Full wwPDB NMR Structure Validation Report

Feb 12, 2022 – 03:55 PM EST

PDB ID	:	1FJE
Title	:	SOLUTION STRUCTURE OF NUCLEOLIN RBD12 IN COMPLEX WITH SNRE RNA
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Deposited on	:	2000-08-08

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/NMRValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

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

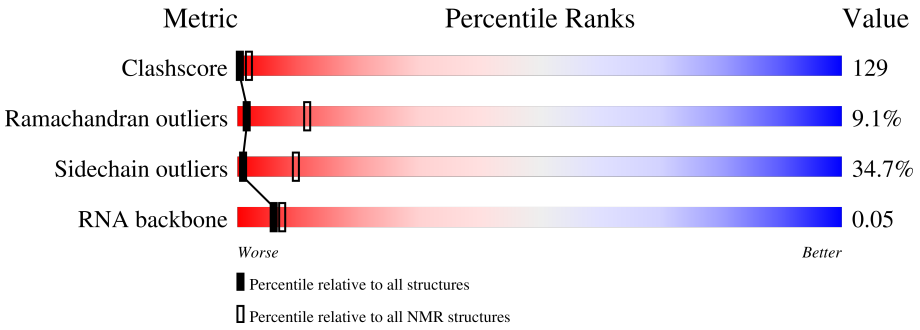
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	2.26
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.26

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 was not calculated.

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
RNA backbone	4643	676

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	22	5% 41% 55%
2	B	175	7% 58% 24% • 10%

2 Ensemble composition and analysis

This entry contains 19 models. Model 10 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	B:10-B:130, B:136-B:172 (158)	0.84	10

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

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

The models can be grouped into 4 clusters and 3 single-model clusters were found.

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

3 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 3444 atoms, of which 1611 are hydrogens and 0 are deuteriums.

- Molecule 1 is a RNA chain called SNRE RNA.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	P	
1	A	22	712	211	242	90	148	21	0

- Molecule 2 is a protein called NUCLEOLIN RBD12.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
2	B	175	2732	856	1369	229	277	1	0

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	1	GLY	LYS	conflict	UNP P08199
B	2	SER	LYS	conflict	UNP P08199
B	3	HIS	GLN	conflict	UNP P08199
B	4	MET	LYS	conflict	UNP P08199
B	37	LEU	PRO	conflict	UNP P08199

4 Residue-property plots

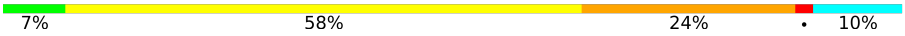
4.1 Average score per residue in the NMR ensemble

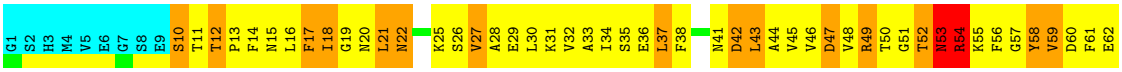
These plots are provided for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outliers are shown as green connectors. Residues which are classified as ill-defined in the NMR ensemble, are shown in cyan with an underline colour-coded according to the previous scheme. Residues which were present in the experimental sample, but not modelled in the final structure are shown in grey.

• Molecule 1: SNRE RNA

Chain A: 

• Molecule 2: NUCLEOLIN RBD12

Chain B: 



4.2 Scores per residue for each member of the ensemble

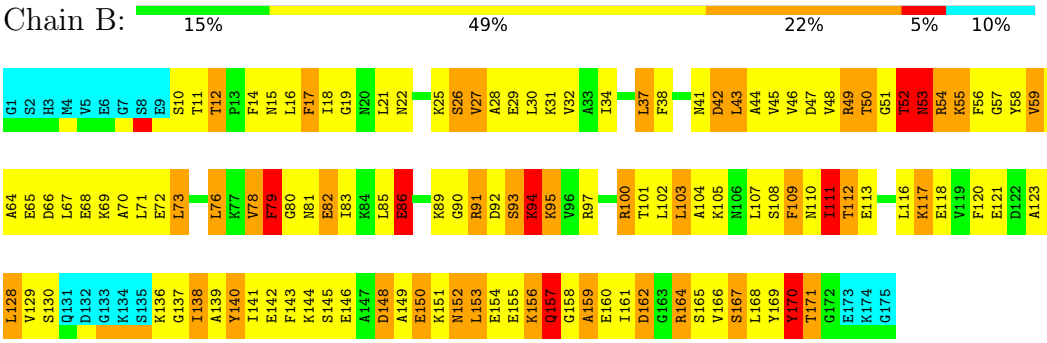
Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

• Molecule 1: SNRE RNA

Chain A: 

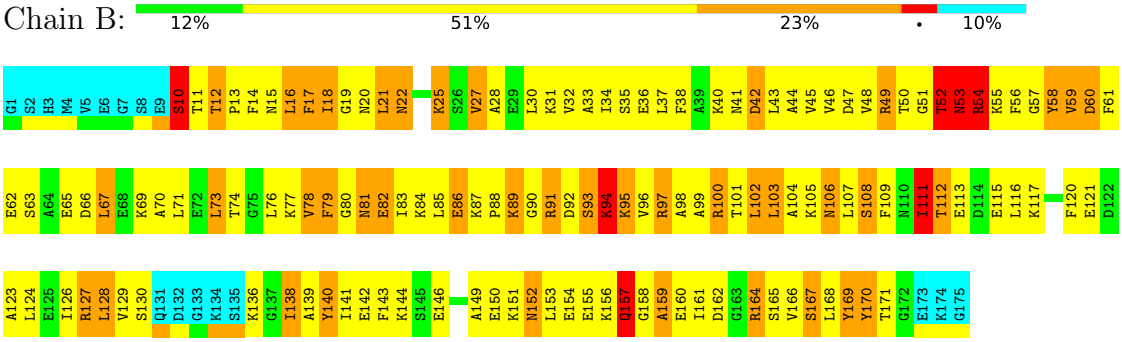
• Molecule 2: NUCLEOLIN RBD12



4.2.2 Score per residue for model 2

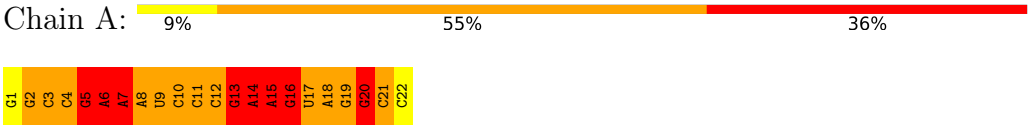
• Molecule 1: SNRE RNA

• Molecule 2: NUCLEOLIN RBD12

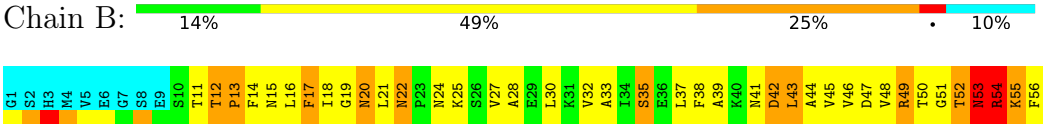


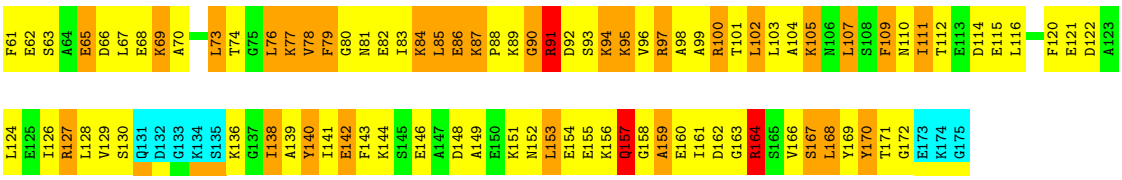
4.2.3 Score per residue for model 3

• Molecule 1: SNRE RNA



• Molecule 2: NUCLEOLIN RBD12





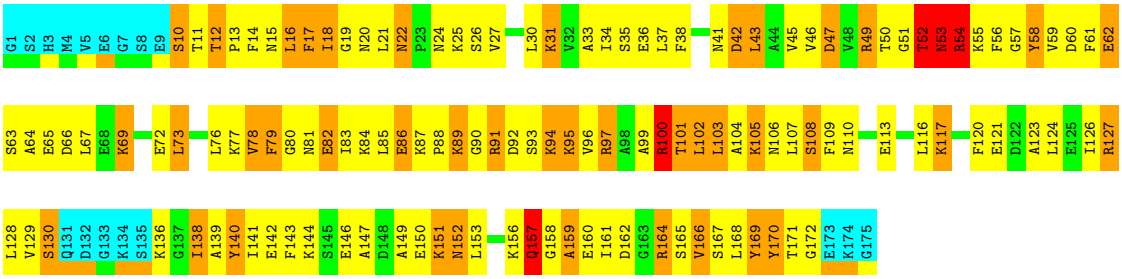
4.2.4 Score per residue for model 4

• Molecule 1: SNRE RNA

Chain A: 50% 50%

• Molecule 2: NUCLEOLIN RBD12

Chain B: 16% 48% 23% 10%



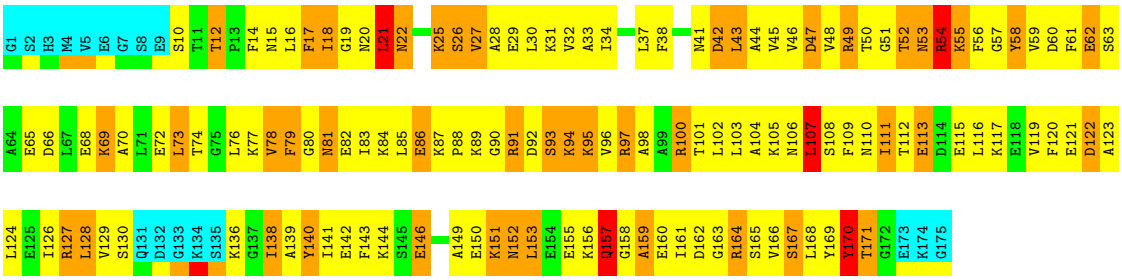
4.2.5 Score per residue for model 5

• Molecule 1: SNRE RNA

Chain A: 5% 50% 45%

• Molecule 2: NUCLEOLIN RBD12

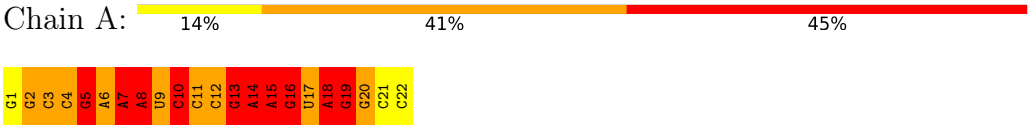
Chain B: 13% 50% 25% 10%



4.2.6 Score per residue for model 6

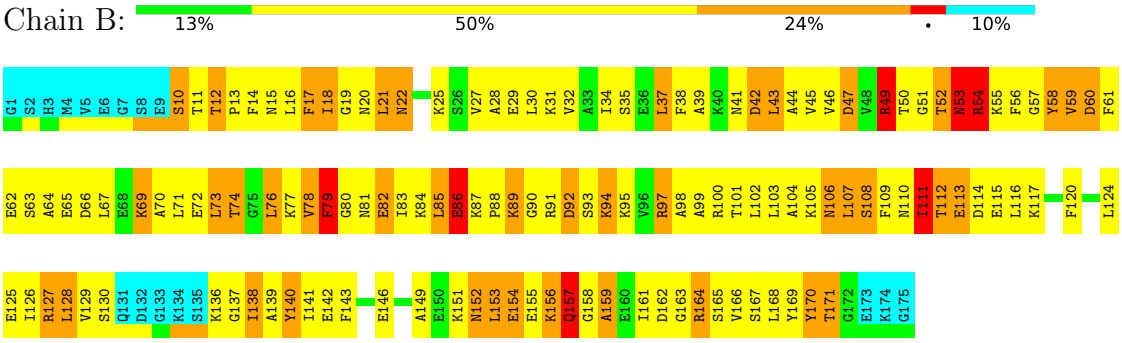
• Molecule 1: SNRE RNA

Chain A:



• Molecule 2: NUCLEOLIN RBD12

Chain B:



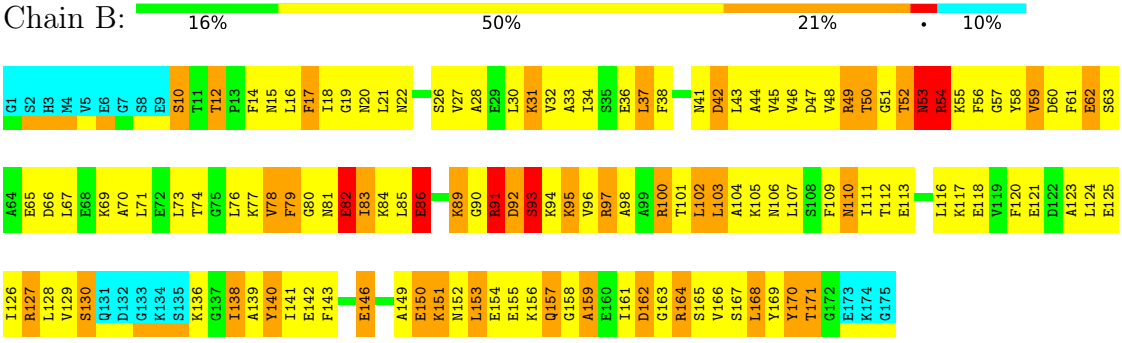
4.2.7 Score per residue for model 7

• Molecule 1: SNRE RNA

Chain A:

• Molecule 2: NUCLEOLIN RBD12

Chain B:



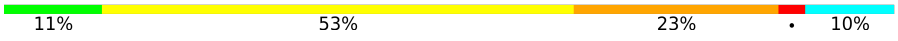
4.2.8 Score per residue for model 8

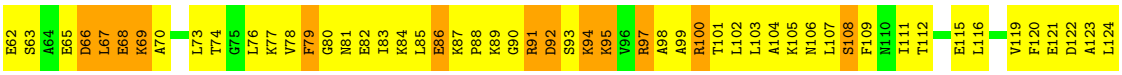
• Molecule 1: SNRE RNA

Chain A:

• Molecule 2: NUCLEOLIN RBD12

Chain B:





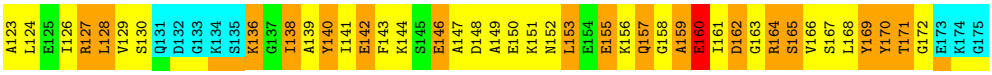
4.2.9 Score per residue for model 9

• Molecule 1: SNRE RNA

Chain A:

• Molecule 2: NUCLEOLIN RBD12

Chain B:



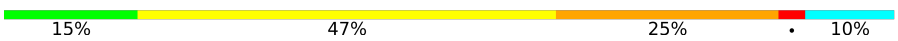
4.2.10 Score per residue for model 10 (medoid)

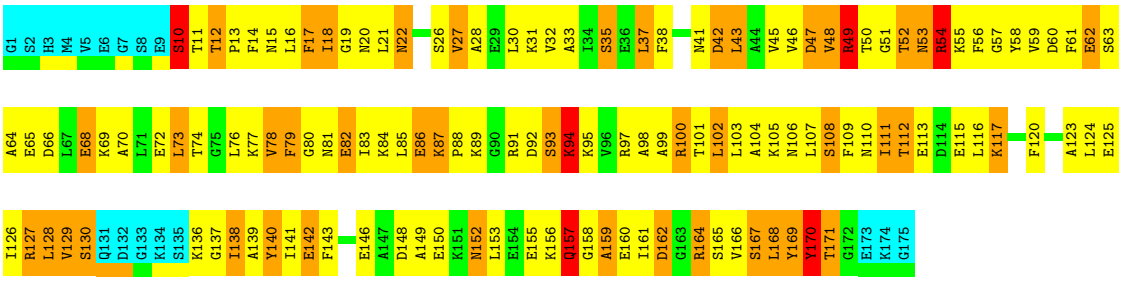
• Molecule 1: SNRE RNA

Chain A:

• Molecule 2: NUCLEOLIN RBD12

Chain B:





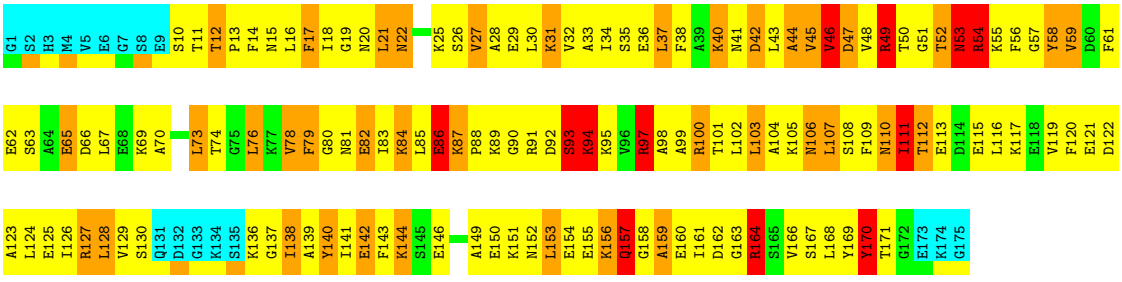
4.2.11 Score per residue for model 11

• Molecule 1: SNRE RNA

Chain A:

• Molecule 2: NUCLEOLIN RBD12

Chain B:



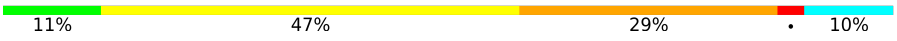
4.2.12 Score per residue for model 12

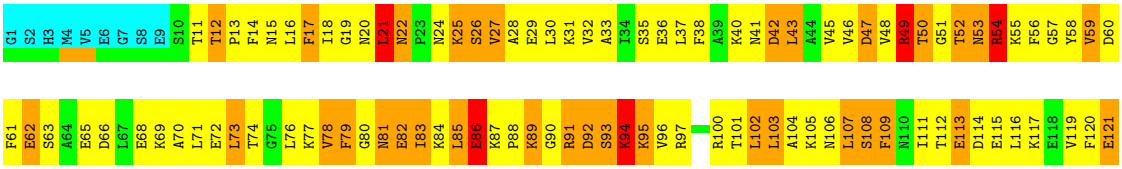
• Molecule 1: SNRE RNA

Chain A:

• Molecule 2: NUCLEOLIN RBD12

Chain B:





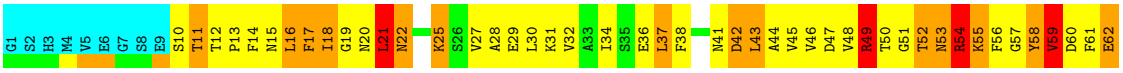
4.2.13 Score per residue for model 13

• Molecule 1: SNRE RNA

Chain A:

• Molecule 2: NUCLEOLIN RBD12

Chain B:



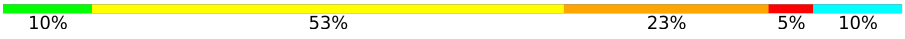
4.2.14 Score per residue for model 14

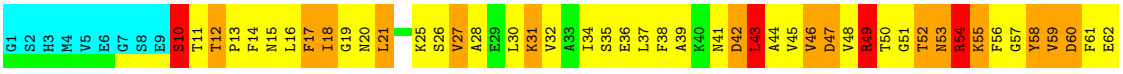
• Molecule 1: SNRE RNA

Chain A:

• Molecule 2: NUCLEOLIN RBD12

Chain B:





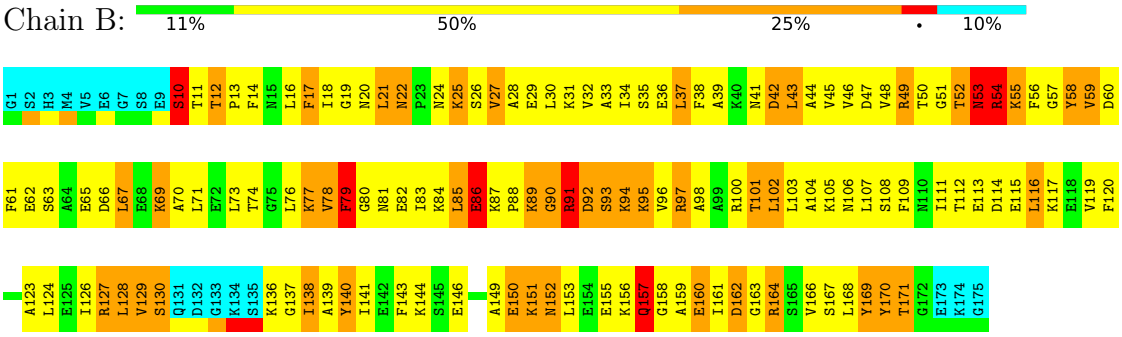
4.2.15 Score per residue for model 15

• Molecule 1: SNRE RNA

Chain A:

• Molecule 2: NUCLEOLIN RBD12

Chain B:



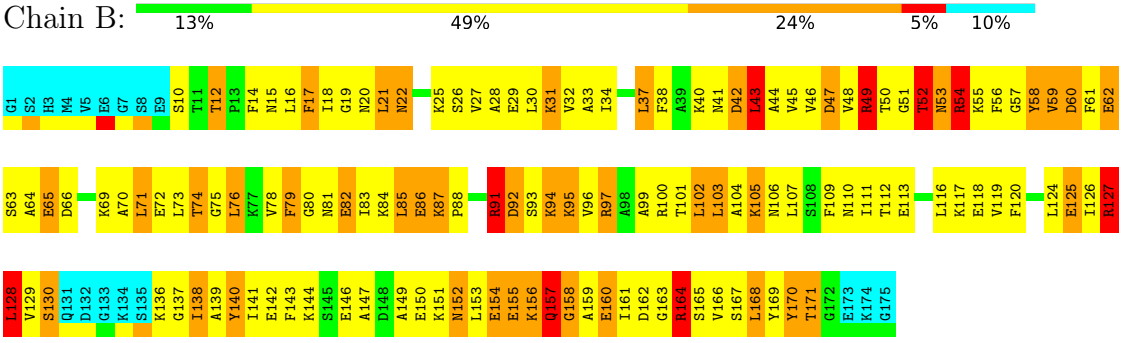
4.2.16 Score per residue for model 16

• Molecule 1: SNRE RNA

Chain A:

• Molecule 2: NUCLEOLIN RBD12

Chain B:



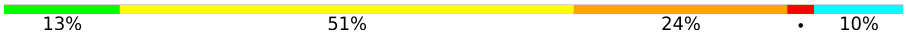
4.2.17 Score per residue for model 17

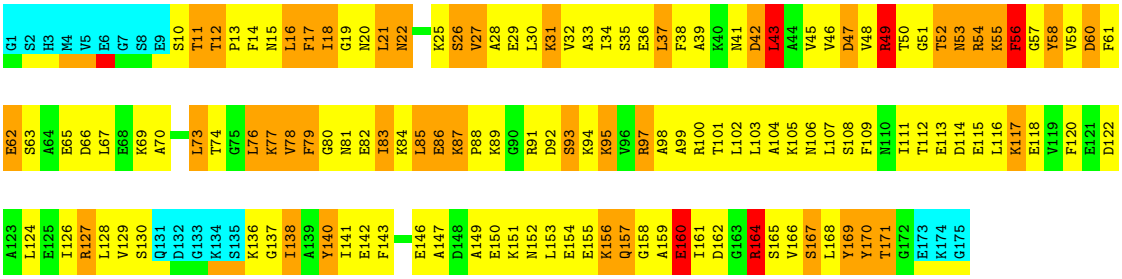
• Molecule 1: SNRE RNA

Chain A:

• Molecule 2: NUCLEOLIN RBD12

Chain B:





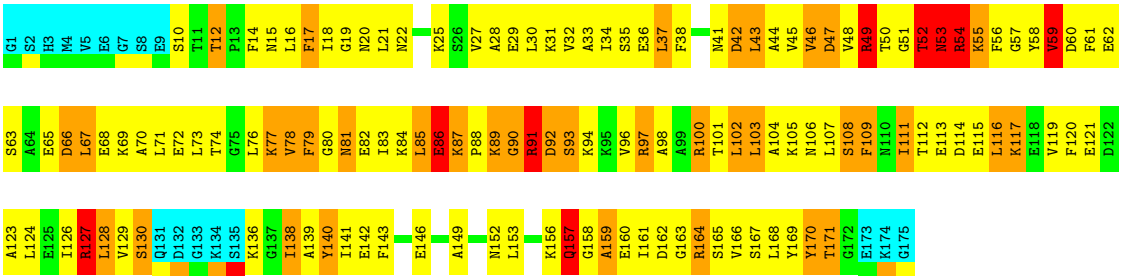
4.2.18 Score per residue for model 18

• Molecule 1: SNRE RNA

Chain A:

• Molecule 2: NUCLEOLIN RBD12

Chain B:



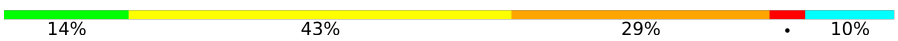
4.2.19 Score per residue for model 19

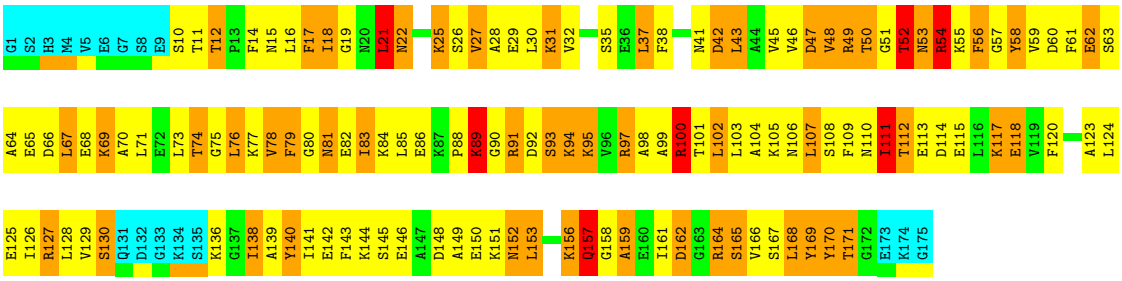
• Molecule 1: SNRE RNA

Chain A:

• Molecule 2: NUCLEOLIN RBD12

Chain B:




G1 S2 H3 M4 V5 E6 G7 S8 E9 S10 T11 T12 P13 F14 N15 L16 F17 I18 G19 N20 L21 N22 K25 S26 V27 A28 E29 L30 K31 V32 S35 E36 L37 F38 N41 D42 L43 A44 V45 V46 D47 V48 R49 T50 G51 T52 N53 R54 K55 F56 G57 Y58 V59 D60 F61 E62 S63
A64 E65 D66 L67 E68 K69 A70 L71 E72 L73 T74 G75 L76 K77 V78 F79 G80 N81 E82 I83 K84 L85 E86 K87 P88 K89 G90 R91 D92 S93 K94 K95 V96 R97 A98 A99 R100 T101 L102 L103 A104 K105 N106 L107 S108 F109 N110 I111 T112 E113 D114 E115 L116 K117 E118 V119 F120 A123 L124
E125 I126 R127 L128 V129 S130 Q131 D132 G133 K134 S135 K136 G137 I138 A139 Y140 I141 E142 F143 K144 S145 E146 A147 D148 A149 E150 K151 N152 L153 K156 Q157 G158 A159 E160 I161 D162 G163 R164 S165 V166 S167 L168 Y169 Y170 T171 G172 E173 K174 G175

5 Refinement protocol and experimental data overview

The models were refined using the following method: *simulated annealing using XPLOR 3.841.*

Of the 40 calculated structures, 19 were deposited, based on the following criterion: *all calculated structures submitted.*

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

Software name	Classification	Version
X-PLOR	refinement	3.841
X-PLOR	structure solution	3.841

No chemical shift data was provided.

6 Model quality (i)

6.1 Standard geometry (i)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#Z>5	RMSZ	#Z>5
1	A	1.21±0.01	0±1/526 (0.1± 0.1%)	2.10±0.01	32±2/819 (3.9± 0.2%)
2	B	1.05±0.01	0±0/1257 (0.0± 0.0%)	1.25±0.01	0±0/1690 (0.0± 0.0%)
All	All	1.10	9/33877 (0.0%)	1.58	614/47671 (1.3%)

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

Mol	Chain	Chirality	Planarity
1	A	0.0±0.0	0.1±0.2
2	B	0.0±0.0	6.8±0.4
All	All	0	131

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
1	A	11	C	N1-C6	-5.76	1.33	1.37	14	1
1	A	10	C	N1-C6	-5.50	1.33	1.37	16	4
1	A	12	C	N1-C6	-5.41	1.33	1.37	18	1
1	A	13	G	N9-C8	-5.28	1.34	1.37	17	3

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	A	13	G	N7-C8-N9	10.33	118.26	113.10	14	19
1	A	5	G	N7-C8-N9	9.73	117.96	113.10	11	19
1	A	20	G	N7-C8-N9	9.51	117.86	113.10	4	19
1	A	1	G	N7-C8-N9	9.39	117.80	113.10	12	19

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})	Models	
								Worst	Total
1	A	16	G	N7-C8-N9	9.36	117.78	113.10	15	19
1	A	19	G	N7-C8-N9	9.32	117.76	113.10	8	19
1	A	2	G	N7-C8-N9	9.28	117.74	113.10	6	19
1	A	15	A	N7-C8-N9	8.44	118.02	113.80	7	19
1	A	8	A	N7-C8-N9	8.15	117.87	113.80	11	19
1	A	7	A	N7-C8-N9	7.97	117.79	113.80	7	19
1	A	16	G	C8-N9-C4	-7.96	103.21	106.40	9	19
1	A	6	A	N7-C8-N9	7.63	117.61	113.80	18	19
1	A	18	A	N7-C8-N9	7.59	117.59	113.80	2	19
1	A	14	A	N7-C8-N9	7.55	117.58	113.80	13	19
1	A	5	G	C8-N9-C4	-7.55	103.38	106.40	8	19
1	A	20	G	C8-N9-C4	-7.26	103.50	106.40	4	19
1	A	1	G	C8-N9-C4	-7.26	103.50	106.40	12	19
1	A	13	G	C8-N9-C4	-7.22	103.51	106.40	5	19
1	A	19	G	C8-N9-C4	-7.02	103.59	106.40	17	19
1	A	2	G	C8-N9-C4	-6.75	103.70	106.40	2	19
2	B	56	PHE	N-CA-CB	-6.12	99.58	110.60	17	1
1	A	13	G	O4'-C1'-N9	5.95	112.96	108.20	11	8
1	A	20	G	O4'-C1'-N9	5.87	112.90	108.20	9	2
1	A	8	A	C5-N7-C8	-5.84	100.98	103.90	17	13
1	A	8	A	C8-N9-C4	-5.83	103.47	105.80	11	19
1	A	18	A	C8-N9-C4	-5.81	103.47	105.80	11	19
1	A	21	C	O4'-C1'-N1	5.78	112.82	108.20	11	3
1	A	7	A	C8-N9-C4	-5.69	103.52	105.80	10	17
1	A	15	A	C5-N7-C8	-5.69	101.06	103.90	17	18
1	A	6	A	C8-N9-C4	-5.67	103.53	105.80	12	19
1	A	16	G	O4'-C1'-N9	5.62	112.69	108.20	13	2
1	A	10	C	C6-N1-C2	5.59	122.54	120.30	16	2
1	A	19	G	C5-N7-C8	-5.57	101.52	104.30	12	15
1	A	13	G	C5-N7-C8	-5.45	101.58	104.30	17	10
1	A	15	A	O4'-C1'-N9	5.44	112.55	108.20	13	4
1	A	14	A	C8-N9-C4	-5.37	103.65	105.80	6	5
2	B	10	SER	N-CA-CB	-5.33	102.50	110.50	15	1
1	A	9	U	O4'-C1'-N1	5.27	112.42	108.20	1	1
1	A	20	G	C5-N7-C8	-5.26	101.67	104.30	18	16
1	A	2	G	C5-N7-C8	-5.24	101.68	104.30	3	17
1	A	5	G	C5-N7-C8	-5.24	101.68	104.30	7	12
1	A	15	A	C8-N9-C4	-5.19	103.72	105.80	12	2
1	A	14	A	C5-N7-C8	-5.18	101.31	103.90	8	8
1	A	1	G	C5-N7-C8	-5.15	101.72	104.30	17	15
1	A	7	A	O4'-C1'-N9	5.09	112.27	108.20	17	1

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})	Models	
								Worst	Total
1	A	14	A	O4'-C1'-N9	5.08	112.27	108.20	14	1
1	A	7	A	C5-N7-C8	-5.07	101.37	103.90	17	2
1	A	16	G	C5-N7-C8	-5.02	101.79	104.30	18	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)
2	B	49	ARG	Sidechain	19
2	B	97	ARG	Sidechain	19
2	B	100	ARG	Sidechain	19
2	B	127	ARG	Sidechain	19
2	B	164	ARG	Sidechain	19
2	B	54	ARG	Sidechain	18
2	B	91	ARG	Sidechain	17
1	A	14	A	Sidechain	1

6.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	470	242	242	172±15
2	B	1241	1259	1259	297±19
All	All	32509	28519	28519	7866

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 129.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:102:LEU:HD21	2:B:149:ALA:HB1	1.14	1.18	3	6
2:B:21:LEU:HD22	2:B:30:LEU:HD22	1.12	1.19	18	1
2:B:102:LEU:HD23	2:B:149:ALA:HB1	1.12	1.18	14	5
2:B:73:LEU:HD12	2:B:76:LEU:HD11	1.11	1.14	12	5

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:3:C:O2'	1:A:4:C:H5'	1.08	1.48	8	11
2:B:104:ALA:HB3	2:B:139:ALA:HB3	1.07	1.25	19	15
2:B:102:LEU:HD11	2:B:149:ALA:HB1	1.06	1.20	12	7
1:A:10:C:O4'	2:B:129:VAL:HG13	1.05	1.51	4	19
2:B:73:LEU:HD13	2:B:76:LEU:HD12	1.04	1.29	7	4
2:B:48:VAL:HG22	2:B:59:VAL:HG13	1.04	1.25	5	2
1:A:5:G:O2'	1:A:6:A:H5"	1.03	1.52	9	11
2:B:12:THR:HG21	2:B:46:VAL:HG11	1.03	1.25	3	11
2:B:38:PHE:CD1	2:B:43:LEU:HD22	1.02	1.88	16	1
2:B:37:LEU:HD13	2:B:76:LEU:HD13	1.02	1.31	19	2
1:A:8:A:N1	1:A:14:A:H1'	1.02	1.70	16	18
1:A:19:G:H2'	1:A:20:G:O4'	1.02	1.54	10	15
2:B:102:LEU:HD21	2:B:143:PHE:CE1	1.01	1.91	8	8
2:B:107:LEU:HD21	2:B:139:ALA:HB2	1.00	1.31	10	2
2:B:38:PHE:CD2	2:B:45:VAL:HG11	0.99	1.92	11	4
1:A:15:A:C4	2:B:52:THR:HG23	0.99	1.92	13	19
2:B:85:LEU:HD13	2:B:86:GLU:N	0.99	1.73	5	1
1:A:13:G:H5'	2:B:90:GLY:O	0.99	1.58	7	2
1:A:13:G:O2'	1:A:15:A:H3'	0.99	1.57	18	1
2:B:73:LEU:HD12	2:B:76:LEU:CD1	0.99	1.87	12	4
2:B:22:ASN:CB	2:B:30:LEU:HD21	0.98	1.87	19	12
1:A:15:A:OP1	1:A:17:U:H1'	0.98	1.56	7	12
2:B:107:LEU:HD23	2:B:166:VAL:HG21	0.98	1.34	15	3
1:A:14:A:O2'	2:B:52:THR:HG21	0.97	1.58	14	11
1:A:11:C:O2'	1:A:12:C:H5'	0.97	1.56	15	10
2:B:102:LEU:HD21	2:B:168:LEU:HD12	0.97	1.34	18	1
1:A:13:G:H3'	1:A:13:G:N3	0.96	1.75	1	19
2:B:38:PHE:CD2	2:B:43:LEU:HD23	0.96	1.95	2	1
2:B:103:LEU:HD11	2:B:171:THR:HG23	0.96	1.38	6	1
2:B:17:PHE:O	2:B:85:LEU:HD12	0.95	1.60	1	1
2:B:12:THR:CG2	2:B:46:VAL:HG11	0.95	1.92	3	16
2:B:48:VAL:HG22	2:B:59:VAL:HG22	0.95	1.38	17	4
1:A:15:A:H4'	1:A:17:U:OP1	0.94	1.60	9	6
2:B:101:THR:C	2:B:102:LEU:HD13	0.94	1.81	12	8
1:A:4:C:H4'	1:A:5:G:OP1	0.94	1.63	1	9
2:B:21:LEU:HD13	2:B:56:PHE:C	0.93	1.84	2	10
2:B:70:ALA:O	2:B:85:LEU:HD13	0.93	1.64	15	4
1:A:10:C:C2	1:A:11:C:C6	0.93	2.57	18	19
2:B:30:LEU:HD12	2:B:31:LYS:N	0.93	1.79	14	1
2:B:37:LEU:HD13	2:B:76:LEU:HD23	0.93	1.41	15	2
2:B:37:LEU:CD2	2:B:76:LEU:HD13	0.92	1.94	7	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:22:ASN:HB3	2:B:30:LEU:HD21	0.92	1.40	19	12
2:B:38:PHE:CD2	2:B:43:LEU:HD13	0.92	2.00	8	8
2:B:102:LEU:HD12	2:B:170:TYR:CD1	0.92	1.99	7	6
2:B:38:PHE:CZ	2:B:73:LEU:HD13	0.92	2.00	9	1
1:A:18:A:O2'	1:A:19:G:H5'	0.92	1.64	19	9
1:A:9:U:O2'	1:A:10:C:H6	0.91	1.48	2	19
2:B:30:LEU:O	2:B:34:ILE:HD12	0.91	1.64	18	5
2:B:107:LEU:CD2	2:B:166:VAL:HG21	0.91	1.94	15	2
2:B:21:LEU:HD22	2:B:56:PHE:O	0.91	1.64	5	11
2:B:73:LEU:CD1	2:B:76:LEU:HD11	0.91	1.95	12	2
1:A:13:G:C8	2:B:58:TYR:CD1	0.91	2.58	18	11
1:A:14:A:H4'	1:A:15:A:OP2	0.91	1.65	18	6
2:B:37:LEU:HD23	2:B:76:LEU:HD13	0.91	1.43	7	3
2:B:73:LEU:O	2:B:76:LEU:HD12	0.90	1.65	1	4
2:B:120:PHE:CZ	2:B:168:LEU:HD11	0.90	2.00	18	10
2:B:28:ALA:O	2:B:32:VAL:HG23	0.90	1.67	16	18
2:B:37:LEU:HD13	2:B:76:LEU:HD12	0.90	1.43	9	1
1:A:5:G:OP2	1:A:5:G:H3'	0.90	1.67	4	3
2:B:73:LEU:CD1	2:B:76:LEU:HD12	0.89	1.97	7	4
2:B:98:ALA:HB1	2:B:171:THR:CG2	0.89	1.96	15	1
2:B:73:LEU:HD22	2:B:76:LEU:HD11	0.89	1.44	13	2
2:B:102:LEU:HD12	2:B:103:LEU:N	0.89	1.82	18	1
1:A:8:A:H5"	1:A:9:U:OP2	0.89	1.68	3	4
1:A:6:A:H4'	1:A:6:A:OP1	0.89	1.68	15	3
2:B:11:THR:HG21	2:B:47:ASP:OD2	0.89	1.68	6	3
2:B:37:LEU:HD11	2:B:76:LEU:HD22	0.89	1.42	14	1
2:B:69:LYS:O	2:B:73:LEU:HD23	0.89	1.67	19	12
1:A:9:U:OP1	1:A:9:U:H3'	0.88	1.67	19	1
1:A:10:C:C1'	2:B:129:VAL:HG13	0.88	1.97	16	19
2:B:127:ARG:CZ	2:B:127:ARG:HB3	0.88	1.99	18	2
2:B:102:LEU:HD23	2:B:149:ALA:CB	0.87	1.98	14	2
1:A:18:A:H2'	1:A:19:G:O4'	0.87	1.69	15	13
2:B:140:TYR:O	2:B:141:ILE:HD13	0.87	1.70	9	6
2:B:38:PHE:CE2	2:B:43:LEU:HD22	0.87	2.03	19	1
2:B:61:PHE:CZ	2:B:70:ALA:HB1	0.87	2.04	9	9
2:B:107:LEU:HD12	2:B:137:GLY:O	0.87	1.69	6	6
1:A:14:A:H8	2:B:52:THR:HG1	0.87	1.12	1	1
1:A:10:C:H2'	1:A:10:C:O2	0.87	1.70	9	19
2:B:103:LEU:HD13	2:B:140:TYR:CE1	0.87	2.05	14	9
2:B:125:GLU:O	2:B:126:ILE:HD13	0.87	1.69	16	2
2:B:102:LEU:HD12	2:B:102:LEU:O	0.87	1.70	11	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:73:LEU:O	2:B:76:LEU:HD22	0.87	1.70	9	1
2:B:37:LEU:HD22	2:B:76:LEU:CD2	0.86	2.00	16	5
2:B:103:LEU:HD13	2:B:140:TYR:CD1	0.86	2.05	14	2
1:A:10:C:C2	2:B:127:ARG:NH2	0.86	2.43	18	2
2:B:107:LEU:CD2	2:B:139:ALA:HB2	0.86	1.99	10	2
2:B:102:LEU:HD21	2:B:149:ALA:CB	0.86	2.01	3	6
1:A:13:G:OP1	1:A:13:G:H4'	0.86	1.68	18	4
2:B:107:LEU:HD23	2:B:166:VAL:HG22	0.86	1.48	18	1
1:A:13:G:C8	2:B:58:TYR:CD2	0.86	2.63	8	5
1:A:14:A:H4'	1:A:14:A:OP2	0.86	1.68	1	1
2:B:102:LEU:HD13	2:B:102:LEU:N	0.86	1.86	10	8
2:B:160:GLU:O	2:B:161:ILE:HD13	0.85	1.69	10	3
2:B:103:LEU:HD21	2:B:140:TYR:CE1	0.85	2.06	10	7
2:B:56:PHE:CD1	2:B:57:GLY:N	0.85	2.44	17	3
1:A:21:C:HO2'	1:A:22:C:H6	0.85	0.88	11	1
1:A:13:G:N3	1:A:13:G:H5'	0.85	1.85	10	6
1:A:10:C:C5	2:B:140:TYR:CZ	0.85	2.64	14	18
2:B:102:LEU:CD1	2:B:168:LEU:HD22	0.85	2.01	4	4
2:B:16:LEU:HD12	2:B:17:PHE:N	0.85	1.87	9	9
1:A:14:A:N3	2:B:94:LYS:HG3	0.85	1.87	11	4
2:B:126:ILE:HG23	2:B:141:ILE:CD1	0.85	2.02	9	2
2:B:67:LEU:HD22	2:B:67:LEU:O	0.84	1.72	8	1
2:B:120:PHE:CE2	2:B:141:ILE:HD13	0.84	2.08	11	4
2:B:102:LEU:CD2	2:B:149:ALA:HB1	0.84	2.02	3	9
2:B:16:LEU:HD22	2:B:17:PHE:N	0.84	1.87	2	4
2:B:21:LEU:HD13	2:B:30:LEU:HD13	0.84	1.48	18	3
2:B:38:PHE:CE2	2:B:43:LEU:HD13	0.83	2.07	19	7
2:B:103:LEU:HD11	2:B:138:ILE:CG2	0.83	2.02	12	5
2:B:37:LEU:HG	2:B:76:LEU:HD13	0.83	1.47	14	1
2:B:21:LEU:HD12	2:B:30:LEU:HD13	0.83	1.50	12	3
1:A:9:U:HO2'	1:A:10:C:H6	0.83	0.84	16	14
2:B:103:LEU:HD11	2:B:140:TYR:CE1	0.83	2.09	4	4
2:B:111:ILE:O	2:B:112:THR:HG23	0.83	1.74	10	16
2:B:103:LEU:HD12	2:B:171:THR:CG2	0.83	2.04	4	1
1:A:10:C:C5	2:B:140:TYR:CE1	0.82	2.67	4	18
2:B:50:THR:C	2:B:56:PHE:O	0.82	2.17	19	1
1:A:14:A:O2'	1:A:15:A:C8	0.82	2.32	17	18
1:A:10:C:C2	2:B:127:ARG:CZ	0.82	2.61	16	1
2:B:153:LEU:HA	2:B:168:LEU:HD13	0.82	1.52	1	4
2:B:34:ILE:HD11	2:B:78:VAL:HG23	0.82	1.52	13	4
1:A:10:C:C2	1:A:11:C:C5	0.81	2.68	13	19

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:130:SER:HA	2:B:136:LYS:HA	0.81	1.49	15	1
2:B:143:PHE:HB2	2:B:149:ALA:HB2	0.81	1.49	16	18
2:B:101:THR:C	2:B:102:LEU:HD23	0.81	1.96	9	1
1:A:8:A:C6	1:A:14:A:C4	0.81	2.69	17	19
1:A:20:G:C5	1:A:21:C:C5	0.81	2.68	8	17
2:B:126:ILE:HG23	2:B:140:TYR:O	0.81	1.75	15	13
2:B:48:VAL:HG13	2:B:59:VAL:CG2	0.81	2.05	18	3
2:B:102:LEU:HD13	2:B:168:LEU:HD22	0.81	1.51	8	4
2:B:111:ILE:HD12	2:B:162:ASP:OD2	0.81	1.76	3	1
2:B:103:LEU:HD23	2:B:129:VAL:HG21	0.81	1.53	9	4
2:B:101:THR:O	2:B:102:LEU:HD13	0.81	1.76	13	5
2:B:102:LEU:CD1	2:B:149:ALA:HB1	0.80	2.05	12	4
2:B:102:LEU:N	2:B:102:LEU:HD22	0.80	1.92	16	7
1:A:14:A:H2'	2:B:52:THR:HG21	0.80	1.54	8	18
2:B:43:LEU:HD21	2:B:69:LYS:HB3	0.80	1.51	14	3
2:B:160:GLU:C	2:B:161:ILE:HD13	0.80	1.95	10	1
2:B:140:TYR:CE2	2:B:171:THR:HG21	0.80	2.12	7	7
2:B:153:LEU:HD23	2:B:154:GLU:N	0.80	1.92	1	5
2:B:102:LEU:HD23	2:B:153:LEU:HD12	0.80	1.49	2	1
2:B:58:TYR:O	2:B:59:VAL:HG23	0.80	1.77	9	8
1:A:14:A:H2'	2:B:52:THR:OG1	0.79	1.76	17	9
2:B:116:LEU:HB3	2:B:126:ILE:HD13	0.79	1.54	6	1
1:A:7:A:O2'	1:A:8:A:P	0.79	2.40	14	4
1:A:10:C:C6	2:B:140:TYR:CE1	0.79	2.71	11	18
1:A:13:G:C8	2:B:49:ARG:HD2	0.79	2.13	12	10
2:B:128:LEU:C	2:B:128:LEU:HD22	0.79	1.96	16	1
2:B:50:THR:O	2:B:56:PHE:O	0.79	2.01	19	1
1:A:11:C:O2'	1:A:12:C:P	0.79	2.40	8	9
1:A:13:G:N3	1:A:13:G:H5"	0.79	1.91	18	9
1:A:10:C:O2	2:B:127:ARG:CZ	0.79	2.31	16	2
2:B:27:VAL:HG23	2:B:54:ARG:NE	0.79	1.93	18	4
2:B:69:LYS:O	2:B:73:LEU:HD13	0.79	1.78	8	4
2:B:102:LEU:HD13	2:B:168:LEU:HD13	0.79	1.53	6	1
2:B:37:LEU:HD22	2:B:76:LEU:CD1	0.79	2.08	9	1
1:A:19:G:C4	1:A:20:G:C8	0.78	2.71	18	17
1:A:10:C:N3	2:B:127:ARG:NH1	0.78	2.31	16	1
1:A:10:C:N3	1:A:11:C:C5	0.78	2.51	16	15
1:A:21:C:O2'	1:A:22:C:H6	0.78	1.61	11	3
2:B:21:LEU:HD13	2:B:56:PHE:O	0.78	1.79	10	10
1:A:10:C:C4	2:B:140:TYR:CZ	0.78	2.71	13	19
2:B:67:LEU:HD13	2:B:68:GLU:N	0.78	1.93	8	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:120:PHE:CE1	2:B:168:LEU:HD11	0.78	2.13	9	8
2:B:16:LEU:HD22	2:B:16:LEU:C	0.78	1.99	17	3
2:B:98:ALA:HB1	2:B:171:THR:HG22	0.78	1.54	15	1
1:A:19:G:O2'	1:A:20:G:P	0.77	2.42	9	7
2:B:120:PHE:CZ	2:B:168:LEU:HD21	0.77	2.14	4	8
1:A:16:G:N7	2:B:27:VAL:HG21	0.77	1.93	9	9
2:B:103:LEU:CD1	2:B:171:THR:HG23	0.77	2.09	6	1
2:B:70:ALA:O	2:B:85:LEU:HD22	0.77	1.79	10	1
2:B:18:ILE:HD13	2:B:59:VAL:CG2	0.77	2.09	19	1
2:B:103:LEU:HD12	2:B:171:THR:HG22	0.77	1.55	4	1
1:A:16:G:H4'	1:A:16:G:OP1	0.77	1.80	18	2
1:A:18:A:O2'	1:A:19:G:P	0.77	2.43	17	2
2:B:85:LEU:HD23	2:B:86:GLU:N	0.77	1.94	7	1
2:B:98:ALA:HB1	2:B:171:THR:O	0.77	1.79	18	4
2:B:102:LEU:HD11	2:B:153:LEU:HD12	0.77	1.55	14	1
1:A:10:C:C4	1:A:11:C:C4	0.77	2.72	14	14
2:B:51:GLY:N	2:B:56:PHE:O	0.77	2.18	17	19
1:A:12:C:O2'	2:B:56:PHE:CE2	0.76	2.37	19	11
2:B:74:THR:HG23	2:B:84:LYS:HA	0.76	1.56	8	2
2:B:16:LEU:C	2:B:16:LEU:HD22	0.76	2.01	13	1
1:A:10:C:C5	2:B:140:TYR:CE2	0.76	2.72	15	1
1:A:2:G:C5	1:A:3:C:C5	0.76	2.74	1	7
2:B:30:LEU:HD11	2:B:31:LYS:HE2	0.76	1.57	14	1
1:A:8:A:C2	1:A:14:A:N3	0.76	2.53	11	19
2:B:30:LEU:HD11	2:B:54:ARG:HB3	0.76	1.55	3	7
1:A:13:G:N7	2:B:58:TYR:CD1	0.76	2.53	12	3
2:B:102:LEU:HD22	2:B:102:LEU:O	0.76	1.81	10	1
1:A:12:C:C2	2:B:17:PHE:CZ	0.76	2.74	6	18
1:A:14:A:C2'	2:B:52:THR:HG21	0.76	2.11	11	15
1:A:13:G:C8	2:B:49:ARG:CD	0.76	2.69	18	5
1:A:2:G:O2'	1:A:3:C:P	0.76	2.43	10	3
2:B:107:LEU:HD11	2:B:139:ALA:HB2	0.75	1.59	4	1
1:A:20:G:O2'	1:A:21:C:P	0.75	2.43	13	3
1:A:1:G:N3	1:A:1:G:H2'	0.75	1.95	12	2
1:A:1:G:O2'	1:A:2:G:P	0.75	2.44	2	3
1:A:12:C:C6	1:A:12:C:P	0.75	2.79	3	5
2:B:37:LEU:HD21	2:B:76:LEU:HB3	0.75	1.56	14	2
2:B:30:LEU:HD23	2:B:78:VAL:HG11	0.75	1.57	16	3
1:A:15:A:C5	2:B:52:THR:CG2	0.75	2.70	1	19
1:A:10:C:C4	2:B:140:TYR:CE2	0.75	2.75	15	5
1:A:19:G:C6	1:A:20:G:N7	0.75	2.55	5	12

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:18:ILE:CG1	2:B:85:LEU:HD12	0.75	2.12	6	1
1:A:9:U:O2'	1:A:10:C:P	0.75	2.44	6	4
2:B:38:PHE:HD2	2:B:45:VAL:HG11	0.75	1.42	11	1
2:B:21:LEU:HD23	2:B:30:LEU:HD13	0.75	1.58	15	8
2:B:17:PHE:CD1	2:B:56:PHE:CE2	0.75	2.75	17	2
2:B:103:LEU:HD12	2:B:138:ILE:HG22	0.75	1.56	1	2
1:A:20:G:C8	1:A:21:C:C5	0.75	2.75	11	6
2:B:70:ALA:HA	2:B:73:LEU:HD22	0.75	1.56	15	4
2:B:78:VAL:HB	2:B:83:ILE:HG23	0.74	1.58	14	9
1:A:13:G:N3	1:A:13:G:C5'	0.74	2.50	17	15
2:B:38:PHE:CE2	2:B:43:LEU:HD23	0.74	2.16	2	1
2:B:104:ALA:O	2:B:107:LEU:HD11	0.74	1.82	6	2
1:A:8:A:H5"	1:A:9:U:O5'	0.74	1.83	11	6
1:A:20:G:H2'	1:A:21:C:O4'	0.74	1.81	11	4
2:B:30:LEU:HD11	2:B:54:ARG:CG	0.74	2.11	16	2
2:B:21:LEU:CD2	2:B:30:LEU:HD22	0.74	2.08	18	1
2:B:17:PHE:C	2:B:18:ILE:HD12	0.74	2.03	12	1
2:B:153:LEU:HD13	2:B:153:LEU:C	0.74	2.01	15	1
1:A:2:G:C6	1:A:3:C:C4	0.74	2.76	3	11
1:A:13:G:N7	2:B:49:ARG:NE	0.74	2.35	19	19
2:B:103:LEU:HD21	2:B:140:TYR:HE1	0.74	1.42	8	4
1:A:21:C:O2'	1:A:22:C:H5"	0.74	1.83	17	2
1:A:4:C:O2'	1:A:5:G:P	0.74	2.46	19	10
1:A:19:G:H4'	1:A:20:G:OP1	0.74	1.83	10	5
2:B:126:ILE:HG23	2:B:141:ILE:HG13	0.74	1.59	10	1
2:B:116:LEU:HD12	2:B:141:ILE:HD11	0.74	1.60	17	1
2:B:140:TYR:C	2:B:141:ILE:HD13	0.74	2.03	7	4
1:A:13:G:C8	2:B:58:TYR:CG	0.73	2.75	7	6
1:A:15:A:C4	1:A:17:U:C5	0.73	2.76	15	16
1:A:4:C:H1'	1:A:5:G:O4'	0.73	1.83	13	7
1:A:13:G:N3	1:A:13:G:C3'	0.73	2.51	10	19
1:A:13:G:N7	2:B:58:TYR:CG	0.73	2.57	1	8
2:B:63:SER:N	2:B:66:ASP:OD2	0.73	2.20	8	3
1:A:7:A:C6	1:A:8:A:C2	0.73	2.76	18	14
2:B:74:THR:OG1	2:B:85:LEU:HD21	0.73	1.84	17	3
1:A:9:U:C5	2:B:103:LEU:HD21	0.73	2.17	16	4
1:A:19:G:O2'	1:A:20:G:H5'	0.73	1.83	6	3
2:B:37:LEU:CG	2:B:76:LEU:HD13	0.73	2.14	14	1
1:A:15:A:OP1	1:A:15:A:H8	0.73	1.67	7	1
2:B:159:ALA:HB3	2:B:166:VAL:HB	0.73	1.61	18	1
2:B:171:THR:HG22	2:B:171:THR:O	0.73	1.83	9	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:10:C:C2	2:B:127:ARG:NH1	0.73	2.56	16	1
1:A:20:G:C2	1:A:21:C:C6	0.73	2.77	9	5
2:B:67:LEU:HD13	2:B:67:LEU:C	0.73	2.04	1	4
1:A:21:C:C2	1:A:22:C:C5	0.73	2.77	14	14
2:B:48:VAL:HG13	2:B:59:VAL:HG23	0.73	1.59	18	3
2:B:44:ALA:HB1	2:B:62:GLU:CG	0.73	2.14	8	1
2:B:103:LEU:HD12	2:B:171:THR:OG1	0.73	1.83	9	1
1:A:20:G:C4	1:A:21:C:C6	0.73	2.77	19	15
1:A:6:A:C5	1:A:18:A:C2	0.73	2.77	16	5
2:B:38:PHE:CG	2:B:43:LEU:HD22	0.73	2.18	16	1
2:B:124:LEU:HD11	2:B:144:LYS:CG	0.73	2.14	16	1
1:A:19:G:C2	1:A:20:G:C4	0.72	2.76	17	9
1:A:2:G:C2	1:A:22:C:C2	0.72	2.77	16	8
2:B:16:LEU:HD12	2:B:16:LEU:C	0.72	2.04	10	10
1:A:10:C:C2	2:B:140:TYR:CD2	0.72	2.77	15	1
2:B:38:PHE:CD2	2:B:43:LEU:HD22	0.72	2.18	19	4
2:B:51:GLY:HA3	2:B:56:PHE:CG	0.72	2.19	11	17
2:B:37:LEU:HD21	2:B:76:LEU:HD22	0.72	1.60	2	2
1:A:15:A:C5	1:A:17:U:C4	0.72	2.77	3	15
1:A:19:G:C5	1:A:20:G:C8	0.72	2.77	18	15
1:A:16:G:H4'	1:A:17:U:OP1	0.72	1.82	13	1
1:A:15:A:H1'	1:A:16:G:OP1	0.72	1.83	18	1
2:B:27:VAL:HG23	2:B:50:THR:HG21	0.72	1.59	19	1
1:A:6:A:C4	1:A:18:A:C2	0.72	2.78	17	11
1:A:11:C:O2'	1:A:12:C:C5'	0.72	2.38	5	13
1:A:13:G:N7	2:B:58:TYR:CD2	0.72	2.58	7	6
1:A:10:C:O4'	2:B:129:VAL:CG1	0.72	2.38	16	13
1:A:10:C:N3	1:A:11:C:C4	0.72	2.57	16	6
1:A:5:G:O2'	1:A:6:A:P	0.72	2.47	4	1
1:A:8:A:H4'	1:A:9:U:OP2	0.72	1.84	8	7
1:A:9:U:H1'	1:A:10:C:OP1	0.72	1.85	9	10
1:A:16:G:O2'	1:A:17:U:P	0.72	2.47	11	2
1:A:8:A:N1	1:A:14:A:N3	0.72	2.38	11	18
1:A:10:C:O2	1:A:11:C:C6	0.72	2.42	16	14
2:B:18:ILE:HD13	2:B:59:VAL:HG21	0.72	1.60	19	2
2:B:38:PHE:CE1	2:B:73:LEU:HD13	0.72	2.20	9	2
1:A:3:C:O2'	1:A:4:C:P	0.72	2.48	1	10
1:A:8:A:N1	1:A:14:A:C1'	0.72	2.53	3	16
1:A:14:A:C4	2:B:94:LYS:CG	0.72	2.73	1	6
1:A:15:A:H4'	1:A:16:G:OP1	0.72	1.84	1	5
2:B:33:ALA:HB2	2:B:79:PHE:CD2	0.72	2.20	17	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:21:C:H4'	1:A:21:C:OP1	0.72	1.83	18	1
1:A:20:G:C5	1:A:21:C:C4	0.72	2.78	2	6
2:B:102:LEU:HD23	2:B:168:LEU:HD23	0.72	1.61	10	1
1:A:20:G:C6	1:A:21:C:C4	0.72	2.78	5	16
2:B:44:ALA:HB1	2:B:62:GLU:HG2	0.71	1.60	5	1
1:A:16:G:C8	2:B:27:VAL:HG21	0.71	2.20	17	11
1:A:12:C:O2'	2:B:56:PHE:CZ	0.71	2.42	14	3
1:A:11:C:O2'	1:A:12:C:OP1	0.71	2.08	5	6
1:A:15:A:C8	1:A:17:U:C2	0.71	2.78	3	13
1:A:14:A:N6	2:B:94:LYS:NZ	0.71	2.39	5	1
2:B:30:LEU:HD23	2:B:78:VAL:CG1	0.71	2.15	8	8
2:B:93:SER:O	2:B:95:LYS:N	0.71	2.23	10	14
2:B:126:ILE:HG12	2:B:141:ILE:HG23	0.71	1.60	5	8
2:B:92:ASP:CA	2:B:96:VAL:HG11	0.71	2.15	16	1
1:A:9:U:O2'	1:A:10:C:C6	0.71	2.43	5	18
2:B:37:LEU:HD13	2:B:76:LEU:CD2	0.71	2.15	15	1
2:B:21:LEU:HD22	2:B:30:LEU:CD2	0.71	2.10	18	1
1:A:4:C:O2'	1:A:5:G:O5'	0.71	2.09	1	19
2:B:103:LEU:HD23	2:B:169:TYR:O	0.71	1.86	5	3
1:A:20:G:N3	1:A:21:C:C6	0.71	2.59	9	5
1:A:3:C:C2	1:A:4:C:C5	0.70	2.78	19	2
2:B:103:LEU:HD12	2:B:138:ILE:CG2	0.70	2.16	1	3
2:B:37:LEU:HD22	2:B:76:LEU:HD21	0.70	1.61	11	2
1:A:12:C:O2'	2:B:56:PHE:CE1	0.70	2.43	6	1
2:B:37:LEU:HD22	2:B:76:LEU:HD22	0.70	1.63	10	1
2:B:41:ASN:O	2:B:42:ASP:CB	0.70	2.40	4	19
1:A:15:A:C5	2:B:52:THR:HG23	0.70	2.20	3	3
2:B:37:LEU:HD23	2:B:76:LEU:CD2	0.70	2.15	3	1
1:A:12:C:C2	1:A:12:C:P	0.70	2.85	6	2
2:B:43:LEU:HD12	2:B:66:ASP:OD1	0.70	1.85	17	2
2:B:38:PHE:CZ	2:B:43:LEU:HD13	0.70	2.22	19	1
1:A:15:A:C4	2:B:52:THR:CG2	0.70	2.75	15	18
1:A:13:G:O2'	1:A:14:A:H5"	0.70	1.85	11	3
1:A:14:A:O2'	1:A:15:A:N7	0.70	2.25	16	15
1:A:19:G:C2'	1:A:20:G:O4'	0.70	2.39	10	8
2:B:103:LEU:HD12	2:B:129:VAL:HG21	0.70	1.62	15	2
1:A:13:G:O2'	2:B:56:PHE:CZ	0.70	2.43	16	3
2:B:77:LYS:O	2:B:78:VAL:O	0.70	2.10	7	8
1:A:13:G:C5	2:B:58:TYR:CE2	0.70	2.80	1	5
2:B:27:VAL:HA	2:B:30:LEU:HD12	0.70	1.61	16	5
2:B:102:LEU:HD22	2:B:141:ILE:O	0.70	1.85	12	4

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:15:A:OP1	1:A:15:A:C8	0.70	2.45	7	1
1:A:15:A:C6	1:A:17:U:C4	0.70	2.80	5	10
2:B:12:THR:HG21	2:B:46:VAL:HG21	0.70	1.64	17	5
2:B:12:THR:HG21	2:B:46:VAL:HB	0.70	1.63	19	1
2:B:12:THR:HG22	2:B:13:PRO:HD2	0.70	1.64	11	6
2:B:129:VAL:HB	2:B:138:ILE:HB	0.69	1.62	10	19
1:A:3:C:N4	1:A:4:C:N4	0.69	2.40	14	2
1:A:21:C:N3	1:A:22:C:C5	0.69	2.60	12	6
2:B:116:LEU:HD23	2:B:141:ILE:HD11	0.69	1.62	8	2
2:B:56:PHE:CD1	2:B:56:PHE:C	0.69	2.66	19	2
2:B:78:VAL:O	2:B:80:GLY:N	0.69	2.24	4	18
2:B:107:LEU:HD11	2:B:139:ALA:CB	0.69	2.17	4	3
1:A:9:U:C5	2:B:138:ILE:HD13	0.69	2.21	17	9
1:A:4:C:OP2	1:A:4:C:H3'	0.69	1.87	8	2
1:A:15:A:C4	1:A:17:U:C4	0.69	2.80	1	15
2:B:126:ILE:HG23	2:B:141:ILE:HD13	0.69	1.64	9	3
2:B:37:LEU:HD21	2:B:76:LEU:CB	0.69	2.16	14	1
2:B:34:ILE:HD11	2:B:83:ILE:HG21	0.69	1.63	14	1
1:A:12:C:C6	1:A:12:C:OP1	0.68	2.46	13	4
1:A:10:C:OP2	1:A:11:C:H5	0.68	1.71	13	1
1:A:8:A:N1	1:A:14:A:C4	0.68	2.61	5	16
1:A:10:C:H1'	2:B:129:VAL:HG22	0.68	1.65	4	19
1:A:19:G:C2	1:A:20:G:N9	0.68	2.61	10	5
2:B:103:LEU:CD2	2:B:140:TYR:CE1	0.68	2.76	10	6
2:B:12:THR:HG22	2:B:13:PRO:CD	0.68	2.18	17	4
1:A:14:A:N7	2:B:94:LYS:NZ	0.68	2.40	7	1
1:A:13:G:O2'	1:A:14:A:P	0.68	2.51	6	5
1:A:15:A:N3	1:A:17:U:C5	0.68	2.61	5	11
1:A:12:C:C5	2:B:17:PHE:CZ	0.68	2.81	3	4
1:A:15:A:C5	2:B:52:THR:HG22	0.68	2.24	8	13
1:A:10:C:N4	1:A:11:C:N4	0.68	2.40	13	3
2:B:78:VAL:HG13	2:B:79:PHE:N	0.68	2.04	18	7
2:B:98:ALA:HB1	2:B:171:THR:HB	0.68	1.63	19	4
2:B:16:LEU:CD2	2:B:85:LEU:HD21	0.68	2.18	6	2
2:B:111:ILE:HD12	2:B:161:ILE:HG21	0.68	1.66	17	1
1:A:14:A:N6	2:B:94:LYS:CE	0.68	2.57	2	4
2:B:37:LEU:HD23	2:B:76:LEU:HD23	0.68	1.66	3	1
1:A:14:A:OP2	1:A:14:A:C8	0.68	2.47	4	2
2:B:74:THR:OG1	2:B:85:LEU:HD11	0.68	1.88	12	1
2:B:157:GLN:HA	2:B:168:LEU:HD12	0.68	1.66	13	4
2:B:38:PHE:CD2	2:B:45:VAL:CG1	0.67	2.78	19	15

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:78:VAL:CG2	2:B:83:ILE:HG21	0.67	2.18	8	10
2:B:102:LEU:HA	2:B:171:THR:HG23	0.67	1.65	2	3
1:A:16:G:N7	2:B:27:VAL:CG2	0.67	2.57	9	11
2:B:153:LEU:HA	2:B:168:LEU:HD22	0.67	1.64	7	3
1:A:13:G:O4'	2:B:56:PHE:CE1	0.67	2.46	17	2
1:A:12:C:C5	1:A:12:C:OP2	0.67	2.47	18	5
2:B:103:LEU:CD1	2:B:140:TYR:CE1	0.67	2.77	4	6
2:B:103:LEU:CG	2:B:140:TYR:CE1	0.67	2.77	11	5
2:B:111:ILE:HD11	2:B:161:ILE:CG2	0.67	2.19	2	1
1:A:19:G:HO2'	1:A:20:G:P	0.67	2.12	7	3
2:B:31:LYS:HG2	2:B:48:VAL:HG13	0.67	1.66	12	3
2:B:102:LEU:CD2	2:B:168:LEU:HD12	0.67	2.18	18	1
2:B:85:LEU:HD23	2:B:85:LEU:N	0.67	2.04	18	3
2:B:130:SER:O	2:B:138:ILE:HD11	0.67	1.89	15	1
2:B:61:PHE:CE2	2:B:70:ALA:HB1	0.67	2.25	12	9
2:B:123:ALA:HB2	2:B:143:PHE:CZ	0.67	2.25	1	6
2:B:69:LYS:C	2:B:73:LEU:HD13	0.67	2.09	8	3
2:B:85:LEU:HD12	2:B:85:LEU:N	0.67	2.04	10	1
2:B:127:ARG:NH2	2:B:140:TYR:HB2	0.67	2.04	18	2
2:B:104:ALA:HB1	2:B:166:VAL:HG11	0.67	1.66	9	1
2:B:107:LEU:HD23	2:B:166:VAL:CG2	0.67	2.17	4	3
1:A:11:C:N3	2:B:94:LYS:HB2	0.67	2.05	18	2
2:B:94:LYS:HG2	2:B:95:LYS:N	0.67	2.03	11	1
1:A:10:C:H4'	2:B:128:LEU:O	0.67	1.90	15	1
2:B:161:ILE:HD12	2:B:166:VAL:HG21	0.67	1.66	17	1
1:A:13:G:O2'	1:A:14:A:C5'	0.67	2.43	8	6
1:A:9:U:C1'	1:A:10:C:OP1	0.67	2.43	8	11
2:B:102:LEU:HD23	2:B:143:PHE:CE1	0.67	2.24	15	4
2:B:46:VAL:HG22	2:B:62:GLU:HG3	0.67	1.64	17	6
2:B:21:LEU:HD12	2:B:56:PHE:O	0.67	1.90	18	2
2:B:127:ARG:NH2	2:B:140:TYR:CG	0.67	2.62	18	1
1:A:7:A:N1	1:A:8:A:C2	0.67	2.63	17	10
2:B:153:LEU:HD23	2:B:153:LEU:C	0.67	2.09	14	4
1:A:5:G:HO2'	1:A:6:A:H5"	0.67	1.47	9	2
1:A:9:U:C4	2:B:138:ILE:HD13	0.67	2.24	4	5
2:B:26:SER:O	2:B:30:LEU:HD13	0.67	1.88	4	2
1:A:8:A:N3	2:B:95:LYS:HD3	0.67	2.05	11	1
1:A:6:A:O2'	1:A:7:A:H5'	0.66	1.90	5	1
1:A:14:A:O3'	1:A:15:A:H8	0.66	1.71	14	3
2:B:102:LEU:HD12	2:B:102:LEU:C	0.66	2.10	18	2
1:A:20:G:C4	1:A:21:C:C5	0.66	2.83	9	13

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:61:PHE:CE2	2:B:70:ALA:CB	0.66	2.79	2	9
2:B:116:LEU:HD13	2:B:126:ILE:HG21	0.66	1.67	3	1
2:B:107:LEU:CD1	2:B:139:ALA:HB2	0.66	2.19	4	2
2:B:102:LEU:HD11	2:B:149:ALA:O	0.66	1.90	17	1
2:B:126:ILE:CG1	2:B:141:ILE:HG23	0.66	2.21	3	4
2:B:37:LEU:HD22	2:B:76:LEU:HD23	0.66	1.67	16	2
1:A:14:A:C6	2:B:94:LYS:CG	0.66	2.78	6	4
1:A:16:G:H1'	1:A:17:U:OP2	0.66	1.89	16	1
2:B:127:ARG:HB3	2:B:127:ARG:NH2	0.66	2.05	16	1
1:A:12:C:C6	1:A:12:C:O5'	0.66	2.48	8	7
1:A:12:C:OP1	1:A:12:C:C5	0.66	2.48	10	5
2:B:48:VAL:HG22	2:B:59:VAL:CG1	0.66	2.13	5	1
1:A:9:U:H1'	2:B:129:VAL:HG12	0.66	1.66	15	1
2:B:73:LEU:HD12	2:B:76:LEU:HD21	0.66	1.67	19	1
1:A:12:C:O3'	1:A:13:G:H4'	0.66	1.91	4	1
1:A:21:C:O2'	1:A:22:C:C5'	0.66	2.44	17	4
2:B:27:VAL:HG22	2:B:31:LYS:HE3	0.66	1.67	19	2
1:A:13:G:N7	2:B:49:ARG:CD	0.66	2.58	19	14
2:B:120:PHE:CE2	2:B:141:ILE:CD1	0.66	2.79	1	8
1:A:11:C:C2'	1:A:12:C:O5'	0.66	2.43	19	9
1:A:3:C:O2'	1:A:4:C:C5'	0.66	2.43	10	16
1:A:13:G:N7	2:B:49:ARG:HD3	0.66	2.06	11	6
1:A:13:G:O2'	1:A:14:A:O5'	0.66	2.14	6	4
1:A:20:G:H3'	1:A:21:C:O4'	0.66	1.91	18	3
2:B:69:LYS:C	2:B:73:LEU:HD23	0.66	2.10	4	7
2:B:102:LEU:HD13	2:B:168:LEU:CD1	0.66	2.20	6	1
1:A:10:C:O2'	2:B:128:LEU:N	0.66	2.29	15	1
1:A:7:A:N1	1:A:8:A:N3	0.66	2.44	4	15
2:B:16:LEU:HD22	2:B:85:LEU:HD21	0.66	1.66	6	1
2:B:128:LEU:HD21	2:B:136:LYS:CB	0.66	2.21	15	1
2:B:21:LEU:HG	2:B:30:LEU:HD22	0.65	1.68	2	3
2:B:116:LEU:CB	2:B:126:ILE:HD13	0.65	2.21	6	1
1:A:4:C:O2'	1:A:5:G:C5'	0.65	2.44	18	9
2:B:61:PHE:CZ	2:B:70:ALA:CB	0.65	2.79	1	7
2:B:103:LEU:HD13	2:B:140:TYR:HE1	0.65	1.52	5	2
2:B:44:ALA:HB3	2:B:66:ASP:OD2	0.65	1.90	11	3
2:B:104:ALA:HB2	2:B:141:ILE:CD1	0.65	2.22	10	1
1:A:14:A:C6	2:B:94:LYS:CE	0.65	2.79	16	4
1:A:20:G:N7	1:A:21:C:C5	0.65	2.65	11	7
1:A:9:U:C5	2:B:138:ILE:HG21	0.65	2.27	14	2
1:A:14:A:N1	2:B:94:LYS:HG3	0.65	2.06	6	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:101:THR:HG23	2:B:141:ILE:O	0.65	1.91	7	3
2:B:102:LEU:HD11	2:B:143:PHE:CE1	0.65	2.26	9	1
1:A:14:A:C5	2:B:94:LYS:HG2	0.65	2.27	15	8
1:A:19:G:N3	1:A:20:G:H1'	0.65	2.05	16	4
1:A:11:C:O2'	1:A:12:C:H5"	0.65	1.90	5	1
2:B:107:LEU:HD21	2:B:166:VAL:HG13	0.65	1.67	7	1
2:B:67:LEU:O	2:B:70:ALA:HB3	0.65	1.92	15	5
2:B:18:ILE:HD12	2:B:59:VAL:CG2	0.65	2.22	10	1
1:A:14:A:C4	2:B:94:LYS:HG3	0.65	2.27	15	4
2:B:59:VAL:CG1	2:B:61:PHE:CZ	0.65	2.80	18	7
1:A:11:C:H4'	1:A:12:C:OP1	0.65	1.89	17	2
1:A:12:C:C4	1:A:12:C:OP2	0.65	2.50	7	5
2:B:21:LEU:HG	2:B:56:PHE:O	0.65	1.92	13	3
1:A:12:C:H4'	1:A:13:G:OP2	0.65	1.89	8	1
2:B:30:LEU:HD23	2:B:78:VAL:HG13	0.65	1.67	19	5
1:A:13:G:HO2'	1:A:14:A:C5'	0.65	2.04	3	2
2:B:103:LEU:HD11	2:B:138:ILE:HG21	0.65	1.67	12	5
1:A:12:C:C2	2:B:17:PHE:CE1	0.65	2.84	14	8
2:B:38:PHE:CB	2:B:45:VAL:HG13	0.65	2.22	9	3
2:B:102:LEU:HD12	2:B:170:TYR:HD1	0.65	1.51	7	1
2:B:105:LYS:CG	2:B:138:ILE:HG23	0.65	2.21	15	3
1:A:19:G:O2'	1:A:20:G:C5'	0.65	2.45	1	5
2:B:27:VAL:CG2	2:B:50:THR:HG21	0.65	2.22	19	3
1:A:13:G:H4'	1:A:14:A:OP1	0.65	1.90	3	2
1:A:19:G:H8	1:A:19:G:OP2	0.65	1.75	11	1
1:A:21:C:O2'	1:A:22:C:P	0.65	2.54	14	2
1:A:7:A:N6	1:A:8:A:N1	0.65	2.44	4	10
1:A:14:A:P	1:A:14:A:C8	0.65	2.90	16	2
2:B:140:TYR:OH	2:B:171:THR:CG2	0.65	2.45	15	4
2:B:30:LEU:HD11	2:B:31:LYS:CE	0.65	2.21	14	1
2:B:128:LEU:HD21	2:B:136:LYS:HB2	0.65	1.69	15	1
1:A:13:G:N2	2:B:92:ASP:O	0.65	2.30	17	1
2:B:102:LEU:HD21	2:B:153:LEU:HD12	0.65	1.69	17	1
2:B:53:ASN:OD1	2:B:55:LYS:CB	0.64	2.45	13	19
1:A:1:G:H4'	1:A:2:G:OP1	0.64	1.91	2	1
1:A:12:C:C2	1:A:12:C:OP1	0.64	2.50	14	4
1:A:8:A:N1	1:A:14:A:O2'	0.64	2.28	13	4
2:B:140:TYR:OH	2:B:171:THR:OG1	0.64	2.10	11	1
1:A:20:G:O2'	1:A:21:C:OP1	0.64	2.14	13	1
1:A:20:G:O2'	1:A:21:C:C5'	0.64	2.46	1	4
1:A:14:A:O4'	1:A:14:A:P	0.64	2.56	2	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:13:G:O2'	2:B:52:THR:OG1	0.64	2.14	14	2
1:A:14:A:C6	2:B:94:LYS:CD	0.64	2.80	13	3
2:B:73:LEU:HD22	2:B:76:LEU:CD1	0.64	2.20	13	1
1:A:4:C:O2'	1:A:5:G:C8	0.64	2.51	8	17
1:A:19:G:C5	1:A:20:G:N7	0.64	2.65	5	11
2:B:104:ALA:HB1	2:B:166:VAL:CG1	0.64	2.22	9	4
2:B:116:LEU:CD1	2:B:139:ALA:HB1	0.64	2.22	10	3
2:B:129:VAL:CB	2:B:138:ILE:HB	0.64	2.23	15	19
1:A:2:G:N1	1:A:22:C:C4	0.64	2.65	10	6
1:A:7:A:H4'	1:A:7:A:OP1	0.64	1.91	14	1
2:B:102:LEU:HD21	2:B:143:PHE:HE1	0.64	1.51	19	1
1:A:12:C:C4	2:B:17:PHE:CZ	0.64	2.86	3	12
1:A:12:C:OP1	1:A:12:C:C4	0.64	2.51	6	2
2:B:38:PHE:CE2	2:B:73:LEU:HD13	0.64	2.27	9	1
2:B:103:LEU:CB	2:B:140:TYR:CD1	0.64	2.80	18	3
1:A:12:C:C2	1:A:12:C:OP2	0.64	2.51	19	4
2:B:16:LEU:CD1	2:B:16:LEU:N	0.64	2.60	13	4
1:A:16:G:C6	2:B:54:ARG:NH1	0.64	2.65	13	2
1:A:9:U:N3	2:B:138:ILE:CD1	0.64	2.60	4	3
2:B:103:LEU:HD11	2:B:171:THR:CG2	0.64	2.20	6	1
1:A:10:C:C6	2:B:140:TYR:CE2	0.64	2.86	15	1
1:A:14:A:OP2	1:A:14:A:C4'	0.64	2.45	3	2
2:B:33:ALA:CB	2:B:78:VAL:HG13	0.64	2.23	3	1
1:A:7:A:O2'	1:A:8:A:O5'	0.64	2.16	14	3
2:B:102:LEU:HD22	2:B:170:TYR:HB3	0.64	1.70	14	1
1:A:11:C:O2	2:B:94:LYS:NZ	0.64	2.31	14	1
1:A:20:G:C6	1:A:21:C:C5	0.64	2.86	3	8
2:B:17:PHE:CD1	2:B:18:ILE:N	0.63	2.66	14	16
2:B:52:THR:O	2:B:53:ASN:CB	0.63	2.46	19	19
1:A:18:A:O2'	1:A:19:G:C5'	0.63	2.46	3	6
2:B:120:PHE:HZ	2:B:168:LEU:HD11	0.63	1.53	18	6
2:B:123:ALA:CB	2:B:141:ILE:HG23	0.63	2.24	11	1
2:B:102:LEU:HD12	2:B:170:TYR:CE1	0.63	2.28	12	1
1:A:13:G:C6	2:B:58:TYR:CE2	0.63	2.85	1	2
1:A:20:G:N1	1:A:21:C:C4	0.63	2.66	9	5
1:A:11:C:N3	2:B:94:LYS:CD	0.63	2.61	2	2
2:B:30:LEU:HD12	2:B:54:ARG:HD2	0.63	1.69	3	6
1:A:14:A:C8	1:A:14:A:P	0.63	2.91	17	2
1:A:14:A:N1	2:B:94:LYS:CG	0.63	2.61	12	3
1:A:7:A:HO2'	1:A:8:A:P	0.63	2.15	10	1
2:B:11:THR:HG21	2:B:47:ASP:CG	0.63	2.13	17	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:16:G:OP1	1:A:16:G:C4'	0.63	2.46	18	1
2:B:33:ALA:HB3	2:B:78:VAL:HG13	0.63	1.70	3	1
2:B:127:ARG:CZ	2:B:140:TYR:CD2	0.63	2.82	12	3
1:A:19:G:O2'	1:A:20:G:O4'	0.63	2.16	15	2
2:B:102:LEU:CA	2:B:171:THR:HG23	0.63	2.24	2	3
2:B:21:LEU:HD23	2:B:30:LEU:HD23	0.63	1.69	4	2
2:B:127:ARG:NH2	2:B:140:TYR:CD2	0.63	2.67	12	5
1:A:8:A:C4'	1:A:9:U:OP2	0.63	2.45	17	5
2:B:34:ILE:CG2	2:B:38:PHE:CE2	0.63	2.82	11	1
2:B:38:PHE:CD1	2:B:43:LEU:CD2	0.63	2.78	16	1
2:B:22:ASN:HB2	2:B:30:LEU:HD21	0.63	1.69	19	6
1:A:17:U:C2'	1:A:18:A:OP1	0.63	2.46	11	1
1:A:19:G:H8	1:A:19:G:O5'	0.63	1.76	13	1
2:B:61:PHE:CE1	2:B:70:ALA:HB1	0.63	2.28	16	1
2:B:38:PHE:CE2	2:B:43:LEU:CD2	0.63	2.82	19	1
1:A:11:C:HO2'	1:A:12:C:H5'	0.63	1.53	1	4
1:A:9:U:C4'	1:A:10:C:OP1	0.63	2.47	16	5
2:B:97:ARG:O	2:B:101:THR:OG1	0.63	2.17	7	11
1:A:15:A:HO2'	1:A:16:G:P	0.63	2.16	5	2
1:A:2:G:N2	1:A:22:C:C6	0.63	2.66	18	3
2:B:38:PHE:CD2	2:B:45:VAL:HG13	0.63	2.29	19	7
2:B:17:PHE:CD1	2:B:17:PHE:C	0.63	2.72	19	5
2:B:18:ILE:HD12	2:B:59:VAL:HG21	0.63	1.69	5	2
1:A:12:C:N3	1:A:12:C:OP1	0.63	2.32	16	1
1:A:12:C:OP2	1:A:12:C:C6	0.63	2.52	19	2
1:A:13:G:N7	2:B:49:ARG:HD2	0.63	2.08	13	4
1:A:13:G:N2	2:B:90:GLY:O	0.63	2.32	6	3
1:A:7:A:O2'	1:A:8:A:OP1	0.63	2.16	14	4
1:A:7:A:N6	1:A:8:A:C2	0.62	2.67	18	8
2:B:17:PHE:CE1	2:B:18:ILE:O	0.62	2.53	6	12
2:B:101:THR:O	2:B:171:THR:OG1	0.62	2.17	10	13
2:B:102:LEU:N	2:B:102:LEU:HD12	0.62	2.09	2	1
1:A:19:G:O2'	1:A:20:G:O5'	0.62	2.17	9	6
2:B:67:LEU:HD22	2:B:67:LEU:C	0.62	2.10	8	1
1:A:13:G:HO2'	1:A:14:A:P	0.62	2.17	9	1
2:B:43:LEU:HD11	2:B:73:LEU:HD21	0.62	1.71	7	2
1:A:14:A:C4	2:B:94:LYS:HG2	0.62	2.29	4	5
1:A:19:G:C2'	1:A:20:G:O5'	0.62	2.47	7	4
2:B:120:PHE:CD2	2:B:141:ILE:HD13	0.62	2.30	5	7
2:B:124:LEU:HD11	2:B:144:LYS:N	0.62	2.10	15	5
2:B:101:THR:OG1	2:B:142:GLU:CG	0.62	2.47	3	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:51:GLY:HA3	2:B:56:PHE:CD2	0.62	2.29	14	3
2:B:107:LEU:HD11	2:B:116:LEU:HD21	0.62	1.70	13	1
2:B:102:LEU:HD12	2:B:168:LEU:HD22	0.62	1.70	9	2
1:A:21:C:O2	1:A:22:C:C6	0.62	2.51	10	8
1:A:15:A:O2'	1:A:16:G:OP2	0.62	2.17	14	7
2:B:161:ILE:HD12	2:B:166:VAL:CG2	0.62	2.24	17	1
1:A:14:A:N3	2:B:95:LYS:HB3	0.62	2.09	8	4
1:A:9:U:H4'	1:A:10:C:OP2	0.62	1.92	19	4
1:A:2:G:N2	1:A:22:C:N1	0.62	2.47	18	4
1:A:4:C:O2'	1:A:5:G:O4'	0.62	2.17	1	18
2:B:51:GLY:HA3	2:B:56:PHE:CD1	0.62	2.30	3	13
1:A:12:C:N3	2:B:17:PHE:CZ	0.62	2.68	19	9
1:A:15:A:H1'	1:A:17:U:OP1	0.62	1.95	8	1
1:A:9:U:O2'	1:A:10:C:O5'	0.62	2.17	6	3
2:B:128:LEU:HD23	2:B:129:VAL:N	0.62	2.10	12	2
2:B:70:ALA:HA	2:B:73:LEU:HD12	0.62	1.71	13	1
2:B:30:LEU:HD12	2:B:30:LEU:C	0.62	2.13	14	1
1:A:8:A:C6	1:A:14:A:N3	0.62	2.68	14	12
1:A:20:G:C2	1:A:21:C:C5	0.62	2.88	9	3
2:B:14:PHE:CE2	2:B:63:SER:O	0.62	2.53	18	1
2:B:128:LEU:HD13	2:B:129:VAL:N	0.62	2.09	2	3
1:A:11:C:N3	2:B:94:LYS:HD2	0.62	2.10	2	2
1:A:20:G:C6	1:A:21:C:N4	0.62	2.68	5	4
2:B:16:LEU:CD1	2:B:85:LEU:HD21	0.62	2.25	5	1
1:A:20:G:HO2'	1:A:21:C:C5'	0.62	2.08	6	1
1:A:12:C:OP2	1:A:12:C:C5	0.62	2.53	9	3
2:B:124:LEU:N	2:B:124:LEU:HD23	0.62	2.08	14	1
2:B:98:ALA:HB1	2:B:171:THR:CB	0.62	2.25	15	1
1:A:17:U:OP2	1:A:17:U:C6	0.62	2.53	16	1
1:A:14:A:C5	2:B:94:LYS:CG	0.62	2.83	15	3
1:A:10:C:C4	1:A:11:C:N4	0.62	2.68	13	4
1:A:15:A:C4	1:A:17:U:C6	0.62	2.88	18	6
2:B:16:LEU:O	2:B:58:TYR:CD2	0.62	2.53	12	5
1:A:11:C:O2'	1:A:12:C:O5'	0.62	2.17	17	3
2:B:30:LEU:CD1	2:B:31:LYS:N	0.62	2.59	14	1
2:B:12:THR:OG1	2:B:15:ASN:ND2	0.62	2.33	19	1
2:B:103:LEU:HB3	2:B:140:TYR:CD1	0.61	2.30	18	2
2:B:103:LEU:CD2	2:B:129:VAL:HG21	0.61	2.24	9	3
2:B:74:THR:CA	2:B:85:LEU:HD21	0.61	2.25	18	1
1:A:14:A:OP1	1:A:14:A:C8	0.61	2.52	9	2
1:A:7:A:OP1	1:A:7:A:C4'	0.61	2.48	14	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:51:GLY:HA3	2:B:56:PHE:O	0.61	1.96	19	2
2:B:34:ILE:O	2:B:38:PHE:CD1	0.61	2.53	15	6
1:A:13:G:O2'	1:A:14:A:OP1	0.61	2.18	9	3
2:B:30:LEU:HD12	2:B:54:ARG:HD3	0.61	1.72	7	1
1:A:8:A:N6	1:A:14:A:N9	0.61	2.48	17	10
2:B:98:ALA:O	2:B:171:THR:OG1	0.61	2.18	3	3
2:B:34:ILE:HD11	2:B:78:VAL:CG2	0.61	2.23	13	2
1:A:15:A:C5	1:A:17:U:N3	0.61	2.69	18	10
2:B:92:ASP:O	2:B:94:LYS:N	0.61	2.33	14	7
1:A:2:G:N2	1:A:22:C:C2	0.61	2.69	15	5
1:A:3:C:HO2'	1:A:4:C:P	0.61	2.19	4	3
1:A:15:A:O2'	1:A:16:G:P	0.61	2.58	5	5
1:A:1:G:C6	1:A:2:G:C5	0.61	2.88	12	3
2:B:12:THR:HG21	2:B:46:VAL:CB	0.61	2.26	19	1
1:A:20:G:O2'	1:A:21:C:O5'	0.61	2.19	6	8
2:B:107:LEU:HD23	2:B:111:ILE:CG2	0.61	2.26	5	1
2:B:92:ASP:CB	2:B:96:VAL:HG11	0.61	2.24	16	1
2:B:63:SER:OG	2:B:66:ASP:CB	0.61	2.49	5	3
1:A:13:G:C2	2:B:92:ASP:O	0.61	2.54	17	1
2:B:156:LYS:O	2:B:157:GLN:C	0.61	2.39	5	18
1:A:14:A:C2	2:B:95:LYS:HB3	0.61	2.31	12	3
2:B:102:LEU:HD22	2:B:102:LEU:H	0.61	1.55	12	7
1:A:18:A:O2'	1:A:19:G:O5'	0.61	2.18	17	3
2:B:16:LEU:HD21	2:B:61:PHE:HE2	0.61	1.56	5	2
2:B:107:LEU:HD12	2:B:111:ILE:CG2	0.61	2.26	11	2
1:A:12:C:C2	2:B:17:PHE:CE2	0.61	2.88	12	1
2:B:14:PHE:CZ	2:B:64:ALA:HB2	0.61	2.31	19	2
2:B:136:LYS:HD3	2:B:138:ILE:HD11	0.61	1.71	7	1
1:A:12:C:O5'	1:A:12:C:N1	0.61	2.34	11	3
1:A:6:A:O2'	1:A:7:A:OP1	0.61	2.17	14	1
1:A:16:G:O2'	1:A:17:U:OP1	0.61	2.19	16	1
1:A:20:G:O2'	1:A:21:C:O4'	0.60	2.19	7	3
1:A:20:G:H4'	1:A:21:C:OP1	0.60	1.96	9	1
2:B:18:ILE:HD12	2:B:59:VAL:HB	0.60	1.72	9	1
2:B:102:LEU:HD23	2:B:168:LEU:CD2	0.60	2.25	10	1
2:B:158:GLY:O	2:B:159:ALA:C	0.60	2.39	18	12
1:A:19:G:O2'	1:A:20:G:OP1	0.60	2.19	7	7
1:A:1:G:C6	1:A:2:G:N7	0.60	2.69	12	2
1:A:2:G:C6	1:A:3:C:C5	0.60	2.89	3	6
1:A:12:C:O2'	1:A:13:G:P	0.60	2.60	15	2
2:B:71:LEU:HD13	2:B:71:LEU:O	0.60	1.96	6	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:12:C:O2'	2:B:56:PHE:CD2	0.60	2.50	7	2
2:B:159:ALA:HB3	2:B:161:ILE:HD11	0.60	1.71	9	1
2:B:22:ASN:CB	2:B:30:LEU:CD2	0.60	2.79	17	3
2:B:44:ALA:HB3	2:B:66:ASP:CG	0.60	2.16	14	2
1:A:1:G:N1	1:A:2:G:C5	0.60	2.70	12	2
1:A:8:A:N6	1:A:14:A:O2'	0.60	2.34	14	7
1:A:9:U:O4	2:B:105:LYS:NZ	0.60	2.34	4	2
1:A:9:U:OP2	1:A:11:C:N4	0.60	2.34	14	2
1:A:14:A:C2	2:B:94:LYS:HG3	0.60	2.30	10	7
2:B:92:ASP:HA	2:B:96:VAL:HG11	0.60	1.71	16	2
2:B:128:LEU:CD2	2:B:136:LYS:CB	0.60	2.79	15	1
2:B:129:VAL:O	2:B:136:LYS:HA	0.60	1.95	15	1
1:A:4:C:HO2'	1:A:5:G:C1'	0.60	2.08	9	15
1:A:10:C:O2'	2:B:128:LEU:O	0.60	2.19	12	13
2:B:21:LEU:O	2:B:22:ASN:HB2	0.60	1.97	12	18
2:B:78:VAL:HG21	2:B:83:ILE:HG21	0.60	1.73	16	7
1:A:21:C:O2'	1:A:22:C:O5'	0.60	2.19	5	9
1:A:14:A:OP2	2:B:94:LYS:CB	0.60	2.49	4	1
2:B:153:LEU:HD23	2:B:154:GLU:HG3	0.60	1.71	7	1
2:B:157:GLN:O	2:B:159:ALA:N	0.60	2.34	16	1
1:A:15:A:C1'	1:A:16:G:OP1	0.60	2.50	18	1
2:B:14:PHE:CE2	2:B:63:SER:CA	0.60	2.85	7	6
2:B:171:THR:O	2:B:171:THR:CG2	0.60	2.49	9	1
2:B:107:LEU:HD12	2:B:138:ILE:HA	0.60	1.73	1	2
2:B:18:ILE:HA	2:B:84:LYS:O	0.60	1.97	13	15
2:B:61:PHE:CD1	2:B:66:ASP:OD1	0.60	2.55	5	1
2:B:71:LEU:HD13	2:B:71:LEU:C	0.60	2.16	6	1
2:B:48:VAL:HG23	2:B:59:VAL:HG23	0.60	1.73	9	1
1:A:10:C:O2	1:A:10:C:C2'	0.60	2.45	16	19
2:B:17:PHE:CE2	2:B:86:GLU:CG	0.60	2.84	4	3
2:B:78:VAL:CG2	2:B:83:ILE:CG2	0.60	2.79	15	9
2:B:123:ALA:CB	2:B:141:ILE:HG22	0.60	2.27	2	3
2:B:156:LYS:O	2:B:158:GLY:N	0.60	2.34	9	4
1:A:3:C:H4'	1:A:4:C:OP1	0.60	1.96	12	5
1:A:15:A:C2	1:A:17:U:C4	0.60	2.90	8	5
1:A:16:G:HO2'	1:A:17:U:P	0.60	2.18	16	2
1:A:12:C:C6	2:B:17:PHE:CE2	0.60	2.89	15	1
2:B:73:LEU:HD12	2:B:76:LEU:CD2	0.60	2.27	19	1
1:A:10:C:C4	1:A:11:C:C5	0.60	2.89	10	9
2:B:21:LEU:O	2:B:78:VAL:HG11	0.60	1.96	4	7
2:B:130:SER:O	2:B:136:LYS:NZ	0.60	2.35	1	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:140:TYR:HE2	2:B:171:THR:HG21	0.60	1.56	1	2
2:B:128:LEU:HD13	2:B:128:LEU:C	0.60	2.16	4	2
2:B:27:VAL:HG23	2:B:54:ARG:HE	0.60	1.56	18	2
2:B:126:ILE:HG13	2:B:141:ILE:HG23	0.60	1.73	3	1
1:A:14:A:O3'	1:A:15:A:C8	0.60	2.53	14	2
2:B:59:VAL:CG1	2:B:61:PHE:CE1	0.60	2.85	18	2
2:B:128:LEU:N	2:B:128:LEU:CD1	0.60	2.65	16	1
2:B:35:SER:HA	2:B:45:VAL:HG21	0.60	1.74	10	3
1:A:11:C:N3	2:B:94:LYS:CE	0.60	2.65	5	6
2:B:38:PHE:CB	2:B:45:VAL:CG2	0.60	2.79	14	3
2:B:158:GLY:O	2:B:159:ALA:HB3	0.60	1.96	16	2
1:A:1:G:O2'	1:A:2:G:O5'	0.59	2.19	4	5
1:A:14:A:N6	2:B:94:LYS:HE3	0.59	2.12	2	2
1:A:20:G:H4'	1:A:20:G:OP1	0.59	1.97	3	1
1:A:18:A:C2'	1:A:19:G:O4'	0.59	2.50	17	6
2:B:43:LEU:HD21	2:B:69:LYS:CB	0.59	2.27	17	3
1:A:12:C:O2'	1:A:13:G:OP1	0.59	2.18	8	2
2:B:124:LEU:HD11	2:B:144:LYS:HG2	0.59	1.73	16	1
2:B:78:VAL:HG23	2:B:83:ILE:HG21	0.59	1.74	6	4
2:B:85:LEU:O	2:B:86:GLU:CB	0.59	2.50	16	19
2:B:116:LEU:HD13	2:B:139:ALA:HB1	0.59	1.74	13	4
2:B:102:LEU:C	2:B:102:LEU:HD12	0.59	2.17	6	1
2:B:107:LEU:CD2	2:B:166:VAL:HG13	0.59	2.26	7	1
1:A:14:A:P	1:A:14:A:O4'	0.59	2.61	9	1
2:B:30:LEU:CD1	2:B:54:ARG:CG	0.59	2.80	16	2
1:A:19:G:C6	1:A:20:G:C5	0.59	2.89	19	9
1:A:19:G:N1	1:A:20:G:C5	0.59	2.70	19	12
1:A:7:A:O2'	1:A:8:A:H5'	0.59	1.97	7	6
1:A:14:A:C5	2:B:94:LYS:HE2	0.59	2.33	9	1
2:B:107:LEU:HD21	2:B:139:ALA:CB	0.59	2.20	10	1
2:B:158:GLY:O	2:B:166:VAL:HG12	0.59	1.97	13	2
1:A:9:U:H5	2:B:103:LEU:HD21	0.59	1.58	16	5
2:B:73:LEU:HD12	2:B:76:LEU:CG	0.59	2.27	10	3
1:A:13:G:H21	2:B:91:ARG:CB	0.59	2.11	9	1
2:B:116:LEU:CD1	2:B:139:ALA:CB	0.59	2.80	10	1
1:A:3:C:O2'	1:A:4:C:O5'	0.59	2.21	11	12
2:B:103:LEU:CD1	2:B:138:ILE:HG22	0.59	2.27	3	2
1:A:11:C:C2	2:B:94:LYS:HE2	0.59	2.32	6	1
2:B:107:LEU:HD13	2:B:138:ILE:C	0.59	2.18	6	3
1:A:14:A:C8	1:A:14:A:OP2	0.59	2.56	16	1
2:B:102:LEU:HD12	2:B:141:ILE:O	0.59	1.96	2	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:103:LEU:HG	2:B:140:TYR:CD1	0.59	2.33	4	4
1:A:14:A:C5	2:B:94:LYS:HD3	0.59	2.32	16	4
2:B:73:LEU:CD1	2:B:76:LEU:HD21	0.59	2.28	19	1
1:A:8:A:C5'	1:A:9:U:O5'	0.59	2.51	11	4
2:B:14:PHE:CE2	2:B:63:SER:C	0.59	2.76	4	9
2:B:29:GLU:CD	2:B:79:PHE:CZ	0.59	2.76	11	6
1:A:15:A:H5"	1:A:16:G:OP1	0.59	1.97	10	3
1:A:9:U:O2'	1:A:10:C:OP1	0.59	2.21	14	5
1:A:18:A:O2'	1:A:19:G:OP1	0.59	2.20	5	2
2:B:48:VAL:CG2	2:B:59:VAL:HG13	0.59	2.16	5	1
2:B:46:VAL:HG21	2:B:61:PHE:O	0.59	1.97	13	6
2:B:21:LEU:HD22	2:B:30:LEU:HB3	0.59	1.73	17	2
1:A:10:C:C4'	2:B:128:LEU:O	0.59	2.50	15	1
2:B:37:LEU:CD2	2:B:73:LEU:HD22	0.59	2.28	16	1
2:B:108:SER:OG	2:B:164:ARG:NH1	0.59	2.36	10	1
2:B:29:GLU:OE1	2:B:79:PHE:CE1	0.59	2.55	17	2
1:A:15:A:C4'	1:A:16:G:OP1	0.59	2.51	6	8
1:A:10:C:C2'	1:A:11:C:OP1	0.59	2.51	2	1
1:A:5:G:O2'	1:A:6:A:O5'	0.59	2.20	18	3
1:A:9:U:C2	2:B:138:ILE:CD1	0.59	2.85	6	3
1:A:14:A:C8	1:A:14:A:OP1	0.59	2.55	16	3
2:B:14:PHE:CZ	2:B:63:SER:C	0.59	2.75	13	2
2:B:107:LEU:HD13	2:B:139:ALA:HB2	0.59	1.75	11	2
2:B:45:VAL:HG23	2:B:45:VAL:O	0.59	1.97	3	12
1:A:11:C:N3	2:B:94:LYS:HE3	0.59	2.13	6	5
2:B:12:THR:CB	2:B:13:PRO:CD	0.59	2.81	13	4
2:B:103:LEU:CD1	2:B:140:TYR:CE2	0.59	2.86	15	1
2:B:65:GLU:OE2	2:B:69:LYS:NZ	0.59	2.35	16	1
2:B:103:LEU:HG	2:B:140:TYR:CE1	0.58	2.33	11	4
2:B:129:VAL:N	2:B:138:ILE:O	0.58	2.36	16	13
1:A:4:C:O2'	1:A:5:G:H8	0.58	1.79	8	10
1:A:9:U:N3	2:B:138:ILE:HD13	0.58	2.13	11	3
1:A:10:C:C5	1:A:11:C:N4	0.58	2.71	15	1
2:B:127:ARG:NH2	2:B:140:TYR:CD1	0.58	2.70	18	1
2:B:63:SER:OG	2:B:66:ASP:OD2	0.58	2.21	11	12
2:B:116:LEU:CD2	2:B:141:ILE:HD11	0.58	2.28	18	2
1:A:14:A:OP1	2:B:52:THR:OG1	0.58	2.22	16	3
1:A:10:C:O2	1:A:11:C:O4'	0.58	2.21	18	1
1:A:15:A:OP1	1:A:17:U:C1'	0.58	2.50	10	7
2:B:50:THR:C	2:B:57:GLY:HA2	0.58	2.18	9	16
2:B:102:LEU:C	2:B:171:THR:HG23	0.58	2.18	13	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:5:G:H4'	1:A:6:A:OP1	0.58	1.97	4	1
1:A:14:A:OP2	1:A:14:A:N9	0.58	2.36	4	2
1:A:19:G:C2	1:A:20:G:C8	0.58	2.92	11	5
1:A:14:A:C6	2:B:94:LYS:HG2	0.58	2.33	8	5
2:B:127:ARG:NH2	2:B:140:TYR:CB	0.58	2.66	18	1
1:A:13:G:N2	2:B:90:GLY:CA	0.58	2.66	3	2
2:B:158:GLY:N	2:B:166:VAL:O	0.58	2.36	9	13
1:A:15:A:C2	1:A:16:G:N3	0.58	2.71	15	3
2:B:34:ILE:N	2:B:34:ILE:CD1	0.58	2.66	9	1
1:A:14:A:OP2	2:B:94:LYS:N	0.58	2.36	19	1
1:A:2:G:C5	1:A:3:C:C6	0.58	2.92	9	2
1:A:9:U:C5	2:B:103:LEU:HD11	0.58	2.33	5	3
1:A:14:A:C6	2:B:94:LYS:HE2	0.58	2.34	2	4
2:B:102:LEU:CD1	2:B:170:TYR:CD1	0.58	2.85	13	4
2:B:58:TYR:C	2:B:59:VAL:CG2	0.58	2.72	19	4
2:B:141:ILE:HG22	2:B:143:PHE:CE1	0.58	2.34	10	4
2:B:61:PHE:CB	2:B:66:ASP:CG	0.58	2.72	18	3
1:A:12:C:H1'	2:B:56:PHE:CE2	0.58	2.34	19	2
2:B:145:SER:N	2:B:148:ASP:OD1	0.58	2.36	19	1
2:B:54:ARG:N	2:B:54:ARG:CD	0.58	2.66	15	8
2:B:169:TYR:O	2:B:170:TYR:O	0.58	2.21	8	17
2:B:12:THR:HG21	2:B:46:VAL:CG1	0.58	2.15	3	4
2:B:104:ALA:O	2:B:107:LEU:HD13	0.58	1.99	10	2
2:B:146:GLU:CG	2:B:170:TYR:OH	0.58	2.52	7	4
2:B:46:VAL:HG22	2:B:62:GLU:CG	0.58	2.28	17	4
1:A:5:G:HO2'	1:A:6:A:C5'	0.58	2.10	15	1
2:B:130:SER:CB	2:B:136:LYS:HD2	0.58	2.29	15	1
1:A:15:A:OP1	1:A:15:A:O4'	0.58	2.21	7	7
1:A:8:A:C5'	1:A:9:U:OP2	0.58	2.52	17	4
1:A:8:A:N6	1:A:14:A:C8	0.58	2.71	17	6
2:B:11:THR:O	2:B:11:THR:HG22	0.58	1.98	3	5
2:B:26:SER:O	2:B:30:LEU:CD1	0.58	2.51	4	2
1:A:13:G:N2	2:B:91:ARG:CB	0.58	2.66	9	1
2:B:73:LEU:O	2:B:75:GLY:N	0.58	2.37	9	4
2:B:21:LEU:CB	2:B:30:LEU:HD22	0.58	2.29	16	1
1:A:14:A:OP1	2:B:94:LYS:N	0.58	2.37	1	2
2:B:105:LYS:N	2:B:167:SER:O	0.58	2.35	9	11
2:B:116:LEU:HD22	2:B:141:ILE:HD11	0.58	1.75	1	1
2:B:156:LYS:O	2:B:157:GLN:O	0.58	2.20	8	12
2:B:107:LEU:HD13	2:B:166:VAL:CG2	0.58	2.29	7	1
2:B:14:PHE:CD1	2:B:67:LEU:HD13	0.58	2.33	9	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:140:TYR:CZ	2:B:171:THR:CG2	0.58	2.87	13	2
2:B:103:LEU:HD13	2:B:140:TYR:CE2	0.58	2.34	15	1
2:B:21:LEU:CD2	2:B:56:PHE:O	0.58	2.52	7	13
2:B:107:LEU:HD12	2:B:138:ILE:CA	0.58	2.29	1	2
2:B:130:SER:HA	2:B:136:LYS:CB	0.58	2.29	10	17
1:A:5:G:O2'	1:A:6:A:C5'	0.58	2.52	4	1
2:B:63:SER:OG	2:B:66:ASP:HB3	0.58	1.98	5	6
1:A:21:C:O2'	1:A:22:C:OP1	0.58	2.22	14	2
2:B:66:ASP:O	2:B:70:ALA:HB2	0.58	1.98	1	8
2:B:158:GLY:O	2:B:166:VAL:N	0.58	2.37	2	12
1:A:6:A:C6	1:A:7:A:C5	0.58	2.92	2	3
1:A:11:C:H2'	1:A:12:C:O5'	0.58	1.99	19	8
1:A:10:C:N3	1:A:11:C:C6	0.58	2.72	11	8
2:B:78:VAL:HG12	2:B:81:ASN:O	0.58	1.98	14	3
2:B:116:LEU:CD2	2:B:139:ALA:CB	0.58	2.82	8	3
2:B:21:LEU:CD2	2:B:78:VAL:HG21	0.58	2.28	9	1
2:B:67:LEU:HD13	2:B:67:LEU:O	0.57	1.98	17	3
2:B:103:LEU:CD1	2:B:138:ILE:CG2	0.57	2.82	3	3
1:A:2:G:O2'	1:A:3:C:O5'	0.57	2.21	12	9
1:A:10:C:H42	2:B:94:LYS:CE	0.57	2.12	8	2
2:B:102:LEU:HD22	2:B:168:LEU:HD12	0.57	1.76	11	2
1:A:15:A:C4'	1:A:17:U:OP1	0.57	2.52	8	1
1:A:3:C:HO2'	1:A:4:C:H5'	0.57	1.57	9	1
2:B:29:GLU:O	2:B:79:PHE:CD2	0.57	2.57	17	1
2:B:103:LEU:HB2	2:B:140:TYR:CD1	0.57	2.33	5	3
2:B:129:VAL:HB	2:B:138:ILE:CB	0.57	2.29	15	19
1:A:13:G:C2'	1:A:14:A:O5'	0.57	2.52	2	4
2:B:74:THR:O	2:B:74:THR:HG22	0.57	1.99	7	6
2:B:37:LEU:HD22	2:B:76:LEU:HD11	0.57	1.75	9	1
2:B:73:LEU:O	2:B:76:LEU:CD2	0.57	2.50	9	1
2:B:145:SER:O	2:B:148:ASP:OD1	0.57	2.22	19	1
1:A:14:A:C2	2:B:94:LYS:HG2	0.57	2.34	16	5
1:A:4:C:C2'	1:A:5:G:O5'	0.57	2.52	11	10
1:A:15:A:O2'	1:A:16:G:O5'	0.57	2.21	5	3
2:B:74:THR:OG1	2:B:85:LEU:HD13	0.57	1.99	10	1
1:A:3:C:HO2'	1:A:4:C:H6	0.57	1.40	12	1
2:B:30:LEU:HD11	2:B:54:ARG:HG2	0.57	1.77	16	1
1:A:2:G:C4	1:A:3:C:C6	0.57	2.92	9	4
2:B:21:LEU:CB	2:B:54:ARG:O	0.57	2.53	3	11
2:B:104:ALA:N	2:B:139:ALA:O	0.57	2.38	19	12
2:B:63:SER:O	2:B:66:ASP:OD2	0.57	2.23	18	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:17:PHE:O	2:B:18:ILE:HD12	0.57	1.99	12	1
2:B:73:LEU:CD1	2:B:76:LEU:CD1	0.57	2.81	7	2
2:B:74:THR:HA	2:B:85:LEU:HD12	0.57	1.76	11	1
1:A:8:A:C2	2:B:95:LYS:HG3	0.57	2.34	13	1
2:B:126:ILE:CD1	2:B:141:ILE:HG23	0.57	2.30	18	1
1:A:8:A:H61	1:A:14:A:C2'	0.57	2.12	14	11
2:B:103:LEU:N	2:B:169:TYR:O	0.57	2.36	3	8
2:B:153:LEU:O	2:B:153:LEU:HD23	0.57	1.99	2	1
1:A:12:C:P	1:A:12:C:C5	0.57	2.97	7	2
1:A:16:G:C5	2:B:27:VAL:CG2	0.57	2.88	6	2
1:A:11:C:C2	2:B:127:ARG:NH2	0.57	2.73	13	1
2:B:83:ILE:CD1	2:B:83:ILE:O	0.57	2.52	14	1
2:B:143:PHE:CD2	2:B:149:ALA:CB	0.57	2.87	18	1
2:B:127:ARG:HB2	2:B:140:TYR:CB	0.57	2.29	8	14
1:A:2:G:C2	1:A:22:C:N3	0.57	2.72	10	4
2:B:22:ASN:O	2:B:54:ARG:CB	0.57	2.53	19	10
2:B:16:LEU:CD2	2:B:17:PHE:O	0.57	2.53	13	4
2:B:66:ASP:OD1	2:B:67:LEU:N	0.57	2.37	18	3
2:B:116:LEU:HD22	2:B:139:ALA:HB1	0.57	1.77	8	1
2:B:37:LEU:CD1	2:B:76:LEU:HD12	0.57	2.25	9	1
2:B:145:SER:OG	2:B:148:ASP:OD2	0.57	2.22	19	1
2:B:28:ALA:O	2:B:32:VAL:CG2	0.57	2.53	13	13
1:A:14:A:OP2	1:A:14:A:O4'	0.57	2.23	4	3
2:B:124:LEU:N	2:B:142:GLU:O	0.57	2.38	8	6
1:A:16:G:C1'	1:A:17:U:OP2	0.57	2.53	16	1
1:A:11:C:N3	2:B:94:LYS:CB	0.57	2.68	18	1
2:B:25:LYS:HE3	2:B:79:PHE:CE1	0.57	2.35	19	1
1:A:16:G:N7	2:B:27:VAL:HB	0.56	2.15	18	10
2:B:14:PHE:CE2	2:B:63:SER:HA	0.56	2.35	7	4
1:A:12:C:OP1	1:A:12:C:C6	0.56	2.58	10	2
2:B:99:ALA:O	2:B:170:TYR:OH	0.56	2.20	3	10
1:A:6:A:C6	1:A:18:A:C4	0.56	2.93	13	2
1:A:9:U:C5	2:B:138:ILE:CD1	0.56	2.87	3	4
2:B:76:LEU:HD13	2:B:83:ILE:HD11	0.56	1.76	13	2
1:A:18:A:H4'	1:A:19:G:OP1	0.56	2.00	17	2
1:A:14:A:C5	2:B:94:LYS:CE	0.56	2.87	7	3
2:B:92:ASP:C	2:B:93:SER:OG	0.56	2.43	14	1
2:B:127:ARG:O	2:B:140:TYR:N	0.56	2.39	15	5
1:A:4:C:C4'	1:A:5:G:OP1	0.56	2.50	18	6
2:B:105:LYS:O	2:B:106:ASN:CB	0.56	2.54	15	14
2:B:18:ILE:HG12	2:B:85:LEU:HD12	0.56	1.77	6	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:12:THR:HG23	2:B:46:VAL:HG11	0.56	1.75	19	3
1:A:19:G:OP2	1:A:19:G:C8	0.56	2.58	11	1
2:B:98:ALA:O	2:B:171:THR:CG2	0.56	2.53	11	1
1:A:11:C:C2	2:B:94:LYS:HD3	0.56	2.35	12	1
2:B:31:LYS:HG2	2:B:48:VAL:HG12	0.56	1.75	17	1
2:B:70:ALA:O	2:B:85:LEU:CD1	0.56	2.53	18	1
2:B:37:LEU:O	2:B:41:ASN:ND2	0.56	2.39	10	8
2:B:161:ILE:O	2:B:164:ARG:N	0.56	2.38	16	18
2:B:16:LEU:CD2	2:B:17:PHE:N	0.56	2.68	4	4
2:B:102:LEU:CD2	2:B:143:PHE:CE1	0.56	2.88	15	4
1:A:10:C:C4	2:B:140:TYR:CE1	0.56	2.93	10	6
2:B:17:PHE:CE2	2:B:86:GLU:HG3	0.56	2.35	4	1
1:A:13:G:N2	2:B:91:ARG:HB3	0.56	2.15	9	1
2:B:27:VAL:HG13	2:B:54:ARG:NE	0.56	2.15	9	2
2:B:38:PHE:CD1	2:B:43:LEU:HD13	0.56	2.35	16	1
2:B:47:ASP:O	2:B:48:VAL:CG2	0.56	2.53	13	7
1:A:15:A:C1'	1:A:17:U:OP1	0.56	2.53	8	1
2:B:94:LYS:NZ	2:B:94:LYS:O	0.56	2.39	8	1
2:B:102:LEU:HD12	2:B:149:ALA:HB1	0.56	1.76	10	1
1:A:14:A:O4'	2:B:95:LYS:CE	0.56	2.53	12	1
2:B:127:ARG:O	2:B:127:ARG:NH1	0.56	2.38	18	1
2:B:21:LEU:O	2:B:78:VAL:CG1	0.56	2.54	9	8
2:B:78:VAL:O	2:B:81:ASN:N	0.56	2.38	8	10
2:B:151:LYS:O	2:B:155:GLU:CB	0.56	2.54	11	8
2:B:101:THR:OG1	2:B:142:GLU:HG3	0.56	2.01	3	2
2:B:24:ASN:O	2:B:25:LYS:CD	0.56	2.54	4	1
2:B:16:LEU:CD1	2:B:17:PHE:N	0.56	2.68	6	9
2:B:85:LEU:C	2:B:85:LEU:CD2	0.56	2.73	12	1
1:A:15:A:N7	1:A:17:U:C2	0.56	2.74	17	7
2:B:111:ILE:O	2:B:112:THR:CG2	0.56	2.53	18	13
1:A:13:G:N2	2:B:90:GLY:HA2	0.56	2.15	3	1
2:B:21:LEU:HD23	2:B:78:VAL:HG21	0.56	1.77	9	1
2:B:94:LYS:NZ	2:B:95:LYS:CE	0.56	2.69	11	1
2:B:92:ASP:CB	2:B:96:VAL:CG2	0.56	2.83	12	1
2:B:102:LEU:O	2:B:141:ILE:N	0.56	2.39	17	3
1:A:10:C:OP1	2:B:129:VAL:CG1	0.56	2.54	19	1
2:B:38:PHE:CE2	2:B:43:LEU:CD1	0.56	2.85	19	1
1:A:12:C:C6	2:B:17:PHE:CZ	0.56	2.94	1	4
2:B:21:LEU:CD1	2:B:56:PHE:O	0.56	2.53	10	8
2:B:158:GLY:O	2:B:159:ALA:O	0.56	2.24	9	13
1:A:1:G:O2'	1:A:2:G:OP1	0.56	2.23	2	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:104:ALA:O	2:B:107:LEU:CD1	0.56	2.53	6	5
2:B:44:ALA:HB1	2:B:62:GLU:HG3	0.56	1.76	8	1
1:A:14:A:C5	2:B:94:LYS:CD	0.56	2.89	16	2
1:A:13:G:O2'	1:A:15:A:C3'	0.56	2.45	18	1
2:B:38:PHE:CG	2:B:45:VAL:CG1	0.56	2.88	5	6
1:A:2:G:C2'	1:A:3:C:O5'	0.56	2.53	6	6
2:B:140:TYR:CE2	2:B:171:THR:CG2	0.56	2.88	13	2
2:B:97:ARG:O	2:B:101:THR:N	0.56	2.39	7	1
2:B:102:LEU:HA	2:B:171:THR:OG1	0.56	2.00	7	2
2:B:103:LEU:CD1	2:B:129:VAL:HG11	0.56	2.31	15	1
2:B:129:VAL:O	2:B:136:LYS:CA	0.56	2.53	15	1
2:B:38:PHE:CE1	2:B:43:LEU:HD22	0.56	2.35	16	1
1:A:13:G:C8	2:B:58:TYR:HB2	0.56	2.35	18	1
2:B:63:SER:OG	2:B:66:ASP:CG	0.56	2.45	19	13
2:B:66:ASP:O	2:B:70:ALA:CB	0.56	2.54	16	4
1:A:6:A:C2	1:A:7:A:N9	0.56	2.73	17	2
2:B:19:GLY:O	2:B:20:ASN:CB	0.56	2.54	17	15
2:B:16:LEU:CD1	2:B:17:PHE:O	0.56	2.54	18	9
1:A:16:G:C5	2:B:27:VAL:HG23	0.56	2.35	6	1
2:B:14:PHE:CE2	2:B:64:ALA:N	0.56	2.74	9	1
2:B:129:VAL:O	2:B:138:ILE:HG13	0.56	2.01	15	1
2:B:47:ASP:C	2:B:48:VAL:HG23	0.56	2.20	17	9
2:B:59:VAL:HG11	2:B:61:PHE:CZ	0.56	2.36	6	6
1:A:13:G:OP1	2:B:93:SER:CB	0.56	2.54	13	2
1:A:13:G:OP2	2:B:89:LYS:CB	0.56	2.54	7	4
2:B:101:THR:CG2	2:B:141:ILE:O	0.56	2.53	16	2
2:B:107:LEU:CD2	2:B:107:LEU:N	0.56	2.69	7	1
1:A:11:C:N4	1:A:14:A:N6	0.56	2.53	9	2
1:A:14:A:N3	2:B:94:LYS:CG	0.56	2.67	11	1
2:B:107:LEU:HD11	2:B:128:LEU:HD11	0.56	1.76	11	1
2:B:159:ALA:O	2:B:160:GLU:C	0.56	2.45	17	4
2:B:102:LEU:N	2:B:141:ILE:O	0.56	2.39	14	2
2:B:130:SER:CA	2:B:136:LYS:HA	0.56	2.29	15	1
2:B:27:VAL:HG12	2:B:28:ALA:N	0.55	2.15	2	4
1:A:9:U:O4'	1:A:10:C:OP1	0.55	2.24	15	4
2:B:146:GLU:O	2:B:150:GLU:CB	0.55	2.54	12	12
1:A:11:C:C2'	1:A:12:C:C5'	0.55	2.84	5	4
2:B:19:GLY:N	2:B:84:LYS:O	0.55	2.39	17	5
2:B:158:GLY:CA	2:B:166:VAL:O	0.55	2.53	8	3
1:A:11:C:N4	1:A:14:A:H61	0.55	1.99	9	3
2:B:38:PHE:CD2	2:B:43:LEU:CD1	0.55	2.88	7	4

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:69:LYS:O	2:B:73:LEU:CD2	0.55	2.54	10	9
2:B:81:ASN:O	2:B:83:ILE:N	0.55	2.39	16	8
2:B:69:LYS:O	2:B:73:LEU:N	0.55	2.39	13	6
2:B:48:VAL:HA	2:B:58:TYR:O	0.55	2.01	19	3
1:A:13:G:C4'	1:A:14:A:OP1	0.55	2.53	6	2
2:B:91:ARG:O	2:B:92:ASP:CB	0.55	2.53	13	3
2:B:38:PHE:CZ	2:B:73:LEU:CD1	0.55	2.86	9	1
1:A:13:G:OP1	2:B:89:LYS:CB	0.55	2.54	13	1
2:B:30:LEU:CD1	2:B:54:ARG:HG3	0.55	2.30	16	2
1:A:1:G:C2'	1:A:2:G:O5'	0.55	2.54	16	6
1:A:18:A:C2'	1:A:19:G:O5'	0.55	2.55	1	3
1:A:12:C:C5	1:A:12:C:P	0.55	2.99	9	2
1:A:14:A:N6	2:B:94:LYS:HE2	0.55	2.17	2	3
1:A:2:G:O2'	1:A:3:C:OP1	0.55	2.24	10	2
2:B:102:LEU:O	2:B:102:LEU:CD2	0.55	2.53	10	1
2:B:103:LEU:CD1	2:B:140:TYR:CD1	0.55	2.87	14	1
2:B:61:PHE:CE1	2:B:70:ALA:CB	0.55	2.89	16	1
2:B:102:LEU:N	2:B:102:LEU:CD1	0.55	2.60	10	7
2:B:46:VAL:CG2	2:B:61:PHE:C	0.55	2.75	13	10
2:B:115:GLU:O	2:B:119:VAL:HG23	0.55	2.01	8	2
2:B:21:LEU:O	2:B:22:ASN:CB	0.55	2.55	9	3
2:B:119:VAL:O	2:B:156:LYS:CE	0.55	2.55	9	1
1:A:9:U:O4	2:B:105:LYS:CE	0.55	2.54	6	4
1:A:11:C:C2	2:B:94:LYS:HE3	0.55	2.36	5	5
2:B:102:LEU:N	2:B:102:LEU:CD2	0.55	2.65	15	5
2:B:141:ILE:CG2	2:B:143:PHE:CE1	0.55	2.89	9	2
1:A:11:C:C4	2:B:94:LYS:HE3	0.55	2.36	13	2
1:A:14:A:N3	2:B:95:LYS:HB2	0.55	2.16	13	1
1:A:11:C:O2	2:B:94:LYS:CE	0.55	2.55	14	1
1:A:13:G:N9	2:B:58:TYR:CD1	0.55	2.74	18	1
1:A:10:C:O2	2:B:127:ARG:NE	0.55	2.40	6	10
2:B:90:GLY:O	2:B:92:ASP:N	0.55	2.40	3	1
1:A:12:C:OP2	2:B:89:LYS:CE	0.55	2.54	5	2
1:A:14:A:C6	2:B:94:LYS:HG3	0.55	2.37	6	1
1:A:4:C:C1'	1:A:5:G:O4'	0.55	2.54	13	3
2:B:155:GLU:O	2:B:156:LYS:CB	0.55	2.55	16	2
1:A:19:G:O2'	1:A:20:G:C4'	0.55	2.54	11	3
2:B:94:LYS:CE	2:B:95:LYS:HE2	0.55	2.32	11	1
2:B:26:SER:OG	2:B:29:GLU:CG	0.55	2.54	12	1
2:B:123:ALA:HB2	2:B:143:PHE:CE1	0.55	2.36	18	1
2:B:70:ALA:O	2:B:85:LEU:CD2	0.55	2.55	1	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:14:A:O2'	2:B:52:THR:CG2	0.55	2.48	14	3
1:A:11:C:C4	2:B:94:LYS:HE2	0.55	2.36	5	4
2:B:158:GLY:O	2:B:165:SER:CA	0.55	2.55	4	4
2:B:38:PHE:CD2	2:B:43:LEU:HB3	0.55	2.37	19	2
2:B:127:ARG:O	2:B:127:ARG:CG	0.55	2.54	6	1
2:B:49:ARG:HB3	2:B:58:TYR:HB2	0.55	1.78	8	1
1:A:14:A:C6	2:B:94:LYS:HE3	0.55	2.36	16	1
1:A:8:A:H5'	1:A:9:U:OP2	0.55	2.01	17	1
2:B:143:PHE:CG	2:B:149:ALA:HA	0.55	2.37	6	18
1:A:1:G:HO2'	1:A:2:G:P	0.55	2.24	4	1
1:A:19:G:N2	1:A:20:G:C4	0.55	2.75	10	3
1:A:15:A:O4'	1:A:17:U:H1'	0.55	2.02	11	3
1:A:21:C:C2	1:A:22:C:C6	0.55	2.95	16	3
1:A:14:A:N6	2:B:94:LYS:HD3	0.55	2.17	13	1
2:B:51:GLY:CA	2:B:56:PHE:O	0.55	2.55	19	2
2:B:46:VAL:CG2	2:B:61:PHE:O	0.55	2.55	16	1
2:B:41:ASN:O	2:B:42:ASP:HB2	0.55	2.00	9	15
2:B:16:LEU:N	2:B:16:LEU:HD13	0.55	2.17	13	4
2:B:14:PHE:CD2	2:B:63:SER:N	0.55	2.75	7	2
2:B:104:ALA:HB2	2:B:141:ILE:HD12	0.55	1.79	11	1
2:B:107:LEU:N	2:B:107:LEU:CD2	0.55	2.69	13	1
2:B:78:VAL:CB	2:B:83:ILE:HG23	0.55	2.30	14	1
2:B:128:LEU:N	2:B:128:LEU:HD13	0.55	2.17	16	1
1:A:13:G:C5	2:B:58:TYR:CZ	0.55	2.95	1	1
1:A:15:A:C1'	1:A:17:U:C6	0.55	2.90	1	4
2:B:103:LEU:HD11	2:B:140:TYR:HE1	0.55	1.57	2	2
2:B:15:ASN:OD1	2:B:15:ASN:N	0.55	2.40	8	9
2:B:38:PHE:CD2	2:B:43:LEU:HG	0.55	2.37	6	5
1:A:20:G:C2'	1:A:21:C:O5'	0.55	2.55	13	1
1:A:14:A:OP2	2:B:91:ARG:O	0.55	2.25	14	1
2:B:127:ARG:CZ	2:B:127:ARG:CB	0.55	2.85	16	2
2:B:161:ILE:O	2:B:164:ARG:O	0.54	2.25	13	5
2:B:16:LEU:HD13	2:B:85:LEU:HD21	0.54	1.77	5	1
2:B:17:PHE:O	2:B:85:LEU:HD22	0.54	2.01	5	1
2:B:46:VAL:HG21	2:B:61:PHE:C	0.54	2.22	13	7
2:B:21:LEU:HB3	2:B:30:LEU:HD22	0.54	1.80	11	2
2:B:92:ASP:CB	2:B:96:VAL:HG21	0.54	2.31	12	1
1:A:14:A:N1	2:B:94:LYS:HE2	0.54	2.18	13	1
2:B:105:LYS:O	2:B:166:VAL:CG2	0.54	2.56	16	1
2:B:116:LEU:HD12	2:B:141:ILE:CD1	0.54	2.32	17	1
1:A:14:A:C5	2:B:94:LYS:HE3	0.54	2.37	7	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:102:LEU:C	2:B:171:THR:CG2	0.54	2.76	13	1
2:B:73:LEU:O	2:B:83:ILE:CD1	0.54	2.55	14	1
2:B:103:LEU:CD1	2:B:129:VAL:HG21	0.54	2.32	17	2
2:B:102:LEU:CD1	2:B:149:ALA:O	0.54	2.54	17	1
2:B:27:VAL:HG22	2:B:31:LYS:CE	0.54	2.31	19	1
1:A:14:A:O4'	1:A:14:A:OP1	0.54	2.25	10	5
2:B:107:LEU:HD23	2:B:111:ILE:HD13	0.54	1.79	8	1
2:B:21:LEU:HD13	2:B:30:LEU:HD23	0.54	1.80	9	1
2:B:74:THR:O	2:B:82:GLU:CG	0.54	2.56	14	1
2:B:93:SER:O	2:B:97:ARG:N	0.54	2.40	14	1
2:B:73:LEU:O	2:B:76:LEU:CD1	0.54	2.56	16	1
1:A:12:C:H1'	2:B:56:PHE:CD2	0.54	2.37	19	2
1:A:8:A:C6	1:A:14:A:N9	0.54	2.76	17	5
2:B:130:SER:O	2:B:136:LYS:CE	0.54	2.55	1	1
2:B:11:THR:O	2:B:11:THR:CG2	0.54	2.55	15	3
2:B:20:ASN:ND2	2:B:82:GLU:O	0.54	2.40	6	5
2:B:27:VAL:O	2:B:30:LEU:N	0.54	2.41	18	3
1:A:19:G:N3	1:A:20:G:C1'	0.54	2.70	4	4
2:B:111:ILE:HD11	2:B:161:ILE:HD12	0.54	1.79	5	1
2:B:111:ILE:C	2:B:112:THR:HG23	0.54	2.22	12	6
2:B:112:THR:OG1	2:B:115:GLU:OE1	0.54	2.24	15	3
1:A:13:G:O4'	2:B:56:PHE:CZ	0.54	2.60	17	1
2:B:170:TYR:N	2:B:170:TYR:CD1	0.54	2.75	17	1
2:B:127:ARG:NH1	2:B:128:LEU:O	0.54	2.40	18	1
2:B:140:TYR:C	2:B:141:ILE:CG1	0.54	2.76	5	8
2:B:34:ILE:CD1	2:B:83:ILE:HG21	0.54	2.33	14	1
1:A:12:C:OP2	2:B:89:LYS:CD	0.54	2.55	18	1
2:B:107:LEU:HB2	2:B:137:GLY:O	0.54	2.03	15	4
2:B:25:LYS:O	2:B:54:ARG:NH1	0.54	2.41	12	2
1:A:7:A:C2'	1:A:8:A:O5'	0.54	2.56	10	1
2:B:116:LEU:CD1	2:B:116:LEU:N	0.54	2.70	14	1
2:B:116:LEU:HD23	2:B:139:ALA:HB1	0.54	1.79	14	1
1:A:17:U:OP2	1:A:17:U:H6	0.54	1.85	16	1
2:B:102:LEU:HD22	2:B:149:ALA:O	0.54	2.03	1	1
2:B:124:LEU:CD1	2:B:144:LYS:N	0.54	2.70	15	4
2:B:146:GLU:OE2	2:B:170:TYR:OH	0.54	2.24	2	1
1:A:13:G:N2	2:B:90:GLY:HA3	0.54	2.16	15	2
2:B:94:LYS:CE	2:B:94:LYS:O	0.54	2.55	8	1
2:B:162:ASP:OD2	2:B:164:ARG:CG	0.54	2.55	9	1
1:A:11:C:C4'	1:A:12:C:OP1	0.54	2.56	17	2
1:A:13:G:OP2	2:B:89:LYS:CG	0.54	2.55	19	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:18:ILE:HD11	2:B:85:LEU:HD23	0.54	1.78	19	1
2:B:53:ASN:OD1	2:B:55:LYS:N	0.54	2.41	18	19
2:B:124:LEU:CD1	2:B:143:PHE:O	0.54	2.56	5	3
2:B:16:LEU:C	2:B:16:LEU:CD1	0.54	2.76	5	4
2:B:93:SER:OG	2:B:97:ARG:HD2	0.54	2.02	9	1
2:B:84:LYS:C	2:B:85:LEU:HD12	0.54	2.23	10	1
1:A:13:G:C4'	1:A:14:A:O5'	0.54	2.56	1	1
2:B:14:PHE:O	2:B:61:PHE:N	0.54	2.39	2	11
2:B:11:THR:C	2:B:12:THR:OG1	0.54	2.45	3	6
2:B:103:LEU:HG	2:B:103:LEU:O	0.54	2.03	5	2
2:B:38:PHE:CD1	2:B:43:LEU:HG	0.54	2.37	4	2
2:B:89:LYS:O	2:B:89:LYS:CG	0.54	2.56	4	1
2:B:92:ASP:CG	2:B:96:VAL:HG12	0.54	2.23	4	1
2:B:105:LYS:HG3	2:B:138:ILE:HG23	0.54	1.80	4	3
1:A:15:A:C2	1:A:17:U:C5	0.54	2.96	5	3
2:B:127:ARG:O	2:B:127:ARG:HG2	0.54	2.03	6	1
1:A:14:A:H5'	1:A:15:A:O5'	0.54	2.02	14	3
2:B:101:THR:CG2	2:B:140:TYR:CD2	0.54	2.91	14	2
2:B:148:ASP:OD1	2:B:149:ALA:N	0.54	2.41	19	1
2:B:38:PHE:HE1	2:B:76:LEU:HD11	0.54	1.63	1	1
1:A:6:A:C6	1:A:7:A:N7	0.54	2.76	2	2
1:A:17:U:OP1	1:A:17:U:O4'	0.54	2.26	8	1
2:B:74:THR:HG23	2:B:85:LEU:HD12	0.54	1.78	16	1
2:B:98:ALA:CB	2:B:171:THR:O	0.54	2.55	18	2
2:B:29:GLU:OE1	2:B:79:PHE:CZ	0.53	2.61	1	4
1:A:15:A:H2'	2:B:52:THR:OG1	0.53	2.02	3	1
1:A:12:C:N4	2:B:84:LYS:NZ	0.53	2.56	15	1
2:B:159:ALA:O	2:B:161:ILE:CG1	0.53	2.56	17	1
1:A:12:C:OP2	1:A:12:C:N3	0.53	2.42	2	2
1:A:19:G:N3	1:A:20:G:C8	0.53	2.76	10	5
1:A:21:C:O2'	1:A:22:C:C6	0.53	2.49	11	3
1:A:11:C:N3	2:B:94:LYS:HG3	0.53	2.18	7	1
2:B:30:LEU:HD21	2:B:54:ARG:HB3	0.53	1.78	9	3
2:B:25:LYS:O	2:B:54:ARG:NH2	0.53	2.42	14	4
2:B:38:PHE:HB3	2:B:45:VAL:CG2	0.53	2.33	14	3
1:A:14:A:OP1	1:A:14:A:O4'	0.53	2.26	9	1
1:A:20:G:H5'	1:A:21:C:OP2	0.53	2.04	10	1
1:A:10:C:O2	2:B:127:ARG:NH2	0.53	2.36	18	2
1:A:10:C:O2'	2:B:127:ARG:NH1	0.53	2.42	18	1
2:B:47:ASP:CB	2:B:60:ASP:OD2	0.53	2.57	1	3
2:B:53:ASN:OD1	2:B:53:ASN:C	0.53	2.46	14	19

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:17:PHE:CD1	2:B:18:ILE:O	0.53	2.61	14	8
2:B:18:ILE:CG1	2:B:85:LEU:CD1	0.53	2.86	6	1
1:A:15:A:C6	2:B:52:THR:HG22	0.53	2.39	12	3
1:A:2:G:N2	1:A:3:C:C2	0.53	2.77	12	1
2:B:47:ASP:O	2:B:48:VAL:HG23	0.53	2.02	13	2
1:A:7:A:C2	1:A:8:A:C4	0.53	2.97	4	10
1:A:16:G:C8	2:B:27:VAL:HG11	0.53	2.39	1	1
2:B:78:VAL:HG12	2:B:81:ASN:CB	0.53	2.34	5	2
2:B:105:LYS:CE	2:B:169:TYR:CD2	0.53	2.92	6	2
2:B:108:SER:CB	2:B:162:ASP:OD2	0.53	2.57	8	3
1:A:14:A:O4'	2:B:94:LYS:CG	0.53	2.56	11	1
2:B:123:ALA:C	2:B:124:LEU:HD23	0.53	2.24	14	1
1:A:17:U:C2'	1:A:18:A:O5'	0.53	2.57	15	1
2:B:93:SER:O	2:B:96:VAL:N	0.53	2.41	18	1
2:B:27:VAL:HG22	2:B:50:THR:HB	0.53	1.79	19	1
2:B:93:SER:HB2	2:B:95:LYS:NZ	0.53	2.18	19	1
1:A:8:A:H61	2:B:52:THR:HG21	0.53	1.62	4	4
1:A:15:A:O3'	1:A:16:G:H4'	0.53	2.03	19	2
2:B:35:SER:O	2:B:39:ALA:HB2	0.53	2.02	8	6
2:B:106:ASN:ND2	2:B:165:SER:O	0.53	2.41	10	5
2:B:43:LEU:CD2	2:B:66:ASP:OD1	0.53	2.57	5	1
1:A:2:G:O2'	1:A:3:C:O4'	0.53	2.27	7	4
2:B:92:ASP:O	2:B:93:SER:CB	0.53	2.57	7	2
2:B:111:ILE:C	2:B:112:THR:CG2	0.53	2.77	13	2
1:A:14:A:C6	2:B:94:LYS:HD3	0.53	2.37	13	1
1:A:21:C:OP1	1:A:21:C:C4'	0.53	2.56	18	1
2:B:51:GLY:HA3	2:B:56:PHE:C	0.53	2.24	7	14
2:B:113:GLU:O	2:B:117:LYS:N	0.53	2.40	1	14
1:A:11:C:N3	2:B:94:LYS:HE2	0.53	2.18	10	2
2:B:12:THR:CG2	2:B:13:PRO:HD2	0.53	2.34	17	5
2:B:38:PHE:CE2	2:B:43:LEU:HG	0.53	2.38	6	1
2:B:38:PHE:CE2	2:B:61:PHE:CE1	0.53	2.97	14	2
2:B:38:PHE:CD2	2:B:45:VAL:HG22	0.53	2.38	8	2
2:B:66:ASP:OD1	2:B:66:ASP:C	0.53	2.46	8	3
2:B:107:LEU:HG	2:B:166:VAL:HG22	0.53	1.81	12	2
2:B:130:SER:O	2:B:138:ILE:CD1	0.53	2.55	15	1
2:B:119:VAL:HG11	2:B:161:ILE:HD11	0.53	1.79	16	1
2:B:157:GLN:CA	2:B:168:LEU:HD12	0.53	2.34	16	1
1:A:13:G:N1	2:B:92:ASP:O	0.53	2.42	17	1
2:B:145:SER:N	2:B:148:ASP:OD2	0.53	2.42	19	1
2:B:53:ASN:OD1	2:B:55:LYS:HB2	0.53	2.04	5	17

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:18:ILE:CA	2:B:84:LYS:O	0.53	2.56	13	9
2:B:60:ASP:OD1	2:B:60:ASP:N	0.53	2.42	19	10
2:B:16:LEU:O	2:B:58:TYR:CD1	0.53	2.61	19	4
2:B:27:VAL:HG13	2:B:31:LYS:HE2	0.53	1.81	7	1
1:A:14:A:P	2:B:94:LYS:HD2	0.53	2.44	9	1
2:B:127:ARG:HB2	2:B:140:TYR:HB2	0.53	1.81	15	6
2:B:18:ILE:N	2:B:57:GLY:O	0.53	2.42	6	5
2:B:26:SER:O	2:B:30:LEU:HD12	0.53	2.03	5	1
2:B:103:LEU:HB3	2:B:140:TYR:CE1	0.53	2.39	5	2
2:B:86:GLU:OE2	2:B:87:LYS:N	0.53	2.42	9	1
1:A:11:C:N3	2:B:94:LYS:HD3	0.53	2.19	10	1
1:A:10:C:HO2'	2:B:128:LEU:N	0.53	2.02	15	1
2:B:62:GLU:CG	2:B:66:ASP:OD2	0.53	2.56	1	2
2:B:37:LEU:CD2	2:B:76:LEU:HD23	0.53	2.33	3	2
1:A:17:U:O2'	1:A:18:A:OP1	0.53	2.27	11	1
1:A:13:G:N2	2:B:91:ARG:HA	0.53	2.19	13	2
1:A:14:A:OP2	2:B:94:LYS:HG2	0.53	2.04	17	1
2:B:47:ASP:C	2:B:48:VAL:CG2	0.52	2.77	8	9
2:B:78:VAL:O	2:B:79:PHE:C	0.52	2.47	8	11
1:A:4:C:C2	1:A:20:G:C2	0.52	2.97	17	4
2:B:119:VAL:O	2:B:156:LYS:NZ	0.52	2.37	15	3
2:B:27:VAL:HG13	2:B:31:LYS:HE3	0.52	1.80	8	2
2:B:21:LEU:CG	2:B:56:PHE:O	0.52	2.57	13	2
2:B:38:PHE:CE1	2:B:76:LEU:HD11	0.52	2.39	3	2
1:A:14:A:OP1	1:A:14:A:N9	0.52	2.42	2	1
2:B:155:GLU:O	2:B:156:LYS:HB3	0.52	2.04	16	2
2:B:153:LEU:CD1	2:B:168:LEU:O	0.52	2.58	17	3
1:A:12:C:C5'	1:A:12:C:C6	0.52	2.92	11	2
1:A:10:C:OP2	1:A:11:C:C5	0.52	2.59	13	1
1:A:10:C:H1'	2:B:129:VAL:HG13	0.52	1.75	15	3
2:B:119:VAL:HG13	2:B:159:ALA:HB1	0.52	1.80	16	1
1:A:15:A:N9	1:A:17:U:C6	0.52	2.77	1	9
2:B:46:VAL:HG22	2:B:62:GLU:HB3	0.52	1.80	5	6
1:A:14:A:C4'	1:A:15:A:OP2	0.52	2.54	4	5
1:A:18:A:HO2'	1:A:19:G:H5'	0.52	1.63	18	2
1:A:5:G:N2	1:A:18:A:H62	0.52	2.02	18	6
2:B:30:LEU:CD2	2:B:78:VAL:HG11	0.52	2.35	8	3
2:B:38:PHE:CG	2:B:43:LEU:HD13	0.52	2.39	8	2
2:B:153:LEU:HD12	2:B:168:LEU:O	0.52	2.03	9	1
2:B:51:GLY:HA2	2:B:56:PHE:CE2	0.52	2.40	18	3
2:B:103:LEU:HD11	2:B:138:ILE:HG22	0.52	1.80	14	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:38:PHE:CZ	2:B:73:LEU:HG	0.52	2.39	17	4
2:B:52:THR:O	2:B:53:ASN:CG	0.52	2.48	12	19
2:B:102:LEU:CD2	2:B:143:PHE:CD1	0.52	2.93	15	5
2:B:21:LEU:CG	2:B:30:LEU:HD22	0.52	2.33	2	2
2:B:37:LEU:CD2	2:B:76:LEU:HD22	0.52	2.33	2	3
2:B:103:LEU:HD21	2:B:140:TYR:CD1	0.52	2.40	2	3
1:A:12:C:P	1:A:12:C:C6	0.52	3.03	18	2
1:A:14:A:OP1	2:B:94:LYS:HB3	0.52	2.04	10	2
2:B:44:ALA:HB3	2:B:66:ASP:OD1	0.52	2.04	14	1
2:B:58:TYR:CE2	2:B:88:PRO:HB3	0.52	2.40	16	1
2:B:29:GLU:O	2:B:79:PHE:CE2	0.52	2.62	17	1
1:A:13:G:O2'	1:A:14:A:H5'	0.52	2.04	8	2
2:B:51:GLY:CA	2:B:56:PHE:CD1	0.52	2.92	3	6
2:B:129:VAL:HB	2:B:138:ILE:O	0.52	2.04	11	12
1:A:14:A:OP2	2:B:93:SER:C	0.52	2.48	3	1
1:A:13:G:C8	2:B:49:ARG:HD3	0.52	2.40	19	4
1:A:19:G:H2'	1:A:20:G:O5'	0.52	2.05	17	3
2:B:153:LEU:C	2:B:153:LEU:HD23	0.52	2.25	17	3
1:A:14:A:N1	2:B:94:LYS:HG2	0.52	2.20	5	2
2:B:127:ARG:O	2:B:128:LEU:O	0.52	2.27	16	2
2:B:71:LEU:C	2:B:71:LEU:HD23	0.52	2.24	15	1
1:A:10:C:C1'	2:B:129:VAL:CG1	0.52	2.83	16	1
2:B:53:ASN:OD1	2:B:55:LYS:HB3	0.52	2.04	17	2
2:B:152:ASN:O	2:B:156:LYS:N	0.52	2.41	2	3
2:B:51:GLY:HA2	2:B:56:PHE:CZ	0.52	2.39	6	2
2:B:149:ALA:O	2:B:153:LEU:CB	0.52	2.58	4	1
2:B:14:PHE:CZ	2:B:64:ALA:CA	0.52	2.93	6	2
2:B:30:LEU:HD11	2:B:54:ARG:CD	0.52	2.35	12	2
1:A:5:G:O2'	1:A:6:A:O4'	0.52	2.28	13	1
2:B:140:TYR:OH	2:B:171:THR:HG21	0.52	2.03	15	2
2:B:152:ASN:OD1	2:B:156:LYS:CE	0.52	2.58	15	1
1:A:7:A:H2'	1:A:8:A:O4'	0.52	2.04	19	1
2:B:52:THR:O	2:B:53:ASN:OD1	0.52	2.27	5	18
1:A:6:A:C4	1:A:7:A:C8	0.52	2.97	17	3
1:A:12:C:C6	1:A:12:C:OP2	0.52	2.62	3	1
2:B:103:LEU:CB	2:B:140:TYR:CE1	0.52	2.92	5	2
1:A:3:C:O2'	1:A:4:C:OP2	0.52	2.27	10	1
2:B:107:LEU:CD1	2:B:137:GLY:O	0.52	2.55	15	2
2:B:111:ILE:CD1	2:B:161:ILE:HG21	0.52	2.34	17	2
1:A:12:C:OP2	1:A:12:C:N1	0.52	2.42	19	1
2:B:76:LEU:O	2:B:82:GLU:HA	0.52	2.04	5	18

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:8:A:N6	1:A:14:A:C4	0.52	2.78	14	7
2:B:102:LEU:CA	2:B:171:THR:OG1	0.52	2.58	7	1
2:B:147:ALA:O	2:B:151:LYS:CB	0.52	2.58	12	5
2:B:93:SER:O	2:B:94:LYS:C	0.52	2.47	14	3
2:B:98:ALA:O	2:B:171:THR:O	0.52	2.27	9	2
2:B:116:LEU:CD2	2:B:139:ALA:HB1	0.52	2.35	16	3
2:B:85:LEU:N	2:B:85:LEU:CD2	0.52	2.70	18	2
1:A:11:C:O2	2:B:94:LYS:HE3	0.52	2.05	14	1
1:A:9:U:O2'	1:A:10:C:O4'	0.52	2.28	15	1
2:B:89:LYS:O	2:B:90:GLY:O	0.52	2.28	18	1
2:B:12:THR:OG1	2:B:60:ASP:HB3	0.52	2.05	19	1
2:B:47:ASP:CB	2:B:60:ASP:OD1	0.52	2.58	2	1
2:B:49:ARG:HD3	2:B:58:TYR:CB	0.52	2.35	17	8
2:B:27:VAL:O	2:B:31:LYS:CE	0.52	2.58	4	1
1:A:14:A:H62	2:B:94:LYS:NZ	0.52	2.01	5	1
2:B:105:LYS:HG2	2:B:138:ILE:HG23	0.52	1.82	15	3
2:B:34:ILE:HG22	2:B:38:PHE:CE2	0.52	2.39	11	1
2:B:94:LYS:C	2:B:94:LYS:CE	0.52	2.79	12	1
2:B:11:THR:C	2:B:12:THR:CG2	0.52	2.78	13	1
2:B:71:LEU:HD23	2:B:71:LEU:O	0.52	2.04	15	1
1:A:14:A:C4	2:B:94:LYS:HD3	0.52	2.40	18	1
2:B:67:LEU:C	2:B:67:LEU:CD1	0.52	2.79	1	4
1:A:10:C:N4	2:B:140:TYR:OH	0.52	2.43	6	4
2:B:103:LEU:CG	2:B:138:ILE:HG22	0.52	2.34	3	2
2:B:69:LYS:O	2:B:73:LEU:CD1	0.52	2.54	8	2
2:B:29:GLU:HB3	2:B:79:PHE:CE1	0.52	2.41	9	1
1:A:7:A:C6	1:A:8:A:C6	0.51	2.98	4	6
2:B:30:LEU:CD1	2:B:54:ARG:HD2	0.51	2.35	19	8
2:B:99:ALA:O	2:B:170:TYR:CZ	0.51	2.63	10	5
2:B:127:ARG:O	2:B:128:LEU:C	0.51	2.48	16	9
1:A:13:G:OP2	2:B:89:LYS:CD	0.51	2.58	6	1
2:B:127:ARG:NH2	2:B:140:TYR:CE2	0.51	2.78	12	3
1:A:12:C:OP2	1:A:12:C:C4	0.51	2.63	12	2
2:B:102:LEU:HD11	2:B:149:ALA:CB	0.51	2.34	16	2
2:B:30:LEU:CD2	2:B:54:ARG:HG3	0.51	2.35	14	1
2:B:120:PHE:HZ	2:B:168:LEU:HD21	0.51	1.63	4	4
2:B:143:PHE:CD1	2:B:143:PHE:N	0.51	2.78	11	5
2:B:101:THR:HG23	2:B:141:ILE:C	0.51	2.24	7	1
1:A:16:G:C2	2:B:54:ARG:NH2	0.51	2.78	8	1
2:B:75:GLY:O	2:B:76:LEU:C	0.51	2.48	16	2
2:B:103:LEU:HB3	2:B:138:ILE:HG22	0.51	1.81	19	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:140:TYR:CZ	2:B:171:THR:HG21	0.51	2.40	13	2
2:B:18:ILE:CG1	2:B:85:LEU:CD2	0.51	2.89	16	1
1:A:6:A:C2	1:A:7:A:C8	0.51	2.98	17	1
1:A:6:A:N7	1:A:15:A:N6	0.51	2.58	18	2
2:B:103:LEU:HD22	2:B:140:TYR:CZ	0.51	2.40	18	2
2:B:120:PHE:CE2	2:B:141:ILE:HD12	0.51	2.40	1	5
2:B:120:PHE:CD2	2:B:141:ILE:CD1	0.51	2.93	1	3
2:B:15:ASN:ND2	2:B:60:ASP:OD2	0.51	2.42	16	8
2:B:104:ALA:O	2:B:139:ALA:N	0.51	2.43	2	3
1:A:5:G:H21	1:A:18:A:H62	0.51	1.49	9	4
2:B:29:GLU:HB3	2:B:79:PHE:CE2	0.51	2.40	8	5
2:B:47:ASP:OD2	2:B:49:ARG:NH1	0.51	2.43	15	2
1:A:14:A:C1'	2:B:94:LYS:HG3	0.51	2.35	11	1
2:B:99:ALA:O	2:B:170:TYR:CE2	0.51	2.63	11	1
2:B:92:ASP:HB3	2:B:96:VAL:CG2	0.51	2.35	12	1
2:B:15:ASN:ND2	2:B:60:ASP:CG	0.51	2.63	13	1
1:A:14:A:C8	2:B:94:LYS:HD3	0.51	2.41	18	1
2:B:103:LEU:CD2	2:B:140:TYR:CD1	0.51	2.94	2	3
1:A:14:A:P	2:B:93:SER:HA	0.51	2.46	5	1
2:B:22:ASN:C	2:B:54:ARG:CB	0.51	2.78	6	1
2:B:105:LYS:HE3	2:B:169:TYR:CD2	0.51	2.41	6	1
2:B:73:LEU:CD2	2:B:76:LEU:HD11	0.51	2.29	13	1
1:A:14:A:OP1	2:B:93:SER:C	0.51	2.49	10	2
2:B:110:ASN:O	2:B:111:ILE:O	0.51	2.28	6	2
2:B:93:SER:O	2:B:94:LYS:HB3	0.51	2.06	17	4
2:B:103:LEU:CD1	2:B:171:THR:OG1	0.51	2.56	9	1
2:B:12:THR:HB	2:B:13:PRO:CD	0.51	2.36	13	1
2:B:22:ASN:N	2:B:54:ARG:O	0.51	2.41	2	2
2:B:102:LEU:CD2	2:B:102:LEU:N	0.51	2.66	3	1
2:B:102:LEU:CD1	2:B:168:LEU:CD1	0.51	2.87	6	1
2:B:103:LEU:CD1	2:B:171:THR:HG22	0.51	2.36	8	1
2:B:12:THR:OG1	2:B:46:VAL:HG11	0.51	2.06	10	1
2:B:46:VAL:CG2	2:B:62:GLU:CG	0.51	2.88	17	6
2:B:143:PHE:CD2	2:B:149:ALA:HA	0.51	2.41	16	2
2:B:22:ASN:ND2	2:B:79:PHE:O	0.51	2.42	5	3
2:B:88:PRO:C	2:B:89:LYS:CG	0.51	2.79	2	1
1:A:20:G:C2	1:A:21:C:N1	0.51	2.79	3	4
2:B:152:ASN:O	2:B:156:LYS:CG	0.51	2.58	19	3
2:B:16:LEU:HD13	2:B:85:LEU:CD2	0.51	2.36	5	1
2:B:146:GLU:HA	2:B:170:TYR:OH	0.51	2.05	18	2
1:A:14:A:C6	2:B:94:LYS:HD2	0.51	2.40	7	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:91:ARG:O	2:B:92:ASP:C	0.51	2.49	16	3
2:B:83:ILE:N	2:B:83:ILE:HD12	0.51	2.20	14	1
2:B:31:LYS:HG3	2:B:48:VAL:CG1	0.51	2.36	16	1
1:A:13:G:C8	2:B:58:TYR:CE1	0.51	2.99	1	2
2:B:14:PHE:CE1	2:B:64:ALA:HA	0.51	2.41	1	3
2:B:46:VAL:CG2	2:B:62:GLU:HB3	0.51	2.36	4	11
2:B:51:GLY:N	2:B:57:GLY:HA2	0.51	2.21	9	10
2:B:17:PHE:CE2	2:B:86:GLU:HB3	0.51	2.41	2	7
1:A:5:G:O2'	1:A:6:A:OP1	0.51	2.21	4	1
1:A:16:G:C8	2:B:27:VAL:CG2	0.51	2.93	6	3
2:B:85:LEU:CD1	2:B:86:GLU:N	0.51	2.64	5	1
2:B:91:ARG:O	2:B:92:ASP:O	0.51	2.29	9	2
2:B:85:LEU:N	2:B:85:LEU:CD1	0.51	2.73	10	1
2:B:93:SER:O	2:B:94:LYS:HE2	0.51	2.06	11	1
1:A:11:C:N3	2:B:94:LYS:NZ	0.51	2.59	14	1
2:B:105:LYS:HG2	2:B:138:ILE:HD13	0.51	1.81	15	1
2:B:103:LEU:O	2:B:169:TYR:N	0.51	2.40	18	1
1:A:10:C:C4'	2:B:129:VAL:HG13	0.51	2.36	16	5
2:B:41:ASN:O	2:B:42:ASP:CG	0.51	2.49	9	4
2:B:76:LEU:HD23	2:B:83:ILE:HD11	0.51	1.81	9	1
1:A:2:G:O2'	1:A:3:C:C6	0.51	2.64	10	2
2:B:59:VAL:HG13	2:B:61:PHE:CE1	0.51	2.41	11	1
2:B:70:ALA:CA	2:B:73:LEU:HD22	0.51	2.36	11	1
1:A:10:C:O2'	2:B:127:ARG:HB3	0.51	2.06	15	1
2:B:129:VAL:CA	2:B:136:LYS:HE2	0.51	2.36	15	1
1:A:11:C:OP1	1:A:11:C:O4'	0.51	2.29	2	1
2:B:17:PHE:HB2	2:B:58:TYR:CE1	0.51	2.41	3	1
2:B:146:GLU:O	2:B:150:GLU:N	0.51	2.43	7	5
2:B:116:LEU:HD21	2:B:139:ALA:CB	0.51	2.36	16	2
2:B:97:ARG:NH1	2:B:142:GLU:OE2	0.51	2.44	16	1
2:B:43:LEU:CD1	2:B:66:ASP:HA	0.51	2.36	17	1
2:B:97:ARG:NH2	2:B:142:GLU:OE2	0.51	2.44	18	1
1:A:3:C:O2'	1:A:4:C:OP1	0.50	2.27	19	3
2:B:25:LYS:HD3	2:B:79:PHE:CD1	0.50	2.42	11	1
2:B:45:VAL:C	2:B:46:VAL:CG2	0.50	2.78	11	1
2:B:107:LEU:O	2:B:107:LEU:HD23	0.50	2.06	11	1
2:B:12:THR:CG2	2:B:46:VAL:CB	0.50	2.89	19	1
1:A:9:U:H4'	1:A:10:C:OP1	0.50	2.07	16	4
1:A:11:C:O4'	2:B:127:ARG:HD2	0.50	2.06	14	11
2:B:76:LEU:HB2	2:B:83:ILE:CG1	0.50	2.36	13	4
2:B:105:LYS:HD3	2:B:138:ILE:HG23	0.50	1.82	5	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:143:PHE:CD1	2:B:149:ALA:HA	0.50	2.41	19	5
2:B:97:ARG:O	2:B:98:ALA:C	0.50	2.50	7	6
1:A:14:A:P	2:B:94:LYS:CD	0.50	2.99	9	1
2:B:22:ASN:C	2:B:22:ASN:OD1	0.50	2.49	9	2
2:B:94:LYS:CE	2:B:95:LYS:CE	0.50	2.89	11	1
1:A:6:A:C6	1:A:18:A:N3	0.50	2.78	16	2
2:B:76:LEU:HD12	2:B:77:LYS:N	0.50	2.20	17	1
2:B:14:PHE:CD2	2:B:63:SER:C	0.50	2.84	16	4
2:B:76:LEU:CB	2:B:83:ILE:HG12	0.50	2.36	13	2
2:B:143:PHE:CE2	2:B:152:ASN:CB	0.50	2.94	6	4
2:B:48:VAL:C	2:B:49:ARG:CG	0.50	2.79	19	1
2:B:18:ILE:CG1	2:B:85:LEU:HD13	0.50	2.35	1	1
2:B:161:ILE:O	2:B:162:ASP:C	0.50	2.49	15	19
2:B:22:ASN:ND2	2:B:25:LYS:HB2	0.50	2.21	3	3
2:B:158:GLY:O	2:B:165:SER:CB	0.50	2.60	4	1
1:A:8:A:C4	1:A:14:A:C2	0.50	2.99	18	2
2:B:61:PHE:HB3	2:B:66:ASP:CG	0.50	2.25	13	4
1:A:2:G:HO2'	1:A:3:C:P	0.50	2.30	7	1
2:B:110:ASN:CB	2:B:162:ASP:OD2	0.50	2.59	7	1
1:A:16:G:OP1	1:A:16:G:O3'	0.50	2.29	18	1
2:B:102:LEU:HD21	2:B:143:PHE:CD1	0.50	2.40	1	5
2:B:13:PRO:HG2	2:B:14:PHE:CD2	0.50	2.41	15	3
1:A:4:C:C2'	1:A:5:G:C8	0.50	2.95	8	8
2:B:105:LYS:O	2:B:106:ASN:HB3	0.50	2.07	15	9
2:B:74:THR:O	2:B:74:THR:CG2	0.50	2.59	7	4
2:B:153:LEU:HD12	2:B:168:LEU:HB3	0.50	1.83	6	1
2:B:129:VAL:CA	2:B:136:LYS:CE	0.50	2.89	15	1
2:B:92:ASP:O	2:B:93:SER:C	0.50	2.49	18	1
2:B:27:VAL:CG2	2:B:50:THR:CG2	0.50	2.89	19	1
1:A:14:A:H2'	2:B:52:THR:CG2	0.50	2.37	10	14
2:B:21:LEU:HB2	2:B:54:ARG:O	0.50	2.07	19	10
2:B:89:LYS:O	2:B:90:GLY:C	0.50	2.50	11	3
2:B:130:SER:HA	2:B:136:LYS:HB2	0.50	1.84	18	9
1:A:4:C:HO2'	1:A:5:G:H8	0.50	1.37	4	1
2:B:143:PHE:CE2	2:B:152:ASN:CG	0.50	2.84	10	2
2:B:38:PHE:CE1	2:B:73:LEU:HG	0.50	2.41	6	2
2:B:71:LEU:C	2:B:71:LEU:CD1	0.50	2.80	6	1
2:B:71:LEU:O	2:B:74:THR:OG1	0.50	2.22	16	2
1:A:3:C:H1'	1:A:4:C:OP1	0.50	2.07	19	3
2:B:129:VAL:HB	2:B:138:ILE:HD12	0.50	1.84	15	1
1:A:15:A:N9	2:B:52:THR:HG23	0.50	2.22	4	5

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:18:ILE:CG2	2:B:19:GLY:N	0.50	2.75	3	9
1:A:12:C:OP2	1:A:12:C:O2	0.50	2.28	6	2
2:B:129:VAL:CG2	2:B:138:ILE:HB	0.50	2.37	19	6
2:B:16:LEU:HA	2:B:88:PRO:CG	0.50	2.37	4	13
2:B:78:VAL:CG1	2:B:79:PHE:N	0.50	2.75	4	5
2:B:129:VAL:HG23	2:B:139:ALA:CA	0.50	2.37	16	8
1:A:4:C:O2'	1:A:5:G:H3'	0.50	2.06	4	1
2:B:38:PHE:CD2	2:B:43:LEU:CG	0.50	2.95	6	1
2:B:126:ILE:HG23	2:B:141:ILE:HD12	0.50	1.81	9	1
1:A:20:G:C6	1:A:21:C:N3	0.50	2.80	11	2
2:B:123:ALA:CB	2:B:141:ILE:CG2	0.50	2.90	11	1
2:B:25:LYS:HG3	2:B:79:PHE:CD1	0.50	2.42	12	1
1:A:9:U:H3'	1:A:9:U:P	0.50	2.47	14	1
2:B:157:GLN:O	2:B:158:GLY:C	0.50	2.49	16	1
1:A:11:C:N3	1:A:14:A:N6	0.50	2.59	17	1
1:A:13:G:OP2	2:B:89:LYS:HG2	0.50	2.07	19	1
2:B:95:LYS:C	2:B:95:LYS:CD	0.50	2.78	19	1
2:B:146:GLU:HG3	2:B:170:TYR:OH	0.50	2.06	7	5
2:B:102:LEU:CD1	2:B:168:LEU:HD13	0.50	2.31	6	1
1:A:13:G:N2	2:B:90:GLY:C	0.50	2.65	7	1
1:A:10:C:HO2'	1:A:11:C:P	0.50	2.30	11	1
1:A:13:G:C5	2:B:58:TYR:CE1	0.50	2.99	12	1
1:A:14:A:O4'	2:B:95:LYS:HE3	0.50	2.07	12	1
2:B:47:ASP:OD1	2:B:49:ARG:NH1	0.50	2.45	13	1
1:A:2:G:HO2'	1:A:3:C:C5'	0.50	2.20	15	1
2:B:105:LYS:O	2:B:166:VAL:HG22	0.50	2.06	15	1
2:B:18:ILE:HG13	2:B:85:LEU:CD2	0.50	2.36	16	1
2:B:33:ALA:HB2	2:B:79:PHE:HD2	0.50	1.63	17	1
1:A:7:A:N1	1:A:8:A:C4	0.49	2.80	4	5
2:B:38:PHE:CD2	2:B:43:LEU:CD2	0.49	2.84	2	2
2:B:58:TYR:O	2:B:59:VAL:HG22	0.49	2.07	5	4
1:A:15:A:O2'	1:A:16:G:H4'	0.49	2.07	11	2
2:B:124:LEU:CD1	2:B:143:PHE:C	0.49	2.80	15	6
2:B:129:VAL:CB	2:B:138:ILE:O	0.49	2.59	11	11
1:A:12:C:O2	2:B:56:PHE:CB	0.49	2.60	3	1
2:B:53:ASN:OD1	2:B:53:ASN:O	0.49	2.29	5	6
2:B:77:LYS:HA	2:B:82:GLU:HA	0.49	1.82	3	9
2:B:16:LEU:C	2:B:16:LEU:CD2	0.49	2.75	17	3
2:B:18:ILE:HG23	2:B:84:LYS:O	0.49	2.07	14	7
2:B:21:LEU:HB3	2:B:30:LEU:CD2	0.49	2.37	5	2
2:B:107:LEU:HD12	2:B:138:ILE:C	0.49	2.27	4	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:14:A:C5	2:B:94:LYS:NZ	0.49	2.81	7	1
2:B:17:PHE:CD2	2:B:86:GLU:HG3	0.49	2.42	7	1
2:B:101:THR:C	2:B:171:THR:HG1	0.49	2.09	12	1
2:B:153:LEU:HD13	2:B:168:LEU:HB3	0.49	1.83	13	1
2:B:51:GLY:CA	2:B:56:PHE:CD2	0.49	2.94	14	2
2:B:21:LEU:O	2:B:78:VAL:HG12	0.49	2.06	15	1
2:B:129:VAL:HA	2:B:136:LYS:HE3	0.49	1.83	15	1
2:B:85:LEU:O	2:B:86:GLU:HB3	0.49	2.07	1	4
2:B:104:ALA:O	2:B:138:ILE:HG22	0.49	2.07	1	4
2:B:154:GLU:HG3	2:B:155:GLU:N	0.49	2.23	3	5
2:B:11:THR:C	2:B:12:THR:HG1	0.49	2.10	3	3
2:B:18:ILE:CD1	2:B:59:VAL:HG21	0.49	2.37	10	2
1:A:20:G:C4'	1:A:21:C:OP1	0.49	2.61	9	1
2:B:25:LYS:HG3	2:B:79:PHE:CG	0.49	2.42	12	1
1:A:10:C:O4'	1:A:10:C:OP1	0.49	2.29	14	2
2:B:83:ILE:O	2:B:83:ILE:HD12	0.49	2.06	14	1
2:B:128:LEU:HD22	2:B:128:LEU:O	0.49	2.06	16	1
1:A:15:A:C5'	1:A:16:G:OP1	0.49	2.60	10	3
2:B:153:LEU:CD1	2:B:168:LEU:HB3	0.49	2.37	13	2
2:B:12:THR:CB	2:B:13:PRO:HD2	0.49	2.38	9	2
2:B:161:ILE:O	2:B:162:ASP:OD1	0.49	2.30	9	1
2:B:30:LEU:CD1	2:B:54:ARG:CD	0.49	2.90	19	1
2:B:14:PHE:CZ	2:B:64:ALA:N	0.49	2.81	1	3
2:B:154:GLU:CG	2:B:155:GLU:N	0.49	2.74	17	4
2:B:111:ILE:HD11	2:B:161:ILE:HG22	0.49	1.84	2	1
2:B:21:LEU:HD23	2:B:30:LEU:CD2	0.49	2.38	5	1
2:B:85:LEU:CD2	2:B:86:GLU:N	0.49	2.73	7	1
2:B:107:LEU:HD13	2:B:166:VAL:HG21	0.49	1.84	7	1
1:A:12:C:N1	2:B:17:PHE:CZ	0.49	2.81	15	4
2:B:17:PHE:CE2	2:B:18:ILE:O	0.49	2.66	12	1
2:B:101:THR:C	2:B:171:THR:CG2	0.49	2.81	18	1
2:B:103:LEU:HD22	2:B:140:TYR:CE1	0.49	2.42	18	2
2:B:104:ALA:HA	2:B:167:SER:O	0.49	2.07	5	14
1:A:13:G:OP2	2:B:89:LYS:HB2	0.49	2.07	17	6
2:B:11:THR:O	2:B:12:THR:HG23	0.49	2.08	4	4
1:A:12:C:O2	2:B:56:PHE:CG	0.49	2.66	3	1
2:B:11:THR:CB	2:B:47:ASP:OD2	0.49	2.61	3	1
2:B:73:LEU:O	2:B:74:THR:C	0.49	2.51	9	4
2:B:105:LYS:HB2	2:B:167:SER:OG	0.49	2.07	6	2
2:B:48:VAL:HG23	2:B:59:VAL:CG2	0.49	2.38	9	1
2:B:94:LYS:CG	2:B:95:LYS:N	0.49	2.75	9	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:44:ALA:O	2:B:66:ASP:OD2	0.49	2.31	11	1
2:B:100:ARG:NE	2:B:142:GLU:OE1	0.49	2.45	11	1
2:B:101:THR:O	2:B:170:TYR:HA	0.49	2.08	17	2
2:B:120:PHE:HE1	2:B:168:LEU:HD11	0.49	1.63	16	1
1:A:13:G:O2'	2:B:51:GLY:HA2	0.49	2.08	17	1
2:B:59:VAL:O	2:B:60:ASP:OD1	0.49	2.31	9	2
1:A:3:C:C4'	1:A:4:C:OP1	0.49	2.60	12	5
2:B:18:ILE:O	2:B:56:PHE:HB2	0.49	2.07	16	5
1:A:15:A:C5	1:A:17:U:C2	0.49	3.01	18	2
2:B:107:LEU:CD1	2:B:138:ILE:CA	0.49	2.91	6	3
2:B:107:LEU:CD1	2:B:138:ILE:HA	0.49	2.38	6	3
2:B:93:SER:O	2:B:97:ARG:NE	0.49	2.45	7	1
2:B:67:LEU:C	2:B:67:LEU:CD2	0.49	2.80	8	1
2:B:38:PHE:CB	2:B:45:VAL:CG1	0.49	2.91	9	1
2:B:78:VAL:O	2:B:81:ASN:OD1	0.49	2.30	9	1
2:B:116:LEU:CD2	2:B:116:LEU:N	0.49	2.75	9	2
2:B:102:LEU:CD2	2:B:168:LEU:CD2	0.49	2.90	10	1
2:B:128:LEU:HD22	2:B:130:SER:OG	0.49	2.07	12	1
1:A:3:C:C1'	1:A:4:C:OP1	0.49	2.61	19	3
1:A:15:A:C8	1:A:17:U:N1	0.49	2.81	2	5
1:A:5:G:OP2	1:A:5:G:C3'	0.49	2.53	4	1
2:B:25:LYS:CD	2:B:79:PHE:HB3	0.49	2.38	5	1
2:B:30:LEU:CD1	2:B:54:ARG:HD3	0.49	2.38	7	2
1:A:14:A:H61	2:B:94:LYS:HE2	0.49	1.67	13	1
2:B:107:LEU:HD22	2:B:166:VAL:HG23	0.49	1.85	13	1
1:A:21:C:H1'	1:A:22:C:OP1	0.49	2.07	14	1
2:B:92:ASP:CA	2:B:96:VAL:CG1	0.49	2.90	16	1
2:B:78:VAL:O	2:B:78:VAL:HG12	0.49	2.06	9	5
2:B:161:ILE:N	2:B:164:ARG:O	0.49	2.43	2	2
1:A:7:A:C2	1:A:8:A:N3	0.49	2.81	17	7
2:B:38:PHE:CE2	2:B:73:LEU:HD21	0.49	2.43	8	1
1:A:13:G:OP2	2:B:89:LYS:N	0.49	2.46	9	1
2:B:120:PHE:CG	2:B:141:ILE:HG21	0.49	2.42	12	1
2:B:14:PHE:O	2:B:60:ASP:OD1	0.49	2.30	13	1
2:B:102:LEU:CD1	2:B:169:TYR:N	0.49	2.76	14	1
1:A:14:A:OP1	1:A:14:A:H8	0.49	1.91	16	1
2:B:14:PHE:CD1	2:B:67:LEU:HG	0.49	2.43	17	1
2:B:14:PHE:CD2	2:B:67:LEU:HD22	0.49	2.42	19	1
1:A:7:A:C6	1:A:8:A:C4	0.49	3.00	4	3
2:B:103:LEU:O	2:B:103:LEU:HG	0.49	2.07	18	2
1:A:4:C:C4'	1:A:5:G:O5'	0.49	2.61	8	7

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:100:ARG:CG	2:B:142:GLU:OE1	0.49	2.60	4	1
2:B:35:SER:O	2:B:39:ALA:CB	0.49	2.61	8	2
2:B:162:ASP:OD2	2:B:162:ASP:O	0.49	2.31	9	1
1:A:10:C:N4	2:B:94:LYS:NZ	0.49	2.61	12	1
2:B:15:ASN:OD1	2:B:60:ASP:OD1	0.49	2.31	13	1
2:B:159:ALA:HB1	2:B:161:ILE:HD11	0.49	1.83	14	1
2:B:152:ASN:OD1	2:B:156:LYS:HE3	0.49	2.08	15	1
2:B:16:LEU:HD11	2:B:18:ILE:HD12	0.49	1.85	19	1
1:A:16:G:O6	2:B:54:ARG:NH2	0.48	2.42	12	3
2:B:27:VAL:CG1	2:B:28:ALA:N	0.48	2.76	19	3
2:B:76:LEU:O	2:B:83:ILE:HG12	0.48	2.08	5	4
1:A:16:G:N7	2:B:27:VAL:CB	0.48	2.76	4	3
2:B:18:ILE:CG1	2:B:85:LEU:HD23	0.48	2.37	5	1
2:B:53:ASN:O	2:B:53:ASN:CG	0.48	2.51	5	1
2:B:94:LYS:C	2:B:94:LYS:CD	0.48	2.79	8	2
2:B:127:ARG:N	2:B:140:TYR:O	0.48	2.43	19	2
2:B:34:ILE:HG21	2:B:59:VAL:HG21	0.48	1.83	14	1
1:A:11:C:O2'	2:B:94:LYS:NZ	0.48	2.43	15	1
2:B:111:ILE:CG1	2:B:116:LEU:HD11	0.48	2.38	16	1
2:B:103:LEU:CG	2:B:140:TYR:CD1	0.48	2.96	4	2
1:A:17:U:H2'	1:A:17:U:O2	0.48	2.08	3	2
2:B:124:LEU:HD12	2:B:143:PHE:O	0.48	2.08	8	2
2:B:107:LEU:O	2:B:164:ARG:NH1	0.48	2.45	14	1
2:B:153:LEU:C	2:B:153:LEU:CD1	0.48	2.76	15	1
1:A:6:A:C8	1:A:18:A:N1	0.48	2.81	17	1
2:B:14:PHE:CD1	2:B:67:LEU:HB2	0.48	2.43	6	3
2:B:105:LYS:HG3	2:B:169:TYR:CD2	0.48	2.43	3	1
1:A:20:G:N2	1:A:21:C:C2	0.48	2.81	6	2
1:A:11:C:HO2'	1:A:12:C:P	0.48	2.31	12	2
1:A:14:A:C2	2:B:94:LYS:CG	0.48	2.97	19	2
2:B:49:ARG:CG	2:B:58:TYR:HB2	0.48	2.38	19	1
2:B:104:ALA:O	2:B:138:ILE:HA	0.48	2.09	12	8
2:B:19:GLY:O	2:B:83:ILE:HA	0.48	2.08	17	7
1:A:4:C:C1'	1:A:5:G:O5'	0.48	2.61	11	9
1:A:7:A:N6	1:A:8:A:C6	0.48	2.82	4	1
1:A:15:A:N1	1:A:17:U:O4	0.48	2.46	5	2
2:B:85:LEU:O	2:B:85:LEU:HD22	0.48	2.07	12	1
2:B:85:LEU:HD13	2:B:85:LEU:H	0.48	1.68	12	1
2:B:113:GLU:OE1	2:B:126:ILE:O	0.48	2.31	16	1
2:B:102:LEU:HD12	2:B:143:PHE:CE1	0.48	2.44	17	1
2:B:90:GLY:O	2:B:92:ASP:OD1	0.48	2.32	18	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:30:LEU:O	2:B:34:ILE:CD1	0.48	2.61	1	3
2:B:38:PHE:CD2	2:B:45:VAL:HG12	0.48	2.44	3	4
2:B:108:SER:OG	2:B:109:PHE:N	0.48	2.45	12	3
1:A:12:C:OP2	2:B:89:LYS:HE3	0.48	2.09	18	2
2:B:102:LEU:CD2	2:B:141:ILE:HB	0.48	2.39	19	3
1:A:20:G:N7	1:A:21:C:C4	0.48	2.81	11	1
1:A:9:U:C6	2:B:138:ILE:CD1	0.48	2.97	13	2
1:A:9:U:OP2	1:A:10:C:OP2	0.48	2.31	13	1
2:B:94:LYS:CA	2:B:94:LYS:HE2	0.48	2.38	14	1
2:B:157:GLN:CB	2:B:168:LEU:HD12	0.48	2.37	16	1
1:A:13:G:H5"	2:B:58:TYR:OH	0.48	2.09	1	1
2:B:76:LEU:O	2:B:83:ILE:N	0.48	2.46	5	5
2:B:122:ASP:O	2:B:143:PHE:CD2	0.48	2.66	3	1
2:B:124:LEU:HD21	2:B:144:LYS:HG2	0.48	1.85	4	1
1:A:2:G:H2'	1:A:3:C:O5'	0.48	2.08	9	3
1:A:13:G:C8	2:B:49:ARG:NE	0.48	2.82	6	2
2:B:43:LEU:HD11	2:B:73:LEU:CD2	0.48	2.39	7	2
2:B:31:LYS:HG2	2:B:48:VAL:HG22	0.48	1.85	11	1
2:B:116:LEU:HD13	2:B:141:ILE:HD11	0.48	1.83	11	1
1:A:14:A:C1'	2:B:95:LYS:HE3	0.48	2.39	12	1
2:B:38:PHE:CE1	2:B:73:LEU:CD1	0.48	2.97	16	1
2:B:111:ILE:CG1	2:B:116:LEU:CD1	0.48	2.92	16	1
2:B:50:THR:HA	2:B:57:GLY:HA2	0.48	1.86	17	1
2:B:16:LEU:HD11	2:B:18:ILE:CD1	0.48	2.39	19	1
2:B:78:VAL:HB	2:B:83:ILE:CG2	0.48	2.38	13	14
2:B:47:ASP:O	2:B:59:VAL:HA	0.48	2.08	13	4
2:B:140:TYR:C	2:B:141:ILE:HG12	0.48	2.28	8	3
1:A:14:A:N6	2:B:94:LYS:HD2	0.48	2.23	7	1
2:B:97:ARG:C	2:B:101:THR:OG1	0.48	2.52	7	1
1:A:4:C:H4'	1:A:5:G:O5'	0.48	2.09	16	4
1:A:14:A:OP1	2:B:94:LYS:HD3	0.48	2.08	9	1
1:A:10:C:O2'	1:A:11:C:OP1	0.48	2.29	11	1
1:A:14:A:OP1	2:B:93:SER:HA	0.48	2.08	15	1
1:A:12:C:C5	2:B:17:PHE:CE2	0.48	3.01	15	3
2:B:102:LEU:HD11	2:B:141:ILE:HB	0.48	1.85	6	1
1:A:13:G:H21	2:B:90:GLY:C	0.48	2.11	7	1
1:A:16:G:N1	2:B:54:ARG:NH2	0.48	2.62	7	1
2:B:29:GLU:HB3	2:B:79:PHE:CD2	0.48	2.44	8	1
2:B:28:ALA:O	2:B:32:VAL:CB	0.48	2.62	11	4
1:A:1:G:C5	1:A:2:G:N7	0.48	2.82	12	1
1:A:12:C:N1	2:B:17:PHE:CE2	0.48	2.81	12	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:14:A:OP1	2:B:92:ASP:CG	0.48	2.52	12	1
1:A:21:C:HO2'	1:A:22:C:P	0.48	2.31	12	2
2:B:74:THR:HA	2:B:85:LEU:HD21	0.48	1.85	18	2
1:A:14:A:P	2:B:94:LYS:HB2	0.48	2.48	19	1
2:B:14:PHE:CE2	2:B:64:ALA:HA	0.48	2.44	19	1
2:B:52:THR:O	2:B:53:ASN:HB3	0.48	2.07	19	14
1:A:4:C:H2'	1:A:5:G:C8	0.48	2.44	13	8
2:B:51:GLY:CA	2:B:56:PHE:CE1	0.48	2.97	3	1
1:A:1:G:H1'	1:A:2:G:OP1	0.48	2.09	4	1
2:B:19:GLY:O	2:B:20:ASN:HB3	0.48	2.08	12	7
2:B:108:SER:OG	2:B:162:ASP:OD2	0.48	2.26	4	1
1:A:10:C:H42	2:B:94:LYS:HE2	0.48	1.68	8	1
2:B:36:GLU:O	2:B:40:LYS:N	0.48	2.45	11	1
2:B:129:VAL:HA	2:B:136:LYS:CE	0.48	2.39	15	1
1:A:10:C:O2'	2:B:129:VAL:HA	0.48	2.08	16	1
2:B:98:ALA:C	2:B:171:THR:O	0.48	2.52	18	1
1:A:7:A:H4'	1:A:8:A:OP1	0.48	2.09	19	1
2:B:73:LEU:CD1	2:B:76:LEU:CD2	0.48	2.91	19	1
2:B:157:GLN:OE1	2:B:168:LEU:N	0.48	2.40	1	2
2:B:86:GLU:O	2:B:87:LYS:C	0.48	2.53	17	15
2:B:128:LEU:HD22	2:B:129:VAL:N	0.48	2.24	4	1
1:A:21:C:C2'	1:A:22:C:O5'	0.48	2.62	5	1
2:B:51:GLY:CA	2:B:56:PHE:CE2	0.48	2.97	14	2
2:B:103:LEU:HD11	2:B:171:THR:HG22	0.48	1.85	8	1
2:B:22:ASN:O	2:B:54:ARG:HB3	0.47	2.09	5	7
2:B:54:ARG:N	2:B:54:ARG:HD3	0.47	2.24	1	1
2:B:152:ASN:O	2:B:156:LYS:CB	0.47	2.63	10	3
2:B:151:LYS:O	2:B:155:GLU:HB2	0.47	2.09	14	8
1:A:14:A:OP2	2:B:91:ARG:HB2	0.47	2.09	7	1
2:B:120:PHE:CD2	2:B:141:ILE:HD12	0.47	2.44	15	1
2:B:18:ILE:CD1	2:B:59:VAL:HB	0.47	2.38	16	2
2:B:37:LEU:HD22	2:B:76:LEU:CG	0.47	2.39	16	1
2:B:126:ILE:HA	2:B:140:TYR:O	0.47	2.09	6	9
2:B:14:PHE:C	2:B:15:ASN:OD1	0.47	2.52	3	4
2:B:78:VAL:HG23	2:B:83:ILE:CG2	0.47	2.39	6	1
2:B:54:ARG:NH1	2:B:54:ARG:HG2	0.47	2.24	8	1
2:B:90:GLY:O	2:B:91:ARG:O	0.47	2.31	8	1
2:B:105:LYS:O	2:B:166:VAL:HA	0.47	2.09	8	1
2:B:146:GLU:O	2:B:150:GLU:HB2	0.47	2.09	15	8
1:A:15:A:O4'	1:A:17:U:C1'	0.47	2.61	9	3
2:B:126:ILE:CG2	2:B:140:TYR:O	0.47	2.58	15	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:124:LEU:HD11	2:B:144:LYS:HA	0.47	1.85	14	1
2:B:89:LYS:O	2:B:91:ARG:HG3	0.47	2.10	15	1
1:A:16:G:C5	2:B:27:VAL:HG21	0.47	2.45	4	2
1:A:19:G:N3	1:A:20:G:N9	0.47	2.62	10	4
2:B:29:GLU:OE1	2:B:79:PHE:CE2	0.47	2.67	16	2
1:A:10:C:N4	2:B:140:TYR:HH	0.47	2.07	6	1
2:B:22:ASN:ND2	2:B:79:PHE:HB3	0.47	2.25	6	2
2:B:129:VAL:HB	2:B:138:ILE:C	0.47	2.29	16	5
2:B:153:LEU:CD2	2:B:168:LEU:O	0.47	2.63	15	1
2:B:12:THR:HG21	2:B:62:GLU:HG2	0.47	1.87	17	1
2:B:46:VAL:O	2:B:47:ASP:CG	0.47	2.53	1	1
1:A:4:C:O2'	1:A:5:G:C4'	0.47	2.63	18	7
2:B:37:LEU:HD21	2:B:76:LEU:HD13	0.47	1.84	5	2
2:B:11:THR:HG23	2:B:12:THR:OG1	0.47	2.10	1	2
2:B:153:LEU:C	2:B:153:LEU:CD2	0.47	2.79	14	2
2:B:92:ASP:HA	2:B:96:VAL:CG1	0.47	2.40	16	2
2:B:111:ILE:HG23	2:B:112:THR:N	0.47	2.25	15	5
2:B:21:LEU:CG	2:B:30:LEU:HD23	0.47	2.39	5	1
2:B:78:VAL:N	2:B:81:ASN:O	0.47	2.47	5	6
2:B:14:PHE:CZ	2:B:64:ALA:HA	0.47	2.44	6	1
2:B:18:ILE:HB	2:B:57:GLY:O	0.47	2.10	17	4
2:B:122:ASP:O	2:B:123:ALA:C	0.47	2.50	8	3
1:A:8:A:C2	2:B:95:LYS:HD3	0.47	2.44	11	1
2:B:115:GLU:O	2:B:119:VAL:CG2	0.47	2.62	11	1
2:B:16:LEU:HA	2:B:88:PRO:CB	0.47	2.40	14	1
2:B:130:SER:CA	2:B:136:LYS:HD2	0.47	2.40	15	1
1:A:19:G:O2'	1:A:20:G:H4'	0.47	2.10	16	1
2:B:34:ILE:O	2:B:38:PHE:CD2	0.47	2.68	16	1
2:B:96:VAL:HG12	2:B:97:ARG:N	0.47	2.25	18	2
2:B:130:SER:O	2:B:136:LYS:HE2	0.47	2.10	1	1
2:B:53:ASN:CG	2:B:53:ASN:O	0.47	2.53	15	12
1:A:13:G:H21	2:B:90:GLY:HA2	0.47	1.70	3	1
2:B:80:GLY:O	2:B:81:ASN:OD1	0.47	2.33	3	2
2:B:84:LYS:HG2	2:B:85:LEU:N	0.47	2.23	16	4
2:B:158:GLY:O	2:B:165:SER:HA	0.47	2.10	6	4
2:B:151:LYS:O	2:B:155:GLU:HB3	0.47	2.09	12	3
2:B:111:ILE:HD11	2:B:161:ILE:HD13	0.47	1.86	8	1
2:B:58:TYR:O	2:B:59:VAL:CG2	0.47	2.59	9	5
1:A:4:C:O2	1:A:20:G:C2	0.47	2.68	10	2
2:B:102:LEU:HB3	2:B:153:LEU:HD13	0.47	1.87	12	1
2:B:146:GLU:O	2:B:150:GLU:HB3	0.47	2.10	12	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:20:G:C5	1:A:21:C:C6	0.47	3.00	14	3
1:A:14:A:H2'	2:B:52:THR:HG1	0.47	1.69	14	1
1:A:21:C:C1'	1:A:22:C:OP1	0.47	2.62	14	2
1:A:21:C:C2'	1:A:22:C:OP1	0.47	2.62	14	2
2:B:112:THR:O	2:B:116:LEU:HD13	0.47	2.10	16	1
1:A:13:G:N7	2:B:58:TYR:CB	0.47	2.78	18	1
2:B:101:THR:O	2:B:171:THR:CG2	0.47	2.62	18	1
1:A:14:A:OP1	2:B:94:LYS:CB	0.47	2.63	19	1
2:B:15:ASN:O	2:B:16:LEU:HB3	0.47	2.10	18	4
1:A:2:G:O2'	1:A:3:C:H6	0.47	1.92	10	2
2:B:43:LEU:HD11	2:B:66:ASP:HA	0.47	1.87	10	1
2:B:31:LYS:CG	2:B:48:VAL:HG22	0.47	2.40	11	1
2:B:107:LEU:CD1	2:B:128:LEU:HD11	0.47	2.39	11	1
1:A:2:G:H4'	1:A:3:C:OP1	0.47	2.08	12	1
1:A:12:C:C1'	2:B:17:PHE:CE2	0.47	2.98	12	1
2:B:111:ILE:HD13	2:B:162:ASP:OD1	0.47	2.09	13	1
1:A:9:U:C1'	2:B:129:VAL:HG12	0.47	2.36	15	1
2:B:130:SER:N	2:B:136:LYS:HD2	0.47	2.24	15	1
2:B:82:GLU:O	2:B:83:ILE:C	0.47	2.53	14	2
2:B:153:LEU:O	2:B:157:GLN:HB2	0.47	2.09	10	7
2:B:103:LEU:HG	2:B:138:ILE:HG22	0.47	1.85	3	2
2:B:31:LYS:NZ	2:B:50:THR:HB	0.47	2.25	14	2
1:A:13:G:OP2	2:B:89:LYS:HB3	0.47	2.09	7	1
1:A:13:G:C5'	2:B:90:GLY:O	0.47	2.51	9	1
2:B:38:PHE:HB3	2:B:45:VAL:HG13	0.47	1.86	9	1
2:B:80:GLY:C	2:B:81:ASN:OD1	0.47	2.53	9	1
2:B:119:VAL:O	2:B:156:LYS:HE2	0.47	2.09	9	1
2:B:29:GLU:OE2	2:B:79:PHE:CZ	0.47	2.68	15	2
2:B:98:ALA:O	2:B:101:THR:N	0.47	2.42	11	1
2:B:89:LYS:O	2:B:91:ARG:CG	0.47	2.63	15	1
1:A:10:C:N4	1:A:11:C:C4	0.47	2.83	16	1
1:A:13:G:H5'	1:A:14:A:OP1	0.47	2.10	18	1
1:A:10:C:H42	2:B:94:LYS:NZ	0.47	2.08	6	2
1:A:16:G:N1	2:B:54:ARG:NH1	0.47	2.63	6	1
2:B:21:LEU:CD1	2:B:30:LEU:HB3	0.47	2.40	6	2
1:A:13:G:H21	2:B:91:ARG:N	0.47	2.07	7	1
2:B:61:PHE:HB2	2:B:66:ASP:OD1	0.47	2.10	18	3
2:B:74:THR:HA	2:B:85:LEU:CD1	0.47	2.40	16	3
2:B:73:LEU:HD22	2:B:76:LEU:HD21	0.47	1.85	13	1
1:A:20:G:C3'	1:A:21:C:O4'	0.47	2.63	16	2
2:B:125:GLU:O	2:B:126:ILE:CD1	0.47	2.54	16	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:20:G:O2'	1:A:21:C:H5'	0.46	2.10	1	2
2:B:18:ILE:CG1	2:B:85:LEU:HG	0.46	2.40	4	5
2:B:46:VAL:O	2:B:47:ASP:OD1	0.46	2.33	3	1
2:B:24:ASN:O	2:B:25:LYS:HD2	0.46	2.09	4	2
2:B:38:PHE:CD2	2:B:43:LEU:CB	0.46	2.98	6	2
2:B:115:GLU:OE2	2:B:161:ILE:HD13	0.46	2.10	6	1
2:B:38:PHE:CD2	2:B:45:VAL:CG2	0.46	2.98	7	1
2:B:93:SER:N	2:B:96:VAL:HB	0.46	2.24	13	2
2:B:101:THR:C	2:B:102:LEU:CD1	0.46	2.81	10	1
1:A:16:G:C4'	1:A:17:U:OP1	0.46	2.60	13	1
1:A:10:C:C4	1:A:11:C:N3	0.46	2.82	14	1
2:B:145:SER:CB	2:B:148:ASP:OD2	0.46	2.63	19	1
2:B:66:ASP:OD1	2:B:66:ASP:O	0.46	2.34	9	2
1:A:10:C:N4	2:B:94:LYS:HE2	0.46	2.24	8	1
2:B:76:LEU:CB	2:B:83:ILE:CG1	0.46	2.93	13	1
2:B:119:VAL:HG21	2:B:161:ILE:HD12	0.46	1.88	13	1
2:B:15:ASN:ND2	2:B:60:ASP:OD1	0.46	2.47	7	3
2:B:105:LYS:HG3	2:B:169:TYR:CD1	0.46	2.45	1	2
1:A:10:C:C4	2:B:140:TYR:OH	0.46	2.68	2	2
1:A:13:G:H2'	1:A:14:A:O5'	0.46	2.09	2	3
2:B:16:LEU:CB	2:B:88:PRO:HD3	0.46	2.41	17	5
1:A:15:A:N1	1:A:17:U:C4	0.46	2.83	5	2
2:B:121:GLU:OE2	2:B:122:ASP:OD2	0.46	2.33	5	1
1:A:14:A:O4'	2:B:95:LYS:HE2	0.46	2.10	7	4
2:B:21:LEU:C	2:B:30:LEU:HD21	0.46	2.31	7	1
2:B:47:ASP:C	2:B:60:ASP:OD1	0.46	2.54	16	2
1:A:10:C:C6	2:B:129:VAL:HG13	0.46	2.45	15	1
2:B:103:LEU:HD12	2:B:140:TYR:CD2	0.46	2.46	15	1
2:B:102:LEU:HD22	2:B:153:LEU:HB2	0.46	1.86	18	1
2:B:49:ARG:HG3	2:B:58:TYR:CB	0.46	2.40	19	1
2:B:107:LEU:HD21	2:B:116:LEU:HD21	0.46	1.86	15	2
2:B:28:ALA:O	2:B:32:VAL:HB	0.46	2.10	11	4
1:A:8:A:C5'	1:A:9:U:P	0.46	3.03	12	1
2:B:158:GLY:O	2:B:161:ILE:CD1	0.46	2.63	15	1
2:B:128:LEU:HD13	2:B:128:LEU:O	0.46	2.10	16	1
2:B:56:PHE:CG	2:B:57:GLY:N	0.46	2.83	17	1
1:A:13:G:C8	2:B:58:TYR:CB	0.46	2.98	18	1
1:A:15:A:H1'	1:A:17:U:C6	0.46	2.45	9	6
1:A:14:A:OP2	2:B:91:ARG:CB	0.46	2.64	7	1
1:A:9:U:H2'	1:A:9:U:OP1	0.46	2.11	9	1
2:B:102:LEU:C	2:B:102:LEU:CD1	0.46	2.78	18	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:125:GLU:C	2:B:126:ILE:CG1	0.46	2.84	12	1
2:B:38:PHE:HB3	2:B:45:VAL:HG23	0.46	1.86	14	1
2:B:101:THR:HG21	2:B:142:GLU:OE2	0.46	2.09	16	1
2:B:127:ARG:HB3	2:B:140:TYR:HB2	0.46	1.86	18	1
2:B:103:LEU:CB	2:B:140:TYR:HA	0.46	2.40	1	2
1:A:9:U:O4	2:B:105:LYS:HD3	0.46	2.11	6	1
1:A:12:C:OP2	1:A:12:C:C2	0.46	2.69	7	1
2:B:91:ARG:O	2:B:92:ASP:HB3	0.46	2.10	18	3
2:B:160:GLU:HA	2:B:165:SER:CA	0.46	2.41	9	1
2:B:101:THR:O	2:B:171:THR:HG22	0.46	2.10	11	2
2:B:125:GLU:O	2:B:142:GLU:N	0.46	2.45	11	1
2:B:77:LYS:O	2:B:78:VAL:C	0.46	2.54	17	3
2:B:114:ASP:O	2:B:118:GLU:N	0.46	2.49	14	1
2:B:155:GLU:HG3	2:B:156:LYS:CD	0.46	2.41	16	1
2:B:12:THR:CG2	2:B:13:PRO:CD	0.46	2.93	17	1
2:B:49:ARG:HD3	2:B:58:TYR:HB2	0.46	1.88	19	1
1:A:16:G:N3	1:A:17:U:H5	0.46	2.09	3	1
1:A:7:A:C6	1:A:8:A:C5	0.46	3.04	4	1
2:B:41:ASN:O	2:B:42:ASP:HB3	0.46	2.08	17	7
2:B:98:ALA:CB	2:B:171:THR:HB	0.46	2.40	5	2
1:A:20:G:O2'	1:A:21:C:H6	0.46	1.94	7	1
2:B:61:PHE:HB2	2:B:66:ASP:CG	0.46	2.31	18	3
2:B:158:GLY:HA2	2:B:166:VAL:O	0.46	2.11	8	3
2:B:105:LYS:O	2:B:166:VAL:HG23	0.46	2.11	16	1
2:B:50:THR:OG1	2:B:54:ARG:HD3	0.46	2.11	19	1
2:B:18:ILE:CG2	2:B:83:ILE:HB	0.46	2.41	19	6
2:B:97:ARG:HG3	2:B:98:ALA:N	0.46	2.25	19	3
2:B:12:THR:O	2:B:15:ASN:OD1	0.46	2.34	13	1
2:B:145:SER:N	2:B:148:ASP:CG	0.46	2.69	19	1
1:A:1:G:C4'	1:A:2:G:OP1	0.46	2.64	2	1
1:A:20:G:H5"	1:A:21:C:OP2	0.46	2.11	2	1
2:B:10:SER:OG	2:B:12:THR:O	0.46	2.34	4	1
2:B:59:VAL:C	2:B:60:ASP:OD1	0.46	2.54	4	4
2:B:100:ARG:HG3	2:B:142:GLU:OE1	0.46	2.10	4	1
2:B:153:LEU:HD13	2:B:170:TYR:CD1	0.46	2.46	5	1
2:B:153:LEU:O	2:B:157:GLN:CG	0.46	2.63	6	1
2:B:157:GLN:OE1	2:B:167:SER:HA	0.46	2.11	6	1
2:B:125:GLU:OE2	2:B:142:GLU:OE1	0.46	2.33	10	1
2:B:126:ILE:HG23	2:B:141:ILE:CG1	0.46	2.37	10	1
2:B:30:LEU:HD12	2:B:31:LYS:CA	0.46	2.39	14	1
2:B:16:LEU:HA	2:B:88:PRO:HD3	0.46	1.89	2	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:111:ILE:CG1	2:B:115:GLU:OE1	0.46	2.64	2	1
1:A:16:G:OP2	2:B:49:ARG:HB3	0.46	2.11	3	1
2:B:101:THR:OG1	2:B:142:GLU:HG2	0.46	2.10	3	1
1:A:13:G:C5'	2:B:90:GLY:HA3	0.46	2.41	4	1
2:B:127:ARG:HB2	2:B:140:TYR:HB3	0.46	1.87	8	5
1:A:13:G:N3	1:A:13:G:C2'	0.46	2.78	9	1
1:A:19:G:C4'	1:A:20:G:OP1	0.46	2.64	15	4
2:B:101:THR:HB	2:B:171:THR:HG21	0.46	1.88	11	1
1:A:14:A:OP1	2:B:95:LYS:CD	0.46	2.63	14	1
2:B:21:LEU:HD21	2:B:30:LEU:HD13	0.46	1.86	14	1
2:B:103:LEU:HD11	2:B:129:VAL:HG11	0.46	1.87	15	1
2:B:140:TYR:OH	2:B:171:THR:HG23	0.46	2.10	15	1
1:A:14:A:O4'	2:B:93:SER:O	0.46	2.35	17	1
2:B:87:LYS:O	2:B:89:LYS:HE2	0.46	2.12	18	1
2:B:94:LYS:O	2:B:98:ALA:HB2	0.46	2.11	18	1
2:B:47:ASP:HB3	2:B:60:ASP:OD2	0.45	2.11	18	5
2:B:116:LEU:HD23	2:B:141:ILE:CD1	0.45	2.39	18	2
2:B:64:ALA:O	2:B:68:GLU:OE1	0.45	2.35	10	1
2:B:116:LEU:HD11	2:B:139:ALA:CB	0.45	2.42	10	1
2:B:140:TYR:OH	2:B:171:THR:HG22	0.45	2.10	10	1
1:A:10:C:O2	1:A:11:C:C1'	0.45	2.64	18	1
2:B:143:PHE:CD2	2:B:149:ALA:HB2	0.45	2.45	18	1
2:B:17:PHE:CE2	2:B:86:GLU:HG2	0.45	2.46	19	1
2:B:90:GLY:O	2:B:91:ARG:HB2	0.45	2.11	2	2
1:A:20:G:OP1	1:A:20:G:C4'	0.45	2.63	3	1
1:A:12:C:C4'	1:A:13:G:OP1	0.45	2.64	5	1
2:B:21:LEU:HD13	2:B:30:LEU:HD22	0.45	1.87	6	1
2:B:86:GLU:HG3	2:B:87:LYS:N	0.45	2.26	13	4
1:A:14:A:O4'	2:B:94:LYS:CD	0.45	2.64	11	1
2:B:107:LEU:CD1	2:B:111:ILE:HG22	0.45	2.41	11	1
2:B:53:ASN:C	2:B:54:ARG:HG2	0.45	2.31	18	9
2:B:102:LEU:HD23	2:B:153:LEU:CD1	0.45	2.32	2	1
2:B:22:ASN:ND2	2:B:79:PHE:HB2	0.45	2.25	3	2
2:B:27:VAL:O	2:B:28:ALA:C	0.45	2.54	18	3
2:B:153:LEU:O	2:B:157:GLN:HG2	0.45	2.11	6	2
2:B:110:ASN:HB3	2:B:162:ASP:OD2	0.45	2.11	7	2
2:B:37:LEU:O	2:B:41:ASN:HB2	0.45	2.12	11	4
2:B:116:LEU:HD22	2:B:139:ALA:CB	0.45	2.41	8	1
2:B:14:PHE:CZ	2:B:63:SER:O	0.45	2.69	13	1
2:B:51:GLY:O	2:B:52:THR:O	0.45	2.35	14	1
1:A:10:C:N1	2:B:140:TYR:CD2	0.45	2.84	15	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:107:LEU:CB	2:B:137:GLY:O	0.45	2.64	15	1
1:A:8:A:C2	2:B:95:LYS:HG2	0.45	2.47	17	1
2:B:159:ALA:O	2:B:161:ILE:HG12	0.45	2.10	17	1
2:B:119:VAL:HG13	2:B:156:LYS:HE3	0.45	1.89	18	1
2:B:12:THR:CG2	2:B:46:VAL:CG1	0.45	2.94	19	1
2:B:61:PHE:CE2	2:B:70:ALA:HB2	0.45	2.45	2	2
2:B:21:LEU:HD13	2:B:56:PHE:CA	0.45	2.42	3	3
2:B:45:VAL:O	2:B:45:VAL:CG2	0.45	2.65	3	1
2:B:163:GLY:O	2:B:164:ARG:HG2	0.45	2.12	5	6
2:B:128:LEU:HD11	2:B:130:SER:OG	0.45	2.12	4	1
2:B:37:LEU:HG	2:B:76:LEU:CD2	0.45	2.42	6	1
1:A:10:C:H5"	1:A:11:C:OP2	0.45	2.11	10	2
2:B:22:ASN:OD1	2:B:24:ASN:N	0.45	2.50	9	1
2:B:38:PHE:CE2	2:B:73:LEU:CD1	0.45	2.99	9	1
2:B:83:ILE:HG13	2:B:83:ILE:O	0.45	2.12	10	2
1:A:13:G:OP2	2:B:89:LYS:HG3	0.45	2.12	14	2
1:A:11:C:C2'	2:B:94:LYS:HZ2	0.45	2.25	15	1
2:B:140:TYR:O	2:B:141:ILE:HG12	0.45	2.11	4	6
2:B:16:LEU:HA	2:B:88:PRO:HB3	0.45	1.87	14	3
2:B:101:THR:HG23	2:B:142:GLU:CA	0.45	2.42	3	1
2:B:127:ARG:O	2:B:140:TYR:HB2	0.45	2.12	11	4
2:B:107:LEU:N	2:B:107:LEU:HD22	0.45	2.25	13	2
1:A:10:C:C5	2:B:140:TYR:OH	0.45	2.70	9	2
2:B:167:SER:C	2:B:168:LEU:HD22	0.45	2.32	18	2
2:B:76:LEU:HB2	2:B:83:ILE:CD1	0.45	2.42	12	2
2:B:85:LEU:HD13	2:B:85:LEU:N	0.45	2.27	12	1
2:B:15:ASN:CG	2:B:60:ASP:OD1	0.45	2.55	13	1
2:B:21:LEU:HD23	2:B:54:ARG:HA	0.45	1.88	14	1
2:B:151:LYS:O	2:B:155:GLU:N	0.45	2.44	16	1
2:B:56:PHE:CD1	2:B:56:PHE:N	0.45	2.83	1	5
2:B:14:PHE:O	2:B:60:ASP:HA	0.45	2.11	3	4
1:A:13:G:O5'	2:B:90:GLY:HA3	0.45	2.12	4	1
2:B:33:ALA:HB2	2:B:79:PHE:CE2	0.45	2.46	4	2
1:A:9:U:C2'	1:A:10:C:OP1	0.45	2.63	8	2
2:B:74:THR:OG1	2:B:85:LEU:CD1	0.45	2.64	8	1
2:B:157:GLN:HG3	2:B:158:GLY:N	0.45	2.26	8	1
1:A:17:U:H2'	1:A:18:A:OP1	0.45	2.11	11	1
1:A:3:C:C2'	1:A:4:C:OP1	0.45	2.63	19	2
1:A:8:A:N1	1:A:14:A:N9	0.45	2.65	13	1
1:A:17:U:H2'	1:A:18:A:O5'	0.45	2.12	15	1
1:A:10:C:N4	2:B:140:TYR:CE2	0.45	2.85	1	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:14:PHE:CD2	2:B:63:SER:CA	0.45	3.00	1	1
2:B:18:ILE:HG12	2:B:85:LEU:HD13	0.45	1.87	1	1
2:B:107:LEU:HD22	2:B:139:ALA:HB2	0.45	1.89	3	2
2:B:18:ILE:HG12	2:B:84:LYS:O	0.45	2.11	10	3
2:B:107:LEU:HD23	2:B:111:ILE:HG21	0.45	1.88	5	1
2:B:73:LEU:O	2:B:83:ILE:HD13	0.45	2.12	14	1
2:B:94:LYS:HE2	2:B:94:LYS:HA	0.45	1.86	14	1
2:B:30:LEU:CD1	2:B:54:ARG:HB3	0.45	2.39	19	1
2:B:47:ASP:C	2:B:60:ASP:OD2	0.45	2.56	1	1
2:B:61:PHE:HB3	2:B:66:ASP:CB	0.45	2.42	11	9
2:B:85:LEU:HD13	2:B:86:GLU:H	0.45	1.67	5	1
2:B:101:THR:HG22	2:B:102:LEU:N	0.45	2.27	5	2
1:A:20:G:C2	1:A:21:C:C2	0.45	3.05	6	2
1:A:16:G:C6	2:B:54:ARG:NH2	0.45	2.85	7	1
2:B:30:LEU:CD2	2:B:78:VAL:CG1	0.45	2.94	15	3
2:B:111:ILE:N	2:B:162:ASP:OD2	0.45	2.50	12	1
1:A:16:G:O6	2:B:54:ARG:NH1	0.45	2.49	15	2
2:B:14:PHE:C	2:B:60:ASP:OD1	0.45	2.55	13	1
2:B:27:VAL:HG12	2:B:31:LYS:HE3	0.45	1.89	16	1
1:A:12:C:O2'	1:A:13:G:O5'	0.45	2.34	17	1
1:A:11:C:O2	2:B:94:LYS:HB3	0.45	2.12	18	1
2:B:143:PHE:HB3	2:B:148:ASP:OD1	0.45	2.12	19	1
1:A:10:C:H2'	1:A:11:C:OP1	0.45	2.12	2	1
2:B:53:ASN:C	2:B:54:ARG:HD3	0.45	2.32	5	3
2:B:124:LEU:HD12	2:B:143:PHE:C	0.45	2.32	7	2
1:A:13:G:OP1	2:B:89:LYS:HB3	0.45	2.12	12	1
2:B:94:LYS:HG3	2:B:95:LYS:N	0.45	2.27	12	1
2:B:34:ILE:HG23	2:B:38:PHE:CE1	0.45	2.46	15	1
2:B:16:LEU:HA	2:B:88:PRO:CD	0.45	2.42	14	5
2:B:59:VAL:CG1	2:B:60:ASP:N	0.45	2.80	2	4
2:B:143:PHE:CG	2:B:149:ALA:CA	0.45	2.99	18	6
2:B:129:VAL:HG23	2:B:139:ALA:HA	0.45	1.89	3	6
1:A:1:G:C1'	1:A:2:G:OP1	0.45	2.65	4	1
2:B:94:LYS:CE	2:B:94:LYS:C	0.45	2.84	8	1
2:B:94:LYS:NZ	2:B:95:LYS:HE2	0.45	2.26	11	1
2:B:46:VAL:CG2	2:B:62:GLU:HG3	0.45	2.42	13	2
1:A:6:A:N1	1:A:7:A:C5	0.44	2.85	17	2
1:A:13:G:OP2	2:B:89:LYS:HD3	0.44	2.12	6	1
1:A:14:A:O5'	1:A:14:A:C8	0.44	2.69	6	1
2:B:74:THR:N	2:B:85:LEU:CD1	0.44	2.80	8	1
2:B:19:GLY:HA2	2:B:56:PHE:CB	0.44	2.42	9	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:12:C:H1'	2:B:17:PHE:CE2	0.44	2.46	12	1
2:B:12:THR:HB	2:B:13:PRO:HD2	0.44	1.87	13	1
2:B:159:ALA:O	2:B:160:GLU:O	0.44	2.35	13	1
2:B:111:ILE:HD13	2:B:161:ILE:CG2	0.44	2.41	16	1
2:B:21:LEU:HD12	2:B:50:THR:OG1	0.44	2.12	17	1
2:B:38:PHE:CE1	2:B:43:LEU:HD13	0.44	2.47	19	1
2:B:110:ASN:O	2:B:111:ILE:C	0.44	2.54	6	2
2:B:47:ASP:HB3	2:B:60:ASP:OD1	0.44	2.12	17	4
2:B:88:PRO:O	2:B:89:LYS:HB3	0.44	2.12	4	1
2:B:18:ILE:HG13	2:B:85:LEU:HD23	0.44	1.89	5	1
2:B:61:PHE:CZ	2:B:70:ALA:HB2	0.44	2.47	5	1
1:A:9:U:C5	2:B:103:LEU:HD22	0.44	2.48	6	1
2:B:125:GLU:HG2	2:B:142:GLU:CG	0.44	2.42	6	1
2:B:123:ALA:HA	2:B:142:GLU:O	0.44	2.12	8	1
2:B:124:LEU:HD11	2:B:144:LYS:CA	0.44	2.42	16	2
1:A:10:C:C2	2:B:140:TYR:CD1	0.44	3.05	10	1
2:B:120:PHE:HB3	2:B:123:ALA:HB2	0.44	1.88	10	1
2:B:105:LYS:HG3	2:B:169:TYR:CG	0.44	2.47	11	1
1:A:14:A:N1	2:B:94:LYS:CE	0.44	2.81	13	1
2:B:14:PHE:CZ	2:B:64:ALA:CB	0.44	2.99	19	1
2:B:25:LYS:O	2:B:54:ARG:CZ	0.44	2.66	4	1
2:B:156:LYS:HB2	2:B:168:LEU:CD1	0.44	2.41	4	2
2:B:168:LEU:N	2:B:168:LEU:CD2	0.44	2.80	6	3
2:B:58:TYR:C	2:B:59:VAL:HG23	0.44	2.32	10	3
2:B:147:ALA:O	2:B:151:LYS:N	0.44	2.46	8	1
2:B:140:TYR:O	2:B:141:ILE:HG13	0.44	2.11	11	1
2:B:125:GLU:O	2:B:126:ILE:HG12	0.44	2.12	12	1
2:B:130:SER:HB3	2:B:136:LYS:HD2	0.44	1.89	15	1
2:B:128:LEU:C	2:B:128:LEU:CD2	0.44	2.72	16	1
2:B:51:GLY:HA3	2:B:56:PHE:HD1	0.44	1.73	19	1
2:B:116:LEU:O	2:B:120:PHE:HB2	0.44	2.13	7	9
2:B:14:PHE:CB	2:B:61:PHE:HB2	0.44	2.42	15	5
2:B:120:PHE:CD2	2:B:141:ILE:HG21	0.44	2.48	9	2
2:B:120:PHE:O	2:B:121:GLU:C	0.44	2.54	11	3
2:B:128:LEU:C	2:B:128:LEU:CD1	0.44	2.85	2	1
1:A:9:U:H5	2:B:103:LEU:HD11	0.44	1.71	5	2
2:B:108:SER:HB3	2:B:162:ASP:OD2	0.44	2.13	6	3
1:A:2:G:N1	1:A:3:C:C2	0.44	2.85	9	1
2:B:92:ASP:O	2:B:93:SER:HB2	0.44	2.12	12	2
2:B:152:ASN:O	2:B:156:LYS:HG2	0.44	2.12	10	1
2:B:101:THR:HG21	2:B:140:TYR:CD2	0.44	2.48	17	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:13:G:OP1	2:B:94:LYS:HB2	0.44	2.11	14	1
2:B:166:VAL:CG1	2:B:167:SER:N	0.44	2.80	14	1
2:B:128:LEU:CD2	2:B:136:LYS:HG3	0.44	2.43	15	1
2:B:31:LYS:HG3	2:B:48:VAL:CG2	0.44	2.42	16	1
2:B:47:ASP:CB	2:B:60:ASP:CG	0.44	2.85	16	1
1:A:14:A:O5'	2:B:94:LYS:CB	0.44	2.65	17	1
1:A:13:G:C5'	1:A:14:A:OP1	0.44	2.66	18	1
1:A:12:C:C2'	1:A:13:G:OP2	0.44	2.66	1	1
2:B:144:LYS:HG2	2:B:148:ASP:CB	0.44	2.43	3	1
1:A:12:C:OP1	1:A:12:C:N1	0.44	2.50	6	1
1:A:10:C:H42	2:B:94:LYS:CD	0.44	2.26	8	1
2:B:162:ASP:OD2	2:B:164:ARG:HG2	0.44	2.12	9	1
1:A:10:C:C2	2:B:140:TYR:CE2	0.44	3.05	15	1
2:B:62:GLU:HG3	2:B:66:ASP:OD2	0.44	2.13	4	2
2:B:155:GLU:OE2	2:B:155:GLU:O	0.44	2.36	1	1
2:B:151:LYS:CE	2:B:155:GLU:OE1	0.44	2.66	3	1
2:B:78:VAL:HG12	2:B:81:ASN:HB2	0.44	1.89	5	1
2:B:112:THR:N	2:B:115:GLU:OE1	0.44	2.51	17	3
1:A:12:C:N3	2:B:17:PHE:HZ	0.44	2.10	6	2
2:B:102:LEU:CD1	2:B:141:ILE:HB	0.44	2.43	6	1
1:A:14:A:P	2:B:91:ARG:HB2	0.44	2.52	7	1
2:B:107:LEU:CD2	2:B:111:ILE:HG21	0.44	2.43	9	1
2:B:25:LYS:HG2	2:B:79:PHE:CD2	0.44	2.48	15	1
1:A:17:U:O2'	1:A:18:A:O5'	0.44	2.32	16	1
2:B:27:VAL:HG12	2:B:31:LYS:CE	0.44	2.43	16	1
1:A:20:G:H2'	1:A:20:G:N3	0.44	2.27	18	1
2:B:103:LEU:CD1	2:B:138:ILE:HG21	0.44	2.43	15	2
2:B:111:ILE:CD1	2:B:162:ASP:HB2	0.44	2.43	2	2
1:A:14:A:C2'	2:B:52:THR:CG2	0.44	2.95	2	1
1:A:11:C:C2	2:B:94:LYS:CE	0.44	3.01	6	2
2:B:98:ALA:CA	2:B:171:THR:HB	0.44	2.42	5	1
2:B:107:LEU:CD1	2:B:138:ILE:C	0.44	2.86	9	2
2:B:61:PHE:CB	2:B:66:ASP:OD1	0.44	2.66	18	2
2:B:92:ASP:OD1	2:B:97:ARG:N	0.44	2.51	8	1
2:B:151:LYS:O	2:B:154:GLU:HG2	0.44	2.12	8	1
2:B:21:LEU:HD22	2:B:30:LEU:HG	0.44	1.89	9	1
2:B:26:SER:OG	2:B:29:GLU:HG2	0.44	2.12	12	1
1:A:14:A:N6	2:B:94:LYS:CD	0.44	2.80	13	1
2:B:18:ILE:HD13	2:B:59:VAL:HB	0.44	1.89	16	1
2:B:105:LYS:HD2	2:B:169:TYR:CE1	0.44	2.47	18	1
2:B:74:THR:CG2	2:B:85:LEU:CD1	0.44	2.96	19	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:20:G:C5'	1:A:21:C:OP2	0.44	2.66	2	1
2:B:44:ALA:CB	2:B:62:GLU:HG2	0.44	2.37	5	1
2:B:61:PHE:HB3	2:B:66:ASP:OD2	0.44	2.13	5	3
2:B:105:LYS:HE3	2:B:169:TYR:CE2	0.44	2.47	6	1
2:B:38:PHE:HB3	2:B:43:LEU:HB2	0.44	1.88	7	1
2:B:101:THR:O	2:B:171:THR:CB	0.44	2.66	7	1
1:A:16:G:C5	2:B:27:VAL:HB	0.44	2.48	8	1
2:B:111:ILE:HG13	2:B:115:GLU:CG	0.44	2.43	9	1
2:B:12:THR:OG1	2:B:46:VAL:CG1	0.44	2.66	10	1
2:B:70:ALA:HA	2:B:73:LEU:CD2	0.44	2.42	11	1
1:A:1:G:C2	1:A:2:G:C8	0.44	3.06	12	1
1:A:13:G:P	2:B:89:LYS:HB2	0.44	2.52	13	1
1:A:12:C:N4	2:B:86:GLU:OE1	0.44	2.50	17	1
2:B:30:LEU:HD13	2:B:50:THR:OG1	0.44	2.12	19	1
1:A:13:G:H4'	1:A:14:A:O5'	0.44	2.13	1	1
2:B:49:ARG:NH2	2:B:60:ASP:OD1	0.44	2.51	1	1
2:B:22:ASN:C	2:B:54:ARG:HB2	0.44	2.33	6	3
2:B:152:ASN:O	2:B:156:LYS:HB2	0.44	2.13	10	4
1:A:14:A:C4	2:B:94:LYS:HB3	0.44	2.47	5	1
2:B:46:VAL:C	2:B:47:ASP:CG	0.44	2.77	5	1
2:B:142:GLU:O	2:B:142:GLU:HG3	0.44	2.13	6	2
2:B:93:SER:HA	2:B:97:ARG:HG3	0.44	1.89	7	1
2:B:19:GLY:HA2	2:B:56:PHE:HA	0.44	1.90	9	1
2:B:73:LEU:C	2:B:76:LEU:HD22	0.44	2.33	9	1
2:B:124:LEU:HB2	2:B:142:GLU:CG	0.44	2.43	10	1
2:B:147:ALA:O	2:B:151:LYS:HB3	0.44	2.12	17	1
2:B:48:VAL:O	2:B:49:ARG:HG2	0.44	2.13	19	1
2:B:90:GLY:O	2:B:91:ARG:CB	0.43	2.64	2	1
2:B:162:ASP:O	2:B:164:ARG:HG3	0.43	2.13	6	6
1:A:12:C:C5	1:A:12:C:OP1	0.43	2.71	3	1
2:B:102:LEU:CD1	2:B:170:TYR:CE1	0.43	3.01	3	1
2:B:43:LEU:HD23	2:B:66:ASP:OD1	0.43	2.13	5	1
1:A:16:G:C6	2:B:54:ARG:CZ	0.43	3.00	6	1
2:B:104:ALA:O	2:B:107:LEU:HD12	0.43	2.12	9	1
2:B:163:GLY:O	2:B:164:ARG:HB3	0.43	2.13	9	4
2:B:43:LEU:CD1	2:B:66:ASP:OD1	0.43	2.66	10	2
2:B:102:LEU:CD2	2:B:102:LEU:C	0.43	2.86	10	1
1:A:9:U:O4	2:B:105:LYS:HE3	0.43	2.13	11	2
2:B:120:PHE:CD1	2:B:141:ILE:HG21	0.43	2.48	12	1
2:B:140:TYR:C	2:B:141:ILE:CD1	0.43	2.83	12	1
2:B:116:LEU:HB3	2:B:126:ILE:HG21	0.43	1.90	13	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:107:LEU:HD12	2:B:111:ILE:HG21	0.43	1.88	19	1
2:B:33:ALA:O	2:B:37:LEU:HB2	0.43	2.13	7	10
2:B:77:LYS:HA	2:B:82:GLU:CA	0.43	2.44	3	2
2:B:147:ALA:O	2:B:151:LYS:HB2	0.43	2.12	16	5
2:B:38:PHE:CD1	2:B:38:PHE:N	0.43	2.86	13	3
2:B:49:ARG:HB3	2:B:58:TYR:CB	0.43	2.42	8	1
2:B:74:THR:OG1	2:B:85:LEU:HD12	0.43	2.13	8	1
2:B:158:GLY:HA3	2:B:166:VAL:CB	0.43	2.43	9	1
2:B:30:LEU:HD11	2:B:54:ARG:HD2	0.43	1.89	11	1
2:B:21:LEU:HB2	2:B:54:ARG:C	0.43	2.34	13	1
1:A:3:C:C2'	1:A:4:C:O5'	0.43	2.66	14	1
2:B:92:ASP:HB3	2:B:96:VAL:CB	0.43	2.43	15	1
2:B:76:LEU:CB	2:B:83:ILE:CD1	0.43	2.96	19	1
1:A:14:A:C5	2:B:94:LYS:HG3	0.43	2.47	2	1
2:B:21:LEU:CD2	2:B:30:LEU:HD23	0.43	2.43	4	1
2:B:37:LEU:HD23	2:B:37:LEU:O	0.43	2.12	4	1
2:B:37:LEU:HD13	2:B:41:ASN:ND2	0.43	2.29	6	1
2:B:69:LYS:O	2:B:73:LEU:HB2	0.43	2.13	9	3
2:B:107:LEU:HD22	2:B:111:ILE:HG21	0.43	1.88	9	1
1:A:10:C:O2'	1:A:11:C:P	0.43	2.76	11	1
2:B:62:GLU:N	2:B:66:ASP:OD2	0.43	2.48	17	1
2:B:111:ILE:HA	2:B:115:GLU:OE1	0.43	2.12	19	1
2:B:115:GLU:CD	2:B:115:GLU:C	0.43	2.77	2	2
2:B:94:LYS:HD2	2:B:94:LYS:O	0.43	2.14	17	2
2:B:120:PHE:CE2	2:B:168:LEU:HD11	0.43	2.49	6	1
1:A:1:G:O6	1:A:2:G:O6	0.43	2.36	12	1
1:A:10:C:C3'	2:B:128:LEU:O	0.43	2.66	15	1
2:B:15:ASN:O	2:B:16:LEU:HB2	0.43	2.14	16	1
2:B:56:PHE:HZ	2:B:58:TYR:CE2	0.43	2.32	19	1
2:B:17:PHE:CD2	2:B:86:GLU:CG	0.43	3.01	1	2
2:B:18:ILE:HG13	2:B:85:LEU:HG	0.43	1.89	16	3
2:B:37:LEU:HD21	2:B:76:LEU:CD2	0.43	2.37	2	1
2:B:102:LEU:HD11	2:B:143:PHE:CD1	0.43	2.49	2	2
2:B:38:PHE:CB	2:B:43:LEU:HB2	0.43	2.44	7	1
2:B:27:VAL:CB	2:B:31:LYS:HE3	0.43	2.43	9	1
2:B:158:GLY:HA3	2:B:166:VAL:HB	0.43	1.89	9	1
2:B:49:ARG:CG	2:B:58:TYR:CB	0.43	2.96	19	1
1:A:9:U:O3'	1:A:10:C:C6	0.43	2.72	1	2
2:B:32:VAL:HA	2:B:35:SER:OG	0.43	2.13	2	1
2:B:69:LYS:HG2	2:B:73:LEU:CD2	0.43	2.43	4	1
2:B:59:VAL:C	2:B:60:ASP:CG	0.43	2.77	15	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:38:PHE:HE2	2:B:73:LEU:HD21	0.43	1.72	8	1
1:A:1:G:N3	1:A:1:G:C2'	0.43	2.76	12	1
2:B:97:ARG:CZ	2:B:142:GLU:OE2	0.43	2.66	18	1
2:B:17:PHE:CE2	2:B:86:GLU:CD	0.43	2.92	4	1
2:B:18:ILE:HD11	2:B:85:LEU:CD1	0.43	2.44	6	1
1:A:17:U:O2'	1:A:18:A:P	0.43	2.77	11	1
2:B:76:LEU:O	2:B:83:ILE:HD12	0.43	2.13	12	1
2:B:15:ASN:CG	2:B:60:ASP:CG	0.43	2.77	13	1
2:B:48:VAL:HG13	2:B:59:VAL:HG22	0.43	1.88	18	1
2:B:66:ASP:CG	2:B:67:LEU:N	0.43	2.71	18	1
2:B:59:VAL:HG13	2:B:61:PHE:CZ	0.43	2.48	1	1
2:B:97:ARG:O	2:B:100:ARG:N	0.43	2.51	19	3
2:B:25:LYS:CE	2:B:79:PHE:CD1	0.43	3.02	8	1
1:A:8:A:H61	1:A:14:A:C1'	0.43	2.27	14	1
1:A:6:A:C8	1:A:18:A:C6	0.43	3.06	17	1
1:A:6:A:N1	1:A:7:A:C4	0.43	2.87	17	1
2:B:73:LEU:HG	2:B:76:LEU:CD1	0.43	2.44	18	1
2:B:41:ASN:C	2:B:42:ASP:CG	0.43	2.76	13	2
2:B:20:ASN:O	2:B:83:ILE:HG22	0.43	2.13	4	2
1:A:4:C:O2'	1:A:5:G:C3'	0.43	2.66	4	1
1:A:5:G:C4'	1:A:6:A:OP1	0.43	2.67	4	1
1:A:10:C:O2	2:B:127:ARG:CD	0.43	2.66	6	2
2:B:94:LYS:HE2	2:B:127:ARG:NH2	0.43	2.28	6	1
2:B:102:LEU:O	2:B:140:TYR:HA	0.43	2.13	9	1
1:A:10:C:C5	1:A:11:C:C4	0.43	3.06	14	1
2:B:37:LEU:HD13	2:B:76:LEU:CG	0.43	2.44	15	1
2:B:153:LEU:HD13	2:B:153:LEU:O	0.43	2.14	15	1
2:B:144:LYS:O	2:B:145:SER:HB3	0.43	2.14	19	1
2:B:159:ALA:O	2:B:165:SER:HA	0.43	2.13	9	2
2:B:50:THR:OG1	2:B:51:GLY:N	0.43	2.51	6	1
2:B:101:THR:C	2:B:171:THR:OG1	0.43	2.58	6	1
2:B:38:PHE:CB	2:B:45:VAL:HG21	0.43	2.44	8	2
2:B:159:ALA:O	2:B:161:ILE:HG13	0.43	2.14	9	5
2:B:153:LEU:HA	2:B:168:LEU:HD12	0.43	1.91	9	1
2:B:61:PHE:CD1	2:B:61:PHE:N	0.43	2.86	11	1
2:B:94:LYS:HE2	2:B:94:LYS:O	0.43	2.13	14	1
2:B:119:VAL:CG1	2:B:159:ALA:HB1	0.43	2.43	16	1
2:B:59:VAL:HG11	2:B:61:PHE:CE1	0.43	2.48	18	1
2:B:130:SER:C	2:B:136:LYS:HB2	0.42	2.34	3	3
2:B:47:ASP:CB	2:B:60:ASP:HB2	0.42	2.44	8	1
2:B:27:VAL:O	2:B:31:LYS:HD2	0.42	2.13	9	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:51:GLY:N	2:B:57:GLY:CA	0.42	2.82	9	1
1:A:6:A:C2'	1:A:7:A:O5'	0.42	2.66	10	1
2:B:94:LYS:HE3	2:B:94:LYS:O	0.42	2.14	10	1
2:B:13:PRO:HG2	2:B:14:PHE:CE2	0.42	2.49	13	2
1:A:10:C:C2'	2:B:128:LEU:O	0.42	2.67	15	1
2:B:95:LYS:O	2:B:95:LYS:HG2	0.42	2.13	19	2
2:B:46:VAL:HG23	2:B:61:PHE:CA	0.42	2.44	18	1
2:B:102:LEU:O	2:B:102:LEU:HG	0.42	2.13	1	1
1:A:19:G:C2	1:A:20:G:H1'	0.42	2.49	17	2
1:A:8:A:C6	1:A:14:A:C5	0.42	3.07	5	1
2:B:118:GLU:OE1	2:B:118:GLU:HA	0.42	2.13	7	1
2:B:38:PHE:N	2:B:38:PHE:CD1	0.42	2.85	8	1
2:B:81:ASN:OD1	2:B:81:ASN:N	0.42	2.52	9	1
2:B:73:LEU:HD22	2:B:76:LEU:CG	0.42	2.43	13	1
2:B:153:LEU:HD23	2:B:168:LEU:HB3	0.42	1.91	15	1
1:A:14:A:O5'	2:B:94:LYS:HB2	0.42	2.15	17	1
2:B:22:ASN:HB2	2:B:30:LEU:CD2	0.42	2.44	17	1
2:B:29:GLU:O	2:B:33:ALA:CB	0.42	2.67	18	1
2:B:47:ASP:O	2:B:48:VAL:HB	0.42	2.13	19	1
2:B:22:ASN:OD1	2:B:25:LYS:CD	0.42	2.67	2	1
2:B:130:SER:HA	2:B:136:LYS:HB3	0.42	1.91	3	2
1:A:20:G:O6	1:A:21:C:N4	0.42	2.52	5	1
2:B:97:ARG:O	2:B:101:THR:CB	0.42	2.67	7	1
1:A:10:C:H42	2:B:94:LYS:HD3	0.42	1.73	8	1
2:B:21:LEU:HD23	2:B:21:LEU:HA	0.42	1.70	18	2
2:B:26:SER:O	2:B:30:LEU:HG	0.42	2.14	17	1
2:B:101:THR:CA	2:B:102:LEU:HD13	0.42	2.43	19	1
2:B:53:ASN:C	2:B:54:ARG:CG	0.42	2.85	1	1
2:B:65:GLU:O	2:B:69:LYS:HD2	0.42	2.15	11	2
2:B:37:LEU:CD2	2:B:76:LEU:CD2	0.42	2.88	4	2
2:B:43:LEU:CD2	2:B:69:LYS:HD2	0.42	2.45	4	1
1:A:12:C:OP1	1:A:12:C:N3	0.42	2.52	6	1
2:B:102:LEU:CD2	2:B:141:ILE:O	0.42	2.64	13	1
2:B:158:GLY:HA2	2:B:166:VAL:N	0.42	2.29	16	3
2:B:136:LYS:HD3	2:B:138:ILE:CD1	0.42	2.45	18	1
2:B:48:VAL:HG22	2:B:59:VAL:HG23	0.42	1.92	1	1
2:B:51:GLY:O	2:B:56:PHE:CE1	0.42	2.71	1	1
1:A:9:U:O4	2:B:105:LYS:HE2	0.42	2.15	7	1
2:B:125:GLU:HG3	2:B:142:GLU:CB	0.42	2.45	8	1
1:A:9:U:OP2	1:A:9:U:H3'	0.42	2.15	14	1
1:A:10:C:O2'	2:B:127:ARG:CB	0.42	2.67	15	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:20:G:N3	1:A:20:G:H2'	0.42	2.30	16	1
2:B:31:LYS:HG2	2:B:48:VAL:CG1	0.42	2.45	17	1
2:B:16:LEU:HD12	2:B:17:PHE:O	0.42	2.14	18	1
1:A:2:G:O6	1:A:3:C:C4	0.42	2.72	1	2
2:B:24:ASN:O	2:B:25:LYS:HD3	0.42	2.15	4	1
2:B:142:GLU:CA	2:B:142:GLU:OE1	0.42	2.68	9	1
2:B:31:LYS:O	2:B:35:SER:HB2	0.42	2.14	11	1
1:A:11:C:O2	2:B:94:LYS:HG2	0.42	2.14	12	1
1:A:15:A:C2	1:A:16:G:C2	0.42	3.08	12	1
2:B:98:ALA:CB	2:B:171:THR:CG2	0.42	2.85	15	1
2:B:128:LEU:HG	2:B:136:LYS:HB3	0.42	1.90	15	1
2:B:139:ALA:O	2:B:141:ILE:CD1	0.42	2.68	15	1
2:B:127:ARG:NH1	2:B:140:TYR:CD2	0.42	2.88	16	1
2:B:158:GLY:O	2:B:159:ALA:CB	0.42	2.64	16	1
2:B:93:SER:HB2	2:B:95:LYS:HZ2	0.42	1.75	19	1
1:A:18:A:H2'	1:A:19:G:O5'	0.42	2.14	1	1
2:B:37:LEU:CD2	2:B:76:LEU:HB3	0.42	2.42	2	1
1:A:16:G:H5"	2:B:50:THR:HG22	0.42	1.91	3	1
2:B:92:ASP:HB3	2:B:96:VAL:CG1	0.42	2.45	3	3
1:A:11:C:O2	2:B:94:LYS:HE2	0.42	2.14	6	1
2:B:37:LEU:HD22	2:B:37:LEU:HA	0.42	1.72	6	1
2:B:18:ILE:HD12	2:B:59:VAL:CB	0.42	2.44	9	1
1:A:20:G:HO2'	1:A:21:C:P	0.42	2.37	13	1
1:A:3:C:C4	1:A:4:C:C4	0.42	3.07	14	1
1:A:9:U:O4'	1:A:9:U:O2	0.42	2.36	15	1
2:B:92:ASP:HB3	2:B:96:VAL:HG12	0.42	1.91	15	1
2:B:161:ILE:CD1	2:B:166:VAL:HB	0.42	2.44	15	1
2:B:62:GLU:O	2:B:63:SER:HB3	0.42	2.15	19	2
2:B:114:ASP:O	2:B:118:GLU:HB2	0.42	2.15	19	2
1:A:11:C:C4	2:B:94:LYS:CE	0.42	3.03	18	1
2:B:49:ARG:CD	2:B:58:TYR:HB2	0.42	2.44	19	1
2:B:26:SER:OG	2:B:29:GLU:HG3	0.42	2.15	1	1
2:B:105:LYS:HG2	2:B:138:ILE:CG2	0.42	2.45	1	1
1:A:13:G:O6	2:B:49:ARG:NH2	0.42	2.52	3	1
2:B:157:GLN:N	2:B:168:LEU:HD12	0.42	2.30	4	1
2:B:92:ASP:HB3	2:B:97:ARG:CG	0.42	2.44	6	1
2:B:54:ARG:NH1	2:B:54:ARG:CG	0.42	2.83	8	1
2:B:73:LEU:O	2:B:76:LEU:HG	0.42	2.15	13	1
2:B:103:LEU:HB3	2:B:169:TYR:O	0.42	2.14	17	2
2:B:159:ALA:O	2:B:161:ILE:CD1	0.42	2.67	13	1
1:A:13:G:OP2	2:B:89:LYS:HD2	0.42	2.14	14	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:76:LEU:O	2:B:83:ILE:HG13	0.42	2.15	14	1
2:B:129:VAL:HG23	2:B:138:ILE:HB	0.42	1.91	15	1
1:A:14:A:O4'	2:B:94:LYS:HB3	0.42	2.15	17	1
2:B:101:THR:O	2:B:170:TYR:CA	0.42	2.68	17	1
2:B:101:THR:HB	2:B:171:THR:CG2	0.42	2.44	18	1
2:B:143:PHE:CD2	2:B:149:ALA:CA	0.42	3.02	18	1
1:A:13:G:OP1	2:B:90:GLY:HA2	0.42	2.15	19	1
2:B:12:THR:HG23	2:B:46:VAL:CG1	0.42	2.45	19	1
2:B:25:LYS:CE	2:B:79:PHE:CE1	0.42	3.03	19	1
2:B:48:VAL:HG23	2:B:58:TYR:O	0.42	2.15	19	1
2:B:62:GLU:HG2	2:B:66:ASP:OD2	0.42	2.15	1	1
2:B:149:ALA:O	2:B:153:LEU:HB2	0.42	2.15	4	2
1:A:9:U:C6	2:B:138:ILE:HD12	0.42	2.49	14	2
1:A:14:A:OP2	2:B:94:LYS:HB2	0.42	2.14	4	1
2:B:74:THR:OG1	2:B:85:LEU:HB3	0.42	2.15	7	1
2:B:117:LYS:O	2:B:121:GLU:N	0.42	2.51	9	1
2:B:127:ARG:NH1	2:B:142:GLU:CD	0.42	2.73	12	1
2:B:66:ASP:O	2:B:70:ALA:N	0.42	2.52	13	1
1:A:7:A:C6	1:A:8:A:N1	0.42	2.88	16	2
1:A:8:A:C6	1:A:14:A:C1'	0.42	3.03	17	2
2:B:31:LYS:HD3	2:B:31:LYS:N	0.42	2.29	16	1
2:B:92:ASP:HB2	2:B:96:VAL:HG11	0.42	1.91	16	1
1:A:18:A:O2'	1:A:19:G:O4'	0.42	2.38	17	1
1:A:13:G:N9	2:B:49:ARG:HD2	0.42	2.30	18	1
2:B:22:ASN:ND2	2:B:25:LYS:CB	0.42	2.83	18	1
1:A:10:C:H1'	2:B:129:VAL:CG2	0.42	2.42	3	1
2:B:38:PHE:CZ	2:B:76:LEU:HD11	0.42	2.50	3	1
2:B:77:LYS:O	2:B:77:LYS:HG3	0.42	2.14	3	1
1:A:21:C:O2'	1:A:22:C:O4'	0.42	2.38	4	1
2:B:17:PHE:O	2:B:85:LEU:HG	0.42	2.15	7	1
2:B:149:ALA:O	2:B:153:LEU:HB3	0.42	2.15	7	1
2:B:38:PHE:CD1	2:B:43:LEU:CG	0.42	3.03	10	1
2:B:107:LEU:CD1	2:B:111:ILE:CG2	0.42	2.97	11	1
1:A:9:U:OP1	1:A:9:U:C6	0.42	2.73	15	1
1:A:1:G:H2'	1:A:2:G:O5'	0.42	2.14	16	1
2:B:153:LEU:O	2:B:157:GLN:CB	0.42	2.67	18	1
1:A:13:G:C5	2:B:58:TYR:CD2	0.41	3.08	7	2
2:B:51:GLY:C	2:B:56:PHE:CE1	0.41	2.94	1	2
2:B:123:ALA:CA	2:B:142:GLU:O	0.41	2.69	8	1
2:B:152:ASN:O	2:B:155:GLU:HB3	0.41	2.15	8	1
2:B:116:LEU:HD21	2:B:139:ALA:HB1	0.41	1.91	12	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:126:ILE:HD12	2:B:141:ILE:HG23	0.41	1.91	13	1
1:A:6:A:C2'	1:A:7:A:OP1	0.41	2.68	14	1
1:A:10:C:N3	1:A:11:C:C2	0.41	2.88	14	1
2:B:103:LEU:HD23	2:B:105:LYS:HD2	0.41	1.92	15	1
2:B:18:ILE:HG13	2:B:85:LEU:CG	0.41	2.45	16	1
2:B:105:LYS:HD2	2:B:169:TYR:CD1	0.41	2.50	18	1
2:B:115:GLU:CG	2:B:161:ILE:HD13	0.41	2.45	3	1
1:A:7:A:C5	1:A:8:A:C5	0.41	3.09	4	1
2:B:89:LYS:O	2:B:89:LYS:HG3	0.41	2.15	4	1
1:A:13:G:H21	2:B:91:ARG:HB2	0.41	1.74	9	1
2:B:92:ASP:CG	2:B:96:VAL:HG21	0.41	2.35	9	1
2:B:162:ASP:OD2	2:B:164:ARG:CD	0.41	2.67	9	1
2:B:102:LEU:HD22	2:B:102:LEU:C	0.41	2.35	10	1
2:B:120:PHE:O	2:B:122:ASP:N	0.41	2.53	11	1
2:B:153:LEU:HD12	2:B:168:LEU:CB	0.41	2.45	11	1
2:B:18:ILE:HD12	2:B:18:ILE:N	0.41	2.30	12	1
2:B:18:ILE:CG1	2:B:84:LYS:O	0.41	2.67	13	1
2:B:113:GLU:O	2:B:117:LYS:HB2	0.41	2.16	17	2
2:B:89:LYS:O	2:B:91:ARG:N	0.41	2.53	15	1
1:A:13:G:C8	2:B:49:ARG:HB3	0.41	2.50	18	1
2:B:27:VAL:CG2	2:B:50:THR:CB	0.41	2.98	19	1
1:A:1:G:O2'	1:A:2:G:C5'	0.41	2.68	2	1
2:B:54:ARG:NH1	2:B:54:ARG:HG3	0.41	2.30	4	1
2:B:77:LYS:C	2:B:78:VAL:O	0.41	2.58	4	2
1:A:2:G:O6	1:A:3:C:N4	0.41	2.53	15	2
2:B:85:LEU:HD13	2:B:85:LEU:C	0.41	2.31	5	1
2:B:155:GLU:CG	2:B:156:LYS:HD3	0.41	2.46	8	1
2:B:119:VAL:CG2	2:B:161:ILE:HD11	0.41	2.45	9	1
1:A:12:C:C2	2:B:17:PHE:HZ	0.41	2.31	10	1
2:B:47:ASP:HB3	2:B:60:ASP:CG	0.41	2.36	10	2
2:B:93:SER:O	2:B:94:LYS:CE	0.41	2.68	11	1
2:B:153:LEU:HD13	2:B:168:LEU:O	0.41	2.14	11	1
1:A:1:G:C6	1:A:2:G:C6	0.41	3.08	12	1
2:B:45:VAL:O	2:B:45:VAL:HG23	0.41	2.16	12	1
1:A:14:A:C8	2:B:52:THR:HB	0.41	2.50	13	1
2:B:73:LEU:O	2:B:76:LEU:HD23	0.41	2.16	19	1
2:B:46:VAL:O	2:B:47:ASP:OD2	0.41	2.38	1	1
2:B:145:SER:OG	2:B:148:ASP:HB2	0.41	2.16	1	1
2:B:20:ASN:O	2:B:81:ASN:HB3	0.41	2.15	2	2
2:B:17:PHE:O	2:B:18:ILE:HG13	0.41	2.16	3	1
1:A:12:C:H1'	2:B:17:PHE:CE1	0.41	2.50	6	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:91:ARG:O	2:B:92:ASP:HB2	0.41	2.15	8	1
2:B:34:ILE:HG23	2:B:38:PHE:CE2	0.41	2.48	11	1
1:A:13:G:C4	2:B:58:TYR:CE1	0.41	3.08	12	1
2:B:121:GLU:HG3	2:B:122:ASP:N	0.41	2.29	12	1
2:B:73:LEU:CD2	2:B:76:LEU:HD21	0.41	2.45	13	1
2:B:102:LEU:HB2	2:B:143:PHE:CD1	0.41	2.49	14	1
2:B:128:LEU:HA	2:B:139:ALA:HA	0.41	1.92	16	1
2:B:69:LYS:HD3	2:B:69:LYS:N	0.41	2.29	17	1
1:A:13:G:C8	2:B:49:ARG:CG	0.41	3.03	18	1
2:B:29:GLU:O	2:B:33:ALA:HB2	0.41	2.15	18	1
2:B:76:LEU:HB2	2:B:83:ILE:HD11	0.41	1.91	19	1
2:B:11:THR:CG2	2:B:12:THR:OG1	0.41	2.68	1	1
2:B:124:LEU:O	2:B:125:GLU:HB3	0.41	2.14	6	1
2:B:20:ASN:HB3	2:B:82:GLU:O	0.41	2.14	8	1
2:B:46:VAL:HG21	2:B:62:GLU:HB3	0.41	1.92	8	1
1:A:13:G:OP1	2:B:90:GLY:C	0.41	2.59	9	1
2:B:38:PHE:CG	2:B:45:VAL:HG13	0.41	2.50	9	1
2:B:73:LEU:HD13	2:B:73:LEU:HA	0.41	1.71	10	1
2:B:116:LEU:O	2:B:120:PHE:N	0.41	2.43	12	1
2:B:111:ILE:O	2:B:112:THR:HG22	0.41	2.15	13	1
2:B:111:ILE:CG2	2:B:112:THR:N	0.41	2.83	18	1
2:B:127:ARG:HB3	2:B:140:TYR:CB	0.41	2.46	18	1
2:B:82:GLU:O	2:B:82:GLU:HG3	0.41	2.14	2	1
1:A:14:A:OP2	1:A:14:A:C1'	0.41	2.69	4	1
1:A:16:G:O5'	1:A:17:U:OP1	0.41	2.38	4	1
2:B:115:GLU:OE2	2:B:161:ILE:CD1	0.41	2.67	6	1
2:B:47:ASP:O	2:B:48:VAL:HG22	0.41	2.16	8	1
2:B:102:LEU:HD23	2:B:102:LEU:N	0.41	2.30	9	1
2:B:111:ILE:HG12	2:B:116:LEU:HD11	0.41	1.91	16	1
2:B:155:GLU:CG	2:B:156:LYS:HG2	0.41	2.45	16	1
2:B:20:ASN:N	2:B:55:LYS:O	0.41	2.54	17	1
2:B:51:GLY:CA	2:B:56:PHE:HD1	0.41	2.27	17	1
2:B:97:ARG:O	2:B:100:ARG:HG2	0.41	2.15	3	1
2:B:107:LEU:CD2	2:B:116:LEU:HD11	0.41	2.45	6	1
1:A:2:G:C2'	1:A:3:C:OP2	0.41	2.68	7	1
1:A:13:G:O3'	2:B:93:SER:HB2	0.41	2.15	8	1
2:B:94:LYS:HE3	2:B:95:LYS:CE	0.41	2.46	11	1
1:A:2:G:O6	1:A:22:C:N4	0.41	2.54	12	1
2:B:108:SER:OG	2:B:164:ARG:NH2	0.41	2.54	14	1
2:B:98:ALA:CB	2:B:171:THR:HG22	0.41	2.35	15	1
2:B:129:VAL:C	2:B:138:ILE:HG13	0.41	2.36	15	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:22:ASN:HB3	2:B:30:LEU:CD2	0.41	2.42	16	1
1:A:14:A:N7	2:B:94:LYS:HE2	0.41	2.31	9	1
2:B:119:VAL:HG22	2:B:159:ALA:CB	0.41	2.45	9	1
2:B:142:GLU:OE1	2:B:143:PHE:N	0.41	2.53	9	1
2:B:21:LEU:HB3	2:B:54:ARG:O	0.41	2.15	14	1
2:B:30:LEU:CD2	2:B:54:ARG:CG	0.41	2.98	14	1
2:B:73:LEU:HD23	2:B:73:LEU:HA	0.41	1.73	16	1
2:B:91:ARG:C	2:B:92:ASP:CG	0.41	2.76	18	2
1:A:20:G:N3	1:A:20:G:C2'	0.41	2.83	18	1
2:B:101:THR:CG2	2:B:142:GLU:HG3	0.41	2.46	19	1
2:B:48:VAL:HG13	2:B:58:TYR:O	0.41	2.15	1	1
2:B:30:LEU:O	2:B:34:ILE:HG13	0.41	2.16	2	1
2:B:120:PHE:CE2	2:B:141:ILE:HG21	0.41	2.51	2	1
2:B:33:ALA:CB	2:B:78:VAL:CG1	0.41	2.97	3	1
2:B:78:VAL:HG13	2:B:79:PHE:H	0.41	1.75	4	1
1:A:14:A:N3	2:B:94:LYS:HB3	0.41	2.30	5	1
1:A:14:A:O5'	2:B:93:SER:HB3	0.41	2.16	5	1
2:B:163:GLY:C	2:B:164:ARG:CG	0.41	2.89	18	2
1:A:14:A:N6	2:B:94:LYS:HG2	0.41	2.30	6	1
2:B:160:GLU:C	2:B:161:ILE:HG13	0.41	2.36	14	2
2:B:107:LEU:HB2	2:B:137:GLY:C	0.41	2.35	10	1
2:B:51:GLY:CA	2:B:56:PHE:CG	0.41	3.00	11	1
2:B:107:LEU:O	2:B:137:GLY:HA2	0.41	2.15	11	1
2:B:163:GLY:C	2:B:164:ARG:HG2	0.41	2.36	11	1
1:A:17:U:O2	1:A:17:U:H2'	0.41	2.16	13	1
2:B:102:LEU:HB2	2:B:143:PHE:CE1	0.41	2.51	14	1
2:B:116:LEU:HD23	2:B:139:ALA:CB	0.41	2.46	14	1
2:B:76:LEU:HD12	2:B:76:LEU:N	0.41	2.30	15	1
2:B:98:ALA:O	2:B:171:THR:HB	0.41	2.15	15	1
2:B:104:ALA:O	2:B:138:ILE:CG2	0.41	2.69	15	1
1:A:6:A:C2	1:A:7:A:C4	0.41	3.08	17	1
2:B:76:LEU:HD12	2:B:76:LEU:C	0.41	2.36	17	1
2:B:95:LYS:C	2:B:95:LYS:HD2	0.41	2.36	19	1
2:B:51:GLY:O	2:B:56:PHE:CD1	0.41	2.74	1	1
2:B:100:ARG:O	2:B:100:ARG:HG3	0.41	2.15	2	1
1:A:6:A:HO2'	1:A:7:A:H5'	0.41	1.76	5	1
2:B:143:PHE:HB2	2:B:149:ALA:CB	0.41	2.43	5	1
2:B:27:VAL:HG13	2:B:31:LYS:CE	0.41	2.46	13	2
1:A:2:G:C6	1:A:22:C:C4	0.41	3.09	12	1
2:B:140:TYR:CE2	2:B:171:THR:CB	0.41	3.04	13	1
2:B:166:VAL:HG13	2:B:167:SER:N	0.41	2.31	15	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:43:LEU:HD13	2:B:73:LEU:HD12	0.41	1.93	16	1
2:B:83:ILE:O	2:B:83:ILE:HG13	0.41	2.15	17	1
2:B:170:TYR:CD1	2:B:170:TYR:C	0.41	2.94	17	1
2:B:106:ASN:HB3	2:B:165:SER:O	0.40	2.16	2	1
2:B:143:PHE:N	2:B:143:PHE:CD1	0.40	2.89	4	1
1:A:9:U:C1'	1:A:10:C:P	0.40	3.09	9	1
2:B:144:LYS:CB	2:B:148:ASP:OD2	0.40	2.69	9	1
2:B:160:GLU:HG3	2:B:165:SER:OG	0.40	2.16	9	1
2:B:129:VAL:O	2:B:136:LYS:HB3	0.40	2.16	10	1
2:B:125:GLU:OE2	2:B:127:ARG:NH1	0.40	2.54	14	1
2:B:143:PHE:CE2	2:B:152:ASN:HB2	0.40	2.51	16	1
2:B:164:ARG:O	2:B:164:ARG:HG3	0.40	2.15	17	1
1:A:3:C:O2'	1:A:4:C:H5"	0.40	2.14	18	1
2:B:73:LEU:HG	2:B:76:LEU:HD12	0.40	1.92	18	1
2:B:47:ASP:HB2	2:B:60:ASP:CG	0.40	2.36	2	1
2:B:93:SER:O	2:B:93:SER:OG	0.40	2.38	8	1
2:B:83:ILE:HD13	2:B:83:ILE:O	0.40	2.16	12	1
2:B:46:VAL:HG21	2:B:62:GLU:CG	0.40	2.47	13	1
1:A:10:C:O2	2:B:127:ARG:HD2	0.40	2.16	14	1
2:B:24:ASN:O	2:B:25:LYS:CE	0.40	2.70	15	1
1:A:17:U:C5	1:A:17:U:OP2	0.40	2.74	16	1
2:B:53:ASN:O	2:B:54:ARG:CB	0.40	2.67	18	1
2:B:127:ARG:CZ	2:B:140:TYR:HB2	0.40	2.46	18	1
2:B:16:LEU:HB3	2:B:59:VAL:HG12	0.40	1.92	1	1
2:B:108:SER:HB2	2:B:164:ARG:CD	0.40	2.46	1	1
2:B:24:ASN:O	2:B:25:LYS:HG2	0.40	2.17	3	1
1:A:8:A:N6	2:B:52:THR:HG21	0.40	2.31	4	1
1:A:14:A:OP1	2:B:93:SER:CB	0.40	2.69	8	1
2:B:17:PHE:CG	2:B:18:ILE:N	0.40	2.89	11	1
1:A:19:G:O5'	1:A:19:G:C8	0.40	2.67	13	1
1:A:15:A:O4'	1:A:15:A:P	0.40	2.80	14	1
2:B:31:LYS:CE	2:B:50:THR:HB	0.40	2.46	14	1
2:B:48:VAL:O	2:B:48:VAL:HG13	0.40	2.16	14	1
2:B:83:ILE:CD1	2:B:83:ILE:N	0.40	2.84	14	1
2:B:24:ASN:O	2:B:25:LYS:HE3	0.40	2.17	15	1
2:B:99:ALA:C	2:B:146:GLU:HG3	0.40	2.37	17	1
1:A:16:G:OP2	1:A:17:U:OP1	0.40	2.40	18	1
2:B:102:LEU:HD22	2:B:153:LEU:HD12	0.40	1.92	18	1
1:A:21:C:O2	1:A:22:C:C5	0.40	2.74	19	1
2:B:105:LYS:HD2	2:B:169:TYR:CG	0.40	2.52	2	1
2:B:140:TYR:C	2:B:141:ILE:HG13	0.40	2.37	5	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:85:LEU:O	2:B:86:GLU:HB2	0.40	2.16	9	3
2:B:37:LEU:HD22	2:B:76:LEU:HD12	0.40	1.89	9	1
2:B:43:LEU:HD13	2:B:43:LEU:HA	0.40	1.70	10	1
1:A:14:A:O4'	2:B:94:LYS:CB	0.40	2.70	11	1
1:A:19:G:H2'	1:A:20:G:C8	0.40	2.52	12	1
1:A:6:A:N3	1:A:18:A:C2	0.40	2.89	13	1
1:A:14:A:C5'	1:A:15:A:O5'	0.40	2.69	14	1
2:B:21:LEU:HD12	2:B:21:LEU:HA	0.40	1.81	14	1
2:B:56:PHE:HZ	2:B:58:TYR:CE1	0.40	2.34	17	1
2:B:68:GLU:CD	2:B:68:GLU:C	0.40	2.79	3	1
2:B:76:LEU:O	2:B:83:ILE:HG23	0.40	2.16	3	1
2:B:77:LYS:HA	2:B:81:ASN:C	0.40	2.36	3	1
1:A:5:G:HO2'	1:A:6:A:P	0.40	2.30	4	1
2:B:38:PHE:CG	2:B:43:LEU:HD12	0.40	2.51	7	1
2:B:94:LYS:C	2:B:94:LYS:HE3	0.40	2.36	8	1
1:A:20:G:N1	1:A:21:C:C5	0.40	2.90	9	1
2:B:41:ASN:O	2:B:42:ASP:OD1	0.40	2.39	10	1
2:B:98:ALA:O	2:B:99:ALA:C	0.40	2.59	11	1
2:B:113:GLU:OE2	2:B:126:ILE:O	0.40	2.40	14	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	
2	B	158/175 (90%)	119±3 (75±2%)	25±2 (16±2%)	14±2 (9±1%)	1	11
All	All	3002/3325 (90%)	2252 (75%)	476 (16%)	274 (9%)	1	11

All 38 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
2	B	42	ASP	19
2	B	52	THR	19
2	B	157	GLN	19

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Mol	Chain	Res	Type	Models (Total)
2	B	79	PHE	18
2	B	170	TYR	17
2	B	53	ASN	16
2	B	86	GLU	16
2	B	159	ALA	15
2	B	22	ASN	15
2	B	94	LYS	12
2	B	21	LEU	12
2	B	82	GLU	10
2	B	44	ALA	9
2	B	78	VAL	9
2	B	92	ASP	7
2	B	10	SER	6
2	B	160	GLU	6
2	B	93	SER	5
2	B	111	ILE	5
2	B	91	ARG	5
2	B	90	GLY	4
2	B	43	LEU	4
2	B	74	THR	3
2	B	13	PRO	2
2	B	89	LYS	2
2	B	128	LEU	2
2	B	83	ILE	2
2	B	156	LYS	2
2	B	76	LEU	2
2	B	48	VAL	2
2	B	59	VAL	2
2	B	81	ASN	1
2	B	20	ASN	1
2	B	107	LEU	1
2	B	45	VAL	1
2	B	46	VAL	1
2	B	162	ASP	1
2	B	158	GLY	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
2	B	134/147 (91%)	87±6 (65±4%)	47±6 (35±4%)	1 10
All	All	2546/2793 (91%)	1662 (65%)	884 (35%)	1 10

All 111 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)
2	B	17	PHE	19
2	B	65	GLU	19
2	B	138	ILE	19
2	B	140	TYR	19
2	B	12	THR	18
2	B	54	ARG	18
2	B	152	ASN	18
2	B	43	LEU	17
2	B	10	SER	16
2	B	31	LYS	15
2	B	95	LYS	15
2	B	157	GLN	14
2	B	58	TYR	14
2	B	37	LEU	13
2	B	53	ASN	13
2	B	59	VAL	13
2	B	102	LEU	13
2	B	108	SER	13
2	B	26	SER	12
2	B	27	VAL	12
2	B	171	THR	12
2	B	93	SER	12
2	B	47	ASP	12
2	B	72	GLU	11
2	B	111	ILE	11
2	B	128	LEU	11
2	B	142	GLU	11
2	B	153	LEU	11
2	B	18	ILE	11
2	B	62	GLU	11
2	B	25	LYS	10
2	B	73	LEU	10
2	B	91	ARG	10
2	B	94	LYS	10
2	B	103	LEU	10
2	B	67	LEU	10

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Mol	Chain	Res	Type	Models (Total)
2	B	85	LEU	10
2	B	55	LYS	9
2	B	86	GLU	9
2	B	165	SER	9
2	B	167	SER	9
2	B	36	GLU	9
2	B	89	LYS	9
2	B	169	TYR	9
2	B	110	ASN	9
2	B	130	SER	9
2	B	49	ARG	9
2	B	52	THR	8
2	B	68	GLU	8
2	B	71	LEU	8
2	B	78	VAL	8
2	B	100	ARG	8
2	B	117	LYS	8
2	B	121	GLU	8
2	B	156	LYS	8
2	B	151	LYS	8
2	B	69	LYS	8
2	B	87	LYS	8
2	B	76	LEU	7
2	B	112	THR	7
2	B	160	GLU	7
2	B	114	ASP	7
2	B	168	LEU	7
2	B	50	THR	6
2	B	109	PHE	6
2	B	77	LYS	6
2	B	107	LEU	6
2	B	164	ARG	6
2	B	148	ASP	5
2	B	150	GLU	5
2	B	162	ASP	5
2	B	170	TYR	5
2	B	60	ASP	5
2	B	113	GLU	5
2	B	144	LYS	5
2	B	35	SER	5
2	B	21	LEU	5
2	B	81	ASN	5

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Mol	Chain	Res	Type	Models (Total)
2	B	83	ILE	5
2	B	79	PHE	4
2	B	118	GLU	4
2	B	16	LEU	4
2	B	40	LYS	4
2	B	106	ASN	4
2	B	84	LYS	4
2	B	122	ASP	4
2	B	82	GLU	4
2	B	92	ASP	4
2	B	97	ARG	4
2	B	124	LEU	3
2	B	74	THR	3
2	B	105	LYS	3
2	B	146	GLU	3
2	B	154	GLU	3
2	B	125	GLU	3
2	B	66	ASP	3
2	B	136	LYS	3
2	B	115	GLU	3
2	B	155	GLU	3
2	B	11	THR	3
2	B	46	VAL	3
2	B	101	THR	2
2	B	166	VAL	2
2	B	141	ILE	2
2	B	129	VAL	2
2	B	116	LEU	2
2	B	127	ARG	2
2	B	56	PHE	2
2	B	15	ASN	1
2	B	34	ILE	1
2	B	24	ASN	1

6.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers	Suiteness
1	A	21/22 (95%)	18±1 (85±6%)	8±1 (38±6%)	0.05±0.04
All	All	401/418 (96%)	339 (85%)	152 (38%)	0.05

The overall RNA backbone suiteness is 0.05.

All unique RNA backbone outliers are listed below:

Mol	Chain	Res	Type	Models (Total)
1	A	5	G	19
1	A	9	U	19
1	A	10	C	19
1	A	12	C	19
1	A	13	G	19
1	A	14	A	19
1	A	15	A	19
1	A	16	G	19
1	A	3	C	18
1	A	17	U	18
1	A	4	C	17
1	A	6	A	17
1	A	7	A	17
1	A	11	C	16
1	A	2	G	15
1	A	20	G	14
1	A	21	C	13
1	A	8	A	12
1	A	19	G	10
1	A	22	C	10
1	A	18	A	10

All unique RNA pucker outliers are listed below:

Mol	Chain	Res	Type	Models (Total)
1	A	4	C	19
1	A	12	C	19
1	A	13	G	19
1	A	15	A	18
1	A	9	U	17
1	A	3	C	9
1	A	11	C	8
1	A	8	A	8
1	A	19	G	7
1	A	16	G	6
1	A	14	A	6
1	A	7	A	4
1	A	1	G	2
1	A	5	G	2
1	A	18	A	2
1	A	20	G	2
1	A	2	G	2

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Mol	Chain	Res	Type	Models (Total)
1	A	21	C	2

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

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

6.5 Carbohydrates (i)

There are no monosaccharides in this entry.

6.6 Ligand geometry (i)

There are no ligands in this entry.

6.7 Other polymers (i)

There are no such molecules in this entry.

6.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

7 Chemical shift validation

No chemical shift data were provided