



# Full wwPDB/EMDatabank EM Map/Model Validation Report ⓘ

Jan 17, 2017 – 07:17 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](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/EMValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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MolProbity : 4.02b-467  
Mogul : unknown  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20028442

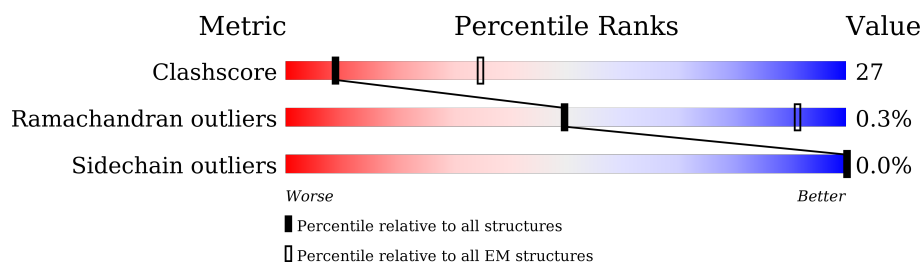
# 1 Overall quality at a glance

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	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686

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  $\geq 3$ , 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	51% 44% . .
1	B	281	68% 22% 9%
1	C	281	70% 23% 7%
1	D	281	58% 16% .. 23%
1	E	281	72% 19% 9%
1	F	281	72% 23% 5%
1	G	281	58% 15% 27%
1	H	281	60% 17% 23%
1	I	281	47% 47% . . .

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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		

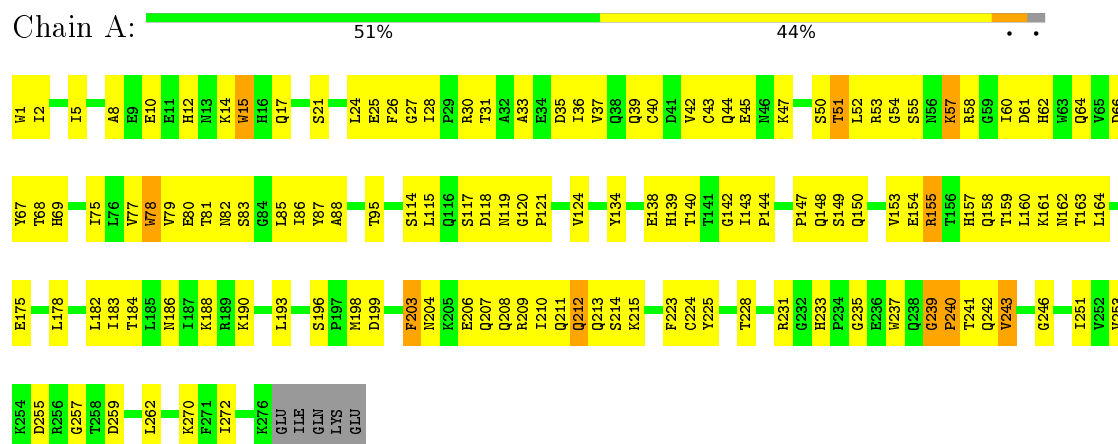
- Molecule 4 is a DNA chain called tDNA.

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		

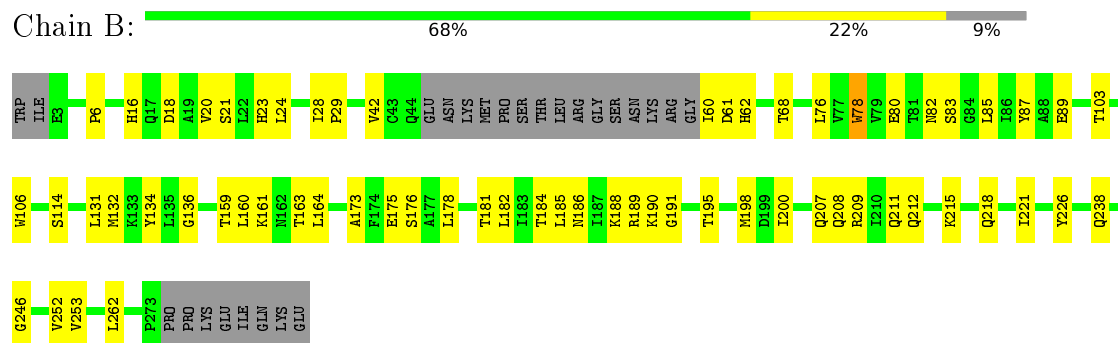
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

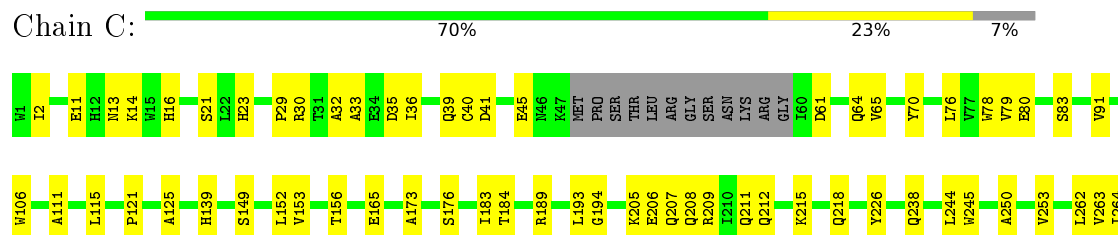
- Molecule 1: integrase

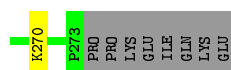


- Molecule 1: integrase



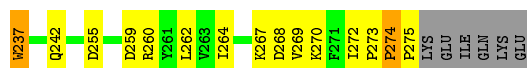
- Molecule 1: integrase





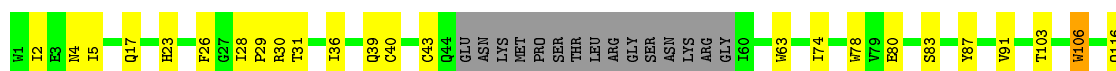
- Molecule 1: integrase

Chain D: 58% 16% 23%



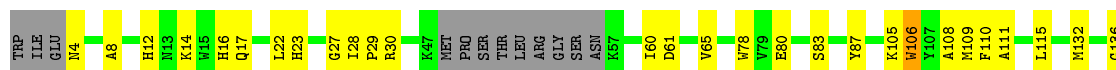
- Molecule 1: integrase

Chain E: 72% 19% 9%



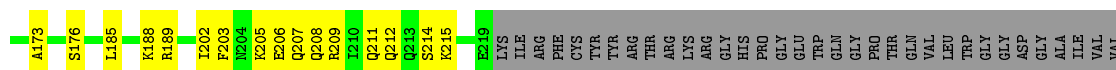
- Molecule 1: integrase

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  
LEU  
ILE  
GLN  
GLU

- Molecule 1: integrase

Chain H:  60% 17% 23%

TRP  
ILE  
GLU  
ASN  
ILE  
PRO  
LEU  
ALA  
GLU  
GLU  
GLU  
HIS  
ASN  
LYS  
TRP  
HIS  
GLN  
ASP  
PHE  
ILE  
VAL  
SER  
LEU  
HIS  
LEU  
PHE  
GLU  
GLN  
GLU  
ILE  
GLY  
ILE  
PRO  
ARG  
THR  
ALA  
ALA  
GLU  
ASP  
ILE  
VAL  
Q148  
Q147  
P147  
Q148  
S149  
Q150  
A151  
L152  
VAL  
CYS  
GLN  
GLU  
ASN  
LYS  
MET  
PRO  
SER  
THR  
LEU  
ARG  
GLY  
SER  
ASN  
LYS  
ARG  
GLY  
I60

Q64  
T68  
I75  
V79  
E90  
S83  
E89  
G93  
E98  
K105  
W106  
Y107  
A108  
M109  
F110  
L115  
M119  
T140  
T141  
G142  
W145  
M146  
P147  
Q148  
S149  
Q150  
A151  
L152  
T156  
L164  
A173  
S176  
A177  
L178  
T181  
T184  
L185  
R189  
I202

F203  
R204  
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% . . .

W1  
I2  
I5  
A8  
E9  
E10  
E11  
H12  
H13  
H16  
K14  
W15  
H16  
Q17  
S21  
F26  
G27  
I28  
P29  
R30  
A33  
I36  
V37  
Q38  
Q39  
C40  
P41  
V42  
C43  
K47  
W48  
P49  
S50  
T51  
L52  
R53  
G54  
S55  
R56  
K57  
R58  
D61  
H62  
W63  
Q64  
V65  
D66  
Y67  
T68  
H69  
I74  
I75

L76  
V77  
W78  
V79  
T80  
H82  
S83  
G84  
L85  
H86  
Y87  
A88  
E94  
T95  
F99  
A108  
A111  
P112  
K113  
S114  
L115  
Q116  
S117  
D118  
N119  
G120  
P121  
A122  
F123  
V124  
A125  
E126  
E138  
H139  
T140  
L141  
G142  
I143  
P144  
W145  
N146  
P147  
Q148  
S149  
Q150  
V153  
D154  
R155  
T156  
H157  
Q158  
T159  
L160

K161  
M162  
T163  
E175  
L178  
L182  
L183  
D185  
H186  
G187  
H188  
K188  
K189  
K190  
L193  
S196  
P197  
M198  
D199  
F203  
R204  
K205  
E206  
Q207  
Q208  
R209  
Q212  
Q213  
S214  
K215  
S216  
K217  
I221  
R222  
F223  
C224  
Y226  
R227  
T228  
R231  
G232  
H233  
P234  
G235  
E236  
K237  
Q238  
G239  
P240  
T241

Q242  
V243  
G246  
I251  
V252  
V253  
R254  
D255  
G257  
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  
SER  
SER  
THR  
ARG  
GLY  
SER  
ASN  
LYS  
ARG  
GLY  
I60  
D61  
H62  
Q64  
T68  
H69  
I75  
W78  
V79  
E80  
S83  
G84  
L85  
I86  
Y87  
A88  
E89  
R90  
V91  
K92  
G93  
M104  
K105

W106  
T107  
A108  
S114  
L115  
Y134  
L135  
E138  
T159  
L160  
K161  
T163  
A173  
S176  
A177  
L178  
A179  
G180  
T181  
T184  
I187  
K190  
T195  
M198  
D199  
I200  
Q208  
R209  
I210  
Q211  
Q212  
R215  
S216  
K217  
Q218  
R222  
W245  
G246  
G247  
A250  
I251  
V252  
V253

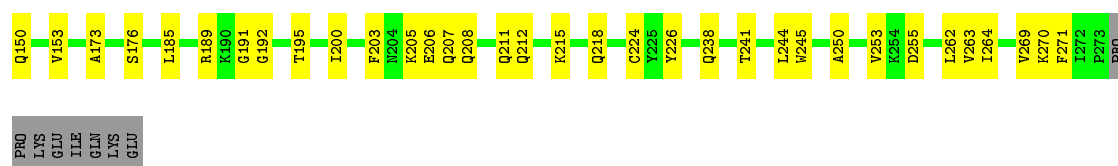
L262  
P273  
PRO  
PRO  
LYS  
GLU  
ILE  
GLN  
LYS  
GLU

- Molecule 1: integrase

Chain K:  71% 22% 7%

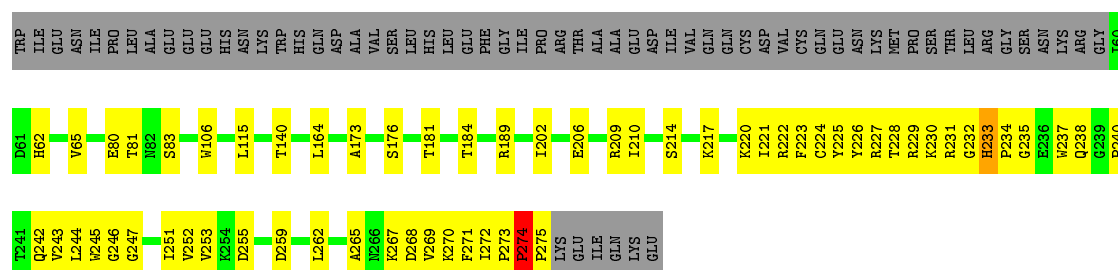
W1  
I2  
E3  
M4  
I5  
P6  
L7  
A8  
E9  
S21  
L22  
H23  
F26  
G27  
I28  
P29  
R30  
T31  
A32  
I36  
C40  
K47  
MET  
PRO  
SER  
SER  
THR  
LEU  
ARG  
GLY  
ASN  
LYS  
ARG  
GLY  
I60  
D61  
H62  
W63  
Q64  
V65  
W78  
V79  
E80  
S83  
W106  
S114  
L115  
T140  
S149





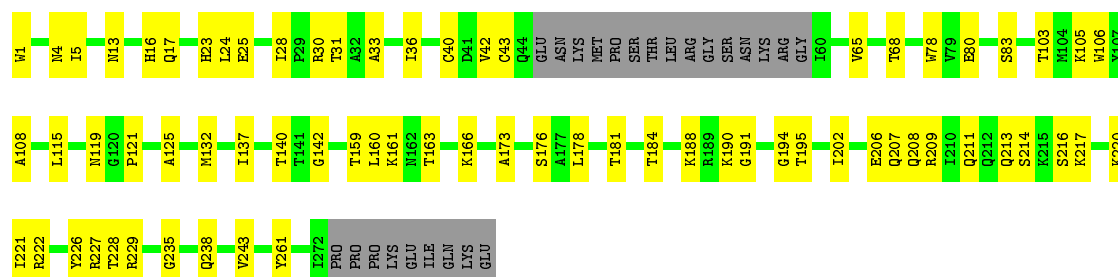
- Molecule 1: integrase

Chain L: 55% 21% 23%



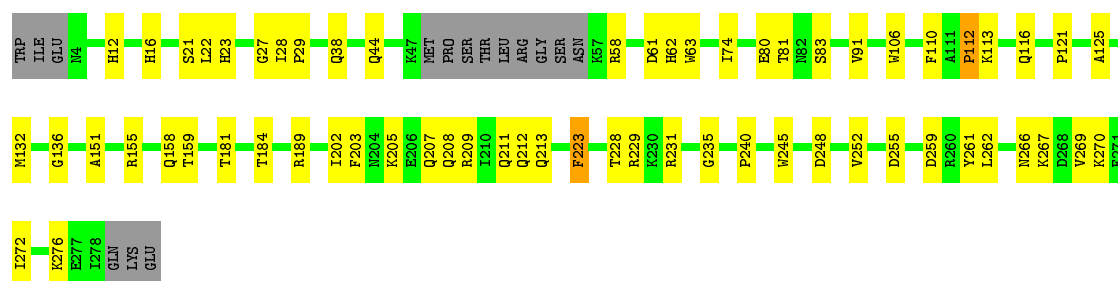
- Molecule 1: integrase

Chain M: 67% 25% 9%



- Molecule 1: integrase

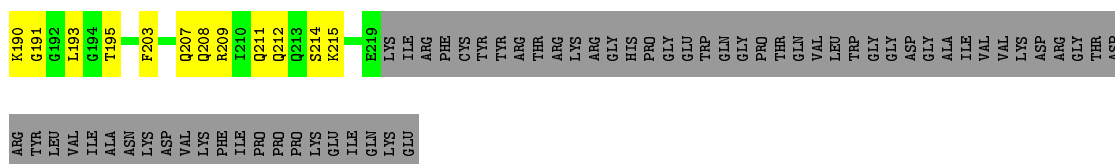
Chain N: 72% 22% 5%



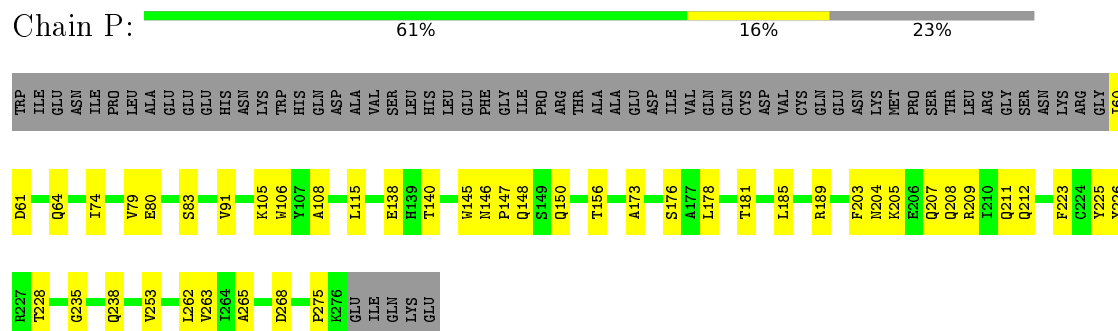
- Molecule 1: integrase

Chain O: 60% 13% 27%

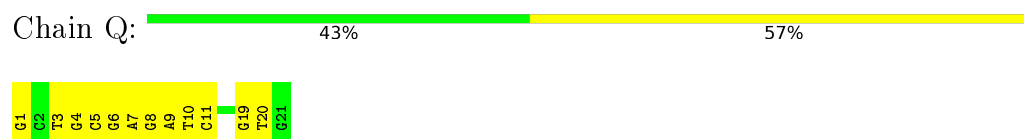




- Molecule 1: integrase



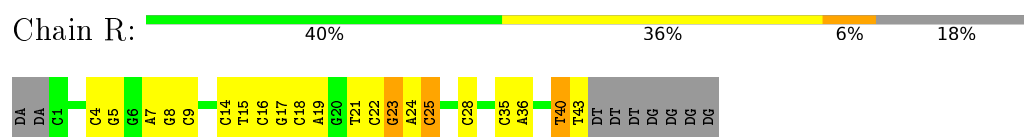
- Molecule 2: vDNA, non-transferred strand



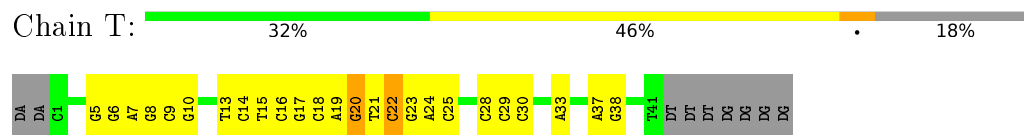
- Molecule 2: vDNA, non-transferred strand



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

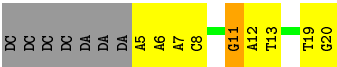


- Molecule 3: vDNA-tDNA, transferred strand, joined to a model tDNA

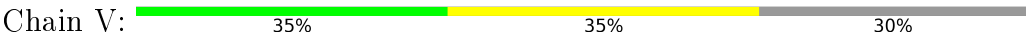


- Molecule 4: tDNA





● Molecule 4: tDNA



## 4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	37021	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Not provided	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	Not provided	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	Depositor
Image detector	Not provided	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:125:ALA:HA	3:T:30:DC:OP1	1.24	1.27

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:203:PHE:CE1	1:I:207:GLN:NE2	2.02	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:154:GLU:HB3	3:R:18:DC:C1'	1.72	1.20

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:223:PHE:CD1	1:I:242:GLN:HG2	1.77	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:121:PRO:C	3:T:29:DC:H4'	1.24	1.19
1:I:95:THR:HA	3:T:28:DC:O3'	1.43	1.19
1:D:274:PRO:CB	1:D:275:PRO:HD3	1.59	1.18
1:I:119:ASN:CB	4:V:19:DT:H4'	1.71	1.18
1:I:69:HIS:O	3:R:21:DT:OP1	1.57	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:F:159:THR:OG1	1:G:48:MET:SD	2.00	1.16
1:G:29:PRO:CG	1:G:211:GLN:CD	2.12	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:231:ARG:HH22	2:S:20:DT:P	1.71	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: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:I:145:TRP:HB2	1:N:229:ARG:HD2	1.13	1.06
1:L:224:CYS:HB3	1:L:271:PHE:HA	1.11	1.06
1:A:14:LYS:CB	1:J:134:TYR:HE1	1.64	1.06
1:A:50:SER:HB2	2:Q:8:DG:H21	1.15	1.06
1:I:146:ASN:OD1	1:I:149:SER:OG	1.72	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:A:147:PRO:HG2	3:T:19:DA:C2	1.82	1.06

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:154:GLU:CB	3:R:18:DC:H2''	1.86	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: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:47:LYS:CG	2:S:9:DA:OP1	2.05	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:94:GLU:HB2	3:T:28:DC:H4'	1.43	1.00
1:I:154:GLU:C	3:R:18:DC:C1'	2.29	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:67:TYR:CE2	1:I:123:PHE:CE1	2.50	1.00
1:I:125:ALA:CA	3:T:30:DC:OP1	2.09	1.00
1:I:237:TRP:CZ3	1:I:270:LYS:N	2.29	0.99
1:I:154:GLU:CB	3:R:18:DC:H1'	1.91	0.99
1:A:148:GLN:NE2	2:S:4:DG:C5	2.29	0.99
1:N:231:ARG:NH2	3:T:25:DC:N4	2.10	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:M:222:ARG:HD2	1:P:203:PHE:CZ	1.97	0.99
1:K:270:LYS:HD2	1:P:145:TRP:CG	1.96	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:D:232:GLY:CA	2:Q:11:DC:H4'	1.96	0.96
1:F:203:PHE:CZ	1:F:207:GLN:NE2	2.32	0.96
1:A:155:ARG:NH1	2:S:7:DA:H5'	1.81	0.96
1:L:220:LYS:NZ	1:L:222:ARG:HD3	1.80	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:225:TYR:HE1	1:A:272:ILE:CD1	1.79	0.95
1:E:31:THR:OG1	3:R:8:DG:C5'	2.14	0.95
1:A:95:THR:HG22	3:R:28:DC:C4'	1.97	0.95
1:A:147:PRO:HG2	3:T:19:DA:H2	1.19	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:A:155:ARG:HE	2:S:6:DG:H1'	0.80	0.94
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: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:D:231:ARG:O	2:Q:11:DC:H4'	1.66	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:A:225:TYR:HE1	1:A:272:ILE:HD11	1.28	0.94
1:I:52:LEU:CD1	3:T:14:DC:H4'	1.98	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:121:PRO:HG3	4:V:18:DG:N2	1.83	0.94
1:I:119:ASN:CB	4:V:19:DT:O5'	2.15	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:K:270:LYS:HG2	1:P:145:TRP:CZ2	2.04	0.92
1:N:29:PRO:CB	1:N:211:GLN:OE1	2.18	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:203:PHE:HZ	1:D:222:ARG:CG	1.83	0.91
1:A:225:TYR:CD2	1:A:239:GLY:O	2.23	0.91
1:A:55:SER:OG	2:S:5:DC:H5'	1.70	0.91
1:G:29:PRO:HG3	1:G:211:GLN:NE2	1.82	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:L:220:LYS:HE2	1:L:222:ARG:HG2	0.93	0.91
1:I:94:GLU:HB2	3:T:28:DC:C4'	2.01	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:B:23:HIS:NE2	1:B:207:GLN:OE1	2.04	0.90
1:A:69:HIS:ND1	3:T:20:DG:O4'	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:G:65:VAL:CG2	1:G:78:TRP:CZ3	2.56	0.89
1:E:222:ARG:NH1	1:H:207:GLN:CG	2.34	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:E:31:THR:OG1	3:R:8:DG:P	2.31	0.88
1:A:14:LYS:HE3	1:J:134:TYR:CD1	1.90	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:I:121:PRO:CD	4:V:18:DG:N2	2.36	0.88
1:A:14:LYS:HZ3	1:J:134:TYR:CA	1.73	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:I:225:TYR:CB	1:I:237:TRP:CB	2.40	0.87
1:A:119:ASN:CB	4:U:19:DT:H4'	2.03	0.87
1:E:222:ARG:CZ	1:H:207:GLN:HG3	2.04	0.87
1:A:207:GLN:CB	1:D:222:ARG:NH2	2.33	0.87
1:A:225:TYR:CE2	1:A:240:PRO:HD3	2.10	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:155:ARG:NE	2:S:6:DG:C1'	2.23	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
2:S:6:DG:N2	3:T:16:DC:O2	2.07	0.86
1:A:69:HIS:HB2	3:T:21:DT:OP1	1.74	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:I:212:GLN:HB3	1:L:217:LYS:HZ1	1.14	0.85
1:L:220:LYS:HE2	1:L:222:ARG:HD3	1.53	0.85
1:I:69:HIS:HB2	3:R:21:DT:OP1	1.75	0.85
1:E:31:THR:OG1	3:R:8:DG:H5''	1.75	0.85
1:I:52:LEU:HA	3:T:15:DT:H5''	1.56	0.85
1:A:155:ARG:NH2	2:S:7:DA:O4'	2.08	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: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:A:149:SER:OG	2:S:3:DT:P	2.35	0.84
1:A:24:LEU:O	1:J:217:LYS:CB	2.25	0.84
1:C:65:VAL:HG21	1:C:78:TRP:CE2	2.12	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:121:PRO:CG	4:V:18:DG:H22	1.90	0.82
1:I:118:ASP:OD2	4:V:20:DG:C5'	2.26	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:I:155:ARG:HD3	3:R:17:DG:N2	1.94	0.82
1:A:24:LEU:C	1:J:217:LYS:HG2	2.00	0.82
1:L:223:PHE:HE2	1:L:240:PRO:CB	1.91	0.82
1:A:155:ARG:HG2	2:S:6:DG:C4'	2.09	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:223:PHE:CD1	1:I:242:GLN:CG	2.53	0.80
1:I:1:TRP:HB2	1:I:28:ILE:HG22	1.63	0.80
1:N:23:HIS:HE1	1:N:211:GLN:NE2	1.80	0.80
1:A:52:LEU:CD1	1:D:233:HIS:CB	2.60	0.80
1:A:54:GLY:HA3	2:S:3:DT:O2	1.80	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:68:THR:CB	1:A:157:HIS:CD2	2.65	0.79
1:A:225:TYR:CE2	1:A:240:PRO:CD	2.66	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:I:154:GLU:CA	3:R:18:DC:H2''	2.12	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: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
1:A:155:ARG:HH12	2:S:7:DA:C4'	1.95	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:F:111:ALA:O	1:F:205:LYS:NZ	2.17	0.77
1:D:231:ARG:O	2:Q:11:DC:C1'	2.32	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: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:K:270:LYS:CD	1:P:145:TRP:CD2	2.37	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: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
1:A:50:SER:CB	2:Q:8:DG:N2	2.39	0.72
2:S:6:DG:H2''	2:S:7:DA:C8	2.24	0.72
1:I:52:LEU:HD11	1:L:232:GLY:N	2.04	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: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:J:208:GLN:O	1:J:212:GLN:HG3	1.90	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:95:THR:HA	3:T:28:DC:C3'	2.20	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:I:155:ARG:NH2	2:Q:6:DG:N3	2.38	0.70
1:A:25:GLU:HA	1:J:217:LYS:CG	2.20	0.70
1:K:208:GLN:O	1:K:212:GLN:HB2	1.90	0.70
1:P:226:TYR:O	1:P:238:GLN:N	2.25	0.70
1:P:61:ASP:OD2	1:P:205:LYS:NZ	2.22	0.70
1:N:203:PHE:CE1	1:N:207:GLN:NE2	2.59	0.70
1:A:24:LEU:O	1:J:217:LYS:HB3	1.92	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:I:240:PRO:HG2	1:P:223:PHE:HE2	1.56	0.70
1:I:212:GLN:HB2	1:L:217:LYS:HZ1	1.50	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:14:LYS:CA	1:J:134:TYR:HE1	2.05	0.69
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: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: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:A:21:SER:OG	1:I:190:LYS:HD2	1.94	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:67:TYR:CD1	1:I:76:LEU:HB2	2.28	0.68
1:I:52:LEU:HD11	1:L:232:GLY:CA	2.24	0.68
1:I:58:ARG:CB	1:I:62:HIS:HD2	2.07	0.68
1:I:61:ASP:O	1:I:63:TRP:NE1	2.27	0.68
1:L:242:GLN:HG2	1:L:244:LEU:HD23	1.77	0.67
1:I:196:SER:N	1:I:199:ASP:OD2	2.27	0.67
1:A:69:HIS:CB	3:T:21:DT:OP1	2.42	0.67
1:I:147:PRO:HB3	3:R:19:DA:H2''	1.77	0.67
1:N:245:TRP:CD1	2:Q:1:DG:O6	2.46	0.67
1:A:159:THR:CG2	2:S:7:DA:C5'	2.72	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:30:ARG:HH22	3:T:9:DC:H3'	1.60	0.67
1:I:52:LEU:HD13	1:L:232:GLY:O	1.94	0.67
1:I:212:GLN:NE2	1:L:214:SER:HA	2.09	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:A:155:ARG:NH2	2:S:6:DG:H1'	2.10	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: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: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:A:159:THR:CG2	2:S:7:DA:H5'	2.26	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:M:220:LYS:NZ	1:O:209:ARG:NH2	2.45	0.65
1:I:158:GLN:CG	3:R:18:DC:H5'	2.27	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: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
1:N:209:ARG:NH1	1:N:213:GLN:OE1	2.30	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:154:GLU:HB3	3:T:18:DC:C2'	2.27	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:154:GLU:HA	3:R:18:DC:H2''	1.77	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: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: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:120:GLY:HA2	4:U:19:DT:H2''	1.81	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:I:118:ASP:OD2	4:V:20:DG:C4'	2.48	0.62
1:L:223:PHE:O	1:L:272:ILE:HB	1.99	0.62
1:L:247:GLY:H	1:L:251:ILE:HG22	1.65	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: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:161:LYS:NZ	3:T:19:DA:OP1	2.33	0.61
1:A:35:ASP:HB3	1:E:2:ILE:HD12	1.80	0.61
1:A:203:PHE:CZ	1:D:222:ARG:CG	2.68	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:G:29:PRO:CG	1:G:211:GLN:NE2	2.56	0.60
1:D:267:LYS:CE	2:S:3:DT:N3	2.65	0.60
1:D:231:ARG:O	2:Q:11:DC:C3'	2.48	0.60
1:G:80:GLU:OE1	1:G:83:SER:N	2.34	0.60
1:C:270:LYS:NZ	1:H:145:TRP:CG	2.45	0.60
1:A:193:LEU:CD1	1:D:223:PHE:HZ	2.15	0.60
1:B:78:TRP:N	1:B:87:TYR:O	2.35	0.60
1:A:237:TRP:CB	1:H:275:PRO:HG2	2.32	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:A:25:GLU:HA	1:J:217:LYS:HG3	1.83	0.60
1:I:154:GLU:CA	3:R:18:DC:C1'	2.72	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:225:TYR:O	1:I:237:TRP:HZ3	1.85	0.59
1:I:212:GLN:HE22	1:L:214:SER:HA	1.68	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:37:VAL:HG13	1:A:43:CYS:HB2	1.84	0.59
1:A:237:TRP:CD1	1:H:275:PRO:HB2	2.38	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:N:158:GLN:HB2	1:O:48:MET:CE	2.29	0.58
1:O:30:ARG:HH22	1:O:207:GLN:HB3	1.67	0.58
1:I:55:SER:HB3	2:Q:4:DG:H4'	1.84	0.58
1:I:121:PRO:CD	4:V:18:DG:H22	2.07	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:66:ASP:H	1:I:153:VAL:HG21	1.67	0.58
1:I:37:VAL:HG13	1:I:43:CYS:HB2	1.84	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:193:LEU:HD11	1:D:223:PHE:HZ	1.69	0.58
1:A:62:HIS:HD1	1:A:114:SER:HG	1.48	0.58
1:F:4:ASN:O	1:F:8:ALA:N	2.35	0.58
1:I:94:GLU:H	3:T:28:DC:C5'	2.14	0.58
1:I:158:GLN:HA	3:R:18:DC:H5'	1.86	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:108:ALA:HB2	1:J:179:ALA:HB1	1.86	0.57
1:I:204:ASN:HA	1:I:207:GLN:HB2	1.85	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:210:ILE:HD12	1:A:211:GLN:HG3	1.86	0.57
1:A:134:TYR:O	1:C:14:LYS:NZ	2.38	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:I:52:LEU:CD2	3:T:14:DC:C4'	2.83	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: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:A:54:GLY:H	2:S:3:DT:H1'	1.71	0.56
1:I:149:SER:CB	2:Q:3:DT:P	2.93	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:I:158:GLN:CD	3:R:17:DG:N3	2.59	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:C:65:VAL:HG22	1:C:78:TRP:HA	1.87	0.56
1:A:52:LEU:HB2	1:D:233:HIS:CB	2.34	0.56
1:D:267:LYS:NZ	2:S:3:DT:O4	2.38	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: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:J:105:LYS:O	1:J:108:ALA:HB3	2.05	0.56
1:I:108:ALA:CB	1:J:179:ALA:HB1	2.35	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:222:ARG:O	1:M:243:VAL:HG23	2.06	0.55
1:M:227:ARG:NH2	1:P:148:GLN:O	2.40	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:A:121:PRO:HD3	4:U:19:DT:H1'	1.89	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: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:L:231:ARG:CB	3:T:13:DT:O3'	2.56	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: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:148:GLN:CD	3:R:19:DA:C2	2.82	0.53
1:I:50:SER:OG	2:S:9:DA:C4'	2.56	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:A:95:THR:HG23	3:R:28:DC:H5''	1.71	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:226:TYR:HB3	1:I:264:ILE:HG13	1.90	0.52
1:I:228:THR:O	1:I:235:GLY:N	2.42	0.52
1:I:223:PHE:HE1	1:I:242:GLN:NE2	2.07	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:D:220:LYS:HG3	1:D:222:ARG:HG3	1.90	0.52
1:A:25:GLU:CA	1:J:217:LYS:CG	2.88	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:K:62:HIS:CG	1:K:114:SER:HG	2.26	0.52
1:I:147:PRO:CB	3:R:19:DA:C1'	2.86	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:67:TYR:HD1	1:I:76:LEU:HB2	1.74	0.51
1:I:56:ASN:HA	1:L:267:LYS:HE3	1.92	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:147:PRO:CB	3:T:19:DA:N3	2.68	0.51
1:A:69:HIS:ND1	3:T:20:DG:C4'	2.73	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:158:GLN:N	3:R:18:DC:C5'	2.74	0.50
1:I:189:ARG:HD2	2:Q:7:DA:OP1	2.12	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:N:158:GLN:CB	1:O:48:MET:HE1	2.36	0.50
1:M:222:ARG:NH2	1:P:207:GLN:HB2	2.27	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:I:158:GLN:HG2	3:R:17:DG:O3'	2.12	0.50
1:N:58:ARG:NH2	1:N:116:GLN:OE1	2.44	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:31:THR:HG22	3:R:9:DC:OP2	2.13	0.49
1:A:207:GLN:HG3	1:D:222:ARG:CD	2.42	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:222:ARG:NH2	1:P:207:GLN:CB	2.76	0.49
1:M:261:TYR:HB2	1:P:263:VAL:HG21	1.93	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:240:PRO:HG3	1:P:223:PHE:CE2	2.48	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: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: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:M:217:LYS:NZ	1:P:209:ARG:HB2	2.28	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:A:240:PRO:HG2	1:H:223:PHE:CD2	2.48	0.48
1:H:146:ASN:O	1:H:150:GLN:HG2	2.14	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:222:ARG:HD2	1:P:203:PHE:HZ	1.70	0.48
1:M:25:GLU:HB2	1:M:190:LYS:NZ	2.29	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:158:GLN:HG2	3:R:18:DC:C5'	2.43	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: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:66:ASP:N	1:A:153:VAL:HG21	2.29	0.47
1:A:155:ARG:HH12	2:S:7:DA:H4'	1.77	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:17:GLN:HG2	1:I:188:LYS:HD2	1.96	0.46
1:A:237:TRP:CG	1:H:275:PRO:CB	2.98	0.46
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: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: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
1:M:132:MET:O	1:M:137:ILE:N	2.47	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:233:HIS:NE2	2:S:21:DG:H5'	2.30	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:223:PHE:HE1	1:I:242:GLN:HE21	1.61	0.46
1:I:237:TRP:CH2	1:I:270:LYS:CA	2.98	0.46
1:J:218:GLN:OE1	1:J:218:GLN:N	2.48	0.46
1:A:143:ILE:HG12	2:S:3:DT:OP1	2.14	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:207:GLN:NE2	1:L:222:ARG:NE	2.61	0.46
1:I:88:ALA:N	1:I:182:LEU:HD21	2.30	0.46
1:K:208:GLN:O	1:K:212:GLN:CB	2.61	0.46
1:A:188:LYS:HB3	1:I:17:GLN:HG2	1.98	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: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:G:111:ALA:HB3	1:G:205:LYS:NZ	2.31	0.46
1:E:227:ARG:NH2	1:H:148:GLN:O	2.48	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:246:GLY:HA2	1:A:251:ILE:HG22	1.99	0.45
1:A:204:ASN:OD1	1:D:222:ARG:NH1	2.50	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:252:VAL:HG11	1:L:245:TRP:CE3	2.51	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
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: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:78:TRP:HZ3	1:M:115:LEU:HD13	1.82	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:O:70:TYR:CD2	1:O:164:LEU:HD13	2.52	0.45
1:A:159:THR:HG22	2:S:7:DA:H4'	1.99	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:14:LYS:C	1:J:134:TYR:HH	2.18	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:M:42:VAL:HG12	1:M:166:LYS:HG2	1.99	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:A:240:PRO:CG	1:H:223:PHE:CD2	3.00	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: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:I:240:PRO:HG3	1:P:223:PHE:CD2	2.53	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:223:PHE:CE1	1:I:242:GLN:CD	2.85	0.44
1:I:1:TRP:CD1	1:I:29:PRO:CD	2.97	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:A:231:ARG:NE	2:Q:19:DG:O3'	2.50	0.43
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
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: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:I:50:SER:HB2	2:S:8:DG:H21	1.82	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:C:270:LYS:HG2	1:H:145:TRP:CZ2	2.54	0.43
1:A:204:ASN:HA	1:D:222:ARG:HH12	1.83	0.43
1:D:64:GLN:N	1:D:79:VAL:O	2.49	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:143:ILE:HG12	2:Q:3:DT:OP1	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:237:TRP:CE2	1:I:270:LYS:HB2	2.53	0.43
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
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:M:222:ARG:CD	1:P:203:PHE:CE1	3.02	0.42
1:N:106:TRP:HH2	1:N:112:PRO:HB3	1.84	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: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:M:78:TRP:CZ3	1:M:115:LEU:HD13	2.55	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:183:ILE:HD13	1:I:15:TRP:CH2	2.56	0.41
1:A:62:HIS:CD2	1:A:81:THR:HG21	2.55	0.41
1:B:175:GLU:OE1	1:B:175:GLU:N	2.52	0.41
1:B:16:HIS:CE1	1:B:42:VAL:HG21	2.56	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: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%)	39	80
1	B	252/281 (90%)	242 (96%)	8 (3%)	2 (1%)	24	69
1	C	257/281 (92%)	249 (97%)	8 (3%)	0	100	100
1	D	214/281 (76%)	203 (95%)	8 (4%)	3 (1%)	14	58
1	E	253/281 (90%)	244 (96%)	8 (3%)	1 (0%)	39	80
1	F	262/281 (93%)	248 (95%)	12 (5%)	2 (1%)	24	69
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%)	39	80
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%)	21	67
1	M	253/281 (90%)	244 (96%)	9 (4%)	0	100	100
1	N	262/281 (93%)	252 (96%)	9 (3%)	1 (0%)	39	80
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%)	50	83

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%)	93	96
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