



Full wwPDB/EMDatabank EM Map/Model Validation Report ⓘ

Jan 16, 2017 – 02:02 PM EST

PDB ID : 5WSG
EMDB ID: : EMD-6684
Title : Cryo-EM structure of the Catalytic Step II spliceosome (C* complex) at 4.0 angstrom resolution
Authors : Yan, C.; Wan, R.; Bai, R.; Huang, G.; Shi, Y.
Deposited on : 2016-12-07
Resolution : 4.00 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

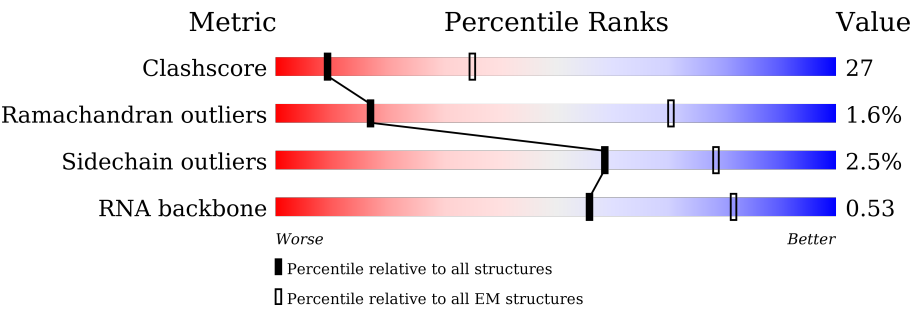
MolProbity : 4.02b-467
Mogul : 1.7.1 (RC1), CSD as537be (2016)
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20028442

1 Overall quality at a glance i

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

The reported resolution of this entry is 4.00 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.




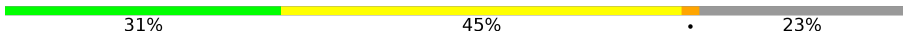
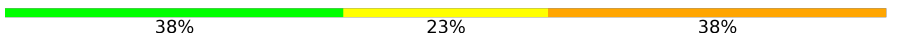
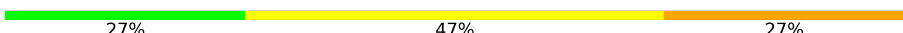
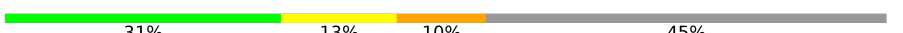
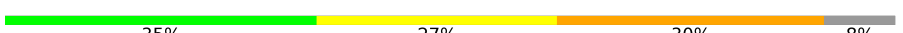



















Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

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 >=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 <=5%

Mol	Chain	Length	Quality of chain
1	A	2413	<div><div>33%</div><div>45%</div><div>•</div><div>20%</div></div>
2	C	1008	<div><div>36%</div><div>49%</div><div>•</div><div>13%</div></div>
3	J	135	<div><div>7%</div><div>13%</div><div>80%</div></div>
4	O	451	<div><div>26%</div><div>45%</div><div>•</div><div>25%</div></div>
5	P	379	<div><div>28%</div><div>22%</div><div>•</div><div>47%</div></div>
6	Q	364	<div><div>17%</div><div>32%</div><div>•</div><div>49%</div></div>
7	R	339	<div><div>27%</div><div>48%</div><div>•</div><div>23%</div></div>
8	S	175	<div><div>18%</div><div>20%</div><div>•</div><div>61%</div></div>


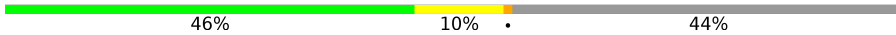
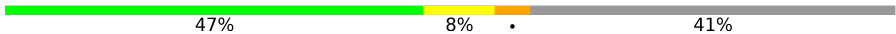
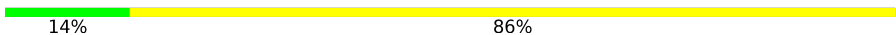


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Mol	Chain	Length	Quality of chain
9	T	157	
10	Z	577	
11	B	13	
12	N	15	
13	D	214	
14	E	112	
15	L	1175	
16	M	23	
17	c	579	
18	d	652	
19	I	215	
20	v	858	
21	n	455	
22	o	503	
22	p	503	
22	q	503	
22	r	503	
23	t	175	
24	F	196	
24	k	196	
25	G	94	
25	i	94	
26	H	86	
26	h	86	
27	K	77	

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Mol	Chain	Length	Quality of chain
27	j	77	
28	U	101	
28	l	101	
29	V	146	
29	m	146	
30	W	110	
30	g	110	
31	X	111	
32	Y	238	
33	b	14	
34	e	1071	
35	f	251	

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
36	GTP	C	1500	-	-	X	-

2 Entry composition

There are 38 unique types of molecules in this entry. The entry contains 76730 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	1931	Total	C	N	O	S	0	0
			15939	10244	2739	2898	58		

- Molecule 2 is a protein called Pre-mRNA-splicing factor SNU114.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	878	Total	C	N	O	S	0	0
			7019	4529	1166	1295	29		

- Molecule 3 is a protein called Pre-mRNA-splicing factor CWC21.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	J	27	Total	C	N	O	0	0
			190	112	38	40		

- Molecule 4 is a protein called Pre-mRNA-splicing factor PRP46.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	O	337	Total	C	N	O	S	0	0
			2646	1669	466	501	10		

- Molecule 5 is a protein called Pre-mRNA-processing protein 45.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	P	201	Total	C	N	O	S	0	0
			1583	988	290	298	7		

- Molecule 6 is a protein called Pre-mRNA-splicing factor SLT11.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	Q	185	Total	C	N	O	S	0	0
			1472	930	256	271	15		

- Molecule 7 is a protein called Pre-mRNA-splicing factor CWC2.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	R	261	Total	C	N	O	S	0	0
			2089	1320	369	388	12		

- Molecule 8 is a protein called Pre-mRNA-splicing factor CWC15.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	S	69	Total	C	N	O	S	0	0
			560	351	112	96	1		

- Molecule 9 is a protein called Pre-mRNA-splicing factor BUD31.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	T	157	Total	C	N	O	S	0	0
			1291	808	240	232	11		

- Molecule 10 is a protein called Pre-mRNA-splicing factor CWC22.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	Z	447	Total	C	N	O	S	0	0
			3651	2343	602	688	18		

- Molecule 11 is a RNA chain called 5'-exon.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	B	13	Total	C	N	O	P	0	0
			275	124	47	91	13		

- Molecule 12 is a RNA chain called 5'-intron-lariat.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	N	15	Total	C	N	O	P	0	0
			312	140	45	112	15		

- Molecule 13 is a RNA chain called U5 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	D	117	Total	C	N	O	P	0	0
			2465	1104	414	830	117		

- Molecule 14 is a RNA chain called Saccharomyces cerevisiae S288c SNR6 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	E	103	Total	C	N	O	P	0	0
			2192	982	391	716	103		

- Molecule 15 is a RNA chain called TPA_inf: *Saccharomyces cerevisiae* S288c chromosome II, complete sequence.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	L	91	Total	C	N	O	P	0	0
			1909	854	309	655	91		

- Molecule 16 is a RNA chain called 3'-intron-lariat.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	M	23	Total	C	N	O	P	0	0
			486	219	86	158	23		

- Molecule 17 is a protein called Pre-mRNA-splicing factor CEF1,Pre-mRNA-splicing factor CEF1,Cef1,Pre-mRNA-splicing factor CEF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	c	436	Total	C	N	O	S	0	0
			2971	1841	549	573	8		

- Molecule 18 is a protein called Pre-mRNA-splicing factor CLF1,Pre-mRNA-splicing factor CLF1,Clf1.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	d	532	Total	C	N	O	S	0	0
			3506	2182	658	658	8		

- Molecule 19 is a protein called Pre-mRNA-splicing factor SYF2.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	I	102	Total	C	N	O	S	0	0
			822	504	152	165	1		

- Molecule 20 is a protein called Syf1,Pre-mRNA-splicing factor SYF1,Syf1,Pre-mRNA-splicing factor SYF1,Syf1,Pre-mRNA-splicing factor SYF1,Syf1.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	v	593	Total	C	N	O	S	0	0
			3183	1953	603	626	1		

- Molecule 21 is a protein called Pre-mRNA-processing factor 17.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	n	296	Total	C	N	O	S	0	0
			1870	1162	337	365	6		

- Molecule 22 is a protein called Pre-mRNA-processing factor 19.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	o	126	Total	C	N	O	S	0	0
			830	525	134	169	2		
22	p	128	Total	C	N	O	S	0	0
			843	532	136	173	2		
22	q	387	Total	C	N	O	S	0	0
			2345	1471	402	464	8		
22	r	125	Total	C	N	O	S	0	0
			823	521	133	167	2		

- Molecule 23 is a protein called Pre-mRNA-splicing factor SNT309.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	t	156	Total	C	N	O	S	0	0
			926	585	160	180	1		

- Molecule 24 is a protein called Small nuclear ribonucleoprotein-associated protein B.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	k	80	Total	C	N	O	S	0	0
			631	403	114	111	3		
24	F	78	Total	C	N	O	S	0	0
			610	389	110	108	3		

- Molecule 25 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	i	75	Total	C	N	O	S	0	0
			575	379	92	101	3		
25	G	75	Total	C	N	O	S	0	0
			575	379	92	101	3		

- Molecule 26 is a protein called Small nuclear ribonucleoprotein F.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	h	70	Total	C	N	O	S	0	0
			554	355	98	100	1		
26	H	70	Total	C	N	O	S	0	0
			554	355	98	100	1		

- Molecule 27 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	j	69	Total	C	N	O	S	0	0
			529	337	93	97	2		
27	K	69	Total	C	N	O	S	0	0
			529	337	93	97	2		

- Molecule 28 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	l	82	Total	C	N	O	S	0	0
			625	399	109	115	2		
28	U	82	Total	C	N	O	S	0	0
			625	399	109	115	2		

- Molecule 29 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	m	82	Total	C	N	O	S	0	0
			644	409	110	123	2		
29	V	82	Total	C	N	O	S	0	0
			644	409	110	123	2		

- Molecule 30 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	g	94	Total	C	N	O	S	0	0
			741	477	141	119	4		
30	W	65	Total	C	N	O	S	0	0
			528	340	102	84	2		

- Molecule 31 is a protein called U2 small nuclear ribonucleoprotein B”.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	X	81	Total	C	N	O	0	0
			513	332	89	92		

- Molecule 32 is a protein called U2 small nuclear ribonucleoprotein A'.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	Y	135	Total	C	N	O	0	0
			841	538	142	161		

- Molecule 33 is a RNA chain called 3'-exon-intron.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	b	14	Total	C	N	O	P	0	0
			208	91	13	90	14		

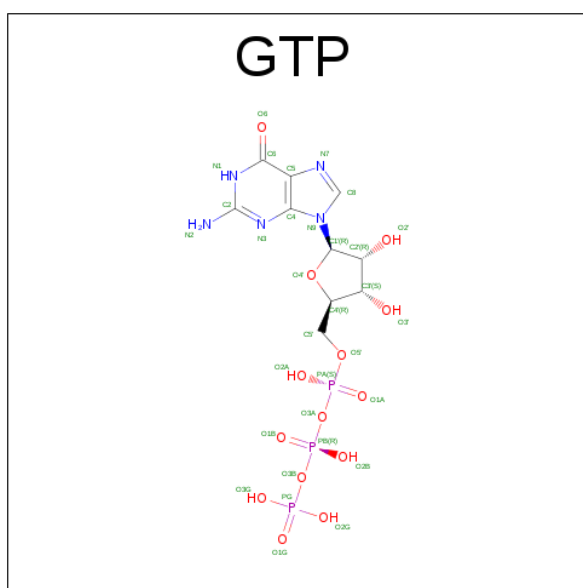
- Molecule 34 is a protein called Pre-mRNA-splicing factor ATP-dependent RNA helicase PRP16.

Mol	Chain	Residues	Atoms				AltConf	Trace
34	e	679	Total	C	N	O	0	0
			3360	2002	679	679		

- Molecule 35 is a protein called Pre-mRNA-splicing factor 18.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	f	148	Total	C	N	O	S	0	0
			1202	780	204	214	4		

- Molecule 36 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



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

- Molecule 37 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
37	B	1	Total	Mg	0
			1	1	
37	C	1	Total	Mg	0
			1	1	
37	E	4	Total	Mg	0
			4	4	

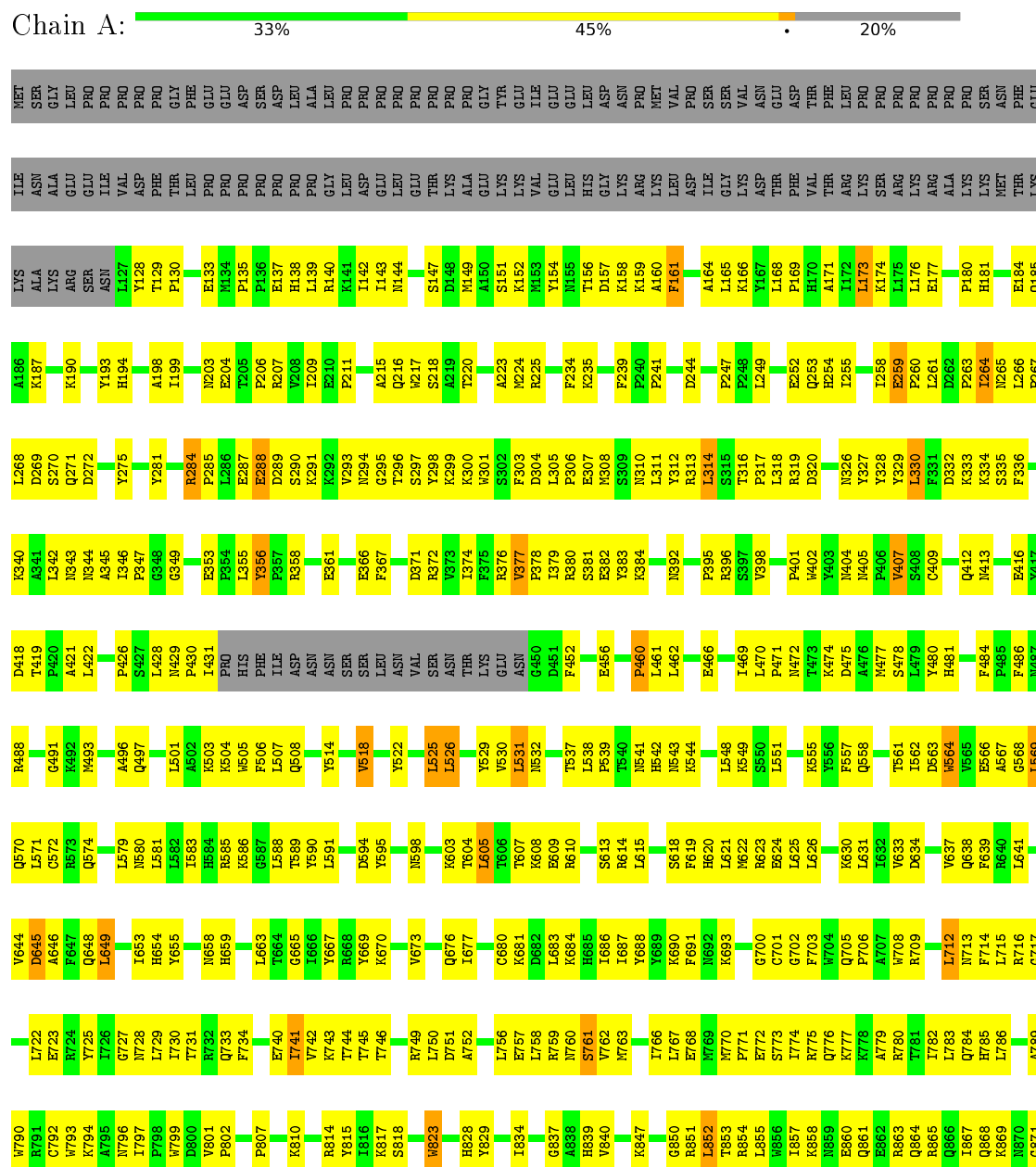
- Molecule 38 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
38	R	1	Total	Zn	0
			1	1	
38	Q	2	Total	Zn	0
			2	2	
38	T	3	Total	Zn	0
			3	3	

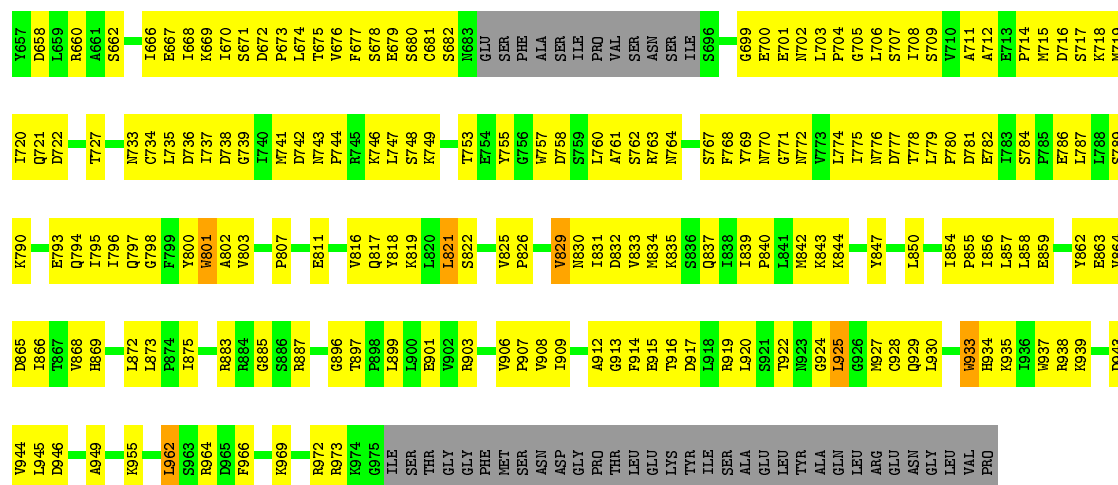
3 Residue-property plots

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

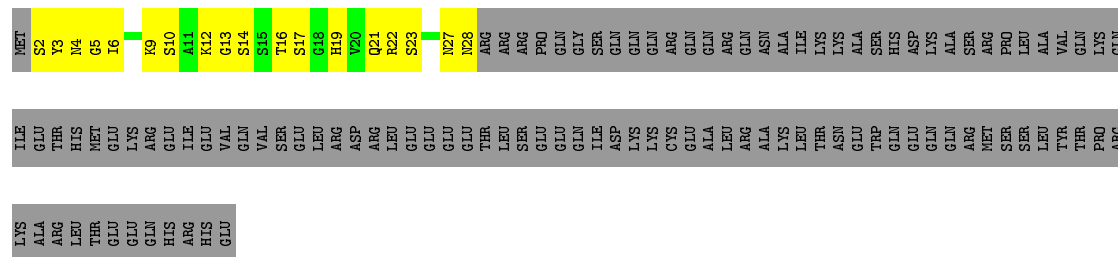




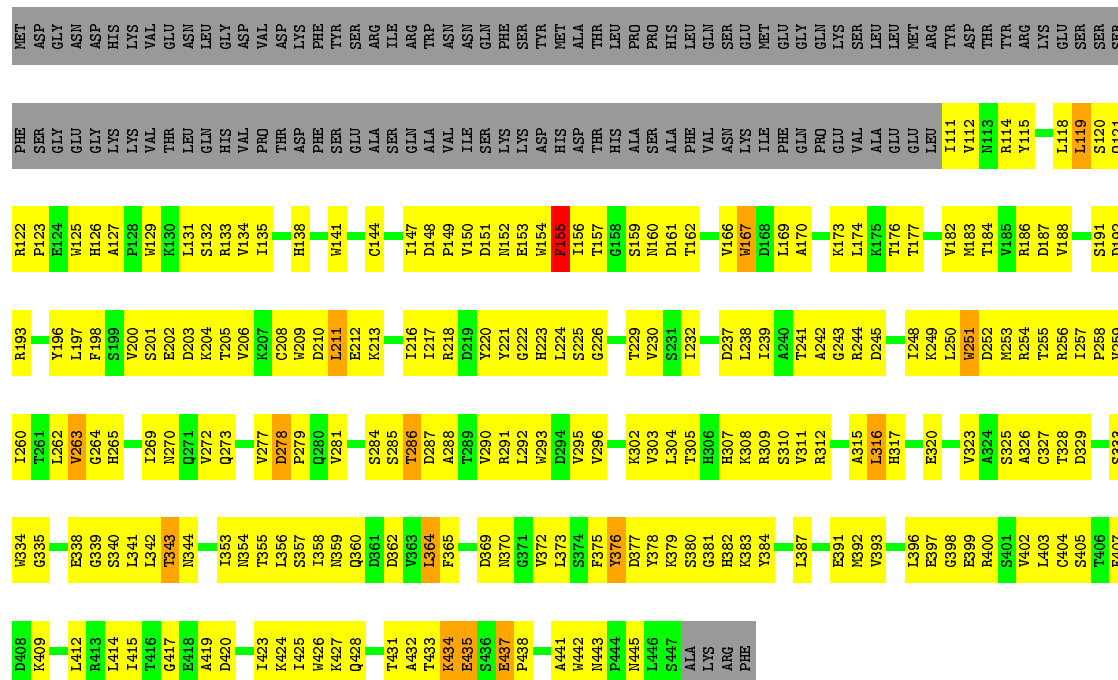
• Molecule 3: Pre-mRNA-splicing factor CWC21

Chain J: 7% 13% 80%

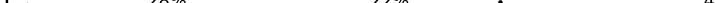


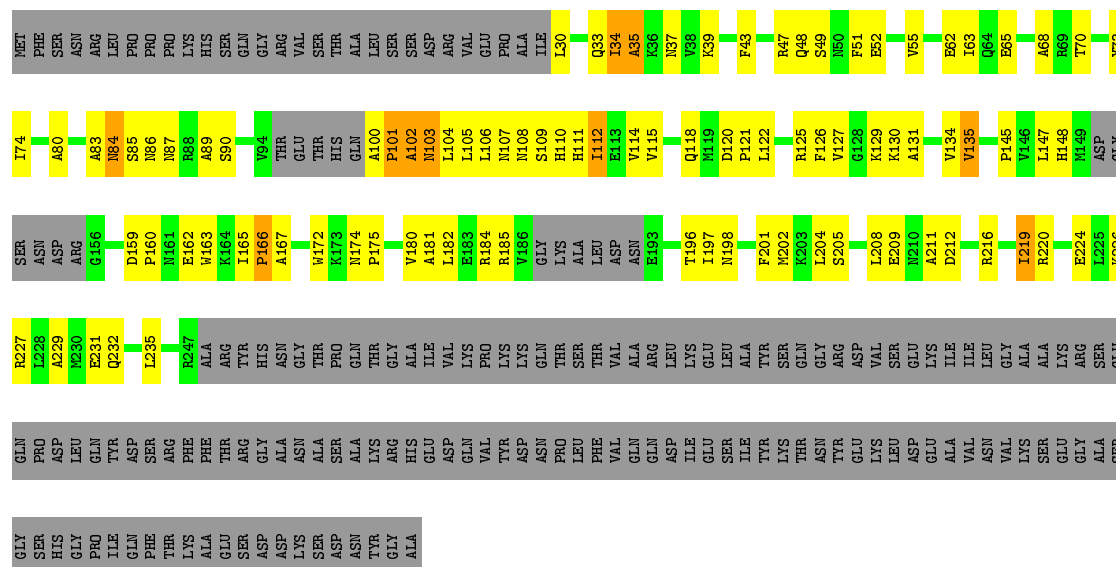
• Molecule 4: Pre-mRNA-splicing factor PRP46

Chain O: 26% 45% 25%



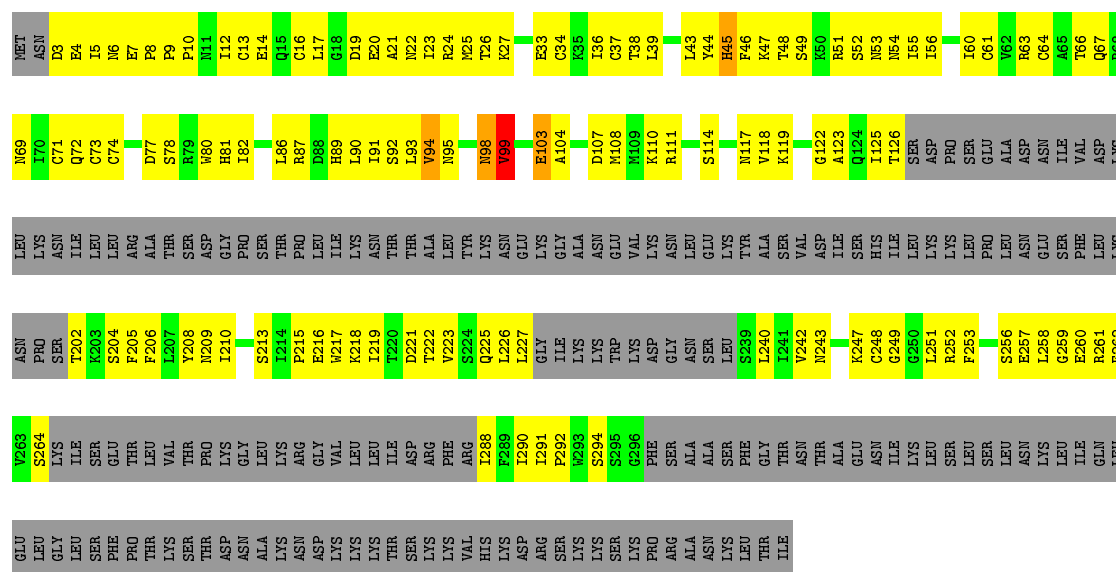
- Molecule 5: Pre-mRNA-processing protein 45

Chain P:  28% 22% • 49%



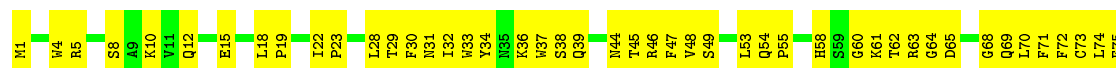
- Molecule 6: Pre-mRNA-splicing factor SLT11

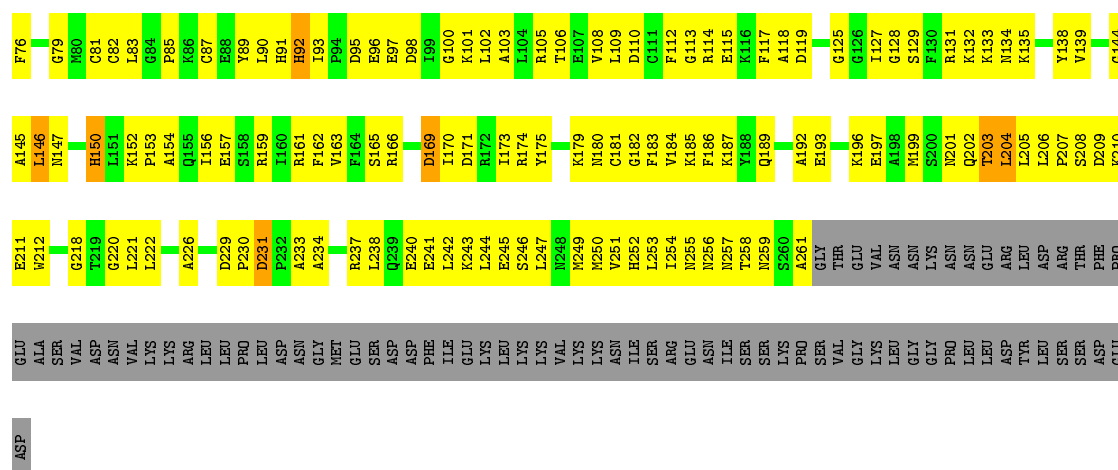
Chain Q: 17% 32% . 49%



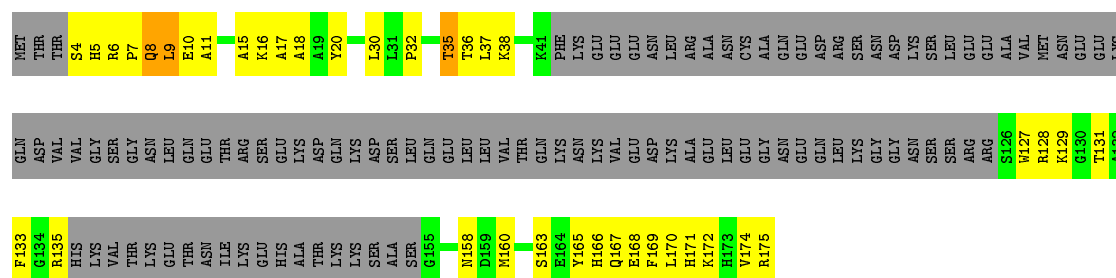
- Molecule 7: Pre-mRNA-splicing factor CWC2

Chain R:  27% 48% • 23%

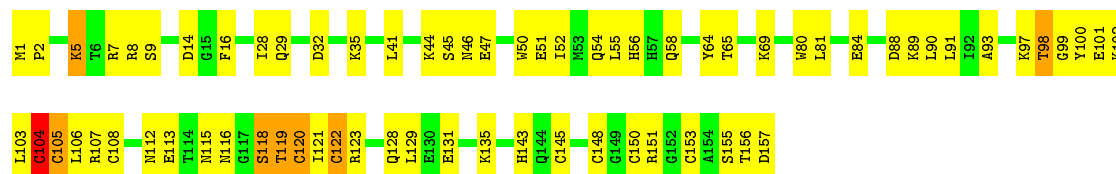




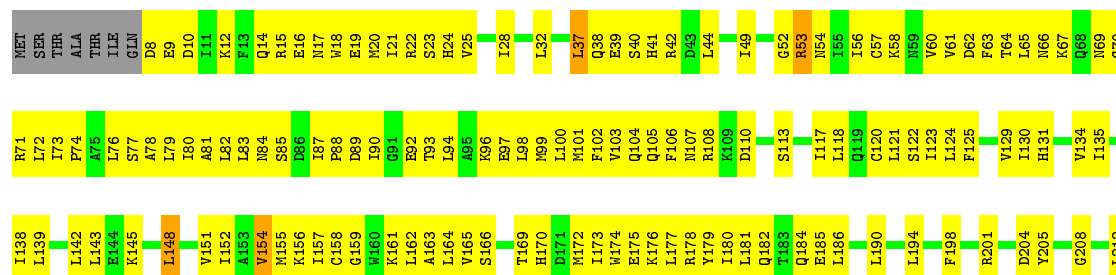
- Molecule 8: Pre-mRNA-splicing factor CWC15

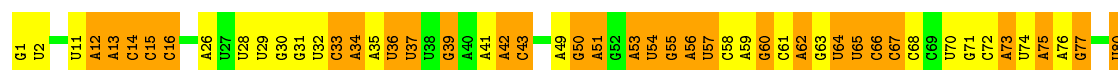


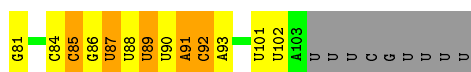
- Molecule 9: Pre-mRNA-splicing factor BUD31



- Molecule 10: Pre-mRNA-splicing factor CWC22

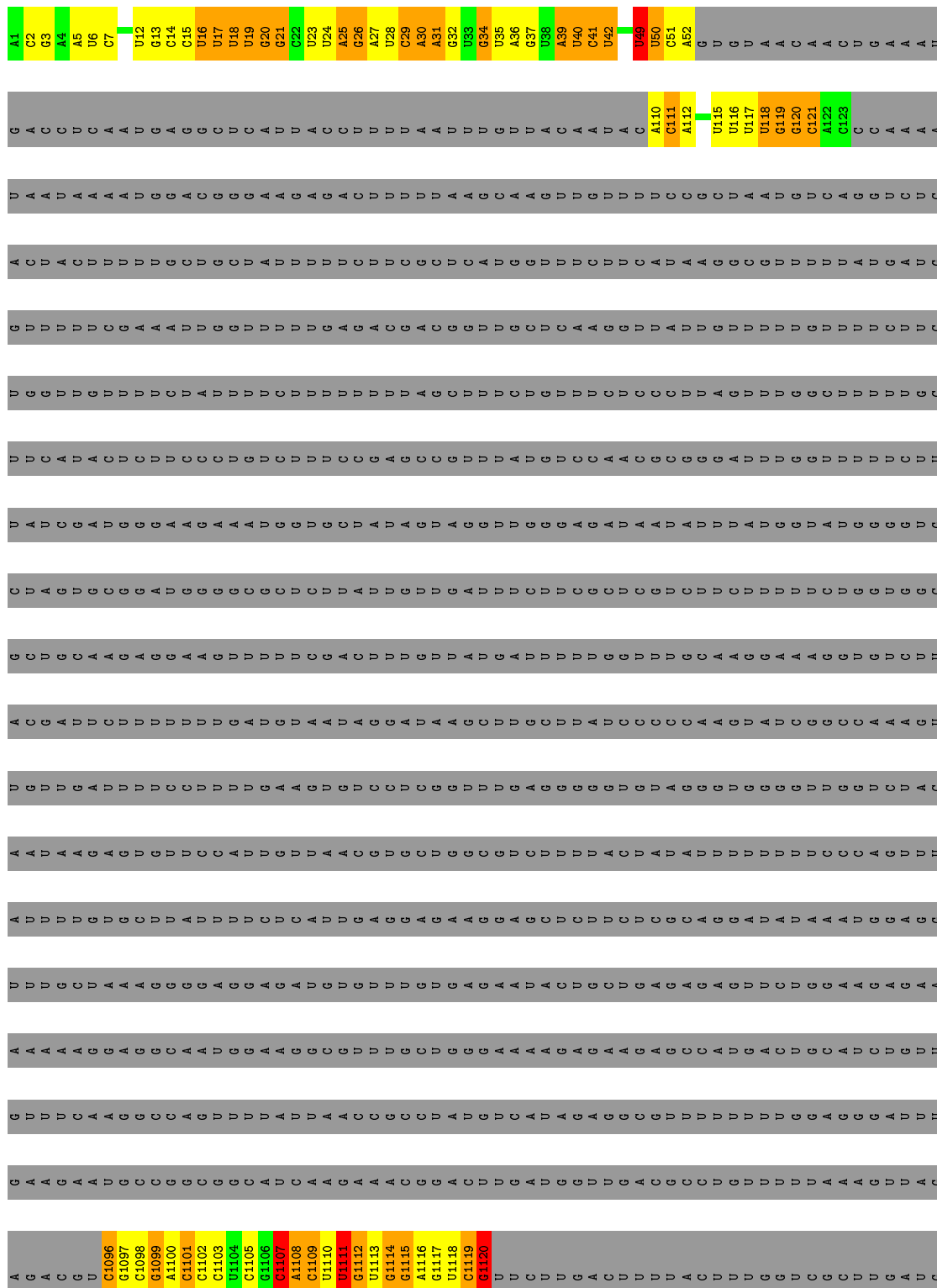


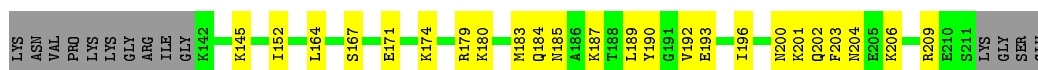




- Molecule 15: TPA_inf: *Saccharomyces cerevisiae* S288c chromosome II, complete sequence

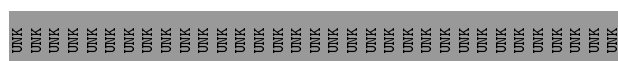
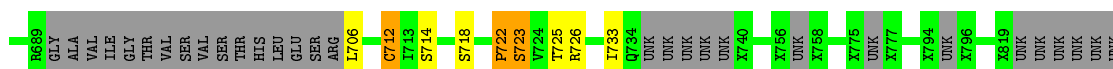
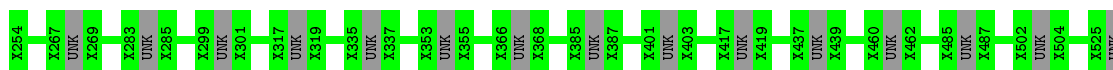
Chain L: . . . 92%





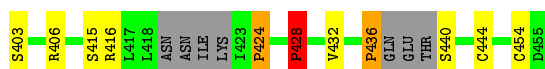
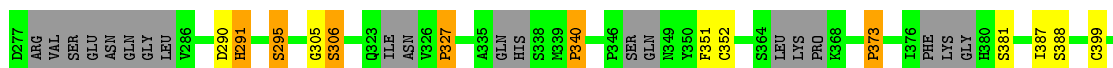
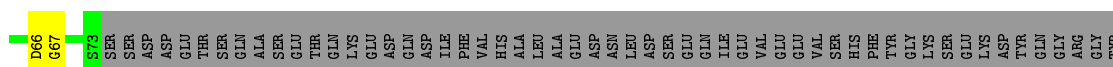
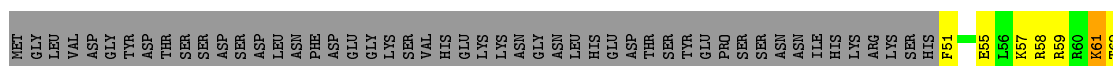
- Molecule 20: Syf1,Pre-mRNA-splicing factor SYF1,Syf1,Pre-mRNA-splicing factor SYF1,Syf1,Pre-mRNA-splicing factor SYF1,Syf1

Chain v:  67% .. 31%



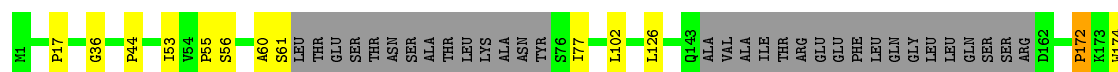
- Molecule 21: Pre-mRNA-processing factor 17

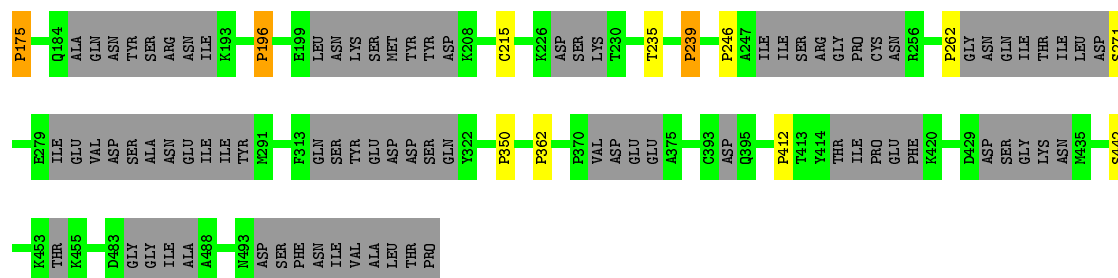
Chain n:  54% 7% 35%



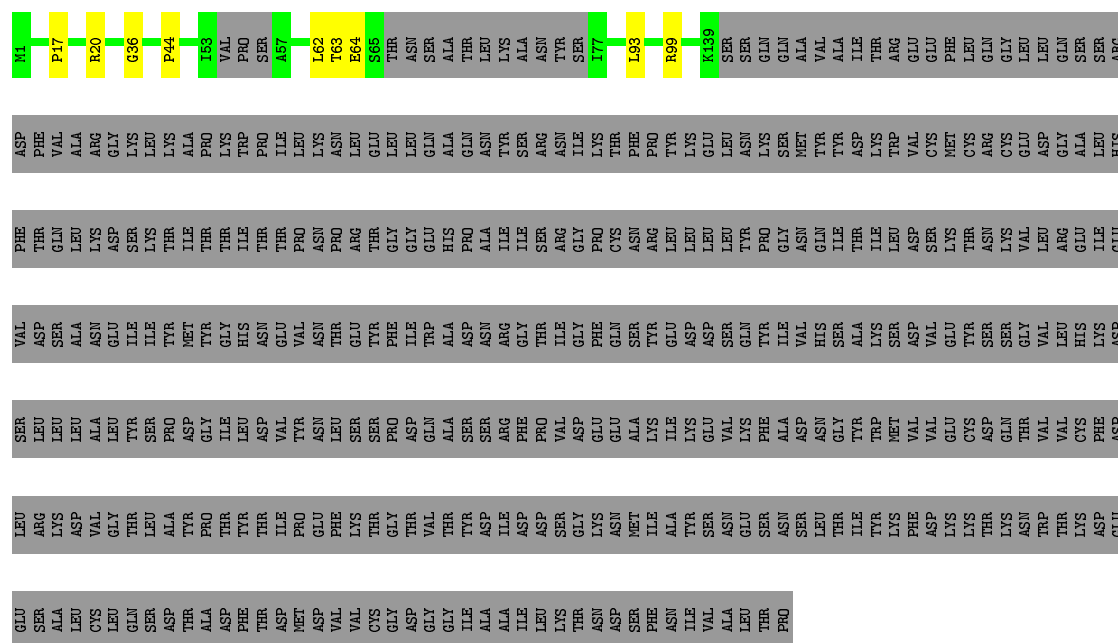
- Molecule 22: Pre-mRNA-processing factor 19

Chain o: 24% 75%

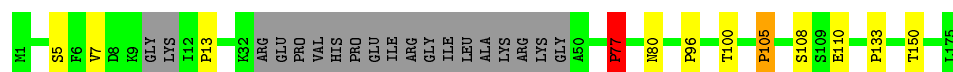
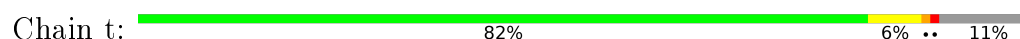




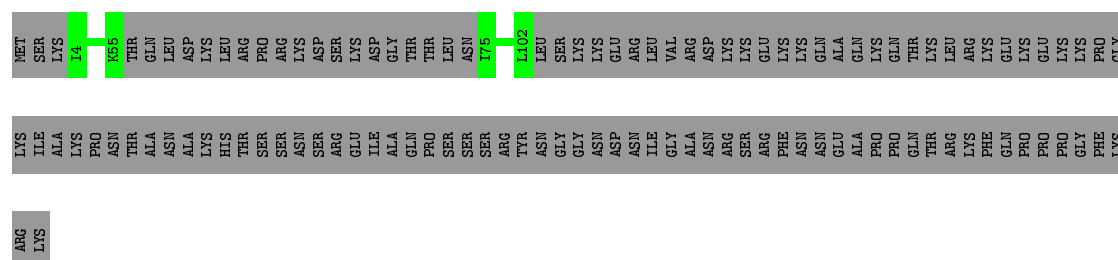
• Molecule 22: Pre-mRNA-processing factor 19



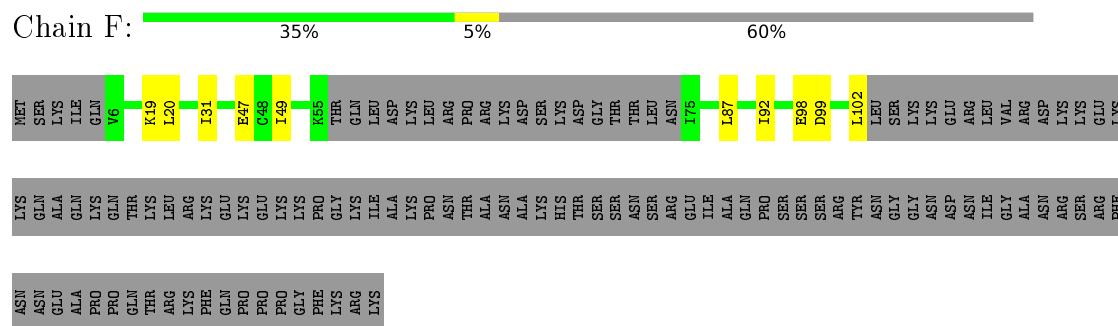
• Molecule 23: Pre-mRNA-splicing factor SNT309



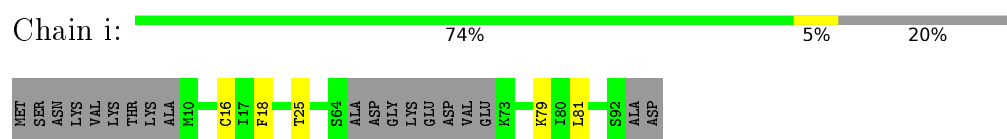
• Molecule 24: Small nuclear ribonucleoprotein-associated protein B



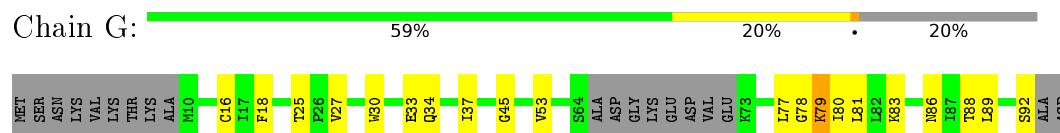
- Molecule 24: Small nuclear ribonucleoprotein-associated protein B



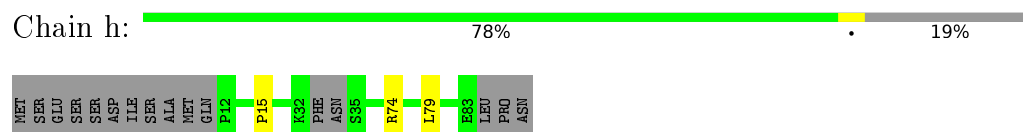
- Molecule 25: Small nuclear ribonucleoprotein E



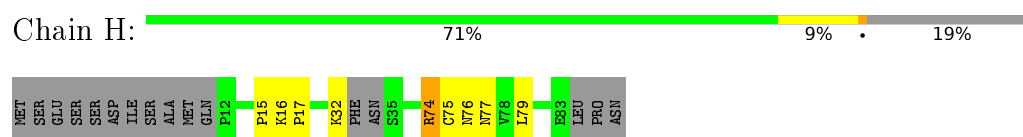
- Molecule 25: Small nuclear ribonucleoprotein E



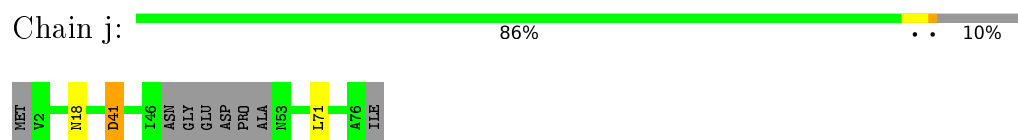
- Molecule 26: Small nuclear ribonucleoprotein F



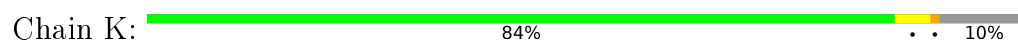
- Molecule 26: Small nuclear ribonucleoprotein F



- Molecule 27: Small nuclear ribonucleoprotein G



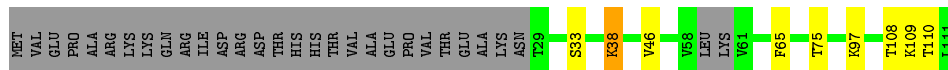
- Molecule 27: Small nuclear ribonucleoprotein G





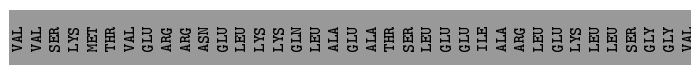
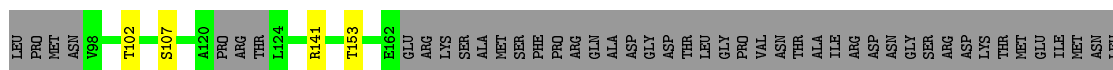
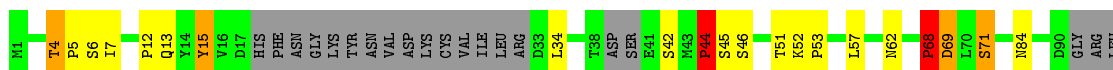
- Molecule 31: U2 small nuclear ribonucleoprotein B'

Chain X: 65% 7% 27%



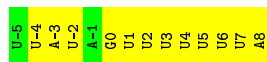
- Molecule 32: U2 small nuclear ribonucleoprotein A'

Chain Y: 46% 8% 43%



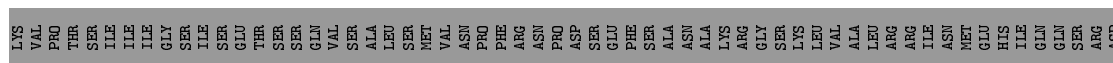
- Molecule 33: 3'-exon-intron

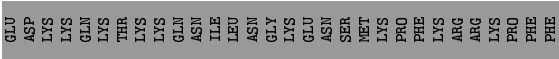
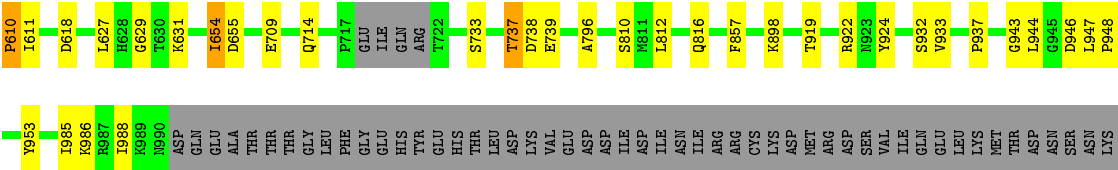
Chain b: 14% 86%



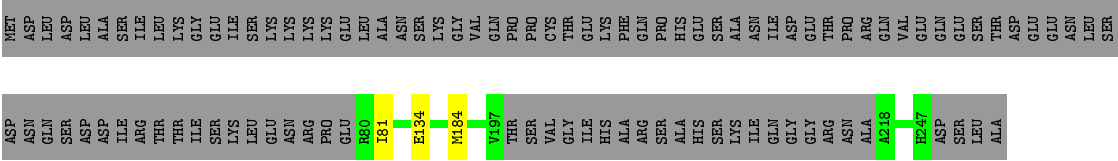
- Molecule 34: Pre-mRNA-splicing factor ATP-dependent RNA helicase PRP16

Chain e: 58% 5% 37%





● Molecule 35: Pre-mRNA-splicing factor 18



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	27558	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Not provided	Depositor
Microscope	FEI TITAN KRIOS	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, ZN, MG

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	0.81	5/16346 (0.0%)	0.81	19/22154 (0.1%)
10	Z	0.55	0/3712	0.75	5/5004 (0.1%)
11	B	0.68	0/307	0.90	0/475
12	N	0.68	0/346	0.86	0/535
13	D	0.73	0/2747	0.92	3/4267 (0.1%)
14	E	0.72	0/2452	0.95	3/3817 (0.1%)
15	L	0.75	13/2123 (0.6%)	1.12	18/3295 (0.5%)
16	M	0.29	0/543	0.72	0/842
17	c	0.38	0/2405	0.54	0/3218
18	d	0.42	0/2107	0.54	0/2852
19	I	0.35	0/826	0.53	0/1097
2	C	0.79	1/7168 (0.0%)	0.80	7/9707 (0.1%)
20	v	1.05	8/905 (0.9%)	0.76	6/1214 (0.5%)
21	n	1.47	17/1878 (0.9%)	0.89	15/2503 (0.6%)
22	o	0.40	0/835	0.53	0/1126
22	p	0.40	0/848	0.55	0/1143
22	q	0.44	0/2342	0.65	0/3139
22	r	0.39	0/828	0.54	1/1117 (0.1%)
23	t	0.42	0/924	0.56	2/1244 (0.2%)
24	F	0.37	0/615	0.61	0/829
24	k	0.37	0/636	0.61	0/856
25	G	0.42	0/585	0.62	0/795
25	i	0.42	0/585	0.62	0/795
26	H	0.44	0/564	0.66	1/761 (0.1%)
26	h	0.44	0/564	0.65	1/761 (0.1%)
27	K	0.37	0/532	0.60	0/715
27	j	0.37	0/532	0.60	0/715
28	U	0.40	0/634	0.70	0/859
28	l	0.40	0/634	0.70	0/859
29	V	0.41	0/649	0.61	0/880
29	m	0.41	0/649	0.61	0/880
3	J	0.70	0/191	0.80	0/254

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
30	W	0.43	0/535	0.66	2/717 (0.3%)
30	g	0.45	0/753	0.69	2/1013 (0.2%)
31	X	0.82	4/514 (0.8%)	1.32	2/686 (0.3%)
32	Y	1.03	9/839 (1.1%)	1.65	11/1127 (1.0%)
33	b	0.20	0/227	0.73	0/346
34	e	0.48	0/3357	1.09	4/4674 (0.1%)
35	f	0.29	0/1227	0.50	0/1665
4	O	0.98	3/2704 (0.1%)	0.89	5/3676 (0.1%)
5	P	0.66	0/1604	0.78	1/2160 (0.0%)
6	Q	0.64	0/1496	0.76	1/2014 (0.0%)
7	R	0.72	0/2135	0.76	2/2871 (0.1%)
8	S	0.70	0/574	0.85	0/766
9	T	0.81	3/1315 (0.2%)	0.79	0/1759
All	All	0.71	63/74292 (0.1%)	0.81	111/102182 (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	24
10	Z	0	2
17	c	0	2
18	d	0	1
2	C	0	10
21	n	0	4
27	K	0	1
27	j	0	1
28	U	0	2
28	l	0	2
30	W	0	2
30	g	0	2
34	e	0	32
4	O	0	10
5	P	0	5
6	Q	0	6
7	R	0	3
8	S	0	1
9	T	0	5
All	All	0	115

All (63) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
21	n	399	CYS	CB-SG	-24.14	1.41	1.82
21	n	444	CYS	CB-SG	-22.91	1.43	1.82
21	n	454	CYS	CB-SG	-19.93	1.48	1.82
21	n	218	CYS	CB-SG	-19.55	1.49	1.82
21	n	352	CYS	CB-SG	-18.81	1.50	1.82
21	n	198	CYS	CB-SG	-17.76	1.52	1.82
20	v	712	CYS	CB-SG	-17.12	1.53	1.82
15	L	1096	C	O3'-P	-10.06	1.49	1.61
20	v	723	SER	CB-OG	8.59	1.53	1.42
20	v	718	SER	CB-OG	8.57	1.53	1.42
20	v	714	SER	CB-OG	7.95	1.52	1.42
21	n	440	SER	CB-OG	7.84	1.52	1.42
20	v	681	SER	CB-OG	7.83	1.52	1.42
9	T	148	CYS	CB-SG	-7.54	1.69	1.82
15	L	1096	C	C1'-N1	7.47	1.59	1.48
32	Y	46	SER	CB-OG	7.46	1.51	1.42
21	n	381	SER	CB-OG	7.34	1.51	1.42
15	L	1120	G	C1'-N9	-7.34	1.36	1.46
15	L	1118	U	C1'-N1	7.33	1.59	1.48
32	Y	45	SER	CB-OG	7.32	1.51	1.42
31	X	33	SER	CB-OG	7.10	1.51	1.42
32	Y	69	ASP	CA-CB	-6.99	1.38	1.53
32	Y	6	SER	CB-OG	6.93	1.51	1.42
20	v	633	SER	CB-OG	6.83	1.51	1.42
15	L	1111	U	C1'-N1	6.77	1.58	1.48
15	L	1101	C	C1'-N1	6.76	1.58	1.48
15	L	1119	C	C1'-N1	6.76	1.58	1.48
1	A	708	TRP	CB-CG	-6.61	1.38	1.50
21	n	415	SER	CB-OG	6.60	1.50	1.42
15	L	1115	G	C1'-N9	-6.59	1.37	1.46
21	n	268	SER	CB-OG	6.59	1.50	1.42
15	L	1109	C	C1'-N1	6.06	1.57	1.48
21	n	220	SER	CB-OG	6.02	1.50	1.42
32	Y	42	SER	CB-OG	5.89	1.50	1.42
21	n	388	SER	CB-OG	5.84	1.49	1.42
21	n	403	SER	CB-OG	5.83	1.49	1.42
1	A	505	TRP	CB-CG	-5.82	1.39	1.50
32	Y	102	THR	CB-OG1	5.80	1.54	1.43
20	v	640	SER	CB-OG	5.72	1.49	1.42
21	n	351	PHE	CB-CG	-5.68	1.41	1.51
4	O	251	TRP	CB-CG	-5.68	1.40	1.50
32	Y	15	TYR	CB-CG	-5.68	1.43	1.51
15	L	121	C	C1'-N1	5.66	1.57	1.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	O	167	TRP	CB-CG	-5.63	1.40	1.50
15	L	1112	G	C1'-N9	-5.61	1.39	1.46
32	Y	51	THR	CB-OG1	5.58	1.54	1.43
21	n	432	VAL	CB-CG1	-5.43	1.41	1.52
21	n	275	TYR	CB-CG	-5.42	1.43	1.51
9	T	105	CYS	CB-SG	-5.36	1.73	1.81
1	A	564	TRP	CB-CG	-5.29	1.40	1.50
20	v	685	GLU	CB-CG	-5.28	1.42	1.52
1	A	823	TRP	CB-CG	-5.24	1.40	1.50
31	X	75	THR	CB-OG1	5.20	1.53	1.43
2	C	933	TRP	CB-CG	-5.20	1.40	1.50
4	O	155	PHE	CB-CG	-5.20	1.42	1.51
31	X	110	THR	CB-OG1	5.20	1.53	1.43
1	A	673	VAL	CB-CG1	-5.15	1.42	1.52
32	Y	153	THR	CB-OG1	5.12	1.53	1.43
15	L	49	U	C1'-N1	5.12	1.56	1.48
9	T	122	CYS	CB-SG	-5.08	1.73	1.81
31	X	65	PHE	CB-CG	-5.08	1.42	1.51
21	n	291	HIS	CA-CB	-5.05	1.42	1.53
15	L	50	U	C1'-N1	5.04	1.56	1.48

All (111) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	L	1110	U	C5-C4-O4	11.94	133.07	125.90
15	L	1107	C	N1-C2-O2	-10.12	112.83	118.90
32	Y	44	PRO	N-CA-CB	8.85	113.92	103.30
15	L	1109	C	O4'-C1'-N1	8.79	115.23	108.20
2	C	656	LEU	CA-CB-CG	-8.46	95.84	115.30
1	A	525	LEU	CA-CB-CG	-8.39	96.01	115.30
15	L	1112	G	P-O3'-C3'	8.35	129.72	119.70
15	L	1107	C	C5'-C4'-O4'	-8.29	99.15	109.10
15	L	1110	U	N3-C4-O4	-8.14	113.70	119.40
34	e	373	GLY	O-C-N	7.94	135.41	122.70
1	A	1339	LEU	CB-CG-CD2	-7.89	97.58	111.00
1	A	1882	LEU	C-N-CA	-7.83	102.14	121.70
15	L	1107	C	P-O3'-C3'	7.58	128.79	119.70
15	L	1110	U	N1-C2-O2	7.51	128.05	122.80
15	L	1107	C	N3-C2-O2	7.49	127.14	121.90
4	O	250	LEU	CA-CB-CG	-7.40	98.29	115.30
21	n	428	PRO	N-CA-CB	7.37	112.14	103.30
32	Y	5	PRO	N-CA-CB	7.22	111.97	103.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	Y	42	SER	N-CA-CB	-7.22	99.66	110.50
15	L	1111	U	P-O5'-C5'	-7.10	109.53	120.90
15	L	1110	U	N3-C2-O2	-6.97	117.32	122.20
15	L	1108	A	O4'-C1'-N9	-6.95	102.64	108.20
7	R	231	ASP	CB-CG-OD1	6.94	124.55	118.30
1	A	569	LEU	CA-CB-CG	-6.90	99.42	115.30
34	e	373	GLY	C-N-CA	6.78	138.64	121.70
32	Y	12	PRO	N-CA-CB	6.73	111.38	103.30
20	v	617	PRO	CA-CB-CG	6.62	117.37	104.80
20	v	613	PRO	N-CA-CB	6.51	111.12	103.30
5	P	135	VAL	C-N-CA	-6.50	105.46	121.70
20	v	722	PRO	N-CA-CB	6.45	111.05	103.30
1	A	526	LEU	CA-CB-CG	-6.45	100.47	115.30
4	O	119	LEU	CA-CB-CG	-6.43	100.52	115.30
1	A	531	LEU	CA-CB-CG	-6.42	100.54	115.30
1	A	1624	LEU	CB-CG-CD2	-6.39	100.13	111.00
32	Y	57	LEU	N-CA-CB	6.35	123.10	110.40
32	Y	4	THR	N-CA-CB	-6.32	98.28	110.30
1	A	1054	LEU	CA-CB-CG	-6.29	100.83	115.30
1	A	1360	LEU	CA-CB-CG	-6.24	100.95	115.30
21	n	159	PRO	N-CA-CB	6.15	110.67	103.30
4	O	211	LEU	CA-CB-CG	-6.12	101.22	115.30
10	Z	37	LEU	CA-CB-CG	6.12	129.38	115.30
21	n	373	PRO	N-CA-CB	6.12	110.64	103.30
21	n	257	PRO	N-CA-CB	6.11	110.63	103.30
21	n	208	PRO	N-CA-CB	6.06	110.57	103.30
20	v	641	PRO	CA-CB-CG	6.01	116.21	104.80
21	n	424	PRO	N-CA-CB	6.00	110.50	103.30
13	D	79	C	C2-N1-C1'	5.98	125.38	118.80
20	v	616	PRO	N-CA-CB	5.95	110.44	103.30
32	Y	141	ARG	CD-NE-CZ	5.92	131.89	123.60
32	Y	7	ILE	CA-CB-CG1	5.92	122.24	111.00
15	L	1107	C	C5-C4-N4	-5.87	116.09	120.20
15	L	1111	U	C5'-C4'-C3'	-5.83	106.68	116.00
15	L	1110	U	O3'-P-O5'	-5.79	93.00	104.00
1	A	605	LEU	CA-CB-CG	-5.78	102.00	115.30
21	n	162	PRO	N-CA-CB	5.78	110.23	103.30
23	t	105	PRO	CA-CB-CG	5.78	115.78	104.80
21	n	373	PRO	CA-CB-CG	5.77	115.76	104.80
34	e	431	TYR	C-N-CA	5.76	136.10	121.70
10	Z	321	LEU	CA-CB-CG	-5.75	102.08	115.30
10	Z	148	LEU	CA-CB-CG	-5.74	102.09	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
21	n	327	PRO	N-CA-CB	5.71	110.15	103.30
21	n	436	PRO	N-CA-CB	5.69	110.13	103.30
1	A	1259	LEU	CB-CG-CD2	-5.68	101.34	111.00
32	Y	68	PRO	N-CA-CB	5.68	110.12	103.30
21	n	436	PRO	CA-CB-CG	5.65	115.54	104.80
10	Z	470	LEU	CA-CB-CG	5.65	128.29	115.30
2	C	109	LEU	CA-CB-CG	5.64	128.27	115.30
2	C	962	LEU	CB-CG-CD2	-5.63	101.43	111.00
1	A	1320	LEU	CA-CB-CG	-5.59	102.45	115.30
30	W	81	GLY	CA-C-N	-5.56	104.97	117.20
30	g	81	GLY	CA-C-N	-5.54	105.02	117.20
21	n	260	PRO	N-CA-CB	5.53	109.94	103.30
21	n	306	SER	N-CA-CB	-5.53	102.21	110.50
34	e	618	ASP	CB-CA-C	5.52	121.44	110.40
1	A	852	LEU	CA-CB-CG	-5.50	102.64	115.30
2	C	873	LEU	CA-CB-CG	-5.48	102.69	115.30
2	C	925	LEU	CA-CB-CG	-5.48	102.70	115.30
14	E	77	G	C6-C5-N7	-5.47	127.12	130.40
1	A	625	LEU	CB-CG-CD1	-5.45	101.74	111.00
1	A	712	LEU	CA-CB-CG	-5.41	102.86	115.30
7	R	204	LEU	C-N-CA	5.41	135.21	121.70
1	A	173	LEU	CB-CG-CD1	-5.39	101.83	111.00
1	A	330	LEU	CA-CB-CG	-5.34	103.02	115.30
6	Q	226	LEU	CA-CB-CG	5.33	127.57	115.30
23	t	77	PRO	CA-CB-CG	5.31	114.89	104.80
1	A	314	LEU	CB-CG-CD2	-5.30	101.99	111.00
15	L	1113	U	O4'-C1'-C2'	-5.29	100.51	105.80
4	O	364	LEU	CB-CG-CD1	-5.28	102.02	111.00
14	E	58	C	C2-N1-C1'	5.28	124.61	118.80
21	n	340	PRO	N-CA-CB	5.27	109.62	103.30
26	H	74	ARG	NE-CZ-NH1	5.27	122.94	120.30
32	Y	71	SER	N-CA-CB	-5.22	102.67	110.50
22	r	62	LEU	CA-CB-CG	-5.22	103.30	115.30
15	L	1119	C	OP1-P-OP2	-5.20	111.80	119.60
26	h	74	ARG	NE-CZ-NH1	5.16	122.88	120.30
21	n	295	SER	N-CA-CB	-5.14	102.80	110.50
1	A	649	LEU	CB-CG-CD1	-5.13	102.28	111.00
4	O	316	LEU	CA-CB-CG	-5.13	103.50	115.30
10	Z	313	LEU	CA-CB-CG	-5.10	103.58	115.30
13	D	90	C	C5-C6-N1	5.10	123.55	121.00
30	W	82	LYS	N-CA-C	5.09	124.76	111.00
2	C	400	LEU	CA-CB-CG	-5.09	103.60	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	v	617	PRO	N-CA-CB	5.08	109.40	103.30
14	E	55	G	N3-C4-N9	5.08	129.05	126.00
30	g	82	LYS	N-CA-C	5.08	124.71	111.00
31	X	46	VAL	CA-CB-CG2	5.07	118.50	110.90
31	X	33	SER	N-CA-CB	5.06	118.09	110.50
32	Y	107	SER	N-CA-CB	-5.06	102.91	110.50
15	L	1096	C	OP2-P-O3'	5.02	116.24	105.20
13	D	90	C	C2-N1-C1'	5.01	124.32	118.80
2	C	821	LEU	CA-CB-CG	-5.01	103.78	115.30

There are no chirality outliers.

All (115) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1014	LYS	Peptide
1	A	1036	SER	Peptide
1	A	1346	PHE	Peptide
1	A	1375	LEU	Peptide
1	A	1409	ALA	Peptide
1	A	1410	SER	Peptide
1	A	1418	THR	Peptide
1	A	1432	GLU	Peptide
1	A	1539	LEU	Peptide
1	A	1588	LYS	Peptide
1	A	1720	THR	Peptide
1	A	1788	GLY	Peptide
1	A	1790	TRP	Peptide
1	A	1809	ASN	Peptide
1	A	1972	ASP	Peptide
1	A	1999	ILE	Peptide
1	A	259	GLU	Peptide
1	A	288	GLU	Peptide
1	A	356	TYR	Peptide
1	A	460	PRO	Peptide
1	A	539	PRO	Peptide
1	A	761	SER	Peptide
1	A	907	ASN	Peptide
1	A	985	ASP	Peptide
2	C	170	LEU	Peptide
2	C	171	GLY	Peptide
2	C	231	ALA	Peptide
2	C	350	GLY	Peptide

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Mol	Chain	Res	Type	Group
2	C	365	GLU	Peptide
2	C	369	LYS	Peptide
2	C	467	THR	Peptide
2	C	554	HIS	Peptide
2	C	70	TYR	Peptide
2	C	82	ASN	Peptide
27	K	41	ASP	Peptide
4	O	123	PRO	Peptide
4	O	155	PHE	Peptide
4	O	278	ASP	Peptide
4	O	305	THR	Peptide
4	O	376	TYR	Peptide
4	O	431	THR	Peptide
4	O	434	LYS	Peptide
4	O	435	GLU	Peptide
4	O	437	GLU	Peptide
4	O	441	ALA	Peptide
5	P	101	PRO	Peptide
5	P	103	ASN	Peptide
5	P	35	ALA	Peptide
5	P	84	ASN	Peptide
5	P	85	SER	Peptide
6	Q	103	GLU	Peptide
6	Q	291	ILE	Peptide
6	Q	45	HIS	Peptide
6	Q	6	ASN	Peptide
6	Q	94	VAL	Peptide
6	Q	98	ASN	Peptide
7	R	125	GLY	Peptide
7	R	150	HIS	Peptide
7	R	203	THR	Peptide
8	S	172	LYS	Peptide
9	T	104	CYS	Peptide
9	T	116	ASN	Peptide
9	T	118	SER	Peptide
9	T	155	SER	Peptide
9	T	5	LYS	Peptide
28	U	81	ALA	Mainchain,Peptide
30	W	81	GLY	Mainchain,Peptide
10	Z	23	SER	Peptide
10	Z	285	SER	Peptide
17	c	65	PHE	Peptide

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Mol	Chain	Res	Type	Group
17	c	81	PRO	Peptide
18	d	212	HIS	Peptide
34	e	309	MET	Peptide
34	e	313	LEU	Peptide
34	e	372	ILE	Peptide
34	e	386	TYR	Peptide
34	e	387	LEU	Peptide
34	e	431	TYR	Peptide
34	e	436	GLU	Peptide
34	e	443	CYS	Peptide
34	e	449	VAL	Peptide
34	e	532	VAL	Peptide
34	e	542	GLN	Peptide
34	e	563	SER	Peptide
34	e	570	MET	Peptide
34	e	595	PHE	Peptide
34	e	604	ASN	Peptide
34	e	610	PRO	Peptide
34	e	627	LEU	Peptide
34	e	631	LYS	Mainchain,Peptide
34	e	654	ILE	Peptide
34	e	709	GLU	Peptide
34	e	733	SER	Peptide
34	e	737	THR	Peptide
34	e	738	ASP	Peptide
34	e	796	ALA	Peptide
34	e	810	SER	Peptide
34	e	857	PHE	Peptide
34	e	898	LYS	Peptide
34	e	924	TYR	Peptide
34	e	947	LEU	Peptide
34	e	953	TYR	Peptide
34	e	986	LYS	Peptide
30	g	81	GLY	Mainchain,Peptide
27	j	41	ASP	Peptide
28	l	81	ALA	Mainchain,Peptide
21	n	290	ASP	Peptide
21	n	305	GLY	Peptide
21	n	67	GLY	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	15939	0	15918	1209	0
2	C	7019	0	7201	530	0
3	J	190	0	186	29	0
4	O	2646	0	2639	223	0
5	P	1583	0	1608	99	0
6	Q	1472	0	1485	126	0
7	R	2089	0	2053	230	0
8	S	560	0	545	48	0
9	T	1291	0	1312	73	0
10	Z	3651	0	3707	273	0
11	B	275	0	138	23	0
12	N	312	0	156	49	0
13	D	2465	0	1251	108	0
14	E	2192	0	1106	167	0
15	L	1909	0	970	216	0
16	M	486	0	246	69	0
17	c	2971	0	2336	0	0
18	d	3506	0	2340	0	0
19	I	822	0	845	63	0
20	v	3183	0	1207	0	0
21	n	1870	0	1392	0	0
22	o	830	0	663	0	0
22	p	843	0	675	0	0
22	q	2345	0	1636	0	0
22	r	823	0	654	0	0
23	t	926	0	606	0	0
24	F	610	0	640	17	0
24	k	631	0	670	0	0
25	G	575	0	597	22	0
25	i	575	0	597	0	0
26	H	554	0	556	22	0
26	h	554	0	556	0	0
27	K	529	0	557	1	0
27	j	529	0	557	0	0
28	U	625	0	647	8	0
28	l	625	0	647	0	0
29	V	644	0	686	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
29	m	644	0	686	0	0
30	W	528	0	573	16	0
30	g	741	0	778	0	0
31	X	513	0	402	12	0
32	Y	841	0	614	17	0
33	b	208	0	106	0	0
34	e	3360	0	1483	0	0
35	f	1202	0	1248	0	0
36	C	32	0	12	11	0
37	B	1	0	0	0	0
37	C	1	0	0	0	0
37	E	4	0	0	0	0
38	Q	2	0	0	0	0
38	R	1	0	0	0	0
38	T	3	0	0	0	0
All	All	76730	0	65487	3115	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 27.

All (3115) 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)
7:R:75:PHE:CE2	14:E:35:A:C8	1.74	1.62
1:A:1587:PHE:CE2	15:L:31:A:H5'	1.33	1.60
7:R:46:ARG:CD	12:N:110:A:H2	1.17	1.56
7:R:75:PHE:CD2	14:E:35:A:N7	1.83	1.45
7:R:46:ARG:CD	12:N:110:A:C2	2.05	1.40
7:R:46:ARG:HD3	12:N:110:A:C2	1.55	1.39
1:A:839:HIS:CD2	13:D:95:C:O2	1.76	1.38
15:L:5:A:C5'	19:I:114:THR:HG21	1.54	1.36
1:A:839:HIS:HD2	13:D:95:C:O2	1.05	1.35
6:Q:215:PRO:HG3	6:Q:217:TRP:CE2	1.62	1.34
2:C:99:LYS:NZ	13:D:43:G:OP2	1.58	1.34
1:A:839:HIS:HD2	13:D:95:C:C2	1.46	1.33
1:A:1666:CYS:O	1:A:1670:ASP:HB2	1.27	1.30
1:A:1587:PHE:CE2	15:L:31:A:C5'	2.11	1.30
6:Q:215:PRO:HG3	6:Q:217:TRP:CZ2	1.69	1.28
6:Q:47:LYS:HE2	14:E:31:G:O6	1.16	1.27
15:L:5:A:H5'	19:I:114:THR:CG2	1.66	1.25
1:A:713:ASN:ND2	13:D:83:C:H4'	1.55	1.22

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1774:MET:O	1:A:1786:ALA:HA	1.40	1.20
24:F:98:GLU:O	32:Y:53:PRO:CB	1.92	1.17
7:R:89:TYR:CD2	14:E:34:A:C2	2.32	1.16
6:Q:47:LYS:CE	14:E:31:G:O6	1.94	1.15
7:R:46:ARG:NH1	12:N:110:A:C2	2.14	1.15
6:Q:217:TRP:O	6:Q:221:ASP:HB2	1.47	1.13
7:R:46:ARG:NH1	12:N:110:A:N3	1.96	1.13
7:R:75:PHE:CD2	14:E:35:A:C8	2.28	1.12
15:L:1109:C:N4	31:X:109:LYS:H	1.48	1.10
6:Q:51:ARG:NH2	14:E:28:U:O2	1.83	1.10
1:A:854:ARG:NH2	15:L:25:A:OP1	1.84	1.10
15:L:1111:U:H5'	15:L:1111:U:C6	1.86	1.09
1:A:614:ARG:NH1	11:B:98:A:H4'	1.68	1.08
7:R:183:PHE:CE2	12:N:113:U:C6	2.41	1.08
1:A:1588:LYS:HD3	15:L:30:A:N3	1.69	1.08
1:A:477:MET:HE2	2:C:278:LYS:HE3	1.32	1.07
1:A:1709:TRP:O	1:A:1728:ILE:HA	1.54	1.07
1:A:1587:PHE:CZ	15:L:31:A:H5'	1.89	1.07
7:R:179:LYS:HB3	12:N:111:U:O2'	1.54	1.07
7:R:46:ARG:HD2	12:N:110:A:C2	1.89	1.06
1:A:1588:LYS:CD	15:L:30:A:C2	2.38	1.06
7:R:183:PHE:HE2	12:N:113:U:C6	1.72	1.06
6:Q:215:PRO:CG	6:Q:217:TRP:CE2	2.38	1.06
24:F:99:ASP:CB	32:Y:53:PRO:CB	2.35	1.05
15:L:1102:C:H2'	15:L:1103:C:C6	1.91	1.04
15:L:1116:A:H2'	15:L:1117:G:H8	1.18	1.04
15:L:15:C:H41	19:I:209:ARG:CG	1.71	1.03
14:E:49:A:C2'	14:E:50:G:H5'	1.89	1.03
1:A:839:HIS:CD2	13:D:95:C:C2	2.39	1.02
13:D:165:A:H4'	13:D:166:U:C5'	1.89	1.02
15:L:110:A:H4'	15:L:111:C:C5'	1.89	1.01
1:A:1588:LYS:HD2	15:L:30:A:C2	1.95	1.01
7:R:75:PHE:CE2	14:E:35:A:N7	2.06	1.01
1:A:1488:ILE:HG23	1:A:1489:PRO:HD3	1.40	1.00
13:D:165:A:C4'	13:D:166:U:H5'	1.92	1.00
1:A:334:LYS:NZ	13:D:77:A:OP2	1.93	1.00
2:C:784:SER:HB2	2:C:787:LEU:HB3	1.42	1.00
1:A:1587:PHE:HE2	15:L:31:A:C5'	1.60	1.00
15:L:1116:A:H2'	15:L:1117:G:C8	1.95	1.00
1:A:934:ARG:HH22	15:L:30:A:H5'	1.25	0.99
14:E:49:A:H2'	14:E:50:G:H5'	1.41	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:L:110:A:C4'	15:L:111:C:H5'	1.92	0.99
15:L:1114:G:O6	31:X:38:LYS:NZ	1.95	0.99
1:A:1851:PHE:O	1:A:1881:THR:HA	1.62	0.99
1:A:2059:ILE:O	1:A:2063:TYR:HB2	1.61	0.99
8:S:6:ARG:NH1	14:E:84:C:O2'	1.96	0.99
16:M:495:A:H2'	16:M:496:U:C6	1.98	0.99
1:A:1775:ILE:HA	1:A:1785:ASP:O	1.62	0.98
7:R:179:LYS:HA	12:N:111:U:O2	1.63	0.98
13:D:75:A:H4'	13:D:76:U:H5'	1.43	0.97
4:O:379:LYS:HA	5:P:47:ARG:HH21	1.27	0.97
1:A:1587:PHE:CZ	15:L:31:A:C5'	2.47	0.96
15:L:1111:U:H5''	15:L:1111:U:H6	1.25	0.96
15:L:1097:G:N2	15:L:1119:C:O2	1.96	0.96
15:L:1101:C:N4	31:X:38:LYS:HZ3	1.64	0.95
1:A:1335:TRP:HD1	1:A:1367:ILE:HD12	1.28	0.95
15:L:1116:A:C2	15:L:1117:G:C4	2.54	0.94
1:A:1666:CYS:O	1:A:1670:ASP:CB	2.15	0.94
15:L:1111:U:O4'	28:U:30:ARG:HD3	1.67	0.94
1:A:1588:LYS:HD3	15:L:30:A:C2	2.00	0.94
7:R:47:PHE:CE1	14:E:37:U:N3	2.35	0.94
2:C:472:VAL:HB	2:C:575:ALA:O	1.68	0.94
7:R:75:PHE:HD2	14:E:35:A:N7	1.52	0.94
1:A:1379:MET:HE1	1:A:1620:TYR:H	1.31	0.94
15:L:1102:C:H2'	15:L:1103:C:C5	2.03	0.94
15:L:110:A:C2	29:V:2:LYS:CE	2.51	0.94
1:A:532:ASN:ND2	13:D:84:A:OP2	1.99	0.93
2:C:340:LYS:O	2:C:343:ASP:HB3	1.68	0.93
1:A:1081:TYR:O	1:A:1085:LYS:HB2	1.69	0.93
10:Z:63:PHE:O	10:Z:69:ASN:ND2	2.01	0.93
1:A:1335:TRP:CD1	1:A:1367:ILE:HD12	2.03	0.93
15:L:110:A:H4'	15:L:111:C:H5'	0.95	0.93
1:A:1588:LYS:HD2	15:L:30:A:H2	1.28	0.92
15:L:1116:A:C6	15:L:1117:G:C6	2.57	0.92
1:A:854:ARG:CZ	15:L:25:A:OP1	2.17	0.92
15:L:1099:G:C5	15:L:1100:A:C8	2.58	0.91
7:R:46:ARG:HD3	12:N:110:A:H2	0.93	0.91
7:R:75:PHE:CZ	14:E:35:A:C8	2.59	0.91
1:A:1594:GLN:O	1:A:1598:LEU:HB3	1.71	0.91
15:L:15:C:H41	19:I:209:ARG:CB	1.84	0.90
1:A:751:ASP:OD1	1:A:752:ALA:N	2.04	0.90
1:A:477:MET:HE1	2:C:278:LYS:HD3	1.50	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:R:75:PHE:CD2	14:E:35:A:C5	2.59	0.90
6:Q:208:TYR:HB2	6:Q:290:ILE:HD12	1.52	0.90
1:A:416:GLU:HG2	1:A:418:ASP:H	1.35	0.90
16:M:499:U:O2'	16:M:500:A:OP1	1.90	0.90
1:A:1860:VAL:HG21	16:M:502:C:H5''	1.54	0.89
7:R:138:TYR:OH	12:N:111:U:OP2	1.90	0.89
2:C:101:GLN:NE2	13:D:75:A:H61	1.71	0.89
7:R:108:VAL:HG23	7:R:109:LEU:HG	1.54	0.89
15:L:110:A:C2	29:V:2:LYS:HE2	2.08	0.89
7:R:234:ALA:HA	7:R:237:ARG:HD3	1.51	0.89
1:A:713:ASN:HD21	13:D:83:C:H4'	1.32	0.89
1:A:854:ARG:HH22	15:L:25:A:H5''	1.37	0.89
15:L:34:G:OP2	15:L:34:G:C8	2.26	0.89
7:R:76:PHE:HB2	7:R:91:HIS:HD2	1.38	0.89
15:L:1099:G:C6	15:L:1100:A:N7	2.41	0.89
1:A:1365:THR:O	1:A:1369:ASN:ND2	2.06	0.88
14:E:89:U:C6	19:I:179:ARG:HG2	2.08	0.88
10:Z:74:PRO:HA	10:Z:123:ILE:HG21	1.55	0.88
1:A:1576:GLU:OE1	1:A:1826:TYR:O	1.92	0.88
1:A:1863:HIS:O	1:A:1871:ALA:HB3	1.73	0.88
15:L:15:C:H41	19:I:209:ARG:HG2	1.36	0.88
7:R:161:ARG:O	7:R:165:SER:HB3	1.73	0.88
1:A:1748:ILE:O	1:A:1751:TYR:N	2.06	0.87
8:S:9:LEU:HD12	8:S:10:GLU:HB2	1.54	0.87
1:A:614:ARG:CZ	11:B:98:A:H4'	2.05	0.87
15:L:110:A:C2	29:V:2:LYS:HE3	2.10	0.87
13:D:165:A:H4'	13:D:166:U:H5'	0.95	0.86
7:R:23:PRO:O	7:R:37:TRP:NE1	2.06	0.86
2:C:266:VAL:HG22	2:C:312:ILE:HB	1.55	0.86
2:C:711:ALA:HB3	2:C:819:LYS:O	1.74	0.86
7:R:89:TYR:HD2	14:E:34:A:C2	1.93	0.86
15:L:1099:G:N7	15:L:1100:A:C8	2.43	0.86
1:A:585:ARG:NH2	1:A:733:GLN:O	2.09	0.86
14:E:91:A:N7	19:I:97:TYR:CE1	2.42	0.86
16:M:483:U:H3'	16:M:484:U:C5	2.10	0.86
7:R:118:ALA:O	7:R:129:SER:OG	1.93	0.85
1:A:839:HIS:CD2	13:D:95:C:N3	2.45	0.85
9:T:41:LEU:HD21	14:E:35:A:C2	2.11	0.85
1:A:320:ASP:OD1	1:A:508:GLN:NE2	2.09	0.85
4:O:407:PHE:HE1	4:O:414:LEU:HD13	1.41	0.85
1:A:1673:LEU:HA	1:A:1678:ILE:HB	1.58	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:365:GLU:HG3	2:C:366:ASN:H	1.41	0.85
1:A:137:GLU:OE2	1:A:140:ARG:NH2	2.10	0.85
15:L:1099:G:C5	15:L:1100:A:N7	2.44	0.85
16:M:484:U:H4'	16:M:485:U:H5'	1.59	0.84
1:A:1046:SER:HA	1:A:1251:TYR:O	1.77	0.84
1:A:366:GLU:HG3	1:A:372:ARG:HH11	1.41	0.84
1:A:1211:SER:O	1:A:1257:ASN:ND2	2.10	0.84
1:A:1405:ILE:HG22	1:A:1406:LEU:H	1.43	0.84
1:A:839:HIS:HD2	13:D:95:C:N3	1.75	0.84
1:A:1860:VAL:HG21	16:M:502:C:C5'	2.06	0.84
7:R:127:ILE:HB	14:E:39:G:N7	1.92	0.84
10:Z:60:VAL:HG13	10:Z:76:LEU:HD22	1.59	0.84
7:R:89:TYR:CD2	14:E:34:A:N3	2.46	0.84
25:G:86:ASN:HD21	26:H:32:LYS:HD3	1.43	0.84
7:R:253:LEU:O	7:R:257:ASN:CB	2.26	0.84
9:T:128:GLN:O	9:T:131:GLU:N	2.10	0.84
1:A:620:HIS:HB3	1:A:669:TYR:CE2	2.13	0.84
1:A:854:ARG:HH22	15:L:25:A:C5'	1.91	0.83
15:L:1102:C:H2'	15:L:1103:C:H6	1.42	0.83
12:N:101:U:O4	14:E:50:G:O2'	1.95	0.83
1:A:1587:PHE:HE2	15:L:31:A:O5'	1.59	0.83
4:O:354:ASN:ND2	4:O:369:ASP:OD1	2.11	0.83
2:C:734:CYS:SG	2:C:755:TYR:OH	2.35	0.83
1:A:128:TYR:HA	9:T:112:ASN:HD21	1.43	0.83
10:Z:60:VAL:O	10:Z:64:THR:OG1	1.97	0.83
2:C:770:ASN:OD1	2:C:771:GLY:N	2.11	0.83
15:L:1109:C:H41	31:X:109:LYS:H	1.21	0.83
3:J:2:SER:O	3:J:4:ASN:ND2	2.11	0.83
7:R:161:ARG:O	7:R:165:SER:CB	2.27	0.82
4:O:379:LYS:HD3	5:P:47:ARG:HH22	1.42	0.82
6:Q:13:CYS:N	6:Q:71:CYS:SG	2.52	0.82
1:A:1485:ASP:O	1:A:1490:ARG:NH2	2.12	0.82
1:A:978:ILE:HB	8:S:174:VAL:HA	1.61	0.82
2:C:308:ASP:HB3	2:C:310:ASN:HD22	1.44	0.82
7:R:75:PHE:HE2	14:E:35:A:C8	1.54	0.82
14:E:89:U:H6	19:I:179:ARG:HG2	1.42	0.82
10:Z:102:PHE:HB2	10:Z:117:ILE:HG21	1.60	0.82
1:A:1670:ASP:HA	1:A:1681:VAL:HG21	1.59	0.82
7:R:127:ILE:O	14:E:39:G:O6	1.96	0.82
7:R:75:PHE:CE2	14:E:35:A:H8	1.55	0.82
15:L:5:A:H5'	19:I:114:THR:HG21	0.83	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:378:LEU:O	2:C:381:LEU:N	2.13	0.82
1:A:1056:GLU:OE1	1:A:1060:LYS:NZ	2.12	0.81
10:Z:174:TRP:HZ3	10:Z:201:ARG:HD2	1.44	0.81
15:L:41:C:O2	16:M:494:G:N2	2.13	0.81
2:C:779:LEU:O	2:C:782:GLU:N	2.12	0.81
1:A:1889:LEU:O	1:A:1988:LEU:HA	1.79	0.81
7:R:73:CYS:HA	14:E:34:A:N1	1.95	0.81
4:O:193:ARG:HH22	4:O:237:ASP:H	1.28	0.81
1:A:2059:ILE:O	1:A:2063:TYR:CB	2.29	0.81
10:Z:201:ARG:NH2	10:Z:205:TYR:OH	2.13	0.81
2:C:748:SER:HB2	2:C:762:SER:HB3	1.63	0.81
24:F:19:LYS:NZ	32:Y:34:LEU:CB	2.44	0.81
1:A:1456:ARG:NH2	1:A:1460:GLU:OE2	2.13	0.81
2:C:712:ALA:HA	2:C:817:GLN:O	1.81	0.81
1:A:353:GLU:CG	13:D:104:G:O5'	2.28	0.81
7:R:87:CYS:HB3	7:R:91:HIS:CE1	2.15	0.81
1:A:381:SER:O	1:A:384:LYS:N	2.13	0.81
6:Q:47:LYS:NZ	14:E:30:G:O6	2.12	0.80
1:A:1538:ASN:OD1	1:A:1539:LEU:N	2.14	0.80
1:A:1711:VAL:HG13	1:A:1789:ASN:HB3	1.62	0.80
2:C:468:LEU:O	2:C:578:TYR:HA	1.82	0.80
26:H:74:ARG:NH2	30:W:64:HIS:O	2.14	0.80
7:R:165:SER:HA	7:R:170:ILE:HD11	1.62	0.80
1:A:1464:LYS:NZ	1:A:1479:GLU:O	2.15	0.80
10:Z:174:TRP:CZ3	10:Z:201:ARG:HD2	2.15	0.80
10:Z:78:ALA:O	10:Z:81:ALA:HB3	1.81	0.80
15:L:1109:C:N4	31:X:109:LYS:N	2.30	0.80
1:A:353:GLU:HG3	13:D:104:G:O5'	1.81	0.80
13:D:81:A:O2'	13:D:82:A:OP1	1.98	0.80
1:A:1195:PHE:HB3	1:A:1217:ARG:HE	1.47	0.80
14:E:89:U:C6	19:I:179:ARG:CG	2.65	0.80
15:L:119:G:H5'	30:W:99:ASP:OD2	1.82	0.80
1:A:1575:TRP:HA	1:A:1825:ILE:HG12	1.64	0.79
15:L:1099:G:H5''	15:L:1099:G:N3	1.97	0.79
15:L:39:A:H2'	15:L:40:U:C5'	2.12	0.79
6:Q:73:CYS:SG	6:Q:74:CYS:N	2.54	0.79
1:A:1859:ARG:O	1:A:1874:ALA:HA	1.83	0.79
1:A:542:HIS:C	1:A:544:LYS:H	1.86	0.79
1:A:681:LYS:O	1:A:684:LYS:HB3	1.81	0.79
1:A:716:ARG:NH2	13:D:112:C:C2	2.51	0.79
15:L:34:G:OP2	15:L:34:G:O4'	2.01	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1750:ARG:O	1:A:1754:ALA:HB2	1.83	0.79
4:O:248:ILE:O	4:O:262:LEU:HB2	1.83	0.79
1:A:1051:GLU:OE1	1:A:1204:ARG:NH2	2.15	0.79
1:A:2034:ILE:HG12	1:A:2041:PRO:HA	1.65	0.79
1:A:2018:ASN:ND2	1:A:2062:GLU:OE1	2.15	0.79
1:A:740:GLU:HG3	1:A:741:ILE:H	1.47	0.79
6:Q:61:CYS:O	6:Q:72:GLN:NE2	2.15	0.79
10:Z:37:LEU:HG	10:Z:79:LEU:HB2	1.65	0.79
16:M:485:U:H2'	16:M:485:U:OP2	1.82	0.79
1:A:1435:LYS:NZ	1:A:1550:LEU:O	2.16	0.78
2:C:252:LEU:O	2:C:255:GLN:N	2.16	0.78
1:A:477:MET:HE2	2:C:278:LYS:CE	2.11	0.78
15:L:18:U:O2	19:I:206:LYS:HD2	1.84	0.78
15:L:41:C:C2	16:M:494:G:N2	2.50	0.78
1:A:1130:ARG:NH1	1:A:1133:ASP:OD2	2.17	0.78
15:L:1101:C:H41	31:X:38:LYS:HZ3	1.29	0.78
4:O:121:GLN:NE2	5:P:49:SER:O	2.17	0.78
7:R:76:PHE:HB2	7:R:91:HIS:CD2	2.17	0.78
1:A:1082:ILE:O	1:A:1085:LYS:N	2.17	0.78
16:M:483:U:H3'	16:M:484:U:C4	2.18	0.78
1:A:1447:TRP:HB3	1:A:1451:PHE:HE2	1.49	0.78
2:C:163:ASP:OD2	2:C:548:ARG:NH1	2.17	0.77
15:L:1100:A:H61	15:L:1116:A:H61	1.30	0.77
1:A:1945:GLU:O	1:A:1948:MET:N	2.16	0.77
6:Q:71:CYS:HB3	6:Q:74:CYS:HB2	1.65	0.77
2:C:397:LYS:HG2	2:C:401:ARG:HH12	1.48	0.77
15:L:1111:U:C5'	15:L:1111:U:C6	2.65	0.77
10:Z:421:LYS:HG3	10:Z:468:ILE:HG12	1.67	0.77
1:A:1305:SER:OG	1:A:1307:GLU:OE1	2.03	0.77
1:A:997:GLN:OE1	1:A:1511:ARG:NH2	2.17	0.77
16:M:484:U:O2'	16:M:485:U:O4'	2.03	0.77
10:Z:129:VAL:HG12	10:Z:130:ILE:HG23	1.66	0.77
2:C:123:MET:HB2	2:C:199:LEU:HD23	1.66	0.77
1:A:353:GLU:HG2	13:D:104:G:P	2.25	0.77
15:L:1100:A:N1	15:L:1116:A:N1	2.33	0.77
10:Z:61:VAL:HA	10:Z:64:THR:HB	1.66	0.77
1:A:1151:GLU:O	1:A:1155:ALA:N	2.17	0.77
3:J:6:ILE:HD11	11:B:90:A:N1	2.00	0.77
1:A:1063:PHE:HE1	1:A:1086:ASN:HD22	1.31	0.77
2:C:833:VAL:O	2:C:837:GLN:HB2	1.84	0.77
7:R:253:LEU:O	7:R:257:ASN:HB3	1.85	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:992:ASP:OD1	1:A:1085:LYS:NZ	2.18	0.77
1:A:1362:LYS:NZ	3:J:13:GLY:O	2.18	0.76
1:A:404:ASN:ND2	2:C:927:MET:SD	2.57	0.76
1:A:1348:GLU:HG2	1:A:1446:THR:HB	1.67	0.76
1:A:763:MET:SD	1:A:783:LEU:HD11	2.25	0.76
2:C:969:LYS:O	2:C:972:ARG:N	2.18	0.76
4:O:127:ALA:HB3	4:O:428:GLN:HE21	1.50	0.76
1:A:1335:TRP:CH2	1:A:1339:LEU:HD13	2.20	0.76
2:C:667:GLU:N	2:C:667:GLU:OE1	2.17	0.76
19:I:114:THR:O	19:I:118:ASN:HB2	1.85	0.76
1:A:1111:SER:O	1:A:1114:PHE:HB3	1.83	0.76
1:A:1315:ARG:O	1:A:1318:GLY:N	2.18	0.76
1:A:1594:GLN:O	1:A:1598:LEU:CB	2.33	0.76
1:A:1180:GLU:HA	1:A:1183:THR:HG22	1.65	0.76
1:A:1717:LEU:HB2	1:A:1786:ALA:HB3	1.67	0.76
1:A:1810:PRO:O	1:A:1813:TYR:N	2.18	0.76
7:R:69:GLN:HG2	7:R:70:LEU:H	1.48	0.76
5:P:174:ASN:OD1	5:P:185:ARG:NH1	2.18	0.76
1:A:1815:LEU:O	1:A:1818:ARG:N	2.19	0.76
16:M:502:C:O2'	16:M:503:A:OP2	2.04	0.76
1:A:1736:VAL:HG22	1:A:1775:ILE:HB	1.68	0.76
10:Z:82:LEU:O	10:Z:85:SER:HB3	1.85	0.76
15:L:1109:C:H41	31:X:109:LYS:N	1.84	0.76
10:Z:475:GLU:OE2	10:Z:478:ARG:NH1	2.19	0.76
6:Q:16:CYS:SG	7:R:105:ARG:NH2	2.58	0.75
2:C:315:SER:O	2:C:319:GLY:N	2.20	0.75
9:T:41:LEU:HD11	14:E:35:A:N3	1.99	0.75
4:O:357:SER:OG	4:O:405:SER:OG	2.02	0.75
1:A:676:GLN:N	1:A:676:GLN:OE1	2.18	0.75
1:A:984:VAL:HG12	1:A:985:ASP:H	1.51	0.75
15:L:15:C:N4	19:I:209:ARG:HB2	2.01	0.75
1:A:158:LYS:NZ	7:R:33:TRP:O	2.18	0.75
1:A:579:LEU:HD22	1:A:619:PHE:HE1	1.52	0.75
2:C:132:ARG:HG3	2:C:206:LYS:HZ1	1.51	0.75
1:A:1870:VAL:HB	16:M:500:A:C5'	2.17	0.75
4:O:391:GLU:HB3	4:O:400:ARG:HB2	1.66	0.75
1:A:333:LYS:O	1:A:336:PHE:N	2.19	0.75
10:Z:454:ASP:HB3	10:Z:457:HIS:HB2	1.67	0.75
6:Q:104:ALA:HB1	6:Q:110:LYS:HB3	1.69	0.75
6:Q:217:TRP:O	6:Q:221:ASP:CB	2.32	0.75
2:C:214:ASP:OD1	2:C:215:ALA:N	2.20	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:F:102:LEU:C	32:Y:13:GLN:HB3	2.07	0.75
10:Z:89:ASP:O	10:Z:93:THR:OG1	2.04	0.75
1:A:340:LYS:O	1:A:343:ASN:N	2.17	0.74
1:A:900:PHE:N	1:A:1075:ASP:OD2	2.19	0.74
1:A:716:ARG:NH2	13:D:112:C:N3	2.36	0.74
2:C:117:ARG:NH2	2:C:156:ASP:O	2.20	0.74
14:E:64:U:O2'	14:E:65:U:OP1	2.05	0.74
4:O:379:LYS:HA	5:P:47:ARG:NH2	2.01	0.74
6:Q:205:PHE:HB2	6:Q:251:LEU:HB3	1.68	0.74
1:A:1338:SER:OG	1:A:1339:LEU:N	2.19	0.74
14:E:89:U:H6	19:I:179:ARG:CG	1.99	0.74
4:O:263:VAL:HG12	4:O:264:GLY:H	1.50	0.74
9:T:120:CYS:HB2	9:T:122:CYS:HB3	1.68	0.74
10:Z:212:LEU:O	10:Z:214:ILE:N	2.20	0.74
1:A:1377:SER:CB	11:B:95:U:OP1	2.36	0.74
4:O:229:THR:HG21	4:O:272:VAL:H	1.51	0.74
10:Z:92:GLU:O	10:Z:227:TYR:OH	2.05	0.74
10:Z:166:SER:OG	10:Z:169:THR:OG1	2.04	0.74
1:A:1122:ASP:OD1	1:A:1161:TYR:OH	2.05	0.74
1:A:790:TRP:O	1:A:793:TRP:N	2.21	0.74
1:A:1776:GLY:O	1:A:1784:TYR:HA	1.88	0.74
1:A:1144:PHE:HD2	1:A:1145:MET:HG2	1.50	0.74
1:A:847:LYS:O	1:A:850:GLY:N	2.21	0.74
4:O:327:CYS:SG	4:O:328:THR:N	2.61	0.74
1:A:796:ASN:ND2	1:A:861:GLN:OE1	2.21	0.73
2:C:360:ARG:HG2	2:C:362:LYS:HB2	1.69	0.73
15:L:5:A:H5''	19:I:114:THR:HG21	1.66	0.73
15:L:15:C:H41	19:I:209:ARG:HB2	1.52	0.73
10:Z:399:MET:SD	10:Z:439:ARG:HB3	2.28	0.73
1:A:1454:SER:HA	1:A:1487:GLY:HA2	1.69	0.73
1:A:326:ASN:ND2	2:C:924:GLY:O	2.22	0.73
1:A:776:GLN:HG2	1:A:777:LYS:H	1.54	0.73
1:A:976:GLN:HE22	1:A:1310:LYS:HD3	1.53	0.73
4:O:407:PHE:CE1	4:O:414:LEU:HD13	2.22	0.73
1:A:1042:SER:OG	1:A:1043:ARG:NH1	2.20	0.73
24:F:47:GLU:HG3	32:Y:15:TYR:CB	2.18	0.73
25:G:86:ASN:HD21	26:H:32:LYS:CD	2.02	0.73
1:A:670:LYS:NZ	13:D:101:C:OP1	2.19	0.73
15:L:1101:C:N4	31:X:38:LYS:NZ	2.36	0.73
10:Z:384:LEU:HB3	10:Z:419:PHE:HE1	1.53	0.73
10:Z:57:CYS:HB3	10:Z:94:LEU:HD13	1.69	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1052:THR:O	1:A:1167:ARG:HA	1.88	0.73
1:A:1282:ASP:OD1	1:A:1283:GLU:N	2.20	0.73
1:A:1058:ALA:O	1:A:1061:ILE:N	2.17	0.73
1:A:2043:PHE:HB3	1:A:2047:GLN:HB2	1.71	0.73
2:C:67:GLU:CD	2:C:68:HIS:H	1.92	0.73
10:Z:384:LEU:O	10:Z:387:PHE:N	2.22	0.73
1:A:1882:LEU:HB2	1:A:1991:ILE:HD11	1.71	0.73
14:E:89:U:C5	19:I:179:ARG:HB3	2.24	0.72
5:P:101:PRO:O	5:P:103:ASN:N	2.23	0.72
6:Q:209:ASN:HD22	6:Q:288:ILE:HA	1.54	0.72
2:C:407:ASN:OD1	2:C:408:LEU:N	2.20	0.72
1:A:329:TYR:CZ	2:C:919:ARG:HD2	2.24	0.72
1:A:488:ARG:NH1	13:D:81:A:H61	1.87	0.72
1:A:1539:LEU:O	1:A:1541:ALA:N	2.23	0.72
4:O:365:PHE:CZ	4:O:373:LEU:HD22	2.25	0.72
7:R:253:LEU:O	7:R:257:ASN:HB2	1.90	0.72
1:A:139:LEU:HG	1:A:570:GLN:HE22	1.54	0.72
6:Q:86:LEU:O	6:Q:89:HIS:N	2.21	0.72
14:E:65:U:O2'	14:E:67:C:OP2	2.07	0.72
12:N:109:U:OP2	12:N:109:U:C6	2.43	0.72
10:Z:122:SER:HB3	10:Z:158:CYS:HB3	1.72	0.72
1:A:1717:LEU:N	1:A:1786:ALA:O	2.21	0.72
2:C:317:LYS:HE2	2:C:418:GLN:HE22	1.55	0.72
1:A:1659:GLU:O	1:A:1663:PHE:HB3	1.90	0.72
2:C:135:ASN:N	2:C:233:ASP:OD2	2.22	0.72
2:C:833:VAL:O	2:C:837:GLN:CB	2.38	0.72
1:A:488:ARG:HH11	13:D:81:A:N6	1.88	0.72
1:A:1442:ARG:NH2	10:Z:302:SER:O	2.21	0.72
1:A:992:ASP:O	1:A:995:LEU:N	2.22	0.71
2:C:317:LYS:N	36:C:1500:GTP:O6	2.18	0.71
2:C:234:LEU:HD23	2:C:443:TYR:HB2	1.70	0.71
4:O:443:ASN:O	4:O:445:ASN:ND2	2.23	0.71
5:P:84:ASN:O	5:P:125:ARG:NH1	2.18	0.71
9:T:44:LYS:O	9:T:47:GLU:N	2.22	0.71
10:Z:471:GLY:O	10:Z:478:ARG:NH2	2.23	0.71
2:C:183:GLN:NE2	2:C:654:CYS:HA	2.04	0.71
4:O:365:PHE:HZ	4:O:373:LEU:HD22	1.55	0.71
1:A:978:ILE:HD12	8:S:174:VAL:HG22	1.72	0.71
2:C:271:ASP:OD2	36:C:1500:GTP:N1	2.23	0.71
2:C:760:LEU:O	2:C:764:ASN:ND2	2.23	0.71
3:J:27:ASN:OD1	3:J:28:ASN:N	2.23	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:Z:77:SER:OG	10:Z:120:CYS:SG	2.49	0.71
2:C:831:ILE:HG13	2:C:832:ASP:H	1.53	0.71
1:A:861:GLN:HE21	1:A:1097:HIS:HB3	1.54	0.71
1:A:1902:GLN:N	1:A:1902:GLN:OE1	2.24	0.71
4:O:362:ASP:OD2	4:O:379:LYS:NZ	2.22	0.71
2:C:775:ILE:HG22	2:C:776:ASN:H	1.55	0.71
13:D:174:G:OP1	13:D:174:G:H4'	1.90	0.71
15:L:41:C:H4'	15:L:42:U:OP1	1.89	0.71
7:R:209:ASP:H	7:R:212:TRP:HB2	1.56	0.71
6:Q:33:GLU:OE1	6:Q:33:GLU:N	2.22	0.71
2:C:682:SER:HA	2:C:714:PRO:HG3	1.73	0.71
2:C:855:PRO:HG2	2:C:944:VAL:HG21	1.71	0.71
15:L:1116:A:C6	15:L:1117:G:C5	2.79	0.71
7:R:206:LEU:HD12	7:R:207:PRO:HD2	1.73	0.71
1:A:342:LEU:HD13	1:A:392:ASN:HD22	1.56	0.71
2:C:706:LEU:HD21	2:C:834:MET:HE1	1.73	0.71
4:O:152:ASN:HD21	4:O:409:LYS:HB3	1.54	0.71
8:S:8:GLN:HB2	14:E:63:G:O2'	1.91	0.70
10:Z:73:ILE:HG23	10:Z:120:CYS:HB2	1.72	0.70
10:Z:392:ILE:HG12	10:Z:397:LEU:HD22	1.73	0.70
10:Z:440:LEU:HD12	10:Z:473:LEU:HD13	1.72	0.70
1:A:1513:GLU:O	1:A:1516:GLN:N	2.17	0.70
1:A:771:PRO:O	4:O:309:ARG:NH2	2.24	0.70
14:E:89:U:C6	19:I:179:ARG:HB3	2.27	0.70
2:C:90:LEU:HD22	4:O:211:LEU:HD22	1.72	0.70
1:A:688:TYR:O	1:A:691:PHE:N	2.20	0.70
2:C:719:MET:O	2:C:722:ASP:N	2.23	0.70
13:D:76:U:O2'	13:D:77:A:OP1	2.07	0.70
5:P:118:GLN:N	5:P:118:GLN:OE1	2.22	0.70
1:A:1142:ASN:OD1	1:A:1148:LYS:NZ	2.25	0.70
1:A:484:PHE:CB	13:D:81:A:N7	2.55	0.70
1:A:579:LEU:HD22	1:A:619:PHE:CE1	2.25	0.70
7:R:254:ILE:O	7:R:258:THR:CB	2.40	0.70
1:A:1860:VAL:HA	1:A:1873:LYS:O	1.92	0.70
19:I:200:ASN:O	19:I:204:ASN:HB2	1.91	0.70
4:O:125:TRP:HE1	4:O:437:GLU:CD	1.95	0.70
5:P:134:VAL:HG22	6:Q:111:ARG:HD3	1.73	0.70
6:Q:217:TRP:CD1	6:Q:218:LYS:N	2.59	0.70
13:D:173:U:H4'	13:D:174:G:OP1	1.91	0.70
10:Z:16:GLU:O	10:Z:20:MET:HB2	1.92	0.70
10:Z:39:GLU:OE2	10:Z:42:ARG:NH1	2.23	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:486:PHE:O	1:A:488:ARG:N	2.24	0.69
1:A:701:CYS:SG	1:A:702:GLY:N	2.64	0.69
2:C:362:LYS:O	2:C:364:PHE:N	2.26	0.69
15:L:1116:A:C2	15:L:1117:G:C5	2.80	0.69
10:Z:103:VAL:O	10:Z:107:ASN:ND2	2.24	0.69
1:A:1590:LEU:HD21	1:A:1598:LEU:HD13	1.74	0.69
1:A:933:GLU:N	1:A:933:GLU:OE1	2.15	0.69
25:G:86:ASN:HD21	26:H:32:LYS:CE	2.06	0.69
7:R:183:PHE:CE2	12:N:113:U:C5	2.80	0.69
1:A:1887:GLY:HA2	1:A:1991:ILE:HD12	1.73	0.69
6:Q:67:GLN:NE2	6:Q:114:SER:O	2.25	0.69
10:Z:88:PRO:HB3	10:Z:223:HIS:CD2	2.28	0.69
1:A:1058:ALA:HB1	1:A:1103:LEU:HB3	1.74	0.69
14:E:91:A:C5	19:I:97:TYR:CD1	2.81	0.69
10:Z:456:GLU:HA	10:Z:459:ARG:HH11	1.58	0.69
1:A:749:ARG:NH1	14:E:76:A:OP2	2.26	0.69
2:C:787:LEU:HD12	2:C:790:LYS:HD2	1.75	0.69
15:L:1116:A:C4	15:L:1117:G:C8	2.80	0.69
28:U:30:ARG:O	28:U:47:VAL:HG23	1.92	0.69
1:A:269:ASP:OD2	1:A:272:ASP:N	2.21	0.69
1:A:709:ARG:HH22	13:D:83:C:P	2.14	0.69
2:C:656:LEU:HD13	2:C:670:ILE:HD13	1.74	0.69
15:L:1102:C:O5'	15:L:1102:C:H6	1.76	0.69
6:Q:202:THR:OG1	6:Q:252:ARG:NE	2.19	0.69
1:A:889:TRP:HD1	1:A:890:LEU:HG	1.58	0.69
15:L:119:G:H4'	15:L:119:G:OP1	1.90	0.69
4:O:292:LEU:HD11	4:O:304:LEU:HD11	1.74	0.69
15:L:119:G:N7	29:V:20:LYS:HE2	2.08	0.69
6:Q:53:ASN:O	14:E:31:G:N1	2.26	0.69
15:L:110:A:H2	29:V:2:LYS:HE2	1.58	0.69
15:L:118:U:H4'	15:L:119:G:OP1	1.91	0.69
15:L:40:U:HO2'	15:L:41:C:H5	1.40	0.69
16:M:484:U:O3'	16:M:485:U:O4'	2.11	0.69
1:A:1280:SER:OG	10:Z:348:GLU:OE1	2.10	0.69
2:C:326:GLU:HG2	2:C:330:TYR:CE2	2.27	0.69
4:O:204:LYS:HE2	4:O:225:SER:HA	1.74	0.69
5:P:108:ASN:O	5:P:111:HIS:N	2.25	0.69
1:A:614:ARG:HH12	11:B:98:A:H4'	1.54	0.69
15:L:15:C:N4	19:I:209:ARG:HG2	2.08	0.69
1:A:1362:LYS:HZ3	3:J:14:SER:HA	1.59	0.68
1:A:590:TYR:OH	1:A:609:GLU:OE1	2.06	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:215:ALA:HB1	2:C:225:THR:HG22	1.74	0.68
4:O:225:SER:OG	4:O:245:ASP:OD1	2.10	0.68
1:A:1899:TRP:HH2	1:A:1909:ALA:HA	1.56	0.68
2:C:183:GLN:HE22	2:C:654:CYS:HA	1.57	0.68
2:C:340:LYS:O	2:C:344:PHE:N	2.24	0.68
14:E:64:U:O2'	14:E:65:U:P	2.51	0.68
1:A:1972:ASP:O	1:A:1975:SER:N	2.26	0.68
2:C:84:GLN:HE22	2:C:90:LEU:HA	1.58	0.68
5:P:226:LYS:O	5:P:229:ALA:N	2.27	0.68
1:A:1376:ASN:O	1:A:1377:SER:OG	2.11	0.68
1:A:416:GLU:HG2	1:A:418:ASP:N	2.08	0.68
2:C:711:ALA:CB	2:C:819:LYS:O	2.41	0.68
7:R:110:ASP:OD1	7:R:114:ARG:N	2.19	0.68
10:Z:402:LEU:HD22	10:Z:445:LEU:HD13	1.75	0.68
1:A:1020:ILE:HG13	1:A:1022:PRO:HD2	1.76	0.68
1:A:1905:LEU:HA	1:A:1908:LEU:HB3	1.75	0.68
1:A:1656:LYS:HD3	1:A:1949:LEU:HD12	1.76	0.68
1:A:1889:LEU:HB2	1:A:1989:PHE:HB2	1.76	0.68
2:C:101:GLN:HA	2:C:104:THR:O	1.93	0.68
2:C:168:VAL:HG21	2:C:175:LEU:HB2	1.76	0.68
1:A:768:GLU:O	4:O:309:ARG:NH1	2.25	0.68
7:R:54:GLN:HB2	7:R:58:HIS:CD2	2.28	0.68
2:C:67:GLU:HB3	2:C:69:PRO:HD2	1.74	0.68
2:C:736:ASP:OD1	2:C:737:ILE:N	2.27	0.68
2:C:775:ILE:N	2:C:818:TYR:O	2.26	0.68
10:Z:437:GLN:HG2	10:Z:473:LEU:HD21	1.76	0.68
1:A:151:SER:OG	1:A:152:LYS:N	2.24	0.68
1:A:1711:VAL:HG21	1:A:1771:THR:HG21	1.76	0.68
1:A:269:ASP:CG	1:A:271:GLN:H	1.97	0.68
2:C:355:HIS:HD2	2:C:360:ARG:HB3	1.59	0.68
2:C:858:LEU:HD22	2:C:937:TRP:HB3	1.74	0.68
15:L:39:A:H2'	15:L:40:U:H5'	1.75	0.68
1:A:618:SER:OG	1:A:725:TYR:HB3	1.93	0.68
1:A:940:ILE:O	1:A:943:ALA:N	2.26	0.68
1:A:477:MET:CE	2:C:278:LYS:HE3	2.17	0.68
15:L:15:C:N4	19:I:209:ARG:CG	2.53	0.68
15:L:120:G:C2	25:G:33:GLU:HG3	2.29	0.68
1:A:1842:GLU:OE1	1:A:1845:ASN:ND2	2.24	0.68
4:O:206:VAL:HG21	4:O:241:THR:HG21	1.74	0.68
1:A:1338:SER:O	1:A:1341:SER:OG	2.04	0.67
1:A:1340:ILE:HD11	1:A:1400:ILE:HD12	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1449:ASN:O	1:A:1452:LEU:N	2.28	0.67
1:A:426:PRO:HB3	10:Z:201:ARG:HE	1.59	0.67
1:A:934:ARG:NH2	15:L:30:A:H5'	2.05	0.67
4:O:284:SER:HB2	4:O:311:VAL:HB	1.77	0.67
6:Q:258:LEU:O	6:Q:262:PHE:CB	2.42	0.67
1:A:1161:TYR:HD1	1:A:1170:MET:HG2	1.60	0.67
4:O:118:LEU:HD21	5:P:48:GLN:HB3	1.76	0.67
1:A:895:PHE:HE2	1:A:1073:ILE:HG13	1.57	0.67
1:A:2041:PRO:HG2	1:A:2043:PHE:CZ	2.29	0.67
2:C:135:ASN:O	2:C:233:ASP:N	2.27	0.67
2:C:145:GLY:O	2:C:148:SER:OG	2.12	0.67
13:D:75:A:H4'	13:D:76:U:C5'	2.21	0.67
15:L:1116:A:C4	15:L:1117:G:N7	2.63	0.67
1:A:783:LEU:O	1:A:786:LEU:N	2.26	0.67
2:C:701:GLU:HG2	2:C:703:LEU:H	1.60	0.67
7:R:208:SER:HA	7:R:212:TRP:CG	2.29	0.67
26:H:74:ARG:NH1	30:W:65:CYS:SG	2.66	0.67
1:A:1169:TYR:CE2	1:A:1262:MET:HG2	2.29	0.67
1:A:1443:TYR:OH	1:A:1545:ASP:OD2	2.09	0.67
1:A:1801:SER:O	1:A:1804:THR:OG1	2.08	0.67
1:A:1576:GLU:CD	1:A:1826:TYR:O	2.33	0.67
2:C:383:LYS:O	2:C:387:TYR:HB2	1.94	0.67
2:C:307:ILE:HA	2:C:324:ILE:HD11	1.76	0.67
10:Z:319:ASN:HA	10:Z:322:LYS:HD3	1.74	0.67
1:A:1414:TRP:O	1:A:1417:GLN:N	2.23	0.67
1:A:1663:PHE:O	1:A:1666:CYS:HB3	1.95	0.67
1:A:269:ASP:OD1	1:A:270:SER:N	2.28	0.67
2:C:576:THR:HG22	2:C:592:PHE:HD2	1.60	0.67
7:R:146:LEU:HD23	7:R:147:ASN:H	1.60	0.67
10:Z:301:SER:O	10:Z:302:SER:OG	2.13	0.67
1:A:1279:VAL:O	1:A:1299:LYS:NZ	2.27	0.67
1:A:1893:ILE:HB	1:A:1985:GLN:H	1.59	0.67
2:C:355:HIS:CD2	2:C:360:ARG:HB3	2.30	0.67
15:L:119:G:C5'	30:W:99:ASP:HB2	2.25	0.67
4:O:285:SER:OG	4:O:287:ASP:OD1	2.13	0.67
6:Q:39:LEU:HD11	6:Q:111:ARG:HG3	1.75	0.67
8:S:8:GLN:NE2	8:S:10:GLU:O	2.28	0.67
1:A:763:MET:HE1	1:A:779:ALA:HB1	1.76	0.67
19:I:196:ILE:H	19:I:200:ASN:HD22	1.42	0.67
4:O:377:ASP:OD2	4:O:380:SER:N	2.27	0.67
2:C:129:ILE:HG22	2:C:131:GLU:H	1.59	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:S:35:THR:OG1	13:D:109:A:OP1	2.13	0.67
16:M:485:U:O2'	16:M:486:A:N7	2.27	0.67
7:R:87:CYS:HB3	7:R:91:HIS:HE1	1.56	0.67
1:A:1445:THR:OG1	1:A:1450:GLU:OE2	2.13	0.66
6:Q:9:PRO:HB2	6:Q:10:PRO:HD2	1.76	0.66
4:O:358:ILE:HG22	4:O:359:ASN:H	1.59	0.66
10:Z:317:ILE:HD13	10:Z:325:VAL:HG21	1.75	0.66
1:A:1034:ASN:ND2	1:A:1289:VAL:O	2.21	0.66
1:A:1362:LYS:O	1:A:1365:THR:OG1	2.13	0.66
1:A:572:CYS:SG	1:A:630:LYS:HD3	2.36	0.66
7:R:254:ILE:O	7:R:258:THR:HB	1.95	0.66
8:S:7:PRO:O	8:S:8:GLN:HB3	1.95	0.66
10:Z:301:SER:OG	10:Z:311:LYS:NZ	2.28	0.66
10:Z:386:LYS:O	10:Z:389:GLY:N	2.28	0.66
1:A:1762:ASP:OD1	1:A:1763:ASN:N	2.29	0.66
1:A:676:GLN:HE21	1:A:714:PHE:HB2	1.60	0.66
2:C:703:LEU:O	2:C:705:GLY:N	2.28	0.66
15:L:15:C:O2'	15:L:16:U:O4'	2.13	0.66
4:O:320:GLU:OE2	5:P:55:VAL:N	2.21	0.66
7:R:180:ASN:HB2	12:N:111:U:C5	2.31	0.66
1:A:1857:VAL:HG13	1:A:1894:ILE:HD13	1.78	0.66
1:A:1914:ALA:HB2	1:A:1943:PRO:HB2	1.78	0.66
13:D:44:A:O2'	13:D:45:A:OP2	2.10	0.66
7:R:8:SER:HA	7:R:61:LYS:HB3	1.77	0.66
9:T:118:SER:HB2	9:T:119:THR:HG23	1.77	0.66
29:V:82:LEU:HD12	29:V:85:ILE:HD11	1.77	0.66
1:A:1067:ASN:O	1:A:1071:ARG:HG2	1.95	0.66
15:L:18:U:C6	19:I:202:GLN:CG	2.79	0.66
1:A:128:TYR:HA	9:T:112:ASN:ND2	2.10	0.66
1:A:1990:ASN:ND2	1:A:1993:ASP:O	2.28	0.66
1:A:934:ARG:HH22	15:L:30:A:C5'	2.04	0.66
2:C:274:ILE:HG12	2:C:275:LEU:HD12	1.78	0.66
2:C:636:VAL:HG12	2:C:637:GLU:H	1.59	0.66
2:C:101:GLN:HE22	13:D:75:A:H61	1.43	0.66
1:A:1870:VAL:HB	16:M:500:A:H5"	1.76	0.66
1:A:905:TYR:HE2	1:A:907:ASN:HB2	1.60	0.66
1:A:1393:GLU:N	1:A:1393:GLU:OE1	2.23	0.66
1:A:834:ILE:HG12	1:A:840:VAL:HG11	1.78	0.66
1:A:960:THR:O	1:A:962:ARG:NH1	2.29	0.66
7:R:183:PHE:CD2	12:N:113:U:C6	2.84	0.66
1:A:402:TRP:HE1	1:A:405:ASN:ND2	1.94	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:634:ASP:O	1:A:637:VAL:N	2.29	0.65
2:C:779:LEU:HD12	2:C:782:GLU:HB2	1.78	0.65
2:C:829:VAL:HG12	2:C:830:ASN:H	1.61	0.65
15:L:39:A:H2'	15:L:40:U:H5''	1.75	0.65
4:O:148:ASP:OD1	4:O:150:VAL:N	2.22	0.65
4:O:187:ASP:OD1	4:O:188:VAL:N	2.27	0.65
1:A:1286:TRP:NE1	1:A:1348:GLU:OE1	2.30	0.65
1:A:220:THR:O	1:A:224:MET:HG2	1.96	0.65
1:A:585:ARG:HB2	7:R:33:TRP:CE3	2.31	0.65
1:A:477:MET:CE	2:C:278:LYS:HD3	2.26	0.65
1:A:374:ILE:HG21	2:C:966:PHE:HE1	1.59	0.65
14:E:56:A:O2'	14:E:57:U:OP1	2.13	0.65
25:G:77:LEU:HD21	25:G:80:ILE:HD12	1.79	0.65
7:R:46:ARG:NE	12:N:110:A:H2	1.91	0.65
2:C:130:PRO:HG2	2:C:558:LYS:NZ	2.10	0.65
6:Q:89:HIS:CD2	7:R:242:LEU:HD21	2.31	0.65
1:A:217:TRP:HZ3	1:A:703:PHE:HA	1.61	0.65
1:A:713:ASN:O	1:A:716:ARG:N	2.30	0.65
14:E:49:A:O2'	14:E:50:G:H5'	1.96	0.65
1:A:784:GLN:NE2	15:L:20:G:H5''	2.11	0.65
6:Q:53:ASN:OD1	6:Q:54:ASN:N	2.29	0.65
1:A:180:PRO:HA	1:A:187:LYS:HE2	1.79	0.65
1:A:295:GLY:O	1:A:298:TYR:N	2.25	0.65
1:A:687:ILE:HD11	1:A:706:PRO:HG2	1.79	0.65
1:A:353:GLU:CG	13:D:104:G:P	2.85	0.65
9:T:46:ASN:OD1	9:T:47:GLU:N	2.30	0.65
10:Z:113:SER:O	10:Z:117:ILE:HG12	1.97	0.65
1:A:1498:ASP:O	1:A:1501:THR:OG1	2.08	0.65
1:A:1561:LEU:O	1:A:1564:GLY:N	2.20	0.65
1:A:1850:LEU:HD13	1:A:1930:PRO:HB3	1.78	0.65
4:O:201:SER:OG	4:O:202:GLU:N	2.29	0.65
6:Q:258:LEU:O	6:Q:262:PHE:HB2	1.96	0.65
1:A:1682:THR:O	1:A:1702:THR:OG1	2.15	0.65
1:A:430:PRO:O	10:Z:182:GLN:NE2	2.22	0.65
1:A:177:GLU:HB3	1:A:712:LEU:HD11	1.78	0.65
1:A:1870:VAL:HG23	16:M:499:U:O2'	1.96	0.65
7:R:72:PHE:CD1	7:R:90:LEU:HB2	2.32	0.65
1:A:1090:ILE:HD11	1:A:1104:ILE:HD11	1.77	0.65
1:A:2077:THR:HA	1:A:2080:LYS:HG2	1.77	0.65
1:A:725:TYR:CD1	14:E:72:C:C1'	2.80	0.65
4:O:230:VAL:HG22	4:O:241:THR:HG22	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1082:ILE:HD13	1:A:1113:ILE:HD11	1.79	0.65
4:O:307:HIS:HD1	4:O:327:CYS:HB2	1.62	0.65
4:O:340:SER:OG	4:O:341:LEU:N	2.29	0.65
10:Z:307:GLU:OE2	10:Z:311:LYS:HE3	1.97	0.65
1:A:1113:ILE:O	1:A:1116:TYR:HB3	1.97	0.64
1:A:1843:LEU:O	1:A:1849:LYS:HD2	1.96	0.64
1:A:676:GLN:O	1:A:680:CYS:N	2.18	0.64
6:Q:242:VAL:O	7:R:161:ARG:NH2	2.30	0.64
7:R:47:PHE:CZ	14:E:37:U:N3	2.65	0.64
7:R:64:GLY:O	7:R:68:GLY:N	2.30	0.64
1:A:2013:ARG:HB3	1:A:2059:ILE:HD11	1.77	0.64
6:Q:77:ASP:OD1	6:Q:78:SER:N	2.29	0.64
1:A:1882:LEU:HB3	1:A:1889:LEU:HD23	1.79	0.64
1:A:929:LEU:O	1:A:934:ARG:NH1	2.31	0.64
12:N:104:G:C6	14:E:49:A:N1	2.65	0.64
1:A:1232:SER:HB2	8:S:135:ARG:NH2	2.12	0.64
16:M:500:A:H2'	16:M:502:C:H5	1.62	0.64
4:O:414:LEU:HB3	4:O:426:TRP:HB2	1.80	0.64
5:P:105:LEU:HD21	6:Q:12:ILE:HB	1.78	0.64
7:R:127:ILE:CB	14:E:39:G:N7	2.59	0.64
1:A:1750:ARG:O	1:A:1754:ALA:CB	2.46	0.64
1:A:563:ASP:OD1	1:A:564:TRP:N	2.30	0.64
1:A:954:ILE:HG12	1:A:991:THR:HG22	1.80	0.64
1:A:1587:PHE:CE2	15:L:31:A:O5'	2.40	0.64
7:R:89:TYR:CG	14:E:34:A:C2	2.84	0.64
1:A:1296:ARG:NH2	10:Z:426:GLU:OE2	2.30	0.64
2:C:272:ARG:HG3	36:C:1500:GTP:N2	2.13	0.64
6:Q:34:CYS:HB3	6:Q:36:ILE:H	1.62	0.64
1:A:1001:TYR:OH	1:A:1005:GLN:NE2	2.31	0.64
1:A:1792:ASN:OD1	1:A:1793:GLY:N	2.31	0.64
12:N:104:G:C6	14:E:49:A:C2	2.86	0.64
16:M:485:U:H4'	16:M:486:A:OP1	1.98	0.64
2:C:701:GLU:OE1	2:C:706:LEU:N	2.30	0.64
7:R:175:TYR:OH	7:R:180:ASN:OD1	2.16	0.64
9:T:101:GLU:OE1	14:E:1:G:O2'	2.14	0.64
1:A:1488:ILE:HG23	1:A:1489:PRO:CD	2.24	0.64
2:C:77:LEU:HD11	4:O:135:ILE:HG12	1.81	0.64
14:E:88:U:O2'	15:L:17:U:OP2	2.10	0.64
4:O:392:MET:HG3	4:O:393:VAL:H	1.63	0.64
1:A:1716:LEU:N	1:A:1719:GLU:OE1	2.30	0.63
26:H:77:ASN:OD1	30:W:49:ARG:HD3	1.97	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1154:LYS:HA	1:A:1159:ARG:NH2	2.13	0.63
1:A:644:VAL:HG12	1:A:648:GLN:HB2	1.80	0.63
1:A:353:GLU:HG2	13:D:104:G:OP1	1.97	0.63
6:Q:13:CYS:SG	6:Q:17:LEU:N	2.71	0.63
6:Q:89:HIS:O	6:Q:92:SER:OG	2.10	0.63
1:A:209:ILE:HG23	1:A:301:TRP:CD1	2.34	0.63
2:C:817:GLN:HE21	2:C:819:LYS:HE3	1.63	0.63
1:A:1377:SER:HB3	11:B:95:U:OP1	1.97	0.63
1:A:1777:ILE:HA	1:A:1783:MET:O	1.98	0.63
7:R:44:ASN:OD1	7:R:45:THR:N	2.31	0.63
10:Z:80:ILE:O	10:Z:84:ASN:N	2.21	0.63
1:A:1797:LEU:O	1:A:1801:SER:OG	2.15	0.63
2:C:398:ASN:OD1	2:C:401:ARG:NH2	2.31	0.63
2:C:946:ASP:HB3	2:C:949:ALA:HB2	1.79	0.63
13:D:83:C:O2'	13:D:84:A:O5'	2.15	0.63
15:L:14:C:OP2	19:I:209:ARG:NH2	2.32	0.63
1:A:1775:ILE:HG12	1:A:1786:ALA:HB2	1.81	0.63
1:A:725:TYR:HD1	14:E:72:C:O4'	1.82	0.63
15:L:1107:C:H6	15:L:1107:C:H5'	1.63	0.63
16:M:483:U:H5''	16:M:484:U:OP2	1.98	0.63
7:R:15:GLU:HA	7:R:18:LEU:HG	1.81	0.63
10:Z:186:LEU:HD23	10:Z:190:LEU:HD22	1.81	0.63
1:A:239:PHE:CD1	1:A:241:PRO:HD3	2.34	0.63
1:A:828:HIS:CE1	8:S:166:HIS:HD1	2.17	0.63
2:C:717:SER:O	2:C:721:GLN:HB2	1.99	0.63
4:O:242:ALA:HB2	4:O:248:ILE:HA	1.79	0.63
4:O:325:SER:HB3	4:O:334:TRP:HE1	1.62	0.63
7:R:97:GLU:O	7:R:100:GLY:N	2.32	0.63
1:A:2070:ASN:OD1	1:A:2071:ILE:N	2.32	0.63
1:A:314:LEU:O	1:A:317:PRO:HD2	1.99	0.63
1:A:676:GLN:NE2	1:A:714:PHE:HB2	2.13	0.63
2:C:317:LYS:HB2	36:C:1500:GTP:C6	2.34	0.63
4:O:156:ILE:HG12	4:O:166:VAL:HG22	1.80	0.63
4:O:308:LYS:HA	5:P:148:HIS:HE1	1.63	0.63
10:Z:178:ARG:NH2	10:Z:182:GLN:OE1	2.31	0.63
1:A:784:GLN:NE2	15:L:20:G:C5'	2.61	0.63
11:B:88:U:H2'	11:B:89:A:H4'	1.81	0.63
2:C:448:LEU:O	2:C:451:ASN:N	2.31	0.63
2:C:85:SER:O	2:C:88:THR:OG1	2.13	0.63
14:E:85:C:O4'	14:E:85:C:OP1	2.17	0.63
4:O:212:GLU:OE1	8:S:38:LYS:NZ	2.27	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:296:THR:CG2	13:D:33:U:OP2	2.47	0.62
2:C:743:ASN:HB3	2:C:746:LYS:HB3	1.81	0.62
1:A:1105:ARG:O	1:A:1110:ALA:HB3	1.99	0.62
1:A:1626:GLN:HE21	1:A:1631:GLY:HA2	1.64	0.62
2:C:269:LYS:HG2	36:C:1500:GTP:C6	2.34	0.62
10:Z:433:LEU:O	10:Z:437:GLN:HG3	1.99	0.62
1:A:1157:PRO:HG3	8:S:127:TRP:CE2	2.34	0.62
15:L:1098:C:H6	15:L:1098:C:O5'	1.83	0.62
15:L:50:U:H2'	15:L:51:C:C6	2.34	0.62
4:O:357:SER:HB2	4:O:365:PHE:HB3	1.80	0.62
5:P:34:ILE:HG23	5:P:35:ALA:H	1.64	0.62
10:Z:18:TRP:CZ2	10:Z:22:ARG:HD3	2.34	0.62
10:Z:386:LYS:HG2	10:Z:426:GLU:HB2	1.81	0.62
1:A:1289:VAL:HA	1:A:1295:GLN:O	1.99	0.62
1:A:1566:GLY:HA3	1:A:1816:ARG:HE	1.64	0.62
1:A:452:PHE:CZ	2:C:347:ARG:HG3	2.34	0.62
2:C:840:PRO:O	2:C:843:LYS:HB3	2.00	0.62
14:E:91:A:N7	19:I:97:TYR:CD1	2.67	0.62
16:M:500:A:C4	16:M:502:C:N4	2.67	0.62
10:Z:446:ASP:O	10:Z:449:PHE:N	2.32	0.62
10:Z:88:PRO:HB3	10:Z:223:HIS:CG	2.33	0.62
1:A:1852:VAL:HA	1:A:1881:THR:HG22	1.80	0.62
2:C:946:ASP:H	2:C:964:ARG:HD3	1.64	0.62
13:D:174:G:O5'	26:H:76:ASN:ND2	230.39	0.62
14:E:42:A:O2'	14:E:43:C:OP1	2.17	0.62
4:O:379:LYS:HD3	5:P:47:ARG:NH2	2.14	0.62
10:Z:161:LYS:HE2	10:Z:165:VAL:HG23	1.81	0.62
10:Z:287:ASN:O	10:Z:290:GLU:HB3	2.00	0.62
1:A:1852:VAL:HB	1:A:1935:VAL:HG22	1.81	0.62
1:A:475:ASP:O	1:A:478:SER:N	2.26	0.62
14:E:89:U:H6	19:I:179:ARG:CB	2.12	0.62
3:J:22:ARG:NH1	3:J:23:SER:O	2.33	0.62
15:L:119:G:O5'	26:H:76:ASN:ND2	2.32	0.62
4:O:223:HIS:CE1	4:O:249:LYS:HD2	2.35	0.62
10:Z:374:GLU:HA	10:Z:415:GLN:OE1	1.98	0.62
15:L:1099:G:C8	15:L:1100:A:C8	2.87	0.62
4:O:420:ASP:O	8:S:158:ASN:ND2	2.32	0.62
7:R:81:CYS:SG	14:E:35:A:N6	2.70	0.62
1:A:1150:LYS:HB3	1:A:1154:LYS:NZ	2.15	0.62
1:A:900:PHE:HA	1:A:1078:ILE:HD11	1.81	0.62
2:C:706:LEU:HD23	2:C:825:VAL:HA	1.80	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:Z:15:ARG:O	10:Z:19:GLU:HB2	2.00	0.62
1:A:1229:GLU:O	1:A:1232:SER:OG	2.16	0.62
1:A:1565:THR:HG1	1:A:1567:PHE:HD2	1.48	0.62
15:L:1120:G:H8	15:L:1120:G:H5''	1.65	0.62
6:Q:215:PRO:CG	6:Q:217:TRP:CD2	2.82	0.62
9:T:81:LEU:O	9:T:84:GLU:N	2.31	0.62
1:A:1212:ARG:HG2	1:A:1213:MET:H	1.64	0.61
1:A:713:ASN:HD22	13:D:83:C:H4'	1.62	0.61
10:Z:355:ARG:O	10:Z:358:GLN:N	2.33	0.61
10:Z:8:ASP:OD1	10:Z:9:GLU:N	2.32	0.61
1:A:2026:LEU:HB3	1:A:2041:PRO:HG3	1.82	0.61
2:C:195:GLY:HA3	2:C:545:LEU:HD13	1.82	0.61
2:C:136:VAL:HA	2:C:234:LEU:O	1.99	0.61
7:R:36:LYS:HZ2	14:E:41:A:H2	1.48	0.61
7:R:161:ARG:HG2	7:R:173:ILE:HD12	1.82	0.61
1:A:1476:ALA:HB3	1:A:1479:GLU:HG2	1.83	0.61
1:A:705:GLN:NE2	1:A:709:ARG:HG3	2.14	0.61
2:C:829:VAL:O	2:C:830:ASN:ND2	2.34	0.61
16:M:495:A:C8	16:M:496:U:C5	2.88	0.61
7:R:75:PHE:O	7:R:81:CYS:N	2.34	0.61
2:C:798:GLY:HA2	2:C:839:ILE:HG23	1.82	0.61
14:E:89:U:C6	19:I:179:ARG:CB	2.83	0.61
7:R:161:ARG:O	7:R:165:SER:OG	2.18	0.61
28:U:20:SER:OG	28:U:30:ARG:HD2	2.01	0.61
1:A:1051:GLU:O	1:A:1246:ALA:HA	2.00	0.61
1:A:815:TYR:O	1:A:818:SER:N	2.33	0.61
3:J:17:SER:O	11:B:91:A:H4'	2.00	0.61
2:C:142:LEU:HD12	2:C:929:GLN:HE21	1.65	0.61
2:C:500:ARG:NH1	2:C:536:SER:OG	2.34	0.61
1:A:1372:LYS:HG2	1:A:1383:PHE:CD2	2.35	0.61
2:C:79:GLU:OE1	4:O:174:LEU:N	2.34	0.61
15:L:18:U:C6	19:I:202:GLN:HG2	2.36	0.61
12:N:108:U:C4'	12:N:109:U:OP2	2.48	0.61
10:Z:14:GLN:NE2	10:Z:245:CYS:HB2	2.16	0.61
10:Z:73:ILE:HA	10:Z:76:LEU:HD12	1.82	0.61
1:A:1576:GLU:OE2	1:A:1826:TYR:O	2.18	0.61
1:A:258:ILE:HG12	1:A:641:LEU:HA	1.83	0.61
1:A:281:TYR:O	9:T:8:ARG:NH2	2.34	0.61
1:A:585:ARG:HD3	7:R:33:TRP:CD2	2.36	0.61
16:M:502:C:O2'	16:M:503:A:P	2.59	0.61
6:Q:103:GLU:HG2	6:Q:104:ALA:HB3	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:780:ARG:HH12	8:S:9:LEU:HD22	1.65	0.61
1:A:430:PRO:HB3	10:Z:198:PHE:HD2	1.65	0.61
2:C:415:TYR:HB2	2:C:420:PHE:HB2	1.82	0.61
13:D:175:G:N7	26:H:32:LYS:HD2	241.02	0.61
6:Q:103:GLU:OE1	7:R:131:ARG:NH1	2.32	0.61
7:R:173:ILE:HG12	7:R:184:VAL:HG13	1.82	0.61
1:A:934:ARG:HD2	15:L:31:A:C5	2.36	0.61
15:L:120:G:N7	26:H:32:LYS:HD2	2.15	0.61
4:O:125:TRP:HE1	4:O:437:GLU:CG	2.14	0.61
10:Z:479:SER:O	10:Z:482:THR:OG1	2.13	0.61
1:A:1667:GLN:O	1:A:1670:ASP:N	2.33	0.61
1:A:353:GLU:HG2	13:D:104:G:O5'	2.01	0.61
1:A:905:TYR:CE2	1:A:907:ASN:HB2	2.36	0.61
2:C:137:GLY:O	2:C:235:VAL:HA	2.01	0.61
2:C:802:ALA:HB2	2:C:843:LYS:HA	1.83	0.61
2:C:901:GLU:OE2	2:C:903:ARG:NE	2.31	0.61
5:P:127:VAL:HG11	14:E:32:U:O4	2.00	0.61
14:E:56:A:O2'	14:E:57:U:P	2.59	0.61
15:L:119:G:OP2	26:H:76:ASN:CB	2.49	0.61
6:Q:213:SER:OG	7:R:237:ARG:NE	2.33	0.61
7:R:152:LYS:HG2	7:R:154:ALA:H	1.66	0.61
7:R:76:PHE:O	7:R:79:GLY:N	2.23	0.61
10:Z:15:ARG:O	10:Z:19:GLU:CB	2.49	0.61
1:A:1386:ALA:O	1:A:1390:THR:HG23	2.02	0.60
1:A:1899:TRP:HB3	1:A:1905:LEU:HD21	1.83	0.60
1:A:608:LYS:NZ	14:E:43:C:H5'	2.16	0.60
1:A:744:THR:O	1:A:749:ARG:NH2	2.34	0.60
1:A:782:ILE:HA	1:A:785:HIS:HD2	1.66	0.60
1:A:890:LEU:O	1:A:894:SER:N	2.33	0.60
15:L:1116:A:N1	15:L:1117:G:C6	2.68	0.60
10:Z:40:SER:O	10:Z:44:LEU:CB	2.49	0.60
19:I:184:GLN:HA	19:I:187:LYS:HZ3	1.65	0.60
15:L:15:C:O2'	15:L:16:U:H5''	2.01	0.60
1:A:1712:SER:HB3	1:A:1724:PHE:HA	1.81	0.60
1:A:304:ASP:OD1	1:A:305:LEU:N	2.32	0.60
7:R:46:ARG:CZ	12:N:110:A:C2	2.84	0.60
7:R:254:ILE:O	7:R:258:THR:OG1	2.16	0.60
1:A:137:GLU:HB3	9:T:52:ILE:HD13	1.81	0.60
1:A:288:GLU:N	1:A:288:GLU:OE1	2.35	0.60
1:A:484:PHE:CG	13:D:81:A:N7	2.70	0.60
25:G:86:ASN:ND2	26:H:32:LYS:HD3	2.13	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:Q:219:ILE:O	6:Q:222:THR:OG1	2.15	0.60
8:S:5:HIS:HB3	15:L:21:G:N7	2.16	0.60
10:Z:40:SER:O	10:Z:44:LEU:HB2	2.01	0.60
1:A:1698:ALA:HB1	1:A:1766:MET:HB2	1.83	0.60
1:A:2013:ARG:NH1	1:A:2085:GLY:O	2.23	0.60
1:A:266:LEU:HD23	1:A:268:LEU:H	1.66	0.60
1:A:852:LEU:O	1:A:855:LEU:N	2.34	0.60
2:C:167:ASN:O	2:C:171:GLY:HA3	2.01	0.60
2:C:738:ASP:HA	2:C:768:PHE:CZ	2.37	0.60
4:O:303:VAL:O	4:O:304:LEU:HD23	2.01	0.60
15:L:119:G:H5''	30:W:99:ASP:HB2	1.82	0.60
10:Z:63:PHE:HD2	10:Z:76:LEU:HD21	1.65	0.60
4:O:160:ASN:HA	4:O:184:THR:OG1	2.01	0.60
10:Z:305:GLY:HA2	10:Z:342:PHE:CD1	2.37	0.60
1:A:933:GLU:HA	1:A:936:GLU:OE1	2.00	0.60
2:C:223:ASP:OD2	2:C:647:ASN:ND2	2.32	0.60
14:E:56:A:HO2'	14:E:57:U:P	2.25	0.60
4:O:111:ILE:HB	4:O:114:ARG:HH21	1.67	0.60
6:Q:257:GLU:OE2	6:Q:261:ARG:NH2	2.35	0.60
7:R:46:ARG:HD2	12:N:110:A:N1	2.15	0.60
1:A:1090:ILE:O	1:A:1096:SER:HA	2.02	0.60
1:A:1176:GLU:O	1:A:1180:GLU:HB2	2.02	0.60
1:A:705:GLN:HE21	1:A:709:ARG:HG3	1.65	0.60
2:C:116:THR:HG21	2:C:120:ARG:NH2	2.17	0.60
2:C:105:ILE:HG22	2:C:180:ASN:O	2.02	0.60
13:D:78:A:O2'	13:D:79:C:P	2.60	0.60
14:E:64:U:HO2'	14:E:65:U:P	2.25	0.60
6:Q:256:SER:O	6:Q:259:GLY:N	2.33	0.60
7:R:245:GLU:HG3	7:R:249:MET:HE2	1.84	0.60
9:T:41:LEU:HD11	14:E:35:A:C2	2.36	0.60
1:A:1156:HIS:CG	1:A:1157:PRO:HD2	2.37	0.60
1:A:1306:GLU:HA	1:A:1309:ILE:HD12	1.84	0.60
1:A:620:HIS:HB3	1:A:669:TYR:CZ	2.36	0.60
2:C:200:CYS:SG	2:C:210:ILE:HD12	2.42	0.60
2:C:326:GLU:O	2:C:329:SER:OG	2.13	0.60
1:A:1411:ASP:HB2	3:J:6:ILE:HG22	1.81	0.60
24:F:98:GLU:C	32:Y:53:PRO:CB	2.70	0.60
1:A:281:TYR:HB3	9:T:8:ARG:HH22	1.67	0.60
1:A:312:TYR:O	1:A:319:ARG:NH2	2.35	0.60
1:A:477:MET:CE	2:C:278:LYS:CE	2.79	0.60
2:C:915:GLU:HG2	2:C:928:CYS:HB3	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:D:174:G:OP2	26:H:76:ASN:CB	229.64	0.60
6:Q:98:ASN:O	6:Q:99:VAL:HG12	2.02	0.60
29:V:3:LEU:HD11	30:W:60:ALA:HB1	1.82	0.60
1:A:1145:MET:HE3	1:A:1160:LEU:HD13	1.84	0.59
2:C:245:VAL:HG11	2:C:295:ILE:HG22	1.84	0.59
2:C:398:ASN:HA	2:C:401:ARG:NH2	2.17	0.59
19:I:190:TYR:CZ	19:I:192:VAL:HB	2.37	0.59
7:R:230:PRO:HG2	12:N:114:U:C5	2.37	0.59
10:Z:305:GLY:HA2	10:Z:342:PHE:CE1	2.37	0.59
1:A:1025:VAL:HG21	1:A:1265:PHE:HD2	1.67	0.59
2:C:231:ALA:HB2	2:C:473:LEU:HD11	1.83	0.59
15:L:24:U:H5"	15:L:25:A:OP2	2.01	0.59
1:A:1682:THR:OG1	1:A:1702:THR:OG1	2.11	0.59
1:A:725:TYR:CE1	14:E:72:C:N1	2.69	0.59
1:A:779:ALA:O	1:A:782:ILE:HG22	2.02	0.59
2:C:778:THR:HG21	2:C:822:SER:HB2	1.85	0.59
1:A:484:PHE:HB2	13:D:81:A:N7	2.16	0.59
1:A:1588:LYS:HE2	15:L:32:G:OP2	2.02	0.59
1:A:1705:SER:HB3	1:A:1709:TRP:CE3	2.37	0.59
9:T:88:ASP:CG	9:T:91:LEU:H	2.05	0.59
3:J:19:HIS:ND1	11:B:91:A:C8	2.71	0.59
4:O:155:PHE:HZ	4:O:425:ILE:HD11	1.68	0.59
1:A:1368:GLN:O	1:A:1372:LYS:HG3	2.02	0.59
4:O:166:VAL:HB	4:O:176:THR:HG22	1.84	0.59
3:J:12:LYS:NZ	13:D:103:A:O4'	2.34	0.59
13:D:79:C:H3'	13:D:79:C:O2	2.03	0.59
15:L:1116:A:N1	15:L:1117:G:C5	2.71	0.59
28:U:66:GLY:HA2	28:U:69:ILE:HD12	1.85	0.59
10:Z:439:ARG:O	10:Z:443:SER:OG	2.12	0.59
2:C:718:LYS:HA	2:C:721:GLN:HB3	1.83	0.59
1:A:488:ARG:NH1	13:D:81:A:N6	2.49	0.59
7:R:241:GLU:O	7:R:244:LEU:HG	2.03	0.59
8:S:16:LYS:HE3	14:E:65:U:OP2	2.03	0.59
9:T:51:GLU:O	9:T:54:GLN:N	2.36	0.59
1:A:1857:VAL:HG13	1:A:1894:ILE:CD1	2.32	0.59
1:A:194:HIS:CD2	5:P:122:LEU:HD22	2.37	0.59
1:A:2050:THR:O	1:A:2053:SER:OG	2.12	0.59
1:A:1063:PHE:O	1:A:1066:LEU:N	2.36	0.59
1:A:143:ILE:HG13	1:A:144:ASN:N	2.18	0.59
1:A:275:TYR:CE2	1:A:306:PRO:HB2	2.38	0.59
1:A:954:ILE:O	1:A:957:TYR:N	2.35	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:277:LEU:HB3	2:C:279:LEU:HD13	1.85	0.59
25:G:83:LYS:NZ	26:H:75:CYS:O	2.35	0.59
19:I:106:GLU:HA	19:I:109:LEU:HD12	1.84	0.59
19:I:92:ARG:N	19:I:93:GLY:HA3	2.18	0.59
4:O:414:LEU:HG	4:O:426:TRP:HD1	1.67	0.59
5:P:209:GLU:O	5:P:212:ASP:HB3	2.03	0.59
6:Q:13:CYS:SG	6:Q:16:CYS:HB3	2.43	0.59
7:R:46:ARG:HH12	7:R:222:LEU:HD11	1.68	0.59
10:Z:405:ILE:HD13	10:Z:420:ILE:HD11	1.85	0.59
1:A:164:ALA:HB2	5:P:122:LEU:HD21	1.85	0.58
1:A:1716:LEU:HD23	1:A:1787:TYR:HB2	1.85	0.58
1:A:1893:ILE:HD12	1:A:1985:GLN:HG2	1.84	0.58
1:A:615:LEU:HD23	1:A:619:PHE:CD2	2.38	0.58
1:A:713:ASN:HD21	13:D:83:C:C4'	2.11	0.58
2:C:201:THR:HG22	2:C:207:SER:HB3	1.85	0.58
2:C:236:LEU:HD11	2:C:439:ILE:HG12	1.83	0.58
19:I:164:LEU:O	19:I:167:SER:OG	2.17	0.58
4:O:308:LYS:HA	5:P:148:HIS:CE1	2.38	0.58
1:A:1011:ASN:HD21	1:A:1142:ASN:HB2	1.67	0.58
1:A:1232:SER:HB2	8:S:135:ARG:CZ	2.32	0.58
1:A:1748:ILE:HG22	1:A:1752:VAL:HG23	1.85	0.58
1:A:284:ARG:NH2	13:D:33:U:C4	2.71	0.58
10:Z:475:GLU:O	10:Z:478:ARG:N	2.36	0.58
7:R:157:GLU:OE2	7:R:161:ARG:NE	2.36	0.58
8:S:6:ARG:NH2	14:E:85:C:OP1	2.36	0.58
10:Z:63:PHE:HZ	10:Z:72:LEU:HD12	1.69	0.58
10:Z:60:VAL:HG11	10:Z:80:ILE:HD11	1.84	0.58
1:A:1129:GLU:O	1:A:1132:THR:N	2.36	0.58
1:A:1052:THR:OG1	1:A:1168:ILE:HB	2.03	0.58
1:A:1925:PRO:O	1:A:1929:GLN:HG3	2.04	0.58
2:C:300:LYS:HG3	2:C:301:GLY:H	1.67	0.58
4:O:285:SER:O	4:O:287:ASP:N	2.36	0.58
4:O:307:HIS:ND1	4:O:327:CYS:HB2	2.17	0.58
6:Q:256:SER:C	6:Q:259:GLY:H	2.06	0.58
7:R:4:TRP:NE1	7:R:60:GLY:O	2.37	0.58
1:A:264:ILE:HG22	1:A:265:ASN:O	2.03	0.58
2:C:132:ARG:HG3	2:C:206:LYS:NZ	2.17	0.58
2:C:75:GLU:OE1	4:O:133:ARG:NE	2.36	0.58
2:C:797:GLN:O	2:C:800:TYR:N	2.36	0.58
2:C:832:ASP:HA	2:C:835:LYS:HG2	1.85	0.58
1:A:728:ASN:ND2	14:E:72:C:O2'	2.29	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:Z:100:LEU:HB2	10:Z:233:ASP:CG	2.23	0.58
1:A:1253:LYS:O	1:A:1274:ARG:NH2	2.35	0.58
1:A:1645:LEU:O	1:A:1648:ILE:N	2.37	0.58
1:A:143:ILE:HD13	1:A:570:GLN:HG2	1.86	0.58
2:C:373:PHE:HD1	2:C:377:ILE:HD12	1.67	0.58
1:A:1463:THR:O	1:A:1466:GLN:N	2.37	0.58
2:C:680:SER:OG	2:C:681:CYS:N	2.36	0.58
6:Q:87:ARG:NH2	6:Q:126:THR:OG1	2.36	0.58
7:R:256:ASN:OD1	7:R:257:ASN:N	2.36	0.58
10:Z:452:GLU:N	10:Z:452:GLU:OE1	2.37	0.58
1:A:2013:ARG:O	1:A:2016:LYS:N	2.34	0.58
1:A:834:ILE:O	1:A:837:GLY:N	2.37	0.58
1:A:923:TYR:HD1	1:A:926:LYS:HD3	1.68	0.58
2:C:269:LYS:HG2	36:C:1500:GTP:N1	2.19	0.58
2:C:373:PHE:CD1	2:C:377:ILE:HD12	2.39	0.58
7:R:117:PHE:CD2	14:E:39:G:C4	2.92	0.58
7:R:72:PHE:HD1	7:R:90:LEU:HB2	1.67	0.58
1:A:1624:LEU:HD21	1:A:1635:HIS:ND1	2.19	0.58
1:A:1797:LEU:O	1:A:1801:SER:CB	2.52	0.58
1:A:2013:ARG:HB3	1:A:2059:ILE:CD1	2.33	0.58
2:C:746:LYS:O	2:C:749:LYS:N	2.37	0.58
14:E:53:A:H5'	14:E:54:U:OP2	2.02	0.58
15:L:120:G:N1	25:G:33:GLU:O	2.36	0.58
16:M:490:A:H2'	16:M:491:C:C6	2.38	0.58
6:Q:34:CYS:SG	6:Q:61:CYS:N	2.76	0.58
1:A:2019:GLU:O	1:A:2022:ALA:N	2.34	0.58
1:A:235:LYS:O	1:A:648:GLN:NE2	2.37	0.58
1:A:717:GLY:HA3	13:D:84:A:O2'	2.04	0.58
14:E:14:C:H4'	14:E:15:C:O5'	2.04	0.58
7:R:180:ASN:ND2	12:N:111:U:C4	2.72	0.58
4:O:125:TRP:HZ2	4:O:432:ALA:HB1	1.68	0.58
4:O:414:LEU:HD12	4:O:415:ILE:H	1.68	0.58
7:R:255:ASN:O	7:R:259:ASN:ND2	2.30	0.58
10:Z:334:LEU:HD22	10:Z:380:GLN:HB3	1.85	0.58
1:A:1181:GLU:O	1:A:1184:ASP:HB2	2.04	0.57
1:A:782:ILE:HD12	1:A:785:HIS:CD2	2.39	0.57
1:A:901:PRO:HB2	1:A:955:LYS:HE3	1.86	0.57
1:A:946:ASN:HB3	1:A:949:ASP:HB3	1.85	0.57
2:C:249:VAL:O	2:C:253:ILE:HG12	2.03	0.57
6:Q:53:ASN:O	14:E:31:G:N2	2.37	0.57
7:R:36:LYS:NZ	14:E:41:A:H2	2.02	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:580:ASN:O	1:A:583:ILE:N	2.36	0.57
1:A:746:THR:OG1	1:A:749:ARG:NH2	2.37	0.57
2:C:326:GLU:HG2	2:C:330:TYR:HE2	1.69	0.57
2:C:89:PRO:O	2:C:91:VAL:N	2.35	0.57
15:L:119:G:C5	29:V:20:LYS:HE2	2.39	0.57
7:R:19:PRO:HB3	14:E:36:U:O4	2.03	0.57
7:R:249:MET:HA	7:R:252:HIS:HD2	1.68	0.57
15:L:112:A:N7	30:W:63:ARG:NE	2.51	0.57
1:A:1265:PHE:HE1	1:A:1346:PHE:HD1	1.52	0.57
1:A:480:TYR:CE2	2:C:275:LEU:HD23	2.39	0.57
2:C:655:LEU:O	2:C:658:ASP:N	2.36	0.57
10:Z:159:GLY:O	10:Z:163:ALA:HB3	2.05	0.57
10:Z:476:ASP:O	10:Z:479:SER:OG	2.16	0.57
1:A:1601:ILE:HG12	1:A:1604:ARG:HH22	1.69	0.57
1:A:1716:LEU:HA	1:A:1787:TYR:HA	1.86	0.57
1:A:933:GLU:O	1:A:936:GLU:N	2.37	0.57
2:C:225:THR:O	2:C:228:ALA:N	2.37	0.57
13:D:78:A:O2'	13:D:79:C:O5'	2.18	0.57
1:A:1860:VAL:HG11	16:M:502:C:H5'	1.87	0.57
4:O:148:ASP:HB2	4:O:154:TRP:CE2	2.39	0.57
7:R:115:GLU:N	7:R:115:GLU:OE1	2.37	0.57
24:F:47:GLU:HG3	32:Y:15:TYR:CG	2.39	0.57
1:A:426:PRO:HB3	10:Z:201:ARG:NE	2.19	0.57
1:A:137:GLU:O	1:A:140:ARG:N	2.37	0.57
1:A:1805:ILE:HG23	1:A:1809:ASN:HD22	1.69	0.57
2:C:682:SER:O	2:C:854:ILE:HB	2.04	0.57
3:J:6:ILE:HD11	11:B:90:A:H61	1.69	0.57
4:O:157:THR:HG21	4:O:423:ILE:HD11	1.85	0.57
6:Q:27:LYS:HG3	6:Q:44:TYR:HE1	1.69	0.57
7:R:159:ARG:HD3	7:R:204:LEU:HB3	1.87	0.57
7:R:47:PHE:CZ	14:E:37:U:C2	2.93	0.57
10:Z:100:LEU:HB2	10:Z:233:ASP:OD2	2.05	0.57
10:Z:85:SER:HB2	10:Z:220:TYR:HE1	1.70	0.57
1:A:1014:LYS:HG3	1:A:1016:SER:OG	2.04	0.57
1:A:347:PRO:HG3	3:J:2:SER:N	2.20	0.57
4:O:382:HIS:CE1	4:O:442:TRP:H	2.22	0.57
10:Z:410:GLU:OE1	10:Z:411:GLU:N	2.38	0.57
10:Z:459:ARG:O	10:Z:463:ASN:HB3	2.05	0.57
1:A:1182:LEU:O	1:A:1185:GLU:N	2.38	0.57
1:A:1335:TRP:HD1	1:A:1367:ILE:CD1	2.12	0.57
1:A:185:GLN:HG2	1:A:263:PRO:HD3	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:R:28:LEU:HG	7:R:29:THR:HG23	1.87	0.57
1:A:570:GLN:O	1:A:574:GLN:HG2	2.05	0.57
6:Q:260:GLU:O	6:Q:264:SER:N	2.32	0.57
1:A:1616:ARG:NH2	1:A:1744:ASP:OD1	2.38	0.57
1:A:374:ILE:HG12	2:C:969:LYS:HG3	1.86	0.57
1:A:725:TYR:CE1	14:E:72:C:C2	2.92	0.57
1:A:725:TYR:HE1	14:E:72:C:N1	2.03	0.57
6:Q:104:ALA:HB1	6:Q:110:LYS:CB	2.35	0.57
1:A:1335:TRP:HH2	1:A:1339:LEU:HD13	1.70	0.57
1:A:1679:GLU:HG2	1:A:1706:VAL:HA	1.87	0.57
1:A:252:GLU:OE1	1:A:252:GLU:N	2.35	0.57
1:A:266:LEU:HG	1:A:267:PRO:HD2	1.86	0.57
2:C:679:GLU:OE1	2:C:807:PRO:HD2	2.05	0.57
2:C:858:LEU:HB3	2:C:937:TRP:CE3	2.40	0.57
5:P:30:LEU:O	5:P:33:GLN:N	2.38	0.57
9:T:122:CYS:HB2	9:T:145:CYS:HB2	1.86	0.57
10:Z:326:VAL:HG11	10:Z:364:THR:HG21	1.87	0.57
14:E:42:A:HO2'	14:E:43:C:P	2.28	0.56
15:L:52:A:H8	15:L:52:A:O5'	1.88	0.56
6:Q:107:ASP:O	6:Q:110:LYS:HG2	2.04	0.56
8:S:7:PRO:HD2	15:L:20:G:N3	2.19	0.56
10:Z:143:LEU:HB3	10:Z:176:LYS:NZ	2.20	0.56
1:A:1710:GLU:HA	1:A:1727:LEU:O	2.04	0.56
1:A:1863:HIS:O	1:A:1871:ALA:CB	2.51	0.56
1:A:320:ASP:O	1:A:508:GLN:NE2	2.37	0.56
1:A:558:GLN:NE2	9:T:107:ARG:HH12	2.03	0.56
2:C:716:ASP:CG	2:C:719:MET:H	2.09	0.56
15:L:12:U:H4'	19:I:92:ARG:HH22	1.70	0.56
4:O:304:LEU:HB3	4:O:334:TRP:CZ3	2.41	0.56
8:S:10:GLU:HG2	8:S:11:ALA:H	1.69	0.56
15:L:119:G:O6	29:V:20:LYS:HB3	2.05	0.56
1:A:1490:ARG:O	1:A:1492:SER:N	2.38	0.56
1:A:1881:THR:OG1	1:A:1890:PHE:HB2	2.05	0.56
1:A:1902:GLN:HE21	1:A:1908:LEU:HD21	1.71	0.56
1:A:2043:PHE:HD2	1:A:2048:TRP:CD2	2.23	0.56
1:A:909:THR:O	1:A:913:VAL:HG23	2.05	0.56
2:C:716:ASP:HB3	2:C:719:MET:CB	2.35	0.56
1:A:296:THR:HB	13:D:32:G:H5"	1.86	0.56
5:P:216:ARG:HA	5:P:219:ILE:HD12	1.88	0.56
7:R:150:HIS:O	7:R:152:LYS:N	2.38	0.56
1:A:1701:ILE:O	1:A:1733:TRP:HA	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:284:ARG:HB2	1:A:287:GLU:OE2	2.04	0.56
2:C:772:ASN:HB3	2:C:816:VAL:H	1.70	0.56
2:C:772:ASN:N	2:C:772:ASN:OD1	2.35	0.56
2:C:858:LEU:HB3	2:C:937:TRP:HE3	1.70	0.56
16:M:497:A:C5	16:M:498:C:N4	2.73	0.56
4:O:154:TRP:CD1	4:O:154:TRP:N	2.73	0.56
6:Q:48:THR:OG1	6:Q:49:SER:N	2.37	0.56
1:A:978:ILE:O	8:S:175:ARG:HB3	2.05	0.56
1:A:376:ARG:O	1:A:377:VAL:HB	2.05	0.56
2:C:99:LYS:HG2	13:D:43:G:C5'	2.36	0.56
9:T:90:LEU:O	9:T:93:ALA:N	2.38	0.56
1:A:1962:ARG:HG3	1:A:2085:GLY:HA3	1.87	0.56
1:A:744:THR:HG22	14:E:75:A:OP1	2.06	0.56
1:A:865:ARG:O	1:A:868:GLN:N	2.36	0.56
2:C:702:ASN:OD1	2:C:844:LYS:NZ	2.36	0.56
2:C:885:GLY:HA2	2:C:907:PRO:HD3	1.88	0.56
15:L:40:U:O2'	15:L:41:C:H5	1.87	0.56
7:R:230:PRO:CG	12:N:114:U:C4	2.88	0.56
1:A:402:TRP:CG	1:A:402:TRP:O	2.59	0.56
2:C:463:THR:O	2:C:465:GLU:HG2	2.06	0.56
6:Q:87:ARG:NH2	6:Q:122:GLY:O	2.37	0.56
29:V:43:VAL:HG11	29:V:85:ILE:HD12	1.87	0.56
10:Z:122:SER:O	10:Z:125:PHE:N	2.38	0.56
1:A:1626:GLN:HB2	1:A:1633:PHE:CE1	2.41	0.56
1:A:421:ALA:HB3	1:A:469:ILE:HD12	1.87	0.56
2:C:116:THR:HG22	2:C:158:HIS:CD2	2.41	0.56
2:C:865:ASP:OD1	2:C:866:ILE:N	2.39	0.56
2:C:242:VAL:HG13	2:C:897:THR:HG21	1.88	0.56
12:N:101:U:H3'	12:N:101:U:H6	1.71	0.56
6:Q:119:LYS:HE3	6:Q:123:ALA:HB1	1.87	0.56
10:Z:368:ASN:HA	10:Z:372:ASP:HB3	1.88	0.56
1:A:1424:HIS:CD2	3:J:6:ILE:HG21	2.40	0.56
1:A:1447:TRP:HB3	1:A:1451:PHE:CE2	2.36	0.56
1:A:209:ILE:HG22	1:A:211:PRO:HD2	1.88	0.56
1:A:854:ARG:NH1	15:L:25:A:OP1	2.39	0.56
15:L:41:C:O2'	15:L:42:U:O5'	2.23	0.56
15:L:51:C:H6	15:L:51:C:O5'	1.89	0.56
1:A:589:THR:OG1	7:R:39:GLN:NE2	2.39	0.56
6:Q:53:ASN:ND2	7:R:69:GLN:HA	2.21	0.56
24:F:19:LYS:HZ3	32:Y:34:LEU:CB	2.18	0.56
1:A:1431:HIS:HB2	1:A:1433:ASP:O	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:Z:118:LEU:HA	10:Z:121:LEU:HD12	1.87	0.56
1:A:1049:LEU:HA	1:A:1170:MET:O	2.05	0.56
1:A:1395:GLY:HA3	1:A:1609:TRP:CD1	2.41	0.56
1:A:740:GLU:HG3	1:A:741:ILE:N	2.20	0.56
1:A:861:GLN:NE2	1:A:1097:HIS:HB3	2.20	0.56
1:A:878:GLU:O	1:A:881:THR:OG1	2.21	0.56
2:C:187:ARG:NH1	2:C:653:ASP:OD2	2.38	0.56
16:M:499:U:C2'	16:M:500:A:H5'	2.35	0.56
4:O:380:SER:OG	4:O:381:GLY:N	2.39	0.56
6:Q:61:CYS:HB3	6:Q:63:ARG:H	1.71	0.56
1:A:1203:ASN:ND2	1:A:1213:MET:O	2.38	0.55
1:A:1050:LEU:HD23	1:A:1248:VAL:HG22	1.87	0.55
1:A:1354:GLU:OE2	1:A:1408:PRO:HG2	2.06	0.55
1:A:461:LEU:HD12	1:A:462:LEU:HD12	1.88	0.55
25:G:77:LEU:HD21	25:G:80:ILE:CD1	2.36	0.55
15:L:15:C:N4	19:I:209:ARG:CB	2.58	0.55
15:L:1100:A:C2	15:L:1101:C:C2	2.95	0.55
15:L:1097:G:N1	15:L:1119:C:N3	2.50	0.55
9:T:98:THR:OG1	9:T:99:GLY:N	2.39	0.55
15:L:1105:C:N4	31:X:97:LYS:NZ	2.54	0.55
1:A:1705:SER:HB3	1:A:1709:TRP:CD2	2.41	0.55
2:C:261:VAL:HG12	2:C:262:ALA:H	1.71	0.55
2:C:660:ARG:HH22	2:C:670:ILE:HD12	1.71	0.55
2:C:84:GLN:HG2	2:C:88:THR:OG1	2.07	0.55
15:L:18:U:C6	19:I:202:GLN:HG3	2.42	0.55
4:O:138:HIS:CE1	4:O:159:SER:HB2	2.41	0.55
4:O:200:VAL:HG11	4:O:230:VAL:HG23	1.88	0.55
7:R:55:PRO:HG2	7:R:166:ARG:HD2	1.88	0.55
10:Z:130:ILE:HD11	10:Z:135:ILE:HD11	1.89	0.55
10:Z:69:ASN:HB3	10:Z:73:ILE:HG13	1.88	0.55
1:A:1508:HIS:HB2	1:A:1529:ASN:ND2	2.21	0.55
1:A:1562:PHE:HB2	1:A:1609:TRP:HH2	1.71	0.55
1:A:1755:LYS:HB3	1:A:1759:TYR:CE2	2.41	0.55
16:M:499:U:O5'	16:M:499:U:H6	1.89	0.55
4:O:155:PHE:HD2	4:O:167:TRP:CD1	2.25	0.55
6:Q:118:VAL:HG23	6:Q:119:LYS:O	2.06	0.55
10:Z:361:TYR:O	10:Z:364:THR:N	2.39	0.55
16:M:496:U:H3'	16:M:497:A:H5''	1.87	0.55
1:A:1870:VAL:HG23	16:M:499:U:C2'	2.36	0.55
4:O:134:VAL:HG22	4:O:424:LYS:HG2	1.88	0.55
4:O:328:THR:OG1	4:O:329:ASP:N	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1679:GLU:HB2	1:A:1704:GLU:O	2.06	0.55
1:A:382:GLU:OE1	1:A:382:GLU:N	2.28	0.55
2:C:291:ILE:O	2:C:294:ASN:N	2.40	0.55
2:C:545:LEU:O	2:C:545:LEU:HD12	2.06	0.55
15:L:7:C:OP1	19:I:174:LYS:CE	2.55	0.55
16:M:499:U:H2'	16:M:500:A:H5'	1.89	0.55
1:A:1183:THR:O	1:A:1187:LEU:HB2	2.06	0.55
2:C:234:LEU:HD11	2:C:439:ILE:HG23	1.88	0.55
7:R:97:GLU:O	7:R:100:GLY:CA	2.55	0.55
2:C:636:VAL:HG12	2:C:637:GLU:N	2.21	0.55
15:L:1102:C:H2'	15:L:1103:C:H5	1.70	0.55
16:M:487:A:H2'	16:M:488:G:H8	1.70	0.55
16:M:495:A:N7	16:M:496:U:C4	2.74	0.55
4:O:333:SER:OG	4:O:334:TRP:N	2.40	0.55
4:O:396:LEU:O	4:O:399:GLU:N	2.21	0.55
1:A:1511:ARG:O	1:A:1515:LYS:HG2	2.06	0.55
1:A:1739:ARG:O	1:A:1778:ASP:HA	2.06	0.55
1:A:327:TYR:HD2	1:A:328:TYR:CD1	2.25	0.55
1:A:665:GLY:HA2	1:A:667:TYR:CE1	2.42	0.55
15:L:28:U:C2'	15:L:29:C:H5'	2.37	0.55
4:O:148:ASP:CG	4:O:150:VAL:H	2.08	0.55
4:O:187:ASP:OD2	4:O:230:VAL:N	2.26	0.55
1:A:742:VAL:HG12	4:O:224:LEU:HD23	1.89	0.55
4:O:414:LEU:O	4:O:425:ILE:HA	2.07	0.55
8:S:8:GLN:CB	14:E:63:G:O2'	2.54	0.55
4:O:244:ARG:HH12	8:S:8:GLN:NE2	2.05	0.55
1:A:1232:SER:O	1:A:1234:VAL:N	2.40	0.55
1:A:1343:PHE:HE2	1:A:1402:ALA:HB3	1.72	0.55
1:A:249:LEU:O	1:A:249:LEU:HD12	2.07	0.55
2:C:897:THR:O	2:C:899:LEU:N	2.37	0.55
15:L:39:A:C2'	15:L:40:U:C5'	2.83	0.55
4:O:125:TRP:HE1	4:O:437:GLU:HG3	1.71	0.55
6:Q:240:LEU:HD13	6:Q:251:LEU:HD13	1.87	0.55
7:R:180:ASN:ND2	12:N:111:U:O4	2.40	0.55
10:Z:105:GLN:HB3	10:Z:110:ASP:HB3	1.88	0.55
1:A:1335:TRP:CZ3	1:A:1339:LEU:HD22	2.42	0.55
2:C:246:THR:O	2:C:249:VAL:N	2.38	0.55
2:C:493:LEU:HB2	2:C:556:ALA:HB3	1.88	0.55
2:C:607:LEU:HD22	2:C:668:ILE:HD12	1.89	0.55
15:L:1116:A:N3	15:L:1117:G:C8	2.74	0.55
15:L:23:U:C4	15:L:26:G:O4'	2.59	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:O:224:LEU:HB2	4:O:245:ASP:OD1	2.07	0.55
32:Y:44:PRO:O	32:Y:69:ASP:CB	2.54	0.55
10:Z:89:ASP:O	10:Z:93:THR:CB	2.54	0.55
1:A:1026:TYR:HA	1:A:1286:TRP:HZ3	1.72	0.54
1:A:1153:GLU:O	1:A:1159:ARG:NE	2.40	0.54
1:A:367:PHE:O	1:A:372:ARG:NH2	2.41	0.54
2:C:145:GLY:HA3	2:C:268:ASN:ND2	2.22	0.54
4:O:259:VAL:HG12	4:O:260:ILE:HG13	1.89	0.54
10:Z:355:ARG:O	10:Z:358:GLN:HB3	2.07	0.54
10:Z:412:SER:O	10:Z:417:ARG:NH1	2.39	0.54
10:Z:459:ARG:O	10:Z:463:ASN:CB	2.55	0.54
1:A:1699:ALA:HB2	1:A:1767:TYR:HD1	1.72	0.54
1:A:366:GLU:HG3	1:A:372:ARG:NH1	2.17	0.54
1:A:551:LEU:HG	1:A:557:PHE:CE2	2.41	0.54
2:C:477:ASP:HB2	2:C:628:TYR:CE2	2.42	0.54
2:C:646:GLY:HA3	2:C:652:MET:HE3	1.89	0.54
2:C:700:GLU:HG2	2:C:701:GLU:O	2.06	0.54
10:Z:455:ALA:HA	10:Z:458:ILE:HD12	1.90	0.54
1:A:1751:TYR:CZ	1:A:1755:LYS:HG3	2.42	0.54
2:C:109:LEU:HD22	2:C:112:ASN:OD1	2.07	0.54
2:C:856:ILE:HA	2:C:944:VAL:HG11	1.88	0.54
4:O:220:TYR:CE1	4:O:256:ARG:HG2	2.42	0.54
6:Q:45:HIS:CE1	14:E:32:U:H5'	2.43	0.54
7:R:92:HIS:ND1	7:R:93:ILE:O	2.34	0.54
1:A:1372:LYS:HG2	1:A:1383:PHE:CE2	2.43	0.54
1:A:557:PHE:O	1:A:558:GLN:NE2	2.40	0.54
1:A:768:GLU:OE2	4:O:310:SER:HB3	2.08	0.54
2:C:184:GLU:CD	2:C:191:ILE:H	2.10	0.54
2:C:271:ASP:OD1	2:C:272:ARG:N	2.40	0.54
2:C:314:ALA:HB1	2:C:321:THR:HG22	1.89	0.54
7:R:47:PHE:CE1	14:E:37:U:C4	2.95	0.54
15:L:1114:G:H2'	15:L:1115:G:C8	2.43	0.54
4:O:265:HIS:CE1	4:O:291:ARG:HG2	2.43	0.54
4:O:414:LEU:HD12	4:O:415:ILE:N	2.21	0.54
7:R:117:PHE:CE2	14:E:39:G:C4	2.96	0.54
10:Z:152:ILE:O	10:Z:156:LYS:HB2	2.08	0.54
10:Z:53:ARG:HG3	10:Z:54:ASN:H	1.73	0.54
1:A:456:GLU:OE1	1:A:456:GLU:N	2.38	0.54
2:C:149:LEU:HD12	2:C:152:LEU:HD12	1.90	0.54
2:C:139:ILE:HD12	2:C:252:LEU:HD22	1.89	0.54
2:C:471:HIS:N	2:C:487:ARG:O	2.34	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:R:95:ASP:OD1	7:R:97:GLU:N	2.39	0.54
9:T:29:GLN:HA	9:T:32:ASP:OD2	2.08	0.54
10:Z:98:LEU:HD23	10:Z:101:MET:HG3	1.89	0.54
10:Z:18:TRP:CD1	10:Z:242:PHE:HB2	2.41	0.54
1:A:1011:ASN:ND2	1:A:1142:ASN:HB2	2.23	0.54
1:A:1029:THR:O	1:A:1032:ILE:N	2.40	0.54
1:A:1464:LYS:HD3	1:A:1479:GLU:HB2	1.89	0.54
1:A:332:ASP:OD1	1:A:332:ASP:N	2.38	0.54
1:A:346:ILE:O	1:A:349:GLY:N	2.40	0.54
1:A:594:ASP:N	1:A:594:ASP:OD1	2.36	0.54
2:C:101:GLN:NE2	13:D:75:A:N6	2.48	0.54
1:A:709:ARG:NH2	13:D:83:C:OP1	2.36	0.54
15:L:7:C:OP1	19:I:174:LYS:HE3	2.07	0.54
5:P:111:HIS:O	5:P:112:ILE:HG13	2.07	0.54
6:Q:37:CYS:HB3	6:Q:64:CYS:SG	2.47	0.54
7:R:95:ASP:OD1	7:R:98:ASP:N	2.35	0.54
32:Y:68:PRO:O	32:Y:69:ASP:CB	2.54	0.54
1:A:402:TRP:HE1	1:A:405:ASN:HD21	1.54	0.54
1:A:430:PRO:HB3	10:Z:198:PHE:CD2	2.42	0.54
2:C:105:ILE:HG12	2:C:106:PHE:H	1.73	0.54
2:C:733:ASN:OD1	2:C:734:CYS:N	2.40	0.54
15:L:1102:C:C2'	15:L:1103:C:C6	2.80	0.54
4:O:184:THR:O	4:O:201:SER:OG	2.07	0.54
7:R:18:LEU:HD11	7:R:82:CYS:SG	2.48	0.54
7:R:207:PRO:O	7:R:212:TRP:NE1	2.41	0.54
9:T:32:ASP:O	9:T:35:LYS:HD3	2.07	0.54
24:F:47:GLU:HG3	32:Y:15:TYR:HB2	1.87	0.54
10:Z:63:PHE:CD2	10:Z:76:LEU:HD21	2.43	0.54
1:A:409:CYS:SG	2:C:272:ARG:NH2	2.81	0.54
2:C:265:PHE:CD2	2:C:295:ILE:HD12	2.43	0.54
3:J:19:HIS:CE1	11:B:91:A:N7	2.76	0.54
5:P:110:HIS:CD2	6:Q:17:LEU:HD22	2.43	0.54
6:Q:215:PRO:HG2	6:Q:217:TRP:CE2	2.40	0.54
1:A:1282:ASP:OD2	10:Z:305:GLY:N	2.40	0.54
1:A:1451:PHE:O	1:A:1454:SER:OG	2.21	0.54
1:A:2049:ILE:O	1:A:2052:GLU:HB2	2.08	0.54
1:A:422:LEU:HD12	1:A:469:ILE:HD11	1.90	0.54
2:C:133:ILE:HG22	2:C:209:MET:HB3	1.89	0.54
2:C:142:LEU:HB3	2:C:143:HIS:HD2	1.73	0.54
2:C:716:ASP:HB3	2:C:719:MET:HB2	1.89	0.54
14:E:61:C:OP2	14:E:80:U:O2'	2.25	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:F:98:GLU:O	32:Y:53:PRO:CA	2.56	0.54
4:O:325:SER:HB3	4:O:334:TRP:NE1	2.22	0.54
7:R:185:LYS:C	7:R:186:PHE:HD1	2.11	0.54
7:R:75:PHE:CZ	14:E:35:A:O2'	2.54	0.54
1:A:977:ASN:HB2	8:S:175:ARG:HH11	1.72	0.54
10:Z:22:ARG:O	10:Z:25:VAL:HB	2.07	0.54
10:Z:66:ASN:OD1	10:Z:67:LYS:N	2.41	0.54
10:Z:92:GLU:OE1	10:Z:96:LYS:HE3	2.07	0.54
1:A:1039:TRP:CD2	1:A:1271:PRO:HB3	2.43	0.54
1:A:1736:VAL:HA	1:A:1775:ILE:O	2.07	0.54
1:A:888:GLU:O	1:A:892:SER:HB3	2.08	0.54
2:C:315:SER:O	2:C:319:GLY:CA	2.56	0.54
2:C:801:TRP:HE1	2:C:843:LYS:HD2	1.72	0.54
4:O:202:GLU:OE1	4:O:226:GLY:HA3	2.08	0.54
7:R:19:PRO:CB	14:E:36:U:O4	2.56	0.54
7:R:244:LEU:O	7:R:247:LEU:HB3	2.08	0.54
10:Z:60:VAL:O	10:Z:64:THR:CB	2.56	0.54
1:A:1034:ASN:HB3	1:A:1291:GLU:HG3	1.89	0.53
1:A:1693:LYS:HE3	1:A:1695:ASN:HB2	1.88	0.53
1:A:762:VAL:HG21	1:A:786:LEU:HD11	1.88	0.53
15:L:41:C:HO2'	15:L:42:U:C5'	2.20	0.53
16:M:498:C:H6	16:M:498:C:O5'	1.92	0.53
4:O:437:GLU:OE1	4:O:438:PRO:HA	2.08	0.53
6:Q:221:ASP:OD1	6:Q:225:GLN:NE2	2.41	0.53
9:T:88:ASP:HB3	9:T:91:LEU:HB3	1.90	0.53
10:Z:326:VAL:CG1	10:Z:364:THR:HG21	2.38	0.53
10:Z:437:GLN:HA	10:Z:473:LEU:HD21	1.89	0.53
10:Z:454:ASP:O	10:Z:458:ILE:HG13	2.08	0.53
1:A:1375:LEU:O	1:A:1376:ASN:ND2	2.41	0.53
1:A:2034:ILE:CG1	1:A:2041:PRO:HA	2.38	0.53
2:C:116:THR:HG21	2:C:120:ARG:CZ	2.38	0.53
2:C:120:ARG:O	2:C:123:MET:HB3	2.08	0.53
2:C:324:ILE:O	2:C:328:VAL:HG23	2.08	0.53
2:C:767:SER:OG	2:C:796:ILE:HD13	2.08	0.53
7:R:47:PHE:CE2	14:E:37:U:O2	2.61	0.53
9:T:120:CYS:HB2	9:T:122:CYS:CB	2.38	0.53
10:Z:408:THR:HB	10:Z:410:GLU:HB3	1.89	0.53
1:A:1281:ASN:HD22	1:A:1285:VAL:CG2	2.21	0.53
1:A:1605:ARG:NE	1:A:1824:GLN:OE1	2.42	0.53
1:A:1753:ARG:O	1:A:1757:LEU:HG	2.09	0.53
2:C:292:ILE:O	2:C:295:ILE:HG12	2.07	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:385:PHE:HE1	2:C:425:LEU:HD11	1.73	0.53
2:C:490:SER:HA	2:C:558:LYS:HD3	1.89	0.53
2:C:608:GLN:O	2:C:668:ILE:HB	2.09	0.53
2:C:807:PRO:HG3	2:C:850:LEU:HD23	1.90	0.53
15:L:15:C:C5	19:I:209:ARG:HG2	2.43	0.53
4:O:198:PHE:HE1	4:O:208:CYS:HG	1.57	0.53
1:A:1910:LYS:O	1:A:1913:THR:OG1	2.25	0.53
1:A:470:LEU:HB3	1:A:471:PRO:HD2	1.90	0.53
5:P:127:VAL:HG11	14:E:32:U:H3	1.74	0.53
15:L:1114:G:O5'	15:L:1114:G:H8	1.91	0.53
5:P:80:ALA:O	5:P:83:ALA:N	2.41	0.53
10:Z:74:PRO:CA	10:Z:123:ILE:HG21	2.32	0.53
10:Z:77:SER:O	10:Z:81:ALA:N	2.28	0.53
1:A:234:PHE:CE2	1:A:700:GLY:HA2	2.43	0.53
1:A:380:ARG:NH2	1:A:382:GLU:OE2	2.41	0.53
1:A:383:TYR:CE1	2:C:913:GLY:HA3	2.44	0.53
1:A:752:ALA:O	1:A:756:LEU:HB2	2.08	0.53
1:A:905:TYR:HB3	1:A:908:ASP:HB2	1.90	0.53
2:C:139:ILE:O	2:C:237:ILE:HA	2.08	0.53
13:D:75:A:C4'	13:D:76:U:H5'	2.28	0.53
1:A:725:TYR:CD1	14:E:72:C:H1'	2.44	0.53
15:L:1102:C:C2'	15:L:1103:C:H6	2.15	0.53
5:P:105:LEU:H	5:P:108:ASN:HA	1.74	0.53
5:P:111:HIS:HB2	6:Q:22:ASN:HA	1.90	0.53
10:Z:28:ILE:HG21	10:Z:44:LEU:HD13	1.90	0.53
1:A:1458:TRP:CZ2	1:A:1489:PRO:HB2	2.43	0.53
1:A:1476:ALA:C	1:A:1478:GLU:H	2.11	0.53
1:A:2063:TYR:HA	1:A:2067:TYR:CD1	2.44	0.53
2:C:473:LEU:HD12	2:C:485:LEU:HD22	1.90	0.53
2:C:715:MET:HB2	2:C:720:ILE:HD11	1.89	0.53
13:D:31:G:C2'	13:D:32:G:H5'	2.39	0.53
1:A:284:ARG:NH2	13:D:33:U:O4	2.42	0.53
15:L:1103:C:C6	15:L:1114:G:N2	2.76	0.53
1:A:564:TRP:O	1:A:567:ALA:N	2.42	0.53
2:C:761:ALA:O	2:C:764:ASN:N	2.41	0.53
13:D:107:C:H2'	13:D:108:C:O4'	2.08	0.53
24:F:31:ILE:HD11	24:F:49:ILE:HD12	1.90	0.53
15:L:1116:A:C5	15:L:1117:G:C5	2.97	0.53
7:R:230:PRO:HG3	12:N:114:U:C4	2.42	0.53
10:Z:102:PHE:HZ	10:Z:142:LEU:HD21	1.73	0.53
1:A:1720:THR:OG1	1:A:1721:ASN:N	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1751:TYR:CE1	1:A:1755:LYS:HG3	2.43	0.53
19:I:193:GLU:OE1	19:I:204:ASN:HB3	2.08	0.53
15:L:28:U:O2'	15:L:29:C:H5'	2.08	0.53
1:A:770:MET:O	4:O:309:ARG:NH2	2.42	0.53
10:Z:172:MET:O	10:Z:175:GLU:HB3	2.09	0.53
10:Z:445:LEU:O	10:Z:449:PHE:HB2	2.08	0.53
1:A:1413:SER:OG	1:A:1414:TRP:N	2.42	0.53
1:A:161:PHE:CE1	1:A:198:ALA:HA	2.44	0.53
1:A:285:PRO:HD2	1:A:298:TYR:OH	2.08	0.53
2:C:485:LEU:HA	2:C:563:LEU:HD23	1.91	0.53
2:C:758:ASP:HB3	2:C:761:ALA:HB3	1.89	0.53
1:A:854:ARG:NH2	15:L:25:A:H5''	2.17	0.53
15:L:119:G:H8	30:W:99:ASP:OD2	1.91	0.53
15:L:1105:C:H42	31:X:97:LYS:NZ	2.07	0.53
1:A:1232:SER:OG	1:A:1233:ARG:N	2.40	0.53
1:A:526:LEU:O	1:A:529:TYR:N	2.41	0.53
1:A:541:ASN:ND2	13:D:40:C:C4	2.77	0.53
1:A:618:SER:O	1:A:621:LEU:N	2.42	0.53
1:A:847:LYS:HG2	15:L:24:U:C6	2.44	0.53
13:D:96:U:H6	13:D:96:U:O5'	1.91	0.53
4:O:358:ILE:HA	4:O:364:LEU:HD12	1.91	0.53
1:A:1505:ASP:OD1	1:A:1506:ARG:N	2.42	0.52
1:A:1576:GLU:OE1	1:A:1826:TYR:HB2	2.09	0.52
1:A:1992:TYR:HB3	1:A:1995:TRP:HB2	1.91	0.52
1:A:239:PHE:HD1	1:A:241:PRO:HD3	1.72	0.52
1:A:374:ILE:HG21	2:C:966:PHE:CE1	2.43	0.52
1:A:514:TYR:HB3	1:A:518:VAL:CG2	2.40	0.52
2:C:115:LYS:O	2:C:116:THR:OG1	2.27	0.52
2:C:428:ILE:HG22	2:C:429:PHE:HD1	1.74	0.52
2:C:142:LEU:HD12	2:C:929:GLN:NE2	2.24	0.52
1:A:783:LEU:N	1:A:783:LEU:HD12	2.24	0.52
2:C:922:THR:OG1	2:C:925:LEU:O	2.14	0.52
13:D:43:G:O2'	13:D:45:A:H5'	2.09	0.52
25:G:27:VAL:HG22	25:G:92:SER:HB2	1.91	0.52
15:L:1116:A:N6	15:L:1117:G:C6	2.78	0.52
15:L:17:U:H4'	15:L:18:U:OP2	2.07	0.52
1:A:1709:TRP:O	1:A:1728:ILE:CA	2.42	0.52
1:A:936:GLU:O	1:A:939:LEU:N	2.43	0.52
2:C:272:ARG:HG3	36:C:1500:GTP:HN21	1.75	0.52
2:C:147:THR:OG1	2:C:214:ASP:OD2	2.24	0.52
2:C:365:GLU:CG	2:C:366:ASN:H	2.18	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:699:GLY:O	2:C:707:SER:OG	2.27	0.52
16:M:484:U:H2'	16:M:485:U:C2	2.43	0.52
4:O:304:LEU:HD13	4:O:334:TRP:CE3	2.43	0.52
7:R:110:ASP:CG	7:R:114:ARG:H	2.09	0.52
1:A:138:HIS:O	1:A:142:ILE:HG12	2.08	0.52
1:A:1624:LEU:HD21	1:A:1635:HIS:CE1	2.45	0.52
1:A:1653:LEU:O	1:A:1657:ILE:HG13	2.08	0.52
1:A:168:LEU:HB3	1:A:622:MET:HE1	1.91	0.52
1:A:2017:THR:HG21	1:A:2059:ILE:HG12	1.91	0.52
1:A:466:GLU:OE1	1:A:466:GLU:N	2.36	0.52
1:A:910:LYS:O	1:A:913:VAL:HB	2.09	0.52
2:C:798:GLY:O	2:C:801:TRP:HB3	2.09	0.52
2:C:831:ILE:O	2:C:835:LYS:HE2	2.10	0.52
14:E:89:U:O2	14:E:89:U:H2'	2.08	0.52
19:I:145:LYS:HG2	19:I:152:ILE:HG13	1.90	0.52
15:L:30:A:H4'	15:L:31:A:OP1	2.09	0.52
16:M:493:A:H2'	16:M:494:G:O4'	2.09	0.52
1:A:514:TYR:HB3	1:A:518:VAL:HG23	1.92	0.52
1:A:930:ASN:OD1	15:L:30:A:OP1	2.27	0.52
2:C:234:LEU:HB2	2:C:262:ALA:O	2.10	0.52
2:C:916:THR:O	2:C:919:ARG:N	2.42	0.52
7:R:117:PHE:HB2	14:E:39:G:N1	2.24	0.52
6:Q:108:MET:SD	14:E:66:C:H1'	2.50	0.52
7:R:183:PHE:CD2	12:N:113:U:C5	2.98	0.52
10:Z:82:LEU:HD21	10:Z:215:LEU:HD21	1.92	0.52
1:A:897:PRO:O	1:A:1006:ARG:NH1	2.43	0.52
1:A:1716:LEU:H	1:A:1719:GLU:HB2	1.74	0.52
1:A:381:SER:OG	1:A:382:GLU:N	2.41	0.52
1:A:839:HIS:HB2	13:D:95:C:N3	2.25	0.52
2:C:429:PHE:N	2:C:429:PHE:CD1	2.77	0.52
9:T:100:TYR:O	9:T:102:LYS:N	2.43	0.52
10:Z:18:TRP:HB2	10:Z:242:PHE:CD1	2.45	0.52
10:Z:69:ASN:OD1	10:Z:72:LEU:HB2	2.09	0.52
1:A:1086:ASN:O	1:A:1088:VAL:HG13	2.10	0.52
1:A:1275:MET:O	1:A:1276:GLU:HG2	2.10	0.52
1:A:472:ASN:O	1:A:474:LYS:N	2.43	0.52
2:C:323:THR:O	2:C:326:GLU:N	2.43	0.52
2:C:749:LYS:O	2:C:753:THR:OG1	2.21	0.52
13:D:103:A:O2'	13:D:104:G:OP2	2.25	0.52
5:P:127:VAL:HG11	14:E:32:U:C4	2.45	0.52
15:L:41:C:H2'	15:L:42:U:C6	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:Q:215:PRO:CG	6:Q:217:TRP:CZ2	2.65	0.52
1:A:1312:PHE:CD1	1:A:1342:LEU:HD13	2.44	0.52
1:A:1431:HIS:CG	1:A:1434:GLU:HA	2.45	0.52
1:A:1856:ASN:HD21	1:A:1968:ALA:HB3	1.75	0.52
2:C:109:LEU:HD23	2:C:111:LYS:HG2	1.92	0.52
2:C:454:ALA:HB1	2:C:459:PRO:HA	1.92	0.52
2:C:775:ILE:HB	2:C:819:LYS:HG2	1.91	0.52
7:R:117:PHE:CD2	14:E:39:G:C5	2.97	0.52
7:R:46:ARG:NH2	7:R:220:GLY:O	2.42	0.52
10:Z:431:LEU:HD12	10:Z:436:LEU:HD13	1.92	0.52
1:A:395:PRO:HB2	1:A:398:VAL:HG21	1.92	0.52
1:A:898:ILE:HG22	1:A:899:PRO:O	2.10	0.52
2:C:268:ASN:HA	2:C:314:ALA:O	2.10	0.52
2:C:277:LEU:HB3	2:C:279:LEU:CD1	2.40	0.52
2:C:360:ARG:C	2:C:362:LYS:H	2.13	0.52
14:E:92:C:O2	15:L:13:G:N2	2.42	0.52
7:R:169:ASP:OD1	7:R:169:ASP:N	2.42	0.52
1:A:1888:HIS:HA	1:A:1989:PHE:O	2.09	0.52
1:A:2043:PHE:HB2	1:A:2048:TRP:CD1	2.45	0.52
1:A:329:TYR:CE1	2:C:919:ARG:HD2	2.45	0.52
2:C:440:THR:O	2:C:443:TYR:N	2.43	0.52
4:O:328:THR:O	4:O:353:ILE:HG12	2.10	0.52
7:R:182:GLY:O	7:R:183:PHE:HD1	1.93	0.52
7:R:237:ARG:O	7:R:240:GLU:HB3	2.09	0.52
10:Z:339:PHE:HE2	10:Z:387:PHE:HA	1.74	0.52
1:A:1137:PRO:HG2	1:A:1140:ASN:HB2	1.92	0.51
1:A:401:PRO:O	1:A:402:TRP:HB3	2.10	0.51
2:C:355:HIS:ND1	2:C:366:ASN:HB2	2.25	0.51
1:A:371:ASP:HB3	2:C:972:ARG:HD3	1.92	0.51
15:L:2:C:O5'	15:L:2:C:H6	1.92	0.51
4:O:182:VAL:HG23	4:O:183:MET:H	1.74	0.51
4:O:152:ASN:ND2	4:O:409:LYS:HB3	2.24	0.51
1:A:143:ILE:O	1:A:147:SER:OG	2.19	0.51
1:A:1587:PHE:CZ	15:L:31:A:H5"	2.42	0.51
1:A:1699:ALA:HB1	1:A:1733:TRP:CG	2.45	0.51
1:A:623:ARG:NH2	1:A:624:GLU:OE2	2.44	0.51
2:C:271:ASP:CG	36:C:1500:GTP:HN1	2.14	0.51
2:C:233:ASP:OD1	2:C:487:ARG:NH2	2.43	0.51
2:C:325:LYS:NZ	2:C:441:ARG:HH12	2.08	0.51
19:I:183:MET:O	19:I:187:LYS:HG2	2.10	0.51
15:L:15:C:H1'	15:L:16:U:C5	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:O:243:GLY:O	4:O:245:ASP:N	2.44	0.51
10:Z:69:ASN:CB	10:Z:73:ILE:HG13	2.40	0.51
1:A:1142:ASN:HB3	1:A:1146:GLN:HB2	1.92	0.51
1:A:1302:LEU:O	1:A:1303:LYS:HG3	2.10	0.51
1:A:1400:ILE:HG23	1:A:1542:TYR:CZ	2.45	0.51
1:A:239:PHE:CE2	1:A:655:TYR:HD2	2.29	0.51
2:C:365:GLU:HG3	2:C:366:ASN:N	2.19	0.51
2:C:717:SER:O	2:C:721:GLN:CB	2.59	0.51
4:O:302:LYS:NZ	4:O:338:GLU:O	2.43	0.51
6:Q:90:LEU:HD21	7:R:246:SER:HB3	1.92	0.51
7:R:89:TYR:CE2	14:E:34:A:C4	2.98	0.51
1:A:1047:ALA:HA	1:A:1172:PHE:O	2.10	0.51
1:A:235:LYS:NZ	1:A:1758:ASP:OD1	2.40	0.51
2:C:711:ALA:O	2:C:818:TYR:HA	2.10	0.51
24:F:47:GLU:CB	32:Y:15:TYR:CG	2.93	0.51
19:I:187:LYS:HA	19:I:201:LYS:NZ	2.24	0.51
15:L:1107:C:H5'	15:L:1107:C:C6	2.44	0.51
1:A:1156:HIS:HD2	1:A:1158:ILE:HB	1.74	0.51
1:A:1051:GLU:HG2	1:A:1169:TYR:HE1	1.75	0.51
1:A:1340:ILE:O	1:A:1344:THR:OG1	2.16	0.51
1:A:1347:ARG:HD2	1:A:1447:TRP:CE2	2.45	0.51
1:A:1944:LEU:O	1:A:1948:MET:HG2	2.09	0.51
1:A:2024:MET:O	1:A:2028:SER:N	2.44	0.51
1:A:562:ILE:HD11	1:A:566:GLU:CD	2.31	0.51
1:A:569:LEU:O	1:A:572:CYS:N	2.43	0.51
2:C:92:GLU:HG2	2:C:93:PRO:O	2.10	0.51
13:D:78:A:H4'	13:D:79:C:OP1	2.11	0.51
19:I:106:GLU:O	19:I:109:LEU:HB2	2.10	0.51
19:I:187:LYS:HA	19:I:201:LYS:HZ1	1.75	0.51
3:J:9:LYS:O	3:J:10:SER:OG	2.21	0.51
15:L:49:U:H6	15:L:49:U:H5''	1.75	0.51
5:P:43:PHE:N	5:P:43:PHE:CD1	2.77	0.51
7:R:174:ARG:HH22	12:N:114:U:C5'	2.24	0.51
8:S:8:GLN:HG2	8:S:10:GLU:H	1.76	0.51
10:Z:480:ARG:HD3	10:Z:483:ILE:HD12	1.92	0.51
1:A:1025:VAL:HG21	1:A:1265:PHE:CD2	2.45	0.51
1:A:1033:ASN:HB2	1:A:1288:LEU:HD13	1.93	0.51
1:A:1559:HIS:CE1	1:A:1743:TYR:CZ	2.99	0.51
2:C:778:THR:HG23	2:C:781:ASP:H	1.75	0.51
16:M:492:U:H2'	16:M:493:A:C8	2.45	0.51
16:M:499:U:HO2'	16:M:500:A:P	2.24	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:R:180:ASN:HB2	12:N:111:U:C6	2.46	0.51
6:Q:25:MET:HB2	6:Q:45:HIS:O	2.10	0.51
8:S:8:GLN:O	8:S:10:GLU:N	2.44	0.51
1:A:176:LEU:O	1:A:176:LEU:HD23	2.10	0.51
1:A:1865:THR:OG1	1:A:1869:ASN:N	2.43	0.51
1:A:255:ILE:O	1:A:258:ILE:HG22	2.11	0.51
1:A:314:LEU:O	1:A:316:THR:N	2.44	0.51
1:A:705:GLN:HB3	1:A:706:PRO:HD3	1.92	0.51
2:C:418:GLN:HB3	2:C:419:PRO:HD3	1.92	0.51
2:C:106:PHE:CZ	2:C:478:TYR:HD2	2.28	0.51
1:A:1150:LYS:HB3	1:A:1154:LYS:HZ3	1.76	0.51
1:A:1303:LYS:NZ	1:A:1353:THR:HG22	2.26	0.51
1:A:223:ALA:HB2	1:A:266:LEU:HD12	1.92	0.51
1:A:639:PHE:HB2	1:A:649:LEU:HD13	1.93	0.51
2:C:315:SER:HB3	2:C:320:PHE:CE1	2.46	0.51
2:C:707:SER:O	2:C:708:ILE:HD13	2.11	0.51
16:M:489:A:H2'	16:M:490:A:H8	1.76	0.51
5:P:43:PHE:HE1	5:P:147:LEU:HD22	1.76	0.51
24:F:99:ASP:CA	32:Y:53:PRO:CB	2.88	0.51
10:Z:159:GLY:O	10:Z:163:ALA:CB	2.58	0.51
1:A:259:GLU:CG	1:A:260:PRO:HD2	2.40	0.51
1:A:307:GLU:O	1:A:310:ASN:N	2.44	0.51
1:A:614:ARG:CZ	11:B:98:A:C4'	2.85	0.51
2:C:246:THR:HG23	2:C:248:VAL:HG12	1.93	0.51
2:C:734:CYS:SG	2:C:735:LEU:N	2.84	0.51
2:C:793:GLU:HA	2:C:796:ILE:HG22	1.92	0.51
2:C:862:TYR:CD2	2:C:930:LEU:HB3	2.46	0.51
15:L:1102:C:O2'	15:L:1103:C:H5'	2.10	0.51
16:M:484:U:H3'	16:M:484:U:H6	1.75	0.51
4:O:380:SER:OG	4:O:382:HIS:N	2.39	0.51
5:P:147:LEU:HD12	5:P:147:LEU:O	2.11	0.51
6:Q:22:ASN:OD1	6:Q:23:ILE:N	2.44	0.51
7:R:127:ILE:HD12	14:E:39:G:C8	2.46	0.51
1:A:1283:GLU:OE1	1:A:1446:THR:HG21	2.10	0.51
1:A:1849:LYS:O	1:A:1884:PRO:HD2	2.11	0.51
1:A:215:ALA:O	1:A:218:SER:N	2.42	0.51
1:A:583:ILE:O	1:A:586:LYS:N	2.40	0.51
1:A:776:GLN:HG2	1:A:777:LYS:N	2.23	0.51
2:C:307:ILE:HG12	2:C:346:THR:HA	1.93	0.51
2:C:497:ASP:OD1	2:C:497:ASP:N	2.43	0.51
14:E:59:A:H3'	14:E:60:G:H5''	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:E:85:C:OP1	14:E:85:C:C4'	2.58	0.51
15:L:20:G:O5'	15:L:20:G:H8	1.93	0.51
7:R:55:PRO:HB3	7:R:93:ILE:HD11	1.92	0.51
1:A:1795:LYS:O	1:A:1799:GLN:HG3	2.10	0.50
1:A:953:ARG:HG2	1:A:957:TYR:CE2	2.46	0.50
2:C:101:GLN:HG2	2:C:101:GLN:O	2.11	0.50
2:C:172:TRP:N	2:C:172:TRP:CD1	2.79	0.50
7:R:34:TYR:CZ	14:E:41:A:H1'	2.46	0.50
14:E:49:A:N7	14:E:50:G:N7	2.59	0.50
2:C:79:GLU:HG3	5:P:202:MET:SD	49.69	0.50
7:R:234:ALA:O	7:R:237:ARG:HB2	2.10	0.50
1:A:1094:ASP:OD1	15:L:25:A:C2	2.64	0.50
1:A:1048:VAL:HA	1:A:1249:SER:O	2.12	0.50
1:A:1878:CYS:SG	1:A:1891:LEU:HD22	2.50	0.50
1:A:542:HIS:C	1:A:544:LYS:N	2.56	0.50
1:A:839:HIS:ND1	1:A:839:HIS:O	2.44	0.50
1:A:953:ARG:HG2	1:A:957:TYR:HE2	1.76	0.50
14:E:91:A:O2'	19:I:100:LEU:HD22	2.11	0.50
15:L:1116:A:C5	15:L:1117:G:N7	2.79	0.50
4:O:162:THR:HG21	4:O:182:VAL:O	2.12	0.50
7:R:22:ILE:HG22	7:R:30:PHE:CZ	2.46	0.50
7:R:233:ALA:O	7:R:237:ARG:HG3	2.11	0.50
7:R:75:PHE:HE2	14:E:35:A:H8	1.04	0.50
26:H:74:ARG:HD3	30:W:101:VAL:O	2.12	0.50
10:Z:159:GLY:HA2	10:Z:162:LEU:HB3	1.92	0.50
1:A:1861:THR:HG21	1:A:1875:ILE:HG13	1.93	0.50
1:A:382:GLU:CD	1:A:382:GLU:H	2.11	0.50
2:C:362:LYS:HD3	2:C:365:GLU:HB3	1.93	0.50
1:A:709:ARG:NH2	13:D:82:A:O3'	2.45	0.50
16:M:493:A:H2'	16:M:494:G:C1'	2.41	0.50
5:P:182:LEU:O	5:P:185:ARG:N	2.39	0.50
9:T:100:TYR:O	9:T:103:LEU:N	2.42	0.50
15:L:1105:C:N4	31:X:97:LYS:HZ3	2.09	0.50
10:Z:354:HIS:CD2	10:Z:356:SER:H	2.29	0.50
1:A:1011:ASN:ND2	1:A:1143:GLU:O	2.44	0.50
1:A:1508:HIS:HB2	1:A:1529:ASN:HD21	1.76	0.50
1:A:1669:LEU:HD23	1:A:1672:GLU:HG3	1.92	0.50
1:A:193:TYR:CE1	1:A:558:GLN:HB2	2.46	0.50
1:A:929:LEU:HD22	1:A:933:GLU:HB3	1.94	0.50
2:C:585:ASP:O	2:C:588:GLN:HB3	2.11	0.50
13:D:83:C:HO2'	13:D:84:A:P	2.35	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:E:13:A:HO2'	14:E:14:C:H5	1.58	0.50
7:R:29:THR:O	7:R:38:SER:OG	2.19	0.50
9:T:121:ILE:HD11	9:T:129:LEU:HD21	1.93	0.50
1:A:982:TYR:HD2	1:A:1106:GLY:H	1.59	0.50
1:A:779:ALA:O	1:A:782:ILE:N	2.44	0.50
2:C:142:LEU:HB3	2:C:143:HIS:CD2	2.46	0.50
2:C:285:TYR:HD2	2:C:286:LEU:HD12	1.76	0.50
2:C:677:PHE:HB2	2:C:811:GLU:OE1	2.10	0.50
6:Q:222:THR:HA	6:Q:225:GLN:OE1	2.10	0.50
1:A:1023:LEU:HB2	1:A:1451:PHE:CE1	2.46	0.50
1:A:1304:VAL:H	1:A:1353:THR:HG21	1.77	0.50
1:A:1343:PHE:HD1	1:A:1350:ILE:HD13	1.76	0.50
1:A:1606:PHE:O	1:A:1609:TRP:N	2.45	0.50
1:A:1922:ARG:HG2	1:A:1951:PHE:CZ	2.46	0.50
1:A:1935:VAL:O	1:A:1959:THR:HG23	2.11	0.50
2:C:499:VAL:HG11	2:C:577:LEU:HG	1.93	0.50
1:A:709:ARG:NH2	13:D:83:C:P	2.84	0.50
14:E:11:U:C2	14:E:12:A:H1'	2.47	0.50
3:J:6:ILE:HD11	11:B:90:A:C6	2.46	0.50
7:R:146:LEU:HD23	7:R:147:ASN:N	2.25	0.50
10:Z:419:PHE:HD2	10:Z:420:ILE:HD12	1.75	0.50
1:A:413:ASN:OD1	1:A:413:ASN:N	2.37	0.50
1:A:614:ARG:CZ	11:B:98:A:C5'	2.90	0.50
2:C:722:ASP:OD2	2:C:755:TYR:OH	2.15	0.50
2:C:817:GLN:NE2	2:C:819:LYS:HE3	2.25	0.50
3:J:6:ILE:HD11	11:B:90:A:N6	2.27	0.50
10:Z:104:GLN:HB3	10:Z:108:ARG:HH22	1.77	0.50
1:A:1077:ASN:O	1:A:1080:ASP:N	2.44	0.50
1:A:1366:ARG:HA	1:A:1369:ASN:HD22	1.77	0.50
1:A:1613:THR:OG1	1:A:1614:ILE:N	2.43	0.50
1:A:2013:ARG:NH2	1:A:2083:ILE:O	2.45	0.50
2:C:261:VAL:HG12	2:C:262:ALA:N	2.27	0.50
15:L:25:A:H2'	15:L:27:A:OP2	2.12	0.50
4:O:392:MET:HG3	4:O:393:VAL:N	2.26	0.50
1:A:1203:ASN:HD22	1:A:1213:MET:HB3	1.77	0.50
1:A:1339:LEU:O	1:A:1342:LEU:N	2.45	0.50
1:A:429:ASN:HB3	1:A:430:PRO:HD2	1.94	0.50
1:A:633:VAL:O	1:A:637:VAL:HG23	2.12	0.50
1:A:745:THR:HG21	4:O:182:VAL:HG21	1.94	0.50
2:C:501:ILE:HD13	2:C:567:ILE:HG21	1.94	0.50
2:C:758:ASP:O	2:C:762:SER:N	2.33	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:P:127:VAL:CG1	14:E:32:U:O4	2.60	0.50
14:E:89:U:H5	19:I:179:ARG:HB3	1.74	0.50
1:A:1362:LYS:NZ	3:J:14:SER:HA	2.26	0.50
5:P:227:ARG:O	5:P:231:GLU:HB2	2.11	0.50
7:R:89:TYR:CE2	14:E:34:A:N3	2.80	0.50
10:Z:104:GLN:HA	10:Z:107:ASN:HD22	1.77	0.50
10:Z:384:LEU:HB3	10:Z:419:PHE:CE1	2.41	0.50
1:A:1286:TRP:NE1	1:A:1302:LEU:HD11	2.27	0.49
1:A:168:LEU:HD21	1:A:626:LEU:HD21	1.94	0.49
1:A:284:ARG:CZ	13:D:33:U:O4	2.60	0.49
1:A:725:TYR:HE1	14:E:72:C:C2	2.30	0.49
1:A:743:LYS:HD3	1:A:749:ARG:CZ	2.42	0.49
2:C:343:ASP:O	2:C:346:THR:OG1	2.24	0.49
2:C:484:SER:O	2:C:563:LEU:HA	2.12	0.49
2:C:863:GLU:OE2	2:C:934:HIS:ND1	2.44	0.49
13:D:174:G:OP2	26:H:76:ASN:HB2	229.73	0.49
14:E:50:G:H8	14:E:50:G:OP2	1.95	0.49
4:O:341:LEU:HG	4:O:342:LEU:O	2.12	0.49
5:P:105:LEU:N	5:P:108:ASN:HA	2.27	0.49
7:R:169:ASP:OD2	7:R:187:LYS:HD2	2.12	0.49
9:T:143:HIS:O	9:T:151:ARG:HG2	2.12	0.49
1:A:1161:TYR:HE1	1:A:1168:ILE:HG23	1.77	0.49
1:A:1390:THR:OG1	1:A:1396:GLY:HA3	2.12	0.49
1:A:1588:LYS:O	1:A:1590:LEU:N	2.45	0.49
1:A:2009:THR:O	1:A:2013:ARG:HG3	2.12	0.49
12:N:108:U:H4'	12:N:109:U:OP2	2.11	0.49
5:P:159:ASP:O	5:P:162:GLU:N	2.45	0.49
7:R:184:VAL:HG12	7:R:186:PHE:HE1	1.76	0.49
10:Z:12:LYS:HG3	10:Z:15:ARG:HH12	1.77	0.49
10:Z:413:CYS:O	10:Z:416:GLY:N	2.44	0.49
1:A:1144:PHE:CD2	1:A:1145:MET:HG2	2.40	0.49
1:A:1624:LEU:HD11	1:A:1635:HIS:CE1	2.47	0.49
1:A:1708:GLU:HA	1:A:1730:ASN:OD1	2.12	0.49
1:A:1902:GLN:HE21	1:A:1908:LEU:CD2	2.26	0.49
1:A:374:ILE:HD13	2:C:966:PHE:CD1	2.47	0.49
2:C:268:ASN:OD1	2:C:316:THR:HG23	2.12	0.49
2:C:348:LEU:HD21	2:C:377:ILE:HD11	1.92	0.49
13:D:103:A:O2'	13:D:104:G:P	2.70	0.49
15:L:119:G:OP2	26:H:76:ASN:HB2	2.12	0.49
15:L:1120:G:H8	15:L:1120:G:C5'	2.25	0.49
4:O:237:ASP:O	4:O:238:LEU:HD23	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:Z:364:THR:O	10:Z:368:ASN:ND2	2.44	0.49
1:A:1117:TYR:OH	1:A:1238:LEU:HD22	2.13	0.49
1:A:1995:TRP:HE3	1:A:2004:ALA:HB1	1.76	0.49
1:A:355:LEU:HD13	13:D:105:A:H5'	1.94	0.49
1:A:677:ILE:O	1:A:681:LYS:HG3	2.13	0.49
2:C:312:ILE:HG12	2:C:323:THR:OG1	2.12	0.49
2:C:825:VAL:HG13	2:C:826:PRO:HD2	1.95	0.49
25:G:86:ASN:HD21	26:H:32:LYS:NZ	2.09	0.49
15:L:30:A:C4'	15:L:31:A:OP1	2.61	0.49
5:P:115:VAL:HG21	6:Q:24:ARG:HH11	1.77	0.49
10:Z:96:LYS:HG3	10:Z:227:TYR:OH	2.13	0.49
1:A:168:LEU:O	1:A:171:ALA:N	2.46	0.49
1:A:355:LEU:CD1	13:D:105:A:H5'	2.42	0.49
1:A:889:TRP:O	1:A:893:ARG:N	2.36	0.49
2:C:138:VAL:HG21	2:C:150:MET:CE	2.43	0.49
2:C:221:PHE:HE1	2:C:651:TYR:HD1	1.60	0.49
2:C:254:LYS:O	2:C:258:LYS:CB	2.60	0.49
2:C:79:GLU:OE2	4:O:173:LYS:HD3	2.12	0.49
1:A:1023:LEU:HD13	1:A:1451:PHE:CD1	2.47	0.49
1:A:168:LEU:HB3	1:A:622:MET:CE	2.42	0.49
1:A:871:GLY:N	5:P:198:ASN:HD22	2.11	0.49
2:C:254:LYS:O	2:C:258:LYS:HB2	2.12	0.49
1:A:538:LEU:HD11	13:D:41:A:C6	2.48	0.49
14:E:87:U:O4'	14:E:87:U:OP1	2.31	0.49
15:L:39:A:C2'	15:L:40:U:H5''	2.42	0.49
7:R:229:ASP:OD1	12:N:113:U:O2'	2.23	0.49
7:R:63:ARG:NH2	9:T:143:HIS:CD2	2.81	0.49
10:Z:449:PHE:HZ	10:Z:465:PHE:HE2	1.61	0.49
1:A:1383:PHE:HB3	1:A:1388:PHE:CE2	2.47	0.49
1:A:1392:LYS:HA	1:A:1396:GLY:O	2.13	0.49
1:A:1111:SER:HB3	1:A:1514:PHE:HD2	1.78	0.49
1:A:203:ASN:O	1:A:204:GLU:HG3	2.12	0.49
1:A:503:LYS:HA	1:A:506:PHE:CE2	2.48	0.49
1:A:532:ASN:HD21	13:D:84:A:P	2.31	0.49
1:A:645:ASP:OD1	1:A:646:ALA:N	2.45	0.49
1:A:1411:ASP:HA	3:J:5:GLY:O	2.13	0.49
4:O:203:ASP:OD1	4:O:205:THR:OG1	2.19	0.49
4:O:254:ARG:HG3	4:O:255:THR:HG23	1.94	0.49
5:P:105:LEU:HD12	5:P:106:LEU:H	1.78	0.49
5:P:62:GLU:O	5:P:65:GLU:N	2.28	0.49
6:Q:38:THR:O	6:Q:39:LEU:HD12	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:R:134:ASN:ND2	7:R:226:ALA:O	2.46	0.49
7:R:15:GLU:OE1	9:T:44:LYS:NZ	2.42	0.49
10:Z:414:PRO:HA	10:Z:417:ARG:HD2	1.95	0.49
10:Z:443:SER:O	10:Z:444:LYS:HG2	2.13	0.49
1:A:1082:ILE:HG21	1:A:1113:ILE:CD1	2.43	0.49
1:A:1580:GLY:C	1:A:1582:GLU:H	2.16	0.49
1:A:1798:ILE:O	1:A:1801:SER:OG	2.28	0.49
2:C:184:GLU:OE2	2:C:192:LYS:N	2.45	0.49
2:C:286:LEU:HD23	10:Z:182:GLN:HB3	1.95	0.49
1:A:462:LEU:HD22	2:C:383:LYS:HB3	1.94	0.49
1:A:428:LEU:HD22	2:C:896:GLY:O	2.12	0.49
5:P:126:PHE:HB3	5:P:129:LYS:HB2	1.94	0.49
1:A:1111:SER:HA	1:A:1514:PHE:CE2	2.48	0.49
1:A:1572:GLY:O	1:A:1827:GLN:NE2	2.46	0.49
1:A:1699:ALA:HB2	1:A:1767:TYR:CD1	2.46	0.49
1:A:194:HIS:HA	1:A:557:PHE:CD1	2.47	0.49
1:A:2017:THR:HB	1:A:2062:GLU:OE2	2.12	0.49
1:A:296:THR:HG21	13:D:33:U:OP2	2.11	0.49
12:N:108:U:H1'	12:N:109:U:OP1	2.13	0.49
4:O:217:ILE:HG22	4:O:218:ARG:HG3	1.95	0.49
1:A:1026:TYR:HD1	1:A:1286:TRP:CZ3	2.31	0.49
1:A:1402:ALA:HB2	1:A:1440:ILE:HG13	1.93	0.49
1:A:342:LEU:HD13	1:A:392:ASN:ND2	2.27	0.49
1:A:377:VAL:HG13	1:A:378:PRO:HD2	1.95	0.49
1:A:923:TYR:CZ	1:A:936:GLU:OE1	2.66	0.49
2:C:74:VAL:HA	4:O:132:SER:O	2.13	0.49
14:E:49:A:C8	14:E:50:G:N7	2.80	0.49
4:O:404:CYS:SG	4:O:417:GLY:N	2.83	0.49
1:A:1380:PRO:HG2	11:B:93:U:C4	2.48	0.48
1:A:1471:GLN:OE1	1:A:1473:ARG:NE	2.46	0.48
1:A:1540:ASN:O	1:A:1543:ARG:N	2.46	0.48
1:A:1629:LEU:H	1:A:1629:LEU:HG	1.34	0.48
1:A:304:ASP:CG	1:A:306:PRO:HD2	2.33	0.48
2:C:352:VAL:O	2:C:372:THR:OG1	2.17	0.48
2:C:928:CYS:SG	2:C:929:GLN:N	2.85	0.48
2:C:99:LYS:HG2	13:D:43:G:H5'	1.95	0.48
9:T:123:ARG:NH2	14:E:26:A:O2'	2.46	0.48
6:Q:258:LEU:O	6:Q:262:PHE:HB3	2.11	0.48
1:A:1157:PRO:HG3	8:S:127:TRP:CZ2	2.48	0.48
9:T:47:GLU:O	9:T:50:TRP:N	2.46	0.48
10:Z:79:LEU:O	10:Z:83:LEU:N	2.34	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:122:TYR:O	2:C:125:SER:HB3	2.13	0.48
2:C:277:LEU:CB	2:C:279:LEU:HD13	2.44	0.48
15:L:51:C:C6	15:L:51:C:O5'	2.66	0.48
4:O:248:ILE:HG13	4:O:269:ILE:HD13	1.95	0.48
5:P:87:ASN:HB2	5:P:90:SER:HB2	1.95	0.48
7:R:119:ASP:OD1	7:R:119:ASP:N	2.45	0.48
7:R:196:LYS:NZ	7:R:197:GLU:OE2	2.46	0.48
9:T:131:GLU:OE2	9:T:135:LYS:NZ	2.32	0.48
15:L:1109:C:N4	31:X:108:THR:HA	2.28	0.48
10:Z:97:GLU:OE2	10:Z:101:MET:HE1	2.11	0.48
1:A:1015:PRO:HB3	1:A:1164:TYR:CE1	2.48	0.48
1:A:1734:PHE:HD1	1:A:1773:VAL:HB	1.79	0.48
1:A:1718:HIS:HE1	1:A:1799:GLN:HG2	1.78	0.48
1:A:1855:THR:HA	1:A:1937:ARG:NH2	2.27	0.48
1:A:2010:LEU:HD21	1:A:2083:ILE:HG23	1.94	0.48
1:A:776:GLN:HG2	1:A:777:LYS:HG2	1.95	0.48
1:A:933:GLU:O	1:A:936:GLU:HB2	2.13	0.48
2:C:274:ILE:HB	2:C:382:TYR:CE1	2.49	0.48
2:C:468:LEU:HD12	2:C:490:SER:O	2.12	0.48
2:C:674:LEU:HD11	2:C:973:ARG:NH2	2.29	0.48
2:C:716:ASP:OD1	2:C:718:LYS:N	2.30	0.48
2:C:794:GLN:HE22	2:C:835:LYS:HD2	1.78	0.48
14:E:49:A:H3'	14:E:50:G:H8	1.79	0.48
5:P:107:ASN:OD1	5:P:109:SER:HB2	2.13	0.48
5:P:216:ARG:O	5:P:219:ILE:HB	2.14	0.48
7:R:65:ASP:OD1	7:R:90:LEU:HD22	2.13	0.48
10:Z:413:CYS:SG	10:Z:415:GLN:HB2	2.53	0.48
1:A:1082:ILE:C	1:A:1085:LYS:H	2.14	0.48
1:A:683:LEU:HD13	1:A:706:PRO:HB2	1.96	0.48
2:C:355:HIS:CE1	2:C:360:ARG:HH21	2.31	0.48
14:E:87:U:C5	14:E:88:U:C4	3.01	0.48
1:A:1235:PRO:HD3	8:S:133:PHE:CE2	2.49	0.48
1:A:1323:SER:HB2	1:A:1326:THR:CG2	2.44	0.48
1:A:1364:GLU:OE1	1:A:1403:SER:HB3	2.13	0.48
1:A:168:LEU:N	1:A:169:PRO:HD2	2.28	0.48
1:A:923:TYR:OH	1:A:936:GLU:OE1	2.31	0.48
2:C:786:GLU:O	2:C:789:SER:N	2.47	0.48
25:G:34:GLN:HE21	25:G:37:ILE:HD12	1.79	0.48
15:L:1116:A:N6	15:L:1117:G:O6	2.46	0.48
16:M:483:U:C3'	16:M:484:U:C5	2.91	0.48
16:M:487:A:H2'	16:M:488:G:C8	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:O:153:GLU:HB2	4:O:154:TRP:HD1	1.79	0.48
4:O:161:ASP:O	4:O:162:THR:OG1	2.24	0.48
4:O:221:TYR:CG	4:O:222:GLY:N	2.82	0.48
4:O:403:LEU:HD11	4:O:419:ALA:HB2	1.93	0.48
6:Q:61:CYS:HB2	6:Q:64:CYS:H	1.78	0.48
7:R:110:ASP:OD1	7:R:113:GLY:N	2.47	0.48
10:Z:157:ILE:HG23	10:Z:208:GLY:O	2.13	0.48
10:Z:398:PRO:HD2	10:Z:401:CYS:SG	2.54	0.48
1:A:1379:MET:HE1	1:A:1620:TYR:N	2.14	0.48
1:A:1478:GLU:HA	1:A:1481:GLU:HB2	1.94	0.48
1:A:1541:ALA:O	1:A:1544:THR:OG1	2.23	0.48
1:A:2011:LEU:HD13	1:A:2040:TRP:CE3	2.49	0.48
1:A:430:PRO:O	1:A:431:ILE:HG22	2.14	0.48
1:A:472:ASN:O	1:A:475:ASP:N	2.42	0.48
2:C:377:ILE:O	2:C:380:PRO:HG2	2.13	0.48
2:C:624:LYS:O	2:C:628:TYR:HD1	1.97	0.48
2:C:646:GLY:HA3	2:C:652:MET:CE	2.44	0.48
2:C:77:LEU:O	2:C:77:LEU:HD12	2.14	0.48
2:C:908:VAL:HG13	2:C:909:ILE:N	2.28	0.48
15:L:15:C:C2'	15:L:16:U:H5"	2.43	0.48
4:O:155:PHE:CD2	4:O:167:TRP:HB2	2.49	0.48
4:O:285:SER:O	4:O:288:ALA:N	2.45	0.48
1:A:164:ALA:HB2	5:P:122:LEU:CD2	2.44	0.48
7:R:117:PHE:HD2	14:E:39:G:C6	2.31	0.48
9:T:156:THR:HG23	9:T:157:ASP:H	1.78	0.48
10:Z:121:LEU:O	10:Z:124:LEU:HB2	2.14	0.48
10:Z:12:LYS:HG3	10:Z:15:ARG:NH1	2.29	0.48
1:A:1382:ARG:HD3	1:A:1614:ILE:O	2.14	0.48
1:A:1678:ILE:N	1:A:1706:VAL:HG23	2.29	0.48
1:A:766:ILE:HG21	1:A:782:ILE:HG21	1.94	0.48
1:A:932:SER:O	1:A:935:GLU:HB3	2.13	0.48
4:O:391:GLU:O	4:O:392:MET:HB2	2.11	0.48
9:T:28:ILE:HG13	9:T:29:GLN:N	2.28	0.48
10:Z:181:LEU:HD11	10:Z:194:LEU:HD22	1.95	0.48
10:Z:422:PHE:O	10:Z:425:GLN:N	2.46	0.48
1:A:1716:LEU:N	1:A:1719:GLU:HB2	2.28	0.48
1:A:2013:ARG:HH22	1:A:2085:GLY:CA	2.27	0.48
1:A:249:LEU:HD13	1:A:254:HIS:HB2	1.95	0.48
1:A:588:LEU:HD11	1:A:613:SER:HA	1.95	0.48
1:A:631:LEU:HD21	1:A:663:LEU:HD13	1.96	0.48
1:A:789:ALA:O	1:A:792:CYS:HB2	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:161:ILE:HG22	2:C:163:ASP:H	1.79	0.48
16:M:489:A:H2'	16:M:490:A:C8	2.48	0.48
16:M:496:U:C3'	16:M:497:A:H5''	2.43	0.48
12:N:101:U:H3'	12:N:101:U:C6	2.49	0.48
1:A:1233:ARG:HD3	8:S:131:THR:HG21	1.96	0.48
1:A:1440:ILE:O	1:A:1443:TYR:N	2.37	0.48
1:A:1648:ILE:HG22	1:A:1649:PHE:CD1	2.48	0.48
1:A:1797:LEU:O	1:A:1801:SER:HB3	2.12	0.48
1:A:772:GLU:HG3	1:A:773:SER:H	1.78	0.48
4:O:149:PRO:HG3	4:O:191:SER:O	2.14	0.48
1:A:135:PRO:HG3	9:T:56:HIS:CD2	2.48	0.48
10:Z:106:PHE:CZ	10:Z:145:LYS:HG3	2.49	0.48
10:Z:465:PHE:HB2	10:Z:474:THR:HG21	1.96	0.48
1:A:137:GLU:O	1:A:138:HIS:C	2.52	0.48
1:A:174:LYS:HA	1:A:174:LYS:HD2	1.63	0.48
1:A:265:ASN:O	1:A:266:LEU:HB2	2.14	0.48
1:A:296:THR:HG22	13:D:33:U:OP2	2.14	0.48
2:C:325:LYS:NZ	2:C:441:ARG:HH22	2.12	0.48
14:E:42:A:H2'	14:E:43:C:O5'	2.13	0.48
4:O:187:ASP:HB3	4:O:200:VAL:CG1	2.44	0.48
5:P:104:LEU:HG	5:P:108:ASN:HB2	1.96	0.48
7:R:102:LEU:O	7:R:105:ARG:N	2.40	0.48
7:R:163:VAL:HG13	7:R:166:ARG:NH2	2.29	0.48
7:R:144:GLY:O	7:R:203:THR:HA	2.14	0.48
7:R:230:PRO:CG	12:N:114:U:C5	2.97	0.48
1:A:1073:ILE:HG23	1:A:1074:VAL:HG23	1.95	0.47
1:A:1051:GLU:HG2	1:A:1169:TYR:CE1	2.49	0.47
1:A:1406:LEU:HD12	10:Z:307:GLU:OE2	2.13	0.47
1:A:1562:PHE:HZ	1:A:1570:TRP:HA	1.78	0.47
1:A:1856:ASN:ND2	1:A:1968:ALA:HB3	2.29	0.47
1:A:1907:GLN:O	1:A:1911:TRP:HD1	1.97	0.47
1:A:2080:LYS:O	1:A:2084:LEU:HG	2.14	0.47
1:A:294:ASN:HB2	1:A:299:LYS:O	2.14	0.47
1:A:522:TYR:O	1:A:525:LEU:N	2.46	0.47
1:A:568:GLY:HA3	1:A:633:VAL:HG11	1.96	0.47
2:C:105:ILE:O	2:C:106:PHE:HB2	2.14	0.47
2:C:142:LEU:HG	2:C:218:HIS:HA	1.95	0.47
2:C:269:LYS:HG2	36:C:1500:GTP:C2	2.49	0.47
2:C:920:LEU:O	2:C:922:THR:N	2.46	0.47
16:M:494:G:O2'	16:M:495:A:OP1	2.29	0.47
16:M:497:A:C6	16:M:498:C:N4	2.82	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:Z:152:ILE:O	10:Z:156:LYS:CB	2.62	0.47
10:Z:228:ILE:O	10:Z:231:ASP:N	2.42	0.47
1:A:1347:ARG:HB2	1:A:1447:TRP:CD1	2.49	0.47
1:A:1527:TRP:CE3	1:A:1528:THR:HG23	2.49	0.47
1:A:156:THR:HG21	14:E:33:C:O2	2.14	0.47
1:A:2014:ALA:HB1	1:A:2058:LEU:HD12	1.96	0.47
1:A:2064:GLY:HA2	1:A:2069:VAL:O	2.13	0.47
1:A:310:ASN:HA	1:A:313:ARG:NH2	2.30	0.47
1:A:992:ASP:HB3	1:A:1108:LYS:HB2	1.96	0.47
2:C:541:GLU:HG2	2:C:542:ILE:N	2.29	0.47
2:C:739:GLY:O	2:C:741:MET:N	2.47	0.47
2:C:872:LEU:HB3	2:C:875:ILE:HD12	1.96	0.47
10:Z:413:CYS:O	10:Z:417:ARG:N	2.37	0.47
10:Z:57:CYS:O	10:Z:61:VAL:HG23	2.13	0.47
10:Z:93:THR:O	10:Z:96:LYS:HB2	2.14	0.47
1:A:1130:ARG:NH2	1:A:1158:ILE:O	2.47	0.47
1:A:926:LYS:HD2	1:A:1521:ARG:HH22	1.79	0.47
1:A:1995:TRP:HZ3	1:A:2008:LEU:HB2	1.79	0.47
1:A:260:PRO:O	1:A:261:LEU:HB3	2.14	0.47
1:A:969:ILE:HD11	1:A:982:TYR:HE1	1.79	0.47
1:A:984:VAL:HG12	1:A:985:ASP:N	2.25	0.47
2:C:107:THR:OG1	2:C:549:TYR:HB3	2.14	0.47
2:C:221:PHE:CE1	2:C:651:TYR:HD1	2.32	0.47
2:C:137:GLY:N	2:C:232:SER:OG	2.47	0.47
2:C:319:GLY:O	2:C:426:GLN:NE2	2.25	0.47
2:C:801:TRP:CD1	2:C:843:LYS:HB2	2.49	0.47
14:E:53:A:C5'	14:E:54:U:OP2	2.63	0.47
15:L:5:A:H2'	15:L:6:U:C6	2.50	0.47
6:Q:125:ILE:HG13	6:Q:126:THR:H	1.79	0.47
7:R:132:LYS:HG2	7:R:133:LYS:O	2.14	0.47
1:A:1559:HIS:O	1:A:1612:PRO:HG2	2.14	0.47
1:A:1677:GLN:HB3	1:A:1706:VAL:HB	1.96	0.47
1:A:1734:PHE:HB3	1:A:1736:VAL:HG23	1.96	0.47
1:A:2075:THR:O	1:A:2079:ILE:HD12	2.15	0.47
2:C:139:ILE:HG22	2:C:215:ALA:HB3	1.95	0.47
15:L:30:A:O3'	15:L:31:A:C4'	2.62	0.47
16:M:500:A:C2'	16:M:502:C:H5	2.24	0.47
4:O:125:TRP:CZ2	4:O:432:ALA:HB1	2.49	0.47
7:R:72:PHE:O	7:R:112:PHE:HD1	1.96	0.47
10:Z:124:LEU:HD22	10:Z:129:VAL:HG11	1.96	0.47
10:Z:184:GLN:HG3	10:Z:185:GLU:H	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1094:ASP:OD1	15:L:25:A:C4	2.67	0.47
1:A:1402:ALA:HA	1:A:1439:THR:HB	1.96	0.47
1:A:1586:GLN:HB2	1:A:1590:LEU:CD1	2.44	0.47
1:A:1626:GLN:NE2	1:A:1631:GLY:HA2	2.27	0.47
1:A:1908:LEU:HD12	1:A:1908:LEU:HA	1.66	0.47
1:A:1925:PRO:HG2	1:A:1928:GLU:HB2	1.95	0.47
1:A:209:ILE:HG23	1:A:301:TRP:NE1	2.30	0.47
2:C:316:THR:OG1	36:C:1500:GTP:N7	2.46	0.47
2:C:489:TYR:O	2:C:558:LYS:HG3	2.14	0.47
12:N:101:U:C3'	12:N:101:U:C6	2.98	0.47
7:R:91:HIS:O	7:R:92:HIS:HB3	2.14	0.47
10:Z:21:ILE:O	10:Z:24:HIS:HB2	2.14	0.47
10:Z:97:GLU:O	10:Z:101:MET:HG2	2.14	0.47
1:A:1286:TRP:CD1	1:A:1448:GLU:OE2	2.68	0.47
1:A:1339:LEU:HD21	1:A:1440:ILE:CD1	2.44	0.47
1:A:1347:ARG:HD3	1:A:1445:THR:O	2.14	0.47
1:A:763:MET:CE	1:A:779:ALA:HB1	2.43	0.47
1:A:477:MET:HE3	2:C:275:LEU:HA	1.95	0.47
2:C:864:VAL:CG2	2:C:906:VAL:HG12	2.44	0.47
19:I:114:THR:O	19:I:118:ASN:CB	2.57	0.47
1:A:1077:ASN:O	1:A:1080:ASP:HB2	2.15	0.47
1:A:1630:THR:O	1:A:1692:TYR:HB2	2.15	0.47
1:A:166:LYS:HE3	1:A:723:GLU:O	2.14	0.47
1:A:1632:ILE:HG12	1:A:1740:TYR:HB3	1.95	0.47
1:A:477:MET:CE	2:C:278:LYS:CD	2.92	0.47
1:A:501:LEU:HD13	1:A:705:GLN:HG2	1.97	0.47
1:A:591:LEU:HA	1:A:591:LEU:HD23	1.54	0.47
2:C:675:THR:OG1	2:C:676:VAL:N	2.47	0.47
1:A:839:HIS:NE2	13:D:95:C:O2	2.38	0.47
15:L:1099:G:N3	15:L:1099:G:C5'	2.73	0.47
15:L:1100:A:C2	15:L:1101:C:N1	2.82	0.47
15:L:1115:G:H2'	15:L:1116:A:C8	2.50	0.47
4:O:150:VAL:HG12	4:O:151:ASP:OD1	2.13	0.47
10:Z:117:ILE:HG22	10:Z:121:LEU:HD11	1.96	0.47
1:A:2050:THR:O	1:A:2054:GLN:HG3	2.14	0.47
1:A:356:TYR:HB3	1:A:396:ARG:NH1	2.30	0.47
2:C:132:ARG:HG2	2:C:132:ARG:O	2.15	0.47
13:D:31:G:H2'	13:D:32:G:H5'	1.96	0.47
19:I:185:ASN:O	19:I:189:LEU:HG	2.15	0.47
7:R:46:ARG:CZ	12:N:110:A:H2	2.26	0.47
6:Q:290:ILE:HG22	6:Q:292:PRO:HD3	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:R:117:PHE:CD2	14:E:39:G:C2	3.02	0.47
9:T:120:CYS:C	9:T:122:CYS:N	2.68	0.47
15:L:119:G:N7	29:V:20:LYS:CE	2.77	0.47
15:L:112:A:N7	30:W:63:ARG:CZ	2.78	0.47
10:Z:413:CYS:HB3	10:Z:416:GLY:H	1.78	0.47
10:Z:58:LYS:O	10:Z:61:VAL:HB	2.15	0.47
1:A:1627:LEU:HD11	1:A:1634:LEU:HD12	1.96	0.47
1:A:225:ARG:NH2	1:A:693:LYS:O	2.47	0.47
1:A:742:VAL:HG23	1:A:743:LYS:N	2.30	0.47
1:A:783:LEU:H	1:A:783:LEU:HD12	1.78	0.47
2:C:286:LEU:CD2	10:Z:182:GLN:HB3	2.44	0.47
5:P:127:VAL:HG11	14:E:32:U:N3	2.30	0.47
15:L:120:G:H4'	15:L:121:C:O4'	2.15	0.47
4:O:437:GLU:N	4:O:438:PRO:HD3	2.30	0.47
5:P:196:THR:OG1	5:P:197:ILE:N	2.48	0.47
9:T:108:CYS:HA	9:T:120:CYS:SG	2.54	0.47
10:Z:98:LEU:O	10:Z:101:MET:HB2	2.13	0.47
1:A:1292:ARG:HG3	1:A:1293:THR:HG23	1.97	0.47
1:A:1437:ILE:HG22	1:A:1438:PRO:O	2.14	0.47
1:A:1805:ILE:HG23	1:A:1809:ASN:ND2	2.30	0.47
1:A:2048:TRP:O	1:A:2052:GLU:HG3	2.15	0.47
1:A:2062:GLU:O	1:A:2066:LYS:HB3	2.15	0.47
1:A:159:LYS:HZ2	1:A:734:PHE:HE1	1.63	0.47
1:A:767:LEU:HD21	1:A:775:ARG:HG3	1.97	0.47
1:A:974:ASN:O	1:A:975:TYR:HB2	2.14	0.47
2:C:727:THR:HG23	2:C:736:ASP:H	1.80	0.47
6:Q:53:ASN:O	14:E:31:G:C2	2.68	0.47
19:I:99:GLN:O	19:I:103:LEU:HG	2.15	0.47
12:N:102:A:H8	12:N:102:A:H5"	1.80	0.47
4:O:157:THR:HG1	4:O:167:TRP:HD1	1.61	0.47
4:O:193:ARG:HH22	4:O:237:ASP:N	2.04	0.47
4:O:377:ASP:OD2	4:O:379:LYS:N	2.48	0.47
6:Q:206:PHE:HB3	6:Q:208:TYR:CZ	2.50	0.47
8:S:10:GLU:HG2	8:S:11:ALA:N	2.30	0.47
1:A:1400:ILE:HG23	1:A:1542:TYR:CE2	2.50	0.47
1:A:412:GLN:N	1:A:412:GLN:OE1	2.40	0.47
1:A:725:TYR:HE1	14:E:72:C:C6	2.32	0.47
2:C:312:ILE:HG23	2:C:323:THR:OG1	2.15	0.47
2:C:779:LEU:HB3	2:C:780:PRO:HD3	1.97	0.47
2:C:938:ARG:HG2	2:C:939:LYS:O	2.15	0.47
14:E:88:U:C6	15:L:17:U:C6	3.03	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:L:34:G:H2'	15:L:35:U:O4'	2.15	0.47
2:C:79:GLU:CB	4:O:167:TRP:HZ3	2.27	0.47
4:O:244:ARG:HH12	8:S:8:GLN:HE22	1.62	0.47
6:Q:217:TRP:C	6:Q:217:TRP:CD1	2.87	0.47
1:A:1296:ARG:HH12	10:Z:390:HIS:CE1	2.32	0.46
1:A:1328:PHE:O	1:A:1331:VAL:N	2.49	0.46
1:A:1343:PHE:CD1	1:A:1350:ILE:HD13	2.50	0.46
1:A:1562:PHE:CZ	1:A:1570:TRP:HA	2.50	0.46
2:C:682:SER:HA	2:C:714:PRO:CG	2.44	0.46
2:C:743:ASN:O	2:C:747:LEU:N	2.39	0.46
13:D:44:A:OP2	13:D:44:A:H4'	2.14	0.46
14:E:1:G:H2'	14:E:2:U:C6	2.50	0.46
4:O:188:VAL:HG13	4:O:197:LEU:HD11	1.97	0.46
4:O:193:ARG:NH2	4:O:237:ASP:H	2.05	0.46
5:P:103:ASN:HD22	5:P:114:VAL:HG21	1.79	0.46
8:S:167:GLN:O	8:S:171:HIS:HB2	2.15	0.46
1:A:1021:PRO:HG2	1:A:1022:PRO:HD3	1.97	0.46
1:A:1058:ALA:HA	1:A:1061:ILE:HG13	1.96	0.46
1:A:1468:ALA:HA	1:A:1473:ARG:HG2	1.96	0.46
1:A:1999:ILE:HD11	1:A:2007:ARG:NH2	2.30	0.46
2:C:412:ALA:HA	2:C:415:TYR:CE2	2.50	0.46
2:C:482:GLU:OE1	2:C:628:TYR:OH	2.32	0.46
13:D:179:U:OP1	25:G:79:LYS:HG2	253.65	0.46
9:T:120:CYS:HA	14:E:29:U:C4'	2.46	0.46
4:O:160:ASN:HA	4:O:184:THR:HG1	1.80	0.46
4:O:307:HIS:CE1	4:O:326:ALA:O	2.68	0.46
5:P:167:ALA:O	5:P:184:ARG:NH2	2.48	0.46
6:Q:3:ASP:O	6:Q:5:ILE:N	2.48	0.46
7:R:62:THR:OG1	7:R:63:ARG:N	2.45	0.46
10:Z:177:LEU:O	10:Z:180:ILE:HB	2.15	0.46
10:Z:312:LEU:HD23	10:Z:312:LEU:HA	1.75	0.46
10:Z:363:GLU:O	10:Z:366:GLU:N	2.48	0.46
10:Z:80:ILE:HG23	10:Z:90:ILE:HG22	1.97	0.46
10:Z:87:ILE:HG22	10:Z:89:ASP:H	1.80	0.46
1:A:1066:LEU:O	1:A:1068:ARG:N	2.49	0.46
1:A:1070:LEU:HD23	1:A:1070:LEU:HA	1.72	0.46
1:A:299:LYS:HA	1:A:493:MET:HG2	1.96	0.46
1:A:461:LEU:H	1:A:461:LEU:HG	1.44	0.46
1:A:801:VAL:HG13	1:A:802:PRO:HD2	1.97	0.46
1:A:960:THR:OG1	1:A:961:GLN:N	2.48	0.46
2:C:470:ALA:CB	2:C:488:ILE:HA	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:634:ILE:HG22	2:C:635:LYS:N	2.31	0.46
13:D:175:G:H4'	13:D:176:A:O4'	2.15	0.46
14:E:50:G:H2'	14:E:50:G:OP2	2.15	0.46
26:H:16:LYS:N	26:H:17:PRO:CD	2.79	0.46
4:O:111:ILE:HB	4:O:114:ARG:HE	1.80	0.46
4:O:221:TYR:O	4:O:251:TRP:HH2	1.99	0.46
5:P:108:ASN:O	5:P:110:HIS:N	2.49	0.46
5:P:35:ALA:O	5:P:37:ASN:N	2.49	0.46
6:Q:33:GLU:HG2	6:Q:34:CYS:O	2.14	0.46
9:T:150:CYS:SG	9:T:151:ARG:N	2.88	0.46
24:F:19:LYS:HZ1	32:Y:34:LEU:CB	2.27	0.46
10:Z:370:THR:OG1	10:Z:371:GLN:N	2.48	0.46
1:A:1313:ASP:HB2	1:A:1359:ILE:HD13	1.97	0.46
1:A:1875:ILE:HG22	1:A:1876:ASN:H	1.80	0.46
1:A:555:LYS:HD2	5:P:118:GLN:HE21	1.80	0.46
4:O:131:LEU:HB2	4:O:426:TRP:CZ3	2.49	0.46
7:R:105:ARG:HG2	7:R:109:LEU:HD11	1.97	0.46
8:S:168:GLU:O	8:S:171:HIS:N	2.48	0.46
10:Z:148:LEU:HD23	10:Z:148:LEU:HA	1.68	0.46
1:A:1051:GLU:OE1	1:A:1247:PHE:HB2	2.15	0.46
1:A:1347:ARG:O	1:A:1441:PHE:CE1	2.69	0.46
1:A:1023:LEU:HB2	1:A:1451:PHE:HE1	1.80	0.46
1:A:173:LEU:HD11	1:A:712:LEU:HD21	1.97	0.46
1:A:758:LEU:HD23	1:A:759:ARG:N	2.30	0.46
2:C:859:GLU:OE2	2:C:907:PRO:HB3	2.15	0.46
9:T:100:TYR:HE1	14:E:26:A:H4'	1.81	0.46
7:R:229:ASP:CG	12:N:113:U:C2	2.89	0.46
4:O:129:TRP:HB2	4:O:375:PHE:HE2	1.81	0.46
4:O:354:ASN:ND2	4:O:402:VAL:O	2.42	0.46
6:Q:38:THR:C	6:Q:39:LEU:HD12	2.36	0.46
7:R:245:GLU:HG3	7:R:249:MET:CE	2.44	0.46
28:U:39:SER:O	28:U:41:ASN:N	2.48	0.46
10:Z:131:HIS:O	10:Z:134:VAL:HG12	2.15	0.46
10:Z:338:THR:HG22	10:Z:339:PHE:N	2.31	0.46
10:Z:405:ILE:HG21	10:Z:420:ILE:HG12	1.98	0.46
1:A:1048:VAL:HG22	1:A:1250:VAL:HA	1.97	0.46
1:A:180:PRO:O	1:A:184:GLU:HB2	2.16	0.46
1:A:1818:ARG:HA	1:A:1821:LYS:HG2	1.97	0.46
1:A:588:LEU:HD22	1:A:590:TYR:CZ	2.50	0.46
1:A:1377:SER:CA	11:B:95:U:OP1	2.63	0.46
2:C:287:LYS:O	2:C:290:HIS:N	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:477:ASP:HB2	2:C:628:TYR:CD2	2.49	0.46
4:O:263:VAL:HG12	4:O:264:GLY:N	2.24	0.46
10:Z:38:GLN:O	10:Z:41:HIS:HB3	2.16	0.46
1:A:1130:ARG:HA	1:A:1130:ARG:HD2	1.75	0.46
1:A:745:THR:CG2	4:O:203:ASP:HB2	2.46	0.46
2:C:136:VAL:HG13	2:C:212:PHE:HA	1.98	0.46
2:C:489:TYR:HE2	2:C:592:PHE:CE1	2.33	0.46
2:C:821:LEU:HD23	2:C:821:LEU:HA	1.66	0.46
2:C:81:LYS:O	2:C:82:ASN:ND2	2.48	0.46
14:E:14:C:C4'	14:E:15:C:OP2	2.63	0.46
14:E:92:C:O2'	14:E:93:A:O4'	2.31	0.46
4:O:358:ILE:HG22	4:O:359:ASN:N	2.30	0.46
1:A:771:PRO:HD3	5:P:163:TRP:CD1	2.51	0.46
5:P:216:ARG:HA	5:P:219:ILE:CD1	2.45	0.46
7:R:89:TYR:HD2	14:E:34:A:N3	2.02	0.46
9:T:55:LEU:O	9:T:58:GLN:N	2.47	0.46
10:Z:368:ASN:O	10:Z:373:ILE:HG12	2.16	0.46
1:A:1036:SER:OG	1:A:1154:LYS:NZ	2.29	0.46
1:A:1458:TRP:HZ2	1:A:1489:PRO:HB2	1.81	0.46
2:C:251:GLN:NE2	2:C:255:GLN:HG2	2.31	0.46
2:C:739:GLY:O	2:C:742:ASP:N	2.21	0.46
2:C:840:PRO:O	2:C:843:LYS:N	2.48	0.46
2:C:869:HIS:CD2	2:C:925:LEU:HD22	2.50	0.46
1:A:752:ALA:HB1	14:E:62:A:O2'	2.16	0.46
14:E:64:U:H2'	14:E:65:U:C6	2.51	0.46
25:G:30:TRP:CE2	25:G:89:LEU:HD22	2.51	0.46
25:G:86:ASN:ND2	26:H:32:LYS:NZ	2.64	0.46
5:P:175:PRO:HG2	15:L:19:U:O2	2.15	0.46
15:L:2:C:H2'	15:L:3:G:C8	2.51	0.46
4:O:187:ASP:HB3	4:O:200:VAL:HG12	1.98	0.46
5:P:37:ASN:ND2	5:P:145:PRO:HD3	2.30	0.46
8:S:15:ALA:O	8:S:18:ALA:N	2.49	0.46
9:T:32:ASP:HA	9:T:35:LYS:HD3	1.98	0.46
29:V:6:PHE:CZ	29:V:10:LEU:HD11	2.51	0.46
1:A:1054:LEU:HD23	1:A:1054:LEU:HA	1.62	0.46
1:A:1151:GLU:O	1:A:1154:LYS:N	2.49	0.46
1:A:1513:GLU:O	1:A:1516:GLN:HG3	2.16	0.46
1:A:1739:ARG:HD2	1:A:1751:TYR:CZ	2.51	0.46
1:A:355:LEU:HG	1:A:356:TYR:CE2	2.50	0.46
1:A:823:TRP:CE2	1:A:851:ARG:HG2	2.50	0.46
2:C:173:LYS:HD3	13:D:76:U:OP1	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:388:ALA:HA	2:C:396:LEU:HD11	1.97	0.46
2:C:600:GLU:HB2	2:C:935:LYS:HE3	1.96	0.46
4:O:148:ASP:OD2	4:O:151:ASP:N	2.35	0.46
4:O:133:ARG:NH1	4:O:170:ALA:O	2.43	0.46
4:O:284:SER:HB3	4:O:290:VAL:HG22	1.97	0.46
1:A:817:LYS:HG2	4:O:399:GLU:OE2	2.15	0.46
6:Q:218:LYS:O	6:Q:221:ASP:HB3	2.16	0.46
9:T:55:LEU:HA	9:T:55:LEU:HD23	1.76	0.46
10:Z:40:SER:O	10:Z:44:LEU:HB3	2.16	0.46
1:A:1094:ASP:OD1	1:A:1094:ASP:N	2.49	0.46
1:A:1281:ASN:HD22	1:A:1285:VAL:HG21	1.80	0.46
1:A:1570:TRP:O	1:A:1572:GLY:N	2.49	0.46
1:A:1590:LEU:HD22	1:A:1595:ARG:HD2	1.97	0.46
1:A:1624:LEU:HA	1:A:1624:LEU:HD23	1.69	0.46
1:A:1782:ASN:ND2	1:A:1816:ARG:HH21	2.13	0.46
1:A:224:MET:O	1:A:225:ARG:C	2.54	0.46
1:A:416:GLU:HB3	1:A:419:THR:HG23	1.98	0.46
1:A:860:GLU:OE2	1:A:863:ARG:NH2	2.49	0.46
2:C:251:GLN:HE21	2:C:255:GLN:HG2	1.81	0.46
2:C:336:ILE:HD11	2:C:341:ILE:HG22	1.98	0.46
15:L:1100:A:H61	15:L:1116:A:N6	2.07	0.46
12:N:105:U:H2'	12:N:106:A:C8	2.51	0.46
5:P:134:VAL:HG12	5:P:135:VAL:N	2.31	0.46
6:Q:216:GLU:O	6:Q:219:ILE:N	2.48	0.46
6:Q:45:HIS:HB3	6:Q:55:ILE:HD11	1.97	0.46
9:T:41:LEU:HD21	14:E:35:A:N1	2.28	0.46
1:A:1068:ARG:O	1:A:1071:ARG:N	2.48	0.45
1:A:1124:LEU:O	1:A:1127:GLY:N	2.49	0.45
1:A:1053:THR:HG22	1:A:1167:ARG:HD2	1.98	0.45
1:A:1859:ARG:NH2	1:A:1876:ASN:O	2.29	0.45
4:O:220:TYR:CD1	4:O:256:ARG:HG2	2.51	0.45
5:P:205:SER:HA	5:P:208:LEU:HD12	1.98	0.45
8:S:160:MET:O	8:S:163:SER:N	2.33	0.45
10:Z:323:LYS:HE2	10:Z:364:THR:HG22	1.97	0.45
1:A:1041:VAL:HG11	1:A:1253:LYS:HA	1.99	0.45
1:A:1403:SER:OG	1:A:1404:HIS:N	2.49	0.45
1:A:1416:LYS:HA	1:A:1416:LYS:HD2	1.74	0.45
1:A:1423:THR:C	1:A:1424:HIS:CG	2.89	0.45
1:A:361:GLU:OE1	1:A:361:GLU:N	2.48	0.45
1:A:713:ASN:O	1:A:716:ARG:HG2	2.16	0.45
1:A:767:LEU:CD2	1:A:775:ARG:HG3	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:865:ARG:HH21	1:A:869:LYS:NZ	2.14	0.45
1:A:953:ARG:O	1:A:956:LYS:HB3	2.16	0.45
1:A:1377:SER:HA	11:B:95:U:OP1	2.16	0.45
19:I:203:PHE:O	19:I:206:LYS:N	2.48	0.45
15:L:1115:G:H2'	15:L:1116:A:H8	1.80	0.45
4:O:120:SER:OG	4:O:121:GLN:OE1	2.35	0.45
6:Q:240:LEU:CD1	6:Q:251:LEU:HD13	2.46	0.45
6:Q:4:GLU:O	6:Q:7:GLU:N	2.41	0.45
1:A:1012:TRP:CZ3	1:A:1013:ILE:HG13	2.51	0.45
1:A:1286:TRP:CE2	1:A:1302:LEU:HD11	2.52	0.45
1:A:1286:TRP:CD1	1:A:1286:TRP:N	2.83	0.45
1:A:1689:ARG:HA	1:A:1692:TYR:CE1	2.51	0.45
1:A:2011:LEU:HD13	1:A:2040:TRP:CZ3	2.51	0.45
1:A:304:ASP:OD1	1:A:306:PRO:HD2	2.17	0.45
1:A:345:ALA:H	3:J:3:TYR:HD2	1.64	0.45
1:A:452:PHE:HE1	2:C:347:ARG:NE	2.13	0.45
7:R:117:PHE:CD2	14:E:39:G:C6	3.04	0.45
14:E:73:A:C6	14:E:75:A:C5	3.04	0.45
7:R:73:CYS:SG	7:R:76:PHE:N	2.88	0.45
10:Z:184:GLN:HG3	10:Z:185:GLU:N	2.31	0.45
10:Z:69:ASN:HB3	10:Z:70:GLY:H	1.56	0.45
1:A:867:ILE:HG21	1:A:1101:TYR:CD1	2.52	0.45
1:A:1431:HIS:NE2	1:A:1434:GLU:HB3	2.32	0.45
1:A:1683:LYS:HB3	1:A:1701:ILE:HG23	1.97	0.45
1:A:857:ILE:O	1:A:860:GLU:N	2.50	0.45
2:C:394:ASP:O	2:C:397:LYS:HB3	2.16	0.45
2:C:500:ARG:HB2	2:C:578:TYR:O	2.16	0.45
9:T:97:LYS:NZ	13:D:123:U:OP2	2.45	0.45
12:N:102:A:C2	14:E:51:A:C8	3.05	0.45
14:E:53:A:H4'	14:E:54:U:OP2	2.16	0.45
15:L:18:U:C5	19:I:202:GLN:CG	2.99	0.45
14:E:88:U:H5''	15:L:17:U:H5	1.82	0.45
10:Z:22:ARG:HA	10:Z:25:VAL:HG23	1.99	0.45
10:Z:369:TYR:CE2	10:Z:405:ILE:HG12	2.51	0.45
1:A:1508:HIS:CD2	1:A:1532:HIS:CD2	3.05	0.45
1:A:1648:ILE:HG22	1:A:1649:PHE:CE1	2.52	0.45
1:A:1798:ILE:O	1:A:1802:MET:HG2	2.17	0.45
1:A:1877:GLY:C	1:A:1894:ILE:HB	2.37	0.45
1:A:988:GLU:O	1:A:991:THR:OG1	2.34	0.45
2:C:449:PHE:O	2:C:453:THR:HG23	2.16	0.45
9:T:89:LYS:HE2	13:D:123:U:O2'	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:O:355:THR:O	4:O:356:LEU:HD23	2.17	0.45
7:R:48:VAL:HG11	7:R:203:THR:HG23	1.99	0.45
7:R:96:GLU:OE2	7:R:187:LYS:NZ	2.47	0.45
7:R:97:GLU:O	7:R:100:GLY:HA3	2.16	0.45
9:T:88:ASP:OD2	9:T:90:LEU:HB2	2.17	0.45
15:L:112:A:N7	30:W:63:ARG:NH1	2.65	0.45
1:A:1161:TYR:OH	1:A:1163:ARG:HB2	2.17	0.45
1:A:1369:ASN:HB3	1:A:1378:LYS:HZ1	1.81	0.45
2:C:265:PHE:CE2	2:C:295:ILE:HD12	2.52	0.45
2:C:777:ASP:O	2:C:778:THR:HB	2.17	0.45
4:O:132:SER:HB3	4:O:427:LYS:HB2	1.99	0.45
1:A:797:ILE:HD12	5:P:172:TRP:HH2	1.82	0.45
10:Z:381:LEU:O	10:Z:422:PHE:HD2	1.99	0.45
10:Z:465:PHE:CD1	10:Z:468:ILE:HD12	2.52	0.45
1:A:1899:TRP:CH2	1:A:1909:ALA:HA	2.43	0.45
1:A:168:LEU:HD12	1:A:199:ILE:HD11	1.99	0.45
1:A:548:LEU:HD23	1:A:548:LEU:HA	1.70	0.45
2:C:201:THR:HA	2:C:207:SER:HA	1.97	0.45
2:C:451:ASN:O	2:C:455:HIS:HB2	2.16	0.45
2:C:585:ASP:O	2:C:588:GLN:N	2.50	0.45
2:C:621:ALA:O	2:C:624:LYS:HB2	2.16	0.45
2:C:706:LEU:HD21	2:C:834:MET:CE	2.44	0.45
2:C:775:ILE:HG22	2:C:776:ASN:N	2.28	0.45
1:A:355:LEU:CD1	13:D:105:A:C5'	2.94	0.45
9:T:119:THR:OG1	14:E:28:U:OP1	2.34	0.45
14:E:42:A:O2'	14:E:43:C:P	2.74	0.45
15:L:1103:C:N1	15:L:1114:G:N2	2.64	0.45
15:L:1116:A:C4	15:L:1117:G:C5	3.05	0.45
10:Z:161:LYS:HD2	10:Z:164:LEU:HB3	1.98	0.45
10:Z:408:THR:CB	10:Z:410:GLU:HB3	2.46	0.45
1:A:1454:SER:HB2	1:A:1488:ILE:HG22	1.99	0.45
1:A:1814:VAL:HG21	1:A:1949:LEU:HD21	1.97	0.45
1:A:828:HIS:O	1:A:829:TYR:C	2.55	0.45
2:C:148:SER:OG	2:C:149:LEU:N	2.49	0.45
2:C:671:SER:OG	2:C:672:ASP:N	2.50	0.45
1:A:376:ARG:NH2	2:C:962:LEU:HD21	2.31	0.45
1:A:537:THR:HG21	13:D:84:A:H62	1.81	0.45
1:A:381:SER:HB3	3:J:3:TYR:O	2.16	0.45
6:Q:215:PRO:HB2	6:Q:217:TRP:CE3	2.52	0.45
6:Q:223:VAL:O	6:Q:227:LEU:HG	2.17	0.45
9:T:120:CYS:HB2	9:T:122:CYS:H	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1069:LEU:O	1:A:1072:LEU:HB2	2.17	0.45
1:A:1348:GLU:OE2	1:A:1448:GLU:HG3	2.17	0.45
1:A:1366:ARG:O	1:A:1369:ASN:HB2	2.16	0.45
1:A:1774:MET:O	1:A:1786:ALA:CA	2.34	0.45
1:A:247:PRO:HB3	1:A:595:TYR:CZ	2.51	0.45
1:A:683:LEU:HA	1:A:683:LEU:HD23	1.64	0.45
2:C:174:PRO:HG2	2:C:176:ARG:HD3	1.99	0.45
2:C:314:ALA:CB	2:C:321:THR:HG22	2.46	0.45
2:C:353:TYR:CD1	2:C:353:TYR:N	2.83	0.45
2:C:428:ILE:HG22	2:C:429:PHE:CD1	2.51	0.45
2:C:829:VAL:CG1	2:C:834:MET:HG3	2.47	0.45
2:C:887:ARG:HE	2:C:938:ARG:NH2	2.14	0.45
1:A:532:ASN:CG	13:D:84:A:OP2	2.54	0.45
25:G:30:TRP:CD2	25:G:89:LEU:HD22	2.52	0.45
15:L:1120:G:C5'	15:L:1120:G:C8	3.00	0.45
16:M:483:U:OP2	16:M:483:U:C5	2.70	0.45
4:O:119:LEU:HA	4:O:119:LEU:HD23	1.60	0.45
4:O:270:ASN:HD21	4:O:286:THR:CG2	2.30	0.45
4:O:315:ALA:O	4:O:323:VAL:HA	2.17	0.45
6:Q:33:GLU:HA	6:Q:39:LEU:O	2.16	0.45
8:S:32:PRO:O	13:D:109:A:H4'	2.17	0.45
8:S:7:PRO:O	8:S:8:GLN:CB	2.64	0.45
9:T:44:LYS:HA	9:T:44:LYS:HD3	1.68	0.45
10:Z:10:ASP:OD2	10:Z:244:LYS:NZ	2.45	0.45
10:Z:452:GLU:CD	10:Z:452:GLU:H	2.20	0.45
1:A:1033:ASN:O	1:A:1035:LEU:N	2.50	0.45
1:A:1270:LEU:HD23	1:A:1270:LEU:HA	1.77	0.45
1:A:157:ASP:O	1:A:160:ALA:HB3	2.16	0.45
1:A:1710:GLU:HB2	1:A:1724:PHE:HB3	1.99	0.45
1:A:1922:ARG:HG2	1:A:1951:PHE:HZ	1.81	0.45
1:A:308:MET:HE2	1:A:486:PHE:O	2.17	0.45
1:A:688:TYR:O	1:A:690:LYS:N	2.49	0.45
1:A:763:MET:HB3	1:A:763:MET:HE3	1.75	0.45
2:C:179:ASP:OD1	2:C:184:GLU:HB3	2.17	0.45
1:A:1411:ASP:H	3:J:6:ILE:HA	1.81	0.45
16:M:483:U:C6	16:M:484:U:O4	2.70	0.45
4:O:370:ASN:OD1	4:O:370:ASN:N	2.44	0.45
5:P:65:GLU:O	5:P:68:ALA:N	2.49	0.45
5:P:110:HIS:CE1	6:Q:19:ASP:HA	2.52	0.45
9:T:14:ASP:C	9:T:16:PHE:H	2.21	0.45
10:Z:360:ALA:O	10:Z:364:THR:HG23	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:Z:414:PRO:N	10:Z:417:ARG:HH11	2.15	0.45
1:A:140:ARG:O	1:A:144:ASN:HB2	2.17	0.44
1:A:1594:GLN:O	1:A:1598:LEU:HB2	2.17	0.44
1:A:1610:TRP:CD1	1:A:1610:TRP:N	2.85	0.44
1:A:1800:ASN:O	1:A:1803:ARG:HB2	2.17	0.44
1:A:194:HIS:CD2	1:A:557:PHE:HE1	2.35	0.44
2:C:103:HIS:ND1	2:C:662:SER:OG	2.50	0.44
2:C:320:PHE:HB2	2:C:429:PHE:CD2	2.52	0.44
2:C:510:ARG:HD2	2:C:591:PHE:CE2	2.52	0.44
2:C:833:VAL:O	2:C:837:GLN:HB3	2.14	0.44
12:N:104:G:O6	14:E:49:A:N1	2.50	0.44
4:O:211:LEU:HA	4:O:211:LEU:HD23	1.77	0.44
7:R:145:ALA:HB2	7:R:204:LEU:HD12	1.99	0.44
7:R:4:TRP:CE2	7:R:92:HIS:CD2	3.06	0.44
10:Z:169:THR:HG1	10:Z:170:HIS:H	1.65	0.44
10:Z:285:SER:O	10:Z:287:ASN:N	2.49	0.44
1:A:1130:ARG:O	1:A:1133:ASP:HB2	2.17	0.44
1:A:1196:GLU:HB3	1:A:1199:ILE:HD12	1.98	0.44
1:A:1424:HIS:NE2	3:J:6:ILE:HD13	2.32	0.44
1:A:1454:SER:OG	1:A:1455:GLN:N	2.50	0.44
1:A:1458:TRP:CZ2	1:A:1491:ILE:HD13	2.52	0.44
1:A:1548:GLN:O	1:A:1551:GLY:N	2.49	0.44
1:A:265:ASN:HA	1:A:281:TYR:CZ	2.52	0.44
2:C:130:PRO:HG2	2:C:558:LYS:HZ1	1.80	0.44
2:C:885:GLY:HA2	2:C:907:PRO:CD	2.46	0.44
15:L:41:C:H42	16:M:494:G:H1	1.66	0.44
16:M:483:U:O3'	16:M:484:U:C6	2.71	0.44
16:M:484:U:O2'	16:M:485:U:C2	2.70	0.44
4:O:147:ILE:HG13	4:O:154:TRP:O	2.17	0.44
5:P:87:ASN:HD22	5:P:90:SER:HB2	1.82	0.44
7:R:31:ASN:OD1	7:R:32:ILE:N	2.50	0.44
10:Z:198:PHE:O	10:Z:201:ARG:HB3	2.17	0.44
10:Z:303:LEU:O	10:Z:304:SER:OG	2.32	0.44
1:A:1111:SER:HA	1:A:1514:PHE:HE2	1.83	0.44
1:A:745:THR:O	1:A:746:THR:HG23	2.17	0.44
1:A:782:ILE:O	1:A:785:HIS:HB2	2.17	0.44
1:A:950:THR:O	1:A:953:ARG:N	2.50	0.44
1:A:1379:MET:HG2	11:B:94:U:H1'	2.00	0.44
14:E:53:A:C4'	14:E:54:U:OP2	2.65	0.44
19:I:203:PHE:O	19:I:206:LYS:HB3	2.17	0.44
15:L:119:G:C8	30:W:99:ASP:OD2	2.69	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:O:317:HIS:HD2	4:O:378:TYR:CE2	2.34	0.44
5:P:165:ILE:HG22	5:P:166:PRO:O	2.18	0.44
7:R:110:ASP:OD2	7:R:114:ARG:NE	2.41	0.44
7:R:146:LEU:CD2	7:R:147:ASN:H	2.28	0.44
1:A:1063:PHE:HE1	1:A:1086:ASN:ND2	2.07	0.44
1:A:1703:MET:HB2	1:A:1732:MET:HB2	2.00	0.44
1:A:180:PRO:O	1:A:181:HIS:HB2	2.18	0.44
1:A:139:LEU:CG	1:A:570:GLN:HE22	2.28	0.44
1:A:649:LEU:HD12	1:A:649:LEU:HA	1.61	0.44
2:C:273:LEU:HA	2:C:273:LEU:HD12	1.78	0.44
2:C:278:LYS:O	2:C:279:LEU:HD12	2.16	0.44
2:C:847:TYR:O	2:C:850:LEU:N	2.48	0.44
7:R:117:PHE:HD2	14:E:39:G:C5	2.35	0.44
24:F:20:LEU:O	24:F:31:ILE:HA	2.16	0.44
6:Q:39:LEU:CD1	6:Q:111:ARG:HG3	2.44	0.44
6:Q:26:THR:HG22	6:Q:27:LYS:N	2.33	0.44
7:R:186:PHE:CD1	7:R:186:PHE:N	2.85	0.44
9:T:156:THR:HG23	9:T:157:ASP:N	2.32	0.44
10:Z:139:LEU:HD21	10:Z:154:VAL:HG11	1.99	0.44
10:Z:344:SER:O	10:Z:348:GLU:HG3	2.17	0.44
1:A:999:LEU:O	1:A:1000:TRP:C	2.55	0.44
1:A:149:MET:HB2	1:A:154:TYR:HD2	1.82	0.44
1:A:1580:GLY:O	1:A:1582:GLU:N	2.51	0.44
1:A:252:GLU:CD	1:A:253:GLN:HG3	2.38	0.44
1:A:773:SER:O	1:A:775:ARG:HB2	2.17	0.44
2:C:580:VAL:HG22	2:C:581:LYS:H	1.83	0.44
2:C:869:HIS:CD2	2:C:925:LEU:HD13	2.52	0.44
14:E:66:C:H6	14:E:66:C:H5'	1.81	0.44
4:O:209:TRP:CZ3	4:O:216:ILE:HG13	2.53	0.44
4:O:317:HIS:CE1	4:O:320:GLU:H	2.35	0.44
5:P:120:ASP:OD1	5:P:121:PRO:HD2	2.18	0.44
5:P:89:ALA:HB2	13:D:111:C:OP1	2.17	0.44
7:R:186:PHE:CD2	7:R:192:ALA:HA	2.52	0.44
7:R:234:ALA:O	7:R:238:LEU:HG	2.18	0.44
7:R:34:TYR:CE2	14:E:41:A:H1'	2.53	0.44
7:R:63:ARG:HG3	7:R:85:PRO:O	2.17	0.44
1:A:263:PRO:HD2	9:T:7:ARG:NH2	2.32	0.44
10:Z:449:PHE:CZ	10:Z:465:PHE:HE2	2.35	0.44
1:A:542:HIS:O	1:A:544:LYS:N	2.51	0.44
2:C:410:GLN:OE1	2:C:413:LEU:HD12	2.17	0.44
15:L:1098:C:H2'	15:L:1099:G:H5''	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:L:51:C:H2'	15:L:52:A:C8	2.52	0.44
16:M:484:U:O3'	16:M:485:U:C6	2.70	0.44
10:Z:104:GLN:O	10:Z:107:ASN:HB2	2.18	0.44
1:A:1049:LEU:HB2	1:A:1249:SER:OG	2.18	0.44
1:A:1716:LEU:HB2	1:A:1719:GLU:HG3	1.99	0.44
1:A:504:LYS:HA	1:A:504:LYS:HD3	1.76	0.44
1:A:549:LYS:HB3	1:A:549:LYS:HE2	1.66	0.44
1:A:999:LEU:HD23	1:A:999:LEU:HA	1.68	0.44
2:C:576:THR:HG22	2:C:592:PHE:CD2	2.48	0.44
2:C:787:LEU:HA	2:C:790:LYS:HE3	1.99	0.44
14:E:15:C:C6	14:E:15:C:OP2	2.70	0.44
14:E:50:G:C8	14:E:50:G:OP2	2.70	0.44
15:L:50:U:H2'	15:L:51:C:H6	1.81	0.44
5:P:34:ILE:HG23	5:P:35:ALA:N	2.32	0.44
7:R:189:GLN:HG3	7:R:193:GLU:OE2	2.17	0.44
7:R:12:GLN:HE22	7:R:76:PHE:HD1	1.64	0.44
9:T:88:ASP:OD1	9:T:90:LEU:N	2.50	0.44
10:Z:176:LYS:O	10:Z:180:ILE:HG13	2.17	0.44
10:Z:302:SER:OG	10:Z:302:SER:O	2.32	0.44
1:A:1266:GLU:HG3	1:A:1305:SER:HB2	2.00	0.44
1:A:129:THR:CG2	1:A:130:PRO:HD2	2.48	0.44
1:A:1434:GLU:OE1	1:A:1434:GLU:N	2.50	0.44
1:A:1860:VAL:HG21	16:M:502:C:H4'	2.00	0.44
1:A:2010:LEU:HD23	1:A:2013:ARG:HD2	1.99	0.44
2:C:465:GLU:HB3	2:C:467:THR:HG23	1.99	0.44
2:C:539:VAL:HG11	2:C:542:ILE:HD11	2.00	0.44
1:A:725:TYR:CD1	14:E:72:C:O4'	2.65	0.44
15:L:20:G:C8	15:L:20:G:O5'	2.70	0.44
4:O:198:PHE:CE1	4:O:239:ILE:HD11	2.52	0.44
4:O:252:ASP:HB2	4:O:259:VAL:CG2	2.48	0.44
1:A:1012:TRP:CE3	1:A:1013:ILE:HG13	2.53	0.44
1:A:1563:LYS:HB2	1:A:1781:TYR:HD1	1.82	0.44
1:A:377:VAL:HG11	2:C:912:ALA:HB3	1.99	0.44
2:C:153:LEU:HD23	2:C:153:LEU:HA	1.78	0.44
2:C:678:SER:O	2:C:857:LEU:HD12	2.18	0.44
2:C:769:TYR:HD2	2:C:803:VAL:HG11	1.82	0.44
14:E:91:A:N7	19:I:97:TYR:HE1	2.06	0.44
15:L:36:A:H2'	15:L:37:G:H8	1.83	0.44
4:O:210:ASP:HB2	4:O:217:ILE:HG13	2.00	0.44
6:Q:66:THR:O	6:Q:69:ASN:N	2.46	0.44
6:Q:80:TRP:CZ3	6:Q:91:ILE:HD11	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:R:246:SER:O	7:R:250:MET:HG3	2.18	0.44
9:T:5:LYS:O	9:T:9:SER:HB3	2.17	0.44
10:Z:58:LYS:C	10:Z:61:VAL:H	2.22	0.44
1:A:180:PRO:HA	1:A:187:LYS:CE	2.47	0.43
2:C:195:GLY:CA	2:C:545:LEU:HD13	2.48	0.43
2:C:883:ARG:HG3	2:C:914:PHE:CD1	2.53	0.43
7:R:153:PRO:O	7:R:156:ILE:HB	2.17	0.43
7:R:48:VAL:HG13	7:R:218:GLY:O	2.18	0.43
1:A:1066:LEU:O	1:A:1069:LEU:N	2.51	0.43
1:A:1147:PHE:C	1:A:1148:LYS:HD2	2.38	0.43
1:A:1165:LEU:HD23	1:A:1165:LEU:HA	1.74	0.43
1:A:1311:LYS:O	1:A:1314:SER:HB2	2.18	0.43
1:A:1687:HIS:CG	1:A:1688:PRO:HD2	2.53	0.43
1:A:1811:ALA:O	1:A:1814:VAL:HB	2.17	0.43
1:A:874:ILE:O	1:A:875:THR:OG1	2.29	0.43
1:A:888:GLU:O	1:A:892:SER:CB	2.66	0.43
1:A:987:LEU:HA	1:A:987:LEU:HD23	1.78	0.43
2:C:727:THR:HG22	2:C:736:ASP:HB2	1.99	0.43
19:I:200:ASN:O	19:I:204:ASN:CB	2.63	0.43
4:O:359:ASN:CG	4:O:360:GLN:H	2.20	0.43
4:O:379:LYS:CD	5:P:47:ARG:HH22	2.21	0.43
6:Q:206:PHE:HB3	6:Q:208:TYR:OH	2.17	0.43
6:Q:23:ILE:HG22	6:Q:24:ARG:N	2.33	0.43
7:R:163:VAL:HG13	7:R:166:ARG:HH21	1.83	0.43
29:V:17:ILE:HG12	29:V:95:ILE:HG23	2.00	0.43
10:Z:297:LEU:O	10:Z:300:LYS:N	2.48	0.43
10:Z:369:TYR:CZ	10:Z:405:ILE:HG12	2.52	0.43
1:A:137:GLU:HB2	9:T:52:ILE:HG21	2.01	0.43
1:A:1619:VAL:HG11	1:A:1635:HIS:HB3	2.00	0.43
1:A:525:LEU:HA	1:A:525:LEU:HD23	1.44	0.43
1:A:244:ASP:HB3	1:A:594:ASP:HB2	2.00	0.43
1:A:716:ARG:NH2	13:D:112:C:C4	2.86	0.43
1:A:727:GLY:O	1:A:731:THR:HG23	2.18	0.43
2:C:469:TRP:HA	2:C:577:LEU:O	2.18	0.43
24:F:47:GLU:HB3	32:Y:15:TYR:CG	2.52	0.43
25:G:45:GLY:HA3	25:G:53:VAL:HG12	2.00	0.43
25:G:88:THR:HG23	27:K:67:SER:CB	2.49	0.43
26:H:16:LYS:CG	26:H:17:PRO:HD3	2.49	0.43
16:M:495:A:C8	16:M:496:U:C4	3.06	0.43
16:M:499:U:O5'	16:M:499:U:C6	2.70	0.43
12:N:108:U:O4'	12:N:109:U:OP2	2.37	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:Q:34:CYS:SG	6:Q:60:ILE:HA	2.59	0.43
6:Q:81:HIS:O	6:Q:82:ILE:HG13	2.17	0.43
9:T:44:LYS:O	9:T:45:SER:C	2.56	0.43
28:U:14:ALA:HA	28:U:78:LEU:HD21	2.01	0.43
10:Z:326:VAL:HG13	10:Z:361:TYR:HE1	1.83	0.43
10:Z:61:VAL:HG11	10:Z:101:MET:CE	2.47	0.43
1:A:1654:TRP:HA	1:A:1657:ILE:HD12	1.99	0.43
1:A:1963:LEU:HA	1:A:1964:PRO:HD3	1.83	0.43
1:A:2053:SER:HA	1:A:2056:ARG:HH11	1.83	0.43
2:C:204:GLU:HB2	2:C:206:LYS:H	1.83	0.43
2:C:313:PHE:HD2	2:C:322:PHE:CE1	2.36	0.43
2:C:604:LYS:HE2	2:C:643:VAL:HG11	2.01	0.43
2:C:749:LYS:O	2:C:753:THR:CB	2.66	0.43
2:C:862:TYR:HE1	2:C:908:VAL:CB	2.31	0.43
15:L:1102:C:C2	15:L:1103:C:C5	3.06	0.43
16:M:485:U:O2'	16:M:486:A:C5	2.71	0.43
4:O:273:GLN:HB3	4:O:316:LEU:HD11	2.01	0.43
5:P:180:VAL:HG12	5:P:181:ALA:O	2.19	0.43
7:R:183:PHE:HD2	12:N:113:U:C2	2.36	0.43
7:R:71:PHE:CE1	7:R:109:LEU:HD13	2.54	0.43
1:A:555:LYS:HA	9:T:113:GLU:OE1	2.17	0.43
1:A:1039:TRP:CE3	1:A:1271:PRO:HB3	2.53	0.43
1:A:1845:ASN:H	1:A:1849:LYS:HZ3	1.67	0.43
1:A:580:ASN:O	1:A:581:LEU:C	2.57	0.43
2:C:194:ASN:OD1	2:C:195:GLY:N	2.52	0.43
2:C:313:PHE:HB2	2:C:322:PHE:CZ	2.53	0.43
2:C:462:SER:OG	2:C:464:PRO:HD3	2.19	0.43
2:C:605:ILE:HG22	2:C:606:VAL:O	2.18	0.43
2:C:614:GLU:HB3	2:C:666:ILE:HD13	2.00	0.43
2:C:635:LYS:HB2	2:C:643:VAL:HB	2.00	0.43
2:C:669:LYS:HB2	2:C:669:LYS:HE3	1.74	0.43
2:C:676:VAL:HG12	2:C:677:PHE:N	2.33	0.43
2:C:862:TYR:HE1	2:C:908:VAL:HB	1.83	0.43
14:E:42:A:C2'	14:E:43:C:O5'	2.65	0.43
24:F:87:LEU:HG	24:F:92:ILE:HD11	2.00	0.43
16:M:495:A:C5	16:M:496:U:C4	3.06	0.43
1:A:760:ASN:ND2	4:O:244:ARG:HE	2.16	0.43
5:P:100:ALA:HB3	5:P:102:ALA:HB2	2.00	0.43
6:Q:45:HIS:CG	6:Q:55:ILE:HD11	2.53	0.43
10:Z:32:LEU:O	10:Z:72:LEU:HD13	2.18	0.43
10:Z:80:ILE:HA	10:Z:83:LEU:HB2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1130:ARG:HD2	1:A:1133:ASP:OD2	2.18	0.43
1:A:312:TYR:CE2	1:A:319:ARG:NH1	2.87	0.43
1:A:333:LYS:O	1:A:336:PHE:HB2	2.18	0.43
1:A:687:ILE:HG22	1:A:687:ILE:O	2.19	0.43
1:A:729:LEU:HD12	1:A:729:LEU:HA	1.78	0.43
1:A:744:THR:OG1	1:A:745:THR:N	2.51	0.43
1:A:480:TYR:HE1	2:C:418:GLN:HB2	1.84	0.43
2:C:502:LEU:HD11	2:C:506:GLN:HB2	1.99	0.43
2:C:737:ILE:HG23	2:C:768:PHE:CD2	2.53	0.43
4:O:213:LYS:HZ2	13:D:107:C:H5"	1.84	0.43
2:C:74:VAL:HG22	4:O:131:LEU:O	2.18	0.43
4:O:196:TYR:HE2	8:S:37:LEU:HD22	1.84	0.43
5:P:65:GLU:OE1	5:P:65:GLU:HA	2.17	0.43
10:Z:181:LEU:CD1	10:Z:194:LEU:HD22	2.48	0.43
10:Z:85:SER:HB2	10:Z:220:TYR:CE1	2.51	0.43
1:A:1442:ARG:HD3	1:A:1442:ARG:HA	1.77	0.43
1:A:1557:LEU:HD13	1:A:1562:PHE:CD2	2.54	0.43
1:A:1813:TYR:O	1:A:1817:GLU:HG3	2.18	0.43
1:A:1840:TYR:O	1:A:1843:LEU:HG	2.18	0.43
1:A:289:ASP:O	1:A:290:SER:C	2.57	0.43
1:A:355:LEU:HG	1:A:356:TYR:CD2	2.52	0.43
1:A:605:LEU:HA	1:A:605:LEU:HD23	1.49	0.43
1:A:758:LEU:O	1:A:761:SER:N	2.51	0.43
2:C:251:GLN:HG2	2:C:933:TRP:CD2	2.54	0.43
2:C:427:LEU:O	2:C:427:LEU:HG	2.17	0.43
2:C:609:PRO:HA	2:C:668:ILE:HG22	2.00	0.43
2:C:829:VAL:HG12	2:C:830:ASN:N	2.32	0.43
2:C:798:GLY:CA	2:C:839:ILE:HG23	2.46	0.43
15:L:1097:G:H2'	15:L:1098:C:C6	2.54	0.43
15:L:28:U:H2'	15:L:29:C:H5'	2.00	0.43
16:M:490:A:H2'	16:M:491:C:H6	1.78	0.43
5:P:232:GLN:OE1	5:P:235:LEU:HD22	2.19	0.43
7:R:117:PHE:O	7:R:129:SER:HA	2.19	0.43
8:S:30:LEU:HA	8:S:30:LEU:HD23	1.71	0.43
10:Z:135:ILE:O	10:Z:138:ILE:HB	2.19	0.43
10:Z:323:LYS:O	10:Z:326:VAL:HB	2.18	0.43
1:A:1077:ASN:O	1:A:1078:ILE:C	2.56	0.43
1:A:667:TYR:OH	1:A:1622:GLY:HA2	2.19	0.43
1:A:1757:LEU:O	1:A:1760:THR:OG1	2.29	0.43
1:A:431:ILE:HG22	10:Z:182:GLN:NE2	2.34	0.43
1:A:460:PRO:HG3	2:C:376:PHE:CD1	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:P:103:ASN:ND2	5:P:114:VAL:HG21	2.33	0.43
6:Q:243:ASN:HB3	6:Q:248:CYS:SG	2.58	0.43
9:T:106:LEU:HA	9:T:106:LEU:HD23	1.71	0.43
9:T:80:TRP:CZ2	9:T:84:GLU:HG3	2.54	0.43
10:Z:169:THR:O	10:Z:173:ILE:HG13	2.19	0.43
10:Z:361:TYR:O	10:Z:362:ASN:C	2.56	0.43
1:A:1028:TRP:CD1	1:A:1260:PHE:CE2	3.07	0.43
1:A:190:LYS:O	1:A:203:ASN:N	2.40	0.43
1:A:851:ARG:O	1:A:855:LEU:HG	2.18	0.43
1:A:864:GLN:NE2	1:A:1100:LYS:H	2.16	0.43
1:A:977:ASN:HB2	8:S:175:ARG:NH1	2.34	0.43
2:C:229:LEU:O	2:C:232:SER:N	2.51	0.43
2:C:318:LEU:HD13	2:C:425:LEU:HD12	2.00	0.43
14:E:70:U:H2'	14:E:71:G:O4'	2.19	0.43
25:G:34:GLN:NE2	25:G:37:ILE:HD12	2.34	0.43
4:O:144:CYS:HB3	4:O:186:ARG:O	2.19	0.43
4:O:206:VAL:HB	4:O:220:TYR:HB2	2.00	0.43
4:O:312:ARG:O	4:O:312:ARG:HG2	2.19	0.43
5:P:70:THR:O	5:P:73:TYR:N	2.51	0.43
10:Z:130:ILE:HG22	10:Z:225:HIS:HD2	1.83	0.43
10:Z:63:PHE:CZ	10:Z:72:LEU:HD12	2.50	0.43
1:A:895:PHE:CE2	1:A:1073:ILE:HG13	2.47	0.43
1:A:1187:LEU:HA	1:A:1187:LEU:HD23	1.78	0.43
1:A:1456:ARG:HG3	1:A:1457:VAL:N	2.34	0.43
1:A:654:HIS:CE1	1:A:658:ASN:HD21	2.37	0.43
1:A:683:LEU:O	1:A:684:LYS:C	2.56	0.43
2:C:159:LYS:HE2	2:C:159:LYS:HB3	1.83	0.43
2:C:656:LEU:HD23	2:C:656:LEU:HA	1.43	0.43
1:A:358:ARG:NH2	13:D:91:U:O2'	2.51	0.43
15:L:120:G:C2	25:G:33:GLU:O	2.71	0.43
15:L:121:C:O2'	29:V:20:LYS:HE3	2.19	0.43
2:C:70:TYR:CE2	4:O:134:VAL:HG21	2.54	0.43
7:R:33:TRP:C	7:R:33:TRP:CD1	2.92	0.43
1:A:1145:MET:SD	1:A:1160:LEU:HD22	2.59	0.42
1:A:1343:PHE:HE2	1:A:1402:ALA:CB	2.32	0.42
1:A:207:ARG:HH12	1:A:299:LYS:HE2	1.84	0.42
1:A:794:LYS:O	1:A:796:ASN:N	2.52	0.42
2:C:153:LEU:HD13	2:C:212:PHE:CZ	2.54	0.42
2:C:317:LYS:HB2	36:C:1500:GTP:C5	2.54	0.42
2:C:340:LYS:O	2:C:343:ASP:CB	2.53	0.42
2:C:431:GLN:H	2:C:431:GLN:CD	2.23	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:925:LEU:HA	2:C:925:LEU:HD23	1.70	0.42
13:D:81:A:HO2'	13:D:82:A:P	2.36	0.42
19:I:118:ASN:OD1	19:I:121:LYS:HD2	2.19	0.42
5:P:106:LEU:HD13	6:Q:14:GLU:HG3	2.01	0.42
6:Q:210:ILE:HD11	6:Q:249:GLY:N	2.34	0.42
6:Q:46:PHE:HD1	6:Q:47:LYS:O	2.02	0.42
7:R:103:ALA:HA	7:R:106:THR:HG23	2.00	0.42
7:R:139:VAL:O	7:R:181:CYS:HA	2.19	0.42
10:Z:106:PHE:HZ	10:Z:145:LYS:HG3	1.84	0.42
10:Z:15:ARG:O	10:Z:19:GLU:HB3	2.19	0.42
10:Z:131:HIS:HB2	10:Z:224:THR:CG2	2.49	0.42
10:Z:297:LEU:HA	10:Z:297:LEU:HD12	1.62	0.42
1:A:1320:LEU:HD23	1:A:1320:LEU:HA	1.62	0.42
1:A:1644:SER:O	1:A:1647:GLN:HB2	2.19	0.42
1:A:206:PRO:HB2	1:A:496:ALA:CB	2.49	0.42
2:C:279:LEU:O	2:C:280:PRO:C	2.55	0.42
2:C:363:PRO:O	2:C:364:PHE:HB3	2.19	0.42
2:C:700:GLU:HG2	2:C:701:GLU:N	2.33	0.42
2:C:715:MET:HG3	2:C:817:GLN:HB2	2.01	0.42
13:D:80:G:C2	13:D:82:A:C2	3.07	0.42
7:R:89:TYR:CB	14:E:34:A:C2	3.02	0.42
3:J:21:GLN:NE2	10:Z:310:HIS:CE1	2.87	0.42
16:M:500:A:H3'	16:M:500:A:H8	1.83	0.42
2:C:79:GLU:HB3	4:O:167:TRP:HZ3	1.84	0.42
4:O:176:THR:OG1	4:O:177:THR:N	2.52	0.42
5:P:201:PHE:O	5:P:204:LEU:N	2.52	0.42
6:Q:46:PHE:O	6:Q:56:ILE:N	2.52	0.42
7:R:231:ASP:C	7:R:231:ASP:OD1	2.56	0.42
7:R:1:MET:HA	7:R:5:ARG:HB3	2.02	0.42
7:R:83:LEU:HA	7:R:83:LEU:HD23	1.81	0.42
9:T:64:TYR:OH	9:T:69:LYS:HE2	2.19	0.42
10:Z:379:ASP:O	10:Z:381:LEU:N	2.53	0.42
1:A:1555:THR:O	1:A:1558:GLU:N	2.52	0.42
1:A:1382:ARG:NH1	1:A:1614:ILE:O	2.53	0.42
1:A:1852:VAL:HB	1:A:1935:VAL:CG2	2.49	0.42
1:A:193:TYR:HD1	1:A:194:HIS:O	2.01	0.42
1:A:1889:LEU:HD12	1:A:1989:PHE:HB2	2.00	0.42
1:A:968:ASP:HB2	1:A:983:SER:OG	2.20	0.42
3:J:19:HIS:ND1	11:B:91:A:N7	2.68	0.42
2:C:121:ASP:O	2:C:124:LEU:HB2	2.19	0.42
2:C:320:PHE:CD1	2:C:425:LEU:HD13	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:D:78:A:HO2'	13:D:79:C:P	2.34	0.42
14:E:91:A:O2'	19:I:100:LEU:CD2	2.67	0.42
5:P:134:VAL:HG13	6:Q:111:ARG:HG2	2.01	0.42
5:P:106:LEU:HD13	6:Q:14:GLU:CG	2.50	0.42
10:Z:155:MET:SD	10:Z:173:ILE:HG21	2.60	0.42
10:Z:49:ILE:HG21	10:Z:56:ILE:HG21	2.01	0.42
10:Z:62:ASP:O	10:Z:66:ASN:HB3	2.19	0.42
10:Z:99:MET:HB2	10:Z:99:MET:HE3	1.42	0.42
1:A:1272:ARG:HA	1:A:1275:MET:SD	2.59	0.42
1:A:1361:VAL:HG21	1:A:1407:ILE:HD11	2.01	0.42
1:A:1423:THR:O	1:A:1424:HIS:CG	2.72	0.42
1:A:288:GLU:O	1:A:288:GLU:HG2	2.19	0.42
1:A:621:LEU:HA	1:A:669:TYR:HD2	1.84	0.42
1:A:644:VAL:O	1:A:645:ASP:HB2	2.19	0.42
1:A:484:PHE:CG	13:D:81:A:C5	3.07	0.42
15:L:24:U:C5'	15:L:25:A:OP2	2.67	0.42
16:M:500:A:C5	16:M:502:C:N4	2.87	0.42
4:O:335:GLY:O	4:O:339:GLY:HA2	2.19	0.42
4:O:396:LEU:O	4:O:398:GLY:N	2.52	0.42
5:P:51:PHE:N	5:P:51:PHE:CD1	2.86	0.42
8:S:128:ARG:HH21	8:S:129:LYS:NZ	2.18	0.42
9:T:1:MET:HB2	9:T:2:PRO:HD3	2.01	0.42
1:A:1275:MET:C	1:A:1277:GLU:H	2.22	0.42
1:A:1634:LEU:HA	1:A:1634:LEU:HD23	1.87	0.42
1:A:531:LEU:HA	1:A:531:LEU:HD23	1.51	0.42
1:A:686:ILE:HA	1:A:686:ILE:HD13	1.74	0.42
1:A:722:LEU:O	1:A:723:GLU:C	2.58	0.42
1:A:857:ILE:O	1:A:858:LYS:C	2.57	0.42
1:A:886:MET:SD	1:A:1120:VAL:HG22	2.59	0.42
1:A:991:THR:O	1:A:992:ASP:C	2.57	0.42
2:C:152:LEU:HA	2:C:152:LEU:HD23	1.81	0.42
2:C:606:VAL:HG12	2:C:607:LEU:N	2.34	0.42
2:C:885:GLY:HA3	2:C:906:VAL:HA	2.01	0.42
4:O:221:TYR:O	4:O:251:TRP:CH2	2.73	0.42
6:Q:17:LEU:HD23	6:Q:17:LEU:O	2.20	0.42
6:Q:215:PRO:CG	6:Q:217:TRP:NE1	2.81	0.42
7:R:138:TYR:HD1	7:R:183:PHE:HE1	1.66	0.42
7:R:135:LYS:HD3	7:R:187:LYS:O	2.20	0.42
9:T:90:LEU:H	9:T:90:LEU:HG	1.66	0.42
28:U:6:ILE:N	28:U:7:PRO:CD	2.82	0.42
10:Z:61:VAL:O	10:Z:65:LEU:HB3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1150:LYS:HB3	1:A:1154:LYS:HZ2	1.85	0.42
1:A:1596:THR:O	1:A:1599:SER:N	2.48	0.42
1:A:1859:ARG:O	1:A:1874:ALA:CA	2.61	0.42
1:A:497:GLN:OE1	1:A:712:LEU:HD22	2.19	0.42
1:A:750:LEU:HD23	1:A:751:ASP:HA	2.01	0.42
1:A:801:VAL:CG1	1:A:802:PRO:HD2	2.49	0.42
1:A:794:LYS:HD3	1:A:854:ARG:HH12	1.84	0.42
1:A:456:GLU:HA	2:C:357:GLY:HA2	2.01	0.42
2:C:352:VAL:HG21	2:C:359:PHE:HB3	2.01	0.42
2:C:681:CYS:O	2:C:714:PRO:HG3	2.18	0.42
16:M:484:U:C2'	16:M:485:U:C2	3.03	0.42
16:M:500:A:H3'	16:M:500:A:C8	2.55	0.42
4:O:414:LEU:HD23	4:O:426:TRP:HB2	2.00	0.42
5:P:115:VAL:HG21	6:Q:24:ARG:NH1	2.35	0.42
8:S:127:TRP:O	8:S:129:LYS:N	2.53	0.42
8:S:170:LEU:HD23	8:S:170:LEU:HA	1.69	0.42
8:S:35:THR:HG1	8:S:35:THR:H	1.47	0.42
10:Z:71:ARG:O	10:Z:74:PRO:HG2	2.20	0.42
10:Z:32:LEU:CD2	10:Z:76:LEU:HD23	2.49	0.42
1:A:1023:LEU:HD13	1:A:1451:PHE:CE1	2.55	0.42
1:A:1206:CYS:HB3	1:A:1303:LYS:HE2	2.01	0.42
1:A:1226:VAL:O	1:A:1229:GLU:HB3	2.20	0.42
1:A:1423:THR:O	1:A:1424:HIS:ND1	2.52	0.42
1:A:1348:GLU:CG	1:A:1446:THR:HB	2.45	0.42
1:A:1454:SER:CB	1:A:1488:ILE:HG22	2.49	0.42
1:A:1498:ASP:OD1	1:A:1498:ASP:N	2.48	0.42
1:A:404:ASN:CG	1:A:405:ASN:N	2.72	0.42
1:A:422:LEU:HD23	1:A:422:LEU:HA	1.91	0.42
1:A:614:ARG:CZ	11:B:98:A:H5"	2.48	0.42
2:C:130:PRO:HG2	2:C:558:LYS:HZ2	1.82	0.42
2:C:281:PRO:HG3	2:C:382:TYR:HD2	1.85	0.42
2:C:70:TYR:HB3	2:C:74:VAL:HG21	2.02	0.42
2:C:774:LEU:HD23	2:C:775:ILE:N	2.35	0.42
2:C:933:TRP:O	2:C:935:LYS:HG3	2.19	0.42
14:E:91:A:C8	19:I:97:TYR:CE1	3.05	0.42
4:O:131:LEU:HA	4:O:131:LEU:HD12	1.81	0.42
4:O:217:ILE:HD12	4:O:217:ILE:HG23	1.70	0.42
4:O:433:THR:OG1	4:O:434:LYS:N	2.53	0.42
1:A:891:GLU:OE2	5:P:219:ILE:HG12	2.20	0.42
6:Q:43:LEU:HD12	6:Q:43:LEU:HA	1.87	0.42
1:A:265:ASN:ND2	9:T:7:ARG:NH2	2.68	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1135:ALA:O	1:A:1141:PRO:HA	2.20	0.42
1:A:1438:PRO:HG3	1:A:1545:ASP:HB3	2.00	0.42
1:A:1618:ASN:N	1:A:1744:ASP:OD2	2.52	0.42
1:A:1875:ILE:HG22	1:A:1876:ASN:N	2.34	0.42
1:A:1905:LEU:HD12	1:A:1905:LEU:N	2.35	0.42
1:A:1920:LEU:O	1:A:1924:LEU:HG	2.19	0.42
1:A:297:SER:HB3	13:D:32:G:OP1	2.20	0.42
1:A:603:LYS:O	1:A:604:THR:C	2.58	0.42
1:A:750:LEU:HD23	1:A:751:ASP:N	2.35	0.42
3:J:6:ILE:CD1	11:B:90:A:N1	2.78	0.42
2:C:68:HIS:HA	2:C:71:GLY:HA2	2.02	0.42
2:C:796:ILE:HG13	2:C:800:TYR:CZ	2.55	0.42
14:E:54:U:O2'	14:E:55:G:N7	2.51	0.42
15:L:1096:C:H2'	15:L:1097:G:H8	1.85	0.42
4:O:204:LYS:HG2	4:O:225:SER:HA	2.02	0.42
5:P:107:ASN:OD1	5:P:107:ASN:N	2.46	0.42
6:Q:251:LEU:HD11	6:Q:253:PHE:CZ	2.55	0.42
7:R:210:LYS:HG3	7:R:211:GLU:N	2.35	0.42
9:T:104:CYS:C	9:T:105:CYS:SG	2.97	0.42
9:T:99:GLY:O	9:T:101:GLU:N	2.52	0.42
1:A:1041:VAL:O	1:A:1041:VAL:HG12	2.19	0.42
1:A:1562:PHE:CG	1:A:1562:PHE:O	2.73	0.42
1:A:1717:LEU:HA	1:A:1790:TRP:CZ2	2.55	0.42
1:A:1884:PRO:O	1:A:1992:TYR:OH	2.14	0.42
1:A:143:ILE:HD13	1:A:570:GLN:NE2	2.35	0.42
1:A:638:GLN:O	1:A:639:PHE:C	2.58	0.42
1:A:655:TYR:CE1	1:A:659:HIS:CD2	3.08	0.42
2:C:718:LYS:CA	2:C:721:GLN:HB3	2.49	0.42
2:C:758:ASP:CG	2:C:761:ALA:H	2.23	0.42
15:L:52:A:C8	15:L:52:A:O5'	2.70	0.42
16:M:484:U:C6	16:M:484:U:C3'	3.03	0.42
6:Q:47:LYS:HB3	6:Q:52:SER:HB3	2.01	0.42
6:Q:94:VAL:O	6:Q:95:ASN:HB3	2.19	0.42
10:Z:323:LYS:CE	10:Z:364:THR:HG22	2.50	0.42
1:A:1042:SER:OG	1:A:1043:ARG:HG3	2.20	0.42
1:A:1050:LEU:HD11	1:A:1230:ILE:HD12	2.01	0.42
1:A:1143:GLU:H	1:A:1146:GLN:CD	2.23	0.42
1:A:1340:ILE:O	1:A:1344:THR:CB	2.68	0.42
1:A:1208:PRO:HB2	1:A:1417:GLN:O	2.20	0.42
1:A:143:ILE:HD13	1:A:570:GLN:HE21	1.85	0.42
1:A:1341:SER:HA	1:A:1525:PHE:CE1	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1654:TRP:O	1:A:1657:ILE:HB	2.19	0.42
1:A:1679:GLU:HG2	1:A:1705:SER:O	2.19	0.42
1:A:1714:PRO:HB2	1:A:1787:TYR:CE2	2.55	0.42
1:A:190:LYS:HG2	1:A:561:THR:HG22	2.02	0.42
2:C:221:PHE:O	2:C:222:MET:C	2.58	0.42
2:C:421:LEU:O	2:C:424:VAL:N	2.53	0.42
2:C:798:GLY:HA3	2:C:842:MET:HB3	2.01	0.42
13:D:32:G:C3'	13:D:33:U:H5"	2.49	0.42
25:G:77:LEU:HD23	25:G:78:GLY:N	2.35	0.42
15:L:7:C:OP1	19:I:174:LYS:HE2	2.19	0.42
15:L:16:U:H2'	19:I:179:ARG:HH21	1.85	0.42
4:O:154:TRP:HZ3	4:O:156:ILE:HD11	1.85	0.42
4:O:387:LEU:HA	4:O:387:LEU:HD23	1.70	0.42
5:P:159:ASP:HB2	5:P:160:PRO:HD3	2.02	0.42
8:S:17:ALA:HA	8:S:20:TYR:CE2	2.54	0.42
30:W:49:ARG:HA	30:W:49:ARG:HD2	1.64	0.42
10:Z:176:LYS:O	10:Z:179:TYR:HB3	2.20	0.42
10:Z:404:ILE:H	10:Z:404:ILE:HD12	1.85	0.42
10:Z:427:LEU:HD21	10:Z:431:LEU:HD12	2.02	0.42
10:Z:92:GLU:O	10:Z:96:LYS:HG3	2.20	0.42
1:A:1041:VAL:HG21	1:A:1274:ARG:NH1	2.35	0.41
1:A:165:LEU:HB3	1:A:730:ILE:HD11	2.02	0.41
1:A:1973:LYS:O	1:A:1976:ASP:HB2	2.20	0.41
1:A:215:ALA:O	1:A:216:GLN:C	2.58	0.41
1:A:291:LYS:H	1:A:291:LYS:HG2	1.70	0.41
1:A:380:ARG:HA	3:J:4:ASN:OD1	2.19	0.41
1:A:583:ILE:HD13	1:A:583:ILE:HG21	1.78	0.41
1:A:481:HIS:NE2	2:C:276:ASP:OD1	2.53	0.41
1:A:452:PHE:CE1	2:C:347:ARG:HG3	2.54	0.41
2:C:916:THR:O	2:C:917:ASP:C	2.58	0.41
14:E:84:C:H3'	14:E:85:C:H5"	2.01	0.41
5:P:110:HIS:HE1	6:Q:19:ASP:HA	1.84	0.41
6:Q:204:SER:O	6:Q:294:SER:HB3	2.20	0.41
7:R:251:VAL:HA	7:R:254:ILE:HG12	2.01	0.41
9:T:104:CYS:N	9:T:153:CYS:SG	2.82	0.41
15:L:112:A:N7	30:W:63:ARG:HB3	2.34	0.41
1:A:1148:LYS:HB2	1:A:1152:VAL:HG21	2.02	0.41
1:A:1229:GLU:OE2	1:A:1233:ARG:NH2	2.53	0.41
1:A:168:LEU:O	1:A:169:PRO:C	2.55	0.41
1:A:294:ASN:CB	1:A:299:LYS:O	2.68	0.41
2:C:135:ASN:HB2	2:C:233:ASP:H	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:257:ILE:HD12	2:C:257:ILE:HA	1.93	0.41
2:C:358:ASN:OD1	2:C:358:ASN:N	2.53	0.41
2:C:362:LYS:HA	2:C:363:PRO:HD3	1.89	0.41
14:E:88:U:H2'	15:L:17:U:C6	2.55	0.41
25:G:88:THR:HG22	25:G:89:LEU:HD12	2.01	0.41
4:O:122:ARG:CZ	4:O:122:ARG:HB2	2.49	0.41
4:O:323:VAL:O	4:O:323:VAL:HG13	2.19	0.41
6:Q:82:ILE:HG23	6:Q:86:LEU:HB3	2.02	0.41
7:R:49:SER:HB3	7:R:202:GLN:HE22	1.84	0.41
28:U:30:ARG:C	28:U:47:VAL:HG23	2.40	0.41
10:Z:337:SER:O	10:Z:338:THR:OG1	2.30	0.41
1:A:1002:GLU:O	1:A:1005:GLN:HB3	2.19	0.41
1:A:1182:LEU:HA	1:A:1182:LEU:HD23	1.82	0.41
1:A:1222:LEU:HD23	1:A:1222:LEU:HA	1.82	0.41
1:A:1893:ILE:HD13	1:A:1981:ALA:HB2	2.02	0.41
1:A:2015:LEU:O	1:A:2019:GLU:HG2	2.19	0.41
1:A:2021:SER:O	1:A:2025:ILE:HG13	2.19	0.41
1:A:2058:LEU:HA	1:A:2058:LEU:HD23	1.81	0.41
1:A:767:LEU:HA	1:A:767:LEU:HD23	1.82	0.41
2:C:274:ILE:HG21	2:C:385:PHE:CD2	2.55	0.41
2:C:602:VAL:O	2:C:676:VAL:HG23	2.20	0.41
19:I:167:SER:O	19:I:171:GLU:HG3	2.20	0.41
1:A:784:GLN:HE22	15:L:19:U:C2'	2.34	0.41
15:L:41:C:O2'	15:L:42:U:P	2.78	0.41
4:O:147:ILE:HD11	4:O:169:LEU:HD22	2.02	0.41
1:A:757:GLU:OE1	4:O:202:GLU:HB3	2.21	0.41
6:Q:4:GLU:O	6:Q:8:PRO:HD2	2.20	0.41
7:R:162:PHE:C	7:R:165:SER:HG	2.24	0.41
7:R:98:ASP:O	7:R:101:LYS:N	2.42	0.41
10:Z:18:TRP:HB2	10:Z:242:PHE:CE1	2.55	0.41
10:Z:194:LEU:O	10:Z:194:LEU:HD23	2.21	0.41
1:A:1441:PHE:CD2	10:Z:303:LEU:HG	2.55	0.41
10:Z:336:GLU:O	10:Z:337:SER:HB3	2.21	0.41
1:A:128:TYR:CZ	13:D:35:A:O4'	2.74	0.41
1:A:1431:HIS:CE1	1:A:1434:GLU:HB3	2.56	0.41
1:A:2080:LYS:HG3	1:A:2081:ASP:N	2.34	0.41
1:A:209:ILE:HG13	1:A:209:ILE:H	1.60	0.41
1:A:590:TYR:OH	1:A:609:GLU:HB3	2.20	0.41
1:A:728:ASN:O	1:A:729:LEU:C	2.58	0.41
2:C:241:VAL:HG13	2:C:242:VAL:N	2.36	0.41
2:C:247:PHE:O	2:C:250:GLU:HB2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:365:GLU:CG	2:C:366:ASN:N	2.81	0.41
2:C:378:LEU:HA	2:C:378:LEU:HD23	1.67	0.41
1:A:784:GLN:HE22	15:L:20:G:H5"	1.81	0.41
16:M:498:C:C4	16:M:499:U:N3	2.89	0.41
12:N:108:U:C1'	12:N:109:U:P	3.08	0.41
2:C:75:GLU:HB2	4:O:133:ARG:HG3	2.02	0.41
2:C:90:LEU:HD12	4:O:176:THR:HG21	2.01	0.41
32:Y:62:ASN:HB2	32:Y:84:ASN:OD1	2.20	0.41
10:Z:434:ASP:O	10:Z:437:GLN:HB2	2.20	0.41
1:A:1427:ALA:O	3:J:16:THR:HB	2.21	0.41
1:A:1460:GLU:O	1:A:1463:THR:OG1	2.25	0.41
1:A:1862:VAL:HA	1:A:1871:ALA:O	2.19	0.41
1:A:2034:ILE:HD13	1:A:2039:LEU:O	2.20	0.41
1:A:259:GLU:HG2	1:A:260:PRO:HD2	2.02	0.41
1:A:275:TYR:HD2	1:A:310:ASN:HD21	1.68	0.41
1:A:340:LYS:NZ	1:A:355:LEU:HD13	2.35	0.41
1:A:615:LEU:HD23	1:A:619:PHE:CE2	2.54	0.41
1:A:653:ILE:HD13	1:A:653:ILE:HG21	1.77	0.41
2:C:172:TRP:HZ2	2:C:416:ASP:OD2	2.03	0.41
2:C:324:ILE:HG13	2:C:325:LYS:N	2.35	0.41
2:C:355:HIS:CD2	2:C:360:ARG:NE	2.88	0.41
13:D:44:A:OP2	13:D:44:A:C4'	2.68	0.41
13:D:45:A:O2'	13:D:45:A:N3	2.46	0.41
14:E:1:G:H2'	14:E:2:U:H6	1.85	0.41
1:A:344:ASN:HA	3:J:3:TYR:CE2	2.56	0.41
15:L:1115:G:C6	15:L:1116:A:N6	2.89	0.41
16:M:483:U:H5"	16:M:484:U:P	2.60	0.41
4:O:257:ILE:HG22	4:O:259:VAL:N	2.35	0.41
4:O:265:HIS:CD2	4:O:269:ILE:HG12	2.55	0.41
7:R:199:MET:HE3	7:R:202:GLN:HG3	2.02	0.41
7:R:36:LYS:HG3	14:E:41:A:C2	2.56	0.41
7:R:53:LEU:HD12	7:R:54:GLN:N	2.36	0.41
10:Z:465:PHE:CE1	10:Z:468:ILE:HD12	2.55	0.41
1:A:1082:ILE:HG21	1:A:1113:ILE:HD11	2.02	0.41
1:A:1423:THR:HB	1:A:1424:HIS:CD2	2.55	0.41
1:A:161:PHE:HE1	1:A:198:ALA:HA	1.85	0.41
1:A:1751:TYR:O	1:A:1755:LYS:HG2	2.20	0.41
1:A:1879:ILE:O	1:A:1891:LEU:HA	2.21	0.41
1:A:299:LYS:HA	1:A:493:MET:CG	2.51	0.41
1:A:311:LEU:HA	1:A:311:LEU:HD23	1.81	0.41
2:C:212:PHE:O	2:C:213:LEU:HD23	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:610:LEU:HD12	2:C:610:LEU:HA	1.76	0.41
2:C:619:LEU:HD23	2:C:619:LEU:HA	1.75	0.41
2:C:603:PHE:HD2	2:C:652:MET:HG3	1.85	0.41
2:C:868:VAL:O	2:C:899:LEU:HA	2.21	0.41
1:A:407:VAL:HG21	2:C:927:MET:HB2	2.02	0.41
1:A:353:GLU:HG3	13:D:104:G:P	2.59	0.41
15:L:34:G:OP2	15:L:34:G:H8	1.94	0.41
16:M:494:G:O2'	16:M:495:A:P	2.78	0.41
4:O:169:LEU:HA	4:O:169:LEU:HD12	1.81	0.41
4:O:238:LEU:HD11	5:P:74:ILE:CD1	2.51	0.41
4:O:251:TRP:HZ3	4:O:258:PRO:HD3	1.85	0.41
5:P:129:LYS:HG2	5:P:130:LYS:N	2.35	0.41
5:P:39:LYS:HB3	5:P:39:LYS:HE2	1.75	0.41
6:Q:215:PRO:HB3	7:R:171:ASP:OD1	2.21	0.41
9:T:65:THR:O	9:T:69:LYS:HB2	2.20	0.41
10:Z:433:LEU:HD21	10:Z:472:LEU:HB2	2.02	0.41
1:A:1880:PHE:CZ	1:A:1882:LEU:HD23	2.55	0.41
1:A:1875:ILE:HA	1:A:1896:THR:HG21	2.03	0.41
1:A:503:LYS:HG2	1:A:507:LEU:HD13	2.03	0.41
1:A:133:GLU:OE2	1:A:561:THR:HG23	2.19	0.41
1:A:852:LEU:O	1:A:853:THR:C	2.58	0.41
2:C:101:GLN:HE22	13:D:75:A:N6	2.13	0.41
2:C:563:LEU:HD23	2:C:563:LEU:HA	1.83	0.41
2:C:611:LEU:HD23	2:C:611:LEU:HA	1.78	0.41
2:C:603:PHE:CD2	2:C:652:MET:HG3	2.55	0.41
2:C:757:TRP:HD1	2:C:762:SER:HG	1.69	0.41
2:C:955:LYS:HA	2:C:955:LYS:HD3	1.90	0.41
19:I:180:LYS:O	19:I:183:MET:HB2	2.21	0.41
4:O:155:PHE:O	4:O:156:ILE:HG13	2.20	0.41
4:O:372:VAL:HA	4:O:387:LEU:O	2.20	0.41
4:O:391:GLU:OE1	4:O:397:GLU:HA	2.21	0.41
4:O:412:LEU:HA	4:O:412:LEU:HD23	1.87	0.41
7:R:10:LYS:HB3	7:R:10:LYS:HE2	1.90	0.41
10:Z:130:ILE:HG22	10:Z:225:HIS:CD2	2.55	0.41
10:Z:204:ASP:O	10:Z:205:TYR:HB2	2.20	0.41
10:Z:32:LEU:HD23	10:Z:76:LEU:HD23	2.03	0.41
10:Z:385:GLY:O	10:Z:423:LEU:HA	2.21	0.41
10:Z:422:PHE:O	10:Z:423:LEU:C	2.58	0.41
10:Z:49:ILE:O	10:Z:52:GLY:N	2.53	0.41
1:A:1003:ALA:O	1:A:1006:ARG:N	2.54	0.41
1:A:1296:ARG:NH1	10:Z:430:GLU:OE2	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:161:PHE:HD1	1:A:161:PHE:HA	1.74	0.41
1:A:1903:LYS:HB3	1:A:1904:ARG:H	1.58	0.41
1:A:318:LEU:HA	1:A:318:LEU:HD23	1.69	0.41
2:C:126:MET:SD	2:C:132:ARG:HD2	2.61	0.41
2:C:67:GLU:N	2:C:76:VAL:HG21	2.35	0.41
2:C:744:PRO:O	2:C:747:LEU:HB3	2.21	0.41
2:C:760:LEU:O	2:C:763:ARG:HB2	2.21	0.41
4:O:149:PRO:HG3	4:O:192:ASP:HA	2.02	0.41
4:O:198:PHE:HD2	4:O:232:ILE:HG12	1.85	0.41
4:O:252:ASP:OD1	4:O:253:MET:N	2.54	0.41
4:O:342:LEU:HB3	5:P:47:ARG:HD3	2.01	0.41
5:P:115:VAL:O	6:Q:26:THR:HA	2.20	0.41
6:Q:210:ILE:HD12	6:Q:247:LYS:C	2.42	0.41
7:R:184:VAL:CG1	7:R:186:PHE:HE1	2.34	0.41
7:R:257:ASN:O	7:R:261:ALA:N	2.53	0.41
8:S:4:SER:O	8:S:5:HIS:CD2	2.74	0.41
10:Z:14:GLN:HA	10:Z:17:ASN:CB	2.50	0.41
1:A:1888:HIS:HB3	1:A:1988:LEU:HD23	2.02	0.41
1:A:2023:LYS:HE3	1:A:2023:LYS:HB2	1.87	0.41
1:A:330:LEU:O	1:A:335:SER:OG	2.39	0.41
1:A:300:LYS:HA	1:A:491:GLY:O	2.21	0.41
1:A:571:LEU:HA	1:A:571:LEU:HD12	1.60	0.41
1:A:687:ILE:HD13	1:A:703:PHE:HD2	1.86	0.41
2:C:656:LEU:HD13	2:C:670:ILE:CD1	2.49	0.41
2:C:709:SER:OG	2:C:821:LEU:HD12	2.20	0.41
14:E:16:C:O5'	14:E:16:C:H6	2.03	0.41
4:O:295:VAL:HG23	4:O:296:VAL:N	2.36	0.41
4:O:277:VAL:CG1	5:P:63:ILE:HG22	2.50	0.41
7:R:74:LEU:HB3	7:R:112:PHE:CD1	2.56	0.41
7:R:221:LEU:HD12	7:R:221:LEU:O	2.21	0.41
1:A:585:ARG:HD3	7:R:33:TRP:CE2	2.56	0.41
9:T:29:GLN:O	9:T:32:ASP:HB2	2.21	0.41
1:A:1066:LEU:O	1:A:1067:ASN:C	2.59	0.41
1:A:898:ILE:HD12	1:A:1074:VAL:HG22	2.02	0.41
1:A:1303:LYS:HZ2	1:A:1353:THR:HG22	1.86	0.41
1:A:1447:TRP:O	1:A:1448:GLU:C	2.60	0.41
1:A:431:ILE:HD12	2:C:287:LYS:HA	2.02	0.41
1:A:852:LEU:HA	1:A:852:LEU:HD23	1.52	0.41
2:C:582:SER:O	2:C:585:ASP:N	2.54	0.41
2:C:761:ALA:HA	2:C:764:ASN:HB2	2.02	0.41
26:H:32:LYS:HG3	26:H:77:ASN:HA	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:L:16:U:OP2	15:L:18:U:C2	2.73	0.41
12:N:104:G:N1	14:E:49:A:C2	2.89	0.41
4:O:156:ILE:HG21	4:O:156:ILE:HD13	1.88	0.41
4:O:162:THR:HG22	4:O:184:THR:HA	2.03	0.41
4:O:376:TYR:CE1	4:O:383:LYS:HG3	2.56	0.41
1:A:807:PRO:HG3	5:P:163:TRP:HH2	1.86	0.41
7:R:159:ARG:CZ	7:R:159:ARG:HB2	2.51	0.41
9:T:51:GLU:O	9:T:52:ILE:C	2.60	0.41
10:Z:135:ILE:HD12	10:Z:135:ILE:HG23	1.80	0.41
1:A:1161:TYR:OH	1:A:1163:ARG:HD3	2.21	0.41
1:A:1203:ASN:ND2	1:A:1212:ARG:HG2	2.35	0.41
1:A:1212:ARG:HG2	1:A:1213:MET:N	2.33	0.41
1:A:1326:THR:O	1:A:1327:THR:OG1	2.21	0.41
1:A:1748:ILE:O	1:A:1749:SER:C	2.59	0.41
1:A:1845:ASN:N	1:A:1849:LYS:HZ3	2.19	0.41
1:A:1940:MET:HE2	1:A:1940:MET:HB3	1.81	0.41
1:A:1932:GLN:NE2	1:A:1957:ARG:HD2	2.36	0.41
1:A:1962:ARG:NH1	1:A:2081:ASP:OD2	2.54	0.41
1:A:526:LEU:HA	1:A:526:LEU:HD23	1.54	0.41
1:A:529:TYR:O	1:A:530:VAL:C	2.58	0.41
1:A:713:ASN:O	1:A:714:PHE:C	2.59	0.41
1:A:779:ALA:O	1:A:780:ARG:C	2.59	0.41
1:A:780:ARG:HA	1:A:783:LEU:HD13	2.02	0.41
1:A:923:TYR:HH	1:A:936:GLU:CD	2.24	0.41
1:A:931:ALA:HA	1:A:934:ARG:NH2	2.36	0.41
2:C:354:TYR:HD1	2:C:359:PHE:CD1	2.39	0.41
2:C:637:GLU:HB2	2:C:639:SER:OG	2.21	0.41
2:C:883:ARG:HE	2:C:914:PHE:HD1	1.68	0.41
2:C:943:ASP:O	2:C:945:LEU:N	2.53	0.41
4:O:112:VAL:O	4:O:115:TYR:N	2.52	0.41
4:O:265:HIS:CE1	4:O:291:ARG:CG	3.04	0.41
7:R:201:ASN:HA	7:R:220:GLY:HA3	2.02	0.41
7:R:205:LEU:HB3	7:R:206:LEU:H	1.66	0.41
7:R:46:ARG:CZ	7:R:222:LEU:HD21	2.51	0.41
7:R:72:PHE:HE1	7:R:90:LEU:HD12	1.86	0.41
1:A:828:HIS:CE1	8:S:169:PHE:CD2	3.09	0.41
10:Z:456:GLU:HA	10:Z:459:ARG:NH1	2.30	0.41
10:Z:53:ARG:NH1	10:Z:89:ASP:OD1	2.54	0.41
1:A:1459:ALA:O	1:A:1462:ALA:HB3	2.21	0.40
1:A:1540:ASN:O	1:A:1541:ALA:C	2.59	0.40
1:A:1550:LEU:HA	1:A:1550:LEU:HD23	1.92	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1999:ILE:HG22	1:A:2000:SER:N	2.34	0.40
1:A:2011:LEU:HB3	1:A:2040:TRP:CH2	2.56	0.40
1:A:215:ALA:HB2	1:A:311:LEU:HD22	2.03	0.40
1:A:569:LEU:HD23	1:A:569:LEU:HA	1.56	0.40
1:A:607:THR:O	1:A:610:ARG:N	2.52	0.40
1:A:670:LYS:HE3	1:A:670:LYS:HB3	1.77	0.40
1:A:910:LYS:O	1:A:913:VAL:N	2.53	0.40
1:A:936:GLU:O	1:A:937:LEU:C	2.59	0.40
2:C:170:LEU:HD12	2:C:171:GLY:HA2	2.03	0.40
2:C:219:VAL:O	2:C:219:VAL:HG22	2.20	0.40
5:P:130:LYS:HG2	5:P:131:ALA:H	1.86	0.40
8:S:165:TYR:O	8:S:168:GLU:N	2.54	0.40
10:Z:41:HIS:ND1	10:Z:83:LEU:HD23	2.36	0.40
1:A:1550:LEU:HB2	1:A:1556:ILE:HD11	2.03	0.40
1:A:1620:TYR:HD2	1:A:1621:VAL:HG22	1.85	0.40
1:A:293:VAL:HG22	1:A:294:ASN:H	1.86	0.40
1:A:319:ARG:HD3	1:A:319:ARG:HH11	1.65	0.40
1:A:551:LEU:HG	1:A:557:PHE:HE2	1.81	0.40
1:A:797:ILE:HG22	1:A:799:TRP:H	1.85	0.40
11:B:88:U:H2'	11:B:89:A:C4'	2.49	0.40
2:C:273:LEU:O	2:C:277:LEU:HB2	2.21	0.40
2:C:289:ASN:ND2	2:C:349:TRP:CZ2	2.89	0.40
2:C:571:TYR:CE1	2:C:573:LYS:O	2.73	0.40
2:C:655:LEU:O	2:C:656:LEU:C	2.59	0.40
2:C:84:GLN:NE2	2:C:90:LEU:HA	2.33	0.40
2:C:84:GLN:NE2	2:C:90:LEU:H	2.17	0.40
9:T:121:ILE:HD13	14:E:28:U:H1'	2.03	0.40
14:E:76:A:C2	14:E:77:G:C4	3.09	0.40
1:A:814:ARG:HG2	4:O:141:TRP:CZ2	2.56	0.40
4:O:292:LEU:HA	4:O:292:LEU:HD23	1.91	0.40
4:O:343:THR:OG1	4:O:344:ASN:N	2.54	0.40
4:O:126:HIS:HB2	4:O:384:TYR:CE2	2.56	0.40
7:R:174:ARG:HH22	12:N:114:U:H5'	1.85	0.40
7:R:231:ASP:OD1	7:R:233:ALA:N	2.54	0.40
10:Z:434:ASP:O	10:Z:437:GLN:N	2.55	0.40
10:Z:64:THR:OG1	10:Z:76:LEU:HD13	2.21	0.40
1:A:1001:TYR:O	1:A:1005:GLN:HB2	2.21	0.40
1:A:1438:PRO:HB2	1:A:1443:TYR:HE2	1.86	0.40
1:A:1339:LEU:HD21	1:A:1440:ILE:HD12	2.03	0.40
1:A:1718:HIS:CE1	1:A:1799:GLN:HG2	2.56	0.40
1:A:173:LEU:HD13	1:A:715:LEU:HD23	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:807:PRO:O	1:A:810:LYS:HB2	2.21	0.40
1:A:967:VAL:HG12	1:A:968:ASP:N	2.37	0.40
2:C:251:GLN:HE22	2:C:255:GLN:HE21	1.68	0.40
2:C:468:LEU:HD13	2:C:492:LEU:N	2.36	0.40
2:C:716:ASP:OD2	2:C:718:LYS:HB3	2.22	0.40
2:C:795:ILE:O	2:C:798:GLY:N	2.54	0.40
2:C:90:LEU:HD23	2:C:90:LEU:O	2.22	0.40
2:C:869:HIS:HD2	2:C:925:LEU:HB3	1.85	0.40
13:D:79:C:H3'	13:D:80:G:H5'	2.03	0.40
14:E:15:C:C4	14:E:16:C:N4	2.89	0.40
7:R:127:ILE:CG1	14:E:39:G:N7	2.84	0.40
7:R:95:ASP:CG	7:R:97:GLU:H	2.25	0.40
10:Z:313:LEU:HA	10:Z:313:LEU:HD23	1.67	0.40
10:Z:346:LEU:HD12	10:Z:346:LEU:HA	1.77	0.40
1:A:1570:TRP:CG	1:A:1571:GLU:N	2.86	0.40
1:A:168:LEU:HD23	1:A:622:MET:HE2	2.03	0.40
1:A:2053:SER:O	1:A:2056:ARG:HB3	2.20	0.40
1:A:303:PHE:HA	1:A:303:PHE:HD1	1.65	0.40
2:C:321:THR:OG1	2:C:432:GLN:HG2	2.22	0.40
2:C:495:ARG:N	2:C:554:HIS:O	2.55	0.40
2:C:68:HIS:N	2:C:69:PRO:HD2	2.36	0.40
14:E:101:U:H2'	14:E:102:U:C6	2.57	0.40
15:L:18:U:O2'	15:L:19:U:OP2	2.38	0.40
16:M:499:U:O2'	16:M:500:A:P	2.77	0.40
4:O:125:TRP:CD1	4:O:437:GLU:OE1	2.74	0.40
4:O:281:VAL:O	4:O:293:TRP:HB2	2.21	0.40
1:A:880:THR:HG23	5:P:211:ALA:HB2	2.02	0.40
5:P:220:ARG:O	5:P:224:GLU:HG2	2.21	0.40
7:R:240:GLU:O	7:R:243:LYS:HB3	2.22	0.40
10:Z:426:GLU:O	10:Z:429:ASN:N	2.55	0.40
10:Z:478:ARG:O	10:Z:481:LEU:HB2	2.21	0.40
1:A:1063:PHE:HB3	1:A:1083:THR:HG23	2.03	0.40
1:A:1323:SER:OG	1:A:1370:ARG:NH2	2.55	0.40
1:A:1369:ASN:HB3	1:A:1378:LYS:NZ	2.37	0.40
1:A:1405:ILE:HG22	1:A:1406:LEU:N	2.24	0.40
1:A:477:MET:HE1	2:C:278:LYS:CD	2.35	0.40
1:A:594:ASP:OD1	1:A:598:ASN:N	2.55	0.40
1:A:631:LEU:O	1:A:634:ASP:HB2	2.22	0.40
1:A:773:SER:OG	1:A:774:ILE:N	2.55	0.40
1:A:936:GLU:O	1:A:940:ILE:HD12	2.21	0.40
1:A:965:LYS:HB3	1:A:966:PRO:HD2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:233:ASP:O	2:C:261:VAL:HG13	2.21	0.40
2:C:253:ILE:HG12	2:C:253:ILE:H	1.74	0.40
2:C:285:TYR:CD2	2:C:286:LEU:HD12	2.56	0.40
2:C:473:LEU:HD12	2:C:485:LEU:CD2	2.51	0.40
2:C:655:LEU:HD23	2:C:655:LEU:HA	1.77	0.40
2:C:603:PHE:CZ	2:C:673:PRO:HB3	2.56	0.40
2:C:737:ILE:HG13	2:C:768:PHE:CD1	2.55	0.40
2:C:831:ILE:HG13	2:C:832:ASP:N	2.29	0.40
2:C:834:MET:HB3	2:C:834:MET:HE3	1.91	0.40
2:C:864:VAL:HG22	2:C:930:LEU:CD2	2.52	0.40
4:O:333:SER:O	4:O:334:TRP:CG	2.75	0.40
5:P:52:GLU:O	5:P:52:GLU:HG3	2.22	0.40
6:Q:117:ASN:O	6:Q:119:LYS:N	2.54	0.40
6:Q:20:GLU:HG3	6:Q:21:ALA:H	1.86	0.40
7:R:127:ILE:HG22	7:R:128:GLY:N	2.37	0.40
7:R:206:LEU:HB3	7:R:208:SER:O	2.22	0.40
30:W:102:ILE:HG22	30:W:103:VAL:HG23	2.01	0.40
10:Z:61:VAL:HG11	10:Z:101:MET:HE3	2.03	0.40
10:Z:143:LEU:HB3	10:Z:176:LYS:HZ1	1.86	0.40
10:Z:148:LEU:HA	10:Z:151:VAL:HG12	2.03	0.40
10:Z:321:LEU:HD23	10:Z:321:LEU:HA	1.77	0.40
10:Z:444:LYS:HG3	10:Z:444:LYS:O	2.21	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	1925/2413 (80%)	1569 (82%)	339 (18%)	17 (1%)	21	66
2	C	872/1008 (86%)	735 (84%)	129 (15%)	8 (1%)	21	66
3	J	25/135 (18%)	21 (84%)	4 (16%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	O	335/451 (74%)	281 (84%)	49 (15%)	5 (2%)	13	58
5	P	193/379 (51%)	160 (83%)	27 (14%)	6 (3%)	5	45
6	Q	177/364 (49%)	145 (82%)	30 (17%)	2 (1%)	17	64
7	R	259/339 (76%)	218 (84%)	40 (15%)	1 (0%)	39	79
8	S	63/175 (36%)	49 (78%)	12 (19%)	2 (3%)	5	44
9	T	155/157 (99%)	123 (79%)	28 (18%)	4 (3%)	7	48
10	Z	443/577 (77%)	369 (83%)	68 (15%)	6 (1%)	14	59
17	c	312/579 (54%)	273 (88%)	35 (11%)	4 (1%)	15	60
18	d	238/652 (36%)	201 (84%)	35 (15%)	2 (1%)	24	69
19	I	98/215 (46%)	85 (87%)	13 (13%)	0	100	100
20	v	121/858 (14%)	110 (91%)	7 (6%)	4 (3%)	5	43
21	n	272/455 (60%)	234 (86%)	28 (10%)	10 (4%)	4	40
22	o	120/503 (24%)	115 (96%)	4 (3%)	1 (1%)	24	69
22	p	122/503 (24%)	116 (95%)	6 (5%)	0	100	100
22	q	355/503 (71%)	327 (92%)	16 (4%)	12 (3%)	5	43
22	r	119/503 (24%)	111 (93%)	5 (4%)	3 (2%)	7	49
23	t	150/175 (86%)	134 (89%)	13 (9%)	3 (2%)	9	54
24	F	74/196 (38%)	67 (90%)	7 (10%)	0	100	100
24	k	76/196 (39%)	69 (91%)	7 (9%)	0	100	100
25	G	71/94 (76%)	65 (92%)	6 (8%)	0	100	100
25	i	71/94 (76%)	65 (92%)	6 (8%)	0	100	100
26	H	66/86 (77%)	61 (92%)	4 (6%)	1 (2%)	13	58
26	h	66/86 (77%)	61 (92%)	4 (6%)	1 (2%)	13	58
27	K	65/77 (84%)	64 (98%)	1 (2%)	0	100	100
27	j	65/77 (84%)	64 (98%)	1 (2%)	0	100	100
28	U	80/101 (79%)	70 (88%)	9 (11%)	1 (1%)	15	60
28	l	80/101 (79%)	70 (88%)	9 (11%)	1 (1%)	15	60
29	V	78/146 (53%)	74 (95%)	4 (5%)	0	100	100
29	m	78/146 (53%)	74 (95%)	4 (5%)	0	100	100
30	W	63/110 (57%)	58 (92%)	4 (6%)	1 (2%)	12	57
30	g	92/110 (84%)	85 (92%)	6 (6%)	1 (1%)	17	64

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
31	X	77/111 (69%)	75 (97%)	2 (3%)	0	100	100
32	Y	125/238 (52%)	111 (89%)	12 (10%)	2 (2%)	12	57
34	e	673/1071 (63%)	563 (84%)	75 (11%)	35 (5%)	2	31
35	f	144/251 (57%)	140 (97%)	4 (3%)	0	100	100
All	All	8398/14235 (59%)	7212 (86%)	1053 (12%)	133 (2%)	17	57

All (133) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	364	PHE
6	Q	99	VAL
10	Z	213	PHE
20	v	616	PRO
21	n	245	HIS
21	n	247	ASN
21	n	428	PRO
22	q	53	ILE
22	q	77	ILE
22	q	172	PRO
22	q	174	TRP
22	q	239	PRO
22	q	246	PRO
22	q	362	PRO
22	q	442	SER
22	r	64	GLU
23	t	77	PRO
32	Y	68	PRO
34	e	374	GLU
34	e	392	TYR
34	e	393	ALA
34	e	434	ARG
34	e	532	VAL
34	e	654	ILE
34	e	714	GLN
34	e	812	LEU
34	e	932	SER
34	e	933	VAL
34	e	948	PRO
34	e	988	ILE
1	A	1405	ILE
1	A	1540	ASN

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Mol	Chain	Res	Type
2	C	363	PRO
4	O	286	THR
5	P	112	ILE
8	S	8	GLN
8	S	9	LEU
20	v	601	VAL
20	v	618	GLU
21	n	61	LYS
21	n	291	HIS
21	n	406	ARG
22	q	196	PRO
23	t	110	GLU
34	e	388	TYR
34	e	428	GLU
34	e	442	GLU
34	e	561	CYS
34	e	611	ILE
34	e	629	GLY
34	e	739	GLU
34	e	919	THR
1	A	1404	HIS
1	A	1581	PHE
1	A	1964	PRO
5	P	102	ALA
10	Z	303	LEU
17	c	230	THR
17	c	231	SER
20	v	634	HIS
21	n	244	LEU
22	o	17	PRO
22	r	20	ARG
23	t	80	ASN
34	e	435	PHE
34	e	462	ASP
34	e	655	ASP
34	e	816	GLN
1	A	645	ASP
1	A	1628	ASP
2	C	655	LEU
2	C	829	VAL
4	O	278	ASP
4	O	435	GLU

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Mol	Chain	Res	Type
10	Z	53	ARG
21	n	267	LEU
28	l	82	PRO
30	g	82	LYS
28	U	82	PRO
30	W	82	LYS
34	e	333	THR
34	e	425	LEU
34	e	610	PRO
34	e	737	THR
34	e	944	LEU
34	e	946	ASP
34	e	985	ILE
1	A	264	ILE
1	A	543	ASN
1	A	1033	ASN
2	C	801	TRP
4	O	279	PRO
5	P	86	ASN
6	Q	93	LEU
7	R	92	HIS
9	T	98	THR
9	T	104	CYS
9	T	119	THR
21	n	416	ARG
22	q	60	ALA
34	e	922	ARG
1	A	1177	ASP
1	A	2002	TYR
2	C	167	ASN
2	C	278	LYS
9	T	115	ASN
10	Z	154	VAL
10	Z	410	GLU
10	Z	415	GLN
18	d	151	ILE
34	e	604	ASN
34	e	937	PRO
4	O	263	VAL
5	P	34	ILE
17	c	16	VAL
17	c	218	VAL

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Mol	Chain	Res	Type
22	q	36	GLY
26	h	15	PRO
26	H	15	PRO
32	Y	52	LYS
1	A	407	VAL
22	q	175	PRO
1	A	741	ILE
21	n	387	ILE
34	e	943	GLY
1	A	377	VAL
1	A	379	ILE
1	A	1752	VAL
5	P	166	PRO
2	C	704	PRO
5	P	219	ILE
18	d	188	ILE
22	r	36	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	1753/2182 (80%)	1745 (100%)	8 (0%)	92	96
2	C	794/910 (87%)	791 (100%)	3 (0%)	93	97
3	J	21/121 (17%)	21 (100%)	0	100	100
4	O	295/397 (74%)	294 (100%)	1 (0%)	94	97
5	P	173/328 (53%)	173 (100%)	0	100	100
6	Q	171/332 (52%)	170 (99%)	1 (1%)	90	95
7	R	224/296 (76%)	222 (99%)	2 (1%)	84	93
8	S	56/151 (37%)	54 (96%)	2 (4%)	42	76
9	T	141/141 (100%)	140 (99%)	1 (1%)	88	94
10	Z	417/538 (78%)	417 (100%)	0	100	100
17	c	212/308 (69%)	206 (97%)	6 (3%)	51	79

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
18	d	219/219 (100%)	219 (100%)	0	100	100
19	I	92/193 (48%)	92 (100%)	0	100	100
20	v	57/152 (38%)	47 (82%)	10 (18%)	2	18
21	n	122/413 (30%)	100 (82%)	22 (18%)	2	17
22	o	59/451 (13%)	52 (88%)	7 (12%)	6	34
22	p	62/451 (14%)	54 (87%)	8 (13%)	5	31
22	q	119/451 (26%)	102 (86%)	17 (14%)	4	28
22	r	60/451 (13%)	55 (92%)	5 (8%)	14	51
23	t	37/165 (22%)	27 (73%)	10 (27%)	0	5
24	F	67/176 (38%)	67 (100%)	0	100	100
24	k	70/176 (40%)	70 (100%)	0	100	100
25	G	65/83 (78%)	60 (92%)	5 (8%)	16	55
25	i	65/83 (78%)	60 (92%)	5 (8%)	16	55
26	H	61/77 (79%)	60 (98%)	1 (2%)	70	88
26	h	61/77 (79%)	60 (98%)	1 (2%)	70	88
27	K	58/66 (88%)	55 (95%)	3 (5%)	29	68
27	j	58/66 (88%)	55 (95%)	3 (5%)	29	68
28	U	69/89 (78%)	67 (97%)	2 (3%)	50	79
28	l	69/89 (78%)	67 (97%)	2 (3%)	50	79
29	V	77/129 (60%)	71 (92%)	6 (8%)	16	54
29	m	77/129 (60%)	71 (92%)	6 (8%)	16	54
30	W	59/103 (57%)	55 (93%)	4 (7%)	20	59
30	g	79/103 (77%)	74 (94%)	5 (6%)	22	61
31	X	26/100 (26%)	25 (96%)	1 (4%)	40	74
32	Y	47/219 (22%)	44 (94%)	3 (6%)	22	61
35	f	134/225 (60%)	131 (98%)	3 (2%)	60	84
All	All	6226/10640 (58%)	6073 (98%)	153 (2%)	59	82

All (153) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	161	PHE
1	A	284	ARG

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Mol	Chain	Res	Type
1	A	518	VAL
1	A	1339	LEU
1	A	1576	GLU
1	A	1588	LYS
1	A	1866	PHE
1	A	1988	LEU
2	C	109	LEU
2	C	193	LEU
2	C	497	ASP
4	O	343	THR
6	Q	99	VAL
7	R	146	LEU
7	R	169	ASP
8	S	35	THR
8	S	36	THR
9	T	120	CYS
17	c	504	PRO
17	c	505	PRO
17	c	517	VAL
17	c	523	LEU
17	c	532	PRO
17	c	550	PRO
20	v	616	PRO
20	v	617	PRO
20	v	641	PRO
20	v	706	LEU
20	v	712	CYS
20	v	722	PRO
20	v	723	SER
20	v	725	THR
20	v	726	ARG
20	v	733	ILE
21	n	51	PHE
21	n	55	GLU
21	n	57	LYS
21	n	58	ARG
21	n	59	ARG
21	n	61	LYS
21	n	62	THR
21	n	66	ASP
21	n	159	PRO
21	n	162	PRO

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Mol	Chain	Res	Type
21	n	208	PRO
21	n	257	PRO
21	n	258	THR
21	n	260	PRO
21	n	295	SER
21	n	306	SER
21	n	327	PRO
21	n	340	PRO
21	n	373	PRO
21	n	424	PRO
21	n	428	PRO
21	n	436	PRO
22	o	17	PRO
22	o	26	SER
22	o	44	PRO
22	o	63	THR
22	o	96	PHE
22	o	109	LEU
22	o	134	SER
22	p	17	PRO
22	p	44	PRO
22	p	63	THR
22	p	80	LEU
22	p	85	GLN
22	p	93	LEU
22	p	99	ARG
22	p	109	LEU
22	q	17	PRO
22	q	44	PRO
22	q	55	PRO
22	q	56	SER
22	q	61	SER
22	q	102	LEU
22	q	126	LEU
22	q	172	PRO
22	q	175	PRO
22	q	196	PRO
22	q	215	CYS
22	q	235	THR
22	q	239	PRO
22	q	262	PRO
22	q	271	SER

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Mol	Chain	Res	Type
22	q	350	PRO
22	q	412	PRO
22	r	17	PRO
22	r	44	PRO
22	r	63	THR
22	r	93	LEU
22	r	99	ARG
23	t	5	SER
23	t	7	VAL
23	t	13	PRO
23	t	77	PRO
23	t	96	PRO
23	t	100	THR
23	t	105	PRO
23	t	108	SER
23	t	133	PRO
23	t	150	THR
25	i	16	CYS
25	i	18	PHE
25	i	25	THR
25	i	79	LYS
25	i	81	LEU
26	h	79	LEU
27	j	18	ASN
27	j	41	ASP
27	j	71	LEU
28	l	10	LEU
28	l	76	ASP
29	m	20	LYS
29	m	26	TRP
29	m	30	GLN
29	m	77	ASP
29	m	99	ASP
29	m	104	ASP
30	g	24	PHE
30	g	49	ARG
30	g	77	THR
30	g	99	ASP
30	g	100	SER
25	G	16	CYS
25	G	18	PHE
25	G	25	THR

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Mol	Chain	Res	Type
25	G	79	LYS
25	G	81	LEU
26	H	79	LEU
27	K	18	ASN
27	K	41	ASP
27	K	71	LEU
28	U	10	LEU
28	U	76	ASP
29	V	20	LYS
29	V	26	TRP
29	V	30	GLN
29	V	77	ASP
29	V	99	ASP
29	V	104	ASP
30	W	49	ARG
30	W	77	THR
30	W	99	ASP
30	W	100	SER
31	X	38	LYS
32	Y	4	THR
32	Y	44	PRO
32	Y	71	SER
35	f	81	ILE
35	f	134	GLU
35	f	184	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (109) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	138	HIS
1	A	146	HIS
1	A	178	ASN
1	A	265	ASN
1	A	343	ASN
1	A	365	ASN
1	A	405	ASN
1	A	429	ASN
1	A	541	ASN
1	A	558	GLN
1	A	570	GLN
1	A	584	HIS
1	A	658	ASN

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Mol	Chain	Res	Type
1	A	659	HIS
1	A	705	GLN
1	A	733	GLN
1	A	760	ASN
1	A	784	GLN
1	A	785	HIS
1	A	796	ASN
1	A	839	HIS
1	A	861	GLN
1	A	864	GLN
1	A	868	GLN
1	A	976	GLN
1	A	1005	GLN
1	A	1011	ASN
1	A	1097	HIS
1	A	1156	HIS
1	A	1173	HIS
1	A	1368	GLN
1	A	1376	ASN
1	A	1431	HIS
1	A	1529	ASN
1	A	1532	HIS
1	A	1559	HIS
1	A	1592	HIS
1	A	1718	HIS
1	A	1782	ASN
1	A	1809	ASN
1	A	1856	ASN
1	A	1888	HIS
2	C	82	ASN
2	C	101	GLN
2	C	143	HIS
2	C	158	HIS
2	C	251	GLN
2	C	289	ASN
2	C	310	ASN
2	C	403	ASN
2	C	418	GLN
2	C	764	ASN
2	C	776	ASN
2	C	794	GLN
2	C	830	ASN

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Mol	Chain	Res	Type
2	C	869	HIS
2	C	929	GLN
3	J	4	ASN
3	J	21	GLN
4	O	223	HIS
4	O	265	HIS
4	O	270	ASN
4	O	382	HIS
4	O	428	GLN
4	O	445	ASN
5	P	103	ASN
5	P	148	HIS
5	P	198	ASN
6	Q	72	GLN
6	Q	106	ASN
6	Q	209	ASN
7	R	91	HIS
7	R	202	GLN
7	R	227	ASN
7	R	252	HIS
8	S	5	HIS
8	S	34	HIS
8	S	173	HIS
9	T	57	HIS
9	T	112	ASN
9	T	143	HIS
10	Z	31	ASN
10	Z	107	ASN
10	Z	131	HIS
10	Z	223	HIS
10	Z	225	HIS
10	Z	354	HIS
10	Z	457	HIS
17	c	72	GLN
17	c	83	GLN
17	c	214	ASN
18	d	67	GLN
19	I	184	GLN
19	I	202	GLN
25	i	34	GLN
25	i	86	ASN
27	j	66	ASN

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Mol	Chain	Res	Type
28	l	41	ASN
29	m	30	GLN
25	G	34	GLN
25	G	86	ASN
26	H	52	GLN
27	K	66	ASN
28	U	41	ASN
29	V	30	GLN
30	W	71	ASN
35	f	87	GLN
35	f	169	HIS
35	f	171	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
11	B	12/13 (92%)	5 (41%)	0
12	N	14/15 (93%)	4 (28%)	1 (7%)
13	D	114/214 (53%)	31 (27%)	3 (2%)
14	E	102/112 (91%)	33 (32%)	6 (5%)
15	L	88/1175 (7%)	30 (34%)	8 (9%)
16	M	22/23 (95%)	13 (59%)	3 (13%)
33	b	12/14 (85%)	12 (100%)	0
All	All	364/1566 (23%)	128 (35%)	21 (5%)

All (128) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
11	B	88	U
11	B	89	A
11	B	90	A
11	B	93	U
11	B	94	U
12	N	101	U
12	N	108	U
12	N	109	U
12	N	110	A
13	D	31	G
13	D	32	G
13	D	33	U
13	D	42	A

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Mol	Chain	Res	Type
13	D	44	A
13	D	45	A
13	D	74	U
13	D	75	A
13	D	76	U
13	D	77	A
13	D	79	C
13	D	80	G
13	D	81	A
13	D	82	A
13	D	84	A
13	D	90	C
13	D	92	U
13	D	94	C
13	D	101	C
13	D	104	G
13	D	113	G
13	D	127	U
13	D	164	C
13	D	165	A
13	D	166	U
13	D	170	U
13	D	171	U
13	D	172	U
13	D	173	U
13	D	174	G
13	D	175	G
14	E	12	A
14	E	13	A
14	E	14	C
14	E	15	C
14	E	16	C
14	E	33	C
14	E	34	A
14	E	36	U
14	E	37	U
14	E	39	G
14	E	43	C
14	E	50	G
14	E	51	A
14	E	54	U
14	E	57	U

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Mol	Chain	Res	Type
14	E	60	G
14	E	62	A
14	E	65	U
14	E	66	C
14	E	67	C
14	E	68	C
14	E	73	A
14	E	74	U
14	E	75	A
14	E	80	U
14	E	81	G
14	E	85	C
14	E	86	G
14	E	87	U
14	E	89	U
14	E	90	U
14	E	91	A
14	E	92	C
15	L	16	U
15	L	17	U
15	L	18	U
15	L	19	U
15	L	20	G
15	L	21	G
15	L	25	A
15	L	26	G
15	L	29	C
15	L	30	A
15	L	31	A
15	L	34	G
15	L	39	A
15	L	41	C
15	L	42	U
15	L	49	U
15	L	111	C
15	L	115	U
15	L	116	U
15	L	117	U
15	L	118	U
15	L	119	G
15	L	120	G
15	L	1099	G

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Mol	Chain	Res	Type
15	L	1107	C
15	L	1108	A
15	L	1111	U
15	L	1112	G
15	L	1114	G
15	L	1120	G
16	M	484	U
16	M	485	U
16	M	486	A
16	M	487	A
16	M	492	U
16	M	494	G
16	M	495	A
16	M	496	U
16	M	497	A
16	M	500	A
16	M	501	A
16	M	502	C
16	M	503	A
33	b	-4	U
33	b	-3	A
33	b	-2	U
33	b	0	G
33	b	1	U
33	b	2	U
33	b	3	U
33	b	4	U
33	b	5	U
33	b	6	U
33	b	7	U
33	b	8	A

All (21) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
12	N	108	U
13	D	78	A
13	D	83	C
13	D	172	U
14	E	14	C
14	E	42	A
14	E	51	A

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Mol	Chain	Res	Type
14	E	53	A
14	E	56	A
14	E	64	U
15	L	17	U
15	L	29	C
15	L	30	A
15	L	40	U
15	L	41	C
15	L	117	U
15	L	1107	C
15	L	1111	U
16	M	483	U
16	M	494	G
16	M	499	U

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 13 ligands modelled in this entry, 12 are monoatomic - leaving 1 for Mogul analysis.

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	$\# Z > 2$
36	GTP	C	1500	37	26,34,34	1.36	3 (11%)	29,54,54	1.63	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
36	GTP	C	1500	37	-	0/18/38/38	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
36	C	1500	GTP	C6-C5	-2.36	1.36	1.41
36	C	1500	GTP	O4'-C4'	-2.12	1.40	1.45
36	C	1500	GTP	C4-N3	-2.04	1.32	1.35

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	C	1500	GTP	C5-C6-N1	-4.21	118.02	123.52
36	C	1500	GTP	C2'-C1'-N9	-3.69	103.58	113.47
36	C	1500	GTP	N3-C2-N1	-3.51	122.79	127.56
36	C	1500	GTP	C6-N1-C2	3.15	119.57	115.88

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
36	C	1500	GTP	11	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.