Full wwPDB NMR Structure Validation Report (i)

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PDB ID	:	2JQG
Title	:	Leader Protease
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This is a Full wwPDB NMR Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
http://wwpdb.org/validation/2016/NMRValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

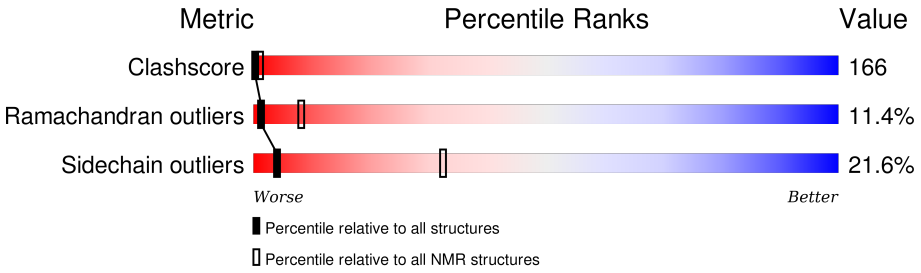
Cyrange	:	Kirchner and Güntert (2011)
NmrClust	:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Mogul	:	unknown
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	rb-20027457
Ideal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

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
SOLUTION NMR

The overall completeness of chemical shifts assignment is 38%.

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



Metric	Whole archive (#Entries)	NMR archive (#Entries)
Clashscore	114402	11133
Ramachandran outliers	111179	9975
Sidechain outliers	111093	9958

The table below summarises the geometric issues observed across the polymeric chains and their fit to the experimental data. The red, orange, yellow and green segments indicate the fraction of residues that contain outliers for >=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	R	167	13% 59% 22% 7%

2 Ensemble composition and analysis

This entry contains 5 models. Model 2 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *lowest energy*.

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

Well-defined (core) protein residues			
Well-defined core	**Residue range (total)**	**Backbone RMSD (Å)**	**Medoid model**
1	R:29-R:184 (156)	1.28	2

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 2 clusters and 1 single-model cluster was found.

Cluster number	Models
1	1, 2
2	3, 5
Single-model clusters	4

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 2612 atoms, of which 1266 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Genome polyprotein.

Mol	Chain	Residues	Atoms						Trace
1	R	167	Total	C	H	N	O	S	0
			2612	871	1266	214	256	5	

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	51	ALA	CYS	ENGINEERED	UNP P03305
R	126	VAL	MET	ENGINEERED	UNP P03305

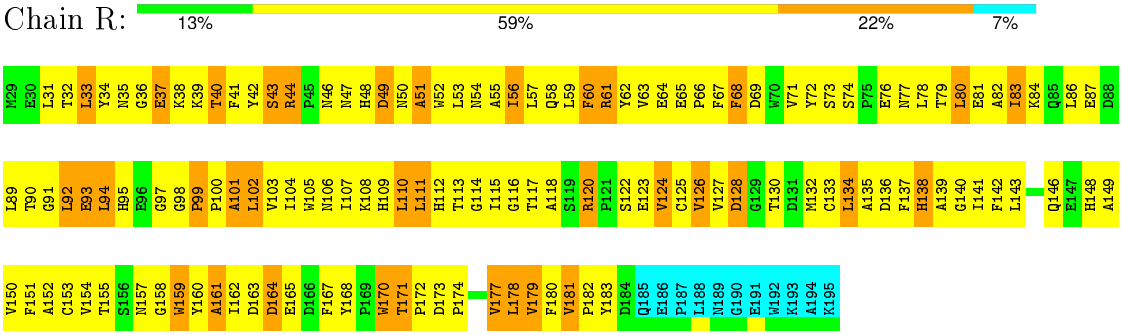
4 Residue-property plots (i)

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: Genome polyprotein

Chain R:



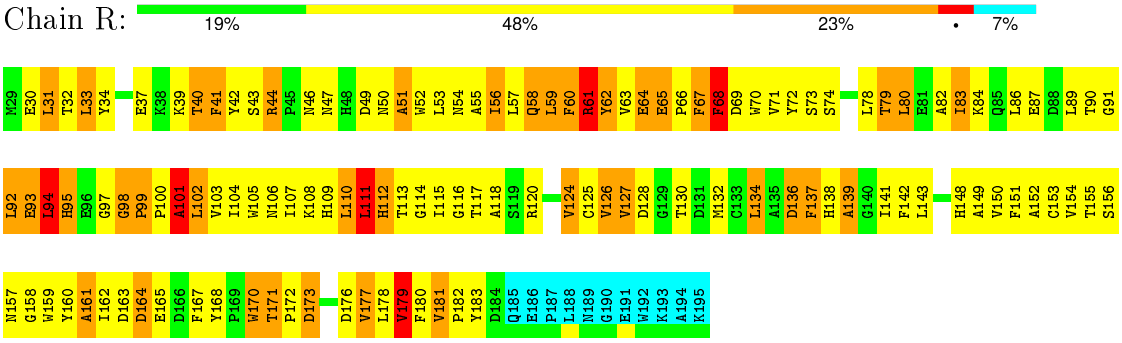
4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

- Molecule 1: Genome polyprotein

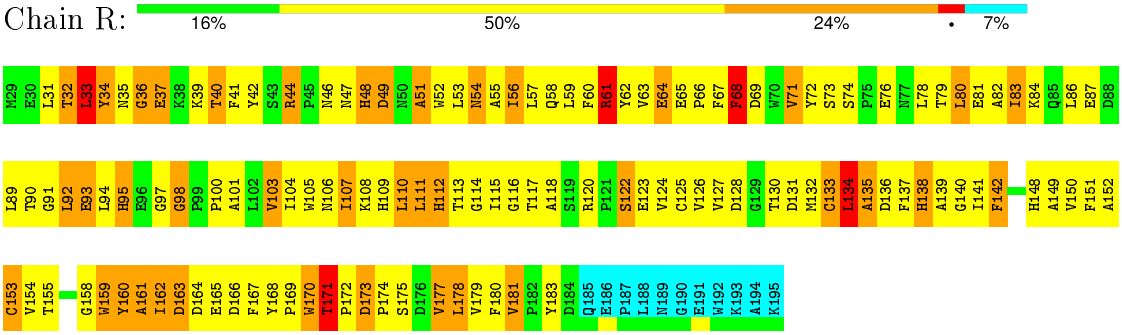
Chain R:



4.2.2 Score per residue for model 2 (medoid)

- Molecule 1: Genome polyprotein

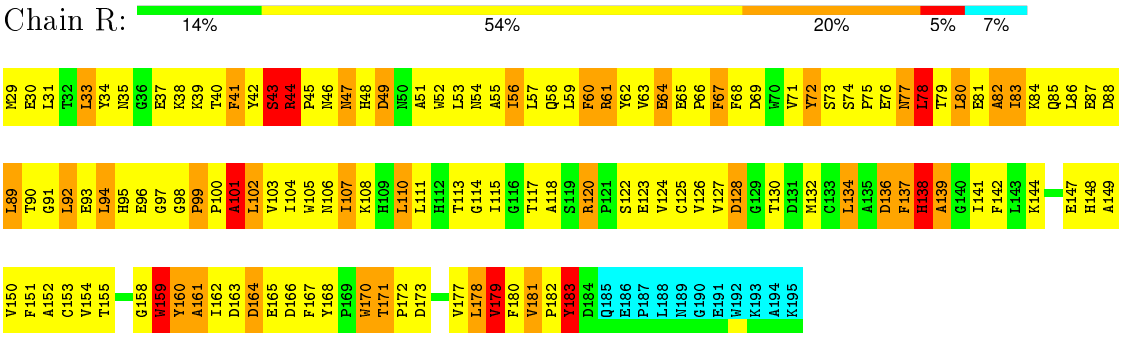
Chain R:



4.2.3 Score per residue for model 3

- Molecule 1: Genome polyprotein

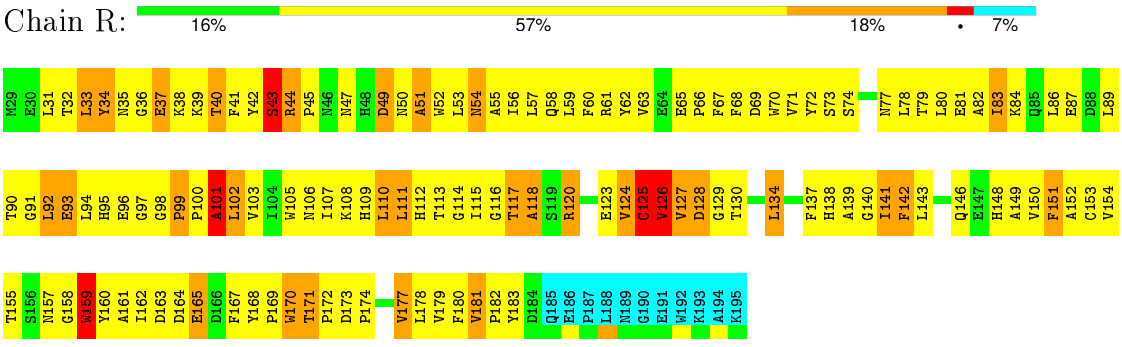
Chain R:



4.2.4 Score per residue for model 4

- Molecule 1: Genome polyprotein

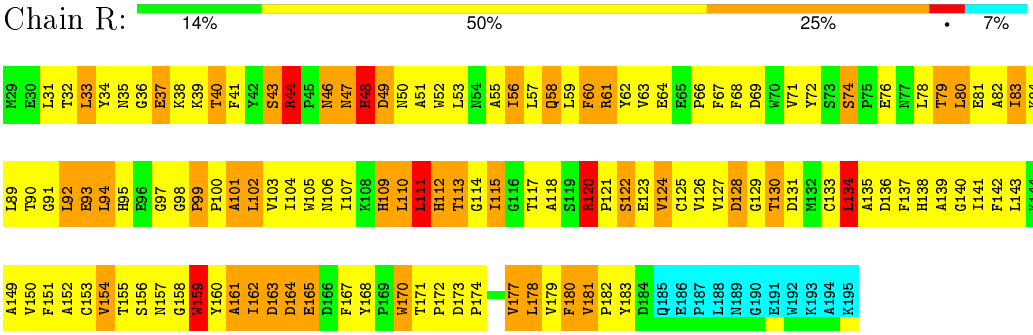
Chain R:



4.2.5 Score per residue for model 5

- Molecule 1: Genome polyprotein

Chain R:



5 Refinement protocol and experimental data overview

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

Of the 100 calculated structures, 5 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
X-PLOR NIH	structure solution	
X-PLOR NIH	refinement	

The following table shows chemical shift validation statistics as aggregates over all chemical shift files. Detailed validation can be found in section 7 of this report.

Chemical shift file(s)	BMRB entry 15278
Number of chemical shift lists	1
Total number of shifts	774
Number of shifts mapped to atoms	774
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	38%

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

6 Model quality

6.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#Z>5	RMSZ	#Z>5
1	R	1.08±0.00	0±0/1296 (0.0±0.0%)	1.31±0.01	3±1/1776 (0.2±0.1%)
All	All	1.08	0/6480 (0.0%)	1.31	17/8880 (0.2%)

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

Mol	Chain	Chirality	Planarity
1	R	0.0±0.0	3.0±0.0
All	All	0	15

There are no bond-length outliers.

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
1	R	118	ALA	N-CA-CB	-6.45	101.08	110.10	4	1
1	R	115	ILE	N-CA-CB	-5.85	97.34	110.80	5	1
1	R	51	ALA	N-CA-CB	-5.79	102.00	110.10	1	3
1	R	126	VAL	CA-CB-CG2	-5.58	102.53	110.90	4	1
1	R	171	THR	N-CA-CB	-5.57	99.72	110.30	3	1
1	R	161	ALA	N-CA-CB	-5.51	102.38	110.10	5	4
1	R	139	ALA	N-CA-CB	-5.32	102.66	110.10	3	1
1	R	101	ALA	N-CA-CB	-5.13	102.91	110.10	1	3
1	R	103	VAL	CA-CB-CG1	-5.01	103.39	110.90	2	1
1	R	82	ALA	N-CA-CB	-5.00	103.09	110.10	3	1

There are no chirality outliers.

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

Mol	Chain	Res	Type	Group	Models (Total)
1	R	44	ARG	Sidechain	5
1	R	120	ARG	Sidechain	5
1	R	61	ARG	Sidechain	5

6.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	R	1254	1178	1175	403±15
All	All	6270	5890	5875	2016

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 166.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:R:115:ILE:HG23	1:R:124:VAL:O	1.22	1.28	5	2
1:R:36:GLY:O	1:R:37:GLU:O	1.22	1.56	2	3
1:R:115:ILE:HD12	1:R:124:VAL:HG22	1.15	1.17	2	3
1:R:134:LEU:HD11	1:R:171:THR:HG22	1.11	1.12	1	4
1:R:86:LEU:HD11	1:R:103:VAL:HG13	1.08	1.23	4	4
1:R:152:ALA:HB2	1:R:161:ALA:HB2	1.06	1.26	1	4
1:R:41:PHE:CE2	1:R:162:ILE:HD11	1.06	1.85	3	1
1:R:33:LEU:N	1:R:33:LEU:HD22	1.05	1.67	2	2
1:R:92:LEU:HD13	1:R:94:LEU:HD23	1.04	1.18	2	3
1:R:115:ILE:CG2	1:R:124:VAL:O	1.04	2.04	5	2
1:R:113:THR:HG23	1:R:115:ILE:HD11	1.03	1.26	2	2
1:R:127:VAL:HG21	1:R:177:VAL:O	1.02	1.54	4	2
1:R:31:LEU:HD13	1:R:162:ILE:HG21	1.01	1.26	3	1
1:R:117:THR:HG23	1:R:126:VAL:HG21	1.01	1.28	5	2
1:R:134:LEU:HD11	1:R:171:THR:HG23	1.00	1.26	5	1
1:R:127:VAL:CG2	1:R:178:LEU:HA	0.98	1.88	4	5
1:R:162:ILE:HG22	1:R:167:PHE:HA	0.98	1.34	3	2
1:R:113:THR:CG2	1:R:115:ILE:HD11	0.98	1.87	2	4
1:R:31:LEU:CD1	1:R:162:ILE:HG21	0.98	1.89	4	2
1:R:141:ILE:HG23	1:R:151:PHE:CE1	0.98	1.94	3	2
1:R:134:LEU:CA	1:R:173:ASP:HB2	0.98	1.88	2	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:R:134:LEU:HD11	1:R:171:THR:CG2	0.97	1.89	3	5
1:R:83:ILE:HG21	1:R:94:LEU:HD11	0.96	1.36	2	2
1:R:111:LEU:O	1:R:113:THR:N	0.95	2.00	5	3
1:R:142:PHE:CG	1:R:177:VAL:HB	0.95	1.95	3	5
1:R:100:PRO:O	1:R:102:LEU:N	0.95	1.99	5	4
1:R:53:LEU:HD11	1:R:83:ILE:HG12	0.95	1.33	4	2
1:R:134:LEU:HA	1:R:173:ASP:HB2	0.94	1.34	2	1
1:R:33:LEU:HD13	1:R:33:LEU:H	0.94	1.17	2	2
1:R:141:ILE:HG23	1:R:151:PHE:CE2	0.94	1.98	1	1
1:R:134:LEU:HD13	1:R:172:PRO:CD	0.93	1.92	2	1
1:R:138:HIS:HB3	1:R:181:VAL:O	0.93	1.62	3	1
1:R:92:LEU:CD1	1:R:94:LEU:HD23	0.93	1.93	2	2
1:R:41:PHE:CZ	1:R:162:ILE:HD11	0.93	1.98	3	1
1:R:142:PHE:CE2	1:R:177:VAL:HG11	0.93	1.99	3	4
1:R:152:ALA:HB1	1:R:160:TYR:O	0.92	1.64	2	2
1:R:31:LEU:HD11	1:R:162:ILE:HD13	0.92	1.39	4	2
1:R:138:HIS:CB	1:R:181:VAL:O	0.92	2.16	3	1
1:R:118:ALA:HB1	1:R:130:THR:HG21	0.91	1.39	1	3
1:R:57:LEU:HG	1:R:71:VAL:HG11	0.91	1.41	5	4
1:R:57:LEU:HD12	1:R:72:TYR:CE1	0.90	2.00	4	1
1:R:118:ALA:HB1	1:R:130:THR:CG2	0.90	1.97	1	3
1:R:115:ILE:HD12	1:R:124:VAL:CG2	0.90	1.97	2	4
1:R:83:ILE:CG2	1:R:94:LEU:HD11	0.90	1.97	4	2
1:R:152:ALA:HA	1:R:161:ALA:HA	0.89	1.42	2	5
1:R:134:LEU:HD13	1:R:172:PRO:HD2	0.89	1.45	2	2
1:R:31:LEU:HD11	1:R:162:ILE:CD1	0.89	1.97	5	3
1:R:31:LEU:HD23	1:R:41:PHE:CD1	0.89	2.02	2	1
1:R:55:ALA:O	1:R:59:LEU:HD23	0.89	1.67	5	1
1:R:52:TRP:CE3	1:R:149:ALA:HB2	0.89	2.03	3	3
1:R:57:LEU:HD12	1:R:72:TYR:CD1	0.88	2.04	4	1
1:R:152:ALA:CB	1:R:161:ALA:HB2	0.88	1.97	3	4
1:R:33:LEU:N	1:R:33:LEU:HD13	0.88	1.82	4	3
1:R:115:ILE:HD12	1:R:124:VAL:CA	0.88	1.98	5	1
1:R:113:THR:HG22	1:R:123:GLU:HA	0.88	1.41	5	1
1:R:126:VAL:CG1	1:R:127:VAL:HG13	0.88	1.99	4	1
1:R:139:ALA:HB3	1:R:181:VAL:CG1	0.87	1.99	4	4
1:R:101:ALA:O	1:R:103:VAL:N	0.87	2.07	3	4
1:R:92:LEU:HD12	1:R:101:ALA:O	0.87	1.69	3	1
1:R:31:LEU:HD22	1:R:167:PHE:CZ	0.87	2.04	4	3
1:R:55:ALA:HB1	1:R:151:PHE:CE1	0.87	2.04	3	1
1:R:141:ILE:O	1:R:177:VAL:HG23	0.86	1.70	3	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:R:86:LEU:CD1	1:R:103:VAL:HG13	0.86	2.00	1	4
1:R:115:ILE:HD12	1:R:124:VAL:HA	0.86	1.46	5	1
1:R:113:THR:HG23	1:R:115:ILE:CD1	0.86	2.00	2	2
1:R:174:PRO:HA	1:R:177:VAL:HG13	0.85	1.48	2	2
1:R:86:LEU:HD22	1:R:90:THR:CG2	0.85	2.01	2	1
1:R:103:VAL:O	1:R:107:ILE:HB	0.85	1.72	3	1
1:R:86:LEU:HD13	1:R:103:VAL:HG13	0.84	1.47	2	1
1:R:92:LEU:HD11	1:R:94:LEU:HD21	0.84	1.46	3	2
1:R:127:VAL:HG23	1:R:178:LEU:HD13	0.84	1.48	3	3
1:R:103:VAL:O	1:R:107:ILE:HG12	0.84	1.73	4	1
1:R:115:ILE:HG23	1:R:124:VAL:CG2	0.84	2.02	3	3
1:R:56:ILE:HG23	1:R:60:PHE:CE2	0.84	2.07	4	1
1:R:134:LEU:CD1	1:R:171:THR:HG23	0.83	2.03	5	1
1:R:86:LEU:HD22	1:R:90:THR:HG23	0.83	1.49	2	1
1:R:53:LEU:CD1	1:R:83:ILE:HG12	0.83	2.03	3	2
1:R:31:LEU:HD13	1:R:162:ILE:CD1	0.83	2.03	1	1
1:R:31:LEU:HD11	1:R:162:ILE:HD11	0.83	1.47	5	1
1:R:31:LEU:HD11	1:R:167:PHE:CZ	0.83	2.09	1	1
1:R:57:LEU:HD11	1:R:71:VAL:HB	0.82	1.49	5	4
1:R:57:LEU:CD2	1:R:71:VAL:HG21	0.82	2.04	2	2
1:R:57:LEU:HD12	1:R:72:TYR:CE2	0.82	2.08	1	1
1:R:127:VAL:CG2	1:R:178:LEU:HD13	0.82	2.04	2	4
1:R:86:LEU:HD12	1:R:94:LEU:HD21	0.82	1.49	4	3
1:R:33:LEU:HA	1:R:37:GLU:CA	0.82	2.05	2	1
1:R:139:ALA:HB3	1:R:181:VAL:HG12	0.82	1.52	4	3
1:R:57:LEU:HD21	1:R:71:VAL:HG21	0.81	1.50	1	5
1:R:126:VAL:HA	1:R:179:VAL:HA	0.81	1.53	2	2
1:R:126:VAL:HG12	1:R:178:LEU:O	0.81	1.73	4	1
1:R:60:PHE:CE1	1:R:111:LEU:HD21	0.81	2.10	2	1
1:R:113:THR:HG22	1:R:115:ILE:CD1	0.80	2.07	4	1
1:R:55:ALA:O	1:R:59:LEU:HB2	0.80	1.75	1	4
1:R:31:LEU:CD1	1:R:162:ILE:HD13	0.80	2.07	4	2
1:R:115:ILE:HG13	1:R:123:GLU:CA	0.80	2.07	5	1
1:R:113:THR:HG23	1:R:115:ILE:HG12	0.80	1.52	5	1
1:R:63:VAL:HG22	1:R:124:VAL:CG1	0.80	2.06	1	2
1:R:134:LEU:HD21	1:R:171:THR:CG2	0.79	2.07	5	2
1:R:33:LEU:CA	1:R:37:GLU:HA	0.79	2.07	2	1
1:R:33:LEU:HA	1:R:37:GLU:HA	0.79	1.54	2	1
1:R:31:LEU:HD21	1:R:41:PHE:CD1	0.79	2.13	5	3
1:R:62:TYR:CZ	1:R:63:VAL:HG23	0.79	2.13	5	2
1:R:62:TYR:HB3	1:R:181:VAL:HG21	0.79	1.52	4	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:R:113:THR:HG23	1:R:115:ILE:CG1	0.79	2.07	5	1
1:R:162:ILE:O	1:R:162:ILE:HG23	0.78	1.75	2	1
1:R:86:LEU:HD13	1:R:86:LEU:C	0.78	1.98	5	2
1:R:86:LEU:HD12	1:R:94:LEU:CD2	0.78	2.09	5	2
1:R:99:PRO:HB2	1:R:100:PRO:CD	0.78	2.09	4	2
1:R:90:THR:OG1	1:R:92:LEU:HD22	0.78	1.79	3	1
1:R:117:THR:HG23	1:R:126:VAL:CG2	0.78	2.06	5	1
1:R:33:LEU:O	1:R:34:TYR:C	0.78	2.20	2	2
1:R:63:VAL:O	1:R:64:GLU:CB	0.78	2.31	1	4
1:R:126:VAL:HG13	1:R:127:VAL:HG13	0.78	1.55	4	1
1:R:115:ILE:HG13	1:R:123:GLU:C	0.78	1.99	5	1
1:R:162:ILE:HG23	1:R:167:PHE:CE1	0.78	2.14	1	1
1:R:142:PHE:CE1	1:R:177:VAL:HG21	0.77	2.14	3	2
1:R:115:ILE:HG23	1:R:124:VAL:C	0.77	2.00	5	1
1:R:57:LEU:HD13	1:R:68:PHE:CG	0.77	2.13	4	1
1:R:117:THR:HA	1:R:126:VAL:HG22	0.77	1.53	2	3
1:R:63:VAL:HG22	1:R:124:VAL:HG12	0.77	1.55	1	2
1:R:171:THR:O	1:R:171:THR:HG22	0.77	1.79	3	1
1:R:59:LEU:HD13	1:R:151:PHE:CE2	0.77	2.13	3	1
1:R:134:LEU:CD1	1:R:171:THR:HG22	0.77	2.08	2	2
1:R:71:VAL:HG23	1:R:82:ALA:HB1	0.77	1.55	3	5
1:R:92:LEU:CD1	1:R:94:LEU:HD21	0.77	2.09	3	2
1:R:99:PRO:HG2	1:R:100:PRO:HD2	0.77	1.57	1	2
1:R:32:THR:C	1:R:33:LEU:HD22	0.77	2.00	2	1
1:R:86:LEU:HD13	1:R:103:VAL:CG1	0.77	2.08	2	1
1:R:53:LEU:HD13	1:R:71:VAL:HG22	0.77	1.56	5	3
1:R:53:LEU:O	1:R:57:LEU:HD23	0.76	1.79	3	4
1:R:142:PHE:CZ	1:R:177:VAL:HG11	0.76	2.15	1	5
1:R:138:HIS:HB2	1:R:154:VAL:HG23	0.76	1.54	2	2
1:R:55:ALA:HA	1:R:151:PHE:CD1	0.76	2.16	3	2
1:R:159:TRP:O	1:R:169:PRO:HA	0.76	1.80	2	1
1:R:118:ALA:HB1	1:R:130:THR:CB	0.76	2.11	2	1
1:R:159:TRP:CG	1:R:171:THR:O	0.76	2.39	3	1
1:R:137:PHE:CE1	1:R:180:PHE:HB2	0.75	2.16	2	2
1:R:33:LEU:H	1:R:33:LEU:CD1	0.75	1.91	2	1
1:R:92:LEU:HD22	1:R:101:ALA:O	0.75	1.82	5	3
1:R:162:ILE:HG22	1:R:162:ILE:O	0.75	1.81	5	1
1:R:55:ALA:HB2	1:R:151:PHE:CZ	0.75	2.16	1	2
1:R:31:LEU:HD23	1:R:31:LEU:N	0.75	1.96	4	2
1:R:110:LEU:HD13	1:R:110:LEU:N	0.75	1.96	4	1
1:R:53:LEU:HD11	1:R:83:ILE:HG13	0.74	1.58	2	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:R:118:ALA:HB2	1:R:130:THR:CG2	0.74	2.12	5	1
1:R:152:ALA:CB	1:R:160:TYR:O	0.74	2.35	2	1
1:R:113:THR:CG2	1:R:123:GLU:HA	0.74	2.12	5	1
1:R:53:LEU:HD13	1:R:71:VAL:CG2	0.74	2.12	5	4
1:R:116:GLY:O	1:R:125:CYS:HB3	0.74	1.83	4	1
1:R:109:HIS:C	1:R:110:LEU:HD13	0.73	2.04	2	4
1:R:62:TYR:CZ	1:R:139:ALA:HB1	0.73	2.18	3	2
1:R:99:PRO:CG	1:R:100:PRO:HD2	0.73	2.13	1	4
1:R:114:GLY:C	1:R:115:ILE:HD13	0.73	2.05	2	3
1:R:83:ILE:CG2	1:R:94:LEU:HD13	0.73	2.14	1	2
1:R:142:PHE:CD1	1:R:177:VAL:HB	0.72	2.19	5	5
1:R:89:LEU:HD23	1:R:90:THR:N	0.72	1.98	1	4
1:R:60:PHE:HA	1:R:66:PRO:HD3	0.72	1.60	1	2
1:R:86:LEU:HD13	1:R:90:THR:OG1	0.72	1.84	3	2
1:R:127:VAL:O	1:R:129:GLY:N	0.72	2.23	4	2
1:R:53:LEU:HD11	1:R:83:ILE:CG1	0.72	2.14	5	4
1:R:127:VAL:HG22	1:R:178:LEU:C	0.72	2.05	3	2
1:R:31:LEU:HD11	1:R:162:ILE:HG21	0.72	1.60	4	1
1:R:123:GLU:O	1:R:124:VAL:HG13	0.72	1.84	5	1
1:R:117:THR:CG2	1:R:126:VAL:HG21	0.72	2.13	5	1
1:R:170:TRP:O	1:R:171:THR:HG23	0.72	1.83	2	1
1:R:53:LEU:HD12	1:R:79:THR:OG1	0.72	1.85	2	3
1:R:55:ALA:HA	1:R:151:PHE:CE2	0.71	2.20	1	1
1:R:31:LEU:CD1	1:R:41:PHE:CD1	0.71	2.73	1	1
1:R:59:LEU:HD13	1:R:151:PHE:HE2	0.71	1.45	3	1
1:R:89:LEU:H	1:R:89:LEU:HD12	0.71	1.46	3	1
1:R:142:PHE:CD2	1:R:177:VAL:CG1	0.71	2.73	2	5
1:R:137:PHE:CG	1:R:180:PHE:CD2	0.71	2.78	4	2
1:R:41:PHE:CD2	1:R:151:PHE:CE2	0.71	2.78	4	1
1:R:31:LEU:CD2	1:R:41:PHE:CD1	0.71	2.74	2	2
1:R:34:TYR:N	1:R:154:VAL:O	0.71	2.24	3	2
1:R:177:VAL:O	1:R:178:LEU:HD22	0.71	1.85	1	4
1:R:162:ILE:HG22	1:R:167:PHE:CA	0.71	2.15	3	2
1:R:139:ALA:HB2	1:R:153:CYS:SG	0.71	2.25	3	1
1:R:93:GLU:C	1:R:94:LEU:HD13	0.71	2.05	3	1
1:R:125:CYS:O	1:R:126:VAL:HG23	0.71	1.85	4	1
1:R:42:TYR:O	1:R:165:GLU:HB3	0.71	1.86	2	1
1:R:57:LEU:HD13	1:R:68:PHE:HD2	0.71	1.45	1	1
1:R:31:LEU:HD21	1:R:41:PHE:CE1	0.71	2.19	3	1
1:R:57:LEU:HD21	1:R:71:VAL:CG2	0.71	2.15	2	3
1:R:149:ALA:HB1	1:R:151:PHE:HZ	0.71	1.44	5	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:R:153:CYS:HB2	1:R:160:TYR:CE2	0.71	2.21	2	1
1:R:142:PHE:CE1	1:R:177:VAL:HG11	0.70	2.20	1	2
1:R:152:ALA:HB2	1:R:161:ALA:CB	0.70	2.15	4	5
1:R:33:LEU:N	1:R:33:LEU:CD2	0.70	2.41	2	1
1:R:107:ILE:HG23	1:R:111:LEU:CG	0.70	2.16	3	1
1:R:44:ARG:HA	1:R:164:ASP:HA	0.70	1.63	5	1
1:R:59:LEU:CD2	1:R:141:ILE:HD11	0.70	2.16	2	1
1:R:107:ILE:HG21	1:R:111:LEU:HD23	0.70	1.63	4	1
1:R:116:GLY:C	1:R:125:CYS:HB3	0.70	2.05	4	1
1:R:164:ASP:O	1:R:165:GLU:CB	0.70	2.40	4	2
1:R:138:HIS:CG	1:R:181:VAL:HG12	0.70	2.21	3	1
1:R:42:TYR:O	1:R:165:GLU:O	0.69	2.09	2	1
1:R:110:LEU:N	1:R:110:LEU:HD13	0.69	2.00	2	4
1:R:92:LEU:CG	1:R:94:LEU:HD21	0.69	2.16	3	1
1:R:126:VAL:HG13	1:R:127:VAL:H	0.69	1.47	4	1
1:R:56:ILE:HD12	1:R:103:VAL:HG11	0.69	1.64	3	1
1:R:90:THR:HG22	1:R:106:ASN:HB2	0.69	1.62	4	4
1:R:60:PHE:C	1:R:60:PHE:CD1	0.69	2.66	1	1
1:R:162:ILE:HA	1:R:166:ASP:O	0.69	1.88	2	2
1:R:155:THR:OG1	1:R:160:TYR:HB2	0.69	1.88	3	4
1:R:43:SER:O	1:R:44:ARG:O	0.69	2.10	3	1
1:R:162:ILE:CG2	1:R:162:ILE:O	0.69	2.39	2	2
1:R:41:PHE:CE2	1:R:162:ILE:HD13	0.69	2.22	5	2
1:R:152:ALA:CA	1:R:161:ALA:HA	0.69	2.17	2	2
1:R:137:PHE:CG	1:R:180:PHE:CD1	0.69	2.80	5	2
1:R:51:ALA:HB1	1:R:149:ALA:HB3	0.68	1.66	4	5
1:R:142:PHE:CD2	1:R:177:VAL:HG12	0.68	2.23	4	3
1:R:114:GLY:O	1:R:115:ILE:HD13	0.68	1.88	5	3
1:R:142:PHE:CG	1:R:177:VAL:CG1	0.68	2.76	2	2
1:R:127:VAL:CB	1:R:178:LEU:HD13	0.68	2.19	1	1
1:R:33:LEU:CD1	1:R:33:LEU:N	0.68	2.56	4	1
1:R:31:LEU:HD13	1:R:167:PHE:CG	0.68	2.22	4	1
1:R:31:LEU:HD21	1:R:162:ILE:HD13	0.68	1.65	4	1
1:R:41:PHE:CD2	1:R:162:ILE:HD11	0.68	2.24	2	1
1:R:71:VAL:HG23	1:R:82:ALA:CB	0.68	2.18	2	3
1:R:139:ALA:HA	1:R:152:ALA:O	0.68	1.88	1	5
1:R:90:THR:HA	1:R:106:ASN:CB	0.68	2.18	2	1
1:R:57:LEU:O	1:R:60:PHE:CD2	0.68	2.47	1	3
1:R:71:VAL:CG2	1:R:82:ALA:HB1	0.68	2.18	1	3
1:R:142:PHE:CE2	1:R:177:VAL:CG1	0.68	2.76	3	4
1:R:118:ALA:CB	1:R:130:THR:HG23	0.68	2.19	3	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:R:151:PHE:C	1:R:151:PHE:CD1	0.68	2.66	4	1
1:R:63:VAL:O	1:R:64:GLU:HB2	0.68	1.89	1	2
1:R:31:LEU:HD22	1:R:162:ILE:HD11	0.67	1.65	1	1
1:R:31:LEU:HD13	1:R:162:ILE:HD13	0.67	1.66	1	1
1:R:142:PHE:O	1:R:150:VAL:HG22	0.67	1.90	2	5
1:R:59:LEU:HD12	1:R:151:PHE:CE1	0.67	2.25	2	1
1:R:41:PHE:CD2	1:R:162:ILE:CD1	0.67	2.76	2	3
1:R:31:LEU:HD11	1:R:167:PHE:CE2	0.67	2.24	1	1
1:R:127:VAL:CG2	1:R:177:VAL:O	0.67	2.40	4	1
1:R:127:VAL:HG23	1:R:178:LEU:HA	0.67	1.66	1	1
1:R:161:ALA:HB3	1:R:168:TYR:CE1	0.67	2.24	1	1
1:R:53:LEU:O	1:R:57:LEU:CB	0.67	2.43	2	1
1:R:150:VAL:O	1:R:151:PHE:CD1	0.67	2.48	5	2
1:R:163:ASP:O	1:R:164:ASP:C	0.67	2.34	3	5
1:R:115:ILE:HB	1:R:122:SER:H	0.67	1.49	5	1
1:R:48:HIS:CD2	1:R:79:THR:HG21	0.67	2.25	5	1
1:R:60:PHE:CD1	1:R:60:PHE:C	0.67	2.67	3	2
1:R:115:ILE:CD1	1:R:124:VAL:HG22	0.66	2.08	2	2
1:R:98:GLY:O	1:R:101:ALA:HB3	0.66	1.89	3	2
1:R:150:VAL:C	1:R:151:PHE:CD1	0.66	2.68	1	1
1:R:53:LEU:HD22	1:R:57:LEU:HD21	0.66	1.65	4	2
1:R:55:ALA:O	1:R:59:LEU:HD22	0.66	1.91	1	1
1:R:111:LEU:O	1:R:112:HIS:C	0.66	2.33	1	3
1:R:49:ASP:O	1:R:79:THR:HG21	0.66	1.89	4	2
1:R:33:LEU:N	1:R:33:LEU:CD1	0.66	2.58	5	2
1:R:56:ILE:HG21	1:R:100:PRO:O	0.66	1.91	2	1
1:R:51:ALA:C	1:R:149:ALA:HB3	0.66	2.11	2	2
1:R:57:LEU:HD12	1:R:72:TYR:CD2	0.66	2.26	1	1
1:R:31:LEU:HB3	1:R:167:PHE:CD2	0.66	2.26	3	1
1:R:63:VAL:HG13	1:R:124:VAL:HG11	0.66	1.67	1	1
1:R:33:LEU:HD21	1:R:37:GLU:HB3	0.66	1.68	3	2
1:R:32:THR:HG22	1:R:38:LYS:HB3	0.66	1.68	4	1
1:R:134:LEU:HD23	1:R:175:SER:OG	0.65	1.91	2	1
1:R:50:ASN:HA	1:R:79:THR:OG1	0.65	1.92	1	1
1:R:116:GLY:O	1:R:125:CYS:CB	0.65	2.44	4	1
1:R:44:ARG:N	1:R:165:GLU:CB	0.65	2.59	5	1
1:R:137:PHE:CE1	1:R:173:ASP:HA	0.65	2.26	2	2
1:R:94:LEU:CD2	1:R:103:VAL:HG22	0.65	2.21	5	3
1:R:134:LEU:HD13	1:R:173:ASP:CG	0.65	2.10	4	1
1:R:92:LEU:HD12	1:R:93:GLU:N	0.65	2.06	2	3
1:R:138:HIS:CG	1:R:159:TRP:CE3	0.65	2.85	5	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:R:33:LEU:HA	1:R:37:GLU:N	0.65	2.07	2	1
1:R:142:PHE:HA	1:R:177:VAL:HA	0.65	1.66	4	4
1:R:31:LEU:HD13	1:R:162:ILE:HD11	0.65	1.69	1	1
1:R:126:VAL:HG13	1:R:127:VAL:N	0.65	2.05	4	1
1:R:127:VAL:HG21	1:R:178:LEU:HA	0.65	1.66	4	3
1:R:107:ILE:HG23	1:R:111:LEU:CD1	0.65	2.22	3	1
1:R:162:ILE:HG23	1:R:167:PHE:CD1	0.65	2.27	1	1
1:R:93:GLU:C	1:R:94:LEU:HG	0.65	2.11	5	2
1:R:137:PHE:HB2	1:R:183:TYR:CE2	0.65	2.27	3	1
1:R:41:PHE:CD2	1:R:162:ILE:HD13	0.64	2.27	1	2
1:R:136:ASP:O	1:R:137:PHE:CD2	0.64	2.50	3	1
1:R:31:LEU:HD21	1:R:162:ILE:CD1	0.64	2.22	4	1
1:R:127:VAL:HG21	1:R:178:LEU:HD13	0.64	1.68	1	1
1:R:124:VAL:O	1:R:125:CYS:HB2	0.64	1.91	4	1
1:R:134:LEU:HD23	1:R:173:ASP:OD2	0.64	1.91	5	1
1:R:160:TYR:CD1	1:R:161:ALA:N	0.64	2.65	2	1
1:R:55:ALA:CB	1:R:151:PHE:CE1	0.64	2.80	5	2
1:R:141:ILE:HG23	1:R:151:PHE:CZ	0.64	2.27	1	2
1:R:57:LEU:HD22	1:R:68:PHE:HB2	0.64	1.70	1	1
1:R:50:ASN:HB3	1:R:79:THR:HG21	0.64	1.68	5	1
1:R:31:LEU:HD12	1:R:41:PHE:CD1	0.64	2.28	1	1
1:R:55:ALA:O	1:R:59:LEU:CD2	0.64	2.45	5	2
1:R:59:LEU:O	1:R:62:TYR:CD1	0.64	2.50	2	2
1:R:31:LEU:HD23	1:R:31:LEU:H	0.64	1.51	4	2
1:R:31:LEU:CG	1:R:162:ILE:HD13	0.64	2.21	4	1
1:R:53:LEU:CD1	1:R:79:THR:HA	0.64	2.23	2	4
1:R:53:LEU:HD21	1:R:83:ILE:HG13	0.64	1.68	1	2
1:R:126:VAL:CG1	1:R:127:VAL:N	0.64	2.61	4	1
1:R:113:THR:HG22	1:R:115:ILE:HD13	0.64	1.70	4	2
1:R:55:ALA:HA	1:R:141:ILE:CG1	0.64	2.23	4	1
1:R:94:LEU:HD23	1:R:103:VAL:HG22	0.64	1.70	5	1
1:R:126:VAL:C	1:R:179:VAL:HA	0.63	2.13	1	1
1:R:42:TYR:O	1:R:43:SER:CB	0.63	2.46	4	2
1:R:173:ASP:O	1:R:177:VAL:CG1	0.63	2.45	4	3
1:R:99:PRO:CB	1:R:100:PRO:CD	0.63	2.76	4	2
1:R:31:LEU:HG	1:R:41:PHE:CE1	0.63	2.28	2	1
1:R:134:LEU:O	1:R:173:ASP:OD2	0.63	2.16	4	1
1:R:57:LEU:HD11	1:R:71:VAL:CG1	0.63	2.24	1	2
1:R:55:ALA:HB2	1:R:151:PHE:CE1	0.63	2.29	5	1
1:R:142:PHE:HB2	1:R:150:VAL:HG23	0.63	1.69	2	3
1:R:78:LEU:O	1:R:82:ALA:HB2	0.63	1.94	2	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:R:137:PHE:CB	1:R:180:PHE:CE1	0.63	2.82	5	1
1:R:56:ILE:O	1:R:60:PHE:CG	0.63	2.52	4	1
1:R:58:GLN:OE1	1:R:140:GLY:O	0.63	2.17	4	1
1:R:117:THR:HB	1:R:120:ARG:O	0.63	1.93	5	1
1:R:83:ILE:HD13	1:R:95:HIS:HA	0.62	1.71	2	2
1:R:57:LEU:HD11	1:R:71:VAL:CB	0.62	2.24	4	4
1:R:31:LEU:CD2	1:R:162:ILE:HD13	0.62	2.24	4	1
1:R:33:LEU:O	1:R:35:ASN:N	0.62	2.31	2	1
1:R:127:VAL:HG22	1:R:178:LEU:HA	0.62	1.71	2	3
1:R:94:LEU:N	1:R:94:LEU:HD13	0.62	2.09	3	1
1:R:86:LEU:CD2	1:R:90:THR:HG23	0.62	2.24	2	1
1:R:107:ILE:CG2	1:R:111:LEU:HD11	0.62	2.24	3	1
1:R:160:TYR:OH	1:R:162:ILE:HD13	0.62	1.94	2	1
1:R:63:VAL:HG11	1:R:113:THR:HG23	0.62	1.71	4	1
1:R:53:LEU:HD11	1:R:79:THR:O	0.62	1.95	1	1
1:R:137:PHE:CZ	1:R:173:ASP:HA	0.62	2.29	2	1
1:R:138:HIS:HB2	1:R:154:VAL:CG2	0.62	2.24	2	3
1:R:42:TYR:O	1:R:165:GLU:CB	0.62	2.47	2	1
1:R:118:ALA:CA	1:R:126:VAL:HG22	0.62	2.24	4	1
1:R:142:PHE:N	1:R:142:PHE:CD1	0.62	2.67	4	1
1:R:137:PHE:CE2	1:R:174:PRO:HD3	0.62	2.30	2	2
1:R:107:ILE:HG22	1:R:107:ILE:O	0.62	1.95	1	1
1:R:83:ILE:HD12	1:R:95:HIS:HA	0.62	1.72	4	1
1:R:107:ILE:HG23	1:R:111:LEU:HG	0.62	1.70	3	1
1:R:118:ALA:HB2	1:R:130:THR:OG1	0.62	1.94	3	2
1:R:126:VAL:CG2	1:R:180:PHE:CD1	0.62	2.82	4	1
1:R:41:PHE:CD1	1:R:41:PHE:N	0.61	2.68	1	3
1:R:90:THR:OG1	1:R:92:LEU:HD11	0.61	1.94	1	4
1:R:53:LEU:O	1:R:57:LEU:HB2	0.61	1.96	5	3
1:R:60:PHE:CG	1:R:61:ARG:N	0.61	2.68	1	2
1:R:59:LEU:HD12	1:R:62:TYR:CZ	0.61	2.30	3	1
1:R:94:LEU:HG	1:R:103:VAL:CG2	0.61	2.25	3	1
1:R:118:ALA:CB	1:R:130:THR:HG21	0.61	2.25	4	1
1:R:139:ALA:HB3	1:R:181:VAL:HB	0.61	1.71	1	3
1:R:43:SER:C	1:R:164:ASP:HA	0.61	2.16	3	1
1:R:124:VAL:O	1:R:125:CYS:CB	0.61	2.48	4	1
1:R:43:SER:CB	1:R:163:ASP:HA	0.61	2.25	4	1
1:R:33:LEU:HD22	1:R:33:LEU:O	0.61	1.95	5	1
1:R:31:LEU:CD1	1:R:162:ILE:HD11	0.61	2.24	5	1
1:R:74:SER:OG	1:R:78:LEU:HD22	0.61	1.96	1	1
1:R:57:LEU:HD22	1:R:68:PHE:HB3	0.61	1.71	3	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:R:127:VAL:HG22	1:R:178:LEU:O	0.61	1.95	5	2
1:R:115:ILE:CG1	1:R:123:GLU:C	0.61	2.69	5	1
1:R:150:VAL:C	1:R:151:PHE:CG	0.61	2.73	5	1
1:R:142:PHE:O	1:R:150:VAL:CG2	0.61	2.49	3	4
1:R:79:THR:O	1:R:83:ILE:HG12	0.61	1.96	3	2
1:R:136:ASP:O	1:R:183:TYR:CZ	0.61	2.54	2	3
1:R:33:LEU:HD13	1:R:33:LEU:N	0.61	2.00	2	2
1:R:139:ALA:HB3	1:R:181:VAL:CB	0.61	2.26	1	4
1:R:118:ALA:CB	1:R:130:THR:CG2	0.61	2.78	1	3
1:R:57:LEU:HD12	1:R:72:TYR:CZ	0.61	2.31	1	1
1:R:152:ALA:HA	1:R:161:ALA:CA	0.61	2.26	5	3
1:R:31:LEU:HD11	1:R:162:ILE:CG1	0.61	2.24	4	1
1:R:107:ILE:CG2	1:R:111:LEU:HD23	0.60	2.26	4	1
1:R:126:VAL:CG1	1:R:178:LEU:O	0.60	2.48	4	1
1:R:55:ALA:C	1:R:59:LEU:HD22	0.60	2.17	1	1
1:R:127:VAL:CG2	1:R:178:LEU:CA	0.60	2.78	3	2
1:R:60:PHE:HB2	1:R:66:PRO:HD2	0.60	1.72	3	2
1:R:100:PRO:HA	1:R:104:ILE:HD12	0.60	1.73	5	1
1:R:180:PHE:CD1	1:R:181:VAL:N	0.60	2.70	5	1
1:R:125:CYS:O	1:R:180:PHE:CD1	0.60	2.55	4	3
1:R:57:LEU:CG	1:R:71:VAL:HG11	0.60	2.23	5	4
1:R:41:PHE:CZ	1:R:162:ILE:CD1	0.60	2.82	3	1
1:R:107:ILE:HA	1:R:110:LEU:HD23	0.60	1.74	3	1
1:R:51:ALA:CB	1:R:149:ALA:HB3	0.60	2.26	4	5
1:R:90:THR:HG22	1:R:106:ASN:CB	0.60	2.26	4	1
1:R:154:VAL:HG13	1:R:158:GLY:HA2	0.60	1.74	4	1
1:R:103:VAL:O	1:R:107:ILE:CG1	0.60	2.48	4	2
1:R:62:TYR:OH	1:R:151:PHE:CD1	0.60	2.55	4	1
1:R:168:TYR:CE2	1:R:170:TRP:CD1	0.60	2.90	5	1
1:R:63:VAL:HG13	1:R:124:VAL:CG1	0.60	2.26	1	1
1:R:54:ASN:OD1	1:R:58:GLN:NE2	0.60	2.35	4	2
1:R:58:GLN:HB2	1:R:151:PHE:CD1	0.60	2.32	4	1
1:R:134:LEU:O	1:R:172:PRO:HG2	0.60	1.97	2	1
1:R:58:GLN:CD	1:R:162:ILE:HG21	0.60	2.17	2	1
1:R:68:PHE:C	1:R:68:PHE:CD1	0.60	2.75	4	2
1:R:55:ALA:CB	1:R:151:PHE:CZ	0.60	2.85	1	2
1:R:155:THR:CG2	1:R:160:TYR:HB2	0.60	2.27	5	3
1:R:167:PHE:CD1	1:R:167:PHE:N	0.60	2.69	3	2
1:R:53:LEU:HD22	1:R:57:LEU:CD2	0.60	2.26	4	2
1:R:53:LEU:O	1:R:57:LEU:N	0.59	2.35	2	1
1:R:99:PRO:CD	1:R:100:PRO:HD2	0.59	2.27	3	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:R:56:ILE:HB	1:R:68:PHE:CE2	0.59	2.32	3	1
1:R:113:THR:CG2	1:R:115:ILE:CG1	0.59	2.79	5	1
1:R:31:LEU:HD11	1:R:167:PHE:CB	0.59	2.28	2	1
1:R:183:TYR:CD1	1:R:183:TYR:N	0.59	2.70	3	1
1:R:115:ILE:HG23	1:R:124:VAL:HG21	0.59	1.73	3	1
1:R:151:PHE:CZ	1:R:162:ILE:HG13	0.59	2.32	4	1
1:R:159:TRP:CD1	1:R:172:PRO:HB3	0.59	2.33	2	1
1:R:63:VAL:HG21	1:R:124:VAL:CG1	0.59	2.27	2	3
1:R:118:ALA:HB2	1:R:128:ASP:HA	0.59	1.74	1	1
1:R:137:PHE:CE1	1:R:159:TRP:NE1	0.59	2.70	3	1
1:R:99:PRO:HG2	1:R:100:PRO:CD	0.59	2.28	5	2
1:R:60:PHE:HB2	1:R:68:PHE:CD2	0.59	2.32	4	1
1:R:115:ILE:CG2	1:R:124:VAL:N	0.59	2.66	5	1
1:R:33:LEU:CA	1:R:37:GLU:CA	0.59	2.77	2	1
1:R:138:HIS:O	1:R:139:ALA:HB2	0.59	1.98	1	2
1:R:134:LEU:HD21	1:R:142:PHE:CZ	0.59	2.33	3	1
1:R:99:PRO:CB	1:R:100:PRO:HD2	0.59	2.28	4	1
1:R:104:ILE:HG22	1:R:111:LEU:HD11	0.59	1.74	2	1
1:R:173:ASP:CB	1:R:174:PRO:CD	0.59	2.81	2	1
1:R:31:LEU:HD12	1:R:160:TYR:CZ	0.59	2.33	2	1
1:R:86:LEU:O	1:R:90:THR:N	0.59	2.35	2	1
1:R:33:LEU:CB	1:R:154:VAL:O	0.59	2.50	1	3
1:R:83:ILE:HG22	1:R:94:LEU:HD13	0.59	1.74	5	1
1:R:154:VAL:HA	1:R:158:GLY:O	0.59	1.98	2	2
1:R:152:ALA:CB	1:R:161:ALA:CB	0.59	2.76	1	4
1:R:118:ALA:CA	1:R:130:THR:HG23	0.59	2.26	3	1
1:R:33:LEU:CD1	1:R:37:GLU:O	0.58	2.51	1	1
1:R:60:PHE:CD2	1:R:68:PHE:CD2	0.58	2.90	1	1
1:R:118:ALA:HB3	1:R:130:THR:CB	0.58	2.27	4	1
1:R:33:LEU:O	1:R:33:LEU:HD22	0.58	1.97	4	1
1:R:107:ILE:HG23	1:R:110:LEU:HD23	0.58	1.75	1	2
1:R:67:PHE:O	1:R:69:ASP:N	0.58	2.36	1	1
1:R:69:ASP:O	1:R:73:SER:CB	0.58	2.51	1	3
1:R:43:SER:HB2	1:R:163:ASP:HA	0.58	1.75	4	1
1:R:104:ILE:HG23	1:R:111:LEU:CD1	0.58	2.27	5	1
1:R:92:LEU:HD23	1:R:102:LEU:HB2	0.58	1.75	1	1
1:R:142:PHE:CZ	1:R:171:THR:O	0.58	2.56	1	1
1:R:53:LEU:CD1	1:R:82:ALA:HB3	0.58	2.28	3	2
1:R:55:ALA:O	1:R:151:PHE:CD2	0.58	2.56	3	1
1:R:115:ILE:HD12	1:R:124:VAL:N	0.58	2.12	5	1
1:R:56:ILE:HG22	1:R:57:LEU:HD22	0.58	1.74	4	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:R:67:PHE:CG	1:R:111:LEU:CD2	0.58	2.87	5	1
1:R:86:LEU:HD13	1:R:86:LEU:O	0.58	1.97	5	1
1:R:55:ALA:HB3	1:R:99:PRO:HB3	0.58	1.75	5	1
1:R:57:LEU:CD1	1:R:68:PHE:HB2	0.58	2.28	2	1
1:R:142:PHE:CZ	1:R:172:PRO:HA	0.58	2.33	4	3
1:R:31:LEU:CD1	1:R:162:ILE:CG2	0.58	2.75	4	2
1:R:66:PRO:O	1:R:68:PHE:HD1	0.58	1.82	1	1
1:R:162:ILE:HG13	1:R:167:PHE:CD1	0.58	2.34	5	1
1:R:126:VAL:HG22	1:R:179:VAL:HA	0.58	1.76	5	1
1:R:134:LEU:HD13	1:R:172:PRO:HD3	0.58	1.72	2	1
1:R:107:ILE:O	1:R:111:LEU:N	0.58	2.37	4	2
1:R:56:ILE:O	1:R:60:PHE:HB3	0.58	1.98	5	2
1:R:62:TYR:CE1	1:R:181:VAL:HG21	0.58	2.34	3	1
1:R:170:TRP:HA	1:R:170:TRP:CE3	0.58	2.33	3	1
1:R:126:VAL:HG12	1:R:179:VAL:HB	0.58	1.75	3	1
1:R:79:THR:O	1:R:83:ILE:CG1	0.58	2.52	3	2
1:R:134:LEU:HD22	1:R:173:ASP:CB	0.58	2.28	4	1
1:R:52:TRP:CD2	1:R:97:GLY:HA2	0.58	2.33	4	1
1:R:54:ASN:OD1	1:R:54:ASN:C	0.58	2.41	4	1
1:R:141:ILE:HB	1:R:179:VAL:CG1	0.58	2.29	1	2
1:R:141:ILE:O	1:R:177:VAL:CG2	0.58	2.49	3	2
1:R:83:ILE:CB	1:R:94:LEU:HD13	0.58	2.29	1	2
1:R:31:LEU:HD13	1:R:162:ILE:CG2	0.58	2.18	3	1
1:R:59:LEU:HD12	1:R:62:TYR:OH	0.58	1.99	3	1
1:R:151:PHE:CD2	1:R:162:ILE:O	0.58	2.57	4	1
1:R:44:ARG:CB	1:R:164:ASP:O	0.58	2.52	4	1
1:R:31:LEU:HD11	1:R:162:ILE:CG2	0.58	2.27	4	1
1:R:94:LEU:HD12	1:R:94:LEU:O	0.58	1.99	4	1
1:R:149:ALA:HB1	1:R:151:PHE:CZ	0.58	2.30	5	1
1:R:89:LEU:CD2	1:R:107:ILE:HG23	0.57	2.29	2	1
1:R:134:LEU:HD13	1:R:173:ASP:OD2	0.57	1.98	4	1
1:R:124:VAL:HB	1:R:180:PHE:O	0.57	1.99	5	1
1:R:69:ASP:O	1:R:73:SER:HB3	0.57	1.99	2	2
1:R:83:ILE:HG21	1:R:94:LEU:CD1	0.57	2.20	2	2
1:R:51:ALA:HB1	1:R:149:ALA:O	0.57	1.99	1	1
1:R:92:LEU:HD13	1:R:94:LEU:CD2	0.57	2.29	1	1
1:R:52:TRP:CG	1:R:97:GLY:HA2	0.57	2.35	1	2
1:R:68:PHE:CE1	1:R:72:TYR:CD2	0.57	2.92	4	1
1:R:86:LEU:CG	1:R:103:VAL:HG13	0.57	2.28	1	2
1:R:68:PHE:CD1	1:R:68:PHE:N	0.57	2.71	3	1
1:R:142:PHE:CA	1:R:177:VAL:HB	0.57	2.28	2	4

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:R:51:ALA:HA	1:R:54:ASN:HB3	0.57	1.75	2	2
1:R:107:ILE:HG23	1:R:111:LEU:HD11	0.57	1.74	3	1
1:R:141:ILE:HG12	1:R:151:PHE:CZ	0.57	2.34	3	1
1:R:151:PHE:CE2	1:R:162:ILE:HG13	0.57	2.34	4	1
1:R:115:ILE:CD1	1:R:123:GLU:C	0.57	2.72	5	1
1:R:53:LEU:HD12	1:R:79:THR:CA	0.57	2.29	2	2
1:R:127:VAL:HG22	1:R:178:LEU:CA	0.57	2.29	3	3
1:R:152:ALA:CA	1:R:160:TYR:O	0.57	2.53	2	1
1:R:142:PHE:CG	1:R:177:VAL:CB	0.57	2.81	3	4
1:R:64:GLU:O	1:R:66:PRO:HD3	0.57	2.00	3	2
1:R:116:GLY:C	1:R:125:CYS:CB	0.57	2.72	4	1
1:R:142:PHE:CD2	1:R:177:VAL:HG11	0.57	2.35	2	2
1:R:134:LEU:HD21	1:R:171:THR:HG23	0.57	1.76	3	1
1:R:53:LEU:HD22	1:R:71:VAL:HG21	0.57	1.76	3	4
1:R:33:LEU:HD23	1:R:35:ASN:OD1	0.57	1.99	3	1
1:R:31:LEU:HD21	1:R:167:PHE:CG	0.57	2.34	1	1
1:R:40:THR:O	1:R:72:TYR:CD1	0.57	2.58	4	1
1:R:126:VAL:C	1:R:127:VAL:HG22	0.56	2.19	4	1
1:R:112:HIS:HA	1:R:122:SER:O	0.56	2.00	5	1
1:R:141:ILE:HD12	1:R:179:VAL:HG11	0.56	1.76	2	3
1:R:170:TRP:O	1:R:171:THR:CG2	0.56	2.52	2	1
1:R:137:PHE:CE1	1:R:159:TRP:CD1	0.56	2.93	3	1
1:R:57:LEU:HG	1:R:71:VAL:CG1	0.56	2.24	5	2
1:R:43:SER:N	1:R:164:ASP:HB2	0.56	2.15	4	1
1:R:57:LEU:N	1:R:57:LEU:CD2	0.56	2.68	4	1
1:R:180:PHE:CD1	1:R:180:PHE:C	0.56	2.78	5	2
1:R:33:LEU:CA	1:R:154:VAL:O	0.56	2.53	5	1
1:R:107:ILE:CG2	1:R:110:LEU:HB2	0.56	2.30	1	2
1:R:118:ALA:HA	1:R:130:THR:HG23	0.56	1.77	3	1
1:R:141:ILE:O	1:R:177:VAL:CB	0.56	2.53	2	2
1:R:171:THR:O	1:R:171:THR:CG2	0.56	2.52	3	1
1:R:164:ASP:O	1:R:165:GLU:HB2	0.56	2.01	4	1
1:R:53:LEU:HD21	1:R:83:ILE:CG1	0.56	2.30	1	3
1:R:102:LEU:HA	1:R:105:TRP:HB3	0.56	1.77	3	1
1:R:139:ALA:HB1	1:R:153:CYS:SG	0.56	2.41	2	1
1:R:31:LEU:CD2	1:R:31:LEU:N	0.56	2.68	4	2
1:R:118:ALA:CB	1:R:130:THR:CB	0.56	2.84	4	2
1:R:134:LEU:N	1:R:173:ASP:CB	0.56	2.69	2	1
1:R:57:LEU:HD13	1:R:60:PHE:CD2	0.56	2.35	3	1
1:R:42:TYR:HA	1:R:164:ASP:HB2	0.56	1.77	4	1
1:R:71:VAL:CG2	1:R:82:ALA:CB	0.56	2.84	3	5

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:R:31:LEU:HD22	1:R:31:LEU:N	0.55	2.16	2	1
1:R:83:ILE:CG2	1:R:94:LEU:HD21	0.55	2.30	2	1
1:R:126:VAL:N	1:R:179:VAL:HA	0.55	2.16	4	1
1:R:68:PHE:N	1:R:68:PHE:CD1	0.55	2.74	5	1
1:R:107:ILE:HG22	1:R:110:LEU:HB2	0.55	1.78	1	2
1:R:118:ALA:CB	1:R:130:THR:HB	0.55	2.31	4	1
1:R:103:VAL:HG12	1:R:107:ILE:HD11	0.55	1.77	4	2
1:R:31:LEU:HD21	1:R:167:PHE:CD2	0.55	2.36	1	1
1:R:31:LEU:HD13	1:R:41:PHE:CD1	0.55	2.35	1	1
1:R:55:ALA:O	1:R:59:LEU:CB	0.55	2.53	1	2
1:R:102:LEU:HD12	1:R:102:LEU:N	0.55	2.17	3	1
1:R:137:PHE:CG	1:R:180:PHE:HD2	0.55	2.19	4	1
1:R:86:LEU:HD11	1:R:90:THR:CG2	0.55	2.31	5	1
1:R:155:THR:CG2	1:R:160:TYR:HB3	0.55	2.31	2	1
1:R:137:PHE:CZ	1:R:174:PRO:CD	0.55	2.89	4	2
1:R:134:LEU:HD21	1:R:171:THR:HB	0.55	1.77	1	2
1:R:118:ALA:HB1	1:R:130:THR:HG23	0.55	1.76	3	1
1:R:43:SER:CA	1:R:165:GLU:HB2	0.55	2.31	5	1
1:R:137:PHE:CB	1:R:180:PHE:CD1	0.55	2.90	1	2
1:R:32:THR:O	1:R:156:SER:N	0.55	2.39	1	2
1:R:59:LEU:HD22	1:R:141:ILE:HD11	0.55	1.78	2	1
1:R:142:PHE:HA	1:R:177:VAL:HB	0.55	1.77	2	3
1:R:86:LEU:C	1:R:86:LEU:CD1	0.55	2.74	5	1
1:R:138:HIS:CB	1:R:154:VAL:HG23	0.55	2.32	5	2
1:R:138:HIS:CG	1:R:154:VAL:HG21	0.55	2.37	1	1
1:R:163:ASP:O	1:R:165:GLU:N	0.55	2.39	3	2
1:R:137:PHE:HA	1:R:183:TYR:CD2	0.55	2.37	4	1
1:R:57:LEU:CD2	1:R:57:LEU:N	0.55	2.69	1	1
1:R:94:LEU:HB2	1:R:97:GLY:O	0.55	2.02	2	2
1:R:142:PHE:HA	1:R:177:VAL:CA	0.55	2.32	4	3
1:R:99:PRO:HG2	1:R:100:PRO:HD3	0.55	1.77	5	2
1:R:60:PHE:CD2	1:R:68:PHE:CE2	0.55	2.95	1	1
1:R:89:LEU:HD12	1:R:89:LEU:N	0.55	2.14	3	1
1:R:92:LEU:H	1:R:92:LEU:CD2	0.55	2.15	3	1
1:R:161:ALA:O	1:R:168:TYR:CD1	0.54	2.60	2	3
1:R:137:PHE:O	1:R:172:PRO:HB2	0.54	2.03	2	1
1:R:141:ILE:O	1:R:177:VAL:HB	0.54	2.02	2	2
1:R:62:TYR:CD2	1:R:153:CYS:SG	0.54	3.00	2	2
1:R:87:GLU:O	1:R:91:GLY:N	0.54	2.39	1	3
1:R:138:HIS:CG	1:R:181:VAL:O	0.54	2.60	3	1
1:R:142:PHE:N	1:R:142:PHE:HD1	0.54	1.98	4	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:R:83:ILE:HG22	1:R:94:LEU:HD11	0.54	1.77	4	1
1:R:123:GLU:O	1:R:124:VAL:CG1	0.54	2.55	5	1
1:R:126:VAL:HG12	1:R:128:ASP:H	0.54	1.63	5	1
1:R:125:CYS:O	1:R:180:PHE:O	0.54	2.25	2	2
1:R:102:LEU:HA	1:R:105:TRP:CB	0.54	2.32	1	4
1:R:138:HIS:HA	1:R:172:PRO:CG	0.54	2.32	5	1
1:R:153:CYS:N	1:R:160:TYR:O	0.54	2.40	2	1
1:R:127:VAL:HG11	1:R:174:PRO:HB3	0.54	1.78	2	1
1:R:92:LEU:HD12	1:R:93:GLU:H	0.54	1.63	4	2
1:R:115:ILE:HD13	1:R:115:ILE:N	0.54	2.16	4	3
1:R:63:VAL:HG13	1:R:113:THR:HG21	0.54	1.79	1	2
1:R:120:ARG:CB	1:R:121:PRO:CD	0.54	2.85	5	1
1:R:101:ALA:O	1:R:104:ILE:HG12	0.54	2.03	2	1
1:R:115:ILE:HG23	1:R:124:VAL:HG23	0.54	1.79	2	1
1:R:33:LEU:H	1:R:33:LEU:HD22	0.54	1.62	1	2
1:R:56:ILE:HD13	1:R:56:ILE:N	0.54	2.17	1	1
1:R:55:ALA:CA	1:R:141:ILE:HD11	0.54	2.33	4	1
1:R:31:LEU:HD21	1:R:162:ILE:HD11	0.54	1.80	5	1
1:R:31:LEU:HD21	1:R:41:PHE:CG	0.54	2.37	5	1
1:R:86:LEU:HD12	1:R:94:LEU:HD22	0.54	1.80	5	1
1:R:53:LEU:HD22	1:R:57:LEU:HD23	0.54	1.79	2	1
1:R:60:PHE:CE2	1:R:67:PHE:HB3	0.54	2.38	2	2
1:R:109:HIS:CD2	1:R:110:LEU:HD22	0.54	2.38	1	1
1:R:126:VAL:O	1:R:128:ASP:N	0.54	2.41	4	1
1:R:35:ASN:O	1:R:62:TYR:HA	0.54	2.02	4	1
1:R:138:HIS:CG	1:R:154:VAL:CG2	0.54	2.91	2	2
1:R:31:LEU:HD12	1:R:160:TYR:CE2	0.54	2.37	2	1
1:R:71:VAL:HG12	1:R:72:TYR:CD1	0.54	2.38	2	1
1:R:180:PHE:CD2	1:R:181:VAL:N	0.54	2.75	4	1
1:R:40:THR:HG22	1:R:40:THR:O	0.54	2.02	2	4
1:R:128:ASP:HB2	1:R:178:LEU:HD12	0.54	1.80	3	1
1:R:155:THR:HG21	1:R:160:TYR:HB3	0.54	1.79	4	2
1:R:90:THR:OG1	1:R:92:LEU:CD1	0.54	2.56	1	3
1:R:160:TYR:HA	1:R:168:TYR:O	0.54	2.02	5	2
1:R:134:LEU:HD22	1:R:173:ASP:HB2	0.54	1.80	4	1
1:R:55:ALA:CA	1:R:151:PHE:CD1	0.54	2.91	3	1
1:R:67:PHE:CE1	1:R:89:LEU:HD21	0.54	2.38	3	1
1:R:33:LEU:HD22	1:R:33:LEU:H	0.54	1.62	3	1
1:R:85:GLN:O	1:R:88:ASP:HB2	0.54	2.03	3	1
1:R:124:VAL:CG2	1:R:124:VAL:O	0.54	2.56	4	1
1:R:116:GLY:H	1:R:125:CYS:HB2	0.54	1.62	4	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:R:137:PHE:CZ	1:R:174:PRO:N	0.54	2.76	4	1
1:R:161:ALA:CB	1:R:170:TRP:CD1	0.53	2.91	3	1
1:R:115:ILE:HG23	1:R:124:VAL:HG22	0.53	1.80	2	1
1:R:51:ALA:O	1:R:54:ASN:HB3	0.53	2.03	1	1
1:R:134:LEU:HD21	1:R:142:PHE:HZ	0.53	1.63	3	1
1:R:92:LEU:HD11	1:R:103:VAL:CG2	0.53	2.33	3	1
1:R:31:LEU:HD11	1:R:162:ILE:CB	0.53	2.33	4	1
1:R:59:LEU:HD13	1:R:62:TYR:CE1	0.53	2.38	5	1
1:R:133:CYS:O	1:R:134:LEU:C	0.53	2.47	2	1
1:R:58:GLN:OE1	1:R:162:ILE:CG2	0.53	2.56	2	1
1:R:33:LEU:HB2	1:R:154:VAL:O	0.53	2.03	1	3
1:R:107:ILE:HG12	1:R:111:LEU:HD21	0.53	1.80	3	1
1:R:40:THR:O	1:R:40:THR:CG2	0.53	2.57	3	1
1:R:125:CYS:O	1:R:180:PHE:HD1	0.53	1.85	4	1
1:R:117:THR:HA	1:R:126:VAL:HB	0.53	1.80	5	1
1:R:153:CYS:O	1:R:160:TYR:CD2	0.53	2.61	2	1
1:R:53:LEU:HG	1:R:83:ILE:HG12	0.53	1.81	2	3
1:R:99:PRO:CG	1:R:100:PRO:CD	0.53	2.86	3	3
1:R:134:LEU:N	1:R:173:ASP:HB2	0.53	2.18	2	1
1:R:94:LEU:O	1:R:95:HIS:C	0.53	2.46	5	5
1:R:118:ALA:HB3	1:R:128:ASP:O	0.53	2.04	1	1
1:R:138:HIS:CD2	1:R:183:TYR:CD2	0.53	2.97	1	1
1:R:162:ILE:CG2	1:R:167:PHE:CD1	0.53	2.92	3	1
1:R:137:PHE:CD1	1:R:180:PHE:CD1	0.53	2.96	5	1
1:R:41:PHE:N	1:R:41:PHE:CD1	0.53	2.77	3	2
1:R:142:PHE:CE2	1:R:172:PRO:HA	0.53	2.39	5	2
1:R:62:TYR:CE2	1:R:181:VAL:HG21	0.53	2.38	5	1
1:R:58:GLN:O	1:R:62:TYR:CE2	0.53	2.62	3	2
1:R:127:VAL:HG22	1:R:178:LEU:HD13	0.53	1.80	2	1
1:R:48:HIS:O	1:R:49:ASP:CB	0.53	2.55	2	1
1:R:59:LEU:HA	1:R:62:TYR:CE1	0.53	2.38	2	2
1:R:53:LEU:CG	1:R:83:ILE:HG12	0.53	2.34	2	2
1:R:89:LEU:CD2	1:R:90:THR:HG23	0.53	2.33	4	3
1:R:83:ILE:O	1:R:86:LEU:N	0.53	2.41	2	5
1:R:154:VAL:CG2	1:R:159:TRP:CD1	0.53	2.92	1	1
1:R:65:GLU:HB2	1:R:68:PHE:CE1	0.53	2.39	1	1
1:R:67:PHE:CE2	1:R:70:TRP:CD1	0.53	2.97	1	1
1:R:113:THR:CG2	1:R:115:ILE:CD1	0.53	2.83	4	2
1:R:137:PHE:CD1	1:R:137:PHE:C	0.53	2.82	2	2
1:R:151:PHE:O	1:R:162:ILE:N	0.53	2.41	2	1
1:R:52:TRP:O	1:R:55:ALA:HB3	0.53	2.04	5	5

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:R:109:HIS:CD2	1:R:110:LEU:CD2	0.53	2.92	1	1
1:R:168:TYR:CD1	1:R:170:TRP:CD1	0.53	2.97	1	1
1:R:77:ASN:O	1:R:78:LEU:CB	0.53	2.56	3	1
1:R:138:HIS:HB3	1:R:172:PRO:HB3	0.52	1.80	2	1
1:R:159:TRP:CD1	1:R:159:TRP:N	0.52	2.75	2	1
1:R:43:SER:O	1:R:164:ASP:CA	0.52	2.57	3	1
1:R:86:LEU:HD11	1:R:90:THR:HG21	0.52	1.79	5	1
1:R:155:THR:CG2	1:R:160:TYR:CD2	0.52	2.92	2	1
1:R:31:LEU:CD1	1:R:160:TYR:CZ	0.52	2.92	2	1
1:R:62:TYR:CE1	1:R:63:VAL:HG23	0.52	2.38	5	2
1:R:62:TYR:CD1	1:R:62:TYR:N	0.52	2.75	1	1
1:R:92:LEU:HD11	1:R:103:VAL:HG22	0.52	1.79	3	1
1:R:43:SER:HA	1:R:51:ALA:HA	0.52	1.80	4	1
1:R:132:MET:O	1:R:173:ASP:OD2	0.52	2.27	2	1
1:R:142:PHE:CD1	1:R:142:PHE:N	0.52	2.77	2	2
1:R:62:TYR:CZ	1:R:139:ALA:CB	0.52	2.90	3	1
1:R:87:GLU:O	1:R:91:GLY:HA2	0.52	2.04	2	4
1:R:127:VAL:HG13	1:R:128:ASP:N	0.52	2.19	1	1
1:R:138:HIS:O	1:R:153:CYS:HA	0.52	2.04	1	2
1:R:31:LEU:CD1	1:R:162:ILE:CD1	0.52	2.84	1	3
1:R:42:TYR:CD1	1:R:42:TYR:N	0.52	2.77	1	1
1:R:138:HIS:HA	1:R:172:PRO:O	0.52	2.04	4	1
1:R:53:LEU:CG	1:R:83:ILE:CG1	0.52	2.88	2	3
1:R:139:ALA:CB	1:R:181:VAL:CG1	0.52	2.84	4	2
1:R:134:LEU:HD12	1:R:159:TRP:CE2	0.52	2.39	1	1
1:R:161:ALA:O	1:R:168:TYR:CD2	0.52	2.62	3	1
1:R:92:LEU:HD23	1:R:92:LEU:C	0.52	2.23	3	1
1:R:68:PHE:CE2	1:R:103:VAL:HG11	0.52	2.39	5	1
1:R:138:HIS:ND1	1:R:154:VAL:CG2	0.52	2.73	2	1
1:R:48:HIS:O	1:R:49:ASP:HB3	0.52	2.03	2	1
1:R:142:PHE:HB2	1:R:150:VAL:CG2	0.52	2.33	1	2
1:R:92:LEU:HD21	1:R:94:LEU:HD21	0.52	1.82	3	1
1:R:124:VAL:CG1	1:R:181:VAL:HG23	0.52	2.35	5	1
1:R:68:PHE:CZ	1:R:103:VAL:HG11	0.52	2.39	5	1
1:R:118:ALA:HB2	1:R:130:THR:HG23	0.52	1.82	5	1
1:R:31:LEU:HD11	1:R:160:TYR:CE1	0.52	2.39	2	1
1:R:92:LEU:O	1:R:93:GLU:O	0.52	2.28	4	2
1:R:181:VAL:O	1:R:181:VAL:HG12	0.52	2.05	3	1
1:R:32:THR:C	1:R:33:LEU:HD13	0.52	2.25	4	2
1:R:60:PHE:HB2	1:R:68:PHE:CE2	0.52	2.39	4	1
1:R:74:SER:OG	1:R:78:LEU:HD23	0.52	2.05	4	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:R:50:ASN:HB3	1:R:79:THR:CG2	0.52	2.35	5	1
1:R:53:LEU:HD12	1:R:79:THR:CB	0.52	2.35	2	2
1:R:54:ASN:O	1:R:58:GLN:HB2	0.52	2.04	2	2
1:R:92:LEU:CD1	1:R:94:LEU:CD2	0.52	2.88	1	2
1:R:32:THR:HG22	1:R:38:LYS:CB	0.52	2.35	4	1
1:R:33:LEU:CD2	1:R:36:GLY:C	0.52	2.78	4	2
1:R:42:TYR:O	1:R:54:ASN:HB2	0.52	2.04	4	1
1:R:80:LEU:O	1:R:84:LYS:CB	0.52	2.58	5	1
1:R:117:THR:CB	1:R:120:ARG:O	0.52	2.58	5	1
1:R:31:LEU:HD22	1:R:167:PHE:CE2	0.52	2.39	3	2
1:R:163:ASP:OD2	1:R:168:TYR:OH	0.52	2.28	3	1
1:R:42:TYR:O	1:R:43:SER:HB2	0.52	2.05	4	1
1:R:115:ILE:HG21	1:R:124:VAL:H	0.52	1.65	5	1
1:R:49:ASP:CB	1:R:95:HIS:O	0.52	2.58	5	1
1:R:104:ILE:HG22	1:R:111:LEU:CD1	0.52	2.35	2	1
1:R:53:LEU:HD22	1:R:71:VAL:CG2	0.52	2.35	1	1
1:R:60:PHE:CD1	1:R:61:ARG:N	0.52	2.78	1	2
1:R:92:LEU:CD1	1:R:101:ALA:O	0.52	2.52	3	1
1:R:99:PRO:CG	1:R:141:ILE:HG21	0.52	2.35	3	1
1:R:160:TYR:HA	1:R:170:TRP:H	0.52	1.64	4	1
1:R:65:GLU:CG	1:R:112:HIS:CE1	0.52	2.93	4	1
1:R:161:ALA:N	1:R:168:TYR:O	0.51	2.43	2	1
1:R:48:HIS:CD2	1:R:80:LEU:HD23	0.51	2.39	2	1
1:R:79:THR:O	1:R:82:ALA:HB3	0.51	2.05	1	3
1:R:60:PHE:HA	1:R:66:PRO:CD	0.51	2.34	1	1
1:R:40:THR:O	1:R:72:TYR:CE1	0.51	2.63	4	1
1:R:92:LEU:O	1:R:93:GLU:HB2	0.51	2.05	5	1
1:R:138:HIS:HA	1:R:172:PRO:HA	0.51	1.81	2	1
1:R:35:ASN:HB2	1:R:154:VAL:N	0.51	2.20	2	1
1:R:53:LEU:CD1	1:R:83:ILE:CG1	0.51	2.88	5	5
1:R:79:THR:HG23	1:R:80:LEU:N	0.51	2.19	4	3
1:R:101:ALA:C	1:R:103:VAL:N	0.51	2.63	5	4
1:R:42:TYR:O	1:R:43:SER:OG	0.51	2.29	3	1
1:R:59:LEU:CD1	1:R:62:TYR:OH	0.51	2.58	3	1
1:R:92:LEU:CD2	1:R:94:LEU:HD21	0.51	2.35	3	1
1:R:98:GLY:O	1:R:101:ALA:CB	0.51	2.58	5	2
1:R:58:GLN:NE2	1:R:151:PHE:HB2	0.51	2.20	4	1
1:R:48:HIS:HD2	1:R:79:THR:HG21	0.51	1.64	5	1
1:R:130:THR:O	1:R:131:ASP:HB2	0.51	2.06	2	1
1:R:137:PHE:CZ	1:R:180:PHE:CB	0.51	2.93	2	1
1:R:138:HIS:ND1	1:R:138:HIS:N	0.51	2.58	2	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:R:53:LEU:CD1	1:R:83:ILE:HG13	0.51	2.34	1	2
1:R:79:THR:O	1:R:83:ILE:CD1	0.51	2.58	5	3
1:R:181:VAL:O	1:R:181:VAL:CG1	0.51	2.58	3	2
1:R:55:ALA:O	1:R:151:PHE:CE2	0.51	2.63	3	1
1:R:62:TYR:CE2	1:R:139:ALA:HB1	0.51	2.40	5	2
1:R:44:ARG:HA	1:R:164:ASP:CA	0.51	2.35	5	1
1:R:41:PHE:CZ	1:R:61:ARG:CB	0.51	2.93	2	1
1:R:31:LEU:CD1	1:R:167:PHE:CE2	0.51	2.93	1	1
1:R:69:ASP:HA	1:R:72:TYR:CD1	0.51	2.40	5	1
1:R:173:ASP:HB3	1:R:174:PRO:CD	0.51	2.36	2	2
1:R:57:LEU:HA	1:R:60:PHE:CD2	0.51	2.40	2	1
1:R:90:THR:HA	1:R:106:ASN:HB3	0.51	1.81	2	1
1:R:31:LEU:HD11	1:R:162:ILE:HD12	0.51	1.77	5	2
1:R:86:LEU:CD1	1:R:94:LEU:HD21	0.51	2.36	5	2
1:R:86:LEU:HD13	1:R:90:THR:HG1	0.51	1.65	3	1
1:R:168:TYR:N	1:R:168:TYR:CD1	0.51	2.78	4	2
1:R:161:ALA:O	1:R:168:TYR:CE1	0.51	2.64	2	2
1:R:53:LEU:O	1:R:57:LEU:HB3	0.51	2.06	2	1
1:R:79:THR:HG23	1:R:80:LEU:H	0.51	1.66	2	4
1:R:102:LEU:O	1:R:103:VAL:C	0.51	2.46	1	3
1:R:137:PHE:CD2	1:R:180:PHE:CD1	0.51	2.99	1	1
1:R:69:ASP:O	1:R:73:SER:HB2	0.51	2.06	4	1
1:R:137:PHE:CB	1:R:183:TYR:CD1	0.51	2.94	2	1
1:R:54:ASN:CB	1:R:58:GLN:OE1	0.51	2.59	2	1
1:R:155:THR:OG1	1:R:160:TYR:CB	0.51	2.58	4	4
1:R:128:ASP:C	1:R:130:THR:N	0.51	2.64	1	1
1:R:168:TYR:CE1	1:R:170:TRP:CD1	0.51	2.99	1	1
1:R:107:ILE:O	1:R:111:LEU:HG	0.51	2.06	3	1
1:R:68:PHE:CZ	1:R:72:TYR:CD2	0.51	2.98	4	1
1:R:55:ALA:HA	1:R:151:PHE:CE1	0.51	2.41	5	1
1:R:48:HIS:CD2	1:R:79:THR:CG2	0.51	2.93	5	1
1:R:115:ILE:CG1	1:R:122:SER:O	0.51	2.59	5	1
1:R:180:PHE:HD1	1:R:181:VAL:N	0.51	2.02	5	1
1:R:58:GLN:CD	1:R:162:ILE:CG2	0.50	2.79	2	1
1:R:141:ILE:H	1:R:179:VAL:HG13	0.50	1.65	2	1
1:R:127:VAL:HG12	1:R:180:PHE:CD1	0.50	2.40	2	1
1:R:63:VAL:CG2	1:R:124:VAL:HG12	0.50	2.36	2	1
1:R:94:LEU:O	1:R:94:LEU:HD12	0.50	2.06	2	1
1:R:142:PHE:CD1	1:R:177:VAL:CB	0.50	2.94	5	5
1:R:67:PHE:CZ	1:R:70:TRP:CD1	0.50	2.99	1	1
1:R:60:PHE:CZ	1:R:72:TYR:CD2	0.50	2.99	3	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:R:125:CYS:O	1:R:126:VAL:CG2	0.50	2.56	4	1
1:R:62:TYR:CE1	1:R:153:CYS:HB3	0.50	2.40	4	1
1:R:94:LEU:HD22	1:R:103:VAL:CG2	0.50	2.36	4	1
1:R:160:TYR:CE1	1:R:162:ILE:N	0.50	2.79	2	1
1:R:52:TRP:CD2	1:R:97:GLY:O	0.50	2.65	3	2
1:R:92:LEU:HD21	1:R:94:LEU:CD2	0.50	2.36	3	1
1:R:104:ILE:HG23	1:R:111:LEU:HG	0.50	1.81	5	1
1:R:170:TRP:O	1:R:171:THR:CB	0.50	2.58	2	1
1:R:53:LEU:CD1	1:R:79:THR:CA	0.50	2.90	2	2
1:R:173:ASP:HB3	1:R:174:PRO:HD2	0.50	1.84	4	2
1:R:94:LEU:N	1:R:94:LEU:HD22	0.50	2.22	3	1
1:R:67:PHE:CD1	1:R:111:LEU:HD22	0.50	2.41	5	1
1:R:115:ILE:CG2	1:R:124:VAL:H	0.50	2.19	5	1
1:R:141:ILE:HG23	1:R:151:PHE:HE1	0.50	1.64	5	1
1:R:71:VAL:HG12	1:R:72:TYR:N	0.50	2.20	2	1
1:R:56:ILE:CG1	1:R:60:PHE:CZ	0.50	2.94	2	1
1:R:60:PHE:HB3	1:R:65:GLU:O	0.50	2.07	2	1
1:R:104:ILE:HA	1:R:111:LEU:HG	0.50	1.83	1	1
1:R:55:ALA:CA	1:R:151:PHE:CZ	0.50	2.95	1	2
1:R:60:PHE:CD1	1:R:65:GLU:HB3	0.50	2.42	3	2
1:R:137:PHE:O	1:R:183:TYR:CD2	0.50	2.64	3	1
1:R:53:LEU:HD21	1:R:83:ILE:HG23	0.50	1.82	4	2
1:R:43:SER:HA	1:R:165:GLU:HB2	0.50	1.83	5	1
1:R:58:GLN:HE21	1:R:59:LEU:HD22	0.50	1.66	5	1
1:R:107:ILE:HG22	1:R:110:LEU:HD23	0.50	1.82	2	1
1:R:107:ILE:O	1:R:110:LEU:N	0.50	2.37	2	2
1:R:155:THR:CG2	1:R:160:TYR:CB	0.50	2.89	2	4
1:R:160:TYR:CD1	1:R:167:PHE:HB2	0.50	2.42	2	1
1:R:138:HIS:CE1	1:R:159:TRP:CD1	0.50	3.00	4	1
1:R:33:LEU:O	1:R:33:LEU:CD2	0.50	2.60	5	1
1:R:44:ARG:N	1:R:165:GLU:HB3	0.50	2.22	5	1
1:R:56:ILE:HG13	1:R:68:PHE:CD1	0.50	2.42	5	1
1:R:57:LEU:O	1:R:60:PHE:HB2	0.50	2.06	2	1
1:R:63:VAL:CG1	1:R:124:VAL:HG11	0.50	2.35	1	1
1:R:123:GLU:O	1:R:181:VAL:HG23	0.50	2.05	4	1
1:R:137:PHE:CZ	1:R:174:PRO:HD3	0.50	2.41	2	2
1:R:137:PHE:HB3	1:R:183:TYR:CD1	0.50	2.42	2	1
1:R:124:VAL:HA	1:R:180:PHE:O	0.50	2.07	4	1
1:R:57:LEU:CD1	1:R:68:PHE:CG	0.50	2.92	4	1
1:R:33:LEU:HA	1:R:155:THR:HA	0.50	1.84	5	1
1:R:89:LEU:HD21	1:R:107:ILE:HG23	0.49	1.84	2	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:R:57:LEU:HA	1:R:68:PHE:CD2	0.49	2.41	4	1
1:R:141:ILE:CG2	1:R:151:PHE:CE2	0.49	2.85	1	1
1:R:167:PHE:N	1:R:167:PHE:CD1	0.49	2.77	1	2
1:R:181:VAL:HG12	1:R:181:VAL:O	0.49	2.06	1	1
1:R:107:ILE:O	1:R:107:ILE:HG22	0.49	2.06	5	1
1:R:49:ASP:O	1:R:79:THR:CG2	0.49	2.61	2	2
1:R:58:GLN:CA	1:R:58:GLN:OE1	0.49	2.60	1	1
1:R:79:THR:CG2	1:R:80:LEU:N	0.49	2.75	1	1
1:R:170:TRP:HA	1:R:170:TRP:HE3	0.49	1.66	3	1
1:R:53:LEU:HD11	1:R:83:ILE:HG23	0.49	1.84	3	1
1:R:155:THR:HG23	1:R:160:TYR:CD2	0.49	2.42	2	1
1:R:160:TYR:HA	1:R:169:PRO:HA	0.49	1.84	2	1
1:R:56:ILE:HA	1:R:59:LEU:HB2	0.49	1.83	2	1
1:R:141:ILE:O	1:R:177:VAL:HA	0.49	2.07	3	1
1:R:142:PHE:CZ	1:R:171:THR:CG2	0.49	2.94	3	1
1:R:43:SER:O	1:R:164:ASP:HA	0.49	2.06	3	1
1:R:159:TRP:HB3	1:R:172:PRO:HD2	0.49	1.84	4	1
1:R:123:GLU:C	1:R:124:VAL:HG13	0.49	2.27	5	1
1:R:137:PHE:CG	1:R:180:PHE:CE1	0.49	3.00	5	1
1:R:54:ASN:HA	1:R:58:GLN:CD	0.49	2.28	2	1
1:R:60:PHE:CZ	1:R:61:ARG:HG2	0.49	2.42	3	1
1:R:101:ALA:C	1:R:103:VAL:H	0.49	2.11	5	3
1:R:89:LEU:C	1:R:89:LEU:HD23	0.49	2.27	4	1
1:R:127:VAL:O	1:R:130:THR:CB	0.49	2.60	2	1
1:R:160:TYR:C	1:R:160:TYR:CD1	0.49	2.86	2	1
1:R:56:ILE:HG12	1:R:60:PHE:CZ	0.49	2.43	2	1
1:R:177:VAL:HG23	1:R:178:LEU:N	0.49	2.23	4	1
1:R:57:LEU:HD11	1:R:71:VAL:HG11	0.49	1.84	2	1
1:R:34:TYR:HB2	1:R:154:VAL:CG1	0.49	2.37	1	1
1:R:142:PHE:CD1	1:R:177:VAL:CG2	0.49	2.96	3	1
1:R:141:ILE:C	1:R:177:VAL:HG23	0.49	2.28	3	1
1:R:92:LEU:CG	1:R:94:LEU:CD2	0.49	2.89	3	1
1:R:55:ALA:CA	1:R:151:PHE:CE1	0.49	2.95	5	2
1:R:31:LEU:CG	1:R:41:PHE:CE1	0.49	2.95	2	1
1:R:163:ASP:HB2	1:R:168:TYR:CE2	0.49	2.43	1	1
1:R:86:LEU:HD21	1:R:107:ILE:HD11	0.49	1.84	1	1
1:R:31:LEU:HD11	1:R:167:PHE:HB2	0.49	1.82	2	1
1:R:56:ILE:CG1	1:R:103:VAL:HG11	0.49	2.38	4	1
1:R:137:PHE:CD2	1:R:180:PHE:CD2	0.49	3.00	2	2
1:R:161:ALA:HB3	1:R:170:TRP:HB2	0.49	1.83	3	1
1:R:47:ASN:O	1:R:48:HIS:HB2	0.49	2.08	3	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:R:57:LEU:CD1	1:R:60:PHE:CD2	0.49	2.96	3	1
1:R:157:ASN:HB2	1:R:160:TYR:CE1	0.49	2.43	4	1
1:R:134:LEU:CD2	1:R:171:THR:CG2	0.49	2.89	5	1
1:R:67:PHE:CE1	1:R:111:LEU:HD22	0.49	2.43	5	1
1:R:105:TRP:O	1:R:108:LYS:HG3	0.48	2.08	1	1
1:R:66:PRO:HG2	1:R:68:PHE:CE2	0.48	2.43	3	1
1:R:62:TYR:CE1	1:R:153:CYS:CB	0.48	2.96	4	1
1:R:92:LEU:CD2	1:R:102:LEU:HB2	0.48	2.37	5	1
1:R:137:PHE:HB2	1:R:181:VAL:O	0.48	2.08	5	1
1:R:153:CYS:CB	1:R:160:TYR:CE2	0.48	2.96	2	1
1:R:128:ASP:C	1:R:130:THR:H	0.48	2.11	1	1
1:R:142:PHE:CE2	1:R:177:VAL:HG12	0.48	2.43	1	1
1:R:134:LEU:CD1	1:R:171:THR:CG2	0.48	2.79	1	2
1:R:65:GLU:CG	1:R:65:GLU:O	0.48	2.61	3	1
1:R:31:LEU:CD1	1:R:160:TYR:CE1	0.48	2.96	2	1
1:R:39:LYS:O	1:R:41:PHE:CE1	0.48	2.66	4	2
1:R:102:LEU:HD23	1:R:106:ASN:HD21	0.48	1.67	3	1
1:R:138:HIS:CD2	1:R:183:TYR:CA	0.48	2.95	3	1
1:R:79:THR:O	1:R:83:ILE:HD12	0.48	2.08	5	1
1:R:138:HIS:ND1	1:R:154:VAL:HG21	0.48	2.23	2	2
1:R:116:GLY:O	1:R:126:VAL:HG13	0.48	2.08	1	1
1:R:118:ALA:CB	1:R:128:ASP:HA	0.48	2.38	1	1
1:R:142:PHE:CZ	1:R:177:VAL:CG1	0.48	2.93	1	1
1:R:31:LEU:CD1	1:R:41:PHE:CG	0.48	2.96	1	1
1:R:33:LEU:CD2	1:R:33:LEU:O	0.48	2.61	4	1
1:R:99:PRO:HD2	1:R:101:ALA:HB2	0.48	1.85	4	1
1:R:31:LEU:HD22	1:R:167:PHE:CE1	0.48	2.43	5	1
1:R:56:ILE:CB	1:R:68:PHE:CE1	0.48	2.96	5	1
1:R:178:LEU:C	1:R:179:VAL:HG12	0.48	2.28	1	2
1:R:126:VAL:HG12	1:R:127:VAL:HG13	0.48	1.81	4	1
1:R:142:PHE:CG	1:R:177:VAL:HG12	0.48	2.43	4	1
1:R:104:ILE:HG23	1:R:111:LEU:CG	0.48	2.38	5	1
1:R:160:TYR:OH	1:R:162:ILE:HB	0.48	2.08	2	1
1:R:83:ILE:HB	1:R:94:LEU:HD13	0.48	1.85	1	1
1:R:31:LEU:HD11	1:R:41:PHE:CZ	0.48	2.44	3	1
1:R:54:ASN:O	1:R:58:GLN:HG3	0.48	2.08	3	1
1:R:66:PRO:HG2	1:R:68:PHE:CD2	0.48	2.43	3	1
1:R:80:LEU:HD12	1:R:81:GLU:N	0.48	2.24	4	1
1:R:142:PHE:CZ	1:R:172:PRO:CA	0.48	2.97	5	1
1:R:47:ASN:C	1:R:48:HIS:CG	0.48	2.85	5	1
1:R:127:VAL:HG23	1:R:128:ASP:N	0.48	2.23	2	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:R:33:LEU:HD11	1:R:37:GLU:O	0.48	2.07	1	1
1:R:157:ASN:CB	1:R:160:TYR:CE1	0.48	2.97	4	2
1:R:92:LEU:N	1:R:92:LEU:CD2	0.48	2.77	3	1
1:R:41:PHE:CD1	1:R:162:ILE:CD1	0.48	2.97	4	1
1:R:134:LEU:O	1:R:138:HIS:CE1	0.48	2.67	5	1
1:R:164:ASP:O	1:R:165:GLU:HB3	0.48	2.09	5	1
1:R:53:LEU:CD2	1:R:83:ILE:HG13	0.48	2.39	1	1
1:R:38:LYS:O	1:R:38:LYS:HG3	0.48	2.09	5	2
1:R:55:ALA:C	1:R:59:LEU:HD23	0.48	2.27	5	1
1:R:90:THR:HB	1:R:92:LEU:HD21	0.48	1.86	5	1
1:R:137:PHE:CB	1:R:183:TYR:CE2	0.48	2.96	3	1
1:R:115:ILE:CD1	1:R:124:VAL:N	0.48	2.77	5	1
1:R:53:LEU:C	1:R:57:LEU:CB	0.47	2.82	2	1
1:R:111:LEU:HD11	1:R:113:THR:OG1	0.47	2.09	4	1
1:R:62:TYR:OH	1:R:151:PHE:CE1	0.47	2.66	4	1
1:R:58:GLN:CG	1:R:59:LEU:HD13	0.47	2.38	4	1
1:R:92:LEU:HD21	1:R:103:VAL:HA	0.47	1.86	4	1
1:R:117:THR:HG23	1:R:126:VAL:CB	0.47	2.38	5	1
1:R:34:TYR:HB2	1:R:154:VAL:HG11	0.47	1.84	1	1
1:R:57:LEU:CD1	1:R:72:TYR:CD2	0.47	2.97	1	1
1:R:89:LEU:HD23	1:R:89:LEU:C	0.47	2.29	1	2
1:R:159:TRP:CD1	1:R:171:THR:O	0.47	2.67	3	1
1:R:107:ILE:O	1:R:111:LEU:HB2	0.47	2.09	4	1
1:R:111:LEU:HD13	1:R:112:HIS:N	0.47	2.24	4	1
1:R:112:HIS:CD2	1:R:112:HIS:O	0.47	2.67	4	1
1:R:168:TYR:CD1	1:R:168:TYR:N	0.47	2.82	2	1
1:R:62:TYR:CE2	1:R:181:VAL:CG2	0.47	2.97	2	1
1:R:43:SER:HB3	1:R:164:ASP:O	0.47	2.08	3	1
1:R:137:PHE:HB3	1:R:180:PHE:CE1	0.47	2.45	5	1
1:R:31:LEU:N	1:R:31:LEU:HD23	0.47	2.24	5	1
1:R:56:ILE:HG21	1:R:68:PHE:CE1	0.47	2.44	5	1
1:R:48:HIS:CD2	1:R:80:LEU:HD22	0.47	2.45	3	1
1:R:63:VAL:O	1:R:64:GLU:HB3	0.47	2.07	2	2
1:R:89:LEU:HD23	1:R:90:THR:CG2	0.47	2.40	5	2
1:R:99:PRO:HB2	1:R:141:ILE:HD13	0.47	1.86	3	1
1:R:60:PHE:CB	1:R:68:PHE:CE2	0.47	2.97	4	1
1:R:52:TRP:CG	1:R:97:GLY:N	0.47	2.83	4	1
1:R:115:ILE:HB	1:R:122:SER:N	0.47	2.23	5	1
1:R:56:ILE:HB	1:R:68:PHE:CD1	0.47	2.45	5	1
1:R:111:LEU:CD1	1:R:112:HIS:N	0.47	2.78	2	1
1:R:136:ASP:O	1:R:183:TYR:CE2	0.47	2.67	2	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:R:139:ALA:CB	1:R:153:CYS:SG	0.47	3.03	2	1
1:R:160:TYR:CE1	1:R:162:ILE:HB	0.47	2.45	2	1
1:R:59:LEU:HD21	1:R:141:ILE:HD11	0.47	1.86	1	2
1:R:55:ALA:HB2	1:R:141:ILE:CD1	0.47	2.40	4	1
1:R:49:ASP:HB2	1:R:95:HIS:O	0.47	2.10	5	1
1:R:153:CYS:O	1:R:160:TYR:HD2	0.47	1.91	2	1
1:R:83:ILE:HG22	1:R:94:LEU:HD21	0.47	1.85	2	1
1:R:67:PHE:CE2	1:R:86:LEU:HD11	0.47	2.45	2	1
1:R:163:ASP:HB2	1:R:168:TYR:CE1	0.47	2.44	5	2
1:R:127:VAL:HB	1:R:178:LEU:HD13	0.47	1.85	1	1
1:R:141:ILE:HB	1:R:179:VAL:HG13	0.47	1.87	1	1
1:R:162:ILE:HG12	1:R:167:PHE:CD1	0.47	2.45	1	1
1:R:71:VAL:HG13	1:R:77:ASN:ND2	0.47	2.24	3	1
1:R:33:LEU:HD22	1:R:33:LEU:N	0.47	2.23	3	1
1:R:34:TYR:HB3	1:R:154:VAL:CG1	0.47	2.40	3	1
1:R:137:PHE:CB	1:R:180:PHE:CD2	0.47	2.97	4	1
1:R:57:LEU:N	1:R:57:LEU:HD22	0.47	2.24	4	1
1:R:46:ASN:HB3	1:R:48:HIS:CE1	0.47	2.45	5	2
1:R:53:LEU:O	1:R:57:LEU:CD2	0.47	2.59	3	1
1:R:57:LEU:C	1:R:57:LEU:HD13	0.47	2.31	2	1
1:R:125:CYS:SG	1:R:180:PHE:CZ	0.47	3.06	1	2
1:R:87:GLU:O	1:R:91:GLY:CA	0.47	2.63	3	4
1:R:57:LEU:HD13	1:R:60:PHE:HD2	0.47	1.70	3	1
1:R:59:LEU:HD12	1:R:62:TYR:CE1	0.47	2.45	3	1
1:R:157:ASN:CB	1:R:160:TYR:CZ	0.47	2.98	5	1
1:R:69:ASP:HA	1:R:73:SER:CB	0.47	2.40	2	1
1:R:94:LEU:HD12	1:R:94:LEU:N	0.47	2.24	1	1
1:R:38:LYS:HG3	1:R:38:LYS:O	0.47	2.09	4	1
1:R:98:GLY:O	1:R:103:VAL:HG21	0.47	2.10	4	1
1:R:115:ILE:HG13	1:R:123:GLU:N	0.47	2.24	5	1
1:R:125:CYS:O	1:R:180:PHE:CD2	0.47	2.68	5	1
1:R:74:SER:CB	1:R:78:LEU:HB2	0.47	2.40	5	1
1:R:134:LEU:CA	1:R:173:ASP:CB	0.46	2.79	2	1
1:R:138:HIS:CD2	1:R:181:VAL:CG1	0.46	2.98	3	1
1:R:67:PHE:CZ	1:R:89:LEU:CD2	0.46	2.97	3	1
1:R:126:VAL:CG1	1:R:127:VAL:H	0.46	2.20	4	1
1:R:127:VAL:CB	1:R:178:LEU:HA	0.46	2.39	1	1
1:R:68:PHE:CD1	1:R:69:ASP:N	0.46	2.84	1	1
1:R:123:GLU:C	1:R:124:VAL:CG1	0.46	2.82	4	1
1:R:170:TRP:O	1:R:172:PRO:HD3	0.46	2.10	4	1
1:R:62:TYR:CE2	1:R:140:GLY:N	0.46	2.83	4	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:R:142:PHE:HA	1:R:177:VAL:CB	0.46	2.39	2	1
1:R:155:THR:OG1	1:R:160:TYR:HB3	0.46	2.10	2	1
1:R:31:LEU:CD2	1:R:41:PHE:CE1	0.46	2.97	3	1
1:R:60:PHE:CB	1:R:68:PHE:CD2	0.46	2.98	4	1
1:R:137:PHE:C	1:R:138:HIS:CD2	0.46	2.89	5	1
1:R:104:ILE:HB	1:R:111:LEU:HD12	0.46	1.86	2	1
1:R:114:GLY:O	1:R:123:GLU:N	0.46	2.48	2	3
1:R:117:THR:O	1:R:125:CYS:SG	0.46	2.73	2	1
1:R:57:LEU:HD22	1:R:68:PHE:CB	0.46	2.40	2	1
1:R:104:ILE:CA	1:R:111:LEU:HG	0.46	2.41	1	1
1:R:71:VAL:HG22	1:R:82:ALA:CB	0.46	2.41	1	2
1:R:161:ALA:HB3	1:R:170:TRP:CB	0.46	2.41	3	1
1:R:116:GLY:O	1:R:117:THR:HG23	0.46	2.11	4	1
1:R:102:LEU:HB3	1:R:105:TRP:HB3	0.46	1.87	5	1
1:R:132:MET:CB	1:R:180:PHE:CZ	0.46	2.98	3	1
1:R:52:TRP:CE3	1:R:97:GLY:HA2	0.46	2.46	4	1
1:R:177:VAL:CG2	1:R:178:LEU:N	0.46	2.79	5	2
1:R:65:GLU:CB	1:R:68:PHE:CE1	0.46	2.98	1	1
1:R:155:THR:OG1	1:R:160:TYR:CG	0.46	2.67	5	1
1:R:170:TRP:C	1:R:171:THR:OG1	0.46	2.52	2	1
1:R:56:ILE:HG12	1:R:60:PHE:CE2	0.46	2.46	2	1
1:R:107:ILE:HG12	1:R:111:LEU:CD2	0.46	2.41	3	1
1:R:142:PHE:CE2	1:R:171:THR:HG23	0.46	2.46	3	1
1:R:58:GLN:HG2	1:R:151:PHE:HB2	0.46	1.86	5	1
1:R:159:TRP:CD2	1:R:172:PRO:HG3	0.46	2.46	2	1
1:R:127:VAL:HG23	1:R:177:VAL:O	0.46	2.11	1	1
1:R:41:PHE:HD1	1:R:41:PHE:N	0.46	2.06	1	1
1:R:141:ILE:HG12	1:R:151:PHE:CE2	0.46	2.46	3	2
1:R:101:ALA:O	1:R:102:LEU:C	0.46	2.54	5	2
1:R:53:LEU:HD13	1:R:82:ALA:HB3	0.46	1.88	3	1
1:R:160:TYR:CA	1:R:168:TYR:O	0.46	2.64	5	1
1:R:58:GLN:HG2	1:R:151:PHE:CB	0.46	2.40	5	1
1:R:117:THR:CA	1:R:126:VAL:HG22	0.46	2.33	2	1
1:R:41:PHE:CG	1:R:162:ILE:HD11	0.46	2.45	2	1
1:R:59:LEU:O	1:R:62:TYR:CE1	0.46	2.69	2	1
1:R:57:LEU:CD1	1:R:71:VAL:HG11	0.46	2.41	1	2
1:R:108:LYS:HA	1:R:112:HIS:H	0.46	1.70	1	1
1:R:137:PHE:CD2	1:R:180:PHE:CE1	0.46	3.04	1	1
1:R:33:LEU:CD1	1:R:61:ARG:NH1	0.46	2.79	1	1
1:R:138:HIS:CB	1:R:181:VAL:HG12	0.46	2.40	3	1
1:R:41:PHE:CD2	1:R:72:TYR:OH	0.46	2.65	4	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:R:51:ALA:O	1:R:54:ASN:ND2	0.46	2.49	4	1
1:R:138:HIS:CB	1:R:154:VAL:CG2	0.46	2.94	2	2
1:R:168:TYR:CE2	1:R:170:TRP:CG	0.46	3.04	2	1
1:R:41:PHE:CE2	1:R:162:ILE:CD1	0.46	2.99	2	3
1:R:57:LEU:CD2	1:R:68:PHE:HB2	0.46	2.41	2	2
1:R:62:TYR:CZ	1:R:153:CYS:HB2	0.46	2.46	1	1
1:R:89:LEU:CD2	1:R:90:THR:CG2	0.46	2.94	5	1
1:R:111:LEU:C	1:R:111:LEU:HD13	0.45	2.32	2	2
1:R:170:TRP:CG	1:R:171:THR:N	0.45	2.84	3	1
1:R:43:SER:O	1:R:164:ASP:CB	0.45	2.63	3	1
1:R:53:LEU:C	1:R:57:LEU:HD23	0.45	2.30	3	1
1:R:152:ALA:HA	1:R:161:ALA:CB	0.45	2.40	5	2
1:R:31:LEU:HB3	1:R:167:PHE:CE2	0.45	2.45	4	1
1:R:159:TRP:CG	1:R:172:PRO:HG3	0.45	2.45	2	1
1:R:33:LEU:CA	1:R:37:GLU:N	0.45	2.79	2	1
1:R:138:HIS:HB3	1:R:181:VAL:HG12	0.45	1.88	3	1
1:R:43:SER:O	1:R:44:ARG:C	0.45	2.54	3	1
1:R:30:GLU:HG2	1:R:40:THR:OG1	0.45	2.11	3	1
1:R:126:VAL:CB	1:R:178:LEU:O	0.45	2.64	4	1
1:R:173:ASP:O	1:R:177:VAL:HG11	0.45	2.12	4	1
1:R:138:HIS:O	1:R:139:ALA:CB	0.45	2.63	1	1
1:R:92:LEU:O	1:R:93:GLU:HB3	0.45	2.12	1	1
1:R:66:PRO:HB3	1:R:68:PHE:CZ	0.45	2.46	4	1
1:R:168:TYR:CZ	1:R:170:TRP:CD1	0.45	3.05	5	1
1:R:117:THR:HA	1:R:126:VAL:CG2	0.45	2.37	2	1
1:R:109:HIS:NE2	1:R:110:LEU:CD2	0.45	2.80	1	1
1:R:104:ILE:O	1:R:111:LEU:HG	0.45	2.12	1	1
1:R:168:TYR:CE1	1:R:170:TRP:CG	0.45	3.04	1	1
1:R:30:GLU:HA	1:R:40:THR:HA	0.45	1.88	1	1
1:R:161:ALA:CB	1:R:170:TRP:CB	0.45	2.95	3	1
1:R:52:TRP:CD1	1:R:96:GLU:C	0.45	2.90	4	1
1:R:58:GLN:HG3	1:R:59:LEU:HD22	0.45	1.87	5	1
1:R:63:VAL:HG21	1:R:124:VAL:HG12	0.45	1.88	2	1
1:R:58:GLN:OE1	1:R:162:ILE:HG21	0.45	2.10	2	1
1:R:118:ALA:CB	1:R:130:THR:OG1	0.45	2.63	3	2
1:R:107:ILE:CG2	1:R:107:ILE:O	0.45	2.64	1	1
1:R:92:LEU:CD2	1:R:101:ALA:O	0.45	2.65	4	1
1:R:159:TRP:O	1:R:160:TYR:CD1	0.45	2.69	4	1
1:R:67:PHE:CD2	1:R:111:LEU:CD2	0.45	2.99	5	1
1:R:53:LEU:O	1:R:54:ASN:C	0.45	2.52	2	2
1:R:53:LEU:CD1	1:R:79:THR:O	0.45	2.64	1	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:R:98:GLY:HA2	1:R:101:ALA:HB2	0.45	1.88	1	1
1:R:138:HIS:CG	1:R:181:VAL:CG1	0.45	2.96	3	1
1:R:150:VAL:CG1	1:R:163:ASP:OD2	0.45	2.65	3	1
1:R:153:CYS:O	1:R:155:THR:HG23	0.45	2.11	3	1
1:R:53:LEU:CG	1:R:83:ILE:HG23	0.45	2.42	3	1
1:R:94:LEU:HD12	1:R:94:LEU:C	0.45	2.31	4	1
1:R:62:TYR:CZ	1:R:63:VAL:CG2	0.45	2.96	5	2
1:R:142:PHE:CE2	1:R:171:THR:OG1	0.45	2.55	3	1
1:R:56:ILE:O	1:R:59:LEU:CB	0.45	2.64	3	1
1:R:103:VAL:HG12	1:R:107:ILE:CD1	0.45	2.42	5	1
1:R:44:ARG:N	1:R:164:ASP:O	0.45	2.50	3	1
1:R:54:ASN:CA	1:R:57:LEU:HB2	0.45	2.41	3	1
1:R:125:CYS:C	1:R:179:VAL:HA	0.45	2.33	4	1
1:R:31:LEU:HD12	1:R:155:THR:HG22	0.45	1.89	5	1
1:R:111:LEU:C	1:R:111:LEU:CD1	0.45	2.84	1	2
1:R:134:LEU:HG	1:R:173:ASP:CA	0.45	2.42	3	1
1:R:141:ILE:C	1:R:142:PHE:HD1	0.45	2.14	4	1
1:R:62:TYR:CE2	1:R:63:VAL:HG23	0.45	2.46	2	2
1:R:57:LEU:CG	1:R:71:VAL:HG21	0.45	2.42	2	1
1:R:117:THR:C	1:R:125:CYS:SG	0.45	2.95	1	1
1:R:67:PHE:CZ	1:R:70:TRP:NE1	0.45	2.85	1	1
1:R:159:TRP:HA	1:R:172:PRO:CD	0.45	2.42	4	1
1:R:162:ILE:HG13	1:R:167:PHE:CE1	0.45	2.46	5	1
1:R:120:ARG:CG	1:R:121:PRO:CD	0.45	2.95	5	1
1:R:107:ILE:O	1:R:108:LYS:C	0.44	2.55	2	4
1:R:90:THR:OG1	1:R:92:LEU:CG	0.44	2.65	2	2
1:R:54:ASN:ND2	1:R:163:ASP:HA	0.44	2.26	1	1
1:R:94:LEU:CD1	1:R:94:LEU:N	0.44	2.78	1	1
1:R:29:MET:HB2	1:R:167:PHE:CE2	0.44	2.47	3	1
1:R:161:ALA:O	1:R:168:TYR:CE2	0.44	2.70	3	1
1:R:42:TYR:CD2	1:R:71:VAL:HG12	0.44	2.47	4	1
1:R:60:PHE:CE1	1:R:66:PRO:HB3	0.44	2.47	5	1
1:R:143:LEU:HD21	1:R:146:GLN:HG2	0.44	1.87	5	1
1:R:90:THR:CB	1:R:92:LEU:HG	0.44	2.42	2	1
1:R:41:PHE:CG	1:R:162:ILE:HD13	0.44	2.48	1	1
1:R:107:ILE:HA	1:R:110:LEU:CD2	0.44	2.40	3	1
1:R:54:ASN:HA	1:R:57:LEU:HB2	0.44	1.88	3	1
1:R:115:ILE:HG22	1:R:125:CYS:SG	0.44	2.52	4	1
1:R:33:LEU:HB3	1:R:155:THR:HA	0.44	1.90	4	1
1:R:57:LEU:CD2	1:R:68:PHE:CB	0.44	2.95	2	1
1:R:59:LEU:HD12	1:R:151:PHE:HE1	0.44	1.67	2	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:R:162:ILE:CG2	1:R:167:PHE:CE1	0.44	2.97	1	1
1:R:33:LEU:CD2	1:R:37:GLU:O	0.44	2.66	1	1
1:R:34:TYR:CG	1:R:35:ASN:N	0.44	2.85	3	1
1:R:112:HIS:CG	1:R:112:HIS:O	0.44	2.70	4	1
1:R:125:CYS:O	1:R:126:VAL:CB	0.44	2.63	4	1
1:R:58:GLN:OE1	1:R:151:PHE:CD1	0.44	2.70	4	1
1:R:115:ILE:HG13	1:R:122:SER:C	0.44	2.33	5	1
1:R:78:LEU:HD12	1:R:81:GLU:OE1	0.44	2.13	5	1
1:R:37:GLU:O	1:R:39:LYS:N	0.44	2.50	2	1
1:R:59:LEU:O	1:R:62:TYR:HD1	0.44	1.93	2	1
1:R:80:LEU:HD12	1:R:81:GLU:HG3	0.44	1.89	3	2
1:R:111:LEU:HD13	1:R:111:LEU:C	0.44	2.33	1	1
1:R:118:ALA:CB	1:R:128:ASP:O	0.44	2.66	1	1
1:R:56:ILE:HD11	1:R:103:VAL:HB	0.44	1.89	4	1
1:R:35:ASN:ND2	1:R:181:VAL:HG11	0.44	2.27	2	1
1:R:40:THR:O	1:R:61:ARG:NH2	0.44	2.51	2	1
1:R:130:THR:HG23	1:R:132:MET:HG3	0.44	1.89	1	1
1:R:67:PHE:CE1	1:R:89:LEU:CD2	0.44	3.00	3	1
1:R:94:LEU:C	1:R:96:GLU:N	0.44	2.70	3	1
1:R:103:VAL:O	1:R:107:ILE:CD1	0.44	2.65	4	1
1:R:33:LEU:HD11	1:R:41:PHE:CE1	0.44	2.47	4	1
1:R:56:ILE:N	1:R:56:ILE:CD1	0.44	2.80	4	1
1:R:63:VAL:CG2	1:R:124:VAL:CG1	0.44	2.89	1	1
1:R:49:ASP:O	1:R:79:THR:HG23	0.44	2.12	1	1
1:R:132:MET:HB3	1:R:180:PHE:CZ	0.44	2.46	3	1
1:R:53:LEU:HD11	1:R:83:ILE:CD1	0.44	2.41	5	1
1:R:31:LEU:CD1	1:R:167:PHE:CB	0.44	2.96	2	1
1:R:168:TYR:CD2	1:R:170:TRP:CE3	0.44	3.06	2	1
1:R:126:VAL:O	1:R:180:PHE:CD2	0.44	2.71	1	1
1:R:98:GLY:CA	1:R:101:ALA:CB	0.44	2.95	1	1
1:R:66:PRO:O	1:R:68:PHE:N	0.44	2.51	3	2
1:R:142:PHE:CD1	1:R:177:VAL:HG21	0.44	2.47	3	1
1:R:44:ARG:HB3	1:R:165:GLU:CB	0.44	2.43	4	1
1:R:58:GLN:CG	1:R:59:LEU:N	0.44	2.81	4	1
1:R:113:THR:HG23	1:R:114:GLY:H	0.44	1.73	5	1
1:R:170:TRP:O	1:R:171:THR:OG1	0.44	2.35	2	1
1:R:43:SER:C	1:R:164:ASP:CA	0.44	2.87	3	1
1:R:126:VAL:HG21	1:R:180:PHE:CD1	0.44	2.46	4	1
1:R:86:LEU:HD11	1:R:103:VAL:CG1	0.44	2.16	4	1
1:R:33:LEU:N	1:R:37:GLU:HA	0.44	2.27	2	1
1:R:66:PRO:CB	1:R:68:PHE:CE1	0.44	3.01	2	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:R:55:ALA:CA	1:R:151:PHE:CE2	0.44	2.96	1	1
1:R:152:ALA:CA	1:R:161:ALA:CB	0.44	2.95	3	3
1:R:143:LEU:N	1:R:143:LEU:CD2	0.44	2.80	4	1
1:R:126:VAL:CA	1:R:179:VAL:HA	0.43	2.43	1	1
1:R:143:LEU:N	1:R:143:LEU:HD22	0.43	2.27	4	2
1:R:137:PHE:HA	1:R:183:TYR:CE2	0.43	2.48	4	1
1:R:94:LEU:HB2	1:R:98:GLY:HA3	0.43	1.88	4	1
1:R:146:GLN:O	1:R:148:HIS:CD2	0.43	2.71	4	2
1:R:125:CYS:HB2	1:R:182:PRO:HG3	0.43	1.89	5	1
1:R:49:ASP:OD1	1:R:49:ASP:O	0.43	2.36	2	1
1:R:90:THR:OG1	1:R:92:LEU:HG	0.43	2.13	2	2
1:R:143:LEU:N	1:R:176:ASP:O	0.43	2.48	1	1
1:R:139:ALA:O	1:R:181:VAL:N	0.43	2.49	3	1
1:R:36:GLY:O	1:R:37:GLU:C	0.43	2.50	4	1
1:R:68:PHE:CE2	1:R:72:TYR:HB2	0.43	2.48	2	1
1:R:71:VAL:HG22	1:R:79:THR:HA	0.43	1.89	2	1
1:R:103:VAL:O	1:R:107:ILE:HG13	0.43	2.13	1	1
1:R:47:ASN:ND2	1:R:80:LEU:HD23	0.43	2.27	1	1
1:R:139:ALA:H	1:R:181:VAL:HG12	0.43	1.72	3	1
1:R:43:SER:HA	1:R:165:GLU:HA	0.43	1.90	5	1
1:R:60:PHE:CE2	1:R:61:ARG:HG2	0.43	2.48	5	1
1:R:33:LEU:N	1:R:37:GLU:CA	0.43	2.81	2	1
1:R:60:PHE:HD1	1:R:65:GLU:HB3	0.43	1.72	3	1
1:R:58:GLN:OE1	1:R:151:PHE:HD1	0.43	1.96	4	1
1:R:92:LEU:HD11	1:R:94:LEU:CD2	0.43	2.44	5	1
1:R:137:PHE:HA	1:R:183:TYR:CD1	0.43	2.48	2	1
1:R:137:PHE:O	1:R:138:HIS:ND1	0.43	2.52	1	1
1:R:41:PHE:CZ	1:R:61:ARG:HB2	0.43	2.49	1	1
1:R:58:GLN:OE1	1:R:151:PHE:O	0.43	2.37	3	1
1:R:138:HIS:CD2	1:R:181:VAL:O	0.43	2.71	3	1
1:R:65:GLU:HG3	1:R:112:HIS:CE1	0.43	2.48	4	1
1:R:43:SER:HA	1:R:164:ASP:O	0.43	2.14	1	1
1:R:68:PHE:CE1	1:R:69:ASP:OD1	0.43	2.71	1	1
1:R:99:PRO:HD2	1:R:100:PRO:HD2	0.43	1.89	3	2
1:R:42:TYR:CD2	1:R:72:TYR:O	0.43	2.72	3	1
1:R:138:HIS:ND1	1:R:183:TYR:CE2	0.43	2.86	4	1
1:R:57:LEU:HD22	1:R:57:LEU:N	0.43	2.29	1	1
1:R:67:PHE:CG	1:R:86:LEU:HD23	0.43	2.49	1	1
1:R:32:THR:O	1:R:155:THR:HA	0.43	2.14	5	2
1:R:180:PHE:CE2	1:R:182:PRO:HB3	0.43	2.48	3	1
1:R:180:PHE:CE2	1:R:182:PRO:N	0.43	2.87	4	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:R:86:LEU:CD1	1:R:94:LEU:CD2	0.43	2.91	5	1
1:R:104:ILE:HG13	1:R:105:TRP:N	0.43	2.29	2	2
1:R:140:GLY:HA3	1:R:179:VAL:O	0.43	2.14	2	1
1:R:142:PHE:HD1	1:R:142:PHE:N	0.43	2.11	2	1
1:R:31:LEU:CD1	1:R:167:PHE:HB2	0.43	2.44	2	1
1:R:61:ARG:NH1	1:R:61:ARG:CG	0.43	2.78	1	1
1:R:128:ASP:CA	1:R:178:LEU:CD1	0.43	2.97	3	1
1:R:77:ASN:O	1:R:78:LEU:HB2	0.43	2.14	3	1
1:R:33:LEU:HD21	1:R:36:GLY:O	0.43	2.14	4	1
1:R:155:THR:HG23	1:R:160:TYR:HB3	0.43	1.91	2	1
1:R:107:ILE:HG23	1:R:110:LEU:CD2	0.43	2.43	1	1
1:R:58:GLN:NE2	1:R:162:ILE:O	0.43	2.51	1	1
1:R:59:LEU:CD1	1:R:62:TYR:CE1	0.43	3.01	5	1
1:R:67:PHE:CZ	1:R:86:LEU:HD21	0.43	2.49	2	1
1:R:134:LEU:HD21	1:R:171:THR:CB	0.43	2.42	1	1
1:R:62:TYR:CD1	1:R:181:VAL:HG21	0.43	2.49	3	1
1:R:69:ASP:HA	1:R:72:TYR:CD2	0.43	2.49	3	1
1:R:83:ILE:HG21	1:R:94:LEU:HB2	0.43	1.90	3	1
1:R:33:LEU:HD21	1:R:37:GLU:CB	0.43	2.41	3	1
1:R:118:ALA:HB3	1:R:130:THR:HB	0.43	1.90	4	1
1:R:115:ILE:HG23	1:R:124:VAL:N	0.43	2.29	5	1
1:R:69:ASP:HA	1:R:73:SER:HB3	0.42	1.90	2	1
1:R:158:GLY:O	1:R:160:TYR:N	0.42	2.51	3	2
1:R:72:TYR:C	1:R:72:TYR:CD1	0.42	2.92	3	1
1:R:89:LEU:CD1	1:R:89:LEU:N	0.42	2.79	3	1
1:R:33:LEU:HD13	1:R:37:GLU:O	0.42	2.13	3	1
1:R:51:ALA:HB1	1:R:149:ALA:H	0.42	1.74	2	1
1:R:151:PHE:CE2	1:R:162:ILE:O	0.42	2.71	4	1
1:R:41:PHE:CD2	1:R:151:PHE:CZ	0.42	3.07	4	1
1:R:136:ASP:HB3	1:R:173:ASP:OD1	0.42	2.14	2	1
1:R:80:LEU:N	1:R:80:LEU:HD12	0.42	2.29	1	1
1:R:70:TRP:HB3	1:R:82:ALA:HA	0.42	1.91	1	1
1:R:98:GLY:HA2	1:R:101:ALA:CB	0.42	2.44	1	1
1:R:53:LEU:HD11	1:R:82:ALA:HB3	0.42	1.92	4	2
1:R:31:LEU:HD22	1:R:167:PHE:CD1	0.42	2.49	5	1
1:R:69:ASP:O	1:R:72:TYR:CD1	0.42	2.72	5	1
1:R:66:PRO:HB2	1:R:68:PHE:CE1	0.42	2.49	2	1
1:R:133:CYS:O	1:R:135:ALA:N	0.42	2.52	5	2
1:R:155:THR:N	1:R:158:GLY:O	0.42	2.47	1	2
1:R:57:LEU:O	1:R:60:PHE:N	0.42	2.52	3	2
1:R:183:TYR:HD1	1:R:183:TYR:N	0.42	2.10	3	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:R:55:ALA:HB1	1:R:99:PRO:HA	0.42	1.91	4	1
1:R:53:LEU:CD2	1:R:57:LEU:CD2	0.42	2.98	4	1
1:R:58:GLN:NE2	1:R:141:ILE:HG12	0.42	2.29	4	1
1:R:60:PHE:N	1:R:60:PHE:CD1	0.42	2.86	4	1
1:R:62:TYR:HE2	1:R:181:VAL:CB	0.42	2.27	5	1
1:R:41:PHE:CD2	1:R:58:GLN:HB2	0.42	2.49	5	1
1:R:59:LEU:HG	1:R:141:ILE:CG1	0.42	2.44	5	1
1:R:53:LEU:CD2	1:R:68:PHE:CD2	0.42	3.02	5	1
1:R:76:GLU:O	1:R:78:LEU:HD13	0.42	2.13	2	1
1:R:151:PHE:CD1	1:R:151:PHE:N	0.42	2.88	1	1
1:R:159:TRP:CD1	1:R:172:PRO:HD3	0.42	2.50	1	1
1:R:127:VAL:HA	1:R:130:THR:OG1	0.42	2.14	3	1
1:R:55:ALA:CB	1:R:141:ILE:CD1	0.42	2.98	4	1
1:R:56:ILE:HG23	1:R:60:PHE:CD2	0.42	2.48	4	1
1:R:39:LYS:HB3	1:R:61:ARG:HD3	0.42	1.92	1	1
1:R:100:PRO:HA	1:R:104:ILE:HG12	0.42	1.92	3	1
1:R:141:ILE:O	1:R:177:VAL:CA	0.42	2.68	3	1
1:R:52:TRP:CD1	1:R:96:GLU:HA	0.42	2.50	4	1
1:R:115:ILE:HG23	1:R:124:VAL:CA	0.42	2.44	5	1
1:R:32:THR:HG22	1:R:38:LYS:HA	0.42	1.91	5	1
1:R:104:ILE:CB	1:R:111:LEU:HD12	0.42	2.44	2	1
1:R:141:ILE:C	1:R:177:VAL:HB	0.42	2.34	2	1
1:R:102:LEU:HD22	1:R:105:TRP:CG	0.42	2.49	1	1
1:R:142:PHE:CE1	1:R:177:VAL:CG1	0.42	2.99	1	1
1:R:55:ALA:HB2	1:R:99:PRO:HB3	0.42	1.89	1	1
1:R:136:ASP:O	1:R:137:PHE:CG	0.42	2.73	3	1
1:R:92:LEU:HG	1:R:93:GLU:N	0.42	2.29	3	1
1:R:56:ILE:HG13	1:R:68:PHE:CG	0.42	2.50	5	1
1:R:86:LEU:HG	1:R:103:VAL:CG1	0.42	2.44	5	1
1:R:94:LEU:O	1:R:97:GLY:N	0.42	2.52	5	1
1:R:127:VAL:CG2	1:R:128:ASP:N	0.42	2.82	2	1
1:R:56:ILE:HA	1:R:59:LEU:CB	0.42	2.44	2	1
1:R:143:LEU:CD2	1:R:143:LEU:N	0.42	2.82	1	1
1:R:58:GLN:CB	1:R:151:PHE:HB3	0.42	2.44	3	1
1:R:62:TYR:CE1	1:R:139:ALA:CB	0.42	3.02	3	1
1:R:116:GLY:O	1:R:125:CYS:SG	0.42	2.78	4	1
1:R:32:THR:HG22	1:R:38:LYS:CA	0.42	2.45	4	1
1:R:58:GLN:O	1:R:62:TYR:CG	0.42	2.73	4	1
1:R:127:VAL:O	1:R:130:THR:HB	0.42	2.15	2	1
1:R:34:TYR:HB2	1:R:154:VAL:HG12	0.42	1.90	2	1
1:R:42:TYR:CD2	1:R:42:TYR:N	0.42	2.88	2	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:R:83:ILE:CG2	1:R:94:LEU:CD1	0.42	2.95	1	1
1:R:84:LYS:O	1:R:87:GLU:HG2	0.42	2.14	1	1
1:R:127:VAL:C	1:R:130:THR:OG1	0.42	2.58	3	1
1:R:168:TYR:OH	1:R:170:TRP:CD1	0.42	2.72	3	1
1:R:69:ASP:HA	1:R:72:TYR:CE2	0.42	2.49	3	1
1:R:34:TYR:CB	1:R:154:VAL:CG1	0.42	2.97	3	1
1:R:140:GLY:HA3	1:R:180:PHE:HA	0.42	1.91	5	1
1:R:157:ASN:HB2	1:R:160:TYR:CZ	0.42	2.50	5	1
1:R:59:LEU:CD1	1:R:151:PHE:CE1	0.42	3.01	2	1
1:R:32:THR:OG1	1:R:155:THR:CB	0.42	2.68	2	1
1:R:31:LEU:CG	1:R:41:PHE:CD1	0.42	3.02	2	1
1:R:60:PHE:HB2	1:R:68:PHE:CG	0.42	2.50	1	1
1:R:52:TRP:CD1	1:R:97:GLY:HA2	0.42	2.49	1	1
1:R:134:LEU:CD2	1:R:173:ASP:CB	0.42	2.98	5	1
1:R:53:LEU:HD12	1:R:79:THR:HA	0.42	1.92	5	1
1:R:86:LEU:CD1	1:R:103:VAL:CG1	0.41	2.92	2	1
1:R:137:PHE:C	1:R:138:HIS:CG	0.41	2.87	2	1
1:R:134:LEU:CD1	1:R:172:PRO:CD	0.41	2.84	2	1
1:R:39:LYS:HG2	1:R:60:PHE:CZ	0.41	2.50	1	1
1:R:39:LYS:O	1:R:41:PHE:CD1	0.41	2.73	4	2
1:R:59:LEU:HD13	1:R:151:PHE:CD2	0.41	2.48	3	1
1:R:60:PHE:CD1	1:R:65:GLU:CB	0.41	3.03	3	1
1:R:42:TYR:CE1	1:R:75:PRO:O	0.41	2.73	3	1
1:R:47:ASN:O	1:R:48:HIS:CB	0.41	2.67	5	1
1:R:137:PHE:CD1	1:R:180:PHE:HB2	0.41	2.50	2	1
1:R:35:ASN:HB3	1:R:153:CYS:CB	0.41	2.45	2	1
1:R:89:LEU:HD23	1:R:90:THR:HG23	0.41	1.91	1	1
1:R:94:LEU:HD12	1:R:95:HIS:N	0.41	2.29	1	1
1:R:144:LYS:O	1:R:148:HIS:CB	0.41	2.68	3	1
1:R:44:ARG:HB3	1:R:164:ASP:C	0.41	2.35	5	1
1:R:136:ASP:C	1:R:183:TYR:CZ	0.41	2.93	2	1
1:R:53:LEU:CD2	1:R:83:ILE:CG1	0.41	2.98	1	2
1:R:99:PRO:HB2	1:R:100:PRO:HD3	0.41	1.92	1	2
1:R:118:ALA:HA	1:R:130:THR:CG2	0.41	2.45	3	1
1:R:60:PHE:CZ	1:R:72:TYR:CG	0.41	3.07	3	1
1:R:126:VAL:C	1:R:127:VAL:CG2	0.41	2.89	4	1
1:R:101:ALA:O	1:R:104:ILE:CG1	0.41	2.67	2	1
1:R:63:VAL:HG21	1:R:124:VAL:HG11	0.41	1.89	2	1
1:R:53:LEU:HD13	1:R:79:THR:HA	0.41	1.93	1	1
1:R:55:ALA:CB	1:R:99:PRO:HB3	0.41	2.46	4	2
1:R:102:LEU:HD12	1:R:102:LEU:H	0.41	1.73	3	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:R:127:VAL:CA	1:R:130:THR:OG1	0.41	2.68	3	1
1:R:33:LEU:CD2	1:R:35:ASN:OD1	0.41	2.67	3	1
1:R:41:PHE:CG	1:R:162:ILE:HD12	0.41	2.50	4	1
1:R:41:PHE:HA	1:R:72:TYR:CE1	0.41	2.51	4	1
1:R:163:ASP:O	1:R:166:ASP:N	0.41	2.43	2	1
1:R:33:LEU:HD12	1:R:61:ARG:NH1	0.41	2.30	1	1
1:R:64:GLU:O	1:R:66:PRO:CD	0.41	2.69	3	1
1:R:76:GLU:O	1:R:78:LEU:N	0.41	2.54	3	1
1:R:94:LEU:O	1:R:96:GLU:N	0.41	2.53	4	1
1:R:58:GLN:CG	1:R:151:PHE:HB2	0.41	2.46	5	1
1:R:55:ALA:CB	1:R:99:PRO:HG3	0.41	2.45	5	1
1:R:67:PHE:C	1:R:69:ASP:H	0.41	2.18	2	2
1:R:61:ARG:HD3	1:R:68:PHE:CZ	0.41	2.50	2	1
1:R:83:ILE:O	1:R:84:LYS:C	0.41	2.58	3	4
1:R:134:LEU:HD12	1:R:159:TRP:CD2	0.41	2.51	1	1
1:R:125:CYS:HB2	1:R:182:PRO:HD3	0.41	1.93	1	1
1:R:60:PHE:HB2	1:R:65:GLU:HA	0.41	1.93	1	1
1:R:102:LEU:HA	1:R:105:TRP:HB2	0.41	1.91	4	3
1:R:139:ALA:CB	1:R:181:VAL:HG12	0.41	2.36	4	1
1:R:39:LYS:HG2	1:R:61:ARG:CA	0.41	2.46	5	1
1:R:111:LEU:HD12	1:R:112:HIS:N	0.41	2.31	2	1
1:R:142:PHE:CE2	1:R:173:ASP:O	0.41	2.74	2	2
1:R:54:ASN:OD1	1:R:58:GLN:CG	0.41	2.69	1	1
1:R:84:LYS:O	1:R:87:GLU:CG	0.41	2.69	1	1
1:R:142:PHE:CD2	1:R:171:THR:OG1	0.41	2.73	3	1
1:R:150:VAL:HG12	1:R:163:ASP:CG	0.41	2.35	3	1
1:R:46:ASN:ND2	1:R:76:GLU:O	0.41	2.54	3	1
1:R:39:LYS:HB3	1:R:61:ARG:HD2	0.41	1.93	3	1
1:R:137:PHE:O	1:R:138:HIS:CD2	0.41	2.73	4	1
1:R:44:ARG:CB	1:R:45:PRO:HD2	0.41	2.46	4	1
1:R:57:LEU:HD13	1:R:68:PHE:CD2	0.41	2.50	4	1
1:R:70:TRP:CZ3	1:R:81:GLU:OE2	0.41	2.74	4	1
1:R:115:ILE:CB	1:R:122:SER:C	0.41	2.89	5	1
1:R:35:ASN:O	1:R:62:TYR:O	0.41	2.38	5	1
1:R:97:GLY:O	1:R:98:GLY:O	0.41	2.39	2	1
1:R:138:HIS:HB3	1:R:154:VAL:CG2	0.41	2.46	1	1
1:R:57:LEU:O	1:R:60:PHE:CB	0.41	2.68	1	1
1:R:44:ARG:H	1:R:165:GLU:CB	0.41	2.26	5	1
1:R:36:GLY:HA3	1:R:62:TYR:HA	0.41	1.92	5	1
1:R:117:THR:N	1:R:120:ARG:O	0.41	2.54	5	1
1:R:56:ILE:CG2	1:R:100:PRO:O	0.41	2.68	2	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:R:62:TYR:HE2	1:R:181:VAL:CG2	0.41	2.29	2	1
1:R:56:ILE:CA	1:R:59:LEU:HB2	0.41	2.46	2	1
1:R:177:VAL:O	1:R:178:LEU:CD2	0.41	2.69	2	1
1:R:67:PHE:C	1:R:69:ASP:N	0.41	2.74	1	1
1:R:168:TYR:CE1	1:R:170:TRP:CB	0.41	3.04	3	1
1:R:93:GLU:O	1:R:94:LEU:HD13	0.41	2.16	3	1
1:R:48:HIS:O	1:R:49:ASP:O	0.41	2.39	3	1
1:R:56:ILE:HD12	1:R:103:VAL:CG1	0.41	2.42	3	1
1:R:40:THR:HG23	1:R:40:THR:O	0.41	2.15	3	1
1:R:107:ILE:HG22	1:R:111:LEU:HB2	0.41	1.93	4	1
1:R:138:HIS:CB	1:R:172:PRO:HG2	0.41	2.46	4	1
1:R:155:THR:HG1	1:R:160:TYR:CB	0.41	2.29	4	1
1:R:90:THR:HB	1:R:92:LEU:CD2	0.41	2.45	5	1
1:R:127:VAL:HG13	1:R:180:PHE:HD2	0.41	1.76	5	1
1:R:69:ASP:HA	1:R:72:TYR:CE1	0.41	2.51	5	1
1:R:54:ASN:ND2	1:R:55:ALA:N	0.41	2.69	2	1
1:R:61:ARG:CD	1:R:68:PHE:CE2	0.41	3.03	2	1
1:R:102:LEU:CD1	1:R:102:LEU:N	0.41	2.83	3	1
1:R:117:THR:HG22	1:R:118:ALA:H	0.41	1.76	3	1
1:R:173:ASP:O	1:R:177:VAL:HG13	0.41	2.13	4	1
1:R:33:LEU:H	1:R:33:LEU:HD13	0.41	1.68	4	1
1:R:42:TYR:CD2	1:R:71:VAL:CG1	0.41	3.04	4	1
1:R:115:ILE:HG21	1:R:123:GLU:N	0.41	2.31	5	1
1:R:179:VAL:O	1:R:179:VAL:HG23	0.41	2.15	5	1
1:R:55:ALA:CB	1:R:99:PRO:CB	0.40	2.99	1	1
1:R:51:ALA:CA	1:R:164:ASP:OD2	0.40	2.69	3	1
1:R:44:ARG:HB3	1:R:164:ASP:O	0.40	2.16	5	1
1:R:83:ILE:HD13	1:R:95:HIS:HB3	0.40	1.92	5	1
1:R:60:PHE:CB	1:R:66:PRO:HD2	0.40	2.46	1	1
1:R:71:VAL:O	1:R:77:ASN:O	0.40	2.39	3	1
1:R:78:LEU:HD12	1:R:81:GLU:HB2	0.40	1.93	3	1
1:R:86:LEU:CD1	1:R:90:THR:OG1	0.40	2.64	3	1
1:R:92:LEU:HG	1:R:94:LEU:CD2	0.40	2.46	3	1
1:R:38:LYS:O	1:R:38:LYS:CG	0.40	2.69	3	1
1:R:38:LYS:C	1:R:39:LYS:HG2	0.40	2.37	4	1
1:R:43:SER:OG	1:R:54:ASN:CG	0.40	2.60	4	1
1:R:68:PHE:CZ	1:R:103:VAL:CG1	0.40	3.04	5	1
1:R:145:GLY:O	1:R:146:GLN:O	0.40	2.40	5	1
1:R:58:GLN:HB3	1:R:151:PHE:CD2	0.40	2.52	2	1
1:R:157:ASN:HB3	1:R:160:TYR:CZ	0.40	2.51	1	1
1:R:154:VAL:HG22	1:R:159:TRP:CD1	0.40	2.52	1	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:R:100:PRO:HA	1:R:104:ILE:CG1	0.40	2.46	3	1
1:R:137:PHE:CZ	1:R:159:TRP:NE1	0.40	2.89	3	1
1:R:168:TYR:C	1:R:168:TYR:CD1	0.40	2.94	3	1
1:R:62:TYR:CB	1:R:181:VAL:HG21	0.40	2.35	4	1
1:R:68:PHE:O	1:R:71:VAL:N	0.40	2.49	4	1
1:R:99:PRO:C	1:R:101:ALA:N	0.40	2.75	4	1
1:R:69:ASP:O	1:R:73:SER:OG	0.40	2.39	4	1
1:R:178:LEU:HD13	1:R:178:LEU:HA	0.40	1.74	5	1
1:R:67:PHE:HB2	1:R:68:PHE:CD1	0.40	2.51	5	1
1:R:56:ILE:HB	1:R:68:PHE:CE1	0.40	2.52	5	1
1:R:76:GLU:CG	1:R:78:LEU:HD23	0.40	2.47	5	1
1:R:137:PHE:CE1	1:R:180:PHE:CB	0.40	2.97	2	1
1:R:142:PHE:CD1	1:R:177:VAL:CG1	0.40	3.04	2	1
1:R:51:ALA:HB1	1:R:149:ALA:CB	0.40	2.46	2	1
1:R:53:LEU:C	1:R:57:LEU:HB2	0.40	2.37	2	1
1:R:116:GLY:N	1:R:122:SER:HB2	0.40	2.31	2	1
1:R:60:PHE:CG	1:R:68:PHE:CD2	0.40	3.09	1	1
1:R:86:LEU:HD11	1:R:103:VAL:HA	0.40	1.93	3	1
1:R:59:LEU:CD2	1:R:141:ILE:HG12	0.40	2.46	5	1
1:R:58:GLN:CG	1:R:151:PHE:CB	0.40	2.99	5	1
1:R:33:LEU:CA	1:R:155:THR:HA	0.40	2.45	5	1
1:R:160:TYR:CD2	1:R:168:TYR:C	0.40	2.95	5	1
1:R:92:LEU:O	1:R:93:GLU:CB	0.40	2.69	5	1
1:R:53:LEU:CD2	1:R:83:ILE:HG12	0.40	2.47	2	1
1:R:59:LEU:CD1	1:R:59:LEU:N	0.40	2.83	1	1
1:R:47:ASN:OD1	1:R:80:LEU:CD2	0.40	2.70	1	1
1:R:94:LEU:H	1:R:94:LEU:HD12	0.40	1.76	1	1
1:R:160:TYR:CZ	1:R:169:PRO:HB3	0.40	2.51	4	1
1:R:59:LEU:HD21	1:R:179:VAL:CG2	0.40	2.46	4	1
1:R:52:TRP:CG	1:R:97:GLY:CA	0.40	3.05	4	1
1:R:155:THR:HG23	1:R:160:TYR:HB2	0.40	1.91	5	1
1:R:139:ALA:O	1:R:180:PHE:HA	0.40	2.17	5	1

6.3 Torsion angles

6.3.1 Protein backbone

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	R	155/167 (93%)	109±3 (70±2%)	29±2 (19±2%)	18±3 (11±2%)	1 8
All	All	775/835 (93%)	543 (70%)	144 (19%)	88 (11%)	1 8

All 48 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	R	99	PRO	4
1	R	49	ASP	4
1	R	101	ALA	4
1	R	93	GLU	4
1	R	102	LEU	4
1	R	164	ASP	3
1	R	159	TRP	3
1	R	37	GLU	3
1	R	112	HIS	3
1	R	128	ASP	3
1	R	43	SER	3
1	R	64	GLU	3
1	R	126	VAL	2
1	R	67	PHE	2
1	R	98	GLY	2
1	R	68	PHE	2
1	R	77	ASN	2
1	R	179	VAL	2
1	R	34	TYR	2
1	R	111	LEU	2
1	R	48	HIS	2
1	R	127	VAL	2
1	R	134	LEU	2
1	R	147	GLU	1
1	R	183	TYR	1
1	R	125	CYS	1
1	R	131	ASP	1
1	R	120	ARG	1
1	R	46	ASN	1
1	R	138	HIS	1
1	R	71	VAL	1
1	R	146	GLN	1
1	R	44	ARG	1
1	R	139	ALA	1
1	R	171	THR	1
1	R	165	GLU	1

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Mol	Chain	Res	Type	Models (Total)
1	R	45	PRO	1
1	R	135	ALA	1
1	R	33	LEU	1
1	R	94	LEU	1
1	R	136	ASP	1
1	R	113	THR	1
1	R	36	GLY	1
1	R	154	VAL	1
1	R	124	VAL	1
1	R	78	LEU	1
1	R	172	PRO	1
1	R	122	SER	1

6.3.2 Protein sidechains (i)

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	R	136/145 (94%)	107±4 (78±3%)	29±4 (22±3%)	4	32
All	All	680/725 (94%)	533 (78%)	147 (22%)	4	32

All 64 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	R	181	VAL	5
1	R	92	LEU	5
1	R	33	LEU	5
1	R	110	LEU	5
1	R	83	ILE	5
1	R	170	TRP	5
1	R	134	LEU	5
1	R	177	VAL	4
1	R	56	ILE	4
1	R	80	LEU	4
1	R	159	TRP	4
1	R	111	LEU	4
1	R	40	THR	4

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Mol	Chain	Res	Type	Models (Total)
1	R	47	ASN	4
1	R	120	ARG	3
1	R	74	SER	3
1	R	44	ARG	3
1	R	171	THR	3
1	R	94	LEU	3
1	R	60	PHE	3
1	R	178	LEU	3
1	R	162	ILE	2
1	R	138	HIS	2
1	R	173	ASP	2
1	R	142	PHE	2
1	R	61	ARG	2
1	R	54	ASN	2
1	R	107	ILE	2
1	R	43	SER	2
1	R	68	PHE	2
1	R	148	HIS	2
1	R	41	PHE	2
1	R	179	VAL	2
1	R	137	PHE	2
1	R	95	HIS	2
1	R	160	TYR	2
1	R	58	GLN	2
1	R	124	VAL	2
1	R	163	ASP	2
1	R	79	THR	2
1	R	122	SER	2
1	R	117	THR	1
1	R	183	TYR	1
1	R	125	CYS	1
1	R	46	ASN	1
1	R	133	CYS	1
1	R	89	LEU	1
1	R	65	GLU	1
1	R	62	TYR	1
1	R	31	LEU	1
1	R	32	THR	1
1	R	153	CYS	1
1	R	180	PHE	1
1	R	130	THR	1
1	R	136	ASP	1

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Mol	Chain	Res	Type	Models (Total)
1	R	141	ILE	1
1	R	48	HIS	1
1	R	165	GLU	1
1	R	109	HIS	1
1	R	50	ASN	1
1	R	59	LEU	1
1	R	78	LEU	1
1	R	151	PHE	1
1	R	72	TYR	1

6.3.3 RNA

There are no RNA molecules in this entry.

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

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

6.5 Carbohydrates

There are no carbohydrates in this entry.

6.6 Ligand geometry

There are no ligands in this entry.

6.7 Other polymers

There are no such molecules in this entry.

6.8 Polymer linkage issues

There are no chain breaks in this entry.

7 Chemical shift validation

The completeness of assignment taking into account all chemical shift lists is 38% for the well-defined parts and 38% for the entire structure.

7.1 Chemical shift list 1

File name: BMRB entry 15278

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	774
Number of shifts mapped to atoms	774
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	1

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	162	-0.27 ± 0.17	None needed (< 0.5 ppm)
$^{13}C_{\beta}$	151	0.18 ± 0.17	None needed (< 0.5 ppm)
$^{13}C'$	161	0.08 ± 0.11	None needed (< 0.5 ppm)
^{15}N	150	0.66 ± 0.25	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 38%, i.e. 722 atoms were assigned a chemical shift out of a possible 1891. 0 out of 28 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	581/760 (76%)	140/302 (46%)	301/312 (96%)	140/146 (96%)
Sidechain	141/892 (16%)	0/520 (0%)	141/347 (41%)	0/25 (0%)

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	Total	^{1}H	^{13}C	^{15}N
Aromatic	0/239 (0%)	0/127 (0%)	0/101 (0%)	0/11 (0%)
Overall	722/1891 (38%)	140/949 (15%)	442/760 (58%)	140/182 (77%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 38%, i.e. 774 atoms were assigned a chemical shift out of a possible 2036. 0 out of 29 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	623/813 (77%)	150/323 (46%)	323/334 (97%)	150/156 (96%)
Sidechain	151/972 (16%)	0/568 (0%)	151/375 (40%)	0/29 (0%)
Aromatic	0/251 (0%)	0/133 (0%)	0/106 (0%)	0/12 (0%)
Overall	774/2036 (38%)	150/1024 (15%)	474/815 (58%)	150/197 (76%)

7.1.4 Statistically unusual chemical shifts (i)

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

Mol	Chain	Res	Type	Atom	Shift, *ppm*	Expected range, *ppm*	Z-score
???	R	155	THR	CB	15.33	78.10 – 61.30	-32.4

7.1.5 Random Coil Index (RCI) plots (i)

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

Random coil index (RCI) for chain R: