



Full wwPDB EM Validation Report ⓘ

Sep 6, 2026 – 06:38 PM EDT

PDB ID : 11IQ / pdb_000011iq
EMDB ID : EMD-75724
Title : Rabbit 80S with eEF2,eIF5A and SERBP1
Authors : Seraj, Z.; Zottig, X.; Huang, C.H.; Loveland, A.B.; Diggs, S.; Sholi, E.; Grigorieff, N.; Korostelev, A.A.
Deposited on : 2026-02-26
Resolution : 2.40 Å(reported)
Based on initial model : 7TOR

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:

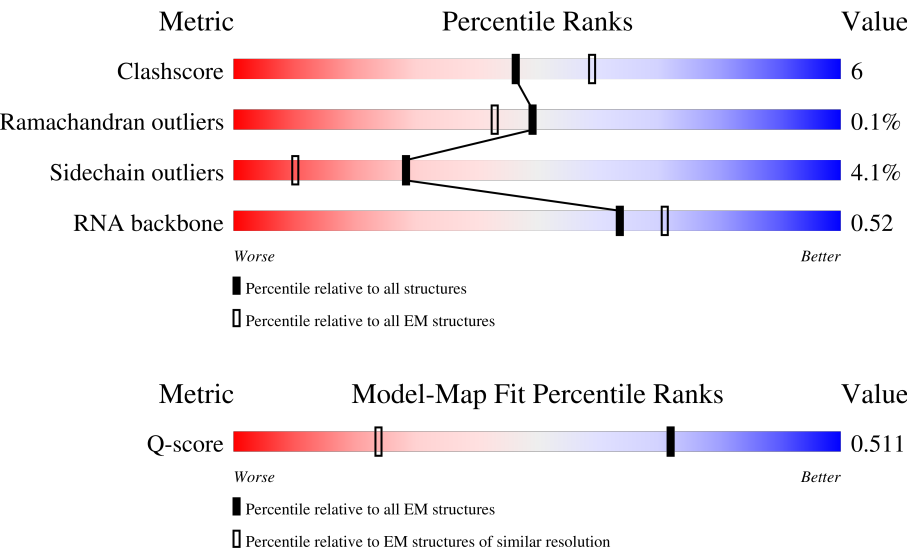
EMDB validation analysis : 0.0.1.dev133
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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) : 2.50

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 2.40 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.



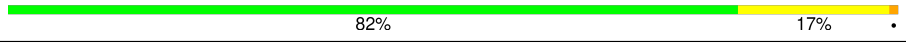
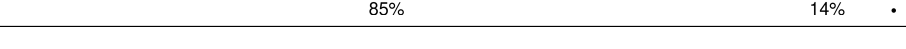
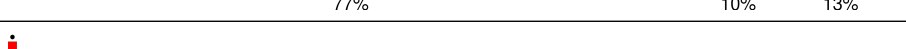
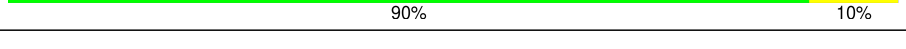
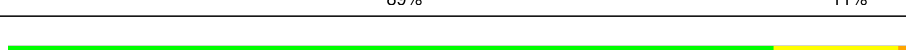
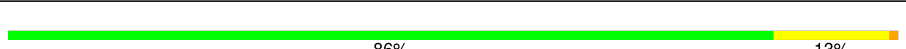
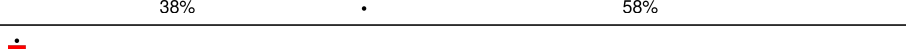
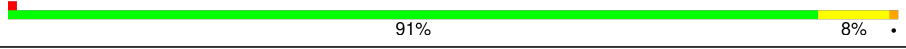
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	5628 (1.90 - 2.90)

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	17	183	14% 86% 12% ..
2	DD	151	89% 5% 5%
3	58	156	47% 47% ..

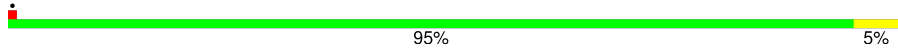
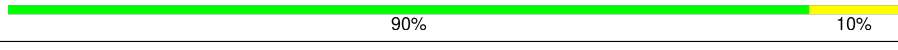
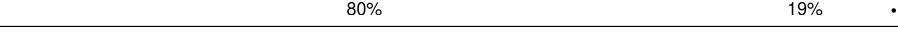
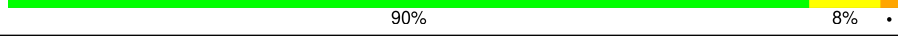
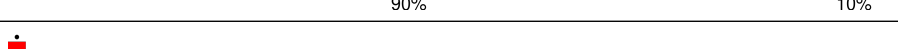
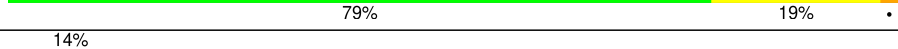
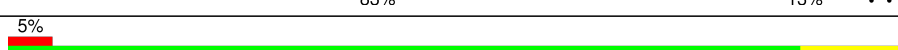
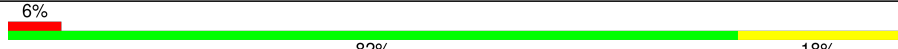
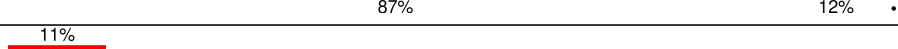
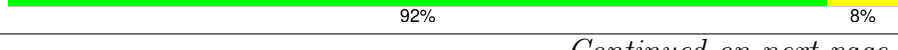
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Mol	Chain	Length	Quality of chain
4	5	120	
5	L8	248	
6	L3	394	
7	L4	362	
8	L5	293	
9	L6	291	
10	L7	253	
11	aa	240	
12	13	241	
13	14	138	
14	15	203	
15	bb	199	
16	20	176	
17	21	159	
18	22	99	
19	cc	118	
20	26	134	
21	27	135	
22	dd	147	
23	29	245	
24	31	107	
25	32	128	
26	ee	109	
27	34	114	
28	35	122	

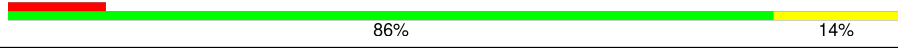
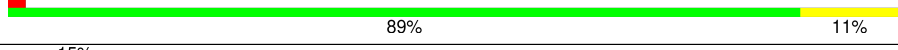
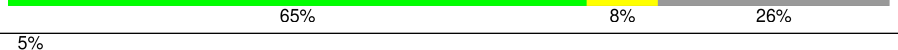
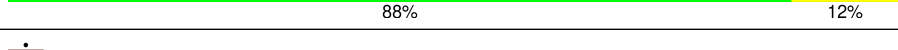
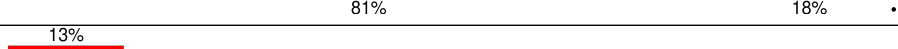
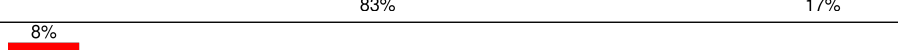
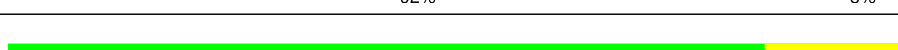
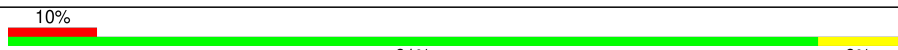
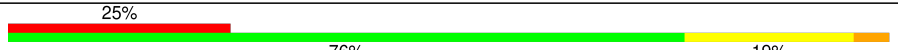
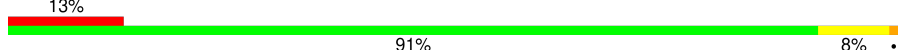
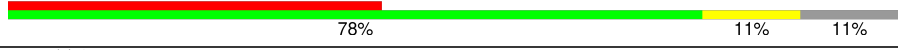
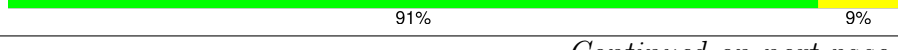
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Mol	Chain	Length	Quality of chain
29	36	102	
30	37	86	
31	38	69	
32	39	50	
33	40	52	
34	41	25	
35	42	104	
36	ff	91	
37	gg	124	
38	s	196	
39	EB	375	
40	Q	188	
41	10	213	
42	L9	190	
43	S7	189	
44	S9	185	
45	S4	262	
46	S6	237	
47	SS	124	
48	RR	141	
49	YY	55	
50	LL	144	
51	11	170	
52	GG	135	
53	23	139	

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Mol	Chain	Length	Quality of chain
54	19	180	
55	v	857	
56	S3	228	
57	FF	149	
58	S8	206	
59	S2	221	
60	BB	295	
61	UU	101	
62	PP	83	
63	JJ	132	
64	AS	213	
65	VV	83	
66	QQ	129	
67	24	157	
68	30	114	
69	ZZ	68	
70	18	1698	
71	MM	141	
72	AA	313	
73	OO	100	
74	RB	407	
75	EE	132	
76	CC	96	
77	II	142	
78	TT	75	

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Mol	Chain	Length	Quality of chain
79	WW	62	
80	XX	55	
81	B	149	
82	u	217	
83	S5	191	
84	A	131	
85	t	153	
86	28	4807	
87	ES	5070	

2 Entry composition

There are 89 unique types of molecules in this entry. The entry contains 224491 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	17	183	Total	C	N	O	S	0	0
			1490	935	287	258	10		

- Molecule 2 is a protein called Small ribosomal subunit protein uS17.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	58	151	Total	C	N	O	P	0	0
			3208	1432	564	1062	150		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	5	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 5 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	L8	248	Total	C	N	O	S	0	0
			1898	1189	389	314	6		

- Molecule 6 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	L3	394	Total	C	N	O	S	0	0
			3172	2020	597	542	13		

- Molecule 7 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	L4	362	Total	C	N	O	S	0	0
			2883	1812	577	480	14		

- Molecule 8 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	L5	293	Total	C	N	O	S	0	0
			2391	1512	438	427	14		

- Molecule 9 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	L6	216	Total	C	N	O	S	0	0
			1729	1115	329	282	3		

- Molecule 10 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L7	225	Total	C	N	O	S	0	0
			1874	1205	358	302	9		

- Molecule 11 is a protein called Large ribosomal subunit protein eL8.

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

- Molecule 12 is a protein called Large ribosomal subunit protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	13	210	Total	C	N	O	S	0	0
			1701	1065	354	278	4		

- Molecule 13 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	14	138	Total	C	N	O	S	0	0
			1137	727	221	182	7		

- Molecule 14 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	15	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 15 is a protein called Large ribosomal subunit protein uL13.

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

- Molecule 16 is a protein called Large ribosomal subunit protein eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	20	176	Total	C	N	O	S	0	0
			1462	930	285	236	11		

- Molecule 17 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	21	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 18 is a protein called Large ribosomal subunit protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	22	99	Total	C	N	O	S	0	0
			809	519	141	147	2		

- Molecule 19 is a protein called Large ribosomal subunit protein uL23.

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

- Molecule 20 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	26	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 21 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	27	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 22 is a protein called 60S ribosomal protein L27a.

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

- Molecule 23 is a protein called Large ribosomal subunit protein eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	29	104	Total	C	N	O	S	0	0
			848	527	189	129	3		

- Molecule 24 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	31	107	Total	C	N	O	S	0	0
			888	560	171	155	2		

- Molecule 25 is a protein called Large ribosomal subunit protein eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	32	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 26 is a protein called Large ribosomal subunit protein eL33.

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

- Molecule 27 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	34	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

- Molecule 28 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	35	122	Total	C	N	O	S	0	0
			1013	640	204	168	1		

- Molecule 29 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	36	102	Total	C	N	O	S	0	0
			830	520	176	129	5		

- Molecule 30 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	37	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 31 is a protein called Large ribosomal subunit protein eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	38	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

- Molecule 32 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	39	50	Total	C	N	O	S	0	0
			447	286	96	64	1		

- Molecule 33 is a protein called Large ribosomal subunit protein eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	40	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 34 is a protein called eL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	41	25	Total	C	N	O	S	0	0
			239	145	64	27	3		

- Molecule 35 is a protein called eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	42	104	Total	C	N	O	S	0	0
			851	533	174	138	6		

- Molecule 36 is a protein called 60S ribosomal protein L37a.

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

- Molecule 37 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	gg	124	Total	C	N	O	S	0	0
			990	615	202	167	6		

- Molecule 38 is a protein called 60S acidic ribosomal protein P0.

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

- Molecule 39 is a protein called Proliferation-associated protein 2G4.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	EB	375	Total	C	N	O	S	0	0
			2932	1844	509	562	17		

- Molecule 40 is a protein called Large ribosomal subunit protein eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Q	187	Total	C	N	O	S	0	0
			1514	946	315	249	4		

- Molecule 41 is a protein called Ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	10	209	Total	C	N	O	S	0	0
			1696	1075	328	280	13		

- Molecule 42 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	L9	190	Total	C	N	O	S	0	0
			1516	954	284	272	6		

- Molecule 43 is a protein called Small ribosomal subunit protein eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	S7	185	Total	C	N	O	S	0	0
			1488	952	271	264	1		

- Molecule 44 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	S9	185	Total	C	N	O	S	0	0
			1525	969	306	248	2		

- Molecule 45 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	S4	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		

- Molecule 46 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	S6	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 47 is a protein called 40S ribosomal protein S24.

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

- Molecule 48 is a protein called 40S ribosomal protein S23.

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

- Molecule 49 is a protein called 40S ribosomal protein S30.

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

- Molecule 50 is a protein called 40S ribosomal protein S18.

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

- Molecule 51 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	11	170	Total	C	N	O	S	0	0
			1362	861	254	241	6		

- Molecule 52 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	GG	135	Total	C	N	O	S	0	0
			1007	615	198	188	6		

- Molecule 53 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	23	139	Total	C	N	O	S	0	0
			1034	648	199	182	5		

- Molecule 54 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	19	180	Total	C	N	O	S	0	0
			1508	933	328	238	9		

- Molecule 55 is a protein called Elongation factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	v	847	Total	C	N	O	S	0	0
			6625	4207	1138	1236	44		

- Molecule 56 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	S3	228	Total	C	N	O	S	0	0
			1768	1126	318	316	8		

- Molecule 57 is a protein called 40S ribosomal protein S13.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
58	S8	206	Total	C	N	O	S	0	0
			1686	1058	332	291	5		

- Molecule 59 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	S2	221	Total	C	N	O	S	0	0
			1716	1111	295	301	9		

- Molecule 60 is a protein called 40S_SA_C domain-containing protein.

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

- Molecule 61 is a protein called eS26.

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

- Molecule 62 is a protein called eS21.

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

- Molecule 63 is a protein called 40S ribosomal protein S17.

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

- Molecule 64 is a protein called 40S ribosomal protein S3a.

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

- Molecule 65 is a protein called 40S ribosomal protein S27.

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

- Molecule 66 is a protein called 40S ribosomal protein S15a.

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

- Molecule 67 is a protein called Large ribosomal subunit protein eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	24	100	Total	C	N	O	S	0	0
			816	512	164	136	4		

- Molecule 68 is a protein called Large ribosomal subunit protein eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	30	114	Total	C	N	O	S	0	0
			884	557	156	164	7		

- Molecule 69 is a protein called 40S ribosomal protein S27a.

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

- Molecule 70 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	18	1662	Total	C	N	O	P	0	0
			35486	15841	6374	11610	1661		

- Molecule 71 is a protein called Small ribosomal subunit protein eS19.

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

- Molecule 72 is a protein called Receptor of activated protein C kinase 1.

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

- Molecule 73 is a protein called 40S ribosomal protein S20.

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

- Molecule 74 is a protein called SERBP1.

Mol	Chain	Residues	Atoms				AltConf	Trace
74	RB	58	Total	C	N	O	0	0
			459	273	93	93		

- Molecule 75 is a protein called 40S ribosomal protein S12.

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

- Molecule 76 is a protein called 40S ribosomal protein S10.

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

- Molecule 77 is a protein called Small ribosomal subunit protein uS9.

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

- Molecule 78 is a protein called 40S ribosomal protein S25.

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

- Molecule 79 is a protein called 40S ribosomal protein S28.

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

- Molecule 80 is a protein called 40S ribosomal protein S29.

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

- Molecule 81 is a protein called Eukaryotic translation initiation factor 5A-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	B	149	Total	C	N	O	S	0	0
			1144	715	195	226	8		

- Molecule 82 is a protein called Ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	u	217	Total	C	N	O	S	0	0
			1743	1114	314	306	9		

- Molecule 83 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	S5	185	Total	C	N	O	S	0	0
			1471	921	277	266	7		

- Molecule 84 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	A	131	Total	C	N	O	S	0	0
			1079	685	205	182	7		

- Molecule 85 is a protein called uL11.

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

- Molecule 86 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
86	28	3498	Total	C	N	O	P	0	0
			75019	33410	13742	24369	3498		

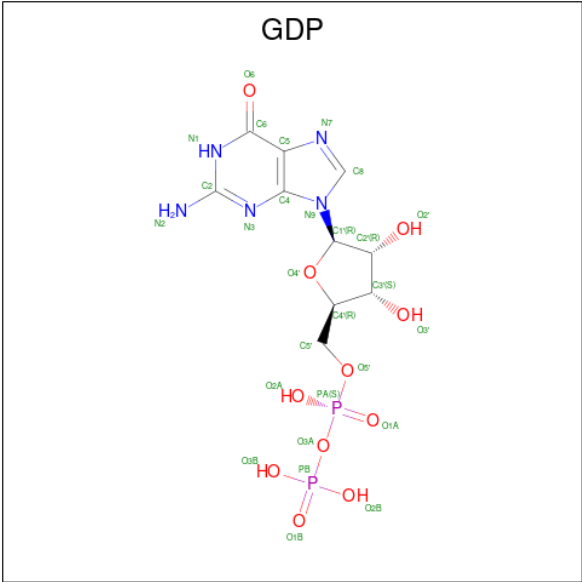
- Molecule 87 is a RNA chain called ES27L.

Mol	Chain	Residues	Atoms					AltConf	Trace
87	ES	35	Total	C	N	O	P	0	0
			756	335	142	244	35		

- Molecule 88 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
88	34	1	Total	Zn	0
			1	1	
88	37	1	Total	Zn	0
			1	1	
88	ff	1	Total	Zn	0
			1	1	
88	GG	1	Total	Zn	0
			1	1	
88	ZZ	1	Total	Zn	0
			1	1	

- Molecule 89 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂) (labeled as "Ligand of Interest" by depositor).

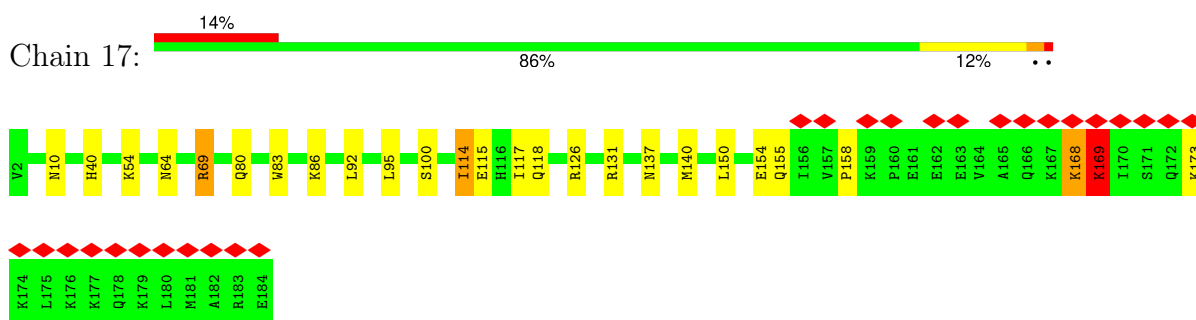


Mol	Chain	Residues	Atoms					AltConf
89	v	1	Total	C	N	O	P	0
			28	10	5	11	2	

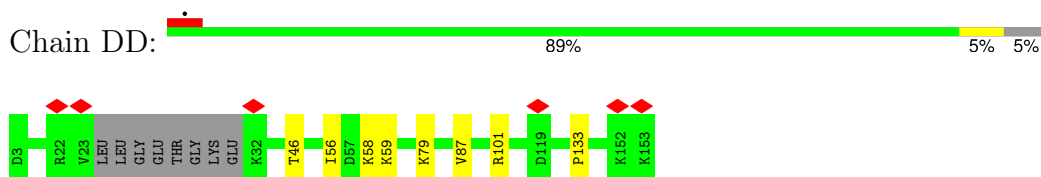
3 Residue-property plots

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

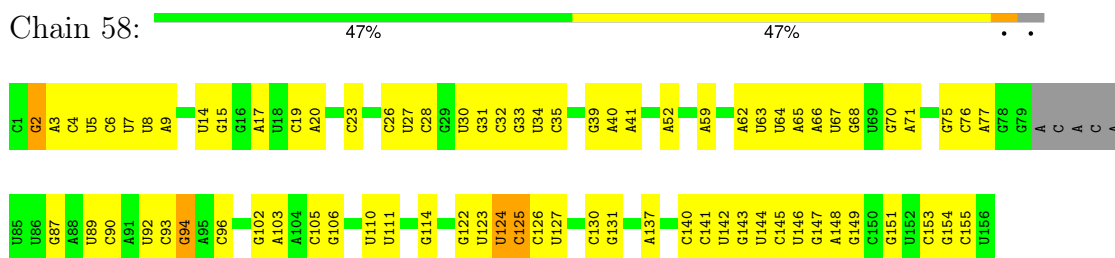
- Molecule 1: Large ribosomal subunit protein uL22



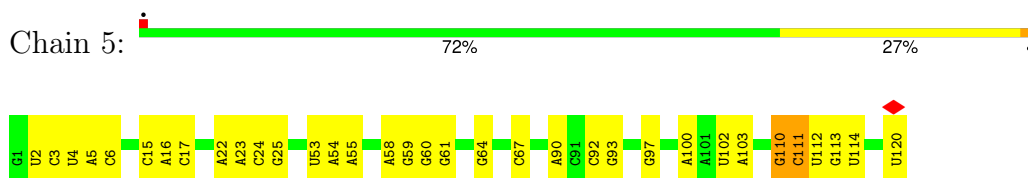
- Molecule 2: Small ribosomal subunit protein uS17



- Molecule 3: 5.8S rRNA

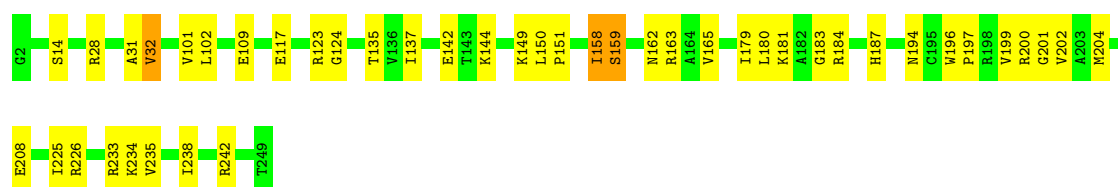


- Molecule 4: 5S rRNA



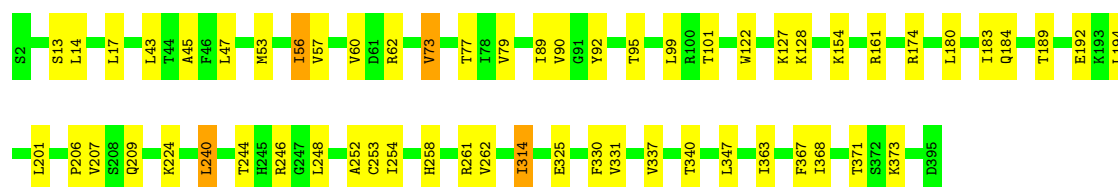
- Molecule 5: 60S ribosomal protein L8

Chain L8:  82% 17%



- Molecule 6: 60S ribosomal protein L3

Chain L3:  85% 14%



- Molecule 7: 60S ribosomal protein L4

Chain L4:  87% 12%



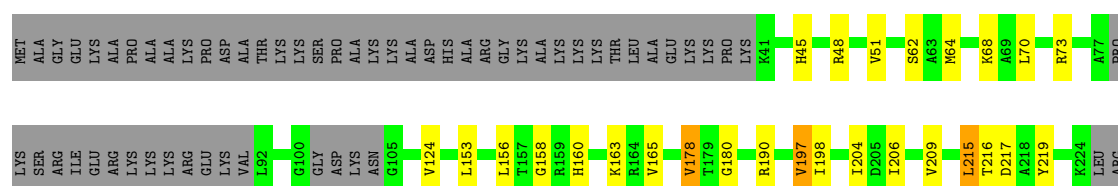
- Molecule 8: 60S ribosomal protein L5

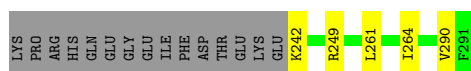
Chain L5:  88% 12%



- Molecule 9: 60S ribosomal protein L6

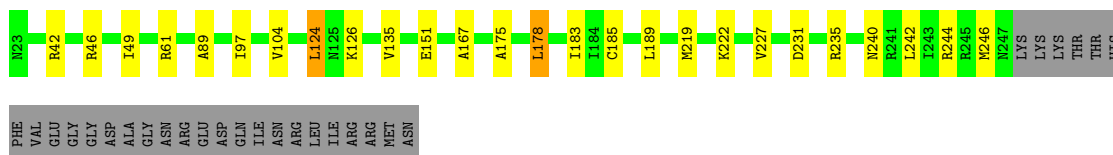
Chain L6:  63% 10% 26%





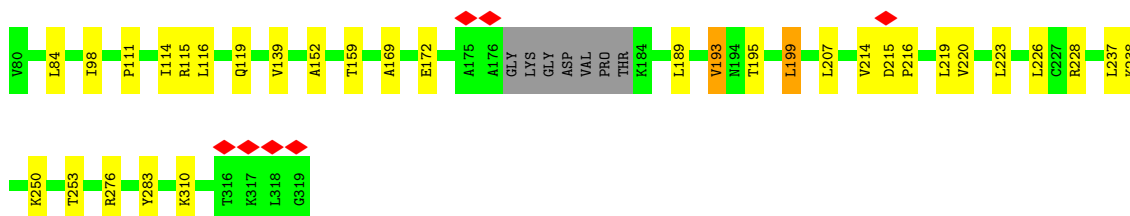
- Molecule 10: 60S ribosomal protein L7

Chain L7: 79% 9% 11%



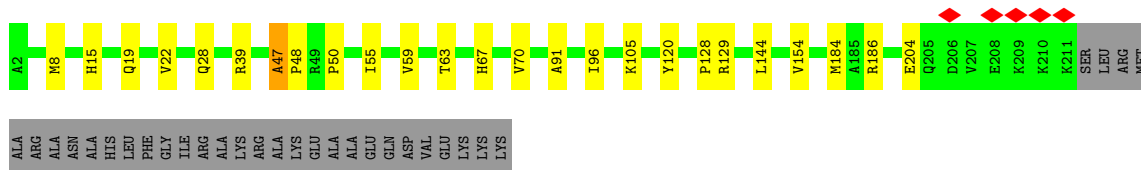
- Molecule 11: Large ribosomal subunit protein eL8

Chain aa: 84% 12%



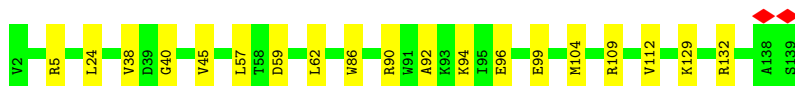
- Molecule 12: Large ribosomal subunit protein eL13

Chain 13: 77% 10% 13%



- Molecule 13: 60S ribosomal protein L14

Chain 14: 86% 14%



- Molecule 14: 60S ribosomal protein L15

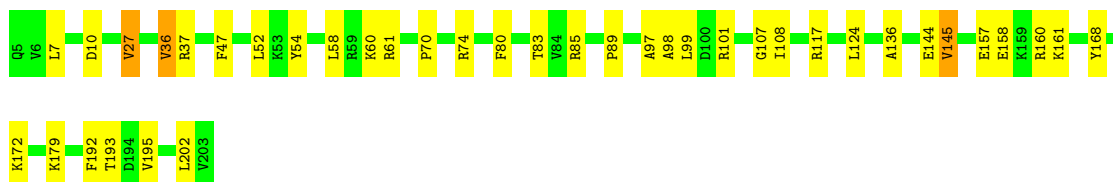
Chain 15: 80% 19%





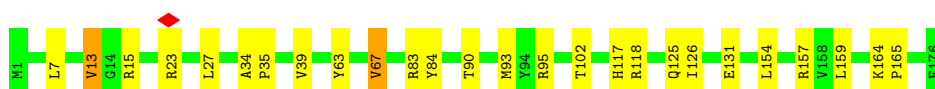
- Molecule 15: Large ribosomal subunit protein uL13

Chain bb: 80% 18%



- Molecule 16: Large ribosomal subunit protein eL20

Chain 20: 85% 14%



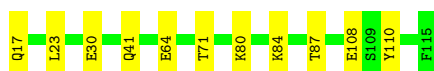
- Molecule 17: 60S ribosomal protein L21

Chain 21: 90% 10%



- Molecule 18: Large ribosomal subunit protein eL22

Chain 22: 89% 11%



- Molecule 19: Large ribosomal subunit protein uL23

Chain cc: 86% 14%



- Molecule 20: 60S ribosomal protein L26

Chain 26: 86% 13%



- Molecule 21: 60S ribosomal protein L27

G2	V11	I25	V43	I46	Y49	P50	R51	K52	V53	T54	M57	R65	I68	V72	I89	P90	L91	V100	L106	E120	R121	F136
----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------

-
- | Layer | Nodes |
|-------|-------|
| P2 | 1 |
| R21 | 2 |
| K24 | 3 |
| A35 | 4 |
| G51 | 5 |
| V56 | 6 |
| G57 | 7 |
| M58 | 8 |
| N66 | 9 |
| P71 | 10 |
| D76 | 11 |
| T86 | 12 |
| A98 | 13 |
| P99 | 14 |
| T100 | 15 |
| Y108 | 16 |
| L117 | 17 |
| P121 | 18 |
| Y122 | 19 |
| I123 | 20 |
| V140 | 21 |
| A148 | 22 |

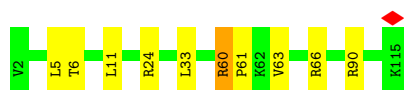
- [illegible]

-
- | Item | Category |
|------|----------|
| E18 | D |
| E19 | D |
| R23 | D |
| T26 | D |
| G37 | D |
| R41 | D |
| A45 | D |
| L46 | D |
| K47 | D |
| E48 | D |
| E56 | D |
| M57 | D |
| I64 | D |
| L68 | D |
| N69 | D |
| K70 | D |
| V86 | D |
| R87 | D |
| L88 | D |
| E94 | A |
| D95 | B |
| E96 | C |
| T106 | D |
| Y108 | D |
| L117 | D |
| V122 | D |
| D123 | D |
| E124 | D |

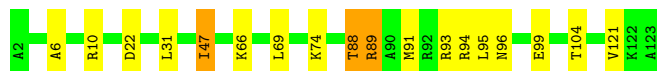
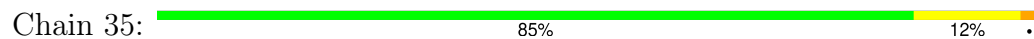
- A2
V13
I31
W35
R44
P56
K67
H68
L85
E86
V87
L88
L89
M90
A115
L118
L129

- | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|----|----|----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|------|------|------|------|------|------|
| S2 | C7 | K8 | A9 | L18 | E23 | L28 | V33 | E38 | R46 | V50 | K54 | N65 | K66 | T67 | R68 | V69 | H78 | V84 | R85 | A86 | R100 | I101 | R102 | V103 | L104 | M105 | V106 | P107 | I110 |
|----|----|----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|------|------|------|------|------|------|

- Chain 34: 91% 8%



- Molecule 28: 60S ribosomal protein L35



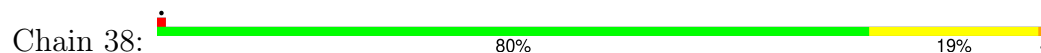
- Molecule 29: 60S ribosomal protein L36



- Molecule 30: 60S ribosomal protein L37



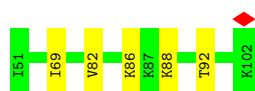
- Molecule 31: Large ribosomal subunit protein eL38



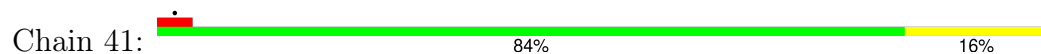
- Molecule 32: 60S ribosomal protein L39

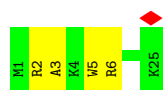


- Molecule 33: Large ribosomal subunit protein eL40



- Molecule 34: eL41





- Molecule 35: eL42

Chain 42: 88% 11%



- Molecule 36: 60S ribosomal protein L37a

Chain ff: 90% 8%



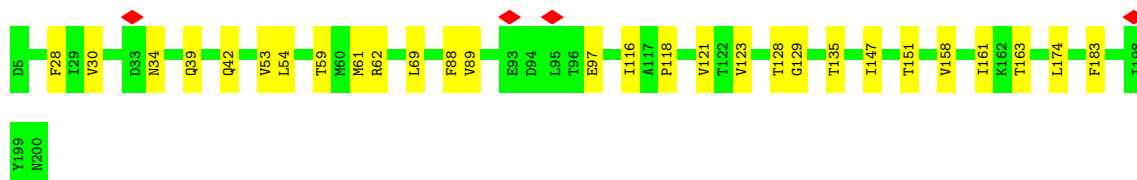
- Molecule 37: 60S ribosomal protein L28

Chain gg: 90% 10%



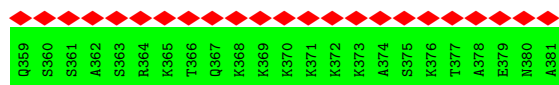
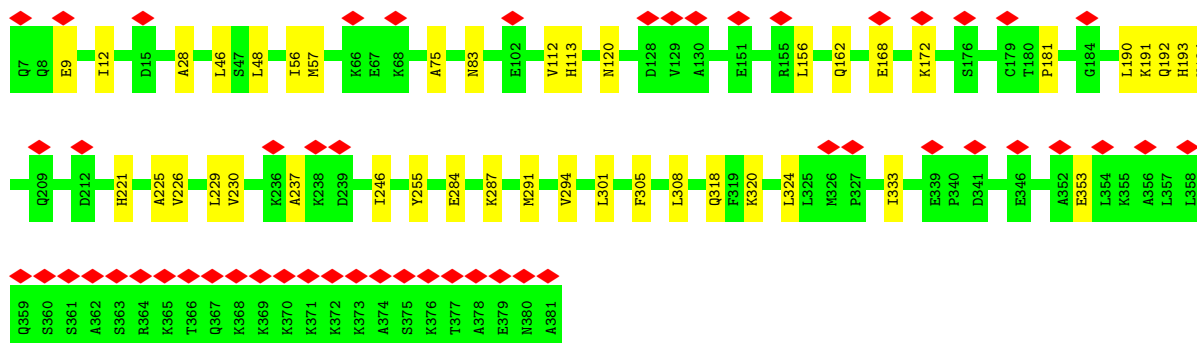
- Molecule 38: 60S acidic ribosomal protein P0

Chain s: 86% 14%



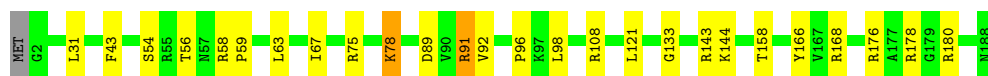
- Molecule 39: Proliferation-associated protein 2G4

Chain EB: 14% 89% 11%



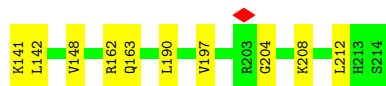
- Molecule 40: Large ribosomal subunit protein eL18

Chain Q:  86% 13% ..



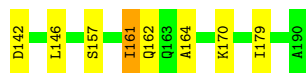
- Molecule 41: Ribosomal protein L10

Chain 10:  80% 17% ..



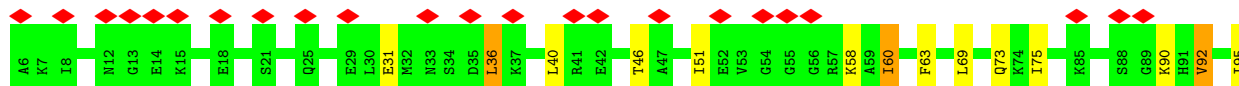
- Molecule 42: 60S ribosomal protein L9

Chain L9:  79% 19% .



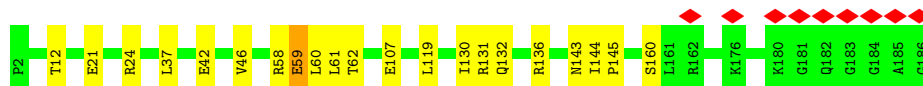
- Molecule 43: Small ribosomal subunit protein eS7

Chain S7:  14% 83% 13% ..

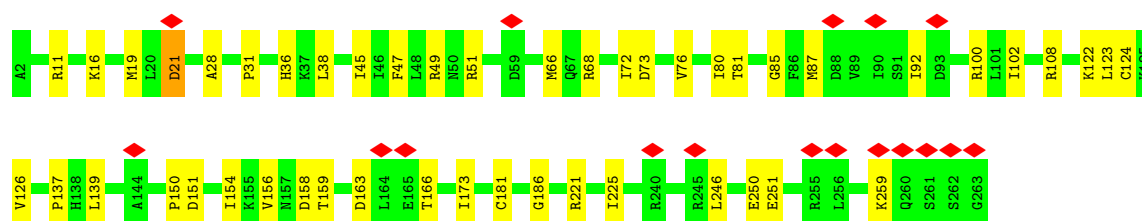
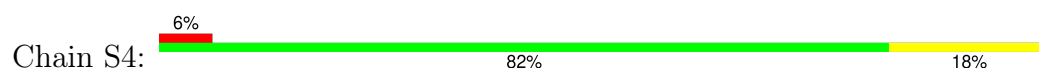


- Molecule 44: 40S ribosomal protein S9

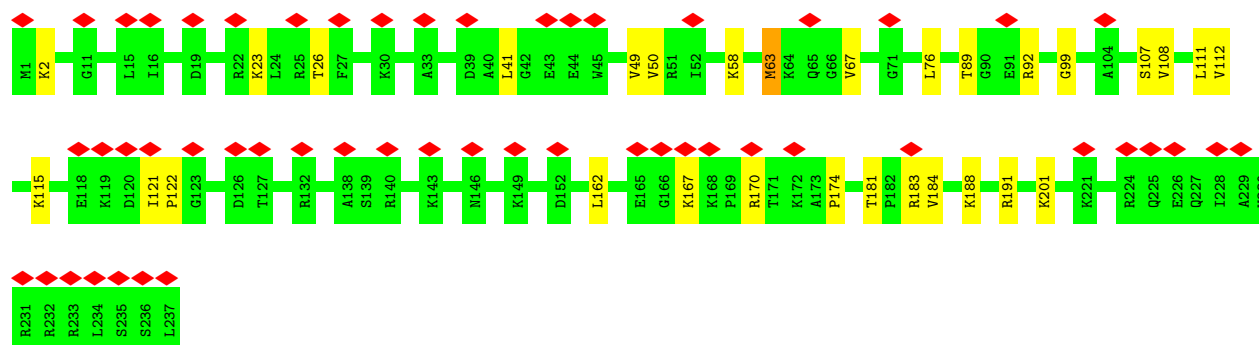
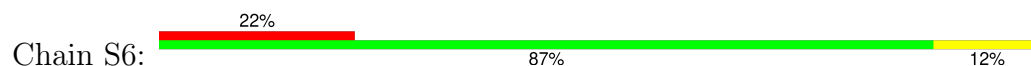
Chain S9:  5% 89% 11% .



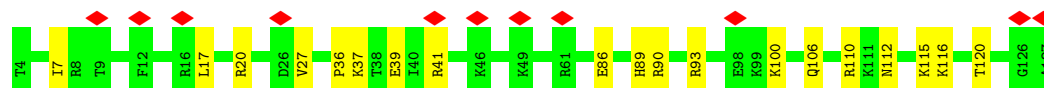
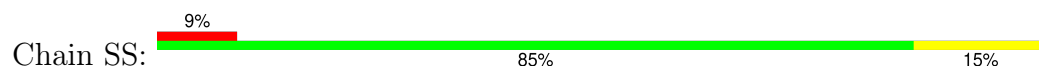
- Molecule 45: 40S ribosomal protein S4



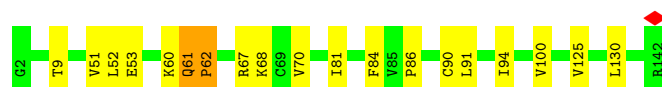
- Molecule 46: 40S ribosomal protein S6



- Molecule 47: 40S ribosomal protein S24



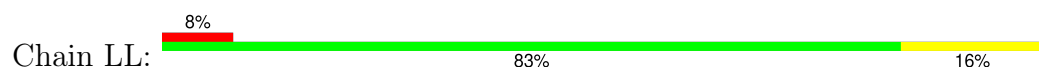
- Molecule 48: 40S ribosomal protein S23

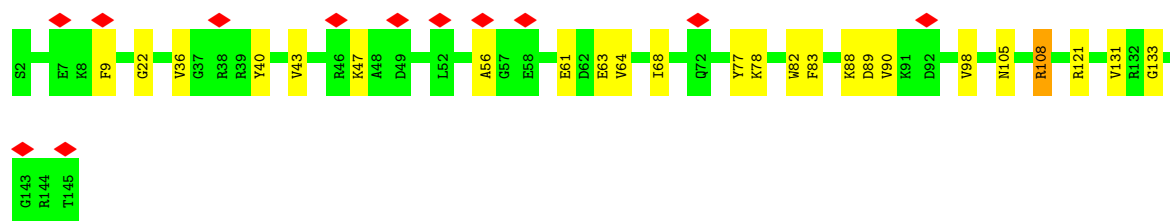


- Molecule 49: 40S ribosomal protein S30



- Molecule 50: 40S ribosomal protein S18





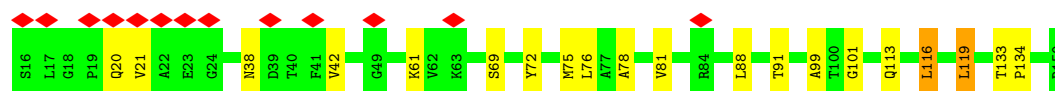
- Molecule 51: 60S ribosomal protein L11

Chain 11: 90% 9% .



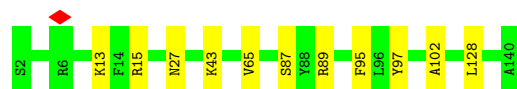
- Molecule 52: Small ribosomal subunit protein uS11

Chain GG: 10% 85% 13% .



- Molecule 53: Large ribosomal subunit protein uL14

Chain 23: 92% 8% .



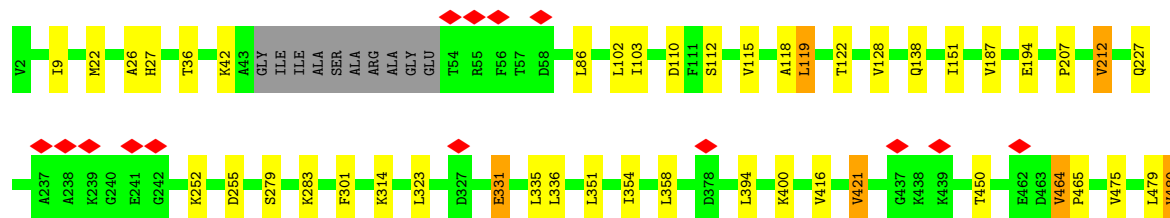
- Molecule 54: 60S ribosomal protein L19

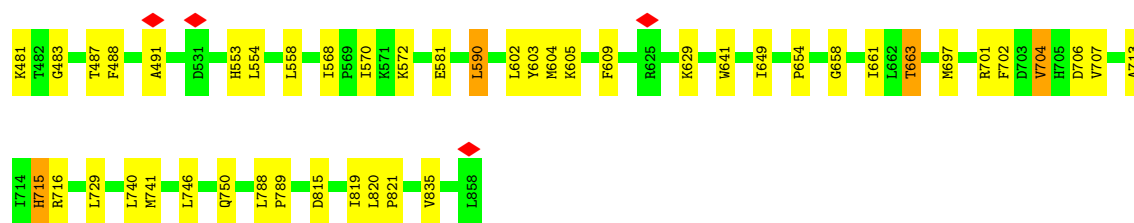
Chain 19: 89% 9% .



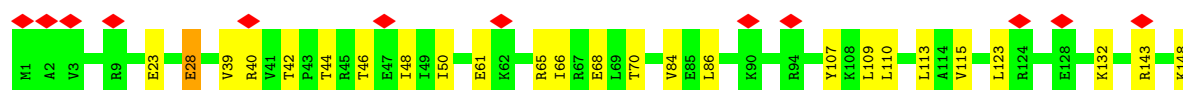
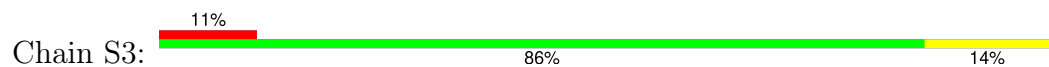
- Molecule 55: Elongation factor 2

Chain v: 88% 10% .

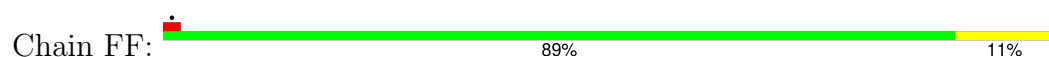




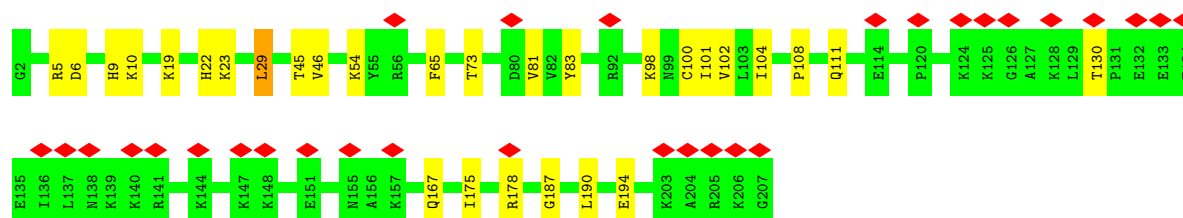
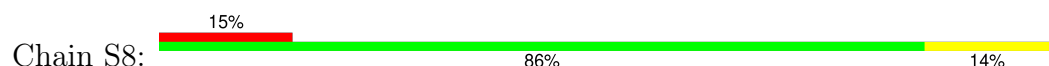
- Molecule 56: 40S ribosomal protein S3



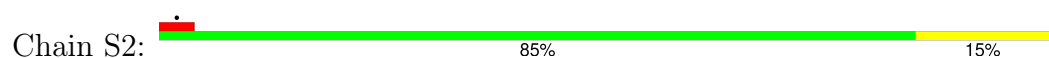
- Molecule 57: 40S ribosomal protein S13



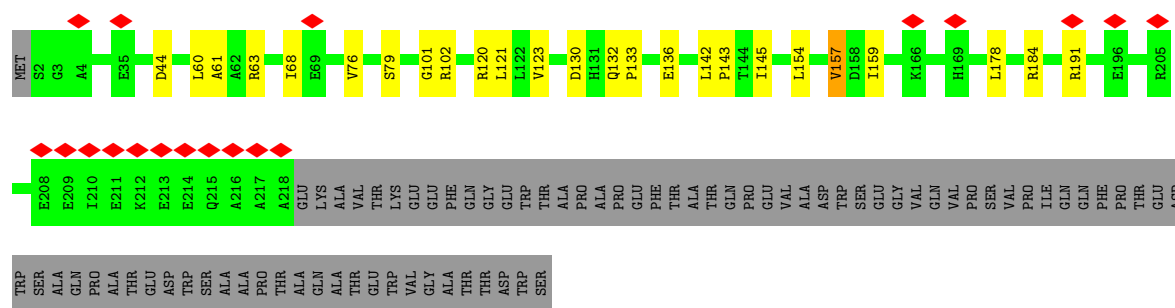
- Molecule 58: 40S ribosomal protein S8



- Molecule 59: 40S ribosomal protein S2



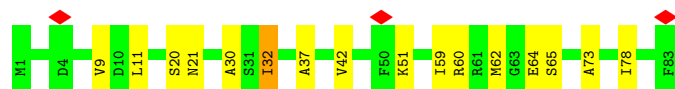
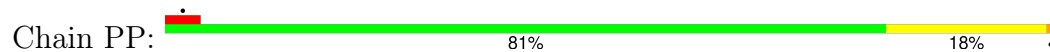
- Molecule 60: 40S_SA_C domain-containing protein



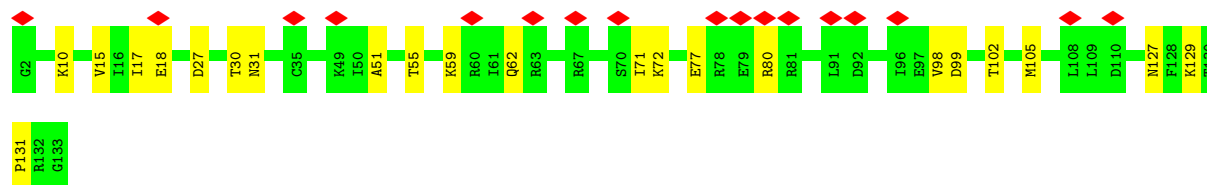
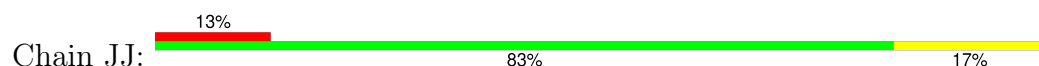
- Molecule 61: eS26



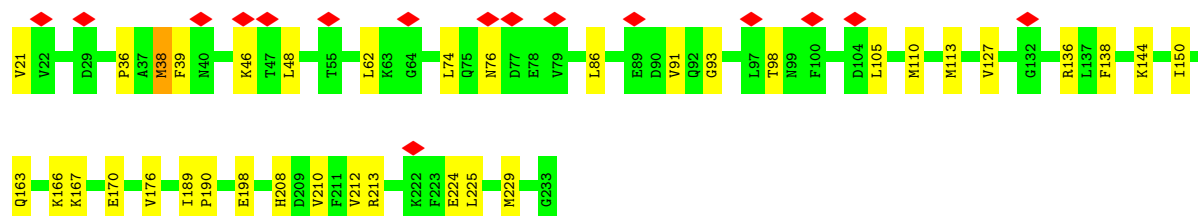
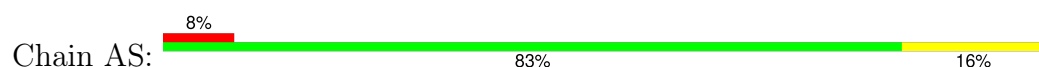
- Molecule 62: eS21



- Molecule 63: 40S ribosomal protein S17



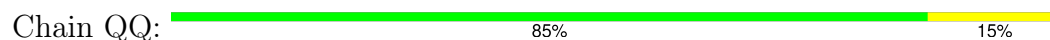
- Molecule 64: 40S ribosomal protein S3a



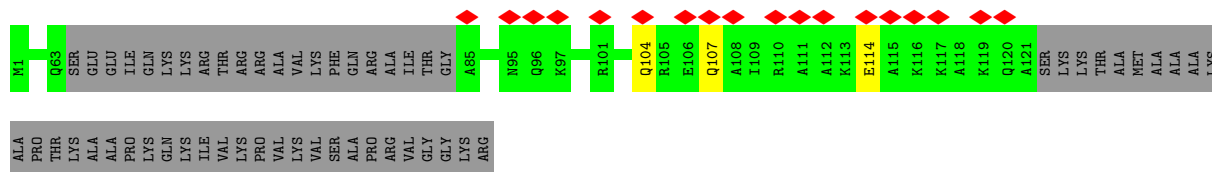
- Molecule 65: 40S ribosomal protein S27



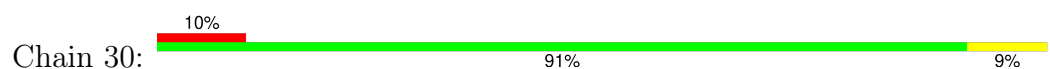
- Molecule 66: 40S ribosomal protein S15a



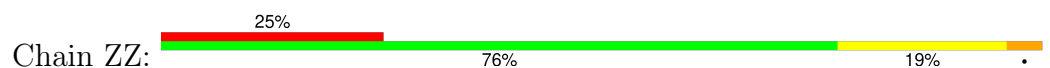
- Molecule 67: Large ribosomal subunit protein eL24



- Molecule 68: Large ribosomal subunit protein eL30

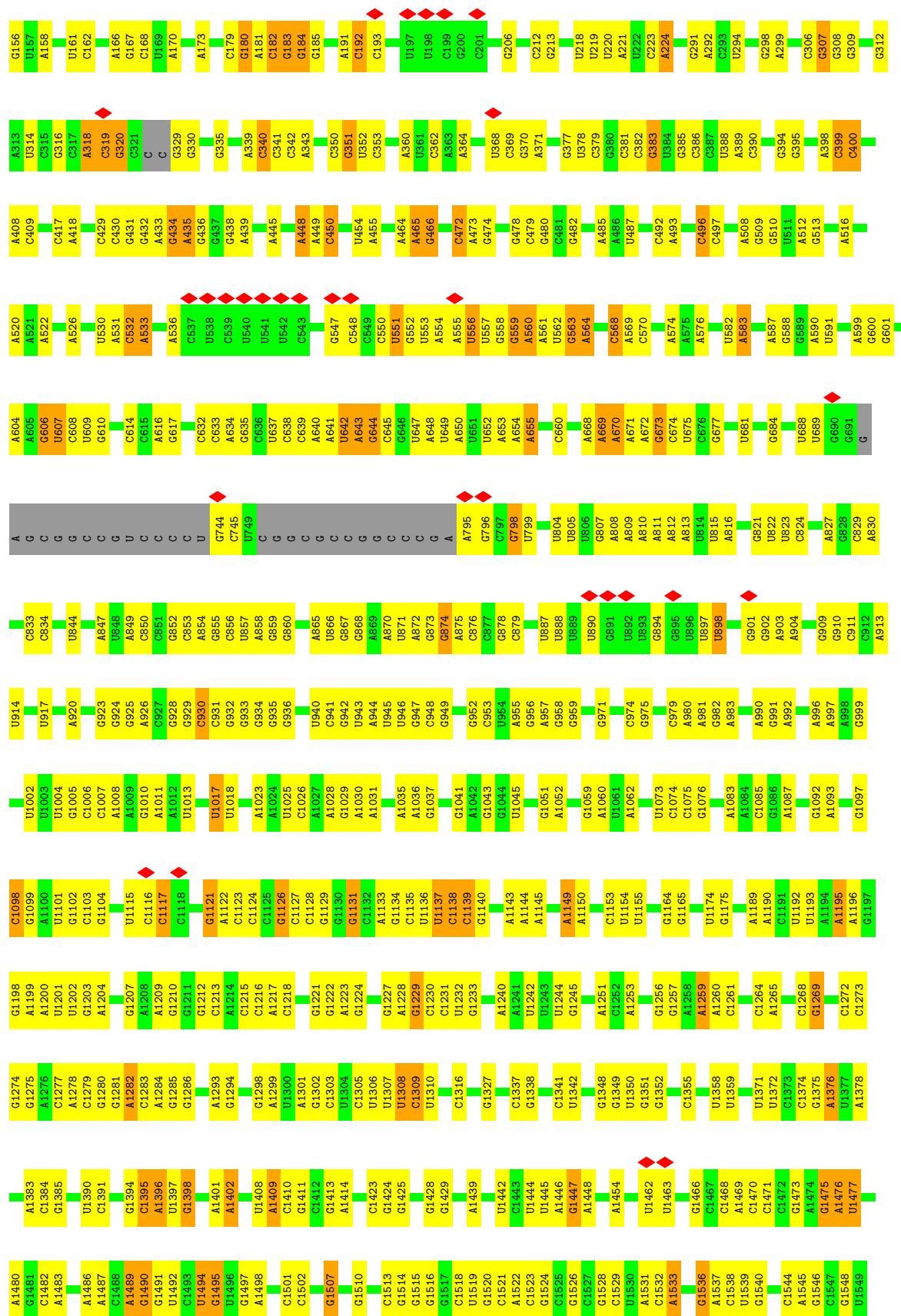


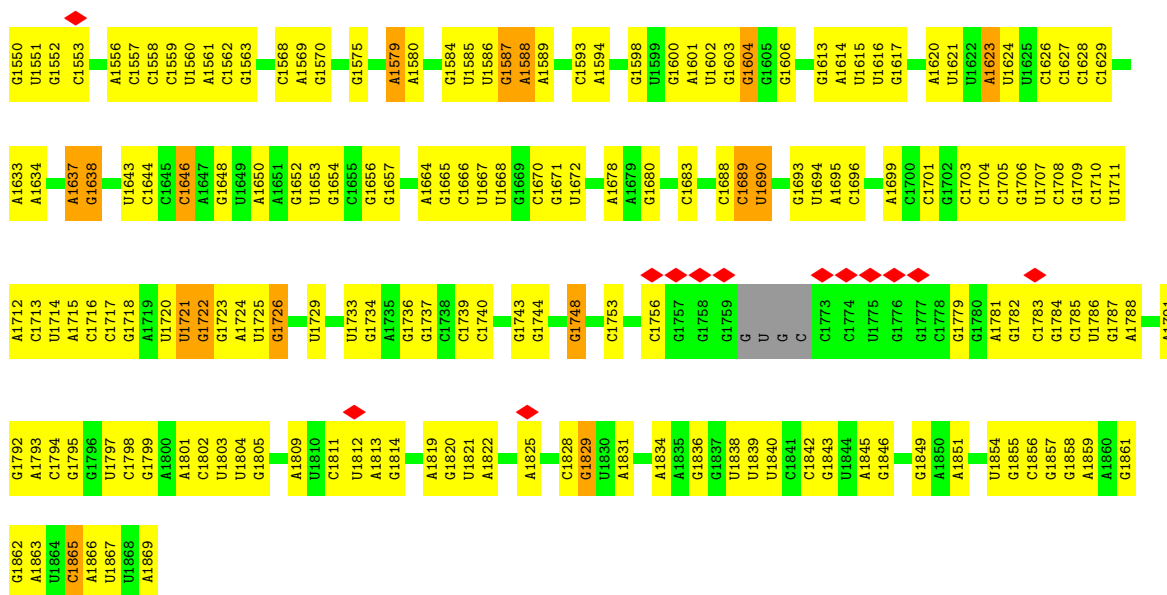
- Molecule 69: 40S ribosomal protein S27a



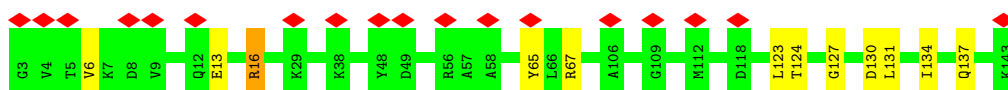
- Molecule 70: 18S rRNA



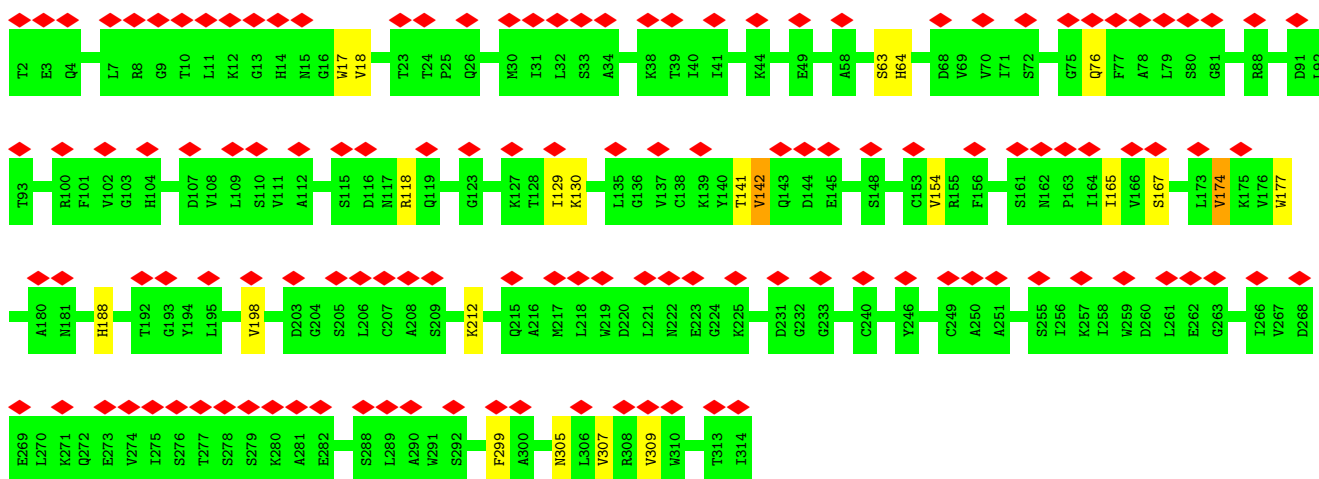
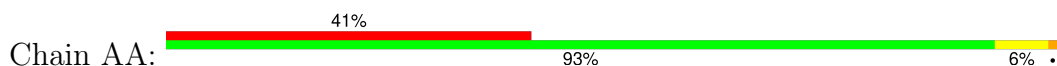




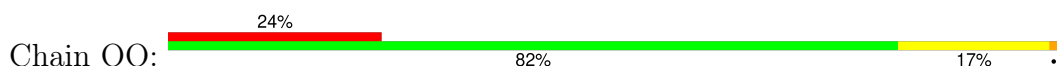
- Molecule 71: Small ribosomal subunit protein eS19



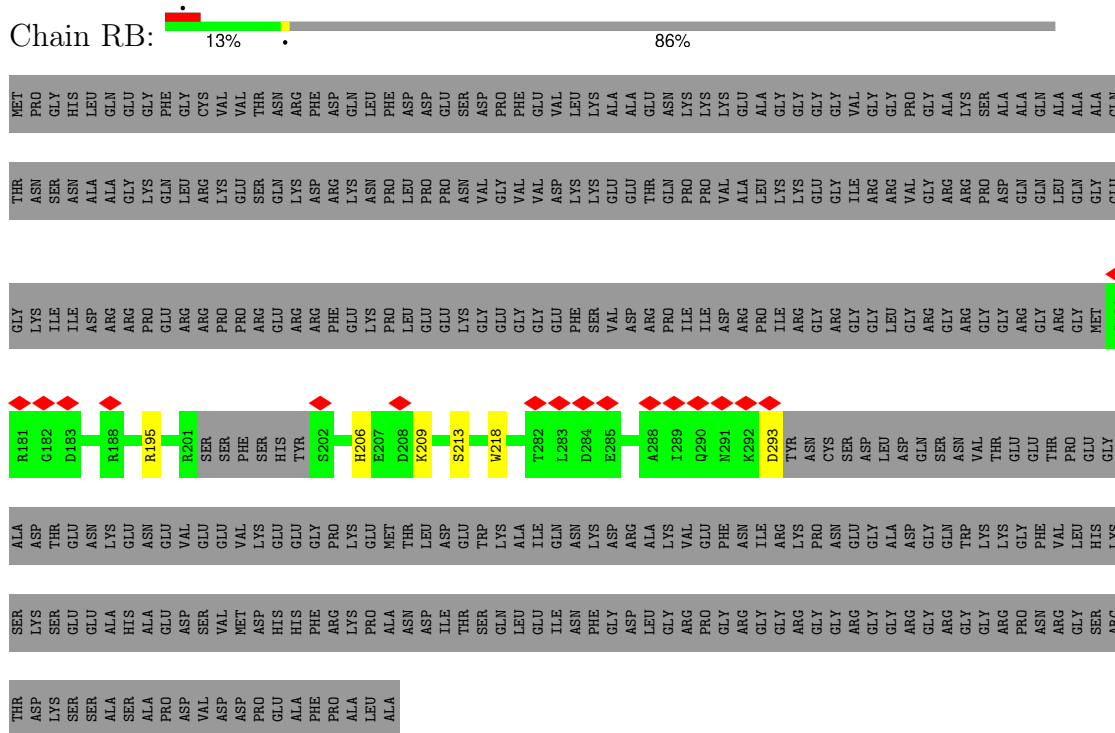
- Molecule 72: Receptor of activated protein C kinase 1



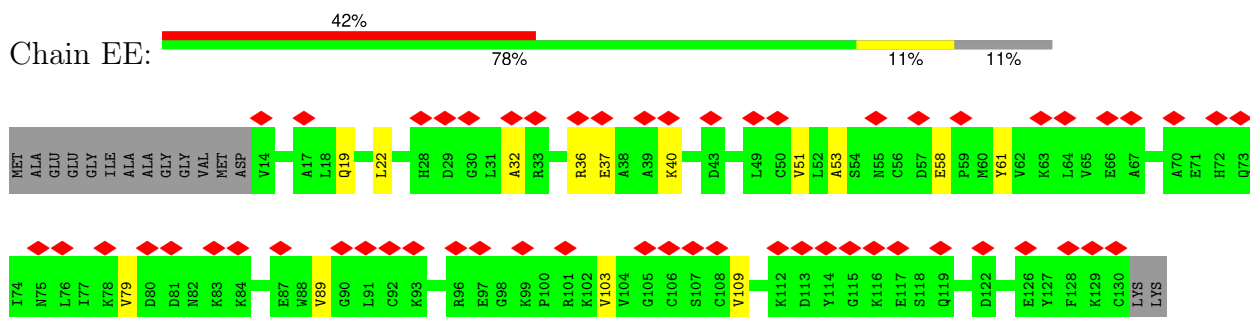
- Molecule 73: 40S ribosomal protein S20



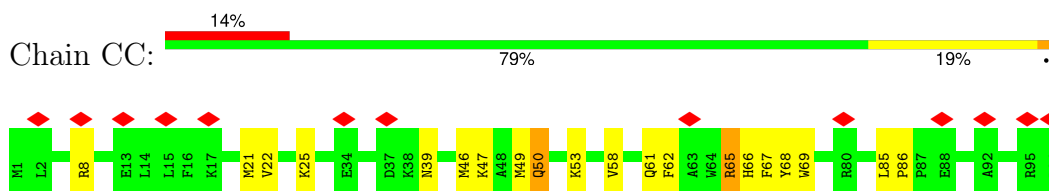
- Molecule 74: SERBP1



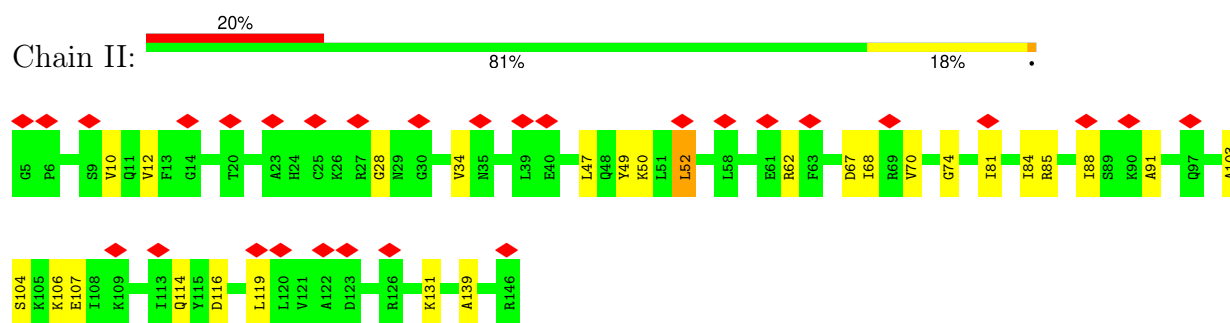
- Molecule 75: 40S ribosomal protein S12



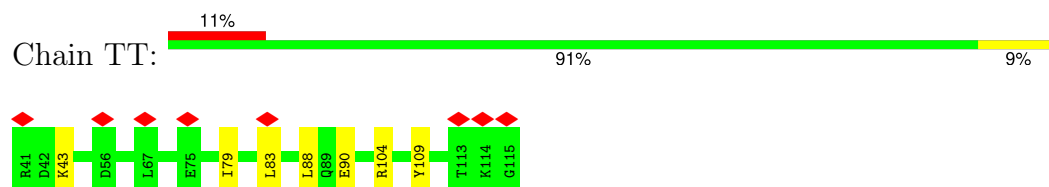
- Molecule 76: 40S ribosomal protein S10



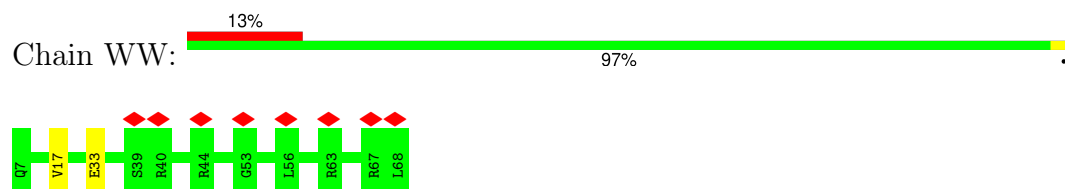
- Molecule 77: Small ribosomal subunit protein uS9



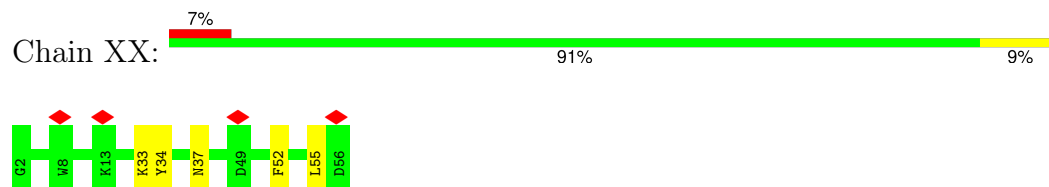
- Molecule 78: 40S ribosomal protein S25



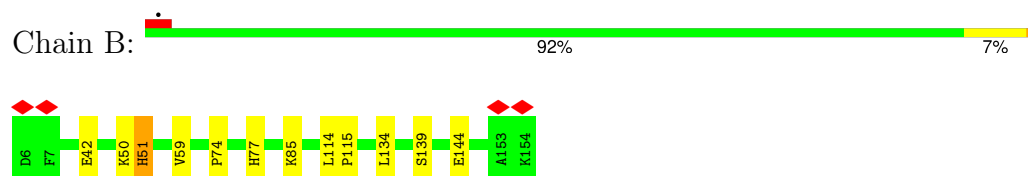
- Molecule 79: 40S ribosomal protein S28



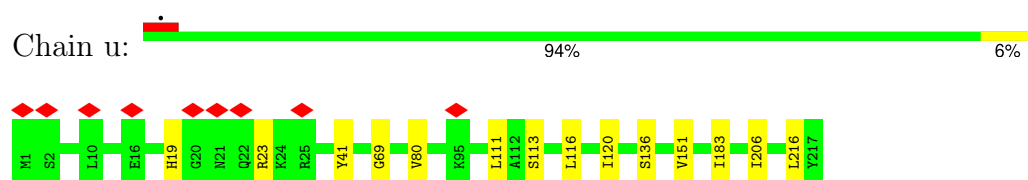
- Molecule 80: 40S ribosomal protein S29



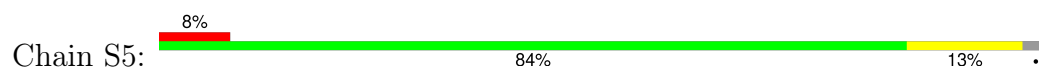
- Molecule 81: Eukaryotic translation initiation factor 5A-1

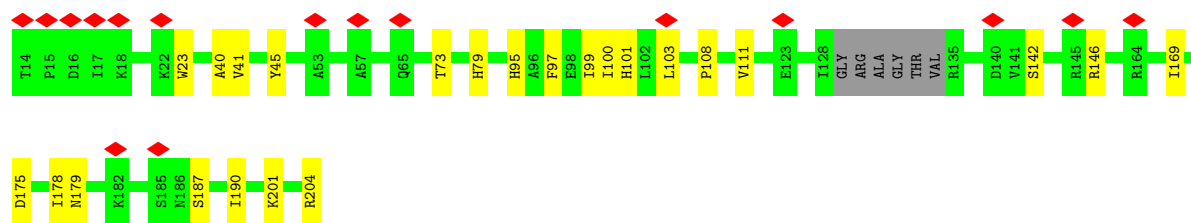


- Molecule 82: Ribosomal protein

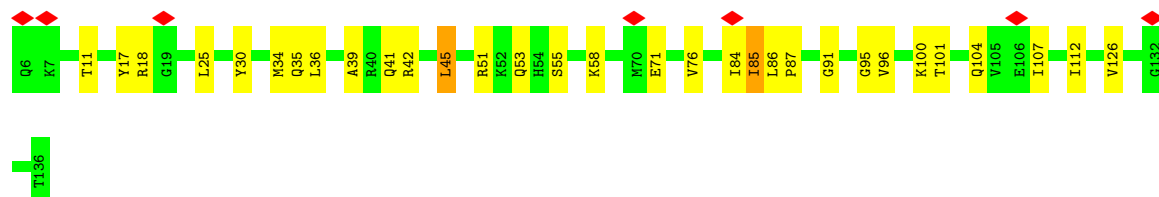
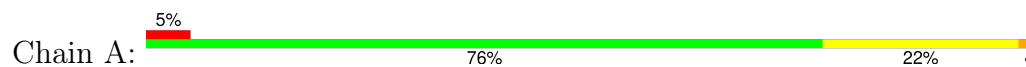


- Molecule 83: Small ribosomal subunit protein uS7

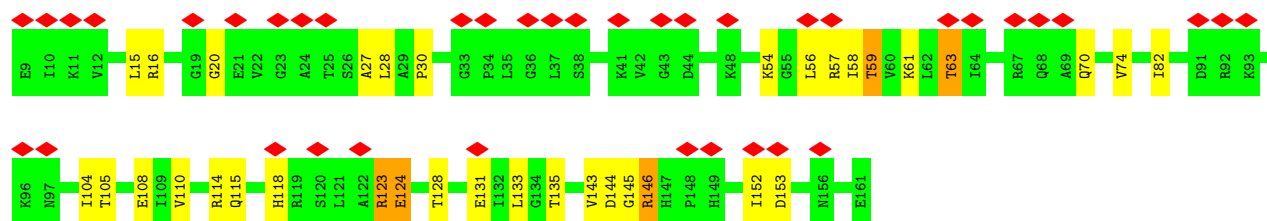
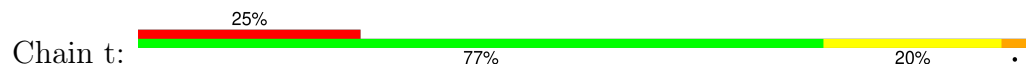




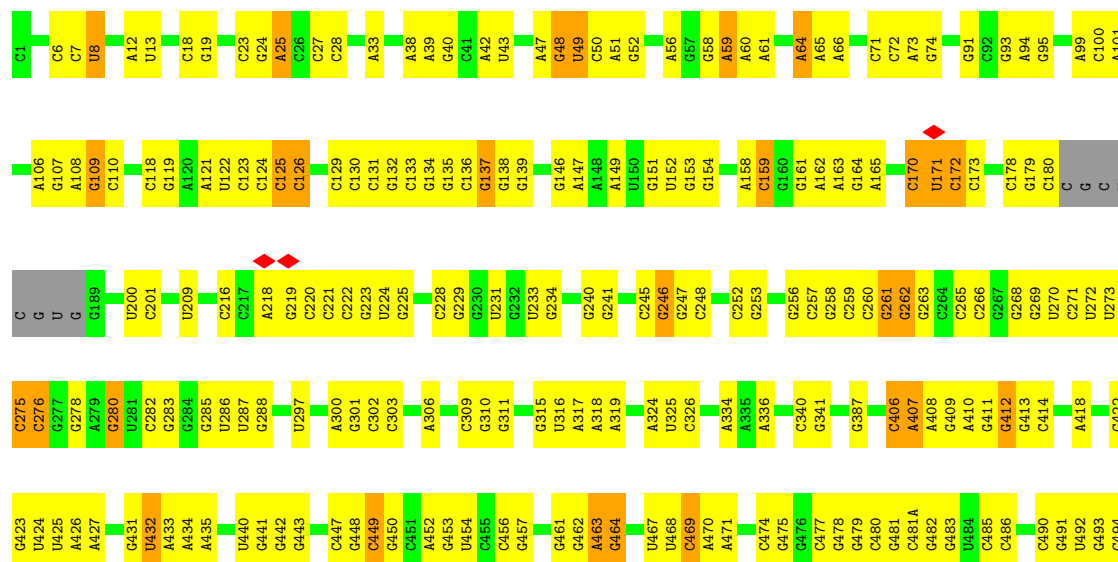
- Molecule 84: Small ribosomal subunit protein uS19



- Molecule 85: uL11



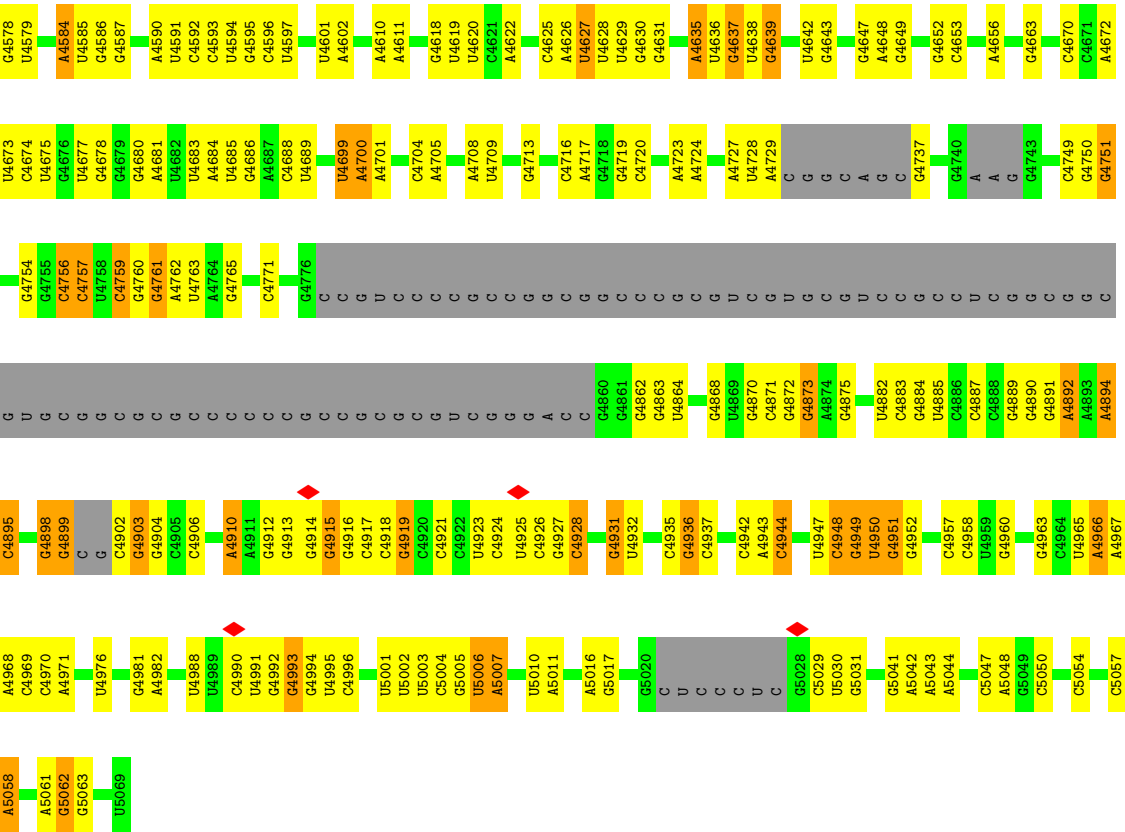
- Molecule 86: 28S rRNA



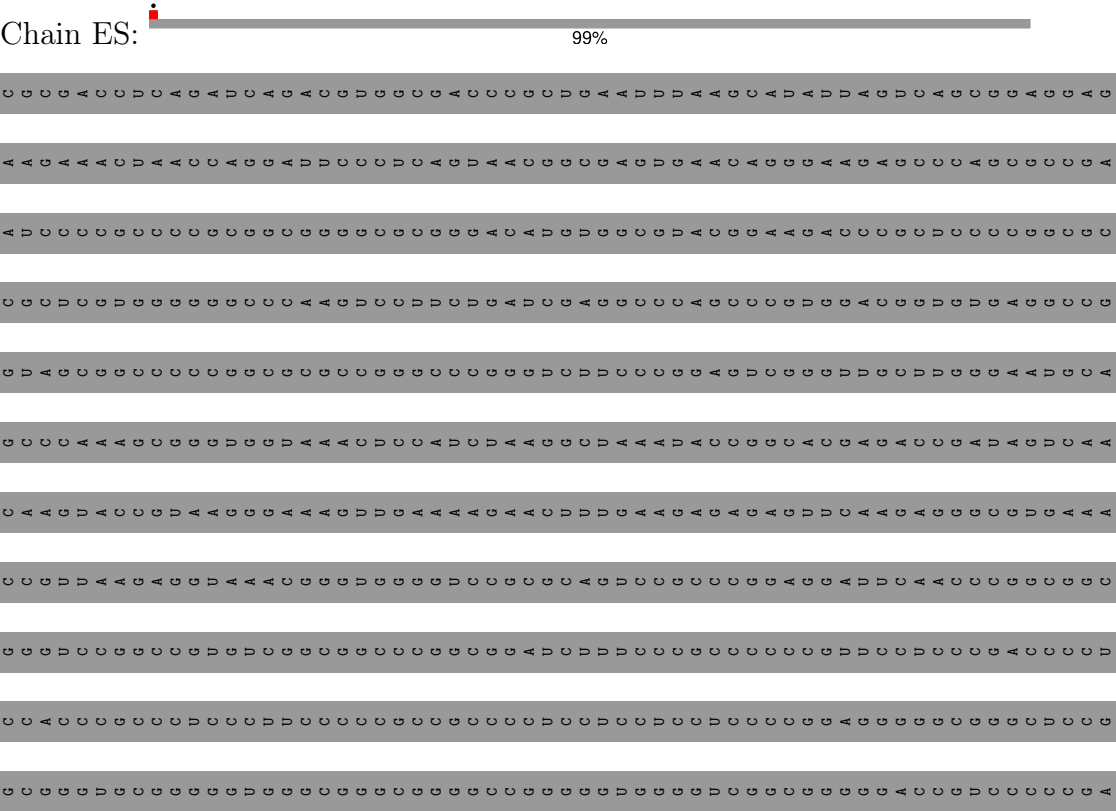
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C1594	G1284	G1349	A1497	G1211	C	C	G933	C	C905	G	G700	G496
U1595	G1285	C1350	G1498	G1212	C	C	C934	C	C906	C	G701	G497
G1596	C1286	G1351	G1499	G1213	U	C	A935	C	C907	C	U702	C498
G1597	G1287	A1354	G1500	C1214	U	C	G935A	C	C908	C	G703	G499
G1604	A1503	G1355	A1502	C1215	U	C	C936	C	C909	C	G704	G500
G1605	G1419	G1356	G1503	C1216	U	C	G939	C	C910	C	G705	U
C1506	A1420	U1357	G1504	G1217	G	C	C940	C	C911	C	C709	U
G1511	A1433	G1358	C1505	G1218	G	C	C941	C	C912	C	A711	C
G1512	C1436	G1359	G1511	G1219	G	C	U945	C	C913	C	C712	U
G1517	C	G1362	G1512	G	G	C	G949	C	C914	C	C713	U
A1518	U1295	C1363	A1517	G	C	C	G950	C	C915	C	G714	U
C1519	G1296	U1364	A1518	G	C	C	G951	C	C916	C	C715	U
C1520	U1297	C	C1519	G	C	C	G952	C	C917	C	C716	U
A1523	G1300	C	G1520	G	C	C	C953	C	C918	C	U717	U
U1528	C1301	A1368	A1523	G	C	C	A956	C	C919	C	C718	U
G1529	U1302	C1369	U1528	G1233	C	C	G957	C	C920	C	C643	U
A1534	A1303	G1370	G1529	G1234	G	C	C958	C	C921	C	G644	U
A1537	C1304	A1371	A1534	C1235	G	C	G959	C	C922	C	C647	U
U1538	C1305	G1377	U1537	C1236	G	C	G961	C	C923	C	A648	U
C1539	C1306	C1378	A1538	A1238	U	C	A964	C	C924	C	C650	U
G1545	A1307	G1379	A1539	C1239	G	C	G965	C	C925	C	C651	U
A1547	C1308	C1380	U1540	G	C	C	A966	C	C926	C	C652	U
C1548	C1313	U1381	G1541	G	C	C	C967	C	C927	C	C653	U
G1549	C1314	G1382	U1542	G	C	C	C968	C	C928	C	C654	U
G1550	G1315	C1383	A1543	G	C	C	C969	C	C929	C	C655	U
C1551	C1316	G1384	U1544	G	C	C	C970	C	C930	C	C656	U
G1552	G1317	C1385	A1545	G	C	C	C971	C	C931	C	C657	U
A1558	U1318	A1387	U1546	G	C	C	C972	C	C932	C	C658	U
C1559	C1322	G1392	A1547	G	C	C	C973	C	C933	C	C659	U
A1563	A1326	G1393	U1548	G	C	C	C974	C	C934	C	C660	U
C1566	C1327	G1394	G1549	G	C	C	C975	C	C935	C	C661	U
G1574	G1328	A1397	U1550	G	C	C	C976	C	C936	C	C662	U
U1577	G1329	C1398	C1551	G	C	C	C977	C	C937	C	C663	U
C1582	A1330	G1404	C1552	G	C	C	C978	C	C938	C	C664	U
U1583	C1331	C	A1553	G	C	C	C979	C	C939	C	C665	U
G1586	C1332	G	U1554	G	C	C	C980	C	C940	C	C666	U
U1587	A1333	C	A1555	G	C	C	C981	C	C941	C	C667	U
C1588	A1334	G	U1556	G	C	C	C982	C	C942	C	C668	U
U1591	C1335	C	U1557	G	C	C	C983	C	C943	C	C669	U
A	G1336	G	U1558	G	C	C	C984	C	C944	C	C670	U
G	U1337	U	U1559	G	C	C	C985	C	C945	C	C671	U
C	G1338	C	U1560	G	C	C	C986	C	C946	C	C672	U
C	U1339	U	U1561	G	C	C	C987	C	C947	C	C673	U
C	C1340	C	U1562	G	C	C	C988	C	C948	C	C674	U
C	U1341	C	U1563	G	C	C	U	C	C949	C	C675	U
C	A1342	G	U1564	G	C	C	C	C	C950	C	C676	U
C	A1343	C	U1565	G	C	C	C	C	C951	C	C677	U
C	U1344	C	U1566	G	C	C	C	C	C952	C	C678	U
C	C1345	C	U1567	G	C	C	C	C	C953	C	C679	U
C	U1346	C	U1568	G	C	C	C	C	C954	C	C680	U
C	C1347	C	U1569	G	C	C	C	C	C955	C	C681	U
C	U1348	C	U1570	G	C	C	C	C	C956	C	C682	U
C	U1349	C	U1571	G	C	C	C	C	C957	C	C683	U
C	U1350	C	U1572	G	C	C	C	C	C958	C	C684	U
C	U1351	C	U1573	G	C	C	C	C	C959	C	C685	U
C	U1352	C	U1574	G	C	C	C	C	C960	C	C686	U
C	U1353	C	U1575	G	C	C	C	C	C961	C	C687	U
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C	U1355	C	U1577	G	C	C	C	C	C963	C	C689	U
C	U1356	C	U1578	G	C	C	C	C	C964	C	C690	U
C	U1357	C	U1579	G	C	C	C	C	C965	C	C691	U
C	U1358	C	U1580	G	C	C	C	C	C966	C	C692	U
C	U1359	C	U1581	G	C	C	C	C	C967	C	C693	U
C	U1360	C	U1582	G	C	C	C	C	C968	C	C694	U
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C	U1362	C	U1584	G	C	C	C	C	C970	C	C696	U
C	U1363	C	U1585	G	C	C	C	C	C971	C	C697	U
C	U1364	C	U1586	G	C	C	C	C	C972	C	C698	U
C	U1365	C	U1587	G	C	C	C	C	C973	C	C699	U
C	U1366	C	U1588	G	C	C	C	C	C974	C	C700	U
C	U1367	C	U1589	G	C	C	C	C	C975	C	C701	U
C	U1368	C	U1590	G	C	C	C	C	C976	C	C702	U
C	U1369	C	U1591	G	C	C	C	C	C977	C	C703	U
C	U1370	C	U1592	G	C	C	C	C	C978	C	C704	U
C	U1371	C	U1593	G	C	C	C	C	C979	C	C705	U
C	U1372	C	U1594	G	C	C	C	C	C980	C	C706	U
C	U1373	C	U1595	G	C	C	C	C	C981	C	C707	U
C	U1374	C	U1596	G	C	C	C	C	C982	C	C708	U
C	U1375	C	U1597	G	C	C	C	C	C983	C	C709	U
C	U1376	C	U1598	G	C	C	C	C	C984	C	C710	U
C	U1377	C	U1599	G	C	C	C	C	C985	C	C711	U
C	U1378	C	U1600	G	C	C	C	C	C986	C	C712	U
C	U1379	C	U1601	G	C	C	C	C	C987	C	C713	U
C	U1380	C	U1602	G	C	C	C	C	C988	C	C714	U
C	U1381	C	U1603	G	C	C	C	C	C989	C	C715	U
C	U1382	C	U1604	G	C	C	C	C	C990	C	C716	U
C	U1383	C	U1605	G	C	C	C	C	C991	C	C717	U
C	U1384	C	U1606	G	C	C	C	C	C992	C	C718	U
C	U1385	C	U1607	G	C	C	C	C	C993	C	C719	U
C	U1386	C	U1608	G	C	C	C	C	C994	C	C720	U
C	U1387	C	U1609	G	C	C	C	C	C995	C	C721	U
C	U1388	C	U1610	G	C	C	C	C	C996	C	C722	U
C	U1389	C	U1611	G	C	C	C	C	C997	C	C723	U
C	U1390	C	U1612	G	C	C	C	C	C998	C	C724	U
C	U1391	C	U1613	G	C	C	C	C	C999	C	C725	U
C	U1392	C	U1614	G	C	C	C	C	C1000	C	C726	U
C	U1393	C	U1615	G	C	C	C	C	C1001	C	C727	U
C	U1394	C	U1616	G	C	C	C	C	C1002	C	C728	U
C	U1395	C	U1617	G	C	C	C	C	C1003	C	C729	U
C	U1396	C	U1618	G	C	C	C	C	C1004	C	C730	U
C	U1397	C	U1619	G	C	C	C	C	C1005	C	C731	U
C	U1398	C	U1620	G	C	C	C	C	C1006	C	C732	U
C	U1399	C	U1621	G	C	C	C	C	C1007	C	C733	U
C	U1400	C	U1622	G	C	C	C	C	C1008	C	C734	U
C	U1401	C	U1623	G	C	C	C	C	C1009	C	C735	U
C	U1402	C	U1624	G	C	C	C	C	C1010	C	C736	U
C	U1403	C	U1625	G	C	C	C	C	C1011	C	C737	U
C	U1404	C	U1626	G	C	C	C	C	C1012	C	C738	U
C	U1405	C	U1627	G	C	C	C	C	C1013	C	C739	U
C	U1406	C	U1628	G	C	C	C	C	C1014	C	C740	U
C	U1407	C	U1629	G	C	C	C	C	C1015	C	C741	U
C	U1408	C	U1630	G	C	C	C	C	C1016	C	C742	U
C	U1409	C	U1631	G	C	C	C	C	C1017	C	C743	U
C	U1410	C	U1632	G	C	C	C	C	C1018	C	C744	U
C	U1411	C	U1633	G	C	C	C	C	C1019	C	C745	U
C	U1412	C	U1634	G	C	C	C	C	C1020	C	C746	U
C	U1413	C	U1635	G	C	C	C	C	C1021	C	C747	U
C	U1414	C	U1636	G	C	C	C	C	C1022	C	C748	U
C	U1415	C	U1637	G	C	C	C	C	C1023	C	C749	U
C	U1416	C	U1638	G	C	C	C	C	C1024	C	C750	U
C	U1417	C	U1639	G	C	C	C	C	C1025	C	C751	U
C	U1418	C	U1640	G	C	C	C	C	C1026	C	C752	U
C	U1419	C	U1641	G	C	C	C	C	C1027	C	C753	U
C	U1420	C	U1642	G	C	C	C	C	C1028	C	C754	U
C	U1421	C	U1643	G	C	C	C	C	C1029	C	C755	U
C	U1422	C	U1644	G	C	C	C	C	C1030	C	C756	U
C	U1423	C	U1645	G	C	C	C	C	C1031	C	C757	U
C	U1424	C	U1646	G	C	C	C	C	C1032	C	C758	U
C	U1425	C	U1647	G	C	C	C	C	C1033	C	C759	U
C	U1426	C	U1648	G	C	C	C	C	C1034	C	C760	U
C	U1427	C	U1649	G	C	C	C	C	C1035	C	C761	U
C	U1428	C	U1650	G	C	C	C	C	C1036	C	C762	U
C	U1429	C	U1651	G	C	C	C	C	C1037	C	C763	U
C	U1430	C	U1652	G	C	C	C	C	C1038	C	C764	U
C	U1431	C	U1653	G	C	C	C	C	C1039	C	C765	U
C	U1432	C	U1654	G	C	C	C	C	C1040			



U4465	A4373	A4273	A4186	C4121	A	C	U3920	C3847	G3740	A3646	C	U
C4466	A4274	A4275	G4187	C4122	C	U	U3921	U3848	U3745	A3647	C	G
U4471	A4276	G4275	U4188	C4125	A	C	G3922	C3850	A3748	A3648	C	G
A4472	A4281	A4281	U4189	C4126	U	C	C3924	U3851	A3748	A3651	C	G
A4473	A4281	A4281	G4191	A4127	C	C	U3927	A3852	G3753	A3652	C	G
A4474	U4290	U4290	G4197	C4134	A	C	A3928	C3855	G3753	A3652	C	G
G4475	C4291	C4291	G4198	C4135	C4057	C	A3929	A3856	A3759	C3858	G	G
C4476	A4297	A4297	C4199	C4136	U4058	C	G3929	U3859	A3760	G3659	C	G
U4489	A4298	A4298	C4199	C4137	C4059	C	U3930	A3861	C3761	C3860	C	G
A4490	U4299	U4299	G4201	C	U4060	C	U3931	A3862	U3762	C3862	C	G
A4495	C4300	C4300	U4202	C	C4061	C	U3932	A3865	A3763	A3663	C	C
A4496	U4301	U4301	A4203	C	C4064	C	G3933	A3865	U3764	C3864	U	C
U4500	U4302	U4302	G	U	C4064	C	G3934	A3865	G3765	G3665	C	G
A4503	C4303	C4303	U4208	G	U4069	C	C3937	A3867	G3765	A3665	C	G
C4504	A4304	A4304	G4209	C	U4070	C	G3938	C3868	U3770	C3867	C	C
C4505	C4305	C4305	C	C	U4071	C	G3939	C3869	C3771	C3867	C	C
C4506	U4306	U4306	A4214	U	C4072	C	U3940	C3870	C3771	C3867	C	C
C4506	C4314	C4314	G4215	C	A4073	C	G3941	A3871	U3773	C3867	C	C
A4507	A4315	A4315	G4216	C	U4076	C	G3944	A3872	U3773	C3867	C	C
C4508	G4316	G4316	A4219	G	C4076	C	G3944	G3873	A3774	C3867	C	C
U4512	A4317	A4317	A4220	C	U4080	C	C3948	G3874	A3775	C3867	C	C
A4513	C4318	C4318	A4228	C	G4081	C	A3949	G3875	G3776	C3867	C	C
C4519	G4320	G4320	U4229	G	G4084	C	A3952	A3877	G3777	C3867	C	C
G4520	A4321	A4321	G4232	G	A4085	C	G3953	C3878	A3783	C3867	C	C
U4521	C4322	C4322	U4233	C	U4086	C	A3953	G3879	A3784	A3702	C	C
G4524	A4325	A4325	A4234	C	G4087	C	A	G3880	A3785	G3703	C	C
C4525	G4236	G4236	G4235	C	G4088	C	G	G3881	U3786	C3706	C	C
U4531	G4237	G4237	G4236	G	G4089	C	U	C3882	G3787	U3707	C	C
C4536	C4238	C4238	G4237	C	G4091	C	G	U3883	C3788	C3708	C	C
C4537	A4239	A4239	G4240	C	G4092	C	U	U3884	G3789	U3709	C	C
G4538	G4240	G4240	G4246	C	G4093	C	G	G3888	G3792	G3710	C	C
U4539	G4247	G4247	G4247	C	G4094	C	A	G3889	U3796	A3599	C	C
A4548	A4251	A4251	A4251	C	G4095	C	A	U3892	C3797	G3600	C	C
C4549	C4252	C4252	C4252	C	C4096	C	U	C3893	G3811	A3604	C	C
G4550	A4253	A4253	U4163	C	G4097	C	A	A3894	U3814	C3605	C	C
U4551	G4254	G4254	C4164	C	G4098	C	A	G3897	A3718	U3607	C	C
U4552	C4166	C4166	C4164	C	C	C	U	U3814	A3719	A3608	C	C
C4560	C4166	C4166	C4166	C	C	C	G	A3817	G3720	G3609	C	C
U4563	A4170	A4170	A4170	C	A	C	G	U3818	G3721	A3610	C	C
A4564	U4174	U4174	C4175	C	G	C	A	G3722	G3722	A3611	C	C
C4565	C4175	C4175	C4176	C	G4108	C	C	A3723	A3723	C3619	C	C
U4566	C4176	C4176	C4177	C	G4109	C	C	G3725	A3724	G3619	C	C
G4567	U4178	U4178	C4179	C	U4113	C	C	A3726	A3726	A3624	C	C
C4573	C4179	C4179	C4179	C	U4116	C	C	A3727	A3727	G3625	C	C
U4574	A4183	A4183	G4183	C	U4117	C	C	A3728	A3728	G3626	C	C
U4575	C4184	C4184	C4184	C	U4118	C	C	A3729	A3729	C3633	C	C
U4577	C4185	C4185	C4185	C	U4119	C	C	A3730	A3730	G3634	C	C
					U4120	C	C	A3731	A3731	A3733	C	C
								A3732	A3732	G3635	C	C
								U3734	U3734	C3636	C	C
								G3735	G3735	U3637	C	C
								A3736	A3736	G3638	C	C
								G3738	G3738	U3641	C	C
								C3739	C3739		C	C



● Molecule 87: ES27L



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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	157683	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	39	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	OTHER	Depositor
Maximum map value	36.663	Depositor
Minimum map value	-14.311	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.783	Depositor
Recommended contour level	2.4	Depositor
Map size ($\text{\AA}$)	664.0, 664.0, 664.0	wwPDB
Map dimensions	800, 800, 800	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.83, 0.83, 0.83	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GDP, ZN, 5CT, DDE

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	17	0.15	0/1518	0.48	2/2029 (0.1%)
2	DD	0.11	0/1195	0.29	0/1597
3	58	0.13	0/3581	0.30	0/5577
4	5	0.12	0/2858	0.27	0/4455
5	L8	0.13	0/1936	0.36	0/2596
6	L3	0.13	0/3240	0.34	0/4339
7	L4	0.12	0/2937	0.33	0/3946
8	L5	0.12	0/2437	0.32	0/3264
9	L6	0.12	0/1762	0.33	0/2362
10	L7	0.12	0/1910	0.31	0/2549
11	aa	0.13	0/1910	0.36	0/2569
12	13	0.13	0/1732	0.35	0/2316
13	14	0.13	0/1158	0.34	0/1547
14	15	0.13	0/1746	0.36	0/2338
15	bb	0.15	0/1662	0.35	0/2222
16	20	0.14	0/1501	0.36	0/2012
17	21	0.12	0/1326	0.31	0/1770
18	22	0.14	0/823	0.37	0/1104
19	cc	0.11	0/984	0.31	0/1323
20	26	0.11	0/1132	0.32	0/1504
21	27	0.13	0/1130	0.34	0/1507
22	dd	0.13	0/1191	0.34	0/1590
23	29	0.12	0/861	0.32	0/1138
24	31	0.12	0/903	0.34	0/1216
25	32	0.12	0/1071	0.33	0/1429
26	ee	0.14	0/895	0.37	0/1198
27	34	0.11	0/916	0.30	0/1220
28	35	0.12	0/1021	0.34	0/1348
29	36	0.11	0/841	0.30	0/1112
30	37	0.13	0/720	0.37	0/952
31	38	0.13	0/575	0.36	0/761
32	39	0.12	0/459	0.32	0/608

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	40	0.11	0/435	0.31	0/575
34	41	0.14	0/240	0.34	0/305
35	42	0.12	0/864	0.35	0/1140
36	ff	0.13	0/718	0.38	0/953
37	gg	0.13	0/1006	0.33	0/1349
38	s	0.14	0/1530	0.35	0/2064
39	EB	0.14	0/2979	0.36	1/4000 (0.0%)
40	Q	0.13	0/1538	0.38	0/2054
41	10	0.13	0/1734	0.35	0/2315
42	L9	0.14	0/1535	0.38	0/2063
43	S7	0.14	0/1510	0.35	0/2022
44	S9	0.13	0/1550	0.34	0/2069
45	S4	0.12	0/2118	0.34	0/2849
46	S6	0.13	0/1946	0.31	0/2590
47	SS	0.13	0/1028	0.32	0/1366
48	RR	0.13	0/1116	0.42	2/1490 (0.1%)
49	YY	0.13	0/447	0.34	0/587
50	LL	0.15	0/1208	0.40	0/1618
51	11	0.13	0/1385	0.39	0/1852
52	GG	0.12	0/1020	0.35	0/1369
53	23	0.11	0/1048	0.33	0/1402
54	19	0.12	0/1524	0.31	0/2013
55	v	0.13	0/6733	0.34	0/9091
56	S3	0.14	0/1796	0.35	0/2417
57	FF	0.12	0/1226	0.30	0/1649
58	S8	0.13	0/1715	0.36	0/2287
59	S2	0.14	0/1753	0.35	0/2369
60	BB	0.12	0/1747	0.33	0/2374
61	UU	0.12	0/828	0.34	0/1109
62	PP	0.12	0/643	0.31	0/860
63	JJ	0.15	0/1082	0.37	0/1452
64	AS	0.12	0/1756	0.32	0/2350
65	VV	0.11	0/665	0.31	0/891
66	QQ	0.14	0/1051	0.36	0/1406
67	24	0.12	0/829	0.31	0/1099
68	30	0.13	0/895	0.33	0/1196
69	ZZ	0.13	0/567	0.39	0/753
70	18	0.11	0/39682	0.31	0/61841
71	MM	0.14	0/1115	0.33	0/1493
72	AA	0.13	0/2493	0.34	0/3394
73	OO	0.12	0/805	0.33	0/1081
74	RB	0.11	0/466	0.27	0/616
75	EE	0.14	0/918	0.38	0/1233

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	CC	0.16	0/834	0.43	0/1125
77	II	0.14	0/1146	0.35	0/1534
78	TT	0.14	0/604	0.30	0/810
79	WW	0.15	0/490	0.40	0/656
80	XX	0.10	0/470	0.31	0/623
81	B	0.15	0/1144	0.36	0/1535
82	u	0.11	0/1771	0.30	0/2375
83	S5	0.13	0/1492	0.32	0/2005
84	A	0.15	0/1099	0.38	0/1465
85	t	0.16	0/1174	0.45	0/1582
86	28	0.14	0/83916	0.33	0/130870
87	ES	0.15	0/844	0.40	0/1314
All	All	0.13	0/240159	0.33	5/350398 (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
1	17	0	1

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	17	168	LYS	CA-C-N	7.83	135.80	121.70
1	17	168	LYS	C-N-CA	7.83	135.80	121.70
48	RR	60	LYS	CA-C-N	5.63	130.05	121.03
48	RR	60	LYS	C-N-CA	5.63	130.05	121.03
39	EB	83	ASN	CB-CA-C	-5.07	110.34	117.23

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	17	169	LYS	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	17	1490	0	1560	17	0
2	DD	1175	0	1249	3	0
3	58	3208	0	1629	49	0
4	5	2558	0	1296	24	0
5	L8	1898	0	1993	28	0
6	L3	3172	0	3310	28	0
7	L4	2883	0	3053	27	0
8	L5	2391	0	2424	19	0
9	L6	1729	0	1887	21	0
10	L7	1874	0	1995	18	0
11	aa	1879	0	2027	15	0
12	13	1701	0	1820	14	0
13	14	1137	0	1211	8	0
14	15	1701	0	1749	26	0
15	bb	1630	0	1778	23	0
16	20	1462	0	1508	10	0
17	21	1298	0	1366	9	0
18	22	809	0	833	3	0
19	cc	967	0	1040	7	0
20	26	1115	0	1205	7	0
21	27	1107	0	1182	8	0
22	dd	1162	0	1209	11	0
23	29	848	0	920	5	0
24	31	888	0	930	11	0
25	32	1053	0	1147	7	0
26	ee	876	0	912	16	0
27	34	906	0	998	7	0
28	35	1013	0	1147	11	0
29	36	830	0	916	3	0
30	37	705	0	737	5	0
31	38	569	0	637	7	0
32	39	447	0	480	3	0
33	40	429	0	469	3	0
34	41	239	0	289	2	0
35	42	851	0	924	6	0
36	ff	708	0	756	4	0
37	gg	990	0	1044	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	s	1507	0	1564	12	0
39	EB	2932	0	2967	16	0
40	Q	1514	0	1634	15	0
41	10	1696	0	1745	19	0
42	L9	1516	0	1597	17	0
43	S7	1488	0	1582	16	0
44	S9	1525	0	1640	12	0
45	S4	2076	0	2177	27	0
46	S6	1923	0	2089	19	0
47	SS	1011	0	1083	10	0
48	RR	1098	0	1167	11	0
49	YY	443	0	492	4	0
50	LL	1190	0	1249	14	0
51	11	1362	0	1399	7	0
52	GG	1007	0	1028	10	0
53	23	1034	0	1097	7	0
54	19	1508	0	1664	9	0
55	v	6625	0	6705	43	0
56	S3	1768	0	1866	18	0
57	FF	1202	0	1289	6	0
58	S8	1686	0	1772	17	0
59	S2	1716	0	1806	15	0
60	BB	1710	0	1708	13	0
61	UU	814	0	864	5	0
62	PP	636	0	637	10	0
63	JJ	1068	0	1121	12	0
64	AS	1729	0	1803	20	0
65	VV	651	0	672	4	0
66	QQ	1034	0	1080	14	0
67	24	816	0	856	1	0
68	30	884	0	931	3	0
69	ZZ	555	0	567	12	0
70	18	35486	0	17916	525	0
71	MM	1097	0	1132	6	0
72	AA	2436	0	2393	8	0
73	OO	795	0	862	9	0
74	RB	459	0	421	8	0
75	EE	908	0	939	6	0
76	CC	810	0	836	9	0
77	II	1128	0	1195	14	0
78	TT	598	0	656	6	0
79	WW	488	0	514	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
80	XX	459	0	452	3	0
81	B	1144	0	1148	6	0
82	u	1743	0	1859	7	0
83	S5	1471	0	1522	10	0
84	A	1079	0	1141	19	0
85	t	1160	0	1218	18	0
86	28	75019	0	37897	1064	0
87	ES	756	0	384	22	0
88	34	1	0	0	0	0
88	37	1	0	0	0	0
88	GG	1	0	0	0	0
88	ZZ	1	0	0	0	0
88	ff	1	0	0	0	0
89	v	28	0	12	0	0
All	All	224491	0	171978	2417	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 (2417) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:17:168:LYS:HA	1:17:169:LYS:HB2	1.46	0.95
56:S3:143:ARG:HH21	74:RB:218:TRP:HB2	1.33	0.93
86:28:2465:C:H1'	86:28:3672:G:H22	1.35	0.92
70:18:1723:G:H2'	70:18:1724:A:H8	1.37	0.86
13:14:40:GLY:HA3	13:14:45:VAL:HB	1.56	0.86
70:18:568:C:H42	70:18:582:U:H3	1.25	0.85
86:28:3717:A:H2'	86:28:3718:A:H8	1.40	0.84
70:18:1652:G:H1	70:18:1672:U:H3	1.25	0.83
69:ZZ:140:TYR:HB2	69:ZZ:147:THR:HG23	1.62	0.82
70:18:957:A:H3'	70:18:958:G:H21	1.43	0.81
86:28:462:G:H2'	86:28:463:A:H8	1.45	0.81
70:18:1656:G:H1	70:18:1668:U:H3	1.28	0.80
70:18:649:U:H2'	70:18:650:A:H8	1.47	0.80
86:28:2745:A:H2'	86:28:2746:A:H8	1.46	0.80
42:L9:94:SER:HB3	42:L9:142:ASP:HB3	1.60	0.80
42:L9:41:ILE:HG21	42:L9:73:ILE:HD11	1.65	0.78
71:MM:124:THR:HG23	71:MM:127:GLY:H	1.50	0.77
86:28:1970:A:H5''	86:28:1971:U:H5'	1.66	0.77
86:28:3717:A:H2'	86:28:3718:A:C8	2.19	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
86:28:2411:C:H2'	86:28:2412:A:H8	1.50	0.77
70:18:1705:C:H2'	70:18:1706:G:C8	2.20	0.77
86:28:1332:C:H2'	86:28:1333:A:H8	1.48	0.77
86:28:2557:G:H1	86:28:2570:U:H3	1.32	0.77
86:28:4949:G:H4'	86:28:4950:U:H5'	1.66	0.76
87:ES:3239:G:H2'	87:ES:3240:A:H8	1.50	0.75
28:35:88:THR:HB	28:35:91:MET:HG2	1.66	0.75
63:JJ:31:ASN:HD21	63:JJ:55:THR:HG22	1.51	0.75
70:18:981:A:H2'	70:18:982:G:C8	2.21	0.75
86:28:4274:A:H2'	86:28:4275:G:H8	1.49	0.75
49:YY:104:ARG:HH22	70:18:526:A:H5'	1.52	0.75
56:S3:70:THR:HG22	56:S3:86:LEU:HD13	1.68	0.75
86:28:461:G:H2'	86:28:462:G:C8	2.21	0.75
86:28:138:G:H2'	86:28:139:G:C8	2.21	0.74
83:S5:201:LYS:HA	83:S5:204:ARG:HD3	1.70	0.74
70:18:928:G:H2'	70:18:929:G:C8	2.23	0.74
70:18:1228:A:H2'	70:18:1229:G:H8	1.53	0.73
10:L7:46:ARG:NH1	86:28:976:G:H5''	2.03	0.73
35:42:69:ARG:HG2	35:42:82:MET:HE1	1.68	0.73
86:28:4967:A:H2'	86:28:4968:A:H8	1.53	0.73
86:28:4992:G:H2'	86:28:4993:G:C8	2.24	0.72
5:L8:234:LYS:HG2	5:L8:238:ILE:HD12	1.71	0.72
11:aa:139:VAL:HG21	11:aa:238:LYS:HG3	1.71	0.72
70:18:857:U:H2'	70:18:858:A:C8	2.23	0.72
70:18:1743:G:H21	70:18:1791:A:H62	1.38	0.72
70:18:1670:C:H2'	70:18:1671:G:H8	1.53	0.72
14:15:75:VAL:HB	14:15:79:ALA:HB3	1.71	0.71
45:S4:19:MET:HE1	45:S4:108:ARG:HH11	1.53	0.71
70:18:1562:C:H2'	70:18:1563:G:H8	1.55	0.71
86:28:4537:C:H2'	86:28:4538:G:H8	1.54	0.71
86:28:4274:A:H2'	86:28:4275:G:C8	2.25	0.71
9:L6:216:THR:H	9:L6:219:TYR:HB3	1.56	0.71
70:18:1445:U:H2'	70:18:1446:A:C8	2.25	0.71
70:18:1480:A:H5'	77:II:131:LYS:HE2	1.73	0.71
45:S4:137:PRO:HB2	45:S4:150:PRO:HD2	1.72	0.71
12:13:129:ARG:HH12	86:28:173:C:H5''	1.54	0.71
26:ee:46:ARG:H	26:ee:107:PRO:HG2	1.55	0.70
86:28:4174:U:H2'	86:28:4175:G:H8	1.55	0.70
86:28:3664:G:H2'	86:28:3665:G:H8	1.56	0.70
86:28:4239:A:H2'	86:28:4240:G:H8	1.54	0.70
21:27:46:ILE:HD11	21:27:49:TYR:HA	1.74	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:18:1228:A:H2'	70:18:1229:G:C8	2.27	0.70
86:28:956:A:H8	86:28:957:G:C8	2.10	0.70
58:S8:98:LYS:HB3	70:18:377:G:H5'	1.74	0.70
70:18:530:U:H2'	70:18:531:A:H8	1.57	0.70
86:28:3709:U:H2'	86:28:3710:G:C8	2.27	0.70
40:Q:108:ARG:HH21	86:28:1354:A:H5'	1.56	0.70
70:18:1723:G:H2'	70:18:1724:A:C8	2.24	0.70
56:S3:46:THR:HB	56:S3:84:VAL:HG12	1.74	0.70
55:v:331:GLU:HA	55:v:335:LEU:HD12	1.73	0.69
70:18:941:C:H2'	70:18:942:G:H8	1.56	0.69
87:ES:3238:C:H2'	87:ES:3239:G:H8	1.57	0.69
50:LL:105:ASN:HA	50:LL:108:ARG:HD3	1.74	0.69
86:28:1306:C:H2'	86:28:1307:A:H8	1.57	0.69
86:28:2745:A:H2'	86:28:2746:A:C8	2.28	0.69
54:19:102:LEU:HD22	54:19:138:LEU:HD12	1.74	0.69
16:20:13:VAL:HG22	16:20:63:TYR:HB3	1.75	0.69
57:FF:136:PRO:HG2	57:FF:139:TRP:HB2	1.75	0.69
5:L8:117:GLU:HB2	5:L8:162:ASN:HB2	1.75	0.69
86:28:3736:A:H2'	86:28:3737:A:C8	2.28	0.69
86:28:2520:C:H2'	86:28:2521:G:H8	1.57	0.69
86:28:258:G:H2'	86:28:259:C:C6	2.28	0.68
87:ES:2943:C:H2'	87:ES:2944:G:H8	1.57	0.68
53:23:15:ARG:HB3	86:28:4618:G:H5''	1.75	0.68
70:18:1232:U:H2'	70:18:1233:G:H8	1.58	0.68
86:28:4594:U:H2'	86:28:4595:G:H8	1.57	0.68
55:v:421:VAL:HG13	55:v:464:VAL:HG13	1.74	0.68
56:S3:148:LYS:HB2	74:RB:206:HIS:CE1	2.28	0.68
86:28:1344:C:H2'	86:28:1345:A:H8	1.58	0.68
26:ee:7:CYS:HB2	26:ee:103:VAL:HG23	1.75	0.68
59:S2:210:PRO:HB3	59:S2:240:THR:HG21	1.75	0.68
86:28:1198:G:H2'	86:28:1199:G:H8	1.59	0.68
86:28:4239:A:H2'	86:28:4240:G:C8	2.28	0.68
86:28:287:U:H2'	86:28:288:G:H8	1.58	0.68
86:28:3736:A:H2'	86:28:3737:A:H8	1.58	0.68
86:28:4635:A:H2	86:28:4663:G:H21	1.42	0.68
70:18:941:C:H2'	70:18:942:G:C8	2.29	0.68
70:18:1518:C:H5''	70:18:1519:U:H5''	1.75	0.68
87:ES:2946:G:H2'	87:ES:2947:G:C8	2.29	0.68
9:L6:156:LEU:HD11	9:L6:198:ILE:HG13	1.76	0.68
86:28:258:G:H2'	86:28:259:C:H6	1.59	0.68
70:18:857:U:H2'	70:18:858:A:H8	1.57	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:18:1854:U:H2'	70:18:1855:G:H8	1.59	0.67
86:28:1942:A:H2'	86:28:1943:A:C8	2.28	0.67
14:15:125:SER:HB3	86:28:3937:C:H1'	1.76	0.67
7:L4:78:ARG:HB3	7:L4:88:GLY:HA2	1.76	0.67
70:18:388:U:H2'	70:18:389:A:H8	1.59	0.67
85:t:143:VAL:C	85:t:145:GLY:H	2.01	0.67
86:28:1346:C:H2'	86:28:1347:G:H8	1.59	0.67
31:38:8:ILE:HD11	31:38:56:LEU:HD13	1.76	0.67
86:28:456:C:H2'	86:28:457:G:H8	1.59	0.67
86:28:3732:A:H2'	86:28:3733:A:C8	2.29	0.67
86:28:3944:G:H1	86:28:4069:U:H3	1.42	0.67
14:15:9:GLU:HB3	29:36:44:ILE:HD12	1.77	0.67
19:cc:81:LEU:HD13	19:cc:97:VAL:HG12	1.75	0.67
86:28:651:C:H2'	86:28:652:G:H8	1.60	0.67
10:L7:104:VAL:HG13	10:L7:135:VAL:HG12	1.76	0.67
86:28:287:U:H2'	86:28:288:G:C8	2.29	0.67
43:S7:31:GLU:HB2	43:S7:40:LEU:HD23	1.77	0.66
9:L6:165:VAL:HG13	9:L6:180:GLY:N	2.11	0.66
39:EB:181:PRO:HA	39:EB:230:VAL:HA	1.76	0.66
52:GG:99:ALA:H	52:GG:133:THR:HG22	1.60	0.66
86:28:679:C:H2'	86:28:680:G:H8	1.61	0.66
86:28:4238:G:H2'	86:28:4239:A:H8	1.59	0.66
3:58:148:A:H2'	3:58:149:G:C8	2.29	0.66
16:20:34:ALA:HB1	16:20:39:VAL:HG23	1.77	0.66
10:L7:227:VAL:HA	16:20:39:VAL:HG12	1.78	0.66
70:18:1781:A:H2'	70:18:1782:G:C8	2.30	0.66
3:58:67:U:H2'	3:58:68:G:H8	1.60	0.66
15:bb:85:ARG:HG2	15:bb:99:LEU:HD11	1.77	0.66
70:18:1670:C:H2'	70:18:1671:G:C8	2.30	0.66
86:28:1857:C:H2'	86:28:1858:A:H8	1.60	0.66
86:28:2411:C:H2'	86:28:2412:A:C8	2.31	0.66
70:18:1004:U:H2'	70:18:1005:G:H8	1.59	0.65
60:BB:76:VAL:HG12	60:BB:123:VAL:HB	1.78	0.65
87:ES:2943:C:H2'	87:ES:2944:G:C8	2.32	0.65
86:28:1538:U:H2'	86:28:1539:G:H8	1.61	0.65
86:28:163:A:H2'	86:28:164:G:H8	1.62	0.65
1:17:118:GLN:HE22	86:28:423:G:H21	1.44	0.65
70:18:795:A:H2'	70:18:796:G:H8	1.62	0.65
86:28:1461:C:H2'	86:28:1462:A:H8	1.61	0.65
86:28:2335:C:H2'	86:28:2336:G:H8	1.62	0.64
86:28:4967:A:H2'	86:28:4968:A:C8	2.32	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:18:744:G:C5	70:18:798:G:C2	2.84	0.64
70:18:1007:C:H2'	70:18:1008:A:C8	2.32	0.64
9:L6:160:HIS:HB3	9:L6:163:LYS:HD2	1.79	0.64
12:13:55:ILE:HD11	12:13:96:ILE:HG12	1.78	0.64
86:28:1186:U:H2'	86:28:1187:G:N3	2.13	0.64
86:28:300:A:H2'	86:28:301:G:H8	1.62	0.64
86:28:1338:G:H4'	86:28:1339:U:H6	1.62	0.64
86:28:137:G:H2'	86:28:138:G:C8	2.33	0.64
86:28:1382:G:H2'	86:28:1383:G:H8	1.62	0.64
70:18:931:C:H2'	70:18:932:G:C8	2.33	0.64
86:28:2647:A:H62	86:28:2686:G:H8	1.45	0.64
86:28:3910:C:H2'	86:28:3911:C:H6	1.63	0.64
11:aa:215:ASP:HB2	11:aa:216:PRO:HD3	1.78	0.63
86:28:4321:U:H2'	86:28:4322:G:C8	2.33	0.63
21:27:50:PRO:HD3	21:27:68:ILE:HG12	1.79	0.63
58:S8:65:PHE:HD2	58:S8:104:ILE:HD13	1.62	0.63
70:18:129:C:H42	70:18:183:G:H22	1.45	0.63
86:28:978:G:N2	86:28:1277:G:H1	1.96	0.63
86:28:1204:C:H2'	86:28:1205:G:H8	1.61	0.63
86:28:1307:A:H2'	86:28:1308:C:H6	1.63	0.63
14:15:50:ARG:HH11	86:28:278:G:H4'	1.64	0.63
21:27:54:THR:H	21:27:57:MET:HE2	1.63	0.63
70:18:1588:A:H2'	70:18:1589:A:C8	2.33	0.63
86:28:4260:U:H2'	86:28:4261:C:H6	1.64	0.63
35:42:98:LYS:HE3	86:28:4233:A:H4'	1.81	0.63
86:28:1669:A:H4'	86:28:1685:G:N2	2.14	0.63
86:28:5030:U:H2'	86:28:5031:G:H8	1.63	0.63
70:18:1447:G:H2'	70:18:1448:A:C8	2.34	0.63
86:28:2492:C:H2'	86:28:2493:G:H8	1.64	0.63
16:20:164:LYS:HB2	16:20:165:PRO:HD3	1.81	0.62
86:28:3868:G:H22	86:28:3900:G:H1'	1.63	0.62
70:18:5:U:H2'	70:18:6:G:H8	1.64	0.62
86:28:1645:C:H2'	86:28:1646:A:C8	2.33	0.62
86:28:3848:U:H2'	86:28:3849:A:H8	1.64	0.62
55:v:110:ASP:HB3	55:v:553:HIS:HB2	1.81	0.62
70:18:1277:C:H2'	70:18:1278:A:H8	1.64	0.62
86:28:978:G:H22	86:28:1277:G:H1	1.47	0.62
86:28:2477:A:H2'	86:28:2478:C:C6	2.34	0.62
42:L9:115:ARG:HG2	42:L9:123:ILE:HG22	1.81	0.62
70:18:677:G:H21	70:18:1028:A:H62	1.45	0.62
86:28:1818:G:O2'	86:28:1819:G:H5'	2.00	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
86:28:4178:A:H2'	86:28:4179:G:C8	2.34	0.62
86:28:1503:A:H4'	86:28:1504:G:H5'	1.80	0.62
86:28:3722:G:H2'	86:28:3723:A:H8	1.64	0.62
86:28:3932:U:H2'	86:28:3933:G:H8	1.65	0.62
86:28:939:G:H2'	86:28:940:C:H6	1.64	0.62
86:28:1332:C:H2'	86:28:1333:A:C8	2.33	0.62
86:28:2486:G:H2'	86:28:2487:G:C8	2.35	0.62
86:28:164:G:H2'	86:28:165:A:H8	1.65	0.62
86:28:1505:C:H2'	86:28:1506:G:H8	1.64	0.62
70:18:1748:G:H1	70:18:1786:U:H3	1.46	0.62
85:t:115:GLN:HA	85:t:118:HIS:CD2	2.35	0.62
1:17:168:LYS:HA	1:17:169:LYS:CB	2.26	0.61
86:28:4178:A:H2'	86:28:4179:G:H8	1.65	0.61
86:28:153:G:H2'	86:28:154:G:H8	1.64	0.61
86:28:5057:C:H2'	86:28:5058:A:C8	2.36	0.61
70:18:866:U:H2'	70:18:867:G:C8	2.35	0.61
11:aa:98:ILE:HG21	86:28:4125:C:H4'	1.82	0.61
27:34:60:ARG:HG3	27:34:61:PRO:HD2	1.82	0.61
87:ES:3238:C:H2'	87:ES:3239:G:C8	2.35	0.61
86:28:3893:C:H2'	86:28:3894:A:H8	1.66	0.61
86:28:1086:C:H2'	86:28:1087:A:H8	1.66	0.61
86:28:1198:G:H2'	86:28:1199:G:C8	2.35	0.61
86:28:3910:C:H2'	86:28:3911:C:C6	2.36	0.61
86:28:318:A:H2'	86:28:319:A:H8	1.65	0.61
6:L3:53:MET:HG2	6:L3:77:THR:HG22	1.83	0.61
86:28:478:G:H2'	86:28:479:G:H8	1.66	0.61
86:28:4088:C:H2'	86:28:4089:G:H8	1.66	0.61
86:28:4260:U:H2'	86:28:4261:C:C6	2.36	0.61
54:19:105:LEU:HD22	54:19:135:LYS:HG3	1.83	0.61
85:t:105:THR:HG22	85:t:108:GLU:HG2	1.82	0.61
86:28:3732:A:H2'	86:28:3733:A:H8	1.64	0.61
3:58:30:U:H2'	3:58:31:G:H8	1.66	0.60
70:18:649:U:H2'	70:18:650:A:C8	2.34	0.60
39:EB:191:LYS:HB2	39:EB:194:VAL:HB	1.83	0.60
70:18:1010:G:H2'	70:18:1011:A:H8	1.66	0.60
86:28:2744:A:H2'	86:28:2745:A:C8	2.36	0.60
34:41:2:ARG:HD3	34:41:5:TRP:CD1	2.35	0.60
63:JJ:131:PRO:HA	64:AS:150:ILE:HG23	1.83	0.60
77:II:34:VAL:HG12	77:II:70:VAL:HB	1.82	0.60
86:28:4459:U:H2'	86:28:4460:U:C6	2.36	0.60
87:ES:3244:U:H2'	87:ES:3245:G:H8	1.65	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:10:54:SER:HB2	41:10:135:ILE:HD11	1.83	0.60
1:17:173:LYS:HG3	86:28:2378:G:H5''	1.82	0.60
70:18:5:U:H2'	70:18:6:G:C8	2.36	0.60
70:18:107:A:H2'	70:18:108:G:C8	2.37	0.60
70:18:508:A:H3'	70:18:509:G:H8	1.65	0.60
70:18:1637:A:H4'	70:18:1638:G:O5'	2.01	0.60
77:II:47:LEU:HD23	77:II:81:ILE:HG21	1.82	0.60
77:II:104:SER:HA	77:II:107:GLU:HG2	1.82	0.60
86:28:4638:U:H2'	86:28:4639:G:N3	2.16	0.60
5:L8:117:GLU:HG2	5:L8:124:GLY:H	1.66	0.60
12:13:91:ALA:HB1	12:13:96:ILE:HB	1.83	0.60
70:18:807:G:H2'	70:18:808:A:C8	2.37	0.60
85:t:123:ARG:HG3	85:t:124:GLU:H	1.66	0.60
86:28:4378:A:O2'	86:28:4379:A:H2'	2.01	0.60
11:aa:111:PRO:HD2	11:aa:114:ILE:HD12	1.82	0.60
16:20:83:ARG:HB3	16:20:125:GLN:HB2	1.84	0.60
43:S7:144:ILE:HB	66:QQ:52:ILE:HG12	1.83	0.60
70:18:28:U:H2'	70:18:29:G:H8	1.66	0.60
70:18:220:U:H2'	70:18:221:A:H8	1.67	0.60
70:18:974:C:H2'	70:18:975:G:H8	1.66	0.60
86:28:3916:G:H2'	86:28:3917:A:C8	2.37	0.60
43:S7:51:ILE:HD11	43:S7:176:VAL:HG22	1.84	0.60
86:28:462:G:H2'	86:28:463:A:C8	2.32	0.60
86:28:4095:G:H1	86:28:4113:U:H3	1.49	0.60
44:S9:37:LEU:HD23	44:S9:42:GLU:HG3	1.82	0.60
86:28:1307:A:H2'	86:28:1308:C:C6	2.37	0.60
86:28:3916:G:H2'	86:28:3917:A:H8	1.66	0.60
41:10:87:ILE:HG12	41:10:138:ILE:HG12	1.83	0.60
5:L8:242:ARG:O	86:28:3658:C:H5''	2.01	0.59
70:18:1616:U:H2'	70:18:1617:G:C8	2.37	0.59
86:28:4238:G:H2'	86:28:4239:A:C8	2.37	0.59
40:Q:67:ILE:HD12	40:Q:96:PRO:HD2	1.83	0.59
70:18:1593:C:H2'	70:18:1594:A:H8	1.67	0.59
86:28:1461:C:H2'	86:28:1462:A:C8	2.38	0.59
86:28:1749:A:H2'	86:28:1750:G:C8	2.37	0.59
86:28:4504:C:H2'	86:28:4505:C:C6	2.37	0.59
55:v:741:MET:HG2	55:v:819:ILE:HA	1.82	0.59
86:28:3708:C:H2'	86:28:3709:U:O2	2.02	0.59
86:28:734:G:C2	86:28:735:G:C8	2.90	0.59
86:28:2007:G:H21	86:28:2012:A:H62	1.49	0.59
9:L6:261:LEU:HD12	9:L6:264:ILE:HD11	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:31:57:MET:HE2	24:31:88:LEU:HD23	1.85	0.59
86:28:1942:A:H2'	86:28:1943:A:H8	1.67	0.59
86:28:2295:C:H2'	86:28:2296:G:H8	1.68	0.59
86:28:2448:G:H2'	86:28:2449:A:C8	2.37	0.59
86:28:3606:U:H2'	86:28:3607:U:H6	1.67	0.59
86:28:3684:G:H2'	86:28:3685:C:C6	2.37	0.59
86:28:4134:C:H2'	86:28:4135:G:H8	1.67	0.59
39:EB:120:ASN:HB3	39:EB:320:LYS:HE3	1.84	0.59
70:18:107:A:H2'	70:18:108:G:H8	1.68	0.59
70:18:1736:G:H2'	70:18:1737:G:H8	1.68	0.59
72:AA:165:ILE:HG13	72:AA:177:TRP:HB2	1.85	0.59
86:28:423:G:H2'	86:28:424:U:H6	1.67	0.59
86:28:4970:C:C2	86:28:4971:A:C8	2.90	0.59
15:bb:27:VAL:HG13	15:bb:98:ALA:HB1	1.84	0.59
20:26:13:LYS:O	20:26:17:ARG:HG2	2.01	0.59
71:MM:13:GLU:HA	71:MM:16:ARG:HD3	1.85	0.59
86:28:137:G:H2'	86:28:138:G:H8	1.68	0.59
86:28:1333:A:H2'	86:28:1334:A:C8	2.38	0.59
86:28:3770:U:H2'	86:28:3771:C:C6	2.38	0.59
86:28:2793:G:H5'	86:28:2794:C:H5''	1.85	0.59
6:L3:240:LEU:HB3	6:L3:244:THR:HG21	1.84	0.58
22:dd:100:ILE:HG13	22:dd:123:ILE:HB	1.84	0.58
38:s:135:THR:HG21	55:v:187:VAL:HG21	1.85	0.58
70:18:795:A:H2'	70:18:796:G:C8	2.39	0.58
70:18:1447:G:H2'	70:18:1448:A:H8	1.66	0.58
86:28:2503:G:H2'	86:28:2504:C:C6	2.39	0.58
86:28:4537:C:H2'	86:28:4538:G:C8	2.35	0.58
53:23:13:LYS:HD2	53:23:128:LEU:HD11	1.85	0.58
59:S2:196:ILE:HB	59:S2:223:TYR:HB2	1.85	0.58
86:28:651:C:H2'	86:28:652:G:C8	2.37	0.58
86:28:2520:C:H2'	86:28:2521:G:C8	2.37	0.58
86:28:3762:U:H3'	86:28:3763:A:H8	1.68	0.58
86:28:4642:U:H2'	86:28:4643:G:H8	1.68	0.58
86:28:949:G:H2'	86:28:950:G:H8	1.67	0.58
86:28:2588:C:H5''	86:28:2589:C:H5''	1.85	0.58
86:28:4761:G:H2'	86:28:4762:A:H8	1.68	0.58
70:18:807:G:H2'	70:18:808:A:H8	1.68	0.58
70:18:946:U:H2'	70:18:947:G:H8	1.69	0.58
86:28:456:C:H2'	86:28:457:G:C8	2.37	0.58
86:28:1504:G:H2'	86:28:1505:C:H6	1.68	0.58
42:L9:146:LEU:HD11	42:L9:161:ILE:HD11	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:v:27:HIS:CD2	55:v:138:GLN:HB2	2.38	0.58
70:18:607:U:H3	74:RB:213:SER:HB2	1.68	0.58
40:Q:144:LYS:HG2	86:28:1460:C:H5''	1.85	0.58
45:S4:16:LYS:HD2	70:18:812:A:H5'	1.85	0.58
70:18:561:A:H2'	70:18:562:U:C6	2.38	0.58
70:18:1259:A:H1'	70:18:1264:C:H42	1.67	0.58
4:5:110:G:H2'	4:5:111:C:C6	2.39	0.58
11:aa:116:LEU:HD21	14:15:29:GLN:HG3	1.86	0.58
70:18:1797:U:H2'	70:18:1798:C:C6	2.38	0.58
86:28:1298:C:H2'	86:28:1299:G:H8	1.68	0.58
3:58:19:C:H2'	3:58:20:A:C8	2.39	0.58
20:26:11:ARG:HG3	86:28:229:G:H5''	1.85	0.58
45:S4:11:ARG:HA	45:S4:28:ALA:HB2	1.85	0.58
86:28:93:G:H2'	86:28:94:A:C8	2.39	0.58
86:28:423:G:H2'	86:28:424:U:C6	2.38	0.58
86:28:1341:U:H2'	86:28:1342:A:H8	1.67	0.58
86:28:4699:U:H1'	86:28:4700:A:H5''	1.84	0.58
87:ES:2945:C:H2'	87:ES:2946:G:H8	1.68	0.58
66:QQ:6:VAL:HG12	66:QQ:34:ILE:HD11	1.84	0.58
70:18:980:A:H2'	70:18:981:A:C8	2.38	0.58
3:58:144:U:H2'	3:58:145:C:C6	2.39	0.58
5:L8:31:ALA:HB2	5:L8:123:ARG:NH2	2.19	0.57
64:AS:91:VAL:HG12	64:AS:93:GLY:H	1.68	0.57
70:18:1144:A:H5'	70:18:1355:C:H41	1.67	0.57
86:28:469:C:H2'	86:28:470:A:H8	1.69	0.57
86:28:4504:C:H2'	86:28:4505:C:H6	1.68	0.57
7:L4:343:GLN:HG2	86:28:724:C:H1'	1.86	0.57
70:18:530:U:H2'	70:18:531:A:C8	2.39	0.57
70:18:1209:A:H2'	70:18:1210:G:H8	1.70	0.57
70:18:1798:C:H2'	70:18:1799:G:O4'	2.03	0.57
86:28:2386:U:H2'	86:28:2387:G:H8	1.69	0.57
86:28:2844:A:O2'	86:28:4631:G:H4'	2.03	0.57
86:28:4591:U:H2'	86:28:4592:C:C6	2.40	0.57
37:gg:108:MET:O	37:gg:112:ARG:HG2	2.05	0.57
70:18:996:A:H2'	70:18:997:A:C8	2.38	0.57
86:28:426:A:H2'	86:28:427:A:H8	1.68	0.57
86:28:3933:G:H2'	86:28:3934:G:H8	1.68	0.57
4:5:58:A:H2'	4:5:59:G:H8	1.68	0.57
70:18:640:A:H2'	70:18:641:A:H8	1.70	0.57
70:18:874:G:H2'	70:18:875:A:H8	1.68	0.57
58:S8:29:LEU:HD13	70:18:448:A:H61	1.70	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:AS:189:ILE:HB	64:AS:190:PRO:HD3	1.86	0.57
70:18:1856:C:H2'	70:18:1857:G:H8	1.69	0.57
86:28:2539:C:H2'	86:28:2540:C:C6	2.40	0.57
86:28:3861:A:H2'	86:28:3862:A:H8	1.69	0.57
70:18:1232:U:H2'	70:18:1233:G:C8	2.39	0.57
86:28:939:G:H2'	86:28:940:C:C6	2.40	0.57
86:28:1346:C:H2'	86:28:1347:G:C8	2.38	0.57
86:28:4704:C:H2'	86:28:4705:A:H8	1.70	0.57
5:L8:137:ILE:HD11	5:L8:149:LYS:HB3	1.86	0.57
30:37:28:HIS:HD2	30:37:31:LYS:H	1.52	0.57
46:S6:121:ILE:HD12	46:S6:122:PRO:HD2	1.85	0.57
70:18:152:U:H2'	70:18:153:G:C8	2.40	0.57
70:18:1244:U:H2'	70:18:1245:G:H8	1.69	0.57
86:28:259:C:H2'	86:28:260:C:C6	2.40	0.57
86:28:1339:U:H2'	86:28:1340:C:C6	2.40	0.57
86:28:3855:C:H2'	86:28:3856:A:H8	1.68	0.57
86:28:4887:C:H42	86:28:4932:U:H3	1.53	0.57
86:28:1308:C:H2'	86:28:1309:C:C6	2.40	0.57
86:28:3911:C:H2'	86:28:3912:U:H6	1.70	0.57
63:JJ:51:ALA:O	63:JJ:55:THR:HG23	2.05	0.57
63:JJ:77:GLU:HA	63:JJ:80:ARG:HG2	1.86	0.57
86:28:1344:C:H2'	86:28:1345:A:C8	2.40	0.57
86:28:2803:U:H2'	86:28:2804:C:H6	1.69	0.57
86:28:3721:U:H2'	86:28:3722:G:H8	1.70	0.57
86:28:4273:A:H2'	86:28:4274:A:C8	2.40	0.57
86:28:4638:U:H3'	86:28:4639:G:H21	1.70	0.57
45:S4:100:ARG:HD2	45:S4:102:ILE:HD11	1.85	0.56
60:BB:63:ARG:HH12	62:PP:78:ILE:HD12	1.70	0.56
70:18:389:A:H2'	70:18:390:C:H6	1.69	0.56
86:28:711:A:H2'	86:28:712:C:C6	2.40	0.56
86:28:1074:G:H2'	86:28:1075:G:C8	2.40	0.56
86:28:3633:C:H2'	86:28:3634:G:C8	2.39	0.56
3:58:144:U:H2'	3:58:145:C:H6	1.69	0.56
12:13:8:MET:HG3	40:Q:166:TYR:HB3	1.86	0.56
86:28:3870:C:H2'	86:28:3871:A:H8	1.70	0.56
86:28:4188:U:H2'	86:28:4189:U:C6	2.41	0.56
4:5:59:G:H4'	8:L5:267:ASN:HD21	1.70	0.56
43:S7:114:GLN:HE22	70:18:874:G:H21	1.54	0.56
58:S8:22:HIS:HB3	70:18:433:A:H5''	1.86	0.56
61:UU:52:ASP:HA	61:UU:55:GLU:HG2	1.87	0.56
70:18:948:C:H2'	70:18:949:G:H8	1.69	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:18:1004:U:H2'	70:18:1005:G:C8	2.39	0.56
86:28:2743:A:H2'	86:28:2744:A:C8	2.41	0.56
15:bb:54:TYR:CD1	15:bb:145:VAL:HG21	2.40	0.56
21:27:51:ARG:HB2	21:27:65:ARG:HG3	1.87	0.56
70:18:1729:U:H3	70:18:1805:G:H1	1.53	0.56
86:28:318:A:H2'	86:28:319:A:C8	2.40	0.56
86:28:3893:C:H2'	86:28:3894:A:C8	2.41	0.56
3:58:19:C:H2'	3:58:20:A:H8	1.71	0.56
84:A:34:MET:HG2	84:A:45:LEU:HD21	1.87	0.56
86:28:1298:C:H2'	86:28:1299:G:C8	2.40	0.56
86:28:4678:G:N2	86:28:4713:G:H1'	2.21	0.56
70:18:432:G:H2'	70:18:433:A:H8	1.69	0.56
86:28:4750:G:H2'	86:28:4751:G:C8	2.40	0.56
56:S3:28:GLU:HG2	76:CC:61:GLN:HG2	1.87	0.56
60:BB:79:SER:HA	60:BB:101:GLY:HA2	1.87	0.56
70:18:106:C:H2'	70:18:107:A:H8	1.71	0.56
86:28:162:A:H2'	86:28:163:A:H8	1.70	0.56
86:28:1333:A:H2'	86:28:1334:A:H8	1.70	0.56
86:28:1505:C:H2'	86:28:1506:G:C8	2.40	0.56
86:28:4915:G:H2'	86:28:4916:G:H8	1.71	0.56
54:19:70:ARG:HH22	86:28:2810:U:H5''	1.70	0.56
70:18:1201:U:H2'	70:18:1202:U:C6	2.41	0.56
7:L4:205:ARG:HG3	86:28:2297:G:H5'	1.86	0.56
31:38:69:LEU:HD21	86:28:2696:A:C5	2.40	0.56
55:v:26:ALA:HB2	55:v:128:VAL:HB	1.88	0.56
86:28:99:A:H2'	86:28:100:C:O2	2.06	0.56
86:28:163:A:H2'	86:28:164:G:C8	2.41	0.56
86:28:1617:G:H1'	86:28:2513:A:N6	2.21	0.56
86:28:4637:G:H2'	86:28:4638:U:C6	2.41	0.56
1:17:114:ILE:HD11	1:17:117:ILE:HB	1.87	0.56
8:L5:62:CYS:HB3	8:L5:105:LEU:HD22	1.88	0.56
25:32:89:LEU:HD13	25:32:118:LEU:HD22	1.88	0.56
70:18:1199:A:H2'	70:18:1200:A:C8	2.41	0.56
87:ES:3239:G:H2'	87:ES:3240:A:C8	2.38	0.56
4:5:15:C:H2'	4:5:16:A:H8	1.71	0.55
70:18:1221:G:H2'	70:18:1222:G:H8	1.71	0.55
70:18:1705:C:H2'	70:18:1706:G:H8	1.71	0.55
70:18:1821:U:H2'	70:18:1822:A:H8	1.71	0.55
86:28:2553:A:H2	86:28:2765:A:H62	1.53	0.55
1:17:154:GLU:HA	1:17:155:GLN:HB2	1.87	0.55
5:L8:32:VAL:HG22	5:L8:163:ARG:HH22	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:ee:50:VAL:HG22	26:ee:69:VAL:HG12	1.89	0.55
86:28:751:G:C4	86:28:752:G:C8	2.95	0.55
3:58:64:U:C2	3:58:65:A:C8	2.95	0.55
14:15:184:ILE:HD12	86:28:99:A:H5''	1.89	0.55
39:EB:75:ALA:HB2	39:EB:113:HIS:HB3	1.88	0.55
50:LL:121:ARG:HG3	50:LL:131:VAL:HG21	1.88	0.55
70:18:388:U:H2'	70:18:389:A:C8	2.41	0.55
10:L7:49:ILE:HD12	10:L7:185:CYS:HB3	1.88	0.55
15:bb:193:THR:HG23	15:bb:202:LEU:HD23	1.88	0.55
24:31:37:GLY:O	24:31:41:ARG:HG3	2.06	0.55
30:37:28:HIS:CD2	30:37:31:LYS:H	2.24	0.55
70:18:1413:G:H2'	70:18:1414:A:H8	1.72	0.55
86:28:654:C:H2'	86:28:655:C:H6	1.70	0.55
5:L8:242:ARG:HG3	86:28:3745:U:H4'	1.89	0.55
52:GG:101:GLY:HA3	52:GG:134:PRO:HG2	1.87	0.55
70:18:151:C:H2'	70:18:152:U:C6	2.41	0.55
70:18:952:G:H2'	70:18:953:C:C6	2.41	0.55
86:28:1933:G:H2'	86:28:1934:A:C8	2.42	0.55
86:28:2485:U:H2'	86:28:2486:G:C8	2.42	0.55
70:18:1103:C:H2'	70:18:1104:G:C8	2.42	0.55
70:18:1491:G:H2'	70:18:1492:U:C6	2.42	0.55
86:28:1317:U:H2'	86:28:1318:C:C6	2.42	0.55
86:28:1504:G:H2'	86:28:1505:C:C6	2.40	0.55
86:28:1683:U:H2'	86:28:1684:A:H8	1.70	0.55
86:28:4563:U:C2	86:28:4564:A:C8	2.94	0.55
86:28:4872:G:H4'	86:28:4873:G:H5'	1.89	0.55
14:15:42:PRO:HA	14:15:61:ILE:HD13	1.89	0.55
52:GG:113:GLN:HG3	61:UU:45:VAL:HG12	1.88	0.55
66:QQ:107:SER:HB3	70:18:860:G:H21	1.71	0.55
70:18:318:A:H3'	70:18:319:C:H5''	1.89	0.55
86:28:1327:C:H2'	86:28:1328:G:C8	2.42	0.55
86:28:1327:C:H2'	86:28:1328:G:H8	1.72	0.55
7:L4:28:PHE:HA	7:L4:129:ALA:HA	1.89	0.55
14:15:40:PRO:HG3	86:28:8:U:H5''	1.89	0.55
20:26:30:MET:HB3	20:26:101:PRO:HG2	1.89	0.55
61:UU:12:LYS:HG3	61:UU:15:ARG:HB2	1.89	0.55
69:ZZ:144:CYS:SG	69:ZZ:146:LEU:HD22	2.47	0.55
70:18:1801:A:H2'	70:18:1802:C:H6	1.71	0.55
86:28:3607:U:H2'	86:28:3608:A:H8	1.71	0.55
13:14:129:LYS:O	13:14:132:ARG:HG3	2.07	0.55
15:bb:58:LEU:HD21	15:bb:74:ARG:HH21	1.72	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:18:942:G:H2'	70:18:943:U:C6	2.41	0.55
76:CC:22:VAL:HG12	76:CC:68:TYR:HD1	1.72	0.55
28:35:6:ALA:O	28:35:10:ARG:HG3	2.06	0.54
70:18:1217:A:H2'	70:18:1218:C:C6	2.42	0.54
86:28:1188:C:H2'	86:28:1189:G:H8	1.71	0.54
86:28:2607:C:H2'	86:28:2608:G:H8	1.71	0.54
70:18:856:C:H2'	70:18:857:U:H6	1.72	0.54
86:28:1345:A:H2'	86:28:1346:C:C6	2.42	0.54
1:17:83:TRP:O	86:28:3856:A:H5''	2.07	0.54
8:L5:246:ALA:HA	8:L5:249:GLU:HG2	1.89	0.54
21:27:100:VAL:HG13	21:27:106:LEU:HB3	1.89	0.54
70:18:946:U:H2'	70:18:947:G:C8	2.42	0.54
86:28:162:A:H2'	86:28:163:A:C8	2.43	0.54
86:28:271:C:H2'	86:28:272:U:H6	1.72	0.54
3:58:67:U:H2'	3:58:68:G:C8	2.41	0.54
86:28:1197:C:H2'	86:28:1198:G:C8	2.43	0.54
86:28:4991:U:H2'	86:28:4992:G:H8	1.72	0.54
3:58:141:C:H2'	3:58:142:U:C6	2.43	0.54
22:dd:21:ARG:HG3	86:28:2282:A:H4'	1.88	0.54
26:ee:33:VAL:HG23	26:ee:38:GLU:HB2	1.88	0.54
86:28:1322:A:C6	86:28:1326:A:C8	2.96	0.54
86:28:1558:A:H2'	86:28:1559:G:H8	1.72	0.54
86:28:2558:C:H2'	86:28:2559:G:H8	1.72	0.54
86:28:3610:A:H2'	86:28:3611:A:H8	1.72	0.54
87:ES:3244:U:H2'	87:ES:3245:G:C8	2.42	0.54
4:5:23:A:H2'	4:5:24:C:C6	2.43	0.54
6:L3:56:ILE:O	6:L3:73:VAL:HA	2.07	0.54
14:15:49:ARG:HH12	86:28:152:U:P	2.31	0.54
70:18:1856:C:H2'	70:18:1857:G:C8	2.43	0.54
75:EE:58:GLU:HB3	75:EE:61:TYR:HB3	1.90	0.54
81:B:114:LEU:HD12	81:B:115:PRO:HD2	1.88	0.54
82:u:206:ILE:HD11	82:u:216:LEU:HD11	1.89	0.54
86:28:252:C:H2'	86:28:253:G:C8	2.43	0.54
86:28:713:C:H2'	86:28:714:G:H8	1.72	0.54
86:28:3633:C:H2'	86:28:3634:G:H8	1.73	0.54
86:28:4246:G:H2'	86:28:4247:G:H8	1.72	0.54
46:S6:2:LYS:HB2	46:S6:108:VAL:HG22	1.89	0.54
54:19:10:LEU:HB3	54:19:41:ILE:HG13	1.89	0.54
56:S3:66:ILE:O	56:S3:70:THR:HG23	2.07	0.54
70:18:16:G:H2'	70:18:17:C:C6	2.42	0.54
86:28:1199:G:H2'	86:28:1200:G:H8	1.73	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
86:28:1341:U:H2'	86:28:1342:A:C8	2.43	0.54
86:28:2093:G:H22	86:28:2262:G:H1	1.55	0.54
39:EB:246:ILE:HB	39:EB:305:PHE:HB2	1.90	0.54
70:18:1030:A:H2'	70:18:1031:A:H8	1.72	0.54
86:28:4232:U:H4'	86:28:4233:A:O5'	2.08	0.54
7:L4:323:ARG:HG3	86:28:1280:C:H2'	1.88	0.54
46:S6:67:VAL:HG11	46:S6:99:GLY:HA2	1.90	0.54
55:v:42:LYS:HE2	55:v:351:LEU:HD11	1.90	0.54
64:AS:110:MET:HA	64:AS:113:MET:HE2	1.90	0.54
70:18:389:A:H2'	70:18:390:C:C6	2.43	0.54
70:18:1035:A:C4	70:18:1036:A:C8	2.96	0.54
70:18:1489:A:H4'	70:18:1490:G:OP2	2.08	0.54
85:t:115:GLN:HA	85:t:118:HIS:NE2	2.23	0.54
86:28:158:A:H5''	86:28:159:C:H2'	1.90	0.54
86:28:2824:C:H2'	86:28:2825:A:C8	2.43	0.54
86:28:3607:U:H2'	86:28:3608:A:C8	2.43	0.54
3:58:30:U:H2'	3:58:31:G:C8	2.42	0.54
42:L9:65:LYS:O	42:L9:69:THR:HG23	2.08	0.54
85:t:131:GLU:O	85:t:135:THR:HG23	2.08	0.54
86:28:3873:G:H2'	86:28:3874:G:C8	2.43	0.54
86:28:4319:C:H2'	86:28:4320:G:H8	1.73	0.54
39:EB:229:LEU:HG	39:EB:318:GLN:HG3	1.88	0.53
56:S3:132:LYS:HB3	56:S3:189:MET:HG2	1.90	0.53
70:18:639:C:H2'	70:18:640:A:H8	1.73	0.53
70:18:640:A:H2'	70:18:641:A:C8	2.43	0.53
70:18:1444:U:H2'	70:18:1445:U:H6	1.73	0.53
86:28:1348:U:H2'	86:28:1349:G:H8	1.73	0.53
86:28:4088:C:H2'	86:28:4089:G:C8	2.43	0.53
8:L5:53:VAL:HG11	8:L5:159:VAL:HA	1.90	0.53
39:EB:56:ILE:HD11	39:EB:112:VAL:HB	1.90	0.53
86:28:1094:G:H2'	86:28:1095:A:H8	1.73	0.53
86:28:2457:G:H21	86:28:3672:G:N2	2.07	0.53
86:28:4704:C:H2'	86:28:4705:A:C8	2.44	0.53
86:28:4890:G:H2'	86:28:4891:G:H8	1.73	0.53
86:28:5062:G:C2	86:28:5063:G:C8	2.96	0.53
3:58:8:U:H2'	3:58:9:A:C8	2.44	0.53
62:PP:32:ILE:HG12	62:PP:60:ARG:HD2	1.91	0.53
81:B:50:5CT:H2	81:B:51:HIS:H	1.74	0.53
86:28:1774:C:C2	86:28:1775:A:C8	2.96	0.53
86:28:4723:A:H2'	86:28:4724:A:C8	2.44	0.53
87:ES:2945:C:H2'	87:ES:2946:G:C8	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:58:8:U:H2'	3:58:9:A:H8	1.72	0.53
14:15:80:THR:HG21	14:15:87:HIS:HA	1.90	0.53
70:18:151:C:H2'	70:18:152:U:H6	1.73	0.53
70:18:432:G:H2'	70:18:433:A:C8	2.42	0.53
86:28:710:G:H2'	86:28:711:A:H8	1.73	0.53
86:28:1204:C:H2'	86:28:1205:G:C8	2.42	0.53
86:28:4594:U:H2'	86:28:4595:G:C8	2.41	0.53
4:5:92:C:H2'	4:5:93:G:H8	1.72	0.53
86:28:3606:U:H2'	86:28:3607:U:C6	2.43	0.53
2:DD:133:PRO:HG3	70:18:383:G:H21	1.72	0.53
4:5:4:U:H2'	4:5:5:A:H8	1.74	0.53
5:L8:233:ARG:HB2	86:28:4184:G:H5'	1.91	0.53
27:34:6:THR:HG22	86:28:2400:G:H21	1.73	0.53
55:v:654:PRO:HD2	55:v:658:GLY:HA3	1.91	0.53
69:ZZ:138:ARG:HG2	69:ZZ:147:THR:HG22	1.89	0.53
70:18:1714:U:H2'	70:18:1715:A:C8	2.44	0.53
86:28:130:C:H2'	86:28:131:C:C6	2.44	0.53
86:28:270:U:H2'	86:28:271:C:H6	1.73	0.53
86:28:4563:U:H2'	86:28:4564:A:H8	1.74	0.53
7:L4:140:LYS:HE2	7:L4:245:HIS:HB2	1.90	0.53
70:18:118:C:H1'	70:18:445:A:C5	2.44	0.53
70:18:532:C:H2'	70:18:533:A:C8	2.44	0.53
70:18:1513:C:H2'	70:18:1514:G:H8	1.73	0.53
70:18:1568:C:H2'	70:18:1569:A:C8	2.44	0.53
86:28:48:G:H1'	86:28:49:U:OP2	2.09	0.53
86:28:697:G:H2'	86:28:698:G:H8	1.72	0.53
86:28:1329:G:H2'	86:28:3865:A:H5'	1.91	0.53
1:17:118:GLN:NE2	86:28:423:G:H21	2.07	0.53
70:18:1653:U:H2'	70:18:1654:G:C8	2.44	0.53
86:28:164:G:H2'	86:28:165:A:C8	2.44	0.53
86:28:643:C:H2'	86:28:644:G:H8	1.74	0.53
86:28:1338:G:H4'	86:28:1339:U:C6	2.44	0.53
86:28:3932:U:H2'	86:28:3933:G:C8	2.43	0.53
86:28:4503:A:H2'	86:28:4504:C:C6	2.43	0.53
15:bb:157:GLU:HA	15:bb:160:ARG:HG2	1.90	0.53
70:18:1144:A:H2'	70:18:1145:A:C8	2.44	0.53
86:28:2503:G:H2'	86:28:2504:C:N1	2.24	0.53
86:28:2735:G:H2'	86:28:2736:G:H8	1.74	0.53
1:17:168:LYS:CA	1:17:169:LYS:HB2	2.30	0.53
10:L7:178:LEU:HB3	10:L7:183:ILE:HB	1.91	0.53
15:bb:36:VAL:HG22	15:bb:107:GLY:O	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
86:28:50:C:C2	86:28:51:A:C8	2.96	0.53
45:S4:31:PRO:HB2	45:S4:38:LEU:HD22	1.91	0.52
55:v:558:LEU:HD13	55:v:572:LYS:HD2	1.91	0.52
41:10:38:ARG:HD3	41:10:83:ASP:HB2	1.90	0.52
86:28:1216:C:C2	86:28:1217:G:C8	2.97	0.52
86:28:2815:A:H2'	86:28:2816:G:C8	2.44	0.52
86:28:3917:A:H2'	86:28:3918:G:H8	1.73	0.52
86:28:4935:C:H2'	86:28:4936:G:H8	1.75	0.52
4:5:58:A:H2'	4:5:59:G:C8	2.44	0.52
5:L8:117:GLU:HG2	5:L8:124:GLY:N	2.24	0.52
45:S4:92:ILE:HG21	47:SS:17:LEU:HD21	1.92	0.52
60:BB:154:LEU:O	60:BB:157:VAL:HG22	2.08	0.52
70:18:1714:U:H2'	70:18:1715:A:H8	1.73	0.52
72:AA:18:VAL:HG21	72:AA:307:VAL:HG23	1.92	0.52
17:21:27:LEU:O	17:21:31:MET:HG2	2.08	0.52
52:GG:116:LEU:HA	52:GG:119:LEU:HD23	1.92	0.52
70:18:644:G:H2'	70:18:645:C:C6	2.44	0.52
86:28:1732:C:H2'	86:28:1733:G:C8	2.45	0.52
86:28:3684:G:H2'	86:28:3685:C:H6	1.73	0.52
86:28:4459:U:H2'	86:28:4460:U:H6	1.74	0.52
50:LL:43:VAL:HG11	50:LL:83:PHE:CZ	2.45	0.52
70:18:1736:G:H2'	70:18:1737:G:C8	2.44	0.52
73:OO:28:ASN:HB3	73:OO:31:SER:OG	2.10	0.52
86:28:262:G:H2'	86:28:263:G:H8	1.73	0.52
86:28:2634:C:H2'	86:28:2635:U:H6	1.75	0.52
41:10:31:ILE:HG22	41:10:62:SER:HB2	1.91	0.52
70:18:352:U:C2	70:18:353:C:C5	2.98	0.52
70:18:434:G:H2'	70:18:435:A:C8	2.45	0.52
70:18:1043:G:N2	70:18:1073:U:C4	2.77	0.52
86:28:4413:C:H5	86:28:4429:C:H42	1.58	0.52
5:L8:183:GLY:HA2	86:28:1613:A:H5''	1.91	0.52
51:11:15:LEU:HD21	51:11:157:ILE:HD13	1.92	0.52
83:S5:175:ASP:O	83:S5:178:ILE:HG13	2.10	0.52
86:28:3848:U:H2'	86:28:3849:A:C8	2.43	0.52
86:28:4474:A:H2'	86:28:4476:C:O5'	2.10	0.52
46:S6:76:LEU:HD22	46:S6:92:ARG:HG2	1.90	0.52
86:28:734:G:H1	86:28:929:A:H62	1.58	0.52
86:28:1450:C:O2'	86:28:2104:A:H1'	2.09	0.52
86:28:2078:C:H2'	86:28:2079:G:C8	2.45	0.52
86:28:3722:G:H2'	86:28:3723:A:C8	2.44	0.52
86:28:4688:C:H2'	86:28:4689:U:C6	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:35:96:ASN:HB2	28:35:99:GLU:HG3	1.92	0.52
38:s:39:GLN:O	38:s:42:GLN:HG3	2.09	0.52
70:18:319:C:H4'	70:18:319:C:OP1	2.10	0.52
70:18:329:G:H2'	70:18:330:G:O4'	2.10	0.52
85:t:20:GLY:H	85:t:54:LYS:HA	1.74	0.52
86:28:1973:G:H2'	86:28:1974:U:C5	2.45	0.52
11:aa:228:ARG:HG3	11:aa:283:TYR:CG	2.45	0.52
50:LL:77:TYR:C	50:LL:78:LYS:HG3	2.34	0.52
59:S2:94:ILE:HD12	59:S2:162:ILE:HD11	1.92	0.52
70:18:12:U:H2'	70:18:13:C:C6	2.46	0.52
70:18:644:G:H2'	70:18:645:C:H6	1.75	0.52
70:18:1036:A:H4'	70:18:1855:G:N2	2.25	0.52
70:18:1103:C:H2'	70:18:1104:G:H8	1.73	0.52
70:18:1384:C:C2	70:18:1385:G:C8	2.97	0.52
70:18:1536:G:H2'	70:18:1537:A:C8	2.44	0.52
70:18:1706:G:H2'	70:18:1707:U:H6	1.74	0.52
80:XX:33:LYS:HE2	80:XX:34:TYR:CZ	2.44	0.52
86:28:3796:U:H2'	86:28:3797:C:C6	2.45	0.52
86:28:4751:G:H1	86:28:4948:C:H5	1.56	0.52
19:cc:77:ILE:HD12	19:cc:116:LEU:HD12	1.91	0.51
26:ee:9:ALA:HB3	26:ee:101:ILE:HG13	1.91	0.51
45:S4:186:GLY:HA3	70:18:809:A:OP1	2.10	0.51
70:18:943:U:C2	70:18:944:A:C8	2.98	0.51
86:28:1072:C:C2	86:28:1073:G:C8	2.98	0.51
86:28:1593:A:H5''	86:28:2839:U:H5''	1.92	0.51
86:28:4344:U:H2'	86:28:4345:C:H6	1.75	0.51
70:18:102:A:H4'	70:18:104:A:C8	2.45	0.51
70:18:1217:A:H2'	70:18:1218:C:H6	1.74	0.51
70:18:1390:U:H2'	70:18:1391:C:H6	1.75	0.51
70:18:1593:C:H2'	70:18:1594:A:C8	2.46	0.51
86:28:271:C:H2'	86:28:272:U:C6	2.46	0.51
86:28:1867:A:H2'	86:28:1868:A:C8	2.45	0.51
86:28:1906:U:H2'	86:28:1907:A:H8	1.75	0.51
86:28:2521:G:H2'	86:28:2522:G:H8	1.75	0.51
86:28:3726:A:H2'	86:28:3727:A:C8	2.45	0.51
86:28:3871:A:H2'	86:28:3872:A:C8	2.45	0.51
28:35:91:MET:HA	28:35:94:ARG:HG3	1.91	0.51
44:S9:131:ARG:NH2	70:18:522:A:H4'	2.24	0.51
70:18:1701:C:C2	74:RB:195:ARG:HG2	2.45	0.51
86:28:1340:C:H2'	86:28:1341:U:H6	1.75	0.51
86:28:1732:C:O2'	86:28:1733:G:H5'	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
86:28:2078:C:H2'	86:28:2079:G:H8	1.76	0.51
86:28:2815:A:H2'	86:28:2816:G:H8	1.74	0.51
46:S6:50:VAL:HG21	46:S6:111:LEU:HB3	1.91	0.51
51:11:110:GLN:HG2	51:11:111:GLU:HG2	1.92	0.51
59:S2:167:ARG:HD3	59:S2:177:PRO:HB2	1.91	0.51
70:18:1470:C:H2'	70:18:1471:C:H6	1.74	0.51
70:18:1588:A:H2'	70:18:1589:A:H8	1.74	0.51
86:28:1296:G:HO2'	86:28:1297:U:H6	1.58	0.51
86:28:1633:G:H5'	86:28:1634:A:OP1	2.11	0.51
86:28:3832:U:H2'	86:28:3833:C:H6	1.74	0.51
86:28:4174:U:H2'	86:28:4175:G:C8	2.42	0.51
9:L6:62:SER:HB2	86:28:1236:C:O2'	2.11	0.51
58:S8:108:PRO:O	58:S8:111:GLN:HG3	2.10	0.51
70:18:1536:G:H2'	70:18:1537:A:H8	1.75	0.51
77:II:12:VAL:HG21	77:II:91:ALA:HA	1.92	0.51
86:28:270:U:H2'	86:28:271:C:C6	2.46	0.51
86:28:4389:C:H2'	86:28:4390:A:H8	1.75	0.51
86:28:4635:A:H8	86:28:5048:A:H61	1.58	0.51
6:L3:224:LYS:HG2	6:L3:340:THR:HB	1.92	0.51
82:u:111:LEU:HD21	82:u:151:VAL:HG21	1.92	0.51
6:L3:161:ARG:HG2	6:L3:184:GLN:HA	1.93	0.51
6:L3:252:ALA:HB3	86:28:4457:U:H1'	1.93	0.51
6:L3:331:VAL:HG21	6:L3:347:LEU:HD21	1.91	0.51
41:10:22:PHE:CZ	86:28:1788:A:H2'	2.46	0.51
63:JJ:129:LYS:HB2	64:AS:150:ILE:HD13	1.92	0.51
64:AS:136:ARG:HD2	64:AS:138:PHE:CZ	2.46	0.51
86:28:129:C:H2'	86:28:130:C:C6	2.45	0.51
86:28:976:G:H22	86:28:1279:A:H2	1.58	0.51
86:28:1662:C:H2'	86:28:1663:C:C6	2.45	0.51
86:28:2376:A:H2'	86:28:2377:C:C6	2.45	0.51
86:28:2858:A:H2'	86:28:2859:G:H8	1.75	0.51
86:28:3920:U:H2'	86:28:3921:U:C6	2.46	0.51
86:28:4892:A:N6	86:28:4928:C:H41	2.08	0.51
86:28:4915:G:H2'	86:28:4916:G:C8	2.46	0.51
87:ES:2953:C:H2'	87:ES:2954:G:C8	2.46	0.51
52:GG:20:GLN:HB2	64:AS:46:LYS:HE3	1.92	0.51
55:v:301:PHE:CE2	55:v:336:LEU:HD21	2.46	0.51
59:S2:193:VAL:HG11	59:S2:240:THR:HG22	1.93	0.51
70:18:1221:G:H2'	70:18:1222:G:C8	2.46	0.51
70:18:1446:A:H5'	73:OO:57:PRO:HA	1.92	0.51
86:28:4344:U:H2'	86:28:4345:C:C6	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
86:28:4642:U:H2'	86:28:4643:G:C8	2.45	0.51
41:10:190:LEU:HB3	41:10:197:VAL:HG21	1.92	0.51
56:S3:40:ARG:HG2	73:OO:108:PRO:HG3	1.93	0.51
86:28:691:C:H2'	86:28:692:A:C8	2.46	0.51
22:dd:117:LEU:HB2	22:dd:140:VAL:HG21	1.92	0.51
41:10:91:LEU:HD12	41:10:135:ILE:HG23	1.92	0.51
42:L9:157:SER:O	42:L9:161:ILE:HG12	2.10	0.51
47:SS:36:PRO:HG2	47:SS:39:GLU:HB2	1.93	0.51
63:JJ:31:ASN:ND2	63:JJ:55:THR:HG22	2.21	0.51
70:18:1743:G:N2	70:18:1791:A:H62	2.06	0.51
86:28:286:U:H2'	86:28:287:U:C6	2.46	0.51
86:28:956:A:C8	86:28:957:G:C8	2.96	0.51
86:28:2386:U:H2'	86:28:2387:G:C8	2.46	0.51
22:dd:71:PRO:HG2	22:dd:108:TYR:HA	1.93	0.50
66:QQ:31:SER:HB3	66:QQ:34:ILE:HG13	1.92	0.50
67:24:104:GLN:HA	67:24:107:GLN:HG2	1.93	0.50
70:18:51:U:H2'	70:18:52:G:H8	1.75	0.50
70:18:532:C:H2'	70:18:533:A:H8	1.76	0.50
70:18:812:A:C4	70:18:813:A:C8	2.99	0.50
84:A:41:GLN:HG2	84:A:84:ILE:HD13	1.93	0.50
86:28:1381:U:H5'	86:28:1382:G:OP2	2.11	0.50
86:28:1494:U:H2'	86:28:1495:G:H8	1.76	0.50
86:28:2293:U:H2'	86:28:2294:G:C8	2.46	0.50
87:ES:2946:G:H2'	87:ES:2947:G:H8	1.77	0.50
9:L6:219:TYR:OH	9:L6:249:ARG:HD3	2.10	0.50
70:18:903:A:H2'	70:18:904:A:H8	1.76	0.50
70:18:1828:C:H2'	70:18:1829:G:C8	2.47	0.50
72:AA:17:TRP:HA	72:AA:305:ASN:HA	1.92	0.50
76:CC:49:MET:HG2	76:CC:69:TRP:CE3	2.46	0.50
86:28:2558:C:H2'	86:28:2559:G:C8	2.47	0.50
86:28:3845:A:H2'	86:28:3846:C:H6	1.76	0.50
2:DD:79:LYS:HB2	2:DD:87:VAL:HB	1.93	0.50
7:L4:89:GLN:HG2	86:28:2353:U:H5''	1.93	0.50
31:38:49:ASP:HB3	31:38:52:LYS:HB2	1.93	0.50
32:39:8:ARG:H	32:39:8:ARG:HD2	1.75	0.50
49:YY:85:VAL:HG21	70:18:616:A:N3	2.27	0.50
55:v:740:LEU:HD11	55:v:835:VAL:HG23	1.93	0.50
70:18:146:G:H1	70:18:173:A:H61	1.58	0.50
70:18:1010:G:H2'	70:18:1011:A:C8	2.44	0.50
70:18:1486:A:H2'	70:18:1487:A:C8	2.46	0.50
70:18:1693:G:H21	70:18:1834:A:H8	1.58	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:t:59:THR:HG23	85:t:74:VAL:HB	1.92	0.50
86:28:4346:U:H2'	86:28:4347:G:C8	2.46	0.50
7:L4:195:LYS:HE3	86:28:2333:G:H5''	1.93	0.50
50:LL:64:VAL:O	50:LL:68:ILE:HG12	2.11	0.50
70:18:935:G:H2'	70:18:936:G:H8	1.75	0.50
70:18:1337:C:H4'	73:OO:67:LYS:HB3	1.92	0.50
73:OO:26:SER:HB3	73:OO:32:LEU:HB2	1.93	0.50
84:A:95:GLY:HA2	84:A:104:GLN:HA	1.93	0.50
86:28:679:C:H2'	86:28:680:G:C8	2.43	0.50
86:28:2704:C:H2'	86:28:2705:G:O4'	2.12	0.50
86:28:4208:U:H2'	86:28:4209:G:H8	1.76	0.50
86:28:4601:U:H2'	86:28:4602:A:H8	1.75	0.50
86:28:4680:G:H2'	86:28:4681:A:C8	2.45	0.50
12:13:19:GLN:HA	12:13:22:VAL:HG23	1.94	0.50
14:15:178:HIS:HA	14:15:181:HIS:NE2	2.27	0.50
70:18:340:C:H2'	70:18:341:C:H6	1.77	0.50
70:18:744:G:C6	70:18:798:G:C4	3.00	0.50
70:18:1600:G:H5''	78:TT:43:LYS:HE2	1.93	0.50
70:18:1801:A:H2'	70:18:1802:C:C6	2.46	0.50
86:28:161:G:H2'	86:28:162:A:H8	1.77	0.50
86:28:4759:C:H2'	86:28:4760:G:C8	2.47	0.50
7:L4:103:ALA:HA	86:28:1517:G:H22	1.76	0.50
10:L7:46:ARG:HH11	86:28:976:G:H5''	1.76	0.50
10:L7:126:LYS:HB2	17:21:133:ALA:HB3	1.93	0.50
47:SS:86:GLU:OE2	47:SS:90:ARG:HD2	2.12	0.50
86:28:2016:C:C2	86:28:2017:A:C8	3.00	0.50
86:28:3739:C:C2	86:28:3740:G:C8	3.00	0.50
10:L7:240:ASN:O	10:L7:244:ARG:HG2	2.12	0.50
15:bb:54:TYR:HD1	15:bb:145:VAL:HG21	1.74	0.50
44:S9:143:ASN:H	70:18:823:U:H5	1.59	0.50
70:18:155:G:H2'	70:18:156:G:C8	2.47	0.50
70:18:1787:G:H2'	70:18:1788:A:H8	1.76	0.50
86:28:1304:C:H2'	86:28:1305:C:H6	1.77	0.50
86:28:2373:C:H2'	86:28:2374:A:H8	1.76	0.50
86:28:2521:G:H2'	86:28:2522:G:C8	2.47	0.50
26:ee:54:LYS:HB3	86:28:443:G:H5''	1.93	0.50
50:LL:88:LYS:HG2	84:A:18:ARG:HG2	1.93	0.50
58:S8:100:CYS:HB2	58:S8:175:ILE:HD12	1.93	0.50
62:PP:11:LEU:HD23	62:PP:11:LEU:H	1.77	0.50
62:PP:21:ASN:HB2	66:QQ:67:GLY:HA3	1.93	0.50
70:18:15:U:H2'	70:18:16:G:O4'	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:18:1722:G:C4	70:18:1723:G:C8	3.00	0.50
86:28:2540:C:H2'	86:28:2541:G:H8	1.77	0.50
86:28:3719:A:C4	86:28:3720:G:C8	3.00	0.50
86:28:3917:A:H2'	86:28:3918:G:C8	2.47	0.50
86:28:4584:A:H2'	86:28:4585:U:O4'	2.11	0.50
4:5:2:U:H2'	4:5:3:C:H6	1.76	0.50
39:EB:291:MET:O	39:EB:294:VAL:HG12	2.12	0.50
46:S6:183:ARG:HH22	70:18:316:G:H3'	1.77	0.50
70:18:1733:U:H2'	70:18:1734:G:O4'	2.12	0.50
86:28:1450:C:H2'	86:28:1451:G:C8	2.47	0.50
31:38:26:LYS:HE2	86:28:2696:A:H5'	1.94	0.49
37:gg:104:PRO:O	37:gg:107:ARG:HG2	2.12	0.49
70:18:1036:A:C4	70:18:1037:G:C8	3.00	0.49
86:28:178:C:H2'	86:28:179:G:C8	2.47	0.49
1:17:40:HIS:CE1	1:17:158:PRO:HG3	2.47	0.49
6:L3:56:ILE:HD11	6:L3:368:ILE:HG12	1.94	0.49
11:aa:250:LYS:HB3	86:28:6:C:H5''	1.94	0.49
42:L9:41:ILE:HG23	42:L9:43:VAL:HG13	1.94	0.49
42:L9:111:LEU:HD21	42:L9:125:ARG:HG3	1.93	0.49
70:18:1101:U:H2'	70:18:1102:G:H8	1.77	0.49
86:28:709:C:H1'	86:28:4942:C:H5	1.77	0.49
86:28:905:C:H2'	86:28:906:C:H6	1.77	0.49
86:28:1209:U:O2'	86:28:1211:G:H5'	2.12	0.49
86:28:3876:A:H4'	86:28:3877:A:OP2	2.12	0.49
86:28:4356:G:C2	86:28:4357:G:C8	2.99	0.49
3:58:5:U:H2'	3:58:6:C:H6	1.77	0.49
6:L3:77:THR:HG21	6:L3:337:VAL:HG22	1.93	0.49
43:S7:157:HIS:HB3	43:S7:190:PRO:HG3	1.95	0.49
54:19:4:LEU:HD11	54:19:29:THR:HG23	1.94	0.49
61:UU:11:ALA:HB3	61:UU:33:ASP:HB2	1.94	0.49
70:18:115:U:H2'	70:18:116:U:C6	2.47	0.49
70:18:1390:U:H2'	70:18:1391:C:C6	2.47	0.49
86:28:223:G:H4'	86:28:225:G:N7	2.27	0.49
86:28:4935:C:H2'	86:28:4936:G:C8	2.48	0.49
10:L7:89:ALA:HB2	10:L7:124:LEU:HD21	1.93	0.49
14:15:108:ARG:HB2	14:15:161:MET:HE1	1.95	0.49
33:40:69:ILE:HD12	86:28:4473:A:H5''	1.94	0.49
40:Q:63:LEU:O	40:Q:67:ILE:HG12	2.12	0.49
57:FF:110:ASP:O	57:FF:114:ARG:HG2	2.13	0.49
70:18:1523:C:H2'	70:18:1524:G:H8	1.77	0.49
85:t:143:VAL:C	85:t:145:GLY:N	2.70	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
86:28:643:C:H2'	86:28:644:G:C8	2.47	0.49
86:28:952:G:H2'	86:28:953:C:H6	1.77	0.49
86:28:1458:C:C2	86:28:1459:A:C8	3.00	0.49
86:28:1739:G:H2'	86:28:1740:C:C6	2.46	0.49
86:28:4303:C:H2'	86:28:4305:G:C8	2.47	0.49
86:28:4440:G:C4	86:28:4441:A:C8	3.01	0.49
3:58:40:A:H2'	3:58:41:A:H8	1.77	0.49
3:58:141:C:H2'	3:58:142:U:H6	1.77	0.49
15:bb:27:VAL:HG22	15:bb:101:ARG:HB2	1.94	0.49
24:31:46:LEU:HD12	24:31:64:ILE:HD12	1.95	0.49
50:LL:133:GLY:HA3	70:18:1623:A:H5''	1.94	0.49
59:S2:145:LYS:HE3	70:18:1348:G:H5'	1.95	0.49
65:VV:34:ASP:O	65:VV:79:PHE:HA	2.13	0.49
70:18:14:C:H2'	70:18:15:U:C6	2.47	0.49
70:18:1626:C:H2'	70:18:1627:C:H6	1.77	0.49
81:B:74:PRO:HB2	81:B:77:HIS:HB2	1.93	0.49
86:28:137:G:N1	86:28:138:G:C6	2.81	0.49
86:28:463:A:C2	86:28:464:G:C8	3.00	0.49
86:28:1683:U:H2'	86:28:1684:A:C8	2.45	0.49
86:28:2292:C:H2'	86:28:2293:U:C6	2.48	0.49
86:28:2402:G:C2	86:28:2403:A:C8	3.00	0.49
86:28:2412:A:H2'	86:28:2413:U:C6	2.47	0.49
86:28:4346:U:H2'	86:28:4347:G:H8	1.77	0.49
86:28:4862:G:H2'	86:28:4863:G:C8	2.48	0.49
5:L8:199:VAL:HG21	86:28:1631:A:C8	2.47	0.49
13:14:104:MET:HE3	13:14:109:ARG:HG3	1.93	0.49
45:S4:87:MET:HE1	45:S4:123:LEU:HB3	1.94	0.49
70:18:71:G:H21	70:18:73:C:H42	1.61	0.49
86:28:275:C:H2'	86:28:276:C:C6	2.47	0.49
86:28:1824:G:H2'	86:28:1825:A:C8	2.47	0.49
86:28:3870:C:H2'	86:28:3871:A:C8	2.48	0.49
86:28:4458:C:H2'	86:28:4459:U:C6	2.47	0.49
86:28:4507:A:H2'	86:28:4508:C:C6	2.47	0.49
86:28:4948:C:H2'	86:28:4949:G:N2	2.27	0.49
3:58:96:C:H5''	28:35:66:LYS:HD3	1.95	0.49
26:ee:69:VAL:HG11	86:28:4944:C:H1'	1.93	0.49
45:S4:45:ILE:HD11	45:S4:49:ARG:HH21	1.77	0.49
49:YY:114:ARG:HH22	70:18:639:C:H5''	1.77	0.49
59:S2:207:ALA:HB2	70:18:4:C:H4'	1.94	0.49
60:BB:184:ARG:HD3	60:BB:191:ARG:HG2	1.93	0.49
70:18:1689:C:H2'	70:18:1690:U:C5	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
86:28:1857:C:H2'	86:28:1858:A:C8	2.43	0.49
86:28:4320:G:H2'	86:28:4321:U:C6	2.48	0.49
86:28:4538:G:H2'	86:28:4539:U:C6	2.47	0.49
86:28:4673:U:H2'	86:28:4674:C:H6	1.78	0.49
86:28:4994:G:H2'	86:28:4995:U:H6	1.76	0.49
42:L9:92:MET:HE2	42:L9:179:ILE:HG22	1.94	0.49
50:LL:61:GLU:O	50:LL:64:VAL:HG22	2.12	0.49
72:AA:174:VAL:HB	72:AA:188:HIS:HB2	1.95	0.49
86:28:4228:G:H5''	86:28:4229:U:O4'	2.13	0.49
86:28:4389:C:H2'	86:28:4390:A:C8	2.46	0.49
86:28:4448:G:H5''	86:28:4449:A:H5'	1.95	0.49
17:21:35:LYS:HE2	86:28:1824:G:H5''	1.94	0.49
40:Q:54:SER:O	40:Q:58:ARG:HG2	2.12	0.49
70:18:980:A:H2'	70:18:981:A:H8	1.78	0.49
70:18:1272:C:H2'	70:18:1273:C:C6	2.48	0.49
86:28:259:C:H2'	86:28:260:C:H6	1.77	0.49
86:28:2689:C:H2'	86:28:2690:C:H6	1.78	0.49
14:15:85:VAL:HG23	86:28:43:U:OP1	2.13	0.49
24:31:23:ARG:HA	24:31:122:VAL:HG22	1.95	0.49
43:S7:144:ILE:HD12	66:QQ:52:ILE:HD11	1.94	0.49
59:S2:60:TRP:CE2	59:S2:92:GLU:HG3	2.48	0.49
70:18:647:U:H2'	70:18:648:A:H8	1.78	0.49
70:18:1562:C:H2'	70:18:1563:G:C8	2.41	0.49
86:28:750:U:C2	86:28:751:G:C8	3.01	0.49
86:28:2518:G:H1'	86:28:2539:C:H1'	1.94	0.49
86:28:2749:C:H2'	86:28:2750:G:H8	1.77	0.49
86:28:4092:G:H2'	86:28:4093:G:H8	1.78	0.49
86:28:4135:G:H2'	86:28:4136:G:H8	1.78	0.49
14:15:9:GLU:HB3	29:36:44:ILE:CD1	2.43	0.48
44:S9:21:GLU:CD	44:S9:24:ARG:HE	2.21	0.48
69:ZZ:139:HIS:NE2	69:ZZ:148:TYR:HB2	2.28	0.48
70:18:12:U:H2'	70:18:13:C:H6	1.78	0.48
70:18:1279:C:H2'	70:18:1280:G:H8	1.77	0.48
70:18:1486:A:H2'	70:18:1487:A:H8	1.77	0.48
75:EE:53:ALA:HA	75:EE:79:VAL:HG12	1.94	0.48
86:28:674:G:H2'	86:28:675:C:C6	2.48	0.48
8:L5:65:ALA:HB2	8:L5:74:ILE:HD13	1.95	0.48
19:cc:110:LYS:HG3	19:cc:121:VAL:HB	1.94	0.48
70:18:181:A:O5'	70:18:182:C:H5''	2.13	0.48
70:18:600:G:H2'	70:18:601:G:H8	1.78	0.48
70:18:1209:A:H2'	70:18:1210:G:C8	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:18:1410:C:H2'	70:18:1411:G:C8	2.48	0.48
85:t:124:GLU:O	85:t:128:THR:HG23	2.13	0.48
86:28:7:C:H2'	86:28:8:U:C6	2.48	0.48
86:28:3845:A:H2'	86:28:3846:C:C6	2.48	0.48
5:L8:179:ILE:HG23	5:L8:184:ARG:HB2	1.94	0.48
26:ee:65:ASN:HB2	26:ee:67:THR:HG22	1.94	0.48
55:v:480:VAL:HG13	55:v:481:LYS:H	1.78	0.48
56:S3:175:VAL:HG13	56:S3:182:LEU:HG	1.95	0.48
57:FF:33:VAL:HG21	57:FF:66:VAL:HG11	1.95	0.48
70:18:394:G:C2	70:18:395:G:C8	3.01	0.48
70:18:1029:G:N2	86:28:1563:A:H61	2.12	0.48
70:18:1550:G:H3'	70:18:1579:A:H61	1.79	0.48
86:28:424:U:H2'	86:28:425:U:H6	1.78	0.48
86:28:1290:G:H2'	86:28:1291:G:C8	2.49	0.48
86:28:1327:C:C2	86:28:1328:G:N7	2.81	0.48
86:28:1460:C:H2'	86:28:1461:C:H6	1.79	0.48
86:28:1505:C:C2	86:28:1506:G:C8	3.01	0.48
86:28:2293:U:H2'	86:28:2294:G:H8	1.78	0.48
86:28:3952:A:H61	86:28:4059:C:H42	1.60	0.48
86:28:4756:C:H5'	86:28:4757:C:OP1	2.13	0.48
15:bb:97:ALA:O	15:bb:101:ARG:HG3	2.13	0.48
15:bb:168:TYR:CE2	15:bb:172:LYS:HD2	2.48	0.48
46:S6:188:LYS:O	46:S6:191:ARG:HG2	2.13	0.48
86:28:23:C:H2'	86:28:24:G:O4'	2.14	0.48
86:28:1503:A:H1'	86:28:1504:G:C8	2.48	0.48
86:28:1669:A:H4'	86:28:1685:G:H22	1.76	0.48
86:28:2538:U:H2'	86:28:2539:C:C6	2.49	0.48
86:28:4994:G:H2'	86:28:4995:U:C6	2.49	0.48
3:58:106:G:H4'	3:58:137:A:H5'	1.96	0.48
6:L3:57:VAL:HB	6:L3:367:PHE:HB3	1.95	0.48
16:20:35:PRO:HD2	16:20:39:VAL:HG21	1.94	0.48
64:AS:163:GLN:O	64:AS:166:LYS:HG2	2.13	0.48
70:18:857:U:C2	70:18:858:A:N7	2.82	0.48
70:18:1718:G:N2	70:18:1814:G:H2'	2.28	0.48
86:28:1604:G:H2'	86:28:1605:G:C8	2.48	0.48
86:28:1662:C:H2'	86:28:1663:C:H6	1.78	0.48
86:28:2079:G:H2'	86:28:2080:U:C6	2.49	0.48
86:28:2264:C:H2'	86:28:2265:G:O4'	2.14	0.48
86:28:2621:A:H2'	86:28:2622:G:C8	2.48	0.48
86:28:4891:G:C2	86:28:4892:A:N7	2.82	0.48
14:15:45:PRO:O	14:15:49:ARG:HG3	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:41:3:ALA:HA	34:41:6:ARG:HG2	1.95	0.48
70:18:145:G:H2'	70:18:146:G:C8	2.47	0.48
86:28:426:A:H2'	86:28:427:A:C8	2.49	0.48
86:28:440:U:H2'	86:28:441:G:H8	1.79	0.48
86:28:978:G:N2	86:28:1277:G:H22	2.10	0.48
86:28:1308:C:H2'	86:28:1309:C:H6	1.79	0.48
86:28:1846:G:H2'	86:28:1847:C:H6	1.77	0.48
86:28:2671:C:H2'	86:28:2672:C:C6	2.49	0.48
86:28:3920:U:H2'	86:28:3921:U:H6	1.79	0.48
86:28:4577:U:H2'	86:28:4578:G:C8	2.48	0.48
86:28:5043:A:H2'	86:28:5044:A:H8	1.78	0.48
4:5:60:G:C2	4:5:61:G:C8	3.02	0.48
11:aa:115:ARG:O	11:aa:119:GLN:HG2	2.13	0.48
16:20:154:LEU:HB3	16:20:157:ARG:HD3	1.95	0.48
51:11:68:ILE:HD11	86:28:4258:C:H5'	1.96	0.48
51:11:111:GLU:HB2	51:11:125:ILE:HD11	1.96	0.48
59:S2:118:ALA:HB1	70:18:1486:A:H4'	1.94	0.48
70:18:1391:C:H4'	80:XX:55:LEU:HD21	1.96	0.48
70:18:1444:U:H2'	70:18:1445:U:C6	2.47	0.48
70:18:1444:U:C2	70:18:1445:U:C5	3.02	0.48
86:28:268:G:H2'	86:28:269:G:H8	1.78	0.48
86:28:324:A:H2'	86:28:325:U:H6	1.78	0.48
86:28:1475:G:H2'	86:28:1476:C:C6	2.49	0.48
22:dd:98:ALA:HB2	22:dd:121:PRO:HB2	1.96	0.48
62:PP:30:ALA:O	62:PP:60:ARG:HD3	2.14	0.48
70:18:220:U:H2'	70:18:221:A:C8	2.49	0.48
77:II:49:TYR:HA	77:II:52:LEU:HB2	1.96	0.48
86:28:324:A:H2'	86:28:325:U:C6	2.48	0.48
86:28:1356:U:H2'	86:28:1357:C:C6	2.48	0.48
86:28:4072:C:C2	86:28:4073:A:C8	3.01	0.48
4:5:6:C:H4'	8:L5:52:ILE:HD13	1.95	0.48
5:L8:225:ILE:HD11	5:L8:233:ARG:HG3	1.96	0.48
9:L6:158:GLY:HA2	86:28:4942:C:H5''	1.95	0.48
11:aa:169:ALA:O	11:aa:172:GLU:HG3	2.14	0.48
24:31:64:ILE:HG22	24:31:106:VAL:HB	1.96	0.48
42:L9:36:ARG:HD3	42:L9:38:PHE:CZ	2.49	0.48
70:18:352:U:H2'	70:18:353:C:C6	2.49	0.48
70:18:945:U:H2'	70:18:946:U:C6	2.48	0.48
86:28:478:G:H2'	86:28:479:G:C8	2.46	0.48
86:28:731:G:C6	86:28:932:A:C4	3.02	0.48
86:28:2478:C:C2	86:28:2479:G:C8	3.02	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
86:28:2749:C:H2'	86:28:2750:G:C8	2.49	0.48
86:28:3707:U:H2'	86:28:3708:C:C6	2.48	0.48
86:28:4215:C:C2	86:28:4216:G:C8	3.02	0.48
22:dd:24:LYS:H	22:dd:24:LYS:HD2	1.77	0.48
22:dd:35:ALA:HB2	86:28:38:A:H5''	1.95	0.48
25:32:35:TRP:CZ2	25:32:56:PRO:HD2	2.49	0.48
46:S6:58:LYS:HA	46:S6:107:SER:HB2	1.96	0.48
70:18:148:U:H2'	70:18:149:A:H8	1.79	0.48
70:18:982:G:H2'	70:18:983:A:H8	1.79	0.48
70:18:1305:C:H2'	70:18:1306:U:C6	2.49	0.48
86:28:519:C:H2'	86:28:520:U:C6	2.49	0.48
86:28:1290:G:H2'	86:28:1291:G:H8	1.79	0.48
86:28:2897:G:H2'	86:28:2898:G:H8	1.79	0.48
86:28:3718:A:C4	86:28:3719:A:C8	3.01	0.48
86:28:4578:G:H2'	86:28:4579:U:C6	2.49	0.48
3:58:27:U:H2'	3:58:28:C:C6	2.49	0.47
46:S6:181:THR:HG22	46:S6:184:VAL:HG23	1.96	0.47
70:18:1277:C:H2'	70:18:1278:A:C8	2.46	0.47
86:28:1804:A:H4'	86:28:1805:A:O5'	2.13	0.47
86:28:1846:G:H2'	86:28:1847:C:C6	2.49	0.47
86:28:2476:G:H2'	86:28:2477:A:C8	2.49	0.47
86:28:3880:G:H2'	86:28:3881:G:C8	2.49	0.47
86:28:5006:U:H4'	86:28:5007:A:H5'	1.95	0.47
6:L3:373:LYS:HE2	86:28:4627:U:H4'	1.96	0.47
26:ee:46:ARG:HD3	26:ee:106:TYR:HE1	1.79	0.47
44:S9:132:GLN:HG2	70:18:562:U:H1'	1.96	0.47
56:S3:50:ILE:HD11	56:S3:86:LEU:HD23	1.96	0.47
58:S8:5:ARG:HD2	70:18:379:C:O2	2.14	0.47
70:18:298:G:H2'	70:18:299:A:H8	1.79	0.47
86:28:222:C:H2'	86:28:223:G:O4'	2.14	0.47
86:28:950:G:H2'	86:28:951:G:H8	1.79	0.47
86:28:1963:C:C4	86:28:1964:A:C2	3.02	0.47
86:28:2081:C:H2'	86:28:2082:G:H8	1.80	0.47
86:28:2417:A:C4	86:28:2418:A:C8	3.01	0.47
86:28:4349:C:H3'	86:28:4350:C:H5'	1.96	0.47
86:28:4460:U:H2'	86:28:4461:C:H6	1.78	0.47
86:28:5004:C:H2'	86:28:5005:G:O4'	2.14	0.47
6:L3:13:SER:HB2	86:28:4622:A:H4'	1.96	0.47
7:L4:207:PRO:HB3	7:L4:249:PHE:CD2	2.48	0.47
7:L4:312:ARG:HB3	86:28:2274:C:H5'	1.95	0.47
17:21:87:LYS:HE3	17:21:87:LYS:HB2	1.57	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:RR:9:THR:HG22	70:18:681:U:H4'	1.95	0.47
56:S3:143:ARG:HG3	74:RB:209:LYS:H	1.79	0.47
59:S2:70:VAL:HG21	59:S2:93:ILE:HG23	1.95	0.47
70:18:1694:U:H2'	70:18:1696:C:H5	1.80	0.47
86:28:2539:C:H2'	86:28:2540:C:H6	1.75	0.47
86:28:2751:G:C2	86:28:2752:G:C8	3.03	0.47
86:28:3775:A:H2'	86:28:3776:G:O4'	2.15	0.47
3:58:70:G:H5''	20:26:27:ARG:CZ	2.45	0.47
36:ff:57:CYS:SG	36:ff:60:CYS:HB2	2.53	0.47
47:SS:37:LYS:O	47:SS:41:ARG:HG3	2.15	0.47
48:RR:51:VAL:HG21	48:RR:94:ILE:HD11	1.95	0.47
54:19:3:MET:HG2	86:28:2385:U:H4'	1.94	0.47
82:u:183:ILE:HD13	82:u:206:ILE:HD13	1.96	0.47
86:28:1551:C:H2'	86:28:1552:G:O4'	2.14	0.47
86:28:2634:C:H2'	86:28:2635:U:C6	2.50	0.47
86:28:4070:U:H2'	86:28:4071:U:H6	1.79	0.47
5:L8:181:LYS:HB2	86:28:1577:G:C5	2.49	0.47
5:L8:183:GLY:CA	86:28:1613:A:H5''	2.44	0.47
6:L3:14:LEU:O	6:L3:17:LEU:HB2	2.14	0.47
6:L3:60:VAL:HG12	6:L3:62:ARG:HG2	1.97	0.47
9:L6:165:VAL:HG11	9:L6:178:VAL:HG13	1.96	0.47
55:v:715:DDE:HD2	55:v:715:DDE:HA	1.56	0.47
58:S8:23:LYS:HD2	70:18:448:A:H3'	1.96	0.47
60:BB:120:ARG:O	60:BB:143:PRO:HD2	2.14	0.47
68:30:38:ILE:HG21	68:30:63:TYR:HB3	1.96	0.47
70:18:28:U:H2'	70:18:29:G:C8	2.48	0.47
70:18:1098:C:H2'	70:18:1099:G:C8	2.49	0.47
86:28:979:C:H42	86:28:1276:C:H42	1.63	0.47
86:28:1284:G:O2'	86:28:1285:U:H5''	2.15	0.47
86:28:1306:C:C2	86:28:1307:A:C8	3.02	0.47
86:28:2080:U:H2'	86:28:2081:C:C6	2.48	0.47
86:28:3927:U:H2'	86:28:3928:A:C8	2.49	0.47
86:28:4495:G:C2	86:28:4496:A:N7	2.82	0.47
3:58:130:C:H2'	3:58:131:G:H8	1.79	0.47
4:5:4:U:H2'	4:5:5:A:C8	2.50	0.47
15:bb:10:ASP:HB2	15:bb:117:ARG:HB3	1.97	0.47
15:bb:47:PHE:HA	15:bb:136:ALA:HB2	1.97	0.47
38:s:118:PRO:HD2	38:s:183:PHE:CE1	2.49	0.47
42:L9:41:ILE:HD11	42:L9:69:THR:HB	1.96	0.47
70:18:1281:G:C6	70:18:1282:A:C6	3.03	0.47
83:S5:108:PRO:HA	83:S5:111:VAL:HG12	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:t:56:LEU:HD13	85:t:82:ILE:HG23	1.97	0.47
86:28:908:G:C2	86:28:909:G:C8	3.02	0.47
86:28:1340:C:H2'	86:28:1341:U:C6	2.50	0.47
86:28:1528:U:H2'	86:28:1529:G:C8	2.48	0.47
86:28:2413:U:H2'	86:28:2414:G:H8	1.79	0.47
86:28:2480:G:H2'	86:28:2481:G:H8	1.79	0.47
86:28:5003:U:H2'	86:28:5004:C:C6	2.50	0.47
6:L3:79:VAL:HB	6:L3:331:VAL:HG23	1.97	0.47
46:S6:174:PRO:HB3	70:18:65:C:C6	2.50	0.47
50:LL:90:VAL:HA	84:A:18:ARG:HH11	1.79	0.47
55:v:36:THR:HG22	55:v:102:LEU:HD21	1.96	0.47
55:v:394:LEU:HB3	55:v:487:THR:HG23	1.96	0.47
58:S8:19:LYS:HE2	70:18:101:U:H5''	1.95	0.47
59:S2:132:ASP:OD1	59:S2:136:HIS:HB2	2.15	0.47
70:18:71:G:H21	70:18:73:C:N4	2.13	0.47
70:18:815:U:C2	70:18:816:A:C8	3.03	0.47
70:18:1128:C:H2'	70:18:1129:G:C8	2.50	0.47
70:18:1201:U:H2'	70:18:1202:U:H6	1.78	0.47
70:18:1240:A:C5	84:A:100:LYS:HD2	2.50	0.47
71:MM:134:ILE:O	71:MM:137:GLN:HG2	2.15	0.47
73:OO:59:LYS:HB2	73:OO:84:ILE:HG23	1.97	0.47
82:u:69:GLY:HA2	82:u:113:SER:HB3	1.97	0.47
86:28:170:C:H2'	86:28:171:U:H4'	1.95	0.47
86:28:690:C:H2'	86:28:691:C:H6	1.80	0.47
86:28:1490:G:H2'	86:28:1491:A:H8	1.80	0.47
86:28:2482:C:H2'	86:28:2483:G:H8	1.80	0.47
86:28:4458:C:H2'	86:28:4459:U:H6	1.79	0.47
86:28:4761:G:H2'	86:28:4762:A:C8	2.47	0.47
14:15:146:PRO:HB2	28:35:104:THR:HG23	1.97	0.47
24:31:45:ALA:O	24:31:48:GLU:HG2	2.14	0.47
32:39:43:HIS:CG	32:39:46:ARG:HH21	2.33	0.47
70:18:218:U:C2	70:18:219:U:C5	3.03	0.47
70:18:854:A:C2	70:18:855:G:C8	3.03	0.47
70:18:909:G:C2	70:18:910:G:C5	3.03	0.47
70:18:1395:C:H2'	70:18:1396:A:N3	2.30	0.47
70:18:1708:C:C2	70:18:1709:G:C8	3.03	0.47
78:TT:88:LEU:HD13	78:TT:109:TYR:CE2	2.50	0.47
83:S5:187:SER:OG	83:S5:190:ILE:HB	2.14	0.47
86:28:272:U:H2'	86:28:273:U:C6	2.50	0.47
86:28:1445:U:H2'	86:28:1446:C:C6	2.50	0.47
86:28:1673:U:H2'	86:28:1674:C:C6	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
86:28:1889:U:H3'	86:28:1890:G:C8	2.50	0.47
86:28:1893:C:H1'	86:28:1937:C:O2	2.14	0.47
86:28:2373:C:H2'	86:28:2374:A:C8	2.49	0.47
86:28:2478:C:H2'	86:28:2479:G:H8	1.80	0.47
86:28:2870:A:H2'	86:28:2871:A:H8	1.80	0.47
86:28:3861:A:H2'	86:28:3862:A:C8	2.50	0.47
86:28:4652:G:H2'	86:28:4653:C:H6	1.79	0.47
6:L3:128:LYS:HG3	86:28:4966:A:H5'	1.97	0.47
19:cc:80:PRO:HB2	19:cc:155:ILE:HG21	1.96	0.47
37:gg:52:GLU:HB2	37:gg:61:VAL:HG23	1.97	0.47
42:L9:23:ARG:HH22	86:28:4763:U:H5''	1.80	0.47
46:S6:49:VAL:HB	46:S6:115:LYS:HB2	1.97	0.47
48:RR:68:LYS:HB3	48:RR:91:LEU:HD13	1.96	0.47
58:S8:46:VAL:HG23	58:S8:54:LYS:HB2	1.96	0.47
70:18:556:U:H2'	70:18:557:U:H6	1.80	0.47
70:18:929:G:H2'	70:18:930:C:O4'	2.14	0.47
70:18:946:U:C2	70:18:947:G:C8	3.03	0.47
70:18:1265:A:H4'	70:18:1327:G:OP2	2.14	0.47
70:18:1298:G:H2'	70:18:1298:G:N3	2.29	0.47
70:18:1408:U:H2'	70:18:1409:A:C8	2.50	0.47
86:28:325:U:H2'	86:28:326:C:C6	2.50	0.47
86:28:2730:U:H2'	86:28:2731:C:C6	2.50	0.47
86:28:4863:G:H2'	86:28:4864:U:H6	1.78	0.47
3:58:6:C:H2'	3:58:7:U:H6	1.80	0.47
25:32:90:MET:HE2	25:32:90:MET:HA	1.96	0.47
55:v:354:ILE:HG23	55:v:358:LEU:HD12	1.97	0.47
70:18:430:C:H2'	70:18:431:G:H8	1.79	0.47
86:28:710:G:H2'	86:28:711:A:C8	2.50	0.47
86:28:1484:G:H2'	86:28:1484:G:N3	2.31	0.47
86:28:1939:A:H5'	86:28:1940:G:H4'	1.97	0.47
86:28:2732:G:H2'	86:28:2733:C:C6	2.50	0.47
86:28:4399:U:C2	86:28:4400:G:C8	3.02	0.47
86:28:5002:U:H2'	86:28:5003:U:H6	1.79	0.47
25:32:90:MET:HG3	37:gg:33:LYS:HA	1.96	0.46
38:s:59:THR:HA	38:s:62:ARG:HG2	1.97	0.46
43:S7:60:ILE:HG23	43:S7:92:VAL:HA	1.96	0.46
57:FF:32:ASP:O	57:FF:35:GLU:HG3	2.15	0.46
58:S8:45:THR:HG22	70:18:307:G:H1'	1.96	0.46
70:18:17:C:H2'	70:18:18:C:H6	1.79	0.46
70:18:431:G:C2	70:18:432:G:C8	3.03	0.46
70:18:1396:A:O2'	70:18:1398:G:C8	2.60	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
86:28:172:C:H1'	86:28:173:C:C5	2.50	0.46
86:28:470:A:C4	86:28:471:A:C8	3.03	0.46
86:28:714:G:H2'	86:28:715:G:H8	1.80	0.46
86:28:905:C:H2'	86:28:906:C:C6	2.50	0.46
86:28:987:C:H2'	86:28:988:C:C6	2.50	0.46
86:28:1326:A:H2'	86:28:1327:C:C6	2.51	0.46
86:28:2281:U:C2	86:28:2282:A:C8	3.03	0.46
86:28:2832:A:C4	86:28:2833:A:C8	3.03	0.46
86:28:2895:A:H2'	86:28:2896:G:C8	2.50	0.46
86:28:4314:C:C2	86:28:4315:A:C8	3.03	0.46
13:14:24:LEU:HD11	13:14:86:TRP:CG	2.50	0.46
21:27:25:ILE:HA	21:27:43:VAL:HG12	1.97	0.46
26:ee:28:LEU:HB2	26:ee:84:VAL:HG12	1.96	0.46
40:Q:59:PRO:HG3	40:Q:143:ARG:HA	1.97	0.46
53:23:87:SER:HA	53:23:97:TYR:HB3	1.97	0.46
70:18:478:G:H2'	70:18:479:C:H6	1.79	0.46
70:18:1134:G:H2'	70:18:1135:C:H6	1.80	0.46
70:18:1358:U:C2	70:18:1359:U:C6	3.03	0.46
82:u:19:HIS:O	82:u:23:ARG:HG3	2.14	0.46
86:28:440:U:H2'	86:28:441:G:C8	2.51	0.46
86:28:1381:U:H3'	86:28:1382:G:H8	1.80	0.46
86:28:1511:U:H2'	86:28:1512:G:H8	1.79	0.46
86:28:2079:G:H2'	86:28:2080:U:H6	1.80	0.46
86:28:2495:U:H2'	86:28:2496:G:H8	1.80	0.46
86:28:2607:C:H2'	86:28:2608:G:C8	2.49	0.46
86:28:4538:G:H2'	86:28:4539:U:H6	1.80	0.46
2:DD:58:LYS:HG3	2:DD:59:LYS:HG3	1.97	0.46
15:bb:60:LYS:HE2	86:28:2046:G:H5'	1.98	0.46
38:s:121:VAL:HB	38:s:161:ILE:HG13	1.97	0.46
43:S7:58:LYS:HB2	43:S7:90:LYS:HG2	1.97	0.46
43:S7:69:LEU:O	43:S7:73:GLN:HG2	2.15	0.46
66:QQ:5:ASN:HB3	66:QQ:8:ALA:HB3	1.97	0.46
86:28:125:C:H2'	86:28:126:C:H6	1.80	0.46
86:28:2404:A:H61	86:28:2787:A:N6	2.14	0.46
86:28:2482:C:H2'	86:28:2483:G:C8	2.51	0.46
86:28:3610:A:H2'	86:28:3611:A:C8	2.51	0.46
86:28:3911:C:H2'	86:28:3912:U:C6	2.49	0.46
86:28:4186:A:H2'	86:28:4187:G:C8	2.49	0.46
86:28:4898:G:H2'	86:28:4899:G:C8	2.51	0.46
3:58:40:A:H2'	3:58:41:A:C8	2.49	0.46
70:18:674:C:H2'	70:18:675:U:C6	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:18:865:A:C6	70:18:866:U:C4	3.03	0.46
85:t:110:VAL:O	85:t:114:ARG:HG2	2.15	0.46
86:28:691:C:C2	86:28:692:A:N7	2.83	0.46
86:28:1479:G:H2'	86:28:1480:C:C6	2.50	0.46
86:28:4475:G:OP2	86:28:4476:C:H5''	2.16	0.46
86:28:4889:G:H2'	86:28:4890:G:H8	1.80	0.46
3:58:124:U:H4'	3:58:125:C:O5'	2.14	0.46
5:L8:150:LEU:HB3	5:L8:151:PRO:HD2	1.98	0.46
6:L3:95:THR:HG22	86:28:4910:A:H4'	1.98	0.46
7:L4:69:THR:OG1	86:28:3906:A:H2'	2.15	0.46
15:bb:89:PRO:HD3	86:28:1914:C:H4'	1.98	0.46
19:cc:146:ALA:HA	19:cc:149:VAL:HG22	1.97	0.46
70:18:69:C:H3'	70:18:70:G:H8	1.81	0.46
70:18:155:G:H2'	70:18:156:G:H8	1.81	0.46
70:18:744:G:C8	70:18:798:G:N2	2.83	0.46
70:18:1025:U:H2'	70:18:1026:C:O4'	2.15	0.46
70:18:1539:U:H2'	70:18:1540:G:H8	1.81	0.46
70:18:1855:G:H2'	70:18:1856:C:H6	1.80	0.46
73:OO:80:PHE:HB3	80:XX:52:PHE:HB3	1.97	0.46
84:A:30:TYR:O	84:A:34:MET:HG3	2.14	0.46
86:28:1291:G:H2'	86:28:1292:C:C6	2.50	0.46
86:28:1588:U:H2'	86:28:1589:C:C6	2.51	0.46
86:28:3832:U:H2'	86:28:3833:C:C6	2.50	0.46
87:ES:2947:G:H1	87:ES:3247:A:H2	1.57	0.46
5:L8:32:VAL:HG22	5:L8:163:ARG:NH2	2.31	0.46
47:SS:7:ILE:HD12	47:SS:27:VAL:HG22	1.98	0.46
51:11:18:ARG:HG3	51:11:135:GLY:HA3	1.97	0.46
70:18:1164:G:O2'	70:18:1165:G:H5'	2.16	0.46
70:18:1222:G:H2'	70:18:1223:A:C8	2.51	0.46
70:18:1693:G:N2	70:18:1834:A:H8	2.13	0.46
70:18:1716:C:H2'	70:18:1717:C:H6	1.80	0.46
86:28:240:G:H2'	86:28:241:G:O4'	2.15	0.46
86:28:285:G:H2'	86:28:286:U:C6	2.51	0.46
86:28:922:C:H2'	86:28:922(A):G:H8	1.81	0.46
86:28:1195:G:H2'	86:28:1196:G:H8	1.80	0.46
86:28:1472:C:H2'	86:28:1473:U:C6	2.51	0.46
86:28:1558:A:H2'	86:28:1559:G:C8	2.50	0.46
86:28:2538:U:H2'	86:28:2539:C:H6	1.79	0.46
86:28:2633:U:H2'	86:28:2634:C:H6	1.81	0.46
8:L5:286:SER:HA	8:L5:289:ARG:HG2	1.98	0.46
13:14:96:GLU:HA	13:14:99:GLU:HG2	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:S6:162:LEU:HB3	70:18:67:C:C5	2.51	0.46
70:18:382:C:H2'	70:18:383:G:C8	2.51	0.46
70:18:642:U:H4'	70:18:643:A:OP1	2.15	0.46
70:18:1351:G:C2	70:18:1352:G:C8	3.04	0.46
70:18:1858:G:C2	70:18:1859:A:C5	3.04	0.46
86:28:132:G:C4	86:28:133:C:H1'	2.50	0.46
86:28:146:G:C2	86:28:147:A:C8	3.04	0.46
86:28:153:G:N3	86:28:154:G:C8	2.84	0.46
86:28:1315:C:H2'	86:28:1316:G:H8	1.79	0.46
86:28:2490:U:H2'	86:28:2491:C:C6	2.50	0.46
86:28:3769:C:H2'	86:28:3770:U:C6	2.51	0.46
5:L8:180:LEU:HD23	5:L8:180:LEU:HA	1.78	0.46
5:L8:187:HIS:HB3	86:28:2740:U:O4'	2.16	0.46
14:15:38:ARG:HB2	14:15:62:TYR:CZ	2.50	0.46
44:S9:58:ARG:O	44:S9:62:THR:HG23	2.16	0.46
70:18:496:C:H2'	70:18:497:C:H6	1.80	0.46
70:18:677:G:N2	70:18:1028:A:H62	2.11	0.46
70:18:858:A:H2'	70:18:859:G:H8	1.81	0.46
70:18:1533:A:N7	70:18:1604:G:H1'	2.30	0.46
86:28:919:C:H2'	86:28:920:C:H6	1.80	0.46
86:28:952:G:H2'	86:28:953:C:C6	2.51	0.46
86:28:2521:G:H5'	86:28:2640:G:H1'	1.98	0.46
86:28:3658:C:H2'	86:28:3659:G:H8	1.81	0.46
86:28:3911:C:C2	86:28:3912:U:C5	3.04	0.46
86:28:4266:G:H2'	86:28:4266:G:N3	2.31	0.46
86:28:4637:G:H2'	86:28:4638:U:H6	1.80	0.46
3:58:142:U:C2	3:58:143:G:C8	3.04	0.46
6:L3:252:ALA:HB1	86:28:4524:G:C2	2.51	0.46
9:L6:45:HIS:O	86:28:980:U:H4'	2.16	0.46
10:L7:242:LEU:HD11	10:L7:246:MET:HE3	1.98	0.46
42:L9:129:ARG:HD3	42:L9:129:ARG:HA	1.83	0.46
63:JJ:15:VAL:HA	63:JJ:18:GLU:HG2	1.98	0.46
70:18:429:C:H2'	70:18:430:C:H6	1.80	0.46
70:18:1423:C:C2	70:18:1424:G:C8	3.04	0.46
70:18:1501:C:H2'	70:18:1502:C:H6	1.80	0.46
70:18:1538:C:N4	78:TT:104:ARG:HH22	2.14	0.46
75:EE:19:GLN:HE21	75:EE:19:GLN:HB2	1.59	0.46
81:B:42:GLU:HB3	81:B:59:VAL:HB	1.96	0.46
84:A:39:ALA:HA	84:A:42:ARG:HB3	1.97	0.46
86:28:4080:C:H2'	86:28:4081:G:H8	1.80	0.46
86:28:4576:U:H2'	86:28:4577:U:C6	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
86:28:4625:C:O2'	86:28:4626:A:H5'	2.16	0.46
4:5:24:C:H2'	4:5:25:G:O4'	2.15	0.46
7:L4:315:LYS:HD2	10:L7:167:ALA:HB1	1.98	0.46
13:14:5:ARG:HB3	13:14:57:LEU:HG	1.98	0.46
25:32:67:LYS:HG2	25:32:68:HIS:CD2	2.51	0.46
43:S7:63:PHE:HA	43:S7:95:ILE:O	2.16	0.46
56:S3:143:ARG:HB2	74:RB:218:TRP:HD1	1.80	0.46
59:S2:204:ILE:HG21	59:S2:211:LYS:HA	1.97	0.46
66:QQ:28:ARG:HB2	66:QQ:29:PRO:HD3	1.98	0.46
70:18:557:U:H2'	70:18:558:G:H8	1.80	0.46
70:18:1628:C:H2'	70:18:1629:C:H6	1.81	0.46
70:18:1811:C:H2'	70:18:1812:U:O4'	2.16	0.46
77:II:84:ILE:O	77:II:88:ILE:HG12	2.16	0.46
86:28:713:C:H2'	86:28:714:G:C8	2.50	0.46
86:28:1306:C:H2'	86:28:1307:A:C8	2.43	0.46
86:28:1774:C:N3	86:28:1775:A:N7	2.63	0.46
86:28:4564:A:H2'	86:28:4565:C:C6	2.51	0.46
86:28:5002:U:H2'	86:28:5003:U:C6	2.51	0.46
3:58:89:U:H2'	3:58:90:C:C6	2.52	0.45
4:5:16:A:H2'	4:5:17:C:C6	2.51	0.45
6:L3:252:ALA:HB1	86:28:4524:G:N3	2.31	0.45
15:bb:61:ARG:HA	15:bb:70:PRO:HD2	1.98	0.45
17:21:106:LEU:O	17:21:110:LYS:HG2	2.16	0.45
38:s:118:PRO:O	38:s:163:THR:HG23	2.16	0.45
43:S7:160:LYS:O	43:S7:163:GLN:HG3	2.16	0.45
54:19:45:ILE:HD13	54:19:50:ILE:HG13	1.98	0.45
55:v:590:LEU:HD22	55:v:605:LYS:HE3	1.98	0.45
69:ZZ:140:TYR:CE1	69:ZZ:145:CYS:HA	2.51	0.45
70:18:219:U:H2'	70:18:220:U:H6	1.81	0.45
86:28:100:C:C6	86:28:101:A:C8	3.04	0.45
86:28:408:A:H4'	86:28:409:G:H3'	1.98	0.45
86:28:1750:G:C2	86:28:1751:A:C8	3.04	0.45
86:28:2479:G:H2'	86:28:2480:G:H8	1.81	0.45
86:28:3611:A:H2	86:28:5016:A:H8	1.64	0.45
86:28:3619:G:H22	86:28:3624:A:H1'	1.80	0.45
86:28:3723:A:H2'	86:28:3724:A:H8	1.80	0.45
86:28:4058:U:H2'	86:28:4059:C:C6	2.51	0.45
86:28:4629:U:C2	86:28:4630:G:C8	3.04	0.45
87:ES:3245:G:H2'	87:ES:3246:G:H8	1.81	0.45
3:58:147:G:H2'	3:58:148:A:H8	1.80	0.45
7:L4:137:VAL:HG21	7:L4:150:LEU:HD21	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:L6:165:VAL:HG13	9:L6:180:GLY:H	1.82	0.45
35:42:68:LEU:HD11	35:42:85:ILE:HD11	1.98	0.45
45:S4:68:ARG:HG3	45:S4:76:VAL:HG11	1.99	0.45
64:AS:198:GLU:HB2	64:AS:210:VAL:HG21	1.98	0.45
70:18:556:U:H2'	70:18:557:U:C6	2.52	0.45
70:18:867:G:H2'	70:18:868:G:C8	2.52	0.45
70:18:1198:G:H2'	70:18:1199:A:H8	1.82	0.45
70:18:1260:A:C2	70:18:1620:A:C4	3.05	0.45
70:18:1468:C:H2'	70:18:1469:A:H8	1.81	0.45
70:18:1643:U:H2'	70:18:1644:C:C6	2.51	0.45
86:28:477:C:H2'	86:28:478:G:H8	1.80	0.45
86:28:693:C:H2'	86:28:694:C:C6	2.51	0.45
86:28:1959:U:O4'	86:28:1961:G:H1'	2.16	0.45
86:28:3734:U:H2'	86:28:3735:G:O4'	2.17	0.45
86:28:4188:U:H2'	86:28:4189:U:H6	1.79	0.45
24:31:70:LYS:HG3	86:28:2389:A:H4'	1.98	0.45
49:YY:85:VAL:O	49:YY:89:THR:HG23	2.17	0.45
55:v:112:SER:HA	55:v:115:VAL:HG12	1.98	0.45
64:AS:39:PHE:CD1	64:AS:74:LEU:HD23	2.52	0.45
70:18:430:C:C2	70:18:431:G:C8	3.04	0.45
70:18:1650:A:H5''	77:II:139:ALA:HB2	1.98	0.45
70:18:1720:U:H5''	70:18:1721:U:H5''	1.99	0.45
70:18:1839:U:H2'	70:18:1840:U:C6	2.51	0.45
86:28:59:A:C4	86:28:60:A:C8	3.04	0.45
86:28:272:U:H2'	86:28:273:U:H6	1.81	0.45
86:28:1684:A:C4	86:28:1685:G:C8	3.05	0.45
86:28:2543:A:H2	86:28:2773:G:H22	1.65	0.45
86:28:2549:G:H2'	86:28:2550:G:H8	1.81	0.45
86:28:3685:C:C2	86:28:3686:G:C8	3.05	0.45
86:28:4357:G:H2'	86:28:4358:U:H6	1.82	0.45
86:28:4889:G:C2	86:28:4890:G:C8	3.04	0.45
86:28:5043:A:H2'	86:28:5044:A:C8	2.51	0.45
3:58:2:G:C4	3:58:3:A:C8	3.04	0.45
7:L4:266:THR:HG22	7:L4:269:LYS:HB3	1.99	0.45
7:L4:339:THR:HA	7:L4:342:ARG:HB3	1.99	0.45
11:aa:193:VAL:HG13	11:aa:253:THR:OG1	2.16	0.45
14:15:120:TRP:HZ2	14:15:123:GLU:HG2	1.81	0.45
70:18:1538:C:H42	78:TT:104:ARG:NH2	2.14	0.45
86:28:221:C:H2'	86:28:222:C:C6	2.51	0.45
86:28:1888:A:C5	86:28:1889:U:C5	3.05	0.45
86:28:1953:U:H2'	86:28:1954:U:C6	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
86:28:2386:U:C2	86:28:2387:G:C8	3.05	0.45
86:28:3637:U:O4	86:28:3651:A:H2	2.00	0.45
86:28:4991:U:H2'	86:28:4992:G:C8	2.50	0.45
7:L4:211:TYR:O	7:L4:232:VAL:HG22	2.17	0.45
15:bb:124:LEU:HD12	15:bb:124:LEU:HA	1.83	0.45
36:ff:8:VAL:HG13	86:28:2875:C:H5'	1.98	0.45
70:18:512:A:C2	70:18:513:G:C8	3.05	0.45
70:18:558:G:H2'	70:18:559:G:C8	2.52	0.45
70:18:1101:U:H2'	70:18:1102:G:C8	2.51	0.45
70:18:1198:G:H2'	70:18:1199:A:C8	2.51	0.45
70:18:1560:U:H2'	70:18:1561:A:H8	1.81	0.45
70:18:1845:A:H2'	70:18:1846:G:C8	2.51	0.45
86:28:247:G:H2'	86:28:248:C:H6	1.81	0.45
86:28:1216:C:C4	86:28:1217:G:N7	2.85	0.45
86:28:1733:G:N3	86:28:4214:A:H2'	2.31	0.45
86:28:2032:U:H2'	86:28:2033:A:C8	2.51	0.45
86:28:4177:C:C2	86:28:4178:A:C8	3.04	0.45
86:28:4863:G:H2'	86:28:4864:U:C6	2.52	0.45
86:28:4951:G:H2'	86:28:4952:G:H8	1.82	0.45
3:58:140:C:H2'	3:58:141:C:C6	2.51	0.45
7:L4:190:ARG:HB2	7:L4:202:ILE:HG23	1.99	0.45
53:23:43:LYS:HD2	86:28:4508:C:H5''	1.99	0.45
59:S2:137:VAL:HB	59:S2:217:ALA:HA	1.96	0.45
60:BB:145:ILE:HG12	60:BB:159:ILE:HB	1.97	0.45
70:18:637:U:H2'	70:18:638:C:H6	1.81	0.45
70:18:1268:C:C4	70:18:1269:G:N7	2.85	0.45
86:28:286:U:H2'	86:28:287:U:H6	1.82	0.45
86:28:1613:A:N7	86:28:3638:G:H1'	2.31	0.45
86:28:2621:A:H2'	86:28:2622:G:H8	1.81	0.45
86:28:4610:A:C4	86:28:4611:A:C8	3.04	0.45
86:28:4647:G:C2	86:28:4648:A:C8	3.04	0.45
86:28:4918:C:H3'	86:28:4919:G:H8	1.81	0.45
86:28:5010:U:H2'	86:28:5011:A:H8	1.80	0.45
14:15:14:LYS:HE2	86:28:280:G:H5''	1.99	0.45
40:Q:176:ARG:O	40:Q:180:ARG:HB2	2.17	0.45
46:S6:170:ARG:NH1	70:18:72:C:H41	2.14	0.45
52:GG:78:ALA:HA	52:GG:81:VAL:HG12	1.98	0.45
55:v:279:SER:OG	55:v:283:LYS:HG2	2.17	0.45
55:v:820:LEU:HD12	55:v:821:PRO:HD2	1.98	0.45
70:18:381:C:H2'	70:18:382:C:C6	2.52	0.45
70:18:1374:C:H2'	70:18:1375:G:C8	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:18:1375:G:H2'	70:18:1376:A:C8	2.52	0.45
70:18:1819:A:H2'	70:18:1820:G:H8	1.82	0.45
86:28:424:U:H2'	86:28:425:U:C6	2.51	0.45
86:28:699:C:H2'	86:28:700:G:H8	1.80	0.45
86:28:1582:U:C2	86:28:1583:A:C8	3.04	0.45
86:28:2777:G:H5''	86:28:2778:G:H5'	1.98	0.45
86:28:4258:C:H2'	86:28:4259:C:H6	1.82	0.45
86:28:4406:U:C2	86:28:4407:G:C8	3.04	0.45
86:28:4890:G:C2	86:28:4891:G:C8	3.05	0.45
16:20:15:ARG:HB3	16:20:27:LEU:HD13	1.99	0.45
50:LL:82:TRP:CD1	50:LL:82:TRP:H	2.33	0.45
55:v:479:LEU:HD22	55:v:483:GLY:HA3	1.98	0.45
70:18:49:C:H2'	70:18:472:C:H41	1.81	0.45
70:18:85:A:H2'	70:18:86:C:H6	1.82	0.45
70:18:298:G:N3	70:18:299:A:C8	2.85	0.45
70:18:865:A:C5	70:18:866:U:C4	3.05	0.45
70:18:1711:U:H2'	70:18:1712:A:H8	1.82	0.45
70:18:1797:U:H2'	70:18:1798:C:H6	1.80	0.45
86:28:257:C:H2'	86:28:258:G:C8	2.51	0.45
86:28:654:C:H2'	86:28:655:C:C6	2.51	0.45
86:28:1589:C:H2'	86:28:1590:C:C6	2.52	0.45
86:28:2292:C:H2'	86:28:2293:U:H6	1.82	0.45
86:28:2549:G:H2'	86:28:2550:G:C8	2.52	0.45
86:28:3641:U:H5	86:28:3646:A:N7	2.14	0.45
86:28:3720:G:H22	86:28:3733:A:H2	1.62	0.45
86:28:4889:G:C6	86:28:4931:G:C6	3.05	0.45
8:L5:53:VAL:HB	8:L5:159:VAL:HG13	1.98	0.45
44:S9:42:GLU:O	44:S9:46:VAL:HG23	2.17	0.45
45:S4:80:ILE:HG13	45:S4:81:THR:HG23	1.98	0.45
47:SS:112:ASN:O	47:SS:116:LYS:HG2	2.16	0.45
56:S3:109:LEU:HD11	56:S3:115:VAL:HG22	1.99	0.45
70:18:903:A:H2'	70:18:904:A:C8	2.51	0.45
70:18:1036:A:H4'	70:18:1855:G:H21	1.81	0.45
70:18:1230:C:H2'	70:18:1231:C:H6	1.82	0.45
70:18:1413:G:H2'	70:18:1414:A:C8	2.50	0.45
70:18:1538:C:H42	78:TT:104:ARG:HH22	1.64	0.45
73:OO:56:MET:HE2	73:OO:56:MET:HB2	1.93	0.45
83:S5:142:SER:O	83:S5:146:ARG:HG3	2.17	0.45
86:28:653:C:H2'	86:28:654:C:H6	1.80	0.45
86:28:1494:U:H2'	86:28:1495:G:C8	2.52	0.45
86:28:2640:G:H2'	86:28:2641:A:C8	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
86:28:2757:A:H2'	86:28:2758:G:C8	2.52	0.45
86:28:3930:U:H2'	86:28:3931:C:C6	2.52	0.45
86:28:4890:G:N3	86:28:4891:G:C8	2.85	0.45
4:5:2:U:H2'	4:5:3:C:C6	2.52	0.45
13:14:90:ARG:O	13:14:94:LYS:HG2	2.17	0.45
17:21:87:LYS:NZ	86:28:4305:G:H22	2.15	0.45
35:42:30:LYS:HB3	35:42:30:LYS:HE2	1.68	0.45
45:S4:122:LYS:HE3	45:S4:124:CYS:SG	2.57	0.45
58:S8:29:LEU:HD13	70:18:448:A:N6	2.32	0.45
70:18:152:U:H2'	70:18:153:G:H8	1.82	0.45
70:18:218:U:H2'	70:18:219:U:H6	1.82	0.45
70:18:1203:G:H2'	70:18:1204:A:C8	2.52	0.45
86:28:2290:C:C2	86:28:2291:G:C8	3.04	0.45
86:28:2676:A:C4	86:28:2677:G:C8	3.05	0.45
86:28:4094:G:C2	86:28:4095:G:C5	3.04	0.45
86:28:4968:A:H2'	86:28:4969:C:H6	1.81	0.45
3:58:5:U:H2'	3:58:6:C:C6	2.50	0.44
11:aa:310:LYS:HE3	11:aa:310:LYS:HB3	1.82	0.44
12:13:47:ALA:HB3	12:13:48:PRO:HD3	1.99	0.44
20:26:89:LYS:HE2	20:26:95:VAL:HG21	1.98	0.44
41:10:204:GLY:HA3	41:10:208:LYS:HE2	1.99	0.44
53:23:89:ARG:HB2	53:23:95:PHE:CE2	2.52	0.44
55:v:488:PHE:HB3	55:v:491:ALA:HB2	1.97	0.44
77:II:28:GLY:HA3	77:II:67:ASP:OD2	2.17	0.44
84:A:35:GLN:HA	84:A:42:ARG:HH21	1.81	0.44
86:28:1645:C:H2'	86:28:1646:A:H8	1.77	0.44
86:28:2756:G:H2'	86:28:2757:A:C8	2.52	0.44
86:28:3707:U:H2'	86:28:3708:C:H6	1.81	0.44
86:28:4197:G:C4	86:28:4198:G:C8	3.05	0.44
1:17:126:ARG:HG3	1:17:140:MET:HE1	1.99	0.44
3:58:6:C:H2'	3:58:7:U:C6	2.52	0.44
3:58:71:A:H2'	20:26:50:ARG:NH1	2.32	0.44
3:58:140:C:H2'	3:58:141:C:H6	1.82	0.44
6:L3:154:LYS:HG3	6:L3:194:LEU:HD23	1.99	0.44
24:31:68:LEU:HA	24:31:108:TYR:HB2	1.99	0.44
38:s:28:PHE:HB2	38:s:89:VAL:HG13	1.99	0.44
40:Q:67:ILE:HD11	40:Q:98:LEU:HD11	1.98	0.44
42:L9:66:GLU:O	42:L9:70:VAL:HG23	2.16	0.44
48:RR:90:CYS:HB3	48:RR:130:LEU:HD11	1.98	0.44
66:QQ:26:LEU:HD11	66:QQ:60:LYS:HB3	2.00	0.44
70:18:192:C:H2'	70:18:193:C:H6	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:18:1051:G:H2'	70:18:1052:A:H8	1.82	0.44
86:28:433:A:C2	86:28:3867:A:H4'	2.53	0.44
86:28:981:C:H42	86:28:1274:A:H61	1.65	0.44
86:28:1199:G:C2	86:28:1200:G:C5	3.05	0.44
86:28:1298:C:C2	86:28:1299:G:C8	3.05	0.44
86:28:1725:U:H2'	86:28:1726:U:H6	1.82	0.44
86:28:2492:C:H2'	86:28:2493:G:C8	2.49	0.44
86:28:2751:G:N3	86:28:2752:G:C8	2.85	0.44
86:28:2858:A:H2'	86:28:2859:G:C8	2.53	0.44
86:28:4400:G:C6	86:28:4401:G:N7	2.85	0.44
86:28:4578:G:H2'	86:28:4579:U:H6	1.81	0.44
7:L4:242:PRO:HB2	86:28:2297:G:H4'	1.99	0.44
8:L5:11:ALA:HB1	86:28:1743:A:H5'	1.98	0.44
9:L6:165:VAL:HG12	9:L6:178:VAL:HG22	1.99	0.44
12:13:50:PRO:HG3	28:35:121:VAL:HG22	1.99	0.44
41:10:95:HIS:HB3	41:10:126:VAL:HG12	2.00	0.44
56:S3:107:TYR:HA	56:S3:110:LEU:HG	1.98	0.44
60:BB:68:ILE:HD11	60:BB:121:LEU:HD13	1.98	0.44
70:18:856:C:C2	70:18:857:U:C5	3.05	0.44
70:18:1739:C:H2'	70:18:1740:C:H6	1.80	0.44
70:18:1855:G:H2'	70:18:1856:C:C6	2.52	0.44
86:28:25:A:C8	86:28:341:G:C8	3.06	0.44
86:28:1084:C:C4	86:28:1216:C:C4	3.06	0.44
86:28:1445:U:H2'	86:28:1446:C:H6	1.81	0.44
86:28:1481:C:H2'	86:28:1481:C:O2	2.17	0.44
86:28:1972:G:C6	86:28:1995:G:C6	3.05	0.44
10:L7:42:ARG:O	10:L7:46:ARG:HG2	2.18	0.44
10:L7:175:ALA:HB1	86:28:2102:G:C8	2.53	0.44
20:26:100:HIS:CD2	86:28:231:U:H4'	2.52	0.44
55:v:713:ALA:HA	55:v:716:ARG:HG2	1.98	0.44
64:AS:86:LEU:HB3	64:AS:98:THR:HB	1.98	0.44
66:QQ:8:ALA:HB2	66:QQ:74:VAL:HG11	1.99	0.44
69:ZZ:140:TYR:CZ	69:ZZ:142:GLY:HA2	2.52	0.44
70:18:212:C:H2'	70:18:213:G:C8	2.52	0.44
70:18:509:G:H2'	70:18:510:G:H8	1.82	0.44
70:18:925:G:C2	70:18:926:A:C8	3.06	0.44
70:18:1212:G:H2'	70:18:1213:C:C6	2.53	0.44
70:18:1375:G:H2'	70:18:1376:A:H8	1.81	0.44
70:18:1424:G:H2'	70:18:1425:G:H8	1.82	0.44
70:18:1533:A:H2'	70:18:1533:A:N3	2.31	0.44
70:18:1656:G:C2	70:18:1657:G:C8	3.06	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
78:TT:79:ILE:HB	78:TT:83:LEU:HD23	2.00	0.44
10:L7:222:LYS:HE3	86:28:1907:A:H4'	1.99	0.44
41:10:15:LYS:HG3	86:28:1863:U:OP1	2.17	0.44
55:v:602:LEU:HD13	55:v:707:VAL:HG12	2.00	0.44
56:S3:172:VAL:HG22	56:S3:185:LYS:HG2	1.98	0.44
70:18:561:A:H2'	70:18:562:U:H6	1.79	0.44
75:EE:32:ALA:HB1	75:EE:37:GLU:HB3	1.99	0.44
76:CC:47:LYS:HA	76:CC:50:GLN:HG2	2.00	0.44
85:t:146:ARG:H	85:t:146:ARG:HD2	1.83	0.44
86:28:425:U:H2'	86:28:426:A:H8	1.82	0.44
86:28:441:G:H2'	86:28:442:G:H8	1.81	0.44
86:28:647:G:H3'	86:28:648:G:H8	1.82	0.44
86:28:1308:C:C2	86:28:1309:C:C5	3.05	0.44
86:28:1309:C:H2'	86:28:1310:C:C6	2.53	0.44
86:28:1956:A:O2'	86:28:1957:U:H5'	2.17	0.44
86:28:2029:A:H2'	86:28:2030:A:C8	2.52	0.44
86:28:2060:G:H2'	86:28:2061:U:C6	2.51	0.44
86:28:4208:U:H2'	86:28:4209:G:C8	2.53	0.44
86:28:4968:A:H2'	86:28:4969:C:C6	2.53	0.44
87:ES:3246:G:H2'	87:ES:3247:A:C8	2.53	0.44
3:58:27:U:H2'	3:58:28:C:H6	1.82	0.44
8:L5:83:LEU:HB3	8:L5:88:VAL:HB	1.99	0.44
28:35:74:LYS:HE2	86:28:133:C:C5	2.51	0.44
41:10:99:ILE:HG22	41:10:123:GLN:HB2	1.99	0.44
41:10:112:GLN:H	41:10:112:GLN:HG2	1.57	0.44
45:S4:36:HIS:CG	45:S4:85:GLY:HA3	2.52	0.44
52:GG:99:ALA:N	52:GG:133:THR:HG22	2.30	0.44
70:18:859:G:N1	70:18:860:G:C5	2.85	0.44
76:CC:22:VAL:HA	76:CC:67:PHE:O	2.17	0.44
81:B:139:SER:HB3	81:B:144:GLU:HG2	1.99	0.44
86:28:2485:U:H2'	86:28:2486:G:H8	1.82	0.44
86:28:2611:A:H2'	86:28:2612:G:C8	2.52	0.44
86:28:2682:G:H2'	86:28:2683:C:H6	1.81	0.44
86:28:4551:U:H2'	86:28:4552:U:C6	2.52	0.44
86:28:4563:U:H2'	86:28:4564:A:C8	2.51	0.44
9:L6:124:VAL:HG21	86:28:702:U:H5'	2.00	0.44
14:15:61:ILE:O	14:15:61:ILE:HG13	2.18	0.44
14:15:76:PRO:O	14:15:79:ALA:HB2	2.17	0.44
39:EB:255:TYR:HB3	39:EB:301:LEU:HD21	1.99	0.44
41:10:66:GLU:CD	41:10:69:ARG:HH21	2.26	0.44
44:S9:59:GLU:HG3	44:S9:60:LEU:N	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:v:252:LYS:HA	55:v:255:ASP:OD2	2.17	0.44
56:S3:143:ARG:HB2	74:RB:218:TRP:CD1	2.53	0.44
68:30:38:ILE:HD11	68:30:46:VAL:HG21	2.00	0.44
70:18:1117:C:O2	70:18:1117:C:H2'	2.17	0.44
84:A:86:LEU:HD12	84:A:87:PRO:HD2	2.00	0.44
85:t:27:ALA:O	85:t:30:PRO:HD2	2.18	0.44
86:28:432:U:H4'	86:28:433:A:H5''	1.98	0.44
86:28:756:G:C6	86:28:908:G:C6	3.06	0.44
86:28:1392:A:H2'	86:28:1393:G:C8	2.52	0.44
86:28:2503:G:C2	86:28:4084:G:C4	3.06	0.44
86:28:3664:G:C2	86:28:3665:G:N7	2.86	0.44
5:L8:196:TRP:HB3	5:L8:197:PRO:HD3	2.00	0.44
8:L5:33:ARG:HH11	17:21:27:LEU:HD12	1.81	0.44
55:v:119:LEU:HG	55:v:151:ILE:HD12	2.00	0.44
70:18:557:U:H2'	70:18:558:G:C8	2.52	0.44
70:18:902:G:H2'	70:18:903:A:H8	1.83	0.44
70:18:1126:G:H2'	70:18:1127:C:H6	1.83	0.44
70:18:1587:G:N7	71:MM:67:ARG:HD3	2.32	0.44
76:CC:25:LYS:HA	76:CC:46:MET:HE3	2.00	0.44
86:28:6:C:H2'	86:28:7:C:C6	2.52	0.44
86:28:411:G:H4'	86:28:412:G:H5''	2.00	0.44
86:28:1199:G:N3	86:28:1200:G:C8	2.86	0.44
86:28:2080:U:H2'	86:28:2081:C:H6	1.83	0.44
86:28:2412:A:H2'	86:28:2413:U:H6	1.82	0.44
86:28:3648:A:H1'	86:28:3785:A:N6	2.32	0.44
86:28:3727:A:H2'	86:28:3728:A:C8	2.52	0.44
86:28:4108:G:H2'	86:28:4109:G:C8	2.52	0.44
86:28:4135:G:H2'	86:28:4136:G:C8	2.53	0.44
86:28:4246:G:H2'	86:28:4247:G:C8	2.53	0.44
6:L3:189:THR:HG22	6:L3:192:GLU:HG2	2.00	0.44
9:L6:206:ILE:O	9:L6:209:VAL:HG22	2.18	0.44
60:BB:61:ALA:HB1	60:BB:145:ILE:HD13	1.99	0.44
70:18:96:C:H2'	70:18:97:U:C6	2.53	0.44
70:18:114:G:O2'	70:18:115:U:H5''	2.17	0.44
70:18:1035:A:H2'	70:18:1036:A:H8	1.83	0.44
70:18:1075:C:C2	70:18:1076:G:C8	3.06	0.44
70:18:1470:C:H2'	70:18:1471:C:C6	2.52	0.44
70:18:1515:G:H2'	70:18:1516:G:H8	1.83	0.44
70:18:1666:C:C2	70:18:1667:U:C6	3.06	0.44
70:18:1723:G:N3	70:18:1724:A:C8	2.85	0.44
86:28:726:G:H2'	86:28:727:C:C6	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
86:28:1802:A:H5''	86:28:1803:G:H5'	2.00	0.44
86:28:2098:G:H2'	86:28:2099:C:C6	2.53	0.44
86:28:2454:U:C2	86:28:2455:G:C8	3.06	0.44
86:28:3723:A:H2'	86:28:3724:A:C8	2.52	0.44
86:28:4385:A:H4'	86:28:4386:C:H5''	2.00	0.44
4:5:113:G:H2'	4:5:114:U:H6	1.83	0.43
5:L8:194:ASN:HB2	86:28:1539:G:H4'	2.00	0.43
22:dd:21:ARG:HB3	86:28:1318:C:OP1	2.18	0.43
31:38:35:LYS:HE2	86:28:2696:A:H62	1.83	0.43
50:LL:22:GLY:HA2	50:LL:56:ALA:HB3	1.98	0.43
70:18:121:U:H2'	70:18:122:G:H8	1.83	0.43
70:18:212:C:H2'	70:18:213:G:H8	1.82	0.43
70:18:298:G:C4	70:18:299:A:C8	3.06	0.43
70:18:855:G:C2	70:18:856:C:C6	3.06	0.43
70:18:1233:G:C6	70:18:1526:G:C6	3.06	0.43
86:28:33:A:H3'	86:28:47:A:H61	1.84	0.43
86:28:1191:C:H2'	86:28:1192:C:C6	2.53	0.43
86:28:1350:C:H2'	86:28:1351:G:C8	2.53	0.43
86:28:1468:C:H2'	86:28:1469:C:H6	1.83	0.43
86:28:2532:C:C2	86:28:2533:C:C5	3.07	0.43
86:28:3933:G:H2'	86:28:3934:G:C8	2.51	0.43
86:28:4254:G:H2'	86:28:4254:G:N3	2.33	0.43
86:28:4400:G:C2	86:28:4401:G:C8	3.05	0.43
86:28:4503:A:H2'	86:28:4504:C:H6	1.83	0.43
86:28:4723:A:H2'	86:28:4724:A:H8	1.83	0.43
87:ES:3239:G:N3	87:ES:3240:A:C8	2.86	0.43
4:5:67:C:OP1	8:L5:14:LYS:HG2	2.19	0.43
4:5:112:U:H2'	4:5:113:G:H8	1.83	0.43
7:L4:338:ASN:C	7:L4:340:ILE:H	2.26	0.43
41:10:55:ASP:HB2	41:10:162:ARG:HG3	2.00	0.43
48:RR:84:PHE:CE2	48:RR:86:PRO:HA	2.52	0.43
54:19:15:LEU:HD12	54:19:15:LEU:HA	1.88	0.43
55:v:788:LEU:HD12	55:v:789:PRO:HD2	1.99	0.43
66:QQ:50:PHE:HB2	66:QQ:63:VAL:HG22	1.99	0.43
70:18:1280:G:C4	70:18:1281:G:C8	3.05	0.43
70:18:1712:A:H2'	70:18:1713:C:C6	2.53	0.43
70:18:1713:C:H2'	70:18:1714:U:C6	2.53	0.43
70:18:1718:G:H22	70:18:1814:G:H2'	1.84	0.43
70:18:1722:G:C6	70:18:1723:G:C5	3.06	0.43
77:II:10:VAL:HG12	77:II:12:VAL:HG23	2.00	0.43
86:28:40:G:N2	86:28:4380:A:H62	2.16	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
86:28:106:A:H2'	86:28:107:G:O4'	2.18	0.43
86:28:717:U:H2'	86:28:718:C:C6	2.53	0.43
86:28:1895:G:H2'	86:28:1896:A:O4'	2.18	0.43
86:28:2546:G:H4'	86:28:2547:G:OP1	2.17	0.43
86:28:3851:U:H2'	86:28:3852:A:O4'	2.18	0.43
86:28:3923:A:H2'	86:28:3924:C:C6	2.52	0.43
86:28:4685:U:H2'	86:28:4686:G:C8	2.52	0.43
3:58:4:C:H2'	3:58:5:U:H6	1.83	0.43
26:ee:106:TYR:CD1	26:ee:107:PRO:HD3	2.52	0.43
30:37:21:ARG:HG2	30:37:37:CYS:SG	2.58	0.43
41:10:86:HIS:HB3	41:10:139:ARG:HG2	2.01	0.43
70:18:389:A:C4	70:18:390:C:C5	3.06	0.43
70:18:1210:G:N2	70:18:1690:U:H3	2.16	0.43
70:18:1531:A:H2'	70:18:1532:C:C6	2.53	0.43
70:18:1709:G:H2'	70:18:1710:C:H6	1.81	0.43
86:28:27:C:H2'	86:28:28:C:H6	1.83	0.43
86:28:441:G:H2'	86:28:442:G:C8	2.54	0.43
86:28:2457:G:H21	86:28:3672:G:H21	1.66	0.43
86:28:3882:C:C2	86:28:3883:U:C5	3.06	0.43
86:28:4235:G:C2	86:28:4236:G:C8	3.06	0.43
4:5:55:A:H4'	51:11:155:HIS:HB2	2.00	0.43
37:gg:90:LEU:HG	37:gg:111:ILE:HG23	1.99	0.43
45:S4:92:ILE:HG23	47:SS:17:LEU:HD11	1.99	0.43
55:v:22:MET:HE2	55:v:22:MET:HB2	1.84	0.43
64:AS:144:LYS:HB2	64:AS:208:HIS:HB3	2.00	0.43
70:18:184:G:C2	70:18:185:G:C8	3.06	0.43
70:18:449:A:O2'	70:18:450:C:H4'	2.18	0.43
70:18:849:A:H2'	70:18:850:C:H6	1.83	0.43
73:OO:24:LEU:HD12	73:OO:112:VAL:HG22	2.00	0.43
82:u:116:LEU:O	82:u:120:ILE:HG13	2.19	0.43
86:28:18:C:H2'	86:28:19:G:H8	1.83	0.43
86:28:262:G:H2'	86:28:263:G:C8	2.53	0.43
86:28:424:U:C2	86:28:425:U:C5	3.07	0.43
86:28:469:C:H2'	86:28:470:A:C8	2.51	0.43
86:28:1932:A:H2'	86:28:1933:G:C8	2.52	0.43
86:28:4700:A:C2	86:28:4701:A:C8	3.06	0.43
3:58:93:C:HO2'	3:58:94:G:H8	1.66	0.43
23:29:105:GLY:O	23:29:109:ARG:HG2	2.19	0.43
26:ee:8:LYS:HB3	26:ee:100:ARG:CZ	2.48	0.43
55:v:42:LYS:HE3	55:v:42:LYS:HB3	1.80	0.43
63:JJ:10:LYS:HB2	63:JJ:10:LYS:HE3	1.62	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
66:QQ:27:ILE:HG13	66:QQ:61:ILE:HB	2.01	0.43
70:18:342:C:C2	70:18:343:A:C8	3.06	0.43
70:18:351:G:C2	70:18:352:U:C6	3.06	0.43
70:18:454:U:H2'	70:18:455:A:H8	1.83	0.43
70:18:609:U:H2'	70:18:610:G:H8	1.82	0.43
70:18:652:U:H2'	70:18:653:A:C8	2.54	0.43
70:18:925:G:H1	70:18:1017:U:H3	1.67	0.43
70:18:1005:G:H2'	70:18:1006:C:H6	1.84	0.43
70:18:1174:U:H2'	70:18:1175:G:H8	1.83	0.43
86:28:910:G:H2'	86:28:911:U:H6	1.82	0.43
86:28:956:A:H1'	86:28:2076:G:H5''	1.99	0.43
86:28:1306:C:O2	86:28:1307:A:C8	2.72	0.43
86:28:3651:A:H2'	86:28:3652:A:C8	2.53	0.43
86:28:4993:G:C2	86:28:4994:G:C8	3.06	0.43
87:ES:2942:C:C2'	87:ES:2943:C:H5'	2.48	0.43
7:L4:26:ALA:HB1	7:L4:267:TRP:CZ3	2.53	0.43
11:aa:152:ALA:HB1	11:aa:189:LEU:HD11	2.00	0.43
21:27:136:PHE:OXT	27:34:90:ARG:HD3	2.19	0.43
30:37:72:ARG:O	30:37:75:ARG:HG2	2.19	0.43
31:38:2:PRO:HB2	86:28:2692:U:O2	2.18	0.43
36:ff:50:ARG:HD2	36:ff:54:ILE:HD11	2.00	0.43
45:S4:126:VAL:HG11	45:S4:139:LEU:HD13	2.00	0.43
55:v:609:PHE:HZ	55:v:661:ILE:HG13	1.83	0.43
56:S3:143:ARG:NH2	74:RB:218:TRP:HB2	2.16	0.43
62:PP:73:ALA:HB1	62:PP:78:ILE:HB	2.01	0.43
70:18:551:U:H2'	70:18:552:G:C8	2.53	0.43
70:18:1136:U:H2'	70:18:1137:U:C6	2.53	0.43
70:18:1337:C:H2'	70:18:1338:G:H8	1.83	0.43
70:18:1693:G:H2'	70:18:1694:U:C6	2.52	0.43
86:28:1348:U:H2'	86:28:1349:G:C8	2.53	0.43
86:28:1728:U:C2	86:28:1729:A:C8	3.06	0.43
86:28:2689:C:C2	86:28:2690:C:C5	3.05	0.43
86:28:2810:U:H2'	86:28:2811:G:O4'	2.18	0.43
86:28:3608:A:H2'	86:28:3609:G:H8	1.83	0.43
86:28:4342:C:H2'	86:28:4343:U:H6	1.84	0.43
86:28:4345:C:H2'	86:28:4346:U:H6	1.84	0.43
86:28:4966:A:H2'	86:28:4967:A:O4'	2.18	0.43
87:ES:3242:U:H2'	87:ES:3243:C:C6	2.53	0.43
1:17:54:LYS:HA	1:17:83:TRP:CD1	2.53	0.43
1:17:64:ASN:HD22	1:17:80:GLN:HE22	1.66	0.43
8:L5:108:ARG:CZ	8:L5:253:TYR:HB2	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:35:31:LEU:HB3	28:35:47:ILE:HG22	2.01	0.43
38:s:129:GLY:HA2	38:s:151:THR:HG21	2.01	0.43
42:L9:50:LYS:HE3	86:28:759:G:O2'	2.19	0.43
55:v:649:ILE:HA	55:v:663:THR:HA	1.99	0.43
55:v:702:PHE:CD1	55:v:729:LEU:HD22	2.53	0.43
60:BB:102:ARG:HD2	60:BB:102:ARG:HA	1.73	0.43
70:18:26:U:H2'	70:18:27:A:H8	1.84	0.43
70:18:1804:U:H2'	70:18:1805:G:H8	1.83	0.43
82:u:111:LEU:HD23	82:u:136:SER:HB2	2.01	0.43
86:28:956:A:C8	86:28:957:G:N7	2.87	0.43
86:28:1334:A:H2'	86:28:1335:G:H8	1.82	0.43
86:28:1995:G:H2'	86:28:1996:C:C6	2.53	0.43
86:28:2417:A:H2'	86:28:2418:A:H8	1.84	0.43
86:28:2751:G:H2'	86:28:2752:G:H8	1.83	0.43
86:28:4385:A:H61	86:28:4531:U:H5'	1.84	0.43
86:28:4489:G:N3	86:28:4708:A:H2'	2.34	0.43
45:S4:181:CYS:SG	45:S4:225:ILE:HG23	2.58	0.43
70:18:957:A:C8	70:18:958:G:N2	2.87	0.43
70:18:1073:U:H2'	70:18:1074:C:H6	1.83	0.43
70:18:1102:G:C6	70:18:1131:G:C6	3.06	0.43
70:18:1670:C:C2	70:18:1671:G:C8	3.07	0.43
70:18:1712:A:H2'	70:18:1713:C:H6	1.84	0.43
84:A:36:LEU:HD23	84:A:36:LEU:HA	1.91	0.43
84:A:51:ARG:NH1	84:A:55:SER:HB2	2.34	0.43
86:28:125:C:H2'	86:28:126:C:C6	2.53	0.43
86:28:178:C:H2'	86:28:179:G:H8	1.83	0.43
86:28:310:G:C4	86:28:311:G:C8	3.07	0.43
86:28:2726:G:H2'	86:28:2727:C:C6	2.53	0.43
86:28:3697:U:H5''	86:28:3698:G:H5'	2.01	0.43
86:28:3867:A:H2'	86:28:3868:G:C8	2.54	0.43
86:28:3938:G:H4'	86:28:3939:G:O5'	2.18	0.43
86:28:4889:G:N3	86:28:4890:G:C8	2.87	0.43
5:L8:28:ARG:HB3	5:L8:123:ARG:HB3	2.01	0.43
6:L3:45:ALA:HB3	6:L3:183:ILE:HG23	2.01	0.43
8:L5:44:TYR:HB2	86:28:1823:G:O2'	2.18	0.43
17:21:65:TYR:CE1	17:21:88:ARG:HB3	2.54	0.43
18:22:64:GLU:HG2	18:22:71:THR:HB	2.01	0.43
45:S4:259:LYS:HD2	45:S4:259:LYS:HA	1.89	0.43
59:S2:102:LEU:HD21	59:S2:130:ILE:HD11	2.00	0.43
60:BB:130:ASP:O	60:BB:133:PRO:HD2	2.19	0.43
64:AS:105:LEU:HD13	64:AS:213:ARG:HA	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:18:29:G:H2'	70:18:30:C:C6	2.53	0.43
70:18:979:C:H2'	70:18:980:A:C8	2.54	0.43
70:18:1189:A:H2'	70:18:1190:A:H8	1.84	0.43
70:18:1819:A:C4	70:18:1820:G:C8	3.07	0.43
77:II:103:ALA:O	77:II:106:LYS:HG3	2.19	0.43
86:28:1874:A:H2'	86:28:1875:C:C6	2.54	0.43
86:28:2477:A:H2'	86:28:2478:C:C5	2.54	0.43
86:28:2676:A:C5	86:28:2677:G:C8	3.07	0.43
86:28:4401:G:C4	86:28:4402:C:C5	3.07	0.43
86:28:4652:G:H2'	86:28:4653:C:C6	2.54	0.43
6:L3:253:CYS:SG	86:28:4521:U:H1'	2.58	0.43
7:L4:289:LEU:HA	7:L4:292:ILE:HB	2.01	0.43
23:29:4:SER:HB2	86:28:1855:G:OP1	2.19	0.43
27:34:24:ARG:HD3	86:28:2638:G:H4'	2.00	0.43
44:S9:136:ARG:HD3	44:S9:160:SER:HA	2.00	0.43
46:S6:167:LYS:HE3	46:S6:167:LYS:HB3	1.87	0.43
55:v:604:MET:HG2	55:v:704:VAL:HA	2.00	0.43
57:FF:38:TYR:CZ	57:FF:78:LYS:HD2	2.54	0.43
70:18:106:C:H2'	70:18:107:A:C8	2.52	0.43
70:18:647:U:H2'	70:18:648:A:C8	2.53	0.43
70:18:1199:A:H2'	70:18:1200:A:H8	1.82	0.43
70:18:1792:G:H2'	70:18:1793:A:H8	1.82	0.43
70:18:1794:C:H2'	70:18:1795:G:C8	2.54	0.43
77:II:50:LYS:HB3	77:II:85:ARG:HD2	2.00	0.43
85:t:15:LEU:HD13	85:t:28:LEU:HD13	2.01	0.43
86:28:282:C:C4	86:28:283:G:C5	3.07	0.43
86:28:406:C:H2'	86:28:407:A:C8	2.54	0.43
86:28:449:C:OP1	86:28:450:G:H5'	2.18	0.43
86:28:1196:G:H2'	86:28:1197:C:C6	2.54	0.43
86:28:1549:G:C2	86:28:1550:G:C8	3.07	0.43
86:28:1737:A:C4	86:28:1738:A:C8	3.07	0.43
86:28:2056:G:C8	86:28:2058:G:C8	3.07	0.43
86:28:2648:G:H2'	86:28:2649:G:H8	1.83	0.43
86:28:2780:C:H2'	86:28:2781:G:H8	1.83	0.43
86:28:4577:U:H2'	86:28:4578:G:H8	1.84	0.43
86:28:4674:C:H2'	86:28:4675:U:C6	2.53	0.43
86:28:4894:A:H5''	86:28:4895:C:C6	2.54	0.43
3:58:102:G:H5''	30:37:39:TYR:HE1	1.83	0.42
70:18:219:U:H2'	70:18:220:U:C6	2.54	0.42
70:18:319:C:H2'	70:18:320:G:C8	2.54	0.42
70:18:874:G:H2'	70:18:875:A:C8	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:18:945:U:H2'	70:18:946:U:H6	1.84	0.42
70:18:1139:C:H41	70:18:1149:A:H62	1.66	0.42
86:28:983:C:H42	86:28:1071:C:H42	1.65	0.42
86:28:1094:G:C6	86:28:1203:G:C6	3.07	0.42
86:28:2374:A:H2'	86:28:2375:A:H8	1.84	0.42
86:28:2413:U:C2	86:28:2414:G:C8	3.07	0.42
86:28:3774:A:H2'	86:28:3775:A:N3	2.34	0.42
86:28:4089:G:H2'	86:28:4090:G:H8	1.83	0.42
86:28:4862:G:H2'	86:28:4863:G:H8	1.83	0.42
86:28:4981:G:H3'	86:28:4982:A:H8	1.84	0.42
11:aa:195:THR:O	11:aa:199:LEU:HG	2.18	0.42
35:42:9:ARG:HD3	86:28:4290:U:OP1	2.19	0.42
39:EB:190:LEU:HD21	39:EB:225:ALA:HB2	2.01	0.42
39:EB:192:GLN:HG3	39:EB:193:HIS:CD2	2.54	0.42
45:S4:21:ASP:HB3	70:18:829:C:H5''	2.01	0.42
63:JJ:59:LYS:O	63:JJ:62:GLN:HG3	2.19	0.42
70:18:465:A:H2'	70:18:465:A:OP2	2.19	0.42
70:18:673:G:H2'	70:18:674:C:H6	1.85	0.42
70:18:897:U:H2'	70:18:898:U:C6	2.54	0.42
70:18:1260:A:C8	70:18:1261:C:C5	3.07	0.42
70:18:1358:U:H2'	70:18:1359:U:H6	1.84	0.42
70:18:1494:U:H4'	70:18:1495:G:H5''	1.99	0.42
70:18:1820:G:H2'	70:18:1821:U:H6	1.84	0.42
86:28:425:U:C2	86:28:426:A:C8	3.06	0.42
86:28:447:C:H2'	86:28:448:G:H8	1.82	0.42
86:28:1586:G:H2'	86:28:1587:G:C8	2.54	0.42
86:28:2081:C:H2'	86:28:2082:G:C8	2.53	0.42
86:28:4219:A:H2'	86:28:4220:A:C8	2.55	0.42
86:28:4236:G:H4'	86:28:4328:G:O2'	2.20	0.42
86:28:4648:A:H2'	86:28:4649:G:H8	1.83	0.42
86:28:4716:C:H2'	86:28:4717:A:H8	1.84	0.42
86:28:5042:A:C4	86:28:5043:A:C8	3.07	0.42
7:L4:330:PRO:HD3	10:L7:46:ARG:HH21	1.84	0.42
14:15:94:PHE:CE2	14:15:96:ARG:HB2	2.54	0.42
14:15:98:LEU:HD12	14:15:128:LYS:HD2	2.00	0.42
25:32:31:ILE:HD11	86:28:2347:A:C4	2.54	0.42
31:38:36:VAL:HG13	31:38:43:TYR:HB2	2.01	0.42
39:EB:168:GLU:O	39:EB:172:LYS:HG2	2.19	0.42
51:11:42:GLN:HE22	51:11:117:ILE:HD13	1.83	0.42
61:UU:92:ARG:HB3	70:18:1865:C:O2	2.19	0.42
70:18:85:A:H2'	70:18:86:C:C6	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:18:179:C:H3'	70:18:180:G:H8	1.84	0.42
70:18:935:G:H2'	70:18:936:G:C8	2.54	0.42
70:18:1725:U:C2	70:18:1726:G:C8	3.07	0.42
86:28:975:C:H2'	86:28:976:G:O4'	2.18	0.42
86:28:2276:A:H2'	86:28:2277:C:O4'	2.19	0.42
86:28:2350:U:O5'	86:28:2351:C:H5''	2.18	0.42
86:28:2439:G:H5'	86:28:2778:G:OP2	2.18	0.42
86:28:3702:A:C2	86:28:3703:G:C8	3.08	0.42
86:28:3927:U:H2'	86:28:3928:A:H8	1.84	0.42
3:58:17:A:H1'	86:28:418:A:C2	2.54	0.42
4:5:92:C:H2'	4:5:93:G:C8	2.52	0.42
12:13:15:HIS:CE1	86:28:95:G:H5'	2.54	0.42
15:bb:36:VAL:HG21	15:bb:108:ILE:HG23	2.00	0.42
15:bb:192:PHE:HA	15:bb:195:VAL:HG22	2.00	0.42
45:S4:126:VAL:HG23	45:S4:156:VAL:O	2.20	0.42
45:S4:126:VAL:HG22	45:S4:158:ASP:O	2.19	0.42
64:AS:225:LEU:HD23	64:AS:229:MET:HG2	2.01	0.42
70:18:298:G:C2	70:18:299:A:C8	3.07	0.42
70:18:654:A:C8	70:18:655:A:H2'	2.55	0.42
70:18:943:U:H2'	70:18:944:A:H8	1.84	0.42
70:18:1308:U:H2'	70:18:1309:C:C6	2.54	0.42
70:18:1348:G:C8	70:18:1349:G:C8	3.07	0.42
70:18:1545:A:H2'	70:18:1546:G:C8	2.54	0.42
70:18:1726:G:H2'	70:18:1726:G:N3	2.35	0.42
70:18:1842:C:H2'	70:18:1843:G:H8	1.84	0.42
75:EE:51:VAL:CG1	75:EE:109:VAL:HB	2.49	0.42
86:28:123:C:H2'	86:28:124:C:H6	1.85	0.42
86:28:260:C:C2	86:28:261:G:C8	3.07	0.42
86:28:1307:A:C4	86:28:1308:C:C5	3.08	0.42
86:28:1382:G:N3	86:28:1383:G:C8	2.87	0.42
86:28:2688:G:H2'	86:28:2689:C:C6	2.54	0.42
86:28:2858:A:C4	86:28:2859:G:C8	3.07	0.42
86:28:4460:U:H2'	86:28:4461:C:C6	2.54	0.42
87:ES:3236:G:O2'	87:ES:3237:G:C8	2.71	0.42
3:58:66:A:H2'	3:58:67:U:C6	2.54	0.42
15:bb:158:GLU:HA	15:bb:161:LYS:HE3	2.00	0.42
15:bb:179:LYS:HA	15:bb:179:LYS:HD3	1.89	0.42
16:20:67:VAL:HA	86:28:729:G:H1	1.85	0.42
22:dd:2:PRO:HA	86:28:2342:G:OP2	2.19	0.42
27:34:63:VAL:HG13	27:34:66:ARG:CZ	2.49	0.42
36:ff:49:ARG:HH21	36:ff:52:VAL:HG13	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:S4:159:THR:OG1	45:S4:173:ILE:HB	2.19	0.42
46:S6:201:LYS:HB3	46:S6:201:LYS:HE3	1.86	0.42
56:S3:65:ARG:HA	56:S3:68:GLU:HG2	2.02	0.42
84:A:87:PRO:HB3	84:A:112:ILE:HD13	2.02	0.42
86:28:949:G:N3	86:28:950:G:C8	2.87	0.42
86:28:1490:G:H2'	86:28:1491:A:C8	2.55	0.42
86:28:2632:U:C2	86:28:2633:U:C5	3.07	0.42
86:28:2689:C:H2'	86:28:2690:C:C6	2.54	0.42
6:L3:92:TYR:HB3	6:L3:99:LEU:HG	2.02	0.42
8:L5:129:GLU:HG3	8:L5:177:THR:HG21	2.01	0.42
9:L6:64:MET:O	9:L6:68:LYS:HG3	2.20	0.42
9:L6:73:ARG:HD3	86:28:983:C:C6	2.55	0.42
12:13:28:GLN:OE1	14:15:202:ARG:HD3	2.20	0.42
39:EB:287:LYS:HB2	39:EB:287:LYS:HE2	1.78	0.42
66:QQ:50:PHE:HB3	66:QQ:63:VAL:HG13	2.02	0.42
68:30:48:LEU:HD21	68:30:60:ILE:HG21	2.02	0.42
70:18:23:G:C5	70:18:24:C:C5	3.07	0.42
70:18:559:G:C2	70:18:560:A:C8	3.08	0.42
70:18:632:C:C2	70:18:633:C:C5	3.07	0.42
70:18:804:U:H2'	70:18:805:U:C6	2.55	0.42
70:18:958:G:C6	70:18:959:G:C6	3.07	0.42
70:18:1308:U:H2'	70:18:1309:C:H6	1.85	0.42
70:18:1410:C:H2'	70:18:1411:G:H8	1.85	0.42
86:28:137:G:C2	86:28:138:G:C5	3.07	0.42
86:28:447:C:H2'	86:28:448:G:C8	2.54	0.42
86:28:1329:G:C2	86:28:3865:A:H1'	2.54	0.42
86:28:1350:C:H2'	86:28:1351:G:H8	1.84	0.42
86:28:1486:C:H2'	86:28:1487:G:H8	1.84	0.42
86:28:1806:G:H2'	86:28:1807:C:H6	1.83	0.42
86:28:1961:G:H2'	86:28:2025:A:H61	1.84	0.42
86:28:2075:G:H2'	86:28:2076:G:H8	1.85	0.42
86:28:2273:G:H2'	86:28:2274:C:H6	1.85	0.42
86:28:2314:G:C6	86:28:2326:G:C6	3.07	0.42
86:28:2338:C:C4	86:28:2339:G:N7	2.88	0.42
86:28:2804:C:C2	86:28:2805:C:C5	3.08	0.42
87:ES:3245:G:H2'	87:ES:3246:G:C8	2.54	0.42
26:ee:28:LEU:HD22	26:ee:86:ALA:HB2	2.01	0.42
26:ee:46:ARG:HD3	26:ee:106:TYR:CE1	2.55	0.42
38:s:34:ASN:HA	86:28:1968:G:O2'	2.20	0.42
43:S7:192:PHE:HB2	65:VV:12:PRO:HG3	2.02	0.42
55:v:581:GLU:HB2	55:v:697:MET:HG2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:S8:65:PHE:HA	58:S8:187:GLY:O	2.19	0.42
62:PP:62:MET:HE2	62:PP:62:MET:HA	2.02	0.42
70:18:1384:C:C4	70:18:1385:G:N7	2.88	0.42
70:18:1482:C:H2'	70:18:1483:A:O4'	2.19	0.42
70:18:1633:A:H2'	70:18:1634:A:C8	2.54	0.42
72:AA:299:PHE:CD2	72:AA:309:VAL:HG12	2.55	0.42
86:28:221:C:H2'	86:28:222:C:H6	1.84	0.42
86:28:422:C:H2'	86:28:423:G:H8	1.85	0.42
86:28:494:C:H2'	86:28:495:C:C6	2.55	0.42
86:28:1177:U:H2'	86:28:1178:G:C8	2.54	0.42
86:28:1384:C:C2	86:28:1385:G:C8	3.08	0.42
86:28:1687:U:H2'	86:28:1688:G:C8	2.54	0.42
86:28:1749:A:H2'	86:28:1750:G:H8	1.85	0.42
86:28:2488:C:H3'	86:28:2490:U:C4	2.54	0.42
86:28:2540:C:H2'	86:28:2541:G:C8	2.54	0.42
86:28:2653:C:H2'	86:28:2654:C:H6	1.85	0.42
86:28:2815:A:C4	86:28:2816:G:C8	3.08	0.42
86:28:4297:G:C2	86:28:4298:A:C8	3.08	0.42
86:28:4343:U:H2'	86:28:4344:U:C6	2.55	0.42
5:L8:226:ARG:N	86:28:3706:C:H5''	2.34	0.42
9:L6:242:LYS:HE2	9:L6:242:LYS:HB2	1.85	0.42
21:27:89:ILE:HD13	21:27:121:ARG:HD2	2.00	0.42
23:29:111:ARG:HB3	23:29:111:ARG:HH11	1.85	0.42
39:EB:237:ALA:HB1	39:EB:308:LEU:HB3	2.01	0.42
41:10:86:HIS:HB3	41:10:139:ARG:CG	2.50	0.42
48:RR:61:GLN:CB	48:RR:62:PRO:HD2	2.49	0.42
48:RR:61:GLN:HB3	48:RR:62:PRO:HD2	2.01	0.42
63:JJ:72:LYS:HE3	63:JJ:72:LYS:HB3	1.83	0.42
65:VV:47:PHE:CE2	65:VV:49:HIS:HB2	2.55	0.42
69:ZZ:97:LYS:HE2	69:ZZ:97:LYS:HB2	1.65	0.42
70:18:909:G:N3	70:18:910:G:C8	2.88	0.42
70:18:929:G:N2	70:18:1104:G:H4'	2.35	0.42
81:B:85:LYS:HB3	81:B:139:SER:OG	2.20	0.42
86:28:149:A:H5''	86:28:151:G:O4'	2.20	0.42
86:28:650:C:H2'	86:28:651:C:H6	1.84	0.42
86:28:1199:G:H2'	86:28:1200:G:C8	2.53	0.42
86:28:2528:G:H4'	86:28:2783:A:H4'	2.02	0.42
86:28:2639:U:H2'	86:28:2694:G:H1	1.85	0.42
86:28:2889:G:H2'	86:28:2890:C:C6	2.55	0.42
86:28:3697:U:H4'	86:28:3698:G:OP2	2.20	0.42
86:28:3769:C:H2'	86:28:3770:U:H6	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
86:28:4300:U:H2'	86:28:4301:U:C6	2.54	0.42
86:28:4407:G:C4	86:28:4408:G:C8	3.07	0.42
86:28:4737:G:C6	86:28:4963:G:C6	3.08	0.42
3:58:14:U:C4	3:58:15:G:C6	3.08	0.42
10:L7:235:ARG:H	10:L7:235:ARG:HG2	1.65	0.42
11:aa:219:LEU:HD23	14:15:7:ILE:HD11	2.02	0.42
23:29:9:THR:HA	23:29:12:GLN:HG2	2.01	0.42
55:v:603:TYR:HB2	55:v:706:ASP:HB3	2.02	0.42
64:AS:127:VAL:HG13	64:AS:176:VAL:HG11	2.02	0.42
69:ZZ:90:LYS:HE2	69:ZZ:90:LYS:HB3	1.90	0.42
70:18:1143:A:H2'	70:18:1144:A:C8	2.54	0.42
70:18:1408:U:H2'	70:18:1409:A:H8	1.85	0.42
83:S5:40:ALA:HB1	83:S5:45:TYR:CG	2.55	0.42
84:A:85:ILE:H	84:A:85:ILE:HG13	1.47	0.42
86:28:246:G:H2'	86:28:247:G:H8	1.85	0.42
86:28:275:C:H4'	86:28:276:C:OP1	2.20	0.42
86:28:739:G:C5	86:28:926:G:C6	3.07	0.42
86:28:1202:C:H2'	86:28:1203:G:H8	1.85	0.42
86:28:1545:G:H2'	86:28:1546:C:C6	2.55	0.42
86:28:1962:A:N3	86:28:1962:A:H2'	2.35	0.42
86:28:2870:A:H2'	86:28:2871:A:C8	2.55	0.42
86:28:3877:A:O2'	86:28:4401:G:H1'	2.20	0.42
1:17:69:ARG:HD2	86:28:4981:G:H1'	2.02	0.42
1:17:154:GLU:HA	1:17:155:GLN:CB	2.48	0.42
7:L4:165:LYS:HE2	7:L4:165:LYS:HB2	1.92	0.42
44:S9:144:ILE:HG12	70:18:824:C:C2	2.54	0.42
45:S4:246:LEU:HD12	45:S4:250:GLU:HG3	2.02	0.42
55:v:641:TRP:CH2	55:v:701:ARG:HD2	2.55	0.42
55:v:746:LEU:HB2	55:v:815:ASP:HB2	2.01	0.42
70:18:582:U:H2'	70:18:583:A:H8	1.85	0.42
70:18:599:A:H2'	70:18:606:G:N2	2.34	0.42
70:18:634:A:H2'	70:18:635:G:H8	1.83	0.42
70:18:1092:G:H2'	70:18:1093:A:H8	1.85	0.42
70:18:1515:G:H2'	70:18:1516:G:C8	2.55	0.42
70:18:1703:C:H2'	70:18:1704:C:O4'	2.19	0.42
70:18:1812:U:H2'	70:18:1813:A:H8	1.85	0.42
86:28:99:A:C2	86:28:100:C:C2	3.08	0.42
86:28:245:C:H4'	86:28:246:G:O5'	2.20	0.42
86:28:1315:C:H2'	86:28:1316:G:C8	2.54	0.42
86:28:1989:G:H2'	86:28:1990:A:H8	1.85	0.42
86:28:2078:C:C2	86:28:2079:G:C8	3.08	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:S4:47:PHE:O	45:S4:51:ARG:HB2	2.20	0.41
70:18:17:C:H2'	70:18:18:C:C6	2.54	0.41
70:18:493:A:C8	70:18:574:A:C8	3.08	0.41
70:18:652:U:H2'	70:18:653:A:H8	1.84	0.41
70:18:1558:C:H2'	70:18:1559:C:C6	2.55	0.41
70:18:1646:C:H2'	70:18:1678:A:N1	2.35	0.41
76:CC:65:ARG:HD2	76:CC:65:ARG:HA	1.82	0.41
86:28:317:A:C2	86:28:4361:U:H1'	2.54	0.41
86:28:979:C:H2'	86:28:980:U:H6	1.85	0.41
86:28:2497:C:H2'	86:28:2498:C:H6	1.84	0.41
13:14:86:TRP:CE2	13:14:92:ALA:HB2	2.55	0.41
18:22:84:LYS:HA	18:22:87:THR:HG22	2.02	0.41
26:ee:104:MET:HG2	26:ee:106:TYR:CE2	2.56	0.41
46:S6:23:LYS:O	46:S6:26:THR:HG22	2.20	0.41
55:v:103:ILE:HG21	55:v:118:ALA:HB1	2.02	0.41
55:v:207:PRO:HG3	55:v:212:VAL:HG21	2.02	0.41
70:18:439:A:C6	70:18:455:A:N6	2.88	0.41
70:18:1528:G:H2'	70:18:1529:C:C6	2.55	0.41
70:18:1539:U:H2'	70:18:1540:G:C8	2.54	0.41
70:18:1628:C:H2'	70:18:1629:C:C6	2.55	0.41
86:28:494:C:H2'	86:28:495:C:H6	1.85	0.41
86:28:980:U:H3	86:28:1275:G:H1	1.68	0.41
86:28:1355:G:H2'	86:28:1356:U:C6	2.55	0.41
86:28:2478:C:H2'	86:28:2479:G:C8	2.54	0.41
86:28:2491:C:H2'	86:28:2492:C:C6	2.54	0.41
86:28:3783:A:N7	86:28:3792:G:C8	2.88	0.41
86:28:4537:C:C2	86:28:4538:G:C8	3.08	0.41
86:28:4628:U:H2'	86:28:4629:U:C6	2.55	0.41
86:28:4902:C:H2'	86:28:4903:G:H8	1.85	0.41
86:28:4917:C:C2	86:28:4918:C:C5	3.08	0.41
1:17:131:ARG:HG3	1:17:137:ASN:ND2	2.35	0.41
3:58:4:C:H2'	3:58:5:U:C6	2.56	0.41
9:L6:48:ARG:HB2	9:L6:64:MET:HE1	2.01	0.41
9:L6:153:LEU:HD13	9:L6:197:VAL:HG11	2.01	0.41
19:cc:65:ALA:HB2	28:35:69:LEU:HD11	2.01	0.41
19:cc:114:LYS:HG3	19:cc:119:ILE:O	2.20	0.41
35:42:61:LYS:HB3	35:42:61:LYS:HE2	1.62	0.41
45:S4:163:ASP:HB3	45:S4:166:THR:HG22	2.02	0.41
53:23:27:ASN:O	53:23:102:ALA:HA	2.20	0.41
70:18:77:A:H2'	70:18:78:C:C6	2.55	0.41
70:18:378:U:C4	70:18:379:C:C4	3.09	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:18:643:A:OP1	70:18:644:G:H5'	2.20	0.41
70:18:928:G:H1	70:18:1013:U:H3	1.68	0.41
70:18:1123:C:C4	70:18:1124:C:C5	3.08	0.41
70:18:1349:G:H2'	70:18:1350:U:C6	2.55	0.41
70:18:1396:A:O2'	70:18:1398:G:H8	2.02	0.41
70:18:1614:A:H2'	70:18:1615:U:C6	2.55	0.41
70:18:1722:G:C6	70:18:1813:A:N6	2.89	0.41
70:18:1787:G:H2'	70:18:1788:A:C8	2.54	0.41
70:18:1794:C:H2'	70:18:1795:G:H8	1.84	0.41
70:18:1856:C:C2	70:18:1857:G:C8	3.09	0.41
76:CC:62:PHE:HA	76:CC:66:HIS:O	2.20	0.41
86:28:52:G:H4'	86:28:1529:G:H4'	2.02	0.41
86:28:909:G:C2	86:28:910:G:C8	3.08	0.41
86:28:983:C:H2'	86:28:984:C:C6	2.55	0.41
86:28:1537:A:H2'	86:28:1538:U:C6	2.55	0.41
86:28:2299:G:C2	86:28:2336:G:C5	3.07	0.41
86:28:2864:A:H2'	86:28:2865:U:C6	2.56	0.41
86:28:3721:U:H2'	86:28:3722:G:C8	2.53	0.41
86:28:3772:U:H2'	86:28:3773:U:C6	2.55	0.41
86:28:4355:G:C2	86:28:4356:G:C8	3.09	0.41
86:28:4435:U:H2'	86:28:4436:U:C6	2.55	0.41
86:28:4565:C:H2'	86:28:4566:U:H6	1.85	0.41
86:28:4566:U:H2'	86:28:4567:G:O4'	2.20	0.41
4:5:113:G:H2'	4:5:114:U:C6	2.56	0.41
8:L5:67:ALA:HA	8:L5:72:ASP:HB3	2.03	0.41
24:31:70:LYS:HE2	86:28:2389:A:H5'	2.01	0.41
39:EB:28:ALA:HB2	39:EB:112:VAL:HG12	2.01	0.41
44:S9:130:ILE:HD13	44:S9:145:PRO:HA	2.02	0.41
48:RR:100:VAL:HG12	48:RR:125:VAL:HG22	2.02	0.41
50:LL:47:LYS:HA	50:LL:47:LYS:HD3	1.78	0.41
62:PP:64:GLU:HG2	65:VV:2:PRO:HA	2.02	0.41
70:18:96:C:H2'	70:18:97:U:H6	1.85	0.41
70:18:673:G:H2'	70:18:674:C:C6	2.56	0.41
70:18:940:U:H2'	70:18:941:C:C6	2.55	0.41
70:18:1121:G:C2	70:18:1122:A:C8	3.08	0.41
70:18:1139:C:H3'	70:18:1140:G:H8	1.85	0.41
70:18:1627:C:H2'	70:18:1628:C:H6	1.85	0.41
70:18:1802:C:C2	70:18:1803:U:C5	3.08	0.41
70:18:1812:U:H2'	70:18:1813:A:C8	2.55	0.41
83:S5:95:HIS:O	83:S5:99:ILE:HG13	2.20	0.41
86:28:434:A:H2'	86:28:435:A:O4'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
86:28:499:G:H2'	86:28:500:G:C8	2.56	0.41
86:28:652:G:H2'	86:28:653:C:H6	1.84	0.41
86:28:677:G:H2'	86:28:678:C:C6	2.55	0.41
86:28:734:G:H1	86:28:929:A:N6	2.19	0.41
86:28:1824:G:H2'	86:28:1825:A:H8	1.86	0.41
86:28:2780:C:C2	86:28:2781:G:C8	3.08	0.41
86:28:4235:G:C6	86:28:4236:G:N7	2.89	0.41
86:28:4593:C:H2'	86:28:4594:U:H6	1.84	0.41
86:28:5001:U:H2'	86:28:5002:U:O4'	2.20	0.41
4:5:90:A:N3	41:10:56:GLU:HG2	2.35	0.41
12:13:128:PRO:HD2	12:13:144:LEU:HD21	2.02	0.41
26:ee:78:HIS:HB2	26:ee:85:ARG:HG3	2.02	0.41
69:ZZ:138:ARG:HG3	69:ZZ:149:CYS:HA	2.02	0.41
70:18:1192:U:H2'	70:18:1193:U:C6	2.56	0.41
70:18:1280:G:H2'	70:18:1281:G:H8	1.85	0.41
70:18:1401:A:H2'	70:18:1402:A:C8	2.55	0.41
70:18:1476:A:H4'	70:18:1477:U:OP2	2.21	0.41
70:18:1782:G:H2'	70:18:1784:G:H8	1.85	0.41
86:28:60:A:C4	86:28:61:A:C8	3.07	0.41
86:28:282:C:C2	86:28:283:G:C8	3.08	0.41
86:28:302:C:H2'	86:28:303:C:C6	2.56	0.41
86:28:325:U:H2'	86:28:326:C:H6	1.84	0.41
86:28:1779:U:H2'	86:28:1780:A:C8	2.56	0.41
86:28:2688:G:H2'	86:28:2689:C:H6	1.86	0.41
86:28:2688:G:C4	86:28:2689:C:C5	3.09	0.41
86:28:2732:G:H2'	86:28:2733:C:H6	1.86	0.41
86:28:2861:C:H2'	86:28:2862:G:O4'	2.20	0.41
3:58:26:C:H2'	3:58:27:U:C6	2.55	0.41
15:bb:37:ARG:HD2	15:bb:108:ILE:HD11	2.01	0.41
17:21:54:HIS:CD2	86:28:4301:U:H4'	2.55	0.41
41:10:140:THR:HG23	41:10:141:LYS:O	2.20	0.41
42:L9:104:VAL:HG13	42:L9:113:GLU:HB2	2.03	0.41
43:S7:115:LYS:HD2	70:18:868:G:C8	2.55	0.41
47:SS:89:HIS:O	47:SS:93:ARG:HG3	2.20	0.41
53:23:89:ARG:HB2	53:23:95:PHE:CZ	2.55	0.41
55:v:464:VAL:HA	55:v:465:PRO:HD3	1.96	0.41
58:S8:10:LYS:HB2	70:18:371:A:OP2	2.20	0.41
62:PP:20:SER:HB3	62:PP:59:ILE:HD11	2.03	0.41
63:JJ:27:ASP:HB3	63:JJ:30:THR:OG1	2.21	0.41
64:AS:136:ARG:NH1	70:18:941:C:H5''	2.36	0.41
70:18:465:A:H4'	70:18:466:G:O5'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:18:509:G:H2'	70:18:510:G:C8	2.55	0.41
70:18:1739:C:H2'	70:18:1740:C:C6	2.55	0.41
71:MM:127:GLY:HA2	71:MM:130:ASP:OD2	2.20	0.41
75:EE:36:ARG:HG3	75:EE:40:LYS:HE3	2.02	0.41
84:A:100:LYS:HG3	84:A:101:THR:HG23	2.02	0.41
85:t:16:ARG:HD3	85:t:57:ARG:HB2	2.02	0.41
86:28:654:C:C2	86:28:655:C:C5	3.08	0.41
86:28:987:C:H2'	86:28:988:C:H6	1.86	0.41
86:28:1315:C:C2	86:28:1316:G:C8	3.09	0.41
86:28:2635:U:H2'	86:28:2636:U:C6	2.54	0.41
3:58:92:U:H2'	3:58:93:C:O4'	2.20	0.41
12:13:105:LYS:HE2	12:13:105:LYS:HB3	1.86	0.41
15:bb:80:PHE:O	15:bb:83:THR:HG22	2.21	0.41
24:31:26:THR:HG23	86:28:4996:C:H4'	2.01	0.41
33:40:86:LYS:HB3	33:40:88:LYS:HG2	2.03	0.41
40:Q:91:ARG:H	40:Q:91:ARG:HG3	1.61	0.41
48:RR:51:VAL:HG22	48:RR:70:VAL:HG11	2.01	0.41
50:LL:89:ASP:O	84:A:18:ARG:HG3	2.20	0.41
54:19:18:GLY:O	54:19:22:VAL:HG23	2.21	0.41
63:JJ:102:THR:O	63:JJ:105:MET:HG3	2.20	0.41
70:18:223:C:H2'	70:18:224:A:C8	2.54	0.41
70:18:563:G:C2	70:18:564:A:C8	3.09	0.41
77:II:116:ASP:HB3	77:II:119:LEU:HD23	2.02	0.41
86:28:517:C:H2'	86:28:518:G:H8	1.85	0.41
86:28:949:G:H2'	86:28:950:G:C8	2.52	0.41
86:28:1912:G:C6	86:28:2057:A:C2	3.09	0.41
86:28:1958:A:O2'	86:28:1959:U:H5''	2.20	0.41
86:28:2397:G:C8	86:28:2399:G:C8	3.08	0.41
86:28:2683:C:H2'	86:28:2684:C:C6	2.56	0.41
86:28:2844:A:HO2'	86:28:4631:G:H4'	1.84	0.41
86:28:4069:U:H2'	86:28:4070:U:C6	2.56	0.41
86:28:4164:C:H2'	86:28:4165:C:H6	1.85	0.41
86:28:4263:C:H2'	86:28:4264:G:O4'	2.20	0.41
86:28:4683:U:H2'	86:28:4684:A:C8	2.56	0.41
3:58:67:U:C2	3:58:68:G:C8	3.09	0.41
5:L8:201:GLY:HA2	5:L8:204:MET:SD	2.61	0.41
6:L3:314:ILE:HG12	6:L3:330:PHE:CE1	2.56	0.41
7:L4:159:GLU:HA	7:L4:217:ILE:HB	2.03	0.41
14:15:159:ARG:HB3	14:15:164:LEU:HB2	2.02	0.41
16:20:93:MET:HE1	16:20:117:HIS:CE1	2.55	0.41
28:35:89:ARG:O	28:35:93:ARG:HD2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:EB:12:ILE:HD11	39:EB:221:HIS:HA	2.03	0.41
40:Q:89:ASP:OD1	40:Q:91:ARG:HG3	2.21	0.41
58:S8:83:TYR:HB3	58:S8:101:ILE:HB	2.03	0.41
70:18:669:A:H2'	70:18:670:A:C4	2.56	0.41
70:18:974:C:H2'	70:18:975:G:C8	2.51	0.41
70:18:1195:A:H2'	70:18:1196:A:H8	1.86	0.41
70:18:1490:G:C2	70:18:1491:G:C5	3.08	0.41
71:MM:65:TYR:HB2	71:MM:123:LEU:HD22	2.02	0.41
86:28:496:G:C6	86:28:659:G:C6	3.09	0.41
86:28:1617:G:H1'	86:28:2513:A:H61	1.82	0.41
86:28:1920:C:H3'	86:28:1921:C:H5''	2.02	0.41
86:28:2682:G:H2'	86:28:2683:C:C6	2.56	0.41
86:28:2776:G:H2'	86:28:2777:G:C8	2.56	0.41
86:28:3664:G:H2'	86:28:3665:G:C8	2.46	0.41
86:28:4164:C:H2'	86:28:4165:C:C6	2.55	0.41
86:28:4260:U:C2	86:28:4261:C:C5	3.08	0.41
86:28:4407:G:H1'	86:28:4438:U:C2	2.54	0.41
3:58:65:A:C4	3:58:66:A:C8	3.09	0.41
3:58:145:C:H2'	3:58:146:U:C6	2.56	0.41
3:58:154:G:H2'	3:58:155:C:C6	2.56	0.41
4:5:22:A:H2'	4:5:23:A:C8	2.56	0.41
5:L8:200:ARG:H	5:L8:200:ARG:HG2	1.69	0.41
6:L3:122:TRP:CE2	6:L3:127:LYS:HE3	2.55	0.41
6:L3:261:ARG:HB3	86:28:4564:A:O2'	2.20	0.41
8:L5:35:ARG:HB2	86:28:4325:A:C2	2.56	0.41
9:L6:215:LEU:HD12	9:L6:215:LEU:O	2.21	0.41
12:13:55:ILE:HD13	12:13:120:TYR:CG	2.55	0.41
23:29:60:ASN:O	23:29:63:LYS:HG3	2.21	0.41
27:34:33:LEU:HD23	27:34:33:LEU:HA	1.92	0.41
32:39:16:LYS:HG3	32:39:49:LEU:HD11	2.03	0.41
43:S7:36:LEU:HD22	43:S7:75:ILE:HD11	2.02	0.41
45:S4:72:ILE:HG22	45:S4:73:ASP:OD2	2.21	0.41
52:GG:42:VAL:HG11	52:GG:81:VAL:HG11	2.03	0.41
55:v:194:GLU:H	55:v:194:GLU:HG2	1.70	0.41
59:S2:191:VAL:HG11	59:S2:236:PHE:HA	2.03	0.41
60:BB:132:GLN:HB3	60:BB:133:PRO:HD3	2.02	0.41
66:QQ:113:HIS:CD2	66:QQ:113:HIS:H	2.39	0.41
69:ZZ:89:LYS:HE3	70:18:1507:G:C8	2.56	0.41
70:18:87:U:C2	70:18:88:G:C8	3.09	0.41
70:18:94:G:C4	70:18:95:G:C8	3.09	0.41
70:18:430:C:H2'	70:18:431:G:C8	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:18:569:A:H2'	70:18:570:C:C6	2.55	0.41
70:18:1350:U:C2	70:18:1351:G:C8	3.09	0.41
70:18:1473:G:N2	70:18:1475:G:H5''	2.35	0.41
70:18:1781:A:H2'	70:18:1782:G:H8	1.83	0.41
70:18:1803:U:H2'	70:18:1804:U:C6	2.56	0.41
72:AA:129:ILE:HB	72:AA:142:VAL:CG2	2.50	0.41
86:28:648:G:C2	86:28:649:A:C8	3.09	0.41
86:28:650:C:H2'	86:28:651:C:C6	2.56	0.41
86:28:1177:U:H2'	86:28:1178:G:H8	1.86	0.41
86:28:1341:U:C2	86:28:1342:A:C8	3.09	0.41
86:28:1472:C:H2'	86:28:1473:U:H6	1.84	0.41
86:28:1519:C:H2'	86:28:1520:C:H6	1.85	0.41
86:28:1730:U:H2'	86:28:1731:C:H6	1.86	0.41
86:28:1804:A:H5''	86:28:1806:G:C8	2.55	0.41
86:28:1957:U:O2'	86:28:1958:A:H8	2.04	0.41
86:28:1979:A:O2'	86:28:1980:U:H5'	2.19	0.41
86:28:2007:G:C2	86:28:2013:A:N6	2.89	0.41
86:28:2060:G:H2'	86:28:2061:U:H6	1.86	0.41
86:28:2413:U:H2'	86:28:2414:G:C8	2.56	0.41
86:28:2477:A:C2	86:28:2478:C:C4	3.09	0.41
86:28:2514:G:C2	86:28:2515:G:C8	3.09	0.41
86:28:2635:U:C4	86:28:2636:U:C4	3.09	0.41
86:28:2859:G:H2'	86:28:2860:C:H6	1.85	0.41
86:28:2895:A:H2'	86:28:2896:G:H8	1.85	0.41
86:28:3883:U:H2'	86:28:3884:U:C6	2.55	0.41
86:28:4175:G:H2'	86:28:4176:C:H6	1.85	0.41
86:28:4356:G:N3	86:28:4357:G:C8	2.89	0.41
86:28:4596:C:C4	86:28:4597:U:C4	3.09	0.41
5:L8:142:GLU:C	5:L8:144:LYS:H	2.29	0.41
8:L5:52:ILE:HA	8:L5:147:ASP:HB3	2.03	0.41
25:32:85:LEU:HD11	25:32:115:ALA:HB2	2.02	0.41
27:34:66:ARG:HD3	86:28:2539:C:H5''	2.02	0.41
29:36:25:ARG:NH1	86:28:159:C:H5'	2.36	0.41
38:s:116:ILE:H	38:s:116:ILE:HG12	1.73	0.41
48:RR:67:ARG:HA	48:RR:67:ARG:HD3	1.90	0.41
64:AS:62:LEU:HD23	64:AS:91:VAL:HG21	2.03	0.41
69:ZZ:140:TYR:HE1	69:ZZ:145:CYS:HA	1.85	0.41
69:ZZ:143:LYS:NZ	70:18:1310:U:H4'	2.35	0.41
70:18:1533:A:H2	70:18:1536:G:N3	2.19	0.41
84:A:42:ARG:HA	84:A:45:LEU:HD23	2.03	0.41
86:28:269:G:H2'	86:28:270:U:H6	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
86:28:474:C:H2'	86:28:475:G:H8	1.85	0.41
86:28:1065:G:H2'	86:28:1066:G:C8	2.56	0.41
86:28:1305:C:H2'	86:28:1306:C:H6	1.86	0.41
86:28:1314:C:C2	86:28:1315:C:C5	3.09	0.41
86:28:1517:G:C2	86:28:1650:A:N6	2.89	0.41
86:28:1779:U:H2'	86:28:1780:A:H8	1.86	0.41
86:28:1823:G:H2'	86:28:1824:G:C8	2.56	0.41
86:28:1875:C:H2'	86:28:1876:U:C6	2.55	0.41
86:28:2627:C:H41	86:28:4649:G:H1	1.68	0.41
86:28:2686:G:H5'	86:28:2687:U:OP1	2.21	0.41
86:28:2696:A:O2'	86:28:2697:A:H8	2.04	0.41
86:28:2752:G:H2'	86:28:2753:G:C8	2.56	0.41
86:28:4060:U:C2	86:28:4061:G:N7	2.89	0.41
5:L8:158:ILE:HG23	5:L8:159:SER:O	2.21	0.40
6:L3:206:PRO:HG2	6:L3:209:GLN:HG2	2.02	0.40
7:L4:134:PRO:HA	7:L4:150:LEU:HD22	2.02	0.40
22:dd:51:GLY:HA2	40:Q:178:ARG:N	2.36	0.40
22:dd:58:MET:HG3	86:28:4364:G:O2'	2.20	0.40
38:s:128:THR:O	38:s:151:THR:HB	2.21	0.40
45:S4:151:ASP:HB3	45:S4:154:ILE:HG13	2.03	0.40
46:S6:112:VAL:HG21	70:18:166:A:H5'	2.02	0.40
52:GG:38:ASN:C	52:GG:69:SER:HB2	2.46	0.40
52:GG:72:TYR:O	52:GG:75:MET:HG3	2.20	0.40
83:S5:97:PHE:HA	83:S5:100:ILE:HG22	2.03	0.40
86:28:950:G:N3	86:28:951:G:C8	2.89	0.40
86:28:1511:U:H2'	86:28:1512:G:C8	2.56	0.40
86:28:1964:A:C5	86:28:1965:G:C8	3.10	0.40
86:28:4336:A:H5''	86:28:4337:C:H5'	2.03	0.40
86:28:4619:U:H2'	86:28:4620:U:C6	2.56	0.40
87:ES:2949:U:H2'	87:ES:2950:G:C8	2.56	0.40
9:L6:204:ILE:HD13	9:L6:264:ILE:HG22	2.04	0.40
12:13:8:MET:HE3	40:Q:168:ARG:HB3	2.04	0.40
18:22:80:LYS:HG2	18:22:110:TYR:CE2	2.55	0.40
33:40:82:VAL:HG21	86:28:1947:U:C4	2.57	0.40
42:L9:124:ARG:HD3	42:L9:164:ALA:O	2.22	0.40
43:S7:135:PHE:CD2	43:S7:136:PRO:HD3	2.55	0.40
43:S7:168:HIS:CE1	43:S7:169:LYS:HE3	2.56	0.40
46:S6:63:MET:H	46:S6:63:MET:HG2	1.61	0.40
64:AS:144:LYS:HD3	64:AS:208:HIS:HB3	2.01	0.40
64:AS:167:LYS:HA	64:AS:167:LYS:HD2	1.88	0.40
70:18:144:U:H2'	70:18:145:G:H8	1.85	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:18:340:C:C2	70:18:341:C:C5	3.09	0.40
70:18:394:G:N3	70:18:395:G:C8	2.89	0.40
70:18:479:C:C2	70:18:480:G:C8	3.09	0.40
70:18:637:U:C2	70:18:638:C:C6	3.09	0.40
70:18:856:C:H2'	70:18:857:U:C6	2.54	0.40
70:18:991:G:C6	70:18:1134:G:H4'	2.56	0.40
70:18:1282:A:H2'	70:18:1283:C:C6	2.56	0.40
84:A:58:LYS:HB3	84:A:58:LYS:HE2	1.91	0.40
86:28:64:A:C4	86:28:109:G:N7	2.89	0.40
86:28:121:A:H5'	86:28:122:U:OP2	2.21	0.40
86:28:1328:G:C6	86:28:1329:G:C6	3.09	0.40
86:28:1594:C:O2'	86:28:1597:G:H1'	2.21	0.40
86:28:1624:G:C5	86:28:1643:A:C8	3.09	0.40
86:28:1893:C:H2'	86:28:1894:C:H6	1.86	0.40
86:28:2015:U:H2'	86:28:2016:C:H6	1.87	0.40
86:28:2385:U:H2'	86:28:2386:U:H6	1.86	0.40
86:28:2634:C:C2	86:28:2635:U:C5	3.09	0.40
86:28:3787:G:H1'	86:28:3789:C:N4	2.36	0.40
86:28:4593:C:H2'	86:28:4594:U:C6	2.55	0.40
86:28:4749:C:H2'	86:28:4750:G:O4'	2.22	0.40
1:17:168:LYS:HB2	1:17:168:LYS:HE3	1.83	0.40
3:58:76:C:C2	3:58:77:A:C8	3.09	0.40
4:5:102:U:C2	4:5:103:A:C8	3.10	0.40
7:L4:283:LYS:HE2	7:L4:283:LYS:HB2	1.85	0.40
40:Q:75:ARG:HA	40:Q:78:LYS:HE3	2.03	0.40
46:S6:89:THR:HG22	70:18:91:A:H61	1.86	0.40
47:SS:115:LYS:HB3	47:SS:115:LYS:HE2	1.82	0.40
48:RR:52:LEU:HD12	48:RR:53:GLU:HG2	2.03	0.40
50:LL:40:TYR:HA	50:LL:43:VAL:HG22	2.03	0.40
60:BB:63:ARG:HD2	62:PP:37:ALA:O	2.22	0.40
70:18:146:G:O2'	70:18:147:A:H8	2.05	0.40
70:18:399:C:H3'	70:18:400:C:H5'	2.03	0.40
70:18:563:G:O2'	70:18:564:A:H8	2.04	0.40
70:18:910:G:H2'	70:18:911:C:C6	2.56	0.40
70:18:979:C:H2'	70:18:980:A:H8	1.86	0.40
70:18:1137:U:O2'	70:18:1138:C:H3'	2.20	0.40
72:AA:130:LYS:HG2	72:AA:141:THR:OG1	2.21	0.40
72:AA:154:VAL:HG12	72:AA:167:SER:HB3	2.04	0.40
76:CC:85:LEU:HA	76:CC:86:PRO:HD3	1.95	0.40
83:S5:23:TRP:HE1	83:S5:101:HIS:CG	2.39	0.40
85:t:104:ILE:O	85:t:143:VAL:HG13	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
86:28:106:A:H1'	86:28:336:A:N3	2.35	0.40
86:28:258:G:C4	86:28:259:C:C5	3.10	0.40
86:28:699:C:C2	86:28:700:G:C8	3.09	0.40
86:28:726:G:H2'	86:28:727:C:H6	1.87	0.40
86:28:910:G:H2'	86:28:911:U:C6	2.57	0.40
86:28:1217:G:C2	86:28:1218:G:N7	2.90	0.40
86:28:2633:U:H2'	86:28:2634:C:C6	2.56	0.40
86:28:2728:U:H2'	86:28:2729:C:C6	2.56	0.40
86:28:2893:U:H2'	86:28:2894:A:H8	1.86	0.40
86:28:4200:G:C4	86:28:4201:G:C8	3.09	0.40
86:28:4390:A:H2'	86:28:4391:G:O4'	2.21	0.40
10:L7:97:ILE:HD12	10:L7:97:ILE:HA	1.93	0.40
24:31:117:LEU:HD13	24:31:117:LEU:HA	1.95	0.40
40:Q:43:PHE:CD1	40:Q:133:GLY:HA3	2.57	0.40
41:10:61:SER:HA	41:10:126:VAL:HG23	2.04	0.40
47:SS:100:LYS:H	47:SS:100:LYS:HG3	1.74	0.40
57:FF:40:LEU:HD13	57:FF:53:ILE:HD11	2.04	0.40
58:S8:81:VAL:HG22	58:S8:102:VAL:HG12	2.02	0.40
64:AS:36:PRO:HB2	64:AS:38:MET:SD	2.62	0.40
70:18:1383:A:H2'	70:18:1384:C:H6	1.87	0.40
70:18:1537:A:H2'	70:18:1538:C:H6	1.86	0.40
70:18:1545:A:H4'	77:II:74:GLY:HA2	2.03	0.40
86:28:301:G:H2'	86:28:302:C:C6	2.56	0.40
86:28:979:C:H2'	86:28:980:U:C6	2.56	0.40
86:28:1278:C:H2'	86:28:1279:A:O4'	2.21	0.40
86:28:1460:C:H2'	86:28:1461:C:C6	2.56	0.40
86:28:1727:U:H2'	86:28:1728:U:H6	1.86	0.40
86:28:2542:G:H2'	86:28:2543:A:C8	2.57	0.40
86:28:3599:A:H2'	86:28:3600:G:C8	2.56	0.40
3:58:32:C:H2'	3:58:33:G:O4'	2.21	0.40
8:L5:223:PHE:HB3	8:L5:226:TYR:HB2	2.02	0.40
10:L7:219:MET:HB3	10:L7:231:ASP:OD2	2.21	0.40
11:aa:139:VAL:HG11	11:aa:238:LYS:HE3	2.02	0.40
12:13:39:ARG:CZ	86:28:1362:G:H5'	2.52	0.40
38:s:61:MET:HE3	38:s:88:PHE:CE2	2.57	0.40
44:S9:12:THR:HG23	70:18:520:A:H5''	2.04	0.40
55:v:400:LYS:HE3	55:v:400:LYS:HB2	1.98	0.40
58:S8:6:ASP:OD2	58:S8:9:HIS:HB3	2.22	0.40
70:18:551:U:H2'	70:18:552:G:H8	1.86	0.40
70:18:583:A:N3	70:18:583:A:H2'	2.37	0.40
70:18:923:G:H2'	70:18:924:G:H8	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:18:924:G:H1	70:18:1018:U:H3	1.69	0.40
70:18:1227:G:C2	70:18:1228:A:C8	3.10	0.40
70:18:1260:A:C8	70:18:1261:C:H5	2.40	0.40
70:18:1620:A:C5	70:18:1624:U:C2	3.10	0.40
83:S5:179:ASN:HB3	83:S5:187:SER:HB3	2.03	0.40
84:A:91:GLY:H	84:A:107:ILE:HG13	1.87	0.40
85:t:63:THR:HG23	85:t:70:GLN:HB2	2.03	0.40
86:28:228:C:H2'	86:28:229:G:H8	1.87	0.40
86:28:490:C:H2'	86:28:491:G:H8	1.87	0.40
86:28:693:C:H2'	86:28:694:C:H6	1.86	0.40
86:28:1173:G:H2'	86:28:1174:G:C8	2.57	0.40
86:28:1195:G:N3	86:28:1196:G:C8	2.90	0.40
86:28:1528:U:H2'	86:28:1529:G:H8	1.86	0.40
86:28:1624:G:C4	86:28:1643:A:C8	3.10	0.40
86:28:2007:G:N2	86:28:2012:A:H62	2.17	0.40
86:28:3941:G:C6	86:28:4073:A:C6	3.10	0.40
86:28:4186:A:H2'	86:28:4187:G:H8	1.85	0.40
86:28:4233:A:C5	86:28:4235:G:C8	3.10	0.40
86:28:4407:G:C6	86:28:4408:G:C5	3.10	0.40
86:28:4727:A:H2'	86:28:4728:U:O4'	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	17	181/183 (99%)	177 (98%)	3 (2%)	1 (1%)	21	32
2	DD	139/151 (92%)	136 (98%)	3 (2%)	0	100	100
5	L8	246/248 (99%)	237 (96%)	8 (3%)	1 (0%)	30	43
6	L3	392/394 (100%)	381 (97%)	11 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	L4	360/362 (99%)	351 (98%)	9 (2%)	0	100	100
8	L5	291/293 (99%)	284 (98%)	7 (2%)	0	100	100
9	L6	208/291 (72%)	201 (97%)	7 (3%)	0	100	100
10	L7	223/253 (88%)	218 (98%)	5 (2%)	0	100	100
11	aa	229/240 (95%)	223 (97%)	6 (3%)	0	100	100
12	13	208/241 (86%)	203 (98%)	3 (1%)	2 (1%)	12	20
13	14	136/138 (99%)	134 (98%)	2 (2%)	0	100	100
14	15	201/203 (99%)	196 (98%)	5 (2%)	0	100	100
15	bb	197/199 (99%)	194 (98%)	3 (2%)	0	100	100
16	20	174/176 (99%)	170 (98%)	4 (2%)	0	100	100
17	21	157/159 (99%)	152 (97%)	5 (3%)	0	100	100
18	22	97/99 (98%)	94 (97%)	3 (3%)	0	100	100
19	cc	116/118 (98%)	114 (98%)	2 (2%)	0	100	100
20	26	132/134 (98%)	132 (100%)	0	0	100	100
21	27	133/135 (98%)	127 (96%)	6 (4%)	0	100	100
22	dd	145/147 (99%)	139 (96%)	6 (4%)	0	100	100
23	29	100/245 (41%)	97 (97%)	3 (3%)	0	100	100
24	31	105/107 (98%)	101 (96%)	4 (4%)	0	100	100
25	32	126/128 (98%)	124 (98%)	2 (2%)	0	100	100
26	ee	107/109 (98%)	106 (99%)	1 (1%)	0	100	100
27	34	112/114 (98%)	112 (100%)	0	0	100	100
28	35	120/122 (98%)	117 (98%)	2 (2%)	1 (1%)	16	25
29	36	100/102 (98%)	99 (99%)	1 (1%)	0	100	100
30	37	84/86 (98%)	84 (100%)	0	0	100	100
31	38	67/69 (97%)	66 (98%)	1 (2%)	0	100	100
32	39	48/50 (96%)	48 (100%)	0	0	100	100
33	40	50/52 (96%)	50 (100%)	0	0	100	100
34	41	23/25 (92%)	23 (100%)	0	0	100	100
35	42	102/104 (98%)	100 (98%)	2 (2%)	0	100	100
36	ff	89/91 (98%)	85 (96%)	4 (4%)	0	100	100
37	gg	122/124 (98%)	120 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
38	s	194/196 (99%)	187 (96%)	7 (4%)	0	100	100
39	EB	373/375 (100%)	361 (97%)	12 (3%)	0	100	100
40	Q	185/188 (98%)	180 (97%)	5 (3%)	0	100	100
41	10	205/213 (96%)	200 (98%)	5 (2%)	0	100	100
42	L9	188/190 (99%)	181 (96%)	7 (4%)	0	100	100
43	S7	181/189 (96%)	178 (98%)	3 (2%)	0	100	100
44	S9	183/185 (99%)	181 (99%)	2 (1%)	0	100	100
45	S4	260/262 (99%)	257 (99%)	3 (1%)	0	100	100
46	S6	235/237 (99%)	235 (100%)	0	0	100	100
47	SS	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
48	RR	139/141 (99%)	134 (96%)	4 (3%)	1 (1%)	18	28
49	YY	53/55 (96%)	53 (100%)	0	0	100	100
50	LL	142/144 (99%)	137 (96%)	5 (4%)	0	100	100
51	11	168/170 (99%)	165 (98%)	3 (2%)	0	100	100
52	GG	133/135 (98%)	132 (99%)	1 (1%)	0	100	100
53	23	137/139 (99%)	135 (98%)	2 (2%)	0	100	100
54	19	178/180 (99%)	176 (99%)	2 (1%)	0	100	100
55	v	842/857 (98%)	832 (99%)	10 (1%)	0	100	100
56	S3	226/228 (99%)	223 (99%)	3 (1%)	0	100	100
57	FF	147/149 (99%)	145 (99%)	2 (1%)	0	100	100
58	S8	204/206 (99%)	200 (98%)	4 (2%)	0	100	100
59	S2	219/221 (99%)	214 (98%)	5 (2%)	0	100	100
60	BB	215/295 (73%)	210 (98%)	5 (2%)	0	100	100
61	UU	99/101 (98%)	97 (98%)	2 (2%)	0	100	100
62	PP	81/83 (98%)	78 (96%)	3 (4%)	0	100	100
63	JJ	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
64	AS	211/213 (99%)	205 (97%)	6 (3%)	0	100	100
65	VV	81/83 (98%)	80 (99%)	1 (1%)	0	100	100
66	QQ	127/129 (98%)	124 (98%)	3 (2%)	0	100	100
67	24	96/157 (61%)	95 (99%)	1 (1%)	0	100	100
68	30	112/114 (98%)	108 (96%)	3 (3%)	1 (1%)	14	22

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
69	ZZ	66/68 (97%)	64 (97%)	2 (3%)	0	100	100
71	MM	139/141 (99%)	136 (98%)	3 (2%)	0	100	100
72	AA	311/313 (99%)	297 (96%)	14 (4%)	0	100	100
73	OO	98/100 (98%)	97 (99%)	1 (1%)	0	100	100
74	RB	54/407 (13%)	52 (96%)	2 (4%)	0	100	100
75	EE	115/132 (87%)	113 (98%)	2 (2%)	0	100	100
76	CC	94/96 (98%)	90 (96%)	3 (3%)	1 (1%)	11	18
77	II	140/142 (99%)	137 (98%)	3 (2%)	0	100	100
78	TT	73/75 (97%)	72 (99%)	1 (1%)	0	100	100
79	WW	60/62 (97%)	59 (98%)	1 (2%)	0	100	100
80	XX	53/55 (96%)	52 (98%)	1 (2%)	0	100	100
81	B	146/149 (98%)	142 (97%)	3 (2%)	1 (1%)	18	28
82	u	215/217 (99%)	210 (98%)	5 (2%)	0	100	100
83	S5	181/191 (95%)	176 (97%)	4 (2%)	1 (1%)	21	32
84	A	129/131 (98%)	121 (94%)	8 (6%)	0	100	100
85	t	151/153 (99%)	139 (92%)	11 (7%)	1 (1%)	18	28
All	All	13211/14215 (93%)	12903 (98%)	297 (2%)	11 (0%)	49	64

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	17	169	LYS
12	13	47	ALA
48	RR	62	PRO
81	B	51	HIS
5	L8	14	SER
12	13	63	THR
68	30	112	THR
28	35	89	ARG
76	CC	65	ARG
83	S5	79	HIS
85	t	144	ASP

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	17	162/162 (100%)	153 (94%)	9 (6%)	19	33
2	DD	130/136 (96%)	127 (98%)	3 (2%)	44	66
5	L8	190/190 (100%)	179 (94%)	11 (6%)	18	32
6	L3	342/342 (100%)	321 (94%)	21 (6%)	17	30
7	L4	302/302 (100%)	293 (97%)	9 (3%)	36	58
8	L5	247/247 (100%)	239 (97%)	8 (3%)	34	56
9	L6	190/251 (76%)	182 (96%)	8 (4%)	26	45
10	L7	196/220 (89%)	191 (97%)	5 (3%)	40	63
11	aa	200/205 (98%)	189 (94%)	11 (6%)	19	34
12	13	175/198 (88%)	168 (96%)	7 (4%)	28	47
13	14	117/117 (100%)	113 (97%)	4 (3%)	32	54
14	15	171/171 (100%)	162 (95%)	9 (5%)	20	36
15	bb	171/171 (100%)	165 (96%)	6 (4%)	32	53
16	20	157/157 (100%)	145 (92%)	12 (8%)	12	21
17	21	139/139 (100%)	133 (96%)	6 (4%)	26	44
18	22	89/89 (100%)	84 (94%)	5 (6%)	19	33
19	cc	106/106 (100%)	101 (95%)	5 (5%)	23	41
20	26	124/124 (100%)	114 (92%)	10 (8%)	11	18
21	27	117/117 (100%)	111 (95%)	6 (5%)	21	37
22	dd	119/119 (100%)	115 (97%)	4 (3%)	32	54
23	29	84/184 (46%)	82 (98%)	2 (2%)	43	65
24	31	98/98 (100%)	89 (91%)	9 (9%)	8	14
25	32	114/114 (100%)	111 (97%)	3 (3%)	40	63
26	ee	88/88 (100%)	81 (92%)	7 (8%)	11	19
27	34	98/98 (100%)	95 (97%)	3 (3%)	35	57
28	35	109/109 (100%)	105 (96%)	4 (4%)	30	51

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
29	36	86/86 (100%)	83 (96%)	3 (4%)	32	53
30	37	73/73 (100%)	71 (97%)	2 (3%)	39	62
31	38	64/64 (100%)	59 (92%)	5 (8%)	11	20
32	39	47/47 (100%)	47 (100%)	0	100	100
33	40	48/48 (100%)	47 (98%)	1 (2%)	47	69
34	41	24/24 (100%)	24 (100%)	0	100	100
35	42	92/92 (100%)	87 (95%)	5 (5%)	20	35
36	ff	74/74 (100%)	70 (95%)	4 (5%)	20	35
37	gg	107/108 (99%)	103 (96%)	4 (4%)	30	51
38	s	164/164 (100%)	155 (94%)	9 (6%)	19	34
39	EB	321/321 (100%)	310 (97%)	11 (3%)	32	54
40	Q	164/165 (99%)	157 (96%)	7 (4%)	26	44
41	10	178/180 (99%)	167 (94%)	11 (6%)	16	29
42	L9	169/169 (100%)	153 (90%)	16 (10%)	8	13
43	S7	165/169 (98%)	160 (97%)	5 (3%)	36	58
44	S9	161/161 (100%)	157 (98%)	4 (2%)	42	64
45	S4	224/224 (100%)	220 (98%)	4 (2%)	51	73
46	S6	207/207 (100%)	205 (99%)	2 (1%)	68	84
47	SS	107/107 (100%)	103 (96%)	4 (4%)	30	51
48	RR	113/113 (100%)	111 (98%)	2 (2%)	51	73
49	YY	46/46 (100%)	46 (100%)	0	100	100
50	LL	125/125 (100%)	120 (96%)	5 (4%)	28	47
51	11	143/143 (100%)	136 (95%)	7 (5%)	22	39
52	GG	105/105 (100%)	98 (93%)	7 (7%)	15	26
53	23	106/106 (100%)	105 (99%)	1 (1%)	70	85
54	19	159/159 (100%)	153 (96%)	6 (4%)	29	49
55	v	723/728 (99%)	700 (97%)	23 (3%)	34	56
56	S3	190/190 (100%)	177 (93%)	13 (7%)	14	25
57	FF	130/130 (100%)	126 (97%)	4 (3%)	35	57
58	S8	178/178 (100%)	171 (96%)	7 (4%)	28	48
59	S2	187/187 (100%)	178 (95%)	9 (5%)	23	40

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
60	BB	180/244 (74%)	174 (97%)	6 (3%)	33	55
61	UU	88/88 (100%)	84 (96%)	4 (4%)	24	42
62	PP	67/67 (100%)	62 (92%)	5 (8%)	12	21
63	JJ	119/119 (100%)	114 (96%)	5 (4%)	26	45
64	AS	194/194 (100%)	187 (96%)	7 (4%)	31	52
65	VV	75/75 (100%)	74 (99%)	1 (1%)	61	80
66	QQ	112/112 (100%)	111 (99%)	1 (1%)	70	85
67	24	82/126 (65%)	81 (99%)	1 (1%)	63	81
68	30	97/97 (100%)	93 (96%)	4 (4%)	27	46
69	ZZ	61/61 (100%)	56 (92%)	5 (8%)	10	18
71	MM	111/111 (100%)	108 (97%)	3 (3%)	39	62
72	AA	272/272 (100%)	264 (97%)	8 (3%)	37	60
73	OO	92/92 (100%)	86 (94%)	6 (6%)	15	27
74	RB	47/326 (14%)	46 (98%)	1 (2%)	47	69
75	EE	99/108 (92%)	96 (97%)	3 (3%)	36	58
76	CC	87/87 (100%)	81 (93%)	6 (7%)	14	24
77	II	117/117 (100%)	113 (97%)	4 (3%)	32	54
78	TT	66/66 (100%)	65 (98%)	1 (2%)	57	77
79	WW	55/55 (100%)	53 (96%)	2 (4%)	31	52
80	XX	48/48 (100%)	47 (98%)	1 (2%)	47	69
81	B	123/123 (100%)	122 (99%)	1 (1%)	73	86
82	u	196/196 (100%)	194 (99%)	2 (1%)	68	84
83	S5	158/161 (98%)	154 (98%)	4 (2%)	42	64
84	A	117/117 (100%)	107 (92%)	10 (8%)	10	16
85	t	126/126 (100%)	116 (92%)	10 (8%)	11	19
All	All	11504/12135 (95%)	11035 (96%)	469 (4%)	28	46

All (469) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	17	10	ASN
1	17	69	ARG
1	17	86	LYS

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Mol	Chain	Res	Type
1	17	92	LEU
1	17	95	LEU
1	17	100	SER
1	17	114	ILE
1	17	115	GLU
1	17	150	LEU
2	DD	46	THR
2	DD	56	ILE
2	DD	101	ARG
5	L8	32	VAL
5	L8	101	VAL
5	L8	102	LEU
5	L8	109	GLU
5	L8	135	THR
5	L8	158	ILE
5	L8	159	SER
5	L8	165	VAL
5	L8	202	VAL
5	L8	208	GLU
5	L8	235	VAL
6	L3	43	LEU
6	L3	47	LEU
6	L3	56	ILE
6	L3	73	VAL
6	L3	89	ILE
6	L3	90	VAL
6	L3	101	THR
6	L3	174	ARG
6	L3	180	LEU
6	L3	201	LEU
6	L3	207	VAL
6	L3	240	LEU
6	L3	246	ARG
6	L3	248	LEU
6	L3	254	ILE
6	L3	258	HIS
6	L3	262	VAL
6	L3	314	ILE
6	L3	325	GLU
6	L3	363	ILE
6	L3	371	THR
7	L4	27	VAL

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Mol	Chain	Res	Type
7	L4	89	GLN
7	L4	154	VAL
7	L4	189	MET
7	L4	205	ARG
7	L4	232	VAL
7	L4	246	VAL
7	L4	291	ARG
7	L4	313	VAL
8	L5	37	VAL
8	L5	110	LEU
8	L5	126	THR
8	L5	191	ASN
8	L5	225	GLN
8	L5	235	MET
8	L5	259	ARG
8	L5	270	LYS
9	L6	51	VAL
9	L6	70	LEU
9	L6	178	VAL
9	L6	190	ARG
9	L6	197	VAL
9	L6	215	LEU
9	L6	217	ASP
9	L6	290	VAL
10	L7	61	ARG
10	L7	124	LEU
10	L7	151	GLU
10	L7	178	LEU
10	L7	189	LEU
11	aa	84	LEU
11	aa	159	THR
11	aa	193	VAL
11	aa	199	LEU
11	aa	207	LEU
11	aa	214	VAL
11	aa	220	VAL
11	aa	223	LEU
11	aa	226	LEU
11	aa	237	LEU
11	aa	276	ARG
12	13	59	VAL
12	13	67	HIS

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Mol	Chain	Res	Type
12	13	70	VAL
12	13	154	VAL
12	13	184	MET
12	13	186	ARG
12	13	204	GLU
13	14	38	VAL
13	14	59	ASP
13	14	62	LEU
13	14	112	VAL
14	15	50	ARG
14	15	64	ILE
14	15	87	HIS
14	15	89	VAL
14	15	151	ILE
14	15	162	ARG
14	15	174	LEU
14	15	189	ARG
14	15	198	LEU
15	bb	7	LEU
15	bb	27	VAL
15	bb	36	VAL
15	bb	52	LEU
15	bb	144	GLU
15	bb	145	VAL
16	20	7	LEU
16	20	13	VAL
16	20	23	ARG
16	20	67	VAL
16	20	84	TYR
16	20	90	THR
16	20	95	ARG
16	20	102	THR
16	20	118	ARG
16	20	126	ILE
16	20	131	GLU
16	20	159	LEU
17	21	40	VAL
17	21	76	VAL
17	21	103	ASP
17	21	111	GLU
17	21	147	GLU
17	21	157	GLU

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Mol	Chain	Res	Type
18	22	17	GLN
18	22	23	LEU
18	22	30	GLU
18	22	41	GLN
18	22	108	GLU
19	cc	62	ARG
19	cc	87	MET
19	cc	95	THR
19	cc	133	GLU
19	cc	155	ILE
20	26	1	MET
20	26	8	THR
20	26	32	SER
20	26	50	ARG
20	26	55	VAL
20	26	79	VAL
20	26	87	ARG
20	26	104	VAL
20	26	119	LEU
20	26	120	GLU
21	27	11	VAL
21	27	53	VAL
21	27	65	ARG
21	27	72	VAL
21	27	91	LEU
21	27	120	GLU
22	dd	56	VAL
22	dd	66	ASN
22	dd	76	ASP
22	dd	86	THR
23	29	27	GLN
23	29	104	LEU
24	31	19	GLU
24	31	23	ARG
24	31	26	THR
24	31	46	LEU
24	31	56	GLU
24	31	86	VAL
24	31	88	LEU
24	31	94	GLU
24	31	122	VAL
25	32	13	VAL

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Mol	Chain	Res	Type
25	32	44	ARG
25	32	87	VAL
26	ee	18	LEU
26	ee	23	GLU
26	ee	33	VAL
26	ee	84	VAL
26	ee	100	ARG
26	ee	101	ILE
26	ee	103	VAL
27	34	5	LEU
27	34	11	LEU
27	34	60	ARG
28	35	22	ASP
28	35	47	ILE
28	35	88	THR
28	35	95	LEU
29	36	3	LEU
29	36	17	VAL
29	36	29	ARG
30	37	58	THR
30	37	69	ILE
31	38	7	GLU
31	38	8	ILE
31	38	12	LEU
31	38	51	GLU
31	38	66	VAL
33	40	92	THR
35	42	43	ARG
35	42	45	GLN
35	42	61	LYS
35	42	96	ASP
35	42	102	GLN
36	ff	30	GLU
36	ff	52	VAL
36	ff	54	ILE
36	ff	86	LEU
37	gg	44	ILE
37	gg	75	THR
37	gg	78	VAL
37	gg	103	HIS
38	s	30	VAL
38	s	53	VAL

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Mol	Chain	Res	Type
38	s	54	LEU
38	s	69	LEU
38	s	97	GLU
38	s	123	VAL
38	s	147	ILE
38	s	158	VAL
38	s	174	LEU
39	EB	9	GLU
39	EB	46	LEU
39	EB	48	LEU
39	EB	57	MET
39	EB	156	LEU
39	EB	162	GLN
39	EB	226	VAL
39	EB	284	GLU
39	EB	324	LEU
39	EB	333	ILE
39	EB	353	GLU
40	Q	31	LEU
40	Q	56	THR
40	Q	78	LYS
40	Q	91	ARG
40	Q	92	VAL
40	Q	121	LEU
40	Q	158	THR
41	10	13	LYS
41	10	43	VAL
41	10	63	GLU
41	10	97	ILE
41	10	112	GLN
41	10	113	THR
41	10	126	VAL
41	10	142	LEU
41	10	148	VAL
41	10	163	GLN
41	10	212	LEU
42	L9	18	ILE
42	L9	26	ILE
42	L9	41	ILE
42	L9	48	LEU
42	L9	55	LEU
42	L9	57	VAL

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Mol	Chain	Res	Type
42	L9	66	GLU
42	L9	74	CYS
42	L9	84	VAL
42	L9	103	VAL
42	L9	107	GLU
42	L9	118	LEU
42	L9	137	SER
42	L9	161	ILE
42	L9	162	GLN
42	L9	170	LYS
43	S7	36	LEU
43	S7	46	THR
43	S7	60	ILE
43	S7	92	VAL
43	S7	134	VAL
44	S9	59	GLU
44	S9	61	LEU
44	S9	107	GLU
44	S9	119	LEU
45	S4	21	ASP
45	S4	66	MET
45	S4	221	ARG
45	S4	251	GLU
46	S6	41	LEU
46	S6	63	MET
47	SS	20	ARG
47	SS	106	GLN
47	SS	110	ARG
47	SS	120	THR
48	RR	61	GLN
48	RR	81	ILE
50	LL	9	PHE
50	LL	36	VAL
50	LL	63	GLU
50	LL	98	VAL
50	LL	108	ARG
51	11	15	LEU
51	11	33	LEU
51	11	38	LYS
51	11	49	VAL
51	11	115	LEU
51	11	148	THR

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Mol	Chain	Res	Type
51	11	168	GLN
52	GG	21	VAL
52	GG	61	LYS
52	GG	76	LEU
52	GG	88	LEU
52	GG	91	THR
52	GG	116	LEU
52	GG	119	LEU
53	23	65	VAL
54	19	15	LEU
54	19	60	ARG
54	19	74	ARG
54	19	106	LEU
54	19	111	GLU
54	19	138	LEU
55	v	9	ILE
55	v	86	LEU
55	v	119	LEU
55	v	122	THR
55	v	212	VAL
55	v	227	GLN
55	v	314	LYS
55	v	323	LEU
55	v	331	GLU
55	v	416	VAL
55	v	421	VAL
55	v	450	THR
55	v	464	VAL
55	v	475	VAL
55	v	480	VAL
55	v	554	LEU
55	v	568	ILE
55	v	570	ILE
55	v	590	LEU
55	v	629	LYS
55	v	663	THR
55	v	704	VAL
55	v	750	GLN
56	S3	23	GLU
56	S3	28	GLU
56	S3	39	VAL
56	S3	42	THR

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Mol	Chain	Res	Type
56	S3	44	THR
56	S3	48	ILE
56	S3	61	GLU
56	S3	113	LEU
56	S3	123	LEU
56	S3	162	ASP
56	S3	175	VAL
56	S3	178	ARG
56	S3	226	GLN
57	FF	46	THR
57	FF	49	GLN
57	FF	84	LEU
57	FF	119	GLU
58	S8	29	LEU
58	S8	73	THR
58	S8	130	THR
58	S8	167	GLN
58	S8	178	ARG
58	S8	190	LEU
58	S8	194	GLU
59	S2	66	LEU
59	S2	78	LEU
59	S2	91	SER
59	S2	92	GLU
59	S2	165	VAL
59	S2	212	LYS
59	S2	213	LEU
59	S2	215	MET
59	S2	260	VAL
60	BB	44	ASP
60	BB	60	LEU
60	BB	136	GLU
60	BB	142	LEU
60	BB	157	VAL
60	BB	178	LEU
61	UU	25	ASN
61	UU	46	GLU
61	UU	74	CYS
61	UU	86	ASN
62	PP	9	VAL
62	PP	32	ILE
62	PP	42	VAL

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Mol	Chain	Res	Type
62	PP	51	LYS
62	PP	65	SER
63	JJ	17	ILE
63	JJ	71	ILE
63	JJ	98	VAL
63	JJ	99	ASP
63	JJ	127	ASN
64	AS	21	VAL
64	AS	38	MET
64	AS	48	LEU
64	AS	76	ASN
64	AS	170	GLU
64	AS	212	VAL
64	AS	224	GLU
65	VV	51	GLN
66	QQ	103	VAL
67	24	114	GLU
68	30	20	LEU
68	30	57	LYS
68	30	94	LEU
68	30	108	MET
69	ZZ	97	LYS
69	ZZ	104	LYS
69	ZZ	110	GLU
69	ZZ	143	LYS
69	ZZ	147	THR
71	MM	6	VAL
71	MM	16	ARG
71	MM	131	LEU
72	AA	63	SER
72	AA	64	HIS
72	AA	76	GLN
72	AA	118	ARG
72	AA	142	VAL
72	AA	174	VAL
72	AA	198	VAL
72	AA	212	LYS
73	OO	21	ARG
73	OO	46	LYS
73	OO	60	THR
73	OO	82	MET
73	OO	84	ILE

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Mol	Chain	Res	Type
73	OO	107	GLU
74	RB	293	ASP
75	EE	22	LEU
75	EE	89	VAL
75	EE	103	VAL
76	CC	8	ARG
76	CC	21	MET
76	CC	39	ASN
76	CC	50	GLN
76	CC	53	LYS
76	CC	58	VAL
77	II	52	LEU
77	II	62	ARG
77	II	68	ILE
77	II	114	GLN
78	TT	90	GLU
79	WW	17	VAL
79	WW	33	GLU
80	XX	37	ASN
81	B	134	LEU
82	u	41	TYR
82	u	80	VAL
83	S5	41	VAL
83	S5	73	THR
83	S5	103	LEU
83	S5	169	ILE
84	A	11	THR
84	A	17	TYR
84	A	25	LEU
84	A	45	LEU
84	A	53	GLN
84	A	71	GLU
84	A	76	VAL
84	A	85	ILE
84	A	96	VAL
84	A	126	VAL
85	t	58	ILE
85	t	59	THR
85	t	61	LYS
85	t	63	THR
85	t	123	ARG
85	t	124	GLU

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Mol	Chain	Res	Type
85	t	133	LEU
85	t	146	ARG
85	t	152	ILE
85	t	153	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (145) such sidechains are listed below:

Mol	Chain	Res	Type
1	17	10	ASN
1	17	25	HIS
1	17	28	ASN
1	17	34	GLN
1	17	56	GLN
1	17	80	GLN
1	17	116	HIS
1	17	118	GLN
1	17	120	ASN
2	DD	11	GLN
5	L8	83	HIS
5	L8	100	ASN
5	L8	215	ASN
5	L8	216	HIS
6	L3	11	HIS
6	L3	138	GLN
6	L3	167	GLN
6	L3	175	GLN
6	L3	184	GLN
6	L3	204	GLN
6	L3	209	GLN
7	L4	329	ASN
7	L4	338	ASN
7	L4	346	ASN
8	L5	42	ASN
9	L6	185	ASN
10	L7	238	GLN
11	aa	119	GLN
11	aa	147	GLN
11	aa	206	GLN
11	aa	261	ASN
12	13	149	GLN
14	15	29	GLN
15	bb	42	ASN

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Mol	Chain	Res	Type
15	bb	50	ASN
15	bb	167	HIS
15	bb	180	GLN
15	bb	184	ASN
16	20	108	GLN
17	21	66	ASN
17	21	69	GLN
17	21	77	ASN
17	21	131	GLN
18	22	41	GLN
18	22	50	ASN
19	cc	57	GLN
20	26	20	ASN
20	26	127	GLN
22	dd	66	ASN
23	29	6	ASN
23	29	61	ASN
24	31	79	ASN
24	31	116	ASN
25	32	52	GLN
25	32	68	HIS
28	35	68	ASN
29	36	20	ASN
30	37	28	HIS
30	37	66	HIS
33	40	64	ASN
35	42	51	GLN
36	ff	92	GLN
37	gg	103	HIS
38	s	72	ASN
39	EB	113	HIS
39	EB	134	GLN
39	EB	171	ASN
39	EB	192	GLN
39	EB	193	HIS
39	EB	209	GLN
39	EB	299	HIS
39	EB	303	GLN
40	Q	7	HIS
40	Q	57	ASN
40	Q	93	GLN
40	Q	188	ASN

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Mol	Chain	Res	Type
41	10	73	ASN
41	10	112	GLN
42	L9	79	ASN
42	L9	98	HIS
42	L9	189	GLN
43	S7	33	ASN
43	S7	114	GLN
43	S7	163	GLN
44	S9	177	ASN
45	S4	67	GLN
45	S4	98	ASN
45	S4	112	HIS
45	S4	138	HIS
45	S4	142	HIS
45	S4	188	ASN
46	S6	225	GLN
48	RR	77	ASN
48	RR	97	ASN
48	RR	127	ASN
49	YY	95	GLN
50	LL	17	ASN
51	11	71	HIS
52	GG	113	GLN
53	23	50	ASN
54	19	141	HIS
54	19	158	GLN
55	v	101	ASN
55	v	243	GLN
55	v	357	HIS
55	v	365	GLN
55	v	468	ASN
55	v	588	ASN
55	v	599	HIS
55	v	696	ASN
56	S3	101	GLN
56	S3	226	GLN
57	FF	13	GLN
57	FF	49	GLN
58	S8	64	ASN
58	S8	167	GLN
59	S2	136	HIS
61	UU	17	HIS

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Mol	Chain	Res	Type
63	JJ	29	HIS
63	JJ	121	GLN
64	AS	101	HIS
64	AS	157	GLN
65	VV	19	HIS
71	MM	51	ASN
71	MM	63	HIS
71	MM	83	GLN
72	AA	26	GLN
72	AA	51	ASN
72	AA	76	GLN
72	AA	133	ASN
72	AA	237	ASN
72	AA	311	GLN
74	RB	206	HIS
75	EE	19	GLN
77	II	11	GLN
77	II	24	HIS
77	II	35	ASN
77	II	48	GLN
78	TT	64	ASN
81	B	78	ASN
81	B	87	ASN
82	u	71	GLN
82	u	73	HIS
82	u	143	ASN
83	S5	148	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	58	149/156 (95%)	24 (16%)	1 (0%)
4	5	119/120 (99%)	8 (6%)	0
70	18	1652/1698 (97%)	335 (20%)	16 (0%)
86	28	3473/4807 (72%)	634 (18%)	46 (1%)
87	ES	34/5070 (0%)	7 (20%)	1 (2%)
All	All	5427/11851 (45%)	1008 (18%)	64 (1%)

All (1008) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
3	58	2	G
3	58	23	C
3	58	34	U
3	58	35	C
3	58	39	G
3	58	52	A
3	58	59	A
3	58	62	A
3	58	63	U
3	58	75	G
3	58	87	G
3	58	94	G
3	58	103	A
3	58	105	C
3	58	110	U
3	58	111	U
3	58	114	G
3	58	122	G
3	58	123	U
3	58	125	C
3	58	126	C
3	58	127	U
3	58	151	G
3	58	153	C
4	5	53	U
4	5	54	A
4	5	64	G
4	5	97	G
4	5	100	A
4	5	110	G
4	5	111	C
4	5	120	U
70	18	2	A
70	18	3	C
70	18	4	C
70	18	25	A
70	18	26	U
70	18	33	G
70	18	41	G
70	18	42	A
70	18	44	U
70	18	45	A
70	18	46	A

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Mol	Chain	Res	Type
70	18	56	G
70	18	58	C
70	18	62	G
70	18	64	A
70	18	67	C
70	18	68	A
70	18	71	G
70	18	72	C
70	18	74	G
70	18	77	A
70	18	79	A
70	18	83	A
70	18	103	A
70	18	110	U
70	18	111	A
70	18	113	G
70	18	115	U
70	18	124	U
70	18	126	G
70	18	127	C
70	18	130	G
70	18	143	U
70	18	146	G
70	18	147	A
70	18	155	G
70	18	158	A
70	18	161	U
70	18	162	C
70	18	167	G
70	18	168	C
70	18	170	A
70	18	180	G
70	18	182	C
70	18	183	G
70	18	184	G
70	18	191	A
70	18	192	C
70	18	206	G
70	18	224	A
70	18	292	A
70	18	294	U
70	18	306	C

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Mol	Chain	Res	Type
70	18	307	G
70	18	308	G
70	18	309	G
70	18	312	G
70	18	314	U
70	18	318	A
70	18	319	C
70	18	320	G
70	18	335	G
70	18	339	A
70	18	340	C
70	18	350	C
70	18	351	G
70	18	360	A
70	18	362	C
70	18	364	A
70	18	368	U
70	18	369	C
70	18	370	G
70	18	383	G
70	18	385	G
70	18	386	C
70	18	398	A
70	18	399	C
70	18	400	C
70	18	408	A
70	18	409	C
70	18	417	C
70	18	418	A
70	18	435	A
70	18	436	G
70	18	438	G
70	18	448	A
70	18	450	C
70	18	464	A
70	18	465	A
70	18	466	G
70	18	472	C
70	18	473	A
70	18	474	G
70	18	482	G
70	18	485	A

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Mol	Chain	Res	Type
70	18	487	U
70	18	492	C
70	18	496	C
70	18	516	A
70	18	532	C
70	18	533	A
70	18	536	A
70	18	547	G
70	18	548	C
70	18	550	C
70	18	551	U
70	18	554	A
70	18	555	A
70	18	556	U
70	18	559	G
70	18	560	A
70	18	563	G
70	18	564	A
70	18	568	C
70	18	576	A
70	18	583	A
70	18	587	A
70	18	588	G
70	18	590	A
70	18	591	U
70	18	604	A
70	18	606	G
70	18	607	U
70	18	608	C
70	18	614	C
70	18	617	G
70	18	643	A
70	18	644	G
70	18	655	A
70	18	660	C
70	18	668	A
70	18	669	A
70	18	670	A
70	18	671	A
70	18	672	A
70	18	673	G
70	18	684	G

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Mol	Chain	Res	Type
70	18	688	U
70	18	689	U
70	18	745	C
70	18	798	G
70	18	799	U
70	18	810	A
70	18	811	A
70	18	821	G
70	18	822	U
70	18	827	A
70	18	830	A
70	18	833	C
70	18	834	C
70	18	844	U
70	18	847	A
70	18	852	G
70	18	853	C
70	18	870	A
70	18	871	U
70	18	872	A
70	18	873	G
70	18	874	G
70	18	876	C
70	18	878	G
70	18	879	C
70	18	887	U
70	18	888	U
70	18	890	U
70	18	894	G
70	18	898	U
70	18	901	G
70	18	913	A
70	18	914	U
70	18	917	U
70	18	920	A
70	18	930	C
70	18	933	G
70	18	934	G
70	18	955	A
70	18	956	G
70	18	971	G
70	18	990	A

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Mol	Chain	Res	Type
70	18	992	A
70	18	999	G
70	18	1002	U
70	18	1017	U
70	18	1023	A
70	18	1041	G
70	18	1045	U
70	18	1059	G
70	18	1060	A
70	18	1062	A
70	18	1083	A
70	18	1085	C
70	18	1087	A
70	18	1097	G
70	18	1098	C
70	18	1115	U
70	18	1116	C
70	18	1117	C
70	18	1121	G
70	18	1126	G
70	18	1131	G
70	18	1133	A
70	18	1138	C
70	18	1139	C
70	18	1149	A
70	18	1150	A
70	18	1153	C
70	18	1154	U
70	18	1155	U
70	18	1195	A
70	18	1207	G
70	18	1215	C
70	18	1216	C
70	18	1224	G
70	18	1229	G
70	18	1242	U
70	18	1251	A
70	18	1253	A
70	18	1256	G
70	18	1257	G
70	18	1259	A
70	18	1269	G

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Mol	Chain	Res	Type
70	18	1274	G
70	18	1275	G
70	18	1282	A
70	18	1284	A
70	18	1285	G
70	18	1286	G
70	18	1293	A
70	18	1294	G
70	18	1299	A
70	18	1301	A
70	18	1302	G
70	18	1303	C
70	18	1307	U
70	18	1308	U
70	18	1309	C
70	18	1316	C
70	18	1341	C
70	18	1342	U
70	18	1371	U
70	18	1372	U
70	18	1376	A
70	18	1378	A
70	18	1395	C
70	18	1396	A
70	18	1397	U
70	18	1398	G
70	18	1402	A
70	18	1409	A
70	18	1428	G
70	18	1429	G
70	18	1439	A
70	18	1442	U
70	18	1447	G
70	18	1454	A
70	18	1462	U
70	18	1463	U
70	18	1466	G
70	18	1475	G
70	18	1476	A
70	18	1477	U
70	18	1489	A
70	18	1490	G

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Mol	Chain	Res	Type
70	18	1494	U
70	18	1495	G
70	18	1497	G
70	18	1498	A
70	18	1507	G
70	18	1510	G
70	18	1521	C
70	18	1522	A
70	18	1533	A
70	18	1536	G
70	18	1544	C
70	18	1548	G
70	18	1551	U
70	18	1552	G
70	18	1553	C
70	18	1556	A
70	18	1557	C
70	18	1570	G
70	18	1575	G
70	18	1579	A
70	18	1580	A
70	18	1584	G
70	18	1585	U
70	18	1586	U
70	18	1587	G
70	18	1588	A
70	18	1598	G
70	18	1601	A
70	18	1602	U
70	18	1603	G
70	18	1604	G
70	18	1606	G
70	18	1613	G
70	18	1621	U
70	18	1623	A
70	18	1637	A
70	18	1638	G
70	18	1646	C
70	18	1648	G
70	18	1665	G
70	18	1680	G
70	18	1683	C

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Mol	Chain	Res	Type
70	18	1688	C
70	18	1689	C
70	18	1690	U
70	18	1695	A
70	18	1699	A
70	18	1721	U
70	18	1722	G
70	18	1726	G
70	18	1744	G
70	18	1748	G
70	18	1753	C
70	18	1756	C
70	18	1779	G
70	18	1783	C
70	18	1785	C
70	18	1809	A
70	18	1825	A
70	18	1829	G
70	18	1831	A
70	18	1836	G
70	18	1838	U
70	18	1849	G
70	18	1851	A
70	18	1861	G
70	18	1862	G
70	18	1863	A
70	18	1865	C
70	18	1866	A
70	18	1867	U
70	18	1869	A
86	28	8	U
86	28	12	A
86	28	13	U
86	28	25	A
86	28	39	A
86	28	42	A
86	28	49	U
86	28	56	A
86	28	58	G
86	28	59	A
86	28	64	A
86	28	65	A

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Mol	Chain	Res	Type
86	28	66	A
86	28	71	C
86	28	72	C
86	28	73	A
86	28	74	G
86	28	91	G
86	28	108	A
86	28	109	G
86	28	110	C
86	28	118	C
86	28	119	G
86	28	126	C
86	28	134	G
86	28	135	G
86	28	136	C
86	28	137	G
86	28	159	C
86	28	170	C
86	28	171	U
86	28	172	C
86	28	180	C
86	28	200	U
86	28	201	C
86	28	209	U
86	28	216	C
86	28	218	A
86	28	219	G
86	28	220	C
86	28	224	U
86	28	233	U
86	28	234	G
86	28	246	G
86	28	256	G
86	28	262	G
86	28	265	C
86	28	266	C
86	28	276	C
86	28	280	G
86	28	297	U
86	28	306	A
86	28	309	C
86	28	315	G

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Mol	Chain	Res	Type
86	28	316	U
86	28	334	A
86	28	340	C
86	28	387	G
86	28	407	A
86	28	410	A
86	28	412	G
86	28	413	G
86	28	414	C
86	28	431	G
86	28	432	U
86	28	449	C
86	28	452	A
86	28	453	G
86	28	454	U
86	28	463	A
86	28	464	G
86	28	467	U
86	28	468	U
86	28	469	C
86	28	481	G
86	28	481(A)	C
86	28	482	G
86	28	483	G
86	28	485	C
86	28	486	C
86	28	492	U
86	28	493	G
86	28	496	G
86	28	497	G
86	28	498	C
86	28	499	G
86	28	505	G
86	28	506	C
86	28	510	U
86	28	517	C
86	28	658	C
86	28	662	C
86	28	666	G
86	28	669	C
86	28	685	C
86	28	686	A

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Mol	Chain	Res	Type
86	28	687	U
86	28	696	C
86	28	697	G
86	28	704	C
86	28	705	G
86	28	730	G
86	28	731	G
86	28	738	C
86	28	739	G
86	28	747	A
86	28	749	G
86	28	750	U
86	28	758	G
86	28	759	G
86	28	905	C
86	28	914	U
86	28	915	A
86	28	917	A
86	28	918	G
86	28	923	C
86	28	925	C
86	28	926	G
86	28	929	A
86	28	931	C
86	28	932	A
86	28	933	G
86	28	934	C
86	28	935	A
86	28	935(A)	G
86	28	936	C
86	28	939	G
86	28	941	C
86	28	945	U
86	28	956	A
86	28	959	G
86	28	960	A
86	28	961	G
86	28	964	A
86	28	965	G
86	28	966	A
86	28	967	C
86	28	969	C

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Mol	Chain	Res	Type
86	28	972	C
86	28	979	C
86	28	983	C
86	28	1068	G
86	28	1070	G
86	28	1072	C
86	28	1073	G
86	28	1079	C
86	28	1082	C
86	28	1179	U
86	28	1180	C
86	28	1187	G
86	28	1193	C
86	28	1195	G
86	28	1210	C
86	28	1211	G
86	28	1212	G
86	28	1214	C
86	28	1215	C
86	28	1234	G
86	28	1235	G
86	28	1236	C
86	28	1237	C
86	28	1238	A
86	28	1239	C
86	28	1244	G
86	28	1277	G
86	28	1284	G
86	28	1285	U
86	28	1287	G
86	28	1292	C
86	28	1293	G
86	28	1295	U
86	28	1296	G
86	28	1301	C
86	28	1303	A
86	28	1304	C
86	28	1313	C
86	28	1326	A
86	28	1330	A
86	28	1337	A
86	28	1354	A

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Mol	Chain	Res	Type
86	28	1358	G
86	28	1359	G
86	28	1371	A
86	28	1377	G
86	28	1378	C
86	28	1379	C
86	28	1380	G
86	28	1381	U
86	28	1387	A
86	28	1394	G
86	28	1397	A
86	28	1398	A
86	28	1416	G
86	28	1419	G
86	28	1420	A
86	28	1433	A
86	28	1436	C
86	28	1445	U
86	28	1446	C
86	28	1456	C
86	28	1457	G
86	28	1477	C
86	28	1482	G
86	28	1483	C
86	28	1484	G
86	28	1497	A
86	28	1498	G
86	28	1502	G
86	28	1523	A
86	28	1534	A
86	28	1547	A
86	28	1563	A
86	28	1566	C
86	28	1574	G
86	28	1578	U
86	28	1591	U
86	28	1596	U
86	28	1612	G
86	28	1613	A
86	28	1624	G
86	28	1625	G
86	28	1631	A

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Mol	Chain	Res	Type
86	28	1633	G
86	28	1638	A
86	28	1640	C
86	28	1641	G
86	28	1654	G
86	28	1661	C
86	28	1676	C
86	28	1677	U
86	28	1734	G
86	28	1742	A
86	28	1750	G
86	28	1755	C
86	28	1756	U
86	28	1759	G
86	28	1760	G
86	28	1761	G
86	28	1773	U
86	28	1774	C
86	28	1776	A
86	28	1781	U
86	28	1787	A
86	28	1804	A
86	28	1805	A
86	28	1808	C
86	28	1818	G
86	28	1819	G
86	28	1821	G
86	28	1828	C
86	28	1834	U
86	28	1836	G
86	28	1837	A
86	28	1842	G
86	28	1855	G
86	28	1869	G
86	28	1882	U
86	28	1897	A
86	28	1910	G
86	28	1918	U
86	28	1920	C
86	28	1921	C
86	28	1922	G
86	28	1930	U

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Mol	Chain	Res	Type
86	28	1931	C
86	28	1935	C
86	28	1940	G
86	28	1948	G
86	28	1955	G
86	28	1957	U
86	28	1958	A
86	28	1961	G
86	28	1962	A
86	28	1974	U
86	28	1976	G
86	28	1978	C
86	28	1980	U
86	28	1983	A
86	28	1984	A
86	28	1985	G
86	28	1987	C
86	28	1991	A
86	28	1992	U
86	28	1997	U
86	28	2001	G
86	28	2002	A
86	28	2003	G
86	28	2004	U
86	28	2011	C
86	28	2025	A
86	28	2046	G
86	28	2047	A
86	28	2048	U
86	28	2052	G
86	28	2055	G
86	28	2056	G
86	28	2062	C
86	28	2064	G
86	28	2069	A
86	28	2084	U
86	28	2089	G
86	28	2090	U
86	28	2092	G
86	28	2093	G
86	28	2094	C
86	28	2095	A

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Mol	Chain	Res	Type
86	28	2097	A
86	28	2100	G
86	28	2102	G
86	28	2104	A
86	28	2105	A
86	28	2107	A
86	28	2108	G
86	28	2110	G
86	28	2267	U
86	28	2268	A
86	28	2275	G
86	28	2279	A
86	28	2289	C
86	28	2300	A
86	28	2301	G
86	28	2306	G
86	28	2313	A
86	28	2314	G
86	28	2333	G
86	28	2348	G
86	28	2351	C
86	28	2360	A
86	28	2395	A
86	28	2398	U
86	28	2421	G
86	28	2422	C
86	28	2425	U
86	28	2433	G
86	28	2441	C
86	28	2453	A
86	28	2469	C
86	28	2475	G
86	28	2488	C
86	28	2489	C
86	28	2490	U
86	28	2491	C
86	28	2503	G
86	28	2505	C
86	28	2506	G
86	28	2513	A
86	28	2529	A
86	28	2530	U

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Mol	Chain	Res	Type
86	28	2537	A
86	28	2544	G
86	28	2545	U
86	28	2546	G
86	28	2547	G
86	28	2554	U
86	28	2564	G
86	28	2575	U
86	28	2583	C
86	28	2586	G
86	28	2587	A
86	28	2589	C
86	28	2627	C
86	28	2638	G
86	28	2653	C
86	28	2661	U
86	28	2662	G
86	28	2669	C
86	28	2686	G
86	28	2687	U
86	28	2694	G
86	28	2695	A
86	28	2696	A
86	28	2702	C
86	28	2703	G
86	28	2707	U
86	28	2708	U
86	28	2710	C
86	28	2711	G
86	28	2712	G
86	28	2714	G
86	28	2725	A
86	28	2726	G
86	28	2740	U
86	28	2743	A
86	28	2744	A
86	28	2753	G
86	28	2754	G
86	28	2760	G
86	28	2761	U
86	28	2763	U
86	28	2764	A

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Mol	Chain	Res	Type
86	28	2769	U
86	28	2787	A
86	28	2788	U
86	28	2790	U
86	28	2798	A
86	28	2807	A
86	28	2808	G
86	28	2826	U
86	28	2827	G
86	28	2842	G
86	28	2855	G
86	28	2856	C
86	28	2875	C
86	28	3604	A
86	28	3605	C
86	28	3625	G
86	28	3626	G
86	28	3635	A
86	28	3648	A
86	28	3662	A
86	28	3663	A
86	28	3673	C
86	28	3674	G
86	28	3698	G
86	28	3711	A
86	28	3714	G
86	28	3748	A
86	28	3753	G
86	28	3759	A
86	28	3760	A
86	28	3761	C
86	28	3762	U
86	28	3764	U
86	28	3765	G
86	28	3772	U
86	28	3773	U
86	28	3776	G
86	28	3777	G
86	28	3783	A
86	28	3784	A
86	28	3786	U
86	28	3811	G

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Mol	Chain	Res	Type
86	28	3814	U
86	28	3817	A
86	28	3819	G
86	28	3822	U
86	28	3824	A
86	28	3838	U
86	28	3839	G
86	28	3840	U
86	28	3876	A
86	28	3877	A
86	28	3878	C
86	28	3879	G
86	28	3889	G
86	28	3892	U
86	28	3897	G
86	28	3901	A
86	28	3905	A
86	28	3906	A
86	28	3907	G
86	28	3908	A
86	28	3915	U
86	28	3916	G
86	28	3917	A
86	28	3918	G
86	28	3938	G
86	28	3948	C
86	28	3949	A
86	28	4064	C
86	28	4069	U
86	28	4076	G
86	28	4084	G
86	28	4085	A
86	28	4086	G
86	28	4088	C
86	28	4095	G
86	28	4097	G
86	28	4116	C
86	28	4118	U
86	28	4119	C
86	28	4120	U
86	28	4121	G
86	28	4122	G

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Mol	Chain	Res	Type
86	28	4125	C
86	28	4127	A
86	28	4137	C
86	28	4158	C
86	28	4162	C
86	28	4163	U
86	28	4165	C
86	28	4166	G
86	28	4170	A
86	28	4183	G
86	28	4184	G
86	28	4191	G
86	28	4203	A
86	28	4228	G
86	28	4229	U
86	28	4233	A
86	28	4238	G
86	28	4251	A
86	28	4253	A
86	28	4254	G
86	28	4266	G
86	28	4268	A
86	28	4271	A
86	28	4273	A
86	28	4281	A
86	28	4291	G
86	28	4297	G
86	28	4304	A
86	28	4305	G
86	28	4306	U
86	28	4314	C
86	28	4317	A
86	28	4318	C
86	28	4319	C
86	28	4329	G
86	28	4330	G
86	28	4332	C
86	28	4336	A
86	28	4349	C
86	28	4354	U
86	28	4355	G
86	28	4373	G

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Mol	Chain	Res	Type
86	28	4376	A
86	28	4377	G
86	28	4378	A
86	28	4380	A
86	28	4387	C
86	28	4391	G
86	28	4394	A
86	28	4395	U
86	28	4401	G
86	28	4419	U
86	28	4421	C
86	28	4422	A
86	28	4444	C
86	28	4448	G
86	28	4449	A
86	28	4453	C
86	28	4464	A
86	28	4466	C
86	28	4471	U
86	28	4475	G
86	28	4500	U
86	28	4512	U
86	28	4513	A
86	28	4519	C
86	28	4520	G
86	28	4524	G
86	28	4525	C
86	28	4531	U
86	28	4536	C
86	28	4548	A
86	28	4549	G
86	28	4560	C
86	28	4567	G
86	28	4573	G
86	28	4574	U
86	28	4575	G
86	28	4577	U
86	28	4584	A
86	28	4586	G
86	28	4587	G
86	28	4590	A
86	28	4627	U

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Mol	Chain	Res	Type
86	28	4635	A
86	28	4636	U
86	28	4637	G
86	28	4639	G
86	28	4656	A
86	28	4670	C
86	28	4672	A
86	28	4677	U
86	28	4700	A
86	28	4709	U
86	28	4720	C
86	28	4729	A
86	28	4751	G
86	28	4754	G
86	28	4756	C
86	28	4757	C
86	28	4759	C
86	28	4761	G
86	28	4765	G
86	28	4771	C
86	28	4868	G
86	28	4870	G
86	28	4871	C
86	28	4873	G
86	28	4875	G
86	28	4882	U
86	28	4883	C
86	28	4885	U
86	28	4892	A
86	28	4894	A
86	28	4895	C
86	28	4899	G
86	28	4903	G
86	28	4904	G
86	28	4906	C
86	28	4910	A
86	28	4912	G
86	28	4913	G
86	28	4914	G
86	28	4915	G
86	28	4919	G
86	28	4921	C

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Mol	Chain	Res	Type
86	28	4923	U
86	28	4924	C
86	28	4925	U
86	28	4926	C
86	28	4927	G
86	28	4928	C
86	28	4931	G
86	28	4937	C
86	28	4943	A
86	28	4944	C
86	28	4948	C
86	28	4949	G
86	28	4950	U
86	28	4951	G
86	28	4957	C
86	28	4958	C
86	28	4960	G
86	28	4965	U
86	28	4966	A
86	28	4976	U
86	28	4988	U
86	28	4990	C
86	28	4993	G
86	28	5006	U
86	28	5007	A
86	28	5017	G
86	28	5029	C
86	28	5041	G
86	28	5047	C
86	28	5050	C
86	28	5054	C
86	28	5058	A
86	28	5061	A
86	28	5062	G
87	ES	2941	G
87	ES	2942	C
87	ES	2943	C
87	ES	2958	C
87	ES	3237	G
87	ES	3238	C
87	ES	3247	A

All (64) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	58	124	U
70	18	110	U
70	18	291	G
70	18	434	G
70	18	465	A
70	18	532	C
70	18	553	U
70	18	642	U
70	18	870	A
70	18	1137	U
70	18	1394	G
70	18	1395	C
70	18	1396	A
70	18	1489	A
70	18	1520	G
70	18	1637	A
70	18	1664	A
86	28	12	A
86	28	48	G
86	28	125	C
86	28	261	G
86	28	275	C
86	28	406	C
86	28	480	C
86	28	485	C
86	28	492	U
86	28	504	G
86	28	696	C
86	28	930	G
86	28	1072	C
86	28	1211	G
86	28	1238	A
86	28	1291	G
86	28	1329	G
86	28	1370	G
86	28	1445	U
86	28	1455	G
86	28	1804	A
86	28	1979	A
86	28	2046	G
86	28	2068	C
86	28	2089	G
86	28	2266	C

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Mol	Chain	Res	Type
86	28	2502	A
86	28	2546	G
86	28	2587	A
86	28	2661	U
86	28	2695	A
86	28	3625	G
86	28	3697	U
86	28	3760	A
86	28	3876	A
86	28	3888	G
86	28	4119	C
86	28	4232	U
86	28	4448	G
86	28	4699	U
86	28	4719	G
86	28	4884	G
86	28	4898	G
86	28	4925	U
86	28	4936	G
86	28	4947	U
87	ES	3236	G

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

2 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
55	DDE	v	715	55	18,20,21	1.04	1 (5%)	17,28,30	1.36	2 (11%)
81	5CT	B	50	81	13,14,15	0.63	0	8,15,17	0.60	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
55	DDE	v	715	55	-	6/20/21/23	0/1/1/1
81	5CT	B	50	81	-	7/13/14/16	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
55	v	715	DDE	CD2-CG	2.37	1.41	1.36

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
55	v	715	DDE	CA-CB-CG	-3.24	105.78	113.77
55	v	715	DDE	CB-CG-CD2	-3.13	122.94	129.33

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
55	v	715	DDE	C-CA-CB-CG
55	v	715	DDE	NAD-CBI-CBW-NCB
81	B	50	5CT	NZ-C1-C2-C3
81	B	50	5CT	NZ-C1-C2-O1
81	B	50	5CT	O1-C2-C3-C4
81	B	50	5CT	C-CA-CB-CG
81	B	50	5CT	CE-CD-CG-CB
55	v	715	DDE	CA-CB-CG-CD2
55	v	715	DDE	CA-CB-CG-ND1
81	B	50	5CT	C2-C1-NZ-CE
55	v	715	DDE	N-CA-CB-CG
81	B	50	5CT	N-CA-CB-CG
55	v	715	DDE	OAG-CBI-CBW-CAU

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
55	v	715	DDE	1	0
81	B	50	5CT	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 5 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
89	GDP	v	900	-	29,30,30	3.43	13 (44%)	45,47,47	1.87	13 (28%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
89	GDP	v	900	-	-	3/16/32/32	0/3/3/3

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
89	v	900	GDP	O6-C6	9.49	1.41	1.23
89	v	900	GDP	C2'-C3'	-7.93	1.31	1.53
89	v	900	GDP	O4'-C4'	-6.52	1.30	1.45
89	v	900	GDP	O4'-C1'	5.46	1.54	1.42
89	v	900	GDP	C2-N2	4.57	1.44	1.34
89	v	900	GDP	C1'-N9	-4.32	1.35	1.47
89	v	900	GDP	PA-O3A	4.26	1.64	1.59
89	v	900	GDP	C3'-C4'	3.61	1.62	1.53
89	v	900	GDP	C6-N1	-3.37	1.32	1.38
89	v	900	GDP	O2'-C2'	2.88	1.50	1.43
89	v	900	GDP	C8-N9	-2.13	1.32	1.37
89	v	900	GDP	C2-N1	-2.10	1.32	1.37
89	v	900	GDP	C5-N7	-2.01	1.35	1.39

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
89	v	900	GDP	C5-C4-N3	-5.87	119.05	128.39
89	v	900	GDP	C2-N3-C4	4.68	120.36	112.30
89	v	900	GDP	N9-C4-N3	4.14	134.22	125.95
89	v	900	GDP	C2'-C3'-C4'	3.13	108.65	102.61
89	v	900	GDP	C8-N7-C5	2.81	109.26	104.26
89	v	900	GDP	C4-C5-N7	-2.69	106.41	110.67
89	v	900	GDP	N9-C8-N7	-2.67	108.45	113.40
89	v	900	GDP	C6-C5-N7	2.41	134.68	130.29
89	v	900	GDP	C3'-C2'-C1'	2.39	105.98	101.46
89	v	900	GDP	O6-C6-C5	-2.32	120.40	126.53
89	v	900	GDP	C2-N1-C6	-2.14	121.23	125.11
89	v	900	GDP	C5-C6-N1	2.12	118.64	113.25
89	v	900	GDP	O4'-C4'-C3'	2.07	109.27	105.15

There are no chirality outliers.

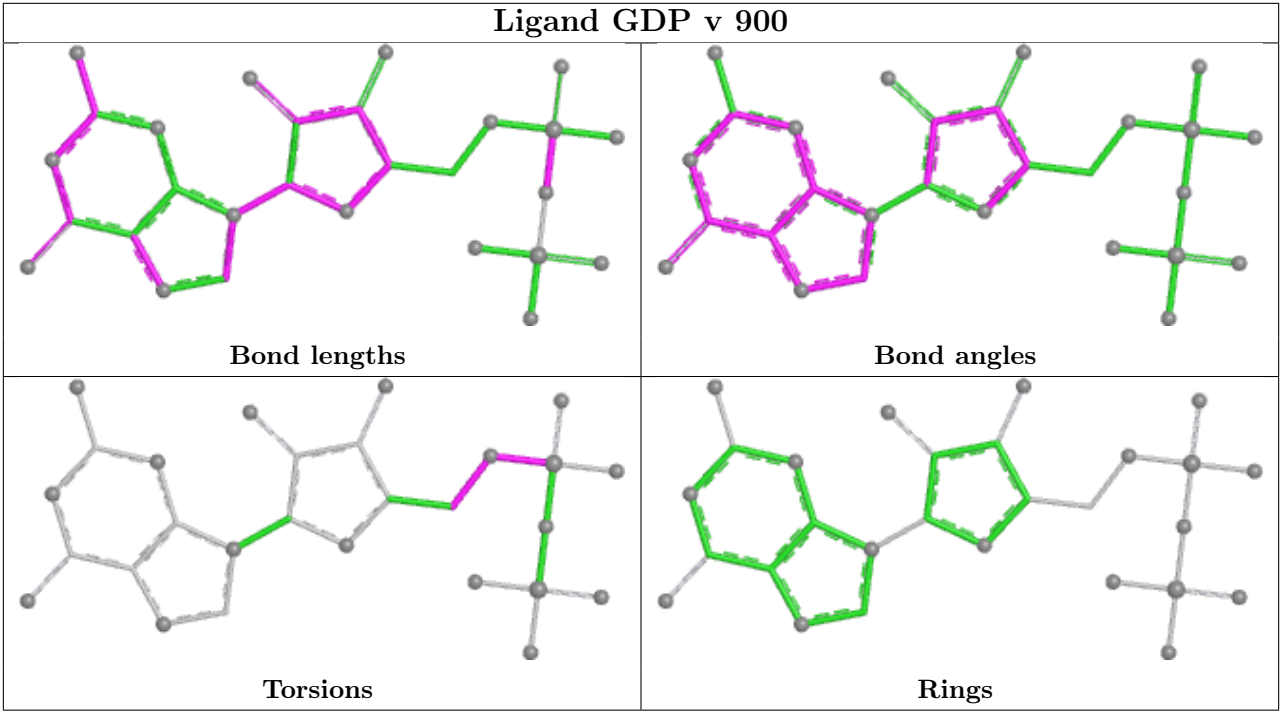
All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
89	v	900	GDP	C5'-O5'-PA-O3A
89	v	900	GDP	C5'-O5'-PA-O2A
89	v	900	GDP	C4'-C5'-O5'-PA

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
70	18	5
74	RB	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	RB	225:LEU	C	282:THR	N	56.11
1	18	834:C	O3'	841:G	P	17.67
1	18	1417:C	O3'	1423:C	P	17.04
1	18	745:C	O3'	749:U	P	7.75
1	18	225:G	O3'	287:U	P	4.54
1	18	1432:U	O3'	1438:A	P	3.22

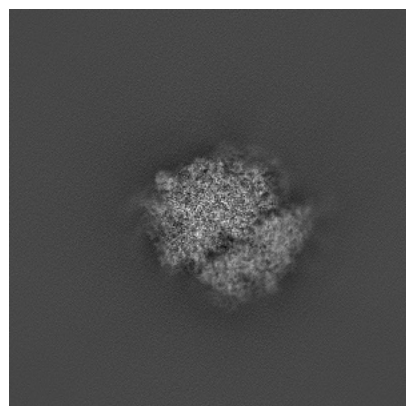
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-75724. These allow visual inspection of the internal detail of the map and identification of artifacts.

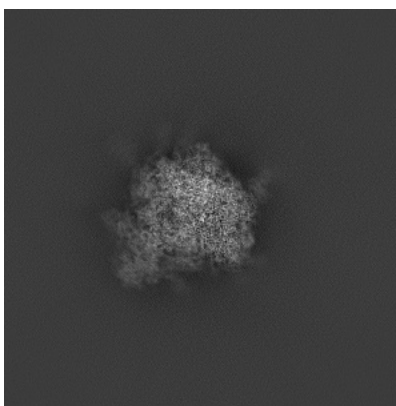
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

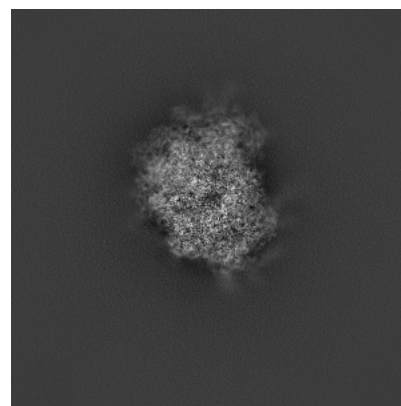
6.1.1 Primary map



X

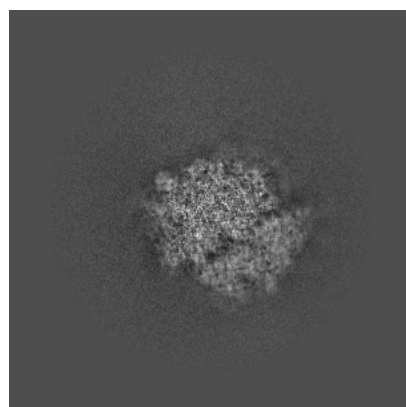


Y

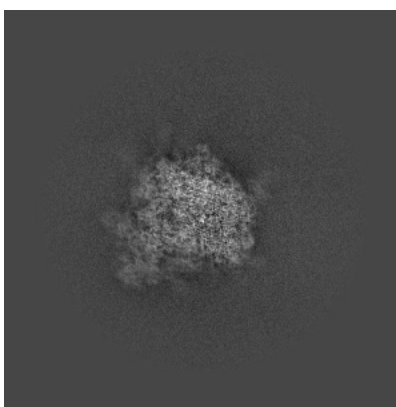


Z

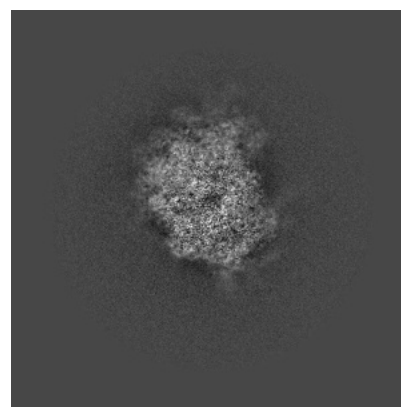
6.1.2 Raw map



X



Y

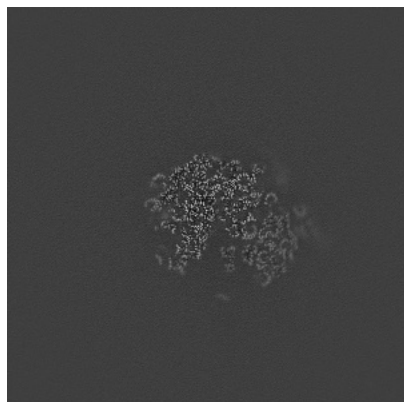


Z

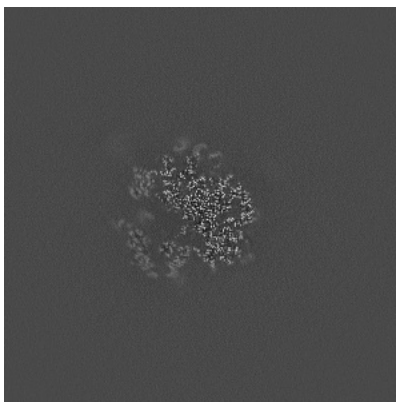
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

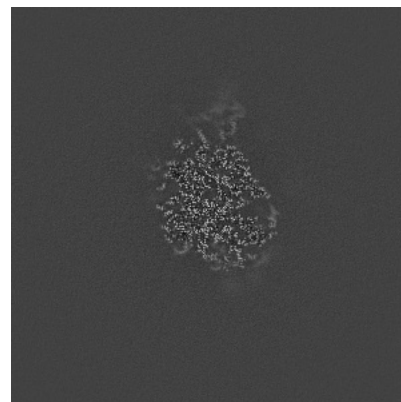
6.2.1 Primary map



X Index: 400

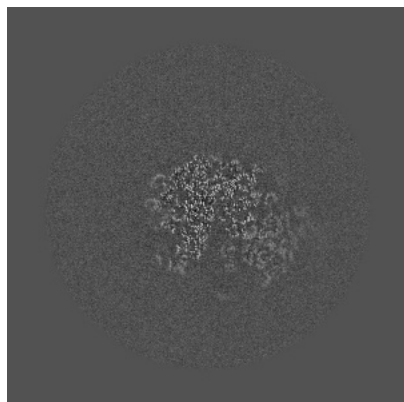


Y Index: 400

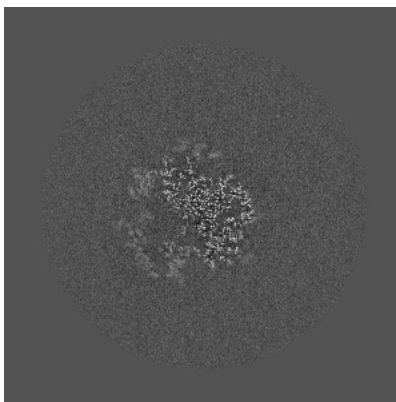


Z Index: 400

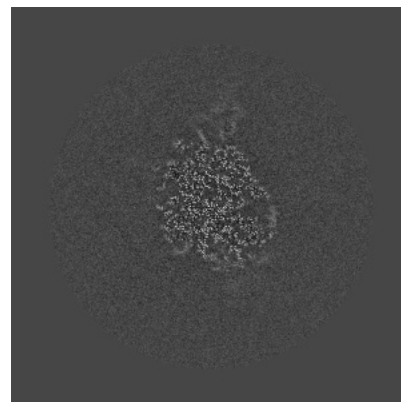
6.2.2 Raw map



X Index: 400



Y Index: 400

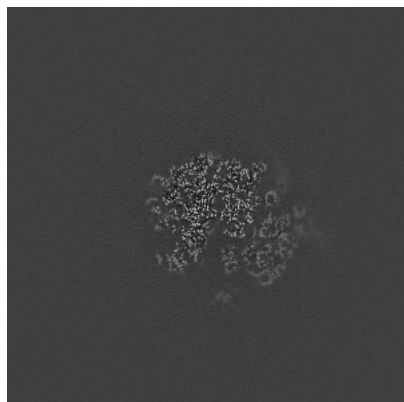


Z Index: 400

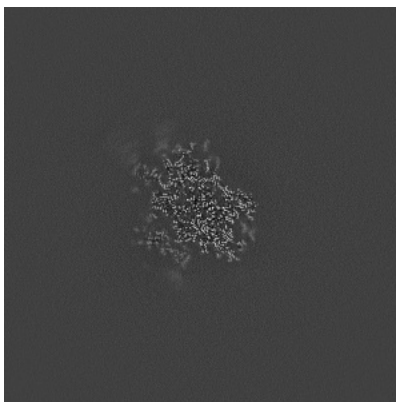
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

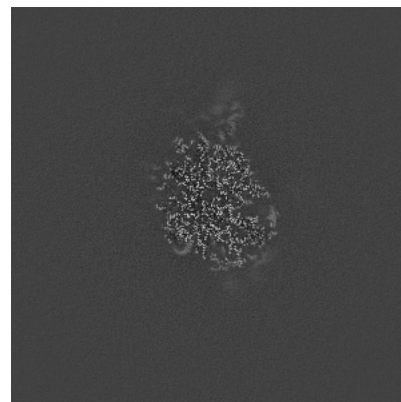
6.3.1 Primary map



X Index: 396

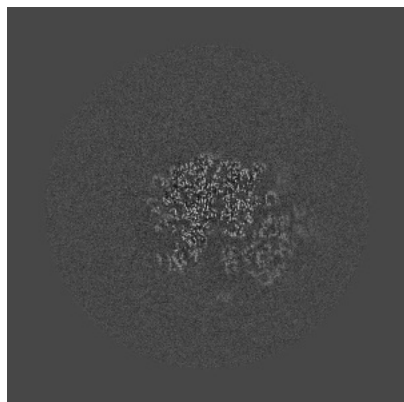


Y Index: 380

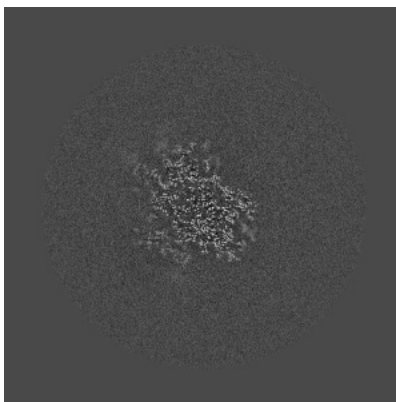


Z Index: 402

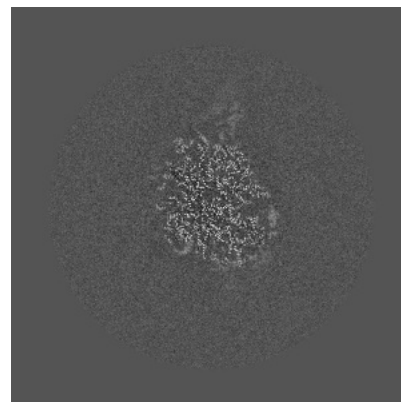
6.3.2 Raw map



X Index: 396



Y Index: 380

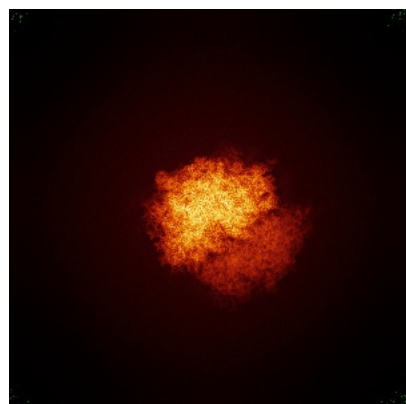


Z Index: 402

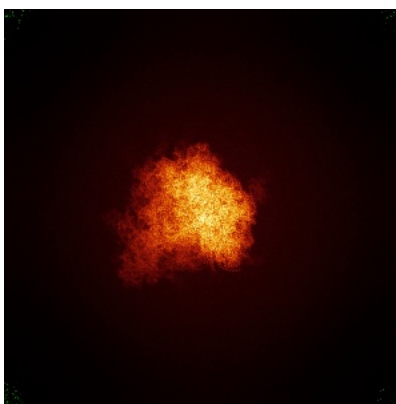
The images above show the largest variance slices of the map in three orthogonal directions.

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

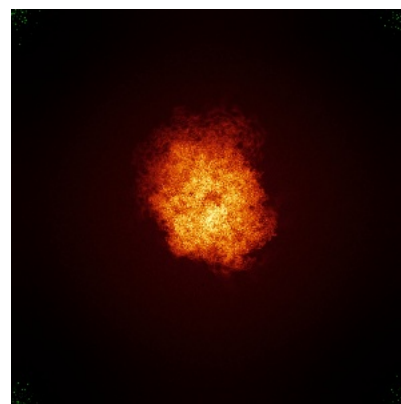
6.4.1 Primary map



X

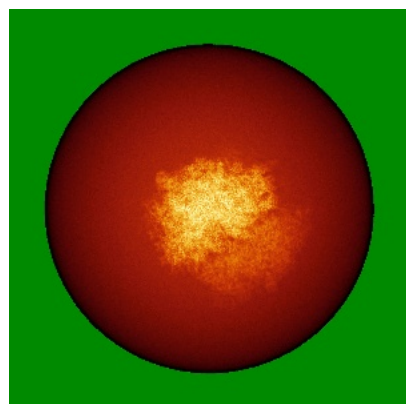


Y

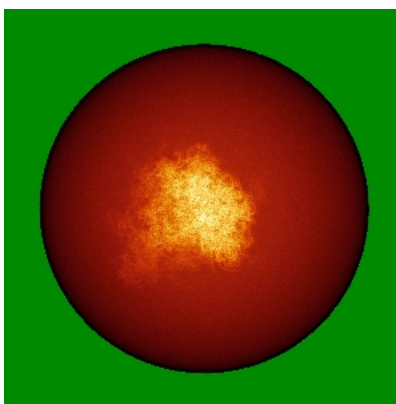


Z

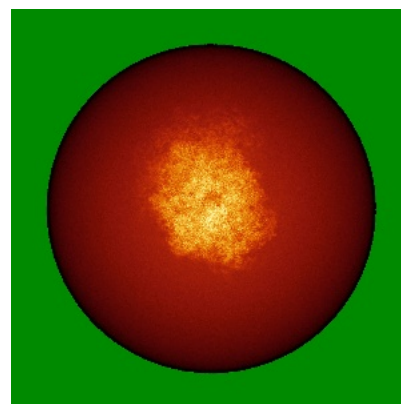
6.4.2 Raw map



X



Y

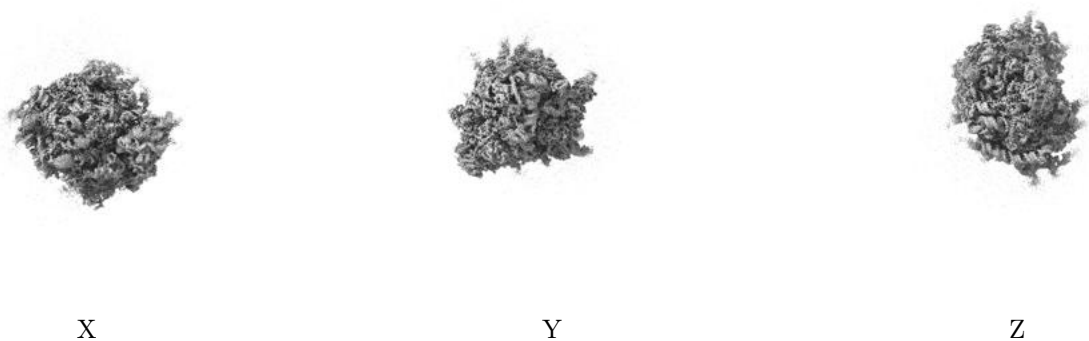


Z

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.

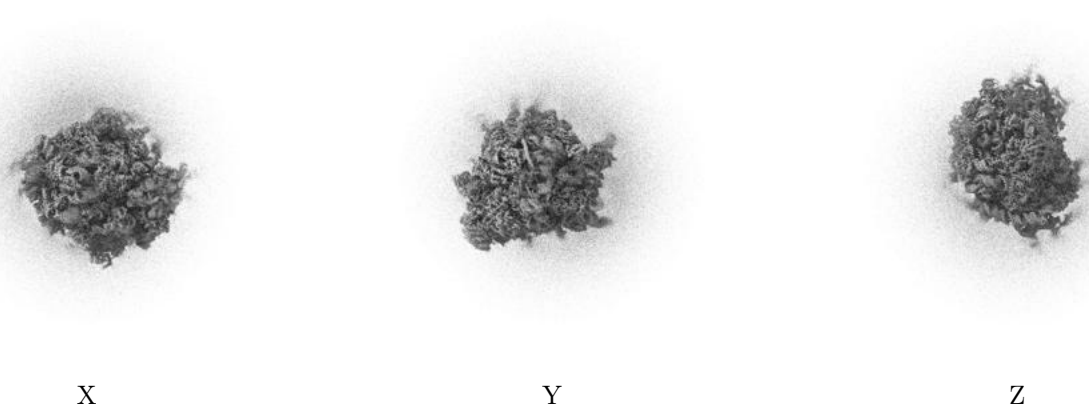
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 2.4. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

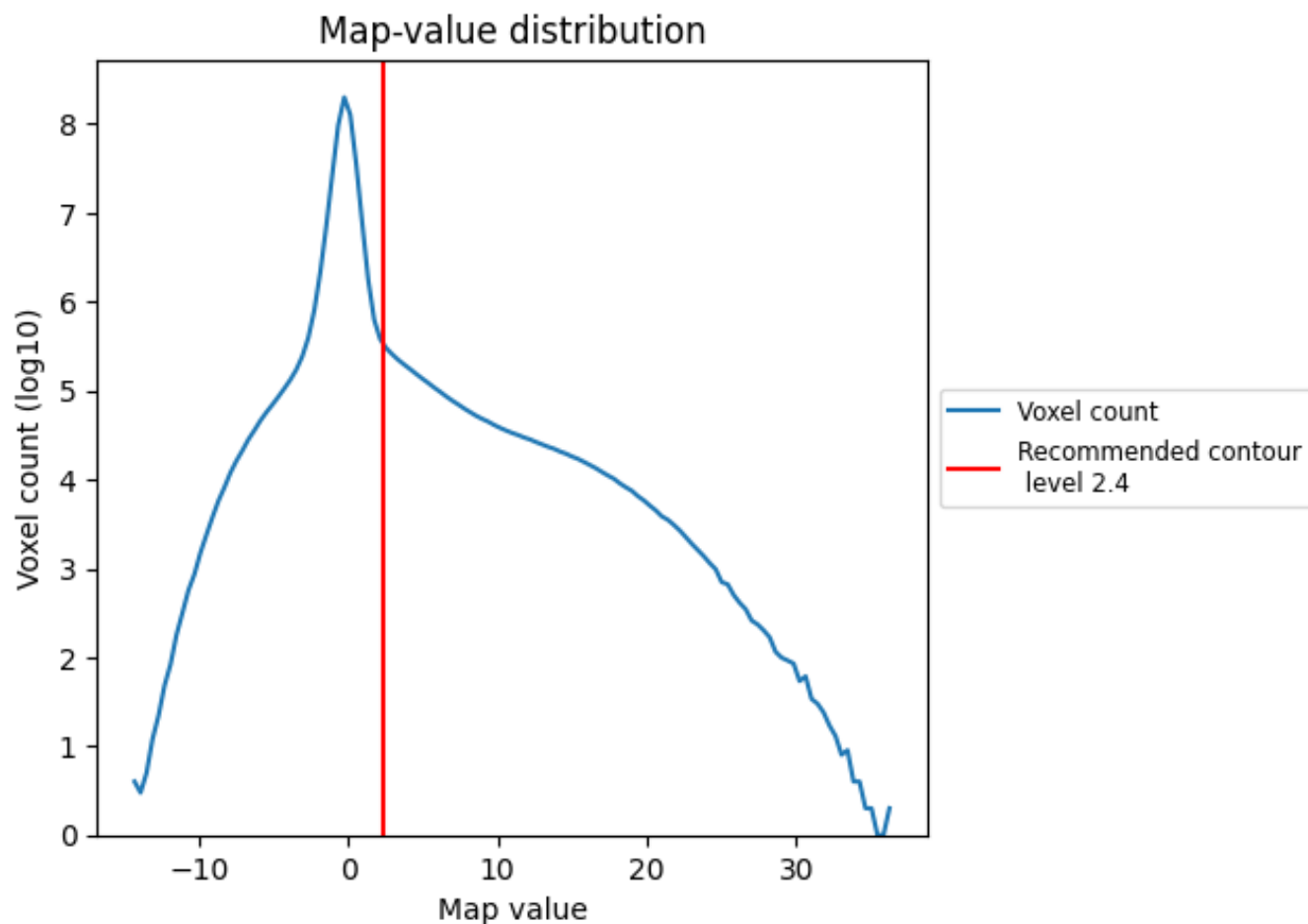
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

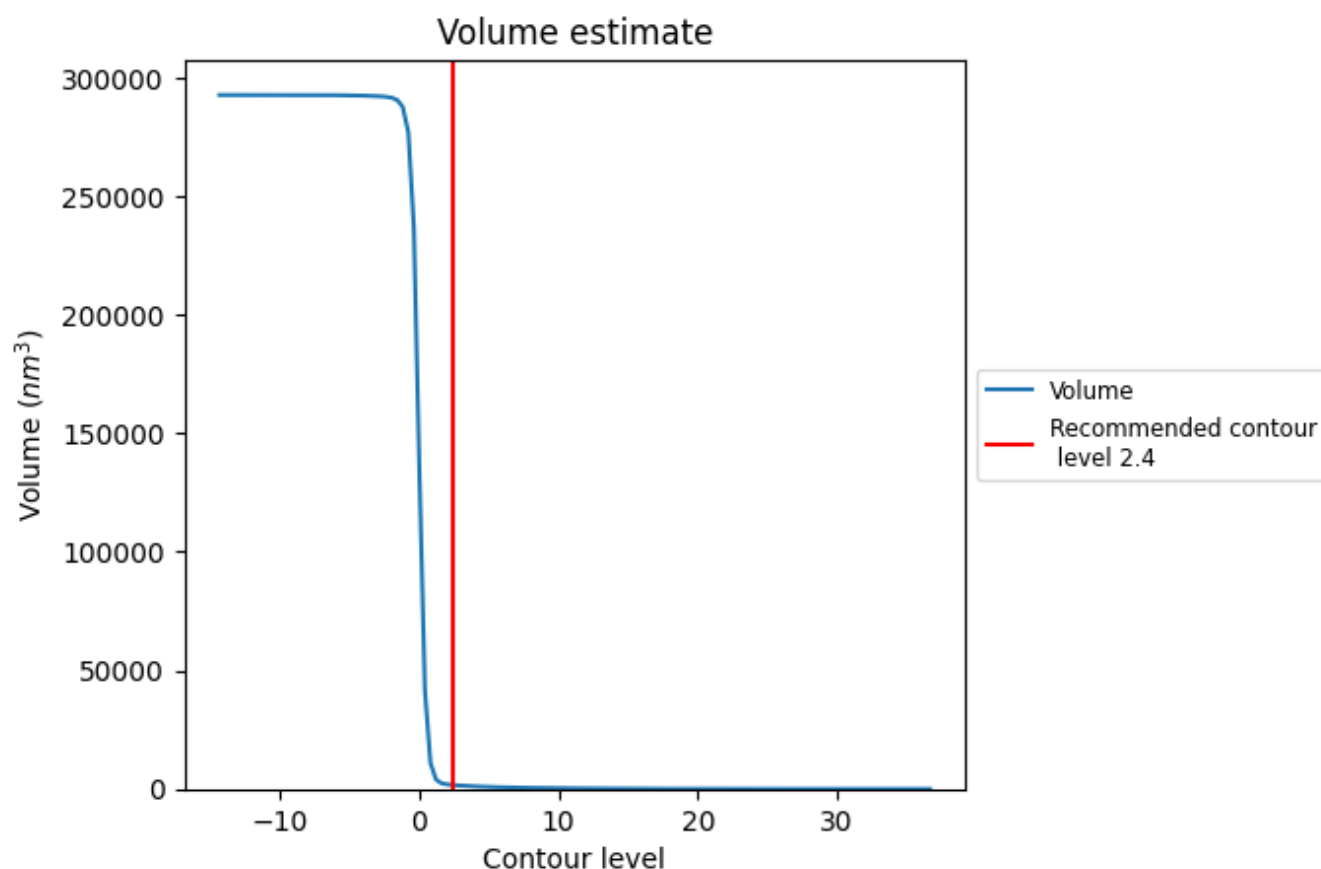
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

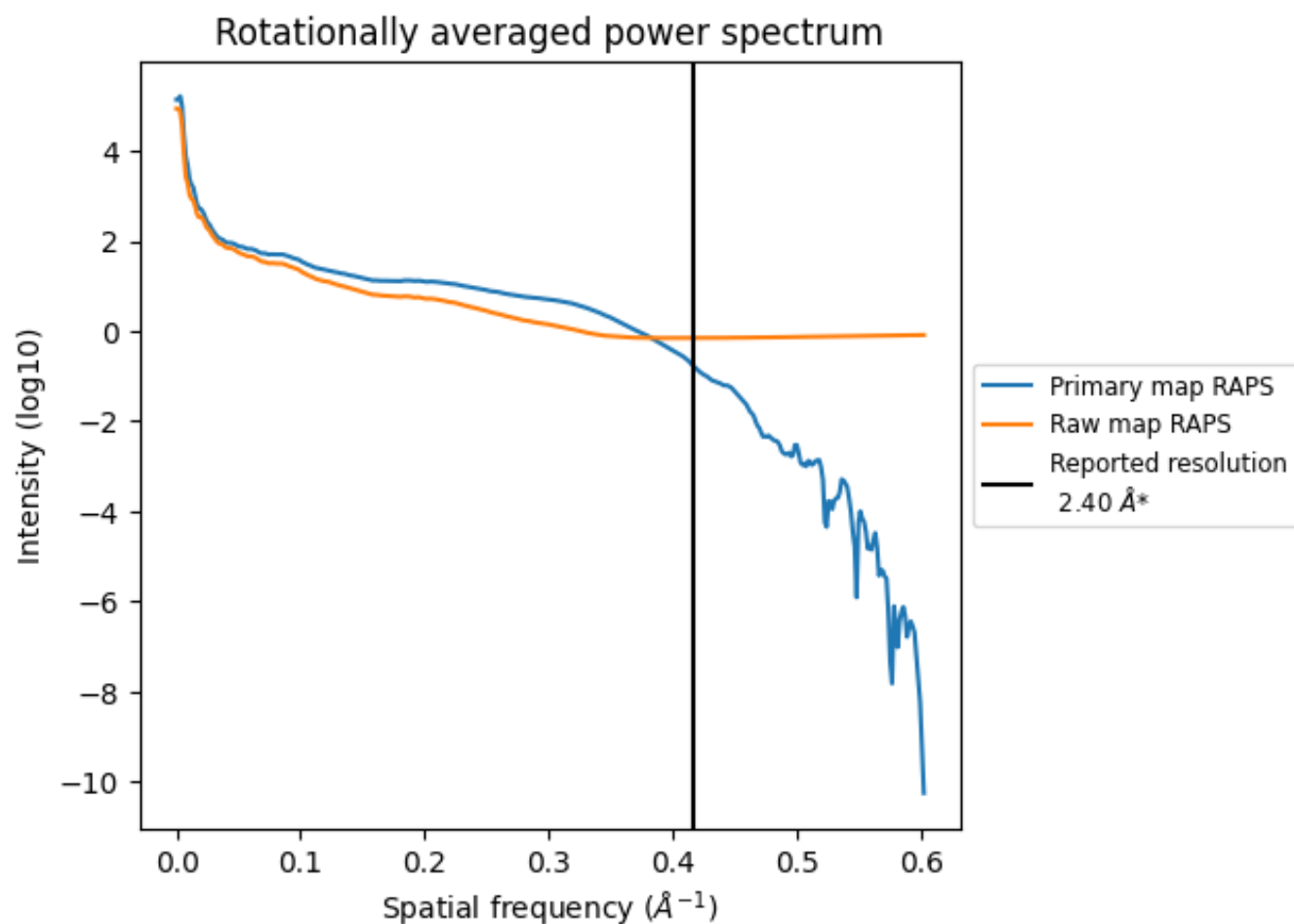
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1691 nm^3 ; this corresponds to an approximate mass of 1528 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 ⓘ

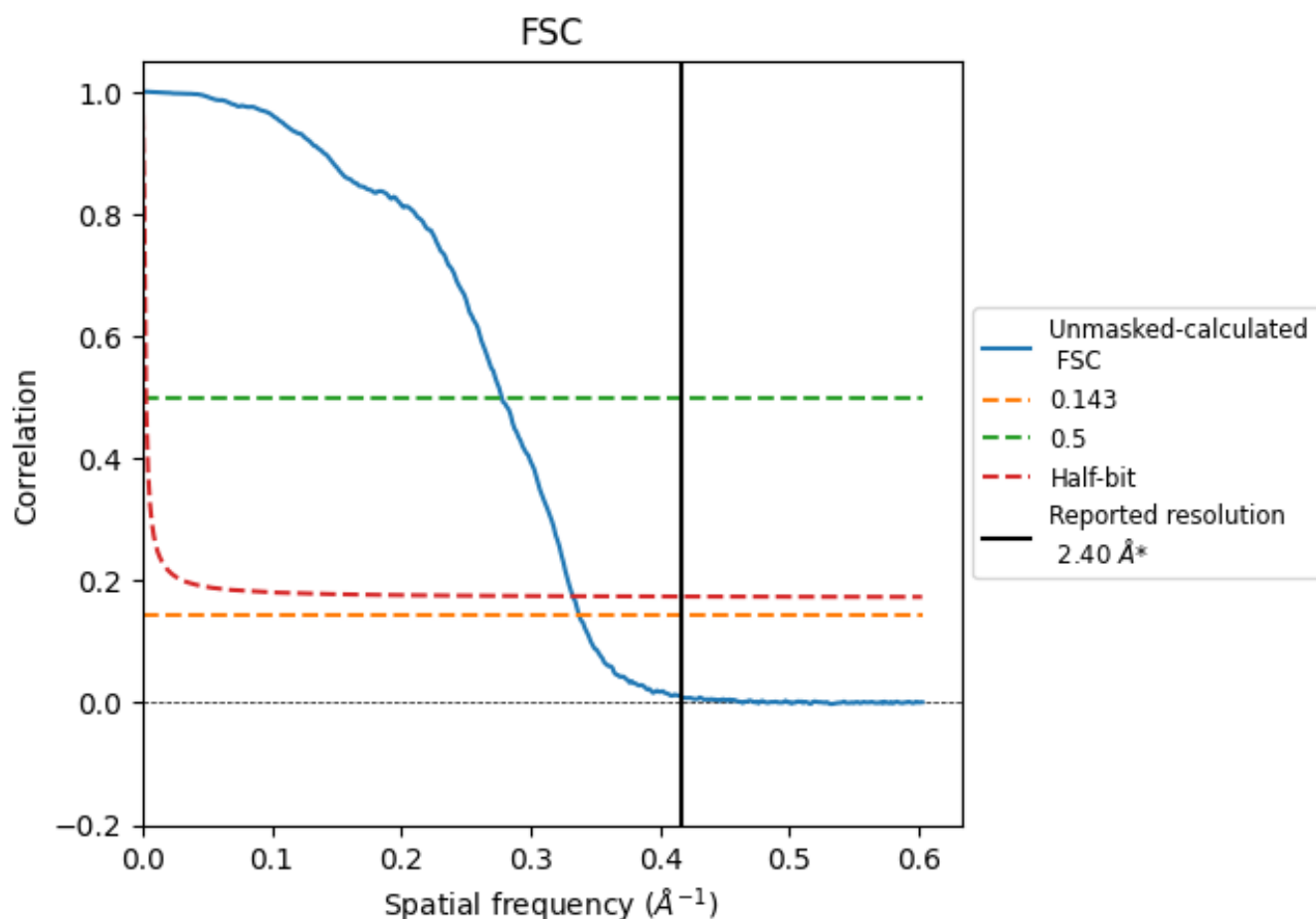


*Reported resolution corresponds to spatial frequency of 0.417 Å⁻¹

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 $0.417 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

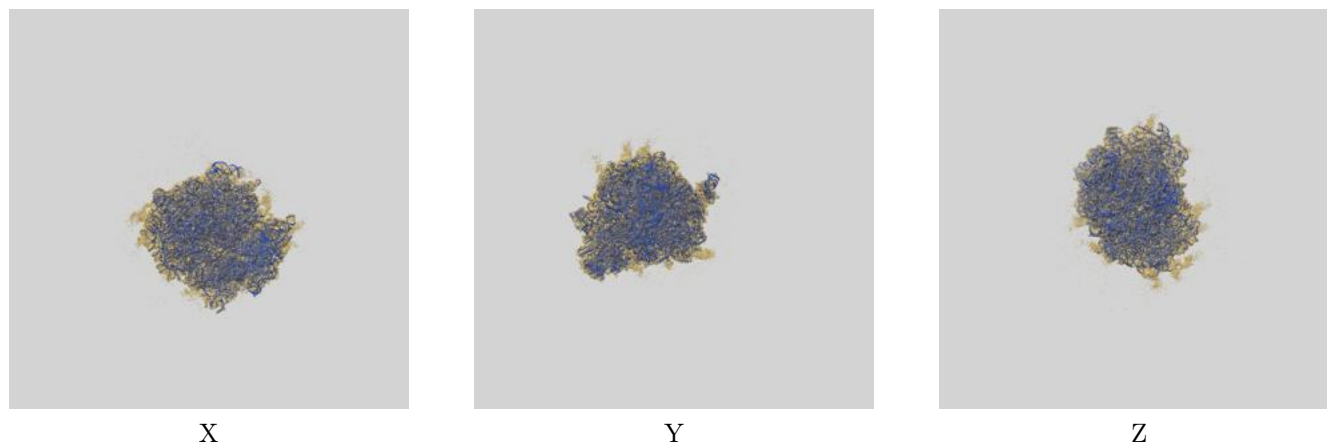
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.40	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	2.96	3.60	3.01

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 2.96 differs from the reported value 2.4 by more than 10 %

9 Map-model fit [i](#)

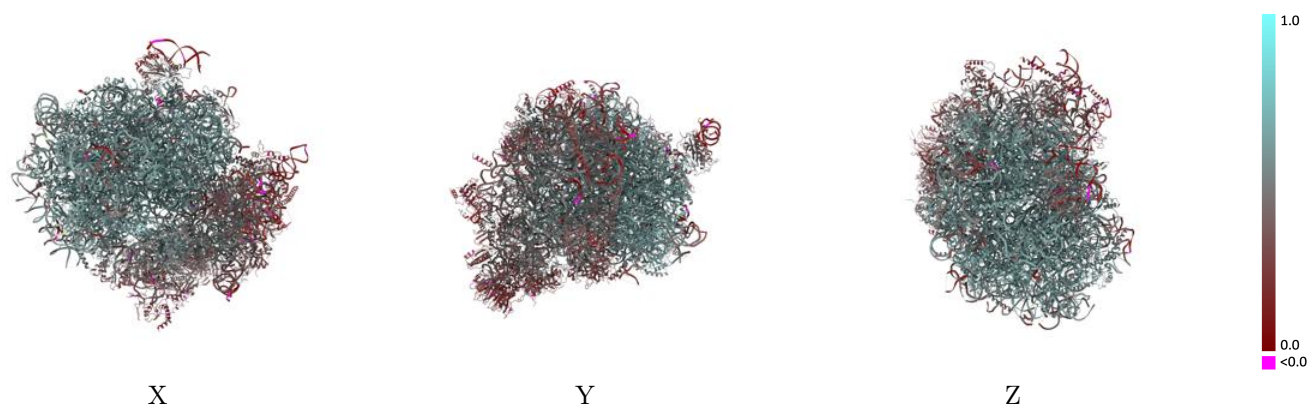
This section contains information regarding the fit between EMDB map EMD-75724 and PDB model 11IQ. Per-residue inclusion information can be found in section 3 on page 21.

9.1 Map-model overlay [i](#)



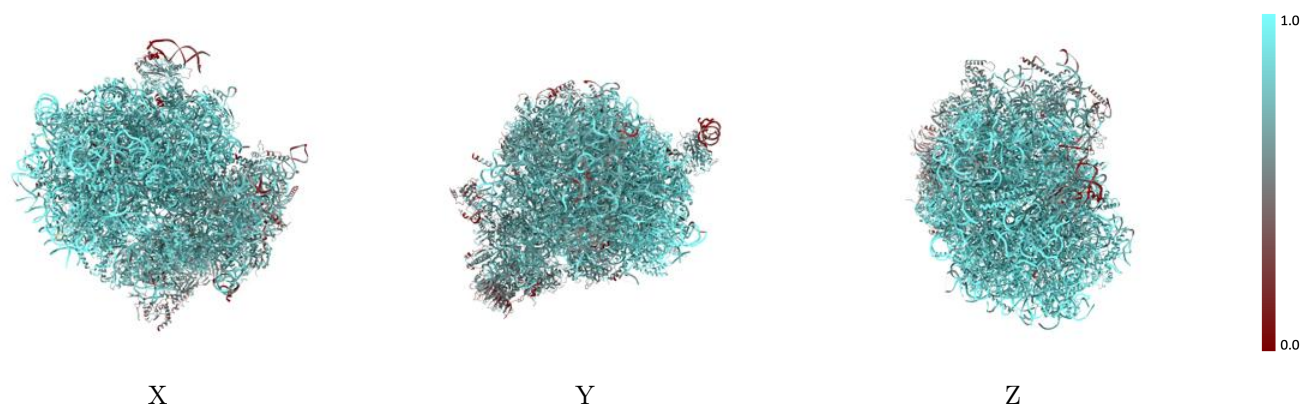
The images above show the 3D surface view of the map at the recommended contour level 2.4 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



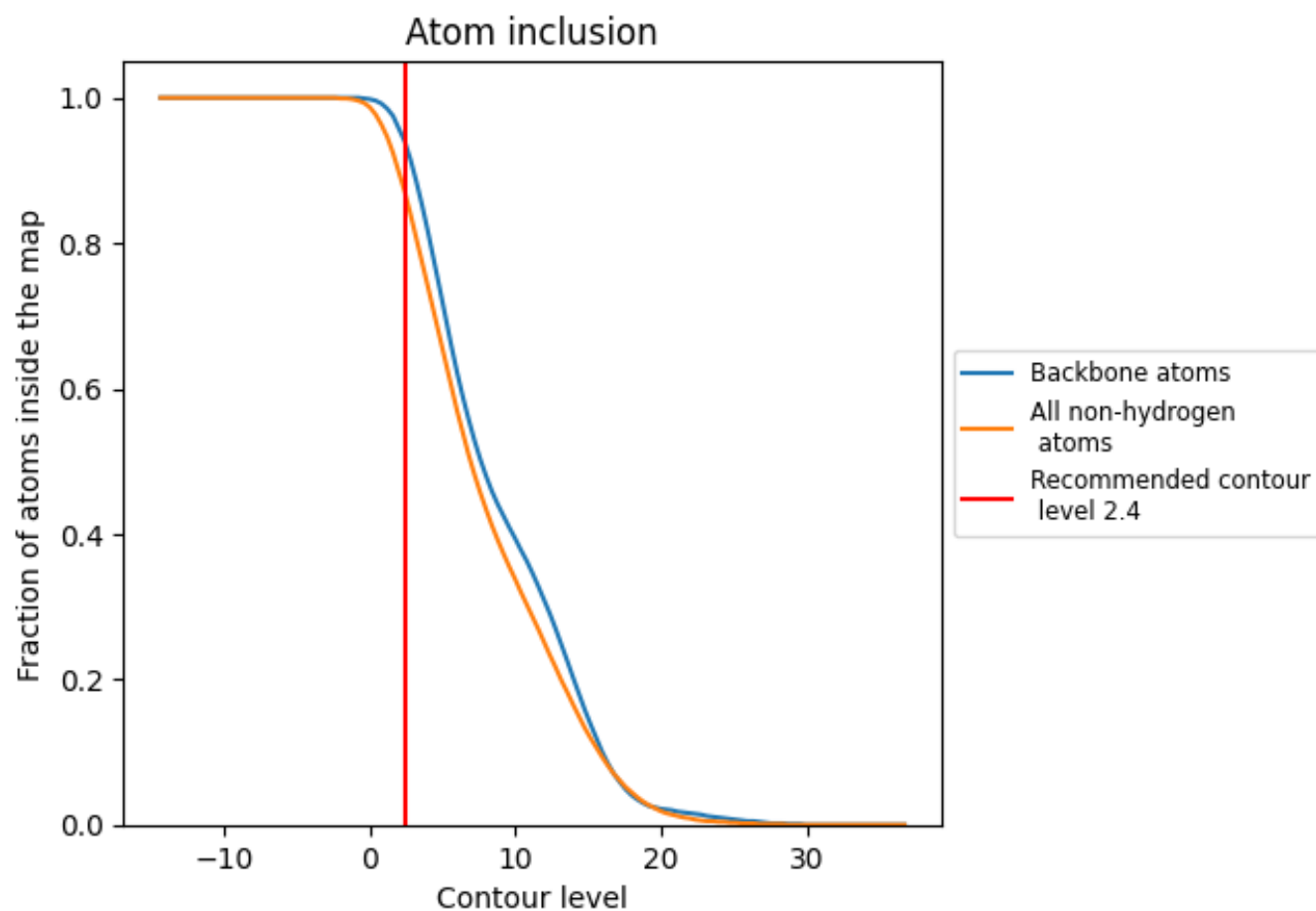
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2.4).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 87% 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 (2.4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8720	 0.5110
10	 0.9180	 0.5890
11	 0.8760	 0.5400
13	 0.9160	 0.5800
14	 0.9250	 0.5780
15	 0.9670	 0.6280
17	 0.7970	 0.5300
18	 0.8800	 0.4320
19	 0.8880	 0.5520
20	 0.9450	 0.6080
21	 0.9290	 0.5850
22	 0.8550	 0.4890
23	 0.9380	 0.6110
24	 0.7360	 0.4660
26	 0.9260	 0.5880
27	 0.9360	 0.5760
28	 0.9690	 0.5770
29	 0.8550	 0.5300
30	 0.8420	 0.5480
31	 0.9090	 0.5660
32	 0.9620	 0.6210
34	 0.9290	 0.5980
35	 0.9190	 0.5820
36	 0.9110	 0.5640
37	 0.9610	 0.6210
38	 0.8400	 0.5330
39	 0.9420	 0.5900
40	 0.9160	 0.5920
41	 0.8390	 0.5300
42	 0.9300	 0.5940
5	 0.9930	 0.6090
58	 0.9750	 0.5890
A	 0.7070	 0.3690
AA	 0.4480	 0.2470
AS	 0.6890	 0.3760



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Chain	Atom inclusion	Q-score
B	 0.8300	 0.5520
BB	 0.6870	 0.4170
CC	 0.6580	 0.3430
DD	 0.7460	 0.4530
EB	 0.6630	 0.4040
EE	 0.4070	 0.2070
ES	 0.1730	 0.1100
FF	 0.7530	 0.4440
GG	 0.6930	 0.3770
II	 0.5930	 0.3330
JJ	 0.5990	 0.3390
L3	 0.9470	 0.6080
L4	 0.9570	 0.6070
L5	 0.9280	 0.5740
L6	 0.9310	 0.5720
L7	 0.9530	 0.6170
L8	 0.9590	 0.6190
L9	 0.9110	 0.5790
LL	 0.6930	 0.3640
MM	 0.6500	 0.3310
OO	 0.5790	 0.3130
PP	 0.7150	 0.4250
Q	 0.9570	 0.6170
QQ	 0.7840	 0.4970
RB	 0.5750	 0.3830
RR	 0.8280	 0.5270
S2	 0.7430	 0.4510
S3	 0.6570	 0.3870
S4	 0.6860	 0.4020
S5	 0.6400	 0.3600
S6	 0.5740	 0.2740
S7	 0.6070	 0.3500
S8	 0.6720	 0.3680
S9	 0.7220	 0.4170
SS	 0.6130	 0.3270
TT	 0.5880	 0.3030
UU	 0.7310	 0.4310
VV	 0.6900	 0.3950
WW	 0.6000	 0.3200
XX	 0.7510	 0.4190
YY	 0.6500	 0.3840
ZZ	 0.5490	 0.2780

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Chain	Atom inclusion	Q-score
aa	 0.8950	 0.5560
bb	 0.9550	 0.6100
cc	 0.9150	 0.5870
dd	 0.9560	 0.6220
ee	 0.9640	 0.6270
ff	 0.9260	 0.5940
gg	 0.9560	 0.6050
s	 0.7600	 0.4210
t	 0.5610	 0.2810
u	 0.7600	 0.4740
v	 0.8020	 0.4950