



## wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 02:12 PM BST

PDB ID : 3JCM  
EMDB ID: : EMD-6561  
Title : Cryo-EM structure of the spliceosomal U4/U6.U5 tri-snRNP  
Authors : Wan, R.; Yan, C.; Bai, R.; Wang, L.; Huang, M.; Wong, C.C.; Shi, Y.  
Deposited on : 2015-12-23  
Resolution : 3.80 Å(reported)

This is a wwPDB EM Map/Model Validation Report for a publicly released PDB/EMDB entry.  
For rigid body fitted models, validation errors reported here could stem from errors in the original structure(s) used in the fitting.  
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>

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MolProbity : 4.02b-467  
Mogul : 1.7.1 (RC1), CSD as537be (2016)  
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) : trunk27241

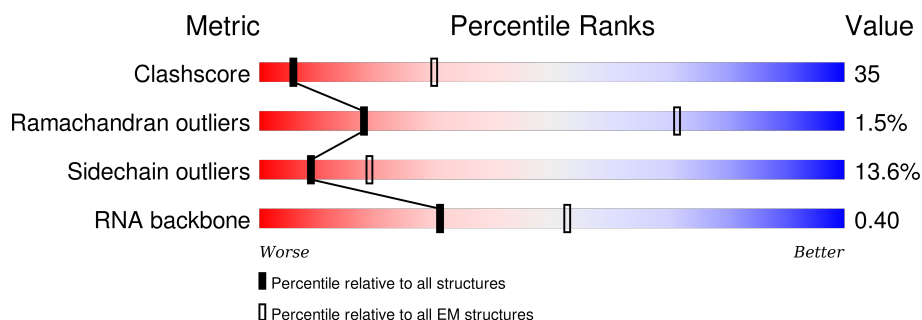
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.80 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.













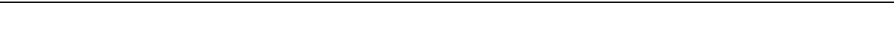

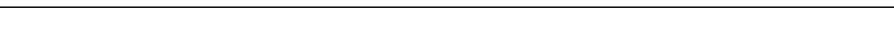
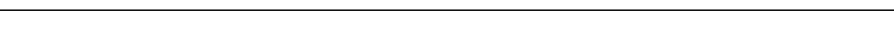



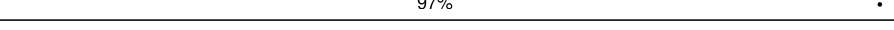







Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

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	2413	54% 28% 8% 10%
2	B	465	40% 43% 9% • 8%
3	I	494	42% 31% 10% • 16%
4	G	899	53% 22% 7% 18%
5	K	469	35% 20% • • 41%
6	L	143	50% 38% 8% • •
7	M	126	75% 21% 5%
8	H	1008	41% 32% 10% • 16%


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Mol	Chain	Length	Quality of chain
9	N	2163	 76% 22%
10	J	101	 76% 22%
10	R	101	 75% 22%
11	O	196	 37% 63%
11	S	196	 37% 63%
12	P	146	 52% 47%
12	T	146	 52% 47%
13	Q	110	 81% 19%
13	U	110	 82% 18%
14	V	94	 77% 23%
14	Y	94	 77% 23%
15	W	86	 77% 19%
15	Z	86	 77% 19%
16	X	77	 91% 9%
16	a	77	 92% 8%
17	b	109	 60% 40%
18	c	95	 97%
19	d	89	 87% 13%
20	e	86	 86% 14%
21	f	93	 82% 17%
22	g	115	 57% 43%
23	h	187	 41% 59%
24	C	20	 10% 10% 80%
25	D	112	 13% 13% 15% 60%
26	E	160	 23% 18% 11% 47%

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Mol	Chain	Length	Quality of chain
27	F	214	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
28	GTP	H	1500	-	-	X	-

## 2 Entry composition

There are 29 unique types of molecules in this entry. The entry contains 58253 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 Pre-mRNA-splicing factor 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	2174	Total	C	N	O	S	0	0
			16889	10715	2978	3138	58		

- Molecule 2 is a protein called U4/U6 small nuclear ribonucleoprotein PRP4.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	429	Total	C	N	O	S	0	0
			3378	2102	610	652	14		

- Molecule 3 is a protein called Pre-mRNA-processing factor 31.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	I	416	Total	C	N	O	S	0	0
			3171	2001	573	585	12		

- Molecule 4 is a protein called Pre-mRNA-splicing factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	G	734	Total	C	N	O	S	0	0
			4927	3063	911	939	14		

- Molecule 5 is a protein called U4/U6 small nuclear ribonucleoprotein PRP3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	K	279	Total	C	N	O	S	0	0
			2328	1476	422	416	14		

- Molecule 6 is a protein called Spliceosomal protein DIB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	L	139	Total	C	N	O	S	0	0
			1146	725	199	211	11		

- Molecule 7 is a protein called 13 kDa ribonucleoprotein-associated protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	M	126	Total	C	N	O	S	0	0
			950	605	163	177	5		

- Molecule 8 is a protein called Pre-mRNA-splicing factor SNU114.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	843	Total	C	N	O	S	0	0
			6732	4350	1119	1235	28		

- Molecule 9 is a protein called Pre-mRNA-splicing helicase BRR2.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	N	1686	Total	C	N	O	0	0
			6744	3372	1686	1686		

- Molecule 10 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	R	79	Total	C	N	O	0	0
			316	158	79	79		
10	J	79	Total	C	N	O	0	0
			316	158	79	79		

- Molecule 11 is a protein called Small nuclear ribonucleoprotein-associated protein B.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	S	73	Total	C	N	O	0	0
			292	146	73	73		
11	O	73	Total	C	N	O	0	0
			292	146	73	73		

- Molecule 12 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	T	77	Total	C	N	O	0	0
			308	154	77	77		
12	P	77	Total	C	N	O	0	0
			308	154	77	77		

- Molecule 13 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	U	90	Total	C	N	O	0	0
			360	180	90	90		
13	Q	89	Total	C	N	O	0	0
			356	178	89	89		

- Molecule 14 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	V	72	Total	C	N	O	0	0
			288	144	72	72		
14	Y	72	Total	C	N	O	0	0
			288	144	72	72		

- Molecule 15 is a protein called Small nuclear ribonucleoprotein F.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	W	70	Total	C	N	O	0	0
			280	140	70	70		
15	Z	70	Total	C	N	O	0	0
			280	140	70	70		

- Molecule 16 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	X	70	Total	C	N	O	0	0
			280	140	70	70		
16	a	71	Total	C	N	O	0	0
			284	142	71	71		

- Molecule 17 is a protein called U6 snRNA-associated Sm-like protein LSm8.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	b	65	Total	C	N	O	0	0
			260	130	65	65		

- Molecule 18 is a protein called U6 snRNA-associated Sm-like protein LSm2.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	c	92	Total	C	N	O	0	0
			368	184	92	92		

- Molecule 19 is a protein called U6 snRNA-associated Sm-like protein LSm3.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	d	77	Total	C	N	O	0	0
			308	154	77	77		

- Molecule 20 is a protein called U6 snRNA-associated Sm-like protein LSm6.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	e	74	Total	C	N	O	0	0
			296	148	74	74		

- Molecule 21 is a protein called U6 snRNA-associated Sm-like protein LSm5.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	f	77	Total	C	N	O	0	0
			308	154	77	77		

- Molecule 22 is a protein called U6 snRNA-associated Sm-like protein LSm7.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	g	66	Total	C	N	O	0	0
			264	132	66	66		

- Molecule 23 is a protein called U6 snRNA-associated Sm-like protein LSm4.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	h	77	Total	C	N	O	0	0
			308	154	77	77		

- Molecule 24 is a RNA chain called pre-mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	C	20	Total	C	N	O	P	0	0
			429	193	79	137	20		

- Molecule 25 is a RNA chain called SNR6 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	D	45	Total	C	N	O	P	0	0
			945	422	170	308	45		

- Molecule 26 is a RNA chain called SNR14 snRNA.

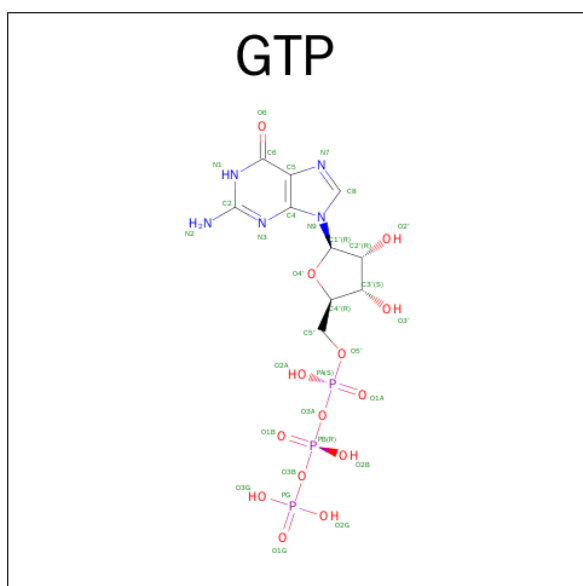


Mol	Chain	Residues	Atoms					AltConf	Trace
26	E	85	Total	C	N	O	P	0	0
			1806	807	309	605	85		

- Molecule 27 is a RNA chain called SNR7-L snRNA.

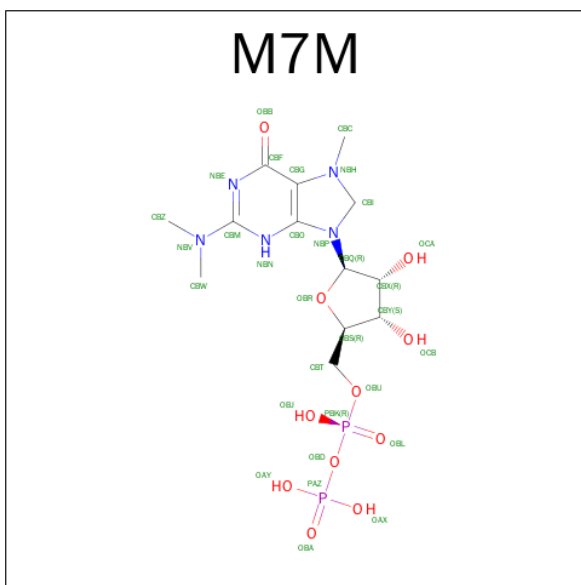
Mol	Chain	Residues	Atoms					AltConf	Trace
27	F	113	Total	C	N	O	P	0	0
			2385	1068	405	799	113		

- Molecule 28 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula:  $C_{10}H_{16}N_5O_{14}P_3$ ).



Mol	Chain	Residues	Atoms					AltConf
28	H	1	Total	C	N	O	P	0
			32	10	5	14	3	

- Molecule 29 is N,N,7-TRIMETHYLGUANOSINE 5'-(TRIHYDROGEN DIPHOSPHATE) (three-letter code: M7M) (formula:  $C_{13}H_{23}N_5O_{11}P_2$ ).

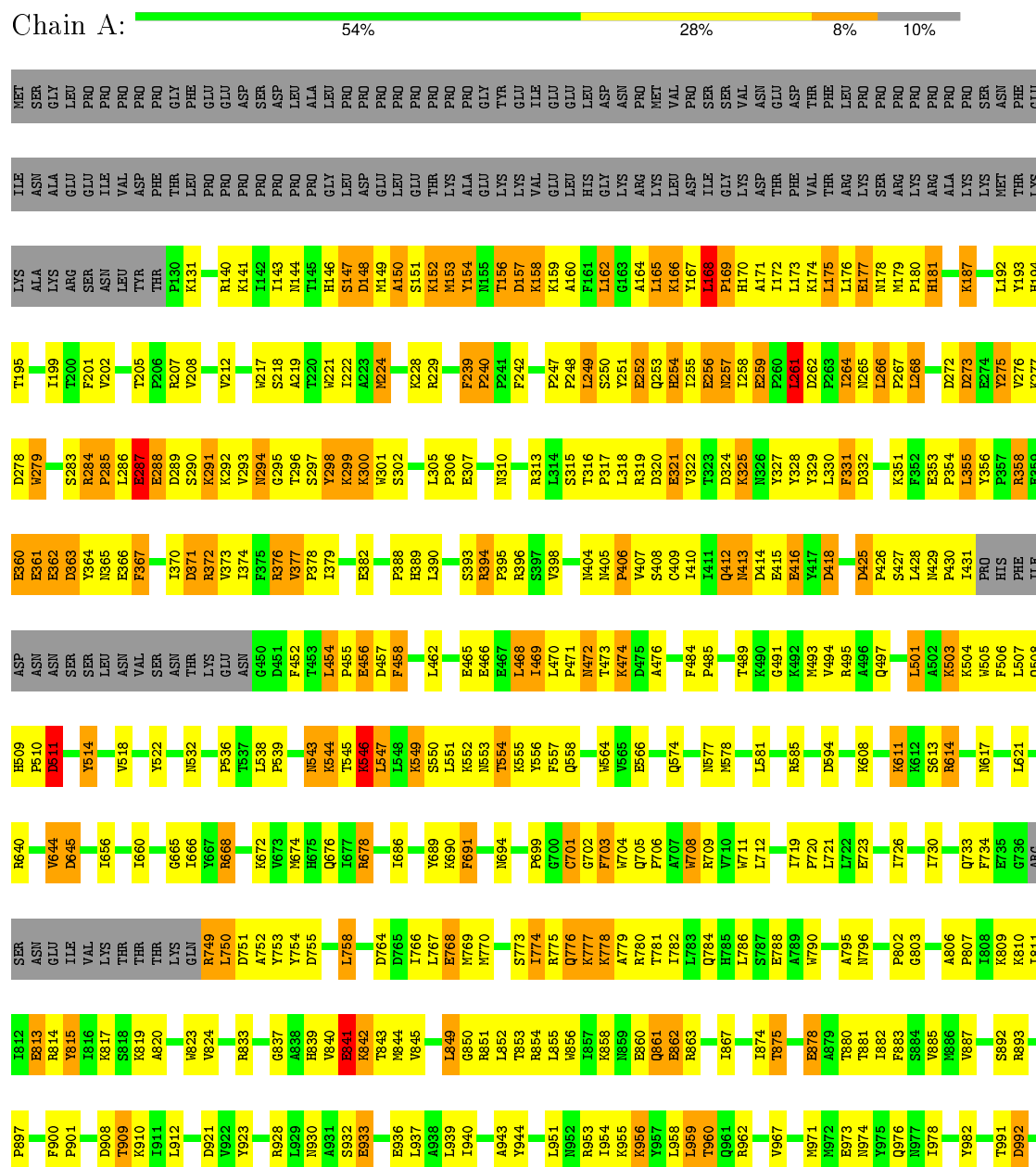


Mol	Chain	Residues	Atoms					AltConf
29	E	1	Total	C	N	O	P	0
			31	13	5	11	2	

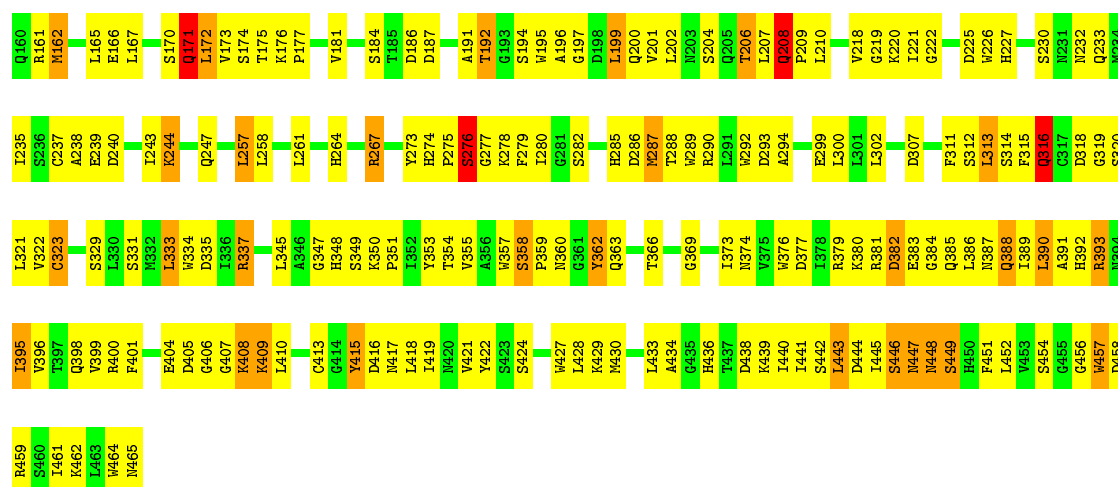
### 3 Residue-property plots

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.

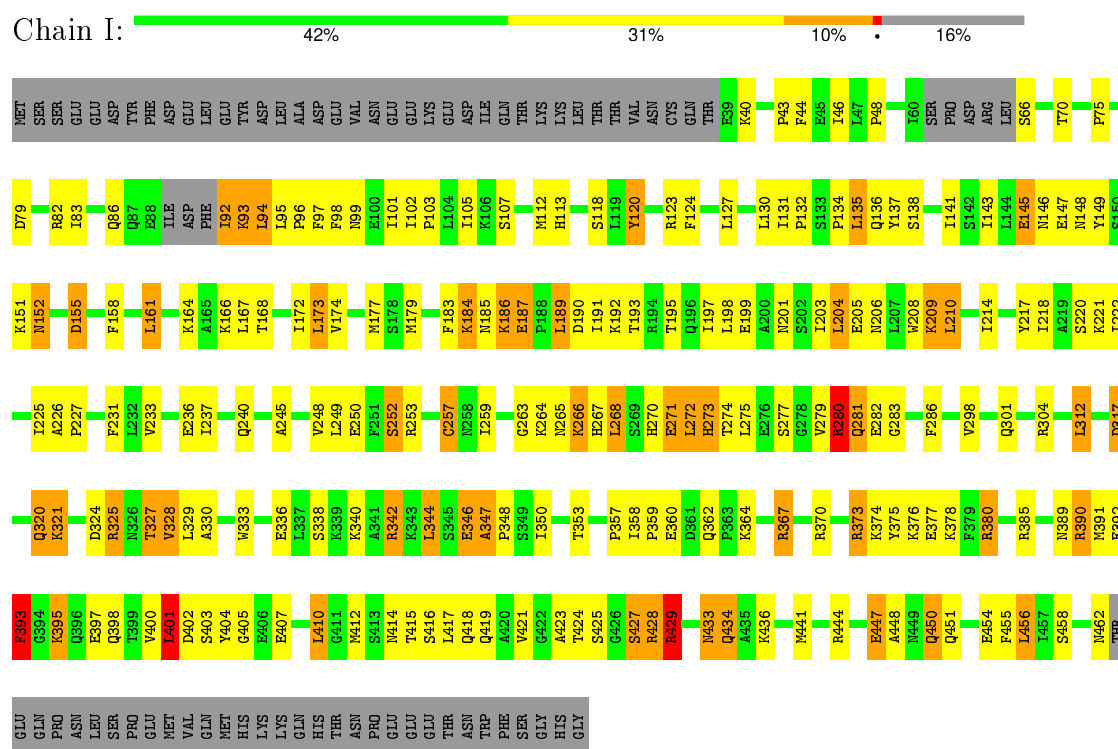
- Molecule 1: Pre-mRNA-splicing factor 8



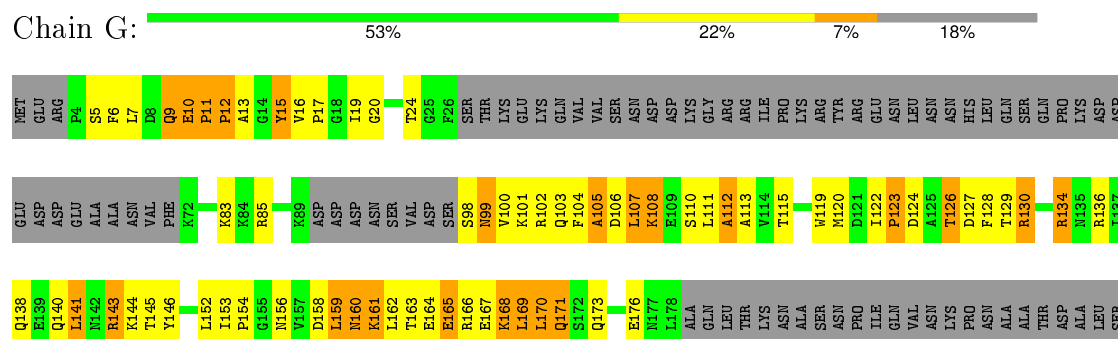


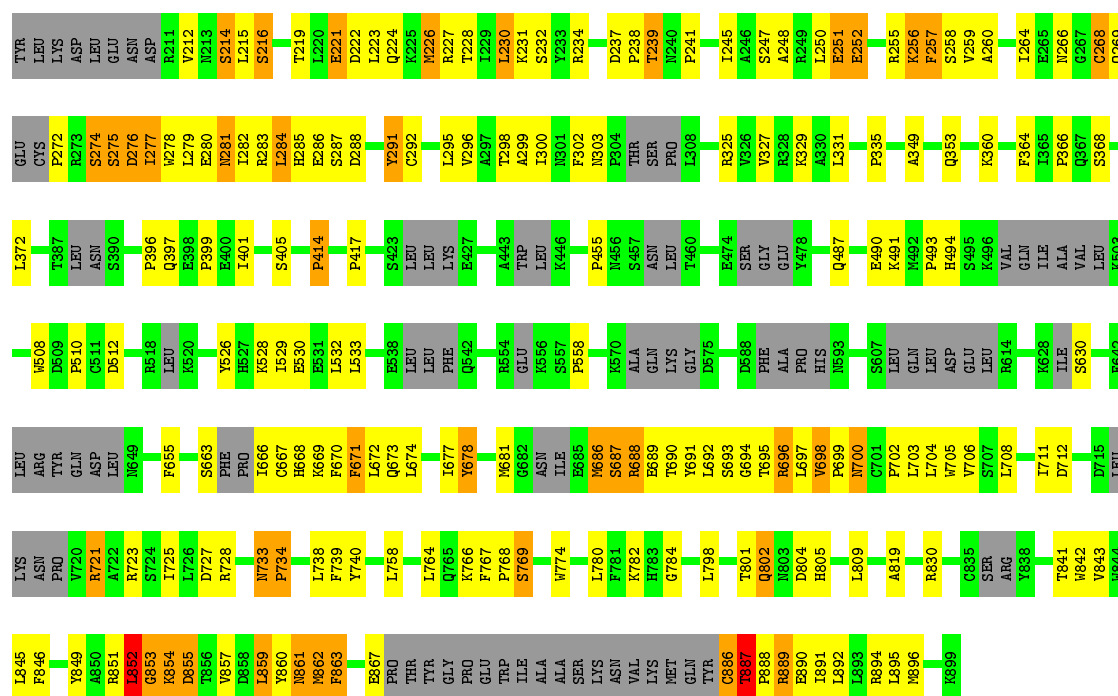


### • Molecule 3: Pre-mRNA-processing factor 31



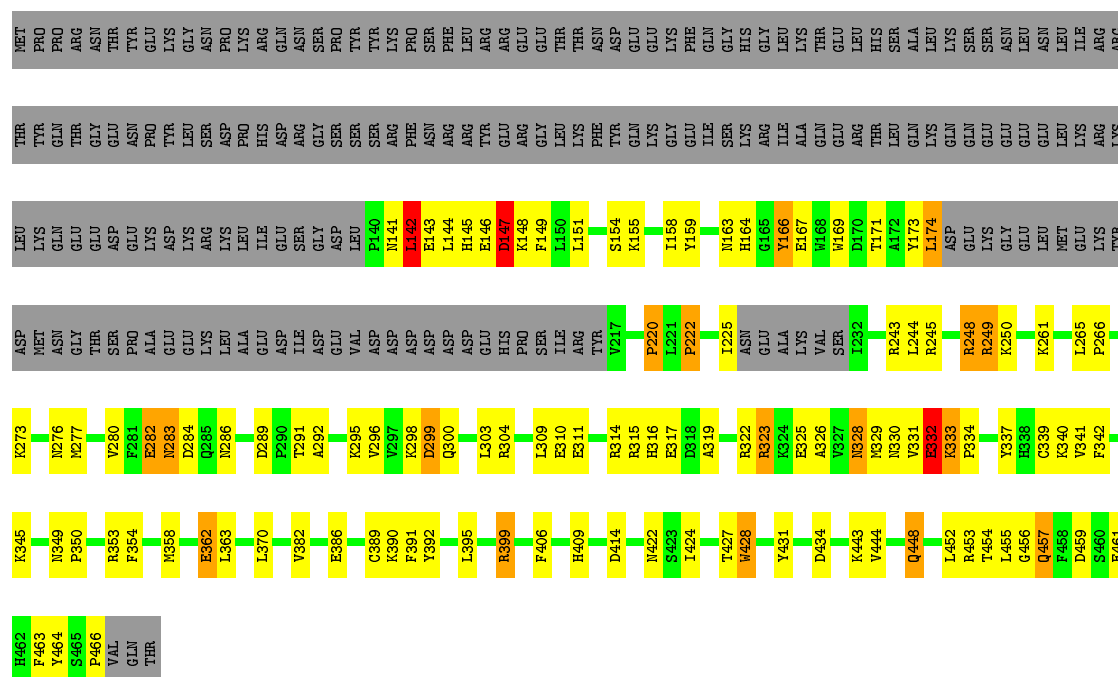
### • Molecule 4: Pre-mRNA-splicing factor 6





- Molecule 5: U4/U6 small nuclear ribonucleoprotein PRP3

Chain K: 35% 20% 41%



- Molecule 6: Spliceosomal protein DIB1

Chain L: 50% 38% 8%





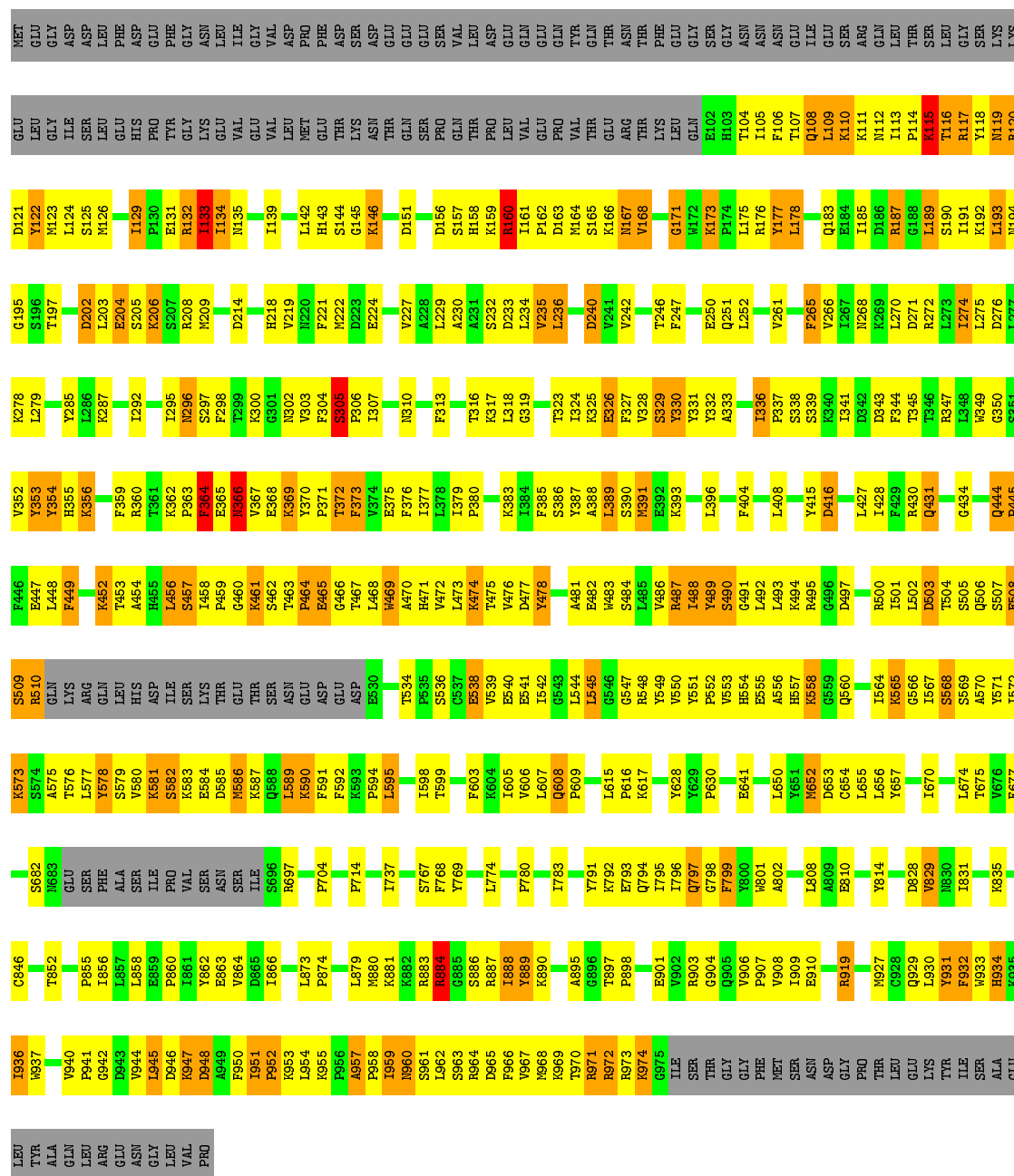
- Molecule 7: 13 kDa ribonucleoprotein-associated protein

Chain M: 75% 21% 5%




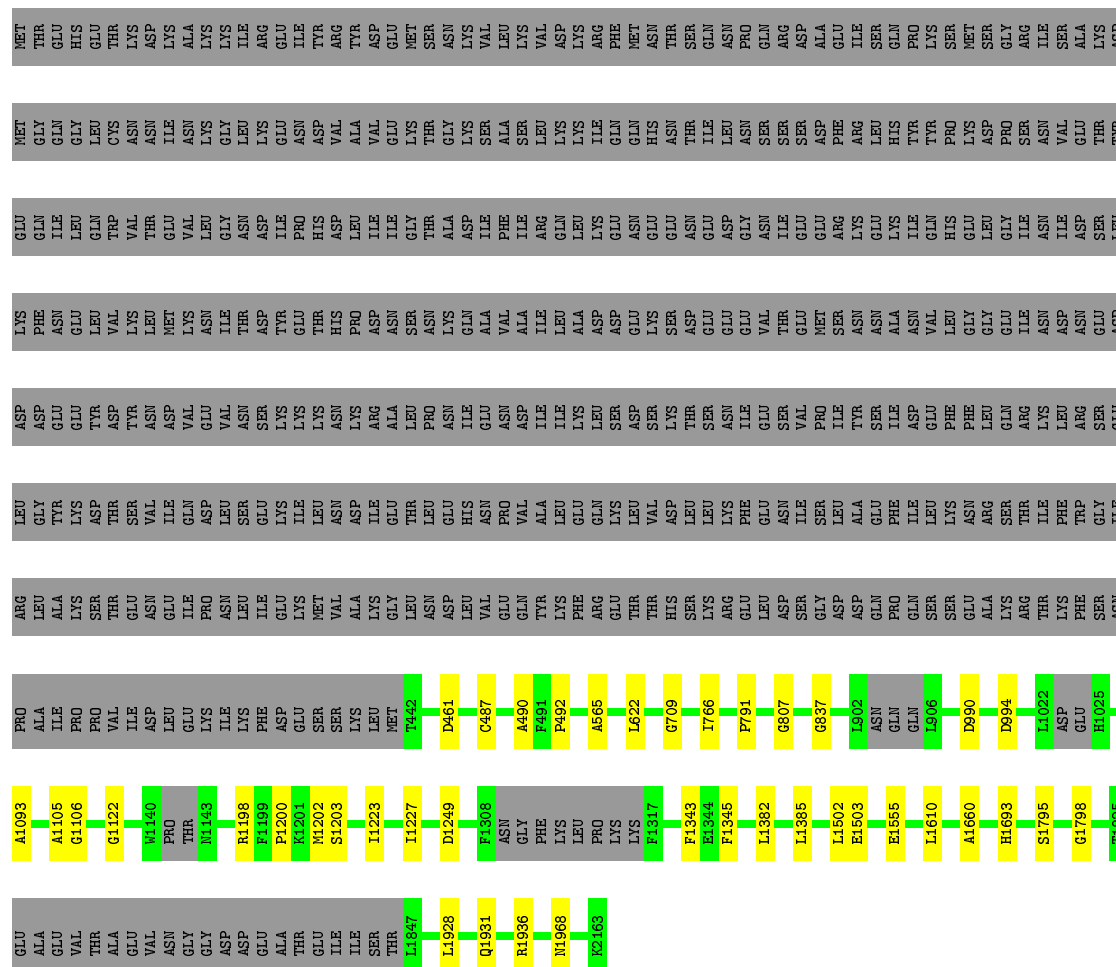
- Molecule 8: Pre-mRNA-splicing factor SNU114

Chain H: 41% 32% 10% 16%



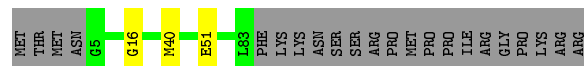
- Molecule 9: Pre-mRNA-splicing helicase BRR2

Chain N:  76% 22%



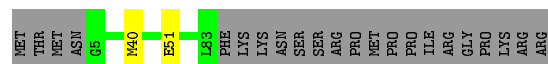
- Molecule 10: Small nuclear ribonucleoprotein Sm D3

Chain R:  75% 22%



- Molecule 10: Small nuclear ribonucleoprotein Sm D3

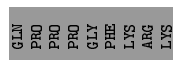
Chain J:  76% 22%



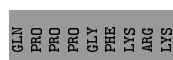
- Molecule 11: Small nuclear ribonucleoprotein-associated protein B

Chain S:  37% 63%

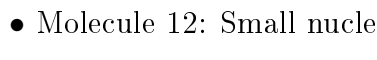




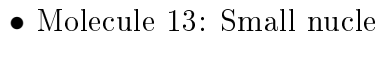
- Chain 0:  37% 63%

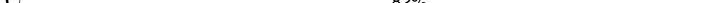


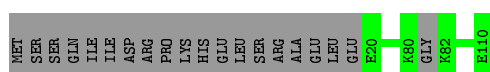
- Chain T:  52% . 47%

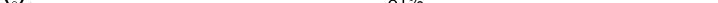


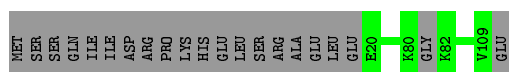
- Chain P:  52% . 47%



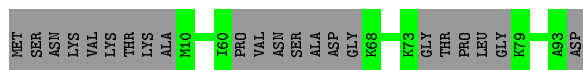
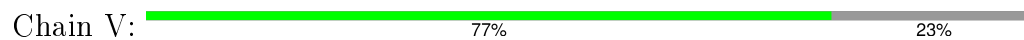
- Chain U:  82% 18%



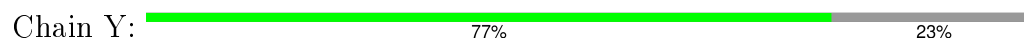
- Chain Q:  81% 19%



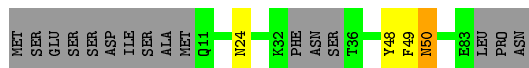
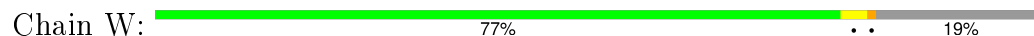
- Molecule 14: Small nuclear ribonucleoprotein E



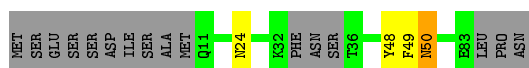
- Molecule 14: Small nuclear ribonucleoprotein E



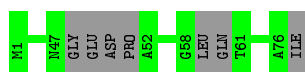
- Molecule 15: Small nuclear ribonucleoprotein F



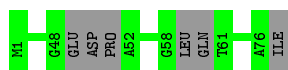
- Molecule 15: Small nuclear ribonucleoprotein F



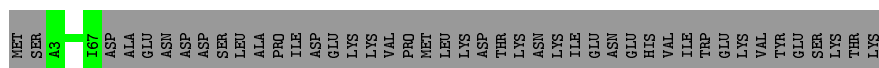
- Molecule 16: Small nuclear ribonucleoprotein G



- Molecule 16: Small nuclear ribonucleoprotein G

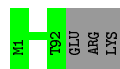


- Molecule 17: U6 snRNA-associated Sm-like protein LSm8



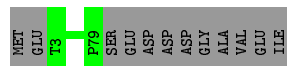
- Molecule 18: U6 snRNA-associated Sm-like protein LSm2

Chain c:  97% 3%



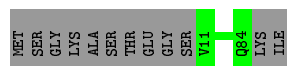
- Molecule 19: U6 snRNA-associated Sm-like protein LSm3

Chain d:  87% 13%

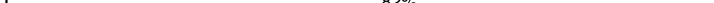


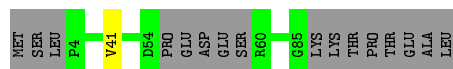
- Molecule 20: U6 snRNA-associated Sm-like protein LSm6

Chain e:  86% 14%



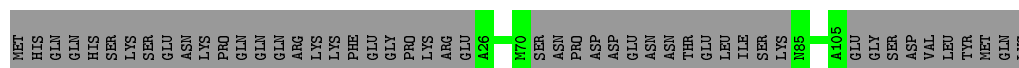
- Molecule 21: U6 snRNA-associated Sm-like protein LSm5

Chain f:  82% • 17%



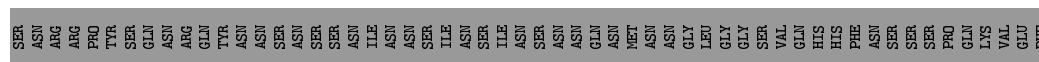
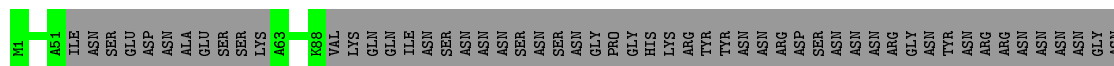
- Molecule 22: U6 snRNA-associated Sm-like protein LSm7

Chain g:  57% 43%



- Molecule 23: U6 snRNA-associated Sm-like protein LSm4

Chain h:  41% 59%



- Molecule 24: pre-mRNA

Chain C:  10% 10% 80%



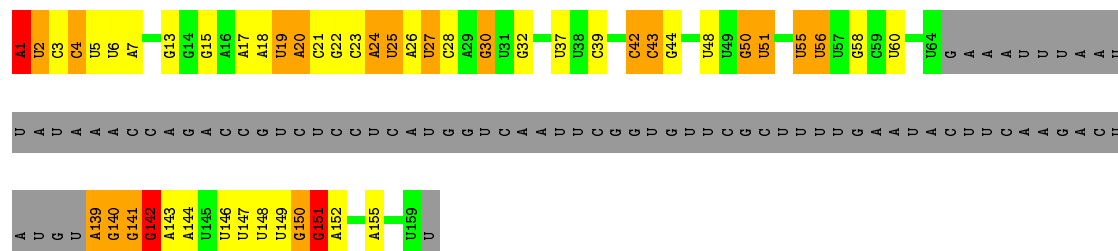
- Molecule 25: SNR6 snRNA

Chain D:  13% 13% 15% 60%

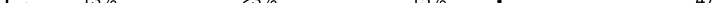


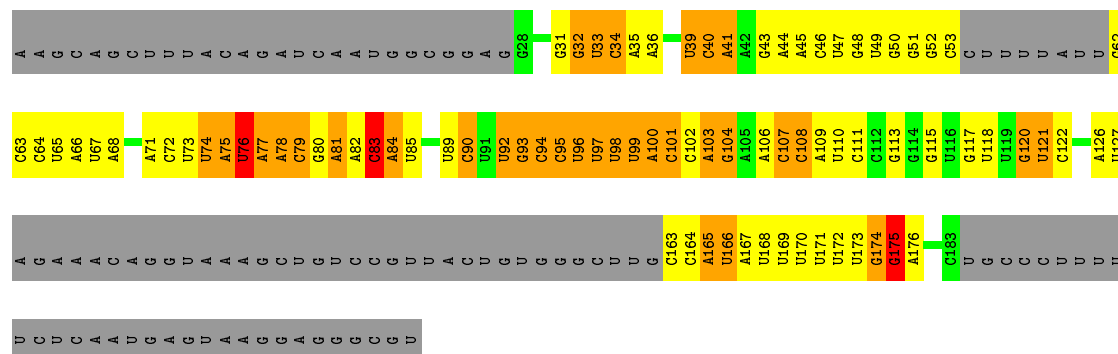
- Molecule 26: SNR14 snRNA

Chain E:  23% 18% 11% 4% 44%



- Molecule 27: SNR7-L snRNA

Chain F:  13% 23% 15% . 47%



## 4 Experimental information

Property	Value	Source
Reconstruction method	Not provided	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	Not provided	Depositor
Resolution determination method	FSC 0.143	Depositor
CTF correction method	Not provided	Depositor
Microscope	FEI TITAN	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 ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: GTP, M7M

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	0.86	22/17296 (0.1%)	0.91	24/23336 (0.1%)
10	J	0.29	0/315	0.46	0/392
10	R	0.29	0/315	0.46	0/392
11	O	0.28	0/290	0.46	0/359
11	S	0.28	0/290	0.46	0/359
12	P	0.27	0/305	0.47	0/376
12	T	0.27	0/305	0.46	0/376
13	Q	0.25	0/354	0.45	0/439
13	U	0.25	0/358	0.45	0/444
14	V	0.29	0/285	0.43	0/351
14	Y	0.29	0/285	0.43	0/351
15	W	0.30	0/278	0.45	0/344
15	Z	0.30	0/278	0.45	0/344
16	X	0.24	0/277	0.46	0/341
16	a	0.27	0/281	0.46	0/346
17	b	0.48	0/259	0.70	0/322
18	c	0.49	0/367	0.66	0/457
19	d	0.58	0/307	0.74	0/382
2	B	0.72	2/3434 (0.1%)	0.86	0/4635
20	e	0.48	0/295	0.68	0/367
21	f	0.50	0/306	0.71	0/379
22	g	0.48	0/262	0.71	0/324
23	h	0.47	0/306	0.68	0/379
24	C	0.34	0/481	0.71	0/747
25	D	0.81	0/1054	0.93	3/1634 (0.2%)
26	E	0.94	8/2016 (0.4%)	1.12	17/3136 (0.5%)
27	F	0.44	2/2659 (0.1%)	0.80	1/4131 (0.0%)
3	I	0.84	1/3219 (0.0%)	0.99	13/4332 (0.3%)
4	G	0.62	3/4967 (0.1%)	0.79	14/6746 (0.2%)
5	K	0.67	1/2376 (0.0%)	0.83	3/3183 (0.1%)
6	L	0.73	0/1167	0.87	0/1571
7	M	0.95	0/963	1.02	2/1310 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >2	RMSZ	# Z  >2
8	H	0.55	2/6874 (0.0%)	0.78	8/9305 (0.1%)
9	N	0.52	0/6738	0.65	0/8412
All	All	0.70	41/59562 (0.1%)	0.84	85/80302 (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	3
2	B	0	2
3	I	0	1
4	G	0	7
5	K	0	1
7	M	0	4
8	H	0	2
All	All	0	20

All (41) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
26	E	1	A	C5-C4	10.58	1.46	1.38
26	E	1	A	N7-C5	-8.64	1.34	1.39
1	A	1335	TRP	CG-CD2	-8.36	1.29	1.43
26	E	1	A	N9-C4	-8.09	1.32	1.37
26	E	1	A	C5-C6	7.52	1.47	1.41
1	A	1335	TRP	CE2-CZ2	-7.42	1.27	1.39
2	B	415	TYR	CE2-CZ	-7.38	1.28	1.38
5	K	428	TRP	CB-CG	-7.31	1.37	1.50
26	E	151	G	C1'-N9	-6.91	1.37	1.46
27	F	175	G	C1'-N9	-6.89	1.37	1.46
4	G	146	TYR	CE1-CZ	-6.75	1.29	1.38
26	E	142	G	C1'-N9	-6.75	1.37	1.46
1	A	856	TRP	CB-CG	-6.67	1.38	1.50
1	A	1335	TRP	CE3-CZ3	-6.46	1.27	1.38
1	A	1081	TYR	CE1-CZ	-6.35	1.30	1.38
1	A	1992	TYR	CE2-CZ	-6.32	1.30	1.38
4	G	146	TYR	CG-CD2	-6.10	1.31	1.39
26	E	155	A	C1'-N9	-6.08	1.38	1.46
1	A	1562	PHE	CB-CG	-6.06	1.41	1.51
1	A	1161	TYR	CB-CG	-5.89	1.42	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1383	PHE	CB-CG	-5.85	1.41	1.51
1	A	1012	TRP	CG-CD2	-5.79	1.33	1.43
2	B	415	TYR	CG-CD1	-5.71	1.31	1.39
26	E	17	A	O3'-P	-5.67	1.54	1.61
1	A	1542	TYR	CG-CD1	-5.61	1.31	1.39
1	A	1610	TRP	CD2-CE3	-5.56	1.32	1.40
4	G	774	TRP	CB-CG	-5.54	1.40	1.50
27	F	76	U	C1'-N1	5.45	1.56	1.48
1	A	1609	TRP	CB-CG	-5.42	1.40	1.50
1	A	708	TRP	CB-CG	-5.42	1.40	1.50
3	I	375	TYR	CG-CD1	-5.38	1.32	1.39
1	A	1116	TYR	CB-CG	-5.33	1.43	1.51
1	A	711	TRP	CB-CG	-5.32	1.40	1.50
8	H	958	PRO	N-CD	5.22	1.55	1.47
8	H	445	PRO	N-CD	5.15	1.55	1.47
1	A	1610	TRP	CG-CD2	-5.12	1.34	1.43
1	A	1117	TYR	CB-CG	-5.07	1.44	1.51
1	A	1542	TYR	CE1-CZ	-5.04	1.31	1.38
1	A	169	PRO	N-CD	5.04	1.54	1.47
1	A	1527	TRP	CE3-CZ3	-5.03	1.29	1.38
1	A	285	PRO	N-CD	5.01	1.54	1.47

All (85) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	E	1	A	C2-N3-C4	20.61	120.90	110.60
4	G	853	GLY	N-CA-C	12.86	145.25	113.10
26	E	1	A	N3-C4-C5	-11.57	118.70	126.80
8	H	951	ILE	C-N-CD	-10.75	96.95	120.60
1	A	1616	ARG	NE-CZ-NH1	10.12	125.36	120.30
26	E	1	A	N1-C2-N3	-9.87	124.37	129.30
26	E	1	A	N3-C4-N9	9.78	135.23	127.40
1	A	854	ARG	NE-CZ-NH2	-9.76	115.42	120.30
1	A	1268	ARG	NE-CZ-NH2	-9.14	115.73	120.30
25	D	61	C	O5'-P-OP2	-8.48	98.06	105.70
26	E	1	A	N9-C1'-C2'	-8.26	102.92	112.00
1	A	1616	ARG	NE-CZ-NH2	-8.16	116.22	120.30
4	G	852	LEU	N-CA-C	8.11	132.89	111.00
26	E	1	A	C4-C5-N7	-8.03	106.69	110.70
3	I	393	PHE	CB-CG-CD2	-7.84	115.31	120.80
26	E	50	G	O5'-P-OP2	7.67	119.91	110.70
3	I	393	PHE	CB-CG-CD1	7.51	126.06	120.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	E	1	A	C8-N9-C4	7.45	108.78	105.80
4	G	493	PRO	N-CA-CB	7.43	112.22	103.30
26	E	1	A	C5-N7-C8	7.38	107.59	103.90
1	A	1818	ARG	NE-CZ-NH2	-7.35	116.63	120.30
5	K	142	LEU	N-CA-C	7.25	130.59	111.00
1	A	1344	THR	CA-CB-CG2	-7.24	102.27	112.40
1	A	1095	MET	CG-SD-CE	-7.08	88.88	100.20
1	A	1263	CYS	CA-CB-SG	-7.00	101.40	114.00
3	I	304	ARG	NE-CZ-NH2	-6.98	116.81	120.30
4	G	396	PRO	N-CA-CB	6.84	111.51	103.30
4	G	399	PRO	N-CA-CB	6.77	111.42	103.30
7	M	79	VAL	CB-CA-C	-6.68	98.70	111.40
4	G	558	PRO	N-CA-CB	6.67	111.31	103.30
3	I	367	ARG	NE-CZ-NH1	-6.67	116.97	120.30
4	G	510	PRO	N-CA-CB	6.64	111.27	103.30
26	E	1	A	P-O3'-C3'	-6.63	111.74	119.70
5	K	222	PRO	N-CA-CB	6.58	111.20	103.30
1	A	668	ARG	NE-CZ-NH1	6.55	123.57	120.30
3	I	48	PRO	N-CA-CB	6.52	111.12	103.30
4	G	417	PRO	N-CA-CB	6.47	111.07	103.30
4	G	455	PRO	N-CA-CB	6.44	111.03	103.30
3	I	43	PRO	N-CA-CB	6.42	111.00	103.30
4	G	414	PRO	N-CA-CB	6.41	110.99	103.30
5	K	220	PRO	N-CA-CB	6.39	110.97	103.30
4	G	366	PRO	N-CA-CB	6.30	110.86	103.30
3	I	75	PRO	N-CA-CB	6.24	110.78	103.30
27	F	83	C	C4'-C3'-O3'	6.19	125.39	113.00
1	A	962	ARG	NE-CZ-NH1	-6.19	117.21	120.30
26	E	42	C	O5'-P-OP1	-6.15	100.16	105.70
1	A	1605	ARG	NE-CZ-NH1	6.11	123.36	120.30
1	A	953	ARG	NE-CZ-NH2	-6.10	117.25	120.30
26	E	1	A	C6-C5-N7	6.00	136.50	132.30
8	H	464	PRO	N-CA-CB	5.95	110.44	103.30
3	I	390	ARG	NE-CZ-NH2	-5.94	117.33	120.30
3	I	401	LEU	CB-CG-CD1	-5.93	100.91	111.00
1	A	394	ARG	NE-CZ-NH2	-5.93	117.33	120.30
1	A	893	ARG	NE-CZ-NH2	-5.89	117.35	120.30
26	E	1	A	N7-C8-N9	-5.86	110.87	113.80
1	A	284	ARG	C-N-CD	5.80	140.57	128.40
8	H	370	TYR	C-N-CD	5.79	140.55	128.40
1	A	1823	LEU	CB-CG-CD1	-5.79	101.17	111.00
1	A	1335	TRP	CD1-NE1-CE2	-5.74	103.83	109.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	H	129	ILE	C-N-CD	5.74	140.45	128.40
1	A	168	LEU	C-N-CD	5.72	140.41	128.40
8	H	444	GLN	C-N-CD	5.68	140.34	128.40
8	H	957	ALA	C-N-CD	5.60	140.16	128.40
1	A	1089	VAL	N-CA-C	-5.58	95.92	111.00
4	G	152	LEU	CB-CG-CD1	-5.55	101.56	111.00
25	D	80	U	C5-C6-N1	-5.50	119.95	122.70
3	I	280	ARG	NE-CZ-NH2	-5.50	117.55	120.30
8	H	607	LEU	CB-CG-CD1	-5.49	101.67	111.00
1	A	1163	ARG	NE-CZ-NH2	-5.48	117.56	120.30
4	G	335	PRO	N-CA-CB	5.46	109.86	103.30
1	A	157	ASP	N-CA-C	5.46	125.73	111.00
26	E	1	A	O3'-P-O5'	5.40	114.25	104.00
3	I	429	ARG	NE-CZ-NH1	5.35	122.97	120.30
1	A	1107	LEU	CB-CG-CD1	-5.26	102.06	111.00
1	A	1068	ARG	NE-CZ-NH2	-5.23	117.69	120.30
26	E	1	A	C3'-C2'-C1'	5.18	105.65	101.50
3	I	120	TYR	CB-CG-CD2	-5.17	117.90	121.00
26	E	50	G	O5'-P-OP1	-5.11	101.10	105.70
26	E	42	C	O5'-P-OP2	5.10	116.82	110.70
3	I	173	LEU	CB-CG-CD1	-5.09	102.35	111.00
25	D	80	U	N1-C2-N3	5.08	117.95	114.90
7	M	9	PHE	C-N-CD	-5.07	109.44	120.60
8	H	884	ARG	CG-CD-NE	-5.07	101.15	111.80
4	G	723	ARG	NE-CZ-NH1	5.05	122.83	120.30
1	A	1739	ARG	NE-CZ-NH2	-5.04	117.78	120.30

There are no chirality outliers.

All (20) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1014	LYS	Peptide
1	A	1867	GLU	Peptide
1	A	694	ASN	Peptide
2	B	208	GLN	Peptide
2	B	316	GLN	Peptide
4	G	12	PRO	Peptide
4	G	123	PRO	Peptide
4	G	733	ASN	Mainchain,Peptide
4	G	767	PHE	Mainchain,Peptide
4	G	802	GLN	Peptide
8	H	160	ARG	Peptide

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Mol	Chain	Res	Type	Group
8	H	171	GLY	Peptide
3	I	410	LEU	Peptide
5	K	282	GLU	Peptide
7	M	59	GLU	Mainchain,Peptide
7	M	9	PHE	Mainchain,Peptide

## 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	16889	0	16134	1106	0
2	B	3378	0	3342	372	0
3	I	3171	0	3140	274	0
4	G	4927	0	4006	390	0
5	K	2328	0	2314	156	0
6	L	1146	0	1133	126	0
7	M	950	0	1004	27	0
8	H	6732	0	6904	868	0
9	N	6744	0	1759	27	0
10	J	316	0	86	0	0
10	R	316	0	86	2	0
11	O	292	0	78	0	0
11	S	292	0	78	0	0
12	P	308	0	78	0	0
12	T	308	0	78	0	0
13	Q	356	0	88	0	0
13	U	360	0	89	0	0
14	V	288	0	74	0	0
14	Y	288	0	74	0	0
15	W	280	0	77	1	0
15	Z	280	0	77	1	0
16	X	280	0	79	0	0
16	a	284	0	82	0	0
17	b	260	0	72	0	0
18	c	368	0	99	0	0
19	d	308	0	80	0	0
20	e	296	0	83	0	0
21	f	308	0	85	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
22	g	264	0	76	0	0
23	h	308	0	85	0	0
24	C	429	0	214	48	0
25	D	945	0	478	73	0
26	E	1806	0	907	49	0
27	F	2385	0	1209	210	0
28	H	32	0	12	10	0
29	E	31	0	20	6	0
All	All	58253	0	44280	3557	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 35.

All (3557) 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)
8:H:856:ILE:HA	8:H:944:VAL:CG1	1.17	1.58
4:G:672:LEU:HD21	4:G:704:LEU:CD2	1.29	1.58
8:H:168:VAL:HG13	8:H:173:LYS:CD	1.09	1.56
8:H:364:PHE:CB	8:H:369:LYS:HG3	1.34	1.54
4:G:672:LEU:CD2	4:G:704:LEU:CD2	1.82	1.52
4:G:274:SER:HB3	4:G:277:ILE:CD1	1.38	1.52
4:G:274:SER:CB	4:G:277:ILE:HD11	1.30	1.50
8:H:168:VAL:CG1	8:H:173:LYS:HD3	1.39	1.50
8:H:500:ARG:CD	8:H:534:THR:HG21	1.40	1.49
8:H:364:PHE:HB2	8:H:369:LYS:CG	1.42	1.49
9:N:807:GLY:CA	9:N:1093:ALA:H	1.28	1.46
8:H:500:ARG:NE	8:H:534:THR:HG21	1.31	1.41
8:H:364:PHE:HD2	8:H:369:LYS:CD	1.33	1.41
9:N:807:GLY:HA2	9:N:1093:ALA:N	1.10	1.38
6:L:105:PHE:CB	6:L:141:ARG:HG2	1.52	1.38
1:A:781:THR:CA	1:A:784:GLN:OE1	1.71	1.37
8:H:488:ILE:CG2	8:H:558:LYS:HA	1.54	1.37
8:H:856:ILE:CA	8:H:944:VAL:CG1	2.00	1.36
8:H:855:PRO:C	8:H:944:VAL:HG11	1.43	1.36
1:A:289:ASP:OD2	1:A:292:LYS:N	1.59	1.36
2:B:389:ILE:CD1	2:B:427:TRP:HB3	1.54	1.35
8:H:168:VAL:CG1	8:H:173:LYS:CD	1.97	1.35
8:H:458:ILE:CG2	8:H:459:PRO:HD2	1.56	1.35
4:G:846:PHE:CE1	4:G:859:LEU:HD21	1.62	1.35
1:A:285:PRO:HD2	1:A:298:TYR:OH	1.27	1.34

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:268:CYS:SG	4:G:278:TRP:CH2	2.21	1.34
1:A:162:LEU:HD21	1:A:730:ILE:CG2	0.88	1.33
8:H:855:PRO:O	8:H:944:VAL:CG1	1.75	1.33
8:H:856:ILE:CA	8:H:944:VAL:HG11	1.56	1.33
8:H:500:ARG:CD	8:H:534:THR:CG2	2.07	1.33
4:G:672:LEU:CD2	4:G:704:LEU:HD21	1.50	1.32
3:I:197:ILE:O	3:I:201:ASN:ND2	1.61	1.32
4:G:630:SER:CB	4:G:670:PHE:CZ	2.11	1.32
1:A:162:LEU:CD2	1:A:730:ILE:HG21	0.85	1.32
9:N:807:GLY:CA	9:N:1093:ALA:N	1.86	1.31
8:H:856:ILE:N	8:H:944:VAL:HG11	1.45	1.30
8:H:810:GLU:OE2	8:H:974:LYS:HG3	1.13	1.28
4:G:863:PHE:CZ	4:G:892:LEU:HD21	1.67	1.28
27:F:73:U:C2'	27:F:74:U:H5'	1.64	1.27
8:H:486:VAL:CG1	8:H:564:ILE:HD11	1.65	1.27
1:A:289:ASP:O	1:A:293:VAL:HG12	1.29	1.27
6:L:105:PHE:CZ	6:L:137:TYR:CE2	2.23	1.26
1:A:611:LYS:CE	24:C:4:G:OP1	1.85	1.25
9:N:807:GLY:CA	9:N:1093:ALA:CA	2.14	1.25
25:D:48:C:O3'	25:D:49:A:C8	1.89	1.24
1:A:165:LEU:HD12	1:A:578:MET:SD	1.78	1.24
1:A:195:THR:HG23	1:A:556:TYR:O	1.34	1.24
8:H:364:PHE:CD2	8:H:369:LYS:HD2	1.73	1.24
8:H:500:ARG:HD3	8:H:534:THR:CG2	1.66	1.23
9:N:807:GLY:HA2	9:N:1093:ALA:CA	1.67	1.23
8:H:364:PHE:CD2	8:H:369:LYS:CD	2.22	1.22
5:K:350:PRO:HA	5:K:353:ARG:CG	1.68	1.22
24:C:8:U:C6	25:D:51:A:N6	2.05	1.22
3:I:226:ALA:HA	3:I:317:ASP:OD2	1.31	1.22
8:H:330:TYR:HE1	8:H:430:ARG:NH2	1.36	1.22
6:L:105:PHE:CE1	6:L:137:TYR:CE2	2.28	1.21
8:H:889:TYR:CD1	8:H:890:LYS:HG2	1.77	1.20
5:K:354:PHE:HE1	5:K:358:MET:CE	1.52	1.20
4:G:672:LEU:CD2	4:G:704:LEU:HD23	1.48	1.20
4:G:630:SER:CB	4:G:670:PHE:CE2	2.24	1.20
4:G:846:PHE:HE1	4:G:859:LEU:CD2	1.55	1.20
6:L:105:PHE:CZ	6:L:137:TYR:CD2	2.29	1.20
8:H:454:ALA:O	8:H:457:SER:O	1.55	1.20
25:D:48:C:H3'	25:D:49:A:N7	1.57	1.19
3:I:123:ARG:HD3	3:I:189:LEU:CD1	1.70	1.19
1:A:1654:TRP:CZ3	1:A:1779:LEU:HD12	1.78	1.19

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:655:PHE:CB	4:G:674:LEU:HD21	1.71	1.19
1:A:1748:ILE:HG22	1:A:1752:VAL:HG22	1.21	1.19
25:D:48:C:C3'	25:D:49:A:C8	2.25	1.18
8:H:116:THR:HG23	8:H:158:HIS:CD2	1.78	1.18
8:H:492:LEU:HD21	8:H:557:HIS:ND1	1.57	1.18
27:F:75:A:C8	27:F:77:A:H5'	1.78	1.18
1:A:286:LEU:HD21	1:A:292:LYS:HB2	1.25	1.17
8:H:510:ARG:HB2	8:H:591:PHE:CE2	1.78	1.17
2:B:389:ILE:HD11	2:B:427:TRP:CB	1.73	1.17
1:A:1755:LYS:O	1:A:1759:TYR:HD2	1.22	1.17
5:K:350:PRO:HA	5:K:353:ARG:HG2	1.20	1.16
1:A:1035:LEU:HD12	1:A:1038:ILE:HG21	1.17	1.16
8:H:354:TYR:CB	8:H:359:PHE:HB3	1.76	1.16
8:H:855:PRO:O	8:H:944:VAL:CG2	1.94	1.15
8:H:163:ASP:OD2	8:H:548:ARG:NH1	1.79	1.15
2:B:316:GLN:HB2	2:B:357:TRP:CD2	1.81	1.15
8:H:117:ARG:HD2	8:H:157:SER:O	1.42	1.15
1:A:468:LEU:HD13	1:A:469:ILE:HD13	1.21	1.15
8:H:501:ILE:CD1	8:H:567:ILE:CG2	2.24	1.15
1:A:162:LEU:HD21	1:A:730:ILE:HG22	1.22	1.15
1:A:1880:PHE:CE2	1:A:1889:LEU:HD21	1.81	1.15
24:C:-3:A:H8	24:C:-2:A:C6	1.65	1.14
6:L:105:PHE:CE1	6:L:137:TYR:CD2	2.35	1.14
1:A:781:THR:HA	1:A:784:GLN:OE1	0.97	1.14
1:A:252:GLU:O	1:A:256:GLU:HG2	1.48	1.14
1:A:779:ALA:HA	1:A:782:ILE:HD12	1.30	1.14
8:H:364:PHE:HD2	8:H:369:LYS:HD2	1.01	1.13
8:H:488:ILE:CD1	8:H:560:GLN:HG2	1.78	1.13
1:A:1654:TRP:CZ3	1:A:1779:LEU:CD1	2.30	1.13
1:A:1490:ARG:NH1	1:A:1536:LEU:HA	1.62	1.13
27:F:44:A:H2'	27:F:45:A:C8	1.83	1.13
8:H:501:ILE:HD11	8:H:567:ILE:CG2	1.78	1.12
8:H:810:GLU:OE2	8:H:974:LYS:CG	1.97	1.12
8:H:330:TYR:CE1	8:H:430:ARG:NH2	2.17	1.12
6:L:105:PHE:HB3	6:L:141:ARG:CG	1.79	1.11
27:F:44:A:H2'	27:F:45:A:H8	0.96	1.11
4:G:272:PRO:HB3	4:G:302:PHE:CD1	1.85	1.11
8:H:330:TYR:HE1	8:H:430:ARG:CZ	1.63	1.11
8:H:488:ILE:HD12	8:H:560:GLN:HG2	1.29	1.11
25:D:48:C:O3'	25:D:49:A:H8	1.22	1.11
8:H:332:TYR:OH	8:H:376:PHE:HB3	1.50	1.11

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:470:ALA:HB1	8:H:486:VAL:HG21	1.26	1.11
1:A:362:GLU:HB3	1:A:1209:LYS:CE	1.81	1.11
1:A:141:LYS:HA	1:A:144:ASN:ND2	1.64	1.11
2:B:329:SER:HB3	2:B:348:HIS:O	1.47	1.11
4:G:691:TYR:HB3	4:G:708:LEU:HD12	1.15	1.10
8:H:486:VAL:HG12	8:H:564:ILE:HD11	1.13	1.10
1:A:297:SER:HB3	27:F:32:G:OP1	1.48	1.10
8:H:168:VAL:HG13	8:H:173:LYS:HD2	1.18	1.10
1:A:162:LEU:HD23	1:A:730:ILE:HG21	1.20	1.10
8:H:677:PHE:CE1	8:H:966:PHE:CD2	2.39	1.10
4:G:286:GLU:HB2	4:G:292:CYS:SG	1.90	1.09
1:A:2077:THR:O	1:A:2080:LYS:HG2	1.52	1.09
8:H:364:PHE:HD2	8:H:369:LYS:HD3	1.17	1.08
24:C:-3:A:H8	24:C:-2:A:C5	1.70	1.08
1:A:141:LYS:HA	1:A:144:ASN:HD21	0.95	1.08
3:I:184:LYS:HD2	3:I:186:LYS:H	1.14	1.08
8:H:582:SER:CB	8:H:585:ASP:OD2	2.01	1.07
8:H:468:LEU:HD21	8:H:577:LEU:HD21	1.33	1.07
8:H:468:LEU:HD11	8:H:493:LEU:HD21	1.31	1.07
1:A:290:SER:OG	1:A:291:LYS:NZ	1.88	1.07
27:F:75:A:C8	27:F:77:A:C5'	2.37	1.07
8:H:488:ILE:HD12	8:H:560:GLN:CG	1.82	1.06
2:B:323:CYS:SG	2:B:355:VAL:HG11	1.95	1.06
8:H:598:ILE:HG22	8:H:933:TRP:CZ3	1.91	1.06
4:G:252:GLU:HG2	4:G:256:LYS:HG3	1.37	1.06
1:A:503:LYS:HA	1:A:506:PHE:CZ	1.89	1.06
8:H:197:THR:CG2	8:H:545:LEU:CD1	2.32	1.06
4:G:668:HIS:HB3	4:G:698:VAL:HG11	1.32	1.06
4:G:672:LEU:HD23	4:G:704:LEU:CD2	1.68	1.06
8:H:458:ILE:HG23	8:H:459:PRO:HD2	1.08	1.06
3:I:123:ARG:CD	3:I:189:LEU:HD13	1.84	1.06
8:H:168:VAL:HG13	8:H:173:LYS:CG	1.85	1.06
5:K:354:PHE:HE1	5:K:358:MET:HE3	1.17	1.06
5:K:428:TRP:HZ2	5:K:463:PHE:CE2	1.74	1.06
3:I:135:LEU:HD23	3:I:136:GLN:N	1.70	1.06
8:H:365:GLU:OE2	8:H:366:ASN:N	1.88	1.05
4:G:274:SER:HB2	4:G:277:ILE:HD11	1.34	1.05
8:H:501:ILE:HD11	8:H:567:ILE:HG23	1.09	1.05
1:A:218:SER:N	1:A:318:LEU:HD21	1.71	1.05
1:A:1755:LYS:O	1:A:1759:TYR:CD2	2.09	1.05
8:H:133:ILE:O	8:H:134:ILE:HG23	1.55	1.05

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1751:TYR:CE1	1:A:1755:LYS:HD3	1.92	1.05
6:L:116:ILE:HD11	6:L:137:TYR:OH	1.57	1.05
1:A:1755:LYS:HG3	1:A:1759:TYR:HE2	1.19	1.05
6:L:140:LYS:HG2	6:L:141:ARG:NH1	1.72	1.04
25:D:83:A:H1'	25:D:84:C:C5	1.93	1.04
5:K:354:PHE:CE1	5:K:358:MET:CE	2.40	1.04
24:C:-3:A:C8	24:C:-2:A:C6	2.45	1.04
8:H:501:ILE:CD1	8:H:567:ILE:HG23	1.87	1.04
4:G:846:PHE:CE1	4:G:859:LEU:CD2	2.35	1.04
1:A:611:LYS:HE2	24:C:4:G:OP1	1.55	1.03
1:A:1998:ARG:O	1:A:1999:ILE:HG13	1.58	1.03
8:H:500:ARG:NE	8:H:534:THR:CG2	2.15	1.03
1:A:1058:ALA:HB2	1:A:1114:PHE:HE1	1.23	1.03
2:B:389:ILE:HD11	2:B:427:TRP:HB3	1.04	1.03
8:H:510:ARG:HB2	8:H:591:PHE:HE2	0.86	1.03
8:H:488:ILE:HG22	8:H:558:LYS:CA	1.88	1.02
1:A:611:LYS:HE3	24:C:4:G:OP1	1.54	1.02
8:H:504:THR:HA	8:H:507:SER:OG	1.59	1.02
4:G:695:THR:HB	4:G:705:TRP:NE1	1.73	1.02
1:A:1748:ILE:O	1:A:1752:VAL:HG23	1.58	1.02
3:I:112:MET:HB3	3:I:204:LEU:HD21	1.38	1.02
8:H:227:VAL:HG11	8:H:474:LYS:HG3	1.37	1.02
4:G:695:THR:O	4:G:699:PRO:HG3	1.58	1.02
27:F:78:A:O2'	27:F:79:C:O5'	1.76	1.02
1:A:1365:THR:O	1:A:1369:ASN:ND2	1.92	1.02
1:A:1035:LEU:HD12	1:A:1038:ILE:CG2	1.90	1.02
3:I:217:TYR:HE1	3:I:221:LYS:NZ	1.58	1.02
8:H:110:LYS:HE2	8:H:552:PRO:HG2	1.42	1.02
9:N:807:GLY:N	9:N:1093:ALA:CA	2.22	1.02
1:A:294:ASN:HB2	1:A:299:LYS:O	1.59	1.02
5:K:350:PRO:O	5:K:353:ARG:HG3	1.60	1.01
1:A:470:LEU:O	1:A:473:THR:HG22	1.60	1.01
1:A:837:GLY:CA	1:A:1317:ARG:NH1	2.23	1.01
27:F:95:C:O2'	27:F:96:U:H5'	1.60	1.01
8:H:388:ALA:HA	8:H:396:LEU:HD11	1.42	1.01
8:H:472:VAL:HG11	8:H:571:TYR:CE2	1.96	1.01
4:G:721:ARG:CD	4:G:725:ILE:HD11	1.90	1.01
8:H:504:THR:O	8:H:507:SER:OG	1.79	1.01
8:H:354:TYR:HB2	8:H:359:PHE:HB3	1.40	1.01
2:B:127:TYR:CE2	2:B:276:SER:HB2	1.96	1.01
8:H:793:GLU:HA	8:H:796:ILE:HG22	1.39	1.01

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:283:ARG:HD2	4:G:284:LEU:HD22	1.43	1.00
8:H:608:GLN:HE22	8:H:641:GLU:HG2	1.25	1.00
1:A:192:LEU:HD11	1:A:557:PHE:HB3	1.42	1.00
27:F:43:G:H2'	27:F:44:A:C8	1.96	1.00
2:B:446:SER:OG	2:B:451:PHE:HD2	1.42	1.00
4:G:691:TYR:O	4:G:695:THR:HG23	1.62	1.00
27:F:39:U:H2'	27:F:40:C:H5'	1.43	1.00
1:A:837:GLY:HA3	1:A:1317:ARG:NH1	1.77	1.00
8:H:488:ILE:CG2	8:H:558:LYS:CA	2.39	1.00
27:F:73:U:H2'	27:F:74:U:C5'	1.90	1.00
8:H:488:ILE:HG21	8:H:557:HIS:C	1.81	0.99
8:H:862:TYR:HE1	8:H:908:VAL:HB	1.27	0.99
1:A:1008:LEU:CD2	1:A:1073:ILE:HD11	1.91	0.99
8:H:500:ARG:HD3	8:H:534:THR:HG23	1.42	0.99
8:H:481:ALA:HB3	8:H:565:LYS:HZ1	1.25	0.99
8:H:582:SER:HB2	8:H:585:ASP:HB2	1.44	0.99
8:H:187:ARG:NH1	8:H:653:ASP:OD2	1.95	0.99
8:H:133:ILE:O	8:H:134:ILE:CG2	2.11	0.99
8:H:576:THR:HG22	8:H:592:PHE:HB2	1.40	0.99
8:H:304:PHE:HD2	8:H:310:ASN:CB	1.76	0.99
8:H:901:GLU:OE2	8:H:903:ARG:NH2	1.95	0.99
4:G:274:SER:CB	4:G:277:ILE:CD1	2.13	0.98
8:H:500:ARG:HE	8:H:534:THR:HG21	1.21	0.98
27:F:73:U:C2'	27:F:74:U:C5'	2.39	0.98
8:H:387:TYR:O	8:H:391:MET:HB2	1.62	0.98
1:A:912:LEU:HD11	1:A:951:LEU:HD21	1.42	0.98
8:H:572:ILE:HD12	8:H:573:LYS:HG3	1.45	0.98
8:H:863:GLU:HB3	8:H:931:TYR:CE1	1.97	0.98
2:B:388:GLN:OE1	2:B:388:GLN:N	1.96	0.98
8:H:855:PRO:O	8:H:944:VAL:HG11	1.45	0.98
2:B:398:GLN:OE1	2:B:442:SER:OG	1.80	0.98
1:A:168:LEU:HB2	1:A:199:ILE:HD12	1.41	0.98
8:H:677:PHE:HE1	8:H:966:PHE:CE2	1.82	0.98
8:H:227:VAL:HG11	8:H:474:LYS:CG	1.92	0.98
6:L:96:GLY:O	6:L:138:ASN:HB3	1.63	0.98
1:A:497:GLN:O	1:A:709:ARG:HD2	1.62	0.98
4:G:230:LEU:HD12	4:G:247:SER:HA	1.40	0.98
8:H:168:VAL:CG1	8:H:173:LYS:CG	2.41	0.97
8:H:889:TYR:CE1	8:H:890:LYS:CG	2.47	0.97
8:H:855:PRO:HG2	8:H:944:VAL:HG21	1.42	0.97
3:I:358:ILE:HG23	3:I:359:PRO:HD2	1.44	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:465:GLU:OE1	8:H:466:GLY:N	1.97	0.97
1:A:322:VAL:HG21	1:A:327:TYR:CE2	1.99	0.97
8:H:855:PRO:C	8:H:944:VAL:CG1	2.26	0.97
24:C:-4:A:H1'	24:C:-3:A:OP1	1.64	0.97
3:I:266:LYS:HG3	3:I:267:HIS:H	1.26	0.97
2:B:235:ILE:CD1	2:B:280:ILE:HD13	1.95	0.97
27:F:43:G:H2'	27:F:44:A:H8	1.26	0.97
8:H:304:PHE:HD2	8:H:310:ASN:HB3	1.25	0.97
25:D:78:G:N2	26:E:4:C:C2	2.33	0.97
4:G:672:LEU:HD21	4:G:704:LEU:CG	1.93	0.97
4:G:251:GLU:OE1	4:G:260:ALA:HB2	1.65	0.97
6:L:116:ILE:CD1	6:L:137:TYR:OH	2.13	0.96
8:H:677:PHE:CE1	8:H:966:PHE:CE2	2.53	0.96
3:I:282:GLU:HG2	3:I:286:PHE:CG	2.00	0.96
8:H:492:LEU:CD2	8:H:557:HIS:ND1	2.28	0.96
4:G:846:PHE:HE1	4:G:859:LEU:HD21	0.91	0.96
8:H:576:THR:HG21	8:H:592:PHE:H	1.26	0.96
8:H:863:GLU:HB3	8:H:931:TYR:HE1	1.27	0.96
1:A:773:SER:OG	1:A:774:ILE:CD1	2.13	0.96
8:H:481:ALA:HB3	8:H:565:LYS:NZ	1.80	0.96
2:B:197:GLY:HA2	2:B:221:ILE:HG13	1.47	0.96
3:I:123:ARG:CD	3:I:189:LEU:CD1	2.41	0.96
8:H:324:ILE:O	8:H:328:VAL:HG23	1.66	0.96
3:I:226:ALA:CA	3:I:317:ASP:OD2	2.13	0.95
1:A:1008:LEU:HD22	1:A:1073:ILE:HD11	1.46	0.95
6:L:105:PHE:CZ	6:L:137:TYR:HE2	1.72	0.95
8:H:458:ILE:CG2	8:H:459:PRO:CD	2.43	0.95
6:L:81:THR:HG21	6:L:102:LYS:NZ	1.80	0.95
27:F:77:A:H4'	27:F:78:A:H5''	1.49	0.95
27:F:44:A:C2'	27:F:45:A:H8	1.78	0.95
8:H:106:PHE:CE2	8:H:554:HIS:CE1	2.55	0.95
4:G:663:SER:CA	4:G:667:CYS:SG	2.55	0.95
4:G:666:ILE:O	4:G:670:PHE:CD2	2.19	0.95
8:H:364:PHE:CD2	8:H:369:LYS:HD3	1.96	0.95
1:A:362:GLU:HB3	1:A:1209:LYS:HE3	1.45	0.95
1:A:1654:TRP:HZ3	1:A:1779:LEU:HD12	1.29	0.95
8:H:501:ILE:CD1	8:H:567:ILE:HG22	1.95	0.95
8:H:458:ILE:HG22	8:H:459:PRO:HD2	1.47	0.95
25:D:49:A:H2'	25:D:50:G:H5''	1.46	0.95
8:H:131:GLU:OE1	8:H:445:PRO:HG3	1.66	0.95
8:H:372:THR:HG22	8:H:376:PHE:CD1	2.01	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:331:TYR:CE1	8:H:404:PHE:HD1	1.84	0.95
1:A:362:GLU:HB3	1:A:1209:LYS:HE2	1.47	0.94
27:F:99:U:O2'	27:F:100:A:OP1	1.84	0.94
27:F:175:G:N2	27:F:176:A:H62	1.65	0.94
8:H:168:VAL:HG11	8:H:173:LYS:HD3	1.46	0.94
1:A:1658:HIS:HA	1:A:1661:ILE:HD12	1.49	0.94
4:G:107:LEU:O	4:G:110:SER:OG	1.86	0.94
6:L:105:PHE:CB	6:L:141:ARG:CG	2.42	0.94
4:G:663:SER:C	4:G:667:CYS:SG	2.45	0.94
1:A:1490:ARG:HH12	1:A:1536:LEU:HA	1.33	0.94
8:H:383:LYS:O	8:H:387:TYR:HB2	1.68	0.94
27:F:175:G:N2	27:F:176:A:N6	2.16	0.94
1:A:366:GLU:HB2	1:A:372:ARG:NH1	1.81	0.94
26:E:151:G:N2	26:E:152:A:H62	1.65	0.94
8:H:488:ILE:CD1	8:H:560:GLN:CG	2.42	0.94
8:H:608:GLN:NE2	8:H:641:GLU:HG2	1.82	0.94
2:B:235:ILE:HD12	2:B:280:ILE:HD13	1.47	0.94
27:F:73:U:H2'	27:F:74:U:H5'	0.95	0.94
4:G:692:LEU:CD2	4:G:708:LEU:HD11	1.98	0.94
1:A:165:LEU:O	1:A:168:LEU:HB3	1.68	0.94
1:A:162:LEU:HG	1:A:734:PHE:HE2	1.32	0.94
8:H:332:TYR:HH	8:H:376:PHE:HD2	1.06	0.93
2:B:290:ARG:NE	2:B:302:LEU:HD13	1.82	0.93
3:I:199:GLU:O	3:I:203:ILE:HG13	1.68	0.93
1:A:168:LEU:HA	1:A:199:ILE:HD11	1.48	0.93
3:I:123:ARG:HD3	3:I:189:LEU:HD13	0.94	0.93
8:H:197:THR:CG2	8:H:545:LEU:HD13	1.96	0.93
1:A:1022:PRO:HD3	1:A:1345:TYR:HE1	1.32	0.93
24:C:2:A:H2	27:F:98:U:H3	1.06	0.93
6:L:96:GLY:O	6:L:138:ASN:CB	2.16	0.93
26:E:151:G:N2	26:E:152:A:N6	2.16	0.93
8:H:489:TYR:HD2	8:H:592:PHE:HZ	1.11	0.93
8:H:486:VAL:HG12	8:H:564:ILE:CD1	1.99	0.93
4:G:286:GLU:O	4:G:288:ASP:N	2.02	0.93
25:D:48:C:H3'	25:D:49:A:C8	1.99	0.93
8:H:219:VAL:HG21	8:H:931:TYR:HB3	1.51	0.93
8:H:855:PRO:O	8:H:944:VAL:HG21	1.67	0.93
1:A:212:VAL:HG11	1:A:285:PRO:HB3	1.46	0.93
8:H:192:LYS:HA	8:H:224:GLU:OE1	1.67	0.93
27:F:45:A:C2	27:F:46:C:C5	2.56	0.93
8:H:510:ARG:CB	8:H:591:PHE:HE2	1.80	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:K:341:VAL:HG21	5:K:428:TRP:HE1	1.32	0.93
4:G:843:VAL:HG21	4:G:895:LEU:HD13	1.51	0.93
8:H:449:PHE:CE1	8:H:453:THR:HG21	2.04	0.92
6:L:105:PHE:HZ	6:L:137:TYR:CE2	1.82	0.92
27:F:98:U:H4'	27:F:99:U:OP1	1.69	0.92
1:A:1621:VAL:HG12	1:A:1622:GLY:H	1.34	0.92
1:A:703:PHE:CE1	1:A:706:PRO:HD3	2.04	0.92
6:L:140:LYS:C	6:L:141:ARG:HD2	1.90	0.92
8:H:468:LEU:HD21	8:H:577:LEU:CD2	1.99	0.92
4:G:285:HIS:CE1	4:G:291:TYR:CE2	2.57	0.92
2:B:358:SER:OG	2:B:401:PHE:CE1	2.20	0.92
3:I:112:MET:CB	3:I:204:LEU:HD21	2.00	0.92
1:A:773:SER:OG	1:A:774:ILE:HD12	1.68	0.92
1:A:455:PRO:HB2	1:A:457:ASP:OD1	1.70	0.92
1:A:781:THR:HA	1:A:784:GLN:CD	1.89	0.92
1:A:1748:ILE:HG22	1:A:1752:VAL:CG2	1.98	0.92
5:K:154:SER:O	5:K:158:ILE:HG23	1.68	0.92
8:H:506:GLN:O	8:H:509:SER:HB2	1.69	0.92
8:H:856:ILE:HA	8:H:944:VAL:HG12	0.94	0.92
8:H:500:ARG:HE	8:H:534:THR:CG2	1.77	0.92
4:G:274:SER:HB3	4:G:277:ILE:HD12	1.50	0.92
8:H:458:ILE:HG23	8:H:459:PRO:CD	1.99	0.92
8:H:330:TYR:CE1	8:H:430:ARG:CZ	2.52	0.91
2:B:115:SER:HA	2:B:118:ILE:CD1	1.99	0.91
8:H:889:TYR:CE1	8:H:890:LYS:HG2	2.04	0.91
8:H:372:THR:CG2	8:H:376:PHE:CE1	2.52	0.91
4:G:668:HIS:CB	4:G:698:VAL:HG11	2.00	0.91
1:A:1256:PRO:HA	1:A:1274:ARG:HH21	1.31	0.91
4:G:663:SER:HA	4:G:667:CYS:SG	2.09	0.91
1:A:1755:LYS:HG3	1:A:1759:TYR:CE2	2.06	0.91
8:H:132:ARG:HH11	8:H:132:ARG:HG2	1.35	0.91
8:H:488:ILE:HG22	8:H:558:LYS:HA	0.93	0.91
8:H:582:SER:HB2	8:H:585:ASP:OD2	1.69	0.91
8:H:489:TYR:CD2	8:H:592:PHE:HZ	1.88	0.91
1:A:286:LEU:CD2	1:A:292:LYS:HB2	2.01	0.91
1:A:288:GLU:OE1	1:A:288:GLU:N	2.04	0.91
4:G:105:ALA:O	4:G:108:LYS:HG3	1.71	0.91
8:H:889:TYR:CD1	8:H:890:LYS:CG	2.53	0.90
8:H:329:SER:HA	8:H:333:ALA:HB2	1.53	0.90
7:M:95:ARG:HG2	7:M:95:ARG:HH11	1.34	0.90
1:A:298:TYR:O	1:A:493:MET:HG3	1.70	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:389:ILE:HD13	2:B:427:TRP:HB3	1.53	0.90
1:A:412:GLN:OE1	1:A:412:GLN:N	2.05	0.90
4:G:695:THR:HB	4:G:705:TRP:HE1	1.33	0.90
8:H:185:ILE:HD13	27:F:75:A:OP2	1.72	0.90
2:B:173:VAL:HG13	2:B:200:GLN:OE1	1.70	0.90
1:A:317:PRO:HG2	1:A:318:LEU:HD12	1.51	0.90
6:L:81:THR:HG21	6:L:102:LYS:HZ1	1.35	0.90
27:F:75:A:N7	27:F:77:A:C5'	2.35	0.90
1:A:322:VAL:HG21	1:A:327:TYR:CD2	2.06	0.90
4:G:668:HIS:O	4:G:672:LEU:HG	1.72	0.90
27:F:75:A:O2'	27:F:76:U:OP2	1.89	0.90
2:B:313:LEU:CD1	2:B:322:VAL:HG23	2.02	0.90
2:B:316:GLN:HB2	2:B:357:TRP:CE2	2.07	0.90
8:H:481:ALA:CB	8:H:565:LYS:NZ	2.35	0.90
8:H:168:VAL:HG13	8:H:173:LYS:HD3	0.93	0.89
1:A:165:LEU:HD22	1:A:730:ILE:HD11	1.51	0.89
4:G:695:THR:O	4:G:699:PRO:CG	2.20	0.89
3:I:184:LYS:CE	3:I:186:LYS:HB2	2.03	0.89
8:H:355:HIS:O	8:H:356:LYS:CG	2.19	0.89
6:L:105:PHE:CZ	6:L:137:TYR:HD2	1.84	0.89
4:G:272:PRO:HB3	4:G:302:PHE:HD1	1.35	0.89
1:A:218:SER:CA	1:A:318:LEU:HD21	2.02	0.89
8:H:598:ILE:HG22	8:H:933:TRP:HZ3	1.32	0.89
8:H:674:LEU:HD13	8:H:973:ARG:HH12	1.35	0.89
6:L:105:PHE:HB3	6:L:141:ARG:HG2	0.89	0.89
25:D:48:C:H4'	25:D:49:A:OP1	1.73	0.89
8:H:500:ARG:CG	8:H:534:THR:HG21	2.03	0.89
8:H:855:PRO:O	8:H:944:VAL:CB	2.21	0.89
4:G:721:ARG:HD3	4:G:725:ILE:HD11	1.53	0.89
8:H:889:TYR:CE1	8:H:890:LYS:HG3	2.06	0.88
4:G:266:ASN:O	4:G:269:GLN:HG3	1.73	0.88
8:H:855:PRO:O	8:H:944:VAL:HG13	1.72	0.88
1:A:294:ASN:CB	1:A:299:LYS:O	2.22	0.88
25:D:83:A:O2'	25:D:84:C:OP2	1.92	0.88
2:B:274:HIS:HD2	2:B:276:SER:H	1.20	0.88
1:A:923:TYR:CE1	1:A:933:GLU:HG3	2.08	0.88
4:G:277:ILE:HD12	4:G:277:ILE:H	1.36	0.88
24:C:7:A:O2'	24:C:8:U:O5'	1.92	0.88
25:D:50:G:O2'	25:D:51:A:O5'	1.91	0.88
5:K:428:TRP:CZ2	5:K:463:PHE:CE2	2.61	0.88
8:H:304:PHE:CD2	8:H:310:ASN:HB3	2.07	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:855:PRO:CG	8:H:944:VAL:HG21	2.03	0.88
2:B:124:LEU:O	2:B:128:SER:OG	1.90	0.88
3:I:373:ARG:HB3	3:I:373:ARG:HH11	1.38	0.88
8:H:582:SER:HB2	8:H:585:ASP:CB	2.03	0.88
3:I:98:PHE:HE2	3:I:217:TYR:CD2	1.91	0.88
1:A:850:GLY:O	1:A:853:THR:HG22	1.73	0.88
2:B:393:ARG:HG2	2:B:393:ARG:HH21	1.37	0.88
1:A:466:GLU:OE2	1:A:466:GLU:N	2.06	0.88
8:H:364:PHE:HB3	8:H:369:LYS:HG3	1.53	0.88
6:L:105:PHE:HB2	6:L:141:ARG:HG2	1.56	0.88
8:H:501:ILE:HD13	8:H:567:ILE:HG22	1.55	0.88
1:A:501:LEU:H	1:A:501:LEU:HD12	1.38	0.88
6:L:101:ASN:O	6:L:102:LYS:HG2	1.73	0.88
8:H:415:TYR:O	8:H:416:ASP:OD1	1.92	0.88
4:G:702:PRO:HB3	4:G:739:PHE:CZ	2.09	0.88
2:B:124:LEU:HD21	2:B:274:HIS:CE1	2.08	0.88
8:H:189:LEU:HD12	8:H:190:SER:N	1.89	0.88
8:H:168:VAL:CG1	8:H:173:LYS:HG3	2.04	0.87
1:A:297:SER:HB2	27:F:32:G:O5'	1.74	0.87
4:G:891:ILE:O	4:G:894:ARG:N	2.07	0.87
2:B:395:ILE:HG22	2:B:396:VAL:H	1.38	0.87
2:B:380:LYS:O	2:B:381:ARG:HG2	1.73	0.87
1:A:141:LYS:CA	1:A:144:ASN:HD21	1.86	0.87
3:I:282:GLU:CD	3:I:286:PHE:CD2	2.48	0.87
2:B:446:SER:OG	2:B:451:PHE:CD2	2.19	0.87
4:G:212:VAL:H	4:G:215:LEU:HD23	1.39	0.87
4:G:691:TYR:HB3	4:G:708:LEU:CD1	2.03	0.87
4:G:282:ILE:O	4:G:286:GLU:HG2	1.73	0.87
5:K:350:PRO:HA	5:K:353:ARG:CD	2.04	0.87
5:K:141:ASN:OD1	5:K:142:LEU:N	2.07	0.87
4:G:692:LEU:HD23	4:G:708:LEU:HD11	1.55	0.87
24:C:8:U:C5	25:D:51:A:N6	2.34	0.87
1:A:358:ARG:HB3	1:A:358:ARG:HH11	1.37	0.87
1:A:266:LEU:HD23	1:A:267:PRO:HD2	1.55	0.87
8:H:306:PRO:HG2	8:H:349:TRP:CZ3	2.09	0.87
27:F:98:U:O2'	27:F:99:U:O5'	1.92	0.87
1:A:1353:THR:O	1:A:1357:LEU:HD12	1.73	0.87
8:H:250:GLU:HB3	8:H:298:PHE:CE2	2.09	0.86
1:A:1373:LEU:HD13	6:L:139:HIS:HE1	1.36	0.86
3:I:282:GLU:OE2	3:I:286:PHE:CD2	2.27	0.86
1:A:168:LEU:HB2	1:A:199:ILE:CD1	2.03	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:274:HIS:CD2	2:B:276:SER:HB3	2.10	0.86
1:A:837:GLY:HA3	1:A:1317:ARG:HH12	1.37	0.86
8:H:968:MET:HE2	8:H:968:MET:HA	1.57	0.86
1:A:1364:GLU:OE1	1:A:1389:TYR:OH	1.92	0.86
2:B:177:PRO:HB3	2:B:457:TRP:HA	1.56	0.86
8:H:489:TYR:CD2	8:H:592:PHE:CZ	2.64	0.86
8:H:488:ILE:HD13	8:H:557:HIS:O	1.74	0.86
3:I:191:ILE:H	3:I:191:ILE:HD12	1.38	0.86
6:L:140:LYS:HB3	6:L:141:ARG:HD2	1.55	0.86
4:G:892:LEU:O	4:G:896:MET:HG2	1.75	0.86
3:I:282:GLU:CD	3:I:286:PHE:CE2	2.49	0.86
2:B:313:LEU:HD13	2:B:322:VAL:HG23	1.57	0.86
1:A:1373:LEU:CD1	6:L:139:HIS:HE1	1.88	0.86
8:H:489:TYR:HD2	8:H:592:PHE:CZ	1.93	0.86
4:G:886:CYS:SG	4:G:888:PRO:HD2	2.16	0.86
8:H:197:THR:HG23	8:H:545:LEU:O	1.76	0.86
1:A:149:MET:HB3	1:A:154:TYR:HD2	1.39	0.86
3:I:231:PHE:CD2	3:I:330:ALA:HB1	2.10	0.86
1:A:162:LEU:CD2	1:A:730:ILE:CG2	1.74	0.85
1:A:1490:ARG:NH1	1:A:1536:LEU:HD23	1.91	0.85
1:A:1875:ILE:HG22	1:A:1876:ASN:H	1.41	0.85
4:G:688:ARG:HH12	4:G:721:ARG:HE	1.24	0.85
8:H:481:ALA:CB	8:H:565:LYS:HZ3	1.89	0.85
2:B:159:LEU:HD13	2:B:430:MET:CE	2.05	0.85
1:A:286:LEU:HD21	1:A:292:LYS:CB	2.05	0.85
8:H:197:THR:CG2	8:H:545:LEU:HD12	2.06	0.85
8:H:608:GLN:HE22	8:H:641:GLU:CG	1.89	0.85
2:B:197:GLY:HA2	2:B:221:ILE:CG1	2.07	0.85
1:A:823:TRP:HZ3	1:A:855:LEU:HD21	1.39	0.85
8:H:492:LEU:HD21	8:H:557:HIS:HD1	1.34	0.85
8:H:117:ARG:CD	8:H:157:SER:O	2.23	0.85
1:A:936:GLU:O	1:A:940:ILE:HD12	1.77	0.85
4:G:691:TYR:CB	4:G:708:LEU:HD12	2.04	0.85
8:H:120:ARG:HG3	8:H:551:TYR:CE1	2.11	0.85
8:H:586:MET:O	8:H:589:LEU:HD23	1.77	0.85
2:B:115:SER:HA	2:B:118:ILE:HD12	1.57	0.85
8:H:235:VAL:HG22	8:H:261:VAL:HG12	1.59	0.85
1:A:1756:PHE:O	1:A:1760:THR:HG23	1.75	0.85
8:H:106:PHE:HE2	8:H:554:HIS:CE1	1.93	0.85
1:A:224:MET:HG3	1:A:701:CYS:O	1.77	0.85
1:A:928:ARG:HH21	4:G:145:THR:HG21	1.42	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:951:ILE:HB	8:H:952:PRO:HD2	1.58	0.85
8:H:855:PRO:HG2	8:H:944:VAL:CG2	2.05	0.85
1:A:162:LEU:HD21	1:A:730:ILE:CB	2.06	0.85
1:A:166:LYS:O	1:A:169:PRO:HD2	1.76	0.85
8:H:247:PHE:HA	8:H:250:GLU:OE1	1.76	0.85
1:A:1498:ASP:OD1	1:A:1502:LEU:CD1	2.25	0.85
2:B:124:LEU:CD2	2:B:274:HIS:CE1	2.60	0.84
1:A:176:LEU:HD23	1:A:708:TRP:HE1	1.42	0.84
8:H:605:ILE:HG13	8:H:652:MET:SD	2.17	0.84
2:B:117:LEU:HD23	2:B:300:LEU:HB3	1.58	0.84
8:H:501:ILE:HD13	8:H:567:ILE:CG2	2.05	0.84
8:H:486:VAL:HG11	8:H:564:ILE:HD11	1.57	0.84
8:H:449:PHE:HE1	8:H:453:THR:HG21	1.40	0.84
8:H:951:ILE:O	8:H:952:PRO:O	1.95	0.84
3:I:158:PHE:HA	3:I:161:LEU:HD12	1.57	0.84
4:G:278:TRP:CZ2	4:G:298:THR:HB	2.12	0.84
8:H:793:GLU:HA	8:H:796:ILE:CG2	2.06	0.84
1:A:251:TYR:HA	1:A:255:ILE:HD12	1.58	0.84
6:L:33:ARG:HD3	6:L:65:ASP:CG	1.98	0.84
1:A:703:PHE:HE1	1:A:706:PRO:HD3	1.40	0.84
8:H:862:TYR:HE1	8:H:908:VAL:CB	1.90	0.84
1:A:691:PHE:CZ	1:A:701:CYS:HA	2.13	0.84
4:G:888:PRO:O	4:G:892:LEU:HD23	1.77	0.84
8:H:504:THR:CA	8:H:507:SER:OG	2.25	0.84
2:B:320:SER:HB2	2:B:337:ARG:NH2	1.92	0.84
2:B:320:SER:HB2	2:B:337:ARG:HH22	1.42	0.84
27:F:39:U:C2'	27:F:40:C:H5'	2.06	0.84
27:F:175:G:H21	27:F:176:A:H62	1.23	0.84
1:A:1877:GLY:O	1:A:1894:ILE:N	2.11	0.84
1:A:175:LEU:O	1:A:175:LEU:HD12	1.76	0.84
25:D:86:G:H5''	25:D:86:G:H8	1.41	0.84
8:H:332:TYR:OH	8:H:376:PHE:CB	2.25	0.84
1:A:1073:ILE:HG23	1:A:1074:VAL:HG23	1.56	0.84
8:H:576:THR:CG2	8:H:592:PHE:HB2	2.07	0.84
1:A:195:THR:CG2	1:A:556:TYR:O	2.24	0.84
8:H:449:PHE:O	8:H:453:THR:HG23	1.77	0.84
1:A:1313:ASP:OD1	1:A:1359:ILE:HD13	1.78	0.84
27:F:78:A:N1	27:F:81:A:C5	2.46	0.84
24:C:-3:A:C8	24:C:-2:A:C5	2.61	0.84
1:A:218:SER:N	1:A:318:LEU:CD2	2.41	0.84
3:I:98:PHE:CE2	3:I:217:TYR:CD2	2.65	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:401:LEU:HD12	4:G:214:SER:HB3	1.58	0.84
1:A:176:LEU:CD2	1:A:708:TRP:HE1	1.90	0.84
1:A:1909:ALA:O	1:A:1913:THR:HG23	1.78	0.84
1:A:160:ALA:HB1	1:A:194:HIS:CE1	2.12	0.84
5:K:354:PHE:CE1	5:K:358:MET:HE3	2.08	0.84
4:G:122:ILE:HG13	4:G:123:PRO:HD2	1.57	0.84
8:H:542:ILE:O	8:H:553:VAL:HB	1.77	0.84
1:A:286:LEU:CD2	1:A:292:LYS:CB	2.56	0.83
1:A:170:HIS:ND1	1:A:547:LEU:HD23	1.93	0.83
1:A:1459:ALA:O	1:A:1463:THR:HG23	1.78	0.83
6:L:105:PHE:HE1	6:L:137:TYR:CE2	1.92	0.83
8:H:576:THR:HG21	8:H:592:PHE:N	1.92	0.83
4:G:863:PHE:HB3	4:G:889:ARG:HH22	1.41	0.83
5:K:350:PRO:CA	5:K:353:ARG:HG2	2.06	0.83
4:G:863:PHE:CE2	4:G:892:LEU:HD21	2.13	0.83
27:F:75:A:C5	27:F:77:A:H5''	2.13	0.83
8:H:576:THR:HB	8:H:592:PHE:HD2	1.41	0.83
27:F:75:A:N7	27:F:77:A:H5'	1.91	0.83
2:B:335:ASP:OD1	2:B:337:ARG:HD2	1.77	0.83
1:A:1214:ARG:HB2	1:A:1255:ASN:OD1	1.78	0.83
8:H:120:ARG:HG3	8:H:551:TYR:CZ	2.13	0.83
1:A:1453:ASP:O	1:A:1456:ARG:HG2	1.77	0.83
9:N:807:GLY:N	9:N:1093:ALA:N	2.23	0.83
27:F:33:U:O2'	27:F:34:C:P	2.37	0.83
4:G:268:CYS:SG	4:G:278:TRP:CZ2	2.72	0.83
26:E:151:G:H21	26:E:152:A:H62	1.23	0.83
1:A:923:TYR:CE1	1:A:933:GLU:CG	2.62	0.83
3:I:373:ARG:HH11	3:I:373:ARG:CB	1.91	0.83
2:B:441:ILE:HD11	2:B:457:TRP:HE1	1.42	0.83
4:G:696:ARG:C	4:G:699:PRO:HD3	1.98	0.83
8:H:307:ILE:HD12	8:H:324:ILE:HD11	1.59	0.83
2:B:197:GLY:HA2	2:B:221:ILE:CD1	2.08	0.83
2:B:47:GLU:O	2:B:51:VAL:HG23	1.78	0.83
3:I:98:PHE:O	3:I:101:ILE:HG22	1.78	0.83
25:D:62:A:C2	26:E:58:G:C2	2.66	0.83
1:A:753:TYR:HE1	6:L:37:ARG:HB3	1.44	0.83
5:K:341:VAL:HG21	5:K:428:TRP:NE1	1.93	0.82
5:K:146:GLU:HA	5:K:149:PHE:CD2	2.14	0.82
1:A:289:ASP:OD2	1:A:292:LYS:CG	2.27	0.82
8:H:372:THR:HG23	8:H:376:PHE:CE1	2.12	0.82
5:K:428:TRP:HZ2	5:K:463:PHE:HE2	1.27	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:116:THR:HG23	8:H:158:HIS:HD2	1.37	0.82
27:F:103:A:O2'	27:F:104:G:O5'	1.96	0.82
8:H:488:ILE:HG21	8:H:558:LYS:HA	1.59	0.82
2:B:389:ILE:HD11	2:B:427:TRP:CG	2.14	0.82
4:G:251:GLU:OE2	4:G:259:VAL:HB	1.79	0.82
1:A:795:ALA:HA	1:A:1095:MET:CE	2.09	0.82
2:B:170:SER:O	2:B:171:GLN:HB2	1.79	0.82
8:H:230:ALA:CB	8:H:595:LEU:HD21	2.09	0.82
25:D:62:A:H2'	25:D:63:G:H5'	1.61	0.82
5:K:164:HIS:ND1	5:K:164:HIS:O	2.13	0.82
8:H:674:LEU:CD1	8:H:973:ARG:HH12	1.93	0.82
2:B:419:ILE:HD11	2:B:443:LEU:CD1	2.10	0.82
8:H:797:GLN:HA	8:H:797:GLN:NE2	1.94	0.82
3:I:184:LYS:HD2	3:I:186:LYS:N	1.93	0.82
2:B:446:SER:OG	2:B:451:PHE:HB2	1.78	0.82
1:A:1350:ILE:HG23	1:A:1356:LEU:CD1	2.09	0.82
8:H:113:ILE:HG22	8:H:114:PRO:HD2	1.62	0.82
4:G:671:PHE:HZ	4:G:693:SER:HG	1.26	0.82
1:A:218:SER:CA	1:A:318:LEU:CD2	2.55	0.82
2:B:202:LEU:HD23	2:B:207:LEU:CD2	2.09	0.82
1:A:149:MET:HG2	1:A:154:TYR:CE2	2.15	0.82
1:A:1415:SER:OG	1:A:1746:HIS:NE2	2.12	0.82
1:A:923:TYR:HE1	1:A:933:GLU:HG3	1.44	0.81
1:A:1908:LEU:O	1:A:1908:LEU:HD12	1.80	0.81
2:B:323:CYS:SG	2:B:355:VAL:CG1	2.68	0.81
4:G:283:ARG:HD2	4:G:284:LEU:CD2	2.09	0.81
8:H:194:ASN:OD1	8:H:547:GLY:HA2	1.80	0.81
5:K:350:PRO:CA	5:K:353:ARG:CG	2.56	0.81
8:H:373:PHE:CD1	8:H:377:ILE:HD12	2.14	0.81
2:B:459:ARG:NH2	4:G:758:LEU:HD22	1.95	0.81
1:A:809:LYS:O	1:A:813:GLU:HG2	1.80	0.81
1:A:404:ASN:OD1	8:H:927:MET:CE	2.28	0.81
8:H:492:LEU:CD2	8:H:557:HIS:CG	2.62	0.81
8:H:230:ALA:HB2	8:H:595:LEU:HD21	1.60	0.81
4:G:104:PHE:O	4:G:107:LEU:N	2.14	0.81
4:G:702:PRO:HB3	4:G:739:PHE:CE1	2.16	0.81
6:L:33:ARG:CD	6:L:65:ASP:CG	2.49	0.81
2:B:51:VAL:HG13	2:B:76:LEU:CD1	2.09	0.81
8:H:810:GLU:CD	8:H:974:LYS:HG3	2.00	0.81
3:I:184:LYS:CD	3:I:186:LYS:HB2	2.10	0.81
4:G:721:ARG:HD2	4:G:725:ILE:HD11	1.60	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:289:ASP:O	1:A:293:VAL:CG1	2.24	0.81
2:B:195:TRP:O	2:B:219:GLY:O	1.99	0.81
8:H:183:GLN:OE1	8:H:657:TYR:CD2	2.34	0.81
1:A:1496:GLN:O	1:A:1499:ARG:HG2	1.81	0.81
8:H:946:ASP:O	8:H:964:ARG:HG2	1.80	0.81
8:H:471:HIS:O	8:H:486:VAL:HG23	1.81	0.81
27:F:32:G:C8	27:F:32:G:H5''	2.15	0.81
25:D:49:A:H2'	25:D:50:G:C5'	2.11	0.81
1:A:176:LEU:O	1:A:176:LEU:HD23	1.79	0.81
8:H:175:LEU:HD23	8:H:176:ARG:N	1.96	0.81
27:F:95:C:C4'	27:F:96:U:OP1	2.29	0.81
4:G:144:LYS:NZ	26:E:55:U:O5'	2.14	0.80
25:D:48:C:C3'	25:D:49:A:N7	2.34	0.80
1:A:149:MET:HG2	1:A:154:TYR:HE2	1.46	0.80
1:A:361:GLU:N	1:A:361:GLU:OE2	2.13	0.80
6:L:140:LYS:HB3	6:L:141:ARG:CD	2.11	0.80
8:H:568:SER:HA	8:H:571:TYR:HE1	1.45	0.80
8:H:769:TYR:CE1	8:H:799:PHE:HE2	1.99	0.80
8:H:369:LYS:O	8:H:369:LYS:HE2	1.80	0.80
8:H:598:ILE:CG2	8:H:933:TRP:CZ3	2.64	0.80
8:H:336:ILE:HD11	8:H:341:ILE:HG22	1.61	0.80
8:H:468:LEU:CD1	8:H:493:LEU:HD21	2.09	0.80
4:G:295:LEU:O	4:G:298:THR:OG1	1.98	0.80
3:I:268:LEU:HD12	3:I:271:GLU:CG	2.11	0.80
1:A:301:TRP:CD1	1:A:491:GLY:O	2.34	0.80
1:A:289:ASP:OD2	1:A:292:LYS:HG2	1.81	0.80
1:A:703:PHE:HE1	1:A:705:GLN:HB3	1.45	0.80
8:H:793:GLU:CA	8:H:796:ILE:HG22	2.11	0.80
8:H:296:ASN:HD21	8:H:304:PHE:H	1.26	0.80
8:H:470:ALA:HB1	8:H:486:VAL:CG2	2.10	0.80
2:B:446:SER:HB2	2:B:451:PHE:H	1.46	0.80
8:H:769:TYR:CE1	8:H:799:PHE:CE2	2.70	0.80
4:G:846:PHE:CD1	4:G:859:LEU:HD21	2.17	0.80
1:A:162:LEU:CG	1:A:730:ILE:CG2	2.58	0.80
8:H:121:ASP:OD1	8:H:122:TYR:N	2.15	0.80
8:H:168:VAL:HG12	8:H:173:LYS:HG3	1.63	0.80
1:A:781:THR:N	1:A:784:GLN:OE1	2.14	0.80
8:H:470:ALA:HB3	8:H:577:LEU:HB3	1.61	0.80
27:F:78:A:C6	27:F:81:A:N7	2.50	0.80
1:A:912:LEU:CD1	1:A:951:LEU:HD21	2.12	0.80
2:B:441:ILE:HD11	2:B:457:TRP:NE1	1.97	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:688:ARG:HH12	4:G:721:ARG:NE	1.79	0.80
1:A:1654:TRP:CH2	1:A:1779:LEU:HD12	2.17	0.80
1:A:305:LEU:HD11	1:A:476:ALA:HB2	1.63	0.80
1:A:166:LYS:HD3	1:A:167:TYR:CE1	2.17	0.79
2:B:316:GLN:HG3	2:B:357:TRP:CZ2	2.16	0.79
1:A:837:GLY:CA	1:A:1317:ARG:HH11	1.95	0.79
3:I:46:ILE:O	3:I:97:PHE:CZ	2.35	0.79
4:G:696:ARG:O	4:G:699:PRO:CD	2.30	0.79
27:F:32:G:H1	27:F:121:U:H3	1.31	0.79
4:G:863:PHE:CE2	4:G:892:LEU:HG	2.17	0.79
4:G:695:THR:O	4:G:699:PRO:CD	2.30	0.79
4:G:251:GLU:OE2	4:G:259:VAL:CG1	2.30	0.79
4:G:691:TYR:HE2	4:G:711:ILE:HD11	1.47	0.79
8:H:488:ILE:HG21	8:H:558:LYS:N	1.97	0.79
8:H:488:ILE:HG21	8:H:558:LYS:CA	2.10	0.79
1:A:585:ARG:HD2	1:A:733:GLN:CD	2.03	0.79
8:H:856:ILE:HA	8:H:944:VAL:HG13	1.59	0.79
8:H:856:ILE:CA	8:H:944:VAL:HG12	1.85	0.79
3:I:123:ARG:NH1	3:I:187:GLU:O	2.14	0.79
1:A:1264:GLY:HA3	1:A:1308:GLU:OE1	1.83	0.79
3:I:197:ILE:C	3:I:201:ASN:HD22	1.85	0.79
4:G:672:LEU:CG	4:G:704:LEU:HD21	2.13	0.79
2:B:389:ILE:CD1	2:B:427:TRP:CB	2.46	0.79
3:I:217:TYR:HE1	3:I:221:LYS:HZ3	0.81	0.79
1:A:456:GLU:OE1	1:A:456:GLU:N	2.14	0.79
8:H:189:LEU:HD13	28:H:1500:GTP:O1G	1.82	0.79
4:G:691:TYR:CE2	4:G:711:ILE:CD1	2.66	0.79
4:G:691:TYR:CE2	4:G:711:ILE:HD11	2.18	0.79
8:H:449:PHE:CE1	8:H:453:THR:CG2	2.65	0.79
2:B:380:LYS:C	2:B:381:ARG:HG2	2.02	0.79
4:G:274:SER:HB3	4:G:277:ILE:HD11	0.79	0.79
25:D:83:A:H1'	25:D:84:C:H5	1.47	0.79
5:K:159:TYR:O	5:K:163:ASN:ND2	2.16	0.79
8:H:500:ARG:HE	8:H:534:THR:CB	1.96	0.78
6:L:140:LYS:CG	6:L:141:ARG:NH1	2.46	0.78
1:A:285:PRO:CD	1:A:298:TYR:OH	2.21	0.78
8:H:197:THR:HG21	8:H:545:LEU:HD12	1.64	0.78
4:G:98:SER:OG	4:G:99:ASN:ND2	2.16	0.78
8:H:167:ASN:ND2	8:H:173:LYS:HG2	1.98	0.78
27:F:77:A:C4'	27:F:78:A:H5''	2.14	0.78
7:M:93:VAL:HG12	7:M:95:ARG:H	1.48	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:468:LEU:HD11	8:H:493:LEU:CD2	2.09	0.78
1:A:1038:ILE:HD11	1:A:1039:TRP:CD2	2.17	0.78
8:H:467:THR:O	8:H:490:SER:HB3	1.82	0.78
3:I:138:SER:HA	3:I:141:ILE:HD12	1.64	0.78
2:B:51:VAL:HG13	2:B:76:LEU:HD11	1.66	0.78
8:H:863:GLU:CB	8:H:931:TYR:HE1	1.96	0.78
2:B:290:ARG:HE	2:B:302:LEU:HD13	1.45	0.78
1:A:923:TYR:HE1	1:A:933:GLU:CG	1.95	0.78
1:A:1755:LYS:CG	1:A:1759:TYR:HE2	1.96	0.78
3:I:266:LYS:HG3	3:I:267:HIS:N	1.98	0.78
6:L:33:ARG:HD2	6:L:65:ASP:OD2	1.83	0.78
9:N:565:ALA:CA	9:N:837:GLY:HA2	2.13	0.78
3:I:184:LYS:HD2	3:I:186:LYS:HB2	1.63	0.78
4:G:863:PHE:CE2	4:G:892:LEU:CG	2.67	0.78
1:A:2079:ILE:HA	1:A:2082:ILE:HD12	1.64	0.78
3:I:266:LYS:CG	3:I:267:HIS:H	1.96	0.78
8:H:116:THR:CG2	8:H:158:HIS:CD2	2.65	0.78
8:H:355:HIS:O	8:H:356:LYS:HG3	1.82	0.78
5:K:457:GLN:OE1	5:K:457:GLN:N	2.17	0.78
1:A:1468:ALA:HB1	1:A:1473:ARG:O	1.83	0.78
8:H:472:VAL:CG1	8:H:571:TYR:CE2	2.67	0.78
1:A:287:GLU:HB2	1:A:288:GLU:OE1	1.84	0.78
4:G:251:GLU:OE2	4:G:259:VAL:HG12	1.84	0.78
4:G:702:PRO:O	4:G:706:VAL:HG23	1.83	0.78
27:F:78:A:N1	27:F:81:A:C4	2.53	0.77
1:A:1697:SER:OG	1:A:1759:TYR:CD1	2.37	0.77
8:H:769:TYR:CZ	8:H:799:PHE:HE2	2.01	0.77
6:L:25:ARG:HB2	6:L:25:ARG:HH11	1.49	0.77
4:G:282:ILE:HA	4:G:295:LEU:HD12	1.66	0.77
8:H:862:TYR:CE1	8:H:908:VAL:HB	2.18	0.77
1:A:511:ASP:HB2	1:A:514:TYR:CE1	2.19	0.77
27:F:75:A:O2'	27:F:76:U:P	2.41	0.77
5:K:428:TRP:CZ2	5:K:463:PHE:HE2	2.01	0.77
1:A:1877:GLY:O	1:A:1894:ILE:HB	1.83	0.77
1:A:377:VAL:HG13	1:A:378:PRO:HD2	1.67	0.77
1:A:212:VAL:HG11	1:A:285:PRO:CB	2.15	0.77
8:H:195:GLY:HA3	8:H:545:LEU:HD22	1.66	0.77
6:L:139:HIS:NE2	27:F:96:U:C5'	2.48	0.77
4:G:212:VAL:HG13	4:G:215:LEU:HB3	1.66	0.77
1:A:823:TRP:CZ3	1:A:855:LEU:HD21	2.19	0.77
1:A:1313:ASP:CG	1:A:1359:ILE:HD13	2.05	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:F:31:G:C2	27:F:32:G:H1'	2.19	0.77
1:A:273:ASP:HB3	1:A:276:VAL:CG2	2.14	0.77
4:G:695:THR:CB	4:G:705:TRP:HE1	1.98	0.77
1:A:1654:TRP:CZ3	1:A:1779:LEU:HD11	2.17	0.77
8:H:794:GLN:OE1	8:H:835:LYS:HG3	1.84	0.77
8:H:947:LYS:CD	8:H:947:LYS:H	1.98	0.77
1:A:168:LEU:HA	1:A:199:ILE:CD1	2.14	0.77
5:K:146:GLU:O	5:K:148:LYS:N	2.18	0.77
8:H:151:ASP:OD1	8:H:175:LEU:HD22	1.85	0.77
2:B:316:GLN:HG3	2:B:357:TRP:CE2	2.20	0.77
1:A:1490:ARG:HH11	1:A:1536:LEU:HA	1.47	0.77
2:B:387:ASN:C	2:B:388:GLN:OE1	2.22	0.77
4:G:252:GLU:HG2	4:G:256:LYS:CG	2.15	0.77
2:B:64:VAL:HG12	2:B:65:GLU:H	1.49	0.77
1:A:317:PRO:HG2	1:A:318:LEU:CD1	2.15	0.77
9:N:1198:ARG:CA	9:N:1227:ILE:H	1.96	0.77
1:A:2064:GLY:O	1:A:2068:ASN:N	2.18	0.77
4:G:285:HIS:HE1	4:G:291:TYR:CE2	2.03	0.76
2:B:459:ARG:CZ	4:G:758:LEU:HD22	2.14	0.76
8:H:883:ARG:O	8:H:884:ARG:HB2	1.81	0.76
3:I:245:ALA:HB1	3:I:250:GLU:HB3	1.66	0.76
9:N:807:GLY:H	9:N:1093:ALA:CA	1.97	0.76
8:H:492:LEU:HD23	8:H:557:HIS:HA	1.66	0.76
1:A:912:LEU:HD11	1:A:951:LEU:CD2	2.16	0.76
8:H:189:LEU:HD21	8:H:218:HIS:HB2	1.67	0.76
8:H:265:PHE:CE2	8:H:295:ILE:HD12	2.20	0.76
2:B:286:ASP:C	2:B:287:MET:HG2	2.05	0.76
8:H:492:LEU:HD21	8:H:557:HIS:CG	2.20	0.76
5:K:350:PRO:HB3	25:D:84:C:C5	2.21	0.76
8:H:951:ILE:O	8:H:951:ILE:HD12	1.85	0.76
3:I:268:LEU:HD12	3:I:271:GLU:HG3	1.66	0.76
8:H:697:ARG:NE	8:H:697:ARG:HA	2.00	0.76
8:H:242:VAL:HG21	8:H:272:ARG:HD3	1.67	0.76
27:F:75:A:N7	27:F:77:A:H5''	2.00	0.76
8:H:545:LEU:H	8:H:545:LEU:HD12	1.51	0.76
8:H:355:HIS:O	8:H:356:LYS:HG2	1.86	0.76
8:H:942:GLY:HA3	8:H:961:SER:HA	1.67	0.76
27:F:106:A:C2'	27:F:107:C:H5'	2.16	0.76
1:A:162:LEU:HG	1:A:734:PHE:CE2	2.17	0.76
1:A:2079:ILE:HG22	1:A:2083:ILE:HD11	1.65	0.76
1:A:1073:ILE:HD12	1:A:1116:TYR:CE1	2.19	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1902:GLN:O	1:A:1905:LEU:HD21	1.85	0.76
4:G:251:GLU:OE2	4:G:259:VAL:CB	2.34	0.76
1:A:1313:ASP:OD1	1:A:1359:ILE:HG21	1.85	0.76
1:A:165:LEU:HD12	1:A:578:MET:CG	2.15	0.76
8:H:372:THR:HG22	8:H:376:PHE:CE1	2.16	0.76
4:G:257:PHE:CG	4:G:258:SER:N	2.52	0.76
3:I:265:ASN:OD1	3:I:266:LYS:N	2.17	0.76
2:B:454:SER:HG	2:B:464:TRP:HE1	1.33	0.76
8:H:338:SER:HA	8:H:341:ILE:HD13	1.66	0.76
1:A:218:SER:HA	1:A:318:LEU:HD21	1.66	0.76
8:H:576:THR:HB	8:H:592:PHE:CD2	2.21	0.75
8:H:197:THR:HG23	8:H:545:LEU:HD13	1.68	0.75
1:A:217:TRP:C	1:A:318:LEU:HD21	2.05	0.75
1:A:1035:LEU:CD1	1:A:1038:ILE:HG21	2.09	0.75
2:B:154:SER:OG	2:B:155:ARG:HD3	1.85	0.75
1:A:928:ARG:NH2	4:G:145:THR:HG21	2.00	0.75
1:A:258:ILE:O	1:A:259:GLU:HB2	1.86	0.75
1:A:1863:HIS:HB2	1:A:1871:ALA:HB3	1.67	0.75
8:H:468:LEU:CD1	8:H:493:LEU:CD2	2.63	0.75
1:A:253:GLN:O	1:A:257:ASN:ND2	2.19	0.75
8:H:118:TYR:HD1	8:H:119:ASN:O	1.69	0.75
8:H:233:ASP:OD1	8:H:487:ARG:NH2	2.17	0.75
1:A:296:THR:CG2	27:F:33:U:OP2	2.34	0.75
8:H:504:THR:C	8:H:507:SER:HG	1.89	0.75
8:H:133:ILE:C	8:H:134:ILE:HG23	2.07	0.75
1:A:543:ASN:HD22	1:A:544:LYS:N	1.83	0.75
2:B:345:LEU:HD13	2:B:376:TRP:CD2	2.20	0.75
8:H:146:LYS:HE2	28:H:1500:GTP:O3G	1.85	0.75
1:A:1647:GLN:HG2	25:D:52:G:OP2	1.86	0.75
1:A:1058:ALA:HB2	1:A:1114:PHE:CE1	2.15	0.75
8:H:304:PHE:CD2	8:H:310:ASN:CB	2.66	0.75
1:A:219:ALA:O	1:A:266:LEU:CD1	2.35	0.75
8:H:860:PRO:HB3	8:H:937:TRP:CZ3	2.21	0.75
4:G:672:LEU:HD21	4:G:704:LEU:HD23	1.15	0.75
6:L:139:HIS:CD2	27:F:96:U:H5"	2.21	0.75
1:A:322:VAL:CG2	1:A:327:TYR:CD2	2.69	0.75
8:H:331:TYR:CE1	8:H:404:PHE:CD1	2.73	0.75
1:A:276:VAL:HG11	1:A:310:ASN:HB3	1.68	0.75
8:H:456:LEU:HD23	8:H:456:LEU:N	2.02	0.75
1:A:1038:ILE:HD11	1:A:1039:TRP:CE3	2.21	0.75
3:I:151:LYS:O	3:I:152:ASN:HB2	1.85	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:510:ARG:HD3	8:H:591:PHE:CE2	2.21	0.75
1:A:806:ALA:O	1:A:810:LYS:HG2	1.87	0.75
27:F:31:G:H2'	27:F:32:G:O4'	1.85	0.74
2:B:121:ARG:O	2:B:125:ILE:HG13	1.86	0.74
3:I:401:LEU:CD1	4:G:214:SER:HA	2.17	0.74
2:B:155:ARG:O	2:B:159:LEU:HG	1.85	0.74
1:A:180:PRO:HA	1:A:187:LYS:CD	2.17	0.74
1:A:192:LEU:HD12	1:A:558:GLN:O	1.87	0.74
8:H:458:ILE:HG22	8:H:459:PRO:CD	2.14	0.74
4:G:863:PHE:HB3	4:G:889:ARG:NH2	2.02	0.74
1:A:1035:LEU:HD21	1:A:1160:LEU:HD11	1.69	0.74
3:I:192:LYS:O	3:I:195:THR:OG1	2.05	0.74
1:A:1629:LEU:HD23	1:A:1630:THR:HG23	1.68	0.74
1:A:1256:PRO:HA	1:A:1274:ARG:NH2	2.03	0.74
8:H:489:TYR:CE2	8:H:592:PHE:CE1	2.76	0.74
1:A:289:ASP:OD2	1:A:292:LYS:CB	2.34	0.74
4:G:863:PHE:HZ	4:G:892:LEU:HD21	1.47	0.74
8:H:476:VAL:CG1	8:H:478:TYR:HD1	2.01	0.74
24:C:2:A:H2	27:F:98:U:N3	1.84	0.74
1:A:1275:MET:HE1	1:A:1299:LYS:HE3	1.69	0.74
1:A:180:PRO:HA	1:A:187:LYS:HD3	1.67	0.74
5:K:315:ARG:NH1	25:D:72:C:O2	2.18	0.74
8:H:306:PRO:HG2	8:H:349:TRP:CE3	2.22	0.74
1:A:1275:MET:HE1	1:A:1299:LYS:CE	2.18	0.74
1:A:299:LYS:HA	1:A:493:MET:HG2	1.69	0.74
8:H:504:THR:C	8:H:507:SER:OG	2.26	0.74
1:A:1922:ARG:HE	1:A:1951:PHE:HZ	1.35	0.74
2:B:195:TRP:O	2:B:220:LYS:HA	1.86	0.74
26:E:139:A:O2'	26:E:140:G:OP2	2.05	0.74
4:G:281:ASN:ND2	4:G:295:LEU:CD1	2.51	0.74
24:C:-5:A:H4'	24:C:-4:A:OP2	1.88	0.74
4:G:863:PHE:CZ	4:G:892:LEU:CD2	2.61	0.74
1:A:173:LEU:HD11	1:A:712:LEU:HD11	1.68	0.74
1:A:773:SER:OG	1:A:774:ILE:HD11	1.87	0.74
5:K:146:GLU:HA	5:K:149:PHE:CE2	2.21	0.74
3:I:231:PHE:HD2	3:I:330:ALA:HB1	1.50	0.74
1:A:404:ASN:OD1	8:H:927:MET:HE1	1.87	0.74
3:I:272:LEU:HD13	3:I:272:LEU:O	1.87	0.74
2:B:410:LEU:HB2	2:B:422:TYR:HB2	1.68	0.74
1:A:874:ILE:O	1:A:875:THR:OG1	2.06	0.74
8:H:305:SER:OG	8:H:307:ILE:HG22	1.87	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:545:LEU:N	8:H:545:LEU:HD12	2.03	0.73
8:H:798:GLY:O	8:H:801:TRP:HB3	1.88	0.73
1:A:174:LYS:HD2	1:A:202:VAL:O	1.88	0.73
8:H:372:THR:HG23	8:H:376:PHE:HE1	1.53	0.73
2:B:115:SER:HA	2:B:118:ILE:CG1	2.17	0.73
1:A:297:SER:CB	27:F:32:G:OP1	2.33	0.73
8:H:354:TYR:CA	8:H:359:PHE:HB3	2.17	0.73
2:B:374:ASN:HB3	2:B:376:TRP:HE1	1.53	0.73
1:A:365:ASN:OD1	1:A:366:GLU:N	2.22	0.73
8:H:326:GLU:HG3	8:H:434:GLY:HA3	1.71	0.73
8:H:132:ARG:HG2	8:H:132:ARG:NH1	2.01	0.73
26:E:2:U:C5	26:E:3:C:C5	2.76	0.73
1:A:930:ASN:HB3	1:A:933:GLU:OE1	1.89	0.73
2:B:232:ASN:HB3	2:B:247:GLN:HE22	1.51	0.73
8:H:500:ARG:CG	8:H:534:THR:CG2	2.62	0.73
27:F:33:U:O2'	27:F:34:C:O5'	2.05	0.73
1:A:1498:ASP:OD1	1:A:1502:LEU:HD11	1.87	0.73
8:H:274:ILE:HG21	8:H:385:PHE:CE2	2.23	0.73
1:A:1065:LEU:HD23	1:A:1069:LEU:HD13	1.70	0.73
4:G:99:ASN:O	4:G:103:GLN:HG3	1.88	0.73
2:B:159:LEU:HD13	2:B:430:MET:HE2	1.71	0.73
3:I:123:ARG:O	3:I:183:PHE:HB2	1.89	0.73
1:A:1857:VAL:O	1:A:1877:GLY:HA3	1.89	0.73
8:H:568:SER:HA	8:H:571:TYR:CE1	2.23	0.73
24:C:8:U:H2'	24:C:9:G:H5'	1.68	0.73
8:H:863:GLU:CB	8:H:931:TYR:CE1	2.71	0.73
4:G:655:PHE:CB	4:G:674:LEU:CD2	2.60	0.73
8:H:336:ILE:CD1	8:H:341:ILE:HG22	2.18	0.73
8:H:489:TYR:HE2	8:H:592:PHE:CE1	2.06	0.73
1:A:289:ASP:OD2	1:A:292:LYS:CA	2.36	0.73
4:G:281:ASN:HD22	4:G:295:LEU:CD1	2.01	0.73
1:A:151:SER:OG	1:A:152:LYS:N	2.22	0.73
5:K:333:LYS:N	5:K:333:LYS:HE2	2.04	0.73
1:A:1414:TRP:HZ3	1:A:1416:LYS:HB2	1.54	0.72
2:B:127:TYR:CE2	2:B:276:SER:CB	2.71	0.72
9:N:1122:GLY:HA3	9:N:1249:ASP:CA	2.18	0.72
27:F:44:A:C4	27:F:45:A:C8	2.76	0.72
1:A:585:ARG:HD2	1:A:733:GLN:NE2	2.03	0.72
1:A:1461:TYR:CE2	1:A:1494:LEU:HD11	2.24	0.72
1:A:1195:PHE:HB3	1:A:1217:ARG:NH1	2.04	0.72
2:B:385:GLN:HA	2:B:385:GLN:OE1	1.88	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:197:THR:HG22	8:H:545:LEU:CD1	2.20	0.72
8:H:959:ILE:CD1	8:H:960:ASN:H	2.00	0.72
1:A:1907:GLN:O	1:A:1910:LYS:HG2	1.89	0.72
1:A:751:ASP:OD1	1:A:752:ALA:N	2.22	0.72
8:H:581:LYS:HB3	8:H:581:LYS:HZ2	1.52	0.72
1:A:842:LYS:HD2	1:A:842:LYS:O	1.89	0.72
1:A:1373:LEU:HD13	6:L:139:HIS:CE1	2.22	0.72
8:H:476:VAL:HG12	8:H:478:TYR:HD1	1.55	0.72
24:C:2:A:C2	27:F:98:U:N3	2.57	0.72
8:H:336:ILE:CG1	8:H:341:ILE:HG22	2.19	0.72
2:B:230:SER:HB2	2:B:232:ASN:HD22	1.53	0.72
8:H:274:ILE:O	8:H:274:ILE:HD13	1.90	0.72
1:A:1464:LYS:O	1:A:1475:LEU:HD21	1.90	0.72
1:A:286:LEU:HD12	1:A:287:GLU:N	2.05	0.72
8:H:307:ILE:CD1	8:H:324:ILE:HD11	2.18	0.72
8:H:197:THR:HG22	8:H:545:LEU:HD13	1.71	0.72
27:F:94:C:N4	27:F:96:U:O2'	2.22	0.72
2:B:199:LEU:N	2:B:199:LEU:HD23	2.04	0.72
1:A:468:LEU:HD13	1:A:469:ILE:CD1	2.10	0.72
1:A:1846:ASN:HA	1:A:1885:LYS:NZ	2.03	0.72
2:B:197:GLY:CA	2:B:221:ILE:HG13	2.18	0.72
2:B:374:ASN:OD1	2:B:388:GLN:HG3	1.90	0.72
5:K:354:PHE:CE1	5:K:358:MET:HE2	2.24	0.72
27:F:95:C:O4'	27:F:96:U:OP1	2.07	0.72
8:H:947:LYS:HG2	8:H:948:ASP:OD1	1.90	0.72
3:I:427:SER:OG	3:I:428:ARG:N	2.20	0.72
3:I:346:GLU:O	3:I:347:ALA:HB3	1.87	0.72
1:A:1880:PHE:CE1	1:A:1882:LEU:HD12	2.25	0.72
1:A:778:LYS:HA	1:A:778:LYS:CE	2.20	0.72
1:A:1008:LEU:HD21	1:A:1073:ILE:HD11	1.70	0.72
8:H:967:VAL:HG12	8:H:968:MET:CE	2.20	0.72
1:A:967:VAL:HG23	1:A:1088:VAL:HG11	1.72	0.72
2:B:369:GLY:HA2	2:B:395:ILE:HG23	1.72	0.71
1:A:298:TYR:O	1:A:493:MET:CG	2.37	0.71
27:F:73:U:O2'	27:F:74:U:C5'	2.39	0.71
1:A:1751:TYR:CZ	1:A:1755:LYS:HD3	2.25	0.71
8:H:347:ARG:O	8:H:352:VAL:HG11	1.90	0.71
1:A:1069:LEU:HB3	1:A:1116:TYR:HE2	1.55	0.71
1:A:779:ALA:HA	1:A:782:ILE:CD1	2.15	0.71
1:A:1653:LEU:O	1:A:1653:LEU:HD12	1.90	0.71
1:A:1629:LEU:HD23	1:A:1630:THR:CG2	2.20	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1216:ILE:HD12	1:A:1254:ASN:HB3	1.72	0.71
2:B:135:ARG:NH1	2:B:139:GLU:OE2	2.23	0.71
8:H:168:VAL:HG12	8:H:173:LYS:CG	2.18	0.71
1:A:298:TYR:CE1	1:A:493:MET:HE1	2.26	0.71
1:A:315:SER:C	1:A:317:PRO:HD2	2.11	0.71
3:I:401:LEU:HD11	4:G:214:SER:HA	1.72	0.71
2:B:153:LEU:O	2:B:157:THR:HG23	1.90	0.71
2:B:220:LYS:HB3	2:B:239:GLU:HB3	1.71	0.71
8:H:944:VAL:HG23	8:H:945:LEU:HG	1.71	0.71
2:B:127:TYR:CD2	2:B:276:SER:HB2	2.26	0.71
3:I:135:LEU:CD2	3:I:136:GLN:HG3	2.20	0.71
5:K:350:PRO:O	5:K:353:ARG:CG	2.37	0.71
1:A:778:LYS:O	1:A:782:ILE:HG13	1.90	0.71
2:B:443:LEU:HD23	2:B:443:LEU:O	1.90	0.71
8:H:265:PHE:CD2	8:H:295:ILE:HD12	2.25	0.71
4:G:666:ILE:HG22	4:G:667:CYS:N	2.05	0.71
1:A:171:ALA:HB2	1:A:201:PHE:CD1	2.25	0.71
27:F:75:A:C8	27:F:77:A:H5''	2.22	0.71
6:L:139:HIS:NE2	27:F:96:U:H5''	2.06	0.71
2:B:313:LEU:CD1	2:B:322:VAL:CG2	2.68	0.71
2:B:415:TYR:OH	7:M:126:ILE:HA	1.91	0.71
27:F:77:A:H1'	27:F:78:A:H5'	1.71	0.71
8:H:332:TYR:CZ	8:H:376:PHE:HB3	2.26	0.71
8:H:799:PHE:CE1	8:H:846:CYS:SG	2.84	0.71
8:H:354:TYR:HA	8:H:359:PHE:HA	1.72	0.71
8:H:677:PHE:CE1	8:H:966:PHE:HD2	2.08	0.71
2:B:446:SER:CB	2:B:451:PHE:HB2	2.20	0.71
1:A:1415:SER:OG	1:A:1746:HIS:CD2	2.43	0.71
1:A:410:ILE:HG13	8:H:276:ASP:OD1	1.90	0.71
4:G:696:ARG:O	4:G:699:PRO:HD3	1.89	0.70
27:F:94:C:H6	27:F:94:C:C5'	2.04	0.70
2:B:359:PRO:HD2	2:B:407:GLY:HA3	1.73	0.70
8:H:501:ILE:HG21	8:H:570:ALA:HB3	1.73	0.70
1:A:162:LEU:HD23	1:A:730:ILE:HD13	1.71	0.70
1:A:770:MET:HE3	1:A:778:LYS:HB2	1.72	0.70
8:H:129:ILE:HD12	8:H:129:ILE:N	2.06	0.70
1:A:614:ARG:CZ	24:C:3:A:OP1	2.39	0.70
2:B:390:LEU:O	2:B:390:LEU:HG	1.91	0.70
1:A:774:ILE:HG23	1:A:777:LYS:HE3	1.73	0.70
5:K:154:SER:O	5:K:158:ILE:CG2	2.39	0.70
2:B:359:PRO:HB2	2:B:406:GLY:O	1.91	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:K:350:PRO:HG3	5:K:353:ARG:CZ	2.21	0.70
1:A:823:TRP:CZ2	1:A:851:ARG:HG2	2.26	0.70
1:A:1877:GLY:O	1:A:1894:ILE:CB	2.38	0.70
1:A:1489:PRO:O	1:A:1533:ASP:O	2.10	0.70
1:A:2071:ILE:O	1:A:2071:ILE:HD13	1.91	0.70
4:G:143:ARG:CZ	4:G:143:ARG:HB3	2.20	0.70
27:F:39:U:H3	27:F:115:G:H1	1.38	0.70
8:H:488:ILE:HG21	8:H:557:HIS:O	1.91	0.70
1:A:2080:LYS:HA	1:A:2083:ILE:HD12	1.74	0.70
2:B:446:SER:HG	2:B:451:PHE:HD2	0.72	0.70
1:A:1846:ASN:HA	1:A:1885:LYS:HZ1	1.56	0.70
4:G:630:SER:CB	4:G:670:PHE:HZ	1.95	0.70
8:H:364:PHE:CB	8:H:369:LYS:CG	2.27	0.70
1:A:1748:ILE:CG2	1:A:1752:VAL:HG22	2.12	0.70
1:A:1704:GLU:HA	1:A:1731:LYS:HG2	1.74	0.70
3:I:145:GLU:HA	3:I:145:GLU:OE2	1.90	0.70
27:F:31:G:C2	27:F:32:G:C4	2.80	0.70
4:G:863:PHE:HE2	4:G:892:LEU:CG	2.04	0.70
4:G:863:PHE:CE2	4:G:892:LEU:CD2	2.74	0.70
24:C:8:U:OP1	24:C:8:U:H4'	1.91	0.70
8:H:586:MET:HA	8:H:589:LEU:HD23	1.73	0.70
1:A:149:MET:HB3	1:A:154:TYR:CD2	2.25	0.70
1:A:514:TYR:HB3	1:A:518:VAL:CG2	2.22	0.70
2:B:362:TYR:HD1	2:B:362:TYR:H	1.38	0.70
1:A:1615:ASN:HD21	1:A:1634:LEU:HD23	1.56	0.70
1:A:1647:GLN:O	1:A:1650:ARG:HG2	1.92	0.70
4:G:98:SER:OG	4:G:99:ASN:N	2.24	0.70
2:B:380:LYS:O	2:B:381:ARG:CG	2.39	0.70
6:L:31:PHE:O	6:L:80:MET:HA	1.92	0.70
8:H:135:ASN:HD22	8:H:487:ARG:NH2	1.90	0.69
8:H:132:ARG:O	8:H:133:ILE:HG12	1.91	0.69
1:A:1022:PRO:HD3	1:A:1345:TYR:CE1	2.22	0.69
4:G:666:ILE:HG22	4:G:667:CYS:H	1.57	0.69
27:F:74:U:O2'	27:F:75:A:H5'	1.92	0.69
27:F:78:A:H61	27:F:81:A:N6	1.90	0.69
8:H:580:VAL:HG22	8:H:582:SER:H	1.57	0.69
8:H:474:LYS:NZ	8:H:630:PRO:HD3	2.06	0.69
4:G:251:GLU:OE2	4:G:260:ALA:N	2.25	0.69
8:H:105:ILE:HA	8:H:108:GLN:CD	2.12	0.69
4:G:862:MET:SD	4:G:862:MET:N	2.65	0.69
26:E:4:C:O2'	26:E:5:U:H5'	1.92	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:131:GLU:HA	8:H:131:GLU:OE2	1.92	0.69
1:A:1756:PHE:CE1	1:A:1760:THR:HG21	2.27	0.69
8:H:113:ILE:HG23	8:H:549:TYR:CD1	2.27	0.69
27:F:78:A:C6	27:F:81:A:C5	2.80	0.69
1:A:1654:TRP:HZ3	1:A:1779:LEU:CD1	1.91	0.69
8:H:187:ARG:NH2	8:H:654:CYS:SG	2.66	0.69
8:H:959:ILE:HD12	8:H:959:ILE:N	2.06	0.69
3:I:93:LYS:O	3:I:96:PRO:HD2	1.91	0.69
8:H:161:ILE:HG23	8:H:162:PRO:HD2	1.75	0.69
8:H:143:HIS:HA	28:H:1500:GTP:O3B	1.91	0.69
1:A:1400:ILE:HG21	1:A:1440:ILE:HD11	1.75	0.69
1:A:305:LEU:HD11	1:A:476:ALA:CB	2.22	0.69
1:A:998:TYR:CE1	1:A:1002:GLU:HG3	2.28	0.69
2:B:274:HIS:CD2	2:B:276:SER:H	2.07	0.69
2:B:115:SER:HA	2:B:118:ILE:HG13	1.75	0.69
2:B:177:PRO:HD2	2:B:195:TRP:CD1	2.28	0.69
27:F:106:A:H2'	27:F:107:C:H5'	1.75	0.69
6:L:53:VAL:HG12	6:L:57:ALA:HB3	1.75	0.69
4:G:666:ILE:O	4:G:670:PHE:HD2	1.73	0.69
8:H:488:ILE:HD12	8:H:560:GLN:HG3	1.73	0.69
27:F:32:G:H4'	27:F:33:U:OP2	1.92	0.69
1:A:1647:GLN:O	1:A:1650:ARG:CG	2.40	0.69
1:A:1051:GLU:OE2	1:A:1261:SER:N	2.21	0.69
9:N:807:GLY:HA2	9:N:1093:ALA:H	0.66	0.69
2:B:235:ILE:HD12	2:B:280:ILE:CD1	2.20	0.69
5:K:141:ASN:HD21	5:K:144:LEU:HD23	1.58	0.69
4:G:851:ARG:O	4:G:852:LEU:HD12	1.92	0.69
1:A:1574:PHE:CE1	3:I:390:ARG:HD3	2.27	0.69
8:H:495:ARG:HH21	8:H:541:GLU:CD	1.96	0.69
8:H:582:SER:HB2	8:H:585:ASP:CG	2.12	0.69
8:H:349:TRP:HZ3	8:H:373:PHE:CE2	2.10	0.69
2:B:176:LYS:HB3	2:B:195:TRP:HB2	1.75	0.69
1:A:431:ILE:HD11	8:H:287:LYS:HA	1.74	0.69
8:H:572:ILE:HD12	8:H:573:LYS:CG	2.22	0.69
8:H:117:ARG:HD2	8:H:157:SER:C	2.13	0.69
3:I:217:TYR:CE1	3:I:221:LYS:NZ	2.45	0.69
2:B:117:LEU:HG	2:B:300:LEU:O	1.93	0.69
8:H:948:ASP:OD1	8:H:948:ASP:N	2.26	0.69
25:D:109:U:H3'	25:D:110:U:H5''	1.75	0.69
27:F:33:U:O2'	27:F:34:C:OP2	2.11	0.68
1:A:1882:LEU:HD13	1:A:1882:LEU:O	1.93	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:19:ILE:HD12	4:G:20:GLY:N	2.07	0.68
4:G:687:SER:O	4:G:690:THR:HG22	1.92	0.68
5:K:350:PRO:HG3	5:K:353:ARG:NH1	2.07	0.68
2:B:274:HIS:HD2	2:B:276:SER:N	1.89	0.68
6:L:101:ASN:O	6:L:102:LYS:CG	2.41	0.68
8:H:495:ARG:HG2	8:H:540:GLU:O	1.94	0.68
1:A:354:PRO:O	1:A:355:LEU:HB3	1.93	0.68
1:A:428:LEU:HD13	8:H:279:LEU:HD11	1.74	0.68
4:G:666:ILE:C	4:G:670:PHE:CD2	2.67	0.68
1:A:168:LEU:CA	1:A:199:ILE:HD11	2.21	0.68
27:F:78:A:N6	27:F:81:A:C5	2.61	0.68
8:H:332:TYR:OH	8:H:376:PHE:CD2	2.44	0.68
1:A:431:ILE:HA	8:H:895:ALA:HB1	1.74	0.68
8:H:470:ALA:HB3	8:H:577:LEU:HD22	1.76	0.68
3:I:183:PHE:CE2	3:I:185:ASN:ND2	2.58	0.68
2:B:419:ILE:HD11	2:B:443:LEU:HD12	1.73	0.68
5:K:303:LEU:C	5:K:303:LEU:HD23	2.13	0.68
3:I:98:PHE:CE2	3:I:217:TYR:HD2	2.09	0.68
6:L:25:ARG:HH11	6:L:25:ARG:CB	2.07	0.68
8:H:105:ILE:O	8:H:109:LEU:HD23	1.93	0.68
4:G:166:ARG:O	4:G:169:LEU:N	2.27	0.68
1:A:2075:THR:HG22	1:A:2077:THR:H	1.58	0.68
3:I:268:LEU:CD1	3:I:271:GLU:HG2	2.24	0.68
3:I:124:PHE:CE2	3:I:127:LEU:HB2	2.28	0.68
4:G:264:ILE:HG21	4:G:281:ASN:HA	1.75	0.68
1:A:837:GLY:HA2	1:A:1317:ARG:HH11	1.56	0.68
2:B:359:PRO:HB2	2:B:406:GLY:C	2.14	0.68
8:H:477:ASP:HB2	8:H:628:TYR:CE1	2.29	0.68
8:H:444:GLN:HE21	8:H:444:GLN:HA	1.57	0.68
4:G:693:SER:O	4:G:697:LEU:HG	1.94	0.68
27:F:78:A:N6	27:F:81:A:N7	2.41	0.68
8:H:330:TYR:HE1	8:H:430:ARG:NE	1.91	0.68
5:K:354:PHE:CE1	5:K:358:MET:SD	2.87	0.68
27:F:40:C:O2'	27:F:41:A:H5''	1.93	0.68
1:A:753:TYR:CE1	6:L:37:ARG:HB3	2.28	0.68
8:H:113:ILE:HD11	8:H:550:VAL:O	1.94	0.68
1:A:404:ASN:OD1	8:H:927:MET:HE3	1.92	0.68
6:L:39:CYS:SG	6:L:80:MET:HB3	2.34	0.68
8:H:142:LEU:HD12	8:H:929:GLN:HE21	1.57	0.68
1:A:358:ARG:CB	1:A:358:ARG:HH11	2.07	0.68
1:A:176:LEU:CD2	1:A:708:TRP:NE1	2.56	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:376:ARG:O	1:A:377:VAL:HB	1.93	0.68
8:H:855:PRO:O	8:H:944:VAL:HG22	1.92	0.67
8:H:577:LEU:C	8:H:577:LEU:HD23	2.15	0.67
1:A:296:THR:HG21	27:F:33:U:OP2	1.94	0.67
2:B:374:ASN:HB3	2:B:376:TRP:NE1	2.09	0.67
8:H:317:LYS:HB2	28:H:1500:GTP:C6	2.29	0.67
1:A:276:VAL:HG13	1:A:310:ASN:HD22	1.59	0.67
8:H:461:LYS:HD2	8:H:461:LYS:C	2.15	0.67
3:I:179:MET:HG3	3:I:183:PHE:CE1	2.28	0.67
8:H:197:THR:HG23	8:H:545:LEU:CD1	2.20	0.67
1:A:325:LYS:HB3	1:A:405:ASN:ND2	2.09	0.67
4:G:281:ASN:ND2	4:G:295:LEU:HD13	2.10	0.67
8:H:246:THR:O	8:H:250:GLU:HG3	1.94	0.67
2:B:159:LEU:HD13	2:B:430:MET:HE1	1.75	0.67
1:A:795:ALA:HA	1:A:1095:MET:HE3	1.75	0.67
9:N:1122:GLY:CA	9:N:1249:ASP:CA	2.73	0.67
4:G:238:PRO:HD2	4:G:239:THR:H	1.59	0.67
1:A:939:LEU:HD11	3:I:441:MET:CE	2.24	0.67
8:H:364:PHE:HB2	8:H:369:LYS:CB	2.21	0.67
8:H:488:ILE:CD1	8:H:560:GLN:HG3	2.23	0.67
1:A:1654:TRP:CH2	1:A:1779:LEU:CD1	2.78	0.67
8:H:116:THR:OG1	8:H:120:ARG:NH2	2.24	0.67
1:A:774:ILE:HG23	1:A:777:LYS:CE	2.24	0.67
1:A:691:PHE:HZ	1:A:701:CYS:HA	1.55	0.67
1:A:276:VAL:HG11	1:A:310:ASN:CB	2.24	0.67
8:H:936:ILE:HD13	8:H:936:ILE:H	1.59	0.67
8:H:364:PHE:HB2	8:H:369:LYS:CD	2.22	0.67
4:G:863:PHE:HE2	4:G:892:LEU:HG	1.58	0.67
8:H:677:PHE:CZ	8:H:966:PHE:CD2	2.82	0.67
6:L:33:ARG:HD2	6:L:65:ASP:CG	2.15	0.67
3:I:312:LEU:HB3	3:I:333:TRP:CH2	2.29	0.67
1:A:1197:ASN:ND2	1:A:1221:ASN:OD1	2.27	0.67
8:H:959:ILE:HD12	8:H:960:ASN:H	1.58	0.67
1:A:1400:ILE:HG22	1:A:1401:SER:H	1.60	0.67
1:A:175:LEU:HD12	1:A:175:LEU:C	2.15	0.67
8:H:105:ILE:HA	8:H:108:GLN:OE1	1.95	0.67
4:G:224:GLN:O	4:G:228:THR:HG23	1.95	0.67
3:I:280:ARG:NH2	26:E:37:U:OP2	2.27	0.67
6:L:105:PHE:HZ	6:L:137:TYR:HE2	1.18	0.67
1:A:165:LEU:CD1	1:A:578:MET:SD	2.72	0.67
27:F:48:G:H1	27:F:67:U:H3	1.41	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:F:77:A:H4'	27:F:78:A:OP1	1.95	0.67
1:A:1651:ALA:C	1:A:1652:HIS:CD2	2.68	0.67
8:H:330:TYR:CE1	8:H:430:ARG:NE	2.61	0.67
8:H:338:SER:O	8:H:341:ILE:HG12	1.95	0.67
3:I:92:ILE:HD12	3:I:92:ILE:N	2.09	0.67
8:H:486:VAL:CG1	8:H:564:ILE:CD1	2.59	0.67
3:I:123:ARG:CD	3:I:189:LEU:HD12	2.23	0.67
27:F:32:G:H8	27:F:32:G:H5"	1.60	0.67
5:K:350:PRO:CB	25:D:84:C:C5	2.78	0.67
8:H:316:THR:OG1	28:H:1500:GTP:N7	2.28	0.67
1:A:1703:MET:HB2	1:A:1732:MET:HB2	1.75	0.67
4:G:688:ARG:HH22	4:G:721:ARG:NH2	1.93	0.66
4:G:672:LEU:HD23	4:G:704:LEU:HD21	1.41	0.66
8:H:331:TYR:OH	8:H:428:ILE:HG23	1.95	0.66
8:H:415:TYR:C	8:H:416:ASP:OD1	2.33	0.66
1:A:511:ASP:HB2	1:A:514:TYR:HE1	1.60	0.66
8:H:271:ASP:O	8:H:274:ILE:HG22	1.94	0.66
1:A:371:ASP:O	8:H:969:LYS:HG3	1.94	0.66
1:A:1892:LYS:HD2	1:A:1916:GLU:CG	2.25	0.66
4:G:692:LEU:HD22	4:G:708:LEU:HD11	1.75	0.66
4:G:721:ARG:CD	4:G:725:ILE:CD1	2.72	0.66
27:F:31:G:N3	27:F:32:G:H1'	2.10	0.66
27:F:31:G:N2	27:F:32:G:H1'	2.10	0.66
8:H:329:SER:O	8:H:333:ALA:HB3	1.96	0.66
1:A:362:GLU:HB2	1:A:1209:LYS:HG2	1.77	0.66
8:H:189:LEU:C	8:H:189:LEU:HD12	2.14	0.66
3:I:231:PHE:CD2	3:I:330:ALA:CB	2.78	0.66
2:B:360:ASN:HB3	2:B:362:TYR:CE1	2.31	0.66
5:K:292:ALA:O	5:K:296:VAL:HG23	1.94	0.66
1:A:909:THR:CG2	1:A:910:LYS:N	2.57	0.66
8:H:329:SER:HA	8:H:333:ALA:CB	2.25	0.66
3:I:112:MET:HB3	3:I:204:LEU:CD2	2.22	0.66
3:I:358:ILE:HG23	3:I:359:PRO:CD	2.21	0.66
2:B:202:LEU:HD23	2:B:207:LEU:HD22	1.77	0.66
8:H:472:VAL:HG11	8:H:571:TYR:CZ	2.30	0.66
8:H:458:ILE:HB	8:H:590:LYS:HD3	1.76	0.66
8:H:219:VAL:CG2	8:H:931:TYR:HB3	2.25	0.66
1:A:1417:GLN:OE1	1:A:1422:ILE:HD11	1.96	0.66
8:H:354:TYR:HB3	8:H:359:PHE:HB3	1.75	0.66
8:H:317:LYS:HB2	28:H:1500:GTP:C5	2.30	0.66
2:B:380:LYS:O	2:B:382:ASP:OD1	2.13	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:456:GLY:O	2:B:459:ARG:N	2.21	0.66
3:I:197:ILE:C	3:I:201:ASN:ND2	2.44	0.66
25:D:51:A:OP1	25:D:51:A:H4'	1.96	0.66
2:B:314:SER:OG	2:B:355:VAL:O	2.10	0.66
8:H:495:ARG:CG	8:H:540:GLU:O	2.43	0.66
1:A:558:GLN:HA	1:A:558:GLN:OE1	1.95	0.66
2:B:177:PRO:HD2	2:B:195:TRP:HD1	1.61	0.66
25:D:109:U:H4'	25:D:110:U:OP2	1.95	0.66
8:H:444:GLN:NE2	8:H:444:GLN:HA	2.11	0.66
1:A:862:GLU:OE2	1:A:862:GLU:HA	1.96	0.66
27:F:50:G:H1	27:F:65:U:H3	1.41	0.66
2:B:274:HIS:CD2	2:B:275:PRO:HD2	2.30	0.66
1:A:362:GLU:CB	1:A:1209:LYS:HE2	2.22	0.66
1:A:1657:ILE:O	1:A:1661:ILE:HG13	1.95	0.66
2:B:313:LEU:HD11	2:B:322:VAL:CG2	2.26	0.66
1:A:923:TYR:CE1	1:A:933:GLU:HG2	2.30	0.66
1:A:1038:ILE:CD1	1:A:1039:TRP:CE3	2.78	0.66
2:B:316:GLN:CB	2:B:357:TRP:CE2	2.78	0.66
4:G:256:LYS:HG2	4:G:257:PHE:H	1.61	0.66
8:H:126:MET:CE	8:H:132:ARG:HH12	2.09	0.66
1:A:366:GLU:HB2	1:A:372:ARG:HH11	1.59	0.66
5:K:141:ASN:O	5:K:142:LEU:HD22	1.96	0.66
1:A:1041:VAL:HG11	1:A:1253:LYS:N	2.11	0.66
8:H:564:ILE:CG2	8:H:567:ILE:HG12	2.26	0.66
27:F:73:U:O2'	27:F:74:U:H5''	1.96	0.66
25:D:78:G:N2	26:E:4:C:O2	2.28	0.66
3:I:124:PHE:CD2	3:I:127:LEU:HB2	2.30	0.66
5:K:349:ASN:HB2	5:K:406:PHE:CE1	2.31	0.66
8:H:855:PRO:C	8:H:944:VAL:HG21	2.16	0.65
4:G:99:ASN:ND2	4:G:99:ASN:H	1.94	0.65
1:A:1591:THR:HG22	1:A:1592:HIS:N	2.11	0.65
8:H:110:LYS:HE2	8:H:552:PRO:CG	2.20	0.65
5:K:154:SER:O	5:K:158:ILE:CG1	2.44	0.65
5:K:155:LYS:O	5:K:158:ILE:HG13	1.96	0.65
8:H:797:GLN:HA	8:H:797:GLN:HE21	1.61	0.65
1:A:325:LYS:HB3	1:A:405:ASN:HD22	1.59	0.65
8:H:165:SER:OG	8:H:168:VAL:HG22	1.96	0.65
3:I:197:ILE:CG2	3:I:201:ASN:HD21	2.09	0.65
1:A:319:ARG:NH1	1:A:485:PRO:HG2	2.11	0.65
25:D:48:C:C2'	25:D:49:A:C8	2.79	0.65
2:B:227:HIS:HD2	2:B:273:TYR:CE1	2.14	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:K:154:SER:O	5:K:158:ILE:HG12	1.97	0.65
3:I:93:LYS:HA	3:I:93:LYS:HZ1	1.61	0.65
6:L:141:ARG:HD2	6:L:141:ARG:N	2.11	0.65
2:B:316:GLN:HB2	2:B:357:TRP:CE3	2.30	0.65
8:H:129:ILE:HG12	10:R:16:GLY:HA3	1.78	0.65
7:M:95:ARG:HG3	7:M:96:PRO:HD2	1.78	0.65
1:A:875:THR:OG1	1:A:878:GLU:HB2	1.96	0.65
8:H:888:ILE:HD12	8:H:888:ILE:H	1.60	0.65
3:I:120:TYR:HE2	3:I:141:ILE:HG12	1.59	0.65
2:B:202:LEU:HB3	2:B:207:LEU:HD23	1.79	0.65
1:A:809:LYS:O	1:A:813:GLU:CG	2.43	0.65
2:B:329:SER:CB	2:B:348:HIS:O	2.36	0.65
3:I:358:ILE:CG2	3:I:360:GLU:H	2.10	0.65
2:B:280:ILE:O	2:B:292:TRP:N	2.29	0.65
4:G:212:VAL:CG1	4:G:215:LEU:HB3	2.25	0.65
8:H:274:ILE:O	8:H:278:LYS:HA	1.96	0.65
2:B:147:ASN:HB3	2:B:150:GLN:OE1	1.95	0.65
4:G:278:TRP:CH2	4:G:298:THR:HB	2.31	0.65
8:H:306:PRO:HG2	8:H:349:TRP:CH2	2.31	0.65
1:A:404:ASN:HA	8:H:919:ARG:HH12	1.61	0.65
1:A:1279:VAL:HG11	1:A:1301:TYR:OH	1.96	0.65
1:A:1578:ALA:HB1	1:A:1602:PRO:HB3	1.78	0.65
3:I:179:MET:HG3	3:I:183:PHE:HE1	1.62	0.65
1:A:2060:LEU:HD21	1:A:2079:ILE:HG23	1.78	0.65
1:A:366:GLU:HB2	1:A:372:ARG:HH12	1.59	0.65
8:H:799:PHE:HE1	8:H:846:CYS:SG	2.20	0.65
8:H:503:ASP:OD1	8:H:571:TYR:HB2	1.97	0.65
1:A:770:MET:CE	1:A:775:ARG:O	2.45	0.65
1:A:173:LEU:HD11	1:A:712:LEU:CD1	2.27	0.65
2:B:381:ARG:HG3	2:B:382:ASP:OD1	1.97	0.65
1:A:875:THR:OG1	1:A:878:GLU:OE1	2.15	0.65
1:A:1145:MET:O	1:A:1146:GLN:HG3	1.97	0.64
8:H:160:ARG:HB3	8:H:161:ILE:HA	1.78	0.64
27:F:95:C:O2'	27:F:96:U:C5'	2.43	0.64
4:G:843:VAL:HG21	4:G:895:LEU:CD1	2.27	0.64
2:B:218:VAL:HG21	2:B:238:ALA:HB3	1.80	0.64
27:F:97:U:H5''	27:F:97:U:C6	2.33	0.64
1:A:1739:ARG:NH2	1:A:1745:SER:OG	2.31	0.64
1:A:767:LEU:HD21	1:A:779:ALA:CB	2.27	0.64
3:I:184:LYS:HE2	3:I:186:LYS:HB2	1.78	0.64
8:H:500:ARG:NE	8:H:534:THR:CB	2.57	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:207:ARG:NH1	1:A:299:LYS:HG2	2.13	0.64
1:A:168:LEU:CB	1:A:199:ILE:CD1	2.74	0.64
8:H:599:THR:CG2	8:H:933:TRP:CZ3	2.80	0.64
8:H:599:THR:HG22	8:H:932:PHE:O	1.98	0.64
8:H:862:TYR:OH	8:H:908:VAL:HG23	1.98	0.64
1:A:173:LEU:HD12	1:A:173:LEU:O	1.98	0.64
1:A:174:LYS:NZ	1:A:177:GLU:OE2	2.30	0.64
1:A:780:ARG:O	1:A:784:GLN:OE1	2.15	0.64
27:F:44:A:N3	27:F:45:A:C8	2.66	0.64
1:A:250:SER:O	1:A:254:HIS:HB2	1.96	0.64
3:I:266:LYS:CG	3:I:267:HIS:N	2.56	0.64
2:B:313:LEU:HD11	2:B:322:VAL:HG23	1.78	0.64
5:K:146:GLU:HA	5:K:149:PHE:HD2	1.62	0.64
6:L:76:LEU:N	6:L:76:LEU:HD12	2.11	0.64
1:A:676:GLN:N	1:A:676:GLN:OE1	2.31	0.64
2:B:374:ASN:CB	2:B:376:TRP:HE1	2.11	0.64
8:H:129:ILE:HD12	8:H:129:ILE:H	1.59	0.64
2:B:235:ILE:HD13	2:B:280:ILE:HD13	1.78	0.64
2:B:393:ARG:CG	2:B:393:ARG:HH21	2.09	0.64
3:I:401:LEU:HD12	4:G:214:SER:CB	2.27	0.64
26:E:24:A:C2	26:E:50:G:C2	2.86	0.64
1:A:1017:ASP:O	1:A:1509:ARG:NH1	2.31	0.64
2:B:48:ASP:OD2	2:B:69:VAL:HG21	1.96	0.64
6:L:91:MET:HE1	6:L:129:GLY:HA2	1.79	0.64
4:G:721:ARG:HD3	4:G:725:ILE:CD1	2.26	0.64
1:A:784:GLN:O	1:A:788:GLU:HG2	1.98	0.64
4:G:281:ASN:ND2	4:G:295:LEU:HD11	2.13	0.64
2:B:316:GLN:CG	2:B:357:TRP:CE2	2.81	0.64
8:H:197:THR:HG21	8:H:545:LEU:CD1	2.21	0.64
1:A:1876:ASN:OD1	1:A:1896:THR:HG23	1.97	0.64
1:A:273:ASP:O	1:A:276:VAL:HG22	1.97	0.64
2:B:311:PHE:CE2	7:M:126:ILE:HD13	2.32	0.64
26:E:1:A:N6	29:E:201:M7M:HBZB	2.13	0.64
27:F:76:U:H4'	27:F:76:U:OP2	1.97	0.64
8:H:164:MET:HG2	8:H:175:LEU:HD12	1.80	0.64
8:H:292:ILE:O	8:H:295:ILE:HG12	1.97	0.64
8:H:167:ASN:HD21	8:H:173:LYS:HG2	1.62	0.64
1:A:294:ASN:OD1	1:A:300:LYS:CE	2.45	0.64
1:A:703:PHE:CE1	1:A:705:GLN:HB3	2.30	0.64
1:A:1621:VAL:HG12	1:A:1622:GLY:N	2.07	0.64
8:H:470:ALA:CB	8:H:577:LEU:HD22	2.28	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:506:PHE:HA	1:A:522:TYR:CE1	2.33	0.64
5:K:304:ARG:NH1	26:E:13:G:OP1	2.31	0.64
5:K:325:GLU:HA	5:K:328:ASN:OD1	1.97	0.64
4:G:693:SER:HA	4:G:696:ARG:HD2	1.80	0.64
3:I:120:TYR:CE2	3:I:141:ILE:HG12	2.33	0.64
26:E:23:C:O2'	26:E:24:A:H5'	1.97	0.64
4:G:843:VAL:CG2	4:G:895:LEU:HD13	2.27	0.63
1:A:1458:TRP:CZ3	1:A:1461:TYR:CD2	2.86	0.63
2:B:415:TYR:HD2	2:B:439:LYS:HD3	1.61	0.63
8:H:105:ILE:HA	8:H:108:GLN:NE2	2.13	0.63
1:A:1076:PRO:O	1:A:1080:ASP:OD2	2.16	0.63
1:A:293:VAL:HG13	1:A:295:GLY:N	2.13	0.63
1:A:767:LEU:HD21	1:A:779:ALA:HB2	1.78	0.63
8:H:227:VAL:O	8:H:473:LEU:HD13	1.99	0.63
25:D:62:A:C2'	25:D:63:G:H5'	2.28	0.63
1:A:273:ASP:OD1	1:A:273:ASP:N	2.31	0.63
3:I:197:ILE:HG23	3:I:201:ASN:HD21	1.61	0.63
27:F:78:A:HO2'	27:F:79:C:P	2.18	0.63
8:H:463:THR:CB	8:H:585:ASP:OD1	2.47	0.63
2:B:273:TYR:CZ	2:B:280:ILE:HD11	2.33	0.63
2:B:114:THR:O	2:B:118:ILE:HG13	1.99	0.63
8:H:947:LYS:H	8:H:947:LYS:HD3	1.62	0.63
8:H:118:TYR:CD1	8:H:119:ASN:O	2.50	0.63
8:H:880:MET:HB3	8:H:886:SER:HA	1.81	0.63
1:A:1613:THR:O	1:A:1616:ARG:HD3	1.97	0.63
8:H:484:SER:HB3	8:H:571:TYR:OH	1.97	0.63
25:D:49:A:C2'	25:D:50:G:H5''	2.23	0.63
1:A:173:LEU:CD1	1:A:712:LEU:CD1	2.76	0.63
6:L:25:ARG:CG	6:L:25:ARG:HH11	2.10	0.63
24:C:10:U:O2'	24:C:11:A:H5'	1.99	0.63
8:H:945:LEU:HD12	8:H:945:LEU:H	1.63	0.63
3:I:98:PHE:CZ	3:I:217:TYR:HD2	2.15	0.63
27:F:40:C:OP2	27:F:40:C:H3'	1.99	0.63
3:I:282:GLU:OE1	3:I:286:PHE:CE2	2.52	0.63
3:I:225:ILE:C	3:I:325:ARG:HH12	2.01	0.63
1:A:1935:VAL:HG11	1:A:1940:MET:HB2	1.81	0.63
4:G:134:ARG:HB3	4:G:134:ARG:CZ	2.28	0.63
8:H:469:TRP:CD1	8:H:578:TYR:HB3	2.34	0.63
1:A:1317:ARG:HH21	1:A:1366:ARG:HH22	1.45	0.63
3:I:358:ILE:HG22	3:I:360:GLU:H	1.64	0.63
8:H:968:MET:CA	8:H:968:MET:HE2	2.29	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:175:LEU:HD11	1:A:564:TRP:CZ2	2.33	0.63
3:I:320:GLN:HG2	3:I:325:ARG:HA	1.80	0.63
3:I:206:ASN:O	3:I:209:LYS:HG2	1.98	0.63
8:H:363:PRO:O	8:H:364:PHE:HB3	1.98	0.63
4:G:886:CYS:C	4:G:888:PRO:HD2	2.19	0.63
8:H:889:TYR:HE1	8:H:890:LYS:HG3	1.57	0.63
27:F:94:C:H6	27:F:94:C:H5''	1.63	0.63
3:I:268:LEU:HD12	3:I:271:GLU:HG2	1.80	0.63
2:B:230:SER:OG	2:B:233:GLN:OE1	2.16	0.63
3:I:402:ASP:OD1	3:I:403:SER:N	2.31	0.63
2:B:391:ALA:O	2:B:392:HIS:HB2	1.97	0.63
1:A:1618:ASN:OD1	1:A:1618:ASN:N	2.31	0.63
1:A:1748:ILE:O	1:A:1752:VAL:CG2	2.41	0.63
1:A:1658:HIS:CA	1:A:1661:ILE:HD12	2.27	0.63
2:B:239:GLU:HA	2:B:267:ARG:HB2	1.81	0.63
5:K:452:LEU:O	5:K:456:GLY:N	2.31	0.63
4:G:279:LEU:N	4:G:279:LEU:HD23	2.13	0.63
1:A:393:SER:O	1:A:394:ARG:HG2	1.98	0.63
3:I:429:ARG:CB	3:I:429:ARG:HH11	2.11	0.63
4:G:666:ILE:C	4:G:670:PHE:HD2	2.02	0.63
4:G:702:PRO:HA	4:G:739:PHE:CE2	2.33	0.63
8:H:942:GLY:O	8:H:963:SER:OG	2.17	0.63
1:A:874:ILE:HD11	1:A:1062:ASP:HB2	1.81	0.63
27:F:92:U:H5''	27:F:92:U:H6	1.64	0.63
1:A:1118:GLY:HA3	1:A:1163:ARG:NH2	2.14	0.63
1:A:297:SER:CB	27:F:32:G:O5'	2.47	0.62
24:C:2:A:O5'	24:C:2:A:H8	1.82	0.62
1:A:1916:GLU:HA	1:A:1916:GLU:OE2	1.98	0.62
4:G:703:LEU:C	4:G:703:LEU:HD13	2.19	0.62
4:G:859:LEU:O	4:G:862:MET:HG2	1.99	0.62
1:A:1653:LEU:HD21	1:A:1815:LEU:HD23	1.80	0.62
8:H:959:ILE:CD1	8:H:960:ASN:N	2.61	0.62
8:H:178:LEU:N	8:H:178:LEU:HD23	2.14	0.62
9:N:807:GLY:H	9:N:1093:ALA:N	1.93	0.62
1:A:770:MET:HE1	1:A:779:ALA:N	2.15	0.62
8:H:126:MET:SD	8:H:132:ARG:NH1	2.72	0.62
3:I:102:ILE:HB	3:I:103:PRO:HD3	1.81	0.62
6:L:96:GLY:O	6:L:138:ASN:HB2	1.96	0.62
8:H:936:ILE:CD1	8:H:936:ILE:H	2.12	0.62
2:B:405:ASP:OD2	2:B:408:LYS:HD3	1.98	0.62
1:A:2018:ASN:HB3	1:A:2021:SER:OG	2.00	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:268:CYS:SG	4:G:278:TRP:HH2	2.15	0.62
8:H:129:ILE:HB	8:H:132:ARG:HB2	1.81	0.62
8:H:793:GLU:O	8:H:796:ILE:HG22	1.99	0.62
1:A:1275:MET:HE3	1:A:1299:LYS:HD2	1.81	0.62
5:K:141:ASN:ND2	5:K:144:LEU:HD23	2.14	0.62
24:C:3:A:O5'	24:C:3:A:H8	1.81	0.62
3:I:146:ASN:ND2	3:I:148:ASN:ND2	2.47	0.62
1:A:1880:PHE:CD2	1:A:1889:LEU:HD21	2.32	0.62
3:I:321:LYS:HD2	3:I:324:ASP:HB3	1.79	0.62
3:I:433:ASN:O	3:I:434:GLN:C	2.37	0.62
4:G:124:ASP:N	4:G:124:ASP:OD1	2.32	0.62
4:G:223:LEU:HD23	4:G:223:LEU:O	2.00	0.62
5:K:166:TYR:OH	5:K:174:LEU:HD12	2.00	0.62
8:H:483:TRP:CH2	8:H:565:LYS:HG3	2.34	0.62
2:B:292:TRP:CD1	2:B:299:GLU:HA	2.34	0.62
3:I:373:ARG:HB3	3:I:373:ARG:NH1	2.14	0.62
1:A:376:ARG:NE	8:H:910:GLU:OE2	2.32	0.62
3:I:433:ASN:O	3:I:434:GLN:O	2.18	0.62
4:G:857:VAL:O	4:G:860:TYR:HB2	1.99	0.62
1:A:840:VAL:HG22	1:A:840:VAL:O	2.00	0.62
8:H:202:ASP:N	8:H:202:ASP:OD1	2.31	0.62
24:C:5:G:H4'	24:C:6:U:OP1	1.98	0.62
8:H:931:TYR:HD1	8:H:931:TYR:O	1.83	0.62
8:H:379:ILE:O	8:H:383:LYS:HG3	1.99	0.62
1:A:1022:PRO:CD	1:A:1345:TYR:HE1	2.09	0.62
1:A:219:ALA:O	1:A:266:LEU:HD12	1.99	0.62
4:G:167:GLU:HG3	4:G:168:LYS:N	2.13	0.62
1:A:1458:TRP:CE3	1:A:1461:TYR:HD2	2.18	0.62
1:A:1887:GLY:HA3	1:A:1992:TYR:HD1	1.64	0.62
5:K:311:GLU:HA	5:K:311:GLU:OE1	2.00	0.62
4:G:688:ARG:HD3	4:G:692:LEU:HD21	1.81	0.62
1:A:780:ARG:C	1:A:784:GLN:OE1	2.38	0.62
1:A:286:LEU:CD2	1:A:292:LYS:HB3	2.28	0.62
8:H:326:GLU:OE1	8:H:330:TYR:HD2	1.82	0.62
8:H:582:SER:OG	8:H:585:ASP:OD2	2.17	0.62
8:H:674:LEU:CD1	8:H:973:ARG:HH22	2.12	0.62
1:A:175:LEU:CD1	1:A:564:TRP:CE2	2.83	0.62
2:B:165:LEU:N	2:B:165:LEU:HD23	2.14	0.62
9:N:487:CYS:O	9:N:490:ALA:N	2.33	0.62
4:G:281:ASN:HD22	4:G:295:LEU:HD13	1.65	0.62
1:A:169:PRO:HA	1:A:172:ILE:HD12	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:129:ILE:HG12	10:R:16:GLY:CA	2.30	0.62
5:K:280:VAL:O	5:K:286:ASN:ND2	2.33	0.62
5:K:282:GLU:O	5:K:284:ASP:N	2.32	0.62
6:L:34:LYS:HD2	6:L:35:ASN:H	1.64	0.62
4:G:285:HIS:CE1	4:G:291:TYR:CZ	2.87	0.61
4:G:230:LEU:HD12	4:G:247:SER:CA	2.23	0.61
1:A:1658:HIS:HA	1:A:1661:ILE:CD1	2.26	0.61
8:H:114:PRO:C	8:H:115:LYS:HG3	2.20	0.61
8:H:389:LEU:N	8:H:389:LEU:HD23	2.15	0.61
5:K:147:ASP:N	5:K:147:ASP:OD1	2.31	0.61
4:G:671:PHE:CE2	4:G:694:GLY:HA2	2.35	0.61
4:G:721:ARG:HD2	4:G:725:ILE:CD1	2.30	0.61
27:F:31:G:N1	27:F:32:G:C4	2.68	0.61
4:G:888:PRO:O	4:G:892:LEU:CD2	2.48	0.61
8:H:373:PHE:CE1	8:H:377:ILE:HD12	2.34	0.61
2:B:124:LEU:CD2	2:B:274:HIS:HE1	2.10	0.61
2:B:192:THR:HB	2:B:461:ILE:HD11	1.82	0.61
2:B:313:LEU:HD13	2:B:322:VAL:CG2	2.26	0.61
3:I:400:VAL:HG21	4:G:154:PRO:HG2	1.81	0.61
8:H:881:LYS:HA	8:H:886:SER:CB	2.30	0.61
1:A:1585:MET:HB3	1:A:1598:LEU:HD13	1.81	0.61
8:H:168:VAL:HG12	8:H:173:LYS:O	2.00	0.61
3:I:184:LYS:CD	3:I:186:LYS:H	2.01	0.61
8:H:581:LYS:HB3	8:H:581:LYS:NZ	2.11	0.61
24:C:11:A:O5'	24:C:11:A:H8	1.83	0.61
8:H:471:HIS:C	8:H:486:VAL:HG23	2.19	0.61
1:A:207:ARG:NH1	1:A:299:LYS:CG	2.63	0.61
1:A:837:GLY:O	1:A:1317:ARG:NH1	2.34	0.61
2:B:395:ILE:HD11	7:M:123:THR:HG23	1.80	0.61
4:G:215:LEU:HD12	4:G:215:LEU:C	2.20	0.61
1:A:1907:GLN:O	1:A:1910:LYS:CG	2.48	0.61
4:G:143:ARG:HH21	4:G:143:ARG:CG	2.14	0.61
3:I:93:LYS:HA	3:I:93:LYS:NZ	2.15	0.61
3:I:263:GLY:O	3:I:283:GLY:HA2	2.00	0.61
3:I:450:GLN:HG3	3:I:451:GLN:N	2.14	0.61
8:H:674:LEU:HD13	8:H:973:ARG:NH1	2.13	0.61
1:A:1340:ILE:O	1:A:1344:THR:OG1	2.18	0.61
4:G:238:PRO:CD	4:G:239:THR:H	2.14	0.61
4:G:6:PHE:CD1	4:G:7:LEU:N	2.68	0.61
1:A:843:THR:HG21	6:L:108:ASP:HB3	1.83	0.61
1:A:769:MET:CE	4:G:112:ALA:HA	2.29	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:956:LYS:HD2	1:A:956:LYS:C	2.21	0.61
9:N:807:GLY:C	9:N:1093:ALA:H	2.00	0.61
8:H:379:ILE:HG22	8:H:383:LYS:HE3	1.81	0.61
1:A:322:VAL:CG2	1:A:327:TYR:CE2	2.80	0.61
1:A:147:SER:O	1:A:150:ALA:HB2	2.00	0.61
1:A:514:TYR:HB3	1:A:518:VAL:HG21	1.83	0.61
8:H:139:ILE:HD12	8:H:252:LEU:HD22	1.81	0.61
1:A:892:SER:CB	1:A:1128:GLN:HE22	2.13	0.61
27:F:32:G:O2'	27:F:33:U:OP1	2.19	0.61
2:B:320:SER:CB	2:B:337:ARG:HH22	2.13	0.61
1:A:141:LYS:CA	1:A:144:ASN:ND2	2.54	0.61
8:H:106:PHE:O	8:H:110:LYS:HG2	2.00	0.61
8:H:968:MET:CE	8:H:968:MET:HA	2.30	0.61
2:B:456:GLY:O	2:B:458:ASP:N	2.34	0.61
1:A:1350:ILE:HG23	1:A:1356:LEU:HD12	1.81	0.61
2:B:206:THR:HB	2:B:208:GLN:OE1	2.00	0.61
27:F:74:U:H6	27:F:74:U:H5'	1.65	0.61
1:A:217:TRP:CD1	1:A:703:PHE:CE2	2.89	0.61
1:A:1275:MET:CE	1:A:1299:LYS:HD2	2.31	0.61
8:H:606:VAL:HG21	8:H:973:ARG:HH21	1.66	0.61
1:A:1468:ALA:CB	1:A:1473:ARG:O	2.49	0.61
24:C:11:A:O2'	24:C:12:U:H5'	2.01	0.61
3:I:393:PHE:C	3:I:393:PHE:CD1	2.73	0.61
8:H:369:LYS:NZ	8:H:369:LYS:H	1.99	0.61
8:H:132:ARG:HH21	8:H:206:LYS:HG3	1.66	0.61
1:A:495:ARG:CZ	1:A:497:GLN:HE21	2.12	0.61
8:H:235:VAL:HG22	8:H:261:VAL:CG1	2.29	0.61
8:H:883:ARG:NH2	8:H:910:GLU:O	2.34	0.61
1:A:355:LEU:HD13	1:A:356:TYR:N	2.16	0.61
1:A:1282:ASP:O	1:A:1285:VAL:HG23	2.01	0.61
1:A:1830:VAL:HG11	1:A:1958:PRO:HG3	1.80	0.61
4:G:668:HIS:HB3	4:G:698:VAL:CG1	2.21	0.61
8:H:576:THR:CB	8:H:592:PHE:HD2	2.11	0.61
1:A:293:VAL:HG22	1:A:294:ASN:H	1.65	0.61
3:I:135:LEU:HD23	3:I:136:GLN:HG3	1.83	0.61
4:G:702:PRO:CB	4:G:739:PHE:CZ	2.83	0.61
3:I:402:ASP:O	3:I:405:GLY:N	2.33	0.61
1:A:1887:GLY:HA3	1:A:1992:TYR:CD1	2.35	0.61
5:K:334:PRO:HG2	5:K:337:TYR:CE1	2.36	0.61
2:B:389:ILE:HD11	2:B:427:TRP:CD1	2.36	0.60
1:A:547:LEU:O	1:A:547:LEU:HD12	2.00	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:862:TYR:CE1	8:H:908:VAL:HG23	2.36	0.60
2:B:175:THR:HA	2:B:459:ARG:HD2	1.83	0.60
1:A:547:LEU:C	1:A:547:LEU:HD12	2.20	0.60
1:A:1998:ARG:C	1:A:1999:ILE:HG13	2.21	0.60
1:A:497:GLN:O	1:A:709:ARG:CD	2.46	0.60
3:I:158:PHE:HA	3:I:161:LEU:CD1	2.28	0.60
1:A:842:LYS:HD2	1:A:842:LYS:C	2.19	0.60
1:A:1158:ILE:HG13	1:A:1172:PHE:HE1	1.65	0.60
1:A:1624:LEU:HD21	1:A:1635:HIS:CE1	2.36	0.60
4:G:692:LEU:HD23	4:G:692:LEU:N	2.17	0.60
1:A:293:VAL:HG13	1:A:295:GLY:H	1.65	0.60
27:F:95:C:HO2'	27:F:96:U:H5'	1.63	0.60
7:M:95:ARG:NH1	7:M:95:ARG:HG2	2.01	0.60
1:A:358:ARG:CD	1:A:360:GLU:HB2	2.31	0.60
4:G:6:PHE:CE1	4:G:7:LEU:HD12	2.36	0.60
1:A:861:GLN:HE21	1:A:1097:HIS:HB3	1.66	0.60
4:G:630:SER:CA	4:G:670:PHE:CZ	2.84	0.60
2:B:127:TYR:CE2	2:B:276:SER:CA	2.85	0.60
2:B:320:SER:HB2	2:B:337:ARG:CZ	2.30	0.60
5:K:457:GLN:CD	5:K:457:GLN:H	1.98	0.60
1:A:325:LYS:HA	1:A:325:LYS:HE2	1.83	0.60
6:L:71:ASP:HA	6:L:76:LEU:HD13	1.82	0.60
27:F:44:A:C4	27:F:45:A:N7	2.69	0.60
24:C:8:U:C5	25:D:51:A:C6	2.90	0.60
3:I:123:ARG:HD2	3:I:189:LEU:CD1	2.31	0.60
27:F:102:C:H6	27:F:102:C:O5'	1.85	0.60
6:L:74:TYR:CD1	6:L:83:MET:HE3	2.37	0.60
5:K:244:LEU:O	5:K:248:ARG:HB2	2.02	0.60
8:H:352:VAL:HG13	8:H:372:THR:OG1	2.02	0.60
5:K:341:VAL:CG2	5:K:428:TRP:NE1	2.65	0.60
3:I:135:LEU:HD23	3:I:136:GLN:H	1.62	0.60
8:H:113:ILE:HG23	8:H:549:TYR:CG	2.37	0.60
2:B:187:ASP:OD2	2:B:447:ASN:HB3	2.01	0.60
4:G:855:ASP:N	4:G:855:ASP:OD1	2.34	0.60
3:I:123:ARG:HD2	3:I:189:LEU:HD12	1.83	0.60
2:B:331:SER:HB3	2:B:345:LEU:HB2	1.83	0.60
8:H:113:ILE:HG22	8:H:114:PRO:CD	2.30	0.60
27:F:32:G:N2	27:F:122:C:C2	2.70	0.60
24:C:8:U:N1	25:D:51:A:N6	2.48	0.60
8:H:349:TRP:HZ3	8:H:373:PHE:HE2	1.47	0.60
3:I:282:GLU:CG	3:I:286:PHE:CG	2.80	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:702:PRO:HB3	4:G:739:PHE:CE2	2.37	0.60
1:A:255:ILE:HG23	1:A:640:ARG:HG2	1.83	0.60
2:B:47:GLU:HB2	2:B:50:GLU:HG3	1.82	0.60
27:F:97:U:C5'	27:F:97:U:C6	2.85	0.60
1:A:1206:CYS:SG	1:A:1306:GLU:HG3	2.41	0.60
8:H:324:ILE:O	8:H:328:VAL:CG2	2.46	0.60
4:G:143:ARG:HH21	4:G:143:ARG:HG3	1.66	0.60
8:H:492:LEU:HD22	8:H:557:HIS:CG	2.36	0.59
1:A:173:LEU:CD1	1:A:712:LEU:HD11	2.32	0.59
3:I:265:ASN:O	3:I:266:LYS:HB2	2.02	0.59
1:A:266:LEU:HD23	1:A:267:PRO:CD	2.32	0.59
27:F:97:U:H5''	27:F:97:U:H6	1.67	0.59
6:L:71:ASP:OD1	6:L:76:LEU:HB2	2.02	0.59
4:G:6:PHE:CZ	6:L:18:ALA:HB2	2.37	0.59
1:A:1025:VAL:O	1:A:1029:THR:HG23	2.01	0.59
5:K:342:PHE:HB3	5:K:424:ILE:HD11	1.84	0.59
1:A:1354:GLU:N	1:A:1354:GLU:OE2	2.35	0.59
4:G:863:PHE:HE2	4:G:892:LEU:CD1	2.16	0.59
1:A:505:TRP:CZ3	1:A:690:LYS:HG3	2.37	0.59
6:L:81:THR:HG21	6:L:102:LYS:HZ3	1.62	0.59
1:A:1275:MET:CE	1:A:1299:LYS:CE	2.80	0.59
2:B:177:PRO:CD	2:B:195:TRP:CD1	2.85	0.59
2:B:177:PRO:HB2	2:B:195:TRP:HE1	1.66	0.59
1:A:1450:GLU:HB3	1:A:1488:ILE:HD11	1.83	0.59
5:K:350:PRO:HB3	5:K:353:ARG:HD2	1.84	0.59
3:I:184:LYS:HD2	3:I:186:LYS:CB	2.31	0.59
3:I:98:PHE:CE2	3:I:217:TYR:CE2	2.91	0.59
1:A:1857:VAL:O	1:A:1877:GLY:CA	2.49	0.59
1:A:1458:TRP:CZ3	1:A:1461:TYR:HD2	2.20	0.59
3:I:347:ALA:HB1	3:I:348:PRO:CD	2.31	0.59
7:M:125:LEU:O	7:M:126:ILE:C	2.39	0.59
8:H:364:PHE:HB2	8:H:369:LYS:HG3	0.63	0.59
8:H:332:TYR:OH	8:H:376:PHE:HD2	1.81	0.59
3:I:98:PHE:HE2	3:I:217:TYR:CE2	2.19	0.59
2:B:177:PRO:HB2	2:B:195:TRP:NE1	2.17	0.59
2:B:131:ARG:HG2	2:B:131:ARG:HH11	1.67	0.59
2:B:320:SER:CB	2:B:337:ARG:NH2	2.65	0.59
2:B:227:HIS:CD2	2:B:273:TYR:CE1	2.90	0.59
3:I:282:GLU:OE2	3:I:286:PHE:CE2	2.52	0.59
6:L:34:LYS:HD2	6:L:35:ASN:N	2.18	0.59
3:I:423:ALA:O	3:I:424:THR:HB	2.03	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:500:ARG:HD3	8:H:534:THR:CB	2.32	0.59
1:A:294:ASN:OD1	1:A:300:LYS:HE2	2.01	0.59
1:A:362:GLU:OE2	1:A:1209:LYS:HE3	2.01	0.59
3:I:112:MET:CB	3:I:204:LEU:CD2	2.79	0.59
2:B:124:LEU:O	2:B:128:SER:N	2.31	0.59
8:H:608:GLN:HG3	8:H:609:PRO:HD2	1.85	0.59
5:K:146:GLU:O	5:K:149:PHE:N	2.33	0.59
1:A:175:LEU:CD1	1:A:564:TRP:NE1	2.64	0.59
8:H:385:PHE:O	8:H:389:LEU:HG	2.03	0.59
3:I:301:GLN:OE1	3:I:344:LEU:HD13	2.01	0.59
1:A:766:ILE:O	1:A:770:MET:HG2	2.03	0.59
2:B:177:PRO:CD	2:B:195:TRP:HD1	2.15	0.59
3:I:233:VAL:HG12	3:I:237:ILE:HB	1.84	0.59
1:A:332:ASP:C	1:A:332:ASP:OD1	2.41	0.59
8:H:369:LYS:H	8:H:369:LYS:HE2	1.67	0.59
8:H:323:THR:OG1	8:H:326:GLU:HB2	2.03	0.59
8:H:932:PHE:O	8:H:933:TRP:CE3	2.56	0.59
8:H:230:ALA:HB3	8:H:473:LEU:HD13	1.84	0.59
3:I:393:PHE:C	3:I:393:PHE:HD1	2.05	0.59
4:G:277:ILE:HD12	4:G:277:ILE:N	2.15	0.59
27:F:44:A:C2'	27:F:45:A:C8	2.67	0.59
27:F:45:A:C2	27:F:46:C:C4	2.91	0.59
1:A:1414:TRP:CZ3	1:A:1416:LYS:HB2	2.37	0.59
1:A:316:THR:N	1:A:317:PRO:CD	2.66	0.59
3:I:94:LEU:HD13	3:I:98:PHE:CZ	2.38	0.59
5:K:141:ASN:HD21	5:K:144:LEU:CD2	2.15	0.59
8:H:959:ILE:HD13	8:H:960:ASN:N	2.17	0.59
1:A:149:MET:O	1:A:153:MET:CG	2.51	0.59
1:A:390:LEU:HD13	8:H:652:MET:SD	2.42	0.59
2:B:51:VAL:HG13	2:B:76:LEU:HD12	1.85	0.59
6:L:75:GLU:C	6:L:76:LEU:HD12	2.24	0.59
1:A:1577:LYS:NZ	3:I:397:GLU:OE2	2.36	0.59
1:A:546:LYS:O	1:A:550:SER:OG	2.18	0.59
5:K:249:ARG:HG2	5:K:249:ARG:HH11	1.67	0.59
8:H:567:ILE:HD13	8:H:567:ILE:N	2.18	0.58
2:B:358:SER:OG	2:B:401:PHE:CZ	2.48	0.58
4:G:702:PRO:HG3	4:G:738:LEU:HB2	1.85	0.58
6:L:33:ARG:NE	6:L:64:ILE:HB	2.18	0.58
1:A:425:ASP:OD2	1:A:426:PRO:HD2	2.03	0.58
8:H:362:LYS:HE2	8:H:365:GLU:HB2	1.84	0.58
1:A:1628:ASP:HB3	25:D:50:G:N2	2.18	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:449:PHE:CD1	8:H:453:THR:CG2	2.86	0.58
8:H:268:ASN:HD21	8:H:316:THR:CG2	2.17	0.58
2:B:456:GLY:O	2:B:457:TRP:C	2.42	0.58
1:A:176:LEU:C	1:A:176:LEU:HD23	2.22	0.58
2:B:415:TYR:OH	7:M:126:ILE:CA	2.51	0.58
25:D:109:U:C3'	25:D:110:U:H5''	2.31	0.58
2:B:405:ASP:OD2	2:B:408:LYS:CD	2.52	0.58
1:A:1158:ILE:CG1	1:A:1172:PHE:CE1	2.86	0.58
1:A:1147:PHE:CD2	1:A:1153:GLU:HG2	2.38	0.58
4:G:12:PRO:HB2	4:G:13:ALA:O	2.03	0.58
8:H:386:SER:O	8:H:390:SER:HB3	2.03	0.58
1:A:297:SER:HB3	27:F:32:G:P	2.41	0.58
2:B:115:SER:CA	2:B:118:ILE:HG13	2.32	0.58
1:A:165:LEU:CD2	1:A:730:ILE:HD11	2.29	0.58
1:A:1739:ARG:HD2	1:A:1751:TYR:CE2	2.38	0.58
2:B:127:TYR:OH	2:B:131:ARG:NH1	2.35	0.58
1:A:1880:PHE:HE2	1:A:1889:LEU:HD21	1.57	0.58
8:H:191:ILE:HG23	8:H:221:PHE:CE1	2.38	0.58
3:I:367:ARG:NH2	26:E:58:G:N7	2.52	0.58
6:L:74:TYR:CD1	6:L:83:MET:CE	2.86	0.58
8:H:881:LYS:HA	8:H:886:SER:HB2	1.84	0.58
1:A:1758:ASP:O	1:A:1762:ASP:HB2	2.04	0.58
1:A:168:LEU:CA	1:A:199:ILE:CD1	2.81	0.58
1:A:506:PHE:HA	1:A:522:TYR:CD1	2.39	0.58
8:H:476:VAL:CG1	8:H:478:TYR:CD1	2.85	0.58
8:H:145:GLY:N	28:H:1500:GTP:O2B	2.31	0.58
8:H:780:PRO:HA	8:H:783:ILE:HB	1.85	0.58
5:K:363:LEU:HD11	5:K:391:PHE:HD2	1.68	0.58
1:A:1664:ASP:O	1:A:1668:ILE:HG13	2.04	0.58
1:A:1854:ASP:OD1	1:A:1879:ILE:HG23	2.04	0.58
3:I:113:HIS:HD2	3:I:134:PRO:HA	1.68	0.58
4:G:630:SER:CA	4:G:670:PHE:HZ	2.16	0.58
8:H:572:ILE:O	8:H:572:ILE:HD12	2.03	0.58
2:B:446:SER:HB2	2:B:451:PHE:N	2.16	0.58
1:A:1496:GLN:O	1:A:1499:ARG:CG	2.51	0.58
24:C:-1:A:N3	24:C:-1:A:H2'	2.18	0.58
7:M:8:ALA:HA	7:M:80:PHE:CE2	2.38	0.58
4:G:849:TYR:O	4:G:853:GLY:N	2.35	0.58
8:H:369:LYS:CA	8:H:369:LYS:HE2	2.33	0.58
8:H:489:TYR:CE2	8:H:592:PHE:HE1	2.20	0.58
8:H:307:ILE:CD1	8:H:324:ILE:CD1	2.81	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1998:ARG:O	1:A:1999:ILE:CG1	2.44	0.58
1:A:839:HIS:NE2	27:F:96:U:C4	2.71	0.58
8:H:862:TYR:HD2	8:H:930:LEU:HB3	1.67	0.58
3:I:282:GLU:HG2	3:I:286:PHE:CD1	2.36	0.58
6:L:133:SER:OG	6:L:135:TYR:O	2.20	0.58
1:A:457:ASP:OD1	1:A:457:ASP:N	2.37	0.58
1:A:255:ILE:O	1:A:258:ILE:HG22	2.03	0.58
1:A:286:LEU:O	1:A:287:GLU:O	2.22	0.58
8:H:507:SER:O	8:H:510:ARG:N	2.37	0.58
8:H:296:ASN:HD21	8:H:304:PHE:N	2.00	0.58
1:A:1256:PRO:CA	1:A:1274:ARG:HH21	2.12	0.58
1:A:149:MET:CG	1:A:154:TYR:HE2	2.16	0.58
1:A:1313:ASP:OD2	1:A:1359:ILE:HD13	2.03	0.58
5:K:295:LYS:O	5:K:299:ASP:HB2	2.04	0.58
4:G:697:LEU:HD23	4:G:697:LEU:N	2.17	0.58
4:G:672:LEU:HD23	4:G:704:LEU:HD23	1.45	0.58
4:G:278:TRP:CE3	4:G:278:TRP:HA	2.38	0.58
1:A:1751:TYR:CE1	1:A:1755:LYS:CD	2.77	0.58
2:B:197:GLY:C	2:B:221:ILE:HD11	2.24	0.58
1:A:249:LEU:HD23	1:A:249:LEU:H	1.69	0.58
1:A:261:LEU:HD12	1:A:261:LEU:C	2.23	0.58
3:I:421:VAL:HG21	4:G:250:LEU:CD1	2.33	0.58
4:G:401:ILE:O	4:G:405:SER:N	2.35	0.58
8:H:489:TYR:HE2	8:H:592:PHE:HE1	1.52	0.57
4:G:867:GLU:OE2	4:G:888:PRO:CG	2.52	0.57
4:G:248:ALA:HB1	4:G:264:ILE:HD11	1.86	0.57
8:H:586:MET:CA	8:H:589:LEU:HD23	2.33	0.57
8:H:354:TYR:HA	8:H:359:PHE:CB	2.33	0.57
1:A:1073:ILE:CG2	1:A:1074:VAL:HG23	2.29	0.57
26:E:19:U:O2'	26:E:20:A:OP2	2.21	0.57
1:A:1308:GLU:OE1	1:A:1346:PHE:HZ	1.87	0.57
2:B:286:ASP:C	2:B:287:MET:CG	2.72	0.57
8:H:500:ARG:HG2	8:H:534:THR:CG2	2.33	0.57
4:G:846:PHE:CE1	4:G:859:LEU:HD23	2.36	0.57
8:H:353:TYR:O	8:H:359:PHE:HB2	2.04	0.57
8:H:349:TRP:CZ3	8:H:373:PHE:CE2	2.92	0.57
2:B:264:HIS:HE1	2:B:290:ARG:HD2	1.69	0.57
1:A:1256:PRO:CA	1:A:1274:ARG:NH2	2.67	0.57
1:A:552:LYS:HG3	1:A:553:ASN:N	2.19	0.57
2:B:278:LYS:C	2:B:279:PHE:HD1	2.08	0.57
4:G:764:LEU:O	4:G:768:PRO:HB3	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:124:LEU:C	2:B:128:SER:HG	2.01	0.57
2:B:443:LEU:HD11	2:B:452:LEU:HD11	1.86	0.57
1:A:833:ARG:HH21	1:A:840:VAL:HG23	1.69	0.57
3:I:147:GLU:CD	3:I:147:GLU:H	2.07	0.57
8:H:336:ILE:HG13	8:H:341:ILE:HG22	1.85	0.57
4:G:170:LEU:C	4:G:170:LEU:HD13	2.24	0.57
1:A:1283:GLU:HG2	1:A:1351:VAL:HB	1.84	0.57
6:L:119:THR:HG22	6:L:131:VAL:CG1	2.35	0.57
4:G:695:THR:CB	4:G:705:TRP:NE1	2.57	0.57
27:F:78:A:HO2'	27:F:79:C:C5'	2.10	0.57
3:I:189:LEU:HD23	3:I:193:THR:OG1	2.03	0.57
2:B:127:TYR:CE2	2:B:276:SER:HA	2.38	0.57
2:B:131:ARG:HG2	2:B:131:ARG:NH1	2.18	0.57
8:H:129:ILE:CD1	8:H:129:ILE:H	2.18	0.57
5:K:163:ASN:O	5:K:164:HIS:HB3	2.03	0.57
3:I:346:GLU:O	3:I:347:ALA:CB	2.53	0.57
8:H:369:LYS:CE	8:H:369:LYS:H	2.16	0.57
8:H:580:VAL:HG11	8:H:586:MET:HG2	1.85	0.57
8:H:132:ARG:NH2	8:H:206:LYS:HG3	2.19	0.57
3:I:217:TYR:O	3:I:220:SER:OG	2.18	0.57
5:K:144:LEU:HD22	5:K:144:LEU:H	1.69	0.57
1:A:251:TYR:CE2	1:A:566:GLU:OE1	2.58	0.57
6:L:74:TYR:HB2	6:L:76:LEU:HD11	1.86	0.57
1:A:1049:LEU:HD13	1:A:1260:PHE:HB3	1.87	0.57
1:A:2007:ARG:NH2	5:K:291:THR:OG1	2.35	0.57
4:G:698:VAL:N	4:G:699:PRO:HD3	2.20	0.57
8:H:306:PRO:O	8:H:324:ILE:HD13	2.04	0.57
8:H:227:VAL:CG1	8:H:474:LYS:HG3	2.25	0.57
1:A:224:MET:CE	1:A:702:GLY:HA3	2.34	0.57
1:A:301:TRP:CE2	1:A:491:GLY:HA3	2.40	0.57
8:H:488:ILE:HD13	8:H:560:GLN:HG2	1.81	0.57
4:G:846:PHE:CB	4:G:896:MET:SD	2.93	0.57
1:A:258:ILE:O	1:A:259:GLU:CB	2.53	0.57
1:A:430:PRO:O	1:A:431:ILE:HG22	2.05	0.57
3:I:344:LEU:HD23	3:I:344:LEU:N	2.20	0.57
6:L:22:GLU:OE2	6:L:58:VAL:HG11	2.04	0.57
7:M:39:GLU:HB2	26:E:32:G:O6	2.05	0.57
4:G:678:TYR:CZ	4:G:686:MET:HG2	2.40	0.57
3:I:155:ASP:OD1	3:I:155:ASP:N	2.35	0.57
1:A:165:LEU:CD2	1:A:726:ILE:HG21	2.35	0.57
27:F:99:U:HO2'	27:F:100:A:P	2.23	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2068:ASN:N	1:A:2068:ASN:OD1	2.38	0.57
8:H:697:ARG:CZ	8:H:697:ARG:HA	2.35	0.57
1:A:543:ASN:ND2	1:A:544:LYS:N	2.53	0.57
4:G:9:GLN:C	4:G:10:GLU:HG3	2.24	0.57
8:H:468:LEU:CD1	8:H:493:LEU:HD23	2.35	0.57
8:H:251:GLN:HG2	8:H:933:TRP:CE2	2.39	0.57
8:H:133:ILE:O	8:H:134:ILE:HG22	2.01	0.57
1:A:1378:LYS:O	1:A:1379:MET:CB	2.53	0.57
8:H:331:TYR:HE1	8:H:404:PHE:HD1	1.50	0.57
1:A:367:PHE:CD1	1:A:367:PHE:C	2.78	0.57
1:A:358:ARG:HD2	1:A:360:GLU:HB2	1.87	0.57
1:A:982:TYR:HB2	1:A:1106:GLY:HA3	1.87	0.57
1:A:1711:VAL:HG13	1:A:1789:ASN:HB3	1.87	0.57
1:A:299:LYS:HA	1:A:493:MET:CG	2.33	0.56
8:H:307:ILE:HD13	8:H:324:ILE:CD1	2.35	0.56
8:H:251:GLN:HG2	8:H:933:TRP:CZ2	2.40	0.56
8:H:599:THR:HG23	8:H:933:TRP:CZ3	2.40	0.56
1:A:389:HIS:HB2	8:H:653:ASP:OD1	2.05	0.56
3:I:158:PHE:CA	3:I:161:LEU:HD12	2.34	0.56
2:B:362:TYR:HB2	2:B:379:ARG:HD2	1.85	0.56
1:A:1020:ILE:HD13	1:A:1488:ILE:HG21	1.87	0.56
1:A:1158:ILE:HG13	1:A:1172:PHE:CE1	2.40	0.56
4:G:296:VAL:HG12	4:G:300:ILE:HD12	1.86	0.56
1:A:1073:ILE:HG23	1:A:1074:VAL:CG2	2.33	0.56
5:K:146:GLU:CA	5:K:149:PHE:HD2	2.18	0.56
1:A:219:ALA:O	1:A:266:LEU:HD11	2.05	0.56
3:I:191:ILE:N	3:I:191:ILE:HD12	2.14	0.56
27:F:103:A:O2'	27:F:104:G:P	2.63	0.56
1:A:1464:LYS:C	1:A:1475:LEU:HD21	2.25	0.56
3:I:455:PHE:O	3:I:458:SER:OG	2.19	0.56
6:L:116:ILE:HD12	6:L:137:TYR:OH	2.02	0.56
1:A:170:HIS:ND1	1:A:547:LEU:CD2	2.68	0.56
25:D:49:A:N6	25:D:50:G:C5	2.73	0.56
1:A:1628:ASP:CB	25:D:50:G:N2	2.68	0.56
1:A:1038:ILE:HD11	1:A:1039:TRP:CE2	2.39	0.56
8:H:328:VAL:O	8:H:333:ALA:N	2.38	0.56
1:A:779:ALA:O	1:A:782:ILE:HB	2.04	0.56
1:A:770:MET:CE	1:A:778:LYS:CB	2.84	0.56
8:H:476:VAL:HG11	8:H:478:TYR:CD1	2.40	0.56
6:L:82:VAL:HB	6:L:103:LEU:HB3	1.87	0.56
8:H:146:LYS:CE	28:H:1500:GTP:O3G	2.51	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:268:ASN:HD21	8:H:316:THR:HG23	1.69	0.56
1:A:224:MET:HE2	1:A:702:GLY:HA3	1.86	0.56
1:A:1498:ASP:HB2	4:G:159:LEU:HB2	1.86	0.56
1:A:180:PRO:HA	1:A:187:LYS:HD2	1.87	0.56
6:L:53:VAL:CG1	6:L:57:ALA:HB3	2.35	0.56
1:A:325:LYS:HA	1:A:325:LYS:CE	2.35	0.56
5:K:296:VAL:O	5:K:300:GLN:HB2	2.05	0.56
1:A:909:THR:HG22	1:A:910:LYS:N	2.20	0.56
3:I:227:PRO:HG3	3:I:325:ARG:HB3	1.86	0.56
3:I:418:GLN:NE2	3:I:425:SER:HB2	2.20	0.56
1:A:208:VAL:HG22	1:A:494:VAL:O	2.05	0.56
8:H:468:LEU:CD2	8:H:577:LEU:CD2	2.80	0.56
8:H:328:VAL:HG21	8:H:345:THR:HG22	1.87	0.56
24:C:-3:A:C8	24:C:-2:A:N6	2.73	0.56
8:H:862:TYR:CE1	8:H:908:VAL:CB	2.80	0.56
8:H:495:ARG:NH2	8:H:541:GLU:OE2	2.38	0.56
1:A:1773:VAL:HG22	1:A:1788:GLY:HA2	1.86	0.56
1:A:1115:GLN:HA	1:A:1115:GLN:NE2	2.20	0.56
8:H:369:LYS:HE2	8:H:369:LYS:N	2.20	0.56
8:H:489:TYR:CE2	8:H:592:PHE:CZ	2.94	0.56
8:H:307:ILE:HA	8:H:324:ILE:HD11	1.87	0.56
27:F:41:A:H5'	27:F:41:A:H8	1.71	0.56
1:A:1275:MET:O	1:A:1277:GLU:O	2.24	0.56
7:M:95:ARG:CG	7:M:96:PRO:HD2	2.36	0.56
2:B:192:THR:CB	2:B:461:ILE:HD11	2.35	0.56
1:A:1364:GLU:O	1:A:1368:GLN:HG3	2.06	0.56
25:D:86:G:H5''	25:D:86:G:C8	2.32	0.56
1:A:272:ASP:HB2	1:A:273:ASP:OD1	2.05	0.56
5:K:300:GLN:HA	5:K:300:GLN:OE1	2.06	0.56
9:N:461:ASP:O	9:N:709:GLY:N	2.35	0.56
1:A:2050:THR:O	1:A:2053:SER:OG	2.20	0.56
2:B:127:TYR:HE2	2:B:276:SER:HB2	1.63	0.56
8:H:132:ARG:HH21	8:H:206:LYS:CD	2.18	0.56
2:B:115:SER:O	2:B:118:ILE:HB	2.06	0.56
1:A:273:ASP:HB3	1:A:276:VAL:HG22	1.86	0.56
4:G:671:PHE:HZ	4:G:693:SER:OG	1.86	0.56
8:H:901:GLU:OE2	8:H:903:ARG:CZ	2.53	0.56
8:H:582:SER:CB	8:H:585:ASP:HB2	2.28	0.56
3:I:217:TYR:HE1	3:I:221:LYS:CE	2.18	0.56
3:I:95:LEU:HA	3:I:98:PHE:HB2	1.88	0.56
1:A:406:PRO:HG2	28:H:1500:GTP:O2'	2.04	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:162:MET:CG	2:B:421:VAL:HG11	2.35	0.56
25:D:46:U:H2'	25:D:47:A:H8	1.69	0.56
7:M:11:LEU:HD23	7:M:12:ALA:O	2.06	0.56
6:L:109:ASP:OD1	6:L:110:LYS:N	2.38	0.56
1:A:1379:MET:HG3	1:A:1380:PRO:HD2	1.87	0.56
1:A:360:GLU:HA	1:A:360:GLU:OE1	2.06	0.56
8:H:118:TYR:CD1	8:H:119:ASN:N	2.74	0.56
1:A:371:ASP:OD2	8:H:972:ARG:NH1	2.38	0.56
1:A:148:ASP:N	1:A:148:ASP:OD1	2.38	0.56
4:G:288:ASP:OD1	4:G:291:TYR:HB2	2.05	0.56
1:A:165:LEU:CD1	1:A:578:MET:HB3	2.35	0.56
3:I:95:LEU:HD23	3:I:98:PHE:HD2	1.69	0.56
2:B:206:THR:O	2:B:207:LEU:HB2	2.05	0.56
8:H:341:ILE:O	8:H:344:PHE:HB3	2.06	0.56
8:H:572:ILE:CD1	8:H:573:LYS:HG3	2.28	0.56
1:A:167:TYR:CD1	1:A:167:TYR:N	2.73	0.56
2:B:320:SER:HB2	2:B:337:ARG:NH1	2.21	0.56
8:H:862:TYR:CE1	8:H:908:VAL:CG2	2.89	0.56
25:D:77:G:N2	26:E:4:C:O2	2.29	0.56
1:A:1389:TYR:CE2	1:A:1401:SER:HB3	2.40	0.56
1:A:176:LEU:O	1:A:179:MET:HG3	2.06	0.56
1:A:749:ARG:HD2	1:A:750:LEU:N	2.20	0.56
1:A:770:MET:CE	1:A:778:LYS:HB2	2.37	0.55
2:B:348:HIS:CD2	2:B:374:ASN:ND2	2.74	0.55
1:A:428:LEU:CD1	8:H:279:LEU:HD11	2.36	0.55
4:G:526:TYR:O	4:G:530:GLU:N	2.35	0.55
4:G:804:ASP:CG	4:G:805:HIS:H	2.10	0.55
1:A:549:LYS:HG2	27:F:35:A:H5'	1.88	0.55
27:F:33:U:H2'	27:F:33:U:O2	2.05	0.55
27:F:44:A:N1	27:F:71:A:N1	2.54	0.55
8:H:862:TYR:CZ	8:H:908:VAL:HG23	2.41	0.55
8:H:483:TRP:CZ3	8:H:565:LYS:CG	2.89	0.55
1:A:1400:ILE:HG22	1:A:1401:SER:N	2.21	0.55
1:A:355:LEU:C	1:A:355:LEU:HD13	2.26	0.55
1:A:939:LEU:HD11	3:I:441:MET:HE1	1.87	0.55
3:I:329:LEU:HD12	3:I:333:TRP:CZ2	2.41	0.55
1:A:1601:ILE:N	1:A:1602:PRO:HD2	2.22	0.55
9:N:1795:SER:O	9:N:1798:GLY:N	2.39	0.55
1:A:2041:PRO:HG2	1:A:2043:PHE:CE2	2.41	0.55
2:B:389:ILE:HD12	2:B:427:TRP:O	2.05	0.55
27:F:78:A:N1	27:F:81:A:C8	2.74	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:D:48:C:C4'	25:D:49:A:OP1	2.52	0.55
27:F:95:C:H4'	27:F:96:U:OP1	2.05	0.55
1:A:149:MET:O	1:A:153:MET:HG2	2.07	0.55
8:H:229:LEU:HD21	8:H:235:VAL:HG11	1.87	0.55
1:A:749:ARG:HD2	1:A:750:LEU:H	1.71	0.55
1:A:992:ASP:OD2	1:A:1109:PHE:CE2	2.60	0.55
4:G:282:ILE:O	4:G:286:GLU:CG	2.51	0.55
4:G:298:THR:O	4:G:302:PHE:HD2	1.88	0.55
8:H:332:TYR:CE2	8:H:376:PHE:HB3	2.41	0.55
1:A:503:LYS:HA	1:A:506:PHE:CE1	2.38	0.55
1:A:1653:LEU:O	1:A:1657:ILE:HG13	2.05	0.55
8:H:605:ILE:CG1	8:H:652:MET:SD	2.92	0.55
25:D:44:A:H2'	25:D:45:A:H8	1.71	0.55
1:A:1831:GLN:HG2	1:A:1832:GLU:N	2.20	0.55
1:A:849:LEU:HG	1:A:973:GLU:HB3	1.88	0.55
4:G:695:THR:O	4:G:699:PRO:HD3	2.06	0.55
8:H:430:ARG:O	8:H:431:GLN:O	2.23	0.55
8:H:586:MET:O	8:H:589:LEU:CD2	2.52	0.55
8:H:380:PRO:HA	8:H:383:LYS:HG3	1.88	0.55
1:A:1065:LEU:HD23	1:A:1065:LEU:O	2.06	0.55
8:H:951:ILE:CD1	8:H:955:LYS:HB2	2.37	0.55
2:B:360:ASN:CB	2:B:362:TYR:HE1	2.20	0.55
1:A:382:GLU:N	1:A:382:GLU:OE1	2.34	0.55
8:H:468:LEU:HB3	8:H:579:SER:HB3	1.89	0.55
2:B:389:ILE:CD1	2:B:427:TRP:O	2.54	0.55
1:A:536:PRO:HG2	27:F:76:U:O4	2.06	0.55
8:H:506:GLN:O	8:H:509:SER:CB	2.49	0.55
1:A:1882:LEU:C	1:A:1882:LEU:HD22	2.26	0.55
1:A:1356:LEU:O	1:A:1356:LEU:HD22	2.06	0.55
1:A:2065:ARG:CD	1:A:2066:LYS:HE2	2.36	0.55
8:H:564:ILE:HG21	8:H:567:ILE:CG1	2.36	0.55
5:K:350:PRO:HB3	25:D:84:C:C6	2.41	0.55
3:I:135:LEU:C	3:I:135:LEU:HD23	2.25	0.55
8:H:387:TYR:HB3	8:H:396:LEU:HD21	1.88	0.55
1:A:160:ALA:CB	1:A:194:HIS:CE1	2.89	0.55
1:A:456:GLU:CD	1:A:456:GLU:H	1.97	0.55
5:K:452:LEU:HB3	5:K:461:GLU:HG2	1.88	0.55
1:A:1163:ARG:NH1	1:A:1165:LEU:O	2.39	0.55
1:A:1341:SER:HA	1:A:1525:PHE:HE1	1.72	0.55
2:B:166:GLU:O	2:B:465:ASN:N	2.39	0.55
1:A:297:SER:CB	27:F:32:G:P	2.95	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:D:51:A:O2'	25:D:52:G:O5'	2.22	0.55
1:A:770:MET:HE2	1:A:775:ARG:O	2.06	0.55
1:A:1074:VAL:HG12	1:A:1075:ASP:N	2.21	0.55
1:A:322:VAL:CB	1:A:327:TYR:CD2	2.90	0.55
8:H:272:ARG:HG3	8:H:276:ASP:HB2	1.89	0.55
4:G:161:LYS:HA	4:G:161:LYS:HE3	1.89	0.55
5:K:332:GLU:O	5:K:332:GLU:HG2	2.05	0.55
1:A:672:LYS:O	1:A:674:MET:N	2.39	0.55
2:B:141:GLU:OE1	2:B:141:GLU:HA	2.07	0.55
6:L:140:LYS:CB	6:L:141:ARG:HD2	2.32	0.55
1:A:1038:ILE:CD1	1:A:1039:TRP:CD2	2.90	0.55
8:H:354:TYR:HA	8:H:359:PHE:CA	2.35	0.55
8:H:474:LYS:HZ2	8:H:630:PRO:HD3	1.71	0.55
2:B:446:SER:HB2	2:B:451:PHE:HB2	1.89	0.55
4:G:691:TYR:CD2	4:G:711:ILE:CD1	2.90	0.55
2:B:275:PRO:HG3	2:B:319:GLY:CA	2.37	0.55
4:G:230:LEU:CD1	4:G:247:SER:HA	2.25	0.55
3:I:282:GLU:OE1	3:I:286:PHE:CZ	2.60	0.55
1:A:1389:TYR:HE2	1:A:1401:SER:HB3	1.72	0.55
1:A:150:ALA:O	1:A:153:MET:HG2	2.07	0.55
2:B:452:LEU:HB3	2:B:464:TRP:HB2	1.89	0.55
1:A:1627:LEU:HB2	1:A:1630:THR:OG1	2.07	0.55
8:H:461:LYS:HD2	8:H:462:SER:N	2.22	0.55
5:K:289:ASP:HB3	5:K:292:ALA:HB3	1.89	0.55
1:A:1559:HIS:O	1:A:1612:PRO:HG2	2.07	0.55
2:B:363:GLN:HG2	2:B:377:ASP:HB3	1.89	0.55
8:H:829:VAL:O	8:H:829:VAL:HG12	2.07	0.55
8:H:132:ARG:C	8:H:133:ILE:HG23	2.27	0.54
4:G:104:PHE:O	4:G:105:ALA:C	2.45	0.54
2:B:441:ILE:HD11	2:B:457:TRP:CD1	2.41	0.54
8:H:337:PRO:O	8:H:341:ILE:HG23	2.07	0.54
1:A:1458:TRP:HZ3	1:A:1461:TYR:CE2	2.24	0.54
1:A:373:VAL:O	8:H:969:LYS:HG2	2.07	0.54
3:I:338:SER:O	3:I:342:ARG:HG3	2.07	0.54
1:A:867:ILE:HD13	1:A:1101:TYR:CD1	2.42	0.54
6:L:140:LYS:HB3	6:L:141:ARG:HH11	1.70	0.54
8:H:303:VAL:HG23	8:H:303:VAL:O	2.07	0.54
8:H:968:MET:CA	8:H:968:MET:CE	2.85	0.54
1:A:1910:LYS:HG3	1:A:1911:TRP:N	2.22	0.54
3:I:146:ASN:HD21	3:I:148:ASN:ND2	2.04	0.54
3:I:418:GLN:HE22	3:I:425:SER:HB2	1.71	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:668:HIS:NE2	4:G:669:LYS:HG3	2.21	0.54
8:H:582:SER:HB3	8:H:585:ASP:OD2	2.03	0.54
8:H:379:ILE:CG2	8:H:383:LYS:CE	2.86	0.54
8:H:767:SER:OG	8:H:796:ILE:HD11	2.07	0.54
3:I:267:HIS:HE1	3:I:273:HIS:CE1	2.25	0.54
2:B:206:THR:CG2	2:B:208:GLN:HE22	2.21	0.54
1:A:410:ILE:N	1:A:410:ILE:HD12	2.22	0.54
3:I:433:ASN:H	3:I:433:ASN:ND2	2.04	0.54
4:G:528:LYS:O	4:G:532:LEU:N	2.39	0.54
4:G:688:ARG:O	4:G:692:LEU:HG	2.07	0.54
4:G:696:ARG:C	4:G:699:PRO:CD	2.74	0.54
8:H:564:ILE:HG21	8:H:567:ILE:HG12	1.89	0.54
1:A:256:GLU:HG3	1:A:257:ASN:N	2.22	0.54
1:A:770:MET:SD	4:G:119:TRP:CZ3	3.01	0.54
27:F:40:C:H3'	27:F:40:C:P	2.48	0.54
2:B:135:ARG:NH2	5:K:167:GLU:OE2	2.40	0.54
1:A:1892:LYS:HD2	1:A:1916:GLU:CD	2.28	0.54
25:D:87:U:P	25:D:87:U:H3'	2.47	0.54
1:A:293:VAL:HG22	1:A:294:ASN:N	2.22	0.54
1:A:296:THR:HG22	27:F:33:U:OP2	2.06	0.54
4:G:846:PHE:HB2	4:G:896:MET:SD	2.48	0.54
1:A:1805:ILE:HG23	1:A:1809:ASN:HD21	1.72	0.54
1:A:413:ASN:ND2	1:A:413:ASN:H	2.06	0.54
1:A:363:ASP:N	1:A:363:ASP:OD1	2.39	0.54
8:H:470:ALA:CB	8:H:486:VAL:HG21	2.19	0.54
8:H:810:GLU:OE2	8:H:974:LYS:CB	2.56	0.54
5:K:141:ASN:OD1	5:K:144:LEU:HD23	2.08	0.54
3:I:191:ILE:H	3:I:191:ILE:CD1	2.14	0.54
1:A:221:TRP:CZ2	1:A:691:PHE:HB3	2.42	0.54
1:A:264:ILE:O	1:A:265:ASN:HB2	2.08	0.54
1:A:860:GLU:OE1	1:A:860:GLU:HA	2.07	0.54
8:H:944:VAL:CG2	8:H:945:LEU:HG	2.37	0.54
4:G:863:PHE:CE2	4:G:892:LEU:HD11	2.43	0.54
27:F:74:U:C5'	27:F:74:U:H6	2.20	0.54
8:H:589:LEU:HD11	8:H:591:PHE:CE1	2.43	0.54
2:B:161:ARG:O	2:B:165:LEU:HD21	2.07	0.54
5:K:249:ARG:HG2	5:K:249:ARG:NH1	2.22	0.54
1:A:1995:TRP:CZ3	1:A:2007:ARG:HD2	2.43	0.54
1:A:158:LYS:HG2	1:A:159:LYS:N	2.23	0.54
5:K:276:ASN:OD1	25:D:61:C:OP1	2.26	0.54
6:L:140:LYS:HG2	6:L:141:ARG:CZ	2.37	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:D:78:G:C2	26:E:4:C:C2	2.96	0.54
6:L:72:GLU:OE2	6:L:72:GLU:HA	2.08	0.54
27:F:31:G:C2	27:F:32:G:C1'	2.89	0.54
8:H:862:TYR:HE1	8:H:908:VAL:CG2	2.20	0.54
1:A:322:VAL:HB	1:A:327:TYR:CD2	2.42	0.54
8:H:769:TYR:CE1	8:H:799:PHE:CD2	2.96	0.54
2:B:64:VAL:HG12	2:B:65:GLU:N	2.20	0.54
2:B:415:TYR:CD2	2:B:439:LYS:HD3	2.42	0.54
3:I:392:GLU:HB2	3:I:412:MET:SD	2.48	0.54
4:G:842:TRP:HA	4:G:845:LEU:HD12	1.90	0.54
6:L:105:PHE:HB2	6:L:141:ARG:CD	2.38	0.54
6:L:105:PHE:HB2	6:L:141:ARG:CG	2.25	0.54
8:H:502:LEU:O	8:H:575:ALA:HB1	2.08	0.54
27:F:78:A:C6	27:F:81:A:C8	2.95	0.54
27:F:72:C:H2'	27:F:73:U:H6	1.73	0.53
24:C:7:A:HO2'	24:C:8:U:P	2.26	0.53
8:H:578:TYR:CD2	8:H:589:LEU:HD13	2.43	0.53
1:A:1038:ILE:HD11	1:A:1039:TRP:CZ3	2.44	0.53
1:A:266:LEU:CD2	1:A:267:PRO:HD2	2.33	0.53
2:B:267:ARG:HG3	2:B:285:HIS:CD2	2.42	0.53
8:H:177:TYR:C	8:H:178:LEU:HD23	2.29	0.53
5:K:455:LEU:C	5:K:457:GLN:OE1	2.47	0.53
1:A:614:ARG:NH1	24:C:3:A:OP1	2.41	0.53
3:I:421:VAL:HG12	3:I:421:VAL:O	2.06	0.53
2:B:279:PHE:CD1	2:B:279:PHE:N	2.76	0.53
3:I:257:CYS:HB2	26:E:42:C:H41	1.72	0.53
4:G:891:ILE:O	4:G:892:LEU:C	2.45	0.53
1:A:166:LYS:HE3	1:A:723:GLU:HB3	1.90	0.53
8:H:307:ILE:CD1	8:H:345:THR:O	2.55	0.53
1:A:1379:MET:HG3	1:A:1380:PRO:CD	2.39	0.53
8:H:331:TYR:OH	8:H:428:ILE:CG2	2.57	0.53
1:A:176:LEU:HD21	1:A:708:TRP:CD1	2.43	0.53
6:L:33:ARG:HE	6:L:64:ILE:HB	1.73	0.53
2:B:201:VAL:C	2:B:202:LEU:HD12	2.28	0.53
5:K:167:GLU:HB3	5:K:169:TRP:CE3	2.43	0.53
24:C:11:A:C2'	24:C:12:U:H5'	2.39	0.53
1:A:1586:GLN:HG2	1:A:1595:ARG:NH1	2.23	0.53
8:H:494:LYS:HE2	8:H:555:GLU:OE1	2.08	0.53
1:A:284:ARG:NH1	27:F:33:U:O4	2.40	0.53
27:F:31:G:C2	27:F:32:G:N9	2.76	0.53
1:A:167:TYR:O	1:A:201:PHE:HE1	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:862:TYR:CD2	8:H:930:LEU:HB3	2.42	0.53
7:M:60:PRO:HB2	7:M:62:GLU:OE1	2.09	0.53
8:H:468:LEU:CD2	8:H:577:LEU:HD21	2.23	0.53
1:A:168:LEU:CB	1:A:199:ILE:HD11	2.38	0.53
1:A:1880:PHE:HE1	1:A:1882:LEU:HD12	1.71	0.53
8:H:114:PRO:O	8:H:115:LYS:O	2.27	0.53
5:K:167:GLU:HB3	5:K:169:TRP:HE3	1.73	0.53
8:H:873:LEU:HB3	8:H:874:PRO:HD3	1.90	0.53
8:H:447:GLU:HA	8:H:447:GLU:OE2	2.08	0.53
3:I:123:ARG:O	3:I:183:PHE:CB	2.56	0.53
1:A:755:ASP:OD2	1:A:819:LYS:HE3	2.08	0.53
4:G:708:LEU:HD22	4:G:725:ILE:HG21	1.90	0.53
4:G:292:CYS:O	4:G:296:VAL:HG23	2.09	0.53
1:A:469:ILE:O	1:A:470:LEU:HD22	2.09	0.53
8:H:677:PHE:HE1	8:H:966:PHE:HE2	1.45	0.53
8:H:599:THR:HG22	8:H:933:TRP:CZ3	2.43	0.53
2:B:322:VAL:HG13	2:B:334:TRP:HB2	1.91	0.53
26:E:19:U:H3'	26:E:19:U:C6	2.44	0.53
8:H:113:ILE:CG2	8:H:114:PRO:HD2	2.34	0.53
8:H:697:ARG:NE	8:H:697:ARG:CA	2.71	0.53
2:B:199:LEU:HD23	2:B:199:LEU:H	1.73	0.53
2:B:360:ASN:HB3	2:B:362:TYR:CD1	2.44	0.53
1:A:674:MET:CE	1:A:678:ARG:HD3	2.38	0.53
1:A:2074:LEU:HD23	1:A:2074:LEU:N	2.22	0.53
4:G:691:TYR:CD2	4:G:711:ILE:HD12	2.44	0.53
4:G:688:ARG:NH1	4:G:721:ARG:NE	2.54	0.53
25:D:49:A:C2'	25:D:50:G:C5'	2.84	0.53
1:A:468:LEU:N	1:A:468:LEU:HD12	2.24	0.53
1:A:837:GLY:C	1:A:1317:ARG:NH1	2.62	0.53
3:I:357:PRO:O	3:I:358:ILE:HG13	2.08	0.53
1:A:239:PHE:O	1:A:240:PRO:C	2.47	0.53
1:A:1500:HIS:HB2	4:G:160:ASN:HD21	1.74	0.53
2:B:75:ARG:HG2	2:B:75:ARG:HH21	1.74	0.53
4:G:158:ASP:OD1	4:G:158:ASP:N	2.40	0.53
4:G:672:LEU:HD21	4:G:704:LEU:HG	1.83	0.53
4:G:846:PHE:HB3	4:G:896:MET:SD	2.49	0.53
27:F:64:C:H2'	27:F:65:U:H6	1.74	0.53
27:F:73:U:C3'	27:F:74:U:C5'	2.87	0.53
8:H:504:THR:OG1	8:H:594:PRO:HG3	2.09	0.53
2:B:176:LYS:HB2	2:B:194:SER:OG	2.09	0.53
1:A:954:ILE:HG23	1:A:991:THR:HG22	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:227:VAL:HG11	8:H:474:LYS:CB	2.39	0.53
1:A:774:ILE:N	1:A:774:ILE:HD12	2.24	0.53
4:G:104:PHE:O	4:G:106:ASP:N	2.41	0.53
2:B:162:MET:N	2:B:162:MET:HE2	2.24	0.53
1:A:944:TYR:O	4:G:166:ARG:NH1	2.41	0.53
1:A:242:PHE:CE1	1:A:249:LEU:HD21	2.44	0.53
8:H:488:ILE:CD1	8:H:557:HIS:O	2.51	0.53
1:A:166:LYS:HD3	1:A:167:TYR:CZ	2.43	0.53
8:H:326:GLU:OE1	8:H:330:TYR:CD2	2.61	0.53
8:H:176:ARG:O	8:H:548:ARG:NH2	2.41	0.53
3:I:358:ILE:HG22	3:I:360:GLU:N	2.24	0.53
4:G:170:LEU:HD13	4:G:171:GLN:N	2.24	0.53
1:A:2065:ARG:HD2	1:A:2066:LYS:HE2	1.91	0.53
1:A:1125:LEU:HD21	1:A:1234:VAL:HG23	1.90	0.53
4:G:630:SER:HA	4:G:670:PHE:HZ	1.72	0.52
6:L:33:ARG:HD3	6:L:65:ASP:N	2.24	0.52
8:H:265:PHE:HE2	8:H:295:ILE:HB	1.73	0.52
5:K:349:ASN:HB2	5:K:406:PHE:CD1	2.44	0.52
3:I:257:CYS:SG	26:E:44:G:O6	2.61	0.52
1:A:1511:ARG:NH2	1:A:1511:ARG:HG3	2.24	0.52
3:I:82:ARG:O	3:I:86:GLN:N	2.35	0.52
1:A:721:LEU:HD11	27:F:85:U:O2'	2.09	0.52
4:G:666:ILE:CG2	4:G:667:CYS:H	2.18	0.52
2:B:316:GLN:NE2	2:B:316:GLN:O	2.42	0.52
1:A:928:ARG:HH21	4:G:145:THR:CG2	2.17	0.52
1:A:881:THR:O	1:A:885:VAL:HG23	2.08	0.52
4:G:126:THR:HB	4:G:128:PHE:CZ	2.44	0.52
1:A:1262:MET:O	1:A:1263:CYS:HB2	2.09	0.52
25:D:64:U:H6	25:D:64:U:H5"	1.74	0.52
1:A:778:LYS:HA	1:A:778:LYS:HE2	1.90	0.52
1:A:1380:PRO:HG3	1:A:1383:PHE:CE1	2.45	0.52
8:H:106:PHE:HE2	8:H:554:HIS:NE2	2.06	0.52
8:H:674:LEU:CD1	8:H:973:ARG:NH1	2.69	0.52
1:A:1468:ALA:O	1:A:1473:ARG:N	2.37	0.52
3:I:347:ALA:HA	4:G:130:ARG:HH11	1.74	0.52
1:A:921:ASP:HB3	3:I:403:SER:HB2	1.91	0.52
3:I:327:THR:O	3:I:328:VAL:HG23	2.09	0.52
1:A:1699:ALA:HA	1:A:1735:ASP:OD1	2.09	0.52
5:K:143:GLU:HA	5:K:145:HIS:CE1	2.45	0.52
4:G:672:LEU:HD21	4:G:704:LEU:HD21	1.28	0.52
4:G:252:GLU:CG	4:G:256:LYS:HG3	2.26	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:283:ARG:NH1	4:G:284:LEU:HD21	2.24	0.52
1:A:1380:PRO:HG3	1:A:1383:PHE:CD1	2.44	0.52
7:M:95:ARG:HG3	7:M:96:PRO:CD	2.40	0.52
26:E:19:U:C3'	26:E:19:U:C6	2.93	0.52
26:E:19:U:O2'	26:E:20:A:P	2.67	0.52
1:A:1613:THR:O	1:A:1616:ARG:CD	2.57	0.52
25:D:44:A:H2'	25:D:45:A:C8	2.44	0.52
4:G:83:LYS:C	4:G:85:ARG:H	2.12	0.52
4:G:671:PHE:CE1	4:G:690:THR:O	2.62	0.52
6:L:140:LYS:HB3	6:L:141:ARG:NH1	2.25	0.52
4:G:288:ASP:OD1	4:G:291:TYR:CB	2.58	0.52
24:C:-4:A:C1'	24:C:-3:A:OP1	2.49	0.52
1:A:1065:LEU:CD2	1:A:1069:LEU:HD13	2.39	0.52
8:H:942:GLY:C	8:H:963:SER:OG	2.47	0.52
1:A:1902:GLN:O	1:A:1905:LEU:CD2	2.56	0.52
4:G:234:ARG:O	4:G:237:ASP:O	2.28	0.52
3:I:398:GLN:NE2	3:I:419:GLN:HG3	2.25	0.52
3:I:336:GLU:O	3:I:340:LYS:HB2	2.09	0.52
7:M:79:VAL:HG13	7:M:121:ILE:HG23	1.91	0.52
5:K:314:ARG:NH2	5:K:314:ARG:HG2	2.23	0.52
8:H:369:LYS:C	8:H:369:LYS:HE2	2.30	0.52
6:L:140:LYS:CB	6:L:141:ARG:NH1	2.73	0.52
5:K:354:PHE:CE1	5:K:358:MET:HG2	2.45	0.52
1:A:770:MET:HB2	1:A:775:ARG:HG3	1.92	0.52
3:I:99:ASN:O	3:I:103:PRO:HD2	2.09	0.52
1:A:691:PHE:CD1	1:A:691:PHE:C	2.82	0.52
1:A:1458:TRP:HZ3	1:A:1461:TYR:CD2	2.25	0.52
8:H:682:SER:HA	8:H:714:PRO:HG3	1.92	0.52
4:G:712:ASP:OD2	4:G:721:ARG:HB3	2.09	0.52
4:G:863:PHE:HE2	4:G:892:LEU:HD11	1.73	0.52
8:H:126:MET:CE	8:H:132:ARG:NH1	2.73	0.52
27:F:95:C:O3'	27:F:96:U:C4'	2.58	0.52
1:A:814:ARG:NH1	4:G:103:GLN:O	2.43	0.52
3:I:400:VAL:HG12	4:G:215:LEU:HA	1.92	0.52
1:A:1342:LEU:HD23	1:A:1342:LEU:C	2.30	0.52
1:A:514:TYR:H	1:A:514:TYR:HD1	1.58	0.52
1:A:377:VAL:CG1	1:A:378:PRO:HD2	2.37	0.52
1:A:261:LEU:HD12	1:A:262:ASP:N	2.24	0.52
8:H:332:TYR:CZ	8:H:376:PHE:HD2	2.27	0.52
8:H:884:ARG:C	8:H:884:ARG:HD3	2.30	0.52
1:A:362:GLU:CB	1:A:1209:LYS:CE	2.72	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:705:GLN:HB3	1:A:706:PRO:HD3	1.91	0.52
3:I:101:ILE:O	3:I:105:ILE:HG13	2.10	0.52
3:I:217:TYR:CE1	3:I:221:LYS:CE	2.92	0.52
2:B:438:ASP:HB2	2:B:458:ASP:HB3	1.91	0.52
1:A:1899:TRP:CH2	1:A:1909:ALA:HB2	2.45	0.52
27:F:103:A:HO2'	27:F:104:G:P	2.29	0.52
1:A:1468:ALA:HB1	1:A:1473:ARG:C	2.29	0.52
8:H:265:PHE:CD1	8:H:265:PHE:N	2.77	0.52
2:B:286:ASP:O	2:B:288:THR:HG23	2.10	0.52
4:G:169:LEU:O	4:G:173:GLN:HG3	2.10	0.52
2:B:68:ASP:OD1	5:K:322:ARG:NH1	2.41	0.52
5:K:314:ARG:HH21	5:K:314:ARG:HG2	1.75	0.52
8:H:270:LEU:HD11	8:H:313:PHE:HB3	1.92	0.52
8:H:168:VAL:HA	8:H:173:LYS:HG3	1.92	0.52
2:B:316:GLN:HB2	2:B:357:TRP:CG	2.42	0.52
1:A:703:PHE:HD1	1:A:704:TRP:N	2.08	0.52
8:H:483:TRP:CZ3	8:H:565:LYS:HG2	2.45	0.52
4:G:702:PRO:CA	4:G:739:PHE:CZ	2.93	0.52
3:I:127:LEU:HD11	3:I:131:ILE:HD12	1.90	0.52
1:A:1285:VAL:O	1:A:1448:GLU:OE2	2.29	0.52
1:A:644:VAL:O	1:A:645:ASP:HB2	2.10	0.52
27:F:77:A:H4'	27:F:78:A:C5'	2.32	0.51
1:A:1416:LYS:HG2	1:A:1417:GLN:N	2.25	0.51
3:I:184:LYS:CD	3:I:186:LYS:CB	2.87	0.51
27:F:100:A:H5'	27:F:101:C:OP2	2.10	0.51
2:B:117:LEU:C	2:B:117:LEU:HD13	2.31	0.51
1:A:1992:TYR:CD2	1:A:2004:ALA:HB1	2.44	0.51
1:A:321:GLU:HA	1:A:508:GLN:OE1	2.11	0.51
4:G:360:LYS:O	4:G:364:PHE:N	2.38	0.51
1:A:471:PRO:HG2	1:A:472:ASN:OD1	2.10	0.51
8:H:227:VAL:HG13	8:H:473:LEU:HB3	1.90	0.51
1:A:376:ARG:O	1:A:377:VAL:CB	2.56	0.51
3:I:347:ALA:HB1	3:I:348:PRO:HD2	1.92	0.51
2:B:360:ASN:CB	2:B:362:TYR:CE1	2.93	0.51
4:G:143:ARG:NH2	4:G:143:ARG:CB	2.73	0.51
1:A:769:MET:HE2	4:G:112:ALA:HA	1.91	0.51
8:H:497:ASP:O	8:H:538:GLU:HA	2.09	0.51
8:H:369:LYS:CE	8:H:369:LYS:N	2.73	0.51
1:A:286:LEU:HD12	1:A:287:GLU:H	1.72	0.51
2:B:275:PRO:CG	2:B:319:GLY:CA	2.88	0.51
1:A:2013:ARG:HG3	1:A:2083:ILE:O	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:217:TRP:CD1	1:A:703:PHE:CZ	2.98	0.51
8:H:478:TYR:HB2	8:H:483:TRP:HD1	1.76	0.51
1:A:228:LYS:CD	1:A:691:PHE:HE1	2.23	0.51
1:A:1342:LEU:HD23	1:A:1350:ILE:HD11	1.91	0.51
9:N:1928:LEU:O	9:N:1931:GLN:N	2.40	0.51
8:H:135:ASN:HD22	8:H:487:ARG:HH21	1.57	0.51
8:H:354:TYR:CE1	8:H:376:PHE:HZ	2.28	0.51
8:H:478:TYR:HB2	8:H:483:TRP:CD1	2.45	0.51
1:A:823:TRP:CE2	1:A:851:ARG:HG2	2.45	0.51
8:H:860:PRO:HB3	8:H:937:TRP:HZ3	1.74	0.51
1:A:1464:LYS:NZ	1:A:1479:GLU:HB3	2.25	0.51
4:G:19:ILE:HD12	4:G:20:GLY:CA	2.40	0.51
1:A:861:GLN:NE2	1:A:1097:HIS:HB3	2.25	0.51
1:A:249:LEU:HD23	1:A:249:LEU:N	2.25	0.51
4:G:9:GLN:C	4:G:11:PRO:HD3	2.30	0.51
4:G:327:VAL:O	4:G:331:LEU:N	2.39	0.51
27:F:62:G:H2'	27:F:63:C:H6	1.75	0.51
5:K:350:PRO:C	5:K:353:ARG:HG3	2.30	0.51
8:H:586:MET:C	8:H:589:LEU:HD23	2.30	0.51
1:A:250:SER:HB2	1:A:252:GLU:OE1	2.11	0.51
6:L:135:TYR:N	6:L:135:TYR:CD1	2.79	0.51
8:H:959:ILE:HD13	8:H:960:ASN:H	1.72	0.51
1:A:1339:LEU:CD2	1:A:1440:ILE:HD12	2.40	0.51
8:H:951:ILE:CB	8:H:952:PRO:CD	2.88	0.51
1:A:1313:ASP:OD2	1:A:1359:ILE:CD1	2.59	0.51
8:H:113:ILE:CG2	8:H:114:PRO:CD	2.89	0.51
8:H:232:SER:OG	8:H:234:LEU:O	2.28	0.51
5:K:316:HIS:C	5:K:316:HIS:CD2	2.83	0.51
1:A:166:LYS:O	1:A:169:PRO:CD	2.53	0.51
8:H:307:ILE:HD11	8:H:345:THR:C	2.30	0.51
8:H:354:TYR:HA	8:H:359:PHE:HB3	1.90	0.51
4:G:101:LYS:O	4:G:105:ALA:N	2.36	0.51
1:A:366:GLU:HG3	1:A:367:PHE:N	2.26	0.51
3:I:401:LEU:HD12	4:G:214:SER:HA	1.93	0.51
2:B:171:GLN:O	2:B:172:LEU:CD1	2.59	0.51
8:H:461:LYS:NZ	8:H:464:PRO:CB	2.73	0.51
2:B:436:HIS:CD2	2:B:440:ILE:HD11	2.45	0.51
6:L:94:ASP:OD1	6:L:132:VAL:HA	2.10	0.51
1:A:291:LYS:H	1:A:291:LYS:NZ	2.09	0.51
8:H:379:ILE:CG2	8:H:383:LYS:HE2	2.40	0.51
1:A:1065:LEU:CD2	1:A:1069:LEU:HD22	2.40	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:497:GLN:HB3	1:A:712:LEU:HD23	1.92	0.51
8:H:178:LEU:HD12	8:H:214:ASP:HB2	1.92	0.51
1:A:2067:TYR:CD1	1:A:2067:TYR:N	2.78	0.51
8:H:953:LYS:O	8:H:954:LEU:HB2	2.10	0.51
1:A:1050:LEU:HD23	1:A:1248:VAL:HG22	1.92	0.51
3:I:376:LYS:O	3:I:378:LYS:N	2.43	0.51
1:A:298:TYR:O	1:A:493:MET:SD	2.69	0.51
27:F:74:U:H2'	27:F:75:A:H3'	1.92	0.51
1:A:522:TYR:CE2	1:A:686:ILE:HD12	2.46	0.51
1:A:273:ASP:HB3	1:A:276:VAL:HG21	1.92	0.51
2:B:415:TYR:OH	7:M:126:ILE:C	2.49	0.51
8:H:945:LEU:O	8:H:945:LEU:HD13	2.11	0.51
27:F:64:C:C2	27:F:65:U:C5	2.99	0.51
2:B:274:HIS:HD2	2:B:276:SER:HB3	1.72	0.51
3:I:112:MET:HB2	3:I:204:LEU:HD21	1.91	0.51
3:I:265:ASN:O	3:I:266:LYS:CB	2.57	0.51
8:H:883:ARG:CZ	8:H:910:GLU:O	2.59	0.51
8:H:697:ARG:NH1	8:H:852:THR:OG1	2.44	0.51
24:C:11:A:C2	24:C:12:U:C4	2.99	0.51
1:A:976:GLN:HE22	1:A:1310:LYS:HB3	1.76	0.51
9:N:1502:LEU:O	9:N:1503:GLU:C	2.47	0.51
27:F:72:C:C2	27:F:73:U:C5	2.98	0.51
8:H:376:PHE:CD1	8:H:376:PHE:N	2.79	0.51
8:H:160:ARG:HB3	8:H:161:ILE:CA	2.40	0.51
2:B:121:ARG:HD2	2:B:337:ARG:O	2.11	0.51
2:B:274:HIS:CD2	2:B:275:PRO:CD	2.93	0.51
1:A:774:ILE:CG2	1:A:777:LYS:HE3	2.38	0.51
1:A:1649:PHE:CE1	1:A:1815:LEU:HD21	2.46	0.51
8:H:143:HIS:HA	28:H:1500:GTP:PB	2.51	0.51
1:A:1511:ARG:CG	1:A:1511:ARG:HH21	2.22	0.51
1:A:1893:ILE:O	1:A:1984:PRO:HA	2.11	0.51
1:A:621:LEU:HD12	1:A:666:ILE:HD11	1.91	0.51
7:M:46:ARG:NH1	26:E:43:C:OP1	2.44	0.51
8:H:247:PHE:CB	8:H:931:TYR:OH	2.59	0.50
8:H:116:THR:CG2	8:H:157:SER:OG	2.59	0.50
8:H:353:TYR:CE2	8:H:371:PRO:HG3	2.47	0.50
2:B:127:TYR:HE2	2:B:276:SER:CB	2.19	0.50
1:A:767:LEU:CD2	1:A:779:ALA:HB2	2.40	0.50
1:A:1490:ARG:NH1	1:A:1535:LYS:O	2.44	0.50
2:B:243:ILE:HD12	2:B:292:TRP:CZ3	2.46	0.50
1:A:806:ALA:N	1:A:807:PRO:HD2	2.26	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:143:ARG:CG	4:G:143:ARG:NH2	2.73	0.50
3:I:447:GLU:OE2	3:I:448:ALA:N	2.45	0.50
3:I:301:GLN:OE1	3:I:344:LEU:CD1	2.60	0.50
2:B:167:LEU:O	4:G:728:ARG:NH2	2.44	0.50
8:H:135:ASN:ND2	8:H:487:ARG:NH2	2.60	0.50
4:G:887:THR:N	4:G:888:PRO:CD	2.74	0.50
27:F:63:C:C2	27:F:64:C:C5	3.00	0.50
1:A:1477:PHE:O	1:A:1481:GLU:N	2.44	0.50
1:A:1498:ASP:OD1	1:A:1502:LEU:HD12	2.07	0.50
3:I:210:LEU:O	3:I:214:ILE:HG13	2.12	0.50
3:I:447:GLU:HA	3:I:450:GLN:HG2	1.93	0.50
27:F:117:G:H2'	27:F:118:U:O4'	2.12	0.50
2:B:354:THR:HG21	2:B:399:VAL:H	1.75	0.50
15:Z:48:TYR:O	15:Z:50:ASN:N	2.45	0.50
1:A:418:ASP:OD1	1:A:418:ASP:N	2.44	0.50
8:H:285:TYR:CD1	8:H:285:TYR:C	2.84	0.50
8:H:305:SER:C	8:H:307:ILE:H	2.15	0.50
1:A:774:ILE:O	1:A:774:ILE:HG22	2.11	0.50
4:G:215:LEU:HD12	4:G:216:SER:O	2.11	0.50
1:A:149:MET:CG	1:A:154:TYR:CE2	2.89	0.50
1:A:251:TYR:CA	1:A:255:ILE:HD12	2.34	0.50
25:D:62:A:H2'	25:D:63:G:C5'	2.38	0.50
2:B:419:ILE:HD11	2:B:443:LEU:HD13	1.91	0.50
1:A:1627:LEU:HD22	1:A:1632:ILE:HB	1.94	0.50
2:B:360:ASN:ND2	2:B:406:GLY:O	2.43	0.50
1:A:299:LYS:O	1:A:300:LYS:HB2	2.12	0.50
8:H:580:VAL:HG13	8:H:580:VAL:O	2.11	0.50
2:B:127:TYR:CZ	2:B:276:SER:HA	2.47	0.50
1:A:1880:PHE:CE2	1:A:1889:LEU:CD2	2.74	0.50
1:A:1882:LEU:HD22	1:A:1883:ASN:N	2.27	0.50
2:B:376:TRP:CD1	2:B:376:TRP:N	2.78	0.50
1:A:505:TRP:O	1:A:522:TYR:HE1	1.93	0.50
1:A:1373:LEU:HD21	1:A:1379:MET:SD	2.51	0.50
8:H:793:GLU:C	8:H:796:ILE:HG22	2.31	0.50
8:H:302:ASN:OD1	8:H:303:VAL:N	2.44	0.50
1:A:1336:ASN:O	1:A:1340:ILE:HG13	2.10	0.50
2:B:171:GLN:O	2:B:172:LEU:HD13	2.12	0.50
8:H:794:GLN:OE1	8:H:835:LYS:CG	2.57	0.50
1:A:1461:TYR:CE2	1:A:1494:LEU:CD1	2.95	0.50
1:A:1709:TRP:HD1	1:A:1730:ASN:O	1.94	0.50
1:A:1892:LYS:HG3	1:A:1916:GLU:HG3	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:6:PHE:HE1	4:G:7:LEU:HD12	1.75	0.50
1:A:1158:ILE:HG12	1:A:1172:PHE:CE1	2.46	0.50
1:A:1735:ASP:O	1:A:1775:ILE:N	2.37	0.50
1:A:754:TYR:CE2	1:A:758:LEU:CD2	2.94	0.50
1:A:764:ASP:O	1:A:768:GLU:N	2.44	0.50
3:I:410:LEU:O	3:I:410:LEU:HD12	2.12	0.50
1:A:1650:ARG:O	1:A:1651:ALA:HB3	2.12	0.50
8:H:354:TYR:CA	8:H:359:PHE:CB	2.86	0.50
8:H:133:ILE:C	8:H:134:ILE:CG2	2.72	0.50
8:H:769:TYR:CD1	8:H:799:PHE:HD2	2.29	0.50
6:L:32:GLY:O	6:L:63:ASP:HA	2.10	0.50
4:G:274:SER:HB2	4:G:277:ILE:CD1	2.15	0.50
6:L:140:LYS:HG2	6:L:141:ARG:HH12	1.69	0.50
1:A:165:LEU:HD21	1:A:726:ILE:HG21	1.93	0.50
1:A:1778:ASP:HB2	1:A:1783:MET:HB2	1.94	0.50
8:H:349:TRP:CZ3	8:H:373:PHE:CD2	2.99	0.50
8:H:160:ARG:NH1	8:H:160:ARG:HG3	2.26	0.50
4:G:252:GLU:O	4:G:256:LYS:HB2	2.11	0.50
1:A:1317:ARG:O	1:A:1321:MET:HG2	2.11	0.50
27:F:39:U:O2'	27:F:40:C:H5'	2.11	0.50
4:G:702:PRO:CB	4:G:739:PHE:CE2	2.95	0.50
5:K:144:LEU:HD22	5:K:144:LEU:N	2.27	0.50
15:W:48:TYR:O	15:W:50:ASN:N	2.45	0.50
25:D:81:G:C6	25:D:82:A:N7	2.80	0.50
1:A:1733:TRP:CE2	1:A:1772:GLY:HA3	2.46	0.50
4:G:241:PRO:HG3	4:G:274:SER:OG	2.12	0.50
1:A:286:LEU:HD21	1:A:289:ASP:HB3	1.92	0.50
1:A:289:ASP:CG	1:A:292:LYS:CG	2.80	0.50
2:B:390:LEU:HD12	5:K:428:TRP:CD1	2.46	0.50
8:H:133:ILE:HA	8:H:209:MET:O	2.11	0.50
8:H:379:ILE:HG22	8:H:383:LYS:CE	2.42	0.50
8:H:862:TYR:OH	8:H:908:VAL:CG2	2.59	0.50
1:A:367:PHE:O	1:A:367:PHE:HD1	1.95	0.50
4:G:143:ARG:CZ	4:G:143:ARG:CB	2.86	0.50
1:A:897:PRO:O	1:A:1006:ARG:NH1	2.44	0.50
1:A:547:LEU:O	1:A:551:LEU:HB2	2.12	0.50
2:B:446:SER:OG	2:B:451:PHE:CB	2.54	0.50
2:B:290:ARG:NE	2:B:299:GLU:OE2	2.42	0.50
2:B:462:LYS:HE2	4:G:727:ASP:OD2	2.12	0.50
26:E:139:A:O2'	26:E:140:G:P	2.69	0.50
27:F:97:U:H2'	27:F:97:U:O2	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:161:LYS:O	4:G:165:GLU:HB2	2.12	0.50
6:L:140:LYS:CG	6:L:141:ARG:CZ	2.90	0.50
8:H:501:ILE:HG21	8:H:570:ALA:CB	2.41	0.50
27:F:32:G:O3'	27:F:33:U:H4'	2.11	0.50
4:G:299:ALA:O	4:G:303:ASN:N	2.43	0.50
27:F:73:U:C2'	27:F:74:U:H5''	2.38	0.50
27:F:75:A:O2'	27:F:76:U:C3'	2.59	0.50
8:H:347:ARG:HG3	8:H:359:PHE:CZ	2.47	0.50
8:H:132:ARG:HH21	8:H:206:LYS:CG	2.25	0.50
1:A:1008:LEU:HD21	1:A:1073:ILE:CD1	2.40	0.50
1:A:221:TRP:CH2	1:A:691:PHE:HB3	2.47	0.50
1:A:1264:GLY:HA3	1:A:1308:GLU:CD	2.33	0.50
1:A:395:PRO:O	1:A:396:ARG:HG3	2.11	0.50
5:K:363:LEU:HD11	5:K:391:PHE:CD2	2.47	0.50
4:G:141:LEU:O	4:G:141:LEU:HD13	2.11	0.50
8:H:250:GLU:HB3	8:H:298:PHE:CD2	2.47	0.49
1:A:291:LYS:N	1:A:291:LYS:NZ	2.60	0.49
1:A:1481:GLU:HA	1:A:1484:TRP:NE1	2.27	0.49
1:A:1275:MET:CE	1:A:1299:LYS:NZ	2.75	0.49
1:A:909:THR:HG22	1:A:910:LYS:H	1.77	0.49
4:G:798:LEU:O	4:G:802:GLN:HA	2.12	0.49
1:A:452:PHE:CZ	8:H:343:ASP:HB3	2.46	0.49
5:K:319:ALA:O	5:K:323:ARG:N	2.44	0.49
3:I:275:LEU:N	3:I:275:LEU:HD23	2.27	0.49
8:H:503:ASP:OD1	8:H:571:TYR:CB	2.59	0.49
4:G:886:CYS:SG	4:G:888:PRO:CD	2.97	0.49
1:A:201:PHE:CE2	1:A:551:LEU:HD21	2.47	0.49
1:A:1759:TYR:HB3	1:A:1767:TYR:OH	2.12	0.49
8:H:474:LYS:HZ2	8:H:630:PRO:CD	2.25	0.49
3:I:401:LEU:HD12	4:G:214:SER:CA	2.42	0.49
8:H:118:TYR:O	8:H:119:ASN:CB	2.60	0.49
1:A:1709:TRP:HB3	1:A:1791:PHE:CE1	2.47	0.49
1:A:1286:TRP:CZ2	1:A:1302:LEU:HD11	2.47	0.49
1:A:1834:PHE:CD1	1:A:1958:PRO:HG2	2.48	0.49
1:A:2065:ARG:NE	1:A:2066:LYS:HE2	2.26	0.49
2:B:143:HIS:CE1	5:K:151:LEU:HD22	2.47	0.49
27:F:62:G:C4	27:F:63:C:C5	3.00	0.49
25:D:50:G:HO2'	25:D:51:A:P	2.27	0.49
1:A:1490:ARG:HH11	1:A:1536:LEU:HD23	1.76	0.49
8:H:379:ILE:CG2	8:H:383:LYS:HE3	2.42	0.49
1:A:149:MET:O	1:A:153:MET:HG3	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1591:THR:HG22	1:A:1592:HIS:H	1.76	0.49
4:G:6:PHE:CD1	4:G:6:PHE:C	2.85	0.49
2:B:448:ASN:O	2:B:449:SER:HB2	2.12	0.49
26:E:141:G:O2'	26:E:142:G:OP2	2.27	0.49
8:H:430:ARG:O	8:H:431:GLN:C	2.50	0.49
8:H:336:ILE:HG13	8:H:341:ILE:CG2	2.43	0.49
1:A:1118:GLY:HA3	1:A:1163:ARG:CZ	2.42	0.49
8:H:539:VAL:HG13	8:H:564:ILE:HG23	1.93	0.49
27:F:31:G:N3	27:F:32:G:C1'	2.74	0.49
27:F:48:G:H2'	27:F:49:U:H6	1.77	0.49
27:F:73:U:H2'	27:F:74:U:H6	1.78	0.49
8:H:160:ARG:HH11	8:H:160:ARG:HG3	1.77	0.49
2:B:276:SER:OG	2:B:277:GLY:N	2.46	0.49
1:A:470:LEU:HB2	1:A:473:THR:HB	1.95	0.49
1:A:1365:THR:C	1:A:1369:ASN:ND2	2.63	0.49
3:I:98:PHE:O	3:I:102:ILE:HG12	2.12	0.49
1:A:1074:VAL:HG12	1:A:1075:ASP:H	1.77	0.49
1:A:912:LEU:CG	1:A:951:LEU:HD21	2.43	0.49
1:A:908:ASP:HB3	1:A:951:LEU:HD11	1.94	0.49
8:H:191:ILE:HG23	8:H:221:PHE:CZ	2.48	0.49
1:A:1922:ARG:NE	1:A:1951:PHE:HZ	2.06	0.49
1:A:356:TYR:HE2	1:A:396:ARG:HB2	1.76	0.49
5:K:331:VAL:O	5:K:332:GLU:HG2	2.13	0.49
1:A:1590:LEU:HB2	1:A:1595:ARG:HH21	1.76	0.49
1:A:1385:PRO:HG3	1:A:1407:ILE:HA	1.95	0.49
1:A:1014:LYS:HD3	1:A:1024:LEU:HD13	1.95	0.49
8:H:470:ALA:HB3	8:H:577:LEU:CB	2.38	0.49
8:H:492:LEU:CD2	8:H:557:HIS:CE1	2.95	0.49
1:A:165:LEU:HD21	1:A:726:ILE:CG2	2.42	0.49
1:A:218:SER:HB2	1:A:317:PRO:HG2	1.95	0.49
2:B:264:HIS:CE1	2:B:290:ARG:HD2	2.47	0.49
1:A:272:ASP:CB	1:A:273:ASP:OD1	2.61	0.49
27:F:92:U:C4	27:F:93:G:N7	2.80	0.49
6:L:119:THR:HG22	6:L:131:VAL:HG11	1.94	0.49
1:A:1207:TRP:HB3	1:A:1211:SER:OG	2.12	0.49
4:G:672:LEU:HD22	4:G:703:LEU:HD12	1.93	0.49
4:G:712:ASP:OD2	4:G:721:ARG:HD2	2.13	0.49
8:H:571:TYR:HD2	8:H:573:LYS:O	1.96	0.49
1:A:201:PHE:CE2	1:A:551:LEU:CD2	2.96	0.49
27:F:77:A:H1'	27:F:78:A:C5'	2.41	0.49
25:D:83:A:HO2'	25:D:84:C:P	2.27	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1373:LEU:CD1	6:L:139:HIS:CE1	2.80	0.49
4:G:843:VAL:CG2	4:G:895:LEU:CD1	2.88	0.49
24:C:11:A:N1	24:C:12:U:C4	2.81	0.49
8:H:864:VAL:HG12	8:H:866:ILE:HG13	1.94	0.49
1:A:1204:ARG:HD2	1:A:1259:LEU:HB3	1.93	0.49
8:H:369:LYS:NZ	8:H:369:LYS:N	2.60	0.49
8:H:492:LEU:CD2	8:H:557:HIS:HA	2.39	0.49
8:H:268:ASN:ND2	8:H:316:THR:HG23	2.28	0.49
1:A:749:ARG:O	1:A:750:LEU:CB	2.61	0.49
3:I:93:LYS:HA	3:I:93:LYS:CE	2.43	0.49
6:L:105:PHE:CE1	6:L:137:TYR:HE2	2.01	0.49
1:A:165:LEU:CD2	1:A:726:ILE:CG2	2.90	0.49
27:F:63:C:H2'	27:F:64:C:H6	1.78	0.49
8:H:589:LEU:HD11	8:H:591:PHE:HE1	1.78	0.49
3:I:217:TYR:CE1	3:I:221:LYS:HE2	2.48	0.49
4:G:101:LYS:O	4:G:105:ALA:CB	2.61	0.49
3:I:400:VAL:HB	4:G:214:SER:HB2	1.94	0.49
2:B:117:LEU:HD22	2:B:117:LEU:O	2.13	0.49
1:A:2071:ILE:C	1:A:2071:ILE:HD13	2.33	0.49
1:A:1865:THR:OG1	1:A:1869:ASN:N	2.34	0.49
1:A:277:LYS:HG3	1:A:278:ASP:N	2.28	0.49
4:G:276:ASP:N	4:G:276:ASP:OD1	2.38	0.49
8:H:383:LYS:O	8:H:387:TYR:CB	2.51	0.49
5:K:159:TYR:CG	5:K:163:ASN:ND2	2.77	0.49
4:G:170:LEU:O	4:G:170:LEU:HD22	2.12	0.49
1:A:1067:ASN:OD1	3:I:270:HIS:HB3	2.11	0.49
1:A:302:SER:HA	1:A:489:THR:O	2.13	0.49
8:H:165:SER:H	8:H:168:VAL:CG2	2.26	0.48
5:K:354:PHE:CE1	5:K:358:MET:CG	2.96	0.48
8:H:578:TYR:CD1	8:H:578:TYR:C	2.86	0.48
1:A:1038:ILE:HG13	1:A:1039:TRP:N	2.28	0.48
24:C:-4:A:H1'	24:C:-3:A:P	2.52	0.48
2:B:197:GLY:CA	2:B:221:ILE:CD1	2.87	0.48
1:A:175:LEU:CD1	1:A:564:TRP:CZ2	2.96	0.48
1:A:276:VAL:CG1	1:A:310:ASN:CB	2.89	0.48
1:A:1629:LEU:H	1:A:1629:LEU:CD2	2.26	0.48
5:K:448:GLN:HE21	5:K:464:TYR:HE2	1.61	0.48
5:K:265:LEU:HD12	5:K:266:PRO:HD2	1.94	0.48
8:H:306:PRO:O	8:H:324:ILE:CD1	2.60	0.48
1:A:140:ARG:NH2	1:A:252:GLU:HB3	2.28	0.48
8:H:677:PHE:CZ	8:H:966:PHE:CE2	3.00	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:282:SER:O	2:B:290:ARG:N	2.40	0.48
8:H:791:TYR:O	8:H:795:ILE:HG13	2.13	0.48
4:G:136:ARG:NH1	26:E:51:U:OP2	2.46	0.48
8:H:945:LEU:HD12	8:H:945:LEU:N	2.29	0.48
27:F:45:A:N3	27:F:45:A:H2'	2.28	0.48
8:H:353:TYR:N	8:H:353:TYR:CD1	2.81	0.48
1:A:839:HIS:CE1	27:F:96:U:C5	3.02	0.48
1:A:192:LEU:HG	1:A:557:PHE:CD2	2.48	0.48
4:G:99:ASN:HD22	4:G:99:ASN:H	1.61	0.48
1:A:1400:ILE:HG23	1:A:1542:TYR:CZ	2.48	0.48
8:H:177:TYR:O	8:H:178:LEU:HG	2.13	0.48
9:N:1198:ARG:CA	9:N:1227:ILE:N	2.71	0.48
1:A:1461:TYR:CZ	1:A:1494:LEU:HD13	2.48	0.48
3:I:376:LYS:O	3:I:377:GLU:C	2.51	0.48
1:A:1594:GLN:HE21	1:A:1594:GLN:N	2.11	0.48
4:G:780:LEU:O	4:G:784:GLY:N	2.45	0.48
8:H:489:TYR:O	8:H:558:LYS:HG3	2.13	0.48
27:F:46:C:H2'	27:F:47:U:H6	1.79	0.48
27:F:74:U:C2'	27:F:75:A:H5'	2.44	0.48
24:C:8:U:H2'	24:C:9:G:C5'	2.42	0.48
8:H:161:ILE:HB	8:H:164:MET:SD	2.54	0.48
8:H:161:ILE:CG2	8:H:162:PRO:HD2	2.41	0.48
1:A:140:ARG:HH21	1:A:252:GLU:HB3	1.77	0.48
1:A:770:MET:HE1	1:A:778:LYS:C	2.33	0.48
8:H:674:LEU:HD11	8:H:973:ARG:HH22	1.77	0.48
1:A:1336:ASN:OD1	1:A:1400:ILE:HG13	2.13	0.48
8:H:936:ILE:HD13	8:H:936:ILE:N	2.27	0.48
1:A:1557:LEU:O	1:A:1560:THR:OG1	2.27	0.48
24:C:8:U:C5	25:D:51:A:N1	2.81	0.48
1:A:1353:THR:O	1:A:1357:LEU:CD1	2.56	0.48
8:H:884:ARG:CB	8:H:910:GLU:HG3	2.44	0.48
8:H:947:LYS:CD	8:H:947:LYS:N	2.73	0.48
8:H:881:LYS:HA	8:H:886:SER:HB3	1.95	0.48
1:A:1183:THR:HG22	1:A:1184:ASP:N	2.29	0.48
3:I:462:ASN:OD1	4:G:830:ARG:NE	2.47	0.48
2:B:60:LYS:HG3	2:B:79:ILE:HD13	1.96	0.48
8:H:490:SER:HA	8:H:558:LYS:HG3	1.96	0.48
27:F:48:G:C4	27:F:49:U:C5	3.02	0.48
1:A:1650:ARG:HD2	25:D:52:G:P	2.53	0.48
5:K:350:PRO:C	5:K:353:ARG:CG	2.81	0.48
1:A:1335:TRP:CZ2	1:A:1339:LEU:CD1	2.97	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:177:PRO:HG2	2:B:195:TRP:HE1	1.79	0.48
2:B:158:GLU:O	2:B:162:MET:HE3	2.14	0.48
1:A:1705:SER:HB3	1:A:1709:TRP:CD1	2.49	0.48
6:L:76:LEU:N	6:L:76:LEU:CD1	2.77	0.48
27:F:46:C:C2	27:F:47:U:C5	3.01	0.48
2:B:357:TRP:CD1	2:B:358:SER:N	2.82	0.48
2:B:345:LEU:HD13	2:B:376:TRP:CE3	2.48	0.48
1:A:290:SER:HG	1:A:291:LYS:NZ	2.05	0.48
1:A:774:ILE:HG23	1:A:777:LYS:NZ	2.28	0.48
6:L:81:THR:CG2	6:L:102:LYS:NZ	2.66	0.48
5:K:146:GLU:C	5:K:148:LYS:N	2.66	0.48
1:A:228:LYS:HD2	1:A:691:PHE:HE1	1.78	0.48
8:H:950:PHE:CZ	8:H:952:PRO:O	2.66	0.48
8:H:858:LEU:HB3	8:H:937:TRP:HB2	1.96	0.48
2:B:359:PRO:CD	2:B:407:GLY:HA3	2.41	0.48
25:D:64:U:C6	25:D:64:U:H5''	2.49	0.48
3:I:130:LEU:HD22	3:I:174:VAL:HG11	1.96	0.48
8:H:491:GLY:O	8:H:492:LEU:HD23	2.14	0.48
27:F:71:A:H2'	27:F:72:C:H6	1.79	0.48
1:A:1657:ILE:O	1:A:1661:ILE:CD1	2.62	0.48
8:H:449:PHE:CD1	8:H:453:THR:HG21	2.45	0.48
5:K:159:TYR:CD2	5:K:163:ASN:ND2	2.82	0.48
2:B:173:VAL:CG1	2:B:200:GLN:OE1	2.54	0.48
1:A:1875:ILE:HG22	1:A:1876:ASN:N	2.18	0.48
1:A:305:LEU:C	1:A:305:LEU:HD23	2.34	0.48
1:A:553:ASN:C	1:A:554:THR:HG23	2.33	0.48
7:M:42:LYS:NZ	26:E:44:G:O6	2.47	0.48
27:F:52:G:C4	27:F:53:C:C5	3.01	0.48
2:B:350:LYS:HE3	5:K:431:TYR:CG	2.49	0.48
2:B:386:LEU:HD12	2:B:386:LEU:C	2.34	0.48
4:G:886:CYS:CB	4:G:888:PRO:HD2	2.44	0.48
2:B:320:SER:HB2	2:B:337:ARG:HH12	1.79	0.48
2:B:345:LEU:HD13	2:B:376:TRP:CG	2.49	0.48
2:B:395:ILE:HG22	2:B:396:VAL:N	2.18	0.48
2:B:177:PRO:CB	2:B:195:TRP:HE1	2.27	0.48
2:B:293:ASP:OD1	2:B:294:ALA:N	2.46	0.48
8:H:538:GLU:HG2	8:H:538:GLU:H	1.47	0.48
1:A:754:TYR:CE2	1:A:758:LEU:HD21	2.49	0.48
1:A:1061:ILE:HG12	1:A:1117:TYR:CE2	2.49	0.48
1:A:292:LYS:NZ	1:A:307:GLU:OE2	2.35	0.48
3:I:248:VAL:O	3:I:252:SER:OG	2.30	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:284:LEU:N	4:G:284:LEU:CD2	2.77	0.48
2:B:312:SER:HB2	2:B:353:TYR:O	2.14	0.48
5:K:141:ASN:C	5:K:142:LEU:HD22	2.33	0.48
1:A:1908:LEU:C	1:A:1908:LEU:HD12	2.34	0.48
26:E:1:A:OP2	29:E:201:M7M:HBI	2.13	0.48
4:G:721:ARG:O	4:G:725:ILE:HD12	2.14	0.47
4:G:286:GLU:OE2	4:G:292:CYS:SG	2.69	0.47
8:H:888:ILE:HA	8:H:904:GLY:HA2	1.96	0.47
26:E:24:A:O2'	26:E:25:U:OP1	2.28	0.47
2:B:404:GLU:O	2:B:405:ASP:HB3	2.13	0.47
2:B:60:LYS:HB3	2:B:61:PRO:HD2	1.95	0.47
3:I:79:ASP:O	3:I:83:ILE:N	2.31	0.47
1:A:2011:LEU:HB3	1:A:2040:TRP:CH2	2.49	0.47
8:H:577:LEU:O	8:H:577:LEU:HD23	2.13	0.47
27:F:73:U:O2'	27:F:74:U:H5'	2.02	0.47
1:A:501:LEU:HD13	1:A:705:GLN:HG2	1.96	0.47
8:H:132:ARG:HE	8:H:206:LYS:HD2	1.80	0.47
3:I:95:LEU:HD23	3:I:98:PHE:CD2	2.49	0.47
1:A:1593:ALA:CB	6:L:118:GLU:OE1	2.63	0.47
6:L:118:GLU:OE2	6:L:122:ARG:NH2	2.26	0.47
8:H:265:PHE:CE2	8:H:295:ILE:HB	2.49	0.47
1:A:874:ILE:O	1:A:874:ILE:HG22	2.15	0.47
6:L:78:ASP:CG	6:L:79:PRO:HD3	2.34	0.47
1:A:1009:PHE:CE1	1:A:1115:GLN:HB3	2.49	0.47
1:A:1014:LYS:NZ	1:A:1016:SER:OG	2.39	0.47
1:A:1211:SER:HA	1:A:1257:ASN:ND2	2.30	0.47
9:N:1203:SER:N	9:N:1223:ILE:O	2.39	0.47
4:G:809:LEU:HD12	4:G:841:THR:HG22	1.96	0.47
4:G:702:PRO:CA	4:G:739:PHE:CE2	2.98	0.47
1:A:1877:GLY:O	1:A:1894:ILE:CA	2.62	0.47
1:A:1731:LYS:O	1:A:1771:THR:OG1	2.32	0.47
8:H:444:GLN:NE2	8:H:444:GLN:CA	2.73	0.47
6:L:18:ALA:HB1	6:L:60:TYR:CE2	2.49	0.47
27:F:36:A:H61	27:F:118:U:H3	1.61	0.47
2:B:77:ALA:O	2:B:81:MET:HG2	2.14	0.47
1:A:1156:HIS:CG	1:A:1157:PRO:HD2	2.50	0.47
9:N:990:ASP:O	9:N:994:ASP:N	2.45	0.47
8:H:233:ASP:HA	8:H:452:LYS:NZ	2.29	0.47
27:F:32:G:HO2'	27:F:33:U:P	2.37	0.47
8:H:889:TYR:N	8:H:903:ARG:O	2.47	0.47
8:H:373:PHE:CE1	8:H:377:ILE:CD1	2.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:446:SER:CB	2:B:451:PHE:H	2.22	0.47
4:G:852:LEU:CD1	4:G:852:LEU:N	2.76	0.47
3:I:209:LYS:HG3	3:I:210:LEU:N	2.29	0.47
1:A:1586:GLN:CG	1:A:1595:ARG:NH1	2.77	0.47
4:G:740:TYR:OH	4:G:766:LYS:NZ	2.42	0.47
1:A:1033:ASN:HD21	1:A:1298:ALA:HB3	1.80	0.47
1:A:2046:GLU:HG2	1:A:2049:ILE:HD12	1.96	0.47
4:G:291:TYR:O	4:G:291:TYR:HD1	1.97	0.47
5:K:350:PRO:CA	5:K:353:ARG:CD	2.85	0.47
8:H:247:PHE:CD1	8:H:903:ARG:NH1	2.83	0.47
25:D:86:G:C5'	25:D:86:G:H8	2.19	0.47
4:G:120:MET:O	4:G:122:ILE:N	2.44	0.47
8:H:769:TYR:CD1	8:H:799:PHE:CD2	3.02	0.47
8:H:118:TYR:O	8:H:119:ASN:HB3	2.14	0.47
8:H:860:PRO:HB3	8:H:937:TRP:CE3	2.48	0.47
1:A:1607:THR:O	1:A:1611:SER:N	2.47	0.47
1:A:1286:TRP:NE1	1:A:1348:GLU:OE1	2.37	0.47
1:A:719:ILE:N	1:A:720:PRO:HD2	2.28	0.47
8:H:941:PRO:HG2	8:H:962:LEU:HD12	1.97	0.47
27:F:71:A:C4	27:F:72:C:C5	3.02	0.47
8:H:175:LEU:HD23	8:H:175:LEU:C	2.34	0.47
1:A:495:ARG:NH1	1:A:497:GLN:HE21	2.12	0.47
25:D:62:A:N3	26:E:58:G:N2	2.62	0.47
1:A:454:LEU:HD22	8:H:336:ILE:HB	1.96	0.47
8:H:104:THR:O	8:H:108:GLN:HG3	2.14	0.47
5:K:282:GLU:C	5:K:284:ASP:H	2.16	0.47
1:A:2041:PRO:HG2	1:A:2043:PHE:CZ	2.50	0.47
1:A:790:TRP:CD2	1:A:819:LYS:HD3	2.49	0.47
1:A:320:ASP:C	1:A:321:GLU:HG3	2.34	0.47
27:F:52:G:H2'	27:F:53:C:H6	1.79	0.47
4:G:672:LEU:HD13	4:G:703:LEU:HD12	1.97	0.47
8:H:492:LEU:HD22	8:H:557:HIS:ND1	2.24	0.47
2:B:321:LEU:HD22	2:B:335:ASP:HA	1.97	0.47
8:H:964:ARG:O	8:H:968:MET:HG2	2.15	0.47
1:A:301:TRP:CZ2	1:A:491:GLY:HA3	2.50	0.47
8:H:581:LYS:CB	8:H:581:LYS:NZ	2.73	0.47
2:B:362:TYR:CD2	2:B:379:ARG:HD2	2.49	0.47
1:A:1730:ASN:C	1:A:1731:LYS:HG3	2.35	0.47
4:G:15:TYR:CE1	6:L:13:TRP:HD1	2.32	0.47
4:G:853:GLY:O	4:G:854:LYS:HB2	2.14	0.47
1:A:553:ASN:O	1:A:554:THR:HG23	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1508:HIS:HA	1:A:1511:ARG:NH2	2.29	0.47
1:A:1262:MET:O	1:A:1263:CYS:CB	2.61	0.47
4:G:368:SER:O	4:G:372:LEU:N	2.47	0.47
2:B:413:CYS:SG	2:B:440:ILE:HG21	2.55	0.47
6:L:105:PHE:CB	6:L:141:ARG:CD	2.92	0.47
27:F:66:A:C4	27:F:67:U:C5	3.02	0.47
8:H:307:ILE:HD13	8:H:345:THR:O	2.15	0.47
2:B:275:PRO:HG3	2:B:319:GLY:N	2.30	0.47
1:A:767:LEU:HA	1:A:770:MET:HG3	1.96	0.47
4:G:144:LYS:O	4:G:145:THR:OG1	2.18	0.47
8:H:336:ILE:HD11	8:H:341:ILE:CG2	2.38	0.47
1:A:174:LYS:O	1:A:178:ASN:ND2	2.39	0.47
1:A:1217:ARG:HD3	1:A:1217:ARG:HA	1.75	0.47
1:A:1591:THR:CG2	1:A:1592:HIS:N	2.78	0.47
2:B:187:ASP:OD2	2:B:447:ASN:CB	2.63	0.47
2:B:120:ALA:HB1	2:B:279:PHE:CE2	2.50	0.47
1:A:239:PHE:CB	1:A:240:PRO:CD	2.92	0.47
2:B:225:ASP:OD1	2:B:226:TRP:N	2.48	0.47
1:A:1527:TRP:CE3	1:A:1528:THR:HG23	2.50	0.47
4:G:672:LEU:HD22	4:G:703:LEU:CD1	2.45	0.47
4:G:288:ASP:O	4:G:292:CYS:SG	2.72	0.47
1:A:1651:ALA:C	1:A:1652:HIS:HD2	2.16	0.47
1:A:470:LEU:H	1:A:473:THR:CG2	2.27	0.47
1:A:470:LEU:H	1:A:473:THR:HG21	1.80	0.47
1:A:1369:ASN:O	1:A:1373:LEU:HG	2.15	0.47
2:B:261:LEU:HD13	2:B:292:TRP:CE3	2.50	0.47
2:B:243:ILE:HD12	2:B:292:TRP:HZ3	1.78	0.47
1:A:691:PHE:HZ	1:A:701:CYS:CA	2.26	0.47
1:A:175:LEU:HD11	1:A:564:TRP:CE2	2.50	0.47
1:A:1623:PHE:CZ	24:C:5:G:C5	3.02	0.47
1:A:1115:GLN:CA	1:A:1115:GLN:NE2	2.78	0.47
5:K:370:LEU:HD21	5:K:454:THR:HG21	1.95	0.47
5:K:340:LYS:HE2	5:K:389:CYS:HB3	1.97	0.47
2:B:181:VAL:HA	2:B:191:ALA:O	2.15	0.47
3:I:277:SER:HB3	3:I:279:VAL:HG23	1.97	0.47
4:G:490:GLU:O	4:G:494:HIS:N	2.48	0.47
4:G:698:VAL:N	4:G:699:PRO:CD	2.78	0.47
4:G:861:ASN:ND2	4:G:862:MET:SD	2.88	0.47
1:A:1145:MET:CE	1:A:1160:LEU:HD13	2.44	0.47
2:B:275:PRO:O	2:B:276:SER:O	2.33	0.47
1:A:845:VAL:HG21	1:A:1321:MET:CE	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:853:THR:OG1	1:A:971:MET:HG2	2.14	0.47
1:A:840:VAL:C	1:A:841:GLU:HG3	2.34	0.47
2:B:161:ARG:O	2:B:165:LEU:CD2	2.62	0.47
6:L:13:TRP:CH2	6:L:17:GLN:NE2	2.83	0.47
8:H:855:PRO:CD	8:H:944:VAL:HG21	2.44	0.46
8:H:500:ARG:CD	8:H:534:THR:HG23	2.10	0.46
8:H:564:ILE:HG22	8:H:567:ILE:HG12	1.95	0.46
1:A:289:ASP:HB3	1:A:292:LYS:HB2	1.97	0.46
27:F:43:G:C2	27:F:44:A:C5	3.02	0.46
8:H:375:GLU:CG	8:H:376:PHE:CE1	2.99	0.46
4:G:101:LYS:O	4:G:105:ALA:HB2	2.15	0.46
3:I:401:LEU:HD12	3:I:401:LEU:H	1.79	0.46
8:H:967:VAL:HB	8:H:968:MET:HE3	1.97	0.46
1:A:251:TYR:HA	1:A:255:ILE:CD1	2.37	0.46
2:B:206:THR:HB	2:B:208:GLN:CD	2.35	0.46
3:I:214:ILE:O	3:I:218:ILE:HG12	2.15	0.46
6:L:108:ASP:OD1	6:L:108:ASP:N	2.48	0.46
27:F:35:A:C4	27:F:120:G:N2	2.82	0.46
8:H:897:THR:HB	8:H:898:PRO:HD2	1.97	0.46
4:G:298:THR:O	4:G:302:PHE:CD2	2.67	0.46
25:D:48:C:H2'	25:D:49:A:C8	2.50	0.46
1:A:315:SER:C	1:A:317:PRO:CD	2.82	0.46
1:A:1704:GLU:HG2	1:A:1731:LYS:HD3	1.97	0.46
1:A:1115:GLN:N	1:A:1115:GLN:HE21	2.12	0.46
2:B:350:LYS:HB3	2:B:351:PRO:HD2	1.98	0.46
1:A:1156:HIS:ND1	1:A:1157:PRO:HD2	2.29	0.46
8:H:941:PRO:HD2	8:H:962:LEU:HB2	1.98	0.46
5:K:395:LEU:HD13	5:K:399:ARG:CZ	2.45	0.46
1:A:815:TYR:CD1	1:A:815:TYR:C	2.88	0.46
8:H:500:ARG:HE	8:H:534:THR:HB	1.75	0.46
8:H:488:ILE:HD11	8:H:556:ALA:HB1	1.97	0.46
1:A:170:HIS:CD2	1:A:170:HIS:C	2.88	0.46
2:B:387:ASN:CA	2:B:388:GLN:OE1	2.64	0.46
1:A:1366:ARG:HA	1:A:1369:ASN:HD22	1.80	0.46
2:B:362:TYR:HD2	2:B:379:ARG:HD2	1.81	0.46
5:K:334:PRO:HG2	5:K:337:TYR:HE1	1.79	0.46
4:G:325:ARG:O	4:G:329:LYS:N	2.37	0.46
27:F:165:A:O2'	27:F:166:U:OP2	2.27	0.46
4:G:691:TYR:CE2	4:G:711:ILE:HD12	2.49	0.46
8:H:167:ASN:C	8:H:167:ASN:ND2	2.69	0.46
1:A:505:TRP:HZ3	1:A:690:LYS:HG3	1.78	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:387:TYR:O	8:H:391:MET:CB	2.50	0.46
8:H:296:ASN:OD1	8:H:303:VAL:HA	2.15	0.46
1:A:1275:MET:CE	1:A:1299:LYS:CD	2.93	0.46
1:A:1899:TRP:CH2	1:A:1909:ALA:CB	2.98	0.46
4:G:122:ILE:CG1	4:G:123:PRO:HD2	2.36	0.46
1:A:1284:GLY:HA2	1:A:1348:GLU:HB3	1.96	0.46
2:B:184:SER:OG	2:B:186:ASP:OD1	2.18	0.46
1:A:2075:THR:HG22	1:A:2076:GLN:N	2.30	0.46
8:H:449:PHE:CD1	8:H:449:PHE:C	2.88	0.46
2:B:313:LEU:HD11	2:B:322:VAL:HG21	1.98	0.46
2:B:177:PRO:CG	2:B:195:TRP:HE1	2.27	0.46
3:I:281:GLN:NE2	26:E:37:U:O4	2.48	0.46
2:B:408:LYS:O	2:B:424:SER:HB3	2.15	0.46
3:I:433:ASN:N	3:I:433:ASN:ND2	2.61	0.46
4:G:13:ALA:O	4:G:15:TYR:N	2.48	0.46
2:B:279:PHE:HD1	2:B:279:PHE:N	2.12	0.46
6:L:45:LEU:HD11	6:L:110:LYS:HA	1.97	0.46
2:B:307:ASP:OD1	5:K:225:ILE:HA	2.16	0.46
1:A:1878:CYS:O	1:A:1878:CYS:SG	2.73	0.46
1:A:1402:ALA:O	1:A:1403:SER:CB	2.63	0.46
1:A:286:LEU:HD22	1:A:292:LYS:HB3	1.96	0.46
1:A:1065:LEU:HG	3:I:177:MET:HE1	1.98	0.46
1:A:1593:ALA:HB3	6:L:118:GLU:OE1	2.16	0.46
1:A:1756:PHE:CD1	1:A:1756:PHE:C	2.89	0.46
8:H:544:LEU:HG	8:H:553:VAL:HG21	1.97	0.46
1:A:514:TYR:CD1	1:A:514:TYR:N	2.84	0.46
8:H:801:TRP:O	8:H:801:TRP:HD1	1.98	0.46
1:A:1216:ILE:HD12	1:A:1254:ASN:CB	2.44	0.46
1:A:1995:TRP:CE3	1:A:2007:ARG:HD2	2.50	0.46
4:G:703:LEU:O	4:G:703:LEU:HD13	2.16	0.46
8:H:247:PHE:HB3	8:H:931:TYR:OH	2.15	0.46
1:A:1417:GLN:OE1	1:A:1422:ILE:CG1	2.64	0.46
24:C:-4:A:C1'	24:C:-3:A:P	3.04	0.46
2:B:290:ARG:CZ	2:B:302:LEU:HD13	2.45	0.46
1:A:810:LYS:HE3	1:A:810:LYS:HA	1.98	0.46
1:A:901:PRO:HD3	1:A:1078:ILE:HD11	1.98	0.46
1:A:1125:LEU:HD21	1:A:1234:VAL:CG2	2.46	0.46
1:A:247:PRO:HB2	1:A:248:PRO:HD2	1.98	0.46
8:H:571:TYR:CD2	8:H:573:LYS:O	2.69	0.46
3:I:226:ALA:CB	3:I:317:ASP:OD2	2.62	0.46
1:A:1038:ILE:HD12	1:A:1039:TRP:CE3	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:321:LEU:HD13	2:B:333:LEU:HD23	1.98	0.46
3:I:136:GLN:NE2	3:I:166:LYS:O	2.49	0.46
1:A:318:LEU:N	1:A:318:LEU:HD12	2.31	0.46
8:H:967:VAL:HG12	8:H:971:ARG:HG3	1.97	0.46
4:G:144:LYS:HE3	26:E:19:U:OP1	2.16	0.46
5:K:453:ARG:O	5:K:457:GLN:CD	2.54	0.46
2:B:422:TYR:HD1	2:B:429:LYS:HA	1.81	0.46
4:G:851:ARG:C	4:G:852:LEU:HD12	2.36	0.46
1:A:1204:ARG:CD	1:A:1259:LEU:HB3	2.46	0.46
7:M:51:PHE:CE2	7:M:53:ILE:HD11	2.50	0.46
1:A:1287:ASP:OD2	1:A:1296:ARG:NH1	2.49	0.46
1:A:656:ILE:O	1:A:660:ILE:HG13	2.16	0.46
8:H:362:LYS:HE2	8:H:365:GLU:CB	2.45	0.46
1:A:141:LYS:HA	1:A:144:ASN:CG	2.19	0.46
4:G:103:GLN:O	4:G:106:ASP:OD1	2.34	0.46
2:B:171:GLN:OE1	2:B:172:LEU:O	2.34	0.46
26:E:2:U:C6	26:E:3:C:C5	3.03	0.46
24:C:10:U:H2'	24:C:11:A:C8	2.50	0.46
4:G:16:VAL:HG13	4:G:17:PRO:HD2	1.98	0.46
3:I:143:ILE:HG23	3:I:149:TYR:HE2	1.81	0.46
1:A:665:GLY:O	1:A:668:ARG:HG2	2.15	0.46
27:F:89:U:C4	27:F:90:C:C5	3.04	0.46
4:G:692:LEU:O	4:G:696:ARG:HG3	2.15	0.46
1:A:175:LEU:HD12	1:A:564:TRP:NE1	2.31	0.46
1:A:532:ASN:ND2	27:F:83:C:O3'	2.49	0.46
3:I:268:LEU:CD1	3:I:271:GLU:CG	2.83	0.46
1:A:1088:VAL:HG12	1:A:1089:VAL:H	1.79	0.46
1:A:1488:ILE:HB	1:A:1489:PRO:HD3	1.97	0.46
6:L:78:ASP:CG	6:L:79:PRO:CD	2.85	0.46
4:G:223:LEU:HD23	4:G:223:LEU:C	2.36	0.46
26:E:32:G:N2	26:E:44:G:N3	2.64	0.46
1:A:1790:TRP:CE3	1:A:1795:LYS:HG3	2.51	0.46
1:A:1521:ARG:CZ	3:I:404:TYR:CD2	2.99	0.46
1:A:1625:VAL:O	1:A:1633:PHE:HA	2.15	0.46
1:A:275:TYR:O	1:A:279:TRP:CE2	2.69	0.46
4:G:769:SER:O	4:G:801:THR:HG22	2.15	0.46
8:H:831:ILE:HG22	8:H:831:ILE:O	2.16	0.46
27:F:73:U:C2	27:F:74:U:C5	3.03	0.45
8:H:328:VAL:HG21	8:H:345:THR:CG2	2.45	0.45
6:L:139:HIS:NE2	27:F:96:U:O5'	2.49	0.45
5:K:159:TYR:CE1	5:K:163:ASN:ND2	2.83	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:853:THR:OG1	1:A:971:MET:CG	2.64	0.45
6:L:36:ASP:HB2	6:L:39:CYS:HB2	1.99	0.45
1:A:1711:VAL:HG12	1:A:1712:SER:N	2.31	0.45
27:F:75:A:C4	27:F:77:A:H5"	2.50	0.45
3:I:123:ARG:HB2	3:I:189:LEU:CD1	2.46	0.45
3:I:359:PRO:O	6:L:122:ARG:NH1	2.50	0.45
2:B:261:LEU:HB3	2:B:292:TRP:CZ3	2.51	0.45
1:A:971:MET:HE3	1:A:978:ILE:HG22	1.99	0.45
8:H:963:SER:O	8:H:967:VAL:HG23	2.17	0.45
2:B:267:ARG:NH1	2:B:285:HIS:NE2	2.64	0.45
2:B:162:MET:N	2:B:162:MET:CE	2.79	0.45
2:B:244:LYS:HG2	2:B:257:LEU:HD23	1.97	0.45
8:H:204:GLU:HA	8:H:204:GLU:OE1	2.17	0.45
26:E:21:C:H2'	26:E:22:G:O4'	2.15	0.45
3:I:98:PHE:CZ	3:I:217:TYR:CD2	2.98	0.45
1:A:495:ARG:CZ	1:A:497:GLN:NE2	2.78	0.45
1:A:388:PRO:HB2	1:A:398:VAL:HG11	1.98	0.45
5:K:337:TYR:CE2	5:K:434:ASP:HA	2.51	0.45
3:I:424:THR:HG22	3:I:425:SER:N	2.30	0.45
1:A:1839:ASN:ND2	1:A:1842:GLU:OE1	2.50	0.45
4:G:487:GLN:O	4:G:491:LYS:N	2.43	0.45
4:G:691:TYR:HE2	4:G:711:ILE:CD1	2.14	0.45
4:G:668:HIS:HB2	4:G:698:VAL:HG11	1.95	0.45
4:G:285:HIS:HE1	4:G:291:TYR:HE2	1.56	0.45
8:H:247:PHE:CD1	8:H:250:GLU:OE1	2.70	0.45
1:A:770:MET:HE1	1:A:778:LYS:CB	2.45	0.45
1:A:362:GLU:CB	1:A:1209:LYS:HG2	2.45	0.45
4:G:255:ARG:HG3	4:G:255:ARG:HH11	1.80	0.45
8:H:379:ILE:HG23	8:H:383:LYS:HE2	1.98	0.45
1:A:883:PHE:HB2	3:I:177:MET:SD	2.56	0.45
5:K:144:LEU:H	5:K:144:LEU:CD2	2.29	0.45
1:A:1335:TRP:CD1	1:A:1367:ILE:HD12	2.52	0.45
2:B:443:LEU:CD1	2:B:452:LEU:HD11	2.47	0.45
2:B:135:ARG:HD3	2:B:360:ASN:O	2.16	0.45
4:G:238:PRO:CD	4:G:239:THR:N	2.79	0.45
1:A:2066:LYS:HB2	1:A:2067:TYR:HD1	1.80	0.45
1:A:1589:LYS:O	1:A:1590:LEU:HD13	2.16	0.45
5:K:273:LYS:O	5:K:277:MET:HB2	2.16	0.45
7:M:67:LEU:HB2	7:M:68:PRO:HD3	1.98	0.45
4:G:219:THR:HG22	4:G:221:GLU:H	1.81	0.45
1:A:162:LEU:CD2	1:A:730:ILE:HD13	2.42	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:F:77:A:C1'	27:F:78:A:C5'	2.95	0.45
6:L:102:LYS:CG	6:L:103:LEU:N	2.78	0.45
8:H:968:MET:HE2	8:H:971:ARG:HG3	1.98	0.45
2:B:155:ARG:CD	2:B:155:ARG:N	2.79	0.45
1:A:1453:ASP:O	1:A:1457:VAL:HG23	2.16	0.45
1:A:874:ILE:O	1:A:875:THR:O	2.34	0.45
3:I:237:ILE:O	3:I:240:GLN:N	2.49	0.45
4:G:733:ASN:HB2	4:G:734:PRO:HA	1.99	0.45
9:N:1105:ALA:O	9:N:1106:GLY:C	2.54	0.45
8:H:306:PRO:HD2	8:H:349:TRP:CE2	2.51	0.45
4:G:252:GLU:CG	4:G:256:LYS:HE3	2.47	0.45
1:A:366:GLU:O	1:A:372:ARG:HD2	2.16	0.45
1:A:251:TYR:O	1:A:255:ILE:HB	2.16	0.45
1:A:795:ALA:O	1:A:796:ASN:HB2	2.17	0.45
8:H:113:ILE:CG2	8:H:549:TYR:CD1	2.99	0.45
8:H:121:ASP:O	8:H:125:SER:N	2.49	0.45
3:I:245:ALA:CB	3:I:250:GLU:HB3	2.40	0.45
8:H:270:LEU:CD1	8:H:313:PHE:HB3	2.45	0.45
2:B:428:LEU:HD11	5:K:466:PRO:HD2	1.97	0.45
1:A:820:ALA:O	1:A:824:VAL:HG23	2.16	0.45
27:F:66:A:H2'	27:F:67:U:H6	1.81	0.45
8:H:675:THR:HG22	8:H:909:ILE:HD13	1.98	0.45
2:B:192:THR:CG2	2:B:200:GLN:HG3	2.47	0.45
27:F:102:C:H2'	27:F:103:A:H5'	1.99	0.45
2:B:202:LEU:CD1	2:B:202:LEU:N	2.80	0.45
8:H:272:ARG:O	8:H:276:ASP:HB2	2.16	0.45
8:H:274:ILE:C	8:H:274:ILE:HD13	2.37	0.45
3:I:92:ILE:O	3:I:96:PRO:HD3	2.16	0.45
1:A:373:VAL:CG1	1:A:374:ILE:N	2.80	0.45
6:L:74:TYR:CG	6:L:83:MET:CE	3.00	0.45
1:A:1974:LEU:O	1:A:1978:VAL:HG23	2.17	0.45
2:B:88:GLU:HA	2:B:91:ASN:HB3	1.98	0.45
1:A:205:THR:HG23	1:A:205:THR:O	2.16	0.45
8:H:500:ARG:HG2	8:H:534:THR:HG21	1.87	0.45
25:D:49:A:H2'	25:D:50:G:O5'	2.16	0.45
8:H:578:TYR:CD1	8:H:578:TYR:O	2.70	0.45
1:A:776:GLN:HG2	1:A:777:LYS:N	2.32	0.45
1:A:176:LEU:C	1:A:176:LEU:CD2	2.85	0.45
2:B:454:SER:OG	2:B:464:TRP:NE1	2.29	0.45
27:F:84:A:C2	27:F:111:C:C2	3.05	0.45
1:A:1611:SER:N	1:A:1612:PRO:HD2	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:447:ASN:ND2	2:B:447:ASN:C	2.70	0.45
3:I:66:SER:O	3:I:70:THR:N	2.50	0.45
9:N:1343:PHE:O	9:N:1345:PHE:N	2.49	0.45
5:K:409:HIS:ND1	5:K:414:ASP:OD1	2.44	0.45
8:H:167:ASN:ND2	8:H:173:LYS:CG	2.76	0.45
8:H:471:HIS:O	8:H:486:VAL:HA	2.17	0.45
1:A:505:TRP:HD1	1:A:505:TRP:H	1.64	0.45
1:A:505:TRP:CE3	1:A:690:LYS:HG3	2.50	0.45
3:I:358:ILE:CG2	3:I:359:PRO:CD	2.94	0.45
8:H:950:PHE:CE1	8:H:951:ILE:O	2.70	0.45
2:B:419:ILE:CG2	2:B:433:LEU:HB2	2.47	0.45
3:I:46:ILE:O	3:I:97:PHE:CE1	2.69	0.45
27:F:107:C:H2'	27:F:108:C:O4'	2.16	0.45
1:A:151:SER:H	1:A:577:ASN:ND2	2.14	0.45
29:E:201:M7M:NBN	29:E:201:M7M:HBX	2.32	0.45
1:A:956:LYS:C	1:A:956:LYS:CD	2.83	0.45
4:G:890:GLU:HA	4:G:890:GLU:OE1	2.17	0.45
1:A:298:TYR:O	1:A:298:TYR:CD1	2.70	0.45
5:K:141:ASN:CG	5:K:144:LEU:HD23	2.37	0.45
24:C:11:A:C2	25:D:47:A:C6	3.05	0.45
8:H:470:ALA:HB3	8:H:577:LEU:CD2	2.46	0.44
8:H:539:VAL:HG22	8:H:567:ILE:HD11	1.99	0.44
27:F:79:C:O2	27:F:79:C:H3'	2.17	0.44
1:A:484:PHE:CD1	27:F:81:A:C6	3.05	0.44
2:B:357:TRP:HD1	2:B:358:SER:N	2.15	0.44
1:A:770:MET:HE3	1:A:775:ARG:O	2.17	0.44
8:H:133:ILE:HG13	8:H:134:ILE:N	2.32	0.44
8:H:481:ALA:HB2	8:H:565:LYS:HZ3	1.77	0.44
2:B:393:ARG:NH2	2:B:393:ARG:CG	2.74	0.44
1:A:1047:ALA:HA	1:A:1172:PHE:O	2.17	0.44
1:A:2029:ASP:HB2	1:A:2032:ILE:HD12	1.98	0.44
1:A:860:GLU:OE2	1:A:863:ARG:NH1	2.51	0.44
8:H:234:LEU:HD23	8:H:234:LEU:H	1.82	0.44
4:G:688:ARG:HH11	4:G:712:ASP:CG	2.20	0.44
25:D:83:A:O2'	25:D:84:C:P	2.75	0.44
8:H:354:TYR:O	8:H:354:TYR:CD1	2.70	0.44
24:C:-3:A:H1'	24:C:-2:A:C8	2.52	0.44
8:H:599:THR:HG23	8:H:933:TRP:HZ3	1.80	0.44
5:K:341:VAL:HG21	5:K:428:TRP:CD1	2.51	0.44
8:H:110:LYS:HD3	8:H:110:LYS:HA	1.79	0.44
3:I:400:VAL:CG2	4:G:154:PRO:HG2	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:401:LEU:HA	3:I:407:GLU:HA	1.97	0.44
8:H:942:GLY:HA2	8:H:960:ASN:O	2.17	0.44
1:A:176:LEU:HD21	1:A:708:TRP:NE1	2.31	0.44
2:B:116:GLU:CD	2:B:117:LEU:N	2.70	0.44
27:F:103:A:C4	27:F:104:G:N7	2.86	0.44
1:A:874:ILE:C	1:A:875:THR:OG1	2.55	0.44
3:I:113:HIS:HD2	3:I:134:PRO:CA	2.30	0.44
6:L:140:LYS:CB	6:L:141:ARG:HH11	2.30	0.44
1:A:165:LEU:HD23	1:A:726:ILE:HG21	1.99	0.44
27:F:50:G:H2'	27:F:51:G:H8	1.82	0.44
1:A:2076:GLN:HA	1:A:2079:ILE:HD12	1.98	0.44
1:A:2075:THR:O	1:A:2079:ILE:HD12	2.17	0.44
1:A:1378:LYS:O	1:A:1379:MET:HB2	2.16	0.44
27:F:95:C:O3'	27:F:96:U:H4'	2.17	0.44
6:L:133:SER:HA	6:L:134:PRO:HD2	1.84	0.44
8:H:449:PHE:CD1	8:H:449:PHE:O	2.70	0.44
1:A:1364:GLU:OE1	1:A:1405:ILE:HD11	2.17	0.44
2:B:154:SER:HG	2:B:155:ARG:HD3	1.79	0.44
1:A:1020:ILE:HD12	1:A:1020:ILE:N	2.32	0.44
3:I:429:ARG:HA	3:I:429:ARG:HH11	1.82	0.44
5:K:143:GLU:O	5:K:145:HIS:CE1	2.70	0.44
8:H:472:VAL:CG1	8:H:571:TYR:HE2	2.29	0.44
24:C:7:A:N6	25:D:51:A:C8	2.85	0.44
8:H:120:ARG:HD3	8:H:120:ARG:HA	1.67	0.44
1:A:1417:GLN:HE22	1:A:1783:MET:HA	1.83	0.44
1:A:1144:PHE:CD2	1:A:1145:MET:HG2	2.53	0.44
8:H:354:TYR:HB2	8:H:359:PHE:CB	2.28	0.44
1:A:1851:PHE:O	1:A:1881:THR:HA	2.17	0.44
1:A:1880:PHE:CD2	1:A:1889:LEU:CD2	3.00	0.44
2:B:390:LEU:CD1	5:K:428:TRP:CD1	3.01	0.44
8:H:595:LEU:HA	8:H:595:LEU:HD13	1.83	0.44
1:A:1373:LEU:HD11	27:F:96:U:OP1	2.17	0.44
2:B:393:ARG:HG2	2:B:393:ARG:NH2	2.17	0.44
1:A:1857:VAL:HG13	1:A:1894:ILE:CD1	2.47	0.44
1:A:1474:ARG:HG2	1:A:1475:LEU:N	2.33	0.44
2:B:359:PRO:HG2	2:B:407:GLY:CA	2.47	0.44
2:B:32:LEU:HD23	2:B:34:HIS:H	1.82	0.44
3:I:456:LEU:HD23	3:I:456:LEU:O	2.18	0.44
1:A:162:LEU:CG	1:A:734:PHE:CE2	2.96	0.44
8:H:375:GLU:HB3	8:H:376:PHE:CD1	2.52	0.44
1:A:1073:ILE:HD12	1:A:1116:TYR:HE1	1.77	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:98:SER:HG	4:G:99:ASN:ND2	2.14	0.44
1:A:1275:MET:HE1	1:A:1299:LYS:CD	2.47	0.44
8:H:950:PHE:CZ	8:H:951:ILE:O	2.70	0.44
27:F:102:C:C2'	27:F:103:A:H5'	2.47	0.44
1:A:543:ASN:C	1:A:543:ASN:HD22	2.21	0.44
1:A:807:PRO:O	1:A:811:ILE:HG13	2.18	0.44
1:A:325:LYS:CA	1:A:325:LYS:CE	2.96	0.44
1:A:275:TYR:N	1:A:275:TYR:CD1	2.72	0.44
1:A:170:HIS:CD2	1:A:170:HIS:O	2.70	0.44
3:I:137:TYR:O	3:I:141:ILE:HG13	2.17	0.44
8:H:230:ALA:HB3	8:H:473:LEU:CD1	2.48	0.44
26:E:151:G:C2	26:E:152:A:N6	2.84	0.44
1:A:358:ARG:CB	1:A:358:ARG:NH1	2.80	0.44
8:H:229:LEU:CD2	8:H:235:VAL:HG11	2.48	0.44
2:B:293:ASP:HB2	2:B:300:LEU:HD11	1.99	0.44
8:H:769:TYR:CZ	8:H:799:PHE:CE2	2.92	0.44
6:L:25:ARG:CG	6:L:25:ARG:NH1	2.75	0.44
4:G:111:LEU:O	4:G:113:ALA:N	2.51	0.44
1:A:429:ASN:HB3	1:A:430:PRO:HD2	1.98	0.44
3:I:398:GLN:OE1	3:I:414:ASN:ND2	2.49	0.44
9:N:1382:LEU:O	9:N:1385:LEU:N	2.50	0.44
4:G:867:GLU:OE2	4:G:888:PRO:HG2	2.17	0.44
8:H:123:MET:SD	8:H:209:MET:HE3	2.58	0.44
8:H:132:ARG:O	8:H:133:ILE:HG23	2.17	0.44
8:H:304:PHE:CD1	8:H:304:PHE:N	2.86	0.44
1:A:1661:ILE:HB	1:A:1736:VAL:HG11	2.00	0.44
2:B:154:SER:O	2:B:158:GLU:HG3	2.18	0.44
1:A:164:ALA:HB2	1:A:194:HIS:CD2	2.53	0.44
1:A:807:PRO:HB2	4:G:111:LEU:HD23	1.99	0.44
8:H:460:GLY:HA3	8:H:461:LYS:HA	1.67	0.44
3:I:277:SER:CB	3:I:279:VAL:HG23	2.48	0.44
1:A:1015:PRO:HG2	1:A:1510:ILE:HG12	1.98	0.44
2:B:416:ASP:O	2:B:417:ASN:HB2	2.18	0.44
5:K:345:LYS:HB2	5:K:422:ASN:HA	2.00	0.44
8:H:484:SER:O	8:H:564:ILE:HD12	2.17	0.44
1:A:171:ALA:HB2	1:A:201:PHE:CE1	2.51	0.44
27:F:99:U:O2'	27:F:100:A:P	2.73	0.44
2:B:171:GLN:NE2	2:B:172:LEU:H	2.15	0.44
1:A:180:PRO:O	1:A:181:HIS:HB2	2.17	0.44
1:A:613:SER:O	1:A:614:ARG:C	2.55	0.44
4:G:166:ARG:O	4:G:167:GLU:C	2.56	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:263:GLY:C	3:I:283:GLY:HA2	2.38	0.44
4:G:6:PHE:CE1	4:G:7:LEU:CD1	2.99	0.44
2:B:448:ASN:O	2:B:449:SER:CB	2.65	0.44
26:E:6:U:H2'	26:E:7:A:H8	1.83	0.44
4:G:272:PRO:CB	4:G:302:PHE:CD1	2.77	0.44
8:H:185:ILE:CD1	27:F:75:A:OP2	2.55	0.44
8:H:306:PRO:HG2	8:H:349:TRP:CD2	2.52	0.44
8:H:354:TYR:CD1	8:H:376:PHE:HZ	2.36	0.44
3:I:282:GLU:CG	3:I:286:PHE:CD2	3.00	0.44
27:F:175:G:H4'	27:F:176:A:O4'	2.18	0.44
4:G:212:VAL:HG22	4:G:214:SER:H	1.83	0.44
3:I:400:VAL:HG21	4:G:154:PRO:CG	2.46	0.44
6:L:25:ARG:HG3	6:L:25:ARG:HH11	1.82	0.44
4:G:161:LYS:CE	4:G:161:LYS:HA	2.48	0.44
1:A:413:ASN:ND2	1:A:413:ASN:N	2.66	0.44
1:A:1836:ASN:H	1:A:1839:ASN:HB3	1.83	0.44
1:A:1276:GLU:N	1:A:1276:GLU:OE2	2.50	0.44
25:D:84:C:C2'	25:D:84:C:O2	2.66	0.43
2:B:316:GLN:O	2:B:319:GLY:N	2.45	0.43
3:I:267:HIS:CE1	3:I:273:HIS:CE1	3.05	0.43
6:L:95:PHE:CE2	6:L:103:LEU:HD13	2.53	0.43
27:F:175:G:C2	27:F:176:A:N6	2.84	0.43
4:G:702:PRO:HB3	4:G:739:PHE:CD1	2.52	0.43
1:A:1285:VAL:HA	1:A:1300:ALA:O	2.18	0.43
2:B:447:ASN:HD22	2:B:447:ASN:C	2.22	0.43
1:A:1393:GLU:HG2	3:I:395:LYS:O	2.18	0.43
1:A:900:PHE:CZ	1:A:959:LEU:HD12	2.52	0.43
1:A:689:TYR:O	1:A:689:TYR:CD1	2.71	0.43
1:A:379:ILE:O	1:A:379:ILE:HG22	2.17	0.43
8:H:488:ILE:HD11	8:H:560:GLN:CG	2.42	0.43
8:H:347:ARG:HG3	8:H:359:PHE:HZ	1.81	0.43
2:B:316:GLN:CG	2:B:357:TRP:CZ2	2.97	0.43
5:K:341:VAL:CG2	5:K:428:TRP:CD1	3.01	0.43
5:K:144:LEU:HB3	5:K:146:GLU:OE2	2.18	0.43
1:A:1894:ILE:HG21	1:A:1899:TRP:CZ2	2.52	0.43
6:L:74:TYR:CD1	6:L:83:MET:HE1	2.52	0.43
1:A:2067:TYR:N	1:A:2067:TYR:HD1	2.15	0.43
1:A:1276:GLU:H	1:A:1276:GLU:CD	2.21	0.43
1:A:1501:THR:HG21	4:G:163:THR:HG21	1.99	0.43
27:F:44:A:H61	27:F:71:A:H61	1.66	0.43
2:B:357:TRP:O	2:B:401:PHE:CD2	2.72	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:505:TRP:N	1:A:505:TRP:CD1	2.86	0.43
2:B:395:ILE:CG2	2:B:396:VAL:H	2.16	0.43
2:B:409:LYS:HA	2:B:422:TYR:O	2.18	0.43
5:K:333:LYS:O	5:K:333:LYS:HD2	2.17	0.43
1:A:750:LEU:HG	1:A:751:ASP:N	2.34	0.43
3:I:391:MET:SD	3:I:397:GLU:HG3	2.58	0.43
3:I:327:THR:O	3:I:328:VAL:CB	2.67	0.43
3:I:298:VAL:O	3:I:298:VAL:HG12	2.18	0.43
8:H:566:GLY:C	8:H:567:ILE:HD13	2.39	0.43
27:F:47:U:H2'	27:F:48:G:H8	1.83	0.43
27:F:67:U:H2'	27:F:68:A:H8	1.82	0.43
8:H:330:TYR:HE1	8:H:430:ARG:HH21	1.25	0.43
8:H:373:PHE:O	8:H:377:ILE:HB	2.17	0.43
2:B:127:TYR:HE2	2:B:276:SER:CA	2.31	0.43
24:C:-4:A:H4'	24:C:-3:A:OP2	2.18	0.43
1:A:1335:TRP:CD1	1:A:1367:ILE:CD1	3.01	0.43
1:A:1342:LEU:HD23	1:A:1350:ILE:CD1	2.49	0.43
3:I:450:GLN:HG3	3:I:451:GLN:H	1.83	0.43
4:G:231:LYS:HA	4:G:234:ARG:HD3	2.00	0.43
1:A:415:GLU:OE1	1:A:416:GLU:HB2	2.18	0.43
8:H:144:SER:HA	8:H:240:ASP:OD2	2.18	0.43
1:A:1019:GLU:HA	1:A:1023:LEU:HD23	2.00	0.43
8:H:360:ARG:HG2	8:H:362:LYS:H	1.82	0.43
1:A:162:LEU:HD11	1:A:730:ILE:HG22	2.01	0.43
3:I:137:TYR:CE2	3:I:141:ILE:HD11	2.54	0.43
3:I:183:PHE:CD2	3:I:185:ASN:ND2	2.86	0.43
1:A:1739:ARG:HD2	1:A:1751:TYR:CD2	2.53	0.43
8:H:349:TRP:CZ3	8:H:373:PHE:HE2	2.31	0.43
2:B:337:ARG:HD3	5:K:173:TYR:OH	2.18	0.43
2:B:192:THR:HG23	2:B:200:GLN:CG	2.48	0.43
6:L:33:ARG:HD3	6:L:65:ASP:H	1.84	0.43
1:A:1664:ASP:O	1:A:1668:ILE:CG1	2.66	0.43
1:A:1381:THR:OG1	1:A:1382:ARG:HG3	2.19	0.43
27:F:31:G:C6	27:F:32:G:C5	3.06	0.43
26:E:151:G:H4'	26:E:152:A:O4'	2.18	0.43
5:K:146:GLU:C	5:K:148:LYS:H	2.21	0.43
27:F:102:C:N4	27:F:103:A:H62	2.16	0.43
27:F:83:C:H4'	27:F:84:A:OP1	2.18	0.43
8:H:769:TYR:HE1	8:H:774:LEU:HB2	1.84	0.43
25:D:109:U:H3'	25:D:110:U:C5'	2.47	0.43
4:G:127:ASP:OD1	4:G:127:ASP:C	2.57	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:143:ILE:HG23	3:I:149:TYR:CE2	2.52	0.43
2:B:222:GLY:N	2:B:237:CYS:O	2.44	0.43
1:A:1168:ILE:O	1:A:1169:TYR:CD1	2.72	0.43
1:A:1580:GLY:HA3	3:I:389:ASN:ND2	2.33	0.43
3:I:380:ARG:CZ	3:I:380:ARG:CB	2.96	0.43
4:G:666:ILE:N	4:G:668:HIS:CD2	2.86	0.43
4:G:697:LEU:C	4:G:699:PRO:HD3	2.39	0.43
8:H:364:PHE:CG	8:H:369:LYS:CD	2.94	0.43
8:H:571:TYR:CB	8:H:575:ALA:HB2	2.49	0.43
1:A:484:PHE:HB3	1:A:485:PRO:HD3	2.00	0.43
1:A:2076:GLN:OE1	5:K:283:ASN:O	2.37	0.43
8:H:132:ARG:CG	8:H:132:ARG:NH1	2.73	0.43
1:A:839:HIS:CE1	27:F:96:U:C6	3.07	0.43
26:E:150:G:C2	26:E:152:A:H4'	2.54	0.43
2:B:382:ASP:N	2:B:382:ASP:OD1	2.50	0.43
4:G:153:ILE:HG23	4:G:154:PRO:HD2	1.99	0.43
8:H:964:ARG:NH1	8:H:968:MET:CE	2.82	0.43
3:I:93:LYS:CA	3:I:93:LYS:CE	2.95	0.43
29:E:201:M7M:HBX	29:E:201:M7M:HNBN	1.82	0.43
3:I:416:SER:HA	3:I:419:GLN:OE1	2.19	0.43
4:G:529:ILE:O	4:G:533:LEU:N	2.52	0.43
5:K:382:VAL:HG11	5:K:392:TYR:CE2	2.53	0.43
1:A:1855:THR:HA	1:A:1937:ARG:NH2	2.34	0.43
1:A:1222:LEU:HD23	1:A:1222:LEU:HA	1.76	0.43
1:A:287:GLU:HB2	1:A:288:GLU:H	1.64	0.43
8:H:379:ILE:O	8:H:383:LYS:CG	2.65	0.43
27:F:174:G:C2	27:F:176:A:H4'	2.54	0.43
8:H:355:HIS:C	8:H:356:LYS:CG	2.86	0.43
1:A:222:ILE:HB	1:A:266:LEU:HD11	2.01	0.43
2:B:73:ARG:O	2:B:76:LEU:HB2	2.19	0.43
2:B:202:LEU:HD12	2:B:202:LEU:N	2.33	0.43
6:L:25:ARG:HG3	6:L:25:ARG:NH1	2.34	0.43
5:K:337:TYR:HE2	5:K:434:ASP:HA	1.82	0.43
1:A:1668:ILE:HD13	1:A:1801:SER:HB2	2.01	0.43
1:A:960:THR:HG21	3:I:455:PHE:CZ	2.54	0.43
1:A:755:ASP:CG	1:A:819:LYS:HE3	2.39	0.43
1:A:2046:GLU:HA	1:A:2049:ILE:HD12	2.01	0.43
8:H:488:ILE:HD11	8:H:560:GLN:HG3	1.99	0.43
1:A:207:ARG:NH1	1:A:299:LYS:HG3	2.34	0.43
27:F:62:G:H2'	27:F:63:C:C6	2.54	0.43
1:A:1647:GLN:O	1:A:1650:ARG:HG3	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:883:PHE:O	1:A:887:VAL:HG23	2.19	0.43
27:F:98:U:O2'	27:F:99:U:P	2.76	0.43
1:A:1657:ILE:O	1:A:1661:ILE:CG1	2.64	0.43
5:K:142:LEU:HA	5:K:142:LEU:HD13	1.74	0.43
5:K:146:GLU:O	5:K:149:PHE:HD2	2.01	0.43
6:L:33:ARG:HD3	6:L:65:ASP:CB	2.49	0.43
2:B:208:GLN:HA	2:B:209:PRO:HA	1.66	0.43
8:H:858:LEU:HB3	8:H:937:TRP:CB	2.48	0.43
1:A:1992:TYR:HD2	1:A:2004:ALA:HB1	1.83	0.43
1:A:1286:TRP:HA	1:A:1448:GLU:OE2	2.19	0.43
1:A:1451:PHE:O	1:A:1455:GLN:OE1	2.35	0.43
8:H:373:PHE:HE1	8:H:377:ILE:HG21	1.84	0.43
8:H:598:ILE:CG2	8:H:933:TRP:CH2	3.01	0.43
1:A:617:ASN:ND2	27:F:99:U:O2'	2.46	0.43
2:B:458:ASP:OD2	2:B:462:LYS:NZ	2.52	0.43
8:H:114:PRO:O	8:H:115:LYS:HG3	2.18	0.43
1:A:410:ILE:N	1:A:410:ILE:CD1	2.82	0.43
3:I:429:ARG:HH11	3:I:429:ARG:CG	2.32	0.43
3:I:321:LYS:O	3:I:324:ASP:O	2.35	0.43
24:C:6:U:O2'	24:C:6:U:O2	2.28	0.43
1:A:1511:ARG:HH21	1:A:1511:ARG:HG3	1.81	0.43
4:G:127:ASP:OD1	4:G:128:PHE:N	2.52	0.43
26:E:6:U:H2'	26:E:7:A:C8	2.53	0.43
1:A:1087:ASN:ND2	3:I:274:THR:OG1	2.45	0.43
1:A:294:ASN:HB2	1:A:300:LYS:HB2	2.01	0.42
3:I:120:TYR:OH	3:I:141:ILE:HG23	2.19	0.42
1:A:291:LYS:H	1:A:291:LYS:HZ2	1.67	0.42
2:B:446:SER:OG	2:B:451:PHE:CG	2.69	0.42
8:H:862:TYR:CD1	8:H:862:TYR:N	2.87	0.42
5:K:155:LYS:HA	5:K:158:ILE:HG12	1.99	0.42
4:G:702:PRO:HA	4:G:739:PHE:CZ	2.54	0.42
1:A:1468:ALA:C	1:A:1473:ARG:O	2.57	0.42
8:H:884:ARG:O	8:H:884:ARG:HD3	2.19	0.42
1:A:1020:ILE:H	1:A:1020:ILE:HD12	1.84	0.42
8:H:940:VAL:HA	8:H:941:PRO:HD3	1.89	0.42
3:I:417:LEU:HB3	4:G:226:MET:HE3	2.00	0.42
6:L:8:GLN:HG2	6:L:61:LEU:HB2	2.01	0.42
1:A:1386:ALA:O	1:A:1390:THR:HG23	2.19	0.42
27:F:73:U:H2'	27:F:74:U:C6	2.54	0.42
8:H:305:SER:C	8:H:307:ILE:N	2.72	0.42
8:H:160:ARG:HD2	8:H:160:ARG:HA	1.70	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:770:MET:SD	4:G:119:TRP:HZ3	2.41	0.42
8:H:129:ILE:N	8:H:129:ILE:CD1	2.73	0.42
1:A:883:PHE:CD1	3:I:177:MET:SD	3.13	0.42
8:H:189:LEU:CD1	8:H:190:SER:O	2.66	0.42
2:B:353:TYR:HE2	2:B:395:ILE:HG21	1.84	0.42
1:A:940:ILE:O	1:A:943:ALA:HB3	2.18	0.42
25:D:62:A:C2	26:E:58:G:N1	2.87	0.42
2:B:422:TYR:CD1	2:B:429:LYS:HA	2.54	0.42
8:H:801:TRP:CD1	8:H:801:TRP:C	2.92	0.42
2:B:247:GLN:HB2	2:B:258:LEU:HD21	1.99	0.42
1:A:1615:ASN:ND2	1:A:1634:LEU:HD23	2.31	0.42
8:H:828:ASP:O	8:H:829:VAL:C	2.57	0.42
2:B:349:SER:O	2:B:350:LYS:HG3	2.19	0.42
1:A:689:TYR:C	1:A:689:TYR:CD1	2.93	0.42
8:H:408:LEU:HD21	8:H:427:LEU:HD22	2.01	0.42
8:H:236:LEU:HD23	8:H:266:VAL:HG21	2.00	0.42
4:G:245:ILE:HG23	4:G:280:GLU:HG2	2.01	0.42
1:A:268:LEU:HD12	1:A:268:LEU:O	2.19	0.42
8:H:470:ALA:N	8:H:577:LEU:O	2.48	0.42
4:G:264:ILE:HG22	4:G:281:ASN:OD1	2.19	0.42
1:A:1739:ARG:O	1:A:1778:ASP:HA	2.18	0.42
2:B:321:LEU:CD2	2:B:335:ASP:HA	2.49	0.42
8:H:933:TRP:HB2	8:H:934:HIS:CE1	2.55	0.42
8:H:483:TRP:CH2	8:H:565:LYS:CG	3.01	0.42
3:I:400:VAL:O	3:I:400:VAL:HG23	2.19	0.42
5:K:333:LYS:CE	5:K:333:LYS:O	2.67	0.42
1:A:901:PRO:HG3	1:A:998:TYR:CD2	2.54	0.42
1:A:396:ARG:O	1:A:398:VAL:HG23	2.19	0.42
4:G:364:PHE:O	4:G:368:SER:N	2.38	0.42
3:I:376:LYS:HE2	26:E:56:U:OP2	2.20	0.42
5:K:323:ARG:O	5:K:326:ALA:HB3	2.19	0.42
8:H:124:LEU:HD12	8:H:124:LEU:O	2.18	0.42
2:B:123:PHE:CD1	2:B:123:PHE:C	2.93	0.42
8:H:167:ASN:HD22	8:H:168:VAL:N	2.16	0.42
3:I:135:LEU:HD21	3:I:136:GLN:HG3	2.01	0.42
1:A:703:PHE:C	1:A:703:PHE:CD1	2.93	0.42
2:B:315:PHE:CE1	2:B:322:VAL:HB	2.54	0.42
3:I:385:ARG:CZ	4:G:153:ILE:HD11	2.50	0.42
1:A:1846:ASN:CA	1:A:1885:LYS:NZ	2.79	0.42
4:G:134:ARG:CB	4:G:134:ARG:CZ	2.96	0.42
4:G:275:SER:O	4:G:279:LEU:HG	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1206:CYS:HB2	1:A:1266:GLU:OE1	2.19	0.42
3:I:168:THR:O	3:I:172:ILE:HD12	2.19	0.42
2:B:119:PHE:C	2:B:119:PHE:CD1	2.93	0.42
5:K:443:LYS:HG2	5:K:444:VAL:H	1.84	0.42
4:G:846:PHE:CD1	4:G:859:LEU:CD2	2.88	0.42
8:H:510:ARG:HD3	8:H:591:PHE:CZ	2.54	0.42
1:A:1697:SER:CB	1:A:1759:TYR:CE1	3.02	0.42
2:B:125:ILE:HA	2:B:128:SER:OG	2.20	0.42
27:F:95:C:C1'	27:F:96:U:OP1	2.67	0.42
5:K:164:HIS:CG	5:K:164:HIS:O	2.71	0.42
8:H:652:MET:HA	8:H:655:LEU:HD12	2.01	0.42
1:A:1877:GLY:C	1:A:1894:ILE:HB	2.40	0.42
1:A:1559:HIS:ND1	1:A:1613:THR:HG21	2.34	0.42
8:H:234:LEU:HD23	8:H:234:LEU:N	2.34	0.42
8:H:957:ALA:HB2	8:H:965:ASP:OD2	2.19	0.42
2:B:112:PRO:O	2:B:113:ALA:HB3	2.19	0.42
5:K:309:LEU:HA	5:K:309:LEU:HD23	1.79	0.42
1:A:294:ASN:C	1:A:294:ASN:ND2	2.73	0.42
2:B:124:LEU:HD22	2:B:274:HIS:HE1	1.84	0.42
2:B:320:SER:O	2:B:321:LEU:HD23	2.20	0.42
1:A:779:ALA:CA	1:A:782:ILE:HD12	2.23	0.42
3:I:95:LEU:O	3:I:98:PHE:HB2	2.20	0.42
8:H:968:MET:CE	8:H:971:ARG:HG3	2.49	0.42
1:A:410:ILE:CG1	8:H:276:ASP:OD1	2.65	0.42
3:I:227:PRO:HG3	3:I:325:ARG:HG2	2.02	0.42
1:A:1834:PHE:CE1	1:A:1958:PRO:HG2	2.53	0.42
8:H:500:ARG:HD3	8:H:534:THR:OG1	2.19	0.42
1:A:173:LEU:CD1	1:A:712:LEU:HD12	2.50	0.42
4:G:251:GLU:CD	4:G:260:ALA:HB2	2.37	0.42
8:H:964:ARG:HA	8:H:964:ARG:HD2	1.77	0.42
1:A:1344:THR:HG22	1:A:1347:ARG:HH21	1.83	0.42
1:A:1335:TRP:HZ3	1:A:1400:ILE:O	2.03	0.42
6:L:33:ARG:HD3	6:L:65:ASP:OD1	2.17	0.42
1:A:939:LEU:HD23	1:A:939:LEU:HA	1.85	0.42
24:C:-1:A:O2'	24:C:0:U:C6	2.73	0.42
1:A:1586:GLN:HB3	1:A:1595:ARG:HH12	1.84	0.42
5:K:143:GLU:HA	5:K:145:HIS:HE1	1.84	0.42
26:E:26:A:O2'	26:E:27:U:P	2.78	0.42
2:B:275:PRO:O	2:B:276:SER:C	2.57	0.42
1:A:1850:LEU:HD23	1:A:1883:ASN:HB3	2.00	0.42
3:I:102:ILE:HB	3:I:103:PRO:CD	2.48	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:193:TYR:CZ	1:A:558:GLN:HB3	2.55	0.42
1:A:908:ASP:HB3	1:A:951:LEU:CD1	2.49	0.42
1:A:1274:ARG:O	1:A:1277:GLU:OE1	2.37	0.42
2:B:159:LEU:HD23	2:B:159:LEU:N	2.34	0.42
1:A:1629:LEU:CD2	1:A:1629:LEU:N	2.82	0.42
8:H:271:ASP:OD2	8:H:318:LEU:HG	2.20	0.42
3:I:93:LYS:HD2	3:I:93:LYS:N	2.34	0.42
4:G:15:TYR:CD1	4:G:15:TYR:O	2.72	0.42
4:G:678:TYR:HD1	4:G:678:TYR:HA	1.74	0.42
1:A:2066:LYS:HB2	1:A:2067:TYR:CD1	2.54	0.42
1:A:370:ILE:HD12	8:H:953:LYS:HD2	2.00	0.42
1:A:974:ASN:C	1:A:976:GLN:H	2.23	0.42
4:G:508:TRP:O	4:G:512:ASP:N	2.52	0.42
2:B:418:LEU:CD2	2:B:434:ALA:HB2	2.50	0.42
4:G:671:PHE:CZ	4:G:693:SER:OG	2.64	0.42
8:H:572:ILE:C	8:H:572:ILE:HD12	2.40	0.42
4:G:282:ILE:HG12	4:G:295:LEU:HB3	2.01	0.42
1:A:1652:HIS:N	1:A:1652:HIS:CD2	2.87	0.42
5:K:350:PRO:CB	5:K:353:ARG:HD2	2.48	0.42
3:I:123:ARG:HB2	3:I:189:LEU:HD11	2.02	0.42
2:B:345:LEU:HB3	2:B:376:TRP:CH2	2.54	0.42
1:A:2075:THR:CG2	1:A:2076:GLN:N	2.82	0.42
1:A:2079:ILE:HG22	1:A:2083:ILE:CD1	2.44	0.42
8:H:483:TRP:CZ3	8:H:565:LYS:HG3	2.54	0.42
8:H:449:PHE:HD1	8:H:449:PHE:O	2.02	0.42
1:A:1629:LEU:HD23	1:A:1630:THR:HG22	1.98	0.42
5:K:280:VAL:HG12	5:K:282:GLU:H	1.85	0.42
3:I:424:THR:CG2	3:I:425:SER:N	2.83	0.42
4:G:349:ALA:O	4:G:353:GLN:N	2.48	0.42
1:A:1715:SER:HB2	1:A:1719:GLU:OE1	2.19	0.42
1:A:2388:ARG:O	1:A:2389:PRO:C	2.57	0.42
4:G:281:ASN:C	4:G:281:ASN:HD22	2.23	0.42
1:A:1851:PHE:HB2	1:A:1882:LEU:HD13	2.01	0.42
4:G:252:GLU:HG3	4:G:284:LEU:CD1	2.50	0.42
1:A:465:GLU:HG3	8:H:387:TYR:OH	2.20	0.42
8:H:475:THR:HG22	8:H:483:TRP:O	2.20	0.42
8:H:968:MET:N	8:H:968:MET:CE	2.82	0.42
1:A:1453:ASP:O	1:A:1456:ARG:CG	2.58	0.42
1:A:276:VAL:CG1	1:A:310:ASN:HB2	2.49	0.42
8:H:798:GLY:O	8:H:802:ALA:N	2.53	0.42
6:L:78:ASP:OD2	6:L:79:PRO:HD2	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:19:ILE:HD12	4:G:20:GLY:HA2	2.02	0.42
1:A:843:THR:HG21	6:L:108:ASP:CB	2.49	0.42
1:A:2026:LEU:HD11	1:A:2040:TRP:HZ3	1.85	0.42
1:A:999:LEU:HD23	1:A:999:LEU:HA	1.78	0.42
27:F:48:G:H2'	27:F:49:U:C6	2.55	0.41
2:B:445:ILE:HG12	2:B:446:SER:N	2.35	0.41
2:B:280:ILE:N	2:B:292:TRP:O	2.45	0.41
7:M:95:ARG:CG	7:M:95:ARG:NH1	2.73	0.41
5:K:146:GLU:CA	5:K:149:PHE:CD2	2.91	0.41
1:A:358:ARG:HD3	1:A:360:GLU:HB2	2.00	0.41
2:B:171:GLN:CD	2:B:172:LEU:H	2.23	0.41
3:I:429:ARG:CA	3:I:429:ARG:HH11	2.33	0.41
4:G:83:LYS:C	4:G:85:ARG:N	2.73	0.41
1:A:1390:THR:HA	1:A:1391:PRO:HD3	1.75	0.41
9:N:1610:LEU:O	9:N:1660:ALA:O	2.38	0.41
27:F:77:A:C4'	27:F:78:A:C5'	2.93	0.41
8:H:372:THR:O	8:H:373:PHE:C	2.58	0.41
2:B:335:ASP:OD1	2:B:337:ARG:CD	2.58	0.41
1:A:474:LYS:CD	1:A:474:LYS:C	2.89	0.41
8:H:933:TRP:C	8:H:934:HIS:CG	2.92	0.41
1:A:703:PHE:HD1	1:A:703:PHE:C	2.23	0.41
1:A:774:ILE:CG2	1:A:777:LYS:NZ	2.83	0.41
8:H:191:ILE:O	8:H:224:GLU:OE1	2.38	0.41
6:L:39:CYS:SG	6:L:79:PRO:O	2.78	0.41
3:I:390:ARG:O	3:I:412:MET:HG2	2.20	0.41
5:K:300:GLN:OE1	5:K:300:GLN:CA	2.68	0.41
2:B:218:VAL:HG23	2:B:240:ASP:CG	2.40	0.41
6:L:74:TYR:CG	6:L:83:MET:HE1	2.55	0.41
6:L:59:ILE:HG22	6:L:60:TYR:N	2.33	0.41
4:G:397:GLN:O	4:G:401:ILE:N	2.38	0.41
1:A:958:LEU:HD22	1:A:1081:TYR:CD2	2.56	0.41
8:H:656:LEU:HD13	8:H:670:ILE:HD13	2.02	0.41
8:H:159:LYS:H	8:H:159:LYS:HG2	1.53	0.41
8:H:571:TYR:H	8:H:571:TYR:HD1	1.69	0.41
1:A:286:LEU:HD22	1:A:292:LYS:CB	2.47	0.41
27:F:32:G:O2'	27:F:33:U:P	2.79	0.41
27:F:45:A:N3	27:F:46:C:C5	2.87	0.41
8:H:507:SER:C	8:H:509:SER:N	2.71	0.41
2:B:316:GLN:OE1	2:B:321:LEU:HB2	2.20	0.41
4:G:115:THR:O	4:G:119:TRP:HD1	2.03	0.41
1:A:217:TRP:NE1	1:A:703:PHE:CE1	2.89	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:289:TRP:HB2	2:B:313:LEU:HD23	2.01	0.41
8:H:879:LEU:O	8:H:883:ARG:HG2	2.20	0.41
1:A:276:VAL:HG11	1:A:310:ASN:HB2	2.01	0.41
8:H:108:GLN:OE1	8:H:109:LEU:HD23	2.19	0.41
3:I:92:ILE:HB	3:I:93:LYS:HD2	2.01	0.41
3:I:441:MET:SD	3:I:444:ARG:NH2	2.93	0.41
1:A:329:TYR:CD2	1:A:330:LEU:HG	2.55	0.41
1:A:1512:ARG:HD2	1:A:1529:ASN:OD1	2.20	0.41
1:A:1714:PRO:HB2	1:A:1787:TYR:CE2	2.55	0.41
1:A:594:ASP:OD1	1:A:594:ASP:C	2.59	0.41
1:A:1626:GLN:HE22	1:A:1694:MET:HG2	1.84	0.41
5:K:354:PHE:CZ	5:K:358:MET:SD	3.14	0.41
1:A:1697:SER:OG	1:A:1759:TYR:CE1	2.64	0.41
8:H:608:GLN:NE2	8:H:641:GLU:CG	2.61	0.41
8:H:177:TYR:O	8:H:178:LEU:CB	2.69	0.41
1:A:1216:ILE:HG21	1:A:1254:ASN:ND2	2.36	0.41
7:M:126:ILE:O	7:M:126:ILE:HG22	2.21	0.41
3:I:329:LEU:HD12	3:I:333:TRP:CH2	2.55	0.41
5:K:362:GLU:HG2	29:E:201:M7M:NBN	2.35	0.41
1:A:1115:GLN:CA	1:A:1115:GLN:HE21	2.33	0.41
1:A:672:LYS:C	1:A:674:MET:N	2.72	0.41
1:A:2020:GLU:HA	1:A:2023:LYS:HB2	2.01	0.41
1:A:1738:LEU:HD23	1:A:1777:ILE:HB	2.01	0.41
8:H:482:GLU:O	8:H:482:GLU:HG2	2.20	0.41
8:H:467:THR:HG23	8:H:579:SER:O	2.21	0.41
3:I:141:ILE:HG21	3:I:197:ILE:HG23	2.03	0.41
1:A:484:PHE:N	1:A:485:PRO:CD	2.83	0.41
27:F:63:C:H2'	27:F:64:C:C6	2.55	0.41
8:H:578:TYR:HD1	8:H:578:TYR:C	2.24	0.41
1:A:1417:GLN:OE1	1:A:1422:ILE:CD1	2.65	0.41
2:B:316:GLN:HE21	2:B:318:ASP:H	1.67	0.41
8:H:327:PHE:HE1	8:H:331:TYR:CD2	2.39	0.41
5:K:159:TYR:CE2	5:K:163:ASN:ND2	2.89	0.41
2:B:174:SER:OG	2:B:175:THR:N	2.54	0.41
8:H:950:PHE:CD1	8:H:951:ILE:N	2.88	0.41
8:H:193:LEU:CB	8:H:214:ASP:O	2.67	0.41
2:B:362:TYR:CB	2:B:379:ARG:HD2	2.48	0.41
1:A:1678:ILE:HD13	1:A:1703:MET:CE	2.50	0.41
1:A:1204:ARG:HG3	1:A:1259:LEU:HD13	2.00	0.41
5:K:386:GLU:HG2	5:K:390:LYS:HE2	2.01	0.41
8:H:325:LYS:HA	8:H:325:LYS:HD2	1.92	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:458:PHE:CD1	1:A:458:PHE:O	2.74	0.41
8:H:362:LYS:CG	8:H:363:PRO:HD2	2.50	0.41
1:A:294:ASN:ND2	27:F:32:G:OP1	2.53	0.41
27:F:49:U:H2'	27:F:50:G:H8	1.84	0.41
4:G:255:ARG:O	4:G:256:LYS:CB	2.68	0.41
8:H:475:THR:CG2	8:H:483:TRP:O	2.68	0.41
5:K:159:TYR:CZ	5:K:163:ASN:ND2	2.88	0.41
1:A:1335:TRP:CH2	1:A:1339:LEU:HD13	2.56	0.41
1:A:1405:ILE:HB	1:A:1437:ILE:HD12	2.03	0.41
2:B:456:GLY:C	2:B:458:ASP:N	2.71	0.41
1:A:1312:PHE:CD1	1:A:1342:LEU:HD12	2.55	0.41
1:A:1461:TYR:O	1:A:1461:TYR:CD1	2.74	0.41
8:H:461:LYS:HZ2	8:H:464:PRO:CB	2.34	0.41
1:A:1578:ALA:CB	1:A:1602:PRO:HB3	2.48	0.41
2:B:405:ASP:OD2	2:B:408:LYS:HD2	2.21	0.41
25:D:87:U:O5'	25:D:87:U:H6	2.04	0.41
1:A:1582:GLU:OE2	1:A:1586:GLN:NE2	2.53	0.41
1:A:1594:GLN:CA	1:A:1594:GLN:NE2	2.83	0.41
1:A:1175:GLU:O	1:A:1179:GLY:N	2.49	0.41
7:M:58:CYS:SG	7:M:98:ILE:HG21	2.60	0.41
7:M:5:ASN:HD21	7:M:61:ILE:HG21	1.85	0.41
1:A:1054:LEU:HA	1:A:1054:LEU:HD23	1.86	0.41
8:H:365:GLU:O	8:H:366:ASN:HB2	2.20	0.41
1:A:166:LYS:C	1:A:169:PRO:HD2	2.39	0.41
25:D:49:A:N6	25:D:50:G:C6	2.88	0.41
8:H:352:VAL:HG13	8:H:352:VAL:O	2.21	0.41
1:A:473:THR:HG23	1:A:474:LYS:N	2.35	0.41
1:A:778:LYS:CA	1:A:778:LYS:HE2	2.50	0.41
8:H:792:LYS:O	8:H:796:ILE:N	2.43	0.41
5:K:159:TYR:CD1	5:K:163:ASN:ND2	2.76	0.41
5:K:158:ILE:HG13	5:K:159:TYR:N	2.34	0.41
2:B:177:PRO:N	2:B:195:TRP:HD1	2.18	0.41
1:A:1308:GLU:OE1	1:A:1346:PHE:CZ	2.70	0.41
1:A:1088:VAL:HG12	1:A:1089:VAL:N	2.36	0.41
1:A:1051:GLU:O	1:A:1246:ALA:HA	2.21	0.41
2:B:408:LYS:O	2:B:424:SER:CB	2.68	0.41
4:G:677:ILE:O	4:G:681:MET:HG2	2.20	0.41
4:G:669:LYS:O	4:G:673:GLN:HG3	2.21	0.41
27:F:46:C:H2'	27:F:47:U:C6	2.55	0.41
24:C:9:G:O5'	24:C:9:G:H8	2.04	0.41
25:D:48:C:O2	25:D:48:C:H2'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1144:PHE:HZ	1:A:1162:THR:HG21	1.85	0.41
8:H:132:ARG:O	8:H:133:ILE:CG1	2.66	0.41
3:I:358:ILE:CG2	3:I:359:PRO:N	2.84	0.41
6:L:95:PHE:HD1	6:L:133:SER:CB	2.33	0.41
2:B:196:ALA:C	2:B:219:GLY:O	2.58	0.41
1:A:691:PHE:O	1:A:691:PHE:CD1	2.73	0.41
1:A:258:ILE:HG21	1:A:640:ARG:HG3	2.03	0.41
8:H:178:LEU:CD2	8:H:178:LEU:N	2.83	0.41
1:A:1195:PHE:HB3	1:A:1217:ARG:HH11	1.82	0.41
1:A:750:LEU:HD23	1:A:752:ALA:HB3	2.03	0.41
4:G:851:ARG:C	4:G:852:LEU:CD1	2.89	0.41
4:G:19:ILE:CD1	4:G:20:GLY:N	2.81	0.41
5:K:303:LEU:CD2	5:K:303:LEU:C	2.84	0.41
3:I:321:LYS:HG3	3:I:324:ASP:O	2.21	0.41
8:H:386:SER:O	8:H:390:SER:CB	2.69	0.41
4:G:804:ASP:OD1	4:G:805:HIS:N	2.53	0.41
5:K:330:ASN:HD22	5:K:331:VAL:HG23	1.85	0.41
1:A:1795:LYS:N	1:A:1796:PRO:HD2	2.36	0.41
1:A:1011:ASN:ND2	1:A:1143:GLU:O	2.54	0.41
3:I:259:ILE:HG21	3:I:259:ILE:HD13	1.76	0.41
8:H:808:LEU:HD11	8:H:855:PRO:HB2	2.01	0.41
25:D:49:A:C2'	25:D:50:G:O5'	2.69	0.41
8:H:586:MET:SD	8:H:586:MET:O	2.79	0.41
8:H:578:TYR:CE2	8:H:589:LEU:CD1	3.04	0.41
2:B:275:PRO:HG3	2:B:319:GLY:HA2	2.02	0.41
1:A:767:LEU:HD21	1:A:779:ALA:HB1	2.00	0.41
4:G:284:LEU:HD22	4:G:284:LEU:N	2.36	0.41
27:F:96:U:O4'	27:F:96:U:P	2.79	0.41
8:H:908:VAL:HG13	8:H:909:ILE:N	2.34	0.41
8:H:449:PHE:CD1	8:H:453:THR:HG23	2.56	0.41
2:B:267:ARG:HG3	2:B:285:HIS:HD2	1.82	0.41
8:H:950:PHE:CG	8:H:951:ILE:N	2.89	0.41
6:L:33:ARG:CD	6:L:65:ASP:OD2	2.54	0.41
2:B:419:ILE:HD13	2:B:419:ILE:HG21	1.89	0.41
3:I:271:GLU:O	3:I:272:LEU:HB3	2.19	0.41
26:E:2:U:C5	26:E:3:C:H5	2.32	0.41
1:A:1461:TYR:CD1	1:A:1461:TYR:C	2.94	0.41
1:A:1464:LYS:HZ2	1:A:1479:GLU:HB3	1.86	0.41
2:B:68:ASP:OD1	2:B:69:VAL:N	2.53	0.41
1:A:2032:ILE:HD13	1:A:2043:PHE:CE1	2.56	0.41
1:A:1067:ASN:HA	1:A:1067:ASN:HD22	1.62	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1594:GLN:HE21	1:A:1594:GLN:CA	2.33	0.41
1:A:1183:THR:CG2	1:A:1184:ASP:N	2.83	0.41
1:A:1174:PHE:HD2	1:A:1222:LEU:HD11	1.85	0.41
1:A:331:PHE:CD2	1:A:509:HIS:CE1	3.09	0.41
8:H:615:LEU:HB3	8:H:616:PRO:HD3	2.02	0.41
8:H:906:VAL:HA	8:H:907:PRO:HD3	1.97	0.41
2:B:383:GLU:HA	2:B:383:GLU:OE1	2.21	0.41
1:A:882:ILE:HD13	1:A:1238:LEU:HD21	2.03	0.41
3:I:40:LYS:O	3:I:44:PHE:N	2.44	0.41
7:M:36:GLY:CA	26:E:30:G:O2'	2.69	0.41
8:H:486:VAL:HG22	8:H:487:ARG:N	2.36	0.41
8:H:576:THR:CG2	8:H:592:PHE:H	2.14	0.41
1:A:294:ASN:OD1	1:A:300:LYS:HE3	2.18	0.41
8:H:117:ARG:NE	8:H:156:ASP:O	2.54	0.41
8:H:116:THR:CG2	8:H:158:HIS:HD2	2.16	0.41
5:K:427:THR:OG1	5:K:428:TRP:N	2.54	0.41
2:B:235:ILE:CD1	2:B:280:ILE:HG21	2.51	0.41
5:K:158:ILE:HG13	5:K:159:TYR:H	1.86	0.41
1:A:160:ALA:HB1	1:A:194:HIS:HE1	1.79	0.41
1:A:795:ALA:HA	1:A:1095:MET:HE2	1.94	0.41
25:D:87:U:H6	25:D:87:U:H3'	1.86	0.41
1:A:863:ARG:NH2	1:A:1059:GLU:HB3	2.36	0.41
2:B:418:LEU:HD23	2:B:434:ALA:HB2	2.02	0.41
8:H:305:SER:O	8:H:307:ILE:N	2.55	0.40
8:H:164:MET:HG2	8:H:175:LEU:CD1	2.50	0.40
1:A:1481:GLU:OE2	4:G:256:LYS:HD3	2.20	0.40
8:H:123:MET:SD	8:H:209:MET:SD	3.19	0.40
8:H:122:TYR:HD1	8:H:122:TYR:O	2.05	0.40
1:A:543:ASN:ND2	1:A:544:LYS:HB2	2.36	0.40
1:A:1623:PHE:CZ	24:C:5:G:C4	3.09	0.40
6:L:9:LEU:HD11	6:L:60:TYR:CB	2.51	0.40
1:A:867:ILE:HG22	1:A:867:ILE:O	2.21	0.40
6:L:97:THR:HG23	6:L:99:ASN:H	1.86	0.40
4:G:302:PHE:O	4:G:303:ASN:OD1	2.39	0.40
8:H:589:LEU:HG	8:H:589:LEU:O	2.20	0.40
8:H:187:ARG:HD3	8:H:650:LEU:HD11	2.02	0.40
2:B:162:MET:HG3	2:B:421:VAL:HG11	2.03	0.40
1:A:175:LEU:HD12	1:A:564:TRP:HE1	1.86	0.40
8:H:178:LEU:HD13	8:H:194:ASN:O	2.20	0.40
26:E:1:A:C6	29:E:201:M7M:HBZB	2.56	0.40
1:A:1049:LEU:HD11	1:A:1258:LEU:HD21	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1029:THR:HG22	1:A:1260:PHE:HZ	1.85	0.40
8:H:737:ILE:HG12	8:H:768:PHE:HB3	2.03	0.40
2:B:366:THR:O	2:B:373:ILE:HA	2.22	0.40
1:A:574:GLN:HA	1:A:574:GLN:OE1	2.21	0.40
1:A:1203:ASN:N	1:A:1203:ASN:OD1	2.54	0.40
8:H:500:ARG:CD	8:H:534:THR:CB	2.88	0.40
4:G:278:TRP:CE2	4:G:298:THR:HB	2.52	0.40
1:A:141:LYS:CA	1:A:144:ASN:CG	2.89	0.40
8:H:796:ILE:HD12	8:H:796:ILE:HA	1.87	0.40
1:A:1653:LEU:CD2	1:A:1815:LEU:HD23	2.48	0.40
8:H:951:ILE:CB	8:H:952:PRO:HD2	2.30	0.40
3:I:161:LEU:HB3	3:I:167:LEU:HD12	2.03	0.40
25:D:62:A:C2'	25:D:63:G:C5'	2.98	0.40
27:F:103:A:C4	27:F:104:G:C8	3.10	0.40
6:L:25:ARG:HB2	6:L:25:ARG:NH1	2.27	0.40
6:L:34:LYS:HD2	6:L:34:LYS:N	2.35	0.40
3:I:222:ILE:HA	3:I:222:ILE:HD13	1.89	0.40
1:A:1182:LEU:HD23	1:A:1182:LEU:HA	1.91	0.40
8:H:135:ASN:ND2	8:H:487:ARG:HH21	2.18	0.40
1:A:287:GLU:HG3	1:A:287:GLU:H	1.47	0.40
1:A:297:SER:HB2	27:F:32:G:P	2.59	0.40
27:F:43:G:N3	27:F:44:A:N7	2.69	0.40
27:F:77:A:C1'	27:F:78:A:H5'	2.45	0.40
3:I:248:VAL:HG11	3:I:317:ASP:HB3	2.03	0.40
8:H:247:PHE:HD1	8:H:903:ARG:NH1	2.18	0.40
8:H:586:MET:SD	8:H:586:MET:C	3.00	0.40
1:A:766:ILE:HG21	1:A:782:ILE:HG21	2.03	0.40
2:B:173:VAL:HA	2:B:200:GLN:OE1	2.20	0.40
8:H:189:LEU:HD12	8:H:190:SER:O	2.22	0.40
1:A:510:PRO:O	1:A:514:TYR:CE1	2.74	0.40
2:B:311:PHE:HE2	7:M:126:ILE:HD13	1.84	0.40
1:A:1887:GLY:O	1:A:1990:ASN:HA	2.21	0.40
3:I:415:THR:O	3:I:418:GLN:N	2.52	0.40
5:K:339:CYS:SG	5:K:340:LYS:N	2.94	0.40
1:A:1790:TRP:CD1	1:A:1795:LYS:HE3	2.56	0.40
1:A:298:TYR:CE1	1:A:493:MET:CE	3.00	0.40
1:A:168:LEU:N	1:A:169:PRO:HD2	2.36	0.40
25:D:49:A:C3'	25:D:50:G:C5'	2.99	0.40
8:H:375:GLU:HG2	8:H:376:PHE:CE1	2.57	0.40
1:A:770:MET:CE	1:A:778:LYS:HB3	2.51	0.40
4:G:256:LYS:O	4:G:257:PHE:HB3	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:F:94:C:C6	27:F:94:C:H5"	2.50	0.40
8:H:942:GLY:CA	8:H:960:ASN:O	2.70	0.40
1:A:305:LEU:N	1:A:306:PRO:HD2	2.36	0.40
3:I:402:ASP:O	3:I:403:SER:C	2.60	0.40
5:K:244:LEU:HD23	5:K:244:LEU:HA	1.69	0.40
1:A:143:ILE:HA	1:A:146:HIS:HB3	2.03	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all 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	2166/2413 (90%)	2019 (93%)	110 (5%)	37 (2%)	11	56
2	B	425/465 (91%)	380 (89%)	36 (8%)	9 (2%)	9	53
3	I	410/494 (83%)	380 (93%)	24 (6%)	6 (2%)	13	59
4	G	684/899 (76%)	604 (88%)	64 (9%)	16 (2%)	8	51
5	K	273/469 (58%)	247 (90%)	21 (8%)	5 (2%)	11	55
6	L	137/143 (96%)	129 (94%)	6 (4%)	2 (2%)	13	59
7	M	124/126 (98%)	118 (95%)	4 (3%)	2 (2%)	12	58
8	H	837/1008 (83%)	770 (92%)	47 (6%)	20 (2%)	7	50
9	N	1674/2163 (77%)	1555 (93%)	109 (6%)	10 (1%)	30	74
10	J	77/101 (76%)	69 (90%)	6 (8%)	2 (3%)	7	48
10	R	77/101 (76%)	69 (90%)	6 (8%)	2 (3%)	7	48
11	O	69/196 (35%)	63 (91%)	6 (9%)	0	100	100
11	S	69/196 (35%)	63 (91%)	6 (9%)	0	100	100
12	P	71/146 (49%)	66 (93%)	4 (6%)	1 (1%)	14	59
12	T	71/146 (49%)	66 (93%)	4 (6%)	1 (1%)	14	59

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
13	Q	85/110 (77%)	82 (96%)	3 (4%)	0	100	100
13	U	86/110 (78%)	83 (96%)	3 (4%)	0	100	100
14	V	66/94 (70%)	62 (94%)	4 (6%)	0	100	100
14	Y	66/94 (70%)	62 (94%)	4 (6%)	0	100	100
15	W	66/86 (77%)	59 (89%)	4 (6%)	3 (4%)	3	34
15	Z	66/86 (77%)	60 (91%)	3 (4%)	3 (4%)	3	34
16	X	64/77 (83%)	58 (91%)	6 (9%)	0	100	100
16	a	65/77 (84%)	59 (91%)	6 (9%)	0	100	100
17	b	63/109 (58%)	61 (97%)	2 (3%)	0	100	100
18	c	90/95 (95%)	83 (92%)	7 (8%)	0	100	100
19	d	75/89 (84%)	71 (95%)	4 (5%)	0	100	100
20	e	72/86 (84%)	70 (97%)	2 (3%)	0	100	100
21	f	73/93 (78%)	69 (94%)	3 (4%)	1 (1%)	14	59
22	g	62/115 (54%)	62 (100%)	0	0	100	100
23	h	73/187 (39%)	72 (99%)	1 (1%)	0	100	100
All	All	8236/10574 (78%)	7611 (92%)	505 (6%)	120 (2%)	18	59

All (120) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	150	ALA
1	A	157	ASP
1	A	239	PHE
1	A	240	PRO
1	A	259	GLU
1	A	264	ILE
1	A	287	GLU
1	A	546	LYS
1	A	645	ASP
1	A	699	PRO
1	A	1044	GLY
1	A	1403	SER
2	B	113	ALA
2	B	171	GLN
2	B	276	SER
2	B	395	ILE
3	I	266	LYS

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Mol	Chain	Res	Type
3	I	328	VAL
3	I	434	GLN
4	G	10	GLU
4	G	287	SER
4	G	700	ASN
5	K	147	ASP
8	H	115	LYS
8	H	133	ILE
8	H	356	LYS
8	H	364	PHE
8	H	431	GLN
8	H	704	PRO
8	H	829	VAL
8	H	884	ARG
8	H	952	PRO
9	N	766	ILE
9	N	1200	PRO
1	A	156	THR
1	A	554	THR
1	A	803	GLY
1	A	1088	VAL
2	B	449	SER
3	I	152	ASN
4	G	112	ALA
5	K	220	PRO
5	K	332	GLU
8	H	146	LYS
8	H	350	GLY
8	H	366	ASN
8	H	367	VAL
8	H	508	GLU
9	N	1693	HIS
10	R	40	MET
12	T	12	ASN
15	W	24	ASN
15	W	49	PHE
10	J	40	MET
12	P	12	ASN
15	Z	24	ASN
15	Z	49	PHE
1	A	261	LEU
1	A	539	PRO

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Mol	Chain	Res	Type
1	A	750	LEU
1	A	875	THR
1	A	1015	PRO
2	B	384	GLY
4	G	11	PRO
4	G	105	ALA
4	G	734	PRO
6	L	75	GLU
8	H	488	ILE
9	N	492	PRO
9	N	1936	ARG
1	A	407	VAL
1	A	511	ASP
1	A	538	LEU
1	A	701	CYS
1	A	1087	ASN
1	A	1621	VAL
1	A	2019	GLU
2	B	204	SER
2	B	210	LEU
2	B	347	GLY
4	G	256	LYS
4	G	769	SER
4	G	819	ALA
5	K	283	ASN
8	H	119	ASN
9	N	1555	GLU
9	N	1968	ASN
1	A	300	LYS
1	A	377	VAL
1	A	841	GLU
1	A	1379	MET
1	A	1380	PRO
4	G	782	LYS
8	H	171	GLY
8	H	305	SER
15	W	50	ASN
15	Z	50	ASN
1	A	802	PRO
4	G	239	THR
4	G	257	PHE
4	G	887	THR

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Mol	Chain	Res	Type
6	L	78	ASP
7	M	60	PRO
8	H	134	ILE
9	N	622	LEU
9	N	1202	MET
10	R	51	GLU
10	J	51	GLU
1	A	406	PRO
4	G	698	VAL
7	M	10	PRO
9	N	791	PRO
4	G	414	PRO
1	A	644	VAL
5	K	222	PRO
21	f	41	VAL
1	A	181	HIS
3	I	132	PRO
3	I	347	ALA
8	H	319	GLY

### 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	1749/2182 (80%)	1543 (88%)	206 (12%)	6	35
2	B	374/410 (91%)	321 (86%)	53 (14%)	4	29
3	I	327/445 (74%)	264 (81%)	63 (19%)	2	13
4	G	361/813 (44%)	295 (82%)	66 (18%)	2	15
5	K	253/436 (58%)	228 (90%)	25 (10%)	10	44
6	L	129/132 (98%)	113 (88%)	16 (12%)	6	33
7	M	104/104 (100%)	98 (94%)	6 (6%)	25	66
8	H	757/910 (83%)	639 (84%)	118 (16%)	3	24
All	All	4054/5432 (75%)	3501 (86%)	553 (14%)	9	30

All (553) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	131	LYS
1	A	147	SER
1	A	148	ASP
1	A	152	LYS
1	A	153	MET
1	A	154	TYR
1	A	156	THR
1	A	158	LYS
1	A	162	LEU
1	A	165	LEU
1	A	166	LYS
1	A	168	LEU
1	A	175	LEU
1	A	177	GLU
1	A	187	LYS
1	A	224	MET
1	A	229	ARG
1	A	249	LEU
1	A	252	GLU
1	A	254	HIS
1	A	256	GLU
1	A	257	ASN
1	A	261	LEU
1	A	266	LEU
1	A	268	LEU
1	A	273	ASP
1	A	275	TYR
1	A	279	TRP
1	A	283	SER
1	A	287	GLU
1	A	288	GLU
1	A	291	LYS
1	A	294	ASN
1	A	298	TYR
1	A	299	LYS
1	A	313	ARG
1	A	321	GLU
1	A	324	ASP
1	A	325	LYS
1	A	328	TYR
1	A	331	PHE
1	A	351	LYS

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Mol	Chain	Res	Type
1	A	353	GLU
1	A	355	LEU
1	A	358	ARG
1	A	360	GLU
1	A	361	GLU
1	A	362	GLU
1	A	363	ASP
1	A	364	TYR
1	A	367	PHE
1	A	371	ASP
1	A	372	ARG
1	A	376	ARG
1	A	408	SER
1	A	409	CYS
1	A	412	GLN
1	A	413	ASN
1	A	414	ASP
1	A	416	GLU
1	A	418	ASP
1	A	425	ASP
1	A	427	SER
1	A	454	LEU
1	A	456	GLU
1	A	458	PHE
1	A	462	LEU
1	A	468	LEU
1	A	469	ILE
1	A	472	ASN
1	A	474	LYS
1	A	501	LEU
1	A	503	LYS
1	A	504	LYS
1	A	507	LEU
1	A	511	ASP
1	A	514	TYR
1	A	543	ASN
1	A	544	LYS
1	A	545	THR
1	A	546	LYS
1	A	547	LEU
1	A	549	LYS
1	A	555	LYS

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Mol	Chain	Res	Type
1	A	581	LEU
1	A	608	LYS
1	A	611	LYS
1	A	614	ARG
1	A	678	ARG
1	A	691	PHE
1	A	703	PHE
1	A	749	ARG
1	A	758	LEU
1	A	768	GLU
1	A	774	ILE
1	A	776	GLN
1	A	777	LYS
1	A	778	LYS
1	A	786	LEU
1	A	813	GLU
1	A	815	TYR
1	A	817	LYS
1	A	841	GLU
1	A	842	LYS
1	A	844	MET
1	A	849	LEU
1	A	852	LEU
1	A	858	LYS
1	A	861	GLN
1	A	862	GLU
1	A	878	GLU
1	A	880	THR
1	A	909	THR
1	A	932	SER
1	A	933	GLU
1	A	937	LEU
1	A	955	LYS
1	A	956	LYS
1	A	959	LEU
1	A	960	THR
1	A	992	ASP
1	A	995	LEU
1	A	1002	GLU
1	A	1035	LEU
1	A	1066	LEU
1	A	1067	ASN

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Mol	Chain	Res	Type
1	A	1068	ARG
1	A	1083	THR
1	A	1088	VAL
1	A	1095	MET
1	A	1105	ARG
1	A	1109	PHE
1	A	1115	GLN
1	A	1128	GLN
1	A	1170	MET
1	A	1183	THR
1	A	1202	ASN
1	A	1214	ARG
1	A	1217	ARG
1	A	1222	LEU
1	A	1262	MET
1	A	1275	MET
1	A	1276	GLU
1	A	1282	ASP
1	A	1314	SER
1	A	1317	ARG
1	A	1329	THR
1	A	1339	LEU
1	A	1344	THR
1	A	1354	GLU
1	A	1356	LEU
1	A	1358	ASP
1	A	1365	THR
1	A	1366	ARG
1	A	1382	ARG
1	A	1383	PHE
1	A	1405	ILE
1	A	1415	SER
1	A	1416	LYS
1	A	1418	THR
1	A	1460	GLU
1	A	1461	TYR
1	A	1465	ARG
1	A	1470	GLN
1	A	1473	ARG
1	A	1490	ARG
1	A	1499	ARG
1	A	1500	HIS

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Mol	Chain	Res	Type
1	A	1509	ARG
1	A	1511	ARG
1	A	1519	LEU
1	A	1590	LEU
1	A	1594	GLN
1	A	1616	ARG
1	A	1618	ASN
1	A	1627	LEU
1	A	1629	LEU
1	A	1650	ARG
1	A	1652	HIS
1	A	1661	ILE
1	A	1663	PHE
1	A	1690	LYS
1	A	1755	LYS
1	A	1762	ASP
1	A	1839	ASN
1	A	1882	LEU
1	A	1885	LYS
1	A	1888	HIS
1	A	1892	LYS
1	A	1908	LEU
1	A	1910	LYS
1	A	1912	LYS
1	A	1915	GLU
1	A	1916	GLU
1	A	1920	LEU
1	A	1951	PHE
1	A	1973	LYS
1	A	2007	ARG
1	A	2013	ARG
1	A	2023	LYS
1	A	2065	ARG
1	A	2067	TYR
1	A	2068	ASN
1	A	2071	ILE
1	A	2076	GLN
1	A	2078	GLU
2	B	47	GLU
2	B	48	ASP
2	B	66	ASN
2	B	73	ARG

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Mol	Chain	Res	Type
2	B	75	ARG
2	B	114	THR
2	B	117	LEU
2	B	119	PHE
2	B	122	ARG
2	B	123	PHE
2	B	128	SER
2	B	129	LEU
2	B	132	SER
2	B	133	ARG
2	B	136	LEU
2	B	137	GLN
2	B	140	MET
2	B	145	LYS
2	B	147	ASN
2	B	155	ARG
2	B	156	ARG
2	B	162	MET
2	B	171	GLN
2	B	172	LEU
2	B	192	THR
2	B	199	LEU
2	B	206	THR
2	B	208	GLN
2	B	244	LYS
2	B	257	LEU
2	B	267	ARG
2	B	276	SER
2	B	287	MET
2	B	313	LEU
2	B	316	GLN
2	B	323	CYS
2	B	333	LEU
2	B	337	ARG
2	B	358	SER
2	B	362	TYR
2	B	382	ASP
2	B	388	GLN
2	B	390	LEU
2	B	393	ARG
2	B	400	ARG
2	B	408	LYS

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Mol	Chain	Res	Type
2	B	409	LYS
2	B	443	LEU
2	B	444	ASP
2	B	446	SER
2	B	447	ASN
2	B	448	ASN
2	B	457	TRP
3	I	92	ILE
3	I	93	LYS
3	I	94	LEU
3	I	107	SER
3	I	118	SER
3	I	135	LEU
3	I	145	GLU
3	I	155	ASP
3	I	161	LEU
3	I	164	LYS
3	I	173	LEU
3	I	184	LYS
3	I	186	LYS
3	I	187	GLU
3	I	189	LEU
3	I	190	ASP
3	I	198	LEU
3	I	204	LEU
3	I	205	GLU
3	I	208	TRP
3	I	209	LYS
3	I	210	LEU
3	I	236	GLU
3	I	249	LEU
3	I	252	SER
3	I	253	ARG
3	I	257	CYS
3	I	264	LYS
3	I	268	LEU
3	I	271	GLU
3	I	272	LEU
3	I	273	HIS
3	I	280	ARG
3	I	281	GLN
3	I	312	LEU

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Mol	Chain	Res	Type
3	I	317	ASP
3	I	320	GLN
3	I	321	LYS
3	I	325	ARG
3	I	327	THR
3	I	342	ARG
3	I	344	LEU
3	I	346	GLU
3	I	350	ILE
3	I	353	THR
3	I	362	GLN
3	I	364	LYS
3	I	370	ARG
3	I	373	ARG
3	I	374	LYS
3	I	380	ARG
3	I	393	PHE
3	I	395	LYS
3	I	401	LEU
3	I	427	SER
3	I	428	ARG
3	I	429	ARG
3	I	433	ASN
3	I	436	LYS
3	I	447	GLU
3	I	450	GLN
3	I	454	GLU
3	I	456	LEU
4	G	5	SER
4	G	9	GLN
4	G	15	TYR
4	G	24	THR
4	G	99	ASN
4	G	100	VAL
4	G	102	ARG
4	G	107	LEU
4	G	108	LYS
4	G	126	THR
4	G	129	THR
4	G	130	ARG
4	G	134	ARG
4	G	138	GLN

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Mol	Chain	Res	Type
4	G	140	GLN
4	G	141	LEU
4	G	143	ARG
4	G	156	ASN
4	G	159	LEU
4	G	160	ASN
4	G	161	LYS
4	G	162	LEU
4	G	164	GLU
4	G	165	GLU
4	G	168	LYS
4	G	169	LEU
4	G	170	LEU
4	G	171	GLN
4	G	176	GLU
4	G	214	SER
4	G	216	SER
4	G	221	GLU
4	G	222	ASP
4	G	226	MET
4	G	227	ARG
4	G	230	LEU
4	G	232	SER
4	G	251	GLU
4	G	252	GLU
4	G	268	CYS
4	G	274	SER
4	G	275	SER
4	G	276	ASP
4	G	277	ILE
4	G	281	ASN
4	G	284	LEU
4	G	291	TYR
4	G	671	PHE
4	G	678	TYR
4	G	686	MET
4	G	687	SER
4	G	688	ARG
4	G	689	GLU
4	G	696	ARG
4	G	700	ASN
4	G	721	ARG

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Mol	Chain	Res	Type
4	G	852	LEU
4	G	854	LYS
4	G	855	ASP
4	G	859	LEU
4	G	861	ASN
4	G	862	MET
4	G	863	PHE
4	G	886	CYS
4	G	887	THR
4	G	889	ARG
5	K	142	LEU
5	K	147	ASP
5	K	166	TYR
5	K	171	THR
5	K	174	LEU
5	K	243	ARG
5	K	245	ARG
5	K	248	ARG
5	K	249	ARG
5	K	250	LYS
5	K	261	LYS
5	K	298	LYS
5	K	299	ASP
5	K	310	GLU
5	K	317	GLU
5	K	323	ARG
5	K	328	ASN
5	K	329	MET
5	K	332	GLU
5	K	333	LYS
5	K	362	GLU
5	K	399	ARG
5	K	448	GLN
5	K	457	GLN
5	K	459	ASP
6	L	25	ARG
6	L	34	LYS
6	L	63	ASP
6	L	73	MET
6	L	77	THR
6	L	78	ASP
6	L	102	LYS

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Mol	Chain	Res	Type
6	L	108	ASP
6	L	113	MET
6	L	118	GLU
6	L	125	ARG
6	L	133	SER
6	L	135	TYR
6	L	137	TYR
6	L	139	HIS
6	L	140	LYS
7	M	7	LYS
7	M	35	LYS
7	M	46	ARG
7	M	94	SER
7	M	95	ARG
7	M	96	PRO
8	H	107	THR
8	H	108	GLN
8	H	109	LEU
8	H	110	LYS
8	H	111	LYS
8	H	112	ASN
8	H	115	LYS
8	H	116	THR
8	H	117	ARG
8	H	120	ARG
8	H	122	TYR
8	H	132	ARG
8	H	133	ILE
8	H	160	ARG
8	H	166	LYS
8	H	167	ASN
8	H	168	VAL
8	H	173	LYS
8	H	177	TYR
8	H	178	LEU
8	H	187	ARG
8	H	189	LEU
8	H	193	LEU
8	H	202	ASP
8	H	203	LEU
8	H	204	GLU
8	H	205	SER

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Mol	Chain	Res	Type
8	H	206	LYS
8	H	208	ARG
8	H	222	MET
8	H	235	VAL
8	H	236	LEU
8	H	240	ASP
8	H	265	PHE
8	H	274	ILE
8	H	275	LEU
8	H	296	ASN
8	H	297	SER
8	H	300	LYS
8	H	305	SER
8	H	326	GLU
8	H	329	SER
8	H	330	TYR
8	H	336	ILE
8	H	339	SER
8	H	353	TYR
8	H	354	TYR
8	H	364	PHE
8	H	366	ASN
8	H	368	GLU
8	H	369	LYS
8	H	372	THR
8	H	373	PHE
8	H	389	LEU
8	H	391	MET
8	H	393	LYS
8	H	416	ASP
8	H	448	LEU
8	H	449	PHE
8	H	452	LYS
8	H	456	LEU
8	H	457	SER
8	H	461	LYS
8	H	465	GLU
8	H	469	TRP
8	H	474	LYS
8	H	478	TYR
8	H	487	ARG
8	H	489	TYR

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Mol	Chain	Res	Type
8	H	490	SER
8	H	503	ASP
8	H	505	SER
8	H	508	GLU
8	H	509	SER
8	H	510	ARG
8	H	536	SER
8	H	538	GLU
8	H	545	LEU
8	H	558	LYS
8	H	565	LYS
8	H	568	SER
8	H	569	SER
8	H	573	LYS
8	H	578	TYR
8	H	581	LYS
8	H	582	SER
8	H	583	LYS
8	H	584	GLU
8	H	586	MET
8	H	587	LYS
8	H	589	LEU
8	H	590	LYS
8	H	595	LEU
8	H	603	PHE
8	H	608	GLN
8	H	617	LYS
8	H	652	MET
8	H	797	GLN
8	H	799	PHE
8	H	814	TYR
8	H	884	ARG
8	H	887	ARG
8	H	888	ILE
8	H	889	TYR
8	H	919	ARG
8	H	931	TYR
8	H	932	PHE
8	H	934	HIS
8	H	936	ILE
8	H	945	LEU
8	H	947	LYS

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Mol	Chain	Res	Type
8	H	948	ASP
8	H	959	ILE
8	H	960	ASN
8	H	970	THR
8	H	971	ARG
8	H	972	ARG
8	H	974	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (84) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	146	HIS
1	A	254	HIS
1	A	310	ASN
1	A	326	ASN
1	A	344	ASN
1	A	392	ASN
1	A	413	ASN
1	A	429	ASN
1	A	497	GLN
1	A	543	ASN
1	A	592	HIS
1	A	868	GLN
1	A	948	HIS
1	A	976	GLN
1	A	1067	ASN
1	A	1115	GLN
1	A	1128	GLN
1	A	1156	HIS
1	A	1496	GLN
1	A	1594	GLN
1	A	1603	ASN
1	A	1615	ASN
1	A	1652	HIS
1	A	1809	ASN
1	A	1839	ASN
2	B	144	GLN
2	B	208	GLN
2	B	227	HIS
2	B	232	ASN
2	B	247	GLN
2	B	274	HIS

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Mol	Chain	Res	Type
2	B	316	GLN
2	B	374	ASN
2	B	392	HIS
2	B	420	ASN
2	B	447	ASN
2	B	448	ASN
2	B	450	HIS
3	I	113	HIS
3	I	146	ASN
3	I	148	ASN
3	I	152	ASN
3	I	196	GLN
3	I	201	ASN
3	I	211	GLN
3	I	267	HIS
3	I	281	GLN
3	I	398	GLN
3	I	414	ASN
3	I	433	ASN
3	I	449	ASN
3	I	461	HIS
4	G	99	ASN
4	G	138	GLN
4	G	140	GLN
4	G	160	ASN
4	G	281	ASN
4	G	285	HIS
4	G	668	HIS
4	G	700	ASN
4	G	805	HIS
5	K	163	ASN
5	K	316	HIS
5	K	330	ASN
6	L	14	HIS
6	L	17	GLN
6	L	87	HIS
6	L	139	HIS
7	M	45	ASN
8	H	112	ASN
8	H	135	ASN
8	H	158	HIS
8	H	167	ASN

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Mol	Chain	Res	Type
8	H	211	ASN
8	H	296	ASN
8	H	334	HIS
8	H	355	HIS
8	H	418	GLN
8	H	444	GLN
8	H	554	HIS
8	H	608	GLN
8	H	721	GLN
8	H	797	GLN
8	H	929	GLN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
24	C	19/20 (95%)	17 (89%)	2 (10%)
25	D	41/112 (36%)	22 (53%)	4 (9%)
26	E	85/160 (53%)	28 (32%)	7 (8%)
27	F	111/214 (51%)	51 (45%)	14 (12%)
All	All	256/506 (50%)	118 (46%)	27 (10%)

All (118) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
24	C	-5	A
24	C	-4	A
24	C	-3	A
24	C	-2	A
24	C	-1	A
24	C	0	U
24	C	1	U
24	C	2	A
24	C	3	A
24	C	4	G
24	C	5	G
24	C	6	U
24	C	7	A
24	C	8	U
24	C	9	G
24	C	10	U
24	C	12	U

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Mol	Chain	Res	Type
25	D	48	C
25	D	49	A
25	D	50	G
25	D	51	A
25	D	52	G
25	D	57	U
25	D	62	A
25	D	63	G
25	D	66	C
25	D	72	C
25	D	75	A
25	D	76	A
25	D	77	G
25	D	78	G
25	D	79	A
25	D	83	A
25	D	84	C
25	D	85	C
25	D	86	G
25	D	87	U
25	D	109	U
25	D	110	U
26	E	2	U
26	E	4	C
26	E	15	G
26	E	18	A
26	E	19	U
26	E	20	A
26	E	25	U
26	E	27	U
26	E	28	C
26	E	30	G
26	E	39	C
26	E	43	C
26	E	48	U
26	E	51	U
26	E	55	U
26	E	56	U
26	E	60	U
26	E	140	G
26	E	141	G
26	E	142	G

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Mol	Chain	Res	Type
26	E	143	A
26	E	144	A
26	E	146	U
26	E	147	U
26	E	148	U
26	E	149	U
26	E	150	G
26	E	151	G
27	F	32	G
27	F	33	U
27	F	34	C
27	F	39	U
27	F	40	C
27	F	41	A
27	F	74	U
27	F	75	A
27	F	76	U
27	F	77	A
27	F	78	A
27	F	79	C
27	F	80	G
27	F	81	A
27	F	82	A
27	F	83	C
27	F	84	A
27	F	90	C
27	F	92	U
27	F	93	G
27	F	94	C
27	F	95	C
27	F	96	U
27	F	97	U
27	F	98	U
27	F	99	U
27	F	100	A
27	F	101	C
27	F	103	A
27	F	104	G
27	F	107	C
27	F	108	C
27	F	109	A
27	F	110	U

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Mol	Chain	Res	Type
27	F	113	G
27	F	120	G
27	F	121	U
27	F	126	A
27	F	127	U
27	F	164	C
27	F	165	A
27	F	166	U
27	F	167	A
27	F	168	U
27	F	169	U
27	F	170	U
27	F	171	U
27	F	172	U
27	F	173	U
27	F	174	G
27	F	175	G

All (27) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
24	C	-4	A
24	C	6	U
25	D	48	C
25	D	50	G
25	D	83	A
25	D	85	C
26	E	1	A
26	E	18	A
26	E	19	U
26	E	24	A
26	E	139	A
26	E	142	G
26	E	148	U
27	F	32	G
27	F	33	U
27	F	75	A
27	F	77	A
27	F	81	A
27	F	83	C
27	F	95	C
27	F	97	U

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Mol	Chain	Res	Type
27	F	98	U
27	F	107	C
27	F	163	C
27	F	166	U
27	F	168	U
27	F	172	U

## 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](#)

2 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
29	M7M	E	201	26	29,33,33	1.13	2 (6%)	32,52,52	3.02	8 (25%)
28	GTP	H	1500	-	26,34,34	1.13	2 (7%)	29,54,54	1.80	4 (13%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
29	M7M	E	201	26	-	1/20/48/48	0/3/3/3
28	GTP	H	1500	-	-	0/18/38/38	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
29	E	201	M7M	CBG-CBO	2.72	1.46	1.39
28	H	1500	GTP	C5-C4	3.06	1.47	1.40
29	E	201	M7M	CBF-CBG	3.39	1.46	1.41
28	H	1500	GTP	C6-C5	3.71	1.48	1.41

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
29	E	201	M7M	CBG-CBO-NBN	-8.85	117.72	126.74
29	E	201	M7M	CBG-CBF-NBE	-5.56	115.11	123.39
28	H	1500	GTP	C5-C6-N1	-4.77	117.29	123.52
29	E	201	M7M	CBW-NBV-CBM	-4.06	117.26	121.34
29	E	201	M7M	CBI-NBP-CBQ	-3.96	110.53	122.43
29	E	201	M7M	OBV-PBK-OBL	-3.27	95.83	109.21
28	H	1500	GTP	N3-C2-N1	-3.07	123.38	127.56
28	H	1500	GTP	C6-C5-C4	-2.84	117.61	120.86
29	E	201	M7M	CBM-NBN-CBO	2.16	118.78	115.42
29	E	201	M7M	OAY-PAZ-OBA	3.53	122.13	110.63
28	H	1500	GTP	C6-N1-C2	5.57	122.41	115.88
29	E	201	M7M	NBN-CBO-NBP	9.45	139.21	126.98

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
29	E	201	M7M	PBK-OBV-CBT-CBS

There are no ring outliers.

2 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
29	E	201	M7M	6	0
28	H	1500	GTP	10	0

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.