1:A:65:THR:CG2	1:A:66:VAL:N	0.47	2.77	38	2
2:A:160:RCY:C1Z	2:A:160:RCY:O1H	0.47	2.62	42	1
1:A:63:ASP:HA	2:A:138:RCY:C1P	0.47	2.40	75	1
2:A:173:RCY:C1U	2:A:187:RCY:O1J	0.47	2.63	55	1
2:A:150:RCY:C1W	2:A:187:RCY:H1CB	0.47	2.37	50	1
1:A:62:THR:OG1	1:A:62:THR:O	0.47	2.32	72	3
1:A:67:ILE:HD13	2:A:138:RCY:O1G	0.47	2.10	72	1
1:A:71:GLU:HB3	2:A:168:RCY:C1M	0.47	2.23	37	1
2:A:160:RCY:C1Y	2:A:176:RCY:O1J	0.47	2.62	71	1
2:A:160:RCY:H1YB	2:A:168:RCY:H1ZB	0.47	1.82	9	1
2:A:173:RCY:H1V	2:A:176:RCY:H1YA	0.47	1.85	54	1
1:A:75:HIS:ND1	1:A:75:HIS:O	0.47	2.48	63	1
2:A:130:RCY:N1V	2:A:160:RCY:H1YA	0.47	2.21	67	1
1:A:68:CYS:C	1:A:70:TRP:N	0.47	2.68	75	9
1:A:69:PRO:C	1:A:71:GLU:N	0.47	2.67	79	15
1:A:60:CYS:C	2:A:160:RCY:O1H	0.47	2.52	29	1
1:A:78:LEU:CD2	2:A:138:RCY:C1V	0.47	2.88	40	1
1:A:72:ALA:HB3	2:A:173:RCY:O1G	0.47	2.09	10	1
1:A:78:LEU:CD1	1:A:78:LEU:C	0.47	2.82	76	3
1:A:64:ILE:HG21	2:A:168:RCY:C1Y	0.47	2.40	95	1
1:A:71:GLU:CD	2:A:168:RCY:H1LA	0.47	2.30	74	1
1:A:64:ILE:CD1	2:A:160:RCY:H1CB	0.47	2.38	96	1
1:A:70:TRP:O	2:A:168:RCY:O1G	0.47	2.32	56	1
2:A:173:RCY:H1VB	2:A:187:RCY:C1W	0.47	2.34	67	1
1:A:59:GLY:O	2:A:168:RCY:H1Z	0.47	2.10	52	1
2:A:187:RCY:C1Q	2:A:187:RCY:C1Z	0.47	2.92	58	1
1:A:71:GLU:CB	2:A:168:RCY:H1C	0.47	2.34	86	1
1:A:71:GLU:O	2:A:173:RCY:C1U	0.47	2.62	94	1
1:A:71:GLU:HG2	2:A:168:RCY:C1L	0.47	2.14	29	1
1:A:69:PRO:HB2	2:A:173:RCY:H1L	0.47	1.86	6	1
1:A:67:ILE:HA	2:A:168:RCY:H1L	0.47	1.85	21	1
2:A:138:RCY:H1V	2:A:150:RCY:C1P	0.47	2.40	80	1
1:A:75:HIS:CE1	1:A:77:GLU:H	0.47	2.28	66	1
1:A:69:PRO:O	1:A:74:ASN:N	0.47	2.48	42	1
2:A:168:RCY:C1M	2:A:176:RCY:C1Y	0.47	2.92	14	2
2:A:168:RCY:H1Z	2:A:176:RCY:C1V	0.47	2.40	84	1
2:A:138:RCY:C1C	2:A:150:RCY:H1M	0.47	2.39	62	1
2:A:168:RCY:C1L	2:A:176:RCY:H1MA	0.47	2.39	62	1
1:A:70:TRP:CE3	2:A:160:RCY:C1Y	0.47	2.91	94	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:71:GLU:OE1	2:A:168:RCY:H1M	0.47	2.09	99	1
1:A:75:HIS:HA	2:A:176:RCY:O1H	0.47	2.10	10	1
1:A:59:GLY:O	1:A:60:CYS:C	0.47	2.52	57	3
2:A:173:RCY:C1Y	2:A:176:RCY:O1J	0.47	2.47	76	2
2:A:110:RCY:C1V	2:A:110:RCY:C1P	0.47	2.88	12	2
2:A:130:RCY:H1Y	2:A:160:RCY:N1V	0.47	2.25	81	1
1:A:70:TRP:CE3	2:A:110:RCY:H1Z	0.47	2.44	59	1
1:A:60:CYS:O	2:A:130:RCY:C1M	0.47	2.59	18	1
1:A:78:LEU:HD23	2:A:187:RCY:C1V	0.47	2.38	91	1
1:A:74:ASN:O	1:A:75:HIS:CD2	0.47	2.67	90	4
2:A:138:RCY:H1CB	2:A:187:RCY:H1VB	0.47	1.86	39	1
1:A:66:VAL:HG11	2:A:121:RCY:H1ZA	0.47	1.85	89	1
2:A:150:RCY:H1Z	2:A:176:RCY:C1S	0.47	2.39	3	1
2:A:150:RCY:H1VA	2:A:173:RCY:C1C	0.47	2.39	31	1
2:A:173:RCY:H1ZA	2:A:187:RCY:O1J	0.47	2.10	31	1
2:A:176:RCY:H1YB	2:A:187:RCY:H1C	0.47	1.79	27	1
1:A:70:TRP:NE1	2:A:173:RCY:C1L	0.47	2.77	93	1
1:A:70:TRP:NE1	2:A:173:RCY:C1P	0.47	2.77	93	1
2:A:176:RCY:C1V	2:A:187:RCY:H1MA	0.47	2.39	97	1
2:A:160:RCY:H1CA	2:A:168:RCY:C1Y	0.47	2.40	17	1
1:A:76:CYS:HB3	2:A:173:RCY:H1L	0.47	1.85	14	1
2:A:138:RCY:H1VA	2:A:160:RCY:H1Y	0.47	1.87	29	1
2:A:176:RCY:C1Y	2:A:187:RCY:C1M	0.47	2.90	69	1
2:A:110:RCY:O1J	2:A:121:RCY:C1W	0.47	2.61	5	1
1:A:70:TRP:HB3	2:A:176:RCY:H1M	0.47	1.79	6	1
1:A:59:GLY:C	2:A:150:RCY:H1L	0.47	2.30	85	1
1:A:64:ILE:HD12	1:A:69:PRO:HD3	0.47	1.86	71	1
1:A:76:CYS:N	2:A:176:RCY:H1ZB	0.47	2.24	44	1
1:A:74:ASN:N	2:A:173:RCY:O1J	0.47	2.47	22	1
2:A:160:RCY:C1Z	2:A:173:RCY:H1YB	0.47	2.40	99	1
1:A:64:ILE:CG2	1:A:68:CYS:SG	0.47	3.03	24	1
2:A:173:RCY:H1VA	2:A:187:RCY:C1Q	0.47	2.40	76	1
1:A:74:ASN:OD1	1:A:75:HIS:CG	0.47	2.67	76	1
1:A:59:GLY:H	2:A:160:RCY:H1ZA	0.47	1.70	91	1
2:A:173:RCY:H1VB	2:A:176:RCY:H1CA	0.47	1.80	49	1
1:A:71:GLU:OE1	1:A:71:GLU:O	0.47	2.32	49	1
1:A:70:TRP:HD1	2:A:176:RCY:C1L	0.47	2.20	32	1
1:A:60:CYS:HB3	2:A:168:RCY:C1C	0.47	2.20	95	1
2:A:173:RCY:N1V	2:A:187:RCY:C1L	0.47	2.60	96	1
2:A:173:RCY:H1Y	2:A:176:RCY:H1C	0.47	1.86	3	1
2:A:160:RCY:H1VA	2:A:168:RCY:C1M	0.47	2.39	93	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:69:PRO:CG	2:A:176:RCY:H1ZA	0.47	2.23	66	1
1:A:69:PRO:HD3	2:A:168:RCY:H1CB	0.47	1.81	66	1
2:A:150:RCY:H1Z	2:A:176:RCY:H1YB	0.47	1.85	83	1
1:A:65:THR:O	2:A:121:RCY:C1Y	0.47	2.62	83	1
2:A:138:RCY:C1S	2:A:150:RCY:C1C	0.47	2.93	43	1
1:A:73:CYS:O	1:A:74:ASN:CG	0.47	2.53	42	11
1:A:61:GLY:C	1:A:62:THR:OG1	0.47	2.53	60	2
1:A:71:GLU:O	1:A:71:GLU:CG	0.47	2.63	88	1
1:A:70:TRP:CA	2:A:168:RCY:H1VB	0.47	2.28	22	1
1:A:75:HIS:O	1:A:76:CYS:CB	0.47	2.60	87	6
2:A:173:RCY:C1Q	2:A:187:RCY:H1CB	0.47	2.35	99	1
2:A:168:RCY:H1U	2:A:173:RCY:O1J	0.47	2.10	10	1
1:A:70:TRP:CB	2:A:176:RCY:H1C	0.47	2.38	13	1
1:A:67:ILE:O	2:A:168:RCY:C1V	0.47	2.63	5	1
2:A:160:RCY:H1M	2:A:168:RCY:H1V	0.47	0.78	48	1
1:A:71:GLU:HB3	2:A:176:RCY:H1C	0.47	1.86	44	1
2:A:150:RCY:H1CB	2:A:176:RCY:N1R	0.47	2.24	82	1
2:A:138:RCY:O1G	2:A:160:RCY:H1CB	0.47	2.10	67	1
1:A:63:ASP:OD2	2:A:121:RCY:N1V	0.46	2.48	42	1
1:A:74:ASN:O	1:A:74:ASN:OD1	0.46	2.32	42	2
1:A:75:HIS:HB3	2:A:176:RCY:H1C	0.46	1.84	84	1
1:A:67:ILE:CG2	1:A:72:ALA:HB2	0.46	2.40	60	1
1:A:75:HIS:C	2:A:176:RCY:C1Q	0.46	2.80	10	1
1:A:67:ILE:HA	2:A:168:RCY:C1L	0.46	2.39	21	1
2:A:138:RCY:N1V	2:A:160:RCY:C1Q	0.46	2.78	73	1
2:A:160:RCY:C1Y	2:A:173:RCY:H1CA	0.46	2.41	73	1
2:A:173:RCY:H1V	2:A:187:RCY:H1ZB	0.46	1.83	36	1
1:A:69:PRO:N	2:A:173:RCY:H1ZA	0.46	2.15	61	1
2:A:160:RCY:C1C	2:A:168:RCY:C1Y	0.46	2.93	17	1
2:A:138:RCY:H1ZA	2:A:176:RCY:C1P	0.46	2.40	22	1
1:A:69:PRO:HD3	2:A:168:RCY:C1U	0.46	2.39	87	2
2:A:173:RCY:H1CB	2:A:176:RCY:H1Z	0.46	1.83	84	1
1:A:72:ALA:HB3	2:A:121:RCY:O1J	0.46	2.10	94	1
2:A:150:RCY:H1YB	2:A:160:RCY:C1Y	0.46	2.38	29	1
1:A:64:ILE:HG21	1:A:67:ILE:C	0.46	2.31	40	2
2:A:110:RCY:H1YB	2:A:121:RCY:H1VA	0.46	1.56	81	1
2:A:168:RCY:O1J	2:A:187:RCY:H1VB	0.46	1.96	70	1
2:A:168:RCY:H1M	2:A:173:RCY:C1V	0.46	2.39	45	1
2:A:138:RCY:C1M	2:A:150:RCY:O1G	0.46	2.38	1	1
2:A:173:RCY:C1Y	2:A:187:RCY:O1J	0.46	2.49	92	2
2:A:150:RCY:H1VB	2:A:160:RCY:C1V	0.46	2.05	42	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:75:HIS:O	2:A:176:RCY:H1L	0.46	2.09	13	1
1:A:59:GLY:C	2:A:160:RCY:O1H	0.46	2.46	91	1
2:A:160:RCY:H1Z	2:A:168:RCY:O1H	0.46	2.09	70	1
2:A:173:RCY:N1V	2:A:176:RCY:H1ZA	0.46	2.26	77	1
1:A:69:PRO:HG3	2:A:150:RCY:H1YA	0.46	1.87	3	1
1:A:66:VAL:HG21	2:A:150:RCY:O1G	0.46	2.10	61	1
2:A:168:RCY:N1V	2:A:187:RCY:C1P	0.46	2.79	88	1
1:A:71:GLU:CD	2:A:173:RCY:O1G	0.46	2.51	17	1
2:A:150:RCY:H1V	2:A:160:RCY:H1YA	0.46	1.61	42	1
2:A:160:RCY:C1Y	2:A:168:RCY:H1L	0.46	2.26	1	2
2:A:173:RCY:C1Y	2:A:176:RCY:H1CB	0.46	2.27	86	1
1:A:71:GLU:HA	2:A:173:RCY:H1CB	0.46	1.87	84	1
1:A:65:THR:C	1:A:66:VAL:CG2	0.46	2.84	34	2
1:A:69:PRO:HG3	2:A:173:RCY:H1L	0.46	1.87	24	1
1:A:67:ILE:CA	2:A:176:RCY:C1V	0.46	2.42	16	1
1:A:64:ILE:CD1	2:A:168:RCY:O1G	0.46	2.22	12	1
1:A:70:TRP:O	2:A:173:RCY:C1Q	0.46	2.63	68	2
1:A:60:CYS:HA	2:A:138:RCY:C1V	0.46	2.40	7	1
2:A:138:RCY:C1Y	2:A:168:RCY:C1Y	0.46	2.73	7	1
1:A:64:ILE:CD1	1:A:68:CYS:SG	0.46	3.02	39	1
1:A:67:ILE:HA	2:A:168:RCY:H1CB	0.46	1.86	27	1
1:A:65:THR:CG2	1:A:66:VAL:HG22	0.46	2.39	38	1
1:A:70:TRP:CE3	2:A:168:RCY:C1X	0.46	2.97	94	1
2:A:138:RCY:H1M	2:A:187:RCY:C1W	0.46	2.38	68	1
2:A:176:RCY:C1V	2:A:187:RCY:H1VA	0.46	0.82	33	1
1:A:69:PRO:CG	2:A:173:RCY:H1MA	0.46	2.41	4	1
2:A:176:RCY:H1VB	2:A:187:RCY:C1Y	0.46	2.34	4	1
2:A:138:RCY:H1Y	2:A:187:RCY:H1MA	0.46	1.88	63	1
2:A:168:RCY:H1C	2:A:176:RCY:H1Z	0.46	1.23	3	1
2:A:138:RCY:O1J	2:A:187:RCY:N1V	0.46	2.48	100	1
1:A:78:LEU:C	1:A:78:LEU:CD1	0.46	2.84	30	3
1:A:69:PRO:O	2:A:150:RCY:O1J	0.46	2.34	34	1
1:A:64:ILE:O	1:A:68:CYS:N	0.46	2.49	93	2
2:A:150:RCY:C1C	2:A:187:RCY:C1Z	0.46	2.94	81	1
2:A:173:RCY:N1R	2:A:176:RCY:O1G	0.46	2.48	59	1
2:A:121:RCY:C1M	2:A:160:RCY:H1ZA	0.46	2.40	44	1
1:A:71:GLU:CB	2:A:176:RCY:C1C	0.46	2.93	44	1
1:A:70:TRP:CB	2:A:168:RCY:O1H	0.46	2.64	44	1
2:A:138:RCY:C1Q	2:A:138:RCY:C1V	0.46	2.84	36	1
2:A:138:RCY:C1X	2:A:173:RCY:C1Z	0.46	2.94	15	1
1:A:67:ILE:HG21	2:A:150:RCY:C1V	0.46	2.38	31	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:77:GLU:HB2	2:A:176:RCY:O1G	0.46	2.11	31	1
1:A:67:ILE:CA	2:A:168:RCY:H1CB	0.46	2.41	27	1
2:A:138:RCY:C1M	2:A:150:RCY:H1VA	0.46	2.35	75	1
1:A:61:GLY:O	1:A:63:ASP:OD1	0.46	2.34	40	3
2:A:150:RCY:O1H	2:A:187:RCY:O1G	0.46	2.34	50	1
1:A:72:ALA:O	1:A:74:ASN:OD1	0.46	2.34	15	4
1:A:65:THR:O	1:A:66:VAL:CG1	0.46	2.59	10	2
1:A:71:GLU:HB3	2:A:176:RCY:O1H	0.46	2.11	76	1
1:A:71:GLU:CB	2:A:173:RCY:H1YA	0.46	2.36	33	1
1:A:64:ILE:C	1:A:65:THR:OG1	0.46	2.53	11	1
2:A:130:RCY:C1L	2:A:130:RCY:H1ZB	0.46	2.41	2	1
2:A:173:RCY:C1C	2:A:187:RCY:C1U	0.46	2.92	88	1
1:A:69:PRO:HB2	2:A:187:RCY:C1V	0.46	2.33	14	1
1:A:71:GLU:O	1:A:74:ASN:OD1	0.46	2.34	50	2
1:A:64:ILE:O	1:A:68:CYS:CB	0.46	2.63	5	1
1:A:70:TRP:HA	2:A:173:RCY:H1YB	0.46	1.85	85	1
2:A:173:RCY:H1VB	2:A:187:RCY:C1P	0.46	2.41	57	1
1:A:71:GLU:OE2	2:A:176:RCY:C1X	0.46	2.54	37	1
1:A:60:CYS:O	1:A:64:ILE:CG2	0.46	2.64	44	1
2:A:168:RCY:C1C	2:A:173:RCY:H1YB	0.46	2.07	21	1
1:A:68:CYS:HB2	1:A:70:TRP:CE2	0.46	2.45	53	2
1:A:61:GLY:CA	2:A:168:RCY:H1MA	0.46	2.41	95	1
2:A:187:RCY:H1VB	2:A:187:RCY:O1G	0.46	2.11	82	1
1:A:74:ASN:CB	2:A:176:RCY:C1L	0.46	2.87	78	1
1:A:64:ILE:CD1	2:A:168:RCY:H1VB	0.46	2.40	58	1
1:A:69:PRO:O	1:A:74:ASN:O	0.46	2.33	59	1
1:A:69:PRO:CD	2:A:150:RCY:H1V	0.46	2.33	85	1
1:A:64:ILE:O	1:A:64:ILE:HD13	0.46	2.11	53	1
1:A:66:VAL:HG12	1:A:67:ILE:HD12	0.46	1.88	95	1
1:A:69:PRO:CG	2:A:168:RCY:C1V	0.46	2.93	63	1
1:A:68:CYS:HB3	1:A:69:PRO:HD2	0.46	1.87	63	1
1:A:71:GLU:N	2:A:176:RCY:O1J	0.46	2.49	77	1
2:A:160:RCY:H1YA	2:A:168:RCY:N1R	0.46	2.22	100	1
2:A:150:RCY:H1YB	2:A:173:RCY:H1Z	0.46	1.87	8	1
1:A:60:CYS:C	2:A:160:RCY:H1S	0.46	2.30	24	1
2:A:176:RCY:C1M	2:A:187:RCY:H1ZA	0.46	2.30	5	1
1:A:60:CYS:C	2:A:130:RCY:C1U	0.46	2.83	18	1
2:A:173:RCY:H1VB	2:A:176:RCY:C1Z	0.46	2.41	2	1
1:A:70:TRP:HE1	2:A:173:RCY:C1L	0.46	2.23	93	1
1:A:72:ALA:C	1:A:74:ASN:ND2	0.46	2.69	87	1
1:A:76:CYS:O	1:A:77:GLU:O	0.45	2.34	90	9

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:73:CYS:O	1:A:74:ASN:OD1	0.45	2.34	62	1
2:A:176:RCY:H1V	2:A:187:RCY:O1G	0.45	2.11	10	1
1:A:77:GLU:OE1	1:A:77:GLU:N	0.45	2.47	47	2
1:A:67:ILE:C	2:A:168:RCY:H1L	0.45	2.30	91	2
2:A:168:RCY:C1W	2:A:173:RCY:H1VA	0.45	1.92	45	1
2:A:150:RCY:N1V	2:A:150:RCY:O1G	0.45	2.50	56	1
2:A:110:RCY:N1V	2:A:110:RCY:O1G	0.45	2.49	42	2
2:A:130:RCY:C1Q	2:A:160:RCY:O1G	0.45	2.64	62	1
1:A:71:GLU:CD	2:A:110:RCY:O1G	0.45	2.52	5	1
1:A:59:GLY:H	2:A:160:RCY:H1S	0.45	1.70	85	1
1:A:64:ILE:N	2:A:138:RCY:H1VB	0.45	2.19	85	1
2:A:138:RCY:H1C	2:A:160:RCY:H1ZA	0.45	1.88	71	1
1:A:75:HIS:C	1:A:75:HIS:HD1	0.45	2.14	33	1
2:A:150:RCY:H1M	2:A:160:RCY:C1Z	0.45	2.41	21	1
2:A:168:RCY:C1P	2:A:173:RCY:H1U	0.45	2.42	21	1
2:A:130:RCY:C1L	2:A:130:RCY:C1Z	0.45	2.92	2	1
2:A:138:RCY:C1P	2:A:187:RCY:C1V	0.45	2.90	39	1
2:A:168:RCY:H1YA	2:A:187:RCY:H1ZB	0.45	1.87	31	1
2:A:168:RCY:C1U	2:A:173:RCY:C1M	0.45	2.83	27	1
1:A:62:THR:OG1	1:A:65:THR:CA	0.45	2.64	87	1
1:A:76:CYS:SG	1:A:78:LEU:O	0.45	2.74	1	1
1:A:69:PRO:HG3	2:A:173:RCY:H1VB	0.45	1.89	30	1
1:A:67:ILE:CG2	2:A:168:RCY:H1U	0.45	2.39	83	1
1:A:73:CYS:C	2:A:173:RCY:C1W	0.45	2.84	22	1
1:A:68:CYS:O	1:A:69:PRO:C	0.45	2.54	90	10
1:A:59:GLY:O	1:A:60:CYS:CB	0.45	2.64	41	1
1:A:72:ALA:O	1:A:76:CYS:SG	0.45	2.74	75	1
2:A:130:RCY:C1C	2:A:173:RCY:O1G	0.45	2.64	18	1
2:A:138:RCY:H1Y	2:A:176:RCY:C1S	0.45	2.42	48	1
1:A:74:ASN:ND2	1:A:74:ASN:O	0.45	2.48	74	1
2:A:173:RCY:C1X	2:A:176:RCY:O1J	0.45	2.65	3	1
2:A:138:RCY:O1J	2:A:150:RCY:C1W	0.45	2.64	43	1
1:A:70:TRP:CD2	1:A:71:GLU:CG	0.45	3.00	86	1
1:A:64:ILE:HA	2:A:168:RCY:C1S	0.45	2.41	5	1
1:A:68:CYS:HB3	2:A:173:RCY:C1Z	0.45	2.41	5	1
1:A:70:TRP:HH2	2:A:168:RCY:C1Z	0.45	2.16	59	1
2:A:150:RCY:C1C	2:A:187:RCY:H1C	0.45	2.33	18	1
2:A:138:RCY:H1MA	2:A:187:RCY:H1C	0.45	1.88	37	1
1:A:71:GLU:O	1:A:71:GLU:OE1	0.45	2.34	37	1
2:A:138:RCY:H1CA	2:A:160:RCY:C1C	0.45	2.23	49	1
2:A:130:RCY:O1J	2:A:160:RCY:C1U	0.45	2.63	23	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:62:THR:O	2:A:160:RCY:H1C	0.45	2.08	46	1
2:A:173:RCY:C1Q	2:A:176:RCY:C1Y	0.45	2.90	77	1
1:A:69:PRO:HD2	2:A:173:RCY:C1C	0.45	2.40	77	1
2:A:176:RCY:C1U	2:A:187:RCY:H1U	0.45	2.28	96	1
2:A:138:RCY:H1S	2:A:160:RCY:N1R	0.45	2.23	27	1
2:A:176:RCY:H1CB	2:A:187:RCY:H1VB	0.45	1.80	93	1
1:A:64:ILE:HG23	1:A:66:VAL:N	0.45	2.23	83	1
1:A:63:ASP:C	2:A:168:RCY:C1Z	0.45	2.73	78	1
1:A:71:GLU:CB	2:A:173:RCY:C1Y	0.45	2.70	78	2
2:A:187:RCY:O1G	2:A:187:RCY:N1V	0.45	2.50	76	2
2:A:173:RCY:O1H	2:A:176:RCY:C1M	0.45	2.63	61	1
2:A:138:RCY:H1MA	2:A:176:RCY:H1LA	0.45	1.86	22	1
2:A:160:RCY:O1G	2:A:160:RCY:N1V	0.45	2.50	52	3
2:A:160:RCY:H1YA	2:A:168:RCY:H1ZA	0.45	1.73	62	1
1:A:64:ILE:HA	1:A:68:CYS:SG	0.45	2.51	63	3
1:A:63:ASP:C	1:A:68:CYS:SG	0.45	2.95	50	1
2:A:160:RCY:H1M	2:A:168:RCY:C1Q	0.45	2.36	34	1
2:A:176:RCY:N1R	2:A:187:RCY:C1M	0.45	2.77	26	1
1:A:70:TRP:HD1	2:A:187:RCY:H1MA	0.45	1.71	16	1
2:A:173:RCY:O1J	2:A:176:RCY:H1CB	0.45	2.11	6	1
1:A:63:ASP:HA	2:A:168:RCY:H1L	0.45	1.88	59	1
1:A:70:TRP:O	1:A:71:GLU:CG	0.45	2.65	28	2
2:A:138:RCY:H1U	2:A:160:RCY:C1C	0.45	2.41	67	1
2:A:160:RCY:C1W	2:A:168:RCY:H1Y	0.45	2.41	78	1
2:A:130:RCY:C1Y	2:A:176:RCY:C1C	0.45	2.92	41	1
2:A:168:RCY:H1VB	2:A:173:RCY:C1Q	0.45	2.42	29	1
1:A:63:ASP:O	1:A:67:ILE:O	0.45	2.35	26	2
1:A:71:GLU:OE2	2:A:168:RCY:C1Q	0.45	2.64	70	1
1:A:75:HIS:CD2	1:A:76:CYS:H	0.45	2.30	6	1
1:A:64:ILE:O	2:A:138:RCY:H1M	0.45	2.12	85	1
1:A:59:GLY:N	2:A:160:RCY:H1S	0.45	2.26	85	1
1:A:59:GLY:O	2:A:150:RCY:C1L	0.45	2.64	85	1
2:A:168:RCY:N1R	2:A:173:RCY:H1U	0.45	2.26	48	1
2:A:160:RCY:C1Y	2:A:168:RCY:C1Y	0.45	2.84	53	1
1:A:78:LEU:HD23	2:A:187:RCY:H1ZA	0.45	1.88	73	1
1:A:69:PRO:HG3	2:A:187:RCY:C1M	0.45	2.42	14	1
2:A:138:RCY:H1MA	2:A:187:RCY:H1U	0.45	1.83	13	1
1:A:71:GLU:O	1:A:72:ALA:O	0.45	2.34	72	1
2:A:160:RCY:C1C	2:A:160:RCY:H1U	0.45	2.36	79	1
1:A:70:TRP:HB2	2:A:168:RCY:H1LA	0.45	1.89	70	1
1:A:71:GLU:HG3	2:A:168:RCY:O1G	0.45	2.07	32	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:62:THR:HB	2:A:160:RCY:O1J	0.45	2.11	46	1
1:A:75:HIS:CD2	2:A:173:RCY:O1H	0.45	2.69	42	1
2:A:138:RCY:O1G	2:A:138:RCY:N1V	0.45	2.50	65	2
1:A:72:ALA:N	2:A:168:RCY:H1CB	0.45	2.26	86	1
2:A:168:RCY:N1V	2:A:187:RCY:H1C	0.45	2.01	40	1
1:A:73:CYS:H	2:A:168:RCY:H1U	0.45	1.71	99	1
2:A:110:RCY:C1W	2:A:121:RCY:C1V	0.45	2.95	5	1
1:A:68:CYS:CB	2:A:173:RCY:C1Z	0.45	2.95	5	1
1:A:64:ILE:H	2:A:138:RCY:C1V	0.45	2.12	85	1
1:A:73:CYS:O	1:A:77:GLU:OE1	0.45	2.34	48	1
2:A:168:RCY:C1L	2:A:176:RCY:C1V	0.45	2.95	49	1
2:A:168:RCY:H1YA	2:A:187:RCY:C1X	0.45	2.40	90	1
1:A:72:ALA:CB	2:A:173:RCY:H1U	0.45	2.36	80	1
2:A:173:RCY:O1J	2:A:176:RCY:H1YB	0.45	2.08	82	1
1:A:71:GLU:O	2:A:176:RCY:H1CA	0.45	2.12	20	1
2:A:138:RCY:H1YB	2:A:160:RCY:H1ZB	0.45	1.89	87	1
2:A:176:RCY:C1U	2:A:187:RCY:O1G	0.45	2.65	97	1
1:A:63:ASP:OD2	2:A:160:RCY:C1L	0.45	2.65	92	1
2:A:176:RCY:O1G	2:A:176:RCY:N1V	0.45	2.50	38	1
2:A:168:RCY:H1CA	2:A:173:RCY:C1S	0.45	2.42	8	1
1:A:67:ILE:HG12	2:A:160:RCY:C1X	0.45	2.42	86	1
2:A:130:RCY:C1C	2:A:160:RCY:H1ZB	0.45	2.34	62	1
1:A:71:GLU:CD	1:A:71:GLU:C	0.45	2.74	60	1
1:A:72:ALA:C	2:A:173:RCY:C1L	0.45	2.78	10	1
1:A:69:PRO:CG	2:A:176:RCY:C1Q	0.45	2.95	59	1
2:A:160:RCY:C1Z	2:A:173:RCY:C1X	0.45	2.89	37	1
2:A:150:RCY:H1M	2:A:160:RCY:O1G	0.45	2.12	91	1
1:A:78:LEU:CD2	2:A:187:RCY:O1J	0.45	2.64	91	1
1:A:66:VAL:O	2:A:173:RCY:H1CA	0.45	2.12	71	1
1:A:77:GLU:O	1:A:77:GLU:OE2	0.45	2.35	49	1
1:A:71:GLU:OE2	2:A:168:RCY:C1S	0.45	2.65	70	1
2:A:150:RCY:C1Z	2:A:168:RCY:H1Y	0.45	2.42	74	1
1:A:64:ILE:HG13	2:A:168:RCY:H1LA	0.45	1.88	15	1
1:A:71:GLU:OE1	2:A:176:RCY:C1C	0.45	2.63	97	1
2:A:121:RCY:O1G	2:A:121:RCY:N1V	0.44	2.50	78	2
2:A:168:RCY:N1V	2:A:173:RCY:O1H	0.44	2.49	8	1
2:A:160:RCY:H1YA	2:A:168:RCY:H1Z	0.44	1.89	62	1
1:A:70:TRP:CZ2	2:A:176:RCY:N1V	0.44	2.84	94	1
2:A:176:RCY:H1CA	2:A:187:RCY:C1Z	0.44	2.42	99	1
1:A:64:ILE:HD11	2:A:121:RCY:O1G	0.44	1.97	68	1
2:A:168:RCY:O1G	2:A:168:RCY:N1V	0.44	2.50	51	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:160:RCY:C1C	2:A:168:RCY:H1YA	0.44	2.42	37	1
2:A:173:RCY:O1H	2:A:176:RCY:N1R	0.44	2.51	70	1
1:A:65:THR:C	1:A:66:VAL:HG22	0.44	2.32	32	1
1:A:64:ILE:CD1	2:A:168:RCY:N1V	0.44	2.79	4	1
2:A:168:RCY:H1YA	2:A:173:RCY:C1V	0.44	0.31	45	1
1:A:77:GLU:HA	2:A:176:RCY:H1MA	0.44	1.89	73	1
1:A:76:CYS:HA	2:A:187:RCY:C1C	0.44	2.36	73	1
1:A:76:CYS:O	2:A:160:RCY:C1C	0.44	2.62	73	1
1:A:64:ILE:HG13	1:A:66:VAL:H	0.44	1.71	89	1
1:A:63:ASP:O	1:A:64:ILE:O	0.44	2.35	8	1
2:A:176:RCY:C1Z	2:A:176:RCY:C1Q	0.44	2.94	94	1
2:A:138:RCY:H1Z	2:A:150:RCY:H1S	0.44	1.87	60	1
2:A:176:RCY:O1H	2:A:187:RCY:C1Z	0.44	2.65	60	1
1:A:75:HIS:O	2:A:176:RCY:C1L	0.44	2.64	13	1
1:A:77:GLU:O	1:A:78:LEU:CB	0.44	2.65	24	4
2:A:150:RCY:O1J	2:A:160:RCY:H1VA	0.44	2.12	6	1
1:A:60:CYS:SG	2:A:130:RCY:H1ZA	0.44	2.38	23	1
1:A:61:GLY:C	1:A:62:THR:CG2	0.44	2.86	23	1
1:A:63:ASP:O	2:A:160:RCY:H1YB	0.44	2.11	47	1
1:A:74:ASN:N	1:A:74:ASN:OD1	0.44	2.49	46	1
1:A:73:CYS:CB	2:A:176:RCY:H1LA	0.44	2.36	63	1
1:A:70:TRP:O	1:A:73:CYS:N	0.44	2.47	74	1
2:A:173:RCY:C1Y	2:A:176:RCY:H1C	0.44	2.41	3	1
2:A:168:RCY:H1YB	2:A:176:RCY:C1Z	0.44	2.41	66	1
1:A:74:ASN:OD1	1:A:74:ASN:O	0.44	2.35	7	2
1:A:69:PRO:CG	2:A:173:RCY:H1S	0.44	2.43	8	1
1:A:73:CYS:SG	2:A:176:RCY:O1H	0.44	2.76	60	1
1:A:77:GLU:O	1:A:78:LEU:C	0.44	2.56	99	4
1:A:75:HIS:CD2	1:A:77:GLU:OE2	0.44	2.70	50	1
1:A:65:THR:CG2	2:A:150:RCY:C1P	0.44	2.67	72	1
2:A:138:RCY:N1R	2:A:187:RCY:C1Z	0.44	2.78	49	1
1:A:72:ALA:HB3	2:A:173:RCY:C1U	0.44	2.39	80	1
2:A:138:RCY:C1M	2:A:150:RCY:H1M	0.44	2.23	1	1
1:A:71:GLU:OE1	2:A:176:RCY:H1C	0.44	2.07	97	1
2:A:173:RCY:C1Y	2:A:176:RCY:O1H	0.44	2.63	61	2
1:A:66:VAL:HG21	2:A:150:RCY:C1L	0.44	2.43	61	1
1:A:75:HIS:C	1:A:75:HIS:CD2	0.44	2.88	42	1
1:A:73:CYS:HB2	2:A:176:RCY:C1W	0.44	2.33	58	1
2:A:130:RCY:H1VA	2:A:187:RCY:H1VA	0.44	1.85	94	1
2:A:138:RCY:C1P	2:A:150:RCY:H1VA	0.44	2.43	94	1
1:A:70:TRP:CD1	2:A:173:RCY:H1ZA	0.44	2.45	94	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:71:GLU:O	1:A:71:GLU:OE2	0.44	2.35	60	1
2:A:173:RCY:H1C	2:A:187:RCY:C1S	0.44	2.37	76	1
2:A:150:RCY:H1MA	2:A:168:RCY:O1H	0.44	2.12	85	1
1:A:62:THR:CG2	2:A:130:RCY:C1Y	0.44	2.88	9	1
1:A:70:TRP:CZ2	2:A:121:RCY:H1VA	0.44	2.46	49	1
1:A:70:TRP:CE3	2:A:168:RCY:C1U	0.44	3.00	49	1
1:A:62:THR:OG1	1:A:66:VAL:CG2	0.44	2.66	54	1
1:A:71:GLU:O	2:A:176:RCY:C1C	0.44	2.64	20	1
2:A:168:RCY:C1Y	2:A:176:RCY:H1L	0.44	2.33	20	1
2:A:138:RCY:H1M	2:A:150:RCY:H1M	0.44	1.80	1	1
1:A:66:VAL:HG11	2:A:121:RCY:C1M	0.44	2.39	83	1
1:A:76:CYS:HB3	2:A:173:RCY:O1H	0.44	2.11	97	1
2:A:168:RCY:C1Z	2:A:176:RCY:H1YA	0.44	2.43	14	1
2:A:176:RCY:H1CA	2:A:187:RCY:N1R	0.44	2.27	86	1
1:A:65:THR:CG2	2:A:168:RCY:O1J	0.44	2.57	24	1
2:A:173:RCY:O1H	2:A:173:RCY:H1CB	0.44	2.13	76	1
2:A:168:RCY:O1J	2:A:173:RCY:C1M	0.44	2.42	91	1
2:A:138:RCY:H1V	2:A:187:RCY:H1Y	0.44	1.89	71	1
2:A:168:RCY:H1VA	2:A:187:RCY:H1Y	0.44	1.88	53	1
2:A:173:RCY:N1V	2:A:176:RCY:C1V	0.44	2.81	63	1
2:A:150:RCY:C1Y	2:A:187:RCY:O1G	0.44	2.66	74	1
2:A:176:RCY:O1J	2:A:187:RCY:C1L	0.44	2.56	96	1
1:A:74:ASN:O	1:A:75:HIS:C	0.44	2.56	90	6
2:A:168:RCY:H1M	2:A:187:RCY:H1CA	0.44	1.89	64	1
2:A:168:RCY:H1VB	2:A:187:RCY:H1ZB	0.44	1.89	64	1
1:A:70:TRP:HE1	1:A:75:HIS:C	0.44	2.15	26	1
1:A:60:CYS:SG	1:A:66:VAL:HG21	0.44	2.52	68	1
2:A:168:RCY:H1ZB	2:A:176:RCY:O1J	0.44	1.93	11	1
1:A:73:CYS:SG	1:A:74:ASN:O	0.44	2.76	90	1
1:A:72:ALA:HA	2:A:173:RCY:C1L	0.44	2.43	21	1
1:A:70:TRP:CZ3	2:A:150:RCY:C1C	0.44	2.98	93	1
1:A:67:ILE:CG2	2:A:130:RCY:C1Y	0.44	2.95	30	1
1:A:61:GLY:O	1:A:64:ILE:CG2	0.44	2.60	94	1
1:A:71:GLU:OE2	2:A:130:RCY:N1R	0.44	2.49	94	1
1:A:69:PRO:CA	2:A:173:RCY:O1G	0.44	2.50	10	1
2:A:176:RCY:O1G	2:A:187:RCY:C1W	0.44	2.62	26	1
1:A:77:GLU:O	1:A:78:LEU:HD22	0.44	2.13	16	1
1:A:70:TRP:CZ3	2:A:110:RCY:H1Z	0.44	2.48	59	1
1:A:59:GLY:CA	2:A:150:RCY:H1L	0.44	2.42	85	1
1:A:68:CYS:SG	1:A:70:TRP:N	0.44	2.90	33	1
2:A:138:RCY:H1CB	2:A:138:RCY:C1P	0.44	2.42	7	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:168:RCY:C1U	2:A:187:RCY:H1VA	0.44	2.38	90	1
2:A:168:RCY:H1CA	2:A:173:RCY:O1J	0.44	2.13	53	1
2:A:173:RCY:O1G	2:A:173:RCY:N1V	0.44	2.50	36	2
1:A:73:CYS:CA	2:A:176:RCY:C1C	0.44	2.82	52	1
1:A:72:ALA:CA	2:A:173:RCY:C1L	0.44	2.93	10	1
1:A:65:THR:HB	2:A:160:RCY:C1L	0.44	2.43	35	1
1:A:70:TRP:CD1	1:A:71:GLU:N	0.44	2.86	35	1
1:A:72:ALA:HB3	1:A:75:HIS:CD2	0.44	2.48	33	1
1:A:60:CYS:CA	2:A:138:RCY:H1V	0.44	2.39	7	1
1:A:70:TRP:CD1	2:A:176:RCY:C1L	0.44	3.00	32	1
1:A:73:CYS:O	1:A:75:HIS:NE2	0.44	2.50	90	1
2:A:168:RCY:O1H	2:A:173:RCY:O1J	0.44	2.35	82	1
1:A:71:GLU:CA	1:A:71:GLU:OE1	0.44	2.66	74	1
1:A:71:GLU:OE2	2:A:173:RCY:H1C	0.44	1.98	89	1
1:A:69:PRO:HG3	2:A:176:RCY:C1U	0.44	2.33	31	1
1:A:71:GLU:HG3	2:A:168:RCY:O1H	0.44	2.08	93	1
1:A:69:PRO:CB	2:A:173:RCY:H1CA	0.44	2.42	92	1
2:A:173:RCY:C1X	2:A:187:RCY:O1J	0.44	2.64	55	1
1:A:70:TRP:NE1	2:A:173:RCY:O1J	0.44	2.51	50	1
2:A:150:RCY:H1ZA	2:A:160:RCY:N1R	0.44	2.27	16	1
2:A:160:RCY:C1Y	2:A:176:RCY:C1Z	0.44	2.95	6	1
2:A:168:RCY:H1CB	2:A:173:RCY:H1V	0.44	1.82	85	1
1:A:62:THR:HG22	1:A:65:THR:OG1	0.44	2.13	46	1
2:A:168:RCY:C1V	2:A:176:RCY:C1P	0.44	2.92	20	1
1:A:70:TRP:N	2:A:173:RCY:C1X	0.44	2.45	92	1
1:A:60:CYS:HB3	2:A:168:RCY:C1W	0.43	2.42	52	1
2:A:173:RCY:O1J	2:A:176:RCY:C1U	0.43	2.65	62	1
1:A:69:PRO:CG	2:A:150:RCY:N1V	0.43	2.80	85	1
1:A:70:TRP:O	2:A:176:RCY:C1Y	0.43	2.66	70	1
1:A:76:CYS:O	2:A:187:RCY:C1Z	0.43	2.66	73	1
1:A:65:THR:OG1	1:A:66:VAL:N	0.43	2.51	96	1
2:A:138:RCY:H1Y	2:A:160:RCY:O1G	0.43	2.13	31	1
2:A:168:RCY:N1R	2:A:173:RCY:H1YA	0.43	2.28	14	1
2:A:150:RCY:C1V	2:A:187:RCY:C1M	0.43	2.96	64	1
1:A:65:THR:HA	2:A:168:RCY:H1L	0.43	1.90	26	1
1:A:69:PRO:HG3	2:A:168:RCY:H1MA	0.43	1.90	81	1
1:A:68:CYS:SG	2:A:150:RCY:H1V	0.43	2.53	85	1
2:A:176:RCY:H1V	2:A:187:RCY:C1V	0.43	0.97	33	1
1:A:67:ILE:CA	2:A:168:RCY:C1Q	0.43	2.94	83	2
1:A:70:TRP:CG	2:A:176:RCY:H1ZA	0.43	2.47	4	1
2:A:173:RCY:H1LA	2:A:176:RCY:N1R	0.43	2.27	20	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:138:RCY:N1V	2:A:150:RCY:H1YA	0.43	2.26	77	1
2:A:173:RCY:H1CB	2:A:176:RCY:H1S	0.43	1.88	96	1
1:A:65:THR:HG23	1:A:66:VAL:H	0.43	1.73	93	1
2:A:168:RCY:C1Z	2:A:176:RCY:C1Y	0.43	2.96	14	1
1:A:70:TRP:CZ2	1:A:71:GLU:OE2	0.43	2.71	86	1
1:A:70:TRP:CA	2:A:168:RCY:H1LA	0.43	2.40	29	1
2:A:168:RCY:H1LA	2:A:173:RCY:H1Y	0.43	1.88	5	1
1:A:70:TRP:CE3	2:A:176:RCY:H1V	0.43	2.48	6	1
2:A:138:RCY:H1Y	2:A:176:RCY:N1R	0.43	2.28	48	1
2:A:173:RCY:N1V	2:A:176:RCY:O1J	0.43	2.51	3	1
2:A:138:RCY:H1CB	2:A:160:RCY:C1Y	0.43	2.16	27	1
2:A:138:RCY:H1U	2:A:150:RCY:O1H	0.43	2.13	98	1
1:A:62:THR:HB	2:A:168:RCY:H1CB	0.43	1.90	97	1
2:A:160:RCY:O1H	2:A:168:RCY:H1YA	0.43	2.14	14	1
1:A:70:TRP:HB2	2:A:176:RCY:C1W	0.43	2.34	18	1
2:A:173:RCY:H1YA	2:A:187:RCY:C1M	0.43	2.43	7	1
1:A:66:VAL:O	1:A:71:GLU:OE2	0.43	2.36	45	1
2:A:150:RCY:H1Z	2:A:176:RCY:C1Q	0.43	2.44	3	1
2:A:168:RCY:C1Y	2:A:187:RCY:C1M	0.43	2.81	97	1
1:A:70:TRP:CD2	1:A:70:TRP:N	0.43	2.86	80	2
1:A:64:ILE:CG2	2:A:150:RCY:C1V	0.43	2.43	16	1
1:A:70:TRP:CE3	2:A:168:RCY:H1YA	0.43	2.43	49	1
2:A:138:RCY:H1YB	2:A:173:RCY:C1M	0.43	2.42	32	1
2:A:138:RCY:H1CB	2:A:187:RCY:C1V	0.43	2.43	39	1
1:A:62:THR:CG2	1:A:62:THR:O	0.43	2.64	14	1
1:A:63:ASP:OD1	1:A:63:ASP:O	0.43	2.37	41	2
1:A:63:ASP:O	1:A:63:ASP:OD1	0.43	2.37	49	4
2:A:150:RCY:N1V	2:A:160:RCY:C1Z	0.43	2.81	29	1
1:A:63:ASP:OD2	1:A:70:TRP:CZ2	0.43	2.72	12	1
1:A:60:CYS:HB2	2:A:160:RCY:H1LA	0.43	1.48	35	2
2:A:160:RCY:H1M	2:A:168:RCY:C1Y	0.43	2.42	9	1
2:A:176:RCY:H1Y	2:A:187:RCY:H1L	0.43	1.88	32	1
1:A:70:TRP:O	1:A:71:GLU:CD	0.43	2.57	21	1
1:A:64:ILE:HD12	2:A:168:RCY:H1YB	0.43	1.89	95	1
2:A:160:RCY:H1YA	2:A:168:RCY:H1CB	0.43	0.50	47	1
2:A:168:RCY:C1V	2:A:173:RCY:H1VB	0.43	2.42	45	1
2:A:150:RCY:H1ZB	2:A:187:RCY:H1LA	0.43	1.85	36	1
2:A:130:RCY:O1G	2:A:130:RCY:N1V	0.43	2.51	78	2
2:A:150:RCY:H1M	2:A:187:RCY:O1G	0.43	2.13	8	1
2:A:173:RCY:H1MA	2:A:176:RCY:C1Z	0.43	2.44	41	1
1:A:74:ASN:ND2	1:A:74:ASN:C	0.43	2.71	75	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:160:RCY:H1VB	2:A:168:RCY:C1Q	0.43	2.44	49	1
1:A:59:GLY:CA	2:A:160:RCY:H1ZB	0.43	2.29	49	1
1:A:73:CYS:CB	2:A:176:RCY:O1G	0.43	2.09	70	1
2:A:150:RCY:H1VA	2:A:187:RCY:C1Z	0.43	2.44	32	1
1:A:60:CYS:C	2:A:168:RCY:C1U	0.43	2.58	95	1
2:A:138:RCY:C1Q	2:A:150:RCY:C1Z	0.43	2.78	82	1
1:A:74:ASN:CG	1:A:74:ASN:O	0.43	2.57	82	1
2:A:176:RCY:H1V	2:A:187:RCY:H1L	0.43	1.86	15	1
1:A:64:ILE:HG23	2:A:168:RCY:H1ZA	0.43	1.74	83	1
1:A:65:THR:O	2:A:168:RCY:H1VB	0.43	2.11	17	1
2:A:173:RCY:C1Y	2:A:187:RCY:C1X	0.43	2.76	64	1
1:A:69:PRO:HA	2:A:173:RCY:C1S	0.43	2.43	24	1
2:A:160:RCY:H1Z	2:A:168:RCY:H1CA	0.43	1.60	69	1
1:A:68:CYS:O	1:A:71:GLU:OE1	0.43	2.37	72	1
2:A:173:RCY:O1J	2:A:176:RCY:C1C	0.43	2.59	6	1
1:A:59:GLY:HA3	2:A:150:RCY:H1L	0.43	1.88	85	1
1:A:70:TRP:O	1:A:71:GLU:OE2	0.43	2.35	7	2
2:A:168:RCY:C1Z	2:A:187:RCY:C1V	0.43	2.96	82	1
2:A:130:RCY:C1M	2:A:130:RCY:N1R	0.43	2.68	25	1
2:A:150:RCY:C1C	2:A:173:RCY:C1C	0.43	2.67	89	1
1:A:65:THR:HB	2:A:168:RCY:C1Q	0.43	2.43	87	1
1:A:67:ILE:HG23	2:A:176:RCY:C1M	0.43	2.44	22	1
1:A:60:CYS:O	1:A:61:GLY:O	0.43	2.37	50	1
2:A:160:RCY:C1Z	2:A:168:RCY:N1V	0.43	2.81	69	1
1:A:59:GLY:O	2:A:150:RCY:O1G	0.43	2.36	85	1
1:A:62:THR:OG1	1:A:65:THR:OG1	0.43	2.35	87	3
2:A:160:RCY:O1H	2:A:168:RCY:C1V	0.43	2.67	44	1
2:A:173:RCY:C1Q	2:A:176:RCY:C1Q	0.43	2.95	70	1
1:A:70:TRP:CB	2:A:187:RCY:H1Z	0.43	2.14	51	1
1:A:67:ILE:C	2:A:173:RCY:C1M	0.43	2.62	80	1
1:A:70:TRP:CZ3	2:A:176:RCY:C1M	0.43	2.95	80	1
2:A:173:RCY:C1Q	2:A:187:RCY:C1Y	0.43	2.97	56	1
2:A:176:RCY:C1P	2:A:187:RCY:O1G	0.43	2.59	88	1
2:A:168:RCY:O1J	2:A:176:RCY:H1ZB	0.43	2.03	17	1
1:A:76:CYS:HB3	2:A:173:RCY:N1R	0.43	2.28	38	1
2:A:138:RCY:C1Y	2:A:150:RCY:H1S	0.43	2.42	60	1
2:A:138:RCY:C1Q	2:A:150:RCY:O1J	0.43	2.66	81	1
1:A:74:ASN:O	2:A:176:RCY:C1Q	0.43	2.66	44	1
1:A:60:CYS:O	1:A:64:ILE:HG22	0.43	2.14	44	1
2:A:160:RCY:H1Y	2:A:176:RCY:C1Y	0.43	2.31	11	1
1:A:71:GLU:HA	2:A:173:RCY:C1M	0.43	2.43	11	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:150:RCY:H1MA	2:A:160:RCY:H1Y	0.43	1.90	21	1
1:A:62:THR:O	1:A:67:ILE:O	0.43	2.36	51	1
1:A:60:CYS:C	1:A:62:THR:N	0.43	2.71	2	1
1:A:70:TRP:CB	2:A:176:RCY:H1YB	0.43	2.35	80	1
2:A:150:RCY:O1J	2:A:176:RCY:H1S	0.43	2.14	3	1
1:A:67:ILE:HG21	2:A:150:RCY:H1VB	0.43	1.90	31	1
1:A:78:LEU:HD12	2:A:176:RCY:H1U	0.43	1.79	56	1
1:A:73:CYS:HB2	2:A:173:RCY:H1LA	0.42	1.66	46	2
1:A:70:TRP:CE2	1:A:71:GLU:CD	0.42	2.92	86	1
1:A:76:CYS:C	1:A:78:LEU:H	0.42	2.17	45	4
2:A:168:RCY:O1H	2:A:173:RCY:H1Z	0.42	2.08	26	1
1:A:72:ALA:CA	2:A:173:RCY:H1S	0.42	2.42	21	1
2:A:138:RCY:C1M	2:A:187:RCY:C1Z	0.42	2.94	3	1
2:A:176:RCY:O1G	2:A:187:RCY:C1Q	0.42	2.66	38	1
1:A:62:THR:N	2:A:160:RCY:O1G	0.42	2.51	19	1
1:A:71:GLU:OE1	2:A:168:RCY:C1P	0.42	2.66	99	1
1:A:69:PRO:HA	2:A:173:RCY:H1L	0.42	1.89	24	1
2:A:160:RCY:H1Y	2:A:176:RCY:C1Z	0.42	2.44	6	1
1:A:64:ILE:HD11	2:A:121:RCY:C1P	0.42	2.39	68	1
2:A:138:RCY:C1L	2:A:150:RCY:O1J	0.42	2.66	81	1
2:A:173:RCY:C1P	2:A:176:RCY:O1G	0.42	2.67	59	1
1:A:69:PRO:HD3	2:A:150:RCY:H1VA	0.42	1.90	85	1
1:A:69:PRO:HB3	2:A:173:RCY:C1M	0.42	2.43	57	1
2:A:160:RCY:H1U	2:A:168:RCY:C1V	0.42	2.39	48	1
2:A:150:RCY:C1Y	2:A:176:RCY:C1Y	0.42	2.76	37	1
1:A:75:HIS:C	2:A:173:RCY:H1CB	0.42	2.34	91	1
1:A:68:CYS:SG	1:A:69:PRO:N	0.42	2.91	33	2
2:A:168:RCY:H1M	2:A:173:RCY:C1C	0.42	2.45	45	1
1:A:63:ASP:CG	2:A:160:RCY:C1V	0.42	2.86	63	1
1:A:62:THR:HG22	2:A:160:RCY:O1G	0.42	1.95	82	1
1:A:64:ILE:HG12	1:A:68:CYS:N	0.42	2.29	89	1
1:A:71:GLU:CD	2:A:173:RCY:C1Q	0.42	2.83	89	1
2:A:150:RCY:H1VA	2:A:187:RCY:C1S	0.42	2.39	87	1
1:A:70:TRP:CZ3	2:A:168:RCY:H1ZB	0.42	2.33	98	1
1:A:63:ASP:OD1	2:A:160:RCY:H1L	0.42	2.13	92	1
1:A:74:ASN:CA	2:A:176:RCY:C1V	0.42	2.91	100	1
1:A:75:HIS:C	2:A:173:RCY:C1Z	0.42	2.83	88	1
1:A:59:GLY:C	2:A:160:RCY:H1S	0.42	2.32	85	2
2:A:138:RCY:C1L	2:A:160:RCY:H1MA	0.42	2.45	18	1
1:A:71:GLU:OE2	2:A:176:RCY:C1U	0.42	2.68	37	1
1:A:76:CYS:N	2:A:176:RCY:C1Z	0.42	2.79	44	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:168:RCY:C1Y	2:A:176:RCY:C1X	0.42	2.95	90	1
1:A:66:VAL:CA	2:A:168:RCY:O1H	0.42	2.67	51	1
1:A:77:GLU:OE1	1:A:77:GLU:C	0.42	2.57	45	1
1:A:66:VAL:HG13	2:A:121:RCY:H1VA	0.42	1.80	83	1
1:A:71:GLU:O	1:A:71:GLU:HG3	0.42	2.14	97	1
2:A:168:RCY:C1M	2:A:187:RCY:H1L	0.42	2.43	100	1
1:A:59:GLY:O	1:A:62:THR:CG2	0.42	2.67	88	1
2:A:168:RCY:O1H	2:A:176:RCY:C1Y	0.42	2.68	17	1
2:A:173:RCY:C1S	2:A:176:RCY:H1CB	0.42	2.44	19	1
2:A:168:RCY:N1V	2:A:176:RCY:H1V	0.42	2.28	84	1
2:A:173:RCY:C1Y	2:A:176:RCY:H1L	0.42	2.43	26	1
2:A:160:RCY:N1V	2:A:168:RCY:H1ZA	0.42	2.29	76	1
1:A:64:ILE:HG12	1:A:65:THR:N	0.42	2.30	49	2
1:A:63:ASP:CG	2:A:150:RCY:O1G	0.42	2.54	85	1
1:A:70:TRP:HH2	2:A:160:RCY:O1J	0.42	1.98	48	1
1:A:77:GLU:N	1:A:77:GLU:CD	0.42	2.72	91	1
1:A:70:TRP:C	1:A:72:ALA:H	0.42	2.17	44	2
1:A:64:ILE:HB	1:A:68:CYS:SG	0.42	2.54	27	1
2:A:130:RCY:C1U	2:A:160:RCY:H1Y	0.42	2.02	67	1
1:A:60:CYS:SG	2:A:130:RCY:H1YA	0.42	2.54	66	1
2:A:138:RCY:H1Y	2:A:187:RCY:H1L	0.42	1.89	42	1
2:A:176:RCY:H1YA	2:A:187:RCY:H1MA	0.42	1.90	19	1
1:A:69:PRO:HD3	2:A:168:RCY:C1Q	0.42	2.45	8	2
2:A:110:RCY:O1G	2:A:110:RCY:H1MA	0.42	2.14	99	1
1:A:69:PRO:CB	2:A:176:RCY:O1H	0.42	2.68	59	1
1:A:68:CYS:SG	2:A:150:RCY:H1YB	0.42	2.51	85	1
1:A:77:GLU:CG	2:A:176:RCY:H1VA	0.42	2.39	7	1
1:A:70:TRP:HB2	2:A:173:RCY:C1X	0.42	2.28	4	1
2:A:138:RCY:O1J	2:A:160:RCY:H1LA	0.42	2.15	73	1
1:A:71:GLU:N	2:A:168:RCY:H1ZB	0.42	2.28	36	1
1:A:70:TRP:N	2:A:168:RCY:H1VB	0.42	2.30	3	1
1:A:77:GLU:N	2:A:176:RCY:C1P	0.42	2.45	31	1
2:A:168:RCY:N1R	2:A:176:RCY:H1ZA	0.42	2.30	98	1
1:A:69:PRO:O	1:A:74:ASN:CA	0.42	2.67	59	2
1:A:69:PRO:HG3	2:A:173:RCY:O1J	0.42	2.14	55	1
2:A:138:RCY:H1YA	2:A:187:RCY:C1V	0.42	2.44	84	1
2:A:173:RCY:H1YA	2:A:176:RCY:C1Z	0.42	2.41	99	1
1:A:63:ASP:OD2	1:A:70:TRP:NE1	0.42	2.53	12	1
2:A:173:RCY:H1V	2:A:187:RCY:H1U	0.42	1.91	57	1
2:A:168:RCY:O1H	2:A:173:RCY:H1U	0.42	2.14	48	1
1:A:64:ILE:CG2	2:A:160:RCY:C1Y	0.42	2.38	49	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:65:THR:HG23	2:A:160:RCY:H1CA	0.42	1.91	70	1
1:A:67:ILE:O	2:A:173:RCY:H1YA	0.42	2.14	80	1
2:A:173:RCY:C1L	2:A:187:RCY:H1VA	0.42	2.44	89	1
2:A:160:RCY:H1U	2:A:168:RCY:H1VA	0.42	1.09	100	1
2:A:168:RCY:C1M	2:A:176:RCY:H1YA	0.42	2.42	14	1
1:A:78:LEU:HD21	2:A:138:RCY:O1J	0.42	1.96	40	1
1:A:61:GLY:CA	2:A:168:RCY:N1R	0.42	2.82	24	1
1:A:67:ILE:CD1	2:A:168:RCY:O1G	0.42	2.64	76	1
2:A:160:RCY:H1YB	2:A:168:RCY:O1J	0.42	2.04	59	1
2:A:138:RCY:C1L	2:A:160:RCY:C1M	0.42	2.92	18	1
2:A:173:RCY:N1V	2:A:173:RCY:O1G	0.42	2.53	57	1
1:A:65:THR:O	2:A:173:RCY:H1CB	0.42	1.94	71	1
1:A:69:PRO:O	2:A:187:RCY:C1C	0.42	2.65	7	1
1:A:64:ILE:HG22	2:A:168:RCY:C1C	0.42	2.36	54	1
1:A:70:TRP:H	2:A:173:RCY:C1M	0.42	2.28	4	1
1:A:70:TRP:O	2:A:173:RCY:H1CB	0.42	1.84	82	1
2:A:160:RCY:C1W	2:A:168:RCY:N1R	0.42	2.83	3	1
1:A:70:TRP:CE3	2:A:150:RCY:H1C	0.42	2.49	93	1
1:A:70:TRP:C	2:A:168:RCY:C1S	0.42	2.83	28	1
1:A:60:CYS:O	1:A:62:THR:OG1	0.42	2.38	43	1
2:A:130:RCY:H1ZA	2:A:160:RCY:H1YA	0.42	1.91	84	1
2:A:160:RCY:C1L	2:A:168:RCY:C1V	0.42	2.98	60	1
2:A:173:RCY:O1G	2:A:187:RCY:C1C	0.42	2.64	99	1
2:A:150:RCY:O1G	2:A:150:RCY:H1MA	0.42	2.14	50	1
1:A:62:THR:HA	2:A:168:RCY:C1C	0.42	2.44	24	1
1:A:60:CYS:SG	1:A:62:THR:N	0.42	2.89	35	1
1:A:72:ALA:O	1:A:73:CYS:O	0.42	2.38	31	1
1:A:68:CYS:HB3	1:A:70:TRP:CE2	0.42	2.49	61	1
1:A:64:ILE:HG22	1:A:65:THR:H	0.42	1.67	38	1
2:A:168:RCY:H1Y	2:A:173:RCY:H1LA	0.42	1.61	99	1
2:A:150:RCY:H1ZB	2:A:187:RCY:C1C	0.42	2.43	50	1
2:A:176:RCY:O1G	2:A:187:RCY:H1ZA	0.42	2.15	26	1
1:A:69:PRO:C	2:A:173:RCY:H1L	0.42	2.22	6	1
1:A:70:TRP:CA	2:A:173:RCY:H1YB	0.42	2.30	85	1
2:A:168:RCY:C1C	2:A:187:RCY:C1Y	0.42	2.93	87	1
2:A:168:RCY:H1MA	2:A:187:RCY:H1MA	0.42	0.83	66	1
1:A:68:CYS:O	1:A:71:GLU:O	0.42	2.37	97	1
2:A:121:RCY:O1G	2:A:121:RCY:H1MA	0.42	2.15	60	1
1:A:75:HIS:CA	2:A:176:RCY:O1H	0.42	2.68	10	1
2:A:173:RCY:H1VA	2:A:176:RCY:H1ZB	0.42	1.84	4	1
1:A:70:TRP:HZ3	2:A:168:RCY:O1G	0.42	1.96	39	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:67:ILE:HD12	1:A:67:ILE:N	0.42	2.28	89	1
2:A:138:RCY:C1X	2:A:173:RCY:H1ZB	0.42	2.45	15	1
1:A:65:THR:OG1	2:A:150:RCY:H1YB	0.42	2.15	31	1
1:A:63:ASP:C	2:A:168:RCY:H1Z	0.41	2.21	78	1
1:A:60:CYS:CA	2:A:130:RCY:C1Z	0.41	2.90	88	1
2:A:138:RCY:N1V	2:A:150:RCY:H1ZB	0.41	1.98	41	1
2:A:168:RCY:C1M	2:A:173:RCY:H1S	0.41	2.37	58	1
2:A:176:RCY:C1C	2:A:187:RCY:C1Q	0.41	2.97	58	1
1:A:75:HIS:O	2:A:176:RCY:C1S	0.41	2.60	84	1
1:A:62:THR:HG1	2:A:168:RCY:C1P	0.41	2.13	72	1
2:A:110:RCY:N1V	2:A:121:RCY:C1M	0.41	2.78	5	1
1:A:67:ILE:C	2:A:173:RCY:O1J	0.41	2.58	31	1
1:A:67:ILE:HG23	1:A:72:ALA:HB2	0.41	1.90	31	1
2:A:168:RCY:H1VA	2:A:173:RCY:H1ZB	0.41	1.87	29	1
2:A:168:RCY:H1V	2:A:173:RCY:H1ZA	0.41	1.85	29	1
1:A:74:ASN:CG	1:A:75:HIS:H	0.41	2.18	46	2
2:A:138:RCY:O1G	2:A:150:RCY:H1S	0.41	2.10	81	1
2:A:173:RCY:H1ZB	2:A:173:RCY:C1P	0.41	2.44	36	2
1:A:74:ASN:HD22	1:A:74:ASN:C	0.41	2.19	74	1
1:A:65:THR:CG2	2:A:160:RCY:H1Y	0.41	2.26	55	1
1:A:67:ILE:C	2:A:168:RCY:O1H	0.41	2.54	86	1
2:A:173:RCY:C1Z	2:A:173:RCY:O1G	0.41	2.68	94	1
1:A:60:CYS:HB3	2:A:160:RCY:H1LA	0.41	1.43	26	1
2:A:168:RCY:H1VB	2:A:176:RCY:O1J	0.41	2.14	16	1
1:A:73:CYS:O	2:A:173:RCY:O1H	0.41	2.39	35	1
1:A:59:GLY:C	2:A:150:RCY:C1L	0.41	2.89	85	1
2:A:138:RCY:C1Y	2:A:176:RCY:H1S	0.41	2.45	48	1
2:A:160:RCY:H1VB	2:A:168:RCY:O1J	0.41	2.12	47	1
1:A:69:PRO:CG	2:A:173:RCY:O1H	0.41	2.68	3	1
1:A:66:VAL:CB	2:A:121:RCY:H1YB	0.41	2.35	83	1
2:A:168:RCY:H1M	2:A:176:RCY:C1Y	0.41	2.43	98	1
1:A:70:TRP:CD1	2:A:168:RCY:C1Q	0.41	3.03	42	1
1:A:68:CYS:SG	1:A:71:GLU:CB	0.41	3.08	52	1
1:A:70:TRP:C	2:A:121:RCY:O1J	0.41	2.59	94	1
1:A:67:ILE:O	2:A:173:RCY:C1C	0.41	2.68	24	1
1:A:63:ASP:OD2	1:A:70:TRP:CE2	0.41	2.73	12	1
2:A:130:RCY:C1Y	2:A:160:RCY:N1V	0.41	2.83	81	1
1:A:69:PRO:CG	2:A:173:RCY:N1V	0.41	2.80	9	1
1:A:70:TRP:CE3	2:A:168:RCY:C1Y	0.41	3.04	49	1
1:A:67:ILE:CB	2:A:176:RCY:C1C	0.41	2.98	53	1
2:A:173:RCY:H1M	2:A:176:RCY:H1CA	0.41	0.77	47	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:176:RCY:H1VA	2:A:187:RCY:H1S	0.41	1.92	98	1
2:A:173:RCY:H1CB	2:A:176:RCY:H1V	0.41	1.92	52	1
2:A:176:RCY:H1MA	2:A:176:RCY:O1G	0.41	2.14	29	2
1:A:70:TRP:CD1	2:A:150:RCY:H1L	0.41	2.23	34	1
1:A:70:TRP:HE1	2:A:168:RCY:H1S	0.41	1.75	24	1
1:A:64:ILE:HG12	1:A:68:CYS:CB	0.41	2.45	76	1
2:A:150:RCY:C1C	2:A:187:RCY:H1Z	0.41	2.46	81	1
2:A:168:RCY:H1U	2:A:173:RCY:H1VA	0.41	1.91	85	1
1:A:74:ASN:ND2	2:A:168:RCY:C1Y	0.41	2.51	91	1
1:A:63:ASP:OD1	1:A:63:ASP:C	0.41	2.57	44	1
1:A:76:CYS:HB2	2:A:176:RCY:H1LA	0.41	1.43	49	2
1:A:63:ASP:O	2:A:160:RCY:H1VA	0.41	1.96	3	1
2:A:173:RCY:C1Z	2:A:176:RCY:H1V	0.41	1.12	31	1
1:A:70:TRP:CA	2:A:130:RCY:O1G	0.41	2.65	27	1
1:A:60:CYS:O	2:A:130:RCY:H1ZB	0.41	2.15	88	1
2:A:160:RCY:O1H	2:A:168:RCY:C1Y	0.41	2.69	14	1
2:A:150:RCY:H1M	2:A:187:RCY:H1MA	0.41	1.92	41	1
2:A:168:RCY:C1S	2:A:173:RCY:H1YA	0.41	2.35	84	1
2:A:176:RCY:C1W	2:A:176:RCY:O1H	0.41	2.64	57	1
2:A:173:RCY:H1VB	2:A:187:RCY:O1G	0.41	2.15	57	1
2:A:150:RCY:C1Z	2:A:187:RCY:C1X	0.41	2.21	37	1
2:A:138:RCY:C1P	2:A:150:RCY:C1Q	0.41	2.70	23	1
2:A:168:RCY:H1U	2:A:187:RCY:C1V	0.41	2.40	90	1
2:A:168:RCY:C1P	2:A:168:RCY:C1C	0.41	2.90	53	1
2:A:138:RCY:H1YB	2:A:187:RCY:H1ZA	0.41	1.92	89	1
2:A:110:RCY:O1G	2:A:110:RCY:N1V	0.41	2.54	78	1
2:A:130:RCY:C1W	2:A:160:RCY:O1H	0.41	2.47	88	1
1:A:71:GLU:CD	2:A:187:RCY:C1Q	0.41	2.84	88	1
2:A:168:RCY:H1CB	2:A:176:RCY:O1J	0.41	1.98	59	1
1:A:60:CYS:SG	1:A:64:ILE:O	0.41	2.78	33	1
2:A:138:RCY:C1S	2:A:187:RCY:H1Z	0.41	2.44	49	1
2:A:150:RCY:C1Q	2:A:187:RCY:H1CB	0.41	2.31	53	1
2:A:173:RCY:H1ZB	2:A:176:RCY:C1P	0.41	2.46	20	1
1:A:74:ASN:CG	2:A:176:RCY:C1Y	0.41	2.87	56	1
2:A:130:RCY:N1V	2:A:130:RCY:O1G	0.41	2.54	43	1
2:A:150:RCY:C1W	2:A:187:RCY:H1YB	0.41	2.42	88	1
2:A:160:RCY:H1LA	2:A:168:RCY:C1V	0.41	2.44	60	1
2:A:130:RCY:H1M	2:A:160:RCY:C1P	0.41	2.44	18	1
1:A:69:PRO:HA	2:A:168:RCY:H1U	0.41	1.46	57	1
2:A:168:RCY:H1C	2:A:173:RCY:H1MA	0.41	1.56	91	1
2:A:121:RCY:C1M	2:A:160:RCY:C1Z	0.41	2.99	44	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:64:ILE:HG21	2:A:168:RCY:H1YB	0.41	1.93	95	1
1:A:74:ASN:OD1	2:A:173:RCY:H1S	0.41	2.05	2	1
1:A:71:GLU:OE2	2:A:168:RCY:N1R	0.41	2.53	93	1
1:A:68:CYS:N	2:A:173:RCY:H1YA	0.41	2.30	100	1
2:A:150:RCY:H1M	2:A:187:RCY:C1C	0.41	2.45	38	1
1:A:72:ALA:O	2:A:173:RCY:C1Y	0.41	2.41	22	1
1:A:66:VAL:O	2:A:176:RCY:H1M	0.41	2.16	22	1
1:A:71:GLU:HA	2:A:173:RCY:H1C	0.41	1.92	19	1
2:A:173:RCY:H1V	2:A:176:RCY:O1G	0.41	2.16	64	1
2:A:176:RCY:O1G	2:A:176:RCY:H1M	0.41	2.16	64	1
1:A:65:THR:HB	2:A:150:RCY:H1LA	0.41	1.92	50	1
1:A:68:CYS:HB3	2:A:168:RCY:H1LA	0.41	1.48	10	2
1:A:78:LEU:HD13	1:A:78:LEU:C	0.41	2.36	26	1
1:A:64:ILE:HG21	1:A:68:CYS:CA	0.41	2.45	76	1
1:A:64:ILE:O	1:A:68:CYS:CA	0.41	2.69	93	2
2:A:173:RCY:H1M	2:A:173:RCY:O1G	0.41	2.16	90	2
1:A:59:GLY:O	2:A:160:RCY:H1MA	0.41	2.10	85	1
2:A:168:RCY:C1P	2:A:173:RCY:H1V	0.41	2.45	11	1
2:A:138:RCY:O1G	2:A:150:RCY:H1VA	0.41	2.15	54	1
1:A:78:LEU:CD2	1:A:78:LEU:H	0.41	2.29	54	1
1:A:60:CYS:CA	2:A:168:RCY:C1P	0.41	2.91	95	1
1:A:69:PRO:HG3	2:A:168:RCY:H1V	0.41	1.91	63	1
1:A:65:THR:OG1	2:A:168:RCY:O1G	0.41	2.34	80	1
2:A:138:RCY:C1C	2:A:187:RCY:O1J	0.41	2.53	3	1
1:A:77:GLU:CD	1:A:77:GLU:C	0.41	2.79	87	1
1:A:71:GLU:CG	2:A:168:RCY:C1S	0.41	2.88	28	1
1:A:68:CYS:HB2	2:A:168:RCY:H1LA	0.41	1.47	67	2
1:A:63:ASP:CG	2:A:160:RCY:H1L	0.41	2.35	92	1
1:A:70:TRP:CE2	2:A:121:RCY:O1H	0.41	2.58	78	1
2:A:168:RCY:O1J	2:A:187:RCY:O1J	0.41	2.39	72	1
1:A:63:ASP:OD1	1:A:64:ILE:N	0.41	2.54	12	1
1:A:70:TRP:CZ2	2:A:176:RCY:C1X	0.41	2.93	4	1
1:A:64:ILE:HG23	2:A:168:RCY:H1LA	0.41	1.93	96	1
1:A:71:GLU:OE1	1:A:71:GLU:C	0.41	2.60	96	1
1:A:65:THR:CA	2:A:168:RCY:O1G	0.41	2.67	97	1
2:A:173:RCY:C1P	2:A:187:RCY:H1Z	0.40	2.44	75	1
2:A:168:RCY:C1M	2:A:187:RCY:C1C	0.40	2.99	64	1
2:A:138:RCY:N1V	2:A:138:RCY:C1S	0.40	2.85	50	1
1:A:69:PRO:HB2	2:A:173:RCY:O1G	0.40	2.15	6	1
1:A:67:ILE:HG23	1:A:72:ALA:HB3	0.40	1.91	81	1
1:A:78:LEU:HD21	2:A:187:RCY:O1J	0.40	2.13	91	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:67:ILE:HG21	2:A:176:RCY:H1CA	0.40	1.92	53	1
2:A:168:RCY:H1M	2:A:173:RCY:H1C	0.40	1.93	45	1
1:A:64:ILE:HG21	2:A:160:RCY:C1C	0.40	2.47	39	1
1:A:76:CYS:HB2	2:A:173:RCY:C1W	0.40	2.47	42	1
1:A:74:ASN:HB3	2:A:176:RCY:C1L	0.40	2.46	52	1
2:A:150:RCY:N1R	2:A:187:RCY:C1Z	0.40	2.78	8	1
2:A:130:RCY:H1MA	2:A:130:RCY:O1G	0.40	2.16	75	1
1:A:60:CYS:CA	2:A:138:RCY:O1G	0.40	2.69	62	1
1:A:76:CYS:H	2:A:176:RCY:H1LA	0.40	1.69	10	1
1:A:69:PRO:HD3	2:A:173:RCY:C1P	0.40	2.39	24	1
2:A:110:RCY:H1YB	2:A:121:RCY:O1J	0.40	2.14	33	1
2:A:130:RCY:H1Y	2:A:138:RCY:H1YB	0.40	1.94	49	1
2:A:138:RCY:O1G	2:A:187:RCY:O1G	0.40	2.38	11	1
1:A:77:GLU:CD	1:A:77:GLU:O	0.40	2.59	45	1
1:A:71:GLU:O	1:A:74:ASN:CG	0.40	2.59	46	1
2:A:176:RCY:H1YB	2:A:187:RCY:O1J	0.40	2.15	82	1
1:A:71:GLU:CA	2:A:168:RCY:H1C	0.40	2.43	86	1
2:A:160:RCY:N1R	2:A:160:RCY:C1M	0.40	2.68	79	1
2:A:168:RCY:O1H	2:A:173:RCY:C1U	0.40	2.69	48	1
2:A:138:RCY:H1VB	2:A:187:RCY:C1Y	0.40	2.46	49	1
1:A:62:THR:HG22	2:A:168:RCY:H1VA	0.40	1.45	7	1
1:A:61:GLY:N	2:A:168:RCY:O1G	0.40	2.54	95	1
2:A:121:RCY:H1M	2:A:121:RCY:O1G	0.40	2.17	80	1
1:A:70:TRP:CA	2:A:176:RCY:H1YB	0.40	2.39	80	1
1:A:76:CYS:CB	2:A:173:RCY:H1L	0.40	2.46	14	1
2:A:173:RCY:H1ZA	2:A:187:RCY:H1YA	0.40	1.94	14	1
1:A:73:CYS:HB2	2:A:176:RCY:H1MA	0.40	1.94	58	1
2:A:168:RCY:H1YA	2:A:176:RCY:C1M	0.40	2.46	94	1
1:A:61:GLY:C	1:A:63:ASP:OD1	0.40	2.59	40	1
1:A:69:PRO:CB	2:A:176:RCY:H1Y	0.40	2.20	72	1
2:A:160:RCY:C1Q	2:A:176:RCY:C1Y	0.40	2.99	71	1
2:A:176:RCY:O1J	2:A:187:RCY:C1Z	0.40	2.67	71	1
2:A:173:RCY:O1G	2:A:173:RCY:H1MA	0.40	2.15	95	1
1:A:76:CYS:HB2	2:A:160:RCY:C1Y	0.40	2.47	73	1
2:A:176:RCY:H1VA	2:A:187:RCY:H1YB	0.40	1.73	36	1
2:A:138:RCY:C1Y	2:A:187:RCY:H1ZA	0.40	2.45	89	1
1:A:63:ASP:CG	1:A:64:ILE:N	0.40	2.74	28	1
2:A:173:RCY:H1YB	2:A:187:RCY:H1Y	0.40	1.42	66	1
2:A:150:RCY:H1YB	2:A:187:RCY:H1VA	0.40	1.88	38	1
2:A:176:RCY:C1Y	2:A:187:RCY:C1U	0.40	2.93	19	1
1:A:71:GLU:OE2	2:A:130:RCY:C1W	0.40	2.64	94	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:70:TRP:CG	2:A:173:RCY:O1J	0.40	2.74	50	1
1:A:73:CYS:HB3	2:A:173:RCY:H1LA	0.40	1.47	16	1
1:A:69:PRO:C	2:A:176:RCY:H1VA	0.40	2.37	72	1
2:A:121:RCY:N1V	2:A:121:RCY:O1G	0.40	2.54	68	1
1:A:69:PRO:CG	2:A:150:RCY:O1J	0.40	2.70	85	1
1:A:62:THR:CB	1:A:65:THR:HG1	0.40	2.30	57	1
1:A:70:TRP:CE2	2:A:168:RCY:H1M	0.40	2.52	37	1
2:A:176:RCY:H1V	2:A:187:RCY:H1VA	0.40	0.67	33	1
2:A:130:RCY:C1C	2:A:160:RCY:H1MA	0.40	2.27	7	1
1:A:77:GLU:CG	2:A:173:RCY:H1CB	0.40	2.46	51	1
2:A:150:RCY:C1P	2:A:187:RCY:H1VB	0.40	2.43	53	1
1:A:61:GLY:HA2	2:A:168:RCY:H1ZB	0.40	1.92	95	1
2:A:168:RCY:C1Y	2:A:173:RCY:H1VB	0.40	1.07	45	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	20/87 (23%)	7±2 (36±10%)	8±2 (38±10%)	5±2 (26±9%)	0	1
All	All	2000/8700 (23%)	723 (36%)	754 (38%)	523 (26%)	0	1

All 18 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	66	VAL	57
1	A	64	ILE	48
1	A	65	THR	41
1	A	77	GLU	39
1	A	69	PRO	33
1	A	76	CYS	31
1	A	61	GLY	31
1	A	60	CYS	31
1	A	62	THR	30

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Mol	Chain	Res	Type	Models (Total)
1	A	75	HIS	30
1	A	72	ALA	28
1	A	74	ASN	27
1	A	63	ASP	25
1	A	73	CYS	22
1	A	78	LEU	21
1	A	59	GLY	18
1	A	70	TRP	6
1	A	71	GLU	5

6.3.2 Protein sidechains (i)

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	17/73 (23%)	14±1 (80±9%)	3±1 (20±9%)	3 33
All	All	1700/7300 (23%)	1356 (80%)	344 (20%)	3 33

All 15 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	68	CYS	48
1	A	70	TRP	41
1	A	73	CYS	32
1	A	62	THR	31
1	A	60	CYS	26
1	A	76	CYS	26
1	A	78	LEU	24
1	A	66	VAL	22
1	A	64	ILE	19
1	A	74	ASN	19
1	A	75	HIS	18
1	A	71	GLU	11
1	A	65	THR	10
1	A	63	ASP	9
1	A	77	GLU	8

6.3.3 RNA

There are no RNA molecules in this entry.

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

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

6.5 Carbohydrates

There are no carbohydrates in this entry.

6.6 Ligand geometry

10 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths		
					Counts	RMSZ	#Z>2
2	RCY	A	130	1	17,18,18	3.70±4.45	2±1 (12±7%)
2	RCY	A	110	1	17,18,18	3.27±0.36	2±0 (12±2%)
2	RCY	A	187	1	17,18,18	3.29±0.45	2±0 (12±2%)
2	RCY	A	138	1	17,18,18	3.29±0.31	2±0 (11±1%)
2	RCY	A	173	1	17,18,18	3.26±0.25	2±0 (12±1%)
2	RCY	A	121	1	17,18,18	3.29±0.33	2±0 (12±2%)
2	RCY	A	150	1	17,18,18	3.28±0.40	2±0 (12±1%)
2	RCY	A	168	1	17,18,18	3.34±0.94	2±1 (12±3%)
2	RCY	A	176	1	17,18,18	3.33±0.64	2±1 (12±3%)
2	RCY	A	160	1	17,18,18	3.28±0.36	2±0 (12±2%)

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

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

Mol	Type	Chain	Res	Link	Bond angles		
					Counts	RMSZ	#Z>2
2	RCY	A	130	1	22,30,30	6.60±8.58	2±2 (7±9%)
2	RCY	A	110	1	22,30,30	4.65±0.36	1±0 (5±1%)
2	RCY	A	187	1	22,30,30	5.09±4.27	1±1 (5±4%)
2	RCY	A	138	1	22,30,30	8.00±11.18	2±2 (8±9%)
2	RCY	A	173	1	22,30,30	5.89±6.82	1±1 (6±5%)
2	RCY	A	121	1	22,30,30	7.14±9.81	1±2 (6±7%)
2	RCY	A	150	1	22,30,30	5.46±5.68	1±1 (5±4%)
2	RCY	A	168	1	22,30,30	5.23±4.15	1±1 (5±5%)
2	RCY	A	176	1	22,30,30	7.26±10.12	2±2 (7±8%)
2	RCY	A	160	1	22,30,30	6.38±8.22	2±2 (7±7%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	RCY	A	187	1	-	0±0,4,40,40	0±0,2,2,2
2	RCY	A	130	1	1±0,1,7,7	0±0,4,40,40	0±0,2,2,2
2	RCY	A	176	1	-	1±0,4,40,40	0±0,2,2,2
2	RCY	A	160	1	1±0,1,7,7	0±0,4,40,40	0±0,2,2,2
2	RCY	A	110	1	-	0±0,4,40,40	0±0,2,2,2
2	RCY	A	173	1	1±0,1,7,7	0±0,4,40,40	0±0,2,2,2
2	RCY	A	150	1	1±0,1,7,7	0±0,4,40,40	0±0,2,2,2
2	RCY	A	138	1	1±0,1,7,7	0±0,4,40,40	0±0,2,2,2
2	RCY	A	168	1	1±0,1,7,7	0±0,4,40,40	0±0,2,2,2
2	RCY	A	121	1	-	0±0,4,40,40	0±0,2,2,2

All unique bond outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
2	A	130	RCY	C1Q-N1R	122.40	3.31	1.39	79	100
2	A	130	RCY	C1U-N1R	100.84	5.00	1.46	79	2
2	A	130	RCY	C1P-N1R	98.88	2.94	1.39	79	100
2	A	130	RCY	C1M-C1U	40.84	2.86	1.53	79	1

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
2	A	168	RCY	C1S-C1Q	33.26	2.51	1.51	79	2
2	A	168	RCY	C1S-C1L	30.78	2.32	1.52	79	1
2	A	176	RCY	C1Q-N1R	24.06	1.77	1.39	25	100
2	A	130	RCY	C1X-N1V	22.60	1.85	1.49	79	2
2	A	130	RCY	C1M-C1W	22.47	2.08	1.54	79	1
2	A	187	RCY	C1Q-N1R	22.29	1.74	1.39	25	100
2	A	130	RCY	C1S-C1Q	19.69	2.10	1.51	79	1
2	A	150	RCY	C1Q-N1R	18.40	1.68	1.39	79	100
2	A	168	RCY	C1Q-N1R	18.11	1.67	1.39	79	99
2	A	130	RCY	C1L-C1P	17.60	2.04	1.51	79	1
2	A	130	RCY	C1S-C1L	17.38	1.97	1.52	79	1
2	A	176	RCY	C1U-N1R	17.37	2.07	1.46	25	2
2	A	160	RCY	C1Q-N1R	16.46	1.65	1.39	79	100
2	A	138	RCY	C1Q-N1R	16.32	1.65	1.39	79	100
2	A	121	RCY	C1Q-N1R	15.93	1.64	1.39	79	100
2	A	110	RCY	C1P-N1R	15.42	1.63	1.39	79	100
2	A	110	RCY	C1Q-N1R	15.20	1.63	1.39	25	100
2	A	176	RCY	C1P-N1R	14.88	1.62	1.39	79	100
2	A	187	RCY	C1P-N1R	14.85	1.62	1.39	79	100
2	A	150	RCY	C1P-N1R	14.75	1.62	1.39	25	100
2	A	173	RCY	C1P-N1R	14.60	1.62	1.39	25	100
2	A	160	RCY	C1P-N1R	14.13	1.61	1.39	25	99
2	A	173	RCY	C1Q-N1R	13.67	1.60	1.39	25	99
2	A	121	RCY	C1P-N1R	12.59	1.59	1.39	25	100
2	A	138	RCY	C1P-N1R	11.57	1.57	1.39	25	100
2	A	160	RCY	C1S-C1Q	11.47	1.85	1.51	25	1
2	A	168	RCY	C1U-N1R	10.95	1.85	1.46	25	2
2	A	168	RCY	C1P-N1R	10.54	1.55	1.39	7	99
2	A	160	RCY	C1U-N1R	10.15	1.82	1.46	25	2
2	A	130	RCY	C1W-N1V	10.09	1.33	1.49	79	1
2	A	130	RCY	C1Z-C1W	9.91	1.75	1.53	79	1
2	A	187	RCY	C1U-N1R	9.12	1.78	1.46	25	2
2	A	176	RCY	C1Z-C1W	8.65	1.34	1.53	25	1
2	A	121	RCY	C1U-N1R	8.62	1.76	1.46	79	2
2	A	138	RCY	C1U-N1R	8.58	1.76	1.46	79	2
2	A	150	RCY	C1U-N1R	8.53	1.76	1.46	79	2
2	A	130	RCY	C1C-C1X	8.43	1.72	1.53	79	1
2	A	130	RCY	C1V-C1X	8.35	1.72	1.53	79	1
2	A	168	RCY	O1G-C1P	8.33	1.04	1.23	25	1
2	A	173	RCY	C1S-C1Q	8.27	1.76	1.51	79	1
2	A	176	RCY	C1X-N1V	8.11	1.62	1.49	79	1

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
2	A	110	RCY	C1U-N1R	7.94	1.74	1.46	79	2
2	A	176	RCY	C1C-C1X	7.92	1.34	1.53	25	1
2	A	138	RCY	C1X-N1V	7.79	1.61	1.49	79	1
2	A	187	RCY	C1X-N1V	7.75	1.61	1.49	25	2
2	A	160	RCY	C1X-N1V	7.54	1.61	1.49	25	1
2	A	121	RCY	C1X-N1V	7.42	1.61	1.49	79	2
2	A	168	RCY	C1X-N1V	7.20	1.60	1.49	25	2
2	A	176	RCY	C1S-C1Q	7.19	1.72	1.51	25	1
2	A	173	RCY	C1U-N1R	7.06	1.71	1.46	25	2
2	A	173	RCY	C1X-N1V	6.65	1.60	1.49	79	2
2	A	130	RCY	O1H-C1Q	6.56	1.37	1.23	79	1
2	A	160	RCY	C1S-C1L	6.52	1.69	1.52	25	1
2	A	130	RCY	O1G-C1P	6.51	1.37	1.23	79	1
2	A	187	RCY	C1W-N1V	6.46	1.59	1.49	25	2
2	A	110	RCY	C1X-N1V	6.44	1.59	1.49	25	2
2	A	150	RCY	C1X-N1V	6.24	1.59	1.49	25	1
2	A	176	RCY	C1W-N1V	6.21	1.59	1.49	79	1
2	A	168	RCY	C1L-C1P	6.10	1.69	1.51	25	1
2	A	110	RCY	C1W-N1V	5.74	1.58	1.49	25	1
2	A	150	RCY	C1W-N1V	5.67	1.58	1.49	25	1
2	A	176	RCY	C1L-C1P	5.30	1.67	1.51	25	1
2	A	168	RCY	C1M-C1W	5.27	1.66	1.54	25	1
2	A	160	RCY	C1L-C1P	5.23	1.66	1.51	25	1
2	A	121	RCY	C1W-N1V	5.18	1.57	1.49	79	1

All unique angle outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})	Models	
								Worst	Total
2	A	138	RCY	C1Q-N1R-C1P	162.55	23.53	112.47	7	100
2	A	121	RCY	C1Q-N1R-C1P	161.99	23.83	112.47	52	100
2	A	173	RCY	C1Q-N1R-C1P	161.99	23.84	112.47	84	100
2	A	176	RCY	C1Q-N1R-C1P	161.96	23.85	112.47	91	100
2	A	130	RCY	C1Q-N1R-C1P	161.95	23.86	112.47	15	100
2	A	150	RCY	C1Q-N1R-C1P	161.93	23.87	112.47	26	100
2	A	160	RCY	C1Q-N1R-C1P	161.92	23.87	112.47	74	100
2	A	187	RCY	C1Q-N1R-C1P	161.86	23.91	112.47	1	100
2	A	168	RCY	C1Q-N1R-C1P	128.04	42.41	112.47	7	100
2	A	138	RCY	C1S-C1Q-N1R	105.35	22.11	107.87	7	9
2	A	121	RCY	C1S-C1Q-N1R	105.23	22.20	107.87	52	7
2	A	176	RCY	C1S-C1Q-N1R	105.23	22.20	107.87	57	8

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})	Models	
								Worst	Total
2	A	130	RCY	C1S-C1Q-N1R	105.22	22.21	107.87	15	6
2	A	160	RCY	C1S-C1Q-N1R	105.19	22.24	107.87	14	5
2	A	173	RCY	C1S-C1Q-N1R	105.19	22.24	107.87	84	4
2	A	150	RCY	C1S-C1Q-N1R	105.18	22.24	107.87	26	2
2	A	187	RCY	C1S-C1Q-N1R	104.91	22.46	107.87	1	2
2	A	138	RCY	C1L-C1P-N1R	92.80	32.32	107.87	6	9
2	A	130	RCY	C1L-C1P-N1R	91.01	33.78	107.87	51	6
2	A	160	RCY	C1L-C1P-N1R	90.97	33.81	107.87	7	6
2	A	176	RCY	C1L-C1P-N1R	90.94	33.84	107.87	85	8
2	A	168	RCY	C1S-C1Q-N1R	85.03	38.65	107.87	7	3
2	A	121	RCY	C1L-C1P-N1R	80.09	42.67	107.87	59	7
2	A	173	RCY	C1L-C1P-N1R	80.06	42.69	107.87	72	4
2	A	168	RCY	C1L-C1P-N1R	80.05	42.70	107.87	7	2
2	A	150	RCY	C1L-C1P-N1R	80.03	42.72	107.87	47	4
2	A	138	RCY	C1L-C1S-C1Q	73.86	25.34	105.23	50	10
2	A	187	RCY	C1L-C1P-N1R	73.21	48.27	107.87	1	2
2	A	121	RCY	C1L-C1S-C1Q	72.90	26.38	105.23	88	6
2	A	150	RCY	C1L-C1S-C1Q	72.90	26.38	105.23	47	2
2	A	173	RCY	C1L-C1S-C1Q	72.89	26.39	105.23	72	4
2	A	130	RCY	C1L-C1S-C1Q	72.89	26.39	105.23	7	5
2	A	168	RCY	C1L-C1S-C1Q	72.87	26.41	105.23	7	3
2	A	130	RCY	C1S-C1L-C1P	69.49	30.07	105.23	51	16
2	A	168	RCY	C1S-C1L-C1P	69.45	30.11	105.23	7	13
2	A	150	RCY	C1S-C1L-C1P	69.45	30.11	105.23	47	12
2	A	173	RCY	C1S-C1L-C1P	69.42	30.14	105.23	82	14
2	A	121	RCY	C1S-C1L-C1P	69.42	30.14	105.23	59	11
2	A	160	RCY	C1L-C1S-C1Q	67.25	32.49	105.23	2	6
2	A	138	RCY	C1S-C1L-C1P	66.40	33.41	105.23	43	24
2	A	160	RCY	C1S-C1L-C1P	64.05	35.95	105.23	2	23
2	A	176	RCY	C1S-C1L-C1P	61.29	38.94	105.23	85	24
2	A	176	RCY	C1L-C1S-C1Q	57.90	42.60	105.23	85	7
2	A	187	RCY	C1L-C1S-C1Q	57.52	43.02	105.23	1	1
2	A	187	RCY	C1S-C1L-C1P	56.53	44.08	105.23	1	15
2	A	110	RCY	C1Q-N1R-C1P	31.10	95.45	112.47	25	100
2	A	130	RCY	C1M-C1W-N1V	25.00	60.29	101.22	79	1
2	A	130	RCY	C1U-N1R-C1P	20.85	169.89	123.55	79	5
2	A	176	RCY	O1G-C1P-N1R	15.07	141.91	124.38	85	6
2	A	130	RCY	O1G-C1P-N1R	15.03	141.87	124.38	51	4
2	A	138	RCY	O1G-C1P-N1R	14.85	141.66	124.38	43	7
2	A	130	RCY	O1H-C1Q-C1S	14.75	89.41	127.08	79	1
2	A	160	RCY	O1G-C1P-N1R	14.03	108.06	124.38	7	4

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})	Models	
								Worst	Total
2	A	138	RCY	O1H-C1Q-N1R	13.69	140.31	124.38	50	8
2	A	176	RCY	C1Z-C1W-C1Y	13.54	79.43	109.45	25	1
2	A	176	RCY	C1V-C1X-C1C	13.16	83.78	110.44	25	1
2	A	168	RCY	O1H-C1Q-N1R	11.79	110.67	124.38	79	3
2	A	130	RCY	C1Z-C1W-C1M	11.59	143.82	112.53	79	1
2	A	130	RCY	C1V-C1X-C1C	11.03	88.09	110.44	79	1
2	A	187	RCY	O1H-C1Q-N1R	10.43	136.51	124.38	1	1
2	A	176	RCY	O1H-C1Q-N1R	10.38	136.46	124.38	86	6
2	A	176	RCY	C1Y-C1W-C1M	10.02	139.59	112.53	25	1
2	A	138	RCY	C1U-N1R-C1P	9.58	144.83	123.55	2	7
2	A	160	RCY	C1U-N1R-C1Q	9.48	144.61	123.55	2	2
2	A	130	RCY	C1U-N1R-C1Q	9.12	143.81	123.55	79	1
2	A	173	RCY	C1U-N1R-C1P	9.01	143.58	123.55	79	4
2	A	130	RCY	O1H-C1Q-N1R	8.85	114.08	124.38	15	5
2	A	173	RCY	O1H-C1Q-N1R	8.85	114.09	124.38	84	4
2	A	160	RCY	O1H-C1Q-N1R	8.84	114.10	124.38	74	4
2	A	130	RCY	C1Z-C1W-C1Y	8.84	89.86	109.45	79	1
2	A	121	RCY	O1H-C1Q-N1R	8.82	114.12	124.38	52	6
2	A	150	RCY	O1H-C1Q-N1R	8.79	114.15	124.38	26	2
2	A	187	RCY	C1U-N1R-C1Q	8.75	143.00	123.55	25	1
2	A	168	RCY	C1U-N1R-C1P	8.71	142.91	123.55	25	2
2	A	130	RCY	C1V-C1X-N1V	8.61	78.89	109.37	79	1
2	A	176	RCY	C1Z-C1W-C1M	8.43	89.78	112.53	25	1
2	A	160	RCY	C1U-N1R-C1P	8.33	142.07	123.55	7	5
2	A	176	RCY	C1U-N1R-C1P	8.31	142.02	123.55	85	6
2	A	176	RCY	C1U-N1R-C1Q	7.90	141.10	123.55	25	1
2	A	121	RCY	C1U-N1R-C1P	7.45	140.11	123.55	52	6
2	A	150	RCY	C1U-N1R-C1P	7.45	140.10	123.55	26	2
2	A	187	RCY	C1U-N1R-C1P	7.44	140.09	123.55	1	1
2	A	176	RCY	O1G-C1P-C1L	7.44	108.08	127.08	85	1
2	A	130	RCY	O1G-C1P-C1L	7.43	108.10	127.08	51	2
2	A	138	RCY	O1G-C1P-C1L	7.37	108.26	127.08	43	2
2	A	138	RCY	C1U-N1R-C1Q	7.36	139.91	123.55	7	4
2	A	168	RCY	O1G-C1P-N1R	6.96	116.29	124.38	25	1
2	A	187	RCY	C1Y-C1W-N1V	6.63	128.10	109.84	25	1
2	A	138	RCY	O1H-C1Q-C1S	6.61	110.19	127.08	50	4
2	A	168	RCY	C1U-N1R-C1Q	6.39	137.75	123.55	79	2
2	A	150	RCY	C1U-N1R-C1Q	5.99	136.87	123.55	79	1
2	A	110	RCY	C1S-C1Q-N1R	5.84	112.62	107.87	79	1
2	A	121	RCY	C1U-N1R-C1Q	5.83	136.49	123.55	79	1
2	A	160	RCY	O1G-C1P-C1L	5.79	141.87	127.08	7	1

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})	Models	
								Worst	Total
2	A	121	RCY	O1G-C1P-N1R	5.57	130.86	124.38	13	4
2	A	150	RCY	O1G-C1P-N1R	5.55	130.84	124.38	26	1
2	A	173	RCY	O1G-C1P-N1R	5.53	130.82	124.38	84	1
2	A	187	RCY	O1G-C1P-N1R	5.50	130.78	124.38	1	1
2	A	176	RCY	O1H-C1Q-C1S	5.48	113.08	127.08	79	2
2	A	130	RCY	C1Y-C1W-N1V	5.48	124.92	109.84	79	1
2	A	187	RCY	C1V-C1X-C1C	5.42	99.46	110.44	25	1
2	A	160	RCY	O1H-C1Q-C1S	5.29	113.57	127.08	25	1
2	A	173	RCY	C1V-C1X-C1C	5.18	99.96	110.44	25	1
2	A	121	RCY	O1H-C1Q-C1S	5.17	113.88	127.08	79	1
2	A	110	RCY	C1U-N1R-C1P	5.11	134.91	123.55	79	1
2	A	187	RCY	O1H-C1Q-C1S	5.10	114.05	127.08	1	1
2	A	110	RCY	C1S-C1L-C1P	5.03	99.79	105.23	22	13
2	A	150	RCY	O1H-C1Q-C1S	5.01	114.28	127.08	25	1

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

Mol	Chain	Res	Type	Atoms	Models (Total)
2	A	160	RCY	C1U	70
2	A	168	RCY	C1U	69
2	A	130	RCY	C1U	61
2	A	187	RCY	C1U	57
2	A	176	RCY	C1U	56
2	A	150	RCY	C1U	53
2	A	138	RCY	C1U	52
2	A	173	RCY	C1U	50
2	A	110	RCY	C1U	47
2	A	121	RCY	C1U	45

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

Mol	Chain	Res	Type	Atoms	Models (Total)
2	A	110	RCY	C1X-C1U-N1R-C1Q	15
2	A	168	RCY	C1X-C1U-N1R-C1Q	14
2	A	160	RCY	C1X-C1U-N1R-C1P	13
2	A	160	RCY	C1X-C1U-N1R-C1Q	12
2	A	130	RCY	C1X-C1U-N1R-C1P	11
2	A	176	RCY	C1X-C1U-N1R-C1Q	11
2	A	121	RCY	C1X-C1U-N1R-C1Q	11
2	A	130	RCY	C1X-C1U-N1R-C1Q	9

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Mol	Chain	Res	Type	Atoms	Models (Total)
2	A	187	RCY	C1X-C1U-N1R-C1Q	9
2	A	150	RCY	C1X-C1U-N1R-C1Q	9
2	A	150	RCY	C1X-C1U-N1R-C1P	8
2	A	138	RCY	C1X-C1U-N1R-C1P	8
2	A	138	RCY	C1X-C1U-N1R-C1Q	7
2	A	187	RCY	C1X-C1U-N1R-C1P	7
2	A	173	RCY	C1X-C1U-N1R-C1Q	7
2	A	168	RCY	C1X-C1U-N1R-C1P	6
2	A	173	RCY	C1X-C1U-N1R-C1P	6
2	A	176	RCY	C1X-C1U-N1R-C1P	6
2	A	110	RCY	C1X-C1U-N1R-C1P	6
2	A	121	RCY	C1X-C1U-N1R-C1P	6

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

Mol	Chain	Res	Type	Atoms	Models (Total)
2	A	130	RCY	C1L-C1P-C1Q-C1S-N1R	1
2	A	130	RCY	C1M-C1U-C1W-C1X-N1V	1

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 68% for the well-defined parts and 64% for the entire structure.

7.1 Chemical shift list 1

File name: input_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	845
Number of shifts mapped to atoms	727
Number of unparsed shifts	0
Number of shifts with mapping errors	118
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

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

- Residue not found in structure. All 118 occurences are reported below.

Chain	Res	Type	Atom	Shift Data		
				Value	Uncertainty	Ambiguity
A	76	LEU	CA	55.995	0.15	1
A	76	LEU	HD23	0.9	0.05	1
A	87	ILE	HG13	1.188	0.05	1
A	38	PHE	CB	40.008	0.15	1
A	76	LEU	HD21	0.9	0.05	1
A	68	ALA	CA	50.582	0.15	1
A	73	PHE	CA	57.985	0.15	1
A	10	ILE	HG23	0.913	0.05	1
A	73	PHE	HD2	7.231	0.05	1
A	68	ALA	H	8.239	0.05	1
A	21	VAL	H	8.376	0.05	1
A	21	VAL	HG21	0.956	0.05	1
A	68	ALA	HB2	1.002	0.05	1
A	76	LEU	HD12	0.863	0.05	1

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Chain	Res	Type	Atom	Shift Data		
				Value	Uncertainty	Ambiguity
A	76	LEU	HD11	0.863	0.05	1
A	76	LEU	CD1	23.706	0.15	1
A	73	PHE	HD1	7.231	0.05	1
A	21	VAL	HA	4.167	0.05	1
A	38	PHE	H	8.373	0.05	1
A	50	PHE	HA	4.632	0.05	1
A	21	VAL	CG2	20.766	0.15	1
A	10	ILE	CD1	12.714	0.15	1
A	87	ILE	CA	66.943	0.15	1
A	30	PHE	CA	57.554	0.15	1
A	87	ILE	HD11	0.848	0.05	1
A	68	ALA	CB	18.099	0.15	1
A	38	PHE	N	122.108	0.15	1
A	10	ILE	HG22	0.913	0.05	1
A	38	PHE	HB3	3.101	0.05	1
A	87	ILE	CB	39.016	0.15	1
A	30	PHE	HD2	7.222	0.05	1
A	87	ILE	HD12	0.848	0.05	1
A	60	LEU	C	177.67	0.15	1
A	60	LEU	HD23	0.907	0.05	1
A	68	ALA	HA	4.361	0.05	1
A	10	ILE	HD11	0.859	0.05	1
A	30	PHE	HA	4.651	0.05	1
A	60	LEU	CA	55.332	0.15	1
A	10	ILE	H	8.289	0.05	1
A	73	PHE	HB3	3.023	0.05	1
A	60	LEU	HA	4.388	0.05	1
A	10	ILE	HG21	0.913	0.05	1
A	38	PHE	HA	4.659	0.05	1
A	68	ALA	HB3	1.002	0.05	1
A	87	ILE	CD1	12.969	0.15	1
A	10	ILE	CB	38.666	0.15	1
A	60	LEU	HD22	0.907	0.05	1
A	87	ILE	HG23	0.895	0.05	1
A	60	LEU	CG	25.049	0.15	1
A	76	LEU	N	122.091	0.15	1
A	21	VAL	HG22	0.956	0.05	1
A	30	PHE	HB2	3.016	0.05	1
A	50	PHE	HB3	3.185	0.05	1
A	38	PHE	CA	57.615	0.15	1
A	87	ILE	HD13	0.848	0.05	1

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Chain	Res	Type	Atom	Shift Data		
				Value	Uncertainty	Ambiguity
A	68	ALA	N	128.782	0.15	1
A	76	LEU	HD13	0.863	0.05	1
A	10	ILE	CG2	17.53	0.15	1
A	73	PHE	HB2	3.129	0.05	1
A	73	PHE	CB	39.356	0.15	1
A	87	ILE	CG2	17.895	0.15	1
A	30	PHE	H	8.168	0.05	1
A	10	ILE	HA	4.166	0.05	1
A	76	LEU	HA	4.287	0.05	1
A	73	PHE	H	7.935	0.05	1
A	60	LEU	CB	42.514	0.15	1
A	60	LEU	HD21	0.907	0.05	1
A	87	ILE	HG22	0.895	0.05	1
A	60	LEU	N	121.371	0.15	1
A	21	VAL	HB	1.962	0.05	1
A	10	ILE	HD13	0.859	0.05	1
A	87	ILE	CG1	27.193	0.15	1
A	76	LEU	HB3	1.642	0.05	1
A	21	VAL	HG23	0.956	0.05	1
A	30	PHE	HB3	3.112	0.05	1
A	76	LEU	CD2	24.084	0.15	1
A	50	PHE	CA	58.008	0.15	1
A	87	ILE	N	127.372	0.15	1
A	60	LEU	HB2	1.648	0.05	1
A	30	PHE	CB	39.988	0.15	1
A	30	PHE	N	121.014	0.15	1
A	76	LEU	HB2	1.568	0.05	1
A	87	ILE	HA	4.426	0.05	1
A	10	ILE	CG1	27.278	0.15	1
A	76	LEU	HD22	0.9	0.05	1
A	50	PHE	C	176.416	0.15	1
A	68	ALA	HB1	1.002	0.05	1
A	10	ILE	HG12	1.214	0.05	1
A	10	ILE	HB	1.88	0.05	1
A	60	LEU	CD2	23.502	0.15	1
A	60	LEU	H	8.124	0.05	1
A	21	VAL	CA	62.522	0.15	1
A	10	ILE	N	123.217	0.15	1
A	21	VAL	C	176.368	0.15	1
A	73	PHE	HA	4.539	0.05	1
A	87	ILE	HG21	0.895	0.05	1

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Chain	Res	Type	Atom	Shift Data		
				Value	Uncertainty	Ambiguity
A	10	ILE	HD12	0.859	0.05	1
A	87	ILE	H	7.855	0.05	1
A	73	PHE	C	175.668	0.15	1
A	76	LEU	CB	42.241	0.15	1
A	87	ILE	HG12	1.433	0.05	1
A	50	PHE	N	119.885	0.15	1
A	50	PHE	CB	39.865	0.15	1
A	60	LEU	HB3	1.663	0.05	1
A	38	PHE	HB2	3.011	0.05	1
A	38	PHE	C	175.417	0.15	1
A	87	ILE	HB	2.018	0.05	1
A	73	PHE	N	117.759	0.15	1
A	76	LEU	C	177.284	0.15	1
A	50	PHE	HB2	3.015	0.05	1
A	10	ILE	HG13	1.501	0.05	1
A	10	ILE	C	176.308	0.15	1
A	21	VAL	N	120.972	0.15	1
A	21	VAL	CB	32.722	0.15	1
A	10	ILE	CA	61.279	0.15	1
A	76	LEU	H	8.166	0.05	1
A	30	PHE	C	175.376	0.15	1
A	50	PHE	H	8.222	0.05	1

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	84	-0.03 ± 0.05	None needed (< 0.5 ppm)
$^{13}C_{\beta}$	74	0.25 ± 0.11	None needed (< 0.5 ppm)
$^{13}C'$	76	-0.07 ± 0.09	None needed (< 0.5 ppm)
^{15}N	76	-0.97 ± 0.26	Should be applied

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 68%, i.e. 145 atoms were assigned a chemical shift out of a possible 213. 1 out of 2 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	76/98 (78%)	29/39 (74%)	32/40 (80%)	15/19 (79%)
Sidechain	67/95 (71%)	39/55 (71%)	28/39 (72%)	0/1 (0%)
Aromatic	2/20 (10%)	2/10 (20%)	0/7 (0%)	0/3 (0%)
Overall	145/213 (68%)	70/104 (67%)	60/86 (70%)	15/23 (65%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 64%, i.e. 658 atoms were assigned a chemical shift out of a possible 1034. 3 out of 6 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	341/415 (82%)	133/164 (81%)	142/174 (82%)	66/77 (86%)
Sidechain	313/583 (54%)	173/352 (49%)	139/201 (69%)	1/30 (3%)
Aromatic	4/36 (11%)	4/18 (22%)	0/13 (0%)	0/5 (0%)
Overall	658/1034 (64%)	310/534 (58%)	281/388 (72%)	67/112 (60%)

7.1.4 Statistically unusual chemical shifts

There are no statistically unusual chemical shifts.

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: