



Full wwPDB EM Validation Report ⓘ

Mar 6, 2026 – 12:04 AM UTC

PDB ID : 5H4P / pdb_00005h4p
EMDB ID : EMD-9569
Title : Structural snapshot of cytoplasmic pre-60S ribosomal particles bound with Nmd3, Lsg1, Tif6 and Reh1
Authors : Ma, C.; Wu, S.; Li, N.; Chen, Y.; Yan, K.; Li, Z.; Zheng, L.; Lei, J.; Woolford, J.L.; Gao, N.
Deposited on : 2016-11-01
Resolution : 3.07 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
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

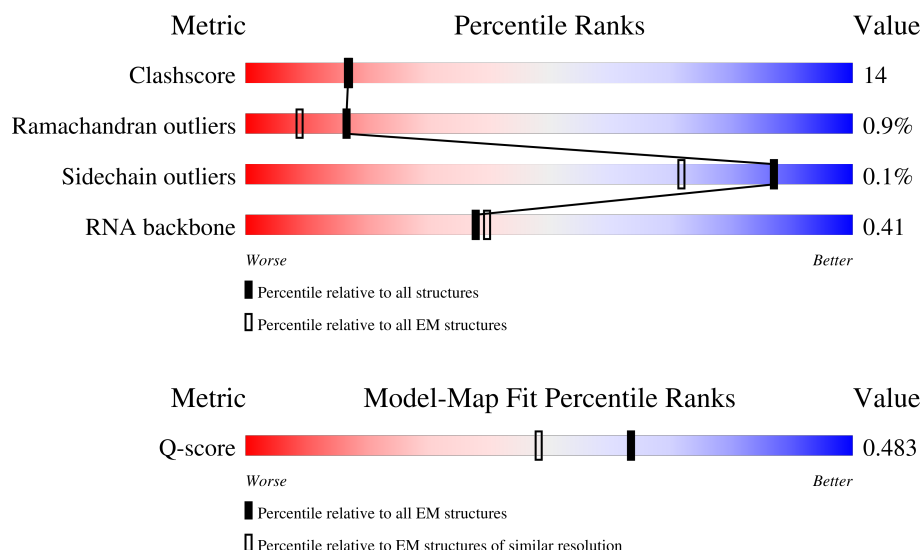
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.07 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	13977 (2.57 - 3.57)

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

Mol	Chain	Length	Quality of chain
1	1	3396	44% 43% 36% 11% 9%
2	3	121	77% 35% 54% 12%
3	4	158	40% 51% 39% 10%

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Mol	Chain	Length	Quality of chain
4	A	246	
5	B	387	
6	C	361	
7	D	297	
8	E	176	
9	F	244	
10	G	256	
11	H	191	
12	J	174	
13	L	199	
14	M	138	
15	N	204	
16	O	199	
17	P	184	
18	Q	186	
19	R	189	
20	S	172	
21	T	160	
22	U	121	
23	V	137	
24	W	155	
25	X	142	
26	Y	127	
27	Z	136	
28	a	149	

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Mol	Chain	Length	Quality of chain
29	b	59	
30	c	105	
31	d	113	
32	e	130	
33	f	107	
34	g	121	
35	h	120	
36	i	100	
37	j	88	
38	k	78	
39	l	51	
40	o	106	
41	p	92	
42	w	248	
43	y	227	
44	z	56	

2 Entry composition

There are 44 unique types of molecules in this entry. The entry contains 122929 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 25S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	3091	Total	C	N	O	P	0	0
			66124	29535	11927	21571	3091		

- Molecule 2 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	3	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 3 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	4	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 4 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	246	Total	C	N	O	S	0	0
			1874	1168	380	325	1		

- Molecule 5 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B	386	Total	C	N	O	S	0	0
			3075	1950	584	533	8		

- Molecule 6 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	C	361	Total	C	N	O	S	0	0
			2748	1729	522	494	3		

- Molecule 7 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	D	296	Total	C	N	O	S	0	0
			2375	1501	414	458	2		

- Molecule 8 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	E	156	Total	C	N	O	S	0	0
			1239	800	222	216	1		

- Molecule 9 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	F	222	Total	C	N	O	S	0	0
			1784	1151	324	308	1		

- Molecule 10 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	G	233	Total	C	N	O	S	0	0
			1804	1151	323	327	3		

- Molecule 11 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	H	191	Total	C	N	O	S	0	0
			1518	963	274	277	4		

- Molecule 12 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	J	169	Total	C	N	O	S	0	0
			1353	847	253	249	4		

- Molecule 13 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	L	193	Total	C	N	O	0	0
			1543	962	315	266		

- Molecule 14 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	M	136	Total	C	N	O	S	0	0
			1053	675	199	177	2		

- Molecule 15 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	N	203	Total	C	N	O	S	0	0
			1720	1077	361	281	1		

- Molecule 16 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	O	197	Total	C	N	O	S	0	0
			1555	1003	289	262	1		

- Molecule 17 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	P	183	Total	C	N	O	S	0	0
			1442	896	287	259			

- Molecule 18 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Q	185	Total	C	N	O	S	0	0
			1441	908	290	241	2		

- Molecule 19 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	R	156	Total	C	N	O	S	0	0
			1258	781	265	212			

- Molecule 20 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	S	172	Total	C	N	O	S	0	0
			1445	930	267	244	4		

- Molecule 21 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	T	159	Total	C	N	O	S	0	0
			1276	805	246	221	4		

- Molecule 22 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	U	100	Total	C	N	O		0	0
			796	516	131	149			

- Molecule 23 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	V	136	Total	C	N	O	S	0	0
			1003	628	189	179	7		

- Molecule 24 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	W	64	Total	C	N	O	S	0	0
			528	340	103	84	1		

- Molecule 25 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	X	121	Total	C	N	O	S	0	0
			964	620	169	173	2		

- Molecule 26 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Y	126	Total	C	N	O		0	0
			993	625	192	176			

- Molecule 27 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Z	135	Total	C	N	O		0	0
			1092	710	202	180			

- Molecule 28 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	a	148	Total	C	N	O	S	0	0
			1173	749	231	190	3		

- Molecule 29 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	b	58	Total	C	N	O		0	0
			462	289	100	73			

- Molecule 30 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	c	97	Total	C	N	O	S	0	0
			743	479	124	139	1		

- Molecule 31 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	d	109	Total	C	N	O	S	0	0
			876	556	167	152	1		

- Molecule 32 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	e	127	Total	C	N	O	S	0	0
			1020	647	205	167	1		

- Molecule 33 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	f	106	Total	C	N	O	S	0	0
			850	540	165	144	1		

- Molecule 34 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	g	112	Total	C	N	O	S	0	0
			880	545	179	152	4		

- Molecule 35 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	h	119	Total	C	N	O	S	0	0
			969	615	186	167	1		

- Molecule 36 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	i	99	Total	C	N	O	S	0	0
			771	481	156	132	2		

- Molecule 37 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	j	87	Total	C	N	O	S	0	0
			681	414	148	114	5		

- Molecule 38 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	k	77	Total	C	N	O		0	0
			612	391	115	106			

- Molecule 39 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	l	50	Total	C	N	O	S	0	0
			436	272	97	65	2		

- Molecule 40 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	o	95	Total	C	N	O	S	0	0
			765	481	154	125	5		

- Molecule 41 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	p	91	Total	C	N	O	S	0	0
			694	429	138	121	6		

- Molecule 42 is a protein called 60S ribosomal export protein NMD3.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	w	248	Total	C	N	O	S	0	0
			1894	1208	318	361	7		

- Molecule 43 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	y	227	Total	C	N	O	S	0	0
			1699	1054	296	342	7		

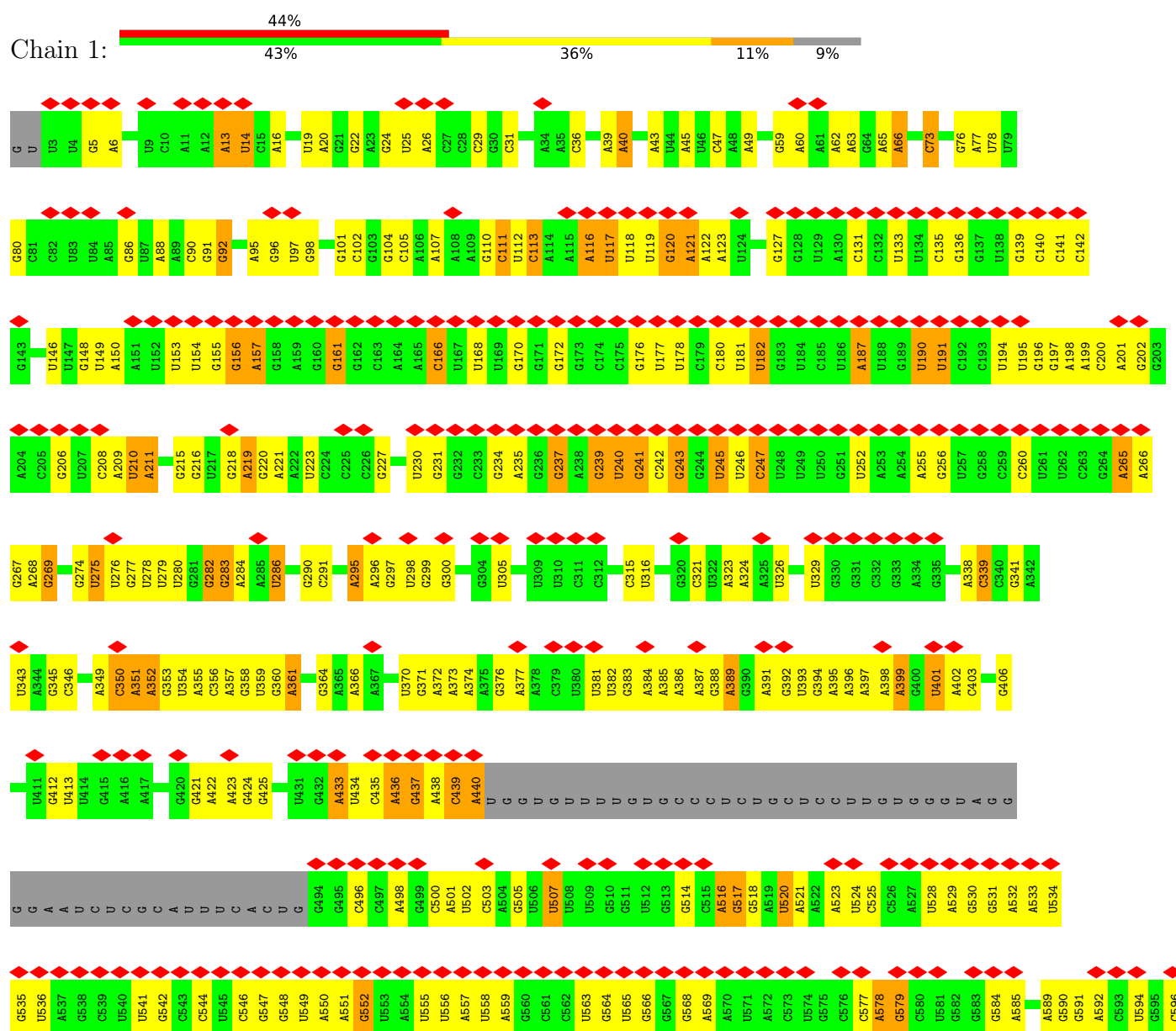
- Molecule 44 is a protein called Cytoplasmic 60S subunit biogenesis factor REH1.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	z	56	Total	C	N	O	S	0	0
			469	289	92	85	3		

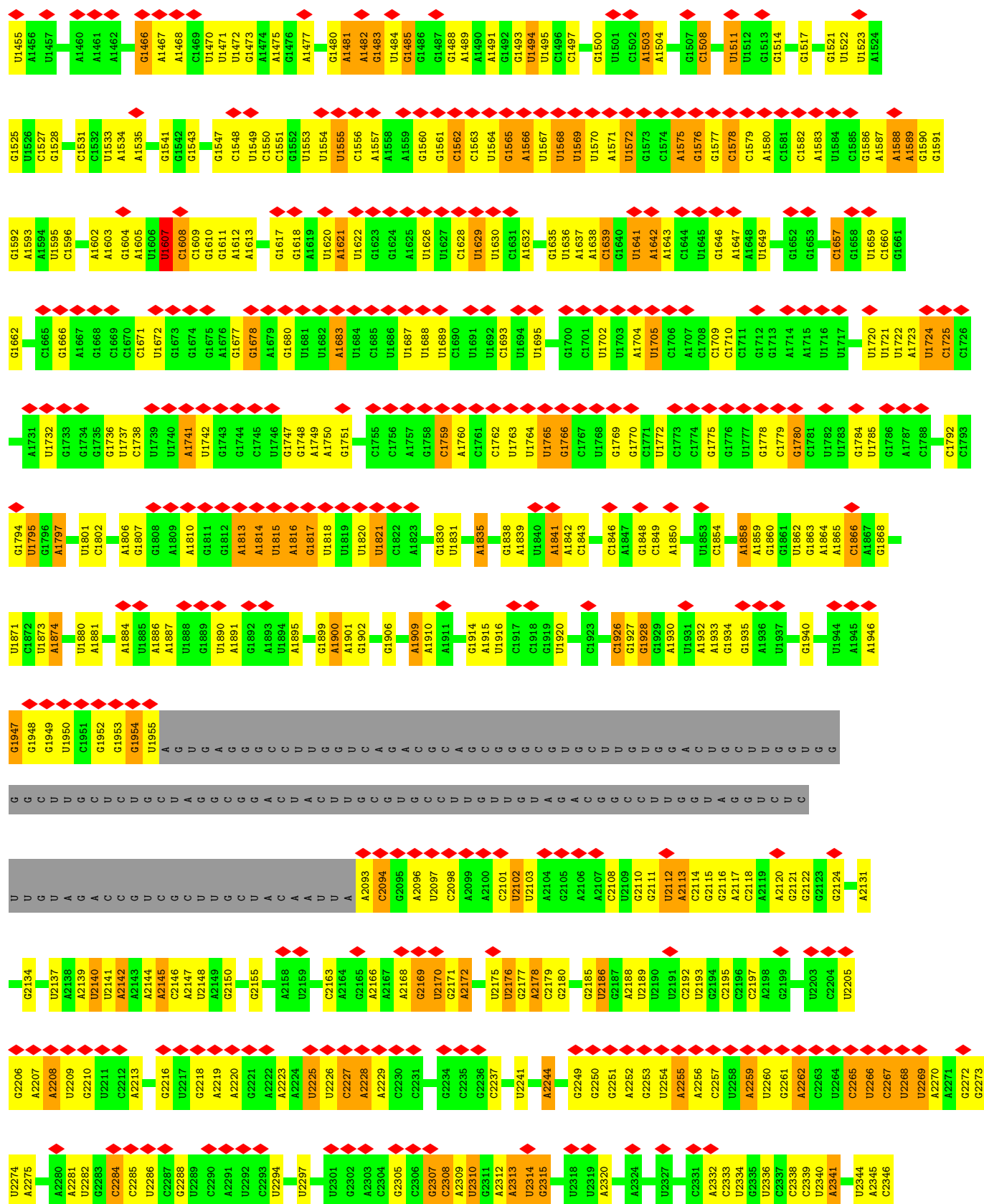
3 Residue-property plots

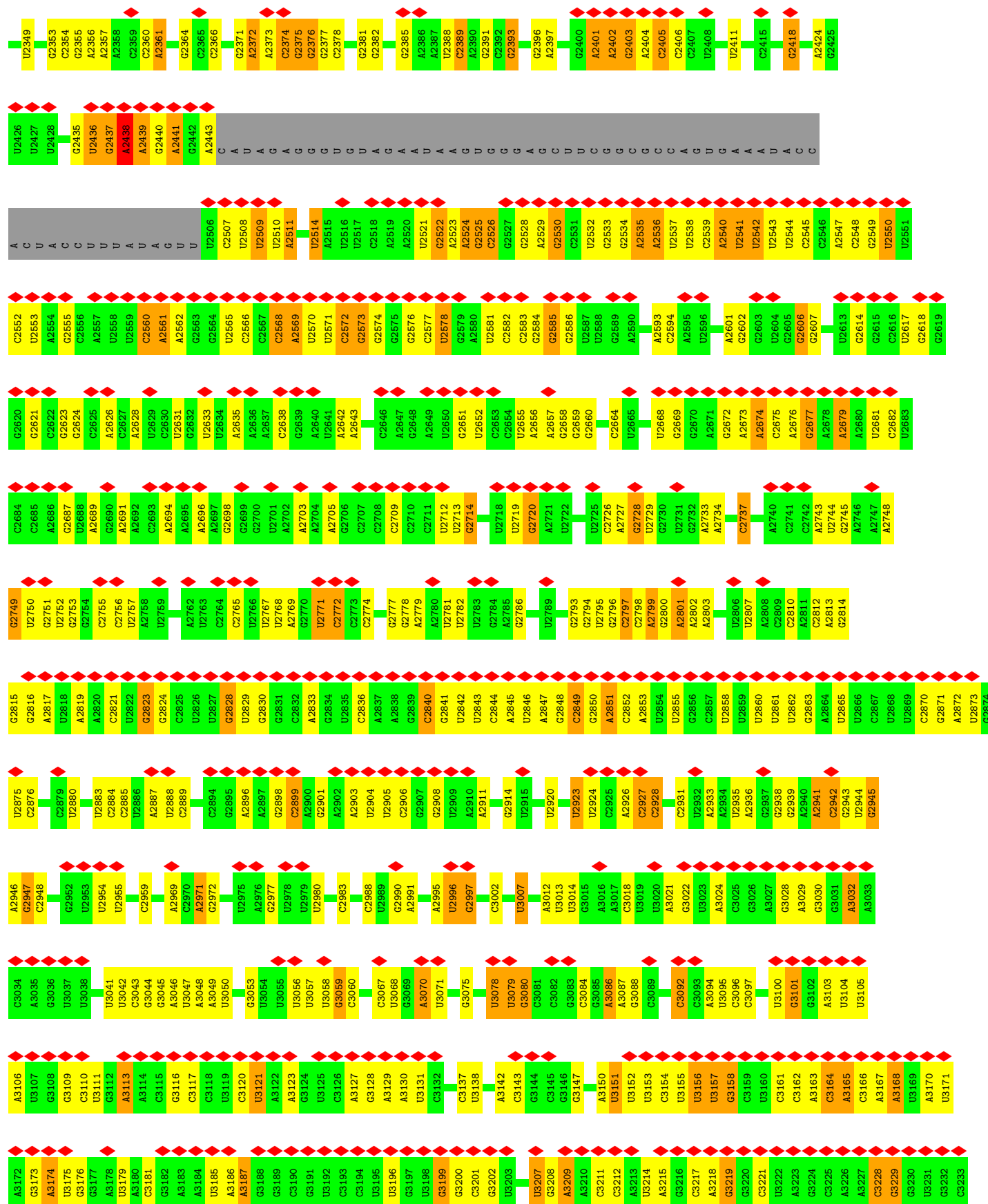
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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.

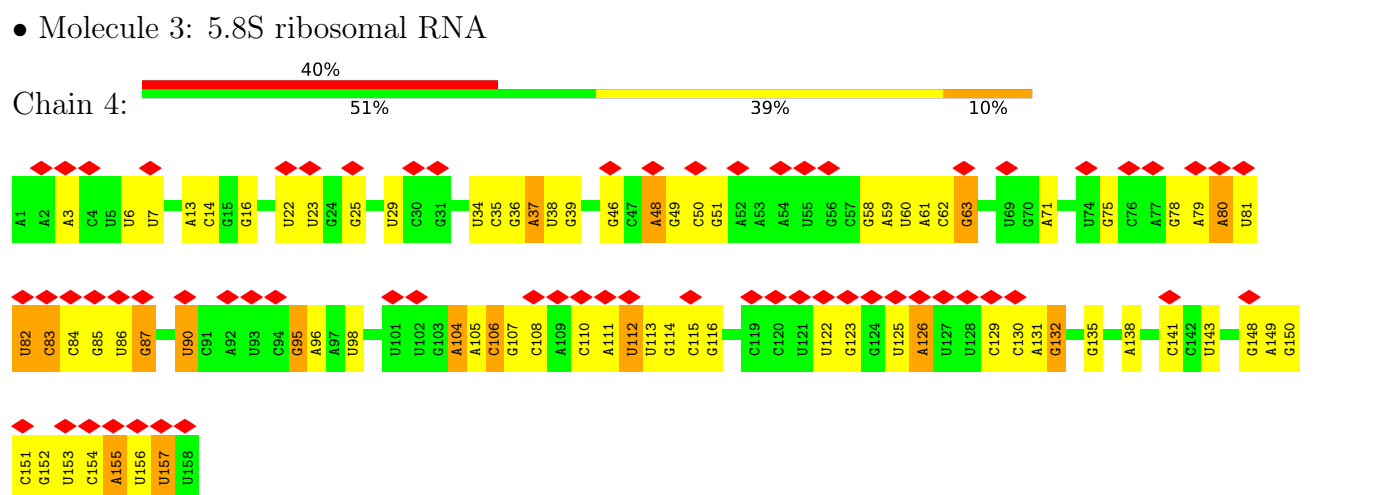
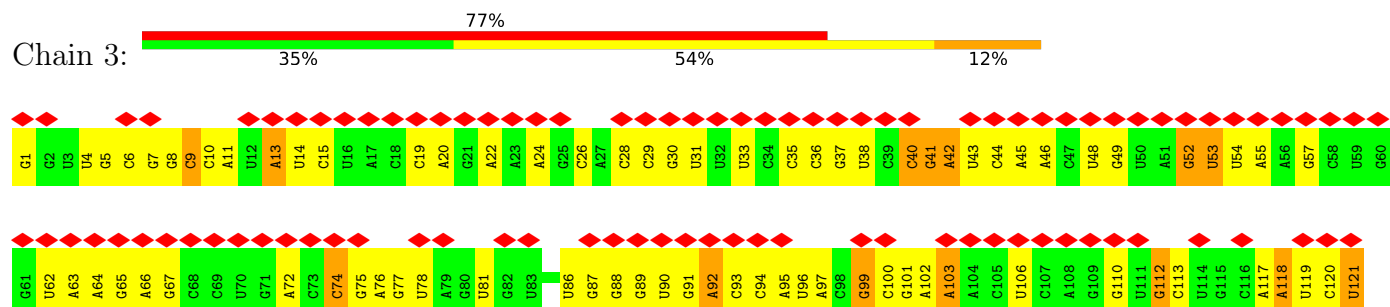
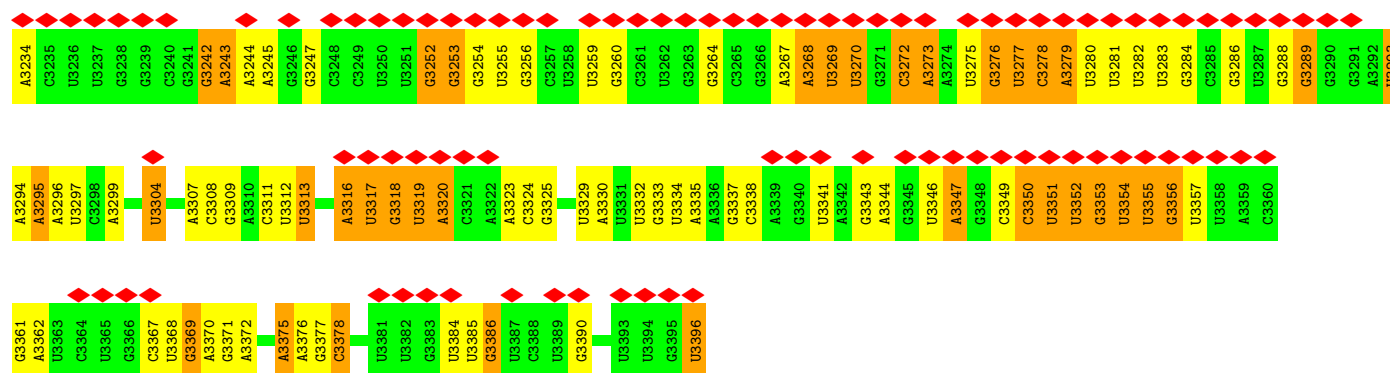
• Molecule 1: 25S ribosomal RNA

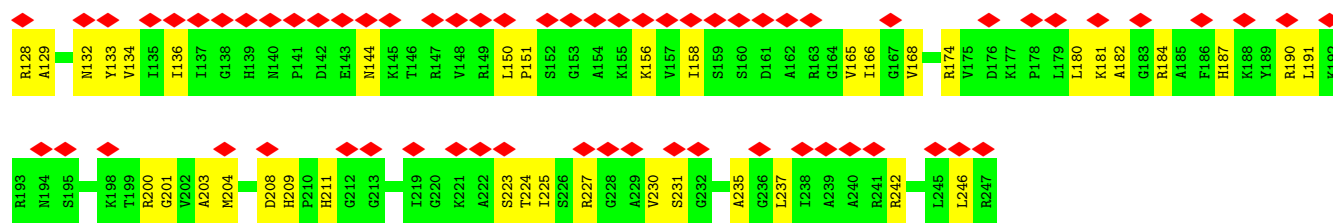




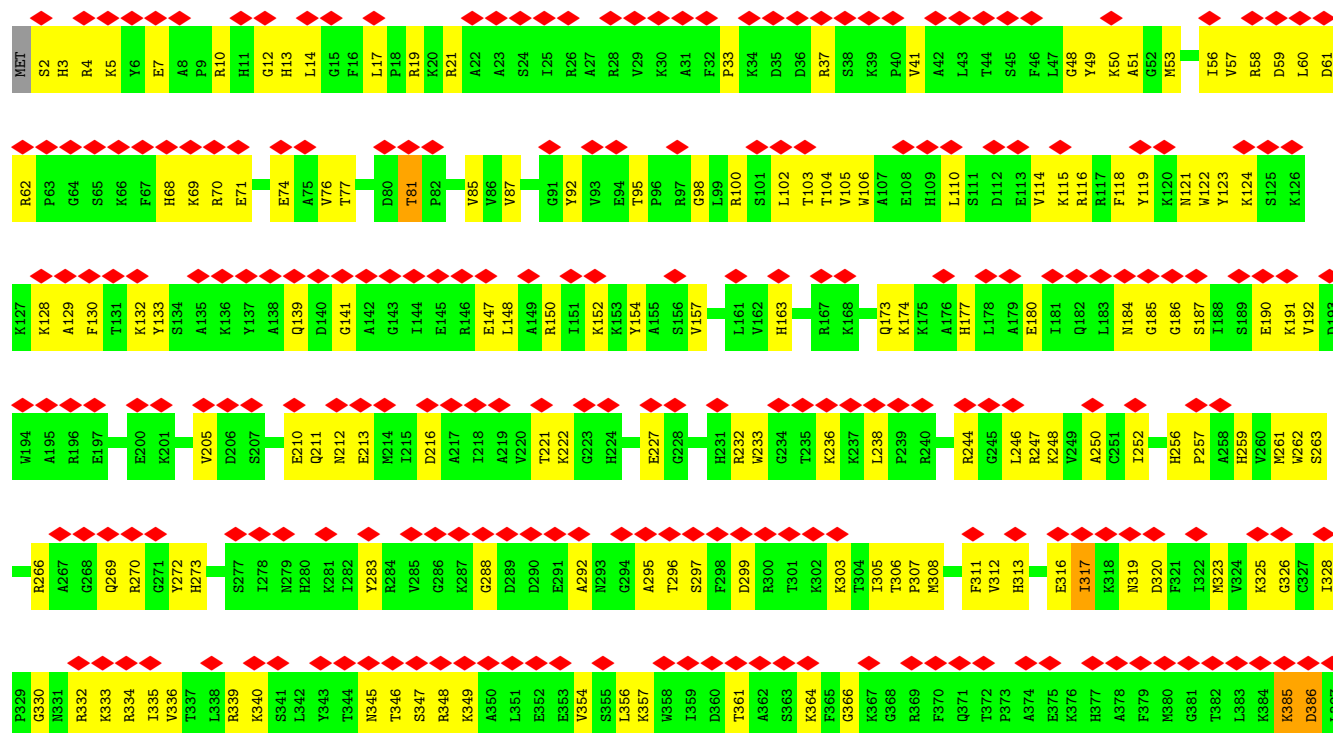




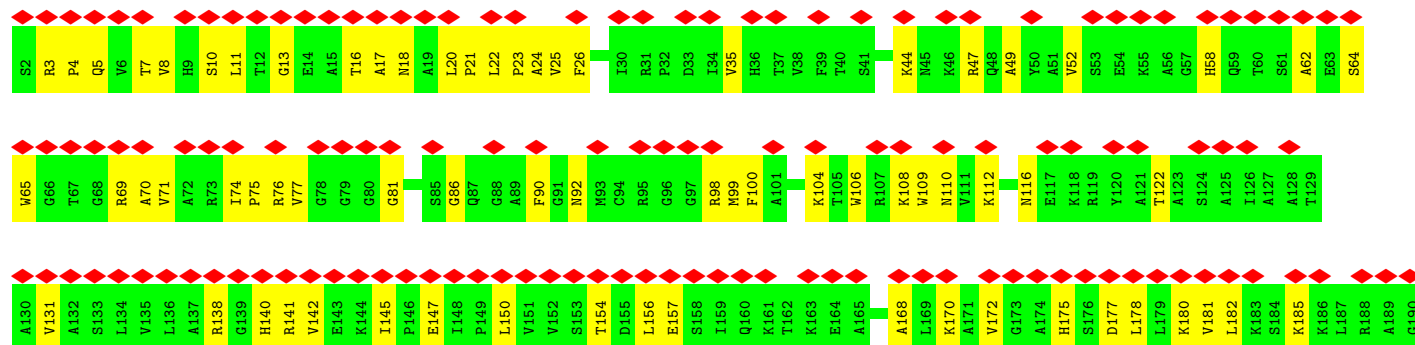
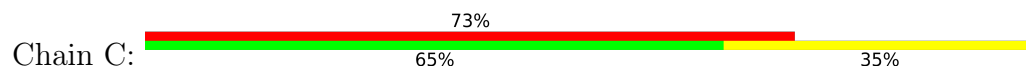


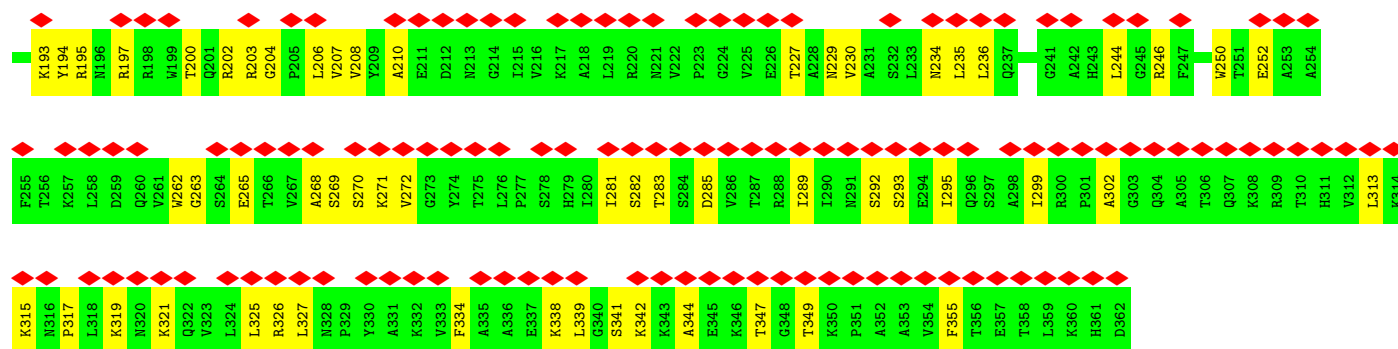


• Molecule 5: 60S ribosomal protein L3

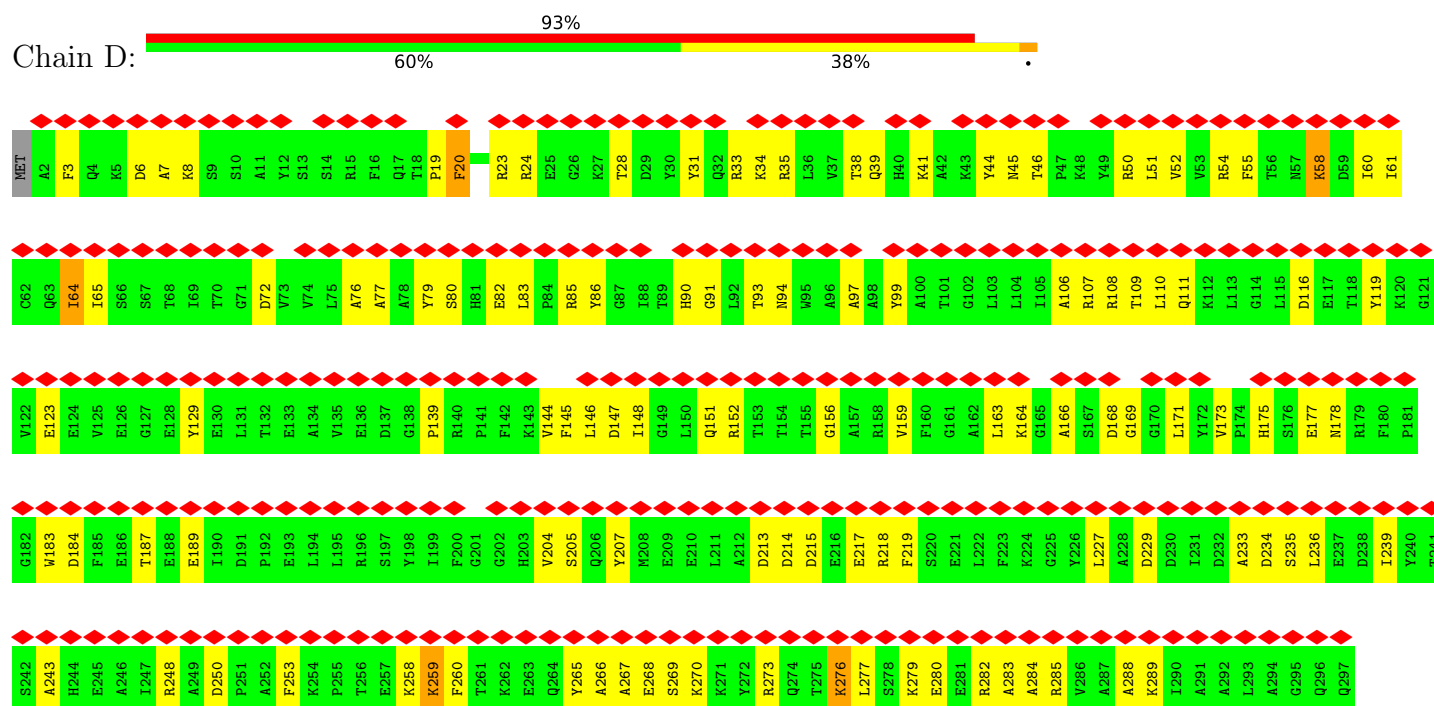


• Molecule 6: 60S ribosomal protein L4-A

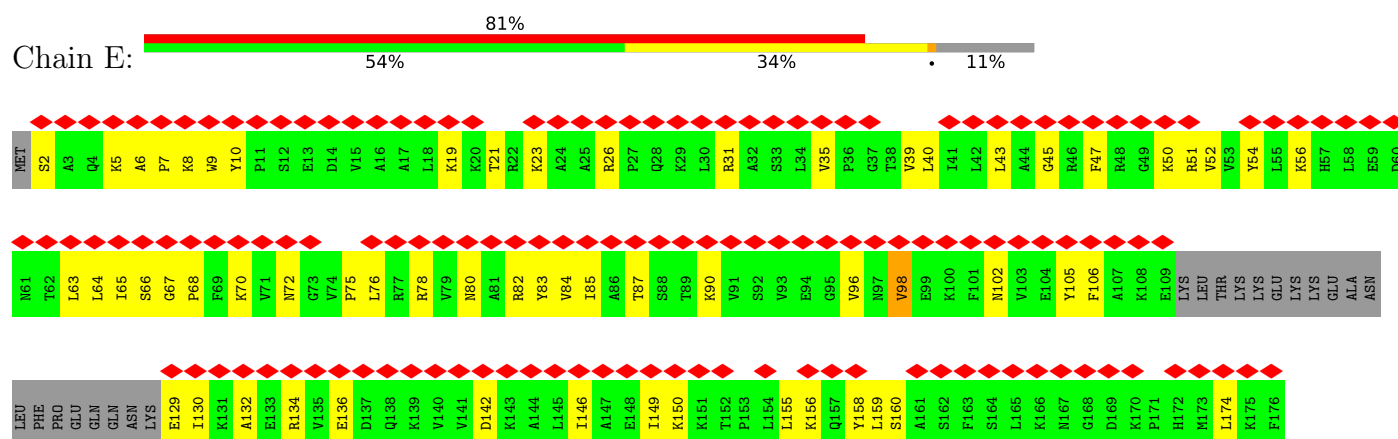




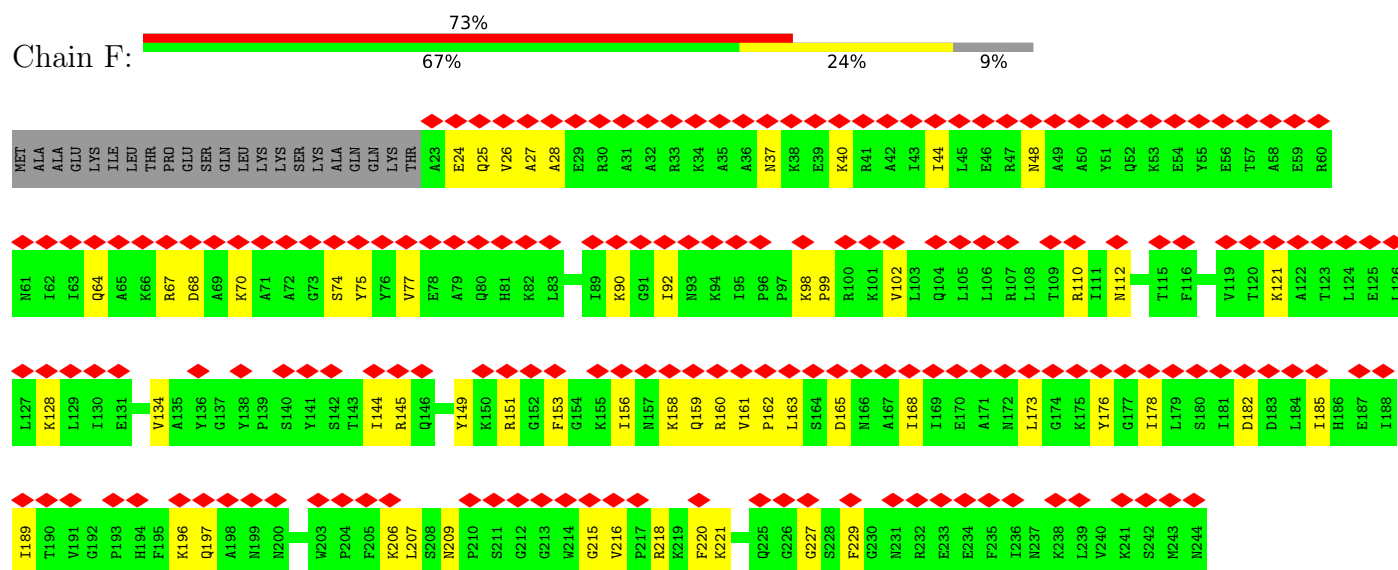
• Molecule 7: 60S ribosomal protein L5



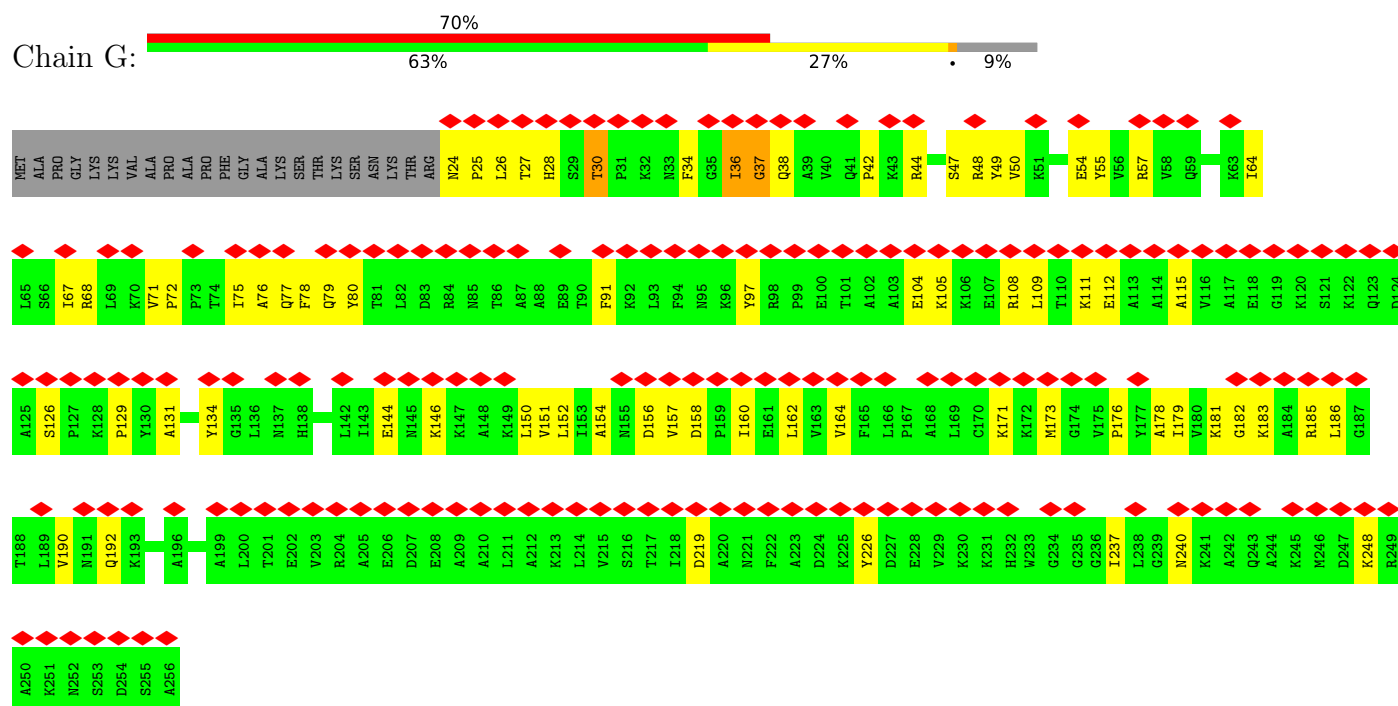
• Molecule 8: 60S ribosomal protein L6-A



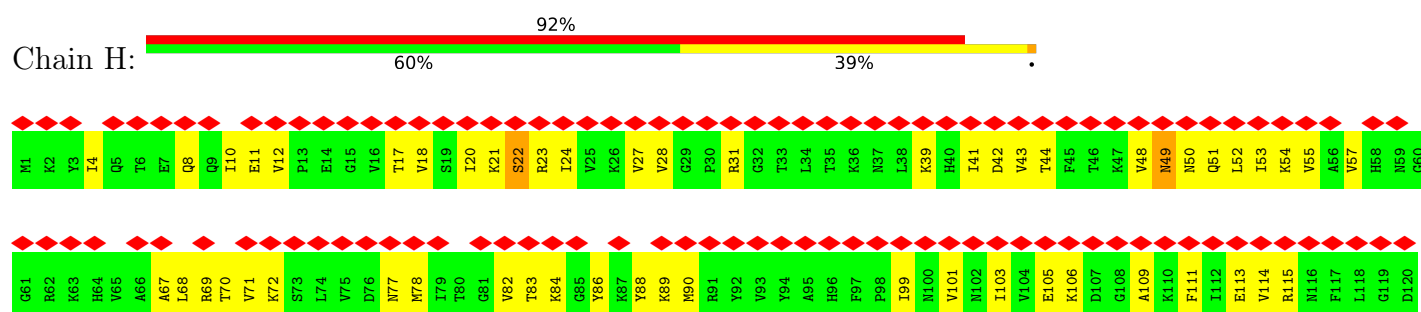
• Molecule 9: 60S ribosomal protein L7-A

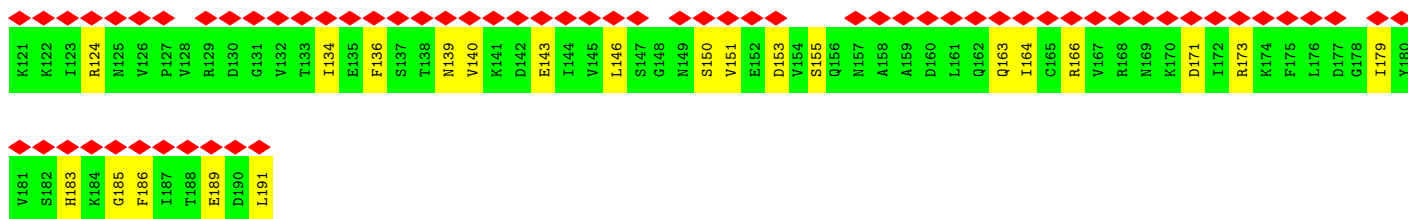


• Molecule 10: 60S ribosomal protein L8-A



• Molecule 11: 60S ribosomal protein L9-A

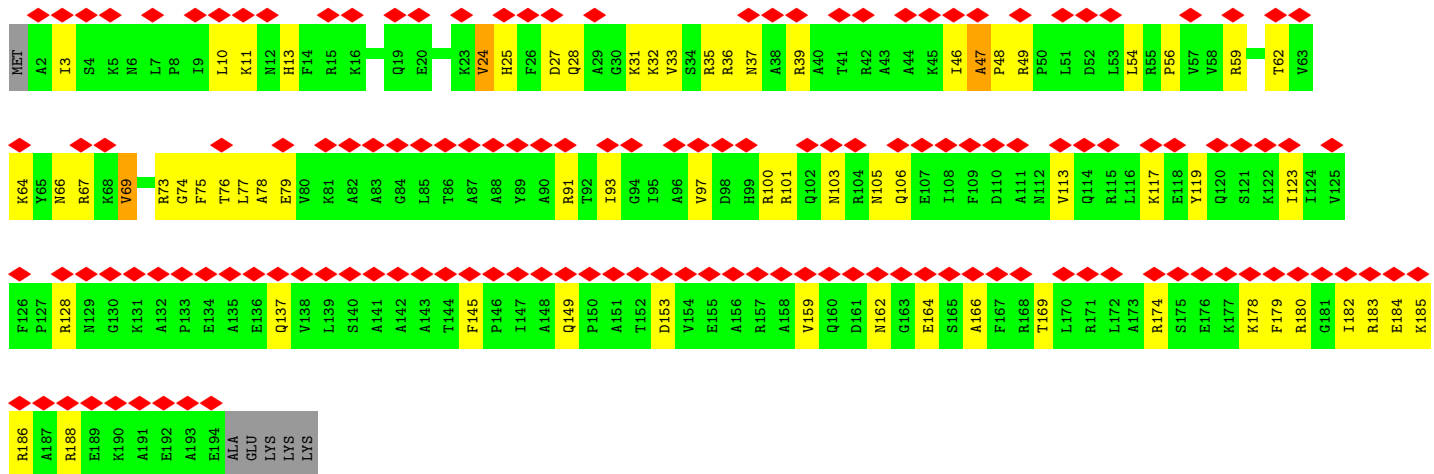




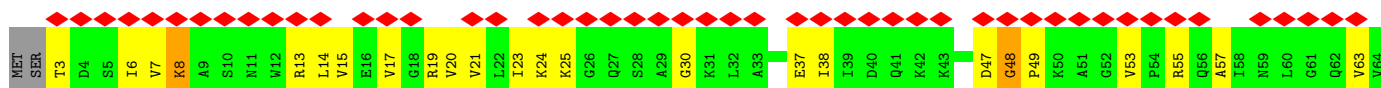
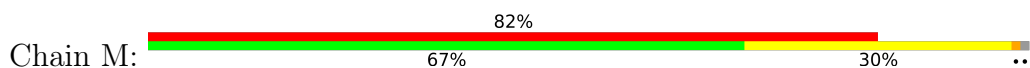
• Molecule 12: 60S ribosomal protein L11-A

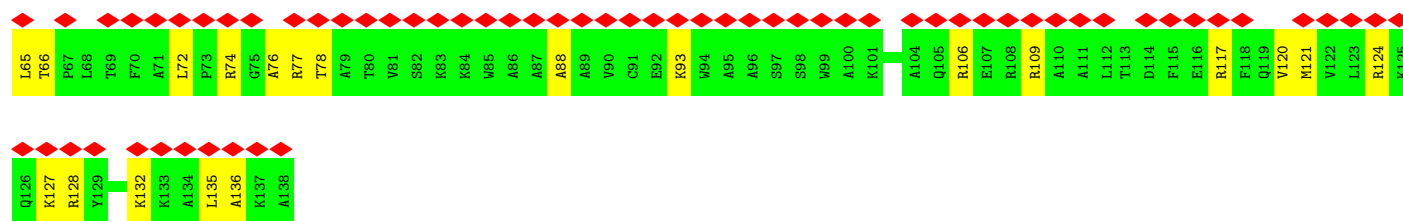


• Molecule 13: 60S ribosomal protein L13-A

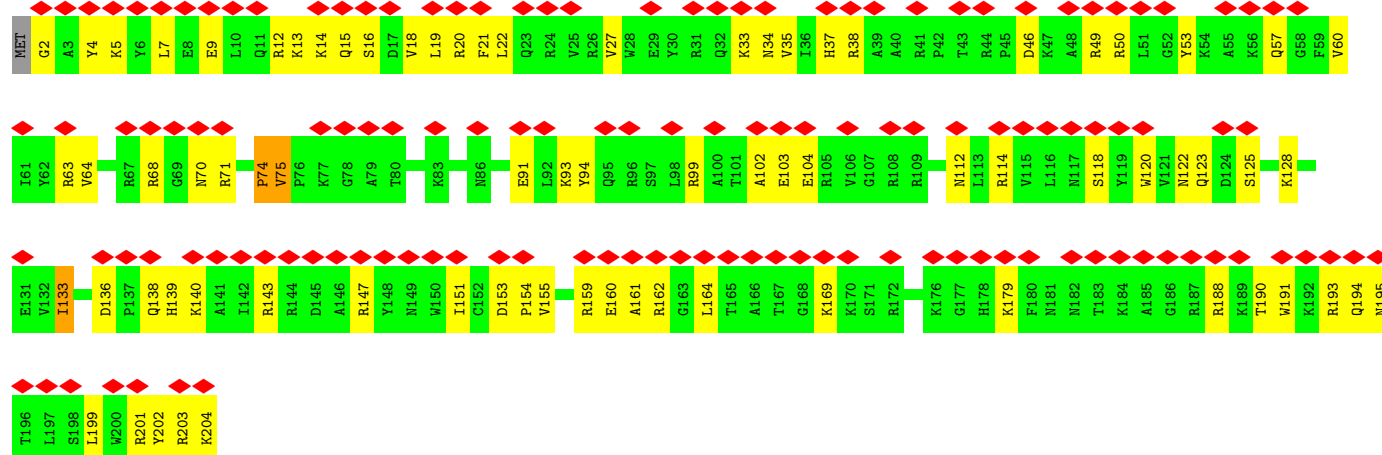


• Molecule 14: 60S ribosomal protein L14-A

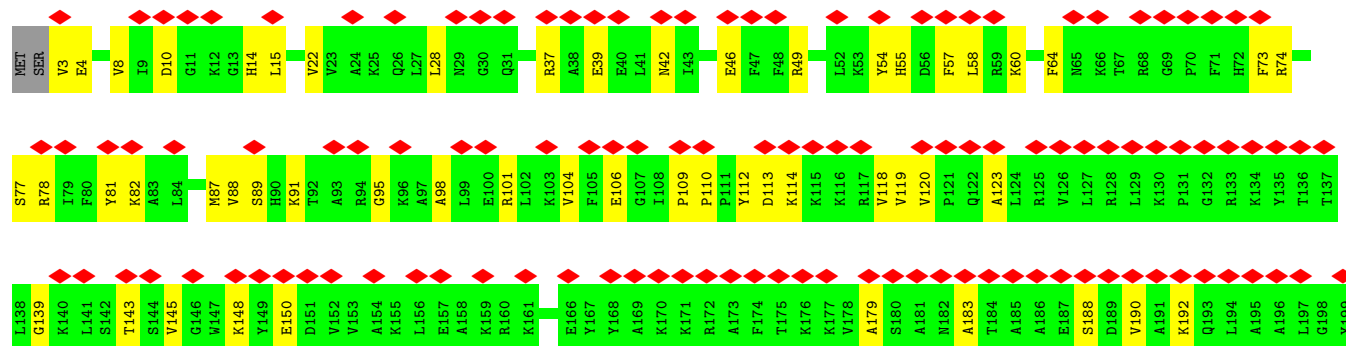
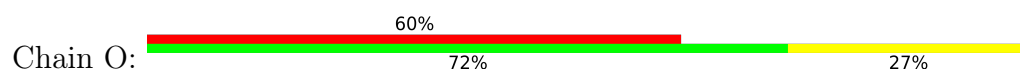




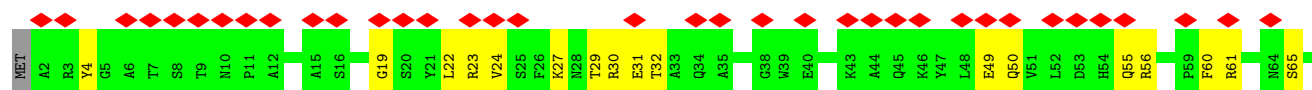
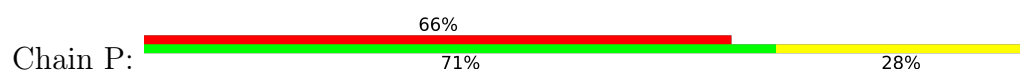
• Molecule 15: 60S ribosomal protein L15-A



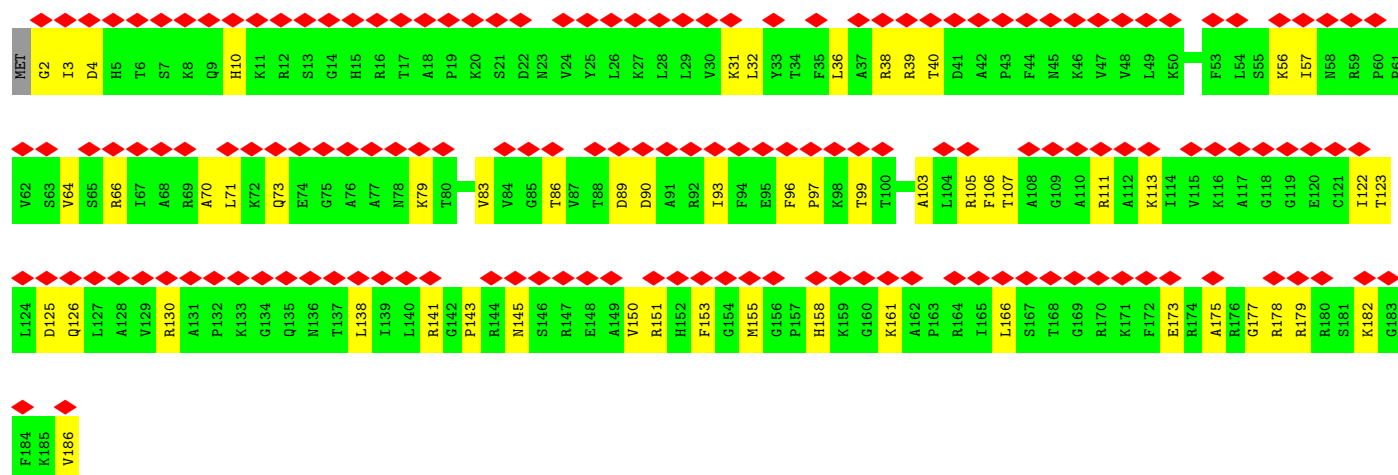
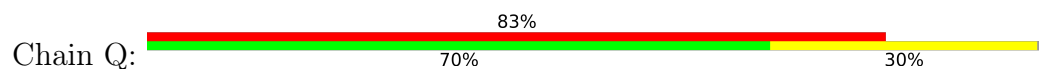
• Molecule 16: 60S ribosomal protein L16-A



• Molecule 17: 60S ribosomal protein L17-A



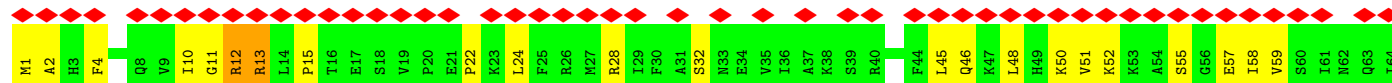
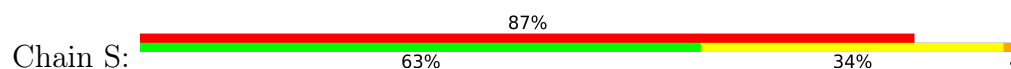
- Molecule 18: 60S ribosomal protein L18-A

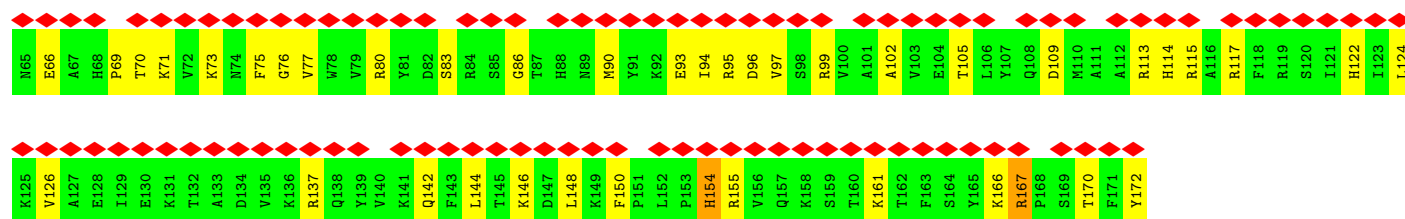


- Molecule 19: 60S ribosomal protein L19-A

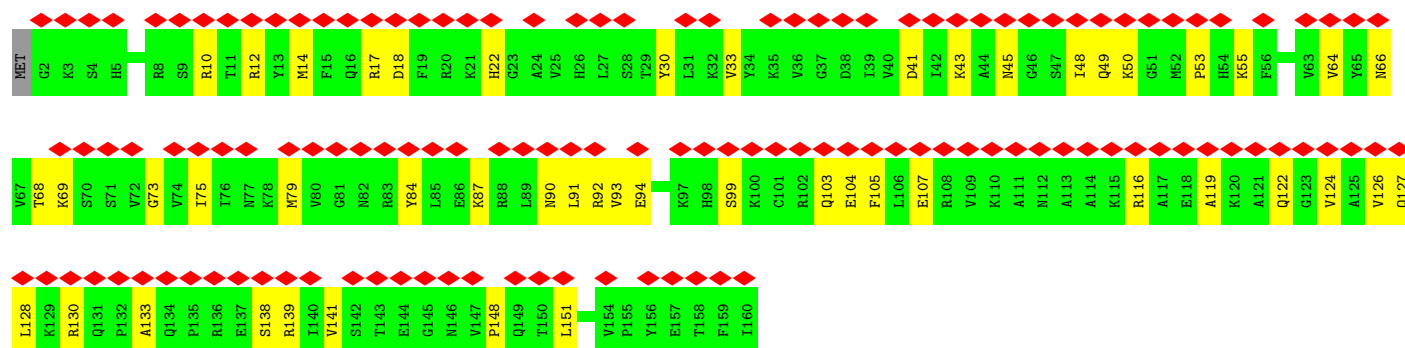
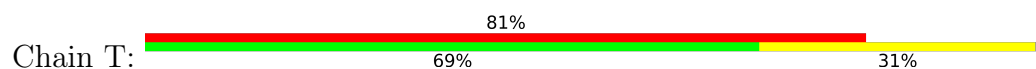


- Molecule 20: 60S ribosomal protein L20-A

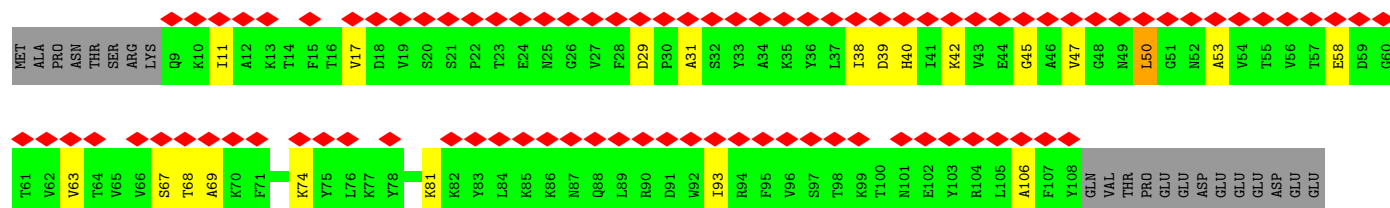
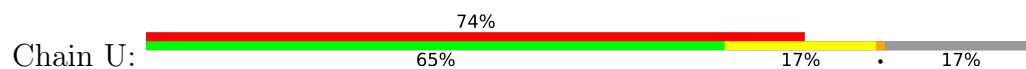




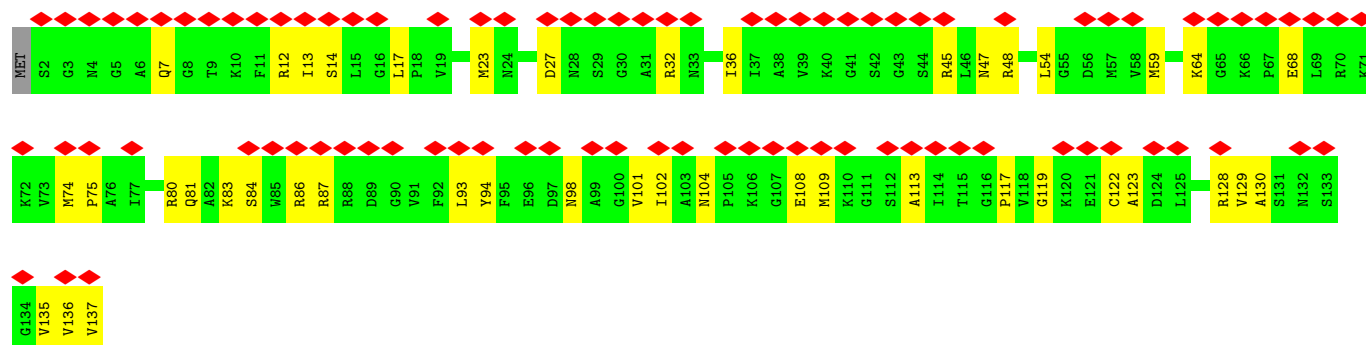
• Molecule 21: 60S ribosomal protein L21-A



• Molecule 22: 60S ribosomal protein L22-A



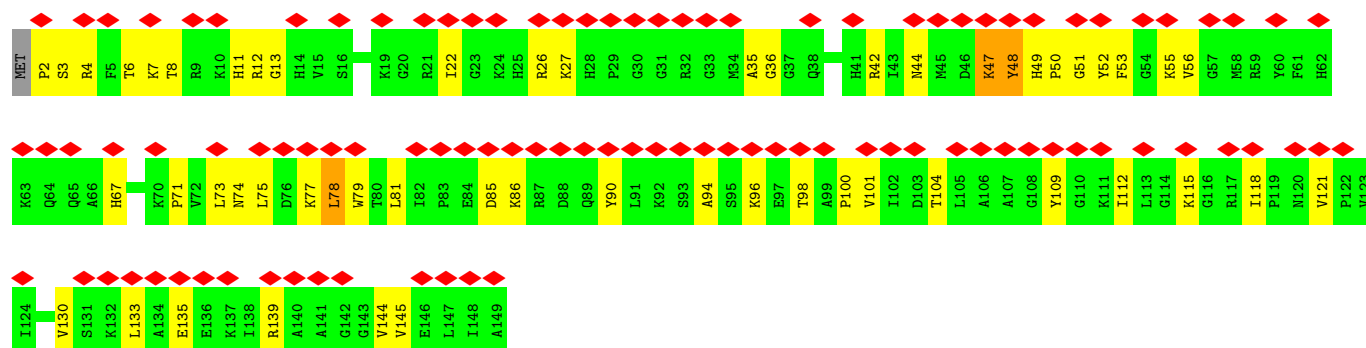
• Molecule 23: 60S ribosomal protein L23-A



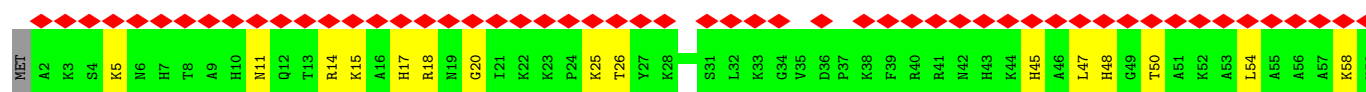
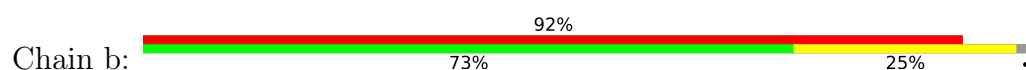
• Molecule 24: 60S ribosomal protein L24-A



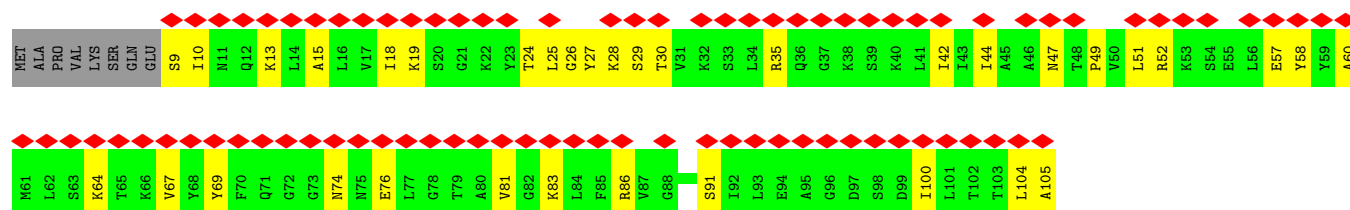
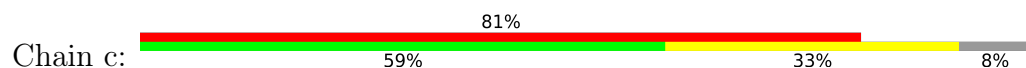
• Molecule 28: 60S ribosomal protein L28



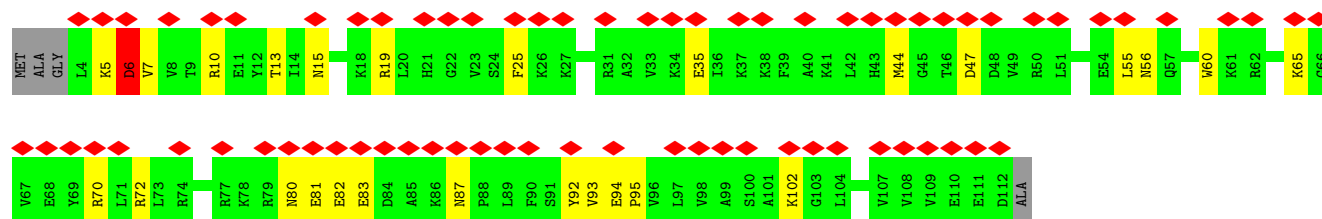
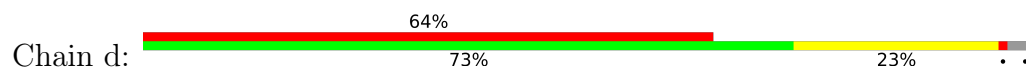
• Molecule 29: 60S ribosomal protein L29



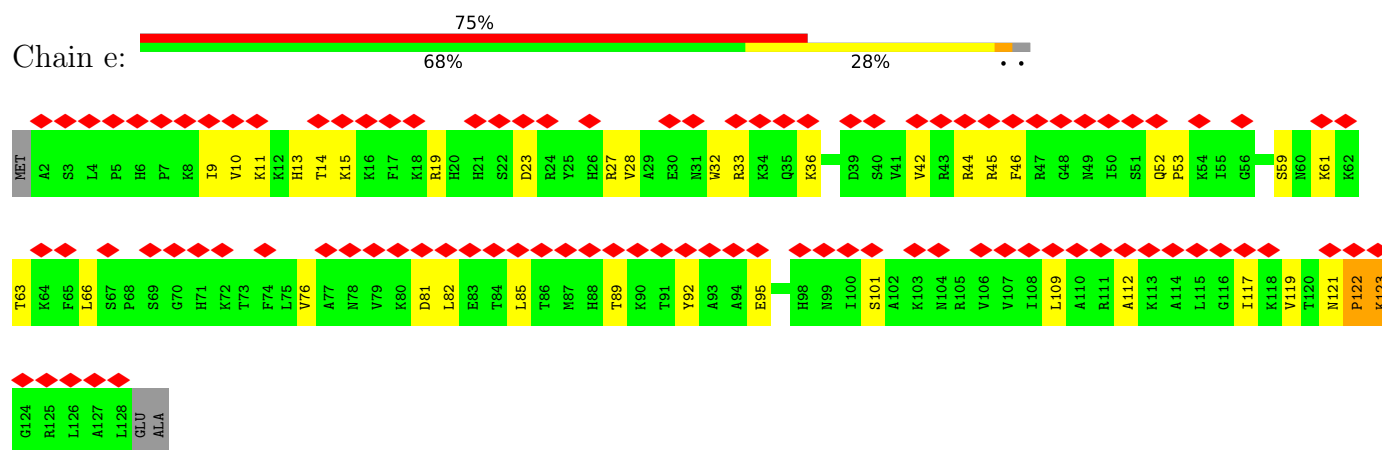
• Molecule 30: 60S ribosomal protein L30



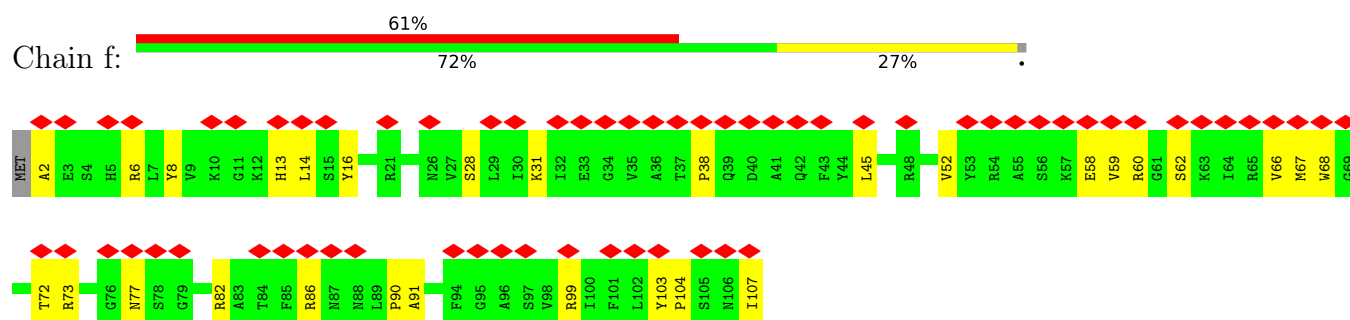
• Molecule 31: 60S ribosomal protein L31-A



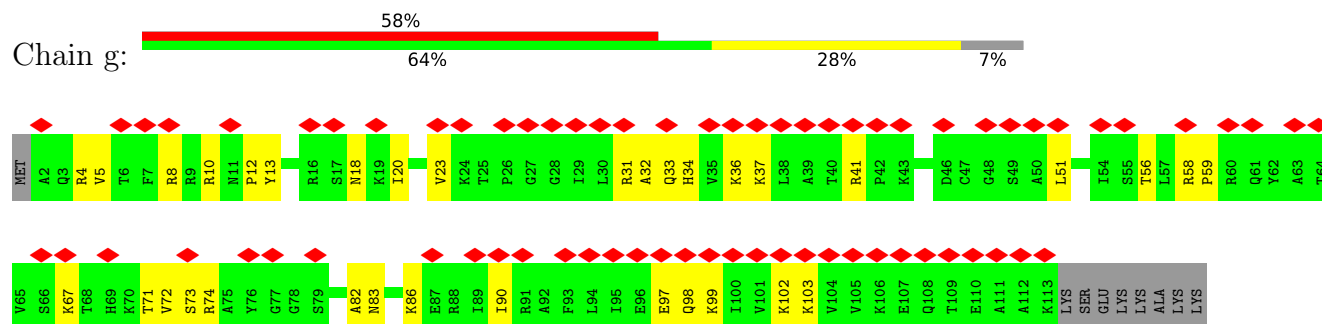
• Molecule 32: 60S ribosomal protein L32



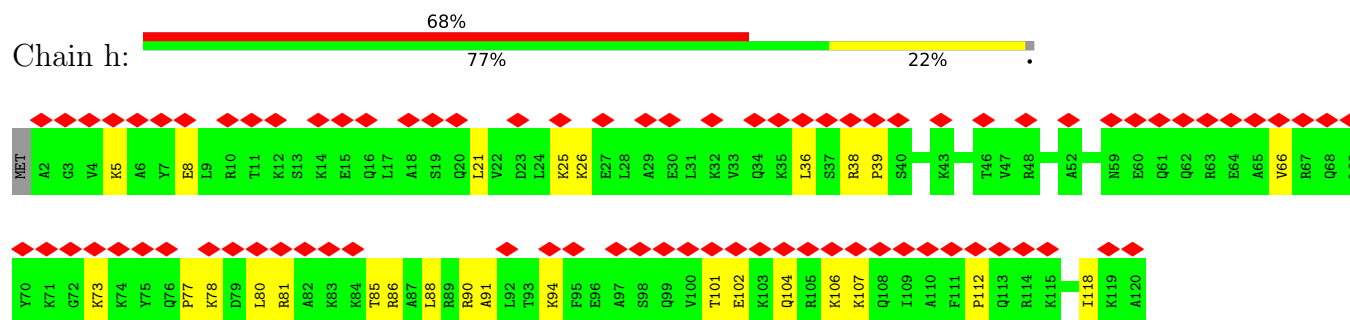
• Molecule 33: 60S ribosomal protein L33-A



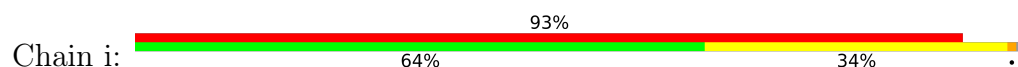
• Molecule 34: 60S ribosomal protein L34-A



• Molecule 35: 60S ribosomal protein L35-A

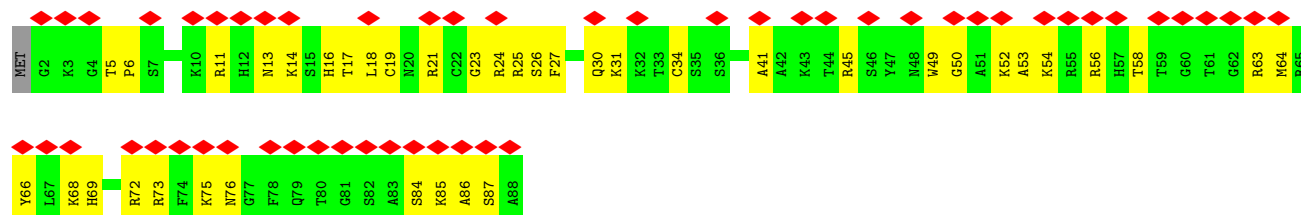


• Molecule 36: 60S ribosomal protein L36-A

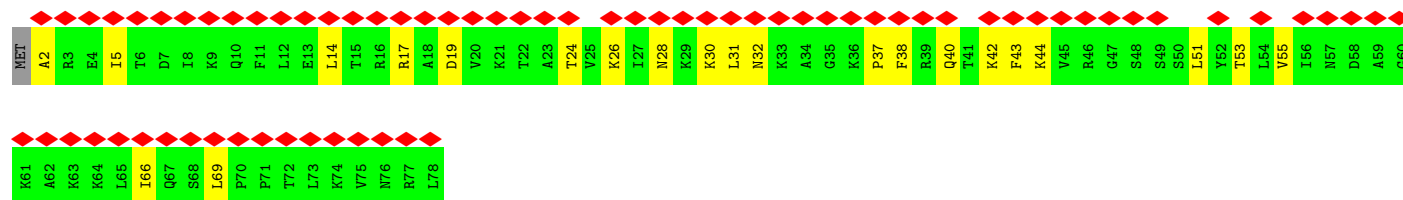




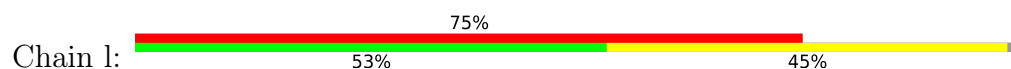
• Molecule 37: 60S ribosomal protein L37-A



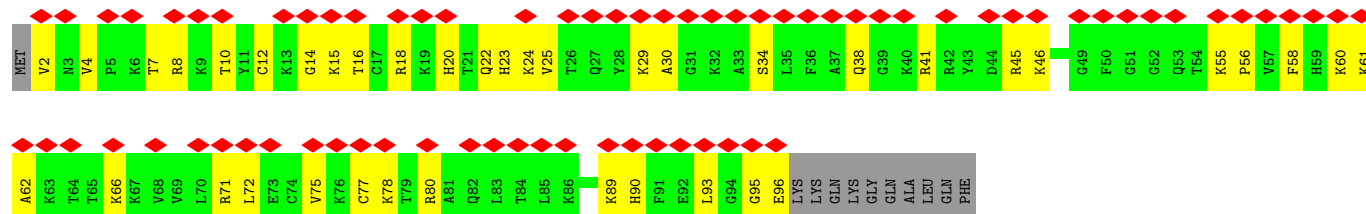
• Molecule 38: 60S ribosomal protein L38



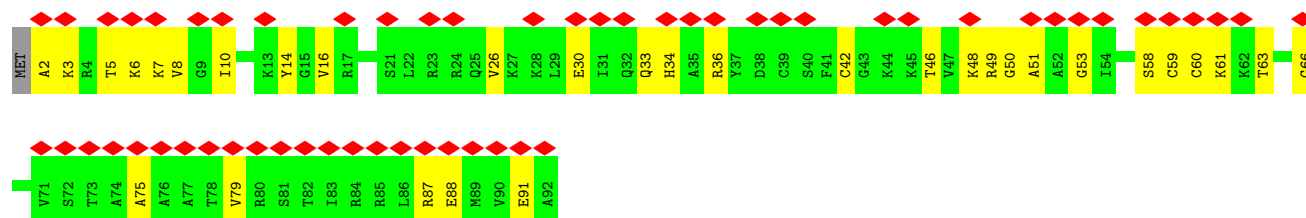
• Molecule 39: 60S ribosomal protein L39



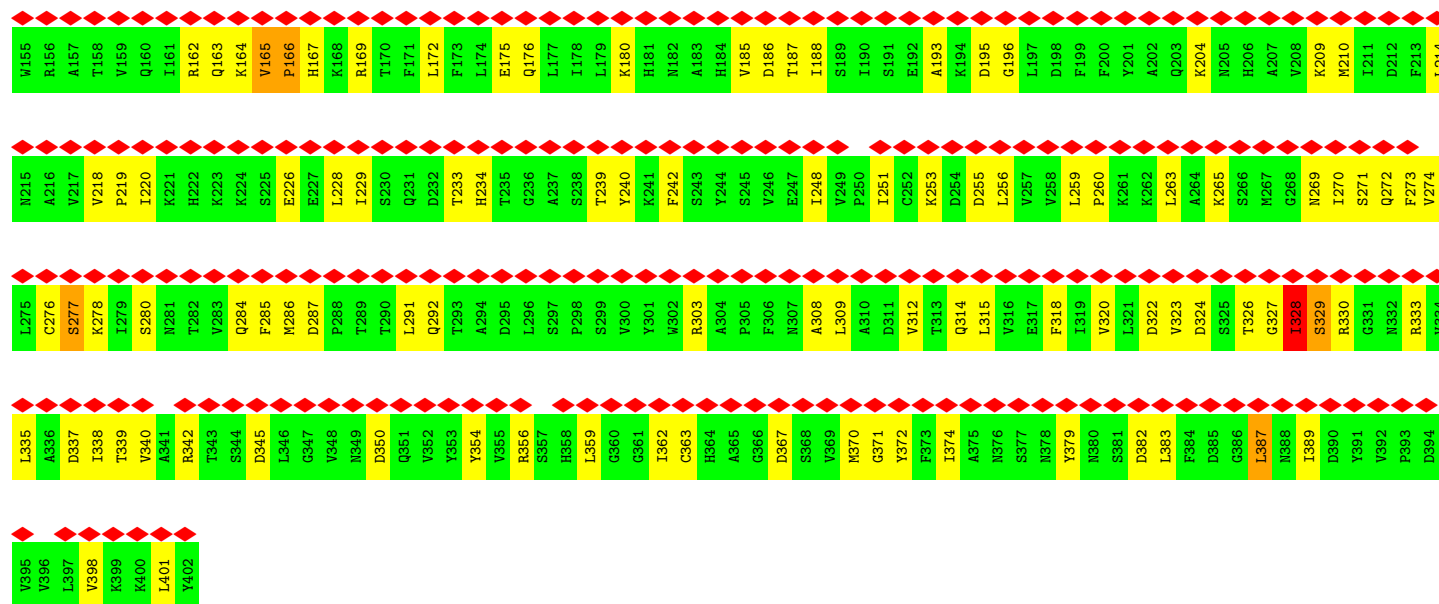
• Molecule 40: 60S ribosomal protein L42-A



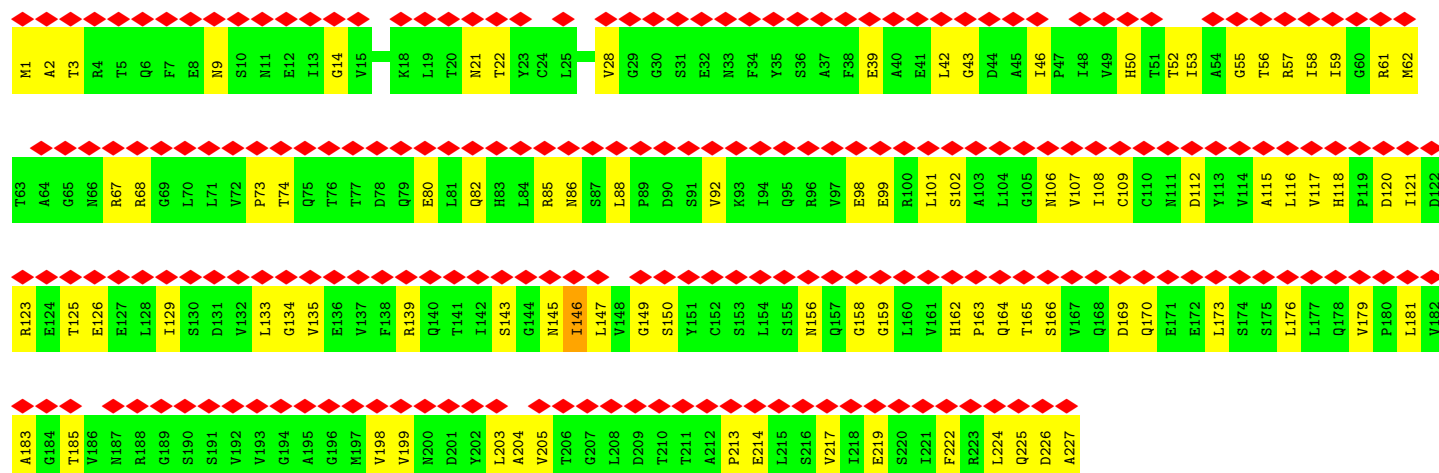
• Molecule 41: 60S ribosomal protein L43-A



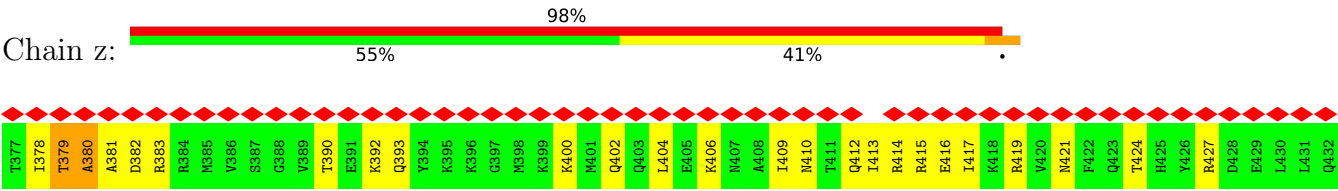
• Molecule 42: 60S ribosomal export protein NMD3



• Molecule 43: Eukaryotic translation initiation factor 6



● Molecule 44: Cytoplasmic 60S subunit biogenesis factor REH1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	84240	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	2	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.483	Depositor
Minimum map value	-0.325	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.021	Depositor
Recommended contour level	0.143	Depositor
Map size ($\text{\AA}$)	388.80002, 388.80002, 388.80002	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.08, 1.08, 1.08	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	1	0.41	0/74017	0.39	2/115398 (0.0%)
2	3	0.34	0/2883	0.32	0/4491
3	4	0.44	0/3746	0.38	0/5832
4	A	0.44	0/1908	0.60	0/2564
5	B	0.43	0/3146	0.60	0/4228
6	C	0.42	0/2800	0.61	0/3790
7	D	0.31	0/2425	0.55	0/3271
8	E	0.33	0/1260	0.54	0/1694
9	F	0.40	0/1821	0.54	0/2451
10	G	0.36	0/1836	0.59	1/2481 (0.0%)
11	H	0.32	0/1539	0.54	1/2073 (0.0%)
12	J	0.28	0/1374	0.57	0/1842
13	L	0.40	0/1568	0.64	0/2106
14	M	0.37	0/1068	0.53	0/1438
15	N	0.46	0/1757	0.66	0/2354
16	O	0.45	1/1585 (0.1%)	0.56	0/2128
17	P	0.41	0/1465	0.62	0/1968
18	Q	0.39	0/1465	0.62	0/1965
19	R	0.38	0/1275	0.60	2/1702 (0.1%)
20	S	0.38	0/1481	0.56	0/1990
21	T	0.36	0/1300	0.56	0/1743
22	U	0.29	0/812	0.52	0/1099
23	V	0.41	0/1018	0.60	0/1369
24	W	0.38	0/540	0.53	0/717
25	X	0.39	0/979	0.56	0/1321
26	Y	0.37	0/1004	0.59	0/1341
27	Z	0.39	1/1118 (0.1%)	0.64	0/1497
28	a	0.42	0/1204	0.69	0/1612
29	b	0.30	0/473	0.50	0/629
30	c	0.34	0/751	0.48	0/1008
31	d	0.40	0/890	0.57	0/1196
32	e	0.40	0/1041	0.60	0/1394
33	f	0.42	0/868	0.54	0/1168
34	g	0.42	0/890	0.57	0/1189

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	h	0.36	0/978	0.55	0/1301
36	i	0.35	0/778	0.68	0/1034
37	j	0.45	0/696	0.66	0/923
38	k	0.32	0/618	0.51	0/826
39	l	0.46	0/443	0.60	0/588
40	o	0.38	0/777	0.63	0/1028
41	p	0.41	0/701	0.56	0/934
42	w	0.58	2/1931 (0.1%)	0.70	4/2629 (0.2%)
43	y	0.32	0/1720	0.51	0/2341
44	z	0.35	0/472	0.70	0/626
All	All	0.40	4/132421 (0.0%)	0.47	10/195279 (0.0%)

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
5	B	0	2
7	D	0	1
10	G	0	1
11	H	0	1
12	J	0	1
13	L	0	1
14	M	0	1
16	O	0	2
17	P	0	1
20	S	0	2
22	U	0	1
27	Z	0	1
31	d	0	1
32	e	0	1
35	h	0	1
39	l	0	1
42	w	0	1
43	y	0	1
All	All	0	21

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
42	w	186	ASP	C-N	20.02	1.59	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
42	w	165	VAL	C-N	6.01	1.48	1.33
16	O	74	ARG	C-N	-5.45	1.22	1.33
27	Z	48	ARG	C-N	-5.01	1.23	1.33

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
42	w	165	VAL	O-C-N	13.82	136.85	121.10
42	w	186	ASP	O-C-N	-8.47	113.44	123.27
1	1	1607	U	C2'-C3'-O3'	6.15	118.73	109.50
1	1	2438	A	C4'-C3'-O3'	5.94	121.91	113.00
10	G	30	THR	N-CA-C	5.64	122.27	109.81
19	R	129	GLY	CA-C-N	-5.54	110.96	121.54
19	R	129	GLY	C-N-CA	-5.54	110.96	121.54
42	w	186	ASP	CA-C-N	5.38	130.92	122.21
42	w	186	ASP	C-N-CA	5.38	130.92	122.21
11	H	22	SER	CB-CA-C	-5.05	110.73	116.54

There are no chirality outliers.

All (21) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	B	385	LYS	Peptide
5	B	81	THR	Peptide
7	D	58	LYS	Peptide
10	G	30	THR	Peptide
11	H	49	ASN	Peptide
12	J	113	GLY	Peptide
13	L	69	VAL	Peptide
14	M	48	GLY	Peptide
16	O	109	PRO	Peptide
16	O	148	LYS	Peptide
17	P	125	GLN	Peptide
20	S	12	ARG	Peptide
20	S	166	LYS	Peptide
22	U	50	LEU	Peptide
27	Z	102	GLU	Peptide
31	d	6	ASP	Peptide
32	e	122	PRO	Peptide
35	h	90	ARG	Peptide
39	l	4	GLN	Peptide
42	w	167	HIS	Peptide

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Mol	Chain	Res	Type	Group
43	y	145	ASN	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	1	66124	0	33228	1249	0
2	3	2579	0	1304	73	0
3	4	3353	0	1695	54	0
4	A	1874	0	1943	81	0
5	B	3075	0	3142	135	0
6	C	2748	0	2859	115	0
7	D	2375	0	2325	104	0
8	E	1239	0	1326	60	0
9	F	1784	0	1862	58	0
10	G	1804	0	1877	62	0
11	H	1518	0	1587	62	0
12	J	1353	0	1383	61	0
13	L	1543	0	1608	63	0
14	M	1053	0	1149	46	0
15	N	1720	0	1779	93	0
16	O	1555	0	1659	36	0
17	P	1442	0	1485	49	0
18	Q	1441	0	1543	65	0
19	R	1258	0	1342	48	0
20	S	1445	0	1487	64	0
21	T	1276	0	1323	46	0
22	U	796	0	812	13	0
23	V	1003	0	1048	39	0
24	W	528	0	558	19	0
25	X	964	0	1025	32	0
26	Y	993	0	1081	25	0
27	Z	1092	0	1155	58	0
28	a	1173	0	1215	52	0
29	b	462	0	491	13	0
30	c	743	0	797	24	0
31	d	876	0	912	26	0
32	e	1020	0	1090	30	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
33	f	850	0	880	26	0
34	g	880	0	945	30	0
35	h	969	0	1078	24	0
36	i	771	0	849	41	0
37	j	681	0	687	35	0
38	k	612	0	682	15	0
39	l	436	0	475	24	0
40	o	765	0	827	46	0
41	p	694	0	738	39	0
42	w	1894	0	1846	94	0
43	y	1699	0	1680	74	0
44	z	469	0	492	28	0
All	All	122929	0	89269	2774	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 14.

All (2774) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:3151:U:OP2	5:B:132:LYS:NZ	1.71	1.22
1:1:912:G:OP2	4:A:9:ARG:NH1	1.74	1.20
1:1:1724:U:OP2	19:R:128:LYS:NZ	1.78	1.16
1:1:1135:A:OP2	29:b:5:LYS:NZ	1.78	1.15
42:w:329:SER:HB2	42:w:333:ARG:O	1.46	1.15
1:1:2436:U:H2'	1:1:2437:G:H5''	1.26	1.14
20:S:109:ASP:OD1	20:S:113:ARG:NH1	1.81	1.12
1:1:3068:U:OP2	19:R:62:ARG:NH1	1.85	1.10
4:A:30:ARG:HH12	4:A:41:ILE:HD13	1.13	1.08
12:J:32:ARG:NH1	12:J:120:ILE:O	1.85	1.08
1:1:2435:G:H2'	1:1:2436:U:H5'	1.12	1.07
15:N:38:ARG:HH12	15:N:60:VAL:HG13	1.16	1.06
42:w:163:GLN:HG2	42:w:169:ARG:CB	1.86	1.05
1:1:1491:A:OP1	37:j:14:LYS:NZ	1.88	1.05
1:1:758:C:OP1	40:o:15:LYS:NZ	1.91	1.03
1:1:1521:G:O6	39:l:17:LYS:NZ	1.92	1.03
1:1:2988:C:O2	5:B:266:ARG:NH1	1.91	1.03
1:1:673:U:O4	18:Q:56:LYS:NZ	1.94	1.00
1:1:1874:A:N7	19:R:20:ARG:NH1	2.11	0.99
28:a:135:GLU:OE2	28:a:139:ARG:NH2	1.94	0.99
5:B:115:LYS:NZ	5:B:129:ALA:O	1.96	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:k:26:LYS:NZ	38:k:28:ASN:OD1	1.97	0.97
33:f:6:ARG:NH1	33:f:8:TYR:O	1.96	0.97
1:1:2103:U:OP1	19:R:81:ARG:NH1	1.98	0.97
1:1:2435:G:H2'	1:1:2436:U:C5'	1.94	0.97
1:1:2713:U:O2'	40:o:8:ARG:NH1	1.98	0.96
42:w:329:SER:CB	42:w:333:ARG:O	2.13	0.96
1:1:284:A:OP2	40:o:41:ARG:NH1	1.98	0.96
1:1:1657:C:O2'	1:1:1797:A:OP2	1.82	0.96
12:J:133:ARG:NH2	12:J:158:ASP:OD2	1.98	0.96
42:w:165:VAL:HG13	42:w:166:PRO:HD2	1.45	0.95
1:1:2338:C:OP1	5:B:236:LYS:NZ	2.00	0.95
5:B:185:GLY:O	5:B:191:LYS:NZ	2.00	0.94
1:1:2251:G:H1	1:1:2265:C:H41	1.16	0.94
1:1:3214:U:OP2	14:M:128:ARG:NH1	1.99	0.94
1:1:596:C:O2	6:C:326:ARG:NH1	2.00	0.94
41:p:36:ARG:HH11	41:p:48:LYS:NZ	1.65	0.94
2:3:31:U:H4'	7:D:218:ARG:HH22	1.33	0.93
15:N:37:HIS:HE1	15:N:63:ARG:HH11	1.03	0.92
41:p:58:SER:O	41:p:61:LYS:NZ	2.01	0.92
1:1:3042:U:OP2	1:1:3092:C:N4	2.03	0.92
9:F:48:ASN:ND2	9:F:182:ASP:OD2	2.03	0.92
3:4:75:G:OP2	26:Y:74:TYR:OH	1.88	0.92
42:w:220:ILE:HG22	42:w:248:ILE:HG12	1.53	0.91
1:1:2435:G:C2'	1:1:2436:U:H5'	2.00	0.91
1:1:1157:G:OP1	9:F:90:LYS:NZ	2.04	0.90
1:1:2991:A:O3'	5:B:21:ARG:NH1	2.04	0.90
1:1:979:U:O2'	1:1:980:A:OP2	1.89	0.90
1:1:2305:G:OP2	1:1:2305:G:N2	2.05	0.90
23:V:135:VAL:HG22	43:y:101:LEU:HA	1.52	0.90
42:w:274:VAL:HG11	42:w:285:PHE:HB3	1.54	0.90
1:1:3309:G:OP2	1:1:3309:G:N2	2.04	0.90
1:1:2945:G:O2'	1:1:2948:C:OP2	1.90	0.89
1:1:1493:G:O6	39:l:2:ALA:N	2.05	0.89
1:1:1305:U:OP2	1:1:2939:G:N2	2.05	0.89
1:1:3276:G:H1	33:f:60:ARG:HH22	1.18	0.89
1:1:97:U:O4	13:L:11:LYS:NZ	2.07	0.88
1:1:123:A:OP1	10:G:105:LYS:NZ	2.06	0.88
31:d:70:ARG:HH12	31:d:102:LYS:HZ3	1.21	0.87
1:1:804:C:OP1	6:C:98:ARG:NH2	2.08	0.86
1:1:2436:U:H2'	1:1:2437:G:C5'	2.05	0.86
1:1:2728:G:N7	21:T:87:LYS:NZ	2.24	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:3:38:U:N3	2:3:41:G:OP2	2.09	0.86
1:1:3308:C:N3	17:P:69:ARG:NH1	2.24	0.86
31:d:70:ARG:HH22	31:d:102:LYS:HZ2	1.22	0.86
42:w:329:SER:HB2	42:w:333:ARG:C	2.01	0.86
17:P:49:GLU:OE2	17:P:92:GLN:NE2	2.08	0.85
36:i:33:ALA:HB1	36:i:38:LYS:NZ	1.91	0.85
1:1:148:G:OP2	15:N:4:TYR:OH	1.94	0.85
1:1:92:G:O5'	40:o:46:LYS:NZ	2.09	0.85
41:p:3:LYS:NZ	41:p:5:THR:O	2.09	0.85
1:1:3092:C:O2'	1:1:3094:A:OP2	1.93	0.85
13:L:128:ARG:HH12	35:h:112:PRO:HG2	1.42	0.85
1:1:2206:G:N2	1:1:2237:C:N3	2.23	0.85
19:R:103:ARG:NH1	19:R:124:TYR:OH	2.09	0.85
27:Z:88:ASP:HB3	27:Z:121:ARG:HH22	1.42	0.85
1:1:3070:A:OP1	19:R:62:ARG:NH2	2.10	0.84
13:L:48:PRO:HA	13:L:137:GLN:HB3	1.58	0.84
23:V:81:GLN:O	23:V:98:ASN:ND2	2.10	0.84
7:D:64:ILE:HD13	7:D:109:THR:HG21	1.60	0.84
1:1:2437:G:H1	1:1:2510:U:H3	1.24	0.84
1:1:2774:C:OP1	13:L:178:LYS:NZ	2.10	0.84
14:M:13:ARG:NH1	20:S:172:TYR:O	2.11	0.84
1:1:2948:C:OP1	5:B:244:ARG:NH2	2.11	0.84
25:X:60:TYR:OH	35:h:26:LYS:NZ	2.10	0.84
1:1:282:G:O2'	1:1:283:G:OP2	1.95	0.83
34:g:8:ARG:NH1	34:g:31:ARG:HD3	1.93	0.83
1:1:1680:G:O6	22:U:81:LYS:NZ	2.10	0.83
1:1:3375:A:O2'	1:1:3378:C:OP2	1.96	0.83
1:1:3316:A:O2'	1:1:3317:U:OP2	1.96	0.83
31:d:10:ARG:HH12	31:d:44:MET:HE1	1.44	0.83
1:1:1179:A:HO2'	1:1:1327:C:HO2'	1.20	0.83
42:w:287:ASP:HB2	42:w:292:GLN:H	1.44	0.83
1:1:743:C:N3	18:Q:141:ARG:NH1	2.27	0.82
7:D:77:ALA:O	7:D:108:ARG:NH1	2.11	0.82
7:D:31:TYR:O	7:D:35:ARG:NH1	2.13	0.82
36:i:70:ARG:NH1	36:i:84:LYS:HG2	1.94	0.82
13:L:182:ILE:HG22	13:L:186:ARG:HH12	1.42	0.82
1:1:801:A:OP1	28:a:27:LYS:NZ	2.10	0.82
1:1:1778:G:O2'	1:1:1780:G:OP2	1.98	0.81
42:w:327:GLY:O	42:w:328:ILE:O	1.97	0.81
1:1:1605:A:O2'	1:1:1607:U:OP2	1.97	0.81
1:1:2745:G:N2	1:1:2748:A:OP2	2.13	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:297:G:O6	15:N:12:ARG:NH1	2.14	0.81
1:1:825:U:O2	1:1:901:G:N2	2.14	0.81
1:1:3162:C:H2'	1:1:3163:A:H8	1.45	0.81
6:C:282:SER:N	18:Q:125:ASP:OD2	2.15	0.80
1:1:31:C:H41	15:N:188:ARG:HH12	1.30	0.80
1:1:2522:G:O6	4:A:70:ARG:NH1	2.14	0.80
1:1:2712:U:HO2'	1:1:2743:A:HO2'	1.21	0.80
1:1:1192:C:N4	1:1:1302:A:OP2	2.13	0.80
1:1:1550:C:H2'	1:1:1551:C:H6	1.46	0.80
1:1:2436:U:C2'	1:1:2437:G:H5''	2.09	0.80
23:V:14:SER:O	23:V:81:GLN:NE2	2.14	0.79
1:1:759:U:P	40:o:18:ARG:HH12	2.06	0.79
7:D:148:ILE:HG23	7:D:151:GLN:HB3	1.64	0.79
24:W:6:ASP:OD2	24:W:9:SER:OG	1.99	0.79
1:1:1721:U:OP2	19:R:124:TYR:OH	2.00	0.79
15:N:37:HIS:CE1	15:N:63:ARG:HH11	1.95	0.79
1:1:1683:A:H61	1:1:3071:U:H3	1.30	0.79
2:3:64:A:OP1	7:D:289:LYS:NZ	2.16	0.79
20:S:13:ARG:NH1	20:S:50:LYS:O	2.14	0.79
1:1:3041:U:OP1	23:V:12:ARG:NH1	2.15	0.79
10:G:144:GLU:CD	36:i:36:ARG:HH12	1.90	0.79
1:1:2219:A:H2'	1:1:2220:A:H8	1.47	0.78
1:1:242:C:O2'	1:1:243:G:OP2	1.99	0.78
15:N:38:ARG:HH12	15:N:60:VAL:CG1	1.96	0.78
28:a:77:LYS:O	28:a:79:TRP:N	2.16	0.78
2:3:121:U:OP2	7:D:265:TYR:OH	2.01	0.78
1:1:852:U:O4	41:p:2:ALA:N	2.17	0.78
1:1:2436:U:C5'	1:1:2436:U:H6	1.97	0.78
43:y:185:THR:OG1	43:y:214:GLU:OE2	2.02	0.78
1:1:525:C:OP2	14:M:77:ARG:NH2	2.17	0.78
1:1:1404:G:N2	1:1:1407:A:OP2	2.17	0.78
43:y:101:LEU:HD13	43:y:107:VAL:HG21	1.64	0.78
1:1:3211:C:P	14:M:109:ARG:HH12	2.06	0.78
1:1:695:C:OP1	6:C:271:LYS:NZ	2.16	0.78
18:Q:86:THR:HG22	18:Q:105:ARG:HB2	1.65	0.78
1:1:1579:C:H42	1:1:1580:A:H62	1.32	0.78
1:1:3349:C:N3	1:1:3356:G:N2	2.32	0.77
1:1:2227:C:H2'	1:1:2228:A:H8	1.49	0.77
36:i:70:ARG:HH12	36:i:84:LYS:HG2	1.47	0.77
1:1:358:G:N2	1:1:361:A:OP2	2.17	0.77
12:J:92:ARG:HB3	12:J:173:ASP:OD2	1.83	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:y:85:ARG:NH2	43:y:92:VAL:O	2.18	0.77
1:1:80:G:OP2	15:N:193:ARG:NH1	2.17	0.77
1:1:2828:G:N1	1:1:2862:U:O2	2.16	0.77
25:X:68:THR:HG21	35:h:36:LEU:HD13	1.66	0.77
43:y:219:GLU:OE2	43:y:225:GLN:HB2	1.85	0.77
11:H:69:ARG:HH12	11:H:72:LYS:NZ	1.83	0.77
1:1:1096:U:OP2	21:T:116:ARG:NH2	2.18	0.77
1:1:2439:A:H2	1:1:2508:U:H3	1.31	0.77
1:1:3350:C:N4	1:1:3353:G:O6	2.17	0.77
4:A:30:ARG:NH1	4:A:41:ILE:HD13	1.96	0.77
20:S:10:ILE:O	20:S:59:VAL:N	2.18	0.77
27:Z:22:LYS:NZ	27:Z:132:SER:O	2.15	0.77
5:B:41:VAL:HA	5:B:185:GLY:HA3	1.64	0.76
1:1:2155:G:O2'	4:A:227:ARG:NH2	2.18	0.76
10:G:36:ILE:HG22	10:G:37:GLY:H	1.50	0.76
1:1:63:A:OP1	15:N:169:LYS:NZ	2.18	0.76
1:1:2254:U:O2	1:1:2262:A:N6	2.18	0.76
1:1:901:G:OP1	37:j:13:ASN:ND2	2.17	0.76
1:1:371:G:N1	1:1:374:A:OP2	2.17	0.76
3:4:135:G:H5''	25:X:49:LYS:HD3	1.65	0.76
20:S:115:ARG:O	20:S:117:ARG:NH2	2.18	0.76
15:N:5:LYS:NZ	36:i:37:THR:HG22	2.00	0.76
1:1:1390:A:N6	1:1:1418:A:O2'	2.19	0.76
42:w:260:PRO:HD2	42:w:263:LEU:HD22	1.66	0.76
1:1:503:C:O5'	8:E:26:ARG:NH1	2.17	0.76
1:1:2405:C:N4	1:1:2870:C:O2	2.19	0.75
1:1:1427:U:OP2	28:a:4:ARG:NH2	2.19	0.75
17:P:122:ALA:HB3	17:P:143:PRO:HB2	1.68	0.75
1:1:1445:U:O2	1:1:2357:A:N6	2.17	0.75
2:3:72:A:N6	2:3:106:U:O4	2.19	0.75
5:B:81:THR:HG21	5:B:205:VAL:HG13	1.68	0.75
1:1:524:U:O4	1:1:568:G:N1	2.15	0.75
8:E:40:LEU:HD13	8:E:84:VAL:HG11	1.68	0.75
25:X:103:TYR:HB3	25:X:135:ILE:HD11	1.67	0.75
14:M:88:ALA:O	14:M:93:LYS:NZ	2.18	0.75
24:W:12:LYS:O	24:W:32:GLN:NE2	2.20	0.74
1:1:1814:A:H4'	1:1:1815:U:H5'	1.68	0.74
41:p:3:LYS:HZ1	41:p:6:LYS:HA	1.51	0.74
7:D:76:ALA:HB3	7:D:109:THR:HG22	1.69	0.74
1:1:1613:A:OP1	38:k:2:ALA:N	2.20	0.74
1:1:1632:A:OP1	27:Z:69:LYS:NZ	2.19	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:920:A:OP1	1:1:923:C:N4	2.21	0.74
20:S:28:ARG:HH11	20:S:99:ARG:CZ	2.00	0.74
1:1:2681:U:O2	12:J:22:SER:OG	2.04	0.73
21:T:119:ALA:HA	21:T:122:GLN:HB3	1.69	0.73
40:o:89:LYS:HD3	42:w:314:GLN:HE22	1.54	0.73
1:1:824:C:H5'	4:A:21:ARG:HD3	1.70	0.73
1:1:2206:G:H8	1:1:2206:G:OP2	1.70	0.73
1:1:2703:A:N6	7:D:28:THR:O	2.21	0.73
1:1:3212:C:OP2	14:M:124:ARG:NH2	2.21	0.73
43:y:39:GLU:O	43:y:43:GLY:N	2.19	0.73
1:1:1591:G:OP1	34:g:37:LYS:NZ	2.21	0.73
23:V:136:VAL:H	43:y:102:SER:HB3	1.54	0.73
42:w:272:GLN:HG3	42:w:387:LEU:HD22	1.68	0.73
1:1:201:A:H2'	1:1:202:G:H8	1.52	0.73
1:1:215:G:OP1	26:Y:12:ARG:NH1	2.22	0.73
1:1:1098:A:O2'	21:T:130:ARG:O	2.06	0.73
2:3:119:U:H3'	7:D:258:LYS:NZ	2.04	0.73
1:1:1101:G:OP2	9:F:196:LYS:HE3	1.89	0.73
23:V:108:GLU:HG2	23:V:128:ARG:NH1	2.04	0.73
1:1:3316:A:OP1	1:1:3318:G:N2	2.16	0.73
15:N:155:VAL:O	15:N:162:ARG:NH2	2.22	0.73
27:Z:89:VAL:HG13	27:Z:93:LYS:HD3	1.71	0.72
1:1:1534:A:OP2	1:1:1586:G:N1	2.13	0.72
6:C:206:LEU:HB2	6:C:246:ARG:HH21	1.54	0.72
41:p:36:ARG:HH11	41:p:48:LYS:HZ3	1.35	0.72
17:P:128:ARG:NH2	44:z:416:GLU:OE2	2.19	0.72
1:1:2703:A:OP2	7:D:23:ARG:NH2	2.22	0.72
5:B:105:VAL:HG11	5:B:148:LEU:HD11	1.71	0.72
7:D:85:ARG:NH1	7:D:86:TYR:OH	2.22	0.72
9:F:24:GLU:HG2	9:F:25:GLN:H	1.53	0.72
1:1:671:U:OP2	18:Q:57:ILE:HD12	1.89	0.72
10:G:78:PHE:O	10:G:79:GLN:HG2	1.89	0.72
25:X:60:TYR:HH	35:h:26:LYS:HZ3	1.35	0.72
27:Z:26:VAL:O	27:Z:93:LYS:NZ	2.19	0.72
42:w:370:MET:HE2	42:w:401:LEU:HD11	1.72	0.72
1:1:1240:A:H3'	1:1:1241:U:H5'	1.72	0.72
39:l:43:ASN:HD22	39:l:46:ARG:NH1	1.87	0.72
1:1:3297:U:O4	5:B:124:LYS:NZ	2.22	0.72
1:1:3367:C:OP2	1:1:3368:U:O2'	2.05	0.72
1:1:2112:U:H4'	1:1:2113:A:OP2	1.90	0.72
4:A:30:ARG:NH1	4:A:41:ILE:HG21	2.04	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1307:G:H5'	16:O:60:LYS:HE2	1.71	0.71
7:D:58:LYS:HA	7:D:93:THR:HG21	1.71	0.71
1:1:1863:G:N1	1:1:1866:C:OP2	2.22	0.71
8:E:35:VAL:HB	8:E:90:LYS:NZ	2.05	0.71
1:1:2435:G:C2'	1:1:2436:U:C5'	2.63	0.71
19:R:99:LEU:HD21	19:R:103:ARG:HH21	1.55	0.71
12:J:133:ARG:HH12	12:J:154:THR:HA	1.55	0.71
13:L:106:GLN:HB3	36:i:18:THR:HG23	1.72	0.71
31:d:70:ARG:NH1	31:d:102:LYS:HZ3	1.88	0.71
1:1:1649:U:O4	1:1:1806:A:N6	2.19	0.71
1:1:2309:A:OP2	42:w:209:LYS:NZ	2.23	0.71
1:1:791:A:OP1	6:C:108:LYS:NZ	2.22	0.71
11:H:113:GLU:OE2	11:H:115:ARG:NE	2.24	0.71
31:d:10:ARG:NH1	31:d:44:MET:HE1	2.06	0.71
1:1:1763:U:H5'	1:1:1764:U:OP2	1.91	0.70
5:B:216:ASP:OD2	5:B:339:ARG:NH2	2.21	0.70
13:L:47:ALA:HB1	13:L:48:PRO:HD2	1.73	0.70
1:1:1940:G:H21	1:1:3362:A:H8	1.39	0.70
1:1:2116:G:OP1	1:1:2118:C:N4	2.24	0.70
1:1:2176:U:OP1	4:A:54:ARG:NH2	2.19	0.70
1:1:2117:A:HO2'	1:1:3080:G:HO2'	1.37	0.70
1:1:2749:G:OP2	1:1:2749:G:H8	1.74	0.70
1:1:796:U:H2'	1:1:797:U:H6	1.55	0.70
1:1:1392:G:HO2'	1:1:1417:G:H1	0.72	0.70
1:1:3252:G:H5''	1:1:3253:G:OP2	1.90	0.70
5:B:10:ARG:NH1	5:B:12:GLY:O	2.24	0.70
1:1:1494:U:OP1	39:l:42:ARG:NH2	2.17	0.70
4:A:118:GLU:HG2	4:A:156:LYS:NZ	2.07	0.70
10:G:162:LEU:HA	15:N:7:LEU:HD11	1.73	0.70
27:Z:54:THR:HG22	27:Z:57:HIS:CD2	2.26	0.70
40:o:71:ARG:HH21	40:o:80:ARG:NH1	1.90	0.70
1:1:2437:G:O6	1:1:2510:U:O4	2.08	0.70
5:B:283:TYR:HB3	5:B:356:LEU:HD11	1.71	0.70
15:N:112:ASN:HB2	15:N:138:GLN:HE22	1.56	0.70
42:w:272:GLN:HG3	42:w:387:LEU:CD2	2.21	0.70
8:E:31:ARG:NE	33:f:107:ILE:O	2.25	0.70
14:M:24:LYS:HE2	14:M:25:LYS:NZ	2.06	0.70
1:1:389:A:OP1	17:P:4:TYR:OH	2.07	0.70
27:Z:3:LYS:NZ	27:Z:30:ASP:OD1	2.22	0.70
10:G:162:LEU:HD23	15:N:7:LEU:HD21	1.74	0.70
25:X:100:LYS:NZ	25:X:106:ASP:OD1	2.24	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:p:3:LYS:NZ	41:p:6:LYS:HA	2.06	0.70
1:1:437:G:H2'	1:1:438:A:O4'	1.92	0.69
1:1:1308:A:H8	1:1:1308:A:OP2	1.73	0.69
17:P:30:ARG:NH1	17:P:31:GLU:OE2	2.25	0.69
27:Z:51:LEU:HB2	27:Z:65:ARG:HD2	1.74	0.69
6:C:112:LYS:HZ1	15:N:204:LYS:HA	1.57	0.69
8:E:43:LEU:HD11	8:E:85:ILE:HG13	1.72	0.69
12:J:38:GLU:O	12:J:42:GLY:N	2.19	0.69
11:H:109:ALA:HB1	11:H:111:PHE:HD2	1.57	0.69
1:1:2140:U:OP2	44:z:427:ARG:NH1	2.22	0.69
5:B:4:ARG:HD2	5:B:7:GLU:HA	1.75	0.69
9:F:92:ILE:HD11	18:Q:4:ASP:HB2	1.73	0.69
19:R:23:TRP:CH2	19:R:25:ASP:HB3	2.28	0.69
1:1:2573:G:H2'	1:1:2574:G:H8	1.56	0.69
1:1:2727:A:OP2	1:1:2728:G:N2	2.25	0.69
1:1:339:C:OP1	1:1:1380:G:O2'	2.10	0.69
1:1:1348:U:OP2	18:Q:38:ARG:NH2	2.26	0.69
1:1:2207:A:H2'	1:1:2208:A:H8	1.58	0.69
2:3:31:U:H4'	7:D:218:ARG:NH2	2.07	0.69
2:3:87:G:H2'	2:3:88:G:H8	1.57	0.69
17:P:56:ARG:NH2	17:P:75:GLU:OE2	2.26	0.69
17:P:128:ARG:NH1	44:z:416:GLU:OE1	2.24	0.69
1:1:1747:G:H21	38:k:2:ALA:HB1	1.58	0.69
6:C:207:VAL:HB	6:C:227:THR:HG22	1.75	0.69
1:1:1308:A:OP2	1:1:1308:A:C8	2.46	0.69
1:1:529:A:H2'	1:1:530:G:H8	1.56	0.68
1:1:1243:G:N2	1:1:1271:A:OP1	2.23	0.68
1:1:2572:C:O2'	1:1:2573:G:O4'	2.10	0.68
11:H:48:VAL:HG13	11:H:49:ASN:H	1.56	0.68
1:1:1720:U:OP2	19:R:110:ARG:NH2	2.25	0.68
1:1:2660:G:N3	1:1:2744:U:O2'	2.25	0.68
7:D:215:ASP:OD2	7:D:218:ARG:HG2	1.92	0.68
12:J:165:GLN:HG2	12:J:166:LYS:H	1.57	0.68
43:y:158:GLY:HA2	43:y:179:VAL:HB	1.74	0.68
1:1:944:C:O2'	32:e:33:ARG:NH1	2.26	0.68
40:o:90:HIS:NE2	42:w:314:GLN:OE1	2.25	0.68
31:d:80:ASN:OD1	31:d:81:GLU:N	2.26	0.68
1:1:2618:G:O2'	1:1:2865:U:OP1	2.12	0.68
1:1:3333:G:H22	1:1:3369:G:H1'	1.58	0.68
16:O:22:VAL:HG21	16:O:120:VAL:HG11	1.76	0.68
18:Q:125:ASP:OD1	18:Q:126:GLN:N	2.27	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:w:342:ARG:HB2	42:w:345:ASP:HB3	1.75	0.68
1:1:321:C:OP1	15:N:159:ARG:NH2	2.26	0.68
1:1:2568:C:O2'	1:1:2569:A:O4'	2.10	0.68
1:1:2714:G:OP2	40:o:8:ARG:NH2	2.27	0.68
43:y:123:ARG:HG3	43:y:126:GLU:OE2	1.94	0.68
1:1:992:A:H5''	21:T:43:LYS:HD2	1.75	0.68
1:1:3275:U:O2'	33:f:99:ARG:NH1	2.27	0.68
5:B:187:SER:O	5:B:190:GLU:N	2.26	0.68
11:H:69:ARG:HH12	11:H:72:LYS:HZ2	1.42	0.68
26:Y:40:ARG:NH1	26:Y:46:LYS:NZ	2.40	0.68
1:1:3018:C:OP1	43:y:9:ASN:ND2	2.27	0.68
24:W:56:ARG:HB3	24:W:61:LYS:HB2	1.76	0.68
4:A:27:ALA:O	4:A:128:ARG:NH2	2.27	0.67
6:C:112:LYS:NZ	15:N:204:LYS:HA	2.09	0.67
40:o:24:LYS:HE3	40:o:75:VAL:HG12	1.76	0.67
42:w:176:GLN:O	42:w:180:LYS:N	2.26	0.67
38:k:24:THR:HG22	38:k:44:LYS:HB2	1.76	0.67
1:1:520:U:H3	6:C:347:THR:HG1	1.43	0.67
1:1:950:G:N1	1:1:1368:U:OP2	2.24	0.67
1:1:1216:C:H42	1:1:1289:G:H1	1.40	0.67
17:P:169:THR:HG21	33:f:60:ARG:NH1	2.08	0.67
1:1:1257:C:H42	1:1:1261:G:H22	1.42	0.67
27:Z:95:VAL:HG11	27:Z:113:VAL:HB	1.76	0.67
31:d:70:ARG:HH22	31:d:102:LYS:NZ	1.91	0.67
1:1:1561:G:O6	1:1:1578:C:N4	2.26	0.67
7:D:280:GLU:HA	7:D:283:ALA:HB3	1.76	0.67
8:E:31:ARG:NH2	8:E:84:VAL:O	2.27	0.67
27:Z:48:ARG:NH1	27:Z:69:LYS:HD2	2.10	0.67
15:N:37:HIS:HE1	15:N:63:ARG:NH1	1.85	0.67
43:y:146:ILE:HG23	43:y:147:LEU:H	1.58	0.67
1:1:353:G:O6	37:j:52:LYS:NZ	2.26	0.67
3:4:36:G:OP2	35:h:85:THR:OG1	2.11	0.67
1:1:364:G:OP2	37:j:52:LYS:HE3	1.94	0.67
1:1:2255:A:N7	1:1:2260:U:N3	2.43	0.67
1:1:3219:G:N7	33:f:2:ALA:N	2.42	0.67
37:j:17:THR:HG22	37:j:18:LEU:H	1.59	0.67
1:1:2139:A:O2'	44:z:427:ARG:NH2	2.28	0.66
1:1:2406:C:H42	1:1:2815:G:H1	1.43	0.66
5:B:53:MET:HG2	5:B:77:THR:HG22	1.78	0.66
11:H:49:ASN:O	11:H:51:GLN:N	2.26	0.66
1:1:2529:A:OP1	10:G:248:LYS:NZ	2.28	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:g:74:ARG:CZ	34:g:82:ALA:HB2	2.24	0.66
15:N:122:ASN:OD1	15:N:123:GLN:N	2.28	0.66
36:i:33:ALA:HB1	36:i:38:LYS:HZ1	1.61	0.66
19:R:102:LEU:HD22	19:R:138:LEU:HD13	1.78	0.66
1:1:187:A:N3	1:1:208:C:O2'	2.27	0.66
1:1:744:A:H1'	18:Q:141:ARG:HD2	1.78	0.66
1:1:2376:G:H2'	1:1:2377:G:C8	2.31	0.66
23:V:27:ASP:OD2	23:V:102:ILE:HG22	1.95	0.66
1:1:401:U:O2'	44:z:400:LYS:NZ	2.29	0.66
1:1:609:G:OP2	6:C:315:LYS:NZ	2.19	0.66
1:1:2799:A:O2'	28:a:42:ARG:NH1	2.29	0.66
1:1:2585:G:O6	10:G:47:SER:OG	2.13	0.66
4:A:104:LEU:HD22	4:A:158:ILE:HD11	1.78	0.66
5:B:76:VAL:HG21	5:B:323:MET:HE3	1.78	0.66
9:F:110:ARG:HH11	18:Q:3:ILE:CG1	2.08	0.66
27:Z:101:PHE:HA	27:Z:107:ARG:HE	1.61	0.66
29:b:11:ASN:OD1	29:b:14:ARG:NH2	2.29	0.66
42:w:164:LYS:HD3	42:w:195:ASP:OD2	1.96	0.66
1:1:502:U:O3'	8:E:26:ARG:NH1	2.26	0.65
23:V:135:VAL:HA	43:y:102:SER:H	1.60	0.65
1:1:76:G:N7	13:L:101:ARG:HB3	2.12	0.65
1:1:3234:A:H2	1:1:3253:G:H22	1.43	0.65
5:B:71:GLU:OE2	24:W:1:MET:N	2.25	0.65
7:D:285:ARG:HA	7:D:288:ALA:HB3	1.77	0.65
1:1:3353:G:H4'	1:1:3354:U:OP2	1.96	0.65
14:M:48:GLY:HA3	14:M:53:VAL:HG13	1.78	0.65
1:1:2781:U:H4'	13:L:185:LYS:HG3	1.79	0.65
7:D:123:GLU:HG2	7:D:248:ARG:HH12	1.62	0.65
21:T:66:ASN:O	21:T:73:GLY:N	2.25	0.65
21:T:79:MET:HB2	21:T:84:TYR:HE1	1.61	0.65
1:1:2186:U:H5	4:A:200:ARG:HD3	1.62	0.65
1:1:2899:C:N3	11:H:173:ARG:NH1	2.44	0.65
31:d:55:LEU:HB2	31:d:95:PRO:HD3	1.78	0.65
6:C:302:ALA:CB	18:Q:39:ARG:HH12	2.10	0.65
11:H:4:ILE:HB	20:S:142:GLN:HE21	1.61	0.65
41:p:36:ARG:NH1	41:p:48:LYS:NZ	2.41	0.65
9:F:110:ARG:HH11	18:Q:3:ILE:HG12	1.61	0.65
10:G:109:LEU:HD23	10:G:112:GLU:OE2	1.97	0.65
1:1:655:C:OP2	32:e:27:ARG:HD3	1.96	0.65
8:E:70:LYS:HG2	8:E:142:ASP:OD2	1.97	0.65
1:1:2219:A:H2'	1:1:2220:A:C8	2.31	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:3308:C:O2	17:P:69:ARG:HD2	1.97	0.64
2:3:112:G:H2'	2:3:113:C:C6	2.32	0.64
25:X:59:SER:HB3	25:X:102:LEU:HD21	1.79	0.64
1:1:1564:U:H2'	1:1:1565:G:C8	2.32	0.64
1:1:3057:U:O2'	1:1:3059:G:OP1	2.14	0.64
9:F:156:ILE:HD11	9:F:168:ILE:HG23	1.79	0.64
19:R:105:LEU:HD12	19:R:135:LYS:HE2	1.79	0.64
1:1:2207:A:H2'	1:1:2208:A:C8	2.31	0.64
5:B:261:MET:HG2	16:O:64:PHE:HA	1.80	0.64
5:B:50:LYS:NZ	5:B:330:GLY:O	2.31	0.64
6:C:317:PRO:C	6:C:319:LYS:H	2.04	0.64
11:H:69:ARG:HH11	11:H:72:LYS:HD3	1.62	0.64
13:L:33:VAL:O	13:L:37:ASN:ND2	2.31	0.64
34:g:8:ARG:HH11	34:g:31:ARG:HD3	1.61	0.64
1:1:784:A:O2'	1:1:785:G:OP2	2.16	0.64
8:E:52:VAL:HG23	8:E:67:GLY:HA2	1.79	0.64
1:1:267:G:N2	15:N:50:ARG:O	2.30	0.64
1:1:989:A:O2'	21:T:104:GLU:OE1	2.15	0.64
1:1:1438:U:H5'	6:C:74:ILE:HD11	1.80	0.64
1:1:1266:G:H8	1:1:1266:G:OP2	1.79	0.64
14:M:21:VAL:HG12	14:M:65:LEU:HD23	1.78	0.64
1:1:901:G:H2'	1:1:902:G:H8	1.63	0.64
1:1:3157:U:H4'	1:1:3158:G:H5'	1.78	0.64
1:1:3333:G:N2	1:1:3369:G:H1'	2.13	0.64
7:D:129:TYR:CG	7:D:177:GLU:HB3	2.33	0.64
11:H:69:ARG:NH1	11:H:72:LYS:HD3	2.13	0.64
13:L:46:ILE:HG22	13:L:49:ARG:HB2	1.80	0.64
29:b:17:HIS:HA	29:b:20:GLY:HA2	1.79	0.64
1:1:359:U:H4'	1:1:817:A:H62	1.63	0.63
1:1:1093:A:N3	1:1:1096:U:N3	2.46	0.63
1:1:1884:A:H2	1:1:2349:U:H3	1.47	0.63
1:1:2250:G:H1	1:1:2266:U:H3	1.46	0.63
14:M:47:ASP:OD2	14:M:49:PRO:HD3	1.98	0.63
15:N:38:ARG:NH1	15:N:60:VAL:HG13	2.01	0.63
1:1:1759:C:N4	1:1:1766:G:O6	2.17	0.63
20:S:13:ARG:HD3	20:S:51:VAL:HG12	1.78	0.63
35:h:102:GLU:OE2	35:h:106:LYS:HE3	1.98	0.63
15:N:53:TYR:HB2	15:N:133:ILE:HD12	1.79	0.63
1:1:2510:U:O2'	1:1:2511:A:H5''	1.98	0.63
27:Z:95:VAL:HG21	27:Z:113:VAL:HG11	1.80	0.63
40:o:8:ARG:HE	40:o:10:THR:HB	1.62	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1618:G:H4'	3:4:129:C:H1'	1.80	0.63
40:o:29:LYS:NZ	42:w:389:ILE:HD13	2.13	0.63
40:o:61:LYS:HZ3	42:w:382:ASP:H	1.47	0.63
1:1:1270:A:N6	1:1:1271:A:N3	2.46	0.63
15:N:91:GLU:O	15:N:93:LYS:NZ	2.28	0.63
1:1:1525:G:H5'	1:1:1830:G:OP2	1.99	0.63
1:1:2228:A:H2'	1:1:2229:A:C8	2.33	0.63
1:1:2698:G:H4'	21:T:12:ARG:NH1	2.13	0.63
1:1:3207:U:OP1	14:M:106:ARG:NH2	2.31	0.63
2:3:110:G:OP2	7:D:279:LYS:NZ	2.32	0.63
1:1:1134:G:O2'	1:1:2642:A:N3	2.30	0.63
3:4:150:G:OP1	25:X:27:ARG:NH2	2.32	0.63
8:E:129:GLU:HG2	8:E:130:ILE:H	1.62	0.63
10:G:36:ILE:O	10:G:38:GLN:N	2.32	0.63
1:1:13:A:H5'	1:1:14:U:OP2	1.99	0.62
1:1:412:G:H5''	17:P:30:ARG:HD2	1.81	0.62
1:1:1186:G:H2'	1:1:1187:C:H6	1.64	0.62
1:1:1693:C:HO2'	1:1:1772:U:HO2'	1.46	0.62
1:1:1814:A:OP1	1:1:1816:A:O2'	2.16	0.62
1:1:2137:U:OP2	1:1:2142:A:N6	2.27	0.62
1:1:2439:A:H8	1:1:2439:A:O5'	1.82	0.62
9:F:77:VAL:HG12	20:S:59:VAL:HA	1.80	0.62
28:a:85:ASP:OD1	28:a:86:LYS:N	2.31	0.62
1:1:92:G:P	40:o:46:LYS:HZ1	2.22	0.62
1:1:2227:C:H2'	1:1:2228:A:C8	2.34	0.62
1:1:2436:U:H6	1:1:2436:U:O5'	1.82	0.62
1:1:3221:C:H42	1:1:3264:G:H1	1.47	0.62
27:Z:88:ASP:HB3	27:Z:121:ARG:NH2	2.13	0.62
1:1:682:U:O2'	13:L:28:GLN:NE2	2.32	0.62
12:J:32:ARG:HB3	12:J:120:ILE:HG23	1.82	0.62
42:w:165:VAL:CG1	42:w:166:PRO:HD2	2.24	0.62
1:1:1763:U:H3'	1:1:1764:U:C6	2.34	0.62
1:1:3376:A:H5'	1:1:3377:G:H5''	1.81	0.62
5:B:269:GLN:NE2	5:B:270:ARG:O	2.32	0.62
5:B:306:THR:OG1	5:B:316:GLU:O	2.12	0.62
1:1:120:G:N1	10:G:126:SER:O	2.31	0.62
2:3:44:C:H2'	2:3:45:A:H8	1.65	0.62
18:Q:173:GLU:HG2	28:a:52:TYR:HA	1.81	0.62
23:V:23:MET:HE2	23:V:36:ILE:HD11	1.82	0.62
1:1:2514:U:OP2	1:1:2586:G:N1	2.27	0.62
1:1:2836:C:H5	1:1:2852:C:H42	1.47	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:H:18:VAL:HG12	11:H:27:VAL:HG22	1.81	0.62
1:1:104:G:O2'	1:1:698:U:O2	2.15	0.62
8:E:174:LEU:HD22	14:M:117:ARG:HH12	1.63	0.62
11:H:23:ARG:NH2	11:H:42:ASP:OD1	2.32	0.62
37:j:53:ALA:HA	37:j:56:ARG:HH11	1.64	0.62
40:o:29:LYS:HG2	40:o:30:ALA:H	1.64	0.62
42:w:265:LYS:HA	42:w:269:ASN:HA	1.81	0.62
2:3:112:G:H2'	2:3:113:C:H6	1.64	0.62
5:B:213:GLU:CD	5:B:340:LYS:HZ2	2.08	0.62
27:Z:46:ILE:HD11	27:Z:49:TYR:CD1	2.35	0.62
43:y:99:GLU:OE2	43:y:125:THR:HG21	1.99	0.62
1:1:503:C:P	8:E:26:ARG:NH1	2.73	0.62
1:1:1748:G:OP1	38:k:44:LYS:HE2	2.00	0.62
1:1:3164:C:H1'	1:1:3165:A:H5'	1.82	0.62
3:4:131:A:H2'	3:4:132:G:H8	1.64	0.62
7:D:107:ARG:NH2	7:D:169:GLY:O	2.33	0.62
1:1:92:G:P	40:o:46:LYS:NZ	2.72	0.61
1:1:959:C:H41	1:1:2801:A:H5''	1.64	0.61
1:1:2660:G:OP1	1:1:2750:U:O2'	2.18	0.61
2:3:88:G:H2'	2:3:89:G:H8	1.64	0.61
8:E:174:LEU:HD22	14:M:117:ARG:NH1	2.14	0.61
14:M:38:ILE:HD11	20:S:150:PHE:CE2	2.35	0.61
4:A:168:VAL:HG13	41:p:79:VAL:HG21	1.82	0.61
7:D:215:ASP:OD2	7:D:217:GLU:HG2	2.00	0.61
13:L:76:THR:CG2	13:L:101:ARG:HG3	2.30	0.61
42:w:328:ILE:O	42:w:329:SER:HB3	1.99	0.61
8:E:40:LEU:HD11	8:E:54:TYR:HB2	1.82	0.61
13:L:182:ILE:HG22	13:L:186:ARG:NH1	2.14	0.61
1:1:237:G:H8	1:1:237:G:OP2	1.82	0.61
1:1:1408:G:OP1	32:e:33:ARG:NH2	2.32	0.61
1:1:1862:U:N3	1:1:1868:G:O6	2.19	0.61
42:w:322:ASP:OD1	42:w:323:VAL:N	2.33	0.61
1:1:1065:A:N6	29:b:26:THR:O	2.34	0.61
1:1:1078:U:H4'	7:D:46:THR:HG21	1.81	0.61
5:B:296:THR:HG22	5:B:297:SER:H	1.65	0.61
10:G:50:VAL:HG12	25:X:30:ALA:HA	1.82	0.61
17:P:24:VAL:HG12	17:P:86:LYS:HG2	1.81	0.61
31:d:92:TYR:HE2	31:d:94:GLU:OE2	1.83	0.61
1:1:503:C:P	8:E:26:ARG:HH11	2.23	0.61
1:1:1626:U:H3	1:1:1817:G:H22	1.46	0.61
1:1:2561:A:HO2'	1:1:2562:A:H8	1.48	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:180:LYS:NZ	6:C:202:ARG:HB3	2.15	0.61
15:N:18:VAL:HG13	15:N:19:LEU:HD12	1.83	0.61
23:V:104:ASN:OD1	23:V:108:GLU:N	2.34	0.61
1:1:63:A:N3	1:1:78:U:O2'	2.28	0.61
1:1:2163:C:O2	1:1:2171:G:N2	2.25	0.61
1:1:2524:A:N1	10:G:44:ARG:NH1	2.49	0.61
2:3:49:G:C8	7:D:58:LYS:HG2	2.35	0.61
4:A:242:ARG:NH1	4:A:246:LEU:HD23	2.16	0.61
7:D:85:ARG:NH1	7:D:86:TYR:CZ	2.69	0.61
1:1:1144:U:OP1	1:1:1367:G:O2'	2.18	0.61
1:1:2113:A:OP2	1:1:2113:A:C8	2.54	0.61
1:1:2312:A:H2'	1:1:2315:G:H21	1.64	0.61
1:1:2437:G:O6	1:1:2510:U:C4	2.54	0.61
4:A:118:GLU:HG2	4:A:156:LYS:HZ3	1.66	0.61
1:1:1175:C:O2'	16:O:87:MET:O	2.17	0.61
1:1:1258:U:H2'	1:1:1260:A:OP2	2.01	0.61
12:J:133:ARG:NH1	12:J:153:LYS:O	2.34	0.61
16:O:14:HIS:HD2	16:O:123:ALA:HB3	1.66	0.61
17:P:131:ARG:HG3	17:P:137:ASN:OD1	2.00	0.61
1:1:2550:U:C6	10:G:37:GLY:HA3	2.35	0.60
1:1:2794:G:O2'	1:1:2795:U:OP2	2.14	0.60
8:E:78:ARG:NH1	8:E:106:PHE:HB2	2.16	0.60
20:S:90:MET:HE1	20:S:114:HIS:CE1	2.36	0.60
1:1:1607:U:H6	1:1:1607:U:H5'	1.65	0.60
1:1:3316:A:N6	5:B:124:LYS:HG2	2.17	0.60
9:F:215:GLY:O	9:F:216:VAL:HG22	2.01	0.60
15:N:104:GLU:HA	15:N:160:GLU:HG3	1.83	0.60
1:1:356:C:O2'	6:C:81:GLY:O	2.17	0.60
11:H:89:LYS:HB3	11:H:143:GLU:OE2	2.00	0.60
13:L:91:ARG:HE	13:L:97:VAL:HB	1.66	0.60
17:P:60:PHE:CE2	17:P:82:ARG:HB2	2.36	0.60
1:1:759:U:OP1	40:o:18:ARG:NH1	2.34	0.60
1:1:1362:G:H2'	1:1:1363:A:C8	2.36	0.60
1:1:1482:A:H4'	1:1:1483:G:OP2	2.01	0.60
1:1:3058:U:O4	31:d:65:LYS:NZ	2.20	0.60
11:H:124:ARG:HD3	11:H:164:ILE:HG13	1.83	0.60
42:w:253:LYS:HG3	42:w:277:SER:O	2.00	0.60
43:y:129:ILE:HG23	43:y:133:LEU:HD12	1.83	0.60
1:1:860:G:OP2	4:A:181:LYS:NZ	2.32	0.60
1:1:2344:U:H2'	1:1:2345:A:C8	2.36	0.60
5:B:70:ARG:NH2	43:y:80:GLU:OE2	2.34	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:o:2:VAL:N	40:o:90:HIS:O	2.35	0.60
1:1:939:U:OP2	28:a:26:ARG:NH2	2.33	0.60
2:3:40:C:O2	12:J:72:ARG:NE	2.22	0.60
6:C:302:ALA:CA	18:Q:39:ARG:HH12	2.14	0.60
42:w:272:GLN:CB	42:w:387:LEU:HD22	2.32	0.60
1:1:1084:A:H4'	7:D:44:TYR:CZ	2.36	0.60
1:1:1447:G:N7	17:P:27:LYS:HB2	2.16	0.60
1:1:1553:U:H4'	1:1:1554:U:H5'	1.83	0.60
1:1:3272:C:OP2	8:E:78:ARG:NH2	2.34	0.60
7:D:151:GLN:HG2	7:D:159:VAL:HG21	1.84	0.60
10:G:24:ASN:HB3	10:G:25:PRO:HD3	1.82	0.60
11:H:90:MET:HE2	11:H:179:ILE:HG22	1.84	0.60
23:V:101:VAL:HB	23:V:109:MET:HE1	1.82	0.60
1:1:349:A:H4'	1:1:350:C:OP2	2.02	0.60
1:1:563:U:OP1	20:S:71:LYS:NZ	2.28	0.60
7:D:7:ALA:C	7:D:8:LYS:HD2	2.27	0.60
7:D:123:GLU:HG2	7:D:248:ARG:NH1	2.16	0.60
34:g:41:ARG:HG2	34:g:56:THR:HG21	1.82	0.60
1:1:111:C:P	13:L:91:ARG:HH12	2.25	0.60
9:F:151:ARG:HH12	9:F:207:LEU:HA	1.67	0.60
9:F:151:ARG:NH1	9:F:207:LEU:HA	2.16	0.60
20:S:12:ARG:HH21	21:T:141:VAL:HG12	1.67	0.60
36:i:33:ALA:HB1	36:i:38:LYS:HZ2	1.67	0.60
1:1:3276:G:H1	33:f:60:ARG:NH2	1.93	0.60
43:y:109:CYS:HB3	43:y:149:GLY:HA2	1.82	0.60
1:1:181:U:O2'	37:j:75:LYS:NZ	2.35	0.59
1:1:1452:A:N3	1:1:2346:C:O2'	2.30	0.59
1:1:3171:U:H3	1:1:3279:A:H61	1.47	0.59
33:f:52:VAL:HG22	33:f:66:VAL:HG22	1.83	0.59
1:1:705:A:H62	28:a:74:ASN:ND2	2.00	0.59
1:1:2441:A:H8	1:1:2441:A:OP2	1.85	0.59
2:3:19:C:H2'	2:3:20:A:C8	2.37	0.59
3:4:80:A:H1'	3:4:82:U:O4	2.03	0.59
32:e:11:LYS:HG3	32:e:14:THR:HG22	1.84	0.59
44:z:390:THR:HG22	44:z:392:LYS:H	1.66	0.59
1:1:2228:A:H2'	1:1:2229:A:H8	1.67	0.59
1:1:2401:A:H5'	6:C:70:ALA:HB2	1.85	0.59
1:1:2767:U:OP1	40:o:34:SER:HB3	2.02	0.59
3:4:95:G:OP2	37:j:72:ARG:NH1	2.35	0.59
4:A:79:ASN:ND2	4:A:166:ILE:O	2.36	0.59
7:D:51:LEU:N	7:D:145:PHE:O	2.26	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:c:60:ALA:O	30:c:64:LYS:N	2.35	0.59
1:1:435:C:H2'	1:1:436:A:C8	2.37	0.59
1:1:1063:G:OP2	1:1:1097:G:H3'	2.03	0.59
1:1:1576:G:H2'	1:1:1577:G:O4'	2.02	0.59
1:1:1813:A:H5'	1:1:1814:A:OP2	2.02	0.59
5:B:17:LEU:HD11	5:B:233:TRP:HH2	1.68	0.59
7:D:60:ILE:HB	7:D:80:SER:HB3	1.83	0.59
10:G:171:LYS:HG2	10:G:226:TYR:CD2	2.37	0.59
23:V:74:MET:SD	23:V:102:ILE:HD11	2.42	0.59
42:w:272:GLN:CG	42:w:387:LEU:HD22	2.32	0.59
1:1:1362:G:H2'	1:1:1363:A:H8	1.66	0.59
1:1:1550:C:H2'	1:1:1551:C:C6	2.35	0.59
1:1:2364:G:H1	1:1:2396:G:H21	1.51	0.59
1:1:3167:A:H5'	1:1:3168:A:OP2	2.03	0.59
20:S:96:ASP:OD1	20:S:97:VAL:N	2.28	0.59
1:1:3277:U:OP1	1:1:3278:C:N4	2.35	0.59
1:1:3277:U:H5''	1:1:3278:C:N3	2.16	0.59
17:P:136:ILE:H	44:z:421:ASN:HD21	1.49	0.59
1:1:1362:G:H4'	9:F:159:GLN:O	2.03	0.59
2:3:121:U:H3	7:D:268:GLU:HG3	1.66	0.59
27:Z:16:GLY:C	27:Z:18:TYR:H	2.10	0.59
32:e:44:ARG:HD2	32:e:46:PHE:CE2	2.37	0.59
32:e:76:VAL:HG11	32:e:82:LEU:HB2	1.83	0.59
1:1:529:A:H2'	1:1:530:G:C8	2.37	0.59
1:1:1353:U:O2'	8:E:8:LYS:O	2.19	0.59
1:1:2424:A:N1	4:A:230:VAL:HG21	2.17	0.59
13:L:76:THR:O	13:L:79:GLU:N	2.36	0.59
26:Y:23:PRO:HD2	26:Y:26:GLN:OE1	2.03	0.59
28:a:7:LYS:O	28:a:11:HIS:ND1	2.23	0.59
43:y:53:ILE:HG12	43:y:59:ILE:HG22	1.85	0.59
43:y:108:ILE:HG12	43:y:117:VAL:HG12	1.85	0.59
1:1:2509:U:H2'	1:1:2510:U:H5'	1.84	0.59
5:B:283:TYR:HD1	5:B:354:VAL:HG21	1.68	0.59
6:C:7:THR:OG1	6:C:147:GLU:OE2	2.17	0.59
6:C:302:ALA:HB2	18:Q:39:ARG:HH12	1.66	0.59
17:P:116:HIS:HB3	17:P:149:VAL:HB	1.83	0.59
17:P:126:ARG:NH1	17:P:140:GLU:OE2	2.36	0.59
43:y:203:LEU:HD21	43:y:205:VAL:HG23	1.84	0.59
44:z:406:LYS:O	44:z:410:ASN:N	2.27	0.59
1:1:40:A:OP2	28:a:36:GLY:N	2.35	0.59
1:1:796:U:H2'	1:1:797:U:C6	2.38	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:939:U:OP2	28:a:26:ARG:NH1	2.35	0.59
1:1:2168:A:C6	1:1:2170:U:H1'	2.37	0.59
1:1:2675:C:H42	12:J:22:SER:HB2	1.66	0.59
1:1:3309:G:H1'	17:P:69:ARG:HD3	1.85	0.59
11:H:4:ILE:HD13	20:S:148:LEU:HD21	1.85	0.59
36:i:34:SER:OG	36:i:37:THR:OG1	2.14	0.59
2:3:11:A:N1	2:3:67:G:O2'	2.35	0.58
6:C:170:LYS:HG2	6:C:175:HIS:HB2	1.85	0.58
13:L:10:LEU:HD23	18:Q:166:LEU:HD11	1.84	0.58
14:M:55:ARG:NH2	14:M:76:ALA:O	2.36	0.58
17:P:114:VAL:HG12	17:P:150:VAL:HG12	1.84	0.58
1:1:709:A:OP1	18:Q:179:ARG:NH1	2.37	0.58
1:1:1523:U:O2'	1:1:1608:C:OP1	2.20	0.58
1:1:3013:U:H2'	1:1:3014:U:C6	2.38	0.58
19:R:25:ASP:OD2	19:R:28:GLU:HG2	2.04	0.58
26:Y:116:LYS:O	26:Y:120:GLN:HG2	2.03	0.58
1:1:346:C:N4	1:1:349:A:OP2	2.19	0.58
1:1:827:A:H2'	1:1:828:A:H8	1.68	0.58
1:1:3211:C:OP2	14:M:109:ARG:NH1	2.35	0.58
6:C:181:VAL:O	6:C:182:LEU:HB2	2.02	0.58
12:J:92:ARG:NH2	12:J:94:ARG:HH11	2.01	0.58
17:P:126:ARG:HH12	17:P:138:LYS:HD2	1.69	0.58
42:w:251:ILE:HG22	42:w:308:ALA:HB2	1.85	0.58
4:A:230:VAL:HG22	4:A:231:SER:H	1.68	0.58
26:Y:112:ASP:H	26:Y:115:ARG:HB2	1.68	0.58
42:w:382:ASP:OD1	42:w:383:LEU:N	2.34	0.58
1:1:502:U:H4'	8:E:26:ARG:HB3	1.86	0.58
1:1:2186:U:C5	4:A:200:ARG:HD3	2.38	0.58
6:C:203:ARG:HB3	6:C:246:ARG:HH12	1.67	0.58
7:D:58:LYS:HA	7:D:93:THR:CG2	2.33	0.58
11:H:23:ARG:HH21	11:H:42:ASP:HA	1.69	0.58
11:H:84:LYS:HB3	11:H:186:PHE:HB3	1.84	0.58
17:P:95:LEU:HD23	17:P:148:LEU:HD21	1.84	0.58
20:S:13:ARG:O	20:S:22:PRO:HG2	2.04	0.58
40:o:8:ARG:NE	40:o:10:THR:HB	2.18	0.58
1:1:1071:U:H3	1:1:1087:G:H1	1.52	0.58
1:1:1110:U:H2'	1:1:1111:U:C6	2.38	0.58
1:1:1514:G:O2'	39:l:45:ARG:NH1	2.32	0.58
1:1:2541:U:H1'	1:1:2542:U:OP2	2.03	0.58
1:1:2843:U:H5''	1:1:2844:C:H5	1.69	0.58
1:1:2991:A:H5''	5:B:21:ARG:NH1	2.18	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:3:96:U:H2'	2:3:97:A:H8	1.68	0.58
1:1:591:G:N2	8:E:19:LYS:O	2.33	0.58
7:D:83:LEU:O	7:D:86:TYR:N	2.36	0.58
25:X:105:VAL:HG12	25:X:106:ASP:H	1.67	0.58
43:y:61:ARG:HH11	43:y:106:ASN:ND2	2.01	0.58
1:1:286:U:O2'	15:N:179:LYS:O	2.21	0.58
1:1:1678:G:O6	22:U:74:LYS:NZ	2.37	0.58
1:1:3086:A:H3'	1:1:3087:A:H8	1.69	0.58
3:4:82:U:O2'	3:4:83:C:OP1	2.20	0.58
6:C:142:VAL:O	6:C:145:ILE:HG12	2.04	0.58
10:G:144:GLU:OE1	36:i:36:ARG:NH1	2.35	0.58
1:1:216:G:OP1	26:Y:16:ARG:NH1	2.37	0.58
1:1:440:A:H8	1:1:440:A:OP2	1.85	0.58
1:1:1108:U:H2'	1:1:1109:U:C6	2.39	0.58
1:1:1229:G:H2'	1:1:1230:G:H8	1.69	0.58
10:G:54:GLU:HG2	10:G:57:ARG:HH21	1.69	0.58
26:Y:51:ARG:HG2	26:Y:52:ARG:H	1.69	0.58
1:1:1270:A:C6	1:1:1271:A:H1'	2.38	0.58
1:1:3255:U:H2'	1:1:3256:G:H8	1.68	0.58
3:4:130:C:H2'	3:4:131:A:H8	1.69	0.58
15:N:190:THR:HA	15:N:193:ARG:HE	1.68	0.58
25:X:67:ILE:HD12	25:X:83:VAL:HG12	1.86	0.58
1:1:498:A:OP1	33:f:86:ARG:NE	2.27	0.57
6:C:302:ALA:HA	18:Q:39:ARG:HH12	1.68	0.57
35:h:5:LYS:HD2	35:h:8:GLU:OE2	2.04	0.57
1:1:1915:A:H5''	19:R:84:THR:HG22	1.86	0.57
1:1:2171:G:H2'	1:1:2172:A:H8	1.68	0.57
16:O:119:VAL:HG11	20:S:167:ARG:HD2	1.86	0.57
1:1:1236:G:N1	1:1:1244:A:OP1	2.35	0.57
5:B:77:THR:HG21	5:B:328:ILE:HG22	1.87	0.57
38:k:31:LEU:HA	38:k:37:PRO:HA	1.86	0.57
43:y:107:VAL:HG13	43:y:118:HIS:HB3	1.85	0.57
1:1:113:C:OP1	15:N:147:ARG:NE	2.30	0.57
1:1:1503:A:C2	44:z:402:GLN:HB3	2.39	0.57
1:1:2341:A:H8	1:1:2341:A:OP2	1.87	0.57
3:4:78:G:H2'	3:4:79:A:C8	2.39	0.57
19:R:28:GLU:O	19:R:31:GLU:N	2.38	0.57
42:w:218:VAL:HG13	42:w:220:ILE:HG23	1.86	0.57
43:y:58:ILE:O	43:y:58:ILE:HG13	2.05	0.57
1:1:685:G:OP2	13:L:35:ARG:NH2	2.38	0.57
1:1:691:A:OP2	1:1:691:A:H8	1.88	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:710:A:H2'	1:1:711:A:C8	2.39	0.57
1:1:1816:A:H2'	1:1:1817:G:C8	2.39	0.57
2:3:6:C:O2'	7:D:72:ASP:OD2	2.10	0.57
6:C:150:LEU:HD21	6:C:172:VAL:HG11	1.86	0.57
16:O:28:LEU:HD11	16:O:88:VAL:HG13	1.85	0.57
18:Q:107:THR:O	18:Q:111:ARG:HG3	2.04	0.57
43:y:143:SER:HB2	43:y:165:THR:HA	1.85	0.57
4:A:44:ILE:HG22	4:A:87:PHE:HD1	1.69	0.57
5:B:139:GLN:HG3	5:B:141:GLY:H	1.69	0.57
6:C:62:ALA:HB3	6:C:90:PHE:CE2	2.39	0.57
7:D:148:ILE:HG12	7:D:159:VAL:HG11	1.86	0.57
7:D:267:ALA:HA	7:D:270:LYS:HD2	1.86	0.57
8:E:96:VAL:HG12	8:E:98:VAL:HG23	1.86	0.57
10:G:26:LEU:HD23	27:Z:123:GLN:HE22	1.68	0.57
42:w:255:ASP:HA	42:w:372:TYR:OH	2.04	0.57
1:1:885:U:H2'	1:1:886:C:H6	1.68	0.57
1:1:1095:U:H3	21:T:127:GLN:NE2	2.02	0.57
1:1:1188:U:OP1	1:1:1210:U:O2'	2.15	0.57
1:1:1203:A:N3	1:1:2855:U:O2'	2.34	0.57
1:1:1224:C:H2'	1:1:1225:A:H8	1.70	0.57
8:E:2:SER:HA	32:e:81:ASP:OD2	2.05	0.57
11:H:163:GLN:HB3	11:H:166:ARG:NH1	2.20	0.57
1:1:156:G:OP2	36:i:25:LYS:HB3	2.05	0.57
1:1:627:U:H2'	1:1:628:A:C8	2.40	0.57
1:1:1831:U:O2'	3:4:114:G:OP1	2.15	0.57
1:1:2206:G:H1	1:1:2237:C:H42	1.52	0.57
4:A:20:THR:HA	4:A:23:ARG:HH11	1.69	0.57
8:E:146:ILE:HD13	8:E:149:ILE:HD12	1.85	0.57
12:J:95:ASN:O	12:J:102:PHE:HA	2.04	0.57
25:X:86:VAL:HG21	25:X:95:ILE:HG12	1.86	0.57
29:b:47:LEU:HA	29:b:50:THR:HG22	1.87	0.57
1:1:1261:G:O2'	1:1:1278:A:N6	2.37	0.57
1:1:2991:A:C3'	5:B:21:ARG:HH12	2.17	0.57
6:C:122:THR:HG22	6:C:235:LEU:HB2	1.86	0.57
18:Q:178:ARG:NH1	28:a:50:PRO:HG2	2.20	0.57
20:S:45:LEU:HB3	20:S:51:VAL:HG21	1.85	0.57
42:w:315:LEU:HD23	42:w:370:MET:HB3	1.87	0.57
1:1:1405:U:OP2	32:e:59:SER:OG	2.16	0.57
1:1:1592:G:OP1	34:g:58:ARG:NH2	2.35	0.57
1:1:2259:A:H2'	1:1:2260:U:C6	2.40	0.57
2:3:44:C:O4'	7:D:152:ARG:NH1	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:i:94:ILE:HA	36:i:98:ARG:HH11	1.69	0.57
1:1:1235:U:H4'	1:1:1236:G:H5'	1.86	0.56
1:1:2439:A:H2'	1:1:2440:G:C8	2.39	0.56
1:1:2526:C:OP2	1:1:2526:C:H6	1.87	0.56
1:1:2573:G:H2'	1:1:2574:G:C8	2.39	0.56
1:1:3048:A:OP2	5:B:222:LYS:NZ	2.27	0.56
1:1:3329:U:H5''	5:B:308:MET:HE2	1.87	0.56
3:4:110:C:O2'	3:4:112:U:OP2	2.19	0.56
25:X:67:ILE:HD11	25:X:115:ARG:HH21	1.70	0.56
1:1:1114:U:H5''	28:a:22:ILE:HD12	1.87	0.56
1:1:2344:U:H2'	1:1:2345:A:H8	1.69	0.56
1:1:2374:C:N4	1:1:2941:A:O4'	2.38	0.56
1:1:2584:G:O2'	10:G:240:ASN:ND2	2.34	0.56
4:A:60:LYS:HB3	4:A:73:GLU:OE2	2.05	0.56
15:N:68:ARG:NH1	15:N:128:LYS:HE3	2.19	0.56
18:Q:64:VAL:HG12	18:Q:90:ASP:H	1.71	0.56
42:w:165:VAL:HG13	42:w:166:PRO:CD	2.28	0.56
1:1:865:U:H2'	1:1:866:A:H8	1.69	0.56
1:1:873:C:H4'	1:1:874:U:OP2	2.05	0.56
1:1:1107:C:P	29:b:25:LYS:HZ3	2.28	0.56
1:1:1229:G:H2'	1:1:1230:G:C8	2.39	0.56
1:1:1815:U:O2'	1:1:1816:A:OP2	2.21	0.56
1:1:2437:G:O2'	1:1:2438:A:H8	1.88	0.56
1:1:3002:C:O2'	5:B:180:GLU:OE2	2.18	0.56
1:1:3094:A:OP1	23:V:14:SER:OG	2.20	0.56
1:1:3174:A:C5	1:1:3279:A:H1'	2.40	0.56
1:1:3295:A:H5'	5:B:119:TYR:HE1	1.70	0.56
3:4:149:A:N3	10:G:55:TYR:OH	2.32	0.56
4:A:201:GLY:HA2	4:A:204:MET:HE3	1.86	0.56
14:M:23:ILE:O	14:M:30:GLY:N	2.30	0.56
15:N:4:TYR:CD1	15:N:46:ASP:HB3	2.40	0.56
15:N:68:ARG:HH12	15:N:128:LYS:HE3	1.69	0.56
20:S:12:ARG:O	20:S:12:ARG:HG3	2.05	0.56
26:Y:3:LYS:HD2	26:Y:8:VAL:HG13	1.87	0.56
43:y:143:SER:HB3	43:y:162:HIS:CE1	2.41	0.56
43:y:204:ALA:HB3	43:y:224:LEU:HD21	1.86	0.56
1:1:651:G:O2'	1:1:1435:A:OP1	2.22	0.56
1:1:1249:G:H2'	1:1:1250:G:C8	2.40	0.56
1:1:3319:U:O2'	1:1:3320:A:OP1	2.22	0.56
3:4:36:G:N2	3:4:37:A:N1	2.54	0.56
30:c:13:LYS:HB3	30:c:100:ILE:HG22	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:209:A:H4'	1:1:211:A:N7	2.20	0.56
1:1:1081:U:O2'	1:1:1082:U:OP2	2.22	0.56
1:1:1568:U:H4'	1:1:1569:U:OP2	2.05	0.56
1:1:2720:G:H8	1:1:2720:G:OP2	1.88	0.56
1:1:3116:G:OP1	1:1:3116:G:N2	2.36	0.56
1:1:3152:U:O2'	1:1:3153:U:H5'	2.06	0.56
5:B:345:ASN:OD1	5:B:346:THR:N	2.38	0.56
11:H:4:ILE:HD11	20:S:150:PHE:CD2	2.41	0.56
1:1:374:A:HO2'	1:1:376:G:H8	1.51	0.56
1:1:1508:C:OP1	17:P:127:ARG:NH2	2.39	0.56
12:J:28:ASP:O	12:J:32:ARG:NE	2.39	0.56
15:N:27:VAL:HB	15:N:122:ASN:HD21	1.71	0.56
15:N:99:ARG:NH2	15:N:118:SER:O	2.38	0.56
15:N:114:ARG:NH1	15:N:151:ILE:O	2.38	0.56
1:1:265:A:H5''	1:1:266:A:OP2	2.04	0.56
1:1:3243:A:H4'	5:B:95:THR:HG22	1.88	0.56
4:A:180:LEU:HD11	41:p:26:VAL:HG21	1.88	0.56
6:C:138:ARG:NH1	6:C:140:HIS:NE2	2.54	0.56
10:G:72:PRO:HG3	15:N:18:VAL:HA	1.88	0.56
15:N:5:LYS:HZ3	36:i:37:THR:HG22	1.70	0.56
15:N:37:HIS:CE1	15:N:63:ARG:HD2	2.41	0.56
23:V:93:LEU:HB3	24:W:20:LEU:HB3	1.86	0.56
28:a:130:VAL:HG11	28:a:145:VAL:HG11	1.86	0.56
3:4:82:U:H4'	3:4:87:G:H5''	1.87	0.56
6:C:62:ALA:HB3	6:C:90:PHE:HE2	1.69	0.56
9:F:110:ARG:HD3	18:Q:3:ILE:HG13	1.88	0.56
21:T:48:ILE:HG13	21:T:94:GLU:HG2	1.87	0.56
1:1:1108:U:H2'	1:1:1109:U:H6	1.70	0.56
1:1:1353:U:H2'	8:E:9:TRP:CE3	2.41	0.56
1:1:3168:A:H61	1:1:3282:U:H3	1.53	0.56
3:4:131:A:H2'	3:4:132:G:C8	2.41	0.56
6:C:263:GLY:HA3	6:C:268:ALA:O	2.06	0.56
7:D:213:ASP:OD1	7:D:214:ASP:N	2.39	0.56
11:H:12:VAL:N	11:H:51:GLN:O	2.39	0.56
15:N:68:ARG:HD3	15:N:125:SER:O	2.05	0.56
19:R:134:HIS:CE1	19:R:136:ARG:HB3	2.41	0.56
32:e:42:VAL:HG12	32:e:52:GLN:HE21	1.70	0.56
1:1:1639:C:N4	34:g:73:SER:HB2	2.21	0.56
1:1:2568:C:OP2	1:1:2568:C:H6	1.89	0.56
1:1:3283:U:H2'	1:1:3284:G:C8	2.40	0.56
2:3:87:G:H2'	2:3:88:G:C8	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:305:ILE:HD11	5:B:317:ILE:HG21	1.87	0.56
28:a:77:LYS:C	28:a:79:TRP:H	2.10	0.56
1:1:653:A:H5''	1:1:2361:A:H5'	1.87	0.55
1:1:1765:U:H5	19:R:46:LYS:HZ3	1.50	0.55
4:A:126:LEU:HD13	4:A:150:LEU:HD21	1.89	0.55
9:F:144:ILE:HG22	9:F:185:ILE:HG23	1.89	0.55
13:L:179:PHE:O	13:L:183:ARG:HG2	2.06	0.55
34:g:98:GLN:HG3	34:g:102:LYS:HE2	1.86	0.55
39:l:28:ARG:HA	39:l:33:ASN:ND2	2.21	0.55
1:1:563:U:H2'	1:1:564:G:C8	2.40	0.55
1:1:2297:U:O2	1:1:2920:U:H5'	2.06	0.55
1:1:3276:G:O2'	1:1:3277:U:OP2	2.23	0.55
5:B:74:GLU:OE1	5:B:283:TYR:OH	2.19	0.55
18:Q:64:VAL:HG22	18:Q:96:PHE:CE1	2.41	0.55
31:d:13:THR:HG23	31:d:72:ARG:HH11	1.72	0.55
1:1:1288:U:H2'	1:1:1289:G:H8	1.70	0.55
3:4:37:A:C2	35:h:86:ARG:NH1	2.74	0.55
20:S:155:ARG:HD2	20:S:172:TYR:HD1	1.71	0.55
22:U:39:ASP:OD1	22:U:40:HIS:ND1	2.37	0.55
33:f:14:LEU:HD11	33:f:31:LYS:HB2	1.88	0.55
35:h:101:THR:HG23	35:h:104:GLN:H	1.70	0.55
1:1:194:U:H2'	1:1:195:U:H6	1.70	0.55
1:1:671:U:H2'	1:1:672:A:H8	1.71	0.55
2:3:52:G:O2'	2:3:53:U:OP1	2.22	0.55
1:1:86:G:O2'	1:1:98:G:O6	2.23	0.55
1:1:155:G:H5''	1:1:156:G:C8	2.41	0.55
1:1:3157:U:H1'	1:1:3158:G:C8	2.41	0.55
6:C:58:HIS:NE2	6:C:98:ARG:HD3	2.22	0.55
33:f:67:MET:HE1	33:f:90:PRO:HD3	1.89	0.55
6:C:5:GLN:HE22	6:C:21:PRO:HG3	1.71	0.55
6:C:10:SER:OG	6:C:13:GLY:O	2.22	0.55
12:J:92:ARG:NH2	12:J:94:ARG:NH1	2.55	0.55
36:i:50:LEU:O	36:i:55:ARG:NH1	2.29	0.55
41:p:88:GLU:HA	41:p:91:GLU:HG2	1.89	0.55
5:B:385:LYS:HG3	5:B:386:ASP:H	1.72	0.55
8:E:52:VAL:HG21	8:E:65:ILE:HD13	1.89	0.55
11:H:77:ASN:HB3	11:H:151:VAL:HG21	1.89	0.55
11:H:105:GLU:HA	11:H:109:ALA:HB3	1.89	0.55
43:y:68:ARG:NH2	43:y:134:GLY:O	2.40	0.55
1:1:149:U:P	15:N:49:ARG:HH12	2.29	0.55
1:1:377:A:H1'	1:1:392:G:N2	2.22	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:551:A:O2'	1:1:552:G:O5'	2.24	0.55
1:1:1097:G:C8	21:T:128:LEU:HD13	2.41	0.55
9:F:110:ARG:NH2	9:F:206:LYS:HZ3	2.04	0.55
13:L:32:LYS:O	13:L:36:ARG:HG3	2.07	0.55
27:Z:46:ILE:HD11	27:Z:49:TYR:CE1	2.41	0.55
1:1:737:G:OP2	1:1:737:G:H8	1.90	0.55
1:1:781:G:OP1	18:Q:151:ARG:HD2	2.07	0.55
1:1:1723:A:OP2	19:R:103:ARG:NH2	2.40	0.55
1:1:3049:A:H4'	5:B:364:LYS:HD2	1.88	0.55
1:1:3163:A:N6	1:1:3288:G:H1	2.03	0.55
2:3:119:U:H3'	7:D:258:LYS:HZ2	1.71	0.55
8:E:102:ASN:OD1	8:E:105:TYR:N	2.33	0.55
12:J:47:GLN:HG2	12:J:67:VAL:HG12	1.87	0.55
14:M:65:LEU:HD12	20:S:172:TYR:HE2	1.72	0.55
44:z:378:ILE:O	44:z:382:ASP:HB2	2.07	0.55
1:1:194:U:H2'	1:1:195:U:C6	2.42	0.55
1:1:1419:A:H5''	6:C:193:LYS:HZ2	1.72	0.55
1:1:2876:C:O2'	42:w:234:HIS:ND1	2.23	0.55
3:4:95:G:OP1	37:j:76:ASN:ND2	2.29	0.55
7:D:106:ALA:HB2	7:D:166:ALA:HA	1.89	0.55
13:L:166:ALA:O	13:L:169:THR:N	2.38	0.55
41:p:42:CYS:HB3	41:p:60:CYS:HB3	1.89	0.55
1:1:676:G:OP2	18:Q:107:THR:HA	2.07	0.54
9:F:151:ARG:NH1	9:F:206:LYS:O	2.40	0.54
13:L:76:THR:HG22	13:L:101:ARG:HG3	1.89	0.54
17:P:126:ARG:NH1	17:P:138:LYS:HD2	2.21	0.54
43:y:222:PHE:HB2	43:y:224:LEU:HD13	1.89	0.54
1:1:661:G:O2'	28:a:8:THR:HG21	2.07	0.54
1:1:3165:A:H2'	1:1:3166:C:H6	1.71	0.54
42:w:228:LEU:HB3	42:w:240:TYR:CE1	2.42	0.54
42:w:272:GLN:CG	42:w:387:LEU:CD2	2.85	0.54
1:1:1245:A:N6	1:1:1272:C:O2'	2.36	0.54
1:1:1348:U:C4	18:Q:31:LYS:HE3	2.43	0.54
1:1:1449:A:H5''	1:1:1450:G:OP2	2.07	0.54
1:1:1612:A:H5''	38:k:51:LEU:HD22	1.88	0.54
1:1:2437:G:O2'	1:1:2438:A:OP2	2.20	0.54
7:D:52:VAL:HG21	7:D:65:ILE:HD12	1.87	0.54
1:1:676:G:H1'	1:1:787:G:H22	1.73	0.54
1:1:1097:G:H1'	1:1:1098:A:OP2	2.07	0.54
1:1:2799:A:H1'	28:a:42:ARG:NH1	2.23	0.54
18:Q:71:LEU:HD13	18:Q:99:THR:HG21	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:i:94:ILE:HA	36:i:98:ARG:NH1	2.22	0.54
1:1:297:G:H2'	36:i:41:ARG:HH12	1.73	0.54
1:1:514:G:N3	6:C:341:SER:OG	2.39	0.54
2:3:26:C:O2	2:3:57:G:N2	2.37	0.54
2:3:53:U:H4'	12:J:8:PRO:HB2	1.89	0.54
6:C:292:SER:OG	6:C:293:SER:N	2.39	0.54
9:F:112:ASN:ND2	9:F:209:ASN:OD1	2.39	0.54
10:G:91:PHE:CE2	10:G:185:ARG:NH1	2.74	0.54
13:L:76:THR:HG23	13:L:101:ARG:NH1	2.23	0.54
1:1:1103:A:H4'	1:1:1103:A:OP2	2.07	0.54
1:1:1222:G:O2'	1:1:1284:C:N4	2.41	0.54
1:1:1258:U:O2'	1:1:1260:A:N7	2.37	0.54
1:1:3164:C:O2'	1:1:3165:A:H8	1.91	0.54
28:a:75:LEU:HB3	28:a:118:ILE:HG23	1.89	0.54
38:k:5:ILE:HD11	38:k:14:LEU:HD12	1.89	0.54
1:1:785:G:H1	18:Q:90:ASP:HA	1.72	0.54
2:3:62:U:O4	2:3:63:A:N6	2.41	0.54
8:E:35:VAL:HB	8:E:90:LYS:HZ2	1.72	0.54
8:E:150:LYS:HE3	8:E:156:LYS:HD2	1.89	0.54
11:H:20:ILE:HD13	14:M:7:VAL:HG22	1.90	0.54
43:y:42:LEU:HD13	43:y:46:ILE:HD11	1.88	0.54
1:1:962:A:N1	1:1:2814:G:O2'	2.36	0.54
1:1:972:A:H2'	1:1:973:A:H8	1.73	0.54
5:B:332:ARG:HH11	5:B:333:LYS:HE2	1.73	0.54
7:D:41:LYS:HB2	21:T:68:THR:O	2.08	0.54
8:E:35:VAL:HB	8:E:90:LYS:HZ1	1.72	0.54
11:H:150:SER:HB3	11:H:153:ASP:HB2	1.89	0.54
12:J:15:GLU:HB3	12:J:130:VAL:HG13	1.89	0.54
1:1:73:C:N3	13:L:59:ARG:NH1	2.56	0.54
1:1:246:U:H2'	1:1:247:C:H6	1.73	0.54
1:1:807:A:H61	1:1:934:G:H22	1.55	0.54
1:1:1107:C:OP2	29:b:25:LYS:NZ	2.41	0.54
7:D:60:ILE:HD11	7:D:93:THR:HA	1.89	0.54
30:c:9:SER:OG	30:c:10:ILE:N	2.40	0.54
40:o:58:PHE:CE1	40:o:60:LYS:HB2	2.42	0.54
1:1:196:G:N2	1:1:198:A:H3'	2.22	0.54
1:1:394:G:N1	1:1:397:A:OP2	2.42	0.54
1:1:655:C:OP1	32:e:27:ARG:N	2.40	0.54
1:1:1795:U:OP1	4:A:191:LEU:HD21	2.07	0.54
1:1:2218:G:H2'	1:1:2219:A:C8	2.43	0.54
1:1:2526:C:O2	10:G:48:ARG:NH2	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:19:ARG:HB2	5:B:232:ARG:HH21	1.73	0.54
28:a:94:ALA:HB1	28:a:121:VAL:HG13	1.91	0.54
1:1:585:A:H4'	33:f:72:THR:HG22	1.90	0.53
1:1:2534:G:H22	1:1:2545:C:H42	1.55	0.53
1:1:3330:A:H4'	5:B:366:GLY:HA3	1.90	0.53
5:B:110:LEU:HD22	5:B:130:PHE:CE2	2.43	0.53
20:S:95:ARG:NH1	20:S:144:LEU:HD21	2.24	0.53
28:a:48:TYR:O	28:a:49:HIS:ND1	2.42	0.53
1:1:743:C:C2	18:Q:141:ARG:NH1	2.76	0.53
1:1:1269:U:H3	1:1:1271:A:H5''	1.73	0.53
1:1:2991:A:N3	17:P:69:ARG:NH2	2.56	0.53
2:3:19:C:H2'	2:3:20:A:H8	1.71	0.53
4:A:113:VAL:HG12	4:A:166:ILE:HD13	1.88	0.53
10:G:26:LEU:HD13	27:Z:53:VAL:HG11	1.90	0.53
41:p:30:GLU:HA	41:p:33:GLN:HG2	1.89	0.53
1:1:815:G:OP2	37:j:31:LYS:NZ	2.40	0.53
3:4:82:U:HO2'	3:4:83:C:P	2.31	0.53
6:C:283:THR:HG22	6:C:285:ASP:H	1.73	0.53
7:D:94:ASN:OD1	7:D:97:ALA:N	2.41	0.53
12:J:7:ASN:OD1	12:J:10:ARG:NH1	2.34	0.53
41:p:6:LYS:HE2	41:p:7:LYS:NZ	2.23	0.53
42:w:165:VAL:CG1	42:w:166:PRO:CD	2.86	0.53
1:1:73:C:H5'	36:i:15:LYS:HB3	1.90	0.53
4:A:116:VAL:HG13	4:A:126:LEU:HB2	1.88	0.53
10:G:152:LEU:HD23	10:G:178:ALA:HB3	1.90	0.53
13:L:153:ASP:OD2	28:a:101:VAL:HG11	2.08	0.53
25:X:105:VAL:HG11	25:X:126:LEU:HD13	1.90	0.53
40:o:61:LYS:NZ	42:w:382:ASP:H	2.05	0.53
1:1:498:A:P	33:f:86:ARG:HE	2.30	0.53
1:1:745:C:H5''	18:Q:145:ASN:ND2	2.24	0.53
1:1:1107:C:P	29:b:25:LYS:NZ	2.81	0.53
1:1:1595:U:OP2	34:g:36:LYS:NZ	2.38	0.53
1:1:1637:A:H4'	27:Z:15:ARG:HB3	1.91	0.53
1:1:1659:U:H2'	1:1:1660:C:C6	2.43	0.53
1:1:3147:G:O2'	5:B:104:THR:OG1	2.12	0.53
6:C:64:SER:HA	6:C:75:PRO:HA	1.91	0.53
23:V:113:ALA:HB2	43:y:146:ILE:HG21	1.90	0.53
40:o:77:CYS:O	40:o:78:LYS:HG2	2.08	0.53
42:w:324:ASP:N	42:w:337:ASP:O	2.36	0.53
1:1:25:U:H4'	1:1:26:A:N7	2.24	0.53
1:1:1635:G:N2	1:1:1638:A:OP2	2.35	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1724:U:H1'	1:1:1725:C:C6	2.43	0.53
7:D:129:TYR:CD1	7:D:177:GLU:HB3	2.44	0.53
10:G:75:ILE:HD11	15:N:22:LEU:HD11	1.89	0.53
12:J:90:GLN:HG2	12:J:170:ASP:HB2	1.90	0.53
27:Z:5:LEU:HD11	30:c:35:ARG:HD2	1.90	0.53
34:g:99:LYS:O	34:g:103:LYS:HD3	2.09	0.53
39:l:27:ILE:HG23	39:l:30:ARG:HH21	1.73	0.53
39:l:44:TRP:CZ2	39:l:45:ARG:HD3	2.42	0.53
42:w:323:VAL:HG11	42:w:363:CYS:SG	2.49	0.53
1:1:2767:U:O2'	40:o:30:ALA:O	2.26	0.53
3:4:46:G:O2'	3:4:61:A:N1	2.39	0.53
3:4:156:U:H5''	3:4:157:U:OP2	2.08	0.53
5:B:272:TYR:HE1	5:B:334:ARG:HH22	1.56	0.53
10:G:78:PHE:C	10:G:80:TYR:H	2.17	0.53
12:J:49:LYS:HB3	12:J:62:ASN:HA	1.90	0.53
16:O:3:VAL:O	16:O:4:GLU:HG3	2.09	0.53
20:S:24:LEU:O	21:T:148:PRO:HA	2.08	0.53
20:S:102:ALA:O	20:S:105:THR:OG1	2.25	0.53
37:j:54:LYS:O	37:j:58:THR:HG23	2.09	0.53
1:1:577:C:O2'	1:1:579:G:OP1	2.16	0.53
1:1:611:A:O2'	1:1:612:U:OP2	2.15	0.53
1:1:1687:U:OP2	22:U:42:LYS:HE3	2.09	0.53
1:1:2255:A:H5'	1:1:2261:G:N2	2.24	0.53
1:1:2927:C:H2'	1:1:2928:C:C6	2.44	0.53
10:G:36:ILE:HG22	10:G:37:GLY:N	2.21	0.53
30:c:27:TYR:HD2	30:c:28:LYS:HG3	1.72	0.53
37:j:27:PHE:HA	37:j:34:CYS:HA	1.91	0.53
1:1:95:A:C5	1:1:96:G:H1'	2.44	0.53
1:1:1350:A:H8	1:1:1351:U:H3'	1.74	0.53
1:1:3344:A:H2	1:1:3361:G:H21	1.54	0.53
7:D:187:THR:HG23	7:D:189:GLU:HG3	1.89	0.53
22:U:17:VAL:HB	22:U:63:VAL:HB	1.91	0.53
37:j:5:THR:HG22	37:j:6:PRO:HD3	1.90	0.53
43:y:99:GLU:OE2	43:y:121:ILE:HD11	2.08	0.53
44:z:380:ALA:HB2	44:z:383:ARG:NH1	2.23	0.53
1:1:600:G:O2'	1:1:602:A:N6	2.35	0.53
1:1:817:A:O2'	37:j:11:ARG:HG3	2.09	0.53
13:L:3:ILE:HG22	28:a:44:ASN:ND2	2.24	0.53
24:W:6:ASP:OD1	24:W:31:PHE:HA	2.09	0.53
1:1:549:U:H2'	1:1:550:A:H8	1.73	0.52
1:1:627:U:H2'	1:1:628:A:H8	1.72	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:839:C:H2'	1:1:840:C:H6	1.74	0.52
1:1:2841:G:H2'	1:1:2844:C:H42	1.73	0.52
3:4:63:G:OP2	3:4:90:U:H4'	2.09	0.52
14:M:48:GLY:HA3	14:M:53:VAL:CG1	2.40	0.52
19:R:23:TRP:CE3	19:R:51:VAL:HG22	2.44	0.52
26:Y:56:VAL:HG21	26:Y:104:LEU:HD13	1.91	0.52
41:p:36:ARG:NH1	41:p:48:LYS:HZ1	2.06	0.52
43:y:109:CYS:SG	43:y:116:LEU:HB2	2.49	0.52
1:1:523:A:O2'	20:S:69:PRO:HD2	2.08	0.52
1:1:945:C:OP1	32:e:36:LYS:NZ	2.42	0.52
1:1:1795:U:N3	41:p:50:GLY:O	2.42	0.52
1:1:2186:U:O2'	1:1:2313:A:N3	2.42	0.52
1:1:2307:G:O2'	1:1:2310:U:OP2	2.25	0.52
1:1:2779:A:O2'	13:L:180:ARG:NH2	2.39	0.52
1:1:3199:G:H2'	1:1:3200:G:H8	1.73	0.52
4:A:80:GLU:HG3	41:p:66:GLY:HA2	1.92	0.52
4:A:224:THR:HA	4:A:237:LEU:O	2.09	0.52
12:J:11:ASP:O	12:J:12:LEU:HB2	2.10	0.52
18:Q:64:VAL:HG11	18:Q:113:LYS:HD2	1.91	0.52
22:U:93:ILE:HA	22:U:106:ALA:O	2.08	0.52
27:Z:90:GLU:HA	27:Z:93:LYS:HG2	1.91	0.52
31:d:13:THR:CG2	31:d:72:ARG:HH11	2.22	0.52
1:1:1446:A:N6	1:1:2356:A:C8	2.77	0.52
6:C:180:LYS:HZ2	6:C:202:ARG:CB	2.22	0.52
25:X:105:VAL:HG12	25:X:106:ASP:N	2.25	0.52
25:X:105:VAL:HG11	25:X:126:LEU:HD22	1.91	0.52
27:Z:81:LEU:HD11	34:g:90:ILE:HD13	1.90	0.52
39:l:21:ARG:HH12	39:l:24:PRO:HG3	1.75	0.52
1:1:1621:A:H2'	1:1:1622:U:C6	2.44	0.52
1:1:1933:A:H4'	1:1:2124:G:H5'	1.91	0.52
1:1:3078:U:H4'	1:1:3079:U:OP2	2.08	0.52
1:1:3255:U:H2'	1:1:3256:G:C8	2.45	0.52
8:E:149:ILE:HG23	8:E:155:LEU:HD23	1.91	0.52
10:G:36:ILE:O	10:G:38:GLN:HG2	2.08	0.52
43:y:3:THR:HB	43:y:205:VAL:HG22	1.92	0.52
1:1:296:A:N3	1:1:299:G:O2'	2.38	0.52
1:1:439:C:H3'	1:1:440:A:H8	1.75	0.52
1:1:898:U:H2'	1:1:899:U:C6	2.44	0.52
1:1:1385:C:H41	6:C:202:ARG:NH2	2.07	0.52
1:1:2436:U:C5'	1:1:2436:U:C6	2.85	0.52
1:1:2997:G:H1'	1:1:3396:U:H5''	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:4:143:U:H4'	15:N:57:GLN:HB3	1.91	0.52
5:B:51:ALA:HB2	5:B:317:ILE:HD11	1.91	0.52
5:B:292:ALA:HB1	5:B:295:ALA:HB3	1.90	0.52
5:B:328:ILE:HD11	5:B:336:VAL:HG11	1.92	0.52
42:w:165:VAL:CG1	42:w:166:PRO:N	2.73	0.52
1:1:502:U:O2'	8:E:26:ARG:NH1	2.43	0.52
1:1:1307:G:H1'	1:1:1308:A:C8	2.45	0.52
1:1:3045:G:OP1	5:B:19:ARG:NH2	2.42	0.52
5:B:221:THR:HB	5:B:273:HIS:H	1.74	0.52
5:B:283:TYR:OH	5:B:325:LYS:HD2	2.10	0.52
13:L:123:ILE:HG22	35:h:118:ILE:HG12	1.90	0.52
14:M:20:VAL:HG13	14:M:66:THR:OG1	2.09	0.52
15:N:191:TRP:O	15:N:195:ASN:ND2	2.43	0.52
17:P:29:THR:HA	17:P:32:THR:HG22	1.91	0.52
18:Q:123:THR:OG1	18:Q:125:ASP:OD1	2.26	0.52
1:1:541:U:H3	1:1:550:A:H61	1.56	0.52
1:1:817:A:C8	1:1:920:A:N1	2.78	0.52
1:1:1389:G:H5''	32:e:101:SER:HB3	1.92	0.52
5:B:332:ARG:NH1	5:B:333:LYS:HE2	2.24	0.52
7:D:234:ASP:OD1	7:D:235:SER:N	2.43	0.52
1:1:914:A:H2	4:A:208:ASP:OD2	1.92	0.52
1:1:1285:G:H8	1:1:1285:G:OP2	1.91	0.52
16:O:98:ALA:HA	16:O:101:ARG:HH11	1.75	0.52
1:1:1603:A:H61	25:X:71:THR:HG21	1.74	0.52
1:1:2284:C:H1'	1:1:2971:A:N6	2.25	0.52
1:1:3351:U:O2'	1:1:3352:U:OP1	2.20	0.52
5:B:114:VAL:HG11	5:B:163:HIS:CD2	2.44	0.52
13:L:75:PHE:O	13:L:79:GLU:HB2	2.10	0.52
14:M:65:LEU:HD12	20:S:172:TYR:CE2	2.44	0.52
17:P:50:GLN:HB3	17:P:55:GLN:HB2	1.92	0.52
19:R:106:LEU:HD11	19:R:138:LEU:HD11	1.92	0.52
23:V:14:SER:HB3	23:V:83:LYS:HZ1	1.74	0.52
26:Y:40:ARG:HH12	26:Y:46:LYS:HZ2	1.56	0.52
42:w:291:LEU:HD13	42:w:335:LEU:HB2	1.91	0.52
1:1:939:U:O2'	1:1:2402:A:N1	2.32	0.52
1:1:1155:C:H2'	1:1:1156:C:H6	1.74	0.52
1:1:2674:A:H8	12:J:126:ASP:OD1	1.93	0.52
10:G:67:ILE:HG23	10:G:237:ILE:HB	1.91	0.52
11:H:86:TYR:CE2	11:H:151:VAL:HG22	2.45	0.52
15:N:15:GLN:HB3	36:i:52:PRO:HD2	1.92	0.52
23:V:32:ARG:HB2	23:V:64:LYS:HB2	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:Y:118:LEU:HD12	26:Y:121:ARG:HH11	1.75	0.52
1:1:291:C:OP1	15:N:68:ARG:HG3	2.09	0.51
1:1:1428:A:OP2	28:a:2:PRO:HA	2.10	0.51
1:1:1843:C:OP1	39:l:48:LYS:NZ	2.38	0.51
4:A:201:GLY:HA3	4:A:209:HIS:CD2	2.46	0.51
16:O:77:SER:OG	16:O:106:GLU:OE2	2.18	0.51
26:Y:126:LEU:HD12	26:Y:126:LEU:O	2.10	0.51
36:i:50:LEU:C	36:i:55:ARG:HH12	2.14	0.51
42:w:359:LEU:HG	42:w:362:ILE:HB	1.92	0.51
1:1:674:G:O2'	6:C:116:ASN:ND2	2.44	0.51
1:1:898:U:H2'	1:1:899:U:H6	1.75	0.51
1:1:1215:U:H2'	1:1:1216:C:O4'	2.10	0.51
1:1:1237:G:H8	1:1:1263:A:C8	2.28	0.51
1:1:2180:G:OP1	4:A:174:ARG:NH2	2.42	0.51
1:1:2841:G:H21	1:1:2847:A:H62	1.57	0.51
5:B:123:TYR:CZ	5:B:124:LYS:HG3	2.45	0.51
7:D:3:PHE:HD2	7:D:6:ASP:OD2	1.92	0.51
11:H:44:THR:O	11:H:55:VAL:HA	2.10	0.51
15:N:5:LYS:HZ1	36:i:37:THR:HG22	1.72	0.51
16:O:110:PRO:O	16:O:112:TYR:N	2.43	0.51
20:S:77:VAL:HG22	20:S:126:VAL:HG22	1.92	0.51
24:W:23:ARG:HG2	24:W:24:GLY:H	1.75	0.51
1:1:903:U:OP2	37:j:30:GLN:NE2	2.37	0.51
1:1:1109:U:H2'	1:1:1110:U:H6	1.75	0.51
1:1:1441:G:OP1	44:z:414:ARG:HD2	2.11	0.51
1:1:2259:A:H2'	1:1:2260:U:H6	1.75	0.51
1:1:2418:G:N3	1:1:2418:G:H2'	2.24	0.51
4:A:44:ILE:HG22	4:A:87:PHE:CD1	2.44	0.51
7:D:41:LYS:HG2	21:T:69:LYS:O	2.11	0.51
14:M:14:LEU:H	14:M:19:ARG:NH1	2.09	0.51
20:S:83:SER:N	20:S:86:GLY:O	2.43	0.51
38:k:17:ARG:NH2	38:k:19:ASP:OD2	2.39	0.51
1:1:149:U:OP2	15:N:49:ARG:NH2	2.41	0.51
1:1:671:U:H2'	1:1:672:A:C8	2.45	0.51
1:1:2677:G:H3'	1:1:2679:A:OP2	2.11	0.51
6:C:326:ARG:HG3	6:C:327:LEU:H	1.75	0.51
14:M:15:VAL:HG13	14:M:65:LEU:HD11	1.92	0.51
31:d:47:ASP:HB2	31:d:87:ASN:HD21	1.75	0.51
36:i:50:LEU:C	36:i:55:ARG:NH1	2.68	0.51
44:z:409:ILE:HA	44:z:412:GLN:HG2	1.93	0.51
1:1:39:A:H5''	28:a:35:ALA:HB2	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1055:A:N3	2:3:81:U:O2'	2.43	0.51
8:E:39:VAL:O	8:E:87:THR:OG1	2.21	0.51
9:F:144:ILE:HD12	9:F:189:ILE:HD12	1.91	0.51
10:G:156:ASP:OD2	10:G:182:GLY:HA2	2.11	0.51
12:J:59:ILE:HG21	12:J:65:ILE:HD12	1.92	0.51
12:J:133:ARG:HH12	12:J:154:THR:CA	2.23	0.51
12:J:163:PHE:CE2	12:J:169:ALA:HB3	2.45	0.51
17:P:19:GLY:HA3	17:P:22:LEU:HD11	1.93	0.51
17:P:23:ARG:NH1	17:P:125:GLN:OE1	2.43	0.51
18:Q:173:GLU:HA	28:a:51:GLY:O	2.10	0.51
25:X:131:ASP:HB3	25:X:134:ASP:OD2	2.11	0.51
1:1:366:A:O2'	44:z:415:ARG:NH1	2.43	0.51
1:1:991:G:H2'	1:1:992:A:C8	2.46	0.51
1:1:1947:G:H5''	1:1:1948:G:OP2	2.11	0.51
6:C:289:ILE:HG21	18:Q:32:LEU:HD11	1.92	0.51
7:D:111:GLN:HA	7:D:116:ASP:HB2	1.92	0.51
16:O:73:PHE:HB3	16:O:78:ARG:HG3	1.92	0.51
22:U:67:SER:OG	22:U:69:ALA:O	2.28	0.51
32:e:82:LEU:HD11	32:e:112:ALA:HB2	1.93	0.51
1:1:116:A:OP2	15:N:2:GLY:HA3	2.10	0.51
1:1:201:A:H2'	1:1:202:G:C8	2.38	0.51
1:1:800:G:H2'	1:1:801:A:N7	2.26	0.51
6:C:234:ASN:OD1	6:C:235:LEU:N	2.44	0.51
8:E:80:ASN:HB3	8:E:83:TYR:HD2	1.74	0.51
37:j:86:ALA:O	37:j:87:SER:OG	2.28	0.51
43:y:88:LEU:HD23	43:y:92:VAL:HG11	1.92	0.51
1:1:1145:G:OP1	32:e:44:ARG:HD3	2.10	0.51
1:1:1471:U:H2'	1:1:1472:U:C6	2.46	0.51
1:1:2561:A:O2'	1:1:2562:A:H8	1.94	0.51
7:D:280:GLU:O	7:D:284:ALA:N	2.39	0.51
19:R:72:GLU:O	19:R:74:ARG:NH1	2.43	0.51
23:V:7:GLN:HG2	43:y:57:ARG:HH22	1.76	0.51
1:1:2096:A:H2'	1:1:2097:U:C6	2.46	0.51
1:1:2244:A:O2'	4:A:223:SER:OG	2.28	0.51
1:1:2816:G:N2	1:1:2819:A:OP2	2.38	0.51
1:1:2861:U:H2'	1:1:2862:U:O4'	2.10	0.51
10:G:154:ALA:HB2	10:G:186:LEU:HD12	1.93	0.51
19:R:28:GLU:HG3	19:R:49:THR:HG23	1.92	0.51
21:T:79:MET:HB2	21:T:84:TYR:CE1	2.42	0.51
28:a:81:LEU:HD21	28:a:109:TYR:HE2	1.73	0.51
42:w:204:LYS:HD2	42:w:242:PHE:CE2	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:w:327:GLY:C	42:w:328:ILE:O	2.54	0.51
1:1:594:U:H2'	1:1:609:G:O6	2.10	0.51
1:1:619:A:OP1	17:P:167:ARG:HD2	2.11	0.51
1:1:1495:U:H2'	1:1:1842:A:C2	2.46	0.51
1:1:2389:C:O2'	1:1:3307:A:N1	2.38	0.51
11:H:57:VAL:HG23	11:H:68:LEU:HD12	1.91	0.51
42:w:323:VAL:HG12	42:w:338:ILE:HG12	1.93	0.51
44:z:379:THR:O	44:z:381:ALA:N	2.44	0.51
1:1:503:C:O2	8:E:23:LYS:HE3	2.10	0.50
20:S:66:GLU:OE2	20:S:73:LYS:HE3	2.11	0.50
25:X:50:ALA:HB2	35:h:77:PRO:HG2	1.93	0.50
29:b:45:HIS:HA	29:b:48:HIS:HB3	1.92	0.50
1:1:277:G:H5'	15:N:91:GLU:OE1	2.10	0.50
1:1:846:A:H2'	1:1:847:A:O4'	2.11	0.50
1:1:3228:C:H1'	1:1:3229:G:OP2	2.11	0.50
13:L:27:ASP:HB2	13:L:31:LYS:HG3	1.94	0.50
20:S:12:ARG:NH1	20:S:15:PRO:HG3	2.26	0.50
26:Y:50:ILE:HD12	26:Y:106:ILE:HD11	1.93	0.50
1:1:372:A:H2'	1:1:373:A:C8	2.46	0.50
1:1:505:G:H4'	6:C:313:LEU:HD21	1.92	0.50
1:1:848:A:N6	1:1:849:C:O2	2.44	0.50
1:1:3296:A:OP2	5:B:121:ASN:HB2	2.10	0.50
5:B:346:THR:O	5:B:348:ARG:N	2.43	0.50
7:D:239:ILE:O	7:D:243:ALA:N	2.43	0.50
14:M:37:GLU:HG2	14:M:38:ILE:H	1.76	0.50
31:d:70:ARG:HH12	31:d:102:LYS:NZ	2.01	0.50
42:w:165:VAL:HG12	42:w:166:PRO:N	2.25	0.50
1:1:916:G:H5'	1:1:917:A:OP1	2.11	0.50
1:1:1480:G:O4'	1:1:1483:G:N2	2.44	0.50
1:1:3050:U:O2'	24:W:16:GLY:O	2.17	0.50
9:F:156:ILE:O	9:F:159:GLN:HB2	2.12	0.50
21:T:17:ARG:NH1	21:T:45:ASN:OD1	2.43	0.50
28:a:75:LEU:HD23	28:a:78:LEU:HD13	1.92	0.50
40:o:29:LYS:HZ1	42:w:389:ILE:HD13	1.75	0.50
1:1:31:C:H5	15:N:188:ARG:HH22	1.60	0.50
1:1:517:G:H5''	9:F:67:ARG:NH2	2.26	0.50
1:1:2712:U:O2'	1:1:2743:A:O2'	2.04	0.50
1:1:2901:G:O2'	1:1:3024:A:N1	2.44	0.50
2:3:15:C:HO2'	7:D:8:LYS:HD3	1.75	0.50
2:3:45:A:H2'	2:3:46:A:C8	2.47	0.50
4:A:20:THR:HA	4:A:23:ARG:NH1	2.27	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:58:ARG:NE	5:B:283:TYR:OH	2.44	0.50
6:C:326:ARG:HG3	6:C:327:LEU:N	2.26	0.50
21:T:66:ASN:HB3	21:T:73:GLY:HA3	1.93	0.50
25:X:53:HIS:CE1	25:X:56:ARG:HG2	2.46	0.50
26:Y:40:ARG:NH1	26:Y:46:LYS:HZ3	2.09	0.50
27:Z:54:THR:HG23	27:Z:56:LYS:H	1.76	0.50
36:i:74:LYS:HD3	36:i:80:PHE:HD1	1.76	0.50
43:y:106:ASN:ND2	43:y:150:SER:HB2	2.27	0.50
1:1:578:A:H2'	6:C:334:PHE:CD2	2.47	0.50
1:1:964:G:H2'	1:1:965:A:C8	2.47	0.50
1:1:1103:A:N6	1:1:1363:A:O2'	2.44	0.50
1:1:1224:C:H2'	1:1:1225:A:C8	2.46	0.50
1:1:2225:U:H2'	1:1:2226:U:H6	1.77	0.50
1:1:3100:U:O2'	1:1:3101:G:OP2	2.27	0.50
1:1:3279:A:H5'	1:1:3280:U:OP2	2.12	0.50
2:3:86:U:O2'	9:F:218:ARG:NH1	2.44	0.50
5:B:288:GLY:N	5:B:320:ASP:OD1	2.45	0.50
6:C:35:VAL:HG21	6:C:244:LEU:HD21	1.94	0.50
11:H:31:ARG:NE	11:H:83:THR:O	2.30	0.50
23:V:59:MET:HE1	23:V:75:PRO:HG3	1.94	0.50
30:c:81:VAL:HG23	30:c:83:LYS:HG2	1.94	0.50
1:1:887:G:H2'	1:1:888:A:C8	2.46	0.50
1:1:1468:A:N1	1:1:1880:U:O2'	2.39	0.50
1:1:2207:A:O2'	1:1:2208:A:H5'	2.11	0.50
6:C:138:ARG:HH11	6:C:140:HIS:CD2	2.30	0.50
9:F:110:ARG:NH1	18:Q:3:ILE:HG12	2.26	0.50
27:Z:25:ILE:HG23	27:Z:41:ALA:HB1	1.93	0.50
1:1:139:G:H2'	1:1:140:C:C6	2.47	0.50
1:1:354:U:H2'	1:1:355:A:H8	1.77	0.50
1:1:900:G:H1'	1:1:1589:A:N6	2.26	0.50
1:1:1450:G:C6	1:1:2355:G:N2	2.80	0.50
5:B:212:ASN:OD1	5:B:354:VAL:HG22	2.12	0.50
9:F:158:LYS:HG2	9:F:159:GLN:H	1.77	0.50
13:L:184:GLU:O	13:L:188:ARG:N	2.32	0.50
24:W:35:LYS:HE2	24:W:51:TRP:CZ2	2.47	0.50
27:Z:22:LYS:HE3	27:Z:134:LEU:HB2	1.94	0.50
42:w:312:VAL:O	42:w:315:LEU:HD13	2.12	0.50
1:1:386:A:C5	1:1:387:A:H1'	2.47	0.50
1:1:618:C:H5''	17:P:169:THR:HG22	1.94	0.50
6:C:180:LYS:HZ2	6:C:202:ARG:HB3	1.77	0.50
7:D:41:LYS:HE2	21:T:93:VAL:HG11	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:D:65:ILE:HG23	7:D:72:ASP:HB3	1.93	0.50
10:G:28:HIS:CE1	27:Z:128:GLN:HG3	2.47	0.50
10:G:78:PHE:HD1	10:G:179:ILE:HD13	1.75	0.50
13:L:56:PRO:HG3	13:L:74:GLY:O	2.12	0.50
37:j:25:ARG:HG2	37:j:25:ARG:O	2.12	0.50
43:y:101:LEU:HD12	43:y:101:LEU:O	2.12	0.50
1:1:406:G:N3	3:4:16:G:C2	2.80	0.49
1:1:520:U:O4	6:C:349:THR:OG1	2.30	0.49
1:1:578:A:H2'	6:C:334:PHE:HD2	1.77	0.49
1:1:813:G:O2'	37:j:45:ARG:NH2	2.45	0.49
1:1:2585:G:C6	25:X:24:LEU:HD13	2.47	0.49
5:B:346:THR:C	5:B:348:ARG:H	2.20	0.49
7:D:164:LYS:HE3	7:D:168:ASP:OD2	2.12	0.49
20:S:12:ARG:HH12	20:S:15:PRO:CG	2.25	0.49
41:p:36:ARG:HH11	41:p:48:LYS:CE	2.25	0.49
1:1:660:A:H5'	6:C:92:ASN:ND2	2.27	0.49
1:1:1213:G:OP1	20:S:137:ARG:NH1	2.45	0.49
1:1:1381:A:OP1	6:C:197:ARG:NE	2.41	0.49
1:1:1548:C:OP2	1:1:1549:U:C2	2.65	0.49
1:1:1603:A:H61	25:X:71:THR:CG2	2.24	0.49
1:1:2765:C:OP1	28:a:55:LYS:NZ	2.36	0.49
1:1:3043:C:P	23:V:48:ARG:HH21	2.35	0.49
1:1:3334:U:H4'	1:1:3335:A:H5'	1.93	0.49
4:A:19:HIS:ND1	4:A:190:ARG:O	2.34	0.49
6:C:269:SER:O	6:C:270:SER:OG	2.25	0.49
11:H:109:ALA:HB1	11:H:111:PHE:CD2	2.43	0.49
17:P:118:GLN:NE2	17:P:147:GLU:OE2	2.46	0.49
20:S:2:ALA:HB3	20:S:32:SER:HB3	1.94	0.49
28:a:104:THR:HG21	28:a:112:ILE:HD11	1.95	0.49
34:g:98:GLN:O	34:g:102:LYS:HG2	2.12	0.49
41:p:49:ARG:HH11	41:p:51:ALA:C	2.19	0.49
1:1:437:G:C8	1:1:437:G:OP2	2.65	0.49
1:1:1485:G:H21	34:g:4:ARG:CZ	2.25	0.49
1:1:3095:U:OP1	23:V:86:ARG:HD3	2.12	0.49
1:1:3221:C:N4	1:1:3264:G:H1	2.09	0.49
14:M:55:ARG:HD3	20:S:70:THR:HB	1.94	0.49
19:R:23:TRP:HB2	19:R:53:LYS:HG3	1.94	0.49
1:1:1841:A:H1'	1:1:1848:G:O4'	2.13	0.49
1:1:2285:C:OP2	1:1:2286:U:O2'	2.17	0.49
1:1:3275:U:H5'	33:f:68:TRP:CZ2	2.47	0.49
4:A:133:TYR:CD2	4:A:168:VAL:HG12	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:F:64:GLN:NE2	9:F:68:ASP:OD1	2.43	0.49
11:H:103:ILE:HG13	11:H:136:PHE:HZ	1.77	0.49
21:T:75:ILE:HA	21:T:87:LYS:O	2.12	0.49
34:g:13:TYR:O	34:g:18:ASN:ND2	2.26	0.49
39:l:9:ILE:HG22	39:l:13:MET:HE3	1.94	0.49
40:o:14:GLY:C	40:o:16:THR:H	2.20	0.49
1:1:112:U:O2'	1:1:113:C:OP2	2.28	0.49
1:1:951:A:OP1	29:b:18:ARG:NH2	2.39	0.49
1:1:964:G:H2'	1:1:965:A:H8	1.78	0.49
1:1:2660:G:O2'	1:1:2744:U:O2	2.29	0.49
1:1:2840:C:H42	1:1:2848:G:H1	1.59	0.49
1:1:3355:U:O2'	1:1:3357:U:OP2	2.29	0.49
4:A:62:VAL:HG21	4:A:71:LEU:HD23	1.94	0.49
7:D:99:TYR:HE1	7:D:164:LYS:HG3	1.77	0.49
13:L:75:PHE:O	13:L:76:THR:OG1	2.26	0.49
23:V:80:ARG:HD3	23:V:117:PRO:HG2	1.93	0.49
23:V:93:LEU:HD22	24:W:20:LEU:HD22	1.94	0.49
23:V:135:VAL:HG11	24:W:26:SER:HB3	1.93	0.49
42:w:286:MET:HE2	42:w:333:ARG:CZ	2.42	0.49
1:1:1440:G:P	44:z:419:ARG:HH12	2.35	0.49
1:1:1765:U:H5	19:R:46:LYS:NZ	2.10	0.49
1:1:1792:C:OP2	41:p:34:HIS:HE1	1.96	0.49
1:1:1807:G:H5''	27:Z:135:ARG:HH22	1.78	0.49
1:1:3350:C:N3	1:1:3356:G:N2	2.60	0.49
2:3:15:C:O2'	7:D:8:LYS:HD3	2.13	0.49
6:C:8:VAL:HG21	6:C:18:ASN:ND2	2.27	0.49
8:E:7:PRO:HG2	8:E:10:TYR:CE1	2.47	0.49
9:F:220:PHE:O	9:F:229:PHE:HE2	1.96	0.49
15:N:34:ASN:O	15:N:37:HIS:HD2	1.96	0.49
33:f:59:VAL:HG23	33:f:60:ARG:H	1.76	0.49
37:j:63:ARG:O	37:j:68:LYS:NZ	2.39	0.49
1:1:216:G:O2'	26:Y:19:TYR:OH	2.25	0.49
1:1:1218:U:H2'	1:1:1219:C:H5'	1.94	0.49
1:1:1494:U:P	39:l:42:ARG:HH22	2.31	0.49
1:1:3313:U:H4'	5:B:173:GLN:HG3	1.95	0.49
2:3:92:A:C5	2:3:93:C:H1'	2.48	0.49
6:C:11:LEU:HD21	6:C:156:LEU:HB2	1.94	0.49
13:L:64:LYS:O	13:L:67:ARG:NH1	2.45	0.49
21:T:64:VAL:HA	21:T:73:GLY:O	2.12	0.49
1:1:1135:A:P	29:b:5:LYS:NZ	2.83	0.49
1:1:3268:A:H1'	8:E:75:PRO:HG3	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:3275:U:H5'	33:f:68:TRP:HZ2	1.76	0.49
3:4:14:C:H5''	17:P:123:PRO:HD3	1.95	0.49
16:O:179:ALA:O	16:O:183:ALA:N	2.45	0.49
25:X:77:GLU:HG2	25:X:133:LEU:HD12	1.94	0.49
42:w:272:GLN:CB	42:w:387:LEU:CD2	2.91	0.49
1:1:255:A:H2'	1:1:256:G:C8	2.48	0.49
1:1:1237:G:H5'	1:1:1238:C:OP2	2.12	0.49
1:1:1886:A:H61	1:1:2391:G:P	2.36	0.49
1:1:2150:G:O2'	1:1:2189:U:OP1	2.31	0.49
2:3:7:G:OP2	7:D:28:THR:OG1	2.17	0.49
2:3:33:U:C2	7:D:207:TYR:CD1	3.00	0.49
5:B:4:ARG:O	5:B:5:LYS:HB3	2.12	0.49
5:B:19:ARG:O	5:B:273:HIS:HE1	1.95	0.49
6:C:69:ARG:NH2	44:z:424:THR:O	2.46	0.49
8:E:72:ASN:HB3	8:E:160:SER:HA	1.95	0.49
11:H:83:THR:OG1	11:H:84:LYS:N	2.41	0.49
15:N:136:ASP:OD2	15:N:139:HIS:HB2	2.13	0.49
21:T:17:ARG:HB3	21:T:22:HIS:CE1	2.48	0.49
43:y:82:GLN:HG3	43:y:86:ASN:HD21	1.78	0.49
1:1:157:A:C8	36:i:26:ILE:HD13	2.47	0.49
1:1:2097:U:H2'	1:1:2098:C:C6	2.48	0.49
1:1:2393:G:H4'	5:B:252:ILE:HG13	1.94	0.49
1:1:2436:U:C6	1:1:2436:U:C4'	2.95	0.49
1:1:2544:U:H2'	1:1:2545:C:C6	2.48	0.49
1:1:2756:C:O4'	21:T:49:GLN:HG2	2.13	0.49
1:1:3084:C:OP1	24:W:38:SER:OG	2.22	0.49
5:B:59:ASP:OD1	5:B:357:LYS:NZ	2.42	0.49
9:F:134:VAL:O	9:F:229:PHE:HB2	2.13	0.49
10:G:64:ILE:O	10:G:68:ARG:HG2	2.12	0.49
10:G:104:GLU:O	10:G:108:ARG:HG2	2.13	0.49
12:J:29:ARG:NH1	12:J:123:PHE:CD1	2.81	0.49
16:O:10:ASP:OD1	16:O:37:ARG:HD3	2.13	0.49
18:Q:173:GLU:OE2	28:a:52:TYR:HD1	1.96	0.49
31:d:10:ARG:NH1	31:d:44:MET:CE	2.75	0.49
42:w:260:PRO:HB2	42:w:263:LEU:HD13	1.93	0.49
1:1:341:G:N7	6:C:195:ARG:NH2	2.58	0.48
1:1:943:U:C4	28:a:12:ARG:NH1	2.81	0.48
1:1:1564:U:H2'	1:1:1565:G:H8	1.78	0.48
4:A:52:SER:HB3	4:A:191:LEU:HD23	1.95	0.48
12:J:139:THR:HG22	12:J:147:THR:HA	1.95	0.48
13:L:35:ARG:HG2	13:L:39:ARG:NH1	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:L:79:GLU:OE2	13:L:103:ASN:ND2	2.40	0.48
30:c:49:PRO:HG2	30:c:52:ARG:HB2	1.94	0.48
42:w:256:LEU:HD11	42:w:273:PHE:HD1	1.77	0.48
1:1:2508:U:H2'	1:1:2509:U:O4'	2.13	0.48
1:1:3386:G:H5'	31:d:10:ARG:NH2	2.27	0.48
2:3:36:C:H2'	2:3:37:G:H8	1.79	0.48
15:N:38:ARG:HH11	15:N:38:ARG:HG3	1.77	0.48
21:T:53:PRO:HD3	21:T:91:LEU:HD22	1.94	0.48
27:Z:5:LEU:HD21	27:Z:82:PRO:HB3	1.94	0.48
30:c:76:GLU:OE1	30:c:76:GLU:N	2.46	0.48
40:o:71:ARG:NH2	40:o:80:ARG:NH1	2.61	0.48
1:1:246:U:H2'	1:1:247:C:C6	2.48	0.48
1:1:762:U:C4	1:1:763:G:H1'	2.48	0.48
1:1:837:A:O2'	41:p:10:ILE:HD13	2.13	0.48
1:1:1062:A:H5''	1:1:1063:G:H5'	1.95	0.48
1:1:1334:U:OP1	9:F:206:LYS:NZ	2.46	0.48
1:1:2577:C:H2'	1:1:2578:U:O4'	2.12	0.48
1:1:3045:G:H2'	1:1:3046:A:O4'	2.12	0.48
1:1:3242:G:H8	5:B:154:TYR:CE2	2.31	0.48
5:B:312:VAL:HG12	5:B:313:HIS:ND1	2.28	0.48
7:D:86:TYR:OH	7:D:250:ASP:O	2.22	0.48
12:J:132:ASN:HA	12:J:154:THR:HG21	1.96	0.48
20:S:52:LYS:N	20:S:55:SER:OG	2.44	0.48
36:i:61:ILE:HD11	36:i:87:VAL:HG13	1.95	0.48
37:j:17:THR:O	37:j:25:ARG:HA	2.13	0.48
42:w:228:LEU:HB3	42:w:240:TYR:CD1	2.47	0.48
1:1:563:U:H2'	1:1:564:G:H8	1.77	0.48
1:1:676:G:N2	1:1:787:G:C6	2.82	0.48
1:1:2139:A:HO2'	44:z:427:ARG:NH2	2.11	0.48
1:1:2171:G:H2'	1:1:2172:A:C8	2.48	0.48
4:A:3:ARG:HG2	4:A:4:VAL:N	2.29	0.48
5:B:49:TYR:OH	5:B:177:HIS:ND1	2.44	0.48
7:D:52:VAL:HG22	7:D:147:ASP:HB3	1.94	0.48
26:Y:51:ARG:HG2	26:Y:52:ARG:N	2.28	0.48
37:j:21:ARG:NH2	37:j:41:ALA:O	2.34	0.48
1:1:117:U:O2	1:1:119:U:H5''	2.13	0.48
1:1:120:G:C8	10:G:129:PRO:HD2	2.48	0.48
1:1:357:A:O4'	6:C:81:GLY:HA3	2.14	0.48
1:1:901:G:H2'	1:1:902:G:C8	2.47	0.48
1:1:1178:G:OP2	1:1:1179:A:OP2	2.31	0.48
1:1:1764:U:H3'	1:1:1765:U:H5''	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2941:A:H8	1:1:2941:A:OP2	1.94	0.48
5:B:70:ARG:HH22	43:y:55:GLY:N	2.11	0.48
11:H:67:ALA:HA	11:H:70:THR:HG22	1.95	0.48
16:O:89:SER:O	16:O:95:GLY:HA3	2.13	0.48
23:V:13:ILE:HD11	23:V:54:LEU:HB3	1.95	0.48
1:1:112:U:O2'	1:1:113:C:P	2.72	0.48
1:1:2274:U:H2'	1:1:2275:A:H8	1.78	0.48
1:1:2673:A:H4'	12:J:104:PHE:HA	1.95	0.48
1:1:2946:A:H5''	1:1:2947:G:H5'	1.95	0.48
1:1:2954:U:H4'	1:1:2955:U:H5'	1.94	0.48
6:C:141:ARG:NH1	6:C:180:LYS:HD3	2.28	0.48
6:C:321:LYS:O	6:C:325:LEU:HG	2.13	0.48
17:P:60:PHE:HE2	17:P:82:ARG:HD2	1.78	0.48
18:Q:126:GLN:O	18:Q:130:ARG:HG3	2.13	0.48
1:1:80:G:P	15:N:193:ARG:NH1	2.87	0.48
1:1:608:A:O2'	6:C:326:ARG:NH1	2.46	0.48
1:1:1472:U:C2	1:1:1473:G:C8	3.02	0.48
1:1:2795:U:OP1	40:o:62:ALA:N	2.30	0.48
6:C:170:LYS:HE2	6:C:175:HIS:ND1	2.29	0.48
15:N:103:GLU:OE2	15:N:118:SER:OG	2.28	0.48
18:Q:177:GLY:O	18:Q:186:VAL:N	2.33	0.48
24:W:8:PHE:CD1	24:W:46:PRO:HG3	2.48	0.48
27:Z:15:ARG:NH2	34:g:83:ASN:OD1	2.47	0.48
1:1:439:C:H3'	1:1:440:A:C8	2.47	0.48
1:1:712:G:OP1	13:L:174:ARG:NH1	2.46	0.48
1:1:1152:G:N3	1:1:1152:G:H2'	2.28	0.48
3:4:37:A:OP2	35:h:86:ARG:HD2	2.13	0.48
6:C:65:TRP:NE1	6:C:76:ARG:HB2	2.28	0.48
10:G:48:ARG:NH1	10:G:49:TYR:CE1	2.82	0.48
16:O:73:PHE:CG	16:O:78:ARG:HG3	2.49	0.48
23:V:122:CYS:SG	23:V:129:VAL:HG11	2.54	0.48
27:Z:88:ASP:O	27:Z:121:ARG:NH2	2.47	0.48
1:1:706:A:C6	1:1:714:G:C2	3.02	0.48
1:1:1621:A:H2'	1:1:1622:U:H6	1.78	0.48
1:1:1864:A:H2'	1:1:1865:A:C8	2.49	0.48
1:1:2382:G:N7	16:O:91:LYS:NZ	2.45	0.48
1:1:2941:A:OP1	1:1:2943:G:O2'	2.30	0.48
1:1:3120:C:O2'	1:1:3121:U:H2'	2.14	0.48
2:3:7:G:OP1	7:D:33:ARG:HD2	2.13	0.48
3:4:58:G:H5''	3:4:98:U:O2	2.14	0.48
37:j:50:GLY:O	37:j:53:ALA:N	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:118:U:O2	1:1:121:A:H5'	2.14	0.48
1:1:295:A:H2	1:1:300:G:H4'	1.78	0.48
1:1:346:C:C2	3:4:25:G:H4'	2.49	0.48
1:1:396:A:C6	1:1:399:A:C6	3.02	0.48
1:1:2112:U:C4'	1:1:2113:A:OP2	2.62	0.48
1:1:2178:A:H5''	4:A:132:ASN:ND2	2.28	0.48
1:1:2227:C:HO2'	1:1:2228:A:P	2.36	0.48
1:1:2631:U:OP1	1:1:2757:U:O2'	2.25	0.48
1:1:3187:A:H5'	11:H:22:SER:HA	1.95	0.48
6:C:92:ASN:HD22	6:C:100:PHE:HB2	1.78	0.48
13:L:166:ALA:HB3	28:a:135:GLU:OE1	2.13	0.48
15:N:153:ASP:CG	15:N:154:PRO:HD2	2.38	0.48
22:U:31:ALA:HA	22:U:58:GLU:OE2	2.12	0.48
1:1:386:A:N6	1:1:387:A:N3	2.62	0.47
1:1:496:C:HO2'	1:1:622:A:H2	1.61	0.47
1:1:612:U:H4'	8:E:21:THR:HG21	1.96	0.47
1:1:1339:C:P	32:e:61:LYS:HZ3	2.36	0.47
1:1:1704:A:O2'	1:1:1705:U:H5''	2.13	0.47
1:1:1813:A:H2'	1:1:1814:A:N7	2.29	0.47
1:1:1864:A:OP1	19:R:88:ARG:NH1	2.47	0.47
1:1:2883:U:H2'	1:1:2884:C:C6	2.49	0.47
1:1:3044:G:O3'	5:B:13:HIS:HB2	2.14	0.47
6:C:269:SER:OG	6:C:271:LYS:O	2.22	0.47
7:D:219:PHE:CE2	7:D:227:LEU:HD11	2.49	0.47
15:N:13:LYS:HB3	15:N:16:SER:HB3	1.96	0.47
20:S:96:ASP:CG	20:S:97:VAL:H	2.18	0.47
21:T:14:MET:HE1	21:T:55:LYS:O	2.14	0.47
27:Z:73:LYS:HG3	27:Z:74:VAL:O	2.13	0.47
30:c:58:TYR:CE1	34:g:97:GLU:HG2	2.48	0.47
38:k:32:ASN:HB3	38:k:38:PHE:CE2	2.48	0.47
43:y:82:GLN:HE21	43:y:86:ASN:HD21	1.62	0.47
43:y:118:HIS:CE1	43:y:120:ASP:HB2	2.49	0.47
1:1:161:G:O6	1:1:260:C:N4	2.43	0.47
1:1:182:U:H3	1:1:234:G:H1	1.62	0.47
1:1:531:G:H2'	1:1:532:A:C8	2.49	0.47
1:1:710:A:H2'	1:1:711:A:H8	1.78	0.47
1:1:1186:G:H2'	1:1:1187:C:C6	2.46	0.47
1:1:3162:C:H2'	1:1:3163:A:C8	2.35	0.47
3:4:71:A:O2'	26:Y:51:ARG:NH2	2.46	0.47
5:B:14:LEU:HD22	5:B:262:TRP:CZ3	2.49	0.47
5:B:95:THR:OG1	5:B:98:GLY:O	2.31	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:E:82:ARG:HD2	33:f:104:PRO:HB3	1.95	0.47
14:M:65:LEU:HB2	20:S:172:TYR:HE2	1.79	0.47
15:N:4:TYR:HD1	15:N:46:ASP:HB3	1.79	0.47
15:N:13:LYS:O	15:N:19:LEU:HD22	2.14	0.47
20:S:13:ARG:CD	20:S:51:VAL:HG12	2.43	0.47
27:Z:124:ALA:O	27:Z:126:LYS:N	2.45	0.47
31:d:19:ARG:HD3	31:d:35:GLU:CG	2.44	0.47
31:d:70:ARG:NH2	31:d:102:LYS:NZ	2.61	0.47
1:1:647:A:N6	1:1:2371:G:O2'	2.45	0.47
1:1:1477:A:OP1	1:1:3075:G:O2'	2.33	0.47
42:w:270:ILE:HG12	42:w:271:SER:H	1.78	0.47
1:1:637:C:H4'	1:1:638:C:OP1	2.14	0.47
1:1:758:C:P	40:o:15:LYS:NZ	2.85	0.47
1:1:1313:G:O2'	1:1:1318:A:N1	2.48	0.47
1:1:1503:A:N1	44:z:402:GLN:NE2	2.62	0.47
1:1:1721:U:OP2	19:R:103:ARG:HD3	2.14	0.47
1:1:1821:U:O2	34:g:67:LYS:HB2	2.14	0.47
1:1:2440:G:N2	1:1:2507:C:N3	2.59	0.47
1:1:2768:U:H2'	1:1:2769:A:C8	2.50	0.47
1:1:3170:A:H61	1:1:3280:U:H3	1.61	0.47
6:C:180:LYS:NZ	6:C:202:ARG:CB	2.77	0.47
16:O:46:GLU:HG3	16:O:49:ARG:H	1.79	0.47
16:O:77:SER:HB2	16:O:104:VAL:HG12	1.97	0.47
27:Z:26:VAL:HG23	27:Z:27:LYS:H	1.79	0.47
27:Z:46:ILE:HA	27:Z:70:PRO:HA	1.96	0.47
30:c:51:LEU:HD11	34:g:90:ILE:HG22	1.97	0.47
1:1:153:U:H2'	1:1:154:U:H5''	1.96	0.47
1:1:824:C:C2	1:1:902:G:N2	2.82	0.47
1:1:825:U:O2	1:1:901:G:C2	2.66	0.47
1:1:1125:U:H2'	1:1:1126:G:H8	1.79	0.47
1:1:1261:G:N2	1:1:1261:G:OP2	2.47	0.47
2:3:24:A:H4'	2:3:120:C:H4'	1.96	0.47
4:A:33:ASP:O	4:A:37:ARG:HG2	2.14	0.47
5:B:256:HIS:HA	5:B:257:PRO:C	2.40	0.47
12:J:29:ARG:NH1	12:J:123:PHE:CE1	2.82	0.47
20:S:57:GLU:OE2	21:T:139:ARG:NH1	2.47	0.47
27:Z:14:VAL:HG22	34:g:86:LYS:HG3	1.96	0.47
27:Z:64:LYS:HD3	27:Z:67:LYS:HZ2	1.79	0.47
36:i:62:ARG:NH1	36:i:98:ARG:CZ	2.78	0.47
1:1:117:U:O2'	1:1:119:U:OP2	2.26	0.47
1:1:903:U:H2'	1:1:904:A:C8	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1060:U:H2'	1:1:1061:A:C8	2.49	0.47
1:1:1470:U:H2'	1:1:1471:U:H6	1.80	0.47
1:1:1646:G:O2'	1:1:1647:A:OP2	2.28	0.47
1:1:2436:U:C6	1:1:2436:U:C3'	2.97	0.47
1:1:3096:C:H2'	1:1:3097:C:C6	2.50	0.47
6:C:3:ARG:NH1	6:C:24:ALA:HA	2.29	0.47
7:D:119:TYR:OH	7:D:139:PRO:O	2.23	0.47
8:E:54:TYR:CE1	8:E:63:LEU:HD22	2.49	0.47
9:F:24:GLU:HB2	9:F:28:ALA:HB3	1.96	0.47
9:F:163:LEU:O	9:F:165:ASP:N	2.48	0.47
9:F:163:LEU:O	9:F:168:ILE:HD12	2.15	0.47
9:F:173:LEU:HD23	9:F:178:ILE:HG21	1.95	0.47
13:L:119:TYR:HD1	13:L:145:PHE:CZ	2.32	0.47
23:V:87:ARG:NH2	23:V:137:VAL:HG21	2.29	0.47
42:w:229:ILE:HG13	42:w:239:THR:HG23	1.97	0.47
42:w:277:SER:OG	42:w:278:LYS:N	2.47	0.47
1:1:374:A:O2'	1:1:376:G:H8	1.97	0.47
1:1:717:C:OP1	1:1:751:A:O2'	2.28	0.47
1:1:991:G:H2'	1:1:992:A:H8	1.78	0.47
1:1:1078:U:H2'	1:1:1080:A:OP2	2.15	0.47
1:1:1381:A:H2'	1:1:1382:G:C8	2.50	0.47
1:1:1384:U:H5''	6:C:138:ARG:O	2.15	0.47
1:1:1497:C:O2'	1:1:1602:A:N3	2.48	0.47
1:1:1816:A:O2'	1:1:1817:G:OP1	2.33	0.47
1:1:2108:C:H1'	1:1:3344:A:C8	2.50	0.47
1:1:2213:A:N3	1:1:2601:A:O2'	2.44	0.47
1:1:2308:C:O2	1:1:2971:A:N6	2.47	0.47
1:1:2659:G:H4'	1:1:2751:G:O2'	2.14	0.47
2:3:93:C:H2'	2:3:94:C:H6	1.79	0.47
4:A:97:ASN:ND2	41:p:87:ARG:NH1	2.63	0.47
6:C:229:ASN:OD1	6:C:230:VAL:N	2.47	0.47
11:H:106:LYS:H	11:H:109:ALA:CB	2.27	0.47
11:H:189:GLU:C	11:H:191:LEU:H	2.21	0.47
12:J:9:MET:HE3	12:J:134:PRO:HB2	1.97	0.47
13:L:76:THR:HG1	13:L:79:GLU:HB2	1.79	0.47
18:Q:36:LEU:O	18:Q:40:THR:OG1	2.21	0.47
26:Y:59:VAL:HG12	26:Y:103:LYS:O	2.14	0.47
34:g:51:LEU:HD12	34:g:51:LEU:O	2.15	0.47
36:i:62:ARG:HH12	36:i:98:ARG:NH2	2.12	0.47
40:o:12:CYS:HB2	40:o:23:HIS:CE1	2.49	0.47
43:y:219:GLU:HA	43:y:224:LEU:HB2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:66:A:P	13:L:100:ARG:HH21	2.37	0.47
1:1:1149:G:C2	1:1:1155:C:N3	2.83	0.47
1:1:2550:U:H6	10:G:37:GLY:HA3	1.79	0.47
1:1:3161:C:H42	1:1:3289:G:H1	1.62	0.47
6:C:71:VAL:HG22	6:C:76:ARG:HH22	1.80	0.47
6:C:175:HIS:HA	6:C:178:LEU:HD12	1.96	0.47
6:C:281:ILE:HG13	18:Q:125:ASP:OD2	2.14	0.47
7:D:34:LYS:O	7:D:38:THR:HG23	2.14	0.47
10:G:158:ASP:O	10:G:160:ILE:HG13	2.15	0.47
11:H:8:GLN:HG2	11:H:68:LEU:HD21	1.97	0.47
35:h:104:GLN:HA	35:h:107:LYS:HB2	1.97	0.47
1:1:981:U:H2'	1:1:982:C:O4'	2.14	0.47
1:1:1194:G:H2'	1:1:1195:A:C8	2.50	0.47
1:1:1561:G:O2'	1:1:1562:C:OP2	2.29	0.47
1:1:1604:G:H4'	1:1:1835:A:H4'	1.96	0.47
1:1:1784:G:H2'	1:1:1785:U:O4'	2.15	0.47
1:1:1909:A:C6	1:1:1910:A:C6	3.03	0.47
1:1:2185:G:O2'	1:1:2314:U:OP2	2.33	0.47
2:3:13:A:H5'	2:3:14:U:H5	1.80	0.47
5:B:56:ILE:HA	5:B:56:ILE:HD13	1.70	0.47
5:B:210:GLU:HG3	5:B:211:GLN:O	2.15	0.47
5:B:303:LYS:HD2	5:B:361:THR:HG21	1.97	0.47
5:B:313:HIS:HB2	5:B:332:ARG:HD2	1.95	0.47
9:F:98:LYS:O	9:F:102:VAL:HG23	2.15	0.47
12:J:133:ARG:HH12	12:J:153:LYS:C	2.23	0.47
16:O:39:GLU:HB2	16:O:139:GLY:HA3	1.97	0.47
18:Q:89:ASP:OD1	18:Q:90:ASP:N	2.48	0.47
26:Y:43:TYR:CE2	26:Y:109:LEU:HD12	2.50	0.47
28:a:90:TYR:CG	28:a:100:PRO:HG3	2.50	0.47
40:o:4:VAL:HG23	40:o:93:LEU:HA	1.97	0.47
43:y:62:MET:O	43:y:73:PRO:HD3	2.14	0.47
43:y:106:ASN:HD22	43:y:150:SER:HB2	1.80	0.47
1:1:354:U:H2'	1:1:355:A:C8	2.50	0.47
1:1:720:A:N7	1:1:783:A:H4'	2.30	0.47
1:1:1100:U:OP2	9:F:196:LYS:HD2	2.14	0.47
1:1:1709:C:H2'	1:1:1710:C:H6	1.80	0.47
1:1:2267:C:H2'	1:1:2268:U:O4'	2.15	0.47
1:1:2529:A:H2'	1:1:2530:G:O4'	2.15	0.47
2:3:40:C:H4'	12:J:43:GLN:NE2	2.31	0.47
3:4:48:A:O2'	3:4:50:C:OP2	2.26	0.47
5:B:347:SER:C	5:B:349:LYS:H	2.22	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:N:138:GLN:HA	15:N:143:ARG:HH11	1.80	0.47
16:O:78:ARG:NH1	16:O:81:TYR:CD2	2.83	0.47
26:Y:107:THR:O	26:Y:108:LYS:HD2	2.15	0.47
30:c:25:LEU:O	30:c:29:SER:OG	2.32	0.47
1:1:372:A:C6	1:1:373:A:C6	3.03	0.46
1:1:831:G:O6	1:1:864:G:N2	2.47	0.46
1:1:848:A:C5	1:1:849:C:HI'	2.50	0.46
1:1:860:G:O5'	4:A:181:LYS:NZ	2.48	0.46
1:1:1326:A:H2'	1:1:1327:C:O4'	2.14	0.46
1:1:1560:G:C2	1:1:1580:A:N1	2.83	0.46
1:1:1687:U:O4	22:U:45:GLY:N	2.48	0.46
1:1:2850:G:H2'	1:1:2851:A:H8	1.80	0.46
1:1:2942:C:H42	42:w:233:THR:HG21	1.80	0.46
1:1:3007:U:H5'	16:O:73:PHE:CD1	2.50	0.46
2:3:36:C:H2'	2:3:37:G:C8	2.49	0.46
4:A:3:ARG:HG2	4:A:4:VAL:H	1.79	0.46
4:A:110:GLY:N	4:A:136:ILE:O	2.28	0.46
4:A:225:ILE:HD11	4:A:235:ALA:O	2.15	0.46
7:D:111:GLN:HG3	7:D:116:ASP:OD2	2.15	0.46
7:D:215:ASP:CG	7:D:217:GLU:HG2	2.40	0.46
33:f:59:VAL:HG23	33:f:60:ARG:N	2.30	0.46
37:j:64:MET:O	37:j:68:LYS:HB2	2.15	0.46
43:y:219:GLU:HA	43:y:224:LEU:HD22	1.97	0.46
1:1:1288:U:H2'	1:1:1289:G:C8	2.50	0.46
1:1:1316:C:H42	20:S:154:HIS:CD2	2.32	0.46
1:1:1504:A:H5''	17:P:125:GLN:HE22	1.80	0.46
1:1:1641:U:O2'	1:1:1642:A:H3'	2.16	0.46
1:1:2771:U:OP2	1:1:2772:C:N3	2.48	0.46
6:C:58:HIS:CE1	6:C:98:ARG:HD3	2.51	0.46
16:O:55:HIS:HA	16:O:58:LEU:HB3	1.95	0.46
20:S:28:ARG:HH11	20:S:99:ARG:NH2	2.13	0.46
22:U:29:ASP:OD2	22:U:31:ALA:HB3	2.16	0.46
27:Z:14:VAL:HG12	27:Z:79:HIS:O	2.16	0.46
30:c:15:ALA:O	30:c:18:ILE:HG22	2.15	0.46
1:1:127:G:OP1	15:N:140:LYS:HG3	2.16	0.46
1:1:1240:A:H8	1:1:1240:A:OP2	1.98	0.46
1:1:3111:U:H4'	11:H:151:VAL:HG12	1.97	0.46
1:1:3228:C:H4'	1:1:3229:G:O5'	2.15	0.46
1:1:3337:G:H2'	1:1:3338:C:C6	2.50	0.46
5:B:115:LYS:NZ	5:B:129:ALA:C	2.72	0.46
12:J:49:LYS:HG2	12:J:64:LYS:H	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:R:60:LYS:HE2	19:R:64:ARG:HH21	1.79	0.46
24:W:20:LEU:HD21	24:W:28:ILE:HG23	1.98	0.46
33:f:13:HIS:NE2	33:f:28:SER:HB3	2.30	0.46
37:j:52:LYS:HB3	37:j:56:ARG:HH12	1.79	0.46
1:1:29:C:O2'	15:N:162:ARG:O	2.31	0.46
1:1:953:G:OP1	29:b:15:LYS:NZ	2.38	0.46
1:1:1481:A:C2	34:g:4:ARG:HD3	2.49	0.46
1:1:1724:U:C5	19:R:125:LYS:NZ	2.83	0.46
2:3:99:G:H4'	9:F:128:LYS:HE3	1.96	0.46
10:G:26:LEU:HD12	10:G:27:THR:N	2.31	0.46
10:G:71:VAL:HG12	15:N:21:PHE:CZ	2.51	0.46
11:H:21:LYS:HG3	14:M:8:LYS:HD2	1.98	0.46
14:M:135:LEU:HD23	14:M:136:ALA:N	2.30	0.46
18:Q:79:LYS:HD3	18:Q:138:LEU:HG	1.97	0.46
33:f:73:ARG:CZ	33:f:82:ARG:NH1	2.78	0.46
1:1:440:A:OP2	1:1:440:A:C8	2.68	0.46
1:1:507:U:HO2'	1:1:1166:G:HO2'	1.59	0.46
1:1:2111:G:H4'	1:1:2112:U:OP2	2.16	0.46
1:1:2375:G:O2'	1:1:2377:G:OP2	2.32	0.46
1:1:2535:A:H2'	1:1:2536:A:O4'	2.16	0.46
1:1:2745:G:N1	1:1:2748:A:OP2	2.47	0.46
1:1:2793:G:H4'	40:o:66:LYS:HE3	1.97	0.46
5:B:53:MET:HE2	5:B:77:THR:HG22	1.98	0.46
6:C:295:ILE:O	6:C:299:ILE:HG12	2.15	0.46
27:Z:47:GLU:N	27:Z:69:LYS:O	2.45	0.46
30:c:18:ILE:HG23	30:c:19:LYS:N	2.31	0.46
37:j:25:ARG:HE	39:l:51:ILE:HD12	1.80	0.46
41:p:58:SER:C	41:p:61:LYS:NZ	2.70	0.46
1:1:413:U:P	17:P:30:ARG:HE	2.39	0.46
1:1:979:U:HO2'	1:1:980:A:P	2.33	0.46
1:1:1385:C:H41	6:C:202:ARG:HH21	1.63	0.46
1:1:1608:C:H5''	25:X:111:ASN:ND2	2.31	0.46
1:1:1928:G:O2'	41:p:16:VAL:HG21	2.15	0.46
10:G:111:LYS:O	10:G:115:ALA:N	2.43	0.46
12:J:125:MET:HG2	12:J:127:PHE:HE1	1.81	0.46
13:L:24:VAL:HG12	15:N:199:LEU:HB2	1.98	0.46
19:R:103:ARG:NH1	19:R:124:TYR:CZ	2.84	0.46
21:T:41:ASP:OD1	21:T:99:SER:HB2	2.16	0.46
30:c:42:ILE:HD12	30:c:44:ILE:HD11	1.97	0.46
41:p:75:ALA:O	41:p:79:VAL:HG23	2.16	0.46
1:1:149:U:N3	1:1:150:A:N7	2.63	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:276:U:O2	15:N:93:LYS:HE2	2.15	0.46
1:1:708:G:N1	1:1:712:G:C6	2.84	0.46
1:1:1176:C:H2'	1:1:1177:G:N2	2.31	0.46
1:1:1281:G:H3'	1:1:1282:G:H8	1.81	0.46
1:1:1427:U:H5'	6:C:44:LYS:NZ	2.31	0.46
1:1:1450:G:O6	1:1:2355:G:N2	2.48	0.46
1:1:1571:A:H2'	1:1:1572:U:O4'	2.14	0.46
1:1:2768:U:H2'	1:1:2769:A:H8	1.80	0.46
1:1:3047:U:O2'	5:B:53:MET:HE1	2.16	0.46
3:4:22:U:OP2	6:C:194:TYR:HD2	1.99	0.46
5:B:87:VAL:HG13	5:B:163:HIS:HD2	1.80	0.46
6:C:355:PHE:CE2	9:F:70:LYS:HE3	2.51	0.46
7:D:276:LYS:O	7:D:277:LEU:HB2	2.15	0.46
15:N:33:LYS:HB3	15:N:37:HIS:CD2	2.51	0.46
15:N:71:ARG:HB2	15:N:94:TYR:HB2	1.97	0.46
32:e:32:TRP:CZ2	32:e:53:PRO:HD2	2.51	0.46
41:p:49:ARG:NH1	41:p:51:ALA:C	2.74	0.46
1:1:860:G:P	4:A:181:LYS:NZ	2.89	0.46
1:1:1566:A:C8	1:1:1566:A:OP2	2.69	0.46
1:1:1688:U:H2'	1:1:1689:U:C6	2.51	0.46
1:1:2371:G:H2'	1:1:2372:A:H5''	1.97	0.46
1:1:2526:C:OP2	1:1:2526:C:C6	2.69	0.46
1:1:3150:A:H5'	5:B:129:ALA:HA	1.98	0.46
1:1:3185:U:O2'	20:S:170:THR:OG1	2.30	0.46
5:B:227:GLU:HG2	5:B:270:ARG:HE	1.81	0.46
8:E:10:TYR:HD1	32:e:92:TYR:CE2	2.34	0.46
13:L:79:GLU:HG3	13:L:103:ASN:OD1	2.15	0.46
43:y:61:ARG:NH1	43:y:106:ASN:ND2	2.64	0.46
1:1:107:A:O2'	1:1:324:A:N3	2.39	0.46
1:1:989:A:H2'	1:1:990:U:O4'	2.16	0.46
1:1:1282:G:H2'	1:1:1283:C:O4'	2.15	0.46
1:1:1579:C:H42	1:1:1580:A:N6	2.07	0.46
1:1:1932:A:C2	1:1:2124:G:H5''	2.51	0.46
1:1:3201:C:H2'	1:1:3202:G:C8	2.50	0.46
4:A:134:VAL:HG12	4:A:151:PRO:HD3	1.97	0.46
7:D:108:ARG:CZ	7:D:253:PHE:HB2	2.46	0.46
12:J:35:LYS:O	12:J:39:GLN:HG2	2.16	0.46
13:L:76:THR:O	13:L:78:ALA:N	2.49	0.46
15:N:16:SER:O	15:N:20:ARG:HG2	2.15	0.46
15:N:191:TRP:NE1	15:N:195:ASN:HD21	2.14	0.46
16:O:57:PHE:CZ	16:O:82:LYS:HE3	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:R:130:ASN:C	19:R:132:PHE:N	2.74	0.46
32:e:122:PRO:O	32:e:123:LYS:HG3	2.15	0.46
33:f:58:GLU:HG3	33:f:62:SER:C	2.41	0.46
43:y:53:ILE:O	43:y:56:THR:OG1	2.30	0.46
1:1:197:G:N2	1:1:372:A:C8	2.84	0.46
1:1:220:G:O2'	1:1:221:A:H5'	2.16	0.46
1:1:241:G:C6	1:1:242:C:C4	3.03	0.46
1:1:338:A:OP1	6:C:47:ARG:HA	2.15	0.46
1:1:599:C:H2'	1:1:600:G:H8	1.81	0.46
1:1:913:A:H2	1:1:2134:G:N3	2.14	0.46
1:1:1561:G:H1	1:1:1578:C:H42	1.64	0.46
1:1:1628:C:H5''	1:1:1629:U:H2'	1.98	0.46
1:1:2436:U:H6	1:1:2436:U:C4'	2.29	0.46
1:1:2521:U:H2'	1:1:2522:G:H5'	1.97	0.46
1:1:2560:C:H41	27:Z:56:LYS:HE3	1.80	0.46
2:3:8:G:C6	2:3:9:C:N4	2.84	0.46
4:A:112:ILE:HD13	41:p:79:VAL:HG22	1.97	0.46
5:B:105:VAL:HG21	5:B:148:LEU:HD12	1.98	0.46
17:P:121:GLN:HA	17:P:144:SER:HA	1.98	0.46
30:c:47:ASN:HD21	30:c:74:ASN:CG	2.24	0.46
32:e:76:VAL:N	32:e:95:GLU:O	2.49	0.46
40:o:61:LYS:HZ1	42:w:382:ASP:CG	2.24	0.46
41:p:46:THR:HG21	41:p:59:CYS:HB2	1.97	0.46
42:w:371:GLY:HA2	42:w:398:VAL:HG23	1.97	0.46
43:y:159:GLY:O	43:y:181:LEU:HA	2.15	0.46
1:1:516:A:H5''	6:C:344:ALA:HB2	1.98	0.45
1:1:1278:A:HO2'	1:1:1279:C:H6	1.61	0.45
1:1:1307:G:H1'	1:1:1308:A:OP2	2.16	0.45
1:1:2117:A:O2'	1:1:3080:G:O2'	2.13	0.45
1:1:2581:U:H2'	1:1:2582:C:H6	1.81	0.45
1:1:2584:G:H5''	1:1:2585:G:OP2	2.15	0.45
5:B:17:LEU:HD11	5:B:233:TRP:CH2	2.48	0.45
11:H:11:GLU:HA	11:H:52:LEU:HD23	1.97	0.45
17:P:126:ARG:HH21	44:z:417:ILE:HD12	1.80	0.45
23:V:14:SER:HB3	23:V:83:LYS:NZ	2.31	0.45
27:Z:15:ARG:HB2	27:Z:79:HIS:HB3	1.98	0.45
35:h:38:ARG:HB2	35:h:39:PRO:HD2	1.98	0.45
42:w:287:ASP:OD2	42:w:292:GLN:HB3	2.16	0.45
43:y:166:SER:HB2	43:y:169:ASP:CG	2.42	0.45
44:z:412:GLN:O	44:z:416:GLU:HB2	2.16	0.45
1:1:190:U:O2'	1:1:191:U:OP2	2.20	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:434:U:H2'	1:1:435:C:H6	1.80	0.45
1:1:2945:G:H5''	1:1:2947:G:C8	2.52	0.45
1:1:3332:U:OP1	24:W:35:LYS:HD2	2.16	0.45
6:C:104:LYS:HD3	6:C:106:TRP:CZ2	2.51	0.45
9:F:121:LYS:HB2	21:T:133:ALA:HB3	1.97	0.45
11:H:86:TYR:CZ	11:H:151:VAL:HG22	2.51	0.45
12:J:133:ARG:NH1	12:J:153:LYS:C	2.74	0.45
12:J:133:ARG:NH1	12:J:154:THR:HG22	2.32	0.45
20:S:28:ARG:HH11	20:S:99:ARG:NE	2.13	0.45
20:S:80:ARG:HH21	20:S:122:HIS:CD2	2.34	0.45
23:V:13:ILE:CD1	23:V:54:LEU:HB3	2.45	0.45
25:X:60:TYR:HH	35:h:26:LYS:NZ	2.01	0.45
27:Z:133:LYS:HG2	27:Z:134:LEU:O	2.17	0.45
42:w:162:ARG:HD2	42:w:195:ASP:HB2	1.97	0.45
1:1:359:U:H4'	1:1:817:A:N6	2.28	0.45
1:1:434:U:H2'	1:1:435:C:C6	2.50	0.45
1:1:534:U:O4	14:M:74:ARG:NH2	2.49	0.45
1:1:565:U:H2'	1:1:566:G:C8	2.51	0.45
1:1:860:G:C6	4:A:181:LYS:HB2	2.51	0.45
1:1:1062:A:H4'	21:T:105:PHE:CE1	2.51	0.45
1:1:2115:G:H22	1:1:2120:A:H1'	1.81	0.45
1:1:2528:G:O3'	10:G:248:LYS:NZ	2.50	0.45
1:1:2633:U:O4	21:T:10:ARG:NH2	2.49	0.45
1:1:2840:C:N3	1:1:2848:G:N2	2.64	0.45
1:1:3088:G:H5''	1:1:3377:G:N2	2.31	0.45
3:4:36:G:O2'	3:4:104:A:N1	2.42	0.45
4:A:168:VAL:CG1	41:p:79:VAL:HG21	2.46	0.45
5:B:296:THR:HG22	5:B:297:SER:N	2.30	0.45
7:D:79:TYR:H	7:D:82:GLU:CD	2.24	0.45
27:Z:74:VAL:HG23	27:Z:101:PHE:CE2	2.51	0.45
30:c:104:LEU:HD12	30:c:105:ALA:N	2.31	0.45
36:i:53:TYR:OH	36:i:86:LYS:HE2	2.15	0.45
40:o:89:LYS:HD3	42:w:314:GLN:NE2	2.27	0.45
1:1:2828:G:OP2	1:1:2829:U:OP2	2.34	0.45
1:1:3028:G:H2'	1:1:3029:A:C8	2.51	0.45
14:M:17:VAL:HG12	14:M:72:LEU:HB2	1.97	0.45
18:Q:122:ILE:HG22	18:Q:123:THR:O	2.17	0.45
22:U:38:ILE:O	22:U:50:LEU:HD11	2.16	0.45
1:1:269:G:H5'	15:N:120:TRP:CE3	2.51	0.45
1:1:715:A:H4'	1:1:716:A:OP1	2.16	0.45
1:1:745:C:H5''	18:Q:145:ASN:HD22	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:3041:U:H2'	1:1:3042:U:C6	2.52	0.45
2:3:29:C:H4'	12:J:9:MET:HE1	1.98	0.45
5:B:116:ARG:NH1	5:B:122:TRP:CD1	2.84	0.45
5:B:173:GLN:O	5:B:174:LYS:HB2	2.17	0.45
5:B:247:ARG:O	5:B:248:LYS:HG3	2.17	0.45
7:D:50:ARG:HD2	7:D:147:ASP:HB2	1.98	0.45
24:W:22:VAL:HG22	24:W:28:ILE:HG12	1.99	0.45
1:1:29:C:H4'	1:1:62:A:H4'	1.98	0.45
1:1:698:U:H2'	1:1:699:A:O4'	2.16	0.45
1:1:1352:A:H1'	1:1:1353:U:O5'	2.16	0.45
1:1:1467:A:N6	1:1:1511:U:O2	2.50	0.45
1:1:1765:U:OP1	1:1:1765:U:H4'	2.16	0.45
1:1:1916:U:H5'	19:R:81:ARG:HH21	1.80	0.45
3:4:14:C:H5''	17:P:123:PRO:CD	2.47	0.45
5:B:62:ARG:H	5:B:68:HIS:HD1	1.65	0.45
15:N:190:THR:O	15:N:194:GLN:HG2	2.15	0.45
27:Z:54:THR:HG23	27:Z:56:LYS:N	2.32	0.45
28:a:3:SER:O	28:a:6:THR:HG22	2.17	0.45
34:g:58:ARG:HB3	34:g:59:PRO:HD2	1.97	0.45
43:y:199:VAL:HG23	43:y:204:ALA:HB2	1.98	0.45
43:y:226:ASP:HA	43:y:227:ALA:HA	1.48	0.45
1:1:210:U:C2	1:1:230:U:H4'	2.52	0.45
1:1:438:A:H2'	1:1:439:C:O4'	2.16	0.45
1:1:584:G:H4'	33:f:45:LEU:C	2.41	0.45
1:1:804:C:O2'	6:C:74:ILE:HG22	2.16	0.45
1:1:820:A:N6	1:1:821:U:O4	2.50	0.45
1:1:1168:U:H2'	1:1:1169:A:H8	1.82	0.45
8:E:39:VAL:HG22	8:E:159:LEU:HD21	1.99	0.45
11:H:10:ILE:O	11:H:52:LEU:HA	2.16	0.45
21:T:103:GLN:O	21:T:107:GLU:HG3	2.16	0.45
27:Z:13:VAL:O	27:Z:19:ALA:HA	2.17	0.45
28:a:96:LYS:C	28:a:98:THR:H	2.25	0.45
30:c:67:VAL:HG12	30:c:69:TYR:CE1	2.52	0.45
35:h:77:PRO:HD2	35:h:80:LEU:HD12	1.99	0.45
38:k:66:ILE:HA	38:k:69:LEU:HD13	1.99	0.45
40:o:7:THR:HB	40:o:22:GLN:NE2	2.31	0.45
43:y:28:VAL:HG12	43:y:50:HIS:HB3	1.99	0.45
43:y:82:GLN:HE21	43:y:86:ASN:ND2	2.15	0.45
1:1:351:A:OP1	39:l:34:THR:HG21	2.16	0.45
1:1:672:A:C2	1:1:673:U:C2	3.04	0.45
1:1:708:G:N1	1:1:712:G:O6	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2664:C:OP2	12:J:142:LYS:NZ	2.38	0.45
2:3:13:A:H5'	2:3:14:U:C5	2.51	0.45
4:A:48:ILE:HD11	41:p:63:THR:HG22	1.98	0.45
6:C:208:VAL:HG11	6:C:250:TRP:CZ3	2.52	0.45
9:F:110:ARG:HG2	18:Q:2:GLY:O	2.17	0.45
16:O:15:LEU:HA	16:O:42:ASN:O	2.16	0.45
20:S:48:LEU:HD13	21:T:151:LEU:HD13	1.99	0.45
37:j:84:SER:O	37:j:85:LYS:HB2	2.16	0.45
1:1:31:C:N4	15:N:188:ARG:HH12	2.08	0.45
1:1:278:U:H2'	1:1:279:U:O4'	2.16	0.45
1:1:1109:U:H2'	1:1:1110:U:C6	2.51	0.45
1:1:1146:C:H4'	1:1:1331:U:C4	2.52	0.45
1:1:1243:G:H1'	1:1:1270:A:C2	2.52	0.45
1:1:2439:A:C8	1:1:2439:A:OP2	2.70	0.45
1:1:2623:G:H2'	1:1:2624:G:O4'	2.17	0.45
1:1:2797:C:H4'	1:1:2798:C:OP2	2.17	0.45
10:G:176:PRO:HB3	10:G:219:ASP:OD1	2.17	0.45
15:N:68:ARG:HH12	15:N:128:LYS:CE	2.30	0.45
16:O:8:VAL:O	16:O:118:VAL:HG22	2.17	0.45
19:R:96:ILE:CG2	19:R:100:ARG:HE	2.30	0.45
21:T:50:LYS:O	21:T:92:ARG:HD3	2.17	0.45
23:V:45:ARG:HB3	23:V:48:ARG:HD2	1.99	0.45
25:X:50:ALA:HB1	35:h:66:VAL:HG11	1.98	0.45
34:g:41:ARG:HG2	34:g:56:THR:CG2	2.47	0.45
42:w:272:GLN:HB3	42:w:387:LEU:CD2	2.47	0.45
1:1:360:G:C2	1:1:361:A:C2	3.05	0.45
1:1:501:A:OP1	8:E:82:ARG:NH2	2.30	0.45
1:1:1168:U:H5	1:1:1329:U:C5	2.35	0.45
1:1:1222:G:H1'	1:1:1285:G:H1	1.80	0.45
1:1:1575:A:N6	1:1:1576:G:O6	2.49	0.45
1:1:1609:C:H2'	1:1:1610:G:C8	2.52	0.45
1:1:1927:G:C8	41:p:16:VAL:HA	2.52	0.45
1:1:2655:U:C5	40:o:4:VAL:HG12	2.51	0.45
1:1:2843:U:H5''	1:1:2844:C:C5	2.49	0.45
1:1:2903:A:H2'	1:1:2904:U:O4'	2.16	0.45
4:A:57:PRO:HD3	41:p:53:GLY:HA3	1.98	0.45
13:L:54:LEU:HD11	13:L:119:TYR:CG	2.52	0.45
13:L:128:ARG:HH12	35:h:112:PRO:CG	2.19	0.45
16:O:143:THR:OG1	16:O:150:GLU:OE1	2.26	0.45
30:c:26:GLY:O	30:c:30:THR:HG23	2.17	0.45
34:g:71:THR:HG22	34:g:72:VAL:O	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:j:24:ARG:O	37:j:24:ARG:HG2	2.17	0.45
40:o:10:THR:O	40:o:20:HIS:HA	2.16	0.45
41:p:61:LYS:HA	41:p:61:LYS:HD3	1.74	0.45
1:1:1096:U:OP2	21:T:128:LEU:HD21	2.17	0.44
1:1:2771:U:HO2'	1:1:2772:C:P	2.39	0.44
2:3:120:C:OP2	7:D:258:LYS:NZ	2.45	0.44
5:B:213:GLU:OE2	5:B:340:LYS:NZ	2.47	0.44
11:H:88:TYR:HE2	11:H:155:SER:HA	1.82	0.44
12:J:167:TYR:O	12:J:169:ALA:N	2.50	0.44
20:S:80:ARG:HH21	20:S:122:HIS:HD2	1.65	0.44
25:X:131:ASP:OD2	25:X:133:LEU:HB3	2.17	0.44
31:d:5:LYS:O	31:d:6:ASP:HB2	2.17	0.44
32:e:109:LEU:HD21	32:e:119:VAL:HG11	2.00	0.44
35:h:78:LYS:HG2	35:h:81:ARG:HE	1.80	0.44
1:1:393:U:H2'	1:1:394:G:C8	2.51	0.44
1:1:885:U:H2'	1:1:886:C:C6	2.50	0.44
1:1:989:A:H4'	21:T:104:GLU:OE2	2.17	0.44
1:1:1926:C:H5'	41:p:8:VAL:HG13	1.99	0.44
1:1:2197:C:N4	1:1:2241:U:H2'	2.32	0.44
1:1:3293:U:H5'	5:B:128:LYS:HE2	1.98	0.44
6:C:35:VAL:HG11	6:C:244:LEU:HD21	1.99	0.44
7:D:38:THR:HG22	21:T:30:TYR:HB3	1.99	0.44
7:D:178:ASN:HA	7:D:183:TRP:CE3	2.53	0.44
10:G:78:PHE:HE2	10:G:164:VAL:HG12	1.82	0.44
11:H:78:MET:O	11:H:82:VAL:N	2.50	0.44
26:Y:89:LYS:HG2	26:Y:90:VAL:H	1.82	0.44
31:d:82:GLU:HG3	31:d:83:GLU:CB	2.47	0.44
37:j:19:CYS:O	37:j:23:GLY:HA2	2.17	0.44
1:1:77:A:N7	13:L:73:ARG:NH1	2.66	0.44
1:1:844:G:N2	1:1:850:U:O2	2.50	0.44
1:1:1488:G:H5''	1:1:1838:G:O6	2.17	0.44
1:1:2927:C:H2'	1:1:2928:C:H6	1.82	0.44
1:1:3317:U:H4'	1:1:3318:G:OP2	2.16	0.44
9:F:110:ARG:NH2	9:F:206:LYS:NZ	2.65	0.44
33:f:16:TYR:OH	33:f:91:ALA:HB2	2.17	0.44
35:h:21:LEU:HD21	35:h:25:LYS:HE3	2.00	0.44
41:p:6:LYS:HE2	41:p:7:LYS:HZ1	1.83	0.44
1:1:180:C:O2	1:1:237:G:N2	2.50	0.44
1:1:528:U:H2'	1:1:529:A:C8	2.52	0.44
1:1:534:U:O2	20:S:146:LYS:HA	2.18	0.44
1:1:965:A:O2'	28:a:44:ASN:HB2	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1367:G:OP1	32:e:45:ARG:NH2	2.50	0.44
1:1:1517:G:H5''	39:l:22:PRO:HG2	1.99	0.44
1:1:1629:U:C4	27:Z:111:LYS:HD2	2.52	0.44
1:1:1795:U:P	4:A:191:LEU:HD21	2.58	0.44
1:1:1873:U:OP2	19:R:20:ARG:NH2	2.51	0.44
1:1:1895:A:O2'	1:1:3053:G:H4'	2.18	0.44
1:1:2843:U:OP2	1:1:2844:C:N4	2.49	0.44
3:4:3:A:H4'	17:P:61:ARG:HH11	1.81	0.44
5:B:238:LEU:HB2	5:B:246:LEU:O	2.17	0.44
7:D:90:HIS:CE1	7:D:229:ASP:OD2	2.71	0.44
12:J:83:GLY:HA3	12:J:127:PHE:HE2	1.81	0.44
14:M:57:ALA:HB2	20:S:97:VAL:HG21	1.99	0.44
18:Q:106:PHE:HB2	18:Q:111:ARG:HH11	1.83	0.44
43:y:82:GLN:HG3	43:y:86:ASN:ND2	2.33	0.44
1:1:425:G:H5'	32:e:23:ASP:OD2	2.18	0.44
1:1:997:A:H61	1:1:1052:U:H3	1.66	0.44
1:1:1105:A:H2'	1:1:1106:G:O4'	2.17	0.44
1:1:2274:U:H2'	1:1:2275:A:C8	2.53	0.44
1:1:3110:C:H2'	1:1:3111:U:C6	2.52	0.44
4:A:184:ARG:NH2	41:p:14:TYR:OH	2.46	0.44
5:B:118:PHE:HE2	5:B:130:PHE:CE2	2.35	0.44
5:B:296:THR:HG21	5:B:356:LEU:O	2.18	0.44
6:C:269:SER:C	6:C:271:LYS:H	2.26	0.44
12:J:12:LEU:HD23	12:J:162:TRP:CG	2.52	0.44
12:J:113:GLY:HA3	12:J:114:ILE:HD12	1.99	0.44
15:N:112:ASN:HB2	15:N:138:GLN:NE2	2.28	0.44
15:N:153:ASP:OD2	15:N:155:VAL:HG22	2.17	0.44
39:l:22:PRO:HG3	39:l:41:ARG:NH1	2.32	0.44
43:y:22:THR:OG1	43:y:67:ARG:HB2	2.17	0.44
1:1:230:U:H2'	1:1:231:G:O4'	2.18	0.44
1:1:791:A:N6	1:1:792:G:O6	2.51	0.44
1:1:816:A:C8	1:1:906:A:N6	2.86	0.44
1:1:1355:A:H1'	1:1:1356:U:OP2	2.18	0.44
1:1:2148:U:O2'	4:A:182:ALA:HB2	2.18	0.44
1:1:2672:G:N2	1:1:2682:C:O2	2.41	0.44
1:1:3165:A:H2'	1:1:3166:C:C6	2.52	0.44
4:A:112:ILE:CD1	41:p:79:VAL:HG22	2.48	0.44
6:C:4:PRO:HD2	6:C:22:LEU:HD12	1.99	0.44
11:H:134:ILE:HG13	11:H:146:LEU:HG	2.00	0.44
14:M:24:LYS:HE2	14:M:25:LYS:HZ3	1.78	0.44
14:M:120:VAL:O	14:M:124:ARG:HG3	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:N:64:VAL:HG11	15:N:102:ALA:HB1	2.00	0.44
20:S:80:ARG:HB2	20:S:124:LEU:HD11	1.99	0.44
25:X:58:ASP:O	25:X:62:VAL:HG23	2.17	0.44
26:Y:56:VAL:CG2	26:Y:104:LEU:HB3	2.48	0.44
37:j:66:TYR:OH	37:j:73:ARG:NH2	2.33	0.44
38:k:14:LEU:HD22	38:k:17:ARG:NH1	2.32	0.44
42:w:219:PRO:HD3	42:w:280:SER:O	2.17	0.44
43:y:2:ALA:N	43:y:224:LEU:HD23	2.32	0.44
1:1:194:U:C2	1:1:195:U:H5	2.35	0.44
1:1:892:U:C4	1:1:893:C:C4	3.06	0.44
1:1:1890:U:O4	1:1:1891:A:N6	2.51	0.44
1:1:2525:G:O2'	1:1:2526:C:OP2	2.25	0.44
1:1:2841:G:N2	1:1:2847:A:H62	2.14	0.44
1:1:3209:A:P	20:S:161:LYS:NZ	2.91	0.44
2:3:88:G:H2'	2:3:89:G:C8	2.49	0.44
6:C:338:LYS:O	6:C:339:LEU:HB2	2.18	0.44
11:H:183:HIS:HE1	11:H:185:GLY:HA3	1.83	0.44
18:Q:182:LYS:HE2	28:a:55:LYS:O	2.18	0.44
22:U:53:ALA:HA	22:U:68:THR:HG22	1.99	0.44
31:d:13:THR:HG22	31:d:72:ARG:HD3	2.00	0.44
35:h:102:GLU:CD	35:h:106:LYS:HE3	2.43	0.44
36:i:33:ALA:O	36:i:34:SER:OG	2.36	0.44
37:j:52:LYS:HB3	37:j:56:ARG:NH1	2.32	0.44
40:o:4:VAL:CG2	40:o:93:LEU:HA	2.48	0.44
43:y:121:ILE:O	43:y:139:ARG:NH2	2.51	0.44
1:1:534:U:H1'	20:S:146:LYS:HD3	2.00	0.44
1:1:845:G:C2	1:1:847:A:OP2	2.71	0.44
1:1:945:C:OP2	1:1:945:C:H6	2.00	0.44
1:1:1577:G:H5''	1:1:1578:C:OP2	2.18	0.44
1:1:2332:A:H2'	1:1:2333:C:O4'	2.18	0.44
1:1:2437:G:O2'	1:1:2438:A:C8	2.69	0.44
1:1:3368:U:O2	1:1:3370:A:H1'	2.18	0.44
2:3:49:G:N7	7:D:58:LYS:HE2	2.32	0.44
2:3:110:G:P	7:D:279:LYS:NZ	2.91	0.44
9:F:24:GLU:HG2	9:F:25:GLN:N	2.27	0.44
12:J:29:ARG:HA	12:J:32:ARG:NH2	2.33	0.44
20:S:1:MET:HE2	20:S:4:PHE:HE1	1.83	0.44
20:S:75:PHE:O	20:S:94:ILE:N	2.37	0.44
43:y:146:ILE:HG13	43:y:147:LEU:HG	2.00	0.44
1:1:40:A:O2'	1:1:937:G:O6	2.22	0.44
1:1:712:G:C2	1:1:713:U:C2	3.06	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1269:U:H5	1:1:1273:A:H62	1.65	0.44
1:1:1534:A:H62	1:1:1586:G:H2'	1.83	0.44
6:C:49:ALA:HA	6:C:109:TRP:CZ2	2.52	0.44
6:C:65:TRP:CD1	6:C:76:ARG:HB2	2.53	0.44
7:D:39:GLN:NE2	7:D:46:THR:O	2.50	0.44
12:J:101:ASN:ND2	12:J:130:VAL:HG23	2.33	0.44
13:L:25:HIS:O	15:N:201:ARG:HG3	2.17	0.44
14:M:38:ILE:HD11	20:S:150:PHE:HE2	1.81	0.44
28:a:73:LEU:HD11	28:a:77:LYS:HB2	2.00	0.44
1:1:589:A:N6	1:1:610:G:O2'	2.44	0.43
1:1:847:A:H2'	1:1:848:A:C8	2.53	0.43
1:1:938:C:H3'	28:a:26:ARG:HH12	1.82	0.43
1:1:1125:U:H2'	1:1:1126:G:C8	2.52	0.43
1:1:1394:A:H2'	1:1:1395:G:O4'	2.18	0.43
1:1:2166:A:H5'	15:N:75:VAL:O	2.18	0.43
1:1:2403:G:N2	1:1:2404:A:H62	2.16	0.43
1:1:2947:G:N3	5:B:250:ALA:HB1	2.32	0.43
2:3:95:A:C6	2:3:96:U:C4	3.06	0.43
4:A:129:ALA:HB3	4:A:132:ASN:ND2	2.32	0.43
5:B:61:ASP:OD1	5:B:68:HIS:HE1	2.01	0.43
10:G:75:ILE:HG22	10:G:76:ALA:N	2.33	0.43
12:J:94:ARG:O	12:J:95:ASN:HB2	2.17	0.43
17:P:126:ARG:HE	44:z:413:ILE:HG22	1.83	0.43
17:P:177:ALA:O	17:P:181:ARG:N	2.50	0.43
20:S:12:ARG:HH12	20:S:15:PRO:HG3	1.82	0.43
30:c:49:PRO:HG2	30:c:52:ARG:CB	2.47	0.43
32:e:85:LEU:HD22	32:e:92:TYR:HB2	1.99	0.43
1:1:166:C:OP2	1:1:166:C:H6	2.01	0.43
1:1:201:A:C4	1:1:202:G:N7	2.86	0.43
1:1:715:A:H8	28:a:115:LYS:HG3	1.81	0.43
1:1:1262:G:H5''	1:1:1263:A:OP2	2.18	0.43
1:1:2093:A:O5'	1:1:2094:C:OP2	2.36	0.43
4:A:187:HIS:HA	4:A:190:ARG:HD3	2.00	0.43
5:B:19:ARG:O	5:B:273:HIS:CE1	2.71	0.43
20:S:57:GLU:HG2	20:S:58:ILE:N	2.34	0.43
27:Z:17:ARG:HA	34:g:74:ARG:HA	1.98	0.43
39:l:36:ARG:HD3	44:z:404:LEU:HD11	2.01	0.43
43:y:117:VAL:HG23	43:y:139:ARG:HG2	2.00	0.43
1:1:36:C:N4	1:1:47:C:O2'	2.51	0.43
1:1:696:C:OP1	6:C:272:VAL:N	2.25	0.43
1:1:1074:U:O3'	1:1:1075:A:H8	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1472:U:H2'	1:1:1473:G:H8	1.82	0.43
1:1:1522:U:H3'	25:X:113:LEU:HD22	2.01	0.43
1:1:1578:C:H5'	1:1:1579:C:OP2	2.18	0.43
1:1:2218:G:H2'	1:1:2219:A:H8	1.82	0.43
1:1:2585:G:H2'	1:1:2585:G:N3	2.32	0.43
1:1:2660:G:H1'	1:1:2744:U:H1'	1.98	0.43
1:1:3113:A:H4'	11:H:69:ARG:HG3	2.00	0.43
2:3:100:C:H2'	2:3:101:G:O4'	2.19	0.43
4:A:96:LEU:HD12	4:A:107:VAL:HG12	1.99	0.43
9:F:176:TYR:CZ	9:F:197:GLN:HG2	2.51	0.43
11:H:8:GLN:HB2	11:H:55:VAL:HG22	2.00	0.43
11:H:17:THR:HG21	14:M:3:THR:HA	2.00	0.43
14:M:49:PRO:HB3	14:M:78:THR:HG23	2.01	0.43
17:P:30:ARG:HA	17:P:119:VAL:HG11	2.00	0.43
21:T:17:ARG:O	21:T:18:ASP:HB2	2.17	0.43
32:e:13:HIS:CE1	32:e:15:LYS:HB3	2.53	0.43
34:g:23:VAL:HG21	34:g:33:GLN:OE1	2.19	0.43
43:y:162:HIS:CD2	43:y:164:GLN:HB2	2.54	0.43
1:1:86:G:N7	13:L:13:HIS:ND1	2.66	0.43
1:1:268:A:OP1	15:N:50:ARG:NH1	2.51	0.43
1:1:297:G:C2'	36:i:41:ARG:HH12	2.31	0.43
1:1:541:U:H2'	1:1:542:G:C8	2.53	0.43
1:1:597:G:OP1	9:F:37:ASN:HB3	2.18	0.43
1:1:1168:U:H1'	9:F:209:ASN:ND2	2.34	0.43
1:1:1265:U:H2'	1:1:1266:G:C8	2.53	0.43
1:1:2703:A:OP2	7:D:23:ARG:CZ	2.66	0.43
3:4:122:U:H2'	3:4:123:G:H8	1.84	0.43
3:4:126:A:O2'	3:4:129:C:N4	2.51	0.43
6:C:185:LYS:HA	6:C:200:THR:O	2.18	0.43
7:D:55:PHE:HE2	7:D:159:VAL:HG22	1.83	0.43
10:G:146:LYS:NZ	10:G:173:MET:O	2.52	0.43
27:Z:16:GLY:O	27:Z:18:TYR:N	2.39	0.43
33:f:38:PRO:HD3	33:f:77:ASN:O	2.18	0.43
42:w:337:ASP:OD2	42:w:354:TYR:CE2	2.72	0.43
43:y:21:ASN:HB2	43:y:67:ARG:HB3	2.00	0.43
1:1:345:G:O2'	3:4:25:G:N3	2.44	0.43
1:1:395:A:C6	1:1:396:A:C6	3.06	0.43
1:1:981:U:H3	1:1:1102:A:H2	1.67	0.43
1:1:1148:G:C6	1:1:1149:G:N7	2.86	0.43
1:1:1354:G:OP2	8:E:9:TRP:HZ3	2.02	0.43
1:1:1618:G:H4'	3:4:129:C:C1'	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1949:G:H2'	1:1:1950:U:C6	2.53	0.43
1:1:2439:A:H8	1:1:2439:A:P	2.41	0.43
1:1:3343:G:H21	1:1:3362:A:H2	1.64	0.43
1:1:3384:U:H2'	1:1:3385:U:H6	1.84	0.43
4:A:30:ARG:HH12	4:A:41:ILE:HG21	1.78	0.43
4:A:225:ILE:HD12	4:A:237:LEU:O	2.18	0.43
5:B:60:LEU:O	5:B:69:LYS:N	2.44	0.43
5:B:92:TYR:HA	5:B:100:ARG:O	2.19	0.43
7:D:19:PRO:HB2	7:D:24:ARG:HG3	1.98	0.43
9:F:98:LYS:HB3	9:F:99:PRO:HD3	1.99	0.43
10:G:26:LEU:HD23	27:Z:123:GLN:NE2	2.33	0.43
10:G:160:ILE:HG22	10:G:164:VAL:CG1	2.47	0.43
24:W:50:ALA:HA	24:W:55:PHE:CD1	2.53	0.43
26:Y:118:LEU:CD1	26:Y:121:ARG:HH11	2.31	0.43
30:c:24:THR:CG2	30:c:91:SER:HB3	2.49	0.43
42:w:272:GLN:HB3	42:w:387:LEU:HD21	2.00	0.43
43:y:115:ALA:HB2	43:y:135:VAL:HG21	2.00	0.43
1:1:146:U:H4'	1:1:148:G:C8	2.53	0.43
1:1:406:G:H1'	3:4:16:G:N2	2.33	0.43
1:1:784:A:HO2'	1:1:785:G:P	2.38	0.43
1:1:854:G:C5	1:1:855:U:C5	3.07	0.43
1:1:1069:C:O2	1:1:1090:G:N2	2.51	0.43
1:1:1155:C:H2'	1:1:1156:C:C6	2.51	0.43
1:1:1724:U:O4	19:R:125:LYS:NZ	2.51	0.43
1:1:2208:A:C8	1:1:2208:A:OP2	2.71	0.43
1:1:3371:G:H2'	1:1:3372:A:C8	2.54	0.43
4:A:209:HIS:HD2	4:A:211:HIS:HB2	1.84	0.43
7:D:205:SER:HB2	7:D:233:ALA:HB1	1.99	0.43
8:E:56:LYS:HD2	8:E:98:VAL:CG1	2.48	0.43
9:F:159:GLN:O	9:F:160:ARG:C	2.62	0.43
15:N:112:ASN:OD1	15:N:112:ASN:N	2.51	0.43
19:R:94:VAL:O	19:R:98:ARG:HG3	2.18	0.43
19:R:148:ASP:OD1	19:R:151:ARG:NH2	2.52	0.43
27:Z:16:GLY:C	27:Z:18:TYR:N	2.76	0.43
36:i:13:LYS:HE2	36:i:13:LYS:HB3	1.85	0.43
38:k:43:PHE:O	38:k:53:THR:HA	2.18	0.43
40:o:55:LYS:HG3	40:o:56:PRO:HD2	2.00	0.43
1:1:283:G:OP1	40:o:45:ARG:NH2	2.51	0.43
1:1:412:G:H1'	17:P:120:ASN:HB3	2.00	0.43
1:1:708:G:H5''	1:1:709:A:OP2	2.17	0.43
1:1:785:G:N2	18:Q:89:ASP:O	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:912:G:N7	4:A:9:ARG:NH2	2.66	0.43
1:1:1125:U:C2	1:1:1126:G:C8	3.06	0.43
1:1:1874:A:C8	19:R:20:ARG:NH1	2.83	0.43
1:1:2169:G:OP2	1:1:2170:U:OP2	2.36	0.43
1:1:2418:G:C4	42:w:303:ARG:HD3	2.54	0.43
1:1:2905:U:H2'	1:1:2906:C:C6	2.53	0.43
1:1:2995:A:H3'	1:1:2996:U:H5''	2.01	0.43
2:3:8:G:N2	2:3:113:C:O2	2.45	0.43
5:B:262:TRP:HD1	16:O:64:PHE:O	2.02	0.43
6:C:16:THR:HG22	6:C:17:ALA:N	2.34	0.43
12:J:29:ARG:HH12	12:J:123:PHE:HD1	1.65	0.43
14:M:21:VAL:HB	14:M:63:VAL:HG22	2.00	0.43
14:M:128:ARG:O	14:M:132:LYS:HG2	2.18	0.43
15:N:139:HIS:O	15:N:143:ARG:HG3	2.19	0.43
18:Q:36:LEU:HD22	18:Q:40:THR:HG21	2.01	0.43
18:Q:155:MET:HA	18:Q:161:LYS:HB2	2.00	0.43
25:X:63:ILE:HD11	25:X:102:LEU:HD12	2.00	0.43
32:e:9:ILE:HG12	32:e:63:THR:HB	1.99	0.43
32:e:89:THR:HG22	32:e:117:ILE:HG12	2.01	0.43
42:w:210:MET:HE3	42:w:214:LEU:HD22	2.01	0.43
42:w:291:LEU:HD23	42:w:291:LEU:O	2.19	0.43
1:1:385:A:C2	1:1:386:A:C4	3.07	0.43
1:1:433:A:H2'	1:1:434:U:C6	2.54	0.43
1:1:679:U:O2'	1:1:788:C:O2	2.18	0.43
1:1:992:A:O2'	1:1:993:G:H5'	2.19	0.43
1:1:2849:C:H2'	1:1:2850:G:O4'	2.18	0.43
1:1:2955:U:OP2	1:1:2977:G:N1	2.23	0.43
2:3:35:C:O2'	7:D:156:GLY:HA3	2.18	0.43
4:A:36:GLU:HG3	4:A:91:GLY:HA2	2.01	0.43
6:C:339:LEU:HA	6:C:342:LYS:HB2	2.01	0.43
11:H:114:VAL:HB	11:H:124:ARG:HB2	2.01	0.43
42:w:318:PHE:CE1	42:w:342:ARG:HG2	2.54	0.43
43:y:163:PRO:HA	43:y:183:ALA:HB1	2.00	0.43
1:1:155:G:O4'	36:i:26:ILE:HD11	2.19	0.43
1:1:589:A:H1'	1:1:1337:A:H5''	2.01	0.43
1:1:818:C:N3	1:1:920:A:H5'	2.33	0.43
1:1:1218:U:H3	1:1:1287:A:N6	2.16	0.43
1:1:1693:C:O2'	1:1:1772:U:O2'	2.17	0.43
1:1:1887:A:C2	1:1:2391:G:H4'	2.54	0.43
1:1:2341:A:OP2	1:1:2341:A:C8	2.69	0.43
1:1:3242:G:C8	5:B:154:TYR:CE2	3.06	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:4:130:C:H2'	3:4:131:A:C8	2.50	0.43
10:G:156:ASP:OD2	10:G:183:LYS:HG2	2.19	0.43
36:i:50:LEU:HD21	36:i:93:ILE:HG21	2.01	0.43
1:1:97:U:OP2	13:L:13:HIS:CD2	2.71	0.43
1:1:352:A:C8	1:1:354:U:C2	3.06	0.43
1:1:1258:U:C2	1:1:1260:A:OP2	2.72	0.43
1:1:1602:A:H5''	19:R:38:ARG:HG3	2.01	0.43
1:1:1709:C:H2'	1:1:1710:C:C6	2.53	0.43
1:1:1954:G:H5''	1:1:1955:U:OP2	2.19	0.43
1:1:2146:C:H5''	4:A:203:ALA:HB1	2.01	0.43
1:1:2320:A:H2	41:p:16:VAL:HG12	1.83	0.43
1:1:2437:G:O2'	1:1:2438:A:P	2.77	0.43
5:B:70:ARG:HH12	43:y:55:GLY:HA3	1.84	0.43
6:C:110:ASN:HB3	15:N:202:TYR:CE1	2.54	0.43
11:H:41:ILE:HD13	11:H:71:VAL:HG22	2.01	0.43
12:J:94:ARG:C	12:J:96:PHE:H	2.27	0.43
15:N:160:GLU:HG2	15:N:161:ALA:N	2.34	0.43
16:O:88:VAL:HG12	16:O:89:SER:N	2.34	0.43
42:w:163:GLN:CG	42:w:169:ARG:CB	2.78	0.43
42:w:339:THR:HG22	42:w:354:TYR:HD1	1.84	0.43
43:y:170:GLN:NE2	43:y:183:ALA:HB2	2.34	0.43
43:y:213:PRO:O	43:y:217:VAL:HG23	2.19	0.43
1:1:19:U:H2'	1:1:20:A:C8	2.54	0.42
1:1:599:C:H2'	1:1:600:G:C8	2.54	0.42
1:1:684:G:H2'	1:1:685:G:C8	2.54	0.42
1:1:705:A:H62	28:a:74:ASN:HD21	1.65	0.42
1:1:998:A:H4'	2:3:103:A:C2	2.54	0.42
1:1:1306:G:O2'	1:1:1307:G:H2'	2.19	0.42
1:1:1332:A:H2'	1:1:1333:C:C6	2.54	0.42
1:1:1342:C:C2	1:1:1343:A:C8	3.07	0.42
1:1:1858:A:O2'	1:1:1859:A:OP2	2.37	0.42
1:1:2529:A:P	10:G:248:LYS:NZ	2.92	0.42
1:1:3047:U:O2'	1:1:3048:A:H5'	2.19	0.42
1:1:3059:G:H2'	1:1:3060:C:C6	2.54	0.42
1:1:3304:U:OP2	1:1:3377:G:C4	2.72	0.42
1:1:3318:G:OP2	1:1:3318:G:C8	2.72	0.42
5:B:385:LYS:HG3	5:B:386:ASP:N	2.34	0.42
10:G:150:LEU:HD23	10:G:151:VAL:N	2.34	0.42
12:J:29:ARG:HH11	12:J:123:PHE:HE1	1.67	0.42
13:L:103:ASN:HB3	36:i:20:MET:SD	2.58	0.42
18:Q:70:ALA:O	18:Q:73:GLN:HB3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:S:155:ARG:CD	20:S:172:TYR:HD1	2.31	0.42
36:i:58:ILE:HD13	36:i:98:ARG:NH2	2.34	0.42
42:w:335:LEU:HD11	42:w:356:ARG:NH1	2.34	0.42
43:y:112:ASP:HB2	43:y:156:ASN:HD21	1.83	0.42
1:1:433:A:H2'	1:1:434:U:H6	1.84	0.42
1:1:520:U:N3	6:C:347:THR:OG1	2.33	0.42
1:1:873:C:H3'	1:1:874:U:H4'	2.01	0.42
1:1:1191:U:H3	1:1:3105:U:H5''	1.84	0.42
1:1:1252:A:H2'	1:1:1253:U:C5	2.54	0.42
1:1:1352:A:H4'	1:1:1353:U:OP1	2.18	0.42
1:1:2525:G:H4'	1:1:2526:C:OP2	2.20	0.42
1:1:2737:C:H4'	21:T:68:THR:OG1	2.19	0.42
1:1:2908:G:HO2'	1:1:3106:A:HO2'	1.64	0.42
5:B:106:TRP:HB2	5:B:133:TYR:CE2	2.53	0.42
5:B:283:TYR:CG	5:B:356:LEU:HD21	2.54	0.42
5:B:288:GLY:HA2	5:B:319:ASN:C	2.43	0.42
5:B:296:THR:H	5:B:299:ASP:HB3	1.84	0.42
7:D:110:LEU:HD13	7:D:171:LEU:HD23	2.01	0.42
11:H:18:VAL:HG21	11:H:53:ILE:HD11	2.01	0.42
23:V:17:LEU:HD21	23:V:98:ASN:CG	2.44	0.42
27:Z:48:ARG:HH12	27:Z:69:LYS:HD2	1.83	0.42
28:a:77:LYS:C	28:a:79:TRP:N	2.73	0.42
32:e:19:ARG:HD2	32:e:28:VAL:CG1	2.49	0.42
32:e:121:ASN:N	32:e:122:PRO:HD3	2.35	0.42
35:h:94:LYS:HB3	35:h:94:LYS:HE3	1.83	0.42
1:1:290:G:O2'	15:N:70:ASN:OD1	2.17	0.42
1:1:384:A:C2	1:1:385:A:C4	3.08	0.42
1:1:798:G:H2'	1:1:799:G:O4'	2.20	0.42
1:1:993:G:N2	1:1:1057:A:N1	2.67	0.42
1:1:1148:G:N1	1:1:1149:G:C5	2.87	0.42
1:1:1217:A:C6	1:1:1218:U:C4	3.06	0.42
1:1:1792:C:HO2'	1:1:1794:G:H8	1.64	0.42
1:1:1946:A:H2'	1:1:1947:G:O4'	2.20	0.42
1:1:3350:C:O2'	1:1:3351:U:OP1	2.37	0.42
2:3:64:A:P	7:D:289:LYS:NZ	2.91	0.42
5:B:216:ASP:HB2	5:B:339:ARG:HB3	2.01	0.42
5:B:307:PRO:HD3	5:B:311:PHE:CE2	2.53	0.42
6:C:5:GLN:HA	6:C:20:LEU:O	2.19	0.42
7:D:52:VAL:HG13	7:D:54:ARG:NH1	2.35	0.42
8:E:40:LEU:CD1	8:E:54:TYR:HB2	2.47	0.42
15:N:191:TRP:CD1	15:N:195:ASN:HD21	2.37	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:U:39:ASP:O	22:U:47:VAL:HB	2.18	0.42
23:V:54:LEU:HD21	23:V:119:GLY:HA3	2.01	0.42
27:Z:64:LYS:HD3	27:Z:67:LYS:NZ	2.34	0.42
36:i:26:ILE:O	36:i:29:LYS:HB2	2.19	0.42
36:i:54:GLU:HB3	36:i:90:MET:HE3	2.01	0.42
37:j:14:LYS:HD2	39:l:51:ILE:HD11	2.00	0.42
42:w:193:ALA:N	42:w:196:GLY:O	2.33	0.42
1:1:39:A:H5''	28:a:35:ALA:CB	2.50	0.42
1:1:589:A:H8	1:1:590:G:C8	2.37	0.42
1:1:1143:A:H4'	1:1:1144:U:OP2	2.19	0.42
1:1:1144:U:C4	1:1:1366:A:C2	3.08	0.42
1:1:3022:G:N2	1:1:3032:A:OP2	2.45	0.42
3:4:58:G:O6	37:j:63:ARG:NH2	2.51	0.42
3:4:106:C:C5'	3:4:108:C:OP2	2.66	0.42
7:D:146:LEU:CD1	7:D:163:LEU:HD12	2.49	0.42
20:S:13:ARG:HA	20:S:13:ARG:HD2	1.68	0.42
32:e:63:THR:HA	32:e:66:LEU:HD12	2.01	0.42
34:g:20:ILE:HD11	34:g:34:HIS:CE1	2.55	0.42
1:1:62:A:H5''	15:N:164:LEU:HD21	2.01	0.42
1:1:116:A:H62	1:1:153:U:H1'	1.85	0.42
1:1:280:U:O2	1:1:282:G:H3'	2.20	0.42
1:1:591:G:N2	1:1:612:U:OP1	2.38	0.42
1:1:664:U:O2'	1:1:665:A:H5'	2.19	0.42
1:1:915:A:H2'	1:1:915:A:N3	2.34	0.42
1:1:943:U:H3'	28:a:13:GLY:HA2	2.00	0.42
1:1:974:G:C2	1:1:975:C:C6	3.08	0.42
1:1:1110:U:C2	1:1:1111:U:C5	3.07	0.42
1:1:1541:G:H22	1:1:1555:U:H2'	1.84	0.42
1:1:1579:C:H5'	1:1:1649:U:H5''	2.02	0.42
1:1:1795:U:H2'	4:A:50:HIS:CD2	2.54	0.42
1:1:1914:G:N2	19:R:81:ARG:O	2.40	0.42
1:1:2418:G:H5''	1:1:2606:G:N2	2.35	0.42
1:1:2617:U:C5	1:1:2621:G:OP2	2.72	0.42
6:C:338:LYS:HA	6:C:338:LYS:HD3	1.82	0.42
8:E:68:PRO:HB3	8:E:142:ASP:OD1	2.19	0.42
12:J:83:GLY:HA2	12:J:112:LEU:HD22	2.02	0.42
13:L:59:ARG:HD2	13:L:66:ASN:O	2.19	0.42
17:P:128:ARG:HH11	44:z:413:ILE:HG12	1.84	0.42
21:T:90:ASN:O	21:T:91:LEU:HD23	2.20	0.42
24:W:50:ALA:HA	24:W:55:PHE:CG	2.55	0.42
25:X:103:TYR:HB3	25:X:135:ILE:CD1	2.45	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:c:24:THR:HG22	30:c:91:SER:HB3	2.00	0.42
36:i:51:SER:O	36:i:54:GLU:N	2.52	0.42
37:j:68:LYS:HD2	37:j:69:HIS:CE1	2.55	0.42
43:y:68:ARG:NH2	43:y:112:ASP:O	2.52	0.42
1:1:116:A:N6	1:1:153:U:H1'	2.34	0.42
1:1:914:A:H2	4:A:208:ASP:CG	2.27	0.42
1:1:1260:A:O2'	1:1:1279:C:O2	2.28	0.42
1:1:1305:U:C2	5:B:257:PRO:HG3	2.54	0.42
1:1:2745:G:C2	1:1:2748:A:OP2	2.72	0.42
1:1:2971:A:OP1	42:w:226:GLU:OE2	2.38	0.42
1:1:3384:U:H2'	1:1:3385:U:C6	2.54	0.42
3:4:39:G:O2'	3:4:105:A:N1	2.42	0.42
4:A:144:ASN:OD1	4:A:144:ASN:N	2.53	0.42
5:B:58:ARG:O	5:B:71:GLU:HA	2.20	0.42
5:B:283:TYR:HE1	5:B:354:VAL:HG11	1.83	0.42
6:C:154:THR:OG1	6:C:252:GLU:HB3	2.19	0.42
6:C:234:ASN:OD1	6:C:236:LEU:N	2.51	0.42
11:H:24:ILE:HD11	11:H:39:LYS:HE2	2.02	0.42
11:H:69:ARG:NH1	11:H:72:LYS:HZ2	2.12	0.42
12:J:18:VAL:HG22	12:J:70:THR:HG22	2.00	0.42
1:1:784:A:C6	18:Q:93:ILE:HG22	2.55	0.42
1:1:1057:A:OP1	9:F:98:LYS:HE3	2.19	0.42
1:1:1103:A:H2'	1:1:1103:A:N3	2.35	0.42
1:1:1250:G:H2'	1:1:1251:A:C8	2.55	0.42
1:1:1814:A:H4'	1:1:1815:U:C5'	2.44	0.42
1:1:2883:U:H6	1:1:2883:U:O5'	2.02	0.42
1:1:3121:U:H3	1:1:3123:A:H62	1.68	0.42
2:3:1:G:C4	7:D:266:ALA:HA	2.54	0.42
2:3:49:G:OP2	7:D:91:GLY:HA2	2.19	0.42
2:3:96:U:H2'	2:3:97:A:C8	2.52	0.42
7:D:58:LYS:HE3	7:D:93:THR:OG1	2.19	0.42
10:G:134:TYR:CD2	10:G:190:VAL:HG23	2.55	0.42
12:J:63:GLU:O	12:J:63:GLU:HG2	2.19	0.42
18:Q:66:ARG:NH2	18:Q:143:PRO:HD3	2.34	0.42
18:Q:83:VAL:O	18:Q:103:ALA:HA	2.20	0.42
18:Q:150:VAL:HA	18:Q:153:PHE:CD2	2.54	0.42
1:1:381:U:H2'	1:1:382:U:C6	2.55	0.42
1:1:827:A:H2'	1:1:828:A:C8	2.51	0.42
1:1:849:C:H2'	1:1:850:U:C6	2.54	0.42
1:1:900:G:C6	1:1:901:G:C6	3.07	0.42
1:1:1279:C:H2'	1:1:1280:C:O4'	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1528:G:O2'	1:1:1588:A:N3	2.49	0.42
1:1:1636:U:H5''	27:Z:73:LYS:HE3	2.01	0.42
1:1:2668:U:H2'	1:1:2669:G:C8	2.54	0.42
1:1:2944:U:O2'	1:1:2947:G:N7	2.47	0.42
1:1:3214:U:OP2	14:M:128:ARG:CZ	2.67	0.42
1:1:3243:A:C8	16:O:110:PRO:HD3	2.55	0.42
2:3:42:A:C5	2:3:43:U:C4	3.08	0.42
6:C:177:ASP:OD2	6:C:204:GLY:HA2	2.20	0.42
8:E:66:SER:HB3	8:E:76:LEU:HD23	2.01	0.42
11:H:171:ASP:OD2	11:H:173:ARG:HG2	2.20	0.42
16:O:188:SER:O	16:O:192:LYS:HG2	2.19	0.42
27:Z:10:VAL:HG11	27:Z:129:TRP:HZ3	1.84	0.42
1:1:971:G:C6	1:1:972:A:C5	3.08	0.42
1:1:1246:G:N3	1:1:1264:G:O2'	2.53	0.42
1:1:1447:G:OP1	17:P:65:SER:OG	2.15	0.42
1:1:1900:A:H1'	1:1:1902:G:N7	2.35	0.42
1:1:2308:C:C2	1:1:2971:A:N6	2.84	0.42
1:1:2528:G:N2	1:1:2582:C:O2	2.51	0.42
1:1:2733:A:H2'	1:1:2734:A:O4'	2.20	0.42
1:1:3067:C:H3'	19:R:62:ARG:NH1	2.35	0.42
1:1:3253:G:C2	1:1:3254:G:C8	3.07	0.42
1:1:3269:U:H4'	1:1:3270:U:O5'	2.19	0.42
1:1:3324:C:OP1	31:d:19:ARG:NH1	2.45	0.42
2:3:28:C:OP1	12:J:137:ARG:NH1	2.51	0.42
6:C:65:TRP:CE3	6:C:69:ARG:NH1	2.88	0.42
8:E:78:ARG:NH1	8:E:106:PHE:CB	2.82	0.42
11:H:139:ASN:OD1	11:H:140:VAL:HG23	2.19	0.42
12:J:54:VAL:HG11	12:J:57:PHE:CD2	2.55	0.42
13:L:113:VAL:O	13:L:117:LYS:HG2	2.20	0.42
15:N:74:PRO:O	15:N:75:VAL:O	2.38	0.42
32:e:10:VAL:HG12	32:e:11:LYS:N	2.35	0.42
37:j:16:HIS:HD2	37:j:26:SER:O	2.03	0.42
1:1:382:U:C2	1:1:388:G:N2	2.88	0.42
1:1:2147:A:H2'	1:1:2148:U:O4'	2.20	0.42
1:1:2340:U:OP1	5:B:236:LYS:HD2	2.20	0.42
1:1:2830:G:H1	1:1:2858:U:H3	1.66	0.42
4:A:242:ARG:HH12	4:A:246:LEU:HD23	1.85	0.42
6:C:302:ALA:HB2	18:Q:39:ARG:NH1	2.34	0.42
7:D:163:LEU:HD21	7:D:175:HIS:CG	2.55	0.42
9:F:40:LYS:O	9:F:44:ILE:HG13	2.19	0.42
9:F:110:ARG:HH11	18:Q:3:ILE:HG13	1.80	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:G:75:ILE:C	10:G:77:GLN:H	2.27	0.42
11:H:18:VAL:CG2	11:H:53:ILE:HD11	2.49	0.42
34:g:74:ARG:NH2	34:g:82:ALA:HB2	2.34	0.42
35:h:85:THR:O	35:h:88:LEU:N	2.47	0.42
39:l:44:TRP:CH2	39:l:45:ARG:HD3	2.55	0.42
42:w:320:VAL:HG12	42:w:367:ASP:O	2.20	0.42
1:1:199:A:C4	1:1:201:A:C8	3.08	0.41
1:1:297:G:H2'	36:i:41:ARG:NH1	2.35	0.41
1:1:423:A:N6	1:1:424:G:C6	2.88	0.41
1:1:674:G:C2	1:1:789:A:C2	3.07	0.41
1:1:1252:A:C8	1:1:1253:U:H5	2.37	0.41
1:1:1269:U:N3	1:1:1271:A:H5''	2.35	0.41
1:1:1704:A:N6	1:1:1741:A:N1	2.68	0.41
1:1:1760:A:OP2	1:1:1760:A:H8	2.03	0.41
1:1:2113:A:OP2	1:1:2113:A:N9	2.53	0.41
1:1:2668:U:O4	1:1:2687:G:N2	2.53	0.41
1:1:2991:A:C4'	5:B:21:ARG:HH12	2.33	0.41
6:C:77:VAL:O	6:C:86:GLY:N	2.53	0.41
10:G:97:TYR:O	10:G:131:ALA:HA	2.20	0.41
12:J:137:ARG:NH1	12:J:141:ARG:HD3	2.35	0.41
18:Q:86:THR:HA	18:Q:105:ARG:O	2.20	0.41
23:V:84:SER:HB3	23:V:94:TYR:CD2	2.55	0.41
27:Z:89:VAL:CG1	27:Z:93:LYS:HD3	2.47	0.41
43:y:74:THR:OG1	43:y:98:GLU:HA	2.20	0.41
1:1:541:U:H3	1:1:550:A:N6	2.17	0.41
1:1:1111:U:H2'	1:1:1112:A:H8	1.85	0.41
1:1:1466:G:H5''	1:1:1467:A:OP2	2.21	0.41
1:1:2781:U:H2'	1:1:2782:U:C6	2.55	0.41
2:3:38:U:C2	2:3:40:C:OP2	2.73	0.41
3:4:141:C:O2	15:N:112:ASN:ND2	2.52	0.41
4:A:79:ASN:ND2	4:A:165:VAL:HG22	2.35	0.41
5:B:2:SER:OG	5:B:3:HIS:N	2.49	0.41
5:B:56:ILE:HD11	5:B:323:MET:HE1	2.02	0.41
6:C:71:VAL:HG21	6:C:76:ARG:HH12	1.85	0.41
6:C:157:GLU:OE2	6:C:210:ALA:N	2.52	0.41
7:D:20:PHE:O	7:D:24:ARG:NH2	2.53	0.41
8:E:47:PHE:O	8:E:50:LYS:HG2	2.20	0.41
14:M:21:VAL:HB	14:M:63:VAL:CG2	2.50	0.41
18:Q:96:PHE:CG	18:Q:97:PRO:HD2	2.55	0.41
27:Z:23:VAL:HG12	27:Z:45:GLY:HA3	2.03	0.41
39:l:29:LEU:HD11	44:z:393:GLN:HE22	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:y:1:MET:HB3	43:y:224:LEU:HG	2.01	0.41
1:1:92:G:P	40:o:46:LYS:HZ2	2.43	0.41
1:1:246:U:O2'	1:1:247:C:H5'	2.20	0.41
1:1:620:U:H5'	17:P:167:ARG:CZ	2.51	0.41
1:1:885:U:C2	1:1:886:C:C5	3.08	0.41
1:1:1230:G:H1	1:1:1279:C:H42	1.67	0.41
1:1:1261:G:OP2	1:1:1261:G:C2	2.74	0.41
2:3:9:C:H5	2:3:10:C:C2	2.38	0.41
2:3:30:G:N2	2:3:48:U:C2	2.88	0.41
5:B:313:HIS:CB	5:B:332:ARG:HD2	2.50	0.41
15:N:38:ARG:NH1	15:N:38:ARG:HG3	2.34	0.41
31:d:55:LEU:HD13	31:d:93:VAL:HG12	2.02	0.41
40:o:29:LYS:HZ3	42:w:389:ILE:HD13	1.85	0.41
1:1:73:C:C2	13:L:59:ARG:NH1	2.88	0.41
1:1:239:G:H2'	1:1:240:U:C2	2.55	0.41
1:1:785:G:N1	18:Q:90:ASP:HA	2.35	0.41
1:1:2145:A:H5'	1:1:2959:C:H5'	2.02	0.41
1:1:2617:U:H5	1:1:2621:G:OP2	2.02	0.41
3:4:153:U:H2'	3:4:154:C:C6	2.56	0.41
5:B:77:THR:HG23	5:B:326:GLY:O	2.20	0.41
7:D:144:VAL:HG13	7:D:173:VAL:HG22	2.03	0.41
7:D:204:VAL:HB	7:D:236:LEU:HD21	2.01	0.41
8:E:51:ARG:NH1	8:E:158:TYR:CE1	2.88	0.41
8:E:64:LEU:HD21	8:E:76:LEU:HD22	2.03	0.41
8:E:105:TYR:OH	8:E:134:ARG:HG2	2.20	0.41
9:F:145:ARG:O	9:F:149:TYR:HD2	2.03	0.41
9:F:153:PHE:CD1	9:F:162:PRO:HA	2.55	0.41
9:F:161:VAL:HG12	9:F:162:PRO:O	2.20	0.41
9:F:221:LYS:O	9:F:227:GLY:HA3	2.20	0.41
10:G:190:VAL:HG22	10:G:192:GLN:HG2	2.00	0.41
12:J:17:LEU:HD13	12:J:129:VAL:HG22	2.02	0.41
14:M:14:LEU:H	14:M:19:ARG:HH11	1.67	0.41
16:O:55:HIS:ND1	16:O:58:LEU:HD23	2.35	0.41
18:Q:175:ALA:HB3	28:a:53:PHE:O	2.19	0.41
21:T:138:SER:O	21:T:139:ARG:HG3	2.21	0.41
30:c:74:ASN:ND2	30:c:86:ARG:HD3	2.34	0.41
33:f:73:ARG:HG3	33:f:82:ARG:HD2	2.03	0.41
41:p:58:SER:C	41:p:61:LYS:HZ1	2.10	0.41
43:y:52:THR:OG1	43:y:80:GLU:OE2	2.34	0.41
43:y:62:MET:HB3	43:y:73:PRO:HG3	2.02	0.41
1:1:2548:C:P	4:A:93:LYS:HZ1	2.43	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2931:C:OP1	23:V:59:MET:HE3	2.20	0.41
1:1:3346:U:H2'	1:1:3347:A:O4'	2.21	0.41
2:3:13:A:C8	2:3:112:G:C4	3.09	0.41
5:B:92:TYR:HB2	5:B:157:VAL:HG23	2.02	0.41
7:D:184:ASP:HB2	7:D:189:GLU:HB2	2.02	0.41
9:F:160:ARG:NH2	9:F:206:LYS:HD3	2.35	0.41
10:G:75:ILE:HG22	10:G:76:ALA:H	1.85	0.41
13:L:159:VAL:HG13	28:a:144:VAL:HG22	2.02	0.41
14:M:127:LYS:HB2	16:O:190:VAL:HG11	2.02	0.41
29:b:54:LEU:HB3	29:b:58:LYS:HG2	2.02	0.41
42:w:286:MET:HE2	42:w:333:ARG:NH1	2.34	0.41
1:1:176:G:H2'	1:1:177:U:O4'	2.20	0.41
1:1:391:A:H2'	1:1:392:G:O4'	2.20	0.41
1:1:929:A:O2'	37:j:49:TRP:O	2.39	0.41
1:1:1155:C:C6	1:1:1156:C:H5	2.39	0.41
1:1:1334:U:H5''	9:F:206:LYS:HB3	2.01	0.41
1:1:1578:C:H3'	1:1:1579:C:C6	2.56	0.41
1:1:1949:G:H1	1:1:2097:U:H3	1.68	0.41
1:1:2642:A:H2'	1:1:2643:A:C8	2.55	0.41
3:4:122:U:H2'	3:4:123:G:C8	2.56	0.41
4:A:45:VAL:HB	4:A:61:VAL:HG22	2.03	0.41
5:B:10:ARG:NH2	5:B:263:SER:O	2.54	0.41
6:C:23:PRO:HD2	6:C:26:PHE:CD2	2.56	0.41
6:C:168:ALA:O	6:C:172:VAL:HG23	2.20	0.41
8:E:78:ARG:HH11	8:E:106:PHE:HB2	1.84	0.41
13:L:162:ASN:HD21	13:L:164:GLU:HB2	1.86	0.41
19:R:81:ARG:HG2	19:R:88:ARG:CZ	2.50	0.41
36:i:9:ILE:HA	36:i:13:LYS:HD3	2.01	0.41
42:w:338:ILE:HG22	42:w:340:VAL:HG23	2.03	0.41
43:y:173:LEU:HA	43:y:176:LEU:HD13	2.01	0.41
44:z:380:ALA:CB	44:z:383:ARG:HH11	2.34	0.41
1:1:221:A:O2'	1:1:223:U:OP2	2.37	0.41
1:1:406:G:H1'	3:4:16:G:H22	1.84	0.41
1:1:880:G:C8	17:P:132:ALA:HA	2.55	0.41
1:1:909:G:C4	1:1:910:G:C8	3.09	0.41
1:1:949:C:OP1	18:Q:10:HIS:ND1	2.53	0.41
1:1:1638:A:N1	1:1:1736:G:O2'	2.49	0.41
1:1:2227:C:O2'	1:1:2228:A:OP1	2.30	0.41
1:1:2366:C:P	5:B:259:HIS:HE2	2.44	0.41
1:1:3277:U:H2'	17:P:175:ARG:NH2	2.36	0.41
1:1:3293:U:OP2	1:1:3293:U:H6	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:3:90:U:H2'	2:3:91:G:O4'	2.21	0.41
6:C:112:LYS:NZ	15:N:203:ARG:O	2.51	0.41
7:D:45:ASN:OD1	21:T:33:VAL:HG21	2.21	0.41
11:H:17:THR:OG1	11:H:28:VAL:HB	2.20	0.41
11:H:43:VAL:HG11	11:H:71:VAL:HG21	2.02	0.41
11:H:163:GLN:HB3	11:H:166:ARG:HH12	1.86	0.41
24:W:50:ALA:HA	24:W:55:PHE:CE1	2.56	0.41
30:c:57:GLU:OE2	30:c:69:TYR:OH	2.34	0.41
31:d:56:ASN:O	31:d:60:TRP:HD1	2.03	0.41
34:g:5:VAL:HG21	34:g:32:ALA:N	2.35	0.41
1:1:423:A:C6	1:1:424:G:C5	3.09	0.41
1:1:437:G:H22	1:1:622:A:H61	1.67	0.41
1:1:715:A:O2'	1:1:752:C:O2'	2.34	0.41
1:1:826:G:C2	1:1:900:G:C6	3.09	0.41
1:1:958:C:C5	1:1:960:U:H1'	2.55	0.41
1:1:1779:C:O5'	19:R:97:ARG:NH2	2.54	0.41
1:1:2353:G:C6	1:1:2354:C:N3	2.89	0.41
1:1:2418:G:H5''	1:1:2606:G:H22	1.84	0.41
1:1:2786:G:H5''	40:o:38:GLN:HB2	2.02	0.41
1:1:2847:A:OP2	1:1:2848:G:OP2	2.38	0.41
2:3:74:C:H2'	2:3:75:G:C8	2.56	0.41
5:B:48:GLY:O	5:B:335:ILE:HD12	2.20	0.41
5:B:283:TYR:CD1	5:B:354:VAL:HG21	2.51	0.41
6:C:265:GLU:OE1	6:C:265:GLU:N	2.40	0.41
11:H:53:ILE:HG22	11:H:54:LYS:N	2.36	0.41
13:L:46:ILE:O	13:L:47:ALA:HB3	2.20	0.41
13:L:93:ILE:HG23	13:L:93:ILE:HD12	1.85	0.41
16:O:113:ASP:OD1	16:O:114:LYS:N	2.53	0.41
19:R:130:ASN:C	19:R:132:PHE:H	2.27	0.41
20:S:155:ARG:HD2	20:S:172:TYR:CD1	2.54	0.41
28:a:47:LYS:HG3	28:a:47:LYS:O	2.21	0.41
38:k:42:LYS:HG2	38:k:55:VAL:HG22	2.02	0.41
39:l:24:PRO:HD2	39:l:27:ILE:HD12	2.03	0.41
40:o:96:GLU:CD	42:w:345:ASP:HA	2.46	0.41
42:w:259:LEU:O	42:w:272:GLN:NE2	2.53	0.41
1:1:199:A:C6	1:1:219:A:N6	2.89	0.41
1:1:502:U:O3'	8:E:26:ARG:HD2	2.21	0.41
1:1:652:G:N1	1:1:2361:A:H1'	2.36	0.41
1:1:802:C:H2'	1:1:803:C:H6	1.85	0.41
1:1:822:G:O6	1:1:904:A:C6	2.73	0.41
1:1:860:G:P	4:A:181:LYS:HZ3	2.42	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:913:A:O2'	1:1:2146:C:O2	2.37	0.41
1:1:1240:A:OP2	1:1:1240:A:C8	2.74	0.41
1:1:1330:A:N7	1:1:1332:A:C6	2.88	0.41
1:1:1353:U:O2	8:E:10:TYR:N	2.38	0.41
1:1:1471:U:H2'	1:1:1472:U:H6	1.86	0.41
1:1:1495:U:H1'	39:I:44:TRP:CZ2	2.55	0.41
1:1:1721:U:C5	19:R:103:ARG:NH1	2.88	0.41
1:1:1737:U:H2'	1:1:1738:C:O4'	2.21	0.41
1:1:1764:U:H3'	1:1:1765:U:C5'	2.51	0.41
1:1:2208:A:H8	1:1:2208:A:OP2	2.04	0.41
1:1:2218:G:C6	1:1:2219:A:C6	3.09	0.41
1:1:2252:A:H2'	1:1:2253:G:H8	1.86	0.41
1:1:2268:U:H3'	1:1:2269:U:H5'	2.03	0.41
1:1:2314:U:H6	1:1:2314:U:H2'	1.73	0.41
1:1:2548:C:P	4:A:93:LYS:NZ	2.94	0.41
1:1:2660:G:H5''	1:1:2750:U:O2'	2.20	0.41
1:1:2712:U:H4'	1:1:2743:A:O3'	2.21	0.41
1:1:2807:U:H5''	1:1:2969:A:OP1	2.21	0.41
1:1:2823:G:H2'	1:1:2824:G:H8	1.85	0.41
1:1:2880:U:OP1	23:V:47:ASN:ND2	2.46	0.41
1:1:3156:U:HO2'	1:1:3157:U:P	2.44	0.41
1:1:3288:G:N3	1:1:3289:G:C8	2.89	0.41
3:4:6:U:H2'	3:4:7:U:C6	2.56	0.41
3:4:115:C:H2'	3:4:116:G:O4'	2.21	0.41
4:A:44:ILE:O	4:A:61:VAL:HA	2.21	0.41
5:B:147:GLU:OE1	5:B:150:ARG:NH1	2.54	0.41
5:B:152:LYS:HG2	5:B:192:VAL:HG11	2.01	0.41
6:C:25:VAL:HG22	6:C:262:TRP:HB2	2.03	0.41
6:C:52:VAL:HG11	6:C:99:MET:HE3	2.03	0.41
7:D:259:LYS:O	7:D:260:PHE:HB2	2.21	0.41
9:F:74:SER:HB3	21:T:141:VAL:O	2.21	0.41
11:H:99:ILE:HG22	11:H:101:VAL:HG23	2.03	0.41
12:J:32:ARG:HD2	12:J:120:ILE:HA	2.03	0.41
13:L:69:VAL:HG12	13:L:149:GLN:OE1	2.21	0.41
14:M:65:LEU:HB2	20:S:172:TYR:CE2	2.56	0.41
15:N:9:GLU:HB3	36:I:44:VAL:HG21	2.03	0.41
16:O:55:HIS:HD1	16:O:58:LEU:HD23	1.85	0.41
18:Q:64:VAL:HG12	18:Q:90:ASP:N	2.35	0.41
19:R:99:LEU:HD21	19:R:103:ARG:NH2	2.28	0.41
20:S:11:GLY:HA3	20:S:57:GLU:O	2.21	0.41
23:V:27:ASP:N	23:V:27:ASP:OD1	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:a:71:PRO:HB2	28:a:109:TYR:HA	2.01	0.41
40:o:25:VAL:HG22	40:o:72:LEU:HD23	2.01	0.41
42:w:272:GLN:HE21	42:w:387:LEU:CD2	2.34	0.41
42:w:278:LYS:HG2	42:w:284:GLN:OE1	2.21	0.41
1:1:31:C:H5	15:N:188:ARG:NH2	2.19	0.41
1:1:177:U:H2'	1:1:178:U:O4'	2.21	0.41
1:1:194:U:C2	1:1:195:U:C5	3.08	0.41
1:1:269:G:H5''	15:N:14:LYS:HE2	2.03	0.41
1:1:678:G:O2'	1:1:787:G:N2	2.54	0.41
1:1:709:A:P	18:Q:179:ARG:HH22	2.44	0.41
1:1:1062:A:N3	21:T:130:ARG:NH2	2.62	0.41
1:1:1287:A:C5	1:1:1288:U:C4	3.09	0.41
1:1:1493:G:C6	39:l:13:MET:HE2	2.55	0.41
1:1:2565:U:H2'	1:1:2566:C:C6	2.56	0.41
1:1:2569:A:H8	1:1:2569:A:OP2	2.04	0.41
1:1:2812:C:H2'	1:1:2813:A:C8	2.56	0.41
1:1:2926:A:H2'	1:1:2927:C:C6	2.55	0.41
2:3:4:U:H2'	2:3:5:G:C8	2.56	0.41
2:3:77:G:N2	2:3:78:U:O4	2.25	0.41
5:B:33:PRO:HB2	5:B:184:ASN:HD21	1.86	0.41
7:D:91:GLY:O	7:D:94:ASN:ND2	2.54	0.41
27:Z:14:VAL:HG12	27:Z:79:HIS:C	2.46	0.41
36:i:58:ILE:HD13	36:i:98:ARG:HH22	1.85	0.41
42:w:276:CYS:O	42:w:276:CYS:SG	2.78	0.41
42:w:359:LEU:HD23	42:w:359:LEU:O	2.21	0.41
43:y:14:GLY:HA2	43:y:198:VAL:HG13	2.03	0.41
1:1:16:A:O3'	25:X:45:LYS:HG2	2.21	0.40
1:1:245:U:H2'	1:1:246:U:C6	2.56	0.40
1:1:869:G:H1'	1:1:891:G:N2	2.36	0.40
1:1:895:A:N7	1:1:897:U:C2	2.90	0.40
1:1:1779:C:H41	1:1:2102:U:P	2.44	0.40
1:1:1801:U:H2'	1:1:1802:C:C6	2.56	0.40
1:1:3215:A:O5'	14:M:121:MET:HE1	2.20	0.40
1:1:3311:C:H2'	1:1:3312:U:O4'	2.21	0.40
3:4:75:G:C8	39:l:30:ARG:HG2	2.57	0.40
5:B:102:LEU:HD12	5:B:103:THR:N	2.36	0.40
7:D:279:LYS:HD2	7:D:282:ARG:HH21	1.86	0.40
8:E:132:ALA:O	8:E:136:GLU:HG2	2.21	0.40
9:F:75:TYR:HB2	21:T:141:VAL:CG2	2.51	0.40
10:G:160:ILE:HG22	10:G:164:VAL:HG13	2.03	0.40
12:J:39:GLN:HE21	12:J:114:ILE:HG23	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:L:93:ILE:HG22	13:L:93:ILE:O	2.21	0.40
18:Q:158:HIS:H	18:Q:186:VAL:HG11	1.86	0.40
19:R:67:ALA:O	19:R:71:ARG:HG3	2.21	0.40
19:R:106:LEU:HB3	19:R:120:TYR:CE1	2.56	0.40
23:V:45:ARG:HB3	23:V:48:ARG:CD	2.51	0.40
23:V:123:ALA:O	23:V:130:ALA:HB2	2.22	0.40
26:Y:83:ASP:OD1	26:Y:84:LYS:N	2.49	0.40
31:d:15:ASN:O	31:d:19:ARG:NH1	2.49	0.40
33:f:103:TYR:HA	33:f:104:PRO:C	2.46	0.40
42:w:187:THR:HG22	42:w:188:ILE:N	2.36	0.40
42:w:240:TYR:HB2	42:w:242:PHE:CZ	2.56	0.40
43:y:166:SER:HB2	43:y:169:ASP:OD2	2.21	0.40
1:1:199:A:C5	1:1:201:A:C5	3.10	0.40
1:1:370:U:C4	1:1:376:G:O6	2.74	0.40
1:1:971:G:C6	1:1:972:A:C6	3.09	0.40
1:1:1440:G:OP2	44:z:419:ARG:NH1	2.52	0.40
1:1:1489:A:N6	1:1:1854:C:H42	2.19	0.40
1:1:2179:C:H4'	1:1:2180:G:OP2	2.20	0.40
1:1:2540:A:OP2	1:1:2540:A:C8	2.74	0.40
1:1:3272:C:OP2	8:E:78:ARG:CZ	2.68	0.40
3:4:155:A:H2'	3:4:156:U:O4'	2.21	0.40
9:F:163:LEU:C	9:F:165:ASP:H	2.29	0.40
10:G:34:PHE:CE1	10:G:42:PRO:HD3	2.56	0.40
13:L:105:ASN:OD1	13:L:106:GLN:N	2.54	0.40
20:S:76:GLY:HA2	20:S:93:GLU:HA	2.03	0.40
21:T:126:VAL:HG23	21:T:127:GLN:H	1.87	0.40
23:V:68:GLU:H	23:V:68:GLU:CD	2.27	0.40
34:g:10:ARG:O	34:g:12:PRO:HD3	2.21	0.40
35:h:73:LYS:HB3	35:h:73:LYS:HE2	1.85	0.40
40:o:95:GLY:O	40:o:96:GLU:HB2	2.21	0.40
44:z:406:LYS:O	44:z:409:ILE:N	2.55	0.40
1:1:274:G:H2'	1:1:275:U:O4'	2.21	0.40
1:1:565:U:H2'	1:1:566:G:H8	1.86	0.40
1:1:945:C:OP2	1:1:945:C:C6	2.74	0.40
1:1:1230:G:H2'	1:1:1231:A:H5'	2.04	0.40
1:1:1239:C:H1'	1:1:1250:G:H22	1.85	0.40
1:1:1304:A:H1'	1:1:2885:C:H1'	2.02	0.40
1:1:1481:A:C8	1:1:1483:G:C6	3.09	0.40
1:1:1543:G:OP1	15:N:35:VAL:HG23	2.21	0.40
1:1:1722:U:OP1	19:R:100:ARG:NH1	2.54	0.40
1:1:2548:C:OP2	4:A:93:LYS:NZ	2.45	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:3215:A:C5'	14:M:121:MET:HE1	2.52	0.40
2:3:117:A:H2'	2:3:118:A:O4'	2.21	0.40
3:4:29:U:H5''	13:L:27:ASP:HB3	2.03	0.40
5:B:57:VAL:HG13	5:B:71:GLU:HB3	2.03	0.40
7:D:269:SER:O	7:D:273:ARG:HG2	2.22	0.40
42:w:204:LYS:HD2	42:w:242:PHE:CD2	2.57	0.40
1:1:101:G:H2'	1:1:102:C:O4'	2.21	0.40
1:1:500:C:H2'	1:1:501:A:C8	2.57	0.40
1:1:672:A:C2	1:1:791:A:C2	3.10	0.40
1:1:715:A:OP1	28:a:133:LEU:HB2	2.22	0.40
1:1:743:C:H2'	1:1:744:A:O4'	2.22	0.40
1:1:839:C:H2'	1:1:840:C:C6	2.53	0.40
1:1:1617:G:H2'	1:1:1618:G:O4'	2.21	0.40
1:1:1859:A:C2	1:1:1860:G:N7	2.90	0.40
1:1:2703:A:C6	7:D:23:ARG:NH1	2.90	0.40
1:1:2923:U:H2'	1:1:2924:U:C6	2.57	0.40
1:1:3021:A:H4'	1:1:3022:G:OP1	2.21	0.40
1:1:3273:A:H5'	8:E:45:GLY:HA2	2.04	0.40
2:3:8:G:O6	2:3:9:C:N4	2.55	0.40
2:3:77:G:H3'	20:S:46:GLN:O	2.21	0.40
3:4:154:C:H5''	10:G:181:LYS:HB3	2.02	0.40
5:B:37:ARG:HD3	5:B:186:GLY:HA2	2.03	0.40
6:C:170:LYS:HE2	6:C:175:HIS:CE1	2.57	0.40
7:D:61:ILE:HG12	7:D:79:TYR:CE1	2.56	0.40
8:E:40:LEU:HB3	8:E:84:VAL:CG1	2.52	0.40
16:O:54:TYR:CD2	16:O:145:VAL:HG11	2.56	0.40
27:Z:4:PHE:O	27:Z:9:LYS:HG3	2.21	0.40
27:Z:26:VAL:HG12	27:Z:89:VAL:HG21	2.03	0.40
30:c:27:TYR:CD1	30:c:52:ARG:HD2	2.57	0.40
31:d:25:PHE:HD1	31:d:65:LYS:HB2	1.85	0.40
38:k:30:LYS:HD2	38:k:40:GLN:OE1	2.21	0.40
42:w:172:LEU:O	42:w:175:GLU:N	2.54	0.40
42:w:309:LEU:HG	42:w:379:TYR:CE1	2.57	0.40
1:1:532:A:O2'	1:1:533:A:H5'	2.22	0.40
1:1:653:A:C8	1:1:2360:C:N4	2.90	0.40
1:1:1258:U:O2	1:1:1261:G:N1	2.54	0.40
1:1:1321:G:H2'	1:1:1322:U:H6	1.87	0.40
1:1:1560:G:H1	1:1:1580:A:H61	1.66	0.40
1:1:1671:C:H2'	1:1:1672:U:O4'	2.21	0.40
1:1:2529:A:C2	1:1:2530:G:H1'	2.56	0.40
4:A:230:VAL:HG22	4:A:231:SER:N	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:F:26:VAL:HG23	9:F:27:ALA:H	1.86	0.40
12:J:91:LEU:HB3	12:J:95:ASN:HD22	1.87	0.40
28:a:47:LYS:HB2	28:a:47:LYS:HE3	1.89	0.40
28:a:67:HIS:CD2	28:a:67:HIS:H	2.40	0.40
42:w:165:VAL:HA	42:w:166:PRO:HD3	1.82	0.40
42:w:326:THR:HB	42:w:335:LEU:HD12	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	A	244/246 (99%)	236 (97%)	8 (3%)	0	100	100
5	B	384/387 (99%)	357 (93%)	25 (6%)	2 (0%)	24	54
6	C	359/361 (99%)	329 (92%)	29 (8%)	1 (0%)	36	64
7	D	294/297 (99%)	267 (91%)	24 (8%)	3 (1%)	12	39
8	E	152/176 (86%)	143 (94%)	6 (4%)	3 (2%)	6	23
9	F	220/244 (90%)	205 (93%)	15 (7%)	0	100	100
10	G	231/256 (90%)	208 (90%)	20 (9%)	3 (1%)	9	33
11	H	189/191 (99%)	174 (92%)	14 (7%)	1 (0%)	24	54
12	J	167/174 (96%)	144 (86%)	18 (11%)	5 (3%)	3	17
13	L	191/199 (96%)	172 (90%)	16 (8%)	3 (2%)	7	28
14	M	134/138 (97%)	123 (92%)	9 (7%)	2 (2%)	8	30
15	N	201/204 (98%)	189 (94%)	10 (5%)	2 (1%)	12	39
16	O	195/199 (98%)	193 (99%)	2 (1%)	0	100	100
17	P	181/184 (98%)	178 (98%)	3 (2%)	0	100	100
18	Q	183/186 (98%)	172 (94%)	11 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	R	154/189 (82%)	147 (96%)	6 (4%)	1 (1%)	21	49
20	S	170/172 (99%)	157 (92%)	10 (6%)	3 (2%)	6	26
21	T	157/160 (98%)	148 (94%)	8 (5%)	1 (1%)	21	49
22	U	98/121 (81%)	86 (88%)	11 (11%)	1 (1%)	12	39
23	V	134/137 (98%)	130 (97%)	4 (3%)	0	100	100
24	W	62/155 (40%)	60 (97%)	2 (3%)	0	100	100
25	X	119/142 (84%)	113 (95%)	6 (5%)	0	100	100
26	Y	124/127 (98%)	115 (93%)	9 (7%)	0	100	100
27	Z	133/136 (98%)	124 (93%)	6 (4%)	3 (2%)	5	21
28	a	146/149 (98%)	131 (90%)	11 (8%)	4 (3%)	4	18
29	b	56/59 (95%)	51 (91%)	5 (9%)	0	100	100
30	c	95/105 (90%)	92 (97%)	3 (3%)	0	100	100
31	d	107/113 (95%)	101 (94%)	4 (4%)	2 (2%)	6	24
32	e	125/130 (96%)	117 (94%)	7 (6%)	1 (1%)	16	44
33	f	104/107 (97%)	98 (94%)	6 (6%)	0	100	100
34	g	110/121 (91%)	105 (96%)	5 (4%)	0	100	100
35	h	117/120 (98%)	110 (94%)	6 (5%)	1 (1%)	14	41
36	i	97/100 (97%)	82 (84%)	13 (13%)	2 (2%)	5	22
37	j	85/88 (97%)	77 (91%)	8 (9%)	0	100	100
38	k	75/78 (96%)	70 (93%)	5 (7%)	0	100	100
39	l	48/51 (94%)	43 (90%)	5 (10%)	0	100	100
40	o	93/106 (88%)	84 (90%)	9 (10%)	0	100	100
41	p	89/92 (97%)	82 (92%)	7 (8%)	0	100	100
42	w	246/248 (99%)	220 (89%)	19 (8%)	7 (3%)	4	18
43	y	225/227 (99%)	220 (98%)	4 (2%)	1 (0%)	30	58
44	z	54/56 (96%)	47 (87%)	5 (9%)	2 (4%)	2	13
All	All	6348/6731 (94%)	5900 (93%)	394 (6%)	54 (1%)	16	41

All (54) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	E	98	VAL
10	G	36	ILE

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Mol	Chain	Res	Type
28	a	78	LEU
32	e	123	LYS
42	w	328	ILE
42	w	329	SER
42	w	387	LEU
7	D	259	LYS
10	G	37	GLY
11	H	50	ASN
12	J	11	ASP
14	M	8	LYS
20	S	13	ARG
27	Z	17	ARG
36	i	13	LYS
43	y	146	ILE
7	D	276	LYS
8	E	5	LYS
12	J	8	PRO
13	L	77	LEU
21	T	124	VAL
28	a	47	LYS
35	h	91	ALA
42	w	185	VAL
44	z	380	ALA
12	J	114	ILE
13	L	62	THR
42	w	277	SER
5	B	386	ASP
7	D	20	PHE
12	J	165	GLN
15	N	74	PRO
15	N	75	VAL
27	Z	102	GLU
28	a	48	TYR
31	d	6	ASP
44	z	379	THR
12	J	12	LEU
13	L	47	ALA
19	R	131	ALA
20	S	154	HIS
42	w	350	ASP
10	G	157	VAL
8	E	6	ALA

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Mol	Chain	Res	Type
20	S	167	ARG
27	Z	125	GLY
42	w	166	PRO
6	C	131	VAL
28	a	56	VAL
31	d	7	VAL
36	i	3	VAL
5	B	317	ILE
14	M	6	ILE
22	U	11	ILE

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	A	189/189 (100%)	189 (100%)	0	100	100
5	B	318/323 (98%)	317 (100%)	1 (0%)	86	85
6	C	288/288 (100%)	288 (100%)	0	100	100
7	D	244/245 (100%)	243 (100%)	1 (0%)	84	84
8	E	134/153 (88%)	134 (100%)	0	100	100
9	F	186/205 (91%)	186 (100%)	0	100	100
10	G	187/208 (90%)	187 (100%)	0	100	100
11	H	171/171 (100%)	171 (100%)	0	100	100
12	J	147/150 (98%)	147 (100%)	0	100	100
13	L	154/159 (97%)	153 (99%)	1 (1%)	78	81
14	M	107/109 (98%)	107 (100%)	0	100	100
15	N	175/176 (99%)	174 (99%)	1 (1%)	78	81
16	O	160/162 (99%)	160 (100%)	0	100	100
17	P	145/146 (99%)	145 (100%)	0	100	100
18	Q	150/151 (99%)	150 (100%)	0	100	100
19	R	129/154 (84%)	129 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
20	S	156/156 (100%)	156 (100%)	0	100	100
21	T	136/137 (99%)	136 (100%)	0	100	100
22	U	87/107 (81%)	87 (100%)	0	100	100
23	V	104/105 (99%)	104 (100%)	0	100	100
24	W	56/129 (43%)	56 (100%)	0	100	100
25	X	104/118 (88%)	103 (99%)	1 (1%)	68	77
26	Y	109/110 (99%)	109 (100%)	0	100	100
27	Z	115/116 (99%)	115 (100%)	0	100	100
28	a	118/119 (99%)	118 (100%)	0	100	100
29	b	46/47 (98%)	46 (100%)	0	100	100
30	c	81/88 (92%)	81 (100%)	0	100	100
31	d	92/97 (95%)	92 (100%)	0	100	100
32	e	109/111 (98%)	109 (100%)	0	100	100
33	f	90/91 (99%)	90 (100%)	0	100	100
34	g	95/103 (92%)	95 (100%)	0	100	100
35	h	104/105 (99%)	104 (100%)	0	100	100
36	i	81/82 (99%)	81 (100%)	0	100	100
37	j	70/71 (99%)	70 (100%)	0	100	100
38	k	68/69 (99%)	68 (100%)	0	100	100
39	l	45/46 (98%)	45 (100%)	0	100	100
40	o	82/91 (90%)	82 (100%)	0	100	100
41	p	71/72 (99%)	71 (100%)	0	100	100
42	w	205/221 (93%)	202 (98%)	3 (2%)	57	73
43	y	189/194 (97%)	189 (100%)	0	100	100
44	z	51/51 (100%)	51 (100%)	0	100	100
All	All	5348/5625 (95%)	5340 (100%)	8 (0%)	87	89

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	B	85	VAL
7	D	64	ILE
13	L	24	VAL

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Mol	Chain	Res	Type
15	N	133	ILE
25	X	63	ILE
42	w	328	ILE
42	w	330	ARG
42	w	374	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (96) such sidechains are listed below:

Mol	Chain	Res	Type
4	A	24	GLN
4	A	79	ASN
4	A	97	ASN
4	A	209	HIS
5	B	3	HIS
5	B	184	ASN
5	B	224	HIS
5	B	231	HIS
5	B	269	GLN
5	B	273	HIS
6	C	5	GLN
6	C	48	GLN
6	C	59	GLN
6	C	114	ASN
6	C	116	ASN
6	C	322	GLN
7	D	90	HIS
7	D	151	GLN
8	E	57	HIS
8	E	167	ASN
9	F	52	GLN
9	F	81	HIS
10	G	138	HIS
10	G	232	HIS
11	H	58	HIS
11	H	96	HIS
11	H	125	ASN
11	H	183	HIS
12	J	39	GLN
12	J	150	ASN
13	L	28	GLN
13	L	112	ASN
13	L	114	GLN

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Mol	Chain	Res	Type
15	N	37	HIS
15	N	138	GLN
15	N	156	HIS
15	N	175	ASN
16	O	50	ASN
16	O	90	HIS
17	P	133	HIS
17	P	137	ASN
19	R	141	HIS
19	R	144	GLN
20	S	114	HIS
20	S	122	HIS
20	S	142	GLN
20	S	154	HIS
21	T	58	GLN
21	T	98	HIS
21	T	112	ASN
21	T	127	GLN
21	T	131	GLN
21	T	134	GLN
22	U	87	ASN
23	V	98	ASN
24	W	42	GLN
24	W	59	HIS
25	X	111	ASN
26	Y	4	GLN
27	Z	36	HIS
27	Z	57	HIS
27	Z	123	GLN
27	Z	128	GLN
28	a	28	HIS
28	a	40	HIS
28	a	65	GLN
28	a	74	ASN
29	b	7	HIS
29	b	43	HIS
30	c	11	ASN
31	d	15	ASN
31	d	87	ASN
32	e	13	HIS
32	e	31	ASN
32	e	71	HIS

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Mol	Chain	Res	Type
32	e	88	HIS
34	g	34	HIS
34	g	98	GLN
36	i	100	HIS
37	j	12	HIS
37	j	16	HIS
37	j	57	HIS
38	k	67	GLN
39	l	11	GLN
40	o	82	GLN
41	p	25	GLN
41	p	33	GLN
41	p	34	HIS
42	w	272	GLN
42	w	332	ASN
43	y	86	ASN
43	y	106	ASN
43	y	145	ASN
43	y	162	HIS
44	z	393	GLN
44	z	402	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	3086/3396 (90%)	747 (24%)	47 (1%)
2	3	120/121 (99%)	20 (16%)	1 (0%)
3	4	157/158 (99%)	39 (24%)	2 (1%)
All	All	3363/3675 (91%)	806 (23%)	50 (1%)

All (806) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	5	G
1	1	6	A
1	1	14	U
1	1	22	G
1	1	24	G
1	1	40	A
1	1	43	A
1	1	45	A

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Mol	Chain	Res	Type
1	1	49	A
1	1	59	G
1	1	60	A
1	1	65	A
1	1	66	A
1	1	73	C
1	1	88	A
1	1	90	C
1	1	91	G
1	1	92	G
1	1	105	C
1	1	110	G
1	1	111	C
1	1	113	C
1	1	116	A
1	1	117	U
1	1	120	G
1	1	121	A
1	1	122	A
1	1	131	C
1	1	133	U
1	1	135	C
1	1	136	G
1	1	141	C
1	1	142	C
1	1	156	G
1	1	157	A
1	1	161	G
1	1	166	C
1	1	168	U
1	1	170	G
1	1	172	G
1	1	182	U
1	1	187	A
1	1	190	U
1	1	191	U
1	1	200	C
1	1	206	G
1	1	210	U
1	1	211	A
1	1	218	G
1	1	219	A

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Mol	Chain	Res	Type
1	1	227	G
1	1	235	A
1	1	237	G
1	1	240	U
1	1	241	G
1	1	243	G
1	1	245	U
1	1	247	C
1	1	252	U
1	1	265	A
1	1	269	G
1	1	275	U
1	1	283	G
1	1	286	U
1	1	295	A
1	1	298	U
1	1	305	U
1	1	315	C
1	1	316	U
1	1	323	A
1	1	326	U
1	1	329	U
1	1	339	C
1	1	343	U
1	1	350	C
1	1	351	A
1	1	352	A
1	1	361	A
1	1	383	G
1	1	389	A
1	1	398	A
1	1	399	A
1	1	401	U
1	1	402	A
1	1	403	C
1	1	421	G
1	1	422	A
1	1	433	A
1	1	436	A
1	1	437	G
1	1	439	C
1	1	440	A

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Mol	Chain	Res	Type
1	1	507	U
1	1	516	A
1	1	517	G
1	1	518	G
1	1	520	U
1	1	521	A
1	1	535	G
1	1	536	U
1	1	544	C
1	1	546	C
1	1	547	G
1	1	548	G
1	1	552	G
1	1	555	U
1	1	556	U
1	1	557	A
1	1	558	U
1	1	559	A
1	1	569	A
1	1	578	A
1	1	579	G
1	1	592	A
1	1	604	G
1	1	609	G
1	1	611	A
1	1	620	U
1	1	621	A
1	1	630	A
1	1	636	C
1	1	638	C
1	1	645	A
1	1	647	A
1	1	648	C
1	1	649	A
1	1	658	G
1	1	661	G
1	1	665	A
1	1	677	A
1	1	681	U
1	1	683	U
1	1	684	G
1	1	690	A

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Mol	Chain	Res	Type
1	1	699	A
1	1	705	A
1	1	706	A
1	1	707	U
1	1	708	G
1	1	709	A
1	1	712	G
1	1	715	A
1	1	716	A
1	1	718	G
1	1	726	G
1	1	735	A
1	1	743	C
1	1	760	G
1	1	762	U
1	1	763	G
1	1	764	U
1	1	765	C
1	1	766	U
1	1	767	U
1	1	768	C
1	1	771	A
1	1	774	G
1	1	775	A
1	1	776	U
1	1	777	U
1	1	780	A
1	1	781	G
1	1	785	G
1	1	786	A
1	1	800	G
1	1	801	A
1	1	806	A
1	1	817	A
1	1	825	U
1	1	830	A
1	1	849	C
1	1	851	C
1	1	854	G
1	1	861	C
1	1	865	U
1	1	869	G

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Mol	Chain	Res	Type
1	1	870	G
1	1	874	U
1	1	878	G
1	1	879	U
1	1	880	G
1	1	895	A
1	1	904	A
1	1	907	G
1	1	908	G
1	1	914	A
1	1	915	A
1	1	916	G
1	1	917	A
1	1	923	C
1	1	924	G
1	1	925	A
1	1	926	A
1	1	929	A
1	1	932	U
1	1	933	A
1	1	937	G
1	1	944	C
1	1	945	C
1	1	946	U
1	1	959	C
1	1	960	U
1	1	979	U
1	1	980	A
1	1	981	U
1	1	982	C
1	1	986	U
1	1	992	A
1	1	994	G
1	1	1064	A
1	1	1065	A
1	1	1069	C
1	1	1072	G
1	1	1079	A
1	1	1081	U
1	1	1082	U
1	1	1083	G
1	1	1093	A

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Mol	Chain	Res	Type
1	1	1094	U
1	1	1095	U
1	1	1097	G
1	1	1098	A
1	1	1103	A
1	1	1104	G
1	1	1106	G
1	1	1117	G
1	1	1129	A
1	1	1130	A
1	1	1131	G
1	1	1144	U
1	1	1151	U
1	1	1152	G
1	1	1153	A
1	1	1155	C
1	1	1156	C
1	1	1159	A
1	1	1177	G
1	1	1178	G
1	1	1180	A
1	1	1181	U
1	1	1182	A
1	1	1191	U
1	1	1192	C
1	1	1196	C
1	1	1200	A
1	1	1201	C
1	1	1202	A
1	1	1208	U
1	1	1209	G
1	1	1211	U
1	1	1216	C
1	1	1221	A
1	1	1222	G
1	1	1227	C
1	1	1232	C
1	1	1236	G
1	1	1237	G
1	1	1238	C
1	1	1241	U
1	1	1242	G

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Mol	Chain	Res	Type
1	1	1243	G
1	1	1244	A
1	1	1245	A
1	1	1246	G
1	1	1248	C
1	1	1249	G
1	1	1252	A
1	1	1262	G
1	1	1263	A
1	1	1264	G
1	1	1266	G
1	1	1270	A
1	1	1271	A
1	1	1272	C
1	1	1274	A
1	1	1275	C
1	1	1278	A
1	1	1279	C
1	1	1281	G
1	1	1285	G
1	1	1286	A
1	1	1287	A
1	1	1292	C
1	1	1294	A
1	1	1295	G
1	1	1307	G
1	1	1308	A
1	1	1309	U
1	1	1313	G
1	1	1330	A
1	1	1333	C
1	1	1349	G
1	1	1350	A
1	1	1351	U
1	1	1352	A
1	1	1353	U
1	1	1355	A
1	1	1356	U
1	1	1357	G
1	1	1359	C
1	1	1383	G
1	1	1386	A

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Mol	Chain	Res	Type
1	1	1399	A
1	1	1400	G
1	1	1417	G
1	1	1418	A
1	1	1419	A
1	1	1421	G
1	1	1433	A
1	1	1434	G
1	1	1437	C
1	1	1438	U
1	1	1446	A
1	1	1453	A
1	1	1455	U
1	1	1466	G
1	1	1475	A
1	1	1481	A
1	1	1482	A
1	1	1483	G
1	1	1485	G
1	1	1494	U
1	1	1500	G
1	1	1503	A
1	1	1508	C
1	1	1511	U
1	1	1527	C
1	1	1531	C
1	1	1533	U
1	1	1535	A
1	1	1547	G
1	1	1555	U
1	1	1556	C
1	1	1557	A
1	1	1562	C
1	1	1563	C
1	1	1565	G
1	1	1566	A
1	1	1567	U
1	1	1568	U
1	1	1569	U
1	1	1570	U
1	1	1572	U
1	1	1575	A

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Mol	Chain	Res	Type
1	1	1576	G
1	1	1578	C
1	1	1582	C
1	1	1583	A
1	1	1587	A
1	1	1588	A
1	1	1589	A
1	1	1590	G
1	1	1593	A
1	1	1596	C
1	1	1607	U
1	1	1608	C
1	1	1611	G
1	1	1620	U
1	1	1621	A
1	1	1629	U
1	1	1630	U
1	1	1639	C
1	1	1641	U
1	1	1642	A
1	1	1643	A
1	1	1657	C
1	1	1662	G
1	1	1666	G
1	1	1677	G
1	1	1678	G
1	1	1683	A
1	1	1695	U
1	1	1702	U
1	1	1705	U
1	1	1724	U
1	1	1725	C
1	1	1732	U
1	1	1741	A
1	1	1742	U
1	1	1749	A
1	1	1750	A
1	1	1751	G
1	1	1759	C
1	1	1762	C
1	1	1765	U
1	1	1766	G

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Mol	Chain	Res	Type
1	1	1769	G
1	1	1770	G
1	1	1775	G
1	1	1780	G
1	1	1795	U
1	1	1797	A
1	1	1810	A
1	1	1813	A
1	1	1814	A
1	1	1816	A
1	1	1817	G
1	1	1818	U
1	1	1820	U
1	1	1821	U
1	1	1835	A
1	1	1839	A
1	1	1841	A
1	1	1846	C
1	1	1849	C
1	1	1850	A
1	1	1858	A
1	1	1866	C
1	1	1871	U
1	1	1874	A
1	1	1881	A
1	1	1899	G
1	1	1900	A
1	1	1901	A
1	1	1906	G
1	1	1909	A
1	1	1920	U
1	1	1926	C
1	1	1928	G
1	1	1930	A
1	1	1934	G
1	1	1935	G
1	1	1947	G
1	1	1952	G
1	1	1953	G
1	1	1954	G
1	1	2094	C
1	1	2101	C

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Mol	Chain	Res	Type
1	1	2102	U
1	1	2110	G
1	1	2112	U
1	1	2113	A
1	1	2114	C
1	1	2121	G
1	1	2122	G
1	1	2131	A
1	1	2140	U
1	1	2141	U
1	1	2142	A
1	1	2144	A
1	1	2145	A
1	1	2169	G
1	1	2170	U
1	1	2172	A
1	1	2175	U
1	1	2176	U
1	1	2177	G
1	1	2178	A
1	1	2186	U
1	1	2188	A
1	1	2192	C
1	1	2193	U
1	1	2195	C
1	1	2205	U
1	1	2208	A
1	1	2209	U
1	1	2210	G
1	1	2216	G
1	1	2223	A
1	1	2225	U
1	1	2228	A
1	1	2244	A
1	1	2249	G
1	1	2255	A
1	1	2256	A
1	1	2257	C
1	1	2259	A
1	1	2262	A
1	1	2265	C
1	1	2266	U

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Mol	Chain	Res	Type
1	1	2267	C
1	1	2268	U
1	1	2269	U
1	1	2270	A
1	1	2272	G
1	1	2273	G
1	1	2281	A
1	1	2282	U
1	1	2284	C
1	1	2288	G
1	1	2294	U
1	1	2307	G
1	1	2308	C
1	1	2310	U
1	1	2313	A
1	1	2314	U
1	1	2315	G
1	1	2334	U
1	1	2336	U
1	1	2339	C
1	1	2341	A
1	1	2361	A
1	1	2372	A
1	1	2373	A
1	1	2374	C
1	1	2375	G
1	1	2376	G
1	1	2378	C
1	1	2381	G
1	1	2385	G
1	1	2388	U
1	1	2389	C
1	1	2393	G
1	1	2397	A
1	1	2401	A
1	1	2402	A
1	1	2403	G
1	1	2405	C
1	1	2411	U
1	1	2418	G
1	1	2436	U
1	1	2437	G

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Mol	Chain	Res	Type
1	1	2438	A
1	1	2439	A
1	1	2441	A
1	1	2443	A
1	1	2509	U
1	1	2511	A
1	1	2514	U
1	1	2522	G
1	1	2523	A
1	1	2524	A
1	1	2525	G
1	1	2526	C
1	1	2530	G
1	1	2532	U
1	1	2533	G
1	1	2535	A
1	1	2537	U
1	1	2538	U
1	1	2539	C
1	1	2540	A
1	1	2541	U
1	1	2542	U
1	1	2543	U
1	1	2547	A
1	1	2549	G
1	1	2550	U
1	1	2552	C
1	1	2553	U
1	1	2555	G
1	1	2560	C
1	1	2561	A
1	1	2568	C
1	1	2569	A
1	1	2570	U
1	1	2571	U
1	1	2572	C
1	1	2573	G
1	1	2576	G
1	1	2578	U
1	1	2583	C
1	1	2585	G
1	1	2593	A

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Mol	Chain	Res	Type
1	1	2594	C
1	1	2602	G
1	1	2606	G
1	1	2607	G
1	1	2614	G
1	1	2626	A
1	1	2628	A
1	1	2635	A
1	1	2638	C
1	1	2651	G
1	1	2652	U
1	1	2656	A
1	1	2657	A
1	1	2658	G
1	1	2674	A
1	1	2676	A
1	1	2677	G
1	1	2679	A
1	1	2689	A
1	1	2691	A
1	1	2694	A
1	1	2696	A
1	1	2705	A
1	1	2709	C
1	1	2714	G
1	1	2719	U
1	1	2720	G
1	1	2726	C
1	1	2728	G
1	1	2729	U
1	1	2737	C
1	1	2749	G
1	1	2752	U
1	1	2753	G
1	1	2755	C
1	1	2772	C
1	1	2777	G
1	1	2778	G
1	1	2796	G
1	1	2797	C
1	1	2799	A
1	1	2800	G

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Mol	Chain	Res	Type
1	1	2801	A
1	1	2802	A
1	1	2803	A
1	1	2810	C
1	1	2817	A
1	1	2821	C
1	1	2823	G
1	1	2828	G
1	1	2833	A
1	1	2840	C
1	1	2842	U
1	1	2845	A
1	1	2846	U
1	1	2849	C
1	1	2851	A
1	1	2853	A
1	1	2860	U
1	1	2863	G
1	1	2871	G
1	1	2872	A
1	1	2873	U
1	1	2875	U
1	1	2887	A
1	1	2888	U
1	1	2889	C
1	1	2896	A
1	1	2898	G
1	1	2899	C
1	1	2911	A
1	1	2914	G
1	1	2923	U
1	1	2927	C
1	1	2928	C
1	1	2933	A
1	1	2935	U
1	1	2936	A
1	1	2938	G
1	1	2941	A
1	1	2942	C
1	1	2945	G
1	1	2947	G
1	1	2971	A

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Mol	Chain	Res	Type
1	1	2972	G
1	1	2980	U
1	1	2983	C
1	1	2990	G
1	1	2996	U
1	1	2997	G
1	1	3007	U
1	1	3012	A
1	1	3030	G
1	1	3032	A
1	1	3056	U
1	1	3059	G
1	1	3070	A
1	1	3078	U
1	1	3079	U
1	1	3080	G
1	1	3086	A
1	1	3092	C
1	1	3101	G
1	1	3103	A
1	1	3104	U
1	1	3109	G
1	1	3113	A
1	1	3117	C
1	1	3121	U
1	1	3127	A
1	1	3128	G
1	1	3129	A
1	1	3130	A
1	1	3131	U
1	1	3137	C
1	1	3138	U
1	1	3142	A
1	1	3143	C
1	1	3151	U
1	1	3154	C
1	1	3155	U
1	1	3156	U
1	1	3157	U
1	1	3158	G
1	1	3164	C
1	1	3165	A

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Mol	Chain	Res	Type
1	1	3168	A
1	1	3173	G
1	1	3174	A
1	1	3175	U
1	1	3176	G
1	1	3179	U
1	1	3181	C
1	1	3186	A
1	1	3187	A
1	1	3196	U
1	1	3199	G
1	1	3207	U
1	1	3208	G
1	1	3209	A
1	1	3217	C
1	1	3218	A
1	1	3219	G
1	1	3229	G
1	1	3242	G
1	1	3243	A
1	1	3244	A
1	1	3245	A
1	1	3247	G
1	1	3252	G
1	1	3253	G
1	1	3259	U
1	1	3260	G
1	1	3267	A
1	1	3268	A
1	1	3269	U
1	1	3270	U
1	1	3272	C
1	1	3273	A
1	1	3276	G
1	1	3277	U
1	1	3278	C
1	1	3279	A
1	1	3281	U
1	1	3286	G
1	1	3289	G
1	1	3293	U
1	1	3294	A

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Mol	Chain	Res	Type
1	1	3295	A
1	1	3299	A
1	1	3304	U
1	1	3313	U
1	1	3316	A
1	1	3317	U
1	1	3318	G
1	1	3319	U
1	1	3320	A
1	1	3323	A
1	1	3325	G
1	1	3341	U
1	1	3347	A
1	1	3351	U
1	1	3352	U
1	1	3353	G
1	1	3354	U
1	1	3355	U
1	1	3356	G
1	1	3369	G
1	1	3375	A
1	1	3378	C
1	1	3386	G
1	1	3390	G
1	1	3396	U
2	3	9	C
2	3	13	A
2	3	22	A
2	3	40	C
2	3	41	G
2	3	42	A
2	3	53	U
2	3	54	U
2	3	55	A
2	3	65	G
2	3	66	A
2	3	74	C
2	3	76	A
2	3	92	A
2	3	99	G
2	3	102	A
2	3	103	A

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Mol	Chain	Res	Type
2	3	112	G
2	3	118	A
2	3	121	U
3	4	13	A
3	4	23	U
3	4	34	U
3	4	35	C
3	4	37	A
3	4	38	U
3	4	48	A
3	4	49	G
3	4	51	G
3	4	59	A
3	4	60	U
3	4	62	C
3	4	63	G
3	4	80	A
3	4	81	U
3	4	82	U
3	4	83	C
3	4	84	C
3	4	85	G
3	4	86	U
3	4	87	G
3	4	90	U
3	4	95	G
3	4	96	A
3	4	104	A
3	4	106	C
3	4	107	G
3	4	111	A
3	4	112	U
3	4	113	U
3	4	125	U
3	4	126	A
3	4	132	G
3	4	138	A
3	4	148	G
3	4	151	C
3	4	152	G
3	4	155	A
3	4	157	U

All (50) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	13	A
1	1	239	G
1	1	282	G
1	1	547	G
1	1	619	A
1	1	637	C
1	1	715	A
1	1	873	C
1	1	916	G
1	1	979	U
1	1	981	U
1	1	1064	A
1	1	1097	G
1	1	1103	A
1	1	1143	A
1	1	1307	G
1	1	1352	A
1	1	1355	A
1	1	1482	A
1	1	1484	U
1	1	1562	C
1	1	1568	U
1	1	1607	U
1	1	1815	U
1	1	1816	A
1	1	2101	C
1	1	2112	U
1	1	2209	U
1	1	2227	C
1	1	2372	A
1	1	2525	G
1	1	2536	A
1	1	2537	U
1	1	2541	U
1	1	2593	A
1	1	2771	U
1	1	3078	U
1	1	3156	U
1	1	3218	A
1	1	3228	C
1	1	3269	U
1	1	3316	A

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Mol	Chain	Res	Type
1	1	3317	U
1	1	3319	U
1	1	3350	C
1	1	3351	U
1	1	3353	G
2	3	52	G
3	4	82	U
3	4	85	G

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](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

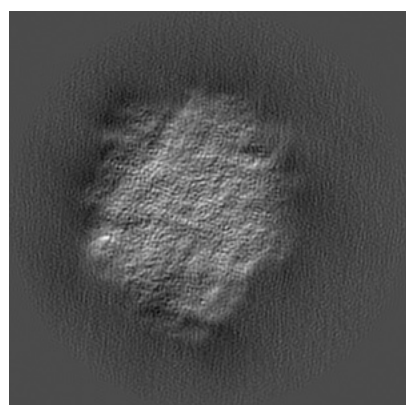
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-9569. These allow visual inspection of the internal detail of the map and identification of artifacts.

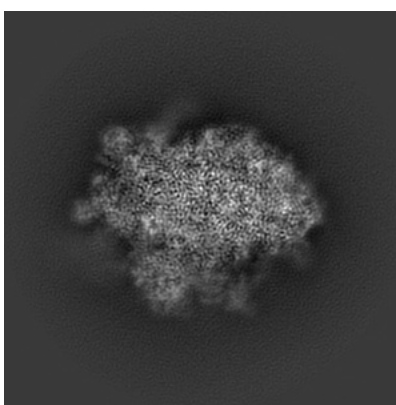
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

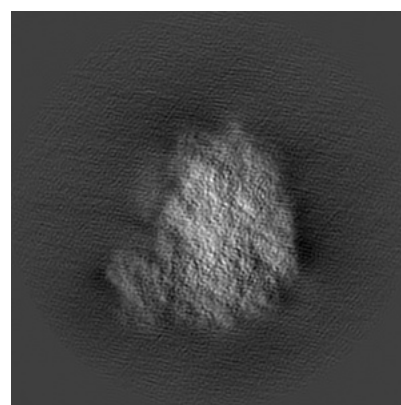
6.1.1 Primary map



X



Y

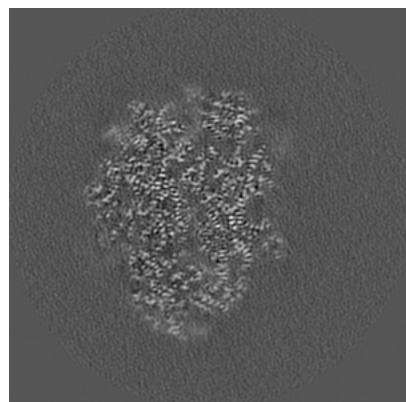


Z

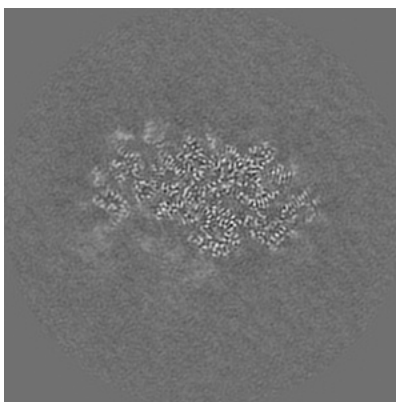
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

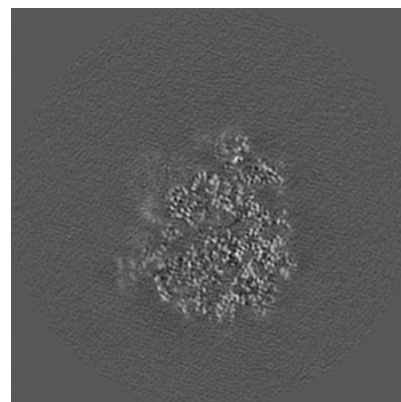
6.2.1 Primary map



X Index: 180



Y Index: 180

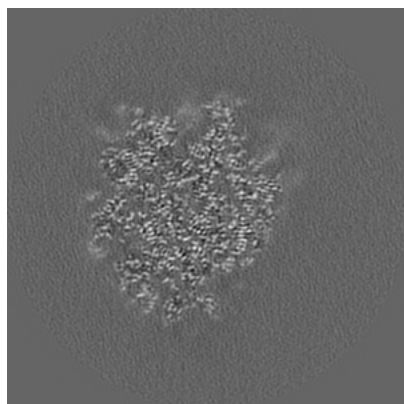


Z Index: 180

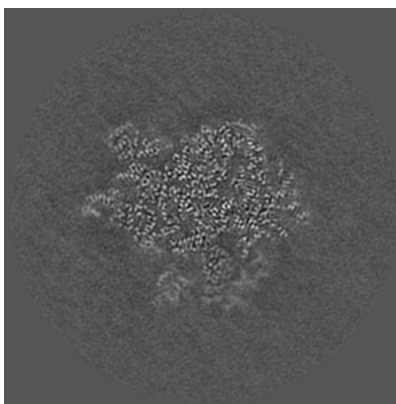
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

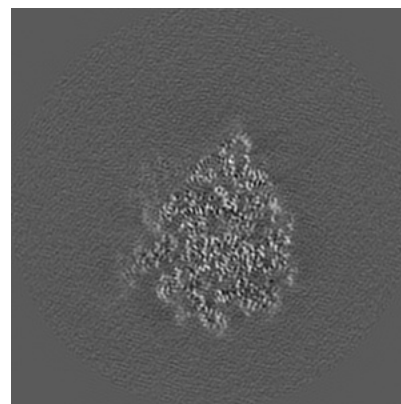
6.3.1 Primary map



X Index: 193



Y Index: 133

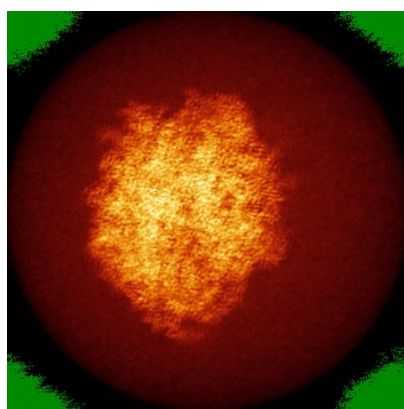


Z Index: 188

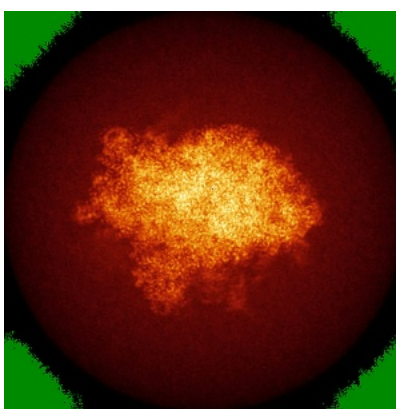
The images above show the largest variance slices of the map in three orthogonal directions.

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

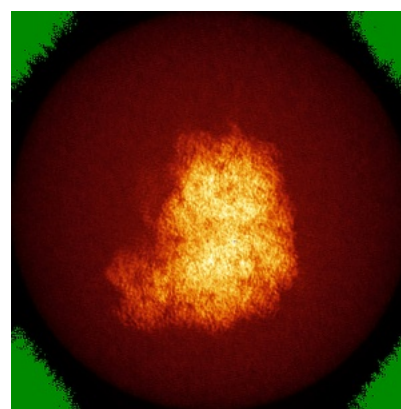
6.4.1 Primary map



X



Y

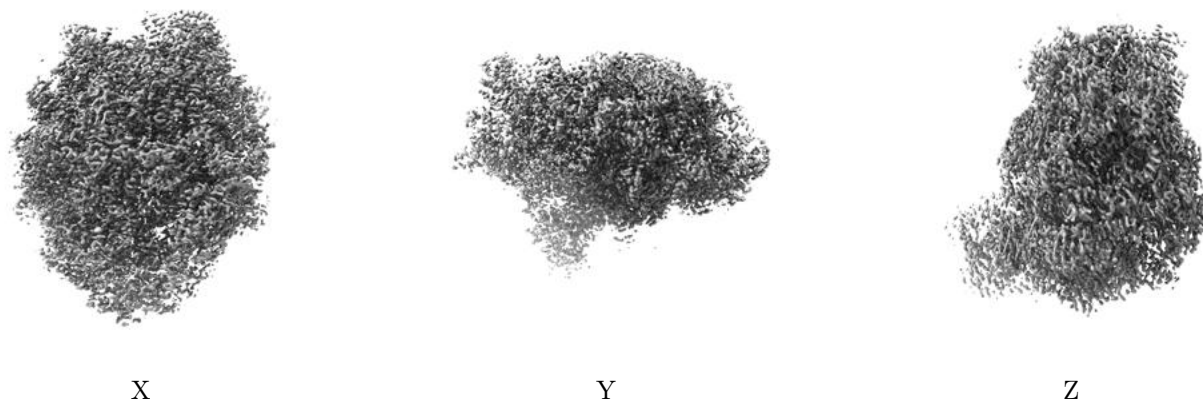


Z

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

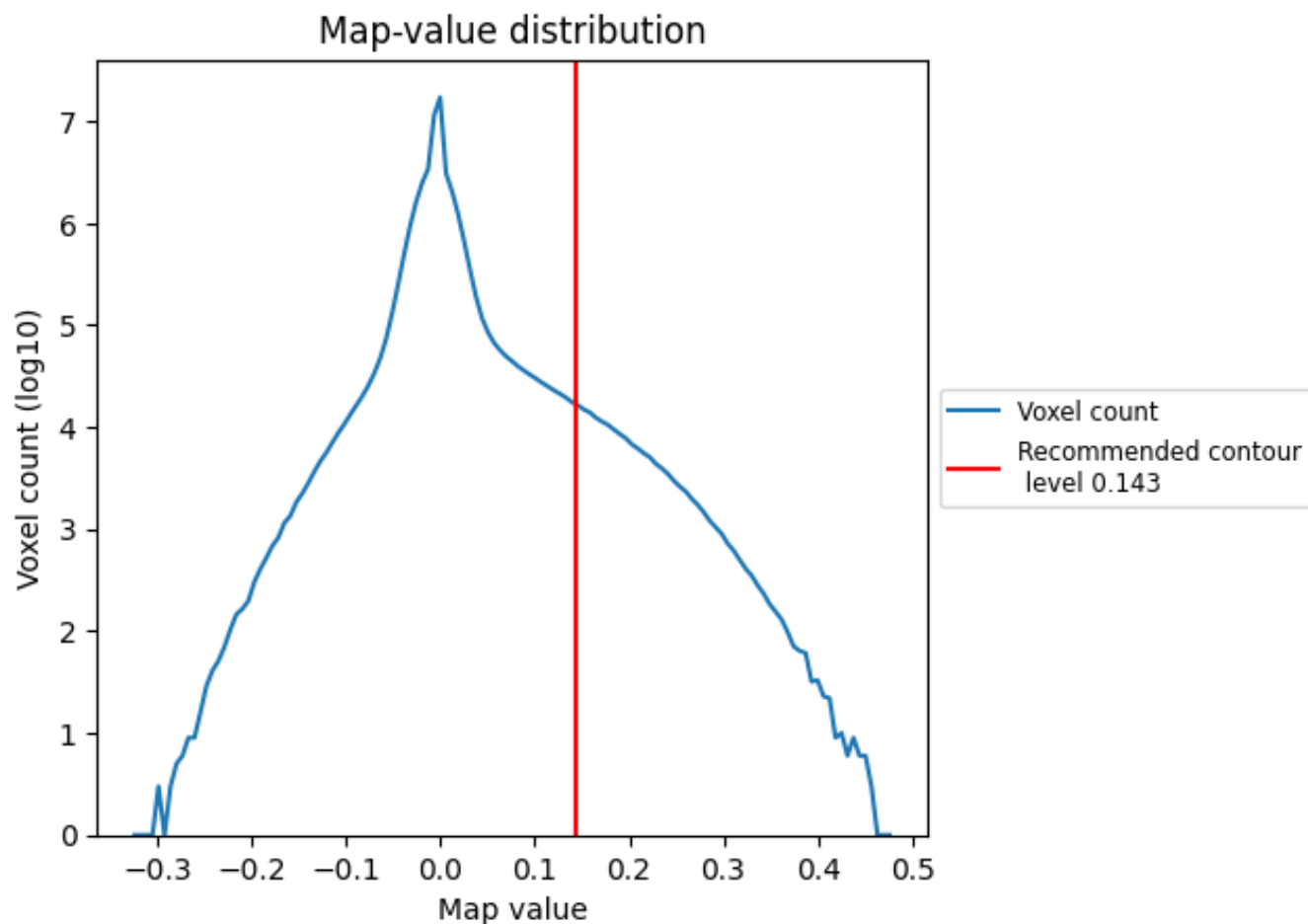
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

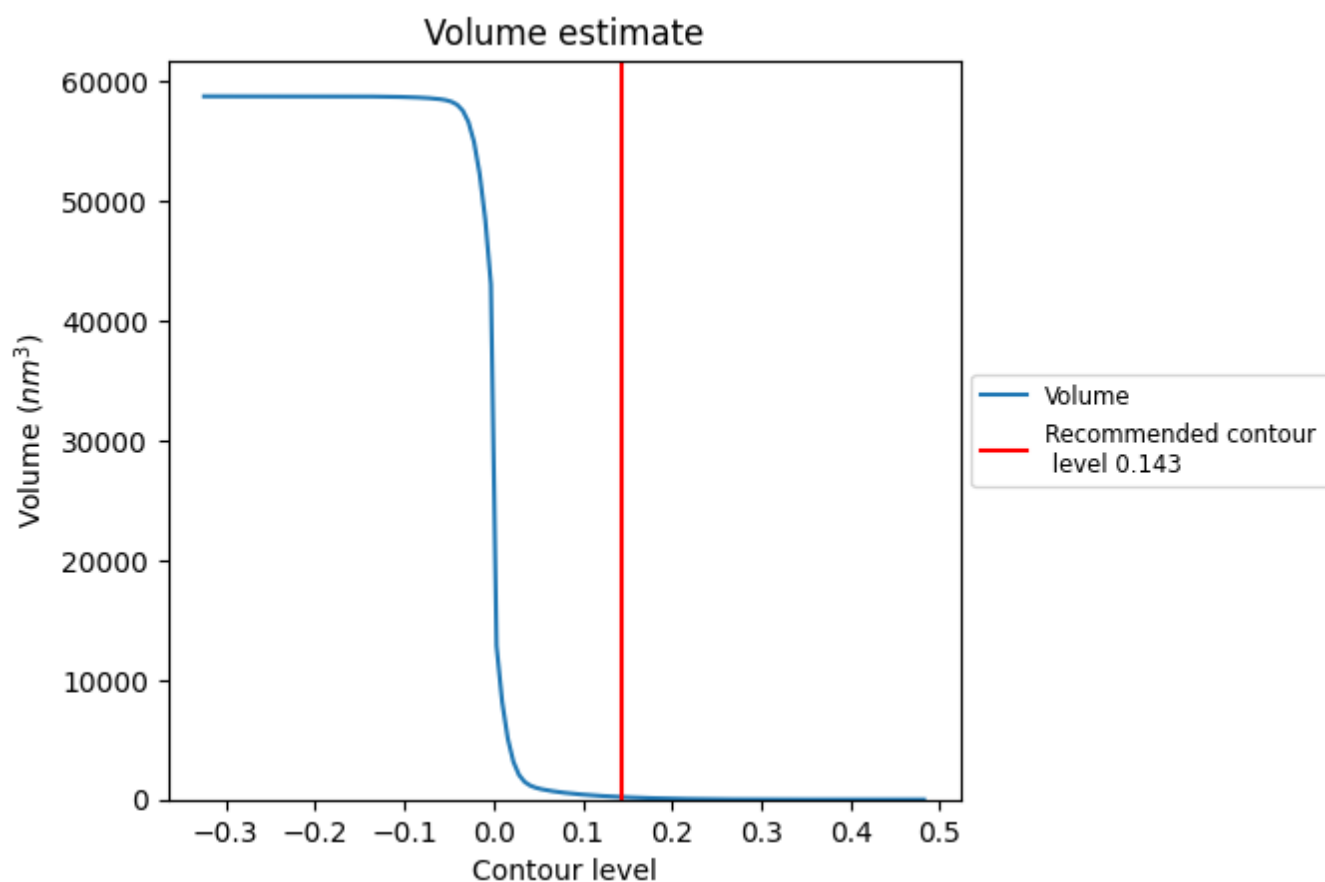
This section contains the results of statistical analysis of the map.

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.

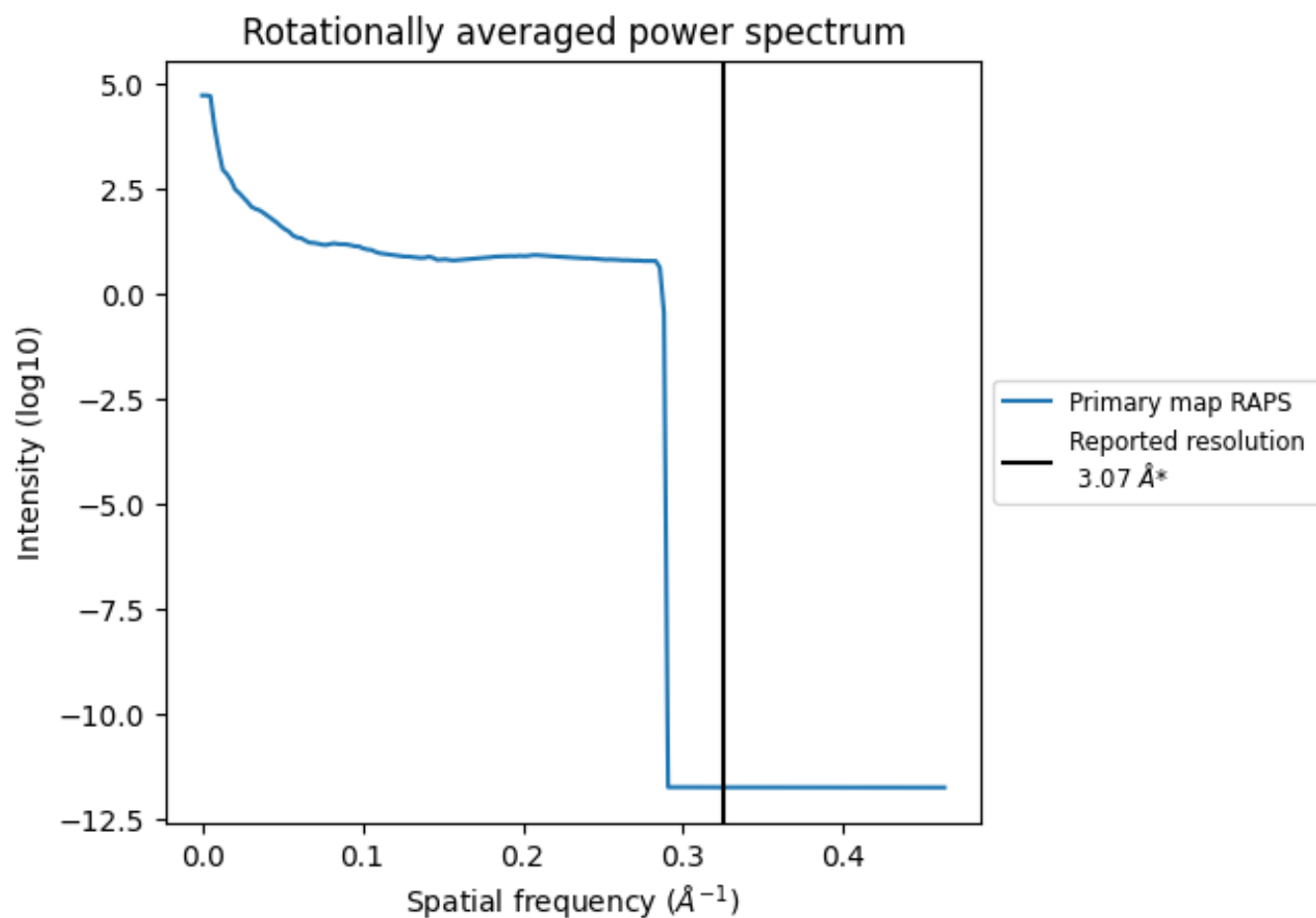
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 212 nm³; this corresponds to an approximate mass of 192 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 0.326 Å⁻¹

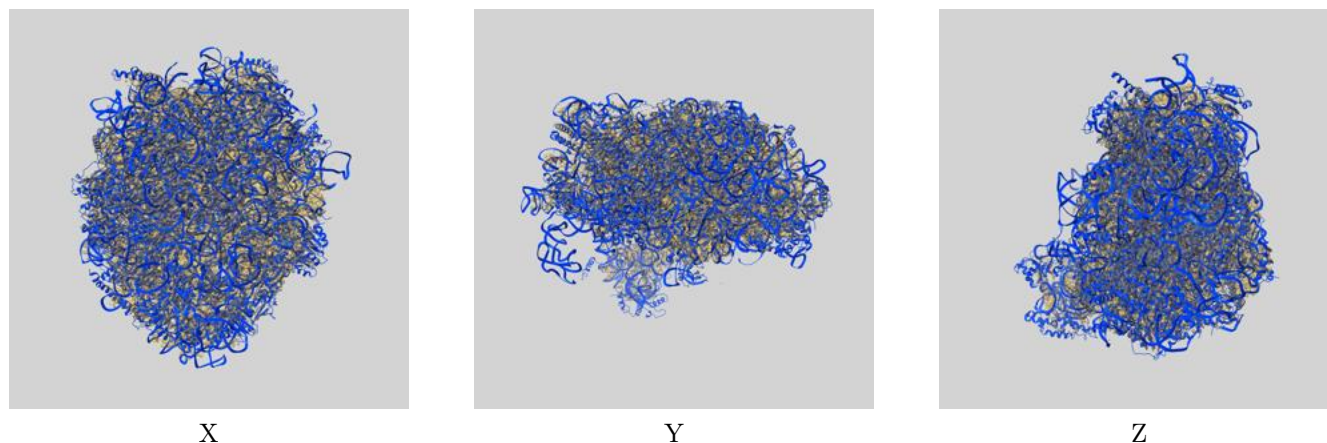
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

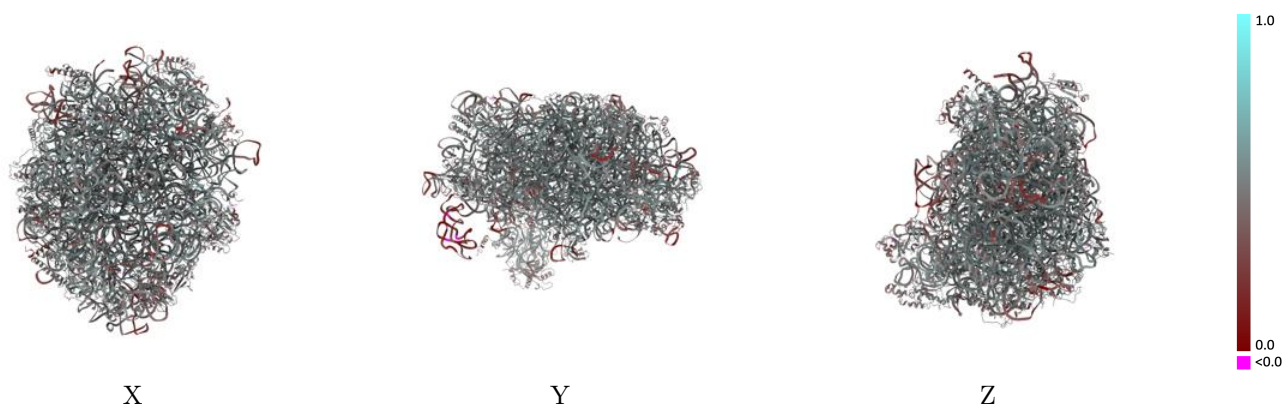
This section contains information regarding the fit between EMDB map EMD-9569 and PDB model 5H4P. Per-residue inclusion information can be found in section 3 on page 12.

9.1 Map-model overlay [i](#)



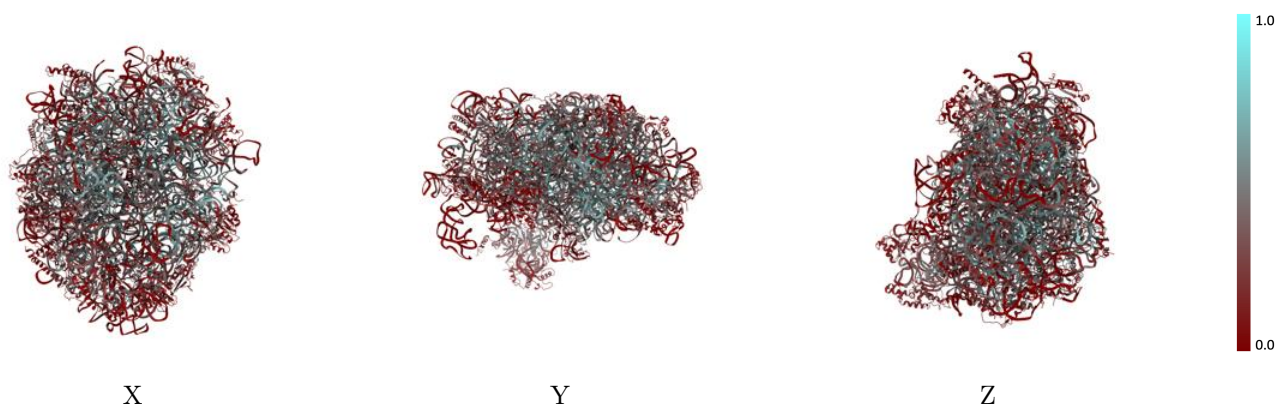
The images above show the 3D surface view of the map at the recommended contour level 0.143 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



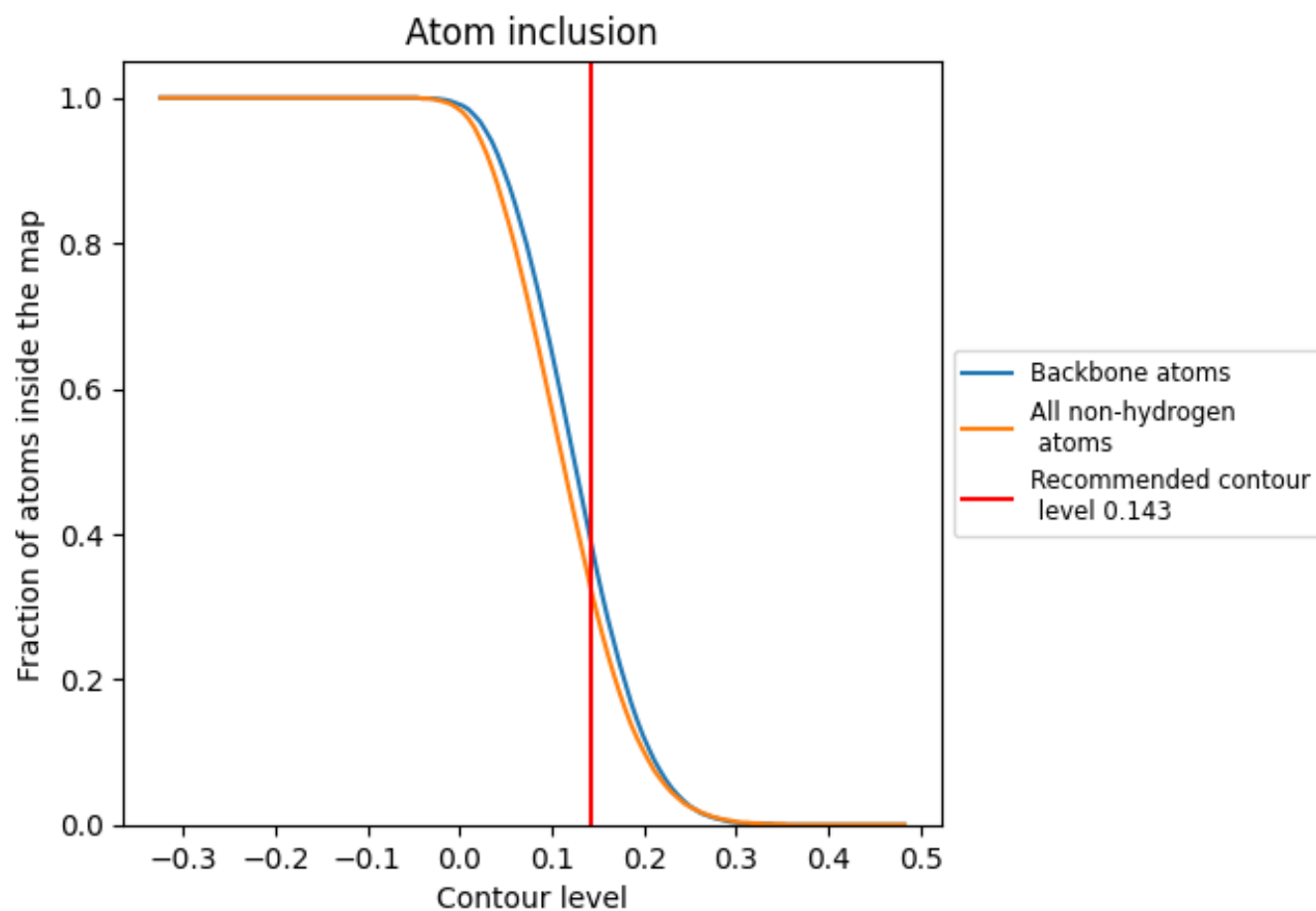
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.143).

9.4 Atom inclusion [i](#)



At the recommended contour level, 38% of all backbone atoms, 32% 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 (0.143) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.3200	 0.4830
1	 0.3760	 0.4820
3	 0.2740	 0.4830
4	 0.4380	 0.5040
A	 0.3590	 0.5090
B	 0.3570	 0.5000
C	 0.2730	 0.4980
D	 0.1030	 0.4330
E	 0.1390	 0.4730
F	 0.2700	 0.5000
G	 0.2380	 0.4730
H	 0.1360	 0.4590
J	 0.0590	 0.4070
L	 0.2540	 0.4830
M	 0.2220	 0.4870
N	 0.3560	 0.5130
O	 0.3360	 0.5110
P	 0.3080	 0.4810
Q	 0.2250	 0.4990
R	 0.3040	 0.4830
S	 0.2070	 0.4840
T	 0.1990	 0.4760
U	 0.1390	 0.4490
V	 0.3060	 0.5020
W	 0.2380	 0.4910
X	 0.3140	 0.4980
Y	 0.2610	 0.4990
Z	 0.2100	 0.4720
a	 0.3010	 0.5060
b	 0.1240	 0.4470
c	 0.1750	 0.4550
d	 0.3070	 0.4890
e	 0.2760	 0.5100
f	 0.3460	 0.5150
g	 0.3350	 0.4920



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Chain	Atom inclusion	Q-score
h	 0.2850	 0.4870
i	 0.1440	 0.4550
j	 0.3770	 0.5170
k	 0.1200	 0.4530
l	 0.3280	 0.5160
o	 0.2780	 0.4800
p	 0.3170	 0.4830
w	 0.0840	 0.4590
y	 0.1050	 0.4390
z	 0.0610	 0.4690