



Full wwPDB/EMDataBank EM Map/Model Validation Report ⓘ

Nov 15, 2018 – 03:35 PM EST

PDB ID : 5M0R
EMDB ID: : EMD-4139
Title : Cryo-EM reconstruction of the maedi-visna virus (MVV) strand transfer complex
Authors : Pye, V.E.; Ballandras-Colas, A.; Maskell, D.; Locke, J.; Kotecha, A.; Costa, A.; Cherepanov, P.
Deposited on : 2016-10-05
Resolution : 8.20 Å(reported)

This is a Full wwPDB/EMDataBank EM Map/Model Validation Report
for a publicly released PDB/EMDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

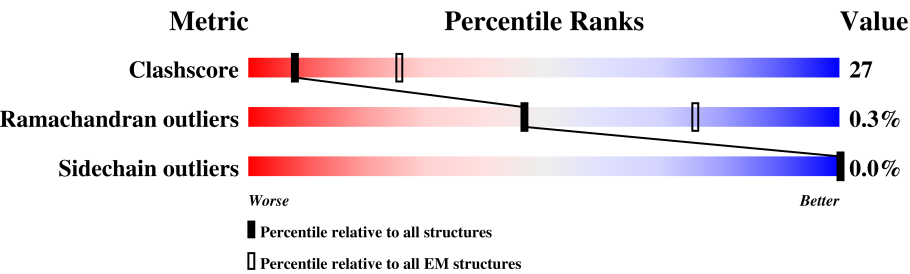
MolProbity : 4.02b-467
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20031633

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 8.20 Å.

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.













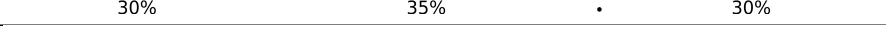
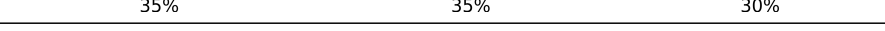
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	136327	1886
Ramachandran outliers	132723	1663
Sidechain outliers	132532	1531

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	281	<div><div>51%</div><div>44%</div><div>.</div><div>.</div></div>
1	B	281	<div><div>68%</div><div>22%</div><div>9%</div></div>
1	C	281	<div><div>70%</div><div>23%</div><div>7%</div></div>
1	D	281	<div><div>58%</div><div>16%</div><div>.</div><div>.</div><div>23%</div></div>
1	E	281	<div><div>72%</div><div>19%</div><div>9%</div></div>
1	F	281	<div><div>72%</div><div>23%</div><div>5%</div></div>
1	G	281	<div><div>58%</div><div>15%</div><div>27%</div></div>
1	H	281	<div><div>60%</div><div>17%</div><div>23%</div></div>
1	I	281	<div><div>47%</div><div>47%</div><div>.</div><div>.</div><div>.</div></div>

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Mol	Chain	Length	Quality of chain
1	J	281	
1	K	281	
1	L	281	
1	M	281	
1	N	281	
1	O	281	
1	P	281	
2	Q	21	
2	S	21	
3	R	50	
3	T	50	
4	U	23	
4	V	23	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 34774 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called integrase.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	276	Total	C	N	O	S	0	0
			2216	1411	387	409	9		
1	B	256	Total	C	N	O	S	0	0
			2075	1321	363	383	8		
1	C	261	Total	C	N	O	S	0	0
			2123	1353	371	391	8		
1	D	216	Total	C	N	O	S	0	0
			1729	1110	297	316	6		
1	E	257	Total	C	N	O	S	0	0
			2090	1333	365	384	8		
1	F	266	Total	C	N	O	S	0	0
			2140	1362	377	393	8		
1	G	205	Total	C	N	O	S	0	0
			1657	1051	284	314	8		
1	H	217	Total	C	N	O	S	0	0
			1761	1129	308	318	6		
1	I	276	Total	C	N	O	S	0	0
			2216	1411	387	409	9		
1	J	256	Total	C	N	O	S	0	0
			2075	1321	363	383	8		
1	K	261	Total	C	N	O	S	0	0
			2123	1353	371	391	8		
1	L	216	Total	C	N	O	S	0	0
			1729	1110	297	316	6		
1	M	257	Total	C	N	O	S	0	0
			2090	1333	365	384	8		
1	N	266	Total	C	N	O	S	0	0
			2140	1362	377	393	8		
1	O	205	Total	C	N	O	S	0	0
			1657	1051	284	314	8		
1	P	217	Total	C	N	O	S	0	0
			1761	1129	308	318	6		

- Molecule 2 is a DNA chain called vDNA, non-transferred strand.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	Q	21	Total	C	N	O	P	0	0
			431	203	79	128	21		
2	S	21	Total	C	N	O	P	0	0
			431	203	79	128	21		

- Molecule 3 is a DNA chain called vDNA-tDNA, transferred strand, joined to a model tDNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	R	41	Total	C	N	O	P	0	0
			834	396	153	244	41		
3	T	41	Total	C	N	O	P	0	0
			834	396	153	244	41		

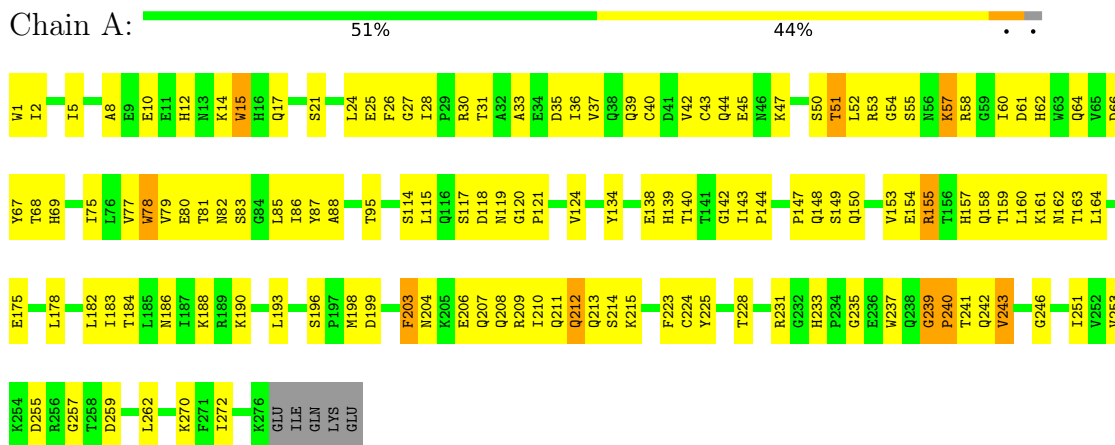
- Molecule 4 is a DNA chain called tDNA.

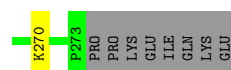
Mol	Chain	Residues	Atoms					AltConf	Trace
4	U	16	Total	C	N	O	P	0	0
			331	159	63	94	15		
4	V	16	Total	C	N	O	P	0	0
			331	159	63	94	15		

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-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 outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

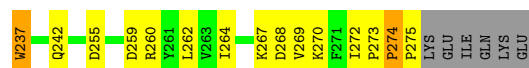
- Molecule 1: integrase





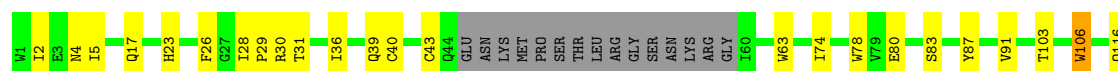
• Molecule 1: integrase

Chain D: 58% 16% 23%



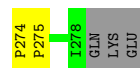
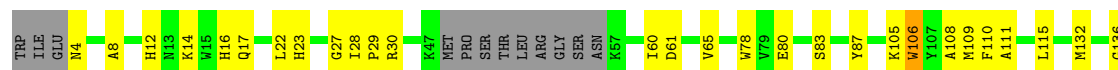
• Molecule 1: integrase

Chain E: 72% 19% 9%



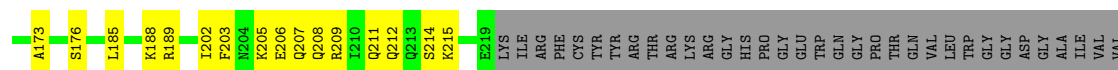
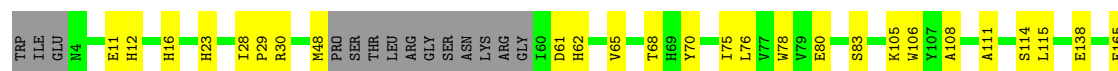
• Molecule 1: integrase

Chain F: 72% 23% 5%



• Molecule 1: integrase

Chain G: 58% 15% 27%



LYS ASP ARG GLY THR ASP ARG LEU LEU VAL ILE ALA ASN LYS ASP VAL LYS PHE ILE PRO PRO PRO LYS LYS LEU ILE GLN LYS GLU

- Molecule 1: integrase

Chain H:  60% 17% 23%

TRP ILE GLU ASN ILE ILE LEU ALA GLU GLU ILE ILE ALA ASN LYS TRP HIS GLN ASP PHE ILE VAL SER LEU HIS LEU LEU PHE GLY ILE PRO ARG THR ALA ALA ASP ILE ILE VAL CYS ASP VAL CYS GLN ASN LYS MET PRO SER THR LEU ARG GLY SER ASN LYS ARG GLY I60

Q64 T68 I75 V79 E80 S83 E89 G93 E98 K105 W106 Y107 A108 M109 F110 L115 N119 T140 T141 G142 W145 N146 P147 Q148 S149 Q150 L152 T156 L164 A173 S176 A177 L178 T181 T184 L185 R189 I202

F203 N204 Q207 Q208 R209 T210 Q211 Q212 F223 Y226 R227 T228 G235 Q238 V252 V263 P275 K276 GLU ILE GLN LYS GLU

- Molecule 1: integrase

Chain I:  47% 47% . . .

V1 I2 I5 A8 E9 E10 E11 H12 N13 N14 W15 H16 Q17 S21 F26 G27 I28 P29 R30 A33 T36 V37 Q38 Q39 C40 P41 V42 C43 K47 W48 P49 S50 T51 R53 R54 S55 N56 K57 R58 D61 H62 W63 Q64 V65 D66 Y67 T68 H69 I74 I75

L76 V77 W78 E80 T81 H82 S83 G84 L85 I86 Y87 A88 E94 T95 F99 A108 A111 P112 K113 S114 L115 Q116 S117 D118 N119 Q120 P121 A122 V124 A125 E126 E138 H139 T140 L141 G142 I143 P144 W145 N146 P147 Q148 S149 Q150 V153 E154 R155 T156 H157 Q158 L160

K161 N162 T163 E175 L178 L182 G184 T183 I184 I185 N186 H187 K188 R189 K190 L193 S196 P197 M198 D199 F203 N204 K205 E206 Q207 Q208 R209 Q212 Q213 S214 K215 S216 K217 I221 R222 F223 C224 Y226 R227 T228 R231 G232 H233 P234 G235 E236 Q237 Q238 G239 P240 T241

Q242 V243 G246 I251 V252 V253 K254 D255 Q257 T258 D259 L262 V263 I264 V269 K270 F271 I272 P273 K276 GLU ILE GLN LYS GLU

- Molecule 1: integrase

Chain J:  69% 21% 9%

TRP ILE E3 H23 I28 P29 A33 I36 C40 Q44 GLU ASN LYS MET PRO SER THR LEU ARG GLY I60 D61 H62 Q64 T68 H69 I75 W78 V79 E80 S83 G84 L85 I86 A89 E89 R90 V91 K92 G93 M104 K105

W106 Y107 A108 S114 L115 Y134 L135 E138 T159 L160 K161 T163 A173 S176 A177 L178 A179 G180 T181 T184 I187 K190 T195 W198 M199 D199 I200 Q208 R209 I210 Q211 Q212 K215 S216 K217 Q218 R222 W245 E246 G247 A250 I251 V252 V253

L262 P273 PRO PRO LYS GLU ILE LYS GLU

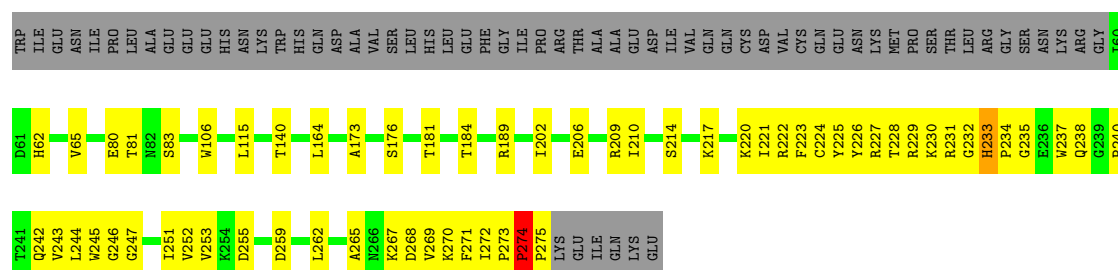
- Molecule 1: integrase

Chain K:  71% 22% 7%

V1 I2 E3 N4 I5 P6 L7 A8 E9 S21 L22 H23 F26 G27 I28 P29 R30 T31 A32 I36 C40 K47 MET PRO SER THR LEU ARG GLY I60 D61 H62 W63 Q64 V65 W78 V79 E80 S83 W106 S114 L115 T140 S149

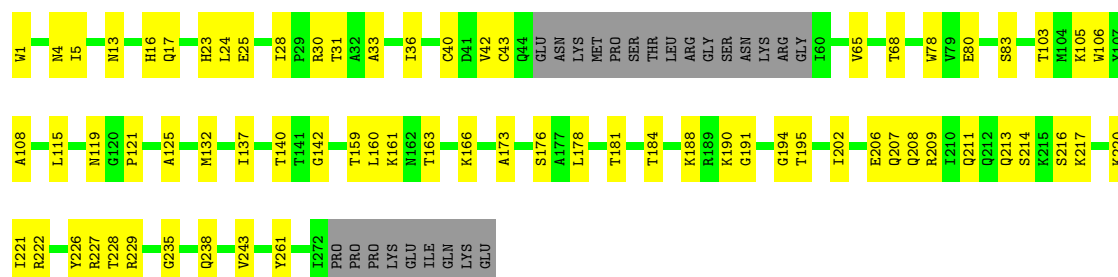
- Molecule 1: integrase

Chain L: 55% 21% 23%



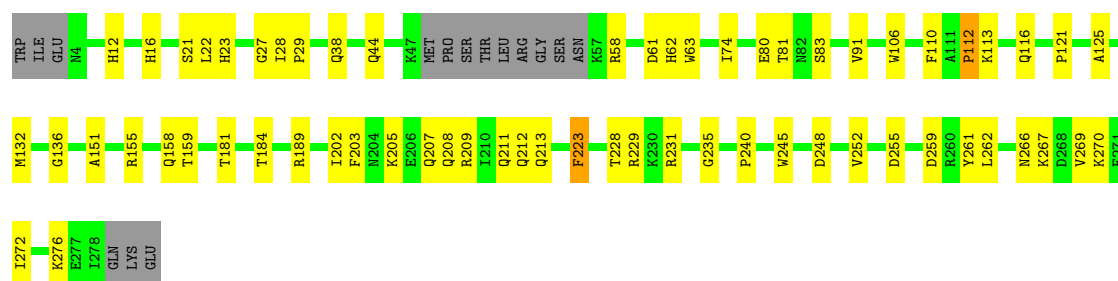
- Molecule 1: integrase

Chain M:  67% 25% 9%



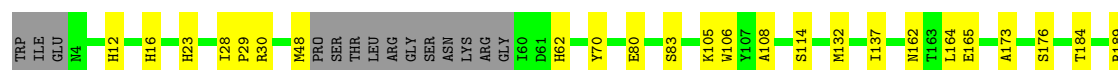
- Molecule 1: integrase

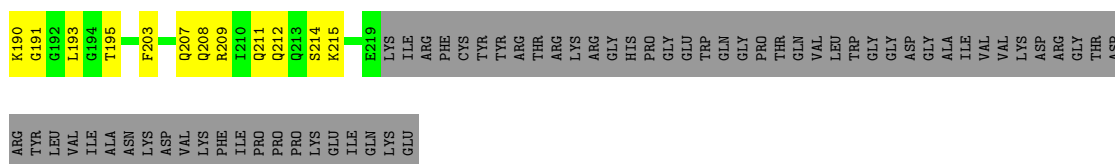
Chain N: 72% 22% • 5%



- Molecule 1: integrase

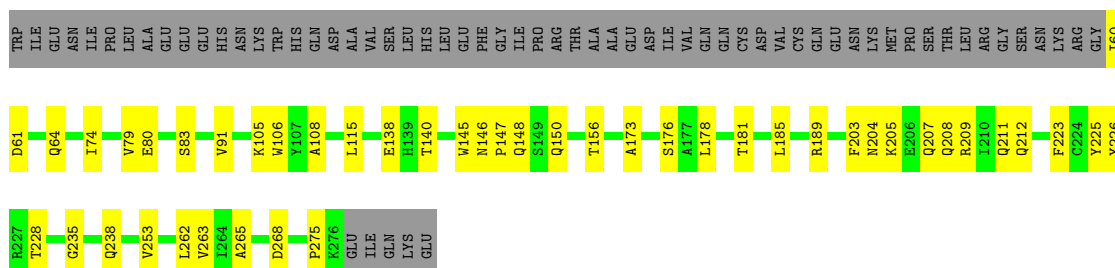
Chain 0:  60% 13% 27%





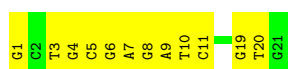
- Molecule 1: integrase

Chain P: 61% 16% 23%



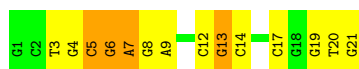
- Molecule 2: vDNA, non-transferred strand

Chain Q: 43% 57%



- Molecule 2: vDNA, non-transferred strand

Chain S: 33% 48% 19%



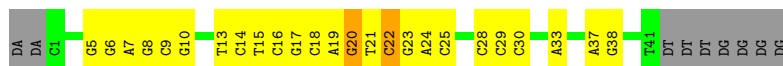
- Molecule 3: vDNA-tDNA, transferred strand, joined to a model tDNA

Chain R: 40% 36% 6% 18%



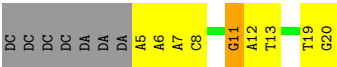
- Molecule 3: vDNA-tDNA, transferred strand, joined to a model tDNA

Chain T: 32% 46% 18%

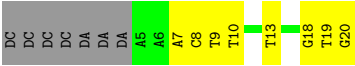
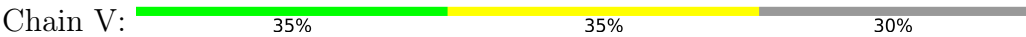


- Molecule 4: tDNA

Chain U: 30% 35% 30%



● Molecule 4: tDNA



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	37021	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.47	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
1	A	0.83	4/2269 (0.2%)	0.85	7/3071 (0.2%)
1	B	0.58	1/2124 (0.0%)	0.73	2/2874 (0.1%)
1	C	0.48	1/2174 (0.0%)	0.65	0/2942
1	D	0.57	3/1772 (0.2%)	0.79	4/2401 (0.2%)
1	E	0.53	1/2140 (0.0%)	0.67	0/2896
1	F	0.62	2/2191 (0.1%)	0.72	0/2966
1	G	0.43	1/1693 (0.1%)	0.60	0/2290
1	H	0.47	1/1805 (0.1%)	0.66	0/2441
1	I	0.89	6/2271 (0.3%)	1.22	12/3077 (0.4%)
1	J	0.59	2/2124 (0.1%)	0.74	1/2874 (0.0%)
1	K	0.47	1/2174 (0.0%)	0.65	1/2942 (0.0%)
1	L	0.66	3/1772 (0.2%)	0.68	1/2401 (0.0%)
1	M	0.54	0/2140	0.67	0/2896
1	N	0.61	0/2191	0.71	1/2966 (0.0%)
1	O	0.43	1/1693 (0.1%)	0.60	0/2290
1	P	0.49	1/1805 (0.1%)	0.68	0/2441
2	Q	0.52	0/482	0.85	0/742
2	S	0.75	3/482 (0.6%)	1.07	4/742 (0.5%)
3	R	1.38	3/934 (0.3%)	0.96	3/1437 (0.2%)
3	T	0.66	2/934 (0.2%)	0.98	4/1437 (0.3%)
4	U	0.69	2/372 (0.5%)	0.92	0/574
4	V	0.48	0/372	0.88	0/574
All	All	0.63	38/35914 (0.1%)	0.77	40/49274 (0.1%)

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 outliers	#Planarity outliers
1	A	0	1
1	I	0	3
All	All	0	4

All (38) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	R	40	DT	O3'-P	-38.12	1.15	1.61
1	I	238	GLN	C-N	17.98	1.65	1.33
1	A	239	GLY	C-N	16.57	1.65	1.34
1	L	221	ILE	C-N	14.47	1.67	1.34
1	I	146	ASN	C-N	10.20	1.53	1.34
1	I	142	GLY	C-N	-9.79	1.11	1.34
3	T	20	DG	C4'-O4'	9.17	1.54	1.45
3	T	22	DC	C4'-O4'	9.11	1.54	1.45
3	R	23	DG	C4'-O4'	8.35	1.53	1.45
2	S	5	DC	O3'-P	-7.78	1.51	1.61
2	S	6	DG	O3'-P	7.57	1.70	1.61
4	U	13	DT	C4'-O4'	7.47	1.52	1.45
1	D	237	TRP	CB-CG	-6.54	1.38	1.50
2	S	7	DA	C4'-O4'	-6.46	1.38	1.45
4	U	11	DG	C4'-O4'	6.33	1.51	1.45
1	H	106	TRP	CB-CG	-6.14	1.39	1.50
1	G	106	TRP	CB-CG	-6.11	1.39	1.50
1	L	106	TRP	CB-CG	-6.07	1.39	1.50
1	A	15	TRP	CB-CG	-6.06	1.39	1.50
1	I	15	TRP	CB-CG	-6.05	1.39	1.50
1	J	106	TRP	CB-CG	-6.00	1.39	1.50
1	A	78	TRP	CB-CG	-5.72	1.40	1.50
1	O	106	TRP	CB-CG	-5.72	1.40	1.50
1	I	78	TRP	CB-CG	-5.67	1.40	1.50
1	F	106	TRP	CB-CG	-5.65	1.40	1.50
1	J	78	TRP	CB-CG	-5.64	1.40	1.50
1	L	237	TRP	CB-CG	-5.62	1.40	1.50
1	A	203	PHE	CB-CG	-5.61	1.41	1.51
1	I	203	PHE	CB-CG	-5.61	1.41	1.51
1	E	106	TRP	CB-CG	-5.53	1.40	1.50
1	B	78	TRP	CB-CG	-5.34	1.40	1.50
1	K	106	TRP	CB-CG	-5.28	1.40	1.50
3	R	24	DA	C4'-O4'	5.21	1.50	1.45
1	F	271	PHE	CB-CG	-5.12	1.42	1.51
1	D	225	TYR	CD1-CE1	-5.11	1.31	1.39
1	C	106	TRP	CB-CG	-5.10	1.41	1.50
1	P	106	TRP	CB-CG	-5.07	1.41	1.50
1	D	106	TRP	CB-CG	-5.00	1.41	1.50

All (40) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	I	238	GLN	O-C-N	30.56	175.16	123.20
1	I	238	GLN	CA-C-N	-29.87	56.45	116.20
1	I	238	GLN	C-N-CA	-16.82	86.99	122.30
1	D	274	PRO	C-N-CD	-15.44	86.63	120.60
2	S	13	DG	OP1-P-O3'	-10.65	81.76	105.20
3	R	24	DA	OP1-P-O3'	-10.65	81.78	105.20
3	T	37	DA	OP1-P-O3'	-10.61	81.87	105.20
1	D	233	HIS	C-N-CD	-10.14	98.28	120.60
3	T	37	DA	OP2-P-O3'	-9.77	83.71	105.20
3	R	24	DA	OP2-P-O3'	-9.72	83.81	105.20
2	S	13	DG	OP2-P-O3'	-9.42	84.48	105.20
1	I	142	GLY	O-C-N	-8.49	109.11	122.70
1	I	142	GLY	C-N-CA	8.20	142.20	121.70
1	I	239	GLY	C-N-CD	-8.19	102.58	120.60
3	R	25	DC	OP1-P-OP2	7.11	130.27	119.60
3	T	38	DG	OP1-P-OP2	7.05	130.18	119.60
2	S	14	DC	OP1-P-OP2	6.96	130.04	119.60
1	L	274	PRO	C-N-CD	-6.58	106.12	120.60
1	A	239	GLY	CA-C-N	-6.51	98.88	117.10
1	A	239	GLY	O-C-N	6.37	133.20	121.10
1	J	178	LEU	CA-CB-CG	6.11	129.35	115.30
3	T	22	DC	C1'-O4'-C4'	-6.04	104.06	110.10
1	K	7	LEU	CA-CB-CG	6.04	129.20	115.30
1	I	225	TYR	O-C-N	-5.92	113.23	122.70
1	D	231	ARG	N-CA-C	-5.89	95.10	111.00
1	A	155	ARG	NE-CZ-NH1	5.72	123.16	120.30
1	I	118	ASP	CB-CG-OD1	5.69	123.42	118.30
1	B	131	LEU	CA-CB-CG	5.69	128.38	115.30
1	A	155	ARG	NE-CZ-NH2	-5.65	117.48	120.30
1	A	118	ASP	CB-CG-OD1	5.63	123.37	118.30
1	D	230	LYS	N-CA-C	5.63	126.20	111.00
1	I	155	ARG	NE-CZ-NH2	-5.63	117.48	120.30
1	I	155	ARG	NE-CZ-NH1	5.62	123.11	120.30
1	A	243	VAL	N-CA-C	-5.30	96.69	111.00
2	S	7	DA	C5'-C4'-O4'	5.30	119.36	109.30
1	N	223	PHE	CB-CG-CD1	5.29	124.51	120.80
1	I	142	GLY	CA-C-N	5.27	128.79	117.20
1	A	57	LYS	N-CA-C	-5.26	96.79	111.00
1	B	178	LEU	CA-CB-CG	5.10	127.04	115.30
1	I	146	ASN	O-C-N	-5.01	111.59	121.10

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	51	THR	Mainchain
1	I	142	GLY	Peptide
1	I	225	TYR	Mainchain
1	I	51	THR	Mainchain

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the 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 within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2216	0	2173	407	0
1	B	2075	0	2046	51	0
1	C	2123	0	2091	85	0
1	D	1729	0	1705	152	0
1	E	2090	0	2061	100	0
1	F	2140	0	2106	51	0
1	G	1657	0	1626	57	0
1	H	1761	0	1764	101	0
1	I	2216	0	2175	484	0
1	J	2075	0	2046	116	0
1	K	2123	0	2095	77	0
1	L	1729	0	1702	160	0
1	M	2090	0	2059	96	0
1	N	2140	0	2105	107	0
1	O	1657	0	1626	60	0
1	P	1761	0	1764	82	0
2	Q	431	0	236	58	0
2	S	431	0	236	93	0
3	R	834	0	461	127	0
3	T	834	0	460	150	0
4	U	331	0	183	12	0
4	V	331	0	182	36	0
All	All	34774	0	32902	1839	0

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 27.

All (1839) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:212:GLN:HB2	1:D:217:LYS:CD	1.21	1.64
1:A:14:LYS:HB3	1:J:134:TYR:CE1	1.27	1.61
1:I:145:TRP:CB	1:N:229:ARG:HD2	1.28	1.61
1:C:270:LYS:HD3	1:H:145:TRP:CE2	1.31	1.59
1:I:119:ASN:HB2	4:V:19:DT:C4'	1.25	1.59
1:L:224:CYS:SG	1:L:269:VAL:HG13	1.39	1.59
1:A:203:PHE:CZ	1:D:222:ARG:HD3	1.27	1.59
1:I:68:THR:CG2	1:I:75:ILE:HB	1.29	1.59
1:L:230:LYS:CB	1:L:235:GLY:CA	1.77	1.57
1:E:30:ARG:CD	3:R:7:DA:H5'	1.26	1.57
1:M:30:ARG:CD	3:T:7:DA:H5''	1.08	1.55
3:R:40:DT:O3'	3:R:43:DT:P	1.15	1.53
1:L:223:PHE:HA	1:L:243:VAL:CG2	1.34	1.53
1:N:252:VAL:HG21	2:Q:1:DG:C2	1.40	1.52
1:E:30:ARG:CG	3:R:7:DA:C5'	1.89	1.51
1:L:274:PRO:HB2	1:L:275:PRO:CD	1.40	1.50
1:O:29:PRO:HG3	1:O:211:GLN:CD	1.13	1.50
1:E:30:ARG:CD	3:R:7:DA:C5'	1.88	1.50
1:L:231:ARG:CB	3:T:14:DC:C5'	1.85	1.50
1:E:30:ARG:CG	3:R:7:DA:H5''	1.41	1.48
1:N:252:VAL:CG2	2:Q:1:DG:N2	1.75	1.48
1:I:212:GLN:CB	1:L:217:LYS:NZ	1.73	1.47
1:K:270:LYS:CD	1:P:145:TRP:CE2	1.98	1.47
1:A:212:GLN:HB2	1:D:217:LYS:CE	1.41	1.46
1:L:220:LYS:CE	1:L:222:ARG:CG	1.91	1.46
1:L:231:ARG:CB	3:T:14:DC:H5'	0.98	1.46
1:L:220:LYS:HE2	1:L:222:ARG:CG	1.01	1.46
1:K:270:LYS:HD3	1:P:145:TRP:CE2	1.49	1.44
1:A:2:ILE:CG2	1:A:5:ILE:HD12	1.48	1.43
1:E:222:ARG:CD	1:H:203:PHE:HZ	1.28	1.43
1:L:220:LYS:CE	1:L:222:ARG:HG2	1.49	1.43
1:C:270:LYS:NZ	1:H:145:TRP:CD1	1.86	1.42
1:I:223:PHE:CE1	1:I:242:GLN:HG2	1.53	1.42
1:A:212:GLN:CB	1:D:217:LYS:CD	1.97	1.41
1:E:222:ARG:NH1	1:H:203:PHE:CE2	1.82	1.41
1:I:67:TYR:CE1	1:I:76:LEU:HD22	1.55	1.41
1:E:30:ARG:HG2	3:R:7:DA:C5'	1.44	1.40
1:E:222:ARG:HD2	1:H:203:PHE:CZ	1.54	1.40
1:A:147:PRO:HG3	3:T:19:DA:N3	1.17	1.40
1:A:203:PHE:CZ	1:D:222:ARG:CD	2.03	1.39
1:I:67:TYR:OH	1:I:99:PHE:CD1	1.73	1.39
1:I:154:GLU:HB3	3:R:18:DC:C2'	1.50	1.39

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:223:PHE:CE1	1:A:242:GLN:HG2	1.55	1.39
1:F:231:ARG:HH22	3:R:25:DC:N4	1.18	1.39
1:L:223:PHE:CA	1:L:243:VAL:HG23	1.36	1.39
1:L:224:CYS:HB2	1:L:270:LYS:C	1.43	1.39
1:A:225:TYR:CZ	1:A:240:PRO:HB3	1.59	1.38
1:A:95:THR:CG2	3:R:28:DC:H5'	1.50	1.38
1:L:230:LYS:CB	1:L:235:GLY:HA3	1.44	1.38
1:L:220:LYS:HE2	1:L:222:ARG:CD	1.52	1.37
1:M:30:ARG:HD2	3:T:7:DA:C5'	0.90	1.37
1:I:145:TRP:CB	1:N:229:ARG:CD	2.02	1.37
1:I:231:ARG:NH2	2:S:20:DT:H5'	1.38	1.36
1:I:121:PRO:CG	3:T:28:DC:O2	1.73	1.36
1:I:53:ARG:CB	2:Q:4:DG:OP1	1.73	1.36
1:M:30:ARG:CD	3:T:7:DA:C5'	1.74	1.36
1:K:270:LYS:HD3	1:P:145:TRP:NE1	1.07	1.36
1:C:270:LYS:HD3	1:H:145:TRP:NE1	1.37	1.35
1:A:147:PRO:HG3	3:T:19:DA:C2	1.61	1.35
1:A:147:PRO:CG	3:T:19:DA:C2	2.08	1.35
1:E:222:ARG:CD	1:H:203:PHE:CZ	2.07	1.34
1:A:24:LEU:O	1:J:217:LYS:CG	1.75	1.33
1:O:29:PRO:CG	1:O:211:GLN:CD	1.95	1.33
1:A:155:ARG:NE	2:S:6:DG:H1'	1.41	1.33
1:A:2:ILE:HG23	1:A:5:ILE:CD1	1.56	1.33
1:E:220:LYS:NZ	1:H:203:PHE:HE1	1.26	1.33
1:I:223:PHE:CE1	1:I:242:GLN:CG	2.10	1.33
1:A:14:LYS:NZ	1:J:134:TYR:HA	1.00	1.33
1:C:65:VAL:CG2	1:C:78:TRP:CE3	2.12	1.32
1:A:35:ASP:CB	1:E:2:ILE:HD11	1.58	1.32
1:K:270:LYS:HD2	1:P:145:TRP:CD2	1.63	1.30
1:D:224:CYS:HB2	1:D:270:LYS:O	1.14	1.30
1:I:225:TYR:CB	1:I:237:TRP:HB3	1.60	1.29
1:A:14:LYS:HE2	1:J:134:TYR:CD1	1.66	1.29
1:I:1:TRP:NE1	1:I:29:PRO:HD3	1.45	1.29
1:C:270:LYS:CD	1:H:145:TRP:CE2	2.16	1.28
1:A:225:TYR:CE1	1:A:272:ILE:HD11	1.67	1.28
1:I:225:TYR:HB2	1:I:237:TRP:CE3	1.66	1.28
1:A:14:LYS:CE	1:J:134:TYR:CD1	2.17	1.27
3:R:40:DT:C3'	3:R:43:DT:P	2.21	1.27
1:N:159:THR:OG1	1:O:48:MET:HE3	1.18	1.27
1:I:121:PRO:O	3:T:29:DC:H4'	1.25	1.27
1:I:203:PHE:CE1	1:I:207:GLN:NE2	2.02	1.27

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:125:ALA:HA	3:T:30:DC:OP1	1.24	1.27
1:A:14:LYS:NZ	1:J:134:TYR:CA	1.96	1.27
1:L:274:PRO:CB	1:L:275:PRO:HD3	1.57	1.27
1:A:207:GLN:HB3	1:D:222:ARG:NH2	1.50	1.26
1:G:29:PRO:HG3	1:G:211:GLN:CD	1.54	1.26
1:A:155:ARG:NH2	2:S:7:DA:C8	2.03	1.26
1:K:270:LYS:CD	1:P:145:TRP:NE1	1.95	1.26
1:M:217:LYS:HD3	1:P:212:GLN:CG	1.66	1.26
1:I:52:LEU:HD22	3:T:14:DC:O3'	1.23	1.26
1:E:222:ARG:NH1	1:H:207:GLN:HG3	1.48	1.25
1:I:121:PRO:C	3:T:29:DC:C4'	2.03	1.25
1:A:15:TRP:CZ2	1:J:135:LEU:HD21	1.71	1.25
1:O:23:HIS:CE1	1:O:207:GLN:OE1	1.89	1.25
1:A:147:PRO:CG	3:T:19:DA:N3	1.95	1.25
1:A:14:LYS:CB	1:J:134:TYR:CE1	2.19	1.25
1:A:212:GLN:CB	1:D:217:LYS:HD2	1.60	1.25
1:K:65:VAL:CG2	1:K:78:TRP:CE3	2.18	1.25
1:C:270:LYS:CD	1:H:145:TRP:CD2	2.20	1.24
1:I:52:LEU:HD12	1:L:232:GLY:CA	1.67	1.24
1:I:154:GLU:C	3:R:18:DC:H1'	1.57	1.24
1:N:252:VAL:HG21	2:Q:1:DG:N2	0.93	1.24
1:I:225:TYR:CB	1:I:237:TRP:CE3	2.19	1.24
1:L:224:CYS:HB2	1:L:270:LYS:O	1.36	1.24
1:N:203:PHE:CZ	1:N:207:GLN:NE2	2.05	1.24
1:A:95:THR:HG22	3:R:28:DC:C5'	1.66	1.23
1:C:208:GLN:O	1:C:212:GLN:HG3	1.10	1.23
1:I:145:TRP:CG	1:N:229:ARG:CD	2.13	1.23
1:G:29:PRO:HG3	1:G:211:GLN:CG	1.69	1.22
1:A:25:GLU:OE1	1:J:217:LYS:NZ	1.73	1.21
1:I:225:TYR:HB3	1:I:237:TRP:CB	1.68	1.21
1:I:212:GLN:HB3	1:L:217:LYS:NZ	0.93	1.21
1:I:47:LYS:HB2	2:S:9:DA:OP1	1.40	1.21
1:B:29:PRO:HG3	1:B:211:GLN:CD	1.58	1.21
1:N:29:PRO:HA	1:N:211:GLN:OE1	1.38	1.21
1:I:119:ASN:HB2	4:V:19:DT:C5'	1.71	1.20
1:I:68:THR:CG2	1:I:75:ILE:CB	2.19	1.20
1:I:61:ASP:O	1:I:63:TRP:CD1	1.94	1.20
1:E:30:ARG:CG	3:R:7:DA:C4'	2.20	1.20
1:G:65:VAL:CG2	1:G:78:TRP:CE3	2.25	1.20
1:O:29:PRO:HG3	1:O:211:GLN:NE2	1.56	1.20
1:I:223:PHE:CD1	1:I:242:GLN:HG2	1.77	1.20

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:154:GLU:HB3	3:R:18:DC:C1'	1.72	1.20
1:A:155:ARG:HE	2:S:6:DG:C1'	1.53	1.19
1:K:270:LYS:NZ	1:P:145:TRP:CD1	2.09	1.19
1:I:47:LYS:HD3	2:S:9:DA:P	1.83	1.19
1:I:68:THR:HG22	1:I:75:ILE:O	1.43	1.19
1:I:154:GLU:O	3:R:18:DC:O4'	1.59	1.19
1:A:212:GLN:CB	1:D:217:LYS:CE	2.02	1.19
1:I:95:THR:HA	3:T:28:DC:O3'	1.43	1.19
1:I:121:PRO:C	3:T:29:DC:H4'	1.24	1.19
1:D:274:PRO:CB	1:D:275:PRO:HD3	1.59	1.18
1:I:69:HIS:O	3:R:21:DT:OP1	1.57	1.18
1:I:119:ASN:CB	4:V:19:DT:H4'	1.71	1.18
1:M:30:ARG:HD2	3:T:7:DA:C4'	1.73	1.18
1:E:30:ARG:CG	3:R:7:DA:H4'	1.72	1.18
1:O:29:PRO:CG	1:O:211:GLN:OE1	1.91	1.18
1:C:270:LYS:HD3	1:H:145:TRP:CD2	1.79	1.18
1:I:95:THR:HA	3:T:29:DC:P	1.83	1.18
1:D:267:LYS:HE3	2:S:3:DT:O4	1.41	1.18
1:A:14:LYS:HE3	1:J:134:TYR:HD1	1.08	1.17
1:N:106:TRP:CZ3	1:N:112:PRO:HG3	1.79	1.17
1:D:237:TRP:CZ2	1:D:270:LYS:HE2	1.78	1.17
1:G:29:PRO:CG	1:G:211:GLN:CD	2.12	1.16
1:F:159:THR:OG1	1:G:48:MET:SD	2.00	1.16
1:N:231:ARG:HH22	3:T:25:DC:N4	1.40	1.16
1:L:230:LYS:CB	1:L:235:GLY:HA2	1.75	1.16
1:I:119:ASN:CB	4:V:19:DT:C4'	2.22	1.16
1:A:25:GLU:HA	1:J:217:LYS:CE	1.75	1.16
1:D:224:CYS:CB	1:D:270:LYS:O	1.92	1.16
1:F:231:ARG:NH2	3:R:25:DC:H41	1.44	1.16
1:I:118:ASP:OD2	4:V:20:DG:O5'	1.64	1.16
1:A:223:PHE:CE1	1:A:242:GLN:CG	2.29	1.15
1:I:146:ASN:ND2	1:I:148:GLN:HB2	1.59	1.15
1:D:227:ARG:HE	1:D:268:ASP:CG	1.50	1.15
1:I:145:TRP:HB3	1:N:229:ARG:CD	1.71	1.15
1:E:220:LYS:NZ	1:H:203:PHE:CE1	2.14	1.15
1:L:224:CYS:SG	1:L:269:VAL:CG1	2.33	1.15
1:C:65:VAL:CG2	1:C:78:TRP:CD2	2.29	1.15
1:L:223:PHE:HE2	1:L:240:PRO:HB2	1.06	1.15
1:A:211:GLN:O	1:A:215:LYS:HG2	1.46	1.15
1:C:208:GLN:O	1:C:212:GLN:CG	1.96	1.14
1:I:122:ALA:HA	3:T:29:DC:H5''	1.29	1.14

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:157:HIS:HB2	3:R:18:DC:H4'	1.30	1.14
1:A:55:SER:O	1:D:227:ARG:NH2	1.79	1.14
1:I:66:ASP:OD2	4:V:20:DG:C3'	1.95	1.14
1:E:30:ARG:HG3	3:R:7:DA:H4'	1.16	1.14
1:B:23:HIS:CE1	1:B:207:GLN:OE1	2.00	1.14
1:A:203:PHE:CE2	1:D:222:ARG:CD	2.31	1.14
1:A:158:GLN:OE1	3:T:17:DG:H1'	1.45	1.14
1:K:65:VAL:CG2	1:K:78:TRP:CD2	2.30	1.14
1:M:30:ARG:HD2	3:T:7:DA:H5'	1.13	1.13
1:A:224:CYS:C	1:A:225:TYR:N	2.02	1.12
1:G:206:GLU:OE2	1:H:203:PHE:HD1	1.32	1.12
1:I:52:LEU:HD12	1:L:232:GLY:C	1.67	1.12
1:I:225:TYR:CG	1:I:237:TRP:HB3	1.85	1.12
1:I:52:LEU:HD23	3:T:15:DT:H5'	1.26	1.12
1:K:270:LYS:CD	1:P:145:TRP:CD1	2.33	1.12
1:I:231:ARG:HH22	2:S:20:DT:P	1.71	1.12
1:G:29:PRO:CB	1:G:211:GLN:HG3	1.78	1.12
1:L:224:CYS:CB	1:L:270:LYS:C	2.17	1.12
1:C:270:LYS:HD3	1:H:145:TRP:CD1	1.85	1.12
1:L:224:CYS:CB	1:L:270:LYS:O	1.96	1.12
1:A:2:ILE:CG2	1:A:5:ILE:CD1	2.20	1.12
1:I:1:TRP:HE1	1:I:29:PRO:HD3	0.98	1.12
1:A:207:GLN:HB2	1:D:222:ARG:HH12	1.15	1.11
1:A:2:ILE:HG23	1:A:5:ILE:HD11	1.29	1.11
1:E:30:ARG:HD2	3:R:7:DA:C5'	1.62	1.11
1:A:24:LEU:O	1:J:217:LYS:HG2	1.40	1.11
1:E:31:THR:OG1	3:R:8:DG:OP1	1.65	1.11
1:L:230:LYS:CB	1:L:235:GLY:N	2.14	1.11
1:I:52:LEU:HD21	3:T:14:DC:H1'	1.19	1.11
1:A:207:GLN:CB	1:D:222:ARG:NH1	2.13	1.10
1:A:203:PHE:HZ	1:D:222:ARG:CD	1.53	1.10
1:I:231:ARG:NH2	2:S:19:DG:O3'	1.84	1.10
1:A:25:GLU:OE1	1:J:217:LYS:CE	1.98	1.10
1:A:207:GLN:CB	1:D:222:ARG:CZ	2.30	1.10
1:G:29:PRO:HB3	1:G:211:GLN:HG3	1.29	1.10
1:C:65:VAL:HG21	1:C:78:TRP:CD2	1.86	1.10
1:M:217:LYS:HZ2	1:P:211:GLN:HB2	1.07	1.10
1:D:274:PRO:HB2	1:D:275:PRO:CD	1.81	1.09
1:I:47:LYS:CB	2:S:9:DA:OP1	2.00	1.09
1:M:30:ARG:CG	3:T:7:DA:H5''	1.82	1.09
1:C:270:LYS:HD2	1:H:145:TRP:CD2	1.81	1.09

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:270:LYS:CD	1:H:145:TRP:CG	2.35	1.09
1:I:225:TYR:CD2	1:I:237:TRP:HB3	1.87	1.09
1:L:220:LYS:CG	1:L:222:ARG:HG3	1.82	1.09
1:I:52:LEU:CD1	1:L:232:GLY:CA	2.31	1.09
1:A:203:PHE:CE2	1:D:222:ARG:HD2	1.88	1.08
1:A:207:GLN:HB2	1:D:222:ARG:NH1	1.67	1.08
1:I:68:THR:HG21	1:I:75:ILE:HB	1.16	1.08
1:N:29:PRO:CA	1:N:211:GLN:OE1	2.00	1.08
1:K:65:VAL:HG21	1:K:78:TRP:CD2	1.88	1.08
1:L:274:PRO:HB2	1:L:275:PRO:HD2	1.35	1.08
1:A:25:GLU:HA	1:J:217:LYS:HE3	1.28	1.08
1:A:52:LEU:HD12	1:D:233:HIS:CB	1.83	1.08
1:L:224:CYS:HB3	1:L:271:PHE:CA	1.84	1.08
1:G:29:PRO:CG	1:G:211:GLN:HG3	1.82	1.07
1:A:2:ILE:HG22	1:A:5:ILE:HD12	1.15	1.07
1:I:52:LEU:HA	3:T:15:DT:C5'	1.84	1.07
1:B:29:PRO:HG3	1:B:211:GLN:CG	1.83	1.07
1:E:222:ARG:HD3	1:H:203:PHE:HZ	1.11	1.07
1:A:15:TRP:CZ2	1:J:135:LEU:CD2	2.36	1.07
1:L:223:PHE:CE2	1:L:240:PRO:HB2	1.90	1.07
1:E:31:THR:HG21	3:R:8:DG:H5'	1.29	1.07
1:I:154:GLU:CB	3:R:18:DC:C2'	2.31	1.07
1:I:52:LEU:HD21	3:T:14:DC:C1'	1.84	1.07
1:A:14:LYS:CE	1:J:134:TYR:HA	1.85	1.07
1:K:270:LYS:HD3	1:P:145:TRP:CD1	1.90	1.07
3:R:40:DT:HO3'	3:R:43:DT:P	1.20	1.07
1:L:224:CYS:HB3	1:L:271:PHE:HA	1.11	1.06
1:I:145:TRP:HB2	1:N:229:ARG:HD2	1.13	1.06
1:A:14:LYS:CB	1:J:134:TYR:HE1	1.64	1.06
1:I:146:ASN:OD1	1:I:149:SER:OG	1.72	1.06
1:A:50:SER:HB2	2:Q:8:DG:H21	1.15	1.06
1:A:212:GLN:HG2	1:D:217:LYS:HG3	1.35	1.06
1:A:68:THR:HB	1:A:157:HIS:CD2	1.89	1.06
1:B:29:PRO:CB	1:B:211:GLN:HG3	1.84	1.06
1:D:231:ARG:O	2:Q:11:DC:C4'	2.03	1.06
1:A:207:GLN:HG3	1:D:222:ARG:NH1	1.70	1.06
1:A:119:ASN:HB3	4:U:19:DT:H4'	1.36	1.06
1:E:31:THR:HG23	3:R:7:DA:O3'	1.54	1.06
1:I:67:TYR:CD1	1:I:76:LEU:HD13	1.90	1.06
1:I:66:ASP:OD2	4:V:20:DG:H3'	1.28	1.06
1:I:154:GLU:CB	3:R:18:DC:H2''	1.86	1.06

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:147:PRO:HG2	3:T:19:DA:C2	1.82	1.06
1:A:50:SER:HB2	2:Q:8:DG:N2	1.69	1.05
1:O:29:PRO:HG2	1:O:211:GLN:OE1	1.50	1.05
1:C:65:VAL:HG21	1:C:78:TRP:CE3	1.85	1.05
1:G:29:PRO:CG	1:G:211:GLN:CG	2.33	1.05
1:N:252:VAL:CG2	2:Q:1:DG:C2	2.27	1.05
1:I:144:PRO:HB3	4:V:19:DT:OP2	1.56	1.05
1:I:149:SER:OG	2:Q:3:DT:P	2.14	1.04
1:C:270:LYS:CD	1:H:145:TRP:CD1	2.39	1.04
1:A:50:SER:CB	2:Q:8:DG:H21	1.70	1.04
1:I:154:GLU:O	3:R:18:DC:C1'	2.06	1.04
1:L:267:LYS:CD	2:Q:3:DT:O4	2.05	1.04
1:L:220:LYS:HE2	1:L:222:ARG:HG3	1.33	1.04
1:J:29:PRO:HG3	1:J:211:GLN:HG3	1.38	1.03
1:A:1:TRP:CH2	1:J:222:ARG:NH2	2.25	1.03
1:I:47:LYS:HD3	2:S:9:DA:OP1	1.56	1.03
1:I:47:LYS:CG	2:S:9:DA:OP1	2.05	1.03
1:A:1:TRP:CZ2	1:J:222:ARG:NH2	2.26	1.03
1:L:220:LYS:HZ3	1:L:222:ARG:HD3	1.23	1.03
1:I:146:ASN:HD21	1:I:148:GLN:CB	1.71	1.03
1:D:223:PHE:O	1:D:272:ILE:HB	1.57	1.03
1:I:149:SER:OG	2:Q:3:DT:OP1	1.76	1.03
1:D:221:ILE:CG2	1:D:242:GLN:OE1	2.08	1.02
1:D:237:TRP:CH2	1:D:270:LYS:HE2	1.94	1.02
1:I:225:TYR:C	1:I:237:TRP:HE3	1.63	1.02
1:A:207:GLN:HG3	1:D:222:ARG:CZ	1.89	1.02
1:I:67:TYR:CE1	1:I:76:LEU:CD2	2.43	1.02
1:A:35:ASP:HB2	1:E:2:ILE:HD11	1.04	1.02
1:I:225:TYR:CD2	1:I:237:TRP:CB	2.42	1.02
1:K:65:VAL:HG21	1:K:78:TRP:CE3	1.93	1.02
1:A:15:TRP:CH2	1:J:135:LEU:HD21	1.94	1.01
1:I:231:ARG:CZ	2:S:20:DT:H5'	1.89	1.01
1:P:60:ILE:HG21	1:P:208:GLN:OE1	1.60	1.01
1:A:155:ARG:HG2	2:S:6:DG:H4'	1.40	1.01
1:I:52:LEU:HD12	1:L:232:GLY:HA3	1.43	1.01
1:I:68:THR:HG23	1:I:75:ILE:HB	1.39	1.01
1:N:231:ARG:NH2	3:T:25:DC:H41	1.58	1.01
1:A:35:ASP:CB	1:E:2:ILE:CD1	2.38	1.00
1:L:231:ARG:CA	3:T:14:DC:H5'	1.89	1.00
1:A:207:GLN:CG	1:D:222:ARG:CZ	2.40	1.00
1:A:14:LYS:HZ1	1:J:134:TYR:CA	1.63	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:145:TRP:CG	1:N:229:ARG:HD3	1.91	1.00
1:N:106:TRP:HZ3	1:N:112:PRO:HG3	1.11	1.00
1:E:222:ARG:HD2	1:H:203:PHE:CE2	1.97	1.00
1:I:154:GLU:C	3:R:18:DC:C1'	2.29	1.00
1:I:94:GLU:HB2	3:T:28:DC:H4'	1.43	1.00
1:I:231:ARG:NH2	2:S:20:DT:C5'	2.24	1.00
1:E:217:LYS:HZ1	1:H:211:GLN:HB2	1.22	1.00
1:I:125:ALA:CA	3:T:30:DC:OP1	2.09	1.00
1:I:67:TYR:CE2	1:I:123:PHE:CE1	2.50	1.00
1:A:148:GLN:NE2	2:S:4:DG:C5	2.29	0.99
1:I:237:TRP:CZ3	1:I:270:LYS:N	2.29	0.99
1:N:231:ARG:NH2	3:T:25:DC:N4	2.10	0.99
1:I:154:GLU:CB	3:R:18:DC:H1'	1.91	0.99
1:A:225:TYR:CE1	1:A:272:ILE:CD1	2.45	0.99
1:A:14:LYS:CE	1:J:134:TYR:HD1	1.63	0.99
1:A:223:PHE:CD1	1:A:242:GLN:HG2	1.98	0.99
1:B:29:PRO:CG	1:B:211:GLN:HG3	1.91	0.99
1:E:222:ARG:HD3	1:H:203:PHE:CZ	1.86	0.99
1:A:207:GLN:CG	1:D:222:ARG:NH1	2.24	0.99
1:E:30:ARG:HG2	3:R:7:DA:C4'	1.88	0.99
1:D:223:PHE:HD1	1:D:274:PRO:HG3	1.22	0.99
1:H:60:ILE:HG21	1:H:208:GLN:OE1	1.63	0.99
1:K:270:LYS:HD2	1:P:145:TRP:CG	1.96	0.99
1:M:222:ARG:HD2	1:P:203:PHE:CZ	1.97	0.99
1:E:217:LYS:HZ3	1:H:209:ARG:CB	1.76	0.99
1:I:121:PRO:HG2	3:T:28:DC:C2	1.97	0.99
1:I:47:LYS:O	1:N:270:LYS:NZ	1.95	0.99
1:F:29:PRO:HB3	1:F:211:GLN:HG3	1.42	0.99
1:I:119:ASN:CB	4:V:19:DT:C5'	2.41	0.99
1:I:146:ASN:HD21	1:I:148:GLN:HB2	0.84	0.98
1:O:23:HIS:NE2	1:O:207:GLN:OE1	1.96	0.98
1:I:52:LEU:CD2	3:T:14:DC:H1'	1.93	0.98
1:I:120:GLY:O	1:I:124:VAL:HG23	1.62	0.98
1:I:225:TYR:HB2	1:I:237:TRP:CD2	1.98	0.98
1:E:31:THR:CG2	3:R:8:DG:H5'	1.94	0.98
1:I:223:PHE:CE1	1:I:242:GLN:HG3	1.98	0.98
1:I:122:ALA:CA	3:T:29:DC:H5''	1.92	0.98
1:I:30:ARG:HH12	3:T:9:DC:C3'	1.75	0.98
1:I:58:ARG:H	1:L:267:LYS:HA	1.27	0.98
1:I:145:TRP:CG	1:N:229:ARG:HD2	1.81	0.98
1:I:30:ARG:NH1	3:T:9:DC:H2'	1.78	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:217:LYS:HD3	1:P:212:GLN:HG3	1.00	0.98
1:B:29:PRO:HB3	1:B:211:GLN:HG3	1.40	0.98
1:I:121:PRO:HD3	4:V:18:DG:N2	1.79	0.97
1:I:1:TRP:HE1	1:I:29:PRO:CD	1.77	0.97
1:I:225:TYR:HB3	1:I:237:TRP:HB3	0.99	0.97
1:A:120:GLY:O	1:A:124:VAL:HG23	1.62	0.97
1:A:95:THR:HG22	3:R:28:DC:H5''	1.00	0.97
1:E:220:LYS:HZ1	1:H:203:PHE:HE1	0.99	0.97
1:L:220:LYS:CE	1:L:222:ARG:CD	2.34	0.97
1:L:274:PRO:CB	1:L:275:PRO:CD	2.22	0.97
1:F:231:ARG:NH2	3:R:25:DC:N4	2.04	0.97
1:C:270:LYS:CE	1:H:145:TRP:CD1	2.47	0.97
1:I:52:LEU:HD13	3:T:14:DC:H4'	1.44	0.97
1:I:52:LEU:HD12	1:L:232:GLY:O	1.63	0.97
1:G:23:HIS:CE1	1:G:207:GLN:OE1	2.18	0.97
1:I:121:PRO:HG2	3:T:28:DC:O2	0.80	0.97
1:I:225:TYR:CB	1:I:237:TRP:HE3	1.70	0.97
1:K:270:LYS:HD2	1:P:145:TRP:CE2	1.84	0.97
1:I:68:THR:HG22	1:I:75:ILE:HB	1.44	0.96
1:A:225:TYR:CZ	1:A:240:PRO:CB	2.48	0.96
1:N:203:PHE:CZ	1:N:207:GLN:CD	2.39	0.96
1:A:44:GLN:C	1:A:45:GLU:N	2.19	0.96
1:C:65:VAL:HG22	1:C:78:TRP:CD2	2.00	0.96
1:F:203:PHE:CZ	1:F:207:GLN:NE2	2.32	0.96
1:D:232:GLY:CA	2:Q:11:DC:H4'	1.96	0.96
1:L:220:LYS:NZ	1:L:222:ARG:HD3	1.80	0.96
1:A:155:ARG:NH1	2:S:7:DA:H5'	1.81	0.96
1:A:204:ASN:O	1:A:208:GLN:HG3	1.65	0.96
1:I:47:LYS:CD	2:S:9:DA:OP1	2.12	0.96
1:A:207:GLN:HB3	1:D:222:ARG:CZ	1.92	0.96
1:I:207:GLN:NE2	1:L:222:ARG:CZ	2.28	0.96
1:D:232:GLY:HA2	2:Q:11:DC:H4'	1.45	0.96
1:I:154:GLU:HB3	3:R:18:DC:H2''	1.44	0.95
1:M:31:THR:CG2	3:T:7:DA:O3'	2.14	0.95
1:D:274:PRO:HB2	1:D:275:PRO:HD3	0.96	0.95
1:I:209:ARG:HH12	1:J:199:ASP:HB3	1.27	0.95
1:I:121:PRO:CG	4:V:18:DG:N2	2.29	0.95
1:I:122:ALA:N	3:T:29:DC:C5'	2.30	0.95
1:D:227:ARG:HG2	1:D:268:ASP:HB3	1.49	0.95
1:D:267:LYS:CE	2:S:3:DT:O4	2.15	0.95
1:G:206:GLU:OE2	1:H:203:PHE:CD1	2.19	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:147:PRO:HG2	3:T:19:DA:H2	1.19	0.95
1:A:225:TYR:HE1	1:A:272:ILE:CD1	1.79	0.95
1:A:95:THR:HG22	3:R:28:DC:C4'	1.97	0.95
1:E:31:THR:OG1	3:R:8:DG:C5'	2.14	0.95
1:I:203:PHE:CZ	1:I:207:GLN:NE2	2.22	0.95
1:L:224:CYS:CB	1:L:271:PHE:HA	1.97	0.95
1:N:159:THR:OG1	1:O:48:MET:CE	2.14	0.95
1:I:64:GLN:OE1	1:I:150:GLN:HA	1.67	0.94
1:M:229:ARG:HH22	1:P:146:ASN:ND2	1.65	0.94
1:A:155:ARG:HE	2:S:6:DG:H1'	0.80	0.94
1:G:65:VAL:CG2	1:G:78:TRP:CD2	2.50	0.94
1:A:64:GLN:OE1	1:A:150:GLN:HA	1.68	0.94
1:I:52:LEU:CD2	3:T:15:DT:H5'	1.97	0.94
1:A:14:LYS:HB3	1:J:134:TYR:CD1	2.03	0.94
1:L:220:LYS:CE	1:L:222:ARG:HD3	1.98	0.94
1:I:52:LEU:CD1	1:L:232:GLY:HA3	1.97	0.94
1:L:274:PRO:HB2	1:L:275:PRO:HD3	0.97	0.94
1:D:231:ARG:O	2:Q:11:DC:H4'	1.66	0.94
1:A:225:TYR:HE1	1:A:272:ILE:HD11	1.28	0.94
1:I:119:ASN:CB	4:V:19:DT:O5'	2.15	0.94
1:I:52:LEU:CD1	1:L:232:GLY:O	2.15	0.94
1:M:31:THR:HG23	3:T:7:DA:O3'	1.68	0.94
1:I:52:LEU:CD1	3:T:14:DC:H4'	1.98	0.94
1:I:121:PRO:HG3	4:V:18:DG:N2	1.83	0.94
1:F:30:ARG:HG2	1:F:211:GLN:HE22	1.28	0.94
1:M:217:LYS:CD	1:P:212:GLN:HG3	1.94	0.94
1:N:61:ASP:OD2	1:N:205:LYS:NZ	2.01	0.93
1:I:225:TYR:CB	1:I:237:TRP:CD2	2.51	0.93
1:M:202:ILE:HG23	1:N:202:ILE:HG23	1.47	0.93
1:I:52:LEU:HA	3:T:15:DT:H5'	1.49	0.93
1:A:203:PHE:CE2	1:D:222:ARG:HD3	1.93	0.93
1:A:35:ASP:HB2	1:E:2:ILE:CD1	1.96	0.93
1:G:65:VAL:HG22	1:G:78:TRP:CD2	2.03	0.93
1:N:203:PHE:HZ	1:N:207:GLN:NE2	1.54	0.93
1:A:117:SER:HG	1:A:139:HIS:HE2	1.11	0.93
1:C:208:GLN:HG2	1:C:212:GLN:OE1	1.68	0.93
1:I:154:GLU:OE1	3:R:18:DC:H2''	1.69	0.93
1:N:252:VAL:CG2	2:Q:1:DG:H21	1.82	0.93
1:A:35:ASP:HB3	1:E:2:ILE:HD11	1.50	0.93
1:L:233:HIS:CB	1:L:234:PRO:CD	2.45	0.93
1:I:225:TYR:C	1:I:237:TRP:CE3	2.42	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:119:ASN:HB2	4:V:19:DT:H4'	0.94	0.93
1:L:220:LYS:HE3	1:L:222:ARG:HG2	1.51	0.93
1:I:67:TYR:HE1	1:I:76:LEU:HD22	1.13	0.92
1:A:212:GLN:HB2	1:D:217:LYS:HD2	0.94	0.92
1:O:29:PRO:HB3	1:O:211:GLN:HG3	1.51	0.92
1:K:65:VAL:HG23	1:K:78:TRP:CE3	2.00	0.92
1:A:225:TYR:HE2	1:A:240:PRO:HD3	1.31	0.92
1:N:29:PRO:CB	1:N:211:GLN:OE1	2.18	0.92
1:K:270:LYS:HG2	1:P:145:TRP:CZ2	2.04	0.92
1:A:159:THR:HG22	2:S:7:DA:C5'	2.00	0.92
1:C:270:LYS:HD2	1:H:145:TRP:CG	2.01	0.92
1:A:155:ARG:CZ	2:S:6:DG:H1'	2.00	0.92
1:C:65:VAL:HG23	1:C:78:TRP:CE3	2.04	0.92
1:L:220:LYS:CD	1:L:222:ARG:HG3	1.99	0.92
1:J:29:PRO:HG3	1:J:211:GLN:CG	2.00	0.92
1:D:267:LYS:HE3	2:S:3:DT:C4	2.04	0.91
1:A:225:TYR:CD2	1:A:239:GLY:O	2.23	0.91
1:A:203:PHE:HZ	1:D:222:ARG:CG	1.83	0.91
1:G:29:PRO:HG3	1:G:211:GLN:NE2	1.82	0.91
1:A:55:SER:OG	2:S:5:DC:H5'	1.70	0.91
1:I:94:GLU:H	3:T:28:DC:H5''	1.35	0.91
1:A:225:TYR:OH	1:A:240:PRO:HB3	1.71	0.91
1:A:24:LEU:O	1:J:217:LYS:HG3	1.68	0.91
1:A:69:HIS:CE1	3:T:20:DG:O4'	2.22	0.91
1:H:204:ASN:O	1:H:208:GLN:HG3	1.71	0.91
1:I:94:GLU:HB2	3:T:28:DC:C4'	2.01	0.91
1:L:220:LYS:HE2	1:L:222:ARG:HG2	0.93	0.91
1:I:52:LEU:HD22	3:T:14:DC:C3'	1.99	0.91
1:I:67:TYR:CG	1:I:76:LEU:HD13	2.05	0.91
1:I:154:GLU:CB	3:R:18:DC:C1'	2.47	0.91
1:B:208:GLN:O	1:B:212:GLN:HG3	1.72	0.90
1:I:61:ASP:HB3	1:I:112:PRO:HA	1.51	0.90
1:A:35:ASP:HB3	1:E:2:ILE:CD1	2.00	0.90
1:I:1:TRP:CD1	1:I:28:ILE:HA	2.06	0.90
1:A:69:HIS:ND1	3:T:20:DG:O4'	2.04	0.90
1:B:23:HIS:NE2	1:B:207:GLN:OE1	2.04	0.90
1:E:217:LYS:NZ	1:H:211:GLN:HB2	1.86	0.90
1:I:30:ARG:HH12	3:T:9:DC:H3'	1.35	0.90
1:N:203:PHE:HZ	1:N:207:GLN:HE22	1.10	0.90
1:F:30:ARG:HG2	1:F:211:GLN:NE2	1.87	0.90
1:I:125:ALA:HA	3:T:30:DC:P	2.11	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:212:GLN:CB	1:D:217:LYS:CG	2.50	0.89
1:D:223:PHE:CD1	1:D:274:PRO:HG3	2.06	0.89
1:I:95:THR:CA	3:T:29:DC:P	2.55	0.89
1:I:121:PRO:C	3:T:29:DC:C5'	2.40	0.89
1:A:203:PHE:HE2	1:D:222:ARG:HD2	1.33	0.89
1:I:61:ASP:O	1:I:63:TRP:HD1	1.47	0.89
1:L:224:CYS:HG	1:L:269:VAL:HG13	1.33	0.89
1:C:270:LYS:HZ2	1:H:145:TRP:HD1	0.92	0.89
1:E:222:ARG:NH1	1:H:207:GLN:CG	2.34	0.89
1:G:65:VAL:CG2	1:G:78:TRP:CZ3	2.56	0.89
1:I:155:ARG:HD3	3:R:17:DG:H21	1.38	0.89
1:I:157:HIS:CB	3:R:18:DC:H4'	2.03	0.89
1:I:30:ARG:HH12	3:T:9:DC:C2'	1.85	0.89
1:D:233:HIS:CB	1:D:234:PRO:CD	2.50	0.89
1:K:65:VAL:HG22	1:K:78:TRP:CD2	2.06	0.89
1:L:224:CYS:CA	1:L:270:LYS:O	2.19	0.89
1:I:212:GLN:CB	1:L:217:LYS:HZ1	1.58	0.89
1:I:223:PHE:HE1	1:I:242:GLN:HG2	1.38	0.89
1:I:154:GLU:CA	3:R:18:DC:H1'	2.03	0.89
1:I:95:THR:HG22	3:T:28:DC:H3'	1.53	0.88
1:A:154:GLU:OE1	3:T:18:DC:H2''	1.73	0.88
1:A:14:LYS:HE3	1:J:134:TYR:CD1	1.90	0.88
1:E:31:THR:OG1	3:R:8:DG:P	2.31	0.88
1:N:252:VAL:HG21	2:Q:1:DG:H22	1.32	0.88
1:I:154:GLU:HB3	3:R:18:DC:H1'	1.51	0.88
1:L:222:ARG:HD2	1:L:273:PRO:HG3	1.55	0.88
1:I:224:CYS:SG	1:I:243:VAL:HG22	2.14	0.88
1:N:158:GLN:HB2	1:O:48:MET:HE1	1.56	0.88
1:G:65:VAL:HG21	1:G:78:TRP:CZ3	2.09	0.88
1:C:270:LYS:CD	1:H:145:TRP:NE1	2.28	0.88
1:A:14:LYS:HZ3	1:J:134:TYR:CA	1.73	0.88
1:I:121:PRO:CD	4:V:18:DG:N2	2.36	0.88
1:I:203:PHE:CE2	1:L:222:ARG:HD2	2.06	0.88
1:L:223:PHE:HA	1:L:243:VAL:HG22	1.55	0.88
1:A:119:ASN:CB	4:U:19:DT:H4'	2.03	0.87
1:I:225:TYR:CB	1:I:237:TRP:CB	2.40	0.87
1:E:222:ARG:CZ	1:H:207:GLN:HG3	2.04	0.87
1:A:225:TYR:CE2	1:A:240:PRO:HD3	2.10	0.87
1:A:207:GLN:CB	1:D:222:ARG:NH2	2.33	0.87
1:D:274:PRO:CB	1:D:275:PRO:CD	2.45	0.87
1:I:121:PRO:HD3	4:V:18:DG:H21	1.40	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:94:GLU:HB2	3:T:28:DC:C5'	2.04	0.87
1:A:15:TRP:NE1	1:J:134:TYR:O	2.08	0.87
1:A:25:GLU:CD	1:J:217:LYS:HE2	1.94	0.87
1:A:119:ASN:HB2	4:U:19:DT:O3'	1.74	0.86
1:I:121:PRO:O	3:T:29:DC:C4'	2.15	0.86
1:A:224:CYS:SG	1:A:243:VAL:HG22	2.15	0.86
1:A:69:HIS:HB2	3:T:21:DT:OP1	1.74	0.86
1:E:222:ARG:NH1	1:H:203:PHE:CD2	2.43	0.86
1:I:237:TRP:CH2	1:I:270:LYS:N	2.44	0.86
1:A:155:ARG:NE	2:S:6:DG:C1'	2.23	0.86
2:S:6:DG:N2	3:T:16:DC:O2	2.07	0.86
1:A:212:GLN:CG	1:D:217:LYS:HG3	2.04	0.86
1:H:60:ILE:CG2	1:H:208:GLN:OE1	2.22	0.86
1:E:222:ARG:NH1	1:H:203:PHE:HE2	1.74	0.86
1:I:67:TYR:HE2	1:I:123:PHE:CE1	1.90	0.86
1:D:237:TRP:CE2	1:D:270:LYS:HE2	2.11	0.86
1:P:204:ASN:O	1:P:208:GLN:HG3	1.76	0.86
1:M:217:LYS:NZ	1:P:211:GLN:HB2	1.90	0.86
1:I:193:LEU:CD1	1:L:274:PRO:O	2.23	0.86
1:I:223:PHE:HA	1:I:242:GLN:HA	1.57	0.86
1:A:154:GLU:HB3	3:T:18:DC:H1'	1.57	0.86
1:I:203:PHE:HE1	1:I:207:GLN:HE21	1.21	0.86
1:I:68:THR:O	1:I:74:ILE:HA	1.76	0.85
1:C:65:VAL:HG21	1:C:78:TRP:CZ3	2.11	0.85
1:I:122:ALA:N	3:T:29:DC:H5'	1.89	0.85
1:G:29:PRO:HG2	1:G:211:GLN:CD	1.93	0.85
1:A:25:GLU:CA	1:J:217:LYS:HE3	2.07	0.85
1:K:270:LYS:CD	1:P:145:TRP:CG	2.58	0.85
1:A:212:GLN:H	1:D:217:LYS:HZ2	1.24	0.85
1:I:67:TYR:CE2	1:I:123:PHE:HE1	1.92	0.85
1:N:29:PRO:HB3	1:N:211:GLN:OE1	1.74	0.85
1:E:31:THR:OG1	3:R:8:DG:H5''	1.75	0.85
1:I:212:GLN:HB3	1:L:217:LYS:HZ1	1.14	0.85
1:I:69:HIS:HB2	3:R:21:DT:OP1	1.75	0.85
1:L:220:LYS:HE2	1:L:222:ARG:HD3	1.53	0.85
1:I:52:LEU:HA	3:T:15:DT:H5''	1.56	0.85
1:I:225:TYR:HB3	1:I:237:TRP:CG	2.11	0.85
1:I:225:TYR:HB3	1:I:237:TRP:CE3	2.09	0.85
1:I:52:LEU:CD1	1:L:232:GLY:N	2.40	0.85
1:A:155:ARG:NH2	2:S:7:DA:O4'	2.08	0.85
1:L:233:HIS:CB	1:L:234:PRO:HD3	2.07	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:154:GLU:O	3:R:18:DC:C4'	2.24	0.84
1:A:207:GLN:HB3	1:D:222:ARG:HH22	1.39	0.84
1:L:244:LEU:HD12	1:L:252:VAL:O	1.76	0.84
1:L:267:LYS:HD2	2:Q:3:DT:O4	1.75	0.84
1:I:68:THR:HG22	1:I:75:ILE:C	1.96	0.84
1:C:270:LYS:HD3	1:H:145:TRP:CG	2.08	0.84
1:I:225:TYR:CD2	1:I:237:TRP:HB2	2.13	0.84
1:D:224:CYS:SG	1:D:269:VAL:HG13	2.17	0.84
1:E:222:ARG:CZ	1:H:203:PHE:CE2	2.61	0.84
1:L:267:LYS:HD3	2:Q:3:DT:O4	1.77	0.84
1:C:65:VAL:HG21	1:C:78:TRP:CE2	2.12	0.84
1:A:24:LEU:O	1:J:217:LYS:CB	2.25	0.84
1:A:149:SER:OG	2:S:3:DT:P	2.35	0.84
1:L:220:LYS:HG3	1:L:222:ARG:HG3	1.59	0.83
1:D:221:ILE:HG22	1:D:242:GLN:OE1	1.76	0.83
1:A:155:ARG:HH22	2:S:7:DA:C1'	1.92	0.83
1:I:30:ARG:NH1	3:T:9:DC:C2'	2.41	0.83
1:L:233:HIS:CB	1:N:248:ASP:OD2	2.27	0.83
3:R:23:DG:O6	3:T:22:DC:N4	2.09	0.83
1:K:270:LYS:HD3	1:P:145:TRP:HE1	1.42	0.83
1:P:207:GLN:O	1:P:212:GLN:NE2	2.12	0.83
1:A:14:LYS:HE2	1:J:134:TYR:CG	2.13	0.83
1:A:14:LYS:HB3	1:J:134:TYR:HE1	1.05	0.83
1:I:50:SER:OG	2:S:9:DA:C1'	2.25	0.83
1:I:193:LEU:HD13	1:L:274:PRO:O	1.79	0.82
1:E:217:LYS:HZ3	1:H:209:ARG:HB2	1.44	0.82
1:I:118:ASP:OD2	4:V:20:DG:C5'	2.26	0.82
1:I:121:PRO:CG	4:V:18:DG:H22	1.90	0.82
1:A:212:GLN:HB2	1:D:217:LYS:NZ	1.93	0.82
1:G:65:VAL:HG22	1:G:78:TRP:CE3	2.12	0.82
1:I:225:TYR:CG	1:I:237:TRP:CB	2.57	0.82
1:K:270:LYS:CE	1:P:145:TRP:CD1	2.63	0.82
1:B:29:PRO:CG	1:B:211:GLN:CG	2.53	0.82
1:N:62:HIS:HD2	1:N:81:THR:HG21	1.41	0.82
1:A:14:LYS:HZ3	1:J:134:TYR:HA	1.00	0.82
1:N:159:THR:N	1:O:48:MET:CE	2.42	0.82
1:A:24:LEU:C	1:J:217:LYS:HG2	2.00	0.82
1:I:155:ARG:HD3	3:R:17:DG:N2	1.94	0.82
1:A:155:ARG:HG2	2:S:6:DG:C4'	2.09	0.82
1:L:223:PHE:HE2	1:L:240:PRO:CB	1.91	0.82
1:A:203:PHE:HZ	1:D:222:ARG:HD3	0.98	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:212:GLN:NE2	1:A:212:GLN:H	1.79	0.81
1:B:29:PRO:CG	1:B:211:GLN:CD	2.45	0.81
1:C:29:PRO:HB3	1:C:211:GLN:HG2	1.63	0.81
1:I:50:SER:OG	2:S:9:DA:O4'	1.99	0.81
1:A:68:THR:HB	1:A:157:HIS:NE2	1.96	0.81
1:L:223:PHE:CA	1:L:243:VAL:CG2	2.18	0.81
1:G:65:VAL:HG21	1:G:78:TRP:CE3	2.12	0.80
1:I:154:GLU:HB3	3:R:18:DC:H2'	1.61	0.80
2:S:17:DC:O2	3:T:5:DG:N2	2.14	0.80
1:E:31:THR:CG2	3:R:7:DA:O3'	2.29	0.80
1:I:147:PRO:CB	3:R:19:DA:H1'	2.11	0.80
1:A:155:ARG:NH2	2:S:7:DA:N9	2.29	0.80
1:I:94:GLU:N	3:T:28:DC:H5''	1.96	0.80
1:I:1:TRP:HB2	1:I:28:ILE:HG22	1.63	0.80
1:I:223:PHE:CD1	1:I:242:GLN:CG	2.53	0.80
1:N:23:HIS:HE1	1:N:211:GLN:NE2	1.80	0.80
1:A:54:GLY:HA3	2:S:3:DT:O2	1.80	0.80
1:A:52:LEU:CD1	1:D:233:HIS:CB	2.60	0.80
1:F:61:ASP:OD2	1:F:205:LYS:NZ	2.13	0.80
1:E:30:ARG:HD2	3:R:7:DA:H5'	0.80	0.80
1:A:158:GLN:OE1	3:T:17:DG:C1'	2.29	0.79
1:A:158:GLN:OE1	3:T:17:DG:N3	2.15	0.79
1:I:146:ASN:OD1	1:I:149:SER:N	2.14	0.79
1:I:47:LYS:HB2	2:S:9:DA:P	2.20	0.79
1:A:25:GLU:CD	1:J:217:LYS:CE	2.49	0.79
1:M:43:CYS:SG	1:M:166:LYS:NZ	2.53	0.79
1:B:29:PRO:HG3	1:B:211:GLN:HG3	1.48	0.79
1:G:29:PRO:HG3	1:G:211:GLN:HG3	1.50	0.79
1:A:225:TYR:CE2	1:A:240:PRO:CD	2.66	0.79
1:A:68:THR:CB	1:A:157:HIS:CD2	2.65	0.79
1:I:154:GLU:CA	3:R:18:DC:H2''	2.12	0.79
1:O:29:PRO:HG3	1:O:211:GLN:CG	2.11	0.79
1:M:229:ARG:HH22	1:P:146:ASN:CG	1.85	0.79
1:C:65:VAL:CG2	1:C:78:TRP:CZ3	2.65	0.79
1:G:65:VAL:HG23	1:G:78:TRP:CE3	2.17	0.79
1:I:68:THR:HG22	1:I:75:ILE:CB	2.04	0.79
1:A:155:ARG:HH12	2:S:7:DA:C4'	1.95	0.78
1:E:30:ARG:HG2	3:R:7:DA:H5''	0.79	0.78
1:N:252:VAL:CB	2:Q:1:DG:N2	2.45	0.78
2:S:8:DG:N2	3:T:14:DC:O2	2.16	0.78
1:D:223:PHE:CD1	1:D:274:PRO:CG	2.64	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:145:TRP:HB3	1:N:229:ARG:HD3	1.59	0.78
1:A:47:LYS:O	1:F:270:LYS:NZ	2.14	0.78
1:I:225:TYR:CB	1:I:237:TRP:CG	2.65	0.78
1:A:215:LYS:NZ	1:D:213:GLN:OE1	2.16	0.78
1:I:58:ARG:N	1:L:267:LYS:HA	1.97	0.78
1:I:2:ILE:HD12	1:I:2:ILE:H	1.48	0.78
1:I:30:ARG:HH12	3:T:9:DC:H2'	1.47	0.78
1:D:221:ILE:HG21	1:D:242:GLN:OE1	1.83	0.78
1:N:207:GLN:O	1:N:211:GLN:HG2	1.83	0.78
1:A:27:GLY:HA3	1:J:217:LYS:O	1.83	0.78
1:I:1:TRP:NE1	1:I:29:PRO:CD	2.37	0.78
1:I:207:GLN:HE21	1:L:222:ARG:NH1	1.80	0.78
1:I:145:TRP:CD2	1:N:229:ARG:HD3	2.19	0.78
1:I:67:TYR:CE1	1:I:76:LEU:HD13	2.19	0.77
1:D:227:ARG:NE	1:D:268:ASP:CG	2.35	0.77
1:G:65:VAL:HG21	1:G:78:TRP:CH2	2.18	0.77
2:S:17:DC:N3	3:T:5:DG:N1	2.31	0.77
1:L:220:LYS:CE	1:L:222:ARG:HG3	1.92	0.77
1:O:208:GLN:O	1:O:212:GLN:HB2	1.84	0.77
1:D:231:ARG:O	2:Q:11:DC:C1'	2.32	0.77
1:F:111:ALA:O	1:F:205:LYS:NZ	2.17	0.77
1:H:152:LEU:O	1:H:156:THR:OG1	2.00	0.77
1:I:122:ALA:CA	3:T:29:DC:C5'	2.61	0.77
1:A:231:ARG:CZ	2:Q:19:DG:O3'	2.32	0.77
1:L:231:ARG:CB	3:T:13:DT:H1'	2.14	0.77
1:I:58:ARG:H	1:L:267:LYS:CA	1.96	0.77
1:M:31:THR:CG2	3:T:8:DG:P	2.73	0.77
1:I:203:PHE:HE1	1:I:207:GLN:NE2	1.76	0.77
1:I:52:LEU:CD2	3:T:14:DC:C1'	2.58	0.77
1:M:31:THR:HG21	3:T:8:DG:H5'	1.66	0.77
1:I:158:GLN:NE2	3:R:17:DG:N3	2.33	0.76
2:S:8:DG:N1	3:T:14:DC:N3	2.31	0.76
1:E:217:LYS:HZ3	1:H:209:ARG:HB3	1.49	0.76
1:O:23:HIS:NE2	1:O:207:GLN:CD	2.39	0.76
1:A:223:PHE:HE1	1:A:242:GLN:HG2	1.41	0.76
1:K:65:VAL:HG21	1:K:78:TRP:CE2	2.20	0.76
1:C:29:PRO:HB3	1:C:211:GLN:CG	2.13	0.76
1:D:237:TRP:CZ2	1:D:270:LYS:CE	2.66	0.76
1:I:209:ARG:NH1	1:J:199:ASP:HB3	1.99	0.76
1:L:229:ARG:O	1:L:233:HIS:O	2.02	0.76
1:A:212:GLN:HG2	1:D:217:LYS:CG	2.15	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:30:ARG:CG	1:F:211:GLN:HE22	1.99	0.76
1:I:68:THR:HG22	1:I:75:ILE:CA	2.15	0.76
1:A:240:PRO:HG2	1:H:223:PHE:CE2	2.20	0.76
1:I:225:TYR:CA	1:I:237:TRP:HE3	1.98	0.76
1:L:222:ARG:CD	1:L:273:PRO:HG3	2.15	0.76
1:M:217:LYS:HD3	1:P:212:GLN:HG2	1.67	0.76
1:G:23:HIS:NE2	1:G:207:GLN:OE1	2.19	0.76
1:M:30:ARG:CD	3:T:7:DA:H5'	1.78	0.76
1:F:231:ARG:HH22	3:R:25:DC:H41	0.77	0.76
1:I:146:ASN:ND2	1:I:148:GLN:CB	2.39	0.76
1:I:199:ASP:OD1	1:J:209:ARG:NH2	2.19	0.75
1:A:225:TYR:CD2	1:A:239:GLY:C	2.60	0.75
2:S:6:DG:N1	3:T:16:DC:N3	2.32	0.75
1:A:199:ASP:OD1	1:B:209:ARG:NH2	2.19	0.75
1:N:29:PRO:HA	1:N:211:GLN:CD	2.07	0.75
1:K:270:LYS:CG	1:P:145:TRP:CE2	2.68	0.75
1:E:31:THR:CB	3:R:8:DG:H5'	2.15	0.75
1:I:50:SER:OG	2:S:9:DA:H1'	1.86	0.75
1:A:184:THR:O	1:A:188:LYS:N	2.20	0.75
1:D:227:ARG:NE	1:D:268:ASP:OD1	2.20	0.75
1:M:217:LYS:HZ1	1:P:209:ARG:HB3	1.49	0.75
1:A:149:SER:HG	2:S:3:DT:P	2.10	0.75
1:C:61:ASP:OD2	1:C:205:LYS:NZ	2.19	0.75
1:D:223:PHE:HD1	1:D:274:PRO:CG	1.99	0.75
1:A:154:GLU:HB3	3:T:18:DC:C1'	2.15	0.75
1:M:229:ARG:NH2	1:P:146:ASN:ND2	2.34	0.75
1:A:53:ARG:O	1:D:234:PRO:HG2	1.87	0.74
1:A:2:ILE:HD12	1:A:2:ILE:N	2.02	0.74
1:I:184:THR:O	1:I:188:LYS:N	2.20	0.74
1:I:240:PRO:HG2	1:P:223:PHE:CE2	2.22	0.74
1:L:220:LYS:CD	1:L:222:ARG:CG	2.59	0.74
1:O:29:PRO:CB	1:O:211:GLN:HG3	2.16	0.74
1:K:270:LYS:CD	1:P:145:TRP:CD2	2.37	0.74
1:I:158:GLN:HG3	3:R:18:DC:O4'	1.87	0.74
1:I:94:GLU:CB	3:T:28:DC:H4'	2.16	0.74
1:J:29:PRO:CG	1:J:211:GLN:HG3	2.16	0.74
1:M:36:ILE:O	1:M:40:CYS:N	2.20	0.74
1:H:115:LEU:O	1:H:140:THR:OG1	2.06	0.73
1:A:143:ILE:HG23	2:S:3:DT:OP1	1.87	0.73
1:I:237:TRP:CH2	1:I:270:LYS:HB2	2.22	0.73
1:K:270:LYS:NZ	1:P:145:TRP:HD1	1.78	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:230:LYS:O	1:D:231:ARG:CB	2.35	0.73
1:K:65:VAL:HG22	1:K:78:TRP:CG	2.23	0.73
1:L:224:CYS:HB3	1:L:271:PHE:N	2.04	0.73
1:A:253:VAL:O	1:A:262:LEU:N	2.22	0.73
1:N:252:VAL:HG11	2:Q:1:DG:N2	2.04	0.73
1:C:65:VAL:HG22	1:C:78:TRP:CE3	2.15	0.72
1:I:253:VAL:O	1:I:262:LEU:N	2.22	0.72
1:I:30:ARG:NH1	3:T:9:DC:H3'	2.04	0.72
1:I:55:SER:O	1:L:227:ARG:NH2	2.22	0.72
1:N:62:HIS:HD2	1:N:81:THR:CG2	2.02	0.72
1:I:231:ARG:NH2	2:S:20:DT:P	2.56	0.72
1:E:217:LYS:NZ	1:H:209:ARG:CB	2.52	0.72
1:D:227:ARG:NH2	1:D:268:ASP:OD1	2.22	0.72
1:I:153:VAL:O	1:I:157:HIS:ND1	2.22	0.72
1:M:217:LYS:HZ1	1:P:209:ARG:CB	2.02	0.72
1:A:50:SER:CB	2:Q:8:DG:N2	2.39	0.72
1:C:209:ARG:HA	1:C:212:GLN:NE2	2.04	0.72
1:L:229:ARG:C	1:L:233:HIS:O	2.28	0.72
2:S:6:DG:H2''	2:S:7:DA:C8	2.24	0.72
1:A:15:TRP:NE1	1:J:134:TYR:CG	2.38	0.72
1:L:231:ARG:CB	3:T:14:DC:C4'	2.67	0.72
1:I:52:LEU:HD11	1:L:232:GLY:N	2.04	0.72
1:E:43:CYS:SG	1:E:166:LYS:NZ	2.59	0.72
1:F:228:THR:O	1:F:235:GLY:N	2.22	0.72
1:I:158:GLN:CA	3:R:18:DC:H5'	2.20	0.72
1:A:159:THR:HG22	2:S:7:DA:H5'	1.70	0.71
1:A:153:VAL:O	1:A:157:HIS:ND1	2.22	0.71
1:A:155:ARG:HH12	2:S:7:DA:H5'	1.50	0.71
1:M:31:THR:HG21	3:T:7:DA:O3'	1.89	0.71
1:J:187:ILE:O	1:J:190:LYS:NZ	2.17	0.71
3:R:40:DT:H3'	3:R:43:DT:P	2.30	0.71
1:E:30:ARG:CD	3:R:7:DA:H5''	1.88	0.71
1:A:64:GLN:OE1	1:A:150:GLN:CA	2.39	0.71
1:I:145:TRP:HB3	1:N:229:ARG:HD2	1.32	0.71
1:N:231:ARG:HH22	3:T:25:DC:H42	1.39	0.71
1:N:252:VAL:CG1	2:Q:1:DG:N2	2.53	0.71
1:I:225:TYR:HB3	1:I:237:TRP:CD2	2.20	0.71
1:K:253:VAL:O	1:K:262:LEU:N	2.23	0.71
3:R:40:DT:H3'	3:R:43:DT:OP2	1.91	0.71
1:E:206:GLU:OE2	1:E:209:ARG:NH2	2.24	0.71
1:I:95:THR:HA	3:T:28:DC:C3'	2.20	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:208:GLN:O	1:J:212:GLN:HG3	1.90	0.71
1:I:212:GLN:CB	1:L:217:LYS:HZ2	1.70	0.71
1:A:14:LYS:HZ1	1:J:134:TYR:HA	0.90	0.71
1:I:147:PRO:HB3	3:R:19:DA:C2'	2.21	0.70
1:L:224:CYS:HA	1:L:270:LYS:O	1.91	0.70
1:A:212:GLN:HB3	1:D:217:LYS:HD2	1.65	0.70
1:A:25:GLU:HA	1:J:217:LYS:CG	2.20	0.70
1:I:155:ARG:NH2	2:Q:6:DG:N3	2.38	0.70
1:K:208:GLN:O	1:K:212:GLN:HB2	1.90	0.70
1:P:61:ASP:OD2	1:P:205:LYS:NZ	2.22	0.70
1:P:226:TYR:O	1:P:238:GLN:N	2.25	0.70
1:N:203:PHE:CE1	1:N:207:GLN:NE2	2.59	0.70
1:A:212:GLN:HB3	1:D:217:LYS:CD	2.13	0.70
1:E:178:LEU:O	1:E:181:THR:OG1	2.07	0.70
1:A:24:LEU:O	1:J:217:LYS:HB3	1.92	0.70
1:I:212:GLN:HB2	1:L:217:LYS:HZ1	1.50	0.70
1:I:240:PRO:HG2	1:P:223:PHE:HE2	1.56	0.70
1:D:267:LYS:CE	2:S:3:DT:C4	2.71	0.70
1:M:31:THR:HG21	3:T:8:DG:P	2.31	0.70
1:A:155:ARG:HH12	2:S:7:DA:C5'	2.03	0.70
1:I:64:GLN:OE1	1:I:150:GLN:CA	2.39	0.70
1:A:25:GLU:HA	1:J:217:LYS:HE2	1.71	0.70
1:A:50:SER:OG	2:Q:9:DA:H1'	1.92	0.70
1:I:117:SER:OG	1:I:139:HIS:NE2	2.22	0.70
1:I:193:LEU:HD11	1:L:274:PRO:O	1.90	0.70
1:A:210:ILE:O	1:A:214:SER:N	2.24	0.70
1:I:2:ILE:N	1:I:2:ILE:HD12	2.06	0.70
1:M:30:ARG:HD2	3:T:7:DA:H4'	1.73	0.70
1:N:62:HIS:CD2	1:N:81:THR:HG21	2.24	0.70
1:A:223:PHE:HA	1:A:242:GLN:HA	1.74	0.69
1:E:217:LYS:NZ	1:H:209:ARG:HB2	2.05	0.69
1:A:14:LYS:CA	1:J:134:TYR:HE1	2.05	0.69
1:K:61:ASP:OD2	1:K:205:LYS:NZ	2.24	0.69
1:I:240:PRO:CG	1:P:223:PHE:CE2	2.74	0.69
3:R:21:DT:H2''	3:R:22:DC:H5''	1.74	0.69
1:L:252:VAL:HG13	1:L:262:LEU:O	1.92	0.69
1:D:227:ARG:CG	1:D:268:ASP:HB3	2.23	0.69
1:C:209:ARG:HA	1:C:212:GLN:HE21	1.57	0.69
1:I:225:TYR:HD2	1:I:237:TRP:CB	2.06	0.69
1:A:225:TYR:HA	1:A:239:GLY:O	1.93	0.69
1:C:36:ILE:O	1:C:40:CYS:N	2.25	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:159:THR:HG22	2:S:7:DA:H5''	1.75	0.69
1:I:237:TRP:CH2	1:I:269:VAL:C	2.66	0.69
1:E:30:ARG:HD2	3:R:7:DA:C4'	2.22	0.69
1:I:53:ARG:CB	2:Q:4:DG:P	2.81	0.68
1:K:65:VAL:HG21	1:K:78:TRP:CZ3	2.27	0.68
1:O:29:PRO:HB3	1:O:211:GLN:CG	2.23	0.68
1:E:227:ARG:NE	1:H:148:GLN:OE1	2.25	0.68
1:I:154:GLU:OE1	3:R:18:DC:C2'	2.42	0.68
1:A:55:SER:H	1:D:227:ARG:HH12	1.41	0.68
1:G:29:PRO:HG2	1:G:211:GLN:OE1	1.94	0.68
1:C:65:VAL:HG22	1:C:78:TRP:CG	2.28	0.68
1:I:119:ASN:HB2	4:V:19:DT:O4'	1.90	0.68
1:K:208:GLN:HG3	1:K:211:GLN:OE1	1.94	0.68
1:N:231:ARG:HH22	3:T:25:DC:H41	1.15	0.68
1:A:21:SER:OG	1:I:190:LYS:HD2	1.94	0.68
1:G:65:VAL:HG21	1:G:78:TRP:CD2	2.23	0.68
1:I:119:ASN:HB3	4:V:19:DT:O5'	1.93	0.68
1:I:51:THR:O	3:T:15:DT:H4'	1.94	0.68
1:L:226:TYR:O	1:L:238:GLN:N	2.25	0.68
1:M:115:LEU:O	1:M:140:THR:OG1	2.12	0.68
1:D:224:CYS:CA	1:D:270:LYS:O	2.42	0.68
1:I:67:TYR:OH	1:I:99:PHE:HD1	1.36	0.68
1:I:145:TRP:HE1	1:N:229:ARG:C	1.97	0.68
1:K:270:LYS:CG	1:P:145:TRP:CZ2	2.75	0.68
1:A:155:ARG:NH1	2:S:7:DA:C5'	2.57	0.68
1:I:52:LEU:HD11	1:L:232:GLY:CA	2.24	0.68
1:I:67:TYR:CD1	1:I:76:LEU:HB2	2.28	0.68
1:I:61:ASP:O	1:I:63:TRP:NE1	2.27	0.68
1:I:58:ARG:CB	1:I:62:HIS:HD2	2.07	0.68
1:L:242:GLN:HG2	1:L:244:LEU:HD23	1.77	0.67
1:A:69:HIS:CB	3:T:21:DT:OP1	2.42	0.67
1:I:196:SER:N	1:I:199:ASP:OD2	2.27	0.67
1:A:159:THR:CG2	2:S:7:DA:C5'	2.72	0.67
1:N:245:TRP:CD1	2:Q:1:DG:O6	2.46	0.67
1:I:147:PRO:HB3	3:R:19:DA:H2''	1.77	0.67
1:L:224:CYS:CB	1:L:271:PHE:N	2.58	0.67
1:D:267:LYS:CE	2:S:3:DT:H3	2.06	0.67
1:A:196:SER:N	1:A:199:ASP:OD2	2.27	0.67
1:I:223:PHE:HE1	1:I:242:GLN:CG	1.95	0.67
1:M:222:ARG:O	1:M:243:VAL:N	2.23	0.67
1:P:60:ILE:CG2	1:P:208:GLN:OE1	2.40	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:203:PHE:CZ	1:I:207:GLN:HE21	1.53	0.67
1:I:212:GLN:NE2	1:L:214:SER:HA	2.09	0.67
1:I:52:LEU:HD13	1:L:232:GLY:O	1.94	0.67
1:I:30:ARG:HH22	3:T:9:DC:H3'	1.60	0.67
1:B:23:HIS:ND1	1:B:28:ILE:O	2.27	0.67
1:M:173:ALA:O	1:M:176:SER:OG	2.13	0.67
2:Q:9:DA:H2''	2:Q:10:DT:H5''	1.76	0.67
1:I:52:LEU:CD2	3:T:14:DC:O3'	2.20	0.67
1:C:41:ASP:O	1:C:45:GLU:N	2.26	0.67
1:A:147:PRO:HG3	3:T:19:DA:C4	2.22	0.67
1:A:15:TRP:CD1	1:J:134:TYR:CZ	2.76	0.67
1:C:270:LYS:NZ	1:H:145:TRP:HD1	1.55	0.67
1:K:80:GLU:OE1	1:K:83:SER:N	2.27	0.67
1:L:223:PHE:HA	1:L:243:VAL:HG23	0.69	0.67
1:O:203:PHE:CE2	1:O:207:GLN:NE2	2.63	0.67
1:A:95:THR:CG2	3:R:28:DC:C5'	2.41	0.66
1:D:231:ARG:O	2:Q:11:DC:O4'	2.13	0.66
1:E:80:GLU:OE1	1:E:83:SER:N	2.27	0.66
1:F:203:PHE:HZ	1:F:207:GLN:HE22	1.42	0.66
1:I:115:LEU:O	1:I:140:THR:N	2.28	0.66
1:G:65:VAL:HG21	1:G:78:TRP:CE2	2.30	0.66
1:B:191:GLY:O	1:B:195:THR:OG1	2.06	0.66
1:J:160:LEU:O	1:J:163:THR:OG1	2.12	0.66
1:L:222:ARG:HB3	1:L:272:ILE:O	1.95	0.66
1:P:253:VAL:O	1:P:262:LEU:N	2.29	0.66
1:A:155:ARG:NH2	2:S:6:DG:H1'	2.10	0.66
1:I:225:TYR:CE2	1:I:240:PRO:HB3	2.30	0.66
1:A:225:TYR:CE1	1:A:240:PRO:HB3	2.26	0.66
1:J:68:THR:OG1	1:J:161:LYS:NZ	2.16	0.66
1:K:36:ILE:O	1:K:40:CYS:N	2.28	0.66
1:A:50:SER:HB3	2:Q:8:DG:N3	2.09	0.66
1:F:231:ARG:CZ	3:R:25:DC:H41	2.08	0.66
1:G:202:ILE:HG23	1:H:202:ILE:HG23	1.78	0.66
1:I:2:ILE:H	1:I:2:ILE:CD1	2.09	0.66
1:A:14:LYS:CE	1:J:134:TYR:CA	2.63	0.66
3:R:40:DT:C3'	3:R:43:DT:OP2	2.44	0.66
1:A:44:GLN:OE1	1:A:47:LYS:HE3	1.96	0.66
1:I:225:TYR:CA	1:I:237:TRP:CE3	2.77	0.66
1:I:67:TYR:CD1	1:I:76:LEU:CD1	2.76	0.66
1:N:151:ALA:HB1	1:N:155:ARG:NH1	2.10	0.66
1:A:115:LEU:O	1:A:140:THR:N	2.28	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:223:PHE:CZ	1:I:242:GLN:HG3	2.30	0.66
1:I:68:THR:CG2	1:I:75:ILE:CA	2.73	0.66
1:J:78:TRP:N	1:J:87:TYR:O	2.29	0.66
1:I:158:GLN:N	3:R:18:DC:H5'	2.11	0.65
1:I:237:TRP:CZ2	1:I:270:LYS:HB2	2.31	0.65
1:I:1:TRP:CD1	1:I:29:PRO:HD3	2.27	0.65
1:A:159:THR:CG2	2:S:7:DA:H5'	2.26	0.65
1:A:212:GLN:HB3	1:D:217:LYS:CG	2.23	0.65
1:D:231:ARG:O	2:Q:11:DC:H1'	1.96	0.65
1:H:209:ARG:O	1:H:212:GLN:HB3	1.97	0.65
1:I:146:ASN:OD1	1:I:149:SER:CB	2.45	0.65
1:M:213:GLN:O	1:M:216:SER:OG	2.12	0.65
1:M:228:THR:O	1:M:235:GLY:N	2.29	0.65
1:A:212:GLN:CB	1:D:217:LYS:HG3	2.22	0.65
1:A:225:TYR:CD1	1:A:272:ILE:HD11	2.29	0.65
1:G:65:VAL:HG21	1:G:78:TRP:CZ2	2.31	0.65
1:K:79:VAL:HG11	1:K:153:VAL:HG22	1.77	0.65
1:N:228:THR:O	1:N:235:GLY:N	2.29	0.65
1:O:62:HIS:ND1	1:O:114:SER:OG	2.22	0.65
1:I:67:TYR:OH	1:I:99:PHE:CG	2.43	0.65
1:M:229:ARG:HH22	1:P:146:ASN:HD21	1.43	0.65
1:N:132:MET:O	1:N:136:GLY:N	2.30	0.65
1:A:204:ASN:O	1:A:208:GLN:N	2.29	0.65
1:C:253:VAL:O	1:C:262:LEU:N	2.29	0.65
1:C:80:GLU:OE1	1:C:83:SER:N	2.29	0.65
1:I:119:ASN:CA	4:V:19:DT:H4'	2.27	0.65
1:A:58:ARG:CB	1:A:62:HIS:HD2	2.10	0.65
1:B:181:THR:O	1:B:184:THR:OG1	2.13	0.65
1:I:158:GLN:CG	3:R:18:DC:H5'	2.27	0.65
1:M:220:LYS:NZ	1:O:209:ARG:NH2	2.45	0.65
1:I:225:TYR:O	1:I:237:TRP:CZ3	2.49	0.64
1:M:80:GLU:OE1	1:M:83:SER:N	2.30	0.64
3:R:40:DT:H2'	3:R:43:DT:C6	2.32	0.64
1:A:225:TYR:OH	1:A:240:PRO:CB	2.42	0.64
1:B:23:HIS:HE1	1:B:207:GLN:OE1	1.76	0.64
1:D:80:GLU:OE1	1:D:83:SER:N	2.30	0.64
1:A:225:TYR:CE2	1:A:240:PRO:HB3	2.28	0.64
1:A:31:THR:CG2	3:R:9:DC:OP2	2.46	0.64
1:A:154:GLU:HB3	3:T:18:DC:C2'	2.27	0.64
1:A:77:VAL:HG13	1:A:88:ALA:HB2	1.79	0.64
1:M:220:LYS:HZ1	1:O:209:ARG:NH2	1.95	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:209:ARG:NH1	1:N:213:GLN:OE1	2.30	0.64
1:E:36:ILE:O	1:E:40:CYS:N	2.30	0.64
1:I:225:TYR:CZ	1:I:240:PRO:HB3	2.33	0.64
1:I:30:ARG:NH2	3:T:10:DG:OP2	2.31	0.64
1:A:119:ASN:OD1	1:A:144:PRO:HB3	1.98	0.64
1:L:231:ARG:CB	3:T:14:DC:O5'	2.46	0.64
1:M:211:GLN:O	1:M:214:SER:OG	2.15	0.64
1:O:23:HIS:CE1	1:O:207:GLN:CD	2.71	0.64
1:A:50:SER:OG	2:Q:9:DA:C1'	2.46	0.64
1:C:173:ALA:O	1:C:176:SER:OG	2.13	0.64
1:D:233:HIS:CB	1:D:234:PRO:HD2	2.26	0.64
1:G:65:VAL:HG11	1:G:76:LEU:HD11	1.80	0.64
1:I:203:PHE:O	1:I:207:GLN:HG2	1.98	0.64
1:M:13:ASN:O	1:M:16:HIS:NE2	2.31	0.64
1:I:154:GLU:HA	3:R:18:DC:H2''	1.77	0.64
1:I:69:HIS:CB	3:R:21:DT:OP1	2.46	0.64
1:I:237:TRP:O	1:I:239:GLY:N	2.30	0.64
1:M:31:THR:HG21	3:T:8:DG:C5'	2.26	0.64
1:A:54:GLY:CA	2:S:3:DT:O2	2.45	0.64
1:I:155:ARG:NH2	2:Q:6:DG:H1'	2.13	0.64
1:B:80:GLU:OE1	1:B:83:SER:N	2.31	0.63
1:I:77:VAL:HG13	1:I:88:ALA:HB2	1.79	0.63
1:A:15:TRP:CZ2	1:J:135:LEU:HD23	2.29	0.63
1:A:255:ASP:O	1:A:259:ASP:N	2.31	0.63
1:C:152:LEU:O	1:C:156:THR:OG1	2.08	0.63
1:J:36:ILE:O	1:J:40:CYS:N	2.30	0.63
1:K:65:VAL:CG2	1:K:78:TRP:CZ3	2.79	0.63
1:A:15:TRP:CE2	1:J:135:LEU:HD23	2.32	0.63
1:I:47:LYS:CD	2:S:9:DA:P	2.75	0.63
1:A:120:GLY:HA2	4:U:19:DT:H2''	1.81	0.63
1:I:158:GLN:HG2	3:R:18:DC:H5'	1.80	0.63
1:I:147:PRO:HB2	3:R:19:DA:H1'	1.78	0.63
1:A:55:SER:O	1:D:227:ARG:CZ	2.46	0.63
1:E:181:THR:O	1:E:184:THR:OG1	2.12	0.63
1:M:30:ARG:NE	3:T:7:DA:C5'	2.28	0.63
1:A:25:GLU:CA	1:J:217:LYS:HG3	2.29	0.63
1:A:95:THR:HG22	3:R:28:DC:H4'	1.80	0.63
1:I:121:PRO:CD	3:T:28:DC:O2	2.47	0.63
1:K:30:ARG:HG2	1:K:211:GLN:HE22	1.64	0.63
1:G:70:TYR:OH	1:G:165:GLU:OE1	2.16	0.63
1:D:206:GLU:OE2	1:D:209:ARG:NH2	2.32	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:255:ASP:O	1:I:259:ASP:N	2.31	0.62
1:L:244:LEU:HD12	1:L:253:VAL:HA	1.79	0.62
1:I:1:TRP:CD1	1:I:28:ILE:HG22	2.35	0.62
1:I:118:ASP:OD2	4:V:20:DG:H4'	1.98	0.62
1:I:1:TRP:O	1:I:5:ILE:HG13	1.99	0.62
1:B:132:MET:O	1:B:136:GLY:N	2.31	0.62
1:I:67:TYR:CZ	1:I:76:LEU:HD22	2.28	0.62
1:N:159:THR:CB	1:O:48:MET:HE3	2.26	0.62
1:I:237:TRP:HZ3	1:I:270:LYS:H	1.43	0.62
1:I:68:THR:HG23	1:I:75:ILE:CB	2.10	0.62
1:M:229:ARG:NH2	1:P:146:ASN:HD21	1.96	0.62
1:E:31:THR:HG1	3:R:8:DG:P	2.12	0.62
1:L:247:GLY:H	1:L:251:ILE:HG22	1.65	0.62
1:L:223:PHE:O	1:L:272:ILE:HB	1.99	0.62
1:I:118:ASP:OD2	4:V:20:DG:C4'	2.48	0.62
1:I:62:HIS:HD1	1:I:114:SER:HG	1.48	0.62
1:N:80:GLU:OE1	1:N:83:SER:N	2.32	0.62
1:C:208:GLN:HG2	1:C:212:GLN:CD	2.19	0.62
1:H:64:GLN:NE2	1:H:150:GLN:OE1	2.31	0.62
1:A:161:LYS:NZ	3:T:19:DA:OP1	2.33	0.61
1:A:2:ILE:HG22	1:A:2:ILE:O	2.00	0.61
1:J:176:SER:O	1:J:179:ALA:HB3	2.00	0.61
1:A:203:PHE:CZ	1:D:222:ARG:CG	2.68	0.61
1:A:35:ASP:HB3	1:E:2:ILE:HD12	1.80	0.61
1:C:29:PRO:CB	1:C:211:GLN:HG2	2.30	0.61
3:T:20:DG:P	3:T:20:DG:H8	2.24	0.61
1:C:218:GLN:NE2	1:C:244:LEU:O	2.34	0.61
1:P:173:ALA:O	1:P:176:SER:OG	2.17	0.61
1:E:23:HIS:ND1	1:E:28:ILE:O	2.33	0.61
1:A:190:LYS:N	1:I:21:SER:OG	2.32	0.61
1:K:65:VAL:HG22	1:K:78:TRP:HA	1.83	0.61
1:L:228:THR:O	1:L:233:HIS:O	2.19	0.61
1:B:160:LEU:O	1:B:163:THR:OG1	2.15	0.61
1:F:80:GLU:OE1	1:F:83:SER:N	2.33	0.61
1:N:23:HIS:CE1	1:N:211:GLN:NE2	2.67	0.61
1:N:261:TYR:O	1:N:262:LEU:HD23	2.00	0.61
1:I:80:GLU:OE1	1:I:83:SER:N	2.34	0.61
1:A:28:ILE:HD11	1:A:33:ALA:HB2	1.83	0.61
1:A:68:THR:HG22	1:A:75:ILE:O	1.99	0.61
1:E:213:GLN:O	1:E:216:SER:OG	2.10	0.61
1:H:80:GLU:OE1	1:H:83:SER:N	2.34	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:121:PRO:CD	4:V:18:DG:H21	2.07	0.61
1:A:14:LYS:O	1:J:134:TYR:OH	2.18	0.61
1:G:23:HIS:NE2	1:G:207:GLN:CD	2.54	0.61
1:I:95:THR:CG2	3:T:28:DC:H3'	2.30	0.61
1:I:28:ILE:HD11	1:I:33:ALA:HB2	1.83	0.60
1:I:78:TRP:O	1:I:87:TYR:N	2.34	0.60
1:G:203:PHE:CE2	1:G:207:GLN:NE2	2.69	0.60
1:I:155:ARG:HH21	2:Q:6:DG:H1'	1.66	0.60
1:A:15:TRP:CD1	1:J:134:TYR:O	2.54	0.60
1:I:68:THR:N	1:I:75:ILE:O	2.35	0.60
1:N:252:VAL:HG11	2:Q:1:DG:H22	1.65	0.60
1:C:65:VAL:HG21	1:C:78:TRP:CH2	2.36	0.60
1:L:244:LEU:CD1	1:L:253:VAL:HA	2.31	0.60
1:I:154:GLU:CA	3:R:18:DC:C2'	2.77	0.60
1:A:80:GLU:OE1	1:A:83:SER:N	2.34	0.60
1:I:237:TRP:HH2	1:I:269:VAL:C	2.04	0.60
1:K:6:PRO:HG2	1:K:263:VAL:HG13	1.82	0.60
1:O:80:GLU:OE1	1:O:83:SER:N	2.35	0.60
1:A:25:GLU:OE1	1:J:217:LYS:HE3	2.00	0.60
1:A:78:TRP:O	1:A:87:TYR:N	2.34	0.60
1:D:221:ILE:HG22	1:D:242:GLN:CD	2.21	0.60
1:D:267:LYS:CE	2:S:3:DT:N3	2.65	0.60
1:G:29:PRO:CG	1:G:211:GLN:NE2	2.56	0.60
1:C:270:LYS:NZ	1:H:145:TRP:CG	2.45	0.60
1:G:80:GLU:OE1	1:G:83:SER:N	2.34	0.60
1:D:231:ARG:O	2:Q:11:DC:C3'	2.48	0.60
1:A:193:LEU:CD1	1:D:223:PHE:HZ	2.15	0.60
1:A:237:TRP:CB	1:H:275:PRO:HG2	2.32	0.60
1:B:78:TRP:N	1:B:87:TYR:O	2.35	0.60
1:L:115:LEU:O	1:L:140:THR:OG1	2.18	0.60
1:A:66:ASP:H	1:A:153:VAL:HG21	1.67	0.60
1:E:211:GLN:O	1:E:214:SER:OG	2.19	0.60
1:I:154:GLU:CA	3:R:18:DC:C1'	2.72	0.60
1:A:25:GLU:HA	1:J:217:LYS:HG3	1.83	0.60
1:M:181:THR:O	1:M:184:THR:OG1	2.15	0.60
1:N:159:THR:H	1:O:48:MET:CE	2.15	0.60
1:B:134:TYR:O	1:I:14:LYS:NZ	2.24	0.59
1:A:31:THR:HG21	3:R:9:DC:OP2	2.00	0.59
1:A:225:TYR:CE2	1:A:240:PRO:CB	2.84	0.59
1:N:38:GLN:OE1	1:N:44:GLN:NE2	2.35	0.59
1:D:221:ILE:O	1:D:221:ILE:HG22	2.01	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:61:ASP:OD2	1:D:205:LYS:NZ	2.27	0.59
1:H:173:ALA:O	1:H:176:SER:OG	2.20	0.59
1:E:222:ARG:CD	1:H:203:PHE:CE2	2.64	0.59
1:I:212:GLN:HE22	1:L:214:SER:HA	1.68	0.59
1:I:225:TYR:O	1:I:237:TRP:HZ3	1.85	0.59
1:L:80:GLU:OE1	1:L:83:SER:N	2.35	0.59
1:M:221:ILE:O	1:M:221:ILE:HG22	2.01	0.59
1:A:237:TRP:CD1	1:H:275:PRO:HB2	2.38	0.59
1:A:37:VAL:HG13	1:A:43:CYS:HB2	1.84	0.59
1:A:52:LEU:HA	3:R:15:DT:H5'	1.84	0.59
1:B:185:LEU:HD22	1:B:189:ARG:NH1	2.17	0.59
1:M:217:LYS:HB3	1:P:212:GLN:HG2	1.83	0.59
1:A:223:PHE:CE1	1:A:242:GLN:HG3	2.30	0.59
1:E:160:LEU:O	1:E:163:THR:OG1	2.12	0.59
1:H:146:ASN:HD21	1:H:148:GLN:HB2	1.68	0.59
1:I:52:LEU:CD1	1:L:232:GLY:H	2.14	0.59
1:G:65:VAL:HG23	1:G:78:TRP:CZ3	2.33	0.59
1:I:119:ASN:CG	4:V:19:DT:C5'	2.65	0.59
1:I:57:LYS:CB	1:L:267:LYS:O	2.50	0.59
1:A:225:TYR:HD2	1:A:239:GLY:O	1.84	0.59
1:A:53:ARG:CB	2:S:4:DG:OP1	2.50	0.59
1:E:173:ALA:O	1:E:176:SER:OG	2.19	0.59
1:E:217:LYS:NZ	1:H:209:ARG:HB3	2.16	0.59
1:I:115:LEU:N	1:I:138:GLU:O	2.36	0.59
1:M:217:LYS:NZ	1:P:209:ARG:HB3	2.18	0.59
1:M:31:THR:HG23	3:T:8:DG:P	2.40	0.59
1:A:115:LEU:N	1:A:138:GLU:O	2.36	0.59
1:I:224:CYS:SG	1:I:243:VAL:CG2	2.90	0.59
1:I:145:TRP:NE1	1:N:229:ARG:C	2.54	0.59
1:I:121:PRO:CD	4:V:18:DG:H22	2.07	0.58
1:O:30:ARG:HH22	1:O:207:GLN:HB3	1.67	0.58
1:N:158:GLN:HB2	1:O:48:MET:CE	2.29	0.58
1:I:55:SER:HB3	2:Q:4:DG:H4'	1.84	0.58
1:C:270:LYS:CE	1:H:145:TRP:CG	2.83	0.58
1:E:31:THR:CB	3:R:8:DG:C5'	2.76	0.58
1:A:14:LYS:C	1:J:134:TYR:OH	2.42	0.58
1:I:183:ILE:HD11	1:J:104:MET:O	2.04	0.58
4:U:11:DG:H2''	4:U:12:DA:H5''	1.85	0.58
1:D:227:ARG:O	1:D:227:ARG:HG3	2.02	0.58
1:I:37:VAL:HG13	1:I:43:CYS:HB2	1.84	0.58
1:I:66:ASP:H	1:I:153:VAL:HG21	1.67	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:66:ASP:OD2	4:V:20:DG:C4'	2.51	0.58
1:A:62:HIS:HD1	1:A:114:SER:HG	1.48	0.58
1:A:193:LEU:HD11	1:D:223:PHE:HZ	1.69	0.58
1:F:4:ASN:O	1:F:8:ALA:N	2.35	0.58
1:I:158:GLN:HA	3:R:18:DC:H5'	1.86	0.58
1:I:94:GLU:H	3:T:28:DC:C5'	2.14	0.58
1:I:52:LEU:CD2	3:T:14:DC:C3'	2.78	0.58
1:B:173:ALA:O	1:B:176:SER:OG	2.22	0.58
1:J:29:PRO:HG3	1:J:211:GLN:CD	2.23	0.58
1:M:222:ARG:CZ	1:P:207:GLN:HG3	2.34	0.58
1:A:207:GLN:HG3	1:D:222:ARG:NE	2.18	0.58
1:I:79:VAL:HG21	1:I:153:VAL:HG23	1.85	0.58
1:B:24:LEU:HD22	1:C:194:GLY:N	2.18	0.58
1:E:222:ARG:CZ	1:H:203:PHE:HE2	2.11	0.58
1:H:207:GLN:O	1:H:212:GLN:OE1	2.21	0.58
1:M:178:LEU:O	1:M:181:THR:OG1	2.20	0.58
1:M:217:LYS:NZ	1:P:209:ARG:CB	2.66	0.58
1:A:58:ARG:CB	1:A:62:HIS:CD2	2.87	0.57
1:I:52:LEU:HD23	3:T:15:DT:C5'	2.18	0.57
1:N:74:ILE:O	1:N:91:VAL:N	2.34	0.57
1:E:30:ARG:NE	3:R:7:DA:C5'	2.40	0.57
1:D:173:ALA:O	1:D:176:SER:OG	2.22	0.57
1:I:204:ASN:HA	1:I:207:GLN:HB2	1.85	0.57
1:I:108:ALA:HB2	1:J:179:ALA:HB1	1.86	0.57
1:B:29:PRO:HG3	1:B:211:GLN:OE1	2.04	0.57
1:G:23:HIS:ND1	1:G:28:ILE:O	2.37	0.57
3:R:16:DC:H2''	3:R:17:DG:C8	2.39	0.57
1:I:237:TRP:CZ3	1:I:270:LYS:HB2	2.39	0.57
1:O:48:MET:O	1:O:48:MET:HG2	2.03	0.57
1:D:223:PHE:HA	1:D:242:GLN:HA	1.84	0.57
1:N:159:THR:H	1:O:48:MET:HE1	1.69	0.57
1:A:148:GLN:NE2	2:S:4:DG:C4	2.72	0.57
1:I:126:GLU:N	3:T:30:DC:OP1	2.37	0.57
1:I:68:THR:HG21	1:I:75:ILE:CB	2.10	0.57
1:L:228:THR:O	1:L:234:PRO:HA	2.04	0.57
1:O:29:PRO:CB	1:O:211:GLN:CG	2.83	0.57
1:A:155:ARG:CG	2:S:6:DG:H4'	2.27	0.57
1:A:207:GLN:HG3	1:D:222:ARG:HH11	1.68	0.57
1:I:212:GLN:HB3	1:L:217:LYS:HZ2	0.74	0.57
1:A:30:ARG:O	1:A:33:ALA:HB3	2.05	0.57
1:A:36:ILE:O	1:A:40:CYS:N	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:29:PRO:HB3	1:B:211:GLN:CG	2.25	0.57
1:F:203:PHE:CZ	1:F:207:GLN:CD	2.77	0.57
1:I:225:TYR:HD2	1:I:237:TRP:HB3	1.58	0.57
1:A:134:TYR:O	1:C:14:LYS:NZ	2.38	0.57
1:A:210:ILE:HD12	1:A:211:GLN:HG3	1.86	0.57
1:F:12:HIS:O	1:F:16:HIS:N	2.38	0.57
1:I:30:ARG:O	1:I:33:ALA:HB3	2.05	0.57
1:M:121:PRO:O	1:M:125:ALA:N	2.38	0.57
1:M:209:ARG:HH12	1:O:193:LEU:CD1	2.18	0.57
1:O:23:HIS:ND1	1:O:28:ILE:O	2.35	0.57
1:I:52:LEU:CD2	3:T:14:DC:C4'	2.83	0.57
1:A:14:LYS:CE	1:J:134:TYR:CG	2.76	0.57
1:M:68:THR:OG1	1:M:161:LYS:NZ	2.18	0.57
1:I:58:ARG:H	1:L:267:LYS:CB	2.16	0.56
1:I:149:SER:CB	2:Q:3:DT:P	2.93	0.56
1:I:158:GLN:CD	3:R:17:DG:N3	2.59	0.56
1:N:106:TRP:O	1:N:110:PHE:N	2.38	0.56
1:N:203:PHE:CE2	1:N:207:GLN:OE1	2.59	0.56
1:A:54:GLY:H	2:S:3:DT:H1'	1.71	0.56
1:G:185:LEU:HD22	1:G:189:ARG:NH1	2.19	0.56
1:L:224:CYS:HB2	1:L:270:LYS:CA	2.32	0.56
1:I:145:TRP:CB	1:N:229:ARG:HD3	2.04	0.56
1:A:52:LEU:HB2	1:D:233:HIS:CB	2.34	0.56
1:C:65:VAL:HG22	1:C:78:TRP:HA	1.87	0.56
1:G:173:ALA:O	1:G:176:SER:OG	2.23	0.56
1:N:155:ARG:O	1:O:48:MET:HE1	2.06	0.56
1:D:267:LYS:NZ	2:S:3:DT:O4	2.38	0.56
1:F:29:PRO:HB3	1:F:211:GLN:CG	2.25	0.56
1:N:12:HIS:O	1:N:16:HIS:N	2.37	0.56
1:M:30:ARG:HG2	3:T:7:DA:H5''	1.82	0.56
1:D:237:TRP:CE2	1:D:270:LYS:CE	2.87	0.56
1:I:79:VAL:HG13	1:I:86:ILE:HG22	1.88	0.56
1:A:159:THR:CG2	2:S:7:DA:H5''	2.35	0.56
1:C:65:VAL:HG21	1:C:78:TRP:CZ2	2.40	0.56
1:I:108:ALA:CB	1:J:179:ALA:HB1	2.35	0.56
1:J:105:LYS:O	1:J:108:ALA:HB3	2.05	0.56
1:A:79:VAL:HG21	1:A:153:VAL:HG23	1.85	0.56
1:L:223:PHE:HB3	1:L:242:GLN:HA	1.86	0.56
1:I:237:TRP:CZ3	1:I:270:LYS:CB	2.89	0.56
1:A:52:LEU:O	3:R:15:DT:OP1	2.24	0.56
1:P:80:GLU:OE1	1:P:83:SER:N	2.37	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:36:ILE:O	1:I:40:CYS:N	2.37	0.55
1:J:23:HIS:ND1	1:J:28:ILE:O	2.37	0.55
1:L:242:GLN:O	1:L:253:VAL:HG12	2.06	0.55
1:A:119:ASN:ND2	1:A:142:GLY:O	2.39	0.55
1:A:240:PRO:CG	1:H:223:PHE:CE2	2.89	0.55
1:I:149:SER:HB3	2:Q:3:DT:OP2	2.07	0.55
1:A:212:GLN:N	1:D:217:LYS:HZ2	2.01	0.55
1:I:153:VAL:HG22	1:I:157:HIS:CE1	2.42	0.55
1:I:61:ASP:OD2	1:I:205:LYS:NZ	2.38	0.55
1:I:67:TYR:CD2	1:I:76:LEU:HD13	2.41	0.55
1:J:69:HIS:O	1:J:161:LYS:NZ	2.33	0.55
1:I:51:THR:HG21	1:N:266:ASN:HB2	1.88	0.55
1:I:58:ARG:CB	1:I:62:HIS:CD2	2.88	0.55
1:C:79:VAL:HG11	1:C:153:VAL:HG22	1.89	0.55
1:D:237:TRP:CZ3	1:D:270:LYS:HE2	2.42	0.55
1:F:253:VAL:O	1:F:262:LEU:N	2.39	0.55
1:I:226:TYR:O	1:I:238:GLN:N	2.33	0.55
1:I:221:ILE:HG21	1:I:242:GLN:CD	2.26	0.55
1:K:65:VAL:HG22	1:K:78:TRP:CE3	2.29	0.55
1:A:209:ARG:NH2	1:C:193:LEU:CD2	2.70	0.55
1:N:63:TRP:CD1	1:N:112:PRO:HB3	2.42	0.55
1:A:79:VAL:HG13	1:A:86:ILE:HG22	1.88	0.55
1:M:227:ARG:NH2	1:P:148:GLN:O	2.40	0.55
1:M:222:ARG:O	1:M:243:VAL:HG23	2.06	0.55
1:A:64:GLN:OE1	1:A:150:GLN:C	2.45	0.55
1:E:202:ILE:HG23	1:F:202:ILE:HG23	1.87	0.55
1:H:146:ASN:OD1	1:H:148:GLN:N	2.33	0.55
1:H:146:ASN:O	1:H:150:GLN:HB2	2.07	0.55
1:I:223:PHE:CE1	1:I:242:GLN:NE2	2.75	0.55
1:M:227:ARG:NE	1:P:148:GLN:OE1	2.39	0.55
1:A:153:VAL:HG22	1:A:157:HIS:CE1	2.42	0.55
1:E:23:HIS:NE2	3:R:7:DA:OP1	2.40	0.55
1:H:226:TYR:O	1:H:238:GLN:N	2.40	0.55
1:I:52:LEU:CA	3:T:15:DT:H5'	2.32	0.55
1:D:223:PHE:O	1:D:272:ILE:CB	2.44	0.54
1:D:227:ARG:CZ	1:D:268:ASP:OD1	2.55	0.54
1:I:30:ARG:NH2	3:T:9:DC:H3'	2.22	0.54
1:F:209:ARG:NH1	1:F:213:GLN:OE1	2.40	0.54
1:H:178:LEU:O	1:H:181:THR:OG1	2.18	0.54
1:I:1:TRP:HB2	1:I:28:ILE:CG2	2.36	0.54
1:J:181:THR:O	1:J:184:THR:OG1	2.21	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:222:ARG:CD	1:P:203:PHE:CZ	2.82	0.54
1:D:267:LYS:NZ	2:S:3:DT:C4	2.75	0.54
1:A:212:GLN:H	1:D:217:LYS:NZ	2.01	0.54
1:B:29:PRO:CG	1:B:211:GLN:OE1	2.56	0.54
1:M:1:TRP:O	1:M:4:ASN:N	2.41	0.54
1:I:155:ARG:CD	3:R:17:DG:H21	2.15	0.54
1:I:64:GLN:OE1	1:I:150:GLN:C	2.45	0.54
1:I:224:CYS:N	1:I:241:THR:O	2.39	0.54
3:R:40:DT:O3'	3:R:43:DT:OP1	2.09	0.54
1:A:121:PRO:HD3	4:U:19:DT:H1'	1.89	0.54
1:A:240:PRO:HG2	1:H:223:PHE:HE2	1.72	0.54
1:C:226:TYR:O	1:C:238:GLN:N	2.34	0.54
1:I:52:LEU:HD22	3:T:14:DC:C4'	2.38	0.54
1:L:274:PRO:HB3	1:L:275:PRO:HD3	1.76	0.54
1:F:105:LYS:O	1:F:108:ALA:HB3	2.08	0.54
1:I:148:GLN:OE1	3:R:19:DA:C2	2.61	0.54
1:E:63:TRP:O	1:E:116:GLN:N	2.41	0.54
1:I:146:ASN:CG	1:I:149:SER:H	2.09	0.54
1:K:149:SER:O	1:K:153:VAL:HG23	2.08	0.53
1:M:226:TYR:O	1:M:238:GLN:N	2.40	0.53
1:N:121:PRO:O	1:N:125:ALA:N	2.41	0.53
1:O:29:PRO:CG	1:O:211:GLN:NE2	2.47	0.53
1:L:231:ARG:CB	3:T:13:DT:O3'	2.56	0.53
1:A:117:SER:OG	1:A:139:HIS:NE2	2.22	0.53
1:I:158:GLN:O	1:I:162:ASN:OD1	2.26	0.53
1:J:80:GLU:OE1	1:J:83:SER:N	2.42	0.53
1:K:173:ALA:O	1:K:176:SER:OG	2.26	0.53
1:G:203:PHE:CZ	1:G:207:GLN:NE2	2.76	0.53
1:C:270:LYS:CG	1:H:145:TRP:CE2	2.90	0.53
1:I:67:TYR:CE1	1:I:76:LEU:CD1	2.88	0.53
1:K:9:GLU:HG3	1:K:36:ILE:HG23	1.90	0.53
1:P:185:LEU:HD22	1:P:189:ARG:NH1	2.23	0.53
1:I:148:GLN:CD	3:R:19:DA:C2	2.82	0.53
1:A:95:THR:HG23	3:R:28:DC:H5''	1.71	0.53
1:I:50:SER:OG	2:S:9:DA:C4'	2.56	0.53
3:T:20:DG:H2'	3:T:21:DT:C6	2.44	0.53
1:I:209:ARG:HH22	1:J:195:THR:HG22	1.73	0.53
1:A:193:LEU:HD13	1:D:274:PRO:O	2.08	0.53
1:P:146:ASN:O	1:P:150:GLN:HB2	2.07	0.53
1:I:40:CYS:SG	1:I:42:VAL:N	2.82	0.53
1:I:67:TYR:HA	1:I:76:LEU:HA	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:64:GLN:O	1:K:79:VAL:N	2.38	0.53
1:D:231:ARG:C	2:Q:11:DC:H4'	2.29	0.53
3:T:23:DG:H2''	3:T:24:DA:C8	2.44	0.53
1:B:188:LYS:NZ	1:C:11:GLU:OE2	2.40	0.53
1:I:52:LEU:HD11	1:L:232:GLY:HA3	1.84	0.53
1:N:151:ALA:HB1	1:N:155:ARG:HH12	1.72	0.53
1:A:60:ILE:O	1:A:61:ASP:HB2	2.09	0.53
1:N:23:HIS:ND1	1:N:28:ILE:O	2.42	0.53
1:O:29:PRO:CG	1:O:211:GLN:CG	2.77	0.53
1:A:158:GLN:O	1:A:162:ASN:OD1	2.26	0.53
1:D:232:GLY:CA	2:Q:11:DC:C4'	2.81	0.53
1:I:1:TRP:CG	1:I:28:ILE:HA	2.44	0.52
1:K:23:HIS:ND1	1:K:28:ILE:O	2.41	0.52
1:C:35:ASP:O	1:C:39:GLN:N	2.37	0.52
1:P:146:ASN:HD21	1:P:148:GLN:HB2	1.74	0.52
1:E:4:ASN:ND2	1:E:26:PHE:O	2.43	0.52
1:I:223:PHE:HE1	1:I:242:GLN:NE2	2.07	0.52
1:I:228:THR:O	1:I:235:GLY:N	2.42	0.52
1:I:226:TYR:HB3	1:I:264:ILE:HG13	1.90	0.52
1:I:94:GLU:HB2	3:T:28:DC:H5'	1.85	0.52
1:A:224:CYS:SG	1:A:243:VAL:CG2	2.94	0.52
1:A:25:GLU:CA	1:J:217:LYS:CG	2.88	0.52
1:D:220:LYS:HG3	1:D:222:ARG:HG3	1.90	0.52
1:N:159:THR:N	1:O:48:MET:HE1	2.20	0.52
1:A:228:THR:O	1:A:235:GLY:N	2.42	0.52
1:K:270:LYS:HZ2	1:P:145:TRP:HD1	1.42	0.52
1:O:132:MET:O	1:O:137:ILE:N	2.43	0.52
1:L:255:ASP:O	1:L:259:ASP:N	2.42	0.52
1:I:148:GLN:CD	3:R:19:DA:H2	2.13	0.52
1:A:40:CYS:SG	1:A:42:VAL:N	2.82	0.52
1:F:274:PRO:N	1:F:275:PRO:HD2	2.24	0.52
1:I:147:PRO:CB	3:R:19:DA:C1'	2.86	0.52
1:K:62:HIS:CG	1:K:114:SER:HG	2.26	0.52
1:B:208:GLN:O	1:B:212:GLN:CG	2.51	0.52
1:D:233:HIS:CB	1:D:234:PRO:HD3	2.34	0.52
1:J:89:GLU:OE2	1:J:105:LYS:NZ	2.36	0.52
1:L:265:ALA:O	1:L:268:ASP:N	2.42	0.52
1:M:220:LYS:HG3	1:M:222:ARG:HG3	1.92	0.52
1:O:173:ALA:O	1:O:176:SER:OG	2.27	0.52
1:O:211:GLN:O	1:O:214:SER:OG	2.14	0.52
3:T:20:DG:H8	3:T:20:DG:O5'	1.93	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:262:LEU:CB	1:D:264:ILE:HD11	2.40	0.52
1:J:64:GLN:O	1:J:79:VAL:N	2.43	0.52
1:K:4:ASN:ND2	1:K:26:PHE:O	2.42	0.52
1:D:231:ARG:O	2:Q:11:DC:O3'	2.28	0.52
1:I:56:ASN:HA	1:L:267:LYS:HE3	1.92	0.51
1:I:67:TYR:HD1	1:I:76:LEU:HB2	1.74	0.51
1:N:159:THR:N	1:O:48:MET:HE2	2.22	0.51
1:B:85:LEU:HD22	1:B:198:MET:HA	1.92	0.51
1:L:245:TRP:O	1:L:251:ILE:HB	2.09	0.51
1:M:1:TRP:O	1:M:5:ILE:N	2.41	0.51
1:L:231:ARG:N	3:T:14:DC:H5'	2.26	0.51
1:A:69:HIS:ND1	3:T:20:DG:C4'	2.73	0.51
1:A:147:PRO:CB	3:T:19:DA:N3	2.68	0.51
1:A:209:ARG:O	1:A:213:GLN:HB2	2.10	0.51
1:F:171:PHE:HB2	1:F:177:ALA:HB2	1.93	0.51
1:K:208:GLN:HA	1:K:211:GLN:CD	2.31	0.51
1:M:217:LYS:CD	1:P:212:GLN:CG	2.61	0.51
1:B:218:GLN:OE1	1:B:218:GLN:N	2.43	0.51
1:I:61:ASP:C	1:I:63:TRP:CD1	2.80	0.51
1:N:106:TRP:CH2	1:N:112:PRO:HG3	2.41	0.51
1:A:25:GLU:C	1:J:217:LYS:HG3	2.31	0.51
1:I:147:PRO:HB3	3:R:19:DA:H1'	1.91	0.51
1:H:228:THR:O	1:H:235:GLY:N	2.43	0.51
1:A:155:ARG:HH21	2:S:6:DG:H1'	1.75	0.51
1:I:36:ILE:O	1:I:39:GLN:N	2.43	0.51
1:L:206:GLU:OE2	1:L:209:ARG:NH2	2.43	0.51
1:I:154:GLU:CG	3:R:18:DC:H2''	2.40	0.51
1:I:237:TRP:HZ3	1:I:270:LYS:N	1.96	0.51
1:M:191:GLY:O	1:M:195:THR:OG1	2.25	0.51
1:O:184:THR:O	1:O:189:ARG:N	2.41	0.51
1:E:252:VAL:HG21	1:H:252:VAL:HG21	1.92	0.50
1:K:218:GLN:NE2	1:K:244:LEU:O	2.44	0.50
1:A:68:THR:CG2	1:A:75:ILE:HB	2.41	0.50
1:A:209:ARG:NH2	1:C:193:LEU:HD22	2.26	0.50
1:F:209:ARG:O	1:F:212:GLN:HB2	2.10	0.50
1:M:65:VAL:HG23	1:M:115:LEU:HD11	1.92	0.50
1:N:252:VAL:CB	2:Q:1:DG:H22	2.23	0.50
1:C:70:TYR:OH	1:C:165:GLU:OE1	2.29	0.50
1:G:111:ALA:HB3	1:G:205:LYS:HZ3	1.76	0.50
1:I:85:LEU:HD12	1:I:186:ASN:OD1	2.12	0.50
1:L:173:ALA:O	1:L:176:SER:OG	2.27	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:36:ILE:O	1:A:39:GLN:N	2.43	0.50
1:F:185:LEU:HD22	1:F:189:ARG:NH1	2.26	0.50
1:L:229:ARG:CA	1:L:233:HIS:O	2.59	0.50
3:R:35:DC:H2''	3:R:36:DA:C8	2.46	0.50
1:B:253:VAL:O	1:B:262:LEU:N	2.45	0.50
1:A:207:GLN:HG3	1:D:222:ARG:HD3	1.93	0.50
1:E:159:THR:O	1:E:163:THR:HG23	2.12	0.50
1:F:151:ALA:HB1	1:F:155:ARG:NH1	2.26	0.50
1:I:189:ARG:HD2	2:Q:7:DA:OP1	2.12	0.50
1:I:158:GLN:N	3:R:18:DC:C5'	2.74	0.50
1:I:273:PRO:O	1:P:225:TYR:OH	2.14	0.50
1:A:24:LEU:C	1:J:217:LYS:CG	2.65	0.50
1:A:55:SER:OG	2:S:5:DC:C5'	2.51	0.50
1:N:110:PHE:C	1:N:112:PRO:HD3	2.31	0.50
1:A:95:THR:HG21	3:R:28:DC:H5''	1.75	0.50
1:G:68:THR:O	1:G:75:ILE:N	2.41	0.50
1:M:222:ARG:NH2	1:P:207:GLN:HB2	2.27	0.50
1:N:158:GLN:CB	1:O:48:MET:HE1	2.36	0.50
1:A:210:ILE:O	1:A:213:GLN:HB3	2.12	0.50
1:A:223:PHE:CZ	1:A:242:GLN:HG3	2.46	0.50
1:C:206:GLU:OE2	1:C:209:ARG:NE	2.44	0.50
1:C:2:ILE:HD13	1:C:250:ALA:HB3	1.92	0.50
1:N:58:ARG:NH2	1:N:116:GLN:OE1	2.44	0.50
1:I:158:GLN:HG2	3:R:17:DG:O3'	2.12	0.50
1:A:2:ILE:HD11	1:E:39:GLN:HE22	1.77	0.49
1:A:14:LYS:CA	1:J:134:TYR:CE1	2.86	0.49
1:I:53:ARG:O	1:L:234:PRO:HD2	2.12	0.49
1:M:207:GLN:O	1:M:211:GLN:HG3	2.11	0.49
1:O:105:LYS:O	1:O:108:ALA:HB3	2.12	0.49
1:M:220:LYS:HZ1	1:O:209:ARG:HH22	1.60	0.49
1:A:154:GLU:CB	3:T:18:DC:H1'	2.34	0.49
1:A:193:LEU:CD1	1:D:274:PRO:O	2.60	0.49
1:F:106:TRP:O	1:F:109:MET:N	2.44	0.49
1:H:146:ASN:O	1:H:150:GLN:CG	2.60	0.49
1:A:203:PHE:CZ	1:D:222:ARG:HG2	2.47	0.49
1:F:203:PHE:CE1	1:F:207:GLN:NE2	2.80	0.49
1:I:231:ARG:CZ	2:S:20:DT:C5'	2.76	0.49
1:I:55:SER:OG	2:Q:5:DC:H5'	2.11	0.49
1:A:154:GLU:C	3:T:18:DC:H1'	2.33	0.49
1:A:207:GLN:HG3	1:D:222:ARG:CD	2.42	0.49
1:A:31:THR:HG22	3:R:9:DC:OP2	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:51:THR:O	3:R:15:DT:C5'	2.61	0.49
1:A:223:PHE:CZ	1:A:242:GLN:CG	2.90	0.49
1:C:149:SER:O	1:C:153:VAL:HG23	2.13	0.49
1:F:78:TRP:N	1:F:87:TYR:O	2.40	0.49
1:A:14:LYS:HZ3	1:J:134:TYR:C	2.13	0.49
1:A:225:TYR:CE2	1:A:240:PRO:N	2.80	0.49
1:A:15:TRP:CG	1:J:134:TYR:CZ	2.97	0.49
1:M:160:LEU:O	1:M:163:THR:OG1	2.20	0.49
1:I:69:HIS:C	3:R:21:DT:OP1	2.46	0.49
1:F:23:HIS:ND1	1:F:28:ILE:O	2.46	0.49
1:M:261:TYR:HB2	1:P:263:VAL:HG21	1.93	0.49
1:M:222:ARG:NH2	1:P:207:GLN:CB	2.76	0.49
1:A:85:LEU:HD12	1:A:186:ASN:OD1	2.12	0.48
1:J:159:THR:O	1:J:163:THR:HG23	2.13	0.48
1:K:191:GLY:O	1:K:195:THR:OG1	2.19	0.48
1:K:3:GLU:HA	1:K:263:VAL:HG11	1.95	0.48
1:A:188:LYS:NZ	1:I:11:GLU:OE2	2.44	0.48
1:I:52:LEU:HD21	3:T:14:DC:O4'	2.13	0.48
1:N:203:PHE:CZ	1:N:207:GLN:OE1	2.65	0.48
1:I:240:PRO:HG3	1:P:223:PHE:CE2	2.48	0.48
1:I:154:GLU:CD	3:R:18:DC:H2''	2.32	0.48
1:A:119:ASN:OD1	1:A:144:PRO:CB	2.61	0.48
1:A:155:ARG:HH22	2:S:7:DA:C4'	2.24	0.48
1:A:225:TYR:OH	1:A:240:PRO:HG3	2.13	0.48
1:B:159:THR:O	1:B:163:THR:HG23	2.12	0.48
1:H:164:LEU:HD23	1:H:181:THR:HG21	1.95	0.48
4:V:7:DA:H4'	4:V:8:DC:OP1	2.13	0.48
1:A:57:LYS:O	1:A:82:ASN:N	2.46	0.48
1:G:105:LYS:O	1:G:108:ALA:HB3	2.13	0.48
1:I:154:GLU:O	3:R:18:DC:H4'	2.09	0.48
1:O:29:PRO:CB	1:O:211:GLN:CD	2.76	0.48
2:S:8:DG:H2''	2:S:9:DA:H5''	1.94	0.48
1:A:15:TRP:HE1	1:J:134:TYR:C	2.16	0.48
1:B:161:LYS:HA	1:B:164:LEU:HD12	1.94	0.48
1:F:106:TRP:O	1:F:110:PHE:N	2.47	0.48
1:G:12:HIS:O	1:G:16:HIS:N	2.42	0.48
1:I:1:TRP:CD1	1:I:28:ILE:CA	2.89	0.48
1:M:217:LYS:NZ	1:P:209:ARG:HB2	2.28	0.48
1:M:30:ARG:NE	3:T:7:DA:H5'	2.14	0.48
1:N:184:THR:O	1:N:189:ARG:N	2.42	0.48
1:E:30:ARG:CD	3:R:7:DA:C4'	2.65	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:193:LEU:HD11	1:D:223:PHE:CZ	2.47	0.48
1:H:146:ASN:O	1:H:150:GLN:HG2	2.14	0.48
1:A:240:PRO:HG2	1:H:223:PHE:CD2	2.48	0.48
1:I:1:TRP:CB	1:I:28:ILE:HG22	2.37	0.48
1:I:67:TYR:CE1	1:I:76:LEU:CG	2.95	0.48
1:A:14:LYS:CG	1:J:134:TYR:CE1	2.93	0.48
1:A:14:LYS:CE	1:J:134:TYR:CB	2.92	0.48
1:M:159:THR:O	1:M:163:THR:HG23	2.14	0.48
1:P:115:LEU:N	1:P:138:GLU:O	2.47	0.48
1:E:30:ARG:NE	3:R:7:DA:H5''	2.21	0.48
1:E:217:LYS:HD3	1:H:212:GLN:HB2	1.95	0.48
1:H:146:ASN:O	1:H:150:GLN:CB	2.62	0.48
1:I:214:SER:O	1:I:217:LYS:HD3	2.14	0.48
1:I:8:ALA:HB2	1:I:26:PHE:CD2	2.49	0.48
1:M:25:GLU:HB2	1:M:190:LYS:NZ	2.29	0.48
1:M:222:ARG:HD2	1:P:203:PHE:HZ	1.70	0.48
1:I:119:ASN:CG	4:V:19:DT:H5'	2.30	0.48
1:J:115:LEU:N	1:J:138:GLU:O	2.46	0.48
1:L:233:HIS:CB	1:L:234:PRO:HD2	2.40	0.48
1:P:228:THR:O	1:P:235:GLY:N	2.45	0.48
1:A:52:LEU:HB3	3:R:14:DC:H4'	1.96	0.48
1:C:211:GLN:O	1:C:215:LYS:N	2.46	0.47
1:K:2:ILE:HD13	1:K:250:ALA:HB3	1.96	0.47
1:L:222:ARG:HG2	1:L:273:PRO:HA	1.96	0.47
1:P:178:LEU:O	1:P:181:THR:OG1	2.25	0.47
1:A:209:ARG:HB2	1:D:217:LYS:NZ	2.29	0.47
1:I:147:PRO:HB3	3:R:19:DA:C1'	2.44	0.47
1:I:85:LEU:HD22	1:I:198:MET:HA	1.96	0.47
1:I:212:GLN:HE22	1:L:214:SER:CA	2.27	0.47
1:A:203:PHE:HZ	1:D:222:ARG:HG2	1.73	0.47
1:D:223:PHE:CE2	1:D:272:ILE:HG21	2.49	0.47
1:I:237:TRP:CZ3	1:I:269:VAL:C	2.86	0.47
1:K:115:LEU:O	1:K:140:THR:OG1	2.30	0.47
1:I:158:GLN:HG2	3:R:18:DC:C5'	2.43	0.47
1:C:111:ALA:HB3	1:C:205:LYS:NZ	2.30	0.47
1:E:229:ARG:HH22	1:H:146:ASN:ND2	2.12	0.47
1:H:146:ASN:ND2	1:H:148:GLN:HB2	2.30	0.47
1:I:206:GLU:O	1:I:209:ARG:HG3	2.14	0.47
1:I:68:THR:CG2	1:I:75:ILE:O	2.36	0.47
1:A:8:ALA:HB2	1:A:26:PHE:CD2	2.49	0.47
1:B:182:LEU:O	1:B:186:ASN:ND2	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:264:ILE:HG22	1:D:269:VAL:CG2	2.44	0.47
1:L:223:PHE:CB	1:L:243:VAL:HG23	2.31	0.47
1:I:47:LYS:HG3	2:S:9:DA:OP1	2.06	0.47
1:L:231:ARG:CB	3:T:14:DC:O4'	2.62	0.47
1:N:21:SER:OG	1:O:190:LYS:N	2.47	0.47
1:P:146:ASN:O	1:P:150:GLN:CB	2.63	0.47
1:A:155:ARG:HH12	2:S:7:DA:H4'	1.77	0.47
1:A:66:ASP:N	1:A:153:VAL:HG21	2.29	0.47
1:D:164:LEU:O	1:D:168:ILE:HG23	2.15	0.47
1:N:61:ASP:O	1:N:113:LYS:HB3	2.14	0.47
1:N:252:VAL:CG1	2:Q:1:DG:H21	2.24	0.47
3:T:20:DG:P	3:T:20:DG:C8	3.07	0.47
1:H:68:THR:O	1:H:75:ILE:N	2.44	0.47
1:I:66:ASP:N	1:I:153:VAL:HG21	2.29	0.47
1:A:209:ARG:HH22	1:C:193:LEU:HD22	1.80	0.47
1:I:183:ILE:HG13	1:J:108:ALA:HB2	1.97	0.47
1:K:211:GLN:HG3	1:K:212:GLN:N	2.30	0.47
1:L:222:ARG:HD2	1:L:273:PRO:CG	2.37	0.47
1:N:23:HIS:HE1	1:N:211:GLN:HE22	1.59	0.47
1:P:115:LEU:O	1:P:140:THR:OG1	2.24	0.47
1:F:65:VAL:HG23	1:F:115:LEU:HD11	1.97	0.47
1:A:88:ALA:N	1:A:182:LEU:HD21	2.30	0.47
1:B:76:LEU:N	1:B:89:GLU:O	2.46	0.47
1:G:65:VAL:CG1	1:G:76:LEU:HD11	2.45	0.47
1:K:32:ALA:HB2	1:K:245:TRP:CE2	2.49	0.47
1:A:57:LYS:CB	1:A:82:ASN:HA	2.44	0.46
1:D:65:VAL:HG23	1:D:115:LEU:HD11	1.96	0.46
1:A:237:TRP:CG	1:H:275:PRO:CB	2.98	0.46
1:A:17:GLN:HG2	1:I:188:LYS:HD2	1.96	0.46
1:I:62:HIS:ND1	1:I:114:SER:OG	2.42	0.46
1:K:191:GLY:N	1:K:195:THR:O	2.48	0.46
1:L:225:TYR:N	1:L:270:LYS:O	2.47	0.46
1:P:79:VAL:HG22	1:P:156:THR:HG21	1.97	0.46
1:D:267:LYS:HE2	2:S:3:DT:H3	1.76	0.46
1:A:14:LYS:HZ1	1:J:134:TYR:N	2.11	0.46
1:A:209:ARG:NH1	1:C:193:LEU:HD21	2.30	0.46
1:I:208:GLN:HG2	1:I:208:GLN:O	2.14	0.46
1:I:233:HIS:NE2	2:S:21:DG:H5'	2.30	0.46
1:K:208:GLN:HA	1:K:211:GLN:HG2	1.98	0.46
1:I:203:PHE:CE2	1:L:222:ARG:CD	2.48	0.46
1:L:62:HIS:CD2	1:L:81:THR:HG21	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:132:MET:O	1:M:137:ILE:N	2.47	0.46
1:A:143:ILE:HG12	2:S:3:DT:OP1	2.14	0.46
1:A:85:LEU:HD22	1:A:198:MET:HA	1.96	0.46
1:D:267:LYS:HE3	2:S:3:DT:N3	2.27	0.46
1:I:149:SER:OG	2:Q:3:DT:O5'	2.32	0.46
1:I:237:TRP:CH2	1:I:270:LYS:CA	2.98	0.46
1:I:223:PHE:HE1	1:I:242:GLN:HE21	1.61	0.46
1:J:218:GLN:OE1	1:J:218:GLN:N	2.48	0.46
1:A:154:GLU:O	3:T:18:DC:H1'	2.15	0.46
1:A:25:GLU:HA	1:J:217:LYS:CD	2.41	0.46
1:C:32:ALA:HB2	1:C:245:TRP:NE1	2.31	0.46
1:F:23:HIS:O	1:F:27:GLY:N	2.47	0.46
1:I:88:ALA:N	1:I:182:LEU:HD21	2.30	0.46
1:I:207:GLN:NE2	1:L:222:ARG:NE	2.61	0.46
1:K:208:GLN:O	1:K:212:GLN:CB	2.61	0.46
1:A:190:LYS:O	1:I:21:SER:OG	2.21	0.46
1:D:237:TRP:CZ3	1:D:270:LYS:HG3	2.50	0.46
1:I:146:ASN:ND2	1:I:148:GLN:H	2.13	0.46
1:A:188:LYS:HB3	1:I:17:GLN:HG2	1.98	0.46
1:J:85:LEU:HD22	1:J:198:MET:HA	1.98	0.46
1:J:215:LYS:NZ	1:J:246:GLY:O	2.41	0.46
1:N:252:VAL:CG1	2:Q:1:DG:H22	2.25	0.46
1:I:52:LEU:O	3:T:15:DT:H5''	2.16	0.46
1:C:30:ARG:HH22	1:C:207:GLN:HB3	1.79	0.46
1:H:184:THR:O	1:H:189:ARG:N	2.49	0.46
1:I:209:ARG:HH12	1:J:199:ASP:CB	2.14	0.46
1:I:255:ASP:OD1	1:I:257:GLY:N	2.47	0.46
1:L:223:PHE:CE2	1:L:240:PRO:CB	2.78	0.46
1:E:227:ARG:NH2	1:H:148:GLN:O	2.48	0.46
1:G:111:ALA:HB3	1:G:205:LYS:NZ	2.31	0.46
1:O:191:GLY:O	1:O:195:THR:OG1	2.15	0.46
3:R:4:DC:H2''	3:R:5:DG:H8	1.81	0.46
1:A:148:GLN:NE2	2:S:4:DG:C6	2.55	0.46
1:I:50:SER:CB	2:S:9:DA:O4'	2.62	0.46
1:I:30:ARG:CZ	3:T:9:DC:H3'	2.46	0.46
1:A:213:GLN:H	1:D:217:LYS:HZ3	1.64	0.46
1:D:262:LEU:HB3	1:D:264:ILE:HD11	1.97	0.46
1:K:29:PRO:O	1:K:32:ALA:HB3	2.16	0.46
1:N:240:PRO:HG2	1:N:276:LYS:NZ	2.30	0.46
3:T:5:DG:H2''	3:T:6:DG:C8	2.51	0.46
1:I:120:GLY:HA2	4:V:19:DT:H1'	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:185:LEU:HD22	1:K:189:ARG:NH1	2.30	0.46
1:A:224:CYS:N	1:A:241:THR:O	2.46	0.46
1:A:225:TYR:OH	1:A:240:PRO:CG	2.63	0.46
1:A:44:GLN:HG3	1:A:45:GLU:N	2.31	0.46
1:A:66:ASP:OD1	1:A:67:TYR:N	2.49	0.46
1:I:237:TRP:CH2	1:I:270:LYS:CB	2.94	0.46
1:L:164:LEU:HD23	1:L:181:THR:HG21	1.98	0.46
3:R:23:DG:N1	3:T:22:DC:N3	2.52	0.46
1:E:191:GLY:O	1:E:195:THR:OG1	2.30	0.45
1:I:207:GLN:NE2	1:L:222:ARG:NH1	2.43	0.45
1:O:12:HIS:O	1:O:16:HIS:N	2.45	0.45
1:O:203:PHE:CZ	1:O:207:GLN:NE2	2.84	0.45
3:R:40:DT:H2'	3:R:43:DT:H6	1.77	0.45
1:A:143:ILE:CG2	2:S:3:DT:OP1	2.60	0.45
1:I:52:LEU:CA	3:T:15:DT:H5''	2.37	0.45
1:A:15:TRP:NE1	1:J:134:TYR:CD1	2.82	0.45
1:A:52:LEU:HD13	3:R:14:DC:H4'	1.98	0.45
1:B:60:ILE:HG22	1:B:61:ASP:H	1.82	0.45
1:I:154:GLU:HB2	3:R:18:DC:O2	2.16	0.45
1:A:52:LEU:CD1	3:R:14:DC:H4'	2.42	0.45
1:B:215:LYS:NZ	1:B:246:GLY:O	2.39	0.45
1:J:247:GLY:N	1:J:250:ALA:O	2.46	0.45
1:K:255:ASP:HB2	1:K:262:LEU:HD11	1.99	0.45
1:L:245:TRP:O	1:L:251:ILE:CG2	2.64	0.45
1:O:209:ARG:O	1:O:212:GLN:HB3	2.16	0.45
1:A:15:TRP:CD1	1:J:134:TYR:CE1	3.03	0.45
1:A:204:ASN:OD1	1:D:222:ARG:NH1	2.50	0.45
1:A:246:GLY:HA2	1:A:251:ILE:HG22	1.99	0.45
1:E:17:GLN:HE21	1:E:188:LYS:HB3	1.82	0.45
1:I:77:VAL:HG12	1:I:79:VAL:CG2	2.47	0.45
1:A:206:GLU:O	1:A:209:ARG:HG3	2.17	0.45
1:C:32:ALA:HB2	1:C:245:TRP:CE2	2.50	0.45
1:D:224:CYS:HA	1:D:270:LYS:O	2.16	0.45
1:F:132:MET:O	1:F:136:GLY:N	2.49	0.45
1:I:246:GLY:HA2	1:I:251:ILE:HG22	1.99	0.45
1:I:1:TRP:HD1	1:I:28:ILE:HG22	1.82	0.45
1:K:211:GLN:HG3	1:K:215:LYS:HE3	1.97	0.45
1:K:263:VAL:O	1:K:264:ILE:HD13	2.15	0.45
1:I:252:VAL:HG11	1:L:245:TRP:CE3	2.51	0.45
3:T:16:DC:H2''	3:T:17:DG:C8	2.52	0.45
4:U:7:DA:H2'	4:U:8:DC:C6	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:159:THR:HG22	2:S:7:DA:H4'	1.99	0.45
1:E:245:TRP:HE3	1:E:252:VAL:HG23	1.82	0.45
1:E:5:ILE:HD11	1:E:29:PRO:HD3	1.98	0.45
1:M:208:GLN:O	1:M:211:GLN:HB2	2.17	0.45
1:M:220:LYS:NZ	1:O:209:ARG:HH22	2.13	0.45
1:M:78:TRP:HZ3	1:M:115:LEU:HD13	1.82	0.45
1:O:70:TYR:CD2	1:O:164:LEU:HD13	2.52	0.45
1:A:224:CYS:O	1:A:225:TYR:N	2.46	0.45
1:A:50:SER:CB	2:Q:8:DG:C2	3.00	0.45
1:B:62:HIS:CG	1:B:114:SER:HG	2.34	0.45
1:I:215:LYS:HD2	1:L:210:ILE:HG12	1.99	0.45
1:A:209:ARG:CZ	1:C:193:LEU:CD2	2.94	0.45
1:A:212:GLN:CB	1:D:217:LYS:NZ	2.65	0.45
1:H:89:GLU:CD	1:H:105:LYS:HZ1	2.19	0.45
1:A:14:LYS:C	1:J:134:TYR:HH	2.18	0.45
1:M:42:VAL:HG12	1:M:166:LYS:HG2	1.99	0.45
1:A:240:PRO:CG	1:H:223:PHE:CD2	3.00	0.45
1:A:50:SER:OG	2:Q:9:DA:O4'	2.34	0.45
1:A:212:GLN:HG3	1:D:213:GLN:HB3	1.98	0.45
1:D:255:ASP:O	1:D:259:ASP:N	2.50	0.45
1:A:2:ILE:CD1	1:E:39:GLN:HE22	2.28	0.45
1:K:64:GLN:NE2	1:K:150:GLN:OE1	2.44	0.45
1:L:242:GLN:CG	1:L:244:LEU:HD23	2.46	0.45
1:M:105:LYS:O	1:M:108:ALA:HB3	2.17	0.45
1:N:63:TRP:NE1	1:N:112:PRO:HB3	2.32	0.45
1:P:105:LYS:O	1:P:108:ALA:HB3	2.16	0.45
1:I:125:ALA:C	3:T:30:DC:OP1	2.55	0.45
1:I:204:ASN:O	1:I:208:GLN:N	2.46	0.45
1:L:184:THR:O	1:L:189:ARG:N	2.49	0.45
1:P:146:ASN:ND2	1:P:148:GLN:HB2	2.31	0.45
1:A:149:SER:OG	2:S:3:DT:OP1	2.35	0.44
1:A:77:VAL:HG12	1:A:79:VAL:CG2	2.47	0.44
1:E:245:TRP:O	1:E:252:VAL:N	2.50	0.44
1:G:211:GLN:O	1:G:214:SER:N	2.50	0.44
1:H:119:ASN:OD1	1:H:142:GLY:N	2.49	0.44
1:I:149:SER:CB	2:Q:3:DT:OP1	2.62	0.44
1:B:190:LYS:N	1:C:21:SER:OG	2.48	0.44
1:F:266:ASN:OD1	1:F:267:LYS:N	2.46	0.44
1:F:274:PRO:N	1:F:275:PRO:CD	2.79	0.44
1:I:175:GLU:HA	1:I:178:LEU:HB3	1.99	0.44
1:N:203:PHE:CE2	1:N:207:GLN:CD	2.90	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1:TRP:CZ2	1:J:222:ARG:CZ	2.99	0.44
1:I:17:GLN:OE1	1:I:17:GLN:N	2.51	0.44
1:L:242:GLN:HG2	1:L:244:LEU:CD2	2.47	0.44
1:I:57:LYS:CB	1:L:267:LYS:C	2.86	0.44
1:L:222:ARG:HA	1:L:274:PRO:HD3	1.98	0.44
1:N:158:GLN:CB	1:O:48:MET:CE	2.94	0.44
2:S:8:DG:O6	3:T:14:DC:N4	2.37	0.44
1:I:67:TYR:CZ	1:I:76:LEU:CD2	2.96	0.44
3:T:20:DG:C8	3:T:20:DG:O5'	2.70	0.44
1:E:78:TRP:N	1:E:87:TYR:O	2.43	0.44
1:H:60:ILE:CB	1:H:208:GLN:OE1	2.65	0.44
1:I:240:PRO:HG3	1:P:223:PHE:CD2	2.53	0.44
1:K:195:THR:HB	1:K:200:ILE:HD11	1.99	0.44
1:K:208:GLN:HA	1:K:211:GLN:CG	2.47	0.44
1:A:17:GLN:N	1:A:17:GLN:OE1	2.51	0.44
1:C:65:VAL:HG23	1:C:78:TRP:CZ3	2.42	0.44
1:A:237:TRP:HB2	1:H:275:PRO:HG2	1.99	0.44
1:I:1:TRP:CD1	1:I:29:PRO:CD	2.97	0.44
1:I:223:PHE:CE1	1:I:242:GLN:CD	2.85	0.44
1:A:175:GLU:HA	1:A:178:LEU:HB3	1.99	0.44
1:A:14:LYS:CG	1:J:134:TYR:CD1	3.01	0.44
1:I:252:VAL:HG11	1:L:245:TRP:CZ3	2.53	0.44
1:M:206:GLU:OE2	1:M:209:ARG:NH2	2.50	0.44
1:A:204:ASN:HA	1:D:222:ARG:NH1	2.33	0.44
1:K:208:GLN:HA	1:K:211:GLN:OE1	2.17	0.44
1:P:74:ILE:O	1:P:91:VAL:N	2.47	0.44
2:S:6:DG:H2''	2:S:7:DA:N7	2.33	0.44
1:C:270:LYS:HD2	1:H:145:TRP:CE3	2.46	0.43
1:A:25:GLU:CA	1:J:217:LYS:CE	2.69	0.43
1:L:229:ARG:HA	1:L:233:HIS:O	2.18	0.43
1:N:23:HIS:O	1:N:27:GLY:N	2.50	0.43
1:A:231:ARG:NE	2:Q:19:DG:O3'	2.50	0.43
4:V:19:DT:H2'	4:V:20:DG:C8	2.54	0.43
1:I:237:TRP:HB2	1:P:275:PRO:HG2	1.53	0.43
4:U:5:DA:H2'	4:U:6:DA:C8	2.53	0.43
1:A:10:GLU:O	1:A:14:LYS:N	2.47	0.43
1:A:68:THR:CB	1:A:157:HIS:HD2	2.27	0.43
1:B:18:ASP:O	1:B:21:SER:N	2.52	0.43
1:D:232:GLY:HA2	2:Q:11:DC:C4'	2.31	0.43
1:L:220:LYS:HG2	1:L:222:ARG:HG3	1.86	0.43
1:N:61:ASP:CB	1:N:113:LYS:H	2.31	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:223:PHE:O	1:N:272:ILE:N	2.51	0.43
1:O:208:GLN:O	1:O:212:GLN:CB	2.60	0.43
1:I:119:ASN:H	4:V:19:DT:H4'	1.83	0.43
1:B:195:THR:HB	1:B:200:ILE:HD11	2.00	0.43
1:E:261:TYR:HB2	1:H:263:VAL:HG21	1.99	0.43
1:I:50:SER:HB2	2:S:8:DG:H21	1.82	0.43
1:N:208:GLN:O	1:N:211:GLN:HB2	2.18	0.43
1:A:155:ARG:NH1	2:S:7:DA:C4'	2.74	0.43
1:A:204:ASN:HA	1:D:222:ARG:HH12	1.83	0.43
1:A:239:GLY:HA2	1:A:240:PRO:HD3	1.77	0.43
1:B:185:LEU:O	1:B:189:ARG:NH2	2.52	0.43
1:D:64:GLN:N	1:D:79:VAL:O	2.49	0.43
1:C:270:LYS:HG2	1:H:145:TRP:CZ2	2.54	0.43
1:H:79:VAL:HG22	1:H:156:THR:HG21	1.99	0.43
1:I:146:ASN:C	1:I:148:GLN:H	2.21	0.43
1:I:49:PRO:HB3	1:N:269:VAL:O	2.18	0.43
1:I:158:GLN:OE1	3:R:17:DG:N3	2.40	0.43
1:D:119:ASN:OD1	1:D:142:GLY:N	2.52	0.43
1:A:160:LEU:O	1:A:163:THR:OG1	2.20	0.43
1:F:188:LYS:NZ	1:G:11:GLU:OE2	2.43	0.43
1:J:68:THR:N	1:J:75:ILE:O	2.48	0.43
1:N:266:ASN:OD1	1:N:267:LYS:N	2.46	0.43
1:O:211:GLN:O	1:O:215:LYS:N	2.51	0.43
4:V:9:DT:H2'	4:V:10:DT:H71	2.01	0.43
1:A:143:ILE:HG23	2:S:3:DT:P	2.59	0.43
1:A:79:VAL:HA	1:A:86:ILE:HG22	2.01	0.43
1:D:262:LEU:HB2	1:D:264:ILE:HD11	2.00	0.43
1:I:231:ARG:HH22	2:S:20:DT:C5'	2.13	0.43
1:I:67:TYR:CZ	1:I:76:LEU:HD13	2.54	0.43
1:J:253:VAL:O	1:J:262:LEU:N	2.47	0.43
1:N:12:HIS:HB2	1:N:22:LEU:HD11	2.01	0.43
1:P:146:ASN:HA	1:P:147:PRO:HD3	1.85	0.43
1:A:12:HIS:CE1	1:A:37:VAL:HG22	2.54	0.43
1:G:62:HIS:CG	1:G:114:SER:HG	2.29	0.43
1:G:209:ARG:NH2	1:H:203:PHE:CD1	2.86	0.43
1:P:146:ASN:O	1:P:150:GLN:HG2	2.18	0.43
1:E:31:THR:HG23	3:R:7:DA:H4'	2.01	0.43
1:B:68:THR:OG1	1:B:161:LYS:NZ	2.39	0.43
1:C:30:ARG:O	1:C:33:ALA:HB3	2.19	0.43
1:F:149:SER:OG	1:F:150:GLN:N	2.52	0.43
1:I:237:TRP:CE2	1:I:270:LYS:HB2	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:224:CYS:CB	1:L:271:PHE:CA	2.68	0.43
1:P:146:ASN:O	1:P:150:GLN:CG	2.67	0.43
1:I:143:ILE:HG12	2:Q:3:DT:OP1	2.19	0.43
4:U:5:DA:H8	4:U:5:DA:HO5'	1.66	0.43
1:A:225:TYR:CG	1:A:239:GLY:O	2.71	0.42
1:A:51:THR:O	3:R:15:DT:H5'	2.19	0.42
1:K:269:VAL:HG11	1:K:271:PHE:CE1	2.54	0.42
1:D:232:GLY:HA3	2:Q:11:DC:H4'	1.96	0.42
1:I:212:GLN:HB2	1:L:217:LYS:HE3	1.34	0.42
1:M:103:THR:HA	1:M:106:TRP:HB3	2.02	0.42
1:M:24:LEU:HD13	1:M:194:GLY:HA2	2.00	0.42
2:S:6:DG:H2''	2:S:7:DA:H8	1.77	0.42
1:A:50:SER:O	1:A:50:SER:OG	2.35	0.42
1:E:171:PHE:CB	1:E:177:ALA:HB2	2.50	0.42
1:M:220:LYS:NZ	1:O:209:ARG:HH21	2.17	0.42
1:M:28:ILE:HD11	1:M:33:ALA:HB2	2.01	0.42
1:I:160:LEU:O	1:I:163:THR:OG1	2.20	0.42
1:L:252:VAL:HA	1:L:262:LEU:O	2.20	0.42
1:I:57:LYS:N	1:L:267:LYS:O	2.43	0.42
2:S:12:DC:C2	2:S:13:DG:N7	2.87	0.42
1:B:6:PRO:HG3	1:B:252:VAL:HG13	2.01	0.42
1:C:115:LEU:HD23	1:C:139:HIS:CD2	2.55	0.42
1:F:17:GLN:HE21	1:G:188:LYS:CB	2.32	0.42
1:H:146:ASN:HA	1:H:147:PRO:HD3	1.82	0.42
1:I:111:ALA:HB3	1:I:205:LYS:HZ1	1.84	0.42
1:I:12:HIS:CE1	1:I:37:VAL:HG22	2.54	0.42
1:I:62:HIS:CD2	1:I:81:THR:HG21	2.55	0.42
4:U:6:DA:H2'	4:U:7:DA:C8	2.55	0.42
1:I:119:ASN:N	4:V:19:DT:H4'	2.34	0.42
1:C:184:THR:O	1:C:189:ARG:N	2.44	0.42
1:F:274:PRO:HD2	1:F:275:PRO:CD	2.49	0.42
1:E:222:ARG:NH1	1:H:203:PHE:CZ	2.49	0.42
1:J:173:ALA:O	1:J:176:SER:OG	2.33	0.42
1:J:200:ILE:HD12	1:K:192:GLY:HA2	2.01	0.42
1:K:270:LYS:HG2	1:P:145:TRP:CH2	2.50	0.42
3:R:40:DT:C2'	3:R:43:DT:P	3.04	0.42
1:A:223:PHE:CD1	1:A:242:GLN:CG	2.79	0.42
1:A:255:ASP:OD1	1:A:257:GLY:N	2.47	0.42
1:A:212:GLN:HB3	1:D:217:LYS:HG3	1.96	0.42
1:H:106:TRP:O	1:H:110:PHE:N	2.53	0.42
1:K:203:PHE:CZ	1:K:207:GLN:HG3	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:106:TRP:HH2	1:N:112:PRO:HB3	1.84	0.42
1:M:222:ARG:CD	1:P:203:PHE:CE1	3.02	0.42
1:A:204:ASN:C	1:A:208:GLN:HG3	2.37	0.42
1:E:31:THR:HG23	3:R:7:DA:C3'	2.45	0.42
1:J:33:ALA:HA	1:J:36:ILE:HD12	2.01	0.42
1:N:209:ARG:O	1:N:212:GLN:HB2	2.19	0.42
1:C:23:HIS:NE2	1:C:207:GLN:OE1	2.35	0.42
1:F:229:ARG:NH1	1:F:232:GLY:O	2.46	0.42
1:H:93:GLY:N	1:H:98:GLU:OE1	2.53	0.42
1:N:61:ASP:HB3	1:N:113:LYS:H	1.84	0.42
1:D:226:TYR:HA	1:D:268:ASP:O	2.19	0.41
1:I:146:ASN:C	1:I:148:GLN:N	2.73	0.41
1:I:66:ASP:OD1	1:I:67:TYR:N	2.51	0.41
1:J:62:HIS:CG	1:J:114:SER:HG	2.38	0.41
1:L:65:VAL:HG23	1:L:115:LEU:HD11	2.01	0.41
1:M:17:GLN:HE21	1:M:188:LYS:HB3	1.85	0.41
1:B:226:TYR:O	1:B:238:GLN:N	2.48	0.41
1:C:263:VAL:O	1:C:264:ILE:HD13	2.20	0.41
1:K:206:GLU:HB2	1:L:202:ILE:HG22	2.01	0.41
1:O:162:ASN:O	1:O:165:GLU:N	2.53	0.41
1:A:119:ASN:HB2	4:U:19:DT:H4'	1.98	0.41
1:A:44:GLN:O	1:A:47:LYS:HG2	2.19	0.41
1:B:207:GLN:O	1:B:211:GLN:HG2	2.21	0.41
1:F:12:HIS:HB2	1:F:22:LEU:HD11	2.01	0.41
1:I:225:TYR:CD2	1:I:239:GLY:O	2.73	0.41
1:I:52:LEU:CD1	3:T:14:DC:C4'	2.85	0.41
1:A:233:HIS:CD2	2:Q:20:DT:O3'	2.68	0.41
1:A:155:ARG:CZ	2:S:7:DA:O4'	2.67	0.41
1:M:30:ARG:CD	3:T:7:DA:H4'	2.42	0.41
4:U:19:DT:H2'	4:U:20:DG:C8	2.54	0.41
1:F:115:LEU:N	1:F:138:GLU:O	2.53	0.41
1:I:61:ASP:OD2	1:I:111:ALA:O	2.38	0.41
1:I:79:VAL:HA	1:I:86:ILE:HG22	2.01	0.41
1:M:78:TRP:CZ3	1:M:115:LEU:HD13	2.55	0.41
1:M:119:ASN:OD1	1:M:142:GLY:N	2.53	0.41
1:M:217:LYS:HZ1	1:P:209:ARG:HE	1.68	0.41
1:A:225:TYR:HD1	1:A:270:LYS:HB3	1.84	0.41
1:C:121:PRO:O	1:C:125:ALA:N	2.51	0.41
1:C:209:ARG:O	1:C:212:GLN:HB2	2.21	0.41
1:I:50:SER:O	1:I:50:SER:OG	2.35	0.41
1:I:79:VAL:HG13	1:I:86:ILE:CG2	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:60:ILE:HG21	1:J:208:GLN:OE1	2.21	0.41
1:K:226:TYR:O	1:K:238:GLN:N	2.44	0.41
1:K:65:VAL:HG21	1:K:78:TRP:CZ2	2.55	0.41
1:L:247:GLY:H	1:L:251:ILE:CG2	2.31	0.41
1:A:62:HIS:CD2	1:A:81:THR:HG21	2.55	0.41
1:B:16:HIS:CE1	1:B:42:VAL:HG21	2.56	0.41
1:B:175:GLU:OE1	1:B:175:GLU:N	2.52	0.41
1:C:183:ILE:HG13	1:D:108:ALA:HB2	2.02	0.41
1:D:184:THR:O	1:D:189:ARG:N	2.52	0.41
1:F:211:GLN:O	1:F:214:SER:OG	2.35	0.41
1:A:183:ILE:HD13	1:I:15:TRP:CH2	2.56	0.41
1:K:224:CYS:N	1:K:241:THR:O	2.50	0.41
1:N:159:THR:CA	1:O:48:MET:CE	2.98	0.41
1:A:12:HIS:CE1	1:A:43:CYS:HG	2.39	0.41
1:A:154:GLU:OE1	3:T:18:DC:C2'	2.57	0.41
1:A:210:ILE:H	1:A:210:ILE:HG13	1.52	0.41
1:A:79:VAL:HG13	1:A:86:ILE:CG2	2.51	0.41
1:D:272:ILE:HG22	1:D:273:PRO:O	2.21	0.41
1:G:115:LEU:N	1:G:138:GLU:O	2.52	0.41
1:G:208:GLN:O	1:G:212:GLN:HB2	2.20	0.41
1:G:65:VAL:CG2	1:G:78:TRP:CE2	2.97	0.41
1:J:190:LYS:N	1:K:21:SER:OG	2.48	0.41
1:A:209:ARG:HB3	1:A:212:GLN:HE22	1.86	0.41
1:H:185:LEU:O	1:H:189:ARG:NE	2.54	0.41
1:I:215:LYS:NZ	1:L:210:ILE:HG12	2.36	0.41
1:M:23:HIS:ND1	1:M:28:ILE:O	2.53	0.41
1:I:94:GLU:CA	3:T:28:DC:H5''	2.50	0.41
1:A:161:LYS:HA	1:A:164:LEU:HD12	2.03	0.41
1:A:212:GLN:HB2	1:D:217:LYS:HZ3	1.83	0.41
1:E:171:PHE:HB2	1:E:177:ALA:HB2	2.03	0.41
1:G:211:GLN:O	1:G:215:LYS:N	2.53	0.41
1:G:61:ASP:OD2	1:G:205:LYS:NZ	2.54	0.41
1:I:10:GLU:O	1:I:14:LYS:N	2.47	0.41
1:J:68:THR:O	1:J:75:ILE:N	2.50	0.41
1:J:64:GLN:N	1:J:79:VAL:O	2.48	0.41
1:A:54:GLY:N	2:S:3:DT:H1'	2.34	0.41
1:B:103:THR:HA	1:B:106:TRP:HB3	2.02	0.41
1:E:160:LEU:O	1:E:163:THR:N	2.54	0.41
1:F:255:ASP:O	1:F:259:ASP:N	2.54	0.41
1:J:245:TRP:O	1:J:252:VAL:N	2.54	0.41
1:L:231:ARG:CB	3:T:13:DT:C1'	2.94	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:T:33:DA:H61	4:V:13:DT:H3	1.69	0.41
1:B:80:GLU:OE1	1:B:82:ASN:N	2.52	0.41
1:D:87:TYR:OH	1:D:89:GLU:OE1	2.39	0.41
1:M:209:ARG:HH12	1:O:193:LEU:HD13	1.86	0.41
1:A:175:GLU:OE1	1:A:175:GLU:N	2.54	0.40
1:G:30:ARG:HH22	1:G:207:GLN:HB3	1.86	0.40
1:H:105:LYS:O	1:H:108:ALA:HB3	2.21	0.40
1:I:69:HIS:HB2	3:R:21:DT:P	2.59	0.40
1:J:91:VAL:HG12	1:J:93:GLY:N	2.35	0.40
1:K:65:VAL:HG21	1:K:78:TRP:CH2	2.55	0.40
1:L:246:GLY:HA2	1:L:251:ILE:HG21	2.03	0.40
1:O:30:ARG:NH2	1:O:207:GLN:HB3	2.34	0.40
1:C:64:GLN:O	1:C:79:VAL:N	2.52	0.40
1:E:103:THR:HA	1:E:106:TRP:HB3	2.02	0.40
1:I:225:TYR:CD1	1:I:272:ILE:HD11	2.56	0.40
1:I:52:LEU:HD11	3:T:14:DC:H4'	1.93	0.40
1:F:191:GLY:O	1:F:195:THR:OG1	2.34	0.40
1:H:60:ILE:HG12	1:H:204:ASN:HB3	2.03	0.40
1:N:181:THR:O	1:N:184:THR:OG1	2.33	0.40
1:C:13:ASN:O	1:C:16:HIS:NE2	2.55	0.40
1:E:74:ILE:O	1:E:91:VAL:N	2.51	0.40
1:E:222:ARG:NE	1:H:203:PHE:CE2	2.90	0.40
1:J:160:LEU:O	1:J:163:THR:N	2.55	0.40
1:L:223:PHE:HB3	1:L:242:GLN:CA	2.49	0.40
1:P:64:GLN:NE2	1:P:150:GLN:OE1	2.53	0.40
1:P:265:ALA:O	1:P:268:ASP:N	2.54	0.40
1:I:94:GLU:CB	3:T:28:DC:C5'	2.87	0.40
4:V:7:DA:H2''	4:V:8:DC:O5'	2.22	0.40
1:A:154:GLU:HB3	3:T:18:DC:H2''	2.03	0.40
1:C:76:LEU:HB2	1:C:91:VAL:HG21	2.04	0.40
1:D:255:ASP:N	1:D:260:ARG:O	2.44	0.40
1:A:51:THR:HB	1:F:266:ASN:HD22	1.87	0.40
1:I:119:ASN:OD1	1:I:142:GLY:O	2.39	0.40
1:N:255:ASP:O	1:N:259:ASP:N	2.54	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	270/281 (96%)	253 (94%)	16 (6%)	1 (0%)	36	77
1	B	252/281 (90%)	242 (96%)	8 (3%)	2 (1%)	21	65
1	C	257/281 (92%)	249 (97%)	8 (3%)	0	100	100
1	D	214/281 (76%)	203 (95%)	8 (4%)	3 (1%)	12	52
1	E	253/281 (90%)	244 (96%)	8 (3%)	1 (0%)	36	77
1	F	262/281 (93%)	248 (95%)	12 (5%)	2 (1%)	21	65
1	G	201/281 (72%)	197 (98%)	4 (2%)	0	100	100
1	H	215/281 (76%)	211 (98%)	4 (2%)	0	100	100
1	I	274/281 (98%)	255 (93%)	18 (7%)	1 (0%)	36	77
1	J	252/281 (90%)	237 (94%)	15 (6%)	0	100	100
1	K	257/281 (92%)	253 (98%)	4 (2%)	0	100	100
1	L	214/281 (76%)	203 (95%)	9 (4%)	2 (1%)	19	61
1	M	253/281 (90%)	244 (96%)	9 (4%)	0	100	100
1	N	262/281 (93%)	252 (96%)	9 (3%)	1 (0%)	36	77
1	O	201/281 (72%)	194 (96%)	7 (4%)	0	100	100
1	P	215/281 (76%)	209 (97%)	6 (3%)	0	100	100
All	All	3852/4496 (86%)	3694 (96%)	145 (4%)	13 (0%)	47	81

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	231	ARG
1	D	233	HIS
1	I	240	PRO
1	L	233	HIS
1	D	234	PRO
1	N	112	PRO

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Mol	Chain	Res	Type
1	A	240	PRO
1	F	14	LYS
1	B	20	VAL
1	E	221	ILE
1	L	274	PRO
1	B	221	ILE
1	F	60	ILE

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	237/246 (96%)	236 (100%)	1 (0%)	92	95
1	B	223/246 (91%)	223 (100%)	0	100	100
1	C	228/246 (93%)	228 (100%)	0	100	100
1	D	183/246 (74%)	183 (100%)	0	100	100
1	E	224/246 (91%)	224 (100%)	0	100	100
1	F	228/246 (93%)	228 (100%)	0	100	100
1	G	181/246 (74%)	181 (100%)	0	100	100
1	H	189/246 (77%)	189 (100%)	0	100	100
1	I	237/246 (96%)	237 (100%)	0	100	100
1	J	223/246 (91%)	223 (100%)	0	100	100
1	K	228/246 (93%)	228 (100%)	0	100	100
1	L	183/246 (74%)	183 (100%)	0	100	100
1	M	224/246 (91%)	224 (100%)	0	100	100
1	N	228/246 (93%)	228 (100%)	0	100	100
1	O	181/246 (74%)	181 (100%)	0	100	100
1	P	189/246 (77%)	189 (100%)	0	100	100
All	All	3386/3936 (86%)	3385 (100%)	1 (0%)	100	100

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	212	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	3
1	I	2
1	L	1
3	R	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	44:GLN	C	45:GLU	N	2.19

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	224:CYS	C	225:TYR	N	2.02
1	L	221:ILE	C	222:ARG	N	1.67
1	A	239:GLY	C	240:PRO	N	1.65
1	I	238:GLN	C	239:GLY	N	1.65
1	R	40:DT	O3'	43:DT	P	1.15
1	I	142:GLY	C	143:ILE	N	1.11