



## Full wwPDB EM Validation Report ⓘ

Dec 3, 2025 – 05:07 PM EST

PDB ID : 9MR4 / pdb\_00009mr4  
EMDB ID : EMD-48552  
Title : NAC: Ribosome nascent chain complex(Oxa1L)  
Authors : Maldosevic, E.; Jomaa, A.  
Deposited on : 2025-01-06  
Resolution : 2.65 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](mailto: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>.

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

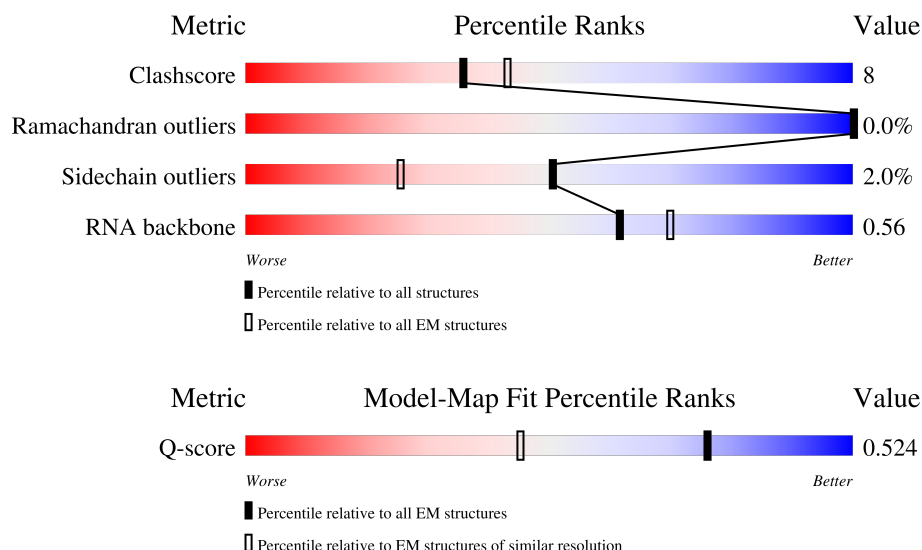
EMDB validation analysis : 0.0.1.dev129  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.46

# 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 2.65 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	210492	15764	-
Ramachandran outliers	207382	16835	-
Sidechain outliers	206894	16415	-
RNA backbone	6643	2191	-
Q-score	-	25397	9050 ( 2.15 - 3.15 )

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  $\geq 3$ , 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	m	128	 6% (red), 33% (green), 6% (yellow), 60% (grey)
2	0	156	 39% (red), 32% (green), 7% (yellow), 61% (grey)
3	4	6	 67% (red), 100% (green)






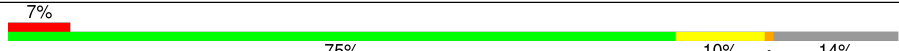
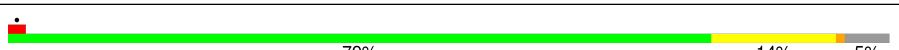

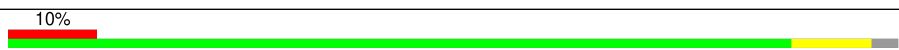

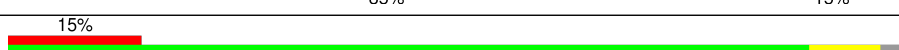


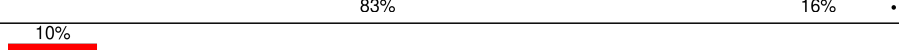
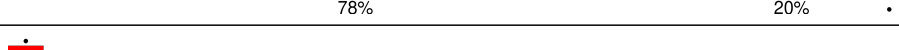
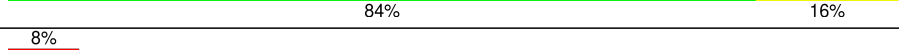





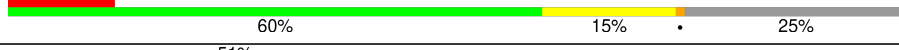



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Mol	Chain	Length	Quality of chain
4	6	317	
5	7	120	
6	9	56	
7	A	257	
8	B	403	
9	C	413	
10	D	297	
11	F	249	
12	G	319	
13	H	192	
14	I	214	
15	J	178	
16	K	4592	
17	L	211	
18	M	218	
19	N	204	
20	O	203	
21	P	183	
22	Q	187	
23	R	196	
24	S	176	
25	T	160	
26	U	128	
27	V	140	
28	W	157	



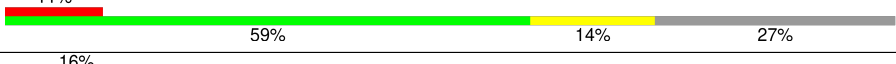


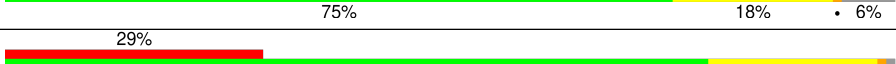
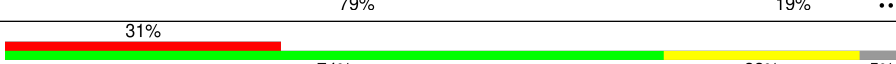
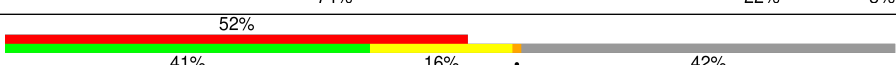
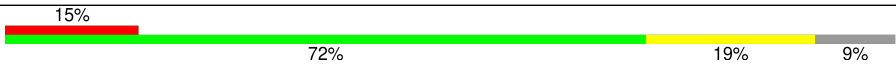
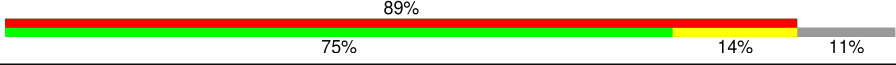

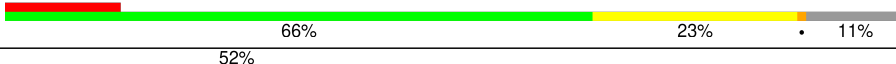


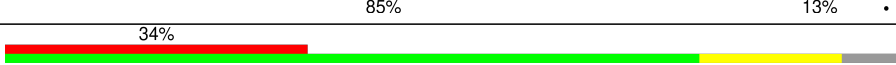






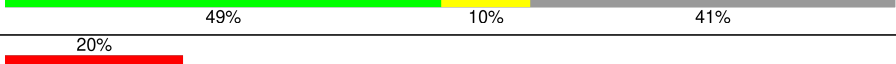



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Mol	Chain	Length	Quality of chain
29	X	156	
30	Y	145	
31	Z	136	
32	a	148	
33	c	115	
34	d	125	
35	e	135	
36	f	110	
37	g	117	
38	h	123	
39	i	105	
40	j	97	
41	k	70	
42	l	51	
43	n	25	
44	o	111	
45	p	92	
46	q	295	
47	r	137	
48	u	264	
49	v	293	
50	w	243	
51	x	263	
52	z	249	
53	2	76	

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Mol	Chain	Length	Quality of chain
54	5	7224	
55	8	156	
56	E	291	
57	b	245	
58	y	204	
59	BB	194	
60	CC	208	
61	DD	194	
62	SS	165	
63	EE	158	
64	RR	132	
65	QQ	151	
66	MM	151	
67	WW	145	
68	UU	146	
69	KK	135	
70	II	152	
71	PP	145	
72	GG	119	
73	HH	83	
74	TT	130	
75	VV	143	
76	NN	133	
77	OO	124	
78	LL	115	

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Mol	Chain	Length	Quality of chain
79	JJ	84	
80	FF	69	
81	AA	133	
82	EF	162	
83	EG	215	
84	EH	33	

## 2 Entry composition [i](#)

There are 86 unique types of molecules in this entry. The entry contains 211175 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 Ubiquitin-ribosomal protein eL40 fusion protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	m	51	Total	C	N	O	S	0	0
			419	260	88	65	6		

- Molecule 2 is a protein called Ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	0	61	Total	C	N	O	S	0	0
			498	314	94	83	7		

- Molecule 3 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	4	6	Total	C	N	O	P	0	0
			128	57	22	43	6		

- Molecule 4 is a protein called RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	6	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 5 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	7	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
7	2	U	N	conflict	GB X06789.1
7	36	C	N	conflict	GB X06789.1
7	102	U	N	conflict	GB X06789.1

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Chain	Residue	Modelled	Actual	Comment	Reference
7	112	U	N	conflict	GB X06789.1
7	114	U	N	conflict	GB X06789.1
7	119	U	C	conflict	GB X06789.1
7	120	U	N	conflict	GB X06789.1

- Molecule 6 is a protein called eS29.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	9	55	Total	C	N	O	S	0	0
			459	286	94	74	5		

- Molecule 7 is a protein called Ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A	248	Total	C	N	O	S	0	0
			1898	1189	389	314	6		

- Molecule 8 is a protein called Ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	B	394	Total	C	N	O	S	0	0
			3172	2020	597	542	13		

- Molecule 9 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	C	362	Total	C	N	O	S	0	0
			2883	1812	577	480	14		

- Molecule 10 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	D	293	Total	C	N	O	S	0	0
			2391	1512	438	427	14		

- Molecule 11 is a protein called uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	F	225	Total	C	N	O	S	0	0
			1875	1205	358	303	9		



- Molecule 12 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	G	233	Total	C	N	O	S	0	0
			1879	1199	361	315	4		

- Molecule 13 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	H	190	Total	C	N	O	S	0	0
			1516	954	284	272	6		

- Molecule 14 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	I	205	Total	C	N	O	S	0	0
			1664	1056	321	274	13		

- Molecule 15 is a protein called Ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	J	170	Total	C	N	O	S	0	0
			1362	861	254	241	6		

- Molecule 16 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	K	1691	Total	C	N	O	P	0	0
			36101	16114	6482	11815	1690		

- Molecule 17 is a protein called Large ribosomal subunit protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	L	210	Total	C	N	O	S	0	0
			1700	1065	352	279	4		

- Molecule 18 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	M	138	Total	C	N	O	S	0	0
			1137	727	221	182	7		

- Molecule 19 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	N	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 20 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	O	199	Total	C	N	O	S	0	0
			1630	1051	319	255	5		

- Molecule 21 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	P	153	Total	C	N	O	S	0	0
			1242	777	241	215	9		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
P	?	-	VAL	deletion	UNP G1SCJ6

- Molecule 22 is a protein called Large ribosomal subunit protein eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Q	187	Total	C	N	O	S	0	0
			1515	946	315	250	4		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Q	4	ASP	ASN	conflict	UNP G1TFE0
Q	14	ARG	TRP	conflict	UNP G1TFE0
Q	53	MET	LEU	conflict	UNP G1TFE0
Q	58	ARG	TRP	conflict	UNP G1TFE0
Q	75	ARG	GLN	conflict	UNP G1TFE0
Q	80	ALA	PRO	conflict	UNP G1TFE0
Q	86	VAL	ILE	conflict	UNP G1TFE0
Q	104	ARG	HIS	conflict	UNP G1TFE0
Q	110	ARG	CYS	conflict	UNP G1TFE0
Q	137	VAL	GLY	conflict	UNP G1TFE0
Q	157	GLY	ARG	conflict	UNP G1TFE0
Q	181	ARG	TRP	conflict	UNP G1TFE0

- Molecule 23 is a protein called Large ribosomal subunit protein eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	R	180	Total	C	N	O	S	0	0
			1507	933	327	238	9		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	38	ARG	HIS	conflict	UNP G1TYL6

- Molecule 24 is a protein called Large ribosomal subunit protein eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	S	176	Total	C	N	O	S	0	0
			1457	924	288	234	11		

- Molecule 25 is a protein called eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	T	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 26 is a protein called Large ribosomal subunit protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	U	105	Total	C	N	O	S	0	0
			874	555	155	162	2		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
U	39	PHE	SER	conflict	UNP G1TSG1

- Molecule 27 is a protein called Ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	V	131	Total	C	N	O	S	0	0
			979	618	184	172	5		

- Molecule 28 is a protein called eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	W	106	Total	C	N	O	S	0	0
			860	538	174	144	4		

- Molecule 29 is a protein called eL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	X	118	Total	C	N	O	S	0	0
			967	618	181	167	1		

- Molecule 30 is a protein called uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Y	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 31 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Z	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 32 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	a	147	Total	C	N	O	S	0	0
			1162	734	239	185	4		

- Molecule 33 is a protein called eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	c	98	Total	C	N	O	S	0	0
			761	481	134	140	6		

- Molecule 34 is a protein called eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	d	107	Total	C	N	O	S	0	0
			888	560	171	155	2		

- Molecule 35 is a protein called Large ribosomal subunit protein eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	e	128	Total	C	N	O	S	0	0
			1058	675	214	164	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
e	108	ARG	CYS	conflict	UNP G1TUN8

- Molecule 36 is a protein called eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	f	109	Total	C	N	O	S	0	0
			876	555	174	143	4		

- Molecule 37 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	g	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

- Molecule 38 is a protein called eL35.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	h	122	Total	C	N	O	S	0	0
			1013	640	204	168	1		

- Molecule 39 is a protein called Large ribosomal subunit protein eL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	i	102	Total	C	N	O	S	0	0
			830	520	176	129	5		

- Molecule 40 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	j	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 41 is a protein called Large ribosomal subunit protein eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	k	69	Total	C	N	O	S	0	0
			568	364	103	100	1		

- Molecule 42 is a protein called eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	l	50	Total	C	N	O	S	0	0
			447	286	96	64	1		

- Molecule 43 is a protein called eL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	n	25	Total	C	N	O	S	0	0
			239	145	64	27	3		

- Molecule 44 is a protein called Large ribosomal subunit protein eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	o	104	Total	C	N	O	S	0	0
			858	541	173	137	7		

- Molecule 45 is a protein called eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	p	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 46 is a protein called uS2 (SA).

Mol	Chain	Residues	Atoms					AltConf	Trace
46	q	217	Total	C	N	O	S	0	0
			1710	1086	300	316	8		

- Molecule 47 is a protein called eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	r	124	Total	C	N	O	S	0	0
			994	616	205	167	6		

- Molecule 48 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	u	213	Total	C	N	O	S	0	0
			1729	1098	309	308	14		

- Molecule 49 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	v	221	Total	C	N	O	S	0	0
			1718	1114	296	299	9		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
v	97	PHE	CYS	conflict	UNP G1SWM1
v	191	VAL	-	insertion	UNP G1SWM1

- Molecule 50 is a protein called Ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	w	226	Total	C	N	O	S	0	0
			1755	1118	316	314	7		

- Molecule 51 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	x	261	Total	C	N	O	S	0	0
			2070	1322	383	356	9		

- Molecule 52 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	z	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 53 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	2	76	Total	C	N	O	P	0	0
			1614	722	287	530	75		

- Molecule 54 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	5	3469	Total	C	N	O	P	0	0
			74394	33129	13626	24170	3469		

- Molecule 55 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	8	151	Total	C	N	O	P	0	0
			3208	1432	564	1062	150		

- Molecule 56 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	E	211	Total	C	N	O	S	0	0
			1697	1095	322	277	3		

- Molecule 57 is a protein called Large ribosomal subunit protein eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	b	104	Total	C	N	O	S	0	0
			848	527	189	129	3		

- Molecule 58 is a protein called Ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	y	184	Total	C	N	O	S	0	0
			1464	917	276	264	7		

- Molecule 59 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	BB	183	Total	C	N	O	S	0	0
			1471	941	268	261	1		

- Molecule 60 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	CC	206	Total	C	N	O	S	0	0
			1686	1058	332	291	5		

There is a discrepancy between the modelled and reference sequences:



Chain	Residue	Modelled	Actual	Comment	Reference
CC	47	ARG	GLY	conflict	UNP G1TJW1

- Molecule 61 is a protein called Ribosomal protein S9 (Predicted).

Mol	Chain	Residues	Atoms					AltConf	Trace
61	DD	185	Total	C	N	O	S	0	0
			1525	969	306	248	2		

- Molecule 62 is a protein called S10\_ plectin domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	SS	95	Total	C	N	O	S	0	0
			802	525	142	130	5		

- Molecule 63 is a protein called Ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	EE	143	Total	C	N	O	S	0	0
			1175	749	222	198	6		

- Molecule 64 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	RR	117	Total	C	N	O	S	0	0
			908	570	161	169	8		

- Molecule 65 is a protein called Ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	QQ	149	Total	C	N	O	S	0	0
			1202	770	228	203	1		

- Molecule 66 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	MM	135	Total	C	N	O	S	0	0
			1004	614	196	188	6		

- Molecule 67 is a protein called uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	WW	122	Total	C	N	O	S	0	0
			1009	643	189	170	7		

- Molecule 68 is a protein called uS9.

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

- Molecule 69 is a protein called eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	KK	132	Total	C	N	O	S	0	0
			1068	670	199	195	4		

- Molecule 70 is a protein called uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	II	142	Total	C	N	O	S	0	0
			1172	736	236	199	1		

- Molecule 71 is a protein called eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	PP	141	Total	C	N	O	S	0	0
			1097	688	211	195	3		

- Molecule 72 is a protein called uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	GG	100	Total	C	N	O	S	0	0
			795	498	152	141	4		

- Molecule 73 is a protein called Small ribosomal subunit protein eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	HH	83	Total	C	N	O	S	0	0
			637	392	117	123	5		

- Molecule 74 is a protein called Ribosomal protein S15a.

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

- Molecule 75 is a protein called uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	VV	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		

- Molecule 76 is a protein called Small ribosomal subunit protein eS24.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	NN	124	Total	C	N	O	S	0	0
			1011	640	198	168	5		

- Molecule 77 is a protein called eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	OO	73	Total	C	N	O	S	0	0
			585	374	108	102	1		

- Molecule 78 is a protein called eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	LL	101	Total	C	N	O	S	0	0
			816	509	170	132	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LL	28	ARG	CYS	conflict	UNP G1TFE8

- Molecule 79 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	JJ	83	Total	C	N	O	S	0	0
			651	408	121	115	7		

- Molecule 80 is a protein called Ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	FF	62	Total	C	N	O	S	0	0
			488	297	97	92	2		

- Molecule 81 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	AA	55	Total	C	N	O	S	0	0
			443	274	97	71	1		

- Molecule 82 is a protein called Transcription factor BTF3.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	EF	110	Total	C	N	O	S	0	0
			854	534	158	158	4		

- Molecule 83 is a protein called Nascent polypeptide-associated complex subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	EG	65	Total	C	N	O	S	0	0
			513	324	93	95	1		

- Molecule 84 is a protein called Nascent Chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	EH	33	Total	C	N	O	S	0	0
			245	161	44	37	3		

- Molecule 85 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
85	m	1	Total	Zn	0
			1	1	
85	g	1	Total	Zn	0
			1	1	
85	j	1	Total	Zn	0
			1	1	
85	o	1	Total	Zn	0
			1	1	
85	p	1	Total	Zn	0
			1	1	
85	LL	1	Total	Zn	0
			1	1	

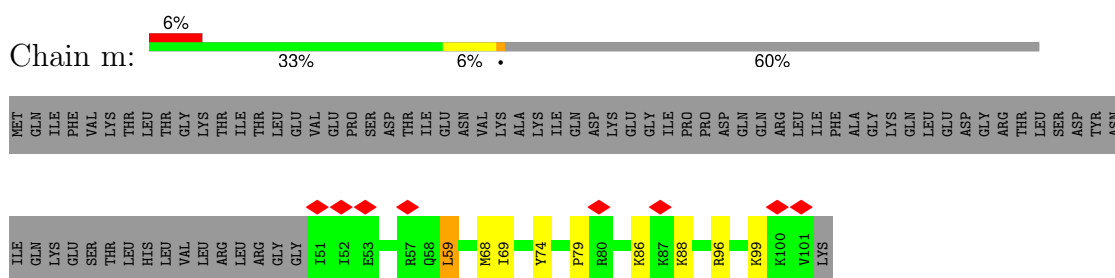
- Molecule 86 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
86	7	6	Total 6	Mg 6	0
86	A	1	Total 1	Mg 1	0
86	B	1	Total 1	Mg 1	0
86	I	1	Total 1	Mg 1	0
86	K	76	Total 76	Mg 76	0
86	P	2	Total 2	Mg 2	0
86	V	1	Total 1	Mg 1	0
86	a	1	Total 1	Mg 1	0
86	g	1	Total 1	Mg 1	0
86	j	2	Total 2	Mg 2	0
86	5	186	Total 186	Mg 186	0
86	8	6	Total 6	Mg 6	0
86	PP	1	Total 1	Mg 1	0

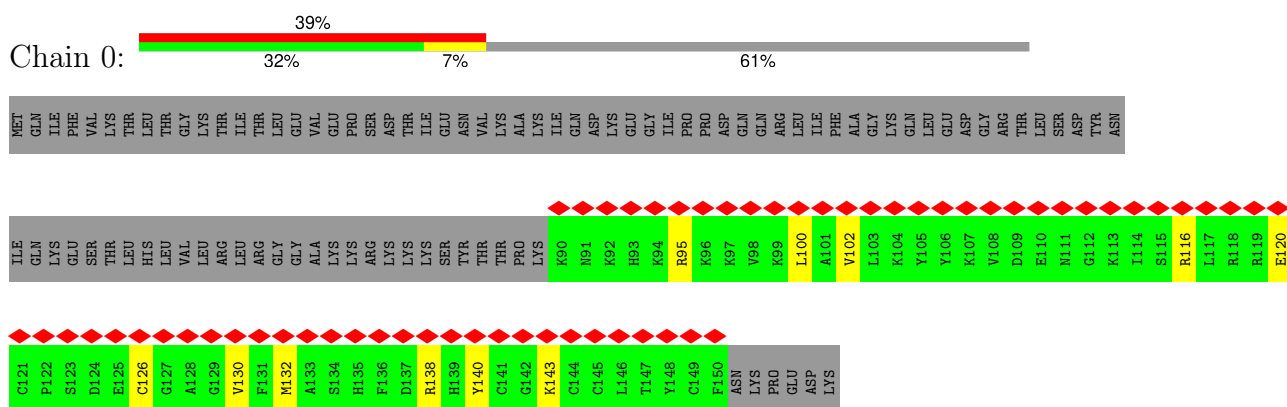
### 3 Residue-property plots

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

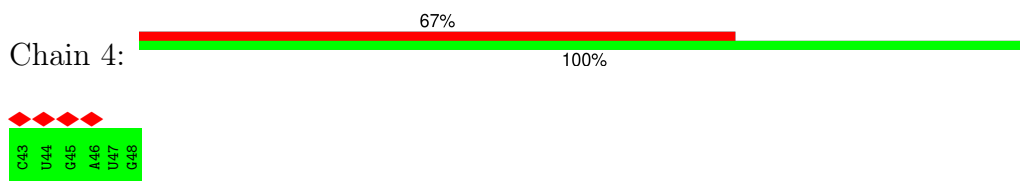
- Molecule 1: Ubiquitin-ribosomal protein eL40 fusion protein



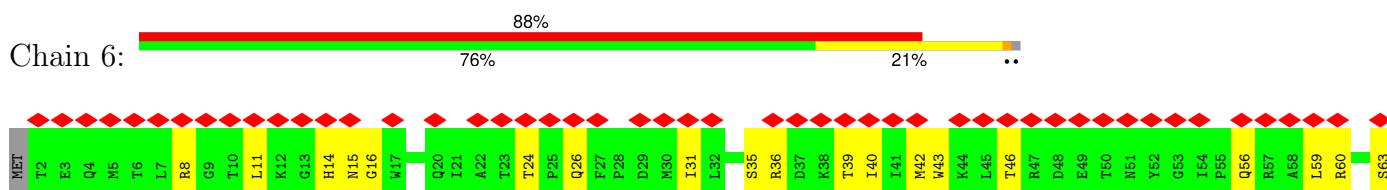
- Molecule 2: Ribosomal protein S27a

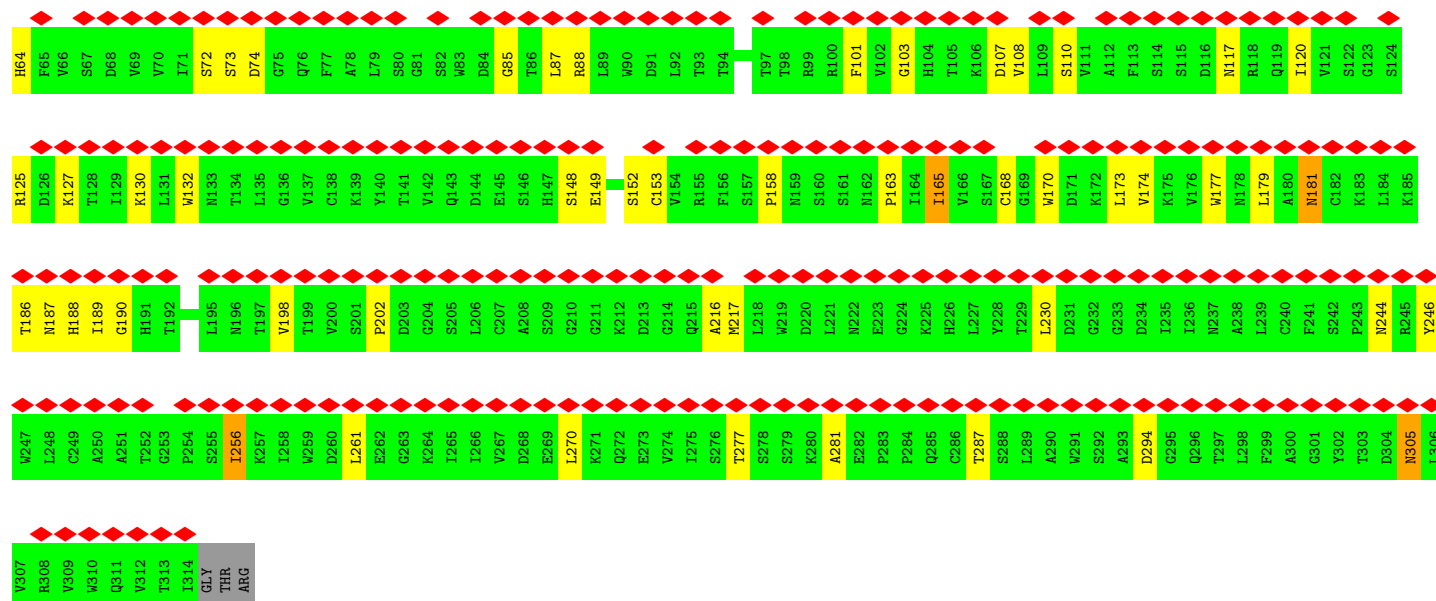


- Molecule 3: mRNA

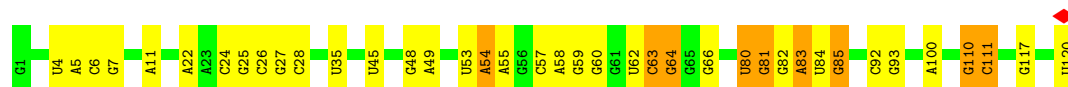


- Molecule 4: RACK1

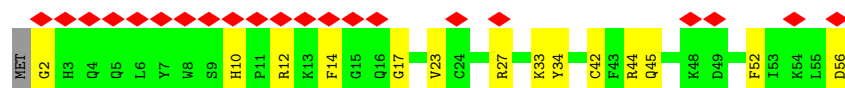




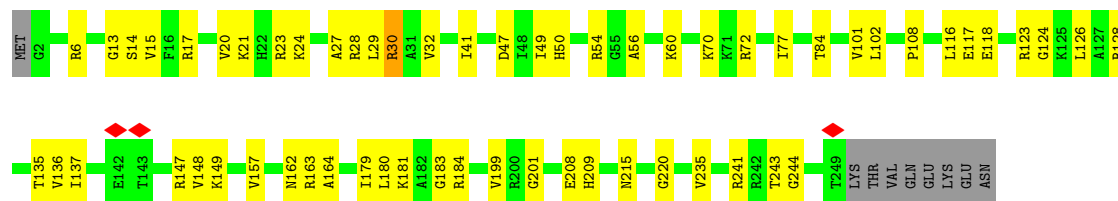
- Molecule 5: 5S rRNA



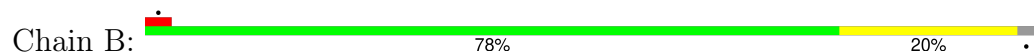
- Molecule 6: eS29

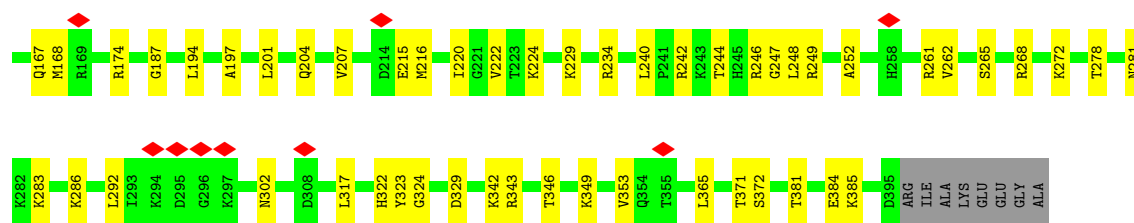


- Molecule 7: Ribosomal protein L8

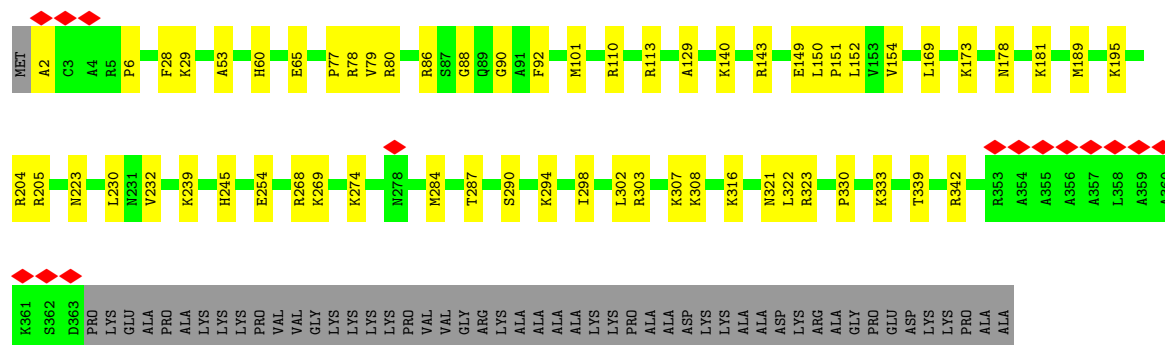


- Molecule 8: Ribosomal protein L3

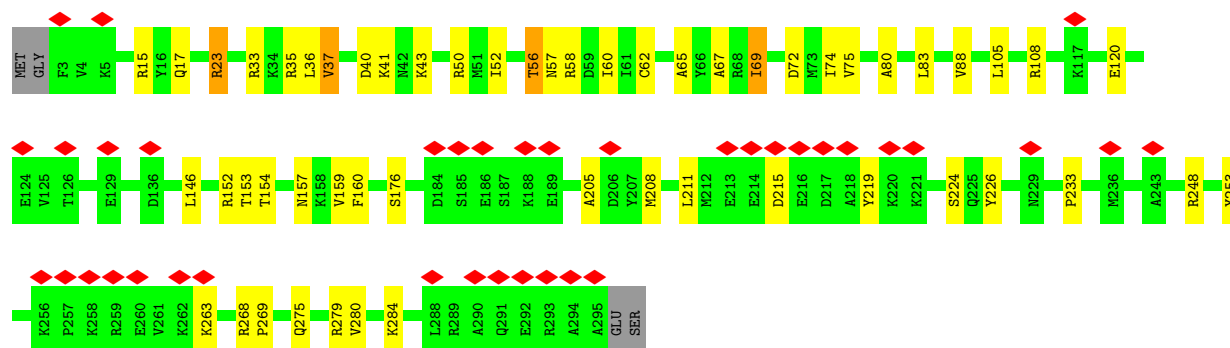
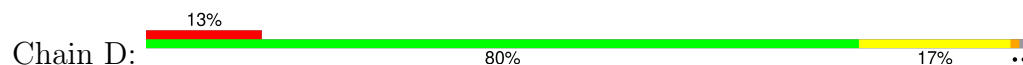




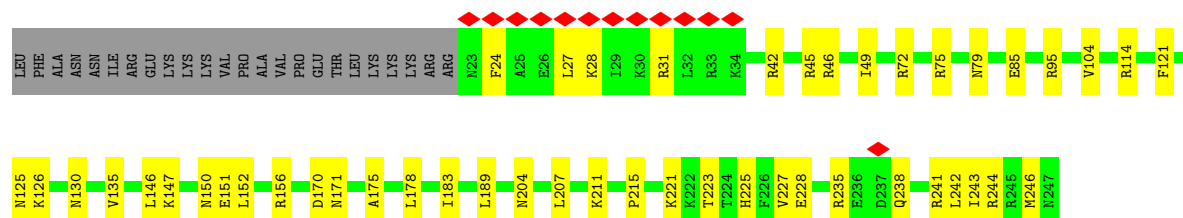
• Molecule 9: 60S ribosomal protein L4



• Molecule 10: Large ribosomal subunit protein uL18

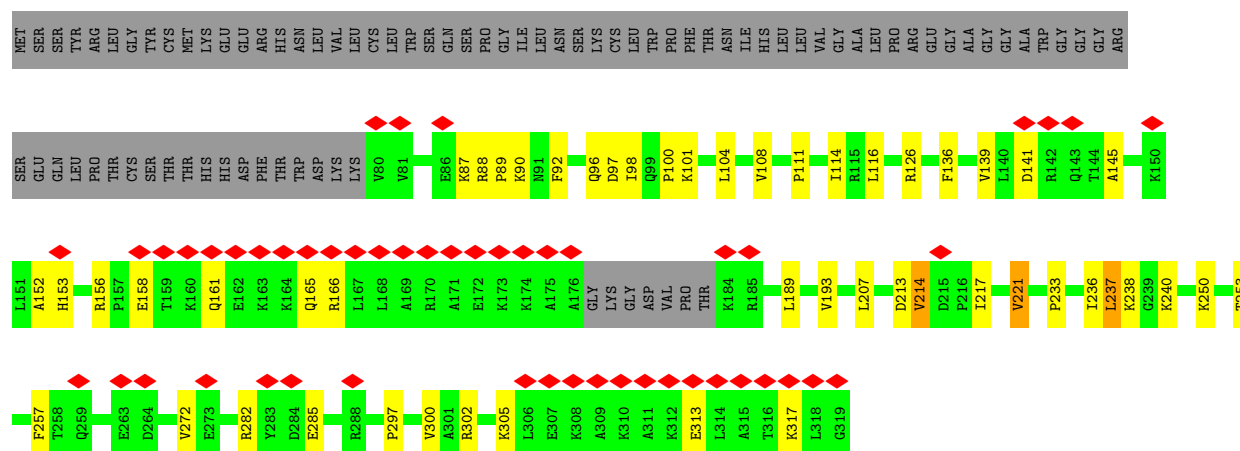


• Molecule 11: uL30

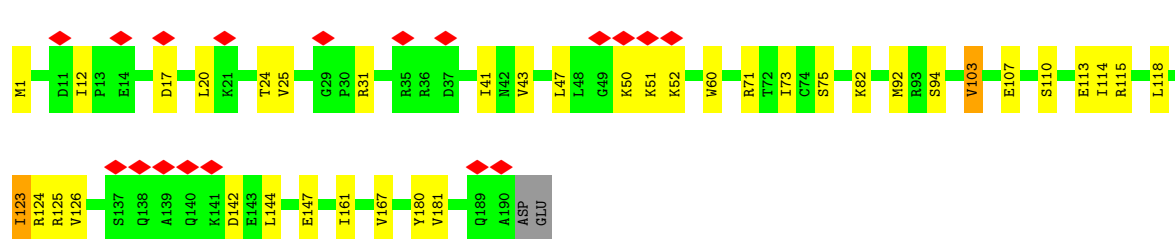
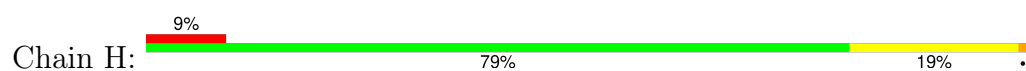


• Molecule 12: 60S ribosomal protein L7a

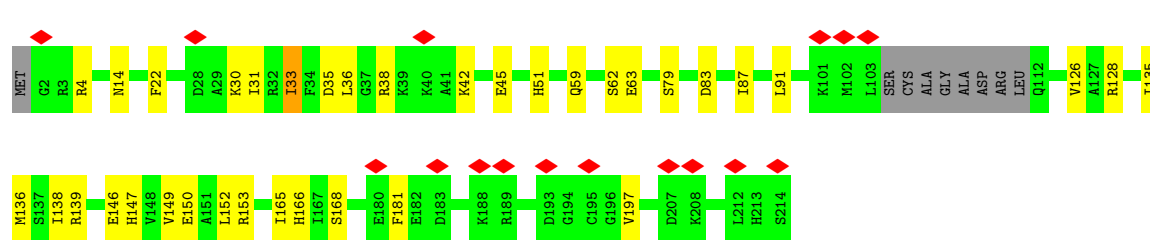
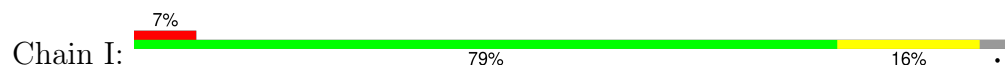




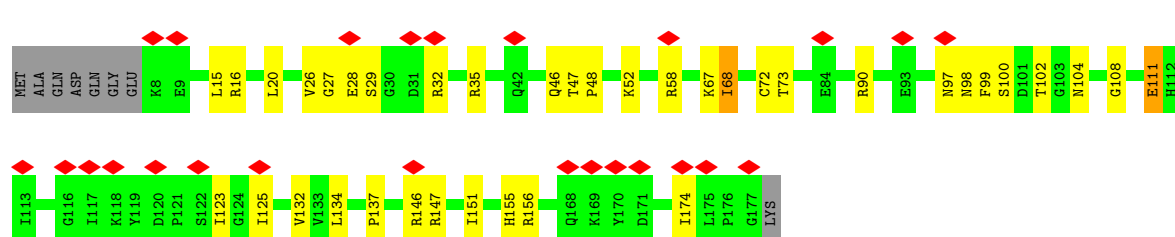
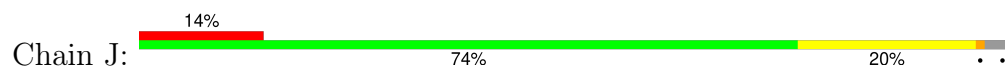
• Molecule 13: 60S ribosomal protein L9



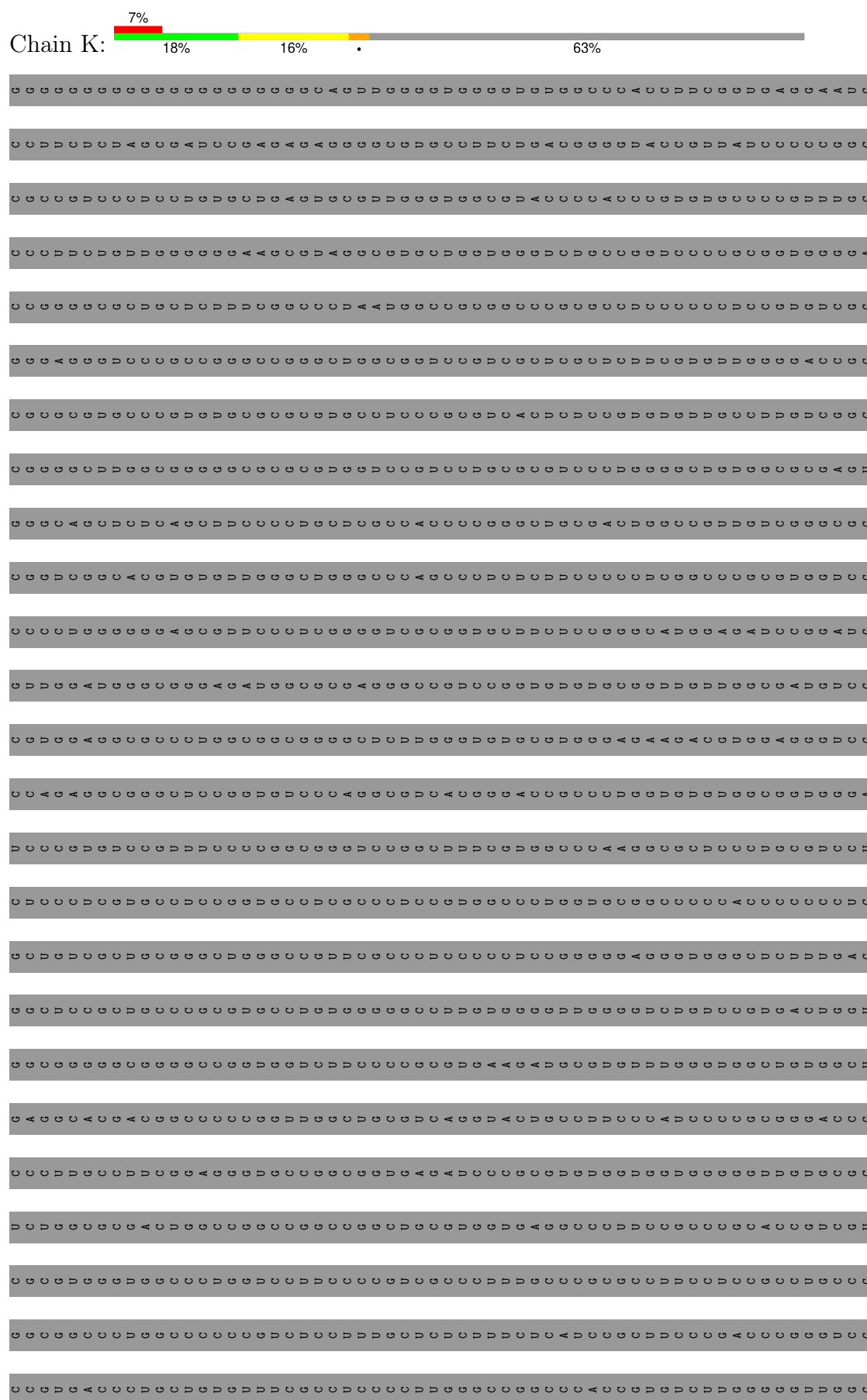
• Molecule 14: 60S ribosomal protein L10



• Molecule 15: Ribosomal protein L11

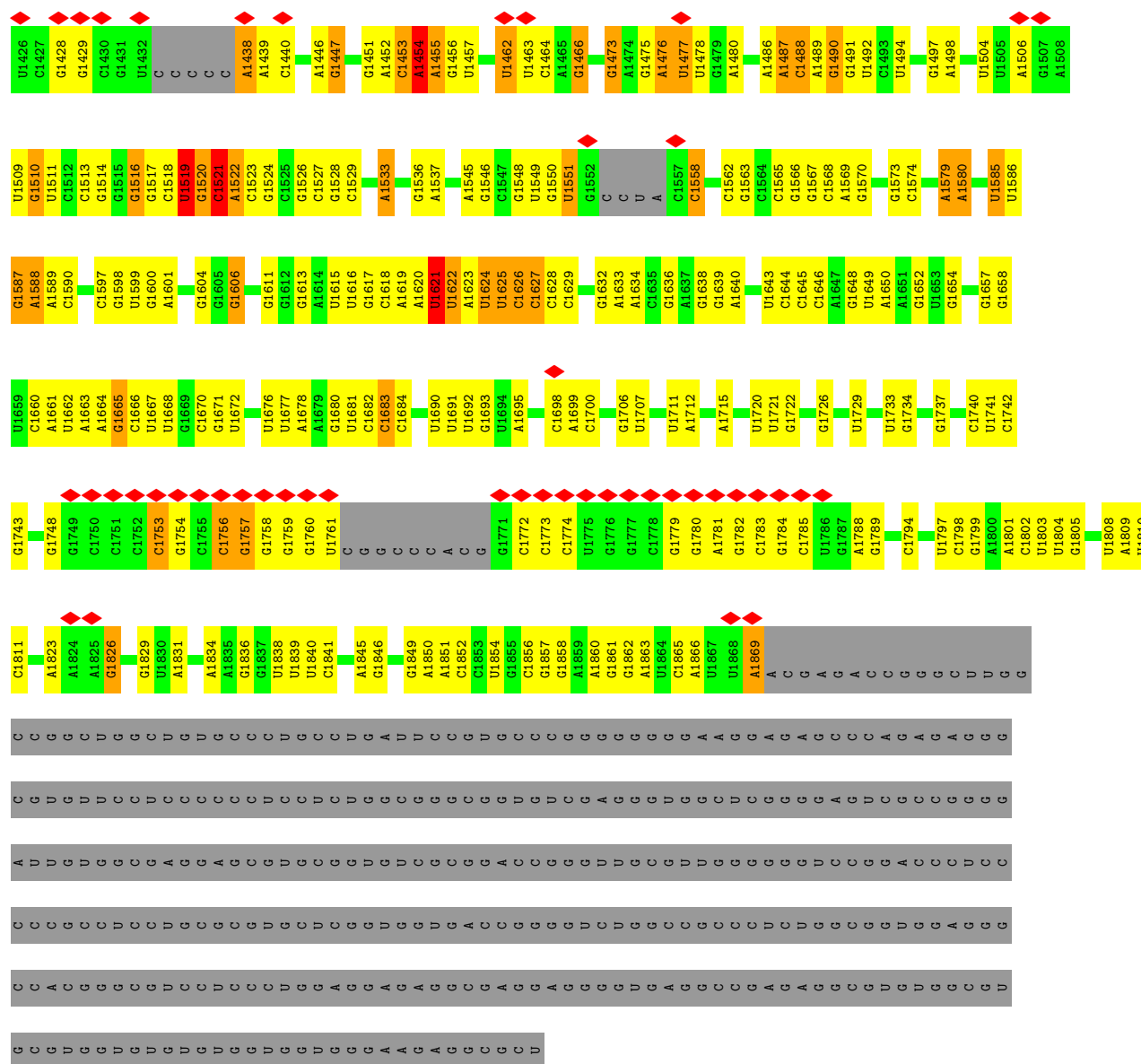


• Molecule 16: 18S rRNA

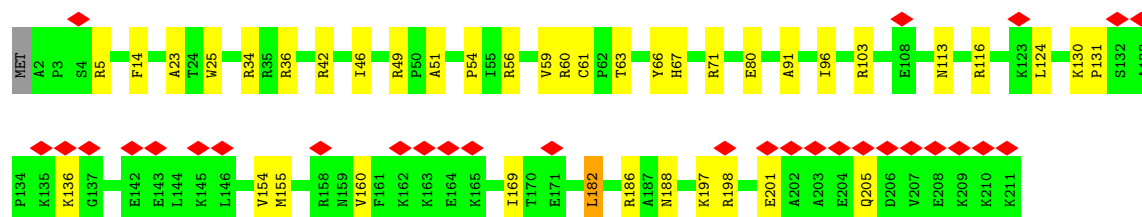
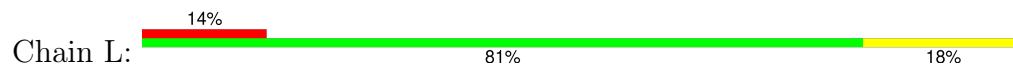






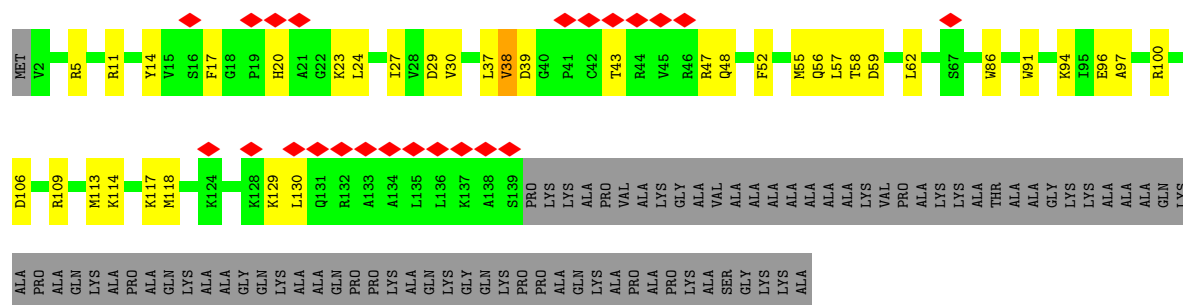


- Molecule 17: Large ribosomal subunit protein eL13

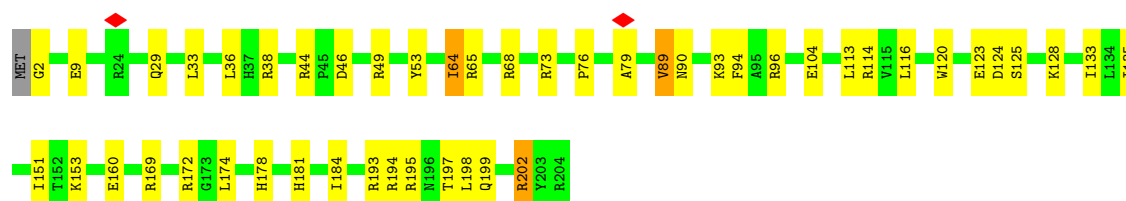
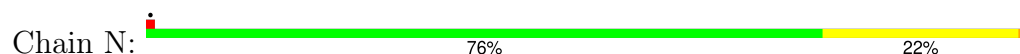


- Molecule 18: 60S ribosomal protein L14

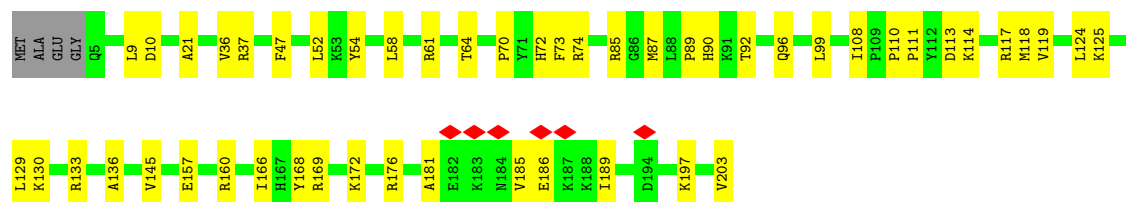




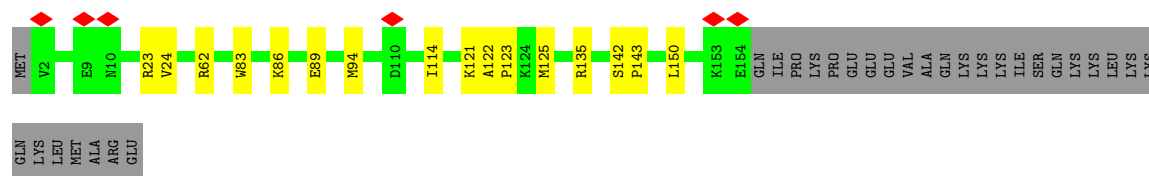
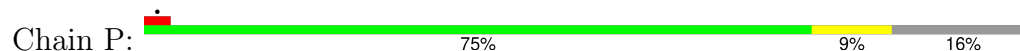
• Molecule 19: Ribosomal protein L15



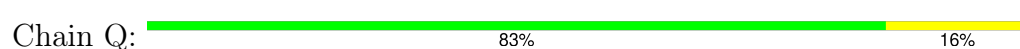
• Molecule 20: Large ribosomal subunit protein uL13



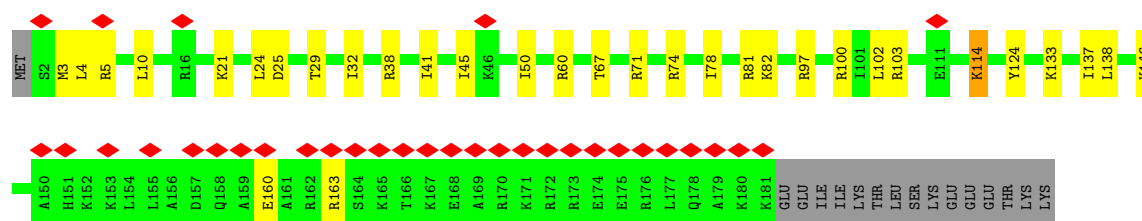
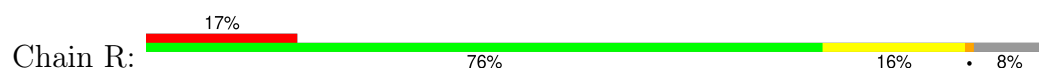
• Molecule 21: Large ribosomal subunit protein uL22



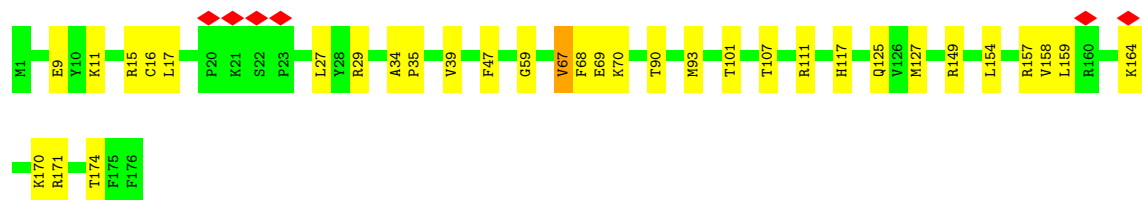
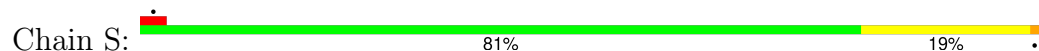
• Molecule 22: Large ribosomal subunit protein eL18



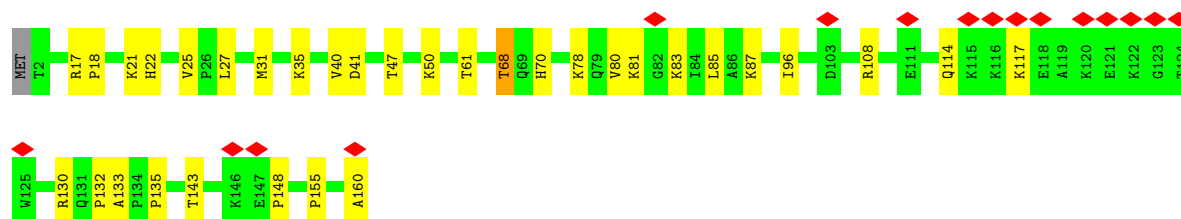
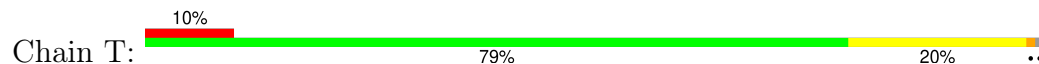
• Molecule 23: Large ribosomal subunit protein eL19



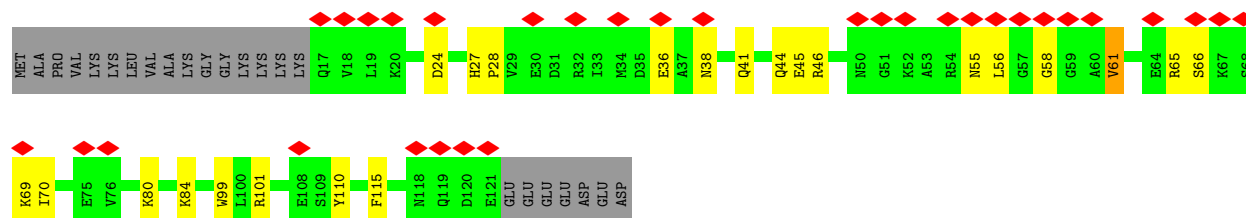
- Molecule 24: Large ribosomal subunit protein eL20



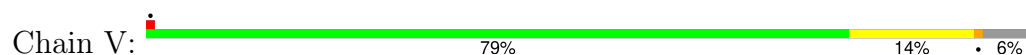
- Molecule 25: eL21



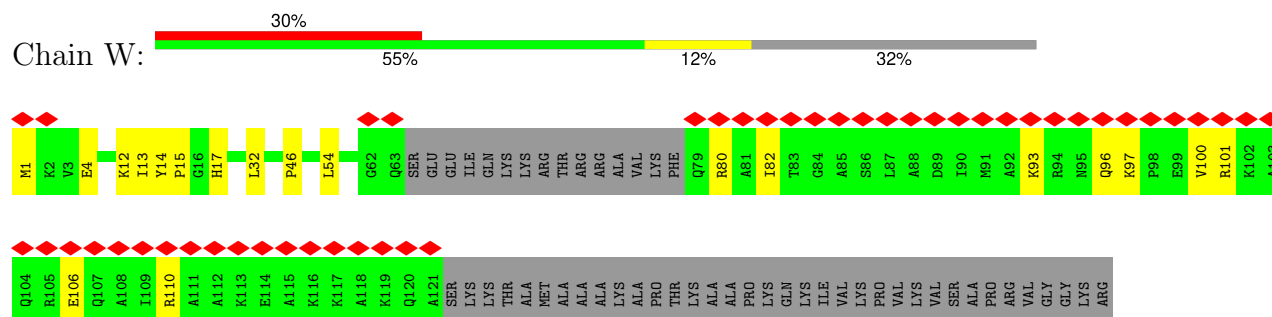
- Molecule 26: Large ribosomal subunit protein eL22



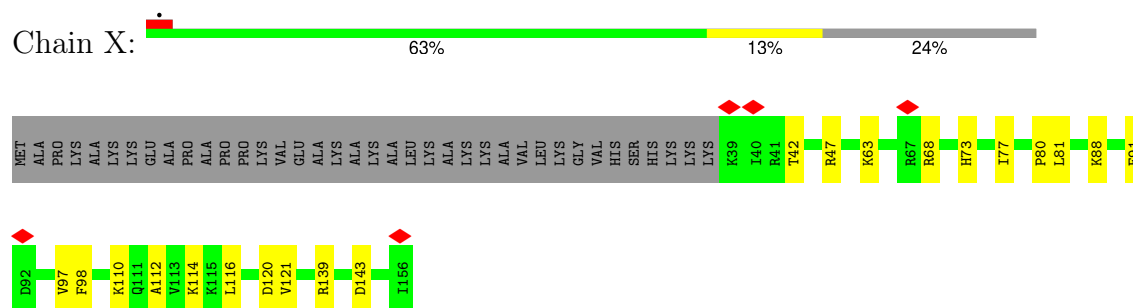
- Molecule 27: Ribosomal protein L23



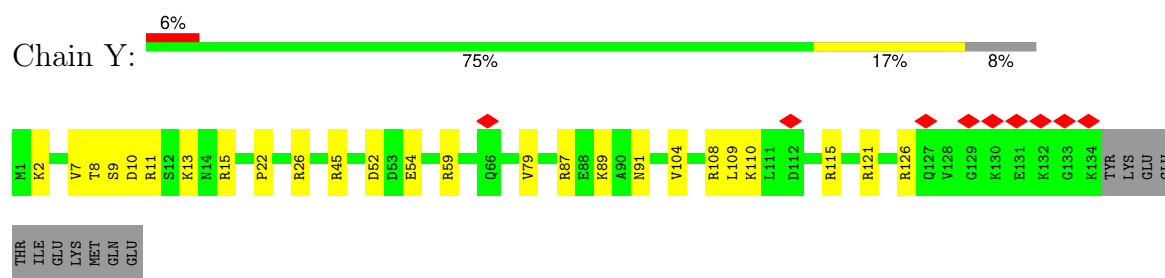
- Molecule 28: eL24



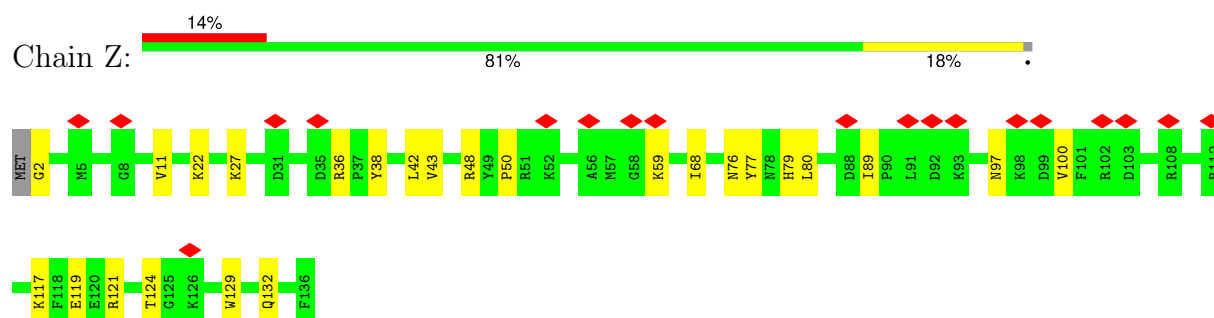
- Molecule 29: eL23



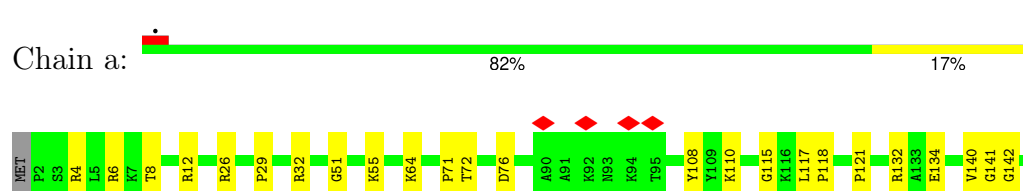
- Molecule 30: uL24



- Molecule 31: 60S ribosomal protein L27

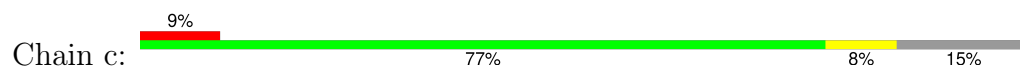


- Molecule 32: 60S ribosomal protein L27a

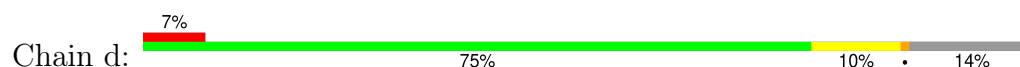




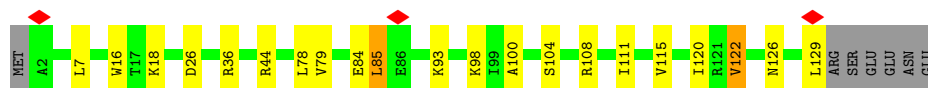
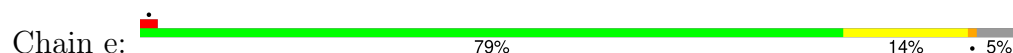
- Molecule 33: eL30



- Molecule 34: eL31



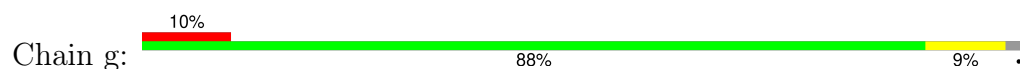
- Molecule 35: Large ribosomal subunit protein eL32



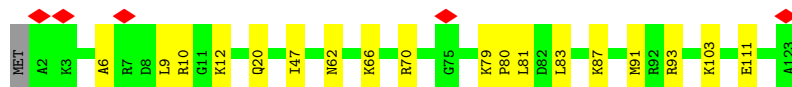
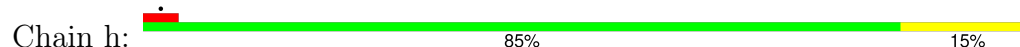
- Molecule 36: eL33



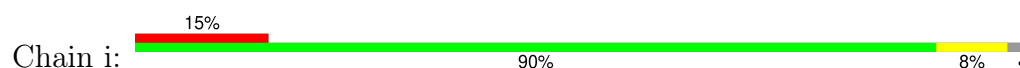
- Molecule 37: 60S ribosomal protein L34



- Molecule 38: eL35

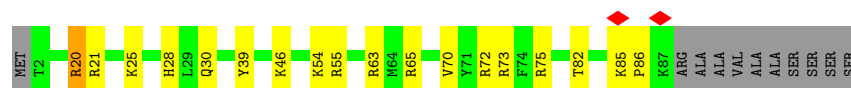


- Molecule 39: Large ribosomal subunit protein eL36

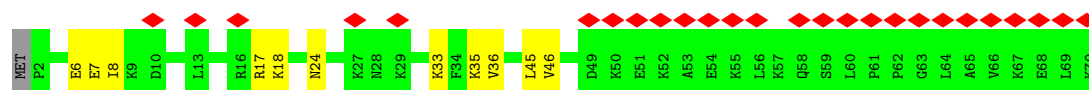
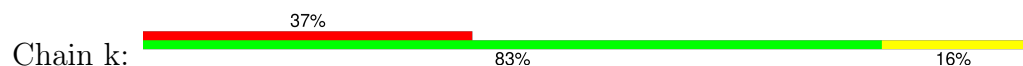




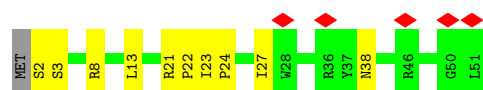
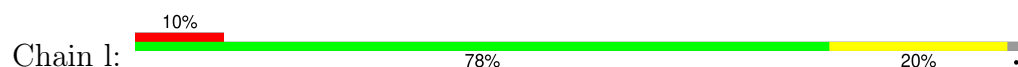
- Molecule 40: Ribosomal protein L37



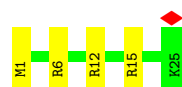
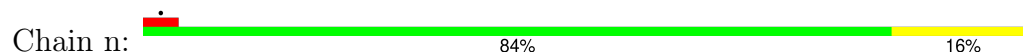
- Molecule 41: Large ribosomal subunit protein eL38



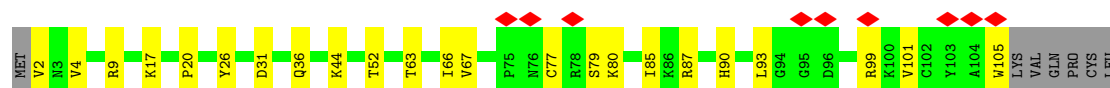
- Molecule 42: eL39



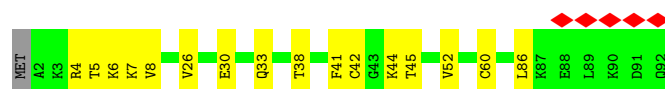
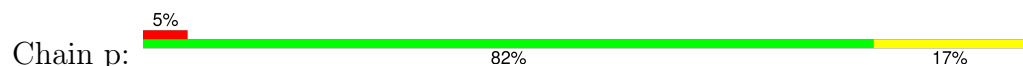
- Molecule 43: eL41



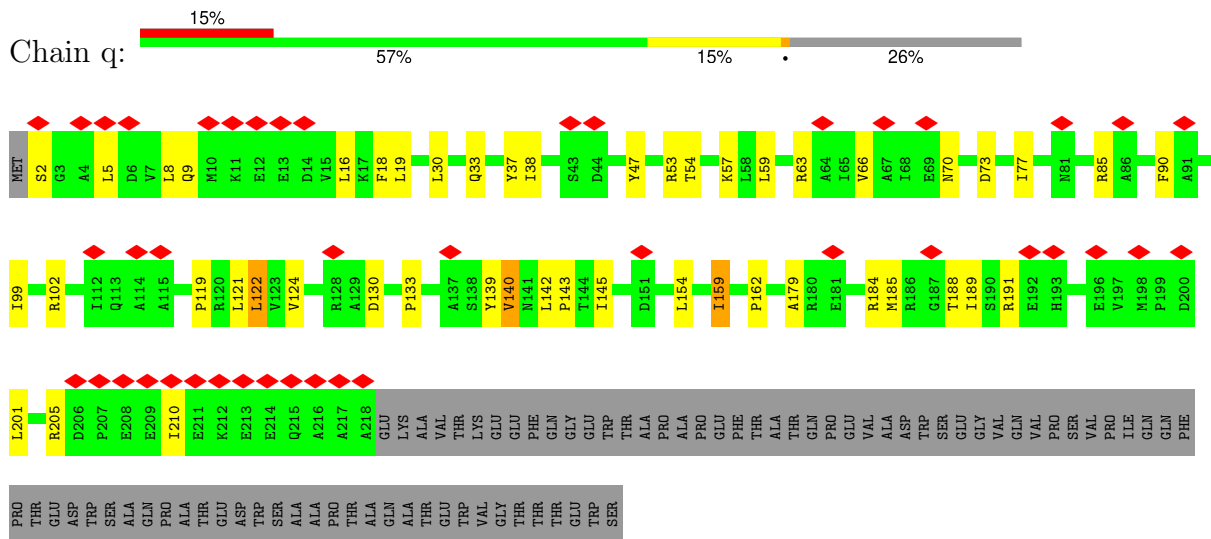
- Molecule 44: Large ribosomal subunit protein eL42



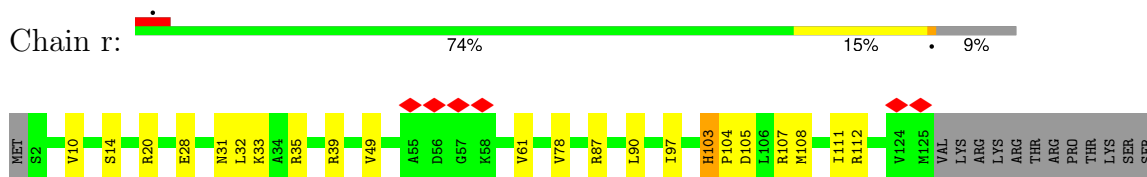
- Molecule 45: eL43



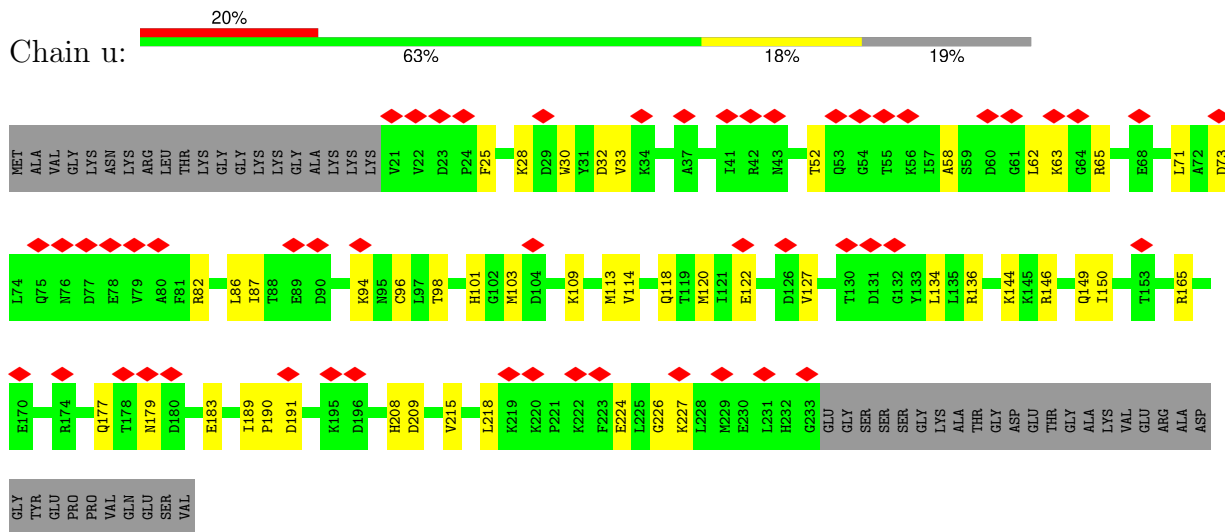
- Molecule 46: uS2 (SA)



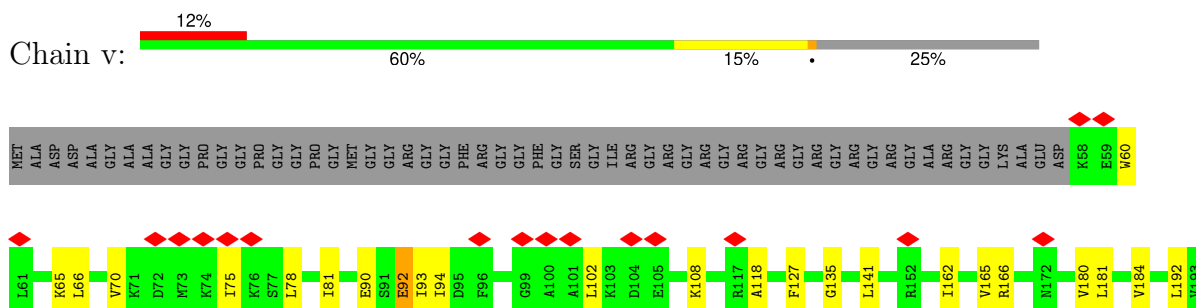
- Molecule 47: eL28

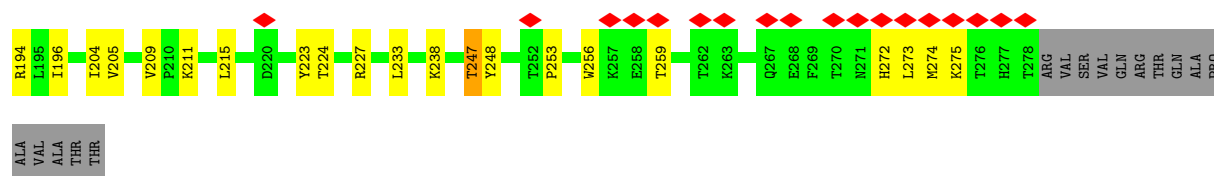


- Molecule 48: 40S ribosomal protein S3a

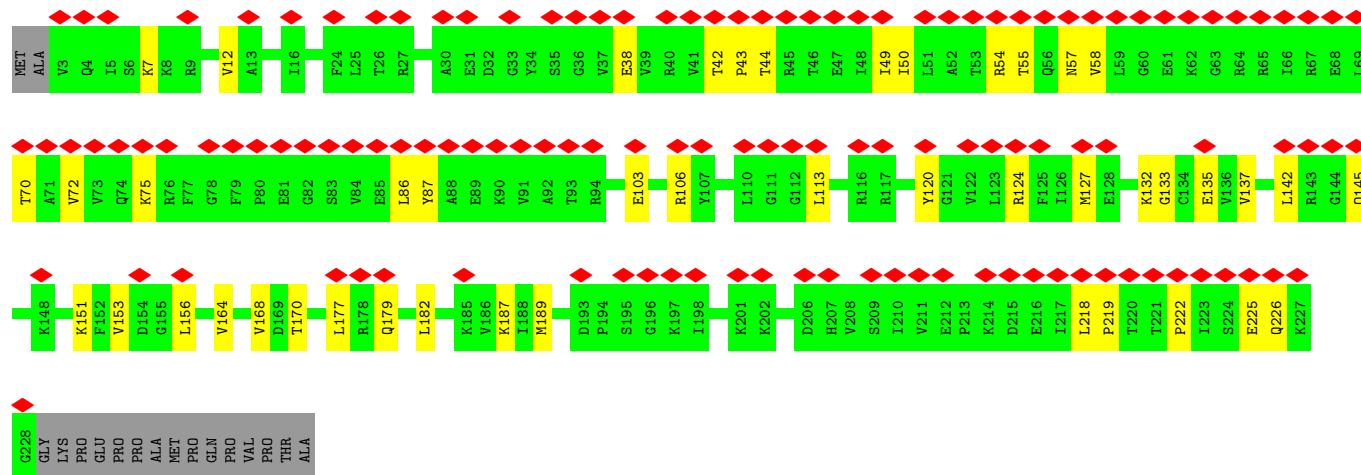


- Molecule 49: Small ribosomal subunit protein uS5

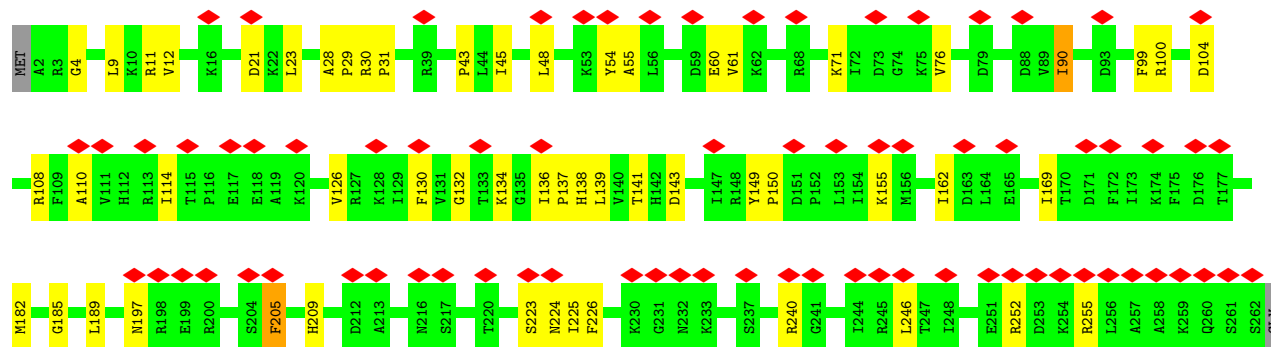
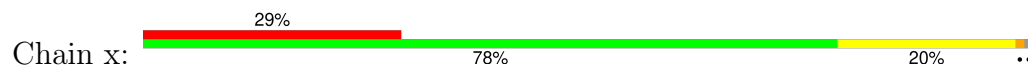




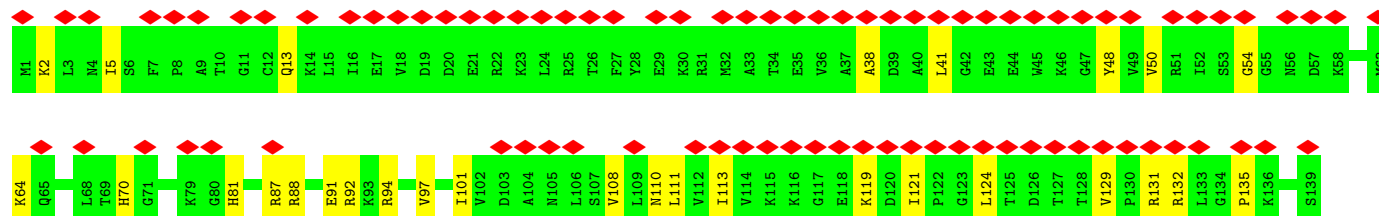
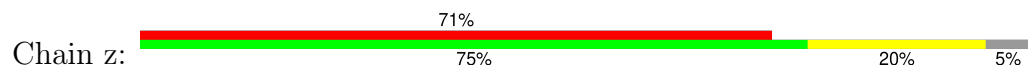
• Molecule 50: Ribosomal protein S3

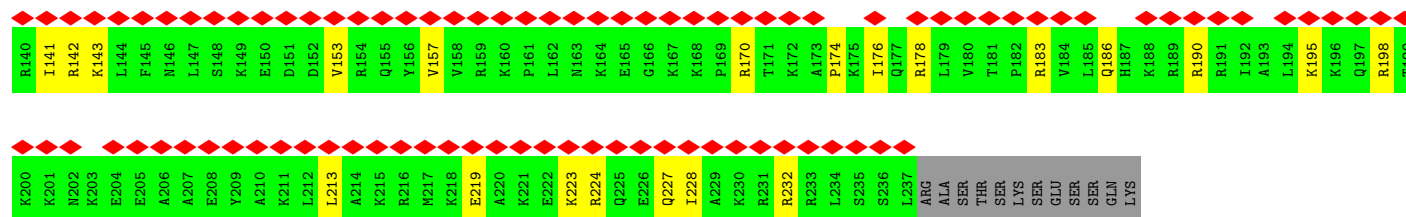


• Molecule 51: 40S ribosomal protein S4

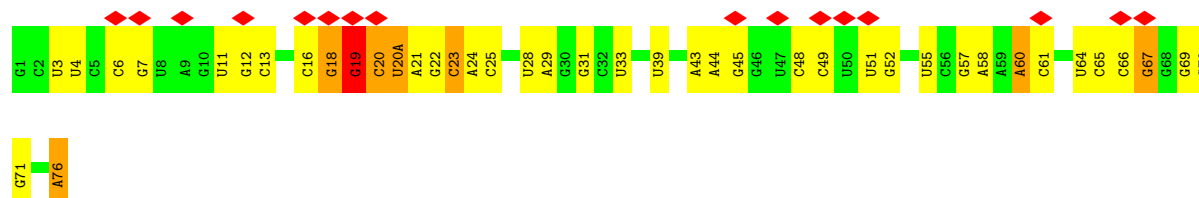
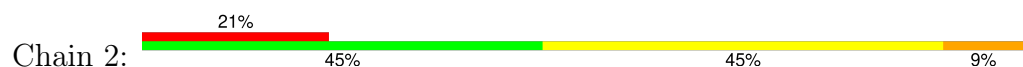


• Molecule 52: 40S ribosomal protein S6

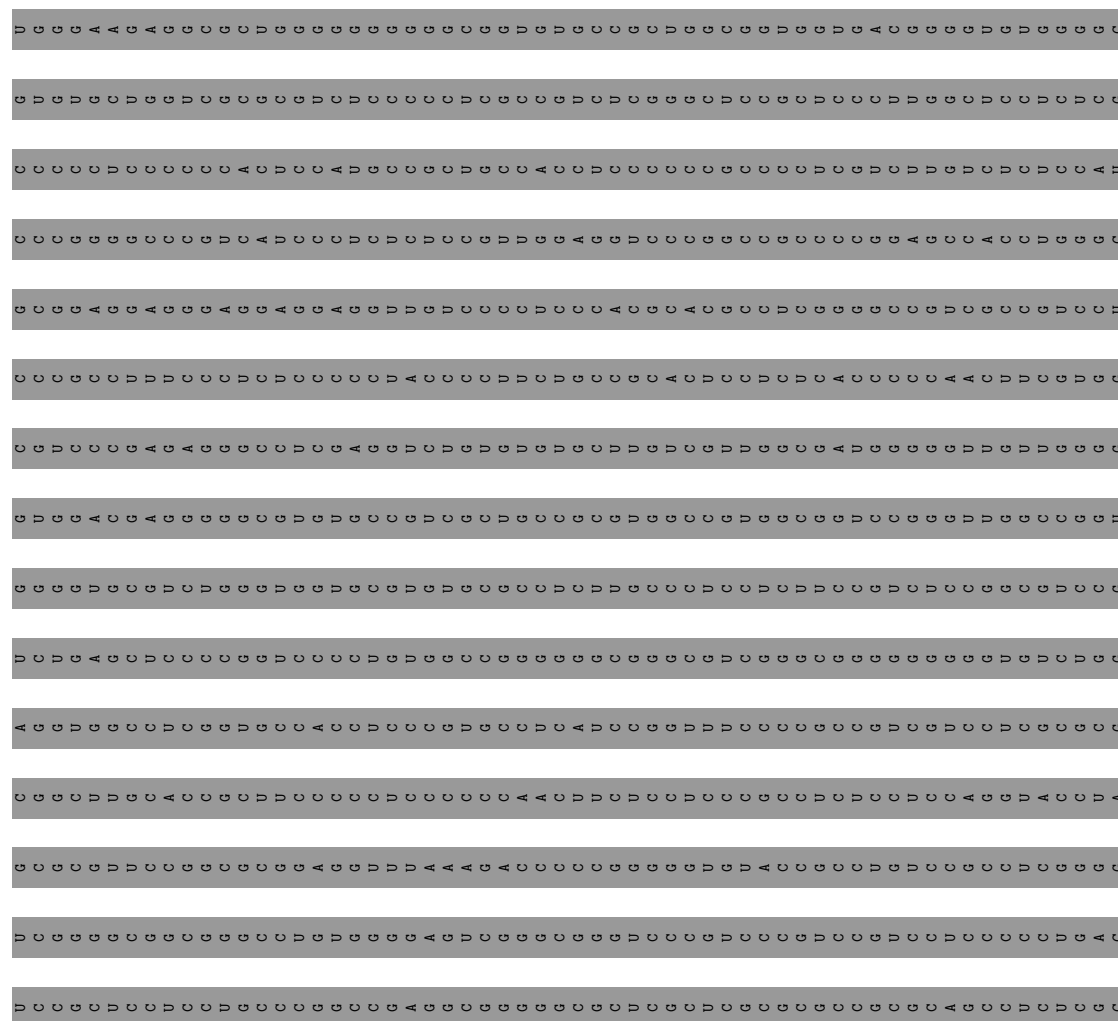




• Molecule 53: tRNA



• Molecule 54: 28S rRNA



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C1

G2

G3

G6

C7

C8

C1

C2

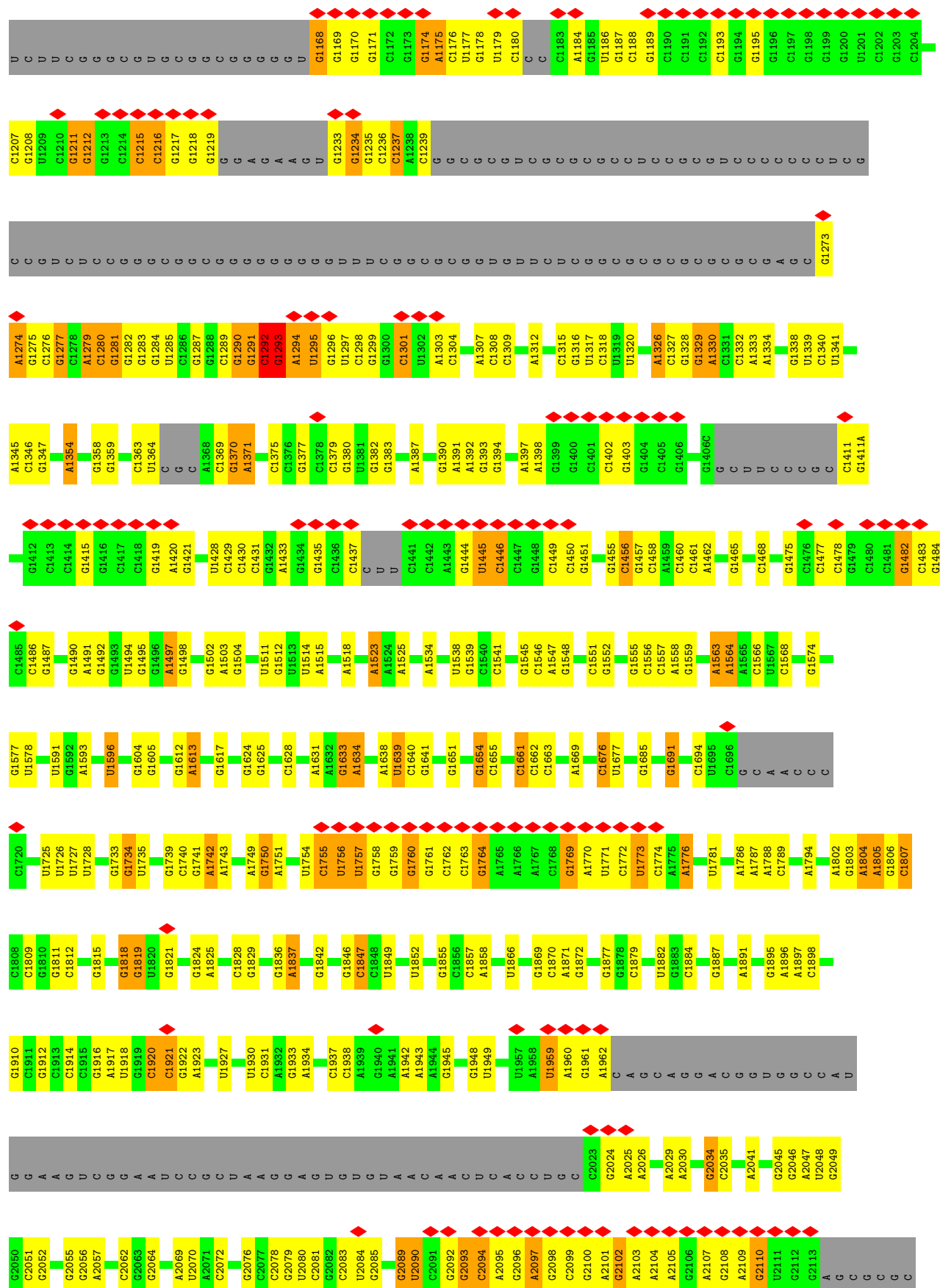
C3

C6

C7

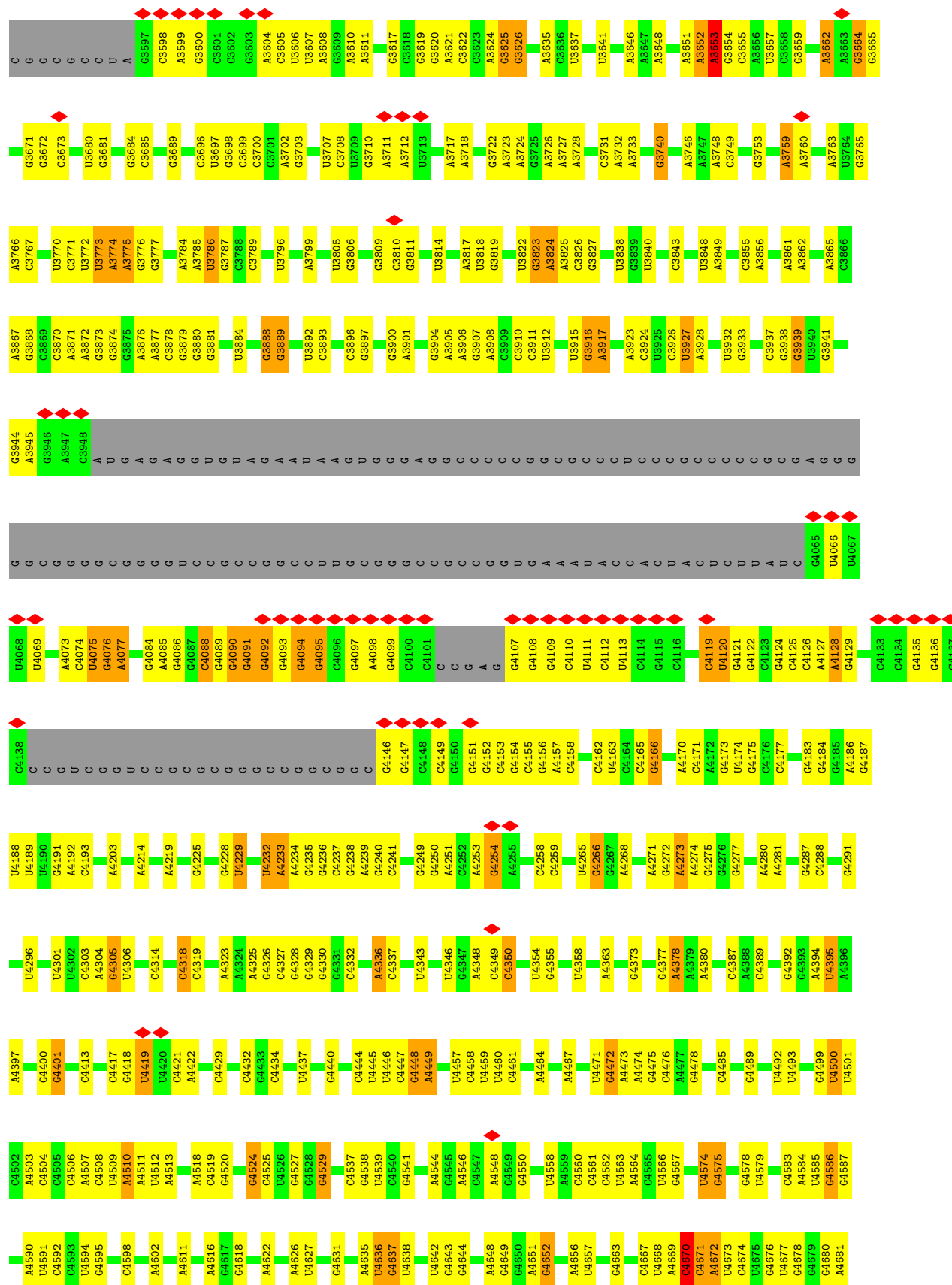
U8

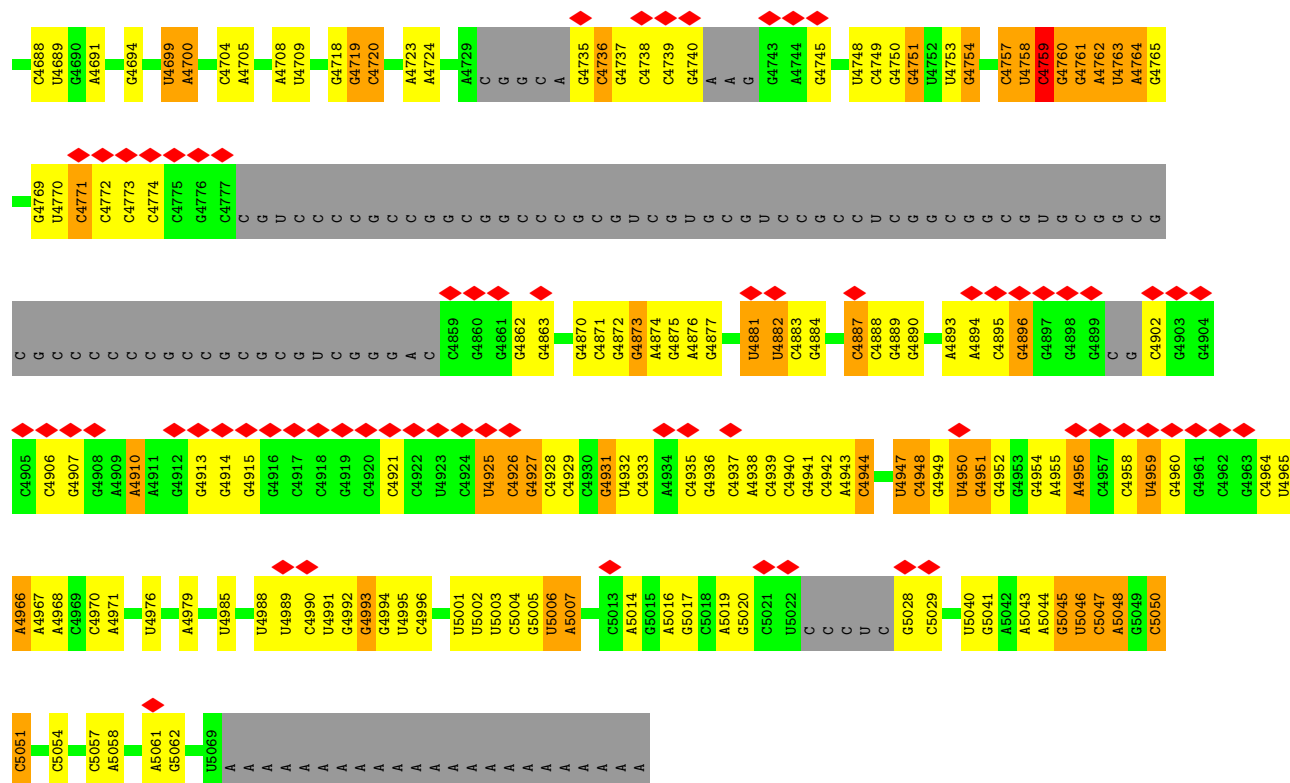




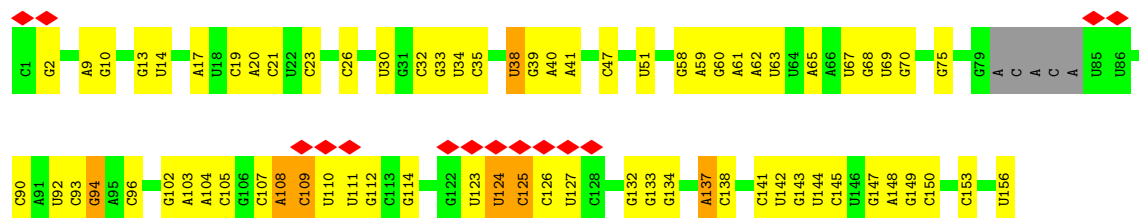




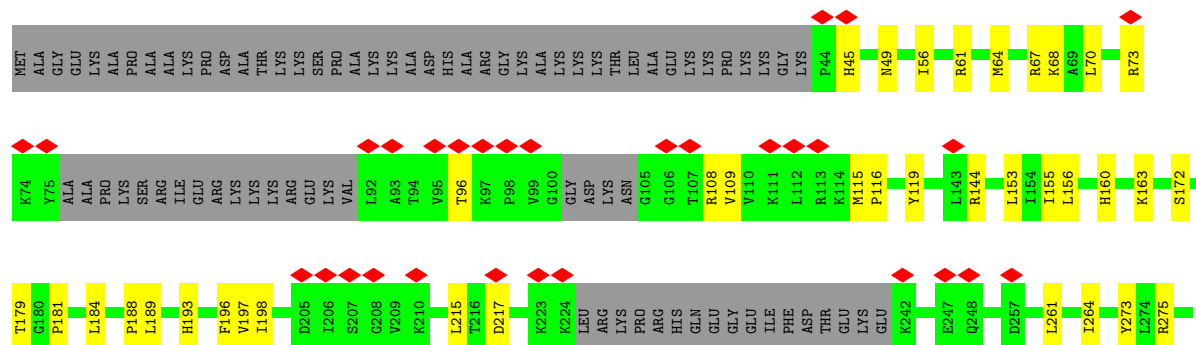


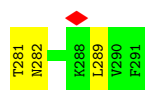


• Molecule 55: 5.8S rRNA

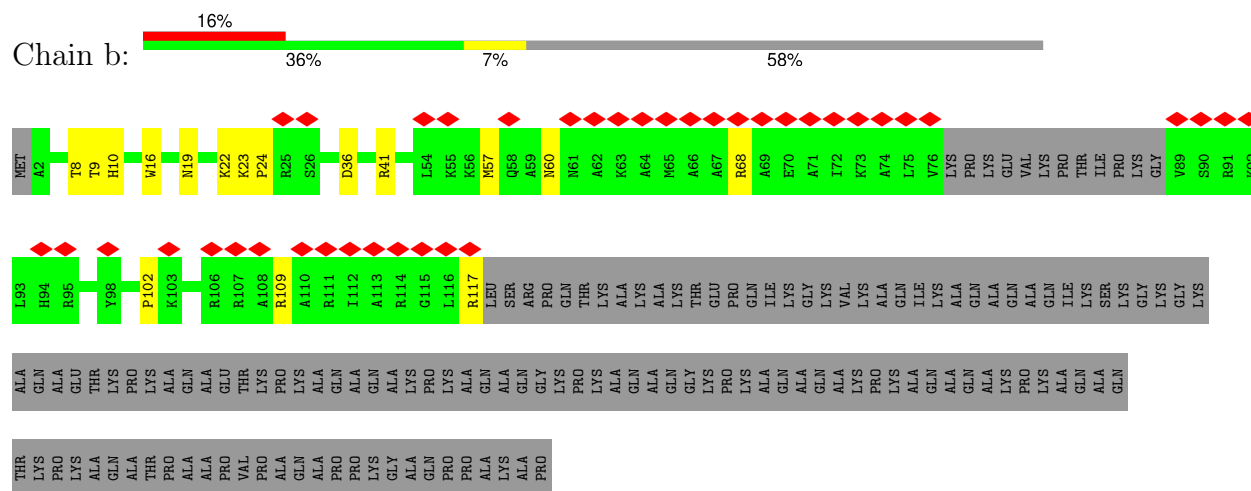


• Molecule 56: 60S ribosomal protein L6

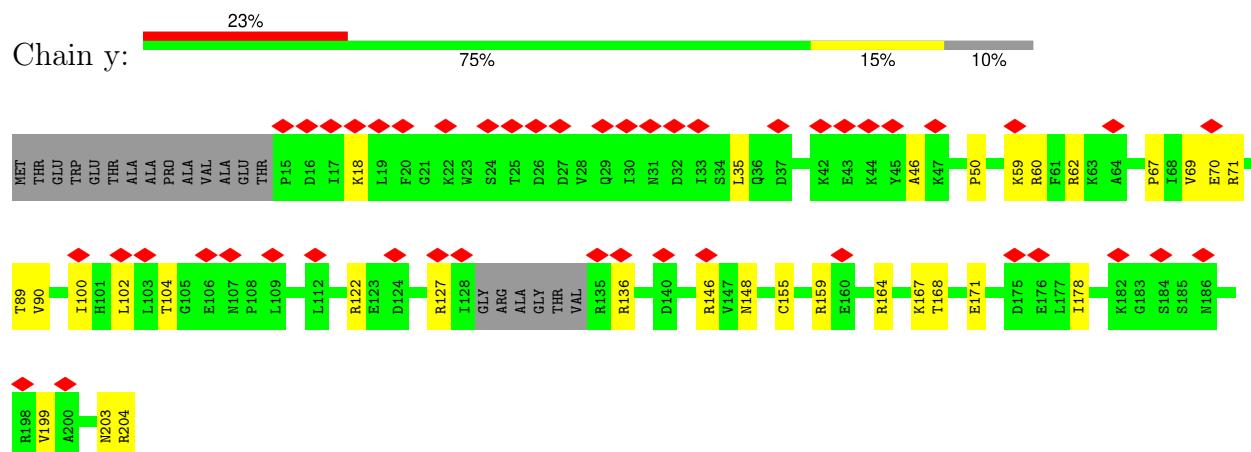




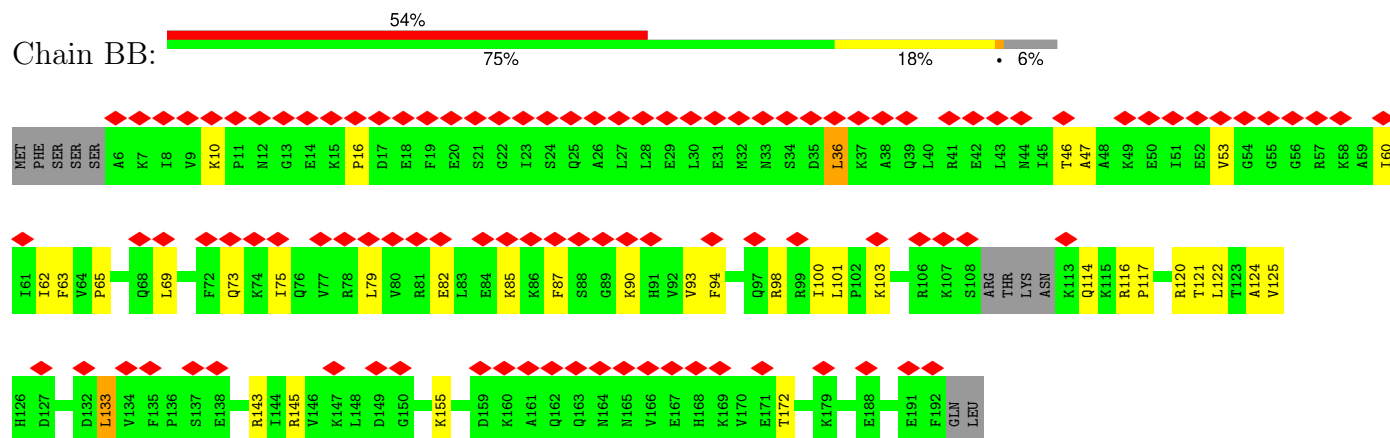
- Molecule 57: Large ribosomal subunit protein eL29




- Molecule 58: Ribosomal protein S5

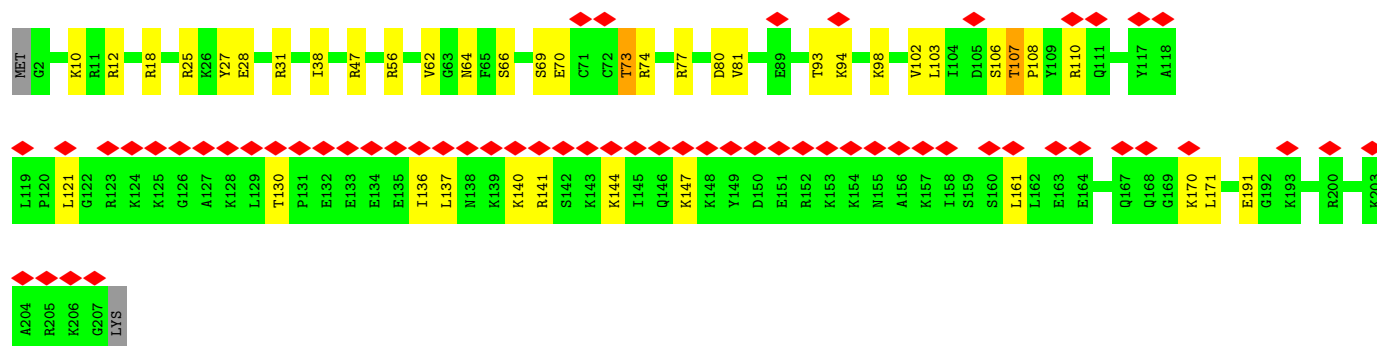


- Molecule 59: 40S ribosomal protein S7




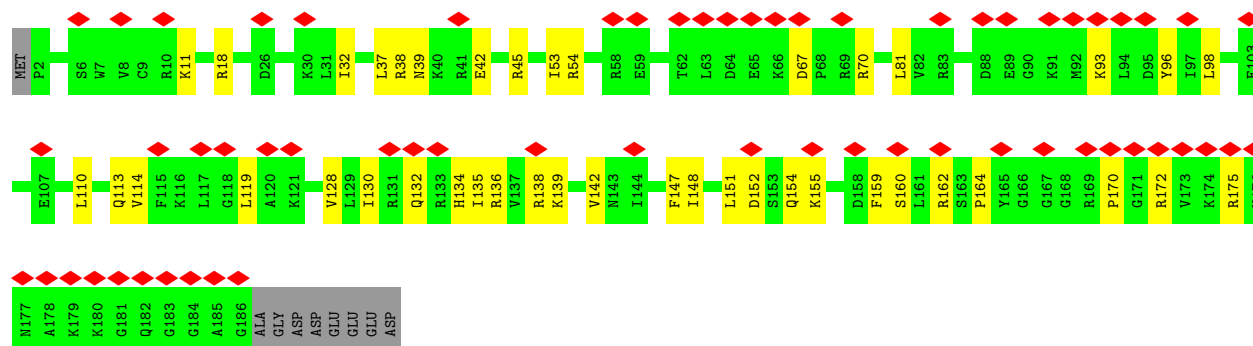
- Molecule 60: 40S ribosomal protein S8

Chain CC: 



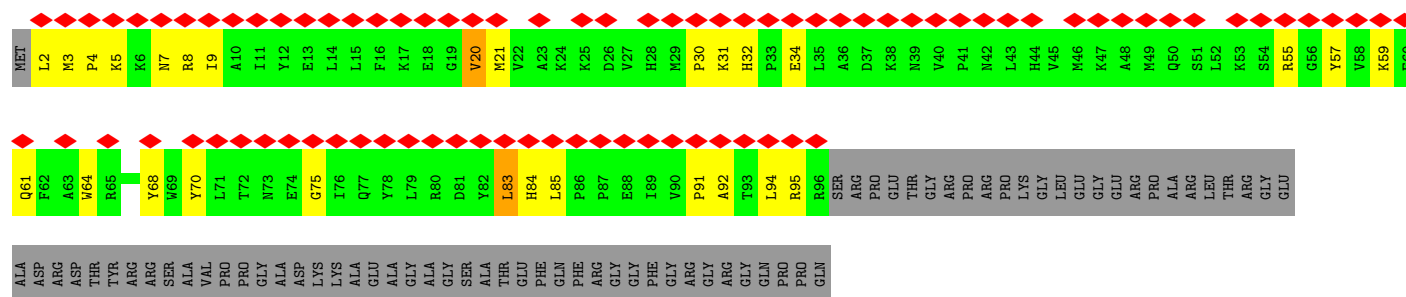
• Molecule 61: Ribosomal protein S9 (Predicted)

Chain DD: 



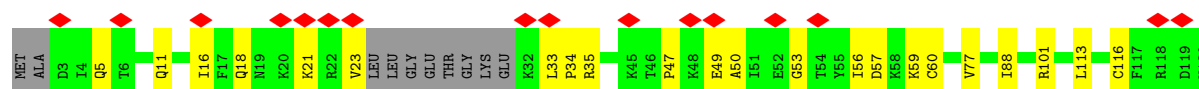
• Molecule 62: S10\_ plectin domain-containing protein

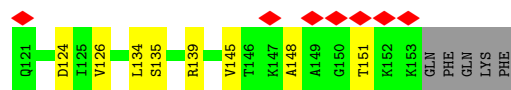
Chain SS: 



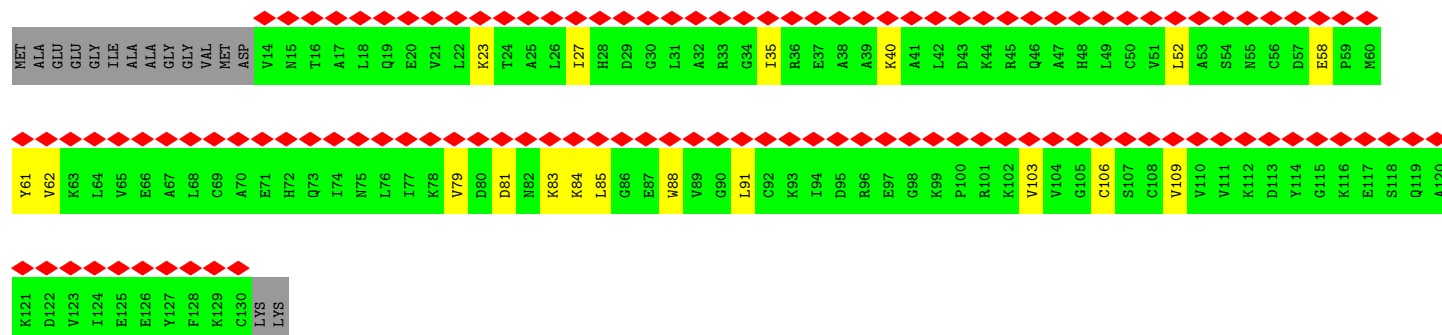
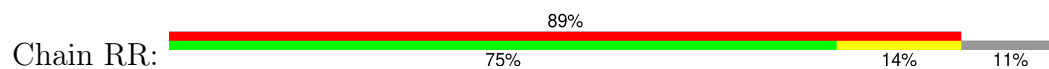
• Molecule 63: Ribosomal protein S11

Chain EE: 

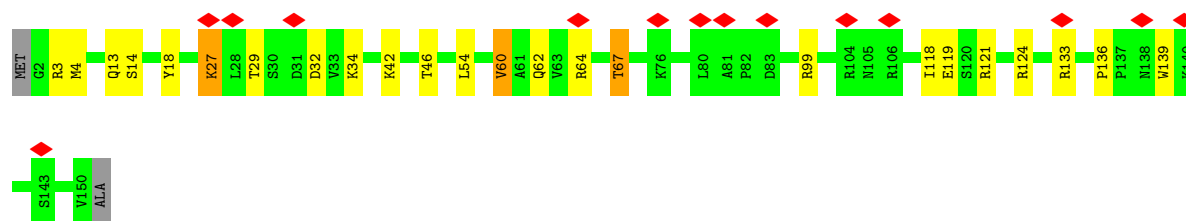
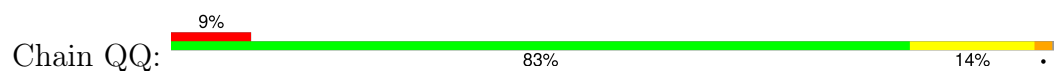




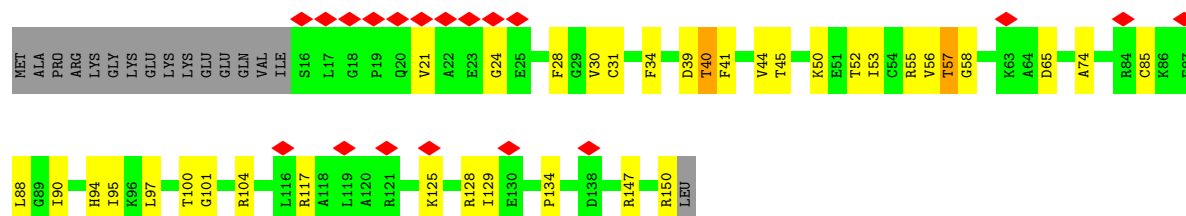
• Molecule 64: 40S ribosomal protein S12



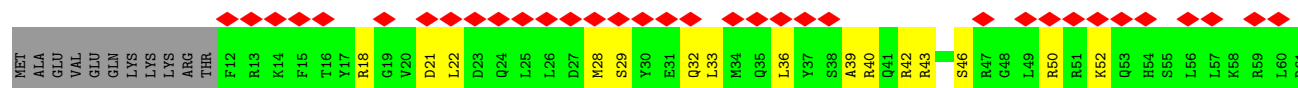
• Molecule 65: Ribosomal protein S13

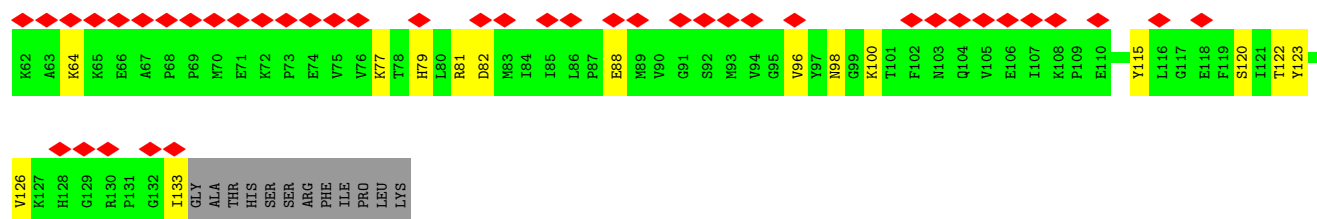


• Molecule 66: Small ribosomal subunit protein uS11

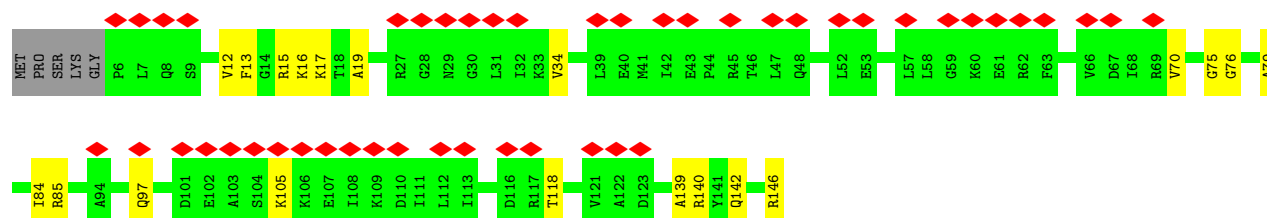
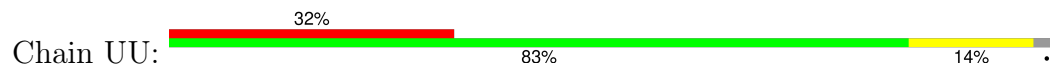


• Molecule 67: uS19

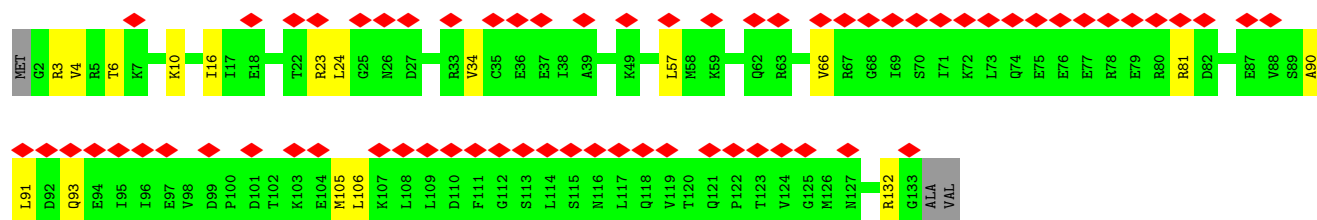
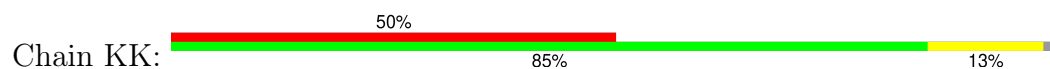




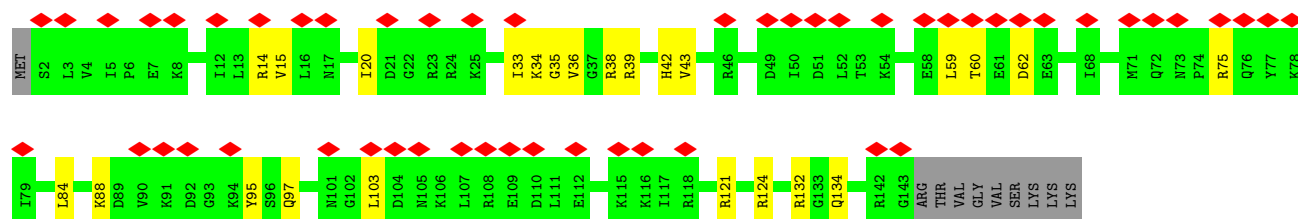
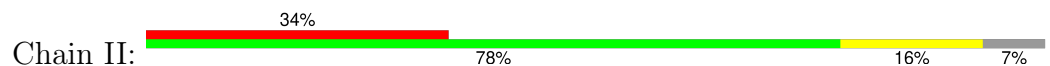
• Molecule 68: uS9



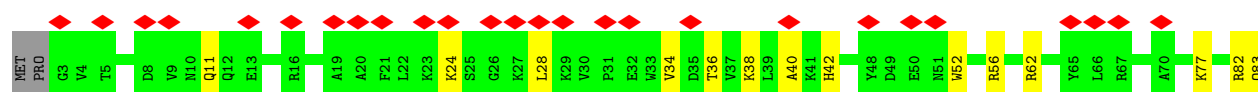
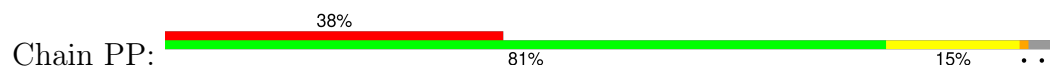
• Molecule 69: eS17

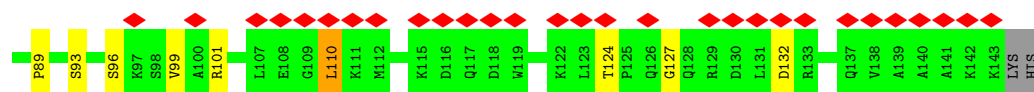


• Molecule 70: uS13

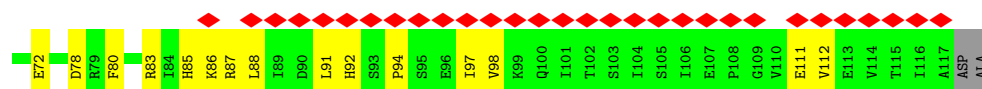
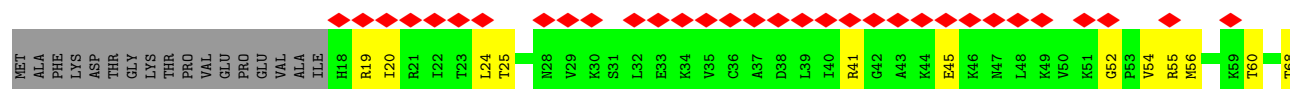


• Molecule 71: eS19

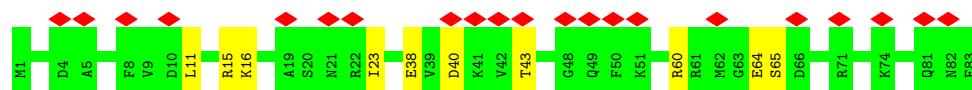




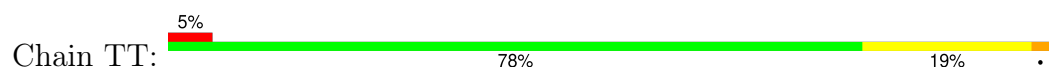
- Molecule 72: uS10



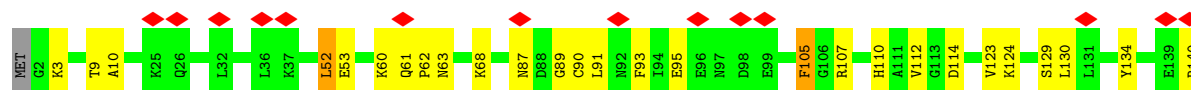
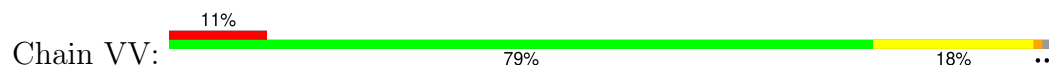
- Molecule 73: Small ribosomal subunit protein eS21



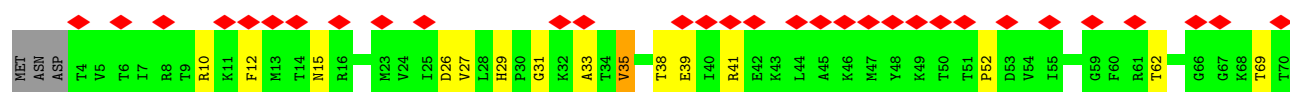
- Molecule 74: Ribosomal protein S15a



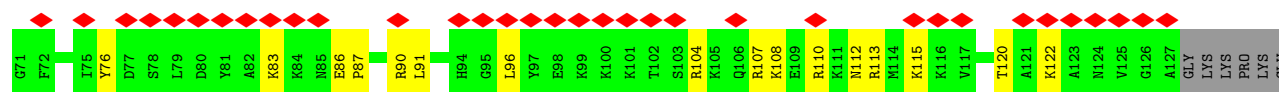
- Molecule 75: uS12



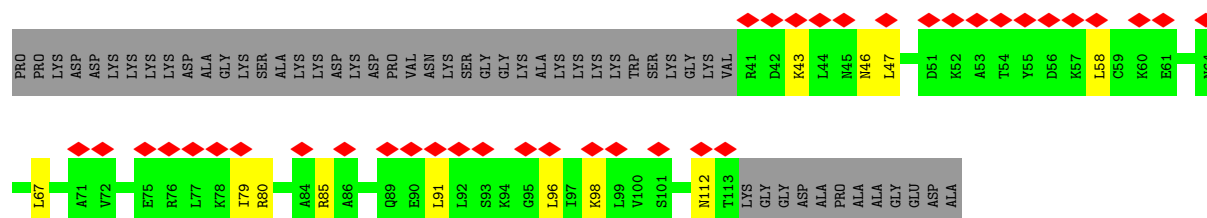
- Molecule 76: Small ribosomal subunit protein eS24



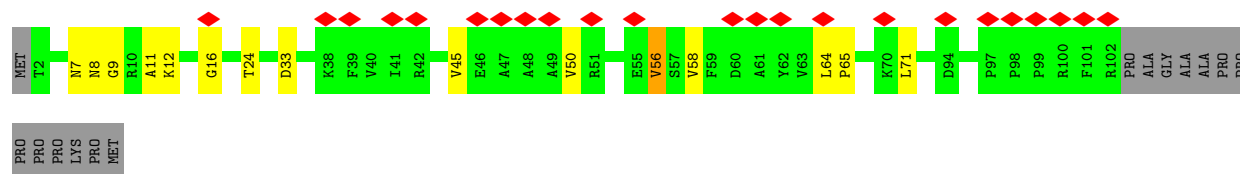
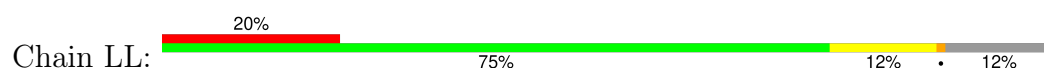




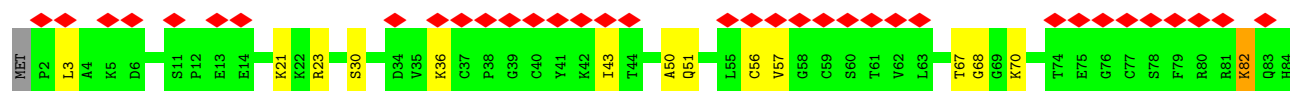
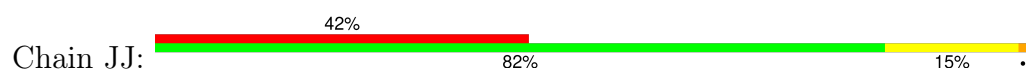
- Molecule 77: eS25



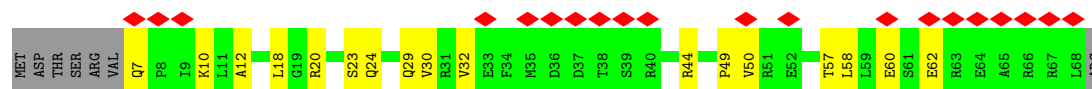
- Molecule 78: eS26



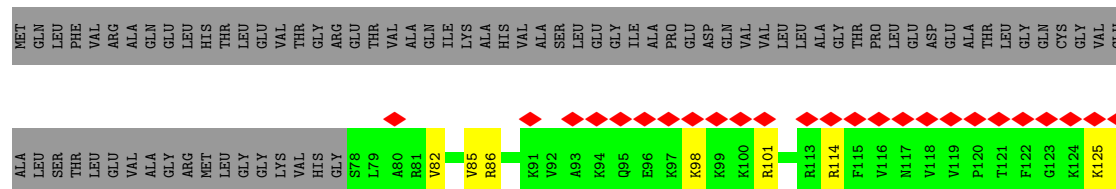
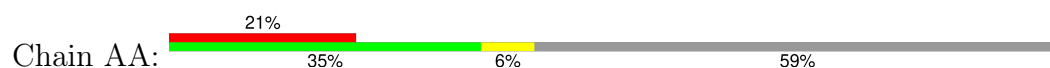
- Molecule 79: 40S ribosomal protein S27



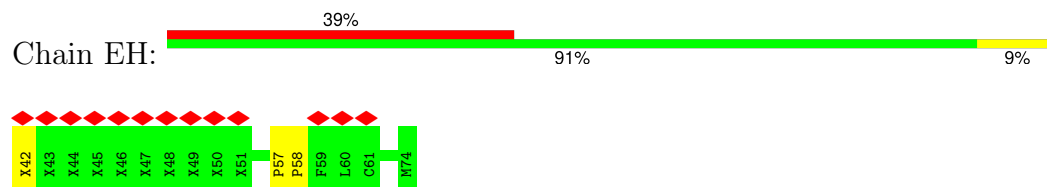
- Molecule 80: Ribosomal protein S28



- Molecule 81: 40S ribosomal protein S30



- Molecule 82: Transcription factor BTF3



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	72007	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	32	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	1400	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.160	Depositor
Minimum map value	-0.658	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.047	Depositor
Recommended contour level	0.11	Depositor
Map size ( $\text{\AA}$ )	424.96, 424.96, 424.96	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	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: ZN, MG

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	m	0.07	0/425	0.23	0/564
2	0	0.06	0/508	0.20	0/673
3	4	0.09	0/142	0.27	0/219
4	6	0.16	0/2493	0.24	0/3394
5	7	0.19	0/2858	0.40	6/4455 (0.1%)
6	9	0.07	0/470	0.19	0/623
7	A	0.08	0/1936	0.24	0/2596
8	B	0.07	0/3240	0.21	0/4339
9	C	0.08	0/2937	0.22	0/3946
10	D	0.13	0/2437	0.23	0/3264
11	F	0.09	0/1911	0.22	0/2549
12	G	0.08	0/1910	0.22	0/2569
13	H	0.07	0/1535	0.22	0/2063
14	I	0.08	0/1702	0.21	0/2272
15	J	0.07	0/1385	0.22	0/1852
16	K	0.17	0/40364	0.37	65/62897 (0.1%)
17	L	0.08	0/1733	0.21	0/2318
18	M	0.08	0/1158	0.22	0/1547
19	N	0.08	0/1746	0.22	0/2338
20	O	0.10	0/1662	0.23	0/2222
21	P	0.08	0/1268	0.24	0/1700
22	Q	0.08	0/1539	0.24	0/2054
23	R	0.08	0/1524	0.19	0/2014
24	S	0.09	0/1497	0.23	0/2008
25	T	0.08	0/1326	0.23	0/1770
26	U	0.08	0/889	0.25	0/1193
27	V	0.07	0/993	0.21	0/1332
28	W	0.07	0/873	0.20	0/1158
29	X	0.07	0/984	0.20	0/1323
30	Y	0.07	0/1132	0.21	0/1504
31	Z	0.07	0/1130	0.20	0/1507
32	a	0.08	0/1191	0.22	0/1590

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	c	0.07	0/771	0.20	0/1034
34	d	0.09	0/903	0.23	0/1216
35	e	0.07	0/1078	0.22	0/1439
36	f	0.08	0/895	0.25	0/1198
37	g	0.08	0/916	0.22	0/1220
38	h	0.07	0/1021	0.19	0/1348
39	i	0.08	0/841	0.19	0/1112
40	j	0.08	0/720	0.23	0/952
41	k	0.07	0/574	0.21	0/761
42	l	0.07	0/459	0.20	0/608
43	n	0.09	0/240	0.18	0/305
44	o	0.08	0/874	0.25	0/1156
45	p	0.07	0/718	0.19	0/953
46	q	0.08	0/1747	0.23	0/2374
47	r	0.08	0/1010	0.25	0/1354
48	u	0.08	0/1756	0.21	0/2350
49	v	0.08	0/1754	0.23	0/2369
50	w	0.07	0/1783	0.22	0/2400
51	x	0.07	0/2112	0.21	0/2841
52	z	0.08	0/1946	0.21	0/2590
53	2	0.25	0/1802	0.51	7/2804 (0.2%)
54	5	0.15	0/83213	0.32	68/129774 (0.1%)
55	8	0.08	0/3581	0.21	0/5577
56	E	0.08	0/1730	0.24	0/2320
57	b	0.07	0/861	0.20	0/1138
58	y	0.08	0/1485	0.24	0/1994
59	BB	0.08	0/1493	0.22	0/1999
60	CC	0.07	0/1715	0.22	0/2287
61	DD	0.07	0/1550	0.19	0/2069
62	SS	0.08	0/826	0.28	0/1115
63	EE	0.07	0/1195	0.21	0/1597
64	RR	0.07	0/918	0.22	0/1233
65	QQ	0.07	0/1226	0.21	0/1649
66	MM	0.07	0/1017	0.20	0/1365
67	WW	0.09	0/1029	0.25	0/1374
68	UU	0.08	0/1142	0.22	0/1528
69	KK	0.06	0/1082	0.17	0/1452
70	II	0.08	0/1190	0.22	0/1594
71	PP	0.08	0/1115	0.23	0/1493
72	GG	0.06	0/805	0.19	0/1081
73	HH	0.14	0/644	0.25	0/862
74	TT	0.08	0/1051	0.22	0/1406
75	VV	0.08	0/1116	0.21	0/1490

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
76	NN	0.06	0/1028	0.20	0/1366
77	OO	0.08	0/591	0.22	0/794
78	LL	0.08	0/830	0.22	0/1112
79	JJ	0.06	0/665	0.21	0/891
80	FF	0.06	0/490	0.17	0/656
81	AA	0.06	0/447	0.20	0/587
82	EF	0.41	0/862	0.54	0/1155
83	EG	0.11	0/518	0.26	0/692
84	EH	0.07	0/206	0.23	0/282
All	All	0.13	0/226439	0.30	146/332169 (0.0%)

There are no bond length outliers.

All (146) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
53	2	20	C	P-O3'-C3'	-9.58	108.20	119.70
5	7	82	G	P-O3'-C3'	-9.36	106.16	120.20
54	5	3655	C	P-O3'-C3'	-8.55	107.38	120.20
16	K	1270	G	P-O3'-C3'	-8.48	107.48	120.20
54	5	2737	C	P-O3'-C3'	-8.48	107.48	120.20
54	5	697	G	P-O3'-C3'	-8.37	107.64	120.20
54	5	451	C	P-O3'-C3'	-8.35	107.67	120.20
16	K	368	U	P-O3'-C3'	-8.29	107.77	120.20
54	5	343	C	P-O3'-C3'	-8.29	107.77	120.20
54	5	341	G	P-O3'-C3'	-8.28	107.78	120.20
16	K	1455	A	P-O3'-C3'	-8.20	107.90	120.20
16	K	1490	G	P-O3'-C3'	-8.16	107.96	120.20
54	5	101	A	P-O3'-C3'	-8.12	108.02	120.20
16	K	664	A	P-O3'-C3'	-8.11	108.04	120.20
16	K	373	G	P-O3'-C3'	-8.07	108.09	120.20
53	2	19	G	P-O3'-C3'	-8.07	108.10	120.20
54	5	4763	U	P-O3'-C3'	-8.04	108.13	120.20
16	K	1268	C	P-O3'-C3'	-8.04	108.14	120.20
16	K	1516	G	P-O3'-C3'	-8.01	108.19	120.20
54	5	344	A	P-O3'-C3'	-8.00	108.20	120.20
16	K	391	C	P-O3'-C3'	-7.93	108.30	120.20
16	K	1267	C	P-O3'-C3'	-7.93	108.31	120.20
54	5	5051	C	P-O3'-C3'	-7.90	108.35	120.20
54	5	4444	C	P-O3'-C3'	-7.89	108.36	120.20
5	7	81	G	P-O3'-C3'	-7.88	108.37	120.20
54	5	4760	G	P-O3'-C3'	-7.84	108.44	120.20
54	5	454	U	P-O3'-C3'	-7.83	108.46	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	K	1624	U	P-O3'-C3'	-7.82	108.47	120.20
16	K	1488	C	P-O3'-C3'	-7.82	108.48	120.20
16	K	1062	A	P-O3'-C3'	-7.79	108.51	120.20
16	K	371	A	P-O3'-C3'	-7.76	108.57	120.20
16	K	1453	C	P-O3'-C3'	-7.76	108.56	120.20
54	5	5044	A	P-O3'-C3'	-7.72	108.61	120.20
54	5	4672	A	P-O3'-C3'	-7.72	108.62	120.20
16	K	388	U	P-O3'-C3'	-7.71	108.63	120.20
16	K	374	G	P-O3'-C3'	-7.70	108.65	120.20
54	5	326	C	P-O3'-C3'	-7.69	108.66	120.20
16	K	1112	U	P-O3'-C3'	-7.68	108.68	120.20
53	2	18	G	P-O3'-C3'	-7.67	108.70	120.20
53	2	23	C	P-O3'-C3'	-7.66	108.71	120.20
16	K	1111	U	P-O3'-C3'	-7.65	108.73	120.20
54	5	342	G	P-O3'-C3'	-7.63	108.75	120.20
5	7	85	G	P-O3'-C3'	-7.63	108.75	120.20
16	K	1057	C	P-O3'-C3'	-7.60	108.80	120.20
16	K	1055	A	P-O3'-C3'	-7.60	108.80	120.20
16	K	369	C	P-O3'-C3'	-7.59	108.82	120.20
16	K	389	A	P-O3'-C3'	-7.59	108.82	120.20
5	7	84	U	P-O3'-C3'	-7.53	108.90	120.20
54	5	5045	G	P-O3'-C3'	-7.53	108.91	120.20
16	K	390	C	P-O3'-C3'	-7.50	108.95	120.20
53	2	20(A)	U	P-O3'-C3'	-7.44	109.03	120.20
5	7	80	U	P-O3'-C3'	-7.41	109.08	120.20
54	5	452	A	P-O3'-C3'	-7.38	109.13	120.20
54	5	455	C	P-O3'-C3'	-7.37	109.14	120.20
16	K	1487	A	P-O3'-C3'	-7.37	109.15	120.20
54	5	450	G	P-O3'-C3'	-7.37	109.15	120.20
54	5	3654	G	P-O3'-C3'	-7.35	109.18	120.20
16	K	1517	G	P-O3'-C3'	-7.34	109.19	120.20
16	K	1271	C	P-O3'-C3'	-7.32	109.22	120.20
16	K	387	C	P-O3'-C3'	-7.31	109.23	120.20
16	K	1627	C	P-O3'-C3'	-7.30	109.24	120.20
54	5	1294	A	P-O3'-C3'	-7.29	109.26	120.20
54	5	695	G	P-O3'-C3'	-7.26	109.31	120.20
16	K	1110	G	P-O3'-C3'	-7.26	109.31	120.20
54	5	4445	U	P-O3'-C3'	-7.26	109.31	120.20
54	5	2741	U	P-O3'-C3'	-7.26	109.32	120.20
16	K	1626	C	P-O3'-C3'	-7.25	109.32	120.20
16	K	1269	G	P-O3'-C3'	-7.23	109.36	120.20
16	K	1056	U	P-O3'-C3'	-7.23	109.36	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	5	4758	U	P-O3'-C3'	-7.21	109.39	120.20
16	K	670	A	P-O3'-C3'	-7.19	109.41	120.20
16	K	372	U	P-O3'-C3'	-7.18	109.43	120.20
54	5	4669	A	P-O3'-C3'	-7.18	109.43	120.20
54	5	2739	C	P-O3'-C3'	-7.15	109.47	120.20
54	5	5050	C	P-O3'-C3'	-7.15	109.47	120.20
16	K	1625	U	P-O3'-C3'	-7.15	109.47	120.20
54	5	453	G	P-O3'-C3'	-7.12	109.52	120.20
16	K	1061	U	P-O3'-C3'	-7.11	109.54	120.20
54	5	345	C	P-O3'-C3'	-7.07	109.60	120.20
54	5	328	A	P-O3'-C3'	-7.05	109.63	120.20
54	5	4671	C	P-O3'-C3'	-7.03	109.66	120.20
54	5	4759	C	P-O3'-C3'	-7.01	109.69	120.20
54	5	4447	C	P-O3'-C3'	-6.99	109.72	120.20
54	5	325	U	P-O3'-C3'	-6.97	109.74	120.20
54	5	1293	G	P-O3'-C3'	-6.94	109.80	120.20
54	5	346	G	P-O3'-C3'	-6.92	109.82	120.20
54	5	100	C	P-O3'-C3'	-6.90	109.85	120.20
54	5	1295	U	P-O3'-C3'	-6.89	109.87	120.20
16	K	665	G	P-O3'-C3'	-6.86	109.91	120.20
54	5	4762	A	P-O3'-C3'	-6.84	109.94	120.20
54	5	1290	G	P-O3'-C3'	-6.83	109.95	120.20
5	7	83	A	P-O3'-C3'	-6.83	109.95	120.20
16	K	367	U	P-O3'-C3'	-6.80	110.00	120.20
16	K	1059	G	P-O3'-C3'	-6.80	110.00	120.20
16	K	1452	A	P-O3'-C3'	-6.80	110.00	120.20
54	5	99	A	P-O3'-C3'	-6.80	110.00	120.20
16	K	1621	U	P-O3'-C3'	-6.77	110.04	120.20
54	5	327	U	P-O3'-C3'	-6.76	110.06	120.20
54	5	4761	G	P-O3'-C3'	-6.76	110.06	120.20
16	K	1113	A	P-O3'-C3'	-6.75	110.07	120.20
16	K	392	A	P-O3'-C3'	-6.75	110.08	120.20
54	5	2740	U	P-O3'-C3'	-6.74	110.10	120.20
16	K	1058	A	P-O3'-C3'	-6.69	110.16	120.20
54	5	1639	U	P-O3'-C3'	-6.68	110.18	120.20
16	K	666	U	P-O3'-C3'	-6.63	110.25	120.20
54	5	3652	A	P-O3'-C3'	-6.62	110.27	120.20
54	5	5048	A	P-O3'-C3'	-6.60	110.30	120.20
53	2	22	G	P-O3'-C3'	-6.57	110.35	120.20
54	5	347	A	P-O3'-C3'	-6.55	110.38	120.20
54	5	4446	U	P-O3'-C3'	-6.52	110.42	120.20
54	5	1292	C	P-O3'-C3'	-6.50	110.45	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	K	1489	A	P-O3'-C3'	-6.38	110.62	120.20
54	5	4757	C	P-O3'-C3'	-6.35	110.68	120.20
54	5	2738	C	P-O3'-C3'	-6.34	110.68	120.20
16	K	668	A	P-O3'-C3'	-6.32	110.72	120.20
16	K	1063	C	P-O3'-C3'	-6.31	110.74	120.20
54	5	5046	U	P-O3'-C3'	-6.28	110.78	120.20
16	K	671	A	P-O3'-C3'	-6.28	110.78	120.20
53	2	21	A	P-O3'-C3'	-6.20	110.90	120.20
54	5	1281	G	P-O3'-C3'	-6.19	110.92	120.20
16	K	667	U	P-O3'-C3'	-6.16	110.96	120.20
54	5	1279	A	P-O3'-C3'	-6.13	111.00	120.20
54	5	2742	G	P-O3'-C3'	-6.11	111.03	120.20
16	K	1521	C	P-O3'-C3'	-6.08	111.07	120.20
54	5	4668	U	P-O3'-C3'	-6.08	111.08	120.20
16	K	669	A	P-O3'-C3'	-6.03	111.16	120.20
16	K	1519	U	P-O3'-C3'	-5.87	111.40	120.20
16	K	672	A	P-O3'-C3'	-5.84	111.44	120.20
16	K	1522	A	P-O3'-C3'	-5.79	111.52	120.20
54	5	1640	C	P-O3'-C3'	-5.78	111.54	120.20
16	K	1622	U	P-O3'-C3'	-5.76	111.55	120.20
54	5	3653	A	P-O3'-C3'	-5.73	111.61	120.20
54	5	1280	C	P-O3'-C3'	-5.60	111.81	120.20
54	5	1289	C	P-O3'-C3'	-5.56	111.86	120.20
54	5	4670	C	P-O3'-C3'	-5.56	111.86	120.20
16	K	1060	A	P-O3'-C3'	-5.55	111.87	120.20
54	5	1282	G	P-O3'-C3'	-5.50	111.95	120.20
54	5	5047	C	P-O3'-C3'	-5.49	111.96	120.20
16	K	1109	C	P-O3'-C3'	-5.40	112.10	120.20
16	K	393	U	P-O3'-C3'	-5.36	112.16	120.20
54	5	5043	A	P-O3'-C3'	-5.32	112.21	120.20
16	K	1486	A	P-O3'-C3'	-5.31	112.24	120.20
16	K	1451	G	P-O3'-C3'	-5.22	112.38	120.20
16	K	1454	A	P-O3'-C3'	-5.19	112.42	120.20
16	K	1266	C	P-O3'-C3'	-5.04	112.63	120.20
16	K	293	C	P-O3'-C3'	-5.02	112.67	120.20

There are no chirality outliers.

There are no planarity outliers.

## 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	m	419	0	452	8	0
2	0	498	0	506	10	0
3	4	128	0	65	0	0
4	6	2436	0	2393	38	0
5	7	2558	0	1296	29	0
6	9	459	0	452	15	0
7	A	1898	0	1993	43	0
8	B	3172	0	3310	57	0
9	C	2883	0	3053	46	0
10	D	2391	0	2424	41	0
11	F	1875	0	1995	38	0
12	G	1879	0	2025	32	0
13	H	1516	0	1597	20	0
14	I	1664	0	1712	21	0
15	J	1362	0	1399	24	0
16	K	36101	0	18235	587	0
17	L	1700	0	1808	28	0
18	M	1137	0	1211	22	0
19	N	1701	0	1749	38	0
20	O	1630	0	1778	33	0
21	P	1242	0	1274	12	0
22	Q	1515	0	1634	24	0
23	R	1507	0	1658	22	0
24	S	1457	0	1492	21	0
25	T	1298	0	1366	27	0
26	U	874	0	885	19	0
27	V	979	0	1039	13	0
28	W	860	0	903	13	0
29	X	967	0	1040	14	0
30	Y	1115	0	1205	18	0
31	Z	1107	0	1182	15	0
32	a	1162	0	1209	20	0
33	c	761	0	794	5	0
34	d	888	0	930	8	0
35	e	1058	0	1156	15	0
36	f	876	0	912	22	0
37	g	906	0	998	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	h	1013	0	1147	14	0
39	i	830	0	914	4	0
40	j	705	0	737	13	0
41	k	568	0	630	6	0
42	l	447	0	480	8	0
43	n	239	0	289	3	0
44	o	858	0	919	13	0
45	p	708	0	757	12	0
46	q	1710	0	1711	28	0
47	r	994	0	1051	16	0
48	u	1729	0	1803	31	0
49	v	1718	0	1816	34	0
50	w	1755	0	1849	31	0
51	x	2070	0	2174	37	0
52	z	1923	0	2089	37	0
53	2	1614	0	822	30	0
54	5	74394	0	37589	1023	0
55	8	3208	0	1629	39	0
56	E	1697	0	1849	29	0
57	b	848	0	920	11	0
58	y	1464	0	1516	19	0
59	BB	1471	0	1563	18	0
60	CC	1686	0	1772	30	0
61	DD	1525	0	1640	33	0
62	SS	802	0	824	20	0
63	EE	1175	0	1249	16	0
64	RR	908	0	939	14	0
65	QQ	1202	0	1289	15	0
66	MM	1004	0	1023	24	0
67	WW	1009	0	1059	23	0
68	UU	1124	0	1193	13	0
69	KK	1068	0	1121	12	0
70	II	1172	0	1229	15	0
71	PP	1097	0	1130	18	0
72	GG	795	0	862	19	0
73	HH	637	0	632	7	0
74	TT	1034	0	1080	19	0
75	VV	1098	0	1167	23	0
76	NN	1011	0	1083	22	0
77	OO	585	0	640	8	0
78	LL	816	0	867	10	0
79	JJ	651	0	672	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
80	FF	488	0	514	11	0
81	AA	443	0	492	10	0
82	EF	854	0	905	15	0
83	EG	513	0	552	10	0
84	EH	245	0	201	2	0
85	LL	1	0	0	0	0
85	g	1	0	0	0	0
85	j	1	0	0	0	0
85	m	1	0	0	0	0
85	o	1	0	0	0	0
85	p	1	0	0	0	0
86	5	186	0	0	0	0
86	7	6	0	0	0	0
86	8	6	0	0	0	0
86	A	1	0	0	0	0
86	B	1	0	0	0	0
86	I	1	0	0	0	0
86	K	76	0	0	0	0
86	P	2	0	0	0	0
86	PP	1	0	0	0	0
86	V	1	0	0	0	0
86	a	1	0	0	0	0
86	g	1	0	0	0	0
86	j	2	0	0	0	0
All	All	211175	0	157519	2731	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 8.

All (2731) 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)
54:5:4887:C:H42	54:5:4932:U:H3	1.11	0.96
54:5:1083:U:H3	54:5:1216:C:H42	1.16	0.94
26:U:99:TRP:HE1	82:EF:15:GLN:HB2	1.36	0.89
54:5:3710:G:H22	54:5:3740:G:H1	1.23	0.87
9:C:323:ARG:HG3	54:5:1280:C:H2'	1.57	0.85
50:w:42:THR:HG23	50:w:43:PRO:HD2	1.58	0.84
16:K:957:A:H3'	16:K:958:G:H21	1.44	0.83
16:K:1276:A:H62	16:K:1321:G:H21	1.25	0.81
54:5:4094:G:H3'	54:5:4095:G:H5''	1.62	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:5:4095:G:H1	54:5:4113:U:H3	1.30	0.80
16:K:1652:G:H1	16:K:1672:U:H3	1.29	0.79
16:K:1058:A:H2'	16:K:1059:G:C8	2.19	0.78
54:5:2845:A:H61	54:5:3843:C:H42	1.32	0.77
14:I:38:ARG:HD3	14:I:83:ASP:HB2	1.66	0.76
54:5:4887:C:N4	54:5:4932:U:H3	1.85	0.75
16:K:568:C:H42	16:K:582:U:H3	1.33	0.75
50:w:42:THR:CG2	50:w:43:PRO:HD2	2.16	0.75
11:F:152:LEU:HD11	11:F:243:ILE:HD11	1.68	0.74
9:C:195:LYS:NZ	55:8:21:C:OP1	2.21	0.74
54:5:982:U:H3	54:5:1273:G:H1	1.36	0.74
71:PP:124:THR:HG23	71:PP:127:GLY:H	1.53	0.73
54:5:4635:A:H8	54:5:5048:A:H61	1.37	0.73
24:S:34:ALA:HB1	24:S:39:VAL:HG23	1.72	0.72
9:C:323:ARG:NH2	54:5:976:G:N3	2.37	0.72
16:K:377:G:H5'	60:CC:98:LYS:HB3	1.71	0.72
54:5:2557:G:H1	54:5:2570:U:H3	1.36	0.72
54:5:3641:U:OP2	54:5:3646:A:N6	2.22	0.72
7:A:215:ASN:ND2	54:5:4546:A:N7	2.39	0.71
54:5:4949:G:H4'	54:5:4950:U:H5'	1.72	0.71
54:5:1083:U:H3	54:5:1216:C:N4	1.87	0.71
16:K:1401:A:H4'	72:GG:52:GLY:HA3	1.73	0.71
56:E:70:LEU:HD23	56:E:73:ARG:HD3	1.70	0.70
16:K:928:G:H2'	16:K:929:G:C8	2.27	0.70
40:j:63:ARG:NH2	55:8:58:G:O6	2.25	0.70
45:p:4:ARG:NH2	54:5:1555:G:O6	2.24	0.70
16:K:1057:C:H1'	16:K:1060:A:H2	1.57	0.70
16:K:1729:U:H3	16:K:1805:G:H1	1.40	0.70
54:5:2489:C:O2'	54:5:2491:C:N4	2.24	0.70
54:5:2457:G:H21	54:5:3672:G:H21	1.37	0.70
75:VV:107:ARG:HB3	75:VV:110:HIS:HB3	1.74	0.69
53:2:23:C:H2'	53:2:24:A:C8	2.26	0.69
16:K:1477:U:OP2	69:KK:3:ARG:NH2	2.26	0.69
50:w:177:LEU:HD23	50:w:179:GLN:HE22	1.56	0.69
12:G:111:PRO:HD2	12:G:114:ILE:HD12	1.75	0.69
21:P:135:ARG:NH2	54:5:1596:U:O2'	2.25	0.69
54:5:1187:G:OP2	54:5:1187:G:N2	2.25	0.69
16:K:639:C:H5''	81:AA:114:ARG:HH22	1.58	0.69
58:y:71:ARG:NH2	58:y:148:ASN:OD1	2.26	0.69
82:EF:7:ASN:H	82:EF:10:LYS:HD3	1.58	0.69
8:B:249:ARG:NH1	54:5:2837:U:OP1	2.25	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:v:196:ILE:HB	49:v:223:TYR:HB2	1.75	0.68
7:A:117:GLU:HB2	7:A:162:ASN:HB2	1.75	0.68
54:5:1332:C:H2'	54:5:1333:A:H8	1.57	0.68
54:5:4098:A:H2'	54:5:4099:G:H8	1.58	0.68
54:5:2647:A:H62	54:5:2686:G:H8	1.42	0.68
54:5:4097:G:N2	54:5:4112:C:O2	2.25	0.68
7:A:6:ARG:HH12	7:A:199:VAL:H	1.38	0.68
54:5:4949:G:H5'	54:5:4951:G:H5'	1.75	0.68
82:EF:62:VAL:HG22	83:EG:96:ILE:HG13	1.75	0.68
8:B:57:VAL:HG22	8:B:73:VAL:HG12	1.75	0.68
8:B:246:ARG:NH2	54:5:4525:C:OP1	2.27	0.68
13:H:71:ARG:HE	54:5:4691:A:H5'	1.59	0.68
54:5:64:A:H1'	54:5:76:A:H1'	1.74	0.68
5:7:49:A:H5''	10:D:224:SER:HB3	1.75	0.68
16:K:1599:U:OP2	77:OO:46:ASN:ND2	2.26	0.68
46:q:210:ILE:HD13	69:KK:81:ARG:HD3	1.76	0.68
23:R:114:LYS:O	23:R:146:LYS:NZ	2.24	0.68
62:SS:3:MET:SD	62:SS:8:ARG:NH2	2.67	0.67
16:K:555:A:OP1	81:AA:98:LYS:NZ	2.26	0.67
54:5:981:C:H42	54:5:1274:A:H61	1.42	0.67
54:5:3809:G:OP2	54:5:3809:G:N2	2.23	0.67
35:e:98:LYS:NZ	54:5:2324:C:O2'	2.24	0.67
49:v:75:ILE:HD12	49:v:81:ILE:HD11	1.77	0.67
66:MM:34:PHE:HB3	66:MM:41:PHE:HB2	1.76	0.67
74:TT:11:LEU:HD12	74:TT:74:VAL:HB	1.77	0.67
16:K:167:G:O2'	28:W:80:ARG:NH2	2.28	0.67
15:J:58:ARG:NH2	53:2:57:G:O2'	2.28	0.67
36:f:100:ARG:NH1	54:5:4753:U:OP1	2.28	0.67
54:5:481:G:OP1	54:5:2094:C:N4	2.28	0.67
54:5:4635:A:H2	54:5:4663:G:H21	1.43	0.66
54:5:286:U:OP2	54:5:296:A:N6	2.28	0.66
35:e:36:ARG:NH2	54:5:2322:G:OP1	2.29	0.66
36:f:7:CYS:HB2	36:f:103:VAL:HG13	1.77	0.66
54:5:664:G:O2'	54:5:668:C:N4	2.25	0.66
64:RR:58:GLU:HB3	64:RR:61:TYR:HB3	1.76	0.66
35:e:36:ARG:NH1	54:5:1661:C:OP1	2.27	0.66
53:2:31:G:H1	53:2:39:U:H3	1.43	0.66
54:5:181:C:H2'	54:5:182:G:C8	2.31	0.66
16:K:532:C:H2'	16:K:533:A:C8	2.31	0.66
16:K:677:G:H21	16:K:1028:A:H62	1.44	0.66
61:DD:170:PRO:O	61:DD:175:ARG:NH1	2.29	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:u:122:GLU:O	48:u:165:ARG:NH1	2.28	0.66
8:B:56:ILE:HG13	8:B:365:LEU:HD22	1.77	0.66
35:e:115:VAL:HG13	35:e:120:ILE:HB	1.77	0.66
54:5:2492:C:H2'	54:5:2493:G:H8	1.61	0.66
4:6:174:VAL:HB	4:6:188:HIS:HB2	1.76	0.65
17:L:23:ALA:HB3	19:N:199:GLN:OE1	1.96	0.65
54:5:2745:A:H2'	54:5:2746:A:H8	1.62	0.65
77:OO:98:LYS:HE3	77:OO:112:ASN:HA	1.78	0.65
48:u:146:ARG:HB2	48:u:149:GLN:HB2	1.78	0.65
54:5:4119:C:O2'	54:5:4120:U:O2	2.14	0.65
58:y:155:CYS:SG	58:y:159:ARG:NH2	2.69	0.65
4:6:127:LYS:HE3	4:6:148:SER:HA	1.77	0.65
7:A:27:ALA:O	7:A:128:ARG:NH2	2.29	0.65
19:N:90:ASN:ND2	54:5:3928:A:OP1	2.29	0.65
48:u:52:THR:HG22	48:u:58:ALA:H	1.61	0.65
50:w:132:LYS:HD3	50:w:156:LEU:HD23	1.77	0.65
58:y:199:VAL:O	58:y:203:ASN:ND2	2.29	0.65
7:A:147:ARG:HG2	7:A:157:VAL:HG22	1.78	0.65
10:D:83:LEU:HB3	10:D:88:VAL:HB	1.78	0.65
16:K:183:G:O2'	16:K:184:G:O5'	2.14	0.65
29:X:81:LEU:HD13	29:X:97:VAL:HG12	1.77	0.65
26:U:101:ARG:NH1	54:5:2623:A:OP1	2.30	0.65
30:Y:8:THR:HG22	30:Y:10:ASP:H	1.62	0.65
16:K:1017:U:OP1	65:QQ:62:GLN:NE2	2.30	0.65
16:K:1670:C:H2'	16:K:1671:G:C8	2.32	0.65
16:K:981:A:H2'	16:K:982:G:C8	2.32	0.65
47:r:87:ARG:NH1	56:E:115:MET:O	2.31	0.64
6:9:52:PHE:HB3	72:GG:80:PHE:HB3	1.78	0.64
16:K:1029:G:O2'	54:5:1564:A:N6	2.26	0.64
16:K:158:A:N6	16:K:466:G:N7	2.46	0.64
54:5:669:C:HO2'	54:5:670:G:H8	1.46	0.64
56:E:160:HIS:HB3	56:E:163:LYS:HD2	1.80	0.64
66:MM:117:ARG:NH2	80:FF:62:GLU:O	2.30	0.64
83:EG:101:ASN:HB3	83:EG:131:LEU:HB3	1.78	0.64
4:6:152:SER:OG	4:6:168:CYS:SG	2.55	0.64
12:G:96:GLN:O	54:5:4124:G:N2	2.31	0.64
16:K:1228:A:H2'	16:K:1229:G:H8	1.63	0.64
29:X:47:ARG:NH1	54:5:2473:A:OP1	2.31	0.64
32:a:72:THR:HG22	32:a:110:LYS:HB3	1.79	0.64
54:5:4541:G:N2	54:5:4544:A:OP2	2.25	0.64
54:5:4594:U:H2'	54:5:4595:G:H8	1.63	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:K:1228:A:H2'	16:K:1229:G:C8	2.32	0.64
54:5:369:G:N2	54:5:372:A:OP2	2.26	0.64
46:q:140:VAL:HB	46:q:142:LEU:HD13	1.79	0.64
54:5:2579:G:N2	54:5:2582:A:OP2	2.23	0.64
54:5:4992:G:H2'	54:5:4993:G:C8	2.33	0.64
16:K:1779:G:H2'	16:K:1780:G:C8	2.33	0.64
38:h:10:ARG:NH2	55:8:65:A:O2'	2.31	0.64
38:h:66:LYS:HD3	55:8:96:C:H5''	1.80	0.64
54:5:2407:G:N2	54:5:2407:G:OP2	2.29	0.64
16:K:1456:G:H2'	16:K:1457:U:H6	1.63	0.64
16:K:1536:G:H2'	16:K:1537:A:H8	1.63	0.64
20:O:85:ARG:HG3	20:O:99:LEU:HD11	1.80	0.64
48:u:30:TRP:HZ2	66:MM:88:LEU:HD21	1.63	0.64
5:7:28:C:H1'	5:7:54:A:H61	1.63	0.64
12:G:90:LYS:NZ	54:5:4126:C:OP1	2.31	0.64
16:K:1276:A:H62	16:K:1321:G:N2	1.96	0.64
16:K:1711:U:H2'	16:K:1712:A:H8	1.61	0.64
70:II:34:LYS:HG2	70:II:103:LEU:HD23	1.80	0.64
16:K:678:U:OP2	16:K:1026:C:N4	2.31	0.63
16:K:885:U:H2'	16:K:886:A:H8	1.61	0.63
61:DD:93:LYS:HB2	61:DD:96:TYR:HD2	1.63	0.63
27:V:35:LYS:HB2	27:V:67:LYS:HG3	1.79	0.63
17:L:136:LYS:NZ	54:5:169:A:O2'	2.30	0.63
16:K:951:C:O2'	66:MM:50:LYS:NZ	2.29	0.63
16:K:1456:G:H2'	16:K:1457:U:C6	2.34	0.63
25:T:35:LYS:HE3	54:5:1824:G:H5''	1.81	0.63
12:G:87:LYS:HG2	12:G:89:PRO:HD3	1.79	0.63
45:p:7:LYS:HE3	54:5:2875:C:H5''	1.80	0.63
54:5:2759:G:O2'	54:5:2762:G:N2	2.32	0.63
56:E:261:LEU:HD12	56:E:264:ILE:HD11	1.81	0.63
41:k:33:LYS:HG2	41:k:46:VAL:HG12	1.80	0.63
54:5:651:C:H2'	54:5:652:G:H8	1.64	0.63
9:C:269:LYS:HD2	54:5:655:C:H5'	1.79	0.63
28:W:93:LYS:O	28:W:101:ARG:NH2	2.31	0.63
31:Z:79:HIS:HD1	54:5:2580:U:HO2'	1.46	0.63
46:q:54:THR:HG22	46:q:162:PRO:HG2	1.79	0.63
63:EE:35:ARG:NH1	63:EE:53:GLY:O	2.31	0.63
10:D:65:ALA:HB2	10:D:74:ILE:HD13	1.80	0.63
16:K:371:A:OP2	60:CC:10:LYS:HB2	1.98	0.63
26:U:66:SER:HB2	26:U:69:LYS:HB3	1.81	0.63
51:x:100:ARG:HB2	51:x:114:ILE:HD13	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:B:13:SER:HB2	54:5:4622:A:H4'	1.81	0.63
11:F:104:VAL:HG13	11:F:135:VAL:HG12	1.80	0.63
13:H:94:SER:HB3	13:H:142:ASP:HB3	1.79	0.63
54:5:1188:C:H2'	54:5:1189:G:H8	1.63	0.63
54:5:2093:G:H4'	54:5:2094:C:H5'	1.79	0.63
9:C:339:THR:HG22	9:C:342:ARG:HH12	1.62	0.62
16:K:925:G:H1	16:K:1017:U:H3	1.46	0.62
37:g:6:THR:HG22	54:5:2400:G:H21	1.64	0.62
16:K:1781:A:H2'	16:K:1782:G:H8	1.64	0.62
20:O:72:HIS:O	20:O:74:ARG:NH1	2.32	0.62
23:R:133:LYS:H	23:R:137:ILE:HD11	1.63	0.62
54:5:4758:U:O5'	54:5:4758:U:O2	2.18	0.62
32:a:76:ASP:HB3	32:a:115:GLY:HA3	1.82	0.62
62:SS:3:MET:SD	62:SS:3:MET:N	2.72	0.62
9:C:149:GLU:HG2	9:C:151:PRO:HD2	1.82	0.62
16:K:561:A:HO2'	61:DD:134:HIS:HE2	1.45	0.62
16:K:1365:G:N2	16:K:1462:U:O4	2.31	0.62
54:5:4635:A:H8	54:5:5048:A:N6	1.97	0.62
59:BB:143:ARG:HB2	59:BB:155:LYS:HB2	1.80	0.62
33:c:28:VAL:HG21	33:c:37:MET:HG3	1.82	0.62
64:RR:85:LEU:HD22	64:RR:106:CYS:HB3	1.81	0.62
52:z:64:LYS:HB2	52:z:97:VAL:HG11	1.82	0.62
54:5:976:G:H1	54:5:1279:A:H2	1.48	0.62
7:A:183:GLY:HA2	54:5:1613:A:H5''	1.81	0.62
16:K:642:U:O2'	16:K:643:A:O5'	2.17	0.62
16:K:1113:A:H2'	16:K:1114:U:C6	2.35	0.62
17:L:42:ARG:NH2	17:L:51:ALA:O	2.33	0.62
17:L:116:ARG:NH2	17:L:155:MET:O	2.32	0.62
54:5:2845:A:H61	54:5:3843:C:N4	1.97	0.62
58:y:59:LYS:HB3	58:y:62:ARG:HB2	1.82	0.62
16:K:1650:A:H5''	68:UU:139:ALA:HB2	1.82	0.62
49:v:192:LEU:HB3	49:v:227:ARG:HB3	1.81	0.62
54:5:2587:A:OP2	54:5:2588:C:N4	2.33	0.62
54:5:2777:G:H5''	54:5:2778:G:H5'	1.81	0.62
59:BB:46:THR:HG23	59:BB:65:PRO:HG3	1.82	0.62
10:D:275:GLN:HE21	54:5:1187:G:H1'	1.64	0.61
15:J:32:ARG:HD2	15:J:35:ARG:HH21	1.65	0.61
16:K:1611:G:OP2	70:II:121:ARG:NH2	2.34	0.61
32:a:117:LEU:HB3	32:a:140:VAL:HG21	1.82	0.61
54:5:1802:A:H5''	54:5:1803:G:H5'	1.82	0.61
5:7:7:G:OP1	10:D:33:ARG:NH1	2.33	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:F:178:LEU:HB3	11:F:183:ILE:HB	1.82	0.61
17:L:56:ARG:O	17:L:116:ARG:NH1	2.33	0.61
6:9:44:ARG:NH1	72:GG:78:ASP:OD2	2.30	0.61
23:R:3:MET:HE1	23:R:5:ARG:HD3	1.82	0.61
64:RR:83:LYS:HE3	64:RR:103:VAL:HG13	1.82	0.61
7:A:128:ARG:NH1	54:5:3681:G:OP2	2.33	0.61
16:K:1781:A:H2'	16:K:1782:G:C8	2.35	0.61
23:R:102:LEU:HD22	23:R:138:LEU:HD13	1.81	0.61
27:V:50:ASN:ND2	54:5:4457:U:OP1	2.32	0.61
54:5:4967:A:H2'	54:5:4968:A:H8	1.65	0.61
2:0:138:ARG:HH21	16:K:1293:A:H1'	1.66	0.61
11:F:85:GLU:HB2	25:T:135:PRO:HB3	1.82	0.61
23:R:100:ARG:NE	54:5:2667:C:OP1	2.32	0.61
9:C:321:ASN:ND2	54:5:715:G:OP1	2.34	0.61
15:J:111:GLU:OE2	70:II:14:ARG:NH2	2.33	0.61
16:K:482:G:N1	16:K:485:A:OP2	2.32	0.61
16:K:1259:A:H1'	16:K:1264:C:H42	1.66	0.61
35:e:16:TRP:NE1	35:e:18:LYS:O	2.34	0.61
36:f:58:VAL:O	54:5:4944:C:N4	2.34	0.61
47:r:39:ARG:NH1	54:5:2266:C:O2'	2.34	0.61
16:K:319:C:H2'	16:K:320:G:H8	1.65	0.61
16:K:639:C:H2'	16:K:640:A:H8	1.64	0.61
16:K:1550:G:H3'	16:K:1579:A:H61	1.66	0.61
22:Q:14:ARG:NH2	54:5:2083:C:OP2	2.34	0.61
34:d:26:THR:HG23	54:5:4996:C:H4'	1.81	0.61
50:w:127:MET:HE1	50:w:133:GLY:HA2	1.82	0.61
54:5:956:A:H1'	54:5:2076:G:H5''	1.83	0.61
54:5:1548:G:O2'	54:5:2812:A:N3	2.34	0.61
54:5:4872:G:H4'	54:5:4873:G:H5'	1.82	0.61
16:K:1014:G:N2	79:JJ:51:GLN:OE1	2.34	0.61
70:II:20:ILE:HD11	70:II:33:ILE:HG13	1.83	0.61
14:I:30:LYS:HD2	14:I:63:GLU:HG3	1.82	0.60
16:K:528:A:H2'	16:K:529:A:H8	1.64	0.60
27:V:57:VAL:HG11	27:V:122:ALA:HB3	1.82	0.60
30:Y:89:LYS:HD2	30:Y:91:ASN:HD21	1.66	0.60
33:c:50:ASN:ND2	33:c:75:SER:O	2.33	0.60
54:5:1177:U:H2'	54:5:1178:G:H8	1.66	0.60
2:0:138:ARG:NH2	16:K:1292:C:N3	2.49	0.60
8:B:216:MET:HE2	8:B:283:LYS:HE2	1.83	0.60
9:C:274:LYS:NZ	54:5:1375:C:OP1	2.34	0.60
24:S:164:LYS:HB3	24:S:165:PRO:HD3	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:a:32:ARG:HD2	54:5:37:U:H4'	1.82	0.60
54:5:1857:C:H2'	54:5:1858:A:H8	1.64	0.60
54:5:2318:G:N2	54:5:2321:G:OP2	2.26	0.60
16:K:1299:A:O2'	67:WW:52:LYS:NZ	2.33	0.60
31:Z:89:ILE:HD11	31:Z:117:LYS:HB3	1.84	0.60
54:5:1332:C:H2'	54:5:1333:A:C8	2.35	0.60
54:5:4238:G:H2'	54:5:4239:A:H8	1.67	0.60
61:DD:128:VAL:O	61:DD:132:GLN:NE2	2.32	0.60
8:B:95:THR:HG22	54:5:4910:A:H4'	1.82	0.60
9:C:65:GLU:OE1	9:C:80:ARG:NH1	2.35	0.60
10:D:15:ARG:HH11	54:5:1743:A:H1'	1.66	0.60
16:K:116:U:H3	16:K:347:G:H22	1.47	0.60
47:r:28:GLU:HB2	47:r:31:ASN:HB2	1.82	0.60
58:y:18:LYS:NZ	58:y:46:ALA:O	2.35	0.60
1:m:74:TYR:O	54:5:4472:G:O2'	2.20	0.60
54:5:408:A:H4'	54:5:409:G:H3'	1.83	0.60
54:5:450:G:H2'	54:5:450:G:N3	2.16	0.60
54:5:521:C:H42	54:5:640:C:H42	1.49	0.60
54:5:1763:C:H2'	54:5:1764:G:C4	2.36	0.60
57:b:19:ASN:O	57:b:22:LYS:NZ	2.34	0.60
16:K:64:A:H2	16:K:83:A:H62	1.50	0.60
16:K:145:G:H2'	16:K:146:G:C8	2.36	0.60
42:l:21:ARG:HG2	42:l:22:PRO:HD2	1.84	0.60
54:5:1503:A:H4'	54:5:1504:G:H5'	1.83	0.60
61:DD:138:ARG:NH2	61:DD:152:ASP:OD2	2.35	0.60
7:A:179:ILE:HG23	7:A:184:ARG:HB2	1.82	0.60
18:M:117:LYS:NZ	54:5:4929:C:OP1	2.34	0.60
19:N:193:ARG:NH2	54:5:28:C:OP2	2.32	0.60
54:5:2587:A:H5'	54:5:2770:C:H5'	1.82	0.60
54:5:4098:A:H2'	54:5:4099:G:C8	2.36	0.60
72:GG:20:ILE:HD13	72:GG:98:VAL:HG21	1.82	0.60
54:5:4274:A:H2'	54:5:4275:G:H8	1.67	0.60
16:K:894:G:H2'	16:K:895:G:C8	2.36	0.60
16:K:896:U:H2'	16:K:897:U:C6	2.37	0.60
16:K:1373:C:O2'	69:KK:10:LYS:NZ	2.35	0.60
54:5:175:C:H2'	54:5:176:G:H8	1.67	0.60
54:5:181:C:H2'	54:5:182:G:H8	1.65	0.60
64:RR:79:VAL:HG11	64:RR:85:LEU:HD12	1.83	0.60
67:WW:33:LEU:HD12	67:WW:36:LEU:HD12	1.82	0.60
4:6:244:ASN:ND2	4:6:294:ASP:O	2.35	0.59
16:K:77:A:H1'	52:z:176:ILE:HG12	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:K:1617:G:O6	67:WW:43:ARG:NH1	2.35	0.59
18:M:117:LYS:NZ	54:5:4882:U:OP1	2.34	0.59
54:5:4174:U:H2'	54:5:4175:G:H8	1.67	0.59
56:E:49:ASN:HB3	56:E:64:MET:HE3	1.83	0.59
62:SS:92:ALA:HA	62:SS:95:ARG:HE	1.66	0.59
11:F:46:ARG:HE	11:F:49:ILE:HD11	1.66	0.59
16:K:1523:C:H2'	16:K:1524:G:H8	1.66	0.59
52:z:54:GLY:O	52:z:110:ASN:ND2	2.36	0.59
54:5:447:C:OP1	54:5:449:C:N4	2.35	0.59
54:5:2704:C:H2'	54:5:2705:G:C8	2.37	0.59
19:N:114:ARG:NH1	19:N:153:LYS:O	2.32	0.59
26:U:65:ARG:HG3	26:U:70:ILE:HG12	1.85	0.59
32:a:132:ARG:NH2	54:5:1468:C:OP1	2.31	0.59
54:5:2638:G:N1	54:5:2718:U:H2'	2.17	0.59
7:A:49:ILE:HD13	7:A:60:LYS:HE3	1.83	0.59
10:D:40:ASP:HB2	10:D:43:LYS:HG2	1.83	0.59
54:5:2587:A:O2'	54:5:2588:C:O4'	2.20	0.59
54:5:2601:A:N6	54:5:2744:A:OP2	2.36	0.59
54:5:4537:C:H2'	54:5:4538:G:H8	1.66	0.59
54:5:4896:G:N2	54:5:4927:G:O6	2.35	0.59
1:m:88:LYS:NZ	54:5:4485:C:O2'	2.36	0.59
11:F:28:LYS:HA	11:F:31:ARG:HD2	1.83	0.59
16:K:1091:C:HO2'	74:TT:2:VAL:N	2.00	0.59
16:K:1658:G:OP2	16:K:1660:C:N4	2.35	0.59
29:X:73:HIS:HD2	29:X:112:ALA:HA	1.66	0.59
36:f:19:ARG:NH2	54:5:1887:G:OP2	2.36	0.59
56:E:96:THR:HG22	56:E:109:VAL:HG22	1.85	0.59
67:WW:28:MET:HG3	67:WW:32:GLN:HG3	1.83	0.59
75:VV:134:TYR:O	81:AA:86:ARG:NH2	2.36	0.59
18:M:100:ARG:NH2	20:O:197:LYS:O	2.34	0.59
44:o:63:THR:O	44:o:87:ARG:NH2	2.35	0.59
7:A:220:GLY:O	54:5:3749:C:O2'	2.21	0.59
16:K:74:G:N2	16:K:78:C:OP2	2.36	0.59
16:K:1298:G:OP2	67:WW:77:LYS:NZ	2.29	0.59
66:MM:30:VAL:HG12	66:MM:94:HIS:HB2	1.84	0.59
16:K:1536:G:H2'	16:K:1537:A:C8	2.38	0.59
16:K:1759:G:H2'	16:K:1760:G:C8	2.38	0.59
23:R:103:ARG:NH1	23:R:124:TYR:OH	2.36	0.59
54:5:126:C:H2'	54:5:127:G:H8	1.68	0.59
54:5:1283:G:N1	54:5:2076:G:OP1	2.34	0.59
58:y:167:LYS:HG2	58:y:171:GLU:HG3	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
67:WW:18:ARG:NH1	70:II:88:LYS:O	2.35	0.59
16:K:311:C:H5''	16:K:312:G:H5''	1.84	0.59
16:K:1194:A:OP1	75:VV:60:LYS:NZ	2.36	0.59
49:v:70:VAL:HG11	49:v:93:ILE:HG12	1.84	0.59
54:5:189:G:H2'	54:5:190:G:H8	1.67	0.59
54:5:504:G:O2'	54:5:505:G:H8	1.85	0.59
54:5:654:C:H2'	54:5:655:C:H6	1.67	0.59
54:5:4274:A:H2'	54:5:4275:G:C8	2.38	0.59
54:5:4527:G:OP2	54:5:4527:G:N2	2.31	0.59
60:CC:69:SER:HB2	63:EE:21:LYS:HD3	1.84	0.59
12:G:139:VAL:HG21	12:G:238:LYS:HG3	1.84	0.59
16:K:1264:C:N3	16:K:1518:C:H5	2.01	0.59
54:5:700:G:H2'	54:5:701:G:H8	1.68	0.59
54:5:1329:G:H2'	54:5:3865:A:H5'	1.85	0.59
18:M:96:GLU:OE2	18:M:100:ARG:NH1	2.36	0.58
19:N:68:ARG:NH2	54:5:303:C:OP2	2.36	0.58
23:R:160:GLU:OE1	23:R:163:ARG:NH2	2.36	0.58
31:Z:36:ARG:NH1	31:Z:38:TYR:OH	2.33	0.58
35:e:7:LEU:HB2	35:e:93:LYS:HB3	1.84	0.58
47:r:10:VAL:HG13	47:r:14:SER:HB3	1.84	0.58
51:x:90:ILE:HG23	51:x:99:PHE:HB2	1.85	0.58
54:5:4759:C:H2'	54:5:4760:G:C8	2.38	0.58
16:K:1062:A:H5''	16:K:1062:A:H8	1.66	0.58
16:K:1275:G:N2	16:K:1506:A:OP2	2.36	0.58
40:j:82:THR:HB	55:8:94:G:H21	1.67	0.58
54:5:1604:G:H2'	54:5:1605:G:C8	2.39	0.58
54:5:2502:A:O2'	54:5:2503:G:O5'	2.16	0.58
54:5:4694:G:N2	54:5:4694:G:OP1	2.35	0.58
62:SS:84:HIS:HB2	64:RR:27:ILE:HG23	1.85	0.58
16:K:367:U:H4'	16:K:371:A:C8	2.38	0.58
16:K:388:U:H2'	16:K:389:A:C8	2.39	0.58
16:K:1621:U:O2'	16:K:1622:U:H2'	2.03	0.58
17:L:5:ARG:HH12	54:5:1849:U:H3'	1.67	0.58
83:EG:98:LYS:HB3	83:EG:102:ILE:HB	1.86	0.58
8:B:268:ARG:NH2	54:5:3896:C:O2'	2.37	0.58
16:K:293:C:O2	16:K:293:C:H2'	2.03	0.58
26:U:99:TRP:NE1	82:EF:15:GLN:HB2	2.15	0.58
27:V:13:LYS:NZ	27:V:59:ASP:OD1	2.37	0.58
48:u:82:ARG:NH2	48:u:191:ASP:OD1	2.37	0.58
54:5:2743:A:H2'	54:5:2744:A:C8	2.38	0.58
16:K:1597:C:OP2	77:OO:85:ARG:NH2	2.34	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:l:21:ARG:NH1	55:8:51:U:OP2	2.36	0.58
52:z:2:LYS:HB2	52:z:108:VAL:HG22	1.84	0.58
54:5:4754:G:N7	56:E:281:THR:OG1	2.37	0.58
54:5:4991:U:H2'	54:5:4992:G:H8	1.68	0.58
63:EE:57:ASP:HB3	63:EE:60:CYS:HB2	1.86	0.58
40:j:85:LYS:HD2	40:j:86:PRO:HD2	1.85	0.58
54:5:2411:C:H2'	54:5:2412:A:H8	1.68	0.58
54:5:4107:G:H2'	54:5:4108:G:C8	2.38	0.58
67:WW:21:ASP:OD1	67:WW:22:LEU:N	2.35	0.58
8:B:89:ILE:HG21	8:B:197:ALA:HB1	1.84	0.58
12:G:126:ARG:NE	54:5:4076:G:OP2	2.37	0.58
25:T:108:ARG:NH1	54:5:1837:A:OP1	2.37	0.58
54:5:4537:C:H2'	54:5:4538:G:C8	2.39	0.58
5:7:92:C:H2'	5:7:93:G:H8	1.68	0.58
7:A:180:LEU:HD21	45:p:26:VAL:HG21	1.86	0.58
54:5:965:G:N2	54:5:2096:G:N3	2.52	0.58
54:5:1273:G:H5''	57:b:117:ARG:HD2	1.86	0.58
54:5:4095:G:O6	54:5:4113:U:O4	2.21	0.58
54:5:4272:G:OP2	54:5:4272:G:N2	2.21	0.58
10:D:23:ARG:NH1	54:5:4280:A:OP2	2.36	0.58
16:K:895:G:H2'	16:K:896:U:C6	2.39	0.58
16:K:1284:A:HO2'	64:RR:106:CYS:HG	1.50	0.58
54:5:1097:C:H2'	54:5:1098:G:C8	2.38	0.58
54:5:2049:G:HO2'	54:5:3884:U:HO2'	1.51	0.58
59:BB:93:VAL:HG21	59:BB:133:LEU:HD13	1.85	0.58
61:DD:164:PRO:HB3	61:DD:170:PRO:HA	1.84	0.58
83:EG:97:ARG:NH1	83:EG:98:LYS:O	2.37	0.58
10:D:17:GLN:O	54:5:4265:U:N3	2.35	0.57
16:K:525:A:OP2	81:AA:101:ARG:NH1	2.37	0.57
19:N:194:ARG:O	19:N:197:THR:HG22	2.04	0.57
35:e:85:LEU:HD21	35:e:111:ILE:HG23	1.86	0.57
54:5:456:C:H2'	54:5:457:G:C8	2.38	0.57
54:5:979:C:H42	54:5:1276:C:H42	1.50	0.57
68:UU:76:GLY:H	68:UU:79:ALA:HB3	1.69	0.57
4:6:42:MET:SD	4:6:56:GLN:NE2	2.77	0.57
5:7:6:C:O2'	10:D:50:ARG:NH2	2.36	0.57
16:K:212:C:H2'	16:K:213:G:C8	2.39	0.57
16:K:1616:U:H3	16:K:1620:A:H2	1.49	0.57
53:2:33:U:OP2	68:UU:146:ARG:NH2	2.37	0.57
54:5:1484:G:O2'	54:5:1486:C:OP2	2.22	0.57
4:6:40:ILE:HB	4:6:59:LEU:HB2	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:6:87:LEU:HD21	4:6:108:VAL:HG11	1.86	0.57
16:K:206:G:O6	60:CC:144:LYS:NZ	2.37	0.57
16:K:1568:C:OP1	71:PP:96:SER:OG	2.22	0.57
54:5:651:C:H2'	54:5:652:G:C8	2.40	0.57
54:5:654:C:H2'	54:5:655:C:C6	2.38	0.57
54:5:1773:U:H2'	54:5:1774:C:C6	2.39	0.57
54:5:2411:C:O2'	54:5:2526:C:O2	2.21	0.57
12:G:250:LYS:HB3	54:5:6:C:H5''	1.87	0.57
14:I:150:GLU:OE2	14:I:153:ARG:NH2	2.38	0.57
16:K:1246:A:O2'	72:GG:72:GLU:OE2	2.22	0.57
44:o:2:VAL:N	44:o:90:HIS:O	2.37	0.57
44:o:26:TYR:HB3	44:o:67:VAL:HB	1.87	0.57
54:5:67:C:OP2	54:5:312:G:N2	2.36	0.57
54:5:1218:G:H2'	54:5:1219:G:C8	2.39	0.57
65:QQ:54:LEU:HB3	65:QQ:60:VAL:HG13	1.87	0.57
16:K:289:G:OP1	51:x:155:LYS:NZ	2.36	0.57
16:K:1293:A:N6	16:K:1294:G:O6	2.37	0.57
54:5:175:C:H2'	54:5:176:G:C8	2.39	0.57
54:5:3699:C:O2'	54:5:3775:A:O2'	2.21	0.57
54:5:4862:G:H2'	54:5:4863:G:C8	2.39	0.57
11:F:95:ARG:NH2	54:5:1895:G:OP1	2.37	0.57
16:K:429:C:O2'	16:K:811:A:N1	2.37	0.57
16:K:1221:G:O2'	16:K:1676:U:O2	2.23	0.57
20:O:72:HIS:N	54:5:4586:G:OP1	2.28	0.57
49:v:204:ILE:O	49:v:211:LYS:NZ	2.37	0.57
50:w:70:THR:HG22	50:w:86:LEU:HD13	1.86	0.57
54:5:4232:U:H4'	54:5:4233:A:O5'	2.04	0.57
56:E:156:LEU:HD11	56:E:198:ILE:HG13	1.87	0.57
11:F:221:LYS:NZ	11:F:223:THR:OG1	2.35	0.57
11:F:242:LEU:HD11	11:F:246:MET:HE3	1.87	0.57
17:L:130:LYS:HD3	17:L:131:PRO:HD2	1.87	0.57
22:Q:108:ARG:NH1	54:5:1354:A:OP1	2.37	0.57
54:5:93:G:H2'	54:5:94:A:C8	2.39	0.57
54:5:1339:U:H2'	54:5:1340:C:C6	2.40	0.57
54:5:1829:G:H21	57:b:68:ARG:HH22	1.51	0.57
83:EG:97:ARG:NH2	83:EG:101:ASN:OD1	2.38	0.57
7:A:116:LEU:HB3	7:A:126:LEU:HB2	1.85	0.57
11:F:146:LEU:O	11:F:150:ASN:ND2	2.36	0.57
16:K:127:C:O2	51:x:134:LYS:NZ	2.37	0.57
16:K:1271:C:H42	16:K:1511:U:H3	1.53	0.57
16:K:1487:A:H2'	16:K:1488:C:C6	2.40	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:K:1533:A:OP2	58:y:164:ARG:NH1	2.37	0.57
16:K:1869:A:N6	48:u:114:VAL:O	2.37	0.57
17:L:36:ARG:NH1	54:5:1364:U:OP2	2.38	0.57
22:Q:75:ARG:HA	22:Q:78:LYS:HE2	1.87	0.57
43:n:12:ARG:HG2	43:n:15:ARG:HH12	1.70	0.57
54:5:62:A:N3	54:5:77:U:O2'	2.31	0.57
54:5:2386:U:H2'	54:5:2387:G:H8	1.70	0.57
16:K:333:G:O6	52:z:186:GLN:NE2	2.37	0.57
16:K:924:G:H1	16:K:1018:U:H3	1.51	0.57
8:B:240:LEU:HB3	8:B:244:THR:HG21	1.85	0.57
8:B:322:HIS:O	8:B:342:LYS:NZ	2.29	0.57
27:V:41:SER:HG	54:5:4507:A:HO2'	1.53	0.57
54:5:450:G:H22	54:5:1297:U:H3	1.52	0.57
54:5:2869:U:O2'	54:5:2881:A:N7	2.36	0.57
22:Q:181:ARG:NH2	54:5:1391:A:OP1	2.31	0.56
23:R:74:ARG:NH1	54:5:2891:U:OP2	2.38	0.56
52:z:38:ALA:HA	52:z:41:LEU:HD23	1.86	0.56
54:5:4884:G:N7	56:E:275:ARG:NH2	2.53	0.56
68:UU:85:ARG:NH2	68:UU:118:THR:OG1	2.38	0.56
9:C:223:ASN:ND2	54:5:223:G:N3	2.53	0.56
13:H:115:ARG:HG2	13:H:123:ILE:HG22	1.86	0.56
16:K:551:U:H2'	16:K:552:G:C8	2.40	0.56
16:K:1621:U:O4	67:WW:82:ASP:HB3	2.05	0.56
28:W:80:ARG:NH1	52:z:129:VAL:O	2.37	0.56
54:5:1933:G:H2'	54:5:1934:A:C8	2.40	0.56
63:EE:101:ARG:HB2	75:VV:10:ALA:HB2	1.87	0.56
11:F:46:ARG:NH1	54:5:976:G:H5''	2.20	0.56
13:H:103:VAL:HG21	13:H:144:LEU:HD11	1.88	0.56
16:K:561:A:O2'	61:DD:134:HIS:NE2	2.29	0.56
16:K:1562:C:H2'	16:K:1563:G:H8	1.69	0.56
18:M:5:ARG:NE	18:M:59:ASP:OD1	2.39	0.56
19:N:93:LYS:NZ	54:5:4177:C:OP1	2.35	0.56
29:X:110:LYS:HG3	29:X:121:VAL:HB	1.87	0.56
31:Z:11:VAL:HG11	31:Z:80:LEU:HB3	1.86	0.56
40:j:55:ARG:NH2	54:5:364:G:O6	2.34	0.56
51:x:141:THR:OG1	51:x:143:ASP:OD1	2.21	0.56
54:5:3880:G:H2'	54:5:3881:G:C8	2.41	0.56
54:5:300:A:H2'	54:5:301:G:H8	1.70	0.56
54:5:2395:A:O2'	54:5:2806:A:H1'	2.05	0.56
59:BB:62:ILE:HD12	59:BB:94:PHE:HE1	1.70	0.56
16:K:107:A:H2'	16:K:108:G:C8	2.40	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:K:874:G:N3	59:BB:114:GLN:NE2	2.51	0.56
16:K:959:G:H1	66:MM:65:ASP:HB3	1.69	0.56
44:o:80:LYS:HE2	54:5:4346:U:H5''	1.87	0.56
54:5:221:C:H2'	54:5:222:C:C6	2.41	0.56
70:II:75:ARG:HH21	70:II:95:TYR:HB2	1.70	0.56
74:TT:8:ALA:HA	74:TT:74:VAL:HG11	1.86	0.56
11:F:241:ARG:NH1	54:5:941:C:OP2	2.37	0.56
16:K:128:U:H3'	16:K:129:C:H6	1.70	0.56
16:K:1033:G:N1	16:K:1080:A:O2'	2.33	0.56
5:7:27:G:N7	10:D:58:ARG:NH2	2.53	0.56
16:K:190:G:O2'	16:K:209:A:N6	2.38	0.56
16:K:1161:U:O4	75:VV:3:LYS:NZ	2.35	0.56
22:Q:15:ARG:HG3	54:5:1691:G:H5'	1.88	0.56
48:u:86:LEU:HB3	48:u:98:THR:HB	1.86	0.56
48:u:224:GLU:OE1	48:u:227:LYS:N	2.35	0.56
54:5:2409:U:H4'	54:5:2428:A:H4'	1.86	0.56
54:5:2519:U:O2'	54:5:2530:U:O2	2.24	0.56
56:E:64:MET:HG3	56:E:68:LYS:HE3	1.86	0.56
15:J:27:GLY:HA2	15:J:68:ILE:HG13	1.88	0.56
16:K:943:U:H2'	16:K:944:A:H8	1.71	0.56
16:K:1518:C:OP1	16:K:1519:U:H2'	2.06	0.56
22:Q:144:LYS:HG2	54:5:1460:C:H5''	1.88	0.56
35:e:115:VAL:HG11	35:e:122:VAL:HG13	1.88	0.56
54:5:33:A:H3'	54:5:47:A:H61	1.71	0.56
54:5:2637:U:O2'	54:5:2718:U:O2'	2.21	0.56
59:BB:87:PHE:HB3	59:BB:90:LYS:HE2	1.87	0.56
8:B:317:LEU:HB2	8:B:372:SER:HB2	1.88	0.56
16:K:152:U:H2'	16:K:153:G:C8	2.41	0.56
40:j:70:VAL:HG22	40:j:73:ARG:HH21	1.70	0.56
49:v:259:THR:HG21	73:HH:15:ARG:HA	1.87	0.56
52:z:219:GLU:OE2	52:z:223:LYS:NZ	2.39	0.56
54:5:115:C:O2'	54:5:276:C:OP1	2.22	0.56
78:LL:12:LYS:HD3	78:LL:16:GLY:H	1.70	0.56
16:K:1580:A:OP1	72:GG:86:LYS:NZ	2.37	0.56
46:q:184:ARG:HD3	46:q:191:ARG:HG3	1.88	0.56
51:x:9:LEU:HB2	51:x:30:ARG:HD3	1.87	0.56
54:5:711:A:H2'	54:5:712:C:C6	2.41	0.56
54:5:3648:A:H1'	54:5:3785:A:H61	1.71	0.56
16:K:528:A:H2'	16:K:529:A:C8	2.41	0.55
16:K:537:C:H2'	16:K:538:U:C6	2.42	0.55
19:N:123:GLU:OE1	19:N:128:LYS:NZ	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:O:89:PRO:HD3	54:5:1914:C:H4'	1.88	0.55
54:5:1169:G:H2'	54:5:1170:G:H8	1.71	0.55
6:9:14:PHE:HB2	16:K:1661:A:C8	2.41	0.55
8:B:329:ASP:OD1	8:B:329:ASP:N	2.38	0.55
9:C:78:ARG:HB3	9:C:88:GLY:HA2	1.87	0.55
16:K:1513:C:H2'	16:K:1514:G:H8	1.70	0.55
21:P:23:ARG:NH1	21:P:125:MET:SD	2.79	0.55
28:W:96:GLN:O	28:W:101:ARG:NH1	2.38	0.55
54:5:3759:A:N6	54:5:3765:G:O2'	2.39	0.55
8:B:153:MET:HG2	8:B:194:LEU:HD11	1.88	0.55
12:G:302:ARG:NH2	54:5:4075:U:OP1	2.39	0.55
14:I:4:ARG:NH1	54:5:1866:U:OP1	2.36	0.55
16:K:57:U:O2'	16:K:499:G:N3	2.38	0.55
16:K:107:A:H2'	16:K:108:G:H8	1.71	0.55
16:K:551:U:H2'	16:K:552:G:H8	1.72	0.55
16:K:897:U:H2'	16:K:898:U:C6	2.41	0.55
16:K:1103:C:H2'	16:K:1104:G:C8	2.41	0.55
27:V:13:LYS:HB2	27:V:128:LEU:HD11	1.87	0.55
65:QQ:4:MET:SD	65:QQ:124:ARG:NH1	2.79	0.55
65:QQ:99:ARG:NH2	65:QQ:119:GLU:OE2	2.39	0.55
76:NN:62:THR:HA	76:NN:69:THR:HG22	1.88	0.55
16:K:5:U:H2'	16:K:6:G:H8	1.72	0.55
16:K:84:A:H5''	76:NN:122:LYS:HD2	1.89	0.55
16:K:1220:A:N3	16:K:1677:U:O2'	2.35	0.55
16:K:1520:G:H2'	16:K:1520:G:N3	2.20	0.55
54:5:456:C:H2'	54:5:457:G:H8	1.69	0.55
75:VV:61:GLN:HG3	75:VV:62:PRO:HD3	1.86	0.55
16:K:792:C:H2'	16:K:793:G:H8	1.72	0.55
16:K:1277:C:H2'	16:K:1278:A:H8	1.71	0.55
16:K:1523:C:H2'	16:K:1524:G:C8	2.41	0.55
31:Z:2:GLY:N	33:c:67:ALA:O	2.39	0.55
32:a:64:LYS:NZ	54:5:70:A:OP2	2.37	0.55
72:GG:60:THR:HG22	72:GG:83:ARG:HG2	1.88	0.55
82:EF:75:ASN:OD1	82:EF:76:ASN:ND2	2.38	0.55
8:B:220:ILE:HB	8:B:346:THR:HB	1.88	0.55
16:K:1758:G:H2'	16:K:1759:G:C8	2.41	0.55
54:5:1100:U:H2'	54:5:1168:G:H8	1.71	0.55
54:5:1333:A:H2'	54:5:1334:A:C8	2.42	0.55
59:BB:98:ARG:HD2	59:BB:125:VAL:HG23	1.88	0.55
8:B:92:TYR:HB2	8:B:159:VAL:HB	1.89	0.55
16:K:656:G:H21	16:K:663:C:H5''	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:K:1680:G:H4'	80:FF:20:ARG:HG3	1.89	0.55
21:P:62:ARG:NH1	54:5:423:G:OP1	2.39	0.55
22:Q:122:THR:OG1	22:Q:124:ASP:OD1	2.24	0.55
32:a:71:PRO:HG2	32:a:108:TYR:HA	1.87	0.55
54:5:1170:G:H2'	54:5:1171:G:H8	1.71	0.55
54:5:2745:A:H2'	54:5:2746:A:C8	2.41	0.55
54:5:3932:U:H2'	54:5:3933:G:H8	1.70	0.55
76:NN:104:ARG:HA	76:NN:107:ARG:HE	1.72	0.55
16:K:928:G:N2	79:JJ:68:GLY:O	2.39	0.55
16:K:1662:U:O4	16:K:1663:A:N6	2.40	0.55
30:Y:11:ARG:HG3	54:5:229:G:H5''	1.88	0.55
48:u:73:ASP:OD1	66:MM:128:ARG:NH1	2.40	0.55
54:5:1170:G:H2'	54:5:1171:G:C8	2.42	0.55
54:5:1942:A:H2'	54:5:1943:A:C8	2.42	0.55
54:5:3848:U:H2'	54:5:3849:A:H8	1.71	0.55
54:5:3868:G:H22	54:5:3900:G:H1'	1.71	0.55
4:6:88:ARG:NH2	16:K:1398:G:O3'	2.40	0.55
7:A:30:ARG:O	7:A:163:ARG:NH2	2.30	0.55
8:B:4:ARG:HH21	54:5:4459:U:H5	1.53	0.55
15:J:29:SER:OG	15:J:67:LYS:O	2.25	0.55
49:v:90:GLU:HG3	49:v:92:GLU:HG2	1.89	0.55
54:5:1211:G:H2'	54:5:1212:G:C8	2.42	0.55
54:5:1523:A:N3	54:5:4389:C:O2'	2.35	0.55
54:5:1333:A:H2'	54:5:1334:A:H8	1.72	0.55
54:5:4088:C:H2'	54:5:4089:G:H8	1.71	0.55
63:EE:135:SER:O	63:EE:139:ARG:NH1	2.38	0.55
76:NN:83:LYS:HE3	76:NN:96:LEU:HD13	1.89	0.55
81:AA:125:LYS:NZ	81:AA:126:LYS:O	2.38	0.55
15:J:35:ARG:HD2	15:J:123:ILE:HA	1.89	0.54
16:K:531:A:H3'	16:K:532:C:H5''	1.89	0.54
16:K:689:U:H2'	16:K:690:G:O4'	2.07	0.54
16:K:919:A:OP2	65:QQ:64:ARG:NH1	2.40	0.54
16:K:1272:C:H2'	16:K:1273:C:C6	2.42	0.54
16:K:1566:G:N2	16:K:1569:A:OP2	2.32	0.54
47:r:35:ARG:NH2	54:5:2265:G:OP1	2.32	0.54
50:w:135:GLU:HG3	50:w:153:VAL:HG22	1.89	0.54
54:5:221:C:H2'	54:5:222:C:H6	1.71	0.54
54:5:673:C:H2'	54:5:674:G:H8	1.72	0.54
54:5:909:G:H2'	54:5:910:G:H8	1.72	0.54
54:5:3717:A:H2'	54:5:3718:A:C8	2.42	0.54
54:5:4862:G:H2'	54:5:4863:G:H8	1.71	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:BB:36:LEU:HD13	59:BB:75:ILE:HD11	1.90	0.54
11:F:130:ASN:ND2	54:5:1727:U:OP1	2.39	0.54
54:5:662:C:H2'	54:5:663:G:C8	2.42	0.54
75:VV:68:LYS:HE2	81:AA:82:VAL:HG22	1.89	0.54
9:C:230:LEU:HD21	9:C:239:LYS:HD2	1.89	0.54
16:K:1153:C:OP2	74:TT:71:LYS:NZ	2.35	0.54
55:8:67:U:H2'	55:8:68:G:H8	1.73	0.54
63:EE:126:VAL:HG22	63:EE:145:VAL:HG12	1.88	0.54
6:9:34:TYR:HB3	50:w:12:VAL:HG21	1.89	0.54
54:5:695:G:H2'	54:5:697:G:OP2	2.07	0.54
54:5:4448:G:H4'	54:5:4449:A:OP2	2.06	0.54
54:5:4967:A:H2'	54:5:4968:A:C8	2.42	0.54
57:b:23:LYS:HG3	57:b:24:PRO:HD2	1.90	0.54
59:BB:145:ARG:HE	74:TT:51:GLU:HB2	1.72	0.54
12:G:282:ARG:NH1	12:G:285:GLU:OE2	2.36	0.54
26:U:45:GLU:OE2	26:U:46:ARG:NH1	2.41	0.54
30:Y:52:ASP:HB2	30:Y:110:LYS:HG3	1.88	0.54
48:u:103:MET:HB3	48:u:215:VAL:HB	1.90	0.54
54:5:520:U:H3	54:5:641:G:H1	1.56	0.54
54:5:4094:G:H2'	54:5:4095:G:O4'	2.07	0.54
16:K:1528:G:O2'	16:K:1666:C:OP1	2.22	0.54
54:5:1959:U:H4'	54:5:1960:A:H5''	1.89	0.54
54:5:2520:C:H2'	54:5:2521:G:H8	1.73	0.54
13:H:92:MET:HB3	13:H:181:VAL:HA	1.90	0.54
14:I:31:ILE:HG22	14:I:62:SER:HB2	1.89	0.54
19:N:104:GLU:HA	19:N:160:GLU:HG3	1.90	0.54
19:N:124:ASP:OD1	54:5:3937:C:O2'	2.25	0.54
54:5:679:C:H2'	54:5:680:G:H8	1.72	0.54
54:5:1369:C:OP2	54:5:1370:G:O2'	2.22	0.54
16:K:72:C:O2'	16:K:74:G:OP2	2.23	0.54
16:K:334:C:H5	52:z:190:ARG:HH12	1.55	0.54
16:K:1670:C:H2'	16:K:1671:G:H8	1.70	0.54
16:K:1693:G:N2	16:K:1834:A:H8	2.06	0.54
23:R:21:LYS:NZ	54:5:2822:G:OP2	2.41	0.54
32:a:12:ARG:NH1	54:5:2345:G:OP2	2.40	0.54
50:w:137:VAL:HG22	50:w:151:LYS:HG3	1.89	0.54
54:5:500:G:O2'	54:5:504:G:O4'	2.24	0.54
54:5:2704:C:H2'	54:5:2705:G:H8	1.71	0.54
54:5:3732:A:H2'	54:5:3733:A:C8	2.42	0.54
54:5:4503:A:H2'	54:5:4504:C:C6	2.43	0.54
16:K:1098:C:H2'	16:K:1099:G:C8	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:K:1324:G:H1	16:K:1504:U:H3	1.55	0.54
16:K:1711:U:H2'	16:K:1712:A:C8	2.41	0.54
20:O:10:ASP:OD2	20:O:37:ARG:NH2	2.41	0.54
22:Q:2:GLY:N	54:5:2072:C:OP1	2.40	0.54
26:U:56:LEU:HB3	26:U:61:VAL:HG13	1.90	0.54
48:u:134:LEU:HG	48:u:218:LEU:HD12	1.90	0.54
54:5:419:A:N3	54:5:1332:C:O2'	2.40	0.54
54:5:1169:G:H2'	54:5:1170:G:C8	2.43	0.54
55:8:47:C:H1'	55:8:61:A:H2'	1.88	0.54
69:KK:90:ALA:O	69:KK:93:GLN:NE2	2.31	0.54
82:EF:36:THR:HG23	82:EF:39:ALA:H	1.73	0.54
7:A:244:GLY:HA3	54:5:3746:A:H5''	1.90	0.54
16:K:1758:G:H2'	16:K:1759:G:H8	1.73	0.54
54:5:4135:G:H2'	54:5:4136:G:H8	1.73	0.54
26:U:55:ASN:HD22	26:U:58:GLY:H	1.56	0.53
52:z:48:TYR:OH	52:z:119:LYS:O	2.26	0.53
54:5:4110:C:H2'	54:5:4111:U:C6	2.43	0.53
67:WW:81:ARG:NH1	67:WW:120:SER:OG	2.41	0.53
5:7:57:C:H2'	5:7:58:A:H8	1.73	0.53
8:B:174:ARG:NH1	54:5:4985:U:O2	2.40	0.53
16:K:538:U:H2'	16:K:539:C:C6	2.44	0.53
16:K:929:G:N2	16:K:1104:G:H4'	2.23	0.53
29:X:139:ARG:NH1	54:5:2533:C:OP1	2.40	0.53
52:z:5:ILE:HD11	52:z:113:ILE:HD11	1.90	0.53
54:5:980:U:H2'	54:5:981:C:H6	1.73	0.53
54:5:1174:G:H2'	54:5:1175:A:C8	2.43	0.53
60:CC:137:LEU:O	60:CC:141:ARG:NH2	2.41	0.53
62:SS:83:LEU:HD11	62:SS:85:LEU:HD23	1.88	0.53
66:MM:45:THR:HG22	66:MM:52:THR:HA	1.90	0.53
4:6:26:GLN:NE2	4:6:73:SER:O	2.41	0.53
16:K:75:G:O2'	16:K:77:A:OP1	2.25	0.53
16:K:319:C:H4'	16:K:319:C:OP1	2.08	0.53
16:K:886:A:N3	16:K:887:U:H1'	2.23	0.53
16:K:1415:C:O2'	71:PP:132:ASP:OD2	2.20	0.53
19:N:125:SER:HB3	54:5:3937:C:H1'	1.90	0.53
45:p:41:PHE:O	54:5:2674:A:N6	2.40	0.53
54:5:2495:U:H2'	54:5:2496:G:H8	1.74	0.53
54:5:3717:A:H2'	54:5:3718:A:H8	1.72	0.53
75:VV:93:PHE:O	75:VV:140:ARG:NH1	2.41	0.53
82:EF:55:ASN:HA	82:EF:80:GLN:HA	1.90	0.53
8:B:10:ARG:HH12	8:B:265:SER:HB2	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:D:62:CYS:HB3	10:D:105:LEU:HD22	1.90	0.53
16:K:110:U:H2'	16:K:111:A:C8	2.43	0.53
16:K:1217:A:H2'	16:K:1218:C:C6	2.44	0.53
16:K:1269:G:H1'	16:K:1298:G:O6	2.08	0.53
16:K:1773:C:H2'	16:K:1774:C:C6	2.44	0.53
54:5:48:G:H4'	54:5:49:U:O5'	2.07	0.53
54:5:2543:A:H2	54:5:2773:G:H1	1.57	0.53
34:d:64:ILE:HG23	34:d:68:LEU:HD23	1.90	0.53
56:E:153:LEU:HD13	56:E:197:VAL:HG11	1.89	0.53
59:BB:53:VAL:HG21	59:BB:172:THR:HA	1.91	0.53
60:CC:12:ARG:HE	60:CC:18:ARG:HB2	1.73	0.53
66:MM:40:THR:HG21	66:MM:74:ALA:HB2	1.90	0.53
73:HH:60:ARG:HA	73:HH:65:SER:HB2	1.90	0.53
11:F:189:LEU:HD21	11:F:207:LEU:HD21	1.91	0.53
14:I:51:HIS:CD2	14:I:168:SER:HB2	2.44	0.53
16:K:212:C:H2'	16:K:213:G:H8	1.73	0.53
54:5:469:C:N3	56:E:108:ARG:NH2	2.50	0.53
54:5:1073:G:H2'	54:5:1074:G:C8	2.44	0.53
54:5:2589:C:HO2'	54:5:2767:U:HO2'	1.56	0.53
5:7:28:C:O2'	5:7:54:A:N1	2.41	0.53
11:F:235:ARG:HB2	11:F:238:GLN:HB2	1.90	0.53
16:K:446:G:OP2	60:CC:47:ARG:NH2	2.41	0.53
31:Z:68:ILE:N	31:Z:119:GLU:OE2	2.40	0.53
51:x:137:PRO:HB2	51:x:150:PRO:HD2	1.91	0.53
54:5:1211:G:O2'	54:5:1212:G:OP1	2.23	0.53
54:5:2539:C:H2'	54:5:2540:C:C6	2.43	0.53
66:MM:28:PHE:HZ	78:LL:58:VAL:HG11	1.73	0.53
7:A:209:HIS:CE1	7:A:235:VAL:HG11	2.44	0.53
10:D:268:ARG:CZ	54:5:1176:C:H5''	2.38	0.53
16:K:1826:G:HO2'	54:5:3759:A:HO2'	1.55	0.53
20:O:87:MET:HE3	54:5:1912:G:H21	1.72	0.53
54:5:1662:C:H2'	54:5:1663:C:C6	2.44	0.53
54:5:2588:C:H5''	54:5:2589:C:H5''	1.90	0.53
54:5:2845:A:N6	54:5:3843:C:H42	2.05	0.53
54:5:3786:U:OP1	54:5:4550:G:O2'	2.25	0.53
54:5:4991:U:H2'	54:5:4992:G:C8	2.42	0.53
60:CC:62:VAL:HA	60:CC:77:ARG:HA	1.91	0.53
15:J:111:GLU:HB2	15:J:125:ILE:HD11	1.91	0.53
18:M:114:LYS:NZ	54:5:4929:C:OP1	2.35	0.53
51:x:54:TYR:O	76:NN:15:ASN:ND2	2.42	0.53
54:5:4888:C:H2'	54:5:4889:G:H8	1.74	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:K:609:U:H2'	16:K:610:G:H8	1.74	0.53
16:K:1365:G:H2'	16:K:1366:G:H8	1.74	0.53
16:K:1565:C:OP2	71:PP:101:ARG:NH1	2.42	0.53
52:z:195:LYS:HG2	52:z:198:ARG:HH21	1.74	0.53
54:5:4112:C:H2'	54:5:4113:U:C6	2.44	0.53
54:5:4239:A:H2'	54:5:4240:G:H8	1.73	0.53
1:m:59:LEU:HD21	13:H:180:TYR:HB2	1.90	0.52
2:0:116:ARG:NH1	2:0:120:GLU:OE2	2.42	0.52
5:7:48:G:OP1	10:D:226:TYR:OH	2.21	0.52
16:K:532:C:O2'	16:K:533:A:OP1	2.26	0.52
16:K:1797:U:H2'	16:K:1798:C:C6	2.44	0.52
27:V:15:ARG:HB2	54:5:4618:G:H5''	1.91	0.52
30:Y:45:ARG:HB2	30:Y:126:ARG:HH22	1.73	0.52
36:f:20:ASN:HB3	36:f:22:ARG:HH12	1.75	0.52
47:r:32:LEU:HD23	47:r:32:LEU:H	1.74	0.52
53:2:3:U:H3	53:2:70:G:H1	1.57	0.52
54:5:1320:U:O2'	54:5:1891:A:N1	2.42	0.52
54:5:2411:C:H2'	54:5:2412:A:C8	2.45	0.52
54:5:4894:A:H5''	54:5:4895:C:H5''	1.91	0.52
66:MM:100:THR:HG21	66:MM:104:ARG:HE	1.74	0.52
16:K:537:C:H2'	16:K:538:U:H6	1.73	0.52
16:K:688:U:H5	59:BB:103:LYS:H	1.57	0.52
16:K:1491:G:H2'	16:K:1492:U:C6	2.44	0.52
46:q:205:ARG:HH21	69:KK:81:ARG:HG3	1.74	0.52
54:5:1177:U:H2'	54:5:1178:G:C8	2.43	0.52
54:5:1734:G:N2	54:5:1735:U:O4	2.31	0.52
76:NN:91:LEU:HB3	76:NN:96:LEU:HD11	1.90	0.52
13:H:60:TRP:HD1	54:5:4764:A:C2	2.27	0.52
74:TT:6:VAL:HG22	74:TT:34:ILE:HD11	1.92	0.52
5:7:59:G:H2'	5:7:60:G:H8	1.74	0.52
9:C:140:LYS:HE2	9:C:245:HIS:HB2	1.92	0.52
15:J:20:LEU:HD13	15:J:132:VAL:HG12	1.91	0.52
16:K:902:G:H2'	16:K:903:A:H8	1.75	0.52
31:Z:27:LYS:HB2	31:Z:42:LEU:HB3	1.92	0.52
53:2:24:A:H2'	53:2:25:C:C6	2.44	0.52
54:5:1669:A:H4'	54:5:1685:G:N2	2.24	0.52
54:5:1877:G:O6	57:b:10:HIS:NE2	2.43	0.52
63:EE:5:GLN:NE2	63:EE:11:GLN:O	2.41	0.52
8:B:14:LEU:O	54:5:4587:G:O2'	2.26	0.52
8:B:224:LYS:NZ	54:5:4626:A:OP2	2.31	0.52
9:C:204:ARG:NH1	9:C:205:ARG:O	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:K:532:C:H2'	16:K:533:A:H8	1.72	0.52
16:K:1545:A:H2'	16:K:1546:G:C8	2.45	0.52
16:K:1798:C:H2'	16:K:1799:G:O4'	2.10	0.52
54:5:1937:C:OP2	54:5:1938:C:O2'	2.25	0.52
54:5:4348:A:O2'	54:5:4350:C:OP2	2.26	0.52
12:G:253:THR:OG1	54:5:150:U:OP2	2.24	0.52
16:K:71:G:N7	52:z:170:ARG:NH1	2.53	0.52
16:K:432:G:H2'	16:K:433:A:C8	2.44	0.52
16:K:1007:C:H2'	16:K:1008:A:C8	2.44	0.52
16:K:1562:C:H2'	16:K:1563:G:C8	2.44	0.52
16:K:1753:C:H2'	16:K:1754:G:H8	1.73	0.52
49:v:94:ILE:HD12	49:v:162:ILE:HD11	1.92	0.52
53:2:58:A:H1'	53:2:60:A:OP2	2.09	0.52
54:5:1676:C:H41	54:5:4378:A:H5''	1.75	0.52
54:5:1879:C:O2'	54:5:1891:A:N3	2.41	0.52
54:5:4583:C:O2'	54:5:4718:G:N2	2.34	0.52
60:CC:80:ASP:OD1	60:CC:81:VAL:N	2.43	0.52
64:RR:23:LYS:NZ	64:RR:88:TRP:O	2.43	0.52
72:GG:94:PRO:HD2	72:GG:97:ILE:HD12	1.91	0.52
7:A:181:LYS:HB2	54:5:1577:G:C5	2.45	0.52
8:B:281:ASN:ND2	54:5:4676:G:OP1	2.43	0.52
12:G:158:GLU:OE1	12:G:166:ARG:NH1	2.43	0.52
15:J:16:ARG:HE	15:J:137:PRO:HG3	1.75	0.52
16:K:106:C:H2'	16:K:107:A:H8	1.75	0.52
25:T:114:GLN:HG2	25:T:117:LYS:HE3	1.91	0.52
54:5:922(B):C:H3'	54:5:923:C:H5''	1.92	0.52
54:5:1315:C:N4	54:5:1316:G:O6	2.43	0.52
54:5:1739:G:N3	54:5:1742:A:N6	2.58	0.52
54:5:4301:U:OP2	54:5:4303:C:N4	2.43	0.52
16:K:1119:A:H2'	16:K:1120:U:H6	1.74	0.52
20:O:186:GLU:HA	20:O:189:ILE:HG12	1.91	0.52
23:R:10:LEU:HB3	23:R:41:ILE:HG13	1.92	0.52
36:f:41:PHE:HE1	36:f:110:ILE:HD11	1.75	0.52
47:r:90:LEU:HG	47:r:111:ILE:HG23	1.90	0.52
49:v:184:VAL:HG11	49:v:247:THR:HA	1.91	0.52
54:5:756:G:H2'	54:5:757:G:H8	1.75	0.52
54:5:1669:A:N3	54:5:1852:U:O2'	2.36	0.52
66:MM:125:LYS:HA	78:LL:56:VAL:HG12	1.92	0.52
68:UU:70:VAL:HG11	68:UU:84:ILE:HG22	1.92	0.52
74:TT:26:LEU:HD11	74:TT:60:LYS:HB3	1.92	0.52
74:TT:102:ILE:HG22	74:TT:128:PHE:HB3	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:K:453:C:O2'	52:z:92:ARG:O	2.22	0.52
16:K:1284:A:C5	64:RR:91:LEU:HD13	2.44	0.52
50:w:132:LYS:HB3	50:w:156:LEU:HB3	1.92	0.52
54:5:2378:G:N2	54:5:2381:A:OP2	2.41	0.52
68:UU:19:ALA:HB2	68:UU:75:GLY:HA3	1.91	0.52
4:6:256:ILE:HG23	4:6:270:LEU:HB2	1.92	0.52
11:F:227:VAL:HA	24:S:39:VAL:HG12	1.92	0.52
16:K:656:G:N2	16:K:663:C:H5''	2.24	0.52
16:K:1566:G:N7	71:PP:101:ARG:NH2	2.57	0.52
31:Z:50:PRO:HD3	31:Z:68:ILE:HG12	1.92	0.52
60:CC:64:ASN:OD1	60:CC:73:THR:OG1	2.26	0.52
62:SS:59:LYS:HG2	62:SS:70:TYR:HB2	1.90	0.52
62:SS:61:GLN:HB2	62:SS:68:TYR:HB2	1.92	0.52
79:JJ:67:THR:OG1	79:JJ:70:LYS:O	2.27	0.52
2:0:140:TYR:OH	16:K:1291:A:O2'	2.27	0.51
16:K:128:U:H3'	16:K:129:C:C6	2.45	0.51
16:K:812:A:O2'	51:x:12:VAL:O	2.22	0.51
19:N:36:LEU:HA	19:N:64:ILE:HG22	1.91	0.51
40:j:46:LYS:HD2	40:j:54:LYS:HE2	1.92	0.51
45:p:30:GLU:HA	45:p:33:GLN:HG2	1.92	0.51
46:q:70:ASN:ND2	49:v:274:MET:SD	2.83	0.51
51:x:31:PRO:HG3	51:x:43:PRO:HG3	1.91	0.51
53:2:18:G:H4'	53:2:60:A:C6	2.45	0.51
54:5:1818:G:O2'	54:5:1819:G:OP1	2.25	0.51
8:B:167:GLN:OE1	8:B:204:GLN:NE2	2.42	0.51
15:J:90:ARG:NH2	15:J:108:GLY:O	2.42	0.51
54:5:1872:G:O2'	54:5:4219:A:N3	2.42	0.51
54:5:3598:C:H2'	54:5:3599:A:H8	1.75	0.51
54:5:3607:U:H2'	54:5:3608:A:C8	2.45	0.51
54:5:4129:G:O6	54:5:4156:G:N2	2.42	0.51
7:A:118:GLU:OE2	54:5:3662:A:O2'	2.29	0.51
11:F:45:ARG:NH2	54:5:2103:A:OP2	2.29	0.51
16:K:1644:C:H4'	68:UU:140:ARG:HB2	1.91	0.51
19:N:2:GLY:N	54:5:115:C:OP1	2.43	0.51
19:N:116:LEU:HD22	19:N:135:ILE:HD11	1.92	0.51
21:P:142:SER:OG	54:5:2361:G:O6	2.28	0.51
42:l:13:LEU:HD22	54:5:2407:G:H2'	1.92	0.51
54:5:517:C:H2'	54:5:518:G:C8	2.45	0.51
54:5:676:C:H2'	54:5:677:G:H8	1.74	0.51
54:5:679:C:H2'	54:5:680:G:C8	2.46	0.51
55:8:141:C:H2'	55:8:142:U:C6	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:BB:101:LEU:O	59:BB:116:ARG:NH1	2.44	0.51
16:K:530:U:H2'	16:K:531:A:C8	2.46	0.51
16:K:1204:A:O2'	16:K:1700:C:OP2	2.29	0.51
16:K:1454:A:C2	16:K:1476:A:H1'	2.45	0.51
16:K:1520:G:H3'	16:K:1521:C:C6	2.46	0.51
54:5:1557:C:H2'	54:5:1558:A:H8	1.75	0.51
54:5:4093:G:O2'	54:5:4094:G:C8	2.64	0.51
54:5:4503:A:H2'	54:5:4504:C:H6	1.74	0.51
54:5:4935:C:H2'	54:5:4936:G:C8	2.45	0.51
58:y:204:ARG:NH1	80:FF:60:GLU:OE1	2.43	0.51
14:I:42:LYS:O	14:I:139:ARG:NH2	2.44	0.51
14:I:79:SER:OG	14:I:147:HIS:ND1	2.43	0.51
16:K:673:G:H2'	16:K:674:C:H6	1.75	0.51
23:R:4:LEU:HD11	23:R:29:THR:HG23	1.92	0.51
26:U:36:GLU:HB3	26:U:65:ARG:HD2	1.91	0.51
38:h:87:LYS:HD3	38:h:91:MET:HE2	1.92	0.51
51:x:205:PHE:HE2	51:x:223:SER:HB2	1.75	0.51
54:5:381:U:H4'	54:5:415:G:H5'	1.91	0.51
54:5:455:C:H2'	54:5:456:C:C6	2.44	0.51
55:8:108:A:H2'	55:8:109:C:O4'	2.10	0.51
4:6:187:ASN:HB2	50:w:225:GLU:HB3	1.92	0.51
10:D:120:GLU:O	10:D:248:ARG:NH2	2.36	0.51
52:z:135:PRO:HB2	52:z:141:ILE:HG12	1.93	0.51
54:5:452:A:H1'	54:5:1293:G:O6	2.11	0.51
54:5:1211:G:OP2	54:5:1215:C:N4	2.44	0.51
54:5:1382:G:H2'	54:5:1383:G:H8	1.75	0.51
54:5:4238:G:H2'	54:5:4239:A:C8	2.45	0.51
67:WW:98:ASN:HB2	67:WW:122:THR:HA	1.92	0.51
16:K:507:G:OP2	76:NN:104:ARG:NH2	2.43	0.51
16:K:673:G:H2'	16:K:674:C:C6	2.46	0.51
16:K:851:C:H5''	16:K:852:G:H5'	1.93	0.51
16:K:915:G:OP2	16:K:915:G:N2	2.39	0.51
16:K:1255:G:OP1	16:K:1256:G:O2'	2.21	0.51
48:u:71:LEU:HD13	48:u:82:ARG:HD2	1.92	0.51
54:5:153:G:H2'	54:5:154:G:H8	1.75	0.51
54:5:757:G:H2'	54:5:758:G:H8	1.75	0.51
54:5:4239:A:H2'	54:5:4240:G:C8	2.45	0.51
63:EE:77:VAL:HG12	63:EE:88:ILE:HG22	1.93	0.51
73:HH:16:LYS:HG2	73:HH:23:ILE:HG22	1.93	0.51
4:6:15:ASN:O	4:6:305:ASN:ND2	2.43	0.51
39:i:28:ARG:HA	54:5:327:U:O4	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:v:209:VAL:HG21	49:v:233:LEU:HD11	1.93	0.51
50:w:72:VAL:HG22	62:ss:20:VAL:HG21	1.93	0.51
54:5:1237:C:H5''	56:E:61:ARG:HG3	1.92	0.51
54:5:2521:G:H5'	54:5:2640:G:H1'	1.92	0.51
54:5:4751:G:H1	54:5:4948:C:H5	1.58	0.51
74:TT:52:ILE:HG22	74:TT:61:ILE:HG12	1.93	0.51
8:B:381:THR:HG23	8:B:384:GLU:H	1.75	0.51
11:F:156:ARG:NH1	11:F:211:LYS:O	2.44	0.51
16:K:128:U:H5'	16:K:215:G:H5'	1.93	0.51
30:Y:2:LYS:HE2	30:Y:9:SER:HB2	1.93	0.51
44:o:31:ASP:OD1	54:5:4343:U:O2'	2.29	0.51
48:u:189:ILE:HB	48:u:190:PRO:HD3	1.93	0.51
54:5:4699:U:H1'	54:5:4700:A:H5''	1.92	0.51
59:BB:10:LYS:HE3	59:BB:16:PRO:HB3	1.93	0.51
63:EE:18:GLN:HB2	63:EE:33:LEU:HD22	1.93	0.51
70:II:35:GLY:O	70:II:97:GLN:NE2	2.44	0.51
5:7:6:C:H4'	10:D:52:ILE:HD13	1.93	0.51
16:K:1438:A:H2'	16:K:1439:A:C8	2.45	0.51
38:h:80:PRO:HD2	38:h:83:LEU:HD12	1.92	0.51
54:5:2052:G:O2'	54:5:2057:A:N1	2.39	0.51
54:5:2459:G:N2	54:5:2462:C:OP2	2.42	0.51
54:5:3911:C:H2'	54:5:3912:U:H6	1.76	0.51
54:5:4108:G:H2'	54:5:4109:G:C8	2.46	0.51
10:D:60:ILE:HB	10:D:80:ALA:HB2	1.93	0.50
16:K:316:G:H3'	52:z:183:ARG:HH22	1.76	0.50
17:L:54:PRO:O	17:L:56:ARG:NH1	2.44	0.50
30:Y:54:GLU:HB2	30:Y:108:ARG:HG2	1.92	0.50
35:e:26:ASP:OD2	54:5:435:A:O2'	2.26	0.50
37:g:90:ARG:HG3	54:5:4122:G:H4'	1.92	0.50
38:h:93:ARG:NH2	54:5:19:G:OP2	2.30	0.50
5:7:110:G:H2'	5:7:111:C:C6	2.46	0.50
6:9:56:ASP:OXT	16:K:1480:A:O2'	2.29	0.50
9:C:178:ASN:OD1	9:C:181:LYS:NZ	2.43	0.50
9:C:268:ARG:HD2	54:5:492:U:H5''	1.93	0.50
15:J:15:LEU:HD21	15:J:134:LEU:HB3	1.93	0.50
16:K:1311:C:OP2	64:RR:40:LYS:NZ	2.40	0.50
16:K:1588:A:H2'	16:K:1589:A:C8	2.45	0.50
16:K:1590:C:OP1	71:PP:82:ARG:NH1	2.45	0.50
36:f:46:ARG:H	36:f:107:PRO:HG2	1.75	0.50
41:k:6:GLU:HG2	41:k:7:GLU:HG2	1.93	0.50
51:x:185:GLY:N	51:x:189:LEU:HD13	2.25	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:5:1233:G:HO2'	54:5:1234:G:H8	1.58	0.50
54:5:1433:A:H62	54:5:1451:G:H21	1.58	0.50
54:5:1662:C:H2'	54:5:1663:C:H6	1.75	0.50
75:VV:95:GLU:HG2	75:VV:140:ARG:HH22	1.77	0.50
8:B:41:VAL:HA	8:B:187:GLY:HA3	1.94	0.50
14:I:152:LEU:HB3	14:I:165:ILE:HD12	1.92	0.50
16:K:51:U:H2'	16:K:52:G:H8	1.76	0.50
16:K:877:C:H2'	16:K:878:G:C8	2.46	0.50
16:K:996:A:H2'	16:K:997:A:C8	2.47	0.50
16:K:1288:U:H1'	16:K:1312:G:H22	1.76	0.50
17:L:23:ALA:CB	19:N:199:GLN:OE1	2.58	0.50
19:N:184:ILE:HG23	19:N:194:ARG:HH22	1.75	0.50
25:T:83:LYS:HE2	25:T:85:LEU:HD21	1.93	0.50
50:w:54:ARG:HE	50:w:57:ASN:HD21	1.58	0.50
54:5:220:C:O2'	54:5:221:C:H6	1.94	0.50
8:B:72:VAL:HA	27:V:92:ASP:HA	1.94	0.50
13:H:50:LYS:HG2	13:H:51:LYS:HG3	1.93	0.50
16:K:334:C:OP2	52:z:190:ARG:NH2	2.44	0.50
16:K:1129:G:H2'	16:K:1130:G:C4	2.46	0.50
16:K:1447:G:OP1	72:GG:85:HIS:ND1	2.43	0.50
29:X:68:ARG:NH2	55:8:60:G:OP1	2.45	0.50
51:x:130:PHE:O	51:x:138:HIS:N	2.43	0.50
54:5:469:C:H2'	54:5:470:A:H8	1.76	0.50
54:5:2658:G:O2'	54:5:2675:G:N2	2.44	0.50
54:5:3697:U:H5''	54:5:3698:G:H5'	1.93	0.50
67:WW:123:TYR:OH	70:II:124:ARG:NH1	2.43	0.50
72:GG:24:LEU:HD22	72:GG:112:VAL:HG22	1.92	0.50
75:VV:123:VAL:HG12	75:VV:124:LYS:HG3	1.94	0.50
2:O:126:CYS:HB2	2:O:130:VAL:HB	1.94	0.50
16:K:530:U:H2'	16:K:531:A:H8	1.77	0.50
20:O:108:ILE:HD13	20:O:117:ARG:HH11	1.76	0.50
42:l:8:ARG:NH2	55:8:109:C:O2'	2.44	0.50
54:5:161:G:H2'	54:5:162:A:H8	1.77	0.50
54:5:1757:U:H2'	54:5:1758:G:C8	2.47	0.50
54:5:4563:U:C2	54:5:4564:A:C8	2.99	0.50
76:NN:112:ASN:HA	76:NN:115:LYS:HE2	1.92	0.50
16:K:17:C:H2'	16:K:18:C:C6	2.47	0.50
16:K:568:C:H2'	16:K:569:A:C8	2.46	0.50
16:K:1057:C:H1'	16:K:1060:A:C2	2.42	0.50
22:Q:42:THR:HB	54:5:1428:U:H5'	1.93	0.50
26:U:44:GLN:HA	26:U:56:LEU:HD21	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:5:3799:A:N3	54:5:4506:C:O2'	2.39	0.50
54:5:3805:U:H2'	54:5:3806:G:H8	1.77	0.50
54:5:5004:C:H2'	54:5:5005:G:O4'	2.12	0.50
55:8:108:A:N6	55:8:112:G:O6	2.45	0.50
56:E:115:MET:N	56:E:115:MET:SD	2.84	0.50
80:FF:44:ARG:HH11	80:FF:58:LEU:HD13	1.75	0.50
10:D:152:ARG:HG3	10:D:154:THR:HG23	1.93	0.50
13:H:31:ARG:NH2	13:H:147:GLU:OE2	2.38	0.50
16:K:126:G:H5''	52:z:195:LYS:HD3	1.93	0.50
16:K:562:U:O2'	61:DD:132:GLN:OE1	2.29	0.50
16:K:1118:C:H2'	16:K:1119:A:O4'	2.12	0.50
16:K:1156:U:O4	49:v:194:ARG:NH1	2.44	0.50
32:a:26:ARG:NH1	54:5:1655:C:OP2	2.44	0.50
54:5:1188:C:H2'	54:5:1189:G:C8	2.44	0.50
54:5:1942:A:H2'	54:5:1943:A:H8	1.75	0.50
54:5:3599:A:H2'	54:5:3600:G:C8	2.47	0.50
54:5:3607:U:H2'	54:5:3608:A:H8	1.77	0.50
66:MM:57:THR:OG1	66:MM:58:GLY:N	2.44	0.50
80:FF:44:ARG:NH1	80:FF:60:GLU:O	2.45	0.50
8:B:246:ARG:NH1	54:5:4558:U:OP2	2.45	0.50
16:K:841:G:H8	76:NN:12:PHE:HB3	1.77	0.50
17:L:103:ARG:HH21	54:5:326:C:P	2.35	0.50
20:O:9:LEU:HD23	20:O:118:MET:HB2	1.94	0.50
42:l:2:SER:N	54:5:2407:G:O6	2.45	0.50
53:2:65:C:H2'	53:2:66:C:H6	1.77	0.50
54:5:1345:A:H2'	54:5:1346:C:C6	2.47	0.50
54:5:3873:G:H2'	54:5:3874:G:C8	2.47	0.50
54:5:4594:U:H2'	54:5:4595:G:C8	2.44	0.50
55:8:124:U:H4'	55:8:125:C:O5'	2.12	0.50
61:DD:113:GLN:OE1	61:DD:154:GLN:NE2	2.44	0.50
7:A:21:LYS:HG2	54:5:1541:C:H5''	1.93	0.50
7:A:70:LYS:HD3	7:A:72:ARG:HH12	1.77	0.50
9:C:323:ARG:HD3	54:5:1280:C:H3'	1.94	0.50
16:K:5:U:H2'	16:K:6:G:C8	2.47	0.50
16:K:215:G:H2'	16:K:216:C:C6	2.47	0.50
16:K:1144:A:H2'	16:K:1145:A:C8	2.47	0.50
22:Q:86:VAL:HB	22:Q:105:VAL:HG13	1.93	0.50
48:u:82:ARG:HD3	48:u:103:MET:HE3	1.94	0.50
54:5:318:A:H2'	54:5:319:A:H8	1.77	0.50
54:5:756:G:H2'	54:5:757:G:C8	2.46	0.50
54:5:4419:U:OP1	54:5:4421:C:N4	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:5:5006:U:H4'	54:5:5007:A:H5'	1.94	0.50
65:QQ:18:TYR:HE1	74:TT:55:ASP:HA	1.76	0.50
7:A:54:ARG:HG2	7:A:56:ALA:H	1.77	0.49
16:K:51:U:H2'	16:K:52:G:C8	2.47	0.49
16:K:191:A:H3'	16:K:192:C:H5''	1.94	0.49
24:S:29:ARG:HB2	25:T:148:PRO:HB2	1.93	0.49
52:z:70:HIS:HB2	52:z:101:ILE:HD11	1.92	0.49
53:2:76:A:H2'	54:5:4397:A:H1'	1.93	0.49
54:5:1857:C:H2'	54:5:1858:A:C8	2.47	0.49
54:5:2562:G:O2'	54:5:2565:A:N6	2.45	0.49
54:5:3664:G:H2'	54:5:3665:G:H8	1.78	0.49
54:5:3689:G:O2'	54:5:3818:U:OP2	2.26	0.49
54:5:3732:A:H2'	54:5:3733:A:H8	1.77	0.49
54:5:4135:G:H2'	54:5:4136:G:C8	2.46	0.49
54:5:4499:G:C2	54:5:4529:G:H1'	2.47	0.49
54:5:4736:C:H2'	54:5:4737:G:H8	1.76	0.49
61:DD:38:ARG:HG2	61:DD:42:GLU:OE2	2.12	0.49
64:RR:81:ASP:HB2	64:RR:84:LYS:HG2	1.93	0.49
54:5:979:C:H2'	54:5:980:U:H6	1.77	0.49
54:5:3823:G:H2'	54:5:3824:A:H8	1.77	0.49
54:5:4467:A:O2'	54:5:4510:A:N3	2.39	0.49
9:C:6:PRO:HB3	54:5:668:C:H4'	1.94	0.49
9:C:53:ALA:O	55:8:26:C:O2'	2.28	0.49
11:F:24:PHE:CD1	11:F:27:LEU:HB2	2.47	0.49
16:K:12:U:H2'	16:K:13:C:C6	2.47	0.49
16:K:319:C:H2'	16:K:320:G:C8	2.47	0.49
16:K:1395:C:HO2'	16:K:1396:A:C5'	2.24	0.49
16:K:1772:C:H2'	16:K:1773:C:C6	2.47	0.49
51:x:132:GLY:N	51:x:136:ILE:O	2.39	0.49
54:5:306:A:H2'	54:5:307:A:C8	2.48	0.49
54:5:1492:G:O2'	57:b:41:ARG:NH1	2.44	0.49
54:5:1617:G:H1'	54:5:2513:A:N6	2.27	0.49
54:5:3610:A:H2'	54:5:3611:A:C8	2.47	0.49
54:5:3871:A:H2'	54:5:3872:A:C8	2.47	0.49
54:5:5057:C:H2'	54:5:5058:A:C8	2.48	0.49
10:D:69:ILE:HA	25:T:31:MET:HE3	1.93	0.49
29:X:63:LYS:HD2	55:8:134:G:H5''	1.94	0.49
42:l:23:ILE:HG23	42:l:38:ASN:HB2	1.93	0.49
47:r:103:HIS:ND1	47:r:105:ASP:OD1	2.45	0.49
71:PP:28:LEU:HD23	71:PP:110:LEU:HD21	1.95	0.49
4:6:87:LEU:HB2	4:6:101:PHE:HB2	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:C:143:ARG:NH1	54:5:2300:A:N7	2.60	0.49
16:K:14:C:H2'	16:K:15:U:C6	2.48	0.49
16:K:1240:A:N7	67:WW:100:LYS:HB2	2.28	0.49
16:K:1643:U:H2'	16:K:1644:C:C6	2.47	0.49
30:Y:2:LYS:NZ	30:Y:7:VAL:O	2.41	0.49
53:2:64:U:H2'	53:2:65:C:H6	1.77	0.49
54:5:516:C:H2'	54:5:517:C:C6	2.47	0.49
54:5:1073:G:H2'	54:5:1074:G:H8	1.77	0.49
54:5:2045:G:O6	54:5:3870:C:O2'	2.31	0.49
54:5:4413:C:H5	54:5:4429:C:H42	1.60	0.49
55:8:137:A:H2'	55:8:138:C:C6	2.48	0.49
66:MM:39:ASP:OD1	66:MM:40:THR:N	2.46	0.49
8:B:371:THR:HG21	28:W:17:HIS:CE1	2.47	0.49
9:C:290:SER:O	9:C:294:LYS:HG2	2.12	0.49
11:F:114:ARG:HD3	22:Q:5:ILE:HD11	1.95	0.49
13:H:20:LEU:HB3	13:H:25:VAL:HG12	1.93	0.49
16:K:17:C:H2'	16:K:18:C:H6	1.77	0.49
16:K:77:A:H4'	52:z:157:VAL:HG11	1.94	0.49
16:K:1244:U:H2'	16:K:1245:G:H8	1.76	0.49
23:R:97:ARG:NH2	54:5:2725:A:OP2	2.44	0.49
31:Z:97:ASN:HB2	31:Z:100:VAL:HG23	1.93	0.49
36:f:110:ILE:OXT	56:E:144:ARG:NE	2.46	0.49
37:g:21:ARG:HH11	37:g:35:THR:HG22	1.78	0.49
46:q:73:ASP:HB2	46:q:119:PRO:HA	1.95	0.49
49:v:166:ARG:HE	49:v:181:LEU:HD13	1.78	0.49
54:5:699:C:H2'	54:5:700:G:H8	1.76	0.49
54:5:2844:A:O2'	54:5:4631:G:H4'	2.13	0.49
54:5:4507:A:H2'	54:5:4508:C:C6	2.48	0.49
16:K:321:C:H2'	16:K:322:C:C6	2.48	0.49
16:K:867:G:H2'	16:K:868:G:C8	2.48	0.49
16:K:1616:U:H2'	16:K:1617:G:C8	2.47	0.49
54:5:2502:A:H4'	54:5:2503:G:OP1	2.13	0.49
54:5:2770:C:H2'	54:5:2771:G:H8	1.76	0.49
1:m:68:MET:HG2	1:m:79:PRO:HA	1.95	0.49
5:7:80:U:H2'	5:7:81:G:C8	2.48	0.49
16:K:16:G:H2'	16:K:17:C:C6	2.48	0.49
20:O:21:ALA:HA	20:O:87:MET:HE1	1.95	0.49
34:d:37:GLY:O	34:d:41:ARG:HG3	2.12	0.49
35:e:44:ARG:NH2	54:5:1312:A:O2'	2.46	0.49
54:5:1281:G:N3	54:5:1281:G:H2'	2.27	0.49
54:5:1346:C:H2'	54:5:1347:G:H8	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:5:3610:A:H2'	54:5:3611:A:H8	1.77	0.49
76:NN:27:VAL:HG11	76:NN:35:VAL:HG11	1.94	0.49
7:A:15:VAL:HG21	54:5:1628:C:H5''	1.95	0.49
8:B:385:LYS:NZ	54:5:5002:U:OP2	2.46	0.49
11:F:147:LYS:O	11:F:151:GLU:HG2	2.12	0.49
13:H:113:GLU:HG2	13:H:125:ARG:HG2	1.94	0.49
16:K:15:U:H2'	16:K:16:G:O4'	2.13	0.49
16:K:394:G:H2'	16:K:394:G:N3	2.28	0.49
18:M:91:TRP:HA	18:M:94:LYS:HE2	1.95	0.49
20:O:90:HIS:O	20:O:96:GLN:NE2	2.46	0.49
24:S:68:PHE:O	24:S:70:LYS:NZ	2.37	0.49
36:f:71:TRP:HB2	36:f:89:ARG:HE	1.78	0.49
46:q:66:VAL:HG21	46:q:185:MET:HB3	1.94	0.49
48:u:144:LYS:HD3	48:u:208:HIS:HB3	1.94	0.49
51:x:126:VAL:HG11	51:x:139:LEU:HD13	1.94	0.49
51:x:185:GLY:H	51:x:189:LEU:HD13	1.78	0.49
54:5:7:C:H2'	54:5:8:U:C6	2.48	0.49
54:5:65:A:N6	54:5:75:G:H1'	2.28	0.49
54:5:2765:A:H2'	54:5:2766:A:C8	2.48	0.49
54:5:3684:G:H2'	54:5:3685:C:C6	2.48	0.49
59:BB:47:ALA:HB3	59:BB:63:PHE:HD2	1.77	0.49
8:B:36:ASP:OD1	8:B:36:ASP:N	2.45	0.49
16:K:880:G:H1	16:K:906:U:H3	1.61	0.49
18:M:27:ILE:HA	18:M:38:VAL:HG23	1.94	0.49
20:O:157:GLU:HA	20:O:160:ARG:HG2	1.94	0.49
25:T:40:VAL:HG11	25:T:96:ILE:HG23	1.94	0.49
47:r:49:VAL:HG21	47:r:97:ILE:HD11	1.94	0.49
49:v:108:LYS:HB2	49:v:233:LEU:HD23	1.95	0.49
49:v:209:VAL:HG11	49:v:233:LEU:HD11	1.95	0.49
53:2:70:G:H2'	53:2:71:G:H8	1.78	0.49
54:5:495:C:H2'	54:5:496:G:C8	2.47	0.49
54:5:1411:C:H2'	54:5:1411(A):G:H8	1.78	0.49
5:7:63:C:H5'	5:7:64:G:H5''	1.95	0.48
7:A:54:ARG:NH2	54:5:3680:U:OP1	2.35	0.48
8:B:248:LEU:N	54:5:2838:G:OP1	2.37	0.48
16:K:671:A:H61	75:VV:3:LYS:NZ	2.12	0.48
16:K:1365:G:H2'	16:K:1366:G:C8	2.48	0.48
19:N:181:HIS:O	19:N:195:ARG:NH2	2.40	0.48
54:5:950:G:H2'	54:5:951:G:H8	1.78	0.48
54:5:2457:G:N2	54:5:3672:G:H21	2.09	0.48
54:5:2708:U:H1'	54:5:2709:C:C4'	2.43	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:5:2824:C:H2'	54:5:2825:A:C8	2.48	0.48
54:5:3766:A:OP2	54:5:3767:C:N4	2.39	0.48
54:5:4459:U:H2'	54:5:4460:U:C6	2.48	0.48
54:5:4642:U:H2'	54:5:4643:G:H8	1.78	0.48
76:NN:41:ARG:NH2	76:NN:52:PRO:O	2.42	0.48
6:9:34:TYR:OH	16:K:1549:U:OP1	2.28	0.48
7:A:28:ARG:HB3	7:A:123:ARG:HB3	1.95	0.48
8:B:60:VAL:HG12	8:B:62:ARG:HG2	1.95	0.48
10:D:37:VAL:HG22	10:D:67:ALA:HB2	1.95	0.48
16:K:153:G:N3	52:z:13:GLN:NE2	2.61	0.48
16:K:204:G:OP2	60:CC:147:LYS:NZ	2.37	0.48
16:K:1550:G:O2'	16:K:1558:C:O2	2.29	0.48
16:K:1737:G:OP1	52:z:94:ARG:NH2	2.46	0.48
17:L:14:PHE:HE1	19:N:198:LEU:HD11	1.78	0.48
19:N:49:ARG:HH12	54:5:152:U:P	2.36	0.48
54:5:1338:G:H4'	54:5:1339:U:H6	1.78	0.48
54:5:1804:A:H4'	54:5:1805:A:O5'	2.12	0.48
54:5:3870:C:H2'	54:5:3871:A:H8	1.78	0.48
4:6:277:THR:HB	4:6:281:ALA:HB3	1.95	0.48
15:J:48:PRO:HB3	15:J:72:CYS:HB3	1.94	0.48
16:K:901:G:H2'	16:K:902:G:H8	1.78	0.48
16:K:929:G:H2'	16:K:930:C:O4'	2.13	0.48
16:K:1628:C:H2'	16:K:1629:C:C6	2.48	0.48
18:M:113:MET:HG3	54:5:4881:U:C4	2.48	0.48
26:U:38:ASN:OD1	26:U:41:GLN:NE2	2.43	0.48
54:5:158:A:H4'	54:5:159:C:H5''	1.95	0.48
54:5:4188:U:H2'	54:5:4189:U:C6	2.47	0.48
54:5:4760:G:H2'	54:5:4761:G:O4'	2.13	0.48
54:5:4993:G:H22	54:5:5058:A:H2	1.59	0.48
63:EE:16:ILE:HG21	63:EE:34:PRO:HG2	1.95	0.48
82:EF:65:PHE:HB2	83:EG:93:ARG:HB3	1.96	0.48
9:C:77:PRO:O	9:C:90:GLY:HA2	2.14	0.48
9:C:308:LYS:N	54:5:2099:C:OP1	2.47	0.48
16:K:508:A:H3'	16:K:509:G:H8	1.78	0.48
16:K:1487:A:O4'	49:v:118:ALA:HB1	2.14	0.48
22:Q:173:LYS:NZ	54:5:88:A:N7	2.62	0.48
24:S:159:LEU:HD23	24:S:174:THR:HG22	1.96	0.48
51:x:185:GLY:O	51:x:224:ASN:ND2	2.30	0.48
54:5:519:C:H2'	54:5:520:U:C6	2.48	0.48
54:5:3611:A:H2	54:5:5016:A:H8	1.61	0.48
54:5:3722:G:H2'	54:5:3723:A:H8	1.77	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:5:4994:G:H2'	54:5:4995:U:C6	2.48	0.48
74:TT:69:LEU:HD21	74:TT:72:CYS:HB2	1.94	0.48
74:TT:80:ASP:OD1	74:TT:80:ASP:N	2.44	0.48
4:6:31:ILE:CG2	4:6:43:TRP:HB2	2.44	0.48
7:A:116:LEU:N	7:A:126:LEU:O	2.46	0.48
8:B:11:HIS:NE2	54:5:4458:C:OP1	2.44	0.48
9:C:189:MET:HG2	9:C:195:LYS:HD3	1.94	0.48
9:C:284:MET:HE2	9:C:287:THR:HA	1.95	0.48
16:K:84:A:N3	16:K:150:A:O2'	2.38	0.48
16:K:223:C:H2'	16:K:224:A:C8	2.48	0.48
16:K:730:C:H2'	16:K:731:G:H8	1.78	0.48
16:K:869:A:H5'	16:K:874:G:H4'	1.96	0.48
16:K:1302:G:H1	16:K:1307:U:H3	1.61	0.48
22:Q:184:ARG:NE	32:a:55:LYS:O	2.47	0.48
54:5:180:C:H2'	54:5:181:C:C6	2.49	0.48
54:5:1216:C:H2'	54:5:1217:G:C8	2.48	0.48
54:5:4648:A:H2'	54:5:4649:G:H8	1.78	0.48
54:5:4723:A:H2'	54:5:4724:A:C8	2.48	0.48
61:DD:42:GLU:HA	61:DD:45:ARG:HG2	1.95	0.48
72:GG:56:MET:HG3	72:GG:86:LYS:HE3	1.95	0.48
5:7:55:A:H4'	15:J:155:HIS:HB2	1.96	0.48
6:9:17:GLY:HA2	6:9:27:ARG:HD3	1.95	0.48
17:L:188:ASN:ND2	54:5:1482:G:N7	2.61	0.48
20:O:113:ASP:OD1	20:O:114:LYS:N	2.47	0.48
31:Z:22:LYS:NZ	31:Z:129:TRP:O	2.36	0.48
49:v:127:PHE:CD2	49:v:141:LEU:HD22	2.48	0.48
54:5:114:G:N2	54:5:276:C:O2'	2.47	0.48
54:5:1069:G:OP2	56:E:67:ARG:NH1	2.47	0.48
54:5:1761:G:C6	54:5:1762:C:C4	3.01	0.48
54:5:4635:A:C8	54:5:5048:A:N6	2.79	0.48
60:CC:161:LEU:HD23	60:CC:161:LEU:H	1.79	0.48
73:HH:11:LEU:H	73:HH:11:LEU:HD23	1.77	0.48
1:m:96:ARG:HH21	1:m:99:LYS:HG2	1.78	0.48
7:A:77:ILE:HD12	7:A:128:ARG:HB2	1.95	0.48
13:H:126:VAL:HG21	13:H:161:ILE:HG22	1.95	0.48
16:K:1760:G:H2'	16:K:1761:U:C6	2.49	0.48
16:K:1780:G:H2'	16:K:1781:A:C8	2.49	0.48
26:U:80:LYS:HG2	26:U:110:TYR:CE2	2.49	0.48
51:x:11:ARG:NH1	51:x:21:ASP:O	2.42	0.48
54:5:252:C:H2'	54:5:253:G:C8	2.49	0.48
54:5:755:C:H2'	54:5:756:G:H8	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:5:3731:C:H2'	54:5:3732:A:H8	1.79	0.48
54:5:4400:G:H2'	54:5:4401:G:H5''	1.94	0.48
54:5:4888:C:H2'	54:5:4889:G:C8	2.48	0.48
60:CC:106:SER:HB3	60:CC:171:LEU:HG	1.96	0.48
65:QQ:136:PRO:HG2	65:QQ:139:TRP:HB2	1.94	0.48
79:JJ:36:LYS:HB2	79:JJ:43:ILE:HG12	1.94	0.48
8:B:261:ARG:HB2	20:O:64:THR:HG21	1.94	0.48
16:K:656:G:H5'	16:K:662:G:N2	2.29	0.48
16:K:952:G:H2'	16:K:953:C:C6	2.48	0.48
16:K:1217:A:H2'	16:K:1218:C:H6	1.77	0.48
16:K:1706:G:H5'	43:n:1:MET:HB2	1.96	0.48
21:P:123:PRO:HG3	55:8:14:U:H5''	1.96	0.48
44:o:36:GLN:HB2	54:5:4363:A:H5''	1.96	0.48
48:u:109:LYS:HE3	48:u:113:MET:HE2	1.96	0.48
49:v:65:LYS:HD3	49:v:273:LEU:HD13	1.96	0.48
54:5:36:U:OP1	54:5:1651:G:N2	2.37	0.48
54:5:4932:U:H2'	54:5:4933:C:H6	1.79	0.48
72:GG:25:THR:HG23	72:GG:111:GLU:HB3	1.96	0.48
75:VV:107:ARG:HG3	75:VV:112:VAL:HG22	1.96	0.48
76:NN:76:TYR:OH	76:NN:86:GLU:OE1	2.27	0.48
2:0:130:VAL:HG11	2:0:143:LYS:HE2	1.95	0.48
11:F:75:ARG:NH2	54:5:728:U:OP1	2.46	0.48
12:G:141:ASP:OD1	12:G:141:ASP:N	2.46	0.48
15:J:97:ASN:ND2	54:5:4250:G:OP1	2.40	0.48
16:K:65:C:C5	52:z:174:PRO:HB3	2.48	0.48
16:K:432:G:H2'	16:K:433:A:H8	1.77	0.48
20:O:168:TYR:CE2	20:O:172:LYS:HD2	2.49	0.48
45:p:7:LYS:HE2	54:5:2875:C:H2'	1.95	0.48
49:v:94:ILE:HG22	49:v:102:LEU:HD11	1.96	0.48
54:5:86:U:H2'	54:5:87:A:C8	2.49	0.48
54:5:516:C:H2'	54:5:517:C:H6	1.78	0.48
54:5:757:G:H2'	54:5:758:G:C8	2.48	0.48
54:5:1292:C:H5'	54:5:1293:G:OP2	2.14	0.48
54:5:2848:G:O2'	54:5:3838:U:O4	2.22	0.48
54:5:3848:U:H2'	54:5:3849:A:C8	2.48	0.48
54:5:4578:G:H2'	54:5:4579:U:C6	2.49	0.48
16:K:385:G:H1'	16:K:387:C:OP2	2.13	0.48
16:K:677:G:N2	16:K:1028:A:H62	2.12	0.48
16:K:807:G:H2'	16:K:808:A:C8	2.48	0.48
16:K:1545:A:C2	16:K:1671:G:H1'	2.49	0.48
18:M:14:TYR:O	18:M:56:GLN:N	2.42	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:q:124:VAL:N	46:q:145:ILE:O	2.41	0.48
54:5:1430:C:H2'	54:5:1431:C:H6	1.78	0.48
62:SS:91:PRO:HG2	62:SS:94:LEU:HD13	1.96	0.48
8:B:229:LYS:HG3	8:B:272:LYS:HD3	1.96	0.47
9:C:316:LYS:HB3	9:C:321:ASN:HD22	1.79	0.47
16:K:1396:A:O2'	16:K:1398:G:N7	2.46	0.47
24:S:35:PRO:HD2	24:S:39:VAL:HG21	1.94	0.47
44:o:77:CYS:SG	44:o:79:SER:OG	2.66	0.47
50:w:42:THR:CG2	50:w:43:PRO:CD	2.89	0.47
54:5:58:G:H4'	54:5:59:A:H4'	1.95	0.47
54:5:669:C:O2'	54:5:670:G:H8	1.97	0.47
54:5:980:U:H3	54:5:1275:G:H1	1.60	0.47
54:5:4680:G:H2'	54:5:4681:A:C8	2.49	0.47
58:y:100:ILE:HG23	58:y:178:ILE:HD11	1.96	0.47
60:CC:103:LEU:HD22	60:CC:170:LYS:HB3	1.96	0.47
62:SS:30:PRO:HB2	62:SS:31:LYS:HD2	1.95	0.47
8:B:384:GLU:OE2	28:W:14:TYR:OH	2.31	0.47
14:I:91:LEU:HD12	14:I:135:ILE:HG23	1.95	0.47
16:K:582:U:H1'	76:NN:33:ALA:HB2	1.96	0.47
44:o:17:LYS:HA	54:5:4318:C:H4'	1.96	0.47
46:q:33:GLN:HB3	46:q:154:LEU:HD12	1.94	0.47
54:5:453:G:H2'	54:5:453:G:N3	2.28	0.47
54:5:4156:G:OP2	54:5:4157:A:O2'	2.28	0.47
58:y:50:PRO:HB3	58:y:69:VAL:HG12	1.97	0.47
5:7:92:C:H2'	5:7:93:G:C8	2.48	0.47
10:D:146:LEU:HD21	10:D:159:VAL:HG12	1.96	0.47
12:G:116:LEU:HD21	19:N:29:GLN:HG3	1.96	0.47
15:J:46:GLN:NE2	15:J:73:THR:O	2.41	0.47
21:P:86:LYS:O	21:P:89:GLU:HG2	2.14	0.47
49:v:205:VAL:O	49:v:224:THR:OG1	2.30	0.47
54:5:406:C:O2'	54:5:407:A:OP1	2.28	0.47
54:5:424:U:H2'	54:5:425:U:C6	2.49	0.47
54:5:1216:C:H2'	54:5:1217:G:H8	1.78	0.47
54:5:3822:U:H2'	54:5:3823:G:C4	2.50	0.47
54:5:3944:G:H2'	54:5:3945:A:H8	1.80	0.47
54:5:4093:G:O2'	54:5:4094:G:H5'	2.13	0.47
83:EG:111:VAL:HG22	83:EG:122:VAL:HG22	1.96	0.47
8:B:286:LYS:NZ	8:B:302:ASN:O	2.34	0.47
16:K:15:U:O2'	16:K:669:A:N6	2.46	0.47
16:K:539:C:H2'	16:K:540:U:O4'	2.13	0.47
16:K:1016:U:H5''	65:QQ:14:SER:HB3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:K:1453:C:C5	16:K:1455:A:H1'	2.49	0.47
30:Y:8:THR:CG2	30:Y:10:ASP:H	2.26	0.47
46:q:30:LEU:HB2	46:q:47:TYR:CZ	2.49	0.47
48:u:136:ARG:HE	48:u:218:LEU:HD21	1.79	0.47
49:v:60:TRP:CE3	49:v:92:GLU:HG3	2.50	0.47
52:z:119:LYS:HZ2	52:z:121:ILE:HG13	1.79	0.47
54:5:974:C:H41	54:5:1281:G:H21	1.62	0.47
54:5:4458:C:H2'	54:5:4459:U:C6	2.49	0.47
55:8:67:U:H2'	55:8:68:G:C8	2.49	0.47
16:K:146:G:OP2	52:z:143:LYS:NZ	2.47	0.47
16:K:538:U:H2'	16:K:539:C:H6	1.77	0.47
16:K:602:G:OP2	16:K:603:C:O2'	2.26	0.47
16:K:1617:G:N2	16:K:1619:A:H3'	2.29	0.47
36:f:69:VAL:HG11	54:5:4944:C:H1'	1.96	0.47
42:l:3:SER:O	54:5:2781:G:O2'	2.32	0.47
48:u:62:LEU:HD12	48:u:65:ARG:HD2	1.96	0.47
54:5:4762:A:H2'	54:5:4763:U:O4'	2.14	0.47
14:I:33:ILE:HD11	14:I:36:LEU:HB3	1.96	0.47
16:K:555:A:C8	81:AA:98:LYS:HE2	2.49	0.47
16:K:1221:G:H2'	16:K:1222:G:C8	2.49	0.47
21:P:121:LYS:O	55:8:13:G:O2'	2.32	0.47
54:5:46:U:OP2	54:5:47:A:O2'	2.31	0.47
54:5:1097:C:H2'	54:5:1098:G:H8	1.78	0.47
54:5:1402:C:H2'	54:5:1403:G:H8	1.79	0.47
54:5:3620:G:OP1	54:5:3622:C:N4	2.48	0.47
54:5:3699:C:HO2'	54:5:3775:A:HO2'	1.52	0.47
54:5:4673:U:H2'	54:5:4674:C:H6	1.80	0.47
66:MM:21:VAL:HG22	66:MM:24:GLY:H	1.79	0.47
72:GG:91:LEU:HD23	72:GG:98:VAL:HG22	1.97	0.47
75:VV:140:ARG:HD2	75:VV:141:PRO:HD2	1.96	0.47
1:m:99:LYS:HB2	54:5:4474:A:H5'	1.96	0.47
4:6:165:ILE:HG12	4:6:177:TRP:HB2	1.97	0.47
9:C:333:LYS:NZ	54:5:977:C:O2'	2.37	0.47
10:D:268:ARG:HD3	10:D:269:PRO:HD2	1.96	0.47
13:H:118:LEU:HD11	13:H:167:VAL:HG22	1.96	0.47
16:K:57:U:OP1	16:K:504:G:O2'	2.32	0.47
16:K:96:C:H2'	16:K:97:U:C6	2.49	0.47
16:K:640:A:H2'	16:K:641:A:C8	2.49	0.47
16:K:642:U:P	61:DD:39:ASN:HB2	2.55	0.47
16:K:847:A:OP1	51:x:108:ARG:NH2	2.48	0.47
16:K:1615:U:O4	67:WW:40:ARG:NH2	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:K:1740:C:H42	16:K:1794:C:H42	1.62	0.47
19:N:73:ARG:HB3	19:N:89:VAL:HG12	1.95	0.47
19:N:89:VAL:HG21	54:5:3928:A:H5'	1.97	0.47
19:N:114:ARG:NH1	19:N:151:ILE:O	2.46	0.47
25:T:18:PRO:HB2	25:T:21:LYS:HD2	1.96	0.47
31:Z:79:HIS:ND1	54:5:2580:U:O2'	2.35	0.47
32:a:117:LEU:HD12	32:a:118:PRO:HD2	1.97	0.47
41:k:24:ASN:HB2	41:k:35:LYS:HB2	1.97	0.47
46:q:77:ILE:HG12	46:q:99:ILE:HB	1.97	0.47
49:v:60:TRP:CD2	49:v:92:GLU:HG3	2.50	0.47
49:v:141:LEU:HD11	49:v:238:LYS:HE3	1.97	0.47
50:w:75:LYS:NZ	62:SS:34:GLU:OE2	2.38	0.47
53:2:64:U:H2'	53:2:65:C:C6	2.49	0.47
54:5:128:C:H2'	54:5:129:C:H6	1.79	0.47
54:5:407:A:O2'	54:5:410:A:OP1	2.20	0.47
54:5:978:G:OP2	56:E:61:ARG:NH1	2.47	0.47
54:5:1292:C:O2	54:5:1292:C:H2'	2.15	0.47
54:5:1557:C:H2'	54:5:1558:A:C8	2.49	0.47
54:5:1942:A:N3	54:5:4432:C:O2'	2.40	0.47
54:5:2362:U:H2'	54:5:2363:A:H8	1.79	0.47
54:5:2454:U:C2	54:5:2455:G:C8	3.03	0.47
54:5:2734:U:H2'	54:5:2735:G:H8	1.79	0.47
54:5:4237:C:OP1	54:5:4327:C:O2'	2.33	0.47
54:5:4303:C:H2'	54:5:4305:G:H8	1.79	0.47
54:5:4748:U:H3	54:5:4952:G:H1	1.62	0.47
61:DD:53:ILE:HD13	61:DD:81:LEU:HD21	1.97	0.47
14:I:14:ASN:O	14:I:128:ARG:NH2	2.45	0.47
16:K:1010:G:H2'	16:K:1011:A:H8	1.79	0.47
16:K:1253:A:OP2	16:K:1526:G:N2	2.43	0.47
16:K:1374:C:H2'	16:K:1375:G:O4'	2.15	0.47
18:M:11:ARG:NH1	18:M:58:THR:O	2.45	0.47
31:Z:59:LYS:N	54:5:4149:C:OP1	2.47	0.47
51:x:48:LEU:HD23	51:x:61:VAL:HG13	1.96	0.47
53:2:49:C:H42	53:2:65:C:H42	1.61	0.47
54:5:504:G:O2'	54:5:505:G:O5'	2.33	0.47
54:5:1755:C:H5''	54:5:1756:U:OP1	2.15	0.47
54:5:1794:A:H5''	54:5:4214:A:H61	1.79	0.47
54:5:1806:G:H2'	54:5:1807:C:C6	2.49	0.47
54:5:2616:C:H2'	54:5:2617:G:H8	1.80	0.47
54:5:4758:U:O2	54:5:4758:U:O4'	2.33	0.47
55:8:102:G:OP2	55:8:104:A:O2'	2.25	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:y:50:PRO:HG2	58:y:90:VAL:HG22	1.96	0.47
4:6:11:LEU:HB3	4:6:43:TRP:CH2	2.50	0.47
8:B:222:VAL:O	8:B:343:ARG:NH1	2.48	0.47
11:F:147:LYS:HD3	11:F:244:ARG:HH21	1.80	0.47
16:K:24:C:H42	16:K:650:A:H61	1.62	0.47
16:K:521:A:OP1	61:DD:45:ARG:NH1	2.44	0.47
16:K:929:G:H21	16:K:1104:G:H4'	1.80	0.47
16:K:987:A:C6	48:u:120:MET:HE1	2.49	0.47
16:K:1657:G:H2'	16:K:1658:G:H8	1.80	0.47
16:K:1804:U:H2'	16:K:1805:G:C8	2.50	0.47
17:L:169:ILE:HD13	32:a:142:GLY:HA2	1.96	0.47
54:5:1:C:H2'	54:5:2:G:H8	1.79	0.47
54:5:469:C:H2'	54:5:470:A:C8	2.50	0.47
54:5:4091:G:H2'	54:5:4092:G:C8	2.50	0.47
54:5:4635:A:OP1	54:5:4636:U:O2'	2.32	0.47
56:E:193:HIS:HB3	56:E:196:PHE:HD2	1.80	0.47
61:DD:67:ASP:HB3	61:DD:70:ARG:HB3	1.96	0.47
66:MM:101:GLY:HA3	66:MM:134:PRO:HG2	1.96	0.47
16:K:640:A:H2'	16:K:641:A:H8	1.80	0.47
16:K:1060:A:N3	16:K:1060:A:H2'	2.30	0.47
16:K:1801:A:H2'	16:K:1802:C:C6	2.50	0.47
26:U:84:LYS:HB2	26:U:110:TYR:CE2	2.50	0.47
27:V:19:GLY:O	54:5:2846:G:O2'	2.29	0.47
47:r:104:PRO:O	47:r:107:ARG:HG2	2.15	0.47
54:5:447:C:H2'	54:5:448:G:C8	2.50	0.47
54:5:956:A:N6	54:5:1283:G:H1'	2.30	0.47
54:5:2417:A:C8	84:EH:42:UNK:HA	2.50	0.47
54:5:2520:C:H2'	54:5:2521:G:C8	2.48	0.47
54:5:2689:C:H2'	54:5:2690:C:C6	2.50	0.47
54:5:3932:U:H2'	54:5:3933:G:C8	2.48	0.47
56:E:172:SER:OG	56:E:217:ASP:OD2	2.33	0.47
74:TT:60:LYS:NZ	79:JJ:23:ARG:O	2.48	0.47
2:0:132:MET:HE3	2:0:132:MET:HB3	1.76	0.46
4:6:110:SER:HB3	4:6:153:CYS:HA	1.97	0.46
12:G:305:LYS:NZ	54:5:4090:G:OP1	2.39	0.46
15:J:98:ASN:HD22	54:5:4250:G:H5''	1.81	0.46
15:J:151:ILE:HD11	15:J:156:ARG:HG2	1.97	0.46
16:K:381:C:H41	60:CC:27:TYR:HB2	1.80	0.46
16:K:794:A:H2'	16:K:795:A:H8	1.79	0.46
20:O:47:PHE:HA	20:O:136:ALA:HB2	1.97	0.46
23:R:78:ILE:HD13	23:R:81:ARG:HH21	1.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:e:78:LEU:HB3	47:r:20:ARG:HD3	1.97	0.46
38:h:70:ARG:HB3	38:h:83:LEU:HD22	1.96	0.46
38:h:81:LEU:HD13	55:8:38:U:H5'	1.97	0.46
51:x:71:LYS:HG2	51:x:76:VAL:HG22	1.96	0.46
54:5:517:C:H2'	54:5:518:G:H8	1.80	0.46
54:5:2765:A:H2'	54:5:2766:A:H8	1.80	0.46
60:CC:66:SER:HA	60:CC:73:THR:HB	1.97	0.46
75:VV:91:LEU:HB3	81:AA:82:VAL:HG11	1.96	0.46
7:A:13:GLY:O	7:A:14:SER:OG	2.33	0.46
14:I:135:ILE:HG22	14:I:136:MET:HG3	1.97	0.46
16:K:115:U:H2'	16:K:116:U:C6	2.50	0.46
16:K:1629:C:OP1	70:II:39:ARG:NH1	2.49	0.46
16:K:1649:U:H2'	16:K:1650:A:H8	1.80	0.46
36:f:106:TYR:HB2	56:E:196:PHE:HD1	1.79	0.46
53:2:43:A:H2'	53:2:44:A:C8	2.50	0.46
54:5:189:G:H2'	54:5:190:G:C8	2.49	0.46
54:5:520:U:H2'	54:5:521:C:C6	2.50	0.46
54:5:674:G:H2'	54:5:675:C:C6	2.50	0.46
54:5:979:C:H2'	54:5:980:U:C6	2.49	0.46
54:5:1290:G:H2'	54:5:1291:G:H8	1.80	0.46
54:5:1329:G:O2'	54:5:1330:A:OP1	2.25	0.46
54:5:1563:A:O2'	54:5:1564:A:H8	1.99	0.46
54:5:2708:U:H1'	54:5:2709:C:H4'	1.97	0.46
54:5:4448:G:H5''	54:5:4449:A:H5'	1.96	0.46
67:WW:39:ALA:HA	67:WW:42:ARG:HG2	1.97	0.46
75:VV:90:CYS:HB3	75:VV:130:LEU:HD11	1.98	0.46
10:D:36:LEU:HD23	54:5:4325:A:H1'	1.96	0.46
16:K:77:A:O2'	52:z:174:PRO:O	2.32	0.46
16:K:561:A:H2'	16:K:562:U:O4'	2.14	0.46
16:K:681:U:H4'	75:VV:9:THR:HG22	1.98	0.46
16:K:804:U:H2'	16:K:805:U:C6	2.51	0.46
16:K:1325:G:H1'	16:K:1510:G:H5''	1.98	0.46
16:K:1808:U:H2'	16:K:1809:A:C8	2.50	0.46
24:S:15:ARG:HB3	24:S:27:LEU:HD23	1.98	0.46
33:c:17:ARG:HE	33:c:104:ILE:HA	1.80	0.46
47:r:108:MET:O	47:r:112:ARG:HG2	2.15	0.46
53:2:11:U:H2'	53:2:12:G:C8	2.50	0.46
54:5:1072:C:H42	54:5:1239:C:H42	1.63	0.46
54:5:1760:G:H2'	54:5:1761:G:C8	2.49	0.46
54:5:2029:A:H2'	54:5:2030:A:C8	2.49	0.46
54:5:2412:A:H2'	54:5:2413:U:C6	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:5:2638:G:H22	54:5:2719:C:P	2.39	0.46
54:5:3598:C:H2'	54:5:3599:A:C8	2.51	0.46
54:5:4670:C:O3'	54:5:4671:C:H3'	2.14	0.46
54:5:4750:G:H2'	54:5:4751:G:C8	2.50	0.46
60:CC:25:ARG:HB2	60:CC:28:GLU:HG2	1.98	0.46
69:KK:16:ILE:HG22	69:KK:24:LEU:HD11	1.98	0.46
82:EF:98:GLN:HB2	82:EF:101:GLU:HG3	1.97	0.46
4:6:72:SER:OG	4:6:74:ASP:OD1	2.24	0.46
7:A:116:LEU:HA	7:A:164:ALA:HB2	1.96	0.46
16:K:211:G:H2'	16:K:212:C:H6	1.81	0.46
16:K:1321:G:H2'	16:K:1322:G:C8	2.50	0.46
29:X:80:PRO:HA	29:X:98:PHE:HA	1.97	0.46
32:a:55:LYS:HD3	54:5:92:C:C2	2.51	0.46
38:h:103:LYS:NZ	38:h:111:GLU:OE1	2.48	0.46
54:5:1080:C:O2'	54:5:1081:C:O4'	2.32	0.46
54:5:1490:G:H2'	54:5:1491:A:H8	1.81	0.46
54:5:3916:G:H2'	54:5:3917:A:C8	2.50	0.46
54:5:4153:C:H2'	54:5:4154:G:H8	1.81	0.46
54:5:4889:G:H2'	54:5:4890:G:H8	1.80	0.46
54:5:4947:U:H2'	54:5:4948:C:C2	2.50	0.46
61:DD:136:ARG:NH1	61:DD:159:PHE:O	2.49	0.46
61:DD:162:ARG:NH2	76:NN:31:GLY:HA2	2.31	0.46
68:UU:97:GLN:HB2	68:UU:105:LYS:HG3	1.96	0.46
79:JJ:56:CYS:SG	79:JJ:57:VAL:N	2.88	0.46
7:A:29:LEU:O	7:A:123:ARG:NE	2.30	0.46
16:K:830:A:C5	16:K:831:G:H1'	2.50	0.46
16:K:902:G:H2'	16:K:903:A:C8	2.50	0.46
16:K:1148:A:H4'	16:K:1149:A:O4'	2.16	0.46
16:K:1310:U:H2'	16:K:1311:C:C5	2.50	0.46
22:Q:178:ARG:H	32:a:51:GLY:HA2	1.79	0.46
49:v:127:PHE:HD2	49:v:141:LEU:HD22	1.80	0.46
52:z:50:VAL:HG21	52:z:111:LEU:HB3	1.98	0.46
54:5:318:A:H2'	54:5:319:A:C8	2.49	0.46
54:5:500:G:H3'	54:5:504:G:H5'	1.98	0.46
54:5:664:G:HO2'	54:5:668:C:H42	1.57	0.46
54:5:734:G:H2'	54:5:735:G:H8	1.81	0.46
54:5:3712:A:H2'	54:5:3712:A:N3	2.30	0.46
54:5:3861:A:H2'	54:5:3862:A:H8	1.80	0.46
54:5:4074:C:H2'	54:5:4075:U:C6	2.50	0.46
54:5:4146:G:H2'	54:5:4147:G:C8	2.51	0.46
54:5:4392:G:N2	54:5:4395:U:O2	2.42	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
82:EF:64:MET:HE1	83:EG:91:VAL:HG13	1.96	0.46
7:A:136:VAL:HA	7:A:148:VAL:HG12	1.96	0.46
10:D:108:ARG:CZ	10:D:253:TYR:HB2	2.46	0.46
13:H:17:ASP:OD1	13:H:17:ASP:N	2.45	0.46
16:K:164:A:H2'	16:K:165:G:C4	2.50	0.46
16:K:1139:C:H41	16:K:1149:A:H62	1.62	0.46
16:K:1625:U:H2'	16:K:1626:C:C6	2.51	0.46
18:M:24:LEU:HB2	18:M:43:THR:HG21	1.98	0.46
32:a:6:ARG:NH2	54:5:1340:C:OP1	2.49	0.46
49:v:66:LEU:HD22	49:v:93:ILE:HD13	1.97	0.46
54:5:1207:C:H2'	54:5:1208:G:H8	1.80	0.46
54:5:1402:C:H2'	54:5:1403:G:C8	2.51	0.46
54:5:1725:U:H2'	54:5:1726:U:H6	1.81	0.46
54:5:1733:G:N3	54:5:4214:A:H2'	2.30	0.46
54:5:4688:C:H2'	54:5:4689:U:C6	2.51	0.46
70:II:60:THR:OG1	70:II:62:ASP:OD1	2.28	0.46
71:PP:83:GLN:HB2	71:PP:93:SER:HB2	1.96	0.46
4:6:149:GLU:HB3	4:6:170:TRP:HB2	1.97	0.46
14:I:42:LYS:N	14:I:45:GLU:OE2	2.48	0.46
16:K:211:G:H2'	16:K:212:C:C6	2.51	0.46
16:K:512:A:C2	16:K:513:G:C8	3.04	0.46
16:K:532:C:H4'	16:K:532:C:OP1	2.14	0.46
16:K:942:G:H2'	16:K:943:U:C6	2.51	0.46
16:K:1298:G:H2'	16:K:1298:G:N3	2.30	0.46
16:K:1473:G:H2'	16:K:1475:G:N2	2.30	0.46
16:K:1619:A:O2'	67:WW:82:ASP:OD2	2.33	0.46
44:o:4:VAL:HG23	44:o:93:LEU:HD13	1.97	0.46
51:x:182:MET:N	51:x:226:PHE:O	2.48	0.46
54:5:426:A:H2'	54:5:427:A:H8	1.80	0.46
54:5:695:G:H3'	54:5:696:C:C4'	2.46	0.46
54:5:738(A):C:O2'	54:5:740:G:OP2	2.31	0.46
54:5:980:U:H2'	54:5:981:C:C6	2.50	0.46
77:OO:47:LEU:HB3	77:OO:79:ILE:HG22	1.98	0.46
11:F:42:ARG:O	11:F:46:ARG:HG2	2.16	0.46
16:K:616:A:H1'	81:AA:85:VAL:HG23	1.97	0.46
16:K:1533:A:H2	16:K:1536:G:N3	2.13	0.46
16:K:1568:C:H2'	16:K:1569:A:C8	2.51	0.46
16:K:1756:C:H2'	16:K:1757:G:H8	1.81	0.46
23:R:67:THR:O	23:R:71:ARG:HG2	2.15	0.46
24:S:93:MET:HE1	24:S:117:HIS:CE1	2.51	0.46
49:v:90:GLU:HB3	49:v:93:ILE:HG13	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:5:700:G:H2'	54:5:701:G:C8	2.49	0.46
54:5:1079:C:H2'	54:5:1080:C:H5''	1.98	0.46
54:5:1084:C:C4	54:5:1216:C:C4	3.04	0.46
54:5:4492:U:H5''	54:5:4493:U:H5'	1.98	0.46
60:CC:69:SER:OG	60:CC:70:GLU:OE1	2.23	0.46
61:DD:54:ARG:NH1	61:DD:98:LEU:O	2.49	0.46
61:DD:114:VAL:HG13	61:DD:119:LEU:HB2	1.96	0.46
71:PP:56:ARG:HH22	71:PP:99:VAL:HB	1.81	0.46
8:B:234:ARG:NH2	54:5:4566:U:O2'	2.43	0.46
10:D:72:ASP:N	10:D:72:ASP:OD1	2.46	0.46
16:K:161:U:O2'	52:z:87:ARG:NH1	2.48	0.46
16:K:184:G:C2	16:K:185:G:C8	3.04	0.46
17:L:61:CYS:SG	17:L:71:ARG:HG3	2.56	0.46
46:q:85:ARG:HH21	46:q:201:LEU:HD12	1.80	0.46
51:x:11:ARG:HA	51:x:28:ALA:HB2	1.98	0.46
51:x:126:VAL:HA	51:x:141:THR:HA	1.98	0.46
54:5:2467:U:H4'	54:5:2468:U:H5'	1.98	0.46
54:5:2517:A:N3	54:5:2539:C:O2'	2.48	0.46
54:5:4460:U:H2'	54:5:4461:C:C6	2.51	0.46
55:8:141:C:H2'	55:8:142:U:H6	1.81	0.46
1:m:69:ILE:HD12	54:5:4473:A:H5''	1.97	0.46
4:6:31:ILE:HG22	4:6:43:TRP:HB2	1.98	0.46
7:A:24:LYS:HG3	7:A:49:ILE:HD12	1.97	0.46
12:G:313:GLU:O	12:G:317:LYS:HG2	2.15	0.46
16:K:436:G:OP1	16:K:471:G:O2'	2.34	0.46
37:g:97:ILE:HG12	54:5:4120:U:C4	2.51	0.46
50:w:170:THR:HG22	50:w:187:LYS:HG2	1.98	0.46
54:5:673:C:H2'	54:5:674:G:C8	2.50	0.46
54:5:3648:A:H1'	54:5:3785:A:N6	2.31	0.46
54:5:3910:C:H2'	54:5:3911:C:H6	1.81	0.46
54:5:4153:C:H2'	54:5:4154:G:C8	2.51	0.46
61:DD:136:ARG:HH11	61:DD:160:SER:HA	1.80	0.46
68:UU:16:LYS:HG3	68:UU:17:LYS:H	1.81	0.46
76:NN:38:THR:OG1	76:NN:39:GLU:OE1	2.29	0.46
7:A:241:ARG:NH1	54:5:3659:G:OP1	2.49	0.45
12:G:161:GLN:O	12:G:165:GLN:HG2	2.17	0.45
16:K:506:G:OP1	76:NN:108:LYS:NZ	2.36	0.45
16:K:1646:C:H2'	16:K:1678:A:N1	2.31	0.45
17:L:34:ARG:NH2	55:8:30:U:OP1	2.44	0.45
20:O:110:PRO:N	20:O:111:PRO:HD2	2.30	0.45
23:R:25:ASP:OD2	82:EF:28:ARG:NH2	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:V:26:ILE:O	27:V:37:LEU:N	2.45	0.45
30:Y:8:THR:OG1	54:5:346:G:OP1	2.33	0.45
31:Z:121:ARG:O	31:Z:124:THR:OG1	2.31	0.45
45:p:38:THR:HA	45:p:45:THR:HA	1.97	0.45
54:5:328:A:H2'	54:5:329:A:C8	2.52	0.45
54:5:745:G:H2'	54:5:746:A:C8	2.51	0.45
54:5:2413:U:H2'	54:5:2414:G:H8	1.81	0.45
54:5:4173:G:H2'	54:5:4174:U:H6	1.80	0.45
54:5:4719:G:O2'	54:5:4720:C:O5'	2.30	0.45
57:b:36:ASP:OD1	57:b:36:ASP:N	2.49	0.45
8:B:116:ARG:HD3	8:B:122:TRP:CD2	2.51	0.45
9:C:302:LEU:HD22	22:Q:38:ARG:HB3	1.99	0.45
13:H:75:SER:OG	54:5:4691:A:OP1	2.33	0.45
16:K:49:C:H2'	16:K:472:C:H41	1.81	0.45
16:K:674:C:H2'	16:K:675:U:C6	2.51	0.45
16:K:1109:C:H2'	16:K:1110:G:H5'	1.97	0.45
25:T:78:LYS:NZ	54:5:4301:U:OP1	2.44	0.45
25:T:81:LYS:O	57:b:16:TRP:NE1	2.49	0.45
36:f:33:VAL:HG23	36:f:38:GLU:HB2	1.98	0.45
46:q:121:LEU:HD12	46:q:143:PRO:HG2	1.98	0.45
54:5:432:U:OP2	54:5:3888:G:N2	2.49	0.45
54:5:447:C:H2'	54:5:448:G:H8	1.81	0.45
54:5:1298:C:H2'	54:5:1299:G:C8	2.51	0.45
54:5:1317:U:H2'	54:5:1318:C:C6	2.51	0.45
54:5:2041:A:N7	54:5:4434:C:O2'	2.49	0.45
54:5:2089:G:H4'	54:5:2090:U:O5'	2.16	0.45
54:5:2640:G:H2'	54:5:2641:A:C8	2.51	0.45
54:5:4188:U:H2'	54:5:4189:U:H6	1.81	0.45
65:QQ:29:THR:HG23	65:QQ:32:ASP:H	1.80	0.45
13:H:41:ILE:HG12	13:H:73:ILE:HD11	1.98	0.45
13:H:107:GLU:HB3	13:H:110:SER:HB2	1.98	0.45
16:K:434:G:H2'	16:K:435:A:C8	2.52	0.45
16:K:828:G:H4'	51:x:23:LEU:HD22	1.98	0.45
16:K:853:C:H2'	16:K:854:A:H8	1.82	0.45
16:K:1473:G:H2'	16:K:1475:G:H22	1.82	0.45
16:K:1545:A:H2	16:K:1671:G:H1'	1.82	0.45
20:O:117:ARG:NH2	54:5:4758:U:O2'	2.49	0.45
20:O:130:LYS:HB2	20:O:133:ARG:HG2	1.97	0.45
20:O:181:ALA:O	20:O:185:VAL:HG23	2.17	0.45
23:R:4:LEU:HD22	23:R:32:ILE:HG22	1.98	0.45
54:5:676:C:H2'	54:5:677:G:C8	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:5:978:G:H21	54:5:1277:G:H1	1.63	0.45
54:5:1072:C:N4	54:5:1239:C:H42	2.15	0.45
7:A:50:HIS:HE1	54:5:2741:U:OP2	2.00	0.45
16:K:988:C:O2'	48:u:118:GLN:O	2.33	0.45
16:K:1600:G:H5'	77:OO:43:LYS:HG3	1.98	0.45
54:5:452:A:H4'	54:5:453:G:C4	2.51	0.45
54:5:1346:C:H2'	54:5:1347:G:C8	2.51	0.45
54:5:4954:G:H2'	54:5:4955:A:H8	1.81	0.45
2:O:95:ARG:HH12	16:K:1289:U:H5	1.63	0.45
7:A:14:SER:H	7:A:17:ARG:HG3	1.81	0.45
15:J:26:VAL:HG23	15:J:28:GLU:H	1.81	0.45
16:K:534:G:H2'	16:K:535:G:H8	1.80	0.45
16:K:917:U:H2'	16:K:918:U:C6	2.52	0.45
16:K:1010:G:H2'	16:K:1011:A:C8	2.52	0.45
16:K:1158:G:H5''	74:TT:76:SER:OG	2.16	0.45
18:M:29:ASP:OD1	18:M:30:VAL:N	2.47	0.45
20:O:58:LEU:HD11	20:O:145:VAL:HG13	1.98	0.45
23:R:82:LYS:O	54:5:2863:G:O2'	2.31	0.45
54:5:674:G:H2'	54:5:675:C:H6	1.81	0.45
54:5:1390:G:N2	54:5:1393:G:OP2	2.39	0.45
54:5:1639:U:O2	54:5:1639:U:H2'	2.16	0.45
54:5:1870:C:H2'	54:5:1871:A:H8	1.82	0.45
54:5:1927:U:OP1	54:5:1949:U:O2'	2.27	0.45
54:5:3911:C:H2'	54:5:3912:U:C6	2.51	0.45
54:5:4266:G:N3	54:5:4266:G:H2'	2.32	0.45
54:5:5019:A:H2'	54:5:5020:G:H8	1.81	0.45
65:QQ:13:GLN:HE21	79:JJ:21:LYS:HE2	1.80	0.45
72:GG:20:ILE:HG23	72:GG:91:LEU:HB3	1.97	0.45
76:NN:29:HIS:ND1	76:NN:29:HIS:O	2.50	0.45
8:B:86:VAL:HG12	8:B:201:LEU:HD12	1.98	0.45
10:D:205:ALA:HB1	10:D:233:PRO:HB3	1.98	0.45
16:K:1278:A:H2'	16:K:1279:C:C6	2.51	0.45
16:K:1845:A:H2'	16:K:1846:G:C8	2.52	0.45
18:M:20:HIS:HB3	18:M:23:LYS:HD2	1.99	0.45
18:M:106:ASP:OD2	56:E:273:TYR:OH	2.30	0.45
25:T:41:ASP:HA	25:T:61:THR:HA	1.99	0.45
50:w:103:GLU:HA	50:w:106:ARG:HG2	1.99	0.45
54:5:220:C:O2'	54:5:221:C:O5'	2.32	0.45
54:5:3727:A:H2'	54:5:3728:A:C8	2.51	0.45
54:5:3944:G:H2'	54:5:3945:A:C8	2.51	0.45
54:5:4077:A:N1	54:5:4171:C:N4	2.61	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:5:4174:U:H2'	54:5:4175:G:C8	2.51	0.45
62:SS:55:ARG:HG3	62:SS:57:TYR:HD2	1.81	0.45
9:C:60:HIS:HA	9:C:92:PHE:HE1	1.80	0.45
16:K:302:A:H4'	60:CC:74:ARG:HH21	1.80	0.45
16:K:550:C:C2	16:K:551:U:C5	3.05	0.45
16:K:815:U:C2	16:K:816:A:C8	3.04	0.45
16:K:1424:G:H2'	16:K:1425:G:H8	1.82	0.45
16:K:1527:C:OP1	68:UU:142:GLN:NE2	2.49	0.45
54:5:432:U:H4'	54:5:433:A:H5''	1.99	0.45
54:5:1761:G:C5	54:5:1762:C:C4	3.04	0.45
54:5:2034:G:H2'	54:5:2035:C:C6	2.51	0.45
54:5:4088:C:H2'	54:5:4089:G:C8	2.51	0.45
54:5:5019:A:H2'	54:5:5020:G:C8	2.51	0.45
55:8:92:U:H2'	55:8:93:C:O4'	2.17	0.45
62:SS:57:TYR:HD1	62:SS:75:GLY:HA2	1.82	0.45
68:UU:34:VAL:HG22	68:UU:70:VAL:HB	1.99	0.45
71:PP:11:GLN:HG2	71:PP:62:ARG:NH2	2.32	0.45
78:LL:24:THR:HG21	78:LL:71:LEU:HA	1.97	0.45
7:A:47:ASP:HA	7:A:84:THR:HG22	1.99	0.45
16:K:171:A:OP1	52:z:178:ARG:HD2	2.16	0.45
16:K:600:G:H2'	16:K:601:G:C8	2.51	0.45
16:K:897:U:H2'	16:K:898:U:H6	1.81	0.45
16:K:1012:A:OP1	65:QQ:3:ARG:NH1	2.49	0.45
16:K:1802:C:H2'	16:K:1803:U:C6	2.51	0.45
20:O:87:MET:HE3	54:5:1912:G:N2	2.31	0.45
24:S:170:LYS:NZ	54:5:4874:A:O2'	2.46	0.45
25:T:87:LYS:HZ2	54:5:4305:G:N2	2.15	0.45
32:a:4:ARG:H	32:a:4:ARG:HD3	1.82	0.45
37:g:69:LYS:HD3	54:5:2769:U:N3	2.32	0.45
49:v:70:VAL:HB	49:v:75:ILE:HD11	1.99	0.45
54:5:23:C:H2'	54:5:24:G:O4'	2.16	0.45
54:5:1069:G:O6	56:E:45:HIS:NE2	2.50	0.45
54:5:1076:C:H2'	54:5:1077:C:C6	2.52	0.45
54:5:1433:A:H62	54:5:1451:G:N2	2.14	0.45
54:5:1920:C:H3'	54:5:1921:C:H5''	1.98	0.45
54:5:3855:C:H2'	54:5:3856:A:H8	1.81	0.45
54:5:4146:G:H2'	54:5:4147:G:H8	1.81	0.45
54:5:4598:C:H2'	54:5:4611:A:H61	1.82	0.45
54:5:4954:G:H2'	54:5:4955:A:C8	2.52	0.45
4:6:173:LEU:HD22	4:6:189:ILE:HG12	1.98	0.45
6:9:27:ARG:HD2	16:K:1263:U:H4'	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:C:323:ARG:HG3	54:5:1280:C:C2'	2.40	0.45
12:G:104:LEU:O	12:G:108:VAL:HG23	2.17	0.45
16:K:449:A:O2'	16:K:450:C:H4'	2.17	0.45
16:K:901:G:H2'	16:K:902:G:C8	2.52	0.45
19:N:44:ARG:NH1	19:N:120:TRP:O	2.50	0.45
30:Y:22:PRO:O	30:Y:26:ARG:HG2	2.16	0.45
46:q:38:ILE:HD12	46:q:47:TYR:HB3	1.99	0.45
58:y:127:ARG:HG3	58:y:136:ARG:HG2	1.99	0.45
74:TT:101:PHE:HA	74:TT:113:HIS:HE1	1.82	0.45
4:6:186:THR:HA	50:w:226:GLN:HA	1.99	0.45
4:6:216:ALA:HB3	4:6:230:LEU:HB2	1.99	0.45
8:B:122:TRP:CE2	8:B:127:LYS:HE3	2.52	0.45
16:K:943:U:H2'	16:K:944:A:C8	2.50	0.45
16:K:1332:A:O2'	50:w:145:GLN:O	2.32	0.45
16:K:1453:C:N3	16:K:1455:A:C8	2.85	0.45
16:K:1598:G:OP1	77:OO:80:ARG:NH2	2.50	0.45
20:O:61:ARG:HA	20:O:70:PRO:HD2	1.98	0.45
24:S:69:GLU:HG3	24:S:101:THR:HG22	1.99	0.45
26:U:115:PHE:HB2	82:EF:14:LEU:HD11	1.99	0.45
26:U:115:PHE:HD1	82:EF:29:LYS:HA	1.81	0.45
30:Y:109:LEU:HD22	30:Y:115:ARG:HH21	1.82	0.45
46:q:90:PHE:HD1	46:q:179:ALA:HB2	1.82	0.45
49:v:78:LEU:HA	49:v:81:ILE:HD13	1.98	0.45
49:v:166:ARG:HD3	49:v:181:LEU:HD22	1.99	0.45
53:2:6:C:H2'	53:2:7:G:C8	2.52	0.45
54:5:275:C:H2'	54:5:276:C:C6	2.51	0.45
54:5:2079:G:H2'	54:5:2080:U:C6	2.52	0.45
54:5:2280:G:N2	54:5:2281:U:O4	2.50	0.45
54:5:4151:G:H2'	54:5:4152:G:H8	1.82	0.45
54:5:4925:U:H4'	54:5:4926:C:O5'	2.16	0.45
72:GG:86:LYS:O	72:GG:87:ARG:NE	2.50	0.45
78:LL:64:LEU:HD12	78:LL:65:PRO:HD2	1.99	0.45
8:B:324:GLY:HA2	54:5:5051:C:H5''	1.99	0.44
9:C:195:LYS:HE2	54:5:2333:G:H5''	1.98	0.44
11:F:24:PHE:HD1	11:F:27:LEU:HB2	1.82	0.44
13:H:92:MET:HG3	13:H:144:LEU:HB2	1.99	0.44
16:K:3:C:O2	61:DD:18:ARG:NH1	2.36	0.44
17:L:60:ARG:HD2	17:L:67:HIS:O	2.17	0.44
20:O:54:TYR:CE1	20:O:145:VAL:HG11	2.53	0.44
20:O:166:ILE:HG12	20:O:169:ARG:HH22	1.82	0.44
34:d:70:LYS:HD3	54:5:2388:A:O2'	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:e:79:VAL:HG13	35:e:84:GLU:HB2	1.99	0.44
41:k:17:ARG:NH1	54:5:2772:C:O2'	2.50	0.44
49:v:135:GLY:HA2	49:v:165:VAL:HG12	1.98	0.44
50:w:218:LEU:HD12	50:w:219:PRO:HD2	1.98	0.44
54:5:18:C:H2'	54:5:19:G:H8	1.81	0.44
54:5:1338:G:H4'	54:5:1339:U:C6	2.52	0.44
54:5:1769:G:H2'	54:5:1770:A:C8	2.52	0.44
54:5:2448:G:H2'	54:5:2449:A:C8	2.53	0.44
54:5:2465:C:H2'	54:5:2466:G:O4'	2.17	0.44
54:5:3910:C:H2'	54:5:3911:C:C6	2.51	0.44
55:8:19:C:H2'	55:8:20:A:C8	2.51	0.44
79:JJ:50:ALA:O	79:JJ:51:GLN:HG2	2.17	0.44
6:9:23:VAL:HA	62:SS:64:TRP:HB3	1.98	0.44
7:A:108:PRO:HG2	45:p:86:LEU:HD23	1.99	0.44
10:D:176:SER:HB3	54:5:4323:A:H4'	2.00	0.44
16:K:1124:C:H5''	48:u:150:ILE:HG12	1.98	0.44
16:K:1406:G:H2'	16:K:1407:U:C6	2.52	0.44
16:K:1579:A:OP2	50:w:7:LYS:HG2	2.17	0.44
16:K:1620:A:H2'	16:K:1620:A:N3	2.33	0.44
16:K:1742:C:H2'	16:K:1743:G:O4'	2.18	0.44
23:R:24:LEU:HD12	23:R:32:ILE:HG21	1.99	0.44
27:V:112:MET:HE2	27:V:135:ASN:HD22	1.82	0.44
50:w:50:ILE:HD11	50:w:86:LEU:HD23	2.00	0.44
53:2:51:U:H2'	53:2:52:G:C8	2.52	0.44
54:5:65:A:H61	54:5:75:G:H1'	1.82	0.44
54:5:452:A:H4'	54:5:453:G:C5	2.52	0.44
54:5:709:C:H1'	54:5:4942:C:C5	2.52	0.44
54:5:976:G:H22	54:5:1279:A:H2	1.59	0.44
56:E:179:THR:HG21	56:E:189:LEU:HD13	1.98	0.44
80:FF:18:LEU:HB2	80:FF:29:GLN:HB3	1.99	0.44
80:FF:30:VAL:HG21	80:FF:50:VAL:HG11	1.99	0.44
6:9:42:CYS:HA	6:9:45:GLN:HG2	1.99	0.44
16:K:532:C:HO2'	16:K:533:A:P	2.39	0.44
16:K:734:C:H2'	16:K:735:C:C6	2.53	0.44
16:K:903:A:H2'	16:K:904:A:C8	2.53	0.44
16:K:974:C:H2'	16:K:975:G:H8	1.83	0.44
18:M:109:ARG:CZ	56:E:289:LEU:HD12	2.47	0.44
22:Q:18:PRO:HD3	22:Q:52:PHE:CD1	2.52	0.44
48:u:25:PHE:HZ	66:MM:53:ILE:HA	1.82	0.44
50:w:49:ILE:HG22	50:w:87:TYR:HB2	1.99	0.44
54:5:1593:A:H5''	54:5:2839:U:H5''	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:5:1759:G:H2'	54:5:1760:G:O4'	2.17	0.44
54:5:2632:U:C2	54:5:2633:U:C5	3.05	0.44
54:5:4561:C:H2'	54:5:4562:C:H6	1.82	0.44
54:5:4749:C:H2'	54:5:4750:G:C8	2.53	0.44
55:8:32:C:H2'	55:8:33:G:O4'	2.18	0.44
55:8:69:U:H2'	55:8:70:G:O4'	2.16	0.44
65:QQ:118:ILE:HD13	65:QQ:121:ARG:HH12	1.83	0.44
70:II:38:ARG:O	70:II:42:HIS:ND1	2.47	0.44
5:7:83:A:H4'	11:F:223:THR:HB	1.99	0.44
16:K:600:G:H2'	16:K:601:G:H8	1.81	0.44
16:K:821:G:H22	61:DD:148:ILE:HG23	1.83	0.44
16:K:1298:G:N7	67:WW:79:HIS:ND1	2.65	0.44
16:K:1606:G:N2	16:K:1632:G:H1'	2.32	0.44
16:K:1839:U:H2'	16:K:1840:U:C6	2.53	0.44
18:M:97:ALA:HB2	20:O:203:VAL:HB	1.98	0.44
19:N:169:ARG:NH2	54:5:63:G:OP1	2.48	0.44
20:O:54:TYR:OH	20:O:73:PHE:O	2.35	0.44
25:T:130:ARG:NH2	54:5:1802:A:N3	2.55	0.44
32:a:121:PRO:HA	32:a:141:GLY:O	2.17	0.44
36:f:106:TYR:CD1	36:f:107:PRO:HD3	2.53	0.44
38:h:12:LYS:NZ	38:h:20:GLN:OE1	2.49	0.44
45:p:6:LYS:H	54:5:2876:G:P	2.40	0.44
50:w:38:GLU:HB3	50:w:49:ILE:HG13	1.98	0.44
54:5:35:U:O2'	54:5:1525:A:N1	2.44	0.44
54:5:710:G:H2'	54:5:711:A:H8	1.82	0.44
54:5:734:G:H1	54:5:929:A:H62	1.65	0.44
54:5:758:G:H2'	54:5:759:G:C8	2.53	0.44
54:5:4739:C:H2'	54:5:4740:G:C8	2.53	0.44
54:5:4761:G:H2'	54:5:4762:A:C8	2.52	0.44
56:E:281:THR:OG1	56:E:282:ASN:N	2.50	0.44
70:II:15:VAL:HG23	70:II:33:ILE:HD11	1.99	0.44
8:B:261:ARG:HB3	54:5:4564:A:O2'	2.18	0.44
14:I:87:ILE:HG12	14:I:138:ILE:HG12	1.98	0.44
16:K:380:G:P	60:CC:56:ARG:HH21	2.40	0.44
16:K:419:G:N2	16:K:661:U:O2	2.51	0.44
16:K:1103:C:H2'	16:K:1104:G:H8	1.81	0.44
16:K:1277:C:H2'	16:K:1278:A:C8	2.50	0.44
16:K:1528:G:H2'	16:K:1529:C:C6	2.53	0.44
16:K:1810:U:H2'	16:K:1811:C:C6	2.53	0.44
16:K:1829:G:H1'	16:K:1850:A:H2	1.83	0.44
17:L:91:ALA:HB1	17:L:96:ILE:HB	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:d:92:ARG:HA	34:d:102:LEU:HD23	1.99	0.44
54:5:4574:U:H3'	54:5:4575:G:H5''	2.00	0.44
54:5:4947:U:O2'	54:5:4948:C:OP1	2.32	0.44
56:E:116:PRO:HG2	56:E:119:TYR:CZ	2.52	0.44
8:B:215:GLU:OE2	8:B:349:LYS:NZ	2.48	0.44
16:K:1199:A:H2'	16:K:1200:A:C8	2.53	0.44
46:q:5:LEU:O	46:q:9:GLN:HG2	2.17	0.44
50:w:55:THR:HA	50:w:58:VAL:HG12	2.00	0.44
51:x:240:ARG:H	51:x:240:ARG:HD2	1.83	0.44
52:z:121:ILE:HG22	52:z:124:LEU:H	1.82	0.44
53:2:4:U:H3	53:2:69:G:H1	1.66	0.44
54:5:50:C:C2	54:5:51:A:C8	3.06	0.44
54:5:86:U:H2'	54:5:87:A:H8	1.82	0.44
54:5:180:C:C4	54:5:181:C:N4	2.86	0.44
54:5:261:G:H2'	54:5:262:G:O4'	2.18	0.44
54:5:2560:C:H2'	54:5:2561:C:C6	2.53	0.44
54:5:2756:G:H2'	54:5:2757:A:C8	2.53	0.44
54:5:3637:U:O4	54:5:3651:A:H2	2.00	0.44
54:5:4336:A:H5''	54:5:4337:C:H5'	1.99	0.44
54:5:4591:U:H2'	54:5:4592:C:C6	2.53	0.44
55:8:9:A:H2'	55:8:10:G:H8	1.82	0.44
5:7:58:A:H2'	5:7:59:G:H8	1.83	0.44
8:B:153:MET:HG3	8:B:157:CYS:SG	2.58	0.44
11:F:225:HIS:HB3	11:F:228:GLU:HG2	2.00	0.44
16:K:218:U:H2'	16:K:219:U:C6	2.52	0.44
16:K:371:A:H2'	16:K:371:A:N3	2.32	0.44
16:K:1237:C:H2'	16:K:1238:U:C6	2.52	0.44
16:K:1267:C:C2	16:K:1516:G:N2	2.86	0.44
16:K:1272:C:H1'	16:K:1274:G:H22	1.83	0.44
16:K:1621:U:C6	67:WW:115:TYR:CD2	3.06	0.44
35:e:104:SER:OG	54:5:2305:U:O2'	2.34	0.44
43:n:1:MET:HG3	43:n:6:ARG:HG3	1.98	0.44
50:w:120:TYR:O	50:w:124:ARG:HG2	2.18	0.44
54:5:257:C:H2'	54:5:258:G:C8	2.52	0.44
54:5:1065:G:H2'	54:5:1066:G:H8	1.83	0.44
54:5:2335:C:H2'	54:5:2336:G:H8	1.83	0.44
54:5:2415:U:H2'	54:5:2416:G:C8	2.52	0.44
54:5:2734:U:H2'	54:5:2735:G:C8	2.53	0.44
54:5:4740:G:H22	54:5:4959:U:H3	1.66	0.44
54:5:4994:G:H2'	54:5:4995:U:H6	1.81	0.44
70:II:43:VAL:HG13	71:PP:36:THR:HG22	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:6:103:GLY:O	4:6:130:LYS:NZ	2.51	0.44
11:F:121:PHE:O	11:F:204:ASN:ND2	2.50	0.44
12:G:145:ALA:HB1	12:G:237:LEU:HD21	2.00	0.44
12:G:153:HIS:CD2	12:G:156:ARG:HD2	2.53	0.44
15:J:100:SER:OG	15:J:104:ASN:O	2.35	0.44
16:K:643:A:H4'	16:K:644:G:H5'	2.00	0.44
16:K:674:C:H2'	16:K:675:U:H6	1.83	0.44
16:K:1733:U:H2'	16:K:1734:G:O4'	2.18	0.44
19:N:178:HIS:HA	19:N:181:HIS:NE2	2.32	0.44
20:O:119:VAL:HG11	24:S:171:ARG:HD3	1.99	0.44
24:S:107:THR:O	24:S:111:ARG:HG2	2.17	0.44
40:j:21:ARG:HH21	40:j:39:TYR:HA	1.82	0.44
48:u:87:ILE:HG22	48:u:101:HIS:HB2	1.99	0.44
50:w:142:LEU:HD21	50:w:182:LEU:HD21	2.00	0.44
53:2:28:U:H2'	53:2:29:A:H8	1.82	0.44
54:5:1490:G:H2'	54:5:1491:A:C8	2.53	0.44
54:5:2080:U:H2'	54:5:2081:C:C6	2.53	0.44
54:5:3861:A:H2'	54:5:3862:A:C8	2.52	0.44
54:5:4947:U:H2'	54:5:4948:C:O2	2.18	0.44
61:DD:135:ILE:HA	61:DD:159:PHE:HA	2.00	0.44
4:6:85:GLY:HA2	4:6:108:VAL:HG23	1.98	0.44
4:6:158:PRO:HG2	4:6:202:PRO:HA	2.00	0.44
5:7:62:U:O2'	5:7:64:G:O4'	2.36	0.44
12:G:233:PRO:HG2	12:G:272:VAL:HG13	1.98	0.44
16:K:841:G:C8	76:NN:12:PHE:HB3	2.52	0.44
16:K:980:A:H2'	16:K:981:A:C8	2.53	0.44
18:M:129:LYS:HD3	18:M:130:LEU:HD22	1.99	0.44
23:R:74:ARG:N	23:R:74:ARG:HD2	2.33	0.44
39:i:48:CYS:SG	39:i:49:GLY:N	2.90	0.44
51:x:224:ASN:OD1	51:x:224:ASN:N	2.47	0.44
53:2:65:C:H2'	53:2:66:C:C6	2.52	0.44
54:5:1216:C:C2	54:5:1217:G:C8	3.06	0.44
54:5:1758:G:H2'	54:5:1759:G:H8	1.83	0.44
54:5:2306:G:H1'	54:5:2332:A:N6	2.33	0.44
54:5:2565:A:H8	54:5:2565:A:O5'	2.01	0.44
54:5:2671:C:H2'	54:5:2672:C:C6	2.53	0.44
54:5:4093:G:O2'	54:5:4094:G:H8	2.00	0.44
61:DD:32:ILE:HA	61:DD:37:LEU:HD23	1.99	0.44
73:HH:64:GLU:HG2	79:JJ:3:LEU:HG	2.00	0.44
10:D:211:LEU:HD13	10:D:219:TYR:HA	2.00	0.43
12:G:152:ALA:HB1	12:G:189:LEU:HD11	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:K:340:C:H2'	16:K:341:C:C6	2.52	0.43
16:K:599:A:H2'	16:K:606:G:N2	2.32	0.43
16:K:652:U:H2'	16:K:653:A:C8	2.53	0.43
16:K:1144:A:H5'	16:K:1355:C:H41	1.83	0.43
16:K:1417:C:N3	16:K:1423:C:N4	2.65	0.43
19:N:9:GLU:HB2	39:i:44:ILE:HG13	1.99	0.43
22:Q:16:LYS:O	22:Q:33:ARG:NH2	2.51	0.43
22:Q:176:ARG:HE	54:5:1497:A:N6	2.16	0.43
24:S:9:GLU:HG3	24:S:67:VAL:HG13	2.00	0.43
26:U:45:GLU:HG3	26:U:46:ARG:HG3	1.99	0.43
54:5:1307:A:H2'	54:5:1308:C:C6	2.53	0.43
54:5:1444:G:N2	54:5:1445:U:O4	2.51	0.43
54:5:1633:G:H5'	54:5:1634:A:OP1	2.18	0.43
54:5:2811:G:N1	54:5:2814:C:OP2	2.41	0.43
54:5:3916:G:H2'	54:5:3917:A:H8	1.83	0.43
60:CC:103:LEU:HD13	60:CC:170:LYS:HD3	2.00	0.43
60:CC:191:GLU:OE1	60:CC:191:GLU:N	2.51	0.43
14:I:166:HIS:ND1	25:T:160:ALA:O	2.50	0.43
16:K:1455:A:H2'	16:K:1455:A:N3	2.34	0.43
18:M:57:LEU:HD23	18:M:57:LEU:H	1.83	0.43
28:W:46:PRO:HB2	28:W:54:LEU:HD12	2.00	0.43
40:j:20:ARG:HD2	40:j:39:TYR:CZ	2.53	0.43
44:o:44:LYS:HE2	44:o:52:THR:HB	2.00	0.43
54:5:270:U:H2'	54:5:271:C:H6	1.82	0.43
54:5:275:C:H4'	54:5:276:C:OP1	2.18	0.43
54:5:2694:G:H5'	54:5:2695:A:C2	2.53	0.43
54:5:2897:G:H2'	54:5:2898:G:C8	2.53	0.43
54:5:4460:U:H2'	54:5:4461:C:H6	1.81	0.43
61:DD:110:LEU:HD22	61:DD:130:ILE:HD11	2.01	0.43
73:HH:38:GLU:OE1	73:HH:38:GLU:N	2.51	0.43
74:TT:94:LEU:HD21	74:TT:102:ILE:HG23	2.00	0.43
4:6:163:PRO:HB2	4:6:179:LEU:HB2	2.01	0.43
5:7:4:U:H2'	5:7:5:A:H8	1.83	0.43
5:7:11:A:N1	5:7:66:G:O2'	2.51	0.43
5:7:35:U:O2	5:7:45:U:O2'	2.34	0.43
10:D:67:ALA:HA	10:D:72:ASP:HB3	1.99	0.43
16:K:849:A:H2'	16:K:850:C:C6	2.53	0.43
16:K:1064:C:H2'	16:K:1065:G:H8	1.83	0.43
36:f:4:ARG:NH1	54:5:4754:G:OP1	2.51	0.43
38:h:6:ALA:O	38:h:10:ARG:HG3	2.17	0.43
47:r:105:ASP:OD1	47:r:105:ASP:N	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:2:24:A:H2'	53:2:25:C:H6	1.83	0.43
54:5:287:U:H2'	54:5:288:G:C8	2.54	0.43
54:5:426:A:H2'	54:5:427:A:C8	2.53	0.43
54:5:1538:U:H2'	54:5:1539:G:H8	1.83	0.43
54:5:3625:G:O2'	54:5:3626:G:OP1	2.33	0.43
54:5:3888:G:O2'	54:5:3889:G:OP1	2.28	0.43
57:b:8:THR:HG22	57:b:10:HIS:H	1.82	0.43
61:DD:38:ARG:HG3	61:DD:39:ASN:ND2	2.33	0.43
4:6:39:THR:HG22	4:6:60:ARG:HG2	2.00	0.43
9:C:298:ILE:O	9:C:302:LEU:HG	2.18	0.43
10:D:35:ARG:HB2	54:5:4325:A:C2	2.54	0.43
11:F:175:ALA:HB1	54:5:2102:G:C8	2.53	0.43
16:K:647:U:H2'	16:K:648:A:C8	2.53	0.43
16:K:1288:U:H1'	16:K:1312:G:N2	2.33	0.43
16:K:1618:C:H4'	67:WW:50:ARG:HH21	1.83	0.43
16:K:1779:G:H2'	16:K:1780:G:H8	1.80	0.43
18:M:52:PHE:HA	18:M:55:MET:HG2	2.00	0.43
26:U:24:ASP:HB3	26:U:69:LYS:HD3	2.00	0.43
35:e:126:ASN:HB3	35:e:129:LEU:HD11	2.00	0.43
46:q:130:ASP:C	46:q:133:PRO:HD2	2.44	0.43
54:5:216:C:H5'	54:5:219:G:O3'	2.18	0.43
54:5:451:C:H2'	54:5:1294:A:C8	2.53	0.43
54:5:678:C:H2'	54:5:679:C:H6	1.83	0.43
54:5:1298:C:N4	54:5:1299:G:O6	2.51	0.43
54:5:1392:A:H2'	54:5:1393:G:C8	2.53	0.43
54:5:1486:C:H2'	54:5:1487:G:C8	2.53	0.43
54:5:3621:A:C8	54:5:4642:U:H1'	2.53	0.43
54:5:4186:A:H2'	54:5:4187:G:C8	2.53	0.43
54:5:4489:G:N3	54:5:4708:A:H2'	2.34	0.43
54:5:4510:A:N1	54:5:4592:C:H4'	2.33	0.43
54:5:4931:G:H2'	54:5:4931:G:N3	2.33	0.43
68:UU:13:PHE:HD2	68:UU:15:ARG:HG3	1.83	0.43
69:KK:132:ARG:H	69:KK:132:ARG:HD2	1.83	0.43
4:6:107:ASP:HB2	4:6:125:ARG:HH11	1.82	0.43
4:6:190:GLY:HA3	50:w:222:PRO:HA	2.01	0.43
4:6:246:TYR:CE2	4:6:261:LEU:HB2	2.54	0.43
8:B:73:VAL:HG22	27:V:93:GLY:HA3	2.01	0.43
12:G:214:VAL:HG23	54:5:150:U:C4	2.54	0.43
16:K:318:A:H3'	16:K:319:C:H5''	2.01	0.43
16:K:370:G:H4'	16:K:371:A:O5'	2.19	0.43
16:K:849:A:H2'	16:K:850:C:H6	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:K:1321:G:H2'	16:K:1322:G:H8	1.83	0.43
16:K:1617:G:N1	16:K:1620:A:OP2	2.50	0.43
17:L:46:ILE:HB	17:L:49:ARG:HB2	1.99	0.43
17:L:201:GLU:OE1	17:L:205:GLN:NE2	2.51	0.43
25:T:17:ARG:HD3	25:T:47:THR:HG23	2.01	0.43
31:Z:48:ARG:NH2	54:5:2576:G:OP1	2.49	0.43
48:u:179:ASN:HB2	48:u:183:GLU:HB3	2.00	0.43
53:2:60:A:OP2	53:2:60:A:H8	2.00	0.43
54:5:709:C:H1'	54:5:4942:C:H5	1.82	0.43
54:5:1450:C:H2'	54:5:1451:G:C8	2.53	0.43
54:5:1824:G:H2'	54:5:1825:A:C8	2.53	0.43
57:b:102:PRO:HA	57:b:109:ARG:HH22	1.84	0.43
62:SS:4:PRO:HD2	62:SS:7:ASN:HD21	1.83	0.43
8:B:80:GLU:OE1	8:B:323:TYR:OH	2.31	0.43
9:C:316:LYS:HD3	9:C:321:ASN:ND2	2.34	0.43
16:K:1230:C:H2'	16:K:1231:C:H6	1.83	0.43
16:K:1239:U:H2'	16:K:1241:A:OP2	2.18	0.43
16:K:1395:C:H4'	16:K:1396:A:OP1	2.19	0.43
16:K:1587:G:H5''	71:PP:77:LYS:HD3	2.00	0.43
16:K:1606:G:H22	16:K:1632:G:H1'	1.84	0.43
28:W:14:TYR:HB2	28:W:17:HIS:HD2	1.83	0.43
49:v:272:HIS:HA	49:v:275:LYS:HG2	2.00	0.43
53:2:51:U:H2'	53:2:52:G:H8	1.82	0.43
54:5:178:C:H2'	54:5:179:G:C8	2.54	0.43
54:5:487:G:H2'	54:5:488:G:H8	1.83	0.43
54:5:1749:A:H2'	54:5:1750:G:C8	2.53	0.43
54:5:1754:U:H2'	54:5:1756:U:H5	1.83	0.43
54:5:4253:A:H5'	54:5:4254:G:C8	2.54	0.43
54:5:4948:C:H2'	54:5:4949:G:N2	2.34	0.43
76:NN:10:ARG:HE	76:NN:26:ASP:CG	2.26	0.43
78:LL:11:ALA:HB3	78:LL:33:ASP:HB2	2.01	0.43
7:A:179:ILE:O	54:5:3653:A:O3'	2.37	0.43
9:C:79:VAL:HG21	9:C:86:ARG:HG2	2.00	0.43
16:K:629:A:O2'	16:K:631:U:OP1	2.37	0.43
16:K:1353:A:OP1	46:q:139:TYR:OH	2.25	0.43
16:K:1692:U:H2'	16:K:1693:G:C8	2.54	0.43
17:L:197:LYS:HD3	54:5:4358:U:H4'	2.00	0.43
19:N:33:LEU:O	19:N:65:ARG:NH2	2.52	0.43
29:X:88:LYS:HA	29:X:91:GLU:HG2	2.01	0.43
44:o:66:ILE:HG13	44:o:85:ILE:HB	2.00	0.43
46:q:19:LEU:HD11	69:KK:106:LEU:HD11	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:w:54:ARG:HE	50:w:57:ASN:ND2	2.17	0.43
52:z:228:ILE:O	52:z:232:ARG:HG2	2.18	0.43
54:5:1551:C:H2'	54:5:1552:G:O4'	2.19	0.43
54:5:2809:G:O2'	54:5:4644:G:OP1	2.27	0.43
54:5:4940:C:H5''	54:5:4941:G:H5''	2.01	0.43
7:A:117:GLU:HG2	7:A:124:GLY:H	1.83	0.43
8:B:220:ILE:HG12	8:B:278:THR:HG23	2.00	0.43
9:C:307:LYS:N	54:5:2099:C:OP1	2.52	0.43
10:D:211:LEU:HB3	10:D:219:TYR:HB2	2.01	0.43
11:F:75:ARG:NE	54:5:730:G:OP2	2.51	0.43
16:K:145:G:H2'	16:K:146:G:H8	1.83	0.43
16:K:389:A:H2'	16:K:390:C:C6	2.54	0.43
16:K:945:U:H2'	16:K:946:U:C6	2.54	0.43
16:K:1563:G:C4	16:K:1573:G:N2	2.87	0.43
17:L:80:GLU:OE2	17:L:113:ASN:ND2	2.51	0.43
19:N:76:PRO:HG2	19:N:79:ALA:HB3	2.00	0.43
22:Q:119:LYS:HD3	22:Q:121:LEU:HD21	2.00	0.43
24:S:154:LEU:HB3	24:S:157:ARG:HD3	2.01	0.43
36:f:50:VAL:HG22	36:f:69:VAL:HG12	2.01	0.43
51:x:136:ILE:HD12	51:x:149:TYR:CE1	2.53	0.43
54:5:1211:G:HO2'	54:5:1212:G:P	2.41	0.43
54:5:2539:C:H2'	54:5:2540:C:H6	1.83	0.43
54:5:3740:G:H2'	54:5:3740:G:N3	2.34	0.43
54:5:3824:A:C4	54:5:3825:A:C8	3.07	0.43
59:BB:82:GLU:HA	59:BB:85:LYS:HE2	2.01	0.43
69:KK:23:ARG:HD2	69:KK:34:VAL:HG13	2.01	0.43
8:B:242:ARG:NH2	54:5:2856:C:O2	2.41	0.43
9:C:269:LYS:HG2	54:5:654:C:H4'	2.00	0.43
9:C:330:PRO:HD3	11:F:46:ARG:HH21	1.83	0.43
11:F:125:ASN:HB2	25:T:132:PRO:HB2	2.00	0.43
16:K:92:A:O2'	51:x:4:GLY:HA3	2.19	0.43
16:K:694:G:H22	16:K:732:U:H3	1.66	0.43
16:K:1093:A:H2'	16:K:1094:C:C6	2.54	0.43
16:K:1690:U:H2'	16:K:1691:U:C6	2.54	0.43
16:K:1780:G:H2'	16:K:1781:A:N9	2.34	0.43
17:L:186:ARG:HE	39:i:9:VAL:HG11	1.83	0.43
46:q:53:ARG:O	46:q:57:LYS:HG2	2.19	0.43
54:5:161:G:H2'	54:5:162:A:C8	2.54	0.43
54:5:264:C:N3	54:5:265:C:N4	2.66	0.43
54:5:271:C:H2'	54:5:272:U:H6	1.83	0.43
54:5:422:C:H2'	54:5:423:G:H8	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:5:4735:G:O2'	54:5:4736:C:O5'	2.37	0.43
54:5:4906:C:H2'	54:5:4907:G:C8	2.54	0.43
54:5:4938:A:H1'	56:E:188:PRO:HB3	2.01	0.43
61:DD:110:LEU:HD12	61:DD:147:PHE:CD1	2.54	0.43
63:EE:151:THR:H	65:QQ:133:ARG:NH1	2.17	0.43
64:RR:52:LEU:HD21	64:RR:62:VAL:HG23	2.00	0.43
65:QQ:27:LYS:H	65:QQ:27:LYS:HD2	1.84	0.43
72:GG:54:VAL:HB	72:GG:88:LEU:HG	1.99	0.43
8:B:194:LEU:HD23	8:B:194:LEU:HA	1.93	0.43
16:K:98:C:OP2	16:K:426:A:O2'	2.28	0.43
16:K:671:A:H61	75:VV:3:LYS:HZ1	1.66	0.43
16:K:1117:C:O2'	16:K:1118:C:O2	2.21	0.43
16:K:1203:G:H2'	16:K:1204:A:C8	2.53	0.43
16:K:1244:U:H2'	16:K:1245:G:C8	2.53	0.43
16:K:1438:A:H2'	16:K:1439:A:H8	1.84	0.43
33:c:17:ARG:NH2	33:c:103:ASP:O	2.44	0.43
34:d:92:ARG:HE	34:d:101:LYS:NZ	2.17	0.43
54:5:262:G:H2'	54:5:263:G:C8	2.54	0.43
54:5:499:G:H2'	54:5:500:G:O4'	2.19	0.43
54:5:655:C:H2'	54:5:656:C:H6	1.84	0.43
54:5:1370:G:H4'	54:5:1371:A:O5'	2.18	0.43
54:5:1786:A:H2'	54:5:1789:C:C5	2.54	0.43
54:5:2521:G:H2'	54:5:2522:G:C8	2.54	0.43
54:5:4951:G:H2'	54:5:4952:G:H8	1.83	0.43
66:MM:129:ILE:O	78:LL:65:PRO:HG3	2.19	0.43
9:C:110:ARG:O	9:C:113:ARG:NH1	2.36	0.42
16:K:344:U:H2'	16:K:345:U:H6	1.83	0.42
16:K:527:C:H2'	16:K:528:A:H8	1.84	0.42
16:K:953:C:O2	66:MM:55:ARG:NH1	2.33	0.42
16:K:1016:U:OP1	79:JJ:30:SER:OG	2.29	0.42
17:L:198:ARG:O	17:L:201:GLU:HG3	2.19	0.42
18:M:39:ASP:HB3	18:M:47:ARG:HD3	2.01	0.42
19:N:53:TYR:HB2	19:N:133:ILE:HD13	2.00	0.42
19:N:94:PHE:CE2	19:N:96:ARG:HB2	2.54	0.42
36:f:36:ARG:O	36:f:39:THR:HG22	2.19	0.42
52:z:142:ARG:HE	52:z:153:VAL:HG21	1.83	0.42
54:5:32:G:H21	54:5:50:C:H5	1.67	0.42
54:5:125:C:O2'	54:5:126:C:H6	2.02	0.42
54:5:670:G:H2'	54:5:671:G:H8	1.84	0.42
54:5:1326:A:H2'	54:5:1327:C:C6	2.54	0.42
54:5:3770:U:H2'	54:5:3771:C:C6	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:5:3888:G:HO2'	54:5:3889:G:P	2.42	0.42
55:8:148:A:H2'	55:8:149:G:C8	2.54	0.42
59:BB:69:LEU:O	59:BB:73:GLN:HG2	2.19	0.42
63:EE:59:LYS:HD3	63:EE:134:LEU:HB3	1.99	0.42
71:PP:34:VAL:HG13	71:PP:52:TRP:CZ2	2.54	0.42
5:7:24:C:H2'	5:7:25:G:O4'	2.19	0.42
5:7:26:C:H5''	10:D:56:THR:HG21	2.00	0.42
12:G:92:PHE:CD1	12:G:100:PRO:HD3	2.54	0.42
15:J:15:LEU:HD21	15:J:134:LEU:HD13	2.00	0.42
16:K:874:G:H2'	16:K:875:A:O4'	2.19	0.42
16:K:984:C:H2'	16:K:985:G:C8	2.54	0.42
16:K:1621:U:OP1	67:WW:115:TYR:HE2	2.02	0.42
16:K:1809:A:H2'	16:K:1810:U:C6	2.54	0.42
19:N:172:ARG:HG2	54:5:29:G:H5''	2.02	0.42
50:w:168:VAL:HG12	50:w:189:MET:HA	2.01	0.42
54:5:746:A:N1	54:5:918:G:O6	2.52	0.42
54:5:1545:G:H2'	54:5:1546:C:C6	2.54	0.42
54:5:4192:A:H2'	54:5:4193:C:H6	1.83	0.42
54:5:4578:G:H2'	54:5:4579:U:H6	1.83	0.42
54:5:4637:G:H2'	54:5:4638:U:C6	2.54	0.42
54:5:4651:A:H2'	54:5:4652:G:O4'	2.18	0.42
76:NN:39:GLU:OE1	76:NN:39:GLU:N	2.52	0.42
4:6:14:HIS:ND1	4:6:35:SER:HB2	2.34	0.42
4:6:120:ILE:HG23	4:6:132:TRP:HB2	2.01	0.42
6:9:10:HIS:HE2	16:K:1261:C:HO2'	1.65	0.42
6:9:33:LYS:HE2	6:9:34:TYR:CZ	2.54	0.42
9:C:169:LEU:O	9:C:173:LYS:HG2	2.19	0.42
9:C:333:LYS:HE3	56:E:56:ILE:HA	2.00	0.42
12:G:297:PRO:HA	12:G:300:VAL:HG12	2.00	0.42
15:J:146:ARG:HG2	15:J:147:ARG:HG2	2.01	0.42
16:K:29:G:H2'	16:K:30:C:C6	2.55	0.42
16:K:39:A:H62	16:K:515:G:H21	1.66	0.42
16:K:55:U:H6	16:K:90:G:H21	1.66	0.42
16:K:443:U:H2'	16:K:444:G:O4'	2.20	0.42
16:K:969:U:OP1	16:K:970:G:O2'	2.22	0.42
16:K:1248:U:H2'	16:K:1249:C:C6	2.54	0.42
16:K:1284:A:O2'	64:RR:106:CYS:SG	2.66	0.42
16:K:1567:G:P	16:K:1567:G:H21	2.41	0.42
16:K:1808:U:H2'	16:K:1809:A:H8	1.84	0.42
19:N:120:TRP:HE1	19:N:123:GLU:HB3	1.83	0.42
26:U:27:HIS:HB2	26:U:28:PRO:HD3	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:k:18:LYS:HB3	41:k:18:LYS:HE3	1.82	0.42
45:p:42:CYS:HB3	45:p:60:CYS:SG	2.59	0.42
51:x:252:ARG:HA	51:x:255:ARG:HG2	2.00	0.42
52:z:224:ARG:HD2	52:z:227:GLN:NE2	2.34	0.42
54:5:446:C:H2'	54:5:447:C:C6	2.54	0.42
54:5:677:G:H2'	54:5:678:C:H6	1.84	0.42
54:5:755:C:H2'	54:5:756:G:C8	2.54	0.42
54:5:1186:U:H2'	54:5:1187:G:N3	2.34	0.42
54:5:1558:A:H2'	54:5:1559:G:H8	1.85	0.42
54:5:1773:U:H2'	54:5:1774:C:H6	1.81	0.42
54:5:3707:U:H2'	54:5:3708:C:C6	2.54	0.42
54:5:3726:A:H2'	54:5:3727:A:C8	2.55	0.42
54:5:4092:G:C6	54:5:4093:G:C2	3.08	0.42
54:5:4538:G:H2'	54:5:4539:U:C6	2.54	0.42
54:5:4761:G:H2'	54:5:4762:A:H8	1.84	0.42
75:VV:63:ASN:HD22	75:VV:114:ASP:CG	2.26	0.42
8:B:128:LYS:HG3	54:5:4966:A:H5'	1.99	0.42
10:D:208:MET:HB2	10:D:233:PRO:HG3	2.01	0.42
12:G:207:LEU:HB3	12:G:257:PHE:HB2	2.00	0.42
16:K:160:U:O2'	16:K:161:U:H3'	2.19	0.42
16:K:297:A:C2	16:K:298:G:C8	3.08	0.42
16:K:344:U:H2'	16:K:345:U:C6	2.54	0.42
16:K:823:U:H6	61:DD:142:VAL:HA	1.84	0.42
16:K:1059:G:C6	16:K:1060:A:N1	2.88	0.42
16:K:1130:G:HO2'	16:K:1131:G:P	2.42	0.42
21:P:24:VAL:HG12	21:P:86:LYS:HG2	2.01	0.42
28:W:106:GLU:O	28:W:110:ARG:HG2	2.19	0.42
32:a:8:THR:OG1	54:5:1339:U:OP1	2.32	0.42
36:f:73:LYS:HD3	54:5:952:G:H5''	2.01	0.42
46:q:59:LEU:O	46:q:63:ARG:HG2	2.19	0.42
54:5:645:G:H2'	54:5:646:G:C8	2.55	0.42
54:5:1301:C:N4	54:5:2316:G:OP2	2.51	0.42
54:5:2386:U:H2'	54:5:2387:G:C8	2.52	0.42
54:5:2607:C:H2'	54:5:2608:G:H8	1.84	0.42
54:5:2730:U:H2'	54:5:2731:C:C6	2.54	0.42
54:5:4237:C:O3'	54:5:4326:G:N2	2.52	0.42
54:5:4303:C:H2'	54:5:4305:G:C8	2.54	0.42
54:5:4563:U:H2'	54:5:4564:A:H8	1.84	0.42
58:y:100:ILE:O	58:y:104:THR:HG22	2.19	0.42
69:KK:105:MET:HE3	69:KK:105:MET:HB3	1.97	0.42
70:II:84:LEU:HD22	70:II:97:GLN:HB2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:K:164:A:H2'	16:K:165:G:N3	2.35	0.42
16:K:178:C:H2'	16:K:179:C:C6	2.54	0.42
16:K:1137:U:O2'	16:K:1138:C:OP1	2.35	0.42
16:K:1856:C:H2'	16:K:1857:G:C8	2.54	0.42
31:Z:76:ASN:OD1	31:Z:77:TYR:N	2.52	0.42
40:j:72:ARG:O	40:j:75:ARG:HG2	2.19	0.42
41:k:8:ILE:HD13	41:k:45:LEU:HD21	2.01	0.42
44:o:105:TRP:NE1	53:2:19:G:C6	2.88	0.42
52:z:88:ARG:HB2	52:z:91:GLU:HB2	2.01	0.42
54:5:2295:C:H2'	54:5:2296:G:H8	1.84	0.42
54:5:2690:C:H2'	54:5:2691:U:O4'	2.20	0.42
54:5:2735:G:H2'	54:5:2736:G:H8	1.84	0.42
54:5:3671:G:H2'	54:5:3672:G:C8	2.54	0.42
54:5:4258:C:H2'	54:5:4259:C:H6	1.84	0.42
54:5:4500:U:H2'	54:5:4501:U:H6	1.84	0.42
58:y:67:PRO:HG2	58:y:70:GLU:HB3	2.00	0.42
60:CC:38:ILE:HD12	60:CC:94:LYS:HD2	2.01	0.42
60:CC:81:VAL:HG22	60:CC:102:VAL:HG12	2.02	0.42
71:PP:24:LYS:HE3	71:PP:24:LYS:HB3	1.88	0.42
83:EG:76:ALA:O	83:EG:80:MET:HG2	2.19	0.42
8:B:252:ALA:HB1	54:5:4524:G:N3	2.34	0.42
11:F:126:LYS:HG3	54:5:1727:U:H4'	2.02	0.42
16:K:12:U:H2'	16:K:13:C:H6	1.84	0.42
16:K:387:C:O5'	16:K:387:C:H6	2.02	0.42
16:K:1395:C:H2'	16:K:1396:A:N3	2.34	0.42
16:K:1636:G:H2'	16:K:1636:G:N3	2.35	0.42
17:L:25:TRP:O	19:N:202:ARG:HD3	2.20	0.42
30:Y:15:ARG:NH1	54:5:230:G:OP1	2.52	0.42
40:j:63:ARG:HD3	40:j:65:ARG:HB3	2.01	0.42
53:2:44:A:H2'	53:2:45:G:C8	2.54	0.42
54:5:158:A:H5''	54:5:159:C:H2'	2.01	0.42
54:5:223:G:H4'	54:5:225:G:N7	2.35	0.42
54:5:1444:G:H21	54:5:2110:G:H1	1.66	0.42
54:5:1846:G:H2'	54:5:1847:C:C6	2.55	0.42
54:5:4099:G:H1	54:5:4109:G:H1	1.67	0.42
54:5:4474:A:H2'	54:5:4476:C:O5'	2.20	0.42
54:5:4970:C:C2	54:5:4971:A:C8	3.07	0.42
59:BB:121:THR:HG23	59:BB:124:ALA:H	1.85	0.42
65:QQ:34:LYS:HE3	65:QQ:67:THR:HG21	2.02	0.42
67:WW:64:LYS:NZ	67:WW:88:GLU:O	2.53	0.42
73:HH:40:ASP:HB3	73:HH:43:THR:HB	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:7:59:G:H2'	5:7:60:G:C8	2.53	0.42
11:F:170:ASP:OD1	11:F:171:ASN:N	2.52	0.42
12:G:97:ASP:OD1	12:G:98:ILE:N	2.50	0.42
14:I:59:GLN:HB3	14:I:126:VAL:HG11	2.01	0.42
16:K:562:U:H4'	61:DD:132:GLN:HG3	2.02	0.42
16:K:663:C:N3	16:K:664:A:C8	2.88	0.42
16:K:1856:C:H2'	16:K:1857:G:H8	1.84	0.42
34:d:33:ILE:HD11	34:d:45:ALA:HA	2.01	0.42
49:v:70:VAL:HG21	49:v:93:ILE:HG23	2.02	0.42
54:5:423:G:H2'	54:5:424:U:C6	2.55	0.42
54:5:451:C:O2'	54:5:1294:A:H5'	2.19	0.42
54:5:1556:C:O2'	54:5:2669:C:OP1	2.34	0.42
54:5:1895:G:H2'	54:5:1896:A:O4'	2.20	0.42
54:5:2521:G:H2'	54:5:2522:G:H8	1.84	0.42
58:y:122:ARG:HD2	80:FF:57:THR:HG21	2.02	0.42
78:LL:7:ASN:O	78:LL:9:GLY:N	2.50	0.42
80:FF:23:SER:OG	80:FF:24:GLN:OE1	2.30	0.42
15:J:52:LYS:HA	15:J:67:LYS:HA	2.01	0.42
16:K:15:U:HO2'	16:K:669:A:N6	2.18	0.42
16:K:85:A:H2'	16:K:86:C:H6	1.85	0.42
16:K:155:G:C2	16:K:164:A:C2	3.08	0.42
16:K:303:C:H2'	16:K:304:C:C6	2.55	0.42
16:K:930:C:H42	16:K:1011:A:H62	1.67	0.42
16:K:941:C:H5''	48:u:136:ARG:NH1	2.34	0.42
16:K:1083:A:N7	16:K:1841:C:O2'	2.48	0.42
16:K:1386:A:H2'	16:K:1387:G:O4'	2.20	0.42
16:K:1446:A:H1'	72:GG:55:ARG:HG2	2.01	0.42
17:L:182:LEU:HD13	17:L:182:LEU:HA	1.93	0.42
20:O:125:LYS:HE3	20:O:125:LYS:HB3	1.93	0.42
21:P:83:TRP:O	54:5:3856:A:H5''	2.19	0.42
25:T:50:LYS:NZ	54:5:4328:G:OP1	2.50	0.42
29:X:77:ILE:HD12	29:X:116:LEU:HD12	2.02	0.42
35:e:100:ALA:O	35:e:108:ARG:NH2	2.53	0.42
36:f:54:LYS:HB3	54:5:443:G:H5''	2.02	0.42
37:g:97:ILE:HD12	54:5:4122:G:N7	2.35	0.42
40:j:25:LYS:HB3	40:j:25:LYS:HE3	1.82	0.42
40:j:28:HIS:HD2	40:j:30:GLN:H	1.67	0.42
46:q:2:SER:N	46:q:8:LEU:HD12	2.34	0.42
54:5:153:G:H2'	54:5:154:G:C8	2.55	0.42
54:5:3923:A:H2'	54:5:3924:C:C6	2.55	0.42
54:5:4566:U:H2'	54:5:4567:G:O4'	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:5:4935:C:H2'	54:5:4936:G:H8	1.82	0.42
55:8:40:A:H2'	55:8:41:A:C8	2.54	0.42
75:VV:87:ASN:HB2	75:VV:90:CYS:SG	2.60	0.42
16:K:300:U:H2'	16:K:301:A:C8	2.54	0.42
16:K:886:A:C2	16:K:887:U:H1'	2.55	0.42
16:K:931:C:H2'	16:K:932:G:C8	2.54	0.42
16:K:1407:U:H2'	16:K:1408:U:C6	2.55	0.42
16:K:1410:C:H2'	16:K:1411:G:H8	1.85	0.42
21:P:114:ILE:HG12	21:P:150:LEU:HD22	2.02	0.42
25:T:27:LEU:O	25:T:31:MET:HG2	2.20	0.42
47:r:97:ILE:HG21	47:r:107:ARG:HB3	2.01	0.42
54:5:2447:U:H2'	54:5:2448:G:H8	1.85	0.42
54:5:2482:C:H2'	54:5:2483:G:C8	2.55	0.42
54:5:3652:A:H8	54:5:3652:A:O5'	2.02	0.42
54:5:3938:G:H4'	54:5:3939:G:O5'	2.20	0.42
54:5:4093:G:C4	54:5:4094:G:N7	2.88	0.42
54:5:4642:U:H2'	54:5:4643:G:C8	2.55	0.42
60:CC:136:ILE:HG23	60:CC:140:LYS:HD2	2.00	0.42
62:SS:5:LYS:HE3	62:SS:9:ILE:HD11	2.02	0.42
7:A:137:ILE:HD11	7:A:149:LYS:HD2	2.01	0.42
11:F:79:ASN:HA	25:T:143:THR:HG22	2.01	0.42
16:K:17:C:H4'	16:K:1166:G:C8	2.54	0.42
16:K:96:C:H2'	16:K:97:U:H6	1.85	0.42
16:K:380:G:OP1	60:CC:31:ARG:HD2	2.20	0.42
16:K:382:C:H2'	16:K:383:G:H8	1.85	0.42
16:K:388:U:H2'	16:K:389:A:H8	1.84	0.42
16:K:613:G:N2	16:K:626:G:OP1	2.52	0.42
16:K:1084:A:OP1	16:K:1858:G:O2'	2.28	0.42
16:K:1633:A:H2'	16:K:1634:A:C8	2.55	0.42
16:K:1681:U:H2'	16:K:1682:C:C6	2.55	0.42
25:T:70:HIS:NE2	54:5:4327:C:OP1	2.52	0.42
29:X:143:ASP:OD1	29:X:143:ASP:N	2.53	0.42
30:Y:59:ARG:NH1	54:5:200:U:O2'	2.39	0.42
36:f:100:ARG:HG2	54:5:4753:U:OP2	2.20	0.42
54:5:2:G:H2'	54:5:3:C:C6	2.54	0.42
54:5:2079:G:H2'	54:5:2080:U:H6	1.85	0.42
54:5:2491:C:H2'	54:5:2492:C:C6	2.55	0.42
54:5:4254:G:N3	54:5:4254:G:H2'	2.34	0.42
54:5:4273:A:H2'	54:5:4274:A:C8	2.55	0.42
54:5:4770:U:H3'	54:5:4771:C:H4'	2.01	0.42
58:y:168:THR:HG22	58:y:171:GLU:HG2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:EE:124:ASP:HA	63:EE:148:ALA:HB2	2.02	0.42
77:OO:91:LEU:HD11	77:OO:96:LEU:HD12	2.02	0.42
16:K:588:G:OP2	16:K:588:G:N2	2.35	0.41
16:K:959:G:H2'	16:K:960:U:C6	2.55	0.41
16:K:1054:G:N2	16:K:1055:A:H1'	2.35	0.41
16:K:1093:A:H2'	16:K:1094:C:H6	1.84	0.41
16:K:1215:C:O2'	16:K:1645:C:OP2	2.33	0.41
16:K:1720:U:O2'	54:5:3796:U:O2'	2.20	0.41
17:L:36:ARG:NE	54:5:1363:C:OP2	2.50	0.41
22:Q:73:PRO:HG2	54:5:1456:C:H4'	2.02	0.41
24:S:127:MET:HE1	25:T:155:PRO:HA	2.02	0.41
38:h:62:ASN:ND2	55:8:60:G:O6	2.36	0.41
51:x:162:ILE:HG22	51:x:169:ILE:HG22	2.02	0.41
53:2:23:C:H2'	53:2:24:A:H8	1.81	0.41
54:5:85:G:O2'	54:5:97:G:O6	2.28	0.41
54:5:1794:A:H5''	54:5:4214:A:N6	2.35	0.41
54:5:2862:G:N3	54:5:3624:A:H2'	2.35	0.41
54:5:4932:U:H2'	54:5:4933:C:C6	2.55	0.41
54:5:5028:G:H2'	54:5:5029:C:C6	2.55	0.41
60:CC:110:ARG:HG3	60:CC:121:LEU:HB3	2.02	0.41
67:WW:43:ARG:O	67:WW:46:SER:OG	2.34	0.41
71:PP:38:LYS:NZ	71:PP:40:ALA:O	2.51	0.41
72:GG:19:ARG:HG3	72:GG:92:HIS:CE1	2.55	0.41
75:VV:89:GLY:HA2	81:AA:82:VAL:HG12	2.01	0.41
76:NN:110:ARG:HG2	76:NN:113:ARG:HH21	1.85	0.41
1:m:86:LYS:HB3	1:m:88:LYS:HG2	2.02	0.41
7:A:20:VAL:HG12	7:A:23:ARG:HD2	2.02	0.41
8:B:262:VAL:HG11	8:B:268:ARG:NH1	2.35	0.41
10:D:279:ARG:HD2	54:5:1177:U:H4'	2.02	0.41
16:K:28:U:H2'	16:K:29:G:H8	1.85	0.41
16:K:158:A:H2'	16:K:159:A:O4'	2.19	0.41
16:K:407:G:H2'	16:K:407:G:N3	2.35	0.41
16:K:822:U:H3	16:K:826:A:H62	1.66	0.41
16:K:1117:C:O2'	16:K:1118:C:O5'	2.37	0.41
16:K:1232:U:H2'	16:K:1233:G:C8	2.55	0.41
16:K:1683:C:H2'	16:K:1684:C:H6	1.85	0.41
16:K:1801:A:H2'	16:K:1802:C:H6	1.85	0.41
24:S:15:ARG:HG3	24:S:16:CYS:O	2.20	0.41
30:Y:87:ARG:NH1	54:5:386:A:O2'	2.53	0.41
36:f:28:LEU:HD13	36:f:101:ILE:HD11	2.02	0.41
38:h:9:LEU:HA	38:h:12:LYS:HE2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:o:9:ARG:HA	44:o:20:PRO:HA	2.02	0.41
54:5:162:A:H2'	54:5:163:A:C8	2.55	0.41
54:5:1211:G:H2'	54:5:1212:G:H8	1.83	0.41
54:5:2573:A:H62	54:5:2761:U:H3	1.68	0.41
4:6:73:SER:OG	4:6:117:ASN:OD1	2.27	0.41
5:7:57:C:H2'	5:7:58:A:C8	2.55	0.41
12:G:136:PHE:HA	12:G:236:ILE:HD13	2.01	0.41
14:I:181:PHE:HE1	14:I:197:VAL:HG21	1.85	0.41
15:J:99:PHE:HE2	15:J:174:ILE:HD13	1.85	0.41
16:K:151:C:O2'	52:z:132:ARG:NE	2.54	0.41
16:K:1269:G:C6	16:K:1270:G:C5	3.09	0.41
16:K:1740:C:H2'	16:K:1741:U:C6	2.55	0.41
18:M:24:LEU:HD11	18:M:86:TRP:CG	2.55	0.41
37:g:40:LYS:NZ	54:5:2599:G:OP1	2.33	0.41
46:q:37:TYR:OH	46:q:57:LYS:NZ	2.48	0.41
48:u:32:ASP:OD1	48:u:33:VAL:N	2.52	0.41
51:x:55:ALA:HB1	51:x:60:GLU:HB2	2.00	0.41
51:x:197:ASN:HB3	51:x:209:HIS:HB2	2.02	0.41
54:5:132:G:H2'	54:5:133:C:O4'	2.19	0.41
54:5:162:A:H2'	54:5:163:A:H8	1.85	0.41
54:5:271:C:H2'	54:5:272:U:C6	2.55	0.41
54:5:325:U:H2'	54:5:326:C:C6	2.56	0.41
54:5:645:G:H2'	54:5:646:G:H8	1.86	0.41
54:5:1770:A:H2'	54:5:1771:U:O4'	2.20	0.41
54:5:2692:U:H2'	54:5:2693:G:O4'	2.20	0.41
70:II:132:ARG:HB2	70:II:134:GLN:HE22	1.83	0.41
71:PP:42:HIS:HB2	71:PP:83:GLN:HA	2.01	0.41
4:6:16:GLY:HA3	4:6:36:ARG:HB2	2.03	0.41
6:9:23:VAL:HG13	62:SS:64:TRP:CG	2.55	0.41
8:B:65:SER:HB3	54:5:4616:A:H4'	2.02	0.41
10:D:15:ARG:NH1	54:5:1743:A:H1'	2.34	0.41
14:I:22:PHE:CZ	54:5:1788:A:H2'	2.56	0.41
16:K:454:U:H5''	52:z:94:ARG:HG2	2.02	0.41
16:K:465:A:H4'	16:K:466:G:O5'	2.20	0.41
16:K:586:G:H3'	61:DD:172:ARG:HH12	1.85	0.41
16:K:1665:G:OP2	71:PP:89:PRO:HD2	2.20	0.41
16:K:1860:A:H3'	78:LL:8:ASN:HB3	2.01	0.41
19:N:46:ASP:OD1	19:N:46:ASP:N	2.54	0.41
23:R:38:ARG:NH2	54:5:2527:A:OP1	2.37	0.41
25:T:17:ARG:HB2	25:T:22:HIS:CE1	2.56	0.41
28:W:4:GLU:HG2	28:W:13:ILE:HB	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:Y:8:THR:HG22	30:Y:10:ASP:N	2.31	0.41
32:a:29:PRO:HA	54:5:1654:G:H5''	2.03	0.41
45:p:5:THR:OG1	45:p:8:VAL:O	2.30	0.41
47:r:87:ARG:NE	54:5:690:C:OP1	2.54	0.41
50:w:151:LYS:HG2	50:w:153:VAL:HG23	2.03	0.41
54:5:1:C:H2'	54:5:2:G:C8	2.55	0.41
54:5:922(A):G:H2'	54:5:922(B):C:C6	2.55	0.41
54:5:1078:A:H2'	54:5:1078:A:N3	2.36	0.41
54:5:1445:U:H2'	54:5:1446:C:C6	2.55	0.41
54:5:1757:U:H2'	54:5:1758:G:H8	1.83	0.41
54:5:2368:A:N6	54:5:2827:G:O2'	2.54	0.41
54:5:2565:A:H2'	54:5:2566:G:O4'	2.20	0.41
54:5:2607:C:H2'	54:5:2608:G:C8	2.55	0.41
54:5:4174:U:C2	54:5:4175:G:N7	2.88	0.41
78:LL:45:VAL:HG11	78:LL:50:VAL:N	2.35	0.41
12:G:217:ILE:HG13	12:G:221:VAL:HG23	2.03	0.41
16:K:375:U:H2'	16:K:376:A:C8	2.56	0.41
16:K:1621:U:O2'	16:K:1622:U:H6	2.03	0.41
16:K:1854:U:OP2	66:MM:147:ARG:NH2	2.54	0.41
17:L:66:TYR:OH	54:5:1382:G:OP1	2.22	0.41
20:O:74:ARG:HD2	20:O:145:VAL:HG12	2.02	0.41
25:T:17:ARG:HG2	54:5:4277:G:H5''	2.03	0.41
34:d:54:MET:HE3	34:d:60:PRO:HA	2.01	0.41
36:f:18:LEU:HB2	54:5:1916:G:O6	2.21	0.41
46:q:102:ARG:HD2	46:q:102:ARG:HA	1.90	0.41
46:q:145:ILE:HG13	46:q:159:ILE:HG23	2.01	0.41
51:x:246:LEU:H	51:x:246:LEU:HD23	1.86	0.41
54:5:281:U:H2'	54:5:282:C:H6	1.85	0.41
54:5:923:C:OP1	54:5:923:C:H4'	2.19	0.41
54:5:2395:A:HO2'	54:5:2806:A:H1'	1.86	0.41
54:5:2588:C:OP1	54:5:2768:C:O2'	2.31	0.41
54:5:3722:G:H2'	54:5:3723:A:C8	2.55	0.41
54:5:3773:U:H2'	54:5:3775:A:H2	1.86	0.41
54:5:3927:U:H2'	54:5:3928:A:C8	2.56	0.41
54:5:4949:G:H4'	54:5:4950:U:C5'	2.48	0.41
66:MM:85:CYS:HB3	66:MM:90:ILE:HB	2.03	0.41
82:EF:55:ASN:HA	82:EF:81:ALA:H	1.84	0.41
5:7:85:G:N3	5:7:85:G:H2'	2.35	0.41
10:D:153:THR:HG21	54:5:4323:A:C6	2.56	0.41
13:H:47:LEU:HG	13:H:52:LYS:HD2	2.01	0.41
16:K:494:C:H41	16:K:509:G:H21	1.68	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:K:870:A:H62	16:K:915:G:H2'	1.85	0.41
16:K:1667:U:H2'	16:K:1668:U:C6	2.56	0.41
19:N:184:ILE:HG23	19:N:194:ARG:NH2	2.36	0.41
21:P:122:ALA:HB3	21:P:143:PRO:HG2	2.01	0.41
51:x:45:ILE:HA	51:x:61:VAL:HG11	2.02	0.41
53:2:18:G:O2'	53:2:60:A:N6	2.54	0.41
53:2:55:U:N3	53:2:58:A:OP2	2.30	0.41
54:5:256:G:H2'	54:5:257:C:H6	1.85	0.41
54:5:347:A:H2'	54:5:348:G:C8	2.55	0.41
54:5:396:A:H2'	54:5:397:G:C8	2.56	0.41
54:5:519:C:H2'	54:5:520:U:H6	1.84	0.41
54:5:710:G:H2'	54:5:711:A:C8	2.56	0.41
54:5:980:U:C2	54:5:981:C:C5	3.09	0.41
54:5:983:C:H2'	54:5:984:C:O4'	2.21	0.41
54:5:1086:C:H2'	54:5:1087:A:C8	2.56	0.41
54:5:1511:U:H2'	54:5:1512:G:H8	1.85	0.41
54:5:2461:G:H2'	54:5:2462:C:C6	2.56	0.41
54:5:2761:U:H4'	54:5:2762:G:O4'	2.21	0.41
54:5:3787:G:H1'	54:5:3789:C:N4	2.35	0.41
54:5:4173:G:H2'	54:5:4174:U:C6	2.56	0.41
74:TT:3:ARG:HH22	74:TT:28:ARG:NH1	2.19	0.41
8:B:247:GLY:HA2	54:5:2838:G:O5'	2.21	0.41
9:C:101:MET:H	9:C:101:MET:HG3	1.65	0.41
13:H:114:ILE:HB	13:H:124:ARG:HB2	2.03	0.41
16:K:106:C:H2'	16:K:107:A:C8	2.55	0.41
16:K:1139:C:N4	16:K:1149:A:H62	2.19	0.41
16:K:1520:G:O3'	16:K:1521:C:H6	2.04	0.41
16:K:1585:U:O2'	16:K:1587:G:OP2	2.39	0.41
16:K:1639:G:H2'	16:K:1640:A:C8	2.55	0.41
19:N:113:LEU:HD11	55:8:141:C:H5'	2.03	0.41
22:Q:178:ARG:N	32:a:51:GLY:HA2	2.34	0.41
29:X:68:ARG:HH22	55:8:60:G:P	2.44	0.41
29:X:114:LYS:HG2	29:X:120:ASP:HA	2.02	0.41
54:5:168:C:H2'	54:5:169:A:C8	2.56	0.41
54:5:433:A:C2	54:5:3867:A:H4'	2.55	0.41
54:5:1577:G:H3'	54:5:1577:G:N3	2.35	0.41
54:5:4509:U:H2'	54:5:4510:A:H2'	2.02	0.41
63:EE:47:PRO:HG2	63:EE:50:ALA:HB2	2.03	0.41
75:VV:124:LYS:HG2	75:VV:129:SER:HA	2.02	0.41
76:NN:87:PRO:HG2	76:NN:90:ARG:HH12	1.86	0.41
5:7:27:G:H5''	10:D:57:ASN:ND2	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:C:28:PHE:HA	9:C:129:ALA:HA	2.03	0.41
10:D:280:VAL:HG12	10:D:284:LYS:HE2	2.01	0.41
11:F:126:LYS:HB2	25:T:133:ALA:HB3	2.02	0.41
12:G:88:ARG:HH21	54:5:4128:A:H4'	1.86	0.41
12:G:101:LYS:HB3	29:X:42:THR:HG23	2.01	0.41
12:G:213:ASP:OD1	12:G:240:LYS:N	2.53	0.41
16:K:153:G:H2'	16:K:154:U:C6	2.55	0.41
16:K:302:A:H1'	60:CC:73:THR:HG23	2.03	0.41
16:K:414:A:OP1	16:K:814:U:O2'	2.27	0.41
16:K:531:A:H2'	16:K:532:C:O4'	2.21	0.41
16:K:1387:G:C2	16:K:1388:A:H1'	2.56	0.41
16:K:1439:A:H2'	16:K:1440:C:C6	2.56	0.41
21:P:94:MET:HE2	21:P:94:MET:HB3	1.95	0.41
23:R:45:ILE:HD13	23:R:50:ILE:HG13	2.02	0.41
26:U:69:LYS:HE2	26:U:69:LYS:HB2	1.91	0.41
38:h:70:ARG:HA	38:h:83:LEU:HD13	2.03	0.41
54:5:18:C:H2'	54:5:19:G:C8	2.54	0.41
54:5:1727:U:H2'	54:5:1728:U:C6	2.55	0.41
54:5:3826:C:O2'	54:5:3827:G:H5'	2.20	0.41
54:5:3941:G:C6	54:5:4073:A:C6	3.09	0.41
54:5:4236:G:H4'	54:5:4328:G:O2'	2.21	0.41
54:5:4287:G:H2'	54:5:4288:C:C6	2.56	0.41
54:5:4458:C:H2'	54:5:4459:U:H6	1.86	0.41
71:PP:56:ARG:NH2	71:PP:99:VAL:HB	2.36	0.41
4:6:181:ASN:O	4:6:181:ASN:ND2	2.51	0.41
6:9:2:GLY:N	16:K:1301:A:OP2	2.54	0.41
6:9:12:ARG:HH22	16:K:1262:C:H4'	1.85	0.41
7:A:32:VAL:HG22	7:A:163:ARG:HH21	1.86	0.41
7:A:135:THR:HB	7:A:149:LYS:HG2	2.03	0.41
9:C:150:LEU:O	9:C:152:LEU:N	2.53	0.41
9:C:154:VAL:O	9:C:254:GLU:N	2.54	0.41
10:D:41:LYS:HB2	25:T:68:THR:O	2.20	0.41
15:J:102:THR:OG1	15:J:104:ASN:OD1	2.39	0.41
16:K:81:U:H3'	16:K:82:G:H8	1.86	0.41
16:K:519:A:H5''	61:DD:11:LYS:HD3	2.02	0.41
16:K:529:A:H2'	16:K:530:U:C6	2.56	0.41
16:K:885:U:H3	16:K:901:G:H1	1.68	0.41
16:K:1019:C:H2'	16:K:1020:A:O4'	2.20	0.41
16:K:1390:U:H2'	16:K:1391:C:C6	2.55	0.41
16:K:1453:C:O2	16:K:1453:C:C2'	2.69	0.41
16:K:1551:U:H1'	16:K:1558:C:C2	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:K:1706:G:H2'	16:K:1707:U:H6	1.86	0.41
23:R:60:ARG:NH1	54:5:2808:G:O2'	2.53	0.41
24:S:11:LYS:HD2	24:S:29:ARG:HD2	2.03	0.41
24:S:16:CYS:HA	24:S:59:GLY:HA2	2.02	0.41
28:W:1:MET:HE2	28:W:15:PRO:HB3	2.03	0.41
30:Y:121:ARG:NH1	54:5:194:C:O2'	2.54	0.41
37:g:12:SER:O	54:5:2803:U:O2'	2.31	0.41
45:p:44:LYS:NZ	54:5:2672:C:OP1	2.31	0.41
46:q:122:LEU:O	46:q:145:ILE:N	2.42	0.41
48:u:25:PHE:HA	48:u:28:LYS:HG2	2.03	0.41
48:u:30:TRP:O	48:u:94:LYS:NZ	2.39	0.41
49:v:253:PRO:HA	49:v:256:TRP:NE1	2.36	0.41
53:2:66:C:H2'	53:2:67:G:C8	2.55	0.41
54:5:379:G:O2'	54:5:380:U:H5'	2.21	0.41
54:5:381:U:H2'	54:5:382:G:O4'	2.21	0.41
54:5:981:C:N4	54:5:1274:A:H61	2.15	0.41
54:5:1308:C:H2'	54:5:1309:C:C6	2.55	0.41
54:5:1327:C:H2'	54:5:1328:G:C8	2.56	0.41
54:5:1461:C:H2'	54:5:1462:A:H8	1.86	0.41
54:5:1486:C:H2'	54:5:1487:G:H8	1.86	0.41
54:5:1514:U:H2'	54:5:1515:A:C8	2.55	0.41
54:5:1811:G:H21	57:b:57:MET:HE3	1.86	0.41
54:5:2292:C:H2'	54:5:2293:U:C6	2.56	0.41
54:5:2708:U:OP1	82:EF:38:THR:HG23	2.20	0.41
54:5:4074:C:O2'	54:5:4075:U:H5'	2.20	0.41
54:5:4094:G:C3'	54:5:4095:G:H5''	2.42	0.41
54:5:4174:U:C2	54:5:4175:G:C8	3.09	0.41
54:5:4704:C:H2'	54:5:4705:A:C8	2.56	0.41
56:E:181:PRO:HG2	56:E:184:LEU:HD12	2.03	0.41
63:EE:49:GLU:HG3	63:EE:116:CYS:O	2.20	0.41
66:MM:31:CYS:SG	66:MM:95:ILE:HG13	2.61	0.41
69:KK:57:LEU:HD12	69:KK:57:LEU:HA	1.94	0.41
79:JJ:82:LYS:HE3	79:JJ:82:LYS:HB2	1.87	0.41
10:D:157:ASN:HB3	10:D:160:PHE:HD2	1.86	0.41
16:K:517:C:H2'	16:K:518:G:O4'	2.20	0.41
16:K:818:A:H2'	16:K:819:G:C8	2.56	0.41
16:K:1588:A:N3	16:K:1654:G:O2'	2.42	0.41
28:W:97:LYS:HB2	28:W:100:VAL:HG23	2.03	0.41
54:5:1084:C:H2'	54:5:1085:C:C6	2.56	0.41
54:5:1091:C:H2'	54:5:1092:G:H8	1.86	0.41
54:5:2078:C:H2'	54:5:2079:G:C8	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:5:2097:A:N3	54:5:2097:A:H2'	2.36	0.41
54:5:2412:A:H2'	54:5:2413:U:H6	1.86	0.41
54:5:2635:U:H2'	54:5:2636:U:C6	2.56	0.41
54:5:3619:G:H22	54:5:3624:A:H1'	1.86	0.41
54:5:3700:C:O2'	54:5:3774:A:H1'	2.21	0.41
54:5:4165:C:C2	54:5:4166:G:C8	3.09	0.41
54:5:5003:U:H2'	54:5:5004:C:C6	2.56	0.41
54:5:5045:G:H2'	54:5:5046:U:O4'	2.21	0.41
55:8:142:U:C2	55:8:143:G:C8	3.09	0.41
59:BB:117:PRO:HG2	59:BB:120:ARG:HD3	2.03	0.41
61:DD:136:ARG:HD2	61:DD:139:LYS:HA	2.03	0.41
66:MM:150:ARG:HD3	66:MM:150:ARG:H	1.86	0.41
2:0:102:VAL:HG21	64:RR:35:ILE:HG13	2.02	0.40
9:C:303:ARG:NH2	22:Q:37:ARG:O	2.53	0.40
14:I:35:ASP:OD1	14:I:35:ASP:N	2.53	0.40
16:K:381:C:N4	60:CC:27:TYR:HB2	2.36	0.40
16:K:527:C:H2'	16:K:528:A:C8	2.56	0.40
16:K:551:U:C2	16:K:552:G:C8	3.09	0.40
16:K:690:G:H2'	16:K:691:G:C8	2.55	0.40
16:K:692:G:H2'	16:K:693:A:H8	1.85	0.40
16:K:975:G:H21	66:MM:50:LYS:HA	1.86	0.40
19:N:38:ARG:NH2	55:8:142:U:OP1	2.42	0.40
49:v:204:ILE:HD12	49:v:215:LEU:HG	2.03	0.40
54:5:27:C:O2'	54:5:60:A:N3	2.51	0.40
54:5:473:C:H2'	54:5:474:C:C6	2.57	0.40
54:5:1085:C:H2'	54:5:1086:C:C6	2.56	0.40
54:5:1669:A:H4'	54:5:1685:G:H21	1.86	0.40
54:5:1776:A:N3	54:5:1776:A:H2'	2.36	0.40
54:5:2413:U:H2'	54:5:2414:G:C8	2.55	0.40
54:5:2727:C:H2'	54:5:2728:U:C6	2.56	0.40
54:5:2897:G:H2'	54:5:2898:G:H8	1.86	0.40
54:5:4094:G:H5'	54:5:4094:G:H8	1.85	0.40
54:5:4228:G:H5''	54:5:4229:U:O4'	2.20	0.40
54:5:4233:A:C5	54:5:4235:G:C8	3.09	0.40
54:5:4417:C:H2'	54:5:4418:G:O4'	2.20	0.40
54:5:4584:A:H2'	54:5:4585:U:O4'	2.21	0.40
61:DD:155:LYS:HE3	61:DD:155:LYS:HB2	1.87	0.40
64:RR:85:LEU:HD21	64:RR:109:VAL:HG21	2.02	0.40
83:EG:72:SER:HA	83:EG:75:LYS:HE2	2.03	0.40
16:K:336:A:H2'	16:K:337:C:C6	2.56	0.40
16:K:1397:U:O4	68:UU:12:VAL:HA	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:K:1613:G:C2	16:K:1627:C:C2	3.09	0.40
20:O:176:ARG:HD3	54:5:4769:G:H5'	2.02	0.40
22:Q:49:LYS:HB3	22:Q:49:LYS:HE2	1.87	0.40
38:h:79:LYS:HE2	38:h:79:LYS:HB3	1.91	0.40
54:5:272:U:H2'	54:5:273:U:C6	2.57	0.40
54:5:965:G:N2	54:5:2096:G:O2'	2.54	0.40
54:5:1639:U:O2	54:5:1639:U:C2'	2.70	0.40
54:5:2728:U:H2'	54:5:2729:C:C6	2.57	0.40
54:5:2870:A:H2'	54:5:2871:A:C8	2.57	0.40
54:5:3702:A:C2	54:5:3703:G:C8	3.09	0.40
54:5:4955:A:H2'	54:5:4956:A:O4'	2.21	0.40
63:EE:49:GLU:HG2	63:EE:116:CYS:HB2	2.02	0.40
75:VV:105:PHE:HB3	75:VV:112:VAL:HG21	2.01	0.40
84:EH:57:PRO:HA	84:EH:58:PRO:HD3	1.94	0.40
7:A:201:GLY:HA3	7:A:209:HIS:CE1	2.57	0.40
8:B:317:LEU:HB3	54:5:5001:U:H4'	2.02	0.40
9:C:2:ALA:N	9:C:29:LYS:HD2	2.36	0.40
11:F:215:PRO:HD3	11:F:246:MET:HE2	2.02	0.40
12:G:317:LYS:HD2	48:u:226:GLY:N	2.37	0.40
14:I:146:GLU:HA	14:I:149:VAL:HG22	2.03	0.40
16:K:17:C:O2'	16:K:1194:A:N1	2.52	0.40
16:K:1119:A:H2'	16:K:1120:U:C6	2.55	0.40
16:K:1788:A:H2'	16:K:1789:G:O4'	2.21	0.40
25:T:96:ILE:HD13	25:T:96:ILE:HA	1.88	0.40
27:V:106:VAL:HG21	27:V:132:ILE:HD11	2.02	0.40
36:f:59:THR:HA	54:5:4944:C:N4	2.36	0.40
48:u:127:VAL:HG23	48:u:177:GLN:HG3	2.03	0.40
54:5:122:U:H2'	54:5:123:C:H6	1.86	0.40
54:5:418:A:C2	55:8:17:A:H1'	2.57	0.40
54:5:699:C:H2'	54:5:700:G:C8	2.56	0.40
54:5:1435:G:H1	54:5:1449:C:H42	1.69	0.40
54:5:1494:U:H2'	54:5:1495:G:C8	2.56	0.40
54:5:1755:C:H4'	54:5:1756:U:H5'	2.03	0.40
54:5:1884:C:H4'	54:5:2070:U:C4	2.56	0.40
54:5:4773:C:H2'	54:5:4774:C:H6	1.87	0.40
58:y:35:LEU:HD21	58:y:146:ARG:HE	1.85	0.40
58:y:60:ARG:HH21	80:FF:49:PRO:HA	1.86	0.40
80:FF:12:ALA:HB1	80:FF:32:VAL:HB	2.03	0.40
2:0:100:LEU:HD21	16:K:1285:G:H21	1.87	0.40
4:6:8:ARG:HA	4:6:8:ARG:HH11	1.86	0.40
5:7:117:G:OP1	10:D:253:TYR:OH	2.39	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:243:THR:HG23	54:5:3746:A:H5'	2.04	0.40
11:F:72:ARG:NH2	54:5:727:C:OP1	2.51	0.40
16:K:470:G:H2'	16:K:471:G:C8	2.57	0.40
16:K:1047:C:H2'	16:K:1048:G:O4'	2.21	0.40
16:K:1159:G:H1'	74:TT:4:MET:HE3	2.02	0.40
16:K:1221:G:H2'	16:K:1222:G:H8	1.85	0.40
22:Q:12:LYS:HB2	22:Q:14:ARG:NH1	2.35	0.40
24:S:67:VAL:HA	54:5:729:G:H1	1.86	0.40
28:W:82:ILE:HG23	52:z:131:ARG:HB2	2.02	0.40
30:Y:8:THR:HG21	30:Y:13:LYS:HB2	2.03	0.40
46:q:188:THR:HG22	46:q:189:ILE:HG13	2.03	0.40
47:r:32:LEU:O	47:r:33:LYS:HB2	2.22	0.40
54:5:128:C:H2'	54:5:129:C:C6	2.54	0.40
54:5:462:G:N2	54:5:694:C:C2	2.90	0.40
54:5:1078:A:C6	54:5:1233:G:C6	3.10	0.40
54:5:2540:C:H2'	54:5:2541:G:H8	1.87	0.40
54:5:3723:A:H2'	54:5:3724:A:C8	2.56	0.40
54:5:3893:C:O2'	54:5:4979:A:N1	2.53	0.40
54:5:4478:G:O2'	54:5:4602:A:N1	2.46	0.40
54:5:4561:C:H2'	54:5:4562:C:C6	2.56	0.40
60:CC:107:THR:HG23	60:CC:108:PRO:HD3	2.02	0.40
62:SS:21:MET:HE2	62:SS:21:MET:HB2	1.94	0.40
72:GG:41:ARG:O	72:GG:45:GLU:HG2	2.22	0.40
16:K:215:G:H2'	16:K:216:C:H6	1.87	0.40
16:K:220:U:H2'	16:K:221:A:C8	2.56	0.40
16:K:496:C:H5'	51:x:29:PRO:HA	2.03	0.40
16:K:682:U:O2'	16:K:1159:G:H4'	2.22	0.40
16:K:796:G:H2'	16:K:797:C:C6	2.57	0.40
16:K:860:G:H21	74:TT:107:SER:HB3	1.86	0.40
16:K:1305:C:H2'	16:K:1306:U:C6	2.56	0.40
16:K:1314:U:H2'	62:SS:2:LEU:HD23	2.03	0.40
16:K:1466:G:H5'	69:KK:4:VAL:HG22	2.03	0.40
16:K:1533:A:H2'	16:K:1533:A:N3	2.37	0.40
20:O:92:THR:O	20:O:96:GLN:HG2	2.22	0.40
24:S:47:PHE:HE1	24:S:125:GLN:HG3	1.85	0.40
40:j:63:ARG:CD	40:j:65:ARG:HB3	2.52	0.40
42:l:24:PRO:HG2	42:l:27:ILE:HB	2.02	0.40
48:u:33:VAL:HA	48:u:96:CYS:HB2	2.04	0.40
51:x:104:ASP:HB2	51:x:110:ALA:HB2	2.03	0.40
54:5:340:C:H4'	54:5:341:G:OP2	2.22	0.40
54:5:1339:U:H2'	54:5:1340:C:H6	1.85	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:5:1340:C:H2'	54:5:1341:U:H6	1.85	0.40
54:5:2051:C:H2'	54:5:2052:G:O4'	2.22	0.40
54:5:2362:U:H2'	54:5:2363:A:C8	2.56	0.40
54:5:2376:A:H2'	54:5:2377:C:C6	2.57	0.40
54:5:2501:C:H2'	54:5:2502:A:C8	2.56	0.40
54:5:2722:G:H2'	54:5:2723:U:O4'	2.22	0.40
54:5:2811:G:H22	54:5:2813:A:H3'	1.87	0.40
54:5:4094:G:C6	54:5:4095:G:C5	3.10	0.40
54:5:4949:G:C5	54:5:4951:G:C8	3.10	0.40
55:8:132:G:H2'	55:8:133:G:H8	1.87	0.40
55:8:144:U:H2'	55:8:145:C:C6	2.57	0.40
58:y:102:LEU:HD21	77:OO:67:LEU:HA	2.04	0.40
62:SS:32:HIS:CD2	62:SS:34:GLU:HB3	2.57	0.40
67:WW:29:SER:HG	67:WW:32:GLN:HG2	1.86	0.40
67:WW:96:VAL:HB	67:WW:120:SER:HB3	2.04	0.40
75:VV:52:LEU:HD12	75:VV:53:GLU:HG2	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	m	49/128 (38%)	47 (96%)	2 (4%)	0	100	100
2	0	59/156 (38%)	56 (95%)	3 (5%)	0	100	100
4	6	311/317 (98%)	297 (96%)	14 (4%)	0	100	100
6	9	53/56 (95%)	53 (100%)	0	0	100	100
7	A	246/257 (96%)	235 (96%)	11 (4%)	0	100	100
8	B	392/403 (97%)	383 (98%)	9 (2%)	0	100	100
9	C	360/413 (87%)	350 (97%)	10 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	D	291/297 (98%)	285 (98%)	5 (2%)	1 (0%)	37	53
11	F	223/249 (90%)	219 (98%)	4 (2%)	0	100	100
12	G	229/319 (72%)	227 (99%)	2 (1%)	0	100	100
13	H	188/192 (98%)	186 (99%)	2 (1%)	0	100	100
14	I	201/214 (94%)	195 (97%)	6 (3%)	0	100	100
15	J	168/178 (94%)	164 (98%)	4 (2%)	0	100	100
17	L	208/211 (99%)	200 (96%)	8 (4%)	0	100	100
18	M	136/218 (62%)	130 (96%)	6 (4%)	0	100	100
19	N	201/204 (98%)	193 (96%)	8 (4%)	0	100	100
20	O	197/203 (97%)	193 (98%)	4 (2%)	0	100	100
21	P	151/183 (82%)	149 (99%)	2 (1%)	0	100	100
22	Q	185/187 (99%)	182 (98%)	3 (2%)	0	100	100
23	R	178/196 (91%)	174 (98%)	4 (2%)	0	100	100
24	S	174/176 (99%)	167 (96%)	7 (4%)	0	100	100
25	T	157/160 (98%)	151 (96%)	6 (4%)	0	100	100
26	U	103/128 (80%)	97 (94%)	6 (6%)	0	100	100
27	V	129/140 (92%)	129 (100%)	0	0	100	100
28	W	102/157 (65%)	100 (98%)	2 (2%)	0	100	100
29	X	116/156 (74%)	114 (98%)	2 (2%)	0	100	100
30	Y	132/145 (91%)	129 (98%)	3 (2%)	0	100	100
31	Z	133/136 (98%)	130 (98%)	3 (2%)	0	100	100
32	a	145/148 (98%)	141 (97%)	4 (3%)	0	100	100
33	c	96/115 (84%)	95 (99%)	1 (1%)	0	100	100
34	d	105/125 (84%)	103 (98%)	2 (2%)	0	100	100
35	e	126/135 (93%)	125 (99%)	1 (1%)	0	100	100
36	f	107/110 (97%)	106 (99%)	1 (1%)	0	100	100
37	g	112/117 (96%)	111 (99%)	1 (1%)	0	100	100
38	h	120/123 (98%)	119 (99%)	1 (1%)	0	100	100
39	i	100/105 (95%)	97 (97%)	3 (3%)	0	100	100
40	j	84/97 (87%)	83 (99%)	1 (1%)	0	100	100
41	k	67/70 (96%)	66 (98%)	1 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
42	l	48/51 (94%)	46 (96%)	2 (4%)	0	100	100
43	n	23/25 (92%)	23 (100%)	0	0	100	100
44	o	102/111 (92%)	96 (94%)	5 (5%)	1 (1%)	13	21
45	p	89/92 (97%)	88 (99%)	1 (1%)	0	100	100
46	q	215/295 (73%)	211 (98%)	4 (2%)	0	100	100
47	r	122/137 (89%)	119 (98%)	3 (2%)	0	100	100
48	u	211/264 (80%)	208 (99%)	3 (1%)	0	100	100
49	v	219/293 (75%)	214 (98%)	5 (2%)	0	100	100
50	w	224/243 (92%)	221 (99%)	3 (1%)	0	100	100
51	x	259/263 (98%)	252 (97%)	7 (3%)	0	100	100
52	z	235/249 (94%)	233 (99%)	2 (1%)	0	100	100
56	E	203/291 (70%)	198 (98%)	5 (2%)	0	100	100
57	b	100/245 (41%)	98 (98%)	2 (2%)	0	100	100
58	y	180/204 (88%)	174 (97%)	6 (3%)	0	100	100
59	BB	179/194 (92%)	177 (99%)	2 (1%)	0	100	100
60	CC	204/208 (98%)	197 (97%)	7 (3%)	0	100	100
61	DD	183/194 (94%)	182 (100%)	1 (0%)	0	100	100
62	SS	93/165 (56%)	86 (92%)	7 (8%)	0	100	100
63	EE	139/158 (88%)	133 (96%)	6 (4%)	0	100	100
64	RR	115/132 (87%)	110 (96%)	5 (4%)	0	100	100
65	QQ	147/151 (97%)	146 (99%)	1 (1%)	0	100	100
66	MM	133/151 (88%)	130 (98%)	3 (2%)	0	100	100
67	WW	120/145 (83%)	114 (95%)	6 (5%)	0	100	100
68	UU	139/146 (95%)	134 (96%)	5 (4%)	0	100	100
69	KK	130/135 (96%)	130 (100%)	0	0	100	100
70	II	140/152 (92%)	137 (98%)	3 (2%)	0	100	100
71	PP	139/145 (96%)	134 (96%)	5 (4%)	0	100	100
72	GG	98/119 (82%)	95 (97%)	3 (3%)	0	100	100
73	HH	81/83 (98%)	80 (99%)	1 (1%)	0	100	100
74	TT	127/130 (98%)	123 (97%)	4 (3%)	0	100	100
75	VV	139/143 (97%)	136 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
76	NN	122/133 (92%)	120 (98%)	2 (2%)	0	100	100
77	OO	71/124 (57%)	71 (100%)	0	0	100	100
78	LL	99/115 (86%)	94 (95%)	5 (5%)	0	100	100
79	JJ	81/84 (96%)	79 (98%)	2 (2%)	0	100	100
80	FF	60/69 (87%)	60 (100%)	0	0	100	100
81	AA	53/133 (40%)	53 (100%)	0	0	100	100
82	EF	108/162 (67%)	105 (97%)	3 (3%)	0	100	100
83	EG	63/215 (29%)	59 (94%)	4 (6%)	0	100	100
84	EH	22/33 (67%)	22 (100%)	0	0	100	100
All	All	11349/13306 (85%)	11069 (98%)	278 (2%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
10	D	263	LYS
44	o	101	VAL

### 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	m	47/116 (40%)	46 (98%)	1 (2%)	48	70
2	0	54/140 (39%)	54 (100%)	0	100	100
4	6	272/275 (99%)	261 (96%)	11 (4%)	27	44
6	9	48/49 (98%)	48 (100%)	0	100	100
7	A	190/199 (96%)	185 (97%)	5 (3%)	41	63
8	B	342/348 (98%)	334 (98%)	8 (2%)	45	67
9	C	302/337 (90%)	300 (99%)	2 (1%)	81	90
10	D	247/250 (99%)	241 (98%)	6 (2%)	44	65
11	F	196/218 (90%)	196 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	G	200/273 (73%)	196 (98%)	4 (2%)	50	71
13	H	169/171 (99%)	162 (96%)	7 (4%)	26	43
14	I	175/181 (97%)	174 (99%)	1 (1%)	84	92
15	J	143/149 (96%)	140 (98%)	3 (2%)	48	70
17	L	175/176 (99%)	169 (97%)	6 (3%)	32	51
18	M	117/161 (73%)	111 (95%)	6 (5%)	20	34
19	N	171/172 (99%)	167 (98%)	4 (2%)	45	67
20	O	171/173 (99%)	167 (98%)	4 (2%)	45	67
21	P	134/162 (83%)	134 (100%)	0	100	100
22	Q	164/164 (100%)	161 (98%)	3 (2%)	54	73
23	R	159/175 (91%)	158 (99%)	1 (1%)	84	92
24	S	154/154 (100%)	149 (97%)	5 (3%)	34	54
25	T	139/140 (99%)	136 (98%)	3 (2%)	47	68
26	U	97/116 (84%)	96 (99%)	1 (1%)	73	85
27	V	101/107 (94%)	99 (98%)	2 (2%)	50	71
28	W	86/126 (68%)	84 (98%)	2 (2%)	45	67
29	X	106/134 (79%)	106 (100%)	0	100	100
30	Y	124/135 (92%)	122 (98%)	2 (2%)	58	76
31	Z	117/118 (99%)	115 (98%)	2 (2%)	56	75
32	a	119/120 (99%)	117 (98%)	2 (2%)	56	75
33	c	84/98 (86%)	83 (99%)	1 (1%)	67	82
34	d	98/110 (89%)	97 (99%)	1 (1%)	73	85
35	e	116/123 (94%)	114 (98%)	2 (2%)	56	75
36	f	88/89 (99%)	85 (97%)	3 (3%)	32	51
37	g	98/100 (98%)	95 (97%)	3 (3%)	35	55
38	h	109/110 (99%)	108 (99%)	1 (1%)	75	87
39	i	86/90 (96%)	83 (96%)	3 (4%)	31	50
40	j	73/80 (91%)	72 (99%)	1 (1%)	62	79
41	k	64/65 (98%)	63 (98%)	1 (2%)	58	76
42	l	47/48 (98%)	47 (100%)	0	100	100
43	n	24/24 (100%)	24 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
44	o	92/99 (93%)	91 (99%)	1 (1%)	70	84
45	p	74/75 (99%)	73 (99%)	1 (1%)	62	79
46	q	180/244 (74%)	175 (97%)	5 (3%)	38	60
47	r	108/121 (89%)	105 (97%)	3 (3%)	38	60
48	u	194/231 (84%)	192 (99%)	2 (1%)	73	85
49	v	186/223 (83%)	182 (98%)	4 (2%)	47	68
50	w	189/202 (94%)	186 (98%)	3 (2%)	58	76
51	x	224/225 (100%)	221 (99%)	3 (1%)	65	80
52	z	207/218 (95%)	205 (99%)	2 (1%)	73	85
56	E	188/251 (75%)	186 (99%)	2 (1%)	70	84
57	b	84/184 (46%)	82 (98%)	2 (2%)	44	65
58	y	157/170 (92%)	156 (99%)	1 (1%)	84	92
59	BB	163/174 (94%)	157 (96%)	6 (4%)	29	48
60	CC	178/180 (99%)	174 (98%)	4 (2%)	47	68
61	DD	161/168 (96%)	160 (99%)	1 (1%)	84	92
62	SS	86/136 (63%)	84 (98%)	2 (2%)	45	67
63	EE	130/142 (92%)	127 (98%)	3 (2%)	45	67
64	RR	99/108 (92%)	99 (100%)	0	100	100
65	QQ	130/131 (99%)	125 (96%)	5 (4%)	28	47
66	MM	104/119 (87%)	99 (95%)	5 (5%)	21	36
67	WW	110/130 (85%)	108 (98%)	2 (2%)	54	73
68	UU	117/121 (97%)	117 (100%)	0	100	100
69	KK	119/121 (98%)	116 (98%)	3 (2%)	42	64
70	II	123/132 (93%)	121 (98%)	2 (2%)	58	76
71	PP	111/116 (96%)	110 (99%)	1 (1%)	75	87
72	GG	92/107 (86%)	91 (99%)	1 (1%)	70	84
73	HH	68/68 (100%)	68 (100%)	0	100	100
74	TT	112/113 (99%)	107 (96%)	5 (4%)	23	39
75	VV	113/115 (98%)	111 (98%)	2 (2%)	54	73
76	NN	107/115 (93%)	105 (98%)	2 (2%)	52	72
77	OO	65/102 (64%)	64 (98%)	1 (2%)	60	77

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
78	LL	89/99 (90%)	88 (99%)	1 (1%)	70	84
79	JJ	75/76 (99%)	74 (99%)	1 (1%)	65	80
80	FF	55/62 (89%)	53 (96%)	2 (4%)	30	48
81	AA	46/106 (43%)	46 (100%)	0	100	100
82	EF	94/136 (69%)	86 (92%)	8 (8%)	8	13
83	EG	58/183 (32%)	55 (95%)	3 (5%)	19	33
84	EH	21/21 (100%)	21 (100%)	0	100	100
All	All	9915/11300 (88%)	9719 (98%)	196 (2%)	50	71

All (196) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	m	59	LEU
4	6	24	THR
4	6	46	THR
4	6	63	SER
4	6	64	HIS
4	6	165	ILE
4	6	181	ASN
4	6	198	VAL
4	6	217	MET
4	6	256	ILE
4	6	287	THR
4	6	305	ASN
7	A	30	ARG
7	A	41	ILE
7	A	101	VAL
7	A	102	LEU
7	A	208	GLU
8	B	43	LEU
8	B	56	ILE
8	B	90	VAL
8	B	138	GLN
8	B	168	MET
8	B	207	VAL
8	B	292	LEU
8	B	353	VAL
9	C	232	VAL
9	C	322	LEU
10	D	23	ARG

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Mol	Chain	Res	Type
10	D	37	VAL
10	D	56	THR
10	D	69	ILE
10	D	75	VAL
10	D	215	ASP
12	G	193	VAL
12	G	214	VAL
12	G	221	VAL
12	G	237	LEU
13	H	1	MET
13	H	12	ILE
13	H	24	THR
13	H	43	VAL
13	H	82	LYS
13	H	103	VAL
13	H	123	ILE
14	I	33	ILE
15	J	47	THR
15	J	68	ILE
15	J	111	GLU
17	L	59	VAL
17	L	63	THR
17	L	124	LEU
17	L	154	VAL
17	L	160	VAL
17	L	182	LEU
18	M	17	PHE
18	M	37	LEU
18	M	38	VAL
18	M	48	GLN
18	M	62	LEU
18	M	118	MET
19	N	64	ILE
19	N	89	VAL
19	N	174	LEU
19	N	202	ARG
20	O	36	VAL
20	O	52	LEU
20	O	124	LEU
20	O	129	LEU
22	Q	5	ILE
22	Q	72	LEU

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Mol	Chain	Res	Type
22	Q	95	VAL
23	R	114	LYS
24	S	17	LEU
24	S	67	VAL
24	S	90	THR
24	S	149	ARG
24	S	158	VAL
25	T	25	VAL
25	T	68	THR
25	T	80	VAL
26	U	61	VAL
27	V	37	LEU
27	V	61	VAL
28	W	12	LYS
28	W	32	LEU
30	Y	79	VAL
30	Y	104	VAL
31	Z	43	VAL
31	Z	132	GLN
32	a	134	GLU
32	a	146	LEU
33	c	92	CYS
34	d	26	THR
35	e	85	LEU
35	e	122	VAL
36	f	33	VAL
36	f	73	LYS
36	f	103	VAL
37	g	5	LEU
37	g	15	THR
37	g	66	ARG
38	h	47	ILE
39	i	30	ARG
39	i	42	ASP
39	i	63	VAL
40	j	20	ARG
41	k	36	VAL
44	o	99	ARG
45	p	52	VAL
46	q	16	LEU
46	q	18	PHE
46	q	122	LEU

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Mol	Chain	Res	Type
46	q	140	VAL
46	q	159	ILE
47	r	61	VAL
47	r	78	VAL
47	r	103	HIS
48	u	63	LYS
48	u	209	ASP
49	v	92	GLU
49	v	180	VAL
49	v	247	THR
49	v	248	TYR
50	w	44	THR
50	w	113	LEU
50	w	164	VAL
51	x	90	ILE
51	x	205	PHE
51	x	225	ILE
52	z	81	HIS
52	z	213	LEU
56	E	155	ILE
56	E	215	LEU
57	b	9	THR
57	b	60	ASN
58	y	89	THR
59	BB	36	LEU
59	BB	60	ILE
59	BB	79	LEU
59	BB	100	ILE
59	BB	122	LEU
59	BB	133	LEU
60	CC	73	THR
60	CC	93	THR
60	CC	107	THR
60	CC	130	THR
61	DD	151	LEU
62	SS	20	VAL
62	SS	83	LEU
63	EE	23	VAL
63	EE	56	ILE
63	EE	113	LEU
65	QQ	27	LYS
65	QQ	42	LYS

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Mol	Chain	Res	Type
65	QQ	46	THR
65	QQ	60	VAL
65	QQ	67	THR
66	MM	40	THR
66	MM	44	VAL
66	MM	56	VAL
66	MM	57	THR
66	MM	97	LEU
67	WW	126	VAL
67	WW	133	ILE
69	KK	6	THR
69	KK	66	VAL
69	KK	91	LEU
70	II	36	VAL
70	II	59	LEU
71	PP	110	LEU
72	GG	68	THR
74	TT	3	ARG
74	TT	63	VAL
74	TT	74	VAL
74	TT	76	SER
74	TT	103	VAL
75	VV	52	LEU
75	VV	105	PHE
76	NN	35	VAL
76	NN	120	THR
77	OO	58	LEU
78	LL	56	VAL
79	JJ	82	LYS
80	FF	7	GLN
80	FF	10	LYS
82	EF	2	LYS
82	EF	11	LEU
82	EF	18	VAL
82	EF	33	VAL
82	EF	54	ASN
82	EF	59	ILE
82	EF	83	LEU
82	EF	86	ASN
83	EG	83	LEU
83	EG	85	LEU
83	EG	105	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (77) such sidechains are listed below:

Mol	Chain	Res	Type
6	9	3	HIS
7	A	50	HIS
7	A	140	ASN
7	A	205	ASN
8	B	55	HIS
8	B	245	HIS
9	C	212	ASN
9	C	329	ASN
10	D	267	ASN
10	D	275	GLN
11	F	55	HIS
12	G	99	GLN
13	H	102	ASN
17	L	205	GLN
18	M	48	GLN
18	M	131	GLN
19	N	32	GLN
19	N	117	ASN
20	O	50	ASN
21	P	75	GLN
21	P	137	ASN
22	Q	44	ASN
22	Q	93	GLN
22	Q	188	ASN
23	R	143	HIS
24	S	37	HIS
24	S	117	HIS
25	T	127	GLN
26	U	105	ASN
26	U	119	GLN
29	X	73	HIS
30	Y	91	ASN
31	Z	97	ASN
32	a	34	ASN
32	a	44	ASN
32	a	89	ASN
34	d	100	ASN
35	e	107	ASN
35	e	126	ASN
38	h	98	HIS
39	i	12	ASN

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Mol	Chain	Res	Type
39	i	15	HIS
39	i	36	HIS
40	j	28	HIS
40	j	66	HIS
41	k	24	ASN
42	l	4	HIS
46	q	111	GLN
46	q	141	ASN
48	u	75	GLN
49	v	178	HIS
49	v	271	ASN
56	E	259	GLN
57	b	6	ASN
58	y	79	HIS
58	y	83	ASN
58	y	118	ASN
58	y	203	ASN
59	BB	33	ASN
59	BB	73	GLN
60	CC	22	HIS
63	EE	18	GLN
63	EE	94	HIS
63	EE	112	HIS
64	RR	55	ASN
66	MM	32	HIS
70	II	19	ASN
70	II	73	ASN
73	HH	33	GLN
74	TT	24	GLN
74	TT	70	ASN
76	NN	19	GLN
76	NN	85	ASN
81	AA	95	GLN
82	EF	17	GLN
82	EF	34	HIS
84	EH	67	GLN

### 5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
16	K	1679/4592 (36%)	289 (17%)	16 (0%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	4	5/6 (83%)	0	0
5	7	119/120 (99%)	9 (7%)	0
53	2	74/76 (97%)	10 (13%)	0
54	5	3445/7224 (47%)	639 (18%)	47 (1%)
55	8	149/156 (95%)	29 (19%)	1 (0%)
All	All	5471/12174 (44%)	976 (17%)	64 (1%)

All (976) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
5	7	22	A
5	7	53	U
5	7	54	A
5	7	63	C
5	7	64	G
5	7	100	A
5	7	110	G
5	7	111	C
5	7	120	U
16	K	2	A
16	K	3	C
16	K	4	C
16	K	25	A
16	K	26	U
16	K	33	G
16	K	41	G
16	K	42	A
16	K	44	U
16	K	45	A
16	K	46	A
16	K	56	G
16	K	67	C
16	K	68	A
16	K	71	G
16	K	77	A
16	K	79	A
16	K	103	A
16	K	111	A
16	K	113	G
16	K	115	U
16	K	126	G
16	K	127	C

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Mol	Chain	Res	Type
16	K	129	C
16	K	130	G
16	K	141	A
16	K	142	C
16	K	143	U
16	K	155	G
16	K	158	A
16	K	162	C
16	K	180	G
16	K	183	G
16	K	184	G
16	K	187	G
16	K	188	C
16	K	191	A
16	K	192	C
16	K	215	G
16	K	302	A
16	K	310	C
16	K	318	A
16	K	319	C
16	K	320	G
16	K	351	G
16	K	360	A
16	K	362	C
16	K	364	A
16	K	368	U
16	K	369	C
16	K	370	G
16	K	371	A
16	K	385	G
16	K	386	C
16	K	400	C
16	K	407	G
16	K	408	A
16	K	409	C
16	K	417	C
16	K	418	A
16	K	435	A
16	K	438	G
16	K	441	C
16	K	448	A
16	K	450	C

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Mol	Chain	Res	Type
16	K	465	A
16	K	466	G
16	K	472	C
16	K	473	A
16	K	474	G
16	K	482	G
16	K	487	U
16	K	492	C
16	K	493	A
16	K	523	A
16	K	525	A
16	K	532	C
16	K	533	A
16	K	536	A
16	K	537	C
16	K	541	U
16	K	542	U
16	K	547	G
16	K	549	C
16	K	550	C
16	K	554	A
16	K	556	U
16	K	559	G
16	K	560	A
16	K	563	G
16	K	564	A
16	K	568	C
16	K	570	C
16	K	576	A
16	K	583	A
16	K	587	A
16	K	588	G
16	K	590	A
16	K	591	U
16	K	606	G
16	K	607	U
16	K	608	C
16	K	614	C
16	K	617	G
16	K	628	A
16	K	631	U
16	K	643	A

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Mol	Chain	Res	Type
16	K	644	G
16	K	660	C
16	K	668	A
16	K	669	A
16	K	671	A
16	K	672	A
16	K	688	U
16	K	689	U
16	K	696	G
16	K	752	G
16	K	753	C
16	K	754	G
16	K	798	G
16	K	799	U
16	K	810	A
16	K	811	A
16	K	821	G
16	K	822	U
16	K	830	A
16	K	834	C
16	K	844	U
16	K	847	A
16	K	870	A
16	K	871	U
16	K	872	A
16	K	873	G
16	K	874	G
16	K	875	A
16	K	876	C
16	K	878	G
16	K	881	G
16	K	887	U
16	K	890	U
16	K	891	G
16	K	901	G
16	K	907	G
16	K	913	A
16	K	914	U
16	K	920	A
16	K	922	A
16	K	933	G
16	K	934	G

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Mol	Chain	Res	Type
16	K	955	A
16	K	971	G
16	K	978	G
16	K	990	A
16	K	992	A
16	K	999	G
16	K	1017	U
16	K	1023	A
16	K	1030	A
16	K	1041	G
16	K	1045	U
16	K	1062	A
16	K	1067	C
16	K	1083	A
16	K	1085	C
16	K	1109	C
16	K	1115	U
16	K	1116	C
16	K	1118	C
16	K	1121	G
16	K	1131	G
16	K	1133	A
16	K	1138	C
16	K	1139	C
16	K	1153	C
16	K	1154	U
16	K	1155	U
16	K	1195	A
16	K	1215	C
16	K	1224	G
16	K	1241	A
16	K	1242	U
16	K	1251	A
16	K	1253	A
16	K	1256	G
16	K	1257	G
16	K	1259	A
16	K	1264	C
16	K	1274	G
16	K	1275	G
16	K	1276	A
16	K	1282	A

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Mol	Chain	Res	Type
16	K	1285	G
16	K	1286	G
16	K	1287	A
16	K	1289	U
16	K	1294	G
16	K	1298	G
16	K	1301	A
16	K	1302	G
16	K	1303	C
16	K	1307	U
16	K	1308	U
16	K	1309	C
16	K	1312	G
16	K	1314	U
16	K	1316	C
16	K	1342	U
16	K	1371	U
16	K	1372	U
16	K	1378	A
16	K	1382	A
16	K	1395	C
16	K	1396	A
16	K	1397	U
16	K	1402	A
16	K	1404	U
16	K	1412	C
16	K	1428	G
16	K	1429	G
16	K	1438	A
16	K	1447	G
16	K	1454	A
16	K	1462	U
16	K	1463	U
16	K	1464	C
16	K	1466	G
16	K	1473	G
16	K	1476	A
16	K	1477	U
16	K	1478	U
16	K	1490	G
16	K	1494	U
16	K	1497	G

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Mol	Chain	Res	Type
16	K	1498	A
16	K	1509	U
16	K	1510	G
16	K	1519	U
16	K	1521	C
16	K	1522	A
16	K	1533	A
16	K	1548	G
16	K	1551	U
16	K	1558	C
16	K	1570	G
16	K	1574	C
16	K	1579	A
16	K	1580	A
16	K	1585	U
16	K	1586	U
16	K	1587	G
16	K	1588	A
16	K	1601	A
16	K	1604	G
16	K	1606	G
16	K	1621	U
16	K	1623	A
16	K	1624	U
16	K	1638	G
16	K	1648	G
16	K	1665	G
16	K	1683	C
16	K	1695	A
16	K	1698	C
16	K	1699	A
16	K	1715	A
16	K	1721	U
16	K	1722	G
16	K	1726	G
16	K	1748	G
16	K	1753	C
16	K	1756	C
16	K	1757	G
16	K	1783	C
16	K	1784	G
16	K	1785	C

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Mol	Chain	Res	Type
16	K	1823	A
16	K	1826	G
16	K	1831	A
16	K	1836	G
16	K	1838	U
16	K	1849	G
16	K	1851	A
16	K	1852	C
16	K	1861	G
16	K	1862	G
16	K	1863	A
16	K	1865	C
16	K	1866	A
16	K	1869	A
53	2	13	C
53	2	16	C
53	2	19	G
53	2	20	C
53	2	20(A)	U
53	2	48	C
53	2	60	A
53	2	61	C
53	2	67	G
53	2	76	A
54	5	12	A
54	5	13	U
54	5	25	A
54	5	39	A
54	5	42	A
54	5	48	G
54	5	49	U
54	5	59	A
54	5	64	A
54	5	65	A
54	5	66	A
54	5	71	C
54	5	73	A
54	5	91	G
54	5	104	G
54	5	109	G
54	5	110	C
54	5	116	G

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Mol	Chain	Res	Type
54	5	118	C
54	5	119	G
54	5	120	A
54	5	126	C
54	5	135	G
54	5	136	C
54	5	143	C
54	5	146	G
54	5	157	U
54	5	159	C
54	5	171	U
54	5	172	C
54	5	173	C
54	5	182	G
54	5	197	A
54	5	200	U
54	5	201	C
54	5	209	U
54	5	216	C
54	5	219	G
54	5	220	C
54	5	221	C
54	5	224	U
54	5	233	U
54	5	234	G
54	5	246	G
54	5	256	G
54	5	258	G
54	5	259	C
54	5	265	C
54	5	266	C
54	5	276	C
54	5	280	G
54	5	297	U
54	5	306	A
54	5	315	G
54	5	316	U
54	5	334	A
54	5	340	C
54	5	350	C
54	5	363	A
54	5	386	A

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Mol	Chain	Res	Type
54	5	387	G
54	5	407	A
54	5	412	G
54	5	431	G
54	5	432	U
54	5	446	C
54	5	449	C
54	5	450	G
54	5	451	C
54	5	452	A
54	5	453	G
54	5	454	U
54	5	457	G
54	5	463	A
54	5	464	G
54	5	467	U
54	5	468	U
54	5	481	G
54	5	481(A)	C
54	5	482	G
54	5	483	G
54	5	485	C
54	5	486	C
54	5	491	G
54	5	492	U
54	5	493	G
54	5	495	C
54	5	498	C
54	5	499	G
54	5	500	G
54	5	505	G
54	5	510	U
54	5	641	G
54	5	647	G
54	5	648	G
54	5	658	C
54	5	659	G
54	5	666	G
54	5	667	A
54	5	669	C
54	5	670	G
54	5	683	C

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Mol	Chain	Res	Type
54	5	684	G
54	5	685	C
54	5	686	A
54	5	687	U
54	5	691	C
54	5	696	C
54	5	697	G
54	5	704	C
54	5	719	C
54	5	730	G
54	5	731	G
54	5	738	C
54	5	742	G
54	5	747	A
54	5	759	G
54	5	914	U
54	5	917	A
54	5	918	G
54	5	923	C
54	5	925	C
54	5	926	G
54	5	929	A
54	5	931	C
54	5	932	A
54	5	933	G
54	5	934	C
54	5	935	A
54	5	935(A)	G
54	5	936	C
54	5	938	C
54	5	939	G
54	5	941	C
54	5	944	A
54	5	945	U
54	5	956	A
54	5	959	G
54	5	960	A
54	5	961	G
54	5	962	C
54	5	965	G
54	5	966	A
54	5	967	C

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Mol	Chain	Res	Type
54	5	969	C
54	5	972	C
54	5	979	C
54	5	983	C
54	5	990	C
54	5	1070	G
54	5	1072	C
54	5	1073	G
54	5	1075	G
54	5	1078	A
54	5	1081	C
54	5	1084	C
54	5	1168	G
54	5	1175	A
54	5	1179	U
54	5	1180	C
54	5	1184	A
54	5	1193	C
54	5	1195	G
54	5	1211	G
54	5	1212	G
54	5	1215	C
54	5	1216	C
54	5	1234	G
54	5	1235	G
54	5	1236	C
54	5	1237	C
54	5	1274	A
54	5	1277	G
54	5	1284	G
54	5	1285	U
54	5	1287	G
54	5	1292	C
54	5	1293	G
54	5	1295	U
54	5	1296	G
54	5	1301	C
54	5	1303	A
54	5	1304	C
54	5	1326	A
54	5	1330	A
54	5	1354	A

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Mol	Chain	Res	Type
54	5	1358	G
54	5	1359	G
54	5	1371	A
54	5	1377	G
54	5	1379	C
54	5	1380	G
54	5	1387	A
54	5	1394	G
54	5	1397	A
54	5	1398	A
54	5	1415	G
54	5	1419	G
54	5	1420	A
54	5	1421	G
54	5	1429	C
54	5	1437	C
54	5	1445	U
54	5	1446	C
54	5	1456	C
54	5	1457	G
54	5	1458	C
54	5	1465	G
54	5	1475	G
54	5	1478	C
54	5	1482	G
54	5	1483	C
54	5	1497	A
54	5	1498	G
54	5	1502	G
54	5	1518	A
54	5	1523	A
54	5	1534	A
54	5	1547	A
54	5	1563	A
54	5	1564	A
54	5	1566	C
54	5	1568	C
54	5	1574	G
54	5	1578	U
54	5	1591	U
54	5	1596	U
54	5	1612	G

*Continued on next page...*



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Mol	Chain	Res	Type
54	5	1613	A
54	5	1624	G
54	5	1625	G
54	5	1631	A
54	5	1633	G
54	5	1634	A
54	5	1638	A
54	5	1641	G
54	5	1654	G
54	5	1661	C
54	5	1676	C
54	5	1677	U
54	5	1691	G
54	5	1694	C
54	5	1734	G
54	5	1740	C
54	5	1741	G
54	5	1742	A
54	5	1750	G
54	5	1751	A
54	5	1755	C
54	5	1756	U
54	5	1757	U
54	5	1760	G
54	5	1764	G
54	5	1769	G
54	5	1772	C
54	5	1773	U
54	5	1776	A
54	5	1781	U
54	5	1787	A
54	5	1804	A
54	5	1805	A
54	5	1807	C
54	5	1809	C
54	5	1812	C
54	5	1815	G
54	5	1819	G
54	5	1821	G
54	5	1828	C
54	5	1836	G
54	5	1837	A

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Mol	Chain	Res	Type
54	5	1842	G
54	5	1847	C
54	5	1855	G
54	5	1869	G
54	5	1882	U
54	5	1897	A
54	5	1898	C
54	5	1910	G
54	5	1917	A
54	5	1918	U
54	5	1920	C
54	5	1921	C
54	5	1922	G
54	5	1923	A
54	5	1930	U
54	5	1931	C
54	5	1945	G
54	5	1948	G
54	5	1959	U
54	5	1961	G
54	5	1962	A
54	5	2024	G
54	5	2025	A
54	5	2026	A
54	5	2034	G
54	5	2047	A
54	5	2048	U
54	5	2055	G
54	5	2056	G
54	5	2062	C
54	5	2064	G
54	5	2069	A
54	5	2084	U
54	5	2085	G
54	5	2089	G
54	5	2090	U
54	5	2092	G
54	5	2093	G
54	5	2094	C
54	5	2095	A
54	5	2097	A
54	5	2098	G

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Mol	Chain	Res	Type
54	5	2100	G
54	5	2101	A
54	5	2102	G
54	5	2104	A
54	5	2105	A
54	5	2107	A
54	5	2108	G
54	5	2109	A
54	5	2110	G
54	5	2259	G
54	5	2260	C
54	5	2267	U
54	5	2268	A
54	5	2275	G
54	5	2289	C
54	5	2300	A
54	5	2301	G
54	5	2306	G
54	5	2313	A
54	5	2316	G
54	5	2331	G
54	5	2333	G
54	5	2345	G
54	5	2348	G
54	5	2351	C
54	5	2360	A
54	5	2395	A
54	5	2396	A
54	5	2399	G
54	5	2417	A
54	5	2422	C
54	5	2425	U
54	5	2433	G
54	5	2471	G
54	5	2475	G
54	5	2488	C
54	5	2489	C
54	5	2490	U
54	5	2491	C
54	5	2503	G
54	5	2504	C
54	5	2505	C

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Mol	Chain	Res	Type
54	5	2506	G
54	5	2513	A
54	5	2529	A
54	5	2530	U
54	5	2537	A
54	5	2544	G
54	5	2546	G
54	5	2547	G
54	5	2564	G
54	5	2583	C
54	5	2586	G
54	5	2589	C
54	5	2601	A
54	5	2618	G
54	5	2620	G
54	5	2627	C
54	5	2638	G
54	5	2653	C
54	5	2662	G
54	5	2669	C
54	5	2686	G
54	5	2687	U
54	5	2689	C
54	5	2694	G
54	5	2695	A
54	5	2696	A
54	5	2697	A
54	5	2706	G
54	5	2708	U
54	5	2709	C
54	5	2710	C
54	5	2711	G
54	5	2714	G
54	5	2716	C
54	5	2724	G
54	5	2725	A
54	5	2726	G
54	5	2740	U
54	5	2743	A
54	5	2744	A
54	5	2753	G
54	5	2754	G

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Mol	Chain	Res	Type
54	5	2760	G
54	5	2761	U
54	5	2763	U
54	5	2769	U
54	5	2787	A
54	5	2788	U
54	5	2790	U
54	5	2798	A
54	5	2814	C
54	5	2826	U
54	5	2827	G
54	5	2828	U
54	5	2837	U
54	5	2838	G
54	5	2842	G
54	5	2855	G
54	5	2875	C
54	5	2897	G
54	5	2898	G
54	5	3604	A
54	5	3605	C
54	5	3606	U
54	5	3617	G
54	5	3625	G
54	5	3626	G
54	5	3635	A
54	5	3653	A
54	5	3657	U
54	5	3662	A
54	5	3664	G
54	5	3673	C
54	5	3696	C
54	5	3711	A
54	5	3740	G
54	5	3748	A
54	5	3753	G
54	5	3759	A
54	5	3760	A
54	5	3763	A
54	5	3772	U
54	5	3773	U
54	5	3774	A

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Mol	Chain	Res	Type
54	5	3775	A
54	5	3776	G
54	5	3777	G
54	5	3784	A
54	5	3786	U
54	5	3810	C
54	5	3811	G
54	5	3814	U
54	5	3817	A
54	5	3819	G
54	5	3823	G
54	5	3824	A
54	5	3840	U
54	5	3877	A
54	5	3878	C
54	5	3879	G
54	5	3889	G
54	5	3892	U
54	5	3897	G
54	5	3901	A
54	5	3905	A
54	5	3906	A
54	5	3907	G
54	5	3908	A
54	5	3915	U
54	5	3916	G
54	5	3917	A
54	5	3926	C
54	5	3927	U
54	5	3939	G
54	5	4066	U
54	5	4069	U
54	5	4076	G
54	5	4077	A
54	5	4084	G
54	5	4085	A
54	5	4086	G
54	5	4088	C
54	5	4090	G
54	5	4091	G
54	5	4092	G
54	5	4094	G

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Mol	Chain	Res	Type
54	5	4095	G
54	5	4119	C
54	5	4120	U
54	5	4121	G
54	5	4125	C
54	5	4127	A
54	5	4128	A
54	5	4155	C
54	5	4158	C
54	5	4162	C
54	5	4163	U
54	5	4166	G
54	5	4170	A
54	5	4183	G
54	5	4184	G
54	5	4191	G
54	5	4203	A
54	5	4225	G
54	5	4229	U
54	5	4232	U
54	5	4233	A
54	5	4234	A
54	5	4241	C
54	5	4249	G
54	5	4251	A
54	5	4254	G
54	5	4266	G
54	5	4268	A
54	5	4271	A
54	5	4273	A
54	5	4281	A
54	5	4291	G
54	5	4296	U
54	5	4304	A
54	5	4305	G
54	5	4306	U
54	5	4314	C
54	5	4318	C
54	5	4319	C
54	5	4329	G
54	5	4330	G
54	5	4332	C

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Mol	Chain	Res	Type
54	5	4336	A
54	5	4349	C
54	5	4350	C
54	5	4354	U
54	5	4355	G
54	5	4373	G
54	5	4377	G
54	5	4378	A
54	5	4380	A
54	5	4387	C
54	5	4394	A
54	5	4395	U
54	5	4401	G
54	5	4419	U
54	5	4422	A
54	5	4437	U
54	5	4440	G
54	5	4448	G
54	5	4449	A
54	5	4464	A
54	5	4471	U
54	5	4472	G
54	5	4475	G
54	5	4500	U
54	5	4510	A
54	5	4511	A
54	5	4512	U
54	5	4513	A
54	5	4518	A
54	5	4519	C
54	5	4520	G
54	5	4524	G
54	5	4529	G
54	5	4548	A
54	5	4560	C
54	5	4574	U
54	5	4575	G
54	5	4586	G
54	5	4590	A
54	5	4627	U
54	5	4636	U
54	5	4637	G

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Mol	Chain	Res	Type
54	5	4652	G
54	5	4656	A
54	5	4657	U
54	5	4667	C
54	5	4670	C
54	5	4672	A
54	5	4677	U
54	5	4678	G
54	5	4700	A
54	5	4709	U
54	5	4719	G
54	5	4720	C
54	5	4736	C
54	5	4738	C
54	5	4745	G
54	5	4751	G
54	5	4754	G
54	5	4757	C
54	5	4759	C
54	5	4764	A
54	5	4765	G
54	5	4771	C
54	5	4772	C
54	5	4870	G
54	5	4871	C
54	5	4873	G
54	5	4875	G
54	5	4876	A
54	5	4877	G
54	5	4881	U
54	5	4882	U
54	5	4883	C
54	5	4887	C
54	5	4893	A
54	5	4896	G
54	5	4902	C
54	5	4910	A
54	5	4913	G
54	5	4914	G
54	5	4915	G
54	5	4921	C
54	5	4925	U

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Mol	Chain	Res	Type
54	5	4926	C
54	5	4927	G
54	5	4928	C
54	5	4931	G
54	5	4937	C
54	5	4939	C
54	5	4943	A
54	5	4944	C
54	5	4948	C
54	5	4950	U
54	5	4951	G
54	5	4956	A
54	5	4959	U
54	5	4960	G
54	5	4964	C
54	5	4965	U
54	5	4966	A
54	5	4976	U
54	5	4988	U
54	5	4989	U
54	5	4990	C
54	5	4993	G
54	5	5006	U
54	5	5007	A
54	5	5014	A
54	5	5017	G
54	5	5040	U
54	5	5041	G
54	5	5047	C
54	5	5050	C
54	5	5054	C
54	5	5061	A
54	5	5062	G
55	8	2	G
55	8	23	C
55	8	34	U
55	8	35	C
55	8	38	U
55	8	39	G
55	8	59	A
55	8	62	A
55	8	63	U

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Mol	Chain	Res	Type
55	8	75	G
55	8	90	C
55	8	94	G
55	8	103	A
55	8	105	C
55	8	107	C
55	8	108	A
55	8	109	C
55	8	110	U
55	8	111	U
55	8	114	G
55	8	123	U
55	8	125	C
55	8	126	C
55	8	127	U
55	8	137	A
55	8	147	G
55	8	150	C
55	8	153	C
55	8	156	U

All (64) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
16	K	110	U
16	K	140	U
16	K	370	G
16	K	434	G
16	K	465	A
16	K	532	C
16	K	553	U
16	K	642	U
16	K	688	U
16	K	752	G
16	K	870	A
16	K	1137	U
16	K	1395	C
16	K	1520	G
16	K	1521	C
16	K	1664	A
54	5	12	A
54	5	47	A

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Mol	Chain	Res	Type
54	5	48	G
54	5	125	C
54	5	275	C
54	5	385	A
54	5	406	C
54	5	480	C
54	5	485	C
54	5	492	U
54	5	499	G
54	5	504	G
54	5	696	C
54	5	930	G
54	5	959	G
54	5	971(A)	G
54	5	1174	G
54	5	1211	G
54	5	1291	G
54	5	1329	G
54	5	1370	G
54	5	1445	U
54	5	1455	G
54	5	1477	C
54	5	1633	G
54	5	1804	A
54	5	1818	G
54	5	2046	G
54	5	2089	G
54	5	2266	C
54	5	2502	A
54	5	2546	G
54	5	2708	U
54	5	3625	G
54	5	3823	G
54	5	3876	A
54	5	3888	G
54	5	3904	G
54	5	4075	U
54	5	4119	C
54	5	4232	U
54	5	4448	G
54	5	4699	U
54	5	4719	G

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Mol	Chain	Res	Type
54	5	4925	U
54	5	4947	U
54	5	4958	C
55	8	124	U

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

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

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 291 ligands modelled in this entry, 291 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
53	2	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	2	16:C	O3'	18:G	P	5.37

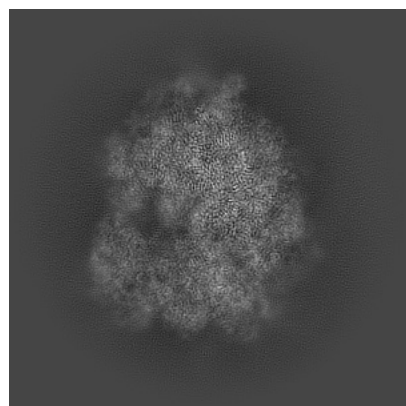
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-48552. These allow visual inspection of the internal detail of the map and identification of artifacts.

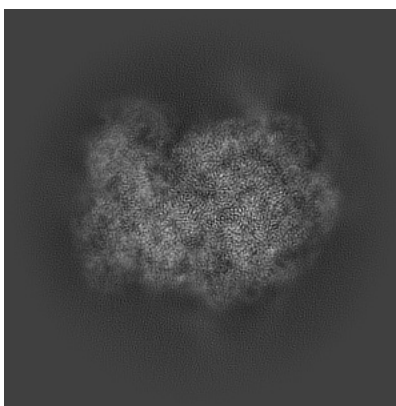
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

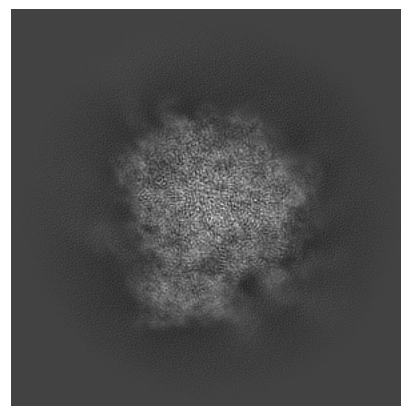
#### 6.1.1 Primary map



X

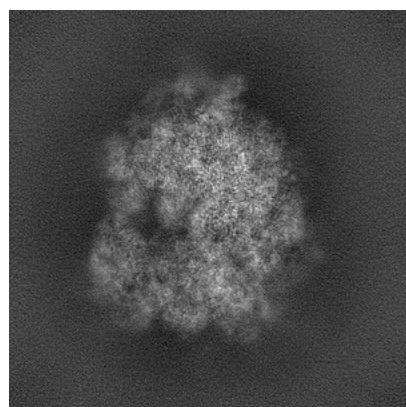


Y

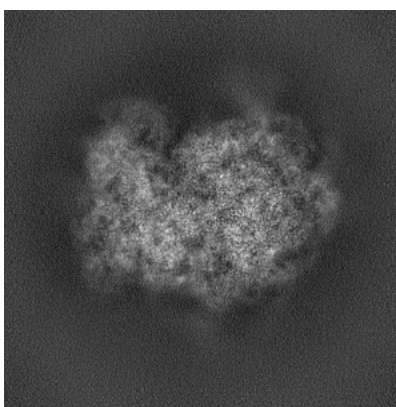


Z

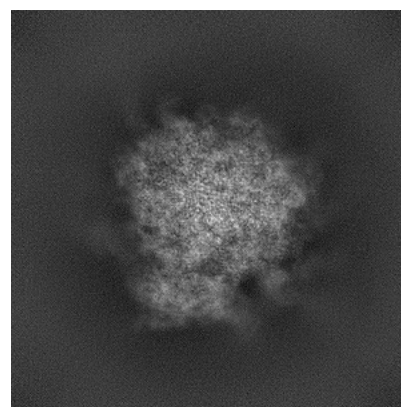
#### 6.1.2 Raw map



X



Y

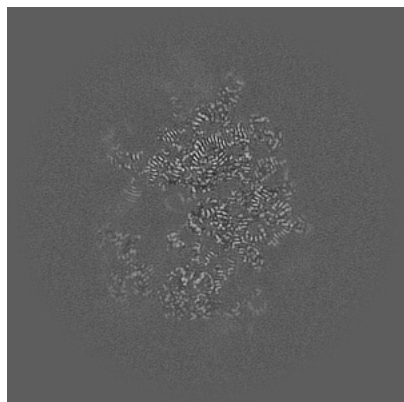


Z

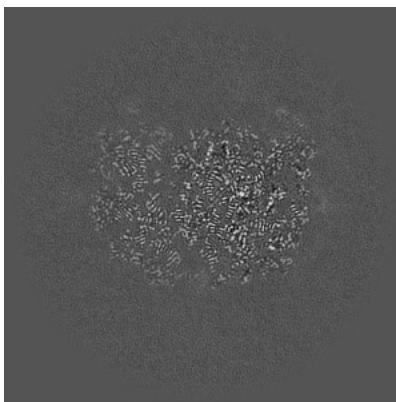
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

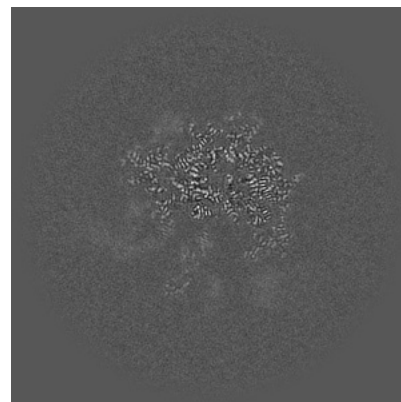
### 6.2.1 Primary map



X Index: 256

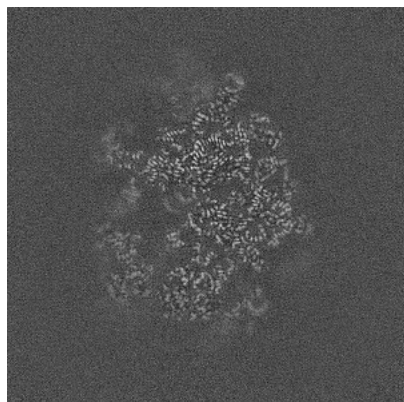


Y Index: 256

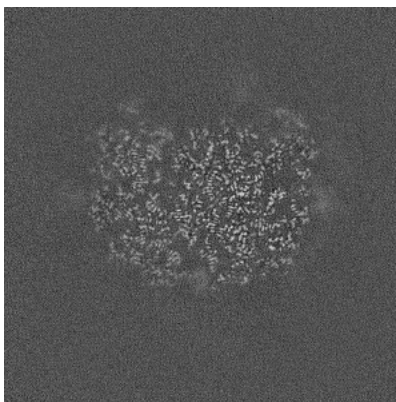


Z Index: 256

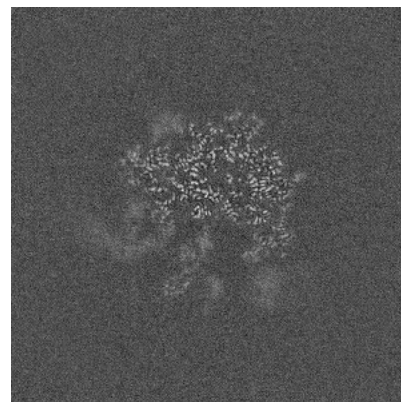
### 6.2.2 Raw map



X Index: 256



Y Index: 256



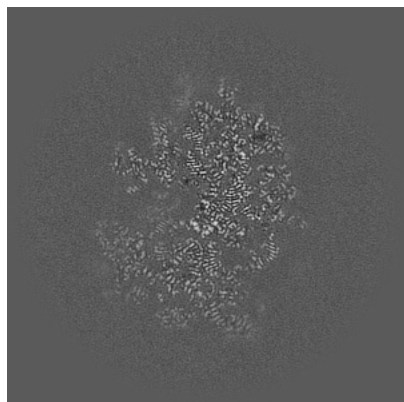
Z Index: 256

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

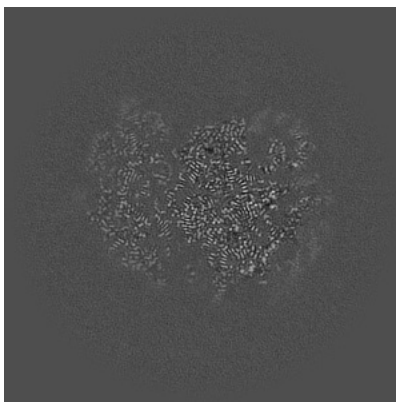


## 6.3 Largest variance slices [i](#)

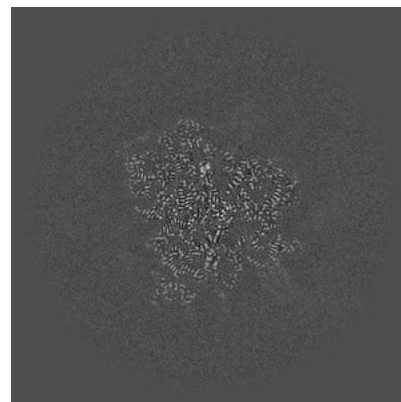
### 6.3.1 Primary map



X Index: 239

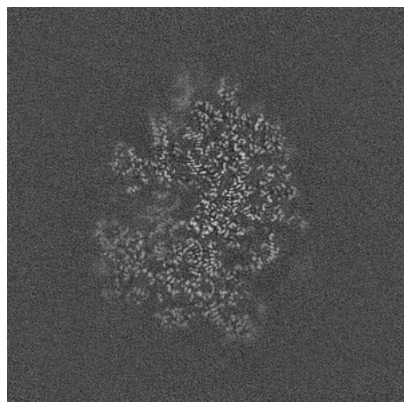


Y Index: 267

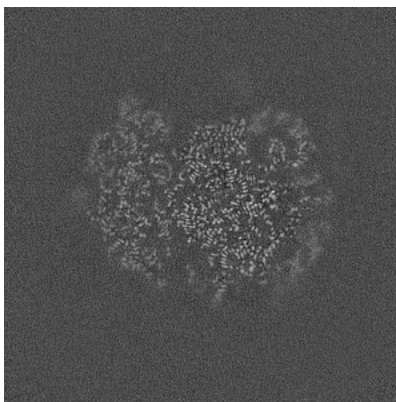


Z Index: 297

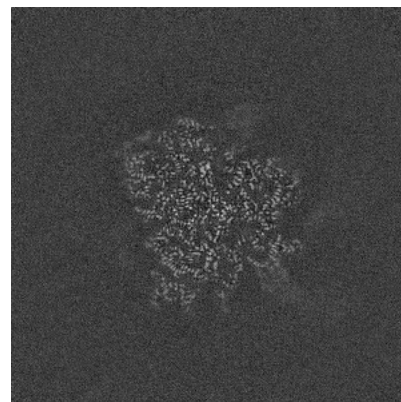
### 6.3.2 Raw map



X Index: 239



Y Index: 267

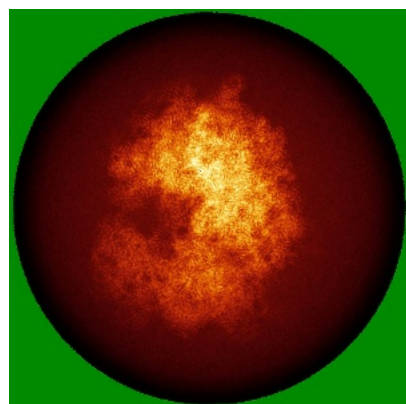


Z Index: 297

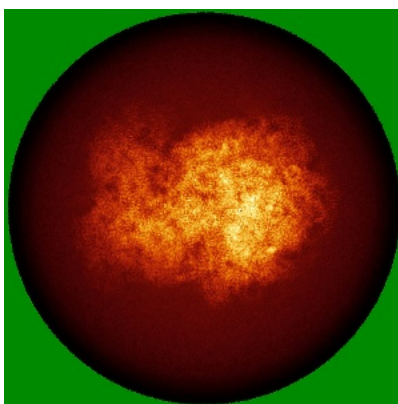
The images above show the largest variance slices of the map in three orthogonal directions.

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

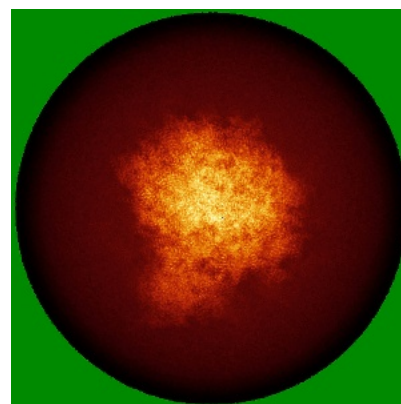
### 6.4.1 Primary map



X

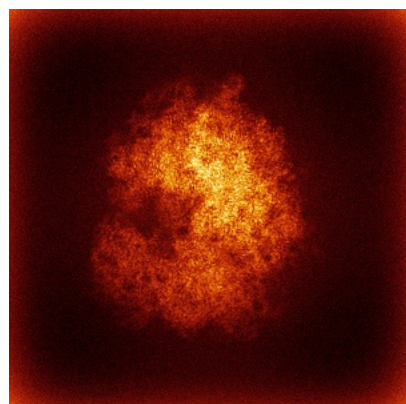


Y

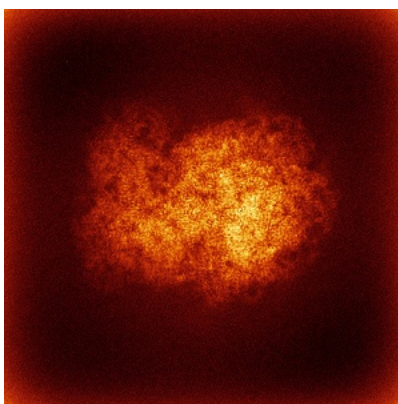


Z

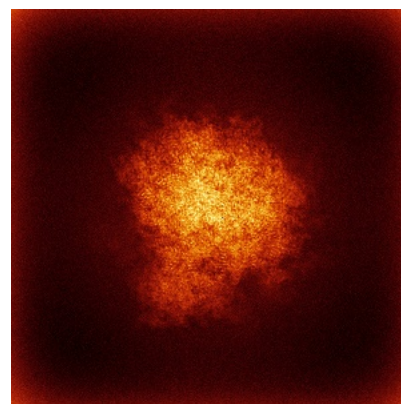
### 6.4.2 Raw map



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



X



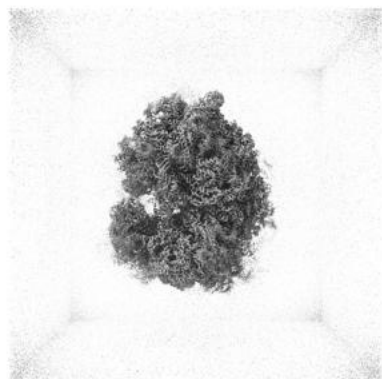
Y



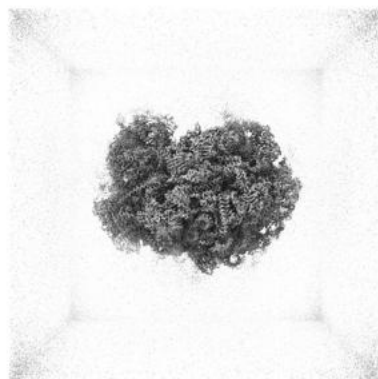
Z

The images above show the 3D surface view of the map at the recommended contour level 0.11. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

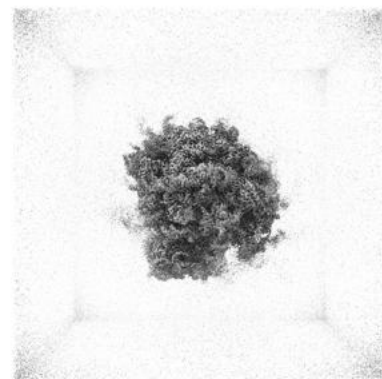
### 6.5.2 Raw map



X



Y



Z

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.

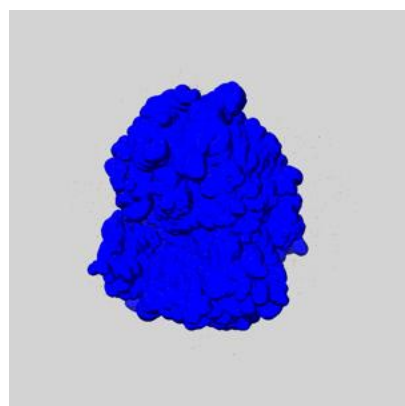
## 6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

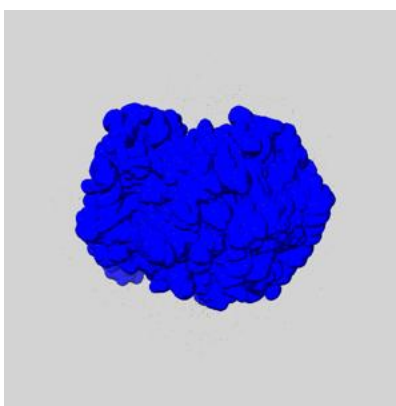
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

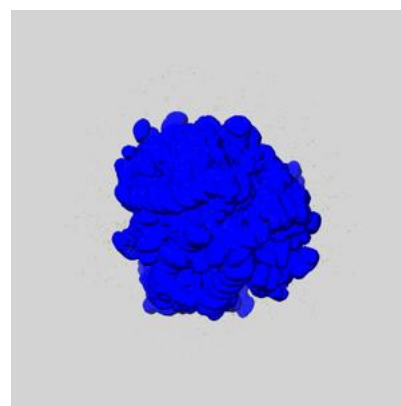
### 6.6.1 emd\_48552\_msk\_1.map [i](#)



X



Y

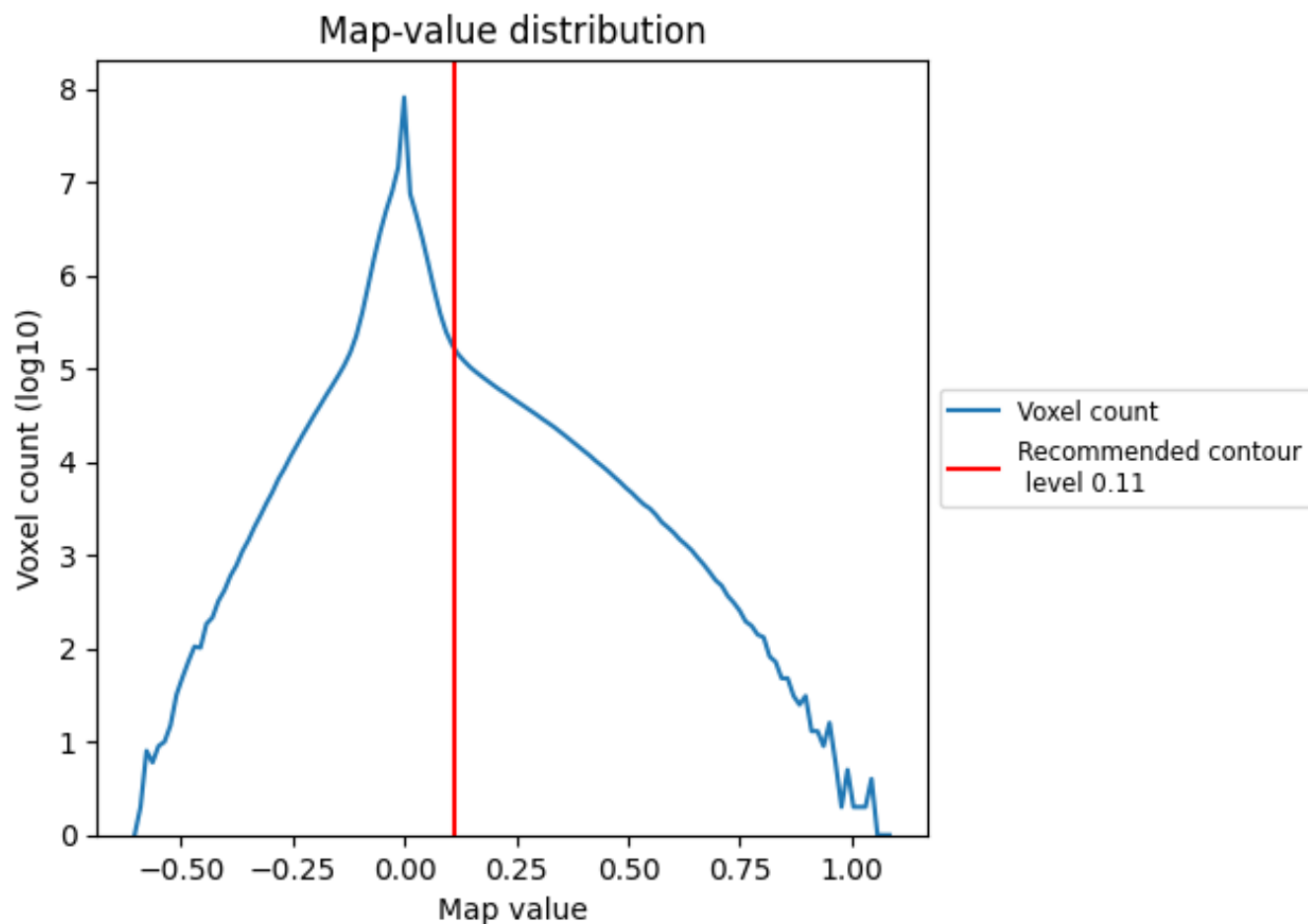


Z

## 7 Map analysis [i](#)

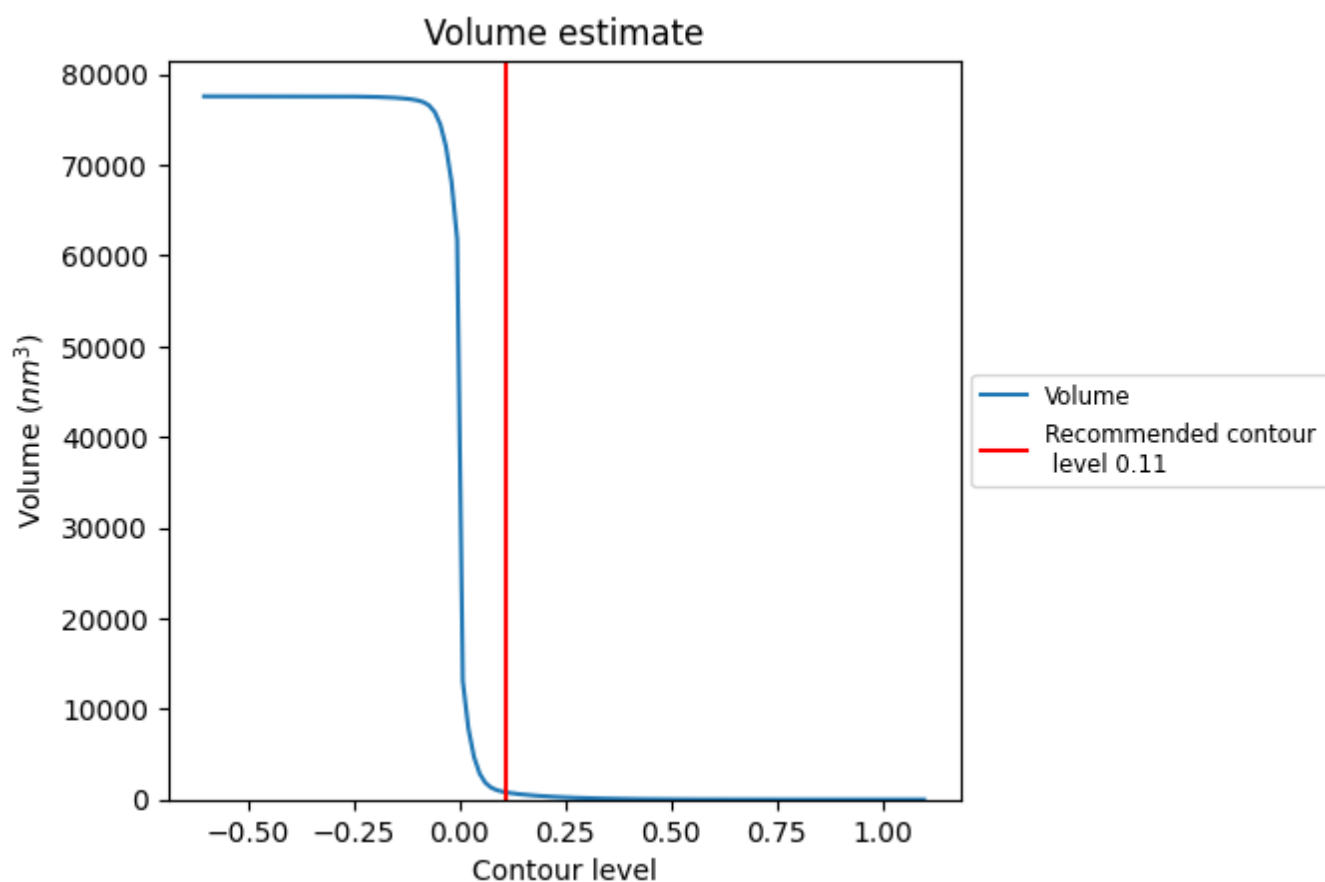
This section contains the results of statistical analysis of the map.

### 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](#)

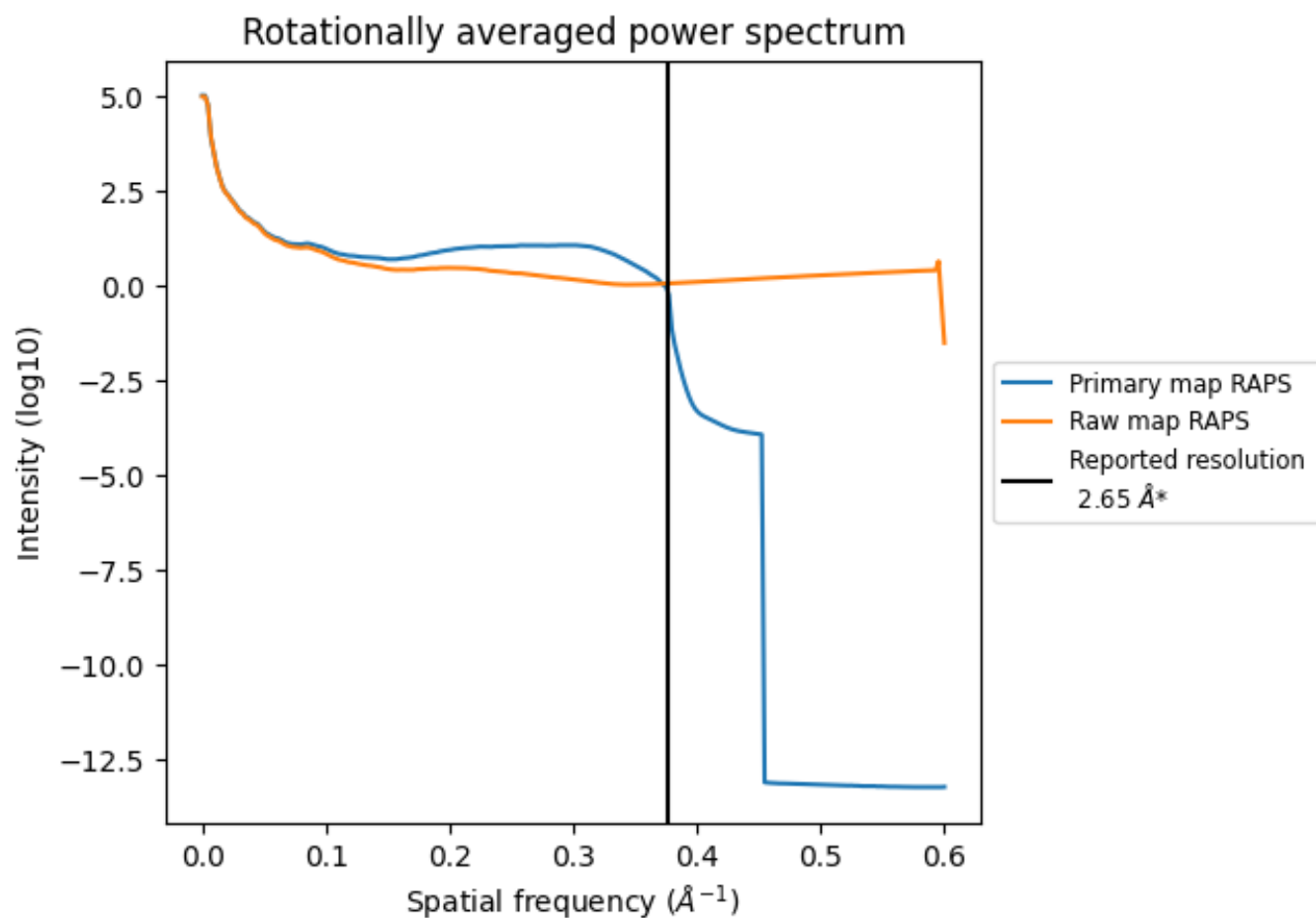


The volume at the recommended contour level is 802 nm<sup>3</sup>; this corresponds to an approximate mass of 725 kDa.

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 ⓘ

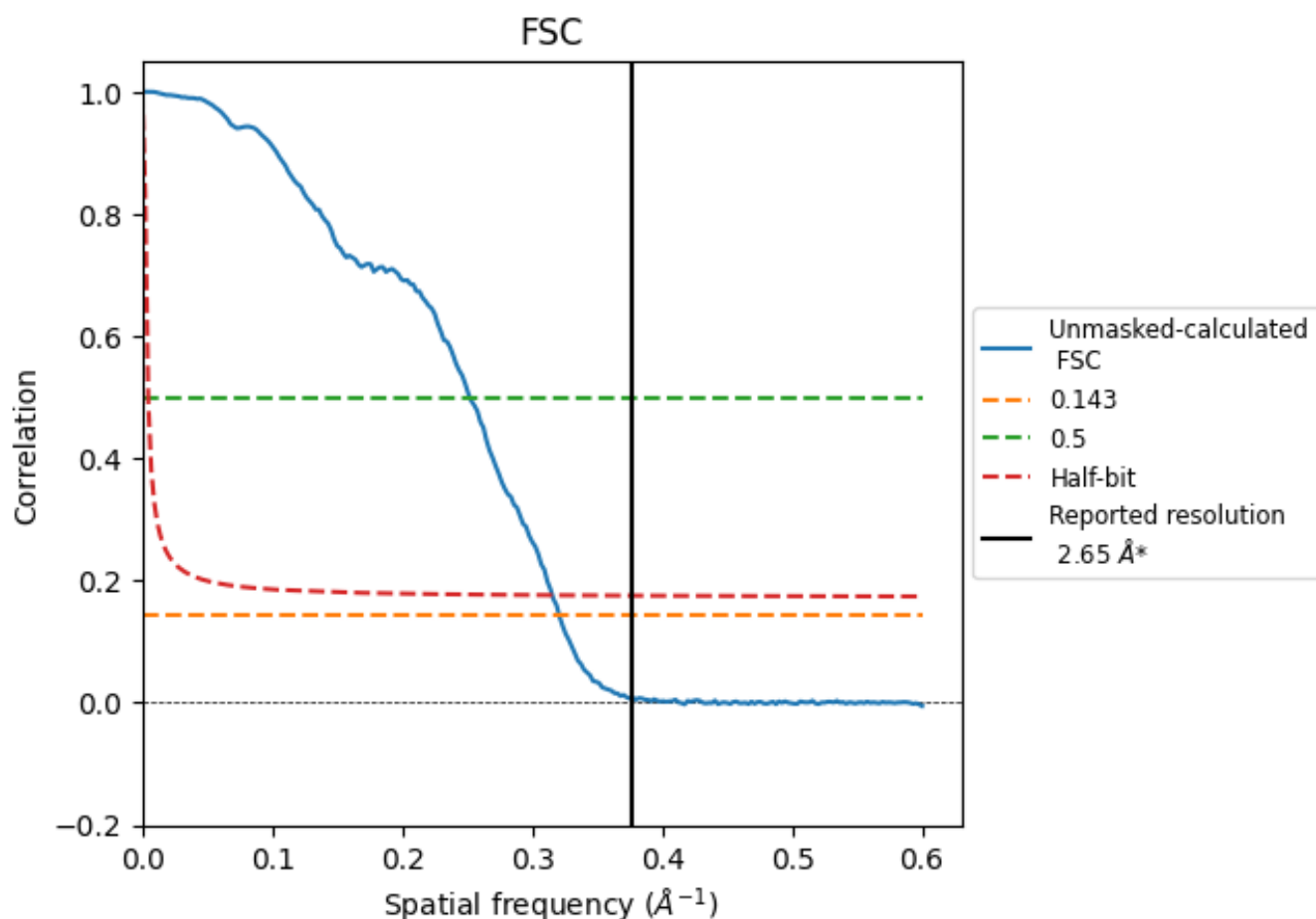


\*Reported resolution corresponds to spatial frequency of 0.377 Å<sup>-1</sup>

## 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 0.377  $\text{\AA}^{-1}$



## 8.2 Resolution estimates [i](#)

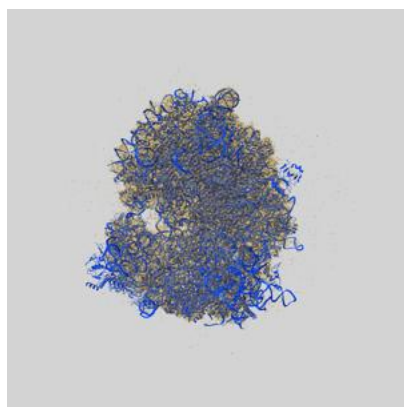
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.65	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.12	3.97	3.17

\*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 3.12 differs from the reported value 2.65 by more than 10 %

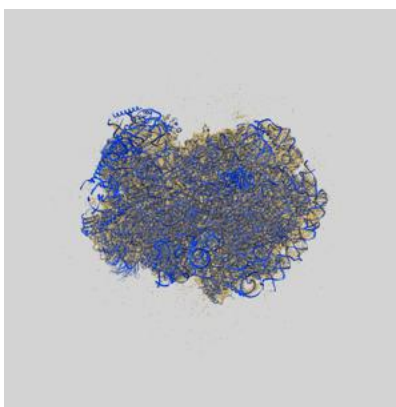
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-48552 and PDB model 9MR4. Per-residue inclusion information can be found in section 3 on page 22.

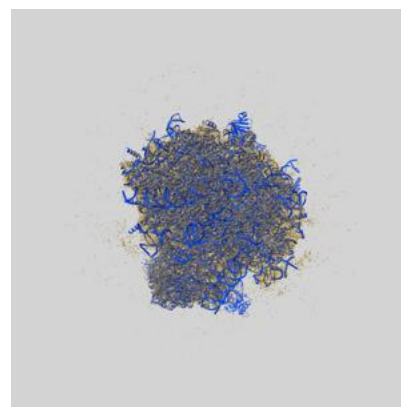
### 9.1 Map-model overlay [i](#)



X



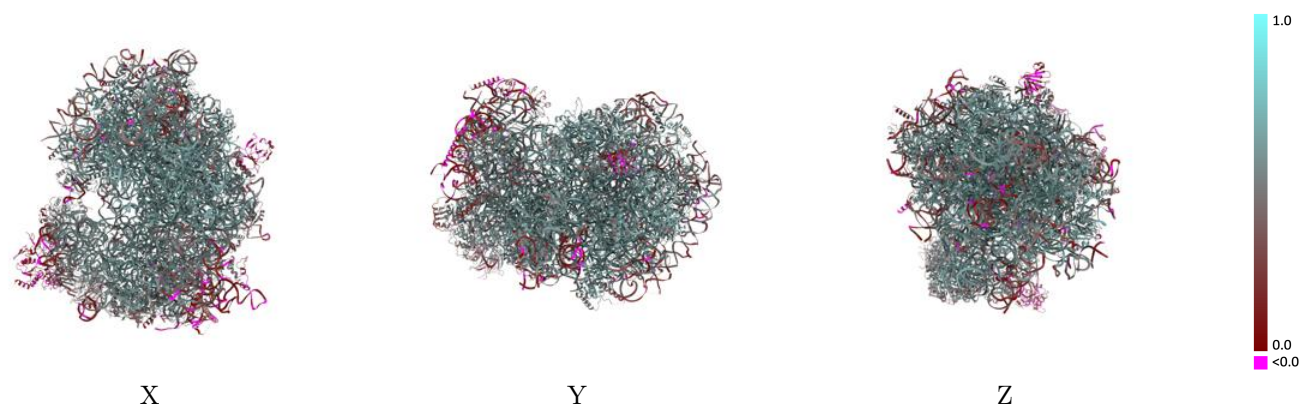
Y



Z

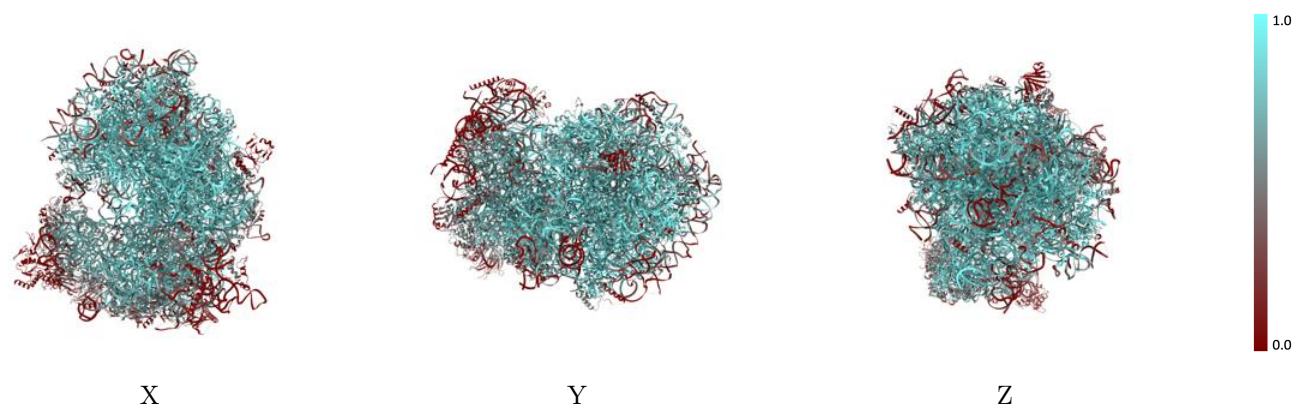
The images above show the 3D surface view of the map at the recommended contour level 0.11 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



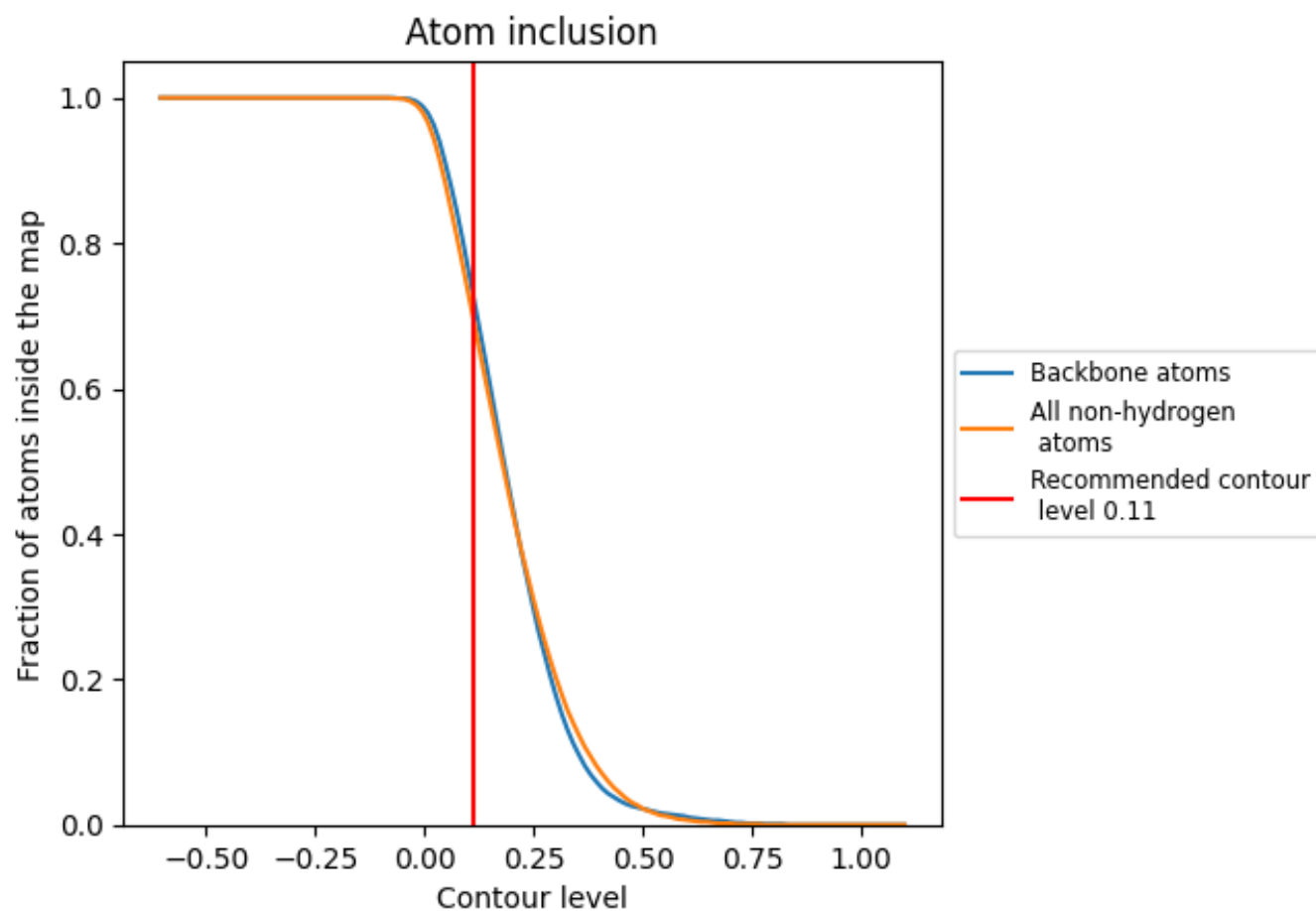
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.11).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 73% of all backbone atoms, 70% 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 (0.11) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7010	 0.5240
0	 0.0020	 0.0720
2	 0.5580	 0.4850
4	 0.2580	 0.4050
5	 0.7830	 0.5480
6	 0.1740	 0.3420
7	 0.9150	 0.6140
8	 0.8380	 0.5710
9	 0.4900	 0.4120
A	 0.8810	 0.6150
AA	 0.3870	 0.3960
B	 0.8500	 0.6050
BB	 0.3660	 0.4030
C	 0.8440	 0.5920
CC	 0.5430	 0.4750
D	 0.7190	 0.5400
DD	 0.5350	 0.4860
E	 0.6820	 0.5220
EE	 0.6660	 0.5300
EF	 0.2000	 0.2490
EG	 0.0060	 0.0700
EH	 0.5830	 0.4940
F	 0.8270	 0.5840
FF	 0.4910	 0.4770
G	 0.6290	 0.5150
GG	 0.3440	 0.3880
H	 0.7140	 0.5520
HH	 0.5710	 0.5060
I	 0.7780	 0.5730
II	 0.4900	 0.4690
J	 0.6160	 0.4960
JJ	 0.4850	 0.4360
K	 0.6810	 0.5040
KK	 0.4280	 0.4540
L	 0.7170	 0.5340



















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Chain	Atom inclusion	Q-score
LL	 0.6430	 0.5030
M	 0.7180	 0.5290
MM	 0.6450	 0.5120
N	 0.8930	 0.6170
NN	 0.3860	 0.4300
O	 0.8520	 0.6020
OO	 0.4170	 0.4700
P	 0.8560	 0.6160
PP	 0.4580	 0.4700
Q	 0.8750	 0.6060
QQ	 0.6830	 0.5400
R	 0.6980	 0.5280
RR	 0.0020	 0.0550
S	 0.8560	 0.6000
SS	 0.1930	 0.3220
T	 0.7780	 0.5680
TT	 0.7390	 0.5520
U	 0.5600	 0.4840
UU	 0.5140	 0.5010
V	 0.8470	 0.6150
VV	 0.7090	 0.5550
W	 0.4900	 0.4190
WW	 0.3370	 0.3940
X	 0.7710	 0.5630
Y	 0.7780	 0.5750
Z	 0.6940	 0.5400
a	 0.8730	 0.6110
b	 0.5780	 0.4740
c	 0.7410	 0.5600
d	 0.7680	 0.5700
e	 0.8540	 0.6000
f	 0.8940	 0.6130
g	 0.7630	 0.5640
h	 0.7370	 0.5440
i	 0.6650	 0.5310
j	 0.8700	 0.6010
k	 0.5360	 0.4910
l	 0.7870	 0.5860
m	 0.6630	 0.5590
n	 0.7980	 0.5940
o	 0.7530	 0.5650
p	 0.8140	 0.5820

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Chain	Atom inclusion	Q-score
q	 0.5960	 0.5080
r	 0.8280	 0.5910
u	 0.5800	 0.4970
v	 0.6350	 0.5260
w	 0.3660	 0.4210
x	 0.5200	 0.4930
y	 0.5330	 0.4870
z	 0.2700	 0.3360