



Full wwPDB EM Validation Report ⓘ

Mar 6, 2026 – 10:44 PM UTC

PDB ID : 6R6G / pdb_00006r6g
EMDB ID : EMD-4735
Title : Structure of XBP1u-paused ribosome nascent chain complex with SRP.
Authors : Shanmuganathan, V.; Cheng, J.; Braunger, K.; Berninghausen, O.; Beatrix, B.; Beckmann, R.
Deposited on : 2019-03-27
Resolution : 3.70 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

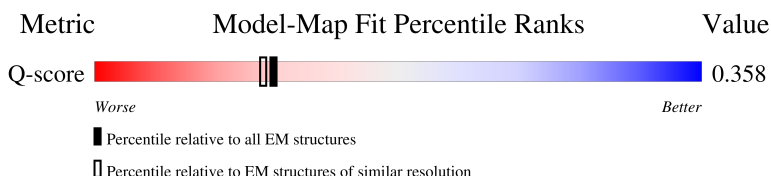
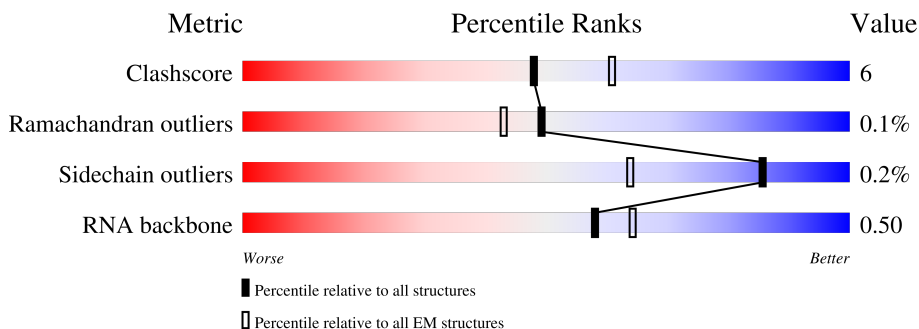
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.70 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	11569 (3.20 - 4.20)

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

Mol	Chain	Length	Quality of chain
1	0	68	79% 82% 18%
2	1	24	8% 38% 33% 25% .
3	2	75	7% 49% 37% 12% .

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Mol	Chain	Length	Quality of chain
4	3	75	
5	4	6	
6	5	3544	
7	6	313	
8	7	120	
9	8	151	
10	9	55	
11	A	248	
12	AA	55	
13	B	394	
14	BB	189	
15	C	362	
16	CC	206	
17	DD	185	
18	D	293	
19	EE	151	
20	E	251	
21	FF	62	
22	F	225	
23	GG	100	
24	G	240	
25	H	190	
26	HH	83	
27	I	213	
28	II	144	

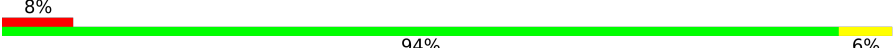
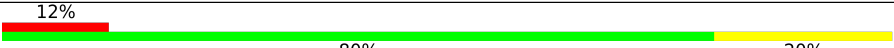
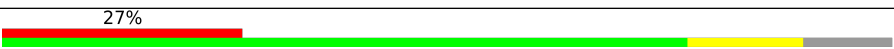
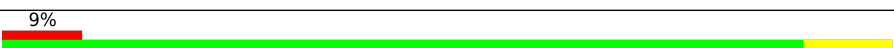
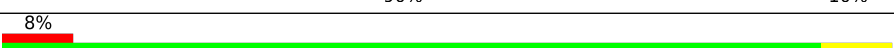
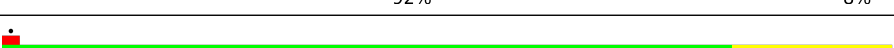
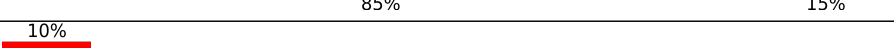
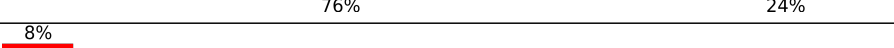
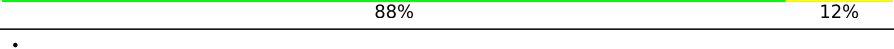
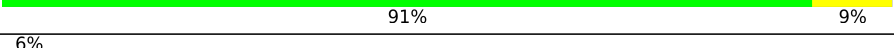
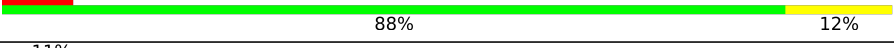
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Mol	Chain	Length	Quality of chain
29	JJ	83	
30	J	170	
31	K	1698	
32	KK	132	
33	L	210	
34	LL	101	
35	M	138	
36	MM	136	
37	N	203	
38	NN	124	
39	O	199	
40	OO	75	
41	P	153	
42	PP	141	
43	Q	187	
44	QQ	149	
45	R	180	
46	RR	117	
47	S	176	
48	SS	96	
49	T	159	
50	TT	129	
51	UU	142	
52	U	99	
53	VV	141	

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Mol	Chain	Length	Quality of chain
54	V	131	
55	W	121	
56	WW	120	
57	X	118	
58	Y	134	
59	Z	135	
60	a	147	
61	b	116	
62	c	98	
63	d	107	
64	e	128	
65	f	109	
66	g	114	
67	h	122	
68	i	102	
69	j	86	
70	k	69	
71	l	50	
72	m	52	
73	n	25	
74	o	104	
75	p	91	
76	q	217	
77	r	124	
78	s	196	

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Mol	Chain	Length	Quality of chain
79	t	153	
80	u	213	
81	v	221	
82	w	228	
83	x	262	
84	y	191	
85	z	237	
86	AB	431	
87	AF	206	
88	AC	105	
89	AI	195	
90	AD	74	
91	AE	94	
92	AG	12	

2 Entry composition [i](#)

There are 94 unique types of molecules in this entry. The entry contains 227187 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 eS31.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	68	Total	C	N	O	S	0	0
			555	351	103	94	7		

- Molecule 2 is a protein called X-box-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	24	Total	C	N	O	S	0	0
			204	137	35	30	2		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	255	ALA	SER	conflict	UNP P17861

- Molecule 3 is a RNA chain called P-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	75	Total	C	N	O	P	0	0
			1594	713	285	522	74		

- Molecule 4 is a RNA chain called E-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	75	Total	C	N	O	P	0	0
			1597	714	287	522	74		

- Molecule 5 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	6	Total	C	N	O	P	0	0
			127	57	21	43	6		

- Molecule 6 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	5	3543	Total	C	N	O	P	0	0
			75972	33833	13910	24686	3543		

- Molecule 7 is a protein called ribosomal protein RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	6	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 8 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	7	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 9 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	8	151	Total	C	N	O	P	0	0
			3208	1432	564	1062	150		

- Molecule 10 is a protein called uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	9	55	Total	C	N	O	S	0	0
			459	286	94	74	5		

- Molecule 11 is a protein called uL2.

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

- Molecule 12 is a protein called 40S ribosomal protein S30.

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

- Molecule 13 is a protein called uL3.

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

- Molecule 14 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	BB	185	Total	C	N	O	S	0	0
			1488	952	271	264	1		

- Molecule 15 is a protein called uL4.

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

- Molecule 16 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	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 17 is a protein called Ribosomal protein S9 (Predicted).

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

- Molecule 18 is a protein called 60S ribosomal protein L5.

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

- Molecule 19 is a protein called Ribosomal protein S11.

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

- Molecule 20 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	E	216	Total	C	N	O	S	0	0
			1729	1115	329	282	3		

- Molecule 21 is a protein called Ribosomal protein S28.

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

- Molecule 22 is a protein called uL30.

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

- Molecule 23 is a protein called Ribosomal protein S20.

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

- Molecule 24 is a protein called eL8.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	244	GLY	CYS	conflict	UNP G1STW0

- Molecule 25 is a protein called uL6.

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

- Molecule 26 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	HH	83	Total	C	N	O	S	0	0
			636	393	117	121	5		

- Molecule 27 is a protein called Ribosomal protein L10 (Predicted).

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

- Molecule 28 is a protein called uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	II	144	Total	C	N	O	S	0	0
			1190	746	241	202	1		

- Molecule 29 is a protein called 40S ribosomal protein S27.

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

- Molecule 30 is a protein called Ribosomal protein L11.

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

- Molecule 31 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	K	1698	Total	C	N	O	P	0	0
			36249	16180	6508	11864	1697		

- Molecule 32 is a protein called eS17.

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

- Molecule 33 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	L	210	Total	C	N	O	S	0	0
			1702	1065	354	279	4		

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	47	ALA	-	insertion	UNP G1TPV0
L	48	PRO	-	insertion	UNP G1TPV0
L	49	ARG	-	insertion	UNP G1TPV0
L	50	PRO	-	insertion	UNP G1TPV0
L	51	ALA	-	insertion	UNP G1TPV0
L	52	ALA	-	insertion	UNP G1TPV0
L	53	GLY	-	insertion	UNP G1TPV0
L	54	PRO	-	insertion	UNP G1TPV0
L	55	ILE	-	insertion	UNP G1TPV0

- Molecule 34 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	LL	101	Total	C	N	O	S	0	0
			814	507	170	132	5		

- Molecule 35 is a protein called Ribosomal protein L14.

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

- Molecule 36 is a protein called 40S ribosomal protein S14.

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

- Molecule 37 is a protein called Ribosomal protein L15.

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

- Molecule 38 is a protein called 40S ribosomal protein S24.

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

- Molecule 39 is a protein called 60S ribosomal protein L13a.

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

- Molecule 40 is a protein called ribosomal protein eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	OO	75	Total	C	N	O	S	0	0
			598	382	111	104	1		

- Molecule 41 is a protein called uL22.

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

- Molecule 42 is a protein called eS19.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
PP	119	GLY	TRP	conflict	UNP G1TN62

- Molecule 43 is a protein called eL18.

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

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Q	6	ARG	LEU	conflict	UNP G1TX70
Q	14	ARG	TRP	conflict	UNP G1TX70
Q	23	ILE	MET	conflict	UNP G1TX70
Q	24	TYR	CYS	conflict	UNP G1TX70
Q	38	ARG	HIS	conflict	UNP G1TX70
Q	57	ASN	LYS	conflict	UNP G1TX70
Q	66	MET	VAL	conflict	UNP G1TX70
Q	74	GLY	ASP	conflict	UNP G1TX70
Q	75	ARG	PRO	conflict	UNP G1TX70
Q	86	VAL	ILE	conflict	UNP G1TX70
Q	110	ARG	HIS	conflict	UNP G1TX70
Q	117	GLY	GLU	conflict	UNP G1TX70
Q	124	ASP	HIS	conflict	UNP G1TX70
Q	150	ARG	GLN	conflict	UNP G1TX70
Q	172	ARG	GLY	conflict	UNP G1TX70
Q	184	ARG	TRP	conflict	UNP G1TX70

- Molecule 44 is a protein called ribosomal protein uS15.

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

- Molecule 45 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	R	180	Total	C	N	O	S	0	0
			1508	933	328	238	9		

- Molecule 46 is a protein called 40S ribosomal protein S12.

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

- Molecule 47 is a protein called eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	S	176	Total	C	N	O	S	0	0
			1462	930	285	236	11		

- Molecule 48 is a protein called eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	SS	96	Total	C	N	O	S	0	0
			810	530	143	131	6		

- Molecule 49 is a protein called eL21.

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

- Molecule 50 is a protein called Ribosomal protein S15a.

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

- Molecule 51 is a protein called Ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	UU	142	Total	C	N	O	S	0	0
			1128	717	213	195	3		

- Molecule 52 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	U	99	Total	C	N	O	S	0	0
			809	519	141	147	2		

- Molecule 53 is a protein called Ribosomal protein S23.

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

- Molecule 54 is a protein called eL14.

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

- Molecule 55 is a protein called Ribosomal protein L24.

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

- Molecule 56 is a protein called uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	WW	120	Total	C	N	O	S	0	0
			997	635	187	168	7		

- Molecule 57 is a protein called uL23.

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

- Molecule 58 is a protein called Ribosomal protein L26.

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

- Molecule 59 is a protein called 60S ribosomal protein L27.

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

- Molecule 60 is a protein called uL15.

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

- Molecule 61 is a protein called eL29.

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

- Molecule 62 is a protein called eL30.

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

- Molecule 63 is a protein called eL31.

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

- Molecule 64 is a protein called eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	e	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 65 is a protein called eL33.

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

- Molecule 66 is a protein called eL34.

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

- Molecule 67 is a protein called uL29.

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

- Molecule 68 is a protein called 60S ribosomal protein L36.

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

- Molecule 69 is a protein called Ribosomal protein L37.

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

- Molecule 70 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	k	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

- Molecule 71 is a protein called eL39.

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

- Molecule 72 is a protein called 60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	m	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 73 is a protein called 60s ribosomal protein l41.

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

- Molecule 74 is a protein called eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	o	104	Total	C	N	O	S	0	0
			851	533	174	138	6		

- Molecule 75 is a protein called ribosomal protein eL43.

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

- Molecule 76 is a protein called uS2.

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

- Molecule 77 is a protein called eL28.

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

- Molecule 78 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	s	196	Total	C	N	O	S	0	0
			1507	959	263	276	9		

- Molecule 79 is a protein called uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	t	153	Total	C	N	O	S	0	0
			1160	722	218	217	3		

- Molecule 80 is a protein called 40S ribosomal protein S3a.

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

- Molecule 81 is a protein called uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	v	221	Total	C	N	O	S	0	0
			1716	1111	295	301	9		

- Molecule 82 is a protein called Ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	w	228	Total	C	N	O	S	0	0
			1768	1126	318	316	8		

- Molecule 83 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	x	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
x	25	GLY	SER	conflict	UNP G1TK17
x	51	ARG	LYS	conflict	UNP G1TK17
x	78	THR	ALA	conflict	UNP G1TK17
x	156	VAL	MET	conflict	UNP G1TK17

- Molecule 84 is a protein called Ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	y	185	Total	C	N	O	S	0	0
			1471	921	277	266	7		

- Molecule 85 is a protein called 40S ribosomal protein S6.

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

- Molecule 86 is a protein called Signal recognition particle 54 kDa protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
86	AB	403	Total	C	N	O	S	0	0
			3126	1978	532	592	24		

- Molecule 87 is a RNA chain called 7S RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
87	AF	206	Total	C	N	O	P	6	0
			4551	2026	836	1477	212		

- Molecule 88 is a protein called Signal recognition particle subunit SRP19.

Mol	Chain	Residues	Atoms					AltConf	Trace
88	AC	105	Total	C	N	O	S	0	0
			844	534	152	152	6		

- Molecule 89 is a protein called Signal recognition particle subunit SRP68.

Mol	Chain	Residues	Atoms					AltConf	Trace
89	AI	179	Total	C	N	O	S	0	0
			1497	939	280	271	7		

- Molecule 90 is a protein called Signal recognition particle 9 kDa protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
90	AD	74	Total	C	N	O	S	0	0
			608	388	105	110	5		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AD	37	ASN	SER	conflict	UNP F1Q0Z5
AD	40	VAL	ILE	conflict	UNP F1Q0Z5
AD	52	LYS	ARG	conflict	UNP F1Q0Z5

- Molecule 91 is a protein called Signal recognition particle 14 kDa protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
91	AE	76	Total	C	N	O	S	0	0
			604	382	105	113	4		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AE	22	THR	LEU	conflict	UNP P16255
AE	27	TYR	PHE	conflict	UNP P16255

- Molecule 92 is a protein called Signal sequence (HR2).

Mol	Chain	Residues	Atoms				AltConf	Trace
92	AG	12	Total	C	N	O	0	0
			96	72	12	12		

- Molecule 93 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
93	5	202	Total 202	Mg 202	0
93	7	6	Total 6	Mg 6	0
93	8	4	Total 4	Mg 4	0
93	A	1	Total 1	Mg 1	0
93	B	1	Total 1	Mg 1	0
93	I	1	Total 1	Mg 1	0
93	K	79	Total 79	Mg 79	0
93	P	2	Total 2	Mg 2	0
93	V	1	Total 1	Mg 1	0
93	a	1	Total 1	Mg 1	0
93	j	1	Total 1	Mg 1	0

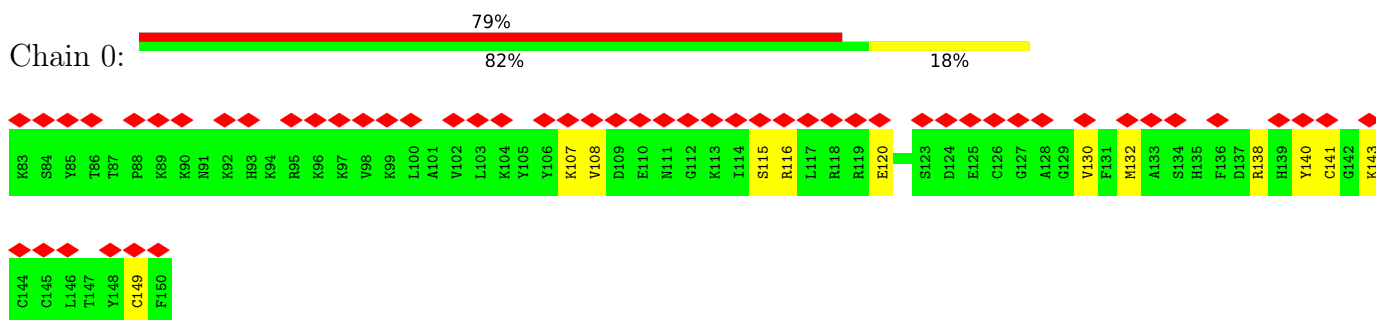
- Molecule 94 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

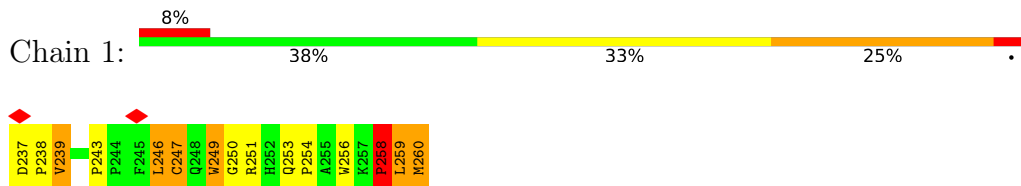
3 Residue-property plots [i](#)

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

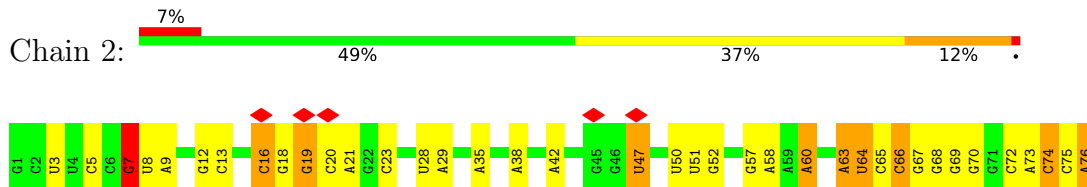
- Molecule 1: eS31



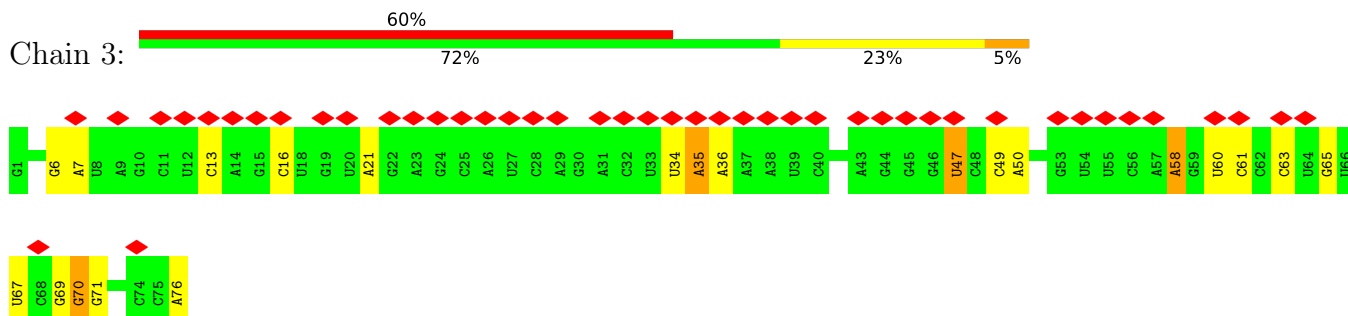
- Molecule 2: X-box-binding protein 1



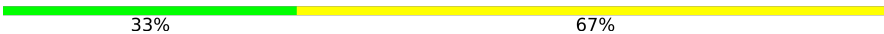
- Molecule 3: P-tRNA



- Molecule 4: E-tRNA



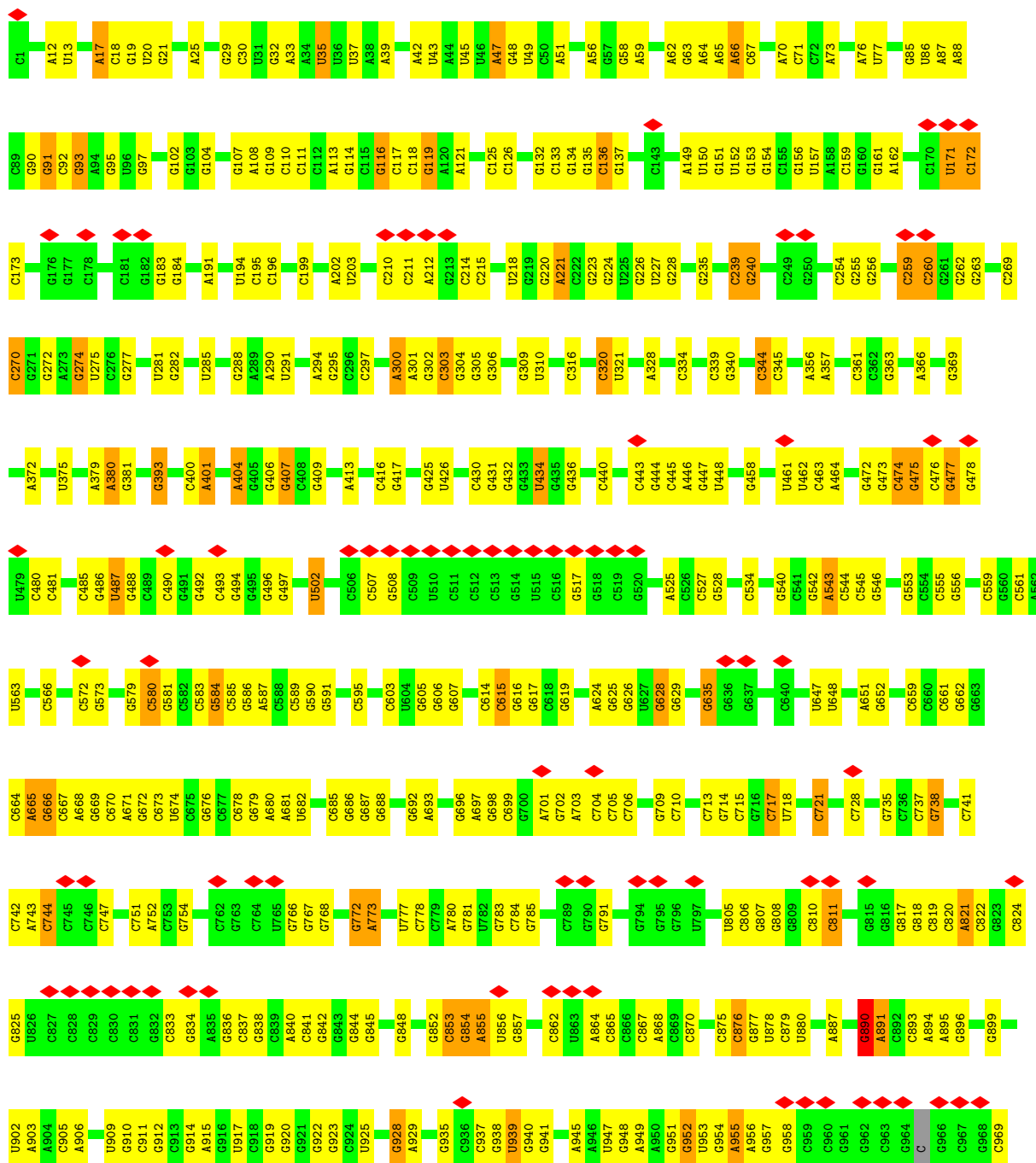
- Molecule 5: mRNA

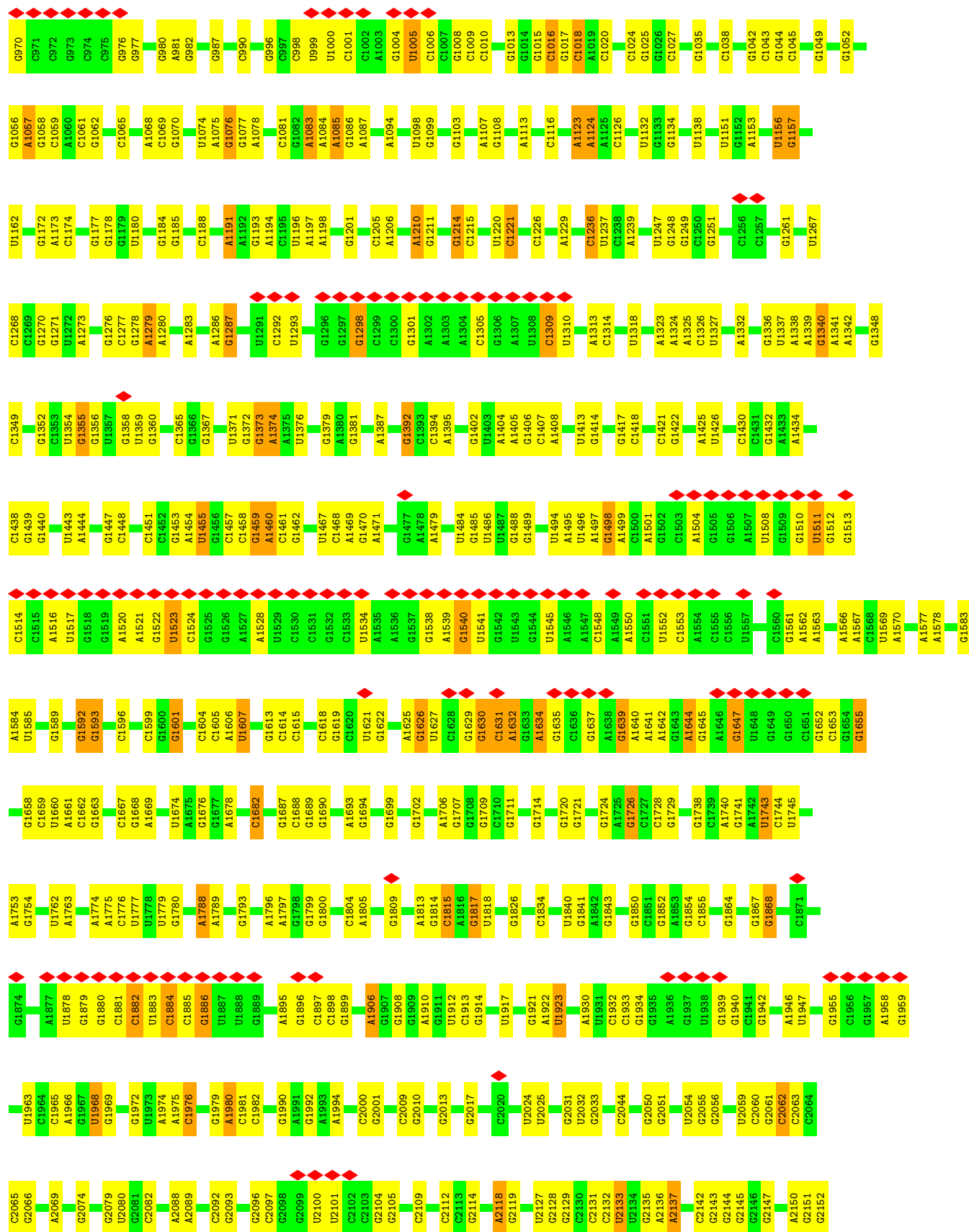
Chain 4:  33% 67%

U43
U44
A45
A46
U47
G48

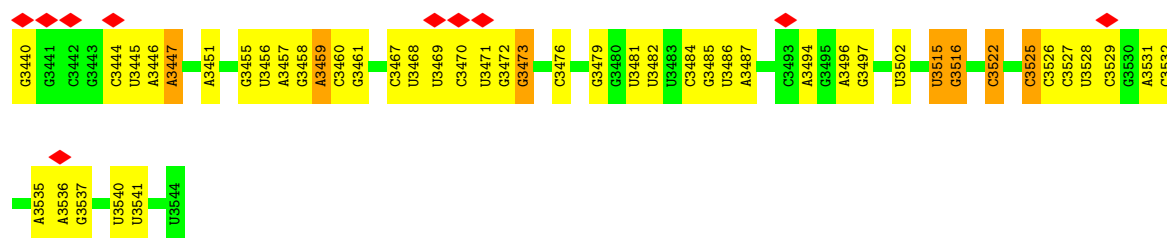
- Molecule 6: 28S ribosomal RNA

Chain 5:  8% 59% 35% 6%

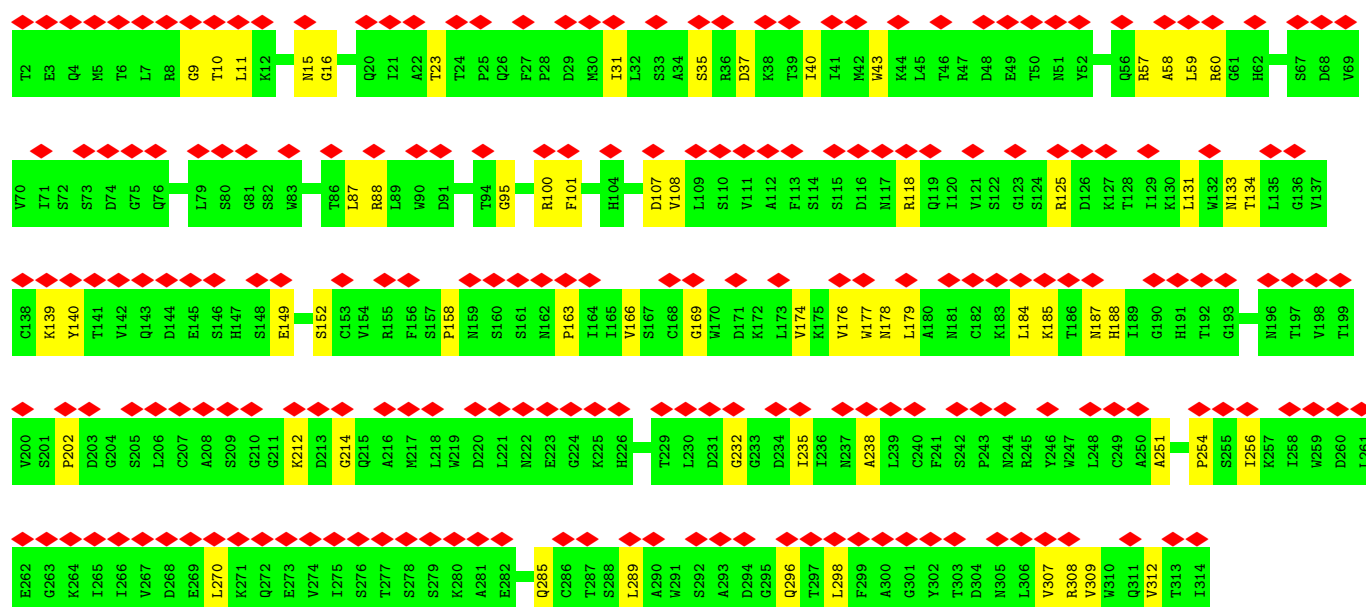
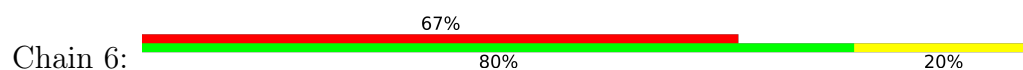




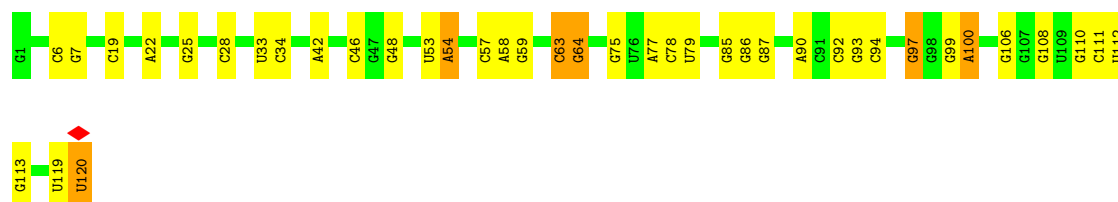




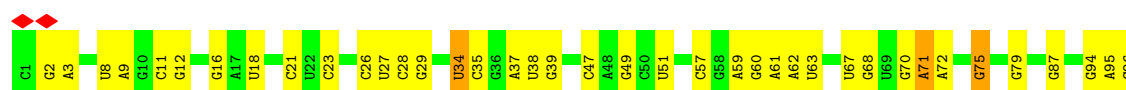
• Molecule 7: ribosomal protein RACK1



• Molecule 8: 5S ribosomal RNA

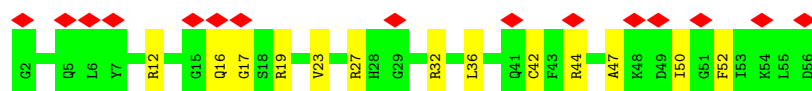
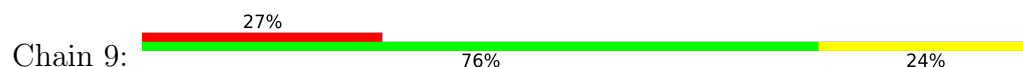


• Molecule 9: 5.8S ribosomal RNA

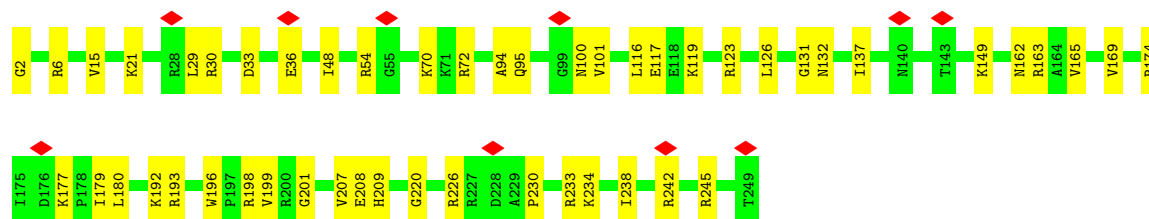
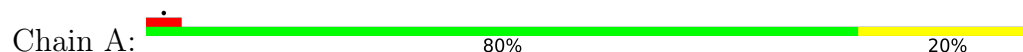




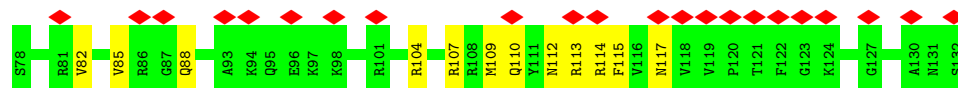
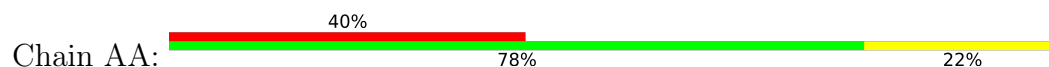
• Molecule 10: uS14



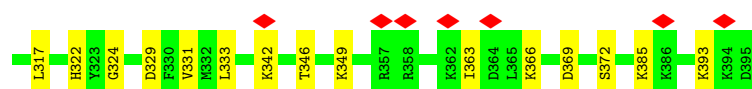
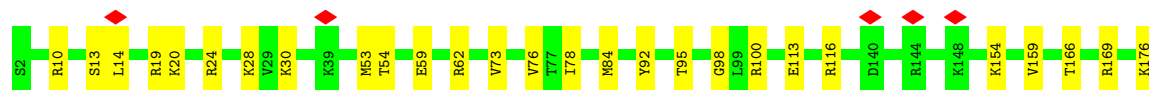
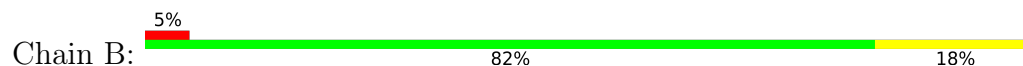
• Molecule 11: uL2



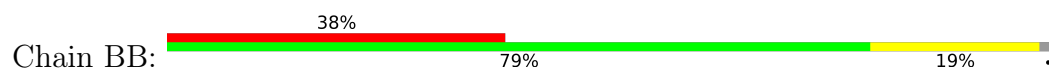
• Molecule 12: 40S ribosomal protein S30

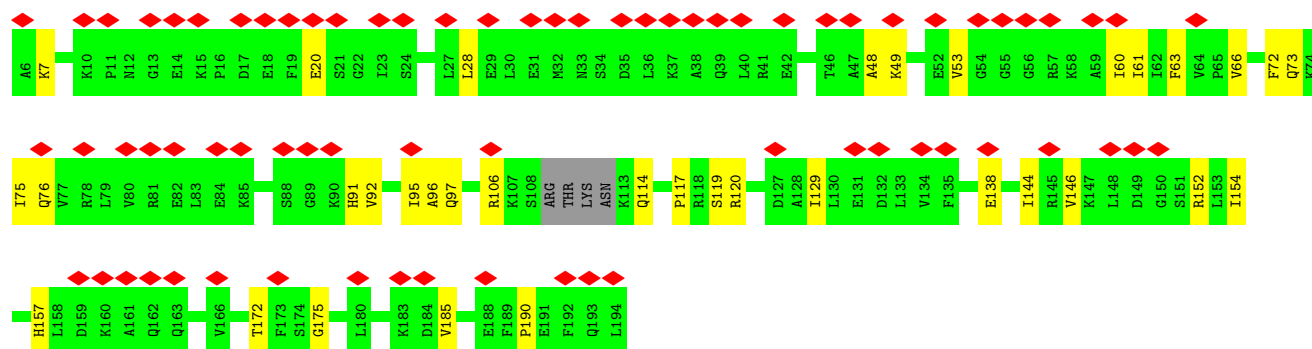


• Molecule 13: uL3

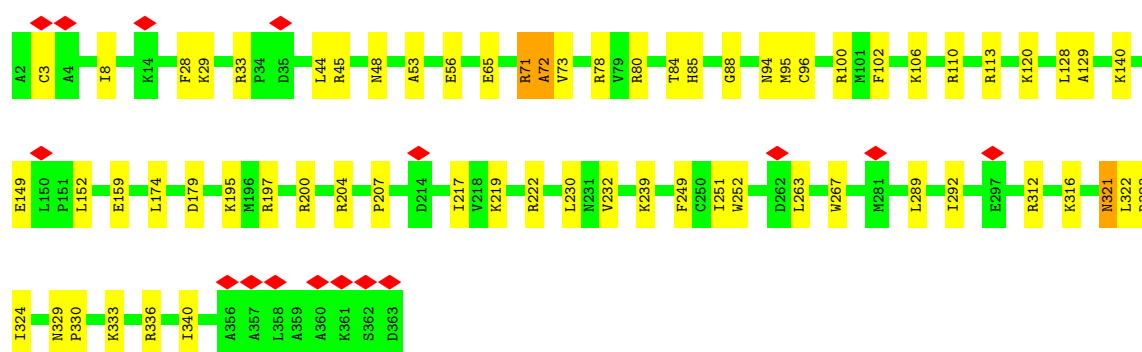
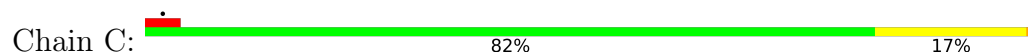


• Molecule 14: 40S ribosomal protein S7

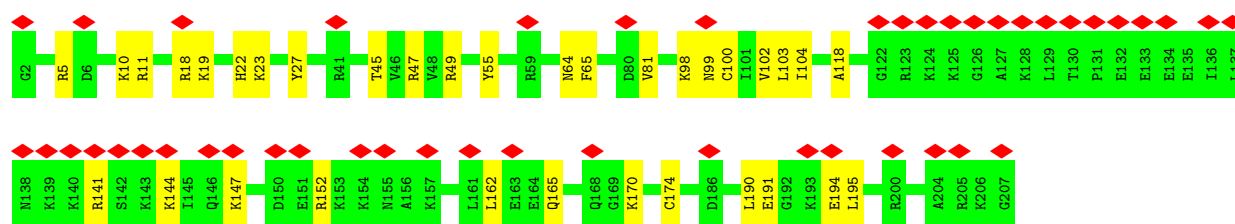
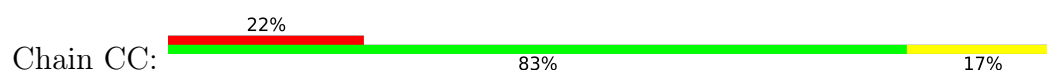




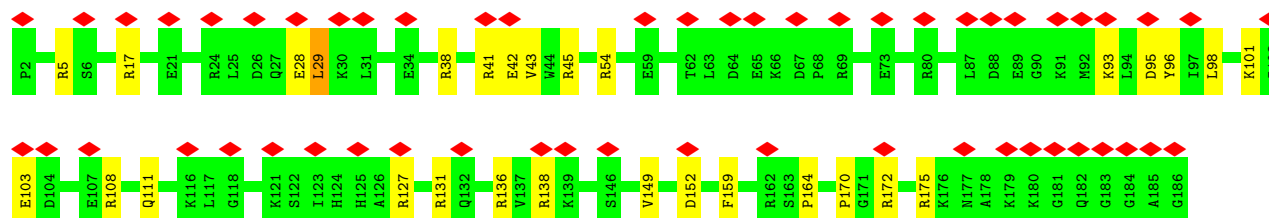
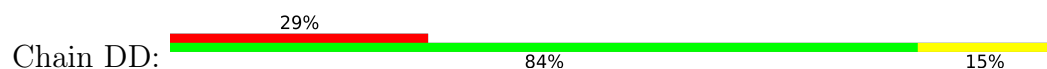
• Molecule 15: uL4



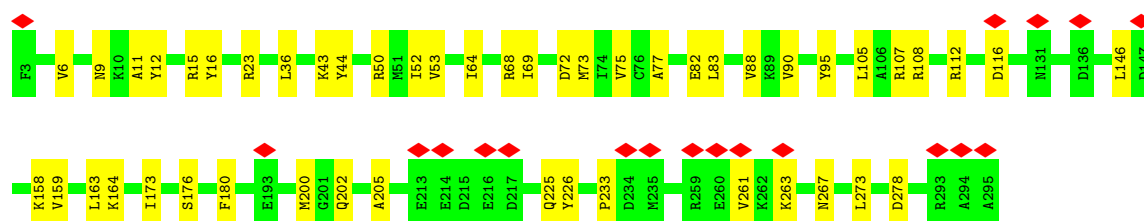
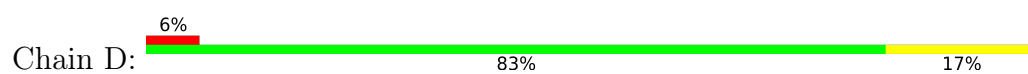
• Molecule 16: 40S ribosomal protein S8



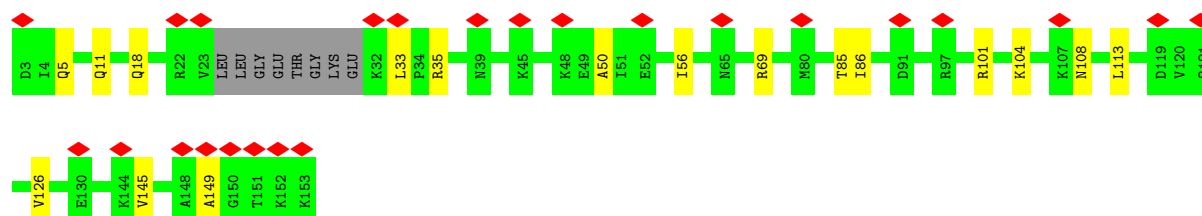
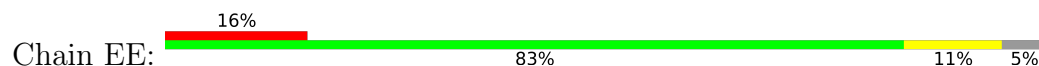
• Molecule 17: Ribosomal protein S9 (Predicted)



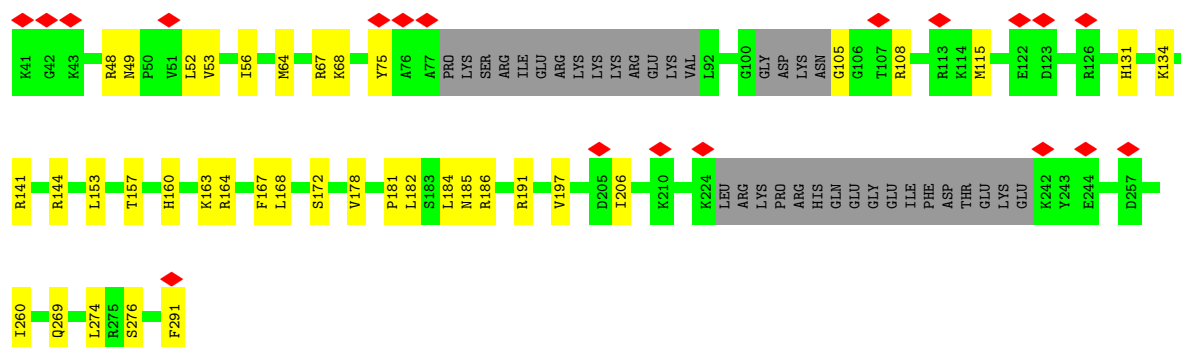
• Molecule 18: 60S ribosomal protein L5



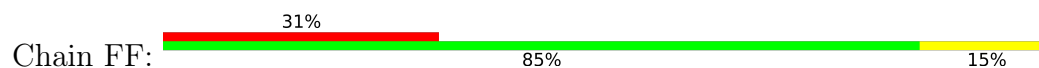
• Molecule 19: Ribosomal protein S11



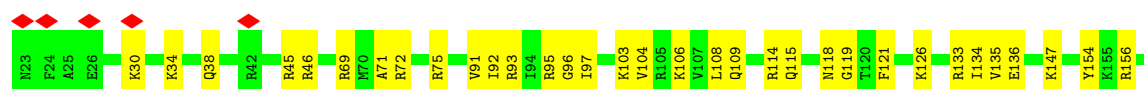
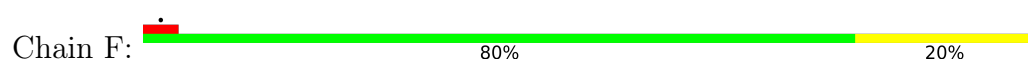
• Molecule 20: 60S ribosomal protein L6



• Molecule 21: Ribosomal protein S28

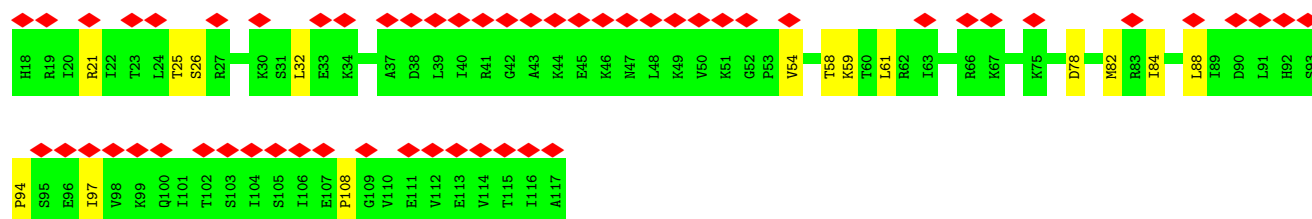
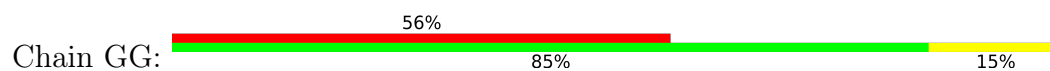


• Molecule 22: uL30

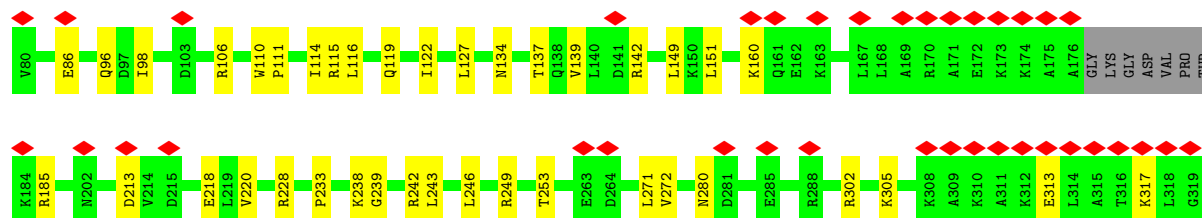
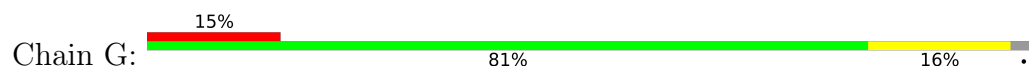




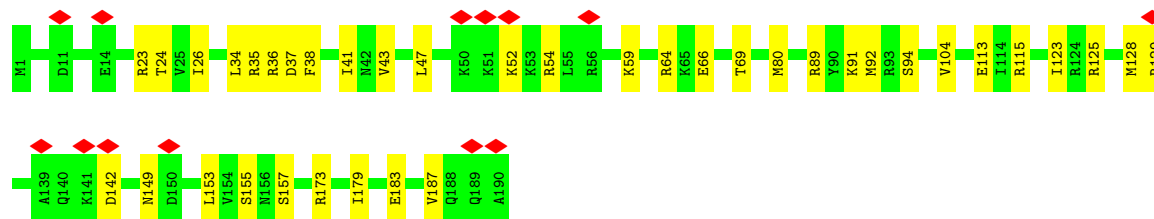
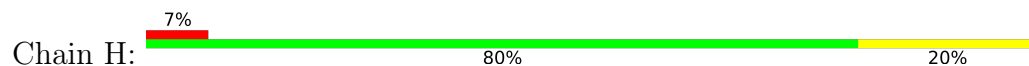
• Molecule 23: Ribosomal protein S20



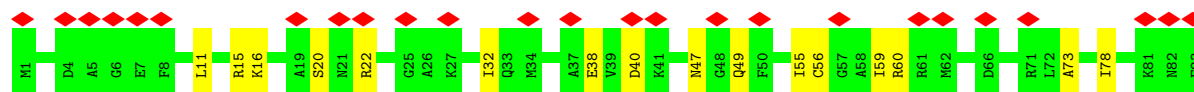
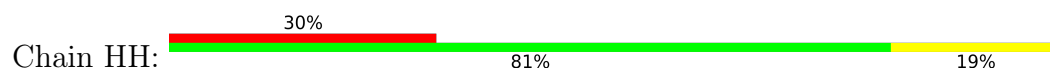
• Molecule 24: eL8



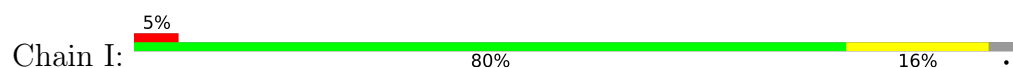
• Molecule 25: uL6

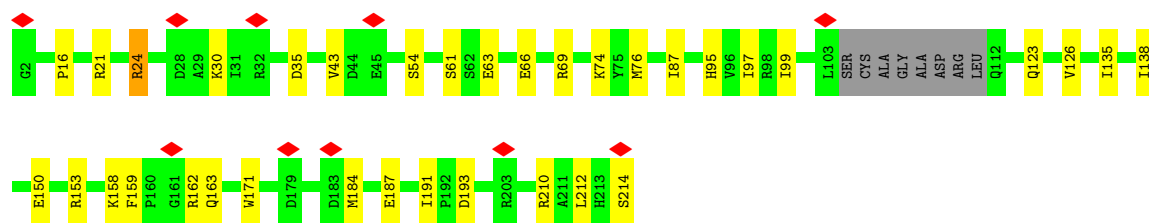


• Molecule 26: 40S ribosomal protein S21

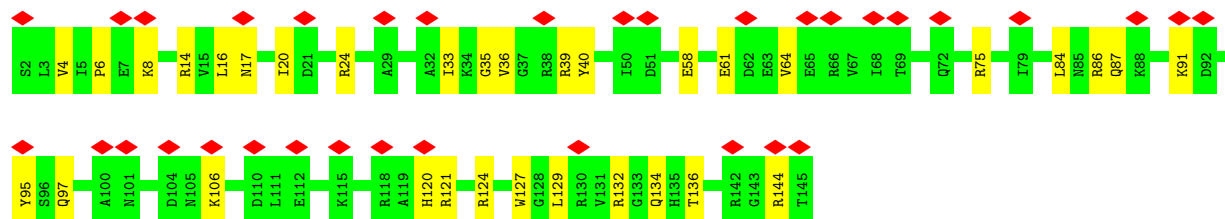
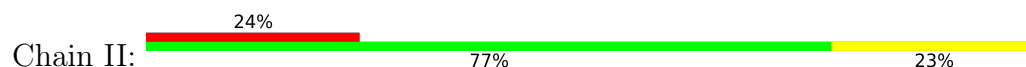


• Molecule 27: Ribosomal protein L10 (Predicted)

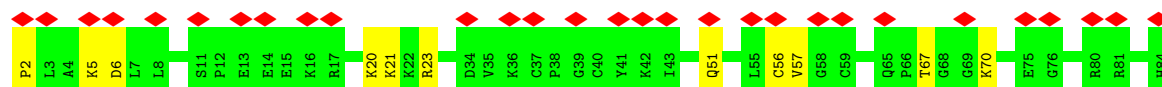
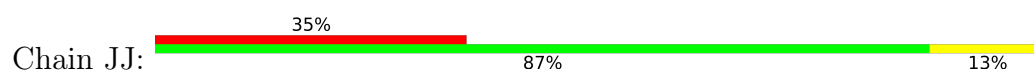




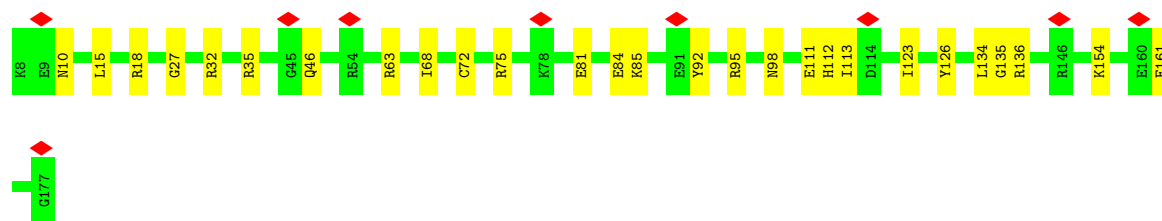
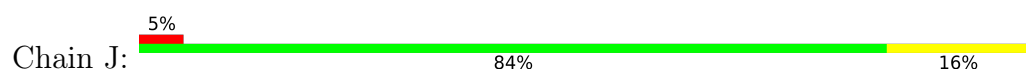
• Molecule 28: uS13



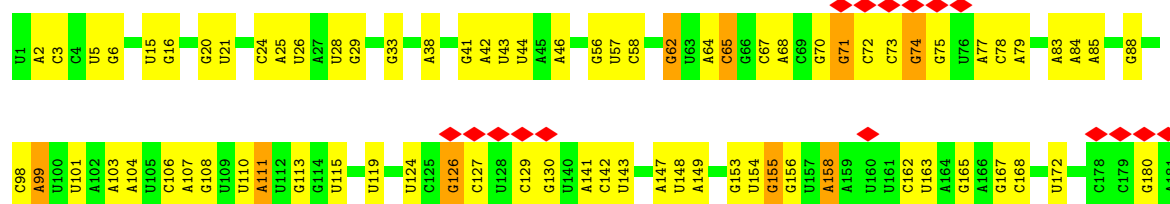
• Molecule 29: 40S ribosomal protein S27

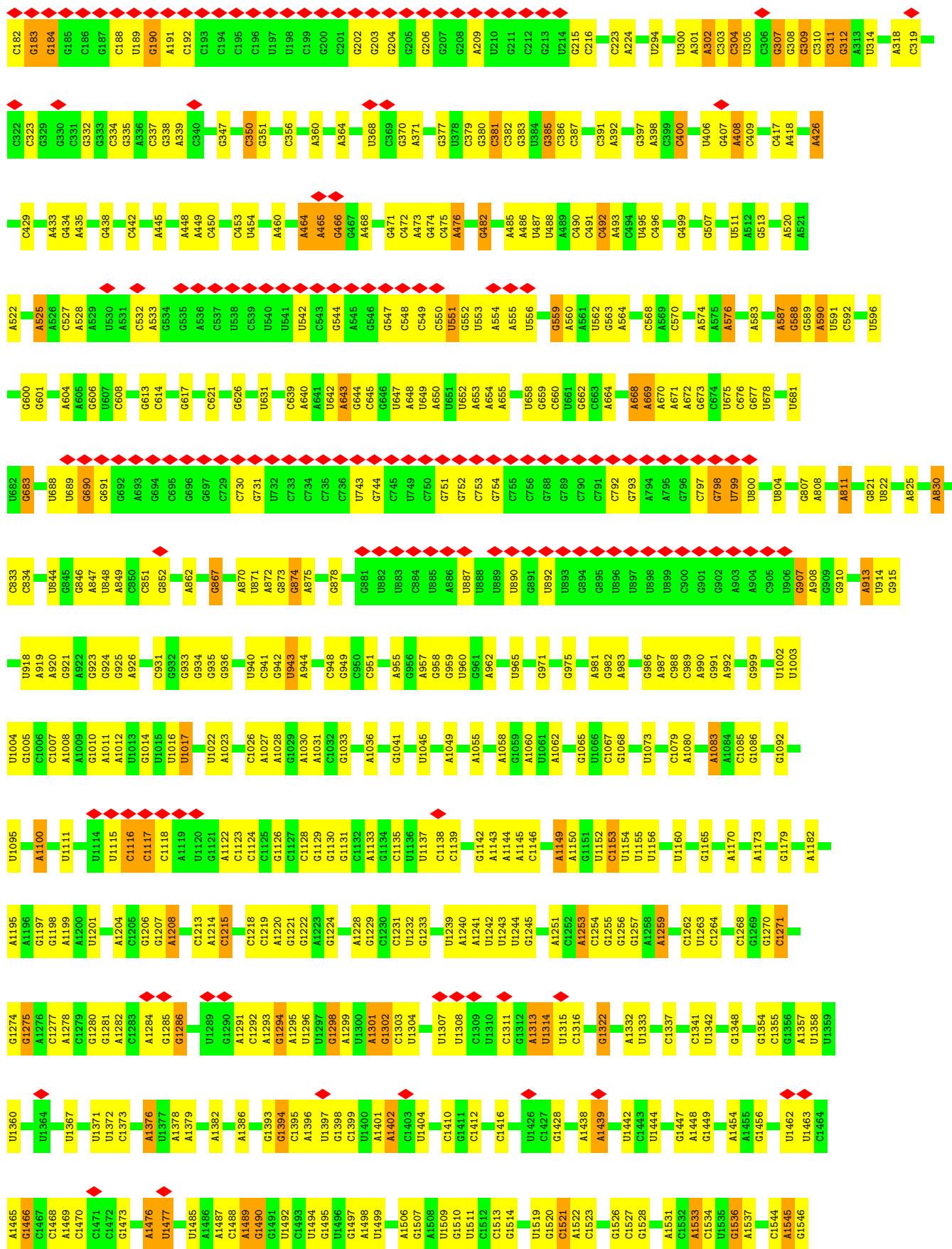


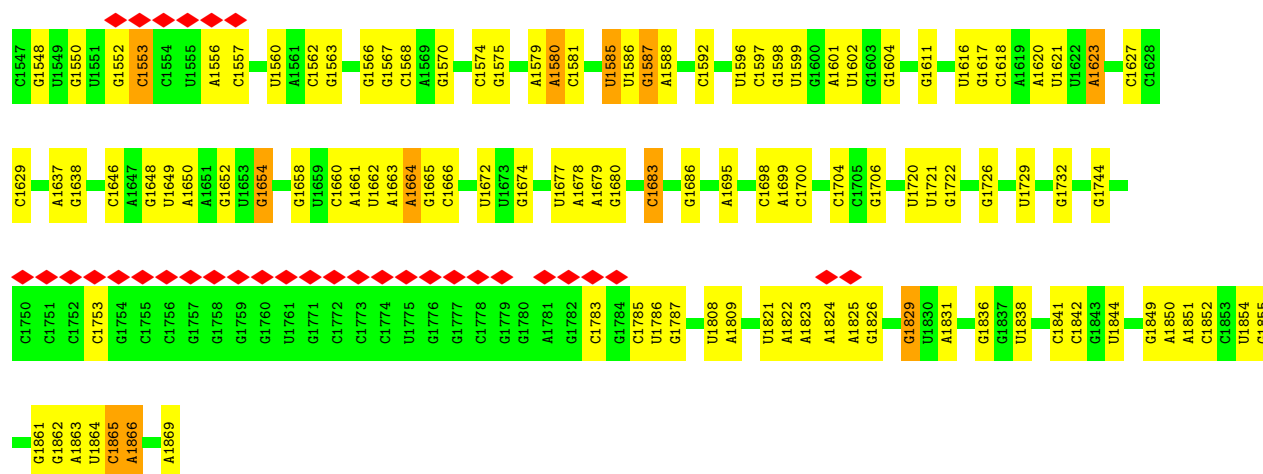
• Molecule 30: Ribosomal protein L11



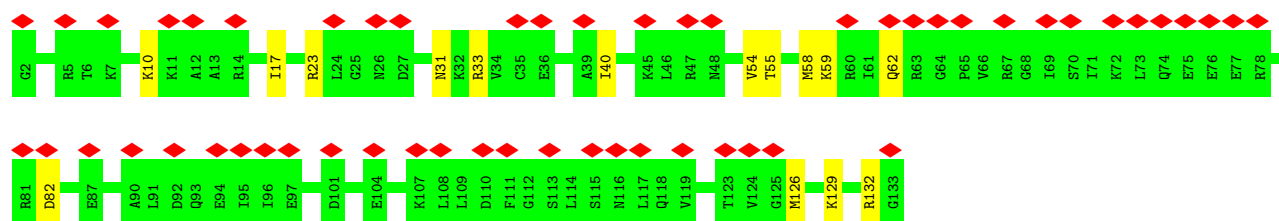
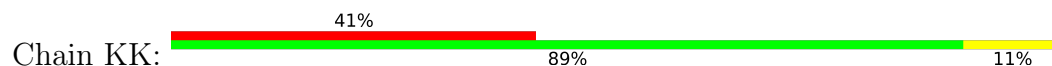
• Molecule 31: 18S ribosomal RNA



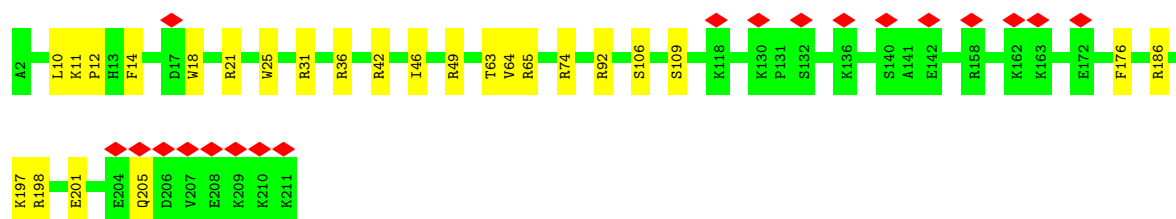
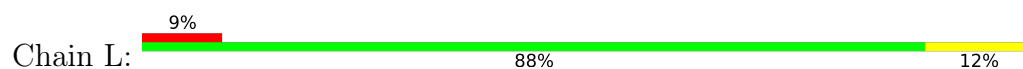




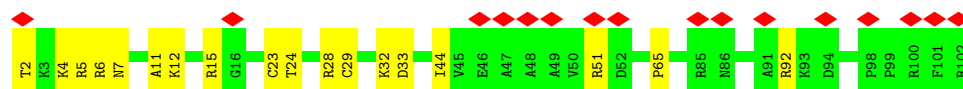
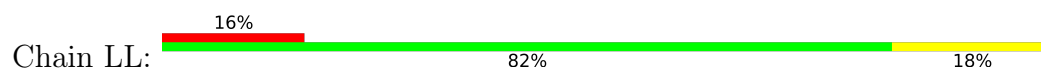
- Molecule 32: eS17



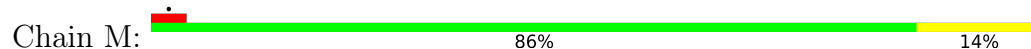
- Molecule 33: 60S ribosomal protein L13



- Molecule 34: 40S ribosomal protein S26

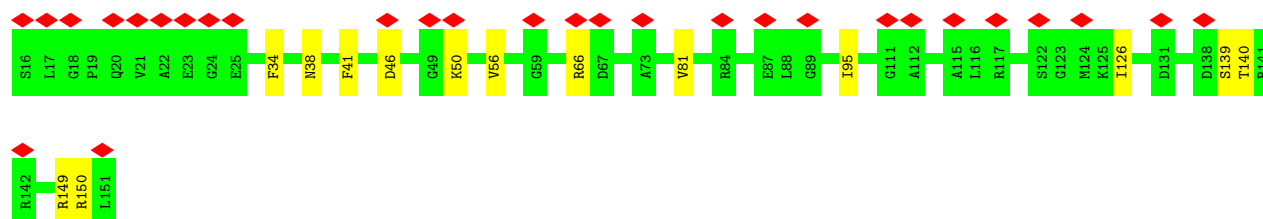


- Molecule 35: Ribosomal protein L14

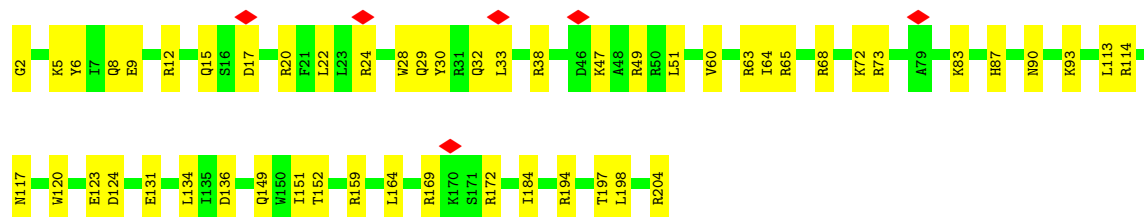
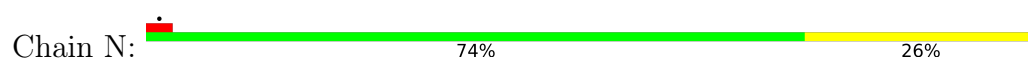




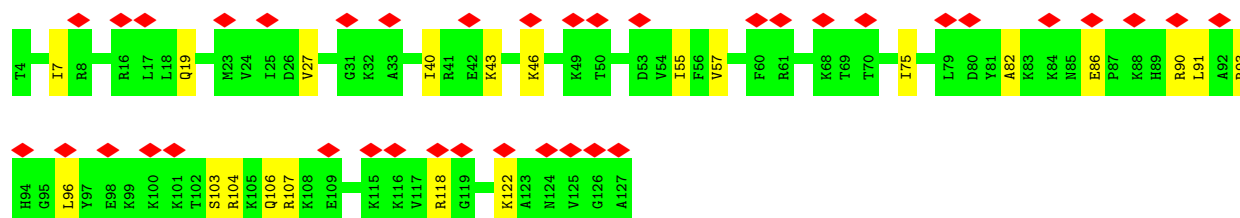
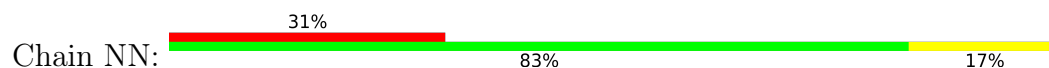
- Molecule 36: 40S ribosomal protein S14



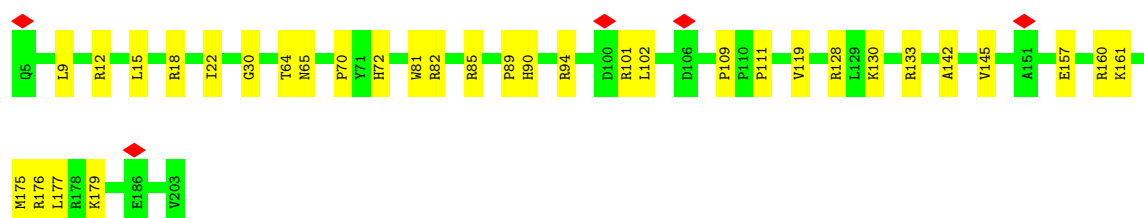
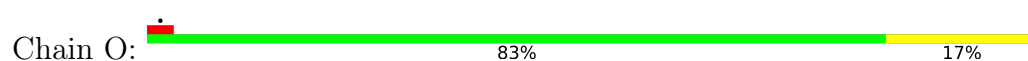
- Molecule 37: Ribosomal protein L15



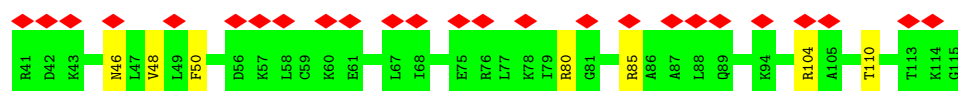
- Molecule 38: 40S ribosomal protein S24



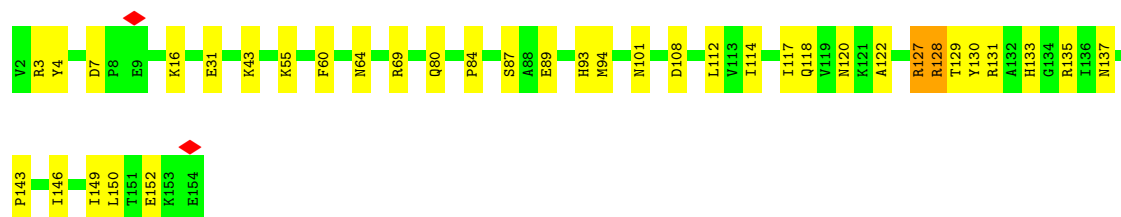
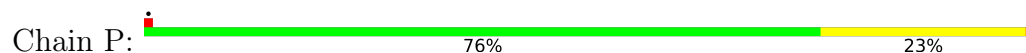
- Molecule 39: 60S ribosomal protein L13a



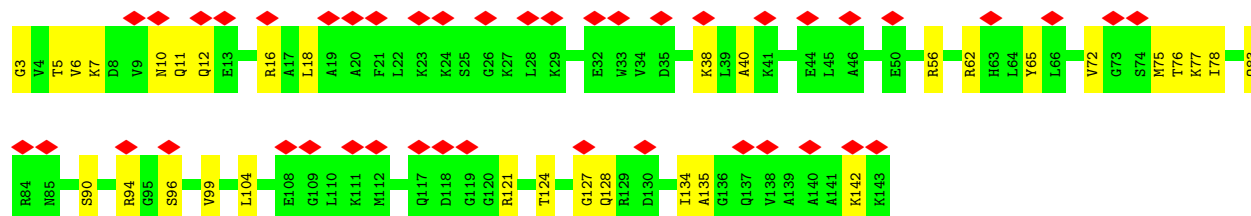
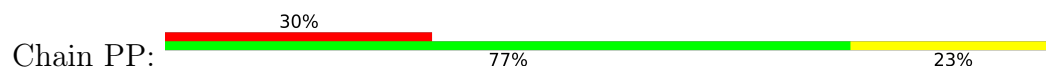
- Molecule 40: ribosomal protein eS25



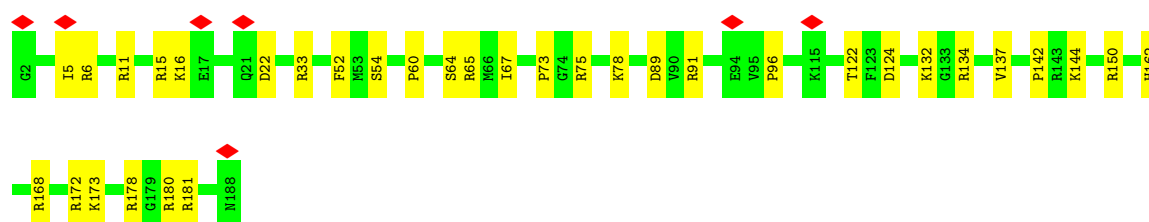
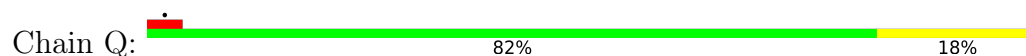
• Molecule 41: uL22



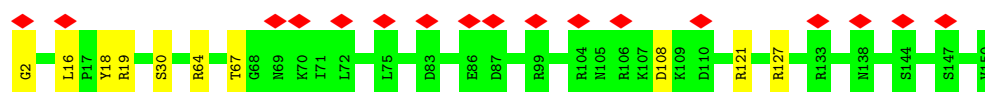
• Molecule 42: eS19



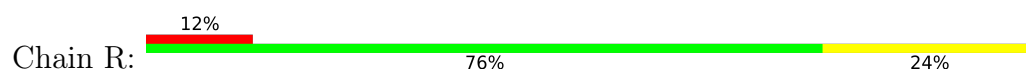
• Molecule 43: eL18

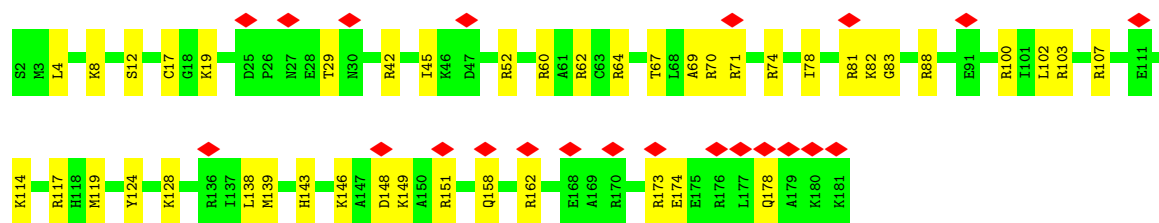


• Molecule 44: ribosomal protein uS15

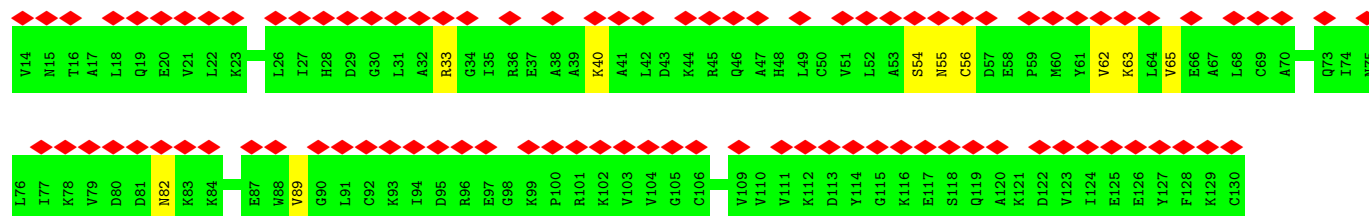
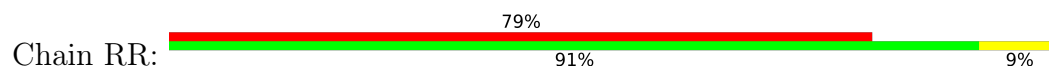


• Molecule 45: 60S ribosomal protein L19

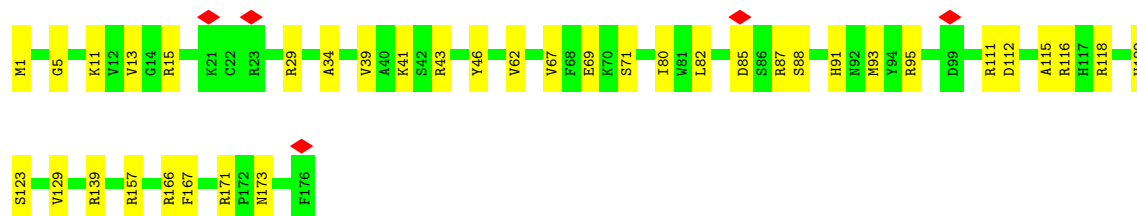
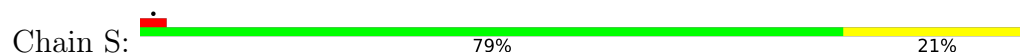




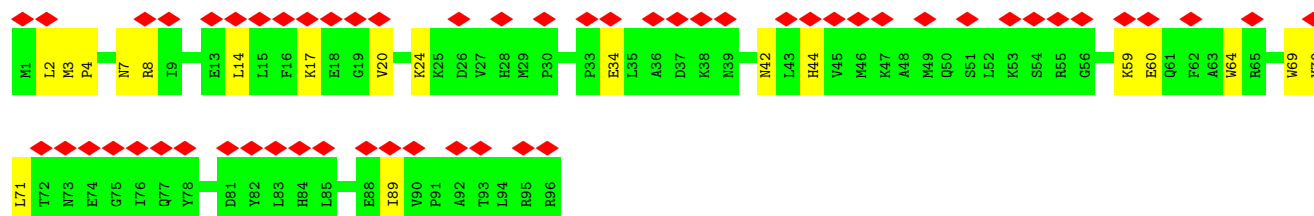
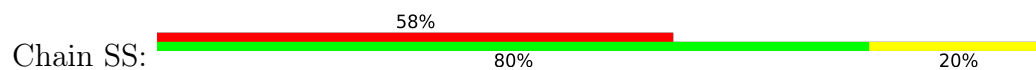
- Molecule 46: 40S ribosomal protein S12



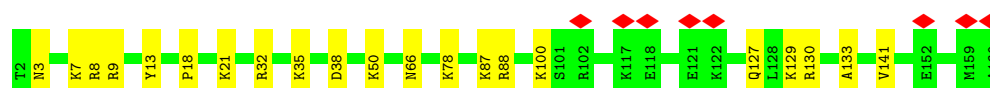
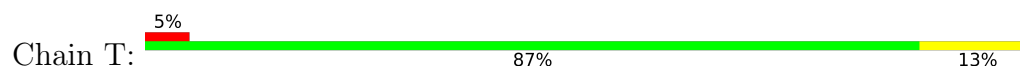
- Molecule 47: eL20



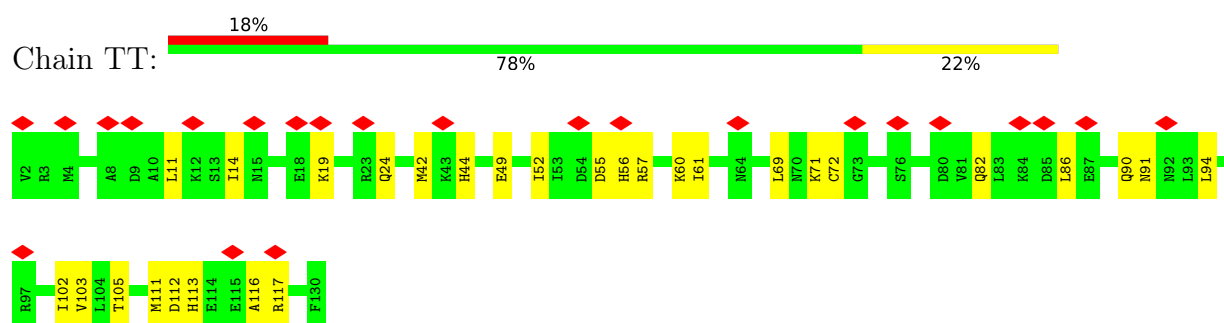
- Molecule 48: eS10



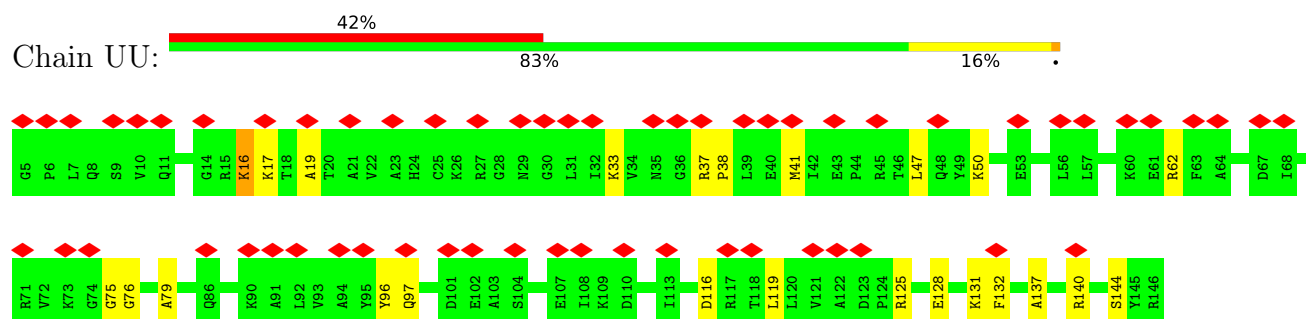
- Molecule 49: eL21



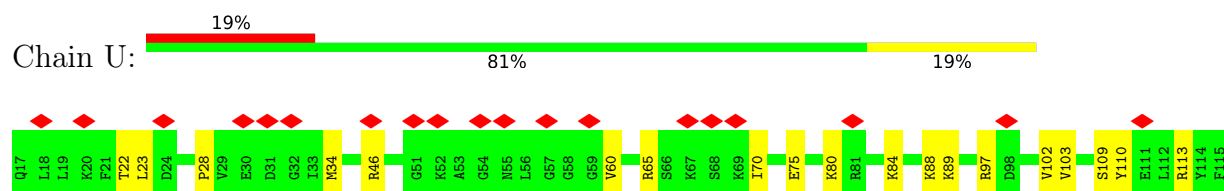
- Molecule 50: Ribosomal protein S15a



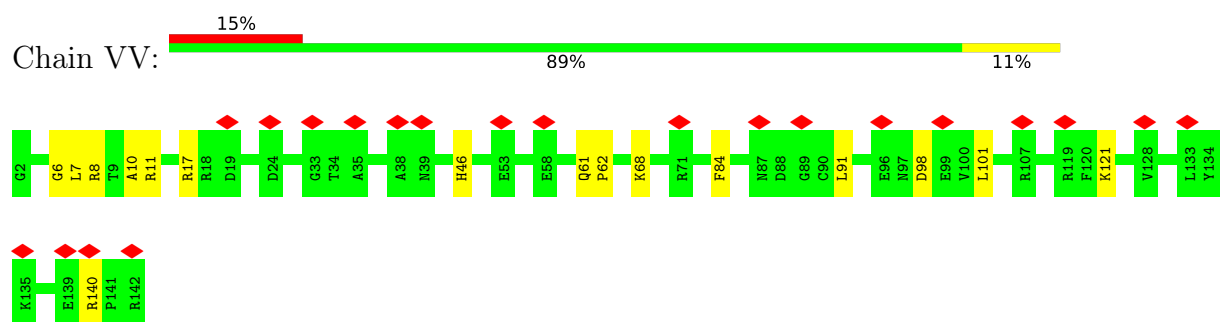
- Molecule 51: Ribosomal protein S16



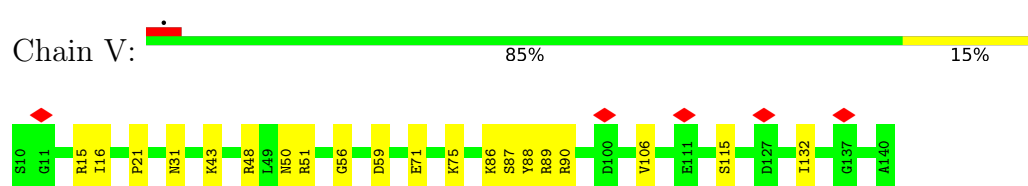
- Molecule 52: 60S ribosomal protein L22



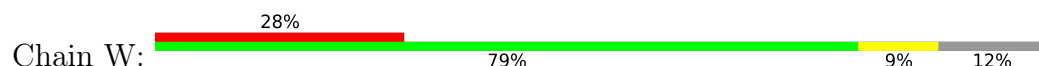
- Molecule 53: Ribosomal protein S23



- Molecule 54: eL14

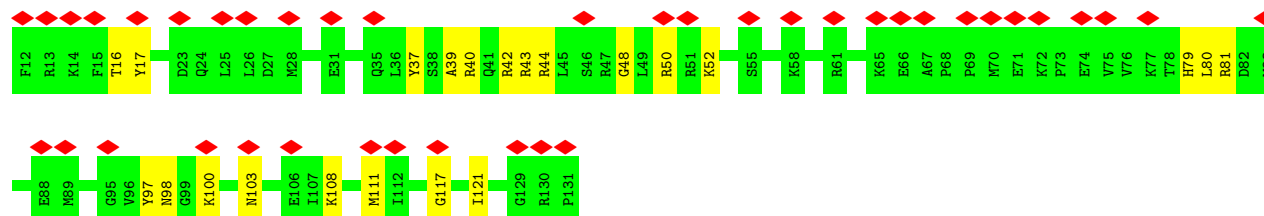
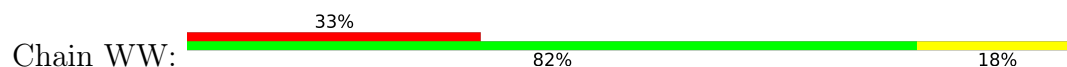


- Molecule 55: Ribosomal protein L24

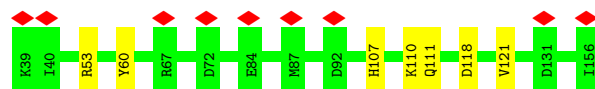




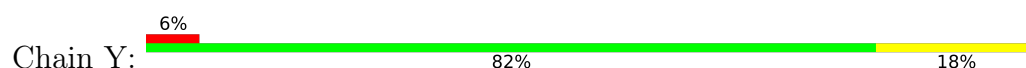
- Molecule 56: uS19



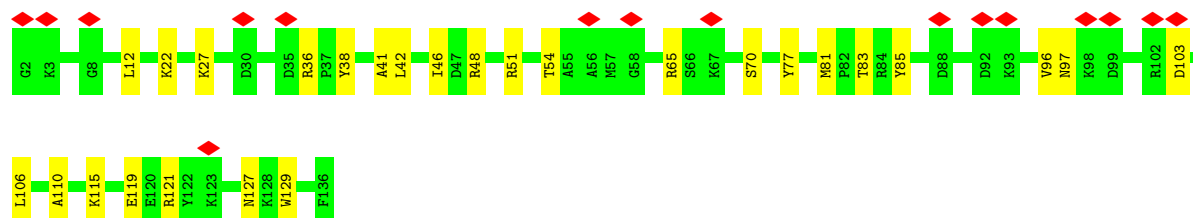
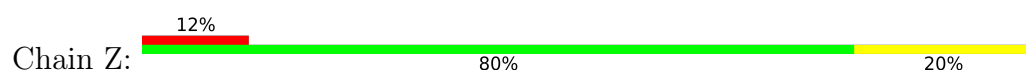
- Molecule 57: uL23



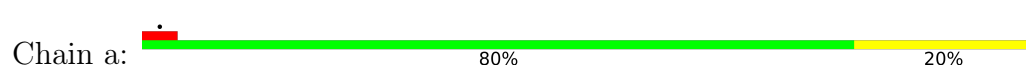
- Molecule 58: Ribosomal protein L26

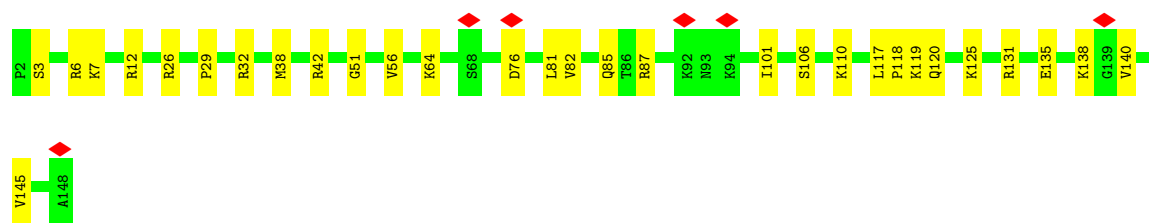


- Molecule 59: 60S ribosomal protein L27

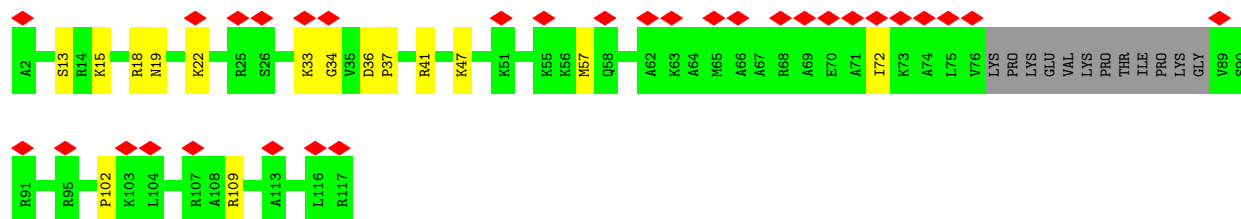
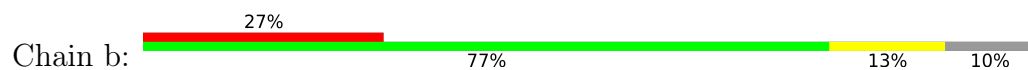


- Molecule 60: uL15

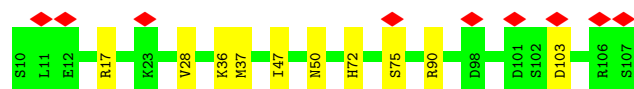
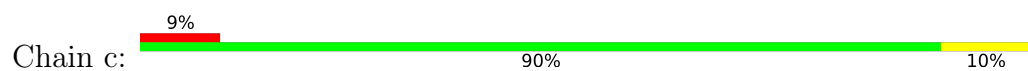




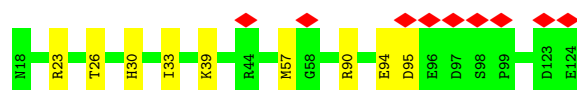
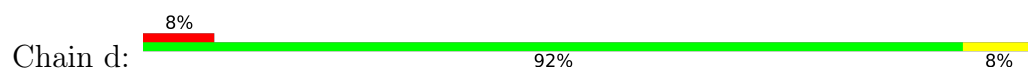
- Molecule 61: eL29



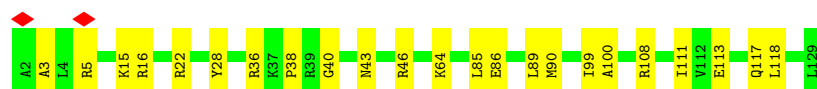
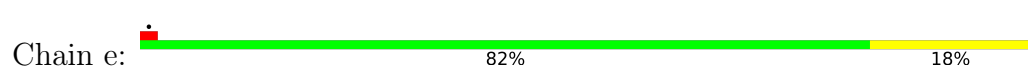
- Molecule 62: eL30



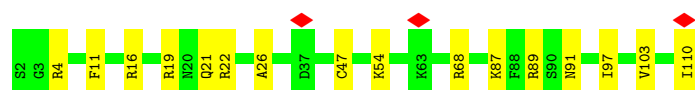
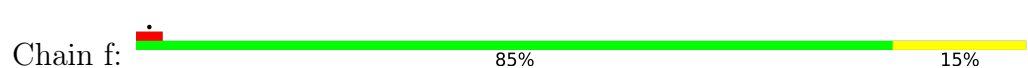
- Molecule 63: eL31



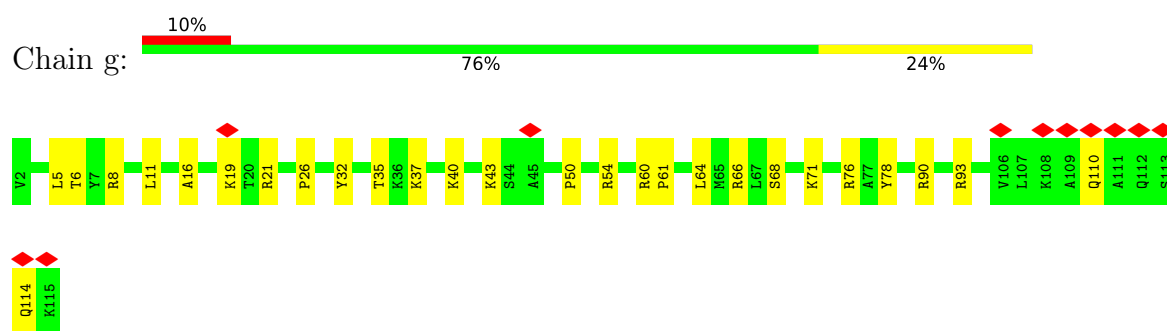
- Molecule 64: eL32



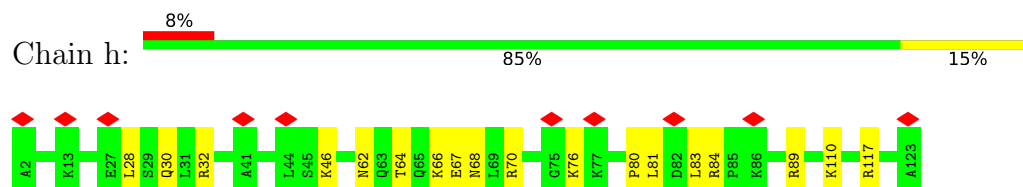
- Molecule 65: eL33



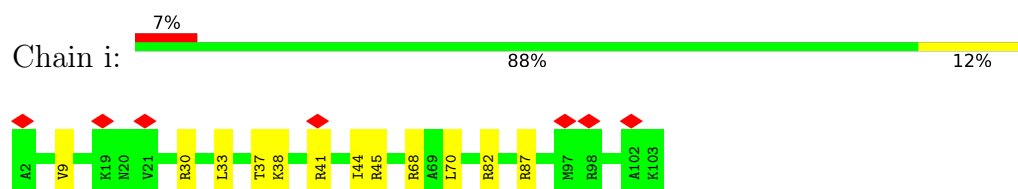
- Molecule 66: eL34



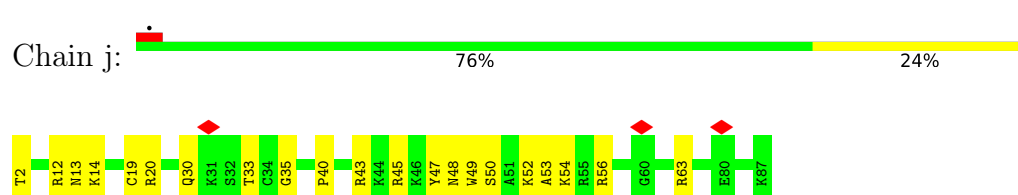
- Molecule 67: uL29



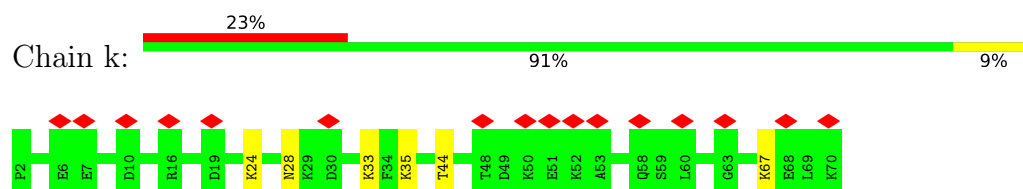
- Molecule 68: 60S ribosomal protein L36



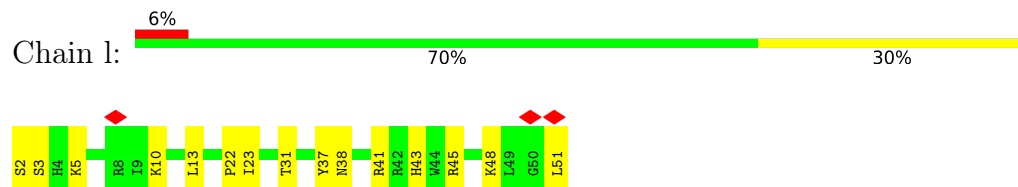
- Molecule 69: Ribosomal protein L37



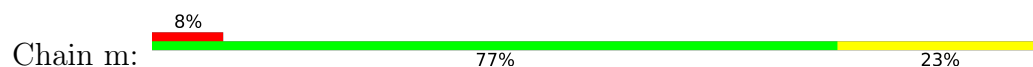
- Molecule 70: 60S ribosomal protein L38

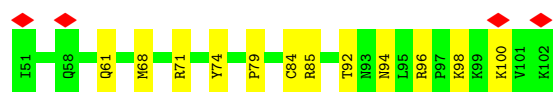


- Molecule 71: eL39

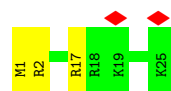
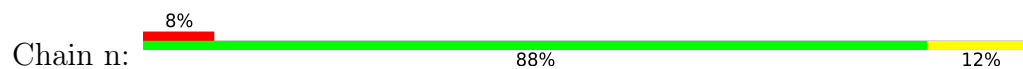


- Molecule 72: 60S ribosomal protein L40

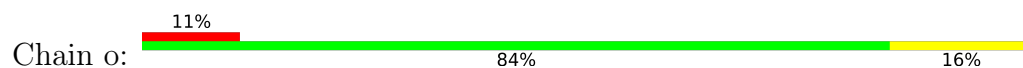




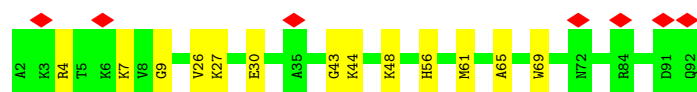
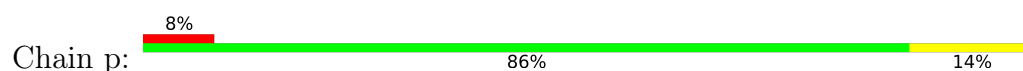
- Molecule 73: 60s ribosomal protein l41



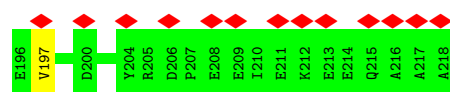
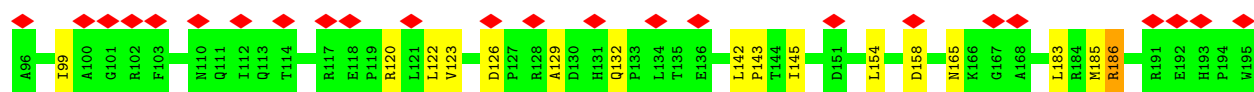
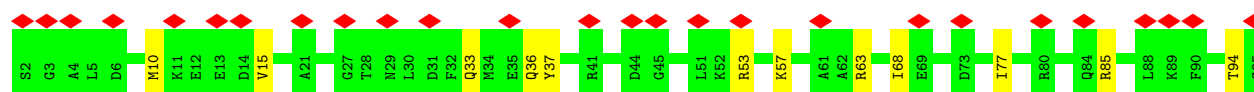
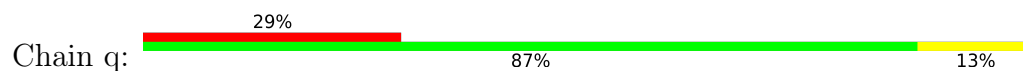
- Molecule 74: eL42



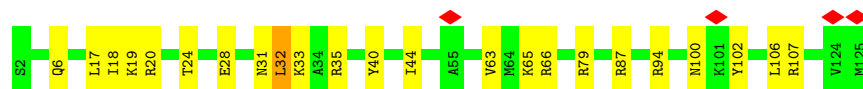
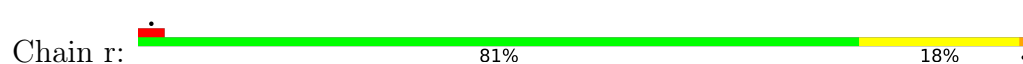
- Molecule 75: ribosomal protein eL43



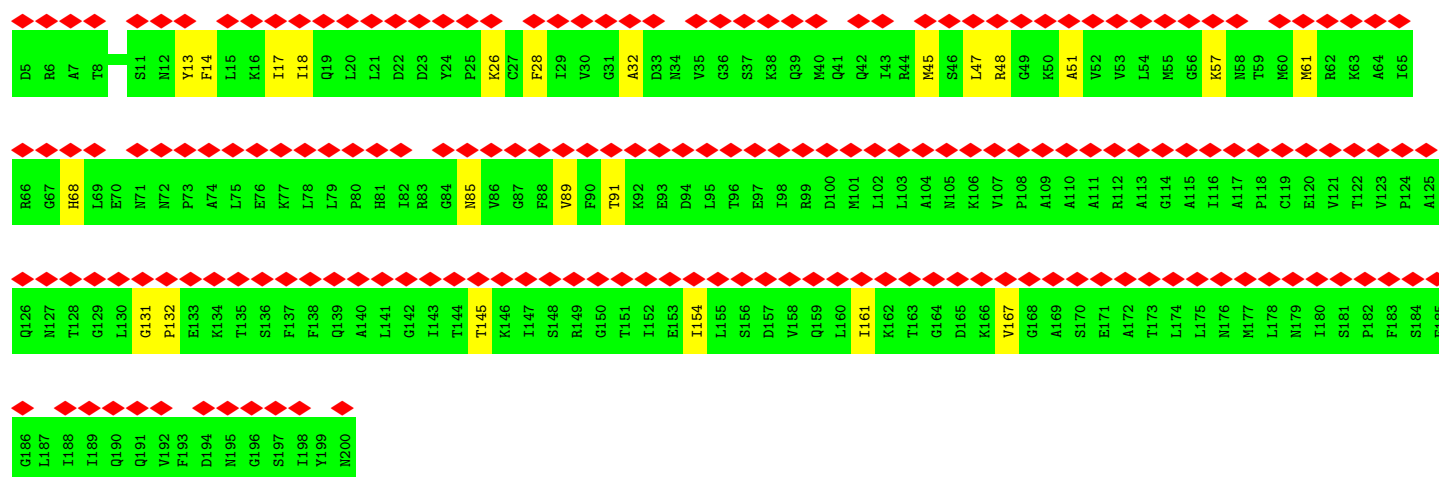
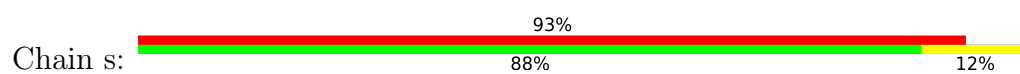
- Molecule 76: uS2



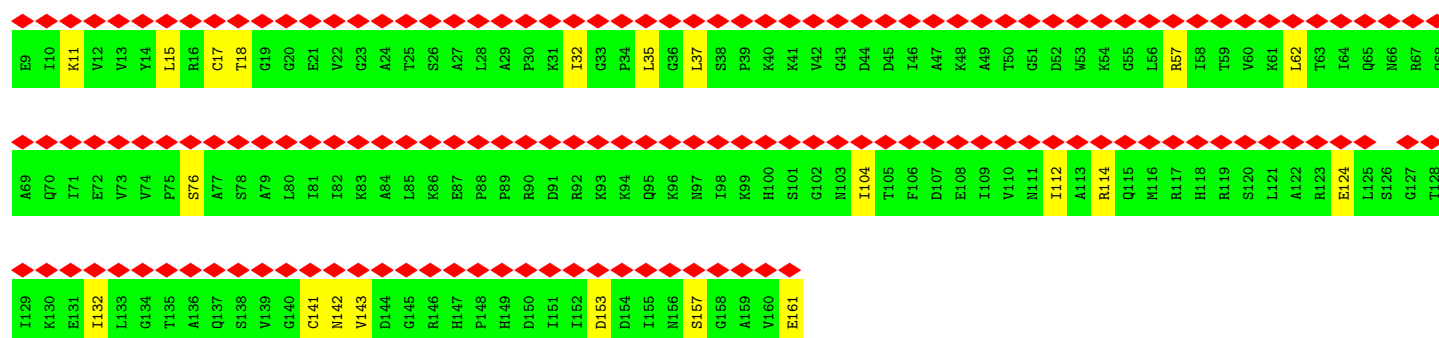
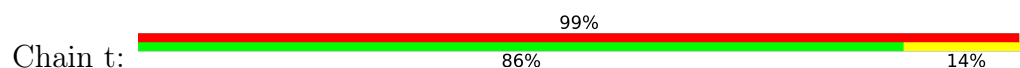
- Molecule 77: eL28



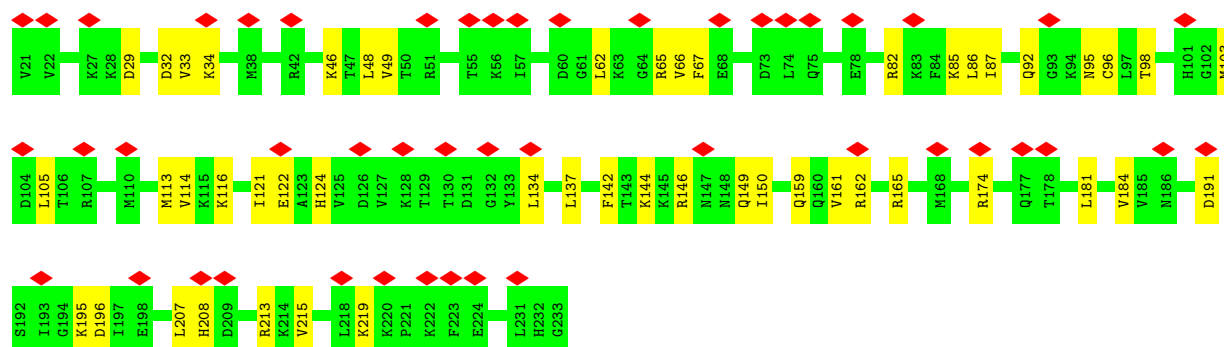
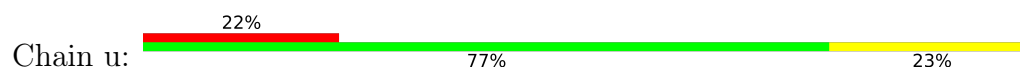
- Molecule 78: 60S acidic ribosomal protein P0



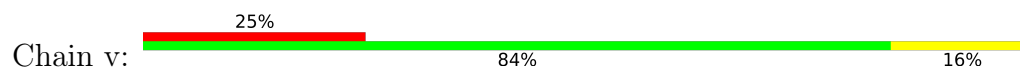
• Molecule 79: uL11

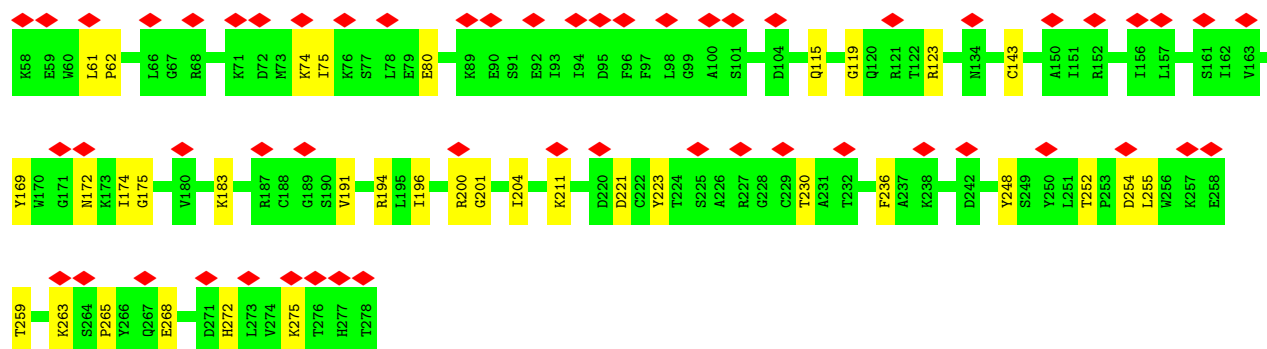


• Molecule 80: 40S ribosomal protein S3a

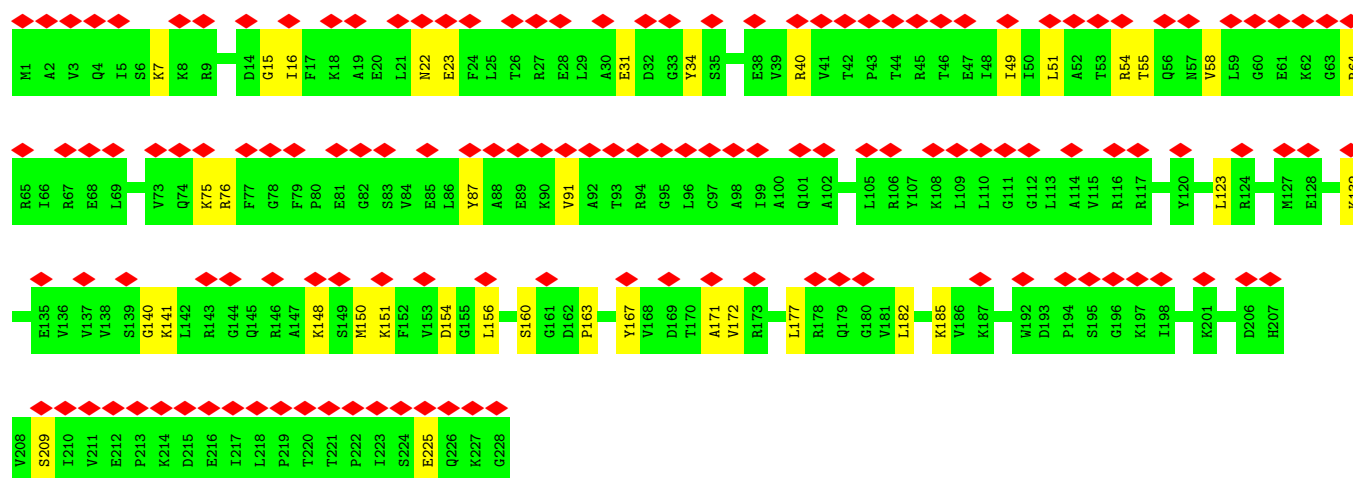
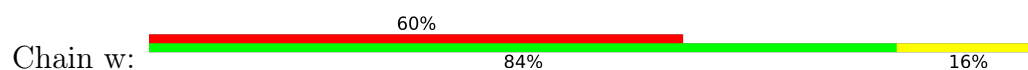


• Molecule 81: uS5

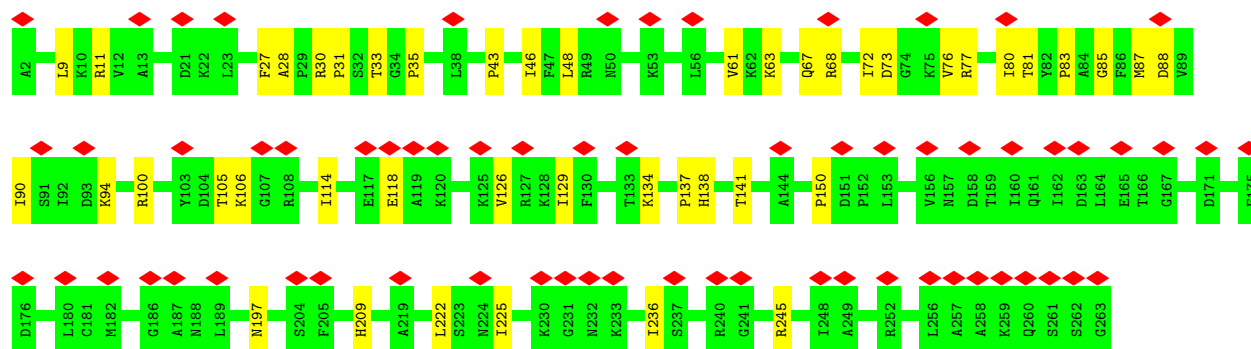
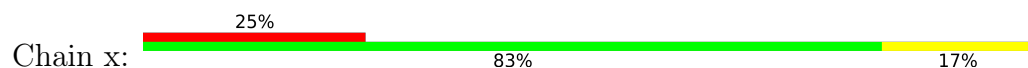




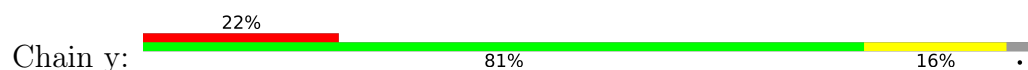
• Molecule 82: Ribosomal protein S3

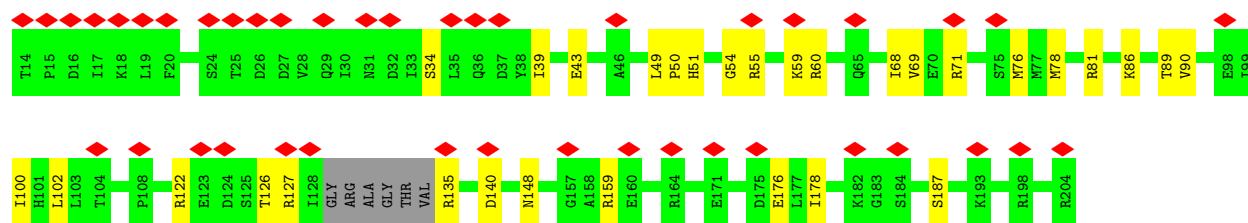


• Molecule 83: 40S ribosomal protein S4

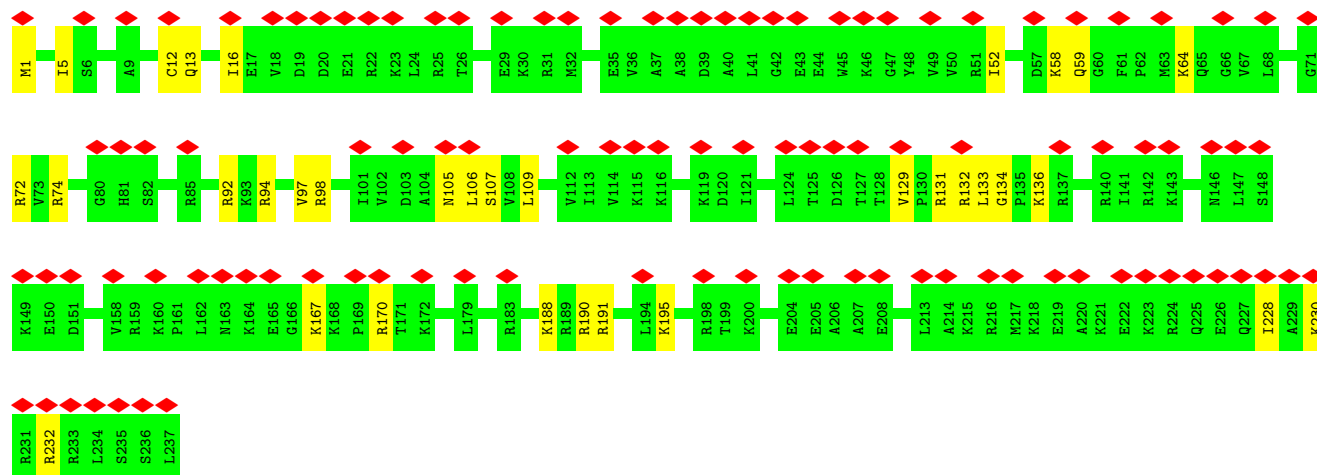
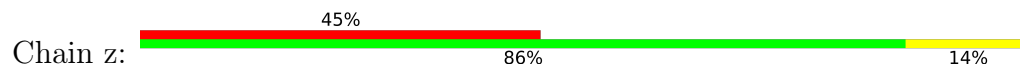


• Molecule 84: Ribosomal protein S5

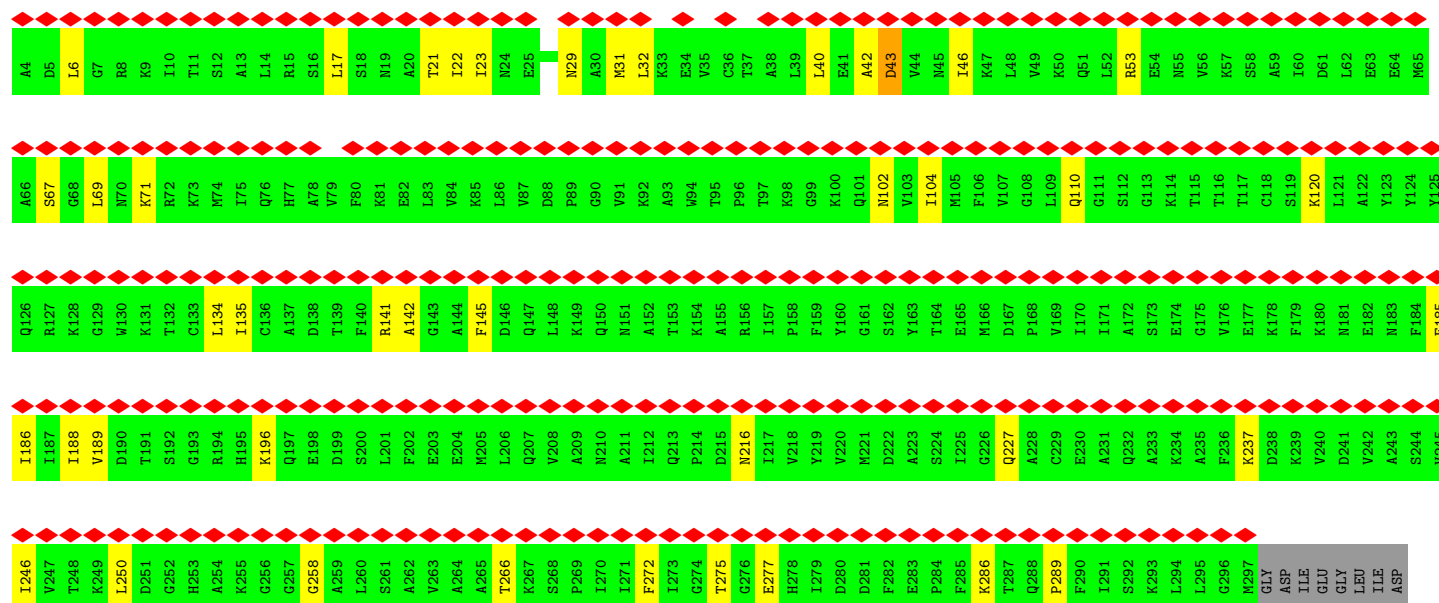
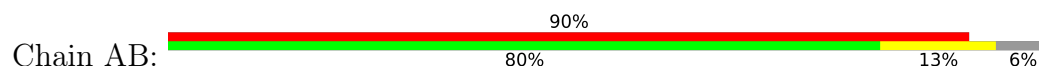


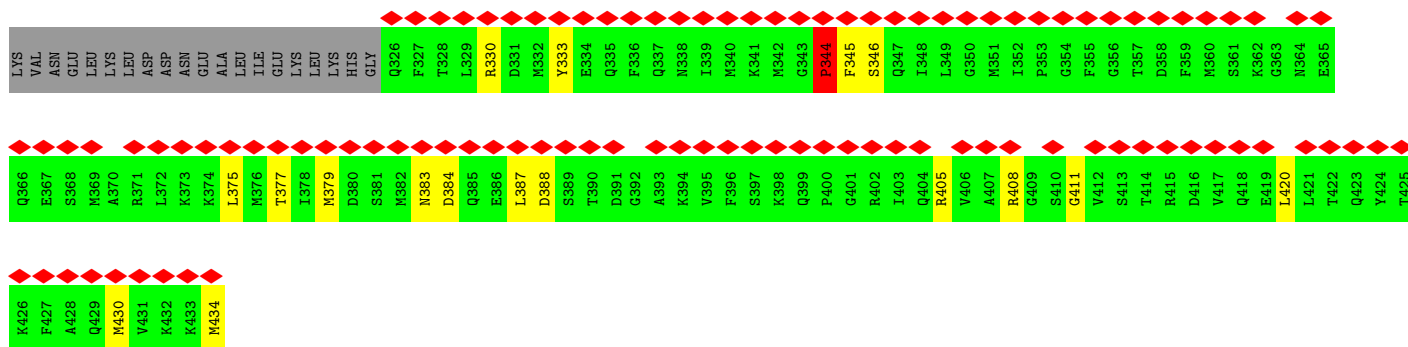


• Molecule 85: 40S ribosomal protein S6

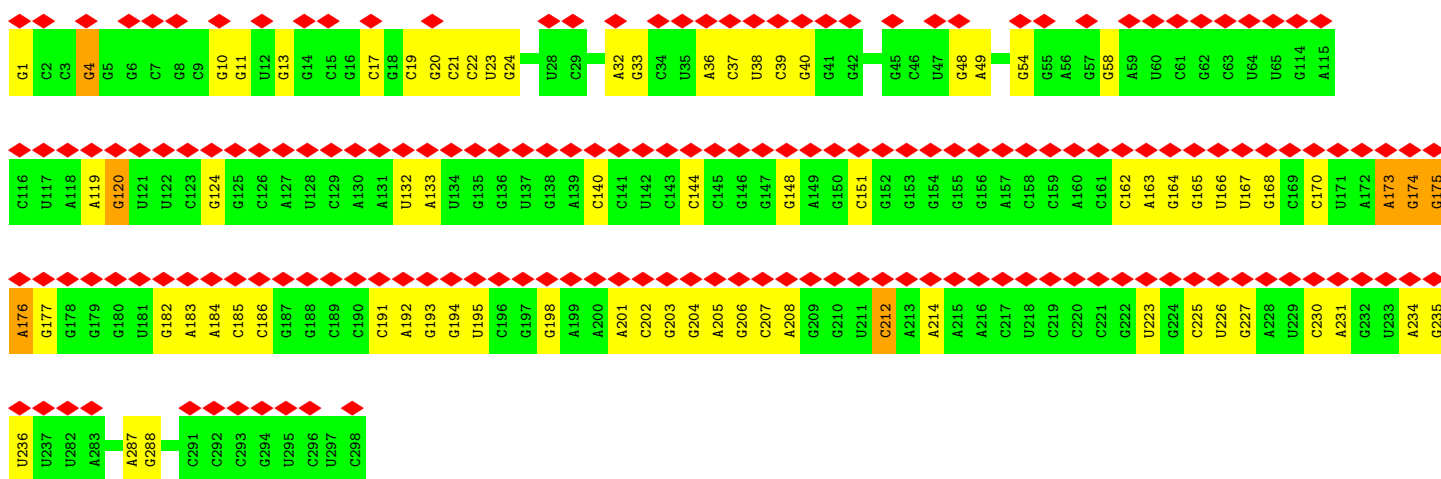
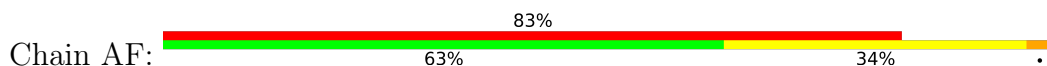


• Molecule 86: Signal recognition particle 54 kDa protein

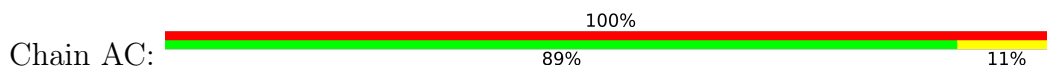




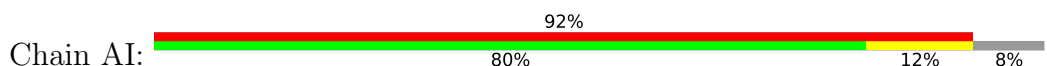
• Molecule 87: 7S RNA



• Molecule 88: Signal recognition particle subunit SRP19

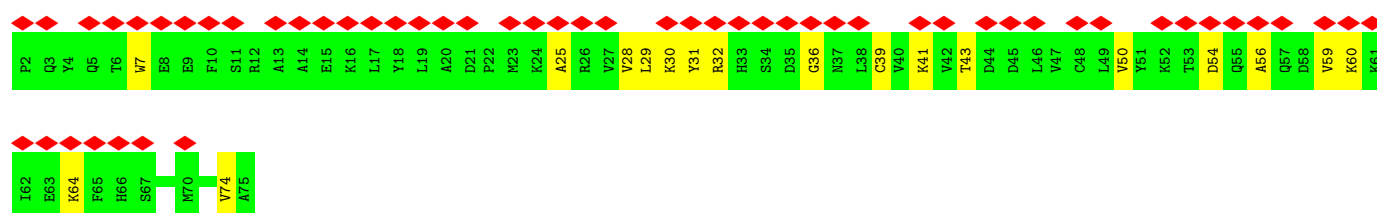
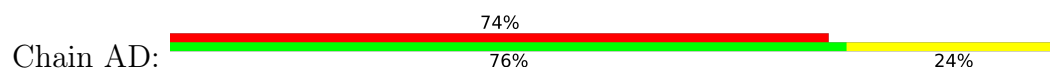


• Molecule 89: Signal recognition particle subunit SRP68

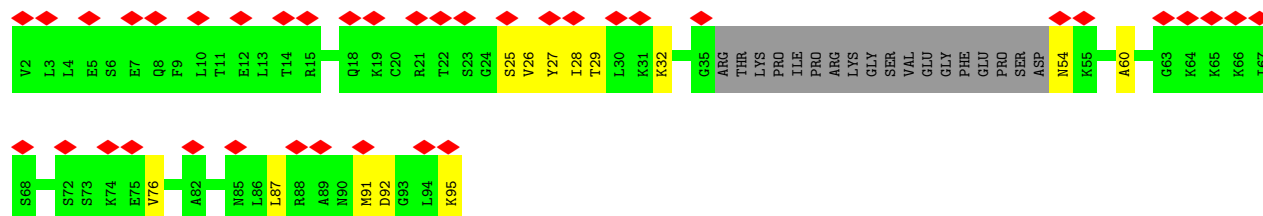
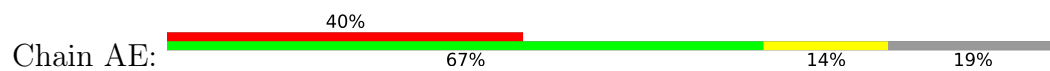




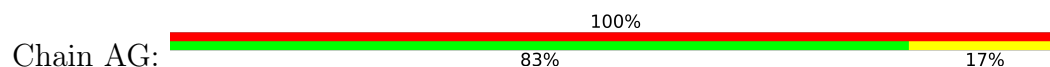
- Molecule 90: Signal recognition particle 9 kDa protein



- Molecule 91: Signal recognition particle 14 kDa protein



- Molecule 92: Signal sequence (HR2)



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	24875	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	28	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.613	Depositor
Minimum map value	-0.452	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.026	Depositor
Recommended contour level	0.08	Depositor
Map size ($\text{\AA}$)	429.264, 429.264, 429.264	wwPDB
Map dimensions	396, 396, 396	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.084, 1.084, 1.084	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	0	0.16	0/567	0.47	0/753
2	1	1.23	2/216 (0.9%)	1.82	5/298 (1.7%)
3	2	0.36	3/1780 (0.2%)	0.46	1/2770 (0.0%)
4	3	0.15	0/1783	0.32	0/2773
5	4	0.12	0/141	0.32	0/217
6	5	0.18	0/84978	0.37	15/132528 (0.0%)
7	6	0.19	0/2493	0.52	0/3394
8	7	0.14	0/2858	0.29	0/4455
9	8	0.16	0/3581	0.33	0/5577
10	9	0.17	0/470	0.48	0/623
11	A	0.20	0/1936	0.55	0/2596
12	AA	0.20	0/447	0.52	0/587
13	B	0.19	0/3240	0.51	2/4339 (0.0%)
14	BB	0.21	0/1510	0.54	0/2022
15	C	0.21	0/2937	0.52	1/3946 (0.0%)
16	CC	0.20	0/1715	0.55	0/2287
17	DD	0.20	0/1550	0.52	0/2069
18	D	0.18	0/2437	0.48	0/3264
19	EE	0.19	0/1195	0.49	0/1597
20	E	0.19	0/1762	0.48	0/2362
21	FF	0.17	0/490	0.51	0/656
22	F	0.21	0/1911	0.51	0/2549
23	GG	0.22	0/805	0.53	0/1081
24	G	0.21	0/1910	0.49	0/2569
25	H	0.20	0/1535	0.55	0/2063
26	HH	0.19	0/643	0.51	0/860
27	I	0.18	0/1702	0.46	0/2272
28	II	0.23	0/1208	0.58	2/1618 (0.1%)
29	JJ	0.18	0/665	0.52	0/891
30	J	0.20	0/1385	0.57	0/1852
31	K	0.16	0/40531	0.36	1/63162 (0.0%)
32	KK	0.19	0/1082	0.44	0/1452

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	L	0.22	0/1733	0.53	0/2316
34	LL	0.20	0/828	0.56	0/1109
35	M	0.21	0/1158	0.51	0/1547
36	MM	0.24	0/1029	0.55	0/1380
37	N	0.21	0/1746	0.53	0/2338
38	NN	0.18	0/1028	0.47	0/1366
39	O	0.20	0/1662	0.51	0/2222
40	OO	0.18	0/604	0.47	0/810
41	P	0.30	0/1268	0.54	0/1700
42	PP	0.20	0/1115	0.52	0/1493
43	Q	0.19	0/1539	0.51	0/2054
44	QQ	0.21	0/1226	0.46	0/1649
45	R	0.19	0/1524	0.48	0/2013
46	RR	0.23	0/918	0.55	0/1233
47	S	0.20	0/1501	0.51	0/2012
48	SS	0.22	0/834	0.63	0/1125
49	T	0.19	0/1326	0.48	0/1770
50	TT	0.21	0/1051	0.54	0/1406
51	UU	0.22	0/1146	0.57	2/1534 (0.1%)
52	U	0.19	0/823	0.53	0/1104
53	VV	0.20	0/1116	0.51	0/1490
54	V	0.18	0/993	0.51	0/1332
55	W	0.21	0/873	0.45	0/1158
56	WW	0.22	0/1017	0.59	0/1358
57	X	0.17	0/984	0.48	0/1323
58	Y	0.17	0/1132	0.47	0/1504
59	Z	0.20	0/1130	0.49	0/1507
60	a	0.16	0/1191	0.44	0/1590
61	b	0.18	0/861	0.47	0/1138
62	c	0.17	0/771	0.43	0/1034
63	d	0.24	0/903	0.58	0/1216
64	e	0.21	0/1071	0.52	0/1429
65	f	0.18	0/895	0.50	0/1198
66	g	0.19	0/916	0.54	0/1220
67	h	0.19	0/1021	0.43	0/1348
68	i	0.19	0/841	0.48	0/1112
69	j	0.18	0/720	0.51	0/952
70	k	0.18	0/575	0.48	0/761
71	l	0.20	0/459	0.50	0/608
72	m	0.17	0/435	0.50	0/575
73	n	0.16	0/240	0.45	0/305
74	o	0.16	0/864	0.46	0/1140
75	p	0.19	0/718	0.51	0/953

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	q	0.24	1/1747 (0.1%)	0.67	2/2374 (0.1%)
77	r	0.21	0/1010	0.58	2/1354 (0.1%)
78	s	0.20	0/1530	0.46	0/2064
79	t	0.23	0/1174	0.63	2/1582 (0.1%)
80	u	0.19	0/1756	0.55	2/2350 (0.1%)
81	v	0.20	0/1753	0.53	0/2369
82	w	0.23	0/1796	0.57	0/2417
83	x	0.19	0/2118	0.50	0/2849
84	y	0.21	0/1492	0.56	1/2005 (0.0%)
85	z	0.21	0/1946	0.52	0/2590
86	AB	0.25	0/3170	0.70	2/4254 (0.0%)
87	AF	0.14	0/5090	0.32	0/7936
88	AC	0.21	0/858	0.51	0/1156
89	AI	0.19	0/1521	0.46	0/2039
90	AD	0.23	0/619	0.64	2/832 (0.2%)
91	AE	0.17	0/608	0.49	0/809
92	AG	0.13	0/95	0.37	0/129
All	All	0.19	6/243531 (0.0%)	0.44	42/357023 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	1	0	1
53	VV	0	1
56	WW	0	2
86	AB	0	4
All	All	0	8

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	1	258	PRO	C-N	8.69	1.45	1.33
2	1	260	MET	CA-C	7.73	1.69	1.52
3	2	7	G	C1'-N9	-6.59	1.37	1.47
3	2	66	C	C1'-N1	5.80	1.57	1.48
76	q	132	GLN	C-N	5.37	1.40	1.33
3	2	60	A	C1'-N9	-5.26	1.39	1.47

All (42) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	1	258	PRO	CA-C-N	-15.02	101.01	122.19
2	1	258	PRO	C-N-CA	-15.02	101.01	122.19
76	q	197	VAL	CA-C-N	14.66	141.31	120.49
76	q	197	VAL	C-N-CA	14.66	141.31	120.49
6	5	3017	C	C2'-C3'-O3'	-14.30	92.25	113.70
6	5	3017	C	C4'-C3'-O3'	11.01	129.51	113.00
6	5	2960	A	C1'-C2'-O2'	-9.84	93.64	108.40
2	1	258	PRO	O-C-N	8.52	134.15	122.64
6	5	2962	G	C1'-C2'-O2'	-7.53	97.11	108.40
15	C	340	ILE	N-CA-C	-7.09	105.46	111.56
6	5	3017	C	C4'-C3'-C2'	-6.89	95.70	102.60
6	5	890	G	C2'-C3'-O3'	6.70	123.75	113.70
6	5	3017	C	C5'-C4'-C3'	6.70	126.05	116.00
84	y	43	GLU	N-CA-CB	-6.52	106.74	114.17
6	5	2601	A	C1'-C2'-O2'	-6.29	98.96	108.40
2	1	243	PRO	C-N-CD	-6.28	99.27	125.00
3	2	51	U	C3'-C2'-O2'	6.25	123.97	114.60
6	5	3017	C	C1'-C2'-O2'	-6.06	99.31	108.40
6	5	3017	C	O4'-C4'-C3'	-6.04	97.96	104.00
6	5	890	G	C4'-C3'-O3'	5.92	121.88	113.00
6	5	2187	C	C1'-C2'-O2'	-5.63	103.35	111.80
80	u	34	LYS	CA-C-N	5.52	132.75	121.48
80	u	34	LYS	C-N-CA	5.52	132.75	121.48
6	5	1743	U	C3'-C2'-O2'	5.51	118.97	110.70
6	5	876	C	C1'-C2'-O2'	-5.46	100.22	108.40
90	AD	7	TRP	CA-C-N	5.45	131.96	121.54
90	AD	7	TRP	C-N-CA	5.45	131.96	121.54
6	5	2576	C	C1'-C2'-O2'	-5.33	103.81	111.80
86	AB	71	LYS	CA-C-N	5.27	131.60	121.54
86	AB	71	LYS	C-N-CA	5.27	131.60	121.54
31	K	1664	A	P-O3'-C3'	5.19	127.99	120.20
51	UU	16	LYS	CA-C-N	5.14	128.53	120.82
51	UU	16	LYS	C-N-CA	5.14	128.53	120.82
13	B	213	GLN	CA-C-N	5.12	129.68	122.46
13	B	213	GLN	C-N-CA	5.12	129.68	122.46
79	t	124	GLU	CA-C-N	5.09	127.82	120.38
79	t	124	GLU	C-N-CA	5.09	127.82	120.38
77	r	32	LEU	CA-C-N	5.08	131.24	121.54
77	r	32	LEU	C-N-CA	5.08	131.24	121.54
2	1	243	PRO	N-CA-C	5.00	116.80	110.70
28	II	16	LEU	CA-C-N	5.00	131.09	121.54
28	II	16	LEU	C-N-CA	5.00	131.09	121.54

There are no chirality outliers.

All (8) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	1	258	PRO	Mainchain
86	AB	196	LYS	Peptide
86	AB	22	ILE	Peptide
86	AB	344	PRO	Peptide
86	AB	43	ASP	Peptide
53	VV	61	GLN	Peptide
56	WW	17	TYR	Peptide
56	WW	37	TYR	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	555	0	567	10	0
2	1	204	0	193	31	0
3	2	1594	0	810	41	0
4	3	1597	0	813	6	0
5	4	127	0	64	1	0
6	5	75972	0	38385	758	0
7	6	2436	0	2393	38	0
8	7	2558	0	1296	30	0
9	8	3208	0	1629	30	0
10	9	459	0	452	12	0
11	A	1898	0	1993	46	0
12	AA	443	0	492	10	0
13	B	3172	0	3310	55	0
14	BB	1488	0	1582	22	0
15	C	2883	0	3053	58	0
16	CC	1686	0	1772	26	0
17	DD	1525	0	1640	20	0
18	D	2391	0	2424	34	0
19	EE	1175	0	1249	13	0
20	E	1729	0	1887	28	0
21	FF	488	0	514	11	0
22	F	1875	0	1995	41	0
23	GG	795	0	862	10	0
24	G	1879	0	2027	29	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
25	H	1516	0	1597	26	0
26	HH	636	0	637	9	0
27	I	1664	0	1712	26	0
28	II	1190	0	1249	23	0
29	JJ	651	0	672	9	0
30	J	1362	0	1399	18	0
31	K	36249	0	18308	384	0
32	KK	1068	0	1121	12	0
33	L	1702	0	1820	26	0
34	LL	814	0	867	13	0
35	M	1137	0	1211	16	0
36	MM	1016	0	1039	12	0
37	N	1701	0	1749	47	0
38	NN	1011	0	1083	14	0
39	O	1630	0	1778	32	0
40	OO	598	0	656	9	0
41	P	1242	0	1274	30	0
42	PP	1097	0	1132	26	0
43	Q	1515	0	1634	33	0
44	QQ	1202	0	1289	9	0
45	R	1508	0	1664	38	0
46	RR	908	0	939	6	0
47	S	1462	0	1508	37	0
48	SS	810	0	836	13	0
49	T	1298	0	1366	19	0
50	TT	1034	0	1080	21	0
51	UU	1128	0	1195	20	0
52	U	809	0	833	13	0
53	VV	1098	0	1167	10	0
54	V	979	0	1039	14	0
55	W	860	0	903	8	0
56	WW	997	0	1045	17	0
57	X	967	0	1040	5	0
58	Y	1115	0	1205	17	0
59	Z	1107	0	1182	19	0
60	a	1162	0	1209	23	0
61	b	848	0	920	14	0
62	c	761	0	794	8	0
63	d	888	0	930	6	0
64	e	1053	0	1147	27	0
65	f	876	0	912	16	0
66	g	906	0	999	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
67	h	1013	0	1147	17	0
68	i	830	0	916	16	0
69	j	705	0	737	19	0
70	k	569	0	637	3	0
71	l	447	0	480	14	0
72	m	429	0	465	10	0
73	n	239	0	289	4	0
74	o	851	0	922	14	0
75	p	708	0	759	16	0
76	q	1710	0	1708	15	0
77	r	994	0	1051	18	0
78	s	1507	0	1564	13	0
79	t	1160	0	1218	11	0
80	u	1729	0	1803	32	0
81	v	1716	0	1806	23	0
82	w	1768	0	1866	29	0
83	x	2076	0	2177	27	0
84	y	1471	0	1522	27	0
85	z	1923	0	2089	27	0
86	AB	3126	0	3190	35	0
87	AF	4551	0	2299	42	0
88	AC	844	0	861	7	0
89	AI	1497	0	1504	18	0
90	AD	608	0	619	15	0
91	AE	604	0	638	12	0
92	AG	96	0	131	1	0
93	5	202	0	0	0	0
93	7	6	0	0	0	0
93	8	4	0	0	0	0
93	A	1	0	0	0	0
93	B	1	0	0	0	0
93	I	1	0	0	0	0
93	K	79	0	0	0	0
93	P	2	0	0	0	0
93	V	1	0	0	0	0
93	a	1	0	0	0	0
93	j	1	0	0	0	0
94	g	1	0	0	0	0
94	j	1	0	0	0	0
94	m	1	0	0	0	0
94	o	1	0	0	0	0
94	p	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	227187	0	169940	2269	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 6.

All (2269) 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)
6:5:2611:G:C2	6:5:2960:A:C2	1.98	1.51
6:5:2611:G:C2	6:5:2960:A:N1	1.79	1.46
2:1:250:GLY:O	6:5:2606:A:C6	1.73	1.41
6:5:2611:G:N3	6:5:2960:A:C2	1.84	1.40
2:1:237:ASP:HB2	2:1:238:PRO:CD	1.48	1.39
31:K:744:G:C4	31:K:798:G:N2	1.97	1.31
2:1:250:GLY:O	6:5:2606:A:C5	1.85	1.28
6:5:2188:A:C8	6:5:2190:C:C5	2.24	1.26
6:5:2188:A:N7	6:5:2190:C:C4	2.09	1.21
3:2:16:C:H5''	3:2:60:A:C2	1.74	1.20
3:2:7:G:C2	3:2:67:G:C2	2.30	1.20
6:5:2611:G:N1	6:5:2960:A:C6	2.10	1.20
6:5:2611:G:C6	6:5:2960:A:N6	2.13	1.17
3:2:7:G:N2	3:2:67:G:N3	1.94	1.16
31:K:744:G:N3	31:K:798:G:N2	1.93	1.16
6:5:3088:A:O2'	6:5:3091:U:OP1	1.61	1.15
6:5:2611:G:C4	6:5:2960:A:N1	2.13	1.15
3:2:16:C:H5''	3:2:60:A:H2	1.03	1.14
3:2:16:C:C5'	3:2:60:A:H2	1.61	1.13
2:1:237:ASP:CB	2:1:238:PRO:CD	2.27	1.10
6:5:2611:G:N1	6:5:2960:A:N1	2.00	1.09
2:1:256:TRP:CD1	6:5:2602:G:H22	1.71	1.07
6:5:2611:G:N3	6:5:2960:A:N1	1.94	1.07
2:1:237:ASP:CB	2:1:238:PRO:HD3	1.82	1.07
6:5:2421:A:OP2	68:i:68:ARG:NH1	1.88	1.06
6:5:1740:A:H2	64:e:28:TYR:CE2	1.72	1.06
6:5:70:A:OP2	60:a:64:LYS:NZ	1.92	1.02
31:K:126:G:OP2	85:z:195:LYS:NZ	1.93	1.02
6:5:1815:C:OP1	41:P:127:ARG:NH2	1.93	1.01
15:C:71:ARG:O	15:C:73:VAL:HG13	1.61	1.00
6:5:2611:G:C2	6:5:2960:A:C6	2.50	0.99
31:K:744:G:C2	31:K:798:G:N2	2.30	0.99
6:5:2268:C:OP2	75:p:7:LYS:NZ	1.96	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2:7:G:N2	3:2:67:G:C2	2.32	0.98
6:5:2611:G:N3	6:5:2960:A:H2	1.54	0.97
31:K:1652:G:H1	31:K:1672:U:H3	1.05	0.97
6:5:2188:A:N7	6:5:2190:C:C5	2.31	0.96
6:5:2611:G:C6	6:5:2960:A:C6	2.52	0.94
3:2:16:C:C5'	3:2:60:A:C2	2.44	0.93
31:K:744:G:C2	31:K:798:G:C2	2.56	0.93
6:5:95:G:OP2	33:L:11:LYS:NZ	2.00	0.93
6:5:2188:A:C8	6:5:2190:C:C4	2.52	0.93
6:5:2129:G:OP2	75:p:48:LYS:NZ	2.02	0.92
27:I:150:GLU:OE2	27:I:153:ARG:NH1	2.02	0.91
4:3:6:G:H1	4:3:67:U:H3	0.94	0.91
31:K:442:C:H42	31:K:449:A:H62	1.19	0.91
6:5:1966:A:H62	6:5:2154:U:H3	1.17	0.91
31:K:1286:G:H21	31:K:1313:A:H62	1.08	0.91
6:5:2611:G:N2	6:5:2960:A:C2	2.39	0.91
9:8:37:A:OP2	67:h:89:ARG:NH1	2.03	0.91
6:5:2611:G:C6	6:5:2960:A:N1	2.39	0.90
13:B:10:ARG:HH12	13:B:14:LEU:HG	1.37	0.89
6:5:2611:G:C5	6:5:2960:A:N1	2.40	0.89
41:P:128:ARG:HH21	41:P:128:ARG:HG3	1.34	0.89
31:K:677:G:H21	31:K:1028:A:H62	1.20	0.88
6:5:3482:U:OP2	13:B:385:LYS:NZ	2.05	0.88
3:2:18:G:O2'	3:2:57:G:N2	2.07	0.87
3:2:7:G:C2	3:2:67:G:N2	2.41	0.87
6:5:1740:A:H2	64:e:28:TYR:CD2	1.91	0.87
2:1:250:GLY:O	6:5:2606:A:N6	2.07	0.87
3:2:7:G:N1	3:2:67:G:C2	2.41	0.87
87:AF:58:G:O6	87:AF:288:G:C2	2.28	0.87
6:5:107:G:OP2	33:L:42:ARG:NH1	2.09	0.86
6:5:2062:C:OP2	45:R:128:LYS:NZ	2.08	0.85
8:7:85:G:OP1	22:F:221:LYS:NZ	2.09	0.85
18:D:50:ARG:NH1	18:D:72:ASP:OD2	2.09	0.85
2:1:256:TRP:NE1	6:5:2602:G:H22	1.74	0.85
6:5:805:U:O3'	22:F:69:ARG:NH1	2.10	0.84
8:7:19:C:OP2	30:J:154:LYS:NZ	2.10	0.84
15:C:219:LYS:HG3	15:C:222:ARG:HH12	1.39	0.84
2:1:237:ASP:HB2	2:1:238:PRO:HD3	0.86	0.84
84:y:71:ARG:NH1	84:y:148:ASN:OD1	2.09	0.84
2:1:256:TRP:CD1	6:5:2602:G:N2	2.46	0.84
6:5:2611:G:C4	6:5:2960:A:C2	2.63	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:5:321:U:O2'	68:i:30:ARG:NH1	2.11	0.83
59:Z:36:ARG:NH1	59:Z:38:TYR:OH	2.10	0.83
1:0:116:ARG:NH1	1:0:120:GLU:OE2	2.11	0.83
6:5:2204:G:N1	6:5:2207:C:OP2	2.10	0.83
31:K:312:G:O2'	85:z:191:ARG:NH1	2.12	0.83
3:2:63:A:H5''	3:2:63:A:C8	2.12	0.83
20:E:141:ARG:NH1	20:E:172:SER:O	2.12	0.83
10:9:44:ARG:NH1	23:GG:78:ASP:OD2	2.11	0.83
59:Z:27:LYS:NZ	59:Z:97:ASN:OD1	2.12	0.83
37:N:33:LEU:O	37:N:65:ARG:NH1	2.12	0.82
76:q:37:TYR:OH	76:q:57:LYS:NZ	2.12	0.82
59:Z:22:LYS:NZ	59:Z:129:TRP:O	2.13	0.82
6:5:3196:A:OP2	13:B:224:LYS:NZ	2.12	0.82
31:K:1841:C:OP2	73:n:2:ARG:NH1	2.11	0.82
82:w:148:LYS:NZ	82:w:150:MET:SD	2.52	0.82
6:5:1655:G:OP1	77:r:107:ARG:NH1	2.12	0.81
41:P:3:ARG:NH1	41:P:7:ASP:OD1	2.13	0.81
76:q:36:GLN:O	76:q:53:ARG:NH1	2.14	0.81
6:5:1287:G:N2	27:I:193:ASP:OD2	2.13	0.81
6:5:1740:A:C2	64:e:28:TYR:CE2	2.65	0.81
37:N:114:ARG:NH1	37:N:151:ILE:O	2.14	0.81
6:5:1486:U:OP1	25:H:64:ARG:NH1	2.14	0.81
66:g:21:ARG:HH11	66:g:35:THR:HG22	1.43	0.80
6:5:1644:A:O2'	22:F:30:LYS:NZ	2.13	0.80
48:SS:34:GLU:OE2	82:w:75:LYS:NZ	2.13	0.80
31:K:1534:C:OP1	84:y:81:ARG:NH1	2.15	0.80
6:5:1052:G:O2'	61:b:41:ARG:NH1	2.15	0.80
6:5:2415:A:OP2	6:5:2433:G:N2	2.15	0.80
6:5:1740:A:C2	64:e:28:TYR:CD2	2.70	0.80
6:5:2339:U:OP2	6:5:2344:A:N6	2.14	0.80
31:K:1156:U:O4	81:v:194:ARG:NH1	2.14	0.80
42:PP:38:LYS:NZ	42:PP:40:ALA:O	2.14	0.80
20:E:115:MET:O	77:r:87:ARG:NH1	2.15	0.79
6:5:1614:C:O2	64:e:15:LYS:NZ	2.15	0.79
31:K:482:G:N1	31:K:485:A:OP2	2.15	0.79
31:K:1286:G:N2	31:K:1313:A:H62	1.81	0.79
6:5:949:A:OP2	43:Q:181:ARG:NH1	2.16	0.79
72:m:61:GLN:OE1	72:m:100:LYS:NZ	2.15	0.79
31:K:1865:C:OP2	34:LL:92:ARG:NH1	2.16	0.78
6:5:2284:U:OP2	45:R:74:ARG:NH2	2.16	0.78
31:K:797:C:H2'	31:K:798:G:O4'	1.82	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:5:1658:G:OP1	77:r:35:ARG:NH1	2.15	0.78
6:5:3128:U:OP2	13:B:246:ARG:NH2	2.17	0.78
31:K:744:G:C5	31:K:798:G:N2	2.51	0.78
67:h:46:LYS:NZ	86:AB:21:THR:OG1	2.16	0.78
6:5:3021:G:H8	6:5:3021:G:H5''	1.46	0.78
9:8:75:G:OP2	58:Y:74:TYR:OH	2.01	0.78
6:5:543:A:O2'	15:C:29:LYS:NZ	2.17	0.78
6:5:1460:A:OP1	35:M:53:LYS:NZ	2.15	0.78
6:5:2507:G:N2	6:5:2507:G:OP2	2.16	0.78
25:H:36:ARG:HH11	25:H:38:PHE:HE1	1.32	0.78
31:K:1658:G:OP2	31:K:1660:C:N4	2.17	0.77
41:P:128:ARG:HG3	41:P:128:ARG:NH2	1.98	0.77
39:O:82:ARG:HH11	39:O:85:ARG:HH21	1.33	0.77
11:A:177:LYS:NZ	75:p:30:GLU:OE1	2.17	0.76
39:O:18:ARG:HH12	39:O:128:ARG:HH11	1.34	0.76
6:5:224:G:OP1	58:Y:15:ARG:NH1	2.18	0.76
6:5:302:G:OP2	6:5:302:G:N2	2.12	0.76
3:2:7:G:N1	3:2:67:G:N1	2.34	0.76
31:K:1596:U:OP2	40:OO:85:ARG:NH2	2.19	0.76
87:AF:58:G:C6	87:AF:288:G:N2	2.53	0.76
2:1:259:LEU:CD1	6:5:2968:C:C6	2.68	0.76
20:E:164:ARG:NH1	20:E:276:SER:OG	2.19	0.76
31:K:744:G:N1	31:K:798:G:C2	2.54	0.76
3:2:63:A:H5''	3:2:63:A:H8	1.50	0.76
6:5:2871:U:OP2	6:5:2873:C:N4	2.19	0.76
6:5:3317:G:OP1	65:f:4:ARG:NH1	2.19	0.76
31:K:1599:U:OP2	40:OO:46:ASN:ND2	2.19	0.76
6:5:19:G:OP2	67:h:89:ARG:NH2	2.19	0.75
31:K:683:G:N1	31:K:1022:U:OP2	2.15	0.75
6:5:890:G:H3'	6:5:890:G:C8	2.21	0.75
10:9:32:ARG:NH1	31:K:1661:A:OP2	2.20	0.75
6:5:107:G:H21	33:L:74:ARG:HH11	1.32	0.75
6:5:475:G:O2'	6:5:477:G:OP2	2.05	0.75
6:5:1402:G:N2	6:5:1405:A:OP2	2.19	0.75
6:5:1966:A:N6	6:5:2154:U:H3	1.85	0.74
31:K:468:A:OP1	85:z:74:ARG:NH1	2.20	0.74
31:K:380:G:N1	31:K:383:G:OP2	2.20	0.74
6:5:3515:U:OP1	13:B:393:LYS:NZ	2.20	0.74
31:K:830:A:OP2	31:K:846:G:N2	2.19	0.74
31:K:1130:G:N2	31:K:1130:G:OP2	2.19	0.74
6:5:2611:G:O6	6:5:2960:A:N6	2.19	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:5:3190:U:OP2	6:5:3240:C:N4	2.21	0.74
6:5:2747:C:OP1	37:N:93:LYS:NZ	2.20	0.74
24:G:228:ARG:NH1	24:G:280:ASN:O	2.20	0.74
31:K:43:U:OP2	31:K:485:A:N6	2.21	0.74
81:v:174:ILE:O	81:v:200:ARG:NH1	2.20	0.73
6:5:925:U:OP2	33:L:36:ARG:NH2	2.20	0.73
31:K:1232:U:H3	31:K:1526:G:H1	1.33	0.73
83:x:85:GLY:N	83:x:88:ASP:OD2	2.22	0.73
6:5:502:U:OP2	60:a:85:GLN:NE2	2.21	0.73
6:5:1522:G:O2'	6:5:1540:G:OP2	2.06	0.73
6:5:2871:U:OP1	49:T:78:LYS:NZ	2.22	0.73
41:P:108:ASP:N	41:P:152:GLU:OE2	2.19	0.73
6:5:714:G:H5''	22:F:46:ARG:NH1	2.04	0.73
9:8:155:C:OP2	24:G:142:ARG:NH2	2.22	0.73
31:K:1354:G:N2	31:K:1357:A:OP2	2.15	0.72
6:5:3097:G:N2	6:5:3097:G:OP2	2.21	0.72
17:DD:38:ARG:NH1	31:K:643:A:OP2	2.18	0.72
6:5:1355:G:N2	6:5:1355:G:OP2	2.22	0.72
6:5:2903:C:O2	49:T:8:ARG:NH1	2.22	0.72
6:5:3240:C:O2'	6:5:3242:A:OP2	2.06	0.72
75:p:7:LYS:O	75:p:27:LYS:NZ	2.22	0.72
6:5:171:U:OP1	6:5:172:C:OP1	2.06	0.72
6:5:615:C:O2'	6:5:617:G:OP2	2.06	0.72
6:5:674:U:H5	35:M:46:ARG:HH11	1.36	0.72
6:5:2387:G:O2'	6:5:2516:U:OP2	2.07	0.72
31:K:167:G:O2'	55:W:80:ARG:NH1	2.23	0.72
2:1:237:ASP:OD1	2:1:238:PRO:HD2	1.90	0.72
6:5:2017:G:OP2	52:U:97:ARG:NH2	2.23	0.72
25:H:89:ARG:HH11	25:H:187:VAL:HG13	1.54	0.71
28:II:121:ARG:NH1	31:K:1611:G:OP2	2.22	0.71
31:K:24:C:H42	31:K:650:A:H61	1.38	0.71
43:Q:65:ARG:HH12	43:Q:142:PRO:HB3	1.55	0.71
9:8:141:C:O2'	37:N:136:ASP:OD2	2.07	0.71
6:5:274:G:N2	6:5:300:A:OP2	2.23	0.71
6:5:2892:G:N2	6:5:2895:A:OP2	2.21	0.71
31:K:72:C:O2'	31:K:74:G:OP2	2.08	0.71
31:K:1204:A:O2'	31:K:1700:C:OP2	2.09	0.71
6:5:3101:U:O2	6:5:3101:U:O2'	2.06	0.71
31:K:1597:C:OP2	40:OO:85:ARG:NH1	2.24	0.71
33:L:11:LYS:H	43:Q:168:ARG:HH12	1.37	0.71
6:5:1440:G:OP1	65:f:87:LYS:NZ	2.21	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:5:2842:G:N2	6:5:2842:G:OP2	2.23	0.70
6:5:1381:G:OP1	61:b:22:LYS:NZ	2.24	0.70
6:5:119:G:H5'	24:G:185:ARG:HH12	1.57	0.70
18:D:75:VAL:O	18:D:112:ARG:NH1	2.24	0.70
31:K:1579:A:O2'	31:K:1581:C:OP2	2.09	0.70
6:5:2605:G:OP1	6:5:2605:G:H4'	1.91	0.70
80:u:82:ARG:NH1	80:u:191:ASP:OD1	2.25	0.70
31:K:165:G:N2	31:K:165:G:OP2	2.25	0.70
62:c:17:ARG:HH12	62:c:103:ASP:HB3	1.57	0.70
6:5:2898:G:OP1	49:T:50:LYS:NZ	2.24	0.70
64:e:113:GLU:OE2	64:e:117:GLN:NE2	2.25	0.70
31:K:751:G:OP1	85:z:230:LYS:NZ	2.20	0.69
86:AB:330:ARG:HB2	86:AB:387:LEU:HB3	1.73	0.69
6:5:2672:G:OP1	24:G:305:LYS:NZ	2.25	0.69
31:K:98:C:OP2	31:K:426:A:O2'	2.10	0.69
2:1:259:LEU:HD11	6:5:2968:C:C6	2.27	0.69
3:2:76:A:OP1	3:2:76:A:H4'	1.91	0.69
6:5:3376:A:H5''	6:5:3377:C:H2'	1.73	0.69
6:5:436:G:OP1	65:f:68:ARG:NH1	2.25	0.69
24:G:149:LEU:HD11	24:G:242:ARG:HH11	1.57	0.69
27:I:162:ARG:HH12	47:S:88:SER:HB2	1.58	0.69
6:5:1740:A:H2	64:e:28:TYR:HE2	1.35	0.68
31:K:744:G:C6	31:K:798:G:N1	2.61	0.68
31:K:959:G:OP2	36:MM:38:ASN:ND2	2.25	0.68
6:5:2918:A:O2'	6:5:2920:C:OP2	2.11	0.68
6:5:1743:U:C4	15:C:73:VAL:O	2.45	0.68
31:K:1215:C:H42	31:K:1220:A:H61	1.40	0.68
54:V:56:GLY:N	54:V:59:ASP:OD2	2.20	0.68
8:7:87:G:N2	8:7:90:A:OP2	2.26	0.68
31:K:1086:G:OP2	34:LL:12:LYS:NZ	2.24	0.68
6:5:2188:A:C8	6:5:2190:C:H5	2.08	0.68
31:K:442:C:N4	31:K:449:A:H62	1.90	0.68
6:5:2230:U:OP1	13:B:249:ARG:NH1	2.26	0.68
6:5:17:A:OP2	57:X:60:TYR:OH	2.10	0.68
6:5:2132:C:O2	11:A:174:ARG:NH1	2.26	0.68
6:5:2202:G:H5'	45:R:60:ARG:HH12	1.58	0.68
24:G:139:VAL:HG11	24:G:238:LYS:HG3	1.76	0.68
6:5:116:G:OP2	37:N:2:GLY:N	2.27	0.67
6:5:272:G:OP2	68:i:30:ARG:NH2	2.22	0.67
31:K:1165:G:OP2	31:K:1165:G:N2	2.17	0.67
43:Q:6:ARG:NH1	61:b:18:ARG:O	2.24	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:5:1711:G:N2	6:5:1714:G:OP2	2.20	0.67
6:5:1955:G:N2	6:5:1958:A:OP2	2.19	0.67
2:1:237:ASP:CG	2:1:238:PRO:HD2	2.19	0.67
31:K:925:G:H1	31:K:1017:U:H3	1.43	0.67
6:5:91:G:O5'	74:o:44:LYS:NZ	2.28	0.67
31:K:678:U:OP2	31:K:1026:C:N4	2.21	0.66
6:5:3111:G:N2	6:5:3114:A:OP2	2.22	0.66
31:K:1179:G:N2	31:K:1182:A:OP2	2.25	0.66
6:5:45:U:O4	37:N:83:LYS:NZ	2.27	0.66
6:5:361:C:O5'	6:5:361:C:H6	1.78	0.66
31:K:1286:G:H21	31:K:1313:A:N6	1.89	0.66
9:8:96:C:H5''	67:h:66:LYS:HD3	1.77	0.66
36:MM:34:PHE:HB3	36:MM:41:PHE:HB2	1.78	0.66
6:5:63:G:OP2	37:N:169:ARG:NH1	2.27	0.66
6:5:3522:C:O2'	6:5:3525:C:OP2	2.13	0.66
8:7:119:U:OP2	8:7:120:U:O2'	2.12	0.65
31:K:1332:A:N3	82:w:141:LYS:NZ	2.37	0.65
49:T:88:ARG:NH1	61:b:33:LYS:O	2.29	0.65
6:5:2962:G:H8	6:5:2962:G:O5'	1.79	0.65
17:DD:5:ARG:HD3	31:K:38:A:H5''	1.76	0.65
3:2:65:C:O5'	3:2:65:C:H6	1.78	0.65
6:5:2302:A:H5''	45:R:71:ARG:HH12	1.61	0.65
31:K:588:G:N2	31:K:588:G:OP2	2.29	0.65
3:2:64:U:H6	3:2:64:U:O5'	1.78	0.65
6:5:948:G:N2	6:5:951:G:OP2	2.24	0.65
6:5:1669:A:OP1	22:F:165:ARG:NH1	2.30	0.65
6:5:1868:G:O2'	57:X:53:ARG:NH1	2.29	0.65
2:1:237:ASP:CB	2:1:238:PRO:HD2	2.22	0.65
31:K:744:G:C6	31:K:798:G:C2	2.85	0.65
6:5:1479:A:OP2	6:5:1577:A:N6	2.29	0.65
13:B:322:HIS:O	13:B:342:LYS:NZ	2.30	0.65
9:8:21:C:OP1	15:C:195:LYS:NZ	2.30	0.64
28:II:14:ARG:NH2	30:J:111:GLU:OE2	2.29	0.64
31:K:677:G:N2	31:K:1028:A:H62	1.93	0.64
15:C:71:ARG:NH1	15:C:71:ARG:HG2	2.10	0.64
86:AB:102:ASN:HB2	86:AB:186:ILE:HA	1.80	0.64
6:5:1972:G:N2	6:5:1975:A:OP2	2.19	0.64
6:5:2608:C:O5'	6:5:2608:C:H6	1.79	0.64
6:5:890:G:H3'	6:5:890:G:H8	1.61	0.64
6:5:2850:A:OP2	18:D:23:ARG:NH2	2.30	0.64
7:6:60:ARG:HE	51:UU:97:GLN:HE22	1.46	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:W:80:ARG:NH2	85:z:129:VAL:O	2.29	0.64
57:X:110:LYS:NZ	57:X:121:VAL:O	2.30	0.64
31:K:851:C:H5''	31:K:852:G:H5'	1.80	0.64
76:q:10:MET:HE2	76:q:15:VAL:HG22	1.80	0.64
6:5:2607:C:C5	6:5:3017:C:N4	2.65	0.63
6:5:2611:G:N1	6:5:2960:A:N6	2.34	0.63
27:I:191:ILE:HD11	27:I:212:LEU:HD11	1.80	0.63
2:1:259:LEU:HD12	6:5:2968:C:C6	2.33	0.63
81:v:123:ARG:NH1	81:v:143:CYS:O	2.31	0.63
6:5:3311:U:H5''	65:f:54:LYS:HE3	1.80	0.63
7:6:187:ASN:HB2	82:w:225:GLU:HB3	1.81	0.63
15:C:330:PRO:HB3	22:F:46:ARG:HH21	1.62	0.63
25:H:26:ILE:HG22	25:H:35:ARG:HG2	1.80	0.63
2:1:249:TRP:CD1	6:5:2602:G:HO2'	2.17	0.63
6:5:714:G:H5''	22:F:46:ARG:HH12	1.64	0.63
6:5:3151:G:OP2	13:B:28:LYS:NZ	2.31	0.63
14:BB:63:PHE:HA	14:BB:95:ILE:O	1.97	0.63
6:5:2188:A:C8	6:5:2190:C:N4	2.67	0.63
56:WW:81:ARG:NH1	56:WW:98:ASN:OD1	2.31	0.63
6:5:1221:C:OP1	64:e:36:ARG:NH2	2.32	0.63
18:D:82:GLU:OE1	18:D:108:ARG:NH1	2.29	0.63
31:K:1617:G:N1	31:K:1620:A:OP2	2.32	0.62
7:6:87:LEU:HB2	7:6:101:PHE:HB2	1.81	0.62
31:K:303:C:C2'	31:K:304:C:H5'	2.30	0.62
31:K:1470:C:OP1	84:y:59:LYS:NZ	2.32	0.62
38:NN:82:ALA:O	38:NN:86:GLU:HB3	1.99	0.62
6:5:297:C:OP2	37:N:68:ARG:NH2	2.32	0.62
6:5:2596:G:H1	6:5:3133:U:H3	1.48	0.62
18:D:200:MET:HB2	18:D:202:GLN:HE22	1.64	0.62
90:AD:32:ARG:O	90:AD:36:GLY:HA2	1.98	0.62
6:5:2782:A:N1	49:T:3:ASN:ND2	2.46	0.62
15:C:71:ARG:HH11	15:C:71:ARG:CG	2.13	0.62
31:K:957:A:H3'	31:K:958:G:H21	1.64	0.62
11:A:36:GLU:HB3	11:A:163:ARG:HH22	1.64	0.62
6:5:1327:U:OP2	49:T:13:TYR:OH	2.12	0.62
56:WW:98:ASN:ND2	56:WW:103:ASN:OD1	2.33	0.62
87:AF:120:G:N7	89:AI:85:ARG:NH2	2.48	0.62
6:5:152:U:P	37:N:49:ARG:HH12	2.22	0.62
6:5:2204:G:OP2	45:R:70:ARG:NH2	2.33	0.62
8:7:42:A:O4'	30:J:75:ARG:NH1	2.31	0.62
6:5:108:A:H5'	33:L:92:ARG:NH1	2.15	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:5:2170:G:H5''	6:5:2171:G:H5'	1.81	0.61
8:7:28:C:H1'	8:7:54:A:H61	1.64	0.61
83:x:72:ILE:HG12	83:x:90:ILE:HG12	1.82	0.61
6:5:718:U:H3	6:5:836:G:H1	1.46	0.61
22:F:93:ARG:HE	22:F:108:LEU:HD13	1.65	0.61
41:P:84:PRO:HB2	41:P:87:SER:HB2	1.82	0.61
48:SS:3:MET:HG2	48:SS:44:HIS:HD2	1.65	0.61
60:a:87:ARG:HG3	60:a:120:GLN:HE22	1.64	0.61
2:1:249:TRP:HZ3	2:1:253:GLN:HG2	1.65	0.61
15:C:71:ARG:HG2	15:C:71:ARG:HH11	1.64	0.61
19:EE:11:GLN:HB3	19:EE:56:ILE:HD11	1.83	0.61
6:5:841:C:O2'	15:C:321:ASN:ND2	2.34	0.61
45:R:102:LEU:HD22	45:R:138:LEU:HD13	1.83	0.61
69:j:35:GLY:O	69:j:45:ARG:NH1	2.34	0.61
16:CC:165:GLN:HE22	16:CC:195:LEU:HD11	1.64	0.61
6:5:1523:U:C4	6:5:1550:A:N6	2.68	0.61
37:N:9:GLU:HG3	37:N:12:ARG:HD2	1.81	0.61
58:Y:77:LYS:NZ	71:l:31:THR:OG1	2.30	0.61
83:x:137:PRO:HB2	83:x:150:PRO:HD2	1.83	0.61
6:5:947:U:H4'	6:5:1056:G:H21	1.65	0.61
15:C:56:GLU:OE2	15:C:106:LYS:NZ	2.27	0.61
26:HH:40:ASP:HB2	26:HH:47:ASN:HD21	1.66	0.61
39:O:22:ILE:HG23	47:S:166:ARG:NH1	2.14	0.61
22:F:104:VAL:HG13	22:F:135:VAL:HG12	1.83	0.61
27:I:87:ILE:HG12	27:I:138:ILE:HG12	1.82	0.61
86:AB:104:ILE:HG12	86:AB:216:ASN:HB2	1.83	0.61
90:AD:74:VAL:HG21	91:AE:76:VAL:HG11	1.82	0.61
6:5:363:G:N2	6:5:366:A:OP2	2.22	0.60
78:s:28:PHE:HB2	78:s:89:VAL:HB	1.83	0.60
6:5:1084:A:H61	6:5:1211:G:H22	1.49	0.60
6:5:1992:G:OP1	66:g:40:LYS:NZ	2.32	0.60
22:F:93:ARG:NH1	22:F:96:GLY:O	2.34	0.60
31:K:1444:U:O2'	31:K:1580:A:N1	2.33	0.60
1:0:138:ARG:NH1	31:K:1292:C:O2	2.35	0.60
3:2:16:C:H5'	3:2:60:A:C2	2.33	0.60
6:5:1229:A:H5''	61:b:15:LYS:HD3	1.83	0.60
18:D:261:VAL:HG12	18:D:263:LYS:H	1.67	0.60
31:K:1854:U:OP1	36:MM:150:ARG:NH1	2.34	0.60
6:5:1432:G:OP1	22:F:95:ARG:NH2	2.35	0.60
19:EE:101:ARG:HB2	53:VV:10:ALA:HB2	1.84	0.60
31:K:975:G:H21	36:MM:50:LYS:HA	1.67	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:c:47:ILE:HG12	62:c:72:HIS:HB3	1.83	0.60
71:l:43:HIS:HD1	71:l:45:ARG:H	1.50	0.60
84:y:50:PRO:HG2	84:y:90:VAL:HG22	1.83	0.60
10:9:12:ARG:NH1	31:K:1262:C:O2'	2.33	0.60
33:L:201:GLU:OE2	33:L:205:GLN:NE2	2.35	0.60
37:N:63:ARG:NE	37:N:131:GLU:OE2	2.35	0.60
31:K:639:C:H2'	31:K:640:A:H8	1.66	0.60
43:Q:64:SER:OG	43:Q:89:ASP:OD2	2.15	0.60
2:1:251:ARG:HB3	2:1:251:ARG:HH11	1.67	0.60
6:5:1932:C:H5''	66:g:66:ARG:HD3	1.82	0.60
13:B:10:ARG:NH1	13:B:14:LEU:HG	2.12	0.60
31:K:1854:U:H2'	31:K:1855:G:H8	1.67	0.60
14:BB:154:ILE:HB	14:BB:185:VAL:HG22	1.82	0.59
15:C:179:ASP:OD1	15:C:204:ARG:NH1	2.35	0.59
31:K:492:C:N4	31:K:507:G:OP2	2.24	0.59
38:NN:7:ILE:HG12	38:NN:27:VAL:HG22	1.84	0.59
2:1:237:ASP:HB2	2:1:238:PRO:HD2	1.68	0.59
31:K:70:G:OP2	85:z:167:LYS:NZ	2.25	0.59
31:K:986:G:OP2	31:K:988:C:N4	2.35	0.59
37:N:28:TRP:O	37:N:32:GLN:NE2	2.34	0.59
86:AB:375:LEU:HD22	86:AB:420:LEU:HD12	1.84	0.59
6:5:987:G:N1	6:5:1018:C:OP2	2.30	0.59
22:F:91:VAL:O	22:F:119:GLY:HA2	2.02	0.59
6:5:1009:C:H5''	43:Q:132:LYS:NZ	2.17	0.59
6:5:1797:A:H1'	69:j:12:ARG:HH11	1.67	0.59
7:6:256:ILE:HB	7:6:270:LEU:HB2	1.85	0.59
48:SS:20:VAL:HA	48:SS:69:TRP:O	2.03	0.59
19:EE:85:THR:HA	19:EE:113:LEU:H	1.67	0.59
25:H:92:MET:HE2	25:H:179:ILE:HG22	1.84	0.59
60:a:131:ARG:NH1	60:a:135:GLU:OE2	2.35	0.59
80:u:49:VAL:HG22	80:u:65:ARG:HH12	1.66	0.59
55:W:56:ARG:HG3	55:W:61:LYS:HB2	1.83	0.59
6:5:2999:C:N3	27:I:158:LYS:NZ	2.51	0.59
7:6:149:GLU:HG2	32:KK:23:ARG:HH12	1.68	0.59
31:K:492:C:OP2	38:NN:107:ARG:NH2	2.34	0.59
31:K:1360:U:O2'	31:K:1379:A:OP2	2.19	0.59
61:b:102:PRO:HA	61:b:109:ARG:HH12	1.67	0.59
74:o:71:GLU:OE2	74:o:78:ARG:NH1	2.25	0.59
6:5:2603:A:H8	6:5:2603:A:H3'	1.68	0.59
6:5:3390:A:H4'	13:B:95:THR:HG22	1.85	0.59
6:5:63:G:P	37:N:169:ARG:HH12	2.24	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:5:890:G:C8	6:5:890:G:C3'	2.85	0.59
8:7:97:G:P	22:F:133:ARG:HH12	2.25	0.59
9:8:153:C:H5'	24:G:238:LYS:HD3	1.85	0.59
31:K:910:G:OP2	45:R:173:ARG:NH2	2.36	0.59
31:K:1373:C:O2'	32:KK:10:LYS:NZ	2.36	0.59
67:h:30:GLN:NE2	86:AB:69:LEU:O	2.36	0.59
81:v:252:THR:HB	81:v:255:LEU:HD23	1.85	0.59
87:AF:226:U:OP2	89:AI:84:ARG:NH1	2.35	0.59
6:5:90:G:OP2	6:5:92:C:N4	2.36	0.58
6:5:413:A:N3	6:5:893:C:O2'	2.36	0.58
6:5:3502:U:O4	16:CC:170:LYS:NZ	2.36	0.58
54:V:31:ASN:HD21	54:V:115:SER:HB2	1.67	0.58
64:e:90:MET:HG2	77:r:33:LYS:HA	1.83	0.58
6:5:717:C:OP1	20:E:49:ASN:ND2	2.35	0.58
6:5:1057:A:N7	43:Q:180:ARG:NH2	2.47	0.58
6:5:3021:G:H5''	6:5:3021:G:C8	2.35	0.58
6:5:1788:A:N6	6:5:2213:C:O2	2.36	0.58
6:5:2788:U:OP2	49:T:9:ARG:NH2	2.37	0.58
38:NN:55:ILE:HG12	38:NN:75:ILE:HG12	1.85	0.58
86:AB:32:LEU:HD13	86:AB:53:ARG:HG3	1.86	0.58
3:2:63:A:C8	3:2:63:A:C5'	2.85	0.58
6:5:3092:G:O2'	6:5:3095:C:OP2	2.20	0.58
31:K:442:C:H42	31:K:449:A:N6	1.97	0.58
31:K:799:U:C4	31:K:867:G:N1	2.72	0.58
64:e:3:ALA:HB3	64:e:5:ARG:HH12	1.69	0.58
87:AF:58:G:O6	87:AF:288:G:N3	2.36	0.58
6:5:2537:G:N2	6:5:2541:C:O2'	2.37	0.58
11:A:29:LEU:O	11:A:123:ARG:NH1	2.34	0.58
12:AA:104:ARG:NH1	31:K:525:A:O2'	2.36	0.58
33:L:25:TRP:HE3	33:L:31:ARG:HH12	1.51	0.58
90:AD:60:LYS:HG2	90:AD:64:LYS:HE2	1.85	0.58
6:5:2659:A:N1	6:5:2741:C:N4	2.48	0.58
7:6:10:THR:HG22	7:6:308:ARG:HG2	1.86	0.58
15:C:94:ASN:HD22	15:C:102:PHE:HB2	1.69	0.58
35:M:24:LEU:HB2	35:M:43:THR:HG21	1.86	0.58
35:M:80:ALA:O	35:M:85:LYS:NZ	2.30	0.58
6:5:3377:C:O2	35:M:132:ARG:NH2	2.36	0.58
3:2:12:G:H1	3:2:23:C:H42	1.52	0.58
6:5:585:C:P	65:f:89:ARG:HH12	2.26	0.58
29:JJ:51:GLN:OE1	31:K:1014:G:N2	2.37	0.58
6:5:93:G:OP2	6:5:2910:U:O2'	2.20	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:5:3429:G:H4'	6:5:3430:U:H5'	1.85	0.58
31:K:962:A:N1	31:K:1055:A:O2'	2.37	0.58
6:5:321:U:HO2'	68:i:30:ARG:HH11	1.47	0.57
13:B:223:THR:HB	13:B:275:HIS:H	1.67	0.57
42:PP:77:LYS:HB2	42:PP:94:ARG:HH12	1.69	0.57
79:t:11:LYS:HD3	79:t:35:LEU:HD21	1.86	0.57
23:GG:108:PRO:HG3	82:w:40:ARG:HG2	1.85	0.57
31:K:15:U:O2'	31:K:669:A:N6	2.35	0.57
6:5:2590:U:O2'	41:P:80:GLN:NE2	2.37	0.57
18:D:83:LEU:HB3	18:D:88:VAL:HB	1.86	0.57
6:5:1123:A:N6	31:K:1028:A:N1	2.52	0.57
6:5:1743:U:N3	15:C:73:VAL:O	2.36	0.57
8:7:86:G:O2'	47:S:87:ARG:NH1	2.37	0.57
10:9:42:CYS:SG	31:K:1495:G:N2	2.76	0.57
31:K:190:G:O2'	31:K:209:A:N6	2.36	0.57
79:t:17:CYS:O	79:t:57:ARG:HA	2.04	0.57
3:2:19:G:H22	30:J:63:ARG:HD3	1.70	0.57
6:5:878:U:OP2	64:e:40:GLY:HA2	2.03	0.57
6:5:1882:C:O2'	6:5:1884:C:N4	2.38	0.57
16:CC:190:LEU:HD12	16:CC:194:GLU:HB3	1.86	0.57
24:G:111:PRO:HD2	24:G:114:ILE:HD12	1.85	0.57
82:w:163:PRO:O	82:w:167:TYR:HB2	2.04	0.57
6:5:2608:C:H3'	6:5:2608:C:C6	2.39	0.57
7:6:107:ASP:HB2	7:6:125:ARG:HD2	1.86	0.57
21:FF:39:SER:OG	34:LL:51:ARG:NH2	2.38	0.57
31:K:1488:C:O2'	31:K:1490:G:OP2	2.14	0.57
45:R:17:CYS:HB3	45:R:52:ARG:HH12	1.70	0.57
47:S:112:ASP:OD1	47:S:116:ARG:NH1	2.37	0.57
80:u:66:VAL:HG22	80:u:87:ILE:HG22	1.86	0.57
83:x:68:ARG:HG3	83:x:76:VAL:HG11	1.85	0.57
7:6:88:ARG:NH2	31:K:1398:G:O2'	2.38	0.57
6:5:3532:C:O2'	63:d:23:ARG:NH2	2.37	0.57
9:8:27:U:H4'	15:C:53:ALA:HB3	1.86	0.57
6:5:2626:A:H61	11:A:230:PRO:HB3	1.68	0.57
16:CC:64:ASN:ND2	31:K:302:A:N3	2.52	0.57
21:FF:26:GLN:NE2	84:y:126:THR:OG1	2.38	0.57
24:G:110:TRP:O	24:G:115:ARG:NH2	2.38	0.57
83:x:31:PRO:HG3	83:x:43:PRO:HG3	1.87	0.57
6:5:603:C:OP1	22:F:72:ARG:NH2	2.37	0.57
23:GG:94:PRO:HD2	23:GG:97:ILE:HD12	1.86	0.57
31:K:1135:C:OP2	34:LL:6:ARG:NH1	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:e:38:PRO:HG2	64:e:46:ARG:HB3	1.85	0.57
72:m:92:THR:HG22	72:m:94:ASN:H	1.69	0.57
83:x:126:VAL:HA	83:x:141:THR:HA	1.87	0.57
31:K:216:C:H42	31:K:309:G:H1	1.52	0.56
31:K:153:G:N3	85:z:13:GLN:NE2	2.52	0.56
67:h:64:THR:O	67:h:68:ASN:ND2	2.37	0.56
6:5:540:G:O2'	6:5:544:C:N4	2.38	0.56
6:5:2385:A:H3'	11:A:198:ARG:HH22	1.69	0.56
6:5:2603:A:H3'	6:5:2603:A:C8	2.40	0.56
6:5:2608:C:C6	6:5:2608:C:C3'	2.87	0.56
6:5:3258:C:HO2'	25:H:155:SER:HG	1.53	0.56
9:8:71:A:OP1	58:Y:27:ARG:NH1	2.34	0.56
50:TT:102:ILE:H	50:TT:113:HIS:HD2	1.51	0.56
78:s:47:LEU:HB3	78:s:51:ALA:HB3	1.86	0.56
80:u:105:LEU:HD23	80:u:213:ARG:HA	1.87	0.56
86:AB:40:LEU:HD11	86:AB:46:ILE:HD13	1.87	0.56
88:AC:33:ARG:NH1	88:AC:35:ILE:O	2.35	0.56
6:5:1461:C:OP1	35:M:34:ASN:ND2	2.38	0.56
8:7:6:C:H4'	18:D:52:ILE:HD13	1.88	0.56
28:II:136:THR:OG1	31:K:1521:C:OP2	2.22	0.56
80:u:146:ARG:HB2	80:u:149:GLN:HB2	1.88	0.56
87:AF:119[A]:A:H61	87:AF:231[A]:A:H61	1.53	0.56
6:5:715:C:O2'	15:C:333:LYS:NZ	2.38	0.56
6:5:1267:U:H4'	49:T:100:LYS:HB2	1.87	0.56
3:2:63:A:H8	3:2:63:A:C5'	2.17	0.56
6:5:3323:G:O3'	39:O:161:LYS:NZ	2.34	0.56
6:5:3391:A:OP2	13:B:100:ARG:NH2	2.38	0.56
37:N:17:ASP:OD1	37:N:20:ARG:NH2	2.38	0.56
55:W:96:GLN:O	55:W:101:ARG:NH1	2.38	0.56
6:5:870:C:O2	65:f:21:GLN:NE2	2.36	0.56
8:7:92:C:H2'	8:7:93:G:H8	1.70	0.56
10:9:36:LEU:HD23	82:w:16:ILE:HD11	1.85	0.56
87:AF:192:A:N6	87:AF:207:C:O2	2.38	0.56
6:5:3135:C:OP1	39:O:65:ASN:ND2	2.38	0.56
8:7:59:G:H4'	18:D:267:ASN:HD21	1.71	0.56
29:JJ:23:ARG:O	50:TT:60:LYS:NZ	2.39	0.56
6:5:1489:G:H5'	47:S:139:ARG:HH11	1.70	0.56
6:5:3253:U:OP2	6:5:3276:G:N1	2.29	0.56
7:6:254:PRO:HA	7:6:285:GLN:HA	1.88	0.56
13:B:113:GLU:OE2	13:B:169:ARG:N	2.39	0.56
13:B:220:ILE:HB	13:B:346:THR:HB	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:K:1275:G:N2	31:K:1506:A:OP2	2.27	0.56
33:L:49:ARG:NH1	67:h:117:ARG:O	2.36	0.56
41:P:94:MET:HE1	41:P:146:ILE:HB	1.87	0.56
66:g:8:ARG:NH2	66:g:32:TYR:O	2.38	0.56
6:5:893:C:H2'	6:5:894:A:H8	1.71	0.56
6:5:2050:G:OP2	62:c:36:LYS:NZ	2.38	0.56
31:K:1012:A:HO2'	31:K:1129:G:H21	1.49	0.56
59:Z:115:LYS:NZ	59:Z:119:GLU:OE2	2.21	0.56
6:5:380:A:O2'	58:Y:87:ARG:NH2	2.38	0.55
6:5:2603:A:C8	6:5:2603:A:C3'	2.90	0.55
15:C:110:ARG:O	15:C:113:ARG:NH1	2.39	0.55
31:K:309:G:H8	31:K:309:G:O5'	1.88	0.55
6:5:1451:C:H4'	39:O:89:PRO:HD3	1.86	0.55
6:5:1966:A:N7	6:5:2154:U:O4	2.39	0.55
6:5:2188:A:C5	6:5:2190:C:C5	2.94	0.55
7:6:289:LEU:HD12	7:6:298:LEU:HD21	1.87	0.55
8:7:86:G:O3'	47:S:87:ARG:NH1	2.37	0.55
31:K:334:C:H5	85:z:190:ARG:HH12	1.54	0.55
41:P:114:ILE:HD11	41:P:117:ILE:HB	1.88	0.55
86:AB:250:LEU:HD12	86:AB:275:THR:HG22	1.87	0.55
1:0:140:TYR:OH	31:K:1291:A:O2'	2.24	0.55
6:5:2626:A:OP1	37:N:90:ASN:ND2	2.39	0.55
31:K:804:U:OP1	50:TT:82:GLN:NE2	2.38	0.55
48:SS:59:LYS:HB3	48:SS:70:TYR:HB2	1.87	0.55
62:c:50:ASN:ND2	62:c:75:SER:O	2.40	0.55
6:5:1394:C:H2'	6:5:1395:A:H8	1.72	0.55
7:6:177:TRP:HA	7:6:184:LEU:HA	1.88	0.55
14:BB:146:VAL:HG22	14:BB:152:ARG:HG2	1.89	0.55
41:P:4:TYR:HE2	41:P:16:LYS:HB3	1.71	0.55
87:AF:173:A:OP1	89:AI:153:LYS:NZ	2.39	0.55
2:1:251:ARG:HH11	2:1:251:ARG:CB	2.18	0.55
6:5:2238:A:H61	6:5:2541:C:H42	1.52	0.55
6:5:3143:G:N2	6:5:3292:G:OP2	2.40	0.55
16:CC:55:TYR:OH	31:K:309:G:OP2	2.22	0.55
58:Y:50:ARG:HB2	58:Y:115:ARG:HH22	1.71	0.55
87:AF:166:U:H5''	89:AI:145:PHE:HZ	1.71	0.55
88:AC:63:GLU:OE1	88:AC:81:ARG:NH2	2.38	0.55
3:2:19:G:C8	3:2:57:G:N2	2.74	0.55
30:J:84:GLU:OE2	30:J:92:TYR:OH	2.24	0.55
41:P:129:THR:HG23	41:P:129:THR:O	2.05	0.55
66:g:37:LYS:HB3	66:g:60:ARG:HH11	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:9:16:GLN:NE2	31:K:1263:U:O2	2.40	0.55
11:A:137:ILE:HD11	11:A:149:LYS:HB3	1.89	0.55
17:DD:170:PRO:O	17:DD:175:ARG:NH1	2.39	0.55
31:K:1585:U:O2'	31:K:1587:G:OP2	2.19	0.55
6:5:2670:C:H2'	6:5:2671:G:H8	1.72	0.55
80:u:113:MET:HB3	80:u:142:PHE:HE2	1.71	0.55
81:v:74:LYS:HZ2	81:v:272:HIS:CG	2.24	0.55
6:5:1077:G:O6	15:C:106:LYS:NZ	2.36	0.55
6:5:2699:G:O3'	66:g:90:ARG:NH1	2.39	0.55
22:F:236:GLU:OE1	47:S:41:LYS:NZ	2.39	0.55
6:5:301:A:OP1	68:i:45:ARG:NH2	2.36	0.55
6:5:2252:G:N2	6:5:2535:C:O2	2.39	0.55
6:5:2318:G:OP1	6:5:2320:C:N4	2.40	0.55
31:K:799:U:O4	31:K:867:G:C6	2.60	0.55
80:u:32:ASP:OD1	80:u:46:LYS:NZ	2.39	0.55
85:z:98:ARG:HH21	85:z:105:ASN:HB3	1.71	0.55
6:5:940:G:H2'	6:5:941:G:H8	1.71	0.54
6:5:1799:G:N7	71:l:2:SER:N	2.55	0.54
6:5:3405:U:H4'	6:5:3406:C:H5'	1.90	0.54
13:B:24:ARG:HH12	13:B:28:LYS:HD2	1.72	0.54
32:KK:58:MET:O	32:KK:62:GLN:NE2	2.39	0.54
6:5:876:C:H5'	64:e:43:ASN:OD1	2.06	0.54
6:5:2188:A:N7	6:5:2190:C:N4	2.53	0.54
6:5:2594:C:H1'	13:B:268:ARG:HH11	1.71	0.54
28:II:127:TRP:O	28:II:144:ARG:NH2	2.38	0.54
6:5:3188:G:H5''	54:V:15:ARG:HB3	1.89	0.54
7:6:296:GLN:NE2	7:6:312:VAL:O	2.41	0.54
11:A:95:GLN:O	11:A:100:ASN:ND2	2.41	0.54
39:O:18:ARG:HH12	39:O:128:ARG:NH1	2.05	0.54
39:O:30:GLY:HA2	39:O:101:ARG:NH1	2.23	0.54
41:P:89:GLU:O	41:P:93:HIS:ND1	2.40	0.54
76:q:183:LEU:HD23	76:q:186:ARG:HE	1.72	0.54
6:5:2133:U:O2'	6:5:2135:G:N2	2.40	0.54
30:J:32:ARG:HD2	30:J:35:ARG:HH11	1.73	0.54
31:K:1270:G:O2'	31:K:1301:A:N7	2.38	0.54
47:S:34:ALA:HB1	47:S:39:VAL:HG23	1.90	0.54
6:5:274:G:O6	37:N:15:GLN:NE2	2.40	0.54
6:5:294:A:H2'	6:5:295:G:H8	1.73	0.54
6:5:1840:U:H2'	6:5:1841:G:H8	1.73	0.54
19:EE:126:VAL:HG23	19:EE:145:VAL:HG22	1.90	0.54
20:E:48:ARG:HB3	20:E:67:ARG:HD3	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:J:136:ARG:NH2	30:J:161:GLU:OE2	2.40	0.54
31:K:965:U:O2	31:K:1065:G:N2	2.41	0.54
80:u:122:GLU:O	80:u:165:ARG:NH2	2.41	0.54
6:5:62:A:OP1	37:N:172:ARG:NH1	2.41	0.54
11:A:116:LEU:HB3	11:A:126:LEU:HB2	1.90	0.54
31:K:158:A:N6	31:K:466:G:O6	2.40	0.54
87:AF:21:C:OP1	90:AD:32:ARG:NH1	2.39	0.54
6:5:113:A:OP2	6:5:156:G:N2	2.37	0.54
6:5:1615:C:OP1	64:e:64:LYS:NZ	2.31	0.54
6:5:1917:U:OP1	45:R:42:ARG:NH1	2.41	0.54
21:FF:9:ILE:HD13	84:y:122:ARG:NH1	2.22	0.54
32:KK:129:LYS:HB2	80:u:150:ILE:HD13	1.89	0.54
50:TT:52:ILE:HG22	50:TT:61:ILE:HG12	1.89	0.54
82:w:31:GLU:O	82:w:54:ARG:NH2	2.40	0.54
6:5:430:C:H2'	6:5:431:G:H8	1.72	0.54
6:5:1578:A:N6	6:5:3004:C:O2	2.41	0.54
6:5:2065:C:OP1	75:p:44:LYS:NZ	2.28	0.54
6:5:2378:U:OP1	11:A:54:ARG:NH2	2.41	0.54
7:6:118:ARG:NH2	7:6:134:THR:OG1	2.40	0.54
39:O:109:PRO:HB2	39:O:111:PRO:HD2	1.90	0.54
6:5:432:G:OP1	64:e:16:ARG:NH2	2.41	0.54
6:5:1804:C:H2'	6:5:1805:A:H8	1.73	0.54
17:DD:172:ARG:NH2	31:K:562:U:O4	2.39	0.54
22:F:34:LYS:O	22:F:38:GLN:NE2	2.41	0.54
22:F:121:PHE:O	22:F:204:ASN:ND2	2.41	0.54
25:H:36:ARG:HB2	25:H:80:MET:HE1	1.89	0.54
29:JJ:20:LYS:NZ	31:K:1016:U:OP2	2.28	0.54
31:K:654:A:OP2	31:K:655:A:O2'	2.17	0.54
60:a:38:MET:O	60:a:42:ARG:NH2	2.41	0.54
86:AB:120:LYS:NZ	86:AB:277:GLU:O	2.41	0.54
6:5:1674:U:H5''	64:e:46:ARG:HH22	1.73	0.54
25:H:129:ARG:HG2	25:H:153:LEU:HD22	1.90	0.54
31:K:941:C:H2'	31:K:942:G:H8	1.72	0.54
43:Q:15:ARG:HH22	43:Q:54:SER:HB3	1.73	0.54
31:K:1079:C:O2'	31:K:1182:A:N1	2.41	0.53
32:KK:17:ILE:HD11	32:KK:54:VAL:HA	1.90	0.53
66:g:110:GLN:O	66:g:114:GLN:NE2	2.40	0.53
87:AF:212:C:O2'	87:AF:214:A:OP1	2.26	0.53
6:5:1913:C:H1'	6:5:2033:G:H21	1.73	0.53
9:8:47:C:H1'	9:8:61:A:H2'	1.90	0.53
24:G:218:GLU:OE2	37:N:22:LEU:HD13	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:K:925:G:H2'	31:K:926:A:H8	1.74	0.53
31:K:1215:C:H42	31:K:1220:A:N6	2.05	0.53
31:K:1215:C:N4	31:K:1220:A:H61	2.05	0.53
31:K:1218:C:H1'	31:K:1683:C:H42	1.73	0.53
45:R:174:GLU:O	45:R:178:GLN:NE2	2.42	0.53
46:RR:33:ARG:HH22	46:RR:89:VAL:HG11	1.74	0.53
54:V:48:ARG:HB3	54:V:51:ARG:HD3	1.89	0.53
6:5:372:A:O2'	6:5:407:G:N2	2.42	0.53
6:5:3378:G:H2'	6:5:3379:G:H8	1.74	0.53
8:7:87:G:H5'	47:S:87:ARG:NH1	2.22	0.53
20:E:52:LEU:HD13	20:E:53:VAL:HG23	1.91	0.53
22:F:126:LYS:HB2	49:T:133:ALA:HB3	1.90	0.53
28:II:35:GLY:O	28:II:97:GLN:NE2	2.41	0.53
31:K:16:G:H5'	31:K:669:A:H61	1.74	0.53
35:M:11:ARG:NH2	35:M:58:THR:O	2.38	0.53
66:g:37:LYS:HB3	66:g:60:ARG:NH1	2.24	0.53
6:5:1976:C:OP2	66:g:76:ARG:NH1	2.42	0.53
6:5:2611:G:N2	6:5:2960:A:N3	2.56	0.53
6:5:2701:G:N2	24:G:96:GLN:O	2.41	0.53
7:6:31:ILE:HG22	7:6:43:TRP:HB2	1.90	0.53
28:II:24:ARG:HH12	31:K:1602:U:H4'	1.72	0.53
31:K:311:C:H3'	31:K:311:C:H6	1.74	0.53
31:K:350:C:O2'	31:K:383:G:N1	2.42	0.53
31:K:1231:C:O2'	31:K:1253:A:N6	2.41	0.53
77:r:6:GLN:HE21	77:r:44:ILE:HG23	1.74	0.53
1:0:108:VAL:HG21	46:RR:63:LYS:HG2	1.89	0.53
6:5:474:C:O2'	6:5:1631:C:N4	2.42	0.53
6:5:844:G:N1	6:5:1613:G:OP1	2.42	0.53
6:5:996:G:N2	6:5:1010:C:N3	2.56	0.53
6:5:2024:U:H5''	6:5:2025:U:H5'	1.90	0.53
6:5:2096:G:H5'	52:U:113:ARG:HH12	1.74	0.53
34:LL:11:ALA:O	34:LL:15:ARG:NH2	2.41	0.53
90:AD:32:ARG:NH2	91:AE:25:SER:OG	2.41	0.53
6:5:735:G:OP2	20:E:67:ARG:NH2	2.42	0.53
6:5:1215:C:OP2	60:a:26:ARG:NH1	2.42	0.53
6:5:1261:G:N2	6:5:1413:U:OP1	2.42	0.53
15:C:316:LYS:HB2	15:C:324:ILE:HG13	1.91	0.53
50:TT:91:ASN:O	81:v:183:LYS:NZ	2.33	0.53
81:v:191:VAL:HG11	81:v:236:PHE:HA	1.91	0.53
6:5:1510:G:OP2	6:5:1511:U:H3'	2.08	0.53
31:K:915:G:OP2	31:K:915:G:N2	2.38	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:5:1076:G:O2'	33:L:18:TRP:NE1	2.37	0.53
6:5:2457:A:H5'	6:5:2463:G:H22	1.73	0.53
6:5:3327:A:H3'	25:H:23:ARG:HH11	1.73	0.53
14:BB:20:GLU:HG2	14:BB:48:ALA:HB3	1.91	0.53
16:CC:22:HIS:ND1	16:CC:23:LYS:O	2.40	0.53
31:K:1485:U:OP1	82:w:151:LYS:NZ	2.37	0.53
31:K:1599:U:OP1	40:OO:80:ARG:NH2	2.42	0.53
41:P:16:LYS:HG2	41:P:149:ILE:HG12	1.91	0.53
66:g:16:ALA:HA	66:g:19:LYS:HE3	1.90	0.53
81:v:272:HIS:HA	81:v:275:LYS:HG2	1.90	0.53
86:AB:411:GLY:HA3	87:AF:195:U:H1'	1.90	0.53
6:5:1800:G:OP2	6:5:1800:G:N2	2.40	0.53
20:E:181:PRO:HG2	20:E:184:LEU:HD12	1.91	0.53
27:I:159:PHE:HB2	27:I:163:GLN:HE22	1.74	0.53
56:WW:108:LYS:HG2	56:WW:111:MET:HE2	1.91	0.53
3:2:3:U:H3	3:2:70:G:H1	1.57	0.53
6:5:202:A:N3	6:5:226:G:O2'	2.42	0.53
6:5:2595:G:N2	6:5:2596:G:O6	2.40	0.53
6:5:3078:C:H4'	54:V:43:LYS:HA	1.91	0.53
16:CC:10:LYS:HB2	31:K:371:A:OP2	2.07	0.53
16:CC:147:LYS:HE2	31:K:204:G:OP2	2.08	0.53
23:GG:26:SER:HB3	23:GG:32:LEU:HD22	1.91	0.53
31:K:491:C:O2	31:K:493:A:N6	2.40	0.53
31:K:1271:C:H42	31:K:1511:U:H3	1.57	0.53
83:x:63:LYS:O	83:x:67:GLN:NE2	2.41	0.53
3:2:19:G:H8	3:2:57:G:N2	2.07	0.52
6:5:1728:C:H2'	6:5:1729:G:H8	1.74	0.52
9:8:142:U:OP1	37:N:38:ARG:NH2	2.39	0.52
20:E:185:ASN:ND2	20:E:274:LEU:O	2.42	0.52
31:K:99:A:H61	31:K:433:A:H1'	1.74	0.52
80:u:49:VAL:HG22	80:u:65:ARG:NH1	2.24	0.52
87:AF:174:G:OP2	89:AI:150:ARG:NH2	2.43	0.52
2:1:251:ARG:CB	2:1:251:ARG:NH1	2.72	0.52
7:6:23:THR:HG22	7:6:31:ILE:HD11	1.91	0.52
11:A:242:ARG:NH1	11:A:245:ARG:O	2.42	0.52
31:K:925:G:OP1	44:QQ:121:ARG:NH2	2.42	0.52
42:PP:124:THR:HG23	42:PP:127:GLY:H	1.74	0.52
6:5:952:G:H5'	33:L:186:ARG:NH1	2.24	0.52
6:5:2494:U:HO2'	31:K:1720:U:HO2'	1.56	0.52
6:5:2893:A:H2	18:D:146:LEU:HD12	1.75	0.52
22:F:147:LYS:HB3	22:F:244:ARG:HH11	1.73	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:I:30:LYS:HD3	27:I:63:GLU:HG2	1.91	0.52
40:OO:110:THR:HG21	84:y:102:LEU:HD22	1.92	0.52
6:5:1968:U:O2	6:5:2151:G:N2	2.42	0.52
6:5:2735:C:OP1	24:G:106:ARG:NH2	2.41	0.52
6:5:3328:G:H21	47:S:173:ASN:HD21	1.57	0.52
13:B:234:ARG:HH21	13:B:235:TRP:HE1	1.57	0.52
74:o:2:VAL:N	74:o:90:HIS:O	2.42	0.52
80:u:86:LEU:HB3	80:u:98:THR:HB	1.91	0.52
87:AF:58:G:C5	87:AF:288:G:N2	2.78	0.52
4:3:47:U:O2'	4:3:50:A:OP1	2.28	0.52
11:A:177:LYS:HE3	75:p:26:VAL:HG13	1.92	0.52
13:B:283:LYS:HD3	13:B:363:ILE:HD11	1.92	0.52
14:BB:53:VAL:HG21	14:BB:172:THR:HA	1.91	0.52
16:CC:81:VAL:HG22	16:CC:102:VAL:HG12	1.91	0.52
18:D:77:ALA:O	18:D:108:ARG:NH2	2.41	0.52
31:K:391:C:H2'	31:K:392:A:H8	1.74	0.52
82:w:123:LEU:HD21	82:w:154:ASP:OD2	2.09	0.52
86:AB:43:ASP:O	86:AB:227:GLN:NE2	2.42	0.52
6:5:1667:C:H5'	15:C:312:ARG:HB3	1.91	0.52
6:5:2807:C:O2'	6:5:2891:U:O2	2.28	0.52
13:B:254:ILE:HG23	13:B:266:VAL:HG11	1.92	0.52
31:K:681:U:H5''	53:VV:8:ARG:HG3	1.92	0.52
31:K:1201:U:HO2'	31:K:1358:U:HO2'	1.56	0.52
50:TT:69:LEU:HD21	50:TT:72:CYS:HB2	1.91	0.52
62:c:17:ARG:NH1	62:c:103:ASP:HB3	2.24	0.52
81:v:123:ARG:NH2	81:v:143:CYS:SG	2.83	0.52
5:4:48:G:OP1	31:K:1704:C:N4	2.41	0.52
7:6:166:VAL:HG22	7:6:176:VAL:HG22	1.92	0.52
11:A:101:VAL:HB	11:A:165:VAL:HG12	1.92	0.52
31:K:64:A:H2	31:K:83:A:H62	1.58	0.52
31:K:1277:C:H2'	31:K:1278:A:H8	1.74	0.52
42:PP:76:THR:HB	42:PP:94:ARG:HB3	1.91	0.52
6:5:3363:U:OP2	35:M:117:LYS:HE2	2.09	0.52
8:7:97:G:O5'	22:F:133:ARG:NH1	2.42	0.52
36:MM:66:ARG:HG3	84:y:135:ARG:HH12	1.73	0.52
72:m:68:MET:HG2	72:m:79:PRO:HA	1.92	0.52
1:0:138:ARG:NH1	31:K:1293:A:H1'	2.25	0.52
6:5:2594:C:H1'	13:B:268:ARG:NH1	2.25	0.52
16:CC:47:ARG:NH1	31:K:445:A:OP2	2.43	0.52
25:H:104:VAL:HG12	25:H:113:GLU:HB2	1.92	0.52
31:K:453:C:O2'	85:z:92:ARG:O	2.27	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:K:454:U:H5''	85:z:94:ARG:HG2	1.91	0.52
31:K:1100:A:O5'	32:KK:132:ARG:NH2	2.43	0.52
77:r:28:GLU:HB2	77:r:31:ASN:HB2	1.91	0.52
6:5:1990:G:H5''	66:g:43:LYS:HZ3	1.75	0.52
6:5:2916:U:O2'	74:o:80:LYS:O	2.27	0.52
16:CC:99:ASN:ND2	16:CC:174:CYS:SG	2.83	0.52
31:K:1598:G:H3'	40:OO:80:ARG:HH21	1.75	0.52
55:W:9:SER:OG	55:W:36:CYS:SG	2.67	0.52
3:2:65:C:H2'	3:2:66:C:C6	2.45	0.51
6:5:1083:A:N3	6:5:2959:C:O2'	2.41	0.51
6:5:1426:U:O2'	6:5:2571:G:N2	2.42	0.51
6:5:2060:C:OP1	45:R:100:ARG:NE	2.43	0.51
6:5:3327:A:C3'	25:H:23:ARG:HH11	2.22	0.51
15:C:329:ASN:ND2	22:F:187:GLU:OE2	2.43	0.51
16:CC:45:THR:HG22	31:K:307:G:H1'	1.92	0.51
54:V:71:GLU:O	54:V:75:LYS:NZ	2.32	0.51
55:W:6:CYS:HB3	55:W:10:GLY:H	1.75	0.51
60:a:3:SER:HA	60:a:6:ARG:HH11	1.74	0.51
1:0:138:ARG:HH11	31:K:1293:A:H1'	1.75	0.51
2:1:250:GLY:O	6:5:2606:A:N7	2.39	0.51
6:5:867:C:H2'	6:5:868:A:H8	1.75	0.51
6:5:1157:G:OP2	41:P:131:ARG:NE	2.31	0.51
6:5:2415:A:N3	6:5:2748:A:O2'	2.39	0.51
9:8:96:C:OP1	67:h:70:ARG:NH2	2.43	0.51
11:A:192:LYS:HD2	11:A:193:ARG:NH1	2.25	0.51
23:GG:59:LYS:HB2	23:GG:84:ILE:HG22	1.91	0.51
31:K:743:U:O4	31:K:798:G:O6	2.28	0.51
43:Q:172:ARG:NH2	60:a:56:VAL:O	2.43	0.51
58:Y:8:THR:HG22	58:Y:10:ASP:H	1.74	0.51
69:j:19:CYS:SG	69:j:20:ARG:N	2.82	0.51
80:u:144:LYS:HD3	80:u:208:HIS:HB3	1.93	0.51
87:AF:132:U:H3	87:AF:165:G:H1	1.58	0.51
6:5:3046:C:O2'	6:5:3048:G:OP2	2.17	0.51
6:5:3156:G:OP1	39:O:72:HIS:N	2.42	0.51
9:8:60:G:O6	67:h:62:ASN:ND2	2.43	0.51
12:AA:115:PHE:HE2	17:DD:29:LEU:HD12	1.75	0.51
19:EE:69:ARG:NH1	31:K:111:A:O2'	2.43	0.51
37:N:113:LEU:HB3	37:N:134:LEU:HB3	1.92	0.51
47:S:1:MET:HB2	47:S:43:ARG:HH11	1.75	0.51
80:u:134:LEU:HD13	80:u:219:LYS:HD2	1.93	0.51
83:x:197:ASN:HB3	83:x:209:HIS:HB2	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
90:AD:32:ARG:HG3	90:AD:36:GLY:H	1.76	0.51
6:5:806:C:P	22:F:69:ARG:HH12	2.32	0.51
6:5:955:A:O2'	6:5:1027:C:O2	2.27	0.51
6:5:1123:A:OP1	31:K:678:U:O2'	2.29	0.51
6:5:1206:A:O2'	69:j:49:TRP:O	2.27	0.51
6:5:1280:A:H1'	18:D:15:ARG:HH21	1.75	0.51
6:5:2985:A:H4'	27:I:74:LYS:NZ	2.25	0.51
7:6:152:SER:H	7:6:169:GLY:HA2	1.76	0.51
9:8:38:U:H5'	67:h:81:LEU:HD13	1.92	0.51
11:A:192:LYS:HD2	11:A:193:ARG:HH12	1.75	0.51
85:z:64:LYS:HE2	85:z:97:VAL:HG11	1.91	0.51
6:5:150:U:OP2	24:G:253:THR:OG1	2.23	0.51
6:5:340:G:OP1	58:Y:8:THR:OG1	2.27	0.51
6:5:1009:C:OP1	43:Q:134:ARG:NH2	2.43	0.51
6:5:1273:A:N3	8:7:78:C:O2'	2.43	0.51
6:5:1738:G:OP2	60:a:12:ARG:NH1	2.42	0.51
31:K:1386:A:OP2	82:w:160:SER:OG	2.27	0.51
31:K:1534:C:P	84:y:81:ARG:HH12	2.29	0.51
31:K:1808:U:H2'	31:K:1809:A:H8	1.75	0.51
6:5:692:G:H5''	6:5:693:A:H5'	1.93	0.51
6:5:2202:G:H5'	45:R:60:ARG:NH1	2.26	0.51
11:A:70:LYS:HB3	11:A:72:ARG:HH12	1.75	0.51
17:DD:131:ARG:NH2	31:K:522:A:O3'	2.44	0.51
26:HH:22:ARG:NH2	26:HH:56:CYS:SG	2.83	0.51
28:II:4:VAL:HA	40:OO:50:PHE:HB2	1.93	0.51
31:K:216:C:C2	31:K:309:G:N2	2.74	0.51
31:K:1144:A:H5'	31:K:1355:C:H41	1.76	0.51
90:AD:59:VAL:HG13	91:AE:91:MET:HE3	1.93	0.51
6:5:37:U:H4'	60:a:32:ARG:HD2	1.91	0.51
6:5:1069:C:H2'	6:5:1070:G:H8	1.75	0.51
6:5:1966:A:H4'	59:Z:115:LYS:HZ1	1.75	0.51
9:8:102:G:OP2	9:8:104:A:O2'	2.25	0.51
11:A:234:LYS:HG2	11:A:238:ILE:HD12	1.93	0.51
28:II:132:ARG:NH1	31:K:1623:A:N7	2.57	0.51
31:K:106:C:H2'	31:K:107:A:H8	1.76	0.51
45:R:148:ASP:OD1	45:R:151:ARG:NH2	2.38	0.51
56:WW:44:ARG:NH1	56:WW:48:GLY:O	2.43	0.51
76:q:126:ASP:OD1	76:q:165:ASN:ND2	2.43	0.51
79:t:112:ILE:HG22	79:t:132:ILE:HD13	1.92	0.51
6:5:751:C:H2'	6:5:752:A:H8	1.75	0.51
6:5:1249:G:OP1	43:Q:11:ARG:NH2	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:6:125:ARG:NH1	32:KK:33:ARG:HG3	2.26	0.51
8:7:77:A:H62	8:7:99:G:H21	1.58	0.51
21:FF:26:GLN:OE1	31:K:1219:C:O2'	2.28	0.51
27:I:43:VAL:O	27:I:171:TRP:NE1	2.43	0.51
28:II:124:ARG:HE	28:II:129:LEU:HB2	1.75	0.51
41:P:122:ALA:HB3	41:P:143:PRO:HG2	1.91	0.51
50:TT:86:LEU:HD23	50:TT:117:ARG:HE	1.75	0.51
53:VV:84:PHE:H	53:VV:121:LYS:HA	1.76	0.51
78:s:18:ILE:HG13	78:s:68:HIS:HE1	1.74	0.51
82:w:140:GLY:HA3	82:w:182:LEU:HG	1.92	0.51
6:5:239:C:O2'	6:5:240:G:OP2	2.23	0.51
6:5:2985:A:H4'	27:I:74:LYS:HZ2	1.76	0.51
18:D:107:ARG:NH2	18:D:116:ASP:OD1	2.44	0.51
31:K:923:G:H2'	31:K:924:G:H8	1.76	0.51
35:M:6:PHE:O	35:M:11:ARG:NE	2.44	0.51
50:TT:103:VAL:HA	50:TT:112:ASP:HA	1.93	0.51
52:U:80:LYS:O	52:U:110:TYR:OH	2.29	0.51
58:Y:50:ARG:NH1	58:Y:112:ASP:OD2	2.38	0.51
69:j:14:LYS:HZ1	71:l:51:LEU:HB3	1.75	0.51
86:AB:430:MET:O	86:AB:434:MET:HB2	2.11	0.51
3:2:74:C:H2'	3:2:74:C:O2	2.11	0.51
3:2:74:C:H5'	6:5:3118:A:H2'	1.92	0.51
6:5:1702:G:O2'	9:8:18:U:O2	2.28	0.51
6:5:2188:A:C5	6:5:2190:C:C6	2.99	0.51
6:5:2361:A:OP1	11:A:119:LYS:NZ	2.41	0.51
12:AA:113:ARG:HA	12:AA:117:ASN:HD22	1.75	0.51
13:B:240:LEU:HB3	13:B:244:THR:HG21	1.93	0.51
41:P:128:ARG:HH21	41:P:128:ARG:CG	2.13	0.51
48:SS:59:LYS:O	48:SS:69:TRP:HA	2.12	0.51
48:SS:71:LEU:O	82:w:64:ARG:NH2	2.44	0.51
87:AF:1:G:HO2'	87:AF:49:A:HO2'	1.59	0.51
2:1:239:VAL:HG12	2:1:239:VAL:O	2.10	0.50
6:5:107:G:N2	33:L:74:ARG:HH11	2.04	0.50
6:5:1108:G:O2'	6:5:2205:A:N3	2.42	0.50
6:5:1921:G:H4'	6:5:2176:A:H4'	1.92	0.50
6:5:3174:G:N2	6:5:3177:A:OP2	2.42	0.50
17:DD:41:ARG:NH1	31:K:643:A:OP1	2.42	0.50
21:FF:44:ARG:HH22	84:y:140:ASP:HB2	1.76	0.50
38:NN:90:ARG:HG3	38:NN:93:ARG:HD2	1.93	0.50
41:P:31:GLU:HG2	41:P:60:PHE:HA	1.92	0.50
51:UU:131:LYS:HB2	51:UU:140:ARG:HH12	1.77	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
71:l:22:PRO:HB3	71:l:41:ARG:NH1	2.26	0.50
77:r:17:LEU:HD21	77:r:19:LYS:HE3	1.93	0.50
82:w:40:ARG:HH12	82:w:49:ILE:HD12	1.76	0.50
86:AB:237:LYS:NZ	86:AB:266:THR:OG1	2.43	0.50
6:5:76:A:N7	33:L:74:ARG:NH2	2.58	0.50
6:5:1455:U:O2	6:5:1601:G:O6	2.30	0.50
6:5:2056:G:O2'	45:R:117:ARG:NH1	2.45	0.50
6:5:2584:G:OP2	39:O:90:HIS:NE2	2.44	0.50
13:B:329:ASP:OD1	13:B:329:ASP:N	2.44	0.50
30:J:81:GLU:OE2	30:J:85:LYS:HE2	2.12	0.50
31:K:989:C:O2	34:LL:32:LYS:NZ	2.43	0.50
31:K:1652:G:O6	31:K:1672:U:O4	2.30	0.50
81:v:252:THR:HG22	81:v:254:ASP:H	1.76	0.50
87:AF:175:G:H3'	87:AF:176:A:H4'	1.94	0.50
1:0:107:LYS:HB2	1:0:115:SER:HB3	1.93	0.50
6:5:2118:A:N6	45:R:88:ARG:O	2.44	0.50
9:8:57:C:N4	69:j:63:ARG:HH12	2.09	0.50
20:E:168:LEU:HD21	20:E:260:ILE:HD11	1.92	0.50
25:H:59:LYS:HE3	25:H:66:GLU:HB3	1.93	0.50
29:JJ:56:CYS:SG	29:JJ:57:VAL:N	2.83	0.50
31:K:57:U:O2'	31:K:499:G:N3	2.41	0.50
31:K:1095:U:H3	31:K:1149:A:H61	1.59	0.50
31:K:1122:A:N3	80:u:146:ARG:NH1	2.59	0.50
39:O:157:GLU:HA	39:O:160:ARG:HG2	1.92	0.50
64:e:22:ARG:HE	64:e:36:ARG:HB2	1.76	0.50
77:r:63:VAL:HG22	77:r:79:ARG:HG2	1.94	0.50
80:u:137:LEU:HG	80:u:215:VAL:HG22	1.93	0.50
6:5:3089:C:H5''	6:5:3090:G:H5''	1.92	0.50
31:K:659:G:HO2'	31:K:662:G:HO2'	1.60	0.50
45:R:158:GLN:HB3	45:R:162:ARG:HH12	1.77	0.50
68:i:70:LEU:HB2	68:i:87:ARG:HH11	1.76	0.50
6:5:1177:G:O2'	69:j:12:ARG:NH2	2.44	0.50
6:5:1793:G:H21	66:g:6:THR:HG22	1.77	0.50
6:5:2889:C:H2'	6:5:2890:G:H8	1.76	0.50
6:5:2893:A:H4'	18:D:176:SER:HB3	1.93	0.50
8:7:6:C:O2'	18:D:50:ARG:NH1	2.45	0.50
31:K:1616:U:OP2	56:WW:43:ARG:NH2	2.40	0.50
43:Q:67:ILE:HD12	43:Q:96:PRO:HD2	1.92	0.50
56:WW:81:ARG:NH2	56:WW:117:GLY:O	2.44	0.50
6:5:1354:U:H4'	18:D:43:LYS:HE2	1.93	0.50
6:5:2968:C:O2	6:5:2968:C:H2'	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:5:3455:G:O2'	6:5:3457:A:N6	2.45	0.50
12:AA:82:VAL:HG22	53:VV:68:LYS:HE2	1.93	0.50
14:BB:119:SER:O	31:K:913:A:N6	2.42	0.50
26:HH:73:ALA:HB1	26:HH:78:ILE:HB	1.92	0.50
31:K:429:C:O2'	31:K:811:A:N1	2.43	0.50
31:K:495:U:O2'	83:x:27:PHE:O	2.30	0.50
31:K:1049:A:OP2	31:K:1068:G:N1	2.39	0.50
31:K:1587:G:H5''	42:PP:77:LYS:HD3	1.93	0.50
50:TT:11:LEU:HA	50:TT:14:ILE:HG12	1.94	0.50
76:q:123:VAL:HG22	76:q:145:ILE:HD12	1.94	0.50
82:w:40:ARG:NH1	82:w:49:ILE:HD12	2.26	0.50
3:2:38:A:O2'	31:K:1058:A:OP1	2.29	0.50
6:5:136:C:N4	67:h:76:LYS:O	2.45	0.50
6:5:917:U:H1'	6:5:1065:C:H1'	1.93	0.50
6:5:1498:G:N2	6:5:1561:G:O2'	2.42	0.50
6:5:1632:A:OP2	6:5:1632:A:H8	1.95	0.50
6:5:1639:G:H3'	22:F:45:ARG:HH22	1.77	0.50
6:5:2699:G:H4'	66:g:90:ARG:HG3	1.92	0.50
25:H:94:SER:HB3	25:H:142:ASP:HB3	1.94	0.50
80:u:121:ILE:HG12	80:u:161:VAL:HG13	1.94	0.50
6:5:1178:G:OP1	69:j:13:ASN:ND2	2.45	0.50
6:5:1214:G:H5''	60:a:29:PRO:HA	1.94	0.50
11:A:192:LYS:HB3	11:A:193:ARG:NH1	2.27	0.50
17:DD:136:ARG:NH1	17:DD:159:PHE:O	2.44	0.50
27:I:66:GLU:CD	27:I:69:ARG:HH11	2.19	0.50
31:K:1528:G:O2'	31:K:1666:C:OP1	2.29	0.50
31:K:1562:C:H2'	31:K:1563:G:H8	1.76	0.50
35:M:47:ARG:HH22	35:M:69:ARG:HA	1.76	0.50
78:s:32:ALA:O	78:s:85:ASN:ND2	2.45	0.50
83:x:80:ILE:HG13	83:x:81:THR:HG23	1.94	0.50
6:5:153:G:H2'	6:5:154:G:H8	1.76	0.50
6:5:1607:U:OP1	65:f:22:ARG:NH2	2.42	0.50
20:E:160:HIS:HB3	20:E:163:LYS:HD2	1.94	0.50
25:H:128:MET:HG3	25:H:157:SER:HB2	1.94	0.50
30:J:15:LEU:HD21	30:J:134:LEU:HD13	1.94	0.50
31:K:931:C:OP2	80:u:159:GLN:HG3	2.12	0.50
31:K:1536:G:H2'	31:K:1537:A:H8	1.77	0.50
33:L:11:LYS:N	43:Q:168:ARG:HH12	2.09	0.50
83:x:100:ARG:NH2	83:x:118:GLU:O	2.45	0.50
90:AD:30:LYS:HB3	90:AD:39:CYS:HB3	1.93	0.50
3:2:63:A:H8	3:2:63:A:OP2	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:5:566:C:OP1	77:r:87:ARG:NE	2.45	0.49
6:5:1004:G:N2	6:5:1005:U:O4	2.44	0.49
6:5:2184:C:OP1	71:l:48:LYS:NZ	2.44	0.49
6:5:2247:G:O6	13:B:243:LYS:NZ	2.45	0.49
6:5:2802:U:H3'	74:o:3:ASN:HB3	1.94	0.49
7:6:11:LEU:HB2	7:6:307:VAL:HB	1.94	0.49
7:6:158:PRO:HG2	7:6:202:PRO:HA	1.94	0.49
13:B:287:ILE:HG12	13:B:331:VAL:HG12	1.94	0.49
14:BB:63:PHE:HB3	14:BB:97:GLN:HB2	1.94	0.49
14:BB:72:PHE:HA	14:BB:75:ILE:HG22	1.94	0.49
21:FF:9:ILE:HD13	84:y:122:ARG:HH12	1.75	0.49
25:H:41:ILE:HD11	25:H:69:THR:HB	1.94	0.49
27:I:162:ARG:NH1	47:S:88:SER:HB2	2.27	0.49
31:K:1616:U:O4	56:WW:40:ARG:NH1	2.36	0.49
51:UU:41:MET:N	51:UU:41:MET:SD	2.85	0.49
67:h:80:PRO:HD2	67:h:83:LEU:HD12	1.94	0.49
88:AC:59:ASN:ND2	88:AC:85:GLN:OE1	2.44	0.49
6:5:1132:U:O4	75:p:4:ARG:NH2	2.42	0.49
6:5:1484:U:O2	6:5:3263:C:N4	2.44	0.49
8:7:57:C:H2'	8:7:58:A:H8	1.77	0.49
15:C:33:ARG:NH1	43:Q:22:ASP:HB2	2.26	0.49
31:K:1259:A:N6	31:K:1519:U:O5'	2.44	0.49
83:x:87:MET:HE1	83:x:236:ILE:HD13	1.94	0.49
87:AF:223:U:H5''	89:AI:76:ARG:HH12	1.77	0.49
91:AE:87:LEU:HB3	91:AE:91:MET:HE2	1.94	0.49
6:5:3269:U:OP2	72:m:85:ARG:HD2	2.12	0.49
6:5:3476:C:H4'	63:d:26:THR:HG23	1.94	0.49
8:7:75:G:N2	8:7:100:A:OP2	2.26	0.49
19:EE:35:ARG:NE	19:EE:50:ALA:O	2.43	0.49
25:H:91:LYS:HB2	25:H:183:GLU:HB3	1.94	0.49
45:R:67:THR:HA	45:R:70:ARG:HB2	1.94	0.49
57:X:107:HIS:O	57:X:111:GLN:NE2	2.44	0.49
86:AB:29:ASN:OD1	86:AB:53:ARG:NH2	2.46	0.49
88:AC:67:MET:SD	88:AC:74:ARG:NH1	2.86	0.49
6:5:35:U:O2'	6:5:1085:A:N1	2.46	0.49
6:5:1630:G:H22	6:5:1655:G:H1	1.61	0.49
6:5:3287:A:H4'	13:B:20:LYS:HD3	1.94	0.49
7:6:100:ARG:NH2	31:K:1399:C:OP1	2.45	0.49
15:C:152:LEU:HD11	15:C:174:LEU:HD22	1.94	0.49
16:CC:98:LYS:HB3	31:K:377:G:H5'	1.94	0.49
31:K:88:G:N2	31:K:499:G:O3'	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:K:991:G:N7	34:LL:7:ASN:ND2	2.61	0.49
76:q:33:GLN:HB3	76:q:154:LEU:HD12	1.93	0.49
6:5:1740:A:C2	64:e:28:TYR:HD2	2.27	0.49
6:5:2755:G:OP1	11:A:2:GLY:N	2.44	0.49
9:8:57:C:O2	9:8:61:A:O2'	2.31	0.49
11:A:2:GLY:HA3	11:A:207:VAL:HB	1.94	0.49
14:BB:138:GLU:OE2	44:QQ:19:ARG:NH1	2.46	0.49
15:C:159:GLU:HA	15:C:217:ILE:HB	1.94	0.49
28:II:120:HIS:HD2	56:WW:121:ILE:HG22	1.77	0.49
31:K:1314:U:O2'	48:SS:8:ARG:NH2	2.45	0.49
32:KK:82:ASP:O	76:q:85:ARG:NH2	2.45	0.49
39:O:12:ARG:HE	47:S:171:ARG:HH22	1.61	0.49
47:S:1:MET:CB	47:S:43:ARG:HH11	2.26	0.49
81:v:115:GLN:NE2	81:v:119:GLY:O	2.45	0.49
86:AB:142:ALA:HA	86:AB:145:PHE:HD2	1.77	0.49
91:AE:32:LYS:HE3	91:AE:54:ASN:HD21	1.77	0.49
4:3:35:A:H2'	4:3:36:A:H8	1.77	0.49
6:5:472:G:OP1	77:r:66:ARG:NH1	2.45	0.49
6:5:1009:C:H5''	43:Q:132:LYS:HZ1	1.77	0.49
6:5:2744:U:H2'	6:5:2745:G:H8	1.78	0.49
13:B:95:THR:OG1	13:B:98:GLY:O	2.26	0.49
25:H:47:LEU:HG	25:H:52:LYS:HD2	1.95	0.49
31:K:681:U:O2'	31:K:1160:U:OP1	2.31	0.49
31:K:1291:A:OP2	31:K:1302:G:O2'	2.28	0.49
31:K:1298:G:N7	56:WW:79:HIS:ND1	2.60	0.49
32:KK:31:ASN:HD21	32:KK:55:THR:HG22	1.78	0.49
51:UU:128:GLU:OE2	51:UU:131:LYS:NZ	2.45	0.49
56:WW:52:LYS:HE3	56:WW:80:LEU:HD21	1.95	0.49
63:d:57:MET:HG2	63:d:90:ARG:NH1	2.27	0.49
85:z:228:ILE:HG22	85:z:232:ARG:NH1	2.28	0.49
11:A:30:ARG:HH12	11:A:33:ASP:CG	2.20	0.49
22:F:114:ARG:HD3	43:Q:5:ILE:HD11	1.94	0.49
31:K:1092:G:OP1	44:QQ:2:GLY:N	2.46	0.49
52:U:23:LEU:HG	52:U:110:TYR:HB2	1.92	0.49
85:z:5:ILE:HD12	85:z:16:ILE:HD13	1.94	0.49
6:5:842:G:H5'	15:C:323:ARG:HB2	1.94	0.49
6:5:890:G:H2'	6:5:891:A:H5''	1.94	0.49
6:5:1348:G:H21	61:b:57:MET:HE2	1.78	0.49
6:5:1630:G:H4'	6:5:1631:C:H5'	1.95	0.49
11:A:117:GLU:O	11:A:162:ASN:ND2	2.46	0.49
13:B:59:GLU:HG2	13:B:366:LYS:HD2	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:DD:138:ARG:NH1	17:DD:152:ASP:OD2	2.46	0.49
19:EE:5:GLN:HG2	19:EE:11:GLN:HB2	1.95	0.49
31:K:1489:A:H4'	31:K:1490:G:OP2	2.13	0.49
51:UU:47:LEU:HG	51:UU:50:LYS:HG3	1.95	0.49
6:5:1593:G:OP1	39:O:128:ARG:NH2	2.46	0.49
6:5:1678:A:OP2	60:a:7:LYS:HE3	2.13	0.49
22:F:227:VAL:HA	47:S:39:VAL:HG12	1.95	0.49
31:K:72:C:H41	85:z:170:ARG:NH1	2.11	0.49
31:K:148:U:H2'	31:K:149:A:H8	1.77	0.49
31:K:1416:C:O2	42:PP:3:GLY:N	2.45	0.49
2:1:249:TRP:HA	2:1:249:TRP:CE3	2.47	0.49
6:5:3301:C:H2'	6:5:3302:G:H8	1.76	0.49
24:G:116:LEU:HD21	37:N:29:GLN:HG3	1.95	0.49
31:K:587:A:H5'	31:K:592:C:H41	1.78	0.49
31:K:1036:A:N3	31:K:1844:U:O2'	2.43	0.49
67:h:70:ARG:HB3	67:h:83:LEU:HD22	1.94	0.49
80:u:62:LEU:HD12	80:u:65:ARG:HD2	1.94	0.49
6:5:285:U:O4	74:o:43:ARG:NH1	2.40	0.48
6:5:369:G:N7	69:j:56:ARG:NH1	2.57	0.48
6:5:2383:C:OP1	11:A:193:ARG:NH1	2.46	0.48
6:5:3192:A:H4'	13:B:13:SER:HB2	1.95	0.48
6:5:3231:G:N2	6:5:3484:C:O3'	2.45	0.48
11:A:30:ARG:HH11	11:A:36:GLU:HG2	1.78	0.48
31:K:1563:G:H5''	42:PP:121:ARG:HH22	1.78	0.48
42:PP:77:LYS:HB2	42:PP:94:ARG:NH1	2.27	0.48
54:V:106:VAL:HG21	54:V:132:ILE:HD11	1.95	0.48
85:z:52:ILE:HD11	85:z:109:LEU:HD22	1.95	0.48
22:F:133:ARG:HA	22:F:136:GLU:HG3	1.95	0.48
31:K:798:G:H5''	31:K:798:G:H8	1.78	0.48
31:K:1627:C:OP1	42:PP:83:GLN:NE2	2.47	0.48
90:AD:28:VAL:HG12	91:AE:29:THR:HG22	1.94	0.48
6:5:32:G:H5''	37:N:73:ARG:NH1	2.28	0.48
6:5:555:C:H2'	6:5:556:G:H8	1.79	0.48
6:5:2551:U:O2'	6:5:3459:A:N3	2.45	0.48
6:5:3045:G:OP2	6:5:3046:C:H5''	2.13	0.48
9:8:72:A:O3'	58:Y:75:ARG:NH2	2.47	0.48
10:9:17:GLY:HA2	10:9:27:ARG:HG2	1.95	0.48
16:CC:11:ARG:O	16:CC:18:ARG:NH1	2.46	0.48
31:K:28:U:H2'	31:K:29:G:H8	1.79	0.48
31:K:337:C:H2'	31:K:338:G:H8	1.78	0.48
31:K:792:C:H2'	31:K:793:G:H8	1.77	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:K:1222:G:H5''	84:y:78:MET:HE3	1.95	0.48
39:O:82:ARG:HH11	39:O:85:ARG:NH2	2.05	0.48
64:e:99:ILE:HG21	64:e:108:ARG:HG2	1.95	0.48
84:y:76:MET:O	84:y:159:ARG:NH2	2.44	0.48
6:5:121:A:OP2	24:G:160:LYS:NZ	2.47	0.48
6:5:840:A:OP1	20:E:134:LYS:NZ	2.37	0.48
6:5:3062:U:H5''	6:5:3063:U:H5'	1.93	0.48
28:II:86:ARG:HH22	28:II:106:LYS:HB3	1.79	0.48
30:J:95:ARG:H	30:J:98:ASN:HD22	1.61	0.48
33:L:46:ILE:HB	33:L:49:ARG:HB2	1.96	0.48
38:NN:82:ALA:O	38:NN:86:GLU:CB	2.60	0.48
78:s:145:THR:HG22	78:s:154:ILE:HG13	1.94	0.48
83:x:222:LEU:HA	83:x:225:ILE:HD12	1.95	0.48
3:2:73:A:O3'	3:2:74:C:H6	1.97	0.48
6:5:3327:A:O2'	25:H:43:VAL:O	2.31	0.48
8:7:48:G:OP1	18:D:226:TYR:OH	2.31	0.48
23:GG:21:ARG:HH21	23:GG:88:LEU:HD22	1.79	0.48
31:K:647:U:H2'	31:K:648:A:H8	1.79	0.48
31:K:948:C:H2'	31:K:949:G:H8	1.78	0.48
31:K:951:C:O2'	36:MM:50:LYS:NZ	2.44	0.48
84:y:39:ILE:HG23	84:y:68:ILE:HD13	1.96	0.48
6:5:583:C:O2'	6:5:3423:A:N1	2.45	0.48
6:5:969:C:H2'	6:5:970:G:H8	1.78	0.48
6:5:1332:A:N3	8:7:79:U:O2'	2.45	0.48
6:5:1990:G:H5''	66:g:43:LYS:NZ	2.29	0.48
6:5:2171:G:N1	9:8:113:C:OP1	2.44	0.48
6:5:2568:C:H2'	6:5:2569:A:H8	1.78	0.48
7:6:131:LEU:HB3	7:6:140:TYR:HB3	1.94	0.48
16:CC:118:ALA:HB2	16:CC:141:ARG:HH11	1.78	0.48
31:K:744:G:C2	31:K:798:G:N3	2.82	0.48
43:Q:15:ARG:NH1	43:Q:52:PHE:O	2.40	0.48
43:Q:122:THR:OG1	43:Q:124:ASP:OD1	2.29	0.48
75:p:56:HIS:NE2	75:p:61:MET:SD	2.78	0.48
87:AF:223:U:OP1	89:AI:76:ARG:NH2	2.44	0.48
6:5:303:C:OP2	68:i:33:LEU:HB2	2.13	0.48
6:5:893:C:H2'	6:5:894:A:C8	2.47	0.48
6:5:1448:C:H1'	6:5:1454:A:H2'	1.96	0.48
6:5:1740:A:C2	64:e:28:TYR:HE2	2.18	0.48
6:5:2711:C:H2'	6:5:2712:G:H8	1.78	0.48
6:5:3354:G:H4'	6:5:3355:G:H5'	1.95	0.48
15:C:84:THR:O	15:C:84:THR:HG23	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:K:743:U:O4	31:K:798:G:C6	2.67	0.48
31:K:1010:G:H2'	31:K:1011:A:H8	1.78	0.48
51:UU:19:ALA:HB2	51:UU:75:GLY:HA3	1.95	0.48
3:2:64:U:H2'	3:2:65:C:C6	2.49	0.48
13:B:19:ARG:HE	13:B:234:ARG:HD2	1.78	0.48
13:B:84:MET:HG2	13:B:166:THR:HA	1.94	0.48
21:FF:29:GLN:HE22	21:FF:67:ARG:HG3	1.78	0.48
24:G:119:GLN:HG3	37:N:28:TRP:HH2	1.77	0.48
31:K:65:C:OP1	85:z:136:LYS:NZ	2.41	0.48
33:L:21:ARG:HB3	37:N:197:THR:HG22	1.96	0.48
72:m:71:ARG:HE	72:m:96:ARG:HB3	1.79	0.48
85:z:59:GLN:HB2	85:z:72:ARG:HH12	1.78	0.48
6:5:221:A:N6	6:5:235:G:O2'	2.47	0.48
6:5:485:C:H2'	6:5:486:G:H8	1.79	0.48
6:5:589:C:H2'	6:5:590:G:H8	1.77	0.48
6:5:1912:U:O2'	6:5:1923:U:O2	2.32	0.48
6:5:1913:C:H2'	6:5:1914:G:H8	1.78	0.48
6:5:2418:G:H22	6:5:2431:A:H2	1.62	0.48
6:5:2546:U:H2'	6:5:2547:A:H8	1.78	0.48
8:7:87:G:H5'	47:S:87:ARG:HH11	1.79	0.48
13:B:73:VAL:HG23	54:V:89:ARG:HH11	1.79	0.48
29:JJ:67:THR:OG1	29:JJ:70:LYS:O	2.32	0.48
6:5:288:G:OP1	74:o:43:ARG:NH1	2.47	0.48
6:5:2590:U:O2	41:P:69:ARG:NH2	2.47	0.48
6:5:3187:G:OP1	13:B:62:ARG:NH1	2.46	0.48
10:9:44:ARG:NH2	31:K:1337:C:OP1	2.42	0.48
16:CC:152:ARG:NH2	31:K:189:U:OP1	2.45	0.48
31:K:1004:U:H2'	31:K:1005:G:H8	1.77	0.48
31:K:1213:C:H2'	31:K:1214:A:H8	1.79	0.48
31:K:1228:A:H2'	31:K:1229:G:H8	1.79	0.48
41:P:118:GLN:HE21	41:P:120:ASN:HD21	1.60	0.48
64:e:3:ALA:HB3	64:e:5:ARG:NH1	2.29	0.48
70:k:35:LYS:HG2	70:k:44:THR:HG22	1.96	0.48
76:q:68:ILE:HG23	76:q:120:ARG:HE	1.79	0.48
77:r:94:ARG:HG3	77:r:107:ARG:HH11	1.79	0.48
6:5:375:U:H4'	6:5:409:G:H5'	1.95	0.47
6:5:853:C:H5'	6:5:854:G:OP2	2.14	0.47
6:5:2152:G:O2'	6:5:2155:G:N2	2.47	0.47
6:5:2368:C:H4'	37:N:72:LYS:NZ	2.29	0.47
6:5:2635:C:O2'	37:N:124:ASP:OD1	2.31	0.47
6:5:3208:U:H1'	6:5:3484:C:H1'	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:6:133:ASN:HD21	7:6:139:LYS:NZ	2.11	0.47
18:D:53:VAL:HG11	18:D:159:VAL:HA	1.96	0.47
21:FF:49:PRO:HA	84:y:60:ARG:HH21	1.79	0.47
31:K:1550:G:H3'	31:K:1579:A:H61	1.79	0.47
57:X:118:ASP:OD2	86:AB:67:SER:N	2.45	0.47
6:5:58:G:H8	9:8:34:U:OP2	1.96	0.47
6:5:345:C:OP2	15:C:197:ARG:NH1	2.45	0.47
6:5:767:G:H2'	6:5:768:G:H8	1.80	0.47
6:5:3015:U:H2'	6:5:3016:U:H5'	1.95	0.47
25:H:89:ARG:NH1	25:H:187:VAL:HG13	2.25	0.47
26:HH:32:ILE:HD12	26:HH:55:ILE:HB	1.96	0.47
82:w:55:THR:HA	82:w:58:VAL:HG22	1.96	0.47
83:x:100:ARG:HB2	83:x:114:ILE:HD13	1.94	0.47
6:5:2136:A:H1'	11:A:21:LYS:NZ	2.30	0.47
6:5:2607:C:H41	6:5:3017:C:N4	2.12	0.47
6:5:3447:A:H61	6:5:3541:U:H3	1.62	0.47
31:K:658:U:O2	53:VV:17:ARG:NH2	2.47	0.47
16:CC:144:LYS:NZ	31:K:206:G:O6	2.47	0.47
43:Q:75:ARG:NH1	43:Q:137:VAL:HG11	2.29	0.47
44:QQ:16:LEU:O	50:TT:57:ARG:NH2	2.47	0.47
64:e:28:TYR:N	64:e:28:TYR:CD1	2.82	0.47
82:w:22:ASN:ND2	82:w:34:TYR:OH	2.47	0.47
86:AB:17:LEU:HD11	86:AB:31:MET:HE2	1.96	0.47
87:AF:120:G:N2	87:AF:230[B]:C:O2	2.40	0.47
6:5:1024:C:H4'	61:b:47:LYS:NZ	2.29	0.47
6:5:3343:G:H2'	6:5:3344:G:H8	1.79	0.47
13:B:215:GLU:OE2	13:B:349:LYS:NZ	2.42	0.47
15:C:322:LEU:HD23	15:C:336:ARG:NH1	2.29	0.47
31:K:918:U:O2'	50:TT:56:HIS:O	2.30	0.47
49:T:66:ASN:ND2	61:b:34:GLY:O	2.47	0.47
52:U:22:THR:O	52:U:109:SER:HA	2.15	0.47
60:a:125:LYS:NZ	60:a:145:VAL:HG11	2.29	0.47
83:x:43:PRO:HD2	83:x:46:ILE:HD12	1.96	0.47
84:y:100:ILE:HA	84:y:178:ILE:HD11	1.97	0.47
87:AF:198:G:N2	87:AF:201:A:OP2	2.46	0.47
6:5:1796:A:N6	6:5:2179:C:O2'	2.47	0.47
6:5:2589:A:O2'	41:P:64:ASN:ND2	2.47	0.47
6:5:3410:C:H5'	20:E:269:GLN:HG2	1.97	0.47
6:5:3467:C:O2'	6:5:3535:A:O2'	2.33	0.47
14:BB:53:VAL:HG23	14:BB:175:GLY:HA3	1.95	0.47
18:D:69:ILE:HD11	49:T:32:ARG:HH21	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:D:90:VAL:HG11	18:D:225:GLN:HB3	1.96	0.47
31:K:155:G:H2'	31:K:156:G:H8	1.80	0.47
31:K:1842:C:OP2	73:n:2:ARG:HD3	2.13	0.47
76:q:143:PRO:HA	76:q:158:ASP:OD2	2.15	0.47
6:5:1068:A:OP1	15:C:110:ARG:NH1	2.48	0.47
6:5:1339:A:O2'	6:5:1374:A:OP1	2.32	0.47
6:5:1404:A:N3	6:5:2973:U:O2'	2.40	0.47
6:5:1552:U:H2'	6:5:1553:C:H6	1.79	0.47
6:5:1682:C:N4	77:r:24:THR:OG1	2.47	0.47
6:5:2607:C:H2'	6:5:2608:C:H5'	1.97	0.47
8:7:34:C:N3	8:7:46:C:O2'	2.46	0.47
8:7:94:C:OP1	47:S:46:TYR:OH	2.32	0.47
28:II:132:ARG:HB2	28:II:134:GLN:HE22	1.78	0.47
31:K:1199:A:H5''	34:LL:2:THR:HB	1.95	0.47
31:K:1864:U:O2'	31:K:1866:A:N7	2.45	0.47
43:Q:91:ARG:HD2	60:a:76:ASP:OD2	2.14	0.47
45:R:12:SER:OG	45:R:17:CYS:O	2.31	0.47
45:R:158:GLN:HB3	45:R:162:ARG:NH1	2.30	0.47
50:TT:44:HIS:NE2	50:TT:112:ASP:OD2	2.48	0.47
77:r:35:ARG:NH1	77:r:40:TYR:HE2	2.13	0.47
6:5:679:G:P	22:F:244:ARG:HH12	2.38	0.47
6:5:2604:A:OP1	15:C:72:ALA:HA	2.15	0.47
13:B:76:VAL:HA	13:B:333:LEU:O	2.15	0.47
20:E:153:LEU:HD13	20:E:197:VAL:HG11	1.97	0.47
31:K:1116:C:O2'	31:K:1117:C:O2	2.33	0.47
31:K:1142:G:H2'	31:K:1144:A:OP2	2.15	0.47
31:K:1476:A:H4'	31:K:1477:U:OP2	2.15	0.47
37:N:6:TYR:HA	68:i:44:ILE:HD11	1.96	0.47
82:w:132:LYS:HG3	82:w:156:LEU:HB3	1.96	0.47
86:AB:377:THR:HB	87:AF:193:G:H21	1.79	0.47
6:5:742:C:OP1	6:5:811:C:O2'	2.33	0.47
6:5:1280:A:N1	6:5:1326:C:O2'	2.45	0.47
6:5:1815:C:HO2'	6:5:2555:G:HO2'	1.61	0.47
6:5:3423:A:OP1	20:E:157:THR:OG1	2.26	0.47
8:7:54:A:O4'	30:J:10:ASN:ND2	2.45	0.47
11:A:174:ARG:HA	75:p:69:TRP:HE1	1.79	0.47
14:BB:95:ILE:HD13	14:BB:129:ILE:HG23	1.96	0.47
18:D:205:ALA:HB1	18:D:233:PRO:HB3	1.97	0.47
31:K:5:U:H2'	31:K:6:G:H8	1.80	0.47
40:OO:48:VAL:HG22	40:OO:80:ARG:HE	1.80	0.47
58:Y:34:LEU:HD23	58:Y:38:LEU:HB3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
81:v:204:ILE:HB	81:v:211:LYS:HG3	1.96	0.47
86:AB:344:PRO:O	86:AB:346:SER:N	2.48	0.47
6:5:302:G:H2'	68:i:41:ARG:HH22	1.79	0.47
6:5:1387:A:N3	6:5:1676:G:O2'	2.44	0.47
15:C:33:ARG:HH11	43:Q:22:ASP:HB2	1.79	0.47
27:I:76:MET:HG3	27:I:87:ILE:HD11	1.95	0.47
28:II:91:LYS:O	56:WW:16:THR:OG1	2.29	0.47
31:K:981:A:H2'	31:K:982:G:C8	2.50	0.47
37:N:30:TYR:O	37:N:65:ARG:NH1	2.48	0.47
37:N:149:GLN:O	37:N:152:THR:OG1	2.28	0.47
79:t:15:LEU:HD12	79:t:62:LEU:HD13	1.96	0.47
86:AB:384:ASP:O	86:AB:388:ASP:HB2	2.15	0.47
1:0:132:MET:HG2	1:0:141:CYS:HB2	1.96	0.46
2:1:251:ARG:NH1	2:1:251:ARG:HB2	2.29	0.46
6:5:18:C:H2'	6:5:19:G:H8	1.79	0.46
6:5:393:G:N2	41:P:101:ASN:OD1	2.44	0.46
6:5:1339:A:H5''	6:5:1340:G:H5'	1.97	0.46
6:5:1688:C:H2'	6:5:1689:G:H8	1.80	0.46
31:K:589:G:H5''	31:K:590:A:OP2	2.15	0.46
31:K:613:G:N2	31:K:626:G:OP1	2.45	0.46
31:K:1293:A:H5'	31:K:1294:G:OP2	2.15	0.46
84:y:127:ARG:NE	84:y:135:ARG:O	2.46	0.46
6:5:738:G:H1	6:5:821:A:H2	1.63	0.46
6:5:1098:U:H2'	6:5:1099:G:H8	1.80	0.46
6:5:2283:C:H42	6:5:2309:A:H61	1.63	0.46
7:6:174:VAL:HB	7:6:188:HIS:HB2	1.98	0.46
9:8:8:U:H2'	9:8:9:A:H8	1.81	0.46
17:DD:101:LYS:HE2	17:DD:103:GLU:HB2	1.97	0.46
22:F:71:ALA:HB1	22:F:75:ARG:HH12	1.80	0.46
31:K:309:G:H8	31:K:309:G:P	2.38	0.46
45:R:103:ARG:NH1	45:R:124:TYR:OH	2.47	0.46
77:r:18:ILE:HD11	77:r:20:ARG:HH12	1.81	0.46
6:5:1511:U:OP1	79:t:76:SER:OG	2.33	0.46
6:5:2386:U:OP2	11:A:198:ARG:NH2	2.48	0.46
6:5:2420:G:H3'	68:i:68:ARG:NH1	2.30	0.46
6:5:2942:U:OP2	74:o:61:LYS:HE3	2.16	0.46
6:5:2976:U:H2'	6:5:2977:G:H8	1.80	0.46
13:B:307:TYR:HD2	13:B:366:LYS:HG2	1.81	0.46
28:II:39:ARG:HG2	31:K:1629:C:H5''	1.97	0.46
31:K:5:U:OP2	81:v:230:THR:OG1	2.18	0.46
31:K:1124:C:O2'	32:KK:126:MET:O	2.32	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:N:184:ILE:HG23	37:N:194:ARG:HH11	1.79	0.46
38:NN:103:SER:OG	38:NN:106:GLN:OE1	2.24	0.46
69:j:33:THR:HG22	69:j:40:PRO:HG2	1.97	0.46
79:t:114:ARG:NH2	79:t:161:GLU:OE2	2.48	0.46
6:5:111:C:OP1	67:h:110:LYS:NZ	2.42	0.46
6:5:953:U:P	33:L:186:ARG:HH12	2.38	0.46
11:A:230:PRO:HG2	11:A:233:ARG:HB3	1.97	0.46
20:E:167:PHE:HD1	20:E:178:VAL:HG22	1.81	0.46
28:II:14:ARG:HE	28:II:17:ASN:HA	1.81	0.46
29:JJ:21:LYS:NZ	31:K:921:G:OP2	2.47	0.46
41:P:31:GLU:HG2	41:P:60:PHE:HD1	1.81	0.46
46:RR:56:CYS:SG	46:RR:82:ASN:ND2	2.89	0.46
47:S:80:ILE:HG12	47:S:129:VAL:HG22	1.97	0.46
48:SS:24:LYS:O	48:SS:42:ASN:ND2	2.48	0.46
51:UU:125:ARG:HG3	84:y:55:ARG:NH1	2.30	0.46
86:AB:286:LYS:HB3	86:AB:289:PRO:HG2	1.97	0.46
6:5:2657:U:OP1	24:G:302:ARG:NH2	2.48	0.46
6:5:3421:G:OP2	20:E:191:ARG:NE	2.48	0.46
6:5:3472:G:H2'	6:5:3473:G:H8	1.81	0.46
20:E:291:PHE:HZ	65:f:110:ILE:HD13	1.80	0.46
28:II:84:LEU:HD22	28:II:97:GLN:HB2	1.98	0.46
31:K:1497:G:H5''	31:K:1499:U:OP2	2.15	0.46
32:KK:40:ILE:HB	82:w:209:SER:HB3	1.98	0.46
42:PP:5:THR:HG23	42:PP:7:LYS:H	1.80	0.46
58:Y:18:HIS:O	58:Y:78:TYR:OH	2.34	0.46
82:w:177:LEU:HD13	82:w:182:LEU:HD13	1.97	0.46
6:5:905:C:H2'	6:5:906:A:H8	1.80	0.46
6:5:2607:C:N4	6:5:3017:C:N4	2.64	0.46
15:C:8:ILE:HG23	15:C:149:GLU:OE2	2.15	0.46
31:K:940:U:H3	31:K:1002:U:H3	1.63	0.46
35:M:20:HIS:HB3	35:M:23:LYS:HD2	1.97	0.46
63:d:30:HIS:HA	63:d:33:ILE:HG22	1.98	0.46
66:g:68:SER:HB3	66:g:71:LYS:HD3	1.97	0.46
79:t:153:ASP:O	79:t:157:SER:OG	2.31	0.46
83:x:35:PRO:HD2	83:x:83:PRO:HG2	1.97	0.46
89:AI:62:GLN:HG2	89:AI:67:LEU:HD12	1.97	0.46
10:9:19:ARG:CZ	10:9:32:ARG:HH11	2.28	0.46
15:C:44:LEU:HD21	15:C:120:LYS:HE2	1.98	0.46
31:K:1268:C:O2	56:WW:97:TYR:OH	2.32	0.46
31:K:1275:G:H4'	31:K:1322:G:H22	1.81	0.46
47:S:115:ALA:O	47:S:118:ARG:NH2	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:Y:80:ILE:HG23	58:Y:101:PRO:HG3	1.98	0.46
6:5:1081:C:OP1	15:C:100:ARG:NH2	2.49	0.46
17:DD:54:ARG:NH2	17:DD:98:LEU:O	2.48	0.46
23:GG:54:VAL:HB	23:GG:88:LEU:HG	1.97	0.46
31:K:74:G:N1	31:K:78:C:OP1	2.44	0.46
31:K:600:G:H2'	31:K:601:G:H8	1.81	0.46
45:R:78:ILE:HA	45:R:81:ARG:NH1	2.30	0.46
51:UU:116:ASP:HB3	51:UU:119:LEU:HD23	1.98	0.46
81:v:265:PRO:HA	81:v:268:GLU:HB2	1.96	0.46
83:x:73:ASP:OD1	83:x:77:ARG:NH2	2.49	0.46
86:AB:40:LEU:HD21	86:AB:46:ILE:HB	1.98	0.46
86:AB:43:ASP:HB2	86:AB:258:GLY:HA3	1.98	0.46
6:5:401:A:O2'	6:5:404:A:OP1	2.32	0.46
6:5:899:G:OP2	6:5:899:G:N2	2.34	0.46
6:5:928:G:OP2	15:C:48:ASN:HB2	2.16	0.46
6:5:1298:G:H1	6:5:1309:C:H42	1.63	0.46
18:D:72:ASP:OD1	18:D:72:ASP:N	2.49	0.46
28:II:20:ILE:HD11	28:II:33:ILE:HD11	1.98	0.46
47:S:82:LEU:HB2	47:S:93:MET:HB2	1.98	0.46
68:i:70:LEU:HD22	68:i:87:ARG:NH1	2.30	0.46
87:AF:10:G:H2'	87:AF:11:G:H8	1.80	0.46
89:AI:218:THR:OG1	89:AI:221:GLN:OE1	2.33	0.46
92:AG:17:LEU:HD23	92:AG:20:LEU:HD12	1.96	0.46
6:5:903:A:OP1	37:N:204:ARG:NH1	2.49	0.46
6:5:911:C:H2'	6:5:912:G:H8	1.81	0.46
6:5:1745:U:H1'	15:C:96:CYS:HA	1.98	0.46
12:AA:112:ASN:O	12:AA:117:ASN:ND2	2.49	0.46
22:F:154:TYR:OH	22:F:187:GLU:OE2	2.34	0.46
31:K:1677:U:H2'	31:K:1678:A:H8	1.81	0.46
43:Q:16:LYS:O	43:Q:33:ARG:NH2	2.49	0.46
71:l:23:ILE:HG23	71:l:38:ASN:HB2	1.97	0.46
81:v:196:ILE:HB	81:v:223:TYR:HB2	1.98	0.46
85:z:58:LYS:HA	85:z:107:SER:HB2	1.97	0.46
3:2:7:G:N1	3:2:67:G:C6	2.84	0.45
3:2:7:G:N3	3:2:67:G:N2	2.64	0.45
6:5:1360:G:O2'	18:D:44:TYR:O	2.34	0.45
6:5:2061:G:N1	6:5:2127:U:O2'	2.44	0.45
6:5:2705:A:H5'	59:Z:54:THR:HG23	1.98	0.45
9:8:141:C:H5''	37:N:60:VAL:HG21	1.98	0.45
13:B:234:ARG:HA	13:B:272:LYS:HD2	1.98	0.45
29:JJ:2:PRO:HG2	29:JJ:5:LYS:HD2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:J:35:ARG:HD2	30:J:123:ILE:HA	1.98	0.45
31:K:5:U:H2'	31:K:6:G:C8	2.51	0.45
33:L:176:PHE:O	60:a:138:LYS:NZ	2.49	0.45
38:NN:104:ARG:HA	38:NN:107:ARG:HE	1.80	0.45
47:S:69:GLU:HG3	47:S:71:SER:H	1.81	0.45
59:Z:96:VAL:HG22	59:Z:110:ALA:HB1	1.99	0.45
76:q:63:ARG:HD3	76:q:185:MET:HE1	1.98	0.45
86:AB:405:ARG:HG3	86:AB:408:ARG:HH21	1.80	0.45
2:1:249:TRP:HA	2:1:249:TRP:HE3	1.81	0.45
3:2:47:U:O2'	3:2:50:U:OP1	2.34	0.45
6:5:62:A:P	37:N:172:ARG:HH12	2.38	0.45
6:5:149:A:C8	24:G:249:ARG:NH1	2.85	0.45
6:5:262:G:H2'	6:5:263:G:H8	1.81	0.45
6:5:628:G:H3'	6:5:629:G:H8	1.81	0.45
6:5:1720:G:H2'	6:5:1721:G:H8	1.81	0.45
6:5:2240:G:H1'	54:V:21:PRO:HD2	1.98	0.45
6:5:2809:A:H2'	6:5:2810:G:C8	2.51	0.45
6:5:2844:A:H2'	6:5:2845:G:H8	1.81	0.45
6:5:3332:G:H5'	39:O:176:ARG:HD3	1.98	0.45
13:B:92:TYR:HB2	13:B:159:VAL:HB	1.98	0.45
14:BB:117:PRO:HG2	14:BB:120:ARG:HD3	1.97	0.45
15:C:65:GLU:HB3	15:C:80:ARG:HD3	1.97	0.45
17:DD:28:GLU:HG2	17:DD:43:VAL:HG11	1.97	0.45
27:I:21:ARG:O	27:I:24:ARG:HD3	2.16	0.45
27:I:210:ARG:O	27:I:214:SER:HB3	2.16	0.45
31:K:476:A:N3	31:K:488:U:O2'	2.41	0.45
31:K:551:U:H2'	31:K:552:G:C8	2.52	0.45
64:e:89:LEU:HB3	64:e:118:LEU:HD13	1.97	0.45
87:AF:162:C:H2'	87:AF:163:A:C8	2.52	0.45
6:5:1226:C:O2'	6:5:1248:G:OP1	2.28	0.45
6:5:2309:A:H2	6:5:3496:A:H8	1.65	0.45
18:D:163:LEU:HD11	18:D:173:ILE:HG21	1.97	0.45
22:F:92:ILE:HA	22:F:118:ASN:O	2.16	0.45
52:U:28:PRO:HB2	52:U:34:MET:HG2	1.99	0.45
86:AB:110:GLN:HG2	86:AB:141:ARG:HH21	1.82	0.45
86:AB:383:ASN:HB3	87:AF:208:A:H5''	1.97	0.45
90:AD:31:TYR:HB3	91:AE:26:VAL:HB	1.97	0.45
6:5:894:A:H2'	6:5:895:A:H8	1.82	0.45
6:5:1980:A:OP2	6:5:1981:C:N4	2.49	0.45
15:C:219:LYS:HG3	15:C:222:ARG:NH1	2.20	0.45
23:GG:58:THR:OG1	23:GG:84:ILE:O	2.33	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:HH:38:GLU:HG3	26:HH:49:GLN:HG3	1.97	0.45
37:N:47:LYS:NZ	37:N:51:LEU:HD21	2.31	0.45
38:NN:91:LEU:HD22	38:NN:96:LEU:HD11	1.98	0.45
50:TT:111:MET:HE3	50:TT:116:ALA:HA	1.97	0.45
51:UU:16:LYS:HG3	51:UU:17:LYS:H	1.81	0.45
52:U:65:ARG:HG3	52:U:70:ILE:HG13	1.98	0.45
59:Z:12:LEU:HB2	59:Z:81:MET:HB3	1.97	0.45
66:g:50:PRO:HG3	75:p:61:MET:HE3	1.97	0.45
6:5:3154:A:H62	6:5:3288:G:H21	1.64	0.45
7:6:118:ARG:HH21	7:6:134:THR:H	1.63	0.45
7:6:163:PRO:O	7:6:178:ASN:ND2	2.50	0.45
11:A:131:GLY:H	11:A:169:VAL:HB	1.81	0.45
14:BB:60:ILE:HG23	14:BB:92:VAL:HA	1.98	0.45
78:s:45:MET:SD	78:s:48:ARG:NH2	2.82	0.45
6:5:301:A:N3	6:5:304:G:O2'	2.47	0.45
6:5:766:G:H2'	6:5:767:G:H8	1.80	0.45
6:5:2546:U:O2'	6:5:3204:U:O4	2.31	0.45
6:5:2751:U:O2'	11:A:226:ARG:NH2	2.50	0.45
6:5:3164:U:H2'	6:5:3165:G:H8	1.81	0.45
24:G:127:LEU:HD23	37:N:24:ARG:NH1	2.31	0.45
31:K:300:U:H2'	31:K:301:A:H8	1.82	0.45
31:K:1674:G:OP1	84:y:51:HIS:NE2	2.38	0.45
34:LL:23:CYS:SG	34:LL:24:THR:N	2.89	0.45
42:PP:7:LYS:HB3	51:UU:37:ARG:HB3	1.97	0.45
51:UU:50:LYS:HD3	84:y:49:LEU:HB2	1.99	0.45
59:Z:121:ARG:NH2	59:Z:127:ASN:OD1	2.40	0.45
79:t:104:ILE:HB	79:t:143:VAL:HG22	1.99	0.45
86:AB:6:LEU:HD21	86:AB:42:ALA:HB2	1.98	0.45
6:5:784:C:H2'	6:5:785:G:H8	1.82	0.45
6:5:1852:G:N2	6:5:1855:C:OP2	2.46	0.45
6:5:2756:A:H1'	37:N:87:HIS:HE2	1.81	0.45
8:7:108:G:OP2	18:D:273:LEU:HD13	2.16	0.45
12:AA:85:VAL:HA	12:AA:88:GLN:HG2	1.98	0.45
13:B:239:LYS:HE3	13:B:249:ARG:HG2	1.99	0.45
14:BB:144:ILE:HD12	50:TT:52:ILE:HD11	1.98	0.45
31:K:465:A:OP2	31:K:465:A:H8	2.00	0.45
31:K:1654:G:OP1	42:PP:90:SER:OG	2.34	0.45
38:NN:19:GLN:HE21	83:x:94:LYS:HE2	1.82	0.45
43:Q:178:ARG:H	60:a:51:GLY:HA2	1.81	0.45
45:R:60:ARG:HB3	45:R:64:ARG:HH12	1.82	0.45
59:Z:115:LYS:HZ3	59:Z:119:GLU:CD	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
69:j:50:SER:HB2	69:j:53:ALA:HB3	1.98	0.45
78:s:132:PRO:HD3	87:AF:13:G:H5''	1.97	0.45
82:w:172:VAL:HG22	82:w:185:LYS:HG2	1.98	0.45
86:AB:135:ILE:HD12	86:AB:189:VAL:HG22	1.98	0.45
87:AF:168:G:O2'	87:AF:170:C:OP2	2.35	0.45
6:5:1634:A:OP1	6:5:1644:A:N6	2.50	0.45
12:AA:114:ARG:HH21	31:K:639:C:H5''	1.82	0.45
18:D:6:VAL:O	18:D:9:ASN:ND2	2.50	0.45
28:II:61:GLU:HA	28:II:64:VAL:HG22	1.98	0.45
59:Z:103:ASP:OD2	59:Z:106:LEU:HD13	2.17	0.45
6:5:21:G:OP2	69:j:43:ARG:NH2	2.50	0.45
6:5:33:A:H3'	6:5:47:A:H61	1.82	0.45
6:5:743:A:H5'	6:5:744:C:OP2	2.17	0.45
6:5:2351:A:OP1	11:A:196:TRP:NE1	2.46	0.45
6:5:3258:C:O2'	25:H:155:SER:OG	2.27	0.45
14:BB:106:ARG:NH1	31:K:800:U:O4	2.47	0.45
19:EE:149:ALA:HB1	31:K:867:G:H5'	1.98	0.45
22:F:134:ILE:HG23	22:F:135:VAL:HG13	1.99	0.45
25:H:34:LEU:HD11	25:H:149:ASN:HB3	1.99	0.45
25:H:115:ARG:NH1	25:H:123:ILE:HG21	2.32	0.45
27:I:95:HIS:HB3	27:I:126:VAL:O	2.17	0.45
31:K:944:A:H61	31:K:982:G:H1	1.65	0.45
33:L:10:LEU:HA	43:Q:168:ARG:NH1	2.31	0.45
45:R:139:MET:O	45:R:143:HIS:ND1	2.38	0.45
52:U:46:ARG:HH22	52:U:89:LYS:HE2	1.81	0.45
76:q:94:THR:O	76:q:186:ARG:NH2	2.50	0.45
6:5:713:C:H41	6:5:842:G:H21	1.65	0.45
6:5:1075:A:H1'	33:L:12:PRO:HB2	1.98	0.45
6:5:1690:G:O3'	15:C:140:LYS:NZ	2.50	0.45
17:DD:38:ARG:HD2	17:DD:127:ARG:HH22	1.81	0.45
17:DD:93:LYS:HB3	17:DD:96:TYR:HD2	1.82	0.45
24:G:134:ASN:ND2	24:G:137:THR:OG1	2.50	0.45
25:H:24:THR:OG1	25:H:37:ASP:OD1	2.35	0.45
31:K:941:C:H2'	31:K:942:G:C8	2.49	0.45
31:K:1003:U:H1'	80:u:124:HIS:HE1	1.83	0.45
42:PP:10:ASN:H	42:PP:142:LYS:NZ	2.15	0.45
67:h:67:GLU:HA	67:h:70:ARG:HG2	1.97	0.45
72:m:84:CYS:SG	72:m:85:ARG:N	2.89	0.45
85:z:1:MET:HE3	85:z:106:LEU:HB2	1.99	0.45
85:z:98:ARG:NE	85:z:105:ASN:O	2.50	0.45
3:2:63:A:C8	3:2:63:A:OP2	2.70	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:5:527:C:H2'	6:5:528:G:H8	1.81	0.44
6:5:772:G:H2'	6:5:773:A:H8	1.81	0.44
31:K:596:U:O2'	31:K:645:C:O2	2.33	0.44
35:M:7:VAL:HG13	35:M:27:ILE:HD13	1.98	0.44
51:UU:33:LYS:HA	51:UU:38:PRO:HA	1.99	0.44
64:e:86:GLU:HA	64:e:89:LEU:HD23	1.98	0.44
68:i:33:LEU:HD11	68:i:38:LYS:HD2	1.98	0.44
80:u:33:VAL:HA	80:u:96:CYS:HB2	1.97	0.44
3:2:19:G:H8	3:2:57:G:H21	1.64	0.44
6:5:590:G:H2'	6:5:591:G:H8	1.82	0.44
6:5:909:U:H2'	6:5:910:G:H8	1.83	0.44
6:5:1392:G:O6	6:5:1417:G:N2	2.50	0.44
6:5:1885:C:H2'	6:5:1886:G:C8	2.52	0.44
6:5:2966:A:N6	6:5:3017:C:N3	2.66	0.44
7:6:40:ILE:HB	7:6:59:LEU:HB2	1.99	0.44
11:A:94:ALA:HB1	11:A:100:ASN:HD21	1.82	0.44
31:K:107:A:H2'	31:K:108:G:H8	1.82	0.44
31:K:744:G:C5	31:K:798:G:C2	3.04	0.44
31:K:1228:A:H2'	31:K:1229:G:C8	2.52	0.44
50:TT:42:MET:HE2	50:TT:49:GLU:HA	1.99	0.44
53:VV:46:HIS:HB3	53:VV:101:LEU:HD11	1.99	0.44
81:v:263:LYS:HD3	81:v:268:GLU:OE2	2.17	0.44
3:2:7:G:C6	3:2:67:G:N1	2.85	0.44
6:5:718:U:OP2	20:E:68:LYS:HE2	2.17	0.44
6:5:877:G:H8	6:5:877:G:O5'	2.00	0.44
6:5:911:C:H2'	6:5:912:G:C8	2.52	0.44
6:5:1191:A:H2	11:A:208:GLU:HG3	1.82	0.44
6:5:1774:A:H1'	6:5:1776:C:OP2	2.16	0.44
6:5:1885:C:H2'	6:5:1886:G:H8	1.82	0.44
7:6:212:LYS:HA	7:6:235:ILE:HG13	2.00	0.44
7:6:214:GLY:O	7:6:232:GLY:N	2.45	0.44
11:A:6:ARG:HH12	11:A:199:VAL:H	1.65	0.44
14:BB:49:LYS:HB2	14:BB:61:ILE:HG23	1.98	0.44
15:C:78:ARG:HB3	15:C:88:GLY:HA2	1.99	0.44
31:K:604:A:N3	31:K:639:C:O2'	2.45	0.44
31:K:652:U:H2'	31:K:653:A:C8	2.52	0.44
31:K:1128:C:H2'	31:K:1129:G:C8	2.53	0.44
31:K:1527:C:H5'	51:UU:144:SER:HB3	1.98	0.44
31:K:1650:A:OP1	51:UU:137:ALA:N	2.51	0.44
60:a:81:LEU:HD22	60:a:106:SER:HB2	1.99	0.44
60:a:82:VAL:HG21	60:a:101:ILE:HG12	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:e:85:LEU:HD11	64:e:111:ILE:HG23	1.99	0.44
78:s:131:GLY:HA2	87:AF:13:G:H5'	1.99	0.44
83:x:9:LEU:HB2	83:x:30:ARG:HD3	1.99	0.44
6:5:102:G:O2'	6:5:939:U:O2'	2.28	0.44
6:5:1016:C:O2'	43:Q:73:PRO:O	2.30	0.44
6:5:2340:A:HO2'	69:j:2:THR:N	2.15	0.44
6:5:2630:U:H2'	6:5:2631:G:H8	1.82	0.44
27:I:66:GLU:OE2	27:I:69:ARG:NH1	2.50	0.44
30:J:112:HIS:ND1	30:J:126:TYR:O	2.44	0.44
31:K:486:A:H1'	31:K:513:G:H22	1.83	0.44
31:K:1206:G:O2'	31:K:1208:A:OP1	2.36	0.44
31:K:1662:U:O4	31:K:1663:A:N6	2.50	0.44
37:N:120:TRP:HE1	37:N:123:GLU:HB3	1.82	0.44
42:PP:6:VAL:O	42:PP:11:GLN:NE2	2.50	0.44
52:U:60:VAL:HG13	52:U:75:GLU:HB2	1.98	0.44
80:u:159:GLN:OE1	80:u:162:ARG:NH1	2.50	0.44
6:5:114:G:N2	6:5:270:C:O2'	2.50	0.44
6:5:635:G:OP1	25:H:54:ARG:NH2	2.50	0.44
6:5:1045:C:H2'	33:L:198:ARG:HH12	1.83	0.44
6:5:1910:A:N3	6:5:1932:C:O2'	2.51	0.44
6:5:2670:C:H2'	6:5:2671:G:C8	2.52	0.44
6:5:3205:A:H2	6:5:3233:G:H21	1.65	0.44
19:EE:108:ASN:ND2	31:K:397:G:OP2	2.50	0.44
39:O:142:ALA:HA	39:O:145:VAL:HG12	1.99	0.44
63:d:94:GLU:HG3	63:d:95:ASP:H	1.83	0.44
65:f:11:PHE:HE1	65:f:26:ALA:HB1	1.82	0.44
72:m:71:ARG:HH11	72:m:96:ARG:HB3	1.81	0.44
83:x:105:THR:HG23	83:x:106:LYS:HD2	1.98	0.44
90:AD:32:ARG:O	90:AD:36:GLY:CA	2.66	0.44
3:2:64:U:C5	3:2:64:U:OP2	2.70	0.44
6:5:693:A:N7	6:5:844:G:O2'	2.46	0.44
6:5:896:G:H21	15:C:95:MET:HB2	1.83	0.44
6:5:1376:U:OP2	22:F:201:LYS:HD2	2.17	0.44
6:5:1425:A:O3'	65:f:19:ARG:NH2	2.51	0.44
6:5:1511:U:H1'	6:5:1513:G:OP2	2.18	0.44
6:5:1570:A:OP1	47:S:88:SER:OG	2.36	0.44
6:5:2044:C:O2'	66:g:54:ARG:NH2	2.49	0.44
6:5:2228:A:O2'	13:B:228:TYR:O	2.27	0.44
6:5:3286:C:OP2	13:B:30:LYS:HG3	2.18	0.44
6:5:3472:G:H2'	6:5:3473:G:C8	2.53	0.44
8:7:42:A:C1'	30:J:75:ARG:HH12	2.28	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:30:ARG:NH1	11:A:36:GLU:HG2	2.33	0.44
23:GG:25:THR:HG21	82:w:7:LYS:HE2	1.99	0.44
25:H:173:ARG:HD3	72:m:98:LYS:HE2	1.99	0.44
31:K:309:G:OP1	31:K:309:G:C8	2.71	0.44
31:K:311:C:C3'	31:K:311:C:C6	3.01	0.44
31:K:527:C:H2'	31:K:528:A:H8	1.83	0.44
31:K:652:U:H2'	31:K:653:A:H8	1.82	0.44
31:K:798:G:H5''	31:K:798:G:C8	2.52	0.44
31:K:1536:G:H2'	31:K:1537:A:C8	2.52	0.44
31:K:1562:C:H2'	31:K:1563:G:C8	2.53	0.44
33:L:186:ARG:HE	68:i:9:VAL:HG11	1.82	0.44
37:N:159:ARG:HB3	37:N:164:LEU:HB2	1.98	0.44
42:PP:56:ARG:NH1	42:PP:99:VAL:HB	2.33	0.44
43:Q:6:ARG:HH12	61:b:18:ARG:C	2.20	0.44
45:R:60:ARG:HB3	45:R:64:ARG:NH1	2.32	0.44
48:SS:60:GLU:OE1	48:SS:69:TRP:NE1	2.51	0.44
74:o:9:ARG:HA	74:o:20:PRO:HA	1.98	0.44
87:AF:19:C:H2'	87:AF:20:G:H8	1.83	0.44
90:AD:54:ASP:OD1	90:AD:54:ASP:N	2.49	0.44
6:5:890:G:C2'	6:5:891:A:H5''	2.48	0.44
6:5:1413:U:H2'	6:5:1414:G:C8	2.53	0.44
6:5:1980:A:H5'	6:5:2163:C:H5'	1.99	0.44
6:5:2136:A:H2'	6:5:2137:A:C8	2.53	0.44
6:5:2591:C:H2'	6:5:2592:A:H8	1.83	0.44
6:5:2614:G:H2'	6:5:2615:A:H8	1.81	0.44
14:BB:7:LYS:HE3	14:BB:28:LEU:HD23	2.00	0.44
20:E:182:LEU:HD11	20:E:186:ARG:NH1	2.32	0.44
31:K:649:U:H2'	31:K:650:A:H8	1.81	0.44
33:L:14:PHE:HE1	37:N:198:LEU:HD11	1.83	0.44
39:O:70:PRO:HB2	39:O:72:HIS:CE1	2.52	0.44
42:PP:65:TYR:HE1	42:PP:128:GLN:HG3	1.82	0.44
45:R:4:LEU:HD11	45:R:29:THR:HG23	2.00	0.44
86:AB:330:ARG:NH2	86:AB:384:ASP:OD1	2.51	0.44
87:AF:120:G:N2	87:AF:230[A]:C:O2	2.41	0.44
89:AI:112:ASP:OD2	89:AI:114:ARG:NH1	2.51	0.44
2:1:246:LEU:N	2:1:246:LEU:HD13	2.32	0.44
6:5:416:C:H2'	6:5:417:G:H8	1.83	0.44
6:5:939:U:H5'	6:5:940:G:OP2	2.18	0.44
6:5:1421:C:H2'	6:5:1422:G:H8	1.82	0.44
6:5:1754:G:O2'	6:5:2557:G:O6	2.30	0.44
6:5:2699:G:H5'	66:g:93:ARG:HD2	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:5:2804:A:OP2	74:o:100:LYS:NZ	2.40	0.44
6:5:3274:C:H2'	6:5:3275:A:H8	1.83	0.44
6:5:3381:G:O6	6:5:3400:C:N4	2.51	0.44
7:6:87:LEU:HD21	7:6:108:VAL:HG11	2.00	0.44
31:K:1244:U:H2'	31:K:1245:G:H8	1.82	0.44
46:RR:54:SER:OG	46:RR:55:ASN:N	2.48	0.44
56:WW:98:ASN:ND2	56:WW:121:ILE:O	2.50	0.44
70:k:24:LYS:HA	70:k:67:LYS:O	2.18	0.44
78:s:13:TYR:OH	78:s:61:MET:SD	2.72	0.44
84:y:50:PRO:HB3	84:y:69:VAL:HG12	2.00	0.44
87:AF:22:C:OP2	91:AE:25:SER:OG	2.27	0.44
6:5:66:A:O2'	6:5:320:C:O2	2.29	0.44
6:5:472:G:H2'	6:5:473:G:H8	1.82	0.44
6:5:1569:U:H2'	6:5:1570:A:H8	1.83	0.44
6:5:1779:U:H2'	6:5:1780:G:H8	1.83	0.44
6:5:2174:G:O2'	71:l:3:SER:O	2.35	0.44
6:5:2607:C:H5	6:5:3017:C:N4	2.11	0.44
7:6:176:VAL:O	7:6:185:LYS:N	2.51	0.44
22:F:213:SER:OG	22:F:246:MET:O	2.36	0.44
24:G:119:GLN:HA	24:G:122:ILE:HB	2.00	0.44
26:HH:20:SER:HB3	26:HH:59:ILE:HD11	2.00	0.44
31:K:1439:A:H8	31:K:1439:A:OP2	2.00	0.44
35:M:53:LYS:HA	47:S:157:ARG:HH22	1.83	0.44
77:r:32:LEU:HD11	77:r:106:LEU:HD12	2.00	0.44
89:AI:238:TYR:O	89:AI:242:ASN:ND2	2.51	0.44
6:5:553:G:H1'	77:r:100:ASN:HD21	1.83	0.43
6:5:1059:C:OP1	43:Q:150:ARG:NH2	2.50	0.43
6:5:1236:C:H41	6:5:2948:A:H5''	1.83	0.43
6:5:1453:G:N3	6:5:1604:C:O2'	2.49	0.43
6:5:2895:A:H1'	18:D:36:LEU:HD23	2.00	0.43
31:K:84:A:H5''	38:NN:122:LYS:HD2	2.00	0.43
31:K:382:C:H2'	31:K:383:G:H8	1.83	0.43
49:T:127:GLN:HE21	49:T:129:LYS:HB2	1.83	0.43
58:Y:51:LYS:HG3	58:Y:72:GLN:HA	1.98	0.43
85:z:12:CYS:SG	85:z:13:GLN:N	2.91	0.43
6:5:259:C:H4'	6:5:260:C:OP2	2.14	0.43
6:5:432:G:H5''	64:e:16:ARG:HH12	1.83	0.43
6:5:2056:G:H4'	45:R:117:ARG:NH1	2.33	0.43
6:5:2202:G:O2'	6:5:3214:G:OP1	2.35	0.43
6:5:2542:U:H2'	6:5:2543:A:H8	1.83	0.43
6:5:2705:A:O2'	24:G:86:GLU:O	2.35	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:5:2744:U:H2'	6:5:2745:G:C8	2.53	0.43
6:5:2950:A:OP1	74:o:58:LYS:NZ	2.51	0.43
6:5:3197:U:H5'	13:B:53:MET:HB2	1.99	0.43
15:C:152:LEU:HD21	15:C:174:LEU:HD13	2.00	0.43
16:CC:65:PHE:HD2	16:CC:104:ILE:HD13	1.82	0.43
31:K:520:A:O2'	31:K:825:A:N3	2.44	0.43
31:K:1033:G:N1	31:K:1080:A:O2'	2.42	0.43
31:K:1592:C:OP2	40:OO:104:ARG:NH2	2.51	0.43
42:PP:104:LEU:HD22	42:PP:121:ARG:HG3	2.01	0.43
66:g:78:TYR:HE2	66:g:90:ARG:HD2	1.83	0.43
87:AF:133:A:H61	87:AF:164:G:H22	1.66	0.43
87:AF:166:U:H5	89:AI:142:ARG:HH12	1.66	0.43
3:2:28:U:H2'	3:2:29:A:H8	1.83	0.43
6:5:67:C:OP2	6:5:306:G:N2	2.50	0.43
6:5:369:G:OP2	69:j:52:LYS:HE3	2.18	0.43
6:5:824:C:H2'	6:5:825:G:H8	1.83	0.43
6:5:1004:G:H21	6:5:1647:G:H1	1.65	0.43
6:5:2351:A:O2'	11:A:179:ILE:O	2.25	0.43
9:8:11:C:H2'	9:8:12:G:H8	1.83	0.43
18:D:12:TYR:O	18:D:16:TYR:HB2	2.17	0.43
28:II:6:PRO:HG2	28:II:58:GLU:HG2	2.01	0.43
31:K:1869:A:N6	80:u:114:VAL:O	2.51	0.43
37:N:47:LYS:HZ3	37:N:51:LEU:HD21	1.84	0.43
37:N:68:ARG:NH1	37:N:124:ASP:O	2.44	0.43
39:O:175:MET:HE3	39:O:179:LYS:HE3	1.99	0.43
60:a:119:LYS:HA	60:a:140:VAL:HG13	2.00	0.43
62:c:90:ARG:HH12	75:p:44:LYS:N	2.15	0.43
76:q:77:ILE:HG12	76:q:99:ILE:HD12	1.99	0.43
78:s:14:PHE:HA	78:s:17:ILE:HG22	2.00	0.43
89:AI:126:ALA:HA	89:AI:150:ARG:HD2	1.99	0.43
6:5:1640:A:C8	22:F:45:ARG:NH1	2.87	0.43
6:5:2913:U:O2'	74:o:31:ASP:OD1	2.36	0.43
13:B:54:THR:OG1	13:B:369:ASP:O	2.29	0.43
31:K:649:U:H2'	31:K:650:A:C8	2.53	0.43
31:K:807:G:H2'	31:K:808:A:C8	2.53	0.43
31:K:1030:A:H2'	31:K:1031:A:H8	1.83	0.43
31:K:1311:C:OP1	46:RR:40:LYS:NZ	2.52	0.43
36:MM:56:VAL:HG12	36:MM:81:VAL:HG23	2.01	0.43
52:U:84:LYS:HG3	52:U:102:VAL:HG11	2.00	0.43
84:y:176:GLU:OE1	84:y:187:SER:OG	2.33	0.43
86:AB:102:ASN:HB2	86:AB:185:GLU:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:5:32:G:H5''	37:N:73:ARG:HH12	1.83	0.43
6:5:584:G:H5'	65:f:89:ARG:HH22	1.83	0.43
6:5:1020:C:H5''	43:Q:144:LYS:HG2	2.01	0.43
6:5:1470:G:H2'	6:5:1471:A:C8	2.54	0.43
6:5:1852:G:H2'	6:5:1854:G:OP2	2.18	0.43
6:5:1966:A:H4'	59:Z:115:LYS:NZ	2.34	0.43
6:5:3540:U:H5''	41:P:43:LYS:HE2	2.00	0.43
31:K:730:C:H2'	31:K:731:G:H8	1.84	0.43
31:K:798:G:H8	31:K:798:G:C5'	2.31	0.43
31:K:1373:C:O2	31:K:1465:A:O2'	2.36	0.43
31:K:1568:C:O2	31:K:1627:C:O2'	2.35	0.43
79:t:15:LEU:HD11	79:t:32:ILE:HD11	2.00	0.43
90:AD:25:ALA:HA	90:AD:43:THR:O	2.18	0.43
4:3:6:G:N2	4:3:67:U:O2	2.35	0.43
6:5:51:A:OP1	69:j:48:ASN:ND2	2.51	0.43
6:5:161:G:H2'	6:5:162:A:H8	1.83	0.43
6:5:281:U:H2'	6:5:282:G:C8	2.54	0.43
6:5:1123:A:O2'	6:5:1124:A:O4'	2.36	0.43
6:5:3353:C:N4	47:S:171:ARG:O	2.52	0.43
7:6:58:ALA:HB3	51:UU:97:GLN:HE21	1.84	0.43
8:7:63:C:H5'	8:7:64:G:H5''	1.99	0.43
28:II:75:ARG:HH21	28:II:95:TYR:HB2	1.83	0.43
31:K:183:G:O2'	31:K:184:G:O5'	2.37	0.43
54:V:87:SER:HB2	55:W:19:ARG:HH11	1.83	0.43
64:e:100:ALA:O	64:e:108:ARG:NH1	2.52	0.43
87:AF:203:G:H2'	87:AF:204:G:H8	1.83	0.43
90:AD:29:LEU:HB3	91:AE:28:ILE:HB	2.00	0.43
6:5:445:C:OP2	6:5:855:A:N6	2.52	0.43
6:5:1578:A:H62	6:5:3004:C:H1'	1.82	0.43
9:8:8:U:H2'	9:8:9:A:C8	2.53	0.43
27:I:54:SER:HB2	27:I:135:ILE:HD11	2.00	0.43
31:K:1533:A:O2'	84:y:81:ARG:NH2	2.52	0.43
65:f:47:CYS:HB3	65:f:103:VAL:HG12	2.00	0.43
81:v:201:GLY:N	81:v:221:ASP:OD2	2.51	0.43
85:z:59:GLN:HB2	85:z:72:ARG:NH1	2.33	0.43
6:5:2205:A:OP1	45:R:83:GLY:N	2.45	0.43
6:5:3218:A:OP1	45:R:62:ARG:NH2	2.51	0.43
17:DD:164:PRO:HB3	17:DD:170:PRO:HA	2.00	0.43
22:F:147:LYS:HB3	22:F:244:ARG:NH1	2.33	0.43
25:H:113:GLU:OE2	25:H:125:ARG:HG2	2.19	0.43
30:J:18:ARG:HG3	30:J:135:GLY:HA3	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:K:1245:G:O2'	31:K:1492:U:OP1	2.37	0.43
31:K:1553:C:H42	82:w:76:ARG:HH22	1.66	0.43
36:MM:95:ILE:HD11	36:MM:126:ILE:HD12	2.01	0.43
45:R:8:LYS:HG2	45:R:19:LYS:HB2	2.00	0.43
45:R:78:ILE:HA	45:R:81:ARG:HH12	1.83	0.43
46:RR:62:VAL:HA	46:RR:65:VAL:HG12	2.01	0.43
51:UU:62:ARG:O	51:UU:96:TYR:OH	2.37	0.43
79:t:18:THR:HA	79:t:57:ARG:HG2	2.01	0.43
80:u:103:MET:HE2	80:u:215:VAL:HG23	2.01	0.43
6:5:288:G:OP2	6:5:290:A:H4'	2.18	0.43
6:5:372:A:HO2'	6:5:407:G:H22	1.66	0.43
6:5:3156:G:O6	6:5:3287:A:N6	2.52	0.43
6:5:3451:A:O2'	41:P:55:LYS:NZ	2.52	0.43
6:5:3471:U:H2'	6:5:3472:G:H8	1.83	0.43
17:DD:17:ARG:O	31:K:21:U:O2'	2.34	0.43
26:HH:32:ILE:HD11	26:HH:60:ARG:HD2	2.00	0.43
31:K:400:C:OP2	31:K:400:C:H6	2.02	0.43
31:K:490:C:O2'	31:K:574:A:N1	2.51	0.43
31:K:600:G:OP2	31:K:631:U:H5''	2.19	0.43
31:K:848:U:H2'	31:K:849:A:H8	1.84	0.43
31:K:987:A:OP2	31:K:988:C:H5	2.02	0.43
31:K:1821:U:H2'	31:K:1822:A:H8	1.84	0.43
33:L:106:SER:OG	33:L:109:SER:OG	2.32	0.43
37:N:5:LYS:HZ3	68:i:37:THR:HG22	1.83	0.43
51:UU:76:GLY:H	51:UU:79:ALA:HB3	1.84	0.43
59:Z:46:ILE:HA	59:Z:70:SER:HA	2.01	0.43
60:a:117:LEU:HB3	60:a:140:VAL:HG21	2.01	0.43
79:t:141:CYS:SG	79:t:142:ASN:N	2.91	0.43
80:u:181:LEU:HA	80:u:184:VAL:HG22	2.01	0.43
86:AB:333:TYR:HD1	86:AB:379:MET:HE3	1.84	0.43
86:AB:411:GLY:O	87:AF:195:U:O2'	2.35	0.43
89:AI:158:ALA:HB2	89:AI:185:LEU:HD12	2.00	0.43
6:5:507:C:H2'	6:5:508:G:H8	1.84	0.43
6:5:1205:C:H2'	6:5:1206:A:C8	2.54	0.43
6:5:1817:G:H8	6:5:1817:G:OP2	2.02	0.43
6:5:2290:G:H2'	6:5:2291:G:H8	1.84	0.43
6:5:2989:U:OP1	6:5:2991:C:N4	2.52	0.43
6:5:3157:G:O2'	13:B:14:LEU:O	2.33	0.43
6:5:3481:U:O2'	13:B:372:SER:OG	2.36	0.43
14:BB:66:VAL:HG22	14:BB:96:ALA:HB1	2.01	0.43
14:BB:114:GLN:NE2	31:K:874:G:N3	2.56	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:K:62:G:O2'	31:K:172:U:OP1	2.36	0.43
31:K:216:C:O2	31:K:309:G:N2	2.52	0.43
31:K:311:C:H3'	31:K:311:C:C6	2.54	0.43
31:K:983:A:OP1	31:K:1073:U:O2'	2.28	0.43
31:K:1007:C:H2'	31:K:1008:A:C8	2.54	0.43
31:K:1083:A:N7	31:K:1841:C:O2'	2.42	0.43
42:PP:11:GLN:CD	42:PP:62:ARG:HH11	2.26	0.43
42:PP:12:GLN:HG3	42:PP:16:ARG:HH22	1.83	0.43
45:R:103:ARG:NH1	45:R:124:TYR:CZ	2.87	0.43
52:U:103:VAL:HG21	52:U:113:ARG:HD3	2.01	0.43
54:V:88:TYR:HE2	54:V:90:ARG:HE	1.66	0.43
59:Z:51:ARG:HB2	59:Z:65:ARG:HD2	2.01	0.43
67:h:81:LEU:HD23	67:h:84:ARG:HD2	1.99	0.43
69:j:14:LYS:NZ	71:l:51:LEU:HB3	2.34	0.43
90:AD:41:LYS:HB2	90:AD:50:VAL:HG23	2.00	0.43
1:0:138:ARG:HB2	1:0:149:CYS:HA	1.99	0.42
6:5:272:G:H5''	37:N:8:GLN:HE22	1.84	0.42
6:5:1056:G:H4'	43:Q:180:ARG:NH1	2.34	0.42
6:5:1086:G:H2'	6:5:1087:A:H8	1.84	0.42
6:5:1116:C:O2'	6:5:2062:C:OP1	2.33	0.42
6:5:1413:U:H2'	6:5:1414:G:H8	1.84	0.42
6:5:2808:G:H2'	6:5:2809:A:H8	1.83	0.42
6:5:3458:G:OP1	13:B:271:GLN:NE2	2.52	0.42
16:CC:27:TYR:HB2	31:K:381:C:H41	1.84	0.42
21:FF:55:VAL:O	84:y:34:SER:OG	2.29	0.42
22:F:106:LYS:HD2	22:F:109:GLN:HE21	1.84	0.42
26:HH:16:LYS:NZ	81:v:255:LEU:O	2.43	0.42
30:J:27:GLY:HA2	30:J:68:ILE:HG23	2.01	0.42
31:K:309:G:H8	31:K:309:G:OP1	2.02	0.42
38:NN:43:LYS:HA	38:NN:46:LYS:HG2	2.01	0.42
44:QQ:18:TYR:HE1	50:TT:55:ASP:HA	1.84	0.42
76:q:122:LEU:HD13	76:q:142:LEU:HB3	2.01	0.42
84:y:86:LYS:HA	84:y:89:THR:HG22	1.99	0.42
87:AF:124:G:O6	87:AF:226:U:O2	2.37	0.42
87:AF:148:G:OP1	88:AC:14:ARG:NH2	2.52	0.42
6:5:29:G:H5''	37:N:172:ARG:HG2	2.00	0.42
6:5:277:G:H1'	68:i:82:ARG:HH12	1.83	0.42
6:5:2142:C:H2'	6:5:2143:G:C8	2.54	0.42
6:5:2174:G:H4'	71:l:5:LYS:HB2	2.02	0.42
6:5:2231:G:OP1	13:B:248:LEU:N	2.43	0.42
6:5:2754:G:H5'	11:A:233:ARG:HB2	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:5:2844:A:H2'	6:5:2845:G:C8	2.54	0.42
6:5:3027:U:OP1	54:V:50:ASN:ND2	2.52	0.42
6:5:3350:G:O2'	6:5:3354:G:OP1	2.37	0.42
6:5:3433:G:H2'	6:5:3434:G:C8	2.55	0.42
6:5:3471:U:H2'	6:5:3472:G:C8	2.54	0.42
8:7:112:U:H2'	8:7:113:G:H8	1.84	0.42
10:9:50:ILE:HG23	82:w:15:GLY:HA3	2.00	0.42
20:E:53:VAL:HB	20:E:56:ILE:HB	2.01	0.42
31:K:65:C:N4	85:z:134:GLY:O	2.49	0.42
31:K:1152:U:O3'	50:TT:19:LYS:NZ	2.51	0.42
31:K:1829:G:H1'	31:K:1850:A:H2	1.84	0.42
47:S:11:LYS:HD2	47:S:29:ARG:HD2	2.01	0.42
61:b:36:ASP:HA	61:b:37:PRO:HD3	1.91	0.42
81:v:75:ILE:HD11	81:v:80:GLU:HB2	2.00	0.42
6:5:356:A:N6	71:l:37:TYR:O	2.49	0.42
6:5:1689:G:H1'	15:C:45:ARG:NH1	2.35	0.42
6:5:1850:G:H21	6:5:2370:G:H21	1.67	0.42
6:5:2766:G:H8	6:5:2766:G:O5'	2.02	0.42
6:5:3042:G:O2'	72:m:74:TYR:O	2.33	0.42
6:5:3460:C:OP2	6:5:3461:G:N2	2.52	0.42
11:A:201:GLY:HA3	11:A:209:HIS:CE1	2.54	0.42
15:C:28:PHE:HA	15:C:129:ALA:HA	2.02	0.42
20:E:144:ARG:NH1	65:f:110:ILE:OXT	2.46	0.42
31:K:1240:A:C5	56:WW:100:LYS:HB2	2.54	0.42
45:R:119:MET:HB2	45:R:149:LYS:NZ	2.35	0.42
47:S:13:VAL:HG23	47:S:62:VAL:HB	2.01	0.42
52:U:84:LYS:HG2	52:U:88:LYS:HE2	2.01	0.42
59:Z:83:THR:HG23	59:Z:85:TYR:H	1.84	0.42
6:5:85:G:O2'	6:5:97:G:O6	2.38	0.42
6:5:586:G:H2'	6:5:587:A:C8	2.54	0.42
6:5:1188:C:H5''	11:A:15:VAL:HG21	1.99	0.42
6:5:2296:C:H2'	6:5:2297:A:C8	2.55	0.42
6:5:2541:C:OP2	54:V:51:ARG:HG2	2.19	0.42
6:5:2904:U:H4'	49:T:7:LYS:HB2	2.01	0.42
7:6:15:ASN:HB2	7:6:37:ASP:OD2	2.20	0.42
9:8:26:C:O2'	15:C:53:ALA:O	2.31	0.42
20:E:48:ARG:HB2	20:E:64:MET:HE1	2.02	0.42
22:F:115:GLN:HB2	22:F:118:ASN:HD21	1.84	0.42
31:K:85:A:H5''	38:NN:118:ARG:HE	1.84	0.42
31:K:309:G:O5'	31:K:309:G:C8	2.70	0.42
31:K:943:U:H2'	31:K:944:A:C8	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:K:1173:A:H5'	73:n:17:ARG:NH1	2.35	0.42
39:O:81:TRP:HD1	39:O:102:LEU:HD23	1.84	0.42
59:Z:27:LYS:HB2	59:Z:42:LEU:HB3	2.01	0.42
86:AB:246:ILE:HG12	86:AB:272:PHE:HB2	2.01	0.42
91:AE:27:TYR:O	91:AE:60:ALA:HA	2.19	0.42
2:1:246:LEU:HD21	41:P:133:HIS:HB3	2.01	0.42
6:5:277:G:H1'	68:i:82:ARG:NH1	2.34	0.42
6:5:1276:G:N3	6:5:1279:A:N6	2.68	0.42
6:5:1286:A:H2'	6:5:1287:G:C8	2.55	0.42
6:5:2144:G:H2'	6:5:2145:G:H8	1.85	0.42
6:5:2175:U:OP2	71:l:10:LYS:NZ	2.52	0.42
7:6:163:PRO:HB2	7:6:179:LEU:HB2	2.01	0.42
17:DD:95:ASP:OD2	81:v:172:ASN:ND2	2.50	0.42
31:K:1786:U:H2'	31:K:1787:G:H8	1.84	0.42
6:5:132:G:H2'	6:5:133:C:O4'	2.20	0.42
6:5:665:A:H3'	6:5:666:G:H8	1.84	0.42
6:5:1800:G:H2'	71:l:13:LEU:HD22	2.00	0.42
6:5:2544:C:H1'	6:5:3202:U:H1'	2.02	0.42
12:AA:109:MET:SD	12:AA:113:ARG:NH2	2.89	0.42
13:B:261:ARG:HB2	39:O:64:THR:HG21	2.01	0.42
31:K:183:G:H2'	31:K:183:G:OP2	2.19	0.42
31:K:310:C:C2'	31:K:311:C:H5'	2.49	0.42
31:K:551:U:H2'	31:K:552:G:H8	1.84	0.42
31:K:1143:A:O3'	31:K:1355:C:N4	2.52	0.42
31:K:1456:G:OP2	32:KK:59:LYS:NZ	2.40	0.42
31:K:1563:G:OP2	42:PP:72:VAL:HG23	2.20	0.42
31:K:1706:G:H5'	73:n:1:MET:HB2	2.02	0.42
47:S:85:ASP:HB2	47:S:123:SER:HB3	2.00	0.42
56:WW:39:ALA:HA	56:WW:42:ARG:HG2	2.02	0.42
60:a:117:LEU:HD12	60:a:118:PRO:HD2	2.01	0.42
80:u:92:GLN:HB3	80:u:95:ASN:HB2	2.00	0.42
80:u:191:ASP:O	80:u:195:LYS:N	2.46	0.42
88:AC:60:VAL:HG12	88:AC:84:VAL:HG22	2.02	0.42
89:AI:83:GLN:OE1	89:AI:125:ARG:NH1	2.43	0.42
6:5:485:C:H2'	6:5:486:G:C8	2.55	0.42
6:5:772:G:H2'	6:5:773:A:C8	2.55	0.42
6:5:1196:U:H5''	6:5:1197:A:H5'	2.00	0.42
6:5:1488:G:O3'	47:S:95:ARG:NH1	2.52	0.42
6:5:1762:U:O2	63:d:39:LYS:NZ	2.51	0.42
6:5:2381:C:OP1	11:A:132:ASN:ND2	2.52	0.42
6:5:2702:C:H4'	24:G:98:ILE:HG21	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:5:3350:G:H4'	35:M:90:ARG:NH1	2.35	0.42
15:C:230:LEU:HD21	15:C:239:LYS:HD2	2.01	0.42
27:I:61:SER:HA	27:I:126:VAL:HG23	2.01	0.42
31:K:385:G:H1'	31:K:387:C:OP2	2.20	0.42
31:K:1618:C:H4'	56:WW:50:ARG:HH21	1.84	0.42
34:LL:4:LYS:HG2	34:LL:5:ARG:HD3	2.02	0.42
34:LL:28:ARG:NH1	34:LL:29:CYS:O	2.52	0.42
59:Z:12:LEU:N	59:Z:81:MET:O	2.52	0.42
83:x:72:ILE:HB	83:x:77:ARG:HD3	2.01	0.42
6:5:487:U:O2'	15:C:3:CYS:SG	2.70	0.42
6:5:1592:G:O5'	39:O:130:LYS:NZ	2.51	0.42
6:5:1804:C:H2'	6:5:1805:A:C8	2.54	0.42
6:5:2241:G:O2'	6:5:2536:U:O4	2.33	0.42
6:5:3324:G:P	39:O:12:ARG:HH12	2.43	0.42
6:5:3526:C:H4'	13:B:324:GLY:HA2	2.01	0.42
7:6:238:ALA:H	7:6:251:ALA:HB3	1.85	0.42
14:BB:73:GLN:HA	14:BB:76:GLN:HB2	2.01	0.42
15:C:200:ARG:HH22	58:Y:11:ARG:CZ	2.33	0.42
30:J:111:GLU:HG3	30:J:113:ILE:HG22	2.01	0.42
31:K:172:U:N3	31:K:337:C:O2'	2.52	0.42
31:K:511:U:O2'	31:K:576:A:N6	2.53	0.42
31:K:935:G:O2'	44:QQ:108:ASP:OD1	2.31	0.42
31:K:1438:A:H2'	31:K:1439:A:C8	2.55	0.42
31:K:1513:C:H2'	31:K:1514:G:H8	1.85	0.42
45:R:114:LYS:O	45:R:146:LYS:NZ	2.53	0.42
75:p:9:GLY:H	75:p:27:LYS:HE2	1.85	0.42
6:5:20:U:H3'	6:5:21:G:H8	1.85	0.42
6:5:86:U:H2'	6:5:87:A:H8	1.84	0.42
6:5:487:U:H3	15:C:267:TRP:CG	2.38	0.42
6:5:842:G:C6	20:E:131:HIS:HB2	2.55	0.42
6:5:1339:A:H1'	49:T:130:ARG:NH1	2.35	0.42
6:5:2223:G:H2'	6:5:2224:G:H8	1.85	0.42
6:5:2296:C:H2'	6:5:2297:A:H8	1.84	0.42
6:5:2428:U:H2'	6:5:2429:C:H6	1.85	0.42
6:5:2808:G:H2'	6:5:2809:A:C8	2.55	0.42
12:AA:82:VAL:HG11	53:VV:91:LEU:HB3	2.01	0.42
13:B:240:LEU:HD21	13:B:252:ALA:HB2	2.02	0.42
15:C:289:LEU:HA	15:C:292:ILE:HD12	2.01	0.42
22:F:147:LYS:HD3	22:F:244:ARG:NH1	2.35	0.42
26:HH:15:ARG:HA	81:v:259:THR:HG21	2.02	0.42
27:I:16:PRO:HA	27:I:95:HIS:CD2	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:K:28:U:H2'	31:K:29:G:C8	2.55	0.42
31:K:1277:C:H2'	31:K:1278:A:C8	2.55	0.42
36:MM:150:ARG:HD3	36:MM:150:ARG:H	1.84	0.42
45:R:69:ALA:HB1	45:R:74:ARG:HB2	2.02	0.42
60:a:125:LYS:HG2	60:a:145:VAL:HB	2.02	0.42
6:5:1280:A:H5'	18:D:11:ALA:HB1	2.02	0.42
6:5:1969:G:OP1	59:Z:48:ARG:NH2	2.52	0.42
6:5:2203:U:H5''	45:R:70:ARG:HH22	1.85	0.42
15:C:321:ASN:HD22	15:C:321:ASN:HA	1.65	0.42
18:D:164:LYS:HB2	18:D:180:PHE:HE1	1.84	0.42
19:EE:18:GLN:HB2	19:EE:33:LEU:HD22	2.01	0.42
31:K:104:A:H62	31:K:356:C:H5	1.68	0.42
42:PP:6:VAL:HG12	42:PP:135:ALA:HB2	2.02	0.42
49:T:35:LYS:HB2	49:T:38:ASP:OD2	2.20	0.42
77:r:18:ILE:HD11	77:r:20:ARG:NH1	2.35	0.42
6:5:605:G:H1	47:S:67:VAL:HA	1.85	0.41
6:5:1057:A:OP2	43:Q:162:HIS:HA	2.19	0.41
6:5:1286:A:H4'	27:I:35:ASP:OD2	2.20	0.41
6:5:1618:C:H2'	6:5:1619:G:H8	1.85	0.41
6:5:2447:C:O2'	11:A:220:GLY:O	2.37	0.41
19:EE:101:ARG:NH1	53:VV:6:GLY:O	2.53	0.41
29:JJ:6:ASP:OD1	29:JJ:6:ASP:N	2.53	0.41
31:K:119:U:O2	83:x:33:THR:OG1	2.35	0.41
31:K:475:C:H1'	31:K:507:G:H1'	2.02	0.41
31:K:960:U:H5''	36:MM:149:ARG:HH21	1.85	0.41
35:M:130:LEU:HB3	39:O:177:LEU:HD22	2.02	0.41
39:O:9:LEU:HD21	47:S:167:PHE:HD1	1.85	0.41
47:S:5:GLY:O	47:S:111:ARG:NH1	2.52	0.41
58:Y:59:ARG:HB2	58:Y:103:LYS:HD2	2.02	0.41
65:f:16:ARG:HA	65:f:21:GLN:HA	2.02	0.41
6:5:2000:C:H2'	6:5:2001:G:C8	2.54	0.41
6:5:2563:A:H2'	6:5:2563:A:N3	2.34	0.41
10:9:23:VAL:HA	48:SS:64:TRP:HB3	2.01	0.41
13:B:317:LEU:HB2	13:B:372:SER:HB2	2.01	0.41
14:BB:91:HIS:HB2	14:BB:172:THR:HG21	2.02	0.41
28:II:36:VAL:HG23	28:II:40:TYR:HD2	1.85	0.41
31:K:907:G:H2'	31:K:908:A:C8	2.55	0.41
31:K:1198:G:H2'	31:K:1199:A:H8	1.85	0.41
31:K:1566:G:O3'	31:K:1567:G:N2	2.50	0.41
31:K:1579:A:OP2	82:w:7:LYS:HG2	2.21	0.41
44:QQ:30:SER:HB2	44:QQ:67:THR:HG22	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:u:174:ARG:NH2	80:u:196:ASP:OD2	2.53	0.41
82:w:51:LEU:HG	82:w:91:VAL:HG22	2.01	0.41
6:5:527:C:H2'	6:5:528:G:C8	2.55	0.41
6:5:721:C:OP1	20:E:75:TYR:OH	2.35	0.41
6:5:781:G:O2'	18:D:278:ASP:OD1	2.38	0.41
6:5:2152:G:H1'	6:5:2157:A:H2	1.84	0.41
6:5:2188:A:N7	6:5:2190:C:N3	2.63	0.41
6:5:2929:U:H5'	33:L:197:LYS:NZ	2.35	0.41
8:7:94:C:H4'	47:S:122:HIS:HB2	2.02	0.41
11:A:29:LEU:H	11:A:123:ARG:HB3	1.85	0.41
27:I:97:ILE:HD12	27:I:97:ILE:HA	1.95	0.41
28:II:87:GLN:O	31:K:1611:G:O2'	2.37	0.41
36:MM:139:SER:OG	36:MM:140:THR:N	2.53	0.41
39:O:82:ARG:NH1	39:O:85:ARG:HH21	2.10	0.41
39:O:119:VAL:HG21	47:S:171:ARG:HE	1.85	0.41
91:AE:92:ASP:N	91:AE:92:ASP:OD1	2.53	0.41
6:5:1113:A:O2'	75:p:9:GLY:O	2.31	0.41
6:5:1340:G:OP2	6:5:1373:G:H5'	2.21	0.41
6:5:1407:C:H2'	6:5:1408:A:H8	1.85	0.41
6:5:2136:A:O2'	11:A:21:LYS:NZ	2.54	0.41
6:5:2485:G:H1'	6:5:2487:C:H41	1.86	0.41
6:5:2681:G:H22	6:5:2686:G:H1	1.68	0.41
6:5:2889:C:H2'	6:5:2890:G:C8	2.54	0.41
6:5:3485:G:N2	6:5:3516:G:O2'	2.53	0.41
7:6:16:GLY:O	7:6:35:SER:OG	2.38	0.41
7:6:57:ARG:HH11	7:6:95:GLY:HA3	1.86	0.41
9:8:28:C:H2'	9:8:29:G:H8	1.86	0.41
9:8:153:C:H4'	24:G:238:LYS:HB3	2.02	0.41
13:B:54:THR:HG22	13:B:78:ILE:HD11	2.03	0.41
16:CC:103:LEU:HD13	16:CC:170:LYS:HD3	2.03	0.41
16:CC:147:LYS:NZ	31:K:203:G:OP2	2.50	0.41
24:G:233:PRO:HG2	24:G:272:VAL:HG13	2.02	0.41
24:G:313:GLU:O	24:G:317:LYS:HG2	2.20	0.41
29:JJ:5:LYS:O	50:TT:24:GLN:NE2	2.42	0.41
31:K:559:G:H8	31:K:559:G:OP2	2.04	0.41
31:K:935:G:H2'	31:K:936:G:H8	1.85	0.41
31:K:1239:U:H2'	31:K:1241:A:OP2	2.20	0.41
39:O:15:LEU:HB2	39:O:18:ARG:HB2	2.02	0.41
51:UU:16:LYS:HG2	51:UU:79:ALA:HA	2.01	0.41
55:W:82:ILE:HA	85:z:131:ARG:HB2	2.02	0.41
62:c:90:ARG:HH12	75:p:43:GLY:C	2.29	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
81:v:61:LEU:HD12	81:v:62:PRO:HD2	2.02	0.41
86:AB:134:LEU:HD23	86:AB:188:ILE:HB	2.02	0.41
6:5:18:C:H2'	6:5:19:G:C8	2.55	0.41
6:5:685:C:H2'	6:5:686:G:H8	1.84	0.41
6:5:1432:G:O2'	6:5:1444:A:N3	2.42	0.41
6:5:1813:A:H5''	6:5:1814:G:H5''	2.01	0.41
6:5:2032:U:H1'	66:g:26:PRO:HB3	2.02	0.41
6:5:2189:G:H5'	71:l:45:ARG:NH2	2.36	0.41
6:5:3421:G:P	20:E:191:ARG:HH11	2.43	0.41
20:E:105:GLY:HA3	20:E:108:ARG:HH12	1.86	0.41
22:F:93:ARG:HH12	22:F:97:ILE:HA	1.85	0.41
31:K:677:G:H21	31:K:1028:A:N6	2.01	0.41
31:K:1402:A:OP2	31:K:1402:A:H8	2.02	0.41
34:LL:44:ILE:HG12	34:LL:65:PRO:HG2	2.03	0.41
43:Q:78:LYS:HB2	43:Q:78:LYS:HE3	1.85	0.41
50:TT:90:GLN:HB2	50:TT:94:LEU:HD12	2.02	0.41
58:Y:71:VAL:N	58:Y:81:TYR:O	2.45	0.41
89:AI:137:ALA:HB2	89:AI:143:LYS:HB2	2.02	0.41
6:5:922:G:H2'	6:5:923:G:H8	1.86	0.41
6:5:1438:C:H2'	6:5:1439:G:H8	1.84	0.41
6:5:1459:G:H2'	6:5:1460:A:H8	1.86	0.41
6:5:1596:C:O2'	47:S:118:ARG:NH1	2.54	0.41
6:5:1625:A:H5''	6:5:1626:G:H3'	2.01	0.41
6:5:2150:A:H2'	6:5:2151:G:C8	2.55	0.41
6:5:2238:A:H61	6:5:2541:C:N4	2.16	0.41
6:5:2875:G:H1	49:T:87:LYS:HZ2	1.68	0.41
6:5:2891:U:H2'	6:5:2892:G:C8	2.56	0.41
6:5:3324:G:H2'	6:5:3325:A:H8	1.85	0.41
15:C:232:VAL:HG12	15:C:263:LEU:HD11	2.03	0.41
16:CC:5:ARG:NH1	31:K:379:C:O2	2.54	0.41
16:CC:162:LEU:HD11	16:CC:191:GLU:HG2	2.02	0.41
18:D:64:ILE:HG13	18:D:105:LEU:HD21	2.02	0.41
22:F:156:ARG:NH2	22:F:211:LYS:O	2.54	0.41
31:K:70:G:N2	31:K:71:G:O6	2.54	0.41
31:K:107:A:H2'	31:K:108:G:C8	2.55	0.41
31:K:1153:C:OP2	50:TT:71:LYS:NZ	2.54	0.41
31:K:1376:A:H8	31:K:1376:A:OP2	2.03	0.41
35:M:11:ARG:HB3	35:M:27:ILE:HD12	2.02	0.41
38:NN:40:ILE:HG21	38:NN:57:VAL:HG11	2.02	0.41
39:O:12:ARG:HE	47:S:171:ARG:HH12	1.67	0.41
39:O:18:ARG:NH1	39:O:128:ARG:HE	2.18	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:S:15:ARG:HH21	49:T:141:VAL:HG22	1.86	0.41
62:c:28:VAL:HG21	62:c:37:MET:HG3	2.02	0.41
69:j:45:ARG:HH21	69:j:47:TYR:HE2	1.69	0.41
78:s:26:LYS:NZ	78:s:91:THR:HG23	2.35	0.41
81:v:169:TYR:OH	81:v:175:GLY:O	2.36	0.41
82:w:171:ALA:O	82:w:185:LYS:HA	2.20	0.41
85:z:132:ARG:HG3	85:z:133:LEU:HD12	2.02	0.41
1:0:130:VAL:HG11	1:0:143:LYS:HZ3	1.85	0.41
6:5:687:G:H2'	6:5:688:G:H8	1.86	0.41
6:5:1933:C:H2'	6:5:1934:G:H8	1.86	0.41
6:5:2131:C:O2'	6:5:2133:U:O2	2.28	0.41
6:5:3395:G:H2'	6:5:3396:G:H8	1.85	0.41
16:CC:27:TYR:HB3	16:CC:49:ARG:HH12	1.86	0.41
31:K:127:C:O2	83:x:134:LYS:NZ	2.54	0.41
31:K:223:C:H2'	31:K:224:A:C8	2.56	0.41
31:K:677:G:N1	31:K:1027:A:OP2	2.21	0.41
31:K:862:A:N3	50:TT:105:THR:OG1	2.47	0.41
31:K:1295:A:H3'	31:K:1296:U:C6	2.56	0.41
31:K:1367:U:O2'	31:K:1466:G:O2'	2.31	0.41
36:MM:46:ASP:OD2	80:u:48:LEU:HG	2.21	0.41
42:PP:11:GLN:HG3	42:PP:62:ARG:HH11	1.85	0.41
77:r:65:LYS:O	77:r:102:TYR:OH	2.27	0.41
82:w:49:ILE:HG12	82:w:87:TYR:HB2	2.01	0.41
87:AF:140:C:H5''	88:AC:28:THR:HG21	2.03	0.41
87:AF:194:G:H1	87:AF:205:A:H61	1.69	0.41
6:5:957:G:H2'	6:5:958:G:H8	1.86	0.41
6:5:1210:A:C5	15:C:100:ARG:NH1	2.89	0.41
6:5:1229:A:OP1	61:b:18:ARG:NH2	2.53	0.41
6:5:1247:U:OP2	61:b:19:ASN:ND2	2.54	0.41
6:5:1323:A:O2'	6:5:1325:A:OP2	2.22	0.41
6:5:1498:G:OP2	78:s:57:LYS:HG2	2.20	0.41
6:5:2059:U:OP1	45:R:107:ARG:NH2	2.53	0.41
6:5:2457:A:N6	6:5:2463:G:O2'	2.54	0.41
6:5:3122:U:H2'	6:5:3123:A:C8	2.56	0.41
13:B:116:ARG:NH1	13:B:176:LYS:HB2	2.36	0.41
17:DD:111:GLN:NE2	17:DD:127:ARG:HB2	2.36	0.41
24:G:243:LEU:HD12	24:G:246:LEU:HD12	2.02	0.41
28:II:86:ARG:HD3	28:II:86:ARG:HA	1.92	0.41
31:K:1036:A:H4'	31:K:1855:G:H21	1.85	0.41
31:K:1568:C:OP1	42:PP:96:SER:OG	2.38	0.41
45:R:42:ARG:HA	45:R:45:ILE:HD12	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:SS:14:LEU:HA	48:SS:17:LYS:HG2	2.01	0.41
66:g:61:PRO:HA	66:g:64:LEU:HD13	2.02	0.41
6:5:254:C:H2'	6:5:255:G:H8	1.86	0.41
6:5:579:G:H2'	6:5:580:C:H4'	2.03	0.41
6:5:914:G:H22	43:Q:60:PRO:HG3	1.85	0.41
6:5:1268:C:OP1	49:T:100:LYS:NZ	2.46	0.41
6:5:1980:A:O2'	6:5:1981:C:O4'	2.31	0.41
6:5:2238:A:N3	54:V:86:LYS:NZ	2.68	0.41
6:5:2457:A:OP2	6:5:2463:G:N1	2.39	0.41
6:5:2568:C:H2'	6:5:2569:A:C8	2.56	0.41
6:5:3015:U:H6	6:5:3015:U:O5'	2.04	0.41
13:B:154:LYS:NZ	13:B:191:ALA:O	2.54	0.41
15:C:207:PRO:HB3	15:C:249:PHE:HD2	1.85	0.41
16:CC:19:LYS:HE2	31:K:101:U:H5''	2.03	0.41
16:CC:100:CYS:O	16:CC:174:CYS:HA	2.21	0.41
18:D:95:TYR:HA	18:D:158:LYS:HG2	2.02	0.41
24:G:151:LEU:HD13	24:G:271:LEU:HD12	2.02	0.41
27:I:99:ILE:HB	27:I:123:GLN:HB2	2.03	0.41
31:K:406:U:H2'	31:K:408:A:H8	1.86	0.41
31:K:464:A:OP1	91:AE:95:LYS:NZ	2.51	0.41
31:K:659:G:O2'	31:K:662:G:O2'	2.35	0.41
31:K:690:G:H2'	31:K:691:G:C8	2.55	0.41
31:K:730:C:H2'	31:K:731:G:C8	2.55	0.41
31:K:919:A:OP2	44:QQ:64:ARG:NH2	2.54	0.41
31:K:1447:G:H2'	31:K:1448:A:H8	1.85	0.41
31:K:1468:C:H2'	31:K:1469:A:C8	2.56	0.41
33:L:63:THR:O	33:L:65:ARG:N	2.53	0.41
37:N:51:LEU:HD22	37:N:117:ASN:HD22	1.85	0.41
42:PP:75:MET:HA	42:PP:78:ILE:HG22	2.03	0.41
48:SS:64:TRP:NE1	82:w:23:GLU:HG2	2.36	0.41
51:UU:125:ARG:HH22	84:y:54:GLY:HA3	1.86	0.41
51:UU:132:PHE:O	51:UU:140:ARG:NH2	2.54	0.41
56:WW:79:HIS:HA	56:WW:97:TYR:HB3	2.03	0.41
74:o:3:ASN:ND2	74:o:95:GLY:O	2.53	0.41
80:u:103:MET:H	80:u:215:VAL:HB	1.86	0.41
83:x:48:LEU:HD23	83:x:61:VAL:HG13	2.03	0.41
83:x:129:ILE:HA	83:x:138:HIS:O	2.21	0.41
87:AF:48:G:H2'	87:AF:49:A:C8	2.56	0.41
87:AF:225:C:OP1	89:AI:84:ARG:NH2	2.54	0.41
3:2:68:G:H2'	3:2:69:G:H8	1.86	0.41
6:5:223:G:H2'	6:5:224:G:H8	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:5:305:G:H2'	6:5:306:G:H8	1.86	0.41
6:5:1180:U:OP2	69:j:30:GLN:HG2	2.21	0.41
6:5:1261:G:N2	61:b:13:SER:OG	2.54	0.41
6:5:1569:U:O2'	47:S:91:HIS:NE2	2.54	0.41
6:5:1879:G:H2'	6:5:1880:G:C8	2.56	0.41
6:5:2151:G:O2'	6:5:2158:A:N3	2.45	0.41
6:5:2599:A:H3'	6:5:2599:A:N3	2.36	0.41
10:9:47:ALA:HB1	10:9:52:PHE:HB2	2.02	0.41
13:B:217:ILE:HD11	13:B:333:LEU:HD21	2.01	0.41
18:D:68:ARG:HG3	18:D:73:MET:HE2	2.03	0.41
19:EE:104:LYS:O	53:VV:11:ARG:NH2	2.54	0.41
31:K:300:U:H2'	31:K:301:A:C8	2.56	0.41
39:O:130:LYS:HB2	39:O:133:ARG:HG2	2.03	0.41
49:T:18:PRO:HB2	49:T:21:LYS:HD2	2.03	0.41
59:Z:41:ALA:HB2	59:Z:77:TYR:HE1	1.86	0.41
80:u:67:PHE:O	80:u:85:LYS:HA	2.20	0.41
83:x:11:ARG:HA	83:x:28:ALA:HB2	2.03	0.41
6:5:62:A:N3	6:5:77:U:O2'	2.41	0.40
6:5:540:G:HO2'	6:5:544:C:H42	1.65	0.40
6:5:1906:A:OP2	66:g:11:LEU:HD12	2.20	0.40
6:5:2009:C:H2'	6:5:2010:G:H8	1.86	0.40
6:5:2671:G:H2'	6:5:2672:G:C8	2.56	0.40
7:6:9:GLY:H	7:6:309:VAL:HG22	1.86	0.40
9:8:67:U:H2'	9:8:68:G:C8	2.56	0.40
11:A:180:LEU:HD21	75:p:26:VAL:HG21	2.03	0.40
20:E:168:LEU:HD23	20:E:206:ILE:HD11	2.02	0.40
21:FF:55:VAL:HB	84:y:34:SER:HA	2.02	0.40
31:K:668:A:H1'	31:K:1197:G:H21	1.86	0.40
31:K:678:U:OP1	44:QQ:127:ARG:NH2	2.53	0.40
31:K:848:U:OP1	83:x:245:ARG:NH2	2.54	0.40
31:K:1144:A:H2'	31:K:1145:A:C8	2.56	0.40
41:P:131:ARG:HG3	41:P:137:ASN:ND2	2.36	0.40
42:PP:11:GLN:CG	42:PP:62:ARG:HH11	2.35	0.40
53:VV:98:ASP:OD2	53:VV:140:ARG:NH2	2.48	0.40
70:k:28:ASN:HD21	70:k:33:LYS:NZ	2.19	0.40
74:o:26:TYR:HB3	74:o:67:VAL:HB	2.04	0.40
4:3:58:A:O2'	4:3:60:U:OP2	2.26	0.40
6:5:1337:U:H2'	6:5:1338:A:C8	2.57	0.40
6:5:1566:A:H2'	6:5:1567:A:C8	2.57	0.40
6:5:2096:G:H5''	52:U:113:ARG:HH22	1.86	0.40
6:5:3372:G:H2'	6:5:3373:G:H8	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:8:130:C:H2'	9:8:131:G:H8	1.86	0.40
17:DD:42:GLU:OE2	17:DD:45:ARG:NH2	2.54	0.40
21:FF:18:LEU:HD12	21:FF:29:GLN:HG2	2.03	0.40
27:I:184:MET:HA	27:I:187:GLU:HG2	2.03	0.40
31:K:142:C:OP2	85:z:188:LYS:NZ	2.44	0.40
31:K:1232:U:H2'	31:K:1233:G:C8	2.56	0.40
42:PP:18:LEU:HD13	42:PP:134:ILE:HD13	2.02	0.40
67:h:28:LEU:HD21	67:h:32:ARG:HE	1.87	0.40
78:s:161:ILE:HD13	78:s:167:VAL:HG22	2.03	0.40
89:AI:153:LYS:HE3	89:AI:157:HIS:CD2	2.55	0.40
6:5:183:G:H2'	6:5:184:G:H8	1.86	0.40
6:5:281:U:H2'	6:5:282:G:H8	1.85	0.40
6:5:344:C:OP1	6:5:1687:G:O2'	2.38	0.40
6:5:954:G:N7	60:a:110:LYS:NZ	2.51	0.40
6:5:1153:A:H4'	6:5:2232:U:H4'	2.04	0.40
6:5:1908:G:O2'	6:5:1992:G:O2'	2.36	0.40
6:5:2092:C:H2'	6:5:2093:G:H8	1.86	0.40
6:5:2256:G:O2'	45:R:82:LYS:O	2.31	0.40
6:5:2778:U:H2'	6:5:2779:G:H8	1.85	0.40
6:5:3481:U:H4'	13:B:317:LEU:HB3	2.03	0.40
15:C:128:LEU:HD22	15:C:252:TRP:HZ2	1.87	0.40
15:C:152:LEU:HD23	15:C:251:ILE:HG12	2.03	0.40
19:EE:86:ILE:HG12	19:EE:113:LEU:HB2	2.03	0.40
31:K:988:C:H5''	80:u:116:LYS:HA	2.03	0.40
31:K:1220:A:N3	31:K:1677:U:O2'	2.45	0.40
34:LL:11:ALA:HB3	34:LL:33:ASP:HB2	2.03	0.40
41:P:130:TYR:CD2	41:P:130:TYR:N	2.89	0.40
72:m:71:ARG:HD3	72:m:96:ARG:HH11	1.86	0.40
76:q:126:ASP:HB3	76:q:129:ALA:HB3	2.03	0.40
80:u:29:ASP:N	80:u:49:VAL:O	2.50	0.40
2:1:259:LEU:HD11	6:5:2968:C:H6	1.82	0.40
4:3:70:G:H2'	4:3:71:G:C8	2.56	0.40
6:5:434:U:O2'	65:f:91:ASN:O	2.30	0.40
6:5:902:U:O3'	37:N:204:ARG:NH1	2.51	0.40
6:5:1726:G:H5''	15:C:195:LYS:HE2	2.03	0.40
6:5:2558:A:H2	41:P:131:ARG:HH22	1.70	0.40
6:5:3088:A:O2'	6:5:3091:U:P	2.74	0.40
11:A:48:ILE:HD13	75:p:65:ALA:HB2	2.03	0.40
12:AA:107:ARG:NH1	12:AA:110:GLN:OE1	2.54	0.40
15:C:219:LYS:HA	15:C:222:ARG:NH1	2.37	0.40
17:DD:108:ARG:NH2	17:DD:149:VAL:O	2.55	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:I:150:GLU:CD	27:I:153:ARG:HH11	2.27	0.40
30:J:46:GLN:NE2	30:J:72:CYS:SG	2.95	0.40
41:P:112:LEU:HD13	41:P:150:LEU:HD13	2.03	0.40
48:SS:4:PRO:HG2	48:SS:7:ASN:HD22	1.87	0.40
87:AF:4:G:H1	87:AF:23:U:H3	1.69	0.40
2:1:249:TRP:HD1	6:5:2602:G:HO2'	1.68	0.40
3:2:76:A:H3'	6:5:3101:U:C5	2.56	0.40
6:5:88:A:N7	43:Q:173:LYS:NZ	2.63	0.40
6:5:463:C:H2'	6:5:464:A:H8	1.87	0.40
6:5:1156:U:O2'	41:P:135:ARG:NH2	2.52	0.40
6:5:2308:A:H2'	6:5:2309:A:H8	1.87	0.40
14:BB:157:HIS:HB3	14:BB:190:PRO:HG3	2.04	0.40
22:F:103:LYS:HE3	22:F:134:ILE:HD11	2.04	0.40
23:GG:61:LEU:HB2	23:GG:82:MET:HB3	2.02	0.40
24:G:213:ASP:OD2	24:G:239:GLY:HA2	2.22	0.40
31:K:675:U:H2'	31:K:676:C:H6	1.87	0.40
31:K:1146:C:O2'	31:K:1150:A:N1	2.45	0.40
31:K:1393:G:H2'	31:K:1394:G:C8	2.55	0.40
31:K:1545:A:H2'	31:K:1546:G:C8	2.56	0.40
31:K:1808:U:H2'	31:K:1809:A:C8	2.55	0.40
39:O:94:ARG:HE	65:f:97:ILE:HG21	1.87	0.40
69:j:48:ASN:HA	69:j:54:LYS:HE3	2.02	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	66/68 (97%)	61 (92%)	5 (8%)	0	100	100
2	1	22/24 (92%)	13 (59%)	5 (23%)	4 (18%)	0	1
7	6	311/313 (99%)	292 (94%)	19 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	9	53/55 (96%)	52 (98%)	1 (2%)	0	100	100
11	A	246/248 (99%)	231 (94%)	15 (6%)	0	100	100
12	AA	53/55 (96%)	53 (100%)	0	0	100	100
13	B	392/394 (100%)	374 (95%)	18 (5%)	0	100	100
14	BB	181/189 (96%)	174 (96%)	7 (4%)	0	100	100
15	C	360/362 (99%)	347 (96%)	11 (3%)	2 (1%)	21	52
16	CC	204/206 (99%)	193 (95%)	11 (5%)	0	100	100
17	DD	183/185 (99%)	180 (98%)	3 (2%)	0	100	100
18	D	291/293 (99%)	281 (97%)	10 (3%)	0	100	100
19	EE	139/151 (92%)	134 (96%)	5 (4%)	0	100	100
20	E	208/251 (83%)	201 (97%)	7 (3%)	0	100	100
21	FF	60/62 (97%)	59 (98%)	1 (2%)	0	100	100
22	F	223/225 (99%)	214 (96%)	9 (4%)	0	100	100
23	GG	98/100 (98%)	94 (96%)	4 (4%)	0	100	100
24	G	229/240 (95%)	218 (95%)	11 (5%)	0	100	100
25	H	188/190 (99%)	182 (97%)	6 (3%)	0	100	100
26	HH	81/83 (98%)	78 (96%)	3 (4%)	0	100	100
27	I	201/213 (94%)	193 (96%)	8 (4%)	0	100	100
28	II	142/144 (99%)	134 (94%)	8 (6%)	0	100	100
29	JJ	81/83 (98%)	80 (99%)	1 (1%)	0	100	100
30	J	168/170 (99%)	163 (97%)	5 (3%)	0	100	100
32	KK	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
33	L	208/210 (99%)	200 (96%)	7 (3%)	1 (0%)	24	56
34	LL	99/101 (98%)	94 (95%)	5 (5%)	0	100	100
35	M	136/138 (99%)	128 (94%)	8 (6%)	0	100	100
36	MM	134/136 (98%)	127 (95%)	7 (5%)	0	100	100
37	N	201/203 (99%)	190 (94%)	11 (6%)	0	100	100
38	NN	122/124 (98%)	120 (98%)	2 (2%)	0	100	100
39	O	197/199 (99%)	193 (98%)	4 (2%)	0	100	100
40	OO	73/75 (97%)	72 (99%)	1 (1%)	0	100	100
41	P	151/153 (99%)	144 (95%)	7 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
42	PP	139/141 (99%)	133 (96%)	6 (4%)	0	100	100
43	Q	185/187 (99%)	177 (96%)	8 (4%)	0	100	100
44	QQ	147/149 (99%)	146 (99%)	1 (1%)	0	100	100
45	R	178/180 (99%)	175 (98%)	3 (2%)	0	100	100
46	RR	115/117 (98%)	105 (91%)	10 (9%)	0	100	100
47	S	174/176 (99%)	166 (95%)	8 (5%)	0	100	100
48	SS	94/96 (98%)	89 (95%)	5 (5%)	0	100	100
49	T	157/159 (99%)	150 (96%)	7 (4%)	0	100	100
50	TT	127/129 (98%)	123 (97%)	4 (3%)	0	100	100
51	UU	140/142 (99%)	136 (97%)	4 (3%)	0	100	100
52	U	97/99 (98%)	94 (97%)	3 (3%)	0	100	100
53	VV	139/141 (99%)	134 (96%)	4 (3%)	1 (1%)	18	50
54	V	129/131 (98%)	127 (98%)	2 (2%)	0	100	100
55	W	102/121 (84%)	100 (98%)	2 (2%)	0	100	100
56	WW	118/120 (98%)	109 (92%)	9 (8%)	0	100	100
57	X	116/118 (98%)	114 (98%)	2 (2%)	0	100	100
58	Y	132/134 (98%)	129 (98%)	3 (2%)	0	100	100
59	Z	133/135 (98%)	128 (96%)	5 (4%)	0	100	100
60	a	145/147 (99%)	141 (97%)	4 (3%)	0	100	100
61	b	100/116 (86%)	97 (97%)	3 (3%)	0	100	100
62	c	96/98 (98%)	93 (97%)	3 (3%)	0	100	100
63	d	105/107 (98%)	101 (96%)	4 (4%)	0	100	100
64	e	126/128 (98%)	123 (98%)	3 (2%)	0	100	100
65	f	107/109 (98%)	103 (96%)	4 (4%)	0	100	100
66	g	112/114 (98%)	111 (99%)	1 (1%)	0	100	100
67	h	120/122 (98%)	118 (98%)	2 (2%)	0	100	100
68	i	100/102 (98%)	97 (97%)	3 (3%)	0	100	100
69	j	84/86 (98%)	81 (96%)	3 (4%)	0	100	100
70	k	67/69 (97%)	67 (100%)	0	0	100	100
71	l	48/50 (96%)	48 (100%)	0	0	100	100
72	m	50/52 (96%)	49 (98%)	1 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
73	n	23/25 (92%)	23 (100%)	0	0	100	100
74	o	102/104 (98%)	98 (96%)	4 (4%)	0	100	100
75	p	89/91 (98%)	86 (97%)	3 (3%)	0	100	100
76	q	215/217 (99%)	208 (97%)	7 (3%)	0	100	100
77	r	122/124 (98%)	114 (93%)	8 (7%)	0	100	100
78	s	194/196 (99%)	184 (95%)	10 (5%)	0	100	100
79	t	151/153 (99%)	135 (89%)	16 (11%)	0	100	100
80	u	211/213 (99%)	205 (97%)	6 (3%)	0	100	100
81	v	219/221 (99%)	213 (97%)	6 (3%)	0	100	100
82	w	226/228 (99%)	220 (97%)	6 (3%)	0	100	100
83	x	260/262 (99%)	250 (96%)	10 (4%)	0	100	100
84	y	181/191 (95%)	170 (94%)	11 (6%)	0	100	100
85	z	235/237 (99%)	233 (99%)	2 (1%)	0	100	100
86	AB	397/431 (92%)	358 (90%)	36 (9%)	3 (1%)	16	48
88	AC	103/105 (98%)	99 (96%)	4 (4%)	0	100	100
89	AI	175/195 (90%)	172 (98%)	3 (2%)	0	100	100
90	AD	72/74 (97%)	65 (90%)	6 (8%)	1 (1%)	9	37
91	AE	72/94 (77%)	71 (99%)	1 (1%)	0	100	100
92	AG	10/12 (83%)	10 (100%)	0	0	100	100
All	All	12370/12723 (97%)	11874 (96%)	484 (4%)	12 (0%)	49	78

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
86	AB	345	PHE
2	1	247	CYS
15	C	85	HIS
2	1	258	PRO
90	AD	56	ALA
86	AB	344	PRO
2	1	249	TRP
15	C	72	ALA
33	L	64	VAL
2	1	254	PRO
53	VV	62	PRO

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Mol	Chain	Res	Type
86	AB	23	ILE

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	61/61 (100%)	61 (100%)	0	100	100
2	1	22/22 (100%)	17 (77%)	5 (23%)	1	6
7	6	272/272 (100%)	272 (100%)	0	100	100
10	9	48/48 (100%)	48 (100%)	0	100	100
11	A	190/190 (100%)	190 (100%)	0	100	100
12	AA	46/46 (100%)	46 (100%)	0	100	100
13	B	342/342 (100%)	341 (100%)	1 (0%)	86	83
14	BB	165/169 (98%)	165 (100%)	0	100	100
15	C	302/302 (100%)	300 (99%)	2 (1%)	76	77
16	CC	178/178 (100%)	178 (100%)	0	100	100
17	DD	161/161 (100%)	160 (99%)	1 (1%)	78	79
18	D	247/247 (100%)	247 (100%)	0	100	100
19	EE	130/136 (96%)	130 (100%)	0	100	100
20	E	190/223 (85%)	190 (100%)	0	100	100
21	FF	55/55 (100%)	55 (100%)	0	100	100
22	F	196/196 (100%)	196 (100%)	0	100	100
23	GG	92/92 (100%)	92 (100%)	0	100	100
24	G	200/205 (98%)	199 (100%)	1 (0%)	81	80
25	H	169/169 (100%)	169 (100%)	0	100	100
26	HH	67/67 (100%)	66 (98%)	1 (2%)	57	68
27	I	175/180 (97%)	174 (99%)	1 (1%)	78	79
28	II	125/125 (100%)	124 (99%)	1 (1%)	73	76
29	JJ	75/75 (100%)	75 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
30	J	143/143 (100%)	143 (100%)	0	100	100
32	KK	119/119 (100%)	119 (100%)	0	100	100
33	L	175/175 (100%)	175 (100%)	0	100	100
34	LL	88/88 (100%)	88 (100%)	0	100	100
35	M	117/117 (100%)	117 (100%)	0	100	100
36	MM	106/106 (100%)	106 (100%)	0	100	100
37	N	171/171 (100%)	170 (99%)	1 (1%)	78	79
38	NN	107/107 (100%)	107 (100%)	0	100	100
39	O	171/171 (100%)	171 (100%)	0	100	100
40	OO	66/66 (100%)	66 (100%)	0	100	100
41	P	134/134 (100%)	132 (98%)	2 (2%)	57	68
42	PP	111/111 (100%)	111 (100%)	0	100	100
43	Q	164/164 (100%)	164 (100%)	0	100	100
44	QQ	130/130 (100%)	130 (100%)	0	100	100
45	R	159/159 (100%)	159 (100%)	0	100	100
46	RR	99/99 (100%)	99 (100%)	0	100	100
47	S	157/157 (100%)	157 (100%)	0	100	100
48	SS	87/87 (100%)	85 (98%)	2 (2%)	44	62
49	T	139/139 (100%)	139 (100%)	0	100	100
50	TT	112/112 (100%)	112 (100%)	0	100	100
51	UU	117/117 (100%)	117 (100%)	0	100	100
52	U	89/89 (100%)	89 (100%)	0	100	100
53	VV	113/113 (100%)	112 (99%)	1 (1%)	70	75
54	V	101/101 (100%)	100 (99%)	1 (1%)	68	74
55	W	86/100 (86%)	86 (100%)	0	100	100
56	WW	109/109 (100%)	109 (100%)	0	100	100
57	X	106/106 (100%)	106 (100%)	0	100	100
58	Y	124/124 (100%)	124 (100%)	0	100	100
59	Z	117/117 (100%)	117 (100%)	0	100	100
60	a	119/119 (100%)	119 (100%)	0	100	100
61	b	84/95 (88%)	83 (99%)	1 (1%)	63	72

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
62	c	84/84 (100%)	84 (100%)	0	100	100
63	d	98/98 (100%)	98 (100%)	0	100	100
64	e	114/114 (100%)	114 (100%)	0	100	100
65	f	88/88 (100%)	88 (100%)	0	100	100
66	g	98/98 (100%)	97 (99%)	1 (1%)	68	74
67	h	109/109 (100%)	109 (100%)	0	100	100
68	i	86/86 (100%)	86 (100%)	0	100	100
69	j	73/73 (100%)	73 (100%)	0	100	100
70	k	64/64 (100%)	64 (100%)	0	100	100
71	l	47/47 (100%)	47 (100%)	0	100	100
72	m	48/48 (100%)	48 (100%)	0	100	100
73	n	24/24 (100%)	24 (100%)	0	100	100
74	o	92/92 (100%)	92 (100%)	0	100	100
75	p	74/74 (100%)	74 (100%)	0	100	100
76	q	180/181 (99%)	179 (99%)	1 (1%)	78	79
77	r	108/108 (100%)	108 (100%)	0	100	100
78	s	164/164 (100%)	164 (100%)	0	100	100
79	t	126/126 (100%)	125 (99%)	1 (1%)	73	76
80	u	194/194 (100%)	193 (100%)	1 (0%)	81	80
81	v	187/187 (100%)	186 (100%)	1 (0%)	81	80
82	w	190/190 (100%)	190 (100%)	0	100	100
83	x	224/224 (100%)	224 (100%)	0	100	100
84	y	158/161 (98%)	158 (100%)	0	100	100
85	z	207/207 (100%)	207 (100%)	0	100	100
86	AB	340/364 (93%)	340 (100%)	0	100	100
88	AC	92/94 (98%)	92 (100%)	0	100	100
89	AI	157/171 (92%)	157 (100%)	0	100	100
90	AD	67/67 (100%)	67 (100%)	0	100	100
91	AE	69/85 (81%)	69 (100%)	0	100	100
92	AG	12/12 (100%)	12 (100%)	0	100	100
All	All	10802/10940 (99%)	10776 (100%)	26 (0%)	85	86

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	1	239	VAL
2	1	246	LEU
2	1	247	CYS
2	1	259	LEU
2	1	260	MET
13	B	262	VAL
15	C	71	ARG
15	C	321	ASN
17	DD	29	LEU
24	G	220	VAL
26	HH	11	LEU
27	I	24	ARG
28	II	8	LYS
37	N	64	ILE
41	P	127	ARG
41	P	128	ARG
48	SS	2	LEU
48	SS	89	ILE
53	VV	7	LEU
54	V	16	ILE
61	b	72	ILE
66	g	5	LEU
76	q	186	ARG
79	t	37	LEU
80	u	207	LEU
81	v	248	TYR

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

Mol	Chain	Res	Type
7	6	76	GLN
7	6	104	HIS
7	6	133	ASN
7	6	159	ASN
7	6	178	ASN
7	6	196	ASN
7	6	305	ASN
10	9	3	HIS
11	A	139	HIS
11	A	194	ASN
12	AA	88	GLN

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Mol	Chain	Res	Type
12	AA	95	GLN
12	AA	117	ASN
13	B	123	HIS
13	B	203	GLN
13	B	236	HIS
14	BB	73	GLN
14	BB	97	GLN
14	BB	186	ASN
14	BB	193	GLN
15	C	38	ASN
15	C	47	ASN
15	C	116	ASN
15	C	321	ASN
15	C	329	ASN
15	C	347	HIS
16	CC	84	ASN
16	CC	87	ASN
16	CC	99	ASN
16	CC	146	GLN
16	CC	165	GLN
17	DD	111	GLN
17	DD	124	HIS
18	D	122	GLN
18	D	157	ASN
18	D	202	GLN
19	EE	19	ASN
19	EE	83	GLN
19	EE	94	HIS
20	E	214	HIS
20	E	253	GLN
21	FF	29	GLN
22	F	38	GLN
22	F	79	ASN
22	F	109	GLN
22	F	118	ASN
22	F	205	ASN
23	GG	47	ASN
24	G	99	GLN
24	G	134	ASN
24	G	259	GLN
24	G	293	ASN
25	H	15	ASN

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Mol	Chain	Res	Type
25	H	76	HIS
25	H	102	ASN
26	HH	2	GLN
26	HH	47	ASN
26	HH	82	ASN
27	I	51	HIS
27	I	73	ASN
27	I	86	HIS
27	I	95	HIS
27	I	100	ASN
27	I	123	GLN
27	I	144	ASN
28	II	72	GLN
28	II	97	GLN
30	J	98	ASN
32	KK	62	GLN
34	LL	17	HIS
35	M	20	HIS
35	M	33	GLN
35	M	83	ASN
36	MM	83	GLN
37	N	32	GLN
37	N	57	GLN
37	N	117	ASN
37	N	149	GLN
37	N	196	ASN
38	NN	63	HIS
38	NN	89	HIS
38	NN	112	ASN
41	P	25	HIS
41	P	64	ASN
41	P	75	GLN
41	P	80	GLN
41	P	120	ASN
41	P	137	ASN
44	QQ	49	GLN
44	QQ	62	GLN
44	QQ	69	ASN
44	QQ	123	HIS
45	R	36	ASN
45	R	58	HIS
45	R	121	HIS

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Mol	Chain	Res	Type
45	R	141	HIS
45	R	178	GLN
46	RR	82	ASN
47	S	50	GLN
47	S	77	ASN
47	S	156	HIS
47	S	163	HIS
48	SS	44	HIS
48	SS	61	GLN
48	SS	84	HIS
49	T	70	HIS
49	T	79	GLN
49	T	127	GLN
50	TT	15	ASN
50	TT	56	HIS
50	TT	113	HIS
51	UU	35	ASN
51	UU	80	GLN
51	UU	86	GLN
51	UU	97	GLN
53	VV	23	HIS
54	V	77	HIS
55	W	17	HIS
55	W	59	HIS
57	X	57	GLN
57	X	73	HIS
57	X	93	ASN
57	X	107	HIS
57	X	111	GLN
58	Y	14	ASN
58	Y	65	GLN
60	a	34	ASN
60	a	62	HIS
60	a	120	GLN
61	b	101	HIS
62	c	51	ASN
63	d	18	ASN
63	d	28	ASN
63	d	34	HIS
63	d	79	ASN
64	e	68	HIS
65	f	24	HIS

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Mol	Chain	Res	Type
65	f	99	HIS
66	g	14	ASN
66	g	18	ASN
67	h	63	GLN
69	j	66	HIS
70	k	28	ASN
71	l	19	GLN
72	m	94	ASN
74	o	102	GLN
76	q	111	GLN
76	q	113	GLN
76	q	141	ASN
76	q	169	HIS
77	r	70	GLN
78	s	39	GLN
78	s	58	ASN
78	s	68	HIS
78	s	85	ASN
78	s	126	GLN
78	s	191	GLN
79	t	100	HIS
79	t	115	GLN
79	t	137	GLN
79	t	147	HIS
80	u	124	HIS
80	u	147	ASN
80	u	157	GLN
81	v	113	GLN
81	v	136	HIS
81	v	272	HIS
82	w	22	ASN
82	w	159	HIS
83	x	36	HIS
83	x	67	GLN
83	x	138	HIS
83	x	142	HIS
83	x	188	ASN
83	x	232	ASN
84	y	31	ASN
84	y	65	GLN
84	y	79	HIS
84	y	114	ASN

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Mol	Chain	Res	Type
85	z	59	GLN
86	AB	70	ASN
86	AB	195	HIS
86	AB	335	GLN
89	AI	65	HIS
89	AI	91	ASN
89	AI	157	HIS
90	AD	66	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	2	73/75 (97%)	20 (27%)	1 (1%)
31	K	1686/1698 (99%)	345 (20%)	21 (1%)
4	3	72/75 (96%)	15 (20%)	0
5	4	5/6 (83%)	3 (60%)	0
6	5	3519/3544 (99%)	782 (22%)	67 (1%)
8	7	119/120 (99%)	14 (11%)	0
87	AF	197/206 (95%)	32 (16%)	4 (2%)
9	8	149/151 (98%)	34 (22%)	1 (0%)
All	All	5820/5875 (99%)	1245 (21%)	94 (1%)

All (1245) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
3	2	5	C
3	2	7	G
3	2	8	U
3	2	9	A
3	2	13	C
3	2	16	C
3	2	19	G
3	2	20	C
3	2	21	A
3	2	35	A
3	2	42	A
3	2	47	U
3	2	52	G
3	2	58	A
3	2	63	A
3	2	64	U

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Mol	Chain	Res	Type
3	2	72	C
3	2	74	C
3	2	75	C
3	2	76	A
4	3	7	A
4	3	13	C
4	3	16	C
4	3	21	A
4	3	34	U
4	3	35	A
4	3	47	U
4	3	49	C
4	3	58	A
4	3	61	C
4	3	63	C
4	3	65	G
4	3	69	G
4	3	70	G
4	3	76	A
5	4	44	U
5	4	45	A
5	4	46	A
6	5	12	A
6	5	13	U
6	5	17	A
6	5	25	A
6	5	30	C
6	5	35	U
6	5	39	A
6	5	42	A
6	5	43	U
6	5	47	A
6	5	48	G
6	5	49	U
6	5	56	A
6	5	59	A
6	5	64	A
6	5	65	A
6	5	66	A
6	5	71	C
6	5	73	A
6	5	91	G

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Mol	Chain	Res	Type
6	5	93	G
6	5	104	G
6	5	109	G
6	5	110	C
6	5	116	G
6	5	117	C
6	5	118	C
6	5	119	G
6	5	126	C
6	5	134	G
6	5	135	G
6	5	136	C
6	5	137	G
6	5	151	G
6	5	157	U
6	5	159	C
6	5	171	U
6	5	172	C
6	5	173	C
6	5	191	A
6	5	194	U
6	5	195	C
6	5	196	C
6	5	199	C
6	5	203	U
6	5	210	C
6	5	211	C
6	5	212	A
6	5	214	C
6	5	215	C
6	5	218	U
6	5	220	G
6	5	221	A
6	5	227	U
6	5	228	G
6	5	240	G
6	5	256	G
6	5	259	C
6	5	260	C
6	5	270	C
6	5	274	G
6	5	275	U

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Mol	Chain	Res	Type
6	5	291	U
6	5	300	A
6	5	303	C
6	5	309	G
6	5	310	U
6	5	316	C
6	5	320	C
6	5	328	A
6	5	334	C
6	5	339	C
6	5	344	C
6	5	357	A
6	5	380	A
6	5	381	G
6	5	393	G
6	5	401	A
6	5	404	A
6	5	406	G
6	5	407	G
6	5	425	G
6	5	426	U
6	5	434	U
6	5	440	C
6	5	443	C
6	5	444	G
6	5	446	A
6	5	447	G
6	5	448	U
6	5	458	G
6	5	461	U
6	5	462	U
6	5	475	G
6	5	476	C
6	5	477	G
6	5	478	G
6	5	480	C
6	5	481	C
6	5	487	U
6	5	488	G
6	5	490	C
6	5	492	G
6	5	493	C

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Mol	Chain	Res	Type
6	5	494	G
6	5	497	G
6	5	502	U
6	5	517	G
6	5	525	A
6	5	534	C
6	5	542	G
6	5	543	A
6	5	545	C
6	5	546	G
6	5	559	C
6	5	561	C
6	5	563	U
6	5	572	C
6	5	573	G
6	5	580	C
6	5	581	G
6	5	584	G
6	5	595	C
6	5	606	G
6	5	607	G
6	5	614	C
6	5	615	C
6	5	616	G
6	5	619	G
6	5	624	A
6	5	625	G
6	5	626	G
6	5	628	G
6	5	635	G
6	5	647	U
6	5	648	U
6	5	651	A
6	5	652	G
6	5	659	C
6	5	661	C
6	5	662	G
6	5	664	C
6	5	665	A
6	5	667	C
6	5	668	A
6	5	669	G

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Mol	Chain	Res	Type
6	5	670	C
6	5	671	A
6	5	672	G
6	5	673	C
6	5	676	G
6	5	678	C
6	5	680	A
6	5	681	A
6	5	682	U
6	5	696	G
6	5	697	A
6	5	698	G
6	5	699	C
6	5	701	A
6	5	702	G
6	5	703	A
6	5	704	C
6	5	705	C
6	5	706	C
6	5	710	C
6	5	717	C
6	5	721	C
6	5	728	C
6	5	737	C
6	5	738	G
6	5	741	C
6	5	744	C
6	5	747	C
6	5	754	G
6	5	773	A
6	5	777	U
6	5	778	C
6	5	780	A
6	5	783	G
6	5	791	G
6	5	807	G
6	5	808	G
6	5	810	C
6	5	811	C
6	5	817	G
6	5	818	G
6	5	819	C

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Mol	Chain	Res	Type
6	5	820	C
6	5	821	A
6	5	822	C
6	5	833	C
6	5	834	G
6	5	837	C
6	5	838	G
6	5	845	G
6	5	848	G
6	5	853	C
6	5	854	G
6	5	855	A
6	5	856	U
6	5	857	G
6	5	862	C
6	5	864	A
6	5	865	C
6	5	875	C
6	5	879	C
6	5	880	U
6	5	887	A
6	5	890	G
6	5	891	A
6	5	915	A
6	5	919	G
6	5	920	G
6	5	929	A
6	5	935	G
6	5	937	C
6	5	938	G
6	5	939	U
6	5	945	A
6	5	952	G
6	5	955	A
6	5	956	A
6	5	976	G
6	5	977	G
6	5	980	G
6	5	981	A
6	5	982	G
6	5	990	C
6	5	998	C

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Mol	Chain	Res	Type
6	5	999	U
6	5	1000	U
6	5	1001	C
6	5	1005	U
6	5	1006	C
6	5	1008	G
6	5	1013	G
6	5	1016	C
6	5	1017	G
6	5	1018	C
6	5	1025	G
6	5	1035	G
6	5	1038	C
6	5	1042	G
6	5	1043	C
6	5	1044	G
6	5	1049	G
6	5	1057	A
6	5	1058	G
6	5	1061	C
6	5	1062	G
6	5	1074	U
6	5	1076	G
6	5	1078	A
6	5	1083	A
6	5	1085	A
6	5	1094	A
6	5	1103	G
6	5	1107	A
6	5	1123	A
6	5	1124	A
6	5	1126	C
6	5	1134	G
6	5	1138	U
6	5	1151	U
6	5	1156	U
6	5	1157	G
6	5	1162	U
6	5	1172	G
6	5	1173	A
6	5	1174	C
6	5	1184	G

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Mol	Chain	Res	Type
6	5	1185	G
6	5	1191	A
6	5	1193	G
6	5	1194	A
6	5	1198	A
6	5	1201	G
6	5	1210	A
6	5	1214	G
6	5	1220	U
6	5	1221	C
6	5	1236	C
6	5	1237	U
6	5	1239	A
6	5	1251	G
6	5	1270	G
6	5	1271	G
6	5	1277	C
6	5	1278	G
6	5	1279	A
6	5	1283	A
6	5	1287	G
6	5	1292	C
6	5	1293	U
6	5	1298	G
6	5	1301	G
6	5	1305	C
6	5	1309	C
6	5	1310	U
6	5	1313	A
6	5	1314	C
6	5	1318	U
6	5	1324	A
6	5	1336	G
6	5	1340	G
6	5	1341	A
6	5	1342	A
6	5	1349	C
6	5	1352	G
6	5	1356	G
6	5	1358	G
6	5	1359	U
6	5	1365	C

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Mol	Chain	Res	Type
6	5	1367	G
6	5	1371	U
6	5	1372	G
6	5	1373	G
6	5	1374	A
6	5	1379	G
6	5	1392	G
6	5	1406	G
6	5	1418	C
6	5	1430	C
6	5	1434	A
6	5	1443	U
6	5	1447	G
6	5	1455	U
6	5	1457	C
6	5	1458	C
6	5	1459	G
6	5	1460	A
6	5	1462	G
6	5	1467	U
6	5	1468	C
6	5	1469	A
6	5	1485	G
6	5	1494	U
6	5	1495	A
6	5	1496	U
6	5	1497	A
6	5	1498	G
6	5	1499	A
6	5	1501	A
6	5	1504	A
6	5	1508	U
6	5	1511	U
6	5	1512	G
6	5	1514	C
6	5	1517	U
6	5	1520	A
6	5	1521	A
6	5	1523	U
6	5	1524	C
6	5	1528	A
6	5	1534	U

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Mol	Chain	Res	Type
6	5	1538	G
6	5	1539	A
6	5	1540	G
6	5	1541	U
6	5	1545	U
6	5	1548	C
6	5	1562	A
6	5	1563	A
6	5	1584	A
6	5	1585	U
6	5	1589	G
6	5	1592	G
6	5	1593	G
6	5	1599	C
6	5	1601	G
6	5	1606	A
6	5	1607	U
6	5	1621	U
6	5	1622	G
6	5	1626	G
6	5	1627	U
6	5	1629	G
6	5	1630	G
6	5	1631	C
6	5	1632	A
6	5	1634	A
6	5	1635	G
6	5	1637	G
6	5	1639	G
6	5	1641	A
6	5	1642	A
6	5	1644	A
6	5	1645	G
6	5	1647	G
6	5	1652	G
6	5	1653	C
6	5	1655	G
6	5	1659	C
6	5	1660	U
6	5	1661	A
6	5	1662	C
6	5	1663	G

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Mol	Chain	Res	Type
6	5	1668	G
6	5	1682	C
6	5	1693	A
6	5	1694	G
6	5	1699	G
6	5	1706	A
6	5	1707	G
6	5	1709	G
6	5	1724	G
6	5	1726	G
6	5	1741	G
6	5	1744	C
6	5	1753	A
6	5	1763	A
6	5	1775	A
6	5	1777	U
6	5	1788	A
6	5	1789	A
6	5	1809	G
6	5	1815	C
6	5	1817	G
6	5	1818	U
6	5	1826	G
6	5	1834	C
6	5	1843	G
6	5	1864	G
6	5	1868	G
6	5	1878	U
6	5	1881	C
6	5	1882	C
6	5	1883	U
6	5	1884	C
6	5	1886	G
6	5	1896	G
6	5	1897	C
6	5	1898	C
6	5	1899	G
6	5	1906	A
6	5	1922	A
6	5	1923	U
6	5	1930	A
6	5	1939	G

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Mol	Chain	Res	Type
6	5	1940	G
6	5	1942	G
6	5	1946	A
6	5	1947	U
6	5	1959	G
6	5	1963	U
6	5	1965	C
6	5	1968	U
6	5	1974	A
6	5	1976	C
6	5	1979	G
6	5	1980	A
6	5	1982	C
6	5	1994	A
6	5	2013	G
6	5	2031	G
6	5	2051	G
6	5	2054	U
6	5	2055	G
6	5	2062	C
6	5	2063	C
6	5	2066	G
6	5	2069	A
6	5	2074	G
6	5	2079	G
6	5	2080	U
6	5	2082	C
6	5	2088	A
6	5	2089	A
6	5	2097	C
6	5	2100	U
6	5	2101	U
6	5	2104	G
6	5	2105	G
6	5	2109	C
6	5	2112	C
6	5	2114	G
6	5	2118	A
6	5	2119	G
6	5	2128	G
6	5	2133	U
6	5	2137	A

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Mol	Chain	Res	Type
6	5	2147	G
6	5	2153	G
6	5	2154	U
6	5	2156	U
6	5	2157	A
6	5	2165	C
6	5	2180	A
6	5	2181	U
6	5	2182	A
6	5	2183	U
6	5	2199	A
6	5	2200	A
6	5	2204	G
6	5	2207	C
6	5	2219	U
6	5	2220	G
6	5	2221	U
6	5	2231	G
6	5	2235	G
6	5	2248	G
6	5	2268	C
6	5	2291	G
6	5	2296	C
6	5	2302	A
6	5	2303	C
6	5	2304	U
6	5	2313	G
6	5	2323	G
6	5	2324	G
6	5	2328	A
6	5	2333	A
6	5	2355	U
6	5	2360	A
6	5	2371	C
6	5	2378	U
6	5	2386	U
6	5	2390	A
6	5	2396	G
6	5	2400	A
6	5	2409	A
6	5	2427	U
6	5	2446	A

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Mol	Chain	Res	Type
6	5	2451	G
6	5	2457	A
6	5	2458	A
6	5	2461	A
6	5	2463	G
6	5	2470	U
6	5	2471	U
6	5	2472	A
6	5	2473	A
6	5	2474	G
6	5	2475	G
6	5	2476	U
6	5	2481	A
6	5	2482	A
6	5	2484	U
6	5	2497	A
6	5	2508	C
6	5	2510	C
6	5	2512	U
6	5	2515	A
6	5	2517	G
6	5	2536	U
6	5	2537	G
6	5	2538	U
6	5	2541	C
6	5	2574	A
6	5	2575	A
6	5	2576	C
6	5	2577	G
6	5	2587	G
6	5	2590	U
6	5	2595	G
6	5	2596	G
6	5	2599	A
6	5	2603	A
6	5	2604	A
6	5	2605	G
6	5	2606	A
6	5	2607	C
6	5	2608	C
6	5	2613	U
6	5	2614	G

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Mol	Chain	Res	Type
6	5	2615	A
6	5	2625	U
6	5	2636	G
6	5	2637	G
6	5	2639	G
6	5	2644	G
6	5	2651	U
6	5	2655	A
6	5	2658	G
6	5	2667	A
6	5	2668	G
6	5	2670	C
6	5	2693	C
6	5	2696	C
6	5	2697	U
6	5	2699	G
6	5	2704	A
6	5	2728	C
6	5	2732	C
6	5	2733	U
6	5	2736	G
6	5	2740	A
6	5	2741	C
6	5	2743	G
6	5	2753	G
6	5	2754	G
6	5	2761	G
6	5	2773	A
6	5	2782	A
6	5	2795	G
6	5	2799	U
6	5	2802	U
6	5	2803	A
6	5	2813	C
6	5	2819	G
6	5	2821	A
6	5	2824	G
6	5	2835	U
6	5	2836	G
6	5	2838	A
6	5	2841	A
6	5	2843	A

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Mol	Chain	Res	Type
6	5	2851	A
6	5	2852	A
6	5	2861	G
6	5	2866	U
6	5	2867	G
6	5	2874	A
6	5	2875	G
6	5	2876	U
6	5	2883	A
6	5	2884	C
6	5	2889	C
6	5	2896	G
6	5	2900	G
6	5	2902	C
6	5	2918	A
6	5	2919	C
6	5	2920	C
6	5	2924	U
6	5	2925	G
6	5	2943	G
6	5	2947	G
6	5	2948	A
6	5	2949	A
6	5	2955	A
6	5	2957	C
6	5	2963	G
6	5	2964	A
6	5	2965	U
6	5	2966	A
6	5	2968	C
6	5	2969	U
6	5	2971	G
6	5	2989	U
6	5	2991	C
6	5	2992	A
6	5	3006	U
6	5	3007	U
6	5	3010	G
6	5	3014	C
6	5	3016	U
6	5	3017	C
6	5	3018	G

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Mol	Chain	Res	Type
6	5	3019	A
6	5	3021	G
6	5	3023	C
6	5	3034	A
6	5	3041	U
6	5	3045	G
6	5	3058	A
6	5	3065	G
6	5	3070	U
6	5	3081	A
6	5	3082	U
6	5	3083	A
6	5	3085	G
6	5	3088	A
6	5	3089	C
6	5	3090	G
6	5	3094	G
6	5	3101	U
6	5	3102	U
6	5	3118	A
6	5	3130	C
6	5	3137	G
6	5	3143	G
6	5	3144	U
6	5	3145	G
6	5	3147	U
6	5	3154	A
6	5	3156	G
6	5	3157	G
6	5	3160	A
6	5	3169	A
6	5	3194	A
6	5	3205	A
6	5	3206	U
6	5	3207	G
6	5	3209	G
6	5	3222	G
6	5	3226	A
6	5	3227	U
6	5	3231	G
6	5	3237	C
6	5	3240	C

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Mol	Chain	Res	Type
6	5	3242	A
6	5	3247	U
6	5	3248	G
6	5	3270	A
6	5	3279	U
6	5	3288	G
6	5	3289	G
6	5	3290	C
6	5	3301	C
6	5	3303	C
6	5	3308	G
6	5	3313	G
6	5	3314	G
6	5	3317	G
6	5	3319	C
6	5	3320	C
6	5	3322	C
6	5	3327	A
6	5	3328	G
6	5	3333	U
6	5	3334	C
6	5	3335	C
6	5	3338	C
6	5	3349	G
6	5	3352	G
6	5	3353	C
6	5	3354	G
6	5	3355	G
6	5	3357	G
6	5	3358	A
6	5	3359	G
6	5	3363	U
6	5	3364	U
6	5	3365	C
6	5	3367	U
6	5	3377	C
6	5	3390	A
6	5	3393	G
6	5	3394	G
6	5	3395	G
6	5	3398	C
6	5	3399	G

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Mol	Chain	Res	Type
6	5	3401	C
6	5	3402	C
6	5	3405	U
6	5	3406	C
6	5	3407	G
6	5	3408	C
6	5	3411	G
6	5	3414	A
6	5	3417	C
6	5	3418	A
6	5	3420	C
6	5	3423	A
6	5	3424	C
6	5	3427	U
6	5	3428	C
6	5	3429	G
6	5	3430	U
6	5	3431	G
6	5	3435	A
6	5	3436	A
6	5	3437	C
6	5	3438	C
6	5	3440	G
6	5	3444	C
6	5	3445	U
6	5	3446	A
6	5	3447	A
6	5	3456	U
6	5	3459	A
6	5	3468	U
6	5	3469	U
6	5	3470	C
6	5	3473	G
6	5	3479	G
6	5	3486	U
6	5	3487	A
6	5	3494	A
6	5	3497	G
6	5	3515	U
6	5	3516	G
6	5	3522	C
6	5	3525	C

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Mol	Chain	Res	Type
6	5	3527	C
6	5	3528	U
6	5	3529	C
6	5	3531	A
6	5	3536	A
6	5	3537	G
8	7	7	G
8	7	22	A
8	7	25	G
8	7	33	U
8	7	53	U
8	7	54	A
8	7	63	C
8	7	64	G
8	7	97	G
8	7	100	A
8	7	106	G
8	7	110	G
8	7	111	C
8	7	120	U
9	8	2	G
9	8	3	A
9	8	16	G
9	8	23	C
9	8	34	U
9	8	35	C
9	8	39	G
9	8	49	G
9	8	51	U
9	8	59	A
9	8	62	A
9	8	63	U
9	8	70	G
9	8	71	A
9	8	75	G
9	8	79	G
9	8	87	G
9	8	94	G
9	8	95	A
9	8	99	U
9	8	103	A
9	8	105	C

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Mol	Chain	Res	Type
9	8	107	C
9	8	109	C
9	8	110	U
9	8	111	U
9	8	114	G
9	8	123	U
9	8	125	C
9	8	126	C
9	8	127	U
9	8	128	C
9	8	147	G
9	8	150	C
31	K	2	A
31	K	3	C
31	K	20	G
31	K	25	A
31	K	26	U
31	K	33	G
31	K	41	G
31	K	42	A
31	K	44	U
31	K	46	A
31	K	56	G
31	K	58	C
31	K	62	G
31	K	65	C
31	K	67	C
31	K	68	A
31	K	71	G
31	K	73	C
31	K	74	G
31	K	75	G
31	K	77	A
31	K	79	A
31	K	99	A
31	K	103	A
31	K	111	A
31	K	113	G
31	K	115	U
31	K	124	U
31	K	126	G
31	K	129	C

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Mol	Chain	Res	Type
31	K	130	G
31	K	141	A
31	K	143	U
31	K	147	A
31	K	154	U
31	K	155	G
31	K	158	A
31	K	162	C
31	K	163	U
31	K	168	C
31	K	180	G
31	K	182	C
31	K	183	G
31	K	184	G
31	K	188	C
31	K	190	G
31	K	191	A
31	K	192	C
31	K	202	G
31	K	215	G
31	K	294	U
31	K	302	A
31	K	304	C
31	K	305	U
31	K	307	G
31	K	308	G
31	K	309	G
31	K	311	C
31	K	312	G
31	K	314	U
31	K	318	A
31	K	319	C
31	K	323	C
31	K	332	G
31	K	335	G
31	K	339	A
31	K	347	G
31	K	350	C
31	K	351	G
31	K	360	A
31	K	364	A
31	K	368	U

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Mol	Chain	Res	Type
31	K	370	G
31	K	381	C
31	K	385	G
31	K	386	C
31	K	398	A
31	K	400	C
31	K	407	G
31	K	408	A
31	K	409	C
31	K	417	C
31	K	418	A
31	K	426	A
31	K	435	A
31	K	438	G
31	K	448	A
31	K	450	C
31	K	460	A
31	K	464	A
31	K	465	A
31	K	466	G
31	K	471	G
31	K	472	C
31	K	473	A
31	K	474	G
31	K	476	A
31	K	482	G
31	K	487	U
31	K	492	C
31	K	496	C
31	K	525	A
31	K	532	C
31	K	533	A
31	K	542	U
31	K	544	G
31	K	547	G
31	K	548	C
31	K	549	C
31	K	550	C
31	K	551	U
31	K	554	A
31	K	555	A
31	K	556	U

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Mol	Chain	Res	Type
31	K	559	G
31	K	560	A
31	K	563	G
31	K	564	A
31	K	568	C
31	K	570	C
31	K	576	A
31	K	583	A
31	K	587	A
31	K	588	G
31	K	590	A
31	K	591	U
31	K	606	G
31	K	608	C
31	K	614	C
31	K	617	G
31	K	621	C
31	K	643	A
31	K	644	G
31	K	660	C
31	K	664	A
31	K	668	A
31	K	669	A
31	K	670	A
31	K	671	A
31	K	672	A
31	K	673	G
31	K	683	G
31	K	688	U
31	K	689	U
31	K	690	G
31	K	752	G
31	K	753	C
31	K	754	G
31	K	798	G
31	K	799	U
31	K	811	A
31	K	821	G
31	K	822	U
31	K	830	A
31	K	833	C
31	K	834	C

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Mol	Chain	Res	Type
31	K	844	U
31	K	847	A
31	K	867	G
31	K	870	A
31	K	871	U
31	K	872	A
31	K	873	G
31	K	874	G
31	K	875	A
31	K	878	G
31	K	887	U
31	K	890	U
31	K	892	U
31	K	907	G
31	K	913	A
31	K	914	U
31	K	920	A
31	K	933	G
31	K	934	G
31	K	943	U
31	K	955	A
31	K	971	G
31	K	990	A
31	K	992	A
31	K	999	G
31	K	1017	U
31	K	1023	A
31	K	1041	G
31	K	1045	U
31	K	1060	A
31	K	1062	A
31	K	1067	C
31	K	1083	A
31	K	1085	C
31	K	1100	A
31	K	1111	U
31	K	1115	U
31	K	1116	C
31	K	1117	C
31	K	1118	C
31	K	1123	C
31	K	1126	G

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Mol	Chain	Res	Type
31	K	1131	G
31	K	1133	A
31	K	1138	C
31	K	1139	C
31	K	1149	A
31	K	1153	C
31	K	1154	U
31	K	1155	U
31	K	1170	A
31	K	1195	A
31	K	1207	G
31	K	1208	A
31	K	1215	C
31	K	1221	G
31	K	1224	G
31	K	1242	U
31	K	1243	U
31	K	1251	A
31	K	1253	A
31	K	1254	C
31	K	1255	G
31	K	1256	G
31	K	1257	G
31	K	1259	A
31	K	1264	C
31	K	1271	C
31	K	1274	G
31	K	1275	G
31	K	1280	G
31	K	1281	G
31	K	1282	A
31	K	1284	A
31	K	1285	G
31	K	1286	G
31	K	1294	G
31	K	1298	G
31	K	1299	A
31	K	1301	A
31	K	1302	G
31	K	1303	C
31	K	1304	U
31	K	1307	U

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Mol	Chain	Res	Type
31	K	1308	U
31	K	1313	A
31	K	1314	U
31	K	1315	U
31	K	1316	C
31	K	1322	G
31	K	1333	U
31	K	1341	C
31	K	1342	U
31	K	1348	G
31	K	1371	U
31	K	1372	U
31	K	1376	A
31	K	1378	A
31	K	1382	A
31	K	1395	C
31	K	1396	A
31	K	1397	U
31	K	1401	A
31	K	1402	A
31	K	1404	U
31	K	1410	C
31	K	1412	C
31	K	1428	G
31	K	1439	A
31	K	1442	U
31	K	1449	G
31	K	1454	A
31	K	1462	U
31	K	1463	U
31	K	1466	G
31	K	1473	G
31	K	1476	A
31	K	1477	U
31	K	1487	A
31	K	1489	A
31	K	1490	G
31	K	1494	U
31	K	1498	A
31	K	1507	G
31	K	1509	U
31	K	1510	G

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Mol	Chain	Res	Type
31	K	1521	C
31	K	1522	A
31	K	1523	C
31	K	1531	A
31	K	1533	A
31	K	1536	G
31	K	1544	C
31	K	1545	A
31	K	1548	G
31	K	1552	G
31	K	1553	C
31	K	1556	A
31	K	1557	C
31	K	1560	U
31	K	1570	G
31	K	1574	C
31	K	1575	G
31	K	1580	A
31	K	1585	U
31	K	1586	U
31	K	1587	G
31	K	1588	A
31	K	1601	A
31	K	1604	G
31	K	1621	U
31	K	1623	A
31	K	1637	A
31	K	1638	G
31	K	1646	C
31	K	1648	G
31	K	1649	U
31	K	1654	G
31	K	1665	G
31	K	1680	G
31	K	1683	C
31	K	1686	G
31	K	1695	A
31	K	1698	C
31	K	1699	A
31	K	1721	U
31	K	1722	G
31	K	1726	G

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Mol	Chain	Res	Type
31	K	1729	U
31	K	1732	G
31	K	1744	G
31	K	1753	C
31	K	1783	C
31	K	1785	C
31	K	1823	A
31	K	1825	A
31	K	1826	G
31	K	1829	G
31	K	1831	A
31	K	1836	G
31	K	1838	U
31	K	1849	G
31	K	1851	A
31	K	1852	C
31	K	1861	G
31	K	1862	G
31	K	1863	A
31	K	1865	C
31	K	1866	A
87	AF	4	G
87	AF	17	C
87	AF	24	G
87	AF	32	A
87	AF	33	G
87	AF	36	A
87	AF	38	U
87	AF	39	C
87	AF	40	G
87	AF	54	G
87	AF	120	G
87	AF	144	C
87	AF	151	C
87	AF	167	U
87	AF	173	A
87	AF	174	G
87	AF	175	G
87	AF	176	A
87	AF	177	G
87	AF	182	G
87	AF	183	A

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Mol	Chain	Res	Type
87	AF	184	A
87	AF	185	C
87	AF	186	C
87	AF	191	C
87	AF	202	C
87	AF	206	G
87	AF	212	C
87	AF	227	G
87	AF	235	G
87	AF	236	U
87	AF	287	A

All (94) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	2	20	C
6	5	47	A
6	5	48	G
6	5	125	C
6	5	134	G
6	5	211	C
6	5	220	G
6	5	239	C
6	5	259	C
6	5	269	C
6	5	379	A
6	5	400	C
6	5	443	C
6	5	474	C
6	5	480	C
6	5	496	G
6	5	572	C
6	5	666	G
6	5	696	G
6	5	703	A
6	5	709	G
6	5	737	C
6	5	772	G
6	5	807	G
6	5	819	C
6	5	821	A
6	5	852	G

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Mol	Chain	Res	Type
6	5	890	G
6	5	928	G
6	5	1000	U
6	5	1005	U
6	5	1015	G
6	5	1193	G
6	5	1341	A
6	5	1355	G
6	5	1371	U
6	5	1372	G
6	5	1458	C
6	5	1516	A
6	5	1520	A
6	5	1583	G
6	5	1605	C
6	5	1626	G
6	5	1659	C
6	5	1867	G
6	5	1895	A
6	5	1939	G
6	5	2054	U
6	5	2088	A
6	5	2187	C
6	5	2323	G
6	5	2395	U
6	5	2574	A
6	5	2586	G
6	5	2606	A
6	5	2696	C
6	5	2740	A
6	5	2802	U
6	5	2963	G
6	5	3018	G
6	5	3019	A
6	5	3101	U
6	5	3269	U
6	5	3289	G
6	5	3366	G
6	5	3405	U
6	5	3416	G
6	5	3427	U
9	8	124	U

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Mol	Chain	Res	Type
31	K	110	U
31	K	182	C
31	K	434	G
31	K	465	A
31	K	532	C
31	K	553	U
31	K	642	U
31	K	688	U
31	K	752	G
31	K	870	A
31	K	1137	U
31	K	1253	A
31	K	1394	G
31	K	1395	C
31	K	1396	A
31	K	1489	A
31	K	1520	G
31	K	1637	A
31	K	1664	A
31	K	1679	A
31	K	1824	A
87	AF	37	C
87	AF	38	U
87	AF	39	C
87	AF	234	A

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 304 ligands modelled in this entry, 304 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
6	5	25
31	K	11
87	AF	2
4	3	2
9	8	1
3	2	1
86	AB	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	AF	237:U	O3'	282:U	P	93.22
1	AF	65:U	O3'	114:G	P	86.59
1	5	1650:G	O3'	1651:C	P	41.09
1	5	831:C	O3'	832:G	P	36.72
1	5	815:G	O3'	816:G	P	22.49
1	5	2646:C	O3'	2647:G	P	19.48
1	5	968:G	O3'	969:C	P	18.41
1	K	697:G	O3'	729:C	P	18.40
1	5	728:C	O3'	729:G	P	18.12
1	K	1761:U	O3'	1771:G	P	17.91
1	5	513:C	O3'	514:G	P	17.83
1	K	756:C	O3'	788:G	P	17.68
1	5	2683:C	O3'	2684:G	P	17.61
1	5	2715:C	O3'	2716:G	P	17.40
1	K	834:C	O3'	841:G	P	17.12
1	K	323:C	O3'	329:G	P	16.83
1	5	3340:C	O3'	3341:C	P	16.53

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	K	130:G	O3'	140:U	P	15.98
1	K	1417:C	O3'	1423:C	P	15.83
1	5	637:G	O3'	638:C	P	15.07
1	5	1256:C	O3'	1257:C	P	15.04
1	5	3502:U	O3'	3503:G	P	14.51
1	5	182:G	O3'	183:G	P	13.41
1	5	2294:G	O3'	2295:G	P	13.31
1	5	925:U	O3'	926:A	P	12.92
1	8	79:G	O3'	85:U	P	12.74
1	5	3299:A	O3'	3300:G	P	9.51
1	5	778:C	O3'	779:C	P	9.49
1	5	504:U	O3'	505:C	P	8.80
1	K	225:G	O3'	287:U	P	8.21
1	K	745:C	O3'	749:U	P	7.79
1	K	736:C	O3'	743:U	P	6.78
1	3	19:G	O3'	20:U	P	6.01
1	5	822:C	O3'	823:G	P	5.85
1	5	495:G	O3'	496:G	P	5.68
1	2	16:C	O3'	18:G	P	5.39
1	5	765:U	O3'	766:G	P	5.23
1	3	16:C	O3'	18:U	P	4.84
1	5	3305:G	O3'	3306:G	P	4.59
1	K	1432:U	O3'	1438:A	P	4.12
1	5	3381:G	O3'	3382:C	P	3.53
1	5	999:U	O3'	1000:U	P	3.35
1	AB	86:LEU	C	87:VAL	N	3.26

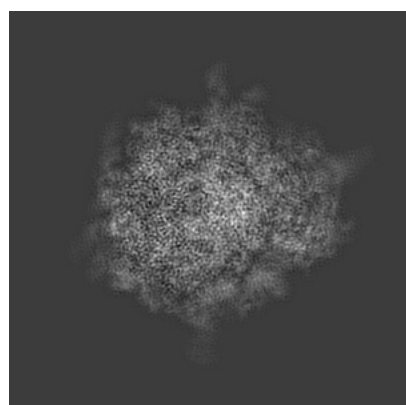
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4735. These allow visual inspection of the internal detail of the map and identification of artifacts.

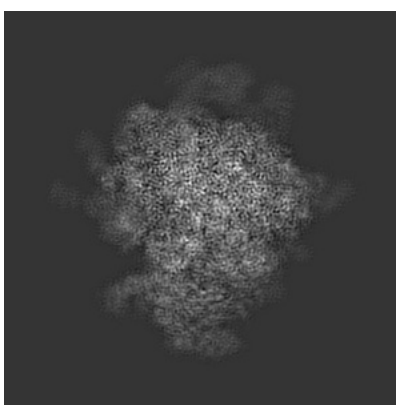
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

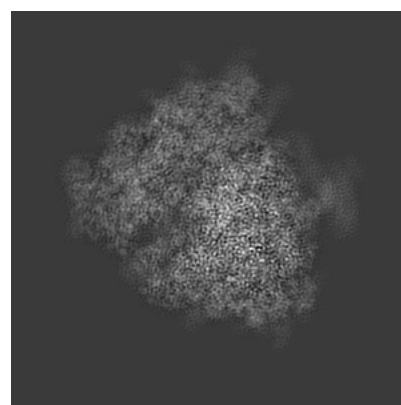
6.1.1 Primary map



X



Y

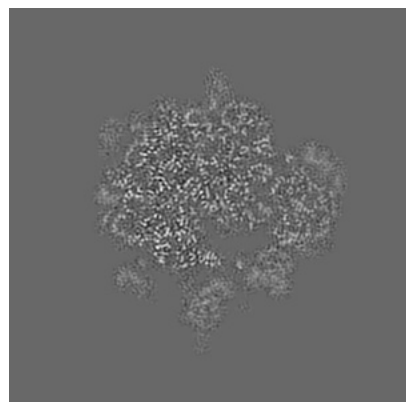


Z

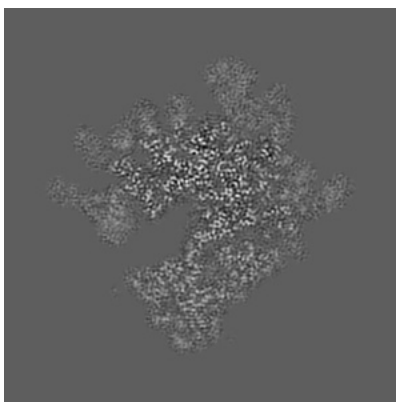
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 198



Y Index: 198

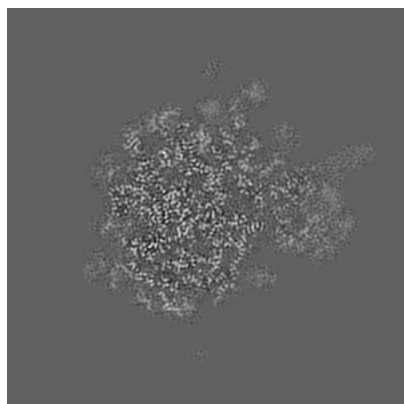


Z Index: 198

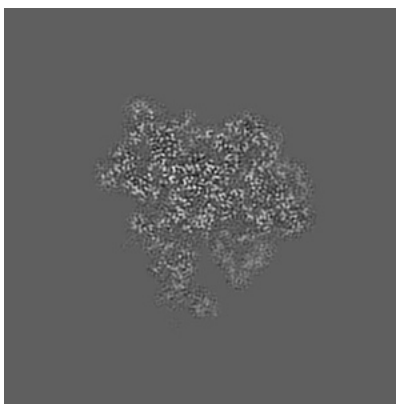
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

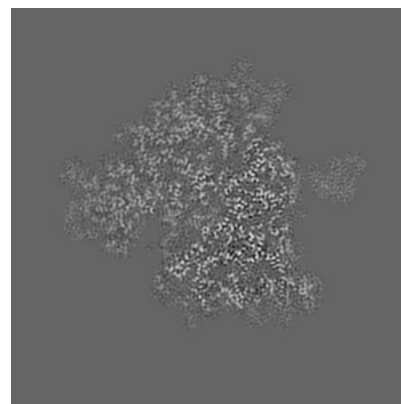
6.3.1 Primary map



X Index: 229



Y Index: 160

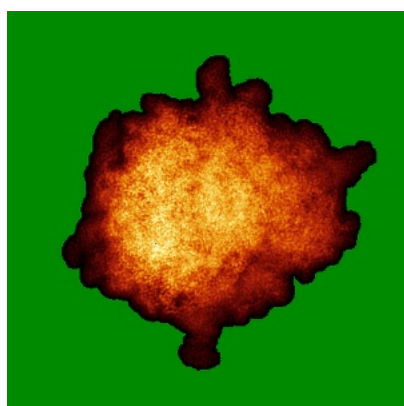


Z Index: 191

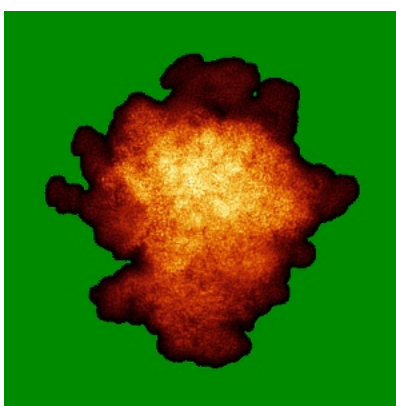
The images above show the largest variance slices of the map in three orthogonal directions.

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

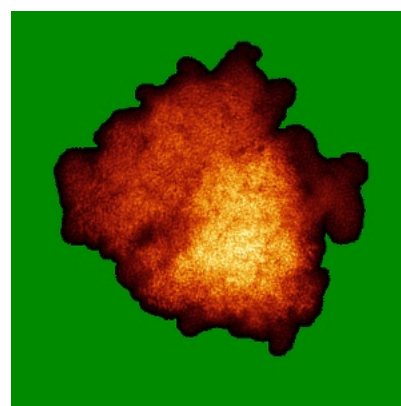
6.4.1 Primary map



X



Y

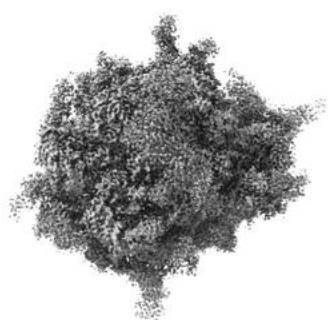


Z

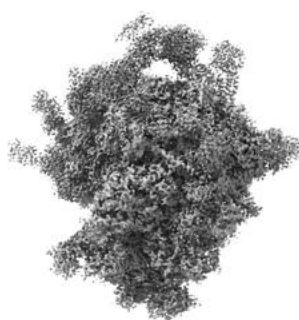
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

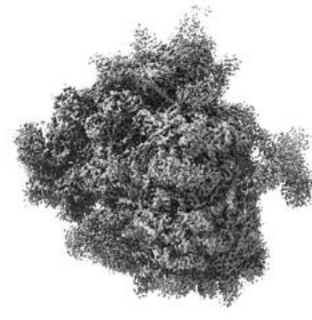
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.08. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

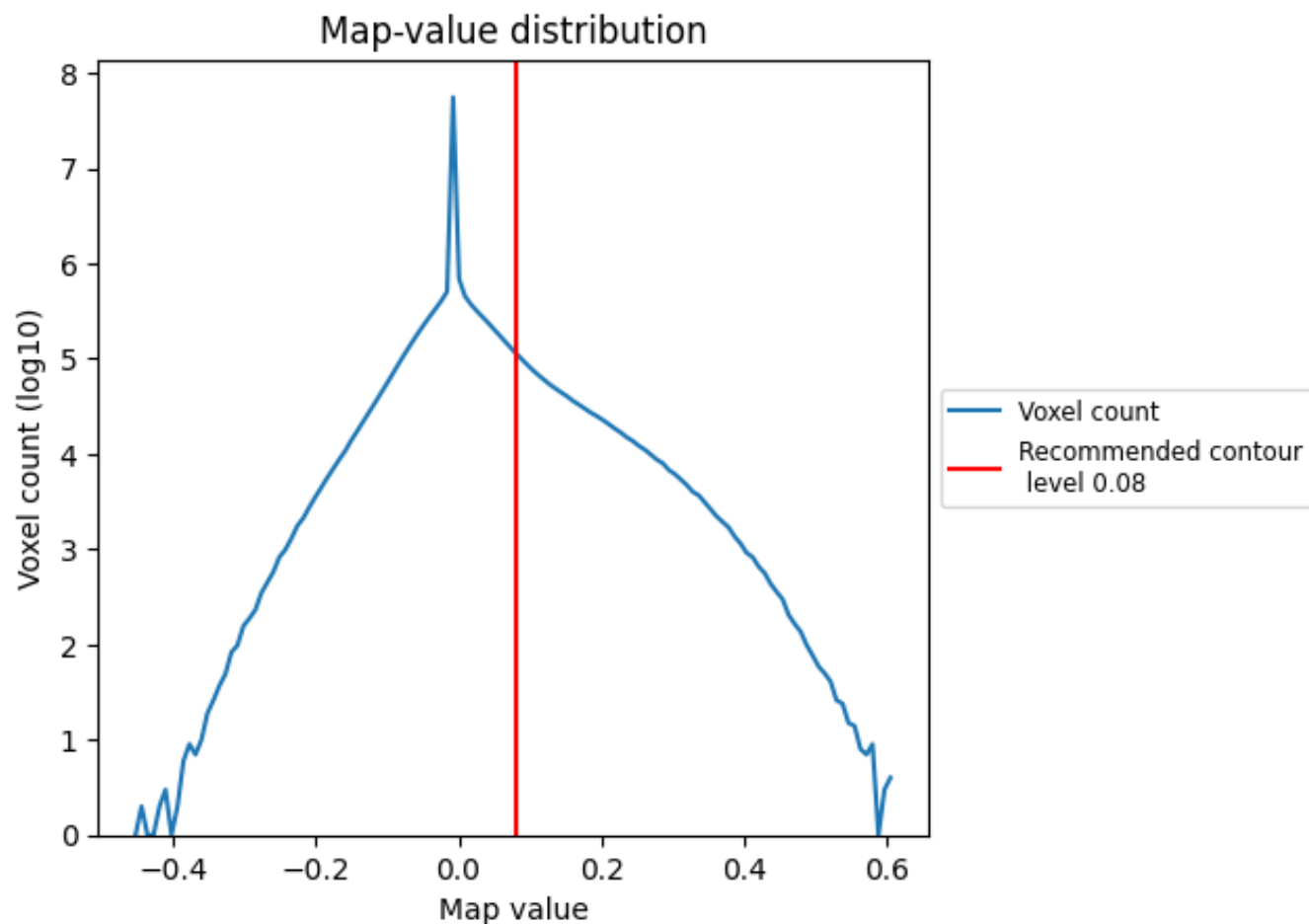
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

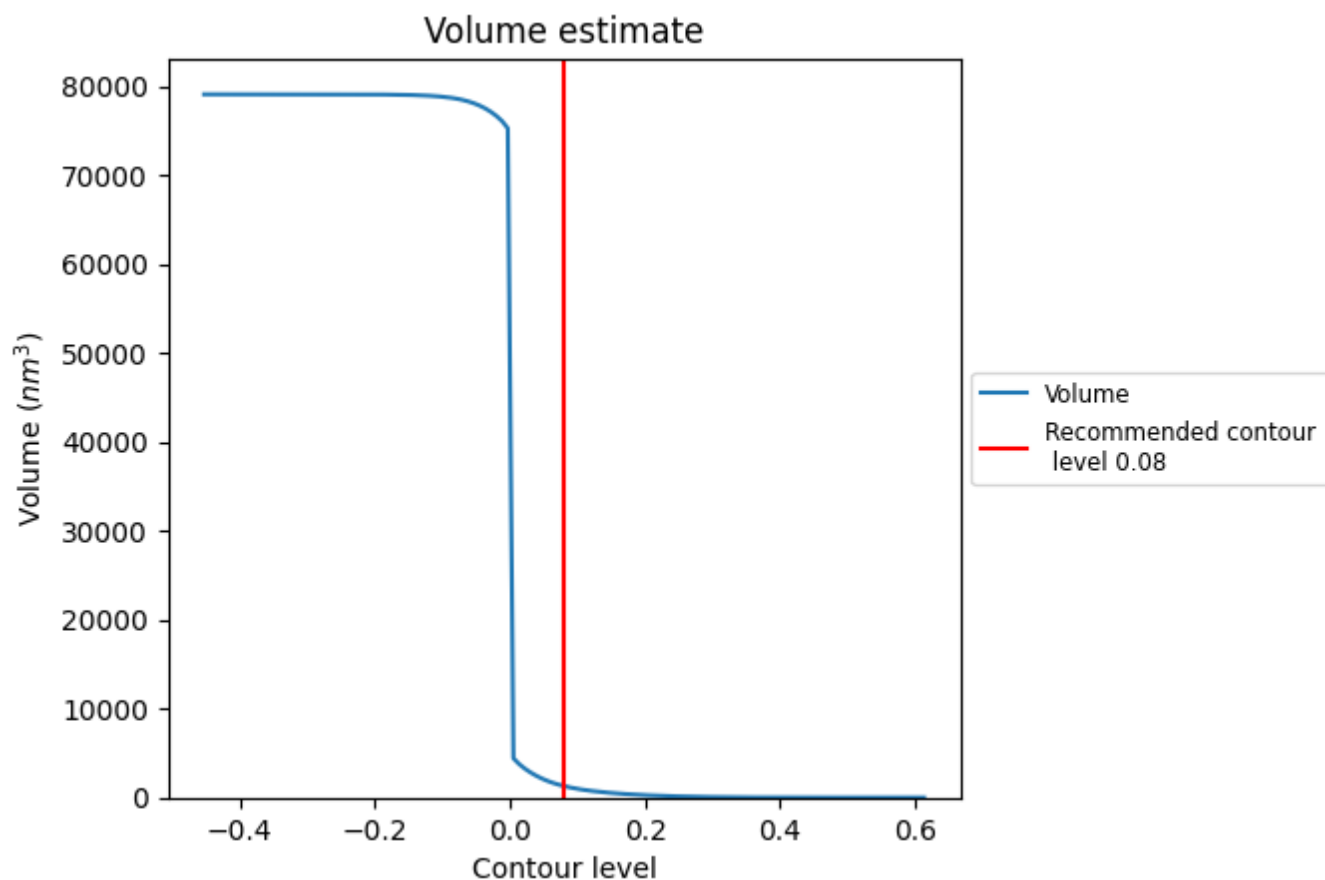
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

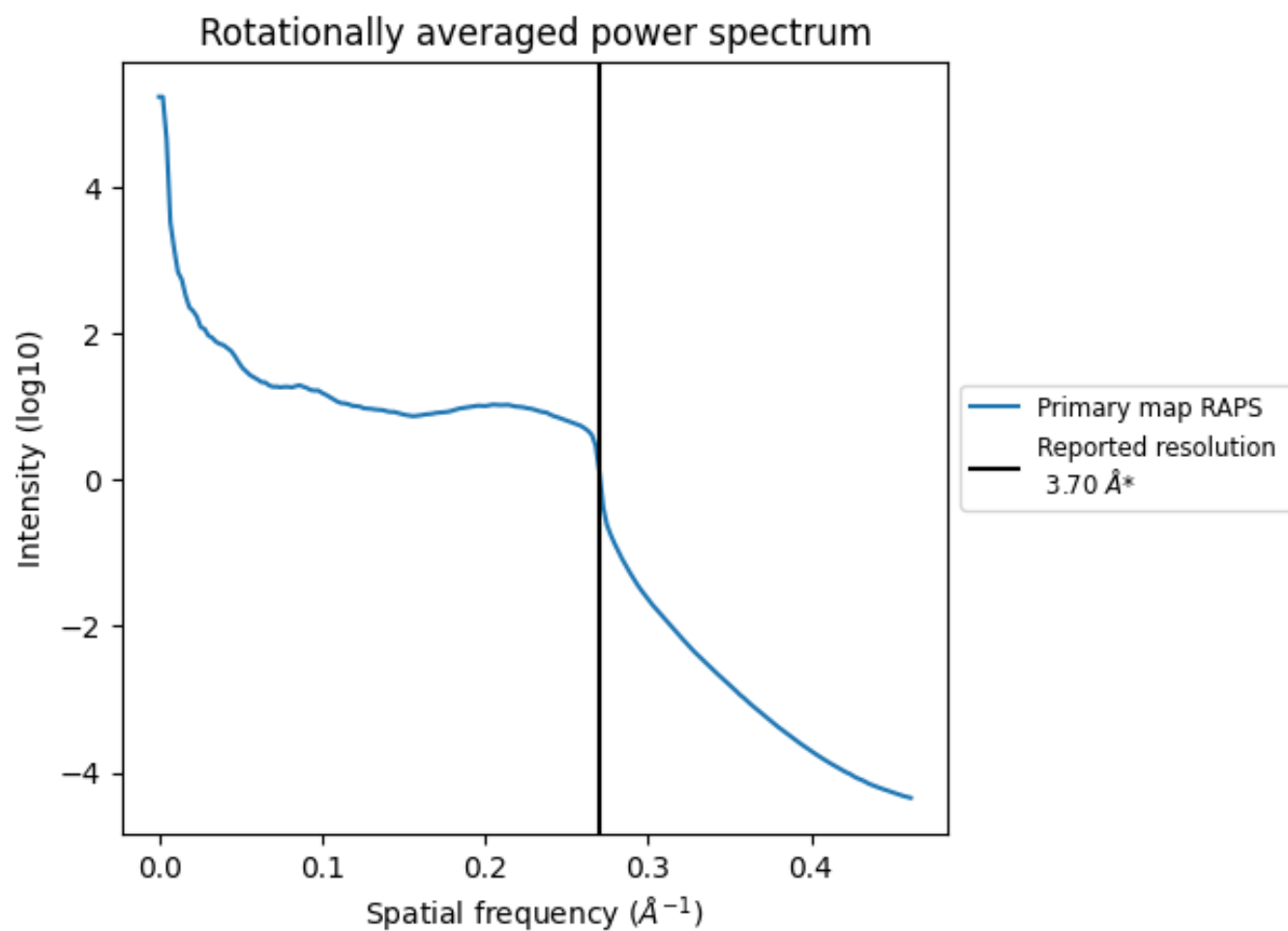
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1300 nm³; this corresponds to an approximate mass of 1174 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 ⓘ

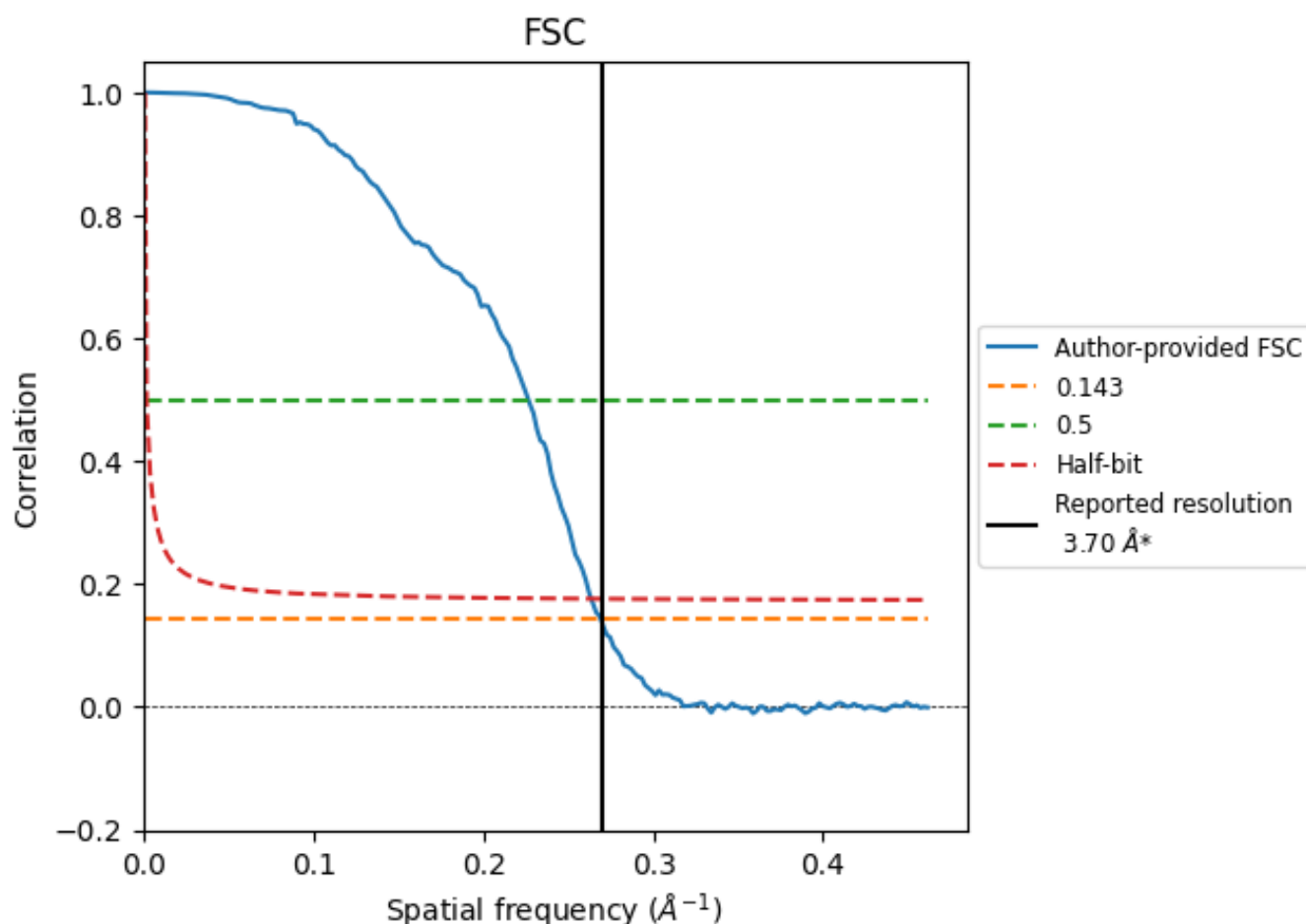


*Reported resolution corresponds to spatial frequency of 0.270 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.270 Å⁻¹

8.2 Resolution estimates [i](#)

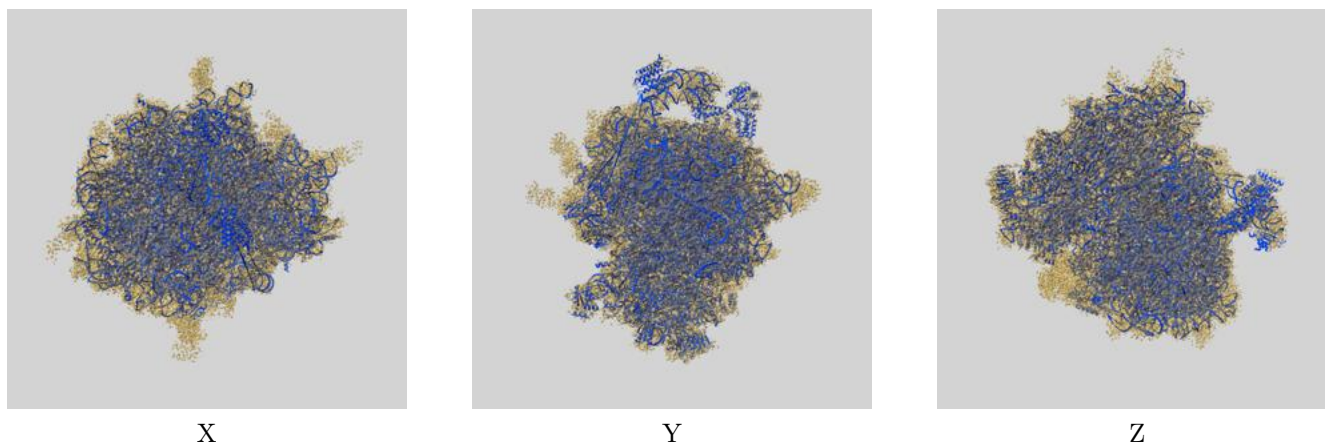
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.70	-	-
Author-provided FSC curve	3.71	4.41	3.79
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

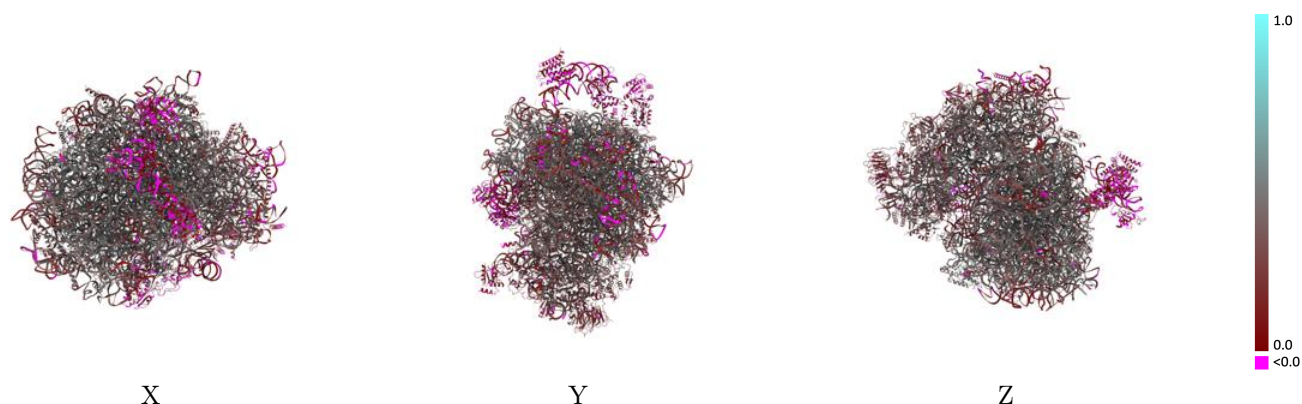
This section contains information regarding the fit between EMDB map EMD-4735 and PDB model 6R6G. Per-residue inclusion information can be found in [section 3](#) on [page 23](#).

9.1 Map-model overlay [i](#)



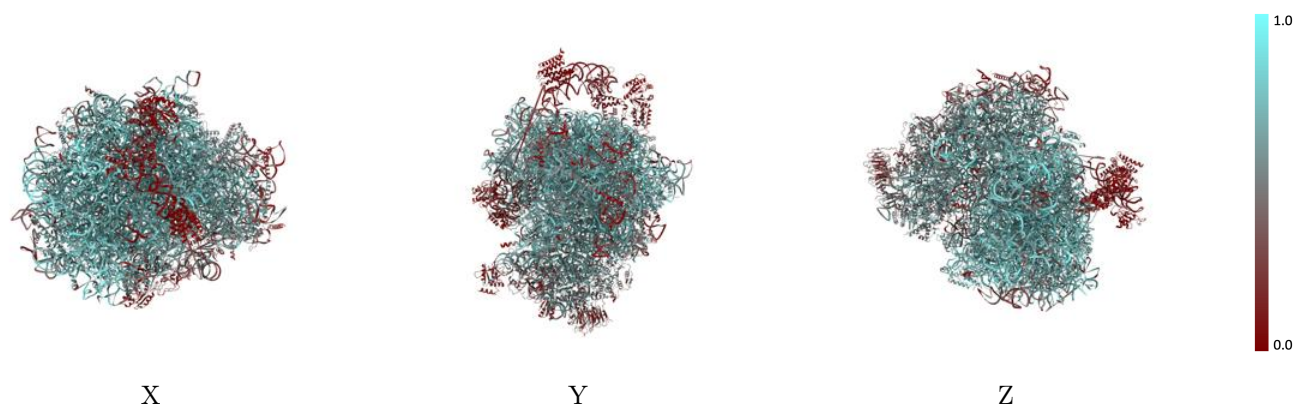
The images above show the 3D surface view of the map at the recommended contour level 0.08 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



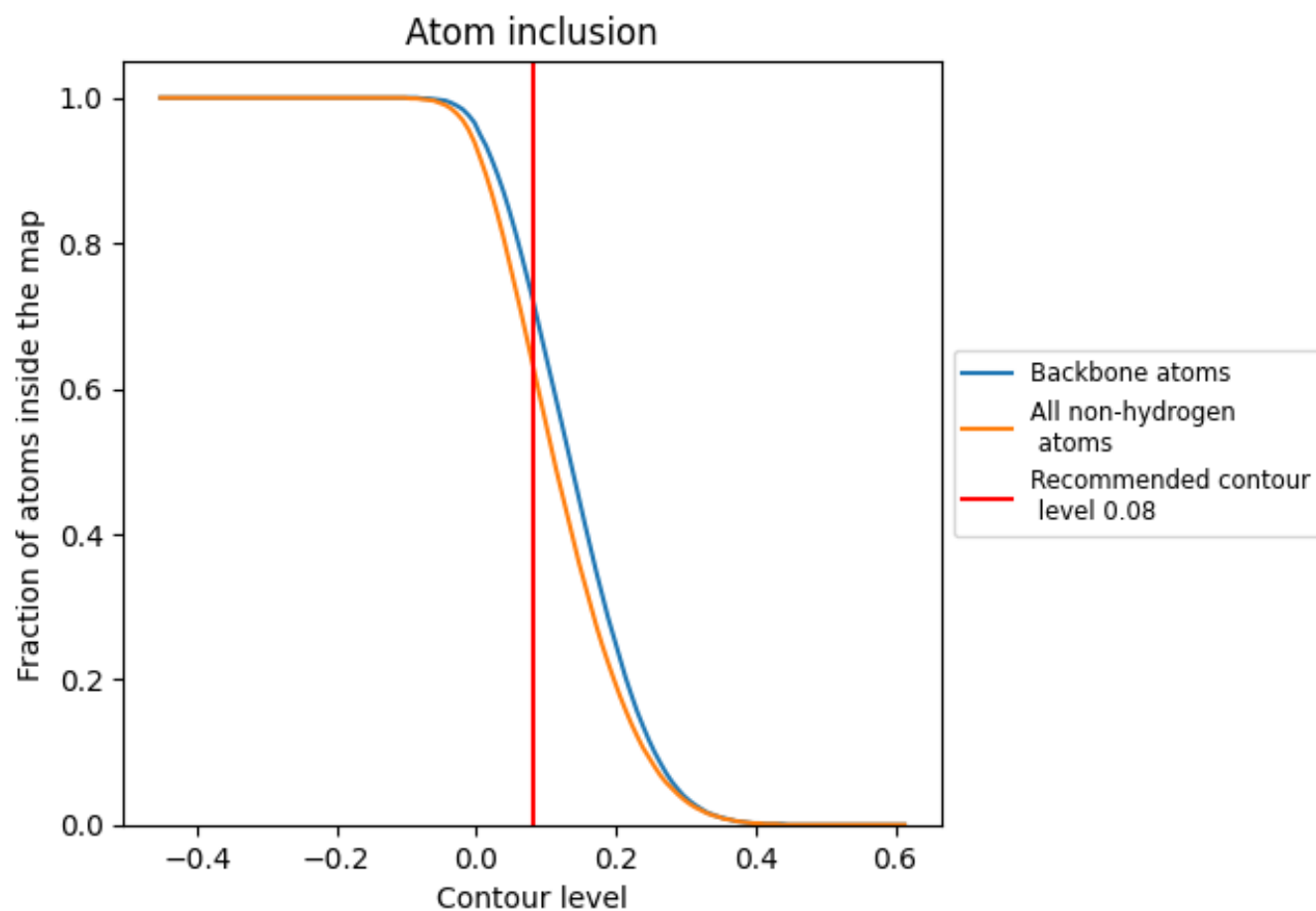
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.08).

9.4 Atom inclusion [i](#)



At the recommended contour level, 72% of all backbone atoms, 64% 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 (0.08) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6360	 0.3580
0	 0.2560	 0.1590
1	 0.7390	 0.5170
2	 0.6320	 0.3240
3	 0.3690	 0.1950
4	 0.6850	 0.4110
5	 0.7500	 0.3910
6	 0.3110	 0.2240
7	 0.8320	 0.4360
8	 0.7680	 0.3970
9	 0.5120	 0.3550
A	 0.6760	 0.4390
AA	 0.4340	 0.3090
AB	 0.0820	 0.0730
AC	 0.0490	 0.0180
AD	 0.2960	 0.1800
AE	 0.3960	 0.2490
AF	 0.2150	 0.0710
AG	 0.0940	 0.0090
AI	 0.0360	 0.0370
B	 0.6970	 0.4450
BB	 0.4700	 0.3030
C	 0.7170	 0.4470
CC	 0.5720	 0.3700
D	 0.6860	 0.4180
DD	 0.5020	 0.3290
E	 0.6770	 0.4130
EE	 0.5690	 0.3960
F	 0.7060	 0.4310
FF	 0.4720	 0.3570
G	 0.6060	 0.3720
GG	 0.3690	 0.2890
H	 0.6580	 0.4190
HH	 0.4980	 0.3330
I	 0.7100	 0.4350



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Chain	Atom inclusion	Q-score
II	0.5330	0.3150
J	0.6610	0.3860
JJ	0.4820	0.3250
K	0.6730	0.3500
KK	0.4450	0.2880
L	0.6460	0.3920
LL	0.5780	0.3870
M	0.7220	0.4330
MM	0.5580	0.3790
N	0.7360	0.4440
NN	0.5000	0.3120
O	0.7110	0.4400
OO	0.4720	0.2890
P	0.7020	0.4460
PP	0.5110	0.2980
Q	0.7100	0.4400
QQ	0.5840	0.3930
R	0.6280	0.3840
RR	0.2140	0.1310
S	0.7220	0.4440
SS	0.3890	0.2530
T	0.6840	0.4240
TT	0.5590	0.4000
U	0.5800	0.3410
UU	0.4660	0.3170
V	0.6810	0.4540
VV	0.5700	0.3910
W	0.5130	0.3170
WW	0.4970	0.2870
X	0.6270	0.4170
Y	0.6740	0.4170
Z	0.6260	0.3970
a	0.7310	0.4460
b	0.5720	0.3600
c	0.6260	0.4050
d	0.6660	0.4200
e	0.7400	0.4560
f	0.7340	0.4530
g	0.6470	0.4190
h	0.6520	0.3900
i	0.6390	0.3760
j	0.7240	0.4510

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Chain	Atom inclusion	Q-score
k	 0.5780	 0.3740
l	 0.6600	 0.4420
m	 0.6800	 0.4340
n	 0.6380	 0.3950
o	 0.6650	 0.4030
p	 0.6390	 0.4230
q	 0.5070	 0.3440
r	 0.7320	 0.4530
s	 0.1030	 0.0510
t	 0.0390	 0.0160
u	 0.5410	 0.3540
v	 0.5330	 0.3540
w	 0.3740	 0.2890
x	 0.5200	 0.3470
y	 0.5330	 0.3370
z	 0.4260	 0.2550