



Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 07:55 PM UTC

PDB ID : 9AXU / pdb_00009axu
EMDB ID : EMD-43973
Title : Non-translating S. pombe ribosome large subunit
Authors : Gluc, M.; Gemin, O.; Purdy, M.; Mattei, S.; Jomaa, A.
Deposited on : 2024-03-06
Resolution : 1.94 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:

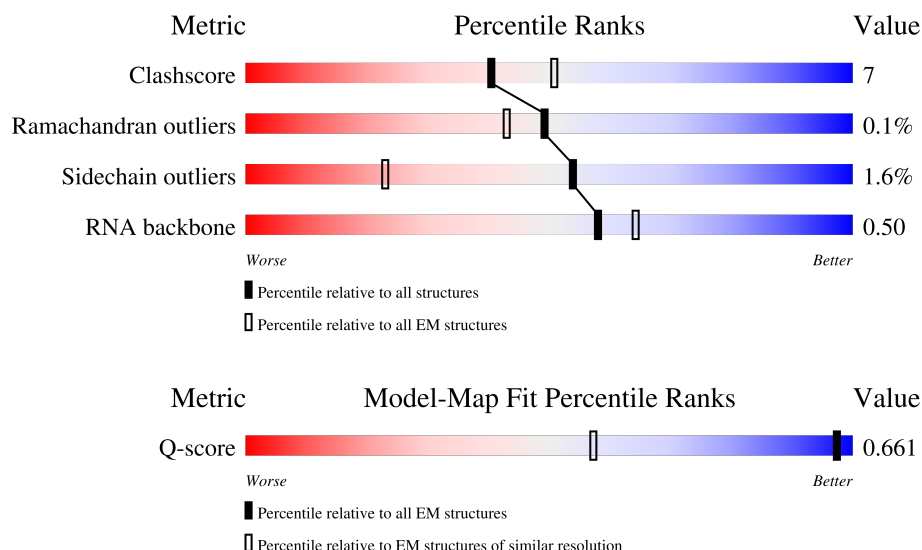
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 1.94 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.



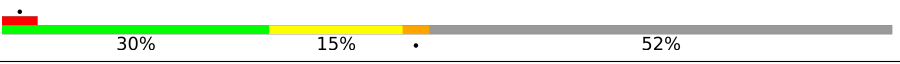
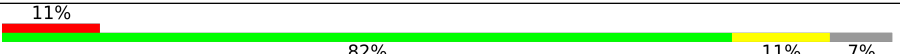
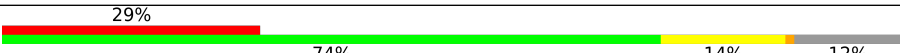
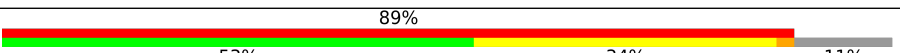
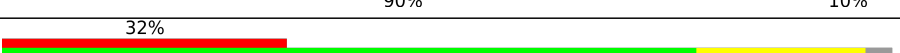
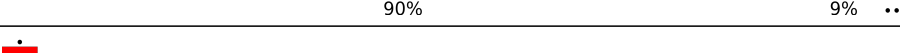
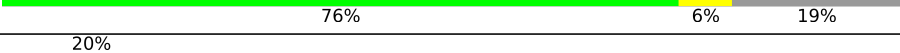
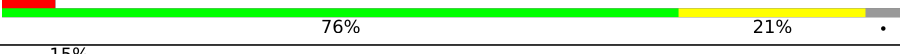
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	1283 (1.45 - 2.44)

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

Mol	Chain	Length	Quality of chain
1	0	106	20% 71% 17% 12%
2	1	94	10% 80% 16% ...
3	2	3498	21% 53% 30% 8% 8%

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Mol	Chain	Length	Quality of chain
4	3	246	
5	4	165	
6	N	253	
7	O	388	
8	P	363	
9	Q	294	
10	R	195	
11	S	251	
12	T	259	
13	U	189	
14	V	221	
15	W	174	
16	X	208	
17	Y	134	
18	Z	201	
19	a	197	
20	b	187	
21	c	187	
22	d	193	
23	e	176	
24	f	160	
25	g	117	
26	h	139	
27	i	149	
28	j	141	

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Mol	Chain	Length	Quality of chain
29	k	126	
30	l	136	
31	m	148	
32	n	61	
33	o	109	
34	p	113	
35	q	127	
36	r	108	
37	s	111	
38	t	122	
39	u	99	
40	v	91	
41	w	74	
42	x	51	
43	y	134	

2 Entry composition

There are 45 unique types of molecules in this entry. The entry contains 123561 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Large ribosomal subunit protein eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	93	Total	C	N	O	S	0	0
			758	479	152	122	5		

- Molecule 2 is a protein called Large ribosomal subunit protein eL43A.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	93	Total	C	N	O	S	0	0
			718	442	147	123	6		

- Molecule 3 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	3212	Total	C	N	O	P	0	0
			68676	30687	12377	22400	3212		

- Molecule 4 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	119	Total	C	N	O	P	0	0
			2539	1133	454	833	119		

- Molecule 5 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	157	Total	C	N	O	P	0	0
			3332	1491	583	1101	157		

- Molecule 6 is a protein called Large ribosomal subunit protein uL2C.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	N	248	Total	C	N	O	S	0	0
			1872	1166	377	324	5		

- Molecule 7 is a protein called Large ribosomal subunit protein uL3A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	O	384	Total	C	N	O	S	0	0
			3050	1929	576	535	10		

- Molecule 8 is a protein called Large ribosomal subunit protein uL4A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	P	362	Total	C	N	O	S	0	0
			2799	1768	538	490	3		

- Molecule 9 is a protein called Large ribosomal subunit protein uL18B.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	Q	287	Total	C	N	O	S	0	0
			2312	1461	410	437	4		

- Molecule 10 is a protein called Large ribosomal subunit protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	R	162	Total	C	N	O	S	0	0
			1251	802	231	215	3		

- Molecule 11 is a protein called Large ribosomal subunit protein uL30C.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	S	233	Total	C	N	O	S	0	0
			1897	1211	349	334	3		

- Molecule 12 is a protein called Large ribosomal subunit protein eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	T	229	Total	C	N	O	S	0	0
			1772	1135	325	309	3		

- Molecule 13 is a protein called Large ribosomal subunit protein uL6B.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	U	168	Total	C	N	O	S	0	0
			1319	828	244	242	5		

- Molecule 14 is a protein called Large ribosomal subunit protein uL16A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	V	191	Total	C	N	O	S	0	0
			1549	982	291	270	6		

- Molecule 15 is a protein called Large ribosomal subunit protein uL5A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	W	167	Total	C	N	O	S	0	0
			1346	854	252	235	5		

- Molecule 16 is a protein called Large ribosomal subunit protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	X	207	Total	C	N	O	S	0	0
			1654	1034	329	290	1		

- Molecule 17 is a protein called Large ribosomal subunit protein eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Y	130	Total	C	N	O	S	0	0
			1038	662	198	174	4		

- Molecule 18 is a protein called Large ribosomal subunit protein eL15B.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Z	200	Total	C	N	O	S	0	0
			1676	1050	348	275	3		

- Molecule 19 is a protein called Large ribosomal subunit protein uL13A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	a	196	Total	C	N	O	S	0	0
			1545	991	294	256	4		

- Molecule 20 is a protein called Large ribosomal subunit protein uL22A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	b	152	Total	C	N	O	S	0	0
			1212	770	229	210	3		

- Molecule 21 is a protein called Large ribosomal subunit protein eL18B.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	c	186	Total	C	N	O	0	0
			1487	937	300	250		

- Molecule 22 is a protein called Large ribosomal subunit protein eL19B.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	d	157	Total	C	N	O	S	0	0
			1301	809	275	212	5		

- Molecule 23 is a protein called Large ribosomal subunit protein eL20A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	e	173	Total	C	N	O	S	0	0
			1423	916	268	234	5		

- Molecule 24 is a protein called Large ribosomal subunit protein eL21B.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	f	159	Total	C	N	O	S	0	0
			1286	810	247	226	3		

- Molecule 25 is a protein called Large ribosomal subunit protein eL22.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	g	99	Total	C	N	O	0	0
			798	518	138	142		

- Molecule 26 is a protein called Large ribosomal subunit protein uL14B.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	h	134	Total	C	N	O	S	0	0
			999	630	184	177	8		

- Molecule 27 is a protein called Large ribosomal subunit protein eL24B.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	i	63	Total	C	N	O	S	0	0
			523	336	102	82	3		

- Molecule 28 is a protein called Large ribosomal subunit protein uL23A.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	j	118	Total	C	N	O	S	0	0
			947	605	175	166	1		

- Molecule 29 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	k	125	Total	C	N	O	S	0	0
			998	622	201	173	2		

- Molecule 30 is a protein called Large ribosomal subunit protein eL27A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	l	135	Total	C	N	O	S	0	0
			1078	698	200	178	2		

- Molecule 31 is a protein called Large ribosomal subunit protein uL15B.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	m	147	Total	C	N	O	S	0	0
			1171	740	235	194	2		

- Molecule 32 is a protein called Large ribosomal subunit protein eL29.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	n	59	Total	C	N	O	0	0
			495	299	112	84		

- Molecule 33 is a protein called Large ribosomal subunit protein eL30A.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	o	94	Total	C	N	O	S	0	0
			705	450	121	130	4		

- Molecule 34 is a protein called Large ribosomal subunit protein eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	p	103	Total	C	N	O	S	0	0
			857	538	167	149	3		

- Molecule 35 is a protein called Large ribosomal subunit protein eL32A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	q	118	Total	C	N	O	S	0	0
			944	591	191	157	5		

- Molecule 36 is a protein called Large ribosomal subunit protein eL33A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	r	104	Total	C	N	O	S	0	0
			831	531	160	137	3		

- Molecule 37 is a protein called Large ribosomal subunit protein eL34B.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	s	106	Total	C	N	O	S	0	0
			858	538	176	142	2		

- Molecule 38 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	t	121	Total	C	N	O		0	0
			999	629	194	176			

- Molecule 39 is a protein called Large ribosomal subunit protein eL36B.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	u	95	Total	C	N	O	S	0	0
			759	472	159	127	1		

- Molecule 40 is a protein called Large ribosomal subunit protein eL37B.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	v	82	Total	C	N	O	S	0	0
			652	399	140	106	7		

- Molecule 41 is a protein called Large ribosomal subunit protein eL38A.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	w	69	Total	C	N	O	S	0	0
			560	355	103	101	1		

- Molecule 42 is a protein called Large ribosomal subunit protein eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	x	50	Total	C	N	O	S	0	0
			436	273	98	64	1		

- Molecule 43 is a protein called Large ribosomal subunit protein eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	y	134	Total	C	N	O	S	0	0
			1039	646	204	187	2		

- Molecule 44 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
44	0	1	Total	Zn	0
			1	1	
44	1	1	Total	Zn	0
			1	1	
44	v	1	Total	Zn	0
			1	1	

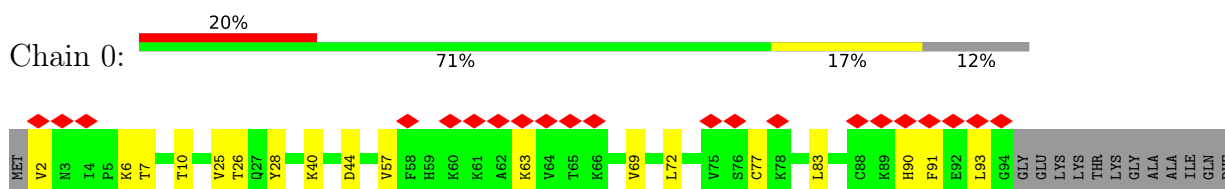
- Molecule 45 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
45	2	91	Total	Mg	0
			91	91	
45	3	2	Total	Mg	0
			2	2	
45	4	1	Total	Mg	0
			1	1	
45	b	1	Total	Mg	0
			1	1	
45	h	1	Total	Mg	0
			1	1	
45	q	1	Total	Mg	0
			1	1	

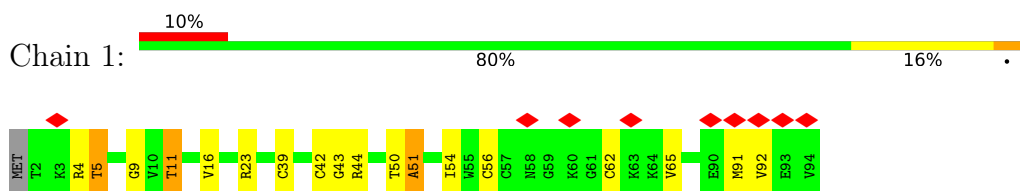
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

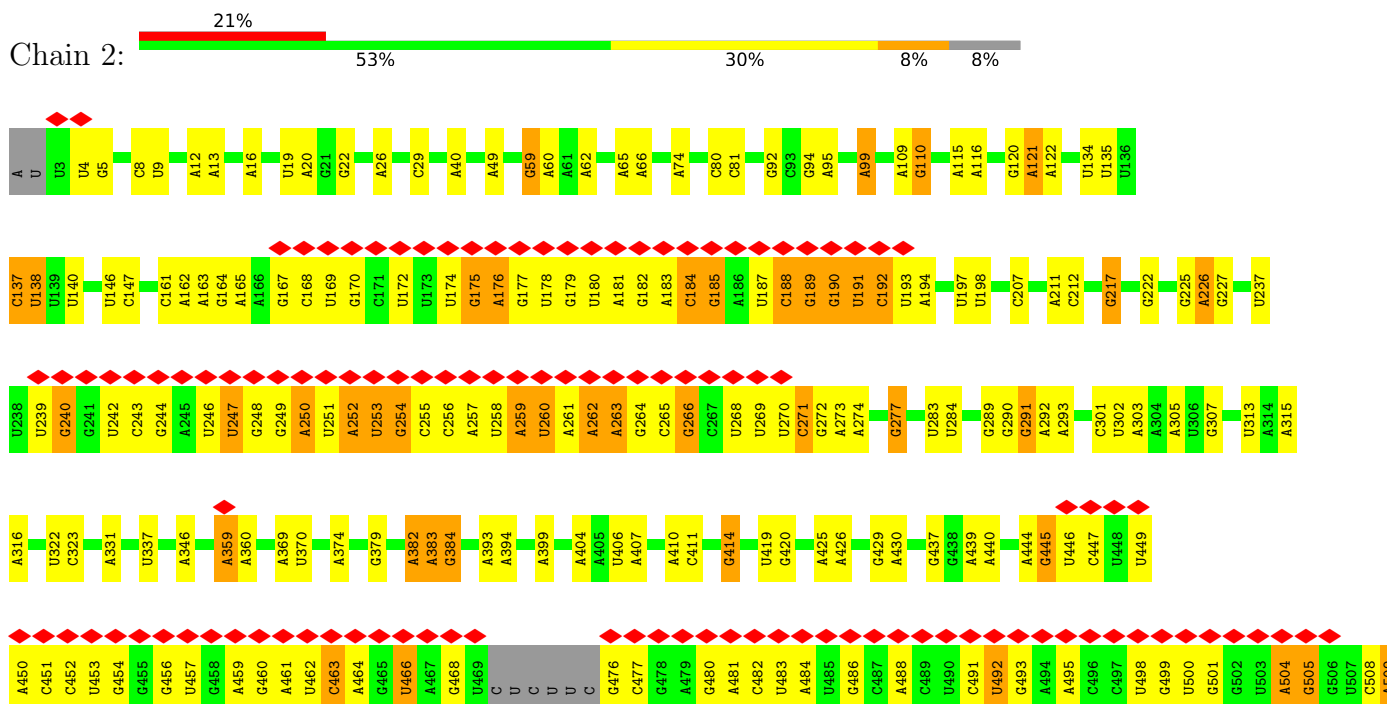
- Molecule 1: Large ribosomal subunit protein eL42

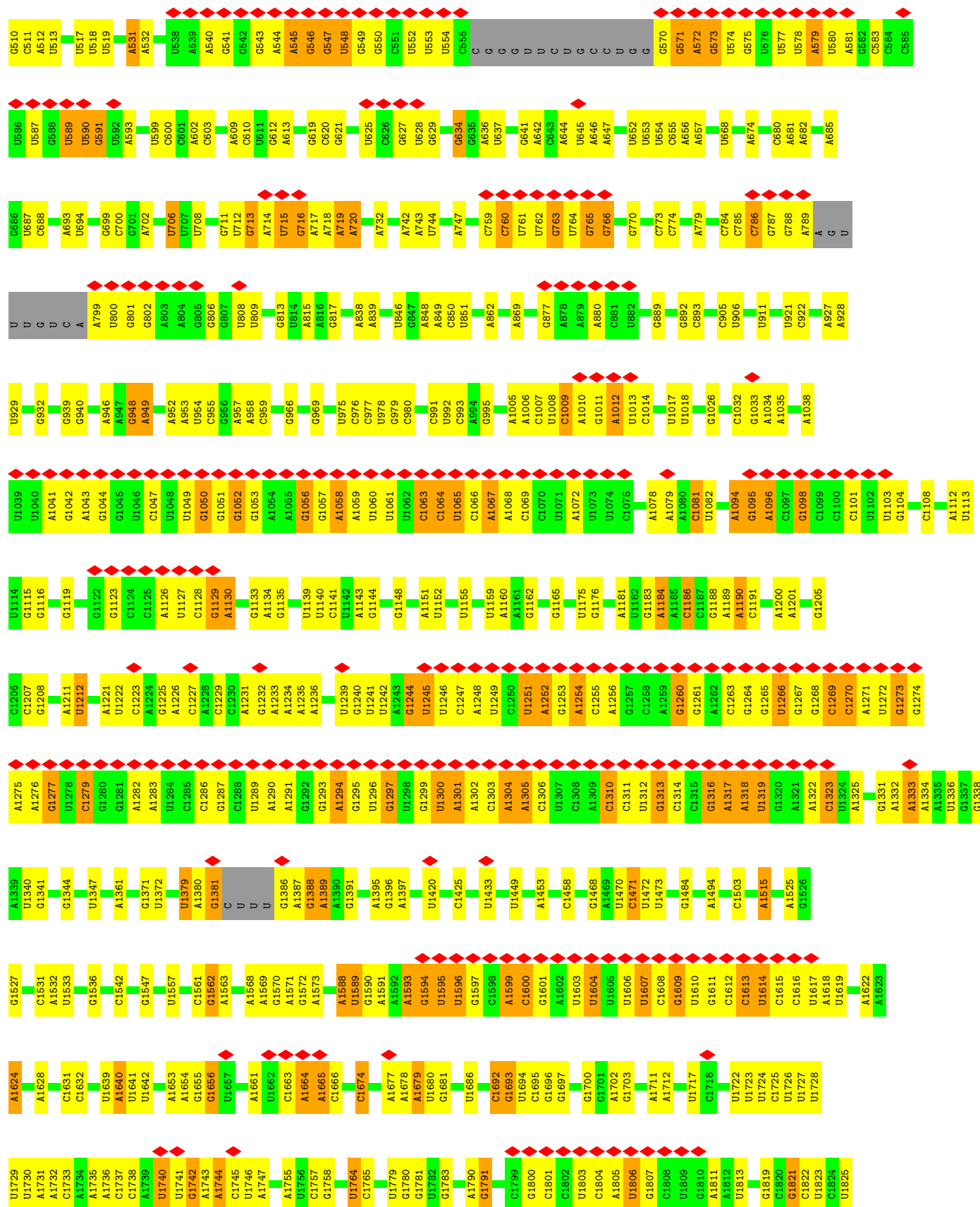


- Molecule 2: Large ribosomal subunit protein eL43A

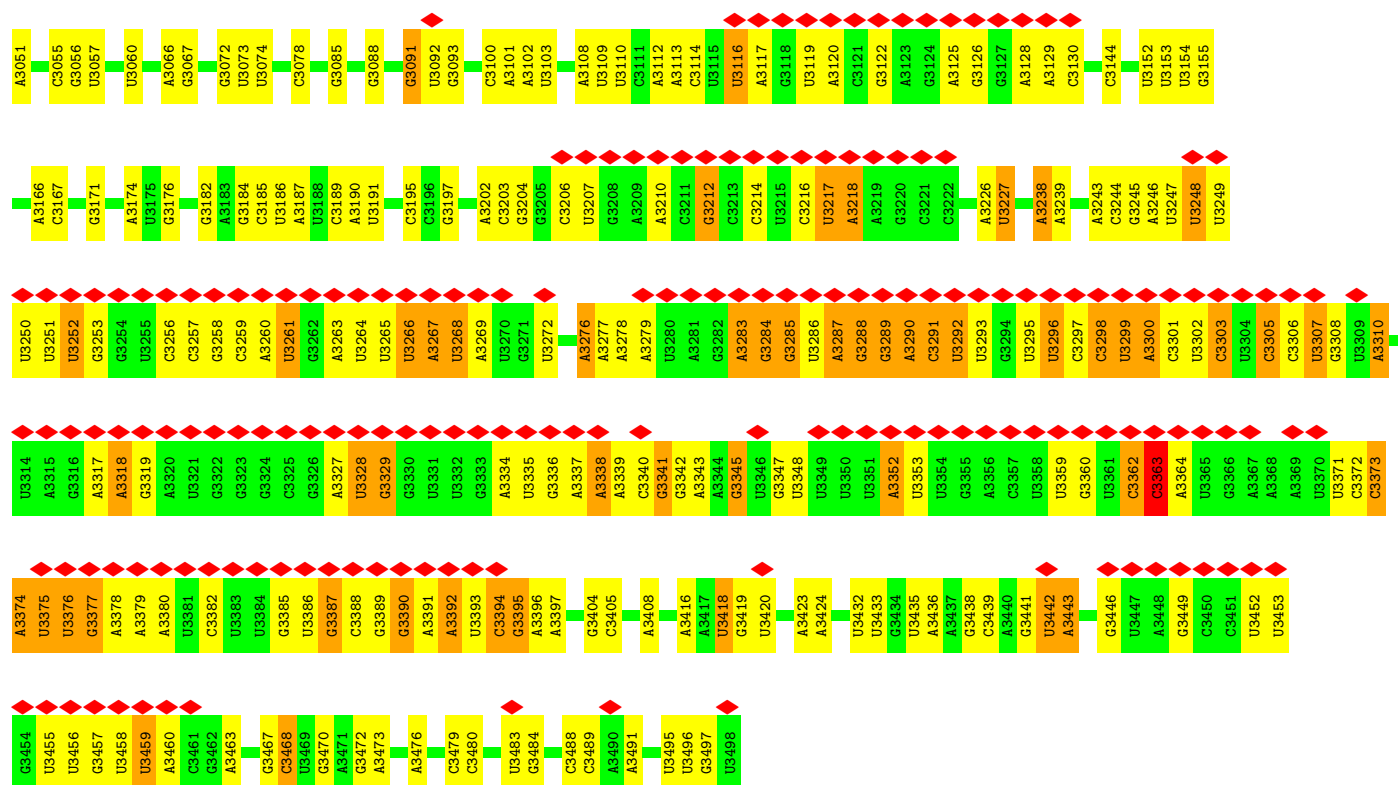


- Molecule 3: 28S ribosomal RNA

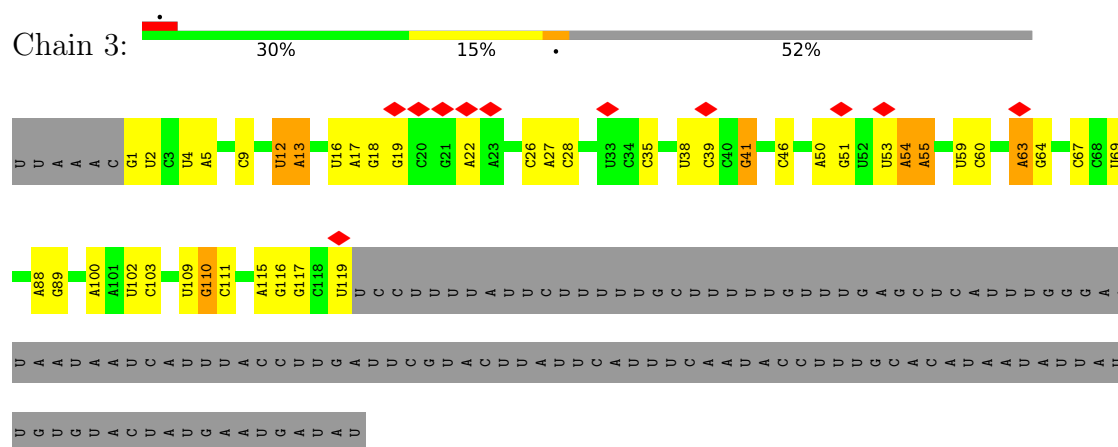








• Molecule 4: 5S ribosomal RNA



• Molecule 5: 5.8S ribosomal RNA



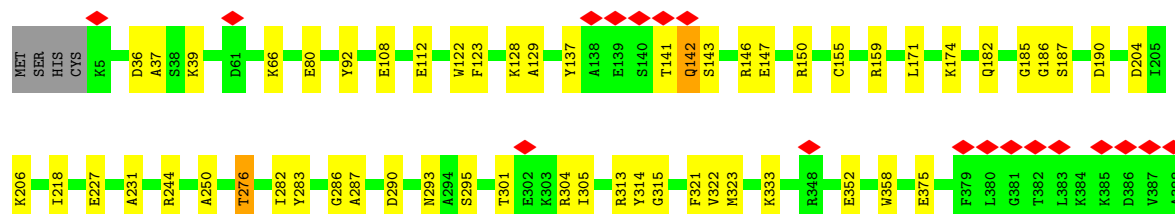
• Molecule 6: Large ribosomal subunit protein uL2C

Chain N:  88% 10%



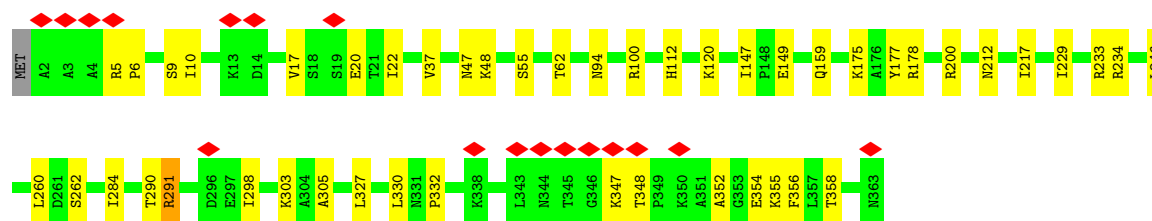
- Molecule 7: Large ribosomal subunit protein uL3A

Chain O:  5% 85% 14%



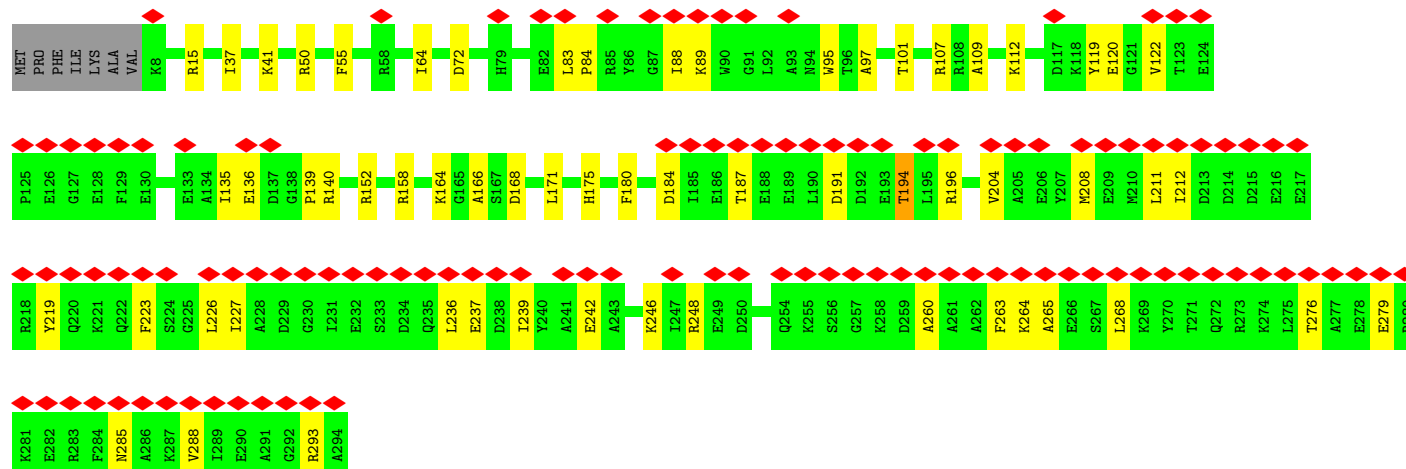
- Molecule 8: Large ribosomal subunit protein uL4A

Chain P:  5% 87% 13%

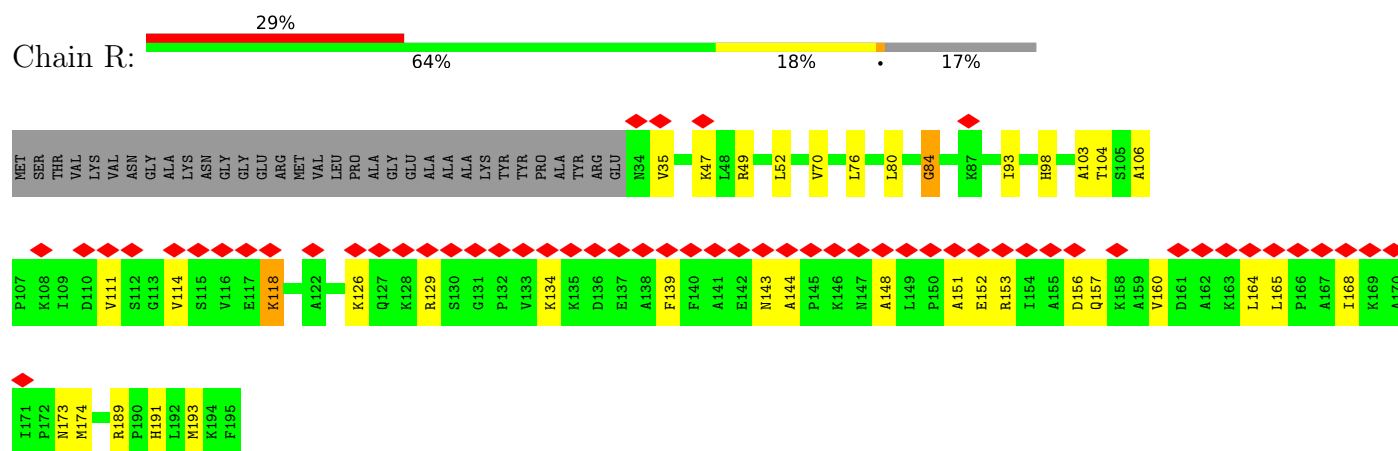


- Molecule 9: Large ribosomal subunit protein uL18B

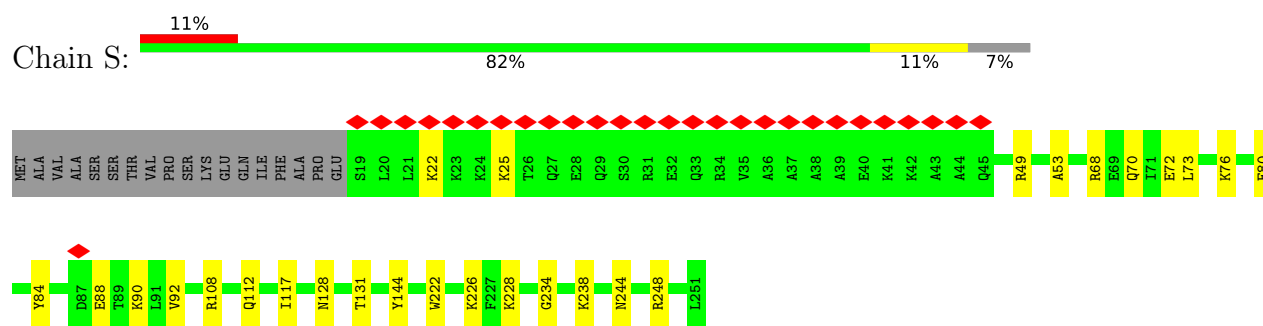
Chain Q:  40% 77% 20%



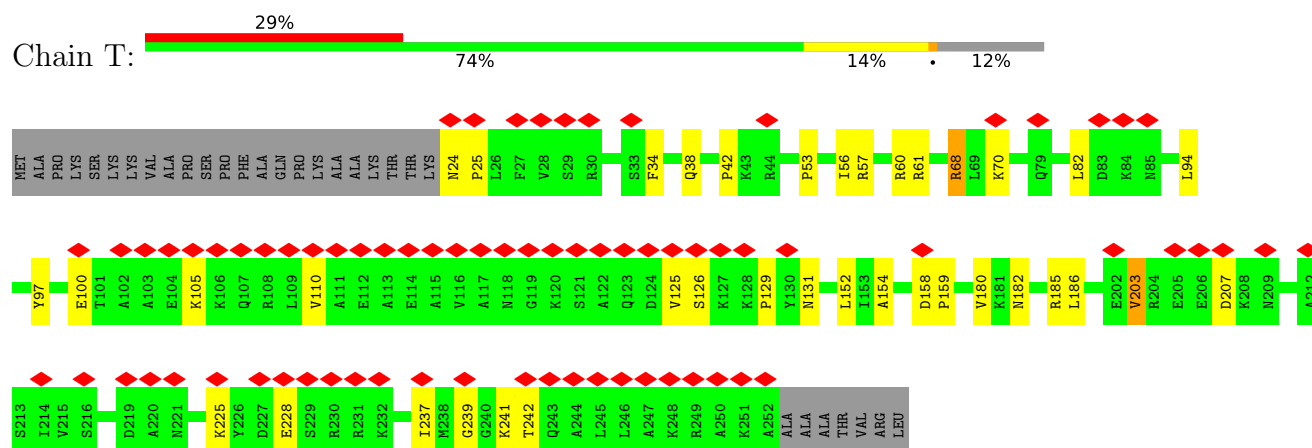
- Molecule 10: Large ribosomal subunit protein eL6



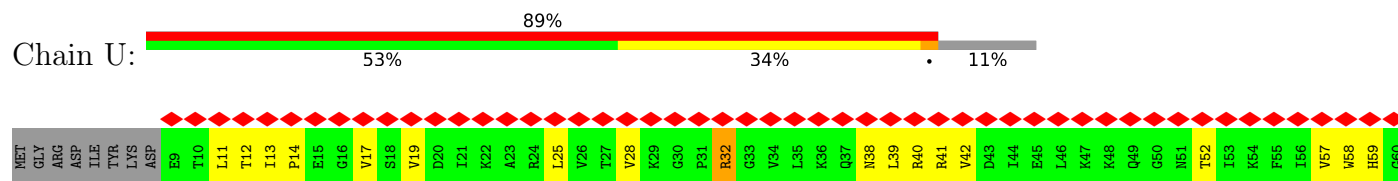
- Molecule 11: Large ribosomal subunit protein uL30C

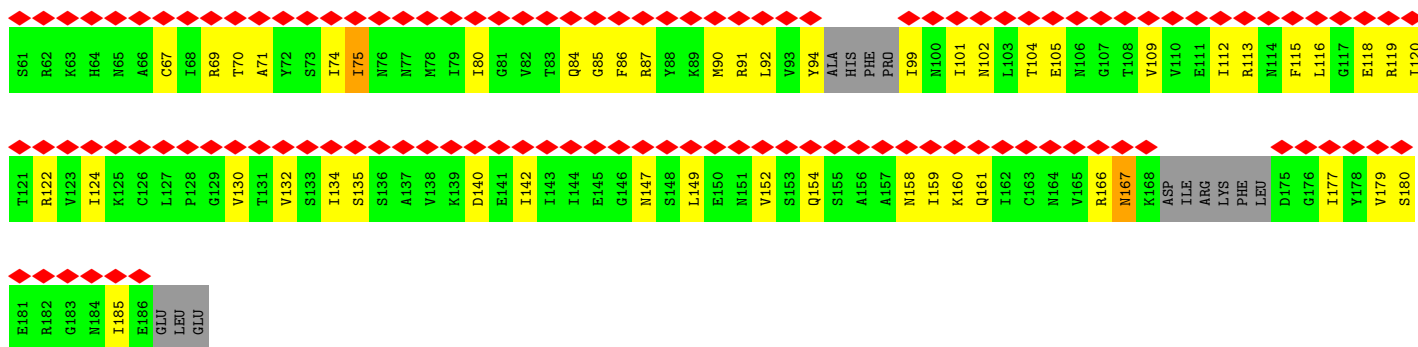


- Molecule 12: Large ribosomal subunit protein eL8

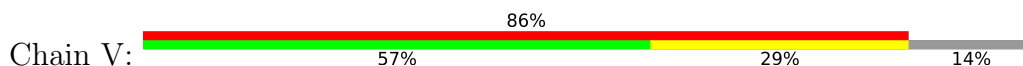


- Molecule 13: Large ribosomal subunit protein uL6B

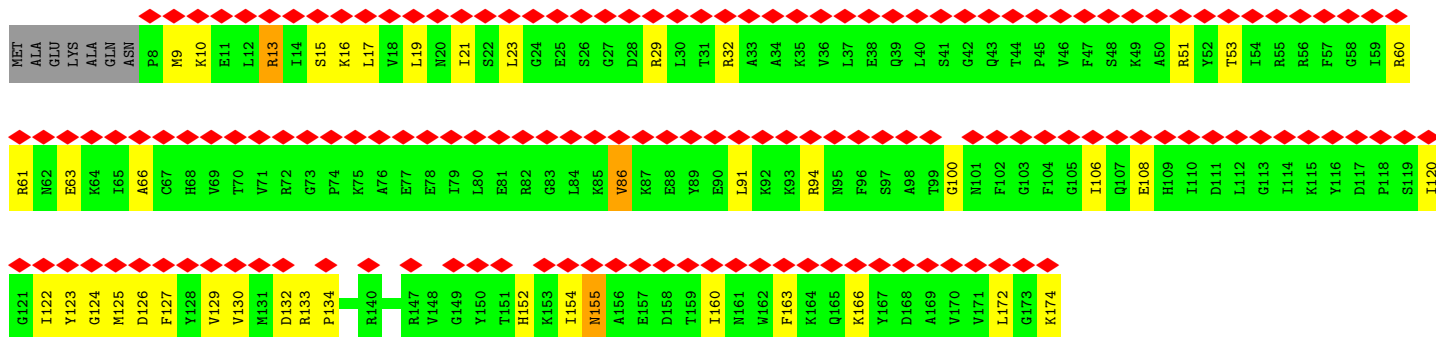
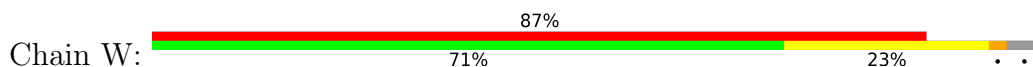




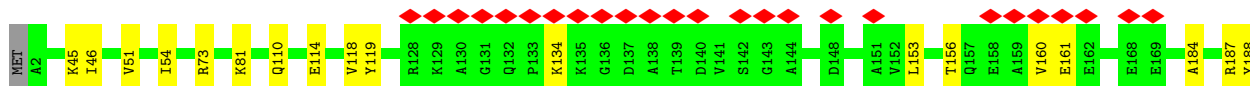
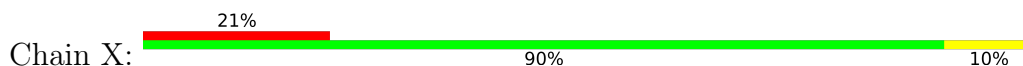
• Molecule 14: Large ribosomal subunit protein uL16A

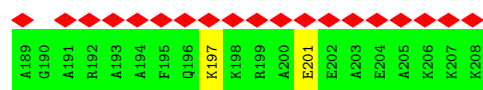


• Molecule 15: Large ribosomal subunit protein uL5A

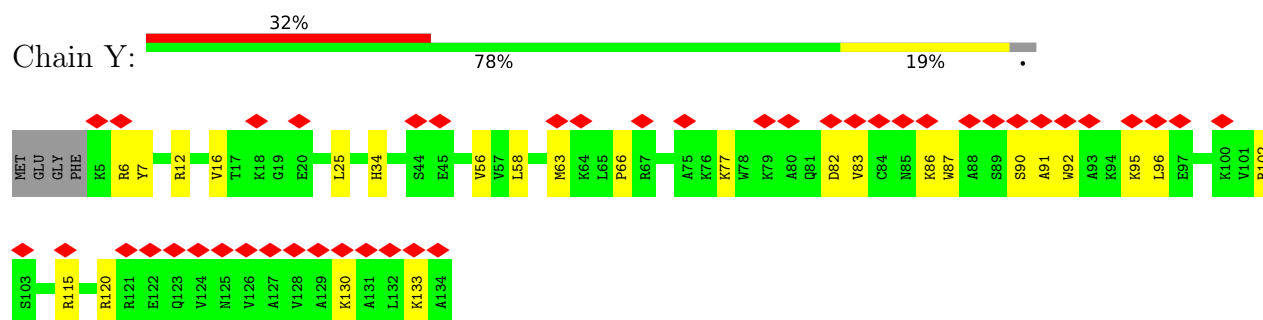


• Molecule 16: Large ribosomal subunit protein eL13

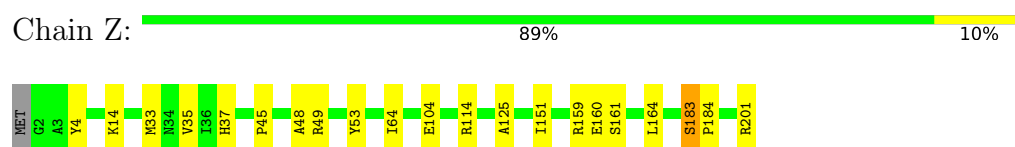




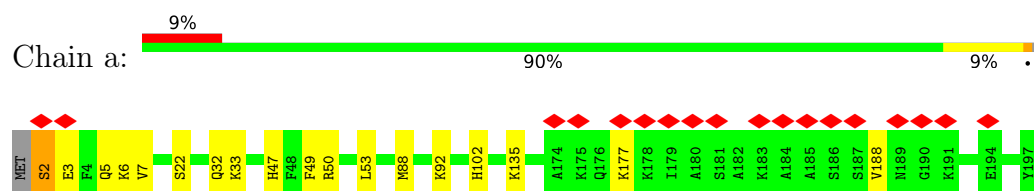
- Molecule 17: Large ribosomal subunit protein eL14



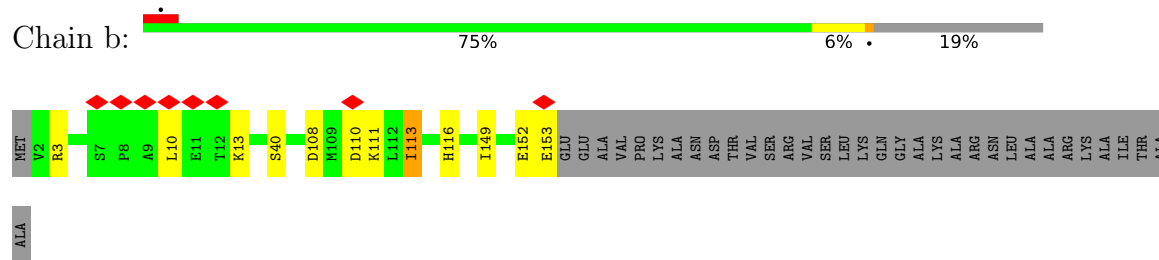
- Molecule 18: Large ribosomal subunit protein eL15B



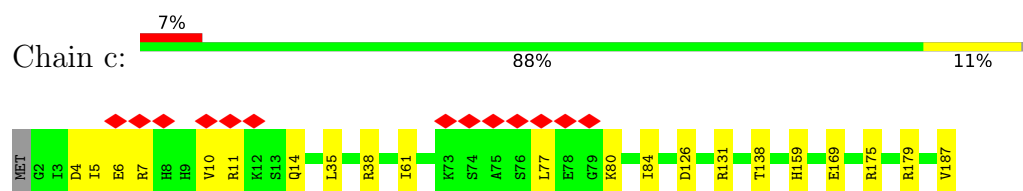
- Molecule 19: Large ribosomal subunit protein uL13A



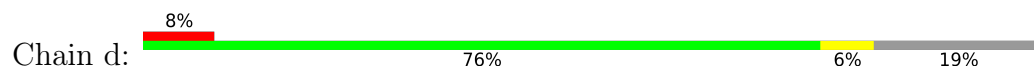
- Molecule 20: Large ribosomal subunit protein uL22A

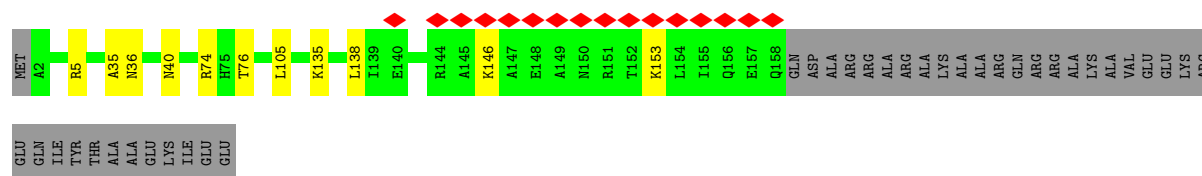


- Molecule 21: Large ribosomal subunit protein eL18B

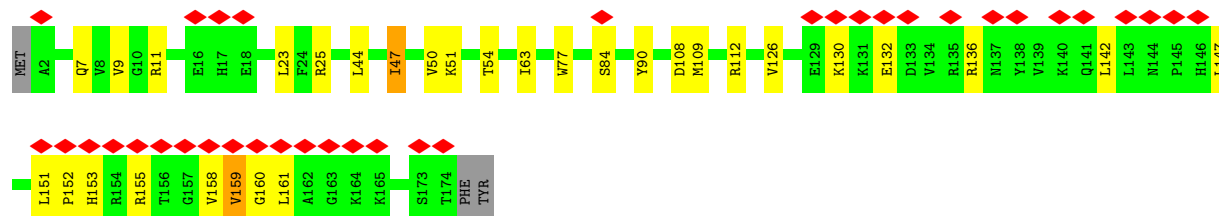
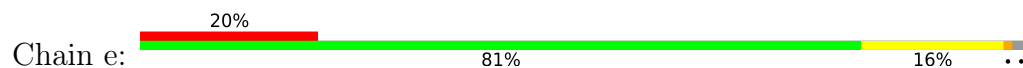


- Molecule 22: Large ribosomal subunit protein eL19B

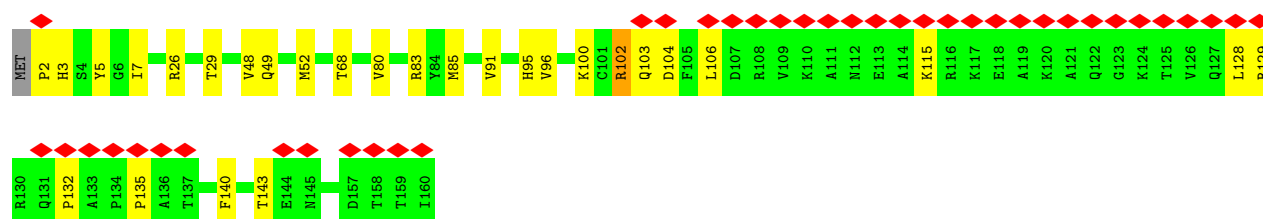
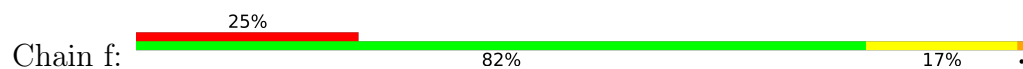




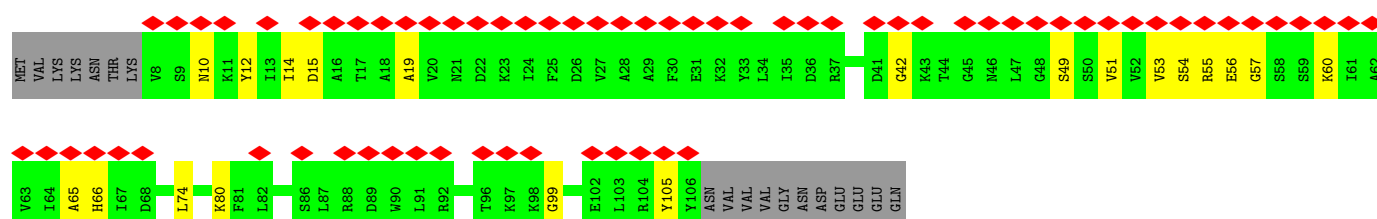
- Molecule 23: Large ribosomal subunit protein eL20A



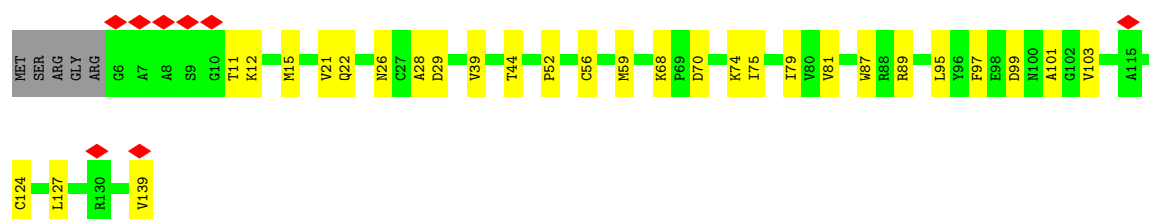
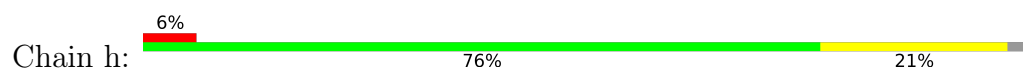
- Molecule 24: Large ribosomal subunit protein eL21B



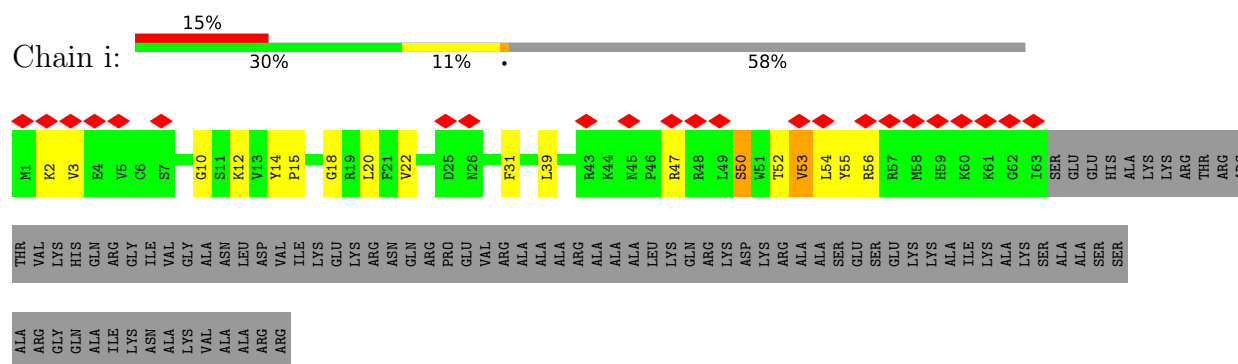
- Molecule 25: Large ribosomal subunit protein eL22



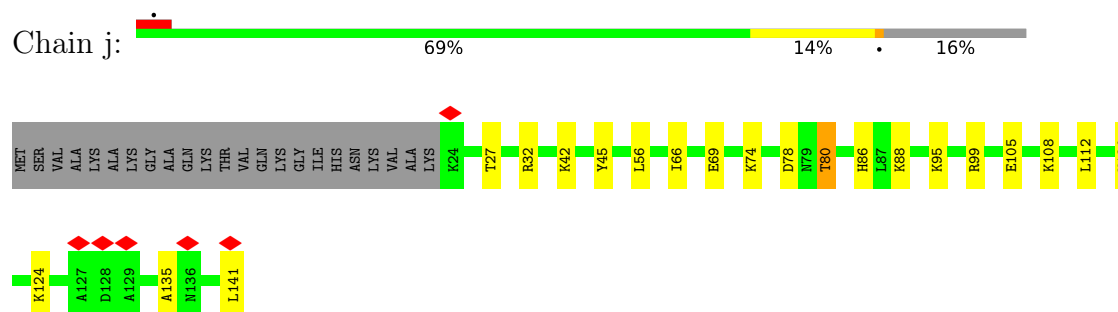
- Molecule 26: Large ribosomal subunit protein uL14B



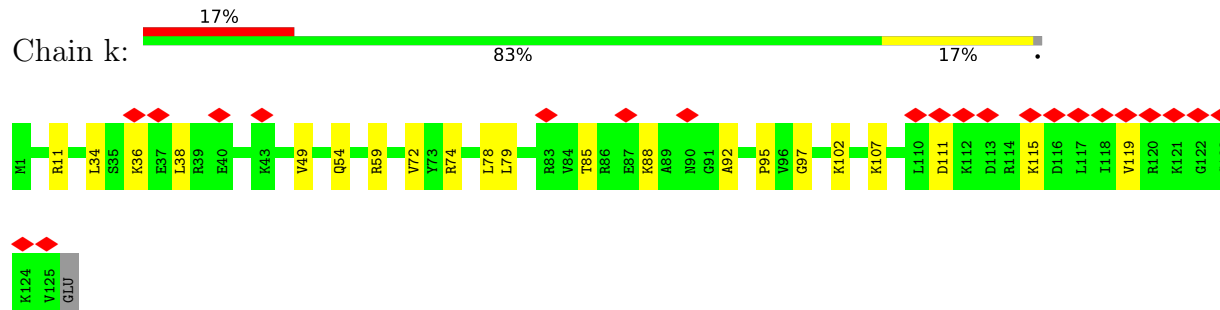
- Molecule 27: Large ribosomal subunit protein eL24B



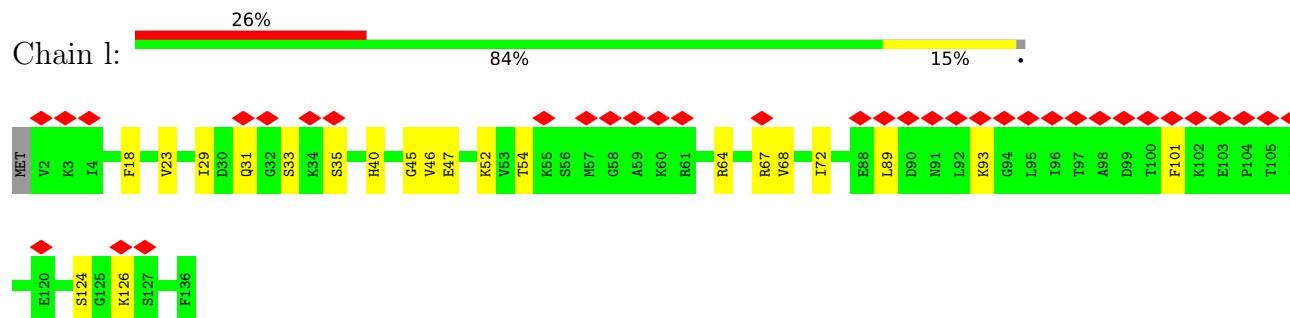
- Molecule 28: Large ribosomal subunit protein uL23A



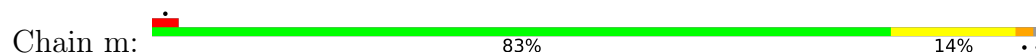
- Molecule 29: Large ribosomal subunit protein uL24



- Molecule 30: Large ribosomal subunit protein eL27A

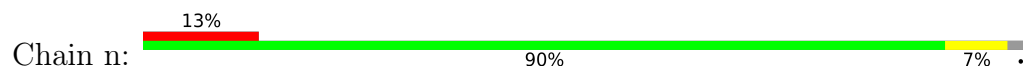


- Molecule 31: Large ribosomal subunit protein uL15B

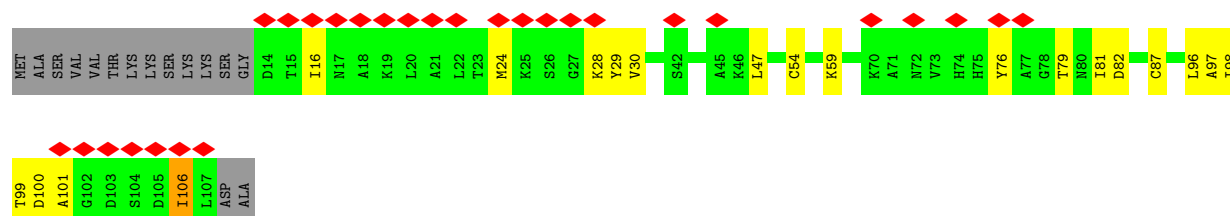




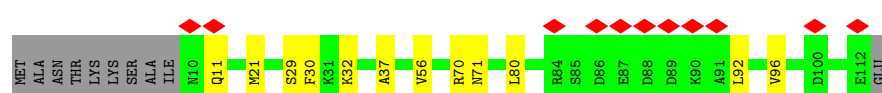
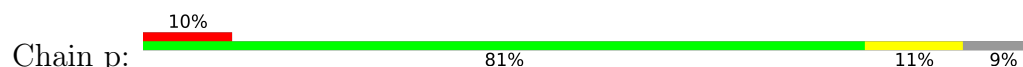
- Molecule 32: Large ribosomal subunit protein eL29



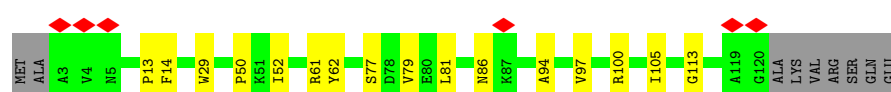
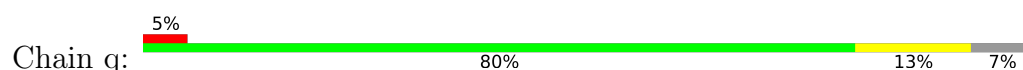
- Molecule 33: Large ribosomal subunit protein eL30A



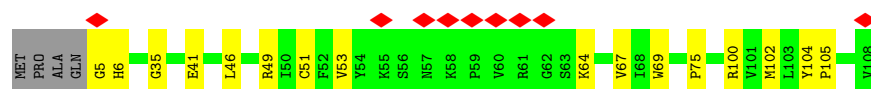
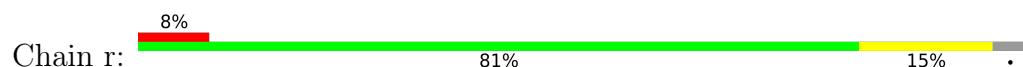
- Molecule 34: Large ribosomal subunit protein eL31



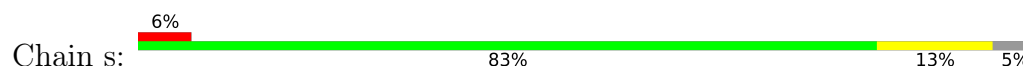
- Molecule 35: Large ribosomal subunit protein eL32A



- Molecule 36: Large ribosomal subunit protein eL33A

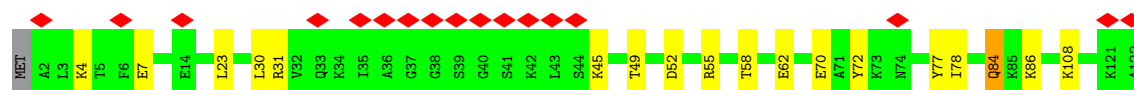
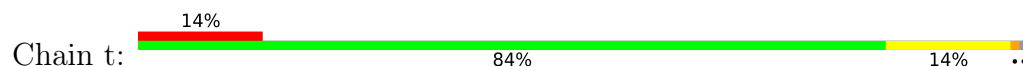


- Molecule 37: Large ribosomal subunit protein eL34B

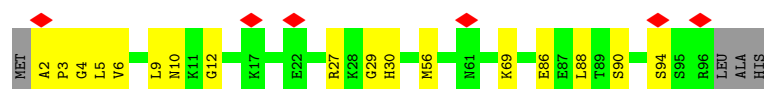




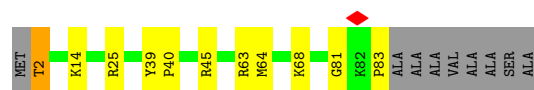
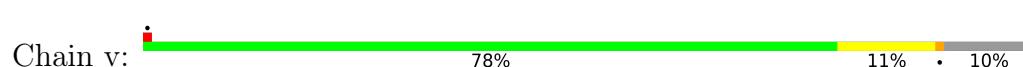
- Molecule 38: Large ribosomal subunit protein uL29



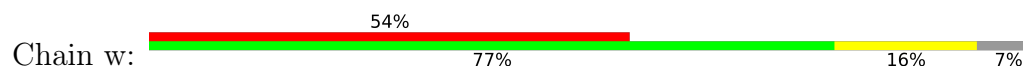
- Molecule 39: Large ribosomal subunit protein eL36B



- Molecule 40: Large ribosomal subunit protein eL37B



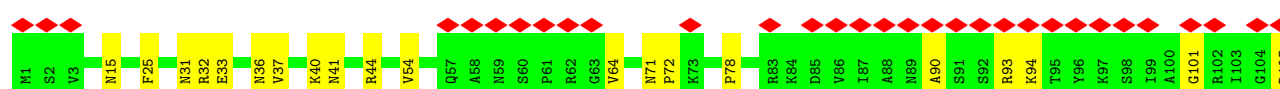
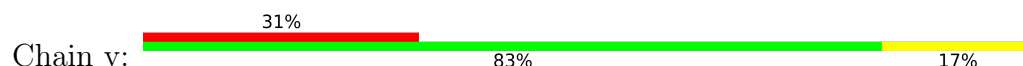
- Molecule 41: Large ribosomal subunit protein eL38A

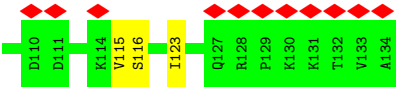


- Molecule 42: Large ribosomal subunit protein eL39



- Molecule 43: Large ribosomal subunit protein eL28





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	820453	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	1600	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	3.551	Depositor
Minimum map value	-1.428	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.080	Depositor
Recommended contour level	0.38	Depositor
Map size (Å)	424.96, 424.96, 424.96	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.83, 0.83, 0.83	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	0	0.30	0/772	0.42	0/1025
2	1	0.31	0/727	0.47	0/973
3	2	0.40	0/76871	0.47	4/119827 (0.0%)
4	3	0.33	0/2838	0.40	0/4422
5	4	0.40	0/3723	0.43	0/5796
6	N	0.32	0/1910	0.49	0/2575
7	O	0.32	0/3116	0.45	0/4190
8	P	0.33	0/2852	0.46	0/3850
9	Q	0.25	0/2361	0.39	0/3173
10	R	0.26	0/1275	0.40	0/1719
11	S	0.30	0/1929	0.40	0/2583
12	T	0.27	0/1801	0.45	0/2430
13	U	0.18	0/1330	0.38	0/1789
14	V	0.17	0/1579	0.35	0/2115
15	W	0.19	0/1369	0.37	0/1830
16	X	0.29	0/1686	0.40	0/2267
17	Y	0.23	0/1054	0.35	0/1413
18	Z	0.38	0/1717	0.54	0/2306
19	a	0.31	0/1575	0.45	0/2109
20	b	0.32	0/1237	0.44	0/1661
21	c	0.31	0/1511	0.46	0/2021
22	d	0.26	0/1320	0.35	0/1757
23	e	0.29	0/1458	0.42	0/1961
24	f	0.29	0/1314	0.42	0/1771
25	g	0.22	0/812	0.44	0/1090
26	h	0.30	0/1015	0.45	0/1369
27	i	0.25	0/534	0.41	0/709
28	j	0.30	0/963	0.46	0/1296
29	k	0.28	0/1008	0.39	0/1341
30	l	0.26	0/1101	0.39	0/1477
31	m	0.35	0/1200	0.53	0/1611
32	n	0.29	0/503	0.43	0/664

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	o	0.27	0/714	0.39	0/961
34	p	0.32	0/872	0.48	0/1172
35	q	0.35	0/958	0.46	0/1278
36	r	0.32	0/853	0.46	0/1146
37	s	0.32	0/870	0.43	0/1165
38	t	0.28	0/1008	0.43	0/1340
39	u	0.28	0/766	0.39	0/1017
40	v	0.37	0/666	0.53	0/881
41	w	0.24	0/566	0.36	0/757
42	x	0.31	0/447	0.51	0/597
43	y	0.27	0/1053	0.45	0/1414
All	All	0.36	0/133234	0.45	4/196848 (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
2	1	0	1
10	R	0	1
All	All	0	2

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	2	3362	C	OP2-P-O3'	-9.53	79.40	108.00
3	2	3362	C	OP1-P-O3'	-8.08	83.75	108.00
3	2	3363	C	OP1-P-OP2	6.14	138.03	119.60
3	2	414	G	O4'-C1'-N9	6.13	117.40	108.20

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	1	51	ALA	Peptide
10	R	84	GLY	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	758	0	815	9	0
2	1	718	0	751	12	0
3	2	68676	0	34522	839	0
4	3	2539	0	1283	30	0
5	4	3332	0	1684	44	0
6	N	1872	0	1917	22	0
7	O	3050	0	3125	40	0
8	P	2799	0	2925	36	0
9	Q	2312	0	2272	41	0
10	R	1251	0	1337	26	0
11	S	1897	0	1984	19	0
12	T	1772	0	1866	28	0
13	U	1319	0	1389	42	0
14	V	1549	0	1591	44	0
15	W	1346	0	1397	34	0
16	X	1654	0	1705	14	0
17	Y	1038	0	1115	18	0
18	Z	1676	0	1712	16	0
19	a	1545	0	1641	17	0
20	b	1212	0	1239	6	0
21	c	1487	0	1597	17	0
22	d	1301	0	1393	8	0
23	e	1423	0	1488	23	0
24	f	1286	0	1310	21	0
25	g	798	0	834	13	0
26	h	999	0	1047	17	0
27	i	523	0	555	12	0
28	j	947	0	1012	19	0
29	k	998	0	1090	14	0
30	l	1078	0	1154	13	0
31	m	1171	0	1215	17	0
32	n	495	0	504	3	0
33	o	705	0	746	16	0
34	p	857	0	891	8	0
35	q	944	0	1005	11	0
36	r	831	0	858	13	0
37	s	858	0	925	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	t	999	0	1092	15	0
39	u	759	0	840	12	0
40	v	652	0	662	13	0
41	w	560	0	608	8	0
42	x	436	0	463	24	0
43	y	1039	0	1092	22	0
44	0	1	0	0	0	0
44	1	1	0	0	0	0
44	v	1	0	0	0	0
45	2	91	0	0	0	0
45	3	2	0	0	0	0
45	4	1	0	0	0	0
45	b	1	0	0	0	0
45	h	1	0	0	0	0
45	q	1	0	0	0	0
All	All	123561	0	88651	1459	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 7.

All (1459) 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)
3:2:1536:G:N2	3:2:1547:G:N7	1.98	1.11
3:2:2298:G:H22	3:2:2322:G:H1	1.09	0.97
3:2:3210:A:H62	3:2:3214:C:H42	0.98	0.95
4:3:2:U:H3	4:3:117:G:H1	1.10	0.95
3:2:1742:G:H1	3:2:1781:G:H1	0.94	0.94
3:2:1183:G:N2	3:2:1231:A:N1	2.16	0.92
3:2:2990:G:H1	3:2:3000:U:H3	1.14	0.91
3:2:3210:A:N6	3:2:3214:C:H42	1.67	0.91
2:1:4:ARG:NH1	3:2:869:A:OP2	2.03	0.90
3:2:3248:U:OP1	3:2:3497:G:N1	2.04	0.89
3:2:3261:U:H3	3:2:3385:G:H1	0.91	0.89
3:2:3335:U:H3'	3:2:3336:G:H21	1.38	0.87
3:2:1728:U:OP1	37:s:28:ASN:ND2	2.08	0.87
10:R:93:ILE:HD11	10:R:160:VAL:HG21	1.55	0.87
28:j:86:HIS:HD2	28:j:88:LYS:H	1.23	0.86
3:2:1744:A:H61	3:2:1779:U:H3	1.22	0.85
17:Y:6:ARG:NH1	17:Y:58:LEU:O	2.09	0.85
3:2:3245:G:O2'	7:O:129:ALA:O	1.93	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:d:35:ALA:O	22:d:40:ASN:ND2	2.11	0.84
3:2:1297:G:N2	3:2:1306:C:O2	2.11	0.83
3:2:1297:G:N1	3:2:1306:C:N3	2.25	0.83
6:N:103:VAL:HA	6:N:106:MET:HE2	1.60	0.83
3:2:1588:A:O4'	3:2:1593:A:N6	2.12	0.83
15:W:108:GLU:HA	15:W:122:ILE:HD11	1.59	0.83
3:2:3210:A:H62	3:2:3214:C:N4	1.76	0.82
3:2:2342:U:O2	3:2:2350:A:N6	2.12	0.82
3:2:2525:G:H1	3:2:2606:U:H3	1.24	0.81
3:2:2304:G:H1	3:2:2317:A:H61	1.30	0.80
3:2:2730:A:H2	3:2:2737:A:H62	1.29	0.80
5:4:132:G:H1	5:4:137:A:H61	1.27	0.80
3:2:359:A:N6	42:x:37:TYR:O	2.15	0.79
13:U:42:VAL:HG21	13:U:71:ALA:HB2	1.65	0.79
2:1:5:THR:HG21	2:1:9:GLY:H	1.48	0.79
3:2:3122:G:N2	3:2:3125:A:OP2	2.15	0.79
8:P:112:HIS:HB3	18:Z:201:ARG:HB3	1.65	0.79
3:2:1995:G:H21	3:2:3463:A:H8	1.32	0.79
14:V:52:LEU:HB2	14:V:152:LEU:HD12	1.65	0.78
3:2:3184:G:OP1	7:O:313:ARG:NH2	2.16	0.78
5:4:92:C:N3	29:k:115:LYS:NZ	2.31	0.78
3:2:1742:G:H22	3:2:1781:G:H22	1.32	0.77
3:2:2769:A:H62	3:2:2775:A:H61	1.30	0.77
3:2:3016:U:O2	3:2:3020:C:N4	2.18	0.77
3:2:2003:G:H22	3:2:2187:A:H2	1.32	0.77
3:2:3247:U:O2'	3:2:3497:G:N2	2.19	0.76
36:r:49:ARG:HD2	36:r:69:TRP:HE3	1.49	0.76
3:2:2680:C:O2	12:T:68:ARG:NH1	2.17	0.76
3:2:1255:C:H2'	3:2:1256:A:H8	1.51	0.76
40:v:25:ARG:HD3	42:x:51:ILE:HD12	1.65	0.76
3:2:110:G:OP2	16:X:73:ARG:NH2	2.19	0.75
3:2:3144:C:H5	3:2:3187:A:H62	1.33	0.75
3:2:706:U:O4	8:P:120:LYS:NZ	2.20	0.75
12:T:53:PRO:HG2	12:T:56:ILE:HD12	1.69	0.75
11:S:73:LEU:HD22	24:f:140:PHE:HZ	1.51	0.75
3:2:191:U:O2'	3:2:192:C:OP1	2.03	0.74
21:c:159:HIS:H	21:c:187:VAL:HG12	1.52	0.73
9:Q:37:ILE:HD12	9:Q:37:ILE:O	1.87	0.73
24:f:103:GLN:NE2	24:f:104:ASP:OD1	2.22	0.73
3:2:466:U:O4	3:2:486:G:N1	2.21	0.73
8:P:37:VAL:HG21	8:P:246:LEU:HD21	1.70	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:j:95:LYS:HE2	28:j:99:ARG:HH22	1.55	0.72
3:2:1223:C:N4	3:2:1332:A:O2'	2.21	0.72
3:2:3000:U:H2'	3:2:3002:G:H1'	1.70	0.72
3:2:481:A:H2'	3:2:482:C:H6	1.54	0.72
3:2:713:G:H1	8:P:234:ARG:HH22	1.37	0.72
29:k:49:VAL:HG21	29:k:79:LEU:HD21	1.72	0.72
3:2:505:G:H1	3:2:644:A:H2	1.38	0.71
5:4:59:G:H8	5:4:60:A:H62	1.36	0.71
3:2:3112:A:H2'	3:2:3113:A:C8	2.26	0.71
3:2:2653:G:N2	12:T:38:GLN:O	2.24	0.71
5:4:83:G:N7	42:x:30:ARG:NH1	2.37	0.71
31:m:125:GLN:HG2	31:m:145:GLU:HG2	1.72	0.71
3:2:3014:A:H61	3:2:3022:C:H42	1.37	0.71
3:2:1764:U:H1'	3:2:1765:C:C6	2.26	0.70
5:4:56:A:O2'	5:4:59:G:N2	2.25	0.70
3:2:1655:G:N2	3:2:1656:G:O6	2.24	0.70
3:2:374:A:N1	42:x:39:MET:HE1	2.07	0.70
6:N:106:MET:HE1	6:N:112:ILE:HG21	1.74	0.70
36:r:49:ARG:HD2	36:r:69:TRP:CE3	2.26	0.70
3:2:1379:U:H5'	3:2:1389:A:N6	2.06	0.70
3:2:1387:A:H5''	3:2:1388:G:H5'	1.74	0.70
3:2:3258:G:N2	3:2:3389:G:N7	2.41	0.69
26:h:26:ASN:ND2	26:h:99:ASP:OD2	2.21	0.69
3:2:3204:G:H21	13:U:161:GLN:HE22	1.40	0.69
33:o:24:MET:HE1	33:o:87:CYS:HB3	1.74	0.69
40:v:14:LYS:HD3	42:x:51:ILE:HD11	1.75	0.69
3:2:359:A:OP1	42:x:34:THR:OG1	2.11	0.69
3:2:167:G:H22	3:2:268:U:H3	1.40	0.69
3:2:3284:G:H3'	3:2:3285:G:H4'	1.73	0.69
16:X:160:VAL:HG11	31:m:105:GLN:HE22	1.58	0.69
15:W:125:MET:HE2	15:W:125:MET:HA	1.75	0.69
3:2:188:C:N3	3:2:190:G:N2	2.41	0.69
3:2:453:U:H2'	3:2:454:G:H8	1.56	0.69
14:V:40:ARG:H	14:V:40:ARG:HD2	1.57	0.68
9:Q:211:LEU:HB3	9:Q:219:TYR:HB2	1.75	0.68
3:2:3268:U:O4	19:a:102:HIS:NE2	2.23	0.68
3:2:3119:U:O2	3:2:3128:A:N7	2.26	0.68
3:2:1275:A:O2'	3:2:1279:C:N4	2.26	0.68
3:2:3212:G:N2	3:2:3212:G:OP1	2.26	0.68
13:U:94:TYR:HD2	13:U:101:ILE:HG12	1.59	0.68
3:2:3329:G:O5'	17:Y:130:LYS:NZ	2.26	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2:2445:A:H2'	3:2:2446:A:C8	2.28	0.67
3:2:2445:A:H2'	3:2:2446:A:H8	1.59	0.67
3:2:476:G:H1	3:2:481:A:H61	1.42	0.67
3:2:1819:G:O2'	3:2:1821:G:OP2	2.11	0.67
3:2:1780:G:N2	3:2:1781:G:O6	2.28	0.67
3:2:3265:U:O2'	3:2:3266:U:O2	2.13	0.67
3:2:3109:U:H2'	3:2:3110:U:C6	2.30	0.67
19:a:47:HIS:CD2	19:a:50:ARG:H	2.14	0.67
3:2:1268:G:O6	3:2:1282:A:N1	2.29	0.66
3:2:3217:U:H1'	3:2:3218:A:H5''	1.77	0.66
9:Q:236:LEU:HA	9:Q:239:ILE:HD12	1.77	0.66
16:X:160:VAL:CG1	31:m:105:GLN:HE22	2.08	0.66
14:V:73:ASN:HB3	14:V:74:LYS:HE2	1.75	0.66
31:m:103:VAL:HG13	31:m:108:TYR:HB2	1.78	0.66
3:2:305:A:H8	39:u:29:GLY:HA2	1.60	0.66
3:2:460:G:H22	3:2:493:G:H1	1.42	0.66
3:2:1674:C:OP2	37:s:74:ARG:NH1	2.24	0.66
38:t:31:ARG:HG2	38:t:31:ARG:HH11	1.59	0.66
3:2:1875:U:OP1	3:2:1876:U:H5'	1.94	0.66
7:O:218:ILE:HG12	7:O:276:THR:HB	1.77	0.66
13:U:41:ARG:HG3	13:U:42:VAL:HG23	1.78	0.66
3:2:1742:G:N2	3:2:1781:G:H22	1.93	0.66
26:h:12:LYS:HB2	26:h:127:LEU:HD11	1.77	0.66
1:O:2:VAL:N	1:O:90:HIS:O	2.29	0.66
2:1:11:THR:HG21	2:1:23:ARG:HB3	1.78	0.65
3:2:140:U:H5''	38:t:84:GLN:HG2	1.77	0.65
14:V:201:ASN:O	14:V:209:LYS:NZ	2.29	0.65
25:g:57:GLY:N	25:g:60:LYS:O	2.29	0.65
3:2:718:A:OP1	8:P:48:LYS:NZ	2.28	0.65
23:e:151:LEU:HD12	23:e:152:PRO:HD2	1.77	0.65
3:2:2188:A:H4'	3:2:2188:A:OP1	1.95	0.65
3:2:2323:C:H2'	3:2:2324:G:C8	2.32	0.65
3:2:3043:C:OP1	7:O:244:ARG:NH2	2.30	0.65
22:d:105:LEU:HD22	22:d:135:LYS:HG2	1.79	0.65
42:x:28:ARG:NH1	42:x:36:HIS:O	2.30	0.65
3:2:1347:U:O4	23:e:153:HIS:NE2	2.29	0.65
10:R:104:THR:HG22	10:R:106:ALA:H	1.62	0.65
3:2:1297:G:O6	3:2:1306:C:N4	2.30	0.65
3:2:2913:U:H6	3:2:2913:U:H5'	1.61	0.65
3:2:980:C:O2'	21:c:11:ARG:NH1	2.31	0.64
27:i:2:LYS:H	27:i:2:LYS:HD3	1.61	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2:459:A:H2'	3:2:460:G:C8	2.33	0.64
3:2:1597:G:OP2	3:2:1597:G:N2	2.29	0.64
3:2:3261:U:O2	3:2:3385:G:N2	2.21	0.64
3:2:3377:G:H2'	3:2:3378:A:C8	2.31	0.64
13:U:14:PRO:HD2	13:U:17:VAL:HG21	1.78	0.64
3:2:1388:G:O2'	3:2:1389:A:OP1	2.16	0.64
3:2:2293:U:H3	3:2:2325:C:H42	1.44	0.64
33:o:47:LEU:HD23	33:o:98:ILE:HD12	1.77	0.64
3:2:180:U:O4	3:2:181:A:N6	2.30	0.64
38:t:52:ASP:OD1	38:t:55:ARG:NH1	2.30	0.64
21:c:77:LEU:HA	21:c:80:LYS:HD3	1.79	0.64
3:2:3283:A:N6	3:2:3288:G:N7	2.42	0.64
3:2:3246:A:H5'	7:O:129:ALA:O	1.97	0.64
5:4:46:U:H5	38:t:84:GLN:O	1.81	0.64
3:2:747:A:O2'	3:2:815:A:O2'	2.14	0.64
3:2:1072:A:O2'	14:V:198:LYS:NZ	2.31	0.64
3:2:2494:C:H2'	3:2:2495:C:C6	2.33	0.64
3:2:3154:U:O4	34:p:70:ARG:NH2	2.31	0.64
3:2:3264:U:H3	3:2:3382:C:H42	1.46	0.64
3:2:3389:G:H5''	3:2:3390:G:C8	2.33	0.64
3:2:445:G:H1	3:2:647:A:H61	1.45	0.63
3:2:3171:G:OP1	34:p:71:ASN:ND2	2.32	0.63
3:2:3289:G:N2	3:2:3299:U:O2'	2.31	0.63
31:m:95:THR:OG1	31:m:97:VAL:O	2.15	0.63
3:2:454:G:H22	3:2:499:G:H22	1.45	0.63
3:2:716:G:N2	3:2:716:G:OP1	2.31	0.63
15:W:21:ILE:HD11	15:W:66:ALA:HA	1.79	0.63
7:O:142:GLN:HG3	7:O:146:ARG:HH22	1.63	0.63
3:2:253:U:H3'	3:2:254:G:H8	1.63	0.63
3:2:1052:G:O2'	3:2:1053:G:O4'	2.17	0.63
29:k:78:LEU:HD13	29:k:97:GLY:HA3	1.79	0.63
7:O:186:GLY:O	7:O:190:ASP:HB2	1.98	0.63
5:4:91:C:O4'	5:4:93:G:N2	2.32	0.63
3:2:454:G:N2	3:2:499:G:H22	1.96	0.63
3:2:2680:C:H42	12:T:237:ILE:HD12	1.64	0.63
3:2:3112:A:H2'	3:2:3113:A:H8	1.62	0.63
31:m:132:ARG:HG3	31:m:132:ARG:HH11	1.63	0.63
3:2:120:G:N2	12:T:126:SER:OG	2.32	0.62
3:2:190:G:O2'	3:2:191:U:O4'	2.17	0.62
3:2:719:A:OP1	18:Z:201:ARG:NH1	2.32	0.62
13:U:19:VAL:HG22	13:U:28:VAL:HG12	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:Q:119:TYR:OH	9:Q:139:PRO:O	2.17	0.62
3:2:277:G:H5''	18:Z:14:LYS:HE2	1.80	0.62
7:O:290:ASP:OD1	7:O:293:ASN:ND2	2.31	0.62
3:2:3119:U:H2'	3:2:3120:A:H8	1.64	0.62
7:O:286:GLY:HA3	7:O:321:PHE:CE1	2.33	0.62
12:T:94:LEU:HD11	12:T:152:LEU:HD13	1.81	0.62
14:V:183:GLU:OE2	14:V:187:ARG:NH2	2.31	0.62
3:2:262:A:H2'	3:2:263:A:C8	2.35	0.62
13:U:104:THR:OG1	13:U:113:ARG:NH1	2.33	0.62
3:2:2631:G:H2'	3:2:2632:A:C2	2.35	0.62
4:3:54:A:O2'	4:3:55:A:H8	1.83	0.62
3:2:217:G:C4	3:2:237:U:H4'	2.34	0.62
3:2:2629:G:H2'	3:2:2630:G:C8	2.34	0.62
3:2:182:G:N2	3:2:248:G:H22	1.98	0.61
26:h:89:ARG:HH22	26:h:139:VAL:HG21	1.65	0.61
3:2:1609:G:H2'	3:2:1610:U:C6	2.35	0.61
39:u:27:ARG:HG2	39:u:30:HIS:CD2	2.36	0.61
15:W:15:SER:HB2	15:W:132:ASP:HB2	1.82	0.61
3:2:1692:C:O2'	3:2:1838:A:OP2	2.13	0.61
3:2:249:G:O6	3:2:250:A:N6	2.33	0.61
3:2:2188:A:H2'	3:2:2189:C:C6	2.36	0.61
3:2:2298:G:N2	3:2:2322:G:H1	1.90	0.61
3:2:3288:G:H2'	3:2:3289:G:H8	1.65	0.61
3:2:3328:U:H5''	17:Y:130:LYS:HE3	1.82	0.61
7:O:305:ILE:O	7:O:305:ILE:HG23	2.00	0.61
3:2:1918:G:N1	3:2:1921:C:OP2	2.30	0.61
3:2:2301:A:H2'	3:2:2302:A:C8	2.35	0.61
11:S:228:LYS:HG3	11:S:234:GLY:HA3	1.83	0.61
15:W:32:ARG:NH1	15:W:120:ILE:O	2.34	0.61
33:o:16:ILE:HD13	33:o:76:TYR:HE2	1.64	0.61
43:y:37:VAL:HG21	43:y:116:SER:HA	1.82	0.61
3:2:3055:C:H2'	3:2:3056:G:C8	2.35	0.61
18:Z:183:SER:HB3	18:Z:184:PRO:HD2	1.83	0.61
27:i:47:ARG:HD3	27:i:54:LEU:HB3	1.83	0.61
3:2:2633:U:O2'	3:2:2639:U:O2	2.19	0.61
3:2:1165:G:O2'	3:2:2737:A:N3	2.32	0.60
3:2:481:A:H2'	3:2:482:C:C6	2.35	0.60
9:Q:265:ALA:HA	9:Q:268:LEU:HD12	1.83	0.60
4:3:16:U:H2'	4:3:17:A:C8	2.37	0.60
4:3:54:A:O3'	15:W:10:LYS:NZ	2.31	0.60
41:w:50:ASP:HB3	41:w:53:LYS:HB2	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2:498:U:H2'	3:2:499:G:C8	2.36	0.60
3:2:1379:U:H5'	3:2:1389:A:H61	1.65	0.60
5:4:88:A:H4'	5:4:89:U:O5'	2.00	0.60
13:U:85:GLY:HA3	13:U:185:ILE:HG22	1.83	0.60
43:y:37:VAL:HG22	43:y:115:VAL:HG12	1.84	0.60
1:0:63:LYS:NZ	3:2:2856:G:N7	2.49	0.60
15:W:17:LEU:HD23	15:W:129:VAL:HG22	1.82	0.60
16:X:45:LYS:HE3	16:X:46:ILE:HG23	1.82	0.60
3:2:2941:U:H4'	3:2:2944:C:H41	1.67	0.60
9:Q:122:VAL:O	9:Q:248:ARG:NH2	2.34	0.60
28:j:86:HIS:CD2	28:j:88:LYS:H	2.12	0.60
3:2:425:A:H2'	3:2:426:A:C8	2.37	0.60
3:2:619:G:N1	3:2:634:G:H5''	2.16	0.60
3:2:1744:A:N6	3:2:1779:U:H3	1.98	0.60
3:2:3040:G:H5'	3:2:3042:G:N7	2.17	0.60
3:2:2632:A:H2'	3:2:2633:U:C6	2.37	0.60
4:3:75:G:N2	23:e:51:LYS:HG3	2.17	0.60
3:2:382:A:N3	3:2:384:G:H5''	2.17	0.60
3:2:2814:U:H2'	3:2:2815:G:C8	2.37	0.60
21:c:169:GLU:OE1	21:c:175:ARG:NH2	2.31	0.60
8:P:354:GLU:O	8:P:358:THR:HG23	2.02	0.59
15:W:23:LEU:HD11	15:W:123:TYR:HA	1.84	0.59
3:2:1387:A:H3'	3:2:1391:G:O2'	2.02	0.59
9:Q:223:PHE:O	9:Q:227:ILE:HG13	2.00	0.59
14:V:75:TYR:HB3	14:V:154:ARG:HH22	1.67	0.59
29:k:59:ARG:HB2	29:k:102:LYS:HG3	1.84	0.59
9:Q:84:PRO:HB3	9:Q:89:LYS:HG2	1.84	0.59
3:2:543:G:H22	3:2:583:C:H5	1.50	0.59
3:2:786:C:H2'	3:2:787:G:C8	2.38	0.59
16:X:187:ARG:NH1	16:X:188:TYR:OH	2.36	0.59
3:2:1255:C:H2'	3:2:1256:A:C8	2.35	0.59
2:1:50:THR:O	2:1:54:ILE:HB	2.02	0.59
3:2:3277:A:N6	3:2:3285:G:OP2	2.27	0.59
41:w:20:ALA:HB1	41:w:37:LEU:HD11	1.84	0.59
3:2:59:G:H2'	5:4:41:A:O2'	2.03	0.58
3:2:548:U:O2'	3:2:550:G:N7	2.36	0.58
3:2:1130:A:H5'	24:f:129:ARG:HD2	1.84	0.58
6:N:28:LEU:O	6:N:29:ARG:HB2	2.02	0.58
3:2:1234:A:H2'	3:2:1235:A:H8	1.68	0.58
3:2:1694:U:H2'	3:2:1695:C:C6	2.38	0.58
3:2:3278:A:H2'	3:2:3279:A:H8	1.68	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2:3470:G:N3	3:2:3470:G:H2'	2.17	0.58
13:U:115:PHE:HE1	13:U:177:ILE:HD12	1.68	0.58
3:2:2354:U:H2'	3:2:2355:C:C6	2.39	0.58
3:2:3288:G:N2	3:2:3300:A:N3	2.50	0.58
43:y:71:ASN:ND2	43:y:72:PRO:HD2	2.17	0.58
3:2:463:C:H2'	3:2:464:A:H8	1.67	0.58
7:O:375:GLU:OE2	27:i:14:TYR:OH	2.21	0.58
19:a:5:GLN:O	19:a:32:GLN:NE2	2.36	0.58
3:2:2515:U:H2'	3:2:2516:U:C6	2.39	0.58
3:2:609:A:H2'	3:2:610:C:C6	2.39	0.58
9:Q:95:TRP:HA	9:Q:158:ARG:HG2	1.86	0.58
3:2:2792:A:H2'	3:2:2793:G:C8	2.38	0.58
3:2:2809:G:H5''	3:2:2811:U:C6	2.39	0.58
3:2:1347:U:H2'	23:e:155:ARG:HH22	1.69	0.58
3:2:3050:U:P	3:2:3072:G:H22	2.27	0.58
6:N:106:MET:HE3	6:N:135:ILE:HD11	1.84	0.58
29:k:88:LYS:HE3	29:k:92:ALA:HB3	1.86	0.58
41:w:52:LYS:O	41:w:56:LYS:HG2	2.04	0.58
3:2:652:U:H2'	3:2:653:U:C6	2.38	0.57
3:2:1731:A:H2'	3:2:1732:A:C8	2.39	0.57
3:2:2672:C:H2'	3:2:2673:U:O4'	2.04	0.57
4:3:69:U:H2'	4:3:70:C:C6	2.39	0.57
39:u:90:SER:O	39:u:94:SER:OG	2.22	0.57
3:2:687:U:H2'	3:2:688:C:C6	2.39	0.57
3:2:3001:C:H4'	3:2:3002:G:O5'	2.04	0.57
3:2:3267:A:H5''	3:2:3268:U:H5'	1.86	0.57
1:0:6:LYS:HG2	1:0:93:LEU:HB3	1.86	0.57
3:2:1653:A:H2'	3:2:1654:A:C8	2.39	0.57
3:2:2935:C:H2'	3:2:2936:G:O4'	2.04	0.57
9:Q:293:ARG:HD2	14:V:210:LEU:HD13	1.86	0.57
33:o:28:LYS:HB2	33:o:100:ASP:HB3	1.87	0.57
3:2:720:A:OP1	8:P:47:ASN:HB2	2.04	0.57
3:2:1064:C:H2'	3:2:1065:U:C6	2.40	0.57
27:i:47:ARG:HE	27:i:54:LEU:HD13	1.70	0.57
35:q:81:LEU:HD21	43:y:32:ARG:HD3	1.86	0.57
3:2:370:U:P	40:v:45:ARG:HH22	2.28	0.57
42:x:28:ARG:HD3	42:x:36:HIS:HA	1.87	0.57
3:2:451:C:H2'	3:2:452:C:C6	2.40	0.57
3:2:1631:C:H2'	3:2:1632:C:C6	2.40	0.57
3:2:1728:U:O2'	3:2:1813:U:O2'	2.22	0.57
10:R:93:ILE:H	10:R:157:GLN:HE22	1.53	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2:1387:A:O3'	43:y:40:LYS:NZ	2.34	0.56
11:S:68:ARG:O	11:S:72:GLU:HG2	2.05	0.56
2:1:42:CYS:HB3	2:1:62:CYS:SG	2.45	0.56
3:2:715:U:C5	3:2:716:G:H2'	2.39	0.56
9:Q:285:ASN:HA	14:V:220:LEU:HD22	1.86	0.56
23:e:159:VAL:HG22	23:e:160:GLY:H	1.70	0.56
30:l:33:SER:OG	30:l:35:SER:O	2.23	0.56
3:2:713:G:H22	8:P:234:ARG:NH2	2.03	0.56
3:2:1244:G:O2'	3:2:1245:U:OP1	2.23	0.56
8:P:305:ALA:HA	21:c:38:ARG:CZ	2.36	0.56
14:V:87:LEU:HA	14:V:138:VAL:HG22	1.86	0.56
15:W:10:LYS:NZ	15:W:152:HIS:HD2	2.04	0.56
33:o:24:MET:HG3	33:o:29:TYR:CE1	2.41	0.56
3:2:932:G:H1'	3:2:1624:A:N6	2.20	0.56
3:2:1494:A:H5'	34:p:56:VAL:O	2.04	0.56
3:2:1891:C:H41	42:x:3:SER:HB3	1.71	0.56
3:2:2383:A:H1'	26:h:75:ILE:HD11	1.88	0.56
34:p:30:PHE:HB3	34:p:70:ARG:HD2	1.88	0.56
3:2:217:G:N3	3:2:237:U:H4'	2.20	0.56
3:2:3328:U:H4'	3:2:3329:G:O5'	2.04	0.56
10:R:156:ASP:O	10:R:160:VAL:HG22	2.06	0.56
3:2:2007:G:H2'	3:2:2008:G:C8	2.41	0.56
3:2:2870:U:H1'	31:m:58:MET:HE1	1.88	0.56
14:V:30:LYS:HG3	14:V:63:GLU:HG3	1.88	0.56
3:2:512:A:H2'	3:2:513:U:C6	2.41	0.56
3:2:1333:A:C2	3:2:2982:A:H5''	2.40	0.56
3:2:3006:A:H4'	3:2:3007:G:C8	2.41	0.56
4:3:4:U:H2'	4:3:5:A:H8	1.71	0.56
5:4:131:G:H2'	5:4:132:G:C8	2.41	0.56
3:2:1063:C:H2'	3:2:1064:C:C2	2.40	0.56
3:2:1386:G:H2'	3:2:1387:A:O4'	2.06	0.56
3:2:2268:G:H2'	3:2:2269:C:C6	2.40	0.56
4:3:38:U:N3	4:3:41:G:OP2	2.35	0.56
5:4:59:G:H8	5:4:60:A:N6	2.04	0.56
27:i:3:VAL:HG11	27:i:12:LYS:HG2	1.87	0.56
3:2:1234:A:H2'	3:2:1235:A:C8	2.39	0.56
3:2:2348:U:H5''	3:2:2349:G:C5	2.41	0.56
3:2:2630:G:O6	3:2:2631:G:N2	2.39	0.56
14:V:93:PRO:HB2	14:V:125:LEU:HB3	1.88	0.56
10:R:168:ILE:HG23	10:R:174:MET:HG3	1.86	0.56
3:2:655:C:H2'	3:2:656:A:C8	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2:1654:A:H61	3:2:1880:A:H61	1.54	0.55
3:2:1741:U:O2'	3:2:1742:G:H8	1.89	0.55
11:S:112:GLN:HA	11:S:117:ILE:HD11	1.88	0.55
14:V:54:SER:HA	14:V:163:GLN:HG3	1.89	0.55
17:Y:120:ARG:HB2	19:a:188:VAL:HG11	1.87	0.55
3:2:2291:U:H2'	3:2:2292:C:C6	2.40	0.55
3:2:2769:A:N6	3:2:2775:A:H61	2.02	0.55
25:g:15:ASP:OD1	25:g:60:LYS:HE3	2.07	0.55
3:2:4:U:H2'	3:2:5:G:C8	2.42	0.55
5:4:20:A:OP1	20:b:3:ARG:NH1	2.39	0.55
34:p:29:SER:HB2	34:p:32:LYS:HD2	1.87	0.55
3:2:393:A:H2'	3:2:394:A:C8	2.41	0.55
3:2:3458:U:H2'	3:2:3459:U:H5'	1.87	0.55
18:Z:33:MET:HG3	18:Z:37:HIS:CE1	2.40	0.55
3:2:454:G:H22	3:2:499:G:H1	1.55	0.55
3:2:773:C:H2'	3:2:774:C:C6	2.42	0.55
3:2:1661:A:N1	3:2:1872:G:O6	2.40	0.55
3:2:3299:U:O2'	3:2:3300:A:H8	1.90	0.55
5:4:92:C:H5'	29:k:111:ASP:HB2	1.87	0.55
3:2:135:U:O2'	3:2:137:C:O2	2.19	0.55
3:2:1005:A:H2'	3:2:1006:A:O4'	2.07	0.55
3:2:2343:A:H8	3:2:2349:G:H21	1.55	0.55
18:Z:183:SER:HB3	18:Z:184:PRO:CD	2.36	0.55
3:2:1332:A:H4'	3:2:1333:A:H5'	1.87	0.55
3:2:2730:A:H2	3:2:2737:A:N6	2.02	0.55
3:2:2769:A:O2'	15:W:126:ASP:OD2	2.13	0.55
26:h:89:ARG:HH22	26:h:139:VAL:CG2	2.20	0.55
42:x:20:ASN:ND2	42:x:42:ARG:O	2.40	0.55
5:4:17:A:H2'	5:4:18:G:C8	2.41	0.55
10:R:173:ASN:OD1	17:Y:115:ARG:NH1	2.40	0.55
3:2:444:A:H2'	3:2:445:G:C8	2.42	0.55
3:2:1735:A:H2'	3:2:1736:A:C8	2.41	0.55
7:O:171:LEU:HD21	7:O:333:LYS:HB2	1.89	0.55
3:2:451:C:H2'	3:2:452:C:H6	1.72	0.54
3:2:453:U:H2'	3:2:454:G:C8	2.38	0.54
3:2:2183:A:H1'	3:2:2184:A:N7	2.22	0.54
3:2:2710:G:H2'	3:2:2711:C:H6	1.72	0.54
14:V:39:LYS:HA	14:V:86:HIS:CD2	2.42	0.54
14:V:48:LEU:HB2	14:V:142:ASP:OD1	2.07	0.54
22:d:105:LEU:HD23	22:d:138:LEU:HD23	1.89	0.54
35:q:79:VAL:HG21	35:q:105:ILE:HG23	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2:1038:A:O2'	14:V:19:LYS:HE2	2.06	0.54
3:2:1268:G:C6	3:2:1282:A:N1	2.74	0.54
3:2:3002:G:H5'	3:2:3003:G:OP2	2.07	0.54
3:2:3416:A:OP1	7:O:174:LYS:NZ	2.38	0.54
15:W:100:GLY:HA3	15:W:154:ILE:HG22	1.90	0.54
38:t:30:LEU:HD11	38:t:45:LYS:HG2	1.87	0.54
3:2:2304:G:N2	3:2:2317:A:N1	2.39	0.54
3:2:3337:A:H2'	3:2:3338:A:O4'	2.08	0.54
12:T:158:ASP:HB3	12:T:159:PRO:HD3	1.89	0.54
28:j:69:GLU:CD	28:j:69:GLU:H	2.13	0.54
3:2:2323:C:H2'	3:2:2324:G:H8	1.71	0.54
9:Q:164:LYS:HG2	9:Q:180:PHE:CZ	2.42	0.54
10:R:126:LYS:HB3	10:R:129:ARG:HH12	1.72	0.54
2:1:39:CYS:HB3	2:1:42:CYS:SG	2.48	0.54
3:2:713:G:H1	8:P:234:ARG:NH2	2.05	0.54
3:2:3278:A:H2'	3:2:3279:A:C8	2.41	0.54
3:2:188:C:O2'	3:2:190:G:O4'	2.24	0.54
3:2:250:A:C4	3:2:252:A:H1'	2.43	0.54
3:2:1052:G:H2'	3:2:1053:G:C8	2.43	0.54
3:2:1599:A:H1'	3:2:1600:C:C5	2.43	0.54
9:Q:122:VAL:HG22	9:Q:168:ASP:HB3	1.90	0.54
23:e:9:VAL:HG22	23:e:25:ARG:HG3	1.89	0.54
24:f:3:HIS:HD2	24:f:5:TYR:CE1	2.25	0.54
29:k:34:LEU:HD23	29:k:38:LEU:HB3	1.90	0.54
3:2:619:G:H1	3:2:634:G:H5''	1.72	0.54
30:l:29:ILE:HD13	30:l:40:HIS:CE1	2.43	0.54
30:l:72:ILE:HD12	30:l:101:PHE:CE1	2.43	0.54
3:2:29:C:H4'	3:2:62:A:H4'	1.89	0.54
3:2:1603:U:C4	3:2:1604:U:H1'	2.42	0.54
6:N:107:PRO:O	6:N:110:THR:HG22	2.08	0.54
11:S:76:LYS:O	11:S:80:GLU:HG3	2.07	0.54
18:Z:159:ARG:HB2	18:Z:164:LEU:HB2	1.90	0.54
24:f:26:ARG:O	24:f:29:THR:HG23	2.08	0.54
3:2:952:A:OP1	3:2:954:U:H5	1.91	0.54
28:j:78:ASP:HB2	28:j:80:THR:HG22	1.90	0.54
3:2:243:C:H2'	3:2:244:G:C8	2.42	0.53
3:2:1742:G:H22	3:2:1781:G:N2	2.04	0.53
3:2:3252:U:H2'	3:2:3253:G:C8	2.44	0.53
5:4:150:C:H2'	5:4:151:U:C6	2.44	0.53
7:O:92:TYR:O	7:O:155:CYS:HA	2.08	0.53
11:S:22:LYS:HA	11:S:25:LYS:HE2	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:U:38:ASN:HD21	13:U:40:ARG:HD2	1.74	0.53
14:V:175:GLN:OE1	14:V:196:TYR:OH	2.26	0.53
3:2:188:C:H4'	3:2:189:G:OP1	2.08	0.53
3:2:3290:A:H2'	3:2:3291:C:C6	2.44	0.53
5:4:60:A:N1	42:x:27:ILE:HG21	2.23	0.53
13:U:42:VAL:HG13	13:U:67:CYS:HB3	1.91	0.53
3:2:463:C:H2'	3:2:464:A:C8	2.42	0.53
3:2:877:G:N2	3:2:880:A:OP2	2.41	0.53
3:2:1968:G:N3	3:2:2208:A:H2'	2.23	0.53
12:T:182:ASN:HB3	12:T:185:ARG:H	1.73	0.53
3:2:1041:A:H2'	3:2:1042:G:H8	1.74	0.53
7:O:227:GLU:HG3	7:O:231:ALA:HB3	1.90	0.53
42:x:3:SER:HA	42:x:5:LYS:NZ	2.24	0.53
3:2:1253:G:O2'	3:2:1316:G:O6	2.27	0.53
3:2:3379:A:H2'	3:2:3380:A:C8	2.44	0.53
4:3:4:U:H2'	4:3:5:A:C8	2.43	0.53
12:T:154:ALA:HB2	12:T:186:LEU:HD12	1.90	0.53
3:2:3055:C:H2'	3:2:3056:G:H8	1.72	0.53
10:R:114:VAL:HG13	10:R:160:VAL:HG12	1.90	0.53
35:q:62:TYR:CG	43:y:25:PHE:HA	2.44	0.53
3:2:591:G:O2'	3:2:593:A:OP2	2.26	0.53
3:2:1425:C:C5	35:q:100:ARG:HD3	2.44	0.53
3:2:2602:U:C2	3:2:2603:C:C5	2.97	0.53
3:2:2706:U:H2'	3:2:2707:U:C6	2.44	0.53
23:e:142:LEU:HA	23:e:147:LEU:HD22	1.91	0.53
26:h:70:ASP:O	26:h:74:LYS:NZ	2.41	0.53
3:2:247:U:O2'	3:2:252:A:N6	2.38	0.53
3:2:257:A:N3	3:2:258:U:N3	2.57	0.53
3:2:1839:A:H2'	3:2:1840:A:C8	2.44	0.53
13:U:91:ARG:HG2	13:U:180:SER:HB2	1.91	0.53
3:2:481:A:H4'	43:y:105:ARG:HH11	1.74	0.52
3:2:3119:U:C2	3:2:3128:A:N7	2.78	0.52
4:3:63:A:N3	14:V:202:LYS:NZ	2.57	0.52
5:4:60:A:O5'	5:4:60:A:H8	1.92	0.52
14:V:195:CYS:SG	14:V:196:TYR:N	2.82	0.52
30:l:46:VAL:HG13	30:l:68:VAL:HG13	1.91	0.52
43:y:101:GLY:HA2	43:y:105:ARG:HG3	1.90	0.52
3:2:713:G:H1	8:P:234:ARG:HH12	1.57	0.52
3:2:1665:A:N7	30:l:64:ARG:NH1	2.56	0.52
3:2:2646:U:H5	6:N:39:TYR:O	1.91	0.52
8:P:284:ILE:HG13	21:c:126:ASP:CG	2.35	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:b:116:HIS:HB3	20:b:149:ILE:HB	1.90	0.52
3:2:1068:A:H2'	3:2:1069:C:C6	2.44	0.52
3:2:2702:G:H5'	6:N:232:GLN:HB3	1.91	0.52
3:2:3091:G:H2'	3:2:3092:U:C6	2.44	0.52
3:2:3256:C:H2'	3:2:3257:C:C6	2.44	0.52
4:3:110:G:H2'	4:3:111:C:C6	2.44	0.52
7:O:159:ARG:HG2	7:O:182:GLN:HA	1.90	0.52
3:2:2791:A:H2'	3:2:2792:A:C8	2.45	0.52
1:0:10:THR:HG22	3:2:2809:G:OP2	2.10	0.52
3:2:253:U:H3'	3:2:254:G:C8	2.44	0.52
9:Q:83:LEU:HB3	9:Q:88:ILE:HB	1.91	0.52
14:V:53:VAL:HG12	14:V:134:ILE:HG13	1.91	0.52
33:o:30:VAL:HG22	33:o:97:ALA:HB3	1.89	0.52
3:2:1241:U:H2'	3:2:1242:U:C6	2.45	0.52
3:2:1381:G:H1'	8:P:290:THR:HG21	1.91	0.52
15:W:155:ASN:OD1	15:W:155:ASN:N	2.32	0.52
31:m:82:VAL:HG12	31:m:87:ARG:HG3	1.92	0.52
3:2:1617:U:H2'	3:2:1618:A:H5''	1.92	0.52
13:U:105:GLU:HG3	13:U:109:VAL:HG13	1.92	0.52
1:0:26:THR:HA	1:0:93:LEU:HD11	1.92	0.52
3:2:1588:A:H4'	3:2:1589:U:H5'	1.91	0.52
3:2:2896:A:O2'	3:2:2897:A:H2'	2.09	0.52
3:2:3017:G:C2	3:2:3047:G:H1'	2.45	0.52
3:2:3378:A:H2'	3:2:3379:A:C8	2.45	0.52
15:W:133:ARG:HG3	15:W:154:ILE:HD11	1.92	0.52
17:Y:7:TYR:H	17:Y:12:ARG:NH2	2.08	0.52
35:q:13:PRO:O	35:q:14:PHE:HB2	2.10	0.52
3:2:2632:A:O2'	3:2:2633:U:O4'	2.27	0.52
10:R:52:LEU:HD13	10:R:80:LEU:HD11	1.91	0.52
19:a:33:LYS:HG2	19:a:102:HIS:HD2	1.75	0.52
37:s:92:ALA:O	37:s:96:GLU:HG2	2.10	0.52
3:2:543:G:H2'	3:2:544:A:C8	2.45	0.52
3:2:2342:U:OP2	3:2:2342:U:H6	1.93	0.52
8:P:332:PRO:HB2	11:S:53:ALA:HB2	1.91	0.52
13:U:11:LEU:HD23	13:U:75:ILE:HG22	1.92	0.52
13:U:59:HIS:HE1	23:e:147:LEU:HD11	1.75	0.52
38:t:72:TYR:HB3	38:t:78:ILE:HG13	1.91	0.51
39:u:27:ARG:HG2	39:u:30:HIS:HD2	1.74	0.51
14:V:71:CYS:O	14:V:154:ARG:NH1	2.43	0.51
3:2:763:G:C5	3:2:765:G:H1'	2.46	0.51
3:2:2400:A:OP1	3:2:2402:U:H5	1.94	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2:1078:A:H2'	3:2:1081:C:C5	2.45	0.51
3:2:1515:A:N1	37:s:2:ALA:N	2.58	0.51
3:2:1686:U:H5''	6:N:70:THR:HG22	1.92	0.51
3:2:3378:A:H2'	3:2:3379:A:H8	1.74	0.51
14:V:71:CYS:SG	14:V:154:ARG:NH1	2.81	0.51
27:i:52:THR:O	27:i:56:ARG:HG3	2.10	0.51
3:2:19:U:H2'	3:2:20:A:C8	2.46	0.51
3:2:222:G:H5''	29:k:11:ARG:HG3	1.92	0.51
3:2:977:C:H2'	3:2:978:U:C6	2.45	0.51
3:2:1043:A:H2'	3:2:1044:G:H8	1.76	0.51
3:2:2622:C:OP1	6:N:36:ARG:NH2	2.36	0.51
26:h:15:MET:HE1	26:h:56:CYS:HB2	1.93	0.51
3:2:1854:A:C4	3:2:1855:U:H5	2.29	0.51
3:2:2003:G:N2	3:2:2187:A:H2	2.04	0.51
3:2:2348:U:H5''	3:2:2349:G:C6	2.45	0.51
3:2:2507:A:H2'	3:2:2508:C:C6	2.46	0.51
9:Q:119:TYR:CZ	9:Q:135:ILE:HG13	2.45	0.51
10:R:151:ALA:O	10:R:152:GLU:HG2	2.11	0.51
11:S:222:TRP:CD1	11:S:226:LYS:HD2	2.46	0.51
18:Z:45:PRO:O	18:Z:49:ARG:HG3	2.10	0.51
3:2:491:C:H5''	3:2:492:U:H5	1.76	0.51
3:2:1274:G:O2'	3:2:1302:A:N3	2.43	0.51
3:2:3267:A:H4'	3:2:3268:U:OP2	2.11	0.51
33:o:98:ILE:HD13	33:o:106:ILE:HD12	1.92	0.51
3:2:261:A:H1'	3:2:262:A:C8	2.45	0.51
3:2:1702:A:H2'	3:2:1703:G:C8	2.46	0.51
3:2:2395:G:O2'	3:2:2398:U:OP2	2.20	0.51
3:2:2931:C:O2'	14:V:158:LYS:NZ	2.44	0.51
3:2:3017:G:N2	3:2:3047:G:H1'	2.25	0.51
13:U:112:ILE:HG22	13:U:122:ARG:HB2	1.92	0.51
27:i:50:SER:HA	27:i:55:TYR:CD1	2.46	0.51
37:s:41:ILE:HG13	37:s:56:ALA:HB2	1.92	0.51
40:v:25:ARG:HH11	42:x:51:ILE:HD12	1.75	0.51
43:y:33:GLU:HG3	43:y:36:ASN:HB2	1.92	0.51
3:2:1096:A:C2	3:2:1098:G:C6	2.99	0.51
3:2:1313:G:N3	3:2:1313:G:H2'	2.26	0.51
3:2:2304:G:H1	3:2:2317:A:N6	2.03	0.51
3:2:2994:C:H2'	3:2:2995:A:O4'	2.11	0.51
3:2:370:U:OP1	40:v:45:ARG:NH2	2.42	0.51
3:2:1325:A:OP1	23:e:84:SER:OG	2.23	0.51
3:2:1941:A:O4'	3:2:3408:A:H5'	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:V:38:ARG:HG3	14:V:83:ASP:HA	1.93	0.51
3:2:712:U:H2'	3:2:713:G:N2	2.26	0.50
31:m:82:VAL:HG13	31:m:86:THR:HB	1.93	0.50
39:u:3:PRO:HB2	39:u:5:LEU:HG	1.92	0.50
3:2:1299:G:O2'	3:2:1300:U:O5'	2.28	0.50
3:2:1804:C:N3	3:2:1805:A:N6	2.59	0.50
3:2:2628:U:H2'	3:2:2629:G:C4	2.46	0.50
19:a:6:LYS:HG3	19:a:7:VAL:HG12	1.93	0.50
3:2:12:A:H2'	3:2:13:A:C8	2.46	0.50
3:2:1717:U:O2	25:g:80:LYS:HG2	2.11	0.50
3:2:2629:G:H2'	3:2:2630:G:N7	2.27	0.50
3:2:2931:C:H5	3:2:2947:C:N4	2.09	0.50
28:j:74:LYS:HB3	28:j:80:THR:HG23	1.93	0.50
7:O:305:ILE:HG21	7:O:321:PHE:CE1	2.46	0.50
3:2:1536:G:N2	3:2:1547:G:C5	2.76	0.50
7:O:287:ALA:O	7:O:293:ASN:ND2	2.38	0.50
34:p:21:MET:HE3	34:p:37:ALA:HB1	1.94	0.50
3:2:1017:U:H2'	3:2:1018:U:C6	2.47	0.50
3:2:1268:G:O6	3:2:1282:A:C6	2.65	0.50
3:2:2954:U:H4'	3:2:2955:U:C5	2.47	0.50
20:b:113:ILE:HD13	20:b:153:GLU:HB2	1.93	0.50
3:2:518:U:H2'	3:2:519:U:C6	2.47	0.50
3:2:2295:A:H2'	3:2:2296:A:H4'	1.94	0.50
3:2:3289:G:H2'	3:2:3289:G:N3	2.26	0.50
11:S:128:ASN:HB2	24:f:132:PRO:HB2	1.93	0.50
15:W:106:ILE:O	15:W:106:ILE:HG13	2.11	0.50
3:2:492:U:H2'	3:2:493:G:C8	2.47	0.50
3:2:1254:A:N1	3:2:1318:A:H1'	2.26	0.50
3:2:1268:G:N1	3:2:1282:A:C2	2.80	0.50
3:2:2977:U:H2'	3:2:2978:U:C6	2.47	0.50
3:2:3459:U:H2'	3:2:3460:A:H8	1.76	0.50
25:g:19:ALA:HA	25:g:105:TYR:OH	2.11	0.50
3:2:257:A:H1'	3:2:258:U:C2	2.47	0.50
3:2:3007:G:H1'	3:2:3227:U:OP1	2.12	0.50
3:2:3305:C:H2'	3:2:3305:C:O2	2.12	0.50
3:2:270:U:H2'	3:2:271:C:O4'	2.12	0.49
3:2:468:G:H1	3:2:484:A:H2	1.58	0.49
3:2:2975:U:H1'	7:O:250:ALA:HB3	1.94	0.49
11:S:88:GLU:HB3	24:f:135:PRO:HB3	1.93	0.49
13:U:25:LEU:HD23	13:U:38:ASN:HA	1.93	0.49
40:v:64:MET:O	40:v:68:LYS:HG3	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2:2320:A:H2'	3:2:2321:A:C8	2.47	0.49
38:t:23:LEU:HD12	38:t:49:THR:HG23	1.93	0.49
3:2:146:U:H2'	3:2:147:C:C6	2.47	0.49
3:2:179:G:H1	3:2:252:A:H2	1.60	0.49
3:2:1970:A:H2'	3:2:1971:U:C6	2.47	0.49
3:2:2925:G:H2'	3:2:2926:G:H8	1.77	0.49
8:P:9:SER:HB2	8:P:149:GLU:OE1	2.12	0.49
3:2:693:A:H2'	3:2:694:U:C6	2.48	0.49
3:2:1068:A:H2'	3:2:1069:C:H6	1.76	0.49
3:2:1806:U:H1'	3:2:1807:G:C8	2.47	0.49
3:2:1846:A:H2'	3:2:1847:C:C6	2.47	0.49
26:h:59:MET:HE3	26:h:79:ILE:HD11	1.94	0.49
3:2:3459:U:H2'	3:2:3460:A:C8	2.48	0.49
21:c:159:HIS:H	21:c:187:VAL:CG1	2.24	0.49
3:2:1723:U:H2'	3:2:1724:U:C6	2.47	0.49
3:2:2842:A:H5'	9:Q:175:HIS:HA	1.93	0.49
3:2:3373:C:HO2'	3:2:3374:A:P	2.36	0.49
8:P:298:ILE:HD12	21:c:35:LEU:HD21	1.95	0.49
9:Q:242:GLU:OE2	9:Q:246:LYS:NZ	2.46	0.49
23:e:90:TYR:O	23:e:136:ARG:NH2	2.45	0.49
3:2:784:C:H2'	3:2:785:C:C6	2.47	0.49
3:2:1722:U:O4	25:g:42:GLY:N	2.42	0.49
9:Q:55:PHE:CZ	9:Q:158:ARG:HB3	2.47	0.49
9:Q:119:TYR:OH	9:Q:135:ILE:HG13	2.13	0.49
14:V:55:ASN:ND2	14:V:164:ARG:HD3	2.28	0.49
14:V:174:SER:OG	14:V:175:GLN:N	2.44	0.49
23:e:159:VAL:HG13	23:e:161:LEU:H	1.77	0.49
33:o:79:THR:N	33:o:82:ASP:OD2	2.38	0.49
3:2:183:A:O2'	3:2:184:C:O5'	2.30	0.49
3:2:641:G:H2'	3:2:642:A:C8	2.47	0.49
3:2:654:U:H2'	3:2:655:C:C6	2.48	0.49
3:2:1594:G:H1'	3:2:1595:U:C5	2.47	0.49
3:2:2662:U:H3	3:2:2669:G:H22	1.60	0.49
3:2:3303:C:H5''	17:Y:91:ALA:HB2	1.95	0.49
4:3:9:C:OP1	24:f:26:ARG:HB2	2.12	0.49
7:O:150:ARG:HG3	7:O:150:ARG:HH11	1.77	0.49
3:2:4:U:H2'	3:2:5:G:H8	1.77	0.49
5:4:45:A:H5''	5:4:47:G:O4'	2.12	0.49
35:q:86:ASN:HD21	35:q:113:GLY:C	2.21	0.49
3:2:656:A:H2'	3:2:657:A:C8	2.48	0.49
3:2:1017:U:H2'	3:2:1018:U:H6	1.77	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:r:46:LEU:HD11	36:r:75:PRO:HD3	1.95	0.48
38:t:31:ARG:HG2	38:t:31:ARG:NH1	2.27	0.48
3:2:1043:A:H2'	3:2:1044:G:C8	2.49	0.48
3:2:1253:G:OP1	3:2:1312:U:H5''	2.13	0.48
4:3:102:U:H2'	4:3:103:C:C6	2.48	0.48
9:Q:50:ARG:NH2	9:Q:72:ASP:OD2	2.46	0.48
3:2:1725:C:H2'	3:2:1726:U:C6	2.49	0.48
7:O:227:GLU:CG	7:O:231:ALA:HB3	2.44	0.48
31:m:132:ARG:HG3	31:m:132:ARG:NH1	2.28	0.48
3:2:799:A:H2'	3:2:800:U:O4'	2.13	0.48
3:2:975:U:OP1	31:m:15:VAL:HA	2.12	0.48
3:2:1050:G:H22	3:2:1066:C:H42	1.61	0.48
3:2:1264:G:N1	3:2:1287:G:O6	2.46	0.48
3:2:2660:U:H2'	3:2:2661:U:H5'	1.95	0.48
15:W:9:MET:HG3	15:W:134:PRO:HG2	1.94	0.48
3:2:979:G:H5''	35:q:52:ILE:HB	1.95	0.48
3:2:1008:U:H2'	3:2:1009:C:O4'	2.14	0.48
3:2:1115:G:H2'	3:2:1116:G:C8	2.49	0.48
3:2:2726:U:OP1	3:2:2852:U:O2'	2.24	0.48
3:2:3073:U:O2'	3:2:3074:U:H5'	2.12	0.48
3:2:3210:A:OP1	13:U:69:ARG:HG3	2.13	0.48
3:2:3438:G:H2'	3:2:3439:C:C6	2.49	0.48
9:Q:204:VAL:O	9:Q:208:MET:HG2	2.13	0.48
25:g:57:GLY:HA3	25:g:60:LYS:HB2	1.94	0.48
3:2:1234:A:H61	3:2:1331:G:H2'	1.79	0.48
9:Q:196:ARG:NH2	9:Q:237:GLU:OE2	2.47	0.48
14:V:72:ALA:HA	14:V:154:ARG:NH2	2.28	0.48
21:c:61:ILE:HG22	21:c:84:ILE:HD13	1.94	0.48
21:c:179:ARG:HH11	21:c:187:VAL:HG22	1.79	0.48
28:j:99:ARG:NH1	28:j:105:GLU:OE1	2.46	0.48
40:v:25:ARG:HH11	42:x:51:ILE:CD1	2.26	0.48
40:v:25:ARG:CD	42:x:51:ILE:HD12	2.39	0.48
3:2:1618:A:H2'	3:2:1619:U:O4'	2.14	0.48
3:2:2200:U:H4'	3:2:2201:A:O5'	2.13	0.48
3:2:2867:C:H5'	3:2:2868:C:H5'	1.96	0.48
4:3:12:U:H4'	4:3:13:A:OP2	2.12	0.48
6:N:106:MET:CE	6:N:112:ILE:HG21	2.44	0.48
13:U:70:THR:O	13:U:74:ILE:HD13	2.13	0.48
28:j:88:LYS:HE2	28:j:88:LYS:HA	1.94	0.48
42:x:27:ILE:HG22	42:x:35:VAL:HG11	1.95	0.48
3:2:226:A:HO2'	3:2:227:G:H21	1.59	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2:266:G:OP1	16:X:81:LYS:HE3	2.14	0.48
3:2:2710:G:H2'	3:2:2711:C:C6	2.49	0.48
18:Z:35:VAL:O	18:Z:64:ILE:HA	2.13	0.48
29:k:85:THR:HG22	29:k:95:PRO:HA	1.96	0.48
35:q:61:ARG:HG2	35:q:62:TYR:CE2	2.48	0.48
36:r:102:MET:HE2	36:r:104:TYR:CZ	2.49	0.48
3:2:1568:A:H2'	3:2:1569:A:C8	2.49	0.48
3:2:1696:G:H2'	3:2:1697:G:C8	2.49	0.48
3:2:2680:C:C4	12:T:239:GLY:HA3	2.48	0.48
3:2:2931:C:H4'	14:V:157:TYR:CG	2.49	0.48
3:2:3347:G:H2'	3:2:3348:U:C6	2.49	0.48
7:O:108:GLU:HG3	7:O:137:TYR:HB3	1.96	0.48
9:Q:208:MET:O	9:Q:212:ILE:HG23	2.13	0.48
29:k:72:VAL:HG12	29:k:74:ARG:HG2	1.94	0.48
36:r:53:VAL:HG22	36:r:67:VAL:HG22	1.95	0.48
3:2:80:C:H2'	3:2:81:C:H6	1.79	0.48
3:2:140:U:H5''	38:t:84:GLN:CG	2.43	0.48
3:2:239:U:H2'	3:2:240:G:C8	2.49	0.48
3:2:250:A:C5	3:2:252:A:H1'	2.49	0.48
3:2:509:A:O2'	3:2:3373:C:H5	1.97	0.48
3:2:1728:U:HO2'	3:2:1813:U:HO2'	1.47	0.48
3:2:2294:G:H4'	3:2:2295:A:H5'	1.96	0.48
32:n:55:ARG:NH2	32:n:56:GLN:HG2	2.29	0.48
3:2:256:C:H2'	3:2:256:C:O2	2.14	0.47
3:2:2457:G:H2'	3:2:2458:G:C8	2.49	0.47
3:2:3088:G:H2'	3:2:3238:A:N6	2.28	0.47
3:2:291:G:OP2	3:2:293:A:H4'	2.14	0.47
3:2:510:G:H2'	3:2:511:C:C6	2.48	0.47
3:2:1386:G:O2'	43:y:44:ARG:HD3	2.15	0.47
6:N:21:LEU:HB3	6:N:51:PRO:HG2	1.96	0.47
7:O:204:ASP:OD1	7:O:206:LYS:HE2	2.14	0.47
25:g:10:ASN:HD22	25:g:65:ALA:HB3	1.79	0.47
30:l:18:PHE:CE1	30:l:47:GLU:HG3	2.49	0.47
3:2:445:G:H1	3:2:647:A:N6	2.10	0.47
3:2:508:C:H2'	3:2:509:A:H5''	1.96	0.47
3:2:531:A:C8	8:P:348:THR:HG23	2.48	0.47
3:2:1300:U:H2'	3:2:1301:A:H3'	1.96	0.47
3:2:1347:U:H3	23:e:153:HIS:CD2	2.33	0.47
3:2:1594:G:C6	28:j:32:ARG:HD3	2.49	0.47
3:2:1971:U:H2'	3:2:1972:C:C6	2.50	0.47
3:2:2663:C:N4	3:2:2665:U:O4'	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:T:82:LEU:HD12	12:T:180:VAL:HG12	1.96	0.47
12:T:100:GLU:OE2	12:T:105:LYS:HD2	2.14	0.47
17:Y:87:TRP:O	17:Y:90:SER:OG	2.26	0.47
30:l:23:VAL:HG12	30:l:45:GLY:HA3	1.96	0.47
3:2:1268:G:H2'	3:2:1268:G:N3	2.29	0.47
3:2:2757:G:H2'	3:2:2758:A:C8	2.49	0.47
3:2:2792:A:H2'	3:2:2793:G:H8	1.78	0.47
3:2:3125:A:O5'	3:2:3125:A:H8	1.97	0.47
3:2:850:C:H2'	3:2:851:U:O4'	2.14	0.47
3:2:1205:G:N2	19:a:88:MET:HE2	2.29	0.47
3:2:1246:U:H2'	3:2:1247:C:C6	2.49	0.47
3:2:2868:C:H2'	3:2:2869:C:C6	2.49	0.47
3:2:2931:C:N4	3:2:2932:A:N1	2.62	0.47
3:2:3001:C:H1'	3:2:3002:G:OP2	2.13	0.47
3:2:3204:G:N2	13:U:161:GLN:HE22	2.08	0.47
3:2:3296:U:O2'	3:2:3297:C:O4'	2.30	0.47
4:3:2:U:O4	4:3:117:G:O6	2.33	0.47
42:x:15:LYS:O	42:x:19:GLN:HG3	2.15	0.47
3:2:419:U:H2'	3:2:420:G:H8	1.79	0.47
3:2:545:A:N7	3:2:577:U:O4	2.47	0.47
3:2:1614:U:OP1	28:j:27:THR:OG1	2.33	0.47
3:2:2680:C:N4	12:T:237:ILE:HD12	2.27	0.47
4:3:54:A:C6	15:W:9:MET:HE3	2.49	0.47
6:N:158:PRO:C	6:N:160:SER:H	2.23	0.47
9:Q:120:GLU:OE1	9:Q:120:GLU:N	2.42	0.47
10:R:70:VAL:HA	10:R:84:GLY:HA3	1.96	0.47
11:S:112:GLN:NE2	21:c:6:GLU:OE1	2.48	0.47
15:W:94:ARG:HB3	15:W:174:LYS:NZ	2.28	0.47
16:X:197:LYS:O	16:X:201:GLU:HB2	2.14	0.47
28:j:56:LEU:HD11	28:j:86:HIS:CE1	2.49	0.47
3:2:169:U:C2	3:2:266:G:N2	2.82	0.47
3:2:460:G:N2	3:2:493:G:H22	2.13	0.47
3:2:482:C:H2'	3:2:483:U:C6	2.49	0.47
3:2:504:A:N6	3:2:505:G:O6	2.48	0.47
3:2:589:U:O2'	3:2:590:U:H3'	2.15	0.47
3:2:1234:A:N3	3:2:2950:U:O2'	2.40	0.47
3:2:1260:G:H2'	3:2:1261:G:C8	2.49	0.47
3:2:1639:U:H4'	3:2:1890:A:H4'	1.97	0.47
3:2:2377:U:H2'	3:2:2378:C:C6	2.50	0.47
3:2:2470:G:N7	19:a:92:LYS:NZ	2.51	0.47
3:2:2521:U:H1'	18:Z:125:ALA:HB2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2:2603:C:C2	3:2:2604:U:C5	3.03	0.47
3:2:2609:U:H5''	12:T:242:THR:HG21	1.97	0.47
3:2:2942:A:H3'	3:2:2943:G:H8	1.80	0.47
5:4:17:A:H2'	5:4:18:G:H8	1.77	0.47
16:X:110:GLN:O	16:X:114:GLU:HG2	2.14	0.47
29:k:115:LYS:O	29:k:119:VAL:HG23	2.14	0.47
35:q:62:TYR:CD1	43:y:25:PHE:HA	2.49	0.47
42:x:15:LYS:HD2	42:x:18:ARG:NH2	2.30	0.47
2:1:56:CYS:SG	2:1:65:VAL:HG22	2.55	0.47
3:2:1664:A:C2'	30:l:67:ARG:HH12	2.28	0.47
3:2:3395:G:H2'	3:2:3396:A:O4'	2.14	0.47
9:Q:285:ASN:HB3	14:V:220:LEU:HD13	1.97	0.47
22:d:35:ALA:O	22:d:36:ASN:ND2	2.48	0.47
3:2:414:G:OP1	3:2:1449:U:O2'	2.29	0.47
3:2:784:C:H2'	3:2:785:C:H6	1.78	0.47
3:2:3256:C:H2'	3:2:3257:C:H6	1.80	0.47
31:m:70:ARG:HD2	31:m:128:TYR:CD2	2.50	0.47
34:p:11:GLN:HB3	34:p:92:LEU:HD11	1.97	0.47
3:2:1379:U:H5'	3:2:1389:A:C6	2.49	0.47
3:2:1525:A:N6	42:x:2:PRO:HA	2.30	0.47
3:2:1825:U:H2'	3:2:1826:C:C6	2.50	0.47
3:2:2778:U:H2'	3:2:2779:C:C6	2.50	0.47
5:4:61:A:O2'	42:x:40:LYS:NZ	2.48	0.47
13:U:13:ILE:HG23	13:U:17:VAL:HB	1.97	0.47
15:W:10:LYS:HZ1	15:W:152:HIS:HD2	1.61	0.47
3:2:22:G:H1'	5:4:112:A:N3	2.30	0.46
3:2:1094:A:H5''	3:2:1095:G:H5'	1.96	0.46
3:2:1654:A:H2'	3:2:1655:G:O4'	2.15	0.46
3:2:2343:A:H8	3:2:2349:G:N2	2.13	0.46
3:2:2666:C:H5	3:2:2667:G:C8	2.33	0.46
3:2:3202:A:H2'	3:2:3203:C:O4'	2.15	0.46
3:2:3307:U:OP1	23:e:158:VAL:HG13	2.15	0.46
3:2:3338:A:H2'	3:2:3339:A:H8	1.80	0.46
6:N:146:ARG:HG3	6:N:156:VAL:HG22	1.98	0.46
16:X:118:VAL:HB	16:X:153:LEU:HD21	1.97	0.46
24:f:115:LYS:HB2	24:f:128:LEU:HD21	1.96	0.46
3:2:2642:C:H4'	3:2:2643:A:OP1	2.15	0.46
3:2:3390:G:O2'	3:2:3391:A:O4'	2.29	0.46
42:x:3:SER:HA	42:x:5:LYS:HZ2	1.80	0.46
3:2:134:U:H5	3:2:140:U:O4	1.99	0.46
3:2:2495:C:H2'	3:2:2496:U:H6	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2:3016:U:C2	3:2:3018:U:H5'	2.50	0.46
3:2:3338:A:H2'	3:2:3339:A:C8	2.49	0.46
5:4:127:U:H2'	5:4:128:U:C6	2.50	0.46
14:V:15:LYS:HB3	14:V:15:LYS:HE2	1.65	0.46
33:o:54:CYS:SG	33:o:59:LYS:HB2	2.55	0.46
39:u:4:GLY:HA2	39:u:12:GLY:O	2.16	0.46
3:2:425:A:H2'	3:2:426:A:H8	1.80	0.46
3:2:1066:C:H2'	3:2:1067:A:C8	2.51	0.46
3:2:1741:U:HO2'	3:2:1742:G:H8	1.59	0.46
3:2:2953:U:H2'	3:2:2954:U:C6	2.50	0.46
17:Y:130:LYS:HA	17:Y:130:LYS:HD3	1.74	0.46
3:2:801:G:H5'	16:X:184:ALA:HB2	1.98	0.46
3:2:1967:U:N3	3:2:2210:G:OP2	2.48	0.46
3:2:3495:U:H2'	3:2:3496:U:C6	2.50	0.46
20:b:108:ASP:OD1	20:b:110:ASP:HB2	2.15	0.46
23:e:7:GLN:HB3	23:e:63:ILE:HD11	1.97	0.46
37:s:16:ARG:HG2	37:s:16:ARG:HH11	1.79	0.46
43:y:31:ASN:ND2	43:y:41:ASN:OD1	2.48	0.46
3:2:481:A:H5'	43:y:105:ARG:HD2	1.98	0.46
3:2:808:U:O2	3:2:2814:U:H1'	2.16	0.46
3:2:2370:U:O2	3:2:2398:U:H4'	2.16	0.46
3:2:3272:U:C4	19:a:6:LYS:HB3	2.51	0.46
22:d:153:LYS:HE2	22:d:153:LYS:HB2	1.76	0.46
3:2:8:C:H2'	3:2:9:U:C6	2.50	0.46
3:2:921:U:H2'	3:2:922:C:O4'	2.15	0.46
3:2:1603:U:C5	3:2:1604:U:H1'	2.50	0.46
3:2:2464:G:O2'	3:2:2465:G:H5'	2.15	0.46
3:2:2603:C:H2'	3:2:2604:U:H6	1.81	0.46
3:2:3206:C:H2'	3:2:3207:U:C6	2.51	0.46
9:Q:288:VAL:HG22	14:V:206:LEU:HD21	1.98	0.46
13:U:86:PHE:CD2	13:U:149:LEU:HD13	2.51	0.46
25:g:12:TYR:HA	25:g:99:GLY:O	2.16	0.46
30:l:18:PHE:HE1	30:l:47:GLU:HG3	1.81	0.46
2:1:51:ALA:HB2	3:2:1836:U:N3	2.31	0.46
3:2:181:A:H2'	3:2:182:G:C8	2.50	0.46
3:2:1095:G:N2	3:2:1095:G:OP2	2.45	0.46
3:2:2000:A:H2'	3:2:2001:A:C8	2.51	0.46
3:2:2226:A:N3	40:v:2:THR:HG22	2.31	0.46
3:2:2863:U:H2'	3:2:2864:G:H8	1.81	0.46
3:2:3391:A:H1'	3:2:3392:A:H5'	1.96	0.46
13:U:105:GLU:CG	13:U:109:VAL:HG13	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Y:92:TRP:O	17:Y:96:LEU:HG	2.15	0.46
19:a:135:LYS:HB2	19:a:135:LYS:HE2	1.69	0.46
33:o:24:MET:HE3	33:o:24:MET:HB2	1.79	0.46
3:2:715:U:H2'	3:2:716:G:H21	1.79	0.46
3:2:1781:G:C4	3:2:1783:G:C8	3.04	0.46
3:2:1850:A:H2'	3:2:1851:A:C8	2.51	0.46
3:2:2662:U:H3	3:2:2669:G:H1	1.63	0.46
4:3:12:U:OP2	4:3:67:C:O2'	2.33	0.46
10:R:111:VAL:HG12	10:R:164:LEU:HD11	1.98	0.46
3:2:1056:G:C2'	3:2:1058:A:H62	2.28	0.46
3:2:1871:U:H2'	3:2:1872:G:C8	2.51	0.46
3:2:2925:G:H2'	3:2:2926:G:C8	2.51	0.46
5:4:153:U:H2'	5:4:154:U:C6	2.51	0.46
5:4:164:U:O5'	5:4:164:U:H6	1.99	0.46
17:Y:16:VAL:HA	17:Y:56:VAL:HG12	1.98	0.46
3:2:80:C:H2'	3:2:81:C:C6	2.50	0.45
3:2:1679:A:OP1	3:2:1874:U:O2'	2.30	0.45
3:2:2294:G:N1	3:2:2324:G:O6	2.48	0.45
3:2:2355:C:H2'	3:2:2356:U:H4'	1.98	0.45
3:2:3259:C:H42	3:2:3387:G:H1	1.63	0.45
3:2:3467:G:H2'	3:2:3468:C:C6	2.51	0.45
7:O:137:TYR:O	7:O:141:THR:HG22	2.16	0.45
26:h:81:VAL:HG12	26:h:124:CYS:SG	2.55	0.45
26:h:87:TRP:HH2	26:h:97:PHE:HE1	1.64	0.45
3:2:137:C:O2	3:2:137:C:H2'	2.15	0.45
3:2:744:U:OP1	3:2:779:A:O2'	2.26	0.45
3:2:1610:U:H2'	3:2:1611:G:O4'	2.16	0.45
3:2:2311:A:H2'	3:2:2312:A:C8	2.50	0.45
3:2:2603:C:H2'	3:2:2604:U:C6	2.51	0.45
3:2:2660:U:H3'	3:2:2661:U:O2	2.16	0.45
3:2:3286:U:H3	3:2:3303:C:H1'	1.80	0.45
3:2:3423:A:H2'	3:2:3424:A:C8	2.52	0.45
12:T:34:PHE:CD1	12:T:42:PRO:HD3	2.51	0.45
14:V:200:LEU:HD12	14:V:213:PHE:CG	2.51	0.45
3:2:1700:G:H4'	3:2:1743:A:O4'	2.16	0.45
3:2:2267:C:H4'	3:2:2268:G:OP2	2.16	0.45
3:2:2446:A:H3'	3:2:2447:C:C6	2.52	0.45
3:2:2857:A:H2'	3:2:2858:U:H6	1.81	0.45
3:2:3276:A:H61	3:2:3285:G:H5'	1.81	0.45
15:W:91:LEU:HD12	15:W:163:PHE:CE2	2.51	0.45
31:m:74:ASN:CG	31:m:114:LYS:HB3	2.40	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:s:103:GLN:HE22	37:s:107:GLN:HE22	1.63	0.45
3:2:2299:U:H3	3:2:2321:A:H61	1.65	0.45
3:2:2862:U:H2'	3:2:2863:U:C6	2.52	0.45
3:2:3042:G:C2	7:O:250:ALA:HB1	2.52	0.45
3:2:3363:C:H2'	3:2:3364:A:H8	1.81	0.45
3:2:3441:G:O2'	3:2:3443:A:OP1	2.26	0.45
17:Y:82:ASP:O	17:Y:86:LYS:N	2.42	0.45
26:h:28:ALA:HB2	26:h:101:ALA:HB1	1.99	0.45
36:r:51:CYS:SG	36:r:100:ARG:HB2	2.57	0.45
43:y:31:ASN:OD1	43:y:33:GLU:HG2	2.16	0.45
3:2:175:G:N2	3:2:176:A:C4	2.84	0.45
3:2:547:G:O6	3:2:579:A:N7	2.50	0.45
3:2:1255:C:O2	3:2:3212:G:N2	2.49	0.45
3:2:2515:U:H2'	3:2:2516:U:H6	1.81	0.45
3:2:2660:U:H2'	3:2:2660:U:O2	2.17	0.45
3:2:3257:C:H2'	3:2:3258:G:O4'	2.16	0.45
5:4:77:U:H2'	5:4:78:G:O4'	2.16	0.45
7:O:80:GLU:OE1	7:O:314:TYR:OH	2.32	0.45
14:V:41:ALA:O	14:V:195:CYS:HA	2.16	0.45
15:W:29:ARG:N	15:W:32:ARG:HH21	2.15	0.45
33:o:28:LYS:HB3	33:o:99:THR:OG1	2.16	0.45
2:1:5:THR:CG2	2:1:9:GLY:H	2.26	0.45
3:2:283:U:H2'	3:2:284:U:C6	2.52	0.45
3:2:454:G:H22	3:2:499:G:N2	2.13	0.45
3:2:1190:A:N3	3:2:1190:A:H2'	2.30	0.45
3:2:1234:A:N6	3:2:1331:G:H2'	2.31	0.45
3:2:2514:U:H2'	3:2:2515:U:C6	2.51	0.45
3:2:2784:A:N3	3:2:2784:A:H2'	2.32	0.45
3:2:3287:A:N1	3:2:3289:G:H4'	2.31	0.45
5:4:159:U:H5''	5:4:160:G:OP1	2.17	0.45
12:T:57:ARG:O	12:T:61:ARG:HG3	2.16	0.45
17:Y:133:LYS:HA	17:Y:133:LYS:HD3	1.77	0.45
23:e:159:VAL:HG13	23:e:160:GLY:N	2.32	0.45
28:j:135:ALA:HB1	28:j:141:LEU:HD13	1.99	0.45
3:2:492:U:H2'	3:2:493:G:H8	1.82	0.45
3:2:1640:A:O2'	3:2:1642:U:OP2	2.35	0.45
3:2:1886:U:O2'	5:4:122:G:OP1	2.23	0.45
3:2:2507:A:H2'	3:2:2508:C:H6	1.81	0.45
3:2:2621:G:N7	6:N:66:TYR:OH	2.43	0.45
3:2:2781:A:H2'	3:2:2782:G:O4'	2.17	0.45
3:2:3266:U:H2'	3:2:3267:A:C8	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:3:12:U:O2'	4:3:109:U:O4'	2.31	0.45
5:4:81:U:H2'	5:4:82:U:O4'	2.17	0.45
7:O:283:TYR:HB2	7:O:323:MET:HG2	1.99	0.45
13:U:130:VAL:HG13	13:U:152:VAL:HG22	1.99	0.45
14:V:51:HIS:CD2	14:V:168:SER:HB2	2.52	0.45
30:l:124:SER:O	30:l:126:LYS:HE2	2.16	0.45
31:m:148:ALA:HA	39:u:6:VAL:HG13	1.98	0.45
3:2:480:G:H2'	3:2:481:A:H8	1.81	0.45
3:2:599:U:H2'	3:2:600:C:C6	2.50	0.45
3:2:1244:G:HO2'	3:2:1245:U:P	2.39	0.45
3:2:2303:A:H2'	3:2:2304:G:C8	2.52	0.45
6:N:28:LEU:HD23	6:N:28:LEU:HA	1.69	0.45
13:U:80:ILE:O	13:U:84:GLN:HB2	2.17	0.45
15:W:16:LYS:HG3	15:W:130:VAL:HB	1.98	0.45
21:c:5:ILE:HG22	21:c:7:ARG:HG3	1.99	0.45
30:l:29:ILE:HG22	30:l:31:GLN:O	2.16	0.45
33:o:87:CYS:SG	33:o:96:LEU:HD11	2.57	0.45
43:y:90:ALA:HB1	43:y:94:LYS:HB2	1.99	0.45
3:2:259:A:H5'	3:2:259:A:N3	2.31	0.45
3:2:1726:U:H2'	3:2:1727:U:C6	2.52	0.45
3:2:2867:C:H4'	3:2:2868:C:OP2	2.17	0.45
3:2:2995:A:H3'	3:2:2996:G:H8	1.82	0.45
8:P:5:ARG:N	8:P:6:PRO:HD3	2.31	0.45
12:T:203:VAL:HG13	12:T:207:ASP:HB2	1.99	0.45
18:Z:4:TYR:CZ	18:Z:49:ARG:HD2	2.51	0.45
23:e:11:ARG:HB3	23:e:23:LEU:HD23	1.98	0.45
24:f:100:LYS:O	24:f:103:GLN:HG3	2.16	0.45
38:t:108:LYS:HE2	38:t:108:LYS:HB3	1.77	0.45
3:2:1234:A:H5''	4:3:88:A:C5	2.52	0.45
3:2:1458:C:H4'	43:y:15:ASN:HD21	1.81	0.45
3:2:1472:U:H2'	3:2:1473:U:C6	2.51	0.45
3:2:1686:U:H5''	6:N:70:THR:CG2	2.47	0.45
3:2:1732:A:H2'	3:2:1733:C:O4'	2.17	0.45
3:2:3252:U:H2'	3:2:3253:G:H8	1.82	0.45
11:S:70:GLN:OE1	11:S:84:TYR:OH	2.32	0.45
16:X:54:ILE:HD12	16:X:119:TYR:HB2	1.99	0.45
26:h:44:THR:HG21	26:h:52:PRO:HB3	1.97	0.45
3:2:419:U:H2'	3:2:420:G:C8	2.52	0.44
3:2:2005:U:H3'	3:2:2006:U:C6	2.51	0.44
10:R:47:LYS:HB2	10:R:47:LYS:HE2	1.74	0.44
15:W:53:THR:HG22	15:W:61:ARG:NH1	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:h:29:ASP:HB3	26:h:103:VAL:HG12	1.99	0.44
27:i:18:GLY:HA3	27:i:31:PHE:O	2.17	0.44
3:2:1261:G:N2	3:2:1291:A:H1'	2.32	0.44
3:2:1379:U:OP2	21:c:38:ARG:HD3	2.17	0.44
3:2:1589:U:H5	3:2:1591:A:N7	2.15	0.44
3:2:3246:A:H4'	7:O:128:LYS:O	2.17	0.44
10:R:139:PHE:HD2	10:R:143:ASN:HD22	1.65	0.44
12:T:97:TYR:HB3	12:T:131:ASN:HA	2.00	0.44
12:T:97:TYR:OH	12:T:207:ASP:OD2	2.15	0.44
12:T:237:ILE:O	12:T:237:ILE:HG13	2.17	0.44
3:2:138:U:H5	38:t:70:GLU:OE2	2.01	0.44
3:2:249:G:C6	3:2:250:A:N7	2.86	0.44
3:2:1425:C:H2'	3:2:1425:C:O2	2.18	0.44
3:2:2750:U:H4'	3:2:2751:A:O4'	2.17	0.44
3:2:3480:C:H4'	7:O:315:GLY:HA2	1.99	0.44
6:N:205:PRO:HG3	6:N:212:GLY:HA3	2.00	0.44
14:V:203:ARG:O	14:V:209:LYS:NZ	2.37	0.44
3:2:572:A:O2'	3:2:573:G:H8	2.01	0.44
3:2:681:A:H2'	3:2:682:A:C8	2.53	0.44
3:2:1599:A:H1'	3:2:1600:C:H5	1.82	0.44
3:2:3335:U:H3'	3:2:3336:G:N2	2.18	0.44
5:4:164:U:H2'	5:4:165:U:O4'	2.17	0.44
10:R:191:HIS:CD2	36:r:41:GLU:HB3	2.52	0.44
18:Z:104:GLU:OE1	18:Z:161:SER:HA	2.18	0.44
23:e:47:ILE:HD13	23:e:47:ILE:HA	1.82	0.44
28:j:99:ARG:NH1	28:j:99:ARG:HB2	2.33	0.44
33:o:16:ILE:HD13	33:o:76:TYR:CE2	2.48	0.44
38:t:58:THR:HG22	38:t:62:GLU:OE2	2.17	0.44
3:2:995:G:O2'	31:m:29:PRO:O	2.35	0.44
3:2:2225:U:C6	3:2:2229:U:C4	3.06	0.44
3:2:3342:G:H5'	3:2:3345:G:H8	1.83	0.44
4:3:115:A:H2'	4:3:116:G:O4'	2.17	0.44
8:P:94:ASN:HA	8:P:100:ARG:O	2.17	0.44
20:b:10:LEU:HB2	20:b:13:LYS:HB2	1.99	0.44
40:v:39:TYR:CD1	40:v:40:PRO:HA	2.52	0.44
3:2:481:A:C5'	43:y:105:ARG:HD2	2.48	0.44
3:2:641:G:H2'	3:2:642:A:H8	1.81	0.44
3:2:2343:A:C5	3:2:2350:A:H1'	2.52	0.44
3:2:2512:A:H2'	3:2:2513:G:O4'	2.18	0.44
3:2:3263:A:H2'	3:2:3264:U:H6	1.82	0.44
3:2:3435:U:H4'	3:2:3436:A:H5'	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:U:124:ILE:HG21	13:U:159:ILE:HG12	1.98	0.44
16:X:46:ILE:HD11	16:X:51:VAL:HA	1.99	0.44
3:2:265:C:C2'	3:2:266:G:H5'	2.47	0.44
3:2:1607:U:OP1	5:4:135:C:N4	2.50	0.44
3:2:1826:C:H5''	37:s:38:LEU:HD22	1.99	0.44
3:2:2238:G:O2'	3:2:2277:U:OP1	2.19	0.44
3:2:2303:A:H2'	3:2:2304:G:O4'	2.18	0.44
3:2:3042:G:H2'	3:2:3043:C:C6	2.53	0.44
12:T:68:ARG:H	12:T:68:ARG:HG2	1.58	0.44
14:V:46:PHE:HB2	14:V:139:ARG:HH11	1.83	0.44
23:e:77:TRP:HZ3	23:e:126:VAL:HG22	1.83	0.44
3:2:948:G:H5'	3:2:949:A:OP1	2.18	0.44
3:2:1336:U:H5	3:2:2455:U:OP1	2.01	0.44
3:2:1975:U:O2'	3:2:1987:A:N7	2.49	0.44
3:2:2495:C:H2'	3:2:2496:U:C6	2.53	0.44
3:2:2989:C:OP2	13:U:166:ARG:NH2	2.51	0.44
3:2:3292:U:OP2	3:2:3292:U:H3'	2.18	0.44
7:O:293:ASN:HB2	7:O:304:ARG:HA	1.99	0.44
10:R:118:LYS:HB3	10:R:118:LYS:HE2	1.64	0.44
13:U:154:GLN:NE2	13:U:158:ASN:OD1	2.50	0.44
16:X:134:LYS:HD2	16:X:134:LYS:HA	1.76	0.44
19:a:3:GLU:OE2	19:a:5:GLN:NE2	2.51	0.44
19:a:177:LYS:HB3	19:a:177:LYS:HE3	1.73	0.44
35:q:94:ALA:HB3	35:q:97:VAL:HG23	2.00	0.44
39:u:30:HIS:ND1	39:u:30:HIS:C	2.76	0.44
3:2:251:U:O2	3:2:253:U:O2'	2.32	0.44
3:2:1064:C:H2'	3:2:1065:U:C5	2.52	0.44
3:2:1140:U:H2'	3:2:1141:C:C6	2.53	0.44
3:2:3019:U:H2'	3:2:3020:C:O4'	2.18	0.44
5:4:27:C:H2'	5:4:28:U:C6	2.53	0.44
8:P:177:TYR:H	8:P:178:ARG:NH2	2.16	0.44
13:U:160:LYS:HE3	13:U:179:VAL:HB	1.99	0.44
15:W:60:ARG:HB2	15:W:63:GLU:HB2	2.00	0.44
41:w:64:ASP:OD1	41:w:64:ASP:N	2.42	0.44
3:2:182:G:H22	3:2:248:G:H1	1.65	0.43
3:2:248:G:H2'	3:2:249:G:C8	2.53	0.43
3:2:1181:A:N7	3:2:1341:G:H5'	2.32	0.43
3:2:1304:A:H2'	3:2:1304:A:N3	2.33	0.43
3:2:1661:A:N1	3:2:1872:G:C6	2.86	0.43
3:2:1977:A:H2'	3:2:1978:C:O4'	2.18	0.43
3:2:2787:A:H2'	3:2:2788:U:O4'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2:3264:U:OP1	36:r:64:LYS:HE2	2.18	0.43
3:2:3472:G:H2'	3:2:3473:A:C8	2.53	0.43
11:S:244:ASN:O	11:S:248:ARG:HG2	2.18	0.43
34:p:80:LEU:CD2	34:p:96:VAL:HG13	2.48	0.43
3:2:265:C:H2'	3:2:266:G:H5'	1.99	0.43
3:2:1108:C:O3'	32:n:38:LYS:HD3	2.18	0.43
3:2:1143:A:H2'	3:2:1144:G:C8	2.53	0.43
3:2:2003:G:C6	3:2:2004:G:N7	2.86	0.43
3:2:2765:G:H2'	3:2:2766:A:C8	2.53	0.43
3:2:2815:G:H22	3:2:2831:A:H2	1.64	0.43
3:2:2868:C:H2'	3:2:2869:C:H6	1.82	0.43
3:2:3056:G:H2'	3:2:3057:U:C6	2.53	0.43
9:Q:276:THR:OG1	9:Q:279:GLU:OE1	2.35	0.43
18:Z:48:ALA:O	18:Z:53:TYR:HB3	2.18	0.43
26:h:21:VAL:HG12	26:h:22:GLN:HG2	1.99	0.43
27:i:10:GLY:HA3	27:i:53:VAL:HG22	1.99	0.43
35:q:29:TRP:CZ2	35:q:50:PRO:HD2	2.54	0.43
2:1:43:GLY:O	33:o:81:ILE:HD11	2.18	0.43
3:2:305:A:C8	3:2:307:G:H1'	2.53	0.43
3:2:1270:C:H2'	3:2:1271:A:O4'	2.18	0.43
3:2:2379:A:H2'	3:2:2380:U:H6	1.83	0.43
3:2:3394:C:OP1	3:2:3394:C:H4'	2.19	0.43
5:4:151:U:H2'	5:4:152:G:O4'	2.19	0.43
24:f:80:VAL:HG21	24:f:85:MET:SD	2.58	0.43
3:2:177:G:H22	3:2:254:G:N2	2.16	0.43
3:2:808:U:C2	3:2:2814:U:H1'	2.53	0.43
3:2:1613:C:N4	3:2:1614:U:O4	2.51	0.43
3:2:1881:U:H2'	3:2:1882:C:C6	2.54	0.43
3:2:3119:U:H2'	3:2:3120:A:C8	2.50	0.43
3:2:3263:A:H2'	3:2:3264:U:C6	2.53	0.43
3:2:3318:A:C5	36:r:5:GLY:HA3	2.54	0.43
8:P:291:ARG:HE	8:P:291:ARG:HB2	1.51	0.43
3:2:188:C:C4	3:2:190:G:N2	2.86	0.43
3:2:369:A:O4'	3:2:846:U:H4'	2.19	0.43
3:2:517:U:H2'	3:2:518:U:O4'	2.18	0.43
3:2:680:C:H2'	3:2:681:A:C8	2.54	0.43
3:2:765:G:N3	3:2:765:G:H2'	2.33	0.43
3:2:1225:G:H2'	3:2:1226:A:C8	2.52	0.43
3:2:1396:G:H2'	3:2:1397:A:C8	2.53	0.43
3:2:2529:A:H2'	3:2:2530:G:C8	2.53	0.43
3:2:2777:C:OP2	15:W:51:ARG:NH2	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2:3217:U:C1'	3:2:3218:A:H5''	2.46	0.43
4:3:75:G:H21	23:e:50:VAL:C	2.26	0.43
9:Q:285:ASN:CG	14:V:220:LEU:HB3	2.43	0.43
3:2:1286:C:H2'	3:2:1287:G:C8	2.54	0.43
3:2:1746:U:H2'	3:2:1747:A:C8	2.53	0.43
3:2:2833:A:H5'	32:n:36:ASP:OD1	2.18	0.43
3:2:3243:A:H2'	3:2:3244:C:O4'	2.19	0.43
9:Q:97:ALA:O	9:Q:101:THR:HG22	2.19	0.43
10:R:189:ARG:HH22	23:e:161:LEU:HD22	1.82	0.43
19:a:2:SER:HB3	36:r:35:GLY:HA2	2.01	0.43
37:s:16:ARG:HG2	37:s:16:ARG:NH1	2.34	0.43
37:s:103:GLN:NE2	37:s:107:GLN:HE22	2.15	0.43
43:y:71:ASN:HD22	43:y:72:PRO:HD2	1.84	0.43
3:2:1470:U:O5'	3:2:1471:C:H5''	2.19	0.43
3:2:1531:C:H2'	3:2:1532:A:C8	2.53	0.43
3:2:3363:C:O4'	3:2:3363:C:P	2.76	0.43
3:2:3375:U:O2'	3:2:3376:U:O5'	2.31	0.43
7:O:37:ALA:HA	7:O:185:GLY:O	2.19	0.43
8:P:347:LYS:HA	8:P:347:LYS:HD3	1.82	0.43
8:P:355:LYS:NZ	24:f:143:THR:OG1	2.52	0.43
11:S:90:LYS:HB2	11:S:90:LYS:HE3	1.64	0.43
20:b:111:LYS:HE3	20:b:152:GLU:HB3	2.00	0.43
23:e:109:MET:HE3	23:e:109:MET:HB3	1.85	0.43
36:r:51:CYS:HB3	36:r:69:TRP:CE3	2.53	0.43
3:2:1388:G:N3	3:2:1388:G:C2'	2.81	0.43
3:2:2683:U:OP1	12:T:241:LYS:NZ	2.50	0.43
3:2:3352:A:H2'	3:2:3353:U:C6	2.53	0.43
6:N:174:ILE:H	6:N:174:ILE:HG13	1.66	0.43
8:P:175:LYS:HA	8:P:178:ARG:NH2	2.33	0.43
9:Q:64:ILE:HD12	9:Q:109:ALA:HB2	2.01	0.43
9:Q:107:ARG:HH12	9:Q:120:GLU:HA	1.84	0.43
9:Q:184:ASP:HB3	9:Q:187:THR:HG22	2.00	0.43
24:f:80:VAL:HG23	24:f:83:ARG:NH1	2.33	0.43
41:w:41:LYS:HG2	41:w:42:TYR:CE2	2.53	0.43
43:y:64:VAL:HG12	43:y:123:ILE:HG21	2.00	0.43
3:2:140:U:C5'	38:t:84:GLN:HG2	2.45	0.43
3:2:699:G:H2'	3:2:700:C:O4'	2.19	0.43
3:2:765:G:H3'	3:2:766:G:H8	1.84	0.43
3:2:1035:A:H1'	9:Q:15:ARG:CZ	2.49	0.43
3:2:1248:A:H2'	3:2:1249:U:C5	2.54	0.43
3:2:2608:C:O2'	3:2:2609:U:H5'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2:3113:A:H2'	3:2:3114:C:C6	2.54	0.43
14:V:58:GLU:HG3	14:V:60:ILE:HG13	2.01	0.43
36:r:102:MET:HE3	36:r:102:MET:HB3	1.89	0.43
3:2:183:A:HO2'	3:2:184:C:C5'	2.31	0.43
3:2:619:G:C8	3:2:634:G:C6	3.07	0.43
3:2:1081:C:H2'	3:2:1082:U:C6	2.53	0.43
3:2:2954:U:H4'	3:2:2955:U:C6	2.54	0.43
3:2:3396:A:H2'	3:2:3397:A:C8	2.54	0.43
9:Q:191:ASP:OD2	9:Q:194:THR:HG22	2.19	0.43
3:2:315:A:H2'	3:2:316:A:C8	2.54	0.42
3:2:379:G:H4'	3:2:404:A:N1	2.34	0.42
3:2:444:A:C6	3:2:445:G:C6	3.07	0.42
3:2:1594:G:O6	28:j:32:ARG:HD3	2.19	0.42
3:2:2657:A:O5'	30:l:52:LYS:NZ	2.52	0.42
3:2:3288:G:H2'	3:2:3289:G:C8	2.49	0.42
5:4:100:A:H2'	5:4:101:U:O4'	2.18	0.42
14:V:49:CYS:HA	14:V:139:ARG:HA	2.01	0.42
3:2:1130:A:O2'	24:f:132:PRO:HD3	2.19	0.42
3:2:1200:A:H2'	3:2:1201:A:C8	2.53	0.42
3:2:1388:G:N3	3:2:1388:G:H2'	2.33	0.42
3:2:1388:G:P	43:y:40:LYS:HZ1	2.40	0.42
3:2:2703:G:O2'	3:2:2704:A:H5'	2.20	0.42
6:N:5:ILE:HG22	6:N:207:ASP:O	2.19	0.42
13:U:99:ILE:HG21	13:U:116:LEU:HA	2.01	0.42
15:W:126:ASP:OD1	15:W:126:ASP:N	2.52	0.42
3:2:121:A:C2	12:T:129:PRO:HB3	2.53	0.42
3:2:1007:C:OP2	21:c:14:GLN:NE2	2.52	0.42
3:2:1056:G:H2'	3:2:1058:A:H62	1.84	0.42
3:2:1186:C:H1'	3:2:1229:C:O2	2.19	0.42
3:2:1322:A:H2'	3:2:1323:C:O4'	2.19	0.42
3:2:1661:A:H2	3:2:1872:G:H1	1.58	0.42
3:2:1791:G:C8	41:w:26:LYS:HD3	2.54	0.42
3:2:2363:A:H2'	3:2:2364:G:O4'	2.19	0.42
3:2:3006:A:H4'	3:2:3007:G:H8	1.82	0.42
3:2:3334:A:H2'	3:2:3335:U:H6	1.84	0.42
13:U:118:GLU:HB3	13:U:120:ILE:HG13	2.01	0.42
13:U:135:SER:HB3	13:U:142:ILE:HA	2.02	0.42
21:c:175:ARG:O	31:m:56:VAL:HG21	2.18	0.42
39:u:9:LEU:HD23	39:u:9:LEU:HA	1.83	0.42
3:2:1261:G:H21	3:2:1291:A:H1'	1.85	0.42
3:2:1594:G:C6	3:2:1614:U:N3	2.88	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2:2379:A:H2'	3:2:2380:U:C6	2.54	0.42
3:2:2680:C:OP1	3:2:2680:C:H6	2.02	0.42
3:2:2908:A:H2'	3:2:2909:G:O4'	2.19	0.42
3:2:3166:A:H2'	3:2:3167:C:H6	1.84	0.42
3:2:3441:G:O3'	3:2:3442:U:H4'	2.19	0.42
4:3:16:U:H2'	4:3:17:A:H8	1.82	0.42
10:R:104:THR:HG22	10:R:106:ALA:N	2.30	0.42
15:W:9:MET:HE2	15:W:9:MET:HB2	1.72	0.42
19:a:3:GLU:HG3	19:a:5:GLN:HG2	2.01	0.42
24:f:7:ILE:HD13	24:f:7:ILE:HA	1.91	0.42
3:2:182:G:H3'	3:2:183:A:H5''	2.00	0.42
3:2:1207:C:H2'	3:2:1208:G:N2	2.35	0.42
3:2:1290:A:N3	3:2:1312:U:H1'	2.34	0.42
3:2:1822:C:H2'	3:2:1823:U:C6	2.55	0.42
3:2:2863:U:H2'	3:2:2864:G:C8	2.54	0.42
3:2:3102:A:H2'	3:2:3103:U:O4'	2.20	0.42
4:3:88:A:H2'	4:3:89:G:O4'	2.19	0.42
7:O:66:LYS:HE2	26:h:11:THR:O	2.19	0.42
7:O:358:TRP:CZ3	27:i:15:PRO:HG2	2.54	0.42
8:P:159:GLN:HA	8:P:217:ILE:HB	2.01	0.42
14:V:25:ALA:O	14:V:122:PRO:HG2	2.18	0.42
28:j:45:TYR:CD1	38:t:77:TYR:HB3	2.54	0.42
28:j:108:LYS:HG2	28:j:124:LYS:HE2	2.01	0.42
41:w:46:LEU:HD21	41:w:57:LEU:HD11	2.00	0.42
2:1:16:VAL:HG12	3:2:1982:G:C8	2.55	0.42
3:2:439:A:H2'	3:2:440:A:C8	2.54	0.42
3:2:589:U:O2'	3:2:590:U:O5'	2.36	0.42
3:2:1371:G:H2'	3:2:1372:U:C6	2.55	0.42
3:2:1737:C:H2'	3:2:1738:C:O4'	2.19	0.42
3:2:2659:G:H2'	3:2:2660:U:H6	1.84	0.42
3:2:3129:A:H2'	3:2:3130:C:C6	2.54	0.42
3:2:3190:A:H2'	3:2:3191:U:C6	2.55	0.42
11:S:22:LYS:HA	11:S:25:LYS:HG2	2.02	0.42
15:W:23:LEU:HD11	15:W:124:GLY:H	1.85	0.42
18:Z:114:ARG:NH1	18:Z:151:ILE:O	2.52	0.42
24:f:48:VAL:O	24:f:52:MET:HE3	2.19	0.42
25:g:14:ILE:HD11	25:g:74:LEU:HD12	2.01	0.42
25:g:53:VAL:HG12	25:g:54:SER:O	2.20	0.42
25:g:55:ARG:HG2	25:g:56:GLU:H	1.85	0.42
39:u:69:LYS:HE2	39:u:69:LYS:HB3	1.86	0.42
3:2:719:A:O3'	18:Z:201:ARG:NH2	2.51	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2:1095:G:H2'	3:2:1129:G:N2	2.35	0.42
3:2:1200:A:H4'	11:S:226:LYS:HD3	2.02	0.42
3:2:1277:G:H8	3:2:1277:G:P	2.42	0.42
3:2:1395:A:H2'	3:2:1396:G:C8	2.55	0.42
3:2:1738:C:O2'	3:2:1740:U:N3	2.51	0.42
3:2:3287:A:C2	3:2:3289:G:H4'	2.55	0.42
4:3:27:A:H2'	4:3:28:C:C6	2.55	0.42
10:R:189:ARG:O	10:R:193:MET:HG3	2.20	0.42
11:S:144:TYR:CE2	11:S:238:LYS:HB3	2.54	0.42
23:e:130:LYS:HE3	23:e:132:GLU:OE2	2.19	0.42
31:m:135:GLU:O	31:m:139:GLN:HG3	2.19	0.42
3:2:1095:G:N2	3:2:1129:G:O2'	2.53	0.42
3:2:1183:G:H1	3:2:1231:A:H61	1.66	0.42
3:2:3259:C:N4	3:2:3387:G:H1	2.18	0.42
6:N:28:LEU:O	6:N:29:ARG:CB	2.68	0.42
9:Q:260:ALA:HA	9:Q:263:PHE:CD2	2.55	0.42
17:Y:63:MET:SD	17:Y:83:VAL:HG21	2.59	0.42
3:2:715:U:H5'	3:2:716:G:H5''	2.01	0.42
3:2:1151:A:H2'	3:2:1152:U:C6	2.54	0.42
3:2:1757:C:H2'	3:2:1758:G:O4'	2.20	0.42
4:3:1:G:C8	9:Q:264:LYS:HD3	2.54	0.42
5:4:61:A:OP1	42:x:19:GLN:NE2	2.53	0.42
10:R:143:ASN:HA	10:R:148:ALA:HB2	2.01	0.42
13:U:92:LEU:HD12	13:U:140:ASP:OD1	2.19	0.42
39:u:2:ALA:HA	39:u:10:ASN:O	2.20	0.42
39:u:56:MET:HG2	39:u:88:LEU:HB3	2.02	0.42
2:1:42:CYS:SG	2:1:44:ARG:HD3	2.60	0.42
3:2:1159:U:H2'	3:2:1160:A:O4'	2.20	0.42
3:2:1562:G:H2'	3:2:1563:A:O4'	2.19	0.42
3:2:1711:A:H2'	3:2:1712:A:C8	2.54	0.42
3:2:2687:G:H4'	3:2:2689:C:C2	2.55	0.42
3:2:3340:C:H2'	3:2:3341:G:H5''	2.02	0.42
3:2:3418:U:H5'	7:O:123:PHE:HE1	1.85	0.42
6:N:28:LEU:HB2	6:N:122:ARG:HA	2.02	0.42
9:Q:112:LYS:HE2	9:Q:112:LYS:HB2	1.83	0.42
13:U:12:THR:HA	13:U:52:THR:HA	2.01	0.42
14:V:145:ARG:NH2	14:V:167:VAL:HG21	2.33	0.42
18:Z:104:GLU:OE1	18:Z:160:GLU:HG2	2.20	0.42
3:2:256:C:H3'	3:2:257:A:H8	1.84	0.41
3:2:301:C:H2'	3:2:302:U:O4'	2.20	0.41
3:2:1527:G:O6	42:x:2:PRO:HD2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2:2501:A:H2'	3:2:2502:G:H8	1.84	0.41
3:2:2730:A:N1	3:2:2737:A:N7	2.68	0.41
3:2:2952:C:H2'	3:2:2953:U:C6	2.55	0.41
10:R:93:ILE:N	10:R:157:GLN:HE22	2.17	0.41
10:R:151:ALA:C	10:R:153:ARG:H	2.28	0.41
16:X:161:GLU:H	16:X:161:GLU:HG2	1.72	0.41
17:Y:12:ARG:HG2	17:Y:58:LEU:HD22	2.00	0.41
22:d:74:ARG:O	22:d:76:THR:HG23	2.20	0.41
23:e:108:ASP:OD1	23:e:112:ARG:NH1	2.53	0.41
1:0:28:TYR:HB3	1:0:69:VAL:HB	2.01	0.41
3:2:573:G:H2'	3:2:574:U:H6	1.84	0.41
3:2:1188:G:H2'	3:2:1189:A:O4'	2.20	0.41
3:2:1251:U:H4'	3:2:1252:A:H5''	2.02	0.41
3:2:1294:A:H2'	3:2:1294:A:N3	2.34	0.41
3:2:2356:U:H2'	3:2:2357:U:C5	2.56	0.41
3:2:2740:G:N7	24:f:2:PRO:HG3	2.35	0.41
7:O:112:GLU:HG3	7:O:122:TRP:CZ2	2.55	0.41
8:P:175:LYS:HA	8:P:178:ARG:HH21	1.85	0.41
8:P:332:PRO:HG3	11:S:49:ARG:CZ	2.50	0.41
12:T:34:PHE:CE1	12:T:42:PRO:HD3	2.55	0.41
13:U:102:ASN:OD1	13:U:113:ARG:HB2	2.21	0.41
17:Y:95:LYS:HB2	17:Y:95:LYS:HE3	1.58	0.41
3:2:359:A:N3	5:4:61:A:H1'	2.36	0.41
3:2:1012:A:H2'	3:2:1013:U:O4'	2.19	0.41
3:2:2759:C:O2'	3:2:2760:U:H5'	2.19	0.41
3:2:3100:C:O2'	3:2:3101:A:H5'	2.21	0.41
5:4:92:C:O4'	29:k:111:ASP:HB2	2.20	0.41
9:Q:166:ALA:HB1	9:Q:171:LEU:HD12	2.02	0.41
15:W:17:LEU:HD21	15:W:127:PHE:CD2	2.55	0.41
15:W:166:LYS:HE3	15:W:166:LYS:HB3	1.82	0.41
29:k:36:LYS:HA	29:k:36:LYS:HD3	1.81	0.41
1:0:25:VAL:HG22	1:0:72:LEU:HD22	2.02	0.41
3:2:191:U:O2'	3:2:192:C:P	2.79	0.41
3:2:382:A:H4'	3:2:383:A:OP1	2.19	0.41
3:2:668:U:O2'	3:2:1184:A:N1	2.49	0.41
3:2:760:C:H5	3:2:763:G:O6	2.03	0.41
3:2:1050:G:N2	3:2:1066:C:H42	2.19	0.41
3:2:1221:A:H5'	3:2:1222:U:OP1	2.20	0.41
3:2:1310:C:H2'	3:2:1311:C:C6	2.55	0.41
3:2:1571:A:H2'	3:2:1572:G:O4'	2.20	0.41
3:2:1597:G:H21	3:2:1597:G:P	2.41	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2:1896:A:H1'	42:x:45:ARG:HH22	1.85	0.41
3:2:1934:A:H2'	3:2:1934:A:N3	2.36	0.41
3:2:2310:A:H2'	3:2:2311:A:C8	2.55	0.41
3:2:2355:C:H3'	3:2:2356:U:H4'	2.02	0.41
8:P:147:ILE:O	43:y:78:PRO:HG2	2.19	0.41
12:T:225:LYS:HD2	12:T:228:GLU:OE2	2.20	0.41
13:U:87:ARG:HG2	13:U:185:ILE:HB	2.03	0.41
14:V:141:LYS:H	14:V:141:LYS:HG2	1.63	0.41
3:2:456:G:H2'	3:2:457:U:C6	2.55	0.41
3:2:1842:U:H2'	3:2:1843:C:C6	2.55	0.41
3:2:2818:U:H2'	3:2:2819:U:C6	2.56	0.41
3:2:2978:U:H2'	3:2:2979:C:C6	2.55	0.41
3:2:3217:U:H4'	3:2:3218:A:OP1	2.20	0.41
5:4:66:G:O6	40:v:63:ARG:NH1	2.52	0.41
5:4:103:G:C5	40:v:83:PRO:HB3	2.56	0.41
10:R:76:LEU:HD23	10:R:76:LEU:HA	1.91	0.41
3:2:192:C:OP1	3:2:192:C:H3'	2.20	0.41
3:2:1212:U:O4	19:a:22:SER:OG	2.37	0.41
3:2:1693:G:H2'	3:2:1694:U:C6	2.56	0.41
3:2:2809:G:H8	3:2:2846:G:H2'	1.86	0.41
3:2:3021:A:H2'	3:2:3022:C:C6	2.56	0.41
3:2:3204:G:H21	13:U:161:GLN:NE2	2.14	0.41
3:2:3389:G:H5''	3:2:3390:G:N7	2.35	0.41
21:c:131:ARG:HE	21:c:131:ARG:HB2	1.69	0.41
43:y:93:ARG:HD2	43:y:93:ARG:HA	1.91	0.41
3:2:445:G:H8	3:2:445:G:H5''	1.85	0.41
3:2:480:G:H2'	3:2:481:A:C8	2.55	0.41
3:2:546:G:H2'	3:2:548:U:C5	2.55	0.41
3:2:892:G:O2'	3:2:927:A:H4'	2.20	0.41
3:2:958:A:H2'	3:2:959:C:C6	2.56	0.41
3:2:1595:U:O2'	3:2:1596:U:P	2.78	0.41
3:2:1725:C:H2'	3:2:1726:U:H6	1.84	0.41
3:2:2770:C:H3'	3:2:2771:A:H8	1.86	0.41
3:2:2913:U:H5'	3:2:2913:U:C6	2.49	0.41
3:2:3432:U:H2'	3:2:3433:U:C6	2.56	0.41
5:4:103:G:O2'	40:v:81:GLY:O	2.35	0.41
7:O:282:ILE:HG23	7:O:322:VAL:HG13	2.03	0.41
8:P:352:ALA:O	8:P:356:PHE:HB3	2.21	0.41
12:T:24:ASN:HB3	12:T:25:PRO:HD3	2.03	0.41
14:V:178:ARG:HH21	14:V:182:ILE:HD11	1.86	0.41
15:W:9:MET:CG	15:W:134:PRO:HG2	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:f:49:GLN:HA	24:f:52:MET:HE3	2.03	0.41
25:g:49:SER:O	25:g:49:SER:OG	2.35	0.41
36:r:104:TYR:HB2	36:r:105:PRO:HD3	2.03	0.41
1:0:91:PHE:CZ	1:0:93:LEU:HG	2.56	0.41
3:2:94:G:H2'	3:2:95:A:C8	2.56	0.41
3:2:175:G:N2	3:2:176:A:N3	2.68	0.41
3:2:653:U:H2'	3:2:654:U:C6	2.56	0.41
3:2:1386:G:C8	3:2:1387:A:C8	3.09	0.41
3:2:1729:U:O2'	3:2:1730:U:H5'	2.21	0.41
3:2:1846:A:H5'	37:s:77:GLY:O	2.20	0.41
3:2:2757:G:H2'	3:2:2758:A:H8	1.84	0.41
3:2:3488:C:H2'	3:2:3489:C:C6	2.56	0.41
8:P:260:LEU:HD23	8:P:260:LEU:HA	1.96	0.41
8:P:303:LYS:HB2	8:P:303:LYS:HE3	1.74	0.41
11:S:108:ARG:NH2	21:c:4:ASP:OD1	2.54	0.41
13:U:167:ASN:OD1	13:U:167:ASN:C	2.64	0.41
25:g:51:VAL:O	25:g:66:HIS:N	2.48	0.41
3:2:222:G:OP1	8:P:200:ARG:HD2	2.21	0.41
3:2:260:U:H4'	3:2:261:A:O4'	2.21	0.41
3:2:1068:A:H2'	3:2:1069:C:O4'	2.20	0.41
3:2:1304:A:C6	3:2:1305:A:C6	3.08	0.41
3:2:1381:G:C1'	8:P:290:THR:HG21	2.51	0.41
3:2:1388:G:HO2'	3:2:1389:A:P	2.43	0.41
3:2:1532:A:H2'	3:2:1533:U:C6	2.55	0.41
3:2:2255:A:H2'	3:2:2256:A:C8	2.56	0.41
3:2:2348:U:H2'	3:2:2349:G:C2	2.55	0.41
3:2:2357:U:H1'	3:2:2359:A:OP2	2.21	0.41
3:2:3374:A:H5'	3:2:3375:U:O5'	2.21	0.41
4:3:51:G:N2	15:W:9:MET:HE1	2.36	0.41
5:4:57:G:H2'	5:4:58:C:C6	2.56	0.41
5:4:112:A:C8	5:4:113:A:C8	3.09	0.41
8:P:10:ILE:HD11	8:P:22:ILE:HG13	2.03	0.41
9:Q:41:LYS:HB2	24:f:68:THR:O	2.20	0.41
10:R:52:LEU:HD23	10:R:103:ALA:HB2	2.02	0.41
13:U:32:ARG:HH21	13:U:147:ASN:HB3	1.86	0.41
27:i:47:ARG:CZ	27:i:54:LEU:HD22	2.51	0.41
28:j:66:ILE:HD12	28:j:120:LYS:HG3	2.02	0.41
29:k:54:GLN:HB3	29:k:107:LYS:HB3	2.03	0.41
3:2:322:U:H2'	3:2:323:C:C6	2.55	0.41
3:2:1268:G:C6	3:2:1269:C:C4	3.09	0.41
3:2:1744:A:H2'	3:2:1744:A:N3	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2:3310:A:OP1	17:Y:102:ARG:NH1	2.51	0.41
5:4:158:G:O3'	12:T:60:ARG:NH2	2.54	0.41
7:O:352:GLU:O	7:O:352:GLU:HG3	2.20	0.41
8:P:212:ASN:O	8:P:233:ARG:NH2	2.54	0.41
24:f:102:ARG:O	24:f:106:LEU:HG	2.21	0.41
3:2:115:A:H2'	3:2:273:A:H2'	2.03	0.40
3:2:164:G:H2'	3:2:165:A:C8	2.57	0.40
3:2:211:A:H2'	3:2:212:C:O4'	2.21	0.40
3:2:570:G:H2'	3:2:570:G:N3	2.35	0.40
3:2:619:G:H2'	3:2:620:C:C6	2.56	0.40
3:2:1273:G:C8	3:2:1274:G:N7	2.89	0.40
3:2:1305:A:H2'	3:2:1306:C:C6	2.57	0.40
3:2:1871:U:H2'	3:2:1872:G:H8	1.84	0.40
3:2:2493:C:O2	3:2:2914:A:N1	2.54	0.40
3:2:2857:A:H2'	3:2:2858:U:C6	2.56	0.40
3:2:3003:G:H2'	3:2:3004:U:C6	2.56	0.40
3:2:3247:U:H5'	3:2:3394:C:N1	2.36	0.40
3:2:3298:C:O2'	3:2:3299:U:P	2.79	0.40
4:3:17:A:H2'	4:3:18:G:O4'	2.21	0.40
4:3:26:C:H2'	4:3:27:A:O4'	2.20	0.40
10:R:49:ARG:NH2	10:R:98:HIS:O	2.54	0.40
15:W:19:LEU:HB2	15:W:125:MET:SD	2.61	0.40
15:W:86:VAL:HG11	15:W:106:ILE:HD13	2.03	0.40
19:a:49:PHE:HE2	19:a:53:LEU:HD11	1.86	0.40
22:d:146:LYS:HE3	22:d:146:LYS:HB3	1.93	0.40
37:s:62:PHE:O	37:s:70:LYS:HD3	2.21	0.40
41:w:41:LYS:HG2	41:w:42:TYR:CD2	2.55	0.40
3:2:99:A:H1'	3:2:289:G:C5	2.56	0.40
3:2:839:A:H61	3:2:966:G:H22	1.70	0.40
3:2:1041:A:H2'	3:2:1042:G:C8	2.54	0.40
3:2:1112:A:OP1	9:Q:140:ARG:HD3	2.21	0.40
3:2:1115:G:C6	3:2:1116:G:C6	3.09	0.40
3:2:1249:U:C4	3:2:1319:U:C4	3.08	0.40
3:2:1265:G:C8	3:2:1266:U:H2'	2.55	0.40
3:2:1594:G:O6	3:2:1614:U:N3	2.54	0.40
3:2:1881:U:H2'	3:2:1882:C:H6	1.86	0.40
3:2:2990:G:C6	3:2:3002:G:C6	3.09	0.40
3:2:3003:G:H2'	3:2:3004:U:H6	1.85	0.40
3:2:3185:C:H2'	3:2:3186:U:O4'	2.21	0.40
3:2:3247:U:H3'	3:2:3394:C:N3	2.36	0.40
3:2:3342:G:O4'	3:2:3345:G:H1'	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:O:36:ASP:HB3	7:O:39:LYS:HG3	2.02	0.40
14:V:71:CYS:SG	14:V:154:ARG:HD3	2.61	0.40
24:f:91:VAL:CG1	24:f:95:HIS:HB2	2.51	0.40
1:O:40:LYS:NZ	1:O:44:ASP:OD1	2.45	0.40
3:2:453:U:C2	3:2:454:G:C8	3.09	0.40
3:2:1317:A:H2'	3:2:1317:A:N3	2.36	0.40
3:2:1387:A:H3'	3:2:1391:G:HO2'	1.86	0.40
3:2:1557:U:H3	28:j:74:LYS:NZ	2.20	0.40
3:2:2501:A:H2'	3:2:2502:G:C8	2.56	0.40
5:4:154:U:H2'	5:4:155:U:C6	2.55	0.40
5:4:163:A:H2'	5:4:164:U:C6	2.57	0.40
7:O:295:SER:OG	7:O:301:THR:O	2.34	0.40
13:U:39:LEU:HD23	13:U:39:LEU:HA	1.76	0.40
15:W:13:ARG:HH21	15:W:134:PRO:HA	1.86	0.40
26:h:68:LYS:HE2	26:h:68:LYS:HB3	1.84	0.40
33:o:98:ILE:HD13	33:o:106:ILE:CD1	2.50	0.40
3:2:509:A:H5''	3:2:509:A:H8	1.86	0.40
3:2:609:A:H2'	3:2:610:C:H6	1.83	0.40
3:2:680:C:H2'	3:2:681:A:H8	1.87	0.40
3:2:1547:G:OP1	22:d:5:ARG:NH1	2.54	0.40
3:2:1836:U:H2'	6:N:49:HIS:CD2	2.56	0.40
3:2:2446:A:H3'	3:2:2447:C:H6	1.86	0.40
3:2:2806:C:O2'	3:2:2839:U:OP1	2.33	0.40
3:2:2942:A:H3'	3:2:2943:G:C8	2.57	0.40
3:2:3116:U:C4'	13:U:119:ARG:HH21	2.33	0.40
3:2:3272:U:O4	19:a:6:LYS:HB3	2.21	0.40
3:2:3298:C:O2'	3:2:3299:U:O2	2.21	0.40
7:O:142:GLN:HG2	7:O:143:SER:N	2.29	0.40
8:P:10:ILE:HD12	8:P:20:GLU:HB3	2.03	0.40
9:Q:208:MET:HE1	9:Q:226:LEU:HD13	2.02	0.40
17:Y:66:PRO:HD3	17:Y:77:LYS:HE2	2.03	0.40
28:j:42:LYS:HE3	28:j:42:LYS:HB3	1.75	0.40
30:l:89:LEU:CD2	30:l:93:LYS:HD3	2.51	0.40
38:t:4:LYS:HD2	38:t:4:LYS:HA	1.88	0.40
3:2:184:C:C2	3:2:185:G:N7	2.89	0.40
3:2:570:G:O2'	3:2:571:G:H5''	2.20	0.40
3:2:1531:C:H2'	3:2:1532:A:H8	1.87	0.40
3:2:2280:C:H2'	3:2:2281:U:O4'	2.21	0.40
3:2:2506:G:H1	3:2:3060:U:H1'	1.87	0.40
3:2:2524:U:H5''	12:T:70:LYS:HD3	2.02	0.40
3:2:2701:G:H2'	3:2:2701:G:N3	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:3:13:A:OP1	4:3:109:U:H1'	2.22	0.40
4:3:59:U:H2'	4:3:60:C:C6	2.57	0.40
10:R:134:LYS:HD3	10:R:134:LYS:HA	2.00	0.40
13:U:185:ILE:HD12	13:U:185:ILE:HA	1.92	0.40
26:h:95:LEU:HA	27:i:20:LEU:O	2.22	0.40
33:o:101:ALA:HA	33:o:106:ILE:HD11	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	91/106 (86%)	86 (94%)	5 (6%)	0	100	100
2	1	91/94 (97%)	83 (91%)	8 (9%)	0	100	100
6	N	246/253 (97%)	233 (95%)	12 (5%)	1 (0%)	30	22
7	O	382/388 (98%)	371 (97%)	10 (3%)	1 (0%)	36	30
8	P	360/363 (99%)	347 (96%)	13 (4%)	0	100	100
9	Q	285/294 (97%)	277 (97%)	8 (3%)	0	100	100
10	R	160/195 (82%)	148 (92%)	11 (7%)	1 (1%)	21	11
11	S	231/251 (92%)	228 (99%)	3 (1%)	0	100	100
12	T	227/259 (88%)	213 (94%)	14 (6%)	0	100	100
13	U	162/189 (86%)	153 (94%)	8 (5%)	1 (1%)	21	11
14	V	187/221 (85%)	179 (96%)	8 (4%)	0	100	100
15	W	165/174 (95%)	158 (96%)	7 (4%)	0	100	100
16	X	205/208 (99%)	200 (98%)	5 (2%)	0	100	100
17	Y	128/134 (96%)	126 (98%)	2 (2%)	0	100	100
18	Z	198/201 (98%)	188 (95%)	9 (4%)	1 (0%)	24	15

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	a	194/197 (98%)	191 (98%)	3 (2%)	0	100	100
20	b	150/187 (80%)	145 (97%)	5 (3%)	0	100	100
21	c	184/187 (98%)	174 (95%)	10 (5%)	0	100	100
22	d	155/193 (80%)	152 (98%)	3 (2%)	0	100	100
23	e	171/176 (97%)	164 (96%)	6 (4%)	1 (1%)	21	11
24	f	157/160 (98%)	149 (95%)	8 (5%)	0	100	100
25	g	97/117 (83%)	83 (86%)	14 (14%)	0	100	100
26	h	132/139 (95%)	123 (93%)	9 (7%)	0	100	100
27	i	61/149 (41%)	60 (98%)	1 (2%)	0	100	100
28	j	116/141 (82%)	111 (96%)	5 (4%)	0	100	100
29	k	123/126 (98%)	120 (98%)	3 (2%)	0	100	100
30	l	133/136 (98%)	119 (90%)	14 (10%)	0	100	100
31	m	145/148 (98%)	140 (97%)	4 (3%)	1 (1%)	18	9
32	n	57/61 (93%)	55 (96%)	2 (4%)	0	100	100
33	o	92/109 (84%)	91 (99%)	1 (1%)	0	100	100
34	p	101/113 (89%)	99 (98%)	2 (2%)	0	100	100
35	q	116/127 (91%)	110 (95%)	6 (5%)	0	100	100
36	r	102/108 (94%)	100 (98%)	2 (2%)	0	100	100
37	s	104/111 (94%)	102 (98%)	2 (2%)	0	100	100
38	t	119/122 (98%)	115 (97%)	3 (2%)	1 (1%)	16	7
39	u	93/99 (94%)	90 (97%)	3 (3%)	0	100	100
40	v	80/91 (88%)	77 (96%)	3 (4%)	0	100	100
41	w	67/74 (90%)	65 (97%)	2 (3%)	0	100	100
42	x	48/51 (94%)	43 (90%)	5 (10%)	0	100	100
43	y	132/134 (98%)	121 (92%)	11 (8%)	0	100	100
All	All	6047/6586 (92%)	5789 (96%)	250 (4%)	8 (0%)	49	41

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	N	29	ARG
10	R	144	ALA
13	U	134	ILE

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Mol	Chain	Res	Type
18	Z	183	SER
23	e	159	VAL
7	O	187	SER
38	t	86	LYS
31	m	28	HIS

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	84/93 (90%)	80 (95%)	4 (5%)	23	10
2	1	74/75 (99%)	70 (95%)	4 (5%)	20	7
6	N	188/192 (98%)	188 (100%)	0	100	100
7	O	318/326 (98%)	315 (99%)	3 (1%)	70	67
8	P	293/294 (100%)	285 (97%)	8 (3%)	39	26
9	Q	235/241 (98%)	232 (99%)	3 (1%)	61	54
10	R	132/155 (85%)	129 (98%)	3 (2%)	44	33
11	S	198/213 (93%)	196 (99%)	2 (1%)	68	64
12	T	182/212 (86%)	178 (98%)	4 (2%)	45	35
13	U	149/168 (89%)	142 (95%)	7 (5%)	23	10
14	V	165/187 (88%)	161 (98%)	4 (2%)	43	31
15	W	141/146 (97%)	136 (96%)	5 (4%)	32	18
16	X	166/167 (99%)	165 (99%)	1 (1%)	78	78
17	Y	110/113 (97%)	108 (98%)	2 (2%)	51	43
18	Z	175/176 (99%)	175 (100%)	0	100	100
19	a	159/160 (99%)	158 (99%)	1 (1%)	78	78
20	b	124/149 (83%)	122 (98%)	2 (2%)	55	46
21	c	157/158 (99%)	155 (99%)	2 (1%)	61	54
22	d	136/163 (83%)	136 (100%)	0	100	100
23	e	151/154 (98%)	148 (98%)	3 (2%)	48	39

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
24	f	138/139 (99%)	136 (99%)	2 (1%)	59	52
25	g	86/103 (84%)	86 (100%)	0	100	100
26	h	103/107 (96%)	102 (99%)	1 (1%)	68	64
27	i	57/121 (47%)	53 (93%)	4 (7%)	14	3
28	j	105/122 (86%)	103 (98%)	2 (2%)	50	40
29	k	110/111 (99%)	110 (100%)	0	100	100
30	l	114/115 (99%)	113 (99%)	1 (1%)	70	67
31	m	122/123 (99%)	118 (97%)	4 (3%)	33	20
32	n	50/51 (98%)	50 (100%)	0	100	100
33	o	75/87 (86%)	74 (99%)	1 (1%)	61	54
34	p	94/102 (92%)	94 (100%)	0	100	100
35	q	100/107 (94%)	99 (99%)	1 (1%)	68	64
36	r	91/94 (97%)	90 (99%)	1 (1%)	65	60
37	s	91/96 (95%)	91 (100%)	0	100	100
38	t	106/107 (99%)	104 (98%)	2 (2%)	50	40
39	u	81/84 (96%)	80 (99%)	1 (1%)	63	57
40	v	68/71 (96%)	67 (98%)	1 (2%)	57	49
41	w	63/66 (96%)	63 (100%)	0	100	100
42	x	46/47 (98%)	46 (100%)	0	100	100
43	y	113/113 (100%)	112 (99%)	1 (1%)	70	67
All	All	5150/5508 (94%)	5070 (98%)	80 (2%)	54	46

All (80) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	0	7	THR
1	0	57	VAL
1	0	77	CYS
1	0	83	LEU
2	1	5	THR
2	1	11	THR
2	1	91	MET
2	1	92	VAL
7	O	142	GLN
7	O	147	GLU

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Mol	Chain	Res	Type
7	O	276	THR
8	P	17	VAL
8	P	55	SER
8	P	62	THR
8	P	229	ILE
8	P	262	SER
8	P	291	ARG
8	P	327	LEU
8	P	330	LEU
9	Q	136	GLU
9	Q	152	ARG
9	Q	194	THR
10	R	35	VAL
10	R	118	LYS
10	R	165	LEU
11	S	92	VAL
11	S	131	THR
12	T	68	ARG
12	T	110	VAL
12	T	125	VAL
12	T	203	VAL
13	U	32	ARG
13	U	57	VAL
13	U	58	TRP
13	U	75	ILE
13	U	90	MET
13	U	132	VAL
13	U	167	ASN
14	V	48	LEU
14	V	130	ASN
14	V	144	SER
14	V	165	ILE
15	W	13	ARG
15	W	86	VAL
15	W	155	ASN
15	W	160	ILE
15	W	172	LEU
16	X	156	THR
17	Y	25	LEU
17	Y	34	HIS
19	a	2	SER
20	b	40	SER

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Mol	Chain	Res	Type
20	b	113	ILE
21	c	10	VAL
21	c	138	THR
23	e	44	LEU
23	e	47	ILE
23	e	54	THR
24	f	96	VAL
24	f	102	ARG
26	h	39	VAL
27	i	22	VAL
27	i	39	LEU
27	i	50	SER
27	i	53	VAL
28	j	80	THR
28	j	112	LEU
30	l	54	THR
31	m	15	VAL
31	m	82	VAL
31	m	103	VAL
31	m	120	THR
33	o	106	ILE
35	q	77	SER
36	r	6	HIS
38	t	7	GLU
38	t	84	GLN
39	u	86	GLU
40	v	2	THR
43	y	54	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (72) such sidechains are listed below:

Mol	Chain	Res	Type
1	0	3	ASN
1	0	59	HIS
2	1	45	ASN
6	N	217	HIS
7	O	198	HIS
7	O	293	ASN
8	P	118	ASN
8	P	201	HIS
8	P	245	HIS
8	P	323	ASN

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Mol	Chain	Res	Type
9	Q	235	GLN
10	R	143	ASN
10	R	157	GLN
11	S	27	GLN
11	S	112	GLN
11	S	118	GLN
12	T	182	ASN
12	T	192	GLN
13	U	76	ASN
13	U	100	ASN
13	U	161	GLN
14	V	163	GLN
15	W	95	ASN
15	W	152	HIS
16	X	11	ASN
16	X	174	ASN
17	Y	49	GLN
18	Z	19	ASN
18	Z	95	GLN
19	a	5	GLN
19	a	47	HIS
19	a	189	ASN
20	b	54	HIS
21	c	14	GLN
22	d	34	ASN
22	d	118	HIS
22	d	141	HIS
23	e	48	ASN
23	e	87	HIS
24	f	3	HIS
24	f	90	ASN
24	f	152	HIS
26	h	35	ASN
26	h	134	ASN
27	i	59	HIS
28	j	86	HIS
28	j	136	ASN
29	k	54	GLN
30	l	123	GLN
31	m	14	HIS
31	m	84	ASN
31	m	105	GLN

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Mol	Chain	Res	Type
31	m	139	GLN
32	n	6	ASN
32	n	10	HIS
33	o	74	HIS
34	p	71	ASN
34	p	74	HIS
35	q	86	ASN
36	r	6	HIS
37	s	107	GLN
38	t	15	ASN
38	t	21	GLN
38	t	99	GLN
39	u	30	HIS
40	v	76	ASN
42	x	19	GLN
43	y	15	ASN
43	y	43	GLN
43	y	57	GLN
43	y	74	ASN
43	y	89	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	2	3204/3498 (91%)	660 (20%)	49 (1%)
4	3	118/246 (47%)	18 (15%)	1 (0%)
5	4	156/165 (94%)	26 (16%)	1 (0%)
All	All	3478/3909 (88%)	704 (20%)	51 (1%)

All (704) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
3	2	16	A
3	2	26	A
3	2	40	A
3	2	49	A
3	2	59	G
3	2	60	A
3	2	65	A
3	2	66	A
3	2	74	A

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Mol	Chain	Res	Type
3	2	92	G
3	2	99	A
3	2	109	A
3	2	110	G
3	2	116	A
3	2	121	A
3	2	122	A
3	2	137	C
3	2	138	U
3	2	161	C
3	2	162	A
3	2	163	A
3	2	168	C
3	2	170	G
3	2	172	U
3	2	174	U
3	2	175	G
3	2	176	A
3	2	178	U
3	2	184	C
3	2	185	G
3	2	187	U
3	2	188	C
3	2	189	G
3	2	190	G
3	2	191	U
3	2	192	C
3	2	193	U
3	2	194	A
3	2	197	U
3	2	198	U
3	2	207	C
3	2	217	G
3	2	225	G
3	2	226	A
3	2	240	G
3	2	242	U
3	2	246	U
3	2	247	U
3	2	250	A
3	2	252	A
3	2	253	U

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Mol	Chain	Res	Type
3	2	254	G
3	2	255	C
3	2	259	A
3	2	260	U
3	2	262	A
3	2	263	A
3	2	264	G
3	2	266	G
3	2	269	U
3	2	271	C
3	2	272	G
3	2	274	A
3	2	277	G
3	2	291	G
3	2	292	A
3	2	303	A
3	2	313	U
3	2	331	A
3	2	337	U
3	2	346	A
3	2	359	A
3	2	360	A
3	2	383	A
3	2	384	G
3	2	399	A
3	2	406	U
3	2	407	A
3	2	410	A
3	2	411	C
3	2	429	G
3	2	430	A
3	2	437	G
3	2	445	G
3	2	446	U
3	2	447	C
3	2	449	U
3	2	450	A
3	2	461	A
3	2	462	U
3	2	463	C
3	2	466	U
3	2	477	C

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Mol	Chain	Res	Type
3	2	488	A
3	2	492	U
3	2	495	A
3	2	500	U
3	2	501	G
3	2	504	A
3	2	505	G
3	2	509	A
3	2	531	A
3	2	532	A
3	2	540	A
3	2	541	G
3	2	545	A
3	2	546	G
3	2	547	G
3	2	548	U
3	2	549	G
3	2	552	U
3	2	553	U
3	2	554	U
3	2	571	G
3	2	572	A
3	2	573	G
3	2	575	G
3	2	578	U
3	2	579	A
3	2	580	U
3	2	581	A
3	2	587	U
3	2	590	U
3	2	591	G
3	2	602	A
3	2	603	C
3	2	612	G
3	2	613	A
3	2	621	G
3	2	625	U
3	2	627	G
3	2	628	U
3	2	629	G
3	2	634	G
3	2	636	A

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Mol	Chain	Res	Type
3	2	637	U
3	2	645	U
3	2	646	A
3	2	674	A
3	2	685	A
3	2	702	A
3	2	706	U
3	2	708	U
3	2	711	G
3	2	713	G
3	2	714	A
3	2	715	U
3	2	716	G
3	2	717	A
3	2	720	A
3	2	732	A
3	2	742	A
3	2	743	A
3	2	759	C
3	2	760	C
3	2	761	U
3	2	762	U
3	2	763	G
3	2	764	U
3	2	765	G
3	2	766	G
3	2	770	G
3	2	786	C
3	2	788	G
3	2	789	A
3	2	802	G
3	2	806	G
3	2	809	U
3	2	813	G
3	2	817	G
3	2	838	A
3	2	849	A
3	2	862	A
3	2	889	G
3	2	893	C
3	2	906	U
3	2	911	U

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Mol	Chain	Res	Type
3	2	928	A
3	2	929	U
3	2	939	G
3	2	940	G
3	2	946	A
3	2	948	G
3	2	949	A
3	2	953	A
3	2	955	C
3	2	957	A
3	2	969	G
3	2	976	C
3	2	991	C
3	2	992	U
3	2	993	C
3	2	1009	C
3	2	1010	A
3	2	1011	G
3	2	1012	A
3	2	1014	C
3	2	1026	G
3	2	1032	C
3	2	1033	G
3	2	1034	A
3	2	1047	C
3	2	1049	U
3	2	1050	G
3	2	1051	G
3	2	1052	G
3	2	1056	G
3	2	1057	G
3	2	1058	A
3	2	1059	A
3	2	1060	U
3	2	1061	U
3	2	1063	C
3	2	1064	C
3	2	1065	U
3	2	1067	A
3	2	1079	A
3	2	1081	C
3	2	1095	G

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Mol	Chain	Res	Type
3	2	1096	A
3	2	1098	G
3	2	1101	C
3	2	1104	G
3	2	1113	U
3	2	1119	G
3	2	1123	G
3	2	1126	A
3	2	1127	U
3	2	1128	C
3	2	1129	G
3	2	1130	A
3	2	1134	A
3	2	1135	G
3	2	1139	U
3	2	1148	G
3	2	1155	U
3	2	1162	G
3	2	1175	U
3	2	1176	G
3	2	1184	A
3	2	1186	C
3	2	1190	A
3	2	1191	C
3	2	1211	A
3	2	1212	U
3	2	1227	C
3	2	1232	G
3	2	1233	A
3	2	1236	A
3	2	1239	U
3	2	1240	G
3	2	1245	U
3	2	1251	U
3	2	1252	A
3	2	1254	A
3	2	1260	G
3	2	1263	C
3	2	1266	U
3	2	1267	G
3	2	1269	C
3	2	1270	C

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Mol	Chain	Res	Type
3	2	1272	U
3	2	1273	G
3	2	1276	A
3	2	1277	G
3	2	1279	C
3	2	1283	A
3	2	1289	U
3	2	1293	G
3	2	1294	A
3	2	1295	G
3	2	1296	U
3	2	1297	G
3	2	1300	U
3	2	1301	A
3	2	1303	C
3	2	1304	A
3	2	1305	A
3	2	1310	C
3	2	1313	G
3	2	1314	C
3	2	1316	G
3	2	1317	A
3	2	1318	A
3	2	1319	U
3	2	1323	C
3	2	1333	A
3	2	1334	A
3	2	1338	G
3	2	1340	U
3	2	1344	G
3	2	1361	A
3	2	1379	U
3	2	1380	A
3	2	1381	G
3	2	1388	G
3	2	1389	A
3	2	1420	U
3	2	1433	U
3	2	1453	A
3	2	1468	G
3	2	1471	C
3	2	1484	G

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Mol	Chain	Res	Type
3	2	1503	C
3	2	1515	A
3	2	1542	C
3	2	1561	C
3	2	1562	G
3	2	1570	G
3	2	1573	A
3	2	1588	A
3	2	1589	U
3	2	1590	G
3	2	1593	A
3	2	1594	G
3	2	1595	U
3	2	1596	U
3	2	1599	A
3	2	1600	C
3	2	1601	G
3	2	1604	U
3	2	1606	U
3	2	1607	U
3	2	1608	C
3	2	1609	G
3	2	1612	C
3	2	1613	C
3	2	1614	U
3	2	1615	C
3	2	1616	C
3	2	1622	A
3	2	1624	A
3	2	1628	A
3	2	1640	A
3	2	1641	U
3	2	1656	G
3	2	1663	C
3	2	1664	A
3	2	1665	A
3	2	1666	C
3	2	1674	C
3	2	1677	A
3	2	1678	A
3	2	1679	A
3	2	1680	U

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Mol	Chain	Res	Type
3	2	1681	G
3	2	1692	C
3	2	1693	G
3	2	1740	U
3	2	1742	G
3	2	1744	A
3	2	1745	C
3	2	1755	A
3	2	1764	U
3	2	1790	A
3	2	1791	G
3	2	1800	G
3	2	1801	C
3	2	1803	U
3	2	1806	U
3	2	1811	A
3	2	1821	G
3	2	1837	G
3	2	1838	A
3	2	1850	A
3	2	1853	A
3	2	1854	A
3	2	1855	U
3	2	1856	G
3	2	1857	G
3	2	1871	U
3	2	1876	U
3	2	1894	A
3	2	1897	A
3	2	1904	C
3	2	1933	G
3	2	1934	A
3	2	1935	U
3	2	1948	A
3	2	1961	G
3	2	2007	G
3	2	2182	C
3	2	2183	A
3	2	2188	A
3	2	2189	C
3	2	2190	U
3	2	2200	U

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Mol	Chain	Res	Type
3	2	2201	A
3	2	2209	G
3	2	2210	G
3	2	2219	A
3	2	2228	U
3	2	2246	A
3	2	2257	G
3	2	2294	G
3	2	2295	A
3	2	2296	A
3	2	2297	U
3	2	2298	G
3	2	2310	A
3	2	2311	A
3	2	2317	A
3	2	2332	A
3	2	2337	G
3	2	2339	G
3	2	2340	A
3	2	2342	U
3	2	2344	A
3	2	2345	C
3	2	2348	U
3	2	2349	G
3	2	2351	C
3	2	2353	C
3	2	2356	U
3	2	2358	A
3	2	2360	G
3	2	2361	G
3	2	2367	A
3	2	2369	A
3	2	2376	G
3	2	2392	C
3	2	2395	G
3	2	2396	C
3	2	2398	U
3	2	2401	A
3	2	2403	G
3	2	2423	G
3	2	2424	U
3	2	2461	A

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Mol	Chain	Res	Type
3	2	2462	C
3	2	2463	G
3	2	2481	G
3	2	2485	A
3	2	2489	A
3	2	2490	A
3	2	2491	G
3	2	2492	A
3	2	2499	U
3	2	2523	G
3	2	2527	A
3	2	2529	A
3	2	2530	G
3	2	2601	U
3	2	2602	U
3	2	2603	C
3	2	2606	U
3	2	2607	A
3	2	2610	U
3	2	2611	A
3	2	2619	A
3	2	2620	A
3	2	2622	C
3	2	2627	U
3	2	2628	U
3	2	2629	G
3	2	2630	G
3	2	2631	G
3	2	2632	A
3	2	2633	U
3	2	2634	U
3	2	2635	U
3	2	2636	A
3	2	2638	U
3	2	2641	C
3	2	2642	C
3	2	2643	A
3	2	2644	U
3	2	2645	A
3	2	2646	U
3	2	2648	C
3	2	2649	U

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Mol	Chain	Res	Type
3	2	2656	A
3	2	2657	A
3	2	2660	U
3	2	2661	U
3	2	2662	U
3	2	2664	U
3	2	2665	U
3	2	2666	C
3	2	2667	G
3	2	2668	C
3	2	2680	C
3	2	2688	A
3	2	2701	G
3	2	2702	G
3	2	2709	G
3	2	2721	A
3	2	2743	G
3	2	2747	U
3	2	2751	A
3	2	2752	A
3	2	2769	A
3	2	2770	C
3	2	2772	G
3	2	2773	A
3	2	2774	A
3	2	2775	A
3	2	2784	A
3	2	2785	G
3	2	2789	A
3	2	2798	A
3	2	2799	A
3	2	2809	G
3	2	2823	G
3	2	2824	U
3	2	2848	G
3	2	2850	C
3	2	2868	C
3	2	2872	G
3	2	2873	A
3	2	2889	G
3	2	2891	G
3	2	2894	A

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Mol	Chain	Res	Type
3	2	2895	G
3	2	2896	A
3	2	2897	A
3	2	2898	A
3	2	2909	G
3	2	2912	A
3	2	2913	U
3	2	2914	A
3	2	2918	G
3	2	2923	G
3	2	2934	G
3	2	2937	U
3	2	2938	U
3	2	2940	A
3	2	2942	A
3	2	2955	U
3	2	2957	U
3	2	2966	G
3	2	2967	A
3	2	2968	U
3	2	2970	U
3	2	2982	A
3	2	2992	A
3	2	2993	G
3	2	2994	C
3	2	2997	A
3	2	3001	C
3	2	3002	G
3	2	3003	G
3	2	3018	U
3	2	3030	U
3	2	3031	A
3	2	3037	C
3	2	3042	G
3	2	3050	U
3	2	3051	A
3	2	3066	A
3	2	3067	G
3	2	3078	C
3	2	3085	G
3	2	3091	G
3	2	3093	G

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Mol	Chain	Res	Type
3	2	3108	A
3	2	3116	U
3	2	3117	A
3	2	3126	G
3	2	3152	U
3	2	3153	U
3	2	3155	G
3	2	3174	A
3	2	3176	G
3	2	3182	G
3	2	3189	C
3	2	3195	C
3	2	3197	G
3	2	3212	G
3	2	3216	C
3	2	3218	A
3	2	3226	A
3	2	3227	U
3	2	3238	A
3	2	3239	A
3	2	3248	U
3	2	3249	U
3	2	3250	U
3	2	3251	U
3	2	3252	U
3	2	3260	A
3	2	3261	U
3	2	3266	U
3	2	3268	U
3	2	3269	A
3	2	3276	A
3	2	3283	A
3	2	3284	G
3	2	3285	G
3	2	3287	A
3	2	3288	G
3	2	3289	G
3	2	3290	A
3	2	3291	C
3	2	3292	U
3	2	3293	U
3	2	3295	U

Continued on next page...

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Mol	Chain	Res	Type
3	2	3296	U
3	2	3298	C
3	2	3299	U
3	2	3300	A
3	2	3301	C
3	2	3302	U
3	2	3303	C
3	2	3305	C
3	2	3306	C
3	2	3307	U
3	2	3308	G
3	2	3310	A
3	2	3317	A
3	2	3318	A
3	2	3319	G
3	2	3327	A
3	2	3328	U
3	2	3329	G
3	2	3338	A
3	2	3341	G
3	2	3343	A
3	2	3345	G
3	2	3352	A
3	2	3359	U
3	2	3360	G
3	2	3362	C
3	2	3363	C
3	2	3371	U
3	2	3372	C
3	2	3373	C
3	2	3374	A
3	2	3375	U
3	2	3376	U
3	2	3377	G
3	2	3386	U
3	2	3387	G
3	2	3388	C
3	2	3390	G
3	2	3392	A
3	2	3393	U
3	2	3394	C
3	2	3395	G

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Mol	Chain	Res	Type
3	2	3404	G
3	2	3405	C
3	2	3418	U
3	2	3419	G
3	2	3420	U
3	2	3442	U
3	2	3443	A
3	2	3446	G
3	2	3449	G
3	2	3452	U
3	2	3453	U
3	2	3455	U
3	2	3456	U
3	2	3457	G
3	2	3459	U
3	2	3468	C
3	2	3476	A
3	2	3479	C
3	2	3483	U
3	2	3484	G
3	2	3491	A
4	3	12	U
4	3	13	A
4	3	19	G
4	3	22	A
4	3	35	C
4	3	39	C
4	3	41	G
4	3	46	C
4	3	50	A
4	3	53	U
4	3	54	A
4	3	55	A
4	3	63	A
4	3	64	G
4	3	75	G
4	3	100	A
4	3	110	G
4	3	119	U
5	4	42	U
5	4	43	C
5	4	56	A

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Mol	Chain	Res	Type
5	4	60	A
5	4	67	A
5	4	70	C
5	4	71	G
5	4	83	G
5	4	88	A
5	4	89	U
5	4	90	U
5	4	91	C
5	4	92	C
5	4	93	G
5	4	94	U
5	4	95	G
5	4	103	G
5	4	113	A
5	4	114	C
5	4	119	A
5	4	121	U
5	4	133	U
5	4	134	U
5	4	135	C
5	4	146	A
5	4	165	U

All (51) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	2	137	C
3	2	191	U
3	2	290	G
3	2	382	A
3	2	446	U
3	2	572	A
3	2	589	U
3	2	612	G
3	2	719	A
3	2	762	U
3	2	764	U
3	2	848	A
3	2	905	C
3	2	928	A
3	2	948	G

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Mol	Chain	Res	Type
3	2	992	U
3	2	1059	A
3	2	1094	A
3	2	1103	U
3	2	1133	G
3	2	1190	A
3	2	1244	G
3	2	1272	U
3	2	1380	A
3	2	1608	C
3	2	1640	A
3	2	1665	A
3	2	1854	A
3	2	1897	A
3	2	2200	U
3	2	2369	A
3	2	2823	G
3	2	2867	C
3	2	2896	A
3	2	2913	U
3	2	2993	G
3	2	3001	C
3	2	3152	U
3	2	3217	U
3	2	3249	U
3	2	3260	A
3	2	3267	A
3	2	3292	U
3	2	3298	C
3	2	3328	U
3	2	3373	C
3	2	3404	G
3	2	3418	U
3	2	3456	U
4	3	12	U
5	4	88	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 100 ligands modelled in this entry, 100 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

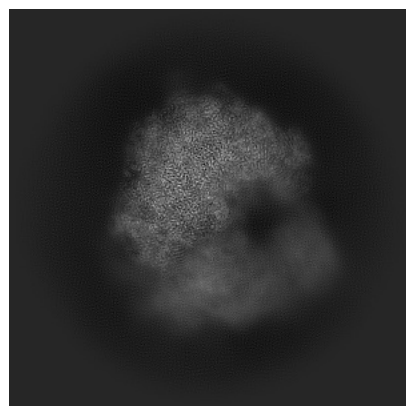
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43973. These allow visual inspection of the internal detail of the map and identification of artifacts.

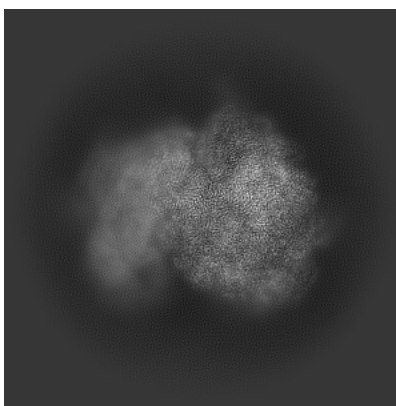
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

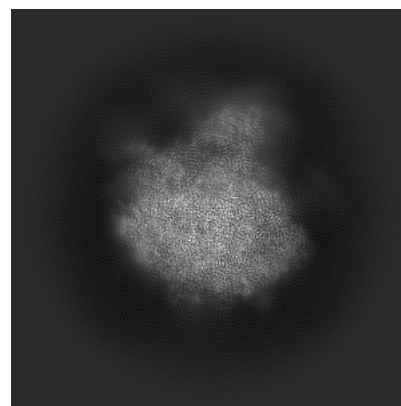
6.1.1 Primary map



X

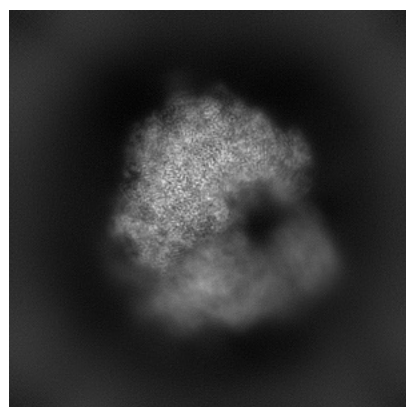


Y

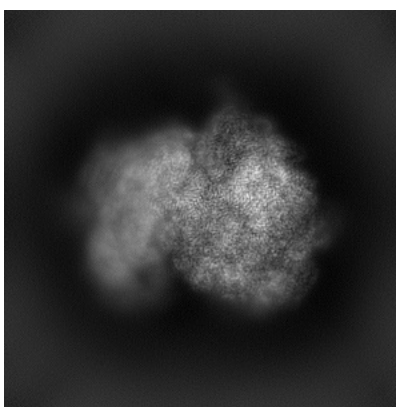


Z

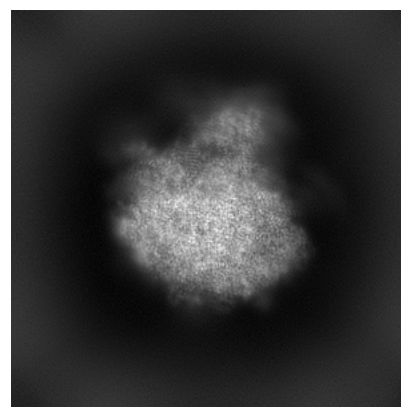
6.1.2 Raw map



X



Y

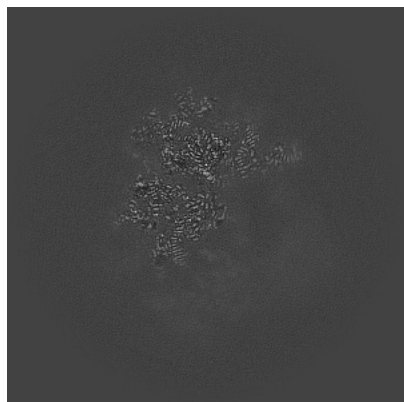


Z

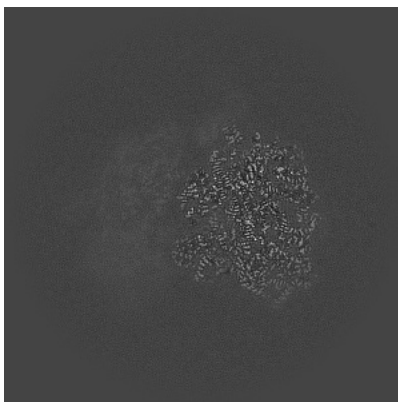
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

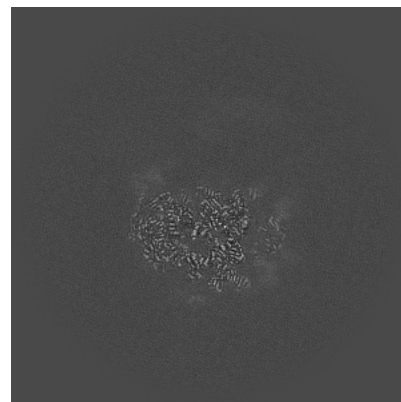
6.2.1 Primary map



X Index: 256

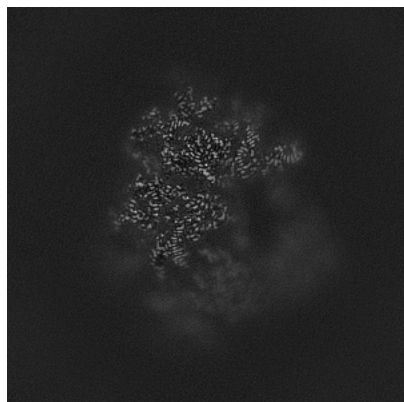


Y Index: 256

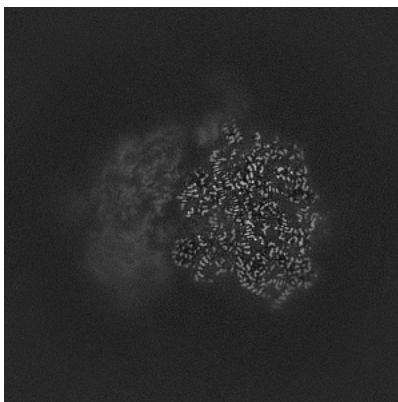


Z Index: 256

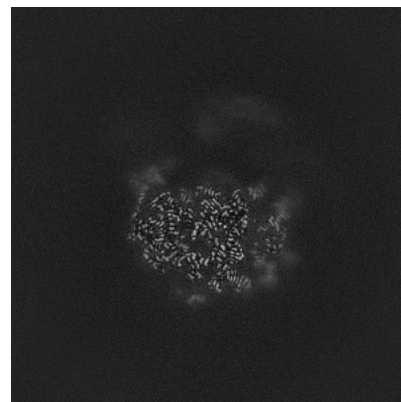
6.2.2 Raw map



X Index: 256



Y Index: 256

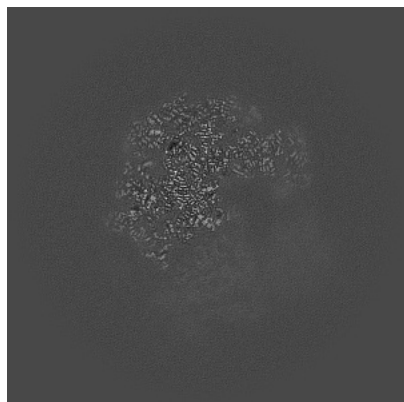


Z Index: 256

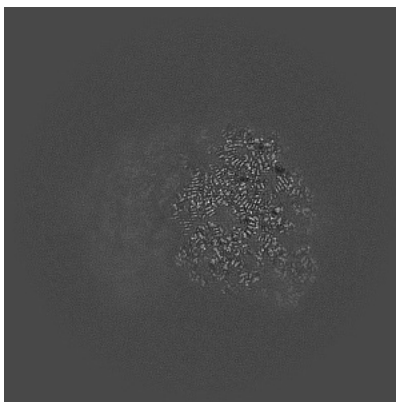
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

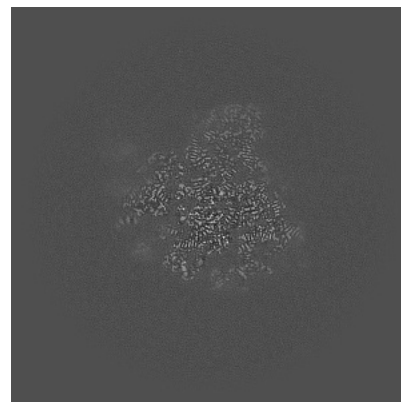
6.3.1 Primary map



X Index: 275

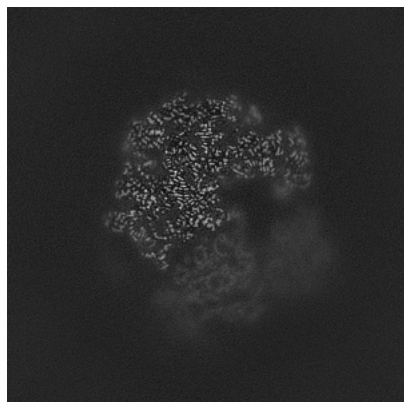


Y Index: 246

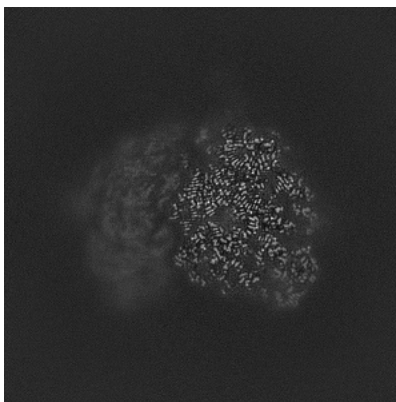


Z Index: 324

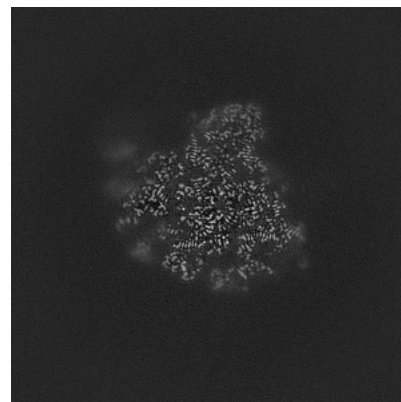
6.3.2 Raw map



X Index: 275



Y Index: 246

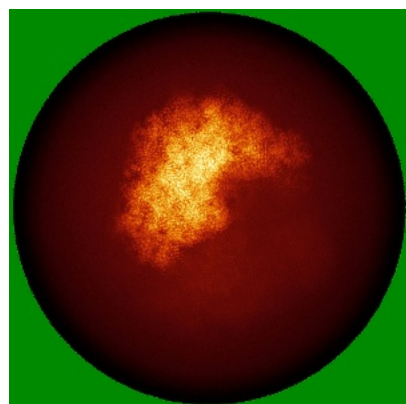


Z Index: 324

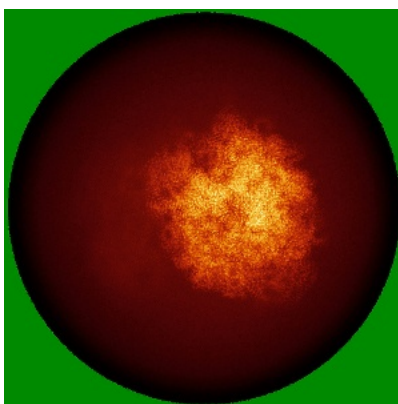
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) ⓘ

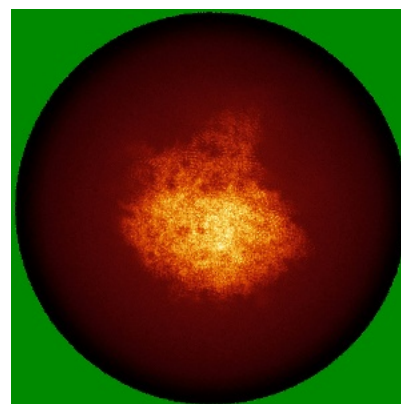
6.4.1 Primary map



X

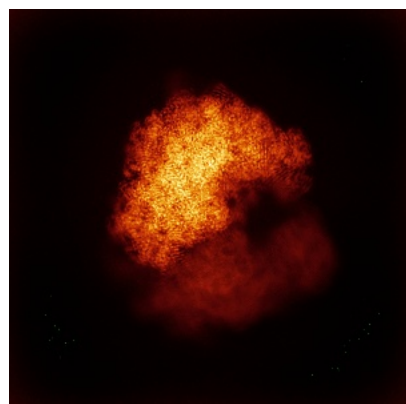


Y

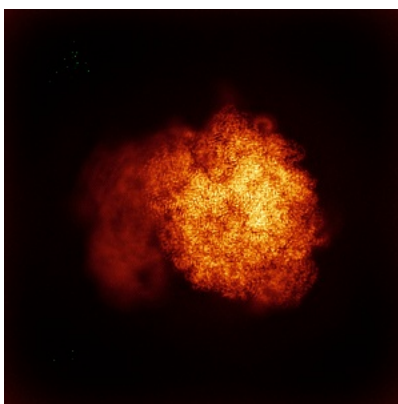


Z

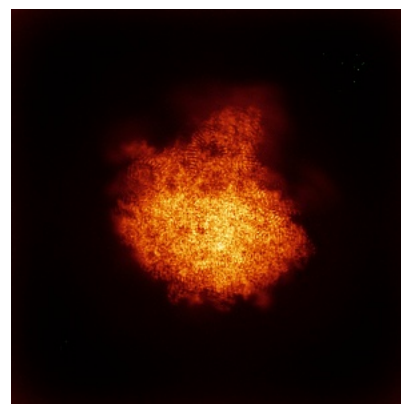
6.4.2 Raw map



X



Y

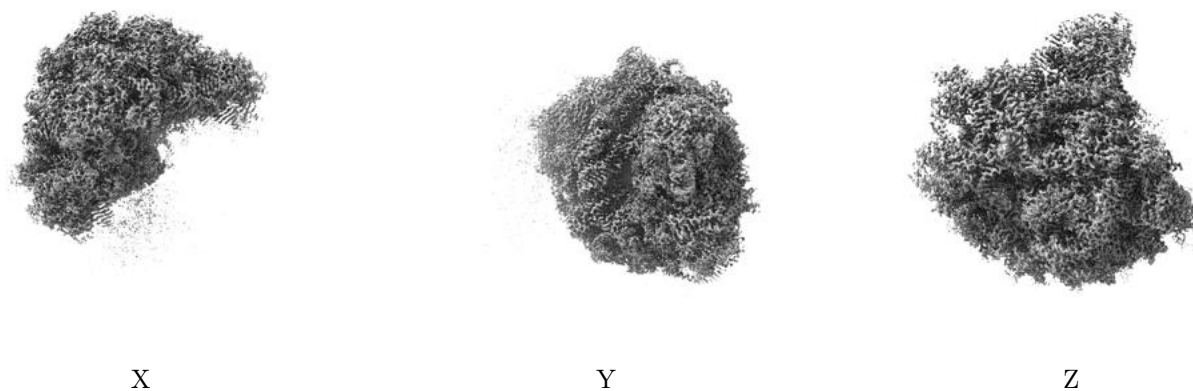


Z

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.

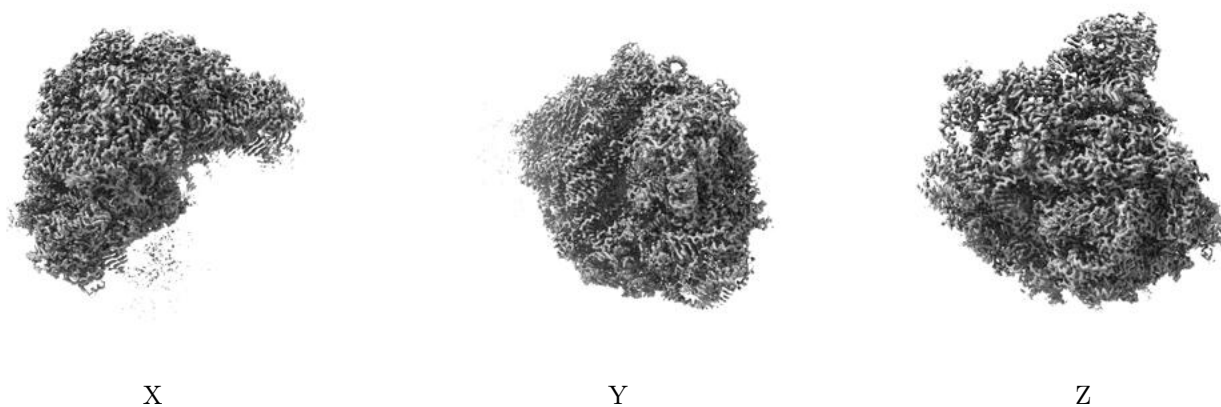
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.38. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

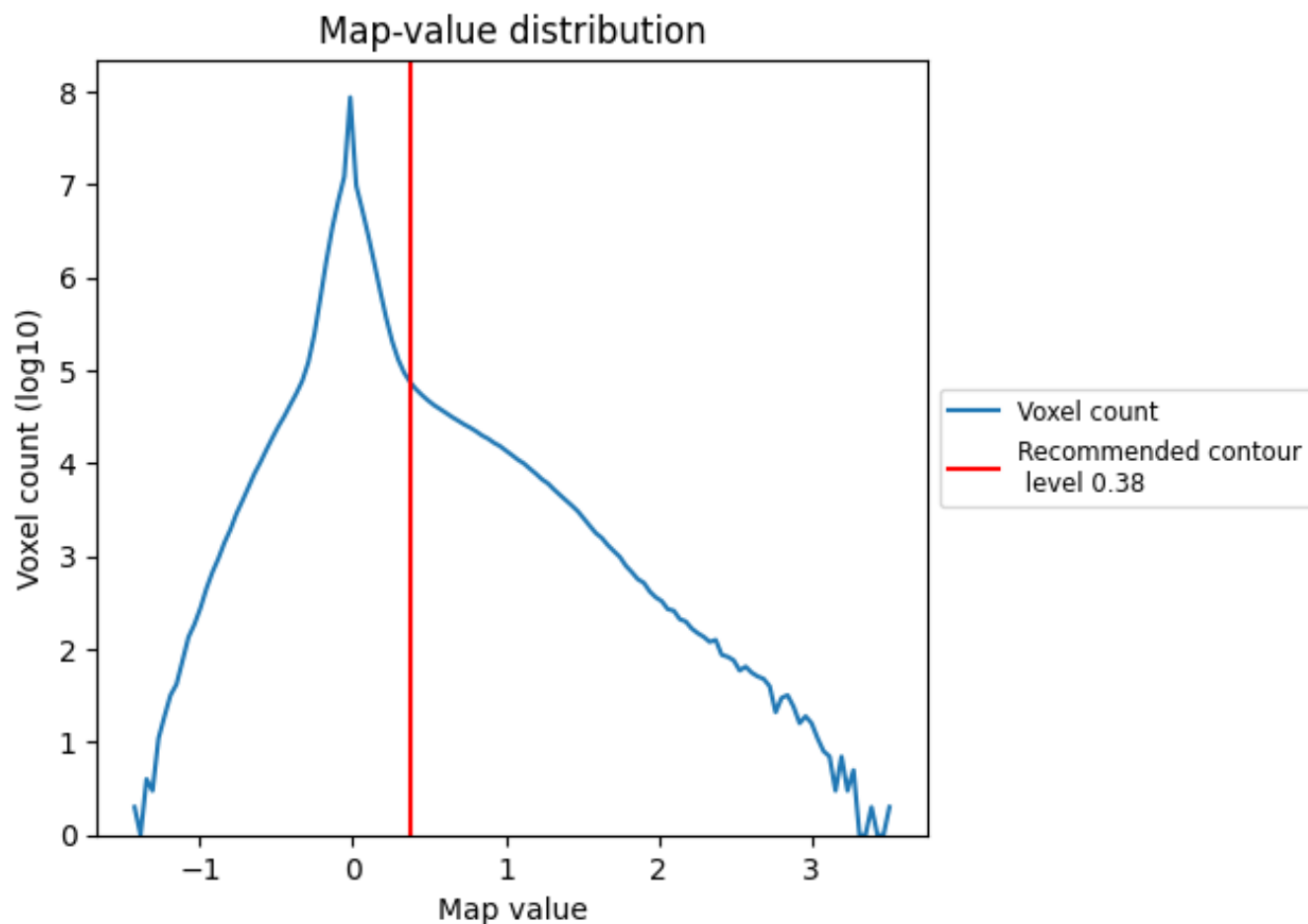
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

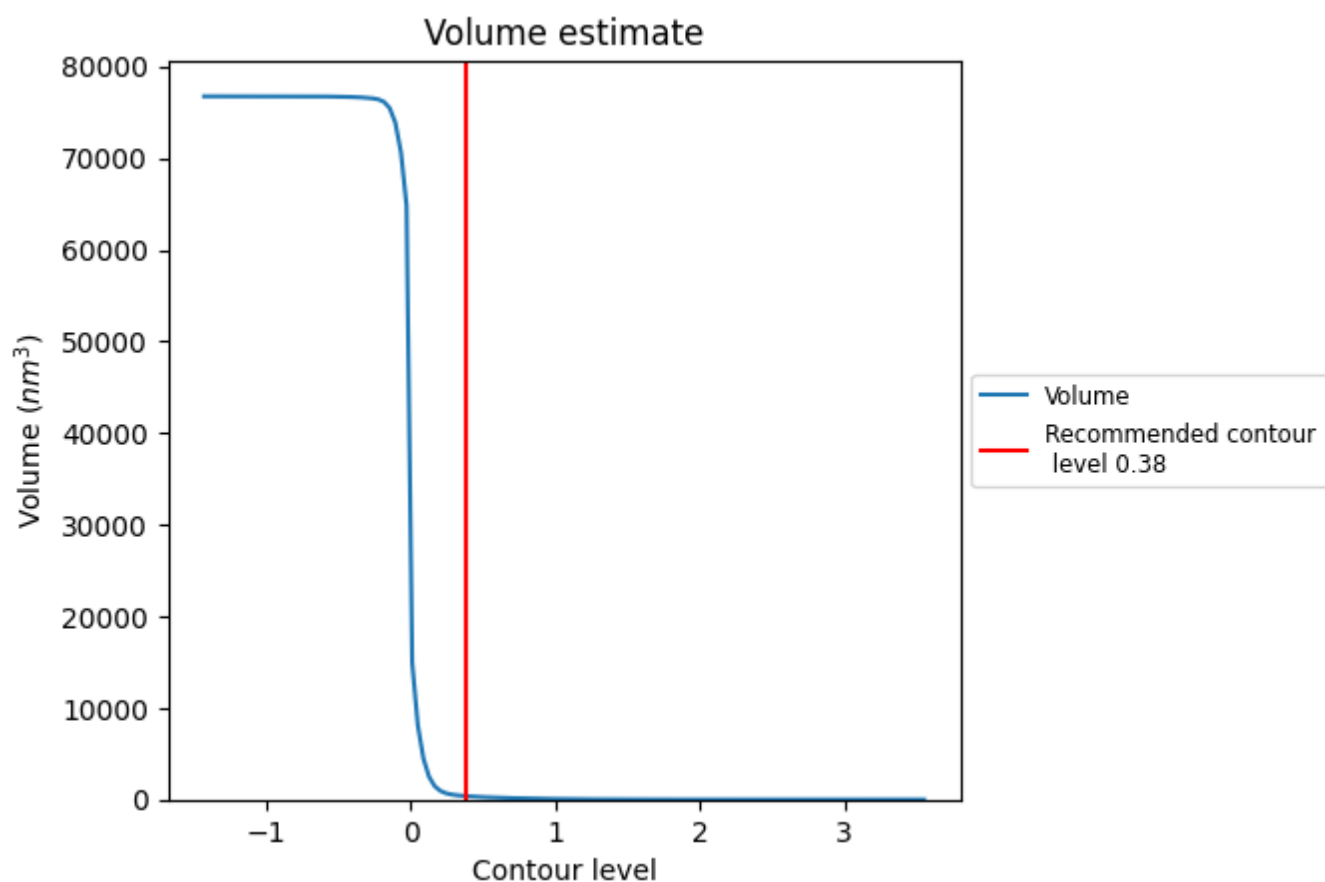
This section contains the results of statistical analysis of the map.

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.

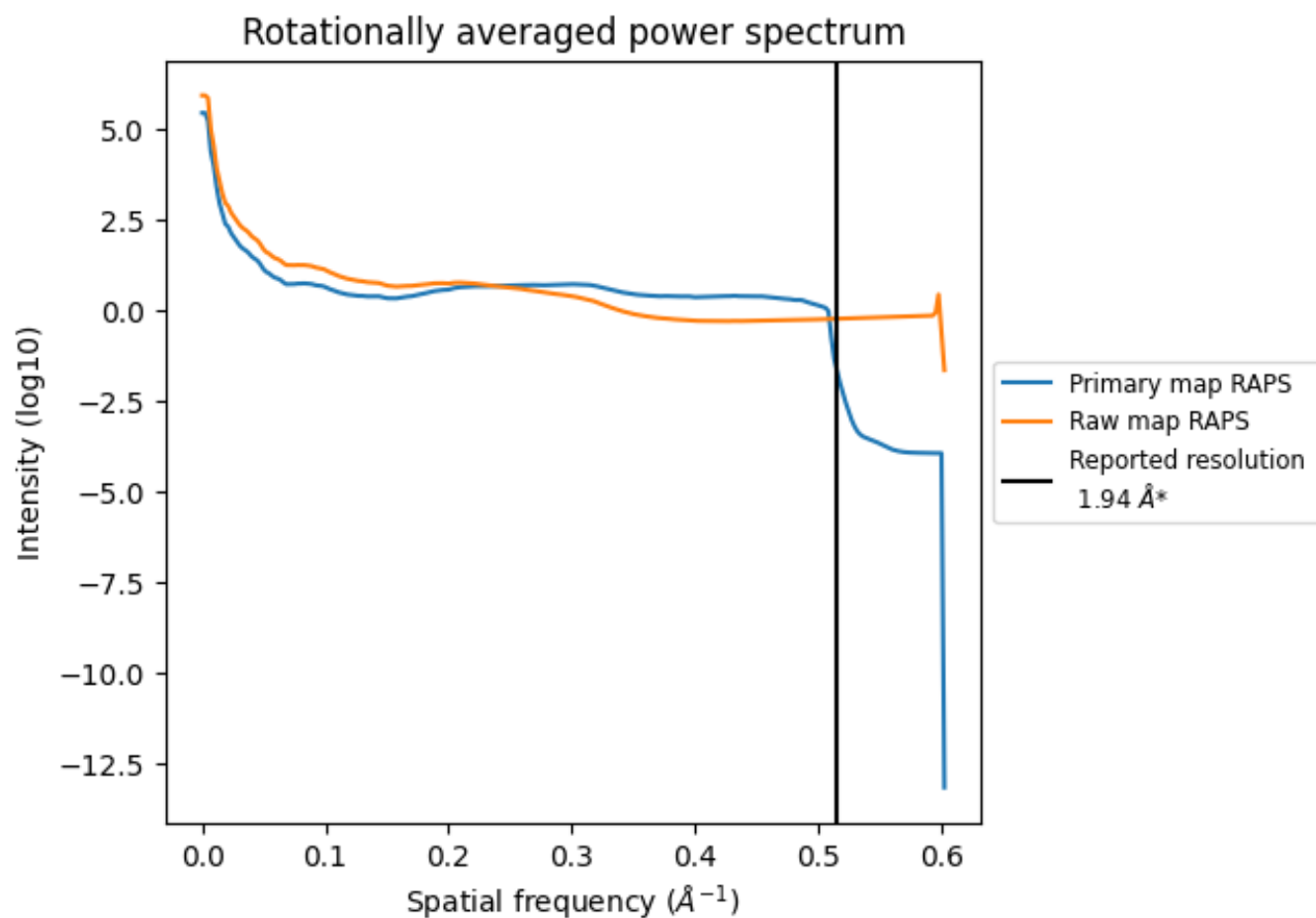
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 381 nm^3 ; this corresponds to an approximate mass of 344 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 ⓘ

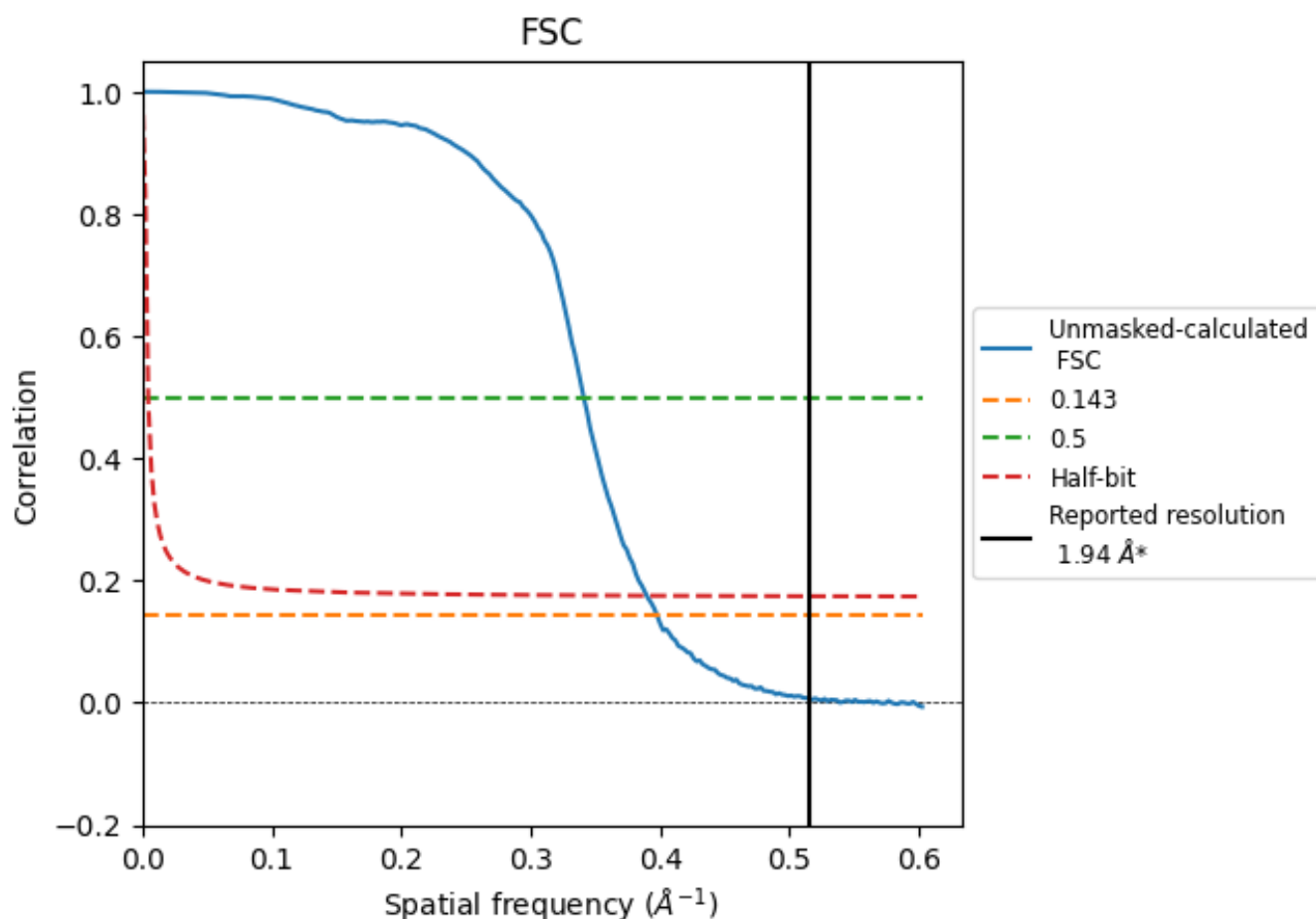


*Reported resolution corresponds to spatial frequency of 0.515 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.515 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

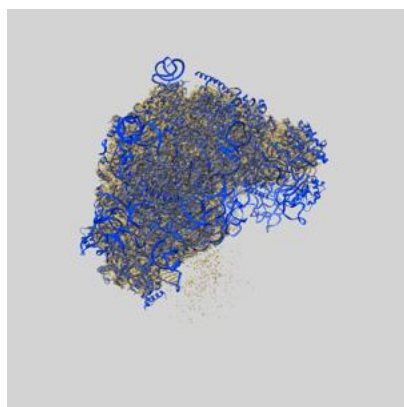
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	1.94	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	2.52	2.93	2.57

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 2.52 differs from the reported value 1.94 by more than 10 %

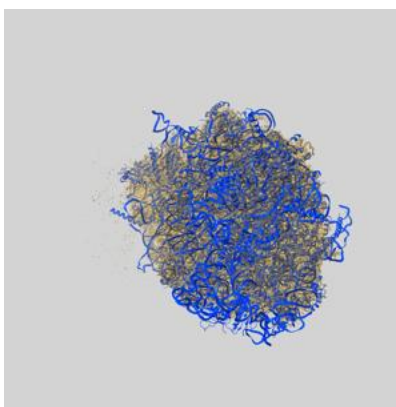
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-43973 and PDB model 9AXU. Per-residue inclusion information can be found in section [3](#) on page [12](#).

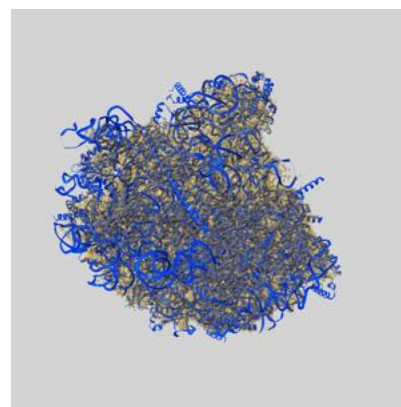
9.1 Map-model overlay [i](#)



X



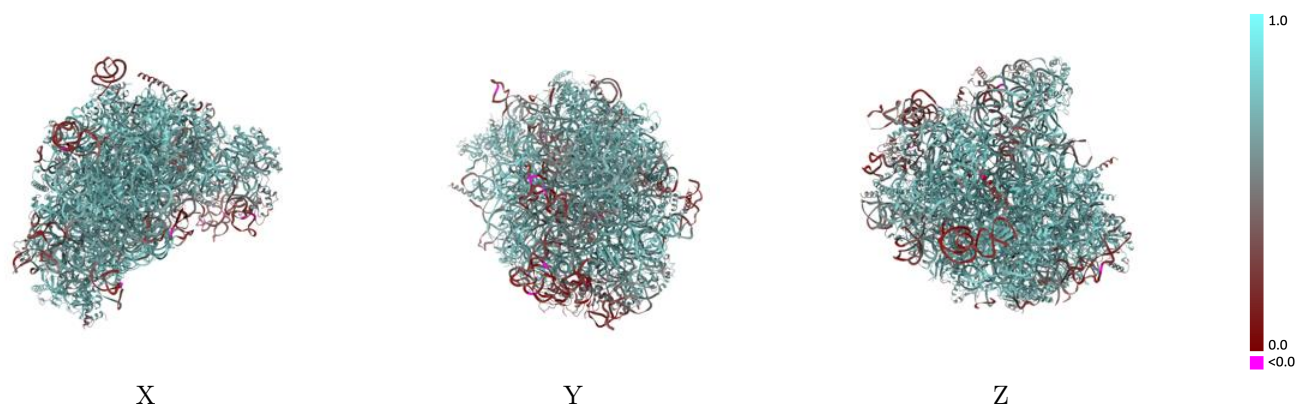
Y



Z

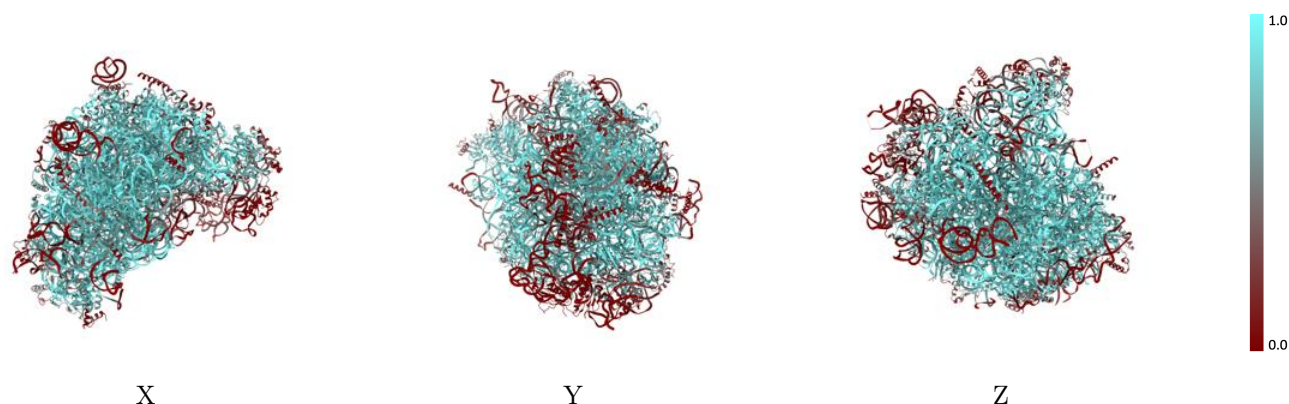
The images above show the 3D surface view of the map at the recommended contour level 0.38 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



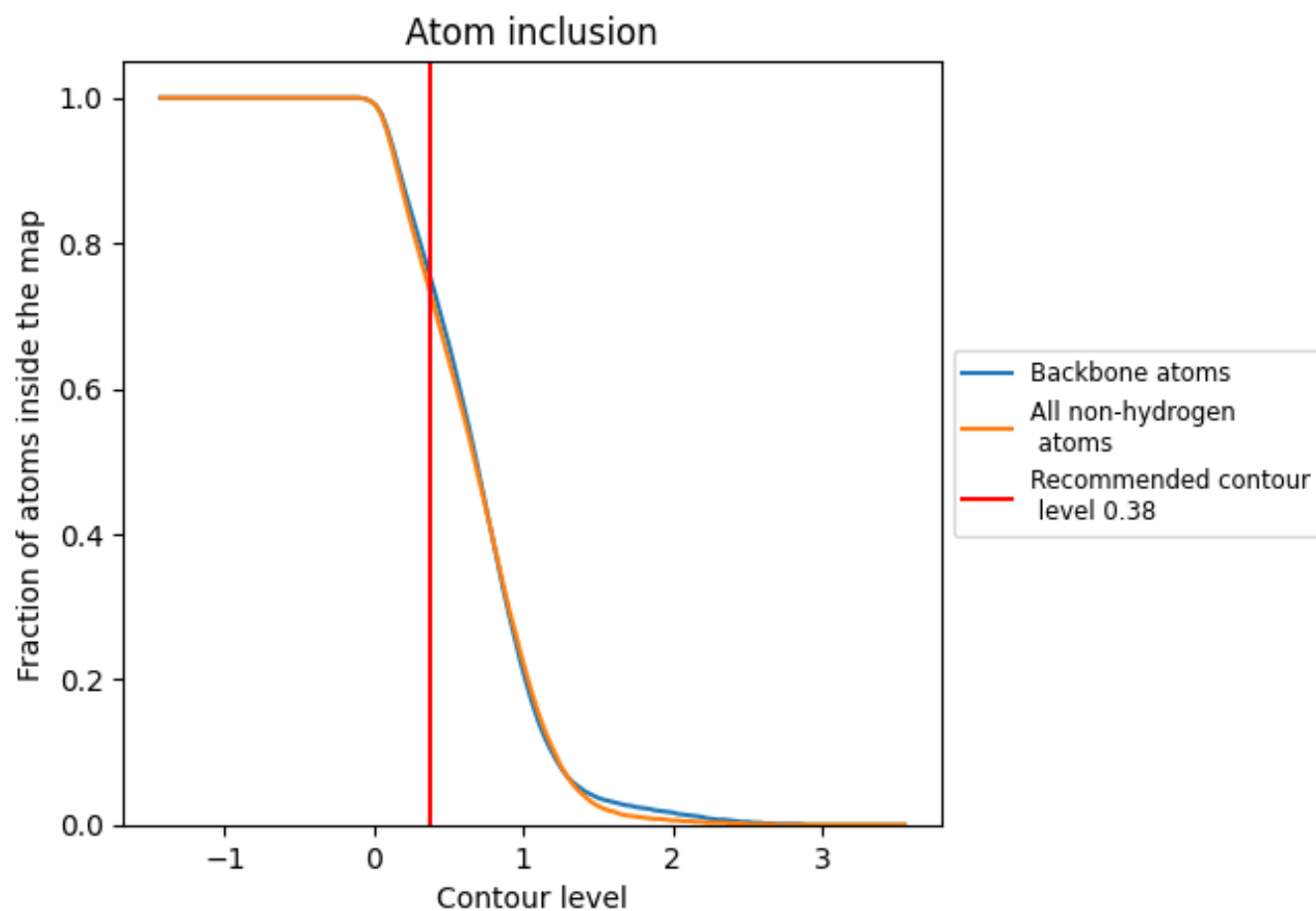
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.38).

9.4 Atom inclusion [i](#)



At the recommended contour level, 75% of all backbone atoms, 73% 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 (0.38) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7290	 0.6610
0	 0.6590	 0.6920
1	 0.7990	 0.7110
2	 0.7360	 0.6390
3	 0.7530	 0.6620
4	 0.8300	 0.6840
N	 0.9360	 0.7670
O	 0.8860	 0.7510
P	 0.8990	 0.7550
Q	 0.5560	 0.6430
R	 0.5680	 0.6300
S	 0.8200	 0.7180
T	 0.6350	 0.6780
U	 0.0030	 0.3280
V	 0.0340	 0.4920
W	 0.0980	 0.4460
X	 0.7390	 0.7060
Y	 0.5390	 0.6550
Z	 0.9830	 0.7810
a	 0.8620	 0.7510
b	 0.8970	 0.7610
c	 0.8850	 0.7540
d	 0.8380	 0.7280
e	 0.7350	 0.6940
f	 0.7040	 0.6870
g	 0.3370	 0.5810
h	 0.8410	 0.7390
i	 0.5790	 0.6840
j	 0.8320	 0.7330
k	 0.7390	 0.7150
l	 0.6230	 0.6720
m	 0.9330	 0.7690
n	 0.7860	 0.7160
o	 0.6120	 0.6610
p	 0.8230	 0.7190



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Chain	Atom inclusion	Q-score
q	 0.8980	 0.7610
r	 0.8770	 0.7450
s	 0.8980	 0.7490
t	 0.7550	 0.7170
u	 0.7950	 0.7210
v	 0.9510	 0.7790
w	 0.3970	 0.5910
x	 0.6240	 0.6430
y	 0.5960	 0.6890