



Full wwPDB EM Validation Report ⓘ

Mar 24, 2026 – 01:07 AM UTC

PDB ID : 6D9J / pdb_00006d9j
EMDB ID : EMD-7836
Title : Mammalian 80S ribosome with a double translocated CrPV-IRES, P-sitetRNA and eRF1.
Authors : Pisareva, V.P.; Pisarev, A.V.; Fernandez, I.S.
Deposited on : 2018-04-30
Resolution : 3.20 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

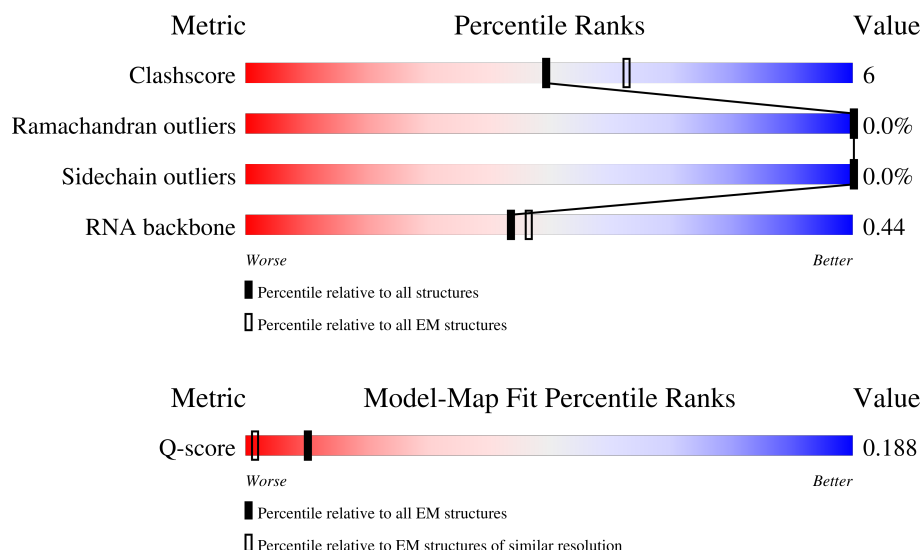
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 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.



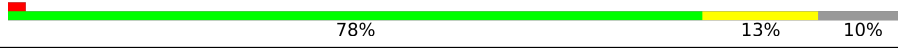
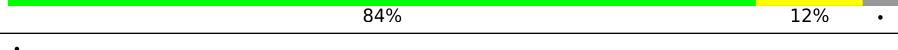
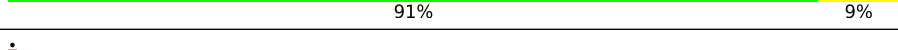
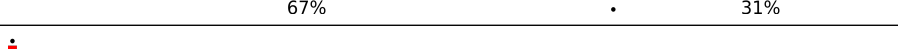
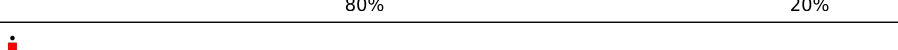
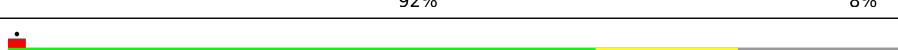
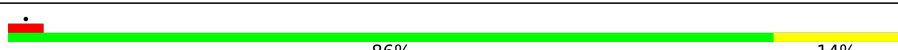
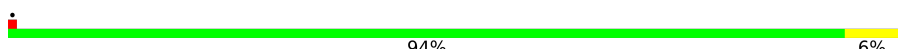
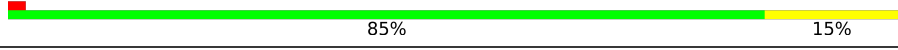
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	15020 (2.70 - 3.70)

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	A	257	
2	B	403	
3	C	392	

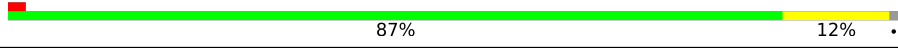
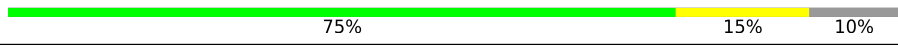
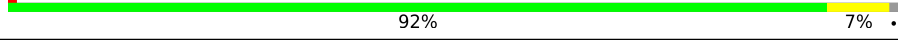
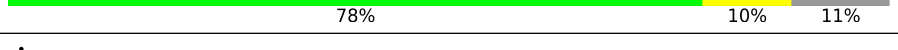
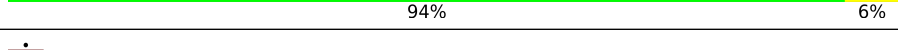
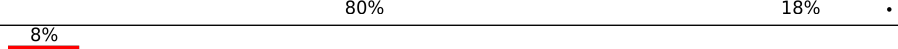
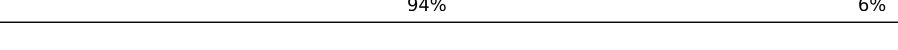
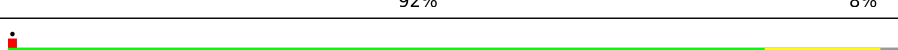
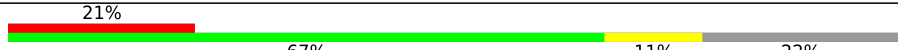
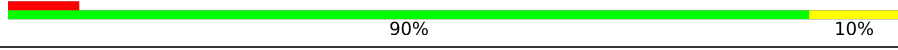
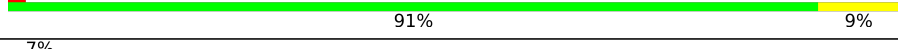
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Mol	Chain	Length	Quality of chain
4	D	297	
5	E	291	
6	F	249	
7	G	242	
8	H	192	
9	I	214	
10	J	178	
11	L	211	
12	M	198	
13	N	204	
14	O	198	
15	P	187	
16	Q	187	
17	R	181	
18	S	176	
19	T	160	
20	U	99	
21	V	140	
22	W	157	
23	X	156	
24	Y	145	
25	Z	136	
26	a	148	
27	b	226	
28	c	115	

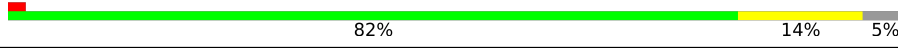
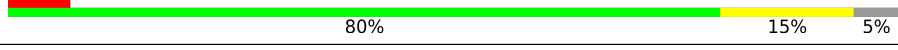
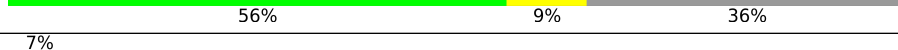
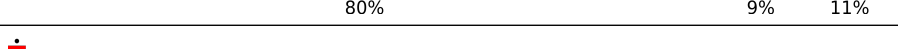
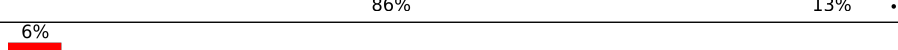
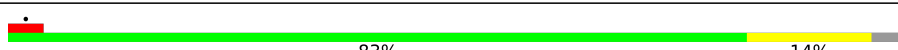
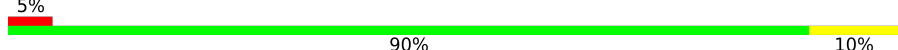
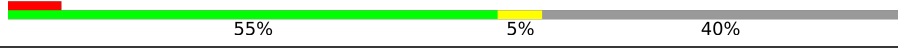
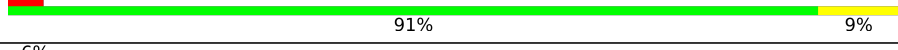
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Mol	Chain	Length	Quality of chain
29	d	125	
30	e	135	
31	f	110	
32	g	126	
33	h	123	
34	i	105	
35	j	97	
36	k	69	
37	l	51	
38	m	52	
39	n	25	
40	o	106	
41	p	92	
42	r	137	
43	s	303	
44	t	195	
45	5	3594	
46	7	119	
47	8	151	
48	K	217	
49	2	1697	
50	BB	217	
51	CC	264	
52	DD	221	
53	EE	281	

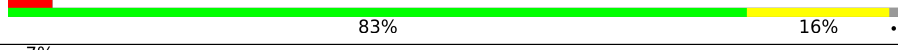
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Mol	Chain	Length	Quality of chain
54	FF	262	
55	GG	204	
56	HH	249	
57	II	194	
58	JJ	206	
59	KK	194	
60	LL	149	
61	MM	158	
62	NN	132	
63	OO	151	
64	PP	151	
65	QQ	145	
66	RR	172	
67	SS	135	
68	TT	152	
69	UU	145	
70	VV	119	
71	WW	83	
72	XX	130	
73	YY	143	
74	ZZ	134	
75	aa	125	
76	bb	101	
77	cc	84	
78	dd	69	

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Mol	Chain	Length	Quality of chain
79	ee	56	
80	ff	133	
81	gg	156	
82	hh	317	
83	3	87	
84	9	856	
85	4	190	

2 Entry composition

There are 87 unique types of molecules in this entry. The entry contains 227188 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 Ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	239	Total	C	N	O	S	0	0
			1777	1110	361	300	6		

- Molecule 2 is a protein called uL3.

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

- Molecule 3 is a protein called Ribosomal protein L4.

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

- Molecule 4 is a protein called Large ribosomal subunit protein uL18.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	1	LYS	-	expression tag	UNP P19949

- Molecule 5 is a protein called 60S ribosomal protein L6.

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

- Molecule 6 is a protein called uL30.

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

- Molecule 7 is a protein called eL8.

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

- Molecule 8 is a protein called 60S ribosomal protein L9.

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

- Molecule 9 is a protein called 60S ribosomal protein L10.

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

- Molecule 10 is a protein called Ribosomal protein L11.

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

- Molecule 11 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	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	46	ILE	-	insertion	UNP G1TPV0
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

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Chain	Residue	Modelled	Actual	Comment	Reference
L	52	ALA	-	insertion	UNP G1TPV0
L	53	GLY	-	insertion	UNP G1TPV0
L	54	PRO	-	insertion	UNP G1TPV0

- Molecule 12 is a protein called Large ribosomal subunit protein eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	M	137	Total	C	N	O	S	0	0
			1130	722	220	181	7		

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	?	-	LYS	deletion	UNP G1SZ12
M	?	-	ALA	deletion	UNP G1SZ12
M	?	-	ALA	deletion	UNP G1SZ12
M	?	-	ALA	deletion	UNP G1SZ12
M	?	-	GLN	deletion	UNP G1SZ12
M	?	-	LYS	deletion	UNP G1SZ12
M	?	-	ALA	deletion	UNP G1SZ12
M	?	-	PRO	deletion	UNP G1SZ12
M	?	-	ALA	deletion	UNP G1SZ12
M	?	-	GLN	deletion	UNP G1SZ12
M	?	-	LYS	deletion	UNP G1SZ12
M	?	-	ALA	deletion	UNP G1SZ12
M	?	-	PRO	deletion	UNP G1SZ12
M	?	-	ALA	deletion	UNP G1SZ12
M	?	-	GLN	deletion	UNP G1SZ12
M	?	-	LYS	deletion	UNP G1SZ12
M	?	-	ALA	deletion	UNP G1SZ12
M	?	-	ALA	deletion	UNP G1SZ12
M	?	-	GLY	deletion	UNP G1SZ12
M	?	-	GLN	deletion	UNP G1SZ12

- Molecule 13 is a protein called Ribosomal protein L15.

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

- Molecule 14 is a protein called uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	O	198	Total	C	N	O	S	0	0
			1623	1046	318	254	5		

- Molecule 15 is a protein called Large ribosomal subunit protein uL22.

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

- Molecule 16 is a protein called eL18.

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

- Molecule 17 is a protein called eL19.

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

- Molecule 18 is a protein called eL20.

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

- Molecule 19 is a protein called eL21.

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

- Molecule 20 is a protein called eL22.

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

- Molecule 21 is a protein called Ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	V	129	Total	C	N	O	S	0	0
			969	613	182	169	5		

- Molecule 22 is a protein called eL24.

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

- Molecule 23 is a protein called eL23.

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

- Molecule 24 is a protein called uL24.

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

- Molecule 25 is a protein called 60S ribosomal protein L27.

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

- Molecule 26 is a protein called uL15.

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

- Molecule 27 is a protein called eL29.

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

- Molecule 28 is a protein called eL30.

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

- Molecule 29 is a protein called eL31.

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

- Molecule 30 is a protein called Ribosomal protein L32.

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

- Molecule 31 is a protein called eL33.

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

- Molecule 32 is a protein called Large ribosomal subunit protein eL34.

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

- Molecule 33 is a protein called eL35.

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

- Molecule 34 is a protein called 60S ribosomal protein L36.

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

- Molecule 35 is a protein called Ribosomal protein L37.

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

- Molecule 36 is a protein called eL38.

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

- Molecule 37 is a protein called eL39.

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

- Molecule 38 is a protein called eL40.

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

- Molecule 39 is a protein called eL41.

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

- Molecule 40 is a protein called Large ribosomal subunit protein eL42.

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

- Molecule 41 is a protein called eL43.

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

- Molecule 42 is a protein called eL28.

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

- Molecule 43 is a protein called 60S acidic ribosomal protein P0.

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

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
s	262	LEU	ALA	conflict	UNP A0A1U7UFL5
s	?	-	GLU	deletion	UNP A0A1U7UFL5
s	266	THR	ALA	conflict	UNP A0A1U7UFL5
s	267	LEU	PHE	conflict	UNP A0A1U7UFL5
s	269	ILE	ALA	conflict	UNP A0A1U7UFL5
s	270	ILE	ASP	conflict	UNP A0A1U7UFL5
s	?	-	SER	deletion	UNP A0A1U7UFL5
s	?	-	ALA	deletion	UNP A0A1U7UFL5
s	?	-	PHE	deletion	UNP A0A1U7UFL5
s	?	-	VAL	deletion	UNP A0A1U7UFL5
s	?	-	ALA	deletion	UNP A0A1U7UFL5
s	?	-	ALA	deletion	UNP A0A1U7UFL5
s	?	-	ALA	deletion	UNP A0A1U7UFL5
s	?	-	PRO	deletion	UNP A0A1U7UFL5
s	?	-	VAL	deletion	UNP A0A1U7UFL5
s	272	VAL	ALA	conflict	UNP A0A1U7UFL5
s	273	ARG	ALA	conflict	UNP A0A1U7UFL5
s	274	ASP	ALA	conflict	UNP A0A1U7UFL5
s	275	SER	ALA	conflict	UNP A0A1U7UFL5
s	276	THR	PRO	conflict	UNP A0A1U7UFL5
s	278	ASP	ALA	conflict	UNP A0A1U7UFL5
s	282	ALA	LEU	conflict	UNP A0A1U7UFL5
s	284	GLN	ALA	conflict	UNP A0A1U7UFL5
s	286	SER	ALA	conflict	UNP A0A1U7UFL5
s	290	PRO	ALA	conflict	UNP A0A1U7UFL5
s	?	-	GLU	deletion	UNP A0A1U7UFL5
s	?	-	GLU	deletion	UNP A0A1U7UFL5
s	?	-	SER	deletion	UNP A0A1U7UFL5
s	?	-	GLU	deletion	UNP A0A1U7UFL5
s	294	ASN	ASP	conflict	UNP A0A1U7UFL5

- Molecule 44 is a protein called Ribosomal protein L12.

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

- Molecule 45 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	5	3594	Total	C	N	O	P	0	0
			77073	34324	14116	25039	3594		

- Molecule 46 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	7	119	Total	C	N	O	P	0	0
			2538	1132	454	834	118		

- Molecule 47 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	8	151	Total	C	N	O	P	0	0
			3208	1432	564	1062	150		

- Molecule 48 is a protein called Ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	K	212	Total	C	N	O	S	0	0
			1705	1091	306	300	8		

- Molecule 49 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	2	1697	Total	C	N	O	P	0	0
			36229	16171	6507	11855	1696		

- Molecule 50 is a protein called uS2.

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

- Molecule 51 is a protein called 40S ribosomal protein S3a.

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

- Molecule 52 is a protein called uS5.

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

- Molecule 53 is a protein called Ribosomal protein S3.

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

- Molecule 54 is a protein called eS4.

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

- Molecule 55 is a protein called Ribosomal protein S5.

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

- Molecule 56 is a protein called 40S ribosomal protein S6.

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

- Molecule 57 is a protein called 40S ribosomal protein S7.

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

- Molecule 58 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	JJ	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
JJ	47	ARG	GLY	conflict	UNP G1TJW1

- Molecule 59 is a protein called Ribosomal protein S9 (Predicted).

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

- Molecule 60 is a protein called S10_ plectin domain-containing protein.

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

- Molecule 61 is a protein called Ribosomal protein S11.

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

- Molecule 62 is a protein called 40S ribosomal protein S12.

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

- Molecule 63 is a protein called Ribosomal protein S13.

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

- Molecule 64 is a protein called Small ribosomal subunit protein uS11.

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

- Molecule 65 is a protein called uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	QQ	115	Total	C	N	O	S	0	0
			956	610	176	163	7		

- Molecule 66 is a protein called Ribosomal protein S16.

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

- Molecule 67 is a protein called eS17.

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

- Molecule 68 is a protein called uS13.

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

- Molecule 69 is a protein called eS19.

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

- Molecule 70 is a protein called uS10.

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

- Molecule 71 is a protein called eS21.

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

- Molecule 72 is a protein called Ribosomal protein S15a.

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

- Molecule 73 is a protein called Ribosomal protein S23.

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

- Molecule 74 is a protein called 40S ribosomal protein S24.

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

- Molecule 75 is a protein called eS25.

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

- Molecule 76 is a protein called eS26.

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

- Molecule 77 is a protein called 40S ribosomal protein S27.

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

- Molecule 78 is a protein called Ribosomal protein S28.

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

- Molecule 79 is a protein called eS29.

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

- Molecule 80 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	ff	57	Total	C	N	O	S	0	0
			457	282	101	73	1		

- Molecule 81 is a protein called Ribosomal protein S27a.

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

- Molecule 82 is a protein called RACK1.

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

- Molecule 83 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	3	87	Total	C	N	O	P	0	0
			1860	829	333	612	86		

- Molecule 84 is a protein called Elongation factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	9	856	Total	C	N	O	S	0	0
			6673	4234	1148	1247	44		

- Molecule 85 is a RNA chain called CrPV IRES.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	4	190	Total	C	N	O	P	0	0
			4020	1802	689	1339	190		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
4	6217	C	-	expression tag	GB 8895506
4	6218	U	-	expression tag	GB 8895506
4	6219	U	-	expression tag	GB 8895506

- Molecule 86 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
86	p	1	Total	Zn	0
			1	1	
86	2	1	Total	Zn	0
			1	1	
86	bb	1	Total	Zn	0
			1	1	
86	gg	1	Total	Zn	0
			1	1	

- Molecule 87 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

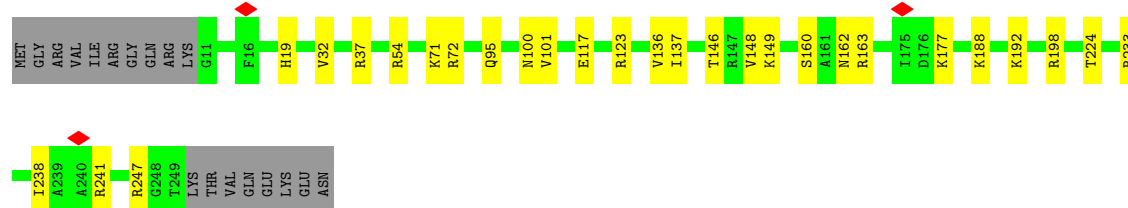
Mol	Chain	Residues	Atoms		AltConf
87	5	2	Total	Mg	0
			2	2	

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.

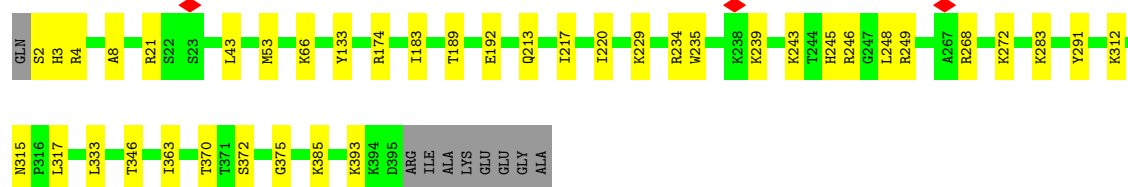
• Molecule 1: Ribosomal protein L8

Chain A: 



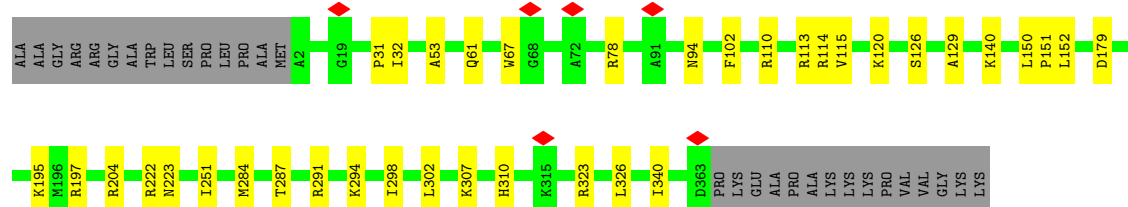
• Molecule 2: uL3

Chain B: 



• Molecule 3: Ribosomal protein L4

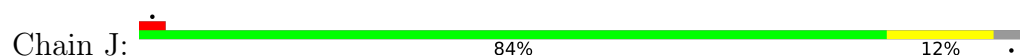
Chain C: 



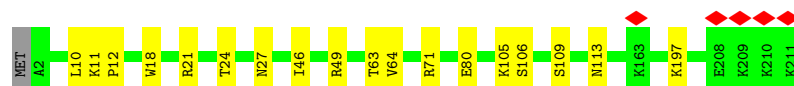
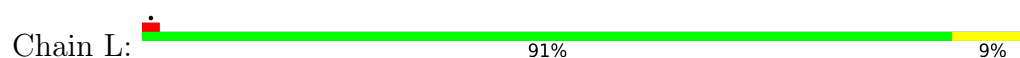
• Molecule 4: Large ribosomal subunit protein uL18

Chain D: 

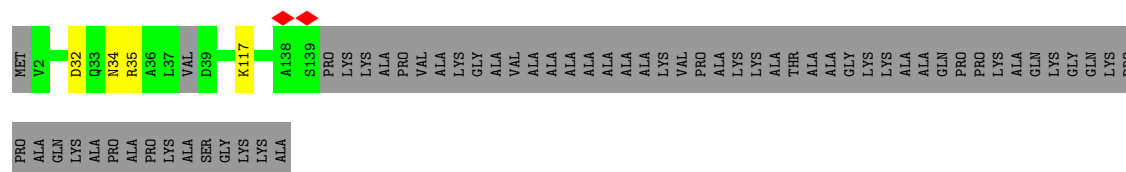
- Molecule 10: Ribosomal protein L11



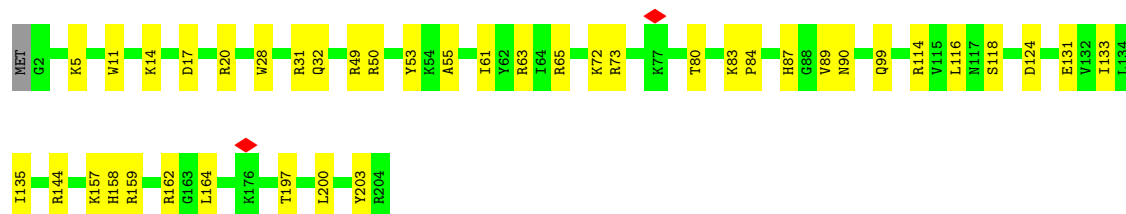
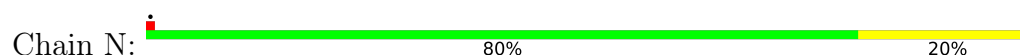
- Molecule 11: 60S ribosomal protein L13



- Molecule 12: Large ribosomal subunit protein eL14



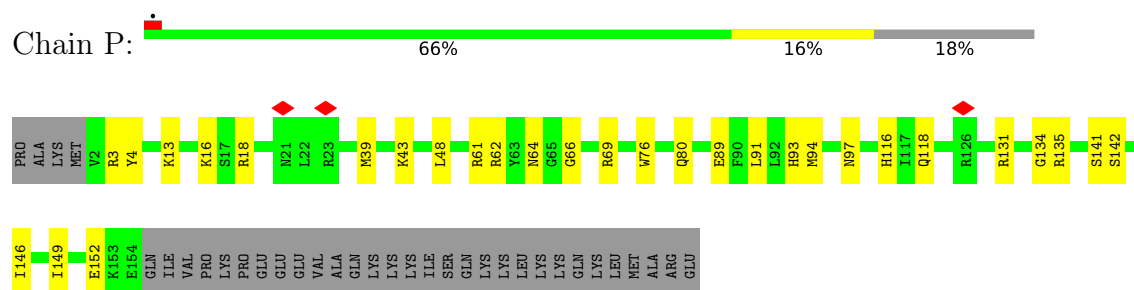
- Molecule 13: Ribosomal protein L15



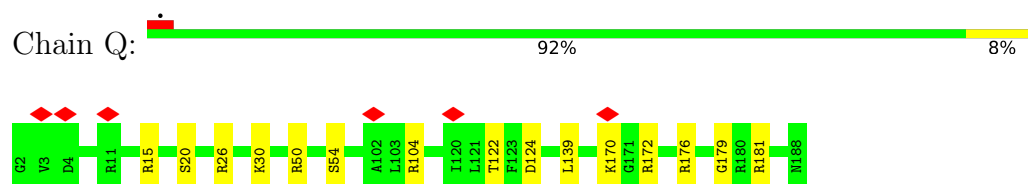
- Molecule 14: uL13



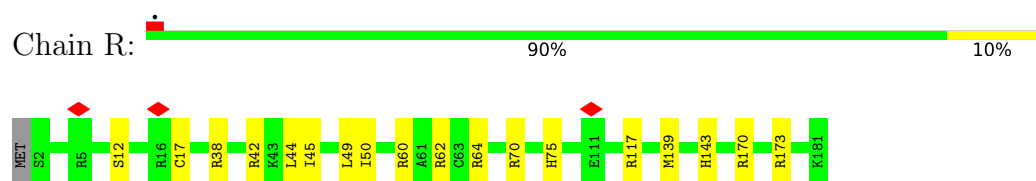
- Molecule 15: Large ribosomal subunit protein uL22



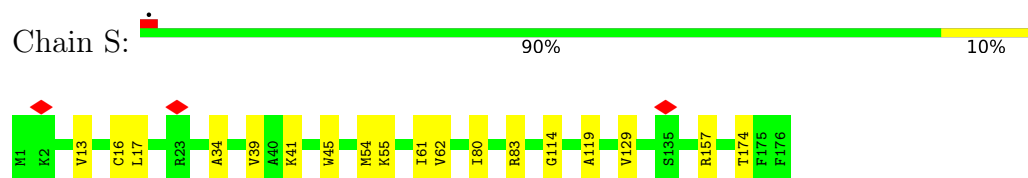
- Molecule 16: eL18



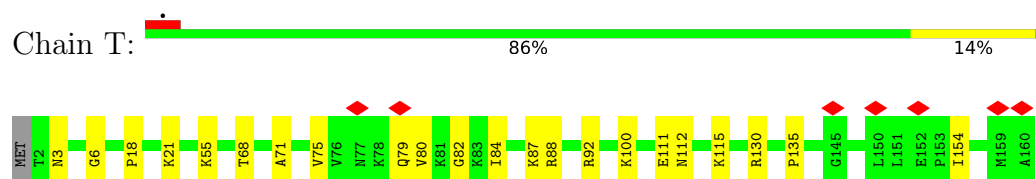
- Molecule 17: eL19



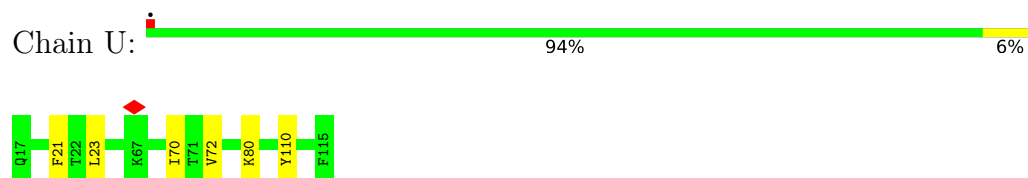
- Molecule 18: eL20



- Molecule 19: eL21



- Molecule 20: eL22



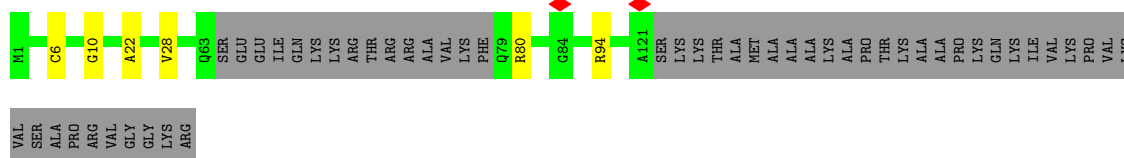
- Molecule 21: Ribosomal protein L23

Chain V: 



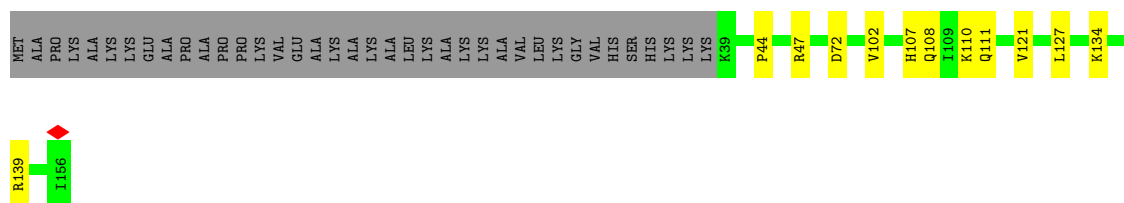
- Molecule 22: eL24

Chain W: 



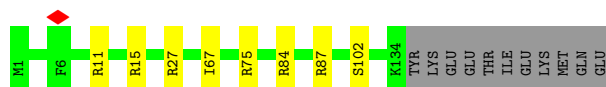
- Molecule 23: eL23

Chain X: 



- Molecule 24: uL24

Chain Y: 



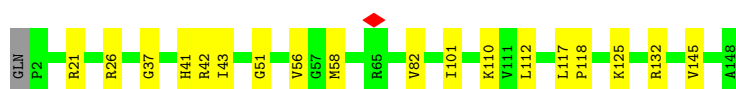
- Molecule 25: 60S ribosomal protein L27

Chain Z: 

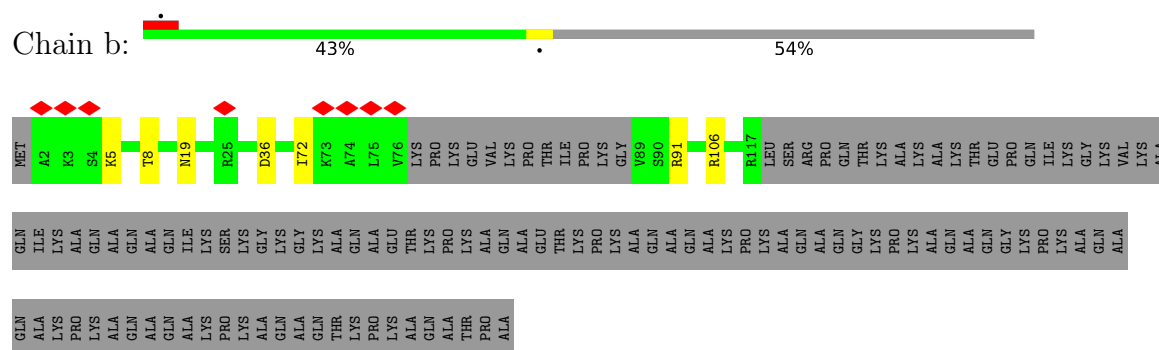


- Molecule 26: uL15

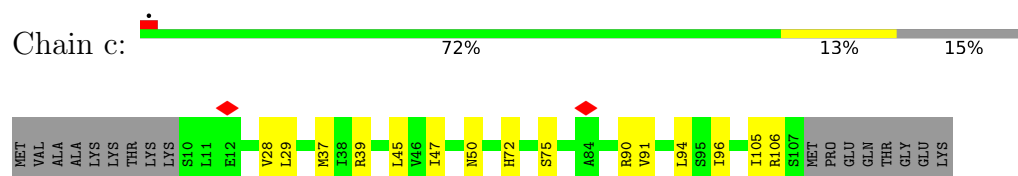
Chain a: 



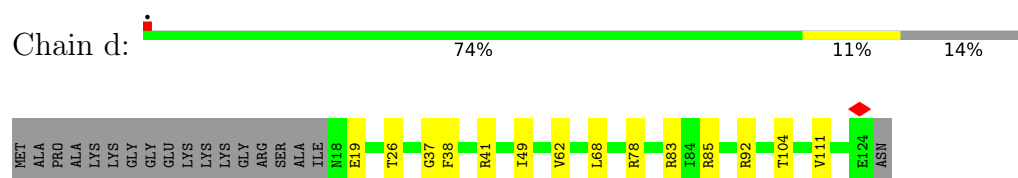
- Molecule 27: eL29



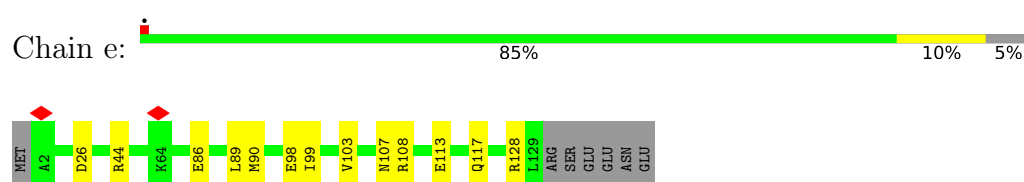
- Molecule 28: eL30



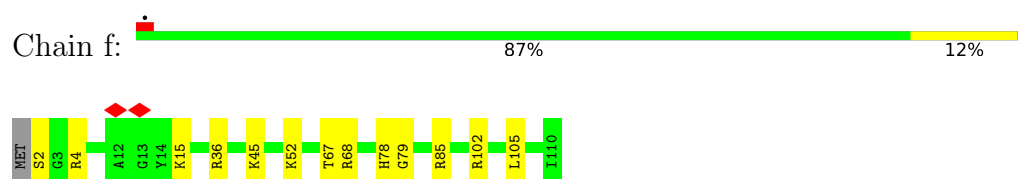
- Molecule 29: eL31



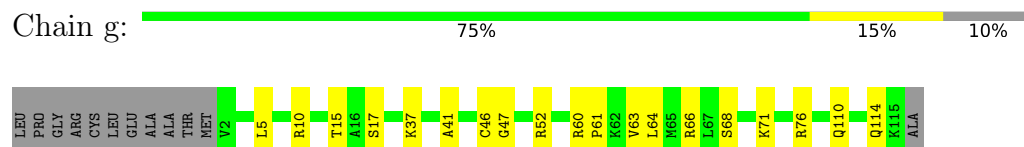
- Molecule 30: Ribosomal protein L32



- Molecule 31: eL33



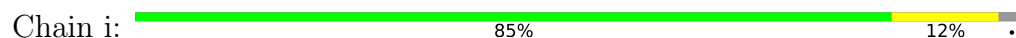
- Molecule 32: Large ribosomal subunit protein eL34



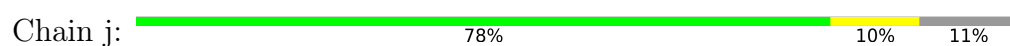
- Molecule 33: eL35



- Molecule 34: 60S ribosomal protein L36



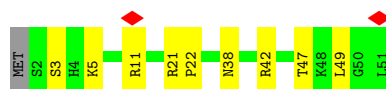
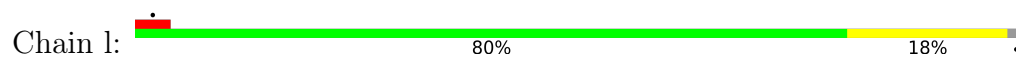
- Molecule 35: Ribosomal protein L37



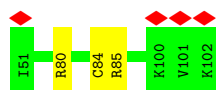
- Molecule 36: eL38



- Molecule 37: eL39



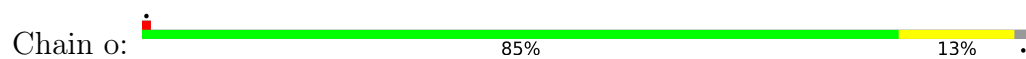
- Molecule 38: eL40



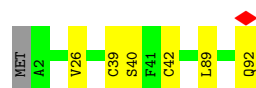
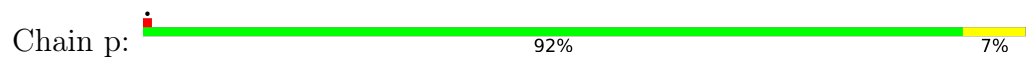
- Molecule 39: eL41



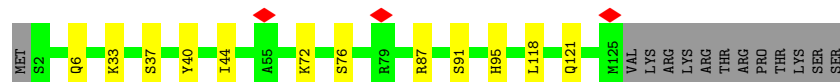
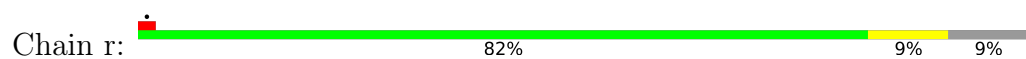
- Molecule 40: Large ribosomal subunit protein eL42



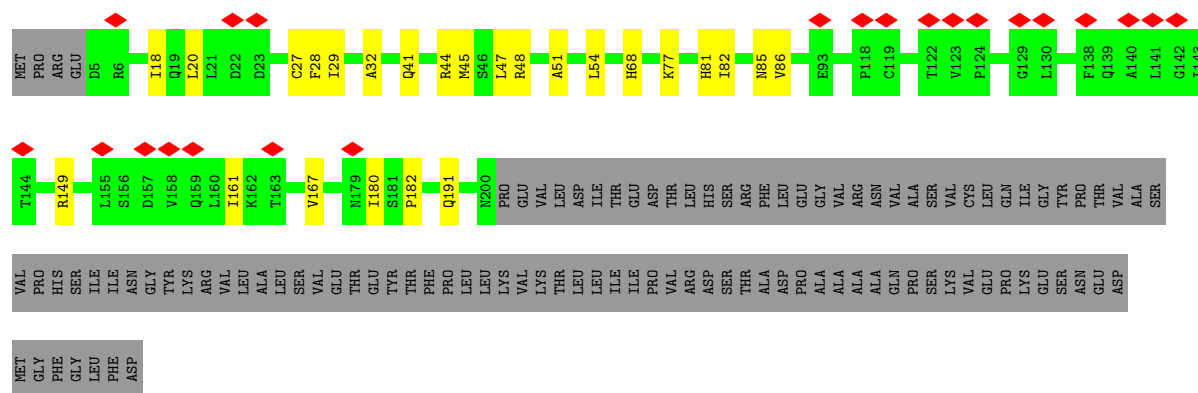
• Molecule 41: eL43



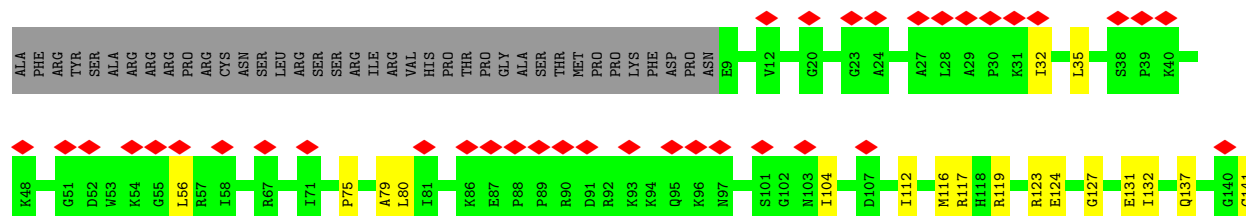
• Molecule 42: eL28

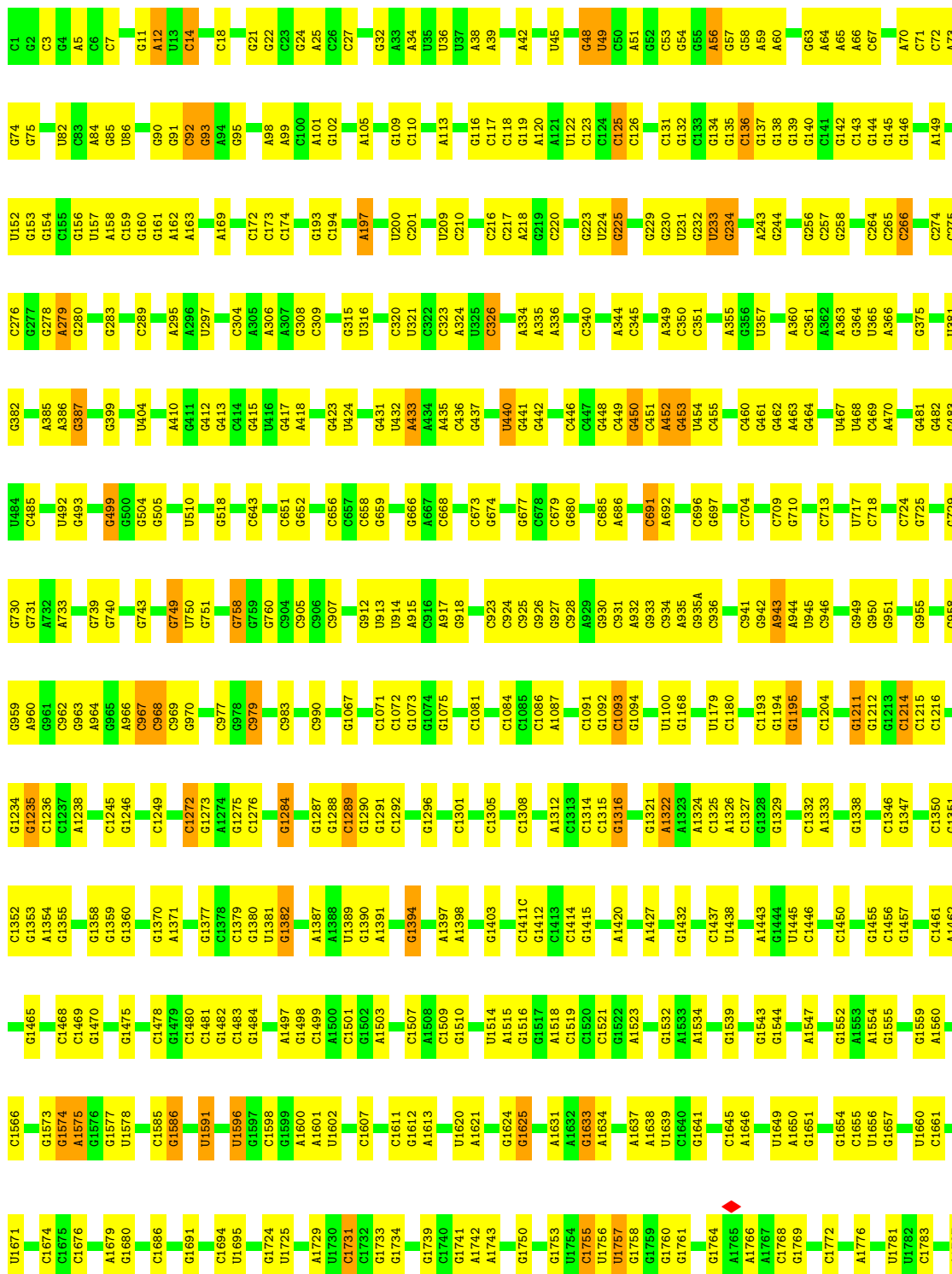


• Molecule 43: 60S acidic ribosomal protein P0

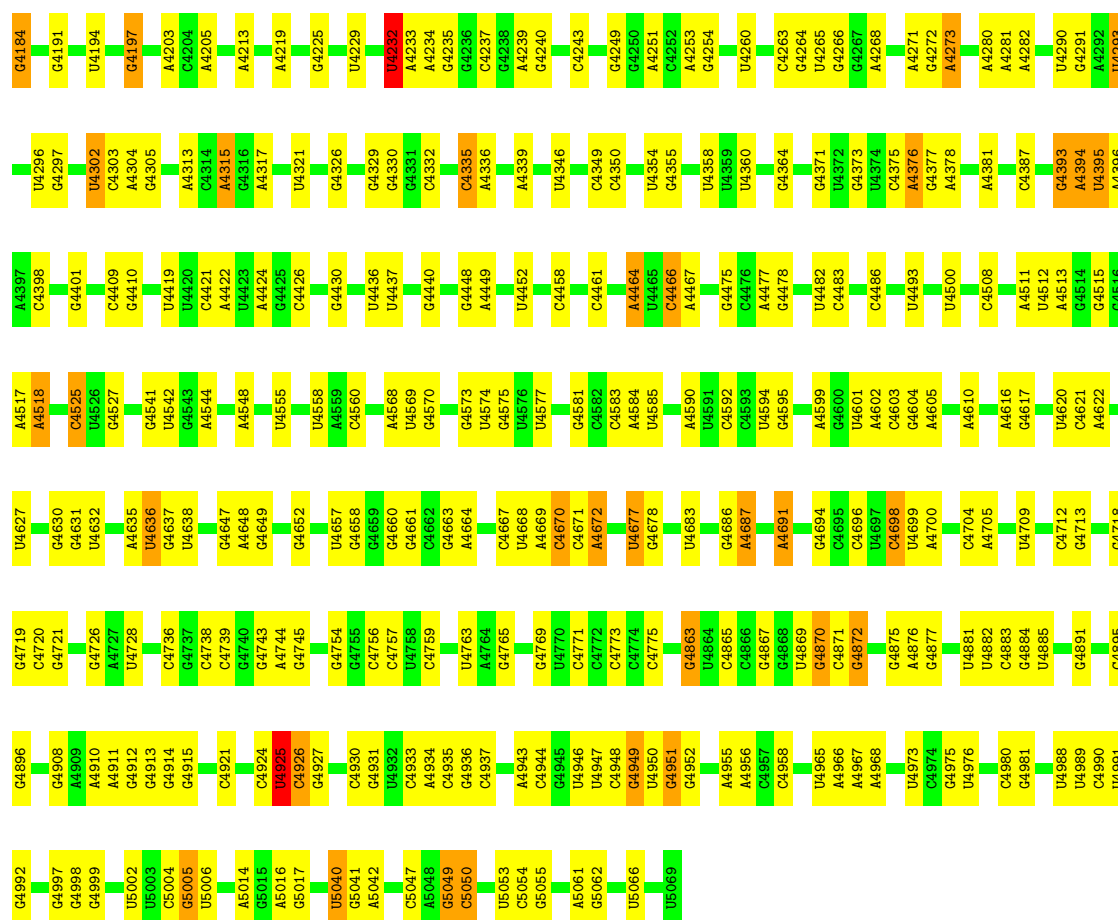


• Molecule 44: Ribosomal protein L12



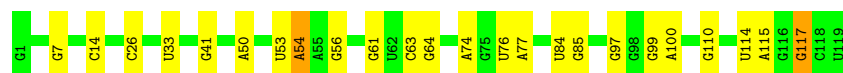


U4066	A3817	U3734	A3643	G2838	A2744	U2830	G2544	C2437	C2325	C2094	U2004	C1920	A1788
U4067	U3818	G3735	A3643	U2839	A2745	U2831	U2545	G2437	G2326	A2097	G2007	C1921	C1789
U4068	G3819	A3917	A3646	G2842	A2746	U2832	G2546	G2443	G2327	A2098	G2008	C1922	U1790
U4069	G3820	G3743	A3647	G2842	G2749	G2838	G2547	G2443	G2328	C2099	A2009	C1923	U1800
C4072	G3823	A3746	A3648	A2845	G2750	G2842	G2548	G2457	U2329	G2100	A2010	C1924	A1801
A4073	A3824	A3747	A3648	G2846	G2751	A2842	G2549	G2458	U2330	A2101	C2011	C1925	A1802
A4074	A3825	A3748	A3653	G2847	G2752	G2843	G2550	C2458	G2331	G2102	A2012		G1803
U4075	C3926	G3753	A3657	G2848	G2753	G2843	A2551	G2461	G2332	A2103	C2013	C1928	A1804
A4076	G3827	G3754	U3658	A2849	G2754	G2844	G2552	G2462	G2333	A2104	C2014	A1929	A1805
A4077	A3828	G3754	G3658	A2849	A2755	A2845	A2553	U2467	G2334	A2105	A2015	U1930	
G4082	G3829	G3754	G3659	C2853	A2756	C2854	G2554	U2468	C2340	G2106	C2016	U1931	
U4083	A3830	A3760	A3682	G2855	A2757	G2855	G2555	C2469	A2341	G2107	C2018	U1932	C1812
A4084	G3839	A3763	A3683	G2855	G2758	G2856	G2556	G2348	A2025	G2108	A2025	A1934	G1815
A4085	U3840	A3763	A3684	G2857	G2759	G2857	G2557	U2349	A2026		A2026	C1936	
A4086	G3841	U3764	G3685	A2857	U2761	G2858	G2558	G2474	A2029	C2258	A2029	C1937	G1818
G4087	C3843	G3765	G3671	U2874	A2764	U2661	A2565	G2475	A2030	C2259	A2030	C1938	U1820
A4088	U3844	U3770	G3672	C2875	C2772	G2662	G2567	G2483	C2360	G2260	C2031	U1821	G1822
G4089	A3845	G3771	G3673	G2876	C2773	G2663	G2568	G2484	U2361	G2261	G2032	U1822	G1823
U3950	C3846	U3772	G3673	G2877	G2774	C2669	G2569	G2486	G2362		U2033	U1947	
G3951	U3851	U3773	G3678	U2880	G2775	G2675	C2572	G2487	U2369	G2266	A2041	G1948	C1827
G3956	A3852	A3774	U3679	A2881	C2776	G2675	A2573	G2488	G2377		A2042	G1951	G1828
U3957	G3855	A3775	U3680	G2882	G2777	G2681	G2574	U2490		C2267	A2043	U1947	G1829
G3958	A3856	G3776	U3688	G2883	G2778	G2682	G2575	U2491	A2381	A2268	A2044	G1948	G1830
U3964	C3866	U3777	G3689	G2884	G2779	G2683	G2576	C2492	A2382	G2269	G2045		G1833
G4121	A3867	U3778	U3690	U2887	G2781	G2687	G2579	G2493	U2386	G2281	A2046	U1959	G1836
A3966	G3868	G3779	G3691	G2888	C2782	U2687	A2581	U2494	G2387	G2282	A2047	G1961	A1837
G3967	U3869	A3780	A3692	G2889	G2783	U2688	C2583	C2501	G2387	G2284	U2048	A1962	
U3968	A3871	A3781	A3695	G2897	U2788	G2694	A2587	C2502	A2395	G2289	G2055	A1963	G1842
A4125	A3872	U3786	G3698	G2898	U2789	A2695	C2588	G2503	G2400	G2295	G2056	A1964	U1849
G3970	C3877	G3787	G3698	C3598	U2790	A2696	G2589	G2504	G2402	G2296	A2057	G1965	A1850
A4127	A3878	G3788	C3701	G3599	G2791	A2697	G2590	G2505	A2403	G2297	G2060	G1969	G1854
G4131	C3702	A3702	A3702	G3600	C2794	G2700	G2597	G2506	A2404		U2061	A1970	G1855
C4134	G3705	A3705	G3705	G3603	A2795	U2708	A2598	A2513	G2405	A2300	C2062	U1971	
G4135	C3706	G3706	C3706	A3604	G2796	C2709	A2599	G2516	G2406	G2301	G2068	G1972	G1878
C4148	U3707	U3707	U3707	U3607	A2798	G2710	A2600	A2517	U2408	C2302	C2069	U1974	
A4157	C3708	C3708	C3708	G3608	G2799	G2711	A2601	G2517	U2409	C2303	A2070	G1975	C1881
C4158	U3709	U3709	U3709	G3609	A2807	G2712	G2602	C2520	C2410	U2304	U2070	G1982	U1882
U4162	G3710	G3710	G3710	A3610	G2807	G2713	C2603	G2521	A2411	U2305	C2073	G1983	A1891
C4163	A3711	A3711	A3711	A3611	G2811	G2714	G2604	G2522	A2412	G2306	C2074	A1892	C1893
C4164	A3717	A3717	A3717	U3616	C2814	C2719	G2605	U2524	G2416	G2309	G2075	G1985	
A4048	U3805	U3805	U3805	G3617	C2814	G2724	G2607	U2525	C2422	A2313	C2078	A1991	A1897
U4049	G3806	G3806	G3806	G3618	A2825	A2725	G2608	A2529	A2423	G2314	G2079	U1992	
A4050	A3807	U3807	U3807	G3619	U2826	G2726	G2609	U2530	G2424	G2315	C2093	C1993	G1910
C4051	G3808	G3808	G3808	G3620	G2827	G2726	G2609	U2530	U2425	G2316	U2084	C1996	C1911
A4052	A3809	A3809	A3809	A3621	U2829	U2730	C2615	G2533	U2426	G2317	G2085	C1996	G1912
A4053	G3810	G3810	G3810	G3622	U2829	U2731	C2616	G2533	G2427	G2318	U2098	U1997	C1915
C4054	A3811	A3811	A3811	G3623	U2833	U2734	G2617	A2537	G2428	G2319	A2088	A1998	C1916
U4055	G3812	G3812	G3812	G3624	C2834	G2735	G2617	G2537	U2432	G2320	G2089	G2001	G1917
A4178	A3813	U3780	U3780	A3635	C2834	G2735	A2623	G2540	U2433	G2321	U2090	A2002	U1918
C4179	U3814	A3731	A3731	A3636	A2835	U2740	U2628	G2541	G2433		G2093	G2003	G1919
G4180	G3815	A3732	A3732	U3639	U2837	A2743	C2629						
G4183	A3816	A3816	A3816										



• Molecule 46: 5S rRNA

Chain 7: 80% 18%



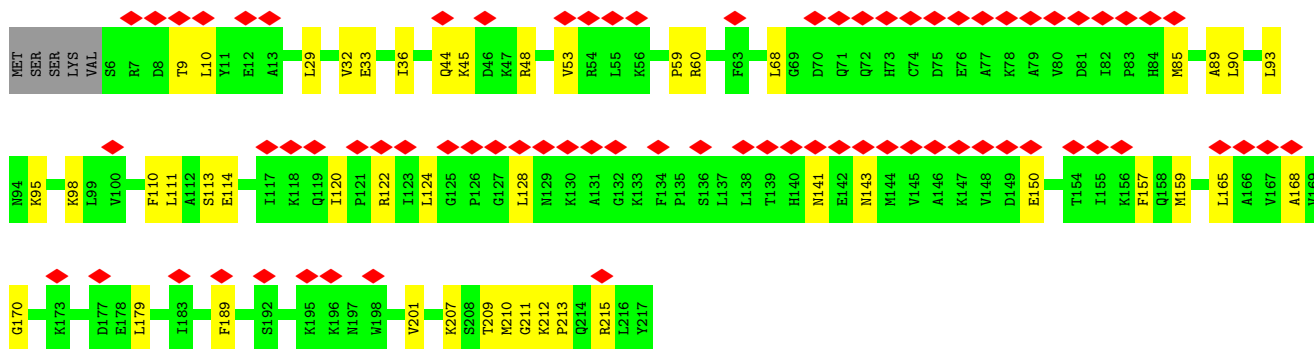
• Molecule 47: 5.8S rRNA

Chain 8: 60% 36%



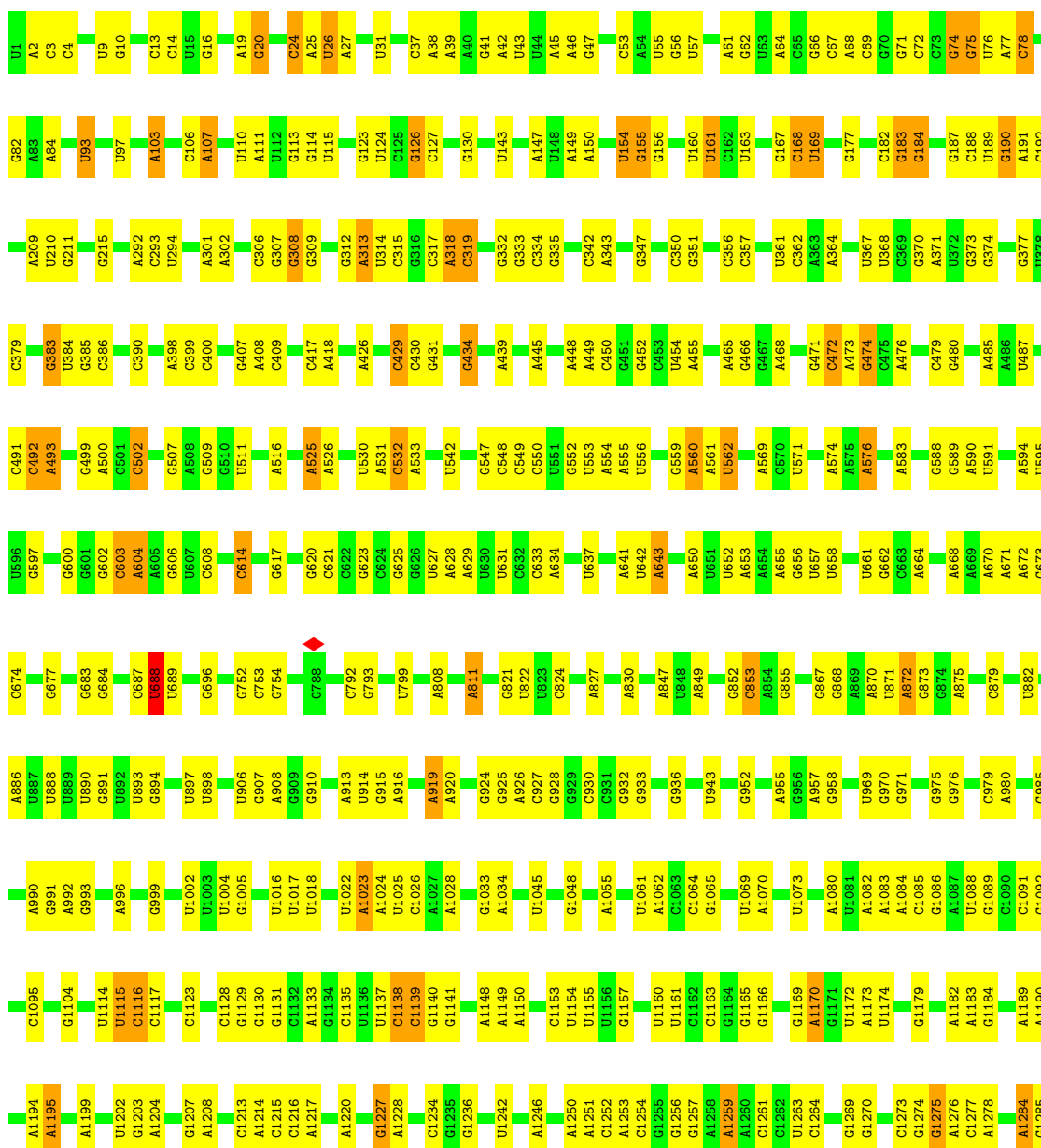
• Molecule 48: Ribosomal protein

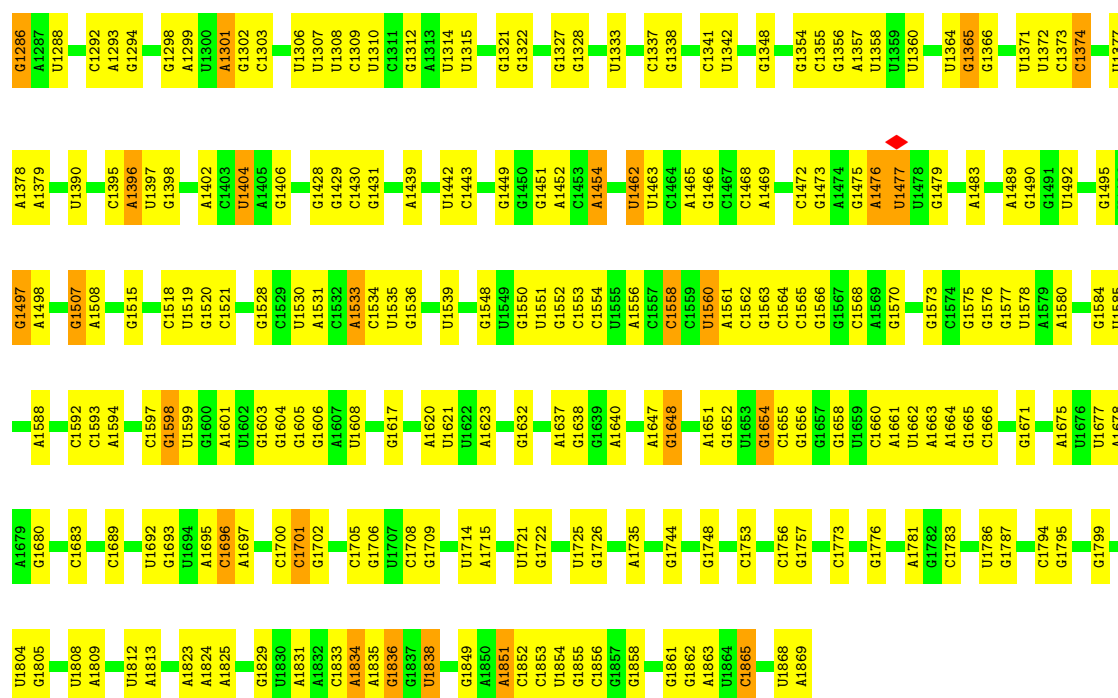
Chain K: 35% 77% 21%



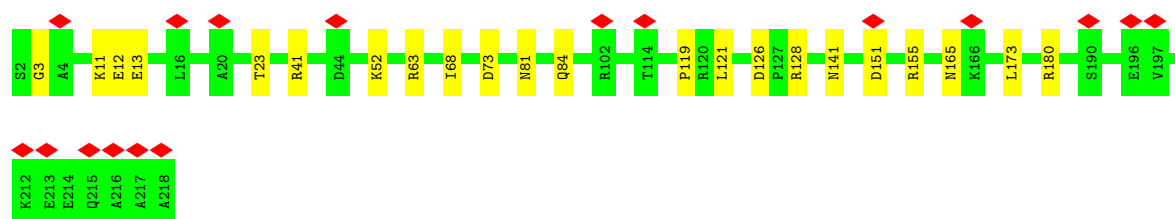
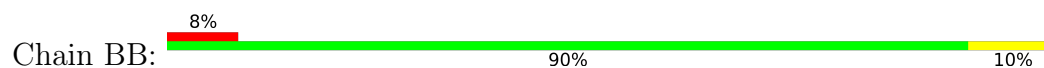
• Molecule 49: 18S rRNA

Chain 2:

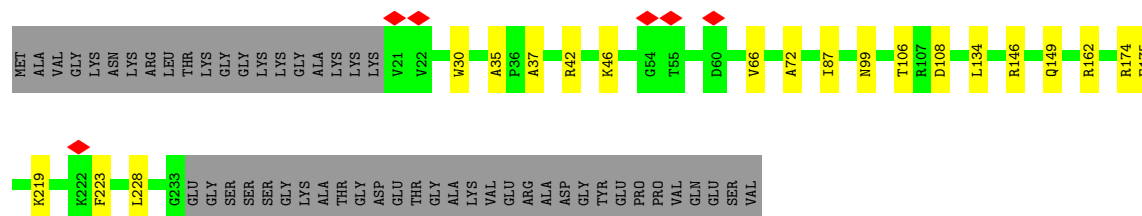
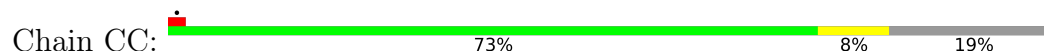




- Molecule 50: uS2



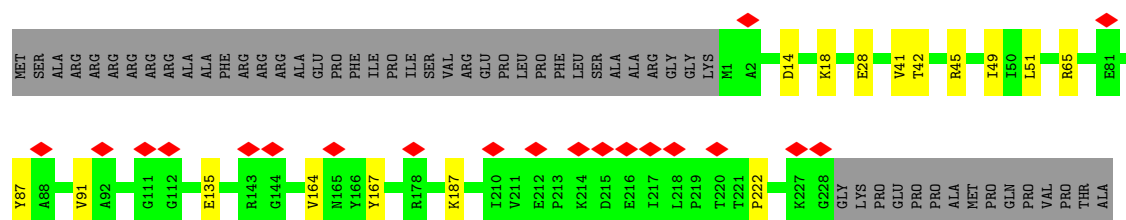
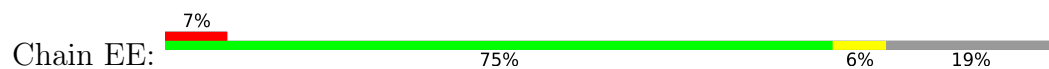
- Molecule 51: 40S ribosomal protein S3a



- Molecule 52: uS5



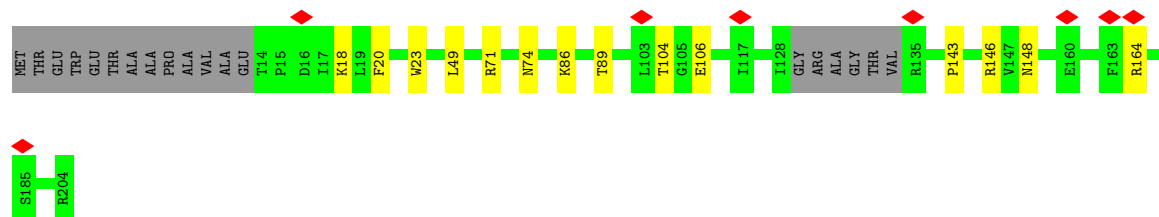
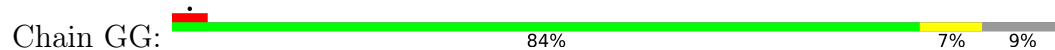
- Molecule 53: Ribosomal protein S3



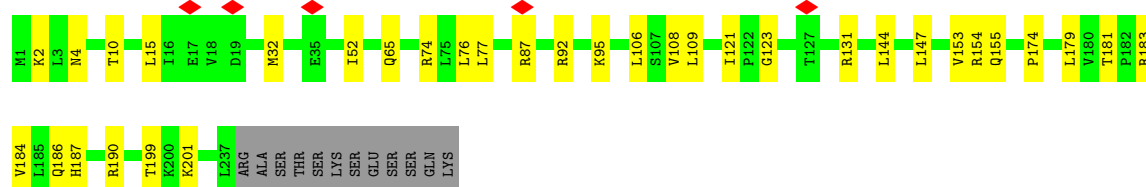
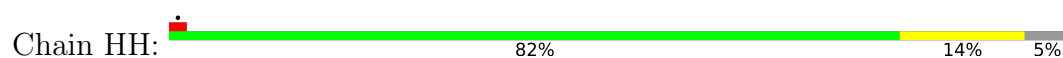
- Molecule 54: eS4



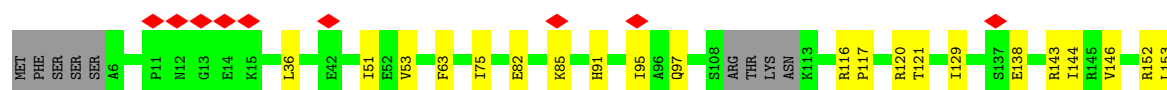
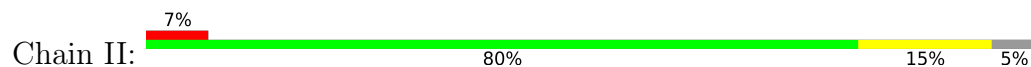
- Molecule 55: Ribosomal protein S5



- Molecule 56: 40S ribosomal protein S6



- Molecule 57: 40S ribosomal protein S7





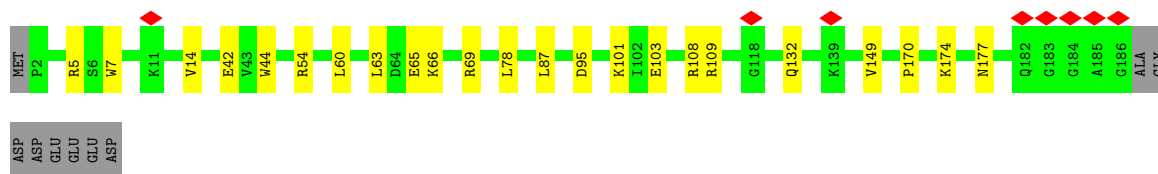
- Molecule 58: 40S ribosomal protein S8

Chain JJ: 88% 12%



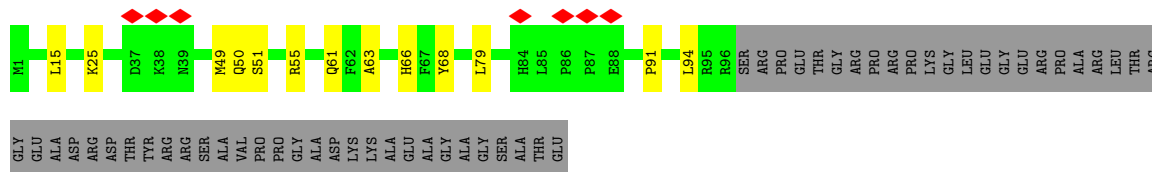
- Molecule 59: Ribosomal protein S9 (Predicted)

Chain KK: 84% 12% 5%



- Molecule 60: S10_pectin domain-containing protein

Chain LL: 5% 56% 9% 36%



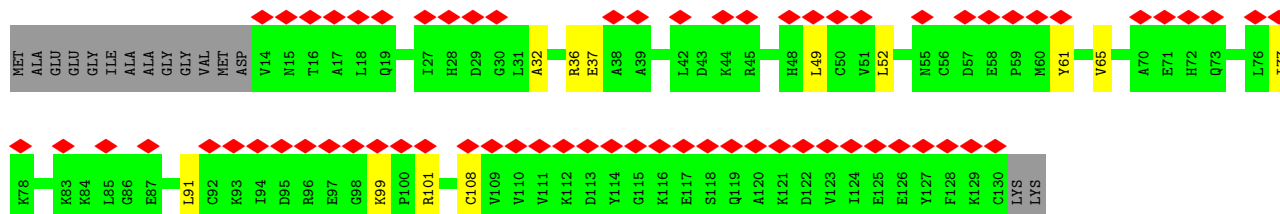
- Molecule 61: Ribosomal protein S11

Chain MM: 7% 83% 8% 9%



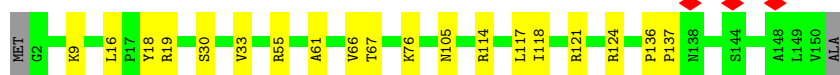
- Molecule 62: 40S ribosomal protein S12

Chain NN: 52% 80% 9% 11%



- Molecule 63: Ribosomal protein S13

Chain OO:  86% 13%



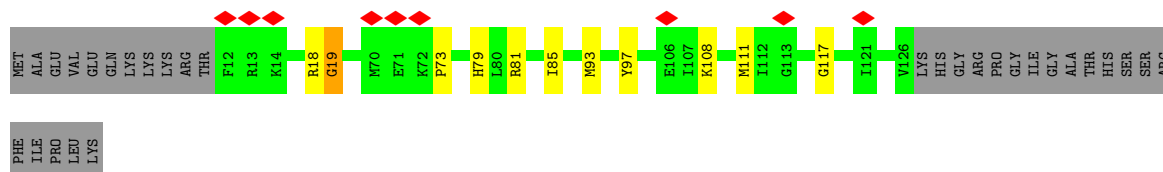
- Molecule 64: Small ribosomal subunit protein uS11

Chain PP:  6% 79% 11% 10%



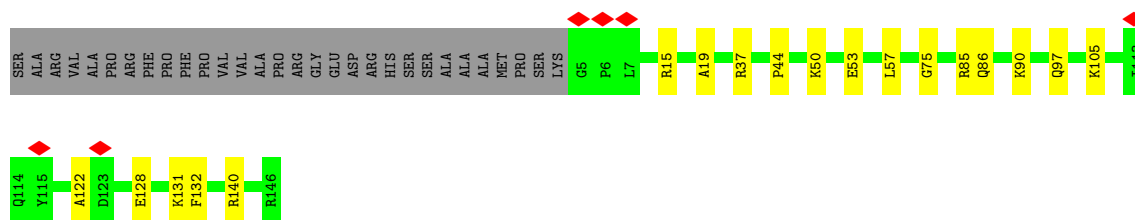
- Molecule 65: uS19

Chain QQ:  6% 72% 7% 21%



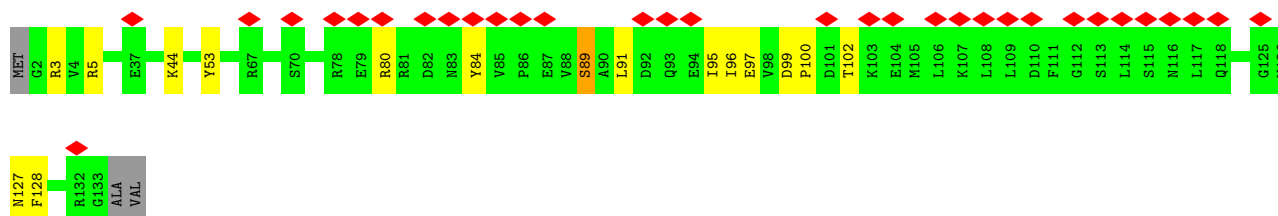
- Molecule 66: Ribosomal protein S16

Chain RR:  72% 10% 17%



- Molecule 67: eS17

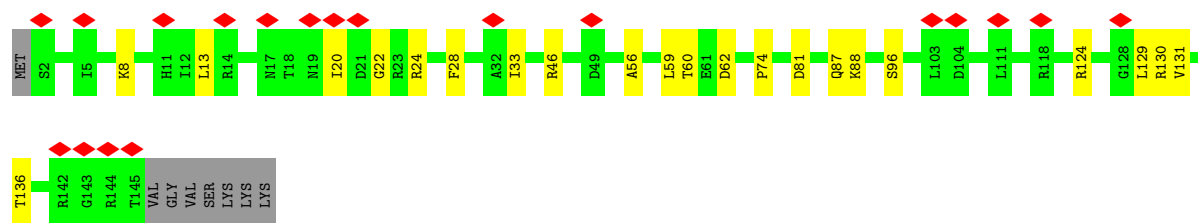
Chain SS:  24% 86% 11% 2%



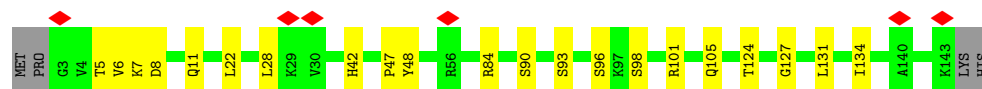
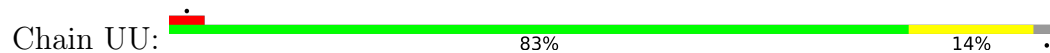
- Molecule 68: uS13

Chain TT:  12% 80% 14% 5%

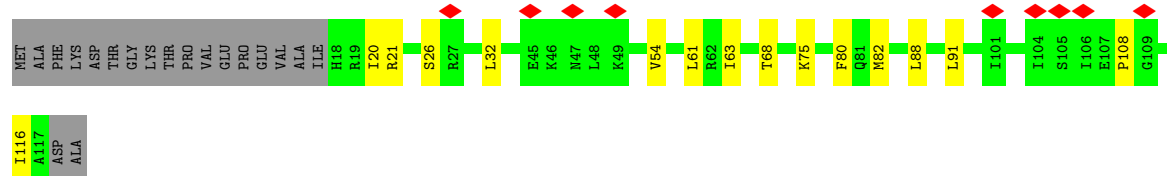
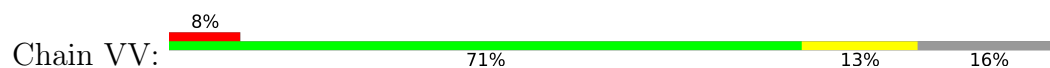




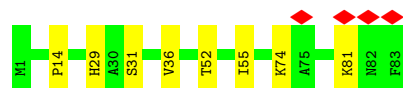
- Molecule 69: eS19



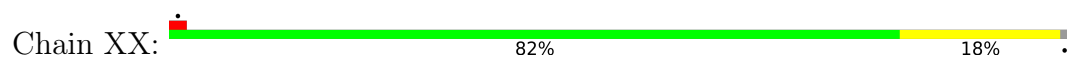
- Molecule 70: uS10



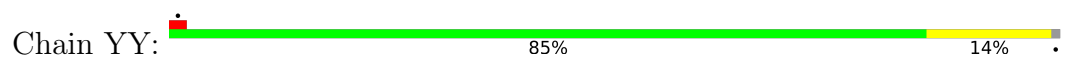
- Molecule 71: eS21



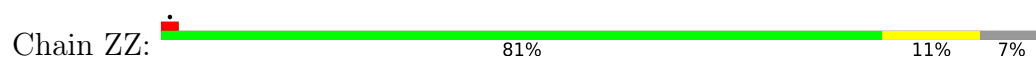
- Molecule 72: Ribosomal protein S15a

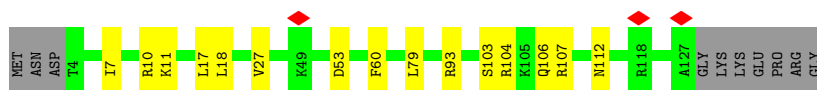


- Molecule 73: Ribosomal protein S23

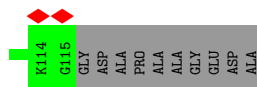
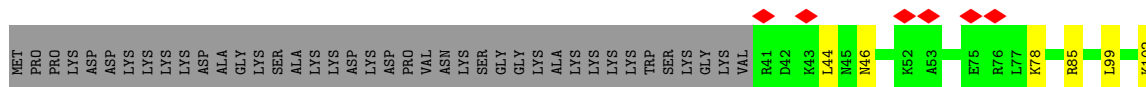


- Molecule 74: 40S ribosomal protein S24

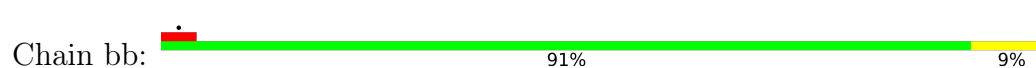




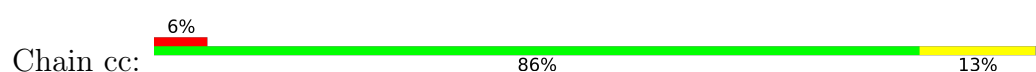
• Molecule 75: eS25



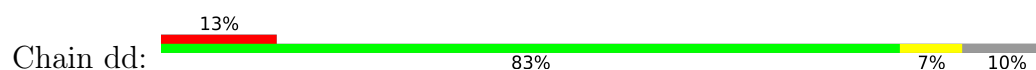
• Molecule 76: eS26



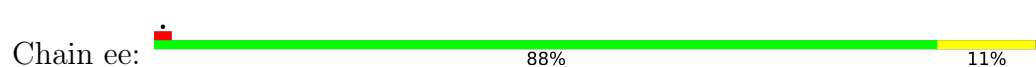
• Molecule 77: 40S ribosomal protein S27



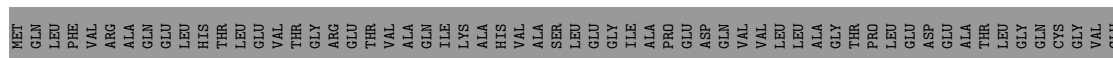
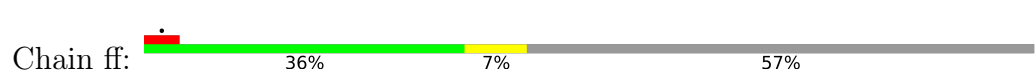
• Molecule 78: Ribosomal protein S28

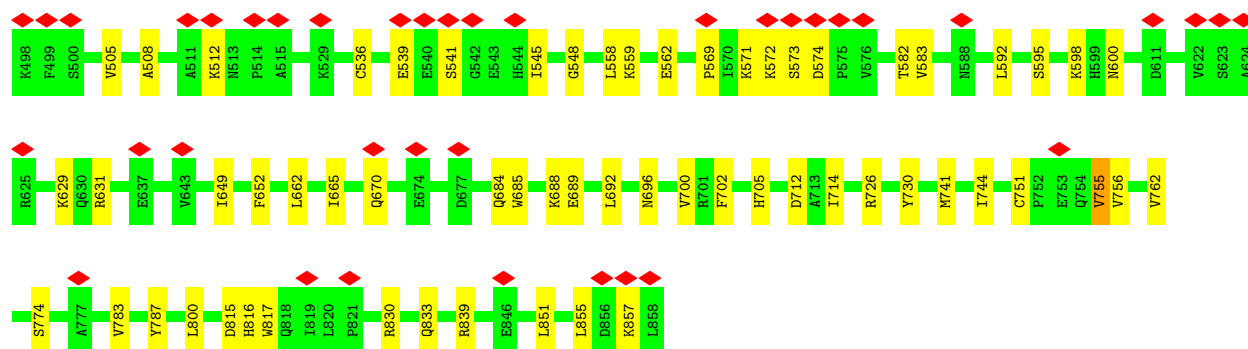


• Molecule 79: eS29

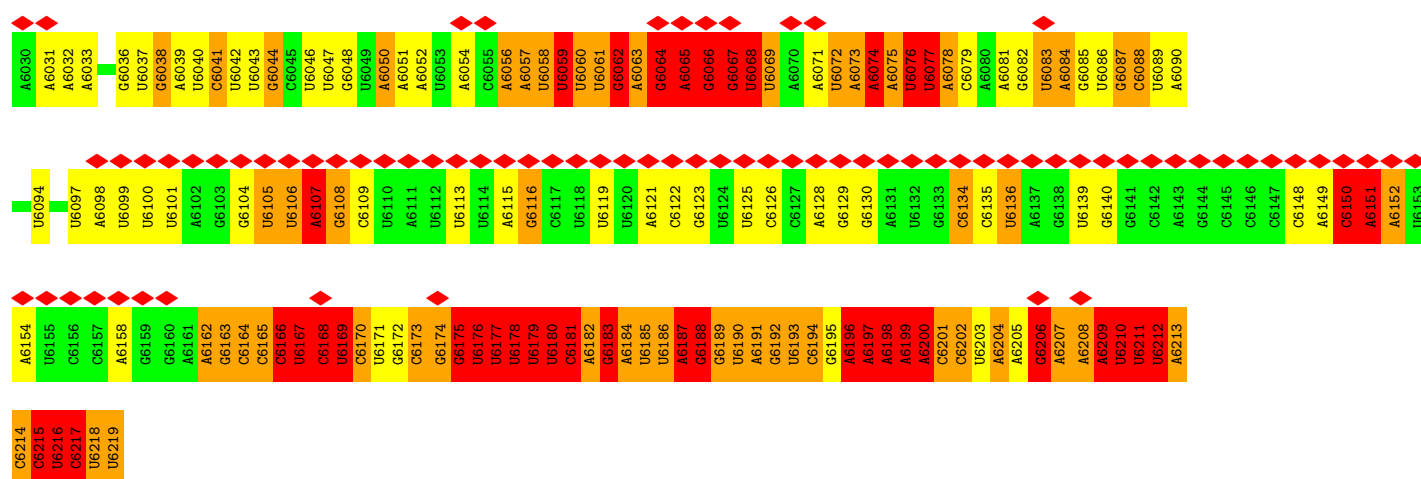
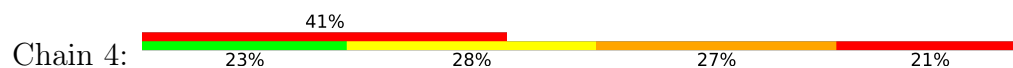


• Molecule 80: 40S ribosomal protein S30





• Molecule 85: CrPV IRES



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	75654	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 ($e^-/\text{\AA}^2$)	64	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.076	Depositor
Minimum map value	-0.013	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.02	Depositor
Map size ($\text{\AA}$)	432.00003, 432.00003, 432.00003	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.08, 1.08, 1.08	Depositor

5 Model quality

5.1 Standard geometry

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	A	0.19	0/1812	0.49	0/2439
2	B	0.18	0/3240	0.48	2/4339 (0.0%)
3	C	0.18	0/2936	0.45	0/3943
4	D	0.17	0/2437	0.43	0/3264
5	E	0.18	0/1762	0.46	0/2362
6	F	0.18	0/1911	0.46	0/2549
7	G	0.19	0/1910	0.47	0/2569
8	H	0.18	0/1535	0.49	0/2063
9	I	0.18	0/1702	0.43	0/2272
10	J	0.18	0/1385	0.48	0/1852
11	L	0.24	0/1733	0.49	0/2316
12	M	0.16	0/1150	0.41	0/1534
13	N	0.17	0/1746	0.45	0/2338
14	O	0.17	0/1653	0.43	0/2206
15	P	0.17	0/1268	0.47	0/1700
16	Q	0.18	0/1539	0.46	0/2054
17	R	0.18	0/1524	0.45	0/2013
18	S	0.17	0/1501	0.45	0/2012
19	T	0.18	0/1326	0.42	0/1770
20	U	0.18	0/823	0.47	0/1104
21	V	0.16	0/983	0.42	0/1319
22	W	0.16	0/873	0.45	0/1158
23	X	0.18	0/984	0.43	0/1323
24	Y	0.18	0/1132	0.43	0/1504
25	Z	0.18	0/1130	0.47	0/1507
26	a	0.16	0/1191	0.42	0/1590
27	b	0.16	0/861	0.40	0/1138
28	c	0.17	0/771	0.41	0/1034
29	d	0.21	0/903	0.54	0/1216
30	e	0.17	0/1071	0.47	0/1429
31	f	0.17	0/895	0.48	0/1198
32	g	0.18	0/916	0.45	0/1220

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	h	0.18	0/1021	0.42	0/1348
34	i	0.17	0/841	0.44	0/1112
35	j	0.23	0/720	0.50	0/952
36	k	0.17	0/575	0.41	0/761
37	l	0.19	0/459	0.48	0/608
38	m	0.18	0/435	0.45	0/575
39	n	0.16	0/240	0.41	0/305
40	o	0.14	0/864	0.37	0/1140
41	p	0.17	0/718	0.44	0/953
42	r	0.18	0/1010	0.47	0/1354
43	s	0.19	0/1530	0.45	0/2064
44	t	0.21	0/1174	0.55	0/1582
45	5	0.14	0/86202	0.31	5/134412 (0.0%)
46	7	0.13	0/2836	0.28	0/4421
47	8	0.14	0/3581	0.30	0/5577
48	K	0.23	0/1730	0.60	0/2315
49	2	0.14	0/40500	0.32	2/63092 (0.0%)
50	BB	0.21	0/1747	0.54	0/2374
51	CC	0.18	0/1756	0.46	0/2350
52	DD	0.18	0/1753	0.45	0/2369
53	EE	0.20	0/1796	0.49	0/2417
54	FF	0.17	0/2118	0.47	0/2849
55	GG	0.20	0/1492	0.49	0/2005
56	HH	0.18	0/1946	0.45	0/2590
57	II	0.19	0/1510	0.47	0/2022
58	JJ	0.18	0/1715	0.48	0/2287
59	KK	0.18	0/1550	0.49	0/2069
60	LL	0.17	0/834	0.43	0/1125
61	MM	0.18	0/1195	0.48	0/1597
62	NN	0.21	0/918	0.53	0/1233
63	OO	0.17	0/1226	0.42	0/1649
64	PP	0.17	0/1029	0.46	0/1380
65	QQ	0.18	0/974	0.54	0/1301
66	RR	0.19	0/1146	0.48	0/1534
67	SS	0.22	0/1082	0.56	1/1452 (0.1%)
68	TT	0.20	0/1208	0.53	0/1618
69	UU	0.19	0/1115	0.46	0/1493
70	VV	0.19	0/805	0.44	0/1081
71	WW	0.18	0/643	0.47	0/860
72	XX	0.17	0/1051	0.43	0/1406
73	YY	0.18	0/1116	0.47	0/1490
74	ZZ	0.19	0/1028	0.47	0/1366
75	aa	0.20	0/604	0.48	0/810

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	bb	0.17	0/828	0.44	0/1109
77	cc	0.18	0/665	0.46	0/891
78	dd	0.14	0/490	0.38	0/656
79	ee	0.16	0/470	0.45	0/623
80	ff	0.17	0/462	0.47	0/607
81	gg	0.16	0/567	0.42	0/753
82	hh	0.16	0/2492	0.46	0/3391
83	3	0.13	0/2077	0.26	0/3238
84	9	0.20	0/6804	0.54	1/9189 (0.0%)
85	4	0.68	14/4490 (0.3%)	1.55	126/6984 (1.8%)
All	All	0.18	14/243741 (0.0%)	0.44	137/357074 (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
3	C	0	1
50	BB	0	1
65	QQ	0	1
67	SS	0	1
73	YY	0	1
84	9	0	1
85	4	1	14
All	All	1	20

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
85	4	6218	U	C1'-N1	7.11	1.59	1.48
85	4	6219	U	C1'-N1	7.05	1.59	1.48
85	4	6065	A	O3'-P	6.87	1.71	1.61
85	4	6078	A	O3'-P	-6.68	1.51	1.61
85	4	6217	C	O3'-P	6.52	1.71	1.61
85	4	6187	A	O3'-P	6.28	1.70	1.61
85	4	6210	U	O3'-P	6.09	1.70	1.61
85	4	6166	C	O3'-P	6.06	1.70	1.61
85	4	6181	C	O3'-P	5.99	1.70	1.61
85	4	6167	U	O5'-C5'	5.78	1.51	1.42
85	4	6217	C	C3'-O3'	5.42	1.50	1.42
85	4	6181	C	C1'-N1	5.31	1.56	1.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
85	4	6212	U	O3'-P	5.25	1.69	1.61
85	4	6066	G	O5'-C5'	5.12	1.50	1.42

All (137) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
85	4	6068	U	O3'-P-O5'	-25.54	65.70	104.00
85	4	6218	U	O3'-P-O5'	-23.73	68.41	104.00
85	4	6176	U	C1'-C2'-O2'	-21.00	76.91	108.40
85	4	6215	C	C4'-C3'-O3'	19.37	142.05	113.00
85	4	6187	A	C1'-C2'-O2'	-17.98	84.84	111.80
85	4	6068	U	OP1-P-O3'	17.92	161.75	108.00
85	4	6204	A	O3'-P-O5'	-17.70	77.46	104.00
85	4	6181	C	C1'-C2'-O2'	-14.87	86.10	108.40
85	4	6166	C	C4'-C3'-O3'	13.92	133.87	113.00
85	4	6065	A	C2'-C3'-O3'	-12.55	94.87	113.70
85	4	6218	U	P-O3'-C3'	12.24	138.56	120.20
85	4	6178	U	C4'-C3'-O3'	11.90	130.85	113.00
85	4	6065	A	C1'-C2'-O2'	-11.84	90.64	108.40
85	4	6197	A	N9-C1'-C2'	11.29	128.93	112.00
85	4	6177	U	N1-C1'-C2'	11.20	128.80	112.00
85	4	6212	U	N1-C1'-C2'	11.01	130.52	114.00
85	4	6215	C	C2'-C3'-O3'	-11.01	97.19	113.70
85	4	6187	A	C2'-C3'-O3'	10.68	125.52	109.50
85	4	6065	A	C3'-C2'-O2'	10.66	126.70	110.70
85	4	6187	A	C4'-C3'-O3'	-10.66	93.41	109.40
85	4	6150	C	C2'-C3'-O3'	10.13	128.90	113.70
85	4	6187	A	C3'-C2'-O2'	10.12	129.78	114.60
85	4	6166	C	C2'-C3'-O3'	-10.11	98.54	113.70
85	4	6068	U	OP2-P-O3'	-9.87	78.40	108.00
85	4	6168	C	N1-C1'-C2'	9.80	126.71	112.00
85	4	6216	U	C4'-C3'-O3'	9.65	127.47	113.00
85	4	6211	U	N1-C1'-C2'	9.62	128.44	114.00
85	4	6210	U	N1-C1'-C2'	9.53	126.30	112.00
85	4	6180	U	C4'-C3'-O3'	-9.51	95.13	109.40
85	4	6177	U	C4'-C3'-O3'	9.50	127.25	113.00
85	4	6179	U	N1-C1'-C2'	9.22	127.83	114.00
85	4	6107	A	C2'-C3'-O3'	9.20	123.29	109.50
85	4	6166	C	C3'-C2'-O2'	9.05	124.28	110.70
85	4	6059	U	C2'-C3'-O3'	8.81	122.71	109.50
85	4	6183	G	C4'-C3'-O3'	-8.69	96.36	109.40
85	4	6077	U	N1-C1'-C2'	-8.67	99.00	112.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
85	4	6181	C	N1-C1'-C2'	8.43	124.64	112.00
85	4	6209	A	C3'-C2'-O2'	8.35	127.12	114.60
85	4	6065	A	C4'-C3'-O3'	8.31	125.47	113.00
85	4	6181	C	C4'-C3'-O3'	8.31	125.46	113.00
85	4	6199	A	N9-C1'-C2'	8.17	126.26	114.00
85	4	6077	U	C4'-C3'-O3'	8.13	125.19	113.00
85	4	6181	C	C3'-C2'-C1'	8.10	109.40	101.30
85	4	6180	U	C2'-C3'-O3'	8.09	121.63	109.50
85	4	6188	G	P-O5'-C5'	7.93	132.80	120.90
85	4	6218	U	OP1-P-O3'	7.84	131.53	108.00
85	4	6206	G	C2'-C3'-O3'	7.68	121.02	109.50
85	4	6210	U	C3'-C2'-O2'	7.51	121.97	110.70
85	4	6188	G	O5'-P-OP2	7.46	130.37	108.00
85	4	6150	C	C4'-C3'-O3'	7.34	124.01	113.00
85	4	6065	A	O4'-C1'-N9	7.28	119.42	108.50
85	4	6064	G	C4'-C3'-O3'	7.19	123.78	113.00
85	4	6198	A	C5'-C4'-C3'	7.18	126.77	116.00
85	4	6059	U	C3'-C2'-O2'	7.17	125.36	114.60
85	4	6169	U	C4'-C3'-O3'	7.14	123.71	113.00
85	4	6210	U	C2'-C3'-O3'	-7.14	102.99	113.70
85	4	6197	A	C4'-C3'-O3'	7.09	123.64	113.00
85	4	6216	U	C2'-C3'-O3'	-7.04	103.14	113.70
85	4	6064	G	N9-C1'-C2'	-6.86	101.72	112.00
85	4	6169	U	N1-C1'-C2'	6.85	122.28	112.00
85	4	6188	G	C5'-C4'-C3'	-6.77	105.84	116.00
85	4	6199	A	O4'-C1'-C2'	6.63	112.43	105.80
84	9	755	VAL	N-CA-C	-6.56	105.94	112.17
85	4	6188	G	C4'-C3'-O3'	6.54	122.81	113.00
85	4	6201	C	N1-C1'-C2'	-6.51	102.23	112.00
67	SS	91	LEU	N-CA-C	6.51	118.96	111.02
85	4	6210	U	O4'-C1'-N1	6.49	118.23	108.50
85	4	6078	A	P-O3'-C3'	-6.46	110.50	120.20
85	4	6210	U	C4'-C3'-O3'	6.45	122.68	113.00
85	4	6067	G	N9-C1'-C2'	6.45	123.68	114.00
85	4	6179	U	C5'-C4'-C3'	6.42	124.83	115.20
85	4	6199	A	C4-N9-C1'	-6.41	107.08	126.30
85	4	6216	U	C3'-C2'-O2'	6.34	120.22	110.70
2	B	213	GLN	CA-C-N	6.32	131.37	122.46
2	B	213	GLN	C-N-CA	6.32	131.37	122.46
85	4	6200	A	C4'-C3'-O3'	6.31	122.46	113.00
85	4	6151	A	C1'-O4'-C4'	-6.28	103.62	109.90
85	4	6178	U	C2'-C3'-O3'	-6.24	104.34	113.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
85	4	6169	U	C2'-C3'-O3'	-6.21	104.39	113.70
85	4	6167	U	O5'-C5'-C4'	6.20	120.80	111.50
85	4	6198	A	O4'-C4'-C3'	6.20	110.19	104.00
85	4	6215	C	N1-C1'-C2'	-6.19	102.72	112.00
85	4	6200	A	N9-C1'-C2'	-6.18	102.73	112.00
85	4	6211	U	O4'-C1'-C2'	6.18	111.98	105.80
85	4	6194	C	C4'-C3'-O3'	6.16	122.25	113.00
85	4	6176	U	N1-C1'-C2'	-6.16	102.76	112.00
85	4	6151	A	O4'-C4'-C3'	-6.13	97.87	104.00
85	4	6166	C	C3'-C2'-C1'	6.04	107.34	101.30
85	4	6074	A	N9-C1'-C2'	-6.02	102.97	112.00
85	4	6198	A	C2'-C3'-O3'	-5.91	104.83	113.70
85	4	6199	A	C8-N9-C1'	5.91	145.43	127.70
85	4	6065	A	C5'-C4'-C3'	5.89	124.84	116.00
85	4	6198	A	N9-C1'-C2'	5.89	120.84	112.00
85	4	6186	U	C4'-C3'-O3'	5.89	118.23	109.40
85	4	6169	U	C3'-C2'-O2'	5.88	119.52	110.70
85	4	6065	A	C8-N9-C1'	-5.84	110.18	127.70
85	4	6074	A	C4'-C3'-O3'	5.82	121.74	113.00
85	4	6183	G	C2'-C3'-O3'	5.79	118.18	109.50
85	4	6215	C	C3'-C2'-C1'	5.75	107.05	101.30
85	4	6210	U	O4'-C1'-C2'	5.74	113.34	107.60
85	4	6199	A	O4'-C1'-N9	5.69	116.73	108.20
85	4	6062	G	N9-C1'-C2'	-5.65	103.52	112.00
85	4	6167	U	C3'-C2'-O2'	5.65	119.17	110.70
85	4	6201	C	C4'-C3'-O3'	5.63	121.44	113.00
85	4	6168	C	C4'-C3'-O3'	5.57	121.35	113.00
85	4	6198	A	C3'-C2'-O2'	5.54	119.01	110.70
85	4	6066	G	P-O5'-C5'	5.48	129.12	120.90
85	4	6176	U	C2'-C3'-O3'	-5.48	105.48	113.70
45	5	4232	U	P-O3'-C3'	5.43	128.35	120.20
85	4	6169	U	C5'-C4'-C3'	5.40	124.10	116.00
85	4	6076	U	N1-C1'-C2'	-5.40	103.90	112.00
85	4	6167	U	C2'-C3'-O3'	-5.40	105.60	113.70
85	4	6196	A	C2'-C3'-O3'	5.38	121.77	113.70
85	4	6175	G	C3'-C2'-O2'	5.36	118.73	110.70
45	5	2695	A	P-O3'-C3'	5.31	128.16	120.20
85	4	6197	A	C8-N9-C1'	-5.30	111.78	127.70
85	4	6201	C	C2'-C3'-O3'	-5.30	105.75	113.70
85	4	6151	A	C5'-C4'-C3'	5.30	123.95	116.00
85	4	6151	A	C5'-C4'-O4'	5.28	117.72	109.80
85	4	6211	U	O4'-C1'-N1	5.28	116.11	108.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
85	4	6167	U	C4'-C3'-C2'	5.23	107.83	102.60
49	2	688	U	P-O3'-C3'	5.22	128.03	120.20
85	4	6201	C	C3'-C2'-O2'	5.21	118.52	110.70
45	5	4925	U	P-O3'-C3'	5.21	128.02	120.20
85	4	6181	C	C2'-C3'-O3'	-5.20	105.90	113.70
85	4	6217	C	O3'-P-O5'	-5.15	96.28	104.00
85	4	6217	C	C3'-C2'-C1'	5.14	106.44	101.30
85	4	6210	U	C1'-C2'-O2'	5.13	116.09	108.40
85	4	6065	A	C1'-O4'-C4'	-5.12	104.78	109.90
85	4	6215	C	C3'-C2'-O2'	5.10	118.35	110.70
85	4	6188	G	O5'-P-OP1	-5.09	92.74	108.00
45	5	2089	G	P-O3'-C3'	5.08	127.82	120.20
85	4	6198	A	C1'-C2'-O2'	5.07	116.01	108.40
85	4	6175	G	C2'-C3'-O3'	-5.04	106.14	113.70
45	5	2046	G	P-O3'-C3'	5.02	127.73	120.20
49	2	532	C	P-O3'-C3'	5.01	127.71	120.20
85	4	6187	A	P-O3'-C3'	5.01	127.71	120.20

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
85	4	6210	U	C1'

All (20) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
85	4	6065	A	Sidechain
85	4	6066	G	Sidechain
85	4	6067	G	Sidechain
85	4	6077	U	Sidechain
85	4	6151	A	Sidechain
85	4	6177	U	Sidechain
85	4	6178	U	Sidechain
85	4	6179	U	Sidechain
85	4	6181	C	Sidechain
85	4	6197	A	Sidechain
85	4	6198	A	Sidechain
85	4	6199	A	Sidechain
85	4	6210	U	Sidechain
85	4	6216	U	Sidechain
84	9	240	GLY	Peptide
50	BB	12	GLU	Peptide

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Mol	Chain	Res	Type	Group
3	C	151	PRO	Peptide
65	QQ	19	GLY	Peptide
67	SS	89	SER	Peptide
73	YY	61	GLN	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1777	0	1819	22	0
2	B	3172	0	3310	31	0
3	C	2883	0	3052	28	0
4	D	2391	0	2424	21	0
5	E	1729	0	1887	17	0
6	F	1875	0	1995	20	0
7	G	1879	0	2025	11	0
8	H	1516	0	1597	14	0
9	I	1664	0	1712	14	0
10	J	1362	0	1399	11	0
11	L	1702	0	1820	15	0
12	M	1130	0	1201	3	0
13	N	1701	0	1749	27	0
14	O	1623	0	1771	11	0
15	P	1242	0	1274	22	0
16	Q	1515	0	1634	11	0
17	R	1508	0	1664	13	0
18	S	1462	0	1508	11	0
19	T	1298	0	1366	15	0
20	U	809	0	833	3	0
21	V	969	0	1031	11	0
22	W	860	0	903	7	0
23	X	967	0	1040	9	0
24	Y	1115	0	1205	7	0
25	Z	1107	0	1182	13	0
26	a	1162	0	1209	14	0
27	b	848	0	920	5	0
28	c	761	0	794	9	0
29	d	888	0	930	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	e	1053	0	1147	10	0
31	f	876	0	912	10	0
32	g	906	0	1002	12	0
33	h	1013	0	1147	7	0
34	i	830	0	916	10	0
35	j	705	0	741	9	0
36	k	569	0	637	2	0
37	l	447	0	480	7	0
38	m	429	0	469	2	0
39	n	239	0	289	2	0
40	o	851	0	924	10	0
41	p	708	0	756	4	0
42	r	994	0	1051	8	0
43	s	1507	0	1564	14	0
44	t	1160	0	1218	12	0
45	5	77073	0	38949	466	0
46	7	2538	0	1286	8	0
47	8	3208	0	1629	24	0
48	K	1705	0	1804	143	0
49	2	36229	0	18309	260	0
50	BB	1710	0	1708	16	0
51	CC	1729	0	1803	12	0
52	DD	1716	0	1806	13	0
53	EE	1768	0	1866	9	0
54	FF	2076	0	2177	14	0
55	GG	1471	0	1522	11	0
56	HH	1923	0	2089	24	0
57	II	1488	0	1582	18	0
58	JJ	1686	0	1772	18	0
59	KK	1525	0	1640	16	0
60	LL	810	0	836	8	0
61	MM	1175	0	1249	10	0
62	NN	908	0	939	7	0
63	OO	1202	0	1289	15	0
64	PP	1016	0	1039	15	0
65	QQ	956	0	1002	6	0
66	RR	1128	0	1195	12	0
67	SS	1068	0	1121	13	0
68	TT	1190	0	1249	13	0
69	UU	1097	0	1130	16	0
70	VV	795	0	862	11	0
71	WW	636	0	637	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
72	XX	1034	0	1080	15	0
73	YY	1098	0	1167	13	0
74	ZZ	1011	0	1083	10	0
75	aa	598	0	656	4	0
76	bb	814	0	865	8	0
77	cc	651	0	672	7	0
78	dd	488	0	514	3	0
79	ee	459	0	451	5	0
80	ff	457	0	502	6	0
81	gg	555	0	565	5	0
82	hh	2436	0	2392	28	0
83	3	1860	0	935	36	0
84	9	6673	0	6750	78	0
85	4	4020	0	2013	738	0
86	2	1	0	0	0	0
86	bb	1	0	0	0	0
86	gg	1	0	0	0	0
86	p	1	0	0	0	0
87	5	2	0	0	0	0
All	All	227188	0	170642	2123	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 (2123) 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)
85:4:6199:A:N6	85:4:6200:A:C5	1.78	1.50
85:4:6180:U:N3	85:4:6196:A:H2	1.08	1.49
48:K:124:LEU:CA	85:4:6088:C:H42	1.25	1.48
85:4:6178:U:C2	85:4:6179:U:C6	2.00	1.48
85:4:6177:U:H2'	85:4:6178:U:C3'	1.39	1.47
85:4:6071:A:C2'	85:4:6072:U:H5'	1.46	1.45
85:4:6177:U:N1	85:4:6178:U:H1'	1.32	1.45
48:K:124:LEU:HA	85:4:6088:C:N4	1.13	1.44
85:4:6066:G:C2	85:4:6167:U:C5	2.06	1.42
85:4:6199:A:C6	85:4:6200:A:C4	2.04	1.42
85:4:6174:G:C6	85:4:6207:A:H1'	1.52	1.41
85:4:6199:A:N6	85:4:6200:A:C6	1.90	1.38
48:K:122:ARG:CG	85:4:6037:U:H4'	0.90	1.37
85:4:6066:G:N2	85:4:6167:U:C6	1.93	1.37

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:4:6178:U:N1	85:4:6179:U:C6	1.93	1.36
48:K:98:LYS:NZ	85:4:6086:U:H4'	1.38	1.35
85:4:6181:C:O2	85:4:6182:A:C5	1.79	1.35
85:4:6181:C:C2	85:4:6182:A:C5	2.15	1.35
48:K:124:LEU:HB2	85:4:6038:G:OP1	1.17	1.34
85:4:6199:A:O2'	85:4:6200:A:C5'	1.73	1.34
85:4:6182:A:H61	85:4:6195:G:N2	1.21	1.34
48:K:124:LEU:CG	85:4:6037:U:H2'	1.57	1.33
85:4:6177:U:C3'	85:4:6178:U:H4'	1.59	1.32
85:4:6198:A:C4	85:4:6199:A:C5	2.17	1.32
48:K:124:LEU:CA	85:4:6088:C:N4	1.84	1.31
48:K:93:LEU:CD2	85:4:6039:A:C2	2.13	1.31
85:4:6199:A:C6	85:4:6200:A:C5	2.17	1.31
83:3:36:A:N1	85:4:6217:C:C2	1.98	1.30
85:4:6148:C:H2'	85:4:6149:A:C8	1.65	1.30
85:4:6050:A:O3'	85:4:6051:A:H3'	1.18	1.29
48:K:122:ARG:HG2	85:4:6037:U:C4'	0.82	1.29
48:K:128:LEU:HD21	85:4:6086:U:C4	1.68	1.28
85:4:6071:A:H2'	85:4:6072:U:C5'	1.64	1.28
85:4:6177:U:C6	85:4:6178:U:H1'	1.69	1.28
85:4:6174:G:N3	85:4:6208:A:N6	1.82	1.27
85:4:6179:U:H3	85:4:6197:A:N6	1.30	1.27
85:4:6199:A:C5	85:4:6200:A:C8	2.23	1.27
48:K:98:LYS:HE3	85:4:6086:U:C5'	1.63	1.27
85:4:6066:G:OP1	85:4:6069:U:C4	1.88	1.27
85:4:6178:U:C6	85:4:6179:U:C5	2.21	1.26
85:4:6214:C:O2'	85:4:6215:C:H5'	1.34	1.25
85:4:6181:C:O2	85:4:6182:A:C4	1.88	1.25
85:4:6174:G:C2	85:4:6208:A:C6	2.25	1.24
85:4:6181:C:C2	85:4:6182:A:N7	2.06	1.24
85:4:6178:U:C4	85:4:6179:U:C4	2.25	1.24
48:K:122:ARG:CB	85:4:6037:U:O3'	1.87	1.23
85:4:6174:G:C2	85:4:6208:A:C5	2.27	1.23
83:3:36:A:N6	85:4:6217:C:C4	2.07	1.23
85:4:6211:U:O2	85:4:6212:U:H5'	1.35	1.22
85:4:6178:U:C5	85:4:6179:U:C5	2.26	1.21
85:4:6148:C:C2'	85:4:6149:A:H8	1.52	1.20
85:4:6177:U:H2'	85:4:6178:U:C2'	1.70	1.20
48:K:122:ARG:HB3	85:4:6037:U:O3'	1.02	1.19
85:4:6057:A:C8	85:4:6058:U:C6	2.30	1.19
85:4:6189:G:N1	85:4:6214:C:O2	1.75	1.19

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:K:124:LEU:HG	85:4:6037:U:C2'	1.71	1.19
48:K:110:PHE:CZ	85:4:6039:A:N6	2.10	1.18
85:4:6182:A:O2'	85:4:6183:G:H5'	1.39	1.18
48:K:93:LEU:CD2	85:4:6039:A:H2	1.50	1.17
48:K:93:LEU:HD21	85:4:6039:A:C2	1.78	1.17
48:K:128:LEU:HD21	85:4:6086:U:O4	1.40	1.17
83:3:36:A:C6	85:4:6217:C:N3	2.12	1.16
45:5:4045:G:O3'	85:4:6044:G:N1	1.79	1.15
85:4:6174:G:N2	85:4:6208:A:C6	2.13	1.15
48:K:93:LEU:HD23	85:4:6039:A:C2	1.73	1.15
85:4:6174:G:N1	85:4:6208:A:N7	1.93	1.15
85:4:6179:U:N3	85:4:6197:A:N6	1.91	1.14
48:K:124:LEU:CB	85:4:6038:G:OP1	1.95	1.14
85:4:6176:U:O2	85:4:6200:A:C2	1.99	1.14
48:K:90:LEU:HD22	85:4:6039:A:H1'	1.18	1.14
85:4:6199:A:N6	85:4:6200:A:C4	2.10	1.14
48:K:90:LEU:CD2	85:4:6039:A:H1'	1.78	1.13
85:4:6068:U:H3'	85:4:6069:U:C5'	1.66	1.13
85:4:6176:U:C2	85:4:6200:A:H2	1.66	1.13
85:4:6198:A:C2	85:4:6199:A:C2	2.36	1.13
85:4:6218:U:H2'	85:4:6219:U:C6	1.83	1.13
85:4:6063:A:N6	85:4:6169:U:O4	1.80	1.12
85:4:6188:G:N2	85:4:6215:C:O2	1.80	1.11
85:4:6066:G:OP1	85:4:6069:U:N3	1.83	1.11
85:4:6179:U:O2'	85:4:6180:U:H5'	1.51	1.11
49:2:1701:C:N3	85:4:6219:U:C2	2.19	1.11
85:4:6198:A:N3	85:4:6199:A:C4	2.18	1.11
85:4:6068:U:C3'	85:4:6069:U:O4'	1.98	1.10
85:4:6180:U:O4	85:4:6196:A:N1	1.84	1.10
85:4:6179:U:C2	85:4:6197:A:N1	2.19	1.10
85:4:6193:U:O2'	85:4:6210:U:O4	1.68	1.10
85:4:6068:U:H3'	85:4:6069:U:C4'	1.80	1.10
85:4:6134:C:C4	85:4:6135:C:N4	2.20	1.09
85:4:6179:U:C4	85:4:6197:A:N6	2.20	1.08
85:4:6194:C:H5'	85:4:6210:U:O4	1.51	1.08
85:4:6050:A:O3'	85:4:6051:A:C3'	2.02	1.08
48:K:122:ARG:HG2	85:4:6037:U:C3'	1.84	1.07
85:4:6179:U:N3	85:4:6197:A:N1	2.00	1.07
85:4:6177:U:O4	85:4:6200:A:C2	2.08	1.07
85:4:6056:A:C2'	85:4:6057:A:H5'	1.84	1.06
85:4:6177:U:C2'	85:4:6178:U:C3'	2.33	1.06

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:4:6178:U:C2	85:4:6179:U:N1	2.20	1.06
85:4:6174:G:C6	85:4:6207:A:C1'	2.38	1.06
83:3:34:U:H5'	85:4:6187:A:C8	1.88	1.06
85:4:6177:U:O4	85:4:6200:A:N3	1.87	1.06
85:4:6068:U:H3'	85:4:6069:U:O4'	1.51	1.06
85:4:6198:A:C6	85:4:6199:A:N6	2.22	1.06
85:4:6200:A:C6	85:4:6201:C:C4	2.42	1.06
85:4:6217:C:H2'	85:4:6218:U:C6	1.91	1.06
85:4:6179:U:O2	85:4:6197:A:N1	1.88	1.05
48:K:128:LEU:CD2	85:4:6086:U:O4	2.03	1.05
48:K:122:ARG:CD	85:4:6037:U:H4'	1.86	1.05
83:3:37:G:C2	85:4:6217:C:C2	2.45	1.04
85:4:6177:U:H3'	85:4:6178:U:H4'	1.05	1.04
85:4:6182:A:N6	85:4:6195:G:N2	2.05	1.04
85:4:6071:A:OP2	85:4:6072:U:C5	2.11	1.03
48:K:93:LEU:HD21	85:4:6039:A:H2	1.09	1.03
85:4:6134:C:H2'	85:4:6135:C:C6	1.93	1.03
85:4:6182:A:O2'	85:4:6183:G:C5'	2.07	1.03
85:4:6198:A:C6	85:4:6199:A:C6	2.47	1.03
64:PP:66:ARG:NH2	85:4:6193:U:OP1	1.90	1.03
85:4:6180:U:C4	85:4:6196:A:C2	2.46	1.03
48:K:45:LYS:NZ	85:4:6047:U:H5''	1.72	1.02
49:2:1640:A:H4'	85:4:6195:G:H5'	1.40	1.02
48:K:45:LYS:NZ	85:4:6047:U:C5'	2.21	1.02
48:K:90:LEU:HD22	85:4:6039:A:C1'	1.88	1.02
48:K:98:LYS:HE3	85:4:6086:U:H5'	1.03	1.02
48:K:124:LEU:CD2	85:4:6089:U:C4	2.42	1.02
85:4:6178:U:C4	85:4:6179:U:C5	2.46	1.01
85:4:6200:A:N6	85:4:6201:C:N4	2.06	1.01
85:4:6198:A:C2	85:4:6199:A:N1	2.28	1.01
85:4:6179:U:O4	85:4:6197:A:N6	1.94	1.01
48:K:124:LEU:CD2	85:4:6088:C:H41	1.74	1.01
85:4:6180:U:C4	85:4:6196:A:H2	1.78	1.01
48:K:122:ARG:CG	85:4:6037:U:C3'	2.39	1.00
48:K:124:LEU:CB	85:4:6088:C:H41	1.73	1.00
85:4:6177:U:C4	85:4:6200:A:N3	2.29	1.00
85:4:6198:A:C2	85:4:6199:A:C6	2.49	1.00
85:4:6199:A:O2'	85:4:6200:A:H5''	0.84	1.00
48:K:124:LEU:CD1	85:4:6037:U:H2'	1.90	1.00
83:3:37:G:C4	85:4:6217:C:O2	2.03	1.00
85:4:6057:A:C8	85:4:6058:U:H6	1.75	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:4:6176:U:O2	85:4:6200:A:H2	1.37	1.00
48:K:124:LEU:CB	85:4:6088:C:N4	2.23	1.00
85:4:6180:U:C4	85:4:6197:A:C6	2.49	1.00
85:4:6199:A:N1	85:4:6200:A:C4	2.29	1.00
85:4:6177:U:H2'	85:4:6178:U:C4'	1.91	1.00
48:K:110:PHE:HZ	85:4:6039:A:N6	1.57	0.99
85:4:6198:A:N3	85:4:6199:A:C5	2.29	0.99
85:4:6057:A:N1	85:4:6165:C:OP2	1.94	0.99
85:4:6148:C:C2'	85:4:6149:A:C8	2.34	0.99
48:K:120:ILE:HA	85:4:6038:G:H5''	1.44	0.99
48:K:124:LEU:CD2	85:4:6088:C:N4	2.25	0.99
85:4:6177:U:C2	85:4:6178:U:O2'	2.15	0.99
85:4:6199:A:C5	85:4:6200:A:N7	2.31	0.99
85:4:6057:A:C2	85:4:6164:C:H3'	1.98	0.98
48:K:98:LYS:CE	85:4:6086:U:H5'	1.94	0.98
48:K:124:LEU:HD23	85:4:6088:C:N4	1.78	0.98
85:4:6066:G:N1	85:4:6166:C:N3	2.11	0.98
85:4:6176:U:C2	85:4:6200:A:C2	2.50	0.98
85:4:6177:U:N1	85:4:6178:U:C1'	2.25	0.98
48:K:48:ARG:HD3	85:4:6082:G:H4'	1.42	0.98
85:4:6218:U:H2'	85:4:6219:U:H6	1.25	0.98
85:4:6178:U:C2	85:4:6179:U:C5	2.50	0.98
85:4:6066:G:N2	85:4:6167:U:C5	2.23	0.98
85:4:6066:G:N3	85:4:6167:U:C4	2.31	0.98
85:4:6174:G:N2	85:4:6208:A:C5	2.29	0.98
48:K:124:LEU:CD2	85:4:6089:U:N3	2.26	0.97
85:4:6056:A:O2'	85:4:6057:A:H5'	1.64	0.97
48:K:122:ARG:HG2	85:4:6037:U:C5'	1.94	0.97
85:4:6198:A:C4	85:4:6199:A:N7	2.33	0.97
48:K:124:LEU:HD21	85:4:6089:U:C4	1.98	0.97
48:K:124:LEU:HD23	85:4:6089:U:N3	1.80	0.97
85:4:6071:A:OP2	85:4:6072:U:H5	1.43	0.97
85:4:6148:C:H2'	85:4:6149:A:H8	0.99	0.96
48:K:128:LEU:HD21	85:4:6086:U:N3	1.80	0.96
85:4:6076:U:O4	85:4:6077:U:O4	1.84	0.96
85:4:6177:U:O4	85:4:6199:A:N1	1.98	0.96
85:4:6177:U:H2'	85:4:6178:U:O3'	1.64	0.95
85:4:6057:A:N7	85:4:6058:U:C6	2.33	0.95
85:4:6199:A:C6	85:4:6200:A:N9	2.33	0.95
85:4:6177:U:O2	85:4:6178:U:O2'	1.83	0.95
85:4:6066:G:N3	85:4:6167:U:C5	2.33	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:4:6134:C:C2	85:4:6135:C:C5	2.54	0.94
85:4:6177:U:H3'	85:4:6178:U:C4'	1.97	0.94
83:3:34:U:C5'	85:4:6187:A:C8	2.49	0.94
48:K:98:LYS:HZ1	85:4:6086:U:H4'	1.17	0.94
85:4:6174:G:C2	85:4:6208:A:N6	2.30	0.94
85:4:6200:A:C5	85:4:6201:C:C5	2.55	0.94
83:3:36:A:N1	85:4:6217:C:O2	1.99	0.94
85:4:6192:G:H1	85:4:6211:U:H3	0.96	0.94
85:4:6180:U:N3	85:4:6196:A:C2	1.96	0.94
85:4:6198:A:N9	85:4:6199:A:C8	2.36	0.94
85:4:6177:U:C2'	85:4:6178:U:H4'	1.97	0.93
48:K:98:LYS:HZ2	85:4:6086:U:H4'	1.21	0.93
85:4:6066:G:C2	85:4:6167:U:C6	2.48	0.93
85:4:6057:A:C6	85:4:6165:C:OP2	2.21	0.93
85:4:6198:A:N9	85:4:6199:A:N7	2.17	0.93
85:4:6217:C:HO2'	85:4:6218:U:H6	1.11	0.93
83:3:36:A:C2	85:4:6217:C:O2	2.22	0.92
64:PP:66:ARG:NH2	85:4:6193:U:P	2.43	0.92
48:K:124:LEU:HD21	85:4:6089:U:O4	1.68	0.92
85:4:6178:U:N1	85:4:6179:U:C5	2.32	0.91
48:K:98:LYS:CE	85:4:6086:U:C5'	2.48	0.91
48:K:45:LYS:HZ3	85:4:6047:U:C5'	1.82	0.91
85:4:6134:C:O2'	85:4:6135:C:H5'	1.71	0.91
48:K:124:LEU:HG	85:4:6037:U:H2'	0.92	0.91
85:4:6071:A:C3'	85:4:6072:U:H5'	2.01	0.90
85:4:6177:U:C2'	85:4:6178:U:C4'	2.50	0.90
85:4:6199:A:HO2'	85:4:6200:A:H5''	1.20	0.90
85:4:6071:A:P	85:4:6072:U:H5	1.94	0.90
64:PP:66:ARG:HH21	85:4:6193:U:P	1.95	0.90
85:4:6178:U:C6	85:4:6179:U:H5	1.83	0.90
85:4:6134:C:N3	85:4:6135:C:C4	2.40	0.90
85:4:6177:U:C6	85:4:6178:U:C1'	2.54	0.90
85:4:6177:U:C2'	85:4:6178:U:C2'	2.50	0.90
85:4:6179:U:O2	85:4:6197:A:C2	2.25	0.90
48:K:98:LYS:NZ	85:4:6086:U:C4'	2.33	0.89
48:K:93:LEU:HD23	85:4:6039:A:N3	1.85	0.89
85:4:6182:A:H61	85:4:6195:G:H22	0.95	0.89
85:4:6217:C:H2'	85:4:6218:U:C5	2.06	0.89
48:K:124:LEU:HD12	85:4:6038:G:OP1	1.71	0.89
85:4:6200:A:H62	85:4:6201:C:N4	1.68	0.89
83:3:35:G:C6	85:4:6218:U:C4	2.61	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:4:6148:C:N1	85:4:6149:A:C8	2.41	0.89
85:4:6217:C:C2'	85:4:6218:U:H6	1.86	0.89
85:4:6177:U:C2'	85:4:6178:U:O2'	2.20	0.89
85:4:6174:G:C6	85:4:6208:A:N7	2.41	0.89
85:4:6176:U:N3	85:4:6200:A:C2	2.42	0.88
85:4:6198:A:N1	85:4:6199:A:C6	2.40	0.88
85:4:6217:C:C2'	85:4:6218:U:C6	2.57	0.88
85:4:6198:A:C5	85:4:6199:A:C6	2.62	0.88
85:4:6071:A:C8	85:4:6072:U:C6	2.62	0.88
85:4:6200:A:N6	85:4:6201:C:C4	2.41	0.88
85:4:6199:A:C6	85:4:6200:A:C8	2.58	0.87
85:4:6150:C:H3'	85:4:6150:C:H6	1.39	0.87
85:4:6188:G:C2	85:4:6215:C:O2	2.26	0.87
49:2:1701:C:C4	85:4:6219:U:C2	2.63	0.87
9:I:6:ALA:O	9:I:10:ARG:HB2	1.74	0.87
85:4:6148:C:C2	85:4:6149:A:C8	2.63	0.86
85:4:6177:U:C4	85:4:6178:U:C2	2.63	0.86
48:K:122:ARG:HG3	85:4:6037:U:O2'	1.75	0.86
85:4:6177:U:C1'	85:4:6178:U:H1'	2.04	0.86
85:4:6057:A:H2	85:4:6164:C:H3'	1.35	0.86
85:4:6183:G:N2	85:4:6184:A:C2	2.43	0.86
85:4:6134:C:H2'	85:4:6135:C:H6	1.37	0.86
85:4:6181:C:C2	85:4:6182:A:C8	2.63	0.86
85:4:6199:A:C4	85:4:6200:A:C8	2.64	0.86
85:4:6056:A:H2'	85:4:6057:A:H5'	1.58	0.86
85:4:6064:G:N1	85:4:6168:C:O2	2.08	0.85
85:4:6194:C:H5'	85:4:6210:U:C4	2.11	0.85
85:4:6060:U:OP1	85:4:6061:U:H5'	1.74	0.85
85:4:6071:A:H2'	85:4:6072:U:H5'	0.85	0.85
85:4:6199:A:HO2'	85:4:6200:A:C5'	1.78	0.85
85:4:6184:A:C8	85:4:6185:U:C4	2.63	0.85
48:K:45:LYS:HZ1	85:4:6047:U:H5''	1.42	0.85
85:4:6068:U:C6	85:4:6069:U:C2	2.64	0.85
85:4:6106:U:N3	85:4:6130:G:N7	2.10	0.85
83:3:36:A:C6	85:4:6217:C:C2	2.61	0.84
85:4:6217:C:O2'	85:4:6218:U:H6	1.60	0.84
85:4:6177:U:C2	85:4:6178:U:O2	2.30	0.84
83:3:37:G:N1	85:4:6217:C:N1	2.07	0.84
85:4:6194:C:C5'	85:4:6210:U:O4	2.26	0.84
85:4:6177:U:C4	85:4:6178:U:N3	2.45	0.84
85:4:6178:U:N1	85:4:6179:U:H6	1.75	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:4:6182:A:H61	85:4:6195:G:H21	1.23	0.84
85:4:6078:A:N1	85:4:6079:C:C4	2.46	0.83
85:4:6180:U:O4	85:4:6196:A:C2	2.29	0.83
85:4:6066:G:C4	85:4:6167:U:C4	2.66	0.83
85:4:6180:U:C5	85:4:6197:A:N1	2.46	0.83
85:4:6197:A:C2	85:4:6198:A:C2	2.67	0.83
85:4:6199:A:C2	85:4:6200:A:C1'	2.62	0.83
48:K:124:LEU:HB2	85:4:6038:G:P	2.19	0.83
85:4:6050:A:HO3'	85:4:6051:A:H3'	1.43	0.83
85:4:6176:U:N3	85:4:6200:A:H2	1.76	0.83
85:4:6174:G:N1	85:4:6207:A:C1'	2.42	0.82
83:3:36:A:N1	85:4:6217:C:N3	2.23	0.82
48:K:122:ARG:CB	85:4:6037:U:H4'	2.06	0.82
85:4:6178:U:C6	85:4:6179:U:C6	2.58	0.82
48:K:122:ARG:HB3	85:4:6038:G:P	2.19	0.82
84:9:714:ILE:CD1	85:4:6219:U:O2'	2.28	0.82
85:4:6068:U:C5	85:4:6069:U:O2	2.31	0.82
84:9:714:ILE:HD13	85:4:6219:U:O2'	1.80	0.82
85:4:6068:U:C6	85:4:6069:U:O2	2.33	0.82
48:K:124:LEU:CD1	85:4:6038:G:OP1	2.26	0.81
85:4:6178:U:N3	85:4:6179:U:C4	2.48	0.81
85:4:6199:A:N7	85:4:6200:A:N7	2.27	0.81
31:f:2:SER:N	45:5:4946:U:HO2'	1.78	0.81
85:4:6065:A:H2	85:4:6167:U:H3	1.24	0.81
85:4:6181:C:N3	85:4:6182:A:C6	2.49	0.81
83:3:35:G:C6	85:4:6218:U:O4	2.33	0.81
85:4:6200:A:C5	85:4:6201:C:C4	2.69	0.81
85:4:6175:G:N7	85:4:6206:G:N2	2.29	0.81
85:4:6198:A:C5	85:4:6199:A:C5	2.68	0.80
85:4:6168:C:C4	85:4:6169:U:C4	2.70	0.80
85:4:6198:A:N1	85:4:6199:A:N1	2.29	0.80
85:4:6199:A:N6	85:4:6200:A:N1	2.28	0.80
85:4:6078:A:C6	85:4:6079:C:C4	2.70	0.80
83:3:37:G:N3	85:4:6217:C:O2	2.14	0.80
85:4:6060:U:H3'	85:4:6061:U:H5''	1.64	0.80
85:4:6178:U:N3	85:4:6179:U:C5	2.50	0.79
85:4:6179:U:N3	85:4:6180:U:C5	2.51	0.79
85:4:6177:U:C2'	85:4:6178:U:O3'	2.29	0.79
85:4:6178:U:C5	85:4:6179:U:H5	1.96	0.79
85:4:6198:A:C4	85:4:6199:A:C6	2.70	0.78
85:4:6177:U:C4	85:4:6200:A:C2	2.70	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:4:6214:C:O2'	85:4:6215:C:C5'	2.25	0.78
85:4:6057:A:N6	85:4:6165:C:OP2	2.16	0.78
85:4:6148:C:C4	85:4:6149:A:C5	2.72	0.78
85:4:6173:C:H4'	85:4:6174:G:OP2	1.83	0.78
48:K:45:LYS:NZ	85:4:6047:U:H5'	1.98	0.78
83:3:37:G:N1	85:4:6217:C:C6	2.51	0.78
85:4:6174:G:N1	85:4:6207:A:O4'	2.16	0.78
85:4:6180:U:H3'	85:4:6180:U:OP2	1.85	0.77
48:K:32:VAL:HA	48:K:207:LYS:O	1.85	0.77
83:3:36:A:N6	85:4:6217:C:N3	2.24	0.77
85:4:6167:U:H2'	85:4:6168:C:H6	1.50	0.77
85:4:6199:A:N6	85:4:6200:A:C2	2.49	0.77
85:4:6199:A:C5	85:4:6200:A:C5	2.71	0.77
85:4:6057:A:H2'	85:4:6058:U:O4'	1.85	0.77
85:4:6148:C:H2'	85:4:6149:A:O4'	1.85	0.77
85:4:6181:C:N3	85:4:6182:A:C5	2.52	0.76
48:K:45:LYS:HZ3	85:4:6047:U:H5'	1.50	0.76
85:4:6148:C:C6	85:4:6149:A:N7	2.53	0.76
7:G:313:GLU:O	7:G:317:LYS:HB2	1.84	0.76
85:4:6066:G:H3'	85:4:6067:G:H3'	1.67	0.76
48:K:48:ARG:CD	85:4:6082:G:H4'	2.16	0.76
85:4:6066:G:OP1	85:4:6069:U:O4	2.04	0.76
85:4:6174:G:N1	85:4:6208:A:C5	2.46	0.76
85:4:6174:G:O6	85:4:6207:A:H1'	1.84	0.76
85:4:6050:A:H5'	85:4:6051:A:OP2	1.86	0.76
85:4:6071:A:C5	85:4:6072:U:H1'	2.21	0.76
85:4:6108:G:C5	85:4:6109:C:C4	2.74	0.75
49:2:924:G:H1	49:2:1018:U:H3	1.34	0.75
49:2:1640:A:H4'	85:4:6195:G:C5'	2.17	0.75
85:4:6066:G:N2	85:4:6167:U:H6	1.75	0.75
48:K:98:LYS:HE2	85:4:6086:U:OP1	1.86	0.75
85:4:6063:A:N6	85:4:6169:U:C4	2.45	0.75
85:4:6168:C:C6	85:4:6169:U:C5	2.74	0.75
85:4:6148:C:C3'	85:4:6149:A:H8	1.98	0.75
85:4:6174:G:C2	85:4:6208:A:N7	2.47	0.75
85:4:6198:A:C5	85:4:6199:A:N6	2.55	0.74
85:4:6179:U:C2	85:4:6180:U:C5	2.75	0.74
85:4:6168:C:C5	85:4:6169:U:C5	2.75	0.74
48:K:124:LEU:HD21	85:4:6089:U:N3	1.97	0.74
85:4:6062:G:O6	85:4:6170:C:O2	2.04	0.74
85:4:6071:A:H2'	85:4:6072:U:C4'	2.16	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:4:6177:U:C1'	85:4:6178:U:O2'	2.34	0.74
83:3:36:A:C6	85:4:6217:C:C4	2.67	0.74
85:4:6182:A:N6	85:4:6195:G:H22	1.73	0.74
85:4:6068:U:H6	85:4:6069:U:C2	2.05	0.73
85:4:6181:C:N3	85:4:6182:A:N6	2.36	0.73
83:3:35:G:N1	85:4:6218:U:C4	2.56	0.73
45:5:3946:G:H1	45:5:4067:U:H3	1.37	0.73
85:4:6177:U:C3'	85:4:6178:U:C4'	2.52	0.73
85:4:6181:C:C2	85:4:6182:A:C6	2.77	0.73
85:4:6134:C:C2	85:4:6135:C:C4	2.77	0.73
85:4:6166:C:O2	85:4:6166:C:O2'	2.05	0.73
85:4:6178:U:O2	85:4:6179:U:N1	2.21	0.72
85:4:6211:U:O4	85:4:6212:U:N3	2.22	0.72
85:4:6180:U:C5	85:4:6197:A:C6	2.77	0.72
48:K:110:PHE:CE1	85:4:6039:A:N6	2.58	0.72
85:4:6068:U:C2'	85:4:6069:U:O4'	2.36	0.72
85:4:6183:G:O2'	85:4:6184:A:C8	2.43	0.72
85:4:6183:G:C2	85:4:6184:A:C6	2.78	0.71
85:4:6071:A:C2'	85:4:6072:U:C5'	2.40	0.71
85:4:6177:U:H2'	85:4:6178:U:O2'	1.86	0.71
48:K:124:LEU:HB3	85:4:6088:C:H41	1.54	0.71
85:4:6192:G:N2	85:4:6211:U:O2	2.23	0.71
85:4:6211:U:O2	85:4:6212:U:C5'	2.27	0.71
49:2:1701:C:C4	85:4:6219:U:N3	2.58	0.71
85:4:6150:C:H3'	85:4:6150:C:C6	2.24	0.71
85:4:6057:A:C8	85:4:6058:U:C5	2.79	0.71
48:K:44:GLN:HG2	85:4:6046:U:O2'	1.91	0.71
83:3:36:A:N6	85:4:6217:C:C5	2.59	0.71
85:4:6198:A:C2	85:4:6199:A:C5	2.75	0.71
85:4:6199:A:N1	85:4:6200:A:N9	2.38	0.71
85:4:6134:C:C4	85:4:6135:C:C4	2.79	0.70
49:2:19:A:H5''	73:YY:107:ARG:HH22	1.57	0.70
85:4:6180:U:C6	85:4:6197:A:C2	2.80	0.70
85:4:6068:U:C4'	85:4:6069:U:O4'	2.40	0.70
85:4:6183:G:N1	85:4:6184:A:C6	2.59	0.70
85:4:6198:A:C2	85:4:6199:A:C4	2.80	0.70
85:4:6198:A:C8	85:4:6199:A:N7	2.60	0.70
48:K:45:LYS:HZ1	85:4:6047:U:C5'	1.97	0.70
48:K:98:LYS:CE	85:4:6086:U:H4'	2.21	0.69
49:2:808:A:H2	49:2:855:G:H1	1.39	0.69
48:K:128:LEU:HD21	85:4:6086:U:H3	1.56	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:19:HIS:HE2	45:5:1539:G:HO2'	1.38	0.69
85:4:6199:A:C2	85:4:6200:A:H1'	2.27	0.69
48:K:124:LEU:CD2	85:4:6089:U:H3	2.03	0.69
85:4:6211:U:O2'	85:4:6212:U:O5'	2.09	0.69
85:4:6184:A:N7	85:4:6185:U:O4	2.26	0.69
83:3:37:G:C2	85:4:6217:C:O2	2.46	0.69
85:4:6177:U:C4	85:4:6199:A:N1	2.61	0.69
48:K:122:ARG:CB	85:4:6037:U:C4'	2.68	0.69
48:K:124:LEU:HD22	85:4:6088:C:H41	1.57	0.69
45:5:234:G:H1	45:5:2304:U:H3	1.39	0.68
48:K:122:ARG:CB	85:4:6037:U:C3'	2.69	0.68
85:4:6174:G:C5	85:4:6207:A:H1'	2.25	0.68
85:4:6193:U:H2'	85:4:6194:C:C6	2.28	0.68
85:4:6197:A:H3'	85:4:6198:A:H4'	1.74	0.68
85:4:6148:C:C2	85:4:6149:A:N9	2.62	0.68
82:hh:87:LEU:HB2	82:hh:101:PHE:HB2	1.76	0.68
48:K:124:LEU:CG	85:4:6088:C:H41	2.07	0.68
85:4:6150:C:H6	85:4:6150:C:C3'	2.06	0.68
85:4:6076:U:C4	85:4:6077:U:C5	2.82	0.68
85:4:6076:U:N3	85:4:6077:U:C5	2.62	0.68
85:4:6150:C:C6	85:4:6150:C:C3'	2.77	0.68
85:4:6176:U:O2	85:4:6177:U:C5	2.47	0.68
85:4:6059:U:H1'	85:4:6060:U:H5''	1.75	0.67
85:4:6078:A:C6	85:4:6079:C:N4	2.61	0.67
85:4:6071:A:C3'	85:4:6072:U:C5'	2.71	0.67
85:4:6218:U:C2'	85:4:6219:U:C6	2.72	0.67
85:4:6060:U:O4	85:4:6167:U:OP1	2.11	0.67
48:K:90:LEU:HD22	85:4:6039:A:O2'	1.95	0.67
85:4:6192:G:N1	85:4:6211:U:N3	2.36	0.67
83:3:37:G:C2	85:4:6217:C:N1	2.60	0.67
85:4:6047:U:OP1	85:4:6073:A:N3	2.28	0.67
85:4:6066:G:H2'	85:4:6067:G:H2'	1.77	0.67
84:9:279:SER:HB3	84:9:283:LYS:H	1.60	0.67
85:4:6181:C:N1	85:4:6182:A:C8	2.63	0.66
49:2:1701:C:O2	85:4:6219:U:H3'	1.94	0.66
17:R:60:ARG:HH12	45:5:2615:C:H5''	1.60	0.66
48:K:124:LEU:CG	85:4:6038:G:OP1	2.42	0.66
84:9:741:MET:SD	84:9:817:TRP:NE1	2.69	0.66
85:4:6066:G:C2	85:4:6167:U:C4	2.75	0.66
85:4:6179:U:N3	85:4:6197:A:C6	2.26	0.66
85:4:6200:A:N7	85:4:6201:C:C5	2.63	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:S:114:GLY:HA2	18:S:119:ALA:H	1.59	0.66
30:e:44:ARG:HH22	45:5:1312:A:H4'	1.60	0.66
49:2:1701:C:N4	85:4:6219:U:O2	2.27	0.66
85:4:6177:U:N1	85:4:6178:U:O2'	2.26	0.66
85:4:6134:C:N4	85:4:6135:C:N4	2.44	0.66
45:5:2007:G:H21	45:5:2012:A:H62	1.44	0.66
85:4:6104:G:O2'	85:4:6105:U:H5'	1.95	0.66
2:B:21:ARG:HH21	45:5:4568:A:H4'	1.61	0.65
15:P:16:LYS:HG2	15:P:149:ILE:HG12	1.78	0.65
49:2:1227:G:H1	49:2:1531:A:H61	1.42	0.65
85:4:6177:U:C5	85:4:6178:U:C2	2.84	0.65
48:K:98:LYS:HZ2	85:4:6086:U:C4'	2.04	0.65
85:4:6214:C:C2'	85:4:6215:C:H5'	2.26	0.65
85:4:6167:U:H2'	85:4:6168:C:C6	2.31	0.65
85:4:6134:C:H2'	85:4:6135:C:C5	2.31	0.65
85:4:6199:A:O2'	85:4:6200:A:P	2.54	0.65
14:O:93:LYS:HG3	45:5:1308:C:H5''	1.78	0.65
85:4:6180:U:C6	85:4:6197:A:N1	2.64	0.65
85:4:6200:A:C6	85:4:6201:C:N3	2.65	0.65
85:4:6198:A:C4	85:4:6199:A:C8	2.84	0.64
48:K:98:LYS:CE	85:4:6086:U:OP1	2.44	0.64
85:4:6066:G:H3'	85:4:6067:G:C3'	2.27	0.64
85:4:6178:U:C2	85:4:6179:U:C2	2.85	0.64
85:4:6217:C:O2'	85:4:6218:U:O4'	2.15	0.64
85:4:6065:A:H2'	85:4:6066:G:H8	1.63	0.64
85:4:6174:G:N1	85:4:6208:A:C8	2.62	0.64
83:3:36:A:N1	85:4:6218:U:C6	1.92	0.64
85:4:6184:A:C8	85:4:6185:U:O4	2.50	0.64
48:K:122:ARG:CG	85:4:6037:U:O3'	2.44	0.64
85:4:6179:U:O2	85:4:6180:U:C6	2.51	0.63
70:VV:20:ILE:HG12	70:VV:116:ILE:HG12	1.79	0.63
85:4:6211:U:H1'	85:4:6212:U:O5'	1.97	0.63
79:ee:43:PHE:O	79:ee:47:ALA:HB2	1.99	0.63
83:3:37:G:C6	85:4:6217:C:C6	2.74	0.63
85:4:6071:A:C8	85:4:6072:U:H6	2.14	0.63
85:4:6078:A:N6	85:4:6079:C:N4	2.46	0.63
85:4:6218:U:C2'	85:4:6219:U:H6	2.06	0.63
85:4:6178:U:C4	85:4:6179:U:O4	2.50	0.63
85:4:6198:A:C4	85:4:6199:A:C4	2.72	0.63
21:V:107:ASN:HD21	21:V:111:GLU:HB2	1.63	0.63
83:3:34:U:C5'	85:4:6187:A:H8	2.11	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:K:122:ARG:CG	85:4:6037:U:C4'	1.78	0.63
68:TT:60:THR:HG22	68:TT:62:ASP:H	1.64	0.63
85:4:6177:U:O4	85:4:6199:A:C6	2.51	0.63
5:E:93:ALA:H	45:5:2258:C:H42	1.45	0.63
85:4:6108:G:H2'	85:4:6109:C:O4'	1.99	0.63
85:4:6182:A:HO2'	85:4:6183:G:H5'	1.60	0.63
49:2:1292:C:N3	81:gg:138:ARG:NH1	2.47	0.62
51:CC:66:VAL:HG22	51:CC:87:ILE:HG22	1.81	0.62
85:4:6108:G:H8	85:4:6108:G:O5'	1.82	0.62
85:4:6177:U:C2	85:4:6178:U:C2	2.86	0.62
45:5:2749:C:H2'	45:5:2750:G:H8	1.64	0.62
49:2:1234:C:H4'	49:2:1246:A:H61	1.65	0.62
85:4:6105:U:O4'	85:4:6152:A:N6	2.32	0.62
10:J:21:CYS:HB2	10:J:131:TYR:HB3	1.80	0.62
85:4:6215:C:N3	85:4:6216:U:C6	2.68	0.62
55:GG:143:PRO:HA	55:GG:146:ARG:HE	1.64	0.62
58:JJ:165:GLN:HE22	58:JJ:195:LEU:HD11	1.64	0.62
48:K:90:LEU:HD22	85:4:6039:A:C2'	2.30	0.62
85:4:6057:A:OP2	85:4:6058:U:C5	2.52	0.62
85:4:6188:G:P	85:4:6188:G:C8	2.93	0.62
85:4:6217:C:H2'	85:4:6218:U:H6	1.43	0.62
2:B:53:MET:HB3	45:5:4627:U:H5'	1.81	0.61
48:K:124:LEU:HG	85:4:6037:U:O2'	1.98	0.61
85:4:6063:A:N6	85:4:6169:U:H3	1.98	0.61
85:4:6168:C:C5	85:4:6169:U:C4	2.88	0.61
48:K:124:LEU:HD21	85:4:6089:U:H3	1.62	0.61
85:4:6057:A:N1	85:4:6165:C:P	2.73	0.61
85:4:6181:C:N1	85:4:6182:A:N7	2.48	0.61
85:4:6183:G:C2	85:4:6184:A:C5	2.88	0.61
85:4:6188:G:C6	85:4:6216:U:C4	2.89	0.61
85:4:6215:C:H2'	85:4:6216:U:C5'	2.30	0.61
3:C:114:ARG:HH11	45:5:1507:C:H5'	1.65	0.61
4:D:261:VAL:HG12	4:D:263:LYS:H	1.65	0.61
68:TT:124:ARG:HE	68:TT:131:VAL:HA	1.65	0.61
85:4:6066:G:C2	85:4:6167:U:H5	2.06	0.61
85:4:6198:A:O3'	85:4:6198:A:OP1	2.19	0.61
45:5:451:C:H5''	45:5:452:A:H5'	1.83	0.61
85:4:6063:A:N6	85:4:6168:C:N4	2.48	0.61
85:4:6104:G:C2'	85:4:6105:U:H5'	2.30	0.61
37:I:5:LYS:HB2	45:5:2781:G:H4'	1.82	0.61
4:D:223:PHE:HB3	4:D:226:TYR:HB2	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:K:124:LEU:CD1	85:4:6037:U:C2'	2.75	0.61
49:2:434:G:H5''	58:JJ:23:LYS:HE3	1.82	0.60
85:4:6148:C:C1'	85:4:6149:A:C8	2.84	0.60
3:C:114:ARG:HB3	13:N:203:TYR:HB3	1.83	0.60
49:2:24:C:H42	49:2:650:A:H61	1.48	0.60
85:4:6176:U:C2	85:4:6177:U:C5	2.89	0.60
85:4:6211:U:C4	85:4:6212:U:C2	2.90	0.60
85:4:6177:U:C1'	85:4:6178:U:C1'	2.77	0.60
8:H:163:GLN:HE22	45:5:4687:A:H4'	1.67	0.60
40:o:8:ARG:HH22	45:5:4232:U:H3	1.49	0.60
85:4:6180:U:C4	85:4:6197:A:N6	2.69	0.60
32:g:63:VAL:HG22	32:g:66:ARG:HH21	1.66	0.60
85:4:6063:A:N6	85:4:6169:U:N3	2.49	0.60
3:C:94:ASN:HD22	3:C:102:PHE:HB2	1.67	0.60
85:4:6057:A:N7	85:4:6058:U:C5	2.69	0.60
48:K:209:THR:HG22	48:K:210:MET:HG3	1.84	0.60
85:4:6108:G:C6	85:4:6109:C:N4	2.70	0.60
45:5:2309:G:O6	45:5:2330:G:N2	2.35	0.59
85:4:6199:A:C2	85:4:6200:A:N9	2.70	0.59
48:K:98:LYS:HE3	85:4:6086:U:O5'	2.02	0.59
25:Z:36:ARG:NH1	25:Z:38:TYR:OH	2.36	0.59
45:5:2422:C:N4	45:5:2829:U:O2'	2.35	0.59
48:K:128:LEU:CD2	85:4:6086:U:H3	2.15	0.59
85:4:6057:A:OP2	85:4:6058:U:H5	1.85	0.59
85:4:6066:G:C6	85:4:6166:C:N3	2.68	0.59
85:4:6198:A:H2	85:4:6199:A:C2	2.10	0.59
85:4:6199:A:N7	85:4:6200:A:C8	2.66	0.59
85:4:6068:U:C3'	85:4:6069:U:C5'	2.56	0.59
49:2:1276:A:H4'	60:LL:50:GLN:HE22	1.66	0.59
15:P:62:ARG:NH2	45:5:423:G:OP1	2.36	0.59
18:S:45:TRP:HE1	18:S:61:ILE:HD11	1.68	0.59
48:K:124:LEU:CD2	85:4:6089:U:O4	2.38	0.59
49:2:1507:G:HO2'	81:gg:83:LYS:N	2.00	0.59
26:a:132:ARG:HH12	45:5:1468:C:H5''	1.66	0.59
39:n:21:ARG:NH1	49:2:1174:U:OP1	2.36	0.59
45:5:1427:A:H4'	45:5:1694:C:H5'	1.85	0.59
45:5:2587:A:H5'	45:5:2770:C:H5'	1.84	0.59
49:2:43:U:OP2	49:2:485:A:N6	2.36	0.59
85:4:6181:C:O2	85:4:6182:A:C8	2.52	0.59
84:9:337:LYS:HG2	84:9:341:ARG:HE	1.68	0.59
85:4:6056:A:O2'	85:4:6057:A:C5'	2.45	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:4:6148:C:C4	85:4:6149:A:C6	2.90	0.59
85:4:6148:C:C6	85:4:6149:A:C8	2.90	0.59
85:4:6148:C:O2	85:4:6149:A:H1'	2.03	0.59
27:b:91:ARG:HG3	45:5:1214:C:H42	1.67	0.59
50:BB:41:ARG:HB2	67:SS:128:PHE:HB3	1.85	0.59
85:4:6211:U:O4	85:4:6212:U:C4	2.56	0.59
45:5:2016:C:H2'	45:5:2017:A:H8	1.68	0.58
84:9:582:THR:HB	84:9:741:MET:HE3	1.84	0.58
85:4:6148:C:C5	85:4:6149:A:N7	2.71	0.58
85:4:6218:U:C2	85:4:6219:U:C5	2.91	0.58
5:E:130:SER:HB2	5:E:133:LYS:HD3	1.85	0.58
35:j:72:ARG:NH2	47:8:94:G:OP2	2.36	0.58
45:5:4077:A:H62	45:5:4169:G:H21	1.51	0.58
84:9:23:SER:HB3	84:9:122:THR:HG21	1.85	0.58
84:9:354:ILE:HG23	84:9:358:LEU:HD12	1.85	0.58
4:D:240:TYR:O	4:D:244:HIS:ND1	2.34	0.58
40:o:26:TYR:HB2	40:o:69:ARG:HB2	1.84	0.58
44:t:75:PRO:HD2	44:t:119:ARG:HH21	1.69	0.58
22:W:6:CYS:HB3	22:W:10:GLY:H	1.68	0.58
32:g:37:LYS:HB3	32:g:60:ARG:HH11	1.68	0.58
45:5:2377:C:H42	45:5:2381:A:H62	1.49	0.58
49:2:511:U:O2'	49:2:576:A:N6	2.34	0.58
85:4:6179:U:O2'	85:4:6180:U:C5'	2.39	0.58
12:M:34:ASN:ND2	45:5:1924:C:OP1	2.37	0.58
45:5:499:G:H1	45:5:656:C:H42	1.52	0.58
49:2:468:A:OP1	56:HH:74:ARG:NH1	2.36	0.58
85:4:6194:C:H5'	85:4:6210:U:C5	2.39	0.58
45:5:4045:G:O3'	85:4:6044:G:C2	2.51	0.58
49:2:1095:C:O2'	72:XX:20:ARG:NH2	2.37	0.58
56:HH:154:ARG:HE	56:HH:179:LEU:HD11	1.69	0.58
7:G:142:ARG:NH1	47:8:154:G:OP1	2.37	0.58
45:5:1555:G:H21	45:5:2669:C:H5'	1.68	0.58
48:K:122:ARG:HG3	85:4:6037:U:C2'	2.34	0.58
49:2:1263:U:O2	79:ee:16:GLN:NE2	2.37	0.58
45:5:63:G:H21	45:5:335:A:H62	1.50	0.58
82:hh:289:LEU:HD12	82:hh:298:LEU:HD21	1.85	0.58
85:4:6106:U:C5	85:4:6130:G:OP2	2.57	0.58
85:4:6181:C:O2	85:4:6182:A:N9	2.36	0.58
32:g:68:SER:HB3	32:g:71:LYS:HD3	1.85	0.58
45:5:3897:G:N2	45:5:3898:G:O6	2.37	0.58
48:K:122:ARG:CG	85:4:6037:U:C2'	2.82	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:DD:266:TYR:O	52:DD:270:THR:HB	2.03	0.58
48:K:124:LEU:HD13	85:4:6087:G:H22	1.68	0.58
49:2:16:G:H21	49:2:1195:A:H62	1.50	0.58
83:3:33:U:O2'	85:4:6187:A:C4	2.56	0.58
85:4:6047:U:OP1	85:4:6073:A:C4	2.57	0.58
85:4:6177:U:C2	85:4:6178:U:H1'	2.31	0.58
45:5:234:G:N2	45:5:2304:U:O4	2.36	0.57
49:2:379:C:O2	58:JJ:5:ARG:NH1	2.37	0.57
49:2:1170:A:H62	49:2:1189:A:H62	1.51	0.57
49:2:1495:G:N2	79:ee:42:CYS:SG	2.77	0.57
14:O:18:ARG:NH1	45:5:2057:A:N7	2.52	0.57
17:R:170:ARG:HH12	49:2:872:A:H5'	1.69	0.57
37:l:47:THR:HG22	37:l:49:LEU:H	1.66	0.57
45:5:2609:G:H1	45:5:2730:U:H3	1.50	0.57
49:2:620:G:O2'	73:YY:107:ARG:NH2	2.37	0.57
85:4:6178:U:C5	85:4:6179:U:C4	2.72	0.57
49:2:10:G:N2	49:2:1357:A:O2'	2.38	0.57
85:4:6108:G:C6	85:4:6109:C:C4	2.93	0.57
85:4:6190:U:O2'	85:4:6191:A:C8	2.55	0.57
45:5:1552:G:N2	45:5:1575:A:N7	2.53	0.57
48:K:124:LEU:HB3	85:4:6087:G:N2	2.20	0.57
57:II:146:VAL:HG22	57:II:152:ARG:HG2	1.86	0.57
85:4:6181:C:O2	85:4:6182:A:C6	2.52	0.57
4:D:120:GLU:OE1	4:D:248:ARG:NH2	2.36	0.57
85:4:6198:A:C2	85:4:6199:A:N3	2.71	0.57
45:5:1625:G:H1	45:5:3918:G:H5''	1.69	0.57
45:5:2616:C:H2'	45:5:2617:G:H8	1.69	0.57
66:RR:86:GLN:HG2	66:RR:90:LYS:HE2	1.87	0.57
85:4:6166:C:O2	85:4:6166:C:C2'	2.52	0.57
85:4:6200:A:N6	85:4:6201:C:H42	1.95	0.57
2:B:234:ARG:HH21	2:B:235:TRP:HE1	1.52	0.57
36:k:35:LYS:HG2	36:k:44:THR:HG22	1.87	0.57
45:5:2457:G:HO2'	45:5:3672:G:HO2'	1.53	0.57
48:K:98:LYS:HZ1	85:4:6086:U:C4'	2.05	0.57
65:QQ:73:PRO:HG2	65:QQ:93:MET:HG2	1.86	0.57
84:9:123:ASP:OD1	84:9:368:ARG:NH1	2.38	0.57
45:5:433:A:N6	45:5:3866:C:O2'	2.36	0.57
84:9:505:VAL:HB	84:9:548:GLY:O	2.05	0.57
7:G:233:PRO:HG2	7:G:272:VAL:HG13	1.85	0.57
19:T:75:VAL:HG22	19:T:88:ARG:HG2	1.87	0.57
21:V:85:ARG:HE	45:5:2846:G:H5''	1.69	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:FF:35:PRO:HB2	54:FF:143:ASP:HB2	1.86	0.57
49:2:919:A:H5''	63:OO:16:LEU:HD12	1.87	0.56
84:9:5:THR:HG23	84:9:8:GLN:H	1.70	0.56
2:B:245:HIS:H	45:5:4525:C:H4'	1.70	0.56
43:s:45:MET:SD	43:s:48:ARG:NH2	2.79	0.56
82:hh:174:VAL:HB	82:hh:188:HIS:HB2	1.87	0.56
2:B:268:ARG:HH12	45:5:3896:C:H1'	1.69	0.56
6:F:69:ARG:NH2	45:5:1211:G:OP1	2.38	0.56
45:5:1075:G:H22	45:5:1235:G:H22	1.54	0.56
69:UU:124:THR:HG23	69:UU:127:GLY:H	1.70	0.56
85:4:6074:A:H2'	85:4:6075:A:C8	2.41	0.56
85:4:6076:U:C4	85:4:6077:U:O4	2.56	0.56
31:f:102:ARG:NH2	45:5:4946:U:O4	2.39	0.56
48:K:95:LYS:HD2	85:4:6041:C:O4'	1.93	0.56
59:KK:170:PRO:HB3	59:KK:174:LYS:HD2	1.87	0.56
83:3:35:G:N1	85:4:6218:U:N3	2.54	0.56
85:4:6190:U:HO2'	85:4:6191:A:H8	1.43	0.56
49:2:1648:G:N2	49:2:1675:A:OP2	2.37	0.56
71:WW:31:SER:HA	71:WW:55:ILE:O	2.05	0.56
84:9:398:ILE:HA	84:9:414:GLY:HA3	1.88	0.56
45:5:5053:U:O2'	45:5:5055:G:N7	2.38	0.56
48:K:128:LEU:HD22	85:4:6086:U:O4	2.01	0.56
49:2:1398:G:O2'	82:hh:88:ARG:NH2	2.39	0.56
28:c:28:VAL:HG21	28:c:37:MET:HG3	1.88	0.56
45:5:4045:G:O3'	85:4:6044:G:C6	2.57	0.56
48:K:68:LEU:H	48:K:111:LEU:HD13	1.71	0.56
48:K:124:LEU:HA	85:4:6088:C:C4	2.23	0.56
48:K:128:LEU:CD2	85:4:6086:U:N3	2.63	0.56
84:9:44:GLY:HA2	84:9:47:ALA:HB3	1.87	0.56
84:9:302:ASP:OD1	84:9:306:ASN:ND2	2.38	0.56
6:F:87:LYS:HE3	19:T:135:PRO:HD2	1.88	0.56
85:4:6071:A:C5	85:4:6072:U:C1'	2.88	0.56
85:4:6071:A:C4	85:4:6072:U:O4'	2.59	0.56
10:J:159:LYS:HG2	10:J:163:MET:HE2	1.87	0.56
13:N:49:ARG:NH1	13:N:53:TYR:O	2.38	0.56
19:T:111:GLU:HG2	19:T:115:LYS:HE3	1.88	0.56
53:EE:135:GLU:HB3	53:EE:187:LYS:HB3	1.88	0.56
44:t:141:CYS:SG	44:t:142:ASN:N	2.80	0.56
49:2:574:A:OP2	74:ZZ:93:ARG:NH2	2.39	0.56
49:2:1865:C:OP2	76:bb:92:ARG:NH1	2.39	0.56
50:BB:11:LYS:HB2	67:SS:95:ILE:HG23	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:4:6182:A:N6	85:4:6195:G:H21	1.86	0.56
85:4:6215:C:C4	85:4:6216:U:C6	2.94	0.56
25:Z:112:ARG:HH22	45:5:2572:C:H1'	1.71	0.55
45:5:2751:G:H2'	45:5:2752:G:H8	1.71	0.55
49:2:1677:U:OP1	55:GG:71:ARG:NH1	2.38	0.55
85:4:6108:G:O6	85:4:6116:G:O6	2.24	0.55
1:A:188:LYS:HG2	1:A:192:LYS:HE2	1.87	0.55
6:F:115:GLN:O	6:F:118:ASN:ND2	2.39	0.55
24:Y:27:ARG:NH1	47:8:71:A:OP1	2.40	0.55
25:Z:136:PHE:HA	45:5:4122:G:H21	1.70	0.55
49:2:925:G:OP1	63:OO:121:ARG:NH2	2.38	0.55
70:VV:63:ILE:HB	70:VV:80:PHE:HB2	1.88	0.55
84:9:830:ARG:HH21	84:9:833:GLN:HG3	1.71	0.55
17:R:173:ARG:NH2	49:2:910:G:OP2	2.39	0.55
28:c:50:ASN:ND2	28:c:75:SER:O	2.40	0.55
45:5:4620:U:OP2	45:5:4670:C:N4	2.37	0.55
53:EE:222:PRO:HA	82:hh:189:ILE:O	2.07	0.55
49:2:334:C:OP2	56:HH:190:ARG:NH2	2.40	0.55
49:2:502:C:N4	54:FF:67:GLN:OE1	2.39	0.55
49:2:637:U:O2	80:ff:129:ASN:ND2	2.40	0.55
49:2:1091:C:O2	72:XX:2:VAL:N	2.40	0.55
85:4:6199:A:N6	85:4:6200:A:N3	2.54	0.55
85:4:6215:C:H2'	85:4:6216:U:H5''	1.87	0.55
85:4:6062:G:C6	85:4:6170:C:O2	2.60	0.55
85:4:6078:A:C2	85:4:6079:C:C4	2.95	0.55
85:4:6201:C:O2'	85:4:6202:C:O4'	2.23	0.55
10:J:140:SER:O	10:J:144:LYS:HB3	2.07	0.55
40:o:61:LYS:NZ	45:5:4371:G:OP1	2.39	0.55
45:5:2550:G:H2'	45:5:2551:A:H8	1.71	0.55
84:9:744:ILE:HD11	84:9:787:TYR:HB3	1.88	0.55
27:b:19:ASN:ND2	45:5:1686:C:OP1	2.40	0.55
45:5:1585:C:N4	45:5:1586:G:O6	2.40	0.55
64:PP:148:GLY:O	64:PP:150:ARG:NH2	2.40	0.55
1:A:95:GLN:O	1:A:100:ASN:ND2	2.40	0.55
2:B:385:LYS:NZ	45:5:5002:U:OP2	2.39	0.55
4:D:200:MET:HB2	4:D:202:GLN:HE22	1.71	0.55
13:N:61:ILE:HG12	13:N:133:ILE:HG12	1.89	0.55
15:P:66:GLY:HA3	45:5:2362:U:H5''	1.87	0.55
56:HH:52:ILE:HD11	56:HH:109:LEU:HD22	1.89	0.55
69:UU:22:LEU:HD22	69:UU:28:LEU:HD11	1.89	0.55
84:9:365:GLN:HA	84:9:368:ARG:HB3	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:133:LYS:NZ	45:5:713:C:O2	2.40	0.55
16:Q:179:GLY:H	26:a:51:GLY:HA2	1.72	0.55
37:l:42:ARG:NH1	45:5:2408:U:OP1	2.39	0.55
45:5:3927:U:H2'	45:5:3928:A:H8	1.72	0.55
80:ff:76:HIS:HB3	80:ff:81:ARG:HH22	1.72	0.55
84:9:120:ARG:O	84:9:368:ARG:NH2	2.38	0.55
85:4:6106:U:H5	85:4:6130:G:OP2	1.90	0.55
85:4:6198:A:N6	85:4:6199:A:N6	2.55	0.55
45:5:1086:C:H2'	45:5:1087:A:H8	1.71	0.54
73:YY:71:ARG:HD2	73:YY:80:LYS:HB3	1.88	0.54
82:hh:158:PRO:HG2	82:hh:202:PRO:HA	1.89	0.54
85:4:6178:U:N3	85:4:6179:U:C6	2.65	0.54
85:4:6199:A:N1	85:4:6200:A:N3	2.53	0.54
5:E:185:ASN:ND2	5:E:274:LEU:O	2.40	0.54
6:F:93:ARG:HH22	6:F:108:LEU:HD13	1.71	0.54
9:I:87:ILE:HG12	9:I:138:ILE:HG12	1.89	0.54
40:o:71:GLU:OE2	40:o:78:ARG:NH1	2.40	0.54
45:5:2845:A:H61	45:5:3843:C:H42	1.54	0.54
50:BB:73:ASP:HB2	50:BB:119:PRO:HA	1.88	0.54
44:t:131:GLU:HB2	45:5:1973:G:H21	1.71	0.54
49:2:1564:C:H5'	69:UU:105:GLN:HE21	1.72	0.54
52:DD:202:THR:OG1	59:KK:54:ARG:NH1	2.40	0.54
59:KK:42:GLU:OE2	59:KK:109:ARG:NH2	2.41	0.54
10:J:22:LEU:HD22	10:J:128:LEU:HD13	1.90	0.54
16:Q:20:SER:O	16:Q:26:ARG:NH2	2.41	0.54
17:R:60:ARG:O	17:R:64:ARG:NH1	2.40	0.54
19:T:79:GLN:HG2	19:T:84:ILE:HG12	1.88	0.54
31:f:68:ARG:NH1	45:5:442:G:OP1	2.40	0.54
49:2:1203:G:H22	49:2:1696:C:H2'	1.72	0.54
49:2:1310:U:OP1	62:NN:36:ARG:NH1	2.41	0.54
85:4:6078:A:C2	85:4:6079:C:C2	2.96	0.54
85:4:6201:C:O2'	85:4:6202:C:O5'	2.25	0.54
2:B:317:LEU:HB2	2:B:372:SER:HB2	1.89	0.54
6:F:216:ARG:NH1	45:5:718:C:OP1	2.40	0.54
29:d:26:THR:HB	29:d:85:ARG:HH11	1.73	0.54
49:2:190:G:O2'	49:2:209:A:N6	2.40	0.54
49:2:1301:A:HO2'	79:ee:2:GLY:N	2.06	0.54
68:TT:81:ASP:O	68:TT:87:GLN:NE2	2.40	0.54
84:9:714:ILE:HD12	85:4:6219:U:O2'	2.05	0.54
4:D:276:LYS:HD3	46:7:61:G:H5'	1.90	0.54
43:s:149:ARG:NH2	84:9:196:GLU:OE2	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:5:1591:U:H3	45:5:4555:U:H5''	1.73	0.54
49:2:683:G:N2	49:2:1022:U:OP2	2.40	0.54
49:2:1179:G:N2	49:2:1182:A:OP2	2.41	0.54
64:PP:142:ARG:NH1	76:bb:23:CYS:O	2.40	0.54
76:bb:22:ARG:HH21	76:bb:27:ALA:HB1	1.72	0.54
18:S:80:ILE:HG12	18:S:129:VAL:HG22	1.90	0.54
33:h:87:LYS:O	33:h:92:ARG:NH1	2.40	0.54
45:5:2443:G:OP1	45:5:2516:G:N2	2.41	0.54
49:2:53:C:OP1	74:ZZ:112:ASN:ND2	2.41	0.54
51:CC:174:ARG:NH2	51:CC:175:GLU:OE2	2.40	0.54
85:4:6078:A:C2	85:4:6079:C:C6	2.95	0.54
85:4:6193:U:O3'	85:4:6210:U:C4	2.61	0.54
2:B:220:ILE:HB	2:B:346:THR:HB	1.89	0.54
6:F:117:PHE:HB3	6:F:212:LEU:HB2	1.90	0.54
45:5:3695:U:H3	45:5:3820:G:H22	1.54	0.54
49:2:1348:G:OP1	52:DD:145:LYS:NZ	2.41	0.54
56:HH:106:LEU:HD13	56:HH:109:LEU:HD21	1.89	0.54
82:hh:256:ILE:HB	82:hh:270:LEU:HB2	1.90	0.54
84:9:26:ALA:HB3	84:9:32:LYS:HD2	1.89	0.54
84:9:558:LEU:HD13	84:9:572:LYS:HD3	1.90	0.54
85:4:6180:U:O4	85:4:6197:A:N6	2.41	0.54
1:A:117:GLU:O	1:A:162:ASN:ND2	2.41	0.54
5:E:115:MET:O	42:r:87:ARG:NH1	2.41	0.54
6:F:102:PRO:HA	6:F:105:ARG:HE	1.73	0.54
13:N:28:TRP:O	13:N:32:GLN:NE2	2.41	0.54
13:N:90:ASN:ND2	45:5:3928:A:OP1	2.41	0.54
15:P:80:GLN:NE2	45:5:3892:U:O2'	2.40	0.54
24:Y:102:SER:OG	45:5:231:U:O2'	2.26	0.54
34:i:28:ARG:NH2	45:5:326:C:OP2	2.41	0.54
45:5:2887:U:OP1	45:5:3618:C:N4	2.41	0.54
49:2:1497:G:N7	60:LL:25:LYS:NZ	2.56	0.54
66:RR:53:GLU:OE1	66:RR:85:ARG:NH2	2.41	0.54
84:9:452:LEU:HD12	84:9:461:ILE:HD12	1.90	0.54
85:4:6176:U:C2	85:4:6177:U:H5	2.25	0.54
3:C:150:LEU:HD23	3:C:152:LEU:HD12	1.90	0.54
15:P:135:ARG:NH2	45:5:1596:U:O2'	2.41	0.54
45:5:4648:A:H2'	45:5:4649:G:H8	1.73	0.54
49:2:301:A:H1'	58:JJ:72:CYS:HA	1.90	0.54
82:hh:244:ASN:ND2	82:hh:294:ASP:O	2.41	0.54
85:4:6176:U:H6	85:4:6176:U:O5'	1.91	0.54
26:a:42:ARG:NH1	45:5:4376:A:O2'	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
77:cc:40:CYS:SG	77:cc:41:TYR:N	2.81	0.53
85:4:6078:A:C2	85:4:6079:C:C5	2.96	0.53
2:B:234:ARG:NH2	2:B:268:ARG:O	2.42	0.53
10:J:146:ARG:HG2	10:J:147:ARG:HG3	1.89	0.53
45:5:673:C:H2'	45:5:674:G:H8	1.73	0.53
45:5:3653:A:OP2	45:5:3691:G:N2	2.42	0.53
45:5:4272:G:N2	45:5:4272:G:OP2	2.39	0.53
49:2:1539:U:H4'	69:UU:47:PRO:HA	1.90	0.53
49:2:1608:U:O4	49:2:1632:G:N2	2.41	0.53
53:EE:51:LEU:HG	53:EE:91:VAL:HG22	1.90	0.53
84:9:120:ARG:NH1	84:9:495:ARG:O	2.38	0.53
84:9:399:SER:N	84:9:413:PHE:O	2.37	0.53
85:4:6179:U:C2	85:4:6180:U:C6	2.96	0.53
1:A:37:ARG:NH1	45:5:4088:C:OP1	2.42	0.53
32:g:10:ARG:NH1	37:l:3:SER:OG	2.41	0.53
48:K:98:LYS:CE	85:4:6086:U:C4'	2.83	0.53
85:4:6060:U:C4	85:4:6167:U:OP1	2.61	0.53
85:4:6178:U:N3	85:4:6179:U:N3	2.56	0.53
5:E:49:ASN:ND2	45:5:979:C:OP1	2.42	0.53
17:R:117:ARG:NH1	45:5:2663:G:O2'	2.41	0.53
21:V:98:PHE:HA	22:W:22:ALA:HB3	1.89	0.53
45:5:3972:A:N6	45:5:4040:C:OP1	2.42	0.53
48:K:111:LEU:HD12	48:K:143:ASN:HD22	1.72	0.53
85:4:6148:C:C2	85:4:6149:A:C4	2.97	0.53
45:5:2877:G:N2	45:5:3824:A:O2'	2.42	0.53
45:5:4677:U:O2	45:5:4713:G:N2	2.42	0.53
61:MM:95:TYR:OH	61:MM:100:ASN:ND2	2.42	0.53
85:4:6148:C:N3	85:4:6149:A:C4	2.77	0.53
4:D:83:LEU:HB3	4:D:88:VAL:HB	1.91	0.53
4:D:104:LEU:HD12	4:D:247:ILE:HG12	1.89	0.53
8:H:23:ARG:NH1	45:5:4763:U:OP1	2.42	0.53
28:c:45:LEU:HD23	28:c:96:ILE:HD12	1.90	0.53
45:5:3944:G:H1	45:5:4069:U:H3	1.55	0.53
45:5:4541:G:N2	45:5:4544:A:OP2	2.41	0.53
48:K:36:ILE:HD11	48:K:201:VAL:HA	1.90	0.53
72:XX:52:ILE:HG22	72:XX:61:ILE:HG12	1.90	0.53
82:hh:29:ASP:OD1	82:hh:47:ARG:NH2	2.41	0.53
85:4:6168:C:H2'	85:4:6169:U:C1'	2.39	0.53
13:N:17:ASP:OD1	13:N:20:ARG:NH2	2.42	0.53
49:2:1130:G:N2	49:2:1130:G:OP2	2.41	0.53
49:2:1199:A:OP1	76:bb:2:THR:N	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
84:9:10:ARG:NH1	84:9:14:ASP:OD1	2.42	0.53
84:9:300:VAL:HG12	84:9:315:LEU:HD21	1.90	0.53
85:4:6178:U:N3	85:4:6179:U:C2	2.77	0.53
7:G:209:VAL:HB	7:G:255:VAL:HB	1.90	0.53
7:G:249:ARG:NH2	45:5:149:A:N7	2.57	0.53
49:2:1708:C:H2'	49:2:1709:G:H8	1.74	0.53
64:PP:34:PHE:HB3	64:PP:41:PHE:HB2	1.91	0.53
77:cc:56:CYS:SG	77:cc:57:VAL:N	2.82	0.53
82:hh:11:LEU:HB2	82:hh:307:VAL:HB	1.91	0.53
85:4:6107:A:H4'	85:4:6108:G:H5'	1.91	0.53
85:4:6174:G:N2	85:4:6208:A:N1	2.56	0.53
85:4:6177:U:H3	85:4:6200:A:H1'	1.73	0.53
29:d:83:ARG:NH1	45:5:4997:G:OP1	2.41	0.53
49:2:374:G:OP1	61:MM:59:LYS:NZ	2.41	0.53
64:PP:95:ILE:HB	64:PP:129:ILE:HG12	1.91	0.53
74:ZZ:7:ILE:HG12	74:ZZ:27:VAL:HG22	1.91	0.53
84:9:316:ILE:HG23	84:9:321:ILE:HB	1.90	0.53
85:4:6217:C:O2'	85:4:6218:U:C6	2.46	0.53
45:5:3839:G:N2	45:5:3843:C:O2'	2.42	0.53
49:2:526:A:OP2	80:ff:101:ARG:NH2	2.42	0.53
85:4:6217:C:C2	85:4:6218:U:C5	2.96	0.53
15:P:3:ARG:NH2	15:P:4:TYR:O	2.42	0.52
28:c:105:ILE:HG13	28:c:106:ARG:HD2	1.91	0.52
30:e:107:ASN:ND2	45:5:2303:C:OP1	2.42	0.52
34:i:48:CYS:SG	34:i:49:GLY:N	2.82	0.52
40:o:23:VAL:HG22	40:o:70:LEU:HG	1.91	0.52
45:5:2604:C:H2'	45:5:2605:G:H8	1.74	0.52
49:2:1662:U:O4	49:2:1663:A:N6	2.42	0.52
13:N:73:ARG:NH2	45:5:32:G:OP1	2.43	0.52
21:V:43:LYS:HE2	45:5:4508:C:H5''	1.90	0.52
45:5:210:C:N4	45:5:233:U:OP2	2.42	0.52
49:2:1701:C:N3	85:4:6219:U:N3	2.57	0.52
56:HH:2:LYS:HB2	56:HH:108:VAL:HG22	1.90	0.52
56:HH:2:LYS:HD3	56:HH:15:LEU:HD11	1.92	0.52
57:II:138:GLU:OE2	63:OO:19:ARG:NH1	2.43	0.52
85:4:6078:A:C6	85:4:6079:C:C5	2.98	0.52
85:4:6180:U:N1	85:4:6197:A:C2	2.77	0.52
4:D:23:ARG:NH2	45:5:4280:A:OP2	2.43	0.52
7:G:302:ARG:NH2	45:5:4075:U:OP2	2.42	0.52
26:a:37:GLY:HA2	26:a:41:HIS:HB2	1.90	0.52
49:2:1092:G:OP1	63:OO:9:LYS:NZ	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:BB:52:LYS:HB3	67:SS:102:THR:HG21	1.90	0.52
50:BB:141:ASN:ND2	71:WW:31:SER:O	2.42	0.52
85:4:6179:U:N3	85:4:6180:U:H5	2.06	0.52
85:4:6183:G:N2	85:4:6184:A:N3	2.57	0.52
11:L:197:LYS:HD2	45:5:4358:U:H4'	1.91	0.52
15:P:69:ARG:NH2	45:5:4980:C:N3	2.57	0.52
45:5:3:C:H42	47:8:156:U:H3	1.56	0.52
49:2:333:G:O6	56:HH:186:GLN:NE2	2.42	0.52
57:II:117:PRO:HG2	57:II:120:ARG:HB2	1.90	0.52
85:4:6177:U:C6	85:4:6178:U:N1	2.76	0.52
85:4:6192:G:N2	85:4:6211:U:C2	2.76	0.52
85:4:6214:C:HO2'	85:4:6215:C:H5'	1.62	0.52
45:5:2405:G:H21	45:5:2791:C:H5'	1.74	0.52
45:5:3911:C:H1'	45:5:4395:U:H3	1.73	0.52
48:K:124:LEU:HD13	85:4:6087:G:N2	2.24	0.52
61:MM:5:GLN:NE2	61:MM:11:GLN:O	2.40	0.52
68:TT:22:GLY:HA2	68:TT:56:ALA:HB3	1.92	0.52
85:4:6180:U:C4	85:4:6197:A:C5	2.98	0.52
85:4:6213:A:H2'	85:4:6214:C:C6	2.45	0.52
21:V:96:LEU:HD11	22:W:22:ALA:HB2	1.90	0.52
22:W:94:ARG:NH1	56:HH:144:LEU:O	2.43	0.52
45:5:1332:C:H2'	45:5:1333:A:H8	1.73	0.52
49:2:1560:U:H2'	49:2:1561:A:H8	1.75	0.52
49:2:1599:U:OP2	75:aa:46:ASN:ND2	2.42	0.52
84:9:692:LEU:O	84:9:839:ARG:NH2	2.41	0.52
8:H:173:ARG:NH2	45:5:4475:G:OP2	2.43	0.52
32:g:110:GLN:O	32:g:114:GLN:NE2	2.43	0.52
37:l:21:ARG:NH2	37:l:22:PRO:O	2.43	0.52
43:s:44:ARG:NH1	45:5:1997:U:O5'	2.41	0.52
50:BB:180:ARG:NH1	67:SS:89:SER:O	2.43	0.52
58:JJ:164:GLU:O	58:JJ:168:GLN:NE2	2.43	0.52
63:OO:118:ILE:HG12	63:OO:121:ARG:HH11	1.74	0.52
84:9:571:LYS:NZ	84:9:573:SER:OG	2.41	0.52
85:4:6057:A:H2'	85:4:6058:U:C4'	2.34	0.52
85:4:6071:A:P	85:4:6072:U:C5	2.86	0.52
85:4:6182:A:O2'	85:4:6183:G:O5'	2.27	0.52
15:P:131:ARG:HH21	45:5:1596:U:H2'	1.75	0.52
85:4:6068:U:C5'	85:4:6069:U:O4'	2.53	0.52
85:4:6148:C:H2'	85:4:6149:A:C1'	2.39	0.52
45:5:3805:U:H2'	45:5:3806:G:H8	1.75	0.52
45:5:3890:A:N6	45:5:4570:G:O2'	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:2:1658:G:OP2	49:2:1660:C:N4	2.42	0.52
85:4:6198:A:C1'	85:4:6199:A:C8	2.92	0.52
5:E:191:ARG:NH1	5:E:220:PHE:O	2.43	0.52
49:2:1396:A:O2'	49:2:1398:G:N7	2.37	0.52
82:hh:40:ILE:HB	82:hh:59:LEU:HB2	1.92	0.52
84:9:592:LEU:HD11	84:9:857:LYS:HA	1.92	0.52
85:4:6105:U:H2'	85:4:6106:U:H4'	1.91	0.52
1:A:72:ARG:NH2	45:5:4084:G:O6	2.44	0.51
1:A:146:THR:HG1	1:A:160:SER:HG	1.56	0.51
6:F:125:ASN:H	6:F:128:SER:HB3	1.75	0.51
32:g:15:THR:HG22	32:g:17:SER:H	1.75	0.51
45:5:967:C:OP2	45:5:968:C:N4	2.43	0.51
45:5:1315:C:N4	45:5:1316:G:O6	2.43	0.51
45:5:4704:C:H2'	45:5:4705:A:H8	1.76	0.51
49:2:936:G:O2'	63:OO:105:ASN:ND2	2.43	0.51
72:XX:7:LEU:HD23	72:XX:34:ILE:HG12	1.90	0.51
84:9:309:LYS:HA	84:9:312:THR:HG22	1.91	0.51
2:B:245:HIS:HB3	45:5:4525:C:H5'	1.91	0.51
2:B:375:GLY:HA2	45:5:4664:A:H4'	1.92	0.51
45:5:4638:U:H1'	45:5:5004:C:H1'	1.93	0.51
45:5:4691:A:H5''	45:5:4696:C:H41	1.76	0.51
58:JJ:103:LEU:HD13	58:JJ:170:LYS:HD3	1.92	0.51
77:cc:64:CYS:SG	77:cc:65:GLN:N	2.82	0.51
80:ff:112:ASN:O	80:ff:117:ASN:ND2	2.44	0.51
85:4:6066:G:C4	85:4:6167:U:O4	2.63	0.51
45:5:3611:A:H2	45:5:5016:A:H8	1.59	0.51
49:2:429:C:O2'	49:2:811:A:N1	2.43	0.51
49:2:1592:C:H4'	66:RR:44:PRO:HB3	1.90	0.51
50:BB:13:GLU:H	67:SS:95:ILE:HG22	1.75	0.51
40:o:75:PRO:HA	40:o:78:ARG:HD3	1.92	0.51
45:5:2562:G:N2	45:5:2565:A:OP2	2.44	0.51
49:2:1404:U:OP2	70:VV:21:ARG:NH1	2.44	0.51
49:2:1477:U:OP2	67:SS:3:ARG:NH2	2.44	0.51
49:2:1617:G:N1	49:2:1620:A:OP2	2.37	0.51
57:II:143:ARG:HB2	57:II:155:LYS:HB2	1.92	0.51
85:4:6169:U:C5	85:4:6170:C:C4	2.99	0.51
85:4:6177:U:O4	85:4:6200:A:C4	2.61	0.51
85:4:6179:U:H2'	85:4:6180:U:H6	1.76	0.51
85:4:6193:U:O3'	85:4:6210:U:O4	2.28	0.51
2:B:4:ARG:HH22	45:5:4458:C:H3'	1.75	0.51
4:D:256:LYS:HD2	46:7:117:G:H5'	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:P:116:HIS:NE2	45:5:424:U:O2'	2.40	0.51
18:S:41:LYS:HD2	18:S:61:ILE:HD13	1.91	0.51
32:g:76:ARG:NH1	45:5:2583:C:OP2	2.44	0.51
45:5:113:A:OP2	45:5:156:G:N2	2.44	0.51
49:2:38:A:H4'	59:KK:7:TRP:HE1	1.75	0.51
49:2:491:C:O2	49:2:493:A:N6	2.42	0.51
49:2:1135:C:OP2	76:bb:6:ARG:NH1	2.39	0.51
82:hh:163:PRO:HB2	82:hh:179:LEU:HB2	1.93	0.51
3:C:115:VAL:O	3:C:120:LYS:NZ	2.44	0.51
4:D:91:GLY:H	4:D:226:TYR:HE1	1.56	0.51
13:N:144:ARG:NH2	45:5:125:C:OP1	2.44	0.51
45:5:4594:U:H2'	45:5:4595:G:H8	1.76	0.51
47:8:8:U:H2'	47:8:9:A:H8	1.76	0.51
49:2:853:C:O2'	61:MM:94:HIS:NE2	2.44	0.51
85:4:6074:A:H2'	85:4:6075:A:H8	1.76	0.51
16:Q:50:ARG:NH1	16:Q:139:LEU:O	2.43	0.51
29:d:37:GLY:O	29:d:41:ARG:NE	2.43	0.51
43:s:32:ALA:O	43:s:85:ASN:ND2	2.43	0.51
45:5:1391:A:H61	45:5:4364:G:H21	1.57	0.51
45:5:2411:C:H2'	45:5:2412:A:H8	1.74	0.51
49:2:614:C:N4	49:2:625:G:OP2	2.44	0.51
49:2:1533:A:OP2	55:GG:164:ARG:NH2	2.43	0.51
49:2:1534:C:O2'	49:2:1598:G:N2	2.41	0.51
66:RR:86:GLN:HE22	66:RR:122:ALA:HB2	1.76	0.51
85:4:6148:C:C3'	85:4:6149:A:C8	2.87	0.51
13:N:50:ARG:NH2	45:5:279:A:OP1	2.41	0.51
17:R:62:ARG:NH2	45:5:4648:A:OP1	2.43	0.51
18:S:55:LYS:NZ	46:7:99:G:OP2	2.44	0.51
20:U:23:LEU:HB2	20:U:70:ILE:HB	1.92	0.51
21:V:73:ARG:NH2	45:5:3798:U:OP2	2.44	0.51
30:e:113:GLU:OE2	30:e:117:GLN:NE2	2.43	0.51
49:2:1605:G:H5''	69:UU:84:ARG:HH11	1.75	0.51
54:FF:126:VAL:HA	54:FF:141:THR:HA	1.93	0.51
59:KK:14:VAL:H	59:KK:44:TRP:HB3	1.76	0.51
82:hh:128:THR:HG22	82:hh:143:GLN:HG2	1.93	0.51
84:9:714:ILE:HD13	85:4:6219:U:HO2'	1.74	0.51
5:E:281:THR:O	31:f:4:ARG:NH2	2.43	0.51
45:5:197:A:N1	45:5:225:G:O2'	2.42	0.51
45:5:2425:U:H5''	45:5:2426:U:H5	1.75	0.51
48:K:9:THR:HG1	48:K:10:LEU:N	2.09	0.51
49:2:75:G:N1	56:HH:155:GLN:O	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:2:1337:C:HO2'	70:VV:68:THR:HG1	1.59	0.51
49:2:1566:G:N7	69:UU:101:ARG:NH2	2.58	0.51
52:DD:172:ASN:ND2	59:KK:95:ASP:OD2	2.44	0.51
58:JJ:37:LYS:HB2	58:JJ:59:ARG:HG2	1.92	0.51
83:3:35:G:O6	85:4:6218:U:C4	2.63	0.51
85:4:6071:A:O5'	85:4:6072:U:C5	2.64	0.51
85:4:6190:U:C2'	85:4:6191:A:H8	2.24	0.51
1:A:241:ARG:NH1	45:5:3659:G:OP1	2.44	0.51
23:X:47:ARG:NH1	45:5:2473:A:O2'	2.44	0.51
37:l:11:ARG:NH2	47:8:45:C:O2'	2.44	0.51
43:s:41:GLN:NE2	45:5:1971:U:O2	2.44	0.51
49:2:149:A:OP2	49:2:168:C:N4	2.39	0.51
61:MM:104:LYS:O	73:YY:11:ARG:NH2	2.43	0.51
85:4:6148:C:N3	85:4:6149:A:C5	2.79	0.51
2:B:375:GLY:HA3	45:5:5002:U:H4'	1.92	0.50
19:T:6:GLY:O	19:T:55:LYS:NZ	2.44	0.50
31:f:15:LYS:HE3	45:5:2068:C:H5''	1.94	0.50
45:5:1322:A:OP2	45:5:3876:A:N6	2.42	0.50
45:5:4686:G:OP2	45:5:4698:C:N4	2.44	0.50
49:2:20:G:OP1	73:YY:107:ARG:NH2	2.44	0.50
49:2:74:G:N2	49:2:78:C:OP2	2.44	0.50
49:2:1005:G:OP1	51:CC:162:ARG:NH1	2.44	0.50
85:4:6190:U:O2'	85:4:6191:A:H8	1.91	0.50
85:4:6194:C:OP2	85:4:6209:A:N6	2.22	0.50
2:B:217:ILE:HD11	2:B:333:LEU:HD21	1.94	0.50
3:C:307:LYS:NZ	45:5:2090:U:OP2	2.45	0.50
5:E:191:ARG:NH2	5:E:217:ASP:OD1	2.44	0.50
6:F:145:ASN:ND2	45:5:942:G:OP1	2.45	0.50
13:N:11:TRP:O	13:N:14:LYS:NZ	2.37	0.50
15:P:97:ASN:HD21	45:5:399:G:H1'	1.76	0.50
32:g:60:ARG:HD3	32:g:61:PRO:HD2	1.93	0.50
43:s:47:LEU:HB3	43:s:51:ALA:HB3	1.92	0.50
45:5:1321:G:H21	45:5:3876:A:H5''	1.77	0.50
45:5:1554:A:H61	45:5:1573:G:H1'	1.75	0.50
45:5:2260:C:O2	45:5:2261:G:N1	2.43	0.50
45:5:4908:G:H21	45:5:4913:G:H1	1.60	0.50
3:C:323:ARG:NH1	45:5:977:C:O2	2.45	0.50
15:P:118:GLN:HE22	45:5:423:G:H21	1.58	0.50
18:S:34:ALA:HB1	18:S:39:VAL:HG23	1.93	0.50
45:5:2601:A:N6	45:5:2744:A:OP2	2.43	0.50
45:5:4670:C:O2'	45:5:4672:A:OP2	2.28	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:2:1286:G:N2	49:2:1312:G:O2'	2.44	0.50
72:XX:102:ILE:H	72:XX:113:HIS:HD2	1.58	0.50
8:H:54:ARG:NH2	45:5:758:G:OP1	2.44	0.50
45:5:1743:A:N1	45:5:1789:C:O2'	2.45	0.50
45:5:2386:U:H2'	45:5:2387:G:H8	1.75	0.50
45:5:2468:U:H4'	45:5:2469:C:H5'	1.93	0.50
45:5:3648:A:OP1	45:5:3827:G:N2	2.45	0.50
49:2:1808:U:H2'	49:2:1809:A:H8	1.75	0.50
73:YY:46:HIS:HB3	73:YY:101:LEU:HD11	1.91	0.50
84:9:688:LYS:HD3	84:9:696:ASN:HD21	1.74	0.50
2:B:4:ARG:NH1	2:B:8:ALA:O	2.44	0.50
7:G:108:VAL:HG22	23:X:44:PRO:HA	1.93	0.50
18:S:16:CYS:SG	18:S:17:LEU:N	2.84	0.50
18:S:83:ARG:NH2	19:T:154:ILE:O	2.45	0.50
39:n:5:TRP:HH2	49:2:1853:C:H41	1.58	0.50
45:5:2811:G:N2	45:5:2814:C:OP2	2.38	0.50
48:K:141:ASN:ND2	48:K:150:GLU:OE2	2.45	0.50
85:4:6078:A:C4	85:4:6079:C:C5	3.00	0.50
85:4:6078:A:C5	85:4:6079:C:C5	2.99	0.50
85:4:6211:U:C2	85:4:6212:U:O4'	2.64	0.50
17:R:70:ARG:HE	17:R:75:HIS:HB2	1.75	0.50
23:X:72:ASP:OD2	33:h:25:LYS:NZ	2.45	0.50
32:g:41:ALA:O	32:g:52:ARG:NH1	2.44	0.50
45:5:469:C:H2'	45:5:470:A:H8	1.77	0.50
45:5:1394:G:N2	45:5:1469:C:O3'	2.45	0.50
45:5:3701:C:OP2	45:5:3746:A:N6	2.45	0.50
2:B:174:ARG:NH2	45:5:4973:U:O2	2.44	0.50
3:C:140:LYS:NZ	45:5:2297:G:O2'	2.41	0.50
44:t:123:ARG:HB3	44:t:127:GLY:H	1.77	0.50
85:4:6195:G:H2'	85:4:6196:A:O4'	2.12	0.50
10:J:43:LEU:HD13	10:J:117:ILE:HD11	1.93	0.50
35:j:48:ASN:ND2	45:5:51:A:OP1	2.45	0.50
36:k:33:LYS:HG2	36:k:46:VAL:HG22	1.94	0.50
45:5:461:G:H2'	45:5:462:G:H8	1.77	0.50
45:5:1633:G:O6	45:5:3918:G:O2'	2.29	0.50
45:5:4869:U:H5''	45:5:4870:G:H5'	1.94	0.50
45:5:4927:G:OP2	45:5:4927:G:N2	2.41	0.50
68:TT:74:PRO:HG3	68:TT:96:SER:HA	1.93	0.50
85:4:6071:A:O5'	85:4:6072:U:H5	1.95	0.50
85:4:6198:A:H4'	85:4:6198:A:OP1	2.10	0.50
16:Q:181:ARG:NH1	45:5:1391:A:OP1	2.36	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:K:110:PHE:CE1	85:4:6039:A:C6	3.00	0.50
85:4:6148:C:H2'	85:4:6149:A:N9	2.19	0.50
2:B:283:LYS:HD3	2:B:363:ILE:HD11	1.94	0.49
23:X:107:HIS:O	23:X:111:GLN:NE2	2.45	0.49
41:p:89:LEU:O	41:p:92:GLN:NE2	2.42	0.49
49:2:1834:A:N6	49:2:1836:G:O6	2.45	0.49
82:hh:79:LEU:HD22	82:hh:111:VAL:HG21	1.94	0.49
85:4:6188:G:C8	85:4:6188:G:OP2	2.64	0.49
3:C:110:ARG:O	3:C:113:ARG:NH1	2.45	0.49
3:C:223:ASN:ND2	45:5:223:G:N3	2.59	0.49
26:a:21:ARG:NH1	45:5:2281:U:O2'	2.42	0.49
45:5:955:G:N2	45:5:1284:G:O5'	2.45	0.49
45:5:4197:G:N2	83:3:86:C:OP2	2.46	0.49
45:5:4743:G:H2'	45:5:4744:A:H8	1.77	0.49
49:2:308:G:OP1	58:JJ:53:LYS:NZ	2.41	0.49
49:2:560:A:OP2	59:KK:177:ASN:ND2	2.45	0.49
49:2:957:A:H3'	49:2:958:G:H21	1.76	0.49
58:JJ:174:CYS:SG	58:JJ:175:ILE:N	2.85	0.49
82:hh:133:ASN:HD21	82:hh:139:LYS:HE3	1.77	0.49
85:4:6065:A:H2'	85:4:6066:G:C8	2.47	0.49
85:4:6176:U:O2	85:4:6200:A:N3	2.39	0.49
85:4:6183:G:C2	85:4:6184:A:C2	3.00	0.49
17:R:38:ARG:NH2	45:5:2525:U:OP2	2.45	0.49
26:a:26:ARG:NH2	45:5:1656:U:OP2	2.45	0.49
31:f:36:ARG:NH2	31:f:79:GLY:O	2.45	0.49
45:5:160:G:H2'	45:5:161:G:H8	1.77	0.49
45:5:1934:A:H5''	45:5:1935:C:H5'	1.94	0.49
45:5:3663:A:N1	45:5:4168:G:O2'	2.43	0.49
49:2:39:A:OP1	59:KK:5:ARG:NH1	2.46	0.49
49:2:1451:G:OP2	67:SS:44:LYS:NZ	2.44	0.49
49:2:1472:C:H42	49:2:1476:A:H62	1.60	0.49
49:2:1528:G:O2'	49:2:1666:C:OP1	2.31	0.49
50:BB:68:ILE:HG13	50:BB:121:LEU:HB2	1.94	0.49
72:XX:57:ARG:NH1	77:cc:26:GLN:OE1	2.45	0.49
85:4:6108:G:H2'	85:4:6109:C:C6	2.47	0.49
85:4:6197:A:N1	85:4:6198:A:C2	2.80	0.49
5:E:96:THR:HG22	5:E:109:VAL:HG22	1.93	0.49
7:G:238:LYS:HD3	47:8:153:C:H4'	1.94	0.49
11:L:106:SER:OG	11:L:109:SER:OG	2.24	0.49
25:Z:26:VAL:HG21	25:Z:96:VAL:HG11	1.94	0.49
50:BB:3:GLY:O	50:BB:63:ARG:NH2	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:PP:30:VAL:HG23	64:PP:94:HIS:HB2	1.94	0.49
75:aa:99:LEU:HD11	75:aa:102:LYS:HD3	1.93	0.49
82:hh:31:ILE:HG22	82:hh:43:TRP:HB2	1.93	0.49
83:3:36:A:O2'	84:9:712:ASP:OD2	2.31	0.49
84:9:26:ALA:HB2	84:9:128:VAL:HB	1.94	0.49
85:4:6071:A:N7	85:4:6072:U:H1'	2.27	0.49
85:4:6071:A:N9	85:4:6072:U:O4'	2.46	0.49
85:4:6178:U:H2'	85:4:6179:U:O4'	2.13	0.49
85:4:6199:A:HO2'	85:4:6200:A:P	2.33	0.49
15:P:64:ASN:ND2	45:5:3891:A:O2'	2.45	0.49
19:T:100:LYS:NZ	45:5:1731:C:OP1	2.44	0.49
49:2:507:G:N7	74:ZZ:104:ARG:NH2	2.59	0.49
49:2:1468:C:H2'	49:2:1469:A:H8	1.78	0.49
85:4:6179:U:O2'	85:4:6179:U:O2	2.27	0.49
5:E:269:GLN:HG2	45:5:4930:C:H5'	1.94	0.49
61:MM:59:LYS:HE2	61:MM:134:LEU:HD12	1.94	0.49
82:hh:57:ARG:NH1	82:hh:94:THR:O	2.45	0.49
85:4:6168:C:C4	85:4:6169:U:O4	2.66	0.49
85:4:6192:G:H2'	85:4:6193:U:C6	2.48	0.49
8:H:21:LYS:NZ	45:5:4863:G:OP1	2.42	0.49
45:5:1324:A:OP1	45:5:1327:C:N4	2.46	0.49
45:5:1353:G:H4'	45:5:1355:G:H4'	1.94	0.49
45:5:2309:G:H1	45:5:2329:U:H3	1.60	0.49
45:5:4603:C:N4	45:5:4604:G:O6	2.46	0.49
2:B:312:LYS:NZ	2:B:370:THR:OG1	2.44	0.49
5:E:193:HIS:HB3	5:E:196:PHE:HD2	1.77	0.49
45:5:90:G:OP2	45:5:92:C:N4	2.44	0.49
45:5:1928:C:OP1	45:5:1948:G:N2	2.44	0.49
48:K:98:LYS:HE3	85:4:6086:U:P	2.53	0.49
49:2:1701:C:C4	85:4:6219:U:O2	2.66	0.49
54:FF:48:LEU:HD23	54:FF:61:VAL:HG22	1.95	0.49
60:LL:63:ALA:HB3	60:LL:66:HIS:HB2	1.94	0.49
67:SS:127:ASN:HD22	67:SS:128:PHE:H	1.60	0.49
81:gg:107:LYS:HB2	81:gg:115:SER:HB3	1.94	0.49
16:Q:172:ARG:NH2	26:a:58:MET:O	2.46	0.49
25:Z:11:VAL:HG11	25:Z:80:LEU:HD13	1.94	0.49
26:a:117:LEU:HD12	26:a:118:PRO:HD2	1.95	0.49
31:f:2:SER:N	45:5:4946:U:O2'	2.43	0.49
46:7:77:A:H62	46:7:99:G:H21	1.60	0.49
49:2:439:A:H4'	49:2:1799:G:H4'	1.95	0.49
49:2:1220:A:N3	49:2:1677:U:O2'	2.44	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:JJ:103:LEU:HD22	58:JJ:170:LYS:HB3	1.95	0.49
59:KK:101:LYS:HE2	59:KK:103:GLU:HB2	1.94	0.49
84:9:665:ILE:HB	84:9:705:HIS:HA	1.95	0.49
85:4:6201:C:O2'	85:4:6202:C:C4'	2.60	0.49
85:4:6217:C:O2'	85:4:6218:U:O5'	2.31	0.49
15:P:39:MET:SD	15:P:43:LYS:NZ	2.80	0.49
25:Z:115:LYS:HE3	45:5:2573:A:H4'	1.95	0.49
38:m:84:CYS:SG	38:m:85:ARG:N	2.86	0.49
45:5:2540:C:H2'	45:5:2541:G:H8	1.77	0.49
45:5:4712:C:H2'	45:5:4713:G:H8	1.78	0.49
49:2:350:C:HO2'	49:2:383:G:H1	1.58	0.49
49:2:1138:C:OP1	50:BB:155:ARG:NH1	2.46	0.49
52:DD:204:ILE:HB	52:DD:211:LYS:HG3	1.94	0.49
60:LL:15:LEU:HD22	60:LL:49:MET:HE1	1.94	0.49
84:9:508:ALA:HB3	84:9:574:ASP:HB2	1.95	0.49
85:4:6076:U:C4	85:4:6077:U:C4	3.01	0.49
85:4:6148:C:C2'	85:4:6149:A:O4'	2.59	0.49
1:A:71:LYS:NZ	45:5:4123:C:OP1	2.46	0.48
11:L:46:ILE:HB	11:L:49:ARG:HB2	1.95	0.48
43:s:161:ILE:HD13	43:s:167:VAL:HG22	1.94	0.48
45:5:709:C:H2'	45:5:710:G:H8	1.78	0.48
45:5:2835:A:N1	45:5:3894:A:O2'	2.45	0.48
45:5:3689:G:O2'	45:5:3818:U:OP2	2.26	0.48
49:2:1275:G:O2'	49:2:1322:G:N2	2.46	0.48
54:FF:45:ILE:HG13	54:FF:61:VAL:HG21	1.95	0.48
82:hh:147:HIS:HD2	82:hh:151:VAL:HG22	1.78	0.48
84:9:583:VAL:HG22	84:9:700:VAL:HG22	1.95	0.48
45:5:3972:A:O2'	45:5:4039:G:N2	2.47	0.48
47:8:11:C:H2'	47:8:12:G:H8	1.75	0.48
49:2:1199:A:H5''	76:bb:2:THR:HB	1.94	0.48
85:4:6211:U:H1'	85:4:6212:U:C5'	2.43	0.48
1:A:32:VAL:HG12	1:A:163:ARG:HH21	1.77	0.48
20:U:21:PHE:HB2	20:U:72:VAL:HB	1.94	0.48
34:i:67:LYS:NZ	45:5:3725:G:N7	2.53	0.48
44:t:137:GLN:NE2	45:5:1993:C:O2'	2.47	0.48
45:5:22:G:H1'	47:8:41:A:H1'	1.94	0.48
45:5:4053:A:H5'	48:K:213:PRO:HA	1.94	0.48
49:2:688:U:OP1	57:II:121:THR:OG1	2.31	0.48
49:2:1025:U:HO2'	49:2:1160:U:HO2'	1.59	0.48
58:JJ:65:PHE:O	58:JJ:109:TYR:OH	2.31	0.48
84:9:268:PRO:HD3	84:9:291:GLN:HE22	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
84:9:652:PHE:O	84:9:684:GLN:NE2	2.46	0.48
85:4:6215:C:H2'	85:4:6216:U:C4'	2.42	0.48
5:E:53:VAL:HB	5:E:56:ILE:HB	1.94	0.48
11:L:21:ARG:HB3	13:N:197:THR:HG22	1.96	0.48
32:g:61:PRO:HA	32:g:64:LEU:HD13	1.95	0.48
45:5:2548:C:H2'	45:5:2549:G:H8	1.76	0.48
45:5:4178:A:H2'	45:5:4179:G:C8	2.49	0.48
49:2:377:G:OP1	58:JJ:98:LYS:NZ	2.43	0.48
49:2:1479:G:N2	79:ee:56:ASP:OD1	2.46	0.48
70:VV:61:LEU:HB2	70:VV:82:MET:HB3	1.95	0.48
85:4:6134:C:N1	85:4:6135:C:C5	2.80	0.48
4:D:50:ARG:NH1	4:D:72:ASP:OD2	2.47	0.48
42:r:6:GLN:HE21	42:r:44:ILE:HG23	1.79	0.48
45:5:2599:G:O2'	45:5:2746:A:N6	2.43	0.48
45:5:3942:A:H2'	45:5:3943:A:H8	1.78	0.48
49:2:1360:U:O2'	49:2:1379:A:OP2	2.30	0.48
53:EE:164:VAL:HA	53:EE:167:TYR:HB2	1.94	0.48
66:RR:37:ARG:HB3	69:UU:7:LYS:HG2	1.95	0.48
45:5:137:G:H2'	45:5:138:G:C8	2.49	0.48
45:5:1469:C:H2'	45:5:1470:G:H8	1.78	0.48
68:TT:46:ARG:NH2	69:UU:48:TYR:O	2.46	0.48
85:4:6068:U:C6	85:4:6069:U:H1'	2.49	0.48
85:4:6197:A:H2'	85:4:6198:A:H1'	1.95	0.48
3:C:284:MET:HE2	3:C:287:THR:HA	1.94	0.48
7:G:285:GLU:O	7:G:289:HIS:HB2	2.14	0.48
9:I:36:LEU:HD11	9:I:87:ILE:HD12	1.95	0.48
11:L:105:LYS:HG2	34:i:19:LYS:HE2	1.95	0.48
49:2:61:A:O2'	49:2:335:G:N2	2.47	0.48
49:2:155:G:H2'	49:2:156:G:H8	1.79	0.48
49:2:454:U:H2'	49:2:455:A:H8	1.79	0.48
49:2:1454:A:OP2	67:SS:3:ARG:NH1	2.47	0.48
49:2:1565:C:OP2	69:UU:101:ARG:NE	2.45	0.48
57:II:154:ILE:HB	57:II:185:VAL:HG22	1.94	0.48
72:XX:2:VAL:HG21	72:XX:4:MET:HE3	1.95	0.48
85:4:6177:U:C1'	85:4:6178:U:C2'	2.92	0.48
1:A:198:ARG:NH2	45:5:3688:U:OP2	2.46	0.48
6:F:45:ARG:HH22	45:5:2102:G:H5'	1.79	0.48
11:L:63:THR:HG21	45:5:101:A:H4'	1.96	0.48
31:f:52:LYS:HA	31:f:67:THR:HA	1.96	0.48
43:s:180:ILE:HG22	43:s:182:PRO:HD3	1.95	0.48
45:5:1305:C:OP1	47:8:7:U:O2'	2.31	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:5:4635:A:OP2	45:5:4663:G:N2	2.47	0.48
45:5:4661:G:N2	45:5:5004:C:O3'	2.47	0.48
45:5:4933:C:H2'	45:5:4934:A:H8	1.79	0.48
49:2:1568:C:OP1	69:UU:96:SER:OG	2.31	0.48
50:BB:81:ASN:OD1	50:BB:84:GLN:NE2	2.46	0.48
59:KK:108:ARG:NH2	59:KK:149:VAL:O	2.46	0.48
66:RR:132:PHE:O	66:RR:140:ARG:NH2	2.44	0.48
68:TT:13:LEU:HB2	68:TT:20:ILE:HB	1.96	0.48
84:9:495:ARG:HD3	84:9:497:MET:HE2	1.96	0.48
85:4:6176:U:O5'	85:4:6176:U:C6	2.66	0.48
10:J:18:ARG:HG3	10:J:135:GLY:HA3	1.95	0.48
15:P:134:GLY:O	45:5:2794:C:N4	2.43	0.48
24:Y:11:ARG:NH1	45:5:229:G:OP1	2.46	0.48
45:5:385:A:H1'	45:5:387:G:H5'	1.95	0.48
45:5:1450:C:O2'	45:5:2104:A:O2'	2.32	0.48
45:5:3607:U:H2'	45:5:3608:A:H8	1.79	0.48
65:QQ:108:LYS:HG2	65:QQ:111:MET:HG2	1.96	0.48
1:A:137:ILE:HD11	1:A:149:LYS:HB2	1.96	0.48
3:C:53:ALA:HB3	47:8:27:U:H4'	1.96	0.48
4:D:291:GLN:NE2	9:I:214:SER:OXT	2.45	0.48
5:E:167:PHE:HA	5:E:178:VAL:HG23	1.96	0.48
9:I:52:MET:HE3	9:I:152:LEU:HD22	1.96	0.48
11:L:80:GLU:OE2	11:L:113:ASN:ND2	2.46	0.48
45:5:4054:C:H5'	48:K:215:ARG:HH21	1.78	0.48
45:5:4601:U:H2'	45:5:4602:A:H8	1.77	0.48
81:gg:116:ARG:NH1	81:gg:120:GLU:OE2	2.44	0.48
2:B:66:LYS:NZ	21:V:12:ALA:O	2.41	0.47
5:E:134:LYS:O	5:E:139:HIS:NE2	2.47	0.47
9:I:112:GLN:HG2	45:5:4440:G:H4'	1.96	0.47
45:5:323:C:H2'	45:5:324:A:H8	1.79	0.47
45:5:2318:G:N1	45:5:2321:G:OP2	2.38	0.47
45:5:2558:C:H2'	45:5:2559:G:H8	1.79	0.47
62:NN:52:LEU:HD13	62:NN:65:VAL:HG21	1.95	0.47
78:dd:31:ARG:HH11	78:dd:43:ILE:HG13	1.79	0.47
85:4:6134:C:C2	85:4:6135:C:C6	3.00	0.47
85:4:6197:A:C2	85:4:6198:A:N3	2.81	0.47
85:4:6211:U:C2'	85:4:6212:U:O5'	2.62	0.47
4:D:24:ARG:NH2	46:7:14:C:OP1	2.47	0.47
24:Y:87:ARG:HH12	45:5:404:U:H4'	1.79	0.47
45:5:1532:G:O2'	45:5:1637:A:N6	2.45	0.47
45:5:3717:A:OP1	45:5:3735:G:N2	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:BB:23:THR:HG21	50:BB:173:LEU:HD12	1.96	0.47
72:XX:86:LEU:HD23	72:XX:117:ARG:HH21	1.79	0.47
84:9:434:TYR:HB3	84:9:493:ASN:HD21	1.79	0.47
2:B:393:LYS:NZ	45:5:5040:U:OP1	2.46	0.47
9:I:43:VAL:O	9:I:171:TRP:NE1	2.47	0.47
17:R:42:ARG:NH1	45:5:2524:U:OP1	2.41	0.47
29:d:38:PHE:HB3	29:d:78:ARG:HG2	1.96	0.47
45:5:1997:U:H2'	45:5:1998:A:H3'	1.95	0.47
45:5:2846:G:H2'	45:5:2847:G:H8	1.80	0.47
45:5:3720:G:H1	45:5:3733:A:H61	1.61	0.47
45:5:4273:A:H62	45:5:4335:C:H42	1.61	0.47
48:K:124:LEU:HD23	85:4:6089:U:C2	2.47	0.47
49:2:943:U:O2'	64:PP:135:ILE:O	2.33	0.47
49:2:1675:A:O2'	55:GG:74:ASN:O	2.32	0.47
65:QQ:18:ARG:HG2	68:TT:88:LYS:HG2	1.97	0.47
82:hh:163:PRO:O	82:hh:178:ASN:ND2	2.47	0.47
85:4:6065:A:H2	85:4:6167:U:N3	2.03	0.47
35:j:52:LYS:HG3	35:j:55:ARG:HE	1.79	0.47
45:5:3846:C:O2'	45:5:4632:U:O2'	2.32	0.47
48:K:48:ARG:HD3	85:4:6082:G:C4'	2.28	0.47
48:K:120:ILE:HG13	85:4:6038:G:H5''	1.95	0.47
49:2:1259:A:N6	49:2:1519:U:O5'	2.48	0.47
49:2:1473:G:N2	49:2:1476:A:OP2	2.43	0.47
65:QQ:85:ILE:HD13	65:QQ:111:MET:HB3	1.96	0.47
82:hh:206:LEU:HD11	82:hh:261:LEU:HD12	1.94	0.47
84:9:121:VAL:O	84:9:415:ARG:NH1	2.48	0.47
85:4:6183:G:C6	85:4:6184:A:C6	3.02	0.47
45:5:2043:A:O2'	45:5:4461:C:O2	2.31	0.47
49:2:1128:C:H2'	49:2:1129:G:C8	2.48	0.47
49:2:1786:U:H2'	49:2:1787:G:H8	1.80	0.47
84:9:130:ASP:HB3	84:9:133:SER:HB3	1.96	0.47
85:4:6065:A:C2	85:4:6066:G:H1'	2.49	0.47
85:4:6078:A:N3	85:4:6079:C:C6	2.82	0.47
45:5:2457:G:O2'	45:5:3672:G:O2'	2.28	0.47
45:5:2777:G:H5''	45:5:2778:G:H5'	1.97	0.47
45:5:4951:G:H2'	45:5:4952:G:H8	1.79	0.47
49:2:126:G:H2'	56:HH:199:THR:HG21	1.96	0.47
52:DD:61:LEU:HD12	52:DD:62:PRO:HD2	1.97	0.47
66:RR:19:ALA:HB2	66:RR:75:GLY:HA3	1.96	0.47
72:XX:3:ARG:HG2	72:XX:6:VAL:HG22	1.96	0.47
85:4:6177:U:C6	85:4:6178:U:C2	3.03	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:4:6177:U:N3	85:4:6178:U:O2	2.48	0.47
2:B:246:ARG:NH2	45:5:4558:U:OP2	2.47	0.47
2:B:248:LEU:HD12	2:B:249:ARG:HG3	1.96	0.47
4:D:119:TYR:OH	4:D:133:GLU:O	2.32	0.47
7:G:104:LEU:HB3	7:G:107:PHE:HB2	1.96	0.47
8:H:91:LYS:HB2	8:H:183:GLU:HB3	1.96	0.47
14:O:81:TRP:HE1	14:O:99:LEU:HD22	1.80	0.47
17:R:45:ILE:HG12	17:R:50:ILE:HD11	1.95	0.47
32:g:5:LEU:O	45:5:2400:G:N2	2.47	0.47
33:h:96:ASN:ND2	45:5:136:C:OP1	2.47	0.47
35:j:46:LYS:NZ	45:5:24:G:OP2	2.41	0.47
45:5:38:A:O2'	45:5:93:G:N2	2.47	0.47
45:5:48:G:O6	45:5:289:C:O2'	2.31	0.47
45:5:3759:A:N6	45:5:3765:G:N3	2.63	0.47
48:K:9:THR:OG1	48:K:10:LEU:N	2.47	0.47
48:K:124:LEU:CG	85:4:6088:C:N4	2.69	0.47
49:2:31:U:O2'	49:2:643:A:N1	2.45	0.47
49:2:373:G:OP1	61:MM:137:THR:OG1	2.32	0.47
49:2:430:C:H2'	49:2:431:G:H8	1.79	0.47
49:2:925:G:H2'	49:2:926:A:H8	1.80	0.47
49:2:1701:C:N4	85:4:6219:U:C2	2.81	0.47
49:2:1735:A:H62	49:2:1799:G:H21	1.63	0.47
50:BB:128:ARG:NH2	50:BB:151:ASP:OD2	2.47	0.47
51:CC:35:ALA:O	51:CC:42:ARG:NH1	2.47	0.47
53:EE:14:ASP:OD2	53:EE:18:LYS:NZ	2.44	0.47
63:OO:30:SER:HB2	63:OO:67:THR:HG22	1.97	0.47
85:4:6169:U:C4	85:4:6170:C:C4	3.03	0.47
15:P:61:ARG:HH22	15:P:76:TRP:HB3	1.79	0.47
30:e:98:GLU:OE2	45:5:2324:C:O2'	2.32	0.47
34:i:84:LYS:NZ	45:5:320:C:OP1	2.40	0.47
45:5:658:C:H2'	45:5:659:G:H8	1.80	0.47
45:5:3844:U:H2'	45:5:3845:A:H8	1.79	0.47
45:5:4051:C:H3'	48:K:211:GLY:HA2	1.96	0.47
52:DD:272:HIS:HA	52:DD:275:LYS:HE2	1.97	0.47
1:A:224:THR:HG21	45:5:3705:G:H21	1.79	0.47
11:L:18:TRP:NE1	45:5:1516:G:O2'	2.48	0.47
45:5:1755:C:O2'	45:5:1757:U:OP2	2.33	0.47
48:K:44:GLN:CG	85:4:6046:U:O2'	2.60	0.47
68:TT:129:LEU:HD22	68:TT:136:THR:HG21	1.96	0.47
84:9:751:CYS:HB2	84:9:755:VAL:HB	1.96	0.47
14:O:173:GLN:HA	14:O:176:ARG:HE	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:i:76:ARG:NH1	45:5:304:C:O3'	2.47	0.47
45:5:460:C:H2'	45:5:461:G:H8	1.80	0.47
49:2:57:U:O2	49:2:499:G:O2'	2.33	0.47
49:2:560:A:H5'	59:KK:174:LYS:HB2	1.96	0.47
49:2:927:C:O2	77:cc:51:GLN:NE2	2.48	0.47
57:II:51:ILE:HD11	57:II:176:VAL:HG22	1.96	0.47
63:OO:114:ARG:HD3	63:OO:117:LEU:HD12	1.97	0.47
64:PP:94:HIS:CD2	64:PP:128:ARG:H	2.33	0.47
68:TT:20:ILE:HD11	68:TT:33:ILE:HD11	1.97	0.47
13:N:159:ARG:HE	13:N:164:LEU:HB2	1.80	0.46
14:O:60:LYS:HD3	45:5:2046:G:H21	1.80	0.46
45:5:4621:C:H2'	45:5:4622:A:H8	1.79	0.46
48:K:124:LEU:HB3	85:4:6088:C:N4	2.16	0.46
49:2:916:A:N1	63:OO:76:LYS:NZ	2.55	0.46
49:2:1854:U:H2'	49:2:1855:G:H8	1.80	0.46
60:LL:91:PRO:HD2	60:LL:94:LEU:HD13	1.97	0.46
85:4:6177:U:N1	85:4:6178:U:C2'	2.78	0.46
3:C:195:LYS:NZ	47:8:21:C:OP1	2.48	0.46
13:N:99:GLN:NE2	13:N:118:SER:O	2.47	0.46
45:5:223:G:O2'	45:5:225:G:OP2	2.31	0.46
48:K:170:GLY:HA2	48:K:179:LEU:HD22	1.96	0.46
49:2:1655:C:H2'	49:2:1656:G:H8	1.80	0.46
49:2:1812:U:H2'	49:2:1813:A:H8	1.80	0.46
45:5:366:A:H62	45:5:375:G:H21	1.63	0.46
45:5:2319:C:N3	45:5:2320:G:N2	2.64	0.46
45:5:2874:U:O4	45:5:3823:G:O2'	2.32	0.46
45:5:3811:G:O2'	45:5:3814:U:OP2	2.33	0.46
49:2:1337:C:O2'	70:VV:68:THR:OG1	2.28	0.46
57:II:82:GLU:HG3	57:II:85:LYS:HE2	1.97	0.46
85:4:6177:U:O2'	85:4:6178:U:O3'	2.33	0.46
10:J:90:ARG:NH2	10:J:108:GLY:O	2.49	0.46
13:N:83:LYS:NZ	45:5:45:U:O4	2.43	0.46
30:e:99:ILE:HG21	30:e:108:ARG:HG2	1.97	0.46
42:r:118:LEU:HA	42:r:121:GLN:HG2	1.96	0.46
49:2:445:A:OP2	58:JJ:47:ARG:NH1	2.46	0.46
49:2:1701:C:C2	85:4:6219:U:C2	3.01	0.46
58:JJ:90:LEU:HD22	58:JJ:95:THR:HB	1.97	0.46
85:4:6168:C:H2'	85:4:6169:U:H1'	1.97	0.46
85:4:6183:G:C6	85:4:6184:A:N6	2.84	0.46
1:A:54:ARG:NH2	45:5:3680:U:OP1	2.47	0.46
9:I:150:GLU:OE2	9:I:153:ARG:NH1	2.47	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:h:67:GLU:HA	33:h:70:ARG:HG2	1.97	0.46
48:K:85:MET:HB3	48:K:89:ALA:HB2	1.96	0.46
49:2:1829:G:H21	49:2:1851:A:H1'	1.80	0.46
54:FF:31:PRO:HG3	54:FF:43:PRO:HG3	1.97	0.46
54:FF:73:ASP:OD1	54:FF:77:ARG:NH2	2.46	0.46
73:YY:93:PHE:O	73:YY:140:ARG:NH1	2.48	0.46
84:9:129:VAL:O	84:9:157:MET:HA	2.15	0.46
84:9:368:ARG:HG2	84:9:372:LEU:HG	1.97	0.46
85:4:6071:A:OP2	85:4:6072:U:C4	2.66	0.46
85:4:6148:C:N4	85:4:6149:A:C6	2.84	0.46
85:4:6215:C:O2'	85:4:6216:U:H4'	2.15	0.46
26:a:132:ARG:NH2	45:5:1468:C:OP1	2.40	0.46
43:s:18:ILE:HG13	43:s:68:HIS:HE1	1.80	0.46
45:5:4097:G:H2'	45:5:4098:A:H8	1.81	0.46
35:j:82:THR:OG1	47:8:94:G:N3	2.45	0.46
49:2:377:G:H5'	58:JJ:98:LYS:HB3	1.98	0.46
55:GG:20:PHE:N	55:GG:23:TRP:O	2.44	0.46
71:WW:74:LYS:HD2	71:WW:81:LYS:HA	1.98	0.46
85:4:6071:A:C8	85:4:6072:U:O4'	2.69	0.46
1:A:238:ILE:O	45:5:3658:C:O2'	2.33	0.46
9:I:193:ASP:OD2	45:5:1750:G:N2	2.49	0.46
12:M:117:LYS:NZ	45:5:4881:U:OP2	2.48	0.46
32:g:46:CYS:SG	32:g:47:GLY:N	2.88	0.46
45:5:3731:C:H2'	45:5:3732:A:H8	1.80	0.46
45:5:4991:U:H2'	45:5:4992:G:H8	1.81	0.46
49:2:1357:A:H5''	52:DD:114:LYS:HB3	1.98	0.46
69:UU:5:THR:HG23	69:UU:8:ASP:H	1.79	0.46
85:4:6066:G:H3'	85:4:6067:G:C2'	2.46	0.46
85:4:6068:U:H2'	85:4:6069:U:O4'	2.15	0.46
85:4:6198:A:N3	85:4:6199:A:N3	2.59	0.46
19:T:80:VAL:HG13	19:T:82:GLY:H	1.81	0.46
34:i:33:LEU:HD11	34:i:38:LYS:HD2	1.98	0.46
45:5:34:A:N6	45:5:49:U:O2	2.49	0.46
45:5:1093:C:H2'	45:5:1094:G:H8	1.80	0.46
45:5:1800:U:H2'	45:5:1801:A:H8	1.81	0.46
45:5:2327:G:H2'	45:5:2328:G:H8	1.81	0.46
57:II:91:HIS:HD2	57:II:169:LYS:HE2	1.80	0.46
73:YY:59:ALA:HB1	73:YY:114:ASP:HB3	1.98	0.46
84:9:18:ASN:ND2	84:9:94:ASP:O	2.48	0.46
85:4:6057:A:N1	85:4:6164:C:H3'	2.29	0.46
8:H:99:PHE:HB2	8:H:118:LEU:HA	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:S:13:VAL:HG23	18:S:62:VAL:HB	1.98	0.46
29:d:19:GLU:HB2	29:d:92:ARG:HH22	1.80	0.46
45:5:1403:G:H1	45:5:1414:C:H42	1.64	0.46
45:5:1849:U:H2'	45:5:1850:A:H8	1.81	0.46
49:2:670:A:O2'	49:2:1163:C:O2	2.34	0.46
49:2:1701:C:N3	85:4:6219:U:N1	2.61	0.46
84:9:244:LEU:HA	84:9:245:GLY:HA2	1.71	0.46
85:4:6050:A:O3'	85:4:6051:A:C2'	2.60	0.46
85:4:6183:G:C2	85:4:6184:A:C4	3.03	0.46
85:4:6211:U:C2	85:4:6212:U:H5'	2.36	0.46
73:YY:19:ASP:O	73:YY:23:HIS:ND1	2.39	0.45
74:ZZ:53:ASP:HB3	74:ZZ:79:LEU:HD21	1.98	0.45
85:4:6148:C:C5	85:4:6149:A:C5	3.03	0.45
23:X:127:LEU:HB3	45:5:2437:C:H5'	1.97	0.45
33:h:56:ARG:NE	47:8:65:A:OP1	2.49	0.45
34:i:82:ARG:HH12	45:5:283:G:H1'	1.81	0.45
43:s:27:CYS:SG	43:s:28:PHE:N	2.88	0.45
49:2:979:C:H2'	49:2:980:A:H8	1.81	0.45
49:2:1033:G:N2	49:2:1080:A:O2'	2.49	0.45
49:2:1854:U:OP1	64:PP:147:ARG:NH2	2.49	0.45
58:JJ:54:LYS:HD3	58:JJ:56:ARG:HE	1.81	0.45
68:TT:24:ARG:HH21	68:TT:28:PHE:HB3	1.81	0.45
85:4:6211:U:N3	85:4:6212:U:C2	2.84	0.45
1:A:233:ARG:HB2	45:5:4184:G:H5'	1.99	0.45
17:R:44:LEU:HD22	17:R:49:LEU:HD12	1.97	0.45
45:5:138:G:H2'	45:5:139:G:C8	2.51	0.45
45:5:2724:G:O2'	45:5:2726:G:OP2	2.35	0.45
54:FF:80:ILE:HG13	54:FF:81:THR:HG23	1.98	0.45
63:OO:33:VAL:HG21	63:OO:66:VAL:HG11	1.97	0.45
84:9:512:LYS:HD3	84:9:569:PRO:HB2	1.99	0.45
85:4:6071:A:N7	85:4:6072:U:C1'	2.79	0.45
15:P:89:GLU:O	15:P:93:HIS:ND1	2.41	0.45
16:Q:30:LYS:NZ	45:5:2269:C:OP1	2.47	0.45
18:S:16:CYS:HB2	18:S:54:MET:HE2	1.99	0.45
49:2:472:C:O2'	49:2:474:G:OP1	2.33	0.45
49:2:915:G:OP1	57:II:120:ARG:NH1	2.43	0.45
16:Q:15:ARG:HH12	16:Q:54:SER:HB3	1.82	0.45
45:5:1645:C:H2'	45:5:1646:A:H8	1.80	0.45
45:5:2658:G:O2'	45:5:2675:G:N2	2.49	0.45
45:5:4583:C:O2'	45:5:4718:G:N2	2.36	0.45
45:5:4967:A:H2'	45:5:4968:A:H8	1.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:8:57:C:O2	47:8:61:A:O2'	2.32	0.45
49:2:930:C:O2'	49:2:1104:G:OP1	2.34	0.45
49:2:1115:U:OP1	49:2:1116:C:N4	2.49	0.45
51:CC:134:LEU:HD13	51:CC:219:LYS:HD2	1.97	0.45
56:HH:76:LEU:HD22	56:HH:92:ARG:HG2	1.98	0.45
61:MM:5:GLN:HG2	61:MM:11:GLN:HB2	1.97	0.45
76:bb:11:ALA:H	76:bb:33:ASP:HB2	1.81	0.45
84:9:27:HIS:HB3	84:9:30:HIS:CE1	2.52	0.45
45:5:2638:G:H1	45:5:2697:A:H61	1.65	0.45
45:5:4134:C:H2'	45:5:4135:G:H8	1.81	0.45
45:5:4393:G:N2	45:5:4396:A:N7	2.63	0.45
49:2:149:A:H62	49:2:169:U:H3	1.65	0.45
49:2:168:C:OP1	56:HH:131:ARG:NE	2.46	0.45
49:2:633:C:H2'	49:2:634:A:H8	1.82	0.45
51:CC:30:TRP:HB3	51:CC:46:LYS:HD3	1.98	0.45
84:9:662:LEU:HD23	84:9:702:PHE:HB2	1.99	0.45
6:F:33:ARG:NH1	45:5:1272:C:OP2	2.50	0.45
6:F:156:ARG:NH2	6:F:211:LYS:O	2.49	0.45
13:N:65:ARG:HH11	45:5:2457:G:H5''	1.82	0.45
25:Z:41:ALA:HB2	25:Z:77:TYR:HE1	1.82	0.45
25:Z:77:TYR:HD2	28:c:39:ARG:HD3	1.81	0.45
25:Z:89:ILE:HD11	25:Z:117:LYS:HB3	1.99	0.45
26:a:125:LYS:HG2	26:a:145:VAL:HB	1.97	0.45
45:5:3868:G:H22	45:5:3900:G:H1'	1.81	0.45
45:5:4486:C:O2'	45:5:4683:U:O2	2.34	0.45
49:2:103:A:H5'	58:JJ:12:ARG:HH22	1.82	0.45
63:OO:55:ARG:NH1	77:cc:49:HIS:O	2.50	0.45
65:QQ:81:ARG:NH2	65:QQ:117:GLY:O	2.50	0.45
74:ZZ:17:LEU:HD12	74:ZZ:18:LEU:HG	1.99	0.45
84:9:10:ARG:HA	84:9:13:MET:HG2	1.98	0.45
85:4:6177:U:C5	85:4:6178:U:N3	2.85	0.45
85:4:6179:U:O4	85:4:6197:A:H61	1.38	0.45
9:I:90:ARG:O	45:5:1783:C:O2'	2.34	0.45
45:5:12:A:O2'	45:5:14:C:OP2	2.28	0.45
45:5:1620:U:H2'	45:5:1621:A:H8	1.82	0.45
45:5:1964:A:H3'	45:5:1965:G:H8	1.81	0.45
45:5:3787:G:H1'	45:5:3789:C:H41	1.82	0.45
45:5:3845:A:H4'	45:5:4668:U:H4'	1.99	0.45
49:2:1062:A:O2'	49:2:1838:U:O4	2.31	0.45
49:2:1259:A:H62	49:2:1518:C:H3'	1.82	0.45
51:CC:72:ALA:HB3	64:PP:128:ARG:HH11	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
67:SS:5:ARG:HG2	67:SS:53:TYR:HB2	1.99	0.45
85:4:6199:A:O2'	85:4:6200:A:OP2	2.32	0.45
2:B:243:LYS:NZ	45:5:2854:G:O6	2.41	0.45
6:F:106:LYS:HD2	6:F:109:GLN:HE21	1.82	0.45
28:c:47:ILE:HG12	28:c:72:HIS:HB3	1.99	0.45
29:d:85:ARG:HG3	29:d:111:VAL:HB	1.99	0.45
42:r:72:LYS:HB2	42:r:76:SER:HB2	1.98	0.45
45:5:3754:G:H1	45:5:3770:U:H3	1.65	0.45
49:2:677:G:OP1	63:OO:124:ARG:NH2	2.50	0.45
49:2:1550:G:O2'	49:2:1558:C:O2	2.34	0.45
70:VV:26:SER:HB3	70:VV:32:LEU:HD22	1.99	0.45
85:4:6148:C:H3'	85:4:6149:A:C8	2.51	0.45
85:4:6184:A:C8	85:4:6185:U:N3	2.85	0.45
85:4:6190:U:C2'	85:4:6191:A:C8	3.00	0.45
9:I:184:MET:HA	9:I:187:GLU:HG2	1.98	0.45
13:N:55:ALA:HB3	45:5:152:U:H5'	1.99	0.45
13:N:116:LEU:HD13	13:N:135:ILE:HD11	1.99	0.45
15:P:48:LEU:HD21	15:P:91:LEU:HD11	1.99	0.45
45:5:382:G:N1	45:5:385:A:OP2	2.49	0.45
45:5:3950:U:H2'	45:5:3951:G:H8	1.81	0.45
49:2:97:U:O2	49:2:434:G:N2	2.49	0.45
49:2:106:C:OP1	49:2:431:G:O2'	2.33	0.45
49:2:161:U:H1'	56:HH:87:ARG:HH22	1.82	0.45
49:2:1084:A:OP1	49:2:1858:G:O2'	2.33	0.45
49:2:1089:G:O6	73:YY:3:LYS:NZ	2.44	0.45
49:2:1172:U:H2'	49:2:1173:A:H8	1.82	0.45
59:KK:60:LEU:HD23	59:KK:63:LEU:HD12	1.99	0.45
83:3:35:G:O6	85:4:6218:U:O4	2.34	0.45
85:4:6083:U:HO2'	85:4:6084:A:H8	1.60	0.45
85:4:6086:U:O2'	85:4:6088:C:OP1	2.27	0.45
22:W:80:ARG:NH1	49:2:167:G:O3'	2.50	0.44
45:5:257:C:H2'	45:5:258:G:H8	1.81	0.44
45:5:3732:A:H2'	45:5:3733:A:C8	2.52	0.44
48:K:124:LEU:HD23	85:4:6088:C:C4	2.49	0.44
49:2:1252:C:OP1	70:VV:75:LYS:NZ	2.42	0.44
49:2:1562:C:H2'	49:2:1563:G:H8	1.82	0.44
56:HH:32:MET:SD	56:HH:65:GLN:NE2	2.89	0.44
85:4:6164:C:OP2	85:4:6164:C:C6	2.70	0.44
8:H:162:GLN:HG3	8:H:180:TYR:HA	1.98	0.44
45:5:1601:A:OP2	45:5:3643:A:N6	2.50	0.44
45:5:4237:C:O2	45:5:4321:U:O2'	2.35	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:5:4660:G:H2'	45:5:4661:G:H8	1.82	0.44
48:K:120:ILE:HG13	85:4:6038:G:C5'	2.47	0.44
49:2:1576:G:H2'	49:2:1577:G:C8	2.52	0.44
53:EE:42:THR:OG1	53:EE:45:ARG:O	2.30	0.44
57:II:36:LEU:HD12	57:II:75:ILE:HD11	1.99	0.44
1:A:247:ARG:HD2	49:2:1069:U:H4'	1.98	0.44
2:B:291:TYR:OH	2:B:315:ASN:ND2	2.50	0.44
19:T:130:ARG:O	45:5:1837:A:O2'	2.34	0.44
45:5:417:G:N2	47:8:16:G:N3	2.65	0.44
48:K:128:LEU:CD2	85:4:6086:U:C4	2.61	0.44
49:2:932:G:HO2'	49:2:993:G:HO2'	1.62	0.44
82:hh:152:SER:OG	82:hh:168:CYS:SG	2.67	0.44
85:4:6189:G:C6	85:4:6214:C:O2	2.62	0.44
17:R:139:MET:O	17:R:143:HIS:ND1	2.38	0.44
43:s:20:LEU:HD12	43:s:54:LEU:HD22	1.99	0.44
44:t:153:ASP:O	44:t:157:SER:OG	2.34	0.44
45:5:53:C:H2'	45:5:54:G:C8	2.53	0.44
45:5:1521:C:N4	45:5:1657:G:O6	2.50	0.44
45:5:4293:U:OP2	45:5:4329:G:O2'	2.35	0.44
49:2:571:U:O2'	74:ZZ:60:PHE:O	2.35	0.44
49:2:1048:G:H21	49:2:1070:A:H62	1.66	0.44
52:DD:259:THR:OG1	71:WW:14:PRO:O	2.33	0.44
58:JJ:70:GLU:HG2	58:JJ:112:TRP:HH2	1.81	0.44
69:UU:6:VAL:O	69:UU:11:GLN:NE2	2.50	0.44
69:UU:131:LEU:HD13	69:UU:134:ILE:HD11	2.00	0.44
78:dd:21:THR:HG22	78:dd:68:LEU:HD13	1.98	0.44
82:hh:37:ASP:OD2	82:hh:39:THR:OG1	2.35	0.44
84:9:595:SER:HB3	84:9:600:ASN:HB2	1.98	0.44
85:4:6134:C:N4	85:4:6135:C:H42	2.16	0.44
85:4:6183:G:N1	85:4:6184:A:N1	2.66	0.44
4:D:209:ARG:NH2	4:D:234:ASP:OD1	2.51	0.44
19:T:68:THR:OG1	19:T:71:ALA:O	2.36	0.44
30:e:90:MET:HG3	42:r:33:LYS:HA	2.00	0.44
45:5:66:A:O2'	45:5:326:C:O2	2.34	0.44
45:5:749:G:N2	45:5:912:G:O2'	2.49	0.44
45:5:2881:A:H3'	45:5:2882:A:H8	1.82	0.44
45:5:4409:C:H2'	45:5:4410:G:H8	1.83	0.44
45:5:4669:A:N3	45:5:4671:C:O2'	2.48	0.44
45:5:5047:C:O2	45:5:5049:G:O2'	2.35	0.44
49:2:1321:G:OP2	84:9:629:LYS:NZ	2.50	0.44
85:4:6174:G:O2'	85:4:6175:G:P	2.75	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:4:6198:A:C5	85:4:6199:A:N7	2.82	0.44
1:A:136:VAL:HG22	1:A:148:VAL:HG22	2.00	0.44
1:A:177:LYS:HD2	41:p:26:VAL:HG13	2.00	0.44
3:C:298:ILE:HG22	3:C:302:LEU:HD11	2.00	0.44
20:U:80:LYS:O	20:U:110:TYR:OH	2.36	0.44
45:5:4925:U:H4'	45:5:4926:C:H5'	1.99	0.44
48:K:124:LEU:HD12	85:4:6037:U:H3'	2.00	0.44
49:2:1566:G:C6	69:UU:98:SER:HB2	2.52	0.44
55:GG:71:ARG:NH1	55:GG:148:ASN:OD1	2.42	0.44
55:GG:86:LYS:HA	55:GG:89:THR:HG22	1.99	0.44
66:RR:97:GLN:HG3	66:RR:105:LYS:HE2	2.00	0.44
68:TT:8:LYS:NZ	68:TT:59:LEU:O	2.51	0.44
85:4:6183:G:C2	85:4:6184:A:N1	2.85	0.44
85:4:6190:U:H2'	85:4:6191:A:H8	1.83	0.44
85:4:6199:A:N3	85:4:6200:A:O4'	2.51	0.44
3:C:179:ASP:OD1	3:C:204:ARG:NH1	2.46	0.44
45:5:1645:C:H2'	45:5:1646:A:C8	2.52	0.44
45:5:2295:C:H2'	45:5:2296:G:H8	1.83	0.44
45:5:3658:C:H2'	45:5:3659:G:H8	1.83	0.44
45:5:4601:U:O2	45:5:4610:A:N7	2.51	0.44
49:2:1202:U:O2'	52:DD:115:GLN:O	2.36	0.44
54:FF:85:GLY:N	54:FF:88:ASP:OD2	2.50	0.44
59:KK:78:LEU:HD22	59:KK:87:LEU:HD22	2.00	0.44
63:OO:18:TYR:HE1	72:XX:55:ASP:HA	1.83	0.44
63:OO:136:PRO:HA	63:OO:137:PRO:HD3	1.90	0.44
82:hh:207:CYS:SG	82:hh:208:ALA:N	2.91	0.44
85:4:6215:C:C2'	85:4:6216:U:O4'	2.65	0.44
8:H:16:VAL:HG21	8:H:81:ILE:HG23	1.99	0.44
24:Y:75:ARG:NH2	47:8:72:A:O2'	2.43	0.44
38:m:80:ARG:NH2	45:5:4696:C:O2'	2.50	0.44
49:2:1593:C:H2'	49:2:1594:A:H8	1.82	0.44
49:2:1701:C:C2	85:4:6219:U:C6	3.06	0.44
50:BB:141:ASN:ND2	71:WW:29:HIS:O	2.51	0.44
74:ZZ:103:SER:OG	74:ZZ:106:GLN:OE1	2.31	0.44
83:3:28:C:OP1	84:9:598:LYS:NZ	2.45	0.44
4:D:44:TYR:O	45:5:1823:G:O2'	2.35	0.44
4:D:205:ALA:HB1	4:D:233:PRO:HB3	1.99	0.44
5:E:117:ARG:NH1	45:5:691:C:OP1	2.50	0.44
16:Q:122:THR:OG1	16:Q:124:ASP:OD1	2.33	0.44
48:K:124:LEU:HD12	85:4:6037:U:H2'	1.91	0.44
49:2:1064:C:H2'	49:2:1065:G:H8	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:FF:206:ASP:HB2	54:FF:222:LEU:HD12	2.00	0.44
64:PP:35:ALA:O	64:PP:109:GLY:N	2.50	0.44
85:4:6059:U:C1'	85:4:6060:U:H5''	2.46	0.44
85:4:6169:U:O2	85:4:6169:U:C2'	2.65	0.44
85:4:6179:U:O2	85:4:6197:A:H2	1.94	0.44
13:N:114:ARG:HH12	13:N:157:LYS:HA	1.83	0.43
19:T:3:ASN:ND2	45:5:4219:A:OP2	2.50	0.43
45:5:4296:U:O4	45:5:4315:A:N6	2.51	0.43
49:2:84:A:N3	49:2:150:A:O2'	2.51	0.43
49:2:93:U:H1'	54:FF:7:LYS:HD2	1.99	0.43
62:NN:61:TYR:HH	62:NN:108:CYS:HG	1.66	0.43
85:4:6108:G:C5	85:4:6109:C:N4	2.85	0.43
85:4:6177:U:H2'	85:4:6178:U:C1'	2.41	0.43
85:4:6199:A:C2'	85:4:6200:A:OP2	2.66	0.43
85:4:6200:A:N6	85:4:6201:C:N3	2.66	0.43
45:5:679:C:H2'	45:5:680:G:H8	1.83	0.43
45:5:3659:G:H21	45:5:3665:G:H1'	1.83	0.43
48:K:113:SER:OG	48:K:114:GLU:N	2.50	0.43
49:2:154:U:O2	56:HH:4:ASN:ND2	2.43	0.43
49:2:183:G:O2'	49:2:184:G:O5'	2.34	0.43
49:2:1202:U:H2'	49:2:1203:G:H8	1.82	0.43
49:2:1328:G:O2'	84:9:670:GLN:NE2	2.51	0.43
49:2:1430:C:H2'	49:2:1431:G:C8	2.52	0.43
85:4:6215:C:H2'	85:4:6216:U:O4'	2.18	0.43
13:N:31:ARG:NH1	13:N:124:ASP:OD1	2.52	0.43
14:O:34:VAL:HG22	14:O:103:LYS:HD2	2.00	0.43
19:T:71:ALA:HA	19:T:92:ARG:HA	1.99	0.43
45:5:651:C:H2'	45:5:652:G:C8	2.53	0.43
45:5:2568:C:N4	45:5:2569:G:O6	2.51	0.43
45:5:2836:A:H2	45:5:3895:G:H4'	1.82	0.43
45:5:3709:U:H2'	45:5:3710:G:C8	2.54	0.43
48:K:95:LYS:HZ3	85:4:6041:C:H6	1.66	0.43
70:VV:20:ILE:HB	70:VV:91:LEU:HB2	1.99	0.43
72:XX:29:PRO:HA	72:XX:58:ALA:HB1	1.99	0.43
83:3:36:A:N6	85:4:6217:C:N4	2.59	0.43
85:4:6149:A:N3	85:4:6149:A:H2'	2.33	0.43
85:4:6169:U:O2	85:4:6169:U:O2'	2.32	0.43
26:a:82:VAL:HG21	26:a:101:ILE:HG12	2.00	0.43
40:o:22:LYS:N	40:o:71:GLU:O	2.50	0.43
45:5:2041:A:O2'	45:5:4464:A:OP1	2.35	0.43
45:5:2630:U:H1'	45:5:4647:G:H22	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:5:5047:C:O2'	45:5:5050:C:OP2	2.37	0.43
49:2:1190:A:N3	49:2:1714:U:O2'	2.48	0.43
49:2:1277:C:H2'	49:2:1278:A:H8	1.84	0.43
57:II:53:VAL:HG21	57:II:172:THR:HA	2.00	0.43
82:hh:133:ASN:HD22	82:hh:137:VAL:HB	1.83	0.43
85:4:6177:U:C2'	85:4:6178:U:C1'	2.96	0.43
4:D:197:LYS:HD3	4:D:202:GLN:HE21	1.83	0.43
22:W:80:ARG:HD3	56:HH:10:THR:HA	2.00	0.43
24:Y:15:ARG:NH1	45:5:230:G:OP1	2.51	0.43
44:t:32:ILE:HA	44:t:35:LEU:HD13	2.01	0.43
45:5:53:C:O2'	45:5:2461:G:O2'	2.28	0.43
45:5:257:C:H2'	45:5:258:G:C8	2.53	0.43
45:5:1289:C:H2'	45:5:1290:G:H8	1.84	0.43
45:5:2074:C:H2'	45:5:2075:G:H8	1.84	0.43
45:5:2579:G:N2	45:5:2582:A:OP2	2.43	0.43
48:K:44:GLN:HG2	85:4:6046:U:H1'	1.62	0.43
49:2:1169:G:H21	49:2:1190:A:H62	1.66	0.43
84:9:689:GLU:O	84:9:730:TYR:OH	2.37	0.43
84:9:851:LEU:O	84:9:855:LEU:HB3	2.19	0.43
85:4:6211:U:O4	85:4:6212:U:C2	2.70	0.43
8:H:102:ASN:HB3	8:H:115:ARG:HB2	2.01	0.43
13:N:84:PRO:HB2	40:o:49:GLY:HA2	2.00	0.43
15:P:69:ARG:HE	45:5:4981:G:H1'	1.84	0.43
42:r:91:SER:O	42:r:95:HIS:ND1	2.38	0.43
48:K:120:ILE:CA	85:4:6038:G:H5''	2.32	0.43
49:2:318:A:H3'	49:2:319:C:H5''	2.01	0.43
49:2:677:G:H21	49:2:1028:A:H62	1.65	0.43
54:FF:125:LYS:H	54:FF:142:HIS:HD2	1.64	0.43
84:9:539:GLU:HG3	84:9:541:SER:H	1.82	0.43
84:9:815:ASP:OD2	84:9:816:HIS:ND1	2.45	0.43
85:4:6174:G:N2	85:4:6208:A:C4	2.82	0.43
3:C:31:PRO:O	3:C:126:SER:OG	2.29	0.43
4:D:12:TYR:O	4:D:16:TYR:HB2	2.18	0.43
23:X:102:VAL:HA	23:X:134:LYS:HE3	2.00	0.43
26:a:110:LYS:HE2	26:a:112:LEU:HD21	2.01	0.43
34:i:60:LEU:HA	34:i:63:VAL:HG22	2.00	0.43
44:t:104:ILE:HB	44:t:143:VAL:HG22	2.00	0.43
45:5:440:U:H2'	45:5:441:G:H8	1.83	0.43
45:5:1100:U:O2	45:5:1195:G:O6	2.37	0.43
45:5:2283:G:H2'	45:5:2284:G:H8	1.82	0.43
49:2:16:G:N2	49:2:1195:A:H62	2.16	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:2:867:G:O2'	49:2:868:G:O4'	2.32	0.43
49:2:1140:G:H2'	49:2:1141:G:C8	2.54	0.43
54:FF:72:ILE:O	54:FF:77:ARG:NH2	2.52	0.43
3:C:67:TRP:HZ3	3:C:78:ARG:HB2	1.84	0.43
25:Z:5:MET:O	25:Z:28:ASN:ND2	2.49	0.43
35:j:19:CYS:SG	35:j:20:ARG:N	2.91	0.43
47:8:124:U:H5'	47:8:126:C:H5	1.83	0.43
49:2:1337:C:H2'	49:2:1338:G:H8	1.83	0.43
49:2:1373:C:O2	49:2:1465:A:O2'	2.32	0.43
60:LL:15:LEU:HD23	60:LL:79:LEU:HD21	2.00	0.43
72:XX:42:MET:HE2	72:XX:49:GLU:HA	2.01	0.43
73:YY:132:ALA:HB1	73:YY:137:LYS:HB2	2.00	0.43
84:9:762:VAL:HG21	84:9:800:LEU:HD12	2.01	0.43
84:9:774:SER:HB2	84:9:783:VAL:HB	2.01	0.43
85:4:6076:U:N3	85:4:6077:U:C4	2.86	0.43
85:4:6168:C:N4	85:4:6169:U:O4	2.52	0.43
30:e:26:ASP:OD2	45:5:435:A:O2'	2.35	0.43
35:j:20:ARG:HD2	35:j:39:TYR:HE1	1.84	0.43
49:2:210:U:H2'	49:2:211:G:H8	1.83	0.43
57:II:178:LYS:HD2	57:II:182:GLY:HA2	2.00	0.43
80:ff:85:VAL:HA	80:ff:88:GLN:HG2	2.01	0.43
82:hh:118:ARG:HH21	82:hh:133:ASN:HB3	1.82	0.43
84:9:685:TRP:HZ3	84:9:726:ARG:HG3	1.83	0.43
6:F:91:VAL:O	6:F:119:GLY:HA2	2.19	0.43
6:F:150:ASN:OD1	45:5:943:A:N6	2.52	0.43
8:H:91:LYS:HG2	8:H:145:VAL:HG22	2.00	0.43
10:J:46:GLN:NE2	10:J:72:CYS:SG	2.91	0.43
11:L:71:ARG:NH1	45:5:102:G:OP1	2.52	0.43
23:X:139:ARG:NH2	45:5:2533:C:OP1	2.52	0.43
30:e:103:VAL:O	30:e:108:ARG:NE	2.51	0.43
45:5:2521:G:H2'	45:5:2522:G:C8	2.54	0.43
45:5:3779:A:H62	45:5:3815:G:H21	1.66	0.43
45:5:4088:C:H2'	45:5:4089:G:C8	2.54	0.43
45:5:4933:C:H2'	45:5:4934:A:C8	2.54	0.43
45:5:4991:U:H2'	45:5:4992:G:C8	2.54	0.43
49:2:77:A:O2'	56:HH:174:PRO:O	2.36	0.43
49:2:975:G:H2'	49:2:976:G:H8	1.84	0.43
74:ZZ:10:ARG:HG2	74:ZZ:11:LYS:HG3	2.00	0.43
77:cc:16:LYS:HA	77:cc:23:ARG:HH21	1.84	0.43
10:J:13:ARG:NH1	46:7:54:A:O2'	2.52	0.42
18:S:157:ARG:O	18:S:174:THR:OG1	2.37	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:t:117:ARG:HH11	44:t:124:GLU:HA	1.84	0.42
45:5:56:A:H2'	45:5:57:G:C8	2.54	0.42
45:5:436:C:H2'	45:5:437:G:H8	1.84	0.42
45:5:1514:U:H2'	45:5:1515:A:C8	2.54	0.42
45:5:1694:C:N4	45:5:1695:U:O4	2.52	0.42
45:5:2597:G:H2'	45:5:2598:A:C8	2.54	0.42
45:5:3701:C:H4'	45:5:3702:A:H5'	2.00	0.42
49:2:603:C:H4'	49:2:604:A:H5'	2.01	0.42
55:GG:49:LEU:HB2	66:RR:50:LYS:HD3	2.00	0.42
65:QQ:79:HIS:HA	65:QQ:97:TYR:HB3	2.01	0.42
84:9:169:LEU:HD22	84:9:174:LEU:HD13	1.99	0.42
84:9:238:ALA:HA	84:9:239:LYS:HA	1.91	0.42
11:L:27:ASN:HD21	47:8:29:G:H5''	1.84	0.42
31:f:45:LYS:HD2	31:f:105:LEU:HA	2.00	0.42
45:5:1573:G:H2'	45:5:1574:G:C4	2.53	0.42
45:5:1959:U:O4'	45:5:2025:A:N6	2.53	0.42
48:K:157:PHE:HB2	48:K:165:LEU:HD11	2.00	0.42
49:2:177:G:H22	49:2:313:A:H5'	1.85	0.42
49:2:342:C:H2'	49:2:343:A:H8	1.84	0.42
49:2:1023:A:H2'	49:2:1024:A:C8	2.54	0.42
49:2:1130:G:H2'	49:2:1131:G:H8	1.85	0.42
49:2:1651:A:H2'	49:2:1652:G:H8	1.84	0.42
61:MM:135:SER:O	61:MM:139:ARG:NH1	2.46	0.42
72:XX:103:VAL:HG13	72:XX:126:LEU:HB2	2.01	0.42
45:5:2340:C:H2'	45:5:2341:A:H8	1.85	0.42
45:5:3870:C:H2'	45:5:3871:A:H8	1.85	0.42
47:8:67:U:H2'	47:8:68:G:H8	1.84	0.42
49:2:979:C:H2'	49:2:980:A:C8	2.54	0.42
49:2:1213:C:H2'	49:2:1214:A:C8	2.54	0.42
78:dd:21:THR:HG23	78:dd:29:GLN:HB2	2.02	0.42
85:4:6169:U:H2'	85:4:6170:C:C6	2.54	0.42
2:B:133:TYR:HB2	45:5:4726:G:H5''	2.01	0.42
17:R:12:SER:OG	17:R:17:CYS:O	2.36	0.42
29:d:62:VAL:HG22	29:d:104:THR:HB	2.01	0.42
40:o:80:LYS:O	45:5:4346:U:O2'	2.35	0.42
43:s:29:ILE:HD12	43:s:191:GLN:HB2	2.01	0.42
44:t:80:LEU:HD13	44:t:112:ILE:HG23	2.02	0.42
45:5:3599:A:H2'	45:5:3600:G:C8	2.55	0.42
49:2:674:C:O2'	49:2:996:A:N3	2.43	0.42
49:2:943:U:N3	64:PP:138:ASP:O	2.50	0.42
72:XX:26:LEU:HD11	72:XX:60:LYS:HB3	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:4:6066:G:N3	85:4:6167:U:C6	2.77	0.42
2:B:3:HIS:HD2	45:5:4515:G:H3'	1.82	0.42
3:C:152:LEU:HD23	3:C:251:ILE:HG12	2.01	0.42
3:C:323:ARG:HG2	3:C:326:LEU:HD12	2.02	0.42
13:N:157:LYS:HD2	45:5:56:A:H4'	1.99	0.42
45:5:2520:C:H2'	45:5:2521:G:H8	1.84	0.42
45:5:3688:U:H2'	45:5:3689:G:H8	1.84	0.42
49:2:792:C:H2'	49:2:793:G:H8	1.84	0.42
56:HH:147:LEU:HD13	56:HH:153:VAL:HG22	2.00	0.42
60:LL:61:GLN:HB3	60:LL:68:TYR:HB2	2.00	0.42
85:4:6078:A:N1	85:4:6079:C:N3	2.66	0.42
3:C:340:ILE:HG21	5:E:52:LEU:HD11	2.02	0.42
9:I:4:ARG:HH22	9:I:100:ASN:HB3	1.84	0.42
13:N:5:LYS:HE2	34:i:37:THR:HG22	2.00	0.42
16:Q:176:ARG:HB2	26:a:56:VAL:HG11	2.01	0.42
28:c:29:LEU:HD23	28:c:94:LEU:HD13	2.01	0.42
43:s:77:LYS:O	43:s:81:HIS:ND1	2.44	0.42
45:5:1091:C:H2'	45:5:1092:G:C8	2.55	0.42
45:5:4239:A:H2'	45:5:4240:G:C8	2.55	0.42
49:2:1004:U:H2'	49:2:1005:G:H8	1.83	0.42
49:2:1288:U:O2'	49:2:1315:U:O2'	2.36	0.42
52:DD:261:PHE:HB2	71:WW:52:THR:HG21	2.02	0.42
69:UU:42:HIS:HB3	69:UU:93:SER:HB3	2.01	0.42
84:9:236:PHE:HA	84:9:237:ALA:HA	1.81	0.42
85:4:6134:C:O2'	85:4:6135:C:C5'	2.56	0.42
85:4:6177:U:N3	85:4:6178:U:C2	2.88	0.42
1:A:101:VAL:HG22	1:A:163:ARG:HB3	2.02	0.42
3:C:61:GLN:OE1	35:j:55:ARG:NH2	2.44	0.42
3:C:183:VAL:HG22	3:C:204:ARG:HB3	2.02	0.42
11:L:24:THR:HG22	13:N:200:LEU:HB2	2.00	0.42
15:P:94:MET:HE1	15:P:146:ILE:HB	2.02	0.42
16:Q:104:ARG:NH2	45:5:1352:C:OP2	2.51	0.42
27:b:106:ARG:NH1	45:5:1437:C:O4'	2.53	0.42
45:5:1509:C:H2'	45:5:1510:G:C8	2.55	0.42
45:5:4630:G:H2'	45:5:4631:G:H8	1.85	0.42
45:5:4980:C:H3'	45:5:4981:G:H21	1.85	0.42
49:2:641:A:OP2	80:ff:107:ARG:NH2	2.43	0.42
49:2:849:A:O2'	59:KK:69:ARG:NH2	2.45	0.42
51:CC:87:ILE:HG13	51:CC:99:ASN:HB3	2.02	0.42
51:CC:223:PHE:HZ	51:CC:228:LEU:HD22	1.85	0.42
52:DD:198:ALA:HB3	52:DD:221:ASP:HB3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:MM:104:LYS:HG2	73:YY:8:ARG:HH11	1.84	0.42
84:9:631:ARG:HE	84:9:649:ILE:HD11	1.84	0.42
4:D:34:LYS:HA	4:D:37:VAL:HG12	2.01	0.42
8:H:71:ARG:HD3	45:5:4691:A:H4'	2.02	0.42
13:N:158:HIS:O	13:N:162:ARG:NE	2.45	0.42
24:Y:67:ILE:O	24:Y:84:ARG:NH2	2.52	0.42
30:e:86:GLU:HA	30:e:89:LEU:HD23	2.01	0.42
42:r:37:SER:HB3	42:r:40:TYR:HD2	1.85	0.42
45:5:450:G:O2'	45:5:453:G:N7	2.47	0.42
48:K:36:ILE:HG22	48:K:165:LEU:HB3	2.02	0.42
73:YY:84:PHE:HB2	73:YY:118:VAL:HG11	2.00	0.42
85:4:6135:C:O4'	85:4:6152:A:H1'	2.20	0.42
14:O:46:ASN:HD21	45:5:1930:U:H5'	1.84	0.42
15:P:4:TYR:HE1	15:P:18:ARG:HD3	1.85	0.42
25:Z:135:ARG:NH1	45:5:2752:G:O2'	2.53	0.42
35:j:12:ARG:NH1	45:5:2404:A:O2'	2.46	0.42
45:5:1657:G:HO2'	45:5:2349:A:HO2'	1.57	0.42
45:5:2458:C:O2'	45:5:3671:G:O2'	2.35	0.42
47:8:36:G:N2	47:8:37:A:N1	2.67	0.42
49:2:927:C:H2'	49:2:928:G:C8	2.55	0.42
49:2:1270:G:O2'	49:2:1301:A:N6	2.46	0.42
49:2:1366:G:O6	49:2:1374:C:N4	2.52	0.42
49:2:1794:C:H2'	49:2:1795:G:H8	1.85	0.42
55:GG:104:THR:HG22	55:GG:106:GLU:H	1.85	0.42
57:II:144:ILE:HD12	72:XX:52:ILE:HD11	2.02	0.42
85:4:6180:U:N3	85:4:6197:A:C5	2.88	0.42
3:C:222:ARG:NH2	45:5:243:A:O2'	2.53	0.42
11:L:11:LYS:NZ	45:5:95:G:OP2	2.41	0.42
44:t:116:MET:HG3	44:t:132:ILE:HD11	2.01	0.42
45:5:2059:C:H2'	45:5:2060:G:H8	1.85	0.42
45:5:3707:U:H3	45:5:3743:G:H1	1.67	0.42
45:5:3878:C:O2'	45:5:4518:A:N6	2.53	0.42
49:2:66:G:OP1	49:2:82:G:N2	2.53	0.42
49:2:1016:U:H6	63:OO:61:ALA:HB2	1.85	0.42
84:9:158:ASN:HD22	84:9:159:LYS:H	1.67	0.42
85:4:6179:U:C2	85:4:6180:U:H5	2.35	0.42
85:4:6191:A:N6	85:4:6213:A:C2	2.88	0.42
2:B:189:THR:HG23	2:B:192:GLU:H	1.85	0.41
3:C:284:MET:HG3	3:C:287:THR:HG22	2.02	0.41
6:F:224:THR:HB	6:F:228:GLU:HG3	2.02	0.41
8:H:92:MET:HE2	8:H:179:ILE:HG22	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:N:80:THR:O	13:N:87:HIS:NE2	2.53	0.41
45:5:1461:C:H2'	45:5:1462:A:H8	1.84	0.41
45:5:2580:U:H2'	45:5:2581:A:C4	2.55	0.41
49:2:602:G:H3'	49:2:603:C:H2'	2.00	0.41
49:2:1804:U:H2'	49:2:1805:G:C8	2.55	0.41
49:2:1854:U:H2'	49:2:1855:G:C8	2.55	0.41
49:2:1856:C:OP1	64:PP:141:ARG:NH1	2.49	0.41
50:BB:126:ASP:OD1	50:BB:165:ASN:ND2	2.53	0.41
52:DD:206:SER:OG	52:DD:207:ALA:N	2.53	0.41
53:EE:49:ILE:HG12	53:EE:87:TYR:HB2	2.02	0.41
75:aa:44:LEU:HD12	75:aa:78:LYS:HE3	2.01	0.41
83:3:36:A:N6	85:4:6217:C:C2	2.83	0.41
84:9:536:CYS:HA	84:9:545:ILE:O	2.20	0.41
45:5:724:C:H2'	45:5:725:G:H8	1.85	0.41
45:5:1461:C:H2'	45:5:1462:A:C8	2.55	0.41
45:5:2078:C:H2'	45:5:2079:G:H8	1.85	0.41
45:5:3942:A:H2'	45:5:3943:A:C8	2.55	0.41
45:5:4179:G:H2'	45:5:4180:G:C8	2.54	0.41
48:K:124:LEU:HD12	85:4:6037:U:C3'	2.50	0.41
49:2:1365:G:N2	49:2:1462:U:O4	2.53	0.41
49:2:1654:G:OP1	69:UU:90:SER:OG	2.35	0.41
56:HH:181:THR:HG23	56:HH:184:VAL:H	1.85	0.41
67:SS:96:ILE:HG22	67:SS:97:GLU:H	1.85	0.41
82:hh:292:SER:OG	82:hh:293:ALA:N	2.53	0.41
85:4:6197:A:H3'	85:4:6198:A:C4'	2.45	0.41
85:4:6201:C:HO2'	85:4:6202:C:C4'	2.32	0.41
12:M:32:ASP:HB3	12:M:35:ARG:HB3	2.02	0.41
25:Z:14:LEU:HB2	25:Z:81:MET:HB2	2.02	0.41
28:c:29:LEU:HD22	28:c:91:VAL:HG21	2.02	0.41
31:f:78:HIS:HB2	31:f:85:ARG:HG3	2.03	0.41
41:p:39:CYS:SG	41:p:40:SER:N	2.93	0.41
45:5:949:G:H2'	45:5:950:G:H8	1.85	0.41
49:2:562:U:H1'	59:KK:132:GLN:HG2	2.02	0.41
49:2:652:U:H2'	49:2:653:A:C8	2.56	0.41
49:2:1530:U:H2'	49:2:1531:A:H8	1.85	0.41
55:GG:143:PRO:HB3	55:GG:146:ARG:HH21	1.85	0.41
56:HH:121:ILE:HG13	56:HH:123:GLY:H	1.86	0.41
57:II:153:LEU:HD21	57:II:186:ASN:HD22	1.84	0.41
82:hh:107:ASP:HB2	82:hh:125:ARG:HD2	2.01	0.41
85:4:6148:C:O2	85:4:6149:A:C1'	2.68	0.41
3:C:310:HIS:O	45:5:2273:G:O2'	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:L:64:VAL:HB	45:5:71:C:H4'	2.02	0.41
19:T:112:ASN:HA	19:T:115:LYS:HZ1	1.86	0.41
42:r:118:LEU:HG	42:r:121:GLN:HE21	1.85	0.41
45:5:4635:A:OP1	45:5:4636:U:O2'	2.35	0.41
45:5:4997:G:H2'	45:5:4998:G:H8	1.85	0.41
49:2:927:C:H2'	49:2:928:G:H8	1.84	0.41
49:2:1139:C:H6	49:2:1139:C:H2'	1.72	0.41
49:2:1284:A:C8	62:NN:91:LEU:HD22	2.55	0.41
54:FF:105:THR:HG23	54:FF:106:LYS:HD2	2.02	0.41
62:NN:99:LYS:HB2	62:NN:101:ARG:HH21	1.85	0.41
3:C:32:ILE:HD11	3:C:129:ALA:HB3	2.02	0.41
6:F:94:ILE:HG13	6:F:95:ARG:HG3	2.01	0.41
6:F:155:LYS:NZ	6:F:247:ASN:O	2.42	0.41
21:V:16:ILE:HD13	21:V:84:GLN:HE22	1.85	0.41
43:s:82:ILE:HA	43:s:86:VAL:HG21	2.03	0.41
44:t:56:LEU:HG	44:t:79:ALA:HA	2.03	0.41
45:5:27:C:O2'	45:5:60:A:N3	2.51	0.41
45:5:3731:C:H2'	45:5:3732:A:C8	2.56	0.41
48:K:124:LEU:CG	85:4:6037:U:C2'	2.51	0.41
49:2:72:C:O2'	49:2:74:G:OP2	2.34	0.41
49:2:1183:A:H2'	49:2:1184:G:H8	1.85	0.41
67:SS:99:ASP:HA	67:SS:100:PRO:HD3	1.90	0.41
85:4:6167:U:HO2'	85:4:6168:C:P	2.44	0.41
85:4:6197:A:C2'	85:4:6198:A:H1'	2.50	0.41
6:F:76:LYS:NZ	45:5:730:G:N7	2.68	0.41
11:L:10:LEU:HG	11:L:12:PRO:HD3	2.01	0.41
45:5:162:A:H2'	45:5:163:A:H8	1.86	0.41
45:5:717:U:H3	45:5:951:G:H1	1.68	0.41
45:5:1850:A:N3	45:5:2283:G:O2'	2.43	0.41
45:5:1854:G:N2	45:5:4394:A:O4'	2.54	0.41
45:5:1937:C:H3'	45:5:1938:C:H2'	2.02	0.41
45:5:2272:C:H2'	45:5:2273:G:H8	1.86	0.41
45:5:2558:C:H2'	45:5:2559:G:C8	2.56	0.41
45:5:2642:A:N6	45:5:2643:G:O6	2.53	0.41
45:5:4949:G:H4'	45:5:4950:U:H5'	2.02	0.41
49:2:492:C:OP2	74:ZZ:107:ARG:NH2	2.42	0.41
49:2:525:A:H2'	49:2:526:A:C8	2.55	0.41
68:TT:124:ARG:NH2	68:TT:130:ARG:O	2.40	0.41
85:4:6066:G:H5''	85:4:6067:G:H3'	2.02	0.41
85:4:6104:G:H2'	85:4:6105:U:H5'	2.01	0.41
85:4:6162:A:H3'	85:4:6163:G:H5''	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:T:18:PRO:HB2	19:T:21:LYS:HD2	2.03	0.41
21:V:109:LYS:HG3	21:V:111:GLU:HG3	2.01	0.41
45:5:1739:G:H22	45:5:1790:U:H1'	1.85	0.41
45:5:4302:U:O2'	45:5:4303:C:O4'	2.37	0.41
48:K:29:LEU:HB3	48:K:60:ARG:HH12	1.86	0.41
49:2:623:G:O2'	49:2:631:U:O4	2.34	0.41
53:EE:41:VAL:H	70:VV:108:PRO:HB3	1.86	0.41
59:KK:65:GLU:HG3	59:KK:66:LYS:HG2	2.03	0.41
62:NN:32:ALA:HB1	62:NN:37:GLU:HB3	2.01	0.41
84:9:403:PRO:HA	84:9:410:PHE:HD1	1.86	0.41
85:4:6197:A:C6	85:4:6198:A:C6	3.08	0.41
7:G:119:GLN:HA	7:G:122:ILE:HD12	2.03	0.41
13:N:63:ARG:NE	13:N:131:GLU:OE2	2.53	0.41
45:5:691:C:H2'	45:5:692:A:C8	2.56	0.41
45:5:4052:C:H5''	48:K:212:LYS:H	1.85	0.41
45:5:4935:C:H2'	45:5:4936:G:C8	2.55	0.41
49:2:26:U:H2'	49:2:27:A:C8	2.56	0.41
49:2:1321:G:H2'	49:2:1322:G:C8	2.56	0.41
84:9:559:LYS:HA	84:9:562:GLU:HG2	2.02	0.41
1:A:123:ARG:NH2	45:5:4082:G:O2'	2.54	0.41
3:C:197:ARG:NH1	45:5:351:C:OP2	2.48	0.41
14:O:28:LEU:HD13	14:O:94:ARG:HH22	1.86	0.41
14:O:201:LEU:O	45:5:4872:G:N2	2.54	0.41
21:V:18:LEU:HD11	21:V:54:ALA:HB1	2.03	0.41
25:Z:9:LYS:HB2	25:Z:25:ILE:HD12	2.03	0.41
26:a:43:ILE:HD11	45:5:1674:C:H1'	2.03	0.41
27:b:36:ASP:OD1	27:b:36:ASP:N	2.54	0.41
29:d:49:ILE:HD13	29:d:68:LEU:HD21	2.01	0.41
33:h:93:ARG:HH21	45:5:18:C:H5'	1.86	0.41
45:5:82:U:O2'	45:5:1382:G:O2'	2.31	0.41
45:5:86:U:O2	45:5:99:A:N6	2.44	0.41
45:5:145:G:H2'	45:5:146:G:H8	1.85	0.41
45:5:740:G:N1	45:5:923:C:O2	2.54	0.41
45:5:1559:G:H2'	45:5:1560:A:H8	1.86	0.41
45:5:2009:A:C8	84:9:756:VAL:HG11	2.56	0.41
45:5:2501:C:H2'	45:5:2502:A:C8	2.56	0.41
45:5:3610:A:H2'	45:5:3611:A:C8	2.56	0.41
45:5:4123:C:O2'	45:5:4124:G:O4'	2.35	0.41
48:K:110:PHE:HZ	85:4:6039:A:H61	1.53	0.41
49:2:492:C:N4	49:2:507:G:OP2	2.44	0.41
51:CC:37:ALA:HB2	51:CC:42:ARG:HH22	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:EE:28:GLU:OE2	53:EE:65:ARG:NH2	2.54	0.41
56:HH:183:ARG:O	56:HH:187:HIS:ND1	2.53	0.41
60:LL:51:SER:O	60:LL:55:ARG:NH1	2.53	0.41
66:RR:128:GLU:OE2	66:RR:131:LYS:NZ	2.54	0.41
82:hh:212:LYS:HA	82:hh:235:ILE:HG13	2.02	0.41
84:9:150:ARG:NH1	84:9:200:MET:SD	2.94	0.41
84:9:182:VAL:HG13	84:9:205:ILE:HG23	2.03	0.41
85:4:6174:G:O6	85:4:6207:A:O3'	2.38	0.41
85:4:6200:A:C6	85:4:6201:C:N4	2.70	0.41
8:H:162:GLN:HE21	8:H:180:TYR:HD1	1.68	0.41
9:I:4:ARG:HA	9:I:5:PRO:HD3	1.87	0.41
30:e:128:ARG:NH2	45:5:2326:G:OP1	2.54	0.41
33:h:66:LYS:HE3	47:8:96:C:H4'	2.02	0.41
45:5:264:C:O2'	45:5:266:C:N4	2.41	0.41
45:5:1329:G:H2'	45:5:3865:A:H5'	2.03	0.41
45:5:1350:C:H2'	45:5:1351:G:C8	2.56	0.41
45:5:1828:C:H2'	45:5:1829:G:H8	1.86	0.41
45:5:4088:C:H2'	45:5:4089:G:H8	1.86	0.41
45:5:4243:C:OP2	45:5:4264:G:N1	2.50	0.41
46:7:114:U:H2'	46:7:115:A:C8	2.56	0.41
48:K:33:GLU:HG2	48:K:168:ALA:HA	2.03	0.41
49:2:13:C:H4'	49:2:1355:C:H1'	2.02	0.41
85:4:6071:A:C8	85:4:6072:U:C1'	3.04	0.41
2:B:2:SER:N	45:5:4517:A:N7	2.69	0.40
2:B:43:LEU:HD23	2:B:183:ILE:HD13	2.03	0.40
6:F:51:GLU:OE1	6:F:54:LYS:NZ	2.54	0.40
9:I:16:PRO:HD3	9:I:128:ARG:HH12	1.85	0.40
14:O:52:LEU:HA	14:O:55:LEU:HB2	2.02	0.40
22:W:22:ALA:HA	22:W:28:VAL:HG13	2.02	0.40
23:X:108:GLN:HE21	47:8:131:G:H5''	1.86	0.40
23:X:110:LYS:HG3	23:X:121:VAL:HB	2.03	0.40
37:l:22:PRO:HA	37:l:38:ASN:HD22	1.85	0.40
45:5:153:G:H2'	45:5:154:G:C8	2.55	0.40
45:5:1543:G:H2'	45:5:1544:G:H8	1.85	0.40
45:5:2734:U:H2'	45:5:2735:G:C8	2.56	0.40
45:5:4605:A:O2'	84:9:27:HIS:NE2	2.37	0.40
46:7:26:C:O2	46:7:56:G:N2	2.55	0.40
48:K:53:VAL:HG23	48:K:189:PHE:HB2	2.03	0.40
49:2:1597:C:OP2	75:aa:85:ARG:NH1	2.54	0.40
85:4:6066:G:H3'	85:4:6067:G:H2'	2.03	0.40
13:N:72:LYS:HB2	13:N:89:VAL:HG22	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:P:141:SER:OG	15:P:142:SER:N	2.55	0.40
16:Q:170:LYS:NZ	45:5:1389:U:OP2	2.53	0.40
19:T:75:VAL:HA	19:T:87:LYS:O	2.21	0.40
45:5:323:C:H2'	45:5:324:A:C8	2.56	0.40
45:5:2607:C:H2'	45:5:2608:G:H8	1.86	0.40
45:5:3943:A:H2'	45:5:3944:G:H8	1.85	0.40
49:2:430:C:H2'	49:2:431:G:C8	2.56	0.40
51:CC:106:THR:HG22	51:CC:108:ASP:H	1.86	0.40
67:SS:80:ARG:O	67:SS:84:TYR:HB2	2.22	0.40
83:3:35:G:C2	85:4:6218:U:N3	2.90	0.40
83:3:37:G:C2	85:4:6217:C:C1'	3.04	0.40
85:4:6164:C:OP2	85:4:6164:C:H6	2.04	0.40
10:J:57:VAL:HG12	10:J:59:SER:H	1.86	0.40
15:P:13:LYS:HE3	15:P:152:GLU:HB2	2.02	0.40
21:V:112:MET:HE1	21:V:135:ASN:HD22	1.85	0.40
28:c:90:ARG:NH1	41:p:42:CYS:O	2.54	0.40
45:5:4466:C:H2'	45:5:4467:A:H8	1.85	0.40
45:5:4949:G:H5''	45:5:4951:G:H5'	2.03	0.40
45:5:5005:G:H1'	45:5:5042:A:H61	1.87	0.40
49:2:106:C:H2'	49:2:107:A:H8	1.86	0.40
49:2:124:U:OP1	56:HH:201:LYS:NZ	2.54	0.40
49:2:906:U:H2'	49:2:907:G:C8	2.57	0.40
49:2:907:G:H2'	49:2:908:A:C8	2.55	0.40
49:2:1562:C:H2'	49:2:1563:G:C8	2.57	0.40
51:CC:146:ARG:HB2	51:CC:149:GLN:HB2	2.04	0.40
55:GG:18:LYS:HE2	66:RR:57:LEU:HD21	2.04	0.40
56:HH:77:LEU:HD12	56:HH:95:LYS:HB2	2.03	0.40
70:VV:54:VAL:HB	70:VV:88:LEU:HG	2.03	0.40
81:gg:132:MET:HE1	81:gg:148:TYR:HD2	1.85	0.40
85:4:6179:U:H4'	85:4:6179:U:OP1	2.21	0.40
85:4:6188:G:OP2	85:4:6188:G:C5	2.75	0.40
1:A:198:ARG:HH21	45:5:3688:U:H5''	1.86	0.40
2:B:229:LYS:HG3	2:B:272:LYS:HD3	2.03	0.40
2:B:239:LYS:HE3	2:B:249:ARG:HG2	2.04	0.40
14:O:78:ARG:NH2	45:5:4584:A:O2'	2.54	0.40
40:o:63:THR:O	40:o:87:ARG:NH1	2.54	0.40
45:5:1346:C:H2'	45:5:1347:G:H8	1.86	0.40
48:K:45:LYS:HZ3	85:4:6047:U:H4'	1.86	0.40
48:K:159:MET:HE3	85:4:6083:U:H5'	2.04	0.40
49:2:907:G:H2'	49:2:908:A:H8	1.86	0.40
49:2:1025:U:O2'	49:2:1160:U:O2'	2.31	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:2:1443:C:O3'	66:RR:15:ARG:NH2	2.55	0.40
57:II:63:PHE:HB3	57:II:97:GLN:HB2	2.03	0.40
57:II:95:ILE:HD13	57:II:129:ILE:HG23	2.04	0.40
76:bb:23:CYS:SG	76:bb:24:THR:N	2.94	0.40
84:9:421:VAL:HG23	84:9:425:LEU:HD13	2.03	0.40
85:4:6136:U:H5''	85:4:6136:U:H6	1.85	0.40
3:C:291:ARG:HA	3:C:294:LYS:HG2	2.03	0.40
11:L:197:LYS:NZ	45:5:4358:U:O3'	2.50	0.40
27:b:5:LYS:HE2	27:b:8:THR:HB	2.04	0.40
45:5:424:U:H3	47:8:10:G:H1	1.69	0.40
45:5:2029:A:H2'	45:5:2030:A:C8	2.57	0.40
49:2:479:C:N4	49:2:480:G:O6	2.54	0.40
49:2:687:C:O2'	57:II:116:ARG:NH2	2.54	0.40
49:2:957:A:H3'	49:2:958:G:N2	2.36	0.40
49:2:1705:C:H2'	49:2:1706:G:C8	2.57	0.40
49:2:1714:U:H2'	49:2:1715:A:H8	1.86	0.40
50:BB:63:ARG:HB3	71:WW:36:VAL:HG13	2.03	0.40
62:NN:49:LEU:HD21	62:NN:77:ILE:HG12	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	237/257 (92%)	223 (94%)	14 (6%)	0	100	100
2	B	392/403 (97%)	381 (97%)	11 (3%)	0	100	100
3	C	358/392 (91%)	341 (95%)	17 (5%)	0	100	100
4	D	291/297 (98%)	281 (97%)	10 (3%)	0	100	100
5	E	208/291 (72%)	198 (95%)	10 (5%)	0	100	100
6	F	223/249 (90%)	214 (96%)	9 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	G	229/242 (95%)	218 (95%)	11 (5%)	0	100	100
8	H	188/192 (98%)	176 (94%)	12 (6%)	0	100	100
9	I	201/214 (94%)	192 (96%)	9 (4%)	0	100	100
10	J	168/178 (94%)	165 (98%)	3 (2%)	0	100	100
11	L	208/211 (99%)	198 (95%)	10 (5%)	0	100	100
12	M	133/198 (67%)	128 (96%)	5 (4%)	0	100	100
13	N	201/204 (98%)	189 (94%)	12 (6%)	0	100	100
14	O	194/198 (98%)	186 (96%)	8 (4%)	0	100	100
15	P	151/187 (81%)	147 (97%)	4 (3%)	0	100	100
16	Q	185/187 (99%)	179 (97%)	6 (3%)	0	100	100
17	R	178/181 (98%)	174 (98%)	4 (2%)	0	100	100
18	S	174/176 (99%)	167 (96%)	7 (4%)	0	100	100
19	T	157/160 (98%)	150 (96%)	7 (4%)	0	100	100
20	U	97/99 (98%)	96 (99%)	1 (1%)	0	100	100
21	V	127/140 (91%)	123 (97%)	4 (3%)	0	100	100
22	W	102/157 (65%)	99 (97%)	3 (3%)	0	100	100
23	X	116/156 (74%)	109 (94%)	7 (6%)	0	100	100
24	Y	132/145 (91%)	129 (98%)	3 (2%)	0	100	100
25	Z	133/136 (98%)	123 (92%)	10 (8%)	0	100	100
26	a	145/148 (98%)	137 (94%)	8 (6%)	0	100	100
27	b	100/226 (44%)	99 (99%)	1 (1%)	0	100	100
28	c	96/115 (84%)	94 (98%)	2 (2%)	0	100	100
29	d	105/125 (84%)	97 (92%)	8 (8%)	0	100	100
30	e	126/135 (93%)	123 (98%)	3 (2%)	0	100	100
31	f	107/110 (97%)	98 (92%)	9 (8%)	0	100	100
32	g	112/126 (89%)	109 (97%)	3 (3%)	0	100	100
33	h	120/123 (98%)	118 (98%)	2 (2%)	0	100	100
34	i	100/105 (95%)	98 (98%)	2 (2%)	0	100	100
35	j	84/97 (87%)	79 (94%)	5 (6%)	0	100	100
36	k	67/69 (97%)	65 (97%)	2 (3%)	0	100	100
37	l	48/51 (94%)	45 (94%)	3 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
38	m	50/52 (96%)	47 (94%)	3 (6%)	0	100	100
39	n	23/25 (92%)	23 (100%)	0	0	100	100
40	o	102/106 (96%)	97 (95%)	5 (5%)	0	100	100
41	p	89/92 (97%)	86 (97%)	3 (3%)	0	100	100
42	r	122/137 (89%)	119 (98%)	3 (2%)	0	100	100
43	s	194/303 (64%)	186 (96%)	8 (4%)	0	100	100
44	t	151/195 (77%)	135 (89%)	16 (11%)	0	100	100
48	K	204/217 (94%)	182 (89%)	21 (10%)	1 (0%)	24	59
50	BB	215/217 (99%)	202 (94%)	13 (6%)	0	100	100
51	CC	211/264 (80%)	197 (93%)	14 (7%)	0	100	100
52	DD	219/221 (99%)	216 (99%)	3 (1%)	0	100	100
53	EE	226/281 (80%)	217 (96%)	9 (4%)	0	100	100
54	FF	260/262 (99%)	244 (94%)	16 (6%)	0	100	100
55	GG	181/204 (89%)	173 (96%)	8 (4%)	0	100	100
56	HH	235/249 (94%)	227 (97%)	8 (3%)	0	100	100
57	II	181/194 (93%)	173 (96%)	8 (4%)	0	100	100
58	JJ	204/206 (99%)	190 (93%)	14 (7%)	0	100	100
59	KK	183/194 (94%)	181 (99%)	2 (1%)	0	100	100
60	LL	94/149 (63%)	90 (96%)	4 (4%)	0	100	100
61	MM	139/158 (88%)	132 (95%)	7 (5%)	0	100	100
62	NN	115/132 (87%)	107 (93%)	8 (7%)	0	100	100
63	OO	147/151 (97%)	145 (99%)	2 (1%)	0	100	100
64	PP	134/151 (89%)	126 (94%)	8 (6%)	0	100	100
65	QQ	113/145 (78%)	102 (90%)	10 (9%)	1 (1%)	14	47
66	RR	140/172 (81%)	133 (95%)	7 (5%)	0	100	100
67	SS	130/135 (96%)	119 (92%)	11 (8%)	0	100	100
68	TT	142/152 (93%)	133 (94%)	9 (6%)	0	100	100
69	UU	139/145 (96%)	133 (96%)	6 (4%)	0	100	100
70	VV	98/119 (82%)	96 (98%)	2 (2%)	0	100	100
71	WW	81/83 (98%)	79 (98%)	2 (2%)	0	100	100
72	XX	127/130 (98%)	120 (94%)	7 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
73	YY	139/143 (97%)	131 (94%)	7 (5%)	1 (1%)	18	52
74	ZZ	122/134 (91%)	120 (98%)	2 (2%)	0	100	100
75	aa	73/125 (58%)	72 (99%)	1 (1%)	0	100	100
76	bb	99/101 (98%)	92 (93%)	7 (7%)	0	100	100
77	cc	81/84 (96%)	78 (96%)	3 (4%)	0	100	100
78	dd	60/69 (87%)	60 (100%)	0	0	100	100
79	ee	53/56 (95%)	48 (91%)	5 (9%)	0	100	100
80	ff	55/133 (41%)	49 (89%)	6 (11%)	0	100	100
81	gg	66/156 (42%)	63 (96%)	3 (4%)	0	100	100
82	hh	310/317 (98%)	292 (94%)	18 (6%)	0	100	100
84	9	854/856 (100%)	801 (94%)	53 (6%)	0	100	100
All	All	12554/14095 (89%)	11964 (95%)	587 (5%)	3 (0%)	100	100

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
48	K	59	PRO
73	YY	62	PRO
65	QQ	19	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	172/199 (86%)	172 (100%)	0	100	100
2	B	342/348 (98%)	342 (100%)	0	100	100
3	C	302/323 (94%)	302 (100%)	0	100	100
4	D	247/250 (99%)	247 (100%)	0	100	100
5	E	190/251 (76%)	190 (100%)	0	100	100
6	F	196/218 (90%)	196 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	G	200/208 (96%)	200 (100%)	0	100	100
8	H	169/171 (99%)	169 (100%)	0	100	100
9	I	175/181 (97%)	175 (100%)	0	100	100
10	J	143/149 (96%)	143 (100%)	0	100	100
11	L	175/176 (99%)	175 (100%)	0	100	100
12	M	116/151 (77%)	116 (100%)	0	100	100
13	N	171/172 (99%)	171 (100%)	0	100	100
14	O	170/170 (100%)	170 (100%)	0	100	100
15	P	134/165 (81%)	134 (100%)	0	100	100
16	Q	164/164 (100%)	164 (100%)	0	100	100
17	R	159/160 (99%)	159 (100%)	0	100	100
18	S	157/157 (100%)	157 (100%)	0	100	100
19	T	139/140 (99%)	139 (100%)	0	100	100
20	U	89/89 (100%)	89 (100%)	0	100	100
21	V	100/107 (94%)	100 (100%)	0	100	100
22	W	86/126 (68%)	86 (100%)	0	100	100
23	X	106/134 (79%)	106 (100%)	0	100	100
24	Y	124/135 (92%)	124 (100%)	0	100	100
25	Z	117/118 (99%)	117 (100%)	0	100	100
26	a	119/120 (99%)	119 (100%)	0	100	100
27	b	84/172 (49%)	83 (99%)	1 (1%)	63	79
28	c	84/98 (86%)	84 (100%)	0	100	100
29	d	98/110 (89%)	98 (100%)	0	100	100
30	e	114/121 (94%)	114 (100%)	0	100	100
31	f	88/89 (99%)	88 (100%)	0	100	100
32	g	98/106 (92%)	98 (100%)	0	100	100
33	h	109/110 (99%)	109 (100%)	0	100	100
34	i	86/89 (97%)	86 (100%)	0	100	100
35	j	73/80 (91%)	73 (100%)	0	100	100
36	k	64/64 (100%)	64 (100%)	0	100	100
37	l	47/48 (98%)	47 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
38	m	48/48 (100%)	48 (100%)	0	100	100
39	n	24/24 (100%)	24 (100%)	0	100	100
40	o	92/94 (98%)	92 (100%)	0	100	100
41	p	74/75 (99%)	74 (100%)	0	100	100
42	r	108/121 (89%)	108 (100%)	0	100	100
43	s	164/258 (64%)	164 (100%)	0	100	100
44	t	126/163 (77%)	126 (100%)	0	100	100
48	K	190/196 (97%)	190 (100%)	0	100	100
50	BB	180/181 (99%)	180 (100%)	0	100	100
51	CC	194/231 (84%)	194 (100%)	0	100	100
52	DD	187/187 (100%)	187 (100%)	0	100	100
53	EE	190/232 (82%)	190 (100%)	0	100	100
54	FF	224/224 (100%)	224 (100%)	0	100	100
55	GG	158/170 (93%)	158 (100%)	0	100	100
56	HH	207/218 (95%)	207 (100%)	0	100	100
57	II	165/174 (95%)	165 (100%)	0	100	100
58	JJ	178/178 (100%)	178 (100%)	0	100	100
59	KK	161/168 (96%)	161 (100%)	0	100	100
60	LL	87/125 (70%)	87 (100%)	0	100	100
61	MM	130/142 (92%)	129 (99%)	1 (1%)	73	82
62	NN	99/108 (92%)	99 (100%)	0	100	100
63	OO	130/131 (99%)	130 (100%)	0	100	100
64	PP	106/119 (89%)	106 (100%)	0	100	100
65	QQ	105/130 (81%)	105 (100%)	0	100	100
66	RR	117/140 (84%)	117 (100%)	0	100	100
67	SS	119/121 (98%)	119 (100%)	0	100	100
68	TT	125/132 (95%)	125 (100%)	0	100	100
69	UU	111/116 (96%)	111 (100%)	0	100	100
70	VV	92/107 (86%)	92 (100%)	0	100	100
71	WW	67/67 (100%)	67 (100%)	0	100	100
72	XX	112/113 (99%)	112 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
73	YY	113/114 (99%)	113 (100%)	0	100	100
74	ZZ	107/115 (93%)	107 (100%)	0	100	100
75	aa	66/103 (64%)	66 (100%)	0	100	100
76	bb	88/88 (100%)	88 (100%)	0	100	100
77	cc	75/76 (99%)	75 (100%)	0	100	100
78	dd	55/62 (89%)	55 (100%)	0	100	100
79	ee	48/49 (98%)	48 (100%)	0	100	100
80	ff	47/106 (44%)	47 (100%)	0	100	100
81	gg	61/140 (44%)	61 (100%)	0	100	100
82	hh	272/275 (99%)	272 (100%)	0	100	100
84	9	728/728 (100%)	727 (100%)	1 (0%)	88	91
All	All	10937/12018 (91%)	10934 (100%)	3 (0%)	100	100

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
27	b	72	ILE
61	MM	42	LEU
84	9	158	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (195) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	22	HIS
1	A	50	HIS
1	A	86	GLN
1	A	139	HIS
1	A	140	ASN
1	A	194	ASN
1	A	205	ASN
1	A	209	HIS
2	B	42	HIS
2	B	203	GLN
2	B	258	HIS
2	B	271	GLN
2	B	315	ASN
3	C	41	HIS

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Mol	Chain	Res	Type
3	C	60	HIS
3	C	85	HIS
3	C	112	HIS
3	C	203	GLN
3	C	245	HIS
3	C	278	ASN
3	C	282	HIS
4	D	202	GLN
5	E	160	HIS
5	E	193	HIS
5	E	253	GLN
5	E	287	HIS
6	F	79	ASN
6	F	109	GLN
6	F	205	ASN
7	G	99	GLN
7	G	153	HIS
7	G	165	GLN
7	G	206	GLN
7	G	259	GLN
7	G	293	ASN
8	H	15	ASN
8	H	42	ASN
8	H	98	HIS
8	H	102	ASN
8	H	106	GLN
8	H	162	GLN
8	H	163	GLN
9	I	95	HIS
9	I	100	ASN
10	J	104	ASN
10	J	155	HIS
11	L	15	HIS
11	L	104	ASN
11	L	159	ASN
12	M	48	GLN
13	N	57	GLN
14	O	143	HIS
14	O	150	GLN
14	O	184	ASN
15	P	34	GLN
15	P	80	GLN

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Mol	Chain	Res	Type
15	P	97	ASN
15	P	120	ASN
17	R	7	GLN
17	R	36	ASN
17	R	58	HIS
17	R	141	HIS
19	T	3	ASN
19	T	49	GLN
19	T	58	HIS
19	T	79	GLN
20	U	17	GLN
20	U	94	ASN
21	V	77	HIS
21	V	84	GLN
21	V	135	ASN
22	W	30	GLN
23	X	111	GLN
24	Y	61	HIS
24	Y	65	GLN
25	Z	79	HIS
26	a	44	ASN
26	a	60	HIS
27	b	60	ASN
27	b	61	ASN
28	c	51	ASN
28	c	72	HIS
29	d	18	ASN
29	d	118	GLN
30	e	52	GLN
31	f	24	HIS
31	f	80	ASN
31	f	99	HIS
32	g	114	GLN
34	i	26	HIS
34	i	80	HIS
35	j	66	HIS
36	k	28	ASN
37	l	19	GLN
37	l	38	ASN
42	r	6	GLN
42	r	103	HIS
42	r	121	GLN

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Mol	Chain	Res	Type
43	s	42	GLN
43	s	68	HIS
43	s	191	GLN
44	t	100	HIS
44	t	137	GLN
48	K	143	ASN
48	K	158	GLN
48	K	182	ASN
50	BB	29	ASN
50	BB	50	ASN
50	BB	81	ASN
50	BB	84	GLN
50	BB	111	GLN
50	BB	113	GLN
50	BB	141	ASN
51	CC	40	ASN
51	CC	118	GLN
51	CC	147	ASN
52	DD	115	GLN
53	EE	57	ASN
53	EE	145	GLN
54	FF	142	HIS
54	FF	201	HIS
54	FF	232	ASN
55	GG	29	GLN
55	GG	79	HIS
56	HH	13	GLN
56	HH	59	GLN
56	HH	65	GLN
57	II	91	HIS
57	II	97	GLN
57	II	186	ASN
57	II	193	GLN
58	JJ	99	ASN
58	JJ	165	GLN
59	KK	143	ASN
60	LL	50	GLN
60	LL	61	GLN
61	MM	19	ASN
61	MM	83	GLN
61	MM	100	ASN
62	NN	72	HIS

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Mol	Chain	Res	Type
62	NN	73	GLN
63	OO	49	GLN
63	OO	62	GLN
63	OO	101	HIS
63	OO	105	ASN
64	PP	94	HIS
66	RR	86	GLN
66	RR	97	GLN
67	SS	74	GLN
67	SS	83	ASN
68	TT	72	GLN
68	TT	101	ASN
68	TT	120	HIS
68	TT	135	HIS
69	UU	11	GLN
69	UU	51	ASN
70	VV	47	ASN
70	VV	81	GLN
70	VV	92	HIS
71	WW	21	ASN
71	WW	35	ASN
71	WW	82	ASN
72	XX	5	ASN
72	XX	15	ASN
72	XX	16	ASN
72	XX	91	ASN
72	XX	113	HIS
73	YY	20	GLN
73	YY	77	ASN
73	YY	127	ASN
74	ZZ	19	GLN
77	cc	84	HIS
80	ff	117	ASN
82	hh	133	ASN
82	hh	159	ASN
82	hh	178	ASN
82	hh	305	ASN
84	9	3	ASN
84	9	18	ASN
84	9	21	ASN
84	9	30	HIS
84	9	101	ASN

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Mol	Chain	Res	Type
84	9	138	GLN
84	9	145	GLN
84	9	158	ASN
84	9	179	GLN
84	9	291	GLN
84	9	468	ASN
84	9	493	ASN
84	9	597	ASN
84	9	600	ASN
84	9	670	GLN
84	9	696	ASN
84	9	811	GLN
84	9	827	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
45	5	3562/3594 (99%)	902 (25%)	29 (0%)
46	7	118/119 (99%)	16 (13%)	0
47	8	149/151 (98%)	37 (24%)	1 (0%)
49	2	1679/1697 (98%)	409 (24%)	14 (0%)
83	3	86/87 (98%)	25 (29%)	0
85	4	188/190 (98%)	124 (65%)	48 (25%)
All	All	5782/5838 (99%)	1513 (26%)	92 (1%)

All (1513) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
45	5	5	A
45	5	7	C
45	5	11	G
45	5	12	A
45	5	14	C
45	5	21	G
45	5	25	A
45	5	36	U
45	5	39	A
45	5	42	A
45	5	48	G
45	5	49	U
45	5	56	A

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Mol	Chain	Res	Type
45	5	58	G
45	5	59	A
45	5	64	A
45	5	65	A
45	5	67	C
45	5	70	A
45	5	72	C
45	5	73	A
45	5	74	G
45	5	75	G
45	5	84	A
45	5	85	G
45	5	91	G
45	5	92	C
45	5	93	G
45	5	98	A
45	5	105	A
45	5	109	G
45	5	110	C
45	5	116	G
45	5	117	C
45	5	118	C
45	5	119	G
45	5	120	A
45	5	122	U
45	5	123	C
45	5	126	C
45	5	131	C
45	5	132	G
45	5	134	G
45	5	135	G
45	5	136	C
45	5	140	G
45	5	142	G
45	5	143	C
45	5	144	G
45	5	157	U
45	5	158	A
45	5	159	C
45	5	169	A
45	5	172	C
45	5	173	C

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Mol	Chain	Res	Type
45	5	174	C
45	5	193	G
45	5	194	C
45	5	197	A
45	5	200	U
45	5	201	C
45	5	209	U
45	5	216	C
45	5	217	C
45	5	218	A
45	5	220	C
45	5	224	U
45	5	225	G
45	5	232	G
45	5	233	U
45	5	234	G
45	5	244	G
45	5	256	G
45	5	265	C
45	5	266	C
45	5	274	C
45	5	276	C
45	5	278	G
45	5	279	A
45	5	280	G
45	5	295	A
45	5	297	U
45	5	306	A
45	5	308	G
45	5	309	C
45	5	315	G
45	5	316	U
45	5	321	U
45	5	326	C
45	5	334	A
45	5	336	A
45	5	340	C
45	5	344	A
45	5	345	C
45	5	349	A
45	5	350	C
45	5	355	A

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Mol	Chain	Res	Type
45	5	357	U
45	5	360	A
45	5	361	C
45	5	363	A
45	5	364	G
45	5	365	U
45	5	381	U
45	5	386	A
45	5	387	G
45	5	410	A
45	5	412	G
45	5	413	G
45	5	415	G
45	5	418	A
45	5	431	G
45	5	432	U
45	5	433	A
45	5	440	U
45	5	446	C
45	5	448	G
45	5	449	C
45	5	450	G
45	5	452	A
45	5	453	G
45	5	454	U
45	5	455	C
45	5	463	A
45	5	464	G
45	5	467	U
45	5	468	U
45	5	481	G
45	5	482	G
45	5	483	G
45	5	485	C
45	5	492	U
45	5	493	G
45	5	499	G
45	5	505	G
45	5	510	U
45	5	518	G
45	5	643	C
45	5	666	G

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Mol	Chain	Res	Type
45	5	668	C
45	5	677	G
45	5	685	C
45	5	686	A
45	5	691	C
45	5	696	C
45	5	697	G
45	5	704	C
45	5	729	G
45	5	731	G
45	5	733	A
45	5	739	G
45	5	743	G
45	5	749	G
45	5	750	U
45	5	751	G
45	5	758	G
45	5	760	G
45	5	905	C
45	5	907	C
45	5	913	U
45	5	914	U
45	5	915	A
45	5	917	A
45	5	918	G
45	5	924	C
45	5	925	C
45	5	926	G
45	5	927	G
45	5	928	C
45	5	931	C
45	5	932	A
45	5	933	G
45	5	934	C
45	5	935	A
45	5	935(A)	G
45	5	936	C
45	5	941	C
45	5	943	A
45	5	944	A
45	5	945	U
45	5	946	C

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Mol	Chain	Res	Type
45	5	958	G
45	5	959	G
45	5	960	A
45	5	962	C
45	5	963	G
45	5	964	A
45	5	966	A
45	5	967	C
45	5	968	C
45	5	969	C
45	5	970	G
45	5	979	C
45	5	983	C
45	5	990	C
45	5	1067	G
45	5	1071	C
45	5	1072	C
45	5	1073	G
45	5	1081	C
45	5	1084	C
45	5	1093	C
45	5	1168	G
45	5	1179	U
45	5	1180	C
45	5	1193	C
45	5	1194	G
45	5	1195	G
45	5	1204	C
45	5	1211	G
45	5	1212	G
45	5	1214	C
45	5	1215	C
45	5	1216	C
45	5	1234	G
45	5	1235	G
45	5	1236	C
45	5	1238	A
45	5	1245	C
45	5	1246	G
45	5	1249	C
45	5	1272	C
45	5	1273	G

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Mol	Chain	Res	Type
45	5	1275	G
45	5	1276	C
45	5	1284	G
45	5	1287	G
45	5	1288	G
45	5	1289	C
45	5	1291	G
45	5	1292	C
45	5	1296	G
45	5	1301	C
45	5	1314	C
45	5	1316	G
45	5	1322	A
45	5	1325	C
45	5	1326	A
45	5	1338	G
45	5	1354	A
45	5	1358	G
45	5	1359	G
45	5	1360	G
45	5	1370	G
45	5	1371	A
45	5	1377	G
45	5	1379	C
45	5	1380	G
45	5	1381	U
45	5	1382	G
45	5	1387	A
45	5	1390	G
45	5	1394	G
45	5	1397	A
45	5	1398	A
45	5	1411(C)	C
45	5	1412	G
45	5	1415	G
45	5	1420	A
45	5	1432	G
45	5	1438	U
45	5	1443	A
45	5	1445	U
45	5	1446	C
45	5	1456	C

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Mol	Chain	Res	Type
45	5	1457	G
45	5	1465	G
45	5	1475	G
45	5	1478	C
45	5	1480	C
45	5	1481	C
45	5	1482	G
45	5	1483	C
45	5	1484	G
45	5	1497	A
45	5	1498	G
45	5	1499	C
45	5	1501	C
45	5	1503	A
45	5	1518	A
45	5	1519	C
45	5	1523	A
45	5	1534	A
45	5	1547	A
45	5	1566	C
45	5	1574	G
45	5	1575	A
45	5	1577	G
45	5	1578	U
45	5	1586	G
45	5	1591	U
45	5	1596	U
45	5	1598	C
45	5	1600	A
45	5	1602	U
45	5	1607	C
45	5	1611	C
45	5	1612	G
45	5	1613	A
45	5	1624	G
45	5	1625	G
45	5	1631	A
45	5	1633	G
45	5	1634	A
45	5	1638	A
45	5	1639	U
45	5	1641	G

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Mol	Chain	Res	Type
45	5	1649	U
45	5	1650	A
45	5	1651	G
45	5	1654	G
45	5	1655	C
45	5	1660	U
45	5	1661	C
45	5	1671	U
45	5	1676	C
45	5	1679	A
45	5	1680	G
45	5	1691	G
45	5	1724	G
45	5	1725	U
45	5	1729	A
45	5	1731	C
45	5	1733	G
45	5	1734	G
45	5	1741	G
45	5	1742	A
45	5	1753	G
45	5	1755	C
45	5	1756	U
45	5	1757	U
45	5	1758	G
45	5	1760	G
45	5	1761	G
45	5	1764	G
45	5	1766	A
45	5	1768	C
45	5	1769	G
45	5	1772	C
45	5	1776	A
45	5	1781	U
45	5	1787	A
45	5	1790	U
45	5	1803	G
45	5	1804	A
45	5	1805	A
45	5	1812	C
45	5	1815	G
45	5	1818	G

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Mol	Chain	Res	Type
45	5	1819	G
45	5	1821	G
45	5	1822	U
45	5	1827	C
45	5	1828	C
45	5	1830	G
45	5	1833	G
45	5	1836	G
45	5	1837	A
45	5	1842	G
45	5	1854	G
45	5	1855	G
45	5	1878	G
45	5	1881	C
45	5	1882	U
45	5	1891	A
45	5	1893	C
45	5	1897	A
45	5	1910	G
45	5	1912	G
45	5	1915	C
45	5	1916	G
45	5	1918	U
45	5	1920	C
45	5	1921	C
45	5	1922	G
45	5	1925	G
45	5	1928	C
45	5	1929	A
45	5	1931	C
45	5	1933	G
45	5	1936	C
45	5	1945	G
45	5	1947	U
45	5	1951	G
45	5	1956	A
45	5	1960	A
45	5	1961	G
45	5	1962	A
45	5	1964	A
45	5	1969	G
45	5	1971	U

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Mol	Chain	Res	Type
45	5	1972	G
45	5	1975	G
45	5	1982	G
45	5	1984	A
45	5	1985	G
45	5	1991	A
45	5	1992	U
45	5	1996	C
45	5	1997	U
45	5	1998	A
45	5	2001	G
45	5	2002	A
45	5	2003	G
45	5	2004	U
45	5	2011	C
45	5	2018	C
45	5	2025	A
45	5	2026	A
45	5	2031	C
45	5	2033	A
45	5	2034	G
45	5	2041	A
45	5	2042	A
45	5	2044	U
45	5	2045	G
45	5	2047	A
45	5	2048	U
45	5	2055	G
45	5	2056	G
45	5	2062	C
45	5	2069	A
45	5	2070	U
45	5	2073	C
45	5	2084	U
45	5	2085	G
45	5	2088	A
45	5	2090	U
45	5	2093	G
45	5	2094	C
45	5	2097	A
45	5	2099	C
45	5	2100	G

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Mol	Chain	Res	Type
45	5	2102	G
45	5	2104	A
45	5	2105	A
45	5	2107	A
45	5	2108	G
45	5	2259	G
45	5	2260	C
45	5	2267	U
45	5	2268	A
45	5	2289	C
45	5	2300	A
45	5	2301	G
45	5	2306	G
45	5	2313	A
45	5	2314	G
45	5	2316	G
45	5	2318	G
45	5	2325	C
45	5	2331	G
45	5	2333	G
45	5	2348	G
45	5	2351	C
45	5	2360	A
45	5	2369	U
45	5	2382	A
45	5	2395	A
45	5	2402	G
45	5	2410	C
45	5	2416	G
45	5	2422	C
45	5	2424	G
45	5	2425	U
45	5	2428	A
45	5	2432	U
45	5	2433	G
45	5	2442	G
45	5	2467	U
45	5	2469	C
45	5	2475	G
45	5	2483	G
45	5	2485	U
45	5	2486	G

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Mol	Chain	Res	Type
45	5	2488	C
45	5	2489	C
45	5	2490	U
45	5	2491	C
45	5	2492	C
45	5	2493	G
45	5	2494	U
45	5	2503	G
45	5	2504	C
45	5	2505	C
45	5	2506	G
45	5	2513	A
45	5	2516	G
45	5	2517	A
45	5	2520	C
45	5	2529	A
45	5	2530	U
45	5	2537	A
45	5	2544	G
45	5	2546	G
45	5	2547	G
45	5	2551	A
45	5	2552	G
45	5	2553	A
45	5	2560	C
45	5	2569	G
45	5	2572	C
45	5	2575	U
45	5	2576	G
45	5	2582	A
45	5	2583	C
45	5	2589	C
45	5	2600	A
45	5	2602	G
45	5	2623	A
45	5	2628	U
45	5	2632	U
45	5	2638	G
45	5	2647	A
45	5	2654	C
45	5	2657	G
45	5	2658	G

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Mol	Chain	Res	Type
45	5	2660	A
45	5	2661	U
45	5	2662	G
45	5	2669	C
45	5	2675	G
45	5	2681	G
45	5	2683	C
45	5	2687	U
45	5	2694	G
45	5	2695	A
45	5	2696	A
45	5	2700	G
45	5	2708	U
45	5	2709	C
45	5	2710	C
45	5	2711	G
45	5	2712	G
45	5	2714	G
45	5	2719	C
45	5	2726	G
45	5	2740	U
45	5	2743	A
45	5	2752	G
45	5	2753	G
45	5	2754	G
45	5	2756	G
45	5	2758	G
45	5	2761	U
45	5	2764	A
45	5	2768	C
45	5	2769	U
45	5	2772	C
45	5	2787	A
45	5	2788	U
45	5	2789	A
45	5	2790	U
45	5	2794	C
45	5	2795	A
45	5	2796	G
45	5	2798	A
45	5	2799	G
45	5	2807	A

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Mol	Chain	Res	Type
45	5	2811	G
45	5	2814	C
45	5	2825	A
45	5	2826	U
45	5	2827	G
45	5	2828	U
45	5	2833	A
45	5	2835	A
45	5	2837	U
45	5	2839	U
45	5	2842	G
45	5	2849	A
45	5	2853	C
45	5	2855	G
45	5	2857	A
45	5	2874	U
45	5	2875	C
45	5	2876	G
45	5	2880	U
45	5	2883	G
45	5	2884	G
45	5	2888	G
45	5	2897	G
45	5	2898	G
45	5	3598	C
45	5	3599	A
45	5	3603	G
45	5	3604	A
45	5	3616	U
45	5	3618	C
45	5	3619	G
45	5	3620	G
45	5	3621	A
45	5	3625	G
45	5	3626	G
45	5	3635	A
45	5	3639	U
45	5	3643	A
45	5	3646	A
45	5	3647	A
45	5	3657	U
45	5	3662	A

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Mol	Chain	Res	Type
45	5	3664	G
45	5	3673	C
45	5	3678	G
45	5	3680	U
45	5	3688	U
45	5	3692	A
45	5	3698	G
45	5	3711	A
45	5	3727	A
45	5	3729	U
45	5	3747	A
45	5	3748	A
45	5	3753	G
45	5	3759	A
45	5	3760	A
45	5	3763	A
45	5	3772	U
45	5	3773	U
45	5	3775	A
45	5	3776	G
45	5	3777	G
45	5	3778	U
45	5	3783	A
45	5	3784	A
45	5	3785	A
45	5	3790	U
45	5	3791	C
45	5	3793	U
45	5	3795	A
45	5	3798	U
45	5	3802	U
45	5	3808	C
45	5	3810	C
45	5	3812	C
45	5	3814	U
45	5	3817	A
45	5	3818	U
45	5	3819	G
45	5	3825	A
45	5	3828	A
45	5	3829	G
45	5	3830	A

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Mol	Chain	Res	Type
45	5	3839	G
45	5	3840	U
45	5	3843	C
45	5	3851	U
45	5	3852	A
45	5	3868	G
45	5	3869	C
45	5	3876	A
45	5	3877	A
45	5	3878	C
45	5	3879	G
45	5	3880	G
45	5	3889	G
45	5	3890	A
45	5	3897	G
45	5	3898	G
45	5	3901	A
45	5	3905	A
45	5	3906	A
45	5	3907	G
45	5	3914	U
45	5	3915	U
45	5	3917	A
45	5	3924	C
45	5	3926	C
45	5	3927	U
45	5	3938	G
45	5	3939	G
45	5	3956	G
45	5	3957	U
45	5	3958	G
45	5	3964	U
45	5	3965	A
45	5	3966	A
45	5	3968	U
45	5	3970	G
45	5	3972	A
45	5	3973	G
45	5	3975	C
45	5	4036	G
45	5	4040	C
45	5	4041	C

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Mol	Chain	Res	Type
45	5	4045	G
45	5	4048	A
45	5	4049	U
45	5	4050	A
45	5	4052	C
45	5	4053	A
45	5	4055	U
45	5	4063	U
45	5	4064	C
45	5	4065	G
45	5	4072	C
45	5	4073	A
45	5	4074	C
45	5	4075	U
45	5	4076	G
45	5	4085	A
45	5	4086	G
45	5	4116	C
45	5	4119	C
45	5	4120	U
45	5	4125	C
45	5	4127	A
45	5	4131	G
45	5	4148	C
45	5	4157	A
45	5	4158	C
45	5	4162	C
45	5	4163	U
45	5	4164	C
45	5	4170	A
45	5	4171	C
45	5	4183	G
45	5	4184	G
45	5	4191	G
45	5	4194	U
45	5	4197	G
45	5	4203	A
45	5	4205	A
45	5	4213	A
45	5	4225	G
45	5	4229	U
45	5	4233	A

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Mol	Chain	Res	Type
45	5	4234	A
45	5	4235	G
45	5	4249	G
45	5	4251	A
45	5	4253	A
45	5	4254	G
45	5	4260	U
45	5	4263	C
45	5	4265	U
45	5	4266	G
45	5	4268	A
45	5	4271	A
45	5	4273	A
45	5	4281	A
45	5	4282	A
45	5	4290	U
45	5	4291	G
45	5	4293	U
45	5	4297	G
45	5	4302	U
45	5	4304	A
45	5	4305	G
45	5	4313	A
45	5	4315	A
45	5	4317	A
45	5	4326	G
45	5	4330	G
45	5	4332	C
45	5	4335	C
45	5	4336	A
45	5	4339	A
45	5	4349	C
45	5	4350	C
45	5	4354	U
45	5	4355	G
45	5	4360	U
45	5	4373	G
45	5	4375	C
45	5	4376	A
45	5	4377	G
45	5	4378	A
45	5	4381	A

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Mol	Chain	Res	Type
45	5	4387	C
45	5	4393	G
45	5	4394	A
45	5	4395	U
45	5	4398	C
45	5	4401	G
45	5	4419	U
45	5	4421	C
45	5	4422	A
45	5	4424	A
45	5	4426	C
45	5	4430	G
45	5	4436	U
45	5	4437	U
45	5	4448	G
45	5	4449	A
45	5	4452	U
45	5	4464	A
45	5	4466	C
45	5	4477	A
45	5	4478	G
45	5	4482	U
45	5	4483	C
45	5	4493	U
45	5	4500	U
45	5	4511	A
45	5	4512	U
45	5	4513	A
45	5	4518	A
45	5	4525	C
45	5	4527	G
45	5	4542	U
45	5	4548	A
45	5	4560	C
45	5	4569	U
45	5	4573	G
45	5	4574	U
45	5	4575	G
45	5	4577	U
45	5	4581	G
45	5	4585	U
45	5	4590	A

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Mol	Chain	Res	Type
45	5	4592	C
45	5	4599	A
45	5	4616	A
45	5	4617	G
45	5	4636	U
45	5	4637	G
45	5	4652	G
45	5	4657	U
45	5	4658	G
45	5	4667	C
45	5	4670	C
45	5	4672	A
45	5	4677	U
45	5	4678	G
45	5	4687	A
45	5	4691	A
45	5	4694	G
45	5	4698	C
45	5	4700	A
45	5	4709	U
45	5	4719	G
45	5	4720	C
45	5	4721	G
45	5	4728	U
45	5	4736	C
45	5	4738	C
45	5	4739	C
45	5	4745	G
45	5	4754	G
45	5	4756	C
45	5	4757	C
45	5	4759	C
45	5	4765	G
45	5	4769	G
45	5	4771	C
45	5	4773	C
45	5	4775	C
45	5	4863	G
45	5	4865	C
45	5	4867	G
45	5	4870	G
45	5	4871	C

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Mol	Chain	Res	Type
45	5	4872	G
45	5	4875	G
45	5	4876	A
45	5	4877	G
45	5	4882	U
45	5	4883	C
45	5	4885	U
45	5	4891	G
45	5	4895	C
45	5	4896	G
45	5	4910	A
45	5	4911	A
45	5	4912	G
45	5	4914	G
45	5	4915	G
45	5	4921	C
45	5	4924	C
45	5	4926	C
45	5	4931	G
45	5	4937	C
45	5	4943	A
45	5	4944	C
45	5	4947	U
45	5	4948	C
45	5	4949	G
45	5	4951	G
45	5	4955	A
45	5	4956	A
45	5	4958	C
45	5	4965	U
45	5	4966	A
45	5	4975	G
45	5	4976	U
45	5	4988	U
45	5	4989	U
45	5	4990	C
45	5	4999	G
45	5	5005	G
45	5	5006	U
45	5	5014	A
45	5	5017	G
45	5	5040	U

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Mol	Chain	Res	Type
45	5	5041	G
45	5	5049	G
45	5	5050	C
45	5	5054	C
45	5	5061	A
45	5	5062	G
45	5	5066	U
46	7	7	G
46	7	33	U
46	7	41	G
46	7	50	A
46	7	53	U
46	7	54	A
46	7	63	C
46	7	64	G
46	7	74	A
46	7	76	U
46	7	84	U
46	7	85	G
46	7	97	G
46	7	100	A
46	7	110	G
46	7	117	G
47	8	2	G
47	8	3	A
47	8	14	U
47	8	16	G
47	8	23	C
47	8	34	U
47	8	35	C
47	8	38	U
47	8	46	G
47	8	51	U
47	8	52	A
47	8	59	A
47	8	62	A
47	8	63	U
47	8	71	A
47	8	72	A
47	8	78	G
47	8	86	U
47	8	87	G

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Mol	Chain	Res	Type
47	8	88	A
47	8	90	C
47	8	94	G
47	8	95	A
47	8	103	A
47	8	105	C
47	8	110	U
47	8	111	U
47	8	114	G
47	8	123	U
47	8	125	C
47	8	126	C
47	8	127	U
47	8	135	C
47	8	137	A
47	8	147	G
47	8	150	C
47	8	151	G
49	2	2	A
49	2	3	C
49	2	4	C
49	2	9	U
49	2	14	C
49	2	20	G
49	2	25	A
49	2	26	U
49	2	37	C
49	2	41	G
49	2	42	A
49	2	45	A
49	2	46	A
49	2	47	G
49	2	55	U
49	2	56	G
49	2	62	G
49	2	64	A
49	2	67	C
49	2	68	A
49	2	69	C
49	2	71	G
49	2	74	G
49	2	75	G

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Mol	Chain	Res	Type
49	2	76	U
49	2	78	C
49	2	93	U
49	2	103	A
49	2	107	A
49	2	110	U
49	2	111	A
49	2	113	G
49	2	114	G
49	2	115	U
49	2	123	G
49	2	126	G
49	2	127	C
49	2	130	G
49	2	143	U
49	2	147	A
49	2	154	U
49	2	155	G
49	2	160	U
49	2	161	U
49	2	163	U
49	2	168	C
49	2	169	U
49	2	183	G
49	2	184	G
49	2	187	G
49	2	188	C
49	2	189	U
49	2	190	G
49	2	191	A
49	2	192	C
49	2	215	G
49	2	292	A
49	2	293	C
49	2	294	U
49	2	302	A
49	2	306	C
49	2	307	G
49	2	308	G
49	2	309	G
49	2	312	G
49	2	313	A

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Mol	Chain	Res	Type
49	2	314	U
49	2	315	C
49	2	317	C
49	2	318	A
49	2	319	C
49	2	332	G
49	2	347	G
49	2	351	G
49	2	356	C
49	2	357	C
49	2	361	U
49	2	362	C
49	2	364	A
49	2	367	U
49	2	368	U
49	2	370	G
49	2	371	A
49	2	383	G
49	2	384	U
49	2	385	G
49	2	386	C
49	2	390	C
49	2	398	A
49	2	399	C
49	2	400	C
49	2	407	G
49	2	408	A
49	2	409	C
49	2	417	C
49	2	418	A
49	2	426	A
49	2	429	C
49	2	434	G
49	2	448	A
49	2	449	A
49	2	450	C
49	2	452	G
49	2	465	A
49	2	466	G
49	2	471	G
49	2	472	C
49	2	473	A

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Mol	Chain	Res	Type
49	2	474	G
49	2	476	A
49	2	487	U
49	2	492	C
49	2	493	A
49	2	500	A
49	2	502	C
49	2	509	G
49	2	516	A
49	2	525	A
49	2	530	U
49	2	531	A
49	2	532	C
49	2	533	A
49	2	542	U
49	2	547	G
49	2	548	C
49	2	549	C
49	2	550	C
49	2	552	G
49	2	554	A
49	2	555	A
49	2	556	U
49	2	559	G
49	2	560	A
49	2	562	U
49	2	569	A
49	2	576	A
49	2	583	A
49	2	588	G
49	2	589	G
49	2	590	A
49	2	591	U
49	2	594	A
49	2	595	U
49	2	597	G
49	2	600	G
49	2	603	C
49	2	604	A
49	2	606	G
49	2	608	C
49	2	614	C

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Mol	Chain	Res	Type
49	2	617	G
49	2	621	C
49	2	627	U
49	2	628	A
49	2	629	A
49	2	642	U
49	2	643	A
49	2	655	A
49	2	656	G
49	2	657	U
49	2	658	U
49	2	661	U
49	2	662	G
49	2	664	A
49	2	668	A
49	2	671	A
49	2	672	A
49	2	673	G
49	2	684	G
49	2	688	U
49	2	689	U
49	2	696	G
49	2	752	G
49	2	753	C
49	2	754	G
49	2	799	U
49	2	811	A
49	2	821	G
49	2	822	U
49	2	824	C
49	2	827	A
49	2	830	A
49	2	847	A
49	2	852	G
49	2	853	C
49	2	870	A
49	2	871	U
49	2	872	A
49	2	873	G
49	2	875	A
49	2	879	C
49	2	882	U

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Mol	Chain	Res	Type
49	2	886	A
49	2	888	U
49	2	890	U
49	2	891	G
49	2	893	U
49	2	894	G
49	2	897	U
49	2	898	U
49	2	913	A
49	2	914	U
49	2	919	A
49	2	920	A
49	2	933	G
49	2	952	G
49	2	955	A
49	2	969	U
49	2	970	G
49	2	971	G
49	2	985	G
49	2	990	A
49	2	991	G
49	2	992	A
49	2	999	G
49	2	1002	U
49	2	1017	U
49	2	1023	A
49	2	1026	C
49	2	1034	A
49	2	1045	U
49	2	1055	A
49	2	1061	U
49	2	1073	U
49	2	1082	A
49	2	1083	A
49	2	1085	C
49	2	1086	G
49	2	1088	U
49	2	1114	U
49	2	1115	U
49	2	1116	C
49	2	1117	C
49	2	1123	C

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Mol	Chain	Res	Type
49	2	1133	A
49	2	1138	C
49	2	1139	C
49	2	1148	A
49	2	1149	A
49	2	1150	A
49	2	1153	C
49	2	1154	U
49	2	1155	U
49	2	1157	G
49	2	1161	U
49	2	1165	G
49	2	1166	G
49	2	1170	A
49	2	1194	A
49	2	1195	A
49	2	1204	A
49	2	1207	G
49	2	1208	A
49	2	1215	C
49	2	1216	C
49	2	1217	A
49	2	1227	G
49	2	1228	A
49	2	1236	G
49	2	1242	U
49	2	1250	A
49	2	1251	A
49	2	1253	A
49	2	1254	C
49	2	1256	G
49	2	1257	G
49	2	1259	A
49	2	1261	C
49	2	1264	C
49	2	1269	G
49	2	1273	C
49	2	1274	G
49	2	1275	G
49	2	1284	A
49	2	1285	G
49	2	1286	G

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Mol	Chain	Res	Type
49	2	1293	A
49	2	1294	G
49	2	1298	G
49	2	1299	A
49	2	1301	A
49	2	1302	G
49	2	1303	C
49	2	1306	U
49	2	1307	U
49	2	1308	U
49	2	1309	C
49	2	1314	U
49	2	1327	G
49	2	1333	U
49	2	1341	C
49	2	1342	U
49	2	1354	G
49	2	1356	G
49	2	1358	U
49	2	1364	U
49	2	1365	G
49	2	1371	U
49	2	1372	U
49	2	1374	C
49	2	1377	U
49	2	1378	A
49	2	1390	U
49	2	1396	A
49	2	1397	U
49	2	1402	A
49	2	1404	U
49	2	1406	G
49	2	1428	G
49	2	1429	G
49	2	1439	A
49	2	1442	U
49	2	1449	G
49	2	1452	A
49	2	1454	A
49	2	1462	U
49	2	1463	U
49	2	1466	G

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Mol	Chain	Res	Type
49	2	1475	G
49	2	1476	A
49	2	1477	U
49	2	1483	A
49	2	1489	A
49	2	1490	G
49	2	1492	U
49	2	1497	G
49	2	1498	A
49	2	1507	G
49	2	1508	A
49	2	1515	G
49	2	1520	G
49	2	1521	C
49	2	1533	A
49	2	1535	U
49	2	1536	G
49	2	1548	G
49	2	1551	U
49	2	1552	G
49	2	1553	C
49	2	1554	C
49	2	1556	A
49	2	1558	C
49	2	1560	U
49	2	1570	G
49	2	1573	G
49	2	1575	G
49	2	1578	U
49	2	1580	A
49	2	1584	G
49	2	1585	U
49	2	1588	A
49	2	1598	G
49	2	1601	A
49	2	1603	G
49	2	1604	G
49	2	1606	G
49	2	1621	U
49	2	1623	A
49	2	1637	A
49	2	1638	G

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Mol	Chain	Res	Type
49	2	1647	A
49	2	1648	G
49	2	1654	G
49	2	1661	A
49	2	1665	G
49	2	1671	G
49	2	1678	A
49	2	1680	G
49	2	1683	C
49	2	1689	C
49	2	1692	U
49	2	1693	G
49	2	1695	A
49	2	1696	C
49	2	1697	A
49	2	1700	C
49	2	1701	C
49	2	1702	G
49	2	1721	U
49	2	1722	G
49	2	1725	U
49	2	1726	G
49	2	1744	G
49	2	1748	G
49	2	1753	C
49	2	1756	C
49	2	1757	G
49	2	1773	C
49	2	1776	G
49	2	1781	A
49	2	1783	C
49	2	1823	A
49	2	1824	A
49	2	1825	A
49	2	1831	A
49	2	1833	C
49	2	1834	A
49	2	1835	A
49	2	1836	G
49	2	1838	U
49	2	1849	G
49	2	1851	A

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Mol	Chain	Res	Type
49	2	1852	C
49	2	1861	G
49	2	1862	G
49	2	1863	A
49	2	1865	C
49	2	1868	U
49	2	1869	A
83	3	8	U
83	3	9	G
83	3	10	G
83	3	13	G
83	3	16	U
83	3	17	U
83	3	18	G
83	3	19	G
83	3	20	U
83	3	21	A
83	3	22	G
83	3	23	A
83	3	24	C
83	3	26	C
83	3	46	G
83	3	49	C
83	3	51	A
83	3	54	G
83	3	55	G
83	3	58	U
83	3	71	U
83	3	77	C
83	3	82	G
83	3	85	C
83	3	86	C
85	4	6031	A
85	4	6032	A
85	4	6033	A
85	4	6036	G
85	4	6038	G
85	4	6040	U
85	4	6041	C
85	4	6042	U
85	4	6043	U
85	4	6044	G

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Mol	Chain	Res	Type
85	4	6048	G
85	4	6050	A
85	4	6052	A
85	4	6054	A
85	4	6056	A
85	4	6057	A
85	4	6058	U
85	4	6059	U
85	4	6060	U
85	4	6061	U
85	4	6062	G
85	4	6063	A
85	4	6064	G
85	4	6065	A
85	4	6066	G
85	4	6067	G
85	4	6068	U
85	4	6069	U
85	4	6072	U
85	4	6073	A
85	4	6074	A
85	4	6075	A
85	4	6076	U
85	4	6077	U
85	4	6081	A
85	4	6083	U
85	4	6084	A
85	4	6085	G
85	4	6087	G
85	4	6088	C
85	4	6090	A
85	4	6094	U
85	4	6097	U
85	4	6098	A
85	4	6099	U
85	4	6100	U
85	4	6101	U
85	4	6105	U
85	4	6106	U
85	4	6107	A
85	4	6108	G
85	4	6113	U

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Mol	Chain	Res	Type
85	4	6115	A
85	4	6116	G
85	4	6119	U
85	4	6121	A
85	4	6122	C
85	4	6123	G
85	4	6125	U
85	4	6126	C
85	4	6128	A
85	4	6129	G
85	4	6134	C
85	4	6136	U
85	4	6139	U
85	4	6140	G
85	4	6150	C
85	4	6151	A
85	4	6152	A
85	4	6154	A
85	4	6158	A
85	4	6162	A
85	4	6163	G
85	4	6164	C
85	4	6165	C
85	4	6166	C
85	4	6167	U
85	4	6168	C
85	4	6169	U
85	4	6170	C
85	4	6171	U
85	4	6172	G
85	4	6173	C
85	4	6174	G
85	4	6175	G
85	4	6176	U
85	4	6177	U
85	4	6178	U
85	4	6179	U
85	4	6180	U
85	4	6181	C
85	4	6182	A
85	4	6183	G
85	4	6184	A

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Mol	Chain	Res	Type
85	4	6185	U
85	4	6186	U
85	4	6187	A
85	4	6188	G
85	4	6189	G
85	4	6190	U
85	4	6191	A
85	4	6192	G
85	4	6193	U
85	4	6196	A
85	4	6197	A
85	4	6198	A
85	4	6199	A
85	4	6200	A
85	4	6202	C
85	4	6203	U
85	4	6204	A
85	4	6205	A
85	4	6206	G
85	4	6207	A
85	4	6208	A
85	4	6209	A
85	4	6210	U
85	4	6211	U
85	4	6212	U
85	4	6213	A
85	4	6214	C
85	4	6215	C
85	4	6216	U
85	4	6217	C

All (92) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
45	5	48	G
45	5	125	C
45	5	275	C
45	5	481	G
45	5	504	G
45	5	930	G
45	5	1072	C
45	5	1211	G

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Mol	Chain	Res	Type
45	5	1291	G
45	5	1445	U
45	5	1455	G
45	5	1633	G
45	5	2046	G
45	5	2089	G
45	5	2266	C
45	5	2502	A
45	5	2661	U
45	5	2695	A
45	5	3603	G
45	5	3625	G
45	5	4054	C
45	5	4170	A
45	5	4232	U
45	5	4448	G
45	5	4699	U
45	5	4719	G
45	5	4884	G
45	5	4925	U
45	5	4947	U
47	8	124	U
49	2	24	C
49	2	110	U
49	2	182	C
49	2	532	C
49	2	553	U
49	2	561	A
49	2	688	U
49	2	752	G
49	2	1137	U
49	2	1253	A
49	2	1395	C
49	2	1489	A
49	2	1637	A
49	2	1664	A
85	4	6057	A
85	4	6058	U
85	4	6059	U
85	4	6060	U
85	4	6061	U
85	4	6066	G

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Mol	Chain	Res	Type
85	4	6067	G
85	4	6068	U
85	4	6072	U
85	4	6073	A
85	4	6076	U
85	4	6107	A
85	4	6150	C
85	4	6151	A
85	4	6163	G
85	4	6164	C
85	4	6165	C
85	4	6166	C
85	4	6167	U
85	4	6170	C
85	4	6171	U
85	4	6172	G
85	4	6173	C
85	4	6174	G
85	4	6175	G
85	4	6176	U
85	4	6179	U
85	4	6180	U
85	4	6181	C
85	4	6182	A
85	4	6183	G
85	4	6184	A
85	4	6185	U
85	4	6186	U
85	4	6187	A
85	4	6188	G
85	4	6189	G
85	4	6190	U
85	4	6196	A
85	4	6199	A
85	4	6206	G
85	4	6208	A
85	4	6209	A
85	4	6210	U
85	4	6211	U
85	4	6212	U
85	4	6213	A
85	4	6214	C

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 6 ligands modelled in this entry, 6 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
45	5	36
49	2	20
48	K	3
47	8	1
82	hh	1
14	O	1
3	C	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	5	2113:G	O3'	2258:C	P	41.98

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	5	1252:C	O3'	1271:G	P	33.40
1	5	1696:C	O3'	1720:C	P	19.99
1	5	1219:G	O3'	1233:G	P	18.35
1	5	523:C	O3'	638:G	P	18.12
1	5	990:C	O3'	1064:G	P	18.08
1	2	756:C	O3'	788:G	P	17.83
1	5	4101:C	O3'	4107:G	P	17.76
1	5	4138:C	O3'	4146:G	P	17.64
1	2	834:C	O3'	841:G	P	17.63
1	2	697:G	O3'	729:C	P	17.51
1	5	3977:C	O3'	4034:G	P	17.44
1	2	1417:C	O3'	1423:C	P	15.35
1	5	5022:U	O3'	5028:G	P	14.94
1	2	1761:U	O3'	1771:G	P	14.63
1	5	4777:C	O3'	4859:C	P	14.47
1	5	760:G	O3'	904:C	P	14.39
1	2	130:G	O3'	141:A	P	13.98
1	5	1364:U	O3'	1368:A	P	13.51
1	2	323:C	O3'	329:G	P	12.90
1	5	1405:C	O3'	1411(A):G	P	12.67
1	5	4045:G	O3'	4047:A	P	12.53
1	5	2901:G	O3'	3597:G	P	11.66
1	5	182:G	O3'	189:G	P	10.37
1	5	4729:A	O3'	4735:G	P	9.24
1	5	1180:C	O3'	1183:C	P	8.44
1	5	971(A):G	O3'	972:C	P	8.39
1	2	689:U	O3'	690:G	P	8.38
1	8	79:G	O3'	85:U	P	7.62
1	hh	2:THR	C	3:GLU	N	7.52
1	K	194:LEU	C	195:LYS	N	7.40
1	5	737:C	O3'	738(A):C	P	7.09
1	5	970:G	O3'	971:U	P	6.80
1	5	500:G	O3'	504:G	P	6.70
1	2	736:C	O3'	743:U	P	6.55
1	5	1957:U	O3'	1958:A	P	6.11
1	2	225:G	O3'	287:U	P	5.99
1	5	751:G	O3'	752:G	P	5.86
1	5	4740:G	O3'	4743:G	P	5.52
1	5	971:U	O3'	971(A):G	P	5.18
1	K	9:THR	C	10:LEU	N	5.03
1	2	1432:U	O3'	1438:A	P	4.80
1	5	1239:C	O3'	1244:G	P	4.77

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	2	322:C	O3'	323:C	P	4.73
1	5	512:U	O3'	515:C	P	4.66
1	K	172:VAL	C	173:LYS	N	4.60
1	5	1438:U	O3'	1440:U	P	4.48
1	5	170:C	O3'	171:U	P	4.34
1	2	745:C	O3'	749:U	P	4.21
1	2	1697:A	O3'	1698:C	P	4.16
1	2	886:A	O3'	887:U	P	4.06
1	2	304:C	O3'	305:U	P	4.01
1	O	109:PRO	C	111:PRO	N	3.99
1	2	903:A	O3'	904:A	P	3.93
1	5	4899:G	O3'	4902:C	P	3.53
1	2	798:G	O3'	799:U	P	3.35
1	5	1100:U	O3'	1168:G	P	3.34
1	5	738(A):C	O3'	739:G	P	3.31
1	5	267:G	O3'	268:G	P	3.29
1	2	902:G	O3'	903:A	P	3.29
1	2	1201:U	O3'	1202:U	P	3.27
1	5	5020:G	O3'	5021:C	P	3.24
1	C	132:ALA	C	133:LEU	N	3.22

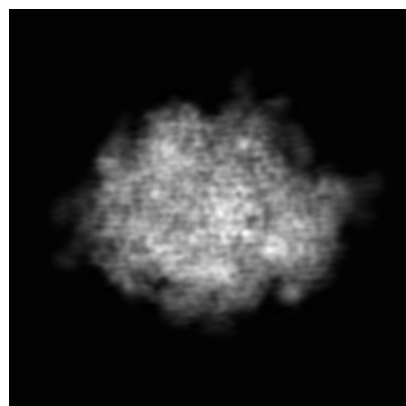
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-7836. These allow visual inspection of the internal detail of the map and identification of artifacts.

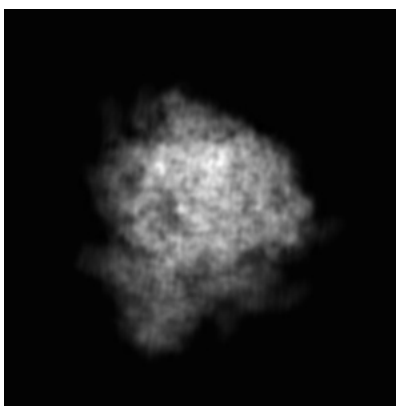
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

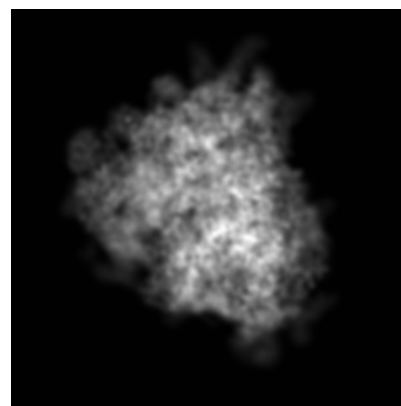
6.1.1 Primary map



X

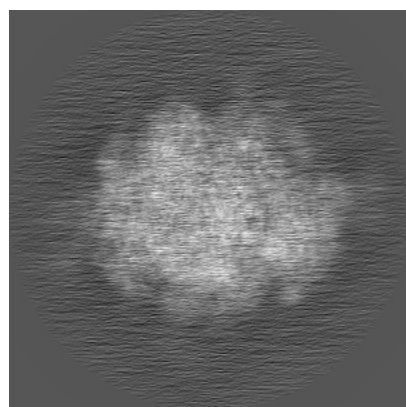


Y

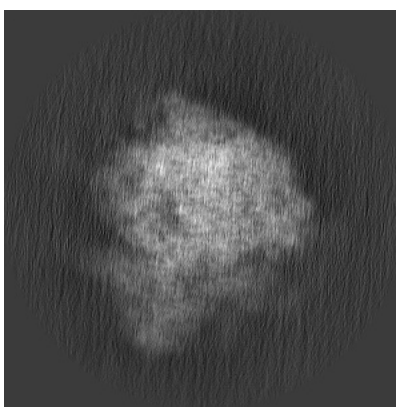


Z

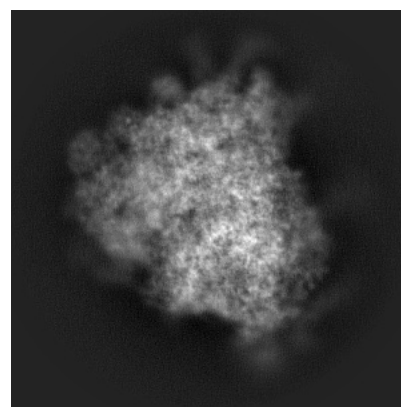
6.1.2 Raw map



X



Y

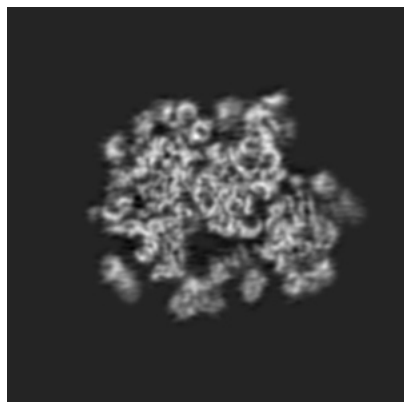


Z

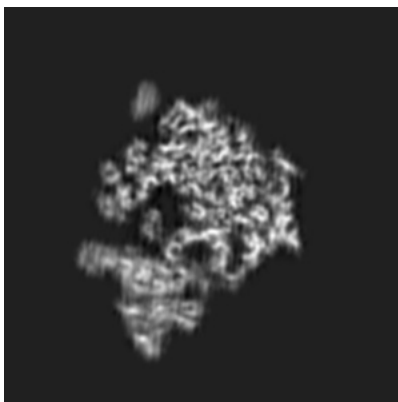
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

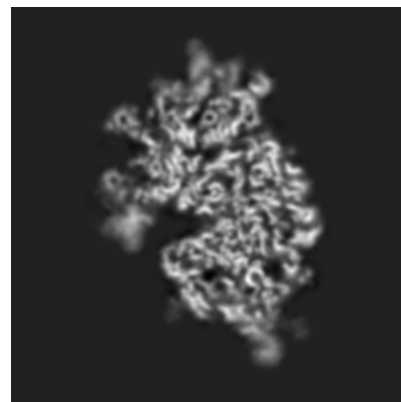
6.2.1 Primary map



X Index: 200

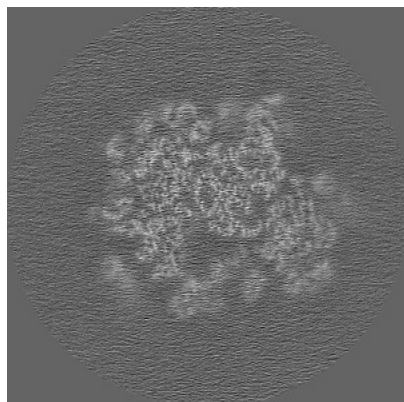


Y Index: 200

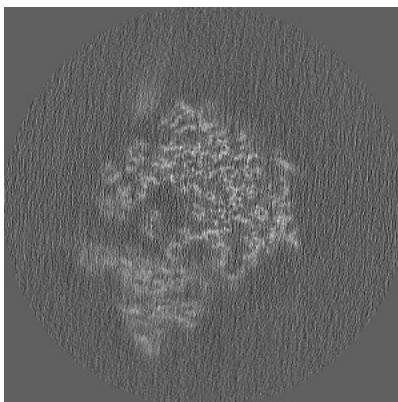


Z Index: 200

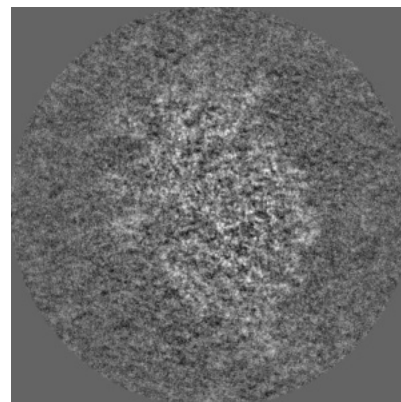
6.2.2 Raw map



X Index: 200



Y Index: 200

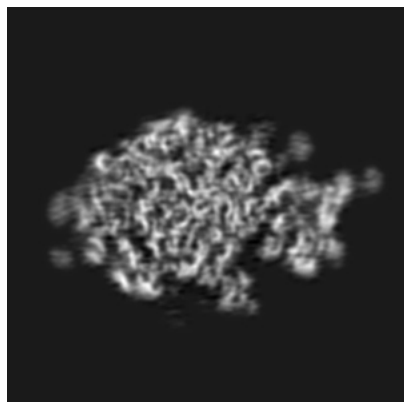


Z Index: 200

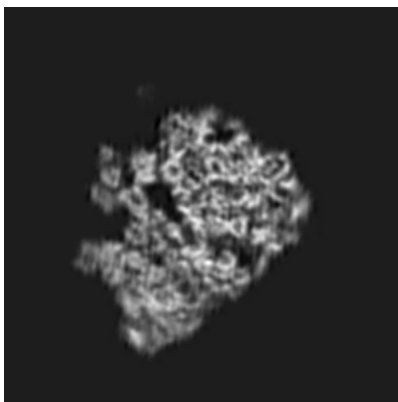
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

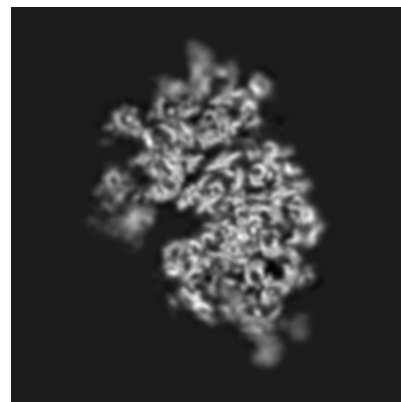
6.3.1 Primary map



X Index: 248

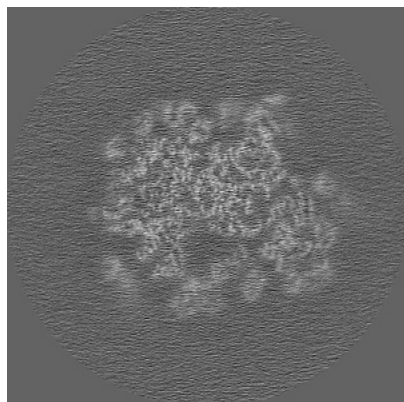


Y Index: 213

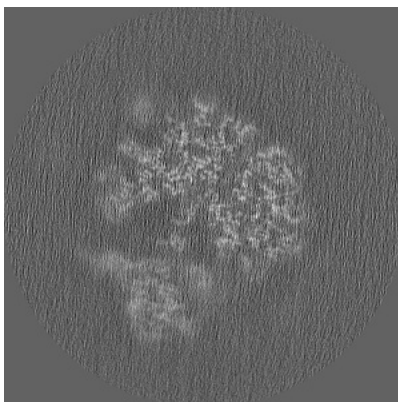


Z Index: 197

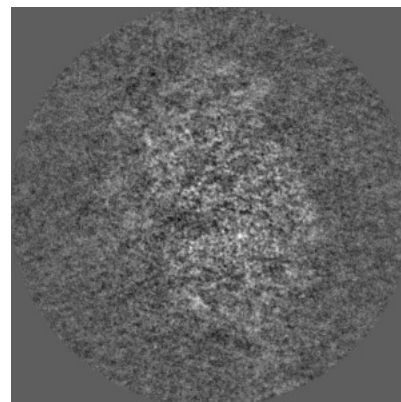
6.3.2 Raw map



X Index: 201



Y Index: 189

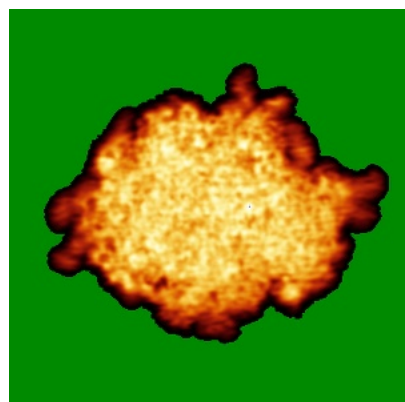


Z Index: 198

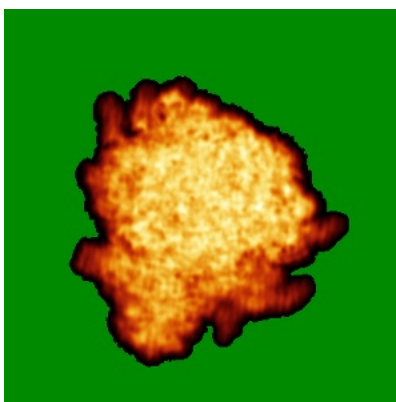
The images above show the largest variance slices of the map in three orthogonal directions.

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

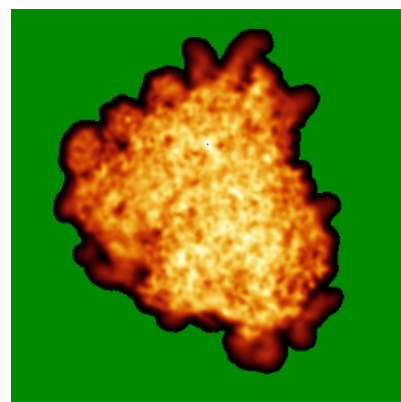
6.4.1 Primary map



X

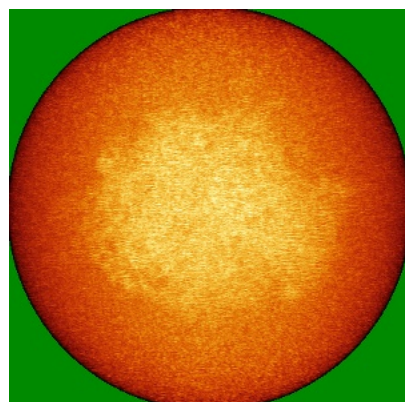


Y

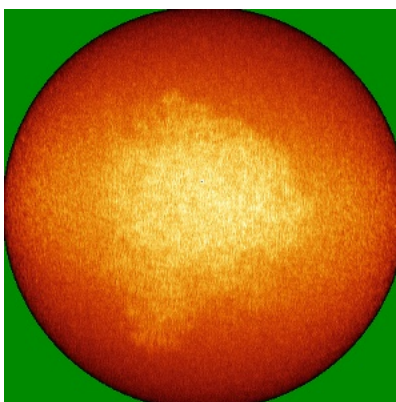


Z

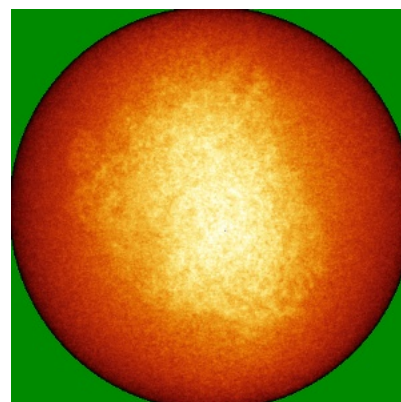
6.4.2 Raw map



X



Y

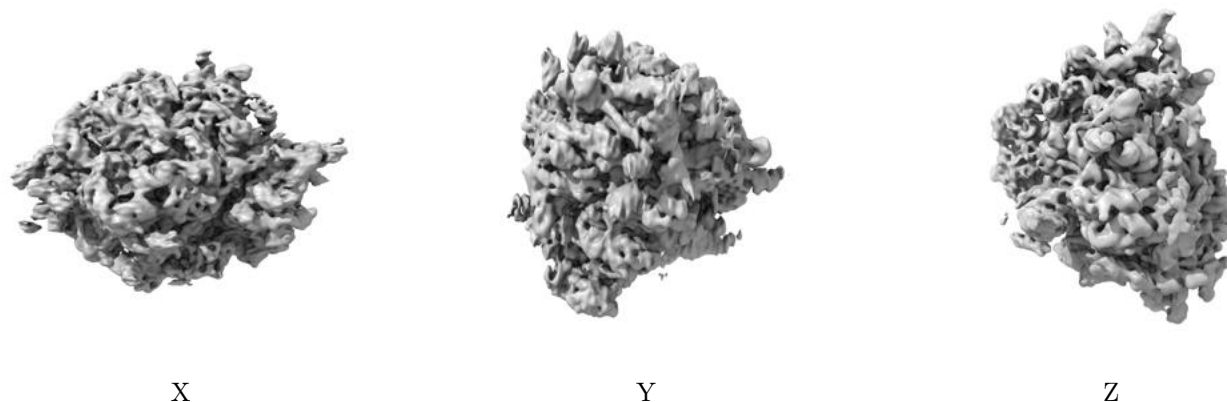


Z

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

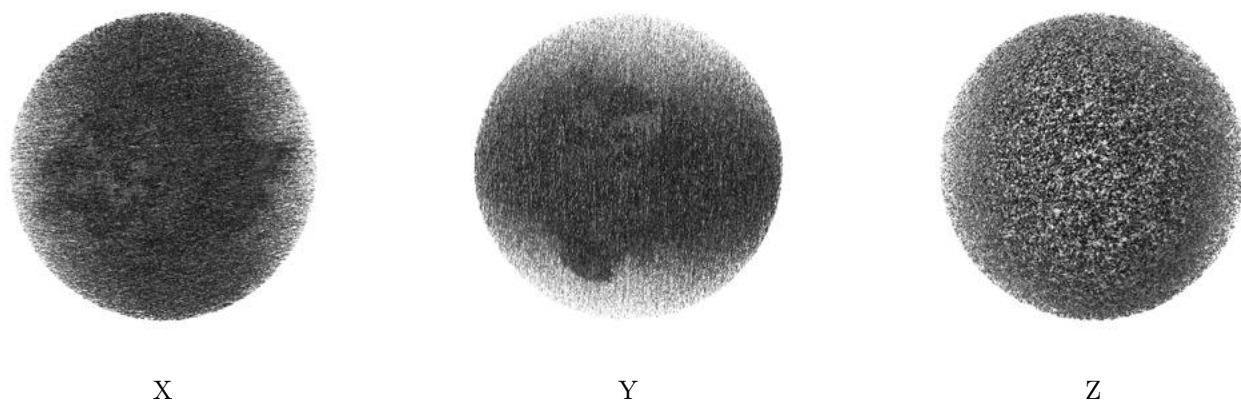
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.02. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

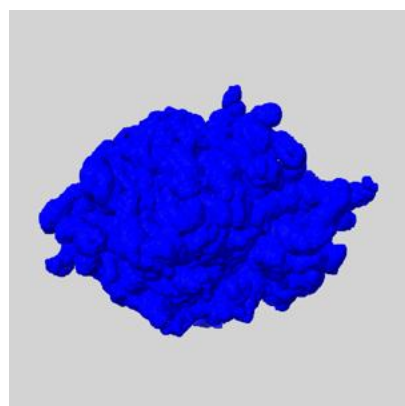
6.6 Mask visualisation [i](#)

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

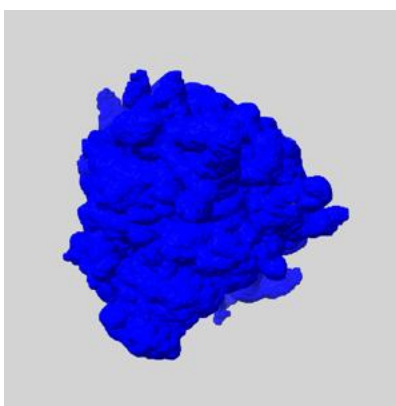
A mask typically either:

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

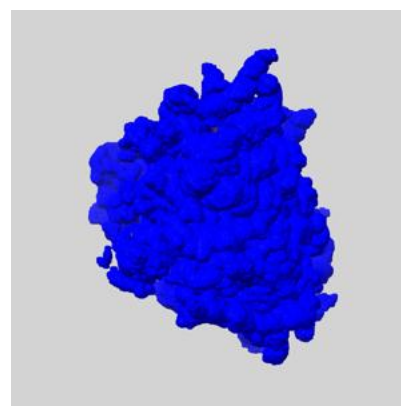
6.6.1 emd_7836_msk_1.map [i](#)



X



Y

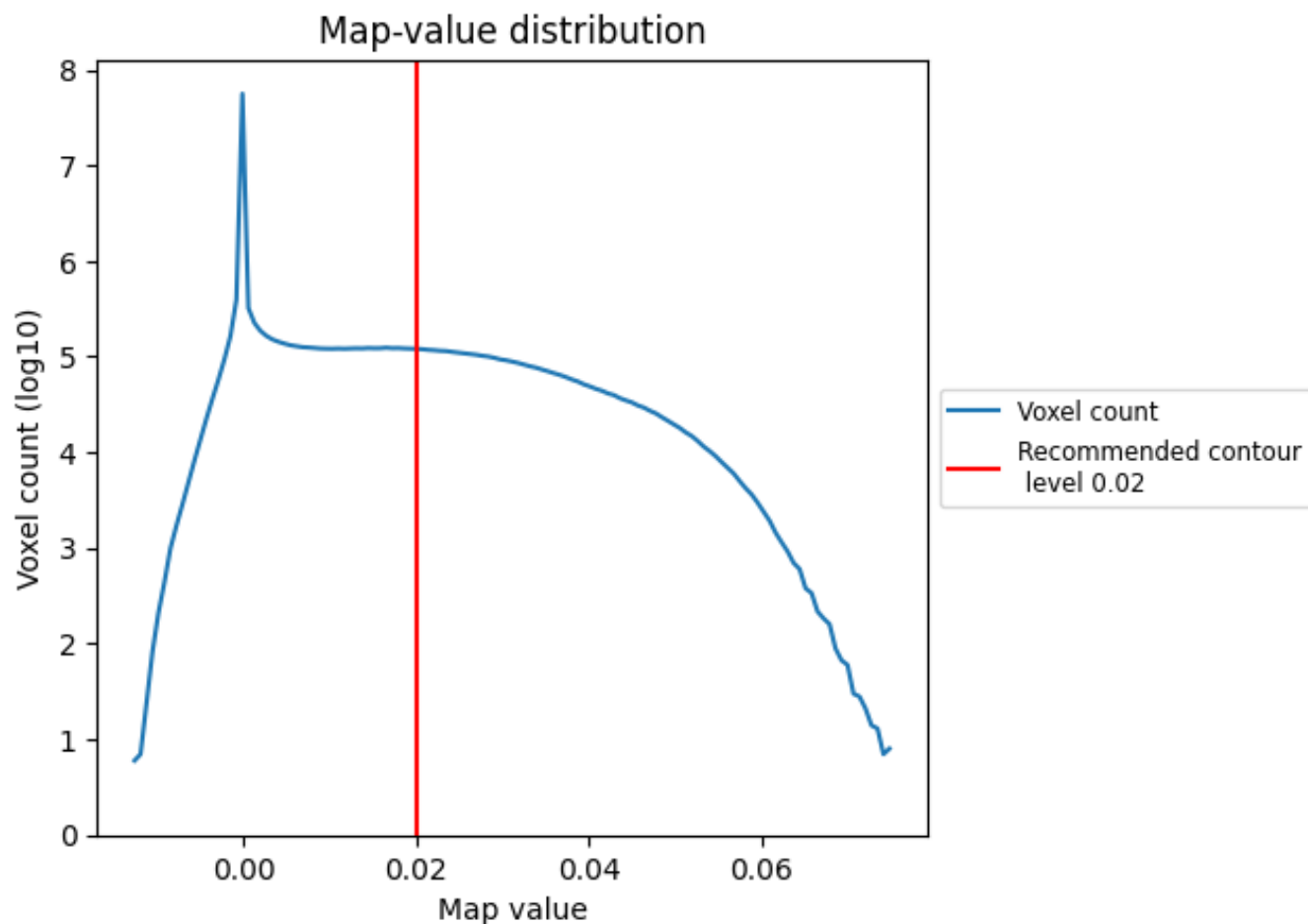


Z

7 Map analysis [i](#)

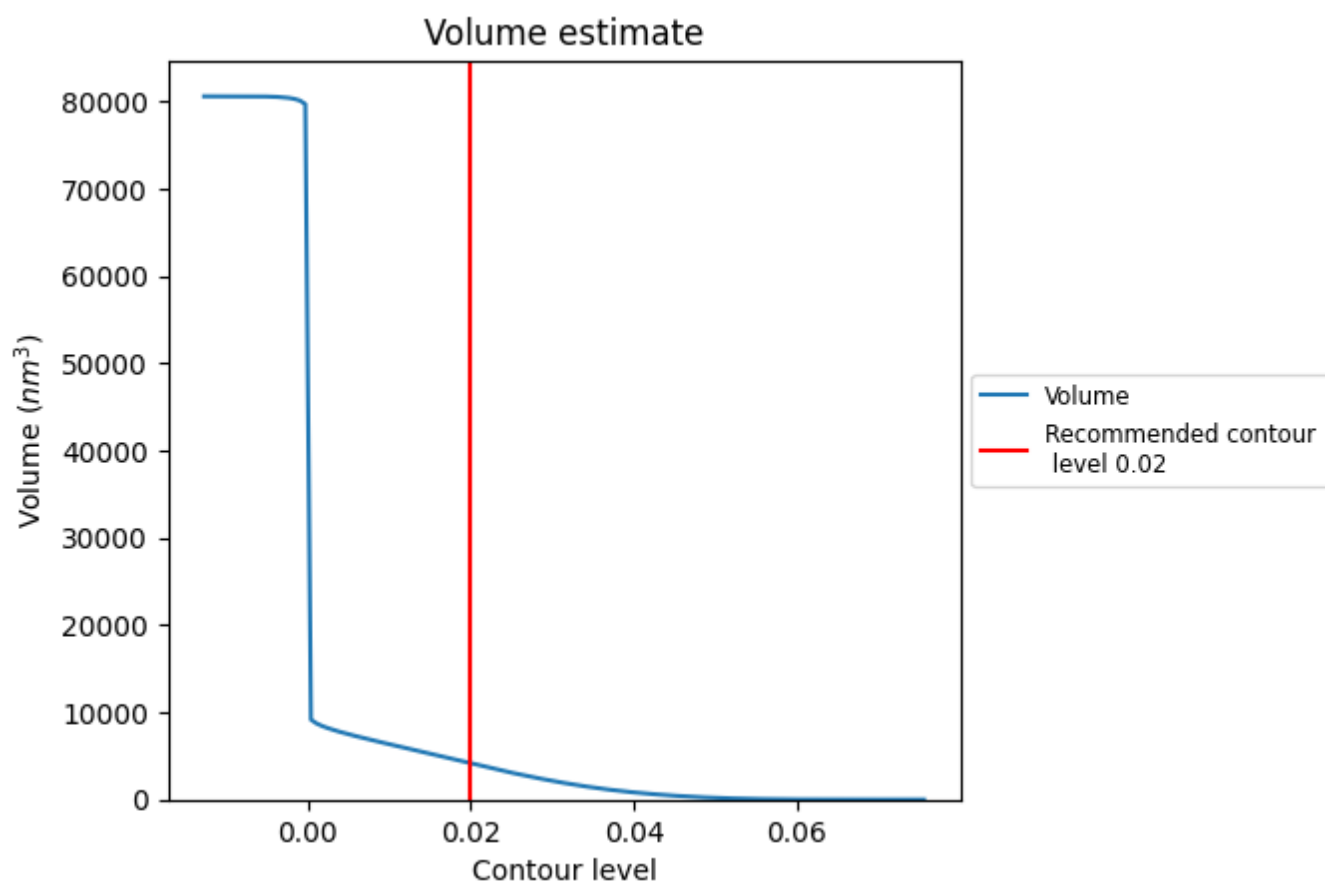
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

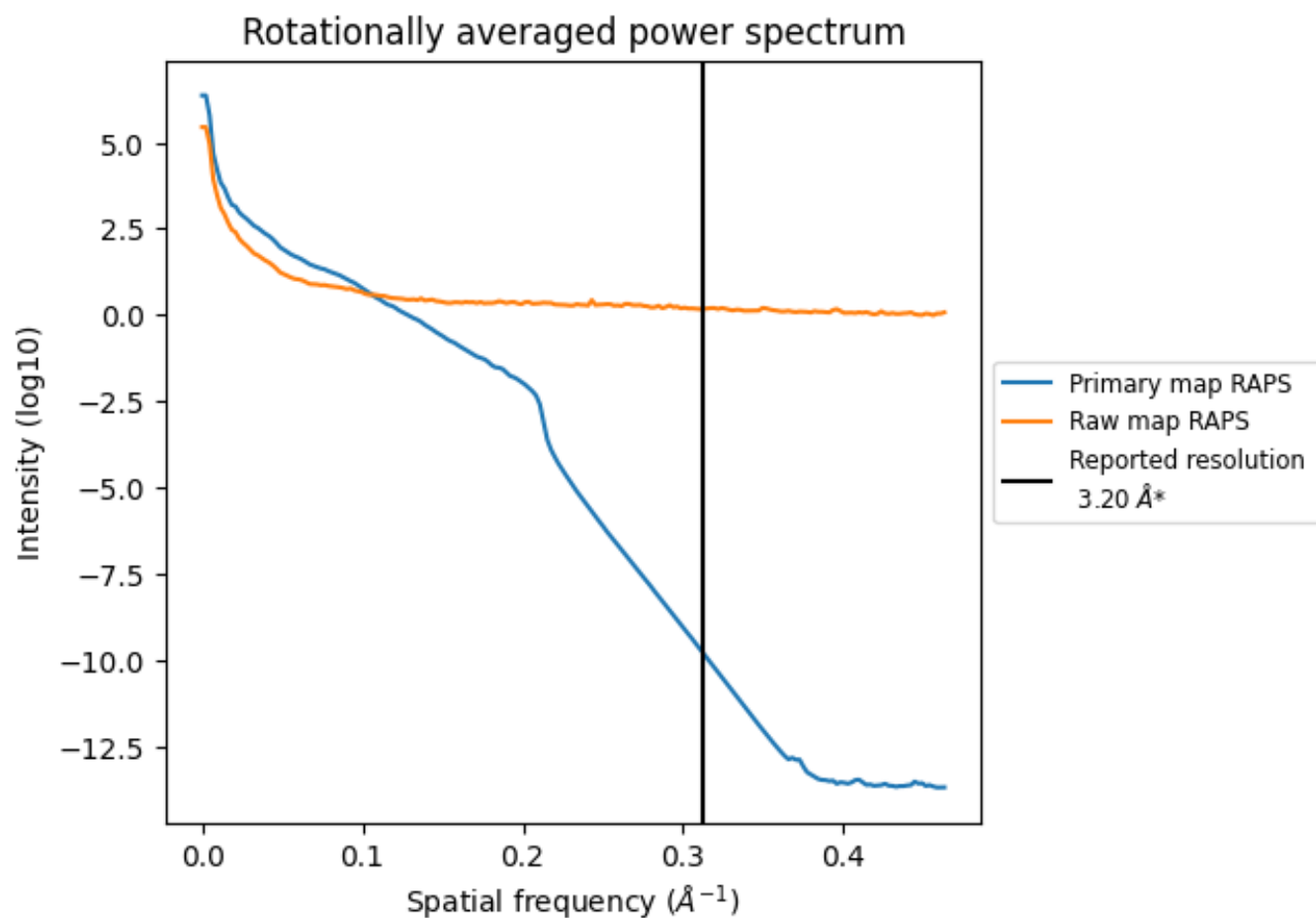
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4136 nm³; this corresponds to an approximate mass of 3736 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 ⓘ

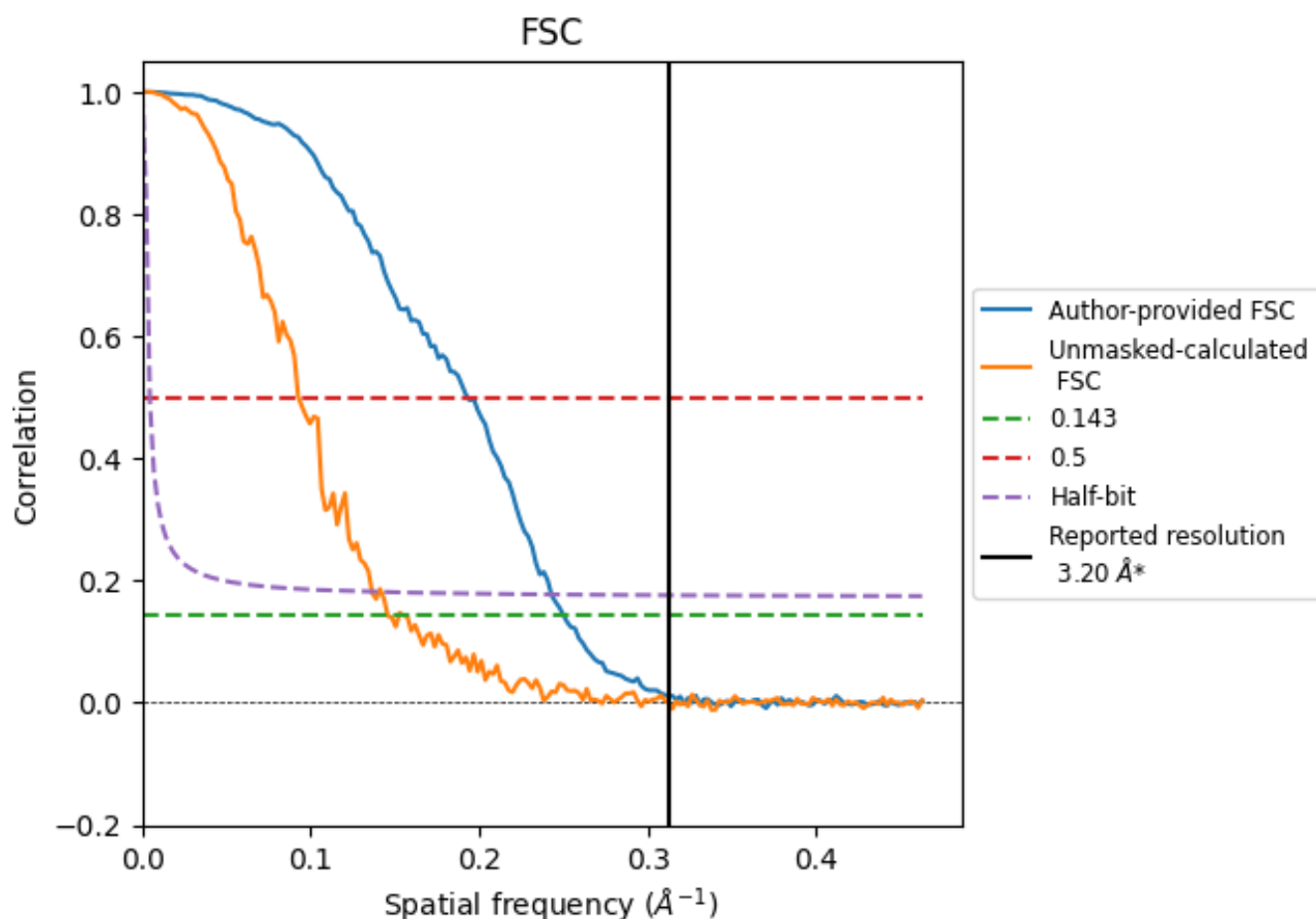


*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

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 $0.312 \text{ \AA}^{-1}$

8.2 Resolution estimates

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	4.00	5.17	4.12
Unmasked-calculated*	6.86	10.79	7.33

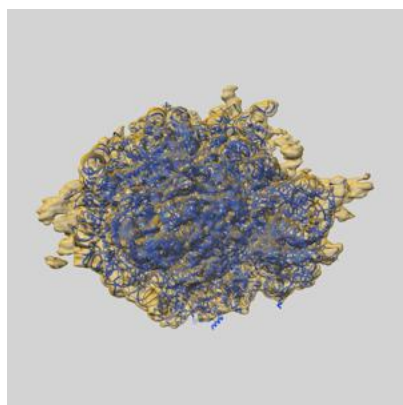
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 4.00 differs from the reported value 3.2 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 6.86 differs from the reported value 3.2 by more than 10 %

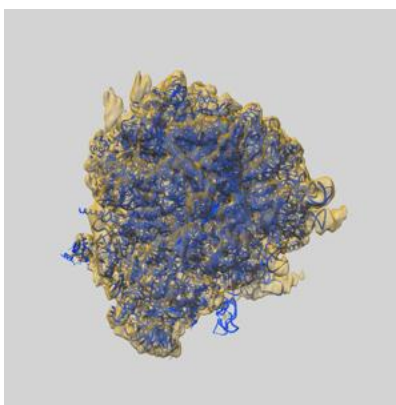
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-7836 and PDB model 6D9J. Per-residue inclusion information can be found in [section 3](#) on [page 22](#).

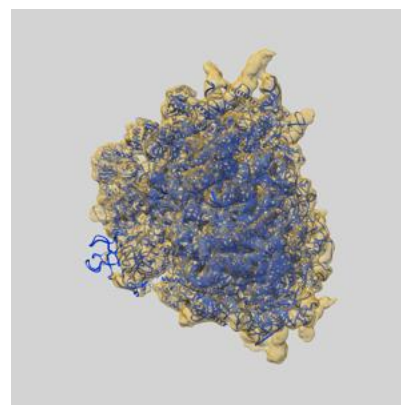
9.1 Map-model overlay [i](#)



X



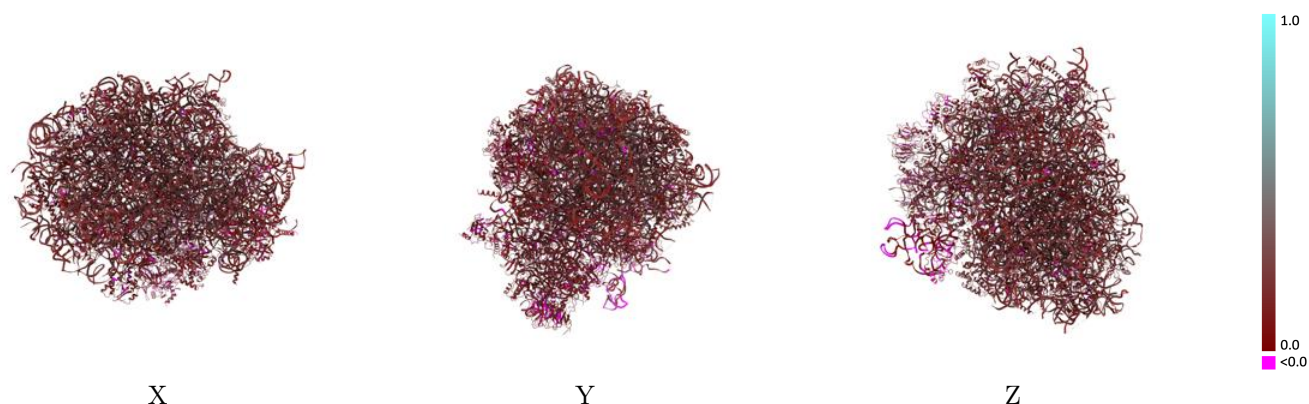
Y



Z

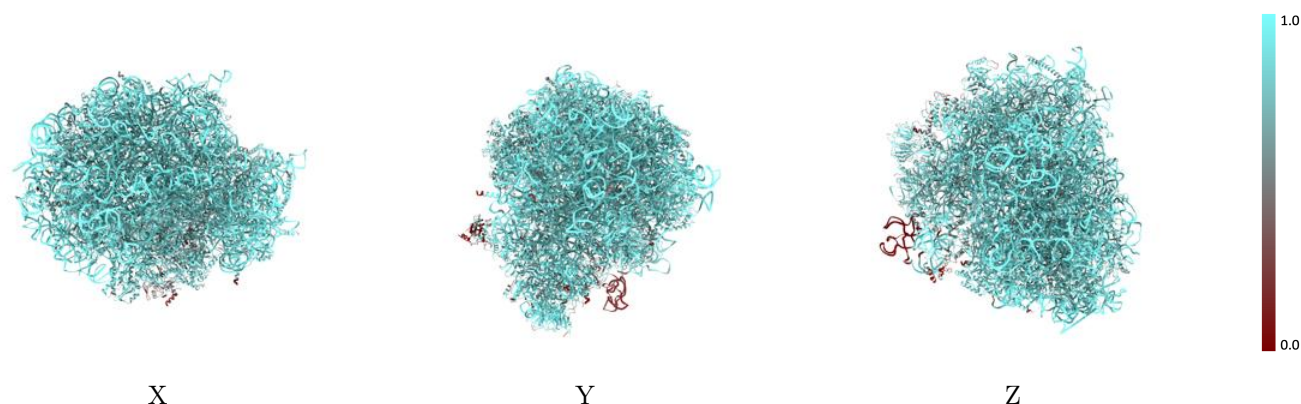
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



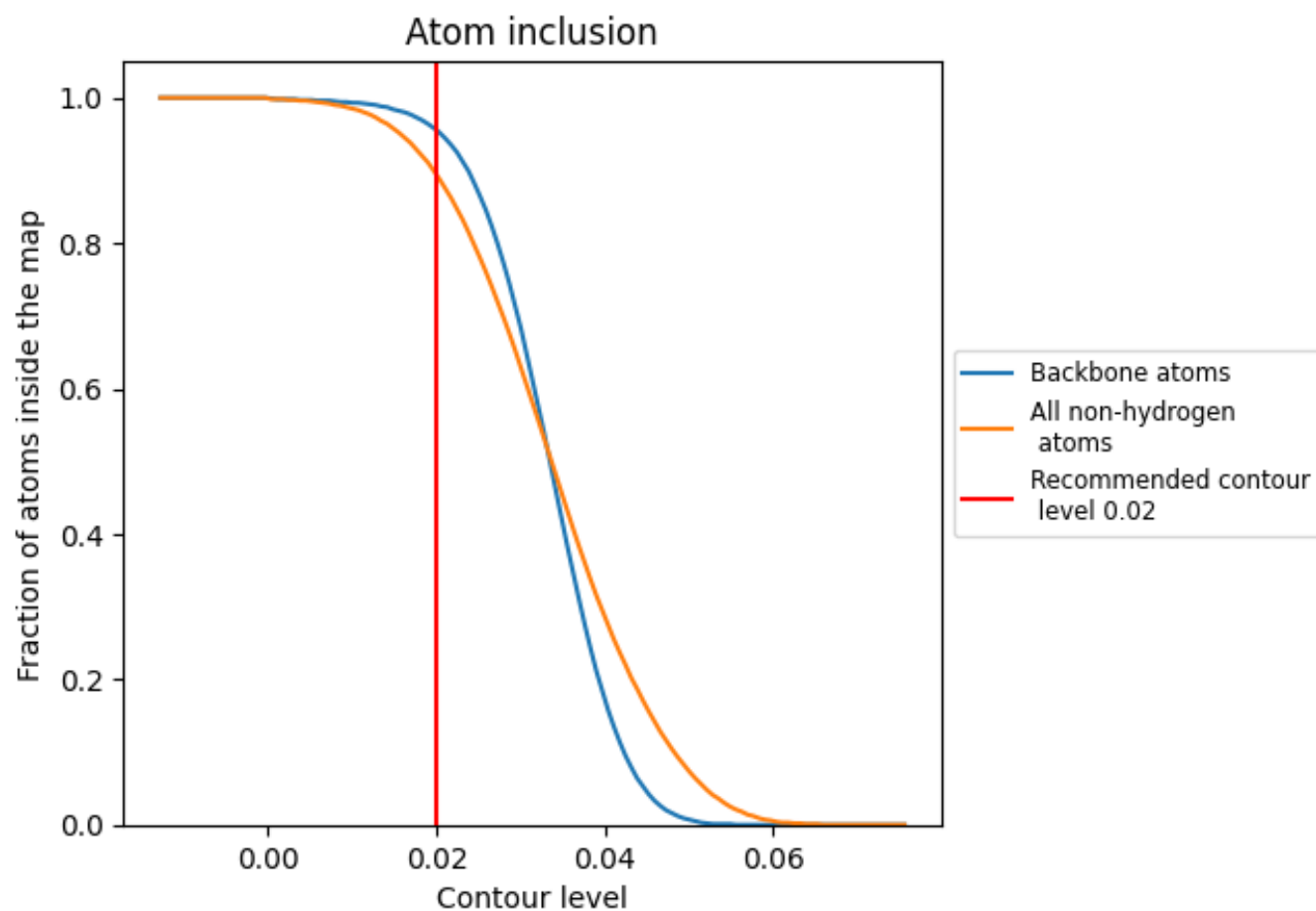
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.02).

9.4 Atom inclusion ⓘ



At the recommended contour level, 96% of all backbone atoms, 90% 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 (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8950	 0.1880
2	 0.9770	 0.2060
3	 0.7770	 0.1720
4	 0.5300	 0.0620
5	 0.9830	 0.2280
7	 0.9960	 0.2340
8	 0.9800	 0.2140
9	 0.7330	 0.1480
A	 0.8350	 0.1770
B	 0.8230	 0.1750
BB	 0.7880	 0.1530
C	 0.8350	 0.1610
CC	 0.8570	 0.1640
D	 0.8940	 0.1680
DD	 0.8000	 0.1630
E	 0.8520	 0.1690
EE	 0.7810	 0.1540
F	 0.7990	 0.1610
FF	 0.8580	 0.1500
G	 0.8270	 0.1690
GG	 0.8030	 0.1470
H	 0.8070	 0.1740
HH	 0.8570	 0.1460
I	 0.8200	 0.1700
II	 0.7960	 0.1670
J	 0.8450	 0.1570
JJ	 0.8490	 0.1540
K	 0.5690	 0.0670
KK	 0.8150	 0.1510
L	 0.8350	 0.1780
LL	 0.8610	 0.1400
M	 0.9020	 0.1660
MM	 0.8120	 0.1870
N	 0.8410	 0.1420
NN	 0.3300	 0.0790



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Chain	Atom inclusion	Q-score
O	 0.8030	 0.1710
OO	 0.8120	 0.1750
P	 0.8720	 0.1570
PP	 0.8460	 0.1530
Q	 0.8000	 0.1630
QQ	 0.8200	 0.1090
R	 0.8240	 0.1720
RR	 0.8210	 0.1110
S	 0.8490	 0.1750
SS	 0.5970	 0.0840
T	 0.8040	 0.1790
TT	 0.7460	 0.1390
U	 0.8410	 0.1780
UU	 0.8590	 0.1220
V	 0.7690	 0.1790
VV	 0.7840	 0.1220
W	 0.8390	 0.1680
WW	 0.7910	 0.1510
X	 0.8170	 0.1620
XX	 0.8150	 0.1770
Y	 0.8820	 0.1560
YY	 0.7550	 0.1600
Z	 0.8910	 0.1650
ZZ	 0.8790	 0.1410
a	 0.8810	 0.1550
aa	 0.7500	 0.1480
b	 0.8070	 0.1590
bb	 0.8250	 0.1560
c	 0.8670	 0.1750
cc	 0.8140	 0.1780
d	 0.8480	 0.1750
dd	 0.7400	 0.1430
e	 0.8280	 0.1830
ee	 0.9050	 0.1340
f	 0.8300	 0.1700
ff	 0.7840	 0.1470
g	 0.8480	 0.1460
gg	 0.5010	 0.0810
h	 0.8320	 0.1750
hh	 0.8710	 0.1260
i	 0.8130	 0.1780
j	 0.8720	 0.1320

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Chain	Atom inclusion	Q-score
k	 0.8260	 0.1720
l	 0.8340	 0.1610
m	 0.8070	 0.1570
n	 0.7660	 0.1230
o	 0.8750	 0.1730
p	 0.8200	 0.1710
r	 0.8450	 0.1740
s	 0.7700	 0.1380
t	 0.6520	 0.0890