



Full wwPDB EM Validation Report ⓘ

Mar 6, 2026 – 01:56 PM UTC

PDB ID : 4UER / pdb_00004uer
EMDB ID : EMD-2845
Title : 40S-eIF1-eIF1A-eIF3-eIF3j translation initiation complex from *Lachancea kluyveri*
Authors : Aylett, C.H.S.; Boehringer, D.; Erzberger, J.P.; Schaefer, T.; Ban, N.
Deposited on : 2014-12-18
Resolution : 6.47 Å(reported)
Based on initial model : 3U5B

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
MolProbity : 4-5-2 with Phenix2.0
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

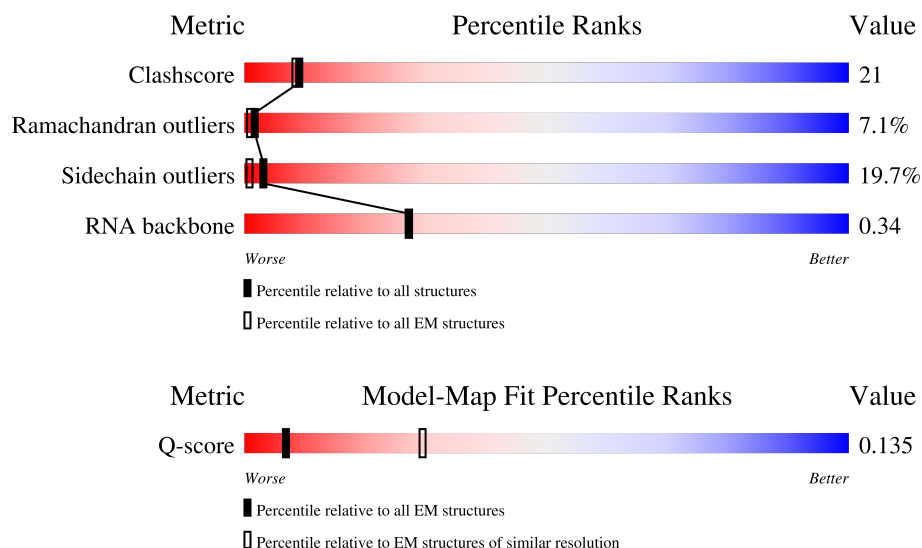
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 6.47 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.



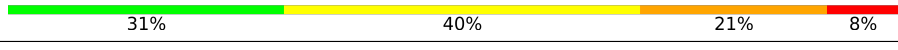
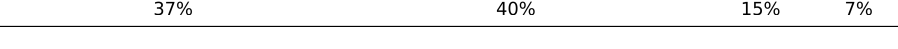
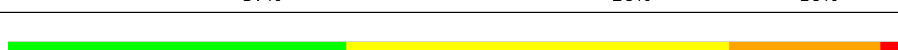
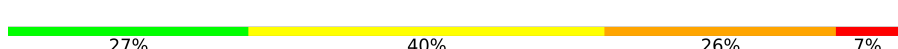
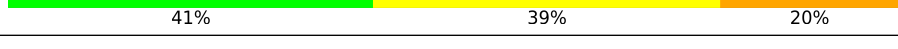
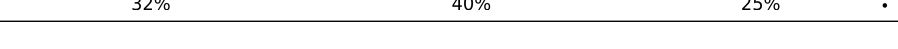
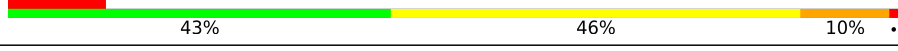
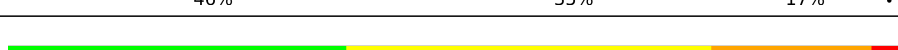
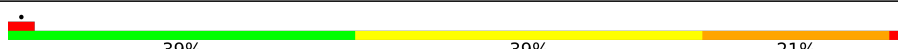
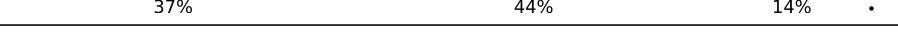
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	499 (5.97 - 6.95)

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	0	100	
2	1	63	
3	2	188	

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Mol	Chain	Length	Quality of chain
4	3	184	
5	4	214	
6	5	97	
7	6	81	
8	7	96	
9	8	70	
10	9	71	
11	A	1781	
12	B	206	
13	C	223	
14	D	185	
15	E	217	
16	F	83	
17	G	206	
18	H	129	
19	I	141	
20	J	107	
21	K	127	
22	L	144	
23	M	145	
24	N	53	
25	O	150	
26	P	134	
27	Q	155	
28	R	318	

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Mol	Chain	Length	Quality of chain
29	S	124	
30	T	143	
31	U	124	
32	V	120	
33	W	260	
34	X	60	
35	Y	226	
36	Z	87	
37	a	964	
38	b	763	
39	c	812	

2 Entry composition

There are 40 unique types of molecules in this entry. The entry contains 89319 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called EIF1A.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	100	Total	C	N	O	S	0	0
			805	495	148	157	5		

- Molecule 2 is a protein called ES28.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	63	Total	C	N	O	S	0	0
			497	306	99	91	1		

- Molecule 3 is a protein called ES8.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	188	Total	C	N	O	S	0	0
			1489	925	298	264	2		

- Molecule 4 is a protein called ES7.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	3	184	Total	C	N	O	0	0
			1481	951	265	265		

- Molecule 5 is a protein called ES1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	214	Total	C	N	O	S	0	0
			1709	1084	310	311	4		

- Molecule 6 is a protein called ES26.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	5	97	Total	C	N	O	S	0	0
			769	475	160	129	5		

- Molecule 7 is a protein called ES27.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	6	81	Total	C	N	O	S	0	0
			610	382	110	113	5		

- Molecule 8 is a protein called ES10.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	7	96	Total	C	N	O	S	0	0
			772	499	126	145	2		

- Molecule 9 is a protein called ES25.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	8	70	Total	C	N	O	0	0
			563	360	104	99		

- Molecule 10 is a protein called ES31.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	9	71	Total	C	N	O	S	0	0
			516	328	93	91	4		

- Molecule 11 is a RNA chain called 18S RRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	A	1781	Total	C	N	O	P	1	0
			37835	16910	6661	12482	1782		

- Molecule 12 is a protein called US2.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	B	206	Total	C	N	O	S	0	0
			1577	1014	278	283	2		

- Molecule 13 is a protein called US3.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	C	223	Total	C	N	O	S	0	0
			1734	1101	313	314	6		

- Molecule 14 is a protein called US4.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	D	185	Total	C	N	O	S	0	0
			1494	943	289	261	1		

- Molecule 15 is a protein called US5.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	E	217	Total	C	N	O	S	0	0
			1635	1047	289	297	2		

- Molecule 16 is a protein called EIF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	F	83	Total	C	N	O	S	0	0
			671	423	124	120	4		

- Molecule 17 is a protein called US7.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	G	206	Total	C	N	O	S	0	0
			1609	1007	300	299	3		

- Molecule 18 is a protein called US8.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	H	129	Total	C	N	O	S	0	0
			1021	650	188	180	3		

- Molecule 19 is a protein called US9.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	I	141	Total	C	N	O	S	0	0
			1105	708	203	194			

- Molecule 20 is a protein called US10.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	J	107	Total	C	N	O	S	0	0
			855	539	156	159	1		

- Molecule 21 is a protein called US11.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	K	127	Total	C	N	O	S	0	0
			891	545	182	163	1		

- Molecule 22 is a protein called US12.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	L	144	Total	C	N	O	S	0	0
			1121	708	220	191	2		

- Molecule 23 is a protein called US13.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	M	145	Total	C	N	O	S	0	0
			1192	743	237	210	2		

- Molecule 24 is a protein called US14.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	N	53	Total	C	N	O	S	0	0
			442	274	92	72	4		

- Molecule 25 is a protein called US15.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	O	150	Total	C	N	O	S	0	0
			1192	759	224	207	2		

- Molecule 26 is a protein called ES24.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	P	134	Total	C	N	O	0	0
			1073	676	208	189		

- Molecule 27 is a protein called US17.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Q	155	Total	C	N	O	S	0	0
			1213	774	230	206	3		

- Molecule 28 is a protein called RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	R	318	Total	C	N	O	S	0	0
			2437	1541	418	470	8		

- Molecule 29 is a protein called US19.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	S	124	Total	C	N	O	S	0	0
			977	622	182	166	7		

- Molecule 30 is a protein called ES19.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	T	143	Total	C	N	O	S	0	0
			1112	694	208	208	2		

- Molecule 31 is a protein called ES12.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	U	124	Total	C	N	O	S	0	0
			890	560	156	172	2		

- Molecule 32 is a protein called ES17.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	V	120	Total	C	N	O	S	0	0
			926	577	177	170	2		

- Molecule 33 is a protein called ES4.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	W	260	Total	C	N	O	S	0	0
			2068	1316	389	360	3		

- Molecule 34 is a protein called ES30.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	X	60	Total	C	N	O	S	0	0
			475	299	98	77	1		

- Molecule 35 is a protein called ES6.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Y	226	Total	C	N	O	S	0	0
			1799	1129	346	321	3		

- Molecule 36 is a protein called ES21.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Z	87	Total	C	N	O	S	0	0
			684	420	125	137	2		

- Molecule 37 is a protein called EIF3A.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	a	449	Total	C	N	O	S	0	0
			3656	2350	616	683	7		

- Molecule 38 is a protein called EIF3B.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	b	572	Total	C	N	O	S	0	92
			3978	2578	667	720	13		

- Molecule 39 is a protein called EIF3C.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	c	544	Total	C	N	O	S	0	0
			4442	2845	736	849	12		

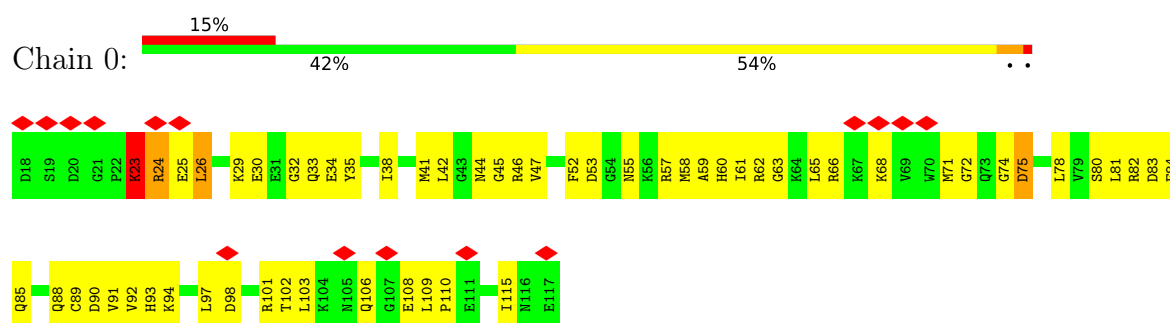
- Molecule 40 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
40	5	1	Total	Zn	0
			1	1	
40	6	1	Total	Zn	0
			1	1	
40	9	1	Total	Zn	0
			1	1	
40	N	1	Total	Zn	0
			1	1	

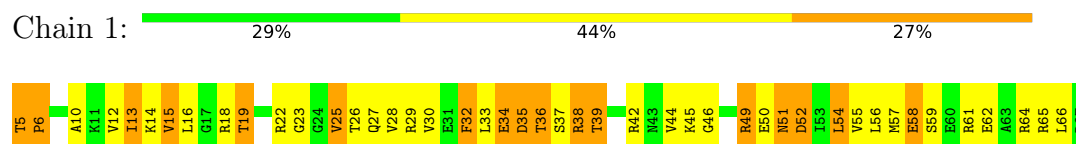
3 Residue-property plots

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.

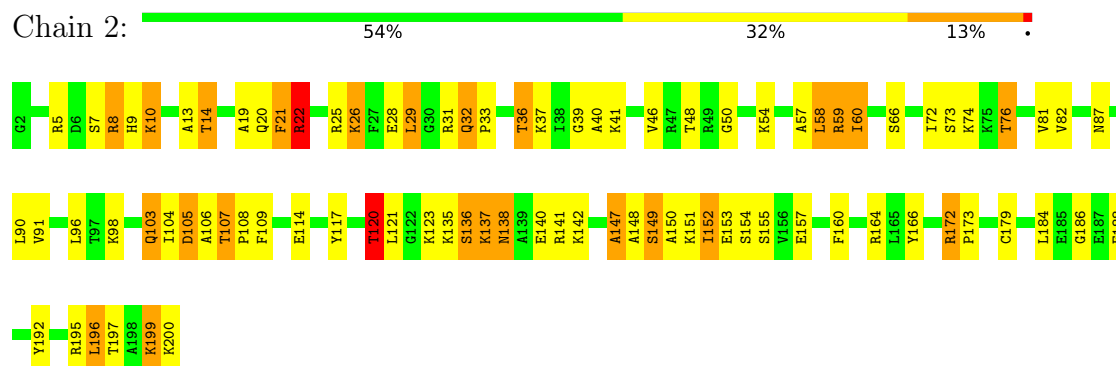
• Molecule 1: EIF1A



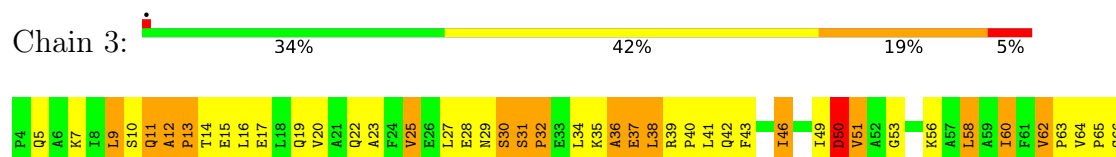
• Molecule 2: ES28

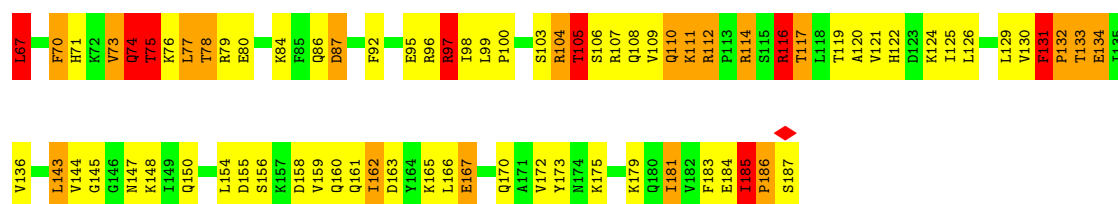


• Molecule 3: ES8



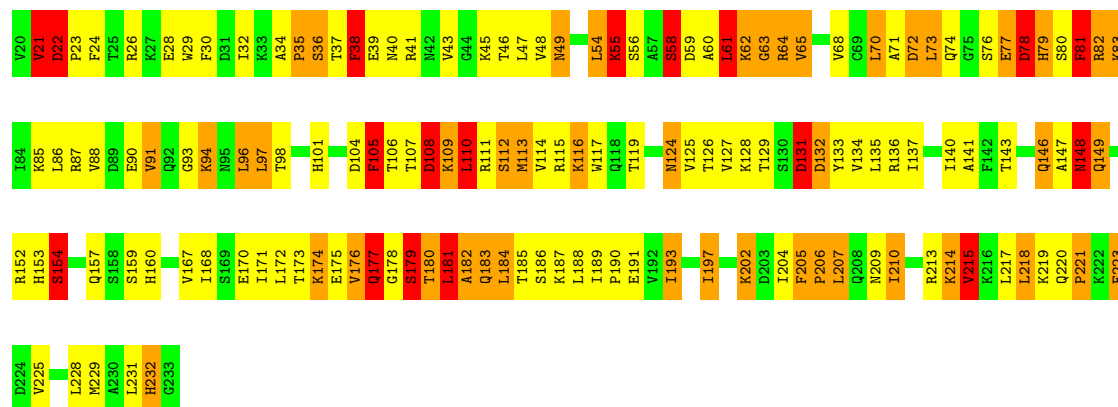
• Molecule 4: ES7





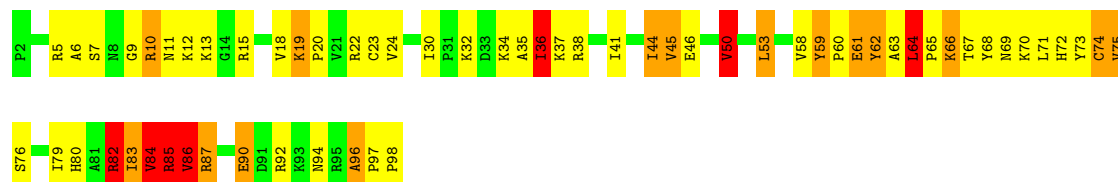
• Molecule 5: ES1

Chain 4: 31% 40% 21% 8%



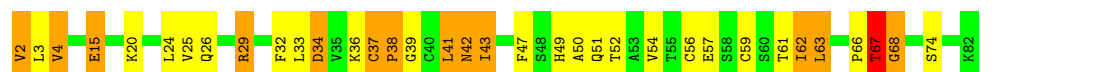
• Molecule 6: ES26

Chain 5: 37% 40% 15% 7%



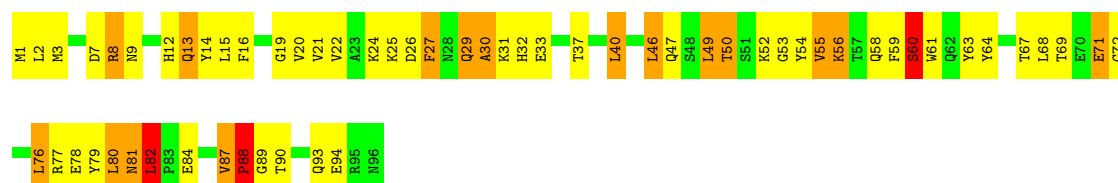
• Molecule 7: ES27

Chain 6: 57% 26% 16%



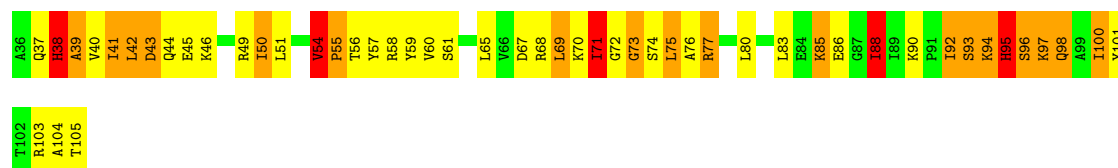
• Molecule 8: ES10

Chain 7: 38% 43% 17%



- Molecule 9: ES25

Chain 8: 27% 40% 26% 7%



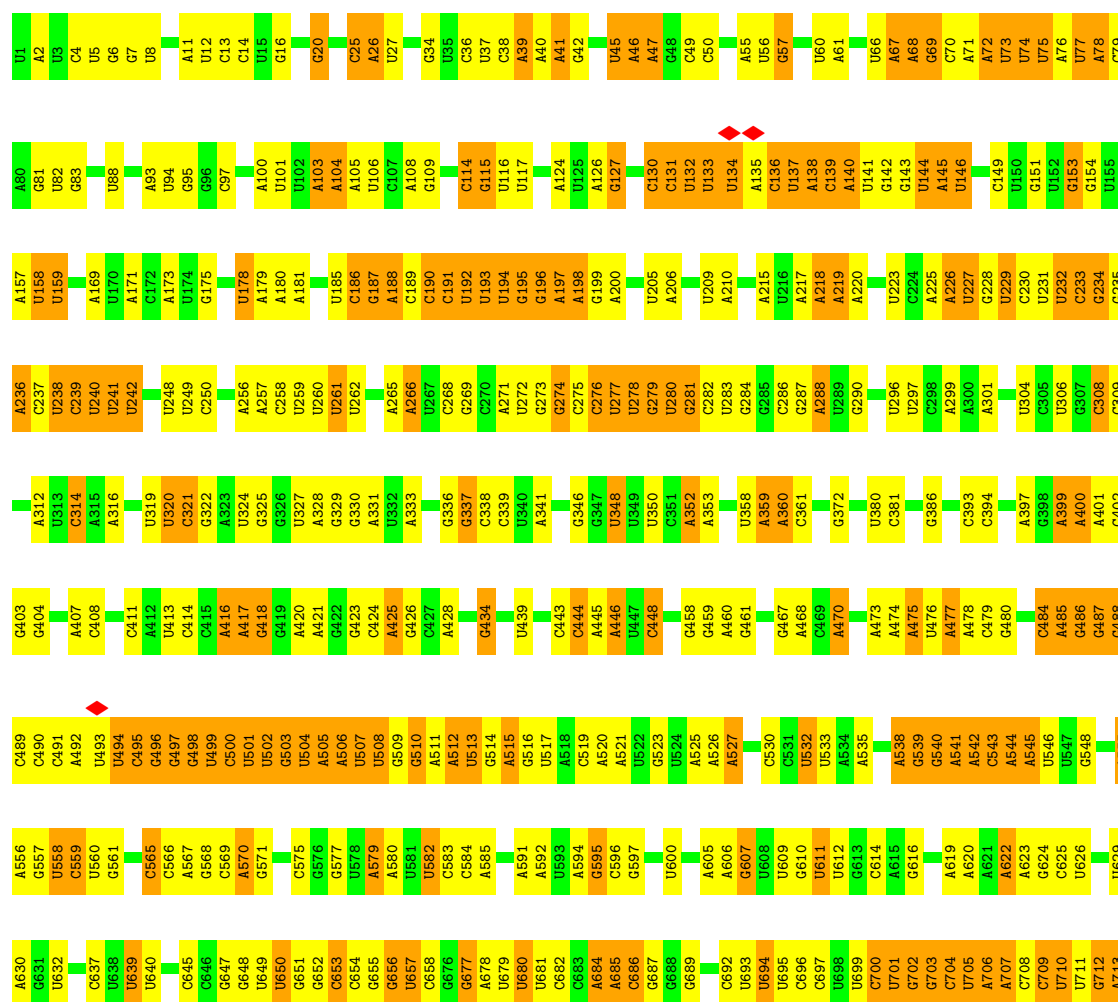
- Molecule 10: ES31

Chain 9: 38% 41% 15% 6%

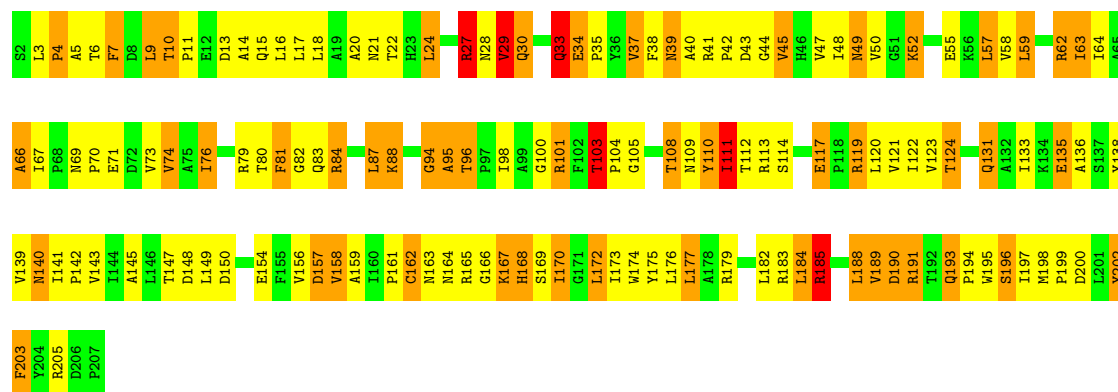


- Molecule 11: 18S RRNA

Chain A: 41% 39% 20%

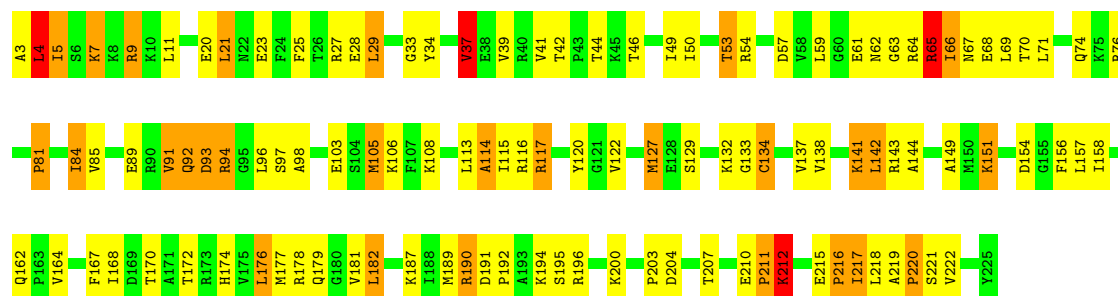






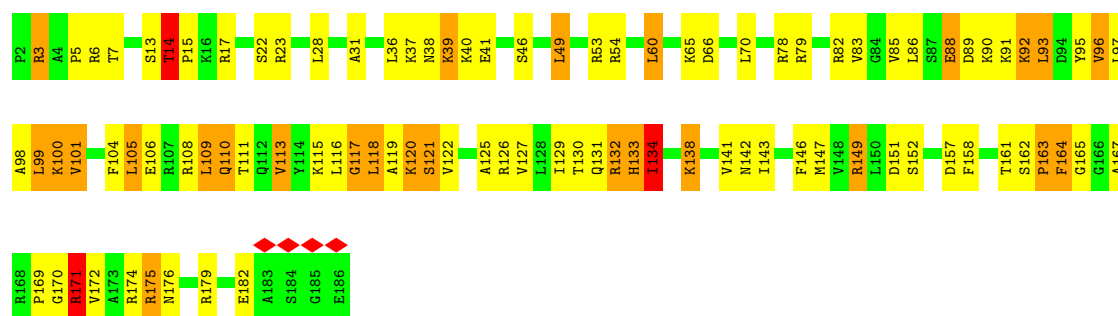
• Molecule 13: US3

Chain C: 48% 37% 13% .



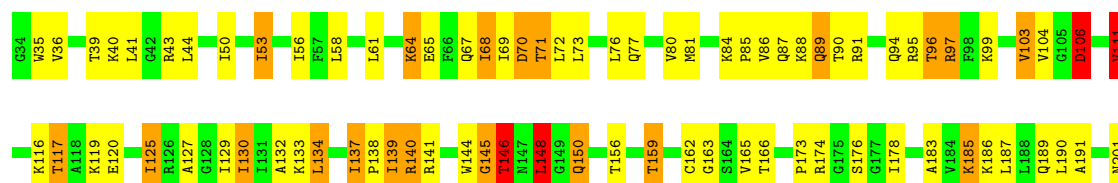
• Molecule 14: US4

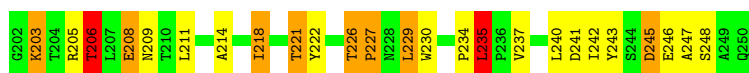
Chain D: 48% 36% 14% .



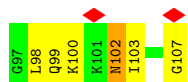
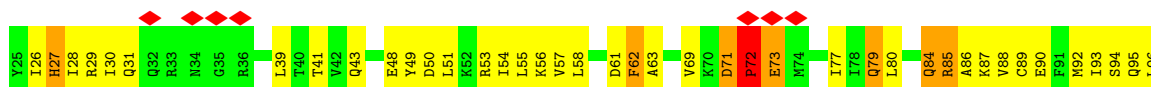
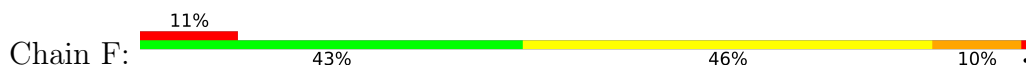
• Molecule 15: US5

Chain E: 51% 33% 13% .

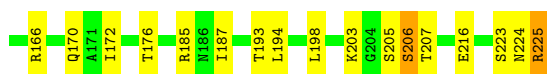




- Molecule 16: EIF1



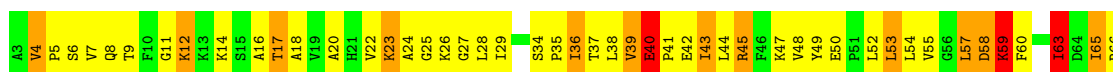
- Molecule 17: US7



- Molecule 18: US8

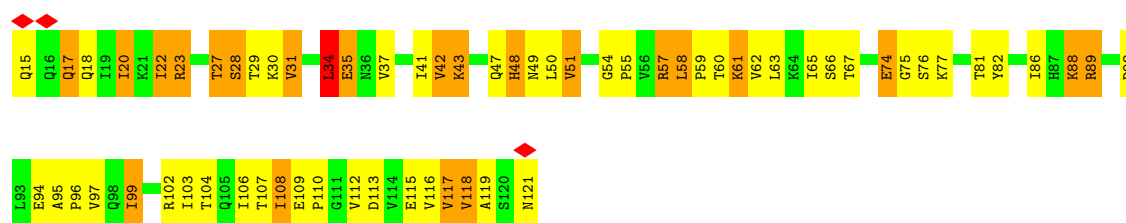


- Molecule 19: US9



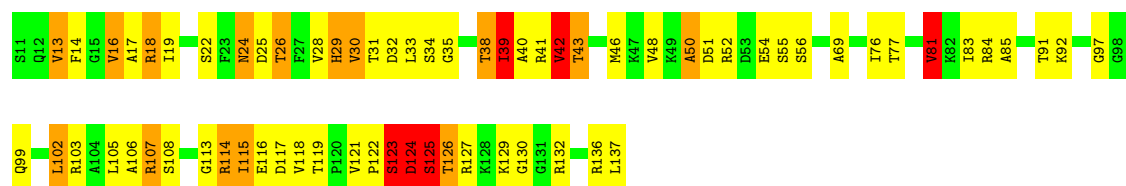
- Molecule 20: US10

Chain J: 



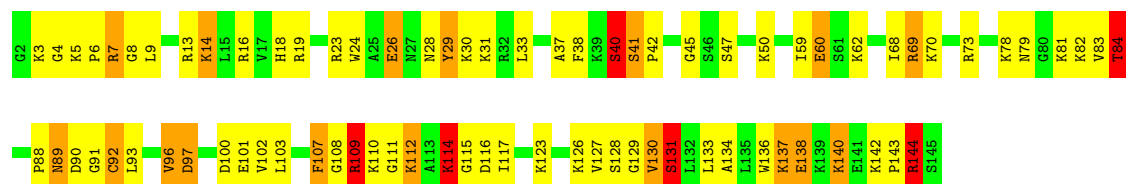
• Molecule 21: US11

Chain K: 



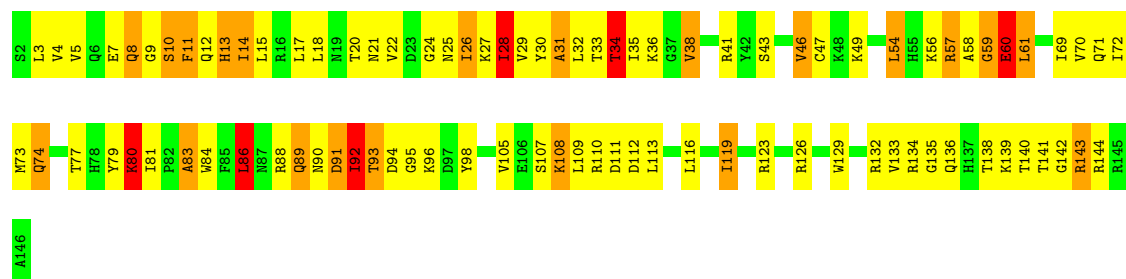
• Molecule 22: US12

Chain L: 



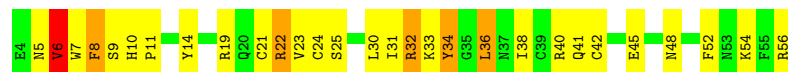
• Molecule 23: US13

Chain M: 

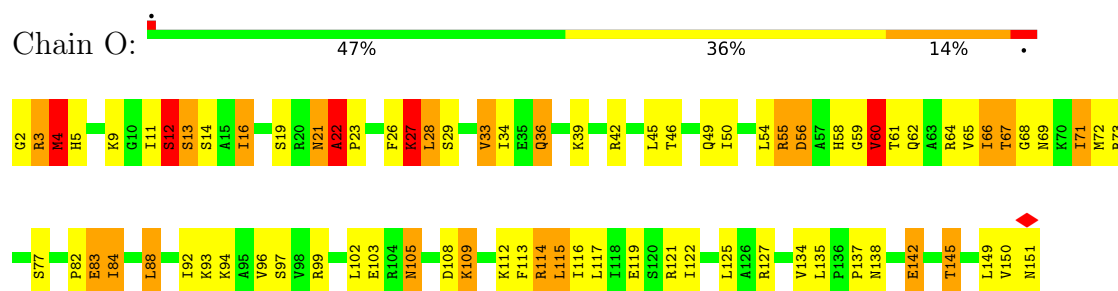


• Molecule 24: US14

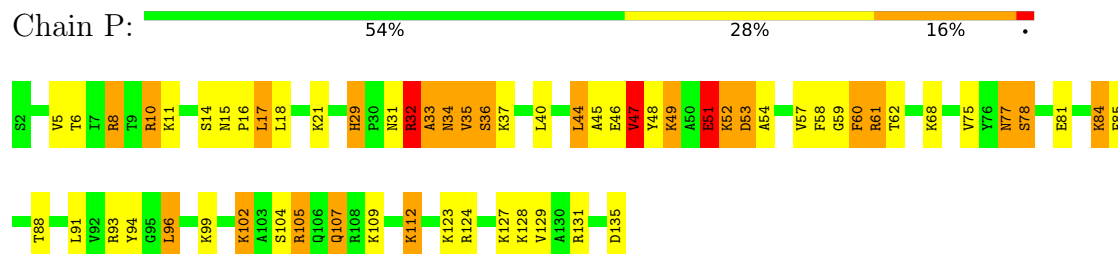
Chain N: 



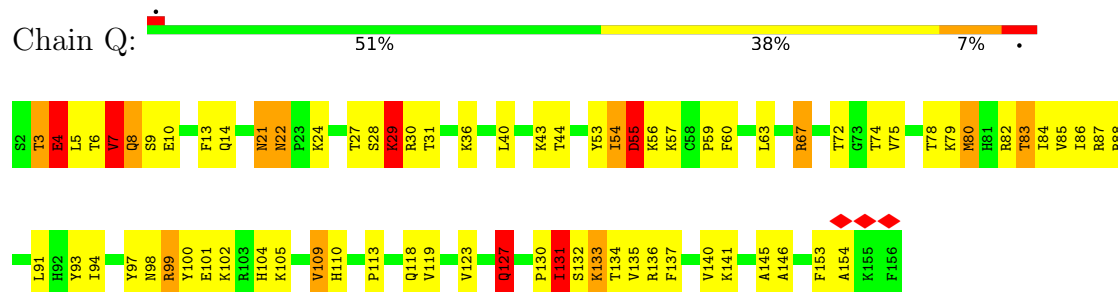
• Molecule 25: US15



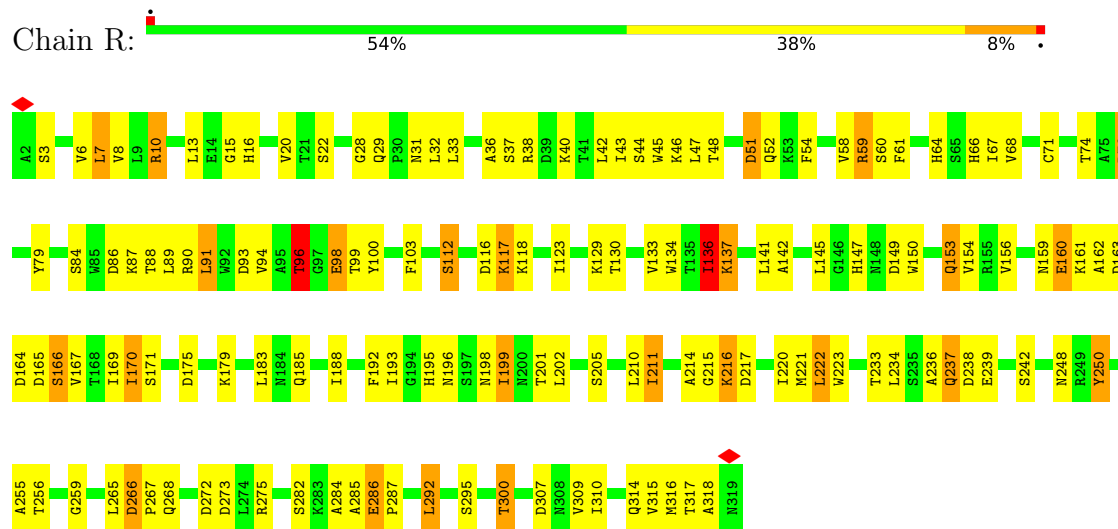
• Molecule 26: ES24



• Molecule 27: US17

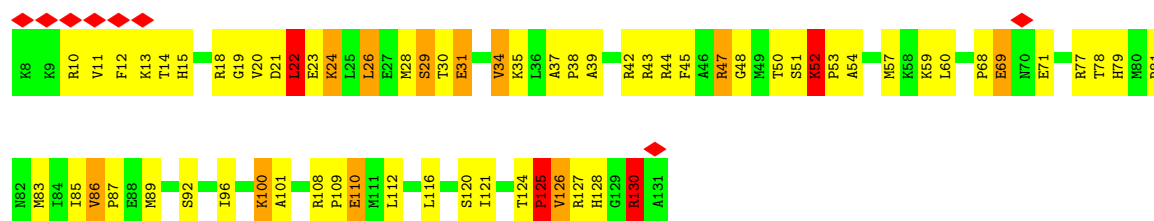


• Molecule 28: RACK1



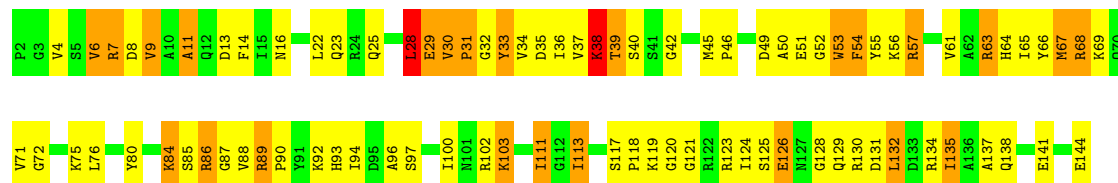
• Molecule 29: US19





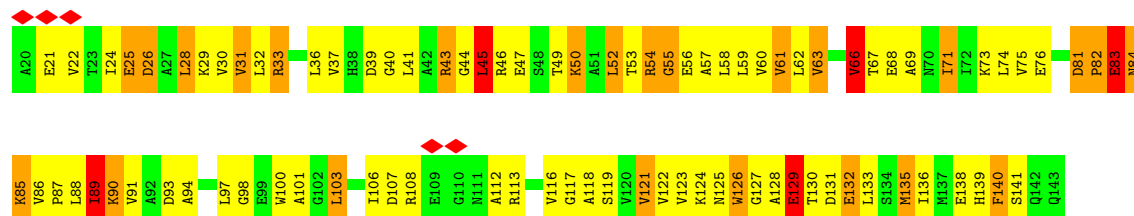
• Molecule 30: ES19

Chain T: 39% 43% 17%



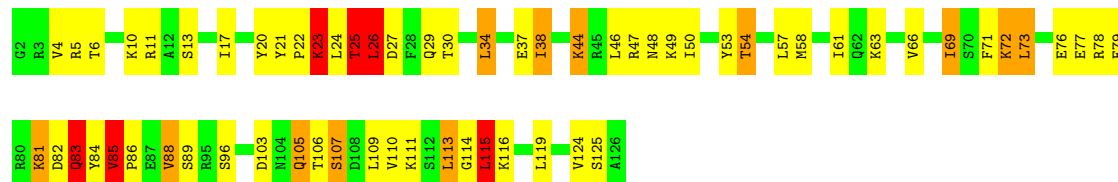
• Molecule 31: ES12

Chain U: 27% 49% 19%



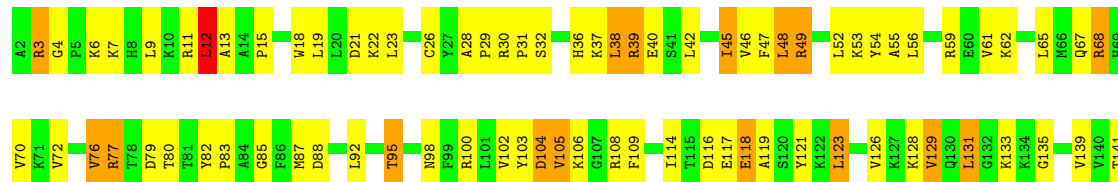
• Molecule 32: ES17

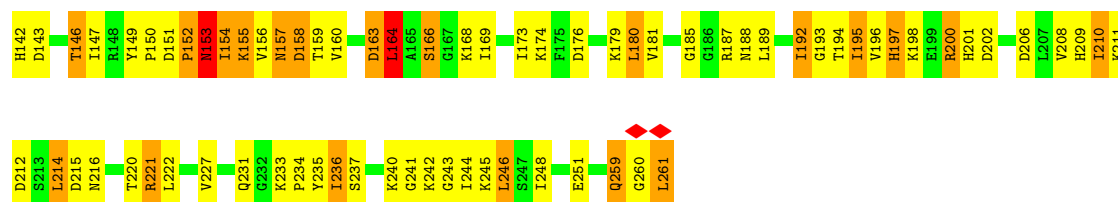
Chain V: 47% 38% 10% 5%



• Molecule 33: ES4

Chain W: 42% 43% 14%

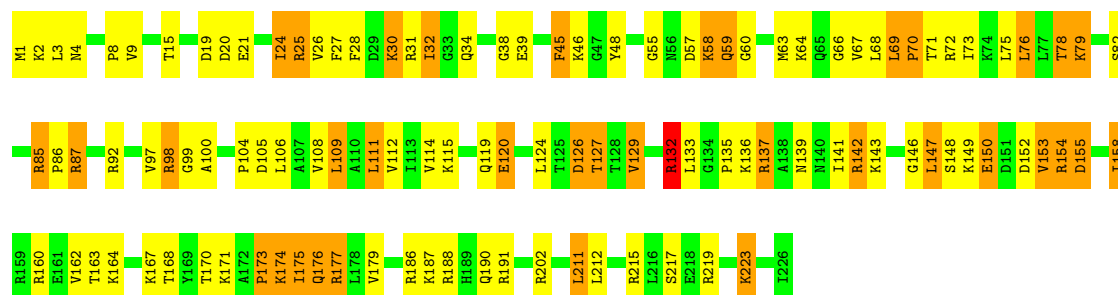




• Molecule 34: ES30



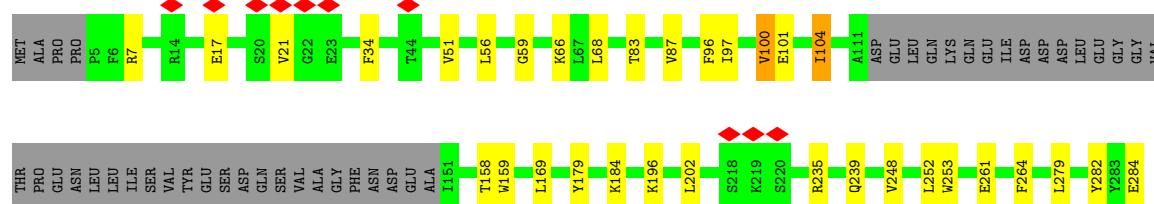
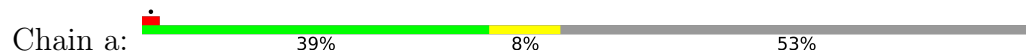
• Molecule 35: ES6



• Molecule 36: ES21

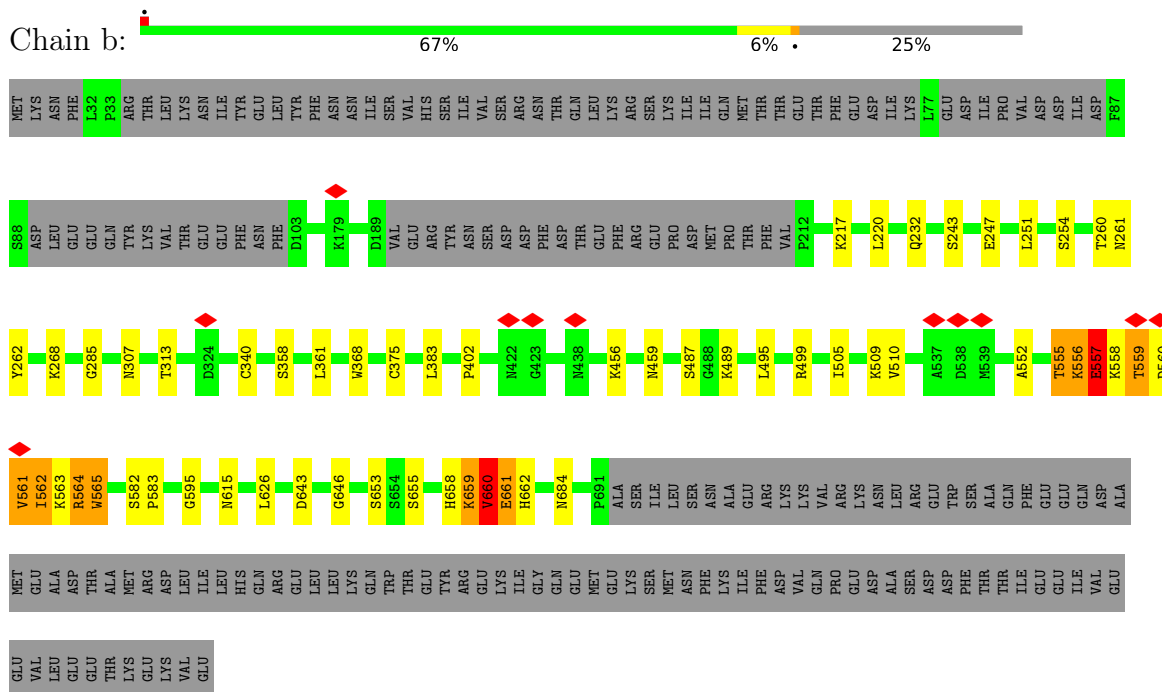


• Molecule 37: EIF3A





- Molecule 38: EIF3B



- Molecule 39: EIF3C



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	27354	Depositor
Resolution determination method	Not provided	
CTF correction method	BY IMAGE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	25	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	100719	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.115	Depositor
Minimum map value	-0.019	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.012	Depositor
Recommended contour level	0.015	Depositor
Map size ($\text{\AA}$)	355.84, 355.84, 355.84	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.39, 1.39, 1.39	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	0	0.86	0/815	1.28	1/1087 (0.1%)
2	1	0.55	0/499	1.08	0/670
3	2	0.85	0/1514	1.18	7/2021 (0.3%)
4	3	0.68	0/1506	1.15	12/2028 (0.6%)
5	4	0.62	0/1735	1.13	11/2335 (0.5%)
6	5	0.76	0/782	1.15	4/1047 (0.4%)
7	6	0.69	0/620	1.23	6/838 (0.7%)
8	7	0.71	0/789	1.20	7/1067 (0.7%)
9	8	0.65	0/571	1.22	4/768 (0.5%)
10	9	0.73	0/404	1.37	5/542 (0.9%)
11	A	0.56	2/42127 (0.0%)	0.60	4/65638 (0.0%)
12	B	0.72	1/1617 (0.1%)	1.22	18/2215 (0.8%)
13	C	0.76	0/1759	1.15	11/2368 (0.5%)
14	D	0.73	0/1519	1.18	7/2035 (0.3%)
15	E	0.81	3/1665 (0.2%)	1.19	6/2263 (0.3%)
16	F	0.91	2/678 (0.3%)	1.47	10/903 (1.1%)
17	G	0.65	0/1629	1.11	7/2202 (0.3%)
18	H	0.83	0/1038	1.23	8/1395 (0.6%)
19	I	0.70	0/1125	1.18	8/1510 (0.5%)
20	J	0.71	0/865	1.19	8/1169 (0.7%)
21	K	0.69	0/901	1.23	7/1217 (0.6%)
22	L	0.91	1/1139 (0.1%)	1.26	6/1518 (0.4%)
23	M	0.74	0/1211	1.14	5/1628 (0.3%)
24	N	0.86	1/452 (0.2%)	1.24	2/600 (0.3%)
25	O	0.80	0/1215	1.17	8/1638 (0.5%)
26	P	0.70	1/1087 (0.1%)	1.08	2/1449 (0.1%)
27	Q	0.86	0/1239	1.17	6/1673 (0.4%)
28	R	0.63	0/2490	1.03	7/3389 (0.2%)
29	S	0.75	0/998	1.21	8/1341 (0.6%)
30	T	0.72	1/1130 (0.1%)	1.09	5/1517 (0.3%)
31	U	0.70	0/898	1.13	4/1220 (0.3%)
32	V	0.73	0/935	1.25	7/1254 (0.6%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	W	0.75	0/2109	1.20	17/2839 (0.6%)
34	X	0.62	0/483	1.13	2/643 (0.3%)
35	Y	0.70	0/1823	1.12	7/2439 (0.3%)
36	Z	0.67	1/693 (0.1%)	1.08	3/935 (0.3%)
37	a	0.40	0/3729	0.80	2/5041 (0.0%)
38	b	0.53	3/3999 (0.1%)	0.85	12/5440 (0.2%)
39	c	0.43	0/4525	0.88	7/6120 (0.1%)
All	All	0.63	16/94313 (0.0%)	0.90	261/136002 (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	0	0	1
4	3	0	1
5	4	0	1
7	6	0	1
9	8	0	3
10	9	0	2
16	F	0	1
21	K	0	1
27	Q	0	1
32	V	0	2
39	c	0	1
All	All	0	15

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	A	1626	U	O3'-P	38.62	2.19	1.61
38	b	565	TRP	C-N	9.98	1.47	1.33
15	E	206	THR	CA-CB	7.60	1.62	1.52
26	P	33	ALA	CA-CB	-7.08	1.43	1.53
38	b	660	VAL	CA-CB	6.53	1.63	1.54
16	F	27	HIS	CG-ND1	-6.23	1.31	1.38
38	b	552	ALA	C-N	6.06	1.40	1.33
15	E	206	THR	CA-C	5.68	1.59	1.52
30	T	39	THR	CA-CB	5.53	1.62	1.53
22	L	84	THR	CA-CB	5.53	1.61	1.53
24	N	6	VAL	CA-CB	5.33	1.61	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
16	F	71	ASP	CG-OD1	5.30	1.35	1.25
12	B	103	THR	CA-CB	5.27	1.61	1.53
11	A	49	C	P-OP2	-5.24	1.38	1.49
36	Z	59	VAL	CA-CB	-5.18	1.48	1.54
15	E	96	THR	CA-CB	5.14	1.59	1.53

All (261) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	A	1626	U	O3'-P-O5'	35.22	156.82	104.00
11	A	1626	U	OP1-P-O3'	-16.65	58.04	108.00
11	A	1626	U	P-O3'-C3'	-15.86	96.41	120.20
16	F	72	PRO	CA-N-CD	-12.50	94.50	112.00
22	L	130	VAL	N-CA-C	11.37	121.34	111.56
8	7	88	PRO	N-CA-CB	10.30	114.07	103.25
14	D	14	THR	CA-C-N	9.72	130.33	119.93
14	D	14	THR	C-N-CA	9.72	130.33	119.93
9	8	95	HIS	N-CA-C	9.63	126.47	108.65
19	I	43	ILE	N-CA-C	-9.39	101.41	110.42
16	F	84	GLN	OE1-CD-NE2	-9.17	113.43	122.60
7	6	37	CYS	CA-C-N	8.88	130.94	119.84
7	6	37	CYS	C-N-CA	8.88	130.94	119.84
38	b	565	TRP	O-C-N	-8.87	112.74	123.30
23	M	58	ALA	N-CA-C	-8.84	101.72	111.36
24	N	9	SER	N-CA-C	8.70	123.63	108.75
16	F	79	GLN	OE1-CD-NE2	-8.54	114.06	122.60
32	V	85	VAL	CA-C-N	8.42	130.37	119.84
32	V	85	VAL	C-N-CA	8.42	130.37	119.84
13	C	210	GLU	CA-C-N	8.31	130.23	119.84
13	C	210	GLU	C-N-CA	8.31	130.23	119.84
23	M	144	ARG	N-CA-C	-8.21	102.02	110.97
39	c	459	ILE	CA-C-N	7.92	129.74	119.84
39	c	459	ILE	C-N-CA	7.92	129.74	119.84
4	3	185	ILE	CA-C-N	-7.92	109.95	119.84
4	3	185	ILE	C-N-CA	-7.92	109.95	119.84
21	K	81	VAL	N-CA-C	7.87	119.93	108.53
8	7	63	TYR	N-CA-C	7.76	125.64	114.39
38	b	562	ILE	N-CA-C	7.70	118.47	110.62
20	J	75	GLY	N-CA-C	-7.59	104.73	111.95
33	W	76	VAL	N-CA-C	7.55	117.63	110.53
38	b	555	THR	N-CA-C	7.52	119.11	111.07
5	4	205	PHE	CA-C-N	7.44	129.14	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	4	205	PHE	C-N-CA	7.44	129.14	119.84
5	4	132	ASP	N-CA-C	7.44	120.02	110.65
24	N	24	CYS	N-CA-C	7.43	122.41	112.30
7	6	43	ILE	N-CA-C	7.41	118.57	107.75
19	I	69	VAL	CB-CA-C	-7.39	100.79	110.84
30	T	38	LYS	N-CA-C	7.38	122.35	113.12
19	I	40	GLU	C-N-CD	-7.38	104.37	120.60
19	I	40	GLU	CA-C-N	7.34	144.62	127.00
19	I	40	GLU	C-N-CA	7.34	144.62	127.00
35	Y	85	ARG	CA-C-N	7.34	127.32	119.76
35	Y	85	ARG	C-N-CA	7.34	127.32	119.76
10	9	146	SER	N-CA-C	-7.20	106.41	114.62
25	O	22	ALA	CA-C-N	7.15	144.16	127.00
25	O	22	ALA	C-N-CA	7.15	144.16	127.00
17	G	44	ASN	N-CA-C	-7.14	102.55	111.11
33	W	28	ALA	CA-C-N	-7.13	112.42	119.90
33	W	28	ALA	C-N-CA	-7.13	112.42	119.90
12	B	3	LEU	CA-C-N	7.09	128.70	119.84
12	B	3	LEU	C-N-CA	7.09	128.70	119.84
15	E	111	VAL	CB-CA-C	-7.08	102.07	111.70
12	B	108	THR	N-CA-C	-7.06	100.07	110.52
33	W	105	VAL	N-CA-C	-6.99	105.24	113.42
27	Q	135	VAL	N-CA-C	6.96	118.02	108.84
25	O	22	ALA	C-N-CD	-6.96	105.30	120.60
16	F	71	ASP	CA-C-N	6.95	128.53	119.84
16	F	71	ASP	C-N-CA	6.95	128.53	119.84
16	F	79	GLN	CG-CD-OE1	6.88	134.57	120.80
3	2	148	ALA	N-CA-C	-6.84	101.95	111.39
13	C	219	ALA	CA-C-N	6.84	128.39	119.84
13	C	219	ALA	C-N-CA	6.84	128.39	119.84
8	7	82	LEU	CA-C-N	6.83	126.86	119.89
8	7	82	LEU	C-N-CA	6.83	126.86	119.89
12	B	202	TYR	N-CA-C	-6.83	101.06	110.35
22	L	45	GLY	N-CA-C	-6.79	105.14	114.64
16	F	71	ASP	CA-CB-CG	6.70	119.30	112.60
8	7	87	VAL	CA-C-N	6.69	128.21	119.84
8	7	87	VAL	C-N-CA	6.69	128.21	119.84
39	c	362	VAL	N-CA-C	-6.69	105.19	111.48
4	3	50	ASP	N-CA-C	6.67	120.24	110.17
16	F	85	ARG	N-CA-C	6.67	119.39	111.33
33	W	30	ARG	CA-C-N	6.66	127.06	119.93
33	W	30	ARG	C-N-CA	6.66	127.06	119.93

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
29	S	52	LYS	CA-C-N	-6.62	114.97	121.65
29	S	52	LYS	C-N-CA	-6.62	114.97	121.65
29	S	100	LYS	N-CA-C	-6.60	99.53	109.96
6	5	96	ALA	CA-C-N	6.57	127.15	120.38
6	5	96	ALA	C-N-CA	6.57	127.15	120.38
21	K	91	THR	N-CA-C	6.55	119.26	111.33
30	T	9	VAL	N-CA-C	6.54	117.44	107.77
17	G	29	ILE	CA-C-N	6.51	127.98	119.84
17	G	29	ILE	C-N-CA	6.51	127.98	119.84
32	V	77	GLU	N-CA-C	-6.51	103.88	110.97
26	P	45	ALA	N-CA-C	-6.50	104.19	111.28
14	D	101	VAL	N-CA-C	6.50	117.24	110.62
9	8	98	GLN	N-CA-C	6.49	119.13	109.59
38	b	552	ALA	CA-C-N	-6.48	113.62	120.03
38	b	552	ALA	C-N-CA	-6.48	113.62	120.03
21	K	56	SER	CA-C-N	6.45	126.67	119.32
21	K	56	SER	C-N-CA	6.45	126.67	119.32
7	6	15	GLU	N-CA-C	-6.41	103.80	111.69
5	4	22	ASP	CA-C-N	6.39	127.83	119.84
5	4	22	ASP	C-N-CA	6.39	127.83	119.84
18	H	94	LEU	CA-C-N	6.36	125.59	118.97
18	H	94	LEU	C-N-CA	6.36	125.59	118.97
25	O	137	PRO	CA-C-O	-6.36	114.09	121.34
33	W	197	HIS	N-CA-C	6.36	116.97	108.38
12	B	167	LYS	CB-CA-C	-6.34	109.28	116.63
9	8	94	LYS	N-CA-C	6.33	121.10	112.68
35	Y	147	LEU	N-CA-C	6.32	121.83	114.62
4	3	30	SER	N-CA-C	-6.31	104.37	113.21
33	W	168	LYS	N-CA-C	6.30	118.44	110.24
4	3	97	ARG	N-CA-C	6.30	117.94	111.14
10	9	106	TYR	N-CA-C	-6.23	97.53	110.80
18	H	105	THR	CB-CA-C	-6.21	100.01	110.19
28	R	286	GLU	CA-C-N	6.20	125.96	119.76
28	R	286	GLU	C-N-CA	6.20	125.96	119.76
10	9	144	CYS	N-CA-C	-6.19	97.61	110.80
22	L	111	GLY	N-CA-C	-6.19	100.50	112.02
15	E	150	GLN	CA-C-N	6.17	126.19	119.90
15	E	150	GLN	C-N-CA	6.17	126.19	119.90
20	J	75	GLY	CA-C-O	-6.14	118.23	122.22
4	3	31	SER	N-CA-C	6.11	123.32	109.81
33	W	149	TYR	CA-C-N	-6.11	114.47	120.52
33	W	149	TYR	C-N-CA	-6.11	114.47	120.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	9	104	SER	N-CA-C	-6.11	105.79	113.18
3	2	104	ILE	N-CA-C	6.11	122.04	109.34
5	4	105	PHE	N-CA-C	-6.11	99.79	109.07
35	Y	38	GLY	N-CA-C	6.10	119.87	112.49
30	T	121	GLY	N-CA-C	6.08	118.64	111.35
12	B	111	ILE	N-CA-C	6.07	121.97	109.34
31	U	26	ASP	N-CA-C	-6.07	105.84	113.18
29	S	124	THR	CA-C-N	6.06	127.41	119.84
29	S	124	THR	C-N-CA	6.06	127.41	119.84
22	L	29	TYR	N-CA-C	-6.04	104.61	111.14
23	M	31	ALA	N-CA-C	-6.04	104.33	111.03
12	B	145	ALA	N-CA-C	6.01	118.29	108.55
18	H	55	ASP	N-CA-C	-5.98	102.47	110.55
25	O	12	SER	N-CA-C	-5.98	99.43	108.52
13	C	203	PRO	CA-C-N	5.97	128.28	120.28
13	C	203	PRO	C-N-CA	5.97	128.28	120.28
33	W	103	TYR	N-CA-C	5.97	119.64	110.20
38	b	582	SER	CA-C-N	5.97	125.65	119.56
38	b	582	SER	C-N-CA	5.97	125.65	119.56
5	4	153	HIS	N-CA-C	5.97	123.51	110.80
7	6	68	GLY	N-CA-C	-5.96	105.44	113.24
35	Y	129	VAL	CA-C-N	5.93	126.23	119.83
35	Y	129	VAL	C-N-CA	5.93	126.23	119.83
21	K	115	ILE	N-CA-C	5.90	116.37	107.75
12	B	67	ILE	CA-C-N	5.88	127.19	119.84
12	B	67	ILE	C-N-CA	5.88	127.19	119.84
30	T	54	PHE	N-CA-C	-5.85	104.85	112.23
20	J	28	SER	N-CA-C	5.80	116.21	108.38
3	2	32	GLN	CA-C-N	5.79	125.69	119.85
3	2	32	GLN	C-N-CA	5.79	125.69	119.85
28	R	59	ARG	N-CA-C	5.78	118.18	109.23
39	c	342	ASN	N-CA-C	5.73	116.48	108.00
4	3	62	VAL	CA-C-N	5.72	126.99	119.84
4	3	62	VAL	C-N-CA	5.72	126.99	119.84
14	D	66	ASP	CA-C-N	5.72	125.19	119.24
14	D	66	ASP	C-N-CA	5.72	125.19	119.24
25	O	122	ILE	CB-CA-C	-5.71	104.67	111.97
29	S	37	ALA	CA-C-N	-5.71	112.71	119.84
29	S	37	ALA	C-N-CA	-5.71	112.71	119.84
12	B	74	VAL	N-CA-C	5.70	116.15	108.17
33	W	3	ARG	N-CA-C	5.70	122.94	110.80
32	V	85	VAL	N-CA-C	5.67	121.13	108.88

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	J	34	LEU	N-CA-C	-5.66	105.19	111.36
18	H	128	PHE	N-CA-C	5.65	117.44	108.79
21	K	124	ASP	N-CA-C	5.65	122.84	110.80
28	R	84	SER	N-CA-C	5.65	117.66	109.07
9	8	83	LEU	N-CA-C	-5.65	106.23	113.23
5	4	131	ASP	CB-CA-C	5.64	119.29	109.65
33	W	105	VAL	CB-CA-C	-5.63	104.75	110.88
7	6	67	THR	N-CA-C	5.63	115.45	108.19
29	S	39	ALA	N-CA-C	5.63	117.89	111.02
36	Z	34	ILE	CB-CA-C	-5.61	104.17	110.96
18	H	98	GLN	N-CA-C	5.61	119.38	112.54
28	R	137	LYS	N-CA-C	-5.59	106.50	113.38
23	M	28	ILE	N-CA-C	5.59	120.96	109.34
38	b	660	VAL	CB-CA-C	5.58	120.45	111.29
4	3	116	ARG	N-CA-C	-5.53	105.46	113.21
35	Y	19	ASP	N-CA-C	-5.52	101.17	109.95
6	5	74	CYS	N-CA-C	5.52	119.32	112.59
36	Z	13	VAL	CA-C-N	5.52	126.74	119.84
36	Z	13	VAL	C-N-CA	5.52	126.74	119.84
16	F	102	ASN	CA-CB-CG	5.51	118.11	112.60
4	3	12	ALA	CA-C-N	5.50	126.72	119.84
4	3	12	ALA	C-N-CA	5.50	126.72	119.84
21	K	22	SER	N-CA-C	-5.49	101.79	109.69
32	V	23	LYS	N-CA-C	-5.48	99.12	110.80
15	E	64	LYS	N-CA-C	-5.46	108.39	114.62
27	Q	131	ILE	N-CA-C	-5.46	107.50	112.96
18	H	93	LEU	N-CA-C	5.46	120.63	112.94
13	C	50	ILE	CB-CA-C	-5.44	106.48	112.68
19	I	63	ILE	N-CA-C	5.43	116.49	108.45
5	4	232	HIS	N-CA-C	5.43	118.31	109.24
27	Q	109	VAL	N-CA-C	5.43	116.10	108.17
13	C	114	ALA	N-CA-C	-5.41	102.17	109.95
6	5	97	PRO	N-CA-C	5.40	117.29	110.70
4	3	183	PHE	N-CA-C	5.40	117.46	109.69
12	B	6	THR	N-CA-C	-5.40	105.92	112.88
31	U	81	ASP	CA-C-N	5.37	126.56	119.84
31	U	81	ASP	C-N-CA	5.37	126.56	119.84
23	M	86	LEU	N-CA-C	5.37	118.23	109.59
38	b	595	GLY	CA-C-N	5.36	125.43	119.32
38	b	595	GLY	C-N-CA	5.36	125.43	119.32
33	W	235	TYR	N-CA-C	-5.35	106.51	114.64
27	Q	22	ASN	CA-C-N	5.35	124.96	119.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
27	Q	22	ASN	C-N-CA	5.35	124.96	119.56
13	C	37	VAL	CB-CA-C	-5.34	103.87	111.19
33	W	154	ILE	CB-CA-C	-5.34	103.36	111.69
5	4	110	LEU	N-CA-C	-5.33	105.47	111.28
20	J	62	VAL	N-CA-C	5.31	115.72	107.28
39	c	342	ASN	CB-CA-C	-5.29	108.93	116.34
31	U	94	ALA	N-CA-C	5.27	116.71	111.07
3	2	172	ARG	CA-C-N	5.27	124.72	119.24
3	2	172	ARG	C-N-CA	5.27	124.72	119.24
26	P	35	VAL	N-CA-C	5.27	116.09	111.56
12	B	143	VAL	N-CA-C	5.26	116.28	107.18
34	X	57	ASN	CA-C-N	-5.26	114.93	120.66
34	X	57	ASN	C-N-CA	-5.26	114.93	120.66
15	E	148	LEU	N-CA-C	5.26	122.00	110.80
28	R	170	ILE	N-CA-C	5.24	115.52	107.77
30	T	39	THR	N-CA-CB	5.24	119.34	110.49
32	V	81	LYS	N-CA-C	-5.23	106.13	112.88
16	F	84	GLN	CG-CD-OE1	5.22	131.24	120.80
1	0	75	ASP	CA-CB-CG	5.22	117.82	112.60
18	H	89	TRP	N-CA-C	5.21	117.38	111.02
17	G	27	THR	CA-C-N	5.21	126.34	120.66
17	G	27	THR	C-N-CA	5.21	126.34	120.66
37	a	7	ARG	CA-C-N	5.21	124.53	118.85
37	a	7	ARG	C-N-CA	5.21	124.53	118.85
5	4	204	ILE	CB-CA-C	-5.20	105.66	111.80
14	D	152	SER	N-CA-C	-5.20	106.04	114.09
38	b	285	GLY	CA-C-N	5.19	125.24	119.32
38	b	285	GLY	C-N-CA	5.19	125.24	119.32
28	R	272	ASP	N-CA-C	5.19	116.18	108.60
12	B	188	LEU	N-CA-C	5.18	121.84	110.80
12	B	63	ILE	CB-CA-C	-5.17	106.33	111.30
8	7	60	SER	N-CA-C	5.17	121.81	110.80
33	W	118	GLU	N-CA-C	-5.17	106.23	112.54
19	I	65	ILE	N-CA-C	5.17	115.30	107.75
12	B	158	VAL	N-CA-C	5.17	120.09	109.34
22	L	129	GLY	CA-C-N	-5.16	117.87	123.08
22	L	129	GLY	C-N-CA	-5.16	117.87	123.08
3	2	22	ARG	N-CA-C	5.16	121.78	110.80
11	A	1626	U	OP2-P-O3'	-5.15	92.54	108.00
13	C	42	THR	CA-C-N	-5.15	114.43	119.99
13	C	42	THR	C-N-CA	-5.15	114.43	119.99
20	J	42	VAL	N-CA-C	5.15	115.37	110.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	W	210	ILE	CB-CA-C	-5.13	103.04	110.63
12	B	166	GLY	N-CA-C	5.12	116.96	110.20
12	B	193	GLN	CA-C-N	5.12	126.24	119.84
12	B	193	GLN	C-N-CA	5.12	126.24	119.84
14	D	138	LYS	N-CA-C	-5.10	106.84	113.16
17	G	66	GLN	CA-C-N	5.07	125.28	120.31
17	G	66	GLN	C-N-CA	5.07	125.28	120.31
10	9	138	ARG	N-CA-C	5.06	121.58	110.80
15	E	206	THR	CB-CA-C	5.06	120.18	111.68
20	J	54	GLY	CA-C-N	5.05	126.15	119.84
20	J	54	GLY	C-N-CA	5.05	126.15	119.84
27	Q	55	ASP	N-CA-C	5.04	121.54	110.80
25	O	112	LYS	N-CA-C	-5.03	105.71	111.14
19	I	74	HIS	N-CA-C	5.03	116.45	111.07
39	c	535	PHE	CA-C-N	5.02	131.12	121.54
39	c	535	PHE	C-N-CA	5.02	131.12	121.54
25	O	4	MET	N-CA-C	5.01	116.55	111.14
32	V	125	SER	N-CA-C	5.01	115.66	108.74

There are no chirality outliers.

All (15) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	0	23	LYS	Peptide
4	3	131	PHE	Peptide
5	4	131	ASP	Peptide
7	6	42	ASN	Peptide
9	8	54	VAL	Peptide
9	8	93	SER	Peptide
9	8	96	SER	Peptide
10	9	105	TYR	Peptide
10	9	138	ARG	Peptide
16	F	62	PHE	Sidechain
21	K	124	ASP	Peptide
27	Q	127	GLN	Peptide
32	V	22	PRO	Peptide
32	V	85	VAL	Peptide
39	c	644	ARG	Peptide

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	805	0	790	148	0
2	1	497	0	535	35	0
3	2	1489	0	1525	59	0
4	3	1481	0	1572	80	0
5	4	1709	0	1784	128	0
6	5	769	0	814	54	0
7	6	610	0	630	45	0
8	7	772	0	727	44	0
9	8	563	0	603	47	0
10	9	516	0	517	43	0
11	A	37835	0	19056	1200	0
12	B	1577	0	1566	222	0
13	C	1734	0	1817	82	0
14	D	1494	0	1573	92	0
15	E	1635	0	1715	89	0
16	F	671	0	707	82	0
17	G	1609	0	1675	72	0
18	H	1021	0	1060	53	0
19	I	1105	0	1166	71	0
20	J	855	0	917	40	0
21	K	891	0	883	65	0
22	L	1121	0	1196	62	0
23	M	1192	0	1222	66	0
24	N	442	0	428	24	0
25	O	1192	0	1255	50	0
26	P	1073	0	1132	41	0
27	Q	1213	0	1257	51	0
28	R	2437	0	2386	79	0
29	S	977	0	1002	42	0
30	T	1112	0	1124	72	0
31	U	890	0	887	47	0
32	V	926	0	930	79	0
33	W	2068	0	2154	73	0
34	X	475	0	523	86	0
35	Y	1799	0	1879	89	0
36	Z	684	0	672	44	0
37	a	3656	0	3708	115	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	b	3978	0	3768	67	0
39	c	4442	0	4474	216	0
40	5	1	0	0	0	0
40	6	1	0	0	0	0
40	9	1	0	0	0	0
40	N	1	0	0	0	0
All	All	89319	0	71629	3291	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 21.

All (3291) 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)
11:A:1151:A:C2'	11:A:1152:A:H5'	1.10	1.57
11:A:1151:A:C6	11:A:1152:A:C8	1.93	1.57
11:A:1293:U:H1'	12:B:111:ILE:CB	1.21	1.57
11:A:1293:U:H1'	12:B:111:ILE:CG1	1.27	1.56
1:0:46:ARG:CD	34:X:3:LYS:HE3	1.39	1.53
11:A:1151:A:H3'	11:A:1152:A:P	1.49	1.53
1:0:46:ARG:HD3	34:X:3:LYS:CE	1.09	1.52
37:a:348:HIS:NE2	39:c:664:PHE:CA	1.74	1.50
37:a:348:HIS:CE1	39:c:664:PHE:HA	1.40	1.49
12:B:42:PRO:CD	32:V:105:GLN:NE2	1.76	1.49
11:A:1151:A:H2'	11:A:1152:A:C5'	0.99	1.47
1:0:82:ARG:NH2	22:L:68:ILE:HD11	1.21	1.44
37:a:348:HIS:NE2	39:c:664:PHE:HA	1.18	1.41
11:A:1296:A:OP1	12:B:138:TYR:CE2	1.73	1.40
11:A:1151:A:N1	11:A:1152:A:C8	1.84	1.39
11:A:579:A:N6	13:C:143:ARG:HA	1.38	1.37
11:A:1293:U:C1'	12:B:111:ILE:CG1	2.01	1.36
11:A:1151:A:C6	11:A:1152:A:N7	1.90	1.36
1:0:85:GLN:NE2	34:X:6:GLY:N	1.71	1.35
1:0:46:ARG:NE	34:X:3:LYS:HG3	1.03	1.33
1:0:88:GLN:NE2	34:X:5:HIS:H	1.28	1.31
1:0:63:GLY:N	11:A:566:C:OP1	1.65	1.29
12:B:42:PRO:HD3	32:V:105:GLN:NE2	1.39	1.29
11:A:1293:U:C1'	12:B:111:ILE:HG12	1.56	1.29
11:A:1293:U:C1'	12:B:111:ILE:HB	1.64	1.28
11:A:579:A:H61	13:C:143:ARG:CA	1.45	1.28
7:6:41:LEU:HD11	39:c:431:ARG:CG	1.63	1.28

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:1295:G:H5'	12:B:108:THR:OG1	1.21	1.28
11:A:1151:A:C2	11:A:1152:A:C8	2.22	1.27
11:A:1151:A:C2'	11:A:1152:A:C5'	1.78	1.27
11:A:1301:U:OP1	15:E:97:ARG:HD3	1.36	1.26
11:A:579:A:N1	13:C:143:ARG:O	1.66	1.26
7:6:41:LEU:CD1	39:c:431:ARG:CG	2.12	1.26
1:0:82:ARG:NH2	22:L:68:ILE:CD1	1.99	1.25
11:A:1151:A:C2	11:A:1152:A:N9	2.04	1.25
37:a:347:PRO:CB	39:c:663:SER:HA	1.66	1.24
11:A:1151:A:C2	11:A:1152:A:C1'	2.21	1.24
1:0:46:ARG:CD	34:X:3:LYS:HG3	1.66	1.23
1:0:85:GLN:HE22	34:X:6:GLY:N	1.30	1.22
11:A:1298:U:O2	15:E:209:ASN:OD1	1.53	1.22
1:0:46:ARG:NE	34:X:3:LYS:CG	2.00	1.22
7:6:41:LEU:CD1	39:c:431:ARG:HG3	1.67	1.22
37:a:347:PRO:HB2	39:c:663:SER:CA	1.71	1.21
11:A:1686:C:H2'	11:A:1687:U:H6	1.07	1.20
11:A:1151:A:N3	11:A:1152:A:O4'	1.76	1.19
7:6:41:LEU:HD13	39:c:431:ARG:NE	1.58	1.18
1:0:85:GLN:NE2	34:X:5:HIS:C	1.85	1.18
1:0:46:ARG:CD	34:X:3:LYS:CE	2.04	1.17
11:A:579:A:N6	13:C:143:ARG:HG3	1.59	1.16
12:B:41:ARG:HG3	32:V:103:ASP:CB	1.76	1.15
37:a:292:VAL:CG1	39:c:667:PRO:CD	2.25	1.15
11:A:1295:G:OP1	12:B:108:THR:HB	1.46	1.15
11:A:1152:A:C2	11:A:1627:U:N3	2.15	1.14
11:A:1151:A:C2'	11:A:1152:A:H5''	1.77	1.12
11:A:1293:U:O3'	12:B:110:TYR:CE1	2.01	1.12
11:A:1320:U:H3'	12:B:101:ARG:NH2	1.64	1.12
11:A:1296:A:OP1	12:B:138:TYR:HE2	0.81	1.12
1:0:88:GLN:CD	34:X:5:HIS:H	1.56	1.12
1:0:88:GLN:CD	34:X:5:HIS:N	2.08	1.12
12:B:38:PHE:CZ	32:V:109:LEU:HA	1.84	1.12
11:A:1151:A:N6	11:A:1152:A:N7	1.97	1.11
11:A:1324:G:O3'	12:B:113:ARG:NH2	1.84	1.11
11:A:12:U:O2'	11:A:1299:G:N2	1.82	1.11
11:A:1324:G:C5'	12:B:113:ARG:NE	2.13	1.11
11:A:1295:G:C5'	12:B:108:THR:OG1	1.99	1.10
16:F:69:VAL:HB	16:F:79:GLN:HE22	1.17	1.09
11:A:1293:U:C1'	12:B:111:ILE:CB	2.14	1.09
11:A:500:C:H5'	38:b:487:SER:O	1.51	1.09

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:1295:G:P	12:B:108:THR:HB	1.92	1.08
1:0:82:ARG:HA	34:X:7:SER:OG	1.54	1.08
11:A:1151:A:C5	11:A:1152:A:C8	2.39	1.08
1:0:88:GLN:HB2	34:X:5:HIS:O	1.53	1.07
11:A:1151:A:C3'	11:A:1152:A:C5'	2.31	1.07
1:0:58:MET:HG3	34:X:3:LYS:HE2	1.31	1.07
11:A:1294:G:O2'	12:B:109:ASN:CB	2.02	1.07
11:A:1151:A:C3'	11:A:1152:A:P	2.43	1.06
12:B:42:PRO:HD2	32:V:105:GLN:NE2	1.46	1.05
11:A:1302:U:OP1	15:E:88:LYS:NZ	1.90	1.05
11:A:1152:A:N3	11:A:1627:U:C2	2.24	1.04
37:a:482:ILE:HD13	39:c:733:TYR:CE1	1.93	1.04
11:A:1061:A:H1'	39:c:594:ASN:CA	1.89	1.03
1:0:46:ARG:CD	34:X:3:LYS:CG	2.37	1.03
11:A:1293:U:H1'	12:B:111:ILE:HB	1.05	1.03
37:a:466:GLU:OE2	39:c:733:TYR:OH	1.75	1.03
1:0:29:LYS:HA	1:0:33:GLN:NE2	1.74	1.02
11:A:1301:U:OP1	15:E:97:ARG:CD	2.06	1.02
37:a:466:GLU:CD	39:c:733:TYR:OH	2.04	1.01
1:0:44:ASN:OD1	11:A:1755:A:N6	1.94	1.01
11:A:1152:A:N1	11:A:1627:U:C4	2.27	1.01
11:A:1324:G:H5''	12:B:113:ARG:CZ	1.91	1.01
11:A:1715:G:O6	11:A:1716:C:N4	1.93	1.01
12:B:41:ARG:HA	32:V:105:GLN:CG	1.90	1.00
11:A:1293:U:O3'	12:B:110:TYR:CZ	2.14	1.00
7:6:41:LEU:HD13	39:c:431:ARG:HE	1.20	1.00
39:c:487:SER:HB2	39:c:506:ASN:HD21	1.27	1.00
11:A:1151:A:H2'	11:A:1152:A:H5''	1.34	1.00
11:A:1152:A:C2	11:A:1627:U:C4	2.50	1.00
12:B:42:PRO:CD	32:V:105:GLN:HE22	1.52	1.00
11:A:1626:U:O3'	11:A:1627:U:P	2.19	1.00
11:A:1294:G:O2'	12:B:109:ASN:HB2	1.16	0.99
11:A:1686:C:H2'	11:A:1687:U:C6	1.98	0.99
11:A:701:U:H3	11:A:737:A:H61	1.07	0.99
1:0:82:ARG:HB3	34:X:8:LEU:N	1.73	0.98
1:0:46:ARG:HD3	34:X:3:LYS:NZ	1.76	0.98
4:3:9:LEU:HD21	4:3:17:GLU:HB3	1.43	0.98
1:0:82:ARG:CA	34:X:7:SER:OG	2.11	0.98
37:a:292:VAL:HG13	39:c:667:PRO:HG3	1.42	0.98
7:6:38:PRO:HG2	39:c:603:ARG:NH1	1.79	0.98
11:A:1293:U:C2'	12:B:111:ILE:HB	1.94	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:1492:A:HO2'	11:A:1493:A:H8	1.00	0.98
11:A:1152:A:C2	11:A:1627:U:C2	2.51	0.98
1:0:29:LYS:HA	1:0:33:GLN:HE21	1.25	0.97
1:0:46:ARG:HD3	34:X:3:LYS:CD	1.93	0.97
7:6:41:LEU:CD1	39:c:431:ARG:HG2	1.94	0.97
11:A:1151:A:C2	11:A:1152:A:O4'	2.15	0.97
11:A:1061:A:C1'	39:c:594:ASN:HB3	1.61	0.97
14:D:60:LEU:HD21	14:D:93:LEU:HD21	1.45	0.97
37:a:292:VAL:HG13	39:c:667:PRO:CG	1.94	0.97
11:A:1300:A:C5'	15:E:117:THR:HG21	1.89	0.97
1:0:82:ARG:CZ	22:L:68:ILE:CD1	2.43	0.97
11:A:1152:A:N3	11:A:1627:U:N3	2.14	0.96
30:T:57:ARG:HH11	30:T:57:ARG:HG3	1.26	0.96
11:A:1588:G:H1	11:A:1608:U:H3	1.13	0.96
11:A:499:U:O2'	38:b:489:LYS:HE2	1.65	0.96
11:A:1324:G:H4'	12:B:113:ARG:HE	1.30	0.95
7:6:41:LEU:HD13	39:c:431:ARG:CG	1.89	0.95
12:B:38:PHE:CD1	32:V:109:LEU:HB2	2.01	0.95
7:6:41:LEU:HD11	39:c:431:ARG:HG3	0.97	0.94
11:A:1151:A:H2'	11:A:1152:A:C4'	1.97	0.94
1:0:82:ARG:HB3	34:X:8:LEU:H	1.26	0.94
12:B:38:PHE:CE1	32:V:109:LEU:HB2	2.02	0.94
1:0:62:ARG:HD2	1:0:92:VAL:HA	1.47	0.94
11:A:1061:A:C1'	39:c:594:ASN:CB	2.44	0.94
17:G:117:THR:HG21	17:G:194:LEU:HD12	1.48	0.94
11:A:1152:A:C6	11:A:1627:U:O4	2.21	0.94
12:B:38:PHE:CE1	32:V:109:LEU:HA	2.02	0.94
37:a:292:VAL:HG13	39:c:667:PRO:CD	1.97	0.94
1:0:63:GLY:HA3	11:A:565:C:C2'	1.98	0.94
11:A:1151:A:N1	11:A:1152:A:N9	2.06	0.94
1:0:85:GLN:CB	34:X:5:HIS:O	2.16	0.93
11:A:579:A:H61	13:C:143:ARG:HA	0.77	0.93
11:A:151:G:O6	26:P:124:ARG:NH2	2.01	0.93
11:A:1294:G:OP1	12:B:110:TYR:HE1	1.50	0.93
1:0:88:GLN:NE2	34:X:5:HIS:N	2.13	0.93
11:A:1644:C:H1'	16:F:63:ALA:HB2	1.50	0.93
12:B:42:PRO:HD3	32:V:105:GLN:CD	1.92	0.93
37:a:293:SER:OG	39:c:664:PHE:CE1	2.22	0.93
37:a:292:VAL:HG12	39:c:667:PRO:CD	1.97	0.93
11:A:1321:A:O5'	12:B:104:PRO:HG2	1.69	0.93
11:A:1324:G:H5'	12:B:113:ARG:NE	1.81	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:1644:C:H1'	16:F:63:ALA:CB	1.98	0.92
1:0:85:GLN:HB3	34:X:5:HIS:O	1.70	0.92
11:A:1324:G:C4'	12:B:113:ARG:HH21	1.82	0.92
11:A:1585:U:H3	11:A:1611:A:H2	0.96	0.92
1:0:88:GLN:CD	34:X:5:HIS:CA	2.36	0.92
1:0:61:ILE:HA	1:0:91:VAL:HG12	1.47	0.92
16:F:30:ILE:HG12	16:F:107:GLY:HA2	1.51	0.92
37:a:466:GLU:CD	39:c:733:TYR:HH	1.78	0.92
37:a:470:LEU:HD11	39:c:733:TYR:CE2	2.04	0.92
1:0:63:GLY:HA3	11:A:565:C:C3'	2.00	0.91
10:9:86:UNK:O	10:9:87:UNK:HG3	1.69	0.91
11:A:1626:U:O3'	11:A:1627:U:OP1	1.88	0.91
11:A:1300:A:O2'	15:E:86:VAL:HB	1.71	0.91
38:b:658:HIS:CG	38:b:659:LYS:H	1.88	0.91
5:4:129:THR:HB	5:4:180:THR:HA	1.51	0.91
5:4:97:LEU:HD13	5:4:98:THR:H	1.34	0.91
11:A:279:G:H3'	11:A:280:U:H5''	1.50	0.91
11:A:475:A:OP2	14:D:126:ARG:NH1	2.04	0.90
21:K:85:ALA:H	21:K:119:THR:HG22	1.36	0.90
11:A:1061:A:H1'	39:c:594:ASN:CB	2.02	0.90
11:A:500:C:O5'	38:b:489:LYS:HA	1.72	0.90
12:B:38:PHE:CE1	32:V:109:LEU:CA	2.54	0.90
37:a:470:LEU:HD11	39:c:733:TYR:HE2	1.33	0.89
11:A:912:U:H4'	11:A:913:G:H3'	1.52	0.89
11:A:1715:G:C6	11:A:1716:C:C4	2.60	0.89
37:a:347:PRO:HG3	39:c:662:LEU:O	1.72	0.89
11:A:1295:G:H5''	12:B:108:THR:HG21	1.55	0.89
11:A:1294:G:O3'	12:B:108:THR:CB	2.21	0.89
11:A:1151:A:C1'	11:A:1152:A:H5'	2.03	0.88
37:a:292:VAL:CG1	39:c:667:PRO:HD2	2.02	0.88
11:A:1151:A:C5	11:A:1152:A:H8	1.88	0.88
1:0:61:ILE:HA	1:0:91:VAL:CG1	2.04	0.88
11:A:1324:G:C3'	12:B:113:ARG:HH21	1.87	0.88
16:F:71:ASP:OD1	16:F:72:PRO:HD2	1.72	0.88
7:6:41:LEU:HD13	39:c:431:ARG:CD	2.03	0.87
11:A:1300:A:H4'	15:E:86:VAL:HG21	1.56	0.87
11:A:1716:C:HO2'	11:A:1717:G:H8	0.89	0.87
14:D:110:GLN:HE22	14:D:126:ARG:HG2	1.39	0.87
37:a:484:HIS:HB2	39:c:735:SER:C	1.98	0.87
11:A:1061:A:H1'	39:c:594:ASN:HB3	1.53	0.87
5:4:32:ILE:HD11	5:4:46:THR:HG23	1.55	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:1299:G:O3'	15:E:99:LYS:HE3	1.75	0.87
22:L:79:ASN:HB3	22:L:81:LYS:H	1.40	0.87
11:A:1324:G:C5'	12:B:113:ARG:CZ	2.52	0.87
11:A:1324:G:H4'	12:B:113:ARG:HH21	1.36	0.87
14:D:116:LEU:CD1	38:b:509:LYS:NZ	2.38	0.87
11:A:1152:A:C4	11:A:1627:U:N3	2.41	0.86
11:A:523:G:OP2	26:P:37:LYS:NZ	2.08	0.86
19:I:58:ASP:O	19:I:60:PHE:N	2.07	0.86
11:A:1324:G:C4'	12:B:113:ARG:HE	1.88	0.86
11:A:579:A:C6	13:C:143:ARG:HA	2.11	0.86
12:B:49:ASN:HB3	12:B:52:LYS:HG3	1.56	0.86
29:S:126:VAL:HG13	29:S:127:ARG:H	1.41	0.86
35:Y:57:ASP:HA	35:Y:106:LEU:HA	1.58	0.86
11:A:500:C:O5'	38:b:489:LYS:CA	2.24	0.86
32:V:25:THR:O	32:V:27:ASP:N	2.07	0.86
37:a:347:PRO:HB2	39:c:663:SER:HA	0.89	0.86
11:A:1293:U:H2'	12:B:109:ASN:OD1	1.76	0.86
11:A:1324:G:H4'	12:B:113:ARG:NE	1.91	0.85
37:a:292:VAL:CG1	39:c:667:PRO:HD3	2.04	0.85
37:a:482:ILE:HG23	39:c:733:TYR:CD1	2.10	0.85
15:E:140:ARG:NH1	36:Z:1:MET:SD	2.49	0.85
33:W:139:VAL:HG13	33:W:150:PRO:HG3	1.58	0.85
11:A:1152:A:C6	11:A:1627:U:C4	2.63	0.85
12:B:24:LEU:O	12:B:163:ASN:ND2	2.08	0.85
11:A:1293:U:H4'	12:B:110:TYR:CE2	2.11	0.85
12:B:41:ARG:HA	32:V:105:GLN:HG3	1.59	0.85
37:a:348:HIS:CE1	39:c:664:PHE:CA	2.36	0.85
1:O:46:ARG:HE	34:X:3:LYS:HG3	1.03	0.85
11:A:1299:G:C4'	15:E:208:GLU:OE2	2.25	0.85
17:G:73:THR:HG23	19:I:114:ARG:HD3	1.58	0.85
1:O:63:GLY:HA3	11:A:565:C:O2'	1.75	0.85
11:A:132:U:H1'	11:A:133:U:OP2	1.77	0.85
11:A:579:A:C2	13:C:143:ARG:O	2.30	0.85
11:A:1300:A:H5''	15:E:117:THR:HG21	1.56	0.84
16:F:98:LEU:HD11	16:F:102:ASN:HB2	1.57	0.84
1:O:82:ARG:HH21	22:L:68:ILE:HD11	1.02	0.84
11:A:1429:G:H1'	20:J:74:GLU:HG2	1.59	0.84
17:G:37:GLN:HG2	19:I:53:LEU:HD13	1.60	0.84
11:A:1151:A:H3'	11:A:1152:A:OP1	1.76	0.83
38:b:556:LYS:HD2	38:b:557:GLU:H	1.43	0.83
11:A:1529:C:OP1	17:G:112:ARG:NH1	2.10	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:1686:C:C2'	11:A:1687:U:H6	1.91	0.83
11:A:1324:G:C4'	12:B:113:ARG:NH2	2.41	0.83
1:0:88:GLN:HB2	34:X:5:HIS:C	2.03	0.83
1:0:88:GLN:OE1	34:X:5:HIS:N	2.10	0.83
11:A:1321:A:O4'	12:B:104:PRO:HB2	1.78	0.83
11:A:1324:G:H4'	12:B:113:ARG:NH2	1.94	0.83
8:7:27:PHE:HB3	8:7:40:LEU:HD23	1.58	0.83
11:A:320:U:H2'	11:A:321:C:H2'	1.58	0.83
14:D:93:LEU:HA	14:D:96:VAL:HG13	1.59	0.83
7:6:29:ARG:HH11	7:6:29:ARG:HG3	1.41	0.83
38:b:659:LYS:O	38:b:662:HIS:NE2	2.12	0.83
11:A:1291:G:N2	11:A:1324:G:H22	1.76	0.83
37:a:470:LEU:HD13	39:c:729:PHE:CD1	2.13	0.82
12:B:38:PHE:CD2	32:V:109:LEU:HD13	2.14	0.82
38:b:556:LYS:O	38:b:558:LYS:N	2.11	0.82
38:b:563:LYS:HE2	38:b:564:ARG:HH22	1.43	0.82
5:4:111:ARG:HG3	6:5:68:TYR:HB2	1.59	0.82
11:A:142:G:H22	11:A:173:A:H2	1.23	0.82
13:C:108:LYS:HG2	13:C:113:LEU:HD12	1.61	0.82
1:0:46:ARG:CD	34:X:3:LYS:CD	2.53	0.82
11:A:1542:G:N2	11:A:1569:A:OP2	2.12	0.82
11:A:829:A:O2'	11:A:830:U:OP2	1.97	0.82
11:A:1300:A:O3'	15:E:86:VAL:HG21	1.79	0.82
11:A:1294:G:P	12:B:110:TYR:CE1	2.72	0.82
16:F:69:VAL:HB	16:F:79:GLN:NE2	1.95	0.82
37:a:292:VAL:HG12	39:c:667:PRO:HD2	1.62	0.81
7:6:41:LEU:HD22	39:c:431:ARG:CZ	2.10	0.81
11:A:1151:A:C4	11:A:1152:A:C8	2.69	0.81
14:D:109:LEU:HB2	14:D:146:PHE:HB3	1.62	0.81
11:A:919:A:H5'	21:K:18:ARG:HH12	1.45	0.81
11:A:1229:G:O2'	11:A:1255:G:N2	2.14	0.81
1:0:83:ASP:OD2	34:X:9:ALA:HA	1.80	0.81
3:2:10:LYS:NZ	11:A:339:C:OP2	2.14	0.81
11:A:500:C:O2'	38:b:487:SER:CB	2.30	0.80
12:B:38:PHE:CG	32:V:109:LEU:HD13	2.16	0.80
11:A:1294:G:O3'	12:B:108:THR:OG1	1.99	0.80
11:A:1644:C:C1'	16:F:63:ALA:HB2	2.11	0.80
12:B:38:PHE:CE1	32:V:109:LEU:CB	2.64	0.80
21:K:50:ALA:O	21:K:52:ARG:N	2.14	0.80
1:0:106:GLN:HE21	1:0:108:GLU:HG3	1.43	0.80
4:3:131:PHE:O	4:3:133:THR:N	2.14	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:6:38:PRO:HG2	39:c:603:ARG:HH12	1.43	0.80
1:0:88:GLN:HG3	34:X:5:HIS:HB2	1.62	0.80
11:A:1151:A:C4	11:A:1152:A:H8	2.00	0.80
11:A:79:C:H1'	35:Y:174:LYS:HD3	1.62	0.80
20:J:27:THR:HG23	20:J:113:ASP:HB3	1.62	0.80
37:a:293:SER:OG	39:c:664:PHE:HE1	1.64	0.80
12:B:42:PRO:HD2	32:V:105:GLN:HE21	1.43	0.80
11:A:1295:G:P	12:B:108:THR:CB	2.70	0.80
1:0:85:GLN:NE2	34:X:6:GLY:O	2.14	0.80
11:A:1151:A:N1	11:A:1152:A:C4	2.50	0.80
22:L:7:ARG:O	27:Q:99:ARG:NH1	2.14	0.79
11:A:1293:U:O4'	12:B:111:ILE:CD1	2.31	0.79
12:B:179:ARG:HD3	12:B:183:ARG:HH11	1.46	0.79
1:0:82:ARG:CZ	22:L:68:ILE:HD13	2.10	0.79
21:K:107:ARG:HG3	21:K:107:ARG:HH11	1.46	0.79
28:R:284:ALA:HB2	32:V:63:LYS:HE2	1.64	0.79
11:A:1681:A:H2'	11:A:1682:U:H5'	1.65	0.79
23:M:69:ILE:HG22	23:M:73:MET:HE2	1.64	0.79
11:A:280:U:O2'	11:A:281:G:OP2	1.99	0.79
11:A:579:A:N6	13:C:143:ARG:CG	2.43	0.79
11:A:868:G:OP1	25:O:121:ARG:NH1	2.15	0.79
32:V:88:VAL:HG22	32:V:89:SER:H	1.47	0.79
12:B:41:ARG:CA	32:V:105:GLN:HG3	2.13	0.78
37:a:348:HIS:NE2	39:c:664:PHE:N	1.94	0.78
11:A:187:G:H4'	11:A:188:A:OP1	1.83	0.78
17:G:62:VAL:HG13	17:G:89:ILE:HG21	1.64	0.78
5:4:39:GLU:HG3	5:4:40:ASN:H	1.47	0.78
16:F:99:GLN:HG2	16:F:102:ASN:ND2	1.99	0.78
25:O:114:ARG:HH11	25:O:114:ARG:HG2	1.48	0.78
11:A:1686:C:C2'	11:A:1687:U:O5'	2.30	0.78
11:A:1686:C:C2	11:A:1687:U:C6	2.72	0.78
11:A:734:A:H5''	11:A:735:C:OP1	1.83	0.78
11:A:579:A:H61	13:C:143:ARG:CB	1.96	0.78
11:A:1291:G:H8	11:A:1291:G:O5'	1.67	0.78
1:0:46:ARG:CZ	34:X:3:LYS:HG3	2.09	0.78
37:a:347:PRO:CG	39:c:662:LEU:O	2.32	0.78
15:E:56:ILE:HG23	15:E:61:LEU:HB2	1.63	0.78
11:A:1716:C:O2'	11:A:1717:G:H8	1.67	0.77
31:U:76:GLU:OE2	31:U:90:LYS:NZ	2.17	0.77
1:0:106:GLN:HE21	1:0:108:GLU:CG	1.96	0.77
11:A:136:C:H4'	11:A:137:U:OP1	1.83	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:276:C:O2'	11:A:277:U:H5''	1.84	0.77
11:A:579:A:C6	13:C:143:ARG:HG3	2.19	0.77
11:A:1369:U:OP1	30:T:119:LYS:NZ	2.16	0.77
11:A:40:A:OP1	14:D:3:ARG:NH2	2.18	0.77
11:A:1299:G:H4'	15:E:208:GLU:OE2	1.84	0.77
11:A:1324:G:C4'	12:B:113:ARG:NE	2.47	0.77
22:L:73:ARG:HE	22:L:84:THR:HG22	1.49	0.77
11:A:1057:U:O2'	11:A:1058:U:OP2	2.02	0.77
10:9:146:SER:HB3	11:A:1234:A:O2'	1.85	0.77
11:A:1061:A:H1'	39:c:594:ASN:N	2.00	0.77
11:A:1293:U:C1'	12:B:111:ILE:CD1	2.62	0.77
11:A:500:C:C5'	38:b:487:SER:O	2.30	0.77
11:A:1229:G:HO2'	11:A:1255:G:N2	1.83	0.77
11:A:1073:G:H2'	11:A:1074:G:H5''	1.66	0.77
5:4:62:LYS:O	5:4:64:ARG:N	2.17	0.77
11:A:1151:A:C3'	11:A:1152:A:H5'	2.04	0.77
2:1:12:VAL:HG22	2:1:28:VAL:HG11	1.66	0.77
11:A:1686:C:H2'	11:A:1687:U:O5'	1.83	0.77
37:a:484:HIS:CG	39:c:736:PHE:HA	2.20	0.77
23:M:84:TRP:HA	23:M:89:GLN:HE22	1.50	0.76
37:a:292:VAL:CG1	39:c:667:PRO:CG	2.59	0.76
1:0:88:GLN:CG	34:X:5:HIS:C	2.58	0.76
11:A:1151:A:N1	11:A:1152:A:C5	2.53	0.76
12:B:41:ARG:CG	32:V:103:ASP:CB	2.61	0.76
3:2:36:THR:HB	3:2:57:ALA:O	1.85	0.76
11:A:1626:U:C3'	11:A:1627:U:P	2.72	0.76
11:A:1293:U:O4'	12:B:111:ILE:HG12	1.83	0.76
11:A:1587:A:H1'	17:G:104:ASN:HD22	1.50	0.76
18:H:27:ILE:HD11	18:H:61:ILE:HD12	1.65	0.76
19:I:40:GLU:HA	19:I:42:GLU:N	2.01	0.76
35:Y:153:VAL:O	35:Y:155:ASP:N	2.16	0.76
23:M:83:ALA:HA	23:M:86:LEU:HD22	1.66	0.76
36:Z:74:GLN:NE2	36:Z:81:ASN:O	2.18	0.76
11:A:484:C:H42	11:A:503:G:H22	1.33	0.76
5:4:181:LEU:O	5:4:184:LEU:N	2.18	0.76
11:A:514:G:H1	11:A:543:C:H5	1.33	0.76
11:A:1715:G:C6	11:A:1716:C:N4	2.54	0.76
14:D:175:ARG:HH11	14:D:175:ARG:HG3	1.51	0.76
4:3:35:LYS:O	4:3:37:GLU:N	2.18	0.76
28:R:89:LEU:HB2	28:R:103:PHE:HB2	1.68	0.76
38:b:563:LYS:HE2	38:b:564:ARG:NH2	2.00	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:5:35:ALA:HB3	6:5:37:LYS:HE3	1.67	0.75
11:A:494:U:O2'	11:A:495:C:O5'	2.01	0.75
18:H:30:SER:HA	18:H:34:ILE:HD12	1.67	0.75
1:0:85:GLN:OE1	34:X:4:VAL:O	1.83	0.75
11:A:488:G:OP1	11:A:488:G:H4'	1.86	0.75
11:A:1559:A:H5''	23:M:135:GLY:HA3	1.67	0.75
5:4:83:LYS:NZ	21:K:116:GLU:OE2	2.18	0.75
11:A:706:A:N1	11:A:734:A:N6	2.34	0.75
12:B:42:PRO:CD	32:V:105:GLN:HE21	1.94	0.75
16:F:77:ILE:HG13	16:F:79:GLN:NE2	2.02	0.75
16:F:27:HIS:HB2	16:F:43:GLN:NE2	2.02	0.75
11:A:1550:A:P	29:S:42:ARG:HH22	2.08	0.75
12:B:42:PRO:HD2	32:V:105:GLN:HE22	1.19	0.75
11:A:1520:U:OP2	30:T:75:LYS:NZ	2.20	0.75
11:A:127:G:N7	35:Y:202:ARG:NH2	2.35	0.74
38:b:556:LYS:CD	38:b:557:GLU:H	1.99	0.74
11:A:1428:G:H5'	11:A:1428:G:H8	1.53	0.74
16:F:27:HIS:O	16:F:43:GLN:HG2	1.87	0.74
19:I:5:PRO:HG2	19:I:24:ALA:HB2	1.69	0.74
31:U:89:ILE:HG23	31:U:90:LYS:H	1.52	0.74
13:C:64:ARG:O	13:C:67:ASN:N	2.20	0.74
5:4:109:LYS:HG3	5:4:113:MET:HE3	1.69	0.74
14:D:116:LEU:CD1	38:b:509:LYS:HZ1	2.00	0.74
23:M:26:ILE:HD11	23:M:31:ALA:N	2.02	0.74
19:I:12:LYS:HD3	19:I:17:THR:HB	1.70	0.74
37:a:292:VAL:HG12	39:c:667:PRO:HD3	1.64	0.74
11:A:818:C:N4	11:A:819:G:O6	2.21	0.74
12:B:200:ASP:HB2	32:V:85:VAL:HG21	1.69	0.74
17:G:144:GLU:OE2	17:G:225:ARG:NH2	2.21	0.74
23:M:123:ARG:HG3	23:M:133:VAL:HG21	1.69	0.74
4:3:50:ASP:OD1	4:3:50:ASP:N	2.21	0.73
11:A:1324:G:C5'	12:B:113:ARG:HE	1.93	0.73
11:A:1521:G:O6	30:T:68:ARG:NH1	2.21	0.73
30:T:57:ARG:HG3	30:T:57:ARG:NH1	2.03	0.73
1:0:106:GLN:NE2	1:0:108:GLU:HG3	2.02	0.73
11:A:582:U:C6	11:A:582:U:H5''	2.24	0.73
11:A:765:G:C2	14:D:149:ARG:HD2	2.23	0.73
11:A:1151:A:H2	11:A:1152:A:C1'	1.94	0.73
14:D:116:LEU:CD1	38:b:509:LYS:HZ2	2.00	0.73
10:9:108:VAL:HG13	31:U:73:LYS:HZ2	1.53	0.73
39:c:487:SER:HB2	39:c:506:ASN:ND2	2.04	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:88:GLN:HG3	34:X:5:HIS:CB	2.18	0.73
1:0:109:LEU:HG	1:0:110:PRO:HD2	1.70	0.73
11:A:1293:U:O4'	12:B:111:ILE:CG1	2.37	0.73
11:A:108:A:H2'	11:A:109:G:C8	2.23	0.73
11:A:649:U:O2'	11:A:650:U:O5'	2.07	0.73
11:A:1293:U:N1	12:B:111:ILE:HG12	2.02	0.73
17:G:40:ILE:HG23	17:G:42:LEU:HD22	1.71	0.73
13:C:7:LYS:NZ	20:J:115:GLU:OE2	2.21	0.72
17:G:57:SER:O	17:G:59:VAL:N	2.20	0.72
21:K:102:LEU:HD22	21:K:105:LEU:HD11	1.71	0.72
38:b:660:VAL:HA	38:b:662:HIS:CE1	2.23	0.72
5:4:202:LYS:NZ	5:4:202:LYS:O	2.23	0.72
11:A:1686:C:O2'	11:A:1687:U:C5'	2.37	0.72
12:B:4:PRO:HB2	12:B:7:PHE:HB2	1.70	0.72
16:F:80:LEU:HB3	16:F:84:GLN:NE2	2.04	0.72
19:I:18:ALA:HB2	19:I:69:VAL:HG13	1.71	0.72
28:R:170:ILE:HG21	28:R:211:ILE:HD11	1.70	0.72
1:0:46:ARG:HE	34:X:3:LYS:CG	1.82	0.72
11:A:74:U:O2'	11:A:75:U:OP2	2.06	0.72
11:A:337:G:H3'	27:Q:133:LYS:HB2	1.69	0.72
13:C:65:ARG:HA	13:C:68:GLU:HG3	1.70	0.72
16:F:39:LEU:HD11	16:F:79:GLN:HB3	1.71	0.72
37:a:482:ILE:CG2	39:c:733:TYR:CD1	2.71	0.72
5:4:157:GLN:O	5:4:159:SER:N	2.20	0.72
11:A:1542:G:N2	11:A:1568:C:H1'	2.04	0.72
32:V:82:ASP:O	32:V:83:GLN:NE2	2.20	0.72
12:B:52:LYS:HD2	36:Z:82:VAL:HA	1.72	0.72
10:9:102:VAL:O	10:9:104:SER:N	2.23	0.72
11:A:1160:A:H2'	11:A:1161:C:C6	2.25	0.72
11:A:1683:C:O2'	11:A:1684:U:O5'	2.07	0.72
14:D:110:GLN:NE2	14:D:126:ARG:HG2	2.04	0.72
6:5:10:ARG:HD2	11:A:1795:U:O2	1.89	0.71
11:A:1290:U:H2'	11:A:1291:G:C8	2.25	0.71
15:E:69:ILE:HD11	15:E:133:LYS:HB3	1.72	0.71
30:T:86:ARG:HH11	30:T:86:ARG:HG3	1.55	0.71
37:a:484:HIS:HB2	39:c:736:PHE:CA	2.20	0.71
37:a:484:HIS:HB2	39:c:736:PHE:N	2.04	0.71
1:0:88:GLN:HE22	34:X:4:VAL:N	1.88	0.71
5:4:173:THR:O	5:4:177:GLN:NE2	2.23	0.71
11:A:12:U:HO2'	11:A:1299:G:H21	1.39	0.71
19:I:113:ASP:CG	19:I:114:ARG:H	1.98	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:V:20:TYR:CE2	32:V:38:ILE:HD11	2.26	0.71
37:a:484:HIS:CB	39:c:736:PHE:HA	2.18	0.71
1:0:63:GLY:CA	11:A:565:C:O2'	2.38	0.71
11:A:1293:U:H1'	12:B:111:ILE:CD1	2.16	0.71
30:T:49:ASP:HB3	30:T:53:TRP:HB3	1.73	0.71
35:Y:24:ILE:O	35:Y:26:VAL:N	2.23	0.71
11:A:584:C:H1'	34:X:18:THR:HG21	1.71	0.71
11:A:717:C:H42	11:A:720:G:H22	1.37	0.71
16:F:28:ILE:HD11	16:F:92:MET:HE1	1.72	0.71
20:J:106:ILE:HG13	20:J:107:THR:H	1.53	0.71
17:G:113:ILE:O	17:G:117:THR:OG1	2.07	0.71
27:Q:78:THR:HG22	27:Q:84:ILE:HG22	1.72	0.71
33:W:79:ASP:HB3	33:W:82:TYR:HB2	1.73	0.71
37:a:482:ILE:CD1	39:c:733:TYR:CE1	2.74	0.71
11:A:614:C:OP2	22:L:5:LYS:NZ	2.24	0.71
11:A:1293:U:O4'	12:B:111:ILE:HD13	1.90	0.71
11:A:1600:A:H4'	11:A:1601:G:OP1	1.90	0.71
11:A:1151:A:C3'	11:A:1152:A:H5''	2.11	0.71
11:A:1324:G:H4'	12:B:113:ARG:CZ	2.20	0.71
12:B:84:ARG:NH2	32:V:82:ASP:OD1	2.23	0.70
13:C:179:GLN:NE2	13:C:179:GLN:O	2.24	0.70
25:O:84:ILE:HG22	25:O:135:LEU:HD21	1.73	0.70
1:0:38:ILE:HG21	1:0:72:GLY:O	1.90	0.70
7:6:38:PRO:CG	39:c:603:ARG:HH12	2.04	0.70
13:C:29:LEU:HD21	13:C:69:LEU:HD11	1.73	0.70
1:0:23:LYS:HZ3	1:0:25:GLU:HG2	1.56	0.70
21:K:29:HIS:HB3	21:K:41:ARG:HG3	1.72	0.70
11:A:159:U:O2'	35:Y:87:ARG:NH1	2.24	0.70
11:A:591:A:H2'	11:A:592:A:C8	2.27	0.70
11:A:1626:U:HO3'	11:A:1627:U:P	2.11	0.70
12:B:185:ARG:HB2	36:Z:45:ALA:HB3	1.72	0.70
14:D:117:GLY:O	14:D:119:ALA:N	2.24	0.70
15:E:203:LYS:O	15:E:206:THR:HG23	1.91	0.70
16:F:80:LEU:HD13	16:F:84:GLN:OE1	1.92	0.70
27:Q:4:GLU:HG3	27:Q:5:LEU:HG	1.74	0.70
4:3:133:THR:HG22	4:3:159:VAL:HG12	1.73	0.70
11:A:1300:A:C4'	15:E:86:VAL:HG21	2.21	0.70
30:T:126:GLU:HA	30:T:129:GLN:HG3	1.74	0.70
1:0:46:ARG:CG	34:X:3:LYS:HE3	2.21	0.70
6:5:15:ARG:NH1	11:A:936:G:N7	2.39	0.70
6:5:32:LYS:NZ	11:A:930:A:OP1	2.23	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:L:91:GLY:O	22:L:93:LEU:N	2.25	0.70
1:0:38:ILE:HG23	1:0:74:GLY:N	2.07	0.70
11:A:1294:G:O3'	12:B:108:THR:HB	1.85	0.70
13:C:53:THR:O	13:C:53:THR:OG1	2.08	0.70
21:K:29:HIS:ND1	21:K:29:HIS:O	2.24	0.70
11:A:12:U:HO2'	11:A:1299:G:N2	1.90	0.70
12:B:167:LYS:HB3	12:B:168:HIS:CD2	2.27	0.70
14:D:60:LEU:CD2	14:D:93:LEU:HD21	2.22	0.70
5:4:154:SER:O	5:4:154:SER:OG	2.09	0.70
39:c:443:LYS:NZ	39:c:451:MET:SD	2.64	0.70
11:A:992:A:H2	11:A:1012:U:H3	1.38	0.69
30:T:28:LEU:HD13	30:T:29:GLU:H	1.56	0.69
1:0:46:ARG:HD3	34:X:3:LYS:HE3	0.70	0.69
11:A:1711:C:H2'	11:A:1712:A:H5''	1.74	0.69
1:0:78:LEU:C	1:0:92:VAL:HG12	2.17	0.69
11:A:579:A:H61	13:C:143:ARG:CG	2.03	0.69
12:B:157:ASP:OD1	36:Z:60:ARG:NH1	2.25	0.69
19:I:97:VAL:HG12	19:I:98:ASP:H	1.57	0.69
1:0:88:GLN:CB	34:X:5:HIS:O	2.37	0.69
5:4:176:VAL:O	5:4:178:GLY:N	2.25	0.69
32:V:50:ILE:O	32:V:54:THR:HG23	1.92	0.69
11:A:701:U:H3	11:A:737:A:N6	1.87	0.69
11:A:1564:U:H2'	11:A:1565:C:C6	2.27	0.69
36:Z:41:GLU:CD	36:Z:41:GLU:H	2.00	0.69
11:A:1533:C:H4'	11:A:1539:G:N1	2.06	0.69
28:R:76:ASP:OD1	28:R:76:ASP:N	2.18	0.69
35:Y:164:LYS:HB3	35:Y:167:LYS:HB3	1.75	0.69
11:A:867:G:OP2	25:O:3:ARG:NH1	2.24	0.69
11:A:1321:A:O4'	12:B:104:PRO:CB	2.40	0.69
31:U:54:ARG:O	31:U:56:GLU:N	2.23	0.69
3:2:114:GLU:HG2	3:2:120:THR:HA	1.75	0.69
8:7:68:LEU:HD11	8:7:76:LEU:HD21	1.73	0.69
11:A:653:C:H2'	11:A:654:C:O4'	1.92	0.69
11:A:1321:A:O5'	12:B:104:PRO:CG	2.40	0.69
11:A:959:U:C6	25:O:61:THR:HB	2.28	0.68
11:A:1294:G:OP1	12:B:110:TYR:CE1	2.39	0.68
11:A:1300:A:H4'	15:E:86:VAL:HG11	1.74	0.68
15:E:116:LYS:HG2	15:E:127:ALA:HB3	1.75	0.68
25:O:55:ARG:NH1	25:O:56:ASP:OD2	2.26	0.68
1:0:88:GLN:CB	34:X:5:HIS:C	2.66	0.68
11:A:226:A:H2'	11:A:227:U:H5'	1.73	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:D:116:LEU:HD12	38:b:509:LYS:NZ	2.08	0.68
14:D:163:PRO:O	14:D:165:GLY:N	2.26	0.68
18:H:15:ASN:HD21	18:H:71:LYS:HA	1.58	0.68
2:1:52:ASP:OD1	2:1:52:ASP:N	2.26	0.68
11:A:1296:A:P	12:B:138:TYR:CE2	2.85	0.68
12:B:193:GLN:O	12:B:195:TRP:N	2.26	0.68
5:4:28:GLU:OE2	5:4:94:LYS:NZ	2.19	0.68
11:A:1339:C:O2'	11:A:1340:U:OP1	2.12	0.68
16:F:39:LEU:HD12	16:F:80:LEU:O	1.93	0.68
22:L:130:VAL:O	22:L:131:SER:HB3	1.93	0.68
11:A:38:C:H2'	11:A:39:A:H5'	1.76	0.68
11:A:499:U:C2'	38:b:489:LYS:HE2	2.23	0.68
33:W:85:GLY:N	33:W:88:ASP:OD2	2.27	0.68
1:0:85:GLN:NE2	34:X:6:GLY:CA	2.56	0.68
39:c:257:ARG:HH21	39:c:282:LEU:HD21	1.59	0.68
3:2:50:GLY:HA2	11:A:397:A:O3'	1.94	0.68
11:A:839:U:H2'	11:A:840:U:H5'	1.75	0.68
11:A:1267:G:H21	11:A:1448:G:H5''	1.59	0.68
11:A:1550:A:OP2	29:S:42:ARG:NH2	2.26	0.68
28:R:300:THR:HG23	28:R:314:GLN:HG3	1.76	0.68
7:6:29:ARG:HG3	7:6:29:ARG:NH1	2.09	0.68
7:6:41:LEU:CD1	39:c:431:ARG:NE	2.47	0.68
11:A:702:G:O6	11:A:736:C:N4	2.19	0.68
11:A:778:G:H22	26:P:10:ARG:NH2	1.90	0.68
11:A:1295:G:C5'	12:B:108:THR:CB	2.72	0.68
14:D:53:ARG:NH1	14:D:97:LEU:O	2.27	0.68
3:2:25:ARG:NH2	11:A:386:G:OP2	2.27	0.67
11:A:1298:U:C2	15:E:209:ASN:OD1	2.44	0.67
31:U:61:VAL:HG13	31:U:121:VAL:HG23	1.74	0.67
1:0:85:GLN:HB2	34:X:5:HIS:O	1.92	0.67
2:1:32:PHE:HE1	2:1:38:ARG:HB3	1.58	0.67
11:A:418:G:O2'	35:Y:59:GLN:NE2	2.27	0.67
11:A:1295:G:H5''	12:B:108:THR:CG2	2.24	0.67
11:A:1324:G:C3'	12:B:113:ARG:NH2	2.53	0.67
1:0:30:GLU:O	1:0:33:GLN:HG2	1.94	0.67
11:A:959:U:H6	25:O:61:THR:HB	1.59	0.67
11:A:1300:A:H5''	15:E:117:THR:CG2	2.24	0.67
12:B:71:GLU:O	12:B:96:THR:HG22	1.95	0.67
18:H:27:ILE:HG12	18:H:61:ILE:HB	1.76	0.67
19:I:50:GLU:OE1	19:I:82:ARG:NH2	2.27	0.67
35:Y:67:VAL:HG21	35:Y:99:GLY:HA2	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:582:U:H5''	11:A:582:U:H6	1.57	0.67
11:A:1449:U:H2'	11:A:1450:U:C6	2.28	0.67
11:A:533:U:H4'	26:P:33:ALA:HB2	1.77	0.67
14:D:169:PRO:HD2	14:D:174:ARG:HD2	1.76	0.67
33:W:31:PRO:HG2	33:W:38:LEU:HD13	1.76	0.67
5:4:76:SER:OG	5:4:78:ASP:OD1	2.12	0.67
11:A:1061:A:H1'	39:c:594:ASN:HA	1.75	0.67
4:3:50:ASP:HA	4:3:56:LYS:HA	1.76	0.67
4:3:50:ASP:HB3	4:3:56:LYS:HG2	1.76	0.67
9:8:41:ILE:HG23	9:8:42:LEU:H	1.59	0.67
11:A:169:A:H5''	35:Y:176:GLN:HG2	1.77	0.67
11:A:1294:G:P	12:B:110:TYR:HE1	2.16	0.67
22:L:96:VAL:HG23	22:L:97:ASP:H	1.60	0.67
1:0:85:GLN:HE21	34:X:6:GLY:C	2.00	0.67
11:A:765:G:N3	14:D:149:ARG:NH1	2.42	0.67
4:3:38:LEU:HD23	4:3:41:LEU:HD12	1.76	0.66
11:A:131:C:O2'	11:A:132:U:OP1	2.11	0.66
11:A:140:A:N6	11:A:281:G:OP1	2.21	0.66
11:A:1199:G:O6	20:J:67:THR:HG23	1.95	0.66
12:B:41:ARG:CA	32:V:105:GLN:CG	2.71	0.66
1:0:63:GLY:HA3	11:A:565:C:H3'	1.76	0.66
7:6:41:LEU:HB3	39:c:431:ARG:HH21	1.61	0.66
11:A:1789:G:H8	11:A:1789:G:H5''	1.60	0.66
12:B:185:ARG:HA	36:Z:44:ARG:HA	1.77	0.66
14:D:109:LEU:HD13	14:D:129:ILE:HD13	1.75	0.66
1:0:88:GLN:HE22	34:X:5:HIS:H	1.38	0.66
11:A:579:A:N1	13:C:143:ARG:C	2.50	0.66
30:T:117:SER:HB2	30:T:123:ARG:HB2	1.77	0.66
10:9:126:CYS:O	10:9:128:ALA:N	2.28	0.66
21:K:81:VAL:H	21:K:115:ILE:HG22	1.61	0.66
11:A:1254:U:OP2	31:U:46:ARG:NH1	2.28	0.66
12:B:10:THR:OG1	12:B:13:ASP:OD2	2.13	0.66
33:W:13:ALA:O	33:W:39:ARG:NH2	2.28	0.66
11:A:1151:A:C2	11:A:1152:A:H1'	2.25	0.66
11:A:1459:C:OP1	23:M:126:ARG:NH2	2.28	0.66
18:H:47:ILE:HG22	18:H:65:LEU:HB3	1.76	0.66
39:c:501:ARG:HG3	39:c:505:TYR:HE2	1.61	0.66
1:0:46:ARG:HD2	34:X:3:LYS:HE3	1.67	0.66
5:4:70:LEU:O	5:4:74:GLN:N	2.28	0.66
11:A:711:U:H1'	11:A:712:G:H5'	1.78	0.66
11:A:1034:C:HO2'	18:H:2:THR:N	1.94	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:F:77:ILE:HG13	16:F:79:GLN:HE22	1.60	0.66
11:A:1756[B]:A:O2'	11:A:1757:G:H5'	1.95	0.66
13:C:120:TYR:OH	15:E:120:GLU:OE2	2.12	0.66
12:B:41:ARG:HA	32:V:105:GLN:CD	2.20	0.66
16:F:62:PHE:HE2	16:F:84:GLN:HB3	1.60	0.66
39:c:659:TYR:CG	39:c:676:LEU:HD21	2.31	0.66
11:A:1688:U:H2'	11:A:1689:A:C8	2.31	0.65
24:N:33:LYS:O	24:N:36:LEU:HD23	1.95	0.65
5:4:206:PRO:O	5:4:207:LEU:HB2	1.95	0.65
11:A:687:G:H5'	18:H:119:LYS:HG2	1.76	0.65
11:A:843:U:H2'	11:A:844:A:C8	2.30	0.65
16:F:96:LEU:O	16:F:96:LEU:HD23	1.96	0.65
18:H:70:ASN:ND2	18:H:130:TYR:O	2.29	0.65
2:1:10:ALA:HA	2:1:32:PHE:HA	1.78	0.65
2:1:36:THR:OG1	2:1:37:SER:N	2.28	0.65
11:A:1041:G:H2'	11:A:1042:G:C8	2.30	0.65
11:A:1536:G:C5	11:A:1538:U:H1'	2.32	0.65
11:A:1686:C:C2'	11:A:1687:U:O4'	2.45	0.65
16:F:50:ASP:OD2	16:F:53:ARG:HG2	1.96	0.65
11:A:1151:A:C6	11:A:1152:A:C5	2.84	0.65
11:A:1686:C:H2'	11:A:1687:U:O4'	1.96	0.65
11:A:765:G:N1	14:D:149:ARG:HB3	2.11	0.65
16:F:31:GLN:CD	16:F:39:LEU:HD23	2.21	0.65
32:V:47:ARG:NH1	32:V:48:ASN:OD1	2.29	0.65
33:W:212:ASP:OD2	33:W:216:ASN:HB2	1.97	0.65
39:c:582:GLN:HE22	39:c:612:ILE:H	1.42	0.65
11:A:819:G:O2'	11:A:820:U:H5'	1.96	0.65
11:A:1606:C:H2'	11:A:1607:G:C8	2.31	0.65
12:B:70:PRO:HB2	12:B:94:GLY:HA3	1.77	0.65
14:D:96:VAL:HA	14:D:99:LEU:HD22	1.78	0.65
16:F:62:PHE:CZ	16:F:87:LYS:HG3	2.31	0.65
11:A:740:A:H2'	11:A:741:C:H5''	1.77	0.65
11:A:1339:C:O2'	11:A:1341:A:N7	2.30	0.65
11:A:1592:A:H2'	11:A:1593:A:H8	1.61	0.65
16:F:58:LEU:HD22	16:F:80:LEU:HD22	1.79	0.65
27:Q:6:THR:O	27:Q:8:GLN:N	2.30	0.65
28:R:195:HIS:CD2	28:R:199:ILE:HD13	2.32	0.65
37:a:463:TRP:CG	39:c:744:LEU:HD22	2.30	0.65
39:c:380:PHE:O	39:c:383:SER:OG	2.15	0.65
8:7:56:LYS:HG3	8:7:67:THR:HB	1.78	0.65
9:8:59:TYR:HE1	9:8:61:SER:HB3	1.61	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:D:99:LEU:O	14:D:100:LYS:HB3	1.97	0.65
11:A:656:G:O2'	11:A:657:U:O4'	2.15	0.65
12:B:41:ARG:HA	32:V:105:GLN:NE2	2.12	0.65
38:b:383:LEU:HB3	38:b:402:PRO:HD2	1.79	0.65
11:A:1151:A:N1	11:A:1152:A:N7	2.20	0.65
1:O:82:ARG:CB	34:X:7:SER:OG	2.26	0.64
11:A:895:G:H1	11:A:917:U:H3	1.45	0.64
11:A:901:G:N2	21:K:54:GLU:OE1	2.29	0.64
19:I:95:LYS:O	28:R:59:ARG:NH2	2.30	0.64
25:O:27:LYS:H	25:O:27:LYS:HE2	1.61	0.64
34:X:14:VAL:O	34:X:18:THR:HG23	1.97	0.64
39:c:681:SER:OG	39:c:686:ASN:O	2.15	0.64
17:G:94:THR:HB	17:G:114:ILE:HG13	1.77	0.64
30:T:30:VAL:O	30:T:32:GLY:N	2.29	0.64
1:O:83:ASP:CG	34:X:9:ALA:HA	2.23	0.64
11:A:1479:A:OP1	30:T:57:ARG:NH1	2.31	0.64
28:R:90:ARG:NH1	28:R:99:THR:OG1	2.31	0.64
8:7:8:ARG:HD2	8:7:12:HIS:HE1	1.63	0.64
23:M:11:PHE:CE1	23:M:59:GLY:HA2	2.32	0.64
6:5:37:LYS:O	6:5:38:ARG:HD2	1.98	0.64
11:A:499:U:O2'	38:b:489:LYS:HG2	1.98	0.64
11:A:867:G:H5'	25:O:4:MET:HE3	1.79	0.64
11:A:901:G:H22	21:K:54:GLU:CD	2.04	0.64
5:4:105:PHE:N	5:4:214:LYS:HZ1	1.96	0.64
5:4:110:LEU:H	5:4:110:LEU:HD12	1.63	0.64
7:6:41:LEU:HB3	39:c:431:ARG:NH2	2.13	0.64
7:6:62:ILE:HG13	7:6:63:LEU:H	1.62	0.64
11:A:1324:G:C4'	12:B:113:ARG:CZ	2.75	0.64
11:A:1585:U:N3	11:A:1611:A:H2	1.82	0.64
11:A:1762:A:H1'	11:A:1783:C:H5'	1.80	0.64
12:B:168:HIS:HB3	12:B:203:PHE:CZ	2.32	0.64
29:S:57:MET:HE1	29:S:89:MET:HE3	1.78	0.64
11:A:66:U:H5	35:Y:173:PRO:HG3	1.63	0.64
11:A:497:G:H4'	11:A:498:G:OP1	1.97	0.64
11:A:647:G:N2	11:A:687:G:H22	1.95	0.64
11:A:1429:G:C1'	20:J:74:GLU:HG2	2.27	0.64
25:O:54:LEU:HB3	25:O:60:VAL:HG21	1.79	0.64
39:c:637:TYR:OH	39:c:653:ARG:NH2	2.31	0.64
8:7:8:ARG:HD2	8:7:12:HIS:CE1	2.33	0.64
11:A:1300:A:C3'	15:E:86:VAL:HG21	2.27	0.64
1:O:58:MET:HG3	34:X:3:LYS:CE	2.18	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:499:U:O2'	11:A:500:C:O4'	2.16	0.63
11:A:1597:A:OP2	24:N:32:ARG:NH2	2.31	0.63
17:G:152:GLY:O	17:G:154:ALA:N	2.31	0.63
37:a:347:PRO:CG	39:c:663:SER:HA	2.26	0.63
39:c:582:GLN:HB3	39:c:611:HIS:CE1	2.33	0.63
1:0:61:ILE:HG12	1:0:91:VAL:HG11	1.80	0.63
11:A:145:A:O2'	11:A:146:U:O5'	2.16	0.63
12:B:110:TYR:HD1	12:B:110:TYR:H	1.46	0.63
39:c:595:ASN:HA	39:c:598:ALA:HB3	1.79	0.63
1:0:62:ARG:CD	1:0:92:VAL:HA	2.27	0.63
8:7:14:TYR:HE1	8:7:21:VAL:HG22	1.64	0.63
11:A:138:A:O2'	35:Y:149:LYS:NZ	2.31	0.63
30:T:86:ARG:NH1	30:T:90:PRO:O	2.32	0.63
37:a:348:HIS:NE2	39:c:664:PHE:CB	2.60	0.63
4:3:114:ARG:NH2	11:A:637:C:O2	2.30	0.63
5:4:134:VAL:HB	5:4:219:LYS:HB2	1.80	0.63
6:5:84:VAL:O	6:5:86:VAL:N	2.30	0.63
11:A:753:A:H5'	33:W:221:ARG:HG3	1.80	0.63
11:A:1498:G:C2'	11:A:1499:G:H5'	2.28	0.63
11:A:1689:A:H2'	11:A:1690:G:H8	1.64	0.63
12:B:183:ARG:NH2	12:B:191:ARG:O	2.32	0.63
6:5:59:TYR:HE2	21:K:113:GLY:HA2	1.64	0.63
11:A:1151:A:H3'	11:A:1152:A:O5'	1.96	0.63
11:A:1623:C:H2'	11:A:1624:C:C6	2.34	0.63
16:F:62:PHE:CE2	16:F:84:GLN:HB3	2.33	0.63
28:R:216:LYS:HA	28:R:239:GLU:HG3	1.80	0.63
33:W:185:GLY:N	33:W:189:LEU:HD13	2.14	0.63
8:7:56:LYS:NZ	13:C:28:GLU:OE1	2.29	0.63
11:A:1015:U:H5''	11:A:1016:C:OP2	1.98	0.63
13:C:114:ALA:HB3	13:C:117:ARG:HB2	1.80	0.63
33:W:259:GLN:O	33:W:261:LEU:N	2.31	0.63
1:0:33:GLN:HE21	1:0:78:LEU:HD11	1.64	0.63
1:0:97:LEU:HG	1:0:115:ILE:HG21	1.80	0.63
5:4:171:ILE:HA	5:4:174:LYS:HE3	1.81	0.63
11:A:158:U:O2'	11:A:159:U:H3'	1.98	0.63
11:A:470:A:C8	11:A:470:A:H5''	2.33	0.63
11:A:1592:A:H2'	11:A:1593:A:C8	2.34	0.63
19:I:115:THR:O	19:I:117:LEU:N	2.32	0.63
37:a:484:HIS:HB2	39:c:736:PHE:HA	1.81	0.63
11:A:38:C:C2'	11:A:39:A:H5'	2.29	0.63
11:A:702:G:HO2'	11:A:703:G:H8	1.47	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:E:129:ILE:O	15:E:133:LYS:HG2	1.99	0.63
15:E:144:TRP:CE2	15:E:173:PRO:HG3	2.34	0.63
16:F:62:PHE:CD2	16:F:84:GLN:OE1	2.52	0.63
17:G:37:GLN:HB3	19:I:53:LEU:HB3	1.80	0.63
19:I:47:LYS:HZ1	19:I:114:ARG:HD2	1.64	0.63
20:J:118:VAL:HG22	20:J:119:ALA:H	1.63	0.63
22:L:109:ARG:HB3	22:L:112:LYS:HB2	1.81	0.63
28:R:136:ILE:HD13	28:R:136:ILE:H	1.63	0.63
39:c:413:LEU:HD12	39:c:459:ILE:HD13	1.81	0.63
1:0:62:ARG:HG3	1:0:91:VAL:O	1.98	0.62
7:6:38:PRO:CG	39:c:603:ARG:NH1	2.59	0.62
28:R:150:TRP:HE1	32:V:37:GLU:HG3	1.64	0.62
11:A:1202:A:N6	11:A:1457:C:H5''	2.13	0.62
14:D:157:ASP:OD1	38:b:459:ASN:ND2	2.32	0.62
23:M:94:ASP:OD2	23:M:98:TYR:OH	2.17	0.62
26:P:91:LEU:HA	26:P:96:LEU:HD12	1.80	0.62
3:2:138:ASN:ND2	11:A:197:A:H61	1.98	0.62
11:A:66:U:C5	35:Y:173:PRO:HG3	2.35	0.62
19:I:34:SER:HB3	19:I:38:LEU:HD12	1.80	0.62
22:L:92:CYS:HG	22:L:136:TRP:CD1	2.17	0.62
38:b:563:LYS:CE	38:b:564:ARG:HH22	2.09	0.62
11:A:497:G:O2'	11:A:498:G:O5'	2.17	0.62
11:A:1151:A:H2	11:A:1152:A:H1'	1.59	0.62
11:A:1428:G:H5'	11:A:1428:G:C8	2.35	0.62
13:C:191:ASP:HB3	13:C:194:LYS:HG3	1.82	0.62
15:E:145:GLY:O	15:E:146:THR:HB	1.98	0.62
16:F:29:ARG:HB2	16:F:41:THR:HB	1.80	0.62
2:1:42:ARG:HH11	2:1:56:LEU:HD22	1.63	0.62
11:A:1320:U:H3'	12:B:101:ARG:HH22	1.62	0.62
11:A:1523:G:N7	30:T:64:HIS:HE1	1.98	0.62
11:A:1612:U:H2'	11:A:1613:U:H5'	1.79	0.62
11:A:1701:N:H3'	11:A:1702:N:H5''	1.80	0.62
16:F:49:TYR:O	16:F:51:LEU:HD12	1.98	0.62
18:H:105:THR:HG23	18:H:110:ILE:HG12	1.81	0.62
32:V:76:GLU:HA	32:V:79:GLU:HB2	1.81	0.62
2:1:10:ALA:HB1	2:1:30:VAL:HB	1.81	0.62
4:3:145:GLY:O	4:3:147:ASN:ND2	2.31	0.62
5:4:112:SER:O	5:4:114:VAL:N	2.32	0.62
11:A:1081:A:H5''	11:A:1082:C:OP1	1.99	0.62
15:E:103:VAL:HG12	15:E:190:LEU:HD12	1.80	0.62
5:4:34:ALA:N	5:4:41:ARG:O	2.29	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:B:41:ARG:N	32:V:105:GLN:HG3	2.15	0.62
16:F:98:LEU:HD21	16:F:102:ASN:HB2	1.81	0.62
37:a:334:SER:OG	37:a:423:PRO:HB2	2.00	0.62
6:5:44:ILE:H	6:5:44:ILE:HD12	1.65	0.62
11:A:702:G:O2'	11:A:703:G:H8	1.82	0.62
11:A:794:U:O2	11:A:794:U:H2'	2.00	0.62
11:A:823:G:O2'	11:A:824:G:P	2.57	0.62
30:T:61:VAL:O	30:T:65:ILE:HG13	2.00	0.62
4:3:11:GLN:HG3	4:3:13:PRO:HD2	1.80	0.61
11:A:843:U:H2'	11:A:844:A:H8	1.64	0.61
11:A:1214:U:OP1	11:A:1246:C:H1'	1.99	0.61
11:A:1291:G:N2	11:A:1324:G:N2	2.45	0.61
18:H:57:ARG:NH2	25:O:16:ILE:HG22	2.15	0.61
33:W:11:ARG:O	33:W:12:LEU:HB2	1.98	0.61
1:0:45:GLY:HA3	1:0:66:ARG:HH12	1.64	0.61
4:3:74:GLN:HE22	4:3:92:PHE:HB2	1.65	0.61
6:5:75:VAL:O	6:5:79:ILE:N	2.27	0.61
11:A:1626:U:H3'	11:A:1627:U:OP2	2.00	0.61
20:J:48:HIS:ND1	20:J:48:HIS:O	2.34	0.61
7:6:38:PRO:CB	39:c:603:ARG:HH12	2.13	0.61
8:7:56:LYS:HE3	8:7:58:GLN:HG2	1.80	0.61
11:A:677:G:H2'	11:A:678:A:C8	2.35	0.61
11:A:820:U:H2'	11:A:821:U:H4'	1.82	0.61
11:A:1474:G:H2'	11:A:1475:A:C8	2.36	0.61
23:M:26:ILE:HD12	23:M:27:LYS:N	2.16	0.61
23:M:70:VAL:HA	23:M:73:MET:HE3	1.80	0.61
27:Q:3:THR:OG1	27:Q:82:ARG:NE	2.34	0.61
10:9:138:ARG:NH2	11:A:1236:A:O4'	2.33	0.61
11:A:1300:A:H4'	15:E:86:VAL:CG2	2.30	0.61
11:A:1657:U:H4'	11:A:1658:G:O5'	1.99	0.61
30:T:52:GLY:O	30:T:54:PHE:N	2.25	0.61
37:a:292:VAL:HG13	39:c:667:PRO:HD3	1.73	0.61
1:0:38:ILE:HD11	1:0:47:VAL:HB	1.82	0.61
2:1:22:ARG:HH21	11:A:1619:C:H1'	1.64	0.61
11:A:1524:A:H2'	11:A:1525:A:C8	2.35	0.61
11:A:1686:C:N1	11:A:1687:U:C6	2.69	0.61
18:H:80:ASN:HD22	18:H:124:LYS:HG2	1.65	0.61
5:4:77:GLU:OE2	21:K:114:ARG:NH2	2.30	0.61
11:A:248:U:H4'	27:Q:36:LYS:HD3	1.82	0.61
11:A:1615:C:H4'	11:A:1616:G:O5'	2.00	0.61
18:H:11:LEU:HD12	18:H:74:VAL:HB	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:L:24:TRP:HE3	22:L:30:LYS:HD3	1.66	0.61
38:b:658:HIS:CG	38:b:659:LYS:N	2.60	0.61
9:8:43:ASP:O	9:8:45:GLU:N	2.34	0.61
11:A:497:G:H2'	11:A:498:G:C8	2.36	0.61
18:H:111:MET:HE1	18:H:121:VAL:HG23	1.81	0.61
11:A:218:A:O2'	11:A:219:A:OP1	2.15	0.61
11:A:1358:G:H2'	11:A:1359:C:C6	2.35	0.61
37:a:482:ILE:HD13	39:c:733:TYR:HE1	1.62	0.61
11:A:732:G:O2'	11:A:733:A:O4'	2.19	0.60
11:A:1299:G:H4'	15:E:99:LYS:CE	2.31	0.60
19:I:49:TYR:HB3	19:I:53:LEU:HD11	1.82	0.60
3:2:25:ARG:HA	11:A:400:A:H5''	1.82	0.60
11:A:1370:U:H4'	11:A:1371:A:C5'	2.32	0.60
14:D:37:LYS:HB3	34:X:33:ARG:HB2	1.81	0.60
32:V:20:TYR:CD2	32:V:38:ILE:HD11	2.36	0.60
11:A:1031:U:H4'	11:A:1032:G:OP2	1.99	0.60
11:A:1168:U:H2'	11:A:1169:G:H5'	1.82	0.60
11:A:1442:U:H2'	11:A:1443:U:C6	2.37	0.60
14:D:146:PHE:CE2	14:D:149:ARG:HD3	2.36	0.60
35:Y:114:VAL:HG12	35:Y:115:LYS:HD3	1.81	0.60
37:a:348:HIS:HE1	39:c:664:PHE:HA	1.46	0.60
37:a:482:ILE:HG23	39:c:733:TYR:CG	2.36	0.60
38:b:556:LYS:HD2	38:b:557:GLU:CD	2.25	0.60
38:b:653:SER:HG	38:b:658:HIS:HE2	1.48	0.60
5:4:181:LEU:HD13	5:4:181:LEU:H	1.66	0.60
10:9:100:UNK:C	10:9:102:VAL:H	2.14	0.60
11:A:143:G:N7	35:Y:177:ARG:NH2	2.49	0.60
11:A:822:U:H2'	11:A:823:G:H5''	1.83	0.60
11:A:1490:C:H4'	11:A:1491:U:OP1	1.99	0.60
9:8:54:VAL:O	9:8:88:ILE:HG21	2.01	0.60
11:A:1542:G:H22	11:A:1568:C:H1'	1.67	0.60
3:2:39:GLY:O	3:2:59:ARG:HB3	2.02	0.60
4:3:13:PRO:HB3	4:3:14:THR:HB	1.82	0.60
15:E:245:ASP:OD1	15:E:245:ASP:N	2.34	0.60
21:K:19:ILE:HB	21:K:83:ILE:HD12	1.84	0.60
28:R:93:ASP:HB2	28:R:100:TYR:HE2	1.67	0.60
31:U:56:GLU:HB3	31:U:124:LYS:HG2	1.84	0.60
11:A:693:U:H5'	11:A:694:U:H5'	1.83	0.60
11:A:703:G:H2'	11:A:704:C:H5'	1.83	0.60
11:A:765:G:H1	14:D:149:ARG:HB3	1.67	0.60
35:Y:135:PRO:HB2	35:Y:141:ILE:HG12	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:5:35:ALA:O	6:5:36:ILE:HG22	2.00	0.60
11:A:1480:G:H4'	30:T:11:ALA:HB1	1.84	0.60
25:O:5:HIS:HB3	25:O:117:LEU:HD13	1.84	0.60
5:4:137:ILE:HD11	5:4:172:LEU:HB3	1.83	0.60
6:5:87:ARG:NH2	6:5:94:ASN:O	2.34	0.60
8:7:60:SER:HB2	13:C:27:ARG:HD2	1.83	0.60
11:A:1299:G:O3'	15:E:99:LYS:CE	2.49	0.60
11:A:1417:A:O3'	19:I:128:LYS:HE2	2.02	0.60
16:F:31:GLN:CG	16:F:39:LEU:HB3	2.32	0.60
11:A:498:G:O2'	11:A:499:U:O5'	2.17	0.60
11:A:500:C:C3'	38:b:487:SER:O	2.48	0.60
11:A:543:C:H5'	11:A:543:C:O2	2.02	0.60
11:A:1381:U:H1'	11:A:1516:A:N6	2.17	0.60
11:A:1672:G:H2'	11:A:1673:G:C8	2.37	0.60
17:G:73:THR:HG23	19:I:114:ARG:CD	2.30	0.60
1:0:84:PHE:CE2	34:X:7:SER:C	2.63	0.59
3:2:5:ARG:HD3	3:2:29:LEU:O	2.02	0.59
11:A:1293:U:O2'	12:B:111:ILE:HB	2.01	0.59
14:D:116:LEU:HD12	38:b:509:LYS:HZ1	1.62	0.59
35:Y:8:PRO:HG3	35:Y:112:VAL:HG13	1.84	0.59
1:0:34:GLU:HG2	1:0:53:ASP:HB2	1.83	0.59
5:4:70:LEU:HD21	5:4:79:HIS:CD2	2.36	0.59
12:B:66:ALA:HB2	36:Z:37:ALA:HB2	1.85	0.59
9:8:42:LEU:HD12	9:8:43:ASP:N	2.17	0.59
11:A:498:G:O2'	11:A:499:U:P	2.60	0.59
11:A:1324:G:H5'	12:B:113:ARG:CD	2.31	0.59
18:H:104:LEU:HB2	18:H:124:LYS:O	2.01	0.59
35:Y:219:ARG:O	35:Y:223:LYS:HB2	2.01	0.59
11:A:229:U:H3	11:A:236:A:H61	1.51	0.59
11:A:1738:U:H2'	11:A:1739:C:C6	2.37	0.59
23:M:54:LEU:H	23:M:54:LEU:HD22	1.66	0.59
36:Z:17:CYS:HB2	36:Z:56:SER:HB3	1.84	0.59
5:4:193:ILE:O	5:4:197:ILE:HG12	2.03	0.59
11:A:1321:A:C1'	12:B:104:PRO:HB2	2.32	0.59
12:B:40:ALA:C	32:V:105:GLN:HG3	2.28	0.59
17:G:145:ASP:OD1	17:G:146:THR:N	2.36	0.59
19:I:40:GLU:HG3	19:I:42:GLU:HB2	1.84	0.59
39:c:501:ARG:HG3	39:c:505:TYR:CE2	2.38	0.59
4:3:185:ILE:HG22	4:3:186:PRO:HD3	1.82	0.59
9:8:60:VAL:HG22	9:8:101:TYR:HB2	1.83	0.59
9:8:92:ILE:HG12	9:8:100:ILE:HG22	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:61:A:H8	11:A:269:G:HO2'	1.48	0.59
11:A:538:A:H8	11:A:543:C:C4	2.20	0.59
11:A:569:C:H41	22:L:69:ARG:HH12	1.49	0.59
11:A:702:G:C6	11:A:737:A:N6	2.71	0.59
11:A:1316:G:HO2'	11:A:1401:A:HO2'	1.50	0.59
13:C:177:MET:SD	13:C:182:LEU:HD11	2.43	0.59
28:R:214:ALA:HB2	28:R:220:ILE:HA	1.85	0.59
35:Y:142:ARG:HA	35:Y:147:LEU:HD12	1.85	0.59
2:1:45:LYS:HG3	17:G:166:ARG:HD3	1.83	0.59
10:9:144:CYS:HB3	10:9:147:VAL:HG13	1.85	0.59
11:A:1293:U:C1'	12:B:111:ILE:HD13	2.30	0.59
30:T:111:ILE:HG23	30:T:113:ILE:HG13	1.84	0.59
2:1:25:VAL:HG11	2:1:66:LEU:HD12	1.85	0.59
7:6:50:ALA:O	7:6:52:THR:N	2.35	0.59
11:A:45:U:O2'	11:A:46:A:H2'	2.03	0.59
11:A:470:A:H5''	11:A:470:A:H8	1.67	0.59
11:A:1716:C:O2'	11:A:1717:G:C8	2.47	0.59
28:R:93:ASP:HB2	28:R:100:TYR:CE2	2.37	0.59
3:2:37:LYS:H	3:2:59:ARG:H	1.51	0.59
4:3:51:VAL:HG23	4:3:53:GLY:H	1.67	0.59
11:A:407:A:H2'	11:A:408:C:C6	2.38	0.59
11:A:702:G:O2'	11:A:703:G:O4'	2.21	0.59
12:B:150:ASP:OD2	12:B:165:ARG:NH2	2.36	0.59
18:H:111:MET:HE3	18:H:116:ALA:HA	1.85	0.59
23:M:46:VAL:HG22	23:M:72:ILE:HG22	1.83	0.59
25:O:67:THR:O	25:O:69:ASN:N	2.36	0.59
6:5:24:VAL:HG11	6:5:71:LEU:HD12	1.85	0.58
11:A:67:A:O3'	11:A:68:A:H3'	2.03	0.58
11:A:1071:U:H2'	11:A:1072:C:C6	2.38	0.58
23:M:91:ASP:O	23:M:92:ILE:HB	2.03	0.58
28:R:36:ALA:HB2	28:R:71:CYS:HB3	1.85	0.58
33:W:37:LYS:HB2	33:W:40:GLU:HG2	1.84	0.58
11:A:992:A:C2	11:A:1012:U:N3	2.65	0.58
11:A:1300:A:O2'	15:E:86:VAL:CB	2.49	0.58
11:A:1657:U:H1'	11:A:1658:G:OP2	2.02	0.58
16:F:27:HIS:HB2	16:F:43:GLN:CD	2.28	0.58
33:W:200:ARG:NH1	33:W:202:ASP:OD2	2.36	0.58
11:A:1715:G:H2'	11:A:1716:C:H5'	1.85	0.58
12:B:169:SER:O	12:B:173:ILE:HG12	2.03	0.58
18:H:103:ILE:HD11	18:H:126:LEU:HD12	1.86	0.58
39:c:523:LEU:HD11	39:c:550:LEU:HD22	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:143:G:H2'	11:A:144:U:H5''	1.85	0.58
11:A:975:C:H5''	25:O:109:LYS:HE2	1.85	0.58
11:A:1166:A:H5''	17:G:101:GLY:H	1.68	0.58
21:K:38:THR:OG1	21:K:39:ILE:N	2.36	0.58
28:R:74:THR:HG23	28:R:79:TYR:HB2	1.85	0.58
11:A:499:U:O2'	38:b:489:LYS:CE	2.46	0.58
11:A:567:A:O2'	22:L:90:ASP:OD1	2.21	0.58
11:A:1300:A:C4'	15:E:86:VAL:HG11	2.33	0.58
21:K:32:ASP:O	21:K:35:GLY:N	2.33	0.58
23:M:26:ILE:HD11	23:M:31:ALA:H	1.68	0.58
30:T:16:ASN:OD1	30:T:56:LYS:NZ	2.35	0.58
11:A:704:C:H3'	11:A:704:C:OP2	2.04	0.58
11:A:1711:C:O2'	11:A:1712:A:OP1	2.14	0.58
12:B:121:VAL:HG23	12:B:141:ILE:HG21	1.84	0.58
26:P:104:SER:HB3	26:P:107:GLN:HB2	1.85	0.58
31:U:28:LEU:HD13	31:U:32:LEU:HD11	1.84	0.58
16:F:30:ILE:HG13	16:F:30:ILE:O	2.04	0.58
19:I:55:VAL:HG21	19:I:105:LEU:HG	1.85	0.58
30:T:14:PHE:HZ	30:T:132:LEU:HD23	1.69	0.58
37:a:470:LEU:HD13	39:c:729:PHE:HD1	1.63	0.58
5:4:141:ALA:HB1	5:4:207:LEU:HD23	1.84	0.58
21:K:107:ARG:HG3	21:K:107:ARG:NH1	2.15	0.58
29:S:28:MET:O	29:S:29:SER:HB3	2.02	0.58
33:W:179:LYS:N	33:W:194:THR:O	2.36	0.58
1:0:88:GLN:CB	34:X:6:GLY:HA2	2.33	0.58
5:4:62:LYS:C	5:4:64:ARG:H	2.12	0.58
6:5:87:ARG:NH1	11:A:1796:C:OP1	2.36	0.58
11:A:324:U:O2'	27:Q:80:MET:HE3	2.03	0.58
11:A:380:U:H5	14:D:5:PRO:HA	1.68	0.58
11:A:1488:G:H3'	11:A:1515:A:H61	1.68	0.58
22:L:59:ILE:HD12	34:X:4:VAL:HG22	1.85	0.58
35:Y:3:LEU:HD13	35:Y:111:LEU:HD11	1.85	0.58
1:0:52:PHE:CZ	1:0:109:LEU:HD11	2.38	0.58
9:8:88:ILE:HA	9:8:104:ALA:HB2	1.85	0.58
11:A:399:A:H4'	33:W:3:ARG:HG2	1.85	0.58
11:A:1332:C:O2'	13:C:162:GLN:HB3	2.04	0.58
11:A:1338:C:H1'	11:A:1410:A:C4	2.39	0.58
21:K:85:ALA:H	21:K:119:THR:CG2	2.15	0.58
33:W:49:ARG:HB2	33:W:55:ALA:HB3	1.85	0.58
3:2:39:GLY:N	3:2:60:ILE:O	2.30	0.57
11:A:918:U:H2'	11:A:919:A:C8	2.39	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:1178:G:H2'	11:A:1179:G:O4'	2.04	0.57
28:R:255:ALA:HB2	28:R:292:LEU:HD22	1.86	0.57
29:S:52:LYS:HG3	29:S:53:PRO:HD3	1.85	0.57
31:U:67:THR:C	31:U:69:ALA:H	2.11	0.57
1:0:58:MET:CG	34:X:3:LYS:HE2	2.22	0.57
4:3:74:GLN:NE2	4:3:92:PHE:HB2	2.19	0.57
11:A:1498:G:H2'	11:A:1499:G:H5'	1.85	0.57
33:W:104:ASP:HB3	33:W:106:LYS:H	1.69	0.57
4:3:63:PRO:C	4:3:65:PRO:HD2	2.29	0.57
4:3:143:LEU:HB2	4:3:147:ASN:HB2	1.85	0.57
11:A:324:U:OP1	27:Q:133:LYS:NZ	2.36	0.57
11:A:542:A:H2'	11:A:543:C:H3'	1.85	0.57
11:A:625:C:H2'	11:A:626:U:C6	2.39	0.57
16:F:98:LEU:HD21	16:F:102:ASN:C	2.30	0.57
3:2:8:ARG:HG3	3:2:8:ARG:O	2.04	0.57
11:A:190:C:N4	11:A:196:G:O6	2.37	0.57
11:A:1595:U:N3	11:A:1600:A:H2	2.02	0.57
34:X:55:ARG:HB3	34:X:58:PRO:HG3	1.87	0.57
3:2:10:LYS:HG2	27:Q:133:LYS:HE3	1.85	0.57
11:A:1242:A:OP1	29:S:59:LYS:NZ	2.37	0.57
11:A:1483:A:H2'	11:A:1484:G:C8	2.39	0.57
16:F:58:LEU:HD23	16:F:58:LEU:C	2.29	0.57
22:L:24:TRP:CE3	22:L:30:LYS:HD3	2.39	0.57
27:Q:80:MET:HB2	27:Q:83:THR:HG23	1.86	0.57
30:T:57:ARG:HH11	30:T:57:ARG:CG	2.09	0.57
33:W:151:ASP:HB3	33:W:154:ILE:HG13	1.87	0.57
11:A:495:C:H3'	11:A:496:G:O4'	2.05	0.57
11:A:780:A:C8	26:P:8:ARG:HB3	2.40	0.57
28:R:16:HIS:CE1	28:R:43:ILE:HG12	2.39	0.57
36:Z:74:GLN:HB2	36:Z:79:LEU:HB2	1.86	0.57
2:1:32:PHE:CE1	2:1:38:ARG:HB3	2.38	0.57
5:4:117:TRP:HE1	5:4:152:ARG:CZ	2.18	0.57
6:5:24:VAL:HG12	6:5:72:HIS:O	2.05	0.57
11:A:68:A:OP1	35:Y:160:ARG:NH1	2.36	0.57
11:A:241:U:H5'	11:A:242:U:OP2	2.04	0.57
11:A:514:G:N1	11:A:543:C:H5	2.00	0.57
13:C:115:ILE:HG23	13:C:116:ARG:HG3	1.87	0.57
17:G:72:HIS:O	19:I:47:LYS:HE2	2.04	0.57
10:9:135:HIS:ND1	10:9:138:ARG:HD2	2.20	0.57
11:A:7:G:N7	15:E:205:ARG:NH1	2.51	0.57
11:A:1099:U:OP1	18:H:71:LYS:NZ	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:1169:G:N1	11:A:1575:G:OP2	2.36	0.57
11:A:1293:U:C4'	12:B:111:ILE:HD13	2.35	0.57
23:M:70:VAL:HG12	23:M:74:GLN:OE1	2.05	0.57
38:b:658:HIS:C	38:b:659:LYS:HD2	2.30	0.57
7:6:37:CYS:O	7:6:39:GLY:N	2.38	0.57
11:A:448:C:OP1	33:W:29:PRO:HD3	2.05	0.57
11:A:1059:U:O5'	37:a:66:LYS:NZ	2.36	0.57
11:A:1152:A:N3	11:A:1627:U:O2	2.36	0.57
12:B:27:ARG:HG3	12:B:44:GLY:O	2.04	0.57
19:I:113:ASP:CG	19:I:115:THR:H	2.12	0.57
19:I:116:LEU:HD22	19:I:116:LEU:H	1.70	0.57
5:4:39:GLU:HB3	5:4:73:LEU:O	2.04	0.57
11:A:116:U:H2'	11:A:117:U:C6	2.40	0.57
11:A:591:A:H2'	11:A:592:A:H8	1.70	0.57
11:A:639:U:OP2	11:A:639:U:H4'	2.04	0.57
11:A:735:C:H2'	11:A:735:C:OP2	2.05	0.57
11:A:855:A:C2	11:A:857:U:H1'	2.40	0.57
35:Y:186:ARG:O	35:Y:190:GLN:HG2	2.04	0.57
1:0:41:MET:HA	1:0:41:MET:HE2	1.85	0.56
5:4:97:LEU:CD1	5:4:98:THR:H	2.11	0.56
11:A:895:G:HO2'	21:K:38:THR:H	1.53	0.56
11:A:990:C:H2'	11:A:991:G:O4'	2.04	0.56
17:G:91:GLU:HA	17:G:94:THR:HG23	1.88	0.56
11:A:66:U:C4	35:Y:158:ILE:HG21	2.40	0.56
11:A:1173:C:H3'	23:M:141:THR:HG21	1.87	0.56
11:A:1226:A:O2'	11:A:1227:A:OP1	2.23	0.56
14:D:17:ARG:O	14:D:23:ARG:NH2	2.38	0.56
21:K:81:VAL:HG13	21:K:115:ILE:HG21	1.87	0.56
1:0:59:ALA:HA	1:0:89:CYS:O	2.05	0.56
1:0:78:LEU:O	1:0:92:VAL:HG12	2.06	0.56
3:2:8:ARG:HH11	3:2:21:PHE:H	1.54	0.56
4:3:107:ARG:NH2	11:A:741:C:O2	2.38	0.56
8:7:2:LEU:HD13	11:A:1258:U:H4'	1.87	0.56
11:A:93:A:O2'	33:W:4:GLY:HA3	2.05	0.56
11:A:104:A:OP2	11:A:308:C:N4	2.37	0.56
11:A:802:G:H21	18:H:107:SER:HB3	1.71	0.56
11:A:885:G:H2'	11:A:886:U:C6	2.40	0.56
11:A:886:U:O2'	21:K:121:VAL:O	2.22	0.56
11:A:1160:A:H2'	11:A:1161:C:H6	1.69	0.56
11:A:1300:A:H5'	15:E:99:LYS:HG3	1.87	0.56
11:A:1413:U:H4'	11:A:1414:U:OP2	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:1525:A:OP1	30:T:93:HIS:ND1	2.36	0.56
12:B:13:ASP:HA	12:B:16:LEU:HD12	1.87	0.56
14:D:38:ASN:HB2	14:D:41:GLU:HG3	1.87	0.56
16:F:98:LEU:HD23	16:F:103:ILE:CG1	2.35	0.56
21:K:81:VAL:HG22	21:K:115:ILE:HB	1.87	0.56
30:T:45:MET:HE3	30:T:46:PRO:HD2	1.87	0.56
1:0:38:ILE:HG23	1:0:74:GLY:H	1.70	0.56
5:4:149:GLN:NE2	11:A:1066:C:H4'	2.20	0.56
10:9:135:HIS:HB2	10:9:138:ARG:CB	2.35	0.56
11:A:180:A:H2'	11:A:181:A:O4'	2.05	0.56
11:A:717:C:N3	11:A:720:G:N1	2.48	0.56
11:A:885:G:H21	21:K:123:SER:HB2	1.70	0.56
12:B:41:ARG:HH11	32:V:103:ASP:CB	2.18	0.56
21:K:13:VAL:HG22	21:K:76:ILE:HA	1.87	0.56
29:S:96:ILE:HD11	29:S:116:LEU:HD22	1.88	0.56
32:V:71:PHE:HE1	32:V:73:LEU:HD22	1.71	0.56
33:W:152:PRO:O	33:W:154:ILE:N	2.39	0.56
35:Y:70:PRO:C	35:Y:98:ARG:HH21	2.14	0.56
35:Y:78:THR:HG23	35:Y:92:ARG:HG2	1.86	0.56
5:4:136:ARG:NH1	11:A:885:G:OP1	2.39	0.56
6:5:23:CYS:HB2	6:5:74:CYS:HB3	1.88	0.56
11:A:1321:A:N9	12:B:104:PRO:HB2	2.21	0.56
30:T:6:VAL:HG13	30:T:66:TYR:CE2	2.41	0.56
37:a:482:ILE:HD13	39:c:733:TYR:CZ	2.38	0.56
11:A:1511:U:H2'	11:A:1512:G:C8	2.41	0.56
14:D:175:ARG:HD3	14:D:179:ARG:NH1	2.21	0.56
26:P:77:ASN:O	26:P:78:SER:HB3	2.05	0.56
31:U:30:VAL:HB	31:U:132:GLU:HG3	1.86	0.56
33:W:194:THR:O	33:W:195:ILE:HB	2.05	0.56
5:4:147:ALA:O	5:4:148:ASN:ND2	2.28	0.56
11:A:312:A:C2	11:A:314:C:H2'	2.40	0.56
11:A:513:U:OP1	14:D:133:HIS:NE2	2.38	0.56
11:A:577:G:H3'	11:A:577:G:H8	1.71	0.56
11:A:1207:C:H42	11:A:1456:C:H5	1.53	0.56
32:V:26:LEU:HD23	32:V:26:LEU:H	1.70	0.56
1:0:82:ARG:NH2	22:L:68:ILE:CG1	2.66	0.56
3:2:138:ASN:O	3:2:141:ARG:HB2	2.06	0.56
11:A:717:C:N4	11:A:720:G:H22	2.03	0.56
11:A:1555:A:OP2	29:S:47:ARG:NH1	2.39	0.56
13:C:64:ARG:O	13:C:66:ILE:N	2.39	0.56
16:F:85:ARG:HA	16:F:88:VAL:HG12	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:F:98:LEU:CD1	16:F:102:ASN:HD22	2.19	0.56
16:F:98:LEU:CD1	16:F:102:ASN:HB2	2.31	0.56
17:G:42:LEU:HB2	17:G:46:TRP:O	2.05	0.56
21:K:13:VAL:N	21:K:77:THR:OG1	2.38	0.56
22:L:102:VAL:HG12	22:L:127:VAL:HG12	1.88	0.56
25:O:12:SER:O	25:O:13:SER:HB3	2.06	0.56
39:c:335:THR:HG21	39:c:339:TYR:HB3	1.88	0.56
11:A:514:G:O2'	11:A:515:A:H5'	2.06	0.56
11:A:852:C:O5'	11:A:852:C:H6	1.88	0.56
11:A:1370:U:O2'	11:A:1371:A:OP2	2.20	0.56
11:A:1489:U:OP2	13:C:9:ARG:NH1	2.38	0.56
16:F:80:LEU:HB3	16:F:84:GLN:HE22	1.70	0.56
19:I:22:VAL:HG22	19:I:65:ILE:HD13	1.88	0.56
33:W:246:LEU:HD13	33:W:251:GLU:HG2	1.88	0.56
4:3:71:HIS:CG	4:3:131:PHE:HZ	2.24	0.56
11:A:1097:U:O4	15:E:201:ASN:ND2	2.39	0.56
12:B:38:PHE:CD1	32:V:109:LEU:CB	2.85	0.56
32:V:5:ARG:O	32:V:10:LYS:HE2	2.05	0.56
1:0:82:ARG:CZ	22:L:68:ILE:HD11	2.06	0.55
3:2:192:TYR:O	3:2:196:LEU:HB2	2.05	0.55
8:7:15:LEU:HD13	8:7:21:VAL:HG23	1.87	0.55
11:A:540:G:O3'	11:A:541:A:H3'	2.06	0.55
7:6:38:PRO:HB2	39:c:603:ARG:HH12	1.71	0.55
11:A:149:C:O2'	35:Y:132:ARG:NH1	2.39	0.55
11:A:238:U:O2'	11:A:239:C:H5'	2.05	0.55
11:A:1625:C:C5'	15:E:91:ARG:NH1	2.43	0.55
14:D:151:ASP:N	14:D:151:ASP:OD1	2.39	0.55
23:M:83:ALA:O	23:M:89:GLN:NE2	2.39	0.55
27:Q:59:PRO:HG2	27:Q:60:PHE:CE2	2.41	0.55
1:0:33:GLN:NE2	1:0:78:LEU:HD11	2.21	0.55
11:A:827:C:H2'	11:A:828:U:C6	2.41	0.55
11:A:896:U:O4'	21:K:38:THR:HG21	2.06	0.55
11:A:1151:A:O3'	11:A:1152:A:H5''	2.07	0.55
11:A:1299:G:H5'	15:E:208:GLU:OE2	2.07	0.55
13:C:29:LEU:HB2	13:C:34:TYR:HB2	1.87	0.55
13:C:141:LYS:HD2	13:C:179:GLN:CG	2.36	0.55
25:O:72:MET:HE1	25:O:82:PRO:HD2	1.87	0.55
39:c:304:PHE:HB3	39:c:375:ARG:HE	1.71	0.55
1:0:103:LEU:HD23	1:0:106:GLN:NE2	2.22	0.55
3:2:48:THR:HG21	3:2:54:LYS:HB2	1.87	0.55
11:A:103:A:H4'	11:A:104:A:OP2	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:489:C:H42	11:A:497:G:H22	1.53	0.55
19:I:50:GLU:OE2	19:I:112:TYR:OH	2.24	0.55
30:T:9:VAL:HG12	30:T:14:PHE:HB2	1.88	0.55
39:c:558:CYS:SG	39:c:712:SER:OG	2.59	0.55
5:4:110:LEU:HD21	5:4:213:ARG:HD2	1.89	0.55
6:5:5:ARG:NH1	11:A:1796:C:OP2	2.39	0.55
7:6:36:LYS:HG2	7:6:43:ILE:HG22	1.88	0.55
7:6:42:ASN:OD1	39:c:427:ARG:NH2	2.40	0.55
9:8:65:LEU:HB3	9:8:71:ILE:HD13	1.89	0.55
11:A:706:A:C6	11:A:734:A:N6	2.75	0.55
11:A:749:U:H2'	11:A:750:U:C6	2.41	0.55
11:A:1650:U:H2'	11:A:1651:A:C8	2.42	0.55
13:C:34:TYR:OH	13:C:37:VAL:HG22	2.07	0.55
19:I:9:THR:HG21	19:I:88:GLY:HA2	1.88	0.55
28:R:64:HIS:ND1	28:R:86:ASP:OD2	2.35	0.55
1:0:46:ARG:HD3	34:X:3:LYS:HZ2	1.71	0.55
1:0:88:GLN:HE22	34:X:4:VAL:H	1.54	0.55
3:2:188:GLU:HG2	27:Q:13:PHE:CD2	2.42	0.55
5:4:34:ALA:HB3	5:4:41:ARG:HA	1.89	0.55
11:A:647:G:N2	11:A:687:G:N2	2.54	0.55
11:A:1157:A:C8	11:A:1157:A:H3'	2.42	0.55
11:A:1291:G:O5'	11:A:1291:G:C8	2.55	0.55
11:A:1420:C:P	24:N:54:LYS:HZ1	2.29	0.55
12:B:179:ARG:HD3	12:B:183:ARG:NH1	2.17	0.55
35:Y:109:LEU:HD13	35:Y:111:LEU:HD21	1.87	0.55
38:b:495:LEU:HB2	38:b:510:VAL:HB	1.88	0.55
1:0:42:LEU:HD11	1:0:58:MET:SD	2.46	0.55
5:4:39:GLU:HG3	5:4:40:ASN:N	2.21	0.55
6:5:9:GLY:HA3	6:5:34:LYS:HE2	1.89	0.55
11:A:190:C:O2'	11:A:191:C:OP2	2.23	0.55
11:A:652:G:H1	11:A:682:C:N4	2.05	0.55
16:F:92:MET:SD	16:F:103:ILE:HG12	2.46	0.55
28:R:93:ASP:OD1	28:R:96:THR:HB	2.06	0.55
33:W:159:THR:HG23	33:W:173:ILE:HD13	1.88	0.55
38:b:660:VAL:HB	38:b:662:HIS:CE1	2.42	0.55
1:0:30:GLU:H	1:0:33:GLN:CD	2.15	0.55
11:A:286:C:H2'	11:A:287:G:H5'	1.89	0.55
14:D:163:PRO:C	14:D:165:GLY:H	2.14	0.55
20:J:57:ARG:HG3	20:J:89:ARG:CZ	2.36	0.55
30:T:42:GLY:HA2	30:T:84:LYS:HB2	1.89	0.55
33:W:158:ASP:OD2	33:W:174:LYS:NZ	2.38	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:W:192:ILE:HG13	33:W:243:GLY:HA3	1.89	0.55
10:9:91:UNK:HG2	11:A:1445:G:C4	2.41	0.55
11:A:1760:G:H2'	11:A:1761:U:H5'	1.88	0.55
11:A:1776:A:H2'	11:A:1777:G:C8	2.42	0.55
16:F:98:LEU:HD11	16:F:102:ASN:HD22	1.71	0.55
18:H:8:ALA:HA	18:H:74:VAL:HG11	1.88	0.55
5:4:34:ALA:HB2	5:4:43:VAL:HG23	1.89	0.55
9:8:60:VAL:CG2	9:8:101:TYR:HB2	2.37	0.55
11:A:197:A:H2'	11:A:198:A:C8	2.42	0.55
11:A:425:A:H5'	11:A:425:A:H8	1.72	0.55
11:A:1433:G:H2'	11:A:1434:U:C6	2.42	0.55
11:A:1514:U:H5'	11:A:1514:U:O2	2.07	0.55
11:A:1783:C:H2'	11:A:1784:C:H6	1.72	0.55
12:B:147:THR:OG1	12:B:159:ALA:HB1	2.07	0.55
22:L:16:ARG:NH1	27:Q:101:GLU:OE1	2.40	0.55
31:U:67:THR:O	31:U:69:ALA:N	2.35	0.55
33:W:104:ASP:HB2	33:W:108:ARG:H	1.72	0.55
35:Y:58:LYS:C	35:Y:60:GLY:H	2.15	0.55
1:0:46:ARG:CD	34:X:3:LYS:HZ2	2.20	0.54
1:0:84:PHE:CZ	34:X:7:SER:O	2.43	0.54
3:2:26:LYS:O	3:2:29:LEU:HB3	2.07	0.54
11:A:142:G:O6	35:Y:177:ARG:NH1	2.36	0.54
11:A:592:A:OP1	14:D:39:LYS:HG2	2.07	0.54
11:A:1157:A:H2'	11:A:1160:A:N7	2.21	0.54
11:A:1625:C:C5'	15:E:91:ARG:HH12	2.09	0.54
37:a:96:PHE:O	37:a:100:VAL:HG12	2.07	0.54
2:1:32:PHE:HZ	2:1:38:ARG:CZ	2.21	0.54
2:1:45:LYS:HB3	17:G:162:VAL:HB	1.90	0.54
6:5:13:LYS:O	11:A:1075:C:O2'	2.20	0.54
11:A:558:U:O2'	11:A:559:C:O5'	2.25	0.54
11:A:896:U:C4'	21:K:38:THR:HG21	2.37	0.54
36:Z:64:GLU:O	36:Z:68:SER:HB2	2.07	0.54
38:b:217:LYS:HB3	38:b:220:LEU:HD12	1.89	0.54
39:c:257:ARG:HE	39:c:282:LEU:HD11	1.72	0.54
1:0:38:ILE:CG2	1:0:75:ASP:H	2.20	0.54
6:5:6:ALA:H	11:A:1796:C:H5	1.50	0.54
9:8:77:ARG:NH2	11:A:1533:C:C5	2.75	0.54
11:A:178:U:C4	35:Y:191:ARG:HD3	2.43	0.54
11:A:970:A:H5'	11:A:971:A:OP2	2.07	0.54
11:A:1559:A:C6	23:M:134:ARG:HD2	2.42	0.54
11:A:1686:C:O2'	11:A:1687:U:H5'	2.06	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:B:58:VAL:O	12:B:62:ARG:HB2	2.07	0.54
16:F:98:LEU:HD11	16:F:102:ASN:CB	2.31	0.54
20:J:28:SER:OG	20:J:29:THR:N	2.38	0.54
26:P:51:GLU:OE1	26:P:53:ASP:N	2.33	0.54
30:T:63:ARG:HG3	30:T:67:MET:HE1	1.90	0.54
37:a:303:TRP:HB3	37:a:328:ILE:HG12	1.89	0.54
4:3:122:HIS:HA	4:3:125:ILE:HD12	1.89	0.54
11:A:93:A:H4'	11:A:94:U:OP2	2.08	0.54
11:A:133:U:OP2	11:A:133:U:H3'	2.07	0.54
31:U:98:GLY:C	31:U:103:LEU:HD21	2.32	0.54
1:0:23:LYS:C	1:0:24:ARG:O	2.50	0.54
4:3:73:VAL:HG12	4:3:77:LEU:HB2	1.90	0.54
4:3:111:LYS:O	4:3:112:ARG:HB2	2.07	0.54
5:4:131:ASP:CG	5:4:180:THR:HG21	2.33	0.54
5:4:180:THR:O	5:4:184:LEU:HB2	2.08	0.54
11:A:480:G:N2	11:A:509:G:H1'	2.22	0.54
11:A:711:U:H4'	11:A:712:G:OP1	2.08	0.54
11:A:1354:G:H5'	11:A:1355:C:OP2	2.07	0.54
11:A:1492:A:O2'	11:A:1493:A:H8	1.80	0.54
14:D:65:LYS:HA	14:D:70:LEU:HD11	1.89	0.54
25:O:114:ARG:HG2	25:O:114:ARG:NH1	2.18	0.54
32:V:20:TYR:CZ	32:V:38:ILE:HD11	2.42	0.54
1:0:45:GLY:HA3	1:0:66:ARG:NH1	2.23	0.54
5:4:61:LEU:HD23	5:4:62:LYS:H	1.72	0.54
5:4:128:LYS:HE3	5:4:132:ASP:HB3	1.90	0.54
11:A:133:U:H4'	11:A:134:U:OP2	2.07	0.54
11:A:878:G:O2'	25:O:108:ASP:OD1	2.26	0.54
11:A:989:U:H2'	11:A:990:C:C6	2.42	0.54
11:A:1293:U:O2'	12:B:111:ILE:N	2.29	0.54
11:A:1352:G:H2'	11:A:1353:U:O4'	2.07	0.54
14:D:125:ALA:O	14:D:129:ILE:HG13	2.08	0.54
14:D:171:ARG:O	14:D:175:ARG:N	2.36	0.54
4:3:35:LYS:NZ	4:3:39:ARG:HD2	2.23	0.54
11:A:1098:U:OP1	15:E:159:THR:HB	2.07	0.54
11:A:1151:A:N6	11:A:1152:A:C5	2.74	0.54
11:A:1332:C:O5'	11:A:1332:C:H6	1.89	0.54
14:D:90:LYS:HB2	14:D:95:TYR:CD2	2.43	0.54
23:M:90:ASN:O	29:S:18:ARG:NH1	2.40	0.54
4:3:16:LEU:HA	4:3:19:GLN:HG3	1.90	0.54
4:3:46:ILE:HG12	4:3:60:ILE:HG23	1.90	0.54
8:7:9:ASN:O	8:7:13:GLN:HB3	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:8:85:LYS:HG3	9:8:86:GLU:N	2.22	0.54
11:A:542:A:O2'	11:A:543:C:O5'	2.26	0.54
12:B:9:LEU:HD22	12:B:10:THR:H	1.72	0.54
14:D:116:LEU:HD13	38:b:509:LYS:HZ2	1.73	0.54
17:G:37:GLN:CD	19:I:53:LEU:HD22	2.32	0.54
18:H:37:PHE:CD2	18:H:103:ILE:HD12	2.43	0.54
24:N:7:TRP:O	24:N:8:PHE:HB2	2.07	0.54
28:R:160:GLU:O	28:R:162:ALA:N	2.35	0.54
37:a:235:ARG:O	37:a:239:GLN:HG3	2.07	0.54
1:0:88:GLN:HB3	34:X:6:GLY:HA2	1.90	0.54
4:3:107:ARG:NH1	11:A:741:C:O2	2.40	0.54
8:7:14:TYR:CE1	8:7:21:VAL:HG22	2.43	0.54
11:A:20:G:H5'	11:A:571:G:C5	2.43	0.54
11:A:115:G:OP1	27:Q:67:ARG:NH1	2.39	0.54
38:b:358:SER:HB2	38:b:361:LEU:HG	1.89	0.54
39:c:322:PHE:CE1	39:c:407:LEU:HG	2.43	0.54
4:3:30:SER:HB2	4:3:34:LEU:HB2	1.90	0.54
11:A:138:A:N6	11:A:266:A:H61	2.06	0.54
11:A:142:G:N2	11:A:173:A:H2	2.00	0.54
11:A:542:A:H5''	11:A:544:A:C8	2.43	0.54
11:A:720:G:H1'	11:A:721:U:H5''	1.90	0.54
11:A:1217:A:H5'	11:A:1217:A:H8	1.73	0.54
11:A:1498:G:H5''	30:T:72:GLY:HA3	1.90	0.54
26:P:36:SER:O	26:P:40:LEU:HG	2.08	0.54
1:0:30:GLU:H	1:0:33:GLN:NE2	2.07	0.53
10:9:86:UNK:C	10:9:87:UNK:HG3	2.38	0.53
10:9:130:VAL:HG11	10:9:143:LYS:HG2	1.89	0.53
10:9:136:LYS:H	10:9:138:ARG:HB2	1.73	0.53
11:A:832:U:H2'	11:A:833:U:H5''	1.89	0.53
11:A:1034:C:OP1	25:O:9:LYS:NZ	2.40	0.53
11:A:1299:G:C5'	15:E:208:GLU:OE2	2.57	0.53
13:C:211:PRO:O	13:C:212:LYS:HB2	2.08	0.53
21:K:107:ARG:HH11	21:K:107:ARG:CG	2.19	0.53
27:Q:6:THR:CB	27:Q:9:SER:HB3	2.38	0.53
39:c:668:PRO:HD3	39:c:677:PHE:CZ	2.43	0.53
2:1:13:ILE:HG13	2:1:29:ARG:O	2.08	0.53
4:3:167:GLU:O	4:3:170:GLN:HB2	2.07	0.53
5:4:72:ASP:OD1	6:5:59:TYR:OH	2.14	0.53
11:A:237:C:H4'	11:A:238:U:H5'	1.90	0.53
11:A:1294:G:O3'	12:B:109:ASN:N	2.40	0.53
11:A:1528:U:OP1	17:G:109:LYS:HG2	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:1535:U:O2'	11:A:1536:G:N3	2.35	0.53
20:J:23:ARG:HD3	20:J:92:ASP:OD1	2.09	0.53
23:M:30:TYR:O	23:M:33:THR:OG1	2.15	0.53
38:b:556:LYS:HD2	38:b:557:GLU:OE2	2.09	0.53
38:b:559:THR:HG23	38:b:561:VAL:HG23	1.90	0.53
39:c:351:ILE:O	39:c:355:PRO:HD2	2.08	0.53
3:2:76:THR:HG22	3:2:108:PRO:HG2	1.90	0.53
5:4:48:VAL:HG13	5:4:61:LEU:HD21	1.89	0.53
11:A:717:C:H2'	11:A:718:U:H5''	1.90	0.53
23:M:31:ALA:O	23:M:34:THR:HG23	2.08	0.53
24:N:22:ARG:HD2	24:N:38:ILE:HD11	1.90	0.53
27:Q:84:ILE:HD12	27:Q:86:ILE:HG23	1.90	0.53
5:4:172:LEU:O	5:4:176:VAL:HG23	2.08	0.53
6:5:79:ILE:HG23	6:5:84:VAL:HG21	1.89	0.53
11:A:503:G:O2'	11:A:504:U:P	2.65	0.53
11:A:513:U:H2'	11:A:514:G:C8	2.44	0.53
11:A:767:U:H5	14:D:142:ASN:H	1.55	0.53
11:A:866:G:OP1	25:O:2:GLY:HA2	2.07	0.53
11:A:1322:A:C2	12:B:109:ASN:ND2	2.76	0.53
18:H:72:CYS:HB3	18:H:129:VAL:HG13	1.90	0.53
32:V:44:LYS:HG2	32:V:48:ASN:HD21	1.74	0.53
38:b:562:ILE:O	38:b:564:ARG:N	2.40	0.53
8:7:12:HIS:NE2	8:7:49:LEU:HD21	2.23	0.53
8:7:33:GLU:CD	8:7:33:GLU:H	2.16	0.53
10:9:86:UNK:O	10:9:87:UNK:CG	2.51	0.53
11:A:1300:A:HO2'	15:E:86:VAL:HB	1.74	0.53
11:A:1595:U:H3	11:A:1600:A:H2	1.56	0.53
13:C:176:LEU:HD12	13:C:176:LEU:H	1.73	0.53
19:I:35:PRO:HG2	19:I:38:LEU:HG	1.90	0.53
21:K:117:ASP:OD1	21:K:119:THR:HG23	2.09	0.53
26:P:94:TYR:HD2	26:P:96:LEU:HD11	1.73	0.53
28:R:273:ASP:CG	28:R:275:ARG:HH22	2.17	0.53
30:T:57:ARG:NH2	30:T:80:TYR:HB3	2.24	0.53
33:W:42:LEU:HD12	33:W:109:PHE:HB2	1.89	0.53
11:A:240:U:H1'	11:A:241:U:P	2.49	0.53
11:A:1149:G:H1'	11:A:1765:A:C4	2.44	0.53
12:B:109:ASN:O	12:B:112:THR:HG22	2.08	0.53
39:c:626:LEU:HD11	39:c:679:ALA:HB2	1.90	0.53
3:2:8:ARG:HH11	3:2:21:PHE:N	2.06	0.53
3:2:36:THR:HG21	3:2:173:PRO:HB2	1.90	0.53
4:3:104:ARG:O	4:3:106:SER:N	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:230:C:H2'	11:A:231:U:H5''	1.90	0.53
11:A:981:U:H2'	11:A:982:U:H5'	1.91	0.53
11:A:1320:U:O2	11:A:1322:A:H5'	2.09	0.53
11:A:1473:U:O2	11:A:1473:U:H2'	2.08	0.53
12:B:14:ALA:O	12:B:18:LEU:HG	2.09	0.53
12:B:81:PHE:HB3	12:B:170:ILE:HD13	1.91	0.53
18:H:83:ILE:HD12	18:H:122:SER:HB2	1.89	0.53
30:T:117:SER:OG	30:T:118:PRO:O	2.20	0.53
3:2:105:ASP:OD2	3:2:107:THR:HG23	2.09	0.53
11:A:226:A:C2'	11:A:227:U:H5'	2.38	0.53
11:A:283:U:H5''	35:Y:188:ARG:HD3	1.90	0.53
11:A:632:U:OP1	27:Q:102:LYS:HG3	2.08	0.53
11:A:649:U:HO2'	11:A:650:U:P	2.31	0.53
11:A:765:G:N1	14:D:149:ARG:HD2	2.24	0.53
11:A:799:A:H5''	33:W:201:HIS:CE1	2.44	0.53
11:A:1241:G:H5''	29:S:77:ARG:HB2	1.90	0.53
22:L:90:ASP:OD1	34:X:12:GLY:HA2	2.08	0.53
28:R:136:ILE:HD13	28:R:136:ILE:N	2.24	0.53
30:T:126:GLU:CD	30:T:126:GLU:H	2.17	0.53
36:Z:72:LEU:O	36:Z:76:ASP:HB2	2.09	0.53
38:b:655:SER:HA	38:b:662:HIS:NE2	2.24	0.53
4:3:96:ARG:CZ	4:3:124:LYS:HB3	2.39	0.53
7:6:4:VAL:HA	18:H:24:GLN:NE2	2.24	0.53
11:A:61:A:H8	11:A:269:G:O2'	1.92	0.53
11:A:420:A:H2'	11:A:421:A:O4'	2.08	0.53
11:A:851:U:H2'	11:A:852:C:C6	2.42	0.53
11:A:1151:A:C3'	11:A:1152:A:O5'	2.55	0.53
11:A:1291:G:H22	11:A:1324:G:N2	2.07	0.53
12:B:49:ASN:HB3	12:B:52:LYS:CG	2.32	0.53
17:G:94:THR:O	17:G:97:LEU:HB2	2.08	0.53
21:K:16:VAL:O	21:K:30:VAL:HA	2.09	0.53
25:O:113:PHE:HA	25:O:116:ILE:HD12	1.90	0.53
27:Q:14:GLN:HB3	27:Q:54:ILE:HG21	1.91	0.53
5:4:179:SER:HB3	5:4:183:GLN:CD	2.34	0.53
9:8:43:ASP:O	9:8:46:LYS:N	2.27	0.53
11:A:114:C:H6	11:A:114:C:H5'	1.74	0.53
11:A:765:G:C4	14:D:149:ARG:CZ	2.92	0.53
11:A:780:A:H8	26:P:8:ARG:HB3	1.73	0.53
11:A:1062:A:H2'	11:A:1063:U:O4'	2.09	0.53
13:C:127:MET:HE1	13:C:133:GLY:HA2	1.91	0.53
17:G:103:ASN:HA	17:G:106:LYS:HD2	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:Q:57:LYS:HB2	27:Q:110:HIS:NE2	2.24	0.53
5:4:157:GLN:H	5:4:160:HIS:HB2	1.74	0.52
11:A:93:A:HO2'	33:W:4:GLY:HA3	1.74	0.52
14:D:88:GLU:HG3	14:D:91:LYS:HE3	1.90	0.52
16:F:100:LYS:HA	16:F:103:ILE:HD12	1.91	0.52
26:P:49:LYS:N	26:P:49:LYS:HD3	2.24	0.52
28:R:192:PHE:HD2	28:R:223:TRP:CE3	2.27	0.52
11:A:6:G:OP2	15:E:205:ARG:HD2	2.10	0.52
11:A:918:U:O3'	21:K:18:ARG:NH1	2.42	0.52
15:E:185:LYS:O	15:E:189:GLN:HG3	2.09	0.52
19:I:47:LYS:HZ1	19:I:114:ARG:CD	2.21	0.52
37:a:351:MET:HA	37:a:354:LEU:HB2	1.91	0.52
8:7:1:MET:HG2	8:7:2:LEU:H	1.73	0.52
11:A:325:G:H4'	27:Q:83:THR:HG21	1.91	0.52
11:A:1760:G:C2'	11:A:1761:U:H5'	2.39	0.52
23:M:26:ILE:HD13	23:M:30:TYR:HB2	1.92	0.52
27:Q:75:VAL:HG12	27:Q:119:VAL:HA	1.91	0.52
38:b:659:LYS:N	38:b:659:LYS:HD2	2.24	0.52
1:0:84:PHE:HZ	34:X:7:SER:O	1.86	0.52
8:7:61:TRP:CD2	13:C:20:GLU:HG3	2.44	0.52
10:9:133:ALA:HB2	11:A:1252:C:O4'	2.10	0.52
11:A:359:A:C2	22:L:38:PHE:HB3	2.45	0.52
28:R:7:LEU:HD23	28:R:315:VAL:HG22	1.90	0.52
28:R:33:LEU:HB3	28:R:45:TRP:HB2	1.90	0.52
5:4:174:LYS:HB2	5:4:174:LYS:NZ	2.25	0.52
5:4:181:LEU:O	5:4:182:ALA:C	2.52	0.52
11:A:79:C:H4'	35:Y:173:PRO:O	2.09	0.52
11:A:611:U:OP2	22:L:5:LYS:HE2	2.09	0.52
11:A:1535:U:H4'	11:A:1535:U:OP1	2.10	0.52
16:F:69:VAL:CB	16:F:79:GLN:HE22	2.06	0.52
33:W:241:GLY:O	33:W:244:ILE:HG12	2.09	0.52
39:c:346:ASP:N	39:c:347:PRO:HD2	2.25	0.52
5:4:127:VAL:HG11	5:4:176:VAL:HG21	1.91	0.52
11:A:927:C:H1'	21:K:125:SER:HB2	1.91	0.52
12:B:167:LYS:HB3	12:B:168:HIS:HD2	1.72	0.52
16:F:85:ARG:NH1	16:F:107:GLY:HA3	2.24	0.52
21:K:29:HIS:HB2	21:K:41:ARG:HA	1.92	0.52
25:O:92:ILE:O	25:O:96:VAL:HG23	2.09	0.52
2:1:34:GLU:O	2:1:35:ASP:HB2	2.10	0.52
9:8:41:ILE:HG13	9:8:42:LEU:HG	1.91	0.52
9:8:77:ARG:NH2	11:A:1533:C:H5	2.08	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:8:94:LYS:HD3	9:8:95:HIS:HB3	1.90	0.52
11:A:579:A:N6	13:C:143:ARG:CA	2.25	0.52
11:A:1059:U:H5'	37:a:66:LYS:HZ1	1.74	0.52
11:A:1061:A:H2'	11:A:1062:A:H5'	1.92	0.52
11:A:1199:G:O6	24:N:31:ILE:HD11	2.10	0.52
11:A:1487:A:H2'	11:A:1488:G:C8	2.44	0.52
11:A:1647:U:O2	34:X:2:ALA:HA	2.10	0.52
12:B:69:ASN:HB3	12:B:71:GLU:CD	2.34	0.52
12:B:189:VAL:HG22	12:B:190:ASP:H	1.75	0.52
19:I:127:LYS:NZ	19:I:131:GLY:O	2.38	0.52
23:M:18:LEU:HD21	23:M:70:VAL:HG13	1.92	0.52
3:2:58:LEU:O	3:2:59:ARG:HB2	2.10	0.52
5:4:128:LYS:CE	5:4:132:ASP:HB3	2.40	0.52
5:4:134:VAL:O	5:4:218:LEU:HD22	2.10	0.52
11:A:520:A:H2'	11:A:521:A:C8	2.45	0.52
11:A:530:C:O2	26:P:61:ARG:NH2	2.43	0.52
11:A:929:A:OP2	11:A:931:C:N4	2.43	0.52
11:A:961:U:H5''	25:O:71:ILE:HD13	1.91	0.52
11:A:1002:G:H2'	11:A:1003:A:H5'	1.92	0.52
11:A:1320:U:C3'	12:B:101:ARG:NH2	2.56	0.52
11:A:1324:G:H5''	12:B:113:ARG:NH2	2.25	0.52
11:A:1474:G:H2'	11:A:1475:A:H8	1.72	0.52
11:A:1676:U:O2'	11:A:1677:C:H5'	2.09	0.52
15:E:67:GLN:HA	15:E:70:ASP:HB2	1.92	0.52
29:S:29:SER:OG	29:S:31:GLU:HG3	2.10	0.52
5:4:133:TYR:CD1	5:4:181:LEU:HD11	2.44	0.52
11:A:256:A:H2'	11:A:257:A:O4'	2.09	0.52
11:A:487:G:H3'	11:A:488:G:H5''	1.92	0.52
11:A:500:C:HO2'	38:b:487:SER:CB	2.16	0.52
11:A:1334:U:H2'	11:A:1335:U:C6	2.45	0.52
12:B:73:VAL:O	12:B:95:ALA:HA	2.09	0.52
13:C:179:GLN:NE2	13:C:179:GLN:C	2.68	0.52
15:E:89:GLN:OE1	15:E:94:GLN:NE2	2.41	0.52
22:L:6:PRO:HG3	22:L:14:LYS:HG2	1.91	0.52
22:L:107:PHE:CE2	22:L:114:LYS:HB2	2.44	0.52
24:N:21:CYS:SG	24:N:23:VAL:HB	2.50	0.52
27:Q:93:TYR:HB2	27:Q:100:TYR:CE2	2.45	0.52
28:R:167:VAL:HG12	28:R:183:LEU:HB2	1.92	0.52
2:1:50:GLU:O	2:1:51:ASN:HB2	2.10	0.52
3:2:117:TYR:CD1	3:2:150:ALA:HB2	2.44	0.52
11:A:555:A:C8	11:A:555:A:H3'	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:710:U:H2'	11:A:711:U:H5'	1.91	0.52
11:A:872:G:H2'	11:A:873:U:O4'	2.09	0.52
11:A:1039:A:H5''	36:Z:62:ARG:NH2	2.24	0.52
11:A:1532:U:O3'	23:M:27:LYS:NZ	2.42	0.52
30:T:52:GLY:C	30:T:54:PHE:H	2.15	0.52
31:U:52:LEU:HD13	31:U:85:LYS:NZ	2.25	0.52
10:9:143:LYS:HA	11:A:1253:U:O2'	2.10	0.51
11:A:577:G:H3'	11:A:577:G:C8	2.45	0.51
11:A:647:G:H22	11:A:687:G:N2	2.09	0.51
14:D:104:PHE:O	14:D:147:MET:HE1	2.10	0.51
14:D:105:LEU:O	14:D:108:ARG:HG3	2.09	0.51
15:E:173:PRO:O	15:E:176:SER:OG	2.27	0.51
19:I:7:VAL:HG22	19:I:22:VAL:HB	1.92	0.51
20:J:117:VAL:HG22	20:J:118:VAL:H	1.75	0.51
27:Q:55:ASP:OD2	27:Q:110:HIS:HE1	1.92	0.51
28:R:295:SER:HB2	28:R:300:THR:HB	1.92	0.51
35:Y:67:VAL:O	35:Y:68:LEU:HB2	2.10	0.51
1:0:46:ARG:CD	34:X:3:LYS:NZ	2.55	0.51
11:A:55:A:OP1	26:P:112:LYS:NZ	2.43	0.51
11:A:56:U:H4'	11:A:57:G:H5'	1.92	0.51
11:A:144:U:O2'	11:A:145:A:H5'	2.10	0.51
11:A:497:G:O2'	11:A:498:G:O4'	2.29	0.51
11:A:1081:A:H4'	11:A:1082:C:O5'	2.10	0.51
13:C:3:ALA:O	13:C:4:LEU:HB2	2.09	0.51
28:R:154:VAL:HG12	28:R:171:SER:HB3	1.93	0.51
30:T:118:PRO:C	30:T:120:GLY:H	2.18	0.51
32:V:13:SER:HA	32:V:54:THR:HG22	1.92	0.51
35:Y:57:ASP:OD2	35:Y:72:ARG:NH1	2.43	0.51
35:Y:139:ASN:HA	35:Y:142:ARG:HB2	1.91	0.51
39:c:304:PHE:CD1	39:c:375:ARG:HG2	2.46	0.51
5:4:186:SER:O	5:4:190:PRO:HD2	2.10	0.51
6:5:10:ARG:HB2	6:5:34:LYS:HG3	1.91	0.51
6:5:22:ARG:HH12	21:K:127:ARG:HG3	1.75	0.51
11:A:501:U:HO2'	11:A:502:U:H6	1.59	0.51
11:A:1061:A:C1'	39:c:594:ASN:N	2.72	0.51
11:A:1502:G:O6	30:T:102:ARG:NH2	2.44	0.51
11:A:1513:G:O2'	11:A:1515:A:N3	2.38	0.51
12:B:74:VAL:HG22	12:B:96:THR:HG23	1.91	0.51
16:F:28:ILE:HD11	16:F:92:MET:CE	2.39	0.51
20:J:106:ILE:C	20:J:108:ILE:H	2.19	0.51
22:L:23:ARG:HA	22:L:26:GLU:OE2	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:U:31:VAL:HG21	31:U:136:ILE:HD13	1.92	0.51
38:b:268:LYS:NZ	38:b:307:ASN:OD1	2.33	0.51
39:c:593:SER:HA	39:c:594:ASN:C	2.36	0.51
5:4:71:ALA:C	5:4:73:LEU:H	2.19	0.51
11:A:523:G:H5''	26:P:59:GLY:O	2.10	0.51
11:A:542:A:O2'	11:A:543:C:P	2.67	0.51
11:A:912:U:H4'	11:A:913:G:O5'	2.10	0.51
11:A:927:C:H2'	11:A:928:U:C6	2.46	0.51
15:E:40:LYS:HA	15:E:43:ARG:NH1	2.25	0.51
16:F:98:LEU:HD23	16:F:103:ILE:HG12	1.93	0.51
19:I:106:LYS:O	19:I:110:THR:HB	2.10	0.51
30:T:137:ALA:O	30:T:141:GLU:HG2	2.10	0.51
38:b:555:THR:O	38:b:556:LYS:HB3	2.09	0.51
3:2:33:PRO:HA	11:A:331:A:H5'	1.92	0.51
4:3:10:SER:HB3	4:3:43:PHE:O	2.11	0.51
11:A:229:U:H2'	11:A:230:C:C6	2.46	0.51
11:A:647:G:H1	11:A:687:G:H1	1.58	0.51
11:A:779:U:OP2	11:A:780:A:H2	1.93	0.51
11:A:902:G:H8	11:A:902:G:O5'	1.93	0.51
11:A:1410:A:H5''	19:I:118:ILE:HD13	1.91	0.51
11:A:1572:G:H1'	17:G:185:ARG:HH22	1.74	0.51
12:B:27:ARG:HG2	12:B:28:ASN:H	1.75	0.51
16:F:54:ILE:HA	16:F:57:VAL:HG12	1.92	0.51
18:H:89:TRP:O	18:H:93:LEU:HD22	2.11	0.51
19:I:114:ARG:O	19:I:115:THR:OG1	2.26	0.51
20:J:102:ARG:O	20:J:106:ILE:HG22	2.10	0.51
32:V:21:TYR:HA	32:V:58:MET:HE1	1.92	0.51
39:c:343:GLU:OE2	39:c:420:LYS:HE3	2.11	0.51
5:4:104:ASP:OD1	5:4:214:LYS:NZ	2.43	0.51
11:A:651:G:C2	11:A:684:A:C6	2.98	0.51
11:A:1229:G:H1	31:U:47:GLU:HG3	1.75	0.51
11:A:1267:G:H21	11:A:1448:G:C5'	2.22	0.51
11:A:1300:A:H5''	15:E:117:THR:CB	2.41	0.51
11:A:1433:G:C8	24:N:41:GLN:HG2	2.46	0.51
12:B:163:ASN:C	12:B:165:ARG:H	2.19	0.51
15:E:234:PRO:O	15:E:235:LEU:HB2	2.09	0.51
11:A:458:G:OP2	26:P:105:ARG:NH2	2.43	0.51
11:A:677:G:H2'	11:A:678:A:H8	1.73	0.51
11:A:868:G:H1	11:A:960:U:H3	1.59	0.51
11:A:1151:A:N3	11:A:1152:A:C8	2.71	0.51
2:1:26:THR:H	2:1:44:VAL:HG22	1.76	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:1686:C:C6	11:A:1687:U:C5	2.99	0.51
12:B:33:GLN:C	12:B:34:GLU:HG2	2.36	0.51
13:C:105:MET:HG2	13:C:122:VAL:HG21	1.92	0.51
17:G:205:SER:O	17:G:207:THR:N	2.43	0.51
29:S:87:PRO:HD3	29:S:112:LEU:HD22	1.92	0.51
9:8:50:ILE:O	9:8:54:VAL:HG23	2.11	0.51
12:B:59:LEU:HD11	36:Z:79:LEU:HD11	1.91	0.51
21:K:25:ASP:N	21:K:55:SER:HB3	2.26	0.51
24:N:10:HIS:CG	24:N:11:PRO:HD2	2.46	0.51
39:c:531:ASN:O	39:c:535:PHE:HD1	1.92	0.51
39:c:705:ASN:OD1	39:c:705:ASN:N	2.38	0.51
39:c:784:ILE:HA	39:c:787:LEU:HD12	1.93	0.51
3:2:76:THR:CG2	3:2:108:PRO:HG2	2.41	0.51
4:3:131:PHE:O	4:3:133:THR:OG1	2.27	0.51
8:7:55:VAL:HA	8:7:69:THR:HG23	1.93	0.51
10:9:138:ARG:NH2	11:A:1235:C:H2'	2.26	0.51
11:A:498:G:HO2'	11:A:499:U:P	2.33	0.51
11:A:542:A:H5''	11:A:544:A:N7	2.25	0.51
11:A:859:A:C6	25:O:73:ARG:HD3	2.46	0.51
11:A:1458:G:H2'	11:A:1458:G:N3	2.26	0.51
14:D:106:GLU:OE2	14:D:115:LYS:HE2	2.11	0.51
14:D:117:GLY:C	14:D:119:ALA:H	2.17	0.51
17:G:69:PHE:HD2	19:I:50:GLU:HG2	1.75	0.51
20:J:22:ILE:HD12	20:J:118:VAL:HA	1.93	0.51
39:c:546:VAL:O	39:c:550:LEU:HD23	2.11	0.51
5:4:119:THR:HB	5:4:143:THR:HG23	1.92	0.50
5:4:124:ASN:N	5:4:124:ASN:OD1	2.43	0.50
9:8:55:PRO:C	9:8:57:TYR:H	2.19	0.50
11:A:279:G:H3'	11:A:279:G:H8	1.75	0.50
11:A:882:U:H2'	11:A:883:C:C6	2.46	0.50
11:A:1381:U:H4'	20:J:59:PRO:HG3	1.93	0.50
14:D:38:ASN:HB3	14:D:40:LYS:H	1.75	0.50
15:E:178:ILE:HB	15:E:185:LYS:HG3	1.93	0.50
23:M:27:LYS:O	23:M:29:VAL:N	2.44	0.50
30:T:40:SER:OG	30:T:96:ALA:HA	2.11	0.50
11:A:446:A:N6	11:A:461:G:H21	2.08	0.50
11:A:503:G:O2'	11:A:504:U:OP1	2.27	0.50
11:A:1300:A:H5'	15:E:99:LYS:NZ	2.26	0.50
30:T:113:ILE:O	30:T:124:ILE:HD12	2.11	0.50
37:a:347:PRO:HB2	39:c:663:SER:N	2.24	0.50
37:a:482:ILE:HG21	39:c:733:TYR:CE1	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:8:71:ILE:HB	9:8:76:ALA:HB2	1.92	0.50
11:A:320:U:H3'	11:A:321:C:H5''	1.94	0.50
11:A:425:A:H5'	11:A:425:A:C8	2.46	0.50
11:A:713:A:H61	11:A:725:U:H3	1.58	0.50
11:A:1298:U:H1'	15:E:162:CYS:SG	2.51	0.50
11:A:1472:C:OP1	17:G:102:ARG:NH2	2.43	0.50
26:P:31:ASN:O	26:P:32:ARG:HB2	2.11	0.50
32:V:24:LEU:HD13	32:V:58:MET:HE3	1.93	0.50
1:0:60:HIS:CE1	1:0:66:ARG:HH21	2.29	0.50
2:1:15:VAL:HA	2:1:28:VAL:HG22	1.92	0.50
3:2:8:ARG:C	3:2:9:HIS:O	2.53	0.50
7:6:34:ASP:N	7:6:34:ASP:OD1	2.43	0.50
11:A:220:A:H5''	11:A:832:U:H1'	1.93	0.50
11:A:393:C:H4'	11:A:1673:G:O2'	2.12	0.50
11:A:478:A:OP1	34:X:37:ARG:NH1	2.44	0.50
11:A:1572:G:H8	17:G:185:ARG:HH12	1.60	0.50
20:J:51:VAL:HG13	20:J:94:GLU:HB2	1.92	0.50
35:Y:28:PHE:CE2	35:Y:104:PRO:HG3	2.46	0.50
36:Z:71:ARG:HG3	36:Z:83:TRP:CH2	2.46	0.50
1:0:65:LEU:HD11	1:0:93:HIS:HA	1.93	0.50
1:0:92:VAL:HG22	1:0:93:HIS:CD2	2.46	0.50
11:A:734:A:O2'	11:A:735:C:H5'	2.11	0.50
11:A:1410:A:H2'	11:A:1411:A:O4'	2.11	0.50
28:R:29:GLN:HG3	28:R:32:LEU:HB2	1.93	0.50
32:V:82:ASP:O	32:V:83:GLN:HB2	2.12	0.50
4:3:23:ALA:O	4:3:27:LEU:HG	2.12	0.50
5:4:184:LEU:O	5:4:188:LEU:HG	2.12	0.50
10:9:135:HIS:HB2	10:9:138:ARG:HB3	1.93	0.50
11:A:336:G:H5'	27:Q:130:PRO:O	2.11	0.50
11:A:1295:G:H5''	12:B:108:THR:CB	2.41	0.50
11:A:1686:C:O2'	11:A:1687:U:O5'	2.30	0.50
14:D:120:LYS:O	14:D:121:SER:HB2	2.12	0.50
15:E:140:ARG:NH2	15:E:226:THR:HG23	2.27	0.50
17:G:43:PHE:HA	17:G:68:ILE:O	2.11	0.50
20:J:20:ILE:HG13	20:J:95:ALA:O	2.11	0.50
32:V:106:THR:O	32:V:109:LEU:HB3	2.10	0.50
3:2:29:LEU:HD23	3:2:29:LEU:C	2.36	0.50
4:3:28:GLU:O	4:3:35:LYS:HB2	2.12	0.50
5:4:126:THR:HG22	5:4:136:ARG:HE	1.76	0.50
11:A:279:G:C3'	11:A:280:U:H5''	2.28	0.50
11:A:818:C:N4	11:A:819:G:C6	2.80	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:1325:A:OP2	32:V:11:ARG:NH1	2.45	0.50
11:A:1686:C:C2'	11:A:1687:U:C6	2.79	0.50
11:A:1716:C:O2'	11:A:1717:G:O5'	2.30	0.50
12:B:41:ARG:HA	32:V:105:GLN:HG2	1.86	0.50
13:C:33:GLY:O	13:C:53:THR:HG23	2.12	0.50
15:E:106:ASP:OD1	15:E:106:ASP:N	2.44	0.50
15:E:139:ILE:CD1	15:E:191:ALA:HB1	2.42	0.50
17:G:145:ASP:CG	17:G:146:THR:H	2.17	0.50
23:M:119:ILE:HD11	29:S:110:GLU:HG3	1.93	0.50
25:O:54:LEU:HB3	25:O:60:VAL:CG2	2.40	0.50
31:U:123:VAL:HG11	31:U:126:TRP:HB3	1.94	0.50
39:c:369:ILE:HA	39:c:372:PHE:HD2	1.77	0.50
39:c:640:ILE:HG13	39:c:730:LYS:HE3	1.93	0.50
1:0:82:ARG:NE	22:L:68:ILE:HD13	2.25	0.50
9:8:46:LYS:HE2	9:8:70:LYS:HD2	1.94	0.50
11:A:498:G:H2'	11:A:499:U:C5	2.47	0.50
11:A:789:A:O2'	33:W:106:LYS:NZ	2.43	0.50
11:A:1365:C:H5''	19:I:28:LEU:HD23	1.94	0.50
15:E:148:LEU:O	36:Z:4:ASP:HB2	2.12	0.50
23:M:88:ARG:NH2	23:M:112:ASP:OD1	2.44	0.50
27:Q:72:THR:O	27:Q:88:ARG:HD2	2.11	0.50
39:c:304:PHE:CG	39:c:375:ARG:HG2	2.47	0.50
1:0:33:GLN:NE2	1:0:78:LEU:HD21	2.27	0.50
4:3:99:LEU:HD12	4:3:116:ARG:HG2	1.92	0.50
11:A:533:U:C4'	26:P:33:ALA:HB2	2.39	0.50
11:A:606:A:H4'	11:A:607:G:H5''	1.94	0.50
11:A:707:A:H2'	11:A:708:C:H5''	1.93	0.50
12:B:84:ARG:HH21	32:V:82:ASP:CG	2.20	0.50
16:F:31:GLN:HG2	16:F:39:LEU:HB3	1.92	0.50
27:Q:6:THR:HB	27:Q:9:SER:HB3	1.92	0.50
39:c:642:VAL:HG21	39:c:763:LEU:HA	1.94	0.50
3:2:26:LYS:O	3:2:26:LYS:HG3	2.12	0.49
11:A:1132:A:OP1	22:L:30:LYS:HE3	2.12	0.49
11:A:1433:G:H22	24:N:45:GLU:CD	2.20	0.49
12:B:29:VAL:HG13	12:B:150:ASP:HB3	1.93	0.49
12:B:136:ALA:HB1	12:B:141:ILE:HB	1.94	0.49
12:B:185:ARG:N	36:Z:45:ALA:H	2.09	0.49
13:C:192:PRO:O	13:C:195:SER:HB2	2.11	0.49
14:D:93:LEU:HA	14:D:96:VAL:CG1	2.38	0.49
20:J:106:ILE:HD12	20:J:108:ILE:HD11	1.93	0.49
29:S:22:LEU:HD21	29:S:109:PRO:HB3	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:T:31:PRO:HG3	30:T:103:LYS:HG2	1.94	0.49
31:U:29:LYS:HE2	31:U:100:TRP:NE1	2.27	0.49
33:W:15:PRO:HG2	33:W:18:TRP:CE2	2.46	0.49
37:a:347:PRO:O	39:c:663:SER:HB3	2.11	0.49
37:a:348:HIS:HD2	39:c:663:SER:HB3	1.76	0.49
4:3:35:LYS:HZ2	4:3:39:ARG:HD2	1.76	0.49
4:3:167:GLU:HG3	4:3:170:GLN:OE1	2.12	0.49
8:7:19:GLY:HA2	8:7:68:LEU:HD23	1.93	0.49
9:8:37:GLN:O	9:8:38:HIS:HB3	2.10	0.49
11:A:1049:U:H2'	11:A:1050:G:C8	2.47	0.49
11:A:1324:G:C5'	12:B:113:ARG:NH2	2.75	0.49
13:C:20:GLU:OE2	13:C:76:ARG:NH2	2.44	0.49
29:S:85:ILE:HD11	29:S:116:LEU:HD23	1.93	0.49
37:a:303:TRP:CZ2	37:a:327:THR:HG21	2.48	0.49
5:4:185:THR:O	5:4:189:ILE:HG13	2.12	0.49
10:9:120:GLU:HG3	10:9:128:ALA:HB1	1.94	0.49
11:A:539:G:H8	11:A:539:G:OP2	1.93	0.49
11:A:765:G:C6	14:D:149:ARG:HB3	2.48	0.49
11:A:1168:U:C2'	11:A:1169:G:H5'	2.41	0.49
18:H:82:LYS:HB2	18:H:85:ASP:OD2	2.12	0.49
19:I:25:GLY:H	19:I:63:ILE:HA	1.76	0.49
19:I:73:GLY:H	19:I:76:SER:HB3	1.76	0.49
19:I:112:TYR:OH	19:I:114:ARG:NH2	2.45	0.49
37:a:484:HIS:N	39:c:735:SER:HB2	2.27	0.49
5:4:62:LYS:HD2	5:4:91:VAL:HB	1.94	0.49
5:4:86:LEU:HB3	5:4:98:THR:OG1	2.11	0.49
5:4:105:PHE:H	5:4:214:LYS:HZ1	1.61	0.49
6:5:85:ARG:O	6:5:86:VAL:HB	2.12	0.49
11:A:190:C:H1'	11:A:191:C:H5'	1.93	0.49
11:A:489:C:H2'	11:A:490:C:C6	2.48	0.49
11:A:749:U:H3	11:A:800:U:H3	1.58	0.49
11:A:881:A:H2'	11:A:882:U:O4'	2.13	0.49
11:A:1622:G:H2'	11:A:1623:C:C6	2.47	0.49
14:D:95:TYR:O	14:D:99:LEU:N	2.45	0.49
17:G:129:PRO:O	17:G:133:VAL:HG23	2.13	0.49
23:M:11:PHE:CD1	23:M:11:PHE:C	2.90	0.49
37:a:264:PHE:CG	37:a:354:LEU:HG	2.47	0.49
37:a:429:MET:SD	37:a:460:LEU:HD12	2.52	0.49
38:b:660:VAL:CG2	38:b:661:GLU:H	2.25	0.49
3:2:138:ASN:OD1	3:2:138:ASN:N	2.42	0.49
5:4:56:SER:OG	5:4:59:ASP:OD1	2.29	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:4:61:LEU:HG	5:4:64:ARG:HH21	1.77	0.49
5:4:125:VAL:HG21	5:4:173:THR:HG22	1.94	0.49
6:5:23:CYS:SG	6:5:74:CYS:HB3	2.52	0.49
7:6:54:VAL:O	7:6:63:LEU:HB2	2.13	0.49
8:7:53:GLY:O	8:7:55:VAL:N	2.39	0.49
11:A:194:U:O2'	11:A:195:G:O4'	2.30	0.49
11:A:501:U:H4'	11:A:502:U:OP1	2.11	0.49
11:A:929:A:N6	11:A:930:A:C6	2.80	0.49
11:A:1459:C:O2	29:S:128:HIS:NE2	2.38	0.49
12:B:119:ARG:HD2	15:E:241:ASP:OD1	2.12	0.49
16:F:27:HIS:HB2	16:F:43:GLN:CG	2.42	0.49
17:G:24:VAL:HG22	17:G:25:LEU:H	1.78	0.49
20:J:104:THR:HG21	20:J:116:VAL:HG21	1.93	0.49
27:Q:97:TYR:O	27:Q:99:ARG:HG2	2.12	0.49
3:2:98:LYS:HB3	11:A:329:G:H5''	1.95	0.49
8:7:77:ARG:HD3	8:7:84:GLU:HA	1.94	0.49
11:A:498:G:C4	11:A:499:U:N3	2.81	0.49
11:A:879:G:O2'	25:O:105:ASN:HB3	2.13	0.49
11:A:1244:A:O2'	11:A:1245:G:OP1	2.29	0.49
11:A:1729:C:H5''	11:A:1730:A:OP2	2.13	0.49
19:I:16:ALA:HB2	19:I:72:GLY:HA3	1.94	0.49
21:K:124:ASP:O	21:K:125:SER:HB2	2.13	0.49
22:L:97:ASP:HB2	22:L:100:ASP:OD2	2.12	0.49
28:R:156:VAL:HG22	28:R:169:ILE:HG22	1.95	0.49
31:U:60:VAL:HG13	31:U:122:VAL:HG22	1.93	0.49
37:a:264:PHE:CD2	37:a:354:LEU:HG	2.48	0.49
37:a:290:PHE:HA	37:a:293:SER:HB2	1.94	0.49
39:c:653:ARG:HA	39:c:656:LEU:HD12	1.94	0.49
1:0:44:ASN:HB3	1:0:46:ARG:NH1	2.28	0.49
1:0:71:MET:HE1	1:0:94:LYS:HB2	1.95	0.49
4:3:158:ASP:O	4:3:160:GLN:N	2.46	0.49
5:4:81:PHE:HA	5:4:106:THR:HG23	1.93	0.49
11:A:778:G:H22	26:P:10:ARG:CZ	2.26	0.49
11:A:1300:A:H4'	15:E:86:VAL:CG1	2.42	0.49
11:A:1482:C:OP2	11:A:1521:G:N2	2.46	0.49
11:A:1553:G:N2	11:A:1555:A:H3'	2.28	0.49
12:B:40:ALA:O	32:V:105:GLN:HG3	2.12	0.49
15:E:183:ALA:HB1	15:E:211:LEU:HD21	1.95	0.49
23:M:24:GLY:O	23:M:26:ILE:N	2.45	0.49
29:S:81:ARG:HH12	29:S:120:SER:HB3	1.78	0.49
30:T:53:TRP:HA	30:T:56:LYS:HB2	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:T:63:ARG:HD2	30:T:67:MET:HE1	1.95	0.49
33:W:163:ASP:O	33:W:164:LEU:HB2	2.11	0.49
39:c:293:ILE:HG22	39:c:294:MET:HE2	1.95	0.49
5:4:109:LYS:HD2	5:4:113:MET:HG3	1.94	0.49
6:5:79:ILE:HA	6:5:84:VAL:HG21	1.94	0.49
8:7:49:LEU:HB3	8:7:55:VAL:CG1	2.42	0.49
11:A:1152:A:C5	11:A:1627:U:N3	2.81	0.49
11:A:1294:G:O2'	12:B:108:THR:OG1	2.29	0.49
11:A:1686:C:O2'	11:A:1687:U:O4'	2.30	0.49
12:B:200:ASP:HB2	32:V:85:VAL:CG2	2.42	0.49
17:G:21:THR:O	17:G:21:THR:OG1	2.31	0.49
18:H:36:LYS:O	18:H:40:VAL:HG23	2.13	0.49
21:K:25:ASP:HA	21:K:54:GLU:O	2.12	0.49
23:M:91:ASP:HB3	23:M:95:GLY:H	1.77	0.49
31:U:33:ARG:O	31:U:37:VAL:HG23	2.13	0.49
35:Y:126:ASP:OD1	35:Y:127:THR:HG22	2.13	0.49
37:a:482:ILE:HG23	39:c:733:TYR:HA	1.94	0.49
39:c:555:PHE:HB2	39:c:563:CYS:SG	2.53	0.49
5:4:61:LEU:HD13	5:4:61:LEU:H	1.77	0.49
5:4:70:LEU:HD11	5:4:79:HIS:HB3	1.95	0.49
6:5:37:LYS:C	6:5:38:ARG:HD2	2.38	0.49
6:5:84:VAL:HG13	6:5:85:ARG:H	1.78	0.49
8:7:80:LEU:O	8:7:82:LEU:N	2.41	0.49
10:9:138:ARG:HH22	11:A:1236:A:C1'	2.26	0.49
11:A:70:C:H2'	11:A:71:A:O4'	2.12	0.49
11:A:393:C:H2'	11:A:394:C:C6	2.48	0.49
11:A:1321:A:O4'	12:B:104:PRO:HG2	2.13	0.49
18:H:77:PRO:HD2	18:H:79:PHE:CE1	2.47	0.49
37:a:347:PRO:HG2	39:c:663:SER:O	2.12	0.49
1:0:88:GLN:NE2	34:X:4:VAL:H	2.11	0.49
11:A:778:G:H22	26:P:10:ARG:HH22	1.57	0.49
11:A:823:G:O2'	11:A:824:G:O5'	2.24	0.49
11:A:1253:U:H2'	11:A:1254:U:C6	2.48	0.49
17:G:120:ILE:O	17:G:124:LEU:HD12	2.13	0.49
18:H:55:ASP:C	18:H:57:ARG:H	2.20	0.49
25:O:22:ALA:HB1	25:O:23:PRO:C	2.38	0.49
28:R:153:GLN:HG2	28:R:202:LEU:HD23	1.95	0.49
36:Z:40:ASP:HB3	36:Z:46:ILE:HD11	1.94	0.49
5:4:22:ASP:O	5:4:24:PHE:N	2.46	0.48
5:4:77:GLU:C	5:4:79:HIS:H	2.21	0.48
10:9:87:UNK:O	10:9:87:UNK:HG2	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:484:C:N4	11:A:503:G:H22	2.05	0.48
11:A:702:G:O6	11:A:737:A:N6	2.45	0.48
11:A:1156:C:C2'	11:A:1157:A:H5'	2.43	0.48
11:A:1437:U:H5'	13:C:176:LEU:HD23	1.95	0.48
21:K:122:PRO:C	21:K:124:ASP:N	2.71	0.48
23:M:22:VAL:CG1	23:M:31:ALA:HB1	2.42	0.48
26:P:15:ASN:OD1	26:P:17:LEU:HD12	2.12	0.48
28:R:130:THR:HG22	28:R:145:LEU:HD22	1.94	0.48
30:T:52:GLY:HA2	30:T:55:TYR:CD2	2.48	0.48
9:8:40:VAL:C	9:8:75:LEU:HD11	2.38	0.48
11:A:196:G:O2'	11:A:197:A:C8	2.66	0.48
11:A:346:G:O2'	27:Q:80:MET:HG2	2.13	0.48
11:A:487:G:H3'	11:A:488:G:C5'	2.43	0.48
11:A:494:U:HO2'	11:A:495:C:P	2.32	0.48
11:A:717:C:H42	11:A:720:G:N2	2.09	0.48
11:A:1059:U:C5'	37:a:66:LYS:NZ	2.76	0.48
11:A:1686:C:C5	11:A:1687:U:C5	3.01	0.48
17:G:59:VAL:O	17:G:60:ASP:HB2	2.12	0.48
17:G:133:VAL:O	17:G:137:ILE:HG12	2.13	0.48
25:O:27:LYS:H	25:O:27:LYS:CE	2.26	0.48
28:R:123:ILE:HG22	28:R:133:VAL:HG22	1.95	0.48
31:U:132:GLU:O	31:U:136:ILE:HG12	2.13	0.48
39:c:377:ASP:O	39:c:380:PHE:HB3	2.13	0.48
3:2:8:ARG:NH1	3:2:21:PHE:HB3	2.28	0.48
5:4:61:LEU:O	5:4:63:GLY:N	2.47	0.48
5:4:146:GLN:H	5:4:149:GLN:NE2	2.11	0.48
11:A:358:U:O2'	11:A:360:A:H5''	2.13	0.48
11:A:694:U:H2'	11:A:695:U:H5	1.78	0.48
11:A:730:G:H21	11:A:731:C:H5''	1.78	0.48
12:B:41:ARG:HA	32:V:105:GLN:HE21	1.77	0.48
12:B:120:LEU:HD13	12:B:142:PRO:HB2	1.94	0.48
13:C:116:ARG:O	13:C:120:TYR:HB2	2.12	0.48
21:K:16:VAL:HG22	21:K:33:LEU:HA	1.95	0.48
23:M:32:LEU:O	23:M:38:VAL:HG21	2.13	0.48
28:R:40:LYS:HG2	28:R:66:HIS:O	2.14	0.48
29:S:15:HIS:O	29:S:21:ASP:HA	2.12	0.48
37:a:34:PHE:CD2	37:a:51:VAL:HG11	2.48	0.48
38:b:368:TRP:CE3	38:b:375:CYS:HB3	2.48	0.48
11:A:130:C:O2'	11:A:131:C:OP1	2.29	0.48
11:A:209:U:H2'	11:A:210:A:C8	2.49	0.48
14:D:122:VAL:O	14:D:125:ALA:HB3	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:42:LEU:HD11	1:0:58:MET:CE	2.44	0.48
3:2:96:LEU:HD13	3:2:179:CYS:SG	2.53	0.48
3:2:197:THR:HA	3:2:200:LYS:HB2	1.96	0.48
6:5:36:ILE:HG23	6:5:73:TYR:HB2	1.95	0.48
11:A:279:G:H3'	11:A:279:G:C8	2.48	0.48
11:A:680:U:H2'	11:A:681:U:C6	2.49	0.48
11:A:1133:A:OP1	22:L:31:LYS:HE2	2.13	0.48
13:C:92:GLN:O	13:C:92:GLN:NE2	2.46	0.48
29:S:86:VAL:HG23	29:S:87:PRO:HD2	1.96	0.48
31:U:29:LYS:HE2	31:U:100:TRP:HE1	1.78	0.48
6:5:7:SER:HB2	6:5:11:ASN:H	1.78	0.48
9:8:70:LYS:HA	9:8:70:LYS:HD3	1.69	0.48
11:A:1202:A:H61	11:A:1457:C:H5''	1.76	0.48
11:A:1639:C:O2	11:A:1763:A:N1	2.46	0.48
17:G:205:SER:O	17:G:205:SER:OG	2.25	0.48
23:M:35:ILE:HB	23:M:38:VAL:HG21	1.96	0.48
32:V:13:SER:OG	32:V:54:THR:HG22	2.14	0.48
35:Y:45:PHE:HA	35:Y:48:TYR:HD2	1.79	0.48
37:a:59:GLY:HA3	37:a:68:LEU:HD21	1.96	0.48
37:a:482:ILE:CD1	39:c:733:TYR:HE1	2.22	0.48
39:c:332:LEU:HB3	39:c:414:TYR:CE1	2.49	0.48
10:9:144:CYS:O	10:9:146:SER:N	2.47	0.48
11:A:190:C:O2'	11:A:191:C:H5'	2.14	0.48
11:A:768:C:C6	14:D:143:ILE:HD13	2.49	0.48
11:A:782:U:H4'	11:A:783:G:OP2	2.14	0.48
11:A:1300:A:O3'	15:E:86:VAL:CG2	2.55	0.48
11:A:1746:A:H2'	11:A:1747:G:O4'	2.13	0.48
22:L:127:VAL:O	22:L:130:VAL:HG22	2.14	0.48
27:Q:22:ASN:OD1	27:Q:24:LYS:HB2	2.14	0.48
28:R:112:SER:CB	28:R:153:GLN:HA	2.43	0.48
35:Y:141:ILE:HG21	35:Y:153:VAL:HG13	1.94	0.48
37:a:284:GLU:O	37:a:287:VAL:HG22	2.13	0.48
38:b:556:LYS:HG3	38:b:559:THR:CG2	2.44	0.48
5:4:157:GLN:NE2	11:A:1046:G:OP1	2.46	0.48
11:A:287:G:O2'	11:A:288:A:OP2	2.24	0.48
11:A:350:U:O2	11:A:352:A:C6	2.66	0.48
11:A:507:U:O2	11:A:507:U:H3'	2.13	0.48
11:A:545:A:H4'	11:A:546:U:OP1	2.14	0.48
11:A:772:G:OP1	33:W:22:LYS:NZ	2.29	0.48
11:A:794:U:O2'	11:A:795:U:O2	2.27	0.48
11:A:812:A:OP1	11:A:858:G:N2	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:992:A:O2'	11:A:1785:U:O2	2.31	0.48
11:A:1244:A:H3'	11:A:1244:A:N3	2.29	0.48
12:B:184:LEU:HB3	36:Z:45:ALA:HB2	1.96	0.48
20:J:48:HIS:O	20:J:48:HIS:CG	2.67	0.48
23:M:93:THR:O	29:S:19:GLY:N	2.47	0.48
39:c:671:LEU:HD12	39:c:672:ARG:N	2.28	0.48
1:0:26:LEU:CD1	1:0:102:THR:HG21	2.44	0.48
7:6:61:THR:HG23	7:6:62:ILE:H	1.79	0.48
8:7:12:HIS:CD2	8:7:79:TYR:CD2	3.02	0.48
11:A:114:C:H5'	11:A:114:C:C6	2.49	0.48
11:A:143:G:C2'	11:A:144:U:H5''	2.44	0.48
11:A:495:C:H3'	11:A:496:G:C4'	2.43	0.48
11:A:558:U:O2	11:A:558:U:H2'	2.14	0.48
11:A:823:G:H2'	11:A:824:G:O4'	2.14	0.48
11:A:1196:A:H1'	11:A:1602:C:O2'	2.13	0.48
11:A:1316:G:O2'	11:A:1401:A:O2'	2.25	0.48
11:A:1347:U:O2	11:A:1516:A:H5'	2.14	0.48
11:A:1486:G:H1'	11:A:1592:A:O2'	2.14	0.48
12:B:35:PRO:C	12:B:37:VAL:H	2.22	0.48
19:I:94:GLN:HB2	19:I:102:LYS:HD2	1.96	0.48
23:M:36:LYS:HB3	23:M:105:VAL:HG11	1.96	0.48
30:T:33:TYR:HD1	30:T:33:TYR:C	2.21	0.48
37:a:169:LEU:HB3	37:a:179:TYR:HB2	1.95	0.48
38:b:556:LYS:CD	38:b:557:GLU:N	2.73	0.48
39:c:397:ARG:HA	39:c:397:ARG:HD2	1.55	0.48
1:0:46:ARG:HE	34:X:3:LYS:CB	2.26	0.48
6:5:19:LYS:HG3	6:5:20:PRO:HD2	1.96	0.48
10:9:143:LYS:HB2	11:A:1253:U:H4'	1.96	0.48
10:9:147:VAL:O	10:9:148:TYR:HB2	2.14	0.48
14:D:91:LYS:O	14:D:92:LYS:HG2	2.13	0.48
15:E:139:ILE:HD11	15:E:191:ALA:HB1	1.96	0.48
17:G:172:ILE:O	17:G:176:THR:HG23	2.14	0.48
19:I:112:TYR:CZ	19:I:114:ARG:NH2	2.82	0.48
20:J:58:LEU:HD12	20:J:88:LYS:C	2.38	0.48
26:P:59:GLY:O	26:P:60:PHE:HB2	2.14	0.48
36:Z:9:VAL:HG22	36:Z:10:GLU:H	1.79	0.48
37:a:292:VAL:CG1	39:c:667:PRO:HG3	2.24	0.48
37:a:347:PRO:O	39:c:663:SER:CB	2.61	0.48
37:a:470:LEU:HD23	37:a:480:ILE:HD11	1.95	0.48
37:a:482:ILE:CG2	39:c:733:TYR:CG	2.97	0.48
3:2:66:SER:HB3	3:2:73:SER:OG	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:8:92:ILE:HG12	9:8:100:ILE:CG2	2.44	0.47
11:A:192:U:O2	11:A:192:U:H2'	2.13	0.47
11:A:526:A:H2'	11:A:527:A:O4'	2.13	0.47
11:A:1597:A:C8	24:N:14:TYR:CD2	3.02	0.47
16:F:71:ASP:CG	16:F:72:PRO:HD2	2.39	0.47
18:H:105:THR:HG23	18:H:110:ILE:CG1	2.44	0.47
23:M:108:LYS:HA	23:M:108:LYS:HD2	1.63	0.47
31:U:82:PRO:O	31:U:83:GLU:HB2	2.13	0.47
34:X:53:LYS:HG3	34:X:54:ARG:H	1.78	0.47
35:Y:63:MET:HG2	35:Y:99:GLY:O	2.14	0.47
35:Y:67:VAL:HG23	35:Y:68:LEU:O	2.13	0.47
39:c:296:TYR:O	39:c:300:ILE:HG12	2.13	0.47
39:c:537:SER:O	39:c:541:ILE:HG12	2.14	0.47
39:c:577:ARG:HG2	39:c:582:GLN:O	2.13	0.47
1:0:88:GLN:HB2	34:X:6:GLY:HA2	1.97	0.47
4:3:30:SER:O	4:3:32:PRO:HD2	2.14	0.47
11:A:190:C:N4	11:A:196:G:C6	2.82	0.47
11:A:499:U:O2'	11:A:500:C:P	2.72	0.47
11:A:823:G:HO2'	11:A:824:G:P	2.34	0.47
11:A:992:A:H2	11:A:1012:U:N3	2.06	0.47
11:A:1064:G:H2'	11:A:1065:A:C8	2.49	0.47
11:A:1480:G:H3'	11:A:1481:C:C6	2.49	0.47
16:F:30:ILE:CG1	16:F:107:GLY:HA2	2.35	0.47
23:M:11:PHE:CD1	23:M:59:GLY:HA2	2.49	0.47
24:N:40:ARG:HG2	24:N:41:GLN:OE1	2.14	0.47
37:a:466:GLU:CG	39:c:733:TYR:OH	2.61	0.47
39:c:370:PHE:CZ	39:c:431:ARG:HB3	2.48	0.47
39:c:652:ILE:O	39:c:656:LEU:HG	2.14	0.47
3:2:8:ARG:HD2	3:2:21:PHE:HD1	1.79	0.47
4:3:114:ARG:C	4:3:116:ARG:H	2.22	0.47
5:4:63:GLY:HA2	5:4:88:VAL:O	2.13	0.47
6:5:44:ILE:H	6:5:44:ILE:CD1	2.24	0.47
7:6:47:PHE:CD2	25:O:55:ARG:HD2	2.49	0.47
9:8:72:GLY:O	9:8:74:SER:N	2.47	0.47
11:A:700:C:H42	11:A:738:G:H1	1.62	0.47
11:A:1321:A:C2	12:B:104:PRO:O	2.67	0.47
16:F:26:ILE:HG13	16:F:98:LEU:HD22	1.96	0.47
28:R:221:MET:HG3	28:R:233:THR:HG23	1.94	0.47
35:Y:63:MET:HE2	35:Y:106:LEU:HD22	1.96	0.47
39:c:395:LEU:O	39:c:399:ARG:HG2	2.14	0.47
5:4:61:LEU:CD2	5:4:62:LYS:H	2.28	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:4:62:LYS:O	5:4:88:VAL:HB	2.15	0.47
9:8:54:VAL:HG22	9:8:57:TYR:CE2	2.50	0.47
11:A:72:A:C3'	11:A:73:U:H5''	2.45	0.47
11:A:74:U:HO2'	11:A:75:U:P	2.33	0.47
11:A:1617:U:O2'	11:A:1618:C:H5'	2.14	0.47
12:B:124:THR:HG22	12:B:174:TRP:CZ2	2.49	0.47
13:C:46:THR:HB	13:C:84:ILE:HG12	1.96	0.47
17:G:36:ALA:HB3	17:G:45:LYS:NZ	2.29	0.47
17:G:133:VAL:HG22	17:G:198:LEU:HD13	1.96	0.47
18:H:53:ILE:HG12	18:H:60:LYS:HB2	1.96	0.47
19:I:60:PHE:HA	19:I:63:ILE:HD11	1.95	0.47
36:Z:11:LEU:H	36:Z:11:LEU:HG	1.34	0.47
39:c:405:TYR:OH	39:c:440:ILE:HD11	2.15	0.47
3:2:87:ASN:O	3:2:90:LEU:HB2	2.14	0.47
5:4:101:HIS:HD2	5:4:217:LEU:HD22	1.80	0.47
6:5:38:ARG:HH21	6:5:83:ILE:HG13	1.78	0.47
8:7:1:MET:O	11:A:1258:U:H5'	2.14	0.47
8:7:26:ASP:OD2	8:7:29:GLN:HG3	2.15	0.47
11:A:11:A:C2'	11:A:12:U:H5'	2.44	0.47
11:A:39:A:OP1	14:D:6:ARG:NH1	2.47	0.47
11:A:132:U:C1'	11:A:133:U:OP2	2.58	0.47
11:A:1152:A:N6	11:A:1627:U:O4	2.47	0.47
11:A:1277:G:O2'	13:C:174:HIS:ND1	2.39	0.47
11:A:1299:G:H4'	15:E:99:LYS:HE3	1.96	0.47
16:F:86:ALA:HA	16:F:89:CYS:SG	2.55	0.47
20:J:65:ILE:HD11	24:N:36:LEU:HD21	1.96	0.47
26:P:102:LYS:H	26:P:102:LYS:HD2	1.79	0.47
28:R:29:GLN:C	28:R:31:ASN:H	2.23	0.47
30:T:52:GLY:HA2	30:T:55:TYR:HD2	1.80	0.47
32:V:17:ILE:HG23	32:V:58:MET:HE2	1.95	0.47
39:c:516:PHE:CE1	39:c:554:ALA:HB2	2.49	0.47
39:c:632:ARG:HB3	39:c:644:ARG:HD3	1.97	0.47
1:0:24:ARG:O	1:0:25:GLU:C	2.57	0.47
4:3:16:LEU:O	4:3:20:VAL:HG23	2.14	0.47
4:3:71:HIS:CG	4:3:131:PHE:CZ	3.02	0.47
6:5:73:TYR:CZ	6:5:82:ARG:HD2	2.50	0.47
7:6:63:LEU:O	7:6:74:SER:N	2.48	0.47
9:8:50:ILE:HG22	9:8:51:LEU:HD12	1.96	0.47
10:9:127:GLY:O	10:9:129:GLY:N	2.47	0.47
11:A:1299:G:H4'	15:E:99:LYS:HE2	1.95	0.47
11:A:1349:G:N2	11:A:1350:U:C2	2.83	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:F:61:ASP:OD2	16:F:62:PHE:CD1	2.67	0.47
20:J:117:VAL:HG13	20:J:118:VAL:N	2.30	0.47
25:O:11:ILE:HG13	25:O:11:ILE:O	2.15	0.47
27:Q:104:HIS:O	27:Q:105:LYS:HG2	2.15	0.47
31:U:136:ILE:O	31:U:140:PHE:HB2	2.14	0.47
33:W:98:ASN:HD22	33:W:119:ALA:HB1	1.80	0.47
39:c:528:VAL:O	39:c:529:GLN:NE2	2.47	0.47
2:1:44:VAL:HA	17:G:161:ASP:O	2.15	0.47
5:4:30:PHE:CE1	5:4:96:LEU:HB3	2.50	0.47
5:4:179:SER:HB3	5:4:183:GLN:NE2	2.30	0.47
6:5:38:ARG:NH2	11:A:1798:U:C5	2.83	0.47
8:7:12:HIS:CD2	8:7:79:TYR:HD2	2.33	0.47
8:7:25:LYS:HD3	8:7:59:PHE:CZ	2.50	0.47
8:7:33:GLU:N	8:7:33:GLU:OE1	2.47	0.47
11:A:196:G:HO2'	11:A:197:A:H8	1.61	0.47
11:A:717:C:O2	11:A:722:G:N1	2.47	0.47
11:A:819:G:C6	11:A:853:G:N1	2.82	0.47
11:A:894:U:H2'	11:A:895:G:C8	2.49	0.47
11:A:920:U:H2'	11:A:921:U:O4'	2.15	0.47
11:A:1071:U:H2'	11:A:1072:C:H6	1.79	0.47
11:A:1321:A:C2	12:B:104:PRO:C	2.93	0.47
11:A:1366:U:O2'	30:T:7:ARG:HD2	2.14	0.47
11:A:1420:C:OP1	24:N:54:LYS:NZ	2.38	0.47
11:A:1524:A:N3	11:A:1590:G:O2'	2.44	0.47
11:A:1533:C:P	23:M:27:LYS:HZ1	2.38	0.47
11:A:1789:G:H5''	11:A:1789:G:C8	2.46	0.47
12:B:140:ASN:HD21	36:Z:29:HIS:HA	1.80	0.47
13:C:21:LEU:HD22	13:C:25:PHE:CE2	2.50	0.47
16:F:89:CYS:HA	16:F:92:MET:HE3	1.97	0.47
18:H:10:ALA:HB1	18:H:27:ILE:HD12	1.97	0.47
18:H:79:PHE:HD2	27:Q:98:ASN:HD22	1.60	0.47
23:M:109:LEU:HG	23:M:113:LEU:HD11	1.96	0.47
26:P:84:LYS:HD2	26:P:85:PHE:CE1	2.50	0.47
28:R:211:ILE:HG22	28:R:223:TRP:CD1	2.50	0.47
29:S:126:VAL:CG1	29:S:127:ARG:H	2.19	0.47
30:T:33:TYR:C	30:T:33:TYR:CD1	2.93	0.47
31:U:54:ARG:C	31:U:56:GLU:H	2.21	0.47
33:W:42:LEU:HD12	33:W:109:PHE:CB	2.45	0.47
37:a:196:LYS:HD3	37:a:252:LEU:HD21	1.96	0.47
39:c:349:ASP:N	39:c:349:ASP:OD1	2.47	0.47
1:0:85:GLN:NE2	34:X:6:GLY:C	2.66	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:4:117:TRP:NE1	5:4:152:ARG:CZ	2.77	0.47
7:6:47:PHE:CD2	7:6:49:HIS:O	2.68	0.47
7:6:56:CYS:SG	7:6:57:GLU:N	2.87	0.47
10:9:108:VAL:HG13	31:U:73:LYS:NZ	2.25	0.47
11:A:131:C:HO2'	11:A:132:U:P	2.33	0.47
11:A:538:A:C8	11:A:543:C:C4	3.03	0.47
11:A:702:G:C6	11:A:737:A:C6	3.03	0.47
11:A:823:G:H2'	11:A:824:G:C8	2.49	0.47
11:A:1152:A:C2	11:A:1627:U:C5	3.02	0.47
11:A:1351:G:C2	11:A:1375:A:C2	3.02	0.47
11:A:1477:G:H2'	11:A:1478:G:C8	2.50	0.47
12:B:52:LYS:HB3	36:Z:82:VAL:HG22	1.97	0.47
14:D:175:ARG:HD3	14:D:179:ARG:HH11	1.78	0.47
18:H:23:ARG:H	18:H:24:GLN:NE2	2.13	0.47
19:I:123:ARG:HG3	19:I:124:PRO:HD2	1.96	0.47
22:L:50:LYS:HD3	22:L:101:GLU:HG2	1.97	0.47
31:U:66:VAL:HG11	31:U:71:ILE:HG21	1.97	0.47
37:a:422:ALA:HB3	37:a:423:PRO:HD3	1.97	0.47
11:A:239:C:H3'	11:A:240:U:O4'	2.15	0.47
11:A:372:G:H1'	11:A:612:U:O2	2.14	0.47
11:A:539:G:OP2	11:A:539:G:C8	2.68	0.47
11:A:629:U:OP1	25:O:127:ARG:NH2	2.47	0.47
11:A:840:U:O2'	11:A:841:U:H5''	2.15	0.47
11:A:1626:U:C2'	11:A:1627:U:P	3.03	0.47
18:H:7:LEU:HD22	18:H:11:LEU:HG	1.97	0.47
33:W:42:LEU:HD23	33:W:46:VAL:HB	1.97	0.47
37:a:414:LYS:HB3	37:a:416:TYR:CE1	2.50	0.47
39:c:416:GLU:HG2	39:c:464:LYS:HB2	1.97	0.47
4:3:14:THR:HG23	4:3:15:GLU:H	1.80	0.47
11:A:78:A:N3	35:Y:175:ILE:HG12	2.29	0.47
11:A:258:C:N4	11:A:259:U:O4	2.48	0.47
11:A:909:U:H2'	11:A:910:C:H6	1.80	0.47
11:A:1280:C:H2'	11:A:1281:G:H8	1.80	0.47
11:A:1509:C:H2'	11:A:1510:U:O4'	2.14	0.47
11:A:1715:G:C5	11:A:1716:C:C5	3.03	0.47
16:F:93:ILE:HG13	16:F:94:SER:N	2.29	0.47
23:M:29:VAL:O	23:M:43:SER:OG	2.29	0.47
39:c:396:ILE:O	39:c:399:ARG:HB2	2.15	0.47
1:0:88:GLN:CG	34:X:5:HIS:CA	2.93	0.46
5:4:231:LEU:C	5:4:232:HIS:CD2	2.93	0.46
6:5:10:ARG:HB3	6:5:34:LYS:HA	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:5:84:VAL:HG13	6:5:85:ARG:N	2.30	0.46
9:8:42:LEU:O	9:8:46:LYS:HB2	2.16	0.46
11:A:269:G:C6	11:A:287:G:C6	3.02	0.46
11:A:705:U:OP1	11:A:705:U:H4'	2.14	0.46
11:A:710:U:HO2'	11:A:729:G:H1	1.63	0.46
11:A:1786:G:OP1	21:K:136:ARG:NH2	2.44	0.46
13:C:179:GLN:C	13:C:179:GLN:HE21	2.23	0.46
23:M:22:VAL:HG13	23:M:31:ALA:HB1	1.96	0.46
23:M:108:LYS:HE3	23:M:111:ASP:OD2	2.15	0.46
27:Q:53:TYR:CD1	27:Q:113:PRO:HG2	2.50	0.46
38:b:261:ASN:ND2	38:b:262:TYR:H	2.13	0.46
2:1:12:VAL:HA	2:1:30:VAL:HG12	1.97	0.46
11:A:192:U:O2'	11:A:193:U:O4'	2.33	0.46
11:A:1004:U:H4'	11:A:1005:A:OP2	2.15	0.46
11:A:1555:A:P	29:S:47:ARG:HH11	2.38	0.46
11:A:1629:G:H2'	11:A:1630:U:C6	2.51	0.46
11:A:1629:G:H2'	11:A:1630:U:H6	1.80	0.46
13:C:133:GLY:HA3	13:C:156:PHE:H	1.79	0.46
13:C:168:ILE:HD12	13:C:168:ILE:O	2.15	0.46
14:D:116:LEU:HD11	38:b:509:LYS:NZ	2.26	0.46
15:E:214:ALA:O	15:E:218:ILE:HG13	2.14	0.46
17:G:64:VAL:HG12	17:G:65:ARG:HD3	1.97	0.46
24:N:5:ASN:C	24:N:7:TRP:H	2.23	0.46
27:Q:5:LEU:O	27:Q:7:VAL:N	2.34	0.46
28:R:149:ASP:HB2	28:R:175:ASP:HB3	1.97	0.46
29:S:125:PRO:O	29:S:126:VAL:HB	2.14	0.46
33:W:196:VAL:N	33:W:209:HIS:O	2.43	0.46
35:Y:148:SER:C	35:Y:150:GLU:H	2.22	0.46
36:Z:80:LYS:NZ	36:Z:80:LYS:HB3	2.30	0.46
37:a:439:LYS:HD3	37:a:440:PHE:CE2	2.49	0.46
37:a:459:ASP:OD1	37:a:459:ASP:N	2.48	0.46
39:c:452:GLU:OE1	39:c:478:TYR:OH	2.31	0.46
1:0:103:LEU:O	1:0:106:GLN:HG2	2.15	0.46
5:4:87:ARG:HE	5:4:87:ARG:HB3	1.49	0.46
6:5:18:VAL:O	6:5:19:LYS:HB2	2.16	0.46
8:7:71:GLU:H	8:7:71:GLU:HG2	1.46	0.46
11:A:747:C:O2'	18:H:80:ASN:ND2	2.47	0.46
11:A:927:C:H1'	21:K:125:SER:CB	2.44	0.46
11:A:1363:U:O2	11:A:1363:U:H2'	2.16	0.46
11:A:1396:U:H2'	11:A:1397:U:C6	2.51	0.46
11:A:1459:C:N4	23:M:139:LYS:HG3	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:1562:G:OP1	30:T:89:ARG:NH2	2.42	0.46
12:B:88:LYS:HE2	12:B:88:LYS:HA	1.97	0.46
13:C:84:ILE:HD13	13:C:85:VAL:H	1.79	0.46
15:E:53:ILE:HG23	15:E:56:ILE:HD12	1.98	0.46
28:R:13:LEU:HB2	28:R:310:ILE:HB	1.97	0.46
1:0:71:MET:HE1	1:0:94:LYS:CB	2.45	0.46
4:3:133:THR:HG21	4:3:162:ILE:HD11	1.96	0.46
6:5:85:ARG:HD3	6:5:85:ARG:HA	1.78	0.46
11:A:544:A:H5''	11:A:545:A:OP2	2.15	0.46
11:A:1450:U:H2'	11:A:1451:C:C6	2.50	0.46
12:B:76:ILE:O	12:B:124:THR:HG23	2.15	0.46
17:G:124:LEU:O	17:G:125:THR:OG1	2.29	0.46
19:I:36:ILE:O	19:I:36:ILE:HG12	2.15	0.46
25:O:67:THR:C	25:O:69:ASN:H	2.24	0.46
28:R:133:VAL:HB	28:R:142:ALA:HB3	1.96	0.46
30:T:63:ARG:HG3	30:T:67:MET:CE	2.45	0.46
32:V:115:LEU:HD13	32:V:116:LYS:H	1.80	0.46
33:W:153:ASN:O	33:W:174:LYS:NZ	2.40	0.46
1:0:42:LEU:CD1	1:0:58:MET:SD	3.03	0.46
11:A:918:U:H2'	11:A:919:A:H8	1.81	0.46
11:A:1194:A:H2'	11:A:1195:C:H5'	1.98	0.46
11:A:1231:U:O5'	11:A:1259:U:H1'	2.14	0.46
11:A:1317:C:H2'	11:A:1318:G:O4'	2.14	0.46
12:B:71:GLU:HA	12:B:95:ALA:N	2.31	0.46
14:D:149:ARG:H	14:D:149:ARG:HG2	1.25	0.46
22:L:33:LEU:HA	22:L:33:LEU:HD23	1.70	0.46
35:Y:78:THR:HG22	35:Y:79:LYS:H	1.80	0.46
37:a:386:GLU:O	37:a:390:ILE:HG12	2.16	0.46
39:c:574:SER:HB3	39:c:650:LYS:NZ	2.29	0.46
1:0:55:ASN:HD22	1:0:57:ARG:NH1	2.13	0.46
1:0:60:HIS:CD2	22:L:60:GLU:OE1	2.69	0.46
3:2:66:SER:HB3	3:2:73:SER:CB	2.46	0.46
3:2:138:ASN:HD22	11:A:197:A:H61	1.63	0.46
7:6:63:LEU:HA	7:6:63:LEU:HD23	1.72	0.46
7:6:66:PRO:HB2	11:A:871:G:O2'	2.16	0.46
11:A:77:U:H4'	11:A:78:A:O5'	2.15	0.46
11:A:1681:A:H2	11:A:1720:G:H21	1.64	0.46
11:A:1698:N:O2'	11:A:1699:N:P	2.74	0.46
12:B:41:ARG:HE	12:B:45:VAL:CG2	2.29	0.46
14:D:60:LEU:HD23	14:D:93:LEU:HD11	1.98	0.46
16:F:30:ILE:HD13	16:F:85:ARG:NH1	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:M:41:ARG:NH1	30:T:38:LYS:HG3	2.30	0.46
25:O:114:ARG:HD3	25:O:114:ARG:HA	1.68	0.46
32:V:113:LEU:HG	32:V:114:GLY:N	2.31	0.46
39:c:536:ASP:OD1	39:c:537:SER:N	2.48	0.46
3:2:141:ARG:NH2	11:A:195:G:O6	2.34	0.46
5:4:38:PHE:HB2	5:4:39:GLU:H	1.47	0.46
11:A:768:C:C2	14:D:143:ILE:HD13	2.49	0.46
11:A:1301:U:H5''	15:E:97:ARG:HH12	1.12	0.46
11:A:1321:A:C4	12:B:104:PRO:HB2	2.51	0.46
13:C:216:PRO:HB2	13:C:217:ILE:H	1.59	0.46
16:F:80:LEU:HD13	16:F:84:GLN:CD	2.40	0.46
17:G:100:ASN:O	17:G:102:ARG:N	2.48	0.46
28:R:43:ILE:HA	28:R:59:ARG:O	2.16	0.46
29:S:20:VAL:HG13	29:S:24:LYS:HD2	1.98	0.46
31:U:45:LEU:O	31:U:49:THR:HG23	2.15	0.46
33:W:32:SER:HB2	33:W:83:PRO:HD3	1.96	0.46
39:c:656:LEU:HD23	39:c:676:LEU:HD12	1.96	0.46
3:2:66:SER:HA	3:2:73:SER:HA	1.98	0.46
11:A:25:C:OP2	11:A:26:A:H2'	2.15	0.46
11:A:711:U:C1'	11:A:712:G:H5'	2.43	0.46
11:A:1082:C:H2'	11:A:1083:G:H5'	1.98	0.46
11:A:1558:U:H3'	11:A:1559:A:H4'	1.98	0.46
12:B:39:ASN:HB3	32:V:105:GLN:HB3	1.98	0.46
12:B:105:GLY:O	12:B:108:THR:O	2.34	0.46
16:F:62:PHE:CD2	16:F:84:GLN:CD	2.93	0.46
16:F:69:VAL:CB	16:F:79:GLN:NE2	2.73	0.46
21:K:17:ALA:HB3	21:K:81:VAL:HB	1.96	0.46
28:R:44:SER:OG	28:R:59:ARG:HB2	2.16	0.46
31:U:125:ASN:C	31:U:127:GLY:H	2.23	0.46
35:Y:153:VAL:HG12	35:Y:154:ARG:N	2.31	0.46
35:Y:211:LEU:O	35:Y:215:ARG:HB2	2.16	0.46
38:b:660:VAL:HA	38:b:662:HIS:NE2	2.30	0.46
39:c:500:LYS:HG2	39:c:528:VAL:HG11	1.97	0.46
2:1:22:ARG:O	11:A:1617:U:H1'	2.16	0.46
3:2:81:VAL:HG12	3:2:91:VAL:HG22	1.98	0.46
5:4:107:THR:OG1	5:4:108:ASP:N	2.49	0.46
8:7:14:TYR:CD1	8:7:14:TYR:C	2.93	0.46
9:8:73:GLY:O	9:8:77:ARG:NH1	2.49	0.46
11:A:66:U:OP1	35:Y:136:LYS:NZ	2.41	0.46
11:A:485:A:H2'	11:A:486:G:O4'	2.15	0.46
11:A:499:U:O2'	11:A:500:C:OP1	2.24	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:505:A:N3	11:A:505:A:H2'	2.30	0.46
11:A:1228:G:OP2	31:U:44:GLY:HA2	2.16	0.46
14:D:14:THR:HA	14:D:15:PRO:HD2	1.69	0.46
18:H:37:PHE:CE2	18:H:103:ILE:HD12	2.50	0.46
22:L:107:PHE:CD2	22:L:114:LYS:HB2	2.51	0.46
33:W:163:ASP:HB3	33:W:166:SER:O	2.16	0.46
39:c:349:ASP:O	39:c:352:GLU:N	2.39	0.46
11:A:124:A:H1'	33:W:146:THR:HG21	1.98	0.46
11:A:507:U:H2'	11:A:508:U:O5'	2.16	0.46
11:A:1299:G:C3'	15:E:99:LYS:HE3	2.46	0.46
11:A:1783:C:H2'	11:A:1784:C:C6	2.49	0.46
16:F:61:ASP:OD2	16:F:62:PHE:CE1	2.69	0.46
21:K:25:ASP:OD1	21:K:26:THR:N	2.44	0.46
23:M:80:LYS:HA	23:M:80:LYS:HD2	1.54	0.46
25:O:99:ARG:O	25:O:103:GLU:HG2	2.16	0.46
28:R:91:LEU:O	28:R:100:TYR:N	2.42	0.46
32:V:44:LYS:HB2	32:V:44:LYS:HE2	1.64	0.46
37:a:463:TRP:CD2	39:c:744:LEU:CD2	2.99	0.46
2:1:46:GLY:HA3	17:G:166:ARG:HB2	1.98	0.45
4:3:159:VAL:O	4:3:162:ILE:HG13	2.16	0.45
11:A:287:G:O2'	11:A:288:A:P	2.74	0.45
11:A:1111:G:C2'	11:A:1112:G:H5'	2.47	0.45
11:A:1138:A:H2'	11:A:1139:A:C8	2.51	0.45
12:B:39:ASN:HB3	32:V:105:GLN:CB	2.46	0.45
12:B:108:THR:HG23	12:B:135:GLU:OE2	2.16	0.45
12:B:140:ASN:ND2	36:Z:29:HIS:HA	2.30	0.45
14:D:118:LEU:HG	14:D:158:PHE:CZ	2.51	0.45
16:F:55:LEU:HD23	16:F:55:LEU:C	2.41	0.45
16:F:62:PHE:CZ	16:F:87:LYS:CG	2.98	0.45
28:R:43:ILE:HD13	28:R:60:SER:HA	1.99	0.45
29:S:34:VAL:HG21	29:S:45:PHE:HB2	1.99	0.45
33:W:42:LEU:HD22	33:W:47:PHE:HB2	1.98	0.45
39:c:350:PHE:HA	39:c:351:ILE:HA	1.66	0.45
39:c:767:ALA:HA	39:c:777:VAL:O	2.16	0.45
4:3:22:GLN:HA	4:3:25:VAL:HG23	1.99	0.45
11:A:240:U:H4'	11:A:240:U:OP1	2.16	0.45
11:A:417:A:H5'	11:A:418:G:C5	2.50	0.45
11:A:725:U:H2'	11:A:726:C:O4'	2.16	0.45
11:A:1541:G:C6	11:A:1542:G:N1	2.84	0.45
12:B:71:GLU:OE1	12:B:71:GLU:N	2.37	0.45
16:F:98:LEU:HD12	16:F:98:LEU:HA	1.75	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:G:97:LEU:HD23	17:G:97:LEU:HA	1.79	0.45
18:H:25:VAL:O	18:H:62:VAL:HA	2.16	0.45
28:R:40:LYS:HA	28:R:68:VAL:HG23	1.98	0.45
35:Y:64:LYS:O	35:Y:67:VAL:HG22	2.17	0.45
39:c:737:SER:OG	39:c:740:LYS:HD3	2.16	0.45
2:1:49:ARG:HG2	2:1:52:ASP:OD1	2.16	0.45
4:3:173:TYR:HE2	4:3:179:LYS:HB2	1.80	0.45
5:4:101:HIS:O	5:4:217:LEU:HD13	2.17	0.45
5:4:110:LEU:HA	5:4:113:MET:HB2	1.98	0.45
11:A:273:G:H1	11:A:283:U:H3	1.65	0.45
11:A:381:C:H1'	11:A:756:A:C2	2.51	0.45
11:A:417:A:H4'	11:A:418:G:O5'	2.17	0.45
11:A:1059:U:H5'	37:a:66:LYS:NZ	2.31	0.45
11:A:1060:U:H5''	11:A:1061:A:OP2	2.16	0.45
11:A:1295:G:OP1	12:B:108:THR:CB	2.39	0.45
14:D:83:VAL:HG23	14:D:85:VAL:HG23	1.99	0.45
18:H:17:ALA:HB2	18:H:25:VAL:HG13	1.97	0.45
20:J:43:LYS:HD2	20:J:43:LYS:HA	1.52	0.45
26:P:35:VAL:O	26:P:36:SER:HB3	2.16	0.45
30:T:124:ILE:HG13	30:T:125:SER:O	2.16	0.45
35:Y:4:ASN:HA	35:Y:15:THR:HG22	1.98	0.45
36:Z:1:MET:HE2	36:Z:13:VAL:HG22	1.99	0.45
39:c:487:SER:OG	39:c:488:THR:N	2.49	0.45
9:8:59:TYR:HD1	9:8:60:VAL:N	2.13	0.45
10:9:131:PHE:HE2	31:U:50:LYS:HZ1	1.60	0.45
11:A:755:A:HO2'	11:A:756:A:P	2.38	0.45
11:A:767:U:H6	14:D:141:VAL:HA	1.81	0.45
11:A:795:U:C5	11:A:796:A:C8	3.04	0.45
11:A:915:A:H5'	11:A:916:U:OP2	2.17	0.45
11:A:960:U:H2'	11:A:961:U:H6	1.81	0.45
11:A:1166:A:H2'	11:A:1167:G:O4'	2.17	0.45
19:I:107:LYS:O	19:I:111:SER:HB2	2.16	0.45
32:V:81:LYS:HE3	32:V:81:LYS:HB2	1.73	0.45
37:a:97:ILE:O	37:a:101:GLU:HB2	2.15	0.45
3:2:8:ARG:NH1	3:2:19:ALA:O	2.49	0.45
11:A:66:U:H5'	35:Y:173:PRO:HA	1.98	0.45
11:A:72:A:C2	11:A:73:U:C4	3.05	0.45
11:A:296:U:H2'	11:A:297:U:C6	2.52	0.45
11:A:861:U:H5'	11:A:862:A:OP2	2.16	0.45
11:A:1200:G:H4'	11:A:1201:G:C5'	2.45	0.45
11:A:1281:G:H2'	11:A:1282:U:H6	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:D:163:PRO:HG2	14:D:164:PHE:CD2	2.51	0.45
22:L:4:GLY:O	22:L:5:LYS:C	2.60	0.45
38:b:555:THR:OG1	38:b:556:LYS:N	2.50	0.45
39:c:301:PRO:HD3	39:c:372:PHE:CE1	2.52	0.45
5:4:180:THR:HB	5:4:181:LEU:HD22	1.98	0.45
11:A:491:C:H42	11:A:496:G:H1	1.63	0.45
11:A:595:G:H2'	11:A:596:C:C6	2.52	0.45
11:A:779:U:O2'	11:A:780:A:H5''	2.16	0.45
11:A:1234:A:O2'	11:A:1235:C:O5'	2.20	0.45
13:C:84:ILE:HD13	13:C:85:VAL:N	2.32	0.45
14:D:174:ARG:HA	14:D:174:ARG:HE	1.81	0.45
20:J:27:THR:HB	20:J:88:LYS:CG	2.47	0.45
22:L:40:SER:HB2	22:L:41:SER:H	1.58	0.45
22:L:107:PHE:HD1	22:L:107:PHE:HA	1.68	0.45
32:V:106:THR:O	32:V:110:VAL:HG23	2.17	0.45
33:W:19:LEU:HD11	33:W:108:ARG:HD2	1.99	0.45
35:Y:28:PHE:C	35:Y:30:LYS:H	2.25	0.45
38:b:563:LYS:CE	38:b:564:ARG:NH2	2.73	0.45
39:c:447:LEU:O	39:c:451:MET:HG3	2.17	0.45
39:c:735:SER:HA	39:c:776:PHE:O	2.16	0.45
5:4:205:PHE:HA	5:4:206:PRO:HD2	1.71	0.45
11:A:196:G:O2'	11:A:197:A:OP2	2.34	0.45
11:A:231:U:O2'	11:A:232:U:H5''	2.17	0.45
11:A:1039:A:O2'	11:A:1040:G:P	2.74	0.45
11:A:1151:A:N9	11:A:1152:A:H5'	2.32	0.45
11:A:1402:G:OP1	32:V:10:LYS:NZ	2.49	0.45
11:A:1519:U:H2'	11:A:1520:U:C5	2.52	0.45
11:A:1612:U:C2'	11:A:1613:U:H5'	2.46	0.45
12:B:80:THR:C	12:B:82:GLY:H	2.24	0.45
12:B:120:LEU:HD12	12:B:142:PRO:O	2.17	0.45
12:B:124:THR:HG22	12:B:174:TRP:HZ2	1.81	0.45
12:B:131:GLN:O	12:B:135:GLU:HB2	2.17	0.45
16:F:31:GLN:HG3	16:F:39:LEU:HB3	1.97	0.45
17:G:109:LYS:O	17:G:113:ILE:HG13	2.17	0.45
22:L:108:GLY:O	22:L:109:ARG:HG2	2.16	0.45
29:S:22:LEU:HD13	29:S:26:LEU:HD11	1.99	0.45
31:U:84:ASN:O	31:U:86:VAL:HG22	2.17	0.45
35:Y:70:PRO:O	35:Y:98:ARG:NH2	2.42	0.45
35:Y:137:ARG:HD3	35:Y:177:ARG:HE	1.80	0.45
35:Y:211:LEU:HD11	35:Y:215:ARG:NH2	2.32	0.45
37:a:484:HIS:CD2	39:c:736:PHE:HA	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:88:GLN:CG	34:X:5:HIS:CB	2.94	0.45
5:4:65:VAL:O	21:K:34:SER:HA	2.16	0.45
10:9:108:VAL:HB	10:9:114:VAL:HG22	1.98	0.45
11:A:281:G:H2'	11:A:282:C:C6	2.52	0.45
11:A:489:C:O5'	11:A:489:C:H6	1.99	0.45
11:A:499:U:H2'	38:b:489:LYS:HE2	1.96	0.45
11:A:600:U:H1'	22:L:47:SER:HB3	1.99	0.45
11:A:616:G:C2	11:A:622:A:N7	2.84	0.45
11:A:702:G:H4'	11:A:702:G:OP1	2.17	0.45
11:A:767:U:C5	14:D:143:ILE:HD12	2.52	0.45
11:A:900:A:OP1	21:K:43:THR:OG1	2.20	0.45
11:A:1061:A:C8	39:c:594:ASN:HB3	2.51	0.45
11:A:1552:U:H2'	11:A:1553:G:O4'	2.16	0.45
15:E:140:ARG:HB3	15:E:221:THR:HB	1.99	0.45
17:G:30:PRO:O	17:G:33:VAL:HB	2.16	0.45
17:G:187:ILE:HD12	17:G:187:ILE:H	1.81	0.45
20:J:82:TYR:HB3	24:N:52:PHE:HB3	1.99	0.45
25:O:115:LEU:O	25:O:119:GLU:HG3	2.16	0.45
27:Q:91:LEU:HD23	27:Q:91:LEU:HA	1.80	0.45
30:T:6:VAL:O	30:T:9:VAL:N	2.39	0.45
36:Z:71:ARG:HG3	36:Z:83:TRP:CZ2	2.52	0.45
39:c:283:LEU:HD11	39:c:299:LEU:HD22	1.98	0.45
39:c:384:LEU:HD21	39:c:397:ARG:HB3	1.99	0.45
39:c:553:SER:HA	39:c:556:LYS:HD2	1.98	0.45
1:0:85:GLN:H	34:X:8:LEU:HG	1.82	0.45
4:3:39:ARG:N	4:3:40:PRO:HD2	2.32	0.45
6:5:50:VAL:O	6:5:53:LEU:HB3	2.16	0.45
7:6:67:THR:HB	7:6:68:GLY:H	1.58	0.45
11:A:139:C:H4'	11:A:140:A:O5'	2.17	0.45
11:A:1051:G:O2'	11:A:1052:U:P	2.75	0.45
11:A:1151:A:H2'	11:A:1152:A:H5'	0.46	0.45
11:A:1225:U:O2	11:A:1230:A:H4'	2.16	0.45
11:A:1578:U:O2'	11:A:1579:U:H5'	2.17	0.45
11:A:1586:A:H1'	11:A:1611:A:N6	2.32	0.45
12:B:142:PRO:HG3	36:Z:32:VAL:HG13	1.99	0.45
12:B:175:TYR:CD2	12:B:199:PRO:HA	2.52	0.45
13:C:11:LEU:HD12	20:J:86:ILE:HG12	1.98	0.45
14:D:132:ARG:HH11	14:D:132:ARG:HG3	1.82	0.45
17:G:25:LEU:HB2	19:I:27:GLY:HA3	1.98	0.45
18:H:90:THR:HB	18:H:94:LEU:HD12	1.98	0.45
22:L:41:SER:HA	22:L:42:PRO:HD3	1.75	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:O:46:THR:HG23	25:O:49:GLN:OE1	2.17	0.45
30:T:49:ASP:OD2	30:T:53:TRP:N	2.48	0.45
33:W:212:ASP:OD1	33:W:214:LEU:N	2.49	0.45
35:Y:2:LYS:HB3	35:Y:108:VAL:HG22	1.99	0.45
37:a:470:LEU:CD1	39:c:733:TYR:HE2	2.16	0.45
39:c:280:GLU:HA	39:c:283:LEU:HG	1.99	0.45
39:c:426:GLU:O	39:c:430:THR:HG23	2.17	0.45
5:4:183:GLN:O	5:4:187:LYS:HG3	2.17	0.45
6:5:5:ARG:HG2	11:A:1796:C:C2	2.52	0.45
6:5:38:ARG:NH2	6:5:83:ILE:HG21	2.32	0.45
8:7:25:LYS:HD3	8:7:59:PHE:HZ	1.81	0.45
11:A:156:A:H2'	11:A:157:A:O4'	2.17	0.45
11:A:260:U:H5'	11:A:261:U:H5''	1.98	0.45
11:A:348:U:OP1	27:Q:85:VAL:HG11	2.17	0.45
11:A:416:A:H4'	11:A:417:A:OP2	2.17	0.45
11:A:730:G:H2'	11:A:730:G:N3	2.31	0.45
11:A:1111:G:H2'	11:A:1112:G:H5'	2.00	0.45
11:A:1171:A:H2'	11:A:1172:G:C8	2.52	0.45
11:A:1217:A:H5'	11:A:1217:A:C8	2.51	0.45
11:A:1231:U:C4	11:A:1255:G:N2	2.85	0.45
12:B:52:LYS:NZ	36:Z:82:VAL:O	2.35	0.45
13:C:97:SER:O	13:C:98:ALA:C	2.60	0.45
14:D:85:VAL:HG12	14:D:99:LEU:HD11	1.98	0.45
14:D:108:ARG:HH11	14:D:110:GLN:HG2	1.82	0.45
16:F:73:GLU:O	16:F:73:GLU:HG3	2.16	0.45
22:L:134:ALA:HB1	22:L:140:LYS:HB2	1.98	0.45
32:V:23:LYS:HB3	32:V:34:LEU:HD11	1.99	0.45
36:Z:71:ARG:HB2	36:Z:83:TRP:CE2	2.51	0.45
39:c:550:LEU:HD12	39:c:566:ILE:HD13	2.00	0.45
4:3:12:ALA:HB3	4:3:13:PRO:HD3	1.98	0.44
5:4:110:LEU:CD2	5:4:213:ARG:HD2	2.46	0.44
5:4:229:MET:HA	5:4:232:HIS:CE1	2.52	0.44
6:5:96:ALA:C	6:5:98:PRO:HD2	2.42	0.44
8:7:24:LYS:HB3	8:7:24:LYS:HE2	1.74	0.44
9:8:90:LYS:HB3	9:8:90:LYS:HE2	1.74	0.44
11:A:782:U:C4'	11:A:783:G:OP2	2.64	0.44
11:A:1686:C:C2	11:A:1687:U:N1	2.85	0.44
15:E:81:MET:HE1	15:E:186:LYS:HB3	1.99	0.44
18:H:78:ARG:CD	18:H:126:LEU:HD23	2.47	0.44
26:P:29:HIS:CE1	26:P:68:LYS:N	2.85	0.44
30:T:14:PHE:CZ	30:T:132:LEU:HD23	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:Y:98:ARG:HD3	35:Y:99:GLY:O	2.17	0.44
38:b:499:ARG:CZ	38:b:565:TRP:CZ3	3.00	0.44
38:b:556:LYS:HA	38:b:556:LYS:HD3	1.75	0.44
7:6:25:VAL:HG13	18:H:55:ASP:HA	1.99	0.44
9:8:71:ILE:H	9:8:71:ILE:HG13	1.64	0.44
11:A:47:A:N1	11:A:386:G:H1'	2.32	0.44
11:A:277:U:H2'	11:A:278:U:OP1	2.17	0.44
11:A:413:U:H2'	11:A:414:C:C6	2.52	0.44
11:A:579:A:N1	13:C:143:ARG:HA	2.31	0.44
11:A:694:U:H2'	11:A:695:U:C5	2.51	0.44
11:A:707:A:H2	11:A:731:C:H2'	1.81	0.44
11:A:1617:U:H2'	11:A:1618:C:C6	2.52	0.44
11:A:1727:G:H2'	11:A:1728:A:C8	2.51	0.44
14:D:129:ILE:HG12	14:D:134:ILE:HD12	2.00	0.44
17:G:25:LEU:H	17:G:25:LEU:HD22	1.82	0.44
28:R:42:LEU:HB2	28:R:61:PHE:HB2	1.98	0.44
32:V:24:LEU:O	32:V:25:THR:HG23	2.18	0.44
4:3:16:LEU:HD22	4:3:58:LEU:HD21	1.98	0.44
9:8:54:VAL:HG13	9:8:57:TYR:HD2	1.81	0.44
11:A:154:G:OP1	35:Y:2:LYS:NZ	2.50	0.44
11:A:477:A:N7	11:A:538:A:N1	2.66	0.44
11:A:729:G:N3	11:A:729:G:H2'	2.33	0.44
11:A:981:U:C2'	11:A:982:U:H5'	2.47	0.44
11:A:1057:U:H1'	11:A:1058:U:H2'	1.99	0.44
11:A:1165:G:C6	11:A:1166:A:C6	3.06	0.44
11:A:1256:A:H4'	11:A:1257:U:O5'	2.17	0.44
11:A:1393:C:H2'	11:A:1394:G:O4'	2.17	0.44
20:J:50:LEU:CD2	20:J:95:ALA:HB2	2.47	0.44
25:O:142:GLU:HG3	25:O:145:THR:HG23	1.99	0.44
28:R:16:HIS:CD2	28:R:20:VAL:HG22	2.52	0.44
28:R:211:ILE:HG22	28:R:223:TRP:HD1	1.83	0.44
35:Y:73:ILE:HD12	35:Y:75:LEU:HD21	1.98	0.44
35:Y:163:THR:HA	35:Y:168:THR:HA	1.98	0.44
38:b:559:THR:CG2	38:b:561:VAL:HG23	2.47	0.44
39:c:717:VAL:O	39:c:721:SER:OG	2.32	0.44
2:1:16:LEU:HB2	2:1:27:GLN:HB2	2.00	0.44
3:2:14:THR:HG21	11:A:353:A:O3'	2.17	0.44
4:3:46:ILE:HD11	4:3:60:ILE:HG12	1.98	0.44
11:A:57:G:OP1	26:P:112:LYS:HE3	2.17	0.44
11:A:105:A:H2'	11:A:106:U:O4'	2.17	0.44
11:A:1157:A:HO2'	11:A:1158:C:P	2.40	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:1196:A:OP1	11:A:1196:A:H3'	2.17	0.44
11:A:1321:A:N3	12:B:104:PRO:O	2.51	0.44
12:B:20:ALA:HB3	12:B:22:THR:HG23	2.00	0.44
12:B:110:TYR:CD1	12:B:110:TYR:N	2.80	0.44
12:B:202:TYR:O	12:B:203:PHE:CG	2.70	0.44
13:C:132:LYS:HB3	13:C:189:MET:HG3	1.99	0.44
15:E:140:ARG:NH2	15:E:229:LEU:HD22	2.32	0.44
18:H:83:ILE:HG13	18:H:117:ARG:HH12	1.80	0.44
22:L:88:PRO:O	22:L:89:ASN:HB2	2.17	0.44
22:L:144:ARG:H	22:L:144:ARG:HG3	1.66	0.44
24:N:19:ARG:HD2	24:N:32:ARG:HD2	1.99	0.44
26:P:52:LYS:C	26:P:54:ALA:H	2.26	0.44
28:R:147:HIS:CE1	28:R:179:LYS:HD2	2.52	0.44
28:R:201:THR:HG21	28:R:242:SER:HA	1.98	0.44
30:T:85:SER:C	30:T:87:GLY:H	2.24	0.44
33:W:180:LEU:HD22	33:W:192:ILE:HG22	1.99	0.44
35:Y:72:ARG:HG2	35:Y:98:ARG:HA	1.99	0.44
7:6:15:GLU:OE2	7:6:24:LEU:N	2.50	0.44
11:A:1300:A:C5'	15:E:99:LYS:HG3	2.47	0.44
11:A:1316:G:H2'	11:A:1317:C:H6	1.81	0.44
11:A:1536:G:C6	11:A:1538:U:H1'	2.52	0.44
14:D:109:LEU:HD22	14:D:113:VAL:HG23	1.98	0.44
20:J:31:VAL:O	20:J:35:GLU:HB2	2.18	0.44
30:T:65:ILE:HG23	30:T:71:VAL:HG22	1.99	0.44
3:2:9:HIS:O	3:2:10:LYS:CB	2.64	0.44
8:7:29:GLN:O	8:7:30:ALA:HB3	2.18	0.44
11:A:71:A:O3'	11:A:72:A:H4'	2.17	0.44
11:A:492:A:H2'	11:A:494:U:H5''	1.98	0.44
11:A:501:U:H2'	11:A:502:U:C6	2.51	0.44
11:A:1250:U:O2'	11:A:1251:U:OP1	2.31	0.44
12:B:48:ILE:HG21	12:B:161:PRO:HB2	1.98	0.44
19:I:47:LYS:NZ	19:I:114:ARG:HG2	2.32	0.44
23:M:26:ILE:CD1	23:M:30:TYR:HB2	2.48	0.44
27:Q:131:ILE:HA	27:Q:131:ILE:HD13	1.45	0.44
2:1:19:THR:O	2:1:23:GLY:HA2	2.17	0.44
6:5:92:ARG:HD3	11:A:1796:C:OP2	2.17	0.44
7:6:59:CYS:O	7:6:61:THR:HG22	2.17	0.44
9:8:56:THR:HA	9:8:103:ARG:HH21	1.83	0.44
11:A:233:C:O2'	11:A:234:G:P	2.76	0.44
11:A:577:G:C8	11:A:577:G:C3'	3.01	0.44
11:A:1244:A:HO2'	11:A:1245:G:P	2.41	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:1277:G:H2'	11:A:1278:G:O4'	2.17	0.44
11:A:1418:G:O2'	24:N:56:ARG:O	2.29	0.44
12:B:182:LEU:HB3	12:B:188:LEU:HD23	2.00	0.44
13:C:137:VAL:HG22	13:C:151:LYS:HG3	1.99	0.44
14:D:60:LEU:HD22	14:D:60:LEU:HA	1.49	0.44
16:F:58:LEU:HD21	16:F:84:GLN:OE1	2.17	0.44
16:F:98:LEU:HD23	16:F:103:ILE:HG13	1.98	0.44
17:G:166:ARG:HH12	17:G:170:GLN:HE22	1.64	0.44
21:K:132:ARG:HH11	21:K:132:ARG:HG3	1.81	0.44
27:Q:21:ASN:HD22	27:Q:31:THR:HA	1.82	0.44
28:R:159:ASN:ND2	28:R:166:SER:O	2.51	0.44
37:a:343:ILE:N	37:a:344:GLY:HA2	2.31	0.44
2:1:26:THR:O	2:1:44:VAL:HG13	2.18	0.44
4:3:86:GLN:CG	4:3:87:ASP:H	2.31	0.44
5:4:81:PHE:HD1	5:4:82:ARG:HG3	1.81	0.44
8:7:88:PRO:C	8:7:90:THR:H	2.26	0.44
11:A:187:G:C4'	11:A:188:A:OP1	2.61	0.44
11:A:268:C:N4	35:Y:186:ARG:HD3	2.33	0.44
11:A:960:U:H2'	11:A:961:U:C6	2.52	0.44
11:A:1248:C:H2'	11:A:1249:U:C6	2.52	0.44
11:A:1299:G:C3'	15:E:99:LYS:CE	2.96	0.44
11:A:1346:A:C8	11:A:1370:U:O2	2.71	0.44
12:B:11:PRO:O	12:B:15:GLN:HG3	2.18	0.44
13:C:57:ASP:N	13:C:57:ASP:OD1	2.50	0.44
19:I:11:GLY:C	19:I:12:LYS:HG2	2.43	0.44
23:M:27:LYS:N	23:M:57:ARG:HH21	2.16	0.44
24:N:6:VAL:HG23	24:N:7:TRP:CZ3	2.53	0.44
35:Y:31:ARG:H	35:Y:34:GLN:HG3	1.82	0.44
36:Z:50:TYR:HB2	36:Z:52:THR:HG22	1.99	0.44
37:a:411:LEU:HA	37:a:411:LEU:HD23	1.60	0.44
37:a:484:HIS:CB	39:c:735:SER:C	2.73	0.44
39:c:254:PHE:HE2	39:c:286:ALA:HB2	1.83	0.44
39:c:398:LEU:HD12	39:c:398:LEU:HA	1.62	0.44
2:1:55:VAL:HG11	17:G:143:ARG:HD3	1.99	0.44
7:6:36:LYS:HE2	7:6:43:ILE:HG21	1.99	0.44
11:A:67:A:OP1	35:Y:171:LYS:NZ	2.48	0.44
11:A:72:A:O2'	11:A:73:U:H5''	2.18	0.44
11:A:1686:C:C4	11:A:1687:U:C4	3.05	0.44
12:B:69:ASN:HB3	12:B:71:GLU:OE1	2.18	0.44
12:B:103:THR:HA	12:B:104:PRO:HD3	1.62	0.44
12:B:120:LEU:HD12	12:B:121:VAL:H	1.81	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:D:36:LEU:O	34:X:33:ARG:HG3	2.18	0.44
17:G:29:ILE:HG21	19:I:57:LEU:HD11	2.00	0.44
23:M:56:LYS:HD3	23:M:60:GLU:HG3	2.00	0.44
25:O:26:PHE:HE2	25:O:59:GLY:O	2.01	0.44
28:R:38:ARG:HG2	28:R:67:ILE:CG2	2.48	0.44
28:R:286:GLU:HA	28:R:287:PRO:HD3	1.62	0.44
34:X:39:LEU:HD12	34:X:43:ARG:NH2	2.33	0.44
4:3:104:ARG:HB2	4:3:105:THR:H	1.45	0.43
6:5:60:PRO:C	6:5:62:TYR:H	2.26	0.43
9:8:39:ALA:HB1	9:8:70:LYS:C	2.43	0.43
11:A:443:C:H2'	11:A:444:C:O4'	2.18	0.43
11:A:712:G:C8	11:A:712:G:H3'	2.53	0.43
11:A:1681:A:H1'	35:Y:66:GLY:HA2	2.00	0.43
12:B:172:LEU:O	12:B:176:LEU:HG	2.17	0.43
16:F:28:ILE:HD13	16:F:88:VAL:HG13	1.99	0.43
21:K:30:VAL:HG13	21:K:39:ILE:O	2.18	0.43
22:L:79:ASN:HD22	22:L:81:LYS:HB2	1.82	0.43
23:M:49:LYS:NZ	23:M:79:TYR:O	2.51	0.43
23:M:129:TRP:CH2	29:S:125:PRO:HG3	2.53	0.43
30:T:64:HIS:CE1	30:T:68:ARG:CZ	3.01	0.43
33:W:147:ILE:HD13	33:W:169:ILE:HG13	2.00	0.43
1:0:62:ARG:HH12	1:0:93:HIS:CE1	2.36	0.43
3:2:31:ARG:NH2	11:A:333:A:OP1	2.51	0.43
3:2:136:SER:OG	3:2:137:LYS:N	2.43	0.43
4:3:74:GLN:O	4:3:78:THR:HG23	2.18	0.43
5:4:55:LYS:HD3	5:4:55:LYS:HA	1.67	0.43
6:5:5:ARG:HG2	11:A:1796:C:N1	2.33	0.43
6:5:61:GLU:O	6:5:62:TYR:HB3	2.18	0.43
10:9:83:UNK:O	10:9:84:UNK:HG3	2.18	0.43
11:A:839:U:O4	11:A:840:U:C4	2.71	0.43
11:A:1318:G:O2'	11:A:1319:A:H5'	2.19	0.43
11:A:1504:G:OP1	30:T:97:SER:HB2	2.18	0.43
11:A:1511:U:H2'	11:A:1512:G:H8	1.84	0.43
13:C:105:MET:O	13:C:106:LYS:C	2.61	0.43
14:D:170:GLY:HA2	14:D:171:ARG:HH21	1.83	0.43
16:F:58:LEU:HD23	16:F:58:LEU:O	2.18	0.43
18:H:24:GLN:HA	18:H:63:VAL:O	2.18	0.43
21:K:29:HIS:CB	21:K:41:ARG:HA	2.48	0.43
23:M:8:GLN:HB2	23:M:9:GLY:H	1.56	0.43
26:P:35:VAL:HG11	26:P:40:LEU:HD11	2.00	0.43
29:S:78:THR:OG1	29:S:79:HIS:N	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:U:66:VAL:HB	31:U:67:THR:H	1.51	0.43
35:Y:215:ARG:HA	35:Y:215:ARG:HD3	1.57	0.43
37:a:184:LYS:HE2	37:a:184:LYS:HB3	1.74	0.43
1:0:23:LYS:NZ	1:0:25:GLU:HG2	2.30	0.43
5:4:116:LYS:HD3	5:4:117:TRP:CZ3	2.53	0.43
11:A:93:A:H1'	33:W:3:ARG:HB3	2.00	0.43
11:A:434:G:H5'	22:L:78:LYS:HB3	1.99	0.43
11:A:886:U:H2'	11:A:887:A:O4'	2.18	0.43
11:A:1142:A:H2'	11:A:1143:A:C8	2.53	0.43
11:A:1321:A:O4'	12:B:104:PRO:CG	2.65	0.43
11:A:1796:C:H4'	11:A:1797:A:OP2	2.18	0.43
15:E:165:VAL:HA	15:E:201:ASN:O	2.17	0.43
16:F:95:GLN:HG2	16:F:95:GLN:O	2.17	0.43
20:J:20:ILE:N	20:J:95:ALA:O	2.50	0.43
28:R:74:THR:CG2	28:R:79:TYR:HB2	2.48	0.43
30:T:9:VAL:CG1	30:T:14:PHE:HB2	2.48	0.43
30:T:118:PRO:O	30:T:119:LYS:HB2	2.18	0.43
30:T:135:ILE:H	30:T:135:ILE:HG13	1.53	0.43
39:c:377:ASP:HA	39:c:404:ILE:HD13	2.01	0.43
39:c:512:LEU:HD23	39:c:512:LEU:HA	1.73	0.43
4:3:97:ARG:H	11:A:856:A:H62	1.66	0.43
8:7:7:ASP:HB3	8:7:37:THR:HG21	2.00	0.43
11:A:12:U:H2'	11:A:13:C:C6	2.54	0.43
11:A:501:U:H2'	11:A:502:U:C5	2.53	0.43
11:A:1002:G:N1	11:A:1761:U:OP1	2.43	0.43
11:A:1149:G:H5''	11:A:1150:G:OP1	2.18	0.43
11:A:1287:A:N6	11:A:1329:A:H5'	2.32	0.43
13:C:28:GLU:OE1	13:C:28:GLU:HA	2.18	0.43
13:C:70:THR:OG1	13:C:71:LEU:N	2.51	0.43
14:D:134:ILE:HA	14:D:158:PHE:HA	2.00	0.43
15:E:227:PRO:HA	15:E:230:TRP:CD1	2.54	0.43
18:H:82:LYS:O	18:H:83:ILE:HG22	2.18	0.43
18:H:103:ILE:HD13	18:H:126:LEU:HB2	2.00	0.43
20:J:20:ILE:HD13	20:J:22:ILE:HD13	2.00	0.43
21:K:125:SER:HB3	21:K:126:THR:H	1.45	0.43
24:N:33:LYS:HD3	24:N:34:TYR:CE2	2.53	0.43
27:Q:57:LYS:HB2	27:Q:110:HIS:CE1	2.54	0.43
27:Q:132:SER:O	27:Q:134:THR:N	2.52	0.43
31:U:129:GLU:O	31:U:133:LEU:HD13	2.18	0.43
34:X:47:VAL:HG22	34:X:48:THR:H	1.82	0.43
37:a:97:ILE:HD13	37:a:97:ILE:HA	1.85	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:c:300:ILE:HG22	39:c:304:PHE:CE2	2.53	0.43
39:c:413:LEU:HD12	39:c:459:ILE:HG21	2.00	0.43
5:4:81:PHE:HB2	5:4:82:ARG:H	1.53	0.43
11:A:719:U:H2'	11:A:719:U:O2	2.18	0.43
11:A:1253:U:H2'	11:A:1254:U:H6	1.83	0.43
11:A:1487:A:H2'	11:A:1488:G:H8	1.83	0.43
15:E:137:ILE:HG12	15:E:138:PRO:HD2	2.01	0.43
16:F:77:ILE:CG1	16:F:79:GLN:NE2	2.77	0.43
19:I:9:THR:OG1	19:I:20:ALA:HB3	2.19	0.43
19:I:53:LEU:H	19:I:53:LEU:HG	1.47	0.43
25:O:29:SER:C	25:O:66:ILE:HD11	2.43	0.43
25:O:34:ILE:HD11	25:O:67:THR:HG21	2.00	0.43
26:P:16:PRO:HG2	33:W:95:THR:HG22	2.00	0.43
32:V:34:LEU:O	32:V:38:ILE:HG22	2.18	0.43
33:W:155:LYS:HE2	33:W:155:LYS:HB3	1.76	0.43
5:4:70:LEU:HD12	5:4:82:ARG:O	2.18	0.43
8:7:46:LEU:HA	8:7:46:LEU:HD13	1.66	0.43
9:8:40:VAL:HA	9:8:75:LEU:HD11	2.01	0.43
10:9:111:GLU:HA	10:9:112:GLY:HA2	1.73	0.43
11:A:66:U:O4	35:Y:158:ILE:HG21	2.19	0.43
11:A:67:A:C2	11:A:69:G:H1'	2.54	0.43
11:A:473:A:C2'	11:A:474:A:H5'	2.49	0.43
11:A:1321:A:C4'	12:B:104:PRO:HG2	2.49	0.43
11:A:1386:G:OP2	32:V:44:LYS:NZ	2.52	0.43
11:A:1480:G:H3'	11:A:1481:C:H6	1.82	0.43
12:B:17:LEU:HD23	12:B:172:LEU:HD13	2.00	0.43
13:C:71:LEU:HD23	13:C:71:LEU:HA	1.85	0.43
14:D:175:ARG:HD2	14:D:176:ASN:N	2.33	0.43
17:G:87:CYS:SG	17:G:92:ARG:HG3	2.59	0.43
17:G:144:GLU:HB2	17:G:160:VAL:O	2.19	0.43
20:J:63:LEU:HD22	24:N:34:TYR:CE1	2.53	0.43
21:K:84:ARG:HA	21:K:119:THR:HG22	2.00	0.43
23:M:26:ILE:HD12	23:M:26:ILE:C	2.42	0.43
24:N:42:CYS:O	24:N:45:GLU:N	2.49	0.43
28:R:282:SER:H	28:R:285:ALA:HB3	1.84	0.43
39:c:441:TYR:CG	39:c:505:TYR:HD1	2.37	0.43
5:4:168:ILE:O	5:4:172:LEU:HG	2.19	0.43
11:A:139:C:HO2'	35:Y:187:LYS:HZ1	1.57	0.43
11:A:517:U:H3	11:A:535:A:H61	1.65	0.43
11:A:740:A:C2'	11:A:741:C:H5''	2.43	0.43
11:A:1151:A:C8	11:A:1152:A:P	3.12	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:1597:A:C8	24:N:14:TYR:HD2	2.36	0.43
12:B:57:LEU:HD23	12:B:177:LEU:HD23	2.00	0.43
16:F:58:LEU:HD11	16:F:80:LEU:HD11	2.00	0.43
19:I:18:ALA:CB	19:I:69:VAL:HG13	2.46	0.43
19:I:113:ASP:CG	19:I:114:ARG:N	2.66	0.43
29:S:83:MET:SD	29:S:89:MET:HE1	2.58	0.43
33:W:104:ASP:HB3	33:W:106:LYS:N	2.33	0.43
37:a:100:VAL:HG21	37:a:158:THR:HA	2.00	0.43
3:2:48:THR:HG21	3:2:54:LYS:HE3	2.00	0.43
4:3:17:GLU:HG2	4:3:46:ILE:HB	2.01	0.43
4:3:131:PHE:CD1	4:3:132:PRO:N	2.87	0.43
11:A:993:A:H4'	11:A:1777:G:O2'	2.19	0.43
12:B:200:ASP:HA	12:B:203:PHE:CE2	2.54	0.43
21:K:126:THR:O	21:K:127:ARG:C	2.62	0.43
22:L:23:ARG:HD2	22:L:26:GLU:OE2	2.18	0.43
28:R:116:ASP:HB2	28:R:117:LYS:HD2	2.01	0.43
28:R:222:LEU:HD23	28:R:234:LEU:CD1	2.49	0.43
32:V:57:LEU:O	32:V:61:ILE:HG13	2.19	0.43
35:Y:63:MET:HA	35:Y:98:ARG:O	2.18	0.43
1:0:32:GLY:O	1:0:81:LEU:HB2	2.19	0.43
2:1:58:GLU:HG2	17:G:225:ARG:CZ	2.48	0.43
5:4:105:PHE:CE1	5:4:213:ARG:HA	2.53	0.43
10:9:109:ASP:HB2	10:9:113:LYS:HG2	2.00	0.43
11:A:186:C:H3'	11:A:187:G:H8	1.82	0.43
11:A:560:U:H2'	11:A:561:G:H8	1.83	0.43
11:A:560:U:H2'	11:A:561:G:C8	2.54	0.43
11:A:709:C:N4	11:A:730:G:C4	2.87	0.43
11:A:720:G:O2'	11:A:721:U:H5'	2.18	0.43
11:A:823:G:O2'	11:A:824:G:OP1	2.36	0.43
11:A:827:C:H2'	11:A:828:U:H6	1.84	0.43
11:A:978:A:H2'	11:A:979:A:O4'	2.19	0.43
11:A:1102:G:OP2	22:L:7:ARG:NH1	2.52	0.43
11:A:1600:A:O2'	11:A:1602:C:N4	2.52	0.43
17:G:157:ARG:HB2	17:G:224:ASN:OD1	2.19	0.43
19:I:6:SER:HA	19:I:23:LYS:HA	2.00	0.43
21:K:24:ASN:O	21:K:25:ASP:HB2	2.19	0.43
22:L:40:SER:O	22:L:41:SER:O	2.36	0.43
23:M:10:SER:OG	23:M:11:PHE:N	2.52	0.43
23:M:90:ASN:O	23:M:91:ASP:C	2.61	0.43
26:P:14:SER:CB	26:P:21:LYS:HE3	2.49	0.43
30:T:135:ILE:HA	30:T:138:GLN:HG3	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:U:24:ILE:C	31:U:26:ASP:H	2.27	0.43
31:U:125:ASN:O	31:U:126:TRP:CD1	2.72	0.43
32:V:107:SER:HA	32:V:110:VAL:HG23	2.01	0.43
38:b:583:PRO:HD2	38:b:646:GLY:HA2	2.01	0.43
39:c:300:ILE:HG12	39:c:300:ILE:H	1.59	0.43
39:c:440:ILE:HG23	39:c:448:ILE:HG12	2.01	0.43
1:O:71:MET:SD	1:O:75:ASP:HB2	2.59	0.43
9:8:97:LYS:HG3	9:8:98:GLN:H	1.84	0.43
10:9:138:ARG:CZ	11:A:1235:C:O2	2.67	0.43
11:A:61:A:C8	11:A:269:G:O2'	2.65	0.43
11:A:498:G:H2'	11:A:499:U:C4	2.54	0.43
11:A:506:A:OP1	11:A:506:A:H3'	2.19	0.43
11:A:763:G:C6	11:A:764:U:C4	3.07	0.43
11:A:781:U:O2'	11:A:782:U:H6	2.02	0.43
11:A:1152:A:C6	11:A:1627:U:N3	2.87	0.43
11:A:1489:U:H2'	11:A:1490:C:OP1	2.19	0.43
11:A:1769:U:O2	21:K:136:ARG:HD2	2.18	0.43
22:L:69:ARG:NH1	22:L:116:ASP:OD2	2.52	0.43
28:R:198:ASN:O	28:R:215:GLY:HA3	2.19	0.43
28:R:256:THR:OG1	28:R:259:GLY:O	2.31	0.43
30:T:28:LEU:O	30:T:29:GLU:HB2	2.17	0.43
32:V:17:ILE:HG12	32:V:58:MET:HE2	2.00	0.43
38:b:562:ILE:O	38:b:563:LYS:HB3	2.18	0.43
4:3:75:THR:OG1	4:3:76:LYS:N	2.52	0.42
4:3:117:THR:HG23	4:3:120:ALA:H	1.84	0.42
4:3:133:THR:O	4:3:134:GLU:HB2	2.19	0.42
11:A:74:U:H1'	11:A:75:U:O5'	2.19	0.42
11:A:768:C:N1	14:D:143:ILE:HD13	2.33	0.42
11:A:805:U:H2'	11:A:806:A:H5''	2.01	0.42
11:A:1340:U:N3	11:A:1378:U:H4'	2.34	0.42
11:A:1491:U:H5''	11:A:1491:U:O2	2.19	0.42
11:A:1540:G:C6	11:A:1541:G:C4	3.07	0.42
12:B:63:ILE:HG12	36:Z:36:VAL:HG22	2.01	0.42
14:D:116:LEU:HD11	38:b:509:LYS:HZ1	1.78	0.42
16:F:98:LEU:CG	16:F:102:ASN:HB2	2.49	0.42
22:L:13:ARG:HA	22:L:16:ARG:HD3	2.01	0.42
29:S:108:ARG:HG2	29:S:109:PRO:HD2	2.01	0.42
31:U:129:GLU:HA	31:U:133:LEU:HD22	2.00	0.42
35:Y:67:VAL:HG23	35:Y:100:ALA:H	1.83	0.42
35:Y:76:LEU:HD22	35:Y:92:ARG:HB3	2.01	0.42
36:Z:3:ASN:O	36:Z:4:ASP:C	2.62	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:a:34:PHE:CE2	37:a:51:VAL:HG21	2.54	0.42
5:4:132:ASP:HB2	5:4:221:PRO:HB3	2.01	0.42
11:A:14:C:OP2	15:E:206:THR:HG21	2.18	0.42
11:A:88:U:H4'	11:A:171:A:O4'	2.19	0.42
11:A:609:U:H4'	11:A:610:G:O5'	2.18	0.42
11:A:1002:G:C2'	11:A:1003:A:H5'	2.48	0.42
11:A:1013:A:H2'	11:A:1014:G:O4'	2.19	0.42
11:A:1133:A:H2'	11:A:1134:C:O4'	2.19	0.42
11:A:1781:A:H2'	11:A:1782:A:O4'	2.19	0.42
12:B:69:ASN:HB3	12:B:71:GLU:OE2	2.19	0.42
12:B:87:LEU:HD12	12:B:87:LEU:HA	1.82	0.42
13:C:61:GLU:O	13:C:63:GLY:N	2.52	0.42
13:C:142:LEU:O	13:C:144:ALA:N	2.44	0.42
14:D:31:ALA:HA	14:D:36:LEU:HD12	2.00	0.42
15:E:125:ILE:O	15:E:129:ILE:HG13	2.19	0.42
17:G:43:PHE:CZ	17:G:90:ILE:HG21	2.54	0.42
19:I:22:VAL:HG22	19:I:65:ILE:CD1	2.49	0.42
24:N:5:ASN:HB3	24:N:7:TRP:NE1	2.34	0.42
30:T:125:SER:OG	30:T:128:GLY:N	2.45	0.42
35:Y:55:GLY:C	35:Y:63:MET:HE3	2.44	0.42
37:a:253:TRP:HB3	39:c:664:PHE:CZ	2.53	0.42
39:c:303:ARG:NH1	39:c:324:ASP:OD2	2.52	0.42
3:2:172:ARG:NH1	11:A:330:G:OP2	2.42	0.42
8:7:54:TYR:N	8:7:54:TYR:CD1	2.86	0.42
8:7:81:ASN:HB3	31:U:37:VAL:HG11	2.01	0.42
11:A:36:C:H2'	11:A:37:U:O4'	2.20	0.42
11:A:380:U:H5	14:D:5:PRO:CA	2.30	0.42
11:A:1365:C:H5''	19:I:28:LEU:CD2	2.49	0.42
11:A:1402:G:H2'	11:A:1403:C:C6	2.53	0.42
11:A:1490:C:O4'	11:A:1490:C:P	2.78	0.42
11:A:1560:U:O2	11:A:1560:U:O4'	2.37	0.42
11:A:1740:A:O2'	11:A:1741:U:H5'	2.19	0.42
12:B:162:CYS:HB3	12:B:163:ASN:H	1.34	0.42
27:Q:3:THR:CG2	27:Q:82:ARG:HH21	2.32	0.42
28:R:42:LEU:O	28:R:61:PHE:HD1	2.02	0.42
33:W:141:THR:O	33:W:143:ASP:N	2.53	0.42
37:a:83:THR:O	37:a:87:VAL:HG23	2.18	0.42
37:a:482:ILE:HG21	39:c:733:TYR:CD1	2.52	0.42
39:c:254:PHE:CE2	39:c:286:ALA:HB2	2.54	0.42
39:c:345:ALA:C	39:c:347:PRO:HD2	2.44	0.42
39:c:627:LEU:HD21	39:c:717:VAL:HG22	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:3:74:GLN:O	4:3:75:THR:C	2.63	0.42
5:4:146:GLN:CB	5:4:149:GLN:HE22	2.32	0.42
7:6:61:THR:HG23	7:6:62:ILE:O	2.19	0.42
8:7:50:THR:HB	8:7:55:VAL:O	2.19	0.42
10:9:101:UNK:HA	11:A:1229:G:OP2	2.19	0.42
11:A:273:G:H2'	11:A:274:G:O4'	2.18	0.42
11:A:484:C:O2'	11:A:485:A:OP1	2.35	0.42
11:A:538:A:H8	11:A:543:C:N4	2.16	0.42
11:A:542:A:O2'	11:A:542:A:H8	2.01	0.42
11:A:1456:C:O2	11:A:1456:C:O4'	2.38	0.42
11:A:1473:U:O2'	17:G:103:ASN:ND2	2.48	0.42
12:B:83:GLN:HG2	12:B:100:GLY:H	1.84	0.42
12:B:185:ARG:HB2	36:Z:45:ALA:CB	2.47	0.42
13:C:134:CYS:N	13:C:157:LEU:HD11	2.34	0.42
18:H:43:LYS:O	18:H:43:LYS:HG3	2.19	0.42
19:I:58:ASP:OD1	19:I:59:LYS:N	2.52	0.42
20:J:28:SER:HB2	20:J:112:VAL:HA	2.02	0.42
23:M:95:GLY:HA3	29:S:18:ARG:O	2.20	0.42
26:P:47:VAL:HG23	26:P:48:TYR:HD1	1.84	0.42
28:R:205:SER:HB3	28:R:210:LEU:HB2	2.02	0.42
2:1:29:ARG:HG3	2:1:39:THR:OG1	2.20	0.42
11:A:40:A:H2'	11:A:41:A:O4'	2.19	0.42
11:A:579:A:H61	13:C:143:ARG:HG3	1.48	0.42
11:A:1300:A:C5'	15:E:117:THR:CG2	2.77	0.42
15:E:44:LEU:HG	15:E:247:ALA:HB2	2.01	0.42
15:E:65:GLU:O	15:E:68:ILE:HB	2.19	0.42
22:L:29:TYR:CZ	22:L:33:LEU:HD12	2.54	0.42
27:Q:6:THR:OG1	27:Q:7:VAL:N	2.52	0.42
27:Q:28:SER:O	27:Q:29:LYS:HB3	2.20	0.42
38:b:660:VAL:HG23	38:b:661:GLU:H	1.85	0.42
39:c:456:TRP:CZ2	39:c:469:SER:HB3	2.55	0.42
39:c:572:SER:O	39:c:650:LYS:HD2	2.19	0.42
1:0:62:ARG:O	1:0:66:ARG:HG3	2.19	0.42
4:3:159:VAL:HG23	4:3:163:ASP:OD1	2.20	0.42
11:A:81:G:C6	11:A:82:U:N3	2.88	0.42
11:A:460:A:H3'	11:A:461:G:H8	1.84	0.42
11:A:714:G:C6	11:A:715:U:C2	3.08	0.42
11:A:1150:G:O2'	11:A:1151:A:OP2	2.33	0.42
11:A:1710:U:H2'	11:A:1711:C:C5	2.54	0.42
12:B:20:ALA:O	12:B:21:ASN:HB2	2.19	0.42
13:C:66:ILE:O	13:C:70:THR:HG23	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:E:104:VAL:HG22	15:E:132:ALA:HB1	2.00	0.42
26:P:14:SER:HB3	26:P:21:LYS:HE3	2.02	0.42
27:Q:87:ARG:HH21	27:Q:104:HIS:CE1	2.38	0.42
32:V:84:TYR:C	32:V:85:VAL:HG23	2.45	0.42
35:Y:1:MET:CE	35:Y:106:LEU:HB2	2.50	0.42
39:c:571:LEU:HD21	39:c:617:ILE:HG22	2.01	0.42
3:2:157:GLU:O	3:2:160:PHE:HB2	2.19	0.42
4:3:35:LYS:NZ	4:3:36:ALA:H	2.18	0.42
5:4:97:LEU:HD12	5:4:232:HIS:NE2	2.35	0.42
11:A:153:G:OP2	26:P:131:ARG:NH2	2.38	0.42
11:A:237:C:C4'	11:A:238:U:H5'	2.49	0.42
11:A:685:A:O2'	11:A:686:C:H5'	2.19	0.42
11:A:1586:A:H2'	11:A:1587:A:C8	2.53	0.42
11:A:1595:U:H5	11:A:1596:C:C5	2.37	0.42
19:I:53:LEU:N	19:I:53:LEU:HD23	2.34	0.42
21:K:129:LYS:HG3	21:K:130:GLY:N	2.35	0.42
25:O:46:THR:HG23	25:O:49:GLN:CD	2.45	0.42
27:Q:127:GLN:HG3	27:Q:137:PHE:CZ	2.54	0.42
28:R:201:THR:CB	28:R:242:SER:HA	2.49	0.42
29:S:57:MET:O	29:S:60:LEU:HB3	2.19	0.42
33:W:106:LYS:HG3	33:W:108:ARG:NH2	2.35	0.42
33:W:131:LEU:HD13	33:W:135:GLY:HA2	2.01	0.42
35:Y:119:GLN:HG3	35:Y:120:GLU:N	2.35	0.42
35:Y:132:ARG:HG2	35:Y:132:ARG:HH11	1.83	0.42
39:c:659:TYR:CD2	39:c:676:LEU:HD21	2.55	0.42
2:1:5:THR:HA	2:1:6:PRO:HD3	1.79	0.42
6:5:23:CYS:CB	6:5:74:CYS:HB3	2.50	0.42
6:5:90:GLU:C	6:5:92:ARG:H	2.27	0.42
11:A:68:A:C8	35:Y:160:ARG:NH1	2.87	0.42
11:A:512:A:HO2'	11:A:513:U:P	2.43	0.42
11:A:1321:A:H4'	11:A:1322:A:O5'	2.19	0.42
11:A:1334:U:H2'	11:A:1335:U:H6	1.83	0.42
11:A:1346:A:H8	11:A:1370:U:O2	2.03	0.42
11:A:1557:U:OP2	11:A:1559:A:O2'	2.33	0.42
13:C:5:ILE:CG2	13:C:9:ARG:HB3	2.50	0.42
13:C:167:PHE:HD1	13:C:190:ARG:HD3	1.85	0.42
14:D:127:VAL:HG12	14:D:131:GLN:NE2	2.35	0.42
15:E:67:GLN:O	15:E:71:THR:HG23	2.20	0.42
19:I:27:GLY:HA2	19:I:63:ILE:O	2.19	0.42
21:K:38:THR:O	21:K:39:ILE:HG23	2.19	0.42
23:M:109:LEU:HG	23:M:113:LEU:CD1	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:R:38:ARG:HG2	28:R:67:ILE:HG23	2.01	0.42
28:R:123:ILE:HD11	28:R:156:VAL:HG23	2.01	0.42
35:Y:76:LEU:HD23	35:Y:76:LEU:HA	1.87	0.42
36:Z:15:ARG:HB3	36:Z:16:LYS:H	1.60	0.42
2:1:32:PHE:N	2:1:32:PHE:CD1	2.87	0.42
8:7:16:PHE:HD2	8:7:76:LEU:HD23	1.84	0.42
10:9:143:LYS:CB	11:A:1253:U:H4'	2.50	0.42
11:A:73:U:C2	11:A:74:U:O2	2.73	0.42
11:A:489:C:N4	11:A:497:G:H22	2.15	0.42
11:A:568:G:O2'	11:A:569:C:H5'	2.20	0.42
11:A:579:A:N1	13:C:143:ARG:CA	2.83	0.42
11:A:812:A:OP1	11:A:814:A:C8	2.72	0.42
11:A:814:A:C5	11:A:816:G:C8	3.08	0.42
11:A:1480:G:H4'	30:T:11:ALA:CB	2.49	0.42
11:A:1568:C:OP1	23:M:36:LYS:HE2	2.20	0.42
13:C:113:LEU:HD23	13:C:113:LEU:HA	1.66	0.42
13:C:127:MET:HG2	13:C:154:ASP:OD2	2.19	0.42
17:G:69:PHE:CD2	19:I:50:GLU:HG2	2.54	0.42
29:S:128:HIS:O	29:S:130:ARG:HG2	2.20	0.42
30:T:65:ILE:HG12	30:T:71:VAL:HG21	2.01	0.42
31:U:55:GLY:HA2	31:U:85:LYS:CD	2.50	0.42
32:V:66:VAL:O	32:V:69:ILE:HG12	2.19	0.42
33:W:156:VAL:O	33:W:157:ASN:HB2	2.20	0.42
35:Y:27:PHE:C	35:Y:30:LYS:HG2	2.45	0.42
1:0:88:GLN:CG	34:X:5:HIS:HB2	2.40	0.42
2:1:42:ARG:NH1	2:1:56:LEU:HD22	2.33	0.42
4:3:51:VAL:HG23	4:3:53:GLY:N	2.34	0.42
5:4:96:LEU:HD23	5:4:96:LEU:O	2.20	0.42
5:4:140:ILE:O	5:4:210:ILE:HA	2.20	0.42
9:8:41:ILE:O	9:8:75:LEU:HD13	2.20	0.42
9:8:71:ILE:HG22	9:8:75:LEU:HD12	2.02	0.42
10:9:140:TYR:OH	11:A:1234:A:H1'	2.20	0.42
11:A:71:A:C2	11:A:72:A:C2	3.08	0.42
11:A:74:U:O2'	11:A:75:U:H5'	2.20	0.42
11:A:279:G:C3'	11:A:279:G:C8	3.03	0.42
11:A:328:A:H2'	11:A:329:G:O4'	2.19	0.42
11:A:476:U:OP1	11:A:477:A:O2'	2.31	0.42
11:A:479:C:O2	11:A:510:G:N2	2.53	0.42
11:A:505:A:H2'	11:A:506:A:OP1	2.19	0.42
11:A:542:A:H8	11:A:543:C:H2'	1.83	0.42
11:A:681:U:O4	11:A:682:C:N4	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:1686:C:C4	11:A:1687:U:C5	3.08	0.42
12:B:30:GLN:NE2	12:B:149:LEU:HD13	2.35	0.42
12:B:64:ILE:HG12	12:B:122:ILE:HD11	2.01	0.42
17:G:128:ASN:HD22	17:G:128:ASN:HA	1.74	0.42
18:H:23:ARG:NH2	36:Z:21:ASN:OD1	2.53	0.42
18:H:30:SER:HB2	18:H:61:ILE:CD1	2.50	0.42
19:I:127:LYS:HA	19:I:134:ALA:HA	2.02	0.42
27:Q:118:GLN:HG3	27:Q:119:VAL:N	2.35	0.42
31:U:98:GLY:CA	31:U:118:ALA:HB2	2.50	0.42
31:U:131:ASP:HB2	31:U:132:GLU:CD	2.45	0.42
35:Y:85:ARG:HA	35:Y:86:PRO:HD3	1.75	0.42
36:Z:28:ASP:C	36:Z:30:ALA:H	2.28	0.42
37:a:340:ILE:HD12	37:a:477:TYR:CG	2.55	0.42
37:a:348:HIS:HD2	39:c:663:SER:CB	2.33	0.42
37:a:482:ILE:CG2	39:c:733:TYR:CE1	3.03	0.42
39:c:355:PRO:C	39:c:357:GLU:H	2.28	0.42
39:c:747:LEU:HD23	39:c:747:LEU:HA	1.92	0.42
3:2:21:PHE:O	3:2:22:ARG:HG2	2.20	0.41
3:2:147:ALA:H	3:2:149:SER:HB3	1.84	0.41
4:3:119:THR:HG23	11:A:639:U:OP1	2.19	0.41
4:3:131:PHE:HB3	4:3:132:PRO:HD3	2.02	0.41
5:4:29:TRP:CZ2	5:4:45:LYS:HB3	2.55	0.41
5:4:131:ASP:OD2	5:4:180:THR:HG21	2.19	0.41
6:5:62:TYR:CZ	21:K:114:ARG:HA	2.54	0.41
9:8:54:VAL:HG13	9:8:57:TYR:CD2	2.55	0.41
10:9:138:ARG:CZ	11:A:1235:C:C2	3.03	0.41
11:A:95:G:HO2'	11:A:460:A:HO2'	1.63	0.41
11:A:425:A:H8	11:A:425:A:C5'	2.32	0.41
11:A:648:G:C4	11:A:687:G:N2	2.88	0.41
11:A:839:U:C2'	11:A:840:U:H5'	2.47	0.41
11:A:1625:C:H5'	15:E:91:ARG:HH12	1.83	0.41
14:D:92:LYS:HA	14:D:92:LYS:HE3	2.01	0.41
15:E:111:VAL:HG21	15:E:218:ILE:HD13	2.01	0.41
19:I:39:VAL:O	19:I:40:GLU:C	2.63	0.41
25:O:83:GLU:H	25:O:83:GLU:HG2	1.55	0.41
27:Q:53:TYR:CD1	27:Q:53:TYR:C	2.97	0.41
28:R:98:GLU:HG3	28:R:99:THR:O	2.20	0.41
29:S:108:ARG:HD2	29:S:110:GLU:OE2	2.19	0.41
34:X:34:ALA:O	34:X:37:ARG:HB3	2.20	0.41
35:Y:109:LEU:HD23	35:Y:109:LEU:HA	1.84	0.41
39:c:376:LEU:HD23	39:c:376:LEU:HA	1.92	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:c:497:ALA:O	39:c:501:ARG:HB2	2.19	0.41
1:0:88:GLN:HB2	34:X:6:GLY:CA	2.50	0.41
5:4:37:THR:C	5:4:38:PHE:CG	2.98	0.41
5:4:72:ASP:OD2	21:K:114:ARG:HD2	2.20	0.41
11:A:778:G:C5	11:A:783:G:N1	2.88	0.41
11:A:781:U:O2'	11:A:782:U:O5'	2.38	0.41
11:A:1344:A:H4'	11:A:1345:A:OP1	2.19	0.41
11:A:1547:A:H5'	23:M:112:ASP:OD2	2.19	0.41
13:C:138:VAL:O	13:C:149:ALA:HA	2.20	0.41
14:D:49:LEU:HD22	14:D:53:ARG:HG3	2.01	0.41
15:E:84:LYS:HA	15:E:85:PRO:HD3	1.79	0.41
21:K:84:ARG:HG3	21:K:119:THR:HA	2.01	0.41
28:R:22:SER:HB3	28:R:36:ALA:HB3	2.02	0.41
30:T:126:GLU:CD	30:T:126:GLU:N	2.76	0.41
31:U:55:GLY:HA2	31:U:85:LYS:HD2	2.02	0.41
39:c:332:LEU:HD23	39:c:332:LEU:HA	1.87	0.41
4:3:96:ARG:O	11:A:694:U:C5	2.73	0.41
10:9:143:LYS:CA	11:A:1253:U:H4'	2.50	0.41
11:A:190:C:C4	11:A:196:G:C6	3.09	0.41
11:A:205:U:H2'	11:A:206:A:O4'	2.21	0.41
11:A:773:C:OP1	33:W:21:ASP:HB2	2.19	0.41
11:A:830:U:O2'	11:A:831:U:OP2	2.34	0.41
11:A:1280:C:H2'	11:A:1281:G:C8	2.56	0.41
11:A:1553:G:O6	29:S:43:ARG:HD3	2.20	0.41
14:D:133:HIS:CD2	14:D:133:HIS:H	2.37	0.41
15:E:230:TRP:CE2	18:H:68:ARG:HB3	2.55	0.41
15:E:242:ILE:HG22	15:E:243:TYR:CE2	2.55	0.41
16:F:85:ARG:NH1	16:F:107:GLY:CA	2.83	0.41
16:F:98:LEU:CD2	16:F:102:ASN:HB2	2.48	0.41
17:G:95:ASN:O	17:G:98:MET:HG2	2.20	0.41
19:I:47:LYS:HZ1	19:I:114:ARG:HH11	1.68	0.41
25:O:21:ASN:HB2	25:O:22:ALA:H	1.66	0.41
26:P:44:LEU:HA	26:P:47:VAL:CG2	2.51	0.41
33:W:61:VAL:HG12	33:W:65:LEU:HD12	2.00	0.41
33:W:68:ARG:NH1	33:W:76:VAL:HG21	2.35	0.41
35:Y:158:ILE:HD12	35:Y:158:ILE:HA	1.77	0.41
36:Z:74:GLN:C	36:Z:76:ASP:N	2.77	0.41
37:a:390:ILE:HD12	37:a:403:GLN:CD	2.45	0.41
39:c:254:PHE:CZ	39:c:291:GLU:HB3	2.55	0.41
39:c:387:ILE:HG22	39:c:388:ASP:N	2.35	0.41
39:c:543:PHE:O	39:c:547:VAL:HG23	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:46:ARG:HD2	34:X:3:LYS:CG	2.45	0.41
1:0:61:ILE:HG22	1:0:66:ARG:HG3	2.02	0.41
2:1:46:GLY:HA2	17:G:166:ARG:HD2	2.02	0.41
3:2:87:ASN:HB3	3:2:90:LEU:HD12	2.02	0.41
4:3:67:LEU:HD23	4:3:67:LEU:HA	1.75	0.41
4:3:181:ILE:HA	4:3:181:ILE:HD12	1.72	0.41
5:4:137:ILE:HG22	5:4:215:VAL:CG2	2.50	0.41
6:5:64:LEU:HD22	6:5:64:LEU:HA	1.89	0.41
11:A:68:A:H3'	11:A:68:A:H8	1.84	0.41
11:A:82:U:H2'	11:A:83:G:O4'	2.21	0.41
11:A:327:U:O2'	27:Q:10:GLU:HG2	2.21	0.41
11:A:336:G:O2'	27:Q:133:LYS:N	2.52	0.41
11:A:478:A:H5'	34:X:33:ARG:NH2	2.35	0.41
11:A:1244:A:O2'	11:A:1245:G:P	2.78	0.41
11:A:1479:A:P	30:T:57:ARG:HH12	2.44	0.41
12:B:63:ILE:HG23	36:Z:35:ASN:O	2.20	0.41
12:B:172:LEU:HD13	12:B:176:LEU:HD11	2.01	0.41
14:D:108:ARG:HG2	14:D:147:MET:HE2	2.02	0.41
15:E:130:ILE:O	15:E:134:LEU:HD22	2.19	0.41
20:J:96:PRO:HG2	20:J:99:ILE:HG22	2.02	0.41
23:M:27:LYS:HA	23:M:57:ARG:HE	1.84	0.41
23:M:47:CYS:HB3	23:M:54:LEU:CD1	2.50	0.41
26:P:105:ARG:O	26:P:109:LYS:HG3	2.20	0.41
30:T:86:ARG:HH11	30:T:86:ARG:CG	2.29	0.41
31:U:29:LYS:HA	31:U:32:LEU:HD12	2.00	0.41
31:U:131:ASP:OD1	31:U:132:GLU:N	2.53	0.41
33:W:114:ILE:HB	33:W:118:GLU:OE1	2.20	0.41
37:a:56:LEU:HD23	37:a:68:LEU:HD22	2.02	0.41
39:c:383:SER:O	39:c:387:ILE:HG13	2.20	0.41
1:0:44:ASN:HB3	1:0:46:ARG:HH12	1.84	0.41
3:2:195:ARG:HA	3:2:195:ARG:HD3	1.85	0.41
4:3:28:GLU:O	4:3:30:SER:N	2.52	0.41
7:6:32:PHE:CZ	25:O:61:THR:HG22	2.56	0.41
10:9:103:LEU:HA	10:9:103:LEU:HD23	1.71	0.41
10:9:138:ARG:NE	11:A:1235:C:O2	2.53	0.41
10:9:143:LYS:N	11:A:1253:U:H4'	2.36	0.41
10:9:144:CYS:CB	10:9:147:VAL:HG13	2.49	0.41
11:A:143:G:C2	11:A:173:A:N3	2.88	0.41
11:A:499:U:H2'	11:A:500:C:C6	2.55	0.41
11:A:637:C:OP1	18:H:32:LYS:HG3	2.21	0.41
11:A:685:A:HO2'	11:A:686:C:P	2.44	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:734:A:H4'	11:A:735:C:H5'	2.03	0.41
11:A:1324:G:H5''	12:B:113:ARG:NE	1.99	0.41
11:A:1756[A]:A:H8	11:A:1756[A]:A:OP2	2.04	0.41
12:B:35:PRO:HG3	36:Z:87:ARG:HH21	1.85	0.41
21:K:26:THR:HG21	21:K:97:GLY:C	2.46	0.41
23:M:11:PHE:HE1	23:M:13:HIS:HA	1.86	0.41
28:R:307:ASP:O	28:R:309:VAL:HG23	2.21	0.41
29:S:96:ILE:CD1	29:S:116:LEU:HD22	2.51	0.41
30:T:6:VAL:C	30:T:8:ASP:N	2.78	0.41
30:T:130:ARG:HH11	30:T:130:ARG:HG2	1.86	0.41
32:V:5:ARG:HD3	32:V:5:ARG:N	2.35	0.41
33:W:87:MET:SD	33:W:123:LEU:HB2	2.60	0.41
38:b:232:GLN:HB2	38:b:684:ASN:HB3	2.02	0.41
39:c:580:LEU:HD23	39:c:580:LEU:HA	1.92	0.41
39:c:734:SER:O	39:c:777:VAL:HA	2.20	0.41
1:0:52:PHE:CE2	1:0:109:LEU:HD11	2.55	0.41
5:4:90:GLU:HG2	5:4:223:PHE:HZ	1.84	0.41
9:8:59:TYR:HE1	9:8:61:SER:CB	2.31	0.41
9:8:69:LEU:HD22	9:8:69:LEU:HA	1.83	0.41
11:A:196:G:O2'	11:A:197:A:H8	2.02	0.41
11:A:240:U:H4'	11:A:241:U:OP2	2.20	0.41
11:A:756:A:H1'	33:W:12:LEU:O	2.21	0.41
11:A:916:U:H3	21:K:41:ARG:NH2	2.19	0.41
11:A:959:U:OP2	25:O:14:SER:HA	2.20	0.41
11:A:1570:A:H2'	11:A:1571:C:O4'	2.20	0.41
13:C:21:LEU:HD23	13:C:21:LEU:HA	1.82	0.41
13:C:211:PRO:HB2	13:C:212:LYS:H	1.63	0.41
29:S:52:LYS:HB2	29:S:52:LYS:HE2	1.98	0.41
32:V:23:LYS:O	32:V:24:LEU:HB2	2.20	0.41
35:Y:32:ILE:HD12	35:Y:100:ALA:HB1	2.02	0.41
37:a:391:ILE:HD13	37:a:428:ILE:HG12	2.01	0.41
38:b:615:ASN:HB2	38:b:626:LEU:O	2.20	0.41
5:4:35:PRO:HB2	5:4:36:SER:H	1.63	0.41
5:4:77:GLU:C	5:4:79:HIS:N	2.78	0.41
11:A:268:C:HO2'	11:A:269:G:H5'	1.86	0.41
11:A:901:G:C6	11:A:902:G:C6	3.08	0.41
11:A:992:A:H2'	11:A:993:A:H5'	2.02	0.41
11:A:1162:C:H5''	11:A:1163:A:OP2	2.20	0.41
11:A:1201:G:H22	11:A:1600:A:H5'	1.85	0.41
11:A:1321:A:C5	12:B:105:GLY:N	2.85	0.41
11:A:1360:A:H2'	11:A:1361:U:C1'	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:1370:U:H4'	11:A:1371:A:H5'	2.01	0.41
11:A:1556:A:C5	11:A:1560:U:C2	3.09	0.41
11:A:1584:G:O2'	11:A:1610:G:O6	2.29	0.41
12:B:200:ASP:CB	32:V:85:VAL:CG2	2.99	0.41
18:H:23:ARG:HD2	18:H:23:ARG:HA	1.80	0.41
20:J:37:VAL:O	20:J:41:ILE:HD13	2.21	0.41
25:O:88:LEU:HD23	25:O:88:LEU:HA	1.88	0.41
33:W:131:LEU:HD22	33:W:131:LEU:HA	1.87	0.41
33:W:208:VAL:HG12	33:W:210:ILE:HD11	2.02	0.41
37:a:104:ILE:HD13	37:a:104:ILE:HA	1.77	0.41
37:a:279:LEU:O	37:a:282:TYR:HB3	2.21	0.41
39:c:456:TRP:NE1	39:c:469:SER:OG	2.54	0.41
39:c:682:MET:HE3	39:c:721:SER:HA	2.02	0.41
1:0:84:PHE:HD2	1:0:85:GLN:HG3	1.86	0.41
3:2:37:LYS:O	3:2:59:ARG:HA	2.20	0.41
4:3:129:LEU:HD21	4:3:172:VAL:HG11	2.02	0.41
7:6:41:LEU:HD22	39:c:431:ARG:NE	2.35	0.41
8:7:3:MET:HE3	8:7:8:ARG:NH1	2.35	0.41
8:7:72:GLY:O	8:7:76:LEU:HD22	2.20	0.41
9:8:67:ASP:C	9:8:69:LEU:H	2.29	0.41
11:A:284:G:N7	35:Y:188:ARG:NH1	2.68	0.41
11:A:532:U:H2'	26:P:33:ALA:HB1	2.03	0.41
11:A:570:A:H5''	11:A:571:G:OP2	2.21	0.41
11:A:794:U:H3'	11:A:794:U:OP2	2.20	0.41
11:A:1053:G:C8	11:A:1053:G:H5'	2.56	0.41
11:A:1096:C:O2	11:A:1096:C:H2'	2.20	0.41
11:A:1337:A:H5'	11:A:1338:C:OP2	2.20	0.41
13:C:195:SER:O	13:C:196:ARG:HB3	2.20	0.41
17:G:65:ARG:HA	17:G:66:GLN:C	2.45	0.41
18:H:80:ASN:HD21	18:H:124:LYS:NZ	2.19	0.41
19:I:45:ARG:O	19:I:48:VAL:HG12	2.21	0.41
22:L:23:ARG:HH11	22:L:23:ARG:HG3	1.85	0.41
22:L:114:LYS:HB3	22:L:115:GLY:H	1.77	0.41
22:L:126:LYS:HA	22:L:131:SER:HA	2.02	0.41
28:R:37:SER:OG	28:R:38:ARG:N	2.54	0.41
28:R:164:ASP:C	28:R:166:SER:H	2.29	0.41
33:W:52:LEU:O	33:W:54:TYR:N	2.54	0.41
36:Z:74:GLN:HE22	36:Z:83:TRP:H	1.68	0.41
37:a:420:TYR:O	37:a:423:PRO:HD2	2.20	0.41
38:b:243:SER:HB3	38:b:247:GLU:OE1	2.21	0.41
38:b:456:LYS:HE3	38:b:505:ILE:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:c:487:SER:HG	39:c:488:THR:H	1.68	0.41
1:0:80:SER:OG	1:0:90:ASP:HB2	2.21	0.41
1:0:98:ASP:O	1:0:101:ARG:HG2	2.21	0.41
1:0:103:LEU:HA	1:0:106:GLN:HG2	2.03	0.41
2:1:18:ARG:HA	2:1:25:VAL:O	2.21	0.41
3:2:21:PHE:CZ	3:2:22:ARG:HD3	2.56	0.41
3:2:103:GLN:NE2	3:2:166:TYR:CE1	2.89	0.41
4:3:99:LEU:HD23	4:3:100:PRO:HD2	2.03	0.41
4:3:162:ILE:HA	4:3:165:LYS:HG3	2.02	0.41
5:4:171:ILE:O	5:4:175:GLU:HG2	2.21	0.41
6:5:76:SER:O	6:5:80:HIS:N	2.53	0.41
6:5:82:ARG:O	6:5:84:VAL:HG12	2.20	0.41
9:8:75:LEU:H	9:8:75:LEU:HG	1.46	0.41
11:A:5:U:H2'	11:A:6:G:H8	1.86	0.41
11:A:11:A:H2'	11:A:12:U:H5'	2.02	0.41
11:A:66:U:O2	35:Y:160:ARG:NE	2.52	0.41
11:A:68:A:H3'	11:A:68:A:C8	2.55	0.41
11:A:73:U:O2'	11:A:74:U:C6	2.74	0.41
11:A:140:A:OP2	35:Y:187:LYS:NZ	2.54	0.41
11:A:304:U:OP1	27:Q:136:ARG:HD3	2.20	0.41
11:A:458:G:H5''	11:A:459:G:OP1	2.21	0.41
11:A:768:C:O2	14:D:143:ILE:HG21	2.21	0.41
11:A:1167:G:OP1	17:G:101:GLY:HA3	2.21	0.41
11:A:1180:C:O2	29:S:128:HIS:HE1	2.04	0.41
11:A:1535:U:H1'	11:A:1536:G:C2	2.55	0.41
11:A:1654:G:H2'	11:A:1745:G:N2	2.35	0.41
11:A:1715:G:C2'	11:A:1716:C:H5'	2.51	0.41
12:B:198:MET:SD	12:B:199:PRO:HD2	2.61	0.41
13:C:53:THR:HG22	13:C:91:VAL:HG11	2.03	0.41
13:C:94:ARG:H	13:C:94:ARG:HG3	1.51	0.41
16:F:77:ILE:CD1	16:F:79:GLN:NE2	2.84	0.41
17:G:49:GLU:O	17:G:51:VAL:HG23	2.21	0.41
19:I:4:VAL:HG12	19:I:5:PRO:HD2	2.03	0.41
19:I:82:ARG:NH2	19:I:114:ARG:HG2	2.36	0.41
20:J:61:LYS:HG3	20:J:86:ILE:HB	2.03	0.41
20:J:77:LYS:H	20:J:77:LYS:HG2	1.66	0.41
20:J:109:GLU:OE1	20:J:110:PRO:HD2	2.20	0.41
22:L:107:PHE:CE1	22:L:123:LYS:HB3	2.56	0.41
23:M:29:VAL:HA	23:M:32:LEU:HD12	2.03	0.41
28:R:38:ARG:HG2	28:R:67:ILE:HD13	2.03	0.41
28:R:117:LYS:HD2	28:R:117:LYS:N	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:R:195:HIS:HD2	28:R:199:ILE:HD13	1.81	0.41
29:S:68:PRO:HG2	29:S:71:GLU:OE1	2.21	0.41
31:U:28:LEU:HD22	31:U:32:LEU:HG	2.02	0.41
31:U:52:LEU:HD23	31:U:122:VAL:HG21	2.03	0.41
32:V:10:LYS:HG2	32:V:53:TYR:CE2	2.56	0.41
33:W:100:ARG:NH2	33:W:121:TYR:O	2.54	0.41
33:W:123:LEU:HD22	33:W:236:ILE:HG23	2.03	0.41
33:W:129:VAL:HB	33:W:139:VAL:HG12	2.03	0.41
35:Y:28:PHE:CZ	35:Y:104:PRO:HG3	2.56	0.41
36:Z:74:GLN:C	36:Z:76:ASP:H	2.29	0.41
37:a:248:VAL:HG13	37:a:253:TRP:CZ3	2.56	0.41
39:c:318:TRP:CG	39:c:397:ARG:HH22	2.38	0.41
5:4:21:VAL:HG23	5:4:22:ASP:H	1.86	0.41
9:8:95:HIS:NE2	17:G:112:ARG:HD3	2.35	0.41
11:A:480:G:H22	11:A:509:G:H1'	1.84	0.41
11:A:487:G:C6	11:A:488:G:C8	3.08	0.41
11:A:952:A:O2'	25:O:114:ARG:HG3	2.21	0.41
11:A:992:A:N3	11:A:992:A:O4'	2.53	0.41
11:A:1042:G:C6	11:A:1043:A:N7	2.89	0.41
11:A:1182:U:O2	11:A:1184:A:H8	2.04	0.41
11:A:1281:G:C5	11:A:1282:U:C5	3.09	0.41
11:A:1301:U:H2'	11:A:1302:U:O4'	2.21	0.41
12:B:148:ASP:OD1	12:B:149:LEU:N	2.45	0.41
16:F:58:LEU:CD2	16:F:80:LEU:HD22	2.48	0.41
16:F:98:LEU:HD11	16:F:102:ASN:ND2	2.36	0.41
16:F:98:LEU:HG	16:F:99:GLN:O	2.21	0.41
18:H:6:VAL:HG13	18:H:29:PRO:HD2	2.02	0.41
21:K:81:VAL:HG13	21:K:115:ILE:CG2	2.50	0.41
22:L:90:ASP:OD2	34:X:15:LYS:N	2.53	0.41
23:M:33:THR:C	23:M:35:ILE:H	2.28	0.41
23:M:92:ILE:O	23:M:92:ILE:HD13	2.21	0.41
27:Q:78:THR:HG22	27:Q:84:ILE:CG2	2.45	0.41
28:R:236:ALA:C	28:R:237:GLN:HG2	2.46	0.41
28:R:266:ASP:HA	28:R:267:PRO:HA	1.89	0.41
30:T:52:GLY:C	30:T:54:PHE:N	2.78	0.41
33:W:104:ASP:OD2	33:W:108:ARG:NE	2.41	0.41
37:a:159:TRP:HH2	37:a:202:LEU:HB2	1.86	0.41
37:a:253:TRP:HB3	39:c:664:PHE:HZ	1.86	0.41
38:b:251:LEU:HD11	38:b:254:SER:HB2	2.03	0.41
39:c:585:LEU:O	39:c:588:ILE:HG13	2.21	0.41
5:4:81:PHE:HA	5:4:106:THR:CG2	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:4:207:LEU:HB3	5:4:210:ILE:HD11	2.02	0.40
7:6:2:VAL:HG22	36:Z:64:GLU:OE1	2.21	0.40
9:8:65:LEU:HB3	9:8:71:ILE:CD1	2.51	0.40
11:A:778:G:H1	26:P:10:ARG:HG2	1.86	0.40
11:A:806:A:H5'	11:A:806:A:H8	1.86	0.40
11:A:817:A:C6	11:A:818:C:N4	2.89	0.40
11:A:1322:A:H2	12:B:109:ASN:HD21	1.62	0.40
11:A:1568:C:H6	11:A:1568:C:H2'	1.71	0.40
12:B:13:ASP:O	12:B:16:LEU:HB2	2.21	0.40
19:I:82:ARG:HH12	19:I:114:ARG:HB3	1.84	0.40
22:L:142:LYS:HA	22:L:143:PRO:HD3	1.88	0.40
30:T:49:ASP:O	30:T:51:GLU:N	2.54	0.40
35:Y:58:LYS:HB2	35:Y:59:GLN:OE1	2.21	0.40
37:a:463:TRP:CD2	39:c:744:LEU:HD22	2.56	0.40
39:c:463:PHE:CZ	39:c:468:THR:HA	2.55	0.40
39:c:496:ILE:HG22	39:c:500:LYS:HE3	2.03	0.40
3:2:106:ALA:O	3:2:109:PHE:N	2.53	0.40
4:3:124:LYS:HD3	4:3:124:LYS:HA	1.99	0.40
4:3:186:PRO:HB2	4:3:187:SER:H	1.64	0.40
11:A:473:A:H2'	11:A:474:A:H5'	2.03	0.40
11:A:488:G:N7	11:A:498:G:N2	2.68	0.40
11:A:645:C:H42	11:A:689:G:H1	1.69	0.40
11:A:964:U:H4'	11:A:965:U:O5'	2.21	0.40
11:A:1181:U:H2'	11:A:1182:U:O4'	2.21	0.40
11:A:1191:U:H5'	19:I:143:ARG:CZ	2.51	0.40
11:A:1340:U:C2	11:A:1378:U:H4'	2.57	0.40
11:A:1462:G:N7	23:M:143:ARG:NH2	2.69	0.40
11:A:1715:G:O6	11:A:1716:C:C4	2.56	0.40
12:B:177:LEU:HD23	12:B:177:LEU:HA	1.94	0.40
12:B:202:TYR:HD1	12:B:202:TYR:H	1.68	0.40
14:D:146:PHE:CZ	14:D:149:ARG:HD3	2.56	0.40
21:K:41:ARG:O	21:K:42:VAL:HG22	2.21	0.40
25:O:33:VAL:HA	25:O:36:GLN:HB2	2.02	0.40
26:P:18:LEU:HD23	26:P:18:LEU:HA	1.89	0.40
29:S:85:ILE:HA	29:S:89:MET:SD	2.61	0.40
33:W:48:LEU:HA	33:W:48:LEU:HD12	1.89	0.40
33:W:98:ASN:HD22	33:W:119:ALA:CB	2.35	0.40
33:W:206:ASP:OD1	33:W:206:ASP:N	2.55	0.40
36:Z:3:ASN:OD1	36:Z:7:GLN:HB2	2.20	0.40
37:a:17:GLU:O	37:a:21:VAL:HG23	2.20	0.40
38:b:313:THR:OG1	38:b:340:CYS:HB2	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:c:300:ILE:HD13	39:c:324:ASP:HB3	2.03	0.40
39:c:406:ASN:OD1	39:c:455:ALA:HA	2.21	0.40
39:c:477:ASP:O	39:c:481:ASN:HB2	2.20	0.40
39:c:722:LEU:HD13	39:c:747:LEU:HD12	2.04	0.40
1:0:29:LYS:HG2	1:0:35:TYR:CE2	2.56	0.40
5:4:28:GLU:HB3	5:4:49:ASN:H	1.86	0.40
9:8:54:VAL:HG22	9:8:57:TYR:HE2	1.85	0.40
11:A:600:U:OP2	22:L:108:GLY:HA2	2.22	0.40
11:A:919:A:H4'	21:K:35:GLY:HA3	2.03	0.40
11:A:1018:U:H2'	11:A:1019:A:C8	2.57	0.40
11:A:1163:A:N6	11:A:1164:G:C6	2.89	0.40
11:A:1172:G:C5	11:A:1173:C:C4	3.09	0.40
13:C:74:GLN:OE1	13:C:81:PRO:HA	2.20	0.40
14:D:86:LEU:HA	14:D:86:LEU:HD12	1.85	0.40
16:F:90:GLU:HA	16:F:93:ILE:HG12	2.04	0.40
17:G:36:ALA:HB3	17:G:45:LYS:HZ3	1.85	0.40
17:G:37:GLN:CG	19:I:53:LEU:HD13	2.41	0.40
28:R:242:SER:HB3	28:R:292:LEU:HD23	2.03	0.40
35:Y:55:GLY:CA	35:Y:63:MET:HE3	2.51	0.40
37:a:434:VAL:O	37:a:437:SER:HB3	2.20	0.40
1:0:62:ARG:NH1	1:0:93:HIS:CE1	2.90	0.40
4:3:62:VAL:HG11	4:3:70:PHE:HD2	1.87	0.40
4:3:70:PHE:HD1	4:3:70:PHE:HA	1.65	0.40
5:4:58:SER:O	5:4:62:LYS:HG3	2.22	0.40
5:4:190:PRO:C	5:4:191:GLU:HG2	2.46	0.40
8:7:52:LYS:HG3	8:7:54:TYR:CE2	2.57	0.40
11:A:781:U:HO2'	11:A:782:U:H6	1.63	0.40
11:A:924:A:O2'	11:A:987:G:OP1	2.36	0.40
11:A:1227:A:C2	31:U:43:ARG:HG2	2.56	0.40
11:A:1321:A:C4	12:B:104:PRO:C	2.99	0.40
19:I:35:PRO:C	19:I:37:THR:H	2.29	0.40
25:O:27:LYS:HD2	25:O:28:LEU:H	1.86	0.40
25:O:28:LEU:HA	25:O:28:LEU:HD23	1.85	0.40
26:P:44:LEU:HA	26:P:47:VAL:HG22	2.03	0.40
28:R:10:ARG:HG2	28:R:54:PHE:CE1	2.56	0.40
29:S:12:PHE:CG	29:S:13:LYS:N	2.88	0.40
30:T:72:GLY:O	30:T:76:LEU:HG	2.22	0.40
31:U:57:ALA:HB3	31:U:85:LYS:NZ	2.36	0.40
34:X:38:LEU:O	34:X:42:ARG:HB2	2.21	0.40
35:Y:39:GLU:HB2	35:Y:46:LYS:HG3	2.03	0.40
37:a:352:TYR:O	37:a:357:LEU:HB2	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:a:470:LEU:O	37:a:474:VAL:HG23	2.20	0.40
38:b:655:SER:HA	38:b:662:HIS:CE1	2.56	0.40
39:c:337:ASP:HA	39:c:339:TYR:CE1	2.56	0.40
39:c:427:ARG:HD2	39:c:427:ARG:HA	1.80	0.40
2:1:54:LEU:HD12	2:1:54:LEU:HA	1.94	0.40
4:3:35:LYS:HE3	4:3:35:LYS:HB3	1.89	0.40
4:3:76:LYS:HE2	4:3:76:LYS:HB3	1.86	0.40
5:4:70:LEU:HD21	5:4:79:HIS:CG	2.56	0.40
5:4:176:VAL:C	5:4:178:GLY:H	2.30	0.40
5:4:185:THR:HA	5:4:188:LEU:HD12	2.03	0.40
10:9:87:UNK:C	10:9:89:UNK:N	2.84	0.40
11:A:142:G:C8	11:A:266:A:N1	2.89	0.40
11:A:686:C:H2'	11:A:687:G:C8	2.56	0.40
11:A:817:A:H2'	11:A:818:C:C6	2.56	0.40
11:A:1138:A:H2'	11:A:1139:A:H8	1.85	0.40
11:A:1295:G:P	12:B:108:THR:OG1	2.79	0.40
11:A:1357:A:C6	11:A:1358:G:C6	3.10	0.40
11:A:1361:U:O2	11:A:1361:U:H2'	2.21	0.40
20:J:34:LEU:HD23	20:J:112:VAL:HG13	2.02	0.40
21:K:105:LEU:HD12	21:K:106:ALA:N	2.36	0.40
21:K:122:PRO:C	21:K:124:ASP:H	2.28	0.40
28:R:250:TYR:N	28:R:250:TYR:CD1	2.90	0.40
33:W:36:HIS:HE2	33:W:88:ASP:CG	2.28	0.40
33:W:42:LEU:CD2	33:W:46:VAL:HB	2.52	0.40
39:c:703:LEU:HA	39:c:704:PRO:HD3	1.96	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	98/100 (98%)	89 (91%)	6 (6%)	3 (3%)	3	22

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	1	61/63 (97%)	47 (77%)	9 (15%)	5 (8%)	0	9
3	2	184/188 (98%)	155 (84%)	14 (8%)	15 (8%)	0	9
4	3	182/184 (99%)	128 (70%)	27 (15%)	27 (15%)	0	3
5	4	212/214 (99%)	132 (62%)	42 (20%)	38 (18%)	0	2
6	5	95/97 (98%)	58 (61%)	20 (21%)	17 (18%)	0	2
7	6	79/81 (98%)	62 (78%)	13 (16%)	4 (5%)	1	15
8	7	94/96 (98%)	66 (70%)	18 (19%)	10 (11%)	0	6
9	8	68/70 (97%)	46 (68%)	11 (16%)	11 (16%)	0	2
10	9	50/71 (70%)	30 (60%)	9 (18%)	11 (22%)	0	1
12	B	204/206 (99%)	143 (70%)	35 (17%)	26 (13%)	0	4
13	C	221/223 (99%)	180 (81%)	28 (13%)	13 (6%)	1	13
14	D	183/185 (99%)	153 (84%)	18 (10%)	12 (7%)	1	12
15	E	215/217 (99%)	187 (87%)	16 (7%)	12 (6%)	1	14
16	F	81/83 (98%)	75 (93%)	5 (6%)	1 (1%)	10	44
17	G	204/206 (99%)	154 (76%)	31 (15%)	19 (9%)	0	8
18	H	127/129 (98%)	114 (90%)	10 (8%)	3 (2%)	4	27
19	I	139/141 (99%)	114 (82%)	14 (10%)	11 (8%)	1	9
20	J	105/107 (98%)	87 (83%)	13 (12%)	5 (5%)	2	16
21	K	125/127 (98%)	94 (75%)	16 (13%)	15 (12%)	0	4
22	L	142/144 (99%)	111 (78%)	13 (9%)	18 (13%)	0	4
23	M	143/145 (99%)	110 (77%)	19 (13%)	14 (10%)	0	7
24	N	51/53 (96%)	42 (82%)	7 (14%)	2 (4%)	2	18
25	O	148/150 (99%)	125 (84%)	15 (10%)	8 (5%)	1	14
26	P	132/134 (98%)	106 (80%)	13 (10%)	13 (10%)	0	7
27	Q	153/155 (99%)	125 (82%)	19 (12%)	9 (6%)	1	13
28	R	316/318 (99%)	273 (86%)	30 (10%)	13 (4%)	2	17
29	S	122/124 (98%)	92 (75%)	15 (12%)	15 (12%)	0	4
30	T	141/143 (99%)	111 (79%)	18 (13%)	12 (8%)	0	9
31	U	122/124 (98%)	66 (54%)	23 (19%)	33 (27%)	0	0
32	V	116/120 (97%)	87 (75%)	17 (15%)	12 (10%)	0	6
33	W	258/260 (99%)	202 (78%)	36 (14%)	20 (8%)	1	9

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	X	58/60 (97%)	49 (84%)	7 (12%)	2 (3%)	3	21
35	Y	224/226 (99%)	190 (85%)	22 (10%)	12 (5%)	1	14
36	Z	85/87 (98%)	64 (75%)	11 (13%)	10 (12%)	0	4
37	a	445/964 (46%)	438 (98%)	7 (2%)	0	100	100
38	b	478/763 (63%)	452 (95%)	24 (5%)	2 (0%)	30	67
39	c	542/812 (67%)	507 (94%)	35 (6%)	0	100	100
All	All	6403/7570 (85%)	5264 (82%)	686 (11%)	453 (7%)	2	11

All (453) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	0	24	ARG
2	1	36	THR
2	1	51	ASN
3	2	13	ALA
3	2	22	ARG
3	2	147	ALA
3	2	149	SER
4	3	31	SER
4	3	36	ALA
4	3	64	VAL
4	3	67	LEU
4	3	98	ILE
4	3	104	ARG
4	3	105	THR
4	3	111	LYS
4	3	112	ARG
4	3	131	PHE
4	3	133	THR
4	3	134	GLU
4	3	155	ASP
5	4	21	VAL
5	4	26	ARG
5	4	49	ASN
5	4	58	SER
5	4	60	ALA
5	4	63	GLY
5	4	113	MET
5	4	116	LYS
5	4	176	VAL

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Mol	Chain	Res	Type
5	4	177	GLN
5	4	179	SER
5	4	182	ALA
5	4	206	PRO
5	4	221	PRO
6	5	19	LYS
6	5	45	VAL
6	5	46	GLU
6	5	62	TYR
6	5	65	PRO
6	5	82	ARG
6	5	84	VAL
6	5	85	ARG
7	6	38	PRO
7	6	62	ILE
8	7	60	SER
8	7	81	ASN
8	7	87	VAL
8	7	88	PRO
8	7	93	GLN
9	8	38	HIS
9	8	39	ALA
9	8	43	ASP
9	8	44	GLN
9	8	54	VAL
9	8	71	ILE
9	8	88	ILE
10	9	102	VAL
10	9	103	LEU
10	9	106	TYR
10	9	111	GLU
10	9	128	ALA
10	9	148	TYR
12	B	4	PRO
12	B	29	VAL
12	B	30	GLN
12	B	39	ASN
12	B	66	ALA
12	B	95	ALA
12	B	111	ILE
12	B	191	ARG
12	B	203	PHE

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Mol	Chain	Res	Type
12	B	205	ARG
13	C	4	LEU
13	C	62	ASN
13	C	65	ARG
13	C	93	ASP
13	C	211	PRO
13	C	212	LYS
13	C	216	PRO
13	C	220	PRO
14	D	98	ALA
14	D	100	LYS
14	D	118	LEU
14	D	121	SER
14	D	164	PHE
15	E	146	THR
15	E	148	LEU
16	F	72	PRO
17	G	26	ALA
17	G	39	GLU
17	G	43	PHE
17	G	63	GLN
17	G	101	GLY
17	G	153	GLY
17	G	206	SER
19	I	41	PRO
19	I	58	ASP
19	I	59	LYS
19	I	114	ARG
19	I	116	LEU
19	I	138	PHE
20	J	17	GLN
20	J	118	VAL
21	K	38	THR
21	K	39	ILE
21	K	124	ASP
21	K	125	SER
21	K	126	THR
22	L	3	LYS
22	L	41	SER
22	L	96	VAL
22	L	114	LYS
22	L	128	SER

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Mol	Chain	Res	Type
22	L	131	SER
22	L	137	LYS
22	L	138	GLU
22	L	144	ARG
23	M	14	ILE
23	M	25	ASN
23	M	28	ILE
23	M	60	GLU
23	M	91	ASP
23	M	92	ILE
24	N	8	PHE
25	O	19	SER
25	O	22	ALA
26	P	32	ARG
26	P	36	SER
26	P	78	SER
27	Q	7	VAL
27	Q	29	LYS
27	Q	133	LYS
28	R	51	ASP
28	R	160	GLU
28	R	318	ALA
29	S	29	SER
29	S	54	ALA
29	S	125	PRO
29	S	126	VAL
30	T	31	PRO
30	T	53	TRP
30	T	69	LYS
31	U	21	GLU
31	U	25	GLU
31	U	45	LEU
31	U	55	GLY
31	U	83	GLU
31	U	87	PRO
31	U	89	ILE
31	U	90	LYS
31	U	93	ASP
31	U	126	TRP
32	V	6	THR
32	V	26	LEU
32	V	85	VAL

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Mol	Chain	Res	Type
32	V	86	PRO
32	V	88	VAL
32	V	96	SER
32	V	124	VAL
33	W	104	ASP
33	W	142	HIS
33	W	153	ASN
33	W	164	LEU
33	W	260	GLY
34	X	47	VAL
35	Y	20	ASP
35	Y	25	ARG
35	Y	154	ARG
35	Y	173	PRO
35	Y	174	LYS
36	Z	4	ASP
36	Z	7	GLN
36	Z	11	LEU
38	b	557	GLU
38	b	661	GLU
2	1	35	ASP
2	1	61	ARG
3	2	40	ALA
3	2	105	ASP
3	2	120	THR
3	2	136	SER
3	2	199	LYS
4	3	32	PRO
4	3	156	SER
4	3	186	PRO
5	4	23	PRO
5	4	55	LYS
5	4	72	ASP
5	4	79	HIS
5	4	82	ARG
5	4	93	GLY
5	4	108	ASP
5	4	148	ASN
5	4	181	LEU
5	4	207	LEU
6	5	36	ILE
6	5	63	ALA

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Mol	Chain	Res	Type
6	5	75	VAL
6	5	86	VAL
7	6	63	LEU
8	7	30	ALA
8	7	64	TYR
8	7	82	LEU
9	8	73	GLY
10	9	118	ARG
10	9	127	GLY
12	B	5	ALA
12	B	49	ASN
12	B	81	PHE
12	B	94	GLY
12	B	190	ASP
12	B	194	PRO
12	B	196	SER
13	C	44	THR
13	C	218	LEU
14	D	134	ILE
14	D	167	ALA
14	D	171	ARG
15	E	35	TRP
15	E	203	LYS
15	E	248	SER
17	G	35	GLN
17	G	45	LYS
17	G	58	LEU
17	G	127	GLN
17	G	150	GLY
17	G	223	SER
18	H	66	ASN
19	I	40	GLU
19	I	113	ASP
21	K	40	ALA
21	K	42	VAL
21	K	46	MET
21	K	50	ALA
21	K	51	ASP
21	K	114	ARG
22	L	8	GLY
22	L	97	ASP
23	M	59	GLY

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Mol	Chain	Res	Type
23	M	61	LEU
23	M	142	GLY
24	N	34	TYR
25	O	13	SER
25	O	28	LEU
25	O	68	GLY
26	P	5	VAL
26	P	11	LYS
28	R	3	SER
28	R	28	GLY
28	R	161	LYS
28	R	217	ASP
29	S	48	GLY
29	S	51	SER
29	S	101	ALA
30	T	11	ALA
30	T	28	LEU
30	T	50	ALA
31	U	54	ARG
31	U	63	VAL
31	U	66	VAL
31	U	84	ASN
31	U	91	VAL
31	U	113	ARG
31	U	128	ALA
32	V	25	THR
33	W	12	LEU
33	W	152	PRO
33	W	157	ASN
33	W	195	ILE
33	W	245	LYS
35	Y	24	ILE
35	Y	146	GLY
35	Y	152	ASP
35	Y	153	VAL
36	Z	12	TYR
3	2	41	LYS
3	2	153	GLU
4	3	5	GLN
4	3	29	ASN
4	3	74	GLN
4	3	75	THR

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Mol	Chain	Res	Type
4	3	110	GLN
5	4	35	PRO
5	4	38	PHE
5	4	62	LYS
5	4	209	ASN
6	5	66	LYS
9	8	41	ILE
9	8	55	PRO
9	8	97	LYS
10	9	138	ARG
12	B	27	ARG
12	B	103	THR
13	C	54	ARG
14	D	163	PRO
15	E	106	ASP
15	E	150	GLN
15	E	235	LEU
17	G	33	VAL
17	G	156	ARG
20	J	55	PRO
21	K	18	ARG
21	K	123	SER
22	L	37	ALA
22	L	40	SER
22	L	89	ASN
23	M	10	SER
23	M	80	LYS
23	M	83	ALA
25	O	27	LYS
26	P	34	ASN
26	P	51	GLU
26	P	53	ASP
27	Q	4	GLU
27	Q	55	ASP
27	Q	146	ALA
27	Q	153	PHE
27	Q	154	ALA
28	R	15	GLY
28	R	96	THR
28	R	98	GLU
29	S	11	VAL
29	S	22	LEU

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Mol	Chain	Res	Type
29	S	52	LYS
30	T	25	GLN
31	U	22	VAL
31	U	81	ASP
31	U	82	PRO
31	U	85	LYS
31	U	112	ALA
31	U	135	MET
32	V	83	GLN
32	V	115	LEU
33	W	200	ARG
36	Z	2	GLU
36	Z	10	GLU
36	Z	15	ARG
1	0	23	LYS
2	1	6	PRO
3	2	59	ARG
3	2	152	ILE
4	3	13	PRO
4	3	84	LYS
4	3	132	PRO
5	4	54	LEU
5	4	61	LEU
5	4	81	PHE
5	4	112	SER
5	4	154	SER
5	4	215	VAL
6	5	64	LEU
8	7	94	GLU
10	9	145	HIS
12	B	33	GLN
12	B	158	VAL
12	B	164	ASN
12	B	185	ARG
12	B	189	VAL
13	C	217	ILE
15	E	39	THR
17	G	51	VAL
17	G	79	ASN
19	I	142	TYR
21	K	69	ALA
22	L	92	CYS

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Mol	Chain	Res	Type
22	L	109	ARG
22	L	112	LYS
25	O	138	ASN
26	P	60	PHE
27	Q	145	ALA
28	R	136	ILE
28	R	163	ASP
28	R	237	GLN
30	T	7	ARG
30	T	23	GLN
30	T	39	THR
31	U	39	ASP
31	U	68	GLU
31	U	106	ILE
31	U	107	ASP
31	U	108	ARG
31	U	129	GLU
31	U	130	THR
32	V	23	LYS
32	V	72	LYS
33	W	77	ARG
33	W	80	THR
33	W	163	ASP
33	W	188	ASN
33	W	193	GLY
34	X	50	VAL
35	Y	69	LEU
36	Z	44	ARG
1	0	68	LYS
4	3	73	VAL
4	3	185	ILE
5	4	64	ARG
7	6	51	GLN
13	C	59	LEU
14	D	162	SER
15	E	36	VAL
17	G	21	THR
17	G	64	VAL
18	H	67	GLY
18	H	83	ILE
20	J	49	ASN
22	L	70	LYS

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Mol	Chain	Res	Type
26	P	6	THR
26	P	47	VAL
26	P	77	ASN
29	S	38	PRO
30	T	29	GLU
31	U	101	ALA
33	W	233	LYS
36	Z	46	ILE
36	Z	49	GLU
3	2	10	LYS
3	2	186	GLY
4	3	11	GLN
5	4	78	ASP
5	4	210	ILE
6	5	10	ARG
12	B	139	VAL
14	D	132	ARG
20	J	117	VAL
23	M	7	GLU
23	M	34	THR
25	O	60	VAL
26	P	58	PHE
29	S	10	ARG
29	S	23	GLU
29	S	69	GLU
29	S	130	ARG
33	W	53	LYS
33	W	234	PRO
35	Y	132	ARG
14	D	117	GLY
19	I	97	VAL
21	K	48	VAL
6	5	59	TYR
12	B	117	GLU
31	U	40	GLY
5	4	197	ILE
6	5	50	VAL
10	9	147	VAL
15	E	145	GLY
19	I	29	ILE
30	T	100	ILE
8	7	89	GLY

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Mol	Chain	Res	Type
31	U	117	GLY
33	W	45	ILE
35	Y	70	PRO
15	E	163	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	86/86 (100%)	85 (99%)	1 (1%)	63	75
2	1	56/56 (100%)	36 (64%)	20 (36%)	0	1
3	2	150/150 (100%)	115 (77%)	35 (23%)	1	5
4	3	165/165 (100%)	116 (70%)	49 (30%)	0	2
5	4	191/191 (100%)	138 (72%)	53 (28%)	0	3
6	5	83/83 (100%)	61 (74%)	22 (26%)	0	3
7	6	70/70 (100%)	60 (86%)	10 (14%)	3	13
8	7	77/89 (86%)	57 (74%)	20 (26%)	0	3
9	8	61/61 (100%)	42 (69%)	19 (31%)	0	2
10	9	43/43 (100%)	31 (72%)	12 (28%)	0	3
12	B	164/173 (95%)	114 (70%)	50 (30%)	0	2
13	C	182/182 (100%)	133 (73%)	49 (27%)	0	3
14	D	158/158 (100%)	121 (77%)	37 (23%)	1	5
15	E	176/176 (100%)	124 (70%)	52 (30%)	0	2
16	F	74/74 (100%)	71 (96%)	3 (4%)	27	48
17	G	173/173 (100%)	139 (80%)	34 (20%)	1	7
18	H	110/110 (100%)	82 (74%)	28 (26%)	0	3
19	I	117/117 (100%)	82 (70%)	35 (30%)	0	2
20	J	100/100 (100%)	69 (69%)	31 (31%)	0	2
21	K	81/96 (84%)	57 (70%)	24 (30%)	0	2

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
22	L	119/119 (100%)	93 (78%)	26 (22%)	1	6
23	M	128/128 (100%)	87 (68%)	41 (32%)	0	2
24	N	47/47 (100%)	40 (85%)	7 (15%)	3	12
25	O	127/127 (100%)	86 (68%)	41 (32%)	0	2
26	P	112/112 (100%)	81 (72%)	31 (28%)	0	3
27	Q	129/136 (95%)	102 (79%)	27 (21%)	1	6
28	R	259/261 (99%)	214 (83%)	45 (17%)	2	9
29	S	101/104 (97%)	81 (80%)	20 (20%)	1	7
30	T	115/115 (100%)	84 (73%)	31 (27%)	0	3
31	U	88/100 (88%)	53 (60%)	35 (40%)	0	1
32	V	94/109 (86%)	72 (77%)	22 (23%)	1	5
33	W	221/221 (100%)	160 (72%)	61 (28%)	0	3
34	X	51/51 (100%)	41 (80%)	10 (20%)	1	7
35	Y	188/193 (97%)	145 (77%)	43 (23%)	1	6
36	Z	74/74 (100%)	53 (72%)	21 (28%)	0	2
37	a	404/846 (48%)	400 (99%)	4 (1%)	68	78
38	b	430/693 (62%)	420 (98%)	10 (2%)	44	64
39	c	506/749 (68%)	481 (95%)	25 (5%)	22	43
All	All	5510/6538 (84%)	4426 (80%)	1084 (20%)	3	7

All (1084) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	0	26	LEU
2	1	5	THR
2	1	13	ILE
2	1	14	LYS
2	1	15	VAL
2	1	19	THR
2	1	25	VAL
2	1	32	PHE
2	1	33	LEU
2	1	34	GLU
2	1	38	ARG
2	1	39	THR
2	1	49	ARG

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Mol	Chain	Res	Type
2	1	52	ASP
2	1	54	LEU
2	1	57	MET
2	1	58	GLU
2	1	59	SER
2	1	62	GLU
2	1	64	ARG
2	1	65	ARG
3	2	7	SER
3	2	8	ARG
3	2	14	THR
3	2	20	GLN
3	2	21	PHE
3	2	26	LYS
3	2	28	GLU
3	2	29	LEU
3	2	32	GLN
3	2	36	THR
3	2	46	VAL
3	2	58	LEU
3	2	60	ILE
3	2	72	ILE
3	2	74	LYS
3	2	76	THR
3	2	82	VAL
3	2	103	GLN
3	2	107	THR
3	2	120	THR
3	2	121	LEU
3	2	123	LYS
3	2	135	LYS
3	2	137	LYS
3	2	138	ASN
3	2	140	GLU
3	2	142	LYS
3	2	151	LYS
3	2	152	ILE
3	2	154	SER
3	2	155	SER
3	2	164	ARG
3	2	184	LEU
3	2	196	LEU

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Mol	Chain	Res	Type
3	2	199	LYS
4	3	7	LYS
4	3	9	LEU
4	3	25	VAL
4	3	37	GLU
4	3	38	LEU
4	3	42	GLN
4	3	46	ILE
4	3	49	ILE
4	3	50	ASP
4	3	51	VAL
4	3	58	LEU
4	3	60	ILE
4	3	66	SER
4	3	67	LEU
4	3	70	PHE
4	3	74	GLN
4	3	75	THR
4	3	77	LEU
4	3	78	THR
4	3	79	ARG
4	3	80	GLU
4	3	87	ASP
4	3	95	GLU
4	3	97	ARG
4	3	103	SER
4	3	105	THR
4	3	108	GLN
4	3	109	VAL
4	3	110	GLN
4	3	114	ARG
4	3	116	ARG
4	3	117	THR
4	3	121	VAL
4	3	126	LEU
4	3	130	VAL
4	3	136	VAL
4	3	143	LEU
4	3	144	VAL
4	3	148	LYS
4	3	150	GLN
4	3	154	LEU

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Mol	Chain	Res	Type
4	3	161	GLN
4	3	162	ILE
4	3	166	LEU
4	3	167	GLU
4	3	175	LYS
4	3	181	ILE
4	3	184	GLU
4	3	185	ILE
5	4	21	VAL
5	4	22	ASP
5	4	36	SER
5	4	38	PHE
5	4	47	LEU
5	4	54	LEU
5	4	55	LYS
5	4	58	SER
5	4	61	LEU
5	4	65	VAL
5	4	68	VAL
5	4	70	LEU
5	4	73	LEU
5	4	77	GLU
5	4	78	ASP
5	4	80	SER
5	4	81	PHE
5	4	83	LYS
5	4	85	LYS
5	4	91	VAL
5	4	94	LYS
5	4	96	LEU
5	4	97	LEU
5	4	105	PHE
5	4	108	ASP
5	4	109	LYS
5	4	110	LEU
5	4	115	ARG
5	4	124	ASN
5	4	131	ASP
5	4	135	LEU
5	4	146	GLN
5	4	148	ASN
5	4	149	GLN

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Mol	Chain	Res	Type
5	4	154	SER
5	4	167	VAL
5	4	170	GLU
5	4	174	LYS
5	4	177	GLN
5	4	179	SER
5	4	180	THR
5	4	181	LEU
5	4	183	GLN
5	4	184	LEU
5	4	193	ILE
5	4	202	LYS
5	4	214	LYS
5	4	215	VAL
5	4	218	LEU
5	4	220	GLN
5	4	223	PHE
5	4	225	VAL
5	4	228	LEU
6	5	12	LYS
6	5	30	ILE
6	5	36	ILE
6	5	41	ILE
6	5	44	ILE
6	5	45	VAL
6	5	50	VAL
6	5	53	LEU
6	5	58	VAL
6	5	61	GLU
6	5	64	LEU
6	5	66	LYS
6	5	67	THR
6	5	69	ASN
6	5	70	LYS
6	5	82	ARG
6	5	83	ILE
6	5	84	VAL
6	5	85	ARG
6	5	86	VAL
6	5	87	ARG
6	5	90	GLU
7	6	2	VAL

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Mol	Chain	Res	Type
7	6	3	LEU
7	6	4	VAL
7	6	20	LYS
7	6	26	GLN
7	6	29	ARG
7	6	33	LEU
7	6	34	ASP
7	6	41	LEU
7	6	67	THR
8	7	8	ARG
8	7	13	GLN
8	7	20	VAL
8	7	22	VAL
8	7	27	PHE
8	7	29	GLN
8	7	31	LYS
8	7	32	HIS
8	7	40	LEU
8	7	46	LEU
8	7	47	GLN
8	7	49	LEU
8	7	50	THR
8	7	55	VAL
8	7	56	LYS
8	7	71	GLU
8	7	76	LEU
8	7	78	GLU
8	7	80	LEU
8	7	82	LEU
9	8	38	HIS
9	8	42	LEU
9	8	49	ARG
9	8	50	ILE
9	8	58	ARG
9	8	68	ARG
9	8	69	LEU
9	8	71	ILE
9	8	75	LEU
9	8	77	ARG
9	8	80	LEU
9	8	85	LYS
9	8	88	ILE

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Mol	Chain	Res	Type
9	8	92	ILE
9	8	93	SER
9	8	95	HIS
9	8	96	SER
9	8	100	ILE
9	8	105	THR
10	9	102	VAL
10	9	108	VAL
10	9	120	GLU
10	9	121	CYS
10	9	125	THR
10	9	130	VAL
10	9	137	ASP
10	9	146	SER
10	9	147	VAL
10	9	149	LYS
10	9	150	VAL
10	9	151	ASN
12	B	7	PHE
12	B	9	LEU
12	B	10	THR
12	B	24	LEU
12	B	27	ARG
12	B	29	VAL
12	B	33	GLN
12	B	34	GLU
12	B	37	VAL
12	B	43	ASP
12	B	45	VAL
12	B	47	VAL
12	B	50	VAL
12	B	52	LYS
12	B	55	GLU
12	B	57	LEU
12	B	59	LEU
12	B	62	ARG
12	B	76	ILE
12	B	79	ARG
12	B	84	ARG
12	B	87	LEU
12	B	88	LYS
12	B	96	THR

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Mol	Chain	Res	Type
12	B	98	ILE
12	B	101	ARG
12	B	103	THR
12	B	110	TYR
12	B	111	ILE
12	B	114	SER
12	B	117	GLU
12	B	119	ARG
12	B	123	VAL
12	B	124	THR
12	B	131	GLN
12	B	133	ILE
12	B	135	GLU
12	B	140	ASN
12	B	154	GLU
12	B	156	VAL
12	B	157	ASP
12	B	162	CYS
12	B	168	HIS
12	B	170	ILE
12	B	172	LEU
12	B	177	LEU
12	B	184	LEU
12	B	185	ARG
12	B	196	SER
12	B	197	ILE
13	C	4	LEU
13	C	5	ILE
13	C	7	LYS
13	C	9	ARG
13	C	21	LEU
13	C	23	GLU
13	C	29	LEU
13	C	37	VAL
13	C	39	VAL
13	C	41	VAL
13	C	49	ILE
13	C	53	THR
13	C	65	ARG
13	C	66	ILE
13	C	81	PRO
13	C	84	ILE

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Mol	Chain	Res	Type
13	C	89	GLU
13	C	91	VAL
13	C	92	GLN
13	C	93	ASP
13	C	94	ARG
13	C	96	LEU
13	C	103	GLU
13	C	105	MET
13	C	117	ARG
13	C	127	MET
13	C	129	SER
13	C	134	CYS
13	C	141	LYS
13	C	142	LEU
13	C	151	LYS
13	C	158	ILE
13	C	164	VAL
13	C	170	THR
13	C	172	THR
13	C	176	LEU
13	C	178	ARG
13	C	181	VAL
13	C	182	LEU
13	C	187	LYS
13	C	190	ARG
13	C	200	LYS
13	C	204	ASP
13	C	207	THR
13	C	212	LYS
13	C	215	GLU
13	C	220	PRO
13	C	221	SER
13	C	222	VAL
14	D	3	ARG
14	D	7	THR
14	D	13	SER
14	D	14	THR
14	D	22	SER
14	D	28	LEU
14	D	39	LYS
14	D	46	SER
14	D	49	LEU

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Mol	Chain	Res	Type
14	D	54	ARG
14	D	60	LEU
14	D	78	ARG
14	D	79	ARG
14	D	82	ARG
14	D	88	GLU
14	D	89	ASP
14	D	92	LYS
14	D	93	LEU
14	D	96	VAL
14	D	99	LEU
14	D	101	VAL
14	D	105	LEU
14	D	109	LEU
14	D	110	GLN
14	D	111	THR
14	D	113	VAL
14	D	120	LYS
14	D	130	THR
14	D	133	HIS
14	D	134	ILE
14	D	138	LYS
14	D	149	ARG
14	D	161	THR
14	D	171	ARG
14	D	172	VAL
14	D	175	ARG
14	D	182	GLU
15	E	41	LEU
15	E	50	ILE
15	E	53	ILE
15	E	58	LEU
15	E	64	LYS
15	E	68	ILE
15	E	70	ASP
15	E	71	THR
15	E	72	LEU
15	E	73	LEU
15	E	76	LEU
15	E	77	GLN
15	E	80	VAL
15	E	87	GLN

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Mol	Chain	Res	Type
15	E	89	GLN
15	E	90	THR
15	E	95	ARG
15	E	96	THR
15	E	97	ARG
15	E	103	VAL
15	E	106	ASP
15	E	111	VAL
15	E	117	THR
15	E	119	LYS
15	E	125	ILE
15	E	130	ILE
15	E	134	LEU
15	E	137	ILE
15	E	139	ILE
15	E	140	ARG
15	E	141	ARG
15	E	146	THR
15	E	148	LEU
15	E	156	THR
15	E	159	THR
15	E	166	THR
15	E	174	ARG
15	E	185	LYS
15	E	187	LEU
15	E	206	THR
15	E	208	GLU
15	E	218	ILE
15	E	221	THR
15	E	222	TYR
15	E	226	THR
15	E	227	PRO
15	E	229	LEU
15	E	235	LEU
15	E	237	VAL
15	E	240	LEU
15	E	245	ASP
15	E	246	GLU
16	F	48	GLU
16	F	56	LYS
16	F	73	GLU
17	G	21	THR

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Mol	Chain	Res	Type
17	G	23	VAL
17	G	24	VAL
17	G	25	LEU
17	G	27	THR
17	G	32	GLU
17	G	41	LYS
17	G	45	LYS
17	G	53	VAL
17	G	63	GLN
17	G	68	ILE
17	G	70	VAL
17	G	79	ASN
17	G	89	ILE
17	G	93	LEU
17	G	94	THR
17	G	109	LYS
17	G	114	ILE
17	G	117	THR
17	G	119	ASP
17	G	130	ILE
17	G	140	THR
17	G	146	THR
17	G	147	THR
17	G	149	VAL
17	G	156	ARG
17	G	160	VAL
17	G	162	VAL
17	G	163	SER
17	G	193	THR
17	G	203	LYS
17	G	206	SER
17	G	216	GLU
17	G	225	ARG
18	H	6	VAL
18	H	7	LEU
18	H	22	LYS
18	H	23	ARG
18	H	24	GLN
18	H	25	VAL
18	H	27	ILE
18	H	30	SER
18	H	43	LYS

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Mol	Chain	Res	Type
18	H	47	ILE
18	H	53	ILE
18	H	56	HIS
18	H	65	LEU
18	H	66	ASN
18	H	69	LEU
18	H	74	VAL
18	H	83	ILE
18	H	86	ILE
18	H	87	GLU
18	H	93	LEU
18	H	98	GLN
18	H	103	ILE
18	H	104	LEU
18	H	105	THR
18	H	114	GLU
18	H	119	LYS
18	H	121	VAL
18	H	129	VAL
19	I	4	VAL
19	I	8	GLN
19	I	12	LYS
19	I	14	LYS
19	I	17	THR
19	I	23	LYS
19	I	26	LYS
19	I	36	ILE
19	I	39	VAL
19	I	43	ILE
19	I	44	LEU
19	I	45	ARG
19	I	52	LEU
19	I	53	LEU
19	I	54	LEU
19	I	57	LEU
19	I	59	LYS
19	I	63	ILE
19	I	66	ARG
19	I	67	VAL
19	I	69	VAL
19	I	76	SER
19	I	90	VAL

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Mol	Chain	Res	Type
19	I	94	GLN
19	I	98	ASP
19	I	101	SER
19	I	106	LYS
19	I	115	THR
19	I	117	LEU
19	I	118	ILE
19	I	123	ARG
19	I	128	LYS
19	I	136	SER
19	I	137	ARG
19	I	141	SER
20	J	15	GLN
20	J	17	GLN
20	J	18	GLN
20	J	20	ILE
20	J	22	ILE
20	J	23	ARG
20	J	27	THR
20	J	30	LYS
20	J	31	VAL
20	J	34	LEU
20	J	35	GLU
20	J	42	VAL
20	J	43	LYS
20	J	47	GLN
20	J	48	HIS
20	J	51	VAL
20	J	57	ARG
20	J	58	LEU
20	J	60	THR
20	J	61	LYS
20	J	66	SER
20	J	74	GLU
20	J	76	SER
20	J	81	THR
20	J	88	LYS
20	J	89	ARG
20	J	97	VAL
20	J	99	ILE
20	J	103	ILE
20	J	108	ILE

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Mol	Chain	Res	Type
20	J	121	ASN
21	K	13	VAL
21	K	14	PHE
21	K	16	VAL
21	K	24	ASN
21	K	26	THR
21	K	28	VAL
21	K	29	HIS
21	K	30	VAL
21	K	31	THR
21	K	39	ILE
21	K	42	VAL
21	K	43	THR
21	K	81	VAL
21	K	92	LYS
21	K	99	GLN
21	K	102	LEU
21	K	103	ARG
21	K	107	ARG
21	K	108	SER
21	K	118	VAL
21	K	123	SER
21	K	124	ASP
21	K	125	SER
21	K	137	LEU
22	L	7	ARG
22	L	9	LEU
22	L	14	LYS
22	L	18	HIS
22	L	19	ARG
22	L	26	GLU
22	L	28	ASN
22	L	40	SER
22	L	60	GLU
22	L	62	LYS
22	L	69	ARG
22	L	82	LYS
22	L	83	VAL
22	L	84	THR
22	L	103	LEU
22	L	107	PHE
22	L	109	ARG

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Mol	Chain	Res	Type
22	L	110	LYS
22	L	114	LYS
22	L	117	ILE
22	L	131	SER
22	L	133	LEU
22	L	137	LYS
22	L	138	GLU
22	L	140	LYS
22	L	144	ARG
23	M	3	LEU
23	M	4	VAL
23	M	5	VAL
23	M	8	GLN
23	M	11	PHE
23	M	12	GLN
23	M	13	HIS
23	M	14	ILE
23	M	15	LEU
23	M	17	LEU
23	M	20	THR
23	M	21	ASN
23	M	26	ILE
23	M	28	ILE
23	M	34	THR
23	M	38	VAL
23	M	46	VAL
23	M	54	LEU
23	M	57	ARG
23	M	60	GLU
23	M	61	LEU
23	M	71	GLN
23	M	74	GLN
23	M	77	THR
23	M	80	LYS
23	M	81	ILE
23	M	86	LEU
23	M	89	GLN
23	M	92	ILE
23	M	93	THR
23	M	96	LYS
23	M	107	SER
23	M	108	LYS

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Mol	Chain	Res	Type
23	M	110	ARG
23	M	116	LEU
23	M	119	ILE
23	M	132	ARG
23	M	136	GLN
23	M	138	THR
23	M	140	THR
23	M	143	ARG
24	N	6	VAL
24	N	22	ARG
24	N	25	SER
24	N	30	LEU
24	N	32	ARG
24	N	36	LEU
24	N	48	ASN
25	O	3	ARG
25	O	4	MET
25	O	12	SER
25	O	16	ILE
25	O	21	ASN
25	O	27	LYS
25	O	33	VAL
25	O	36	GLN
25	O	39	LYS
25	O	42	ARG
25	O	45	LEU
25	O	50	ILE
25	O	55	ARG
25	O	56	ASP
25	O	58	HIS
25	O	60	VAL
25	O	62	GLN
25	O	64	ARG
25	O	65	VAL
25	O	66	ILE
25	O	67	THR
25	O	71	ILE
25	O	77	SER
25	O	83	GLU
25	O	84	ILE
25	O	88	LEU
25	O	93	LYS

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Mol	Chain	Res	Type
25	O	94	LYS
25	O	97	SER
25	O	102	LEU
25	O	105	ASN
25	O	109	LYS
25	O	114	ARG
25	O	115	LEU
25	O	125	LEU
25	O	134	VAL
25	O	142	GLU
25	O	145	THR
25	O	149	LEU
25	O	150	VAL
25	O	151	ASN
26	P	8	ARG
26	P	10	ARG
26	P	17	LEU
26	P	29	HIS
26	P	32	ARG
26	P	34	ASN
26	P	44	LEU
26	P	46	GLU
26	P	47	VAL
26	P	49	LYS
26	P	51	GLU
26	P	52	LYS
26	P	57	VAL
26	P	61	ARG
26	P	62	THR
26	P	75	VAL
26	P	81	GLU
26	P	84	LYS
26	P	88	THR
26	P	93	ARG
26	P	96	LEU
26	P	99	LYS
26	P	102	LYS
26	P	105	ARG
26	P	107	GLN
26	P	112	LYS
26	P	123	LYS
26	P	127	LYS

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Mol	Chain	Res	Type
26	P	128	LYS
26	P	129	VAL
26	P	135	ASP
27	Q	3	THR
27	Q	4	GLU
27	Q	7	VAL
27	Q	8	GLN
27	Q	21	ASN
27	Q	27	THR
27	Q	29	LYS
27	Q	30	ARG
27	Q	40	LEU
27	Q	43	LYS
27	Q	44	THR
27	Q	54	ILE
27	Q	56	LYS
27	Q	63	LEU
27	Q	67	ARG
27	Q	74	THR
27	Q	79	LYS
27	Q	80	MET
27	Q	83	THR
27	Q	94	ILE
27	Q	99	ARG
27	Q	109	VAL
27	Q	123	VAL
27	Q	127	GLN
27	Q	131	ILE
27	Q	140	VAL
27	Q	141	LYS
28	R	6	VAL
28	R	7	LEU
28	R	8	VAL
28	R	10	ARG
28	R	46	LYS
28	R	47	LEU
28	R	48	THR
28	R	51	ASP
28	R	52	GLN
28	R	58	VAL
28	R	76	ASP
28	R	87	LYS

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Mol	Chain	Res	Type
28	R	88	THR
28	R	91	LEU
28	R	94	VAL
28	R	96	THR
28	R	112	SER
28	R	117	LYS
28	R	118	LYS
28	R	129	LYS
28	R	134	TRP
28	R	136	ILE
28	R	137	LYS
28	R	141	LEU
28	R	153	GLN
28	R	165	ASP
28	R	166	SER
28	R	185	GLN
28	R	188	ILE
28	R	193	ILE
28	R	196	ASN
28	R	199	ILE
28	R	211	ILE
28	R	216	LYS
28	R	222	LEU
28	R	238	ASP
28	R	248	ASN
28	R	250	TYR
28	R	265	LEU
28	R	266	ASP
28	R	268	GLN
28	R	292	LEU
28	R	300	THR
28	R	316	MET
28	R	317	THR
29	S	14	THR
29	S	22	LEU
29	S	24	LYS
29	S	26	LEU
29	S	30	THR
29	S	31	GLU
29	S	34	VAL
29	S	35	LYS
29	S	44	ARG

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Mol	Chain	Res	Type
29	S	47	ARG
29	S	50	THR
29	S	52	LYS
29	S	69	GLU
29	S	86	VAL
29	S	92	SER
29	S	100	LYS
29	S	110	GLU
29	S	121	ILE
29	S	125	PRO
29	S	130	ARG
30	T	4	VAL
30	T	6	VAL
30	T	13	ASP
30	T	22	LEU
30	T	28	LEU
30	T	30	VAL
30	T	33	TYR
30	T	34	VAL
30	T	35	ASP
30	T	36	ILE
30	T	37	VAL
30	T	38	LYS
30	T	57	ARG
30	T	63	ARG
30	T	67	MET
30	T	68	ARG
30	T	84	LYS
30	T	86	ARG
30	T	88	VAL
30	T	89	ARG
30	T	92	LYS
30	T	94	ILE
30	T	103	LYS
30	T	111	ILE
30	T	113	ILE
30	T	126	GLU
30	T	131	ASP
30	T	132	LEU
30	T	134	ARG
30	T	135	ILE
30	T	144	GLU

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Mol	Chain	Res	Type
31	U	25	GLU
31	U	28	LEU
31	U	31	VAL
31	U	33	ARG
31	U	36	LEU
31	U	41	LEU
31	U	43	ARG
31	U	45	LEU
31	U	50	LYS
31	U	52	LEU
31	U	53	THR
31	U	58	LEU
31	U	59	LEU
31	U	61	VAL
31	U	62	LEU
31	U	63	VAL
31	U	66	VAL
31	U	71	ILE
31	U	74	LEU
31	U	75	VAL
31	U	83	GLU
31	U	88	LEU
31	U	89	ILE
31	U	97	LEU
31	U	103	LEU
31	U	116	VAL
31	U	119	SER
31	U	121	VAL
31	U	129	GLU
31	U	132	GLU
31	U	135	MET
31	U	138	GLU
31	U	139	HIS
31	U	140	PHE
31	U	141	SER
32	V	4	VAL
32	V	25	THR
32	V	26	LEU
32	V	29	GLN
32	V	30	THR
32	V	34	LEU
32	V	38	ILE

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Mol	Chain	Res	Type
32	V	44	LYS
32	V	46	LEU
32	V	49	LYS
32	V	54	THR
32	V	69	ILE
32	V	72	LYS
32	V	73	LEU
32	V	78	ARG
32	V	83	GLN
32	V	105	GLN
32	V	107	SER
32	V	111	LYS
32	V	113	LEU
32	V	115	LEU
32	V	119	LEU
33	W	6	LYS
33	W	7	LYS
33	W	9	LEU
33	W	12	LEU
33	W	23	LEU
33	W	26	CYS
33	W	38	LEU
33	W	39	ARG
33	W	45	ILE
33	W	48	LEU
33	W	49	ARG
33	W	56	LEU
33	W	59	ARG
33	W	62	LYS
33	W	67	GLN
33	W	68	ARG
33	W	70	VAL
33	W	72	VAL
33	W	77	ARG
33	W	92	LEU
33	W	95	THR
33	W	102	VAL
33	W	105	VAL
33	W	116	ASP
33	W	117	GLU
33	W	123	LEU
33	W	126	VAL

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Mol	Chain	Res	Type
33	W	128	LYS
33	W	129	VAL
33	W	131	LEU
33	W	133	LYS
33	W	146	THR
33	W	153	ASN
33	W	155	LYS
33	W	158	ASP
33	W	160	VAL
33	W	164	LEU
33	W	166	SER
33	W	176	ASP
33	W	180	LEU
33	W	181	VAL
33	W	187	ARG
33	W	192	ILE
33	W	197	HIS
33	W	198	LYS
33	W	211	LYS
33	W	214	LEU
33	W	215	ASP
33	W	220	THR
33	W	221	ARG
33	W	222	LEU
33	W	227	VAL
33	W	231	GLN
33	W	236	ILE
33	W	237	SER
33	W	240	LYS
33	W	242	LYS
33	W	246	LEU
33	W	248	ILE
33	W	259	GLN
33	W	261	LEU
34	X	3	LYS
34	X	20	LYS
34	X	21	VAL
34	X	25	GLU
34	X	28	LYS
34	X	29	LYS
34	X	42	ARG
34	X	48	THR

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Mol	Chain	Res	Type
34	X	49	LEU
34	X	50	VAL
35	Y	9	VAL
35	Y	21	GLU
35	Y	25	ARG
35	Y	30	LYS
35	Y	32	ILE
35	Y	45	PHE
35	Y	58	LYS
35	Y	59	GLN
35	Y	69	LEU
35	Y	71	THR
35	Y	76	LEU
35	Y	78	THR
35	Y	79	LYS
35	Y	82	SER
35	Y	87	ARG
35	Y	97	VAL
35	Y	98	ARG
35	Y	105	ASP
35	Y	109	LEU
35	Y	111	LEU
35	Y	120	GLU
35	Y	124	LEU
35	Y	126	ASP
35	Y	127	THR
35	Y	129	VAL
35	Y	132	ARG
35	Y	133	LEU
35	Y	137	ARG
35	Y	142	ARG
35	Y	143	LYS
35	Y	150	GLU
35	Y	155	ASP
35	Y	158	ILE
35	Y	162	VAL
35	Y	170	THR
35	Y	175	ILE
35	Y	176	GLN
35	Y	177	ARG
35	Y	179	VAL
35	Y	211	LEU

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Mol	Chain	Res	Type
35	Y	212	LEU
35	Y	217	SER
35	Y	223	LYS
36	Z	1	MET
36	Z	2	GLU
36	Z	3	ASN
36	Z	5	LYS
36	Z	7	GLN
36	Z	11	LEU
36	Z	24	ILE
36	Z	25	LYS
36	Z	32	VAL
36	Z	38	LYS
36	Z	41	GLU
36	Z	49	GLU
36	Z	50	TYR
36	Z	52	THR
36	Z	60	ARG
36	Z	62	ARG
36	Z	68	SER
36	Z	69	LEU
36	Z	74	GLN
36	Z	78	LEU
36	Z	80	LYS
37	a	100	VAL
37	a	104	ILE
37	a	261	GLU
37	a	397	VAL
38	b	260	THR
38	b	556	LYS
38	b	557	GLU
38	b	559	THR
38	b	560	ASP
38	b	561	VAL
38	b	564	ARG
38	b	643	ASP
38	b	659	LYS
38	b	660	VAL
39	c	300	ILE
39	c	309	ASN
39	c	326	SER
39	c	348	ILE

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Mol	Chain	Res	Type
39	c	407	LEU
39	c	416	GLU
39	c	473	LEU
39	c	482	LEU
39	c	483	ILE
39	c	529	GLN
39	c	550	LEU
39	c	571	LEU
39	c	582	GLN
39	c	589	SER
39	c	590	LEU
39	c	606	LEU
39	c	630	ILE
39	c	640	ILE
39	c	645	ILE
39	c	648	SER
39	c	652	ILE
39	c	705	ASN
39	c	738	VAL
39	c	771	ASP
39	c	778	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (90) such sidechains are listed below:

Mol	Chain	Res	Type
1	0	33	GLN
1	0	55	ASN
1	0	106	GLN
3	2	64	ASN
3	2	94	ASN
3	2	116	HIS
4	3	108	GLN
5	4	101	HIS
5	4	149	GLN
8	7	62	GLN
9	8	95	HIS
10	9	151	ASN
12	B	168	HIS
13	C	159	HIS
13	C	179	GLN
14	D	48	GLN
14	D	110	GLN

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Mol	Chain	Res	Type
14	D	112	GLN
14	D	131	GLN
15	E	82	ASN
15	E	89	GLN
15	E	94	GLN
15	E	189	GLN
15	E	199	GLN
15	E	201	ASN
16	F	27	HIS
16	F	79	GLN
16	F	95	GLN
16	F	99	GLN
16	F	102	ASN
16	F	106	HIS
17	G	35	GLN
17	G	79	ASN
17	G	104	ASN
17	G	128	ASN
17	G	139	ASN
17	G	170	GLN
18	H	24	GLN
18	H	39	GLN
18	H	64	GLN
18	H	80	ASN
19	I	62	ASN
19	I	103	ASN
20	J	47	GLN
22	L	75	GLN
23	M	6	GLN
23	M	21	ASN
23	M	78	HIS
23	M	89	GLN
23	M	104	ASN
24	N	53	ASN
26	P	133	ASN
27	Q	21	ASN
27	Q	92	HIS
27	Q	110	HIS
27	Q	127	GLN
28	R	29	GLN
28	R	101	GLN
28	R	153	GLN

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Mol	Chain	Res	Type
28	R	196	ASN
29	S	82	ASN
29	S	103	ASN
29	S	104	GLN
30	T	64	HIS
30	T	127	ASN
31	U	125	ASN
32	V	62	GLN
32	V	101	ASN
32	V	104	ASN
32	V	105	GLN
33	W	50	ASN
33	W	98	ASN
33	W	157	ASN
34	X	46	ASN
35	Y	22	HIS
35	Y	65	GLN
36	Z	74	GLN
37	a	239	GLN
37	a	402	GLN
37	a	406	ASN
38	b	338	GLN
38	b	459	ASN
38	b	469	HIS
38	b	473	GLN
38	b	491	GLN
39	c	390	HIS
39	c	529	GLN
39	c	575	HIS
39	c	582	GLN
39	c	770	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
11	A	1763/1781 (98%)	547 (31%)	86 (4%)

All (547) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
11	A	2	A

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Mol	Chain	Res	Type
11	A	4	C
11	A	8	U
11	A	16	G
11	A	20	G
11	A	25	C
11	A	26	A
11	A	27	U
11	A	34	G
11	A	39	A
11	A	41	A
11	A	42	G
11	A	45	U
11	A	46	A
11	A	47	A
11	A	50	C
11	A	57	G
11	A	60	U
11	A	67	A
11	A	68	A
11	A	69	G
11	A	72	A
11	A	73	U
11	A	74	U
11	A	75	U
11	A	76	A
11	A	77	U
11	A	78	A
11	A	97	C
11	A	100	A
11	A	101	U
11	A	104	A
11	A	114	C
11	A	115	G
11	A	126	A
11	A	127	G
11	A	131	C
11	A	132	U
11	A	133	U
11	A	134	U
11	A	135	A
11	A	136	C
11	A	137	U

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Mol	Chain	Res	Type
11	A	138	A
11	A	139	C
11	A	140	A
11	A	141	U
11	A	144	U
11	A	145	A
11	A	146	U
11	A	153	G
11	A	158	U
11	A	159	U
11	A	175	G
11	A	178	U
11	A	179	A
11	A	185	U
11	A	186	C
11	A	187	G
11	A	188	A
11	A	189	C
11	A	190	C
11	A	191	C
11	A	192	U
11	A	193	U
11	A	194	U
11	A	195	G
11	A	196	G
11	A	197	A
11	A	198	A
11	A	199	G
11	A	200	A
11	A	215	A
11	A	218	A
11	A	219	A
11	A	223	U
11	A	225	A
11	A	226	A
11	A	227	U
11	A	228	G
11	A	229	U
11	A	233	C
11	A	234	G
11	A	235	G
11	A	236	A

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Mol	Chain	Res	Type
11	A	238	U
11	A	239	C
11	A	240	U
11	A	241	U
11	A	242	U
11	A	249	U
11	A	250	C
11	A	261	U
11	A	262	U
11	A	265	A
11	A	266	A
11	A	271	A
11	A	272	U
11	A	274	G
11	A	275	C
11	A	276	C
11	A	277	U
11	A	278	U
11	A	279	G
11	A	280	U
11	A	281	G
11	A	288	A
11	A	290	G
11	A	299	A
11	A	301	A
11	A	306	U
11	A	308	C
11	A	309	C
11	A	314	C
11	A	316	A
11	A	319	U
11	A	320	U
11	A	321	C
11	A	322	G
11	A	337	G
11	A	338	C
11	A	341	A
11	A	348	U
11	A	352	A
11	A	359	A
11	A	360	A
11	A	361	C

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Mol	Chain	Res	Type
11	A	399	A
11	A	400	A
11	A	401	A
11	A	402	C
11	A	403	G
11	A	404	G
11	A	411	C
11	A	416	A
11	A	417	A
11	A	418	G
11	A	423	G
11	A	424	C
11	A	425	A
11	A	426	G
11	A	428	A
11	A	434	G
11	A	439	U
11	A	444	C
11	A	445	A
11	A	446	A
11	A	448	C
11	A	467	G
11	A	468	A
11	A	470	A
11	A	475	A
11	A	477	A
11	A	484	C
11	A	485	A
11	A	486	G
11	A	487	G
11	A	488	G
11	A	493	U
11	A	494	U
11	A	495	C
11	A	496	G
11	A	497	G
11	A	498	G
11	A	499	U
11	A	500	C
11	A	502	U
11	A	503	G
11	A	504	U

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Mol	Chain	Res	Type
11	A	505	A
11	A	506	A
11	A	507	U
11	A	508	U
11	A	510	G
11	A	511	A
11	A	512	A
11	A	513	U
11	A	515	A
11	A	516	G
11	A	519	C
11	A	525	A
11	A	527	A
11	A	532	U
11	A	538	A
11	A	539	G
11	A	540	G
11	A	541	A
11	A	542	A
11	A	543	C
11	A	544	A
11	A	545	A
11	A	548	G
11	A	555	A
11	A	556	A
11	A	557	G
11	A	558	U
11	A	559	C
11	A	565	C
11	A	570	A
11	A	575	C
11	A	579	A
11	A	580	A
11	A	582	U
11	A	583	C
11	A	585	A
11	A	594	A
11	A	595	G
11	A	597	G
11	A	605	A
11	A	607	G
11	A	611	U

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Mol	Chain	Res	Type
11	A	619	A
11	A	620	A
11	A	622	A
11	A	623	A
11	A	624	G
11	A	630	A
11	A	639	U
11	A	640	U
11	A	650	U
11	A	653	C
11	A	655	G
11	A	656	G
11	A	657	U
11	A	658	C
11	A	677	G
11	A	679	U
11	A	680	U
11	A	684	A
11	A	685	A
11	A	686	C
11	A	692	C
11	A	694	U
11	A	696	C
11	A	697	C
11	A	699	U
11	A	700	C
11	A	701	U
11	A	702	G
11	A	703	G
11	A	704	C
11	A	705	U
11	A	706	A
11	A	707	A
11	A	709	C
11	A	710	U
11	A	712	G
11	A	713	A
11	A	714	G
11	A	717	C
11	A	718	U
11	A	719	U
11	A	720	G

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Mol	Chain	Res	Type
11	A	721	U
11	A	722	G
11	A	723	G
11	A	725	U
11	A	727	U
11	A	728	U
11	A	729	G
11	A	730	G
11	A	731	C
11	A	732	G
11	A	733	A
11	A	734	A
11	A	735	C
11	A	736	C
11	A	737	A
11	A	738	G
11	A	742	U
11	A	743	U
11	A	745	U
11	A	754	A
11	A	755	A
11	A	756	A
11	A	758	U
11	A	765	G
11	A	766	U
11	A	771	A
11	A	774	A
11	A	775	G
11	A	778	G
11	A	780	A
11	A	781	U
11	A	782	U
11	A	783	G
11	A	784	C
11	A	785	U
11	A	787	G
11	A	789	A
11	A	793	A
11	A	794	U
11	A	795	U
11	A	806	A
11	A	811	A

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Mol	Chain	Res	Type
11	A	812	A
11	A	813	U
11	A	815	G
11	A	816	G
11	A	818	C
11	A	819	G
11	A	820	U
11	A	821	U
11	A	823	G
11	A	824	G
11	A	829	A
11	A	830	U
11	A	831	U
11	A	832	U
11	A	833	U
11	A	837	G
11	A	838	G
11	A	840	U
11	A	846	G
11	A	848	C
11	A	849	C
11	A	854	U
11	A	862	A
11	A	863	A
11	A	864	U
11	A	873	U
11	A	876	G
11	A	892	A
11	A	896	U
11	A	898	A
11	A	912	U
11	A	913	G
11	A	914	G
11	A	921	U
11	A	928	U
11	A	933	A
11	A	935	U
11	A	942	G
11	A	944	A
11	A	951	A
11	A	959	U
11	A	960	U

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Mol	Chain	Res	Type
11	A	961	U
11	A	966	A
11	A	968	U
11	A	982	U
11	A	988	A
11	A	992	A
11	A	993	A
11	A	995	A
11	A	997	G
11	A	1003	A
11	A	1004	U
11	A	1005	A
11	A	1020	A
11	A	1021	C
11	A	1026	A
11	A	1028	C
11	A	1031	U
11	A	1039	A
11	A	1040	G
11	A	1052	U
11	A	1053	G
11	A	1058	U
11	A	1059	U
11	A	1060	U
11	A	1061	A
11	A	1064	G
11	A	1073	G
11	A	1074	G
11	A	1079	U
11	A	1080	U
11	A	1082	C
11	A	1083	G
11	A	1084	A
11	A	1086	A
11	A	1087	A
11	A	1091	A
11	A	1092	A
11	A	1093	A
11	A	1096	C
11	A	1097	U
11	A	1100	G
11	A	1104	U

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Mol	Chain	Res	Type
11	A	1111	G
11	A	1138	A
11	A	1139	A
11	A	1146	G
11	A	1149	G
11	A	1151	A
11	A	1155	G
11	A	1157	A
11	A	1158	C
11	A	1160	A
11	A	1162	C
11	A	1167	G
11	A	1185	U
11	A	1188	G
11	A	1191	U
11	A	1194	A
11	A	1196	A
11	A	1197	C
11	A	1199	G
11	A	1200	G
11	A	1202	A
11	A	1207	C
11	A	1208	A
11	A	1217	A
11	A	1218	G
11	A	1219	A
11	A	1221	A
11	A	1226	A
11	A	1227	A
11	A	1228	G
11	A	1229	G
11	A	1235	C
11	A	1243	G
11	A	1244	A
11	A	1245	G
11	A	1250	U
11	A	1251	U
11	A	1257	U
11	A	1258	U
11	A	1260	U
11	A	1269	U
11	A	1286	U

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Mol	Chain	Res	Type
11	A	1301	U
11	A	1314	U
11	A	1315	U
11	A	1321	A
11	A	1329	A
11	A	1337	A
11	A	1339	C
11	A	1340	U
11	A	1341	A
11	A	1344	A
11	A	1345	A
11	A	1349	G
11	A	1354	G
11	A	1361	U
11	A	1363	U
11	A	1364	G
11	A	1370	U
11	A	1371	A
11	A	1372	U
11	A	1379	C
11	A	1382	A
11	A	1383	G
11	A	1388	A
11	A	1390	U
11	A	1398	U
11	A	1399	C
11	A	1400	A
11	A	1412	G
11	A	1413	U
11	A	1414	U
11	A	1415	U
11	A	1420	C
11	A	1421	A
11	A	1427	A
11	A	1428	G
11	A	1429	G
11	A	1431	C
11	A	1445	G
11	A	1446	A
11	A	1448	G
11	A	1454	G
11	A	1457	C

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Mol	Chain	Res	Type
11	A	1459	C
11	A	1461	C
11	A	1462	G
11	A	1471	A
11	A	1473	U
11	A	1474	G
11	A	1475	A
11	A	1478	G
11	A	1482	C
11	A	1486	G
11	A	1488	G
11	A	1489	U
11	A	1490	C
11	A	1491	U
11	A	1492	A
11	A	1493	A
11	A	1499	G
11	A	1500	C
11	A	1506	G
11	A	1514	U
11	A	1516	A
11	A	1518	C
11	A	1521	G
11	A	1522	U
11	A	1523	G
11	A	1524	A
11	A	1535	U
11	A	1536	G
11	A	1537	C
11	A	1538	U
11	A	1539	G
11	A	1540	G
11	A	1557	U
11	A	1559	A
11	A	1569	A
11	A	1573	A
11	A	1574	G
11	A	1575	G
11	A	1584	G
11	A	1590	G
11	A	1601	G
11	A	1616	G

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Mol	Chain	Res	Type
11	A	1619	C
11	A	1624	C
11	A	1625	C
11	A	1627	U
11	A	1631	A
11	A	1635	A
11	A	1649	G
11	A	1657	U
11	A	1658	G
11	A	1663	G
11	A	1680	G
11	A	1682	U
11	A	1683	C
11	A	1684	U
11	A	1685	G
11	A	1686	C
11	A	1687	U
11	A	1693	A
11	A	1712	A
11	A	1713	G
11	A	1716	C
11	A	1717	G
11	A	1727	G
11	A	1729	C
11	A	1731	A
11	A	1759	C
11	A	1760	G
11	A	1761	U
11	A	1762	A
11	A	1766	A
11	A	1768	G
11	A	1769	U
11	A	1770	U
11	A	1780	G
11	A	1782	A
11	A	1783	C
11	A	1789	G
11	A	1792	G
11	A	1793	G
11	A	1794	A
11	A	1795	U
11	A	1796	C

All (86) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
11	A	2	A
11	A	25	C
11	A	45	U
11	A	68	A
11	A	73	U
11	A	74	U
11	A	76	A
11	A	103	A
11	A	114	C
11	A	126	A
11	A	130	C
11	A	131	C
11	A	132	U
11	A	133	U
11	A	136	C
11	A	139	C
11	A	144	U
11	A	158	U
11	A	187	G
11	A	217	A
11	A	218	A
11	A	232	U
11	A	239	C
11	A	240	U
11	A	278	U
11	A	280	U
11	A	320	U
11	A	400	A
11	A	417	A
11	A	484	C
11	A	495	C
11	A	497	G
11	A	498	G
11	A	499	U
11	A	501	U
11	A	503	G
11	A	507	U
11	A	512	A
11	A	542	A
11	A	543	C
11	A	555	A
11	A	558	U

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Mol	Chain	Res	Type
11	A	582	U
11	A	685	A
11	A	704	C
11	A	720	G
11	A	721	U
11	A	734	A
11	A	755	A
11	A	781	U
11	A	782	U
11	A	794	U
11	A	811	A
11	A	815	G
11	A	819	G
11	A	823	G
11	A	829	A
11	A	913	G
11	A	1051	G
11	A	1058	U
11	A	1081	A
11	A	1137	A
11	A	1157	A
11	A	1187	U
11	A	1195	C
11	A	1196	A
11	A	1207	C
11	A	1226	A
11	A	1234	A
11	A	1244	A
11	A	1250	U
11	A	1339	C
11	A	1344	A
11	A	1370	U
11	A	1428	G
11	A	1481	C
11	A	1489	U
11	A	1490	C
11	A	1521	G
11	A	1568	C
11	A	1572	G
11	A	1573	A
11	A	1615	C
11	A	1657	U

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Mol	Chain	Res	Type
11	A	1711	C
11	A	1761	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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
11	A	3
3	2	1
32	V	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	2	123:LYS	C	135:LYS	N	19.74
1	A	658:C	O3'	676:G	P	17.56
1	V	89:SER	C	95:ARG	N	3.95
1	A	1151:A	O3'	1152:A	P	3.15
1	A	1626:U	O3'	1627:U	P	2.19

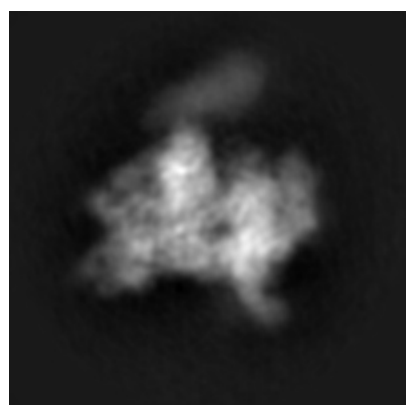
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-2845. These allow visual inspection of the internal detail of the map and identification of artifacts.

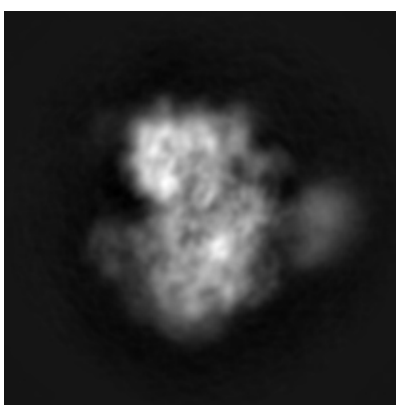
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

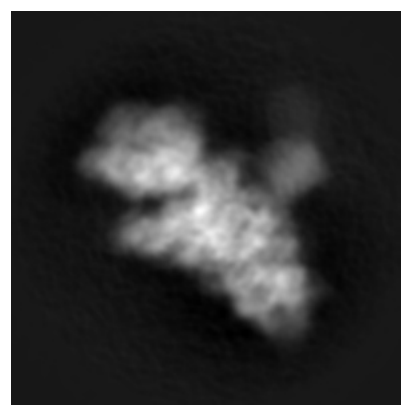
6.1.1 Primary map



X



Y

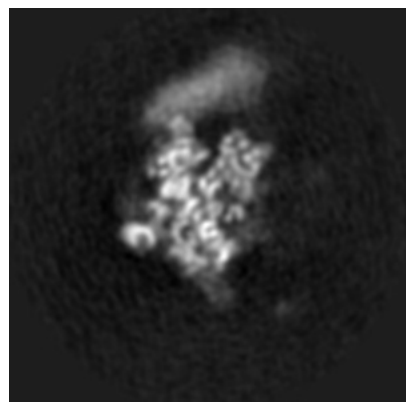


Z

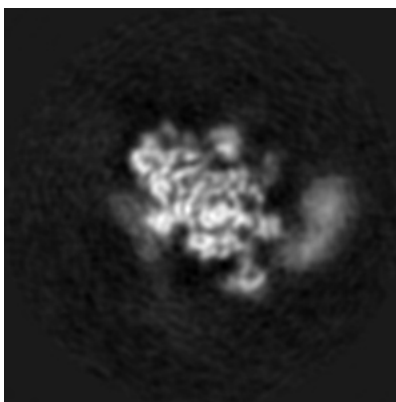
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

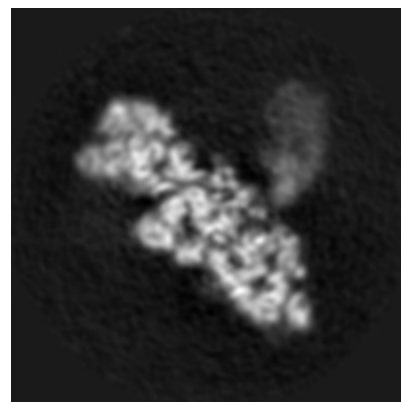
6.2.1 Primary map



X Index: 128



Y Index: 128

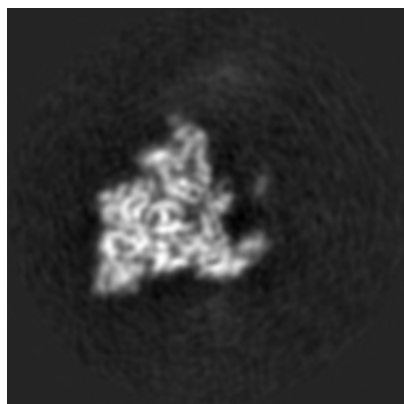


Z Index: 128

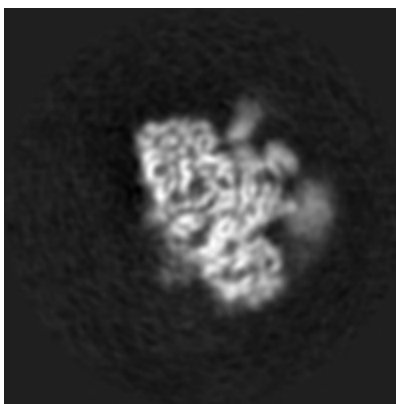
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

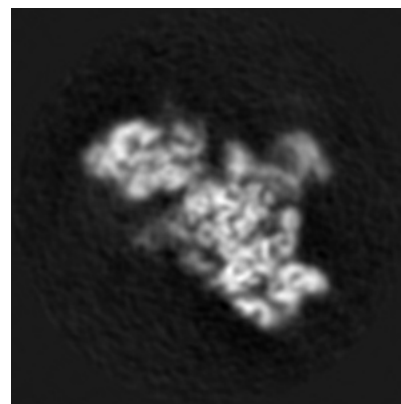
6.3.1 Primary map



X Index: 150



Y Index: 108

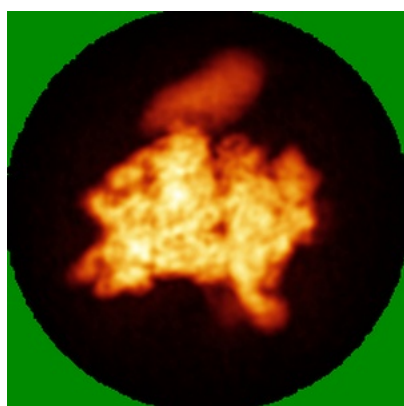


Z Index: 103

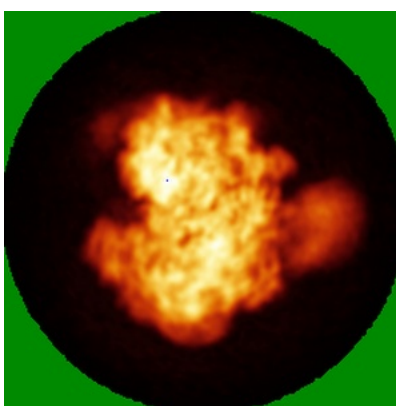
The images above show the largest variance slices of the map in three orthogonal directions.

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

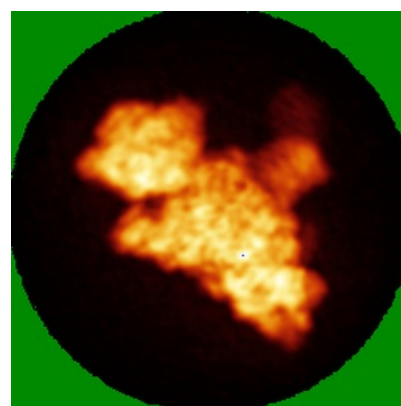
6.4.1 Primary map



X



Y

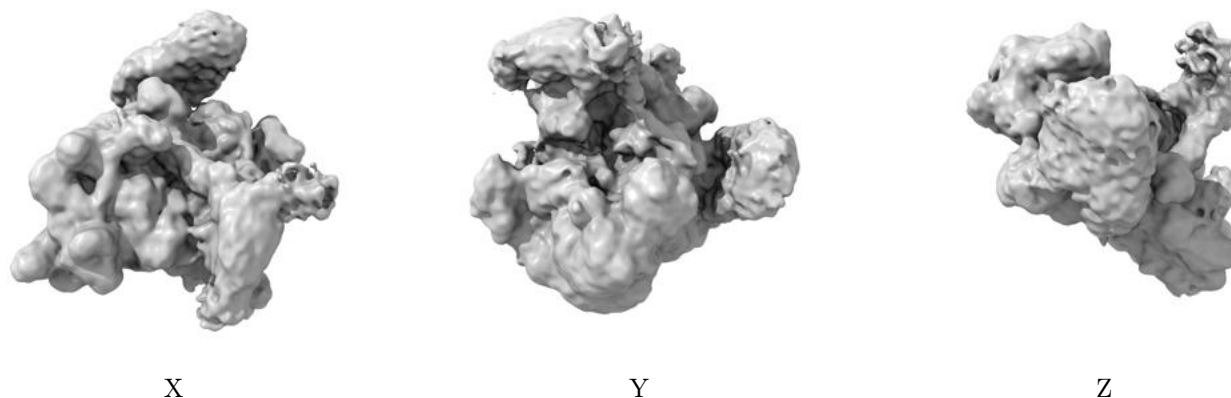


Z

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 0.015. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

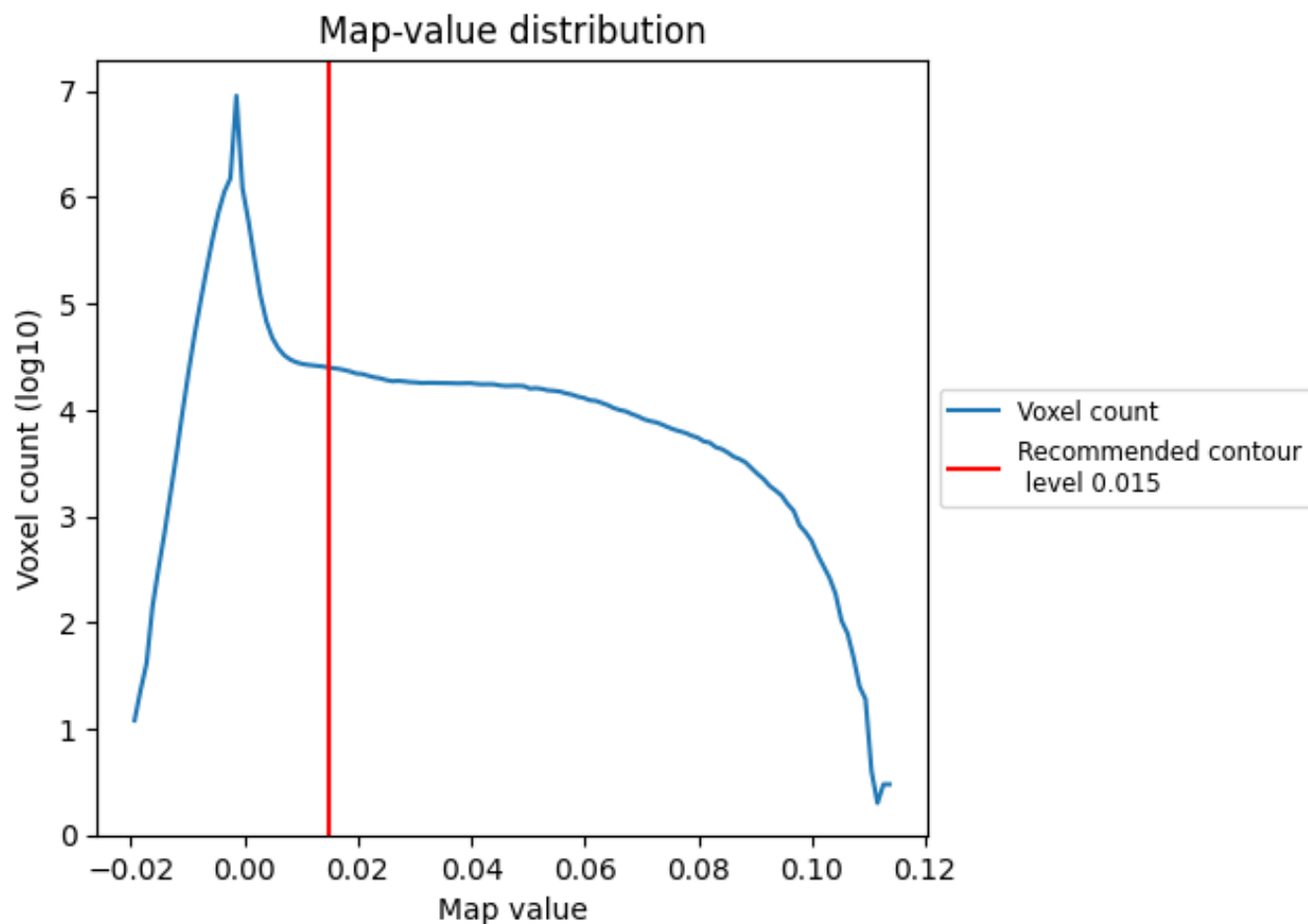
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

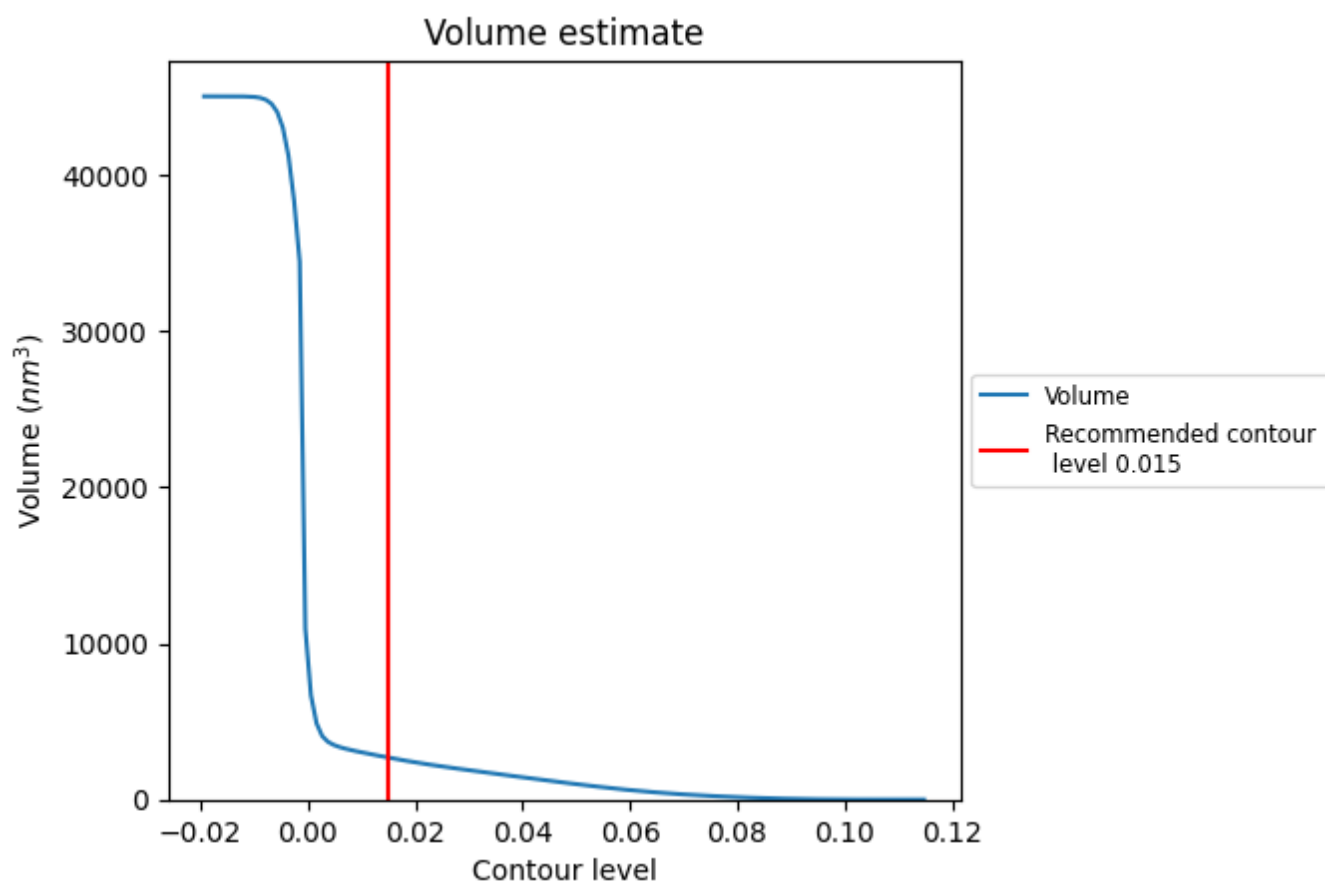
This section contains the results of statistical analysis of the map.

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.

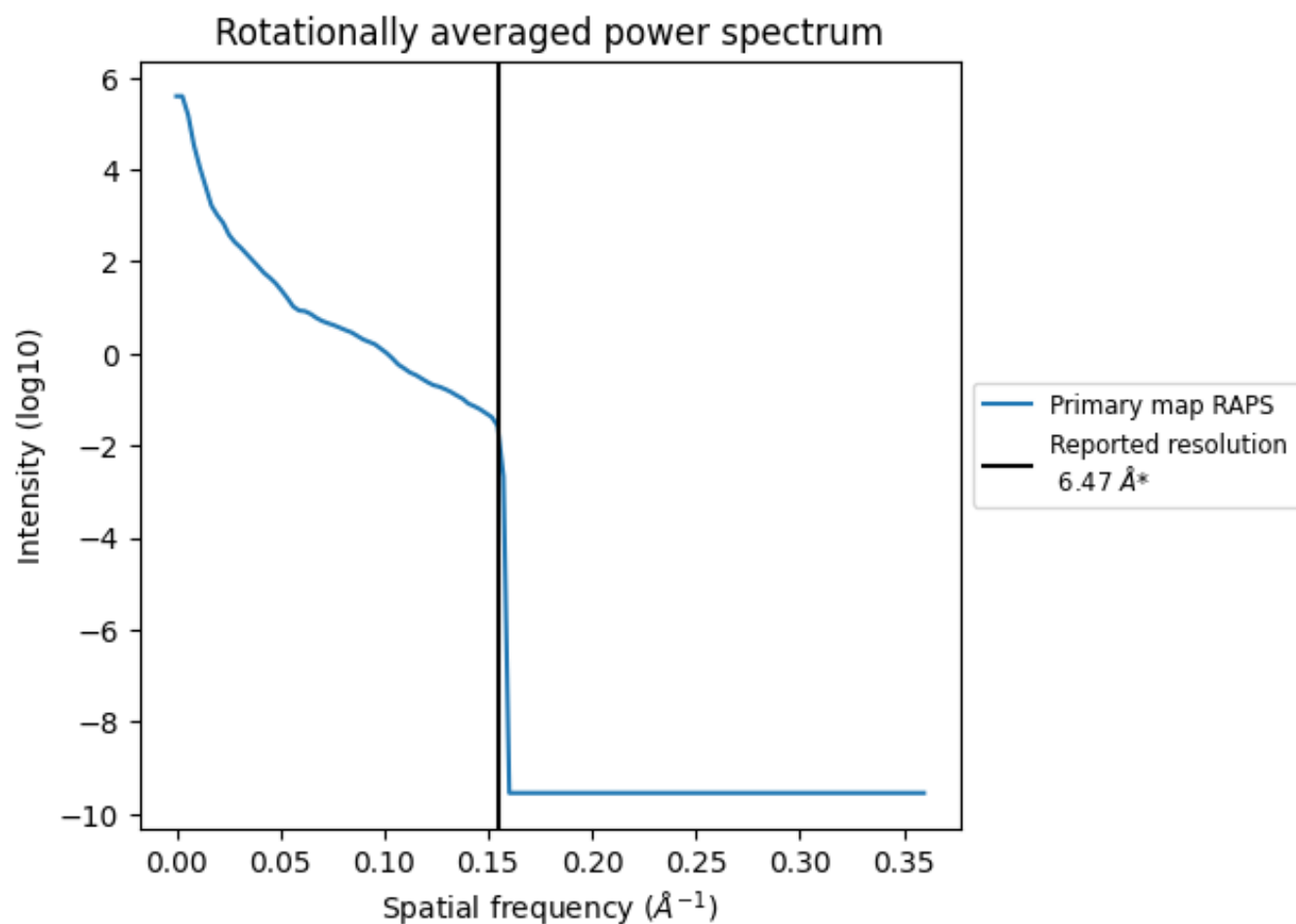
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2691 nm³; this corresponds to an approximate mass of 2431 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 0.155 Å⁻¹

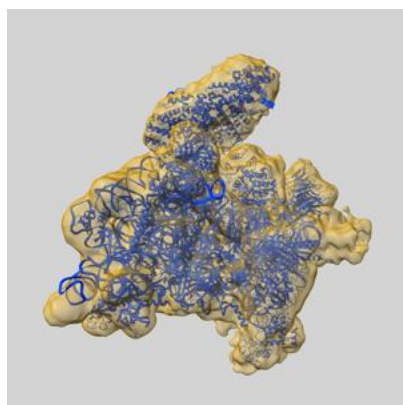
8 Fourier-Shell correlation

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

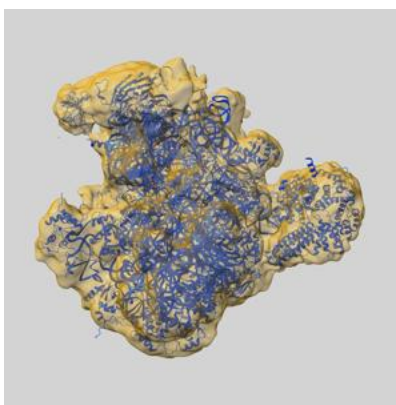
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-2845 and PDB model 4UER. Per-residue inclusion information can be found in section 3 on page 11.

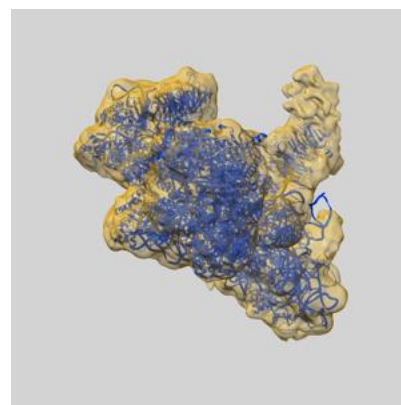
9.1 Map-model overlay [i](#)



X



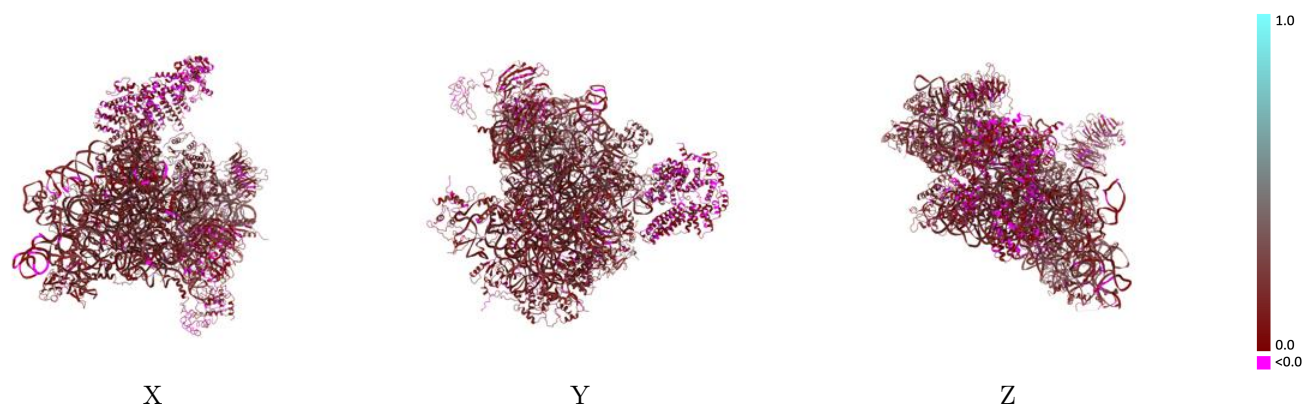
Y



Z

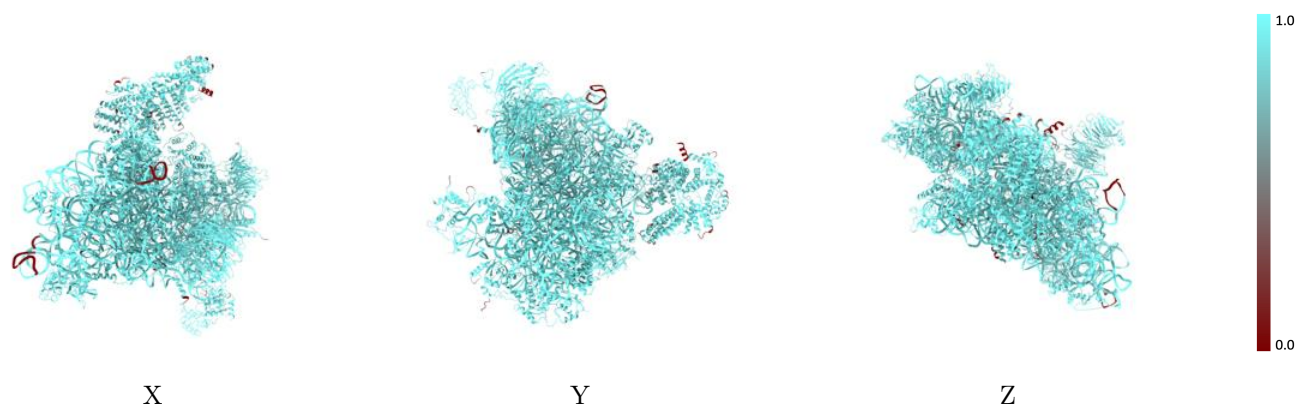
The images above show the 3D surface view of the map at the recommended contour level 0.015 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



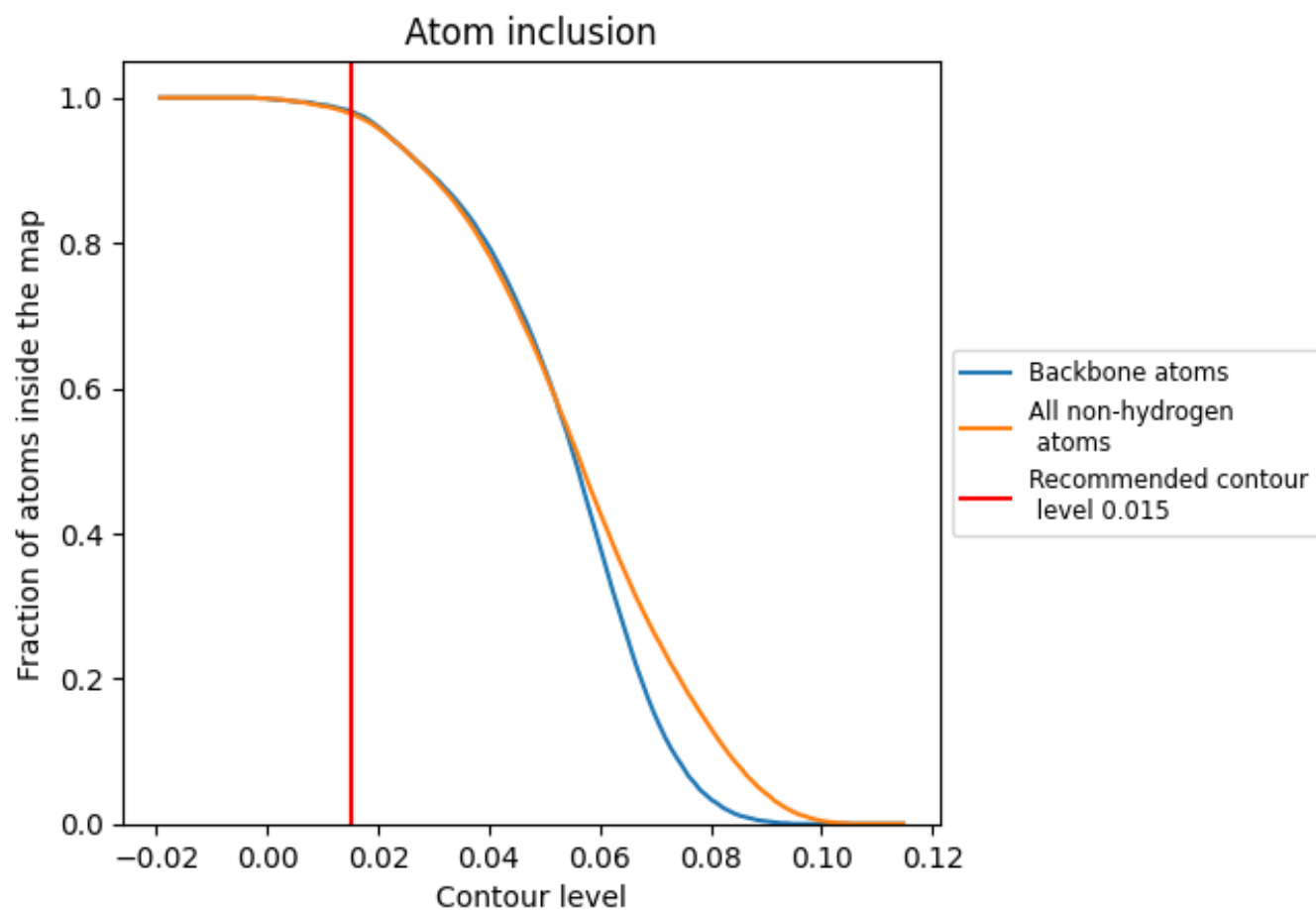
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.015).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 98% 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 (0.015) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9780	 0.1350
0	 0.8020	 0.0540
1	 0.9620	 0.1270
2	 1.0000	 0.1290
3	 0.9840	 0.1470
4	 0.9960	 0.1490
5	 0.9890	 0.1260
6	 0.9920	 0.1280
7	 0.9960	 0.1280
8	 0.9840	 0.1230
9	 0.9700	 0.0710
A	 0.9860	 0.1700
B	 0.9960	 0.1640
C	 0.9870	 0.1340
D	 0.9710	 0.1340
E	 0.9940	 0.1390
F	 0.8670	 0.0800
G	 0.9910	 0.1300
H	 0.9980	 0.1310
I	 1.0000	 0.1110
J	 0.9680	 0.1150
K	 1.0000	 0.1160
L	 0.9950	 0.1310
M	 0.9960	 0.0980
N	 1.0000	 0.0830
O	 0.9890	 0.1440
P	 0.9950	 0.1390
Q	 0.9810	 0.1280
R	 0.9910	 0.1140
S	 0.9370	 0.0960
T	 1.0000	 0.1060
U	 0.9500	 0.0950
V	 0.9820	 0.1350
W	 0.9930	 0.1350
X	 0.9670	 0.0830



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Chain	Atom inclusion	Q-score
Y	 0.9940	 0.1210
Z	 0.9900	 0.1390
a	 0.9480	 0.0430
b	 0.9750	 0.0910
c	 0.9070	 0.0430