



Full wwPDB EM Validation Report ⓘ

Mar 30, 2026 – 01:03 AM UTC

PDB ID : 6YAM / pdb_00006yam
EMDB ID : EMD-10761
Title : Mammalian 48S late-stage translation initiation complex (LS48S+eIF3 IC)
with beta-globin mRNA
Authors : Bochler, A.; Simonetti, A.; Guca, E.; Hashem, Y.
Deposited on : 2020-03-12
Resolution : 3.60 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

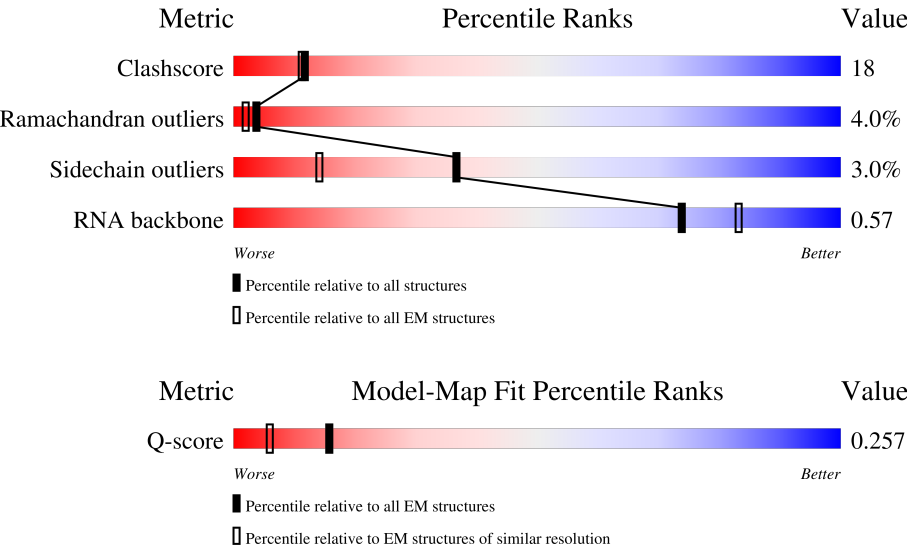
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

The reported resolution of this entry is 3.60 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	12797 (3.10 - 4.10)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	1	75	
2	1	25	
3	C	208	

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Mol	Chain	Length	Quality of chain
4	D	264	
5	E	226	
6	F	227	
7	G	263	
8	H	191	
9	I	237	
10	J	190	
11	K	206	
12	L	182	
13	M	98	
14	N	158	
15	O	132	
16	P	150	
17	Q	151	
18	S	141	
19	T	135	
20	V	145	
21	W	119	
22	X	82	
23	Y	130	
24	Z	142	
25	a	133	
26	b	115	
27	c	84	
28	d	69	

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Mol	Chain	Length	Quality of chain
29	e	53	
30	f	71	
31	g	313	
32	n	75	
33	i	59	
34	2	1863	
35	A	266	
36	B	422	
37	j	144	
38	k	595	
39	U	152	
40	R	145	
41	3	45	
42	m	548	
43	y	1350	
44	v	913	
45	w	445	
46	q	272	
47	r	352	
48	s	218	
49	t	564	
50	u	374	

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
34	C4J	2	1244	X	-	-	-
51	SF4	k	701	-	-	X	-
51	SF4	k	702	-	-	X	-
53	GNP	k	704	-	-	X	-
53	GNP	k	705	-	-	X	-

2 Entry composition

There are 53 unique types of molecules in this entry. The entry contains 118536 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 RNA chain called initiator methionylated tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	75	Total	C	N	O	P	0	0
			1614	722	299	519	74		

- Molecule 2 is a protein called 60s ribosomal protein l41.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	25	Total	C	N	O	S	0	0
			240	145	64	28	3		

- Molecule 3 is a protein called 40S ribosomal protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	208	Total	C	N	O	S	0	0
			1643	1045	289	301	8		

- Molecule 4 is a protein called 40S ribosomal protein eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	215	Total	C	N	O	S	0	0
			1741	1107	309	310	15		

- Molecule 5 is a protein called 40S ribosomal protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	226	Total	C	N	O	S	0	0
			1743	1127	300	307	9		

- Molecule 6 is a protein called 40S ribosomal protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	227	Total	C	N	O	S	0	0
			1765	1124	317	316	8		

- Molecule 7 is a protein called 40S ribosomal protein eS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	263	Total	C	N	O	S	0	0
			2083	1329	385	359	10		

- Molecule 8 is a protein called 40S ribosomal protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	191	Total	C	N	O	S	0	0
			1509	943	286	273	7		

- Molecule 9 is a protein called 40S ribosomal protein eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	237	Total	C	N	O	S	0	0
			1924	1200	387	330	7		

- Molecule 10 is a protein called ribosomal protein eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	190	Total	C	N	O	S	0	0
			1530	975	281	273	1		

- Molecule 11 is a protein called 40S ribosomal protein eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	206	Total	C	N	O	S	0	0
			1680	1054	329	292	5		

- Molecule 12 is a protein called 40S ribosomal protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	182	Total	C	N	O	S	0	0
			1499	952	300	245	2		

- Molecule 13 is a protein called 40S ribosomal protein eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	98	Total	C	N	O	S	0	0
			828	539	148	135	6		

- Molecule 14 is a protein called 40S ribosomal protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	158	Total	C	N	O	S	0	0
			1296	827	241	221	7		

- Molecule 15 is a protein called 40S ribosomal protein eS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	124	Total	C	N	O	S	0	0
			958	600	170	179	9		

- Molecule 16 is a protein called ribosomal protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	150	Total	C	N	O	S	0	0
			1208	773	229	205	1		

- Molecule 17 is a protein called 40S ribosomal protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	136	Total	C	N	O	S	0	0
			1016	621	199	190	6		

- Molecule 18 is a protein called 40S ribosomal protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	S	141	Total	C	N	O	S	0	0
			1124	715	212	194	3		

- Molecule 19 is a protein called 40S ribosomal protein eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	T	126	Total	C	N	O	S	0	0
			1019	639	188	187	5		

- Molecule 20 is a protein called 40S ribosomal protein eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	V	141	Total	C	N	O	S	0	0
			1112	701	213	195	3		

- Molecule 21 is a protein called 40S ribosomal protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	W	104	Total	C	N	O	S	0	0
			822	514	156	148	4		

- Molecule 22 is a protein called 40S ribosomal protein eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	X	82	Total	C	N	O	S	0	0
			620	378	117	120	5		

- Molecule 23 is a protein called 40S ribosomal protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Y	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 24 is a protein called 40S ribosomal protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Z	142	Total	C	N	O	S	0	0
			1107	698	220	185	4		

- Molecule 25 is a protein called 40S ribosomal protein eS24.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	a	126	Total	C	N	O	S	0	0
			1021	645	198	173	5		

- Molecule 26 is a protein called 40S ribosomal protein eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	b	99	Total	C	N	O	S	0	0
			789	491	162	130	6		

- Molecule 27 is a protein called 40S ribosomal protein eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	c	84	Total	C	N	O	S	0	0
			659	413	122	116	8		

- Molecule 28 is a protein called 40S ribosomal protein eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	d	64	Total	C	N	O	S	0	0
			506	308	102	94	2		

- Molecule 29 is a protein called ribosomal protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	e	53	Total	C	N	O	S	0	0
			445	278	90	72	5		

- Molecule 30 is a protein called ribosomal protein eS31.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	f	71	Total	C	N	O	S	0	0
			582	367	109	99	7		

- Molecule 31 is a protein called ribosomal protein RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	g	313	Total	C	N	O	S	0	0
			2437	1535	424	466	12		

- Molecule 32 is a protein called ribosomal protein eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	n	75	Total	C	N	O	S	0	0
			599	382	111	105	1		

- Molecule 33 is a protein called 40S ribosomal protein eS30.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	i	59	Total	C	N	O	S	0	0
			473	293	104	75	1		

- Molecule 34 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	2	1743	Total	C	N	O	P	0	0
			37187	16605	6660	12182	1740		

- Molecule 35 is a protein called eukaryotic translation initiation factor 2 subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	A	266	Total	C	N	O	S	0	0
			2147	1354	376	406	11		

- Molecule 36 is a protein called eukaryotic translation initiation factor 2 subunit gamma.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	B	422	Total	C	N	O	S	0	0
			3214	2044	561	592	17		

- Molecule 37 is a protein called eukaryotic translation initiation factor 1A.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	j	109	Total	C	N	O	S	0	0
			882	549	168	161	4		

- Molecule 38 is a protein called ATP-binding cassette sub-family E member 1 (ABCE1).

Mol	Chain	Residues	Atoms					AltConf	Trace
38	k	595	Total	C	N	O	S	0	0
			4693	2995	802	865	31		

- Molecule 39 is a protein called 40S ribosomal protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	U	145	Total	C	N	O	S	0	0
			1194	747	243	203	1		

- Molecule 40 is a protein called 40S ribosomal protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	R	140	Total	C	N	O	S	0	0
			1154	733	219	195	7		

- Molecule 41 is a RNA chain called beta-globin mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	3	45	Total	C	N	O	P	0	0
			960	430	179	306	45		

- Molecule 42 is a protein called eukaryotic translation initiation factor 3 subunit d.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	m	365	Total	C	N	O	S	0	0
			2955	1856	517	564	18		

- Molecule 43 is a protein called Eukaryotic translation initiation factor 3 subunit A.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	y	603	Total	C	N	O	S	0	0
			4971	3133	897	920	21		

- Molecule 44 is a protein called Eukaryotic translation initiation factor 3 subunit C.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	v	554	Total	C	N	O	S	0	0
			4508	2830	800	845	33		

- Molecule 45 is a protein called Eukaryotic translation initiation factor 3 subunit E.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	w	419	Total	C	N	O	S	0	0
			3465	2220	586	639	20		

- Molecule 46 is a protein called Eukaryotic translation initiation factor 3 subunit F.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	q	272	Total	C	N	O	S	0	0
			2111	1330	359	410	12		

- Molecule 47 is a protein called eukaryotic translation initiation factor 3 subunit h.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	r	324	Total	C	N	O	S	0	0
			2624	1654	452	503	15		

- Molecule 48 is a protein called Eukaryotic translation initiation factor 3 subunit K.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	s	215	Total	C	N	O	S	0	0
			1737	1109	285	330	13		

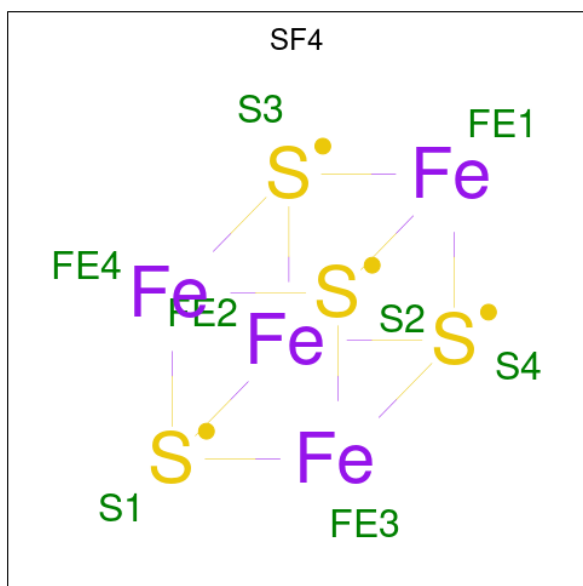
- Molecule 49 is a protein called eukaryotic translation initiation factor 3 subunit l.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	t	372	Total	C	N	O	S	0	0
			3109	2010	519	563	17		

- Molecule 50 is a protein called Eukaryotic translation initiation factor 3 subunit M.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	u	365	Total	C	N	O	S	0	0
			2918	1850	493	558	17		

- Molecule 51 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe_4S_4).

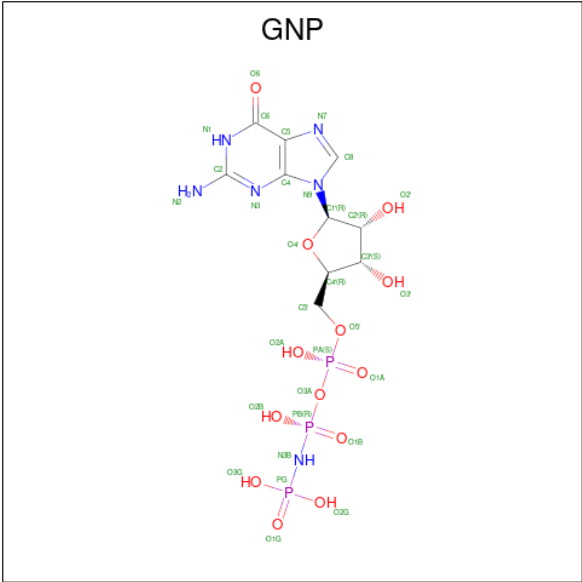


Mol	Chain	Residues	Atoms			AltConf
51	k	1	Total	Fe	S	0
			8	4	4	
51	k	1	Total	Fe	S	0
			8	4	4	

- Molecule 52 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
52	k	1	Total	Mg	0
			1	1	

- Molecule 53 is PHOSPHOAMINOPHOSPHONIC ACID-GUANYLATE ESTER (CCD ID: GNP) (formula: $\text{C}_{10}\text{H}_{17}\text{N}_6\text{O}_{13}\text{P}_3$).

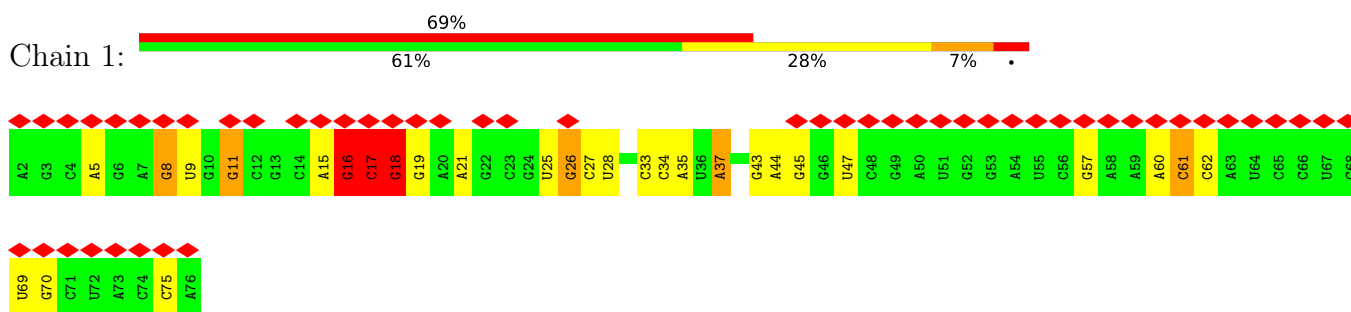


Mol	Chain	Residues	Atoms					AltConf
53	k	1	Total	C	N	O	P	0
			32	10	6	13	3	
53	k	1	Total	C	N	O	P	0
			32	10	6	13	3	

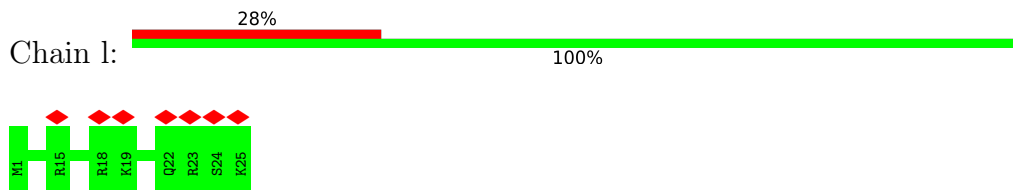
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. 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. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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.

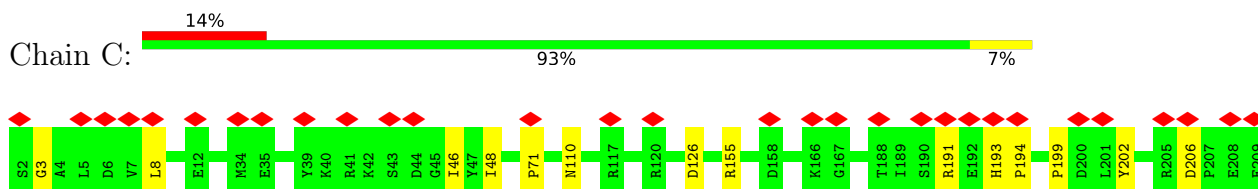
- Molecule 1: initiator methionylated tRNA



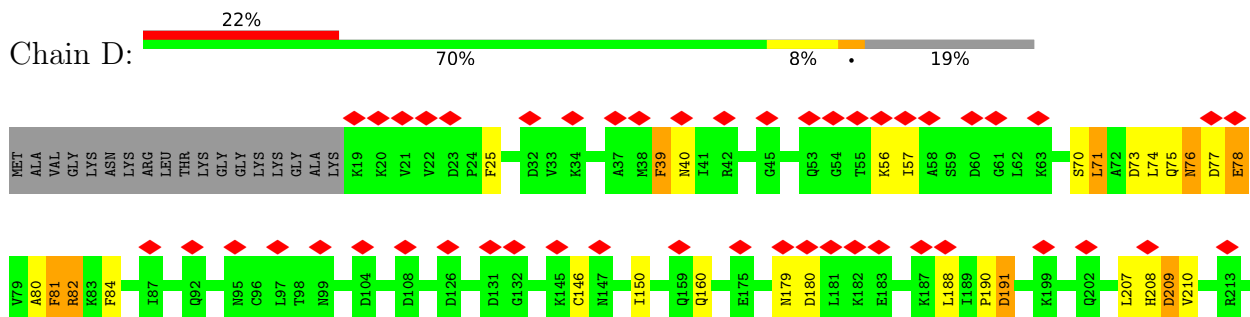
- Molecule 2: 60s ribosomal protein l41

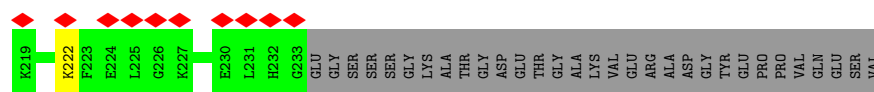


- Molecule 3: 40S ribosomal protein uS2

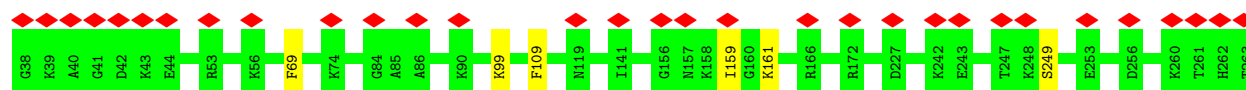


- Molecule 4: 40S ribosomal protein eS1

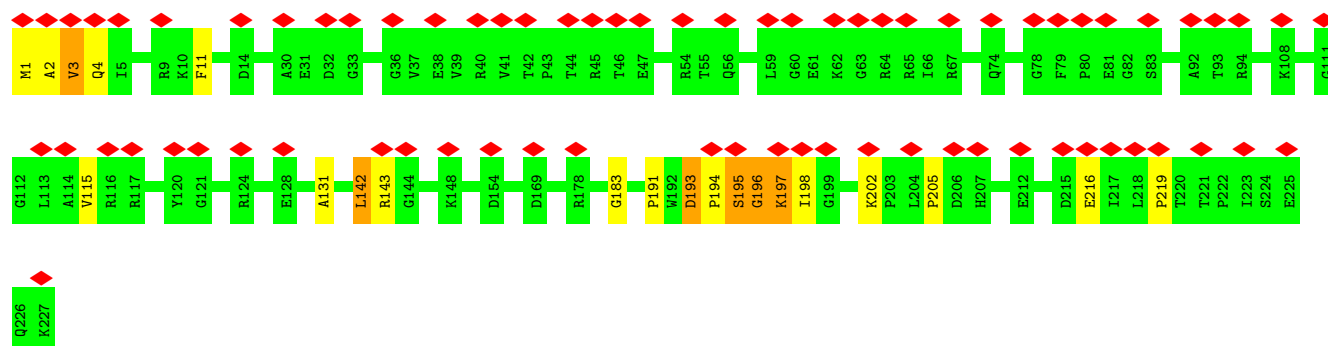




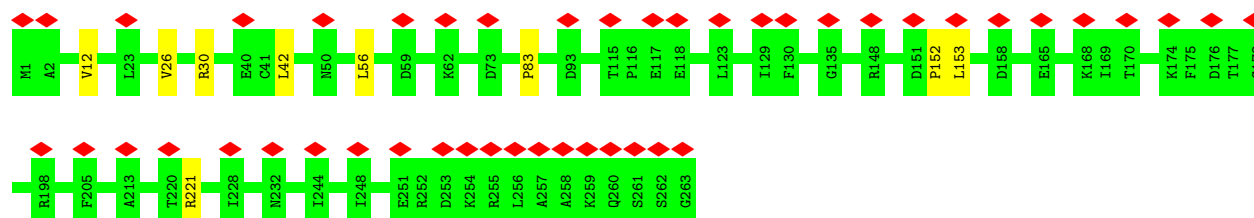
• Molecule 5: 40S ribosomal protein uS5



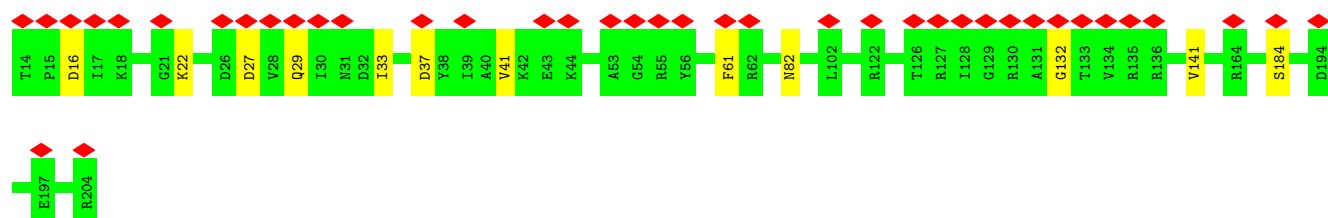
• Molecule 6: 40S ribosomal protein uS3



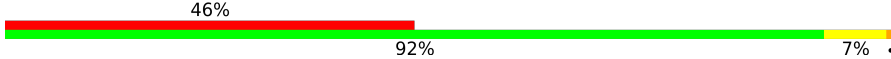
• Molecule 7: 40S ribosomal protein eS4

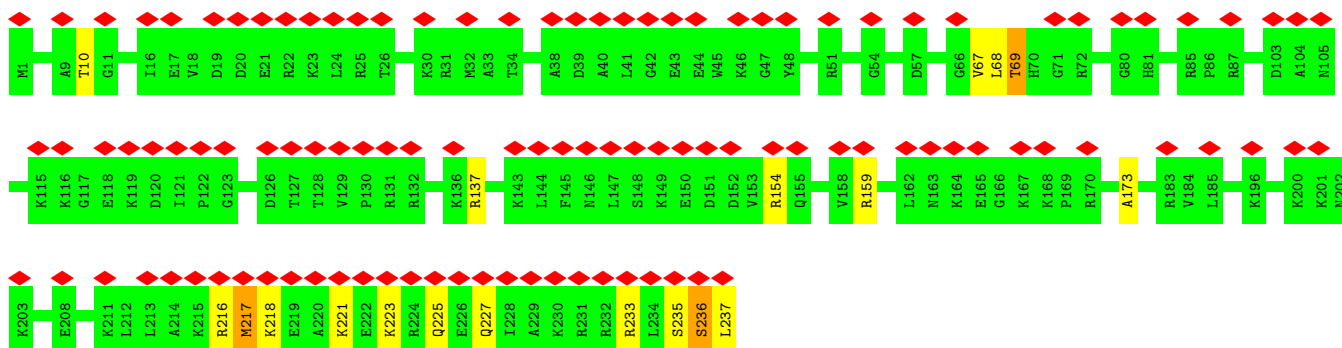


• Molecule 8: 40S ribosomal protein uS7

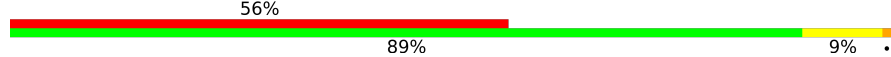


• Molecule 9: 40S ribosomal protein eS6

Chain I: 

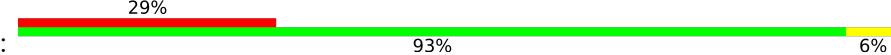


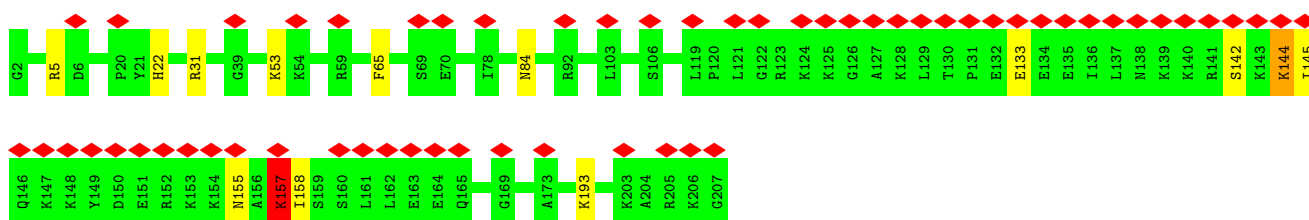
• Molecule 10: ribosomal protein eS7

Chain J: 

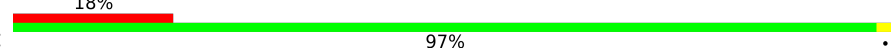


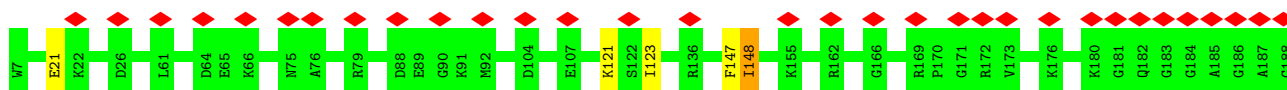
• Molecule 11: 40S ribosomal protein eS8

Chain K: 



• Molecule 12: 40S ribosomal protein uS4

Chain L: 

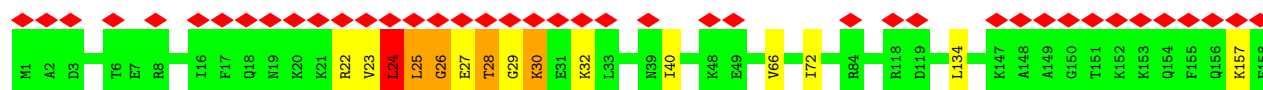
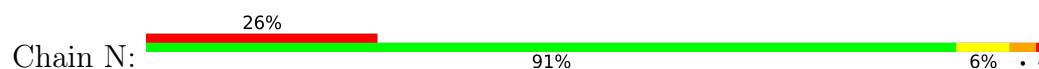


• Molecule 13: 40S ribosomal protein eS10

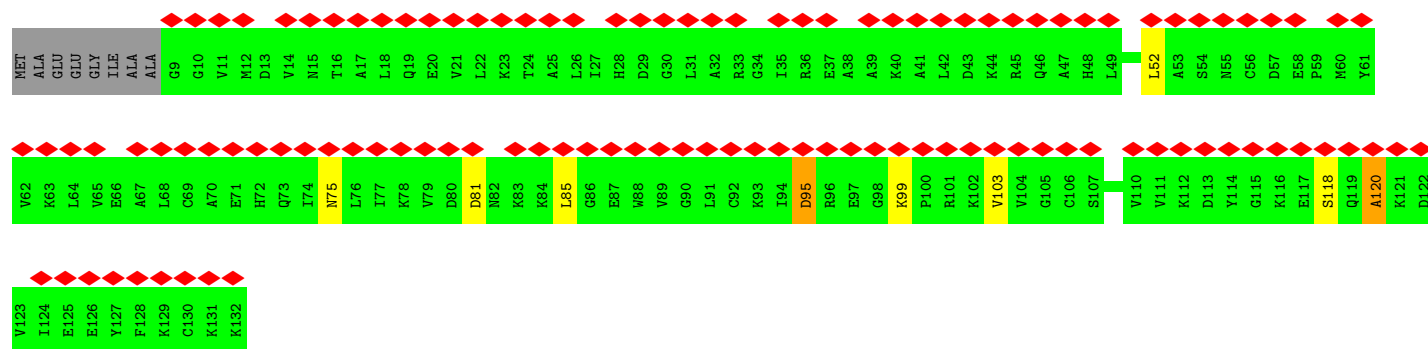
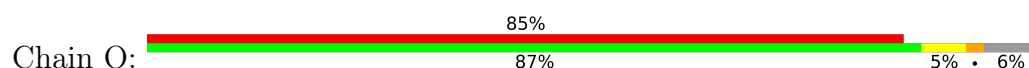
Chain M: 



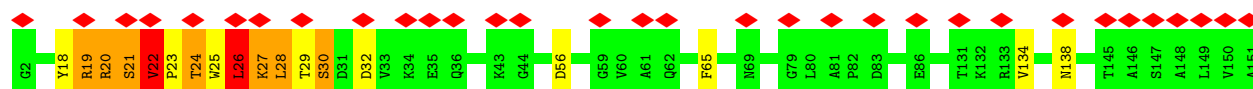
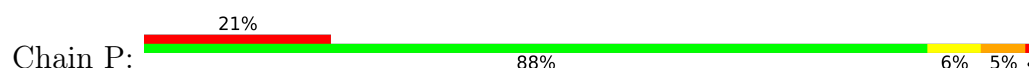
- Molecule 14: 40S ribosomal protein uS17



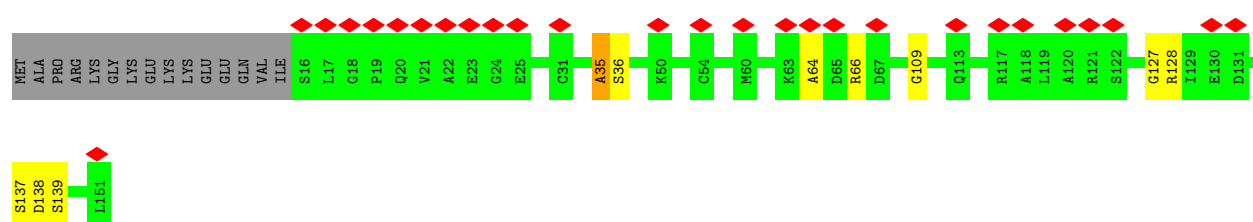
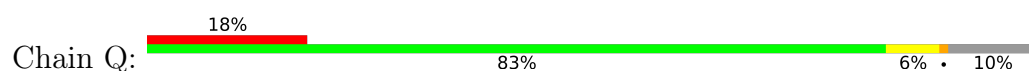
- Molecule 15: 40S ribosomal protein eS12



- Molecule 16: ribosomal protein uS15

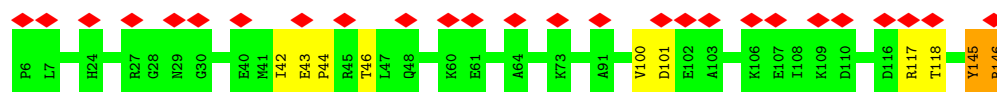


- Molecule 17: 40S ribosomal protein uS11

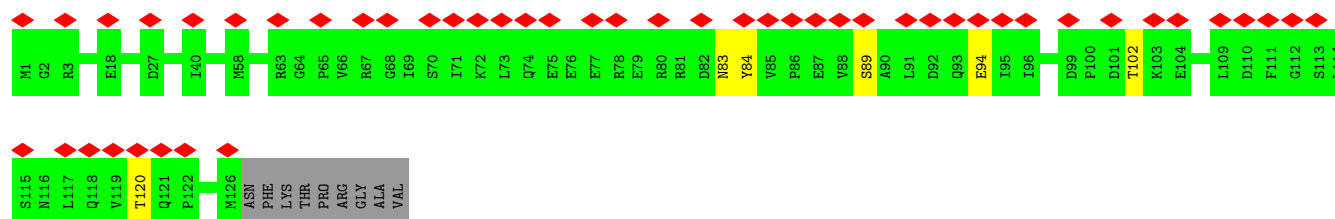
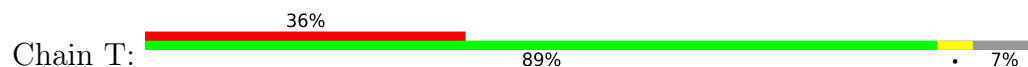


- Molecule 18: 40S ribosomal protein uS9

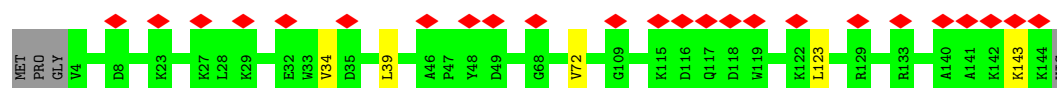




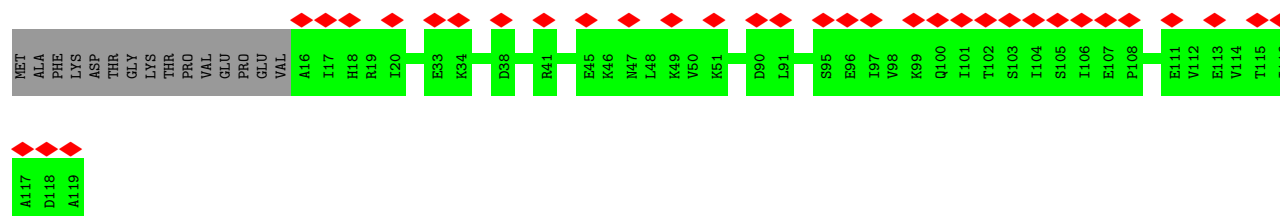
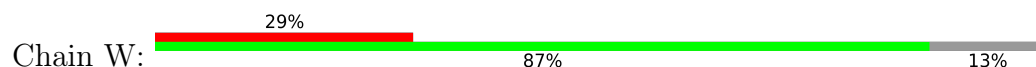
- Molecule 19: 40S ribosomal protein eS17



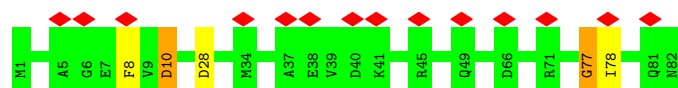
- Molecule 20: 40S ribosomal protein eS19



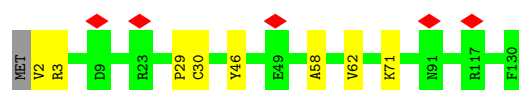
- Molecule 21: 40S ribosomal protein uS10



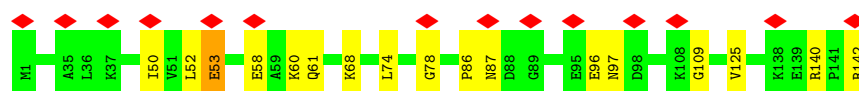
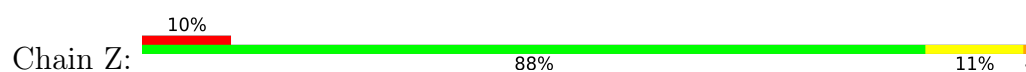
- Molecule 22: 40S ribosomal protein eS21



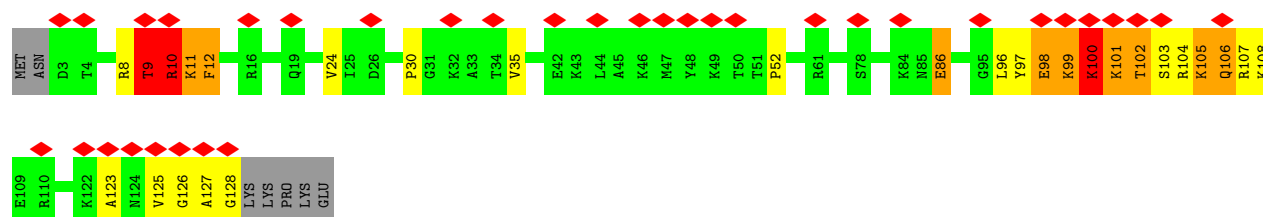
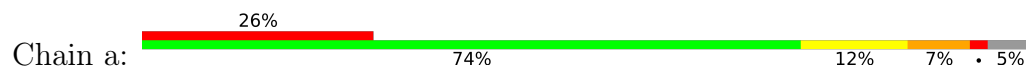
- Molecule 23: 40S ribosomal protein uS8



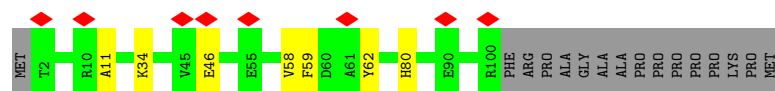
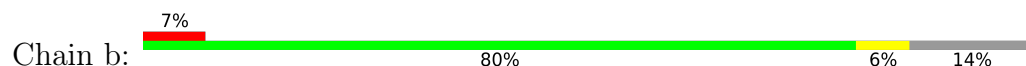
- Molecule 24: 40S ribosomal protein uS12



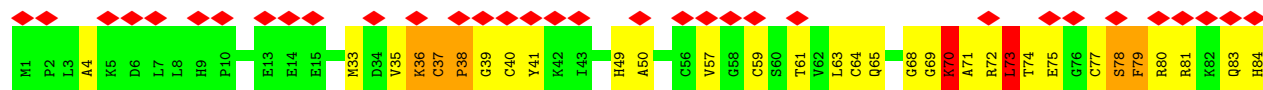
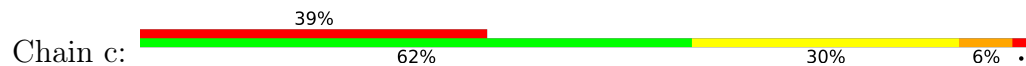
• Molecule 25: 40S ribosomal protein eS24



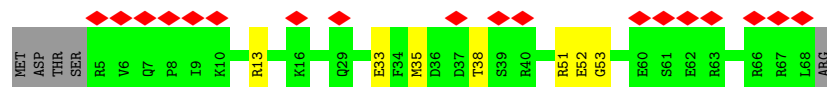
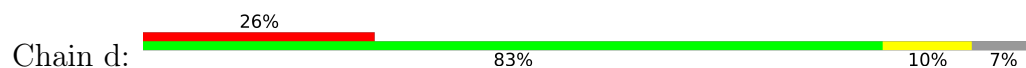
• Molecule 26: 40S ribosomal protein eS26



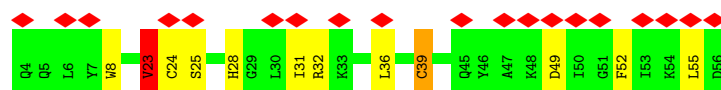
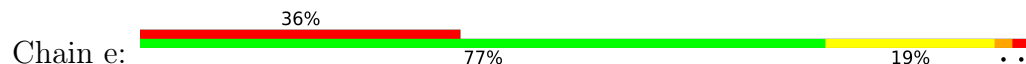
• Molecule 27: 40S ribosomal protein eS27



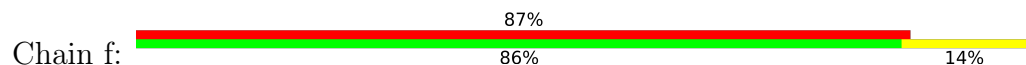
• Molecule 28: 40S ribosomal protein eS28

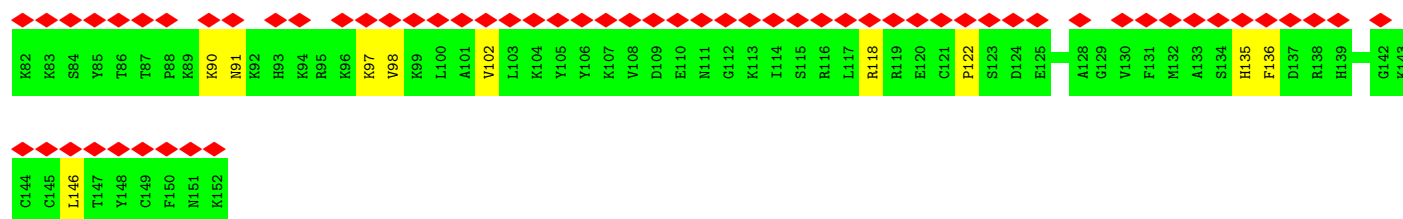


• Molecule 29: ribosomal protein uS14

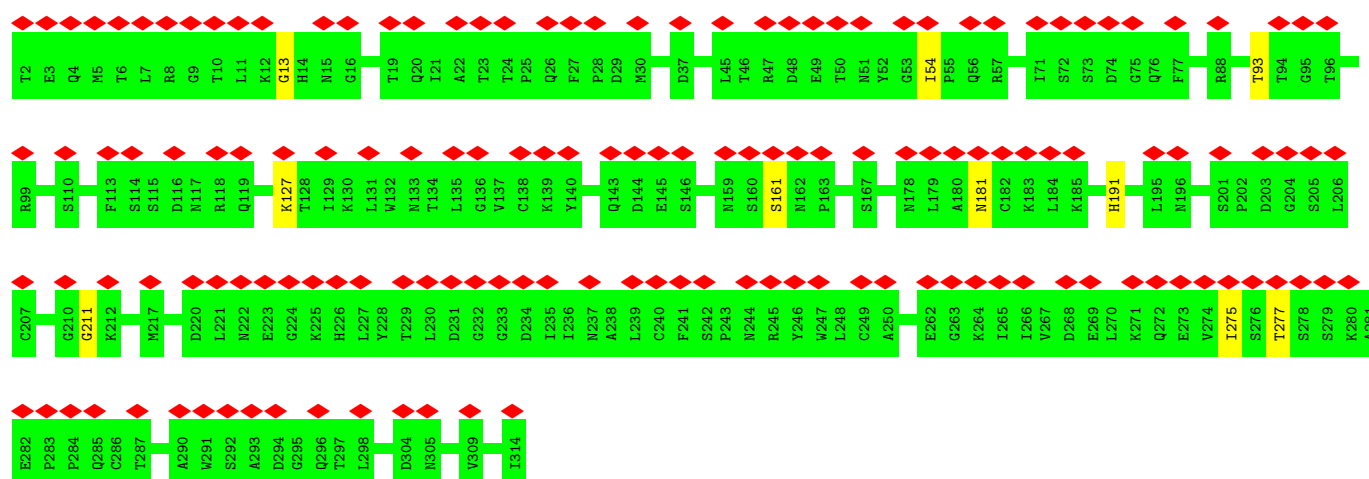


• Molecule 30: ribosomal protein eS31

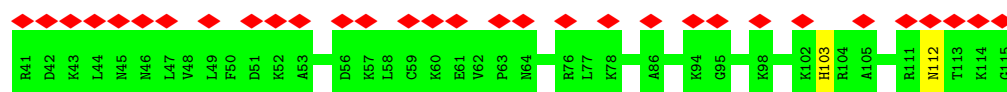
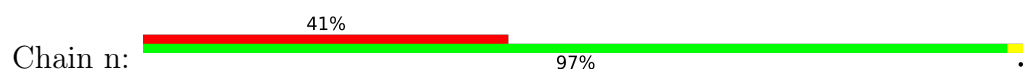




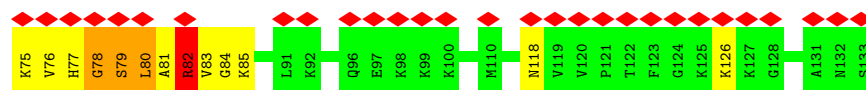
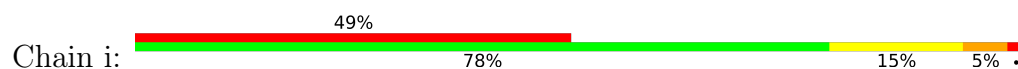
• Molecule 31: ribosomal protein RACK1



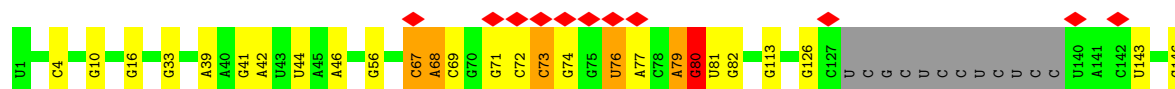
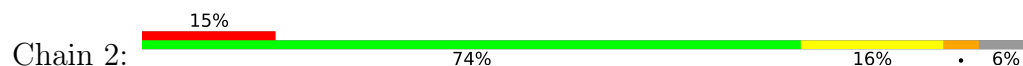
• Molecule 32: ribosomal protein eS25

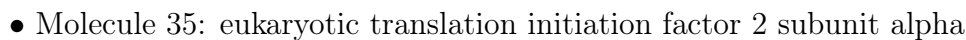


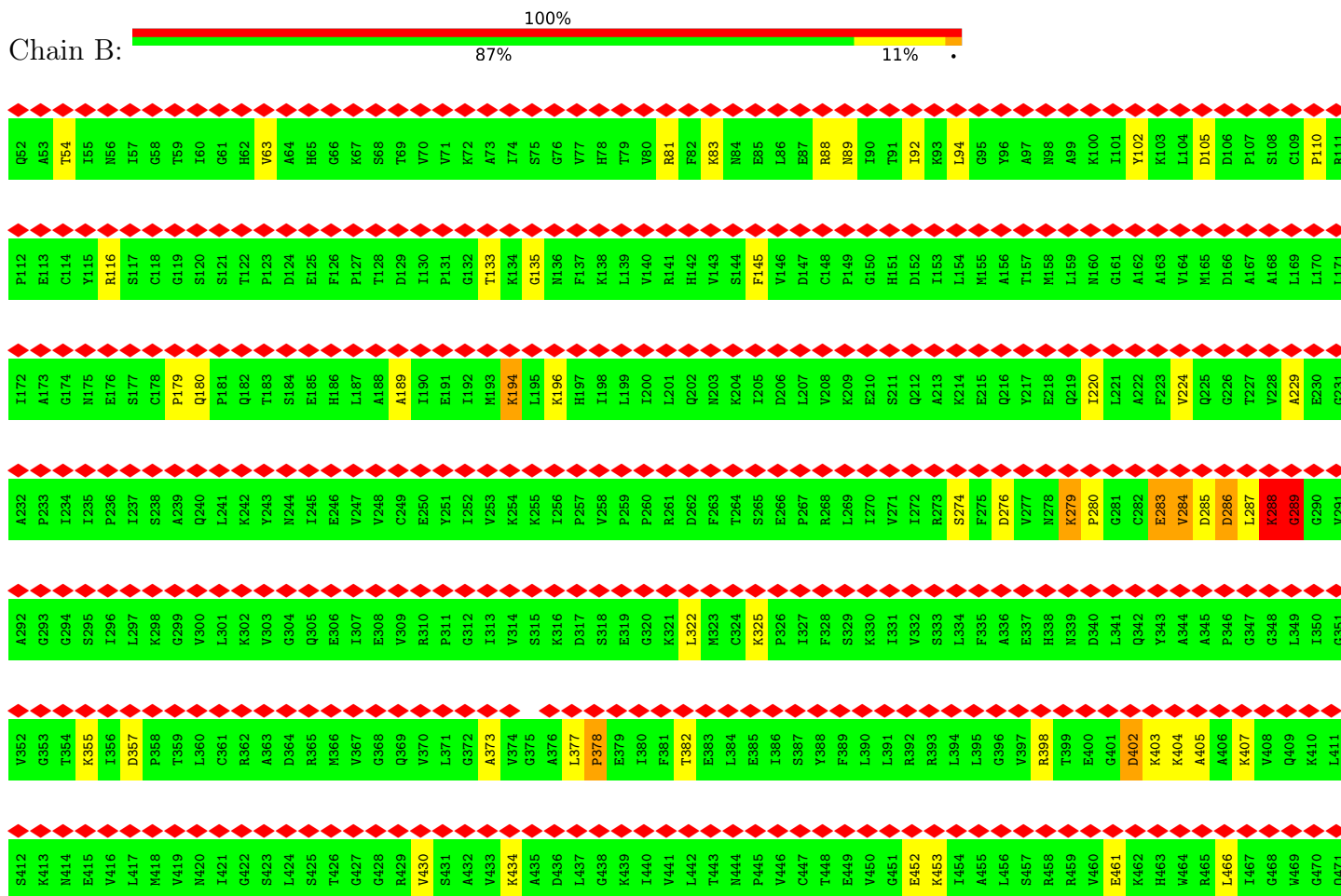
• Molecule 33: 40S ribosomal protein eS30



• Molecule 34: 18S ribosomal RNA

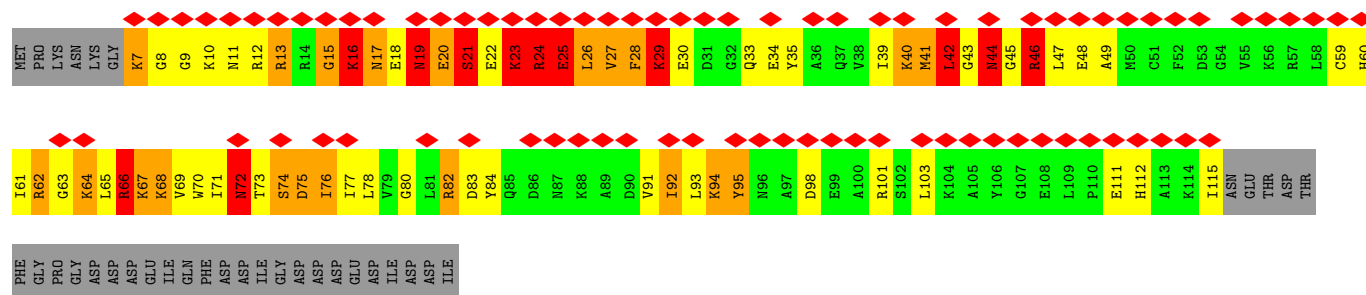
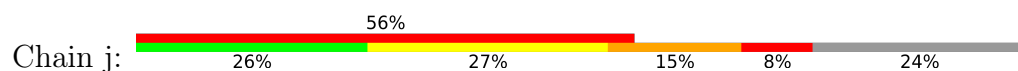




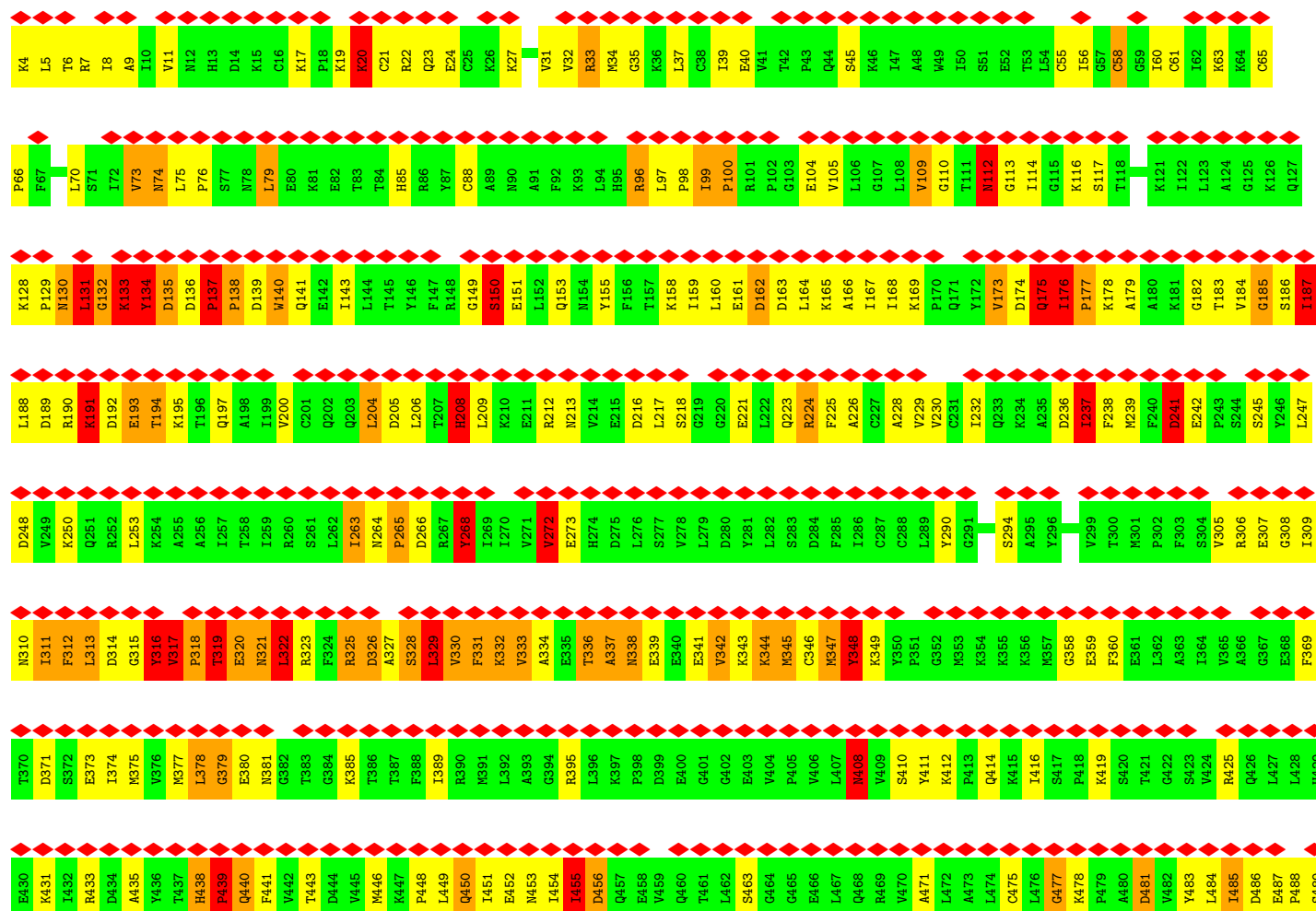
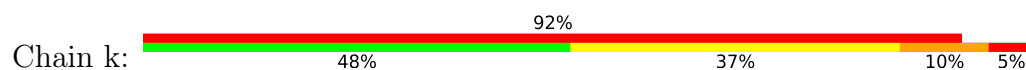


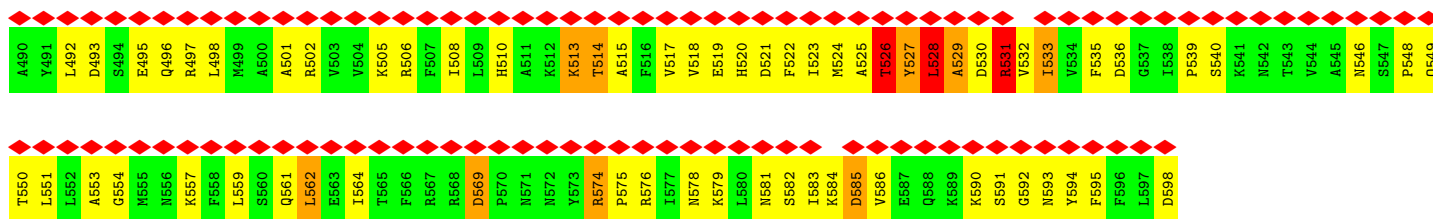


- Molecule 37: eukaryotic translation initiation factor 1A

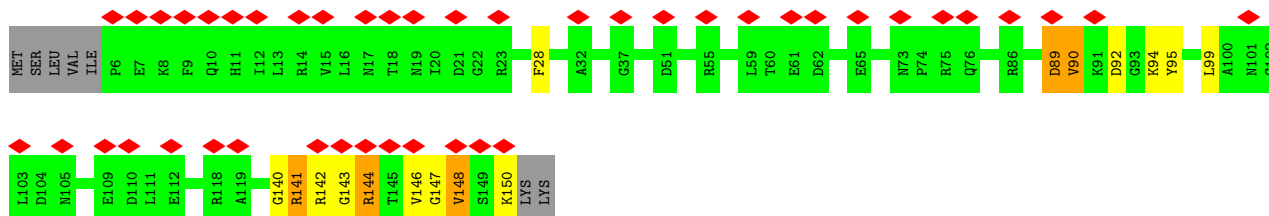
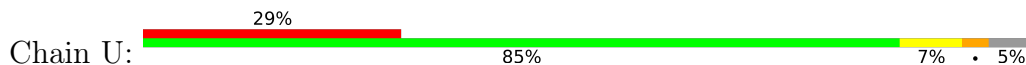


- Molecule 38: ATP-binding cassette sub-family E member 1 (ABCE1)

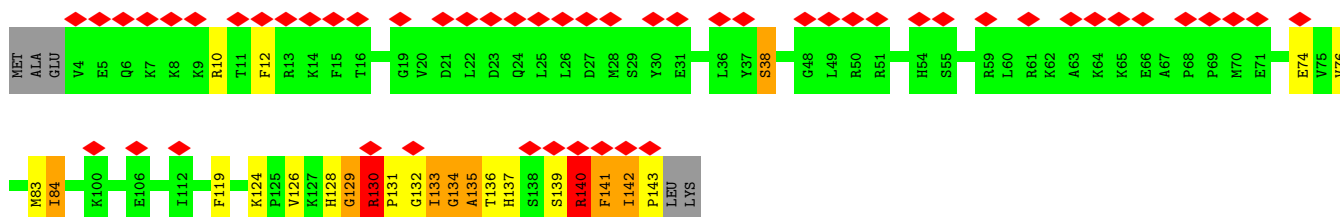
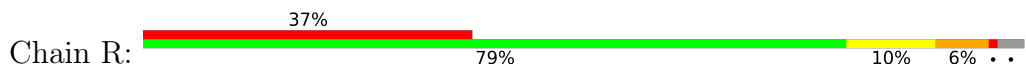




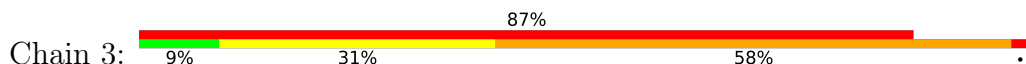
• Molecule 39: 40S ribosomal protein uS13



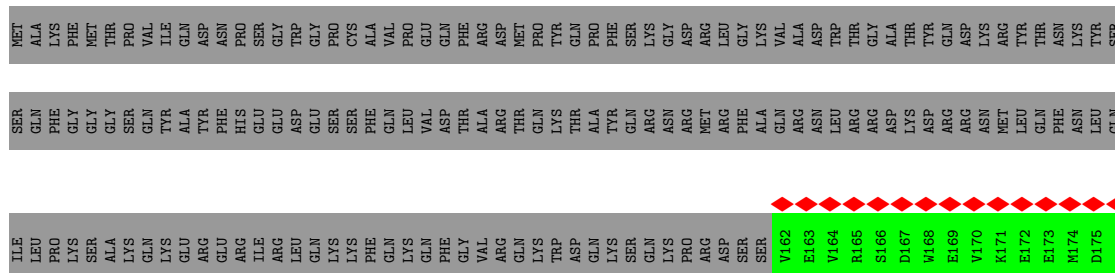
• Molecule 40: 40S ribosomal protein uS19

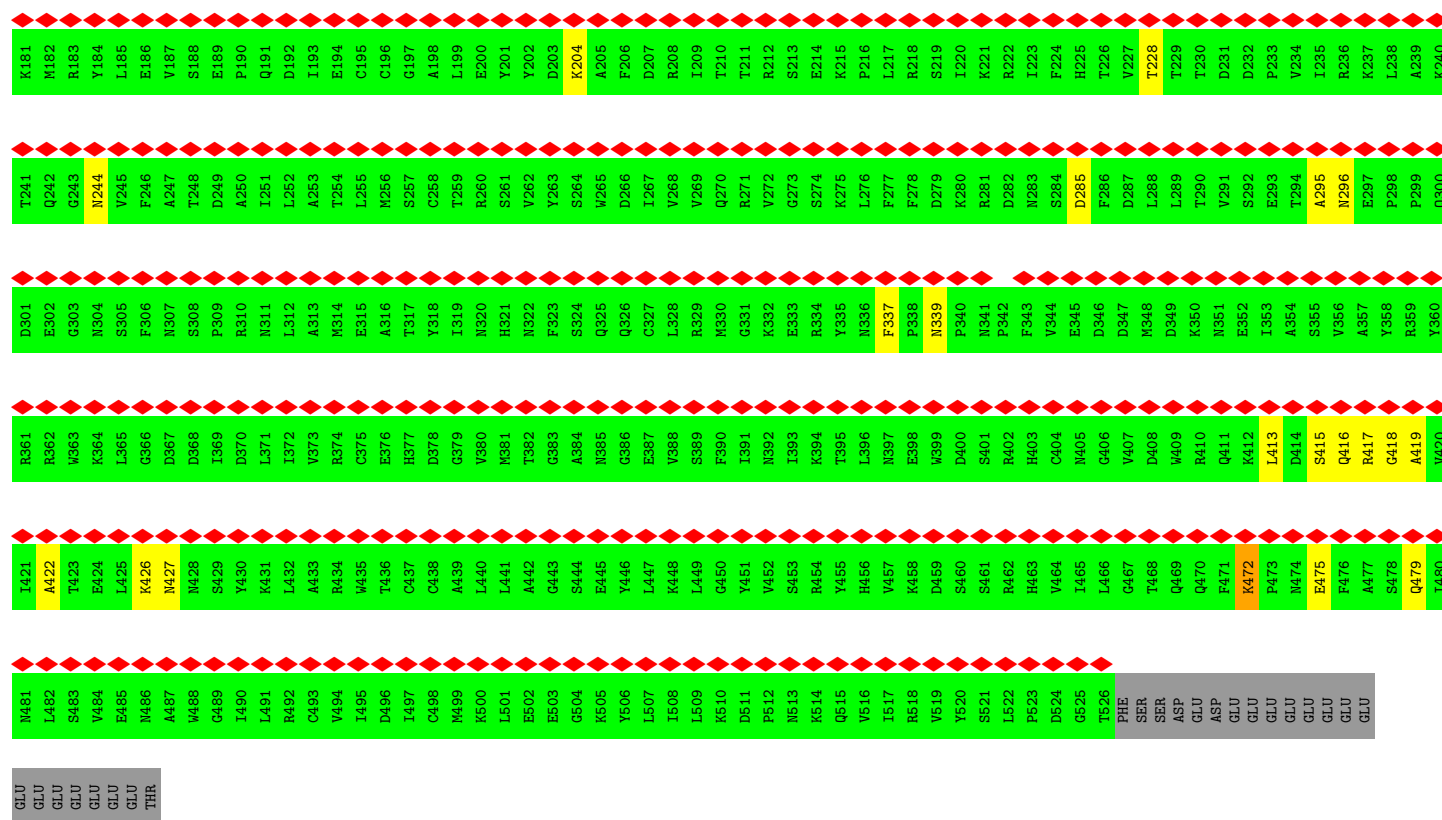


• Molecule 41: beta-globin mRNA

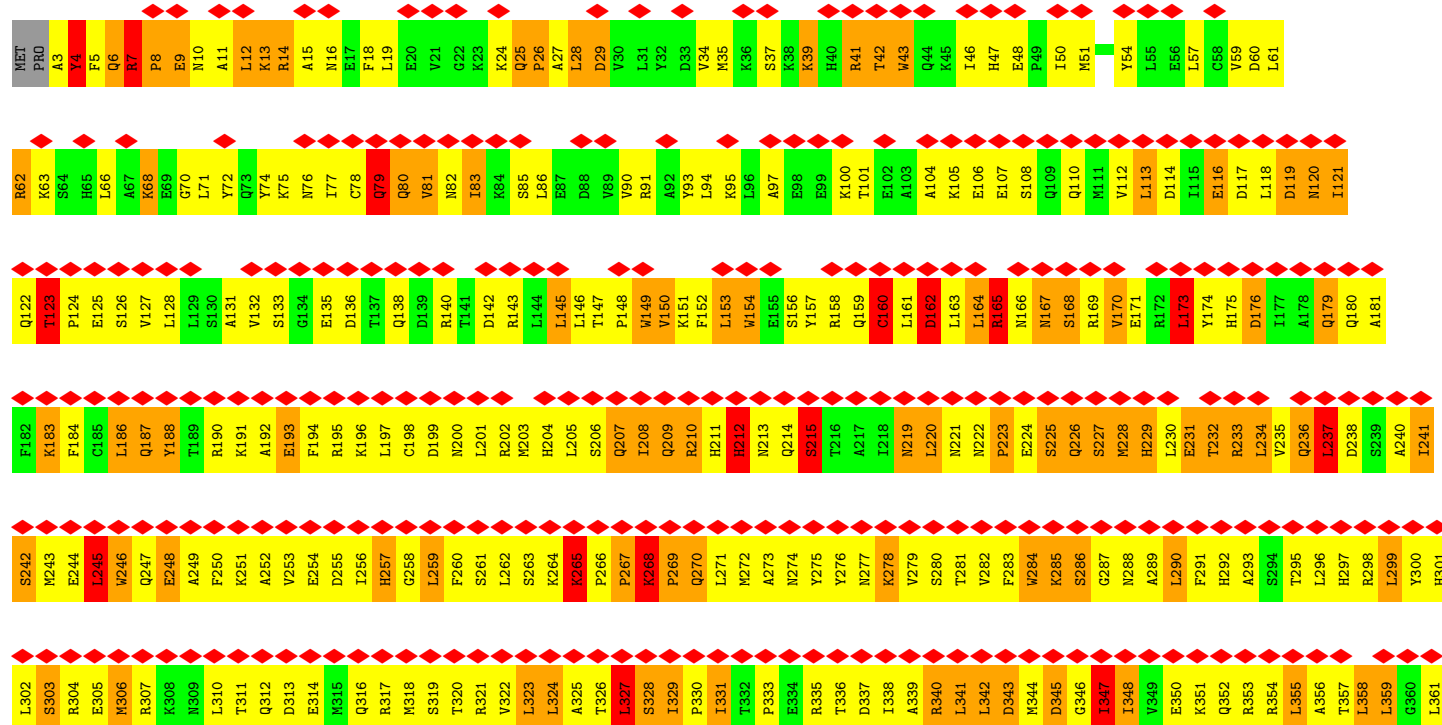
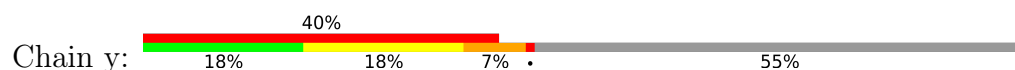


• Molecule 42: eukaryotic translation initiation factor 3 subunit d





• Molecule 43: Eukaryotic translation initiation factor 3 subunit A



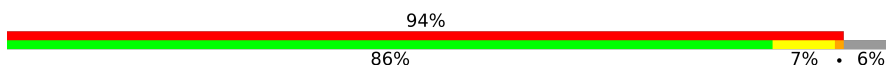
[illegible]

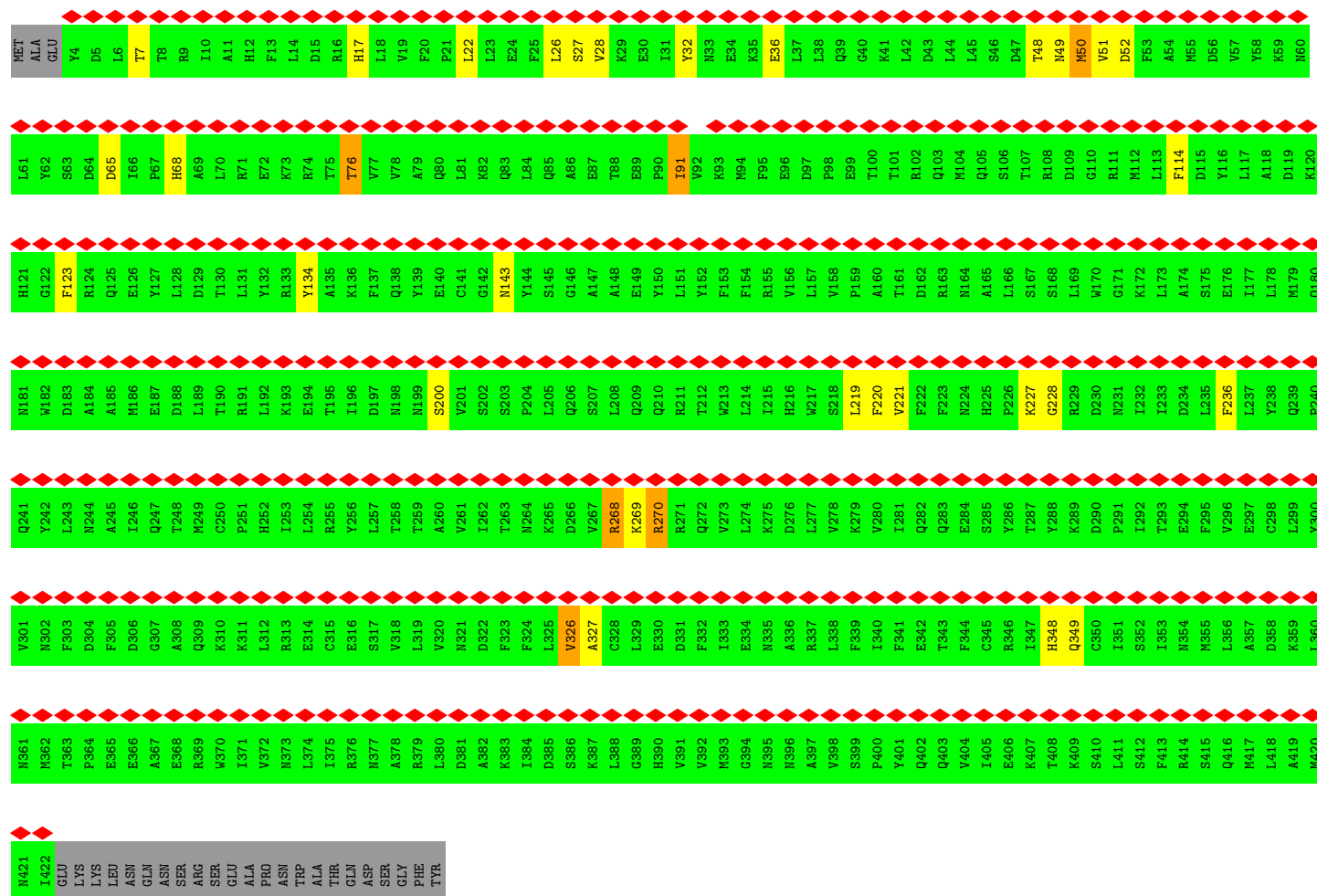
- Molecule 44: Eukaryotic translation initiation factor 3 subunit C



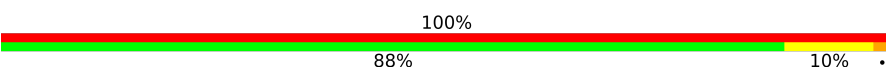
GLY
TYR
ARG
GLN
GLN
SER
GLN
THR
ALA
TYR

• Molecule 45: Eukaryotic translation initiation factor 3 subunit E

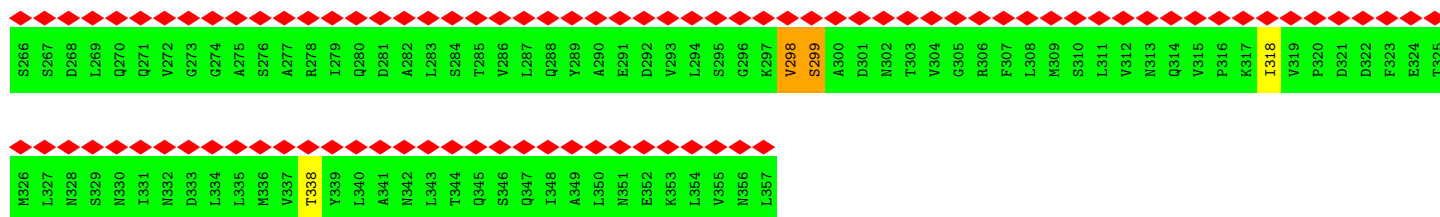
Chain w: 



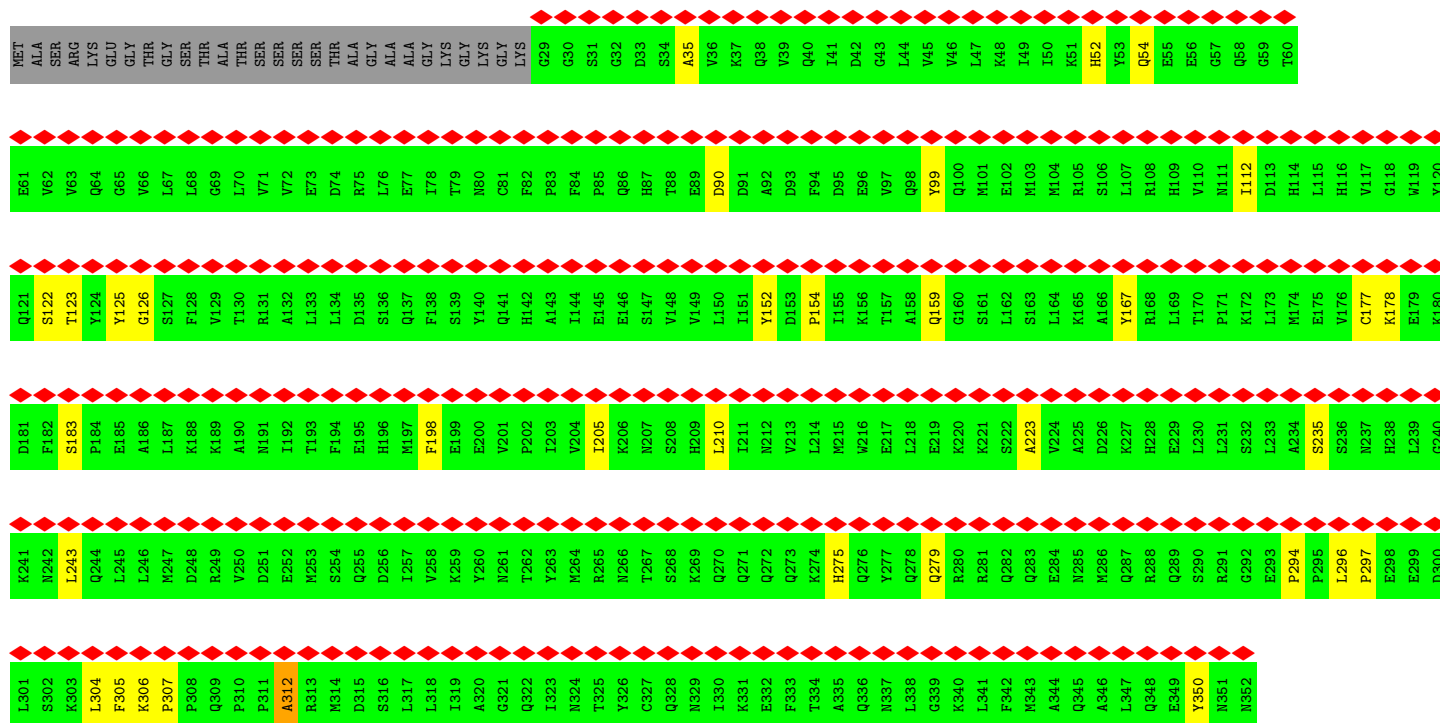
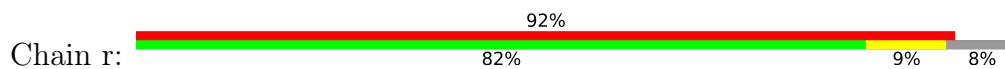
• Molecule 46: Eukaryotic translation initiation factor 3 subunit F

Chain q: 

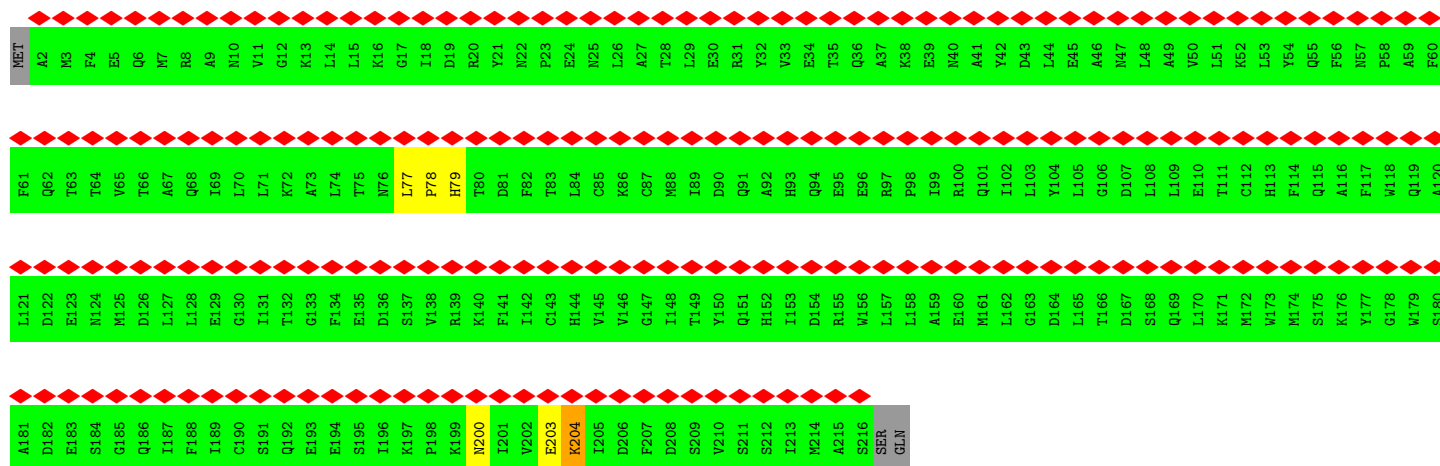




• Molecule 47: eukaryotic translation initiation factor 3 subunit h



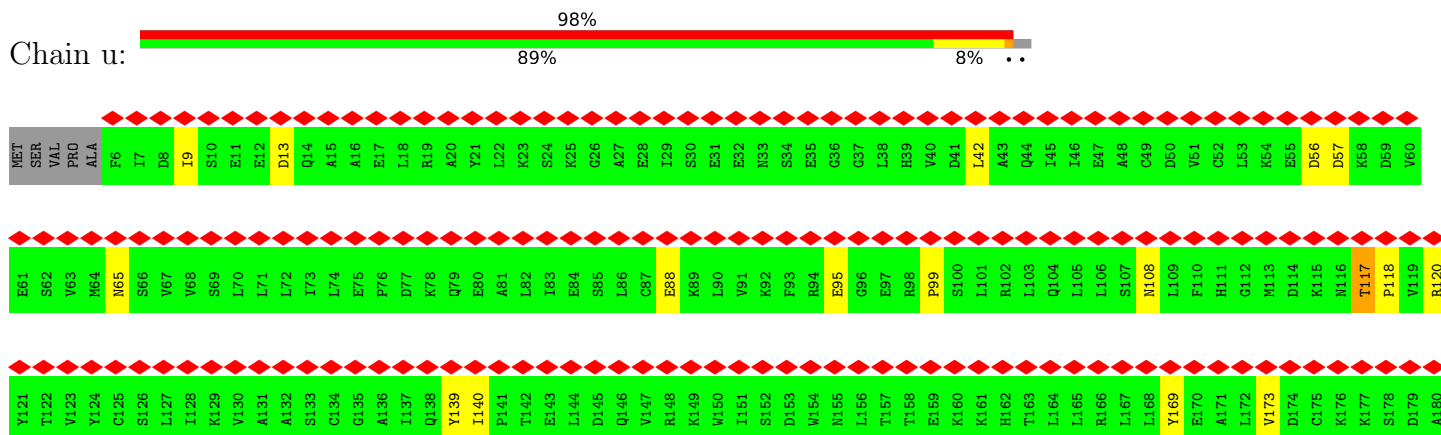
• Molecule 48: Eukaryotic translation initiation factor 3 subunit K



Chain t:



Chain u:





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	43450	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	26	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.119	Depositor
Minimum map value	-0.073	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.02	Depositor
Map size ($\text{\AA}$)	422.40002, 422.40002, 422.40002	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.1, 1.1, 1.1	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: GNP, T6A, C4J, MG, SF4

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 >5	RMSZ	# Z >5
1	1	1.44	8/1770 (0.5%)	1.29	11/2759 (0.4%)
2	l	1.60	0/241	1.35	0/305
3	C	1.24	0/1680	1.43	4/2283 (0.2%)
4	D	1.15	0/1769	1.41	15/2367 (0.6%)
5	E	1.18	0/1779	1.34	4/2399 (0.2%)
6	F	1.24	1/1793 (0.1%)	1.36	5/2412 (0.2%)
7	G	1.26	0/2125	1.36	7/2856 (0.2%)
8	H	1.26	0/1531	1.40	1/2059 (0.0%)
9	I	1.28	1/1947 (0.1%)	1.33	3/2590 (0.1%)
10	J	1.22	0/1553	1.43	6/2079 (0.3%)
11	K	1.29	0/1709	1.42	6/2278 (0.3%)
12	L	1.33	1/1523 (0.1%)	1.40	0/2031
13	M	1.25	0/852	1.49	7/1147 (0.6%)
14	N	1.22	0/1319	1.30	3/1761 (0.2%)
15	O	1.20	0/968	1.50	5/1296 (0.4%)
16	P	1.19	0/1232	1.43	3/1656 (0.2%)
17	Q	1.31	0/1029	1.45	4/1380 (0.3%)
18	S	1.31	0/1142	1.45	6/1528 (0.4%)
19	T	1.25	0/1031	1.39	2/1383 (0.1%)
20	V	1.25	0/1132	1.45	4/1517 (0.3%)
21	W	1.29	0/832	1.37	0/1117
22	X	1.42	1/627 (0.2%)	1.44	4/839 (0.5%)
23	Y	1.28	0/1051	1.39	2/1406 (0.1%)
24	Z	1.28	0/1125	1.35	0/1500
25	a	1.37	1/1038 (0.1%)	1.47	7/1380 (0.5%)
26	b	1.30	0/802	1.35	1/1076 (0.1%)
27	c	1.10	0/673	1.33	1/902 (0.1%)
28	d	1.39	0/508	1.17	0/680
29	e	1.35	0/455	1.47	3/603 (0.5%)
30	f	1.24	0/594	1.47	3/786 (0.4%)
31	g	1.23	0/2494	1.33	6/3394 (0.2%)
32	n	1.25	0/605	1.34	2/810 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	i	1.35	0/478	1.40	2/628 (0.3%)
34	2	0.89	8/41548 (0.0%)	0.99	23/64753 (0.0%)
35	A	0.98	3/2178 (0.1%)	1.50	11/2935 (0.4%)
36	B	1.19	2/3267 (0.1%)	1.46	24/4415 (0.5%)
37	j	0.96	2/892 (0.2%)	1.54	10/1186 (0.8%)
38	k	2.27	16/4772 (0.3%)	2.46	72/6428 (1.1%)
39	U	1.31	0/1211	1.45	3/1618 (0.2%)
40	R	1.25	0/1177	1.40	8/1571 (0.5%)
41	3	0.43	0/1074	0.71	2/1671 (0.1%)
42	m	1.23	0/3015	1.36	8/4078 (0.2%)
43	y	0.89	3/5059 (0.1%)	1.24	23/6832 (0.3%)
44	v	1.15	2/4585 (0.0%)	1.52	26/6185 (0.4%)
45	w	1.19	0/3538	1.51	23/4786 (0.5%)
46	q	1.18	0/2149	1.46	15/2920 (0.5%)
47	r	1.19	0/2675	1.51	20/3609 (0.6%)
48	s	1.12	0/1772	1.40	3/2396 (0.1%)
49	t	1.18	0/3185	1.47	16/4296 (0.4%)
50	u	1.14	0/2963	1.53	20/3998 (0.5%)
All	All	1.17	49/124467 (0.0%)	1.33	434/176884 (0.2%)

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	1	3	2
3	C	0	1
4	D	0	1
9	I	0	3
10	J	0	2
11	K	0	2
12	L	0	2
13	M	0	5
17	Q	0	2
18	S	0	2
22	X	0	1
25	a	0	1
26	b	0	1
27	c	0	1
29	e	0	4
30	f	0	1

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
33	i	0	3
34	2	1	46
35	A	0	7
36	B	0	8
37	j	0	12
38	k	0	33
39	U	0	3
43	y	0	8
44	v	0	53
45	w	0	10
46	q	0	6
47	r	0	10
48	s	0	1
49	t	0	5
50	u	0	9
All	All	4	245

All (49) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
38	k	455	ILE	C-N	-63.41	0.45	1.33
38	k	562	LEU	C-N	-59.61	0.52	1.33
38	k	408	ASN	C-N	-48.19	0.68	1.33
38	k	481	ASP	C-N	-43.96	0.79	1.33
38	k	378	LEU	C-N	42.03	1.94	1.33
38	k	104	GLU	C-N	-39.88	0.75	1.33
38	k	440	GLN	C-N	37.04	1.85	1.33
44	v	748	ASP	C-N	34.42	1.81	1.33
38	k	531	ARG	C-N	-30.25	0.82	1.33
38	k	109	VAL	C-N	29.14	1.79	1.34
1	1	17	C	O3'-P	25.68	1.99	1.61
38	k	241	ASP	C-N	-23.71	0.84	1.33
38	k	268	TYR	C-N	-22.67	1.02	1.33
1	1	17	C	C2'-O2'	-22.55	1.07	1.41
38	k	513	LYS	C-N	22.20	1.64	1.33
38	k	150	SER	C-N	-22.03	1.02	1.33
38	k	160	LEU	C-N	-20.81	1.05	1.33
25	a	9	THR	C-N	19.41	1.60	1.33
1	1	37	T6A	O3'-P	18.89	1.75	1.56
38	k	493	ASP	C-N	-18.76	1.09	1.33
34	2	80	G	O3'-P	-17.59	1.34	1.61
1	1	18	G	O3'-P	17.37	1.87	1.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	2	239	U	O3'-P	-16.48	1.36	1.61
1	1	18	G	C3'-O3'	-15.58	1.18	1.42
34	2	350	A	O3'-P	15.19	1.83	1.61
22	X	77	GLY	C-N	15.17	1.54	1.33
36	B	289	GLY	N-CA	-14.42	1.24	1.45
44	v	762	ASN	C-N	-13.26	1.12	1.33
37	j	95	TYR	C-N	-11.96	1.16	1.33
35	A	184	LEU	C-N	11.45	1.57	1.33
34	2	351	U	O3'-P	-10.84	1.44	1.61
1	1	16	G	O3'-P	-10.13	1.46	1.61
38	k	179	ALA	C-N	10.05	1.48	1.33
34	2	1170	U	O3'-P	-8.22	1.48	1.61
1	1	18	G	C1'-N9	-8.11	1.35	1.48
37	j	19	ASN	C-N	-7.66	1.23	1.33
34	2	1171	G	O3'-P	-7.36	1.50	1.61
9	I	217	MET	C-N	-7.08	1.25	1.33
36	B	288	LYS	C-N	-6.47	1.24	1.33
34	2	1170	U	C1'-N1	6.30	1.57	1.48
34	2	67	C	O3'-P	6.17	1.70	1.61
1	1	17	C	C3'-O3'	-5.88	1.34	1.43
35	A	10	GLN	C-O	-5.79	1.17	1.24
43	y	43	TRP	NE1-CE2	-5.44	1.31	1.37
12	L	121	LYS	CA-C	-5.30	1.50	1.53
35	A	10	GLN	C-N	5.24	1.40	1.33
43	y	265	LYS	C-N	5.06	1.39	1.33
43	y	363	ALA	C-N	5.06	1.39	1.33
6	F	183	GLY	CA-C	-5.01	1.48	1.52

All (434) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	k	531	ARG	CA-C-N	-67.19	35.70	122.37
38	k	531	ARG	C-N-CA	-67.19	35.70	122.37
38	k	160	LEU	O-C-N	53.44	178.76	122.12
44	v	762	ASN	O-C-N	38.88	163.33	122.12
38	k	160	LEU	CA-C-N	-38.24	59.17	122.65
38	k	160	LEU	C-N-CA	-38.24	59.17	122.65
38	k	408	ASN	O-C-N	-30.93	81.45	122.59
38	k	481	ASP	O-C-N	-27.17	88.52	122.21
44	v	762	ASN	CA-C-N	-26.54	60.77	121.82
44	v	762	ASN	C-N-CA	-26.54	60.77	121.82
38	k	348	TYR	O-C-N	-25.84	88.23	122.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	17	C	C4'-C3'-O3'	24.16	145.64	109.40
38	k	531	ARG	O-C-N	23.99	154.72	122.57
38	k	378	LEU	CA-C-N	-22.61	77.09	121.41
38	k	378	LEU	C-N-CA	-22.61	77.09	121.41
38	k	104	GLU	O-C-N	-22.57	97.82	123.33
38	k	481	ASP	CA-C-N	22.52	157.16	122.70
38	k	481	ASP	C-N-CA	22.52	157.16	122.70
38	k	513	LYS	O-C-N	-20.71	95.05	122.59
38	k	104	GLU	CA-C-N	19.86	149.07	121.66
38	k	104	GLU	C-N-CA	19.86	149.07	121.66
38	k	455	ILE	O-C-N	-19.79	97.83	122.57
38	k	493	ASP	O-C-N	18.10	148.82	122.76
38	k	493	ASP	CA-C-N	-17.96	96.22	120.28
38	k	493	ASP	C-N-CA	-17.96	96.22	120.28
1	1	17	C	O3'-P-O5'	17.58	130.37	104.00
1	1	18	G	O3'-P-O5'	16.99	129.49	104.00
34	2	271	G	P-O3'-C3'	16.76	145.34	120.20
1	1	16	G	O3'-P-O5'	16.74	129.11	104.00
38	k	109	VAL	O-C-N	-16.62	98.10	122.20
25	a	12	PHE	CB-CA-C	16.48	139.78	109.46
38	k	455	ILE	CA-C-N	-15.51	91.92	121.54
38	k	455	ILE	C-N-CA	-15.51	91.92	121.54
34	2	351	U	P-O3'-C3'	14.61	142.11	120.20
37	j	29	LYS	CA-C-N	-14.19	94.44	121.54
37	j	29	LYS	C-N-CA	-14.19	94.44	121.54
44	v	748	ASP	O-C-N	-13.91	105.02	122.68
43	y	245	LEU	O-C-N	-13.71	105.89	123.16
37	j	29	LYS	O-C-N	-13.70	104.37	122.59
38	k	510	HIS	O-C-N	-13.51	107.50	122.09
34	2	1171	G	O3'-P-O5'	13.17	123.76	104.00
34	2	1854	A	P-O3'-C3'	12.32	138.69	120.20
38	k	268	TYR	O-C-N	-12.28	107.61	123.21
38	k	272	VAL	O-C-N	11.77	135.56	122.97
34	2	350	A	O3'-P-O5'	-11.49	86.76	104.00
38	k	241	ASP	O-C-N	11.38	136.22	123.13
38	k	513	LYS	CA-C-N	11.26	143.04	121.54
38	k	513	LYS	C-N-CA	11.26	143.04	121.54
38	k	317	VAL	C-N-CD	-11.22	79.01	125.00
34	2	351	U	O3'-P-O5'	10.29	119.43	104.00
43	y	7	ARG	C-N-CD	-10.21	83.15	125.00
22	X	78	ILE	N-CA-CB	-10.02	94.47	111.50
36	B	288	LYS	CA-C-N	9.90	140.81	121.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	B	288	LYS	C-N-CA	9.90	140.81	121.41
45	w	65	ASP	CA-C-N	9.75	126.38	120.24
45	w	65	ASP	C-N-CA	9.75	126.38	120.24
38	k	263	ILE	N-CA-C	9.67	119.62	110.53
43	y	245	LEU	CA-C-N	-9.33	95.74	122.15
43	y	245	LEU	C-N-CA	-9.33	95.74	122.15
11	K	142	SER	CA-C-N	9.19	138.23	121.70
11	K	142	SER	C-N-CA	9.19	138.23	121.70
35	A	184	LEU	CA-C-N	9.11	144.03	121.80
35	A	184	LEU	C-N-CA	9.11	144.03	121.80
30	f	135	HIS	CA-CB-CG	8.95	122.75	113.80
38	k	408	ASN	CA-C-N	8.93	138.04	121.97
38	k	408	ASN	C-N-CA	8.93	138.04	121.97
38	k	109	VAL	CA-C-N	8.87	130.88	121.48
38	k	109	VAL	C-N-CA	8.87	130.88	121.48
45	w	268	ARG	CA-C-N	8.80	137.54	121.70
45	w	268	ARG	C-N-CA	8.80	137.54	121.70
38	k	150	SER	CA-C-N	-8.77	106.07	120.71
38	k	150	SER	C-N-CA	-8.77	106.07	120.71
34	2	1766	C	O3'-P-O5'	8.77	117.15	104.00
38	k	272	VAL	CA-C-N	-8.72	102.13	122.19
38	k	272	VAL	C-N-CA	-8.72	102.13	122.19
35	A	184	LEU	O-C-N	8.72	136.03	122.61
1	1	8	G	P-O3'-C3'	8.52	132.98	120.20
38	k	112	ASN	CA-CB-CG	-8.48	104.12	112.60
49	t	486	PHE	CA-C-N	8.46	136.93	121.70
49	t	486	PHE	C-N-CA	8.46	136.93	121.70
31	g	181	ASN	N-CA-C	-8.28	105.19	114.62
38	k	510	HIS	CA-C-N	8.23	138.77	122.31
38	k	510	HIS	C-N-CA	8.23	138.77	122.31
35	A	269	PHE	CA-CB-CG	-8.10	105.70	113.80
34	2	1170	U	P-O3'-C3'	8.04	132.25	120.20
34	2	67	C	O3'-P-O5'	-7.99	92.01	104.00
37	j	19	ASN	CA-C-N	7.93	136.68	121.54
37	j	19	ASN	C-N-CA	7.93	136.68	121.54
22	X	78	ILE	N-CA-C	7.82	132.89	111.00
38	k	241	ASP	CA-C-N	-7.77	102.84	121.80
38	k	241	ASP	C-N-CA	-7.77	102.84	121.80
34	2	351	U	OP1-P-O3'	-7.76	84.71	108.00
25	a	125	VAL	CA-C-N	-7.76	106.21	121.41
25	a	125	VAL	C-N-CA	-7.76	106.21	121.41
31	g	54	ILE	N-CA-C	-7.72	102.86	109.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	v	748	ASP	CA-C-N	7.65	136.15	121.54
44	v	748	ASP	C-N-CA	7.65	136.15	121.54
38	k	150	SER	O-C-N	7.58	134.52	122.61
34	2	1218	G	O3'-P-O5'	-7.51	92.73	104.00
44	v	603	PRO	N-CA-C	7.47	119.82	110.70
16	P	22	VAL	C-N-CD	7.46	137.01	120.60
38	k	208	HIS	CA-CB-CG	7.45	121.25	113.80
1	1	16	G	OP2-P-O3'	-7.41	85.78	108.00
41	3	40	C	O3'-P-O5'	7.35	115.03	104.00
1	1	18	G	C4'-C3'-O3'	7.34	124.01	113.00
37	j	95	TYR	CA-C-N	7.26	134.48	122.07
37	j	95	TYR	C-N-CA	7.26	134.48	122.07
38	k	440	GLN	O-C-N	-7.22	112.98	122.59
45	w	143	ASN	CA-C-N	7.10	134.48	121.70
45	w	143	ASN	C-N-CA	7.10	134.48	121.70
25	a	86	GLU	N-CA-CB	7.05	122.92	110.37
34	2	1671	U	P-O3'-C3'	7.03	130.74	120.20
36	B	94	LEU	CA-C-N	7.00	126.99	120.34
36	B	94	LEU	C-N-CA	7.00	126.99	120.34
34	2	834	G	O4'-C1'-N9	6.98	118.97	108.50
47	r	123	THR	N-CA-C	-6.97	96.36	108.69
38	k	136	ASP	CA-C-N	-6.89	113.29	120.38
38	k	136	ASP	C-N-CA	-6.89	113.29	120.38
35	A	206	ASP	CA-CB-CG	-6.87	105.73	112.60
36	B	289	GLY	N-CA-C	6.86	129.44	113.18
38	k	529	ALA	N-CA-C	6.85	121.04	110.42
5	E	69	PHE	CA-CB-CG	-6.82	106.98	113.80
36	B	286	ASP	CA-C-N	-6.78	111.44	122.82
36	B	286	ASP	C-N-CA	-6.78	111.44	122.82
23	Y	46	TYR	N-CA-C	-6.77	106.22	114.75
39	U	28	PHE	CA-CB-CG	-6.72	107.08	113.80
50	u	195	ASP	CA-C-N	6.69	133.75	121.70
50	u	195	ASP	C-N-CA	6.69	133.75	121.70
18	S	46	THR	N-CA-C	-6.65	106.37	114.75
34	2	80	G	O3'-P-O5'	6.62	113.92	104.00
38	k	35	GLY	N-CA-C	6.59	121.50	113.79
13	M	1	MET	CA-C-N	6.56	133.51	121.70
13	M	1	MET	C-N-CA	6.56	133.51	121.70
6	F	197	LYS	CA-C-N	6.56	133.50	121.70
6	F	197	LYS	C-N-CA	6.56	133.50	121.70
4	D	25	PHE	CA-CB-CG	-6.52	107.28	113.80
1	1	17	C	P-O3'-C3'	6.49	129.93	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
18	S	145	TYR	CA-C-N	-6.48	110.04	121.70
18	S	145	TYR	C-N-CA	-6.48	110.04	121.70
36	B	220	ILE	N-CA-CB	6.46	118.11	110.55
15	O	120	ALA	CA-C-N	6.46	129.26	120.54
15	O	120	ALA	C-N-CA	6.46	129.26	120.54
38	k	116	LYS	CA-C-N	6.43	128.90	120.28
38	k	116	LYS	C-N-CA	6.43	128.90	120.28
47	r	210	LEU	CA-C-N	6.39	129.54	120.53
47	r	210	LEU	C-N-CA	6.39	129.54	120.53
37	j	98	ASP	CA-CB-CG	-6.37	106.23	112.60
49	t	348	SER	CA-C-N	6.34	133.11	121.70
49	t	348	SER	C-N-CA	6.34	133.11	121.70
44	v	659	ASN	CA-C-N	6.32	129.58	120.79
44	v	659	ASN	C-N-CA	6.32	129.58	120.79
6	F	115	VAL	N-CA-C	-6.32	106.38	111.81
44	v	520	GLN	N-CA-C	-6.31	105.41	113.23
42	m	472	LYS	CA-C-N	6.23	125.91	119.56
42	m	472	LYS	C-N-CA	6.23	125.91	119.56
14	N	72	ILE	N-CA-C	-6.22	100.14	108.35
45	w	270	ARG	N-CA-C	-6.21	106.92	114.75
50	u	139	TYR	CA-C-N	6.20	124.14	120.24
50	u	139	TYR	C-N-CA	6.20	124.14	120.24
18	S	117	ARG	N-CA-C	-6.19	104.54	113.21
38	k	162	ASP	CA-CB-CG	6.19	118.79	112.60
44	v	394	LYS	CA-C-N	-6.16	113.28	119.56
44	v	394	LYS	C-N-CA	-6.16	113.28	119.56
44	v	662	GLN	N-CA-C	-6.16	105.79	113.55
50	u	288	GLU	N-CA-C	6.16	117.99	111.28
45	w	49	ASN	CA-C-N	6.12	132.72	121.70
45	w	49	ASN	C-N-CA	6.12	132.72	121.70
34	2	1671	U	O3'-P-O5'	6.09	113.14	104.00
34	2	848	G	P-O3'-C3'	6.09	129.33	120.20
39	U	92	ASP	N-CA-C	-6.07	107.70	114.62
10	J	107	LYS	N-CA-C	-6.04	107.14	114.75
46	q	220	SER	CA-C-N	6.03	132.56	121.70
46	q	220	SER	C-N-CA	6.03	132.56	121.70
29	e	23	VAL	N-CA-CB	6.03	117.60	110.55
47	r	52	HIS	CA-CB-CG	-5.98	107.82	113.80
9	I	10	THR	N-CA-C	-5.98	106.97	114.56
31	g	211	GLY	CA-C-N	5.98	128.29	120.28
31	g	211	GLY	C-N-CA	5.98	128.29	120.28
1	1	18	G	OP1-P-O3'	-5.97	90.07	108.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	v	524	THR	N-CA-C	-5.97	99.96	109.04
44	v	653	ARG	N-CA-C	-5.96	105.33	114.16
36	B	54	THR	N-CA-C	-5.95	107.84	114.62
29	e	55	LEU	N-CA-C	-5.94	107.26	114.75
4	D	150	ILE	N-CA-C	-5.94	106.47	113.42
41	3	40	C	OP2-P-O3'	-5.91	90.27	108.00
19	T	102	THR	N-CA-C	-5.88	105.77	113.12
46	q	95	HIS	N-CA-C	-5.88	102.93	108.22
38	k	463	SER	CA-C-N	5.88	126.63	119.99
38	k	463	SER	C-N-CA	5.88	126.63	119.99
43	y	265	LYS	CA-C-N	-5.86	114.34	120.38
43	y	265	LYS	C-N-CA	-5.86	114.34	120.38
34	2	1407	G	P-O3'-C3'	5.83	128.95	120.20
43	y	363	ALA	CA-C-N	-5.83	114.37	120.38
43	y	363	ALA	C-N-CA	-5.83	114.37	120.38
37	j	21	SER	N-CA-CB	5.80	120.30	110.49
49	t	379	PRO	CA-C-N	5.80	132.14	121.70
49	t	379	PRO	C-N-CA	5.80	132.14	121.70
22	X	8	PHE	CA-CB-CG	-5.78	108.02	113.80
49	t	438	GLU	CA-C-N	5.78	125.64	119.28
49	t	438	GLU	C-N-CA	5.78	125.64	119.28
43	y	564	GLU	CA-C-N	5.78	128.29	120.38
43	y	564	GLU	C-N-CA	5.78	128.29	120.38
38	k	237	ILE	O-C-N	-5.77	115.36	122.57
16	P	56	ASP	N-CA-C	5.76	117.64	111.36
36	B	357	ASP	CA-C-N	5.76	127.04	119.84
36	B	357	ASP	C-N-CA	5.76	127.04	119.84
7	G	56	LEU	N-CA-C	-5.75	107.50	114.75
44	v	603	PRO	CA-C-O	-5.75	112.22	120.56
34	2	536	G	O3'-P-O5'	5.73	112.60	104.00
38	k	378	LEU	O-C-N	5.73	130.22	122.59
45	w	76	THR	N-CA-C	-5.72	98.61	110.80
44	v	386	ASN	CA-C-N	-5.72	112.69	119.84
44	v	386	ASN	C-N-CA	-5.72	112.69	119.84
45	w	36	GLU	CA-C-N	5.71	128.73	120.79
45	w	36	GLU	C-N-CA	5.71	128.73	120.79
3	C	202	TYR	N-CA-C	-5.70	106.37	113.38
11	K	65	PHE	CA-CB-CG	-5.70	108.10	113.80
22	X	10	ASP	N-CA-CB	5.68	120.09	110.49
36	B	180	GLN	CA-C-N	5.68	126.94	119.84
36	B	180	GLN	C-N-CA	5.68	126.94	119.84
49	t	347	LYS	N-CA-C	-5.68	107.60	114.75

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	B	145	PHE	CA-CB-CG	-5.67	108.13	113.80
36	B	377	LEU	CA-C-N	5.66	126.92	119.84
36	B	377	LEU	C-N-CA	5.66	126.92	119.84
40	R	119	PHE	CA-CB-CG	-5.66	108.14	113.80
42	m	285	ASP	CA-C-N	5.66	127.86	120.28
42	m	285	ASP	C-N-CA	5.66	127.86	120.28
47	r	294	PRO	N-CA-C	5.65	117.59	110.70
13	M	91	PRO	N-CA-C	-5.64	106.74	114.98
50	u	288	GLU	CA-C-N	5.64	131.85	121.70
50	u	288	GLU	C-N-CA	5.64	131.85	121.70
38	k	439	PRO	N-CA-C	5.63	124.07	112.47
35	A	185	THR	N-CA-C	5.62	122.23	109.81
5	E	109	PHE	CA-CB-CG	-5.61	108.19	113.80
4	D	57	ILE	CA-C-N	5.61	128.11	120.54
4	D	57	ILE	C-N-CA	5.61	128.11	120.54
13	M	85	LEU	CA-C-N	5.60	126.14	120.38
13	M	85	LEU	C-N-CA	5.60	126.14	120.38
1	l	17	C	OP2-P-O3'	-5.59	91.23	108.00
49	t	417	CYS	CA-C-N	5.58	125.26	119.56
49	t	417	CYS	C-N-CA	5.58	125.26	119.56
38	k	438	HIS	CA-C-N	5.58	126.81	119.84
38	k	438	HIS	C-N-CA	5.58	126.81	119.84
34	2	73	C	P-O3'-C3'	5.58	128.56	120.20
47	r	123	THR	N-CA-CB	5.58	120.18	110.81
34	2	1219	A	P-O3'-C3'	-5.57	111.84	120.20
48	s	204	LYS	N-CA-CB	5.57	119.91	110.49
47	r	52	HIS	CA-C-N	5.56	128.52	120.79
47	r	52	HIS	C-N-CA	5.56	128.52	120.79
32	n	103	HIS	CA-C-N	5.55	127.72	120.28
32	n	103	HIS	C-N-CA	5.55	127.72	120.28
35	A	232	PRO	N-CA-C	5.53	117.44	110.70
36	B	194	LYS	N-CA-CB	5.52	119.82	110.49
4	D	188	LEU	CA-C-N	5.52	124.74	120.33
4	D	188	LEU	C-N-CA	5.52	124.74	120.33
47	r	297	PRO	CA-C-N	5.51	131.62	121.70
47	r	297	PRO	C-N-CA	5.51	131.62	121.70
3	C	8	LEU	N-CA-C	-5.51	107.81	114.75
7	G	26	VAL	N-CA-C	5.51	116.24	110.62
46	q	299	SER	N-CA-C	5.51	122.53	110.80
46	q	259	PRO	CA-C-N	5.50	131.61	121.70
46	q	259	PRO	C-N-CA	5.50	131.61	121.70
40	R	130	ARG	CA-C-N	-5.50	114.29	119.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
40	R	130	ARG	C-N-CA	-5.50	114.29	119.90
50	u	88	GLU	CA-C-N	5.48	127.63	120.28
50	u	88	GLU	C-N-CA	5.48	127.63	120.28
7	G	12	VAL	N-CA-C	-5.47	105.36	113.39
42	m	228	THR	CA-C-N	5.47	127.55	120.44
42	m	228	THR	C-N-CA	5.47	127.55	120.44
50	u	140	ILE	CB-CA-C	-5.45	108.57	114.35
39	U	90	VAL	N-CA-C	-5.45	98.01	109.34
25	a	35	VAL	CA-C-N	5.44	125.44	119.89
25	a	35	VAL	C-N-CA	5.44	125.44	119.89
50	u	226	LEU	CA-C-N	5.44	127.76	120.58
50	u	226	LEU	C-N-CA	5.44	127.76	120.58
27	c	57	VAL	N-CA-C	-5.44	107.50	113.43
43	y	483	ARG	CA-C-N	5.43	127.90	120.46
43	y	483	ARG	C-N-CA	5.43	127.90	120.46
44	v	415	ASN	CA-C-N	-5.42	113.06	119.84
44	v	415	ASN	C-N-CA	-5.42	113.06	119.84
38	k	162	ASP	N-CA-C	5.42	119.05	111.90
50	u	95	GLU	N-CA-C	-5.42	100.07	108.90
36	B	325	LYS	CA-C-N	5.41	125.41	119.89
36	B	325	LYS	C-N-CA	5.41	125.41	119.89
19	T	89	SER	N-CA-C	-5.40	106.56	114.39
45	w	227	LYS	CA-C-N	5.40	126.08	120.03
45	w	227	LYS	C-N-CA	5.40	126.08	120.03
15	O	95	ASP	N-CA-CB	5.39	119.60	110.49
23	Y	62	VAL	N-CA-C	-5.38	100.09	108.81
35	A	10	GLN	N-CA-CB	5.38	118.03	110.12
44	v	765	VAL	CA-C-N	5.38	127.49	120.28
44	v	765	VAL	C-N-CA	5.38	127.49	120.28
16	P	134	VAL	N-CA-C	-5.38	107.57	113.43
34	2	1067	G	O3'-P-O5'	5.37	112.05	104.00
20	V	72	VAL	CA-C-N	5.36	125.78	119.94
20	V	72	VAL	C-N-CA	5.36	125.78	119.94
4	D	39	PHE	CA-CB-CG	-5.35	108.45	113.80
11	K	157	LYS	CA-C-N	5.33	131.57	121.97
11	K	157	LYS	C-N-CA	5.33	131.57	121.97
33	i	118	ASN	CA-C-N	5.33	131.30	121.70
33	i	118	ASN	C-N-CA	5.33	131.30	121.70
46	q	338	THR	CA-C-N	5.33	127.37	120.44
46	q	338	THR	C-N-CA	5.33	127.37	120.44
36	B	189	ALA	CA-C-N	5.32	127.37	120.56
36	B	189	ALA	C-N-CA	5.32	127.37	120.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	u	360	ASN	CA-C-N	5.32	127.72	120.54
50	u	360	ASN	C-N-CA	5.32	127.72	120.54
43	y	542	ILE	N-CA-C	-5.31	107.65	112.96
49	t	296	ASN	CA-C-N	5.31	127.34	120.70
49	t	296	ASN	C-N-CA	5.31	127.34	120.70
4	D	209	ASP	N-CA-CB	5.31	119.47	110.49
40	R	38	SER	CA-C-N	5.30	128.77	120.82
40	R	38	SER	C-N-CA	5.30	128.77	120.82
50	u	173	VAL	N-CA-C	-5.29	107.56	112.43
7	G	42	LEU	CA-C-N	5.29	125.29	119.89
7	G	42	LEU	C-N-CA	5.29	125.29	119.89
45	w	68	HIS	CA-CB-CG	-5.29	108.51	113.80
14	N	134	LEU	N-CA-C	-5.29	107.38	113.88
36	B	382	THR	N-CA-C	-5.29	107.48	114.04
43	y	384	VAL	CA-C-N	-5.29	113.23	119.84
43	y	384	VAL	C-N-CA	-5.29	113.23	119.84
50	u	13	ASP	CA-C-N	5.29	131.22	121.70
50	u	13	ASP	C-N-CA	5.29	131.22	121.70
14	N	40	ILE	N-CA-C	-5.29	107.67	112.96
45	w	228	GLY	CA-C-N	5.28	127.30	120.44
45	w	228	GLY	C-N-CA	5.28	127.30	120.44
47	r	296	LEU	CA-C-N	5.27	125.27	119.89
47	r	296	LEU	C-N-CA	5.27	125.27	119.89
47	r	279	GLN	CA-C-N	5.27	127.34	120.28
47	r	279	GLN	C-N-CA	5.27	127.34	120.28
42	m	337	PHE	CA-CB-CG	-5.27	108.53	113.80
42	m	427	ASN	N-CA-C	-5.27	107.87	114.56
31	g	93	THR	N-CA-C	-5.27	108.62	114.62
44	v	463	ASP	CA-C-N	-5.26	113.27	119.84
44	v	463	ASP	C-N-CA	-5.26	113.27	119.84
50	u	13	ASP	CA-CB-CG	5.26	117.86	112.60
46	q	298	VAL	N-CA-C	-5.24	106.57	111.45
38	k	137	PRO	CA-C-N	-5.23	113.30	119.84
38	k	137	PRO	C-N-CA	-5.23	113.30	119.84
46	q	150	MET	CA-C-N	5.23	127.81	120.28
46	q	150	MET	C-N-CA	5.23	127.81	120.28
13	M	72	THR	CA-C-N	5.22	127.28	120.28
13	M	72	THR	C-N-CA	5.22	127.28	120.28
38	k	176	ILE	CA-C-N	-5.22	113.31	119.84
38	k	176	ILE	C-N-CA	-5.22	113.31	119.84
47	r	294	PRO	CA-C-O	-5.22	112.99	120.56
40	R	124	LYS	CA-C-N	5.22	125.27	119.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
40	R	124	LYS	C-N-CA	5.22	125.27	119.32
10	J	7	LYS	N-CA-C	-5.22	108.67	114.62
11	K	155	ASN	N-CA-C	-5.22	104.72	111.71
38	k	128	LYS	CA-C-N	-5.22	113.32	119.84
38	k	128	LYS	C-N-CA	-5.22	113.32	119.84
45	w	123	PHE	CA-C-N	5.21	127.22	120.44
45	w	123	PHE	C-N-CA	5.21	127.22	120.44
17	Q	139	SER	CA-C-N	5.21	128.48	120.82
17	Q	139	SER	C-N-CA	5.21	128.48	120.82
35	A	171	ASP	CA-C-N	5.21	127.26	120.28
35	A	171	ASP	C-N-CA	5.21	127.26	120.28
46	q	205	SER	CA-C-N	5.21	127.26	120.28
46	q	205	SER	C-N-CA	5.21	127.26	120.28
3	C	48	ILE	CA-C-N	5.21	127.47	120.50
3	C	48	ILE	C-N-CA	5.21	127.47	120.50
5	E	249	SER	CA-C-N	5.21	124.52	118.85
5	E	249	SER	C-N-CA	5.21	124.52	118.85
47	r	223	ALA	N-CA-CB	5.20	119.28	110.49
36	B	92	ILE	N-CA-C	-5.20	108.06	113.10
1	1	18	G	P-O3'-C3'	5.19	127.98	120.20
4	D	210	VAL	N-CA-C	-5.18	101.17	108.27
43	y	533	ALA	CA-C-N	5.17	127.20	120.28
43	y	533	ALA	C-N-CA	5.17	127.20	120.28
45	w	134	TYR	N-CA-C	-5.16	107.05	113.55
10	J	35	ASP	CA-CB-CG	5.16	117.76	112.60
15	O	81	ASP	CA-C-N	5.14	127.89	120.38
15	O	81	ASP	C-N-CA	5.14	127.89	120.38
6	F	11	PHE	CA-CB-CG	-5.14	108.66	113.80
4	D	222	LYS	CA-C-N	5.13	127.92	120.79
4	D	222	LYS	C-N-CA	5.13	127.92	120.79
43	y	417	GLN	N-CA-C	5.13	121.14	109.81
20	V	123	LEU	CA-C-N	5.12	128.44	120.60
20	V	123	LEU	C-N-CA	5.12	128.44	120.60
36	B	434	LYS	N-CA-C	-5.11	102.22	110.14
46	q	178	ASP	CA-C-N	5.11	131.16	121.97
46	q	178	ASP	C-N-CA	5.11	131.16	121.97
9	I	137	ARG	CA-C-N	5.10	127.39	120.65
9	I	137	ARG	C-N-CA	5.10	127.39	120.65
40	R	76	VAL	N-CA-C	-5.10	101.13	108.53
48	s	203	GLU	CA-C-N	5.10	131.28	121.54
48	s	203	GLU	C-N-CA	5.10	131.28	121.54
25	a	9	THR	O-C-N	5.10	129.37	122.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	A	11	HIS	ND1-CG-CD2	5.10	111.20	106.10
43	y	471	ILE	N-CA-C	-5.10	106.71	111.45
34	2	317	G	P-O3'-C3'	5.09	127.84	120.20
50	u	65	ASN	CA-CB-CG	5.09	117.69	112.60
7	G	221	ARG	CA-C-N	5.09	127.11	120.28
7	G	221	ARG	C-N-CA	5.09	127.11	120.28
17	Q	137	SER	CA-C-N	5.09	131.26	121.54
17	Q	137	SER	C-N-CA	5.09	131.26	121.54
45	w	268	ARG	N-CA-C	5.08	116.63	111.14
6	F	142	LEU	N-CA-CB	5.08	119.08	110.49
8	H	82	ASN	CA-CB-CG	-5.08	107.52	112.60
49	t	269	LEU	CA-C-N	5.08	125.17	120.34
49	t	269	LEU	C-N-CA	5.08	125.17	120.34
37	j	112	HIS	CB-CG-CD2	-5.07	124.61	131.20
4	D	146	CYS	CA-C-N	5.06	127.38	120.54
4	D	146	CYS	C-N-CA	5.06	127.38	120.54
47	r	235	SER	CA-C-N	5.06	127.02	120.44
47	r	235	SER	C-N-CA	5.06	127.02	120.44
10	J	114	GLN	CA-C-N	5.06	127.06	120.28
10	J	114	GLN	C-N-CA	5.06	127.06	120.28
38	k	161	GLU	CA-C-N	5.06	129.52	122.08
38	k	161	GLU	C-N-CA	5.06	129.52	122.08
43	y	454	ARG	CA-C-N	5.06	127.77	120.38
43	y	454	ARG	C-N-CA	5.06	127.77	120.38
30	f	97	LYS	CA-C-N	5.05	131.07	121.97
30	f	97	LYS	C-N-CA	5.05	131.07	121.97
44	v	625	LEU	CA-C-N	5.05	127.31	120.38
44	v	625	LEU	C-N-CA	5.05	127.31	120.38
38	k	11	VAL	N-CA-C	5.05	119.85	109.34
4	D	180	ASP	CA-C-N	5.04	128.39	120.82
4	D	180	ASP	C-N-CA	5.04	128.39	120.82
10	J	106	ARG	N-CA-CB	5.04	119.01	110.49
26	b	34	LYS	N-CA-C	-5.04	108.16	114.56
49	t	291	ILE	N-CA-C	-5.04	107.56	112.29
18	S	117	ARG	CA-C-N	5.03	131.16	121.54
18	S	117	ARG	C-N-CA	5.03	131.16	121.54
45	w	114	PHE	CA-C-N	5.03	126.98	120.44
45	w	114	PHE	C-N-CA	5.03	126.98	120.44
29	e	23	VAL	CB-CA-C	-5.01	105.56	111.97
31	g	277	THR	N-CA-C	-5.01	101.45	109.07
34	2	79	A	C4'-C3'-C2'	-5.00	97.59	102.60
43	y	486	HIS	CA-C-N	5.00	126.99	120.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
43	y	486	HIS	C-N-CA	5.00	126.99	120.28
47	r	198	PHE	CA-C-N	5.00	127.81	120.71
47	r	198	PHE	C-N-CA	5.00	127.81	120.71

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	1	17	C	C3',C2'
1	1	18	G	C3'
34	2	1244	C4J	C4'

All (245) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	1	18	G	Sidechain
1	1	26	G	Sidechain
34	2	1044	G	Sidechain
34	2	1161	G	Sidechain
34	2	1170	U	Sidechain
34	2	1171	G	Sidechain
34	2	1182	U	Sidechain
34	2	1183	G	Sidechain
34	2	1191	A	Sidechain
34	2	1192	A	Sidechain
34	2	1236	A	Sidechain
34	2	1252	G	Sidechain
34	2	1255	A	Sidechain
34	2	126	G	Sidechain
34	2	1304	U	Sidechain
34	2	1405	A	Sidechain
34	2	1427	G	Sidechain
34	2	1437	U	Sidechain
34	2	1438	U	Sidechain
34	2	146	G	Sidechain
34	2	148	U	Sidechain
34	2	1547	G	Sidechain
34	2	1564	A	Sidechain
34	2	1599	G	Sidechain
34	2	1616	U	Sidechain
34	2	1738	G	Sidechain
34	2	1750	C	Sidechain
34	2	1769	U	Sidechain

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Mol	Chain	Res	Type	Group
34	2	1776	G	Sidechain
34	2	1784	A	Sidechain
34	2	1840	G	Sidechain
34	2	195	C	Sidechain
34	2	211	U	Sidechain
34	2	240	C	Sidechain
34	2	318	U	Sidechain
34	2	39	A	Sidechain
34	2	435	A	Sidechain
34	2	526	A	Sidechain
34	2	554	A	Sidechain
34	2	574	A	Sidechain
34	2	576	G	Sidechain
34	2	660	A	Sidechain
34	2	71	G	Sidechain
34	2	76	U	Sidechain
34	2	82	G	Sidechain
34	2	869	G	Sidechain
34	2	951	A	Sidechain
34	2	997	A	Sidechain
35	A	150	TYR	Sidechain
35	A	184	LEU	Peptide
35	A	185	THR	Peptide
35	A	186	PRO	Peptide
35	A	187	GLN	Peptide
35	A	192	ARG	Sidechain
35	A	39	TYR	Sidechain
36	B	110	PRO	Peptide
36	B	133	THR	Peptide
36	B	287	LEU	Peptide
36	B	288	LYS	Peptide,Mainchain
36	B	289	GLY	Peptide
36	B	322	LEU	Peptide
36	B	373	ALA	Peptide
3	C	193	HIS	Peptide
4	D	208	HIS	Peptide
9	I	217	MET	Mainchain
9	I	68	LEU	Peptide
9	I	69	THR	Peptide
10	J	105	THR	Peptide
10	J	66	VAL	Peptide
11	K	144	LYS	Peptide

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Mol	Chain	Res	Type	Group
11	K	157	LYS	Peptide
12	L	147	PHE	Peptide
12	L	148	ILE	Peptide
13	M	1	MET	Peptide
13	M	34	GLU	Peptide
13	M	35	LEU	Peptide
13	M	43	LEU	Peptide
13	M	96	ARG	Sidechain
17	Q	35	ALA	Peptide
17	Q	36	SER	Peptide
18	S	42	ILE	Peptide
18	S	43	GLU	Peptide
39	U	89	ASP	Peptide
39	U	94	LYS	Peptide
39	U	99	LEU	Peptide
22	X	77	GLY	Mainchain
25	a	126	GLY	Peptide
26	b	46	GLU	Peptide
27	c	81	ARG	Peptide
29	e	28	HIS	Peptide
29	e	32	ARG	Peptide
29	e	49	ASP	Peptide
29	e	52	PHE	Peptide
30	f	90	LYS	Peptide
33	i	126	LYS	Peptide
33	i	78	GLY	Peptide
33	i	82	ARG	Sidechain
37	j	15	GLY	Peptide
37	j	16	LYS	Peptide
37	j	18	GLU	Peptide
37	j	19	ASN	Peptide
37	j	22	GLU	Peptide
37	j	23	LYS	Peptide
37	j	24	ARG	Peptide
37	j	25	GLU	Peptide
37	j	28	PHE	Peptide
37	j	29	LYS	Peptide,Mainchain
37	j	92	ILE	Peptide
38	k	129	PRO	Peptide
38	k	130	ASN	Peptide
38	k	131	LEU	Peptide
38	k	132	GLY	Peptide

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Mol	Chain	Res	Type	Group
38	k	133	LYS	Peptide
38	k	134	TYR	Peptide
38	k	137	PRO	Peptide
38	k	138	PRO	Peptide
38	k	150	SER	Mainchain
38	k	173	VAL	Peptide
38	k	175	GLN	Peptide
38	k	176	ILE	Peptide
38	k	192	ASP	Peptide
38	k	193	GLU	Peptide
38	k	208	HIS	Sidechain
38	k	237	ILE	Mainchain
38	k	241	ASP	Mainchain
38	k	268	TYR	Mainchain
38	k	272	VAL	Mainchain
38	k	290	TYR	Sidechain
38	k	348	TYR	Peptide,Mainchain
38	k	408	ASN	Mainchain
38	k	438	HIS	Peptide
38	k	455	ILE	Peptide,Mainchain
38	k	481	ASP	Mainchain
38	k	513	LYS	Mainchain
38	k	531	ARG	Mainchain
38	k	535	PHE	Sidechain
38	k	569	ASP	Peptide
38	k	574	ARG	Sidechain
38	k	96	ARG	Sidechain
46	q	108	ARG	Peptide
46	q	173	TYR	Sidechain
46	q	190	TYR	Sidechain
46	q	194	ALA	Peptide
46	q	223	VAL	Peptide
46	q	298	VAL	Peptide
47	r	122	SER	Peptide
47	r	126	GLY	Peptide
47	r	152	TYR	Sidechain
47	r	177	CYS	Peptide
47	r	243	LEU	Peptide
47	r	304	LEU	Peptide
47	r	306	LYS	Peptide
47	r	307	PRO	Peptide
47	r	350	TYR	Sidechain

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Mol	Chain	Res	Type	Group
47	r	99	TYR	Sidechain
48	s	200	ASN	Peptide
49	t	317	TYR	Sidechain
49	t	350	PHE	Peptide
49	t	375	LEU	Peptide
49	t	376	THR	Peptide
49	t	434	ASN	Peptide
50	u	117	THR	Peptide
50	u	120	ARG	Sidechain
50	u	169	TYR	Sidechain
50	u	217	ALA	Peptide
50	u	249	LEU	Peptide
50	u	259	ASN	Peptide
50	u	335	SER	Peptide
50	u	42	LEU	Peptide
50	u	56	ASP	Peptide
44	v	325	THR	Peptide
44	v	346	ASP	Peptide
44	v	356	LEU	Peptide
44	v	363	GLU	Peptide
44	v	365	ASN	Peptide
44	v	366	LEU	Peptide
44	v	367	GLY	Peptide
44	v	368	GLU	Peptide
44	v	369	GLY	Peptide
44	v	383	TYR	Peptide
44	v	385	TYR	Peptide
44	v	386	ASN	Peptide
44	v	390	ALA	Peptide
44	v	392	TYR	Peptide
44	v	408	LEU	Peptide
44	v	412	LEU	Peptide
44	v	413	PHE	Peptide
44	v	414	ALA	Peptide
44	v	415	ASN	Peptide
44	v	416	PRO	Peptide
44	v	418	ILE	Peptide
44	v	419	PHE	Peptide
44	v	425	LEU	Peptide
44	v	426	GLU	Peptide
44	v	427	GLU	Peptide
44	v	429	GLU	Peptide

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Mol	Chain	Res	Type	Group
44	v	431	LEU	Peptide
44	v	434	VAL	Peptide
44	v	437	PRO	Peptide
44	v	462	THR	Peptide
44	v	463	ASP	Peptide
44	v	466	SER	Peptide
44	v	467	GLN	Peptide
44	v	468	GLU	Peptide
44	v	469	TYR	Peptide
44	v	489	TYR	Peptide
44	v	490	LEU	Peptide
44	v	492	GLU	Peptide
44	v	495	THR	Peptide
44	v	496	THR	Peptide
44	v	499	ILE	Peptide
44	v	501	ARG	Peptide
44	v	513	LYS	Peptide
44	v	523	LEU	Peptide
44	v	556	TYR	Peptide
44	v	557	ALA	Peptide
44	v	558	LYS	Peptide
44	v	559	ASP	Peptide
44	v	583	TYR	Sidechain
44	v	655	LEU	Peptide
44	v	656	GLN	Peptide
44	v	697	TYR	Sidechain
44	v	725	PRO	Peptide
45	w	17	HIS	Peptide
45	w	219	LEU	Peptide
45	w	220	PHE	Peptide
45	w	236	PHE	Peptide
45	w	268	ARG	Peptide
45	w	27	SER	Peptide
45	w	270	ARG	Sidechain
45	w	32	TYR	Peptide
45	w	50	MET	Peptide
45	w	52	ASP	Peptide
43	y	245	LEU	Mainchain
43	y	368	ILE	Peptide
43	y	385	PRO	Peptide
43	y	398	PHE	Peptide
43	y	417	GLN	Peptide

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Mol	Chain	Res	Type	Group
43	y	43	TRP	Peptide
43	y	495	SER	Peptide
43	y	505	ALA	Peptide

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in 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	1	1614	0	822	49	0
2	l	240	0	289	0	0
3	C	1643	0	1646	0	0
4	D	1741	0	1814	39	0
5	E	1743	0	1836	1	0
6	F	1765	0	1863	21	0
7	G	2083	0	2189	0	0
8	H	1509	0	1563	28	0
9	I	1924	0	2089	16	0
10	J	1530	0	1627	21	0
11	K	1680	0	1762	12	0
12	L	1499	0	1608	0	0
13	M	828	0	854	1	0
14	N	1296	0	1374	29	0
15	O	958	0	993	1	0
16	P	1208	0	1294	60	0
17	Q	1016	0	1039	5	0
18	S	1124	0	1193	7	0
19	T	1019	0	1075	0	0
20	V	1112	0	1149	0	0
21	W	822	0	887	0	0
22	X	620	0	622	0	0
23	Y	1034	0	1080	1	0
24	Z	1107	0	1179	48	0
25	a	1021	0	1085	76	0
26	b	789	0	839	9	0
27	c	659	0	682	82	0
28	d	506	0	536	44	0
29	e	445	0	442	1	0
30	f	582	0	599	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
31	g	2437	0	2393	0	0
32	n	599	0	656	0	0
33	i	473	0	524	34	0
34	2	37187	0	18772	486	0
35	A	2147	0	2191	132	0
36	B	3214	0	3353	50	0
37	j	882	0	903	254	0
38	k	4693	0	4798	733	0
39	U	1194	0	1252	60	0
40	R	1154	0	1213	93	0
41	3	960	0	489	139	0
42	m	2955	0	2896	71	0
43	y	4971	0	5032	945	0
44	v	4508	0	4502	724	0
45	w	3465	0	3446	3	0
46	q	2111	0	2105	5	0
47	r	2624	0	2592	1	0
48	s	1737	0	1706	1	0
49	t	3109	0	3084	1	0
50	u	2918	0	2950	5	0
51	k	16	0	0	13	0
52	k	1	0	0	0	0
53	k	64	0	26	31	0
All	All	118536	0	100913	3745	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 18.

All (3745) 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)
38:k:73:VAL:HB	38:k:322:LEU:CD2	1.29	1.61
44:v:375:LYS:CG	44:v:408:LEU:HD11	1.15	1.61
10:J:109:ARG:CB	34:2:740:G:H1'	1.18	1.60
43:y:104:ALA:CB	43:y:149:TRP:CD1	1.80	1.60
43:y:208:ILE:HD11	43:y:262:LEU:CD2	1.18	1.60
43:y:104:ALA:HB3	43:y:149:TRP:CD1	1.34	1.59
35:A:229:LEU:HD22	36:B:284:VAL:CG2	1.14	1.59
35:A:235:TYR:CD1	36:B:285:ASP:CG	1.76	1.59
43:y:330:PRO:HB2	43:y:431:LEU:CD1	1.12	1.59
38:k:332:LYS:HG2	38:k:527:TYR:CD2	1.25	1.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:v:553:LYS:C	44:v:557:ALA:HB2	1.24	1.57
37:j:92:ILE:HG22	37:j:93:LEU:CG	1.27	1.56
43:y:230:LEU:CG	43:y:271:LEU:HD22	1.30	1.56
43:y:277:ASN:HA	43:y:299:LEU:CD1	1.15	1.55
37:j:92:ILE:CG2	37:j:93:LEU:HG	1.31	1.55
44:v:521:ARG:HD3	44:v:542:GLU:CG	1.37	1.54
44:v:413:PHE:HD1	44:v:489:TYR:CZ	1.21	1.53
44:v:413:PHE:CD1	44:v:489:TYR:CZ	1.94	1.53
44:v:554:TYR:HA	44:v:557:ALA:CB	1.11	1.53
44:v:554:TYR:CA	44:v:557:ALA:HB3	1.31	1.53
39:U:146:VAL:CG1	40:R:131:PRO:CG	1.83	1.53
38:k:73:VAL:CB	38:k:322:LEU:HD22	1.38	1.51
34:2:1693:C:C6	41:3:58:C:N4	1.79	1.51
44:v:739:ALA:CB	44:v:755:PHE:CE1	1.86	1.51
43:y:241:ILE:HG21	43:y:282:VAL:CG2	1.41	1.49
34:2:1518:C:C4'	39:U:144:ARG:HA	1.41	1.49
35:A:229:LEU:CD2	36:B:284:VAL:HG21	1.43	1.49
43:y:331:ILE:HG23	43:y:430:GLN:CD	1.34	1.49
44:v:375:LYS:HG2	44:v:408:LEU:CD2	1.36	1.49
43:y:208:ILE:CD1	43:y:262:LEU:CD2	1.88	1.49
38:k:241:ASP:C	38:k:242:GLU:CA	1.84	1.47
16:P:20:ARG:HD2	16:P:65:PHE:CE1	1.48	1.47
27:c:59:CYS:CB	44:v:450:ARG:HD3	1.42	1.47
43:y:233:ARG:HD2	43:y:256:ILE:CD1	1.45	1.47
44:v:373:LYS:HZ2	44:v:440:VAL:CG2	1.28	1.47
39:U:146:VAL:CG1	40:R:131:PRO:HG3	1.01	1.46
43:y:284:TRP:CZ2	43:y:426:GLN:CG	1.98	1.46
44:v:490:LEU:HD13	44:v:499:ILE:CD1	1.42	1.46
44:v:554:TYR:CA	44:v:557:ALA:CB	1.85	1.46
27:c:35:VAL:HG13	27:c:78:SER:CB	1.42	1.45
38:k:414:GLN:CD	38:k:486:ASP:HB3	1.05	1.45
38:k:414:GLN:NE2	38:k:486:ASP:CB	1.78	1.45
38:k:414:GLN:CD	38:k:486:ASP:CB	1.86	1.45
44:v:375:LYS:HG3	44:v:408:LEU:CD1	0.99	1.45
44:v:348:ALA:HB2	44:v:385:TYR:CE1	1.52	1.44
44:v:499:ILE:HG23	44:v:503:TYR:CE2	1.53	1.44
34:2:1705:C:H1'	37:j:42:LEU:CD2	1.49	1.43
43:y:284:TRP:CZ2	43:y:426:GLN:HG3	1.49	1.43
39:U:146:VAL:HG13	40:R:131:PRO:CG	1.43	1.43
10:J:109:ARG:CB	34:2:740:G:C1'	1.98	1.42
28:d:51:ARG:HH21	42:m:416:GLN:CG	1.27	1.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:k:521:ASP:HB3	38:k:524:MET:CB	1.46	1.42
28:d:51:ARG:NH2	42:m:416:GLN:HG2	1.31	1.42
43:y:276:TYR:OH	43:y:298:ARG:CG	1.69	1.41
37:j:8:GLY:HA2	40:R:140:ARG:NH2	1.29	1.41
43:y:277:ASN:CA	43:y:299:LEU:HD11	0.95	1.40
43:y:277:ASN:CB	43:y:299:LEU:HD11	1.49	1.40
44:v:499:ILE:CG2	44:v:503:TYR:HE2	1.34	1.39
16:P:20:ARG:CD	16:P:65:PHE:CE1	2.05	1.39
43:y:233:ARG:CD	43:y:256:ILE:HD13	1.52	1.39
38:k:332:LYS:HG2	38:k:527:TYR:CE2	1.58	1.39
44:v:748:ASP:C	44:v:749:TRP:N	1.81	1.39
44:v:347:ARG:O	44:v:385:TYR:CD1	1.73	1.38
38:k:241:ASP:CA	38:k:242:GLU:N	1.84	1.38
38:k:109:VAL:C	38:k:110:GLY:N	1.79	1.38
43:y:230:LEU:HG	43:y:271:LEU:CD2	1.54	1.38
44:v:375:LYS:HG2	44:v:408:LEU:CG	1.54	1.37
43:y:101:THR:HG22	43:y:149:TRP:CB	1.51	1.37
38:k:332:LYS:HE3	38:k:334:ALA:CB	1.52	1.37
43:y:347:ILE:HD13	44:v:723:ARG:NH2	1.26	1.37
43:y:175:HIS:CE1	43:y:228:MET:SD	2.17	1.36
43:y:277:ASN:CA	43:y:299:LEU:CD1	1.77	1.36
44:v:752:CYS:SG	44:v:783:ILE:HG21	1.62	1.36
38:k:204:LEU:HG	38:k:224:ARG:NH1	1.34	1.35
43:y:236:GLN:CG	43:y:252:ALA:HB2	1.56	1.35
37:j:70:TRP:CD1	40:R:143:PRO:HA	1.60	1.35
43:y:101:THR:HA	43:y:149:TRP:CD1	1.61	1.35
44:v:739:ALA:HB3	44:v:755:PHE:CE1	1.05	1.35
44:v:736:HIS:CG	44:v:759:GLU:CG	2.01	1.34
44:v:413:PHE:CE1	44:v:489:TYR:CE1	2.16	1.34
44:v:736:HIS:CB	44:v:759:GLU:HG3	1.53	1.34
43:y:236:GLN:HG2	43:y:252:ALA:CB	1.57	1.34
43:y:330:PRO:CB	43:y:431:LEU:CD1	2.03	1.34
44:v:554:TYR:N	44:v:557:ALA:HB2	1.38	1.34
38:k:440:GLN:C	38:k:441:PHE:N	1.85	1.33
43:y:101:THR:CG2	43:y:149:TRP:HB3	1.55	1.33
43:y:104:ALA:HB2	43:y:149:TRP:NE1	1.03	1.33
43:y:306:MET:O	43:y:310:LEU:N	1.59	1.33
43:y:330:PRO:CB	43:y:431:LEU:HD13	1.58	1.33
10:J:109:ARG:HB2	34:2:740:G:C1'	1.56	1.33
43:y:205:LEU:CD1	43:y:209:GLN:HE21	1.41	1.33
27:c:72:ARG:CD	34:2:1116:U:OP2	1.74	1.32

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:k:522:PHE:O	38:k:526:THR:HG22	1.29	1.32
43:y:205:LEU:O	43:y:209:GLN:HG3	1.18	1.32
27:c:35:VAL:CG1	27:c:78:SER:HB3	1.55	1.32
43:y:293:ALA:CB	43:y:328:SER:HB2	1.59	1.31
9:I:237:LEU:HD12	34:2:784:G:O3'	1.30	1.31
35:A:235:TYR:CG	36:B:285:ASP:OD2	1.82	1.31
28:d:53:GLY:O	42:m:419:ALA:HB2	1.17	1.30
44:v:351:ILE:HG12	44:v:381:SER:OG	1.21	1.30
37:j:8:GLY:CA	40:R:140:ARG:HH22	1.44	1.30
43:y:230:LEU:CD1	43:y:271:LEU:HD22	1.60	1.30
34:2:1327:C:H41	37:j:15:GLY:C	1.37	1.30
35:A:229:LEU:CD2	36:B:284:VAL:CG2	2.02	1.30
38:k:183:THR:O	38:k:187:ILE:HG22	1.23	1.30
40:R:143:PRO:HG2	41:3:55:G:N3	1.45	1.30
43:y:205:LEU:HD11	43:y:209:GLN:NE2	1.47	1.30
38:k:332:LYS:O	38:k:334:ALA:N	1.65	1.29
44:v:413:PHE:HD1	44:v:489:TYR:OH	1.11	1.29
44:v:449:GLU:CD	44:v:505:ARG:HH21	1.40	1.29
4:D:40:ASN:ND2	4:D:75:GLN:HE22	1.29	1.29
25:a:104:ARG:NH2	25:a:108:LYS:NZ	1.79	1.29
44:v:351:ILE:CG1	44:v:381:SER:OG	1.80	1.29
39:U:143:GLY:O	39:U:144:ARG:CG	1.78	1.29
44:v:375:LYS:CG	44:v:408:LEU:CG	2.10	1.29
34:2:1705:C:C1'	37:j:42:LEU:HD21	1.61	1.28
43:y:175:HIS:HA	43:y:231:GLU:OE2	1.12	1.28
44:v:409:MET:CG	44:v:485:ARG:HH11	1.43	1.28
44:v:490:LEU:CD1	44:v:499:ILE:HD13	1.60	1.28
38:k:414:GLN:HG3	38:k:486:ASP:C	1.54	1.28
28:d:53:GLY:HA3	42:m:416:GLN:OE1	1.23	1.28
43:y:368:ILE:O	43:y:371:ILE:HG22	1.16	1.28
8:H:61:PHE:CZ	42:m:415:SER:HB3	1.68	1.28
24:Z:68:LYS:HG3	37:j:84:TYR:OH	1.21	1.28
43:y:7:ARG:O	43:y:9:GLU:HG3	1.28	1.28
44:v:752:CYS:SG	44:v:783:ILE:CG2	2.21	1.28
38:k:332:LYS:CE	38:k:334:ALA:HB2	1.63	1.27
44:v:748:ASP:OD2	44:v:750:LYS:HD2	1.15	1.27
43:y:390:LEU:CD2	43:y:410:VAL:HB	1.40	1.27
44:v:553:LYS:O	44:v:557:ALA:HB2	1.32	1.27
24:Z:58:GLU:OE1	37:j:60:HIS:CE1	1.88	1.26
38:k:318:PRO:CG	38:k:322:LEU:HA	1.63	1.26
38:k:183:THR:O	38:k:187:ILE:CG2	1.82	1.26

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:k:414:GLN:NE2	38:k:486:ASP:HB3	0.93	1.26
43:y:222:ASN:O	43:y:226:GLN:HG2	1.22	1.26
37:j:70:TRP:HZ2	41:3:55:G:C2'	1.47	1.26
38:k:209:LEU:CD1	38:k:221:GLU:HG3	1.64	1.26
27:c:35:VAL:CG1	27:c:78:SER:CB	2.01	1.25
27:c:59:CYS:HB2	44:v:450:ARG:CD	1.64	1.25
37:j:93:LEU:O	37:j:94:LYS:O	1.54	1.25
43:y:7:ARG:O	43:y:9:GLU:N	1.67	1.25
44:v:409:MET:HG3	44:v:485:ARG:CD	1.65	1.25
43:y:257:HIS:NE2	43:y:358:LEU:HA	1.50	1.24
38:k:374:ILE:HD11	38:k:529:ALA:C	1.63	1.24
6:F:3:VAL:HG11	34:2:1573:U:O4	1.35	1.24
43:y:8:PRO:HB3	43:y:39:LYS:CD	1.67	1.23
34:2:740:G:H21	34:2:794:G:C1'	1.50	1.23
44:v:736:HIS:CG	44:v:759:GLU:HG3	1.53	1.23
35:A:229:LEU:CG	36:B:284:VAL:HG21	1.68	1.23
44:v:375:LYS:CG	44:v:408:LEU:HD21	1.68	1.23
37:j:8:GLY:C	40:R:140:ARG:HH22	1.47	1.22
38:k:329:LEU:O	38:k:498:LEU:HD12	1.37	1.22
34:2:1812:A:C2	34:2:1813:A:C8	2.28	1.22
35:A:58:SER:OG	35:A:61:LYS:HG2	1.37	1.22
38:k:332:LYS:CG	38:k:527:TYR:CD2	2.21	1.21
27:c:72:ARG:NE	34:2:1116:U:OP2	1.73	1.21
38:k:374:ILE:CD1	38:k:528:LEU:O	1.88	1.21
43:y:201:LEU:HD21	43:y:255:ASP:OD2	1.39	1.21
43:y:241:ILE:CG2	43:y:282:VAL:CG2	2.17	1.21
44:v:413:PHE:CD1	44:v:489:TYR:CE1	2.27	1.21
1:1:17:C:O3'	1:1:18:G:P	1.99	1.21
34:2:1102:C:C2'	34:2:1103:G:H5'	1.71	1.21
44:v:553:LYS:O	44:v:557:ALA:CB	1.86	1.21
43:y:104:ALA:CB	43:y:149:TRP:NE1	1.87	1.20
11:K:193:LYS:HZ3	14:N:32:LYS:NZ	1.38	1.20
34:2:1518:C:H4'	39:U:144:ARG:CA	1.70	1.20
34:2:1519:G:P	39:U:144:ARG:HB3	1.80	1.20
43:y:204:HIS:O	43:y:208:ILE:HG22	1.35	1.20
44:v:373:LYS:NZ	44:v:440:VAL:CG2	2.03	1.20
34:2:1116:U:H2'	34:2:1117:G:C5'	1.73	1.19
38:k:315:GLY:HA2	38:k:326:ASP:C	1.66	1.19
44:v:521:ARG:CD	44:v:542:GLU:HG2	1.70	1.19
25:a:104:ARG:HH22	25:a:108:LYS:NZ	1.37	1.19
34:2:478:U:OP1	38:k:150:SER:HB2	1.38	1.19

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:U:143:GLY:O	39:U:144:ARG:HG3	1.07	1.19
43:y:184:PHE:CE1	43:y:188:TYR:CD2	2.30	1.19
38:k:411:TYR:C	38:k:412:LYS:N	2.01	1.19
43:y:175:HIS:HD1	43:y:231:GLU:CD	1.50	1.19
34:2:1706:U:H2'	34:2:1707:A:H8	1.03	1.19
1:1:18:G:H4'	1:1:61:C:OP1	1.43	1.19
34:2:1707:A:C2	34:2:1708:C:C2	2.30	1.19
43:y:283:PHE:CE1	43:y:287:GLY:HA3	1.78	1.19
25:a:12:PHE:CE1	34:2:836:C:O2'	1.94	1.18
44:v:469:TYR:CE1	44:v:473:LEU:HD21	1.78	1.18
34:2:1693:C:N1	41:3:58:C:N4	1.76	1.18
43:y:327:LEU:CD2	43:y:424:LEU:HA	1.66	1.18
44:v:553:LYS:O	44:v:557:ALA:CA	1.92	1.17
35:A:235:TYR:CD1	36:B:285:ASP:OD2	1.92	1.17
38:k:591:SER:C	38:k:592:GLY:N	2.02	1.17
44:v:521:ARG:HD3	44:v:542:GLU:CB	1.73	1.17
34:2:158:A:OP1	38:k:583:ILE:CG2	1.92	1.17
43:y:398:PHE:CE1	43:y:512:GLN:OE1	1.96	1.17
24:Z:97:ASN:OD1	38:k:34:MET:HE1	1.41	1.17
11:K:193:LYS:NZ	14:N:32:LYS:NZ	1.93	1.16
43:y:8:PRO:CB	43:y:39:LYS:HD2	1.74	1.16
38:k:315:GLY:CA	38:k:326:ASP:O	1.93	1.16
33:i:78:GLY:N	37:j:33:GLN:OE1	1.76	1.16
44:v:347:ARG:O	44:v:385:TYR:HD1	1.08	1.16
44:v:449:GLU:OE1	44:v:505:ARG:NH2	1.76	1.16
35:A:157:VAL:CG1	35:A:180:ILE:HG21	1.76	1.16
38:k:204:LEU:CG	38:k:224:ARG:NH1	2.08	1.16
11:K:193:LYS:NZ	14:N:32:LYS:HZ1	1.40	1.16
33:i:80:LEU:CD2	37:j:62:ARG:HH21	1.57	1.16
37:j:8:GLY:CA	40:R:140:ARG:NH2	2.04	1.16
24:Z:58:GLU:OE1	37:j:60:HIS:HE1	1.23	1.15
38:k:378:LEU:O	38:k:385:LYS:HD3	1.43	1.15
40:R:143:PRO:CG	41:3:55:G:N3	2.09	1.15
38:k:17:LYS:HZ3	38:k:20:LYS:HE2	1.10	1.15
38:k:332:LYS:CE	38:k:502:ARG:HD3	1.75	1.15
38:k:375:MET:HE1	38:k:531:ARG:CD	1.76	1.15
44:v:553:LYS:C	44:v:557:ALA:CB	2.19	1.15
37:j:70:TRP:CZ2	41:3:55:G:H2'	1.80	1.15
43:y:330:PRO:HB2	43:y:431:LEU:HD11	1.16	1.15
28:d:35:MET:HA	42:m:426:LYS:HE2	1.28	1.15
41:3:76:A:H2'	41:3:77:A:H5'	1.26	1.15

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:y:245:LEU:HB3	43:y:248:GLU:CD	1.70	1.15
1:l:34:C:N4	41:3:54:G:O6	1.80	1.15
33:i:82:ARG:HH22	33:i:84:GLY:C	1.54	1.15
8:H:37:ASP:OD2	42:m:418:GLY:N	1.80	1.14
24:Z:78:GLY:HA2	38:k:60:ILE:HD11	1.19	1.14
38:k:209:LEU:HD11	38:k:221:GLU:CG	1.76	1.14
38:k:375:MET:SD	38:k:533:ILE:HG23	1.88	1.14
43:y:291:PHE:CE1	43:y:359:LEU:HD13	1.81	1.14
43:y:297:HIS:CE1	43:y:325:ALA:HB1	1.83	1.14
44:v:375:LYS:CG	44:v:408:LEU:CD1	1.83	1.14
24:Z:97:ASN:OD1	38:k:34:MET:CE	1.95	1.14
43:y:276:TYR:OH	43:y:298:ARG:HG2	0.98	1.14
43:y:385:PRO:HB3	43:y:388:LYS:HD3	1.28	1.14
44:v:375:LYS:CG	44:v:408:LEU:CD2	2.21	1.14
27:c:59:CYS:SG	44:v:450:ARG:HD3	1.88	1.14
28:d:53:GLY:CA	42:m:416:GLN:OE1	1.96	1.14
37:j:70:TRP:CZ2	41:3:55:G:C2'	2.29	1.14
43:y:347:ILE:CD1	44:v:723:ARG:HH21	1.59	1.14
38:k:378:LEU:C	38:k:379:GLY:CA	2.15	1.14
35:A:227:ILE:CD1	35:A:237:MET:HE2	1.76	1.14
24:Z:78:GLY:CA	38:k:60:ILE:HD11	1.78	1.13
38:k:315:GLY:HA2	38:k:326:ASP:O	1.46	1.13
38:k:315:GLY:O	38:k:325:ARG:O	1.63	1.13
43:y:300:TYR:HA	43:y:321:ARG:HH11	1.07	1.13
44:v:373:LYS:NZ	44:v:420:VAL:HG11	1.61	1.13
44:v:373:LYS:HE2	44:v:431:LEU:CD2	1.78	1.13
44:v:486:VAL:O	44:v:502:VAL:CG2	1.95	1.13
35:A:229:LEU:HD22	36:B:284:VAL:HG23	1.24	1.13
43:y:175:HIS:CA	43:y:231:GLU:OE2	1.95	1.13
43:y:283:PHE:HE1	43:y:287:GLY:CA	1.62	1.13
44:v:752:CYS:HB3	44:v:783:ILE:HD13	1.30	1.13
38:k:73:VAL:CB	38:k:322:LEU:CD2	2.09	1.13
38:k:412:LYS:HB3	38:k:485:ILE:HA	1.19	1.12
43:y:293:ALA:CA	43:y:328:SER:HB2	1.78	1.12
43:y:340:ARG:N	43:y:340:ARG:HD3	1.64	1.13
38:k:412:LYS:HD3	38:k:485:ILE:HG13	1.31	1.12
44:v:373:LYS:NZ	44:v:440:VAL:HG21	1.59	1.12
35:A:185:THR:HB	35:A:187:GLN:HB2	1.28	1.12
43:y:230:LEU:HD11	43:y:271:LEU:HB3	1.26	1.12
43:y:277:ASN:N	43:y:299:LEU:HD11	1.63	1.12
34:2:1327:C:H41	37:j:16:LYS:N	1.48	1.12

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:k:332:LYS:HE2	38:k:502:ARG:CD	1.79	1.12
10:J:109:ARG:HB3	34:2:740:G:C1'	1.66	1.12
34:2:740:G:N2	34:2:794:G:H1'	1.62	1.12
43:y:241:ILE:HG21	43:y:282:VAL:HG23	1.22	1.12
44:v:391:THR:CG2	44:v:392:TYR:H	1.63	1.12
44:v:394:LYS:O	44:v:397:MET:HG3	1.48	1.12
34:2:472:G:OP1	38:k:63:LYS:HE3	1.50	1.11
35:A:157:VAL:HG21	35:A:180:ILE:CG2	1.80	1.11
34:2:1102:C:H2'	34:2:1103:G:H5'	1.26	1.11
35:A:58:SER:CB	35:A:61:LYS:HG2	1.81	1.11
38:k:374:ILE:HD12	38:k:528:LEU:C	1.76	1.11
38:k:374:ILE:HD12	38:k:528:LEU:O	0.94	1.11
43:y:306:MET:O	43:y:310:LEU:CB	1.98	1.11
44:v:490:LEU:HD22	44:v:499:ILE:HG12	1.25	1.11
1:1:17:C:N4	1:1:60:A:N3	1.99	1.11
8:H:16:ASP:OD2	42:m:204:LYS:CE	1.99	1.11
35:A:227:ILE:HD11	35:A:237:MET:HE2	1.25	1.11
38:k:318:PRO:CB	38:k:322:LEU:HA	1.80	1.11
43:y:105:LYS:HG3	43:y:146:LEU:HD22	1.31	1.11
43:y:113:LEU:HD11	43:y:138:GLN:HB2	1.19	1.11
44:v:499:ILE:O	44:v:502:VAL:HG12	1.49	1.11
43:y:208:ILE:CD1	43:y:262:LEU:HD23	1.78	1.11
43:y:208:ILE:HD13	43:y:262:LEU:HD23	1.32	1.11
43:y:331:ILE:HG22	43:y:430:GLN:NE2	1.56	1.11
44:v:414:ALA:HB3	44:v:415:ASN:OD1	1.50	1.11
38:k:332:LYS:CG	38:k:527:TYR:CE2	2.32	1.10
43:y:100:LYS:O	43:y:149:TRP:NE1	1.83	1.10
4:D:40:ASN:ND2	4:D:75:GLN:NE2	1.99	1.10
34:2:1707:A:C2	34:2:1708:C:N1	2.20	1.10
38:k:17:LYS:HG2	38:k:20:LYS:CE	1.81	1.10
43:y:241:ILE:CG2	43:y:282:VAL:HG21	1.78	1.10
43:y:306:MET:O	43:y:310:LEU:HB3	1.46	1.10
38:k:486:ASP:C	38:k:487:GLU:N	2.09	1.10
41:3:36:A:H4'	41:3:37:C:OP1	1.45	1.10
44:v:373:LYS:HZ2	44:v:440:VAL:HG21	1.06	1.10
44:v:451:MET:HE1	44:v:479:VAL:CG2	1.81	1.10
44:v:760:LYS:HB3	44:v:766:TRP:HB2	1.32	1.10
44:v:398:TRP:HE1	44:v:475:ASP:HB3	0.97	1.10
44:v:736:HIS:HB3	44:v:759:GLU:HG3	1.15	1.10
1:1:18:G:H1'	1:1:61:C:H5'	1.24	1.09
28:d:35:MET:HA	42:m:426:LYS:CE	1.79	1.09

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:A:157:VAL:HG11	35:A:180:ILE:HG21	1.26	1.09
38:k:217:LEU:HG	38:k:221:GLU:HG2	1.27	1.09
43:y:276:TYR:CZ	43:y:298:ARG:CG	2.35	1.09
1:l:35:A:C4'	37:j:8:GLY:O	2.00	1.09
24:Z:60:LYS:NZ	34:2:1817:A:OP1	1.84	1.09
35:A:235:TYR:CE1	36:B:285:ASP:CG	2.29	1.09
44:v:409:MET:HG3	44:v:485:ARG:HH11	1.09	1.09
44:v:420:VAL:HG23	44:v:437:PRO:O	1.48	1.09
38:k:375:MET:HE1	38:k:531:ARG:HD2	1.12	1.09
44:v:409:MET:HE2	44:v:485:ARG:HG2	1.34	1.09
44:v:739:ALA:CB	44:v:755:PHE:HE1	1.39	1.09
28:d:53:GLY:O	42:m:419:ALA:CB	1.99	1.09
24:Z:97:ASN:CG	38:k:34:MET:HE1	1.77	1.09
41:3:58:C:O2	41:3:59:A:C5	2.05	1.09
43:y:293:ALA:HB2	43:y:328:SER:HB2	1.21	1.09
44:v:334:ASN:O	44:v:338:GLN:HG3	1.53	1.09
44:v:409:MET:HE2	44:v:485:ARG:CG	1.82	1.09
43:y:104:ALA:HB2	43:y:149:TRP:CD1	1.64	1.08
44:v:380:ALA:HA	44:v:383:TYR:HD2	1.18	1.08
39:U:146:VAL:HG12	40:R:131:PRO:HG3	1.23	1.08
39:U:146:VAL:HG11	40:R:131:PRO:HB3	1.35	1.08
44:v:521:ARG:CD	44:v:542:GLU:CB	2.30	1.08
38:k:498:LEU:HD11	38:k:523:ILE:HD12	1.29	1.08
43:y:208:ILE:HD11	43:y:262:LEU:HD22	1.12	1.08
43:y:241:ILE:HG21	43:y:282:VAL:HG21	1.10	1.08
43:y:344:MET:HA	43:y:345:ASP:HB3	1.31	1.08
44:v:521:ARG:CD	44:v:542:GLU:CG	2.29	1.08
38:k:332:LYS:HE3	38:k:334:ALA:HB2	1.09	1.08
38:k:412:LYS:N	38:k:484:LEU:O	1.86	1.08
43:y:205:LEU:HD12	43:y:209:GLN:HG2	1.08	1.08
44:v:373:LYS:HZ2	44:v:440:VAL:HG22	1.14	1.08
8:H:16:ASP:OD2	42:m:204:LYS:HE3	1.54	1.08
37:j:67:LYS:HE3	41:3:56:U:C4'	1.83	1.08
37:j:78:LEU:CD2	37:j:93:LEU:HD12	1.82	1.08
38:k:212:ARG:HD2	38:k:359:GLU:OE2	1.52	1.08
43:y:297:HIS:HE1	43:y:325:ALA:HB1	1.08	1.08
44:v:373:LYS:HZ3	44:v:420:VAL:CG1	1.65	1.08
40:R:133:ILE:HG23	40:R:134:GLY:H	0.96	1.07
43:y:284:TRP:HA	43:y:292:HIS:CG	1.87	1.07
44:v:499:ILE:CG2	44:v:503:TYR:CE2	2.23	1.07
39:U:143:GLY:C	39:U:144:ARG:HD2	1.79	1.07

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:v:326:HIS:HA	44:v:329:VAL:CG2	1.84	1.07
8:H:61:PHE:CE1	42:m:415:SER:HB3	1.90	1.07
25:a:104:ARG:HH21	25:a:108:LYS:CE	1.66	1.07
38:k:65:CYS:SG	51:k:702:SF4:FE3	1.44	1.07
35:A:157:VAL:HG11	35:A:180:ILE:CG2	1.83	1.07
37:j:67:LYS:HE3	41:3:56:U:H4'	1.10	1.07
37:j:78:LEU:HD23	37:j:93:LEU:HB2	1.25	1.07
38:k:330:VAL:HG21	38:k:574:ARG:HD3	1.35	1.07
38:k:501:ALA:HB1	38:k:528:LEU:HD11	1.35	1.07
43:y:181:ALA:CB	43:y:196:LYS:HE2	1.85	1.07
43:y:277:ASN:CB	43:y:299:LEU:CD1	2.17	1.07
6:F:3:VAL:HG22	6:F:4:GLN:H	1.15	1.07
38:k:4:LYS:HA	38:k:79:LEU:CG	1.84	1.07
43:y:150:VAL:CG1	43:y:188:TYR:CD1	2.35	1.07
43:y:300:TYR:HA	43:y:321:ARG:NH1	1.68	1.07
44:v:391:THR:HG22	44:v:392:TYR:N	1.62	1.07
26:b:58:VAL:HG23	26:b:59:PHE:CD1	1.90	1.06
27:c:33:MET:HE1	27:c:73:LEU:HD11	1.29	1.06
38:k:330:VAL:HG22	38:k:575:PRO:HD2	1.33	1.06
38:k:347:MET:O	38:k:348:TYR:O	1.73	1.06
43:y:368:ILE:O	43:y:371:ILE:CG2	2.03	1.06
34:2:158:A:OP1	38:k:583:ILE:HG21	1.54	1.06
35:A:229:LEU:CB	36:B:284:VAL:HG21	1.85	1.06
43:y:158:ARG:O	43:y:162:ASP:OD2	1.72	1.06
37:j:10:LYS:HG2	37:j:11:ASN:N	1.58	1.06
38:k:451:ILE:HG13	38:k:452:GLU:N	1.69	1.06
43:y:175:HIS:HE1	43:y:228:MET:HA	1.13	1.06
43:y:205:LEU:O	43:y:209:GLN:CG	2.03	1.06
43:y:320:THR:HA	43:y:323:LEU:HD23	1.09	1.06
44:v:367:GLY:HA3	44:v:369:GLY:HA3	1.34	1.06
44:v:461:ASN:O	44:v:462:THR:HG23	1.54	1.06
25:a:104:ARG:HH21	25:a:108:LYS:HE3	1.18	1.05
34:2:1706:U:H2'	34:2:1707:A:C8	1.90	1.05
37:j:10:LYS:CG	37:j:11:ASN:H	1.67	1.05
43:y:291:PHE:CD1	43:y:359:LEU:HD22	1.90	1.05
43:y:327:LEU:HD23	43:y:424:LEU:HA	1.10	1.05
4:D:40:ASN:HD22	4:D:75:GLN:NE2	1.50	1.05
35:A:235:TYR:CD1	36:B:285:ASP:CB	2.38	1.05
44:v:326:HIS:HA	44:v:329:VAL:HG21	1.07	1.05
25:a:104:ARG:O	25:a:105:LYS:HB2	1.49	1.05
38:k:204:LEU:CB	38:k:224:ARG:CZ	2.28	1.05

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:k:311:ILE:HA	38:k:317:VAL:HG21	1.35	1.05
38:k:375:MET:CE	38:k:531:ARG:HD2	1.87	1.05
43:y:291:PHE:HZ	43:y:356:ALA:HA	1.15	1.05
43:y:333:PRO:HG3	43:y:437:LEU:HD23	1.34	1.05
43:y:339:ALA:HB3	43:y:340:ARG:CZ	1.87	1.05
16:P:22:VAL:HG12	16:P:26:LEU:HG	1.32	1.04
34:2:1115:A:H5'	34:2:1116:U:C4	1.92	1.04
38:k:209:LEU:CD1	38:k:221:GLU:CG	2.31	1.04
44:v:496:THR:O	44:v:555:ILE:HD13	1.56	1.04
33:i:82:ARG:NH2	33:i:84:GLY:C	2.15	1.04
39:U:146:VAL:HG11	40:R:131:PRO:CB	1.84	1.04
43:y:283:PHE:HE1	43:y:287:GLY:HA3	1.12	1.04
43:y:331:ILE:CB	43:y:430:GLN:NE2	2.20	1.04
35:A:170:GLU:O	35:A:172:GLU:N	1.90	1.04
38:k:330:VAL:HG21	38:k:574:ARG:CD	1.83	1.04
39:U:146:VAL:CG1	40:R:131:PRO:CB	2.36	1.04
43:y:79:GLN:O	43:y:81:VAL:N	1.89	1.04
43:y:230:LEU:CG	43:y:271:LEU:CD2	2.24	1.04
43:y:346:GLY:HA2	43:y:347:ILE:HG13	1.39	1.04
34:2:1518:C:OP1	39:U:143:GLY:CA	2.04	1.04
43:y:390:LEU:HD21	43:y:410:VAL:HB	1.10	1.04
44:v:393:MET:SD	44:v:454:GLU:HG2	1.97	1.04
37:j:70:TRP:NE1	40:R:143:PRO:HB3	1.72	1.04
38:k:70:LEU:CD1	51:k:702:SF4:S2	2.46	1.04
38:k:518:VAL:C	38:k:519:GLU:N	2.16	1.04
41:3:58:C:O2	41:3:59:A:C4	2.10	1.04
43:y:205:LEU:CD1	43:y:209:GLN:HG2	1.87	1.04
34:2:1116:U:H2'	34:2:1117:G:H5''	1.05	1.03
1:1:35:A:O2'	37:j:8:GLY:HA3	1.57	1.03
37:j:41:MET:HA	37:j:47:LEU:HD13	1.38	1.03
38:k:294:SER:OG	53:k:704:GNP:O3'	1.74	1.03
43:y:284:TRP:HA	43:y:292:HIS:CD2	1.93	1.03
38:k:187:ILE:HG23	38:k:188:LEU:H	1.23	1.03
43:y:159:GLN:HG3	43:y:163:LEU:HD22	1.36	1.03
43:y:175:HIS:NE2	43:y:228:MET:SD	2.31	1.03
43:y:291:PHE:CZ	43:y:356:ALA:HA	1.94	1.03
37:j:63:GLY:O	37:j:64:LYS:HG3	1.59	1.03
43:y:181:ALA:HB2	43:y:196:LYS:NZ	1.74	1.03
43:y:300:TYR:CA	43:y:321:ARG:HH11	1.70	1.03
43:y:320:THR:HG23	43:y:421:GLU:CG	1.89	1.03
43:y:327:LEU:HD23	43:y:424:LEU:CA	1.89	1.03

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:22:VAL:H	16:P:23:PRO:HA	1.23	1.02
43:y:78:CYS:SG	43:y:86:LEU:HD11	1.99	1.02
43:y:208:ILE:HD11	43:y:262:LEU:HD21	1.07	1.02
43:y:277:ASN:HA	43:y:299:LEU:HD12	1.04	1.02
43:y:347:ILE:CD1	44:v:723:ARG:NH2	2.21	1.02
18:S:145:TYR:O	18:S:146:ARG:HG2	1.56	1.02
34:2:1518:C:H5'	39:U:144:ARG:HG3	1.36	1.02
43:y:367:ARG:HG2	43:y:368:ILE:H	1.23	1.02
44:v:373:LYS:HD2	44:v:420:VAL:HG12	1.37	1.02
44:v:532:SER:C	44:v:533:GLU:N	2.16	1.02
38:k:164:LEU:HD21	38:k:237:ILE:HB	1.41	1.02
44:v:392:TYR:CD1	44:v:461:ASN:ND2	2.27	1.02
44:v:425:LEU:HD12	44:v:426:GLU:H	1.21	1.02
38:k:218:SER:HB3	53:k:705:GNP:O2'	1.60	1.02
43:y:293:ALA:CB	43:y:328:SER:CB	2.37	1.02
43:y:293:ALA:HB2	43:y:328:SER:CB	1.87	1.02
44:v:449:GLU:CG	44:v:505:ARG:NH2	2.22	1.02
38:k:253:LEU:HD11	38:k:564:ILE:CD1	1.90	1.02
43:y:164:LEU:O	43:y:165:ARG:HG3	1.60	1.02
35:A:157:VAL:HG21	35:A:180:ILE:HG22	1.39	1.01
38:k:451:ILE:O	38:k:454:ILE:N	1.67	1.01
40:R:141:PHE:C	40:R:142:ILE:HD12	1.85	1.01
40:R:143:PRO:CB	41:3:55:G:H1'	1.91	1.01
43:y:276:TYR:CE2	43:y:298:ARG:HG3	1.94	1.01
38:k:411:TYR:C	38:k:412:LYS:CA	2.34	1.01
38:k:521:ASP:CB	38:k:524:MET:CB	2.37	1.01
43:y:327:LEU:CD2	43:y:424:LEU:CA	2.27	1.01
44:v:398:TRP:HH2	44:v:451:MET:SD	1.83	1.01
24:Z:78:GLY:HA2	38:k:60:ILE:CD1	1.91	1.01
38:k:329:LEU:O	38:k:498:LEU:CD1	2.08	1.01
38:k:374:ILE:HD11	38:k:529:ALA:CA	1.91	1.01
38:k:521:ASP:HB3	38:k:524:MET:HB2	1.35	1.01
43:y:331:ILE:CG2	43:y:430:GLN:NE2	0.86	1.01
16:P:27:LYS:HZ2	16:P:28:LEU:HD23	1.25	1.01
34:2:742:C:C2'	34:2:743:U:H5'	1.91	1.01
37:j:67:LYS:CE	41:3:56:U:H4'	1.90	1.01
38:k:241:ASP:O	38:k:242:GLU:N	1.93	1.01
43:y:175:HIS:CE1	43:y:228:MET:HA	1.95	1.01
6:F:196:GLY:HA2	6:F:197:LYS:C	1.85	1.01
26:b:58:VAL:HG23	26:b:59:PHE:CE1	1.95	1.01
44:v:748:ASP:OD2	44:v:750:LYS:CD	2.08	1.01

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:y:150:VAL:HG11	43:y:188:TYR:CD1	1.96	1.00
44:v:451:MET:CE	44:v:479:VAL:HG23	1.90	1.00
44:v:486:VAL:O	44:v:502:VAL:HG21	1.57	1.00
8:H:61:PHE:CE1	42:m:415:SER:CB	2.44	1.00
37:j:70:TRP:HZ2	41:3:55:G:H2'	1.17	1.00
38:k:4:LYS:CA	38:k:79:LEU:HG	1.91	1.00
38:k:425:ARG:CZ	38:k:455:ILE:HD12	1.89	1.00
43:y:347:ILE:CD1	44:v:723:ARG:HE	1.73	1.00
24:Z:68:LYS:CG	37:j:84:TYR:OH	2.07	1.00
38:k:4:LYS:N	38:k:79:LEU:HG	1.76	1.00
38:k:578:ASN:HD21	38:k:585:ASP:HB2	1.24	1.00
43:y:221:ASN:HB3	43:y:224:GLU:OE2	1.61	1.00
43:y:371:ILE:HA	43:y:374:MET:SD	2.01	1.00
44:v:345:THR:CG2	44:v:347:ARG:HB2	1.92	1.00
34:2:683:G:N2	34:2:731:C:N3	2.10	1.00
34:2:737:C:H3'	34:2:738:U:H5''	1.42	1.00
6:F:2:ALA:HB1	6:F:3:VAL:HA	1.41	1.00
34:2:1518:C:H5'	39:U:143:GLY:O	1.62	1.00
35:A:157:VAL:CG1	35:A:180:ILE:HD13	1.92	1.00
38:k:492:LEU:O	38:k:497:ARG:NE	1.95	1.00
34:2:1518:C:C5'	39:U:144:ARG:HA	1.91	1.00
37:j:94:LYS:HG2	37:j:95:TYR:N	1.74	0.99
38:k:521:ASP:HB3	38:k:524:MET:HB3	1.05	0.99
10:J:106:ARG:HD3	34:2:794:G:O6	1.60	0.99
34:2:1705:C:C1'	37:j:42:LEU:CD2	2.27	0.99
44:v:393:MET:O	44:v:397:MET:HE3	1.55	0.99
34:2:478:U:O4	38:k:99:ILE:HD11	1.62	0.99
38:k:521:ASP:CB	38:k:524:MET:HB3	1.91	0.99
1:1:35:A:O4'	37:j:8:GLY:O	1.81	0.99
38:k:65:CYS:SG	51:k:702:SF4:S4	2.60	0.99
43:y:230:LEU:CD1	43:y:271:LEU:CD2	2.38	0.99
34:2:1327:C:N4	37:j:15:GLY:C	2.20	0.99
34:2:1518:C:O3'	39:U:144:ARG:HB3	1.62	0.99
35:A:235:TYR:CE1	36:B:285:ASP:OD1	2.15	0.99
34:2:749:C:H3'	34:2:750:G:H5''	1.43	0.99
34:2:1696:C:O2	37:j:10:LYS:HG3	1.63	0.99
35:A:58:SER:CB	35:A:61:LYS:CG	2.41	0.99
38:k:319:THR:CB	38:k:320:GLU:HB2	1.93	0.99
43:y:158:ARG:C	43:y:162:ASP:OD2	2.05	0.99
44:v:413:PHE:HE1	44:v:489:TYR:CE1	1.67	0.99
38:k:212:ARG:CD	38:k:359:GLU:OE2	2.10	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:v:490:LEU:HD13	44:v:499:ILE:CG1	1.92	0.99
44:v:760:LYS:NZ	44:v:765:VAL:HG11	1.78	0.99
6:F:193:ASP:H	6:F:194:PRO:HD2	1.25	0.98
35:A:205:ILE:HD12	36:B:288:LYS:HB2	1.44	0.98
43:y:113:LEU:HD11	43:y:138:GLN:CB	1.93	0.98
43:y:390:LEU:HG	43:y:410:VAL:HG21	1.45	0.98
37:j:47:LEU:HD12	37:j:48:GLU:H	1.25	0.98
37:j:70:TRP:NE1	40:R:143:PRO:CB	2.26	0.98
38:k:150:SER:HG	38:k:151:GLU:N	1.55	0.98
38:k:318:PRO:HG2	38:k:322:LEU:HA	1.42	0.98
44:v:348:ALA:CB	44:v:385:TYR:CE1	2.47	0.98
6:F:3:VAL:HG22	6:F:4:GLN:N	1.76	0.98
34:2:1707:A:C6	34:2:1708:C:C4	2.50	0.98
35:A:58:SER:HB3	35:A:61:LYS:CG	1.92	0.98
37:j:78:LEU:HD23	37:j:93:LEU:HD12	1.45	0.98
38:k:311:ILE:CA	38:k:317:VAL:HG21	1.92	0.98
44:v:393:MET:SD	44:v:454:GLU:CG	2.48	0.98
44:v:449:GLU:HG3	44:v:505:ARG:CZ	1.93	0.98
34:2:1819:A:N6	37:j:66:ARG:O	1.94	0.98
44:v:469:TYR:HE1	44:v:473:LEU:HD21	1.24	0.98
25:a:12:PHE:HE1	34:2:836:C:C2'	1.76	0.98
34:2:472:G:OP1	38:k:63:LYS:CE	2.10	0.98
43:y:114:ASP:O	43:y:118:LEU:HB2	1.64	0.98
38:k:85:HIS:HB2	38:k:130:ASN:ND2	1.77	0.98
44:v:409:MET:HG3	44:v:485:ARG:HD2	1.43	0.98
44:v:409:MET:CG	44:v:485:ARG:HD3	1.94	0.98
34:2:158:A:OP1	38:k:583:ILE:HG22	1.63	0.97
34:2:740:G:H21	34:2:794:G:H1'	0.81	0.97
38:k:332:LYS:HE3	38:k:334:ALA:HB3	1.41	0.97
40:R:133:ILE:HG23	40:R:134:GLY:N	1.78	0.97
43:y:101:THR:HA	43:y:149:TRP:CG	1.98	0.97
44:v:392:TYR:CE1	44:v:461:ASN:ND2	2.31	0.97
44:v:499:ILE:HG23	44:v:503:TYR:HE2	0.81	0.97
34:2:684:A:C2	34:2:731:C:N3	2.32	0.97
44:v:411:ILE:O	44:v:415:ASN:ND2	1.97	0.97
24:Z:50:ILE:CD1	38:k:58:CYS:HB3	1.94	0.97
43:y:210:ARG:HG3	43:y:212:HIS:CE1	1.99	0.97
38:k:414:GLN:CD	38:k:486:ASP:CG	2.32	0.97
44:v:752:CYS:SG	44:v:783:ILE:HG23	2.05	0.97
27:c:59:CYS:CB	44:v:450:ARG:CD	2.33	0.97
35:A:55:ARG:HG2	35:A:55:ARG:HH11	1.29	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:k:17:LYS:HG2	38:k:20:LYS:HG2	1.46	0.97
43:y:383:VAL:HG13	43:y:388:LYS:HG2	1.46	0.97
44:v:409:MET:CG	44:v:485:ARG:NH1	2.27	0.97
35:A:235:TYR:CB	36:B:285:ASP:OD2	2.12	0.97
41:3:76:A:C2'	41:3:77:A:H5'	1.94	0.97
43:y:295:THR:OG1	43:y:359:LEU:HD21	1.65	0.97
44:v:455:PHE:CZ	44:v:476:GLU:HB2	1.99	0.97
43:y:339:ALA:HB3	43:y:340:ARG:NH1	1.78	0.97
44:v:409:MET:HG3	44:v:485:ARG:HD3	1.44	0.97
35:A:229:LEU:HB2	36:B:284:VAL:HG11	1.43	0.96
34:2:1115:A:H5'	34:2:1116:U:C5	2.00	0.96
43:y:367:ARG:O	43:y:370:LEU:N	1.97	0.96
25:a:123:ALA:O	25:a:127:ALA:N	1.98	0.96
38:k:217:LEU:HD23	38:k:221:GLU:HB3	1.47	0.96
44:v:375:LYS:HG2	44:v:408:LEU:HD21	0.97	0.96
37:j:70:TRP:CD1	40:R:143:PRO:CA	2.48	0.96
37:j:70:TRP:NE1	40:R:143:PRO:HA	1.79	0.96
38:k:17:LYS:HZ3	38:k:20:LYS:CE	1.79	0.96
35:A:235:TYR:OH	36:B:286:ASP:OD2	1.83	0.96
25:a:123:ALA:O	25:a:127:ALA:HB3	1.66	0.96
37:j:70:TRP:HZ2	41:3:55:G:O2'	1.48	0.96
43:y:181:ALA:CB	43:y:196:LYS:CE	2.43	0.96
35:A:157:VAL:HG13	35:A:180:ILE:HD13	1.47	0.96
43:y:175:HIS:ND1	43:y:231:GLU:CD	2.22	0.96
14:N:30:LYS:HE2	14:N:30:LYS:N	1.81	0.96
38:k:378:LEU:C	38:k:379:GLY:O	2.09	0.96
43:y:7:ARG:O	43:y:9:GLU:CG	2.13	0.96
44:v:326:HIS:CA	44:v:329:VAL:HG21	1.95	0.96
44:v:486:VAL:O	44:v:502:VAL:HG23	1.62	0.96
34:2:1707:A:C2	34:2:1708:C:C6	2.53	0.96
38:k:17:LYS:NZ	38:k:20:LYS:CE	2.29	0.96
44:v:409:MET:HG3	44:v:485:ARG:NH1	1.80	0.96
16:P:20:ARG:CG	16:P:65:PHE:CE1	2.48	0.96
25:a:12:PHE:CE1	34:2:836:C:H1'	2.00	0.95
34:2:1116:U:C2'	34:2:1117:G:H5''	1.95	0.95
35:A:229:LEU:HD22	36:B:284:VAL:HG22	1.45	0.95
43:y:347:ILE:HD13	44:v:723:ARG:CZ	1.96	0.95
44:v:391:THR:HG22	44:v:392:TYR:H	0.79	0.95
44:v:554:TYR:O	44:v:558:LYS:HE3	1.65	0.95
34:2:1693:C:C5	41:3:58:C:N4	2.33	0.95
38:k:375:MET:SD	38:k:533:ILE:CG2	2.54	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:k:61:CYS:HG	51:k:701:SF4:FE3	0.66	0.95
38:k:414:GLN:HG3	38:k:486:ASP:O	1.67	0.95
43:y:166:ASN:CB	43:y:203:MET:SD	2.54	0.95
43:y:333:PRO:CG	43:y:437:LEU:HD23	1.96	0.95
44:v:521:ARG:HD3	44:v:542:GLU:HG2	0.96	0.95
43:y:106:GLU:O	43:y:110:GLN:HG2	1.65	0.95
37:j:71:ILE:HD13	37:j:77:ILE:CD1	1.97	0.95
38:k:332:LYS:HE2	38:k:502:ARG:HD3	0.95	0.95
44:v:332:LYS:HA	44:v:335:GLU:HG3	1.48	0.95
44:v:736:HIS:O	44:v:755:PHE:CD1	2.18	0.95
34:2:740:G:N2	34:2:794:G:C1'	2.22	0.95
35:A:235:TYR:CG	36:B:285:ASP:CG	2.39	0.95
38:k:4:LYS:HA	38:k:79:LEU:HG	1.43	0.95
40:R:141:PHE:O	40:R:142:ILE:HD12	1.64	0.95
44:v:345:THR:HG23	44:v:347:ARG:HB2	1.47	0.95
1:1:34:C:N3	41:3:54:G:N1	2.15	0.95
24:Z:61:GLN:HG2	34:2:1818:A:OP1	1.67	0.95
37:j:92:ILE:HG21	37:j:93:LEU:CD1	1.97	0.95
44:v:409:MET:HE2	44:v:485:ARG:CD	1.95	0.95
25:a:101:LYS:NZ	25:a:107:ARG:CZ	2.30	0.95
34:2:478:U:C5	38:k:99:ILE:HD13	2.01	0.95
34:2:1707:A:N3	34:2:1708:C:C6	2.35	0.95
44:v:449:GLU:HG3	44:v:505:ARG:NH2	1.81	0.95
25:a:101:LYS:HG3	25:a:107:ARG:NH2	1.82	0.94
37:j:74:SER:O	37:j:75:ASP:HB2	1.65	0.94
39:U:143:GLY:O	39:U:144:ARG:CD	2.14	0.94
43:y:101:THR:CA	43:y:149:TRP:CD1	2.50	0.94
44:v:429:GLU:HG3	44:v:430:ASN:CA	1.96	0.94
1:1:16:G:C6	1:1:17:C:H5	1.85	0.94
28:d:33:GLU:CG	42:m:426:LYS:HZ3	1.79	0.94
37:j:70:TRP:HZ2	41:3:55:G:HO2'	1.13	0.94
43:y:284:TRP:CA	43:y:292:HIS:CD2	2.51	0.94
43:y:291:PHE:HZ	43:y:356:ALA:CA	1.79	0.94
44:v:398:TRP:NE1	44:v:475:ASP:HB3	1.82	0.94
4:D:76:ASN:HA	4:D:77:ASP:HB3	1.49	0.94
38:k:431:LYS:HE3	38:k:477:GLY:C	1.91	0.94
41:3:75:G:H2'	41:3:76:A:H5'	1.49	0.94
43:y:181:ALA:CB	43:y:196:LYS:NZ	2.30	0.94
43:y:284:TRP:CG	43:y:427:TYR:HH	1.85	0.94
44:v:394:LYS:HD3	44:v:394:LYS:H	1.32	0.94
14:N:22:ARG:HH21	14:N:24:LEU:HB2	1.33	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:c:59:CYS:HB2	44:v:450:ARG:HD3	0.96	0.94
44:v:366:LEU:HD12	44:v:367:GLY:N	1.82	0.94
44:v:373:LYS:HZ3	44:v:420:VAL:HG11	0.77	0.94
44:v:425:LEU:HD12	44:v:426:GLU:N	1.81	0.94
37:j:92:ILE:CG2	37:j:93:LEU:CD1	2.44	0.94
43:y:320:THR:CG2	43:y:421:GLU:HG3	1.98	0.94
10:J:109:ARG:HB2	34:2:740:G:O4'	1.67	0.94
43:y:276:TYR:CZ	43:y:298:ARG:HG3	2.01	0.94
1:1:18:G:H1'	1:1:61:C:C5'	1.98	0.94
1:1:37:T6A:ODB	41:3:51:C:O2'	1.84	0.94
34:2:745:U:H2'	34:2:746:C:C6	2.01	0.94
38:k:73:VAL:CG2	38:k:322:LEU:CD2	2.45	0.94
44:v:368:GLU:N	44:v:368:GLU:OE1	2.01	0.94
44:v:409:MET:CG	44:v:485:ARG:CD	2.45	0.94
44:v:363:GLU:OE1	44:v:363:GLU:N	2.01	0.94
25:a:128:GLY:O	38:k:264:ASN:HB3	1.67	0.93
28:d:51:ARG:HH21	42:m:416:GLN:HG3	1.33	0.93
34:2:1244:C4J:O36	34:2:1244:C4J:C3	2.14	0.93
43:y:297:HIS:HE1	43:y:325:ALA:CB	1.82	0.93
43:y:306:MET:O	43:y:310:LEU:CA	2.15	0.93
43:y:320:THR:CA	43:y:323:LEU:HD23	1.99	0.93
34:2:1817:A:O2'	37:j:46:ARG:NH2	2.02	0.93
38:k:241:ASP:C	38:k:242:GLU:N	0.84	0.93
43:y:381:GLN:HE21	43:y:381:GLN:HA	1.32	0.93
44:v:423:ASN:C	44:v:424:ILE:HD12	1.92	0.93
11:K:193:LYS:CE	14:N:32:LYS:NZ	2.31	0.93
43:y:208:ILE:CD1	43:y:262:LEU:HD21	1.76	0.93
44:v:760:LYS:HD3	44:v:765:VAL:HB	1.49	0.93
25:a:104:ARG:NH2	25:a:108:LYS:HZ1	1.48	0.93
34:2:680:G:H1	34:2:734:C:H42	1.00	0.93
37:j:8:GLY:HA2	40:R:140:ARG:HH21	1.17	0.93
38:k:578:ASN:ND2	38:k:585:ASP:HB2	1.83	0.93
44:v:490:LEU:CD2	44:v:499:ILE:HG12	1.98	0.93
28:d:33:GLU:OE2	42:m:426:LYS:HD3	1.69	0.93
40:R:133:ILE:CG2	40:R:134:GLY:H	1.81	0.93
43:y:302:LEU:O	43:y:306:MET:SD	2.27	0.93
44:v:374:ILE:H	44:v:374:ILE:HD12	1.29	0.93
39:U:146:VAL:HG11	40:R:131:PRO:CG	1.96	0.93
43:y:293:ALA:HB2	43:y:328:SER:C	1.93	0.93
43:y:346:GLY:HA2	43:y:347:ILE:CG1	1.99	0.93
44:v:449:GLU:CG	44:v:505:ARG:HH21	1.80	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:v:752:CYS:CB	44:v:783:ILE:HD13	1.98	0.93
34:2:738:U:O2'	34:2:740:G:OP2	1.86	0.93
34:2:742:C:O2'	34:2:743:U:H5'	1.68	0.93
38:k:411:TYR:CA	38:k:412:LYS:N	2.32	0.93
43:y:48:GLU:OE2	43:y:85:SER:HB3	1.68	0.93
44:v:326:HIS:C	44:v:327:ALA:N	2.25	0.93
44:v:461:ASN:O	44:v:462:THR:CG2	2.17	0.93
34:2:1518:C:H4'	39:U:144:ARG:HA	0.95	0.93
37:j:48:GLU:OE2	37:j:49:ALA:N	2.02	0.92
38:k:374:ILE:CD1	38:k:528:LEU:C	2.40	0.92
43:y:227:SER:HB2	43:y:228:MET:HE2	1.51	0.92
1:1:18:G:O4'	1:1:61:C:H5''	1.68	0.92
34:2:742:C:H2'	34:2:743:U:H5'	1.49	0.92
34:2:1108:U:C2'	34:2:1109:A:H5'	1.99	0.92
43:y:42:THR:HG22	43:y:77:ILE:HA	1.50	0.92
43:y:330:PRO:CB	43:y:431:LEU:HD11	1.79	0.92
34:2:478:U:O4	38:k:99:ILE:CD1	2.16	0.92
40:R:141:PHE:O	40:R:142:ILE:CD1	2.17	0.92
43:y:158:ARG:O	43:y:162:ASP:HB2	1.69	0.92
26:b:58:VAL:CG2	26:b:59:PHE:CE1	2.53	0.92
43:y:339:ALA:CB	43:y:340:ARG:NH1	2.32	0.92
34:2:605:C:OP1	37:j:63:GLY:HA3	1.69	0.92
37:j:70:TRP:NE1	40:R:143:PRO:CA	2.33	0.92
1:1:35:A:H4'	37:j:8:GLY:O	1.65	0.92
8:H:61:PHE:CZ	42:m:415:SER:CB	2.53	0.92
24:Z:68:LYS:HG3	37:j:84:TYR:HH	1.31	0.92
38:k:583:ILE:HG23	38:k:584:LYS:H	1.33	0.92
44:v:739:ALA:HB1	44:v:755:PHE:CE1	2.05	0.92
34:2:1519:G:OP1	39:U:144:ARG:HB3	1.70	0.92
43:y:329:ILE:HB	43:y:330:PRO:HD2	1.50	0.92
1:1:18:G:N2	1:1:57:G:O6	2.02	0.92
16:P:27:LYS:NZ	16:P:28:LEU:HD23	1.85	0.92
27:c:65:GLN:HE22	44:v:343:LYS:HG3	1.34	0.92
38:k:61:CYS:SG	51:k:701:SF4:FE3	1.61	0.92
43:y:347:ILE:CD1	44:v:723:ARG:NE	2.31	0.92
44:v:358:VAL:HG13	44:v:359:GLN:H	1.34	0.92
25:a:106:GLN:OE1	38:k:266:ASP:OD2	1.86	0.92
37:j:78:LEU:HD23	37:j:93:LEU:CB	2.00	0.92
43:y:280:SER:HB2	43:y:295:THR:HG22	1.49	0.92
34:2:683:G:H1	34:2:731:C:H42	1.18	0.92
36:B:284:VAL:HG13	36:B:285:ASP:HB3	1.52	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:R:143:PRO:CG	41:3:55:G:H1'	2.00	0.92
41:3:49:A:H5'	41:3:49:A:N3	1.85	0.92
43:y:184:PHE:CD1	43:y:188:TYR:CD2	2.57	0.92
37:j:43:GLY:O	37:j:45:GLY:N	2.01	0.91
38:k:414:GLN:CG	38:k:486:ASP:C	2.43	0.91
34:2:478:U:OP1	38:k:150:SER:CB	2.17	0.91
37:j:78:LEU:CD2	37:j:93:LEU:HB2	1.99	0.91
43:y:184:PHE:CE1	43:y:188:TYR:CE2	2.58	0.91
25:a:128:GLY:HA3	38:k:264:ASN:C	1.95	0.91
28:d:51:ARG:HH21	42:m:416:GLN:HG2	0.76	0.91
38:k:55:CYS:SG	51:k:701:SF4:S3	2.67	0.91
38:k:188:LEU:O	38:k:191:LYS:HB2	1.70	0.91
38:k:412:LYS:HD3	38:k:485:ILE:CG1	2.00	0.91
43:y:8:PRO:CD	43:y:39:LYS:HD3	2.00	0.91
43:y:323:LEU:CD1	43:y:424:LEU:HB2	2.01	0.91
44:v:373:LYS:NZ	44:v:440:VAL:HG22	1.76	0.91
34:2:1102:C:O2'	34:2:1103:G:H5'	1.70	0.91
43:y:241:ILE:CG2	43:y:282:VAL:HG23	1.91	0.91
38:k:17:LYS:HG2	38:k:20:LYS:HE2	1.51	0.91
38:k:521:ASP:O	38:k:525:ALA:N	2.02	0.91
41:3:58:C:O2	41:3:59:A:C8	2.23	0.91
43:y:245:LEU:HB3	43:y:248:GLU:OE1	1.69	0.91
43:y:318:MET:HG2	43:y:382:TYR:HB3	1.52	0.91
44:v:398:TRP:CH2	44:v:451:MET:SD	2.64	0.91
38:k:411:TYR:C	38:k:412:LYS:HA	1.95	0.91
43:y:128:LEU:HD21	44:v:516:TYR:CD2	2.06	0.91
6:F:193:ASP:H	6:F:194:PRO:CD	1.81	0.91
38:k:17:LYS:CG	38:k:20:LYS:HG2	1.99	0.91
38:k:377:MET:HB3	38:k:385:LYS:HD2	1.52	0.91
43:y:326:THR:HG21	43:y:391:TYR:CE2	2.05	0.91
27:c:68:GLY:O	34:2:1101:G:H5''	1.70	0.91
35:A:157:VAL:CG1	35:A:180:ILE:CD1	2.49	0.91
37:j:92:ILE:CG2	37:j:93:LEU:CG	2.11	0.91
44:v:328:VAL:CG1	44:v:332:LYS:HE2	2.00	0.91
44:v:373:LYS:HA	44:v:376:PHE:HD2	1.34	0.91
8:H:27:ASP:HA	42:m:472:LYS:NZ	1.84	0.91
33:i:80:LEU:HD23	37:j:62:ARG:HH21	1.34	0.91
43:y:78:CYS:SG	43:y:86:LEU:CD1	2.58	0.91
43:y:320:THR:HA	43:y:323:LEU:CD2	1.98	0.91
34:2:1707:A:C2'	34:2:1708:C:H5'	2.00	0.91
38:k:241:ASP:O	38:k:242:GLU:CA	2.18	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:y:7:ARG:C	43:y:9:GLU:H	1.79	0.91
43:y:390:LEU:CD2	43:y:410:VAL:CB	2.34	0.91
25:a:123:ALA:O	25:a:127:ALA:CB	2.19	0.90
34:2:1815:U:H2'	34:2:1816:A:H5''	1.53	0.90
37:j:40:LYS:HB2	37:j:40:LYS:NZ	1.84	0.90
38:k:378:LEU:C	38:k:379:GLY:C	2.39	0.90
44:v:451:MET:HE1	44:v:479:VAL:HG23	0.94	0.90
43:y:8:PRO:CB	43:y:39:LYS:CD	2.40	0.90
43:y:269:PRO:O	43:y:272:MET:HG3	1.70	0.90
34:2:680:G:H1	34:2:734:C:N4	1.68	0.90
34:2:733:G:N7	34:2:738:U:O4	2.04	0.90
34:2:1518:C:C4'	39:U:144:ARG:CA	2.37	0.90
34:2:1518:C:OP1	39:U:143:GLY:HA3	1.71	0.90
38:k:331:PHE:O	38:k:498:LEU:HD13	1.71	0.90
43:y:12:LEU:CD2	43:y:16:ASN:HD21	1.85	0.90
43:y:166:ASN:HB3	43:y:203:MET:SD	2.12	0.90
44:v:510:THR:O	44:v:513:LYS:HG2	1.71	0.90
44:v:760:LYS:HZ3	44:v:765:VAL:HG11	1.34	0.90
4:D:40:ASN:HD21	4:D:75:GLN:HE22	1.12	0.90
38:k:411:TYR:HA	38:k:412:LYS:N	1.87	0.90
38:k:412:LYS:CD	38:k:485:ILE:HG13	2.01	0.90
43:y:300:TYR:CA	43:y:321:ARG:NH1	2.33	0.90
43:y:320:THR:CG2	43:y:421:GLU:CG	2.50	0.90
25:a:12:PHE:CZ	34:2:836:C:O2'	2.15	0.90
44:v:348:ALA:HB2	44:v:385:TYR:HE1	1.08	0.90
38:k:164:LEU:CD2	38:k:237:ILE:HB	2.02	0.90
43:y:293:ALA:HA	43:y:328:SER:HB2	1.51	0.90
44:v:376:PHE:HZ	44:v:441:ARG:NH2	1.69	0.90
38:k:200:VAL:HG11	38:k:228:ALA:HA	1.54	0.90
43:y:108:SER:HB2	43:y:145:LEU:CD2	2.01	0.90
27:c:59:CYS:HB2	44:v:450:ARG:CG	2.02	0.90
38:k:315:GLY:HA3	38:k:326:ASP:O	1.72	0.90
43:y:48:GLU:HG2	43:y:74:TYR:OH	1.71	0.90
43:y:320:THR:HG23	43:y:421:GLU:HG2	1.53	0.90
33:i:80:LEU:CD2	37:j:62:ARG:NH2	2.35	0.90
38:k:492:LEU:O	38:k:497:ARG:CZ	2.20	0.90
34:2:734:C:H2'	34:2:735:C:H5''	1.53	0.89
35:A:58:SER:CB	35:A:61:LYS:CD	2.49	0.89
39:U:143:GLY:C	39:U:144:ARG:CD	2.45	0.89
43:y:75:LYS:HA	43:y:78:CYS:SG	2.13	0.89
1:1:16:G:C5	1:1:17:C:H5	1.89	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:2:787:C:H2'	34:2:788:C:C6	2.06	0.89
38:k:381:ASN:HB3	53:k:705:GNP:O1G	1.71	0.89
16:P:20:ARG:HD2	16:P:65:PHE:HE1	0.86	0.89
38:k:521:ASP:CB	38:k:524:MET:HB2	2.00	0.89
40:R:133:ILE:O	40:R:139:SER:OG	1.89	0.89
43:y:181:ALA:HB3	43:y:196:LYS:HE2	1.52	0.89
25:a:12:PHE:HE1	34:2:836:C:C1'	1.85	0.89
25:a:104:ARG:NH2	25:a:108:LYS:CE	2.31	0.89
25:a:104:ARG:HH22	25:a:108:LYS:HZ1	0.97	0.89
43:y:71:LEU:HB3	43:y:164:LEU:HD21	1.53	0.89
43:y:104:ALA:HB2	43:y:149:TRP:CE2	2.07	0.89
43:y:291:PHE:HD1	43:y:359:LEU:HD22	1.33	0.89
38:k:17:LYS:NZ	38:k:20:LYS:HE2	1.85	0.89
43:y:8:PRO:HD3	43:y:39:LYS:HD3	1.53	0.89
44:v:380:ALA:HA	44:v:383:TYR:CD2	2.07	0.89
44:v:392:TYR:HD1	44:v:461:ASN:HD22	1.08	0.89
34:2:739:U:O2'	34:2:740:G:OP1	1.88	0.89
38:k:332:LYS:NZ	38:k:334:ALA:HB2	1.86	0.89
43:y:140:ARG:HG3	44:v:465:HIS:O	1.72	0.89
16:P:26:LEU:HD22	16:P:27:LYS:N	1.88	0.89
35:A:157:VAL:HG11	35:A:180:ILE:CB	2.03	0.89
38:k:112:ASN:HA	53:k:704:GNP:O3G	1.72	0.89
35:A:185:THR:HB	35:A:187:GLN:CB	2.02	0.89
38:k:450:GLN:HG3	38:k:453:ASN:OD1	1.72	0.89
43:y:222:ASN:O	43:y:226:GLN:CG	2.16	0.89
37:j:70:TRP:CE2	40:R:143:PRO:HB3	2.07	0.89
38:k:425:ARG:NH2	38:k:455:ILE:HD12	1.87	0.89
44:v:373:LYS:HE2	44:v:431:LEU:HD21	1.53	0.89
1:1:18:G:C1'	1:1:61:C:H5'	2.03	0.88
27:c:63:LEU:O	27:c:74:THR:HG23	1.73	0.88
44:v:367:GLY:HA3	44:v:369:GLY:CA	2.03	0.88
44:v:396:GLU:N	44:v:396:GLU:OE2	2.05	0.88
44:v:398:TRP:HE1	44:v:475:ASP:CB	1.84	0.88
34:2:1818:A:O2'	34:2:1819:A:OP2	1.90	0.88
38:k:55:CYS:SG	51:k:701:SF4:FE2	1.65	0.88
38:k:492:LEU:CB	38:k:497:ARG:HG3	2.03	0.88
44:v:455:PHE:CZ	44:v:476:GLU:CB	2.56	0.88
44:v:506:ARG:O	44:v:510:THR:HG23	1.71	0.88
34:2:1707:A:N1	34:2:1708:C:N3	2.20	0.88
35:A:157:VAL:CG2	35:A:180:ILE:HG21	2.03	0.88
43:y:104:ALA:HB2	43:y:149:TRP:HE1	1.10	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:Z:50:ILE:HD11	38:k:58:CYS:HB3	1.52	0.88
34:2:1707:A:N1	34:2:1708:C:C4	2.41	0.88
38:k:164:LEU:HD21	38:k:237:ILE:HD13	1.53	0.88
38:k:294:SER:HG	53:k:704:GNP:HO3'	1.12	0.88
44:v:382:LEU:CD1	44:v:400:LYS:HE3	2.04	0.88
43:y:14:ARG:HG2	43:y:14:ARG:HH11	1.37	0.88
43:y:105:LYS:HG3	43:y:146:LEU:CD2	2.02	0.88
44:v:554:TYR:CA	44:v:557:ALA:HB2	1.73	0.88
37:j:78:LEU:HD21	37:j:93:LEU:HD12	1.54	0.88
43:y:143:ARG:O	43:y:147:THR:OG1	1.91	0.88
43:y:399:ASN:OD1	43:y:400:PRO:HD2	1.74	0.88
34:2:605:C:OP1	37:j:63:GLY:CA	2.21	0.88
34:2:751:C:O2'	34:2:752:C:H5'	1.74	0.88
38:k:492:LEU:HB3	38:k:497:ARG:HG3	1.55	0.88
43:y:175:HIS:HE1	43:y:228:MET:CA	1.87	0.88
44:v:409:MET:HB3	44:v:413:PHE:HE2	1.38	0.88
27:c:72:ARG:HD2	34:2:1116:U:OP2	1.71	0.87
37:j:78:LEU:HD23	37:j:93:LEU:CD1	2.03	0.87
41:3:60:C:C3'	41:3:61:C:H4'	2.03	0.87
43:y:190:ARG:HB3	43:y:243:MET:SD	2.15	0.87
27:c:72:ARG:CZ	34:2:1116:U:OP2	2.22	0.87
44:v:398:TRP:HD1	44:v:475:ASP:OD2	1.57	0.87
43:y:184:PHE:CD1	43:y:188:TYR:HD2	1.92	0.87
44:v:455:PHE:HZ	44:v:476:GLU:HB2	1.33	0.87
24:Z:97:ASN:CG	38:k:34:MET:CE	2.43	0.87
43:y:390:LEU:HG	43:y:410:VAL:CG2	1.70	0.87
25:a:128:GLY:C	38:k:264:ASN:HB3	1.99	0.87
25:a:104:ARG:NH2	25:a:108:LYS:HZ2	1.68	0.87
27:c:72:ARG:HD3	34:2:1116:U:OP2	1.72	0.87
34:2:746:C:H2'	34:2:747:G:C8	2.10	0.87
38:k:345:MET:HG3	38:k:346:CYS:H	1.39	0.87
43:y:108:SER:HB2	43:y:145:LEU:HD22	1.56	0.87
43:y:236:GLN:CD	43:y:252:ALA:HB2	2.00	0.87
34:2:742:C:O2'	34:2:743:U:C5'	2.23	0.87
24:Z:58:GLU:CD	37:j:60:HIS:CE1	2.53	0.87
34:2:685:G:N2	34:2:730:C:N3	2.22	0.87
37:j:78:LEU:CD2	37:j:93:LEU:CD1	2.53	0.87
43:y:48:GLU:OE2	43:y:85:SER:CB	2.22	0.87
28:d:33:GLU:HG2	42:m:426:LYS:HZ3	1.39	0.86
43:y:284:TRP:H	43:y:292:HIS:CD2	1.93	0.86
27:c:35:VAL:HG12	27:c:78:SER:CB	2.05	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:k:21:CYS:SG	51:k:702:SF4:FE2	1.66	0.86
25:a:101:LYS:HZ3	25:a:107:ARG:CZ	1.87	0.86
34:2:1108:U:O2'	34:2:1109:A:C5'	2.24	0.86
43:y:230:LEU:HG	43:y:271:LEU:HD22	0.87	0.86
44:v:351:ILE:HG13	44:v:381:SER:OG	1.73	0.86
34:2:1327:C:N4	37:j:16:LYS:N	2.21	0.86
35:A:235:TYR:HB3	36:B:285:ASP:OD2	1.73	0.86
38:k:204:LEU:HG	38:k:224:ARG:HH11	1.05	0.86
43:y:48:GLU:CG	43:y:74:TYR:OH	2.22	0.86
35:A:229:LEU:HB2	36:B:284:VAL:CG1	2.04	0.86
38:k:315:GLY:HA2	38:k:326:ASP:HB3	1.57	0.86
38:k:4:LYS:HG3	38:k:79:LEU:HD12	1.58	0.86
33:i:82:ARG:NH2	33:i:85:LYS:N	2.23	0.86
38:k:345:MET:CG	38:k:346:CYS:H	1.89	0.86
39:U:143:GLY:C	39:U:144:ARG:CG	2.46	0.86
43:y:181:ALA:HB2	43:y:196:LYS:HZ3	1.36	0.86
16:P:20:ARG:CG	16:P:65:PHE:CD1	2.58	0.86
38:k:311:ILE:CB	38:k:317:VAL:HG21	2.04	0.86
37:j:63:GLY:C	37:j:64:LYS:HG3	1.99	0.86
38:k:204:LEU:HB3	38:k:224:ARG:NE	1.90	0.86
38:k:209:LEU:HD11	38:k:221:GLU:HG3	0.87	0.86
38:k:318:PRO:CB	38:k:322:LEU:CA	2.52	0.86
44:v:402:LEU:HD22	44:v:482:ILE:HD11	1.58	0.86
44:v:469:TYR:CE1	44:v:473:LEU:CD2	2.57	0.86
44:v:760:LYS:HZ3	44:v:765:VAL:CG1	1.89	0.86
43:y:159:GLN:CG	43:y:163:LEU:HD22	2.05	0.85
44:v:375:LYS:CB	44:v:408:LEU:HD11	2.05	0.85
44:v:553:LYS:O	44:v:557:ALA:HA	1.75	0.85
34:2:740:G:N1	34:2:793:C:C2	2.44	0.85
35:A:229:LEU:HB2	36:B:284:VAL:HG21	1.57	0.85
43:y:346:GLY:CA	43:y:348:ILE:HG13	2.06	0.85
44:v:373:LYS:HD2	44:v:420:VAL:CG1	2.05	0.85
25:a:101:LYS:O	25:a:102:THR:OG1	1.92	0.85
38:k:182:GLY:HA2	38:k:187:ILE:HD13	1.57	0.85
43:y:124:PRO:HG2	43:y:127:VAL:N	1.89	0.85
16:P:22:VAL:CG1	16:P:26:LEU:HG	2.04	0.85
16:P:22:VAL:HB	16:P:24:THR:N	1.90	0.85
25:a:101:LYS:HG3	25:a:107:ARG:HH21	1.40	0.85
33:i:76:VAL:HG11	33:i:80:LEU:HD23	1.55	0.85
34:2:684:A:H2'	34:2:685:G:C8	2.12	0.85
43:y:201:LEU:CD2	43:y:255:ASP:OD2	2.23	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:y:284:TRP:HZ2	43:y:426:GLN:HG3	0.91	0.85
43:y:368:ILE:HG23	43:y:371:ILE:HG21	1.56	0.85
35:A:229:LEU:HD22	36:B:284:VAL:HG21	0.98	0.85
44:v:375:LYS:CB	44:v:408:LEU:HD21	2.05	0.85
38:k:217:LEU:HB3	38:k:221:GLU:HB2	1.59	0.85
41:3:67:C:C2'	41:3:68:C:H5'	2.06	0.85
43:y:204:HIS:O	43:y:208:ILE:CG2	2.24	0.85
25:a:101:LYS:CG	25:a:107:ARG:NH2	2.40	0.85
34:2:732:C:H2'	34:2:733:G:O4'	1.76	0.85
44:v:326:HIS:CA	44:v:329:VAL:CG2	2.52	0.85
44:v:376:PHE:CZ	44:v:441:ARG:NH2	2.45	0.85
44:v:402:LEU:CD2	44:v:482:ILE:HD11	2.07	0.85
34:2:1518:C:OP1	39:U:143:GLY:C	2.20	0.85
35:A:108:VAL:CG2	35:A:150:TYR:HD1	1.90	0.85
37:j:25:GLU:HG2	37:j:26:LEU:HG	1.58	0.85
37:j:71:ILE:HD13	37:j:77:ILE:HD11	1.58	0.85
38:k:332:LYS:C	38:k:334:ALA:H	1.84	0.85
43:y:344:MET:HA	43:y:345:ASP:CB	2.05	0.85
44:v:328:VAL:HG13	44:v:332:LYS:HE2	1.56	0.85
39:U:146:VAL:HG13	40:R:131:PRO:CD	2.07	0.85
43:y:205:LEU:HD12	43:y:209:GLN:CG	2.02	0.85
25:a:12:PHE:HE1	34:2:836:C:O2'	1.42	0.84
34:2:1109:A:O2'	34:2:1110:U:H5'	1.76	0.84
41:3:74:A:O2'	41:3:75:G:H5'	1.76	0.84
43:y:306:MET:C	43:y:310:LEU:HB3	2.00	0.84
43:y:331:ILE:CG2	43:y:430:GLN:CD	2.12	0.84
35:A:55:ARG:HH11	35:A:55:ARG:CG	1.89	0.84
38:k:216:ASP:O	53:k:705:GNP:C4	2.25	0.84
34:2:740:G:N1	34:2:793:C:O2	2.09	0.84
35:A:178:ASN:O	35:A:182:ARG:HG2	1.78	0.84
43:y:8:PRO:CG	43:y:39:LYS:HD3	2.07	0.84
43:y:101:THR:HA	43:y:149:TRP:HD1	1.43	0.84
34:2:731:C:H2'	34:2:732:C:H5''	1.57	0.84
38:k:204:LEU:HB3	38:k:224:ARG:CZ	2.06	0.84
27:c:63:LEU:O	27:c:74:THR:CG2	2.25	0.84
34:2:1705:C:C2'	37:j:42:LEU:HD21	2.07	0.84
38:k:550:THR:C	38:k:551:LEU:N	2.35	0.84
43:y:297:HIS:CE1	43:y:325:ALA:CB	2.59	0.84
6:F:3:VAL:CG2	6:F:4:GLN:H	1.90	0.84
37:j:10:LYS:HG2	37:j:11:ASN:H	0.76	0.84
38:k:522:PHE:O	38:k:526:THR:CG2	2.21	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:v:420:VAL:CG2	44:v:437:PRO:O	2.26	0.84
44:v:521:ARG:HD2	44:v:542:GLU:CB	2.06	0.84
37:j:72:ASN:HD22	37:j:72:ASN:H	1.24	0.84
41:3:73:G:OP2	41:3:74:A:N6	2.11	0.84
35:A:157:VAL:CG2	35:A:180:ILE:CG2	2.55	0.84
43:y:5:PHE:C	43:y:6:GLN:HG2	2.03	0.84
43:y:278:LYS:HD2	43:y:279:VAL:N	1.91	0.84
43:y:224:GLU:O	43:y:228:MET:HE2	1.78	0.84
43:y:347:ILE:HD11	44:v:723:ARG:NE	1.91	0.84
43:y:285:LYS:O	43:y:287:GLY:O	1.95	0.84
43:y:331:ILE:HG23	43:y:430:GLN:CG	2.07	0.84
44:v:470:VAL:O	44:v:474:LYS:HG3	1.77	0.84
1:1:11:G:H1	1:1:25:U:H3	1.21	0.83
39:U:143:GLY:C	39:U:144:ARG:HG3	2.01	0.83
41:3:74:A:H2'	41:3:75:G:C8	2.12	0.83
43:y:150:VAL:HG12	43:y:188:TYR:CG	2.13	0.83
43:y:230:LEU:HD11	43:y:271:LEU:CB	2.07	0.83
28:d:35:MET:CA	42:m:426:LYS:HE2	2.07	0.83
34:2:1116:U:C2'	34:2:1117:G:C5'	2.53	0.83
38:k:317:VAL:N	38:k:318:PRO:HD3	1.87	0.83
43:y:175:HIS:HE1	43:y:228:MET:SD	1.97	0.83
44:v:348:ALA:CB	44:v:385:TYR:HE1	1.87	0.83
43:y:205:LEU:CD1	43:y:209:GLN:NE2	2.20	0.83
44:v:346:ASP:OD2	44:v:349:ALA:HB3	1.79	0.83
44:v:398:TRP:CD1	44:v:475:ASP:OD2	2.31	0.83
27:c:37:CYS:HB2	27:c:38:PRO:CD	2.07	0.83
35:A:235:TYR:HD1	36:B:285:ASP:CB	1.90	0.83
38:k:70:LEU:HD11	51:k:702:SF4:S2	2.16	0.83
43:y:28:LEU:HD23	43:y:29:ASP:N	1.93	0.83
43:y:250:PHE:O	43:y:253:VAL:HG22	1.79	0.83
43:y:277:ASN:HB3	43:y:299:LEU:HD11	1.58	0.83
34:2:1518:C:C3'	39:U:144:ARG:HA	2.07	0.83
38:k:188:LEU:HD12	38:k:225:PHE:HE1	1.43	0.83
38:k:311:ILE:HA	38:k:317:VAL:CG2	2.08	0.83
43:y:250:PHE:CE2	44:v:726:LEU:HD11	2.13	0.83
38:k:318:PRO:HB3	38:k:322:LEU:N	1.94	0.83
43:y:68:LYS:HE3	43:y:163:LEU:HD23	1.58	0.83
28:d:51:ARG:NH2	42:m:416:GLN:CG	2.09	0.83
43:y:268:LYS:HA	43:y:268:LYS:HE3	1.60	0.83
34:2:478:U:C4	38:k:99:ILE:HD13	2.14	0.82
34:2:1108:U:O2'	34:2:1109:A:H5'	1.77	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:2:1112:C:O2'	34:2:1113:C:OP1	1.95	0.82
38:k:489:SER:N	38:k:524:MET:HE1	1.94	0.82
10:J:109:ARG:HB3	34:2:740:G:H1'	0.83	0.82
11:K:193:LYS:CE	14:N:32:LYS:HZ3	1.91	0.82
35:A:229:LEU:HB2	36:B:284:VAL:CB	2.08	0.82
41:3:35:A:O2'	41:3:36:A:H5'	1.79	0.82
43:y:363:ALA:HB1	43:y:364:PRO:CD	2.09	0.82
1:1:18:G:C1'	1:1:61:C:C5'	2.57	0.82
35:A:108:VAL:HG23	35:A:150:TYR:HD1	1.43	0.82
38:k:253:LEU:HD11	38:k:564:ILE:HD11	1.61	0.82
38:k:318:PRO:HB3	38:k:321:ASN:C	2.04	0.82
40:R:143:PRO:HG2	41:3:55:G:H1'	1.59	0.82
10:J:108:SER:OG	34:2:737:C:O2'	1.86	0.82
36:B:284:VAL:HG13	36:B:285:ASP:CB	2.08	0.82
38:k:204:LEU:HG	38:k:224:ARG:CZ	2.08	0.82
43:y:276:TYR:O	43:y:279:VAL:HG12	1.79	0.82
24:Z:97:ASN:ND2	38:k:34:MET:SD	2.53	0.82
34:2:1693:C:C2	41:3:58:C:N4	2.37	0.82
43:y:75:LYS:HG3	43:y:165:ARG:HH12	1.43	0.82
43:y:158:ARG:CA	43:y:162:ASP:OD2	2.27	0.82
43:y:291:PHE:CE1	43:y:359:LEU:CD1	2.63	0.82
34:2:1705:C:H1'	37:j:42:LEU:HD23	1.59	0.82
38:k:414:GLN:HE21	38:k:486:ASP:HB3	1.43	0.82
43:y:347:ILE:HD11	44:v:723:ARG:HE	1.44	0.82
27:c:35:VAL:HG13	27:c:78:SER:HB3	0.84	0.82
38:k:17:LYS:HG2	38:k:20:LYS:CG	2.09	0.82
43:y:68:LYS:C	43:y:68:LYS:HD3	2.04	0.82
27:c:59:CYS:SG	44:v:450:ARG:CD	2.67	0.82
38:k:318:PRO:HB3	38:k:322:LEU:CA	2.10	0.82
38:k:319:THR:H	38:k:320:GLU:C	1.88	0.82
40:R:130:ARG:HH11	40:R:130:ARG:HB2	1.41	0.82
24:Z:96:GLU:HG2	38:k:34:MET:CE	2.10	0.82
28:d:38:THR:OG1	42:m:296:ASN:ND2	2.13	0.82
44:v:375:LYS:HG2	44:v:408:LEU:HG	1.62	0.82
34:2:1102:C:C2'	34:2:1103:G:C5'	2.58	0.82
41:3:75:G:C2'	41:3:76:A:H5'	2.09	0.82
43:y:390:LEU:HD21	43:y:410:VAL:CB	2.03	0.82
24:Z:96:GLU:HG2	38:k:34:MET:HE1	1.62	0.81
35:A:235:TYR:HD1	36:B:285:ASP:CG	1.85	0.81
43:y:181:ALA:HB1	43:y:196:LYS:HE2	1.62	0.81
43:y:184:PHE:HE1	43:y:188:TYR:CE2	1.97	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:y:253:VAL:O	43:y:256:ILE:HG22	1.79	0.81
43:y:291:PHE:CD1	43:y:359:LEU:HD13	2.15	0.81
16:P:20:ARG:HD3	16:P:65:PHE:CE1	2.15	0.81
38:k:70:LEU:HD13	51:k:702:SF4:S2	2.20	0.81
43:y:236:GLN:HG2	43:y:252:ALA:HB2	0.85	0.81
44:v:366:LEU:HD12	44:v:367:GLY:H	1.44	0.81
16:P:20:ARG:CD	16:P:65:PHE:HE1	1.64	0.81
16:P:22:VAL:N	16:P:23:PRO:HA	1.93	0.81
24:Z:52:LEU:O	38:k:34:MET:SD	2.39	0.81
39:U:140:GLY:O	39:U:141:ARG:HB2	1.77	0.81
43:y:277:ASN:HB3	43:y:299:LEU:CD1	2.09	0.81
43:y:302:LEU:HG	43:y:306:MET:SD	2.20	0.81
28:d:35:MET:HA	42:m:426:LYS:HE3	1.61	0.81
34:2:1517:A:H5'	39:U:142:ARG:NH2	1.95	0.81
39:U:148:VAL:HG21	40:R:131:PRO:O	1.80	0.81
43:y:295:THR:OG1	43:y:359:LEU:CD2	2.27	0.81
43:y:394:LEU:HD21	43:y:435:THR:CG2	2.10	0.81
34:2:1705:C:H1'	37:j:42:LEU:HD22	1.62	0.81
38:k:209:LEU:HD13	38:k:221:GLU:CG	2.10	0.81
38:k:591:SER:C	38:k:593:ASN:H	1.88	0.81
43:y:279:VAL:O	43:y:282:VAL:HG12	1.79	0.81
11:K:193:LYS:HE2	14:N:32:LYS:NZ	1.96	0.81
34:2:1814:G:O2'	34:2:1815:U:H5'	1.79	0.81
38:k:176:ILE:HA	38:k:178:LYS:H	1.45	0.81
38:k:315:GLY:O	38:k:316:TYR:CB	2.29	0.81
43:y:229:HIS:O	43:y:233:ARG:HG2	1.80	0.81
43:y:368:ILE:C	43:y:371:ILE:HG22	2.05	0.81
44:v:760:LYS:HZ3	44:v:765:VAL:CB	1.93	0.81
28:d:38:THR:HG23	42:m:296:ASN:CG	2.04	0.81
44:v:365:ASN:O	44:v:367:GLY:HA2	1.79	0.81
34:2:1327:C:H5	37:j:16:LYS:H	1.25	0.81
34:2:1518:C:O3'	39:U:144:ARG:CB	2.29	0.81
37:j:16:LYS:HE2	41:3:57:G:O2'	1.81	0.81
38:k:55:CYS:SG	51:k:701:SF4:S1	2.78	0.81
38:k:315:GLY:C	38:k:316:TYR:CD1	2.59	0.81
43:y:156:SER:O	43:y:160:CYS:HB2	1.81	0.81
43:y:330:PRO:C	43:y:431:LEU:HD13	2.05	0.81
6:F:3:VAL:CG1	34:2:1573:U:O4	2.26	0.81
43:y:302:LEU:HD11	43:y:306:MET:HE1	1.63	0.81
38:k:241:ASP:HA	38:k:242:GLU:N	1.93	0.81
38:k:307:GLU:O	38:k:311:ILE:HG23	1.81	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:k:315:GLY:O	38:k:316:TYR:CG	2.34	0.81
41:3:58:C:H2'	41:3:59:A:C8	2.16	0.81
43:y:101:THR:HG22	43:y:149:TRP:CA	2.10	0.81
43:y:101:THR:CB	43:y:149:TRP:HB3	2.11	0.81
43:y:175:HIS:ND1	43:y:231:GLU:OE1	2.13	0.81
43:y:370:LEU:O	43:y:373:ASP:HB2	1.79	0.81
37:j:30:GLU:H	37:j:33:GLN:HB3	1.46	0.80
40:R:128:HIS:HB3	40:R:129:GLY:HA3	1.62	0.80
43:y:291:PHE:CE1	43:y:359:LEU:HD22	2.15	0.80
43:y:380:LEU:HD23	43:y:380:LEU:H	1.46	0.80
24:Z:68:LYS:HG3	37:j:84:TYR:CZ	2.16	0.80
34:2:605:C:OP1	37:j:63:GLY:N	2.14	0.80
34:2:1816:A:O2'	34:2:1817:A:C8	2.35	0.80
44:v:372:VAL:HG22	44:v:411:ILE:CG2	2.11	0.80
44:v:372:VAL:O	44:v:375:LYS:HB3	1.81	0.80
38:k:73:VAL:CB	38:k:322:LEU:HD21	2.09	0.80
38:k:166:ALA:HA	38:k:237:ILE:CG2	2.11	0.80
1:1:17:C:H2'	1:1:18:G:H5'	1.63	0.80
16:P:24:THR:O	16:P:26:LEU:HD12	1.81	0.80
34:2:1707:A:N1	34:2:1708:C:C2	2.50	0.80
37:j:70:TRP:HE1	40:R:143:PRO:HB3	1.46	0.80
43:y:346:GLY:HA2	43:y:348:ILE:HG13	1.62	0.80
38:k:315:GLY:CA	38:k:326:ASP:HB3	2.11	0.80
43:y:226:GLN:OE1	43:y:269:PRO:HG3	1.82	0.80
44:v:409:MET:CE	44:v:485:ARG:HD3	2.11	0.80
9:I:237:LEU:HB2	34:2:785:G:OP1	1.81	0.80
34:2:1518:C:P	39:U:143:GLY:HA3	2.22	0.80
35:A:58:SER:HB3	35:A:61:LYS:CD	2.12	0.80
43:y:291:PHE:CD1	43:y:359:LEU:CD2	2.65	0.80
33:i:82:ARG:HH21	33:i:85:LYS:N	1.79	0.80
40:R:143:PRO:HG2	41:3:55:G:C4	2.15	0.80
43:y:166:ASN:HA	43:y:203:MET:SD	2.22	0.80
43:y:257:HIS:NE2	43:y:358:LEU:HD23	1.95	0.80
44:v:499:ILE:HG13	44:v:502:VAL:HG11	1.61	0.80
1:1:34:C:O2	37:j:10:LYS:HA	1.81	0.80
43:y:326:THR:HG21	43:y:391:TYR:HE2	1.42	0.80
34:2:1108:U:H2'	34:2:1109:A:H5'	1.63	0.79
37:j:40:LYS:HD3	37:j:41:MET:H	1.48	0.79
43:y:302:LEU:CD1	43:y:306:MET:HE1	2.11	0.79
25:a:12:PHE:HE1	34:2:836:C:H1'	1.41	0.79
14:N:25:LEU:HD22	14:N:28:THR:O	1.81	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:2:743:U:H1'	34:2:744:C:C1'	2.12	0.79
38:k:150:SER:OG	38:k:151:GLU:N	2.01	0.79
38:k:166:ALA:HA	38:k:237:ILE:HG22	1.65	0.79
43:y:319:SER:O	43:y:322:VAL:HG22	1.81	0.79
44:v:362:SER:C	44:v:363:GLU:OE1	2.24	0.79
44:v:365:ASN:C	44:v:367:GLY:HA2	2.07	0.79
27:c:79:PHE:O	27:c:80:ARG:NH1	2.15	0.79
34:2:1518:C:OP1	39:U:143:GLY:O	2.00	0.79
41:3:58:C:C2	41:3:59:A:C5	2.71	0.79
16:P:20:ARG:HG2	16:P:65:PHE:CD1	2.17	0.79
34:2:1116:U:O2'	34:2:1117:G:O5'	2.00	0.79
38:k:584:LYS:C	38:k:586:VAL:H	1.91	0.79
43:y:230:LEU:HD12	43:y:271:LEU:HD22	1.61	0.79
43:y:390:LEU:HD11	43:y:410:VAL:C	2.00	0.79
44:v:458:ILE:O	44:v:460:GLN:N	2.14	0.79
6:F:3:VAL:HG11	34:2:1573:U:C4	2.15	0.79
27:c:35:VAL:HG12	27:c:36:LYS:H	1.47	0.79
37:j:41:MET:HA	37:j:47:LEU:CD1	2.13	0.79
43:y:68:LYS:CG	43:y:163:LEU:CD2	2.61	0.79
43:y:230:LEU:CD1	43:y:271:LEU:HB3	2.10	0.79
43:y:284:TRP:CH2	43:y:426:GLN:CG	1.96	0.79
43:y:284:TRP:N	43:y:292:HIS:CD2	2.50	0.79
34:2:743:U:O2'	34:2:744:C:O4'	2.01	0.79
34:2:748:G:O2'	34:2:749:C:O5'	2.01	0.79
34:2:1111:U:H6	34:2:1113:C:H41	1.30	0.79
43:y:68:LYS:HB2	43:y:159:GLN:OE1	1.81	0.79
43:y:150:VAL:CG1	43:y:188:TYR:CG	2.66	0.79
43:y:397:GLU:HG3	43:y:398:PHE:O	1.83	0.79
44:v:323:GLU:HG3	44:v:324:ILE:HG13	1.64	0.79
44:v:490:LEU:CD1	44:v:499:ILE:CD1	2.39	0.79
44:v:521:ARG:CD	44:v:542:GLU:HB3	2.12	0.79
34:2:1707:A:O2'	34:2:1708:C:H5'	1.82	0.79
38:k:188:LEU:HD13	38:k:225:PHE:CD1	2.17	0.79
38:k:414:GLN:CG	38:k:486:ASP:HB3	2.13	0.79
43:y:280:SER:HB2	43:y:295:THR:CG2	2.13	0.79
44:v:409:MET:HG2	44:v:485:ARG:HH11	1.46	0.79
41:3:55:G:H5'	41:3:56:U:OP2	1.81	0.79
38:k:319:THR:OG1	38:k:320:GLU:HB2	1.81	0.78
38:k:412:LYS:HB3	38:k:485:ILE:CA	2.08	0.78
40:R:133:ILE:HG12	40:R:139:SER:HB3	1.64	0.78
38:k:414:GLN:CG	38:k:486:ASP:CB	2.60	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:2:1812:A:N1	34:2:1813:A:N7	2.32	0.78
44:v:499:ILE:HG21	44:v:503:TYR:HE2	1.42	0.78
43:y:113:LEU:CD1	43:y:138:GLN:HB2	2.09	0.78
43:y:394:LEU:CD2	43:y:435:THR:HG23	2.13	0.78
44:v:760:LYS:HZ3	44:v:765:VAL:HG21	1.47	0.78
4:D:39:PHE:CD1	4:D:74:LEU:HD22	2.18	0.78
18:S:145:TYR:O	18:S:146:ARG:CG	2.31	0.78
38:k:330:VAL:CG2	38:k:575:PRO:HD2	2.13	0.78
41:3:35:A:C2'	41:3:36:A:H5'	2.14	0.78
41:3:43:A:H2'	41:3:44:C:C6	2.19	0.78
43:y:221:ASN:CB	43:y:224:GLU:OE2	2.32	0.78
4:D:76:ASN:ND2	4:D:77:ASP:HB3	1.99	0.78
34:2:734:C:C2'	34:2:735:C:H5''	2.13	0.78
38:k:374:ILE:CD1	38:k:529:ALA:CA	2.61	0.78
44:v:413:PHE:CD1	44:v:489:TYR:OH	2.00	0.78
34:2:604:G:OP2	37:j:64:LYS:NZ	2.16	0.78
34:2:1705:C:O2'	37:j:42:LEU:HD21	1.84	0.78
38:k:311:ILE:HB	38:k:317:VAL:HG21	1.66	0.78
38:k:492:LEU:HB2	38:k:497:ARG:CG	2.13	0.78
44:v:333:LEU:O	44:v:337:LEU:HG	1.82	0.78
1:1:16:G:H2'	1:1:17:C:H5''	1.66	0.78
28:d:13:ARG:HG2	42:m:426:LYS:HZ1	1.48	0.78
35:A:205:ILE:HD12	36:B:288:LYS:CB	2.13	0.78
38:k:237:ILE:C	38:k:238:PHE:CD2	2.62	0.78
38:k:431:LYS:HE3	38:k:478:LYS:N	1.99	0.78
41:3:67:C:H2'	41:3:68:C:H5'	1.63	0.78
43:y:347:ILE:CD1	44:v:723:ARG:CZ	2.58	0.78
4:D:76:ASN:CA	4:D:77:ASP:HB3	2.14	0.78
24:Z:97:ASN:OD1	38:k:34:MET:HE2	1.81	0.78
43:y:166:ASN:CA	43:y:203:MET:SD	2.72	0.78
43:y:230:LEU:HD12	43:y:271:LEU:CD2	2.12	0.78
44:v:521:ARG:HD2	44:v:542:GLU:HB2	1.64	0.78
38:k:241:ASP:C	38:k:242:GLU:C	2.51	0.78
38:k:272:VAL:HG12	38:k:273:GLU:N	1.98	0.78
38:k:337:ALA:O	38:k:338:ASN:HB2	1.83	0.78
38:k:378:LEU:O	38:k:385:LYS:CD	2.30	0.78
43:y:140:ARG:CZ	44:v:465:HIS:O	2.32	0.78
43:y:270:GLN:HG3	43:y:271:LEU:H	1.47	0.78
37:j:29:LYS:HA	37:j:33:GLN:O	1.84	0.77
38:k:319:THR:HG23	38:k:320:GLU:CB	2.13	0.77
43:y:59:VAL:CG2	43:y:93:TYR:HE1	1.97	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:v:470:VAL:HG12	44:v:474:LYS:HE3	1.66	0.77
44:v:521:ARG:CG	44:v:542:GLU:HG2	2.14	0.77
10:J:106:ARG:CD	34:2:794:G:O6	2.32	0.77
43:y:320:THR:HG23	43:y:421:GLU:HG3	1.57	0.77
16:P:27:LYS:NZ	16:P:27:LYS:HB2	1.99	0.77
34:2:1102:C:H2'	34:2:1103:G:C5'	2.11	0.77
38:k:76:PRO:HG3	38:k:323:ARG:CG	2.15	0.77
34:2:1244:C4J:C31	34:2:1244:C4J:O2	2.31	0.77
38:k:519:GLU:CD	38:k:524:MET:HG2	2.10	0.77
44:v:748:ASP:CG	44:v:750:LYS:HD2	2.08	0.77
34:2:452:C:O2'	38:k:306:ARG:HD3	1.83	0.77
38:k:487:GLU:N	38:k:518:VAL:O	2.16	0.77
43:y:8:PRO:HB3	43:y:39:LYS:HD2	0.83	0.77
44:v:379:ILE:HD11	44:v:447:LEU:HD13	1.66	0.77
4:D:39:PHE:CG	4:D:74:LEU:HD22	2.20	0.77
35:A:229:LEU:HB2	36:B:284:VAL:CG2	2.14	0.77
43:y:284:TRP:HZ2	43:y:426:GLN:CG	1.62	0.77
43:y:293:ALA:HA	43:y:328:SER:CB	2.15	0.77
44:v:409:MET:HB3	44:v:413:PHE:CE2	2.19	0.77
34:2:743:U:O4	34:2:791:A:N1	2.17	0.77
35:A:111:ILE:HD11	35:A:183:ARG:HH12	1.48	0.77
37:j:8:GLY:C	40:R:140:ARG:NH2	2.32	0.77
37:j:27:VAL:HG12	37:j:28:PHE:H	1.48	0.77
38:k:414:GLN:HG2	38:k:486:ASP:OD1	1.83	0.77
44:v:478:GLN:O	44:v:481:ALA:HB3	1.85	0.77
16:P:19:ARG:HH22	16:P:23:PRO:HB2	1.49	0.77
38:k:450:GLN:HG3	38:k:453:ASN:CG	2.09	0.77
38:k:488:PRO:HG2	38:k:524:MET:HE2	1.66	0.77
44:v:736:HIS:CD2	44:v:759:GLU:HB3	2.19	0.77
43:y:158:ARG:O	43:y:162:ASP:CB	2.32	0.77
43:y:201:LEU:HD21	43:y:255:ASP:CG	2.10	0.77
43:y:330:PRO:HB2	43:y:431:LEU:HD13	0.77	0.77
44:v:351:ILE:HG12	44:v:381:SER:CB	2.14	0.77
14:N:22:ARG:NH2	14:N:24:LEU:HB2	2.00	0.76
44:v:382:LEU:HD11	44:v:400:LYS:HE3	1.66	0.76
44:v:736:HIS:CD2	44:v:759:GLU:CB	2.68	0.76
27:c:33:MET:HE1	27:c:73:LEU:CD1	2.13	0.76
38:k:17:LYS:HG2	38:k:20:LYS:CD	2.16	0.76
38:k:378:LEU:C	38:k:379:GLY:HA3	2.10	0.76
24:Z:97:ASN:ND2	38:k:34:MET:CE	2.48	0.76
38:k:183:THR:O	38:k:187:ILE:CB	2.33	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:k:4:LYS:HA	38:k:79:LEU:CB	2.16	0.76
38:k:226:ALA:O	38:k:229:VAL:HG12	1.84	0.76
44:v:554:TYR:N	44:v:557:ALA:CB	2.17	0.76
43:y:236:GLN:CG	43:y:252:ALA:CB	2.35	0.76
27:c:75:GLU:CG	44:v:388:ASN:HB2	2.16	0.76
35:A:54:ARG:HH21	35:A:54:ARG:CB	1.99	0.76
35:A:157:VAL:HG11	35:A:180:ILE:CD1	2.16	0.76
38:k:73:VAL:CG2	38:k:322:LEU:HD21	2.15	0.76
38:k:498:LEU:CD1	38:k:523:ILE:HD12	2.14	0.76
44:v:409:MET:HE2	44:v:485:ARG:HD3	1.64	0.76
38:k:4:LYS:HA	38:k:79:LEU:CD1	2.15	0.76
41:3:73:G:N7	41:3:74:A:C5	2.54	0.76
43:y:284:TRP:H	43:y:292:HIS:HD2	1.33	0.76
10:J:109:ARG:CG	34:2:740:G:H1'	2.15	0.76
25:a:100:LYS:HA	25:a:101:LYS:C	2.09	0.76
34:2:749:C:H2'	34:2:750:G:O4'	1.86	0.76
38:k:188:LEU:CD1	38:k:225:PHE:CE1	2.69	0.76
43:y:329:ILE:HB	43:y:330:PRO:CD	2.16	0.76
43:y:399:ASN:OD1	50:u:313:ILE:HG21	1.85	0.76
38:k:489:SER:CA	38:k:524:MET:HE1	2.16	0.76
38:k:546:ASN:OD1	38:k:557:LYS:NZ	2.18	0.76
43:y:283:PHE:CZ	43:y:287:GLY:HA3	2.21	0.76
38:k:253:LEU:CD1	38:k:564:ILE:CD1	2.64	0.76
38:k:345:MET:CG	38:k:346:CYS:N	2.48	0.76
43:y:12:LEU:CD2	43:y:16:ASN:ND2	2.49	0.76
43:y:42:THR:HA	43:y:77:ILE:HB	1.68	0.76
43:y:291:PHE:HE1	43:y:359:LEU:HB2	1.51	0.76
44:v:449:GLU:HG3	44:v:505:ARG:NE	2.01	0.76
44:v:498:GLU:O	44:v:500:CYS:N	2.19	0.76
1:1:16:G:C5	1:1:17:C:C5	2.74	0.75
38:k:378:LEU:C	38:k:385:LYS:NZ	2.44	0.75
43:y:100:LYS:O	43:y:149:TRP:CD1	2.38	0.75
44:v:379:ILE:CD1	44:v:447:LEU:HD13	2.16	0.75
44:v:429:GLU:HG3	44:v:430:ASN:HA	1.66	0.75
9:I:237:LEU:CD1	34:2:784:G:O3'	2.25	0.75
9:I:237:LEU:CB	34:2:785:G:OP1	2.34	0.75
37:j:70:TRP:CH2	41:3:55:G:H2'	2.20	0.75
27:c:75:GLU:HG3	44:v:389:LEU:H	1.50	0.75
34:2:1116:U:C2'	34:2:1117:G:O5'	2.34	0.75
34:2:1812:A:C2	34:2:1813:A:N7	2.54	0.75
35:A:227:ILE:CD1	35:A:237:MET:CE	2.62	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:k:305:VAL:O	38:k:309:ILE:HG13	1.86	0.75
44:v:438:LEU:HA	44:v:441:ARG:HB3	1.68	0.75
44:v:455:PHE:CZ	44:v:476:GLU:CG	2.70	0.75
44:v:760:LYS:HZ3	44:v:765:VAL:CG2	1.99	0.75
38:k:319:THR:CG2	38:k:320:GLU:HB2	2.15	0.75
41:3:49:A:N3	41:3:49:A:C5'	2.49	0.75
43:y:277:ASN:CB	43:y:299:LEU:HD13	2.13	0.75
44:v:394:LYS:H	44:v:394:LYS:CD	1.99	0.75
16:P:20:ARG:HD2	16:P:65:PHE:CD1	2.21	0.75
27:c:75:GLU:HG3	44:v:388:ASN:HB2	1.68	0.75
43:y:293:ALA:HB2	43:y:328:SER:O	1.86	0.75
44:v:326:HIS:C	44:v:329:VAL:CG2	2.59	0.75
1:1:35:A:HO2'	37:j:8:GLY:HA3	1.51	0.75
14:N:22:ARG:NH2	14:N:24:LEU:HD13	2.02	0.75
38:k:217:LEU:HG	38:k:221:GLU:CG	2.14	0.75
38:k:412:LYS:CB	38:k:484:LEU:O	2.35	0.75
27:c:36:LYS:H	27:c:78:SER:HB2	1.52	0.75
38:k:591:SER:C	38:k:593:ASN:N	2.45	0.75
40:R:141:PHE:O	40:R:142:ILE:CG1	2.34	0.75
43:y:104:ALA:HB3	43:y:149:TRP:HD1	0.97	0.75
43:y:205:LEU:HD11	43:y:209:GLN:HE21	0.63	0.75
43:y:330:PRO:O	43:y:331:ILE:HG12	1.85	0.75
43:y:367:ARG:NH1	43:y:368:ILE:HD12	2.02	0.75
44:v:490:LEU:HD11	44:v:499:ILE:HB	1.68	0.75
35:A:58:SER:CB	35:A:61:LYS:HD2	2.16	0.75
43:y:158:ARG:HA	43:y:162:ASP:OD2	1.86	0.75
44:v:455:PHE:HZ	44:v:476:GLU:CB	1.94	0.75
43:y:291:PHE:HD1	43:y:359:LEU:CD2	1.98	0.75
44:v:760:LYS:HB3	44:v:766:TRP:CB	2.15	0.75
38:k:526:THR:HG23	38:k:527:TYR:H	1.51	0.74
38:k:412:LYS:HB3	38:k:484:LEU:O	1.87	0.74
41:3:73:G:C8	41:3:74:A:N7	2.55	0.74
43:y:245:LEU:C	43:y:246:TRP:CE3	2.66	0.74
44:v:498:GLU:C	44:v:500:CYS:H	1.96	0.74
44:v:748:ASP:OD1	44:v:750:LYS:HG3	1.87	0.74
38:k:165:LYS:H	38:k:236:ASP:HB3	1.49	0.74
43:y:140:ARG:O	44:v:466:SER:CB	2.35	0.74
34:2:1518:C:C5'	39:U:144:ARG:CA	2.64	0.74
43:y:268:LYS:HA	43:y:268:LYS:CE	2.17	0.74
44:v:453:GLU:O	44:v:456:THR:OG1	2.03	0.74
34:2:597:U:O2	41:3:61:C:N4	2.21	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:2:1327:C:C5	37:j:16:LYS:N	2.56	0.74
35:A:114:HIS:CE1	35:A:175:VAL:HG21	2.23	0.74
37:j:92:ILE:HG21	37:j:93:LEU:HD12	1.68	0.74
43:y:293:ALA:HB2	43:y:328:SER:CA	2.16	0.74
6:F:193:ASP:N	6:F:194:PRO:HD2	2.02	0.74
28:d:13:ARG:CG	42:m:426:LYS:HZ1	2.01	0.74
38:k:345:MET:HG3	38:k:371:ASP:HB3	1.69	0.74
41:3:58:C:O2	41:3:59:A:N7	2.19	0.74
34:2:1709:U:O4	34:2:1813:A:N6	2.18	0.74
35:A:202:TYR:HB2	36:B:355:LYS:HB3	1.69	0.74
43:y:5:PHE:O	43:y:6:GLN:HG2	1.88	0.74
43:y:259:LEU:O	43:y:263:SER:OG	2.05	0.74
25:a:103:SER:OG	25:a:104:ARG:N	2.21	0.74
38:k:311:ILE:HB	38:k:317:VAL:CG2	2.18	0.74
43:y:283:PHE:CE1	43:y:287:GLY:CA	2.50	0.74
43:y:368:ILE:CG2	43:y:371:ILE:HG21	2.18	0.74
16:P:19:ARG:HH22	16:P:23:PRO:CB	2.00	0.74
38:k:519:GLU:OE1	38:k:524:MET:HG2	1.87	0.74
43:y:238:ASP:O	43:y:242:SER:HB2	1.87	0.74
43:y:107:GLU:HG3	43:y:145:LEU:HD21	1.70	0.74
44:v:455:PHE:O	44:v:458:ILE:HB	1.88	0.74
17:Q:127:GLY:O	26:b:59:PHE:CE2	2.41	0.73
38:k:188:LEU:HD12	38:k:225:PHE:CE1	2.23	0.73
38:k:348:TYR:HD2	38:k:369:PHE:O	1.71	0.73
43:y:94:LEU:HD22	43:y:157:TYR:CE1	2.23	0.73
43:y:296:LEU:HD13	43:y:324:LEU:HB3	1.70	0.73
35:A:58:SER:HB3	35:A:61:LYS:HD2	1.70	0.73
38:k:21:CYS:HG	51:k:702:SF4:FE2	0.49	0.73
43:y:329:ILE:HD12	43:y:370:LEU:HB2	1.70	0.73
44:v:425:LEU:O	44:v:426:GLU:HG3	1.88	0.73
35:A:58:SER:HB2	35:A:61:LYS:HE3	1.70	0.73
43:y:240:ALA:HB1	43:y:245:LEU:O	1.88	0.73
44:v:499:ILE:HG23	44:v:503:TYR:CD2	2.19	0.73
34:2:454:A:C2	38:k:578:ASN:OD1	2.42	0.73
38:k:519:GLU:OE1	38:k:524:MET:HE2	1.89	0.73
38:k:583:ILE:HG23	38:k:584:LYS:N	2.03	0.73
44:v:374:ILE:H	44:v:374:ILE:CD1	2.00	0.73
38:k:425:ARG:CZ	38:k:455:ILE:CD1	2.66	0.73
44:v:521:ARG:CD	44:v:542:GLU:HB2	2.19	0.73
34:2:748:G:C2	34:2:749:C:C2	2.77	0.73
43:y:71:LEU:HB3	43:y:164:LEU:CD2	2.18	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:y:124:PRO:HG2	43:y:127:VAL:H	1.50	0.73
44:v:490:LEU:CD1	44:v:499:ILE:CG1	2.65	0.73
44:v:530:SER:HB2	44:v:535:ASP:OD2	1.89	0.73
16:P:27:LYS:C	16:P:28:LEU:HG	2.12	0.73
27:c:68:GLY:O	34:2:1101:G:C5'	2.37	0.73
35:A:202:TYR:HB2	36:B:355:LYS:CB	2.17	0.73
38:k:253:LEU:CD1	38:k:564:ILE:HD12	2.18	0.73
43:y:25:GLN:HG2	43:y:26:PRO:HD3	1.70	0.73
44:v:383:TYR:CE1	44:v:450:ARG:HG2	2.23	0.73
16:P:19:ARG:NH1	27:c:84:HIS:CE1	2.57	0.73
38:k:187:ILE:HG23	38:k:188:LEU:N	2.02	0.73
38:k:591:SER:N	38:k:592:GLY:N	2.36	0.73
40:R:134:GLY:HA2	40:R:139:SER:HB2	1.71	0.73
41:3:58:C:O2	41:3:59:A:N9	2.22	0.73
43:y:83:ILE:H	43:y:83:ILE:HD12	1.54	0.73
16:P:26:LEU:C	16:P:26:LEU:HD13	2.14	0.73
37:j:70:TRP:CE2	40:R:143:PRO:CB	2.72	0.73
38:k:332:LYS:HG2	38:k:527:TYR:CG	2.14	0.73
43:y:300:TYR:C	43:y:321:ARG:NH1	2.46	0.73
43:y:327:LEU:O	43:y:331:ILE:HG12	1.88	0.73
43:y:353:ARG:HD3	43:y:353:ARG:C	2.13	0.73
44:v:490:LEU:HD13	44:v:499:ILE:HD13	0.75	0.72
37:j:73:THR:O	37:j:74:SER:OG	2.05	0.72
38:k:319:THR:CA	38:k:320:GLU:HB2	2.20	0.72
43:y:83:ILE:HD12	43:y:83:ILE:N	2.03	0.72
43:y:157:TYR:O	43:y:162:ASP:OD2	2.07	0.72
43:y:234:LEU:N	43:y:234:LEU:HD23	2.03	0.72
44:v:461:ASN:C	44:v:462:THR:HG23	2.14	0.72
44:v:760:LYS:HD3	44:v:765:VAL:CB	2.19	0.72
44:v:760:LYS:CB	44:v:766:TRP:HB2	2.17	0.72
4:D:190:PRO:O	4:D:191:ASP:CG	2.32	0.72
25:a:12:PHE:CE1	34:2:836:C:C1'	2.65	0.72
34:2:684:A:C2	34:2:731:C:C4	2.78	0.72
37:j:63:GLY:C	37:j:64:LYS:CG	2.61	0.72
44:v:409:MET:CE	44:v:485:ARG:CD	2.68	0.72
44:v:423:ASN:OD1	44:v:424:ILE:N	2.23	0.72
44:v:736:HIS:HB3	44:v:759:GLU:CG	2.09	0.72
38:k:164:LEU:HD21	38:k:237:ILE:CB	2.19	0.72
38:k:414:GLN:NE2	38:k:486:ASP:CA	2.52	0.72
40:R:130:ARG:HA	40:R:130:ARG:NH1	2.04	0.72
43:y:140:ARG:NH1	44:v:465:HIS:O	2.23	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:y:301:HIS:HE1	43:y:377:PHE:CZ	2.08	0.72
44:v:490:LEU:HD12	44:v:492:GLU:HB3	1.71	0.72
39:U:146:VAL:HG12	40:R:131:PRO:CG	1.91	0.72
43:y:158:ARG:O	43:y:162:ASP:CG	2.31	0.72
43:y:293:ALA:CB	43:y:328:SER:C	2.61	0.72
44:v:495:THR:OG1	44:v:496:THR:HG23	1.88	0.72
24:Z:78:GLY:HA3	38:k:60:ILE:HD11	1.69	0.72
34:2:749:C:C3'	34:2:750:G:H5''	2.18	0.72
35:A:55:ARG:C	35:A:56:ILE:HD12	2.14	0.72
37:j:40:LYS:HD3	37:j:42:LEU:N	2.04	0.72
37:j:40:LYS:O	37:j:47:LEU:HD11	1.89	0.72
38:k:159:ILE:O	38:k:162:ASP:N	2.22	0.72
38:k:272:VAL:CG1	38:k:273:GLU:N	2.50	0.72
43:y:245:LEU:HB3	43:y:248:GLU:CG	2.19	0.72
1:1:18:G:H4'	1:1:61:C:P	2.29	0.72
1:1:33:C:OP2	18:S:146:ARG:NH1	2.22	0.72
4:D:76:ASN:HA	4:D:77:ASP:CB	2.13	0.72
4:D:190:PRO:C	4:D:191:ASP:CG	2.56	0.72
38:k:521:ASP:CG	38:k:524:MET:HB2	2.14	0.72
43:y:12:LEU:HD23	43:y:16:ASN:ND2	2.05	0.72
25:a:104:ARG:O	25:a:105:LYS:CB	2.34	0.72
34:2:683:G:H1	34:2:731:C:N4	1.87	0.72
38:k:76:PRO:HG3	38:k:323:ARG:HG3	1.72	0.72
43:y:68:LYS:HG2	43:y:163:LEU:CD2	2.19	0.72
43:y:374:MET:O	43:y:379:VAL:HG21	1.89	0.72
44:v:329:VAL:HG23	44:v:330:ILE:N	2.05	0.72
1:1:18:G:O4'	1:1:61:C:C5'	2.38	0.72
33:i:82:ARG:HH22	33:i:84:GLY:CA	2.03	0.72
38:k:310:ASN:O	38:k:314:ASP:N	2.22	0.72
38:k:328:SER:O	38:k:329:LEU:HD22	1.90	0.72
43:y:75:LYS:O	43:y:79:GLN:HG2	1.90	0.72
43:y:159:GLN:O	43:y:163:LEU:HB3	1.89	0.72
43:y:375:VAL:HG22	43:y:379:VAL:HG11	1.72	0.72
44:v:373:LYS:CD	44:v:420:VAL:CG1	2.67	0.72
44:v:504:LEU:HD21	44:v:508:LEU:HD11	1.70	0.72
34:2:1518:C:C5'	39:U:143:GLY:O	2.38	0.72
34:2:1707:A:H2	34:2:1708:C:C2	2.01	0.72
38:k:174:ASP:O	38:k:177:PRO:HD2	1.89	0.71
38:k:204:LEU:CD1	38:k:224:ARG:NH1	2.53	0.71
43:y:101:THR:HG22	43:y:149:TRP:HB3	0.76	0.71
43:y:124:PRO:HG2	43:y:128:LEU:N	2.05	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:y:179:GLN:CA	43:y:179:GLN:HE21	2.00	0.71
43:y:227:SER:CB	43:y:228:MET:HE2	2.20	0.71
43:y:366:THR:O	43:y:370:LEU:HG	1.90	0.71
38:k:164:LEU:HD21	38:k:237:ILE:CD1	2.20	0.71
41:3:70:G:H3'	41:3:70:G:N3	2.04	0.71
43:y:8:PRO:CG	43:y:39:LYS:CD	2.66	0.71
34:2:748:G:N2	34:2:749:C:O2	2.23	0.71
37:j:21:SER:O	37:j:23:LYS:HG3	1.90	0.71
38:k:450:GLN:HE21	38:k:452:GLU:HB3	1.55	0.71
43:y:11:ALA:HB2	43:y:34:VAL:HG21	1.71	0.71
44:v:425:LEU:HD12	44:v:427:GLU:HG2	1.71	0.71
6:F:3:VAL:CG2	6:F:4:GLN:N	2.49	0.71
35:A:54:ARG:HH21	35:A:54:ARG:HB2	1.53	0.71
43:y:150:VAL:CG1	43:y:188:TYR:CE1	2.72	0.71
43:y:166:ASN:HB3	43:y:203:MET:CG	2.20	0.71
44:v:426:GLU:H	44:v:427:GLU:HG2	1.55	0.71
44:v:512:TYR:CZ	44:v:674:HIS:HE1	2.08	0.71
25:a:104:ARG:HH22	25:a:108:LYS:HZ2	1.29	0.71
38:k:315:GLY:O	38:k:316:TYR:HB3	1.89	0.71
43:y:179:GLN:O	43:y:183:LYS:HD2	1.89	0.71
34:2:683:G:H2'	34:2:684:A:C8	2.24	0.71
34:2:733:G:C5	34:2:738:U:O4	2.44	0.71
43:y:91:ARG:NH1	43:y:173:LEU:HD12	2.06	0.71
43:y:179:GLN:HE21	43:y:179:GLN:N	1.88	0.71
43:y:210:ARG:CG	43:y:212:HIS:CE1	2.73	0.71
43:y:299:LEU:O	43:y:321:ARG:NH1	2.23	0.71
43:y:323:LEU:HG	43:y:324:LEU:N	2.04	0.71
35:A:205:ILE:HD13	36:B:288:LYS:HG3	1.71	0.71
37:j:40:LYS:HD3	37:j:41:MET:N	2.04	0.71
38:k:412:LYS:CB	38:k:485:ILE:HA	2.10	0.71
43:y:208:ILE:CD1	43:y:262:LEU:HD22	1.89	0.71
43:y:333:PRO:CG	43:y:437:LEU:CD2	2.68	0.71
44:v:418:ILE:HD12	44:v:418:ILE:N	2.06	0.71
44:v:521:ARG:HH11	44:v:542:GLU:HG3	1.54	0.71
27:c:73:LEU:HD22	27:c:73:LEU:N	2.05	0.71
38:k:237:ILE:O	38:k:238:PHE:CD2	2.42	0.71
40:R:143:PRO:HG3	41:3:55:G:N3	2.05	0.71
44:v:376:PHE:O	44:v:378:ILE:N	2.22	0.71
44:v:517:LYS:O	44:v:542:GLU:OE2	2.09	0.71
44:v:554:TYR:C	44:v:557:ALA:H	1.99	0.71
28:d:38:THR:O	42:m:296:ASN:OD1	2.09	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:2:80:G:H2'	34:2:81:U:H6	1.56	0.71
38:k:218:SER:HB3	53:k:705:GNP:C2'	2.19	0.71
33:i:82:ARG:HH21	33:i:85:LYS:CA	2.03	0.70
34:2:745:U:H2'	34:2:746:C:C5	2.25	0.70
37:j:70:TRP:CE2	40:R:143:PRO:HG3	2.27	0.70
41:3:60:C:H3'	41:3:61:C:H4'	1.72	0.70
24:Z:96:GLU:OE2	38:k:34:MET:HE3	1.91	0.70
34:2:1518:C:O3'	39:U:144:ARG:CA	2.38	0.70
27:c:33:MET:SD	27:c:79:PHE:CE1	2.84	0.70
34:2:1112:C:HO2'	34:2:1113:C:P	2.13	0.70
34:2:1707:A:C4	34:2:1708:C:C5	2.79	0.70
38:k:188:LEU:CD1	38:k:225:PHE:HE1	2.03	0.70
38:k:318:PRO:HB3	38:k:322:LEU:HA	1.65	0.70
43:y:323:LEU:O	43:y:327:LEU:HD13	1.91	0.70
43:y:330:PRO:CA	43:y:431:LEU:HD13	2.19	0.70
44:v:553:LYS:O	44:v:557:ALA:N	2.24	0.70
34:2:80:G:H2'	34:2:81:U:C6	2.26	0.70
34:2:1112:C:O2'	34:2:1113:C:P	2.50	0.70
34:2:1707:A:C4	34:2:1708:C:C6	2.80	0.70
44:v:373:LYS:HA	44:v:376:PHE:CD2	2.24	0.70
44:v:402:LEU:O	44:v:405:ILE:HG22	1.90	0.70
37:j:47:LEU:CD1	37:j:48:GLU:H	2.03	0.70
38:k:319:THR:HG23	38:k:320:GLU:HB2	1.70	0.70
38:k:374:ILE:CD1	38:k:529:ALA:HA	2.21	0.70
44:v:499:ILE:HG21	44:v:503:TYR:CE2	2.19	0.70
34:2:740:G:N2	34:2:794:G:O4'	2.23	0.70
43:y:147:THR:O	43:y:150:VAL:HG23	1.90	0.70
43:y:363:ALA:HB1	43:y:364:PRO:HD3	1.71	0.70
43:y:381:GLN:HA	43:y:381:GLN:NE2	2.06	0.70
44:v:554:TYR:C	44:v:557:ALA:HB3	2.14	0.70
37:j:47:LEU:HD12	37:j:48:GLU:N	2.04	0.70
38:k:591:SER:C	38:k:592:GLY:CA	2.63	0.70
40:R:133:ILE:C	40:R:139:SER:HG	1.98	0.70
43:y:167:ASN:O	43:y:168:SER:HB3	1.90	0.70
44:v:358:VAL:HG13	44:v:359:GLN:N	2.02	0.70
44:v:424:ILE:HD12	44:v:424:ILE:N	2.06	0.70
25:a:128:GLY:CA	38:k:264:ASN:HB3	2.22	0.70
34:2:1327:C:N4	37:j:15:GLY:O	2.25	0.70
43:y:385:PRO:HA	43:y:388:LYS:HG3	1.73	0.70
41:3:71:A:H5''	41:3:73:G:H1'	1.74	0.70
44:v:332:LYS:HA	44:v:335:GLU:CG	2.21	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:v:438:LEU:O	44:v:442:GLY:N	2.25	0.70
4:D:160:GLN:NE2	34:2:1118:A:OP1	2.23	0.70
16:P:19:ARG:NH1	27:c:84:HIS:NE2	2.39	0.70
1:1:16:G:C6	1:1:17:C:C5	2.75	0.69
34:2:1108:U:O2'	34:2:1109:A:H5''	1.90	0.69
35:A:185:THR:OG1	35:A:186:PRO:HA	1.92	0.69
38:k:311:ILE:O	38:k:317:VAL:HG23	1.92	0.69
43:y:108:SER:HB2	43:y:145:LEU:HB3	1.73	0.69
43:y:340:ARG:N	43:y:340:ARG:CD	2.48	0.69
44:v:336:ILE:HD12	44:v:354:LEU:CD2	2.22	0.69
44:v:434:VAL:HG12	44:v:435:ASP:H	1.57	0.69
1:1:35:A:OP2	18:S:146:ARG:NH2	2.25	0.69
43:y:386:GLU:OE2	43:y:414:VAL:HA	1.92	0.69
24:Z:96:GLU:CD	38:k:34:MET:HE3	2.16	0.69
40:R:130:ARG:HH11	40:R:130:ARG:CB	2.05	0.69
41:3:58:C:N3	41:3:59:A:C6	2.60	0.69
44:v:413:PHE:CE1	44:v:489:TYR:CD1	2.79	0.69
28:d:51:ARG:CZ	42:m:415:SER:HB2	2.22	0.69
33:i:80:LEU:HD23	37:j:62:ARG:NH2	2.04	0.69
43:y:108:SER:CB	43:y:145:LEU:HD22	2.20	0.69
43:y:205:LEU:CD1	43:y:209:GLN:CG	2.66	0.69
10:J:109:ARG:CG	34:2:794:G:H1'	2.22	0.69
43:y:237:LEU:O	43:y:241:ILE:HG12	1.92	0.69
43:y:276:TYR:HH	43:y:298:ARG:HG2	1.52	0.69
43:y:323:LEU:HG	43:y:324:LEU:H	1.57	0.69
43:y:323:LEU:HD13	43:y:424:LEU:HB2	1.74	0.69
43:y:326:THR:CG2	43:y:391:TYR:CE2	2.74	0.69
43:y:375:VAL:HG13	43:y:379:VAL:HB	1.74	0.69
44:v:347:ARG:C	44:v:385:TYR:CD1	2.67	0.69
44:v:400:LYS:O	44:v:400:LYS:HD2	1.92	0.69
44:v:469:TYR:HE1	44:v:473:LEU:CD2	2.01	0.69
34:2:1818:A:O4'	37:j:44:ASN:O	2.11	0.69
38:k:223:GLN:HG2	38:k:247:LEU:HD11	1.73	0.69
43:y:276:TYR:HD2	43:y:302:LEU:HD22	1.57	0.69
43:y:331:ILE:CD1	43:y:427:TYR:O	2.40	0.69
44:v:438:LEU:O	44:v:438:LEU:HD23	1.92	0.69
44:v:469:TYR:CE1	44:v:473:LEU:HD11	2.28	0.69
38:k:316:TYR:C	38:k:318:PRO:HD3	2.18	0.69
43:y:280:SER:O	43:y:292:HIS:HD2	1.75	0.69
38:k:85:HIS:HB2	38:k:130:ASN:HD21	1.57	0.69
38:k:375:MET:SD	38:k:531:ARG:HB2	2.32	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:y:6:GLN:C	43:y:7:ARG:HG3	2.18	0.69
43:y:166:ASN:HB3	43:y:203:MET:HG2	1.73	0.69
43:y:276:TYR:CZ	43:y:298:ARG:HB3	2.28	0.69
43:y:384:VAL:O	43:y:387:VAL:HG12	1.93	0.69
27:c:36:LYS:N	27:c:78:SER:HB2	2.07	0.69
27:c:73:LEU:O	27:c:74:THR:HG22	1.93	0.69
34:2:737:C:C3'	34:2:738:U:H5''	2.22	0.69
38:k:85:HIS:HA	38:k:131:LEU:H	1.56	0.69
38:k:492:LEU:CB	38:k:497:ARG:CG	2.69	0.69
41:3:63:G:H3'	41:3:63:G:N3	2.08	0.69
43:y:249:ALA:O	43:y:253:VAL:HG13	1.92	0.69
43:y:300:TYR:O	43:y:321:ARG:NH1	2.25	0.69
6:F:196:GLY:CA	6:F:197:LYS:C	2.66	0.69
38:k:5:LEU:C	38:k:5:LEU:HD12	2.18	0.69
38:k:204:LEU:CG	38:k:224:ARG:CZ	2.61	0.69
38:k:331:PHE:CG	38:k:332:LYS:N	2.58	0.69
43:y:12:LEU:HD22	43:y:16:ASN:HD21	1.55	0.69
43:y:42:THR:HB	43:y:77:ILE:O	1.92	0.69
43:y:398:PHE:HE1	43:y:512:GLN:OE1	1.70	0.69
44:v:484:GLU:O	44:v:487:GLN:HB3	1.93	0.69
11:K:193:LYS:CE	14:N:32:LYS:HZ1	1.97	0.68
34:2:1518:C:H5'	39:U:143:GLY:C	2.17	0.68
43:y:116:GLU:OE1	43:y:138:GLN:HA	1.93	0.68
43:y:121:ILE:HD12	43:y:121:ILE:C	2.17	0.68
44:v:345:THR:HG21	44:v:347:ARG:HB2	1.71	0.68
44:v:379:ILE:HD11	44:v:447:LEU:CD1	2.23	0.68
44:v:760:LYS:NZ	44:v:765:VAL:HG21	2.08	0.68
25:a:127:ALA:C	38:k:265:PRO:HB3	2.18	0.68
34:2:1518:C:H5'	39:U:144:ARG:CG	2.18	0.68
43:y:276:TYR:CZ	43:y:298:ARG:CB	2.75	0.68
43:y:380:LEU:H	43:y:380:LEU:CD2	2.06	0.68
33:i:75:LYS:NZ	37:j:27:VAL:CG2	2.56	0.68
38:k:311:ILE:HB	38:k:317:VAL:CB	2.24	0.68
38:k:315:GLY:HA2	38:k:326:ASP:CB	2.22	0.68
43:y:270:GLN:CG	43:y:271:LEU:H	2.05	0.68
44:v:445:LEU:HD23	44:v:445:LEU:C	2.19	0.68
6:F:2:ALA:HA	6:F:3:VAL:O	1.93	0.68
8:H:61:PHE:CE1	42:m:415:SER:HB2	2.28	0.68
33:i:75:LYS:HZ3	37:j:27:VAL:CG2	2.06	0.68
34:2:793:C:O2'	34:2:794:G:H4'	1.93	0.68
38:k:164:LEU:HD11	38:k:237:ILE:HD13	1.73	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:v:441:ARG:NE	44:v:441:ARG:HA	2.09	0.68
38:k:332:LYS:O	38:k:332:LYS:NZ	2.26	0.68
44:v:458:ILE:C	44:v:460:GLN:H	2.02	0.68
16:P:27:LYS:HG3	16:P:28:LEU:CD2	2.24	0.68
35:A:58:SER:HB2	35:A:61:LYS:CD	2.23	0.68
43:y:166:ASN:CG	43:y:203:MET:SD	2.77	0.68
43:y:246:TRP:CE3	43:y:246:TRP:HA	2.28	0.68
43:y:257:HIS:CD2	43:y:358:LEU:HD23	2.29	0.68
44:v:372:VAL:HG22	44:v:411:ILE:HG21	1.74	0.68
44:v:375:LYS:CG	44:v:408:LEU:HG	2.14	0.68
18:S:145:TYR:C	18:S:146:ARG:CG	2.66	0.68
24:Z:97:ASN:O	38:k:56:ILE:HD12	1.94	0.68
38:k:412:LYS:CA	38:k:484:LEU:O	2.40	0.68
34:2:795:U:OP2	34:2:795:U:H4'	1.93	0.68
38:k:73:VAL:CA	38:k:322:LEU:HD22	2.21	0.68
41:3:74:A:H2'	41:3:75:G:H8	1.59	0.68
34:2:685:G:N2	34:2:730:C:C2	2.62	0.68
38:k:241:ASP:O	38:k:242:GLU:C	2.37	0.68
34:2:1705:C:O2'	37:j:42:LEU:CD2	2.42	0.68
43:y:331:ILE:HG21	43:y:430:GLN:NE2	1.01	0.68
8:H:16:ASP:OD2	42:m:204:LYS:CD	2.41	0.67
43:y:48:GLU:HG3	43:y:74:TYR:OH	1.93	0.67
43:y:124:PRO:HG2	43:y:128:LEU:H	1.56	0.67
43:y:278:LYS:O	43:y:281:THR:OG1	2.12	0.67
6:F:196:GLY:HA2	6:F:198:ILE:N	2.08	0.67
27:c:65:GLN:NE2	44:v:343:LYS:HG3	2.06	0.67
35:A:111:ILE:HD11	35:A:183:ARG:NH1	2.09	0.67
38:k:412:LYS:CD	38:k:485:ILE:CG1	2.67	0.67
43:y:246:TRP:HA	43:y:246:TRP:HE3	1.59	0.67
43:y:284:TRP:HB2	43:y:292:HIS:NE2	2.09	0.67
43:y:326:THR:HB	43:y:391:TYR:OH	1.94	0.67
44:v:504:LEU:HD23	44:v:504:LEU:C	2.19	0.67
25:a:123:ALA:O	25:a:127:ALA:CA	2.42	0.67
37:j:9:GLY:N	40:R:140:ARG:HH22	1.90	0.67
38:k:532:VAL:HG21	38:k:551:LEU:HA	1.76	0.67
40:R:141:PHE:O	40:R:142:ILE:HG13	1.92	0.67
43:y:240:ALA:CB	43:y:249:ALA:HB2	2.24	0.67
44:v:335:GLU:HA	44:v:338:GLN:CD	2.19	0.67
44:v:438:LEU:O	44:v:441:ARG:HB3	1.92	0.67
34:2:1518:C:C5'	39:U:143:GLY:C	2.67	0.67
38:k:229:VAL:O	38:k:232:ILE:HG22	1.93	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:A:185:THR:CB	35:A:187:GLN:HB2	2.15	0.67
38:k:212:ARG:NE	38:k:359:GLU:OE2	2.27	0.67
38:k:451:ILE:CG1	38:k:452:GLU:N	2.53	0.67
38:k:488:PRO:HG2	38:k:524:MET:CE	2.23	0.67
44:v:736:HIS:O	44:v:755:PHE:CE1	2.47	0.67
25:a:100:LYS:HG2	25:a:101:LYS:O	1.95	0.67
34:2:472:G:OP1	38:k:63:LYS:NZ	2.28	0.67
35:A:235:TYR:CD1	36:B:285:ASP:HB2	2.28	0.67
38:k:218:SER:CB	53:k:705:GNP:O2'	2.38	0.67
44:v:499:ILE:HG13	44:v:502:VAL:CG1	2.23	0.67
34:2:740:G:O6	34:2:793:C:N3	2.27	0.67
38:k:329:LEU:HG	38:k:495:GLU:HA	1.76	0.67
38:k:412:LYS:HB2	38:k:483:TYR:CE1	2.30	0.67
43:y:277:ASN:OD1	43:y:278:LYS:N	2.28	0.67
43:y:367:ARG:HG2	43:y:368:ILE:N	2.04	0.67
43:y:394:LEU:CD2	43:y:435:THR:CG2	2.72	0.67
44:v:335:GLU:OE2	44:v:336:ILE:HG23	1.94	0.67
44:v:391:THR:O	44:v:392:TYR:HB3	1.95	0.67
44:v:441:ARG:HA	44:v:441:ARG:HE	1.60	0.67
44:v:449:GLU:CD	44:v:505:ARG:NH2	2.21	0.67
44:v:455:PHE:CE1	44:v:476:GLU:HA	2.29	0.67
44:v:512:TYR:CZ	44:v:674:HIS:CE1	2.83	0.67
33:i:81:ALA:CB	37:j:82:ARG:HD3	2.25	0.67
38:k:578:ASN:ND2	38:k:585:ASP:CB	2.58	0.67
43:y:232:THR:HB	43:y:233:ARG:NH2	2.10	0.67
44:v:455:PHE:CZ	44:v:476:GLU:HG2	2.30	0.67
27:c:75:GLU:OE2	44:v:389:LEU:C	2.37	0.67
43:y:8:PRO:CB	43:y:39:LYS:HD3	2.25	0.67
43:y:399:ASN:CG	50:u:313:ILE:HG21	2.19	0.67
34:2:1518:C:H5'	39:U:144:ARG:CA	2.25	0.66
38:k:85:HIS:HB2	38:k:130:ASN:CG	2.18	0.66
38:k:431:LYS:CE	38:k:477:GLY:C	2.68	0.66
44:v:429:GLU:HG3	44:v:430:ASN:N	2.10	0.66
8:H:16:ASP:OD2	42:m:204:LYS:NZ	2.28	0.66
38:k:321:ASN:O	38:k:322:LEU:HB2	1.94	0.66
44:v:409:MET:CB	44:v:485:ARG:HH11	2.08	0.66
44:v:438:LEU:HD23	44:v:438:LEU:C	2.19	0.66
38:k:4:LYS:HA	38:k:79:LEU:HD12	1.77	0.66
38:k:241:ASP:C	38:k:242:GLU:CB	2.68	0.66
38:k:431:LYS:HB3	38:k:477:GLY:O	1.94	0.66
8:H:27:ASP:HA	42:m:472:LYS:HZ3	1.58	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:k:17:LYS:HZ2	38:k:20:LYS:CE	2.08	0.66
38:k:139:ASP:O	38:k:140:TRP:C	2.37	0.66
44:v:477:ALA:O	44:v:480:CYS:HB2	1.95	0.66
33:i:80:LEU:HD21	37:j:62:ARG:HH21	1.56	0.66
34:2:1705:C:O4'	37:j:42:LEU:HD21	1.96	0.66
34:2:471:C:P	38:k:7:ARG:HH22	2.18	0.66
38:k:165:LYS:O	38:k:237:ILE:HG22	1.95	0.66
38:k:200:VAL:CG1	38:k:228:ALA:HA	2.25	0.66
43:y:289:ALA:O	43:y:328:SER:O	2.12	0.66
25:a:9:THR:C	25:a:10:ARG:CG	2.68	0.66
16:P:19:ARG:O	16:P:20:ARG:HB2	1.96	0.66
25:a:101:LYS:HZ2	25:a:107:ARG:CZ	2.07	0.66
34:2:1518:C:O5'	39:U:143:GLY:C	2.39	0.66
34:2:1707:A:C5	34:2:1708:C:C5	2.84	0.66
44:v:336:ILE:HD12	44:v:354:LEU:HD23	1.77	0.66
34:2:1102:C:O2'	34:2:1103:G:C5'	2.43	0.66
38:k:489:SER:O	38:k:497:ARG:NH2	2.29	0.66
43:y:241:ILE:HG22	43:y:282:VAL:CG2	2.23	0.66
43:y:291:PHE:HE1	43:y:359:LEU:CB	2.08	0.66
44:v:429:GLU:HG3	44:v:430:ASN:C	2.21	0.66
37:j:70:TRP:CZ2	41:3:55:G:O2'	2.34	0.66
38:k:332:LYS:O	38:k:333:VAL:C	2.38	0.66
43:y:128:LEU:HD21	44:v:516:TYR:HD2	1.60	0.66
43:y:276:TYR:OH	43:y:298:ARG:CB	2.43	0.66
43:y:117:ASP:OD1	43:y:121:ILE:HG22	1.96	0.65
43:y:147:THR:HA	43:y:150:VAL:CG2	2.27	0.65
43:y:320:THR:O	43:y:323:LEU:HG	1.96	0.65
39:U:148:VAL:CG2	40:R:131:PRO:O	2.44	0.65
37:j:40:LYS:HB2	37:j:40:LYS:HZ3	1.59	0.65
38:k:337:ALA:O	38:k:338:ASN:CB	2.45	0.65
38:k:348:TYR:CD2	38:k:369:PHE:O	2.48	0.65
43:y:150:VAL:HG13	43:y:188:TYR:CE1	2.30	0.65
43:y:231:GLU:O	43:y:235:VAL:HG23	1.96	0.65
44:v:376:PHE:O	44:v:379:ILE:HG12	1.97	0.65
44:v:760:LYS:HD3	44:v:765:VAL:CG1	2.27	0.65
28:d:38:THR:C	42:m:296:ASN:OD1	2.40	0.65
34:2:80:G:C5	34:2:81:U:C4	2.84	0.65
38:k:412:LYS:HD3	38:k:485:ILE:CB	2.25	0.65
44:v:330:ILE:O	44:v:333:LEU:HB3	1.96	0.65
44:v:422:GLU:N	44:v:422:GLU:OE1	2.29	0.65
44:v:492:GLU:HG2	44:v:494:GLY:O	1.97	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:A:58:SER:HB2	35:A:61:LYS:CE	2.25	0.65
44:v:348:ALA:HB2	44:v:385:TYR:CD1	2.26	0.65
44:v:504:LEU:CD2	44:v:508:LEU:HD11	2.26	0.65
43:y:234:LEU:HD23	43:y:234:LEU:H	1.61	0.65
44:v:340:ARG:NH1	44:v:384:ASP:OD2	2.30	0.65
44:v:499:ILE:O	44:v:501:ARG:N	2.30	0.65
24:Z:52:LEU:HD22	38:k:33:ARG:CD	2.27	0.65
38:k:591:SER:CA	38:k:592:GLY:N	2.60	0.65
38:k:237:ILE:O	38:k:238:PHE:CG	2.50	0.65
38:k:311:ILE:CA	38:k:317:VAL:CG2	2.68	0.65
38:k:582:SER:H	38:k:585:ASP:HB3	1.60	0.65
27:c:73:LEU:HD22	27:c:73:LEU:H	1.61	0.65
34:2:739:U:H4'	34:2:740:G:OP2	1.95	0.65
34:2:785:G:N2	34:2:786:C:O2	2.29	0.65
37:j:7:LYS:HG3	37:j:8:GLY:H	1.60	0.65
37:j:70:TRP:CZ2	41:3:55:G:C1'	2.79	0.65
38:k:135:ASP:O	38:k:138:PRO:HD3	1.96	0.65
38:k:489:SER:O	38:k:497:ARG:CZ	2.45	0.65
43:y:283:PHE:HE1	43:y:287:GLY:N	1.94	0.65
43:y:380:LEU:HD23	43:y:380:LEU:N	2.11	0.65
44:v:425:LEU:CD1	44:v:427:GLU:HG2	2.26	0.65
43:y:68:LYS:NZ	43:y:72:TYR:HB2	2.12	0.65
44:v:377:ASN:O	44:v:380:ALA:HB3	1.96	0.65
16:P:25:TRP:O	16:P:26:LEU:HB3	1.95	0.64
16:P:27:LYS:HZ2	16:P:27:LYS:HB2	1.61	0.64
34:2:1707:A:H2'	34:2:1708:C:H5'	1.77	0.64
38:k:73:VAL:HG21	38:k:322:LEU:HD21	1.78	0.64
43:y:205:LEU:CG	43:y:209:GLN:NE2	2.60	0.64
43:y:347:ILE:O	43:y:348:ILE:HG12	1.96	0.64
43:y:398:PHE:CZ	43:y:512:GLN:OE1	2.48	0.64
4:D:76:ASN:CG	4:D:77:ASP:HB3	2.23	0.64
11:K:157:LYS:HD3	14:N:23:VAL:HG11	1.77	0.64
34:2:743:U:H1'	34:2:744:C:H1'	1.78	0.64
34:2:1518:C:P	39:U:143:GLY:C	2.80	0.64
35:A:229:LEU:CB	36:B:284:VAL:HG11	2.23	0.64
37:j:30:GLU:N	37:j:33:GLN:O	2.30	0.64
43:y:291:PHE:CE1	43:y:359:LEU:HB2	2.32	0.64
25:a:128:GLY:HA3	38:k:264:ASN:HB3	1.80	0.64
27:c:59:CYS:CB	44:v:450:ARG:HB2	2.28	0.64
34:2:1109:A:C5	34:2:1110:U:C4	2.84	0.64
37:j:74:SER:O	37:j:75:ASP:CB	2.40	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:k:188:LEU:HD13	38:k:225:PHE:CE1	2.31	0.64
43:y:338:ILE:HG23	43:y:339:ALA:N	2.12	0.64
24:Z:97:ASN:HD21	38:k:34:MET:CE	2.10	0.64
33:i:82:ARG:HH21	33:i:85:LYS:HA	1.63	0.64
35:A:185:THR:OG1	35:A:186:PRO:N	2.30	0.64
38:k:191:LYS:HG3	38:k:229:VAL:HG23	1.79	0.64
43:y:28:LEU:HD11	43:y:66:LEU:HD13	1.78	0.64
44:v:373:LYS:HE2	44:v:431:LEU:HD22	1.75	0.64
44:v:375:LYS:HA	44:v:378:ILE:HG22	1.79	0.64
44:v:429:GLU:OE1	44:v:431:LEU:CB	2.45	0.64
44:v:502:VAL:HG13	44:v:503:TYR:N	2.12	0.64
39:U:146:VAL:HG13	40:R:131:PRO:HG3	0.64	0.64
41:3:69:U:H5	41:3:70:G:C8	2.15	0.64
43:y:14:ARG:HG2	43:y:14:ARG:NH1	2.08	0.64
43:y:118:LEU:O	43:y:119:ASP:HB2	1.97	0.64
43:y:193:GLU:O	43:y:197:LEU:HG	1.98	0.64
4:D:81:PHE:O	4:D:82:ARG:C	2.39	0.64
25:a:104:ARG:NH2	25:a:108:LYS:HE3	2.00	0.64
34:2:478:U:C4	38:k:99:ILE:CD1	2.78	0.64
44:v:409:MET:CG	44:v:485:ARG:HD2	2.20	0.64
34:2:1819:A:N1	37:j:70:TRP:HA	2.13	0.64
38:k:131:LEU:HD12	38:k:143:ILE:HG22	1.78	0.64
43:y:181:ALA:HB3	43:y:196:LYS:CE	2.20	0.64
43:y:280:SER:O	43:y:292:HIS:CD2	2.51	0.64
25:a:10:ARG:HB2	25:a:24:VAL:HB	1.79	0.64
37:j:13:ARG:C	37:j:13:ARG:HD3	2.23	0.64
37:j:94:LYS:CE	37:j:95:TYR:O	2.45	0.64
43:y:331:ILE:HD12	43:y:430:GLN:HG3	1.80	0.64
44:v:409:MET:CB	44:v:485:ARG:NH1	2.61	0.64
34:2:683:G:C6	34:2:684:A:C6	2.86	0.64
43:y:327:LEU:CD1	43:y:327:LEU:H	2.11	0.64
44:v:392:TYR:HE1	44:v:461:ASN:ND2	1.95	0.64
27:c:59:CYS:HB3	44:v:450:ARG:HB2	1.78	0.64
34:2:1327:C:H5	37:j:16:LYS:N	1.94	0.64
37:j:72:ASN:HD22	37:j:72:ASN:N	1.91	0.64
38:k:217:LEU:CG	38:k:221:GLU:HG2	2.17	0.64
40:R:141:PHE:C	40:R:142:ILE:CD1	2.67	0.64
41:3:76:A:H2'	41:3:77:A:C5'	2.17	0.64
27:c:37:CYS:HB2	27:c:38:PRO:HD3	1.80	0.63
35:A:185:THR:OG1	35:A:186:PRO:CA	2.46	0.63
38:k:330:VAL:CG2	38:k:574:ARG:CD	2.70	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:y:175:HIS:CE1	43:y:228:MET:CA	2.72	0.63
43:y:277:ASN:N	43:y:299:LEU:CD1	2.39	0.63
43:y:307:ARG:HH21	43:y:321:ARG:HH21	1.47	0.63
38:k:218:SER:N	53:k:705:GNP:O2'	2.31	0.63
43:y:154:TRP:HH2	43:y:196:LYS:HB2	1.62	0.63
37:j:63:GLY:O	37:j:64:LYS:CG	2.43	0.63
34:2:743:U:H1'	34:2:744:C:O4'	1.98	0.63
34:2:784:G:H2'	34:2:785:G:H5'	1.79	0.63
38:k:159:ILE:HD13	38:k:164:LEU:HB3	1.81	0.63
43:y:300:TYR:HA	43:y:321:ARG:CZ	2.28	0.63
44:v:366:LEU:N	44:v:367:GLY:HA2	2.12	0.63
35:A:54:ARG:HB2	35:A:54:ARG:NH2	2.13	0.63
35:A:205:ILE:CD1	36:B:288:LYS:HG3	2.28	0.63
43:y:366:THR:O	43:y:370:LEU:CD1	2.47	0.63
44:v:354:LEU:HB3	44:v:378:ILE:HD12	1.80	0.63
37:j:94:LYS:HE2	37:j:95:TYR:O	1.99	0.63
43:y:175:HIS:NE2	43:y:227:SER:HB3	2.13	0.63
43:y:330:PRO:O	43:y:331:ILE:CG1	2.47	0.63
44:v:502:VAL:HG13	44:v:503:TYR:H	1.62	0.63
25:a:101:LYS:C	25:a:102:THR:HG1	2.02	0.63
34:2:1107:U:C4	34:2:1108:U:C5	2.87	0.63
35:A:108:VAL:HG23	35:A:150:TYR:CD1	2.32	0.63
38:k:22:ARG:O	38:k:23:GLN:HG2	1.97	0.63
44:v:409:MET:HB2	44:v:485:ARG:NH1	2.13	0.63
44:v:484:GLU:HG3	44:v:488:ARG:HH12	1.63	0.63
34:2:790:A:O5'	34:2:790:A:H8	1.81	0.63
35:A:157:VAL:CB	35:A:180:ILE:HG21	2.27	0.63
35:A:235:TYR:CZ	36:B:285:ASP:OD1	2.52	0.63
38:k:7:ARG:C	38:k:8:ILE:HG12	2.22	0.63
38:k:450:GLN:O	38:k:453:ASN:HB2	1.94	0.63
44:v:374:ILE:HD12	44:v:374:ILE:N	2.06	0.63
16:P:29:THR:N	16:P:32:ASP:OD2	2.32	0.63
35:A:235:TYR:CE1	36:B:285:ASP:CB	2.78	0.63
43:y:7:ARG:CB	43:y:9:GLU:OE2	2.47	0.63
43:y:224:GLU:H	43:y:224:GLU:CD	2.05	0.63
43:y:285:LYS:O	43:y:286:SER:C	2.41	0.63
43:y:346:GLY:HA3	43:y:348:ILE:HG13	1.81	0.63
44:v:455:PHE:HZ	44:v:476:GLU:CG	2.09	0.63
44:v:471:GLU:HA	44:v:474:LYS:HD2	1.80	0.63
38:k:441:PHE:CZ	38:k:454:ILE:HG21	2.33	0.62
38:k:486:ASP:CA	38:k:487:GLU:N	2.62	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:y:19:LEU:HD21	43:y:57:LEU:HD21	1.81	0.62
43:y:108:SER:CA	43:y:145:LEU:HD22	2.29	0.62
43:y:212:HIS:O	43:y:213:ASN:HB2	1.97	0.62
43:y:291:PHE:CE2	43:y:355:LEU:HB3	2.34	0.62
44:v:469:TYR:CZ	44:v:473:LEU:HD21	2.31	0.62
34:2:740:G:C6	34:2:793:C:N3	2.68	0.62
35:A:181:ASN:O	35:A:185:THR:HG23	2.00	0.62
38:k:17:LYS:HG2	38:k:20:LYS:HE3	1.78	0.62
43:y:9:GLU:HB3	43:y:46:ILE:HG12	1.79	0.62
44:v:349:ALA:O	44:v:353:LEU:HG	1.99	0.62
44:v:373:LYS:CD	44:v:420:VAL:HG11	2.29	0.62
35:A:157:VAL:HG11	35:A:180:ILE:HB	1.80	0.62
37:j:92:ILE:HG22	37:j:93:LEU:CB	2.22	0.62
41:3:42:A:O5'	41:3:42:A:H8	1.81	0.62
43:y:3:ALA:O	43:y:4:TYR:HB2	2.00	0.62
43:y:149:TRP:HA	43:y:149:TRP:CE3	2.35	0.62
44:v:337:LEU:C	44:v:337:LEU:HD12	2.24	0.62
11:K:193:LYS:HZ3	14:N:32:LYS:HZ1	0.69	0.62
34:2:685:G:H1	34:2:730:C:H42	1.47	0.62
34:2:740:G:C2	34:2:793:C:O2	2.52	0.62
38:k:32:VAL:O	38:k:32:VAL:HG12	2.00	0.62
38:k:112:ASN:CA	53:k:704:GNP:O3G	2.45	0.62
43:y:366:THR:O	43:y:370:LEU:CG	2.47	0.62
44:v:469:TYR:CE1	44:v:473:LEU:CG	2.82	0.62
25:a:9:THR:C	25:a:10:ARG:HG2	2.23	0.62
28:d:13:ARG:HD3	42:m:426:LYS:NZ	2.14	0.62
35:A:229:LEU:CB	36:B:284:VAL:CG2	2.68	0.62
41:3:34:C:O2'	41:3:35:A:H5'	1.99	0.62
44:v:736:HIS:O	44:v:755:PHE:CG	2.52	0.62
14:N:22:ARG:HH21	14:N:24:LEU:CB	2.10	0.62
34:2:688:U:O5'	34:2:688:U:H6	1.83	0.62
34:2:746:C:H2'	34:2:747:G:N7	2.14	0.62
43:y:161:LEU:O	43:y:165:ARG:N	2.33	0.62
44:v:373:LYS:NZ	44:v:420:VAL:CG1	2.42	0.62
38:k:168:ILE:HG22	38:k:239:MET:HB2	1.81	0.62
38:k:176:ILE:CA	38:k:178:LYS:H	2.13	0.62
38:k:272:VAL:CG1	38:k:273:GLU:H	2.13	0.62
43:y:113:LEU:CD1	43:y:138:GLN:CB	2.72	0.62
34:2:1707:A:C2	34:2:1708:C:C5	2.88	0.62
43:y:368:ILE:CG2	43:y:371:ILE:CG2	2.78	0.62
44:v:383:TYR:HE1	44:v:450:ARG:CG	2.12	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:c:61:THR:OG1	44:v:340:ARG:NH2	2.32	0.62
35:A:235:TYR:CE1	36:B:285:ASP:HB2	2.34	0.62
38:k:414:GLN:CG	38:k:486:ASP:CG	2.73	0.62
43:y:121:ILE:HD12	43:y:121:ILE:O	1.99	0.62
43:y:298:ARG:NH2	43:y:361:LEU:CD1	2.62	0.62
44:v:383:TYR:HE1	44:v:450:ARG:HG2	1.63	0.62
44:v:383:TYR:CE2	44:v:447:LEU:HD22	2.35	0.62
27:c:61:THR:CG2	44:v:384:ASP:OD2	2.48	0.61
34:2:1111:U:H6	34:2:1113:C:N4	1.97	0.61
34:2:1232:G:O2'	40:R:135:ALA:HB2	2.00	0.61
38:k:346:CYS:C	38:k:347:MET:HG3	2.25	0.61
41:3:36:A:C4'	41:3:37:C:OP1	2.33	0.61
44:v:370:VAL:HG22	44:v:370:VAL:O	2.00	0.61
44:v:379:ILE:HA	44:v:382:LEU:HD12	1.82	0.61
44:v:425:LEU:HD12	44:v:425:LEU:C	2.24	0.61
9:I:235:SER:O	9:I:236:SER:C	2.43	0.61
37:j:70:TRP:CE2	40:R:143:PRO:CG	2.83	0.61
43:y:213:ASN:C	43:y:215:SER:H	2.08	0.61
44:v:329:VAL:HG23	44:v:330:ILE:H	1.64	0.61
34:2:471:C:OP2	38:k:7:ARG:NH2	2.33	0.61
37:j:39:ILE:HB	37:j:48:GLU:HG3	1.81	0.61
44:v:358:VAL:CG1	44:v:359:GLN:H	2.10	0.61
44:v:366:LEU:HD12	44:v:366:LEU:C	2.24	0.61
1:1:16:G:C4	1:1:17:C:C5	2.89	0.61
33:i:81:ALA:HB1	37:j:82:ARG:CD	2.30	0.61
34:2:1518:C:P	39:U:143:GLY:CA	2.87	0.61
38:k:517:VAL:HG12	38:k:519:GLU:HG2	1.82	0.61
41:3:37:C:H3'	41:3:38:C:H5'	1.82	0.61
43:y:326:THR:O	43:y:330:PRO:HD2	2.00	0.61
43:y:330:PRO:O	43:y:431:LEU:HD13	2.00	0.61
44:v:492:GLU:HG2	44:v:494:GLY:C	2.26	0.61
38:k:39:ILE:HD11	51:k:701:SF4:S4	2.41	0.61
41:3:43:A:O2'	41:3:44:C:H5'	1.99	0.61
43:y:344:MET:O	43:y:344:MET:HE3	2.00	0.61
44:v:760:LYS:CD	44:v:765:VAL:HB	2.25	0.61
34:2:745:U:O2'	34:2:746:C:O4'	2.18	0.61
44:v:490:LEU:CD1	44:v:499:ILE:HB	2.31	0.61
28:d:53:GLY:C	42:m:419:ALA:HB2	2.16	0.61
35:A:229:LEU:CD1	36:B:284:VAL:HG21	2.29	0.61
40:R:134:GLY:C	40:R:136:THR:H	2.08	0.61
40:R:143:PRO:HB3	41:3:55:G:H1'	1.80	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:20:ARG:HG3	16:P:65:PHE:CE1	2.36	0.61
34:2:682:G:C2	34:2:683:G:N7	2.69	0.61
34:2:733:G:N7	34:2:738:U:C4	2.69	0.61
38:k:441:PHE:HZ	38:k:454:ILE:HG21	1.66	0.61
43:y:366:THR:O	43:y:370:LEU:HD11	2.00	0.61
44:v:375:LYS:HA	44:v:378:ILE:CG2	2.31	0.61
25:a:98:GLU:N	25:a:98:GLU:OE2	2.31	0.61
34:2:751:C:H2'	34:2:752:C:C6	2.35	0.61
34:2:1816:A:C2	34:2:1817:A:N6	2.68	0.61
38:k:345:MET:HG3	38:k:346:CYS:N	2.13	0.61
38:k:584:LYS:C	38:k:586:VAL:N	2.57	0.61
41:3:67:C:O2'	41:3:68:C:H5'	2.00	0.61
43:y:18:PHE:HB2	43:y:27:ALA:HB2	1.81	0.61
43:y:175:HIS:CB	43:y:231:GLU:OE2	2.47	0.61
43:y:397:GLU:HG3	43:y:406:ARG:NH1	2.16	0.61
44:v:500:CYS:HA	44:v:503:TYR:CD2	2.35	0.61
34:2:734:C:C3'	34:2:735:C:H5''	2.31	0.61
34:2:790:A:C6	34:2:791:A:N6	2.69	0.61
34:2:1766:C:O2'	34:2:1767:C:H5'	2.01	0.61
43:y:108:SER:CB	43:y:145:LEU:HB3	2.31	0.61
43:y:276:TYR:HE1	43:y:295:THR:HG23	1.65	0.61
43:y:340:ARG:HD3	43:y:340:ARG:H	1.63	0.61
43:y:368:ILE:HG23	43:y:371:ILE:CG2	2.30	0.61
37:j:78:LEU:HD23	37:j:93:LEU:CG	2.30	0.60
38:k:250:LYS:HE2	38:k:562:LEU:HD22	1.82	0.60
38:k:309:ILE:O	38:k:313:LEU:HD23	2.01	0.60
43:y:163:LEU:HD23	43:y:163:LEU:O	2.00	0.60
43:y:181:ALA:HB2	43:y:196:LYS:HZ1	1.62	0.60
43:y:181:ALA:HB1	43:y:196:LYS:CE	2.24	0.60
43:y:291:PHE:HZ	43:y:356:ALA:N	1.98	0.60
43:y:339:ALA:HB1	43:y:340:ARG:NH1	2.14	0.60
43:y:346:GLY:HA2	43:y:347:ILE:C	2.25	0.60
44:v:386:ASN:O	44:v:388:ASN:N	2.34	0.60
44:v:556:TYR:O	44:v:559:ASP:N	2.34	0.60
27:c:33:MET:SD	27:c:79:PHE:HE1	2.22	0.60
37:j:24:ARG:HA	37:j:25:GLU:HB2	1.83	0.60
43:y:222:ASN:HB3	43:y:226:GLN:CD	2.26	0.60
43:y:226:GLN:O	43:y:230:LEU:HD23	2.01	0.60
43:y:333:PRO:HG2	43:y:437:LEU:CD2	2.31	0.60
44:v:420:VAL:HG21	44:v:440:VAL:HG13	1.81	0.60
34:2:470:G:OP1	38:k:74:ASN:ND2	2.34	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:k:527:TYR:O	38:k:528:LEU:HD12	2.01	0.60
43:y:325:ALA:O	43:y:329:ILE:HG12	2.02	0.60
44:v:326:HIS:C	44:v:329:VAL:HG22	2.25	0.60
44:v:372:VAL:HG22	44:v:411:ILE:HG22	1.83	0.60
8:H:27:ASP:HA	42:m:472:LYS:HZ1	1.65	0.60
33:i:81:ALA:HB1	37:j:82:ARG:HD3	1.82	0.60
44:v:429:GLU:OE1	44:v:431:LEU:HB3	2.01	0.60
34:2:793:C:C2'	34:2:794:G:H4'	2.31	0.60
38:k:188:LEU:HD13	38:k:225:PHE:HD1	1.63	0.60
38:k:311:ILE:HB	38:k:317:VAL:HB	1.82	0.60
43:y:330:PRO:HB3	43:y:431:LEU:HD11	1.80	0.60
43:y:371:ILE:HG23	43:y:372:ASN:H	1.66	0.60
4:D:77:ASP:O	4:D:78:GLU:HB2	2.01	0.60
35:A:178:ASN:O	35:A:182:ARG:CG	2.50	0.60
38:k:158:LYS:O	38:k:163:ASP:HB2	2.01	0.60
38:k:498:LEU:HD11	38:k:523:ILE:CD1	2.19	0.60
44:v:438:LEU:HA	44:v:441:ARG:CB	2.31	0.60
4:D:190:PRO:O	4:D:191:ASP:OD1	2.17	0.60
14:N:23:VAL:O	14:N:23:VAL:HG13	2.02	0.60
34:2:472:G:P	38:k:63:LYS:NZ	2.74	0.60
34:2:478:U:H5	38:k:99:ILE:HD13	1.60	0.60
34:2:744:C:C4	34:2:745:U:O4	2.55	0.60
35:A:55:ARG:CG	35:A:55:ARG:NH1	2.57	0.60
37:j:13:ARG:HD3	37:j:13:ARG:O	2.01	0.60
38:k:330:VAL:HG22	38:k:330:VAL:O	2.02	0.60
43:y:208:ILE:HD12	43:y:208:ILE:O	2.00	0.60
44:v:418:ILE:HG23	44:v:441:ARG:HD2	1.83	0.60
27:c:35:VAL:HG12	27:c:78:SER:HB3	1.69	0.60
33:i:76:VAL:HG11	37:j:62:ARG:NH2	2.16	0.60
37:j:61:ILE:HG22	37:j:62:ARG:N	2.17	0.60
38:k:17:LYS:CG	38:k:20:LYS:CE	2.69	0.60
41:3:49:A:OP2	41:3:49:A:H2	1.84	0.60
43:y:149:TRP:HA	43:y:149:TRP:HE3	1.67	0.60
43:y:291:PHE:CD1	43:y:359:LEU:CD1	2.83	0.60
38:k:188:LEU:CD1	38:k:225:PHE:CD1	2.85	0.60
38:k:425:ARG:NH1	38:k:455:ILE:CD1	2.65	0.60
41:3:69:U:H3'	41:3:69:U:OP2	2.02	0.60
44:v:421:GLY:HA3	44:v:437:PRO:HB3	1.83	0.60
37:j:15:GLY:O	37:j:16:LYS:CG	2.50	0.60
41:3:53:U:O5'	41:3:53:U:H6	1.85	0.60
43:y:124:PRO:CG	43:y:128:LEU:N	2.65	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:y:165:ARG:HH11	43:y:165:ARG:CG	2.15	0.60
44:v:327:ALA:HA	44:v:330:ILE:HG22	1.84	0.60
25:a:101:LYS:HZ3	25:a:107:ARG:NE	1.99	0.59
34:2:479:A:H4'	38:k:150:SER:C	2.27	0.59
38:k:109:VAL:O	38:k:110:GLY:N	2.31	0.59
38:k:414:GLN:OE1	38:k:486:ASP:CG	2.45	0.59
38:k:533:ILE:HG22	38:k:548:PRO:HB3	1.83	0.59
43:y:91:ARG:O	43:y:95:LYS:HG3	2.01	0.59
43:y:329:ILE:HD11	43:y:374:MET:HE1	1.83	0.59
44:v:413:PHE:CD1	44:v:489:TYR:CE2	2.81	0.59
10:J:109:ARG:HD2	34:2:794:G:H1'	1.83	0.59
34:2:1117:G:C5'	34:2:1117:G:H8	2.15	0.59
34:2:1693:C:C1'	41:3:58:C:N4	2.65	0.59
43:y:91:ARG:NH1	43:y:173:LEU:CD1	2.65	0.59
43:y:245:LEU:CB	43:y:248:GLU:CG	2.80	0.59
43:y:248:GLU:CD	43:y:248:GLU:H	2.07	0.59
44:v:327:ALA:O	44:v:331:LYS:HG3	2.01	0.59
44:v:414:ALA:CB	44:v:415:ASN:OD1	2.39	0.59
34:2:1812:A:C2	34:2:1813:A:N9	2.69	0.59
38:k:204:LEU:HD12	38:k:224:ARG:HH12	1.68	0.59
44:v:400:LYS:HD2	44:v:400:LYS:C	2.26	0.59
44:v:409:MET:HG3	44:v:485:ARG:CZ	2.32	0.59
1:1:18:G:C1'	1:1:61:C:H5''	2.29	0.59
24:Z:52:LEU:HD22	38:k:33:ARG:HD3	1.84	0.59
34:2:686:G:H8	34:2:686:G:O5'	1.84	0.59
34:2:1818:A:C4'	37:j:44:ASN:O	2.49	0.59
37:j:76:ILE:HD13	37:j:76:ILE:N	2.16	0.59
38:k:112:ASN:HB3	53:k:704:GNP:O3G	2.01	0.59
43:y:169:ARG:HG2	43:y:170:VAL:HG13	1.83	0.59
28:d:35:MET:CA	42:m:426:LYS:CE	2.70	0.59
34:2:1115:A:H5'	34:2:1116:U:O4	2.02	0.59
38:k:450:GLN:O	38:k:453:ASN:CB	2.47	0.59
41:3:59:A:H8	41:3:59:A:O5'	1.86	0.59
44:v:325:THR:HG23	44:v:326:HIS:NE2	2.17	0.59
44:v:376:PHE:HZ	44:v:441:ARG:HH22	1.48	0.59
27:c:75:GLU:OE2	44:v:389:LEU:O	2.21	0.59
37:j:10:LYS:HB2	41:3:54:G:H21	1.68	0.59
37:j:62:ARG:NH1	37:j:64:LYS:HD2	2.18	0.59
38:k:486:ASP:HA	38:k:487:GLU:N	2.17	0.59
43:y:279:VAL:HG13	43:y:280:SER:N	2.18	0.59
44:v:455:PHE:CE1	44:v:476:GLU:HB2	2.37	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:2:790:A:H2'	34:2:791:A:C8	2.37	0.59
37:j:40:LYS:HB2	37:j:40:LYS:HZ2	1.67	0.59
38:k:325:ARG:O	38:k:326:ASP:HB2	2.03	0.59
43:y:293:ALA:CB	43:y:328:SER:O	2.51	0.59
44:v:376:PHE:HZ	44:v:441:ARG:HH21	1.45	0.59
25:a:101:LYS:HG2	25:a:107:ARG:NH2	2.17	0.59
27:c:35:VAL:HG12	27:c:36:LYS:N	2.17	0.59
34:2:682:G:C2	34:2:683:G:C5	2.91	0.59
34:2:1117:G:H8	34:2:1117:G:H5'	1.67	0.59
37:j:41:MET:HE2	37:j:47:LEU:HD22	1.85	0.59
38:k:184:VAL:O	38:k:186:SER:N	2.36	0.59
38:k:329:LEU:CD2	38:k:495:GLU:OE1	2.51	0.59
43:y:154:TRP:CH2	43:y:196:LYS:HB2	2.38	0.59
44:v:325:THR:HG23	44:v:326:HIS:CD2	2.38	0.59
44:v:391:THR:CG2	44:v:392:TYR:N	2.35	0.59
44:v:394:LYS:HD3	44:v:394:LYS:N	2.09	0.59
24:Z:74:LEU:O	38:k:60:ILE:HD12	2.02	0.59
25:a:12:PHE:HZ	34:2:836:C:O2'	1.85	0.59
34:2:743:U:C6	34:2:744:C:C2	2.91	0.59
37:j:70:TRP:HD1	40:R:143:PRO:HA	1.51	0.59
43:y:181:ALA:CB	43:y:196:LYS:HZ3	2.04	0.59
43:y:244:GLU:HB3	44:v:731:GLU:HG3	1.83	0.59
43:y:316:GLN:O	43:y:319:SER:OG	2.17	0.59
44:v:473:LEU:O	44:v:476:GLU:HB3	2.03	0.59
44:v:557:ALA:N	44:v:558:LYS:HB3	2.17	0.59
27:c:73:LEU:C	27:c:74:THR:CG2	2.75	0.59
34:2:1108:U:C2'	34:2:1109:A:C5'	2.78	0.59
34:2:1112:C:C2'	34:2:1113:C:O5'	2.51	0.59
38:k:332:LYS:CD	38:k:527:TYR:CE2	2.85	0.59
38:k:590:LYS:C	38:k:592:GLY:N	2.61	0.59
41:3:43:A:C2'	41:3:44:C:C6	2.86	0.59
43:y:140:ARG:HG3	44:v:466:SER:HA	1.84	0.59
43:y:274:ASN:HA	43:y:277:ASN:ND2	2.18	0.59
43:y:291:PHE:CZ	43:y:356:ALA:CA	2.68	0.59
1:1:35:A:H4'	37:j:8:GLY:C	2.28	0.58
34:2:683:G:N2	34:2:731:C:C2	2.66	0.58
43:y:313:ASP:O	43:y:314:GLU:HG2	2.03	0.58
43:y:318:MET:O	43:y:322:VAL:HG13	2.03	0.58
44:v:325:THR:HG22	44:v:325:THR:O	2.02	0.58
44:v:373:LYS:CE	44:v:420:VAL:HG11	2.33	0.58
44:v:427:GLU:HB3	44:v:428:SER:OG	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:j:40:LYS:CD	37:j:41:MET:H	2.14	0.58
38:k:492:LEU:HB2	38:k:497:ARG:HG2	1.83	0.58
43:y:75:LYS:HA	43:y:86:LEU:HD11	1.84	0.58
43:y:86:LEU:HD22	43:y:165:ARG:NH2	2.18	0.58
44:v:499:ILE:C	44:v:501:ARG:H	2.11	0.58
16:P:27:LYS:HG3	16:P:28:LEU:HD21	1.84	0.58
27:c:38:PRO:HD2	27:c:39:GLY:H	1.69	0.58
34:2:1407:G:H3'	34:2:1408:C:H5''	1.85	0.58
35:A:58:SER:OG	35:A:61:LYS:CG	2.30	0.58
37:j:19:ASN:CG	37:j:20:GLU:HA	2.28	0.58
38:k:348:TYR:O	38:k:349:LYS:HB3	2.01	0.58
38:k:550:THR:OG1	38:k:553:ALA:CB	2.51	0.58
41:3:72:G:H8	41:3:72:G:O5'	1.86	0.58
43:y:250:PHE:CZ	44:v:726:LEU:HD11	2.38	0.58
43:y:394:LEU:HD21	43:y:435:THR:HG21	1.85	0.58
44:v:408:LEU:HD23	44:v:411:ILE:HD12	1.85	0.58
44:v:426:GLU:HB2	44:v:427:GLU:CD	2.27	0.58
16:P:22:VAL:HB	16:P:24:THR:H	1.68	0.58
34:2:683:G:N1	34:2:684:A:C6	2.71	0.58
35:A:205:ILE:CD1	36:B:288:LYS:CG	2.81	0.58
38:k:375:MET:HE1	38:k:531:ARG:HD3	1.80	0.58
38:k:521:ASP:OD2	38:k:524:MET:HB2	2.04	0.58
41:3:73:G:N7	41:3:74:A:N7	2.51	0.58
43:y:201:LEU:CD2	43:y:255:ASP:CG	2.74	0.58
43:y:357:THR:HA	43:y:361:LEU:O	2.04	0.58
44:v:375:LYS:O	44:v:378:ILE:HG22	2.03	0.58
44:v:393:MET:O	44:v:394:LYS:C	2.47	0.58
44:v:500:CYS:HB3	44:v:555:ILE:CG2	2.34	0.58
34:2:682:G:H2'	34:2:683:G:H8	1.68	0.58
37:j:19:ASN:CB	37:j:20:GLU:HA	2.34	0.58
43:y:307:ARG:O	43:y:311:THR:N	2.36	0.58
44:v:430:ASN:HD22	44:v:431:LEU:N	2.01	0.58
44:v:760:LYS:CD	44:v:765:VAL:CG1	2.81	0.58
16:P:19:ARG:NH2	16:P:21:SER:OG	2.37	0.58
28:d:53:GLY:C	42:m:416:GLN:OE1	2.46	0.58
34:2:1707:A:C6	34:2:1708:C:C5	2.92	0.58
37:j:70:TRP:CZ2	40:R:143:PRO:HB3	2.39	0.58
38:k:414:GLN:HE21	38:k:486:ASP:CB	2.04	0.58
44:v:441:ARG:HE	44:v:441:ARG:CA	2.16	0.58
16:P:23:PRO:O	16:P:25:TRP:N	2.37	0.58
34:2:793:C:H4'	34:2:793:C:OP1	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:k:229:VAL:HA	38:k:232:ILE:HG22	1.86	0.58
43:y:39:LYS:HG3	43:y:41:ARG:HH21	1.67	0.58
43:y:61:LEU:O	43:y:62:ARG:HG3	2.02	0.58
43:y:79:GLN:C	43:y:81:VAL:N	2.61	0.58
43:y:267:PRO:O	43:y:268:LYS:HB2	2.03	0.58
43:y:394:LEU:O	43:y:438:ARG:NH1	2.37	0.58
44:v:489:TYR:O	44:v:490:LEU:HB2	2.03	0.58
44:v:490:LEU:HD21	44:v:499:ILE:HG21	1.84	0.58
44:v:492:GLU:H	44:v:494:GLY:N	2.01	0.58
40:R:133:ILE:C	40:R:135:ALA:H	2.10	0.58
43:y:124:PRO:O	43:y:125:GLU:HB3	2.03	0.58
43:y:199:ASP:OD1	43:y:202:ARG:NH2	2.37	0.58
43:y:383:VAL:O	43:y:388:LYS:HD2	2.03	0.58
43:y:393:TRP:HA	43:y:397:GLU:HB3	1.86	0.58
1:1:27:C:C4	1:1:28:U:C5	2.92	0.58
4:D:73:ASP:HB2	17:Q:128:ARG:HH22	1.67	0.58
34:2:784:G:C5	34:2:785:G:N7	2.71	0.58
35:A:157:VAL:CG1	35:A:180:ILE:HD12	2.33	0.58
35:A:235:TYR:CD1	36:B:285:ASP:OD1	2.33	0.58
38:k:4:LYS:CG	38:k:79:LEU:HD12	2.32	0.58
38:k:331:PHE:HA	38:k:523:ILE:CG2	2.34	0.58
53:k:705:GNP:H3'	53:k:705:GNP:O1A	2.04	0.58
44:v:373:LYS:CE	44:v:440:VAL:HG21	2.33	0.58
44:v:438:LEU:CA	44:v:441:ARG:HB3	2.34	0.58
10:J:106:ARG:HD3	34:2:794:G:C6	2.38	0.58
16:P:27:LYS:HE3	16:P:28:LEU:CD2	2.34	0.58
27:c:75:GLU:OE1	44:v:388:ASN:CG	2.46	0.58
34:2:743:U:H3	34:2:791:A:H2	1.51	0.58
34:2:784:G:C2'	34:2:785:G:H5'	2.33	0.58
38:k:319:THR:HG23	38:k:320:GLU:HB3	1.85	0.58
38:k:373:GLU:O	38:k:514:THR:HA	2.03	0.58
43:y:59:VAL:CG2	43:y:93:TYR:CE1	2.85	0.58
44:v:355:GLN:O	44:v:358:VAL:HG12	2.04	0.58
44:v:469:TYR:CD1	44:v:473:LEU:HD11	2.39	0.58
44:v:511:TYR:HB2	44:v:575:HIS:NE2	2.19	0.58
27:c:75:GLU:OE2	44:v:390:ALA:CB	2.51	0.57
34:2:471:C:P	38:k:7:ARG:NH2	2.76	0.57
34:2:526:A:H62	34:2:537:G:H21	1.51	0.57
34:2:683:G:O2'	34:2:684:A:H5'	2.04	0.57
34:2:1170:U:H2'	34:2:1171:G:C8	2.39	0.57
38:k:105:VAL:HG23	38:k:263:ILE:HG12	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:y:48:GLU:OE2	43:y:85:SER:HA	2.03	0.57
43:y:297:HIS:NE2	43:y:329:ILE:HD11	2.19	0.57
43:y:399:ASN:ND2	50:u:313:ILE:HG21	2.19	0.57
44:v:383:TYR:O	44:v:385:TYR:N	2.37	0.57
33:i:80:LEU:HD11	37:j:92:ILE:HD13	1.85	0.57
34:2:1112:C:H2'	34:2:1113:C:O5'	2.04	0.57
38:k:508:ILE:HD12	38:k:515:ALA:HB2	1.86	0.57
43:y:329:ILE:HD12	43:y:370:LEU:CB	2.34	0.57
44:v:407:GLU:O	44:v:410:ASP:HB2	2.04	0.57
4:D:71:LEU:O	4:D:75:GLN:HB3	2.03	0.57
8:H:16:ASP:OD2	42:m:204:LYS:HD2	2.04	0.57
25:a:123:ALA:C	25:a:127:ALA:HB3	2.27	0.57
27:c:35:VAL:O	27:c:36:LYS:HB2	2.02	0.57
44:v:455:PHE:CE1	44:v:476:GLU:CA	2.86	0.57
43:y:186:LEU:HA	43:y:243:MET:HE2	1.86	0.57
43:y:245:LEU:O	43:y:246:TRP:HE3	1.88	0.57
43:y:323:LEU:HD13	43:y:424:LEU:HD22	1.84	0.57
43:y:331:ILE:HD12	43:y:430:GLN:CG	2.35	0.57
44:v:434:VAL:HG12	44:v:435:ASP:N	2.18	0.57
11:K:193:LYS:HE2	14:N:32:LYS:HZ3	1.63	0.57
27:c:75:GLU:OE2	44:v:390:ALA:HB3	2.04	0.57
34:2:746:C:C2'	34:2:747:G:C8	2.86	0.57
36:B:284:VAL:CG1	36:B:285:ASP:HB3	2.31	0.57
37:j:19:ASN:HB3	37:j:20:GLU:HA	1.86	0.57
38:k:229:VAL:HG13	38:k:230:VAL:N	2.19	0.57
38:k:217:LEU:HB3	38:k:221:GLU:CB	2.32	0.57
38:k:331:PHE:O	38:k:498:LEU:HD22	2.05	0.57
43:y:227:SER:HB2	43:y:228:MET:CE	2.30	0.57
43:y:233:ARG:CD	43:y:256:ILE:CD1	2.38	0.57
43:y:259:LEU:O	43:y:263:SER:CB	2.53	0.57
43:y:284:TRP:CG	43:y:427:TYR:OH	2.55	0.57
43:y:374:MET:O	43:y:374:MET:HG2	2.05	0.57
44:v:382:LEU:HD13	44:v:400:LYS:HE3	1.84	0.57
44:v:429:GLU:OE1	44:v:431:LEU:HB2	2.05	0.57
44:v:504:LEU:O	44:v:507:ILE:HG12	2.05	0.57
33:i:77:HIS:HA	37:j:33:GLN:HE22	1.68	0.57
37:j:9:GLY:CA	40:R:140:ARG:HH12	2.18	0.57
38:k:322:LEU:HG	38:k:323:ARG:N	2.18	0.57
38:k:348:TYR:O	38:k:349:LYS:CB	2.52	0.57
43:y:68:LYS:HG3	43:y:163:LEU:CD2	2.35	0.57
1:1:18:G:O6	35:A:107:THR:HG21	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:2:750:G:C6	34:2:751:C:N4	2.73	0.57
34:2:787:C:H2'	34:2:788:C:C5	2.38	0.57
34:2:1707:A:C2	34:2:1708:C:C4	2.92	0.57
37:j:28:PHE:O	37:j:78:LEU:HD11	2.05	0.57
38:k:414:GLN:HE21	38:k:486:ASP:CA	2.17	0.57
43:y:26:PRO:HD2	43:y:27:ALA:H	1.70	0.57
43:y:371:ILE:HG23	43:y:372:ASN:N	2.20	0.57
43:y:380:LEU:O	43:y:388:LYS:NZ	2.38	0.57
43:y:385:PRO:CB	43:y:388:LYS:HD3	2.19	0.57
44:v:379:ILE:HG22	44:v:382:LEU:HD12	1.86	0.57
44:v:445:LEU:O	44:v:448:VAL:HG12	2.04	0.57
34:2:454:A:N1	38:k:578:ASN:OD1	2.37	0.57
34:2:683:G:C6	34:2:684:A:N6	2.73	0.57
35:A:197:VAL:HG21	35:A:235:TYR:HE2	1.68	0.57
38:k:237:ILE:HG13	38:k:238:PHE:H	1.70	0.57
44:v:331:LYS:O	44:v:334:ASN:HB2	2.05	0.57
34:2:740:G:H2'	34:2:741:C:H5''	1.87	0.57
34:2:1518:C:OP1	39:U:143:GLY:N	2.37	0.57
34:2:1518:C:O3'	39:U:144:ARG:HA	2.01	0.57
34:2:1696:C:C2	37:j:11:ASN:OD1	2.58	0.57
38:k:139:ASP:O	38:k:141:GLN:N	2.38	0.57
38:k:583:ILE:CG2	38:k:584:LYS:H	2.13	0.57
43:y:63:LYS:HD2	43:y:66:LEU:HD12	1.87	0.57
43:y:107:GLU:CG	43:y:145:LEU:HD21	2.35	0.57
43:y:390:LEU:HD11	43:y:410:VAL:O	2.03	0.57
14:N:25:LEU:CD2	14:N:29:GLY:HA3	2.35	0.56
34:2:472:G:P	38:k:63:LYS:HZ1	2.28	0.56
37:j:16:LYS:HE2	41:3:57:G:HO2'	1.68	0.56
43:y:159:GLN:O	43:y:159:GLN:HG2	2.05	0.56
43:y:283:PHE:O	43:y:285:LYS:N	2.38	0.56
44:v:409:MET:CB	44:v:485:ARG:HD3	2.34	0.56
44:v:411:ILE:O	44:v:411:ILE:HG22	2.04	0.56
34:2:1117:G:H5'	34:2:1117:G:C8	2.39	0.56
43:y:270:GLN:C	43:y:272:MET:H	2.13	0.56
4:D:71:LEU:CD1	4:D:84:PHE:CZ	2.88	0.56
34:2:1109:A:C5	34:2:1110:U:N3	2.73	0.56
37:j:94:LYS:HG2	37:j:95:TYR:H	1.65	0.56
38:k:315:GLY:HA2	38:k:326:ASP:CA	2.35	0.56
41:3:49:A:H2'	41:3:50:C:O4'	2.05	0.56
43:y:153:LEU:HD22	43:y:157:TYR:CE2	2.40	0.56
43:y:257:HIS:CD2	43:y:358:LEU:CD2	2.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:v:332:LYS:CA	44:v:335:GLU:HG3	2.30	0.56
44:v:507:ILE:O	44:v:511:TYR:HB3	2.06	0.56
43:y:74:TYR:O	43:y:78:CYS:SG	2.64	0.56
43:y:259:LEU:O	43:y:263:SER:N	2.38	0.56
43:y:275:TYR:CD1	43:y:278:LYS:NZ	2.73	0.56
44:v:431:LEU:CD1	44:v:434:VAL:HB	2.35	0.56
1:l:17:C:N4	1:l:60:A:C2	2.66	0.56
44:v:373:LYS:O	44:v:376:PHE:HB2	2.06	0.56
44:v:389:LEU:O	44:v:390:ALA:HB2	2.06	0.56
44:v:431:LEU:O	44:v:431:LEU:HG	2.05	0.56
4:D:39:PHE:HB3	4:D:74:LEU:CD2	2.35	0.56
4:D:75:GLN:HG3	4:D:75:GLN:O	2.06	0.56
28:d:33:GLU:CD	42:m:426:LYS:NZ	2.64	0.56
34:2:745:U:C2	34:2:746:C:C4	2.94	0.56
38:k:21:CYS:O	38:k:24:GLU:OE2	2.22	0.56
41:3:65:C:H1'	41:3:66:U:C6	2.40	0.56
43:y:24:LYS:HD3	43:y:61:LEU:HG	1.86	0.56
43:y:278:LYS:HD2	43:y:278:LYS:C	2.30	0.56
44:v:358:VAL:HA	44:v:361:ALA:HB3	1.86	0.56
44:v:393:MET:O	44:v:397:MET:CE	2.36	0.56
4:D:39:PHE:CG	4:D:74:LEU:CD2	2.89	0.56
25:a:104:ARG:HD2	34:2:482:C:OP2	2.05	0.56
38:k:19:LYS:O	38:k:19:LYS:HG3	2.06	0.56
43:y:184:PHE:CD1	43:y:188:TYR:CE2	2.92	0.56
43:y:288:ASN:C	43:y:290:LEU:H	2.13	0.56
44:v:487:GLN:OE1	44:v:502:VAL:HG22	2.05	0.56
24:Z:58:GLU:OE1	37:j:60:HIS:ND1	2.34	0.56
34:2:1707:A:C6	34:2:1708:C:N4	2.73	0.56
38:k:489:SER:CA	38:k:524:MET:CE	2.84	0.56
43:y:223:PRO:HB2	43:y:224:GLU:OE1	2.06	0.56
16:P:29:THR:O	16:P:30:SER:C	2.48	0.56
34:2:734:C:C5	34:2:737:C:N4	2.73	0.56
34:2:848:G:H3'	34:2:849:C:H5''	1.87	0.56
38:k:183:THR:O	38:k:187:ILE:HB	2.05	0.56
38:k:441:PHE:HZ	38:k:454:ILE:CG2	2.14	0.56
43:y:154:TRP:HA	43:y:154:TRP:HE3	1.71	0.56
44:v:739:ALA:HB3	44:v:755:PHE:HE1	0.75	0.56
44:v:760:LYS:HZ2	44:v:765:VAL:HG11	1.65	0.56
25:a:104:ARG:HB2	34:2:481:C:P	2.46	0.56
34:2:80:G:C4	34:2:81:U:C5	2.93	0.56
34:2:1518:C:H4'	39:U:144:ARG:C	2.31	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:y:150:VAL:HG12	43:y:188:TYR:CD2	2.40	0.56
43:y:291:PHE:CE1	43:y:359:LEU:CG	2.89	0.56
44:v:375:LYS:CA	44:v:378:ILE:HG22	2.36	0.56
44:v:397:MET:SD	44:v:398:TRP:N	2.79	0.56
6:F:1:MET:O	6:F:2:ALA:HB2	2.06	0.55
38:k:76:PRO:CG	38:k:323:ARG:HG3	2.36	0.55
38:k:330:VAL:HG22	38:k:575:PRO:CD	2.23	0.55
38:k:489:SER:HA	38:k:524:MET:HE1	1.85	0.55
16:P:27:LYS:O	16:P:28:LEU:HG	2.06	0.55
35:A:263:GLU:HG2	35:A:269:PHE:CD1	2.41	0.55
38:k:187:ILE:CG2	38:k:188:LEU:H	2.06	0.55
38:k:204:LEU:HD12	38:k:224:ARG:NH1	2.21	0.55
38:k:212:ARG:NH2	53:k:705:GNP:N3	2.53	0.55
44:v:490:LEU:HG	44:v:490:LEU:O	2.06	0.55
14:N:22:ARG:NH2	14:N:23:VAL:O	2.38	0.55
16:P:22:VAL:HB	16:P:23:PRO:C	2.31	0.55
43:y:48:GLU:OE2	43:y:85:SER:CA	2.53	0.55
43:y:205:LEU:CG	43:y:209:GLN:HE21	2.08	0.55
43:y:342:LEU:HD22	44:v:702:GLU:HG3	1.89	0.55
43:y:353:ARG:HD3	43:y:353:ARG:O	2.05	0.55
10:J:75:ILE:HG23	10:J:76:GLN:H	1.70	0.55
38:k:204:LEU:CB	38:k:224:ARG:NH1	2.57	0.55
38:k:492:LEU:C	38:k:497:ARG:NE	2.63	0.55
38:k:315:GLY:O	38:k:316:TYR:CD1	2.58	0.55
38:k:318:PRO:C	38:k:319:THR:HG22	2.32	0.55
38:k:318:PRO:O	38:k:319:THR:HG22	2.06	0.55
43:y:273:ALA:HA	43:y:302:LEU:HD23	1.87	0.55
27:c:73:LEU:H	27:c:73:LEU:CD2	2.19	0.55
28:d:33:GLU:CD	42:m:426:LYS:HZ3	2.14	0.55
38:k:315:GLY:C	38:k:326:ASP:HB3	2.31	0.55
38:k:559:LEU:HB2	38:k:594:TYR:CD2	2.41	0.55
41:3:73:G:C5	41:3:74:A:C5	2.94	0.55
43:y:300:TYR:HE1	43:y:318:MET:HE3	1.72	0.55
43:y:366:THR:C	43:y:370:LEU:HG	2.31	0.55
4:D:78:GLU:HG3	43:y:10:ASN:ND2	2.21	0.55
16:P:22:VAL:CG2	16:P:24:THR:H	2.20	0.55
25:a:128:GLY:HA3	38:k:264:ASN:CB	2.35	0.55
34:2:681:U:O2	34:2:681:U:H2'	2.07	0.55
34:2:1112:C:O2	34:2:1113:C:C2	2.59	0.55
38:k:165:LYS:N	38:k:236:ASP:HB3	2.22	0.55
38:k:309:ILE:HG22	38:k:313:LEU:HD21	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:y:114:ASP:O	43:y:118:LEU:CB	2.47	0.55
43:y:179:GLN:HG3	43:y:183:LYS:HZ1	1.72	0.55
43:y:258:GLY:O	43:y:261:SER:OG	2.18	0.55
43:y:326:THR:O	43:y:329:ILE:HB	2.06	0.55
44:v:378:ILE:O	44:v:381:SER:HB3	2.06	0.55
8:H:16:ASP:CG	42:m:204:LYS:HE3	2.29	0.55
34:2:1327:C:C4	37:j:16:LYS:N	2.75	0.55
37:j:40:LYS:HD3	37:j:41:MET:C	2.31	0.55
38:k:385:LYS:HE2	38:k:518:VAL:HG13	1.89	0.55
38:k:530:ASP:O	38:k:532:VAL:HG23	2.06	0.55
38:k:582:SER:H	38:k:585:ASP:CB	2.19	0.55
43:y:331:ILE:HG23	43:y:430:GLN:NE2	0.68	0.55
44:v:373:LYS:CE	44:v:431:LEU:HD21	2.33	0.55
44:v:492:GLU:HG3	44:v:493:LYS:C	2.32	0.55
11:K:5:ARG:HH22	34:2:372:C:H41	1.55	0.55
38:k:204:LEU:HA	38:k:224:ARG:NH1	2.13	0.55
38:k:316:TYR:N	38:k:316:TYR:HD1	2.05	0.55
38:k:336:THR:O	38:k:337:ALA:HB2	2.05	0.55
40:R:129:GLY:O	40:R:130:ARG:HB3	2.06	0.55
43:y:291:PHE:CZ	43:y:355:LEU:C	2.84	0.55
43:y:378:ASN:O	43:y:382:TYR:HD2	1.89	0.55
10:J:109:ARG:CD	34:2:794:G:H1'	2.37	0.55
14:N:30:LYS:HE2	14:N:30:LYS:CA	2.38	0.55
34:2:687:G:H2'	34:2:688:U:H5'	1.89	0.55
37:j:29:LYS:CA	37:j:33:GLN:O	2.55	0.55
37:j:49:ALA:HB3	37:j:59:CYS:SG	2.47	0.55
38:k:319:THR:CA	38:k:320:GLU:CB	2.85	0.55
38:k:451:ILE:HG22	38:k:454:ILE:HG23	1.89	0.55
43:y:246:TRP:N	43:y:248:GLU:OE1	2.40	0.55
43:y:276:TYR:CD2	43:y:302:LEU:HD22	2.41	0.55
43:y:291:PHE:CE1	43:y:359:LEU:CD2	2.87	0.55
43:y:329:ILE:HD11	43:y:374:MET:CE	2.37	0.55
16:P:27:LYS:CE	16:P:28:LEU:HD23	2.36	0.54
34:2:787:C:N3	34:2:788:C:N4	2.55	0.54
38:k:318:PRO:HG2	38:k:322:LEU:CA	2.26	0.54
43:y:82:ASN:ND2	43:y:85:SER:OG	2.40	0.54
43:y:140:ARG:O	44:v:466:SER:HB3	2.06	0.54
43:y:154:TRP:HA	43:y:154:TRP:CE3	2.42	0.54
44:v:341:GLY:O	44:v:342:LYS:O	2.24	0.54
44:v:559:ASP:OD1	44:v:560:ARG:C	2.50	0.54
34:2:739:U:O2	34:2:739:U:H2'	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:k:374:ILE:HD11	38:k:529:ALA:O	2.03	0.54
38:k:381:ASN:CB	53:k:705:GNP:O1G	2.49	0.54
41:3:71:A:N6	41:3:72:G:O6	2.40	0.54
43:y:291:PHE:CZ	43:y:356:ALA:N	2.75	0.54
43:y:329:ILE:CB	43:y:330:PRO:CD	2.85	0.54
44:v:325:THR:C	44:v:326:HIS:CD2	2.86	0.54
44:v:325:THR:CG2	44:v:326:HIS:CD2	2.90	0.54
44:v:431:LEU:HD12	44:v:434:VAL:HB	1.89	0.54
44:v:752:CYS:HB3	44:v:783:ILE:CD1	2.19	0.54
8:H:29:GLN:HE21	42:m:472:LYS:NZ	2.06	0.54
25:a:128:GLY:O	38:k:264:ASN:CB	2.49	0.54
34:2:684:A:H8	34:2:684:A:O5'	1.91	0.54
35:A:197:VAL:CG2	35:A:235:TYR:HE2	2.20	0.54
38:k:520:HIS:HE1	53:k:705:GNP:O1G	1.91	0.54
41:3:43:A:H2'	41:3:44:C:H6	1.71	0.54
43:y:108:SER:HB2	43:y:145:LEU:HD23	1.87	0.54
16:P:27:LYS:CE	16:P:28:LEU:CD2	2.86	0.54
34:2:1109:A:C6	34:2:1110:U:N3	2.74	0.54
37:j:70:TRP:HE1	40:R:143:PRO:CB	2.08	0.54
38:k:241:ASP:O	38:k:242:GLU:CB	2.56	0.54
38:k:316:TYR:CD1	38:k:316:TYR:N	2.73	0.54
38:k:475:CYS:HB3	38:k:483:TYR:CE1	2.43	0.54
43:y:68:LYS:HZ3	43:y:72:TYR:HB2	1.72	0.54
43:y:277:ASN:HB2	43:y:299:LEU:CD1	2.30	0.54
4:D:82:ARG:NH2	4:D:82:ARG:HG3	2.23	0.54
9:I:237:LEU:HD12	34:2:784:G:C3'	2.33	0.54
17:Q:127:GLY:O	26:b:59:PHE:HE2	1.87	0.54
27:c:36:LYS:H	27:c:78:SER:CB	2.20	0.54
34:2:80:G:C5	34:2:81:U:C5	2.95	0.54
35:A:58:SER:CB	35:A:61:LYS:HE3	2.37	0.54
38:k:374:ILE:CD1	38:k:529:ALA:N	2.71	0.54
43:y:320:THR:HG23	43:y:323:LEU:HD21	1.90	0.54
44:v:383:TYR:HE2	44:v:447:LEU:HD22	1.70	0.54
44:v:445:LEU:HD23	44:v:445:LEU:O	2.08	0.54
14:N:30:LYS:HE2	14:N:30:LYS:H	1.66	0.54
16:P:26:LEU:HD13	16:P:26:LEU:O	2.07	0.54
34:2:1110:U:O2'	34:2:1111:U:O2	2.18	0.54
38:k:113:GLY:HA2	53:k:704:GNP:O3A	2.07	0.54
38:k:164:LEU:CD2	38:k:237:ILE:HD13	2.31	0.54
38:k:312:PHE:CD1	38:k:312:PHE:C	2.86	0.54
38:k:312:PHE:O	38:k:326:ASP:OD2	2.25	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:k:410:SER:OG	38:k:475:CYS:O	2.18	0.54
40:R:133:ILE:CG1	40:R:139:SER:HB3	2.37	0.54
43:y:91:ARG:CZ	43:y:173:LEU:CD1	2.85	0.54
43:y:371:ILE:O	43:y:375:VAL:HG23	2.07	0.54
43:y:395:GLU:HA	43:y:438:ARG:HH12	1.73	0.54
44:v:327:ALA:O	44:v:330:ILE:HG22	2.08	0.54
1:l:16:G:C2'	1:l:17:C:H5''	2.37	0.54
40:R:143:PRO:HG2	41:3:55:G:C1'	2.34	0.54
43:y:174:TYR:OH	43:y:203:MET:HE1	2.08	0.54
43:y:230:LEU:O	43:y:234:LEU:HG	2.08	0.54
43:y:237:LEU:CD1	43:y:278:LYS:NZ	2.53	0.54
34:2:786:C:H6	34:2:786:C:O5'	1.90	0.54
38:k:374:ILE:HD11	38:k:529:ALA:HA	1.77	0.54
40:R:140:ARG:NH2	40:R:140:ARG:HG2	2.22	0.54
44:v:438:LEU:C	44:v:441:ARG:HB3	2.33	0.54
44:v:454:GLU:O	44:v:458:ILE:HG12	2.08	0.54
44:v:486:VAL:O	44:v:486:VAL:HG12	2.07	0.54
35:A:58:SER:HB2	35:A:61:LYS:HD2	1.85	0.54
38:k:414:GLN:CG	38:k:486:ASP:OD1	2.55	0.54
38:k:489:SER:N	38:k:524:MET:CE	2.67	0.54
41:3:58:C:N3	41:3:59:A:C5	2.76	0.54
43:y:78:CYS:SG	43:y:86:LEU:CG	2.96	0.54
38:k:209:LEU:HD13	38:k:221:GLU:CB	2.37	0.54
40:R:143:PRO:HB2	41:3:55:G:H1'	1.87	0.54
43:y:94:LEU:HD22	43:y:157:TYR:HE1	1.73	0.54
43:y:340:ARG:O	43:y:343:ASP:O	2.25	0.54
44:v:500:CYS:HA	44:v:503:TYR:HD2	1.73	0.54
14:N:22:ARG:HG3	14:N:23:VAL:N	2.23	0.53
16:P:22:VAL:HG11	16:P:26:LEU:CD1	2.37	0.53
38:k:174:ASP:O	38:k:176:ILE:N	2.38	0.53
41:3:58:C:O2	41:3:58:C:H2'	2.08	0.53
43:y:378:ASN:OD1	43:y:381:GLN:HB3	2.08	0.53
44:v:469:TYR:HE1	44:v:473:LEU:HD11	1.72	0.53
9:I:237:LEU:HB3	34:2:785:G:OP1	2.07	0.53
38:k:378:LEU:C	38:k:385:LYS:CE	2.81	0.53
41:3:57:G:H3'	41:3:57:G:OP2	2.09	0.53
41:3:60:C:C2'	41:3:61:C:H4'	2.38	0.53
43:y:240:ALA:HB3	43:y:249:ALA:HB2	1.90	0.53
43:y:330:PRO:C	43:y:331:ILE:HG12	2.33	0.53
44:v:392:TYR:HD1	44:v:461:ASN:ND2	1.86	0.53
38:k:73:VAL:HB	38:k:322:LEU:CG	2.28	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:k:165:LYS:H	38:k:236:ASP:CB	2.20	0.53
43:y:132:VAL:O	43:y:132:VAL:HG12	2.07	0.53
44:v:334:ASN:O	44:v:337:LEU:HD12	2.08	0.53
44:v:391:THR:O	44:v:392:TYR:CB	2.54	0.53
10:J:109:ARG:HB3	34:2:740:G:C2'	2.35	0.53
35:A:108:VAL:CG2	35:A:150:TYR:CD1	2.82	0.53
37:j:93:LEU:C	37:j:94:LYS:O	2.36	0.53
38:k:321:ASN:O	38:k:322:LEU:CB	2.56	0.53
38:k:492:LEU:O	38:k:497:ARG:NH2	2.41	0.53
43:y:28:LEU:HD23	43:y:28:LEU:C	2.33	0.53
43:y:175:HIS:ND1	43:y:231:GLU:OE2	2.35	0.53
44:v:387:PRO:O	44:v:388:ASN:HB3	2.08	0.53
44:v:504:LEU:CD2	44:v:508:LEU:CD1	2.86	0.53
34:2:1815:U:H2'	34:2:1816:A:C5'	2.31	0.53
37:j:71:ILE:CD1	37:j:77:ILE:HD11	2.34	0.53
38:k:237:ILE:C	38:k:238:PHE:CG	2.86	0.53
41:3:71:A:H8	41:3:71:A:O5'	1.92	0.53
43:y:302:LEU:CG	43:y:306:MET:SD	2.95	0.53
43:y:340:ARG:HD2	43:y:348:ILE:HD12	1.89	0.53
44:v:333:LEU:O	44:v:336:ILE:HG12	2.09	0.53
25:a:10:ARG:C	25:a:11:LYS:HG3	2.33	0.53
28:d:35:MET:HE3	42:m:422:ALA:CB	2.38	0.53
38:k:208:HIS:CE1	38:k:540:SER:N	2.77	0.53
43:y:35:MET:HE1	43:y:47:HIS:ND1	2.24	0.53
43:y:183:LYS:O	43:y:187:GLN:HG3	2.08	0.53
43:y:335:ARG:HH12	43:y:352:GLN:HE21	1.55	0.53
43:y:347:ILE:HG13	43:y:348:ILE:HG13	1.91	0.53
44:v:521:ARG:HD3	44:v:542:GLU:HB3	1.74	0.53
25:a:101:LYS:NZ	25:a:107:ARG:NH2	2.56	0.53
38:k:315:GLY:C	38:k:316:TYR:CG	2.84	0.53
38:k:451:ILE:HB	38:k:454:ILE:HG23	1.91	0.53
43:y:101:THR:HA	43:y:149:TRP:CB	2.38	0.53
43:y:224:GLU:O	43:y:228:MET:CE	2.52	0.53
43:y:236:GLN:CD	43:y:252:ALA:CB	2.75	0.53
44:v:332:LYS:O	44:v:336:ILE:HG23	2.09	0.53
44:v:345:THR:HG23	44:v:347:ARG:CB	2.31	0.53
44:v:554:TYR:C	44:v:557:ALA:CB	2.73	0.53
34:2:687:G:C5	34:2:729:C:N4	2.77	0.53
37:j:70:TRP:CD2	40:R:143:PRO:HG3	2.44	0.53
43:y:12:LEU:HD22	43:y:16:ASN:ND2	2.19	0.53
43:y:327:LEU:HB3	43:y:427:TYR:CB	2.39	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:y:375:VAL:O	43:y:375:VAL:HG12	2.07	0.53
44:v:521:ARG:HH11	44:v:542:GLU:CG	2.20	0.53
44:v:530:SER:CB	44:v:535:ASP:OD2	2.56	0.53
34:2:682:G:N3	34:2:683:G:C8	2.76	0.53
34:2:685:G:H1	34:2:730:C:N4	2.06	0.53
34:2:744:C:C5	34:2:745:U:O4	2.62	0.53
34:2:1696:C:N3	37:j:11:ASN:OD1	2.42	0.53
41:3:60:C:H3'	41:3:61:C:C4'	2.38	0.53
34:2:1115:A:H3'	34:2:1116:U:C6	2.44	0.53
35:A:154:LYS:HD2	35:A:184:LEU:CD2	2.39	0.53
37:j:93:LEU:O	37:j:94:LYS:C	2.39	0.53
43:y:375:VAL:HA	43:y:379:VAL:CG2	2.39	0.53
44:v:476:GLU:O	44:v:479:VAL:HG12	2.09	0.53
44:v:556:TYR:C	44:v:558:LYS:HB3	2.34	0.53
10:J:109:ARG:CB	34:2:740:G:O4'	2.40	0.52
34:2:743:U:HO2'	34:2:744:C:C1'	2.21	0.52
38:k:345:MET:HG2	38:k:346:CYS:N	2.24	0.52
40:R:133:ILE:C	40:R:139:SER:OG	2.48	0.52
43:y:116:GLU:C	43:y:118:LEU:H	2.17	0.52
43:y:237:LEU:HD13	43:y:278:LYS:NZ	2.18	0.52
43:y:381:GLN:HE21	43:y:381:GLN:CA	2.07	0.52
44:v:423:ASN:O	44:v:424:ILE:HD12	2.07	0.52
1:1:16:G:C2	1:1:17:C:C5	2.97	0.52
27:c:73:LEU:O	27:c:74:THR:CG2	2.57	0.52
34:2:1519:G:OP1	39:U:144:ARG:CB	2.51	0.52
38:k:319:THR:N	38:k:320:GLU:CB	2.72	0.52
43:y:335:ARG:NH1	43:y:352:GLN:HE21	2.07	0.52
44:v:372:VAL:CG2	44:v:411:ILE:CG2	2.86	0.52
44:v:375:LYS:C	44:v:378:ILE:HG22	2.34	0.52
25:a:10:ARG:HH21	25:a:11:LYS:CE	2.22	0.52
34:2:469:C:O2'	38:k:319:THR:O	2.28	0.52
34:2:1112:C:N3	34:2:1113:C:N3	2.58	0.52
37:j:27:VAL:HG12	37:j:28:PHE:N	2.22	0.52
38:k:176:ILE:HG23	38:k:176:ILE:O	2.07	0.52
38:k:455:ILE:HG13	38:k:456:ASP:N	2.23	0.52
43:y:156:SER:O	43:y:160:CYS:N	2.39	0.52
43:y:297:HIS:HE1	43:y:325:ALA:CA	2.22	0.52
44:v:409:MET:HG3	44:v:485:ARG:NE	2.23	0.52
8:H:37:ASP:OD2	42:m:418:GLY:CA	2.56	0.52
9:I:223:LYS:HE2	9:I:227:GLN:NE2	2.24	0.52
14:N:22:ARG:HH21	14:N:24:LEU:HD13	1.73	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:2:683:G:C2	34:2:684:A:C4	2.97	0.52
34:2:1109:A:C2'	34:2:1110:U:H5'	2.39	0.52
34:2:1115:A:C5'	34:2:1116:U:C5	2.85	0.52
34:2:1705:C:O2'	37:j:42:LEU:HD11	2.10	0.52
37:j:24:ARG:HG3	37:j:25:GLU:N	2.23	0.52
38:k:177:PRO:O	38:k:178:LYS:HG3	2.09	0.52
43:y:61:LEU:C	43:y:62:ARG:HG3	2.34	0.52
43:y:230:LEU:HG	43:y:271:LEU:CG	2.33	0.52
9:I:235:SER:O	9:I:237:LEU:N	2.43	0.52
34:2:682:G:H8	34:2:682:G:O5'	1.92	0.52
37:j:30:GLU:N	37:j:33:GLN:HB3	2.21	0.52
38:k:451:ILE:CG2	38:k:454:ILE:HG23	2.39	0.52
41:3:34:C:C2'	41:3:35:A:H5'	2.40	0.52
43:y:13:LYS:CB	43:y:13:LYS:NZ	2.73	0.52
43:y:170:VAL:O	43:y:171:GLU:HB2	2.09	0.52
44:v:480:CYS:O	44:v:483:ILE:HG12	2.09	0.52
44:v:496:THR:O	44:v:555:ILE:CD1	2.45	0.52
4:D:70:SER:OG	4:D:71:LEU:N	2.42	0.52
4:D:71:LEU:HD12	4:D:84:PHE:CZ	2.44	0.52
34:2:225:C:H3'	34:2:226:A:C5'	2.40	0.52
37:j:61:ILE:CG2	37:j:62:ARG:N	2.73	0.52
41:3:70:G:N3	41:3:70:G:C3'	2.73	0.52
43:y:78:CYS:SG	43:y:86:LEU:HG	2.49	0.52
43:y:298:ARG:NH2	43:y:361:LEU:HD11	2.24	0.52
43:y:375:VAL:HA	43:y:379:VAL:HG21	1.92	0.52
43:y:385:PRO:HB3	43:y:388:LYS:CD	2.18	0.52
44:v:390:ALA:O	44:v:391:THR:OG1	2.26	0.52
44:v:499:ILE:O	44:v:502:VAL:CG1	2.41	0.52
8:H:37:ASP:OD2	42:m:417:ARG:C	2.51	0.52
34:2:747:G:O5'	34:2:747:G:H8	1.91	0.52
38:k:360:PHE:HE2	53:k:705:GNP:N3	2.07	0.52
43:y:68:LYS:HD3	43:y:68:LYS:O	2.10	0.52
43:y:257:HIS:CE1	43:y:358:LEU:HD23	2.44	0.52
43:y:338:ILE:CG2	43:y:339:ALA:N	2.73	0.52
44:v:389:LEU:CD2	44:v:389:LEU:N	2.73	0.52
44:v:752:CYS:HG	44:v:783:ILE:CG2	2.17	0.52
9:I:221:LYS:HE2	9:I:225:GLN:NE2	2.24	0.52
14:N:30:LYS:C	14:N:32:LYS:H	2.18	0.52
27:c:61:THR:CB	44:v:340:ARG:HH22	2.19	0.52
38:k:217:LEU:CD2	38:k:221:GLU:HB3	2.28	0.52
38:k:332:LYS:CE	38:k:334:ALA:CB	2.37	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:k:378:LEU:C	38:k:385:LYS:HZ1	2.17	0.52
38:k:385:LYS:HE2	38:k:518:VAL:CG1	2.40	0.52
43:y:59:VAL:O	43:y:59:VAL:HG12	2.08	0.52
43:y:165:ARG:HH11	43:y:165:ARG:HG2	1.74	0.52
43:y:168:SER:OG	43:y:169:ARG:N	2.42	0.52
43:y:265:LYS:N	43:y:266:PRO:CD	2.73	0.52
44:v:329:VAL:CG2	44:v:330:ILE:N	2.73	0.52
44:v:429:GLU:CG	44:v:430:ASN:N	2.73	0.52
14:N:26:GLY:O	14:N:27:GLU:HB2	2.09	0.52
33:i:82:ARG:NH2	33:i:83:VAL:O	2.43	0.52
37:j:28:PHE:HB3	37:j:35:TYR:OH	2.10	0.52
38:k:113:GLY:N	53:k:704:GNP:N3B	2.53	0.52
38:k:532:VAL:CG2	38:k:551:LEU:HA	2.39	0.52
39:U:143:GLY:CA	39:U:144:ARG:HD2	2.38	0.52
37:j:68:LYS:HG2	41:3:57:G:O6	2.10	0.52
38:k:217:LEU:C	53:k:705:GNP:O2'	2.53	0.52
43:y:7:ARG:HB2	43:y:9:GLU:OE2	2.09	0.52
43:y:68:LYS:CG	43:y:163:LEU:HD21	2.40	0.52
43:y:330:PRO:O	43:y:331:ILE:CD1	2.58	0.52
44:v:325:THR:CG2	44:v:326:HIS:NE2	2.73	0.52
44:v:326:HIS:CA	44:v:329:VAL:HG22	2.38	0.52
44:v:413:PHE:HE1	44:v:489:TYR:HE1	1.45	0.52
49:t:486:PHE:H	49:t:487:ARG:HB3	1.75	0.52
1:1:16:G:N1	1:1:17:C:H5	2.08	0.51
25:a:105:LYS:C	25:a:107:ARG:H	2.18	0.51
27:c:38:PRO:CD	27:c:39:GLY:H	2.23	0.51
34:2:734:C:C3'	34:2:735:C:C5'	2.88	0.51
34:2:745:U:H3'	34:2:745:U:H6	1.75	0.51
34:2:794:G:O2'	34:2:795:U:OP1	2.20	0.51
43:y:367:ARG:NH1	43:y:368:ILE:CD1	2.73	0.51
6:F:195:SER:HA	6:F:202:LYS:HD2	1.92	0.51
27:c:73:LEU:N	27:c:73:LEU:CD2	2.73	0.51
34:2:1112:C:H2'	34:2:1112:C:O2	2.09	0.51
38:k:209:LEU:CD1	38:k:221:GLU:HG2	2.35	0.51
38:k:381:ASN:HB3	53:k:705:GNP:PG	2.50	0.51
38:k:450:GLN:CG	38:k:453:ASN:CG	2.83	0.51
38:k:455:ILE:CG1	38:k:456:ASP:N	2.73	0.51
40:R:133:ILE:CG2	40:R:134:GLY:N	2.52	0.51
43:y:7:ARG:HB3	43:y:9:GLU:OE2	2.10	0.51
43:y:68:LYS:HG2	43:y:163:LEU:HD23	1.90	0.51
43:y:227:SER:CB	43:y:228:MET:CE	2.86	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:y:283:PHE:HD1	43:y:283:PHE:C	2.18	0.51
43:y:313:ASP:C	43:y:314:GLU:HG2	2.35	0.51
43:y:331:ILE:HD13	43:y:431:LEU:HB2	1.91	0.51
1:l:16:G:N1	1:l:17:C:C5	2.78	0.51
8:H:33:ILE:HB	42:m:479:GLN:HG2	1.93	0.51
35:A:170:GLU:C	35:A:172:GLU:H	2.00	0.51
38:k:112:ASN:HB3	53:k:704:GNP:O1G	2.10	0.51
40:R:140:ARG:HH21	40:R:140:ARG:HG2	1.76	0.51
43:y:222:ASN:N	43:y:223:PRO:CD	2.73	0.51
43:y:279:VAL:CG1	43:y:280:SER:N	2.73	0.51
43:y:318:MET:HG2	43:y:382:TYR:CB	2.33	0.51
44:v:354:LEU:HD13	44:v:378:ILE:HA	1.92	0.51
44:v:373:LYS:HZ1	44:v:440:VAL:CG2	2.15	0.51
8:H:29:GLN:NE2	42:m:472:LYS:HG3	2.26	0.51
34:2:80:G:C4	34:2:81:U:C6	2.99	0.51
43:y:68:LYS:HE3	43:y:163:LEU:O	2.11	0.51
25:a:105:LYS:C	25:a:107:ARG:N	2.67	0.51
34:2:790:A:C5	34:2:791:A:N6	2.78	0.51
37:j:78:LEU:HD21	37:j:93:LEU:CD1	2.31	0.51
38:k:212:ARG:CZ	53:k:705:GNP:HN22	2.24	0.51
43:y:232:THR:CB	43:y:233:ARG:NH2	2.74	0.51
43:y:245:LEU:O	43:y:246:TRP:CE3	2.62	0.51
44:v:380:ALA:O	44:v:383:TYR:HB2	2.11	0.51
44:v:418:ILE:N	44:v:418:ILE:CD1	2.73	0.51
44:v:424:ILE:N	44:v:424:ILE:CD1	2.73	0.51
44:v:487:GLN:NE2	44:v:548:MET:CE	2.73	0.51
44:v:748:ASP:CG	44:v:750:LYS:CD	2.75	0.51
34:2:687:G:C6	34:2:729:C:N4	2.78	0.51
34:2:795:U:O2	34:2:863:G:H1'	2.11	0.51
38:k:508:ILE:HD12	38:k:515:ALA:CB	2.39	0.51
43:y:230:LEU:HG	43:y:271:LEU:HD21	1.78	0.51
43:y:255:ASP:O	43:y:259:LEU:HD12	2.11	0.51
43:y:276:TYR:CE1	43:y:295:THR:HG23	2.46	0.51
43:y:277:ASN:HB2	43:y:299:LEU:HD13	1.91	0.51
43:y:346:GLY:CA	43:y:348:ILE:N	2.73	0.51
44:v:379:ILE:HD12	44:v:447:LEU:HD13	1.93	0.51
33:i:82:ARG:HA	37:j:83:ASP:OD2	2.11	0.51
34:2:682:G:C4	34:2:683:G:N7	2.79	0.51
38:k:134:TYR:H	38:k:135:ASP:HA	1.73	0.51
38:k:329:LEU:HD23	38:k:495:GLU:OE1	2.11	0.51
41:3:77:A:O5'	41:3:77:A:H8	1.94	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:y:121:ILE:HG13	43:y:122:GLN:HE21	1.76	0.51
44:v:451:MET:SD	44:v:451:MET:C	2.94	0.51
8:H:61:PHE:HE1	42:m:415:SER:CB	2.18	0.51
34:2:1117:G:C5'	34:2:1117:G:C8	2.94	0.51
34:2:1709:U:C2	34:2:1814:G:C2	2.99	0.51
38:k:22:ARG:O	38:k:23:GLN:CG	2.58	0.51
38:k:32:VAL:HG13	38:k:37:LEU:HD23	1.93	0.51
38:k:378:LEU:CA	38:k:385:LYS:HE3	2.40	0.51
38:k:450:GLN:NE2	38:k:452:GLU:HB3	2.25	0.51
38:k:451:ILE:CB	38:k:454:ILE:HG23	2.41	0.51
39:U:148:VAL:HG21	40:R:132:GLY:O	2.11	0.51
40:R:130:ARG:NH1	40:R:130:ARG:CB	2.73	0.51
43:y:205:LEU:CD1	43:y:209:GLN:CD	2.83	0.51
43:y:368:ILE:CD1	43:y:438:ARG:NH2	2.74	0.51
44:v:373:LYS:HZ1	44:v:440:VAL:HG21	1.66	0.51
44:v:409:MET:CE	44:v:485:ARG:HG2	2.24	0.51
44:v:752:CYS:HG	44:v:783:ILE:HG21	1.67	0.51
24:Z:96:GLU:CG	38:k:34:MET:CE	2.86	0.51
34:2:1693:C:C4	41:3:58:C:N4	2.78	0.51
38:k:164:LEU:HD21	38:k:237:ILE:CG1	2.41	0.51
38:k:489:SER:O	38:k:497:ARG:NE	2.44	0.51
43:y:7:ARG:N	43:y:8:PRO:CD	2.67	0.51
43:y:167:ASN:O	43:y:168:SER:CB	2.58	0.51
43:y:327:LEU:CD1	43:y:327:LEU:N	2.73	0.51
43:y:347:ILE:HD12	44:v:723:ARG:HE	1.68	0.51
44:v:325:THR:C	44:v:326:HIS:CG	2.89	0.51
44:v:376:PHE:O	44:v:377:ASN:C	2.53	0.51
44:v:476:GLU:HA	44:v:479:VAL:HG12	1.92	0.51
25:a:105:LYS:O	25:a:107:ARG:N	2.44	0.51
34:2:687:G:C2'	34:2:688:U:H5'	2.41	0.51
38:k:21:CYS:C	38:k:23:GLN:H	2.18	0.51
38:k:73:VAL:HB	38:k:322:LEU:HD22	0.55	0.51
38:k:455:ILE:CB	38:k:456:ASP:N	2.37	0.51
38:k:522:PHE:HZ	38:k:595:PHE:CD1	2.29	0.51
44:v:397:MET:SD	44:v:397:MET:C	2.94	0.51
44:v:452:ASP:O	44:v:456:THR:HG23	2.11	0.51
16:P:20:ARG:CD	16:P:65:PHE:CZ	2.84	0.50
16:P:20:ARG:HD3	16:P:65:PHE:CZ	2.46	0.50
28:d:38:THR:HG23	42:m:296:ASN:OD1	2.10	0.50
28:d:38:THR:CG2	42:m:296:ASN:HA	2.41	0.50
34:2:749:C:H3'	34:2:750:G:C5'	2.29	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:2:787:C:H6	34:2:787:C:O5'	1.94	0.50
37:j:62:ARG:HH11	37:j:64:LYS:CD	2.24	0.50
38:k:221:GLU:CD	38:k:221:GLU:H	2.19	0.50
38:k:226:ALA:O	38:k:230:VAL:HG23	2.10	0.50
38:k:485:ILE:HD11	38:k:488:PRO:HG3	1.92	0.50
41:3:38:C:O2'	41:3:39:U:H5''	2.11	0.50
43:y:140:ARG:O	44:v:466:SER:HB2	2.09	0.50
43:y:181:ALA:CB	43:y:196:LYS:HZ1	2.22	0.50
43:y:274:ASN:O	43:y:277:ASN:ND2	2.44	0.50
43:y:283:PHE:C	43:y:283:PHE:CD1	2.86	0.50
44:v:369:GLY:C	44:v:371:ILE:H	2.17	0.50
1:1:34:C:N4	41:3:54:G:C6	2.66	0.50
33:i:75:LYS:NZ	37:j:27:VAL:HG22	2.26	0.50
34:2:1819:A:C6	37:j:66:ARG:O	2.64	0.50
38:k:113:GLY:H	53:k:704:GNP:PB	2.34	0.50
38:k:174:ASP:C	38:k:176:ILE:H	2.19	0.50
39:U:143:GLY:N	39:U:144:ARG:HD2	2.25	0.50
41:3:63:G:N3	41:3:63:G:C2'	2.73	0.50
43:y:59:VAL:HG22	43:y:152:PHE:CZ	2.46	0.50
43:y:105:LYS:CG	43:y:146:LEU:HD22	2.22	0.50
43:y:107:GLU:HG3	43:y:145:LEU:CD2	2.40	0.50
44:v:448:VAL:HG11	44:v:486:VAL:HG11	1.93	0.50
27:c:79:PHE:O	27:c:80:ARG:HG2	2.11	0.50
34:2:1115:A:H2'	34:2:1116:U:OP1	2.10	0.50
38:k:449:LEU:HG	38:k:496:GLN:OE1	2.11	0.50
43:y:165:ARG:CG	43:y:165:ARG:NH1	2.73	0.50
43:y:329:ILE:CD1	43:y:374:MET:HE1	2.41	0.50
44:v:362:SER:C	44:v:363:GLU:CD	2.80	0.50
38:k:204:LEU:HG	38:k:224:ARG:HD2	1.92	0.50
38:k:412:LYS:HB2	38:k:483:TYR:HE1	1.76	0.50
43:y:8:PRO:HG3	43:y:39:LYS:CD	2.42	0.50
43:y:59:VAL:HG23	43:y:93:TYR:HE1	1.75	0.50
43:y:71:LEU:CB	43:y:164:LEU:CD2	2.89	0.50
44:v:487:GLN:HE21	44:v:548:MET:CE	2.24	0.50
33:i:75:LYS:NZ	37:j:27:VAL:HG21	2.26	0.50
37:j:92:ILE:CG2	37:j:93:LEU:HD12	2.34	0.50
38:k:17:LYS:NZ	38:k:20:LYS:NZ	2.60	0.50
38:k:131:LEU:CD1	38:k:143:ILE:HG22	2.41	0.50
38:k:318:PRO:HG3	38:k:322:LEU:HA	1.79	0.50
38:k:450:GLN:CG	38:k:453:ASN:ND2	2.60	0.50
40:R:134:GLY:O	40:R:136:THR:N	2.41	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:y:238:ASP:HA	43:y:241:ILE:CG1	2.41	0.50
44:v:334:ASN:O	44:v:338:GLN:CG	2.43	0.50
44:v:422:GLU:O	44:v:424:ILE:HD12	2.11	0.50
16:P:27:LYS:HB2	16:P:27:LYS:HZ3	1.74	0.50
38:k:139:ASP:O	38:k:141:GLN:OE1	2.30	0.50
40:R:133:ILE:O	40:R:135:ALA:N	2.44	0.50
41:3:49:A:O2'	41:3:50:C:H5'	2.11	0.50
43:y:204:HIS:HE1	43:y:259:LEU:HG	1.77	0.50
43:y:205:LEU:HA	43:y:208:ILE:CG2	2.41	0.50
43:y:221:ASN:C	43:y:223:PRO:HD2	2.37	0.50
43:y:333:PRO:HG3	43:y:434:ASN:ND2	2.27	0.50
44:v:455:PHE:CE1	44:v:476:GLU:CB	2.95	0.50
35:A:229:LEU:HD13	36:B:285:ASP:CB	2.42	0.50
37:j:7:LYS:O	40:R:140:ARG:HG2	2.12	0.50
37:j:15:GLY:O	37:j:16:LYS:CB	2.60	0.50
38:k:294:SER:CB	53:k:704:GNP:O3'	2.58	0.50
38:k:492:LEU:HB2	38:k:497:ARG:HE	1.77	0.50
38:k:523:ILE:HA	38:k:526:THR:CG2	2.42	0.50
43:y:270:GLN:CG	43:y:271:LEU:N	2.74	0.50
43:y:399:ASN:O	43:y:400:PRO:C	2.54	0.50
44:v:354:LEU:CB	44:v:378:ILE:HG13	2.42	0.50
4:D:73:ASP:HB2	17:Q:128:ARG:NH2	2.26	0.50
35:A:227:ILE:HD11	35:A:237:MET:CE	2.18	0.50
43:y:346:GLY:CA	43:y:347:ILE:C	2.85	0.50
44:v:336:ILE:HD12	44:v:354:LEU:HD21	1.92	0.50
44:v:500:CYS:O	44:v:503:TYR:HB2	2.12	0.50
15:O:85:LEU:HD23	15:O:85:LEU:H	1.77	0.50
25:a:12:PHE:CD1	34:2:836:C:H1'	2.46	0.50
27:c:59:CYS:HB2	44:v:450:ARG:CB	2.42	0.50
28:d:38:THR:HG21	42:m:296:ASN:N	2.27	0.50
34:2:1817:A:HO2'	37:j:46:ARG:HH22	1.52	0.50
38:k:173:VAL:O	38:k:177:PRO:HD3	2.12	0.50
38:k:315:GLY:C	38:k:326:ASP:CB	2.85	0.50
41:3:63:G:N3	41:3:63:G:C3'	2.73	0.50
44:v:347:ARG:HD3	44:v:385:TYR:O	2.12	0.50
44:v:354:LEU:HB3	44:v:378:ILE:CD1	2.42	0.50
44:v:383:TYR:HB2	44:v:384:ASP:OD1	2.12	0.50
35:A:229:LEU:CD2	36:B:284:VAL:HG23	2.06	0.49
38:k:248:ASP:HB2	38:k:381:ASN:OD1	2.12	0.49
38:k:331:PHE:H	38:k:498:LEU:CD1	2.25	0.49
43:y:105:LYS:HB2	43:y:146:LEU:HD13	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:y:230:LEU:HD12	43:y:271:LEU:HD23	1.92	0.49
44:v:394:LYS:O	44:v:397:MET:CG	2.41	0.49
6:F:3:VAL:HG13	6:F:4:GLN:N	2.27	0.49
8:H:27:ASP:HA	42:m:472:LYS:CE	2.41	0.49
24:Z:68:LYS:CD	37:j:84:TYR:OH	2.57	0.49
27:c:75:GLU:HB2	44:v:389:LEU:HB2	1.93	0.49
27:c:79:PHE:O	27:c:80:ARG:HD3	2.12	0.49
28:d:13:ARG:HD3	42:m:426:LYS:HZ2	1.76	0.49
34:2:745:U:N3	34:2:746:C:N4	2.60	0.49
34:2:1755:U:H3	34:2:1765:G:H1	1.60	0.49
38:k:112:ASN:CB	53:k:704:GNP:O3G	2.59	0.49
43:y:159:GLN:HG3	43:y:163:LEU:CD2	2.26	0.49
43:y:161:LEU:CD2	43:y:174:TYR:HA	2.42	0.49
43:y:277:ASN:N	43:y:299:LEU:CG	2.75	0.49
43:y:298:ARG:HH21	43:y:361:LEU:HD11	1.77	0.49
44:v:345:THR:HG21	44:v:347:ARG:NE	2.27	0.49
44:v:409:MET:SD	44:v:485:ARG:CD	3.01	0.49
44:v:445:LEU:C	44:v:445:LEU:CD2	2.86	0.49
34:2:679:U:H2'	34:2:680:G:C8	2.47	0.49
38:k:315:GLY:C	38:k:316:TYR:HD1	2.16	0.49
38:k:319:THR:H	38:k:320:GLU:CA	2.24	0.49
38:k:550:THR:OG1	38:k:553:ALA:HB3	2.13	0.49
38:k:559:LEU:HB2	38:k:594:TYR:CE2	2.48	0.49
43:y:331:ILE:CD1	43:y:430:GLN:HG3	2.41	0.49
44:v:376:PHE:C	44:v:378:ILE:H	2.20	0.49
44:v:507:ILE:HA	44:v:510:THR:OG1	2.13	0.49
9:I:237:LEU:HD12	34:2:785:G:P	2.49	0.49
24:Z:52:LEU:O	24:Z:53:GLU:HB3	2.12	0.49
34:2:683:G:C2	34:2:684:A:C5	3.00	0.49
37:j:11:ASN:O	37:j:12:ARG:HG2	2.12	0.49
37:j:94:LYS:HG2	37:j:95:TYR:O	2.12	0.49
38:k:320:GLU:O	38:k:321:ASN:HB2	2.13	0.49
43:y:221:ASN:C	43:y:223:PRO:CD	2.86	0.49
43:y:240:ALA:C	43:y:242:SER:H	2.19	0.49
43:y:363:ALA:CB	43:y:364:PRO:CD	2.87	0.49
44:v:347:ARG:O	44:v:385:TYR:CE1	2.52	0.49
44:v:372:VAL:CG2	44:v:411:ILE:HG22	2.42	0.49
38:k:416:ILE:HD13	38:k:471:ALA:CB	2.42	0.49
43:y:278:LYS:C	43:y:278:LYS:CD	2.86	0.49
43:y:323:LEU:CG	43:y:324:LEU:N	2.73	0.49
44:v:347:ARG:O	44:v:347:ARG:HG2	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:v:366:LEU:C	44:v:366:LEU:CD1	2.85	0.49
44:v:425:LEU:CD1	44:v:425:LEU:C	2.86	0.49
44:v:469:TYR:CE1	44:v:473:LEU:CD1	2.94	0.49
1:1:69:U:H2'	1:1:69:U:O2	2.12	0.49
28:d:38:THR:CG2	42:m:296:ASN:CG	2.83	0.49
28:d:51:ARG:NH2	42:m:415:SER:C	2.70	0.49
33:i:82:ARG:NH2	33:i:85:LYS:HA	2.27	0.49
34:2:741:C:N3	34:2:792:G:O6	2.46	0.49
34:2:743:U:O4	34:2:791:A:C2	2.65	0.49
38:k:17:LYS:CG	38:k:20:LYS:HE2	2.33	0.49
43:y:101:THR:HG22	43:y:149:TRP:C	2.38	0.49
43:y:176:ASP:O	43:y:180:GLN:HG2	2.12	0.49
43:y:228:MET:SD	43:y:228:MET:N	2.85	0.49
44:v:351:ILE:HD11	44:v:381:SER:O	2.13	0.49
34:2:740:G:C3'	34:2:741:C:H5''	2.43	0.49
38:k:209:LEU:HD13	38:k:221:GLU:HB3	1.95	0.49
43:y:237:LEU:HD11	43:y:278:LYS:HZ3	1.78	0.49
4:D:82:ARG:HG3	4:D:82:ARG:HH21	1.78	0.49
34:2:795:U:C2	34:2:863:G:N3	2.80	0.49
38:k:332:LYS:O	38:k:334:ALA:CA	2.57	0.49
43:y:86:LEU:HD22	43:y:165:ARG:HH21	1.78	0.49
43:y:241:ILE:HA	43:y:246:TRP:CZ3	2.48	0.49
44:v:413:PHE:CE1	44:v:489:TYR:HE1	2.10	0.49
44:v:413:PHE:O	44:v:415:ASN:N	2.44	0.49
44:v:492:GLU:CG	44:v:493:LYS:C	2.86	0.49
34:2:16:G:H21	34:2:1191:A:H62	1.60	0.49
34:2:1519:G:P	39:U:144:ARG:CB	2.75	0.49
35:A:216:LEU:HD13	35:A:250:VAL:HG22	1.94	0.49
37:j:40:LYS:CG	37:j:41:MET:N	2.73	0.49
38:k:167:ILE:HG23	38:k:238:PHE:HA	1.94	0.49
38:k:378:LEU:C	38:k:385:LYS:HZ2	2.19	0.49
40:R:139:SER:O	40:R:140:ARG:HD2	2.13	0.49
41:3:34:C:H2'	41:3:34:C:O2	2.12	0.49
43:y:54:TYR:OH	43:y:66:LEU:HD22	2.13	0.49
43:y:68:LYS:HG3	43:y:163:LEU:HD21	1.95	0.49
37:j:64:LYS:C	37:j:66:ARG:H	2.21	0.49
38:k:209:LEU:CD1	38:k:221:GLU:CB	2.91	0.49
38:k:373:GLU:C	38:k:374:ILE:N	2.70	0.49
40:R:134:GLY:HA2	40:R:139:SER:CB	2.41	0.49
43:y:276:TYR:HB3	43:y:299:LEU:HG	1.95	0.49
45:w:326:VAL:HG13	45:w:327:ALA:H	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:c:69:GLY:C	27:c:70:LYS:O	2.55	0.48
34:2:740:G:H3'	34:2:741:C:H5''	1.94	0.48
38:k:318:PRO:C	38:k:319:THR:CG2	2.86	0.48
38:k:342:VAL:HG13	38:k:342:VAL:O	2.13	0.48
43:y:166:ASN:HD22	43:y:203:MET:HG3	1.77	0.48
43:y:283:PHE:CE1	43:y:287:GLY:N	2.77	0.48
43:y:301:HIS:CE1	43:y:377:PHE:CE2	3.02	0.48
43:y:361:LEU:HD22	43:y:365:PRO:HG3	1.95	0.48
44:v:409:MET:SD	44:v:485:ARG:HD3	2.53	0.48
33:i:79:SER:OG	37:j:80:GLY:CA	2.62	0.48
34:2:479:A:O4'	38:k:149:GLY:O	2.30	0.48
37:j:10:LYS:CG	37:j:11:ASN:N	2.40	0.48
43:y:25:GLN:OE1	43:y:25:GLN:N	2.45	0.48
43:y:219:ASN:O	43:y:220:LEU:HD22	2.13	0.48
44:v:358:VAL:O	44:v:361:ALA:N	2.37	0.48
44:v:379:ILE:HA	44:v:382:LEU:CG	2.42	0.48
27:c:36:LYS:N	27:c:78:SER:CB	2.77	0.48
34:2:1407:G:H3'	34:2:1408:C:C5'	2.43	0.48
34:2:1812:A:H2	34:2:1813:A:N9	2.10	0.48
37:j:27:VAL:CG1	37:j:28:PHE:H	2.23	0.48
37:j:40:LYS:CD	37:j:42:LEU:N	2.73	0.48
38:k:169:LYS:HE2	38:k:242:GLU:O	2.13	0.48
38:k:523:ILE:HG23	38:k:575:PRO:HG3	1.94	0.48
43:y:14:ARG:NH1	43:y:14:ARG:CG	2.73	0.48
43:y:35:MET:SD	43:y:50:ILE:HG21	2.53	0.48
43:y:163:LEU:O	43:y:164:LEU:HB2	2.12	0.48
43:y:335:ARG:NH1	43:y:352:GLN:NE2	2.60	0.48
44:v:325:THR:HA	44:v:326:HIS:HD2	1.79	0.48
44:v:490:LEU:CD1	44:v:492:GLU:HB3	2.41	0.48
5:E:99:LYS:HA	34:2:10:G:H21	1.77	0.48
34:2:1812:A:C2	34:2:1813:A:C5	3.01	0.48
38:k:5:LEU:C	38:k:5:LEU:CD1	2.86	0.48
43:y:61:LEU:C	43:y:62:ARG:CG	2.86	0.48
43:y:165:ARG:C	43:y:167:ASN:H	2.21	0.48
6:F:143:ARG:HD3	41:3:62:U:H5'	1.94	0.48
10:J:109:ARG:HG3	34:2:794:G:C4	2.48	0.48
16:P:29:THR:O	16:P:32:ASP:N	2.45	0.48
34:2:1707:A:N6	34:2:1708:C:N4	2.61	0.48
38:k:131:LEU:C	38:k:131:LEU:CD2	2.86	0.48
43:y:273:ALA:O	43:y:299:LEU:HD21	2.13	0.48
43:y:385:PRO:HA	43:y:388:LYS:CG	2.42	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:v:337:LEU:C	44:v:337:LEU:CD1	2.86	0.48
44:v:467:GLN:HA	44:v:469:TYR:HB2	1.95	0.48
44:v:748:ASP:OD1	44:v:750:LYS:CG	2.60	0.48
4:D:74:LEU:HD23	4:D:74:LEU:O	2.13	0.48
16:P:22:VAL:CB	16:P:24:THR:H	2.27	0.48
24:Z:50:ILE:CD1	38:k:58:CYS:CB	2.82	0.48
25:a:128:GLY:HA3	38:k:264:ASN:O	2.11	0.48
34:2:784:G:C6	34:2:785:G:C5	3.01	0.48
38:k:414:GLN:HG2	38:k:486:ASP:CG	2.37	0.48
38:k:584:LYS:O	38:k:586:VAL:N	2.47	0.48
40:R:136:THR:OG1	40:R:137:HIS:N	2.44	0.48
43:y:270:GLN:O	43:y:272:MET:N	2.40	0.48
43:y:296:LEU:HD11	43:y:324:LEU:CD2	2.44	0.48
43:y:298:ARG:NH2	43:y:361:LEU:HD12	2.28	0.48
44:v:376:PHE:C	44:v:378:ILE:N	2.71	0.48
9:I:237:LEU:HB2	34:2:785:G:P	2.53	0.48
25:a:10:ARG:HH21	25:a:11:LYS:HE3	1.79	0.48
38:k:216:ASP:O	53:k:705:GNP:N9	2.46	0.48
38:k:550:THR:OG1	38:k:553:ALA:HB2	2.13	0.48
43:y:262:LEU:O	43:y:265:LYS:HE3	2.13	0.48
43:y:347:ILE:C	43:y:348:ILE:CG1	2.86	0.48
44:v:394:LYS:O	44:v:397:MET:N	2.47	0.48
44:v:417:ASN:H	44:v:419:PHE:HZ	1.62	0.48
27:c:73:LEU:C	27:c:74:THR:HG23	2.39	0.48
35:A:244:ARG:HH22	35:A:251:LEU:HD22	1.78	0.48
37:j:25:GLU:HG2	37:j:26:LEU:CG	2.35	0.48
38:k:32:VAL:HG13	38:k:37:LEU:CD2	2.44	0.48
38:k:164:LEU:HD11	38:k:237:ILE:CD1	2.40	0.48
40:R:130:ARG:NH1	40:R:130:ARG:CA	2.75	0.48
41:3:58:C:C2	41:3:59:A:N7	2.82	0.48
43:y:76:ASN:HA	43:y:79:GLN:HG3	1.96	0.48
43:y:128:LEU:O	43:y:131:ALA:HB3	2.14	0.48
43:y:368:ILE:HG22	43:y:371:ILE:CG2	2.44	0.48
43:y:399:ASN:O	43:y:401:LEU:N	2.46	0.48
44:v:441:ARG:NE	44:v:441:ARG:CA	2.73	0.48
8:H:29:GLN:HG3	42:m:475:GLU:CD	2.39	0.48
24:Z:50:ILE:HD12	38:k:58:CYS:HB3	1.90	0.48
34:2:745:U:C2	34:2:746:C:N4	2.81	0.48
38:k:212:ARG:NH1	38:k:540:SER:HB3	2.28	0.48
38:k:378:LEU:HD12	38:k:379:GLY:HA3	1.01	0.48
43:y:166:ASN:HD22	43:y:203:MET:CG	2.27	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:y:297:HIS:CE1	43:y:374:MET:HG3	2.49	0.48
43:y:327:LEU:HB3	43:y:427:TYR:HB2	1.96	0.48
44:v:504:LEU:O	44:v:508:LEU:HG	2.14	0.48
10:J:109:ARG:HG3	34:2:794:G:H1'	1.94	0.48
25:a:127:ALA:O	38:k:264:ASN:HB2	2.12	0.48
38:k:112:ASN:HB3	53:k:704:GNP:PG	2.54	0.48
43:y:143:ARG:HA	43:y:147:THR:HG23	1.96	0.48
34:2:921:G:H1	34:2:1013:U:H3	1.62	0.47
38:k:229:VAL:CG1	38:k:230:VAL:N	2.76	0.47
40:R:128:HIS:CB	40:R:129:GLY:HA3	2.36	0.47
43:y:164:LEU:O	43:y:165:ARG:CG	2.48	0.47
43:y:284:TRP:CE3	43:y:285:LYS:HD2	2.48	0.47
44:v:367:GLY:HA3	44:v:368:GLU:C	2.39	0.47
44:v:463:ASP:OD1	44:v:464:PRO:HD3	2.13	0.47
10:J:106:ARG:CG	34:2:794:G:O6	2.61	0.47
34:2:1276:G:H1	34:2:1313:U:H3	1.62	0.47
34:2:1705:C:O2'	37:j:42:LEU:CD1	2.62	0.47
38:k:166:ALA:HA	38:k:237:ILE:HG21	1.91	0.47
38:k:581:ASN:HA	38:k:585:ASP:OD2	2.15	0.47
41:3:73:G:N7	41:3:74:A:C6	2.82	0.47
43:y:303:SER:H	43:y:321:ARG:NH1	2.12	0.47
43:y:353:ARG:NH2	43:y:357:THR:OG1	2.47	0.47
43:y:394:LEU:HD21	43:y:435:THR:OG1	2.14	0.47
44:v:396:GLU:N	44:v:396:GLU:CD	2.72	0.47
34:2:597:U:C2	41:3:61:C:N4	2.81	0.47
34:2:1114:C:H5'	34:2:1115:A:OP2	2.13	0.47
35:A:55:ARG:O	35:A:56:ILE:HG13	2.13	0.47
37:j:62:ARG:HH11	37:j:64:LYS:HD2	1.78	0.47
38:k:22:ARG:HB3	38:k:27:LYS:NZ	2.29	0.47
38:k:208:HIS:CE1	38:k:539:PRO:C	2.92	0.47
38:k:375:MET:SD	38:k:533:ILE:HG21	2.50	0.47
38:k:412:LYS:CD	38:k:485:ILE:CB	2.92	0.47
38:k:518:VAL:CA	38:k:519:GLU:N	2.75	0.47
43:y:7:ARG:C	43:y:9:GLU:HG3	2.24	0.47
43:y:26:PRO:CD	43:y:27:ALA:H	2.27	0.47
43:y:327:LEU:HD13	43:y:327:LEU:H	1.78	0.47
43:y:340:ARG:CD	43:y:340:ARG:H	2.23	0.47
4:D:80:ALA:C	4:D:81:PHE:CD2	2.92	0.47
34:2:742:C:O2'	34:2:743:U:H5''	2.09	0.47
37:j:72:ASN:N	37:j:72:ASN:ND2	2.60	0.47
43:y:59:VAL:HG11	43:y:97:ALA:HA	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:y:149:TRP:CA	43:y:149:TRP:CE3	2.98	0.47
43:y:232:THR:HB	43:y:233:ARG:CZ	2.43	0.47
43:y:250:PHE:CE2	44:v:726:LEU:CD1	2.91	0.47
43:y:336:THR:HG23	43:y:336:THR:O	2.14	0.47
9:I:159:ARG:HH11	9:I:173:ALA:HB2	1.79	0.47
14:N:22:ARG:HH22	14:N:24:LEU:HD13	1.79	0.47
16:P:26:LEU:HD22	16:P:27:LYS:CA	2.44	0.47
26:b:58:VAL:HG21	26:b:59:PHE:CE1	2.47	0.47
34:2:1815:U:C2'	34:2:1816:A:H5''	2.35	0.47
34:2:1819:A:N7	37:j:66:ARG:O	2.47	0.47
35:A:205:ILE:HD12	36:B:288:LYS:CG	2.44	0.47
41:3:37:C:C3'	41:3:38:C:C5'	2.92	0.47
43:y:91:ARG:CZ	43:y:173:LEU:HD12	2.44	0.47
43:y:237:LEU:HD11	43:y:278:LYS:NZ	2.30	0.47
44:v:372:VAL:CG2	44:v:411:ILE:HG21	2.44	0.47
8:H:29:GLN:NE2	42:m:472:LYS:NZ	2.63	0.47
34:2:80:G:C6	34:2:81:U:C4	3.02	0.47
34:2:743:U:O2'	34:2:744:C:O5'	2.32	0.47
34:2:886:U:H5'	34:2:887:G:H5''	1.96	0.47
35:A:263:GLU:HG2	35:A:269:PHE:HD1	1.78	0.47
38:k:6:THR:HB	38:k:75:LEU:O	2.14	0.47
38:k:212:ARG:HH12	38:k:540:SER:HB3	1.79	0.47
38:k:331:PHE:O	38:k:498:LEU:CD1	2.52	0.47
38:k:414:GLN:OE1	38:k:486:ASP:CB	2.52	0.47
38:k:536:ASP:CG	38:k:561:GLN:HE22	2.23	0.47
43:y:230:LEU:HD21	43:y:271:LEU:HD13	1.97	0.47
43:y:327:LEU:N	43:y:327:LEU:HD12	2.29	0.47
44:v:366:LEU:N	44:v:367:GLY:CA	2.76	0.47
44:v:484:GLU:HG3	44:v:488:ARG:NH1	2.28	0.47
44:v:736:HIS:CB	44:v:759:GLU:CG	2.47	0.47
24:Z:125:VAL:HG11	24:Z:140:ARG:HH12	1.80	0.47
25:a:101:LYS:HZ3	25:a:107:ARG:NH2	2.12	0.47
33:i:81:ALA:HB1	37:j:82:ARG:HD2	1.96	0.47
34:2:784:G:C4	34:2:785:G:C8	3.02	0.47
41:3:65:C:O2	41:3:65:C:O2'	2.26	0.47
43:y:7:ARG:HA	43:y:8:PRO:HD2	1.56	0.47
43:y:224:GLU:OE1	43:y:224:GLU:N	2.32	0.47
43:y:230:LEU:HG	43:y:271:LEU:CD1	2.45	0.47
43:y:240:ALA:HA	43:y:245:LEU:HB2	1.96	0.47
43:y:288:ASN:C	43:y:290:LEU:N	2.73	0.47
43:y:327:LEU:C	43:y:329:ILE:N	2.73	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:y:367:ARG:CG	43:y:368:ILE:H	2.04	0.47
44:v:325:THR:HA	44:v:326:HIS:CD2	2.49	0.47
44:v:356:LEU:O	44:v:357:LEU:HD23	2.15	0.47
44:v:382:LEU:HD11	44:v:400:LYS:CE	2.41	0.47
44:v:434:VAL:CG1	44:v:435:ASP:N	2.77	0.47
44:v:437:PRO:O	44:v:440:VAL:HG13	2.14	0.47
44:v:438:LEU:C	44:v:438:LEU:CD2	2.85	0.47
44:v:487:GLN:NE2	44:v:548:MET:HE2	2.29	0.47
25:a:100:LYS:HA	25:a:101:LYS:O	2.14	0.47
34:2:684:A:H2'	34:2:685:G:H8	1.73	0.47
34:2:784:G:P	34:2:784:G:H8	2.38	0.47
35:A:189:VAL:HG21	35:A:241:THR:HA	1.96	0.47
38:k:334:ALA:O	38:k:336:THR:OG1	2.33	0.47
38:k:381:ASN:CB	53:k:705:GNP:PG	3.02	0.47
38:k:518:VAL:C	38:k:519:GLU:CA	2.88	0.47
41:3:37:C:H3'	41:3:38:C:C5'	2.44	0.47
43:y:132:VAL:C	44:v:768:LEU:HD22	2.40	0.47
44:v:351:ILE:HG13	44:v:381:SER:HG	1.77	0.47
44:v:399:GLN:HA	44:v:399:GLN:NE2	2.30	0.47
27:c:59:CYS:CB	44:v:450:ARG:CB	2.92	0.47
34:2:741:C:H3'	34:2:741:C:H6	1.80	0.47
34:2:742:C:H3'	34:2:742:C:H6	1.80	0.47
37:j:40:LYS:CD	37:j:41:MET:N	2.73	0.47
38:k:520:HIS:CE1	53:k:705:GNP:O1G	2.68	0.47
41:3:60:C:O3'	41:3:61:C:H4'	2.12	0.47
43:y:128:LEU:CD2	44:v:516:TYR:CD2	2.91	0.47
43:y:333:PRO:HG2	43:y:437:LEU:HD21	1.96	0.47
44:v:368:GLU:N	44:v:368:GLU:CD	2.73	0.47
44:v:426:GLU:N	44:v:427:GLU:HG2	2.26	0.47
44:v:490:LEU:CD1	44:v:499:ILE:CB	2.92	0.47
14:N:25:LEU:CD1	14:N:29:GLY:HA3	2.45	0.47
28:d:33:GLU:CB	42:m:426:LYS:HZ3	2.26	0.47
35:A:170:GLU:C	35:A:172:GLU:N	2.66	0.47
37:j:70:TRP:HE1	40:R:143:PRO:CA	2.19	0.47
38:k:7:ARG:O	38:k:8:ILE:HD13	2.15	0.47
38:k:130:ASN:O	38:k:133:LYS:N	2.48	0.47
38:k:425:ARG:NH1	38:k:455:ILE:HD13	2.29	0.47
41:3:43:A:C1'	41:3:44:C:C5	2.98	0.47
43:y:51:MET:HE3	43:y:70:GLY:O	2.16	0.47
44:v:354:LEU:HB2	44:v:378:ILE:HG13	1.97	0.47
44:v:355:GLN:NE2	44:v:355:GLN:HA	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:v:498:GLU:O	44:v:499:ILE:C	2.58	0.47
44:v:512:TYR:CE1	44:v:674:HIS:CE1	3.03	0.47
44:v:521:ARG:HH21	44:v:522:GLN:HE21	1.63	0.47
27:c:36:LYS:HG2	27:c:36:LYS:O	2.14	0.46
34:2:682:G:C2	34:2:683:G:C8	3.03	0.46
34:2:731:C:C2'	34:2:732:C:H5''	2.37	0.46
38:k:159:ILE:CD1	38:k:164:LEU:HD22	2.45	0.46
38:k:378:LEU:N	38:k:385:LYS:HE3	2.30	0.46
38:k:526:THR:O	38:k:528:LEU:N	2.48	0.46
38:k:582:SER:OG	38:k:583:ILE:N	2.48	0.46
43:y:166:ASN:ND2	43:y:203:MET:SD	2.88	0.46
43:y:224:GLU:CD	43:y:224:GLU:N	2.73	0.46
44:v:335:GLU:HA	44:v:338:GLN:OE1	2.15	0.46
44:v:350:GLN:O	44:v:354:LEU:HG	2.16	0.46
44:v:467:GLN:HG3	44:v:469:TYR:H	1.80	0.46
44:v:504:LEU:C	44:v:504:LEU:CD2	2.85	0.46
44:v:752:CYS:SG	44:v:783:ILE:HD13	2.54	0.46
23:Y:2:VAL:HG23	23:Y:3:ARG:H	1.79	0.46
34:2:685:G:H8	34:2:685:G:O5'	1.98	0.46
34:2:749:C:C3'	34:2:750:G:C5'	2.90	0.46
34:2:793:C:H2'	34:2:794:G:H4'	1.97	0.46
37:j:84:TYR:CD1	37:j:84:TYR:N	2.84	0.46
40:R:133:ILE:C	40:R:135:ALA:N	2.73	0.46
43:y:247:GLN:O	43:y:251:LYS:HD2	2.15	0.46
43:y:367:ARG:C	43:y:369:GLY:N	2.73	0.46
44:v:363:GLU:N	44:v:363:GLU:CD	2.73	0.46
28:d:33:GLU:CG	42:m:426:LYS:NZ	2.65	0.46
37:j:9:GLY:N	40:R:140:ARG:NH2	2.60	0.46
37:j:47:LEU:CD1	37:j:48:GLU:N	2.73	0.46
41:3:66:U:H3'	41:3:66:U:O2	2.15	0.46
43:y:301:HIS:HE1	43:y:377:PHE:CE2	2.33	0.46
44:v:375:LYS:O	44:v:379:ILE:HG12	2.15	0.46
9:I:237:LEU:CD1	34:2:784:G:O2'	2.63	0.46
29:e:23:VAL:HG22	29:e:39:CYS:SG	2.55	0.46
34:2:1105:C:O2	34:2:1105:C:H3'	2.14	0.46
38:k:22:ARG:HB3	38:k:27:LYS:HZ1	1.80	0.46
38:k:486:ASP:C	38:k:487:GLU:CA	2.87	0.46
40:R:135:ALA:O	40:R:136:THR:HB	2.16	0.46
41:3:40:C:H2'	41:3:41:A:H5'	1.97	0.46
43:y:7:ARG:HD3	43:y:9:GLU:OE2	2.16	0.46
43:y:8:PRO:HG3	43:y:39:LYS:HD3	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:y:25:GLN:H	43:y:25:GLN:CD	2.21	0.46
43:y:161:LEU:HD23	43:y:174:TYR:HD1	1.81	0.46
43:y:259:LEU:C	43:y:263:SER:HG	2.19	0.46
44:v:347:ARG:C	44:v:385:TYR:CE1	2.94	0.46
44:v:364:ASN:O	44:v:365:ASN:HB3	2.16	0.46
44:v:413:PHE:HE1	44:v:489:TYR:CD1	2.20	0.46
44:v:445:LEU:HA	44:v:448:VAL:HG12	1.96	0.46
1:l:62:C:O2'	35:A:186:PRO:HD3	2.16	0.46
34:2:479:A:H5'	38:k:150:SER:HA	1.97	0.46
34:2:745:U:C2'	34:2:746:C:C6	2.89	0.46
38:k:167:ILE:HG21	38:k:238:PHE:CD1	2.50	0.46
38:k:217:LEU:HD23	38:k:221:GLU:CB	2.32	0.46
43:y:230:LEU:CD2	43:y:271:LEU:HD13	2.45	0.46
44:v:379:ILE:HA	44:v:382:LEU:CD1	2.45	0.46
44:v:383:TYR:C	44:v:385:TYR:H	2.23	0.46
46:q:117:ILE:HB	46:q:139:HIS:CG	2.50	0.46
8:H:29:GLN:HE21	42:m:472:LYS:HZ3	1.63	0.46
24:Z:97:ASN:O	38:k:56:ILE:CD1	2.61	0.46
34:2:1115:A:H3'	34:2:1116:U:C5	2.51	0.46
37:j:15:GLY:O	37:j:16:LYS:CD	2.64	0.46
37:j:64:LYS:C	37:j:66:ARG:N	2.73	0.46
38:k:168:ILE:HG22	38:k:239:MET:CB	2.45	0.46
38:k:174:ASP:C	38:k:176:ILE:N	2.73	0.46
38:k:450:GLN:HG3	38:k:453:ASN:ND2	2.30	0.46
43:y:386:GLU:O	43:y:410:VAL:HG13	2.16	0.46
44:v:329:VAL:CG2	44:v:330:ILE:H	2.28	0.46
44:v:487:GLN:HA	44:v:502:VAL:HG21	1.97	0.46
44:v:492:GLU:HG3	44:v:493:LYS:O	2.14	0.46
16:P:22:VAL:H	16:P:23:PRO:CA	2.11	0.46
34:2:452:C:O2'	38:k:306:ARG:CD	2.59	0.46
34:2:741:C:H2'	34:2:742:C:O4'	2.15	0.46
34:2:1110:U:O2'	34:2:1111:U:H3'	2.15	0.46
34:2:1518:C:C5'	39:U:144:ARG:N	2.79	0.46
35:A:121:TYR:HA	35:A:126:GLN:HG3	1.98	0.46
38:k:218:SER:N	38:k:221:GLU:OE1	2.42	0.46
43:y:301:HIS:CE1	43:y:377:PHE:CZ	2.97	0.46
44:v:382:LEU:CD2	44:v:400:LYS:HE3	2.45	0.46
4:D:39:PHE:CB	4:D:74:LEU:CD2	2.94	0.46
25:a:99:LYS:O	25:a:100:LYS:HB2	2.16	0.46
33:i:79:SER:OG	37:j:80:GLY:HA3	2.16	0.46
34:2:748:G:N2	34:2:749:C:C2	2.84	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:j:71:ILE:HG22	37:j:71:ILE:O	2.15	0.46
38:k:4:LYS:CA	38:k:79:LEU:CD1	2.92	0.46
38:k:475:CYS:SG	38:k:483:TYR:CE1	3.09	0.46
43:y:128:LEU:CD2	44:v:516:TYR:HD2	2.27	0.46
43:y:154:TRP:CE2	43:y:192:ALA:HB1	2.51	0.46
43:y:167:ASN:CG	43:y:207:GLN:NE2	2.73	0.46
43:y:298:ARG:HD3	43:y:298:ARG:HA	1.68	0.46
44:v:420:VAL:CG2	44:v:440:VAL:HG13	2.46	0.46
11:K:157:LYS:HE2	14:N:23:VAL:HB	1.97	0.46
34:2:1327:C:C6	37:j:17:ASN:ND2	2.84	0.46
37:j:9:GLY:N	40:R:140:ARG:HH12	2.14	0.46
38:k:250:LYS:CE	38:k:562:LEU:HD22	2.45	0.46
38:k:341:GLU:C	38:k:342:VAL:HG12	2.41	0.46
43:y:138:GLN:O	43:y:142:ASP:HB2	2.15	0.46
43:y:236:GLN:OE1	43:y:252:ALA:HB2	2.16	0.46
44:v:412:LEU:HD23	44:v:444:ILE:HD13	1.98	0.46
34:2:751:C:C2'	34:2:752:C:H5'	2.44	0.46
35:A:58:SER:CB	35:A:61:LYS:CE	2.88	0.46
35:A:195:ILE:HG21	35:A:235:TYR:HD2	1.81	0.46
41:3:68:C:O5'	41:3:68:C:H6	1.98	0.46
43:y:277:ASN:CG	43:y:278:LYS:N	2.73	0.46
44:v:369:GLY:O	44:v:371:ILE:N	2.36	0.46
44:v:389:LEU:N	44:v:389:LEU:HD22	2.31	0.46
16:P:22:VAL:N	16:P:23:PRO:CA	2.73	0.45
34:2:1547:G:C8	34:2:1547:G:OP2	2.69	0.45
35:A:185:THR:CB	35:A:186:PRO:HA	2.46	0.45
38:k:332:LYS:HA	38:k:332:LYS:HD2	1.70	0.45
38:k:517:VAL:CG1	38:k:519:GLU:HG2	2.45	0.45
41:3:60:C:O2'	41:3:61:C:H4'	2.16	0.45
43:y:112:VAL:HG21	43:y:145:LEU:HD13	1.98	0.45
44:v:345:THR:C	44:v:347:ARG:N	2.74	0.45
44:v:434:VAL:CG1	44:v:435:ASP:H	2.26	0.45
1:1:17:C:H2'	1:1:18:G:C5'	2.41	0.45
34:2:1813:A:C6	34:2:1814:G:C5	3.05	0.45
35:A:205:ILE:CD1	36:B:288:LYS:CB	2.91	0.45
38:k:17:LYS:NZ	38:k:20:LYS:HE3	2.24	0.45
38:k:450:GLN:CG	38:k:453:ASN:OD1	2.54	0.45
43:y:191:LYS:HD3	43:y:194:PHE:CE2	2.51	0.45
43:y:213:ASN:C	43:y:215:SER:N	2.74	0.45
43:y:330:PRO:O	43:y:331:ILE:HD13	2.16	0.45
44:v:748:ASP:CG	44:v:750:LYS:CG	2.89	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:216:ARG:C	9:I:218:LYS:H	2.22	0.45
34:2:679:U:H3'	34:2:679:U:H6	1.81	0.45
34:2:740:G:C2'	34:2:741:C:H5''	2.46	0.45
34:2:785:G:C2	34:2:786:C:C2	3.04	0.45
40:R:84:ILE:H	40:R:84:ILE:HD12	1.81	0.45
43:y:245:LEU:HD13	43:y:248:GLU:OE2	2.15	0.45
43:y:340:ARG:C	43:y:342:LEU:N	2.74	0.45
44:v:504:LEU:HD23	44:v:504:LEU:O	2.15	0.45
18:S:100:VAL:HG12	18:S:101:ASP:H	1.81	0.45
33:i:75:LYS:HZ2	37:j:27:VAL:CG2	2.29	0.45
37:j:10:LYS:HB2	41:3:54:G:N2	2.31	0.45
38:k:330:VAL:O	38:k:523:ILE:HG21	2.17	0.45
38:k:450:GLN:HB3	38:k:453:ASN:HD21	0.75	0.45
43:y:39:LYS:HB2	43:y:39:LYS:HZ3	1.80	0.45
43:y:75:LYS:HD3	43:y:79:GLN:OE1	2.17	0.45
43:y:302:LEU:CD1	43:y:306:MET:CE	2.89	0.45
43:y:368:ILE:CD1	43:y:510:HIS:CE1	3.00	0.45
44:v:368:GLU:O	44:v:368:GLU:HG2	2.16	0.45
44:v:409:MET:O	44:v:410:ASP:C	2.59	0.45
8:H:61:PHE:CZ	42:m:415:SER:CA	2.99	0.45
37:j:41:MET:CE	37:j:47:LEU:HD22	2.47	0.45
37:j:46:ARG:H	37:j:46:ARG:HG2	1.56	0.45
37:j:47:LEU:CG	37:j:48:GLU:N	2.79	0.45
38:k:105:VAL:CG2	38:k:263:ILE:HG12	2.46	0.45
39:U:147:GLY:C	39:U:148:VAL:HG23	2.42	0.45
43:y:312:GLN:OE1	43:y:317:ARG:HD2	2.16	0.45
6:F:196:GLY:C	6:F:198:ILE:HA	2.42	0.45
27:c:79:PHE:O	27:c:80:ARG:CG	2.65	0.45
34:2:190:A:H3'	34:2:191:C:H5''	1.98	0.45
34:2:684:A:H2	34:2:731:C:N3	2.08	0.45
38:k:431:LYS:HE3	38:k:477:GLY:O	2.14	0.45
43:y:150:VAL:HA	43:y:184:PHE:HZ	1.81	0.45
43:y:179:GLN:HE21	43:y:179:GLN:HA	1.79	0.45
43:y:246:TRP:HE1	44:v:729:PRO:HD2	1.80	0.45
44:v:760:LYS:CE	44:v:765:VAL:HB	2.47	0.45
37:j:11:ASN:C	37:j:13:ARG:N	2.73	0.45
37:j:68:LYS:C	37:j:69:VAL:HG23	2.42	0.45
38:k:385:LYS:CE	38:k:518:VAL:HG13	2.47	0.45
41:3:43:A:N9	41:3:44:C:C5	2.85	0.45
43:y:276:TYR:CE1	43:y:298:ARG:HB3	2.51	0.45
44:v:412:LEU:HG	44:v:412:LEU:O	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:v:459:MET:HE1	44:v:469:TYR:OH	2.17	0.45
28:d:13:ARG:CD	42:m:426:LYS:NZ	2.80	0.45
41:3:38:C:O2	41:3:38:C:H2'	2.15	0.45
43:y:169:ARG:HG2	43:y:170:VAL:N	2.30	0.45
43:y:297:HIS:CE1	43:y:325:ALA:CA	2.99	0.45
43:y:366:THR:H	43:y:370:LEU:HD21	1.82	0.45
43:y:375:VAL:HG22	43:y:379:VAL:CG1	2.46	0.45
44:v:487:GLN:NE2	44:v:503:TYR:CE1	2.85	0.45
8:H:29:GLN:NE2	42:m:472:LYS:HZ2	2.15	0.45
35:A:111:ILE:CD1	35:A:183:ARG:HH12	2.24	0.45
37:j:19:ASN:CB	37:j:20:GLU:CA	2.95	0.45
37:j:67:LYS:O	37:j:70:TRP:CZ3	2.70	0.45
43:y:124:PRO:CG	43:y:128:LEU:H	2.24	0.45
43:y:276:TYR:HD2	43:y:302:LEU:CD2	2.27	0.45
44:v:379:ILE:O	44:v:383:TYR:CD2	2.69	0.45
16:P:22:VAL:CG1	16:P:26:LEU:CG	2.86	0.45
16:P:25:TRP:O	16:P:25:TRP:CD2	2.70	0.45
16:P:25:TRP:O	16:P:25:TRP:CG	2.70	0.45
26:b:62:TYR:CD2	26:b:62:TYR:O	2.70	0.45
28:d:33:GLU:HG2	42:m:426:LYS:NZ	2.22	0.45
34:2:743:U:H2'	34:2:743:U:OP2	2.17	0.45
34:2:1818:A:H4'	37:j:44:ASN:O	2.16	0.45
35:A:54:ARG:CB	35:A:54:ARG:NH2	2.73	0.45
37:j:11:ASN:C	37:j:13:ARG:H	2.24	0.45
38:k:22:ARG:HD3	38:k:22:ARG:HA	1.71	0.45
38:k:74:ASN:OD1	38:k:74:ASN:N	2.50	0.45
38:k:140:TRP:CE3	38:k:140:TRP:HA	2.52	0.45
38:k:347:MET:C	38:k:348:TYR:O	2.52	0.45
38:k:414:GLN:CG	38:k:486:ASP:CA	2.95	0.45
40:R:142:ILE:HB	40:R:143:PRO:HD3	1.99	0.45
43:y:303:SER:O	43:y:307:ARG:HB2	2.17	0.45
44:v:373:LYS:HE2	44:v:431:LEU:HD23	1.88	0.45
16:P:22:VAL:HG11	16:P:26:LEU:HD11	1.98	0.44
25:a:98:GLU:C	25:a:98:GLU:CD	2.85	0.44
26:b:80:HIS:CE1	41:3:48:C:C4	3.05	0.44
34:2:1707:A:C8	34:2:1707:A:OP2	2.70	0.44
38:k:250:LYS:HE2	38:k:562:LEU:CD2	2.46	0.44
38:k:344:LYS:O	38:k:345:MET:HB2	2.17	0.44
38:k:412:LYS:CD	38:k:485:ILE:HB	2.47	0.44
43:y:68:LYS:CB	43:y:159:GLN:OE1	2.60	0.44
44:v:325:THR:O	44:v:327:ALA:N	2.49	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:c:71:ALA:O	27:c:73:LEU:HD22	2.16	0.44
34:2:743:U:C5	34:2:744:C:N3	2.85	0.44
37:j:72:ASN:H	37:j:72:ASN:ND2	2.01	0.44
38:k:76:PRO:HD3	38:k:323:ARG:HG3	1.98	0.44
38:k:185:GLY:O	38:k:189:ASP:HB2	2.16	0.44
43:y:291:PHE:HZ	43:y:355:LEU:C	2.23	0.44
43:y:347:ILE:HD13	44:v:723:ARG:HH21	0.66	0.44
34:2:684:A:C6	34:2:685:G:O6	2.70	0.44
34:2:1518:C:P	39:U:143:GLY:O	2.73	0.44
37:j:19:ASN:HB3	37:j:20:GLU:CA	2.47	0.44
38:k:4:LYS:CA	38:k:79:LEU:CG	2.61	0.44
38:k:492:LEU:C	38:k:497:ARG:HE	2.25	0.44
44:v:393:MET:C	44:v:397:MET:CG	2.91	0.44
27:c:50:ALA:H	27:c:71:ALA:HB2	1.81	0.44
30:f:118:ARG:H	30:f:118:ARG:HD3	1.81	0.44
34:2:792:G:P	34:2:792:G:H8	2.40	0.44
34:2:1815:U:C2'	34:2:1816:A:C5'	2.94	0.44
43:y:76:ASN:HA	43:y:79:GLN:CG	2.48	0.44
16:P:27:LYS:HE3	16:P:28:LEU:HD21	1.99	0.44
27:c:49:HIS:ND1	27:c:70:LYS:HA	2.32	0.44
27:c:65:GLN:OE1	27:c:72:ARG:NH2	2.51	0.44
34:2:784:G:C5	34:2:785:G:C5	3.05	0.44
34:2:1109:A:C5	34:2:1110:U:O4	2.70	0.44
37:j:29:LYS:HE2	37:j:35:TYR:CE2	2.53	0.44
37:j:62:ARG:HD3	37:j:63:GLY:O	2.16	0.44
37:j:71:ILE:HD13	37:j:77:ILE:HD12	1.95	0.44
43:y:230:LEU:H	43:y:230:LEU:HD22	1.81	0.44
44:v:338:GLN:O	44:v:340:ARG:N	2.50	0.44
44:v:410:ASP:C	44:v:412:LEU:H	2.25	0.44
1:1:17:C:H2'	1:1:18:G:P	2.58	0.44
4:D:80:ALA:O	4:D:81:PHE:CD2	2.70	0.44
17:Q:35:ALA:HB1	17:Q:109:GLY:H	1.82	0.44
34:2:1115:A:OP1	34:2:1116:U:C5	2.70	0.44
35:A:229:LEU:HD11	35:A:231:ALA:O	2.18	0.44
41:3:36:A:C8	41:3:36:A:OP2	2.70	0.44
43:y:75:LYS:HG3	43:y:165:ARG:NH1	2.23	0.44
43:y:212:HIS:O	43:y:212:HIS:CG	2.71	0.44
44:v:347:ARG:HG2	44:v:385:TYR:CD1	2.53	0.44
44:v:430:ASN:ND2	44:v:431:LEU:N	2.66	0.44
16:P:23:PRO:O	16:P:25:TRP:CD1	2.71	0.44
25:a:97:TYR:CE2	25:a:98:GLU:O	2.71	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:a:101:LYS:CG	25:a:107:ARG:HH21	2.12	0.44
28:d:35:MET:N	42:m:426:LYS:HE2	2.32	0.44
34:2:472:G:P	38:k:63:LYS:CE	3.05	0.44
34:2:1709:U:C2	34:2:1814:G:N2	2.86	0.44
37:j:67:LYS:NZ	41:3:56:U:H4'	2.32	0.44
38:k:21:CYS:O	38:k:22:ARG:HB2	2.17	0.44
38:k:168:ILE:HG22	38:k:239:MET:CG	2.47	0.44
38:k:206:LEU:HD23	38:k:224:ARG:HG3	2.00	0.44
41:3:53:U:C2'	41:3:54:G:O5'	2.66	0.44
43:y:101:THR:CG2	43:y:149:TRP:CB	2.44	0.44
43:y:122:GLN:O	43:y:123:THR:O	2.35	0.44
43:y:229:HIS:C	43:y:233:ARG:HG2	2.42	0.44
43:y:260:PHE:O	43:y:264:LYS:HB2	2.18	0.44
44:v:482:ILE:O	44:v:486:VAL:HG23	2.18	0.44
4:D:80:ALA:O	4:D:81:PHE:HD2	2.00	0.44
33:i:80:LEU:HD22	37:j:62:ARG:NH2	2.27	0.44
34:2:682:G:H2'	34:2:683:G:C8	2.52	0.44
34:2:735:C:H3'	34:2:736:C:H5''	2.00	0.44
34:2:737:C:H3'	34:2:738:U:C5'	2.30	0.44
34:2:1116:U:O2'	34:2:1117:G:C5'	2.62	0.44
35:A:154:LYS:HD2	35:A:184:LEU:HD23	1.99	0.44
38:k:17:LYS:CG	38:k:20:LYS:HE3	2.42	0.44
38:k:229:VAL:C	38:k:232:ILE:HG22	2.42	0.44
43:y:48:GLU:HG3	43:y:74:TYR:HH	1.80	0.44
43:y:150:VAL:CA	43:y:184:PHE:HZ	2.29	0.44
44:v:413:PHE:HA	44:v:489:TYR:CE2	2.53	0.44
44:v:476:GLU:C	44:v:476:GLU:CD	2.86	0.44
16:P:18:TYR:O	16:P:19:ARG:O	2.36	0.44
34:2:1812:A:H2	34:2:1813:A:C4	2.36	0.44
38:k:113:GLY:HA2	53:k:704:GNP:H5'1	1.99	0.44
38:k:182:GLY:CA	38:k:187:ILE:HD13	2.38	0.44
38:k:332:LYS:HD3	38:k:527:TYR:CE2	2.53	0.44
38:k:412:LYS:HD3	38:k:485:ILE:CA	2.48	0.44
41:3:58:C:OP2	41:3:58:C:C6	2.70	0.44
43:y:68:LYS:C	43:y:68:LYS:CD	2.86	0.44
44:v:408:LEU:CD2	44:v:411:ILE:HD12	2.47	0.44
44:v:409:MET:HB3	44:v:485:ARG:HD3	1.99	0.44
34:2:682:G:N3	34:2:683:G:N7	2.66	0.43
34:2:787:C:O5'	34:2:787:C:C6	2.71	0.43
34:2:1816:A:C2	34:2:1817:A:C6	3.06	0.43
38:k:17:LYS:C	38:k:19:LYS:H	2.26	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:k:140:TRP:HA	38:k:140:TRP:HE3	1.83	0.43
38:k:164:LEU:CD1	38:k:237:ILE:HD13	2.47	0.43
43:y:245:LEU:CB	43:y:248:GLU:CD	2.63	0.43
44:v:373:LYS:NZ	44:v:420:VAL:CB	2.81	0.43
44:v:375:LYS:CD	44:v:408:LEU:HD11	2.23	0.43
44:v:490:LEU:CD1	44:v:499:ILE:HG12	2.48	0.43
4:D:39:PHE:HB3	4:D:74:LEU:HD22	1.99	0.43
24:Z:58:GLU:CD	37:j:60:HIS:ND1	2.75	0.43
28:d:13:ARG:HH11	42:m:419:ALA:HB1	1.83	0.43
33:i:82:ARG:NH2	33:i:85:LYS:CA	2.73	0.43
34:2:745:U:C2	34:2:746:C:N3	2.86	0.43
38:k:100:PRO:HG3	38:k:155:TYR:CE1	2.54	0.43
41:3:69:U:H3'	41:3:69:U:H6	1.82	0.43
41:3:71:A:C6	41:3:72:G:O6	2.70	0.43
43:y:132:VAL:O	44:v:768:LEU:HD22	2.18	0.43
43:y:143:ARG:HG3	43:y:147:THR:HG21	1.99	0.43
43:y:257:HIS:CD2	43:y:358:LEU:HG	2.54	0.43
43:y:271:LEU:O	43:y:272:MET:C	2.61	0.43
44:v:349:ALA:HA	44:v:352:GLU:CG	2.48	0.43
44:v:354:LEU:CD1	44:v:378:ILE:HG13	2.48	0.43
44:v:424:ILE:HG22	44:v:425:LEU:N	2.33	0.43
34:2:683:G:H2'	34:2:684:A:H8	1.78	0.43
34:2:1103:G:N2	34:2:1104:G:H1'	2.33	0.43
35:A:20:VAL:CG2	35:A:71:VAL:HG23	2.49	0.43
35:A:120:GLU:O	35:A:126:GLN:HG3	2.18	0.43
35:A:193:ALA:HB3	35:A:237:MET:H	1.83	0.43
37:j:40:LYS:CG	37:j:48:GLU:HB3	2.48	0.43
37:j:77:ILE:HG13	37:j:94:LYS:HA	2.01	0.43
38:k:241:ASP:O	38:k:242:GLU:HB3	2.17	0.43
38:k:250:LYS:NZ	38:k:562:LEU:CD2	2.82	0.43
38:k:322:LEU:HG	38:k:323:ARG:H	1.83	0.43
43:y:68:LYS:HG2	43:y:163:LEU:HD22	1.99	0.43
43:y:124:PRO:CG	43:y:127:VAL:H	2.25	0.43
43:y:331:ILE:CG1	43:y:430:GLN:NE2	2.81	0.43
44:v:392:TYR:O	44:v:392:TYR:CD2	2.70	0.43
44:v:502:VAL:CG1	44:v:503:TYR:H	2.30	0.43
44:v:502:VAL:CG1	44:v:503:TYR:N	2.80	0.43
4:D:76:ASN:ND2	4:D:77:ASP:CB	2.76	0.43
28:d:13:ARG:CG	42:m:426:LYS:NZ	2.77	0.43
34:2:785:G:C2	34:2:786:C:O2	2.71	0.43
43:y:39:LYS:HB2	43:y:39:LYS:NZ	2.32	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:y:276:TYR:HE2	43:y:298:ARG:HG3	1.69	0.43
44:v:373:LYS:HG3	44:v:420:VAL:HG11	2.00	0.43
44:v:406:ASN:HA	44:v:485:ARG:HH12	1.83	0.43
44:v:427:GLU:OE1	44:v:427:GLU:HA	2.18	0.43
27:c:69:GLY:HA2	34:2:1010:G:O2'	2.18	0.43
28:d:38:THR:HG23	42:m:296:ASN:HA	1.99	0.43
34:2:734:C:H5	34:2:737:C:N4	2.17	0.43
34:2:790:A:H8	34:2:790:A:P	2.41	0.43
34:2:1708:C:H2'	34:2:1709:U:C6	2.53	0.43
38:k:345:MET:HG2	38:k:346:CYS:H	1.77	0.43
38:k:488:PRO:C	38:k:524:MET:HE1	2.43	0.43
43:y:146:LEU:C	43:y:148:PRO:CD	2.91	0.43
43:y:271:LEU:O	43:y:274:ASN:HB3	2.17	0.43
43:y:331:ILE:HD11	43:y:427:TYR:HB3	2.00	0.43
43:y:367:ARG:CG	43:y:368:ILE:N	2.73	0.43
44:v:325:THR:CA	44:v:326:HIS:CD2	3.01	0.43
44:v:530:SER:HB2	44:v:535:ASP:CG	2.44	0.43
25:a:12:PHE:CE1	34:2:836:C:C2'	2.66	0.43
27:c:79:PHE:O	27:c:80:ARG:CD	2.67	0.43
34:2:158:A:P	38:k:583:ILE:HG22	2.55	0.43
34:2:746:C:H5''	34:2:747:G:OP2	2.19	0.43
34:2:748:G:O2'	34:2:749:C:C6	2.71	0.43
35:A:229:LEU:HD13	36:B:285:ASP:HB3	2.00	0.43
38:k:17:LYS:HZ2	38:k:20:LYS:HE3	1.80	0.43
41:3:35:A:H2'	41:3:36:A:H5'	1.99	0.43
43:y:296:LEU:CD1	43:y:324:LEU:HB3	2.44	0.43
43:y:346:GLY:CA	43:y:347:ILE:CG1	2.85	0.43
44:v:384:ASP:C	44:v:386:ASN:H	2.27	0.43
24:Z:52:LEU:O	38:k:34:MET:CG	2.66	0.43
34:2:684:A:H2'	34:2:685:G:N7	2.32	0.43
41:3:35:A:C8	41:3:35:A:OP2	2.71	0.43
43:y:296:LEU:HD11	43:y:324:LEU:HD22	2.00	0.43
43:y:322:VAL:HG23	43:y:323:LEU:N	2.34	0.43
43:y:327:LEU:HB3	43:y:427:TYR:CD2	2.53	0.43
43:y:390:LEU:HB2	43:y:410:VAL:HG11	1.90	0.43
44:v:374:ILE:O	44:v:378:ILE:HG22	2.19	0.43
44:v:453:GLU:O	44:v:457:LYS:HG3	2.18	0.43
44:v:503:TYR:HD1	44:v:548:MET:SD	2.41	0.43
1:1:27:C:N3	1:1:28:U:C5	2.87	0.43
8:H:132:GLY:HA3	41:3:49:A:H61	1.84	0.43
14:N:30:LYS:CA	14:N:30:LYS:CE	2.97	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:k:4:LYS:CA	38:k:79:LEU:HD12	2.46	0.43
38:k:216:ASP:HB3	53:k:705:GNP:N1	2.34	0.43
38:k:229:VAL:CA	38:k:232:ILE:HG22	2.48	0.43
38:k:441:PHE:CZ	38:k:454:ILE:CG2	2.96	0.43
41:3:71:A:C5	41:3:72:G:O6	2.72	0.43
43:y:116:GLU:C	43:y:118:LEU:N	2.76	0.43
43:y:327:LEU:O	43:y:329:ILE:N	2.51	0.43
44:v:417:ASN:HB2	44:v:419:PHE:CE1	2.53	0.43
44:v:422:GLU:O	44:v:424:ILE:CD1	2.66	0.43
44:v:510:THR:HB	44:v:513:LYS:HE2	2.01	0.43
44:v:521:ARG:NH2	44:v:522:GLN:HE21	2.17	0.43
4:D:70:SER:HB3	4:D:73:ASP:HB3	2.01	0.43
34:2:682:G:N1	34:2:683:G:C5	2.87	0.43
34:2:1111:U:O2	34:2:1111:U:H3'	2.19	0.43
38:k:159:ILE:C	38:k:162:ASP:H	2.23	0.43
38:k:331:PHE:C	38:k:498:LEU:HD13	2.41	0.43
38:k:412:LYS:HD2	38:k:483:TYR:OH	2.18	0.43
38:k:416:ILE:HD13	38:k:471:ALA:HB2	2.00	0.43
43:y:13:LYS:NZ	43:y:13:LYS:HB3	2.33	0.43
44:v:339:ALA:HB1	44:v:342:LYS:HE3	2.00	0.43
44:v:373:LYS:CE	44:v:431:LEU:CD2	2.72	0.43
44:v:661:GLU:OE1	44:v:661:GLU:N	2.51	0.43
46:q:187:HIS:CG	46:q:228:MET:HG2	2.54	0.43
27:c:75:GLU:CD	44:v:388:ASN:HB2	2.44	0.43
34:2:1706:U:C2'	34:2:1707:A:H8	1.97	0.43
34:2:1706:U:O2'	34:2:1707:A:O5'	2.27	0.43
43:y:378:ASN:O	43:y:382:TYR:CD2	2.71	0.43
44:v:328:VAL:HG12	44:v:332:LYS:HE2	1.91	0.43
44:v:453:GLU:HG3	44:v:457:LYS:HE3	2.01	0.43
44:v:487:GLN:OE1	44:v:502:VAL:CG2	2.66	0.43
4:D:39:PHE:CB	4:D:74:LEU:HD22	2.48	0.42
24:Z:52:LEU:O	24:Z:53:GLU:CB	2.66	0.42
34:2:734:C:H3'	34:2:735:C:C5'	2.49	0.42
34:2:790:A:N6	34:2:791:A:N6	2.67	0.42
37:j:7:LYS:CG	37:j:8:GLY:N	2.82	0.42
38:k:164:LEU:HD23	38:k:237:ILE:HB	1.94	0.42
38:k:451:ILE:HA	38:k:453:ASN:HB2	0.90	0.42
38:k:502:ARG:HH22	38:k:506:ARG:HH21	1.67	0.42
40:R:143:PRO:HB3	41:3:55:G:O2'	2.19	0.42
43:y:6:GLN:O	43:y:7:ARG:HG3	2.18	0.42
43:y:108:SER:OG	43:y:145:LEU:HB3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:y:194:PHE:N	43:y:194:PHE:CD1	2.86	0.42
43:y:233:ARG:HD2	43:y:256:ILE:HD13	0.57	0.42
43:y:289:ALA:HA	43:y:292:HIS:HB3	2.01	0.42
44:v:443:CYS:O	44:v:447:LEU:HG	2.19	0.42
35:A:144:ARG:HB2	35:A:145:PRO:HD3	2.01	0.42
43:y:135:GLU:HB3	43:y:136:ASP:H	1.70	0.42
43:y:146:LEU:C	43:y:148:PRO:HD2	2.44	0.42
43:y:175:HIS:CE1	43:y:228:MET:N	2.87	0.42
43:y:289:ALA:O	43:y:293:ALA:HB2	2.18	0.42
43:y:378:ASN:HB3	43:y:382:TYR:HE2	1.83	0.42
43:y:399:ASN:HD21	50:u:313:ILE:CG2	2.32	0.42
44:v:373:LYS:CG	44:v:420:VAL:HG11	2.49	0.42
44:v:392:TYR:CE1	44:v:461:ASN:HD22	1.75	0.42
44:v:447:LEU:O	44:v:450:ARG:HB3	2.18	0.42
44:v:487:GLN:HE21	44:v:548:MET:HE1	1.84	0.42
44:v:760:LYS:HD3	44:v:765:VAL:HG12	2.01	0.42
34:2:737:C:H5'	34:2:738:U:OP2	2.19	0.42
38:k:549:GLN:NE2	38:k:557:LYS:HZ1	2.17	0.42
38:k:550:THR:O	38:k:554:GLY:N	2.43	0.42
43:y:75:LYS:CA	43:y:78:CYS:SG	2.95	0.42
43:y:175:HIS:NE2	43:y:228:MET:CE	2.81	0.42
43:y:265:LYS:H	43:y:265:LYS:HG2	1.49	0.42
44:v:349:ALA:HA	44:v:352:GLU:HG3	2.02	0.42
44:v:407:GLU:OE1	44:v:407:GLU:HA	2.19	0.42
44:v:454:GLU:OE1	44:v:454:GLU:HA	2.19	0.42
44:v:484:GLU:HA	44:v:484:GLU:OE2	2.19	0.42
44:v:736:HIS:HD2	44:v:759:GLU:HB3	1.75	0.42
10:J:100:ILE:HG13	34:2:736:C:O2	2.19	0.42
37:j:15:GLY:O	37:j:16:LYS:HG3	2.19	0.42
38:k:31:VAL:C	38:k:33:ARG:H	2.27	0.42
38:k:176:ILE:O	38:k:176:ILE:HG12	2.19	0.42
38:k:378:LEU:HD13	38:k:379:GLY:HA2	0.95	0.42
43:y:68:LYS:HB2	43:y:159:GLN:CD	2.43	0.42
43:y:68:LYS:CE	43:y:163:LEU:HD23	2.41	0.42
43:y:125:GLU:OE1	43:y:125:GLU:HA	2.19	0.42
43:y:205:LEU:HG	43:y:209:GLN:NE2	2.32	0.42
43:y:356:ALA:HB1	43:y:363:ALA:O	2.19	0.42
24:Z:52:LEU:HD13	38:k:33:ARG:NH2	2.34	0.42
34:2:1751:G:H1	34:2:1769:U:H3	1.66	0.42
37:j:7:LYS:HG3	37:j:8:GLY:N	2.30	0.42
37:j:70:TRP:CZ2	41:3:55:G:H1'	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:y:371:ILE:CG2	43:y:372:ASN:H	2.31	0.42
43:y:397:GLU:OE1	43:y:397:GLU:HA	2.19	0.42
44:v:464:PRO:CG	44:v:465:HIS:H	2.33	0.42
44:v:557:ALA:N	44:v:558:LYS:CB	2.81	0.42
48:s:77:LEU:HA	48:s:79:HIS:H	1.84	0.42
4:D:82:ARG:HH21	4:D:82:ARG:CG	2.33	0.42
34:2:791:A:C8	34:2:791:A:O5'	2.72	0.42
37:j:68:LYS:HD2	37:j:68:LYS:HA	1.55	0.42
43:y:233:ARG:CG	43:y:256:ILE:HD13	2.39	0.42
43:y:344:MET:CA	43:y:345:ASP:HB3	2.23	0.42
44:v:402:LEU:O	44:v:405:ILE:CG2	2.63	0.42
44:v:430:ASN:HD22	44:v:431:LEU:H	1.65	0.42
44:v:469:TYR:CD1	44:v:473:LEU:HG	2.55	0.42
1:l:33:C:P	18:S:146:ARG:NH1	2.93	0.42
25:a:10:ARG:HE	25:a:10:ARG:HB3	1.48	0.42
25:a:11:LYS:N	34:2:837:G:O6	2.42	0.42
25:a:101:LYS:HG2	25:a:107:ARG:HH22	1.85	0.42
38:k:7:ARG:O	38:k:8:ILE:HG12	2.20	0.42
38:k:331:PHE:H	38:k:498:LEU:HD13	1.83	0.42
43:y:105:LYS:O	43:y:106:GLU:C	2.63	0.42
43:y:274:ASN:HA	43:y:277:ASN:HD21	1.83	0.42
43:y:323:LEU:O	43:y:326:THR:OG1	2.28	0.42
43:y:331:ILE:HD11	43:y:427:TYR:O	2.18	0.42
43:y:342:LEU:CD2	44:v:702:GLU:HG3	2.50	0.42
44:v:375:LYS:CB	44:v:408:LEU:CD2	2.82	0.42
44:v:429:GLU:HA	44:v:429:GLU:OE2	2.20	0.42
44:v:453:GLU:OE1	44:v:453:GLU:HA	2.19	0.42
46:q:117:ILE:HB	46:q:139:HIS:CD2	2.54	0.42
27:c:74:THR:OG1	27:c:75:GLU:N	2.50	0.42
34:2:786:C:O5'	34:2:786:C:C6	2.70	0.42
34:2:1327:C:O2'	37:j:17:ASN:ND2	2.47	0.42
34:2:1457:G:H3'	34:2:1459:U:H3	1.84	0.42
38:k:315:GLY:CA	38:k:326:ASP:CB	2.88	0.42
43:y:268:LYS:HE3	43:y:269:PRO:CD	2.50	0.42
43:y:303:SER:O	43:y:307:ARG:HG3	2.19	0.42
44:v:324:ILE:O	44:v:324:ILE:HG22	2.20	0.42
44:v:372:VAL:HG12	44:v:376:PHE:CE2	2.55	0.42
44:v:760:LYS:NZ	44:v:765:VAL:CG1	2.56	0.42
16:P:23:PRO:HG2	16:P:25:TRP:NE1	2.35	0.42
25:a:99:LYS:O	25:a:100:LYS:CB	2.68	0.42
34:2:737:C:C3'	34:2:738:U:C5'	2.96	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:2:791:A:O5'	34:2:791:A:H8	2.03	0.42
37:j:67:LYS:HE2	37:j:67:LYS:HB2	1.88	0.42
38:k:159:ILE:O	38:k:162:ASP:HA	2.20	0.42
38:k:475:CYS:SG	38:k:483:TYR:HE1	2.42	0.42
43:y:284:TRP:CD1	43:y:284:TRP:C	2.96	0.42
44:v:469:TYR:CD1	44:v:473:LEU:CD1	3.03	0.42
44:v:701:HIS:CE1	44:v:708:ARG:HB2	2.54	0.42
25:a:8:ARG:CZ	34:2:831:C:H5	2.32	0.42
34:2:795:U:C4	34:2:863:G:C2	3.07	0.42
34:2:1327:C:C2'	37:j:17:ASN:HD21	2.33	0.42
34:2:1707:A:C2	34:2:1708:C:C1'	3.00	0.42
38:k:21:CYS:HB2	38:k:66:PRO:HG2	2.02	0.42
43:y:28:LEU:HD23	43:y:29:ASP:CA	2.49	0.42
43:y:81:VAL:HB	43:y:82:ASN:H	1.73	0.42
44:v:345:THR:O	44:v:346:ASP:HB3	2.20	0.42
24:Z:58:GLU:CG	37:j:60:HIS:CE1	3.01	0.41
37:j:62:ARG:NH1	37:j:64:LYS:CD	2.83	0.41
38:k:414:GLN:HE21	38:k:486:ASP:N	2.18	0.41
43:y:100:LYS:C	43:y:149:TRP:CD1	2.97	0.41
34:2:1112:C:N3	34:2:1113:C:C2	2.87	0.41
34:2:1819:A:OP1	37:j:66:ARG:HD3	2.20	0.41
35:A:229:LEU:HD13	36:B:284:VAL:CG2	2.50	0.41
38:k:133:LYS:C	38:k:134:TYR:CG	2.97	0.41
38:k:193:GLU:O	38:k:197:GLN:HG2	2.19	0.41
38:k:485:ILE:HD11	38:k:488:PRO:HB3	2.02	0.41
38:k:591:SER:C	38:k:592:GLY:C	2.88	0.41
40:R:140:ARG:O	40:R:141:PHE:HB2	2.20	0.41
43:y:59:VAL:HG13	43:y:152:PHE:CE2	2.54	0.41
27:c:61:THR:HG22	44:v:384:ASP:OD2	2.18	0.41
34:2:745:U:C4	34:2:746:C:N4	2.88	0.41
38:k:374:ILE:HD13	38:k:505:LYS:NZ	2.36	0.41
41:3:63:G:N3	41:3:63:G:H2'	2.34	0.41
43:y:291:PHE:CE1	43:y:359:LEU:CB	2.94	0.41
44:v:355:GLN:HA	44:v:355:GLN:HE21	1.84	0.41
34:2:741:C:C3'	34:2:741:C:C6	3.03	0.41
37:j:71:ILE:O	37:j:72:ASN:O	2.38	0.41
38:k:209:LEU:HD13	38:k:221:GLU:HG2	1.96	0.41
43:y:147:THR:HA	43:y:150:VAL:HG21	2.01	0.41
43:y:316:GLN:HG3	43:y:317:ARG:N	2.36	0.41
44:v:375:LYS:C	44:v:408:LEU:HD11	2.45	0.41
38:k:8:ILE:HG22	38:k:9:ALA:N	2.34	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:k:167:ILE:CG2	38:k:238:PHE:HA	2.50	0.41
38:k:194:THR:HB	38:k:195:LYS:H	1.68	0.41
43:y:15:ALA:HA	43:y:27:ALA:HB1	2.02	0.41
43:y:86:LEU:O	43:y:90:VAL:HG12	2.21	0.41
43:y:121:ILE:C	43:y:121:ILE:CD1	2.87	0.41
43:y:291:PHE:O	43:y:359:LEU:HD21	2.21	0.41
43:y:323:LEU:HD13	43:y:424:LEU:CB	2.49	0.41
43:y:327:LEU:CB	43:y:427:TYR:HD2	2.33	0.41
43:y:344:MET:O	43:y:344:MET:SD	2.79	0.41
43:y:370:LEU:O	43:y:374:MET:SD	2.79	0.41
44:v:399:GLN:HA	44:v:399:GLN:HE21	1.85	0.41
44:v:502:VAL:HG13	44:v:503:TYR:CD2	2.56	0.41
44:v:512:TYR:OH	44:v:674:HIS:CE1	2.73	0.41
13:M:1:MET:HA	13:M:3:MET:H	1.85	0.41
34:2:68:A:C6	34:2:69:C:C4	3.09	0.41
34:2:790:A:H2'	34:2:791:A:H8	1.83	0.41
34:2:1116:U:HO2'	34:2:1117:G:C5'	2.25	0.41
35:A:20:VAL:HG23	35:A:71:VAL:HG23	2.02	0.41
38:k:451:ILE:HG22	38:k:454:ILE:CG2	2.51	0.41
41:3:65:C:H4'	41:3:66:U:OP1	2.20	0.41
43:y:79:GLN:HB3	43:y:80:GLN:H	1.67	0.41
43:y:175:HIS:CG	43:y:231:GLU:OE2	2.73	0.41
43:y:262:LEU:O	43:y:265:LYS:CE	2.69	0.41
27:c:69:GLY:O	27:c:70:LYS:O	2.39	0.41
34:2:686:G:O5'	34:2:686:G:C8	2.70	0.41
34:2:742:C:C3'	34:2:742:C:C6	3.04	0.41
37:j:21:SER:O	37:j:23:LYS:CG	2.66	0.41
37:j:28:PHE:HD1	37:j:35:TYR:OH	2.03	0.41
38:k:308:GLY:HA2	38:k:311:ILE:HG12	2.03	0.41
38:k:318:PRO:HB2	38:k:322:LEU:HB2	2.02	0.41
38:k:330:VAL:O	38:k:331:PHE:HB2	2.21	0.41
38:k:347:MET:HB2	38:k:347:MET:HE3	1.66	0.41
38:k:451:ILE:C	38:k:452:GLU:N	2.79	0.41
41:3:49:A:OP2	41:3:49:A:C2	2.69	0.41
41:3:73:G:C5	41:3:74:A:N7	2.89	0.41
43:y:51:MET:CE	43:y:70:GLY:O	2.68	0.41
43:y:63:LYS:CD	43:y:66:LEU:HD12	2.49	0.41
43:y:194:PHE:HE1	43:y:248:GLU:OE2	2.02	0.41
43:y:284:TRP:CB	43:y:292:HIS:NE2	2.82	0.41
43:y:522:GLN:HE21	43:y:526:MET:HE3	1.85	0.41
1:1:18:G:O6	35:A:107:THR:CG2	2.68	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:c:38:PRO:C	27:c:40:CYS:N	2.76	0.41
34:2:745:U:C3'	34:2:745:U:C6	3.03	0.41
34:2:746:C:C3'	34:2:747:G:C8	3.03	0.41
38:k:229:VAL:HA	38:k:232:ILE:CG2	2.50	0.41
38:k:498:LEU:HD21	38:k:523:ILE:HB	2.02	0.41
40:R:140:ARG:HH21	40:R:140:ARG:CG	2.32	0.41
43:y:161:LEU:HD23	43:y:174:TYR:HA	2.03	0.41
43:y:193:GLU:OE1	43:y:245:LEU:HD12	2.21	0.41
43:y:213:ASN:O	43:y:215:SER:N	2.48	0.41
43:y:323:LEU:CD1	43:y:424:LEU:HD22	2.50	0.41
43:y:399:ASN:HD21	50:u:313:ILE:HG21	1.84	0.41
24:Z:96:GLU:CG	38:k:34:MET:HE3	2.48	0.41
24:Z:140:ARG:HE	24:Z:142:ARG:HE	1.69	0.41
26:b:62:TYR:O	26:b:62:TYR:CG	2.74	0.41
33:i:80:LEU:HD11	37:j:92:ILE:CD1	2.49	0.41
34:2:734:C:H41	34:2:737:C:N4	2.19	0.41
35:A:52:SER:OG	35:A:54:ARG:HG2	2.21	0.41
38:k:4:LYS:CB	38:k:79:LEU:HD12	2.51	0.41
38:k:377:MET:HE1	38:k:389:ILE:HD11	2.02	0.41
38:k:521:ASP:CA	38:k:524:MET:HB3	2.48	0.41
43:y:37:SER:C	43:y:39:LYS:N	2.76	0.41
43:y:327:LEU:HD23	43:y:424:LEU:C	2.44	0.41
43:y:368:ILE:HD12	43:y:510:HIS:CE1	2.55	0.41
43:y:371:ILE:CG2	43:y:372:ASN:N	2.84	0.41
44:v:356:LEU:O	44:v:357:LEU:HG	2.21	0.41
44:v:396:GLU:CD	44:v:396:GLU:H	2.29	0.41
44:v:402:LEU:HA	44:v:405:ILE:HG22	2.02	0.41
44:v:483:ILE:HG13	44:v:484:GLU:N	2.36	0.41
44:v:489:TYR:O	44:v:490:LEU:CB	2.66	0.41
44:v:752:CYS:CB	44:v:783:ILE:HG21	2.45	0.41
46:q:172:TRP:CZ2	46:q:199:HIS:CD2	3.09	0.41
1:1:26:G:H1	1:1:44:A:H61	1.68	0.41
34:2:158:A:P	38:k:583:ILE:CG2	3.01	0.41
38:k:169:LYS:CE	38:k:241:ASP:O	2.69	0.41
43:y:299:LEU:C	43:y:321:ARG:HH11	2.28	0.41
44:v:367:GLY:CA	44:v:368:GLU:C	2.94	0.41
34:2:1705:C:C4'	37:j:42:LEU:HD21	2.50	0.40
35:A:202:TYR:HB2	36:B:355:LYS:HB2	2.00	0.40
38:k:133:LYS:O	38:k:134:TYR:CG	2.74	0.40
38:k:183:THR:O	38:k:187:ILE:HG21	2.04	0.40
38:k:329:LEU:HD13	38:k:329:LEU:HA	1.80	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:y:190:ARG:CB	43:y:243:MET:SD	3.00	0.40
44:v:382:LEU:HD21	44:v:400:LYS:CE	2.51	0.40
44:v:512:TYR:CE1	44:v:674:HIS:ND1	2.89	0.40
44:v:554:TYR:C	44:v:557:ALA:N	2.75	0.40
47:r:275:HIS:CE1	47:r:312:ALA:HA	2.56	0.40
38:k:175:GLN:O	38:k:176:ILE:HB	2.20	0.40
38:k:431:LYS:CE	38:k:478:LYS:N	2.77	0.40
40:R:141:PHE:C	40:R:142:ILE:CG1	2.93	0.40
41:3:56:U:H6	41:3:56:U:H5''	1.85	0.40
43:y:338:ILE:CG1	44:v:745:LYS:HD2	2.51	0.40
43:y:347:ILE:HG13	43:y:348:ILE:CG1	2.51	0.40
43:y:436:ILE:HG21	43:y:467:LEU:HD11	2.02	0.40
46:q:200:LEU:HD13	46:q:213:ILE:HD11	2.02	0.40
6:F:3:VAL:HG13	6:F:4:GLN:H	1.85	0.40
9:I:233:ARG:O	9:I:236:SER:HB2	2.21	0.40
38:k:6:THR:O	38:k:74:ASN:HA	2.22	0.40
41:3:73:G:C4	41:3:74:A:C8	3.09	0.40
43:y:24:LYS:HG3	43:y:61:LEU:HD11	2.02	0.40
43:y:68:LYS:CG	43:y:163:LEU:HD22	2.50	0.40
43:y:150:VAL:HA	43:y:184:PHE:CZ	2.56	0.40
43:y:300:TYR:HA	43:y:321:ARG:NE	2.37	0.40
43:y:307:ARG:HH21	43:y:321:ARG:HD2	1.86	0.40
43:y:329:ILE:HG21	43:y:371:ILE:HB	2.04	0.40
43:y:337:ASP:O	43:y:341:LEU:HB2	2.21	0.40
44:v:495:THR:OG1	44:v:496:THR:N	2.54	0.40
1:1:5:A:C2	1:1:70:G:C4	3.10	0.40
38:k:73:VAL:HG23	38:k:322:LEU:CD2	2.43	0.40
43:y:348:ILE:O	43:y:348:ILE:HG22	2.20	0.40
44:v:837:GLN:H	45:w:348:HIS:CE1	2.39	0.40
24:Z:50:ILE:HD11	38:k:58:CYS:CB	2.36	0.40
34:2:679:U:C6	34:2:679:U:C3'	3.04	0.40
34:2:739:U:HO2'	34:2:740:G:P	2.42	0.40
34:2:744:C:OP1	34:2:744:C:H4'	2.21	0.40
34:2:1708:C:H2'	34:2:1709:U:H6	1.87	0.40
37:j:15:GLY:O	37:j:16:LYS:HD2	2.21	0.40
38:k:6:THR:HB	38:k:75:LEU:CB	2.52	0.40
38:k:21:CYS:C	38:k:23:GLN:N	2.80	0.40
38:k:213:ASN:O	38:k:217:LEU:HD13	2.21	0.40
41:3:73:G:C5	41:3:74:A:C8	3.10	0.40
43:y:165:ARG:C	43:y:167:ASN:N	2.79	0.40
43:y:174:TYR:OH	43:y:203:MET:CE	2.70	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:v:334:ASN:HA	44:v:337:LEU:HD11	2.04	0.40
44:v:476:GLU:OE1	44:v:477:ALA:N	2.54	0.40
44:v:479:VAL:O	44:v:483:ILE:HG23	2.21	0.40
44:v:841:THR:HG22	45:w:349:GLN:HE22	1.86	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	
2	I	23/25 (92%)	23 (100%)	0	0	100	100
3	C	206/208 (99%)	177 (86%)	21 (10%)	8 (4%)	2	20
4	D	213/264 (81%)	186 (87%)	21 (10%)	6 (3%)	4	26
5	E	224/226 (99%)	208 (93%)	14 (6%)	2 (1%)	14	46
6	F	225/227 (99%)	202 (90%)	14 (6%)	9 (4%)	2	20
7	G	261/263 (99%)	233 (89%)	24 (9%)	4 (2%)	8	37
8	H	189/191 (99%)	169 (89%)	17 (9%)	3 (2%)	7	36
9	I	235/237 (99%)	209 (89%)	22 (9%)	4 (2%)	7	35
10	J	188/190 (99%)	161 (86%)	18 (10%)	9 (5%)	2	16
11	K	204/206 (99%)	178 (87%)	20 (10%)	6 (3%)	3	26
12	L	180/182 (99%)	167 (93%)	11 (6%)	2 (1%)	11	43
13	M	96/98 (98%)	74 (77%)	16 (17%)	6 (6%)	1	12
14	N	156/158 (99%)	130 (83%)	22 (14%)	4 (3%)	4	27
15	O	122/132 (92%)	105 (86%)	13 (11%)	4 (3%)	3	24
16	P	148/150 (99%)	130 (88%)	11 (7%)	7 (5%)	2	17
17	Q	134/151 (89%)	119 (89%)	12 (9%)	3 (2%)	5	30

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	S	139/141 (99%)	126 (91%)	11 (8%)	2 (1%)	9	38
19	T	124/135 (92%)	112 (90%)	8 (6%)	4 (3%)	3	24
20	V	139/145 (96%)	128 (92%)	8 (6%)	3 (2%)	5	30
21	W	102/119 (86%)	93 (91%)	9 (9%)	0	100	100
22	X	80/82 (98%)	71 (89%)	7 (9%)	2 (2%)	4	28
23	Y	127/130 (98%)	117 (92%)	6 (5%)	4 (3%)	3	25
24	Z	140/142 (99%)	129 (92%)	7 (5%)	4 (3%)	3	26
25	a	124/133 (93%)	104 (84%)	10 (8%)	10 (8%)	1	8
26	b	97/115 (84%)	86 (89%)	10 (10%)	1 (1%)	12	45
27	c	82/84 (98%)	56 (68%)	16 (20%)	10 (12%)	0	4
28	d	62/69 (90%)	57 (92%)	4 (6%)	1 (2%)	7	36
29	e	51/53 (96%)	40 (78%)	7 (14%)	4 (8%)	1	8
30	f	69/71 (97%)	51 (74%)	12 (17%)	6 (9%)	0	7
31	g	311/313 (99%)	273 (88%)	33 (11%)	5 (2%)	7	36
32	n	73/75 (97%)	69 (94%)	3 (4%)	1 (1%)	9	38
33	i	57/59 (97%)	49 (86%)	7 (12%)	1 (2%)	6	34
35	A	264/266 (99%)	233 (88%)	25 (10%)	6 (2%)	5	30
36	B	420/422 (100%)	352 (84%)	48 (11%)	20 (5%)	2	16
37	j	107/144 (74%)	64 (60%)	27 (25%)	16 (15%)	0	2
38	k	577/595 (97%)	431 (75%)	95 (16%)	51 (9%)	0	7
39	U	141/152 (93%)	123 (87%)	12 (8%)	6 (4%)	2	18
40	R	138/145 (95%)	107 (78%)	18 (13%)	13 (9%)	0	6
42	m	363/548 (66%)	336 (93%)	25 (7%)	2 (1%)	21	54
43	y	601/1350 (44%)	457 (76%)	85 (14%)	59 (10%)	0	6
44	v	548/913 (60%)	446 (81%)	72 (13%)	30 (6%)	1	14
45	w	417/445 (94%)	349 (84%)	57 (14%)	11 (3%)	4	27
46	q	270/272 (99%)	226 (84%)	32 (12%)	12 (4%)	2	18
47	r	322/352 (92%)	267 (83%)	42 (13%)	13 (4%)	2	20
48	s	213/218 (98%)	201 (94%)	10 (5%)	2 (1%)	14	46
49	t	370/564 (66%)	328 (89%)	38 (10%)	4 (1%)	11	43
50	u	363/374 (97%)	308 (85%)	47 (13%)	8 (2%)	5	30

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	9695/11534 (84%)	8260 (85%)	1047 (11%)	388 (4%)	4	20

All (388) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	191	ARG
4	D	78	GLU
4	D	209	ASP
6	F	3	VAL
6	F	193	ASP
6	F	219	PRO
8	H	41	VAL
9	I	69	THR
10	J	106	ARG
11	K	158	ILE
12	L	148	ILE
13	M	35	LEU
14	N	66	VAL
14	N	157	LYS
15	O	95	ASP
16	P	19	ARG
16	P	20	ARG
20	V	34	VAL
23	Y	30	CYS
25	a	10	ARG
25	a	100	LYS
25	a	102	THR
25	a	105	LYS
27	c	36	LYS
27	c	37	CYS
27	c	73	LEU
27	c	77	CYS
29	e	25	SER
30	f	102	VAL
35	A	171	ASP
35	A	185	THR
35	A	266	ARG
36	B	194	LYS
36	B	279	LYS
36	B	280	PRO
36	B	283	GLU
36	B	289	GLY

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Mol	Chain	Res	Type
36	B	402	ASP
36	B	405	ALA
37	j	16	LYS
37	j	20	GLU
37	j	21	SER
37	j	24	ARG
37	j	44	ASN
37	j	66	ARG
37	j	72	ASN
37	j	75	ASP
37	j	94	LYS
38	k	20	LYS
38	k	58	CYS
38	k	134	TYR
38	k	140	TRP
38	k	176	ILE
38	k	316	TYR
38	k	318	PRO
38	k	331	PHE
38	k	333	VAL
38	k	348	TYR
38	k	435	ALA
38	k	439	PRO
38	k	456	ASP
38	k	526	THR
38	k	528	LEU
39	U	90	VAL
39	U	144	ARG
40	R	126	VAL
40	R	142	ILE
43	y	4	TYR
43	y	7	ARG
43	y	8	PRO
43	y	79	GLN
43	y	80	GLN
43	y	123	THR
43	y	160	CYS
43	y	164	LEU
43	y	173	LEU
43	y	219	ASN
43	y	284	TRP
43	y	329	ILE

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Mol	Chain	Res	Type
43	y	345	ASP
44	v	342	LYS
44	v	376	PHE
44	v	391	THR
44	v	392	TYR
44	v	464	PRO
44	v	490	LEU
44	v	499	ILE
44	v	558	LYS
44	v	749	TRP
45	w	50	MET
45	w	51	VAL
45	w	200	SER
45	w	221	VAL
46	q	224	PRO
46	q	299	SER
46	q	318	ILE
47	r	305	PHE
48	s	204	LYS
50	u	334	VAL
50	u	335	SER
50	u	336	HIS
3	C	46	ILE
4	D	81	PHE
5	E	159	ILE
6	F	131	ALA
10	J	17	ASP
10	J	67	PRO
10	J	139	ILE
13	M	34	GLU
13	M	36	ALA
14	N	24	LEU
15	O	118	SER
16	P	24	THR
17	Q	66	ARG
17	Q	138	ASP
18	S	44	PRO
20	V	143	LYS
22	X	10	ASP
23	Y	58	ALA
24	Z	87	ASN
25	a	86	GLU

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Mol	Chain	Res	Type
27	c	70	LYS
30	f	98	VAL
36	B	63	VAL
36	B	224	VAL
36	B	229	ALA
36	B	398	ARG
36	B	403	LYS
36	B	452	GLU
37	j	29	LYS
37	j	46	ARG
38	k	132	GLY
38	k	185	GLY
38	k	187	ILE
38	k	322	LEU
38	k	329	LEU
38	k	338	ASN
38	k	342	VAL
38	k	345	MET
38	k	358	GLY
38	k	408	ASN
38	k	514	THR
38	k	527	TYR
40	R	12	PHE
40	R	133	ILE
40	R	134	GLY
40	R	135	ALA
43	y	62	ARG
43	y	116	GLU
43	y	120	ASN
43	y	167	ASN
43	y	168	SER
43	y	188	TYR
43	y	241	ILE
43	y	270	GLN
43	y	286	SER
43	y	331	ILE
44	v	377	ASN
44	v	422	GLU
44	v	458	ILE
44	v	459	MET
44	v	487	GLN
44	v	498	GLU

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Mol	Chain	Res	Type
45	w	28	VAL
46	q	179	ILE
46	q	240	ALA
47	r	159	GLN
47	r	205	ILE
49	t	378	TYR
50	u	57	ASP
4	D	207	LEU
6	F	205	PRO
8	H	22	LYS
9	I	236	SER
10	J	13	GLY
12	L	21	GLU
15	O	75	ASN
16	P	30	SER
18	S	118	THR
19	T	83	ASN
19	T	94	GLU
23	Y	71	LYS
24	Z	86	PRO
24	Z	109	GLY
25	a	30	PRO
25	a	52	PRO
25	a	106	GLN
27	c	38	PRO
27	c	78	SER
27	c	83	GLN
28	d	52	GLU
29	e	24	CYS
31	g	13	GLY
31	g	161	SER
32	n	112	ASN
33	i	79	SER
35	A	55	ARG
36	B	89	ASN
36	B	135	GLY
36	B	179	PRO
36	B	378	PRO
37	j	42	LEU
37	j	74	SER
38	k	88	CYS
38	k	98	PRO

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Mol	Chain	Res	Type
38	k	175	GLN
38	k	327	ALA
38	k	380	GLU
38	k	395	ARG
38	k	448	PRO
38	k	477	GLY
38	k	585	ASP
40	R	10	ARG
40	R	83	MET
43	y	42	THR
43	y	187	GLN
43	y	211	HIS
43	y	212	HIS
43	y	214	GLN
43	y	215	SER
43	y	223	PRO
43	y	267	PRO
43	y	328	SER
43	y	348	ILE
43	y	373	ASP
43	y	399	ASN
43	y	540	ALA
44	v	339	ALA
44	v	370	VAL
44	v	383	TYR
44	v	390	ALA
44	v	428	SER
44	v	493	LYS
44	v	655	LEU
46	q	228	MET
47	r	35	ALA
47	r	167	TYR
47	r	312	ALA
49	t	273	SER
49	t	500	LEU
50	u	108	ASN
3	C	71	PRO
3	C	155	ARG
4	D	56	LYS
5	E	161	LYS
7	G	30	ARG
7	G	153	LEU

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Mol	Chain	Res	Type
10	J	6	ALA
10	J	37	LYS
10	J	116	ARG
11	K	22	HIS
11	K	31	ARG
11	K	144	LYS
13	M	94	LEU
15	O	120	ALA
16	P	22	VAL
16	P	26	LEU
16	P	138	ASN
17	Q	64	ALA
19	T	84	TYR
22	X	28	ASP
24	Z	53	GLU
25	a	9	THR
26	b	11	ALA
27	c	41	TYR
29	e	8	TRP
30	f	91	ASN
30	f	122	PRO
31	g	127	LYS
35	A	40	ASN
38	k	133	LYS
38	k	265	PRO
38	k	321	ASN
38	k	337	ALA
38	k	446	MET
38	k	450	GLN
39	U	89	ASP
39	U	95	TYR
40	R	140	ARG
42	m	244	ASN
42	m	295	ALA
43	y	41	ARG
43	y	119	ASP
43	y	162	ASP
43	y	165	ARG
43	y	231	GLU
43	y	363	ALA
43	y	486	HIS
43	y	497	LEU

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Mol	Chain	Res	Type
43	y	505	ALA
44	v	431	LEU
44	v	707	ARG
45	w	26	LEU
45	w	76	THR
46	q	109	ARG
46	q	114	ALA
46	q	178	ASP
47	r	54	GLN
47	r	90	ASP
50	u	192	TYR
3	C	199	PRO
4	D	179	ASN
6	F	142	LEU
6	F	216	GLU
7	G	83	PRO
8	H	184	SER
11	K	53	LYS
11	K	133	GLU
19	T	120	THR
20	V	39	LEU
25	a	96	LEU
27	c	4	ALA
30	f	136	PHE
30	f	146	LEU
35	A	59	ILE
36	B	196	LYS
36	B	461	GLU
37	j	25	GLU
38	k	191	LYS
38	k	330	VAL
38	k	379	GLY
39	U	141	ARG
39	U	148	VAL
40	R	38	SER
40	R	74	GLU
40	R	130	ARG
43	y	81	VAL
43	y	225	SER
43	y	227	SER
43	y	229	HIS
43	y	233	ARG

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Mol	Chain	Res	Type
43	y	237	LEU
43	y	268	LYS
43	y	421	GLU
44	v	416	PRO
44	v	423	ASN
45	w	326	VAL
46	q	94	LEU
47	r	125	TYR
47	r	154	PRO
47	r	178	LYS
47	r	183	SER
49	t	294	LEU
50	u	118	PRO
3	C	126	ASP
3	C	206	ASP
6	F	191	PRO
9	I	154	ARG
13	M	2	LEU
29	e	36	LEU
31	g	191	HIS
36	B	105	ASP
37	j	23	LYS
37	j	27	VAL
38	k	319	THR
43	y	26	PRO
43	y	327	LEU
44	v	358	VAL
45	w	22	LEU
45	w	48	THR
50	u	193	THR
3	C	3	GLY
7	G	152	PRO
13	M	3	MET
14	N	26	GLY
38	k	99	ILE
38	k	100	PRO
38	k	137	PRO
43	y	347	ILE
44	v	374	ILE
47	r	112	ILE
43	y	121	ILE
45	w	91	ILE

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Mol	Chain	Res	Type
46	q	138	PRO
6	F	196	GLY
10	J	45	ILE
23	Y	29	PRO
31	g	275	ILE
38	k	177	PRO
38	k	237	ILE
43	y	170	VAL
43	y	269	PRO
44	v	324	ILE
44	v	424	ILE
46	q	87	PRO
9	I	67	VAL
40	R	129	GLY
48	s	78	PRO

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all 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	
2	l	24/24 (100%)	24 (100%)	0	100	100
3	C	174/174 (100%)	172 (99%)	2 (1%)	65	74
4	D	196/231 (85%)	192 (98%)	4 (2%)	48	66
5	E	187/187 (100%)	187 (100%)	0	100	100
6	F	190/190 (100%)	189 (100%)	1 (0%)	81	80
7	G	225/225 (100%)	225 (100%)	0	100	100
8	H	161/161 (100%)	160 (99%)	1 (1%)	78	79
9	I	207/207 (100%)	207 (100%)	0	100	100
10	J	170/170 (100%)	169 (99%)	1 (1%)	78	79
11	K	177/177 (100%)	175 (99%)	2 (1%)	65	74
12	L	157/157 (100%)	156 (99%)	1 (1%)	78	79
13	M	89/89 (100%)	89 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	N	142/142 (100%)	138 (97%)	4 (3%)	38	60
15	O	104/108 (96%)	101 (97%)	3 (3%)	37	60
16	P	130/130 (100%)	125 (96%)	5 (4%)	29	55
17	Q	106/119 (89%)	106 (100%)	0	100	100
18	S	117/117 (100%)	116 (99%)	1 (1%)	70	76
19	T	114/121 (94%)	114 (100%)	0	100	100
20	V	113/116 (97%)	113 (100%)	0	100	100
21	W	94/107 (88%)	94 (100%)	0	100	100
22	X	67/67 (100%)	67 (100%)	0	100	100
23	Y	112/113 (99%)	112 (100%)	0	100	100
24	Z	114/114 (100%)	114 (100%)	0	100	100
25	a	108/115 (94%)	102 (94%)	6 (6%)	19	47
26	b	87/99 (88%)	87 (100%)	0	100	100
27	c	76/76 (100%)	72 (95%)	4 (5%)	20	48
28	d	57/62 (92%)	57 (100%)	0	100	100
29	e	47/47 (100%)	44 (94%)	3 (6%)	16	43
30	f	64/64 (100%)	64 (100%)	0	100	100
31	g	272/272 (100%)	272 (100%)	0	100	100
32	n	66/66 (100%)	66 (100%)	0	100	100
33	i	49/49 (100%)	47 (96%)	2 (4%)	27	53
35	A	238/238 (100%)	232 (98%)	6 (2%)	42	63
36	B	354/354 (100%)	337 (95%)	17 (5%)	23	50
37	j	92/123 (75%)	67 (73%)	25 (27%)	0	3
38	k	523/523 (100%)	466 (89%)	57 (11%)	6	27
39	U	125/132 (95%)	124 (99%)	1 (1%)	73	77
40	R	126/130 (97%)	122 (97%)	4 (3%)	34	58
42	m	329/494 (67%)	327 (99%)	2 (1%)	78	79
43	y	554/1233 (45%)	468 (84%)	86 (16%)	2	16
44	v	501/812 (62%)	490 (98%)	11 (2%)	45	65
45	w	384/406 (95%)	381 (99%)	3 (1%)	73	77
46	q	239/239 (100%)	237 (99%)	2 (1%)	73	77

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
47	r	293/310 (94%)	293 (100%)	0	100	100
48	s	190/193 (98%)	190 (100%)	0	100	100
49	t	342/515 (66%)	341 (100%)	1 (0%)	86	83
50	u	327/335 (98%)	323 (99%)	4 (1%)	63	73
All	All	8613/10133 (85%)	8354 (97%)	259 (3%)	37	59

All (259) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	110	ASN
3	C	194	PRO
4	D	71	LEU
4	D	76	ASN
4	D	82	ARG
4	D	191	ASP
6	F	195	SER
8	H	141	VAL
10	J	66	VAL
11	K	84	ASN
11	K	145	ILE
12	L	123	ILE
14	N	24	LEU
14	N	25	LEU
14	N	28	THR
14	N	30	LYS
15	O	52	LEU
15	O	99	LYS
15	O	103	VAL
16	P	21	SER
16	P	22	VAL
16	P	26	LEU
16	P	27	LYS
16	P	28	LEU
18	S	146	ARG
25	a	10	ARG
25	a	11	LYS
25	a	98	GLU
25	a	99	LYS
25	a	100	LYS
25	a	101	LYS
27	c	64	CYS

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Mol	Chain	Res	Type
27	c	70	LYS
27	c	73	LEU
27	c	79	PHE
29	e	23	VAL
29	e	31	ILE
29	e	39	CYS
33	i	80	LEU
33	i	82	ARG
35	A	38	GLU
35	A	54	ARG
35	A	55	ARG
35	A	157	VAL
35	A	185	THR
35	A	205	ILE
36	B	81	ARG
36	B	83	LYS
36	B	88	ARG
36	B	102	TYR
36	B	116	ARG
36	B	274	SER
36	B	276	ASP
36	B	279	LYS
36	B	283	GLU
36	B	284	VAL
36	B	378	PRO
36	B	402	ASP
36	B	404	LYS
36	B	407	LYS
36	B	430	VAL
36	B	453	LYS
36	B	466	LEU
37	j	7	LYS
37	j	13	ARG
37	j	17	ASN
37	j	26	LEU
37	j	29	LYS
37	j	34	GLU
37	j	40	LYS
37	j	41	MET
37	j	42	LEU
37	j	44	ASN
37	j	46	ARG

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Mol	Chain	Res	Type
37	j	62	ARG
37	j	64	LYS
37	j	65	LEU
37	j	66	ARG
37	j	67	LYS
37	j	68	LYS
37	j	72	ASN
37	j	76	ILE
37	j	82	ARG
37	j	91	VAL
37	j	101	ARG
37	j	103	LEU
37	j	111	GLU
37	j	115	ILE
38	k	20	LYS
38	k	33	ARG
38	k	40	GLU
38	k	45	SER
38	k	73	VAL
38	k	74	ASN
38	k	79	LEU
38	k	96	ARG
38	k	97	LEU
38	k	112	ASN
38	k	114	ILE
38	k	117	SER
38	k	131	LEU
38	k	133	LYS
38	k	135	ASP
38	k	150	SER
38	k	153	GLN
38	k	176	ILE
38	k	187	ILE
38	k	190	ARG
38	k	191	LYS
38	k	194	THR
38	k	204	LEU
38	k	205	ASP
38	k	224	ARG
38	k	245	SER
38	k	268	TYR
38	k	311	ILE

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Mol	Chain	Res	Type
38	k	312	PHE
38	k	313	LEU
38	k	316	TYR
38	k	317	VAL
38	k	319	THR
38	k	320	GLU
38	k	322	LEU
38	k	325	ARG
38	k	326	ASP
38	k	328	SER
38	k	329	LEU
38	k	332	LYS
38	k	336	THR
38	k	339	GLU
38	k	343	LYS
38	k	344	LYS
38	k	347	MET
38	k	419	LYS
38	k	433	ARG
38	k	439	PRO
38	k	443	THR
38	k	485	ILE
38	k	526	THR
38	k	528	LEU
38	k	533	ILE
38	k	569	ASP
38	k	576	ARG
38	k	579	LYS
38	k	598	ASP
39	U	150	LYS
40	R	84	ILE
40	R	130	ARG
40	R	140	ARG
40	R	141	PHE
42	m	339	ASN
42	m	413	LEU
43	y	4	TYR
43	y	6	GLN
43	y	9	GLU
43	y	12	LEU
43	y	13	LYS
43	y	14	ARG

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Mol	Chain	Res	Type
43	y	25	GLN
43	y	28	LEU
43	y	29	ASP
43	y	39	LYS
43	y	60	ASP
43	y	68	LYS
43	y	79	GLN
43	y	83	ILE
43	y	113	LEU
43	y	120	ASN
43	y	123	THR
43	y	126	SER
43	y	133	SER
43	y	145	LEU
43	y	149	TRP
43	y	150	VAL
43	y	151	LYS
43	y	153	LEU
43	y	154	TRP
43	y	160	CYS
43	y	162	ASP
43	y	165	ARG
43	y	173	LEU
43	y	176	ASP
43	y	179	GLN
43	y	183	LYS
43	y	186	LEU
43	y	193	GLU
43	y	195	ARG
43	y	198	CYS
43	y	200	ASN
43	y	206	SER
43	y	207	GLN
43	y	208	ILE
43	y	209	GLN
43	y	210	ARG
43	y	212	HIS
43	y	215	SER
43	y	220	LEU
43	y	225	SER
43	y	226	GLN
43	y	228	MET

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Mol	Chain	Res	Type
43	y	232	THR
43	y	234	LEU
43	y	236	GLN
43	y	237	LEU
43	y	242	SER
43	y	246	TRP
43	y	248	GLU
43	y	254	GLU
43	y	257	HIS
43	y	259	LEU
43	y	265	LYS
43	y	268	LYS
43	y	278	LYS
43	y	285	LYS
43	y	290	LEU
43	y	299	LEU
43	y	303	SER
43	y	304	ARG
43	y	305	GLU
43	y	306	MET
43	y	323	LEU
43	y	324	LEU
43	y	327	LEU
43	y	340	ARG
43	y	341	LEU
43	y	342	LEU
43	y	343	ASP
43	y	347	ILE
43	y	350	GLU
43	y	351	LYS
43	y	354	ARG
43	y	355	LEU
43	y	358	LEU
43	y	359	LEU
43	y	380	LEU
43	y	381	GLN
43	y	420	LYS
43	y	530	LEU
44	v	342	LYS
44	v	374	ILE
44	v	389	LEU
44	v	396	GLU

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Mol	Chain	Res	Type
44	v	418	ILE
44	v	424	ILE
44	v	478	GLN
44	v	521	ARG
44	v	542	GLU
44	v	707	ARG
44	v	842	VAL
45	w	7	THR
45	w	91	ILE
45	w	269	LYS
46	q	187	HIS
46	q	249	VAL
49	t	544	ILE
50	u	9	ILE
50	u	99	PRO
50	u	117	THR
50	u	237	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (187) such sidechains are listed below:

Mol	Chain	Res	Type
3	C	24	HIS
3	C	110	ASN
4	D	40	ASN
4	D	76	ASN
4	D	95	ASN
5	E	100	GLN
5	E	121	HIS
5	E	262	HIS
6	F	101	GLN
6	F	159	HIS
6	F	207	HIS
7	G	98	ASN
7	G	112	HIS
7	G	142	HIS
7	G	188	ASN
8	H	29	GLN
8	H	31	ASN
8	H	74	ASN
8	H	95	HIS
8	H	114	ASN
8	H	118	ASN

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Mol	Chain	Res	Type
8	H	149	GLN
9	I	4	ASN
9	I	65	GLN
9	I	105	ASN
9	I	177	GLN
10	J	44	ASN
10	J	68	GLN
10	J	73	GLN
10	J	164	ASN
10	J	165	ASN
11	K	35	ASN
11	K	44	HIS
11	K	84	ASN
11	K	181	GLN
12	L	75	ASN
14	N	100	ASN
14	N	108	ASN
14	N	112	HIS
15	O	55	ASN
16	P	69	ASN
16	P	90	HIS
17	Q	79	GLN
18	S	11	GLN
18	S	24	HIS
18	S	29	ASN
18	S	48	GLN
18	S	97	GLN
19	T	121	GLN
20	V	42	HIS
20	V	85	ASN
21	W	85	HIS
21	W	92	HIS
23	Y	56	HIS
23	Y	92	ASN
24	Z	16	HIS
24	Z	46	HIS
26	b	25	ASN
26	b	80	HIS
27	c	51	GLN
28	d	7	GLN
29	e	5	GLN
30	f	135	HIS

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Mol	Chain	Res	Type
30	f	139	HIS
31	g	14	HIS
31	g	76	GLN
31	g	117	ASN
31	g	133	ASN
31	g	162	ASN
31	g	187	ASN
31	g	188	HIS
31	g	191	HIS
31	g	226	HIS
31	g	305	ASN
31	g	311	GLN
35	A	60	ASN
37	j	17	ASN
37	j	60	HIS
37	j	72	ASN
37	j	112	HIS
38	k	44	GLN
38	k	112	ASN
38	k	153	GLN
38	k	208	HIS
38	k	274	HIS
38	k	426	GLN
38	k	450	GLN
38	k	468	GLN
38	k	520	HIS
38	k	549	GLN
38	k	556	ASN
38	k	578	ASN
40	R	79	HIS
40	R	114	HIS
42	m	225	HIS
42	m	242	GLN
42	m	244	ASN
42	m	283	ASN
42	m	296	ASN
42	m	307	ASN
42	m	325	GLN
42	m	336	ASN
42	m	377	HIS
42	m	456	HIS
42	m	474	ASN

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Mol	Chain	Res	Type
42	m	479	GLN
43	y	10	ASN
43	y	73	GLN
43	y	80	GLN
43	y	82	ASN
43	y	120	ASN
43	y	122	GLN
43	y	179	GLN
43	y	180	GLN
43	y	204	HIS
43	y	207	GLN
43	y	209	GLN
43	y	229	HIS
43	y	236	GLN
43	y	274	ASN
43	y	292	HIS
43	y	301	HIS
43	y	309	ASN
43	y	352	GLN
43	y	381	GLN
43	y	434	ASN
43	y	565	HIS
44	v	326	HIS
44	v	338	GLN
44	v	355	GLN
44	v	377	ASN
44	v	399	GLN
44	v	430	ASN
44	v	465	HIS
44	v	522	GLN
44	v	576	HIS
44	v	599	GLN
44	v	630	HIS
44	v	631	ASN
44	v	662	GLN
44	v	674	HIS
44	v	715	HIS
44	v	717	GLN
44	v	736	HIS
44	v	784	GLN
44	v	837	GLN
45	w	17	HIS

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Mol	Chain	Res	Type
45	w	33	ASN
45	w	39	GLN
45	w	49	ASN
45	w	198	ASN
45	w	216	HIS
45	w	239	GLN
45	w	244	ASN
45	w	282	GLN
45	w	416	GLN
46	q	139	HIS
46	q	187	HIS
46	q	199	HIS
46	q	342	ASN
47	r	54	GLN
47	r	109	HIS
47	r	116	HIS
47	r	141	GLN
47	r	279	GLN
47	r	324	ASN
47	r	329	ASN
47	r	348	GLN
48	s	22	ASN
48	s	93	HIS
48	s	113	HIS
48	s	144	HIS
48	s	169	GLN
48	s	200	ASN
49	t	281	HIS
49	t	366	GLN
49	t	387	HIS
49	t	427	ASN
49	t	443	GLN
49	t	495	HIS
49	t	546	GLN
50	u	39	HIS
50	u	108	ASN
50	u	146	GLN
50	u	196	ASN
50	u	327	GLN
50	u	339	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	74/75 (98%)	13 (17%)	3 (4%)
34	2	1736/1863 (93%)	248 (14%)	8 (0%)
41	3	44/45 (97%)	29 (65%)	2 (4%)
All	All	1854/1983 (93%)	290 (15%)	13 (0%)

All (290) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	9	U
1	1	11	G
1	1	15	A
1	1	16	G
1	1	17	C
1	1	18	G
1	1	19	G
1	1	21	A
1	1	43	G
1	1	45	G
1	1	47	U
1	1	61	C
1	1	75	C
34	2	4	C
34	2	33	G
34	2	41	G
34	2	42	A
34	2	44	U
34	2	46	A
34	2	56	G
34	2	67	C
34	2	68	A
34	2	72	C
34	2	73	C
34	2	74	G
34	2	76	U
34	2	77	A
34	2	79	A
34	2	80	G
34	2	113	G
34	2	143	U
34	2	147	A
34	2	148	U
34	2	181	A
34	2	182	C

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Mol	Chain	Res	Type
34	2	191	C
34	2	197	U
34	2	202	U
34	2	223	A
34	2	226	A
34	2	274	G
34	2	277	U
34	2	278	U
34	2	296	U
34	2	297	C
34	2	299	G
34	2	300	G
34	2	309	A
34	2	310	G
34	2	311	C
34	2	315	C
34	2	316	C
34	2	317	G
34	2	322	G
34	2	337	G
34	2	347	C
34	2	352	C
34	2	354	A
34	2	358	U
34	2	373	G
34	2	375	G
34	2	376	C
34	2	399	C
34	2	418	U
34	2	438	A
34	2	439	A
34	2	440	C
34	2	457	G
34	2	462	C
34	2	463	A
34	2	464	G
34	2	472	G
34	2	477	U
34	2	483	A
34	2	492	C
34	2	515	A
34	2	522	C

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Mol	Chain	Res	Type
34	2	542	G
34	2	543	U
34	2	546	U
34	2	547	U
34	2	554	A
34	2	558	C
34	2	577	A
34	2	579	G
34	2	580	A
34	2	583	C
34	2	584	A
34	2	596	G
34	2	597	U
34	2	598	C
34	2	618	A
34	2	633	A
34	2	658	A
34	2	659	A
34	2	661	A
34	2	662	A
34	2	678	U
34	2	679	U
34	2	680	G
34	2	681	U
34	2	682	G
34	2	729	C
34	2	732	C
34	2	733	G
34	2	734	C
34	2	735	C
34	2	736	C
34	2	737	C
34	2	738	U
34	2	739	U
34	2	740	G
34	2	741	C
34	2	742	C
34	2	743	U
34	2	744	C
34	2	746	C
34	2	747	G
34	2	748	G

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Mol	Chain	Res	Type
34	2	749	C
34	2	750	G
34	2	751	C
34	2	785	G
34	2	786	C
34	2	787	C
34	2	788	C
34	2	789	G
34	2	790	A
34	2	791	A
34	2	793	C
34	2	794	G
34	2	795	U
34	2	807	A
34	2	818	U
34	2	819	U
34	2	835	C
34	2	843	A
34	2	849	C
34	2	864	G
34	2	865	A
34	2	868	A
34	2	869	G
34	2	870	G
34	2	874	G
34	2	883	U
34	2	884	U
34	2	906	G
34	2	907	C
34	2	909	A
34	2	913	U
34	2	916	A
34	2	929	G
34	2	951	A
34	2	967	G
34	2	986	A
34	2	987	G
34	2	988	A
34	2	1004	A
34	2	1013	U
34	2	1019	A
34	2	1045	A

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Mol	Chain	Res	Type
34	2	1057	U
34	2	1058	A
34	2	1081	C
34	2	1082	G
34	2	1103	G
34	2	1107	U
34	2	1109	A
34	2	1111	U
34	2	1112	C
34	2	1113	C
34	2	1115	A
34	2	1116	U
34	2	1117	G
34	2	1144	A
34	2	1145	A
34	2	1150	U
34	2	1211	C
34	2	1217	G
34	2	1219	A
34	2	1238	U
34	2	1247	A
34	2	1252	G
34	2	1253	G
34	2	1255	A
34	2	1260	C
34	2	1270	G
34	2	1271	G
34	2	1280	A
34	2	1281	G
34	2	1296	U
34	2	1297	A
34	2	1298	G
34	2	1299	C
34	2	1311	U
34	2	1367	U
34	2	1374	A
34	2	1391	C
34	2	1399	C
34	2	1406	C
34	2	1408	C
34	2	1413	C
34	2	1414	C

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Mol	Chain	Res	Type
34	2	1415	C
34	2	1420	G
34	2	1427	G
34	2	1431	C
34	2	1433	C
34	2	1450	A
34	2	1471	G
34	2	1472	A
34	2	1473	U
34	2	1485	A
34	2	1486	G
34	2	1503	G
34	2	1506	G
34	2	1507	U
34	2	1516	C
34	2	1517	A
34	2	1539	C
34	2	1547	G
34	2	1548	C
34	2	1549	C
34	2	1551	A
34	2	1575	A
34	2	1580	U
34	2	1583	A
34	2	1596	A
34	2	1616	U
34	2	1618	A
34	2	1632	A
34	2	1643	G
34	2	1659	A
34	2	1660	G
34	2	1666	G
34	2	1675	G
34	2	1678	C
34	2	1683	C
34	2	1706	U
34	2	1707	A
34	2	1708	C
34	2	1716	U
34	2	1717	G
34	2	1743	G
34	2	1747	C

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Mol	Chain	Res	Type
34	2	1748	G
34	2	1777	C
34	2	1778	G
34	2	1816	A
34	2	1818	A
34	2	1819	A
34	2	1820	G
34	2	1823	G
34	2	1825	A
34	2	1829	A
34	2	1846	C
34	2	1855	G
34	2	1856	G
34	2	1858	U
34	2	1859	C
34	2	1863	A
41	3	34	C
41	3	35	A
41	3	36	A
41	3	37	C
41	3	39	U
41	3	40	C
41	3	41	A
41	3	42	A
41	3	43	A
41	3	45	A
41	3	47	A
41	3	48	C
41	3	49	A
41	3	55	G
41	3	56	U
41	3	57	G
41	3	58	C
41	3	59	A
41	3	61	C
41	3	62	U
41	3	65	C
41	3	66	U
41	3	67	C
41	3	69	U
41	3	70	G
41	3	71	A

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Mol	Chain	Res	Type
41	3	72	G
41	3	73	G
41	3	74	A

All (13) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	8	G
1	1	17	C
1	1	18	G
34	2	74	G
34	2	739	U
34	2	912	A
34	2	1012	U
34	2	1112	C
34	2	1270	G
34	2	1716	U
34	2	1857	A
41	3	36	A
41	3	39	U

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

2 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
1	T6A	1	37	1	31,34,35	1.42	4 (12%)	43,49,52	2.51	18 (41%)
34	C4J	2	1244	34	25,29,30	1.04	2 (8%)	28,42,45	2.92	2 (7%)

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
1	T6A	1	37	1	-	6/23/41/42	0/3/3/3
34	C4J	2	1244	34	1/1/7/7	8/16/34/35	0/2/2/2

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	37	T6A	C5-C4	4.80	1.47	1.39
34	2	1244	C4J	C4-C5	-3.51	1.39	1.47
1	1	37	T6A	C5-C6	2.78	1.48	1.41
1	1	37	T6A	C5-N7	-2.32	1.34	1.39
1	1	37	T6A	C8-N7	2.23	1.36	1.31
34	2	1244	C4J	C1'-C5	-2.15	1.45	1.50

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	2	1244	C4J	C1'-C5-C4	14.44	139.53	117.61
1	1	37	T6A	C12-N11-C10	8.52	136.15	121.99
1	1	37	T6A	C5-C4-N3	-5.57	119.05	126.72
1	1	37	T6A	N3-C4-N9	4.47	134.76	127.17
1	1	37	T6A	C14-C12-C13	3.73	116.53	110.03
1	1	37	T6A	C2-N3-C4	3.71	120.89	111.83
34	2	1244	C4J	C4-N3-C2	-3.67	121.10	125.62
1	1	37	T6A	N3-C2-N1	-3.66	123.04	128.58
1	1	37	T6A	C2'-C1'-N9	-3.59	104.38	113.30
1	1	37	T6A	C4-C5-N7	-3.59	106.48	110.58
1	1	37	T6A	C6-C5-N7	3.52	136.26	132.43
1	1	37	T6A	C4-N9-C8	2.83	108.71	105.74
1	1	37	T6A	O10-C10-N6	-2.82	118.62	123.64
1	1	37	T6A	C5-N7-C8	2.73	107.74	103.45
1	1	37	T6A	C14-C12-N11	2.61	118.61	111.70
1	1	37	T6A	C2-N1-C6	2.23	122.64	115.24
1	1	37	T6A	N9-C8-N7	-2.15	110.89	113.94
1	1	37	T6A	N6-C10-N11	2.13	116.70	113.77
1	1	37	T6A	O4'-C1'-N9	2.12	112.15	108.09
1	1	37	T6A	N6-C6-N1	2.04	122.83	117.54

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
34	2	1244	C4J	C4'

All (14) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	1	37	T6A	C14-C12-N11-C10
34	2	1244	C4J	C31-C3-N3-C2
34	2	1244	C4J	C31-C3-N3-C4
34	2	1244	C4J	C3-C31-C32-C34
34	2	1244	C4J	C3-C31-C32-N33
1	1	37	T6A	N11-C12-C13-ODB
1	1	37	T6A	N11-C12-C13-ODA
34	2	1244	C4J	N3-C3-C31-C32
1	1	37	T6A	O4'-C4'-C5'-O5'
34	2	1244	C4J	N33-C32-C34-O35
34	2	1244	C4J	C31-C32-C34-O36
1	1	37	T6A	C13-C12-N11-C10
1	1	37	T6A	C13-C12-C14-C15
34	2	1244	C4J	C31-C32-C34-O35

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	1	37	T6A	1	0
34	2	1244	C4J	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 1 is monoatomic - leaving 4 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	$\# Z > 2$
51	SF4	k	702	38	0,12,12	-	-	-		

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
53	GNP	k	704	52	34,34,34	1.34	3 (8%)	47,54,54	0.88	2 (4%)
53	GNP	k	705	-	34,34,34	1.38	3 (8%)	47,54,54	0.90	2 (4%)
51	SF4	k	701	38	0,12,12	-	-	-	-	-

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
51	SF4	k	702	38	-	-	0/6/5/5
53	GNP	k	704	52	-	3/18/38/38	0/3/3/3
53	GNP	k	705	-	-	4/18/38/38	0/3/3/3
51	SF4	k	701	38	-	-	0/6/5/5

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
53	k	705	GNP	PG-O2G	-4.63	1.44	1.56
53	k	704	GNP	PG-O2G	-4.62	1.44	1.56
53	k	705	GNP	PB-O2B	-4.09	1.45	1.56
53	k	704	GNP	PB-O2B	-3.80	1.46	1.56
53	k	705	GNP	PA-O3A	2.65	1.62	1.59
53	k	704	GNP	PA-O3A	2.35	1.62	1.59

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
53	k	704	GNP	O2G-PG-O3G	-2.51	100.83	107.59
53	k	705	GNP	O2G-PG-O3G	-2.48	100.93	107.59
53	k	704	GNP	O3G-PG-O1G	-2.15	108.06	113.45
53	k	705	GNP	O3G-PG-O1G	-2.11	108.17	113.45

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
53	k	704	GNP	PG-N3B-PB-O1B
53	k	704	GNP	PG-N3B-PB-O3A
53	k	704	GNP	PA-O3A-PB-O2B

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Mol	Chain	Res	Type	Atoms
53	k	705	GNP	PG-N3B-PB-O1B
53	k	705	GNP	C5'-O5'-PA-O3A
53	k	705	GNP	C5'-O5'-PA-O2A
53	k	705	GNP	C4'-C5'-O5'-PA

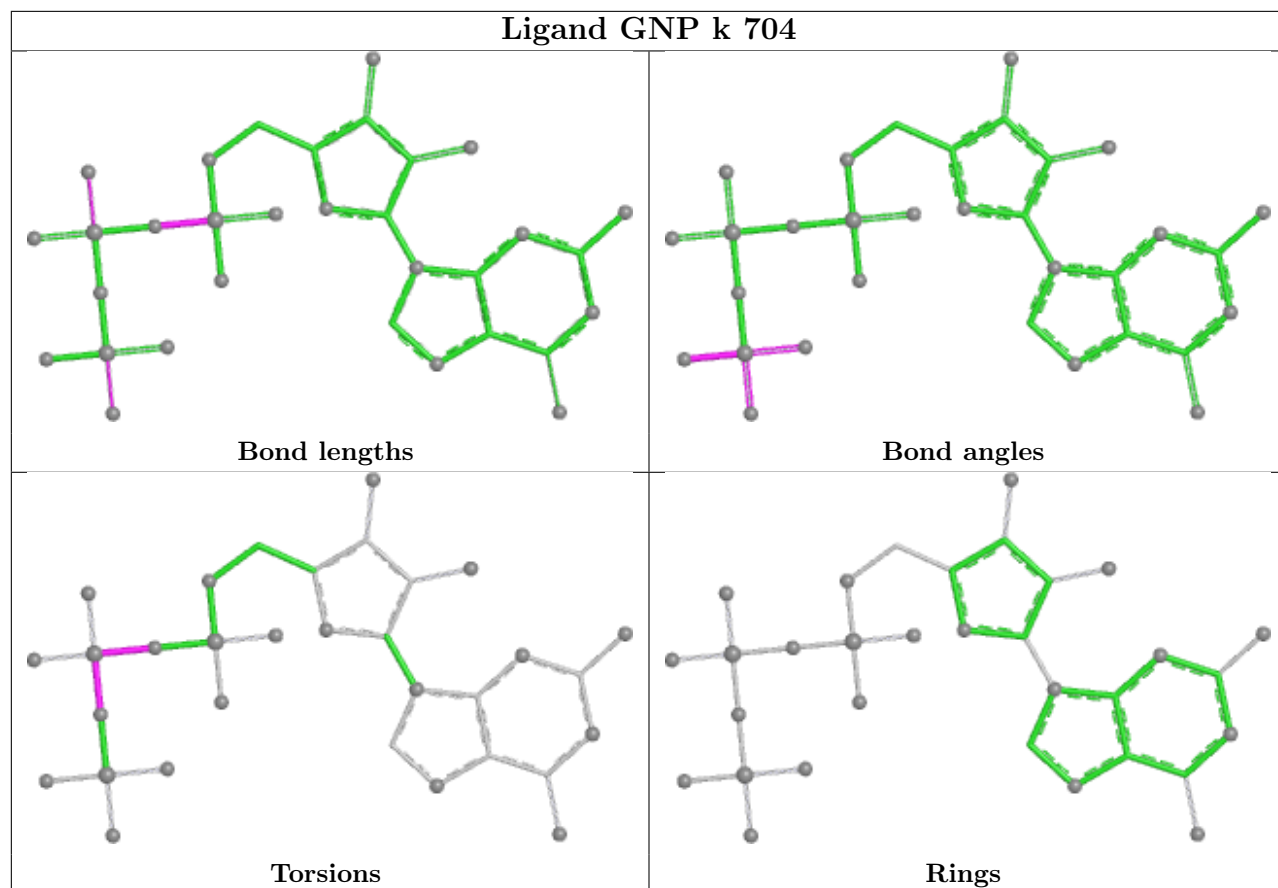
There are no ring outliers.

4 monomers are involved in 44 short contacts:

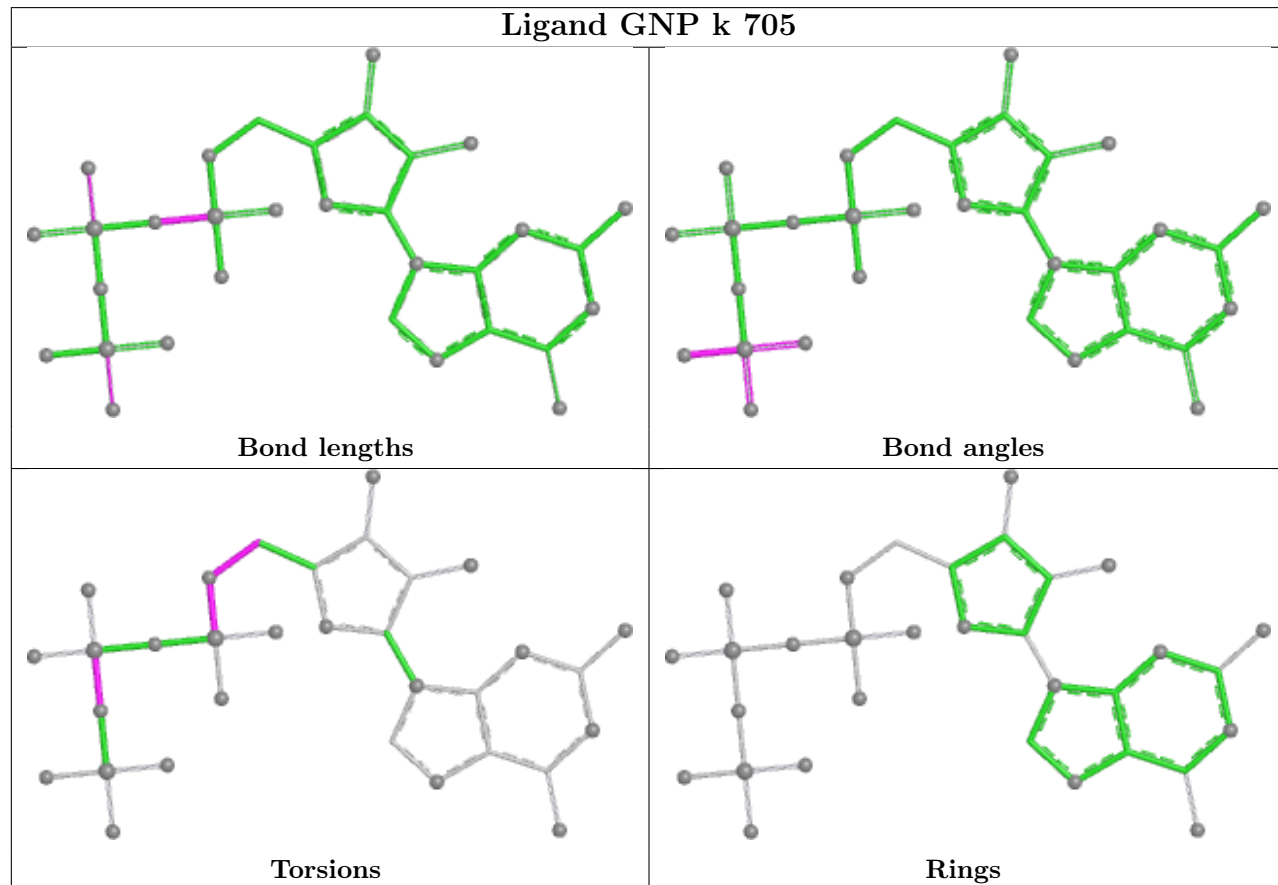
Mol	Chain	Res	Type	Clashes	Symm-Clashes
51	k	702	SF4	7	0
53	k	704	GNP	13	0
53	k	705	GNP	18	0
51	k	701	SF4	6	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand GNP k 704



Ligand GNP k 705



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
38	k	23
34	2	4
44	v	4
1	1	2
39	U	1
25	a	1
37	j	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	2	730:C	O3'	731:C	P	8.58
1	k	521:ASP	C	522:PHE	N	2.98
1	U	142:ARG	C	143:GLY	N	2.92
1	k	451:ILE	C	452:GLU	N	2.79
1	k	373:GLU	C	374:ILE	N	2.70
1	k	550:THR	C	551:LEU	N	2.35
1	v	326:HIS	C	327:ALA	N	2.25
1	k	518:VAL	C	519:GLU	N	2.16
1	v	532:SER	C	533:GLU	N	2.16
1	k	486:ASP	C	487:GLU	N	2.09
1	k	591:SER	C	592:GLY	N	2.02
1	k	411:TYR	C	412:LYS	N	2.01
1	1	17:C	O3'	18:G	P	1.99
1	k	378:LEU	C	379:GLY	N	1.94
1	1	18:G	O3'	19:G	P	1.87
1	k	440:GLN	C	441:PHE	N	1.85
1	2	350:A	O3'	351:U	P	1.83
1	v	748:ASP	C	749:TRP	N	1.81
1	k	109:VAL	C	110:GLY	N	1.79
1	k	513:LYS	C	514:THR	N	1.64
1	a	9:THR	C	10:ARG	N	1.60
1	2	239:U	O3'	240:C	P	1.36
1	2	80:G	O3'	81:U	P	1.34
1	j	95:TYR	C	96:ASN	N	1.16

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	v	762:ASN	C	763:GLY	N	1.12
1	k	493:ASP	C	494:SER	N	1.09
1	k	160:LEU	C	161:GLU	N	1.05
1	k	150:SER	C	151:GLU	N	1.02
1	k	268:TYR	C	269:ILE	N	1.02
1	k	241:ASP	C	242:GLU	N	0.84
1	k	531:ARG	C	532:VAL	N	0.82
1	k	481:ASP	C	482:VAL	N	0.79
1	k	104:GLU	C	105:VAL	N	0.75
1	k	408:ASN	C	409:VAL	N	0.68
1	k	562:LEU	C	563:GLU	N	0.52
1	k	455:ILE	C	456:ASP	N	0.44

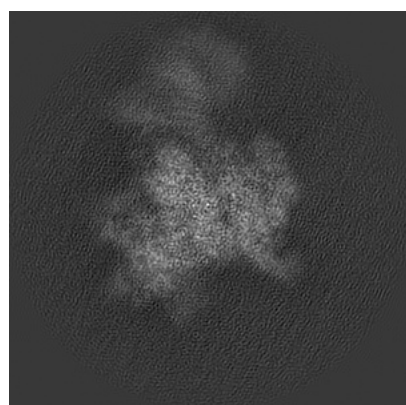
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10761. These allow visual inspection of the internal detail of the map and identification of artifacts.

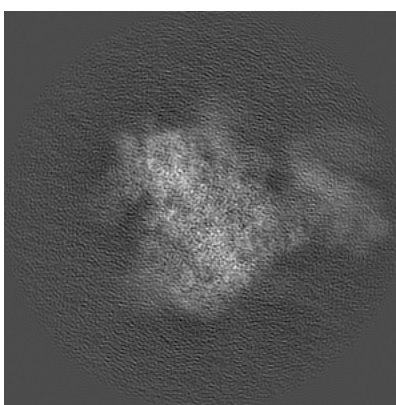
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

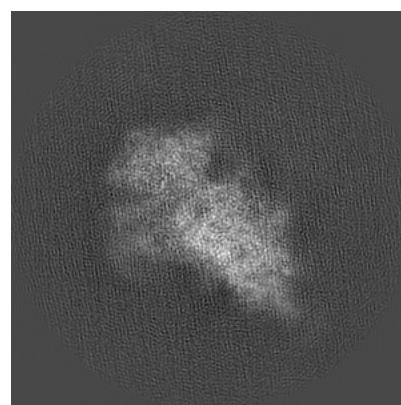
6.1.1 Primary map



X



Y

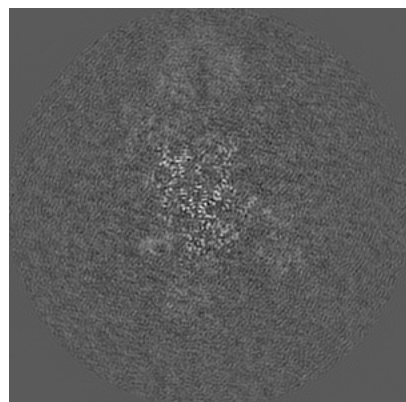


Z

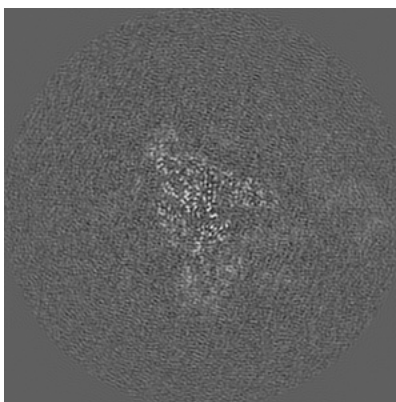
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

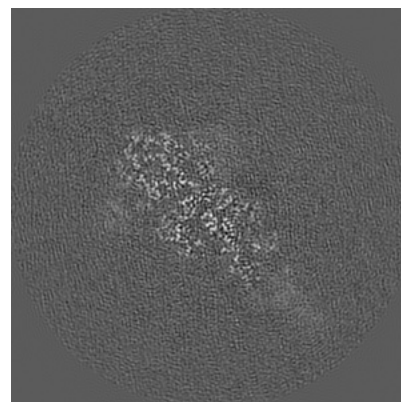
6.2.1 Primary map



X Index: 192



Y Index: 192

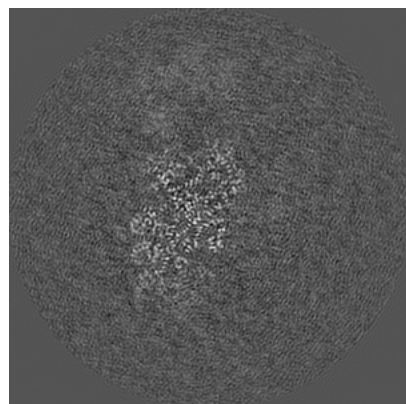


Z Index: 192

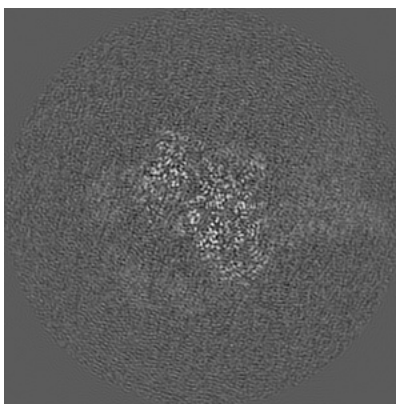
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

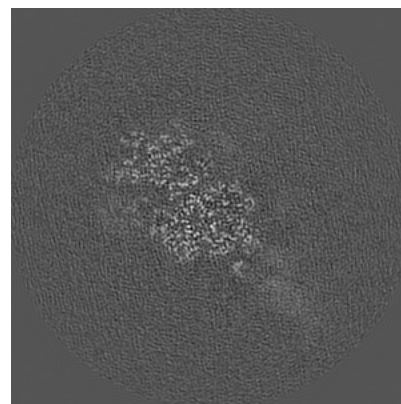
6.3.1 Primary map



X Index: 210



Y Index: 165

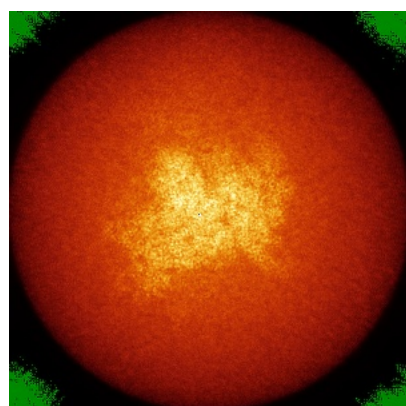


Z Index: 199

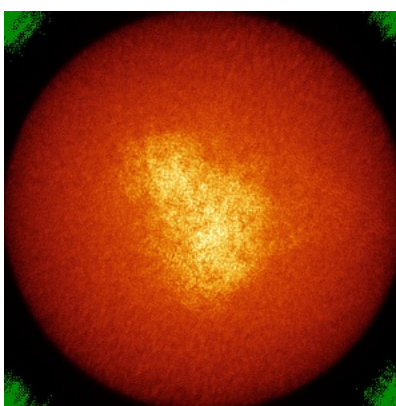
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

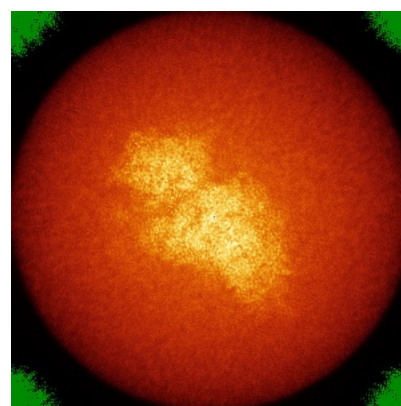
6.4.1 Primary map



X



Y

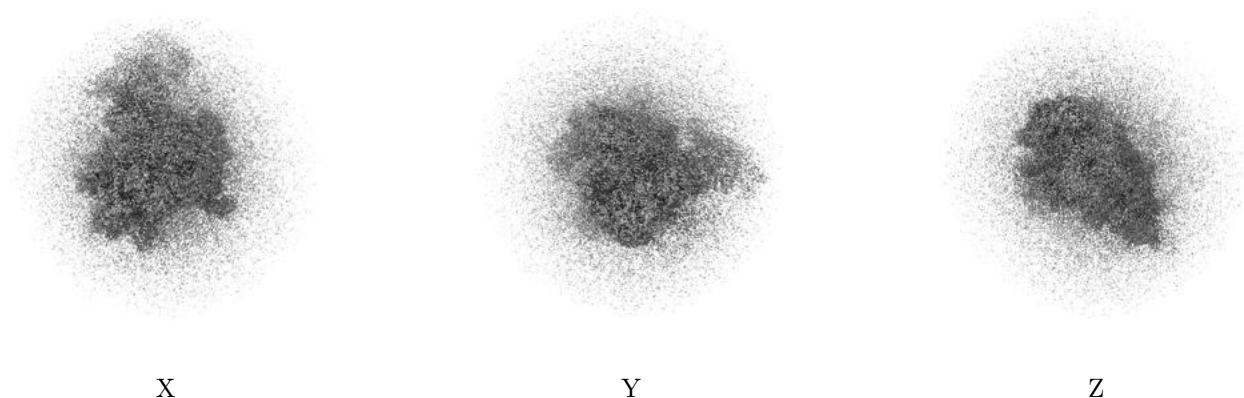


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.02. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

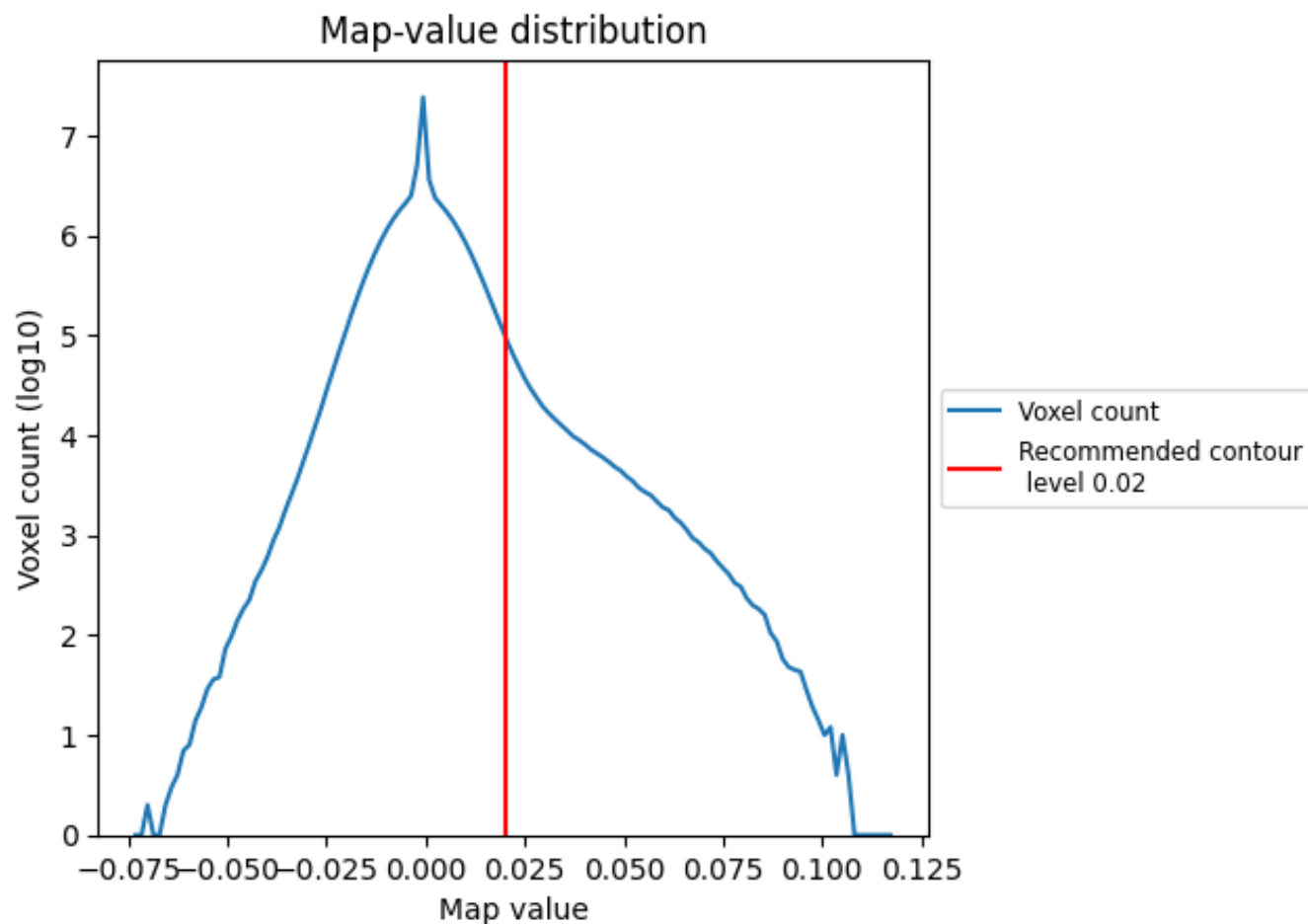
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

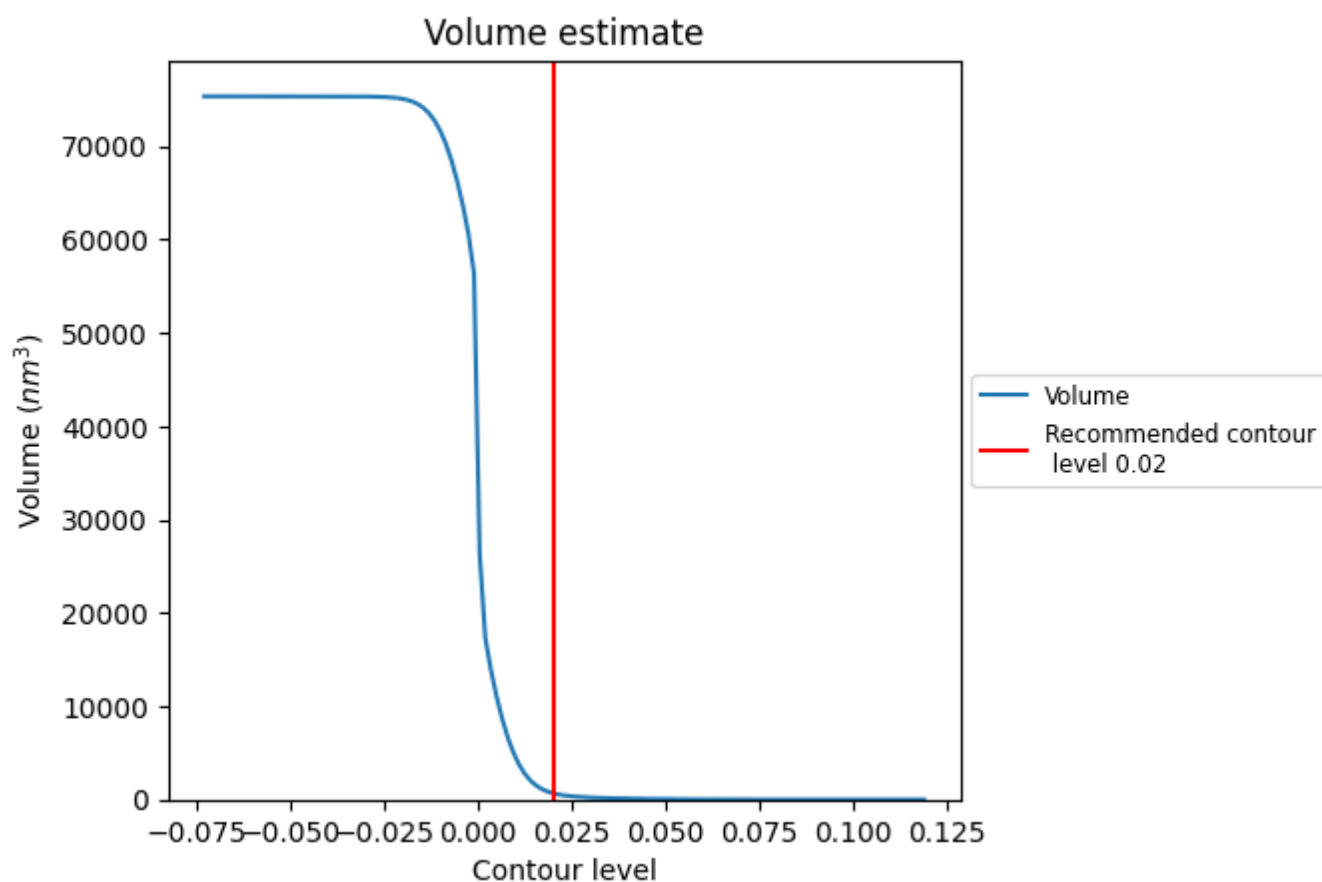
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

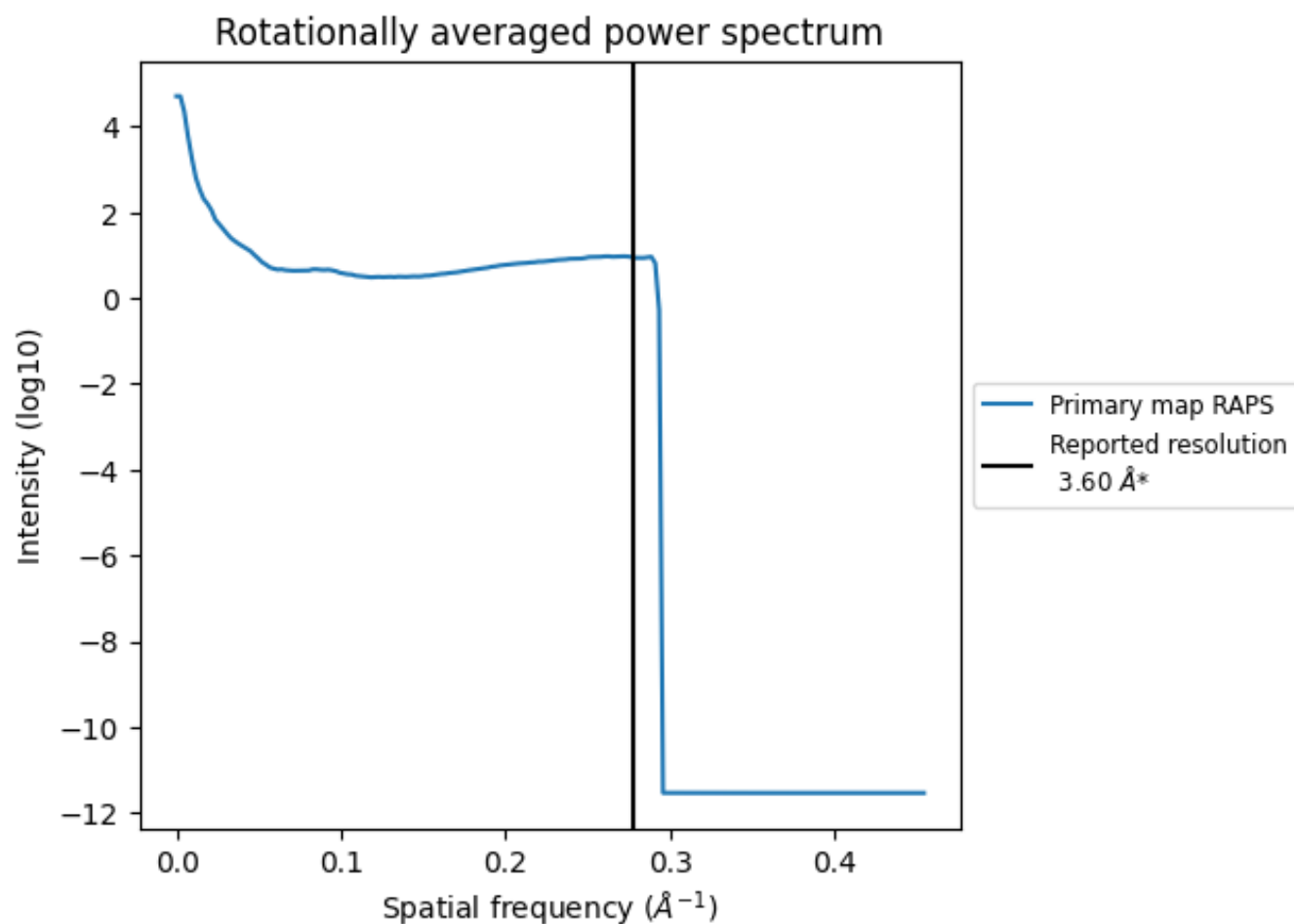
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 665 nm³; this corresponds to an approximate mass of 600 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.278 Å⁻¹

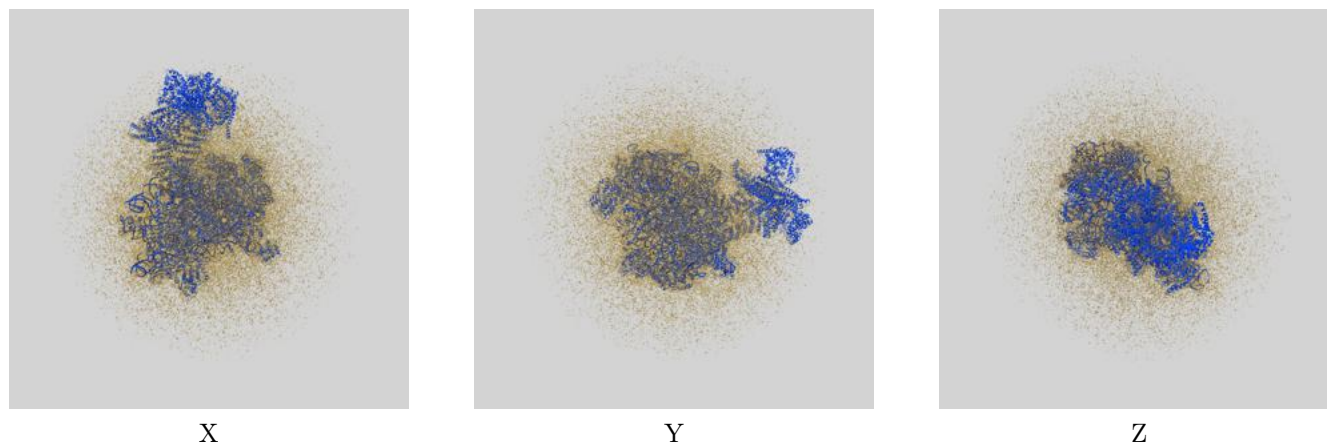
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

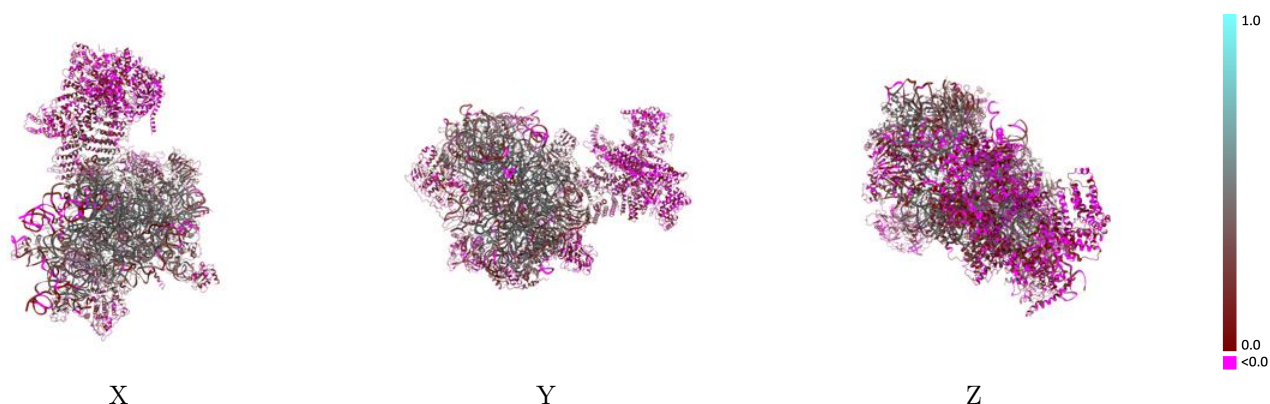
This section contains information regarding the fit between EMDB map EMD-10761 and PDB model 6YAM. Per-residue inclusion information can be found in [section 3](#) on [page 15](#).

9.1 Map-model overlay [i](#)



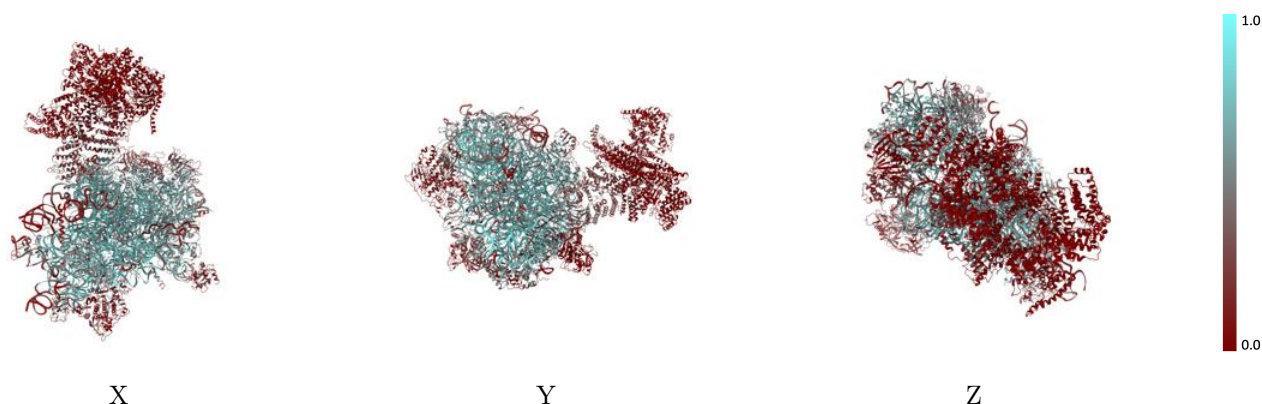
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



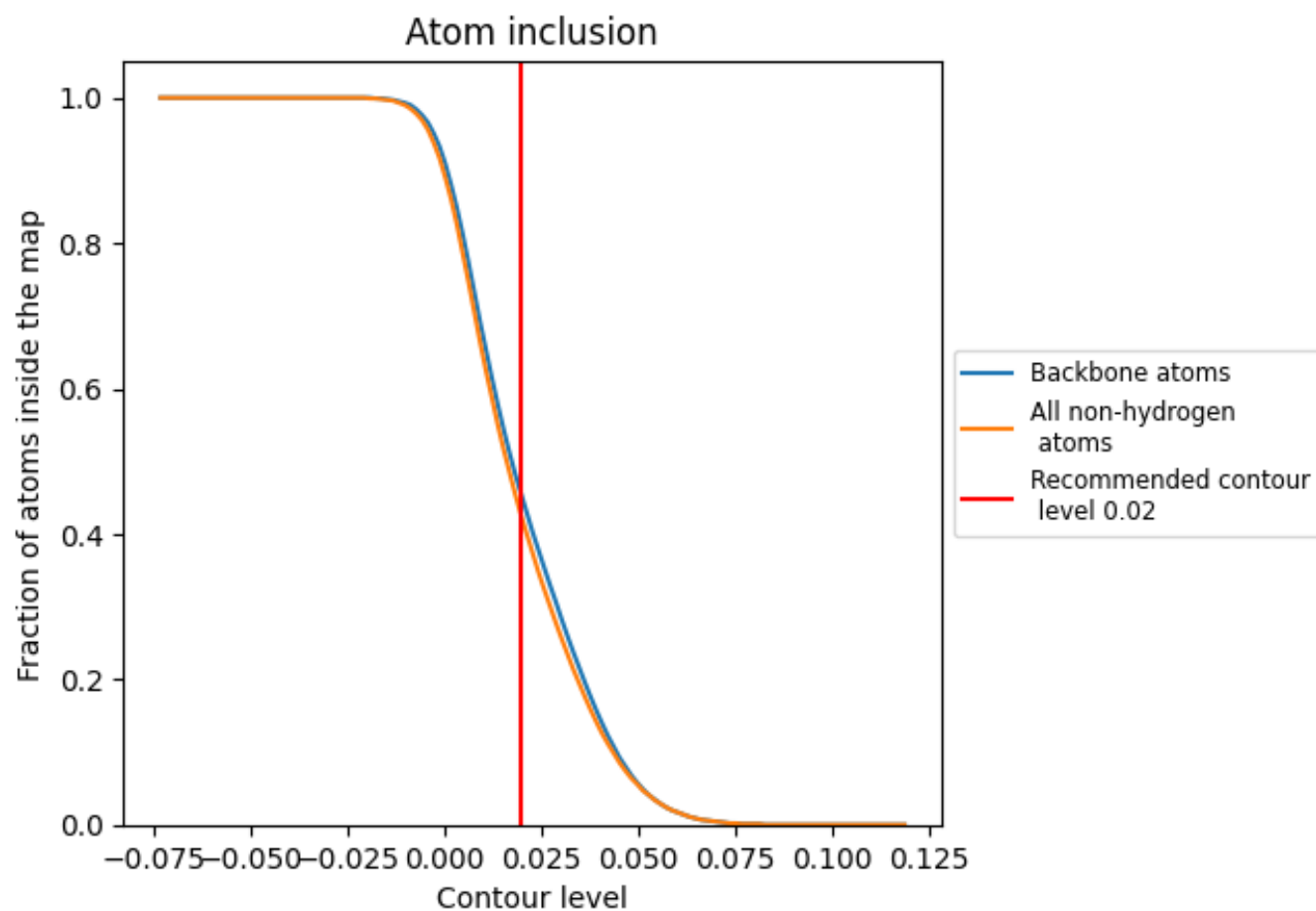
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.02).

9.4 Atom inclusion [i](#)



At the recommended contour level, 45% of all backbone atoms, 42% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.4230	 0.2570
1	 0.3490	 0.1490
2	 0.6960	 0.3870
3	 0.1620	 0.0600
A	 0.1180	 0.1080
B	 0.0240	 0.0050
C	 0.6030	 0.3790
D	 0.5460	 0.3610
E	 0.6360	 0.4040
F	 0.5000	 0.3230
G	 0.6070	 0.3860
H	 0.5760	 0.3590
I	 0.4210	 0.2830
J	 0.3600	 0.2360
K	 0.5100	 0.3180
L	 0.6150	 0.3760
M	 0.4890	 0.2770
N	 0.5550	 0.3550
O	 0.1390	 0.0940
P	 0.5750	 0.3590
Q	 0.5710	 0.3550
R	 0.4470	 0.2960
S	 0.6060	 0.3790
T	 0.4870	 0.2970
U	 0.5170	 0.3340
V	 0.5880	 0.3760
W	 0.4870	 0.3130
X	 0.5810	 0.3810
Y	 0.6950	 0.4320
Z	 0.6580	 0.4060
a	 0.5160	 0.3190
b	 0.6540	 0.4120
c	 0.4990	 0.3270
d	 0.5230	 0.3360
e	 0.5150	 0.2410



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Chain	Atom inclusion	Q-score
f	 0.1920	 0.1410
g	 0.4210	 0.2840
i	 0.4080	 0.2680
j	 0.2650	 0.2090
k	 0.1380	 0.1510
l	 0.5110	 0.3240
m	 0.0210	 0.0430
n	 0.4280	 0.2780
q	 0.0160	 0.0020
r	 0.0150	 -0.0050
s	 0.0010	 0.0140
t	 0.0030	 0.0140
u	 0.0090	 0.0180
v	 0.1510	 0.1240
w	 0.0330	 0.0340
y	 0.1500	 0.1290