



Full wwPDB EM Validation Report ⓘ

Sep 6, 2026 – 07:12 PM EDT

PDB ID : 11JJ / pdb_000011jj
EMDB ID : EMD-75740
Title : Rabbit 80S with eEF2,IFRD2 and LARP1,40S-head-swiveled
Authors : Seraj, Z.; Zottig, X.; Huang, C.H.; Loveland, A.B.; Diggs, S.; Sholi, E.; Grigorieff, N.; Korostelev, A.A.
Deposited on : 2026-02-27
Resolution : 2.90 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

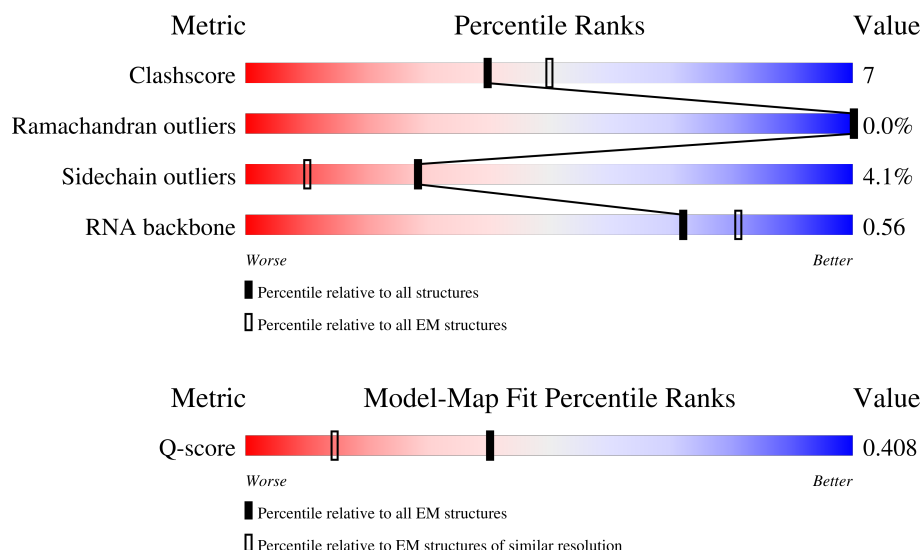
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.90 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	13054 (2.40 - 3.40)

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	IF	442	
2	BB	217	
3	S2	221	

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Mol	Chain	Length	Quality of chain
4	PP	83	
5	DD	151	
6	58	156	
7	6	120	
8	L8	248	
9	L3	394	
10	L4	362	
11	L5	293	
12	L6	291	
13	L7	225	
14	aa	240	
15	10	213	
16	13	210	
17	14	138	
18	15	203	
19	bb	199	
20	17	153	
21	19	180	
22	20	176	
23	21	159	
24	22	99	
25	cc	118	
26	26	134	
27	27	135	
28	dd	147	

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Mol	Chain	Length	Quality of chain
29	29	245	
30	30	98	
31	31	107	
32	32	128	
33	ee	109	
34	34	114	
35	35	122	
36	36	102	
37	37	86	
38	38	69	
39	39	50	
40	40	52	
41	41	25	
42	42	104	
43	ff	91	
44	gg	124	
45	AS	213	
46	FF	149	
47	VV	83	
48	s	196	
49	t	153	
50	F	358	
51	Q	188	
52	ZZ	68	
53	EE	132	

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Mol	Chain	Length	Quality of chain
54	TT	75	
55	S5	191	
56	WW	62	
57	II	142	
58	CC	96	
59	AA	313	
60	OO	100	
61	MM	141	
62	LL	144	
63	XX	55	
64	RR	141	
65	SS	124	
66	S6	237	
67	S4	262	
68	S9	185	
69	S7	189	
70	YY	55	
71	S3	214	
72	RS	132	
73	WX	129	
74	S8	206	
75	W	121	
76	GG	135	
77	UU	101	
78	11	170	

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Mol	Chain	Length	Quality of chain
79	L9	190	6%84%15%
80	18	1698	19%46%47%6%
81	v	857	54%78%18%
82	LA	1096	95%
83	A	121	69%80%18%
84	ES	5070	99%
85	28	4808	39%29%27%
86	23	139	8%87%13%

2 Entry composition

There are 88 unique types of molecules in this entry. The entry contains 224036 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 IFRD2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	IF	346	Total	C	N	O	S	0	0
			2692	1702	484	493	13		

- Molecule 2 is a protein called 40S_SA_C domain-containing protein.

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

- Molecule 3 is a protein called 40S ribosomal protein S2.

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

- Molecule 4 is a protein called eS21.

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

- Molecule 5 is a protein called Small ribosomal subunit protein uS17.

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

- Molecule 6 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	58	151	Total	C	N	O	P	0	0
			3208	1432	564	1062	150		

- Molecule 7 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	6	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 8 is a protein called 60S ribosomal protein L8.

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

- Molecule 9 is a protein called 60S ribosomal protein L3.

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

- Molecule 10 is a protein called 60S ribosomal protein L4.

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

- Molecule 11 is a protein called 60S ribosomal protein L5.

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

- Molecule 12 is a protein called 60S ribosomal protein L6.

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

- Molecule 13 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	L7	225	Total	C	N	O	S	0	0
			1875	1205	358	303	9		

- Molecule 14 is a protein called Large ribosomal subunit protein eL8.

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

- Molecule 15 is a protein called Ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	10	205	Total	C	N	O	S	0	0
			1664	1056	321	274	13		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
16	13	210	Total	C	N	O	S	0	0
			1702	1065	354	279	4		

- Molecule 17 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	14	138	Total	C	N	O	S	0	0
			1137	727	221	182	7		

- Molecule 18 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	15	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 19 is a protein called Large ribosomal subunit protein uL13.

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

- Molecule 20 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	17	153	Total	C	N	O	S	0	0
			1242	777	241	215	9		

- Molecule 21 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	19	180	Total	C	N	O	S	0	0
			1508	933	328	238	9		

- Molecule 22 is a protein called Large ribosomal subunit protein eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	20	176	Total	C	N	O	S	0	0
			1462	930	285	236	11		

- Molecule 23 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	21	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 24 is a protein called Large ribosomal subunit protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	22	99	Total	C	N	O	S	0	0
			809	519	141	147	2		

- Molecule 25 is a protein called Large ribosomal subunit protein uL23.

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

- Molecule 26 is a protein called 60S ribosomal protein L26.

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

- Molecule 27 is a protein called 60S ribosomal protein L27.

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

- Molecule 28 is a protein called 60S ribosomal protein L27a.

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

- Molecule 29 is a protein called Large ribosomal subunit protein eL29.

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

- Molecule 30 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	30	98	Total	C	N	O	S	0	0
			761	481	134	140	6		

- Molecule 31 is a protein called 60S ribosomal protein L31.

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

- Molecule 32 is a protein called Large ribosomal subunit protein eL32.

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

- Molecule 33 is a protein called Large ribosomal subunit protein eL33.

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

- Molecule 34 is a protein called 60S ribosomal protein L34.

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

- Molecule 35 is a protein called 60S ribosomal protein L35.

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

- Molecule 36 is a protein called 60S ribosomal protein L36.

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

- Molecule 37 is a protein called 60S ribosomal protein L37.

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

- Molecule 38 is a protein called Large ribosomal subunit protein eL38.

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

- Molecule 39 is a protein called 60S ribosomal protein L39.

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

- Molecule 40 is a protein called Large ribosomal subunit protein eL40.

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

- Molecule 41 is a protein called eL41.

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

- Molecule 42 is a protein called eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	42	102	Total	C	N	O	S	0	0
			834	522	171	135	6		

- Molecule 43 is a protein called 60S ribosomal protein L37a.

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

- Molecule 44 is a protein called 60S ribosomal protein L28.

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

- Molecule 45 is a protein called 40S ribosomal protein S3a.

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

- Molecule 46 is a protein called 40S ribosomal protein S13.

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

- Molecule 47 is a protein called 40S ribosomal protein S27.

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

- Molecule 48 is a protein called 60S acidic ribosomal protein P0.

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

- Molecule 49 is a protein called uL11.

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

- Molecule 50 is a protein called Proliferation-associated protein 2G4.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	F	358	Total	C	N	O	S	0	0
			2798	1762	482	537	17		

- Molecule 51 is a protein called Large ribosomal subunit protein eL18.

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

- Molecule 52 is a protein called 40S ribosomal protein S27a.

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

- Molecule 53 is a protein called 40S ribosomal protein S12.

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

- Molecule 54 is a protein called 40S ribosomal protein S25.

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

- Molecule 55 is a protein called Small ribosomal subunit protein uS7.

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

- Molecule 56 is a protein called 40S ribosomal protein S28.

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

- Molecule 57 is a protein called Small ribosomal subunit protein uS9.

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

- Molecule 58 is a protein called 40S ribosomal protein S10.

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

- Molecule 59 is a protein called Receptor of activated protein C kinase 1.

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

- Molecule 60 is a protein called 40S ribosomal protein S20.

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

- Molecule 61 is a protein called Small ribosomal subunit protein eS19.

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

- Molecule 62 is a protein called 40S ribosomal protein S18.

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

- Molecule 63 is a protein called 40S ribosomal protein S29.

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

- Molecule 64 is a protein called 40S ribosomal protein S23.

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

- Molecule 65 is a protein called 40S ribosomal protein S24.

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

- Molecule 66 is a protein called 40S ribosomal protein S6.

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

- Molecule 67 is a protein called 40S ribosomal protein S4.

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

- Molecule 68 is a protein called 40S ribosomal protein S9.

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

- Molecule 69 is a protein called Small ribosomal subunit protein eS7.

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

- Molecule 70 is a protein called 40S ribosomal protein S30.

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

- Molecule 71 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	S3	214	Total	C	N	O	S	0	0
			1662	1060	302	292	8		

- Molecule 72 is a protein called 40S ribosomal protein S17.

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

- Molecule 73 is a protein called 40S ribosomal protein S15a.

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

- Molecule 74 is a protein called 40S ribosomal protein S8.

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

- Molecule 75 is a protein called Ribosomal protein L24.

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

- Molecule 76 is a protein called Small ribosomal subunit protein uS11.

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

- Molecule 77 is a protein called eS26.

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

- Molecule 78 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	11	170	Total	C	N	O	S	0	0
			1362	861	254	241	6		

- Molecule 79 is a protein called 60S ribosomal protein L9.

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

- Molecule 80 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	18	1688	Total	C	N	O	P	0	0
			36043	16088	6476	11792	1687		

- Molecule 81 is a protein called Elongation factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	v	829	Total	C	N	O	S	0	0
			6470	4114	1108	1205	43		

- Molecule 82 is a protein called LARP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	LA	51	Total	C	N	O	S	0	0
			421	264	74	82	1		

- Molecule 83 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	A	121	Total	C	N	O	S	0	0
			983	622	184	170	7		

- Molecule 84 is a RNA chain called ES27L.

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

- Molecule 85 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	28	3502	Total	C	N	O	P	0	0
			75105	33448	13761	24394	3502		

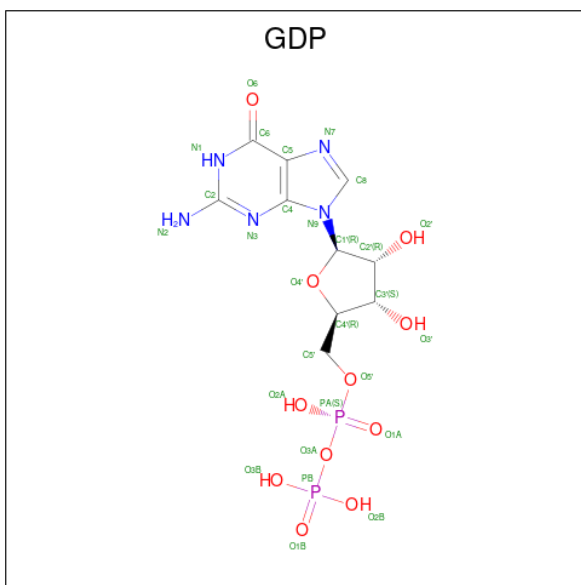
- Molecule 86 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
86	23	139	Total	C	N	O	S	0	0
			1034	648	199	182	5		

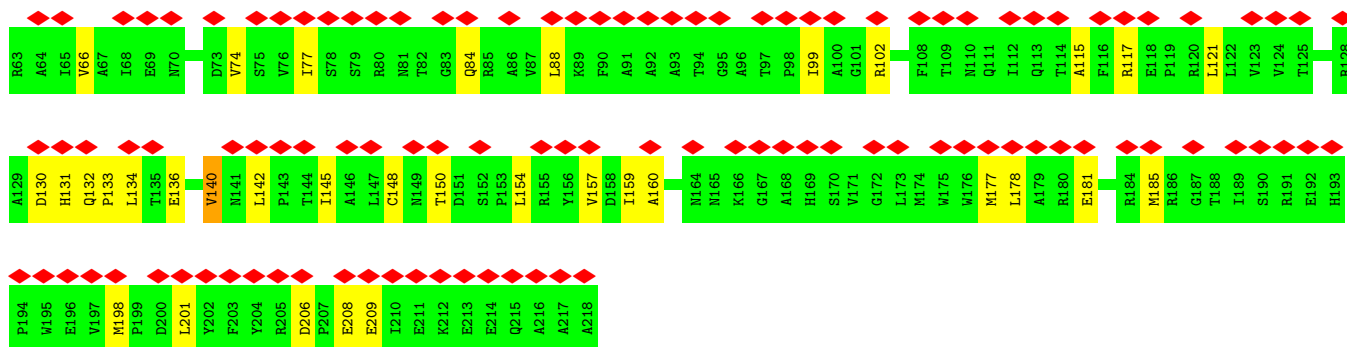
- Molecule 87 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
87	34	1	Total	Zn	0
			1	1	
87	37	1	Total	Zn	0
			1	1	
87	ff	1	Total	Zn	0
			1	1	
87	UU	1	Total	Zn	0
			1	1	

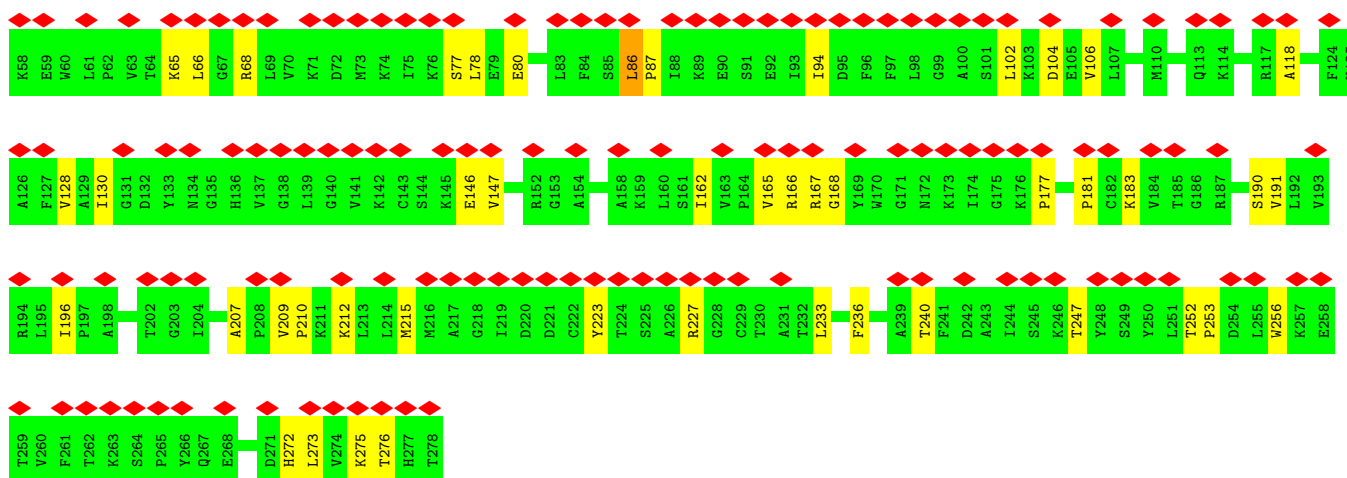
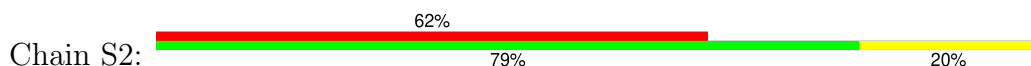
- Molecule 88 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).



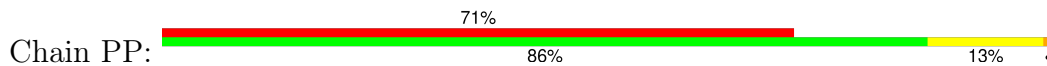
Mol	Chain	Residues	Atoms					AltConf
88	v	1	Total	C	N	O	P	0
			28	10	5	11	2	



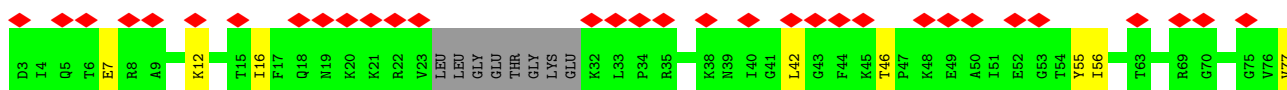
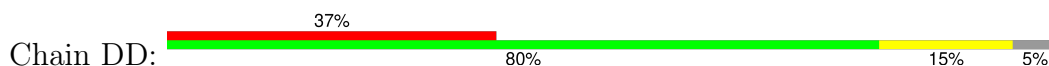
• Molecule 3: 40S ribosomal protein S2

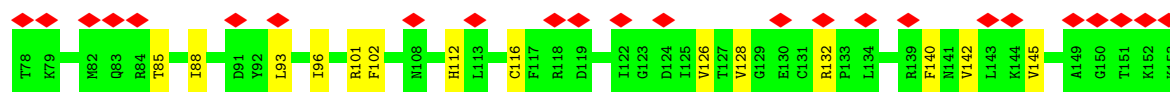


• Molecule 4: eS21



• Molecule 5: Small ribosomal subunit protein uS17





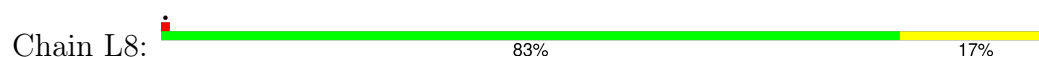
• Molecule 6: 5.8S rRNA



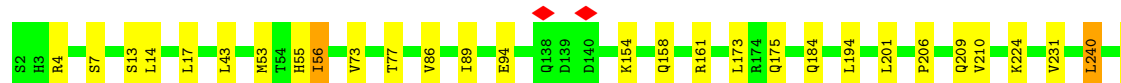
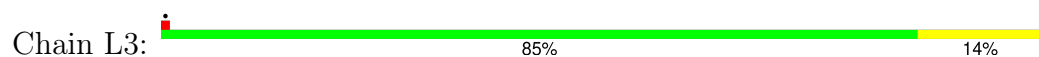
• Molecule 7: 5S rRNA



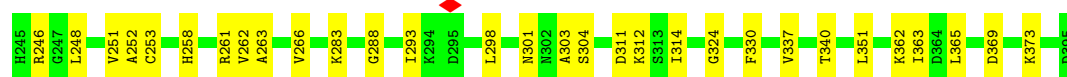
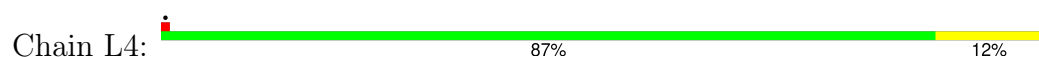
• Molecule 8: 60S ribosomal protein L8

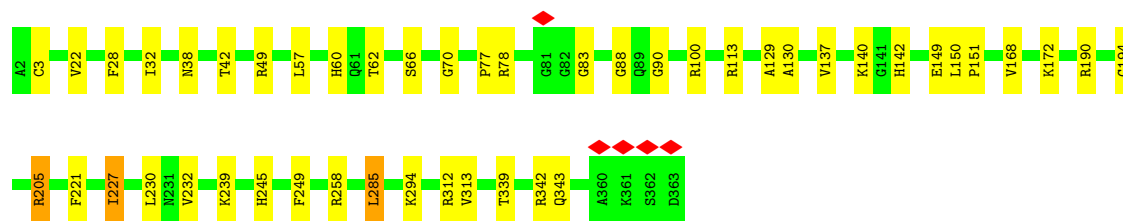


• Molecule 9: 60S ribosomal protein L3

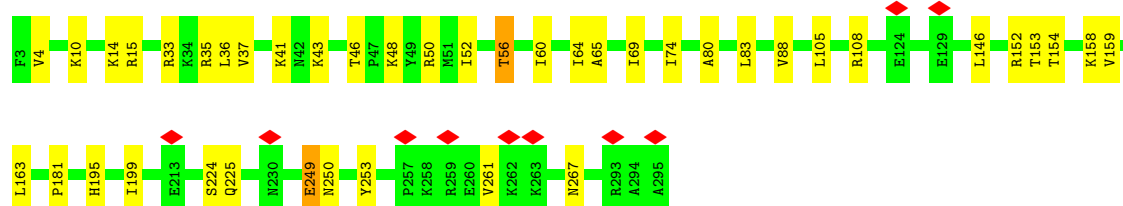
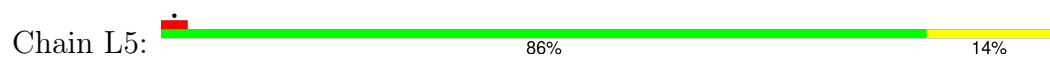


• Molecule 10: 60S ribosomal protein L4

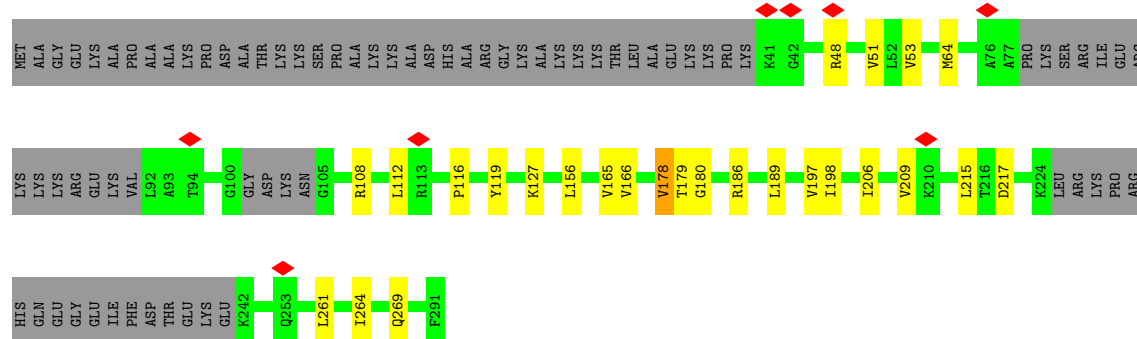




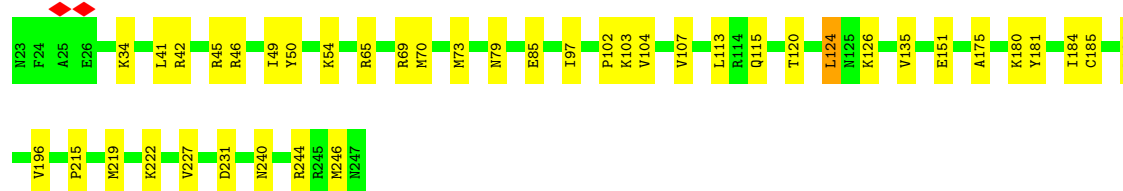
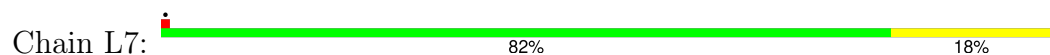
• Molecule 11: 60S ribosomal protein L5



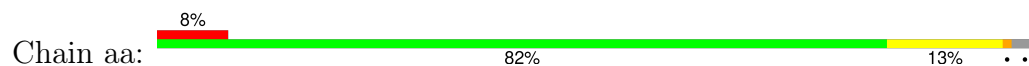
• Molecule 12: 60S ribosomal protein L6

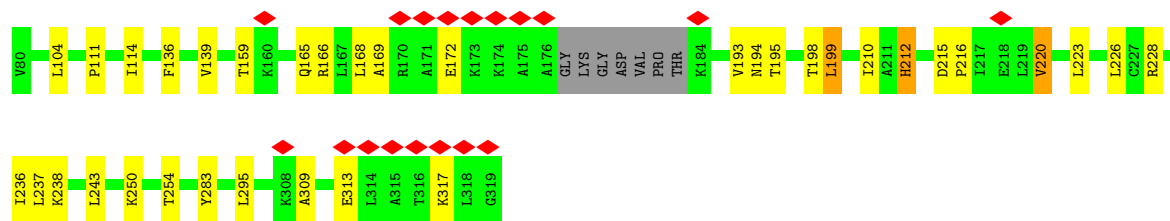


• Molecule 13: 60S ribosomal protein L7

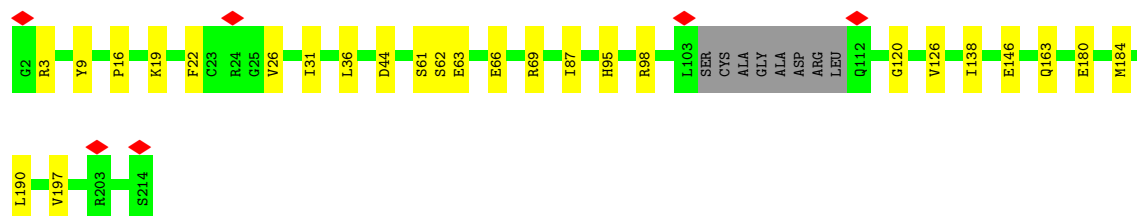
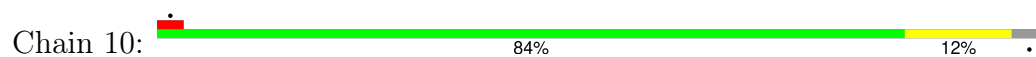


• Molecule 14: Large ribosomal subunit protein eL8

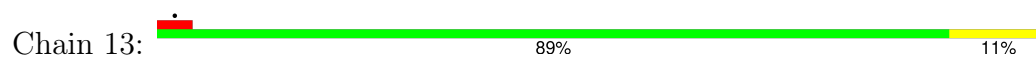




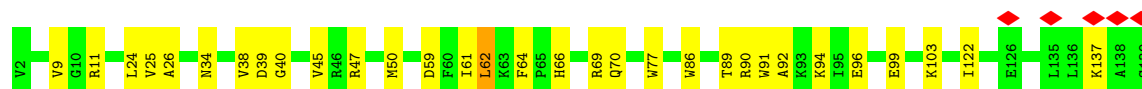
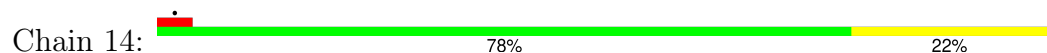
• Molecule 15: Ribosomal protein L10



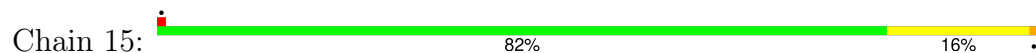
• Molecule 16: Large ribosomal subunit protein eL13



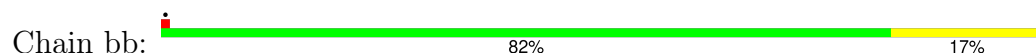
• Molecule 17: 60S ribosomal protein L14



• Molecule 18: 60S ribosomal protein L15



• Molecule 19: Large ribosomal subunit protein uL13



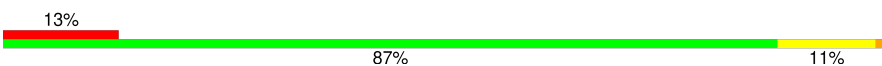


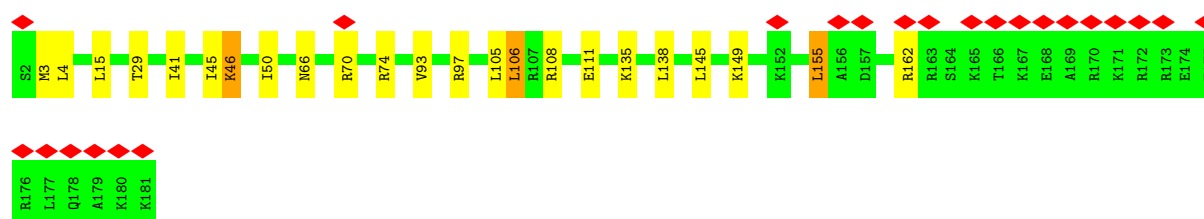
- Molecule 20: 60S ribosomal protein L17

Chain 17: 



- Molecule 21: 60S ribosomal protein L19

Chain 19: 



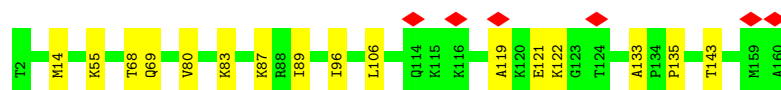
- Molecule 22: Large ribosomal subunit protein eL20

Chain 20: 

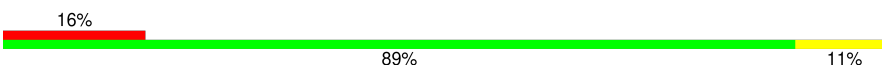


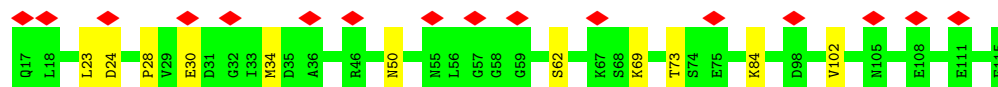
- Molecule 23: 60S ribosomal protein L21

Chain 21: 



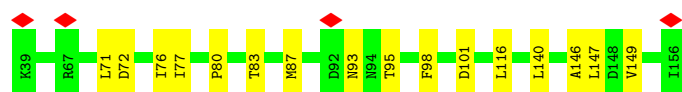
- Molecule 24: Large ribosomal subunit protein eL22

Chain 22: 

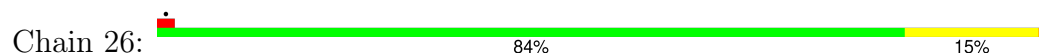


- Molecule 25: Large ribosomal subunit protein uL23

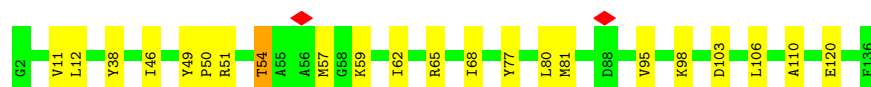
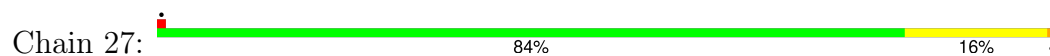
Chain cc: 



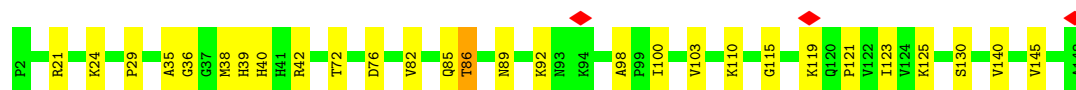
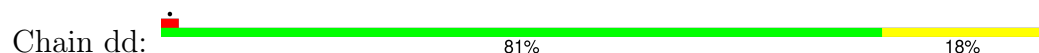
- Molecule 26: 60S ribosomal protein L26



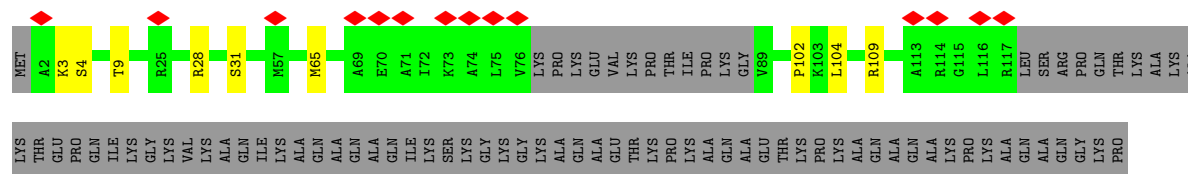
- Molecule 27: 60S ribosomal protein L27



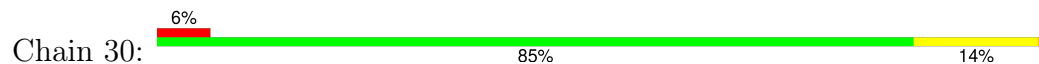
- Molecule 28: 60S ribosomal protein L27a



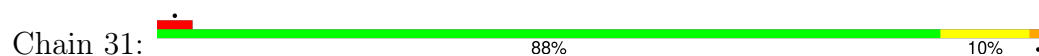
- Molecule 29: Large ribosomal subunit protein eL29

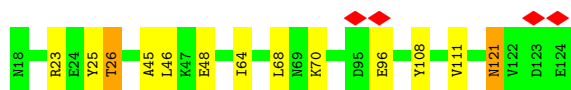


- Molecule 30: 60S ribosomal protein L30

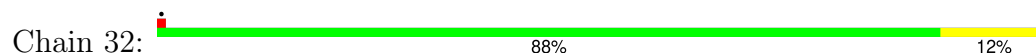


- Molecule 31: 60S ribosomal protein L31

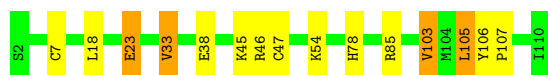




- Molecule 32: Large ribosomal subunit protein eL32



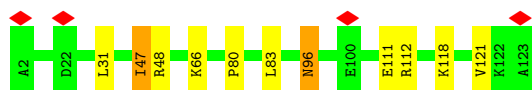
- Molecule 33: Large ribosomal subunit protein eL33



- Molecule 34: 60S ribosomal protein L34



- Molecule 35: 60S ribosomal protein L35



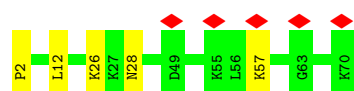
- Molecule 36: 60S ribosomal protein L36



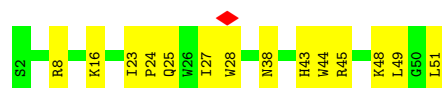
- Molecule 37: 60S ribosomal protein L37



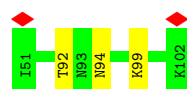
- Molecule 38: Large ribosomal subunit protein eL38



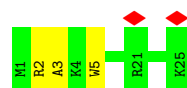
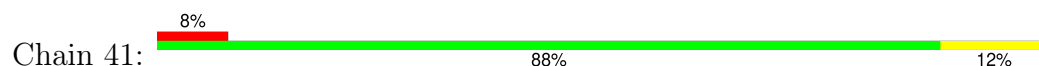
- Molecule 39: 60S ribosomal protein L39



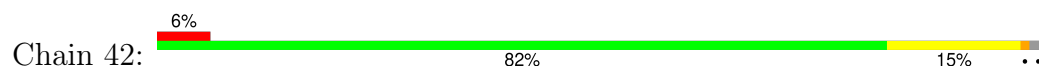
- Molecule 40: Large ribosomal subunit protein eL40



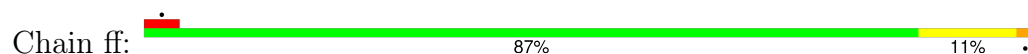
- Molecule 41: eL41



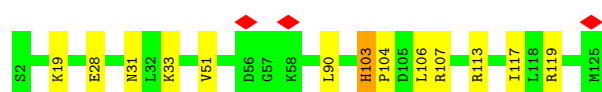
- Molecule 42: eL42



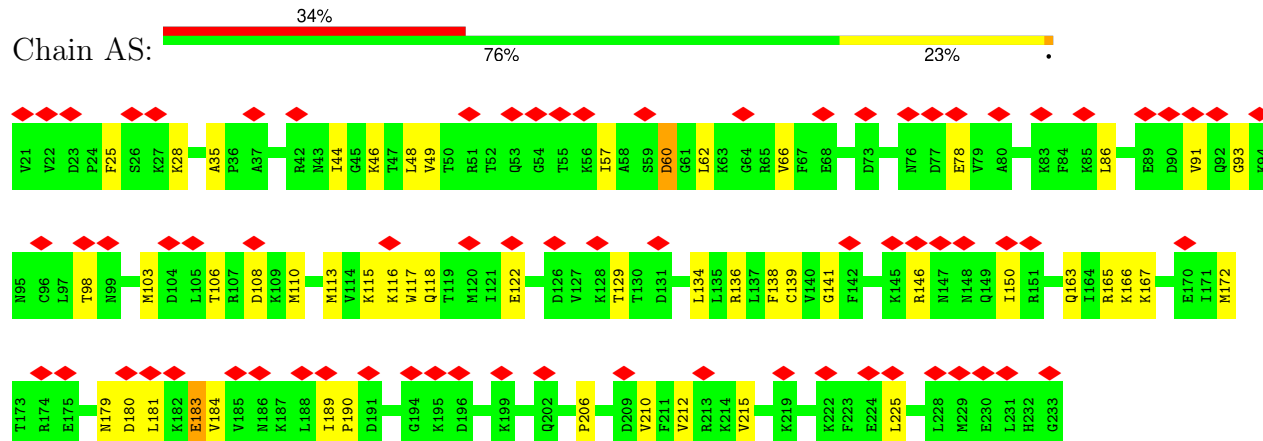
- Molecule 43: 60S ribosomal protein L37a



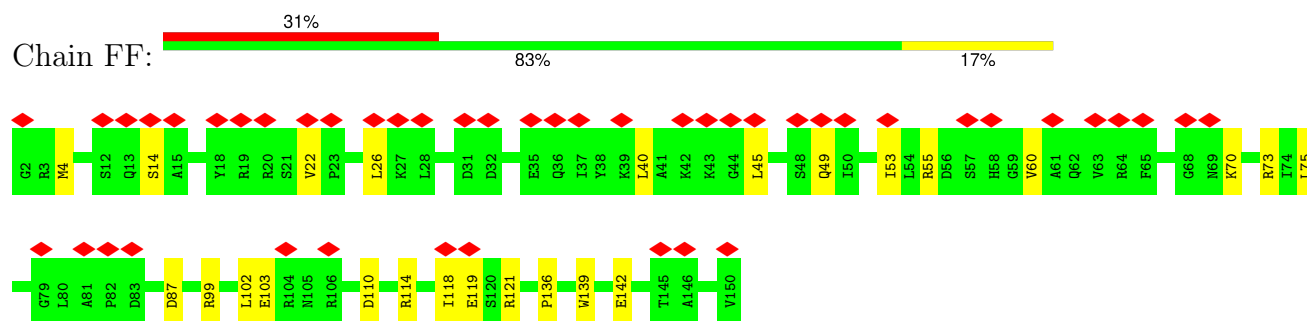
- Molecule 44: 60S ribosomal protein L28



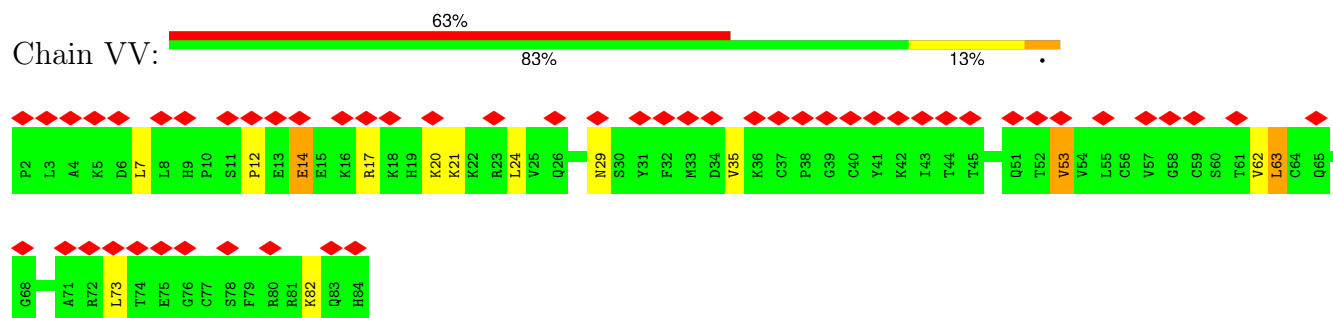
- Molecule 45: 40S ribosomal protein S3a



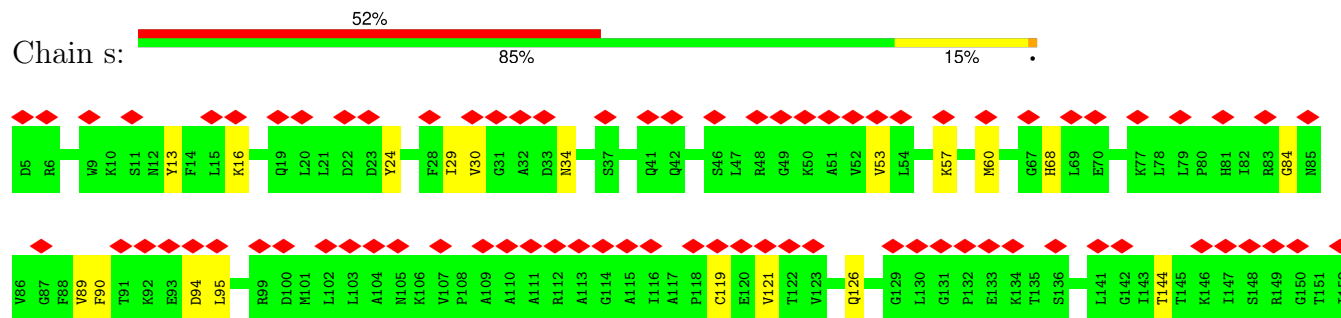
- Molecule 46: 40S ribosomal protein S13

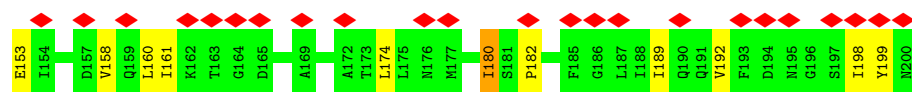


- Molecule 47: 40S ribosomal protein S27

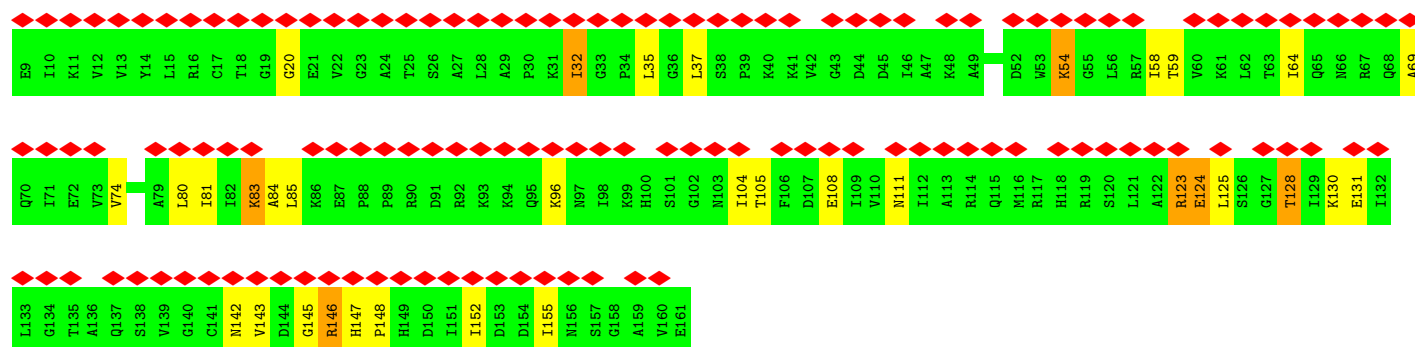
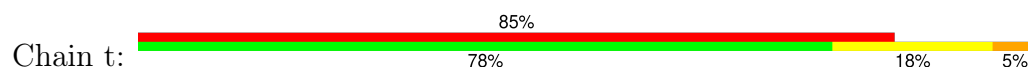


- Molecule 48: 60S acidic ribosomal protein P0

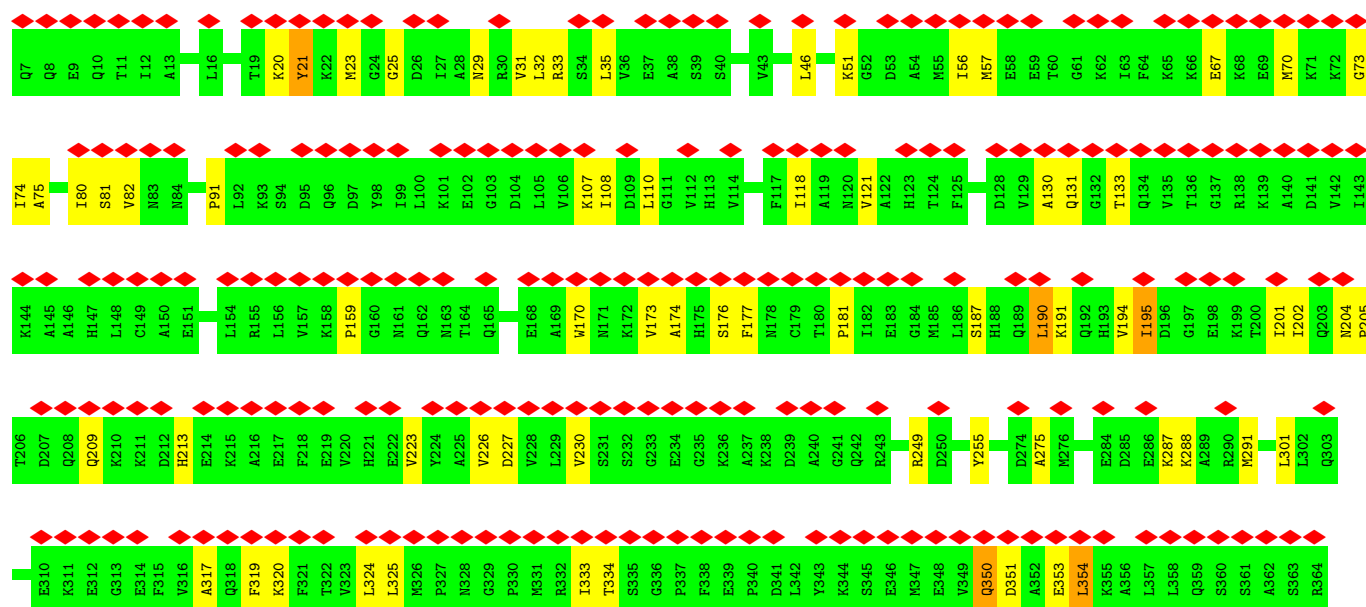
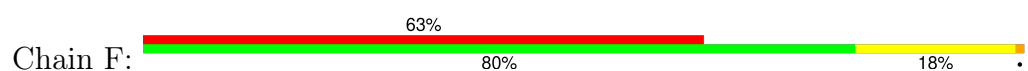




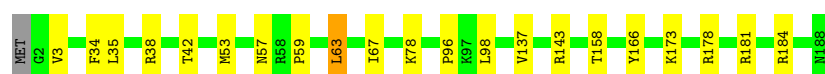
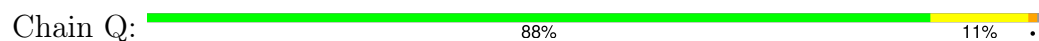
• Molecule 49: uL11



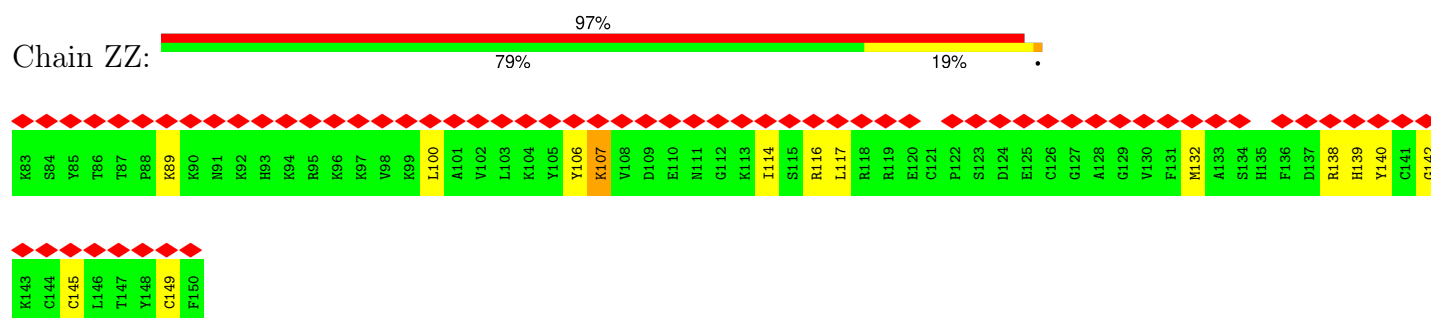
• Molecule 50: Proliferation-associated protein 2G4



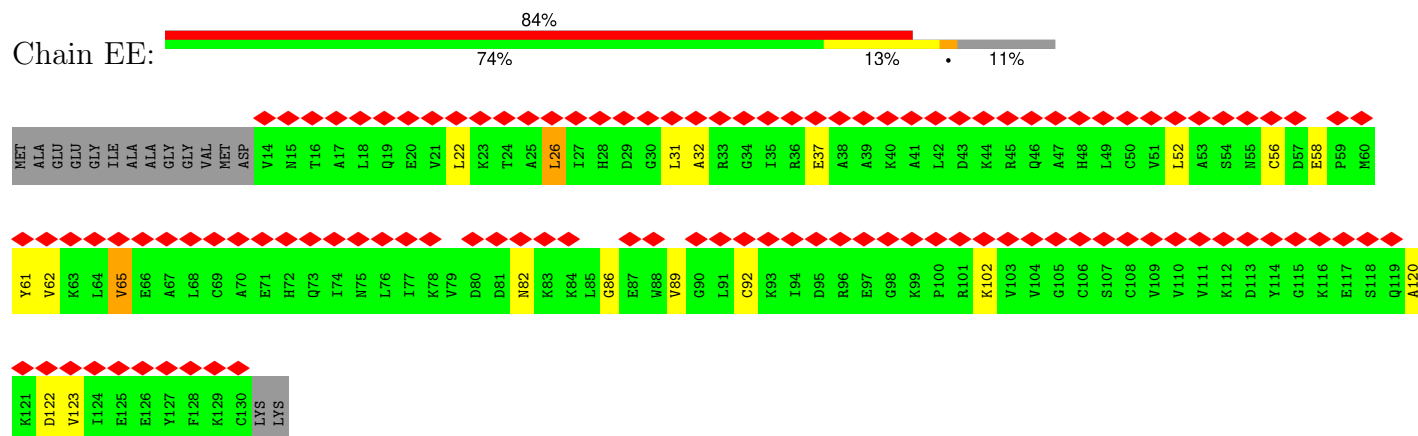
• Molecule 51: Large ribosomal subunit protein eL18



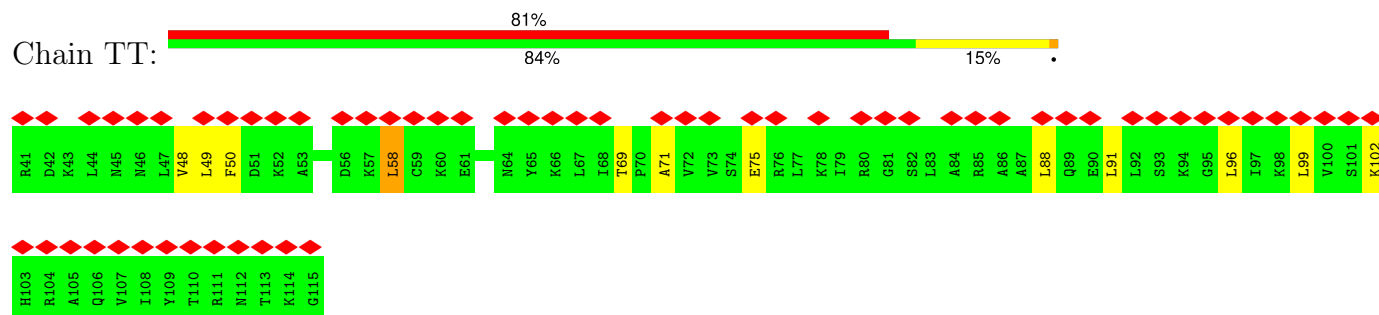
• Molecule 52: 40S ribosomal protein S27a



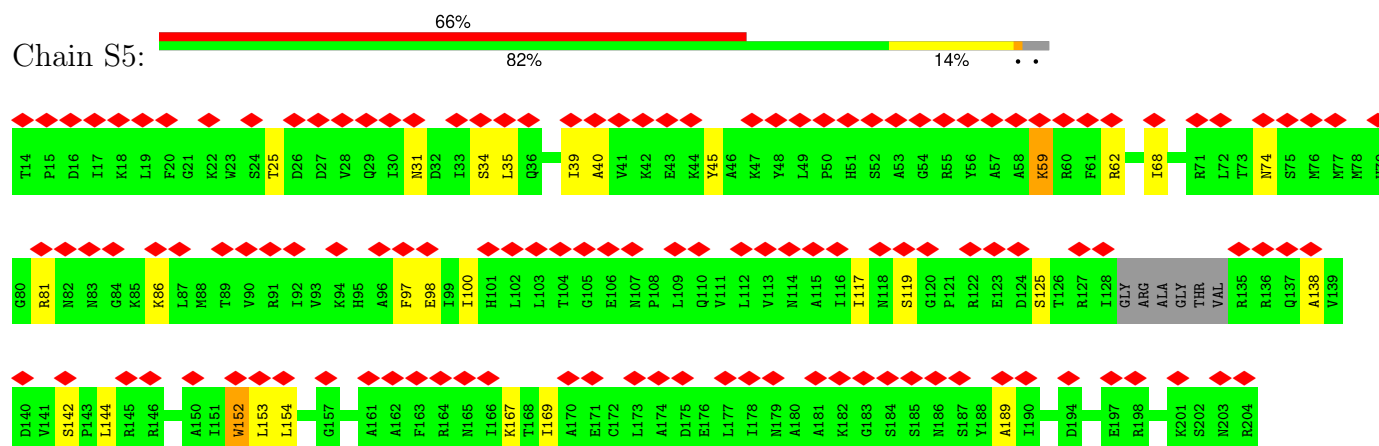
- Molecule 53: 40S ribosomal protein S12



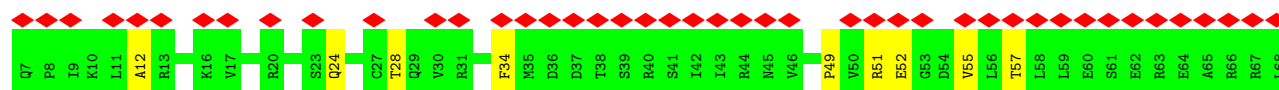
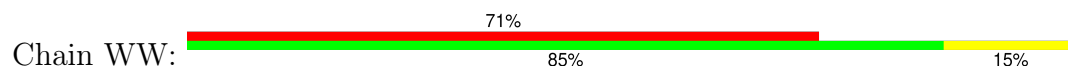
- Molecule 54: 40S ribosomal protein S25



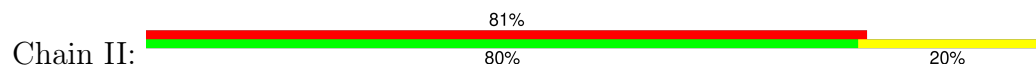
- Molecule 55: Small ribosomal subunit protein uS7



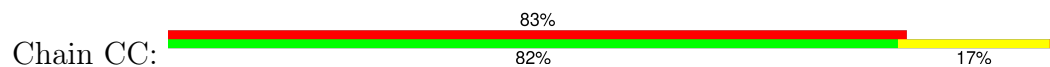
- Molecule 56: 40S ribosomal protein S28



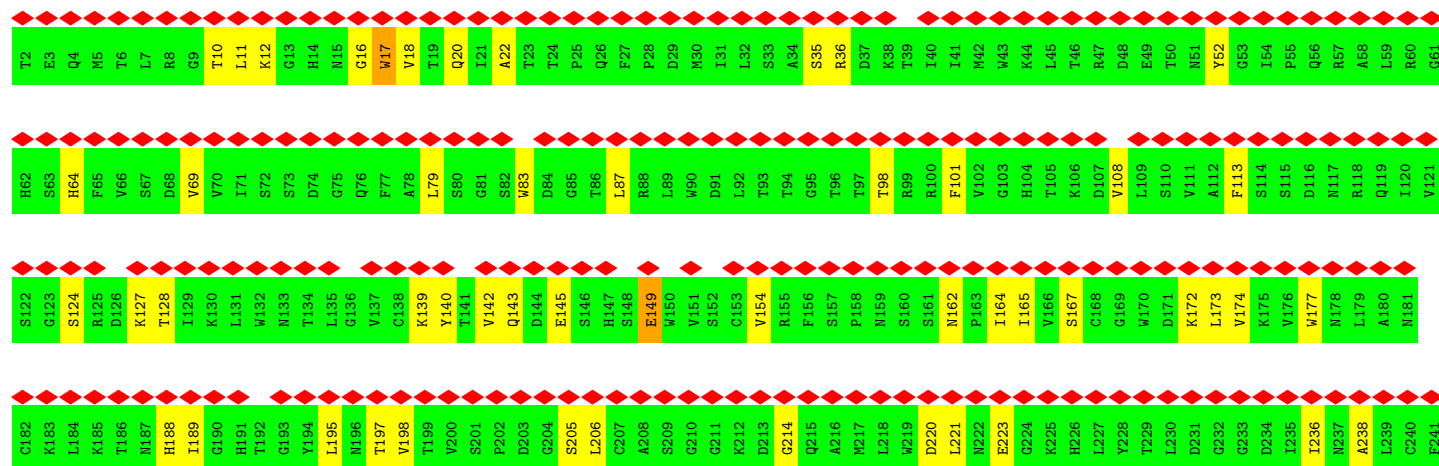
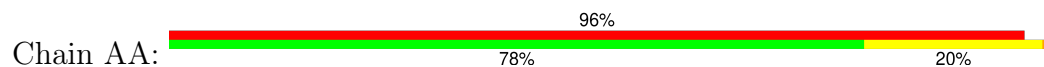
- Molecule 57: Small ribosomal subunit protein uS9

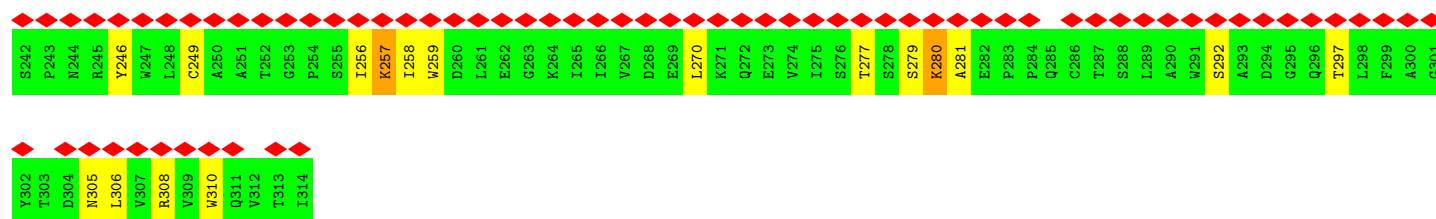


- Molecule 58: 40S ribosomal protein S10

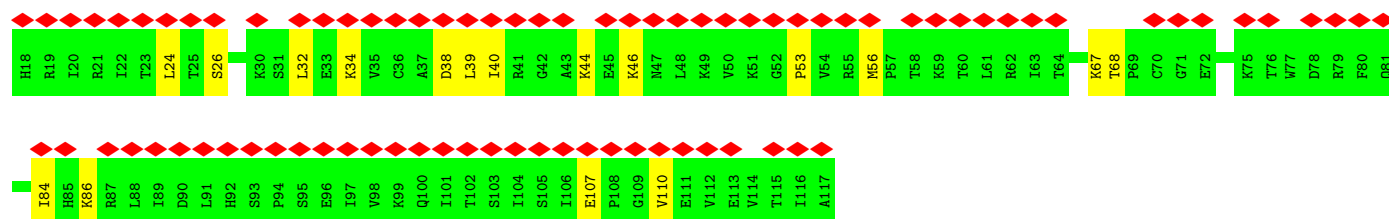
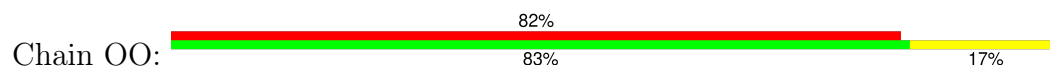


- Molecule 59: Receptor of activated protein C kinase 1

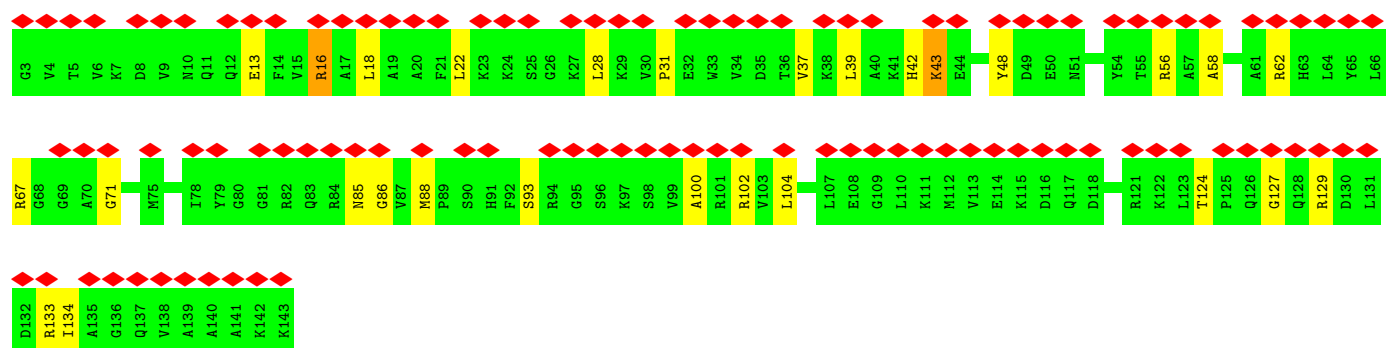
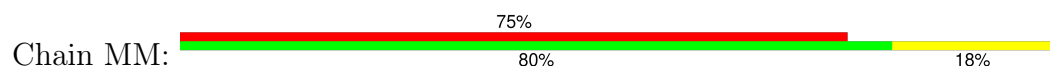




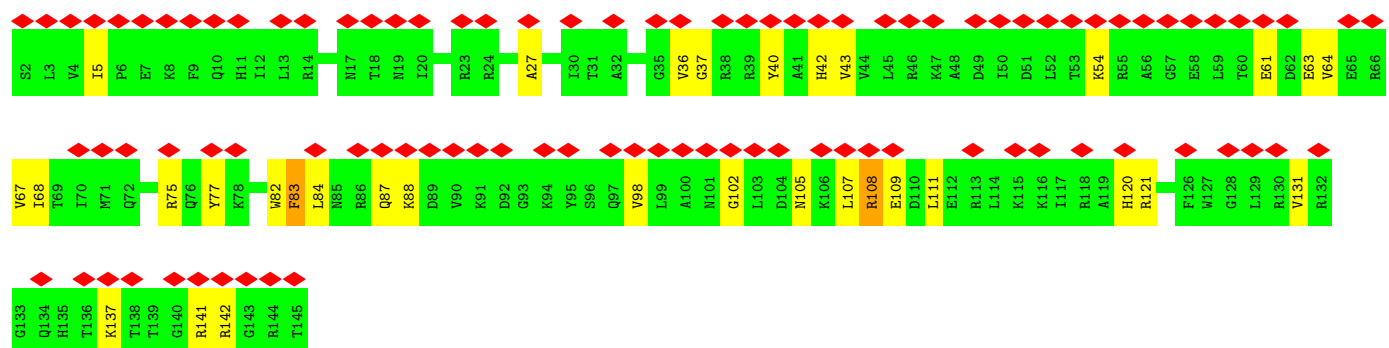
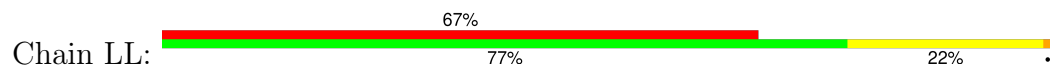
• Molecule 60: 40S ribosomal protein S20



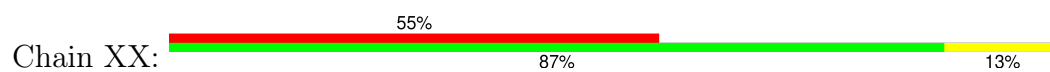
• Molecule 61: Small ribosomal subunit protein eS19



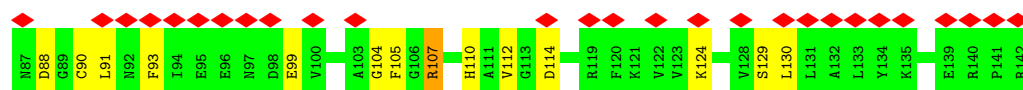
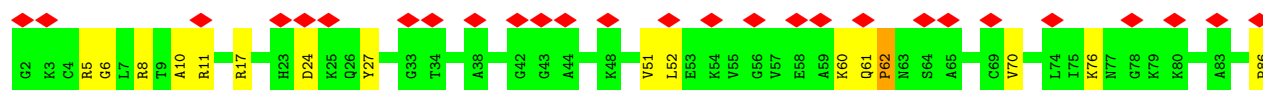
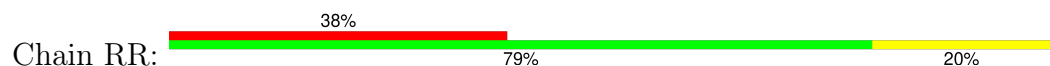
• Molecule 62: 40S ribosomal protein S18



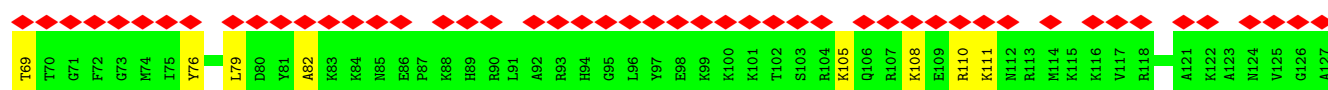
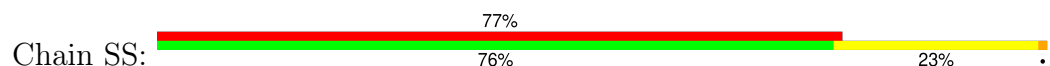
• Molecule 63: 40S ribosomal protein S29



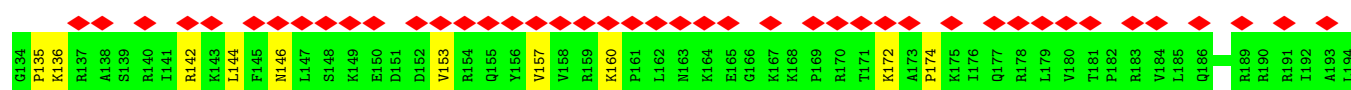
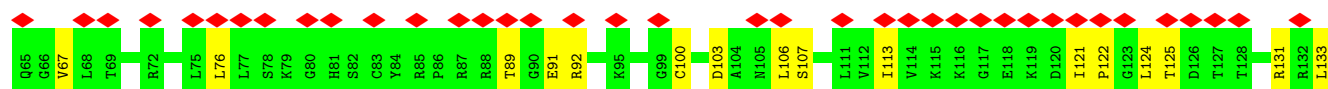
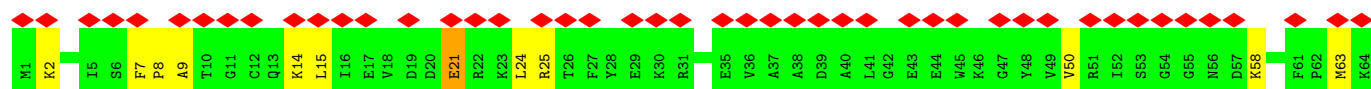
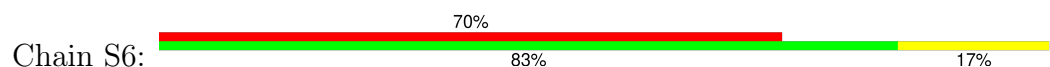
• Molecule 64: 40S ribosomal protein S23



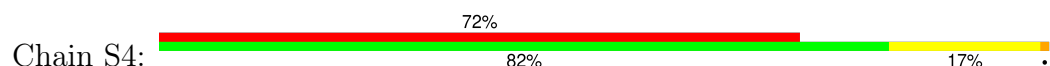
• Molecule 65: 40S ribosomal protein S24

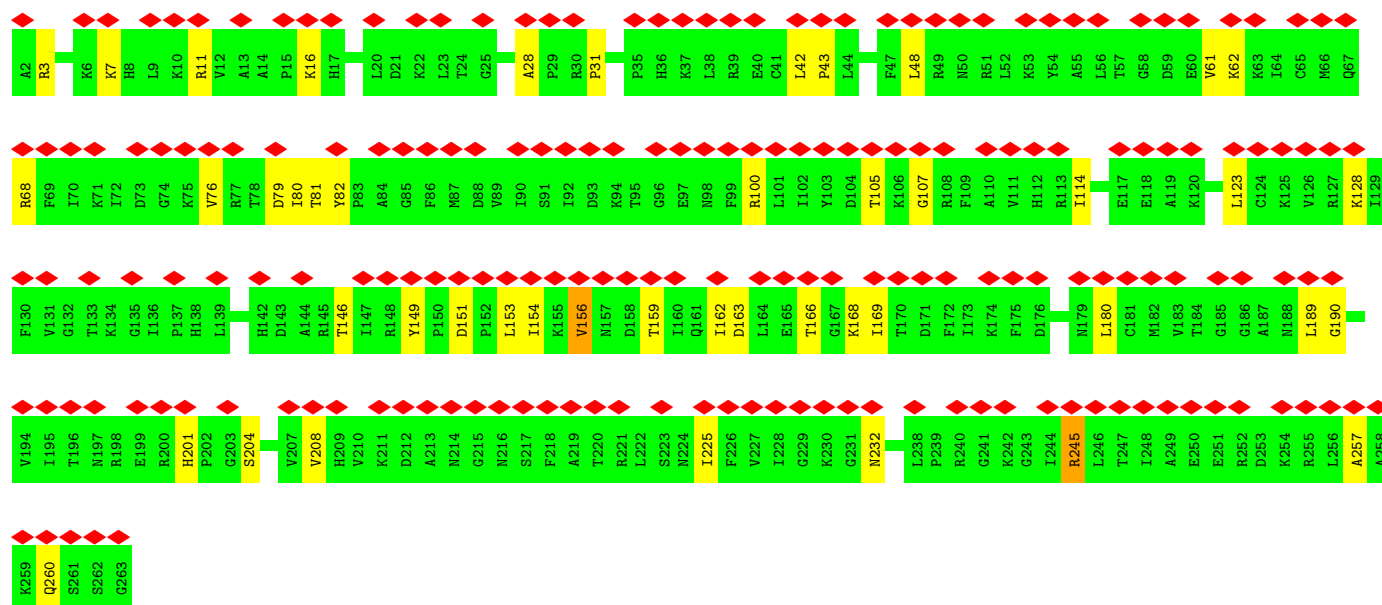


• Molecule 66: 40S ribosomal protein S6

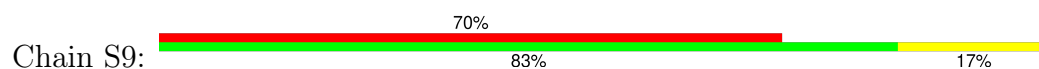


• Molecule 67: 40S ribosomal protein S4

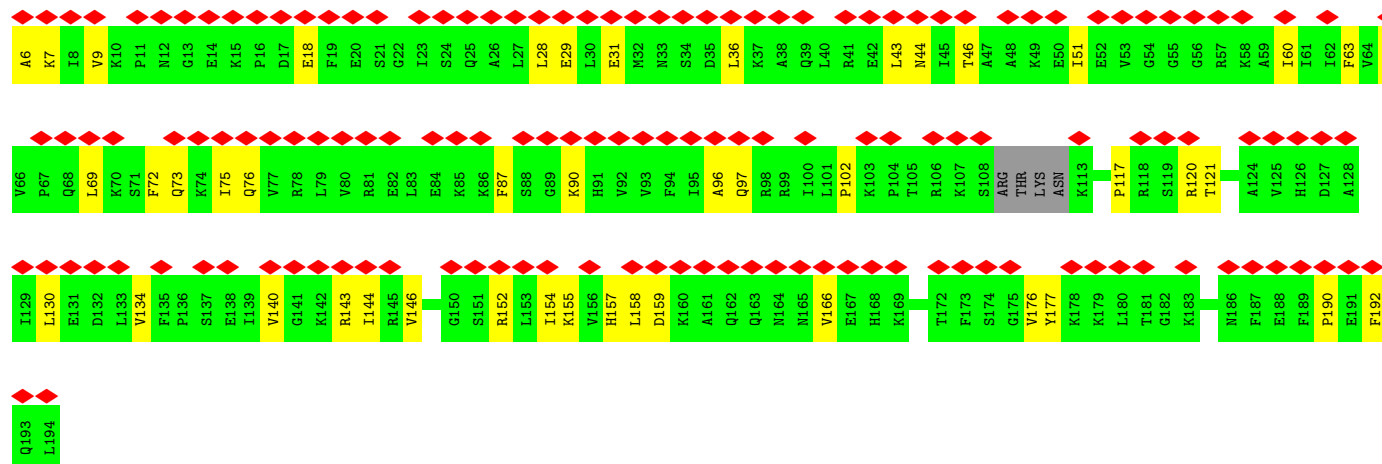
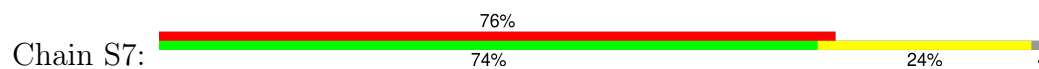




- Molecule 68: 40S ribosomal protein S9



- Molecule 69: Small ribosomal subunit protein eS7



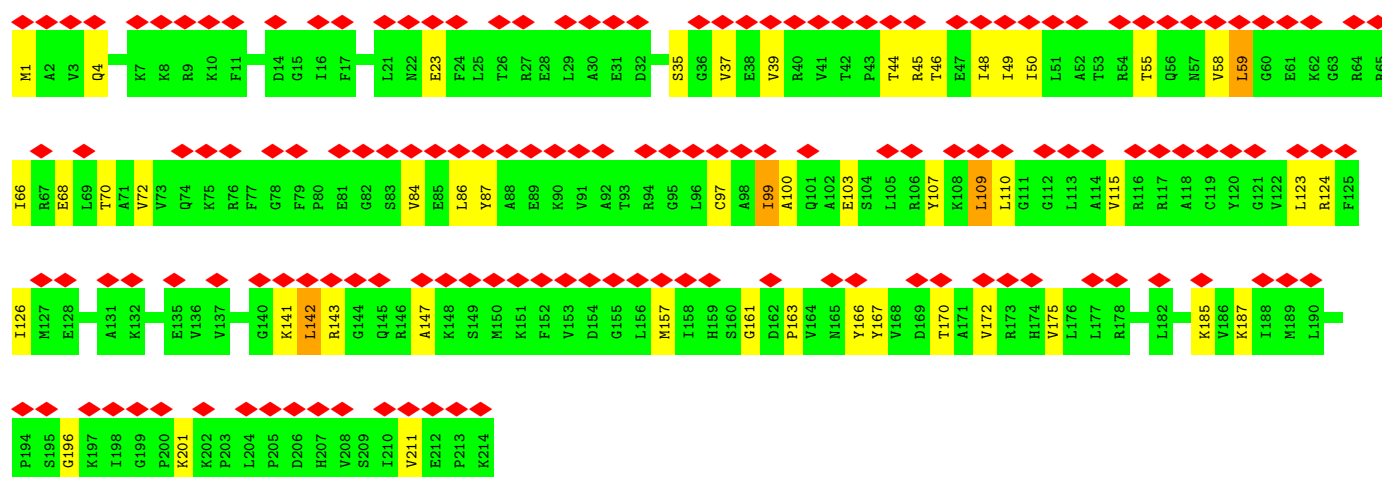
- Molecule 70: 40S ribosomal protein S30

Chain YY: 



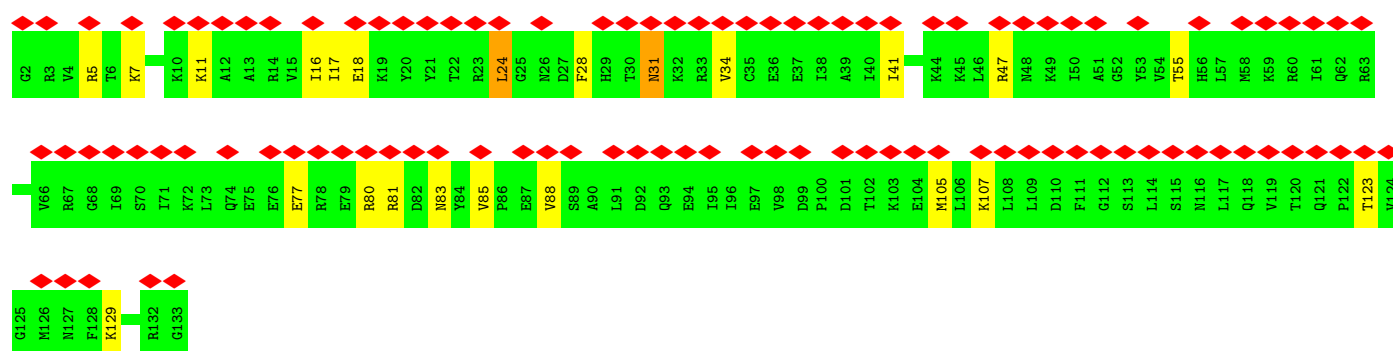
- Molecule 71: Small ribosomal subunit protein uS3

Chain S3: 

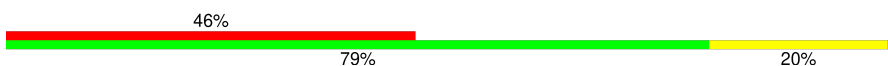


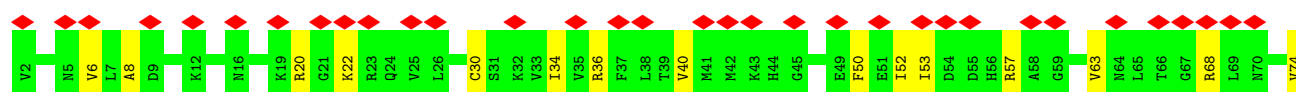
- Molecule 72: 40S ribosomal protein S17

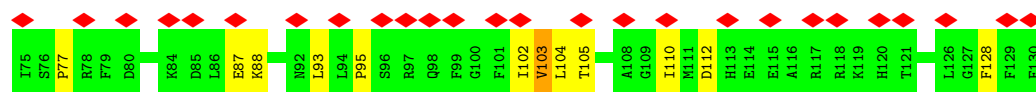
Chain RS: 



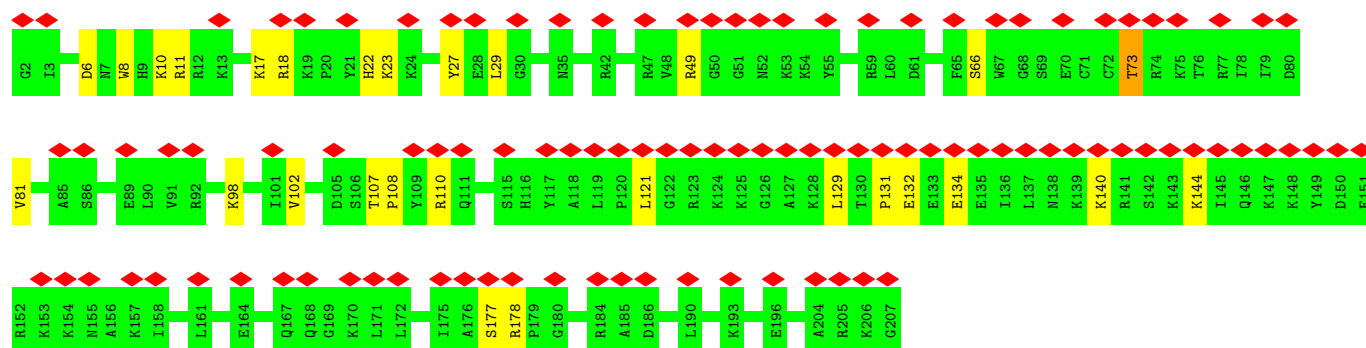
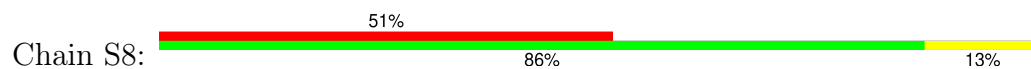
- Molecule 73: 40S ribosomal protein S15a

Chain WX: 

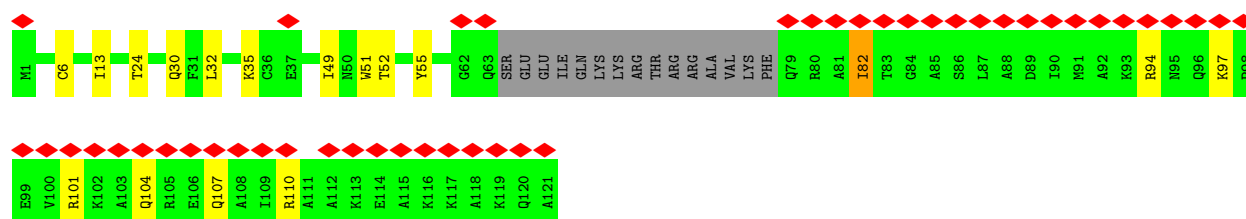
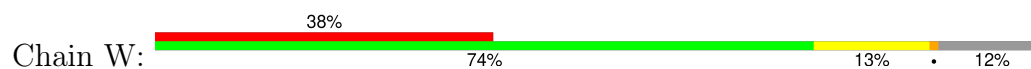




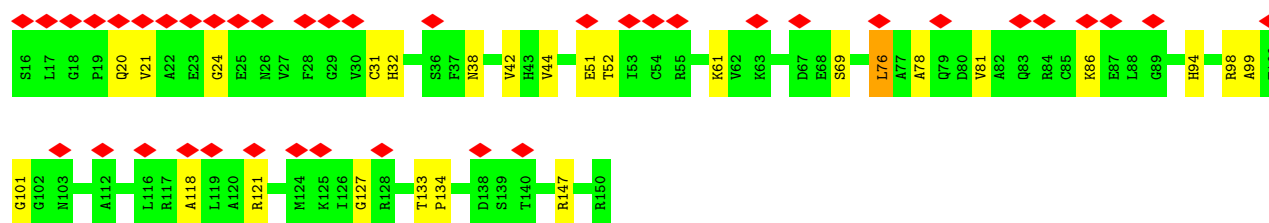
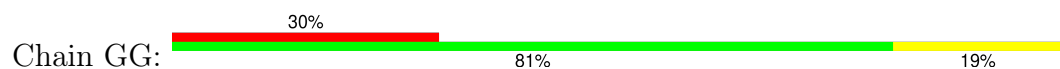
- Molecule 74: 40S ribosomal protein S8



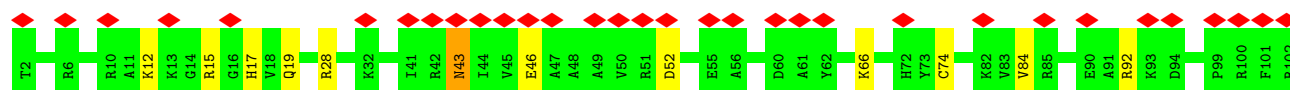
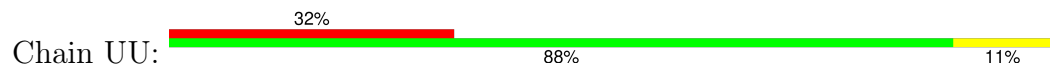
- Molecule 75: Ribosomal protein L24



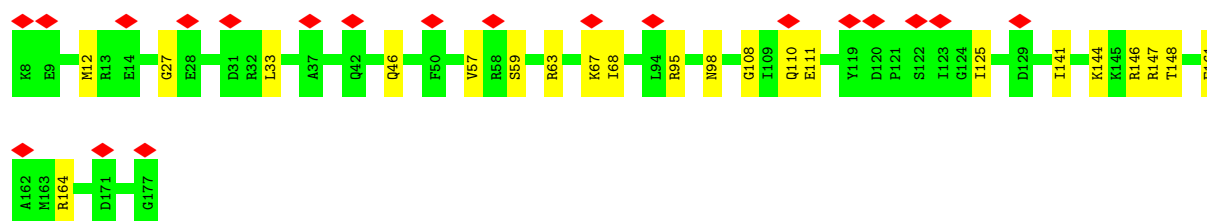
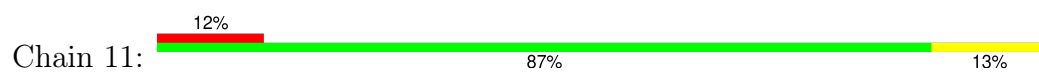
- Molecule 76: Small ribosomal subunit protein uS11



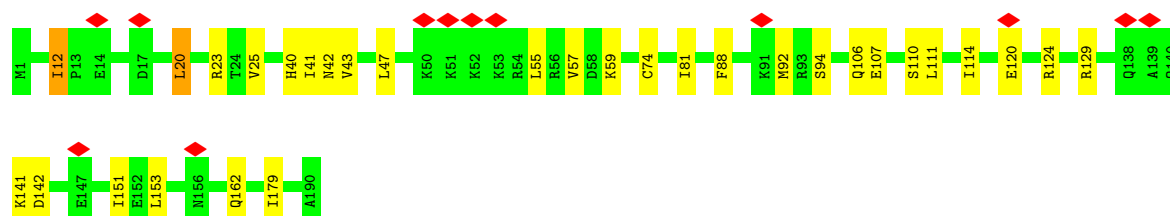
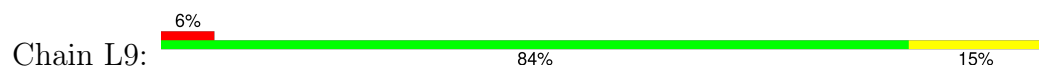
- Molecule 77: eS26



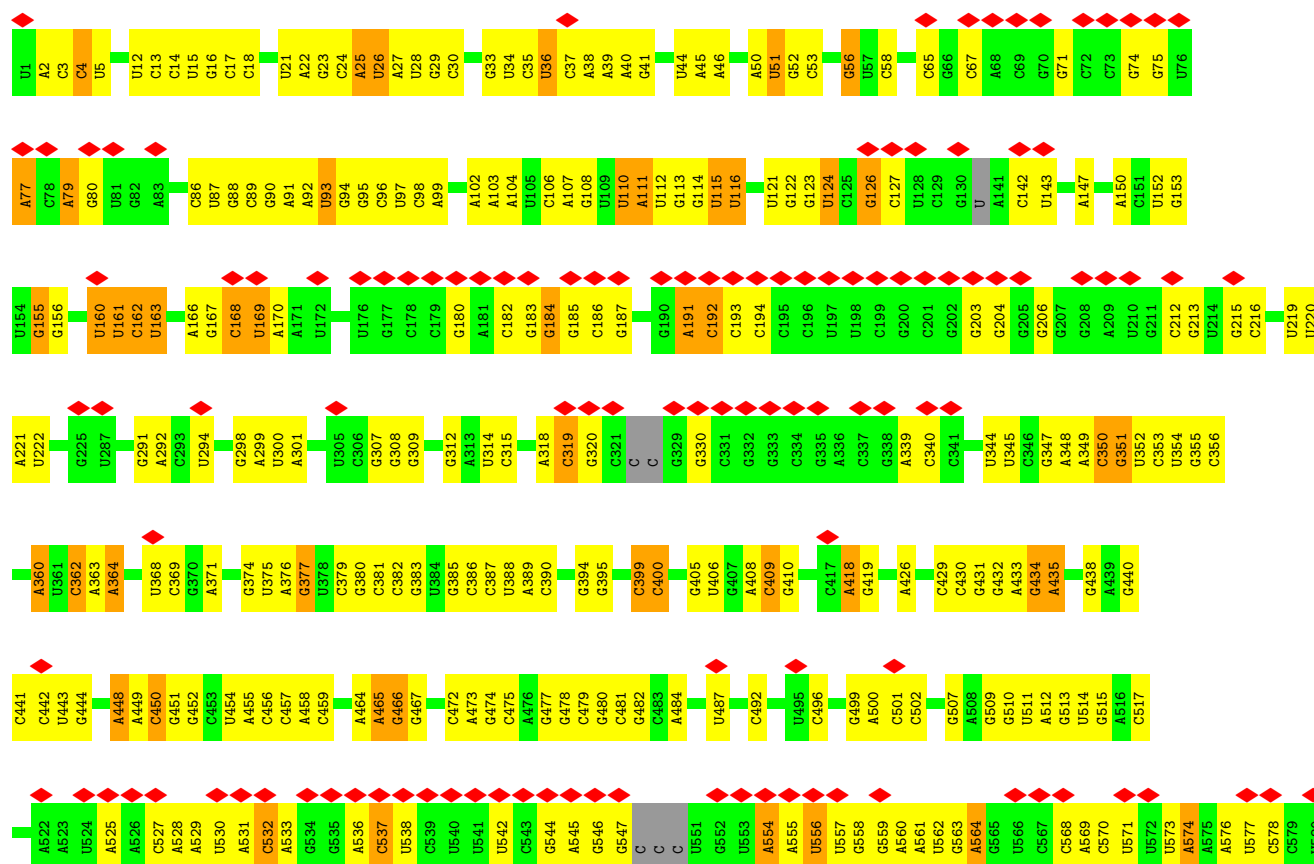
- Molecule 78: 60S ribosomal protein L11

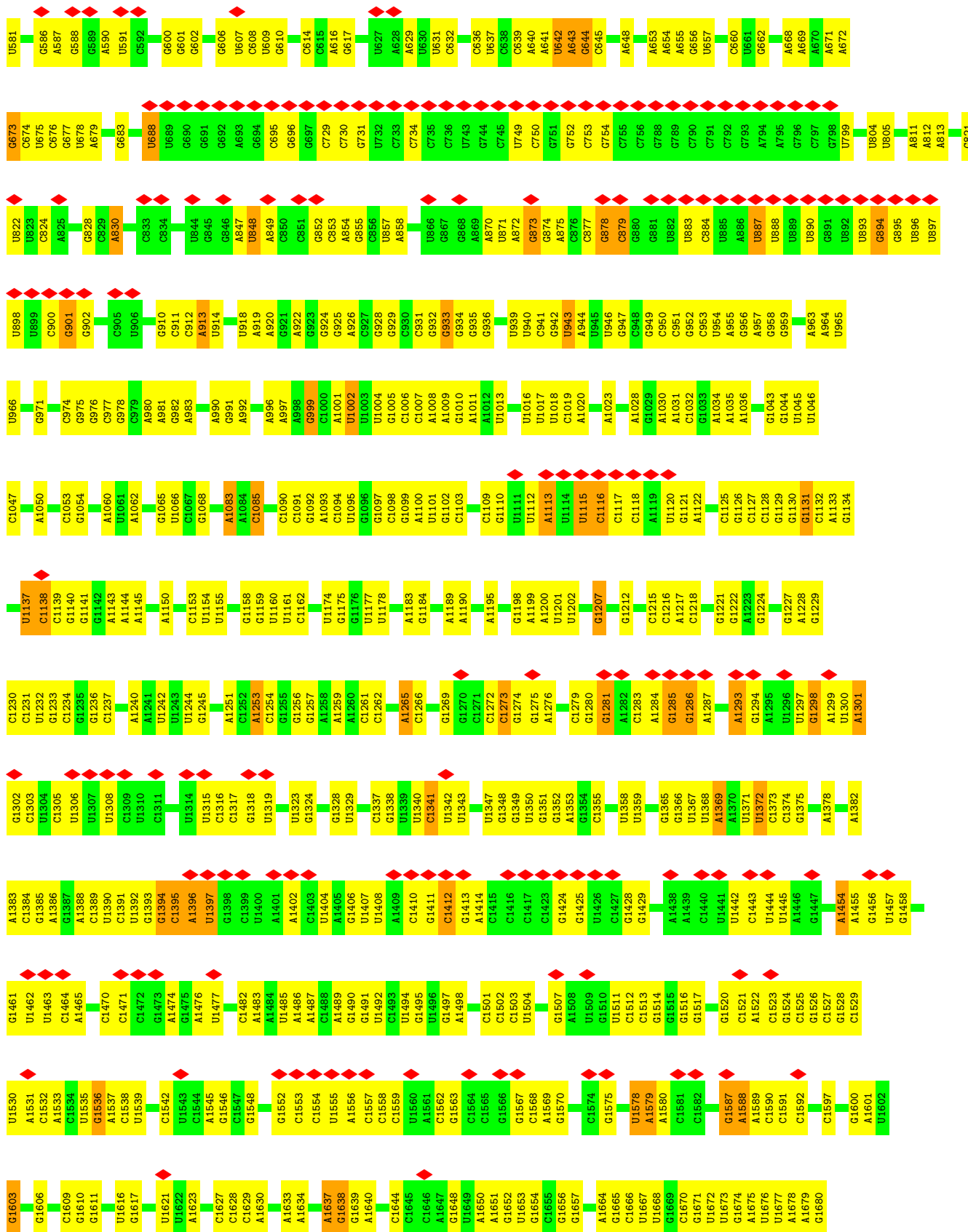


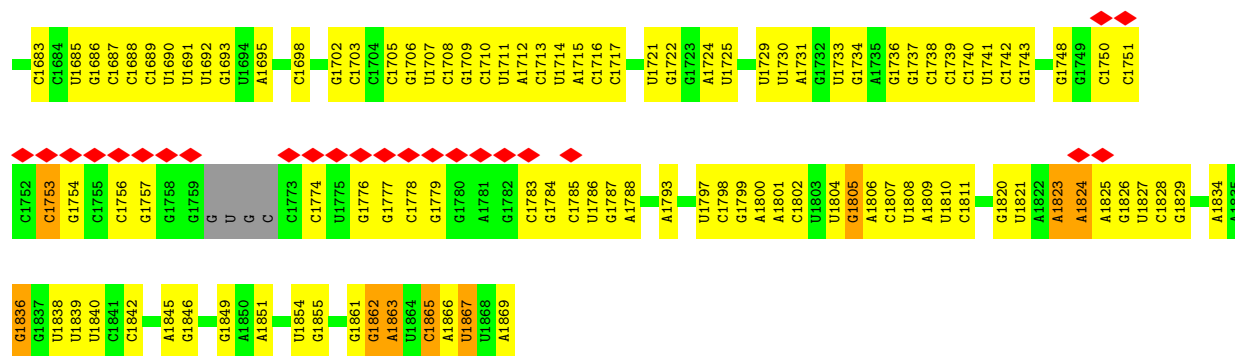
- Molecule 79: 60S ribosomal protein L9



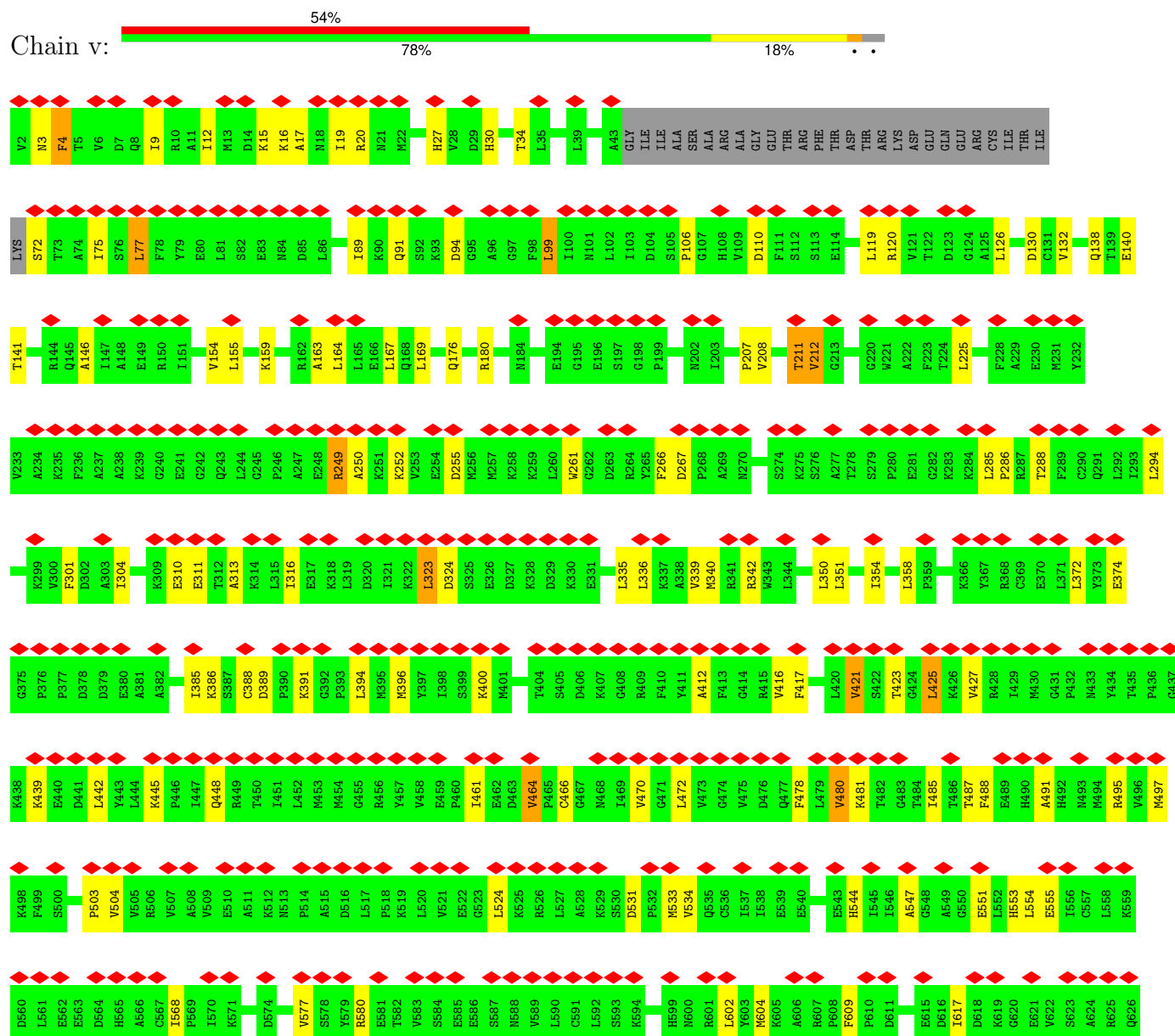
- Molecule 80: 18S rRNA

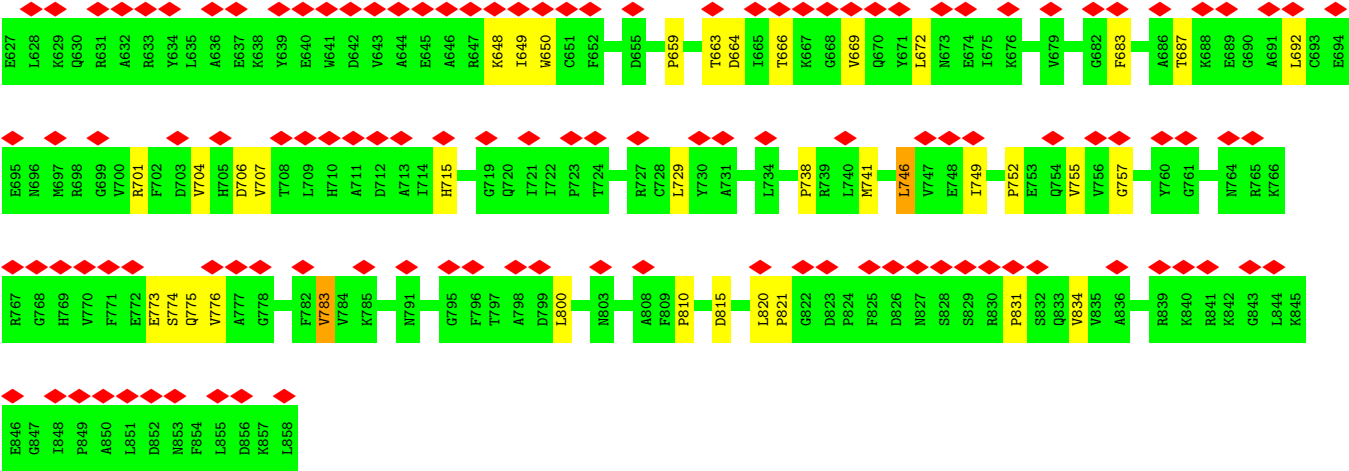




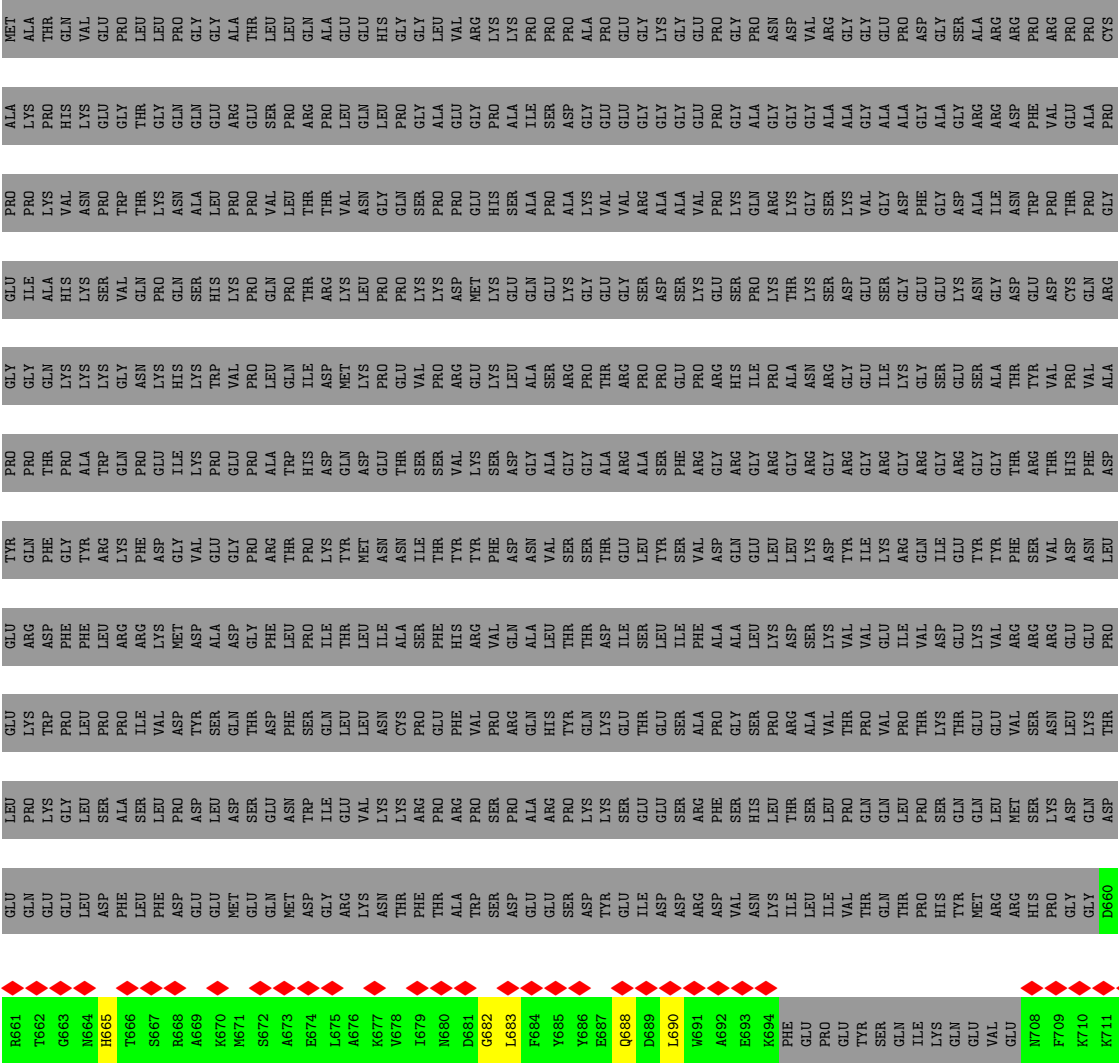


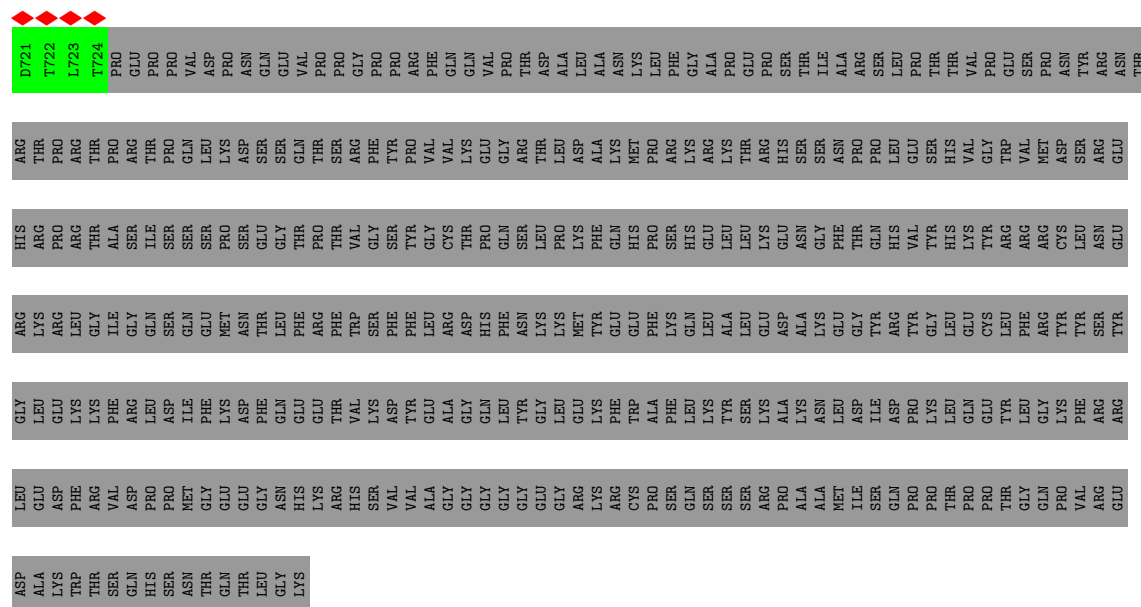
• Molecule 81: Elongation factor 2



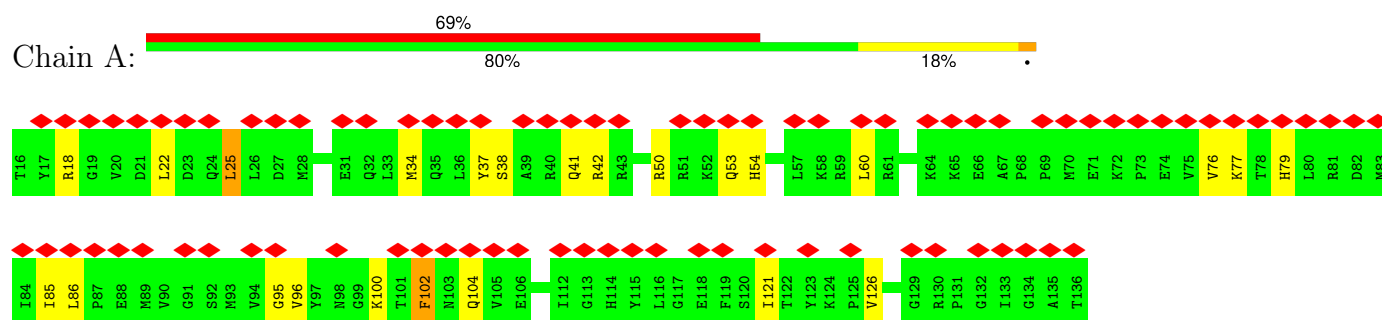


● Molecule 82: LARP1

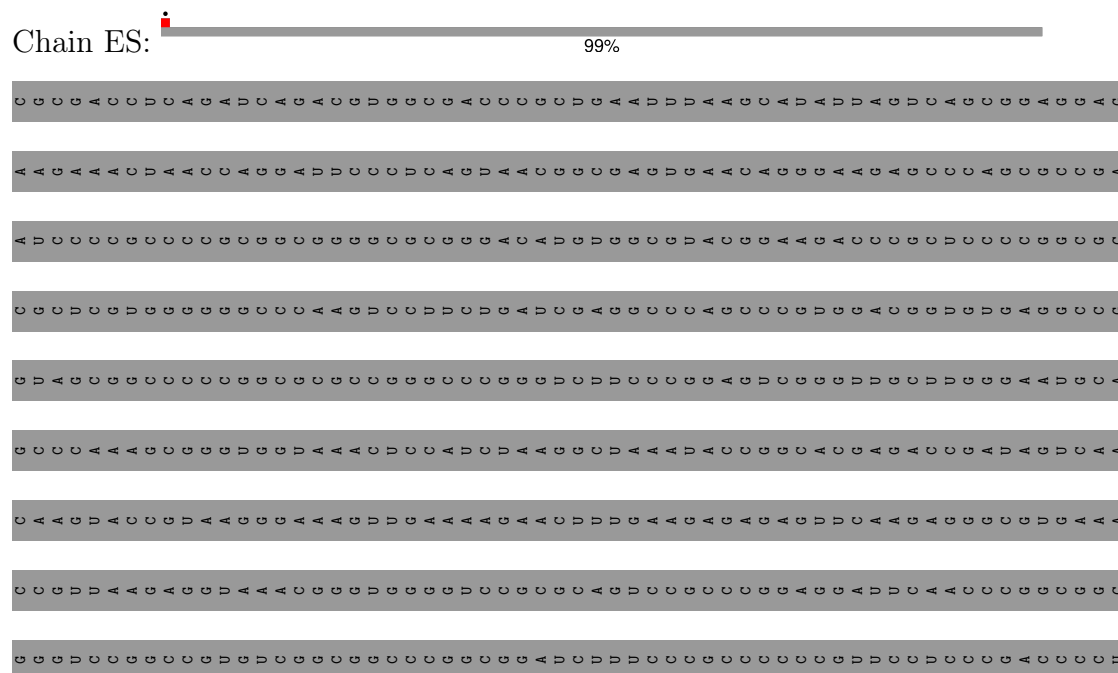




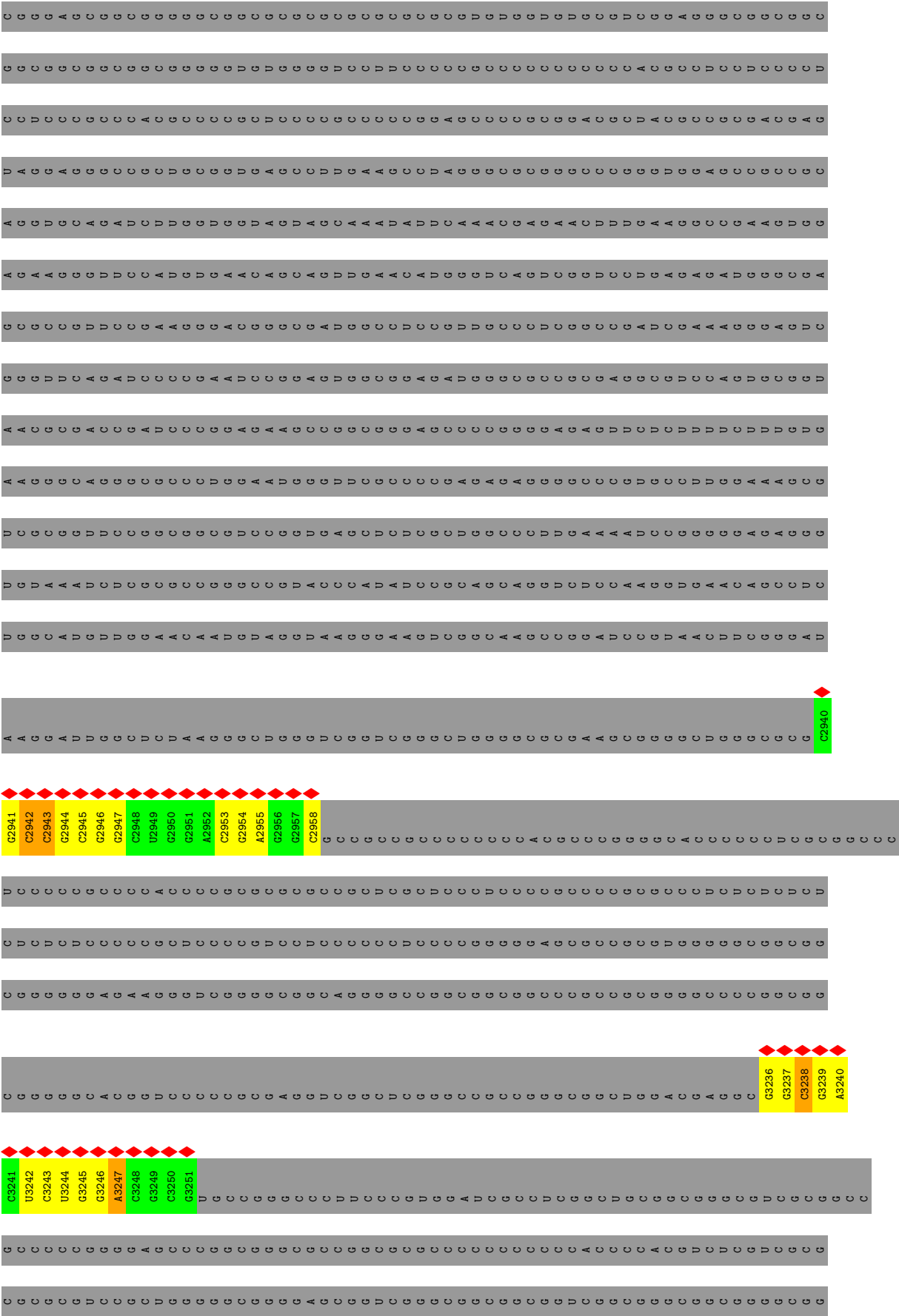
- Molecule 83: Small ribosomal subunit protein uS19



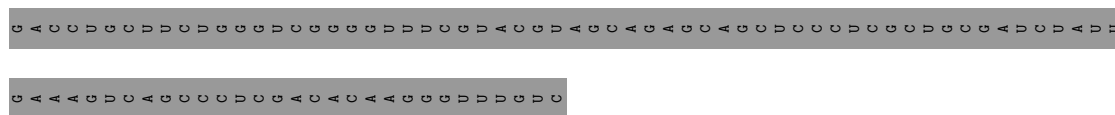
- Molecule 84: ES27L





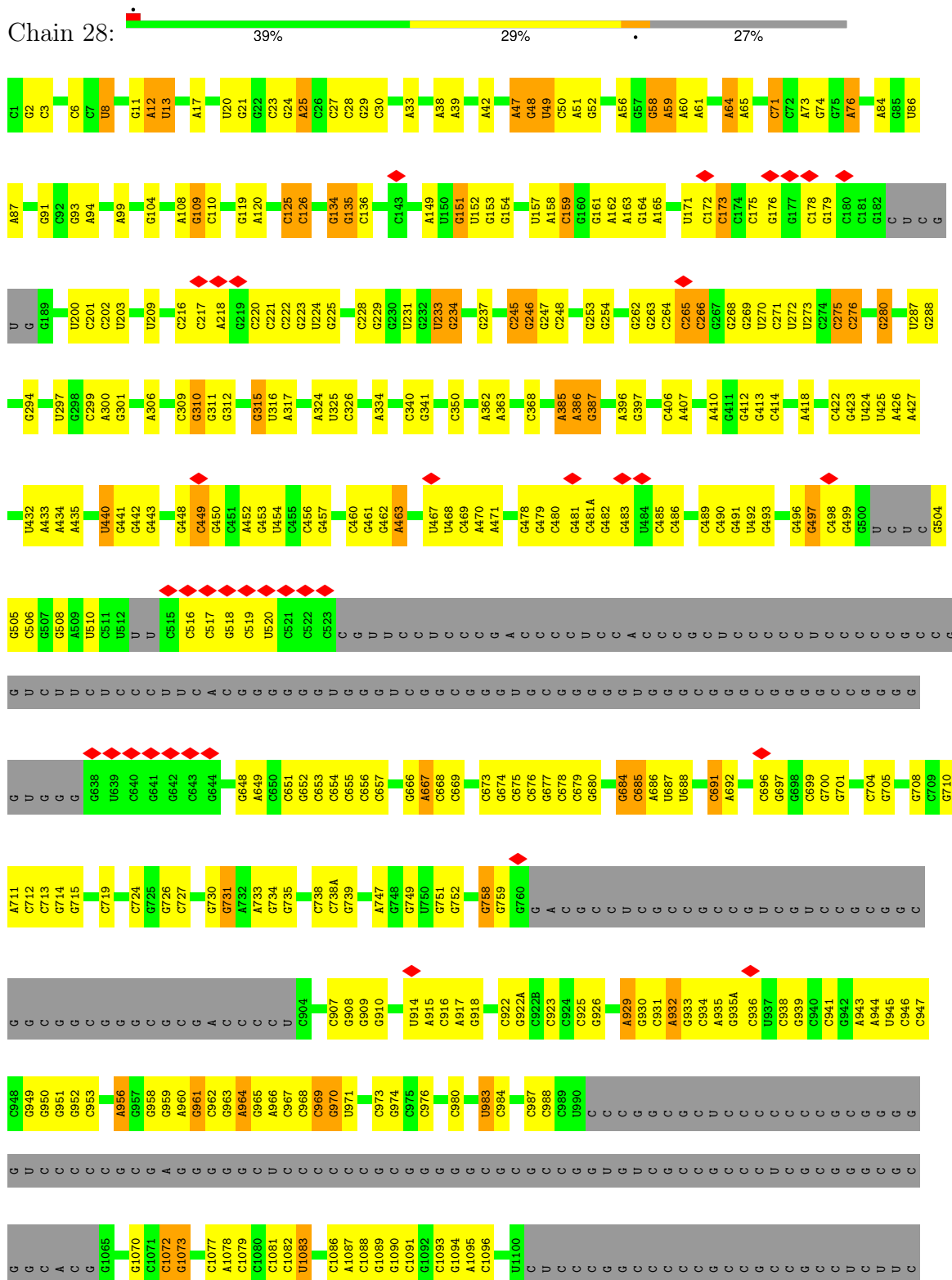






Molecule 85: 28S rRNA

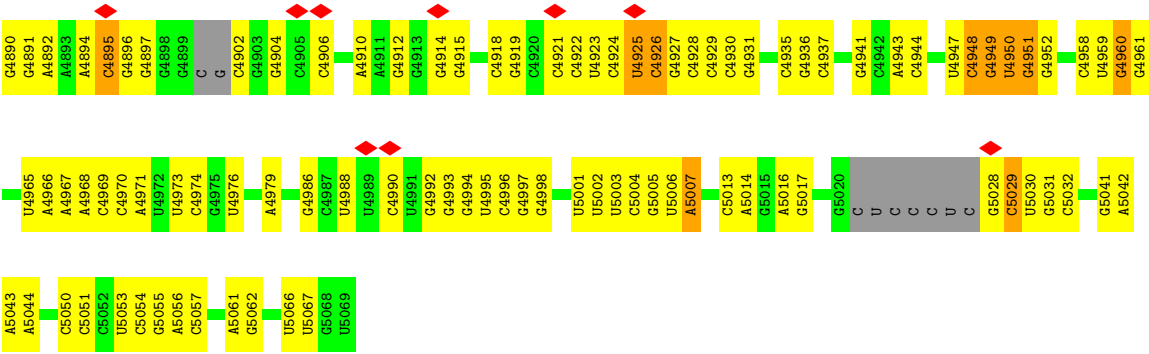
Chain 28:



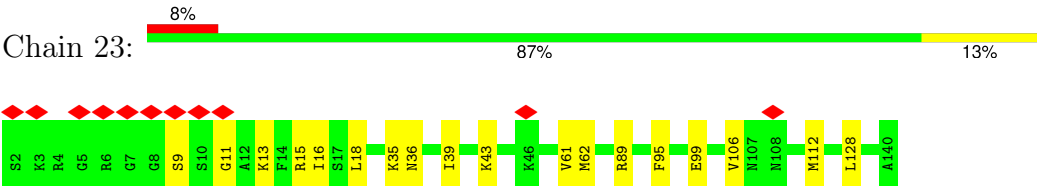








● Molecule 86: Large ribosomal subunit protein uL14



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	16727	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	20.804	Depositor
Minimum map value	-10.773	Depositor
Average map value	0.005	Depositor
Map value standard deviation	0.853	Depositor
Recommended contour level	3.2	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: DDE, ZN, GDP

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	IF	0.31	0/2731	0.66	8/3681 (0.2%)
2	BB	0.13	0/1747	0.35	0/2374
3	S2	0.13	0/1753	0.31	0/2369
4	PP	0.12	0/643	0.29	0/860
5	DD	0.13	0/1195	0.31	0/1597
6	58	0.16	0/3581	0.29	0/5577
7	6	0.16	0/2858	0.26	0/4455
8	L8	0.16	0/1936	0.33	0/2596
9	L3	0.15	0/3240	0.34	0/4339
10	L4	0.15	0/2937	0.32	0/3946
11	L5	0.14	0/2437	0.33	0/3264
12	L6	0.14	0/1762	0.33	0/2362
13	L7	0.15	0/1911	0.29	0/2549
14	aa	0.15	0/1910	0.34	0/2569
15	10	0.14	0/1702	0.31	0/2272
16	13	0.14	0/1733	0.30	0/2316
17	14	0.15	0/1158	0.34	0/1547
18	15	0.16	0/1746	0.32	0/2338
19	bb	0.16	0/1662	0.32	0/2222
20	17	0.15	0/1268	0.33	0/1700
21	19	0.15	0/1524	0.30	0/2013
22	20	0.15	0/1501	0.29	0/2012
23	21	0.13	0/1326	0.28	0/1770
24	22	0.14	0/823	0.36	0/1104
25	cc	0.14	0/984	0.31	0/1323
26	26	0.13	0/1132	0.32	0/1504
27	27	0.13	0/1130	0.29	0/1507
28	dd	0.16	0/1191	0.35	0/1590
29	29	0.14	0/861	0.30	0/1138
30	30	0.13	0/771	0.28	0/1034
31	31	0.16	0/903	0.33	0/1216
32	32	0.15	0/1071	0.33	0/1429

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	ee	0.15	0/895	0.33	0/1198
34	34	0.15	0/916	0.33	0/1220
35	35	0.14	0/1021	0.32	0/1348
36	36	0.13	0/841	0.29	0/1112
37	37	0.15	0/720	0.35	0/952
38	38	0.12	0/575	0.29	0/761
39	39	0.15	0/459	0.31	0/608
40	40	0.12	0/435	0.28	0/575
41	41	0.14	0/240	0.27	0/305
42	42	0.15	0/847	0.31	0/1117
43	ff	0.14	0/718	0.35	0/953
44	gg	0.14	0/1006	0.30	0/1349
45	AS	0.14	0/1756	0.35	0/2350
46	FF	0.14	0/1226	0.36	0/1649
47	VV	0.13	0/665	0.30	0/891
48	s	0.14	0/1530	0.38	0/2064
49	t	0.16	0/1174	0.41	0/1582
50	F	0.20	1/2845 (0.0%)	0.34	0/3828
51	Q	0.15	0/1539	0.37	0/2054
52	ZZ	0.13	0/567	0.35	0/753
53	EE	0.14	0/918	0.36	0/1233
54	TT	0.21	0/604	0.38	1/810 (0.1%)
55	S5	0.14	0/1492	0.37	0/2005
56	WW	0.12	0/490	0.29	0/656
57	II	0.15	0/1146	0.35	0/1534
58	CC	0.15	0/834	0.41	0/1125
59	AA	0.13	0/2493	0.34	0/3394
60	OO	0.13	0/805	0.33	0/1081
61	MM	0.14	0/1115	0.33	0/1493
62	LL	0.14	0/1208	0.39	0/1618
63	XX	0.13	0/470	0.33	0/623
64	RR	0.13	0/1116	0.35	0/1490
65	SS	0.13	0/1028	0.31	0/1366
66	S6	0.14	0/1946	0.36	1/2590 (0.0%)
67	S4	0.21	1/2118 (0.0%)	0.34	0/2849
68	S9	0.14	0/1550	0.33	0/2069
69	S7	0.14	0/1510	0.35	0/2022
70	YY	0.13	0/447	0.34	0/587
71	S3	0.15	0/1688	0.34	0/2269
72	RS	0.13	0/1082	0.34	0/1452
73	WX	0.14	0/1051	0.36	0/1406
74	S8	0.13	0/1715	0.33	0/2287
75	W	0.15	0/873	0.32	0/1158

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	GG	0.13	0/1020	0.35	0/1369
77	UU	0.13	0/828	0.31	0/1109
78	11	0.14	0/1385	0.32	0/1852
79	L9	0.15	0/1535	0.33	0/2063
80	18	0.14	0/40302	0.30	0/62804
81	v	0.13	0/6577	0.33	0/8883
82	LA	0.13	0/426	0.32	0/568
83	A	0.14	0/1001	0.37	0/1339
84	ES	0.17	0/844	0.41	0/1314
85	28	0.17	0/84014	0.31	1/131028 (0.0%)
86	23	0.15	0/1048	0.32	0/1402
All	All	0.16	2/239781 (0.0%)	0.32	11/350090 (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
48	s	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
50	F	204	ASN	C-O	-7.68	1.20	1.23
67	S4	149	TYR	C-O	7.15	1.27	1.23

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	IF	337	LEU	O-C-N	15.62	140.49	122.22
1	IF	337	LEU	CA-C-N	-12.08	103.14	120.29
1	IF	337	LEU	C-N-CA	-12.08	103.14	120.29
1	IF	328	ARG	N-CA-C	8.86	123.19	112.38
1	IF	320	TYR	O-C-N	8.37	133.18	122.39
1	IF	327	ARG	NE-CZ-NH2	6.05	124.65	119.20
66	S6	67	VAL	N-CA-C	-5.66	108.33	113.71
1	IF	330	ARG	NE-CZ-NH2	5.16	123.84	119.20
54	TT	88	LEU	N-CA-C	-5.07	108.84	114.62
85	28	3904	G	C2'-C3'-O3'	5.01	117.02	109.50
1	IF	330	ARG	NE-CZ-NH1	-5.00	116.50	121.50

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
48	s	119	CYS	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	IF	2692	0	2763	93	0
2	BB	1710	0	1708	22	0
3	S2	1716	0	1806	27	0
4	PP	636	0	637	5	0
5	DD	1175	0	1249	12	0
6	58	3208	0	1629	55	0
7	6	2558	0	1296	30	0
8	L8	1898	0	1993	25	0
9	L3	3172	0	3310	31	0
10	L4	2883	0	3053	28	0
11	L5	2391	0	2424	27	0
12	L6	1729	0	1887	16	0
13	L7	1875	0	1995	25	0
14	aa	1879	0	2027	20	0
15	10	1664	0	1712	13	0
16	13	1702	0	1820	15	0
17	14	1137	0	1211	14	0
18	15	1701	0	1749	22	0
19	bb	1630	0	1778	20	0
20	17	1242	0	1274	9	0
21	19	1508	0	1664	12	0
22	20	1462	0	1508	15	0
23	21	1298	0	1366	10	0
24	22	809	0	833	4	0
25	cc	967	0	1040	11	0
26	26	1115	0	1205	10	0
27	27	1107	0	1182	14	0
28	dd	1162	0	1209	18	0
29	29	848	0	920	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	30	761	0	794	10	0
31	31	888	0	930	8	0
32	32	1053	0	1147	7	0
33	ee	876	0	912	11	0
34	34	906	0	1000	5	0
35	35	1013	0	1147	8	0
36	36	830	0	916	5	0
37	37	705	0	738	4	0
38	38	569	0	637	2	0
39	39	447	0	480	10	0
40	40	429	0	469	2	0
41	41	239	0	289	2	0
42	42	834	0	905	10	0
43	ff	708	0	758	7	0
44	gg	990	0	1044	7	0
45	AS	1729	0	1803	31	0
46	FF	1202	0	1289	11	0
47	VV	651	0	672	7	0
48	s	1507	0	1564	11	0
49	t	1160	0	1218	24	0
50	F	2798	0	2809	37	0
51	Q	1515	0	1634	14	0
52	ZZ	555	0	567	9	0
53	EE	908	0	939	10	0
54	TT	598	0	656	6	0
55	S5	1471	0	1522	15	0
56	WW	488	0	514	4	0
57	II	1128	0	1195	17	0
58	CC	810	0	836	12	0
59	AA	2436	0	2393	36	0
60	OO	795	0	862	10	0
61	MM	1097	0	1132	18	0
62	LL	1190	0	1249	18	0
63	XX	459	0	452	4	0
64	RR	1098	0	1167	21	0
65	SS	1011	0	1083	18	0
66	S6	1923	0	2089	25	0
67	S4	2076	0	2177	25	0
68	S9	1525	0	1640	19	0
69	S7	1488	0	1582	23	0
70	YY	443	0	492	5	0
71	S3	1662	0	1760	27	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
72	RS	1068	0	1121	11	0
73	WX	1034	0	1080	17	0
74	S8	1686	0	1772	18	0
75	W	860	0	903	10	0
76	GG	1007	0	1028	16	0
77	UU	814	0	865	9	0
78	11	1362	0	1399	12	0
79	L9	1516	0	1597	16	0
80	18	36043	0	18202	636	0
81	v	6470	0	6548	77	0
82	LA	421	0	405	2	0
83	A	983	0	1030	10	0
84	ES	756	0	384	20	0
85	28	75105	0	37942	1058	0
86	23	1034	0	1097	10	0
87	34	1	0	0	0	0
87	37	1	0	0	0	0
87	UU	1	0	0	0	0
87	ff	1	0	0	0	0
88	v	28	0	12	1	0
All	All	224036	0	171095	2811	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

All (2811) 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:IF:350:VAL:CG1	1:IF:357:LEU:HB3	1.67	1.25
1:IF:350:VAL:HG13	1:IF:357:LEU:HB3	1.31	1.12
1:IF:349:ILE:H	1:IF:349:ILE:HD13	1.23	1.03
1:IF:116:ARG:HG3	1:IF:117:LEU:N	1.72	1.03
1:IF:400:LEU:H	1:IF:400:LEU:HD13	1.28	0.99
1:IF:215:PHE:CE2	1:IF:235:LEU:HD21	1.99	0.98
80:18:677:G:H21	80:18:1028:A:H62	1.18	0.90
1:IF:278:ILE:HG23	1:IF:332:THR:HG21	1.50	0.89
1:IF:116:ARG:NH1	1:IF:116:ARG:HB2	1.87	0.89
62:LL:37:GLY:H	80:18:1630:A:H5'	1.38	0.89
1:IF:215:PHE:CD1	1:IF:227:VAL:HG22	2.07	0.88
80:18:639:C:H2'	80:18:640:A:H8	1.38	0.88
1:IF:215:PHE:HD1	1:IF:227:VAL:HG22	1.38	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:IF:116:ARG:HH22	1:IF:158:LEU:HB2	1.37	0.88
80:18:730:C:H2'	80:18:731:G:C8	2.09	0.86
85:28:2492:C:H2'	85:28:2493:G:H8	1.40	0.86
85:28:2457:G:H21	85:28:3672:G:H21	1.24	0.85
85:28:2478:C:H2'	85:28:2479:G:H8	1.41	0.84
85:28:4949:G:H4'	85:28:4950:U:H5'	1.58	0.84
1:IF:116:ARG:HD2	1:IF:154:LYS:HD2	1.59	0.83
85:28:3751:G:H21	85:28:3775:A:H8	1.23	0.83
58:CC:64:TRP:HB3	63:XX:23:VAL:HA	1.60	0.82
85:28:2486:G:H2'	85:28:2487:G:C8	2.15	0.82
1:IF:350:VAL:HB	1:IF:359:MET:HE1	1.62	0.82
1:IF:116:ARG:NH2	1:IF:158:LEU:HB2	1.95	0.81
85:28:3717:A:H2'	85:28:3718:A:H8	1.41	0.81
85:28:4618:G:H5''	86:23:15:ARG:HB3	1.63	0.80
85:28:2492:C:H2'	85:28:2493:G:C8	2.17	0.80
18:15:125:SER:HB3	85:28:3937:C:H1'	1.63	0.80
6:58:85:U:H5''	6:58:86:U:H3'	1.64	0.80
80:18:639:C:H2'	80:18:640:A:C8	2.17	0.80
80:18:957:A:H3'	80:18:958:G:H21	1.46	0.80
80:18:1410:C:H2'	80:18:1411:G:H8	1.47	0.79
85:28:1970:A:H5''	85:28:1971:U:H5'	1.65	0.79
85:28:2411:C:H2'	85:28:2412:A:H8	1.48	0.79
85:28:3717:A:H2'	85:28:3718:A:C8	2.19	0.78
81:v:17:ALA:HB3	81:v:94:ASP:HB2	1.64	0.78
53:EE:32:ALA:HB1	53:EE:37:GLU:HB3	1.66	0.77
80:18:1486:A:H2'	80:18:1487:A:H8	1.48	0.77
80:18:116:U:H3	80:18:347:G:H1	1.29	0.77
2:BB:66:VAL:HG21	2:BB:185:MET:HB3	1.65	0.77
85:28:1198:G:H2'	85:28:1199:G:C8	2.20	0.77
1:IF:400:LEU:HD13	1:IF:400:LEU:N	2.00	0.77
80:18:530:U:H2'	80:18:531:A:H8	1.50	0.76
85:28:1857:C:H2'	85:28:1858:A:H8	1.48	0.76
85:28:4992:G:H2'	85:28:4993:G:C8	2.20	0.76
85:28:1538:U:H2'	85:28:1539:G:H8	1.51	0.76
1:IF:215:PHE:HE2	1:IF:235:LEU:HD21	1.51	0.76
85:28:2478:C:H2'	85:28:2479:G:C8	2.20	0.76
67:S4:201:HIS:HB3	67:S4:204:SER:HB3	1.68	0.75
1:IF:400:LEU:H	1:IF:400:LEU:CD1	1.98	0.75
8:L8:234:LYS:HG2	8:L8:238:ILE:HD12	1.68	0.75
80:18:1536:G:H2'	80:18:1537:A:H8	1.51	0.75
85:28:2335:C:H2'	85:28:2336:G:H8	1.50	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
79:L9:43:VAL:HG12	79:L9:59:LYS:HD3	1.69	0.75
58:CC:61:GLN:HB3	58:CC:68:TYR:HB2	1.68	0.75
1:IF:116:ARG:HG3	1:IF:117:LEU:H	1.50	0.74
85:28:2707:U:H3'	85:28:2708:U:H5''	1.69	0.74
80:18:730:C:H2'	80:18:731:G:H8	1.53	0.74
80:18:1004:U:H2'	80:18:1005:G:H8	1.52	0.74
85:28:2477:A:H2'	85:28:2478:C:C6	2.22	0.74
67:S4:163:ASP:HB3	67:S4:166:THR:HG22	1.68	0.74
85:28:4967:A:H2'	85:28:4968:A:H8	1.50	0.74
34:34:60:ARG:HG3	34:34:61:PRO:HD2	1.70	0.74
80:18:1670:C:H2'	80:18:1671:G:C8	2.22	0.74
52:ZZ:132:MET:HG3	52:ZZ:139:HIS:HB3	1.68	0.73
81:v:267:ASP:HA	81:v:285:LEU:HD11	1.70	0.73
81:v:354:ILE:HG23	81:v:358:LEU:HD12	1.70	0.73
80:18:1711:U:H2'	80:18:1712:A:H8	1.53	0.73
1:IF:215:PHE:CD2	1:IF:235:LEU:HD11	2.23	0.73
66:S6:58:LYS:HA	66:S6:107:SER:HB2	1.71	0.73
85:28:2745:A:H2'	85:28:2746:A:H8	1.53	0.73
20:17:118:GLN:HE22	85:28:423:G:H21	1.35	0.72
81:v:604:MET:HE3	81:v:704:VAL:HG12	1.69	0.72
85:28:1332:C:H2'	85:28:1333:A:H8	1.52	0.72
80:18:941:C:H2'	80:18:942:G:C8	2.24	0.72
59:AA:87:LEU:HB2	59:AA:101:PHE:HB2	1.70	0.72
80:18:640:A:H2'	80:18:641:A:C8	2.24	0.72
85:28:1169:G:H2'	85:28:1170:G:H8	1.54	0.72
85:28:2480:G:H2'	85:28:2481:G:C8	2.24	0.72
85:28:3868:G:H22	85:28:3900:G:H1'	1.55	0.72
14:aa:111:PRO:HD2	14:aa:114:ILE:HD12	1.71	0.72
81:v:488:PHE:HB3	81:v:491:ALA:HB2	1.71	0.72
64:RR:61:GLN:HB3	64:RR:62:PRO:HD3	1.71	0.71
80:18:1776:G:H2'	80:18:1777:G:H8	1.54	0.71
85:28:1769:G:H2'	85:28:1770:A:C8	2.24	0.71
58:CC:64:TRP:HE1	71:S3:23:GLU:HG2	1.55	0.71
81:v:77:LEU:HD21	81:v:351:LEU:HD21	1.73	0.71
85:28:1197:C:H2'	85:28:1198:G:C8	2.26	0.71
80:18:1711:U:H2'	80:18:1712:A:C8	2.25	0.71
16:13:8:MET:HG3	51:Q:166:TYR:HB3	1.72	0.71
69:S7:134:VAL:HG13	69:S7:166:VAL:HG21	1.73	0.71
80:18:1098:C:H2'	80:18:1099:G:C8	2.25	0.71
85:28:2744:A:H2'	85:28:2745:A:C8	2.25	0.71
21:19:162:ARG:HB3	80:18:873:G:H5'	1.71	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:18:1221:G:H2'	80:18:1222:G:H8	1.55	0.71
68:S9:5:ARG:HD3	80:18:38:A:H5''	1.71	0.70
81:v:531:ASP:HB3	81:v:534:VAL:HG22	1.73	0.70
80:18:894:G:H2'	80:18:895:G:H8	1.55	0.70
80:18:75:G:H21	80:18:77:A:H5''	1.57	0.70
80:18:1101:U:H2'	80:18:1102:G:H8	1.57	0.70
67:S4:31:PRO:HG3	67:S4:43:PRO:HG3	1.74	0.70
80:18:511:U:H2'	80:18:512:A:H8	1.56	0.70
50:F:57:MET:HE3	50:F:74:ILE:HG13	1.73	0.70
80:18:1776:G:H2'	80:18:1777:G:C8	2.27	0.70
85:28:4761:G:H2'	85:28:4762:A:H8	1.57	0.70
67:S4:11:ARG:HA	67:S4:28:ALA:HB2	1.74	0.70
71:S3:37:VAL:HG12	71:S3:50:ILE:HA	1.72	0.70
80:18:58:C:H5''	80:18:499:G:H21	1.56	0.70
85:28:4967:A:H2'	85:28:4968:A:C8	2.27	0.70
75:W:101:ARG:HA	75:W:104:GLN:HG2	1.72	0.70
80:18:1486:A:H2'	80:18:1487:A:C8	2.26	0.70
1:IF:350:VAL:HG13	1:IF:350:VAL:O	1.89	0.70
51:Q:78:LYS:HG2	51:Q:137:VAL:HG23	1.74	0.70
84:ES:3238:C:H2'	84:ES:3239:G:H8	1.57	0.70
85:28:4321:U:H2'	85:28:4322:G:C8	2.27	0.70
25:cc:93:ASN:HB3	25:cc:95:THR:HG23	1.74	0.69
85:28:2520:C:H2'	85:28:2521:G:H8	1.56	0.69
1:IF:330:ARG:NH1	80:18:965:U:OP1	2.24	0.69
85:28:4537:C:H2'	85:28:4538:G:H8	1.57	0.69
80:18:1410:C:H2'	80:18:1411:G:C8	2.27	0.69
85:28:1086:C:H2'	85:28:1087:A:H8	1.58	0.69
50:F:57:MET:HE1	50:F:73:GLY:HA2	1.73	0.69
80:18:1692:U:H2'	80:18:1693:G:C8	2.28	0.69
50:F:190:LEU:HB2	50:F:223:VAL:HG23	1.74	0.69
84:ES:3239:G:H2'	84:ES:3240:A:H8	1.57	0.69
85:28:1461:C:H2'	85:28:1462:A:H8	1.56	0.68
1:IF:215:PHE:CD2	1:IF:235:LEU:HD21	2.28	0.68
80:18:1007:C:H2'	80:18:1008:A:C8	2.28	0.68
85:28:2607:C:H2'	85:28:2608:G:H8	1.57	0.68
80:18:300:U:H2'	80:18:301:A:C8	2.29	0.68
85:28:1327:C:H2'	85:28:1328:G:H8	1.57	0.68
11:L5:4:VAL:HG11	85:28:4247:G:H5''	1.76	0.68
80:18:1536:G:H2'	80:18:1537:A:C8	2.29	0.68
85:28:2486:G:H2'	85:28:2487:G:H8	1.58	0.68
59:AA:17:TRP:HA	59:AA:305:ASN:HA	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
79:L9:12:ILE:HG22	79:L9:81:ILE:HD11	1.75	0.68
85:28:1358:G:N2	85:28:1381:U:O4	2.27	0.68
80:18:928:G:H1	80:18:1013:U:H3	1.42	0.68
84:ES:2946:G:H2'	84:ES:2947:G:C8	2.29	0.68
12:L6:165:VAL:HG13	12:L6:180:GLY:N	2.08	0.67
22:20:147:ASP:HB3	22:20:150:ILE:HB	1.75	0.67
80:18:1144:A:H5'	80:18:1355:C:H41	1.59	0.67
85:28:1414:C:H2'	85:28:1415:G:C8	2.28	0.67
85:28:2411:C:H2'	85:28:2412:A:C8	2.29	0.67
1:IF:215:PHE:CD2	1:IF:235:LEU:CD1	2.77	0.67
81:v:464:VAL:HG11	81:v:470:VAL:HG11	1.76	0.67
85:28:1344:C:H2'	85:28:1345:A:H8	1.56	0.67
32:32:90:MET:HG3	44:gg:33:LYS:HA	1.76	0.67
45:AS:110:MET:HA	45:AS:113:MET:HE2	1.75	0.67
54:TT:48:VAL:HG23	54:TT:49:LEU:HG	1.75	0.67
67:S4:107:GLY:HA2	67:S4:189:LEU:HD23	1.76	0.67
51:Q:67:ILE:HD12	51:Q:96:PRO:HD2	1.76	0.67
85:28:1306:C:H2'	85:28:1307:A:H8	1.59	0.67
1:IF:193:VAL:HG11	1:IF:388:LEU:HD21	1.77	0.67
10:L4:60:HIS:HE1	10:L4:100:ARG:HD3	1.60	0.67
17:14:40:GLY:HA3	17:14:45:VAL:HB	1.76	0.67
80:18:640:A:H2'	80:18:641:A:H8	1.59	0.67
85:28:1669:A:H4'	85:28:1685:G:N2	2.10	0.67
85:28:1942:A:H2'	85:28:1943:A:C8	2.28	0.67
50:F:159:PRO:HD3	50:F:325:LEU:HD11	1.76	0.67
61:MM:124:THR:HG23	61:MM:127:GLY:H	1.59	0.67
80:18:1244:U:H2'	80:18:1245:G:H8	1.59	0.67
85:28:2448:G:H2'	85:28:2449:A:C8	2.30	0.67
85:28:4896:G:H2'	85:28:4897:G:H8	1.60	0.67
85:28:4134:C:H2'	85:28:4135:G:H8	1.58	0.67
85:28:4274:A:H2'	85:28:4275:G:H8	1.60	0.67
85:28:1190:C:H2'	85:28:1191:C:C6	2.29	0.67
11:L5:83:LEU:HB3	11:L5:88:VAL:HB	1.77	0.66
80:18:874:G:H2'	80:18:875:A:H8	1.60	0.66
1:IF:215:PHE:CE1	1:IF:227:VAL:HG13	2.31	0.66
26:26:30:MET:HB3	26:26:101:PRO:HG2	1.77	0.66
80:18:981:A:H2'	80:18:982:G:C8	2.30	0.66
12:L6:165:VAL:HG11	12:L6:178:VAL:HG13	1.77	0.66
51:Q:178:ARG:HA	51:Q:184:ARG:HB3	1.77	0.66
80:18:1424:G:H2'	80:18:1425:G:H8	1.60	0.66
76:GG:21:VAL:HG22	76:GG:24:GLY:H	1.59	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:28:4260:U:H2'	85:28:4261:C:C6	2.31	0.66
85:28:4319:C:H2'	85:28:4320:G:H8	1.61	0.66
1:IF:349:ILE:H	1:IF:349:ILE:CD1	2.06	0.66
1:IF:215:PHE:CD2	1:IF:235:LEU:CD2	2.79	0.66
68:S9:136:ARG:HE	68:S9:139:LYS:HA	1.61	0.66
85:28:1683:U:H2'	85:28:1684:A:C8	2.31	0.66
1:IF:105:SER:HA	1:IF:378:GLY:HA3	1.77	0.65
85:28:1327:C:H2'	85:28:1328:G:C8	2.31	0.65
85:28:3848:U:H2'	85:28:3849:A:H8	1.61	0.65
1:IF:116:ARG:CG	1:IF:117:LEU:N	2.53	0.65
43:ff:17:ARG:HH22	85:28:1578:U:H5''	1.60	0.65
50:F:255:TYR:HB3	50:F:301:LEU:HD21	1.77	0.65
80:18:24:C:H2'	80:18:25:A:C8	2.31	0.65
80:18:677:G:N2	80:18:1028:A:H62	1.93	0.65
71:S3:196:GLY:HA3	71:S3:201:LYS:HE3	1.78	0.65
80:18:1221:G:H2'	80:18:1222:G:C8	2.31	0.65
85:28:2485:U:H2'	85:28:2486:G:C8	2.32	0.65
64:RR:24:ASP:HB3	64:RR:27:TYR:HB3	1.78	0.65
85:28:4274:A:H2'	85:28:4275:G:C8	2.31	0.65
50:F:333:ILE:HG23	50:F:334:THR:HG23	1.77	0.65
69:S7:46:THR:HG23	69:S7:65:PRO:HG3	1.78	0.65
85:28:1358:G:C2	85:28:1381:U:O4	2.50	0.65
80:18:110:U:H2'	80:18:111:A:C8	2.31	0.65
80:18:941:C:H2'	80:18:942:G:H8	1.61	0.65
80:18:126:G:H21	80:18:180:G:H21	1.45	0.65
80:18:894:G:H2'	80:18:895:G:C8	2.31	0.65
85:28:2015:U:H2'	85:28:2016:C:H6	1.61	0.65
85:28:3684:G:H2'	85:28:3685:C:C6	2.32	0.65
3:S2:102:LEU:HD21	3:S2:130:ILE:HD11	1.79	0.64
80:18:1854:U:H2'	80:18:1855:G:H8	1.61	0.64
84:ES:2943:C:H2'	84:ES:2944:G:H8	1.62	0.64
27:27:103:ASP:HB3	27:27:106:LEU:HB2	1.77	0.64
50:F:187:SER:HB3	50:F:201:ILE:HB	1.80	0.64
76:GG:61:LYS:HB3	76:GG:76:LEU:HD12	1.78	0.64
85:28:3736:A:H2'	85:28:3737:A:C8	2.32	0.64
1:IF:251:SER:HB3	1:IF:294:LEU:HD23	1.77	0.64
65:SS:108:LYS:HD3	80:18:53:C:H4'	1.79	0.64
85:28:1193:C:H2'	85:28:1194:G:C8	2.32	0.64
50:F:29:ASN:HD21	50:F:334:THR:HA	1.63	0.64
71:S3:70:THR:HG22	71:S3:86:LEU:HD13	1.79	0.64
85:28:175:C:H2'	85:28:176:G:H8	1.63	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:10:87:ILE:HG12	15:10:138:ILE:HG12	1.80	0.64
80:18:1101:U:H2'	80:18:1102:G:C8	2.32	0.64
27:27:59:LYS:HA	27:27:62:ILE:HB	1.79	0.64
80:18:374:G:H2'	80:18:375:U:C6	2.33	0.64
80:18:389:A:H2'	80:18:390:C:C6	2.33	0.64
80:18:804:U:H2'	80:18:805:U:C6	2.32	0.64
80:18:1217:A:H2'	80:18:1218:C:C6	2.33	0.64
85:28:710:G:H2'	85:28:711:A:H8	1.62	0.64
85:28:1073:G:H1	85:28:1238:A:H2	1.45	0.64
75:W:24:THR:HG23	86:23:99:GLU:HB3	1.79	0.63
85:28:1344:C:H2'	85:28:1345:A:C8	2.33	0.63
85:28:1984:A:H2'	85:28:2011:C:H5'	1.79	0.63
46:FF:136:PRO:HG2	46:FF:139:TRP:HB2	1.80	0.63
2:BB:34:MET:HE3	2:BB:154:LEU:HD11	1.80	0.63
84:ES:2943:C:H2'	84:ES:2944:G:C8	2.34	0.63
85:28:3598:C:H2'	85:28:3599:A:C8	2.34	0.63
85:28:3911:C:H2'	85:28:3912:U:H6	1.64	0.63
8:L8:137:ILE:HD11	8:L8:149:LYS:HB3	1.81	0.63
50:F:176:SER:HB3	50:F:350:GLN:H	1.64	0.63
85:28:3917:A:H2'	85:28:3918:G:H8	1.63	0.63
85:28:1414:C:H2'	85:28:1415:G:H8	1.63	0.63
85:28:2640:G:H2'	85:28:2641:A:H8	1.63	0.63
80:18:940:U:H3	80:18:1002:U:H3	1.47	0.63
1:IF:330:ARG:NH1	80:18:966:U:OP2	2.30	0.62
27:27:54:THR:H	27:27:57:MET:HE2	1.63	0.62
81:v:746:LEU:HB2	81:v:815:ASP:HB2	1.79	0.62
85:28:4239:A:H2'	85:28:4240:G:C8	2.34	0.62
6:58:67:U:H2'	6:58:68:G:H8	1.63	0.62
1:IF:116:ARG:HB2	1:IF:116:ARG:CZ	2.29	0.62
45:AS:86:LEU:HB3	45:AS:98:THR:HB	1.81	0.62
47:VV:14:GLU:HA	47:VV:17:ARG:HD3	1.80	0.62
58:CC:64:TRP:NE1	71:S3:23:GLU:HG2	2.14	0.62
80:18:1010:G:H2'	80:18:1011:A:C8	2.34	0.62
80:18:1845:A:H2'	80:18:1846:G:C8	2.33	0.62
80:18:1198:G:H2'	80:18:1199:A:C8	2.35	0.62
85:28:1503:A:H4'	85:28:1504:G:H5'	1.81	0.62
85:28:1503:A:H1'	85:28:1504:G:C8	2.34	0.62
85:28:3910:C:H2'	85:28:3911:C:H6	1.65	0.62
15:10:61:SER:HA	15:10:126:VAL:HG23	1.81	0.62
18:15:14:LYS:HE2	85:28:280:G:H5''	1.81	0.62
68:S9:164:PRO:HG3	80:18:561:A:H5''	1.80	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
76:GG:101:GLY:HA3	76:GG:134:PRO:HG2	1.81	0.62
80:18:14:C:H2'	80:18:15:U:C6	2.34	0.62
85:28:233:U:H2'	85:28:234:G:C8	2.35	0.62
85:28:3736:A:H2'	85:28:3737:A:H8	1.64	0.62
59:AA:10:THR:HB	59:AA:306:LEU:HD11	1.80	0.62
80:18:122:G:H2'	80:18:123:G:H8	1.65	0.62
85:28:1093:C:H2'	85:28:1094:G:H8	1.65	0.62
85:28:1332:C:H2'	85:28:1333:A:C8	2.33	0.62
80:18:381:C:H2'	80:18:382:C:C6	2.35	0.62
85:28:1307:A:H2'	85:28:1308:C:H6	1.65	0.62
85:28:2480:G:H2'	85:28:2481:G:H8	1.64	0.62
85:28:3848:U:H2'	85:28:3849:A:C8	2.34	0.62
85:28:4504:C:H2'	85:28:4505:C:C6	2.35	0.62
85:28:983:U:H2'	85:28:984:C:C6	2.35	0.62
85:28:3664:G:H2'	85:28:3665:G:H8	1.65	0.62
85:28:3893:C:H2'	85:28:3894:A:C8	2.34	0.62
85:28:4680:G:H2'	85:28:4681:A:C8	2.35	0.62
59:AA:197:THR:HG21	59:AA:238:ALA:HA	1.82	0.62
80:18:1125:C:H2'	80:18:1126:G:C8	2.35	0.62
81:v:266:PHE:HB2	81:v:288:THR:HG22	1.81	0.62
84:ES:3244:U:H2'	84:ES:3245:G:H8	1.63	0.62
80:18:28:U:H2'	80:18:29:G:H8	1.64	0.62
85:28:1857:C:H2'	85:28:1858:A:C8	2.33	0.62
24:22:28:PRO:HB2	24:22:34:MET:HG2	1.81	0.61
45:AS:91:VAL:HG12	45:AS:93:GLY:H	1.65	0.61
80:18:16:G:H2'	80:18:17:C:C6	2.35	0.61
85:28:1512:G:H2'	85:28:1513:U:H6	1.64	0.61
18:15:67:ARG:HD2	85:28:2458:C:H5''	1.82	0.61
79:L9:120:GLU:HG2	85:28:4611:A:H2	1.65	0.61
80:18:121:U:H2'	80:18:122:G:C8	2.35	0.61
73:WX:6:VAL:HG12	73:WX:34:ILE:HD11	1.82	0.61
80:18:874:G:H2'	80:18:875:A:C8	2.36	0.61
80:18:1125:C:H2'	80:18:1126:G:H8	1.64	0.61
69:S7:143:ARG:HB2	69:S7:155:LYS:HB2	1.81	0.61
80:18:152:U:H2'	80:18:153:G:C8	2.35	0.61
80:18:729:C:H2'	80:18:730:C:C6	2.35	0.61
85:28:3910:C:H2'	85:28:3911:C:C6	2.36	0.61
85:28:1683:U:H2'	85:28:1684:A:H8	1.66	0.61
25:cc:83:THR:HG21	85:28:2434:G:H4'	1.82	0.61
79:L9:114:ILE:HB	79:L9:124:ARG:HG3	1.82	0.61
80:18:1797:U:H2'	80:18:1798:C:C6	2.36	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:28:4095:G:H22	85:28:4113:U:H3	1.48	0.61
5:DD:126:VAL:HG22	5:DD:145:VAL:HG22	1.83	0.61
50:F:351:ASP:HB3	50:F:354:LEU:HD21	1.82	0.61
56:WW:12:ALA:HA	56:WW:34:PHE:HA	1.82	0.61
85:28:3610:A:H2'	85:28:3611:A:H8	1.66	0.61
13:L7:227:VAL:HA	22:20:39:VAL:HG12	1.83	0.61
81:v:119:LEU:HD21	81:v:146:ALA:HA	1.82	0.61
85:28:963:G:HO2'	85:28:964:A:H8	1.47	0.61
13:L7:46:ARG:NH1	85:28:976:C:H5''	2.15	0.61
71:S3:35:SER:HA	71:S3:99:ILE:HG13	1.83	0.61
1:IF:350:VAL:HG11	1:IF:357:LEU:HB3	1.73	0.61
69:S7:144:ILE:HB	73:WX:52:ILE:HB	1.82	0.61
85:28:1198:G:H2'	85:28:1199:G:H8	1.62	0.61
85:28:1436:C:H42	85:28:1448:G:H1	1.49	0.61
85:28:1461:C:H2'	85:28:1462:A:C8	2.36	0.61
22:20:13:VAL:HG23	22:20:62:VAL:HB	1.82	0.60
49:t:80:LEU:HA	49:t:83:LYS:HG2	1.81	0.60
84:ES:3238:C:H2'	84:ES:3239:G:C8	2.36	0.60
85:28:1341:U:H2'	85:28:1342:A:H8	1.66	0.60
85:28:1402:C:H2'	85:28:1403:G:C8	2.37	0.60
18:15:75:VAL:HG23	18:15:78:GLY:HA2	1.83	0.60
45:AS:189:ILE:HB	45:AS:190:PRO:HD3	1.82	0.60
48:s:13:TYR:HA	48:s:16:LYS:HG2	1.83	0.60
64:RR:91:LEU:HB3	70:YY:82:VAL:HG21	1.84	0.60
80:18:1705:C:H2'	80:18:1706:G:C8	2.36	0.60
84:ES:2945:C:H2'	84:ES:2946:G:H8	1.66	0.60
1:IF:350:VAL:CG1	1:IF:357:LEU:CB	2.62	0.60
50:F:202:ILE:HG12	50:F:205:PRO:HB3	1.83	0.60
85:28:5006:U:H4'	85:28:5007:A:H5'	1.83	0.60
80:18:106:C:H2'	80:18:107:A:H8	1.65	0.60
80:18:1845:A:H2'	80:18:1846:G:H8	1.66	0.60
85:28:517:C:H2'	85:28:518:G:H8	1.66	0.60
13:L7:104:VAL:HG13	13:L7:135:VAL:HG12	1.84	0.60
55:S5:39:ILE:HG23	55:S5:68:ILE:HG21	1.84	0.60
80:18:1382:A:H2'	80:18:1383:A:C8	2.36	0.60
83:A:22:LEU:HA	83:A:25:LEU:HD23	1.84	0.60
85:28:2607:C:H2'	85:28:2608:G:C8	2.35	0.60
85:28:3619:G:H22	85:28:3624:A:H1'	1.66	0.60
80:18:530:U:H3	80:18:554:A:H61	1.48	0.60
85:28:1093:C:H2'	85:28:1094:G:C8	2.36	0.60
60:OO:40:ILE:HD11	60:OO:53:PRO:HG3	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
81:v:72:SER:HB3	81:v:106:PRO:HD3	1.83	0.60
85:28:1307:A:H2'	85:28:1308:C:C6	2.36	0.60
9:L3:240:LEU:HB3	9:L3:244:THR:HG21	1.84	0.60
10:L4:343:GLN:HG2	85:28:724:C:H1'	1.82	0.60
11:L5:64:ILE:HG13	11:L5:105:LEU:HD21	1.83	0.60
80:18:1128:C:H2'	80:18:1129:G:H8	1.66	0.60
85:28:679:C:H2'	85:28:680:G:H8	1.67	0.60
67:S4:162:ILE:HG22	67:S4:169:ILE:HA	1.84	0.59
80:18:1714:U:H2'	80:18:1715:A:C8	2.36	0.59
85:28:3598:C:H2'	85:28:3599:A:H8	1.65	0.59
85:28:3861:A:H2'	85:28:3862:A:H8	1.67	0.59
85:28:4948:C:H2'	85:28:4949:G:H21	1.67	0.59
4:PP:32:ILE:HD12	4:PP:55:ILE:HB	1.84	0.59
49:t:146:ARG:HB3	49:t:148:PRO:HD2	1.83	0.59
80:18:1382:A:H2'	80:18:1383:A:H8	1.67	0.59
85:28:1317:U:H2'	85:28:1318:C:C6	2.37	0.59
5:DD:77:VAL:HA	5:DD:88:ILE:HG22	1.84	0.59
80:18:115:U:H2'	80:18:116:U:C6	2.37	0.59
80:18:441:C:H41	80:18:448:A:H1'	1.67	0.59
85:28:1382:G:H2'	85:28:1383:G:H8	1.68	0.59
85:28:2745:A:H2'	85:28:2746:A:C8	2.35	0.59
85:28:2845:A:H61	85:28:3843:C:H42	1.49	0.59
85:28:4448:G:H5''	85:28:4449:A:H5''	1.85	0.59
74:S8:110:ARG:HG3	74:S8:121:LEU:HB3	1.84	0.59
85:28:3721:U:H2'	85:28:3722:G:H8	1.67	0.59
85:28:3893:C:H2'	85:28:3894:A:H8	1.67	0.59
32:32:104:SER:HB2	85:28:2303:C:H5''	1.85	0.59
75:W:104:GLN:O	75:W:107:GLN:HG3	2.02	0.59
80:18:556:U:H2'	80:18:557:U:H6	1.67	0.59
17:14:96:GLU:HA	17:14:99:GLU:HG2	1.84	0.59
80:18:1777:G:H2'	80:18:1778:C:H6	1.67	0.59
85:28:2457:G:H21	85:28:3672:G:N2	1.97	0.59
85:28:4239:A:H2'	85:28:4240:G:H8	1.66	0.59
85:28:4458:C:H2'	85:28:4459:U:C6	2.37	0.59
20:17:114:ILE:HD11	20:17:117:ILE:HB	1.85	0.59
70:YY:113:ARG:HG3	70:YY:114:ARG:HG3	1.85	0.59
85:28:1769:G:H2'	85:28:1770:A:H8	1.67	0.59
1:IF:159:PHE:HZ	1:IF:187:LEU:HD12	1.66	0.59
9:L3:13:SER:HB2	85:28:4622:A:H4'	1.84	0.59
45:AS:141:GLY:HA2	45:AS:210:VAL:HG22	1.85	0.59
66:S6:14:LYS:HB2	66:S6:124:LEU:HD11	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
76:GG:78:ALA:HB3	76:GG:118:ALA:HB3	1.84	0.59
85:28:1326:A:H2'	85:28:1327:C:C6	2.38	0.59
9:L3:56:ILE:O	9:L3:73:VAL:HA	2.02	0.59
1:IF:320:TYR:HE1	1:IF:321:ARG:CZ	2.16	0.58
19:bb:185:VAL:HG22	19:bb:188:LYS:HB3	1.83	0.58
80:18:107:A:H2'	80:18:108:G:C8	2.38	0.58
80:18:931:C:H2'	80:18:932:G:C8	2.38	0.58
80:18:952:G:H2'	80:18:953:C:C6	2.38	0.58
1:IF:349:ILE:O	1:IF:349:ILE:HG12	2.02	0.58
28:dd:21:ARG:HG3	85:28:2282:A:H4'	1.83	0.58
85:28:3606:U:H2'	85:28:3607:U:C6	2.38	0.58
28:dd:36:GLY:HA2	28:dd:39:HIS:HB2	1.84	0.58
79:L9:94:SER:HB3	79:L9:142:ASP:HB3	1.84	0.58
80:18:878:G:C2	80:18:879:C:H1'	2.38	0.58
80:18:1854:U:H2'	80:18:1855:G:C8	2.39	0.58
84:ES:3244:U:H2'	84:ES:3245:G:C8	2.39	0.58
85:28:2409:U:H4'	85:28:2428:A:H4'	1.85	0.58
3:S2:78:LEU:HD23	3:S2:78:LEU:H	1.67	0.58
3:S2:167:ARG:HB2	3:S2:177:PRO:HB2	1.84	0.58
20:17:118:GLN:NE2	85:28:423:G:H21	2.01	0.58
50:F:118:ILE:HG13	50:F:195:ILE:HG22	1.85	0.58
59:AA:128:THR:HG22	59:AA:143:GLN:HA	1.86	0.58
85:28:4173:G:H2'	85:28:4174:U:C6	2.39	0.58
6:58:148:A:H2'	6:58:149:G:C8	2.37	0.58
14:aa:317:LYS:HG2	45:AS:225:LEU:HB3	1.84	0.58
51:Q:59:PRO:HG3	51:Q:143:ARG:HA	1.85	0.58
1:IF:116:ARG:HB2	1:IF:116:ARG:HH11	1.65	0.58
8:L8:90:CYS:HB3	8:L8:101:VAL:HG13	1.84	0.58
27:27:46:ILE:HD11	27:27:49:TYR:HA	1.85	0.58
67:S4:146:THR:HB	80:18:123:G:H1'	1.85	0.58
85:28:4091:G:H2'	85:28:4092:G:H8	1.67	0.58
3:S2:190:SER:HB2	80:18:1143:A:H5'	1.85	0.58
80:18:382:C:H2'	80:18:383:G:H8	1.67	0.58
19:bb:5:GLN:HG2	19:bb:6:VAL:HG23	1.86	0.58
79:L9:107:GLU:HG3	79:L9:110:SER:HB2	1.84	0.58
80:18:318:A:H3'	80:18:319:C:H5''	1.85	0.58
80:18:556:U:H2'	80:18:557:U:C6	2.38	0.58
85:28:448:G:H3'	85:28:449:C:H5''	1.84	0.58
85:28:1088:C:H2'	85:28:1089:G:H8	1.68	0.58
85:28:4260:U:H2'	85:28:4261:C:H6	1.66	0.58
85:28:4635:A:H2	85:28:4663:G:H21	1.50	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:39:24:PRO:HG2	39:39:27:ILE:HG12	1.85	0.58
64:RR:51:VAL:HG22	64:RR:70:VAL:HG11	1.86	0.58
75:W:52:THR:HG23	75:W:55:TYR:H	1.69	0.58
77:UU:43:ASN:HA	77:UU:66:LYS:HA	1.85	0.58
80:18:219:U:H2'	80:18:220:U:C6	2.38	0.58
50:F:227:ASP:HB3	50:F:320:LYS:HD3	1.86	0.58
80:18:1201:U:H2'	80:18:1202:U:C6	2.39	0.58
85:28:651:C:H2'	85:28:652:G:H8	1.69	0.58
1:IF:215:PHE:CD1	1:IF:227:VAL:HG13	2.38	0.57
18:15:40:PRO:HG3	85:28:8:U:H5''	1.86	0.57
62:LL:84:LEU:HB2	62:LL:87:GLN:HG2	1.86	0.57
85:28:469:C:H2'	85:28:470:A:H8	1.69	0.57
85:28:4232:U:H4'	85:28:4233:A:O5'	2.04	0.57
6:58:19:C:H2'	6:58:20:A:C8	2.40	0.57
68:S9:172:ARG:HH12	80:18:586:G:H3'	1.69	0.57
74:S8:29:LEU:HD13	80:18:448:A:H62	1.68	0.57
80:18:93:U:H2'	80:18:94:G:O4'	2.04	0.57
80:18:1004:U:H2'	80:18:1005:G:C8	2.36	0.57
85:28:2870:A:H2'	85:28:2871:A:H8	1.69	0.57
80:18:314:U:H2'	80:18:315:C:C6	2.39	0.57
85:28:300:A:H2'	85:28:301:G:H8	1.69	0.57
85:28:1770:A:H2'	85:28:1771:U:C6	2.38	0.57
85:28:4699:U:H1'	85:28:4700:A:H5''	1.85	0.57
3:S2:86:LEU:HD13	3:S2:87:PRO:HD2	1.86	0.57
27:27:11:VAL:HG11	27:27:80:LEU:HB3	1.85	0.57
29:29:3:LYS:HD3	85:28:4194:U:H3'	1.87	0.57
72:RS:28:PHE:HA	72:RS:55:THR:HG21	1.86	0.57
85:28:1468:C:H2'	85:28:1469:C:H6	1.68	0.57
85:28:1512:G:H2'	85:28:1513:U:C6	2.40	0.57
85:28:2413:U:H2'	85:28:2414:G:H8	1.69	0.57
85:28:3648:A:H1'	85:28:3785:A:N6	2.20	0.57
85:28:1204:C:H2'	85:28:1205:G:H8	1.69	0.57
85:28:3911:C:H2'	85:28:3912:U:C6	2.39	0.57
48:s:121:VAL:HG13	48:s:182:PRO:HG2	1.87	0.57
80:18:1511:U:H2'	80:18:1512:C:C6	2.39	0.57
85:28:163:A:H2'	85:28:164:G:H8	1.68	0.57
85:28:1338:G:H4'	85:28:1339:U:H6	1.69	0.57
85:28:1964:A:C8	85:28:1965:G:C8	2.93	0.57
85:28:2496:G:H2'	85:28:2497:C:C6	2.40	0.57
85:28:2521:G:H5'	85:28:2640:G:H1'	1.87	0.57
85:28:4948:C:H2'	85:28:4949:G:N2	2.20	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
81:v:159:LYS:HG2	88:v:900:GDP:C6	2.39	0.57
81:v:666:THR:HG22	81:v:706:ASP:HA	1.86	0.57
85:28:1942:A:H2'	85:28:1943:A:H8	1.69	0.57
18:15:104:GLU:HA	18:15:160:GLU:HG3	1.87	0.57
80:18:674:C:H2'	80:18:675:U:C6	2.40	0.57
80:18:1801:A:H2'	80:18:1802:C:C6	2.40	0.57
85:28:265:C:H4'	85:28:266:C:OP2	2.05	0.57
85:28:1339:U:H2'	85:28:1340:C:C6	2.40	0.57
61:MM:42:HIS:HB3	61:MM:93:SER:HB3	1.86	0.57
85:28:134:G:H4'	85:28:135:G:O5'	2.05	0.57
85:28:1505:C:H2'	85:28:1506:G:H8	1.70	0.57
10:L4:78:ARG:HB3	10:L4:88:GLY:HA2	1.85	0.57
80:18:1748:G:H1	80:18:1786:U:H3	1.53	0.57
85:28:2706:G:H2'	85:28:2708:U:H5'	1.86	0.57
85:28:4080:C:H2'	85:28:4081:G:H8	1.70	0.57
85:28:4774:C:H2'	85:28:4775:C:C6	2.40	0.57
1:IF:350:VAL:HG13	1:IF:357:LEU:CB	2.22	0.56
7:6:110:G:H2'	7:6:111:C:C6	2.40	0.56
9:L3:224:LYS:HG2	9:L3:340:THR:HB	1.87	0.56
10:L4:312:ARG:HB3	85:28:2274:C:H5'	1.85	0.56
81:v:602:LEU:HB3	81:v:604:MET:HE1	1.88	0.56
85:28:4591:U:H2'	85:28:4592:C:C6	2.40	0.56
85:28:4992:G:H2'	85:28:4993:G:H8	1.68	0.56
86:23:9:SER:HB2	86:23:128:LEU:HD12	1.87	0.56
12:L6:48:ARG:HB2	12:L6:64:MET:HE1	1.86	0.56
80:18:912:C:H3'	80:18:913:A:H5''	1.86	0.56
80:18:1714:U:H2'	80:18:1715:A:H8	1.70	0.56
81:v:580:ARG:HB2	81:v:741:MET:HB2	1.87	0.56
85:28:1341:U:H2'	85:28:1342:A:C8	2.41	0.56
85:28:4344:U:H2'	85:28:4345:C:C6	2.40	0.56
1:IF:81:VAL:HG13	1:IF:119:LEU:HD21	1.88	0.56
10:L4:77:PRO:O	10:L4:90:GLY:HA2	2.06	0.56
30:30:38:ILE:HG21	30:30:63:TYR:HB3	1.87	0.56
54:TT:99:LEU:HD21	54:TT:102:LYS:HB2	1.86	0.56
57:II:12:VAL:HG21	57:II:91:ALA:HA	1.88	0.56
57:II:103:ALA:O	57:II:106:LYS:HG3	2.06	0.56
80:18:942:G:H2'	80:18:943:U:C6	2.41	0.56
80:18:1692:U:H2'	80:18:1693:G:H8	1.69	0.56
81:v:820:LEU:HD12	81:v:821:PRO:HD2	1.87	0.56
85:28:1298:C:H2'	85:28:1299:G:H8	1.70	0.56
85:28:5030:U:H2'	85:28:5031:G:H8	1.71	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:42:6:LYS:HG2	42:42:93:LEU:HB3	1.88	0.56
42:42:98:LYS:HE3	85:28:4233:A:H4'	1.87	0.56
74:S8:129:LEU:HG	74:S8:131:PRO:HD2	1.86	0.56
85:28:440:U:H2'	85:28:441:G:H8	1.70	0.56
85:28:3720:G:H22	85:28:3733:A:H2	1.52	0.56
85:28:4537:C:H2'	85:28:4538:G:C8	2.37	0.56
55:S5:153:LEU:HB3	55:S5:189:ALA:HA	1.88	0.56
61:MM:71:GLY:HA3	80:18:1562:C:H5''	1.87	0.56
80:18:963:A:H2'	80:18:964:A:C8	2.40	0.56
84:ES:2945:C:H2'	84:ES:2946:G:C8	2.39	0.56
85:28:2844:A:O2'	85:28:4631:G:H4'	2.05	0.56
1:IF:349:ILE:HD13	1:IF:349:ILE:N	2.04	0.56
8:L8:233:ARG:HB2	85:28:4184:G:H5'	1.88	0.56
12:L6:156:LEU:HD11	12:L6:198:ILE:HG13	1.87	0.56
21:19:41:ILE:O	21:19:45:ILE:HG12	2.06	0.56
22:20:13:VAL:HG22	22:20:63:TYR:HB3	1.88	0.56
80:18:1494:U:H4'	80:18:1495:G:H5''	1.87	0.56
80:18:1801:A:H2'	80:18:1802:C:H6	1.69	0.56
59:AA:172:LYS:HA	59:AA:195:LEU:HG	1.88	0.56
76:GG:31:CYS:HB3	76:GG:44:VAL:HG22	1.88	0.56
80:18:1637:A:H4'	80:18:1638:G:O5'	2.05	0.56
83:A:34:MET:HB3	83:A:42:ARG:HG3	1.87	0.56
85:28:162:A:H2'	85:28:163:A:C8	2.41	0.56
85:28:1333:A:H2'	85:28:1334:A:C8	2.41	0.56
85:28:2483:G:H1	85:28:2495:U:H3	1.51	0.56
85:28:3870:C:H2'	85:28:3871:A:H8	1.71	0.56
85:28:4970:C:C2	85:28:4971:A:C8	2.93	0.56
33:ee:7:CYS:HB2	33:ee:103:VAL:HG23	1.87	0.56
39:39:45:ARG:NH2	85:28:2796:G:H5'	2.21	0.56
50:F:80:ILE:HG12	50:F:108:ILE:HG12	1.87	0.56
80:18:454:U:H2'	80:18:455:A:H8	1.71	0.56
85:28:2493:G:H2'	85:28:2494:U:H6	1.70	0.56
85:28:3606:U:H2'	85:28:3607:U:H6	1.71	0.56
85:28:4070:U:H2'	85:28:4071:U:C6	2.41	0.56
1:IF:188:GLY:HA2	1:IF:245:LEU:HD11	1.88	0.56
6:58:19:C:H2'	6:58:20:A:H8	1.71	0.56
16:13:62:PRO:HG3	85:28:74:G:H1'	1.88	0.56
80:18:112:U:H2'	80:18:115:U:H5	1.71	0.56
80:18:418:A:H3'	80:18:419:G:H8	1.69	0.56
80:18:1008:A:H2'	80:18:1009:A:C8	2.41	0.56
85:28:478:G:H2'	85:28:479:G:H8	1.71	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:28:2528:G:H4'	85:28:2783:A:H4'	1.88	0.56
85:28:3845:A:H2'	85:28:3846:C:H6	1.71	0.56
85:28:4884:G:H2'	85:28:4885:U:O4'	2.06	0.56
46:FF:99:ARG:O	46:FF:103:GLU:HG2	2.06	0.56
69:S7:157:HIS:HB3	69:S7:190:PRO:HG3	1.86	0.56
80:18:382:C:H2'	80:18:383:G:C8	2.41	0.56
80:18:545:A:H2'	80:18:546:G:C8	2.41	0.56
80:18:1130:G:C8	80:18:1131:G:C8	2.94	0.56
80:18:1280:G:H2'	80:18:1281:G:C8	2.40	0.56
80:18:1337:C:H2'	80:18:1338:G:H8	1.71	0.56
81:v:412:ALA:HB3	81:v:472:LEU:H	1.71	0.56
85:28:674:G:H2'	85:28:675:C:H6	1.71	0.56
85:28:4894:A:H5''	85:28:4895:C:H2'	1.87	0.56
39:39:43:HIS:HE2	85:28:2429:A:H5''	1.71	0.55
85:28:713:C:H2'	85:28:714:G:H8	1.71	0.55
85:28:2539:C:H2'	85:28:2540:C:C6	2.41	0.55
1:IF:315:THR:O	1:IF:330:ARG:HD3	2.06	0.55
14:aa:136:PHE:HB3	14:aa:212:HIS:HB2	1.88	0.55
30:30:105:ILE:HD12	30:30:106:ARG:HG3	1.88	0.55
80:18:1513:C:H2'	80:18:1514:G:H8	1.71	0.55
28:dd:98:ALA:HB2	28:dd:121:PRO:HB2	1.88	0.55
49:t:142:ASN:HA	49:t:146:ARG:HH11	1.72	0.55
68:S9:50:LEU:O	68:S9:54:ARG:HG3	2.05	0.55
80:18:1207:G:P	80:18:1207:G:H8	2.30	0.55
45:AS:25:PHE:HA	45:AS:28:LYS:HG2	1.88	0.55
66:S6:121:ILE:HD12	66:S6:122:PRO:HD2	1.87	0.55
80:18:379:C:H2'	80:18:380:G:C8	2.41	0.55
80:18:643:A:H4'	80:18:644:G:H5'	1.88	0.55
80:18:925:G:H1	80:18:1017:U:H3	1.51	0.55
80:18:1347:U:H2'	80:18:1348:G:N3	2.21	0.55
80:18:1736:G:H2'	80:18:1737:G:C8	2.42	0.55
85:28:1893:C:H1'	85:28:1937:C:O2	2.06	0.55
85:28:4238:G:H2'	85:28:4239:A:H8	1.71	0.55
35:35:31:LEU:HB3	35:35:47:ILE:HG22	1.88	0.55
80:18:389:A:H2'	80:18:390:C:H6	1.69	0.55
49:t:59:THR:HG23	49:t:74:VAL:HB	1.87	0.55
49:t:85:LEU:HD21	49:t:104:ILE:HB	1.87	0.55
80:18:511:U:H2'	80:18:512:A:C8	2.41	0.55
80:18:1470:C:H2'	80:18:1471:C:H6	1.71	0.55
81:v:649:ILE:HG22	81:v:663:THR:HG22	1.89	0.55
85:28:3796:U:H2'	85:28:3797:C:C6	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:28:3873:G:H2'	85:28:3874:G:C8	2.41	0.55
85:28:4637:G:H2'	85:28:4638:U:C6	2.42	0.55
54:TT:71:ALA:HB1	55:S5:167:LYS:HA	1.88	0.55
85:28:4736:C:H2'	85:28:4737:G:H8	1.71	0.55
85:28:5028:G:H2'	85:28:5029:C:O4'	2.06	0.55
1:IF:199:GLN:HG3	1:IF:199:GLN:O	2.03	0.55
37:37:33:THR:HG22	37:37:40:PRO:HG2	1.88	0.55
85:28:1338:G:H4'	85:28:1339:U:C6	2.42	0.55
3:S2:207:ALA:HB2	80:18:4:C:H4'	1.88	0.55
9:L3:53:MET:HG2	9:L3:77:THR:HG22	1.89	0.55
16:13:62:PRO:O	85:28:71:C:H1'	2.07	0.55
25:cc:93:ASN:ND2	85:28:2533:C:H5'	2.21	0.55
45:AS:103:MET:HE3	45:AS:215:VAL:HG23	1.89	0.55
77:UU:12:LYS:HG3	77:UU:15:ARG:HB2	1.88	0.55
80:18:1010:G:H2'	80:18:1011:A:H8	1.70	0.55
85:28:2521:G:H2'	85:28:2522:G:H8	1.71	0.55
85:28:4577:U:H2'	85:28:4578:G:C8	2.42	0.55
8:L8:209:HIS:CE1	8:L8:235:VAL:HG11	2.42	0.55
27:27:38:TYR:HB3	85:28:2656:U:H5''	1.87	0.55
65:SS:35:VAL:HG21	65:SS:40:ILE:HD11	1.89	0.55
79:L9:129:ARG:HG2	79:L9:153:LEU:HD22	1.88	0.55
80:18:1424:G:H2'	80:18:1425:G:C8	2.41	0.55
85:28:3707:U:H2'	85:28:3708:C:C6	2.42	0.55
19:bb:60:LYS:HE2	85:28:2046:G:H5'	1.89	0.54
54:TT:49:LEU:HB3	62:LL:5:ILE:HG12	1.89	0.54
62:LL:121:ARG:HG3	62:LL:131:VAL:HG21	1.89	0.54
80:18:857:U:H2'	80:18:858:A:C8	2.42	0.54
80:18:1301:A:H2'	80:18:1303:C:O2	2.07	0.54
80:18:1616:U:H2'	80:18:1617:G:C8	2.42	0.54
85:28:922:C:H2'	85:28:922(A):G:C8	2.42	0.54
85:28:2568:C:H2'	85:28:2569:G:C8	2.42	0.54
5:DD:93:LEU:HB3	5:DD:102:PHE:HB3	1.90	0.54
52:ZZ:138:ARG:HB2	52:ZZ:149:CYS:HA	1.89	0.54
67:S4:48:LEU:HD23	67:S4:61:VAL:HG22	1.89	0.54
69:S7:146:VAL:HG22	69:S7:152:ARG:HG2	1.89	0.54
85:28:3684:G:H2'	85:28:3685:C:H6	1.71	0.54
85:28:3861:A:H2'	85:28:3862:A:C8	2.42	0.54
85:28:93:G:H2'	85:28:94:A:C8	2.42	0.54
85:28:1094:G:H1	85:28:1202:C:H42	1.56	0.54
85:28:1760:G:O6	85:28:1773:U:O2	2.24	0.54
85:28:4238:G:H2'	85:28:4239:A:C8	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:L7:126:LYS:HB2	23:21:133:ALA:HB3	1.89	0.54
23:21:87:LYS:NZ	85:28:4305:G:H22	2.05	0.54
60:OO:26:SER:HB2	60:OO:110:VAL:HG13	1.90	0.54
80:18:514:U:H2'	80:18:515:G:O4'	2.07	0.54
85:28:674:G:H2'	85:28:675:C:C6	2.43	0.54
85:28:907:C:H2'	85:28:908:G:H8	1.72	0.54
85:28:1669:A:H4'	85:28:1685:G:H22	1.71	0.54
85:28:2093:G:H22	85:28:2262:G:H1	1.55	0.54
85:28:2412:A:H2'	85:28:2413:U:C6	2.42	0.54
85:28:2539:C:H2'	85:28:2540:C:H6	1.72	0.54
85:28:4563:U:H2'	85:28:4564:A:H8	1.73	0.54
85:28:4577:U:H2'	85:28:4578:G:H8	1.72	0.54
1:IF:159:PHE:CZ	1:IF:187:LEU:HD12	2.43	0.54
10:L4:339:THR:HG22	10:L4:342:ARG:NH2	2.22	0.54
60:OO:26:SER:HB3	60:OO:32:LEU:HB2	1.89	0.54
80:18:455:A:H2'	80:18:456:C:C6	2.42	0.54
85:28:648:G:H2'	85:28:649:A:H8	1.73	0.54
85:28:1645:C:H2'	85:28:1646:A:C8	2.42	0.54
85:28:2080:U:H2'	85:28:2081:C:C6	2.42	0.54
85:28:3916:G:H2'	85:28:3917:A:C8	2.42	0.54
85:28:3932:U:H2'	85:28:3933:G:H8	1.73	0.54
85:28:4594:U:H2'	85:28:4595:G:H8	1.73	0.54
16:13:59:VAL:HG22	85:28:74:G:H5'	1.90	0.54
66:S6:50:VAL:HG12	66:S6:113:ILE:HD13	1.89	0.54
80:18:121:U:H2'	80:18:122:G:H8	1.71	0.54
85:28:164:G:H2'	85:28:165:A:H8	1.73	0.54
85:28:496:G:H2'	85:28:497:G:H5'	1.88	0.54
85:28:1088:C:H2'	85:28:1089:G:C8	2.42	0.54
85:28:1504:G:H2'	85:28:1505:C:C6	2.42	0.54
85:28:2640:G:H2'	85:28:2641:A:C8	2.41	0.54
18:15:187:SER:H	18:15:190:ALA:HB3	1.71	0.54
80:18:1232:U:H2'	80:18:1233:G:H8	1.73	0.54
85:28:1749:A:H2'	85:28:1750:G:H8	1.72	0.54
85:28:4188:U:H2'	85:28:4189:U:C6	2.42	0.54
6:58:144:U:H2'	6:58:145:C:C6	2.43	0.54
55:S5:34:SER:HA	56:WW:55:VAL:HB	1.90	0.54
80:18:677:G:H21	80:18:1028:A:N6	1.97	0.54
80:18:1708:C:H2'	80:18:1709:G:H8	1.73	0.54
85:28:2078:C:H2'	85:28:2079:G:C8	2.43	0.54
85:28:2602:G:H2'	85:28:2603:C:C6	2.43	0.54
85:28:2634:C:H2'	85:28:2635:U:H6	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
66:S6:142:ARG:HG2	66:S6:153:VAL:HG11	1.89	0.54
80:18:1279:C:H2'	80:18:1280:G:H8	1.72	0.54
80:18:1283:C:H4'	80:18:1287:A:H5'	1.89	0.54
80:18:1395:C:H4'	80:18:1396:A:OP1	2.08	0.54
81:v:323:LEU:HD13	81:v:324:ASP:H	1.72	0.54
85:28:162:A:H2'	85:28:163:A:H8	1.72	0.54
85:28:3871:A:H2'	85:28:3872:A:C8	2.43	0.54
34:34:66:ARG:HD3	85:28:2539:C:H5''	1.90	0.54
45:AS:35:ALA:HB2	45:AS:44:ILE:HD11	1.88	0.54
69:S7:144:ILE:HG12	69:S7:154:ILE:HG13	1.89	0.54
85:28:2859:G:H2'	85:28:2860:C:H6	1.72	0.54
85:28:4471:U:H2'	85:28:4472:G:H8	1.73	0.54
85:28:4629:U:C2	85:28:4630:G:C8	2.96	0.54
9:L3:56:ILE:HD12	9:L3:365:LEU:HD22	1.90	0.53
80:18:1633:A:H2'	80:18:1634:A:C8	2.43	0.53
85:28:2465:C:H2'	85:28:2466:G:O4'	2.07	0.53
85:28:2890:C:H2'	85:28:2891:U:C6	2.43	0.53
85:28:4993:G:H2'	85:28:4994:G:H8	1.73	0.53
1:IF:330:ARG:NE	80:18:965:U:OP1	2.38	0.53
3:S2:272:HIS:HA	3:S2:275:LYS:HG2	1.91	0.53
6:58:8:U:H2'	6:58:9:A:C8	2.44	0.53
15:10:22:PHE:CZ	85:28:1788:A:H2'	2.43	0.53
49:t:108:GLU:HA	49:t:111:ASN:ND2	2.23	0.53
50:F:107:LYS:HD3	50:F:317:ALA:HA	1.89	0.53
80:18:848:U:H2'	80:18:849:A:H8	1.73	0.53
81:v:503:PRO:HD3	81:v:533:MET:HE2	1.90	0.53
85:28:1662:C:H2'	85:28:1663:C:C6	2.43	0.53
85:28:2414:G:H2'	85:28:2415:U:H6	1.73	0.53
85:28:2566:G:H2'	85:28:2567:G:C8	2.43	0.53
85:28:4601:U:H2'	85:28:4602:A:H8	1.72	0.53
32:32:100:ALA:HB3	32:32:103:VAL:HG23	1.91	0.53
48:s:160:LEU:HG	48:s:161:ILE:HG23	1.90	0.53
65:SS:66:GLY:HA2	80:18:581:U:H4'	1.89	0.53
84:ES:2953:C:H2'	84:ES:2954:G:C8	2.43	0.53
85:28:423:G:H2'	85:28:424:U:C6	2.43	0.53
85:28:1558:A:H2'	85:28:1559:G:H8	1.73	0.53
85:28:2560:C:H42	85:28:2567:G:H1	1.56	0.53
85:28:4652:G:H2'	85:28:4653:C:H6	1.73	0.53
10:L4:168:VAL:O	10:L4:172:LYS:HG2	2.08	0.53
19:bb:125:LYS:HG3	19:bb:129:LEU:HD12	1.90	0.53
80:18:35:C:H2'	80:18:36:U:C6	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:18:79:A:H3'	80:18:80:G:H8	1.73	0.53
80:18:1523:C:H2'	80:18:1524:G:H8	1.73	0.53
85:28:418:A:H4'	85:28:2311:C:H5'	1.90	0.53
85:28:4163:U:H5'	85:28:4164:C:H5''	1.90	0.53
1:IF:306:LEU:O	1:IF:309:VAL:HG12	2.08	0.53
14:aa:139:VAL:HG11	14:aa:238:LYS:HD2	1.90	0.53
45:AS:46:LYS:HE3	76:GG:20:GLN:HB2	1.89	0.53
59:AA:16:GLY:HA3	59:AA:36:ARG:HB2	1.90	0.53
78:11:146:ARG:HG2	78:11:147:ARG:HG2	1.91	0.53
80:18:17:C:H2'	80:18:18:C:H6	1.74	0.53
80:18:432:G:H2'	80:18:433:A:H8	1.73	0.53
85:28:710:G:H2'	85:28:711:A:C8	2.41	0.53
85:28:734:G:H1	85:28:929:A:H62	1.56	0.53
71:S3:99:ILE:H	71:S3:99:ILE:HD13	1.72	0.53
85:28:2684:C:H2'	85:28:2685:C:C6	2.44	0.53
52:ZZ:140:TYR:CE1	52:ZZ:145:CYS:HA	2.43	0.53
55:S5:97:PHE:HA	55:S5:100:ILE:HD12	1.88	0.53
65:SS:108:LYS:HB3	80:18:53:C:H5''	1.90	0.53
80:18:1102:G:H2'	80:18:1103:C:C6	2.43	0.53
85:28:922:C:H2'	85:28:922(A):G:H8	1.74	0.53
13:L7:42:ARG:O	13:L7:46:ARG:HG2	2.09	0.53
58:CC:8:ARG:O	58:CC:11:ILE:HG12	2.09	0.53
80:18:96:C:H2'	80:18:97:U:C6	2.44	0.53
80:18:1006:C:H2'	80:18:1007:C:C6	2.43	0.53
85:28:1329:G:C2	85:28:3865:A:H1'	2.43	0.53
6:58:65:A:H2'	6:58:66:A:H8	1.74	0.53
7:6:66:G:H5'	11:L5:10:LYS:HG3	1.90	0.53
28:dd:72:THR:HG22	28:dd:110:LYS:HB3	1.89	0.53
53:EE:56:CYS:SG	53:EE:82:ASN:HB2	2.48	0.53
80:18:418:A:H3'	80:18:419:G:C8	2.44	0.53
80:18:573:U:H2'	80:18:574:A:H5''	1.90	0.53
80:18:1008:A:H2'	80:18:1009:A:H8	1.72	0.53
80:18:1228:A:H2'	80:18:1229:G:C8	2.44	0.53
85:28:3845:A:H2'	85:28:3846:C:C6	2.44	0.53
20:17:16:LYS:HG2	20:17:149:ILE:HG12	1.90	0.53
67:S4:62:LYS:HE2	80:18:502:C:H4'	1.90	0.53
85:28:1333:A:H2'	85:28:1334:A:H8	1.73	0.53
85:28:4258:C:H2'	85:28:4259:C:H6	1.74	0.53
85:28:4552:U:H2'	85:28:4553:A:C8	2.44	0.53
1:IF:307:CYS:HA	1:IF:310:LEU:HB2	1.91	0.52
6:58:141:C:H2'	6:58:142:U:C6	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:6:59:G:H4'	11:L5:267:ASN:HD21	1.74	0.52
8:L8:14:SER:H	8:L8:17:ARG:HG3	1.74	0.52
13:L7:70:MET:HA	13:L7:73:MET:HE2	1.92	0.52
51:Q:181:ARG:HB2	51:Q:184:ARG:HB2	1.90	0.52
69:S7:51:ILE:HD11	69:S7:176:VAL:HG22	1.91	0.52
85:28:1340:C:H2'	85:28:1341:U:C6	2.44	0.52
85:28:3607:U:H2'	85:28:3608:A:H8	1.74	0.52
85:28:3611:A:H2	85:28:5016:A:H8	1.57	0.52
85:28:4756:C:H5'	85:28:4757:C:OP1	2.09	0.52
21:19:46:LYS:HE3	85:28:2710:C:H41	1.73	0.52
70:YY:112:ASN:HA	70:YY:116:VAL:HG12	1.90	0.52
80:18:1131:G:H2'	80:18:1132:C:C6	2.44	0.52
80:18:1687:C:H2'	80:18:1688:C:H6	1.74	0.52
85:28:456:C:H2'	85:28:457:G:H8	1.73	0.52
85:28:667:A:H5''	85:28:668:C:H5	1.74	0.52
85:28:4344:U:H2'	85:28:4345:C:H6	1.74	0.52
1:IF:116:ARG:CG	1:IF:117:LEU:H	2.18	0.52
1:IF:265:LEU:HD11	1:IF:287:LEU:HD12	1.90	0.52
7:6:3:C:H2'	7:6:4:U:H6	1.73	0.52
48:s:180:ILE:HG12	48:s:182:PRO:HD3	1.90	0.52
80:18:1017:U:H2'	80:18:1018:U:H6	1.74	0.52
80:18:1558:C:H2'	80:18:1559:C:C6	2.45	0.52
85:28:233:U:H2'	85:28:234:G:H8	1.74	0.52
85:28:2413:U:H2'	85:28:2414:G:C8	2.44	0.52
59:AA:79:LEU:HB2	59:AA:113:PHE:CZ	2.44	0.52
59:AA:162:ASN:HB3	59:AA:164:ILE:HD12	1.91	0.52
60:OO:24:LEU:HB3	60:OO:32:LEU:HD11	1.92	0.52
62:LL:63:GLU:O	62:LL:67:VAL:HG23	2.10	0.52
80:18:354:U:H2'	80:18:355:G:C8	2.45	0.52
80:18:1337:C:H2'	80:18:1338:G:C8	2.45	0.52
85:28:2376:A:H2'	85:28:2377:C:C6	2.45	0.52
85:28:4091:G:H2'	85:28:4092:G:C8	2.44	0.52
85:28:4458:C:H2'	85:28:4459:U:H6	1.75	0.52
12:L6:108:ARG:HD2	85:28:470:A:H1'	1.91	0.52
38:38:2:PRO:HB2	85:28:2692:U:O2	2.09	0.52
85:28:1505:C:H2'	85:28:1506:G:C8	2.44	0.52
85:28:2553:A:H2	85:28:2765:A:H62	1.55	0.52
7:6:2:U:H2'	7:6:3:C:H6	1.75	0.52
50:F:21:TYR:CD1	50:F:324:LEU:HD21	2.45	0.52
66:S6:131:ARG:HG3	75:W:82:ILE:HG22	1.92	0.52
80:18:344:U:H2'	80:18:345:U:C6	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:18:1305:C:H2'	80:18:1306:U:C6	2.45	0.52
80:18:1627:C:H2'	80:18:1628:C:C6	2.45	0.52
85:28:2704:C:H2'	85:28:2705:G:O4'	2.10	0.52
85:28:4343:U:H2'	85:28:4344:U:C6	2.44	0.52
1:IF:357:LEU:HD11	1:IF:393:PHE:HB3	1.91	0.52
3:S2:166:ARG:HB3	3:S2:247:THR:HB	1.90	0.52
12:L6:165:VAL:HG13	12:L6:180:GLY:H	1.74	0.52
26:26:11:ARG:HG3	85:28:229:G:H5''	1.90	0.52
28:dd:100:ILE:HG13	28:dd:123:ILE:HB	1.91	0.52
29:29:4:SER:HB2	85:28:1855:G:OP1	2.09	0.52
80:18:440:G:H2'	80:18:441:C:O4'	2.10	0.52
85:28:517:C:H2'	85:28:518:G:C8	2.44	0.52
85:28:1204:C:H2'	85:28:1205:G:C8	2.44	0.52
85:28:2521:G:H2'	85:28:2522:G:C8	2.45	0.52
16:13:50:PRO:HG3	35:35:121:VAL:HG22	1.90	0.52
59:AA:205:SER:HA	59:AA:221:LEU:HB2	1.91	0.52
67:S4:166:THR:HG23	67:S4:168:LYS:H	1.75	0.52
80:18:5:U:O2'	80:18:602:G:H4'	2.09	0.52
80:18:21:U:H2'	80:18:22:A:C8	2.45	0.52
80:18:1457:U:H2'	80:18:1458:G:H8	1.75	0.52
80:18:1537:A:H2'	80:18:1538:C:C6	2.44	0.52
81:v:138:GLN:HA	81:v:141:THR:HG22	1.91	0.52
81:v:692:LEU:HD11	81:v:738:PRO:HB2	1.90	0.52
85:28:426:A:H2'	85:28:427:A:H8	1.75	0.52
85:28:1340:C:H2'	85:28:1341:U:H6	1.74	0.52
85:28:4578:G:H2'	85:28:4579:U:C6	2.45	0.52
1:IF:253:GLN:NE2	1:IF:253:GLN:HA	2.24	0.52
16:13:91:ALA:HB1	16:13:96:ILE:HB	1.91	0.52
53:EE:52:LEU:HD13	53:EE:65:VAL:HG11	1.92	0.52
53:EE:86:GLY:O	53:EE:89:VAL:HG12	2.09	0.52
55:S5:125:SER:HA	55:S5:138:ALA:HA	1.92	0.52
74:S8:66:SER:HA	74:S8:73:THR:HB	1.92	0.52
75:W:13:ILE:HD11	75:W:32:LEU:HB2	1.91	0.52
85:28:462:G:H2'	85:28:463:A:C8	2.45	0.52
85:28:1749:A:H2'	85:28:1750:G:C8	2.45	0.52
85:28:4173:G:H2'	85:28:4174:U:H6	1.75	0.52
85:28:4174:U:H2'	85:28:4175:G:H8	1.75	0.52
85:28:4459:U:H2'	85:28:4460:U:C6	2.43	0.52
1:IF:215:PHE:CE1	1:IF:228:PRO:HD2	2.45	0.52
2:BB:198:MET:HB3	72:RS:85:VAL:HG11	1.90	0.52
45:AS:146:ARG:HD3	45:AS:206:PRO:HG3	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
71:S3:107:TYR:HA	71:S3:110:LEU:HB2	1.90	0.52
72:RS:41:ILE:HG21	72:RS:47:ARG:HB2	1.91	0.52
80:18:910:G:H2'	80:18:911:C:C6	2.45	0.52
80:18:958:G:H2'	80:18:959:G:O4'	2.10	0.52
80:18:982:G:H2'	80:18:983:A:H8	1.75	0.52
85:28:1504:G:H2'	85:28:1505:C:H6	1.75	0.52
85:28:1662:C:H2'	85:28:1663:C:H6	1.75	0.52
85:28:3610:A:H2'	85:28:3611:A:C8	2.44	0.52
85:28:4716:C:H2'	85:28:4717:A:H8	1.75	0.52
2:BB:132:GLN:HB3	2:BB:133:PRO:HD3	1.91	0.51
16:13:48:PRO:HG3	35:35:118:LYS:HE3	1.92	0.51
53:EE:52:LEU:HD11	53:EE:62:VAL:HG23	1.91	0.51
80:18:1501:C:H2'	80:18:1502:C:H6	1.74	0.51
80:18:1798:C:H2'	80:18:1799:G:O4'	2.10	0.51
85:28:1494:U:H2'	85:28:1495:G:H8	1.75	0.51
85:28:4319:C:H2'	85:28:4320:G:C8	2.44	0.51
8:L8:183:GLY:HA2	85:28:1613:A:H5''	1.92	0.51
19:bb:157:GLU:HA	19:bb:160:ARG:HG2	1.92	0.51
26:26:89:LYS:HG2	26:26:90:ALA:H	1.75	0.51
33:ee:45:LYS:HD2	33:ee:105:LEU:HA	1.92	0.51
61:MM:100:ALA:O	61:MM:104:LEU:HG	2.11	0.51
78:11:110:GLN:HG2	78:11:111:GLU:HG2	1.92	0.51
80:18:949:G:H2'	80:18:950:C:C6	2.45	0.51
80:18:1189:A:H2'	80:18:1190:A:H8	1.76	0.51
80:18:1232:U:H2'	80:18:1233:G:C8	2.45	0.51
80:18:1511:U:H2'	80:18:1512:C:H6	1.74	0.51
81:v:683:PHE:O	81:v:687:THR:HG22	2.11	0.51
85:28:245:C:H4'	85:28:246:G:O5'	2.10	0.51
6:58:67:U:H2'	6:58:68:G:C8	2.43	0.51
6:58:106:G:H4'	6:58:137:A:H5'	1.92	0.51
14:aa:317:LYS:HE3	45:AS:225:LEU:HB2	1.92	0.51
80:18:509:G:H2'	80:18:510:G:H8	1.75	0.51
80:18:1712:A:H2'	80:18:1713:C:H6	1.75	0.51
85:28:268:G:H2'	85:28:269:G:H8	1.75	0.51
85:28:676:C:H2'	85:28:677:G:H8	1.75	0.51
85:28:1867:A:H2'	85:28:1868:A:C8	2.46	0.51
85:28:2568:C:H2'	85:28:2569:G:H8	1.74	0.51
85:28:3732:A:H2'	85:28:3733:A:C8	2.45	0.51
85:28:4973:U:H2'	85:28:4974:C:C6	2.45	0.51
6:58:8:U:H2'	6:58:9:A:H8	1.74	0.51
6:58:153:C:H2'	6:58:154:G:H8	1.76	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:bb:168:TYR:CE2	19:bb:172:LYS:HD2	2.45	0.51
31:31:64:ILE:HD11	85:28:2373:C:H4'	1.91	0.51
57:II:140:ARG:HB2	80:18:1644:C:H4'	1.91	0.51
71:S3:141:LYS:HA	71:S3:147:ALA:HA	1.91	0.51
85:28:4584:A:H2'	85:28:4585:U:O4'	2.10	0.51
5:DD:96:ILE:HD12	64:RR:10:ALA:HB1	1.93	0.51
7:6:26:C:H5''	11:L5:56:THR:HG21	1.91	0.51
33:ee:47:CYS:HB3	33:ee:103:VAL:HG12	1.92	0.51
85:28:1169:G:H2'	85:28:1170:G:C8	2.40	0.51
85:28:1345:A:H2'	85:28:1346:C:C6	2.45	0.51
85:28:2683:C:H2'	85:28:2684:C:C6	2.45	0.51
85:28:3721:U:H2'	85:28:3722:G:C8	2.46	0.51
8:L8:194:ASN:HB2	85:28:1539:G:H4'	1.91	0.51
11:L5:181:PRO:HG2	11:L5:195:HIS:HD2	1.75	0.51
54:TT:50:PHE:CZ	54:TT:58:LEU:HD13	2.45	0.51
80:18:1159:G:H2'	80:18:1160:U:H6	1.76	0.51
80:18:1690:U:H2'	80:18:1691:U:H6	1.76	0.51
85:28:1346:C:H2'	85:28:1347:G:H8	1.76	0.51
85:28:2078:C:H2'	85:28:2079:G:H8	1.76	0.51
11:L5:108:ARG:CZ	11:L5:253:TYR:HB2	2.41	0.51
21:19:108:ARG:HA	21:19:111:GLU:HG2	1.91	0.51
45:AS:179:ASN:HB3	45:AS:183:GLU:HB2	1.93	0.51
59:AA:174:VAL:HB	59:AA:188:HIS:HB2	1.91	0.51
80:18:528:A:H2'	80:18:529:A:H8	1.76	0.51
80:18:1140:G:H2'	80:18:1141:G:H8	1.74	0.51
83:A:77:LYS:HE2	83:A:79:HIS:CE1	2.45	0.51
85:28:677:G:H2'	85:28:678:C:H6	1.74	0.51
85:28:734:G:H1	85:28:929:A:N6	2.09	0.51
85:28:2544:G:H5''	85:28:2545:U:H5	1.75	0.51
85:28:3607:U:H2'	85:28:3608:A:C8	2.46	0.51
85:28:4704:C:H2'	85:28:4705:A:C8	2.46	0.51
49:t:143:VAL:C	49:t:145:GLY:H	2.18	0.51
80:18:29:G:H2'	80:18:30:C:C6	2.45	0.51
80:18:126:G:H21	80:18:180:G:N2	2.06	0.51
85:28:325:U:H2'	85:28:326:C:C6	2.45	0.51
85:28:734:G:C2	85:28:735:G:C8	2.99	0.51
85:28:1348:U:H2'	85:28:1349:G:H8	1.75	0.51
85:28:1398:A:H61	85:28:1419:G:H2'	1.76	0.51
85:28:2079:G:H2'	85:28:2080:U:C6	2.46	0.51
85:28:4092:G:H2'	85:28:4093:G:H8	1.76	0.51
6:58:124:U:H4'	6:58:125:C:O5'	2.09	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:F:31:VAL:HG21	50:F:56:ILE:HG22	1.91	0.51
50:F:46:LEU:HB3	50:F:91:PRO:HG2	1.92	0.51
59:AA:270:LEU:HB3	59:AA:310:TRP:CZ2	2.46	0.51
71:S3:59:LEU:HA	71:S3:66:ILE:HG13	1.92	0.51
80:18:1035:A:C4	80:18:1036:A:C8	2.98	0.51
80:18:1183:A:H2'	80:18:1184:G:H8	1.76	0.51
80:18:1350:U:C2	80:18:1351:G:C8	2.99	0.51
85:28:163:A:H2'	85:28:164:G:C8	2.46	0.51
85:28:1933:G:H2'	85:28:1934:A:C8	2.46	0.51
85:28:2015:U:H2'	85:28:2016:C:C6	2.46	0.51
85:28:2277:C:H2'	85:28:2278:G:C8	2.46	0.51
85:28:3707:U:H2'	85:28:3708:C:H6	1.76	0.51
85:28:3727:A:H2'	85:28:3728:A:C8	2.46	0.51
85:28:4320:G:H2'	85:28:4321:U:C6	2.46	0.51
6:58:70:G:N2	6:58:87:G:H1'	2.26	0.51
68:S9:108:ARG:HA	68:S9:113:GLN:HE21	1.76	0.51
80:18:957:A:H3'	80:18:958:G:N2	2.21	0.51
85:28:1329:G:H2'	85:28:3865:A:H5'	1.92	0.51
85:28:1965:G:H2'	85:28:1966:C:C6	2.46	0.51
85:28:4538:G:H2'	85:28:4539:U:C6	2.46	0.51
1:IF:181:LEU:HG	1:IF:237:ALA:HB2	1.92	0.50
6:58:5:U:H2'	6:58:6:C:H6	1.76	0.50
6:58:64:U:C2	6:58:65:A:C8	2.99	0.50
66:S6:2:LYS:HB3	66:S6:15:LEU:HD11	1.93	0.50
76:GG:121:ARG:HD3	77:UU:52:ASP:HB2	1.93	0.50
80:18:729:C:H2'	80:18:730:C:H6	1.75	0.50
80:18:1590:C:H3'	80:18:1591:C:H6	1.75	0.50
80:18:1627:C:H2'	80:18:1628:C:H6	1.76	0.50
85:28:1306:C:H2'	85:28:1307:A:C8	2.43	0.50
85:28:1591:U:OP1	85:28:1592:G:H5'	2.10	0.50
85:28:2556:G:H2'	85:28:2557:G:H8	1.77	0.50
6:58:147:G:H2'	6:58:148:A:H8	1.76	0.50
11:L5:65:ALA:HB2	11:L5:74:ILE:HD13	1.93	0.50
67:S4:257:ALA:HA	67:S4:260:GLN:HG3	1.93	0.50
80:18:935:G:H2'	80:18:936:G:H8	1.77	0.50
80:18:1121:G:C2	80:18:1122:A:C8	2.99	0.50
81:v:524:LEU:HD21	81:v:544:HIS:HB3	1.93	0.50
85:28:270:U:H2'	85:28:271:C:H6	1.76	0.50
85:28:2478:C:C2	85:28:2479:G:N7	2.79	0.50
85:28:4563:U:C2	85:28:4564:A:C8	3.00	0.50
17:14:25:VAL:HG11	17:14:50:MET:HE1	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:18:482:G:N2	80:18:484:A:H3'	2.26	0.50
80:18:949:G:H2'	80:18:950:C:H6	1.77	0.50
80:18:1633:A:H2'	80:18:1634:A:H8	1.76	0.50
80:18:1712:A:H2'	80:18:1713:C:C6	2.46	0.50
85:28:1538:U:H2'	85:28:1539:G:C8	2.38	0.50
6:58:47:C:H1'	6:58:61:A:H2'	1.94	0.50
21:19:66:ASN:O	21:19:70:ARG:HG2	2.11	0.50
42:42:63:THR:HG21	42:42:87:ARG:HB3	1.93	0.50
48:s:34:ASN:HA	85:28:1968:G:O2'	2.10	0.50
72:RS:5:ARG:NH2	80:18:1454:A:H5'	2.27	0.50
80:18:1365:G:H2'	80:18:1366:G:H8	1.76	0.50
85:28:460:C:H2'	85:28:461:G:H8	1.75	0.50
85:28:1420:A:H4'	85:28:1421:G:H5'	1.94	0.50
85:28:2412:A:H2'	85:28:2413:U:H6	1.76	0.50
85:28:2633:U:H2'	85:28:2634:C:H6	1.77	0.50
85:28:3692:A:H62	85:28:3823:G:H21	1.60	0.50
6:58:5:U:H2'	6:58:6:C:C6	2.45	0.50
41:41:2:ARG:HD3	41:41:5:TRP:CD1	2.47	0.50
49:t:123:ARG:NH1	49:t:123:ARG:HA	2.27	0.50
49:t:128:THR:HA	49:t:131:GLU:HG2	1.93	0.50
55:S5:35:LEU:HD23	55:S5:35:LEU:H	1.77	0.50
55:S5:40:ALA:HB1	55:S5:45:TYR:CD2	2.46	0.50
59:AA:292:SER:HB2	59:AA:297:THR:HB	1.93	0.50
75:W:6:CYS:HB2	75:W:13:ILE:HD11	1.94	0.50
80:18:186:C:H2'	80:18:187:G:H8	1.76	0.50
80:18:1545:A:H2'	80:18:1546:G:C8	2.46	0.50
85:28:223:G:H4'	85:28:225:G:N7	2.26	0.50
85:28:3732:A:H2'	85:28:3733:A:H8	1.76	0.50
85:28:3832:U:H2'	85:28:3833:C:H6	1.77	0.50
85:28:5066:U:H2'	85:28:5067:U:C6	2.46	0.50
9:L3:263:ALA:HB3	9:L3:266:VAL:HG23	1.94	0.50
14:aa:210:ILE:HA	14:aa:254:THR:HG22	1.93	0.50
32:32:90:MET:HE2	32:32:90:MET:HA	1.94	0.50
80:18:1112:U:H2'	80:18:1113:A:C8	2.47	0.50
85:28:653:C:H2'	85:28:654:C:H6	1.76	0.50
85:28:1804:A:H4'	85:28:1805:A:O5'	2.10	0.50
85:28:1958:A:H4'	85:28:1962:A:H1'	1.93	0.50
1:IF:142:LEU:HD12	1:IF:162:LEU:HD12	1.94	0.50
6:58:144:U:H2'	6:58:145:C:H6	1.77	0.50
9:L3:161:ARG:HG2	9:L3:184:GLN:HA	1.94	0.50
10:L4:140:LYS:HE3	10:L4:245:HIS:HB2	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:AS:48:LEU:HG	76:GG:51:GLU:HG2	1.94	0.50
46:FF:110:ASP:O	46:FF:114:ARG:HG2	2.11	0.50
50:F:174:ALA:HB2	50:F:181:PRO:HD3	1.93	0.50
80:18:110:U:H2'	80:18:111:A:H8	1.73	0.50
80:18:1828:C:H2'	80:18:1829:G:C8	2.47	0.50
85:28:164:G:H2'	85:28:165:A:C8	2.47	0.50
85:28:262:G:H2'	85:28:263:G:H8	1.76	0.50
85:28:424:U:H2'	85:28:425:U:H6	1.77	0.50
85:28:711:A:H2'	85:28:712:C:C6	2.46	0.50
85:28:1676:C:H41	85:28:4378:A:H5''	1.77	0.50
85:28:2373:C:H2'	85:28:2374:A:H8	1.76	0.50
85:28:2726:G:H2'	85:28:2727:C:C6	2.46	0.50
85:28:4716:C:H2'	85:28:4717:A:C8	2.46	0.50
35:35:80:PRO:HD2	35:35:83:LEU:HD12	1.94	0.50
69:S7:117:PRO:HG2	69:S7:120:ARG:HD3	1.94	0.50
74:S8:22:HIS:HB3	80:18:433:A:H5''	1.93	0.50
74:S8:98:LYS:HB3	80:18:377:G:H5'	1.94	0.50
80:18:17:C:H2'	80:18:18:C:C6	2.47	0.50
80:18:212:C:H2'	80:18:213:G:C8	2.47	0.50
80:18:479:C:C2	80:18:480:G:C8	3.00	0.50
80:18:1035:A:H2'	80:18:1036:A:H8	1.77	0.50
80:18:1240:A:C4	83:A:100:LYS:HD2	2.47	0.50
85:28:64:A:H1'	85:28:76:A:H1'	1.93	0.50
85:28:1727:U:H2'	85:28:1728:U:C6	2.47	0.50
85:28:3917:A:H2'	85:28:3918:G:C8	2.45	0.50
3:S2:209:VAL:HG21	3:S2:233:LEU:HD11	1.94	0.50
13:L7:85:GLU:HB2	23:21:135:PRO:HB3	1.93	0.50
28:dd:85:GLN:HE22	85:28:508:G:H21	1.59	0.50
42:42:64:LYS:HD2	85:28:4370:G:H5''	1.92	0.50
57:II:74:GLY:HA2	80:18:1545:A:H4'	1.93	0.50
73:WX:105:THR:HB	73:WX:110:ILE:HG12	1.93	0.50
85:28:175:C:H2'	85:28:176:G:C8	2.45	0.50
85:28:478:G:H2'	85:28:479:G:C8	2.46	0.50
85:28:1524:A:H61	85:28:1651:G:H22	1.59	0.50
85:28:2292:C:H2'	85:28:2293:U:C6	2.47	0.50
85:28:3697:U:H5''	85:28:3698:G:H5'	1.94	0.50
14:aa:250:LYS:HB3	85:28:6:C:H5''	1.93	0.49
31:31:26:THR:HG23	85:28:4996:C:H4'	1.93	0.49
80:18:430:C:C2	80:18:431:G:C8	3.00	0.49
80:18:1253:A:H4'	80:18:1254:C:H5''	1.94	0.49
81:v:617:ILE:HD12	81:v:659:PRO:HA	1.92	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:28:2732:G:H2'	85:28:2733:C:C6	2.47	0.49
85:28:3784:A:O2'	85:28:3785:A:H3'	2.12	0.49
85:28:3933:G:H2'	85:28:3934:G:H8	1.76	0.49
85:28:4563:U:H2'	85:28:4564:A:C8	2.46	0.49
5:DD:101:ARG:HB2	64:RR:10:ALA:HB2	1.94	0.49
8:L8:24:LYS:HG3	8:L8:49:ILE:HD12	1.94	0.49
9:L3:206:PRO:HD2	9:L3:209:GLN:HG3	1.93	0.49
24:22:62:SER:HB3	24:22:73:THR:HG23	1.94	0.49
46:FF:14:SER:HB2	80:18:1016:U:H5''	1.93	0.49
77:UU:17:HIS:HB3	80:18:999:G:C8	2.47	0.49
80:18:557:U:H2'	80:18:558:G:C8	2.47	0.49
80:18:1244:U:H2'	80:18:1245:G:C8	2.43	0.49
80:18:1750:C:H2'	80:18:1751:C:H6	1.77	0.49
81:v:310:GLU:HG2	81:v:311:GLU:N	2.27	0.49
85:28:433:A:C2	85:28:3867:A:H4'	2.47	0.49
85:28:1199:G:H2'	85:28:1200:G:H8	1.77	0.49
85:28:1875:C:H2'	85:28:1876:U:C6	2.47	0.49
85:28:2293:U:H2'	85:28:2294:G:C8	2.48	0.49
85:28:2682:G:H2'	85:28:2683:C:C6	2.47	0.49
85:28:4398:C:H2'	85:28:4399:U:H6	1.76	0.49
85:28:4642:U:H2'	85:28:4643:G:H8	1.76	0.49
85:28:4968:A:H2'	85:28:4969:C:C6	2.47	0.49
11:L5:37:VAL:HG23	11:L5:48:LYS:O	2.12	0.49
57:II:104:SER:HA	57:II:107:GLU:HG3	1.93	0.49
80:18:12:U:H2'	80:18:13:C:C6	2.47	0.49
80:18:1323:U:H2'	80:18:1324:G:C8	2.48	0.49
85:28:2555:G:H2'	85:28:2556:G:H8	1.76	0.49
85:28:2743:A:H2'	85:28:2744:A:C8	2.47	0.49
85:28:4551:U:H2'	85:28:4552:U:C6	2.48	0.49
6:58:70:G:H5''	26:26:27:ARG:CZ	2.42	0.49
6:58:127:U:H2'	6:58:128:C:O4'	2.12	0.49
8:L8:116:LEU:HA	8:L8:164:ALA:HB2	1.95	0.49
10:L4:28:PHE:HA	10:L4:129:ALA:HA	1.94	0.49
18:15:49:ARG:HH12	85:28:152:U:P	2.36	0.49
50:F:121:VAL:HB	50:F:334:THR:HB	1.94	0.49
64:RR:86:PRO:HG2	64:RR:130:LEU:HD22	1.93	0.49
76:GG:42:VAL:HG11	76:GG:81:VAL:HG11	1.94	0.49
80:18:160:U:H3'	80:18:161:U:H5''	1.95	0.49
80:18:1189:A:H2'	80:18:1190:A:C8	2.47	0.49
81:v:89:ILE:HG13	81:v:91:GLN:H	1.77	0.49
85:28:50:C:C2	85:28:51:A:C8	3.00	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:28:440:U:H2'	85:28:441:G:C8	2.47	0.49
85:28:1566:C:H2'	85:28:1567:U:H6	1.76	0.49
85:28:3870:C:H2'	85:28:3871:A:C8	2.48	0.49
85:28:4652:G:H2'	85:28:4653:C:C6	2.47	0.49
3:S2:196:ILE:HB	3:S2:223:TYR:HB2	1.94	0.49
80:18:192:C:H2'	80:18:193:C:C6	2.47	0.49
80:18:434:G:H2'	80:18:435:A:C8	2.48	0.49
80:18:441:C:H2'	80:18:442:C:H6	1.77	0.49
80:18:1228:A:H2'	80:18:1229:G:H8	1.77	0.49
80:18:1347:U:H3'	80:18:1348:G:H21	1.78	0.49
80:18:1688:C:H2'	80:18:1689:C:C6	2.47	0.49
80:18:1737:G:H1	80:18:1797:U:H3	1.61	0.49
85:28:2051:C:H2'	85:28:2052:G:O4'	2.12	0.49
85:28:2566:G:H2'	85:28:2567:G:H8	1.77	0.49
85:28:2634:C:H2'	85:28:2635:U:C6	2.46	0.49
85:28:2689:C:H2'	85:28:2690:C:H6	1.77	0.49
1:IF:116:ARG:HH11	1:IF:116:ARG:CB	2.25	0.49
5:DD:85:THR:HG22	5:DD:112:HIS:HA	1.93	0.49
6:58:70:G:H22	6:58:87:G:H1'	1.77	0.49
10:L4:149:GLU:HG2	10:L4:151:PRO:HD2	1.94	0.49
10:L4:190:ARG:HD2	10:L4:194:GLY:HA3	1.95	0.49
80:18:509:G:H2'	80:18:510:G:C8	2.48	0.49
80:18:925:G:C2	80:18:926:A:C8	3.01	0.49
80:18:1739:C:H2'	80:18:1740:C:C6	2.48	0.49
80:18:1806:A:H2'	80:18:1807:C:C6	2.47	0.49
85:28:1593:A:H5''	85:28:2839:U:H5''	1.94	0.49
85:28:2676:A:C4	85:28:2677:G:C8	3.01	0.49
85:28:4761:G:H2'	85:28:4762:A:C8	2.44	0.49
85:28:4968:A:H2'	85:28:4969:C:H6	1.78	0.49
85:28:4996:C:C2	85:28:4997:G:C8	3.01	0.49
7:6:49:A:H5''	11:L5:224:SER:HB3	1.95	0.49
22:20:34:ALA:HB1	22:20:39:VAL:HG23	1.95	0.49
53:EE:26:LEU:HD12	53:EE:31:LEU:HD21	1.94	0.49
68:S9:86:VAL:HG12	68:S9:100:LEU:HD11	1.93	0.49
80:18:1030:A:H2'	80:18:1031:A:H8	1.78	0.49
80:18:1102:G:H2'	80:18:1103:C:H6	1.78	0.49
85:28:1527:A:H2'	85:28:1528:U:C6	2.47	0.49
85:28:3719:A:H2'	85:28:3720:G:H8	1.77	0.49
85:28:4383:U:H2'	85:28:4384:U:C6	2.48	0.49
85:28:4688:C:H2'	85:28:4689:U:C6	2.48	0.49
85:28:5003:U:H2'	85:28:5004:C:C6	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:S2:65:LYS:HD3	3:S2:273:LEU:HD13	1.95	0.49
58:CC:20:VAL:HG21	71:S3:72:VAL:HG22	1.93	0.49
71:S3:211:VAL:HG12	82:LA:715:ILE:HG13	1.95	0.49
80:18:107:A:H2'	80:18:108:G:H8	1.77	0.49
80:18:656:G:H5'	80:18:662:G:N2	2.27	0.49
80:18:996:A:H2'	80:18:997:A:C8	2.47	0.49
81:v:208:VAL:HG12	81:v:261:TRP:HB3	1.94	0.49
84:ES:3239:G:H2'	84:ES:3240:A:C8	2.45	0.49
85:28:158:A:H5''	85:28:159:C:H2'	1.95	0.49
85:28:222:C:H2'	85:28:223:G:O4'	2.13	0.49
85:28:4925:U:H1'	85:28:4926:C:OP2	2.13	0.49
19:bb:54:TYR:CD1	19:bb:145:VAL:HG21	2.48	0.49
30:30:29:LEU:HD23	30:30:94:LEU:HD13	1.95	0.49
45:AS:48:LEU:HD23	45:AS:48:LEU:H	1.78	0.49
61:MM:37:VAL:HG23	80:18:1567:G:H4'	1.93	0.49
64:RR:60:LYS:HB2	64:RR:114:ASP:OD1	2.13	0.49
80:18:122:G:H2'	80:18:123:G:C8	2.46	0.49
80:18:192:C:H2'	80:18:193:C:H6	1.76	0.49
80:18:577:U:H2'	80:18:578:C:H6	1.78	0.49
80:18:1092:G:H2'	80:18:1093:A:H8	1.78	0.49
80:18:1393:G:H2'	80:18:1394:G:C8	2.47	0.49
80:18:1670:C:H2'	80:18:1671:G:H8	1.76	0.49
85:28:287:U:H2'	85:28:288:G:C8	2.48	0.49
85:28:652:G:H2'	85:28:653:C:C6	2.48	0.49
85:28:2499:C:H2'	85:28:2500:U:C6	2.48	0.49
85:28:3855:C:H2'	85:28:3856:A:H8	1.78	0.49
3:S2:147:VAL:HB	82:LA:682:GLY:HA3	1.95	0.49
7:6:6:C:H4'	11:L5:52:ILE:HD13	1.94	0.49
22:20:35:PRO:HD2	22:20:39:VAL:HG21	1.94	0.49
44:gg:103:HIS:CD2	44:gg:106:LEU:HD22	2.48	0.49
45:AS:57:ILE:HB	45:AS:60:ASP:HB3	1.94	0.49
64:RR:107:ARG:HB2	64:RR:112:VAL:HG22	1.95	0.49
65:SS:62:THR:HA	65:SS:69:THR:HG22	1.95	0.49
69:S7:87:PHE:HB3	69:S7:90:LYS:HD3	1.94	0.49
71:S3:115:VAL:HG11	71:S3:142:LEU:HD21	1.95	0.49
84:ES:2947:G:H1	84:ES:3247:A:H2	1.56	0.49
85:28:714:G:H2'	85:28:715:G:H8	1.78	0.49
85:28:1684:A:C4	85:28:1685:G:C8	3.01	0.49
85:28:2417:A:C4	85:28:2418:A:C8	3.00	0.49
85:28:2699:C:H2'	85:28:2700:G:H8	1.77	0.49
85:28:5031:G:H2'	85:28:5032:C:C6	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:28:5031:G:H2'	85:28:5032:C:H6	1.78	0.49
1:IF:300:TYR:CZ	1:IF:302:ASP:HB2	2.48	0.48
39:39:16:LYS:HG3	39:39:49:LEU:HD11	1.94	0.48
44:gg:19:LYS:HG3	85:28:2337:C:H4'	1.95	0.48
61:MM:18:LEU:HD13	61:MM:134:ILE:HD13	1.95	0.48
80:18:356:C:O2	80:18:356:C:H2'	2.13	0.48
80:18:1174:U:H2'	80:18:1175:G:H8	1.77	0.48
80:18:1372:U:H2'	80:18:1373:C:O4'	2.13	0.48
80:18:1597:C:H4'	80:18:1603:G:C6	2.48	0.48
80:18:1628:C:H2'	80:18:1629:C:H6	1.79	0.48
85:28:263:G:H2'	85:28:264:C:C6	2.48	0.48
85:28:423:G:H2'	85:28:424:U:H6	1.76	0.48
85:28:1170:G:H2'	85:28:1171:G:H8	1.77	0.48
85:28:1447:C:H2'	85:28:1448:G:C8	2.48	0.48
85:28:3739:C:C2	85:28:3740:G:C8	3.01	0.48
85:28:4433:G:H2'	85:28:4434:C:H6	1.78	0.48
85:28:4593:C:H2'	85:28:4594:U:H6	1.76	0.48
85:28:4685:U:H2'	85:28:4686:G:C8	2.47	0.48
8:L8:87:PHE:CE2	85:28:4120:U:H5'	2.48	0.48
14:aa:215:ASP:HB2	14:aa:216:PRO:HD3	1.95	0.48
65:SS:10:ARG:HB3	65:SS:24:VAL:HB	1.95	0.48
67:S4:189:LEU:HD12	67:S4:190:GLY:H	1.77	0.48
80:18:441:C:H2'	80:18:442:C:C6	2.47	0.48
80:18:1297:U:H2'	80:18:1298:G:H2'	1.94	0.48
80:18:1455:A:H2'	80:18:1456:G:H8	1.78	0.48
80:18:1628:C:H2'	80:18:1629:C:C6	2.48	0.48
85:28:1447:C:H2'	85:28:1448:G:H8	1.78	0.48
85:28:1557:C:H2'	85:28:1558:A:C8	2.48	0.48
85:28:1829:G:H2'	85:28:1830:G:C8	2.48	0.48
85:28:2290:C:C2	85:28:2291:G:C8	3.00	0.48
85:28:2292:C:H2'	85:28:2293:U:H6	1.77	0.48
6:58:27:U:H2'	6:58:28:C:H6	1.79	0.48
7:6:2:U:H2'	7:6:3:C:C6	2.48	0.48
57:II:31:LEU:HD21	57:II:33:LYS:HE3	1.96	0.48
74:S8:177:SER:HB3	80:18:220:U:H5'	1.94	0.48
80:18:28:U:H2'	80:18:29:G:C8	2.47	0.48
80:18:1706:G:H2'	80:18:1707:U:H6	1.77	0.48
85:28:490:C:H2'	85:28:491:G:C8	2.48	0.48
85:28:2075:G:H2'	85:28:2076:G:H8	1.78	0.48
85:28:3722:G:H2'	85:28:3723:A:H8	1.77	0.48
85:28:4208:U:H2'	85:28:4209:G:H8	1.77	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:28:4889:G:H2'	85:28:4890:G:H8	1.78	0.48
1:IF:198:ILE:HD11	78:11:63:ARG:HH22	1.77	0.48
9:L3:231:VAL:HG21	9:L3:251:VAL:HG23	1.95	0.48
50:F:181:PRO:HA	50:F:230:VAL:HA	1.95	0.48
51:Q:53:MET:HB3	51:Q:57:ASN:HB2	1.94	0.48
80:18:15:U:H2'	80:18:16:G:O4'	2.13	0.48
80:18:939:U:H2'	80:18:940:U:C6	2.48	0.48
80:18:1413:G:H2'	80:18:1414:A:H8	1.78	0.48
80:18:1839:U:H2'	80:18:1840:U:C6	2.49	0.48
84:ES:3242:U:H2'	84:ES:3243:C:C6	2.49	0.48
85:28:652:G:H2'	85:28:653:C:H6	1.78	0.48
85:28:3719:A:C4	85:28:3720:G:C8	3.00	0.48
85:28:4993:G:H2'	85:28:4994:G:C8	2.48	0.48
25:cc:71:LEU:HG	25:cc:76:ILE:HG22	1.94	0.48
45:AS:129:THR:HB	45:AS:180:ASP:HA	1.95	0.48
72:RS:17:ILE:HD13	72:RS:24:LEU:HD23	1.94	0.48
76:GG:99:ALA:N	76:GG:133:THR:HG22	2.28	0.48
78:11:141:ILE:HG23	78:11:144:LYS:HE2	1.95	0.48
80:18:89:C:H2'	80:18:90:G:C8	2.48	0.48
80:18:749:U:H2'	80:18:750:C:C6	2.48	0.48
80:18:1017:U:H2'	80:18:1018:U:C6	2.48	0.48
80:18:1528:G:H2'	80:18:1529:C:C6	2.48	0.48
80:18:1677:U:C2	80:18:1678:A:C8	3.01	0.48
85:28:684:G:H5'	85:28:685:C:OP2	2.14	0.48
85:28:1291:G:H2'	85:28:1292:C:C6	2.48	0.48
85:28:2732:G:H2'	85:28:2733:C:H6	1.79	0.48
85:28:2780:C:H2'	85:28:2781:G:H8	1.78	0.48
85:28:4349:C:H3'	85:28:4350:C:H5'	1.96	0.48
1:IF:274:VAL:HG22	1:IF:277:ARG:HH22	1.79	0.48
6:58:141:C:H2'	6:58:142:U:H6	1.79	0.48
10:L4:221:PHE:HB3	10:L4:227:ILE:HG21	1.95	0.48
20:17:28:ASN:O	20:17:32:THR:HG22	2.13	0.48
51:Q:67:ILE:HD13	51:Q:98:LEU:HD11	1.95	0.48
80:18:1318:G:H2'	80:18:1319:U:C6	2.49	0.48
80:18:1537:A:H2'	80:18:1538:C:H6	1.77	0.48
80:18:1667:U:H2'	80:18:1668:U:C6	2.49	0.48
80:18:1740:C:H2'	80:18:1741:U:C6	2.49	0.48
83:A:38:SER:HB3	83:A:41:GLN:OE1	2.14	0.48
85:28:956:A:H1'	85:28:2076:G:H5''	1.96	0.48
85:28:3930:U:H2'	85:28:3931:C:C6	2.48	0.48
85:28:4508:C:N3	85:28:4512:U:H5	2.11	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:BB:32:PHE:HA	2:BB:35:GLU:HG3	1.96	0.48
6:58:27:U:H2'	6:58:28:C:C6	2.49	0.48
9:L3:373:LYS:HE2	85:28:4627:U:H4'	1.96	0.48
13:L7:175:ALA:HB1	85:28:2102:G:C8	2.49	0.48
27:27:59:LYS:HE2	85:28:4148:C:H5''	1.96	0.48
38:38:26:LYS:HE3	38:38:28:ASN:HB3	1.95	0.48
42:42:5:PRO:HD3	85:28:4232:U:C2	2.48	0.48
49:t:152:ILE:HD12	49:t:155:ILE:HD12	1.96	0.48
57:II:34:VAL:HG12	57:II:70:VAL:HB	1.94	0.48
62:LL:40:TYR:HA	62:LL:43:VAL:HG22	1.95	0.48
73:WX:88:LYS:HE2	80:18:419:G:H4'	1.95	0.48
78:11:108:GLY:HA3	85:28:4251:A:H5''	1.94	0.48
80:18:431:G:C2	80:18:432:G:C8	3.02	0.48
80:18:1651:A:H2'	80:18:1652:G:H8	1.79	0.48
85:28:1298:C:H2'	85:28:1299:G:C8	2.47	0.48
85:28:1308:C:H2'	85:28:1309:C:C6	2.49	0.48
85:28:1617:G:H1'	85:28:2513:A:N6	2.29	0.48
85:28:2540:C:H2'	85:28:2541:G:H8	1.79	0.48
85:28:4178:A:H2'	85:28:4179:G:C8	2.49	0.48
85:28:4460:U:H2'	85:28:4461:C:H6	1.78	0.48
1:IF:198:ILE:CD1	78:11:63:ARG:HH22	2.27	0.48
6:58:30:U:H2'	6:58:31:G:H8	1.78	0.48
8:L8:3:ARG:HD3	85:28:1628:C:H42	1.79	0.48
12:L6:165:VAL:HG12	12:L6:178:VAL:HG22	1.95	0.48
14:aa:223:LEU:HD12	14:aa:254:THR:HG21	1.95	0.48
21:19:70:ARG:HH22	85:28:2810:U:H5''	1.77	0.48
46:FF:26:LEU:HD21	46:FF:60:VAL:HG12	1.94	0.48
62:LL:43:VAL:HG11	62:LL:83:PHE:CZ	2.48	0.48
63:XX:21:CYS:HA	63:XX:30:LEU:HD11	1.96	0.48
74:S8:81:VAL:HG22	74:S8:102:VAL:HG12	1.96	0.48
80:18:220:U:H2'	80:18:221:A:H8	1.78	0.48
80:18:1126:G:H2'	80:18:1127:C:C6	2.49	0.48
85:28:1519:C:H2'	85:28:1520:C:C6	2.49	0.48
85:28:1565:A:C5	85:28:1566:C:H1'	2.48	0.48
85:28:2080:U:H2'	85:28:2081:C:H6	1.79	0.48
85:28:2373:C:H2'	85:28:2374:A:C8	2.49	0.48
85:28:2708:U:O2'	85:28:2709:C:H5'	2.13	0.48
85:28:3726:A:H2'	85:28:3727:A:C8	2.49	0.48
85:28:4228:G:H5''	85:28:4229:U:O4'	2.14	0.48
85:28:4970:C:H2'	85:28:4971:A:H8	1.78	0.48
7:6:15:C:H2'	7:6:16:A:H8	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:10:98:ARG:HB3	15:10:120:GLY:HA3	1.96	0.48
21:19:3:MET:HG2	85:28:2385:U:H4'	1.96	0.48
69:S7:73:GLN:HA	69:S7:76:GLN:HG2	1.95	0.48
80:18:409:C:H2'	80:18:410:G:H8	1.78	0.48
80:18:544:G:C2	80:18:545:A:C5	3.01	0.48
80:18:1236:G:H2'	80:18:1237:C:C6	2.48	0.48
85:28:1460:C:H2'	85:28:1461:C:H6	1.79	0.48
85:28:1463:C:H2'	85:28:1464:C:C6	2.49	0.48
85:28:1590:C:H4'	85:28:2857:A:H5'	1.96	0.48
85:28:3762:U:H2'	85:28:3763:A:O4'	2.13	0.48
85:28:4273:A:H2'	85:28:4274:A:C8	2.49	0.48
17:14:9:VAL:HG11	17:14:66:HIS:HA	1.95	0.48
24:22:84:LYS:HG3	24:22:102:VAL:HG11	1.95	0.48
27:27:51:ARG:HD2	27:27:65:ARG:HD2	1.96	0.48
50:F:191:LYS:HB2	50:F:194:VAL:HB	1.96	0.48
55:S5:31:ASN:HB2	55:S5:117:ILE:HD13	1.96	0.48
78:11:27:GLY:HA2	78:11:68:ILE:HB	1.96	0.48
80:18:102:A:H4'	80:18:104:A:C8	2.49	0.48
80:18:1128:C:H2'	80:18:1129:G:C8	2.48	0.48
80:18:1144:A:H2'	80:18:1145:A:C8	2.49	0.48
85:28:424:U:H2'	85:28:425:U:C6	2.49	0.48
85:28:1824:G:H2'	85:28:1825:A:C8	2.49	0.48
1:IF:84:LEU:HD12	1:IF:119:LEU:HD22	1.96	0.47
2:BB:148:CYS:SG	2:BB:160:ALA:HB1	2.54	0.47
2:BB:201:LEU:HD11	72:RS:83:ASN:HA	1.96	0.47
3:S2:104:ASP:HB3	3:S2:130:ILE:HG13	1.96	0.47
5:DD:132:ARG:HD3	80:18:114:G:H5'	1.96	0.47
9:L3:303:ALA:HB3	9:L3:312:LYS:HG3	1.96	0.47
23:21:119:ALA:HA	23:21:122:LYS:HB2	1.96	0.47
59:AA:12:LYS:HB3	59:AA:306:LEU:HD13	1.96	0.47
80:18:399:C:H3'	80:18:400:C:H5'	1.95	0.47
80:18:574:A:H2'	80:18:574:A:N3	2.29	0.47
80:18:1562:C:H2'	80:18:1563:G:H8	1.79	0.47
85:28:1192:C:H2'	85:28:1193:C:C6	2.49	0.47
85:28:3769:C:H2'	85:28:3770:U:C6	2.48	0.47
85:28:4254:G:H2'	85:28:4254:G:N3	2.29	0.47
85:28:4357:G:H2'	85:28:4358:U:H6	1.79	0.47
85:28:4737:G:H2'	85:28:4738:C:C6	2.49	0.47
85:28:5002:U:H2'	85:28:5003:U:H6	1.78	0.47
28:dd:85:GLN:NE2	85:28:508:G:H21	2.12	0.47
67:S4:7:LYS:HB2	80:18:93:U:O2'	2.13	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
67:S4:128:LYS:HA	67:S4:156:VAL:HG13	1.96	0.47
80:18:87:U:C2	80:18:88:G:C8	3.02	0.47
80:18:409:C:H2'	80:18:410:G:C8	2.49	0.47
80:18:636:C:H2'	80:18:637:U:O4'	2.13	0.47
80:18:1375:G:H5'	80:18:1464:C:O2	2.14	0.47
80:18:1407:U:H2'	80:18:1408:U:H6	1.79	0.47
80:18:1671:G:H2'	80:18:1672:U:H6	1.79	0.47
85:28:678:C:H2'	85:28:679:C:H6	1.78	0.47
85:28:1072:C:C2	85:28:1073:G:C8	3.01	0.47
85:28:1802:A:H5''	85:28:1803:G:H5'	1.94	0.47
85:28:2477:A:H2'	85:28:2478:C:C5	2.49	0.47
85:28:4266:G:H2'	85:28:4266:G:N3	2.29	0.47
85:28:4625:C:O2'	85:28:4626:A:H5'	2.14	0.47
85:28:4737:G:H2'	85:28:4738:C:H6	1.80	0.47
6:58:32:C:H2'	6:58:33:G:O4'	2.15	0.47
58:CC:50:GLN:HE22	80:18:1276:A:H4'	1.77	0.47
62:LL:107:LEU:O	62:LL:111:LEU:HG	2.15	0.47
69:S7:63:PHE:HB3	69:S7:97:GLN:HB2	1.96	0.47
80:18:1348:G:C8	80:18:1349:G:C8	3.02	0.47
81:v:551:GLU:O	81:v:555:GLU:HG2	2.15	0.47
85:28:270:U:H2'	85:28:271:C:C6	2.48	0.47
85:28:1564:A:H2'	85:28:1565:A:C8	2.49	0.47
85:28:1957:U:O2'	85:28:1958:A:H5'	2.14	0.47
85:28:2771:G:H2'	85:28:2772:C:O4'	2.14	0.47
85:28:4507:A:H2'	85:28:4508:C:C6	2.49	0.47
85:28:4578:G:H2'	85:28:4579:U:H6	1.78	0.47
1:IF:266:PRO:HG3	1:IF:306:LEU:HD12	1.97	0.47
1:IF:379:MET:HE3	1:IF:383:LEU:HD11	1.96	0.47
12:L6:53:VAL:HG11	85:28:947:C:H5''	1.97	0.47
13:L7:184:ILE:HG21	85:28:2102:G:C6	2.50	0.47
14:aa:195:THR:O	14:aa:199:LEU:HG	2.14	0.47
18:15:172:ARG:HG2	85:28:29:G:H5''	1.97	0.47
28:dd:29:PRO:HA	85:28:1654:G:H5''	1.96	0.47
74:S8:27:TYR:HB2	80:18:381:C:H41	1.78	0.47
80:18:26:U:H2'	80:18:27:A:H8	1.78	0.47
80:18:1090:C:H2'	80:18:1091:C:H6	1.80	0.47
85:28:125:C:H2'	85:28:126:C:H6	1.78	0.47
85:28:178:C:H2'	85:28:179:G:C8	2.48	0.47
85:28:1846:G:H2'	85:28:1847:C:H6	1.79	0.47
85:28:2264:C:H2'	85:28:2265:G:O4'	2.14	0.47
85:28:2402:G:C2	85:28:2403:A:C8	3.02	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:28:4495:G:C2	85:28:4496:A:N7	2.83	0.47
85:28:4734:A:H1'	85:28:4735:G:C8	2.49	0.47
46:FF:55:ARG:HE	80:18:1017:U:H5'	1.79	0.47
59:AA:214:GLY:HA2	59:AA:236:ILE:HG12	1.95	0.47
79:L9:92:MET:HE2	79:L9:179:ILE:HG22	1.96	0.47
80:18:1198:G:H2'	80:18:1199:A:H8	1.79	0.47
80:18:1230:C:H2'	80:18:1231:C:C6	2.49	0.47
80:18:1656:G:C2	80:18:1657:G:C8	3.02	0.47
81:v:389:ASP:HB2	81:v:391:LYS:HE3	1.96	0.47
85:28:731:G:C6	85:28:932:A:C4	3.02	0.47
85:28:970:G:H2'	85:28:971:U:O4'	2.14	0.47
85:28:2293:U:H2'	85:28:2294:G:H8	1.80	0.47
85:28:4208:U:H2'	85:28:4209:G:C8	2.50	0.47
85:28:4300:U:H2'	85:28:4301:U:C6	2.50	0.47
1:IF:334:ARG:O	1:IF:338:HIS:HB2	2.15	0.47
13:L7:50:TYR:CD1	85:28:1237:C:H2'	2.49	0.47
42:42:44:LYS:HE3	42:42:52:THR:HB	1.96	0.47
50:F:81:SER:HB2	50:F:107:LYS:HE2	1.97	0.47
59:AA:18:VAL:HA	59:AA:35:SER:HA	1.95	0.47
77:UU:17:HIS:HB3	80:18:999:G:N7	2.29	0.47
80:18:319:C:H4'	80:18:319:C:OP1	2.12	0.47
80:18:479:C:H2'	80:18:480:G:H8	1.79	0.47
80:18:950:C:H2'	80:18:951:C:H6	1.79	0.47
84:ES:2946:G:H2'	84:ES:2947:G:H8	1.74	0.47
85:28:519:C:H2'	85:28:520:U:C6	2.50	0.47
85:28:648:G:H2'	85:28:649:A:C8	2.50	0.47
85:28:1528:U:H2'	85:28:1529:G:C8	2.49	0.47
85:28:2588:C:H5''	85:28:2589:C:H5''	1.97	0.47
85:28:4233:A:C8	85:28:4235:G:C8	3.02	0.47
85:28:4704:C:H2'	85:28:4705:A:H8	1.80	0.47
1:IF:265:LEU:HD13	1:IF:284:ILE:HG12	1.97	0.47
3:S2:106:VAL:HG22	3:S2:128:VAL:HG22	1.97	0.47
5:DD:126:VAL:HG13	5:DD:142:VAL:HG13	1.97	0.47
6:58:65:A:H2'	6:58:66:A:C8	2.50	0.47
7:6:36:C:H2'	7:6:37:G:C8	2.49	0.47
8:L8:125:LYS:HB3	85:28:3681:G:C6	2.50	0.47
9:L3:293:ILE:HA	9:L3:298:LEU:HA	1.97	0.47
20:17:83:TRP:O	85:28:3856:A:H5''	2.15	0.47
40:40:99:LYS:HG3	85:28:4474:A:H5'	1.97	0.47
50:F:32:LEU:HD12	50:F:110:LEU:HD21	1.95	0.47
51:Q:63:LEU:O	51:Q:67:ILE:HG12	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:AA:277:THR:HB	59:AA:281:ALA:HB3	1.97	0.47
62:LL:102:GLY:HA2	62:LL:105:ASN:HB2	1.97	0.47
62:LL:120:HIS:HD2	83:A:121:ILE:HG22	1.79	0.47
66:S6:63:MET:HE3	66:S6:100:CYS:HA	1.97	0.47
66:S6:131:ARG:HB3	80:18:168:C:O2'	2.15	0.47
67:S4:79:ASP:HB3	67:S4:82:TYR:HB2	1.97	0.47
67:S4:80:ILE:HG23	67:S4:81:THR:HG23	1.96	0.47
80:18:98:C:H2'	80:18:426:A:H4'	1.96	0.47
80:18:123:G:H3'	80:18:124:U:H5''	1.97	0.47
80:18:537:C:H2'	80:18:538:U:C5	2.50	0.47
80:18:887:U:H2'	80:18:888:U:H5''	1.97	0.47
80:18:1395:C:H2'	80:18:1396:A:C2	2.49	0.47
80:18:1591:C:H2'	80:18:1592:C:C6	2.49	0.47
80:18:1687:C:H2'	80:18:1688:C:C6	2.49	0.47
81:v:27:HIS:HB3	81:v:30:HIS:CE1	2.50	0.47
81:v:30:HIS:CE1	81:v:130:ASP:H	2.33	0.47
81:v:324:ASP:HB3	81:v:342:ARG:HH12	1.80	0.47
81:v:648:LYS:HB3	81:v:664:ASP:HB3	1.95	0.47
85:28:271:C:H2'	85:28:272:U:C6	2.50	0.47
85:28:673:C:H2'	85:28:674:G:H8	1.79	0.47
85:28:1450:C:H2'	85:28:1451:G:C8	2.49	0.47
85:28:1739:G:H2'	85:28:1740:C:C6	2.49	0.47
85:28:4399:U:C2	85:28:4400:G:C8	3.02	0.47
85:28:5004:C:H2'	85:28:5005:G:O4'	2.14	0.47
86:23:11:GLY:H	86:23:128:LEU:HD13	1.80	0.47
8:L8:21:LYS:HG2	85:28:1541:C:H5''	1.96	0.47
74:S8:129:LEU:HD23	74:S8:132:GLU:H	1.80	0.47
77:UU:84:VAL:HG12	80:18:1867:U:C4	2.50	0.47
80:18:51:U:H2'	80:18:52:G:H8	1.80	0.47
80:18:89:C:H2'	80:18:90:G:H8	1.80	0.47
80:18:387:C:H2'	80:18:388:U:C6	2.50	0.47
80:18:465:A:H5''	80:18:466:G:C4	2.49	0.47
80:18:953:C:H2'	80:18:954:U:O4'	2.15	0.47
80:18:991:G:C6	80:18:1134:G:H4'	2.50	0.47
80:18:1482:C:H2'	80:18:1483:A:O4'	2.15	0.47
80:18:1673:U:H2'	80:18:1674:G:O4'	2.15	0.47
80:18:1709:G:H2'	80:18:1710:C:H6	1.79	0.47
81:v:110:ASP:HB3	81:v:553:HIS:HB2	1.97	0.47
85:28:963:G:O2'	85:28:964:A:H8	1.96	0.47
85:28:2749:C:H2'	85:28:2750:G:C8	2.50	0.47
85:28:2870:A:H2'	85:28:2871:A:C8	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:IF:205:LEU:HD11	1:IF:246:LEU:HD23	1.97	0.47
61:MM:48:TYR:HB2	80:18:1539:U:H1'	1.96	0.47
77:UU:28:ARG:HD3	77:UU:74:CYS:SG	2.55	0.47
80:18:348:A:H2'	80:18:349:A:C8	2.50	0.47
80:18:644:G:H2'	80:18:645:C:C6	2.49	0.47
80:18:812:A:C5	80:18:813:A:C8	3.03	0.47
80:18:928:G:H2'	80:18:929:G:C8	2.50	0.47
80:18:1090:C:H2'	80:18:1091:C:C6	2.50	0.47
85:28:2079:G:H2'	85:28:2080:U:H6	1.79	0.47
85:28:3770:U:H2'	85:28:3771:C:C6	2.49	0.47
2:BB:39:TYR:CE2	72:RS:105:MET:HB3	2.51	0.47
7:6:112:U:H2'	7:6:113:G:H8	1.80	0.47
25:cc:77:ILE:HD12	25:cc:116:LEU:HD12	1.96	0.47
50:F:249:ARG:HB3	50:F:275:ALA:HA	1.97	0.47
68:S9:12:THR:O	68:S9:45:ARG:HA	2.14	0.47
74:S8:49:ARG:HD3	80:18:381:C:C5	2.50	0.47
78:11:111:GLU:HB2	78:11:125:ILE:HD11	1.97	0.47
80:18:89:C:O2'	80:18:499:G:H5''	2.15	0.47
80:18:193:C:H2'	80:18:194:C:H6	1.80	0.47
80:18:481:C:H2'	80:18:482:G:C8	2.49	0.47
80:18:883:U:H2'	80:18:884:C:C6	2.50	0.47
81:v:503:PRO:HB2	81:v:547:ALA:HB1	1.97	0.47
85:28:654:C:H2'	85:28:655:C:H6	1.80	0.47
85:28:1829:G:H2'	85:28:1830:G:H8	1.80	0.47
85:28:1831:G:H2'	85:28:1832:C:O4'	2.15	0.47
85:28:2502:A:H4'	85:28:2503:G:OP2	2.15	0.47
85:28:2608:G:H2'	85:28:2609:G:H8	1.80	0.47
1:IF:431:ARG:O	1:IF:435:ARG:HG3	2.15	0.46
6:58:130:C:H2'	6:58:131:G:H8	1.80	0.46
7:6:16:A:H2'	7:6:17:C:C6	2.50	0.46
27:27:95:VAL:HG12	27:27:110:ALA:HA	1.96	0.46
28:dd:125:LYS:HG2	28:dd:145:VAL:HB	1.95	0.46
44:gg:28:GLU:HB2	44:gg:31:ASN:HB2	1.96	0.46
58:CC:3:MET:HE3	58:CC:44:HIS:HB3	1.97	0.46
68:S9:164:PRO:HB3	68:S9:170:PRO:HA	1.97	0.46
69:S7:36:LEU:HD22	69:S7:75:ILE:HD11	1.96	0.46
80:18:901:G:H2'	80:18:902:G:H8	1.79	0.46
80:18:976:G:H2'	80:18:977:C:O4'	2.16	0.46
80:18:1031:A:H2'	80:18:1032:C:C6	2.50	0.46
80:18:1199:A:H2'	80:18:1200:A:C8	2.50	0.46
85:28:1236:C:H2'	85:28:1238:A:C8	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:28:1744:U:C2	85:28:1745:G:C8	3.03	0.46
1:IF:351:ARG:HG2	1:IF:356:VAL:HG22	1.97	0.46
45:AS:139:CYS:HB3	45:AS:172:MET:HE3	1.98	0.46
59:AA:220:ASP:HB3	59:AA:223:GLU:O	2.15	0.46
61:MM:85:ASN:HB2	61:MM:88:MET:HB2	1.97	0.46
71:S3:161:GLY:CA	80:18:1388:A:H61	2.28	0.46
80:18:677:G:H2'	80:18:678:U:C6	2.50	0.46
80:18:896:U:H2'	80:18:897:U:C6	2.51	0.46
81:v:421:VAL:HA	81:v:425:LEU:HG	1.96	0.46
85:28:1206:C:H2'	85:28:1207:C:H6	1.81	0.46
85:28:1468:C:C2	85:28:1469:C:C5	3.03	0.46
85:28:1920:C:H3'	85:28:1921:C:H5''	1.97	0.46
85:28:2542:G:H2'	85:28:2543:A:C8	2.49	0.46
85:28:4130:C:H2'	85:28:4131:G:H8	1.80	0.46
85:28:4189:U:H2'	85:28:4190:U:O4'	2.15	0.46
85:28:4244:A:H2'	85:28:4245:G:O4'	2.15	0.46
85:28:4406:U:C2	85:28:4407:G:C8	3.03	0.46
85:28:4565:C:H2'	85:28:4566:U:H6	1.81	0.46
85:28:4586:G:C2	85:28:4587:G:C8	3.04	0.46
85:28:5002:U:H2'	85:28:5003:U:C6	2.50	0.46
1:IF:211:VAL:HG12	1:IF:235:LEU:HD23	1.97	0.46
9:L3:301:ASN:HB3	9:L3:311:ASP:HA	1.96	0.46
17:14:26:ALA:HB2	17:14:77:TRP:HZ3	1.81	0.46
28:dd:35:ALA:HB2	85:28:38:A:H5''	1.97	0.46
45:AS:115:LYS:H	45:AS:118:GLN:NE2	2.12	0.46
55:S5:74:ASN:HD21	55:S5:86:LYS:HE3	1.80	0.46
64:RR:90:CYS:HA	64:RR:93:PHE:CD1	2.50	0.46
72:RS:77:GLU:HA	72:RS:80:ARG:HG2	1.96	0.46
80:18:152:U:H2'	80:18:153:G:H8	1.81	0.46
80:18:394:G:C2	80:18:395:G:C8	3.04	0.46
80:18:464:A:H3'	80:18:465:A:H5'	1.97	0.46
80:18:1531:A:H2'	80:18:1532:C:C6	2.50	0.46
85:28:1846:G:H2'	85:28:1847:C:C6	2.51	0.46
1:IF:167:VAL:HG13	1:IF:207:CYS:SG	2.54	0.46
3:S2:66:LEU:HD12	3:S2:86:LEU:HD12	1.97	0.46
9:L3:301:ASN:HB2	9:L3:304:SER:HB2	1.97	0.46
11:L5:195:HIS:CE1	11:L5:199:ILE:HD11	2.50	0.46
15:10:36:LEU:HD23	15:10:69:ARG:HH11	1.80	0.46
18:15:5:LYS:NZ	36:36:37:THR:HG22	2.30	0.46
20:17:54:LYS:HA	20:17:83:TRP:CD1	2.50	0.46
26:26:100:HIS:CD2	85:28:231:U:H4'	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:27:11:VAL:CG1	27:27:80:LEU:HB3	2.44	0.46
50:F:75:ALA:HB1	50:F:118:ILE:HG23	1.97	0.46
59:AA:270:LEU:HD22	59:AA:310:TRP:CE3	2.50	0.46
71:S3:39:VAL:HA	71:S3:48:ILE:HG22	1.96	0.46
80:18:126:G:N2	80:18:180:G:H21	2.10	0.46
80:18:569:A:H2'	80:18:570:C:C6	2.51	0.46
80:18:1177:U:H2'	80:18:1178:U:C6	2.50	0.46
80:18:1265:A:H5''	80:18:1266:C:OP2	2.16	0.46
80:18:1461:G:H1'	80:18:1465:A:N6	2.30	0.46
80:18:1554:C:H2'	80:18:1555:U:C5	2.50	0.46
85:28:317:A:C2	85:28:4361:U:H1'	2.50	0.46
85:28:1468:C:H2'	85:28:1469:C:C6	2.50	0.46
85:28:4594:U:C2	85:28:4595:G:C8	3.03	0.46
2:BB:140:VAL:HB	2:BB:142:LEU:HG	1.97	0.46
3:S2:272:HIS:O	3:S2:276:THR:HG22	2.16	0.46
6:58:65:A:C4	6:58:66:A:C8	3.04	0.46
7:6:46:C:OP1	11:L5:158:LYS:HG3	2.16	0.46
10:L4:78:ARG:HA	10:L4:90:GLY:HA2	1.98	0.46
17:14:39:ASP:OD2	17:14:70:GLN:HG2	2.15	0.46
59:AA:10:THR:HG22	59:AA:308:ARG:HB3	1.98	0.46
64:RR:105:PHE:HB3	64:RR:112:VAL:HG21	1.98	0.46
80:18:432:G:H2'	80:18:433:A:C8	2.50	0.46
80:18:600:G:C2	80:18:601:G:C8	3.03	0.46
80:18:1653:U:H2'	80:18:1654:G:C8	2.51	0.46
85:28:1201:U:H2'	85:28:1202:C:C6	2.50	0.46
85:28:1804:A:H5''	85:28:1806:G:C8	2.51	0.46
85:28:2499:C:H2'	85:28:2500:U:H6	1.81	0.46
85:28:2547:G:H2'	85:28:2548:C:C6	2.50	0.46
85:28:5042:A:C4	85:28:5043:A:C8	3.04	0.46
4:PP:39:VAL:HG22	4:PP:44:GLY:HA2	1.98	0.46
6:58:96:C:H5''	35:35:66:LYS:HG2	1.97	0.46
8:L8:244:GLY:HA3	85:28:3746:A:H5''	1.98	0.46
32:32:35:TRP:CZ2	32:32:56:PRO:HD2	2.51	0.46
68:S9:42:GLU:HA	68:S9:45:ARG:HB3	1.97	0.46
80:18:1161:U:H2'	80:18:1162:C:C6	2.50	0.46
85:28:963:G:N3	85:28:964:A:C8	2.83	0.46
85:28:1472:C:H2'	85:28:1473:U:C6	2.51	0.46
85:28:1519:C:H2'	85:28:1520:C:H6	1.81	0.46
85:28:4605:A:H2'	85:28:4606:G:O4'	2.16	0.46
1:IF:314:ALA:O	1:IF:330:ARG:HG2	2.15	0.46
47:VV:35:VAL:HG11	47:VV:63:LEU:HG	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:CC:52:LEU:HB3	58:CC:57:TYR:HB2	1.97	0.46
68:S9:117:LEU:HD23	68:S9:119:LEU:HD11	1.98	0.46
80:18:530:U:H2'	80:18:531:A:C8	2.40	0.46
80:18:609:U:H2'	80:18:610:G:H8	1.80	0.46
85:28:2479:G:H2'	85:28:2480:G:H8	1.80	0.46
85:28:2682:G:H2'	85:28:2683:C:H6	1.81	0.46
85:28:3768:U:H2'	85:28:3769:C:H6	1.81	0.46
85:28:3794:C:H2'	85:28:3795:A:H8	1.81	0.46
85:28:4708:A:N3	85:28:4709:U:H5'	2.31	0.46
6:58:132:G:H2'	6:58:133:G:H8	1.81	0.46
16:13:72:ALA:HA	16:13:157:ILE:HD12	1.98	0.46
21:19:105:LEU:HD22	21:19:135:LYS:HG3	1.98	0.46
25:cc:76:ILE:HA	25:cc:101:ASP:HB2	1.98	0.46
26:26:8:THR:HG21	26:26:13:LYS:HB2	1.97	0.46
39:39:8:ARG:H	39:39:8:ARG:HD2	1.81	0.46
42:42:9:ARG:HA	42:42:20:PRO:HA	1.97	0.46
61:MM:22:LEU:HB3	61:MM:28:LEU:HD11	1.98	0.46
66:S6:21:GLU:O	66:S6:25:ARG:HD3	2.16	0.46
79:L9:20:LEU:HB3	79:L9:25:VAL:HG12	1.97	0.46
80:18:438:G:H8	80:18:1800:A:H4'	1.80	0.46
80:18:537:C:H2'	80:18:538:U:C6	2.50	0.46
80:18:1006:C:H2'	80:18:1007:C:H6	1.81	0.46
80:18:1367:U:H2'	80:18:1368:U:C6	2.51	0.46
80:18:1501:C:H2'	80:18:1502:C:C6	2.51	0.46
85:28:247:G:H2'	85:28:248:C:H6	1.79	0.46
85:28:956:A:N6	85:28:1283:G:H1'	2.31	0.46
85:28:1346:C:H2'	85:28:1347:G:C8	2.50	0.46
85:28:1463:C:H2'	85:28:1464:C:H6	1.80	0.46
85:28:3690:U:H2'	85:28:3691:G:O4'	2.15	0.46
85:28:4595:G:H2'	85:28:4596:C:C6	2.51	0.46
86:23:13:LYS:HB2	86:23:128:LEU:HD21	1.97	0.46
86:23:43:LYS:HE2	86:23:62:MET:SD	2.56	0.46
1:IF:116:ARG:NH1	1:IF:116:ARG:CB	2.71	0.46
2:BB:206:ASP:HB3	2:BB:209:GLU:HG3	1.98	0.46
3:S2:210:PRO:HB3	3:S2:240:THR:HG21	1.98	0.46
11:L5:33:ARG:HA	11:L5:36:LEU:HB2	1.97	0.46
33:ee:46:ARG:HD2	33:ee:106:TYR:OH	2.15	0.46
49:t:104:ILE:HG23	49:t:143:VAL:HG22	1.98	0.46
65:SS:53:ASP:HB3	65:SS:79:LEU:HD13	1.98	0.46
80:18:166:A:C6	80:18:167:G:N7	2.83	0.46
80:18:501:C:H2'	80:18:502:C:H5''	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:18:577:U:H2'	80:18:578:C:C6	2.51	0.46
80:18:1046:U:H2'	80:18:1047:C:C6	2.51	0.46
80:18:1217:A:H2'	80:18:1218:C:H6	1.78	0.46
80:18:1733:U:H2'	80:18:1734:G:O4'	2.16	0.46
81:v:252:LYS:HA	81:v:255:ASP:OD2	2.16	0.46
81:v:445:LYS:HG3	81:v:478:PHE:CZ	2.51	0.46
85:28:12:A:H5'	85:28:13:U:OP2	2.16	0.46
85:28:1195:G:H2'	85:28:1196:G:H8	1.80	0.46
85:28:2633:U:H2'	85:28:2634:C:C6	2.51	0.46
85:28:3769:C:H2'	85:28:3770:U:H6	1.81	0.46
85:28:4760:G:H2'	85:28:4761:G:O4'	2.16	0.46
85:28:4890:G:H2'	85:28:4891:G:H8	1.80	0.46
3:S2:253:PRO:HA	3:S2:256:TRP:CE2	2.51	0.46
9:L3:261:ARG:HB2	19:bb:64:THR:HG21	1.97	0.46
10:L4:113:ARG:HG3	85:28:1508:A:OP1	2.15	0.46
13:L7:45:ARG:O	13:L7:49:ILE:HG12	2.16	0.46
61:MM:67:ARG:HD3	80:18:1587:G:N7	2.31	0.46
80:18:1018:U:H2'	80:18:1019:C:C6	2.51	0.46
80:18:1159:G:H2'	80:18:1160:U:C6	2.51	0.46
80:18:1384:C:C2	80:18:1385:G:C8	3.04	0.46
80:18:1686:G:H2'	80:18:1687:C:C6	2.51	0.46
80:18:1716:C:H2'	80:18:1717:C:H6	1.81	0.46
81:v:425:LEU:HD12	81:v:427:VAL:HG13	1.98	0.46
85:28:1664:U:H2'	85:28:1665:C:C6	2.51	0.46
85:28:1730:U:H2'	85:28:1731:C:C6	2.51	0.46
85:28:1973:G:OP2	85:28:1974:U:H3'	2.15	0.46
85:28:2538:U:H2'	85:28:2539:C:C6	2.51	0.46
85:28:2567:G:H2'	85:28:2568:C:H6	1.81	0.46
85:28:2591:A:H2'	85:28:2592:U:C6	2.50	0.46
85:28:2664:G:H4'	85:28:2677:G:H4'	1.97	0.46
6:58:67:U:C2	6:58:68:G:C8	3.04	0.45
7:6:3:C:H2'	7:6:4:U:C6	2.52	0.45
7:6:59:G:H2'	7:6:60:G:H8	1.81	0.45
9:L3:324:GLY:HA2	85:28:5051:C:H4'	1.98	0.45
44:gg:104:PRO:O	44:gg:107:ARG:HG2	2.16	0.45
59:AA:154:VAL:HG12	59:AA:167:SER:HB2	1.98	0.45
66:S6:172:LYS:HE2	80:18:65:C:H4'	1.97	0.45
74:S8:23:LYS:HD2	80:18:448:A:H3'	1.98	0.45
75:W:49:ILE:O	75:W:52:THR:HG22	2.16	0.45
79:L9:23:ARG:HH22	85:28:4763:U:H5''	1.81	0.45
80:18:26:U:H2'	80:18:27:A:C8	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:18:456:C:H2'	80:18:457:C:H6	1.81	0.45
80:18:1457:U:H2'	80:18:1458:G:C8	2.51	0.45
85:28:1239:C:H4'	85:28:1244:G:P	2.56	0.45
85:28:4092:G:H2'	85:28:4093:G:C8	2.51	0.45
85:28:4503:A:H2'	85:28:4504:C:H6	1.81	0.45
1:IF:350:VAL:HG12	1:IF:357:LEU:HB3	1.84	0.45
6:58:140:C:H2'	6:58:141:C:H6	1.80	0.45
9:L3:252:ALA:HB3	85:28:4457:U:H1'	1.98	0.45
15:10:16:PRO:HA	15:10:95:HIS:CD2	2.50	0.45
17:14:24:LEU:HD11	17:14:86:TRP:CG	2.51	0.45
27:27:51:ARG:HB2	27:27:65:ARG:HG3	1.97	0.45
33:ee:54:LYS:HE2	85:28:4748:U:H5''	1.97	0.45
39:39:44:TRP:CZ3	39:39:45:ARG:HD3	2.51	0.45
43:ff:52:VAL:HG21	85:28:2739:C:H4'	1.99	0.45
49:t:35:LEU:HD11	49:t:37:LEU:HB2	1.99	0.45
59:AA:108:VAL:HA	59:AA:124:SER:HA	1.99	0.45
61:MM:18:LEU:HB3	61:MM:58:ALA:HB1	1.97	0.45
62:LL:108:ARG:NH1	62:LL:109:GLU:HA	2.31	0.45
80:18:528:A:H2'	80:18:529:A:C8	2.50	0.45
80:18:1101:U:C2	80:18:1102:G:N7	2.84	0.45
80:18:1724:A:H2'	80:18:1725:U:C6	2.51	0.45
85:28:58:G:H4'	85:28:59:A:H4'	1.99	0.45
85:28:271:C:H2'	85:28:272:U:H6	1.81	0.45
85:28:1458:C:C2	85:28:1459:A:C8	3.04	0.45
85:28:2386:U:C2	85:28:2387:G:C8	3.04	0.45
85:28:2610:G:H2'	85:28:2611:A:H8	1.80	0.45
85:28:3832:U:H2'	85:28:3833:C:C6	2.51	0.45
85:28:3904:G:H1'	85:28:3905:A:OP1	2.16	0.45
85:28:4293:U:N3	85:28:4294:C:C5	2.84	0.45
1:IF:124:GLU:HB2	1:IF:162:LEU:HD21	1.98	0.45
9:L3:4:ARG:HD2	9:L3:7:SER:HA	1.98	0.45
9:L3:253:CYS:SG	85:28:4521:U:H1'	2.56	0.45
10:L4:339:THR:HA	10:L4:342:ARG:HB3	1.98	0.45
13:L7:79:ASN:HA	23:21:143:THR:HG22	1.98	0.45
14:aa:104:LEU:HD11	85:28:4086:G:C4	2.52	0.45
22:20:83:ARG:HB3	22:20:125:GLN:HB2	1.99	0.45
25:cc:87:MET:HG3	50:F:291:MET:HE1	1.97	0.45
45:AS:163:GLN:O	45:AS:167:LYS:HG2	2.17	0.45
49:t:146:ARG:HE	49:t:147:HIS:H	1.64	0.45
80:18:219:U:H2'	80:18:220:U:H6	1.81	0.45
80:18:319:C:H2'	80:18:320:G:H8	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:18:454:U:H2'	80:18:455:A:C8	2.51	0.45
80:18:527:C:H2'	80:18:528:A:H8	1.81	0.45
80:18:1174:U:H2'	80:18:1175:G:C8	2.52	0.45
81:v:132:VAL:HG13	81:v:167:LEU:HD11	1.99	0.45
85:28:2308:A:H4'	85:28:2334:C:H4'	1.98	0.45
85:28:2683:C:H2'	85:28:2684:C:H6	1.81	0.45
85:28:4134:C:H2'	85:28:4135:G:C8	2.45	0.45
85:28:4378:A:O2'	85:28:4379:A:H2'	2.17	0.45
37:37:12:ARG:HH11	85:28:2404:A:H1'	1.81	0.45
43:ff:50:ARG:HB3	43:ff:54:ILE:HD13	1.99	0.45
49:t:83:LYS:HG3	49:t:84:ALA:N	2.30	0.45
68:S9:33:GLY:HA3	70:YY:111:TYR:CD1	2.50	0.45
69:S7:7:LYS:HB3	69:S7:44:ASN:HA	1.98	0.45
80:18:168:C:H2'	80:18:169:U:H5'	1.98	0.45
80:18:354:U:H2'	80:18:355:G:H8	1.81	0.45
80:18:1065:G:H2'	80:18:1066:U:C6	2.51	0.45
80:18:1688:C:H2'	80:18:1689:C:H6	1.82	0.45
81:v:388:CYS:HB2	81:v:466:CYS:SG	2.57	0.45
85:28:149:A:H5''	85:28:151:G:O4'	2.16	0.45
85:28:153:G:H2'	85:28:154:G:H8	1.80	0.45
85:28:1077:C:C4	85:28:1078:A:N7	2.85	0.45
85:28:4345:C:H2'	85:28:4346:U:H6	1.80	0.45
85:28:5043:A:H2'	85:28:5044:A:C8	2.52	0.45
1:IF:352:PHE:HE1	1:IF:357:LEU:HB2	1.81	0.45
3:S2:166:ARG:HG2	3:S2:181:PRO:HG3	1.99	0.45
5:DD:102:PHE:H	64:RR:8:ARG:HA	1.81	0.45
13:L7:65:ARG:CZ	85:28:1210:C:H41	2.30	0.45
47:VV:20:LYS:HG3	47:VV:21:LYS:HG2	1.98	0.45
52:ZZ:106:TYR:CE2	52:ZZ:116:ARG:HG2	2.51	0.45
55:S5:59:LYS:HB3	55:S5:62:ARG:HB2	1.98	0.45
64:RR:124:LYS:HA	64:RR:129:SER:HA	1.97	0.45
80:18:37:C:H2'	80:18:38:A:O4'	2.16	0.45
80:18:92:A:H5'	80:18:93:U:C5	2.52	0.45
80:18:350:C:C2	80:18:351:G:C8	3.05	0.45
80:18:609:U:H2'	80:18:610:G:C8	2.51	0.45
80:18:1391:C:H2'	80:18:1392:U:C6	2.52	0.45
80:18:1491:G:H2'	80:18:1492:U:C6	2.52	0.45
81:v:480:VAL:HG13	81:v:481:LYS:H	1.81	0.45
85:28:221:C:H2'	85:28:222:C:C6	2.52	0.45
85:28:489:C:H2'	85:28:490:C:C6	2.51	0.45
85:28:516:C:H2'	85:28:517:C:H6	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:28:679:C:H2'	85:28:680:G:C8	2.48	0.45
85:28:726:G:H2'	85:28:727:C:C6	2.52	0.45
85:28:1956:A:O2'	85:28:1957:U:H5'	2.17	0.45
85:28:1964:A:H2'	85:28:1965:G:H8	1.81	0.45
85:28:2635:U:C4	85:28:2636:U:C4	3.04	0.45
85:28:4400:G:C6	85:28:4401:G:N7	2.84	0.45
3:S2:168:GLY:HA2	4:PP:1:MET:HE1	1.99	0.45
6:58:30:U:H2'	6:58:31:G:C8	2.51	0.45
11:L5:152:ARG:HG3	11:L5:154:THR:HG23	1.98	0.45
13:L7:69:ARG:O	13:L7:73:MET:HG3	2.17	0.45
25:cc:80:PRO:HA	25:cc:98:PHE:HA	1.98	0.45
30:30:105:ILE:H	30:30:105:ILE:HG13	1.54	0.45
45:AS:165:ARG:HD2	80:18:1004:U:OP1	2.16	0.45
68:S9:144:ILE:HG21	80:18:824:C:H1'	1.99	0.45
79:L9:106:GLN:HB2	79:L9:111:LEU:HB3	1.97	0.45
80:18:642:U:H4'	80:18:643:A:OP1	2.16	0.45
81:v:609:PHE:CE1	81:v:701:ARG:HB2	2.51	0.45
85:28:269:G:H2'	85:28:270:U:H6	1.80	0.45
85:28:469:C:H2'	85:28:470:A:C8	2.49	0.45
85:28:490:C:H2'	85:28:491:G:H8	1.80	0.45
85:28:2425:U:H5'	85:28:2426:U:H5	1.81	0.45
85:28:3851:U:H2'	85:28:3852:A:O4'	2.16	0.45
85:28:4345:C:H2'	85:28:4346:U:C6	2.52	0.45
85:28:4460:U:H2'	85:28:4461:C:C6	2.51	0.45
3:S2:118:ALA:HB2	80:18:1486:A:H4'	1.99	0.45
7:6:23:A:H2'	7:6:24:C:C6	2.51	0.45
9:L3:55:HIS:HB2	9:L3:369:ASP:HB2	1.99	0.45
10:L4:230:LEU:HD11	10:L4:239:LYS:HB2	1.99	0.45
13:L7:222:LYS:HE3	85:28:1907:A:H4'	1.99	0.45
18:15:64:ILE:HG21	18:15:106:ALA:HB2	1.98	0.45
49:t:32:ILE:HG22	49:t:37:LEU:HB3	1.98	0.45
50:F:32:LEU:HA	50:F:35:LEU:HG	1.99	0.45
71:S3:170:THR:HB	71:S3:187:LYS:HG2	1.99	0.45
80:18:1412:C:C2	80:18:1413:G:C8	3.05	0.45
85:28:1348:U:H2'	85:28:1349:G:C8	2.52	0.45
85:28:2016:C:C2	85:28:2017:A:C8	3.04	0.45
85:28:2358:G:H2'	85:28:2359:U:O4'	2.17	0.45
85:28:4356:G:C2	85:28:4357:G:C8	3.04	0.45
2:BB:53:ARG:O	2:BB:57:LYS:HG2	2.17	0.45
6:58:142:U:C2	6:58:143:G:C8	3.05	0.45
9:L3:154:LYS:HG3	9:L3:194:LEU:HD23	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:L5:15:ARG:CZ	85:28:1743:A:H1'	2.46	0.45
39:39:25:GLN:HG3	39:39:28:TRP:CZ2	2.52	0.45
46:FF:87:ASP:HB3	80:18:924:G:H21	1.81	0.45
48:s:84:GLY:C	85:28:2021:G:H4'	2.41	0.45
50:F:20:LYS:O	50:F:23:MET:HG2	2.16	0.45
67:S4:16:LYS:HD2	80:18:812:A:H5'	1.99	0.45
76:GG:78:ALA:O	76:GG:81:VAL:HG12	2.17	0.45
80:18:527:C:H2'	80:18:528:A:C8	2.52	0.45
80:18:1365:G:H2'	80:18:1366:G:C8	2.52	0.45
80:18:1591:C:H2'	80:18:1592:C:H6	1.81	0.45
85:28:287:U:H2'	85:28:288:G:H8	1.82	0.45
85:28:678:C:H2'	85:28:679:C:C6	2.52	0.45
85:28:950:G:H2'	85:28:951:G:H8	1.82	0.45
85:28:1090:G:H2'	85:28:1091:C:C6	2.52	0.45
85:28:1475:G:H2'	85:28:1476:C:C6	2.52	0.45
85:28:1558:A:H2'	85:28:1559:G:C8	2.52	0.45
85:28:1690:C:H2'	85:28:1691:G:O4'	2.17	0.45
85:28:3920:U:H2'	85:28:3921:U:C6	2.52	0.45
2:BB:102:ARG:HD2	2:BB:102:ARG:HA	1.67	0.45
6:58:140:C:H2'	6:58:141:C:C6	2.51	0.45
65:SS:42:GLU:O	65:SS:46:LYS:HG3	2.17	0.45
80:18:531:A:H3'	80:18:532:C:H5''	1.98	0.45
80:18:828:G:N2	80:18:830:A:H1'	2.32	0.45
80:18:933:G:H1'	80:18:1001:A:H5'	1.98	0.45
80:18:1007:C:H2'	80:18:1008:A:H8	1.76	0.45
80:18:1862:G:H4'	80:18:1863:A:OP1	2.17	0.45
81:v:154:VAL:HG12	81:v:211:THR:HG22	1.98	0.45
85:28:713:C:H2'	85:28:714:G:C8	2.51	0.45
85:28:1959:U:H1'	85:28:1961:G:N3	2.31	0.45
85:28:3932:U:H2'	85:28:3933:G:C8	2.51	0.45
6:58:92:U:H2'	6:58:93:C:O4'	2.16	0.45
14:aa:139:VAL:HG23	14:aa:236:ILE:HG22	1.98	0.45
14:aa:309:ALA:O	14:aa:313:GLU:HG2	2.16	0.45
21:19:4:LEU:HD11	21:19:29:THR:HG23	1.98	0.45
34:34:56:VAL:HG13	34:34:72:LYS:HA	1.99	0.45
50:F:67:GLU:O	50:F:70:MET:HG2	2.17	0.45
59:AA:257:LYS:HD2	59:AA:259:TRP:CZ2	2.52	0.45
67:S4:180:LEU:HG	67:S4:232:ASN:HA	1.99	0.45
80:18:887:U:H2'	80:18:887:U:O2	2.17	0.45
80:18:1639:G:H2'	80:18:1640:A:C8	2.52	0.45
81:v:207:PRO:HG2	81:v:261:TRP:CE2	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:28:987:C:H2'	85:28:988:C:H6	1.82	0.45
85:28:2106:G:C6	85:28:2108:G:N7	2.85	0.45
85:28:2662:G:H2'	85:28:2663:G:C8	2.52	0.45
85:28:2832:A:C4	85:28:2833:A:C8	3.05	0.45
85:28:2858:A:H2'	85:28:2859:G:H8	1.79	0.45
85:28:4178:A:H2'	85:28:4179:G:H8	1.82	0.45
19:bb:54:TYR:HD1	19:bb:145:VAL:HG21	1.82	0.44
22:20:164:LYS:HB3	22:20:165:PRO:HD3	1.99	0.44
24:22:24:ASP:HB3	24:22:69:LYS:HG3	1.99	0.44
28:dd:24:LYS:HE2	28:dd:24:LYS:HB2	1.75	0.44
39:39:44:TRP:CH2	39:39:45:ARG:HD3	2.52	0.44
56:WW:51:ARG:HG2	56:WW:52:GLU:H	1.81	0.44
66:S6:89:THR:HG22	80:18:91:A:H61	1.82	0.44
77:UU:84:VAL:HB	80:18:1866:A:N6	2.32	0.44
80:18:112:U:H2'	80:18:115:U:C5	2.51	0.44
80:18:934:G:C2	80:18:935:G:C8	3.04	0.44
80:18:974:C:H2'	80:18:975:G:H8	1.82	0.44
80:18:1823:A:N7	80:18:1824:A:H1'	2.32	0.44
81:v:752:PRO:HG2	81:v:755:VAL:HG22	1.98	0.44
85:28:33:A:H3'	85:28:47:A:H61	1.81	0.44
85:28:233:U:C2'	85:28:234:G:C8	3.00	0.44
85:28:1170:G:H2'	85:28:1171:G:C8	2.52	0.44
85:28:1514:U:H2'	85:28:1515:A:C8	2.52	0.44
85:28:1664:U:H2'	85:28:1665:C:H6	1.82	0.44
85:28:1672:U:H2'	85:28:1673:U:C6	2.52	0.44
85:28:2858:A:H2'	85:28:2859:G:C8	2.52	0.44
85:28:2864:A:H2'	85:28:2865:U:C6	2.52	0.44
8:L8:47:ASP:HA	8:L8:84:THR:HG22	1.99	0.44
8:L8:183:GLY:CA	85:28:1613:A:H5''	2.47	0.44
50:F:202:ILE:HB	50:F:213:HIS:CD2	2.52	0.44
61:MM:31:PRO:HG3	61:MM:102:ARG:HG2	1.99	0.44
80:18:86:C:H1'	80:18:170:A:N1	2.32	0.44
80:18:92:A:H5'	80:18:93:U:H5	1.82	0.44
80:18:1160:U:H2'	80:18:1161:U:H6	1.82	0.44
80:18:1358:U:H2'	80:18:1359:U:H6	1.81	0.44
80:18:1689:C:H2'	80:18:1690:U:H6	1.82	0.44
85:28:25:A:C8	85:28:341:G:C8	3.05	0.44
85:28:48:G:H1'	85:28:49:U:OP2	2.18	0.44
85:28:86:U:H2'	85:28:87:A:H8	1.82	0.44
85:28:1557:C:H2'	85:28:1558:A:H8	1.82	0.44
85:28:2520:C:H2'	85:28:2521:G:C8	2.43	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:28:4350:C:C2	85:28:4351:U:C5	3.05	0.44
85:28:4503:A:H2'	85:28:4504:C:C6	2.52	0.44
85:28:4565:C:H2'	85:28:4566:U:C6	2.53	0.44
1:IF:322:ALA:HA	85:28:3743:G:P	2.57	0.44
1:IF:350:VAL:CG1	1:IF:350:VAL:O	2.62	0.44
7:6:80:U:C2	7:6:81:G:C8	3.05	0.44
9:L3:14:LEU:O	9:L3:17:LEU:HB2	2.17	0.44
10:L4:66:SER:HA	10:L4:77:PRO:HA	1.99	0.44
32:32:126:ASN:HD22	32:32:129:LEU:HD11	1.83	0.44
48:s:24:TYR:CG	48:s:90:PHE:HB3	2.52	0.44
53:EE:120:ALA:HA	53:EE:123:VAL:HG12	1.98	0.44
71:S3:68:GLU:O	71:S3:72:VAL:HG23	2.17	0.44
73:WX:30:CYS:HA	73:WX:34:ILE:HD12	1.99	0.44
73:WX:50:PHE:HB3	73:WX:63:VAL:HG13	2.00	0.44
73:WX:93:LEU:HB3	73:WX:102:ILE:HD11	1.99	0.44
80:18:449:A:O2'	80:18:450:C:H4'	2.17	0.44
80:18:1031:A:H2'	80:18:1032:C:H6	1.82	0.44
80:18:1140:G:H2'	80:18:1141:G:C8	2.52	0.44
85:28:1199:G:C2	85:28:1200:G:C5	3.06	0.44
85:28:2421:G:OP2	85:28:2828:U:H1'	2.17	0.44
85:28:3890:A:N7	85:28:4571:A:H1'	2.33	0.44
85:28:4300:U:H2'	85:28:4301:U:H6	1.82	0.44
7:6:58:A:H2'	7:6:59:G:H8	1.81	0.44
49:t:54:LYS:O	49:t:54:LYS:HG2	2.18	0.44
50:F:29:ASN:O	50:F:33:ARG:HG2	2.17	0.44
52:ZZ:140:TYR:CE2	52:ZZ:142:GLY:HA2	2.53	0.44
61:MM:42:HIS:CD2	61:MM:43:LYS:HG2	2.53	0.44
62:LL:88:LYS:HG2	83:A:18:ARG:HD3	1.99	0.44
69:S7:43:LEU:HD23	69:S7:72:PHE:CE1	2.53	0.44
72:RS:7:LYS:O	72:RS:11:LYS:HG2	2.17	0.44
80:18:1609:C:H2'	80:18:1610:G:H8	1.82	0.44
81:v:9:ILE:HA	81:v:12:ILE:HG22	1.99	0.44
83:A:95:GLY:HA2	83:A:104:GLN:HA	1.99	0.44
85:28:253:G:H2'	85:28:254:G:C8	2.52	0.44
85:28:969:C:H42	85:28:2095:A:H61	1.65	0.44
85:28:2386:U:H2'	85:28:2387:G:H8	1.82	0.44
85:28:2730:U:H2'	85:28:2731:C:C6	2.52	0.44
85:28:2845:A:H61	85:28:3843:C:N4	2.15	0.44
85:28:3696:C:H2'	85:28:3697:U:O4'	2.17	0.44
15:10:9:TYR:HE1	85:28:1866:U:H5'	1.83	0.44
25:cc:72:ASP:O	25:cc:76:ILE:HG23	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:VV:24:LEU:HD11	73:WX:53:ILE:HD12	2.00	0.44
59:AA:12:LYS:H	59:AA:12:LYS:HD3	1.83	0.44
60:OO:67:LYS:HB3	80:18:1337:C:H4'	1.99	0.44
66:S6:91:GLU:HG2	66:S6:92:ARG:N	2.32	0.44
80:18:1043:G:H2'	80:18:1044:G:O4'	2.17	0.44
80:18:1804:U:H2'	80:18:1805:G:O4'	2.17	0.44
80:18:1823:A:C5	80:18:1824:A:H1'	2.52	0.44
81:v:155:LEU:O	81:v:212:VAL:HA	2.18	0.44
81:v:249:ARG:HG3	81:v:250:ALA:N	2.31	0.44
85:28:161:G:H2'	85:28:162:A:H8	1.82	0.44
85:28:272:U:H2'	85:28:273:U:C6	2.53	0.44
85:28:1201:U:H2'	85:28:1202:C:H6	1.82	0.44
85:28:1445:U:H2'	85:28:1446:C:C6	2.53	0.44
85:28:2815:A:C4	85:28:2816:G:C8	3.05	0.44
85:28:4198:G:H2'	85:28:4199:C:H6	1.82	0.44
1:IF:300:TYR:HB3	1:IF:303:MET:HB2	2.00	0.44
2:BB:30:LEU:HD21	2:BB:35:GLU:HG2	1.98	0.44
6:58:62:A:H4'	6:58:63:U:O5'	2.18	0.44
9:L3:56:ILE:HA	9:L3:56:ILE:HD13	1.72	0.44
27:27:50:PRO:HD3	27:27:68:ILE:HD13	1.99	0.44
28:dd:76:ASP:HB2	28:dd:115:GLY:HA3	1.99	0.44
45:AS:150:ILE:HD13	72:RS:129:LYS:HB2	1.99	0.44
49:t:105:THR:HG22	49:t:108:GLU:CD	2.41	0.44
53:EE:58:GLU:HB3	53:EE:61:TYR:HB3	1.99	0.44
59:AA:11:LEU:HD21	59:AA:52:TYR:HB3	2.00	0.44
62:LL:64:VAL:O	62:LL:68:ILE:HG12	2.18	0.44
72:RS:31:ASN:HA	72:RS:34:VAL:HB	1.99	0.44
80:18:353:C:H2'	80:18:354:U:C6	2.53	0.44
80:18:1808:U:H2'	80:18:1809:A:H8	1.82	0.44
85:28:27:C:H2'	85:28:28:C:H6	1.82	0.44
85:28:1963:C:C2	85:28:1964:A:C2	3.05	0.44
85:28:2404:A:H61	85:28:2787:A:H61	1.64	0.44
85:28:2862:G:N3	85:28:3624:A:H2'	2.32	0.44
85:28:2885:A:H2'	85:28:2886:U:C6	2.53	0.44
85:28:4419:U:C4	85:28:4420:U:C5	3.06	0.44
5:DD:101:ARG:HD2	64:RR:6:GLY:O	2.18	0.44
62:LL:137:LYS:HE2	80:18:1234:C:N4	2.33	0.44
73:WX:8:ALA:HA	73:WX:74:VAL:HG11	1.98	0.44
73:WX:36:ARG:HB2	73:WX:110:ILE:HD12	2.00	0.44
80:18:1094:C:H2'	80:18:1095:U:C6	2.52	0.44
80:18:1369:A:H8	80:18:1369:A:OP1	2.01	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:18:1610:G:H2'	80:18:1611:G:C8	2.53	0.44
85:28:396:A:H2'	85:28:397:G:C8	2.53	0.44
85:28:673:C:C2	85:28:674:G:C8	3.06	0.44
85:28:677:G:H2'	85:28:678:C:C6	2.52	0.44
85:28:1077:C:C2	85:28:1078:A:C8	3.06	0.44
85:28:1334:A:H2'	85:28:1335:G:H8	1.81	0.44
85:28:1964:A:H2'	85:28:1965:G:O4'	2.17	0.44
85:28:2385:U:H2'	85:28:2386:U:H6	1.83	0.44
85:28:2815:A:H2'	85:28:2816:G:H8	1.82	0.44
85:28:4263:C:H2'	85:28:4264:G:O4'	2.17	0.44
85:28:5043:A:H2'	85:28:5044:A:H8	1.83	0.44
15:10:3:ARG:NH2	85:28:4430:G:H5'	2.33	0.44
25:cc:140:LEU:HD11	25:cc:149:VAL:HG21	1.99	0.44
39:39:48:LYS:HD2	39:39:48:LYS:HA	1.75	0.44
49:t:130:LYS:HD3	49:t:130:LYS:HA	1.84	0.44
57:II:16:LYS:HG3	57:II:17:LYS:H	1.83	0.44
57:II:113:ILE:HG23	57:II:117:ARG:HD3	2.00	0.44
66:S6:133:LEU:HD22	80:18:65:C:C2	2.52	0.44
73:WX:20:ARG:HG2	73:WX:22:LYS:HE2	2.00	0.44
74:S8:10:LYS:HB2	80:18:371:A:OP2	2.18	0.44
85:28:4504:C:H2'	85:28:4505:C:H6	1.83	0.44
1:IF:323:LYS:N	85:28:3743:G:OP1	2.47	0.44
1:IF:330:ARG:CZ	80:18:965:U:OP1	2.66	0.44
9:L3:288:GLY:HA3	9:L3:330:PHE:CE1	2.53	0.44
12:L6:156:LEU:HD13	33:ee:105:LEU:HD13	1.99	0.44
19:bb:85:ARG:HG3	19:bb:99:LEU:HD11	1.99	0.44
48:s:53:VAL:HA	48:s:89:VAL:HA	2.00	0.44
57:II:104:SER:HA	57:II:107:GLU:CG	2.47	0.44
62:LL:61:GLU:O	62:LL:64:VAL:HG22	2.18	0.44
66:S6:7:PHE:CD2	66:S6:125:THR:HG22	2.53	0.44
71:S3:109:LEU:HD13	71:S3:109:LEU:HA	1.91	0.44
84:ES:3245:G:H2'	84:ES:3246:G:H8	1.83	0.44
85:28:221:C:H2'	85:28:222:C:H6	1.83	0.44
85:28:324:A:H2'	85:28:325:U:C6	2.53	0.44
85:28:2374:A:H2'	85:28:2375:A:H8	1.82	0.44
85:28:4958:C:H2'	85:28:4959:U:C6	2.53	0.44
85:28:4960:G:H2'	85:28:4961:G:C8	2.53	0.44
86:23:39:ILE:HG12	86:23:61:VAL:HG11	2.00	0.44
2:BB:59:LEU:HD22	2:BB:181:GLU:HG2	2.00	0.43
11:L5:60:ILE:HB	11:L5:80:ALA:HB2	2.00	0.43
11:L5:249:GLU:HG3	11:L5:250:ASN:N	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:10:66:GLU:CD	15:10:69:ARG:HH21	2.26	0.43
15:10:180:GLU:O	15:10:184:MET:HG3	2.18	0.43
35:35:112:ARG:HG2	85:28:173:C:H1'	1.99	0.43
66:S6:7:PHE:HD1	66:S6:8:PRO:HD2	1.82	0.43
77:UU:92:ARG:HB3	80:18:1865:C:O2	2.18	0.43
79:L9:41:ILE:HG22	79:L9:43:VAL:HG13	1.99	0.43
80:18:22:A:C2	80:18:23:G:C8	3.06	0.43
80:18:349:A:H2'	80:18:350:C:C6	2.53	0.43
80:18:512:A:C2	80:18:513:G:C8	3.06	0.43
80:18:1369:A:OP1	80:18:1369:A:C8	2.71	0.43
85:28:385:A:H4'	85:28:386:A:OP1	2.18	0.43
85:28:653:C:H2'	85:28:654:C:C6	2.53	0.43
85:28:2478:C:C2	85:28:2479:G:C8	3.06	0.43
85:28:2519:U:H1'	85:28:2520:C:C6	2.52	0.43
85:28:2689:C:H2'	85:28:2690:C:C6	2.53	0.43
85:28:2858:A:H2'	85:28:2859:G:O4'	2.18	0.43
85:28:3768:U:H2'	85:28:3769:C:C6	2.53	0.43
85:28:4628:U:C2	85:28:4629:U:C5	3.06	0.43
85:28:4994:G:H2'	85:28:4995:U:H6	1.82	0.43
2:BB:41:ARG:HB2	2:BB:47:TYR:CE1	2.53	0.43
9:L3:77:THR:HG21	9:L3:337:VAL:HG22	2.00	0.43
13:L7:240:ASN:O	13:L7:244:ARG:HG2	2.18	0.43
19:bb:26:GLN:HG3	22:20:167:PHE:HZ	1.82	0.43
30:30:38:ILE:HD13	30:30:43:ALA:HB3	1.99	0.43
51:Q:34:PHE:CE1	51:Q:38:ARG:HD3	2.53	0.43
74:S8:129:LEU:HD22	74:S8:134:GLU:HB2	2.00	0.43
80:18:111:A:H2'	80:18:112:U:C6	2.53	0.43
80:18:184:G:C2	80:18:185:G:H1'	2.52	0.43
80:18:1284:A:OP1	80:18:1286:G:H5'	2.19	0.43
80:18:1839:U:H2'	80:18:1840:U:H6	1.83	0.43
81:v:394:LEU:HD22	81:v:427:VAL:HG11	2.00	0.43
85:28:460:C:H2'	85:28:461:G:C8	2.53	0.43
85:28:1732:C:O2'	85:28:1733:G:H5'	2.18	0.43
85:28:4594:U:H2'	85:28:4595:G:C8	2.52	0.43
85:28:5055:G:H2'	85:28:5056:A:H8	1.83	0.43
4:PP:8:PHE:CZ	4:PP:10:ASP:HB2	2.53	0.43
14:aa:194:ASN:O	14:aa:198:THR:HG23	2.18	0.43
16:13:105:LYS:HB3	16:13:105:LYS:HE2	1.80	0.43
18:15:68:ARG:HG2	18:15:128:LYS:HG3	1.99	0.43
31:31:68:LEU:HA	31:31:108:TYR:HB2	2.00	0.43
53:EE:22:LEU:HD21	53:EE:89:VAL:HB	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:18:150:A:H62	80:18:168:C:H42	1.65	0.43
80:18:360:A:C2	80:18:362:C:H2'	2.53	0.43
80:18:950:C:H2'	80:18:951:C:C6	2.53	0.43
80:18:1666:C:H2'	80:18:1667:U:C6	2.53	0.43
81:v:19:ILE:HD12	81:v:99:LEU:HB3	2.01	0.43
85:28:2056:G:C8	85:28:2058:G:C8	3.06	0.43
85:28:2310:C:H2'	85:28:2311:C:C6	2.53	0.43
85:28:4674:C:H2'	85:28:4675:U:C6	2.53	0.43
3:S2:256:TRP:CE2	73:WX:68:ARG:HB3	2.53	0.43
7:6:60:G:C2	7:6:61:G:C8	3.06	0.43
8:L8:28:ARG:HD3	8:L8:123:ARG:HD3	2.00	0.43
64:RR:11:ARG:CZ	80:18:399:C:H4'	2.49	0.43
64:RR:88:ASP:HB2	80:18:617:G:H4'	2.01	0.43
68:S9:39:ASN:HB2	80:18:642:U:P	2.58	0.43
80:18:106:C:H2'	80:18:107:A:C8	2.51	0.43
80:18:443:U:H2'	80:18:444:G:C8	2.54	0.43
81:v:774:SER:HB3	81:v:783:VAL:HG13	2.00	0.43
85:28:951:G:H2'	85:28:952:G:H8	1.84	0.43
85:28:1588:U:H2'	85:28:1589:C:C6	2.53	0.43
85:28:1958:A:C4'	85:28:1962:A:H1'	2.49	0.43
85:28:2629:C:H2'	85:28:2630:U:O4'	2.17	0.43
85:28:2689:C:C2	85:28:2690:C:C5	3.05	0.43
85:28:4440:G:C4	85:28:4441:A:C8	3.06	0.43
9:L3:252:ALA:HB1	85:28:4524:G:C2	2.54	0.43
13:L7:115:GLN:HG3	51:Q:3:VAL:HG12	2.00	0.43
21:19:155:LEU:HD13	21:19:155:LEU:HA	1.85	0.43
22:20:93:MET:HE1	22:20:117:HIS:CE1	2.54	0.43
32:32:108:ARG:HD3	32:32:127:ALA:HB3	2.00	0.43
45:AS:116:LYS:HG2	45:AS:117:TRP:CD2	2.53	0.43
46:FF:70:LYS:HG2	46:FF:73:ARG:HD2	1.99	0.43
57:II:51:LEU:HD21	57:II:81:ILE:HG13	2.00	0.43
57:II:81:ILE:O	57:II:84:ILE:HG12	2.19	0.43
60:OO:34:LYS:HD3	60:OO:107:GLU:HG3	2.00	0.43
62:LL:82:TRP:CD1	62:LL:82:TRP:H	2.35	0.43
78:11:95:ARG:HB2	78:11:98:ASN:OD1	2.19	0.43
79:L9:88:PHE:CE2	79:L9:151:ILE:HB	2.53	0.43
80:18:382:C:C2	80:18:383:G:N7	2.86	0.43
80:18:1739:C:H2'	80:18:1740:C:H6	1.81	0.43
80:18:1742:C:H2'	80:18:1743:G:O4'	2.19	0.43
83:A:50:ARG:H	83:A:53:GLN:NE2	2.16	0.43
85:28:1298:C:C2	85:28:1299:G:C8	3.07	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:28:2404:A:H61	85:28:2787:A:N6	2.17	0.43
85:28:2555:G:C2	85:28:2556:G:C5	3.06	0.43
85:28:2561:C:H42	85:28:2566:G:H1	1.66	0.43
85:28:2894:A:H2'	85:28:2895:A:C8	2.53	0.43
85:28:4454:G:H2'	85:28:4455:G:H8	1.84	0.43
85:28:5013:C:H4'	85:28:5014:A:H5''	1.99	0.43
86:23:89:ARG:HB2	86:23:95:PHE:CE2	2.54	0.43
18:15:178:HIS:HA	18:15:181:HIS:NE2	2.34	0.43
20:17:131:ARG:HG3	20:17:137:ASN:ND2	2.34	0.43
22:20:34:ALA:HB1	22:20:39:VAL:CG2	2.48	0.43
35:35:47:ILE:HG13	35:35:48:ARG:N	2.32	0.43
36:36:74:LYS:HA	36:36:83:ALA:HB2	2.00	0.43
57:II:71:ARG:CZ	80:18:1407:U:H4'	2.49	0.43
80:18:1053:C:H2'	80:18:1054:G:H8	1.84	0.43
80:18:1126:G:H2'	80:18:1127:C:H6	1.83	0.43
80:18:1340:U:H2'	80:18:1341:C:C5	2.54	0.43
80:18:1676:U:C4	80:18:1677:U:C5	3.06	0.43
81:v:126:LEU:HA	81:v:154:VAL:HG23	1.99	0.43
81:v:163:ALA:HB1	81:v:169:LEU:HD12	2.00	0.43
81:v:372:LEU:HD22	81:v:417:PHE:CZ	2.53	0.43
81:v:650:TRP:HZ2	81:v:672:LEU:HD21	1.84	0.43
85:28:426:A:H2'	85:28:427:A:C8	2.53	0.43
85:28:1545:G:H2'	85:28:1546:C:C6	2.54	0.43
85:28:1737:A:H2'	85:28:1738:A:O4'	2.18	0.43
85:28:2605:G:H2'	85:28:2606:G:H8	1.82	0.43
85:28:2634:C:C2	85:28:2635:U:C5	3.07	0.43
85:28:2690:C:C4	85:28:2691:U:C4	3.07	0.43
85:28:3722:G:H2'	85:28:3723:A:C8	2.54	0.43
85:28:4152:G:H2'	85:28:4153:C:C6	2.54	0.43
85:28:4401:G:H2'	85:28:4402:C:H6	1.82	0.43
17:14:90:ARG:O	17:14:94:LYS:HG2	2.18	0.43
42:42:26:TYR:HB2	42:42:82:MET:HE1	2.00	0.43
55:S5:169:ILE:HG12	80:18:1535:U:C5	2.53	0.43
59:AA:142:VAL:HG11	59:AA:145:GLU:HB3	2.00	0.43
65:SS:29:HIS:HE1	65:SS:69:THR:HG23	1.84	0.43
68:S9:84:ILE:HG13	68:S9:86:VAL:HG23	2.00	0.43
69:S7:102:PRO:HA	80:18:688:U:C5	2.54	0.43
76:GG:32:HIS:CD2	80:18:975:G:H4'	2.54	0.43
80:18:375:U:H2'	80:18:376:A:C8	2.54	0.43
80:18:848:U:O2	80:18:849:A:C8	2.71	0.43
80:18:1588:A:H2'	80:18:1589:A:C8	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
81:v:374:GLU:HB3	81:v:495:ARG:HG2	2.00	0.43
85:28:432:U:H4'	85:28:433:A:H5''	1.99	0.43
85:28:1382:G:N3	85:28:1383:G:C8	2.86	0.43
85:28:3664:G:H2'	85:28:3665:G:C8	2.50	0.43
85:28:3923:A:H2'	85:28:3924:C:C6	2.53	0.43
85:28:4130:C:H2'	85:28:4131:G:C8	2.53	0.43
85:28:4723:A:H2'	85:28:4724:A:C8	2.53	0.43
1:IF:204:CYS:O	1:IF:208:LEU:HG	2.19	0.43
1:IF:215:PHE:CE2	1:IF:235:LEU:HD11	2.54	0.43
3:S2:77:SER:O	3:S2:80:GLU:HG2	2.18	0.43
9:L3:43:LEU:HB2	9:L3:210:VAL:HG22	2.00	0.43
17:14:86:TRP:CE2	17:14:92:ALA:HB2	2.53	0.43
19:bb:26:GLN:HG3	22:20:167:PHE:CZ	2.54	0.43
30:30:64:ALA:HB1	30:30:69:THR:O	2.18	0.43
33:ee:23:GLU:CD	33:ee:23:GLU:H	2.27	0.43
49:t:123:ARG:HG3	49:t:124:GLU:H	1.84	0.43
50:F:288:LYS:HE3	50:F:288:LYS:HB2	1.69	0.43
57:II:142:GLN:HG2	80:18:1527:C:OP1	2.19	0.43
66:S6:230:LYS:O	66:S6:234:LEU:HG	2.18	0.43
80:18:363:A:H4'	80:18:364:A:H4'	2.00	0.43
80:18:673:G:H2'	80:18:674:C:C6	2.54	0.43
80:18:946:U:H2'	80:18:947:G:C8	2.54	0.43
80:18:1092:G:C2	80:18:1093:A:N7	2.86	0.43
80:18:1349:G:H2'	80:18:1350:U:C6	2.54	0.43
80:18:1394:G:N2	80:18:1474:A:H2	2.17	0.43
80:18:1525:C:H2'	80:18:1526:G:H8	1.83	0.43
80:18:1730:U:C2	80:18:1731:A:C8	3.07	0.43
85:28:1460:C:H2'	85:28:1461:C:C6	2.52	0.43
85:28:2587:A:H5''	85:28:2588:C:C5	2.54	0.43
85:28:4343:U:H2'	85:28:4344:U:H6	1.82	0.43
85:28:4407:G:H1'	85:28:4438:U:C2	2.54	0.43
85:28:4477:A:C4	85:28:4478:G:C8	3.06	0.43
2:BB:115:ALA:O	2:BB:117:ARG:HG2	2.19	0.43
7:6:67:C:OP1	11:L5:14:LYS:HG2	2.19	0.43
8:L8:83:HIS:HB3	43:ff:64:VAL:HG22	2.01	0.43
10:L4:285:LEU:HD22	10:L4:285:LEU:HA	1.92	0.43
11:L5:153:THR:HG21	85:28:4323:A:C6	2.53	0.43
12:L6:186:ARG:HA	12:L6:186:ARG:HD2	1.84	0.43
19:bb:188:LYS:HD3	85:28:4892:A:H5''	2.00	0.43
28:dd:89:ASN:HA	28:dd:92:LYS:HG2	2.00	0.43
31:31:70:LYS:HG3	85:28:2389:A:H4'	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:39:23:ILE:HG23	39:39:38:ASN:HB2	2.01	0.43
71:S3:55:THR:O	71:S3:58:VAL:HG22	2.19	0.43
80:18:71:G:C8	80:18:79:A:C6	3.07	0.43
80:18:1568:C:H2'	80:18:1569:A:C8	2.53	0.43
81:v:749:ILE:O	81:v:783:VAL:HA	2.19	0.43
85:28:973:C:H2'	85:28:974:G:H8	1.84	0.43
85:28:1191:C:H2'	85:28:1192:C:H6	1.84	0.43
85:28:1582:U:C2	85:28:1583:A:C8	3.07	0.43
85:28:1633:G:H5'	85:28:1634:A:OP1	2.19	0.43
85:28:2413:U:C2	85:28:2414:G:C8	3.07	0.43
85:28:5001:U:H2'	85:28:5002:U:O4'	2.19	0.43
2:BB:130:ASP:C	2:BB:133:PRO:HD2	2.44	0.43
6:58:126:C:HO2'	6:58:127:U:H5	1.66	0.43
6:58:147:G:H2'	6:58:148:A:C8	2.52	0.43
10:L4:22:VAL:HG22	10:L4:258:ARG:NH1	2.33	0.43
17:14:11:ARG:NH2	17:14:61:ILE:HD11	2.34	0.43
37:37:3:LYS:HB3	85:28:3642:A:C4	2.54	0.43
45:AS:66:VAL:HA	45:AS:86:LEU:O	2.17	0.43
50:F:170:TRP:HA	50:F:173:VAL:HG22	2.01	0.43
59:AA:64:HIS:HB3	59:AA:83:TRP:HB2	2.01	0.43
69:S7:69:LEU:HD13	69:S7:96:ALA:HB2	2.01	0.43
71:S3:49:ILE:HG22	71:S3:87:TYR:HB2	2.01	0.43
80:18:350:C:N3	80:18:351:G:C8	2.87	0.43
80:18:351:G:C2	80:18:352:U:C6	3.06	0.43
80:18:458:A:H2'	80:18:459:C:C6	2.54	0.43
80:18:676:C:H2'	80:18:677:G:O4'	2.18	0.43
80:18:980:A:H2'	80:18:981:A:C8	2.54	0.43
80:18:1034:A:C4	80:18:1035:A:C8	3.06	0.43
80:18:1201:U:H2'	80:18:1202:U:H6	1.83	0.43
85:28:60:A:C4	85:28:61:A:C8	3.07	0.43
85:28:223:G:H4'	85:28:225:G:C8	2.54	0.43
85:28:275:C:H2'	85:28:276:C:C6	2.53	0.43
85:28:299:C:H2'	85:28:300:A:C8	2.54	0.43
85:28:311:G:H2'	85:28:312:G:H8	1.84	0.43
85:28:325:U:H2'	85:28:326:C:H6	1.83	0.43
85:28:758:G:H2'	85:28:759:G:O4'	2.19	0.43
85:28:2627:C:H41	85:28:4649:G:H1	1.67	0.43
85:28:2724:G:H4'	85:28:2725:A:OP1	2.18	0.43
85:28:4307:A:H2'	85:28:4308:C:H6	1.83	0.43
85:28:5056:A:H2'	85:28:5057:C:C6	2.54	0.43
86:23:106:VAL:HG12	86:23:112:MET:HA	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:L3:283:LYS:HE3	9:L3:363:ILE:HD13	2.01	0.42
12:L6:179:THR:OG1	12:L6:189:LEU:HD23	2.18	0.42
12:L6:261:LEU:HD12	12:L6:264:ILE:HD11	2.00	0.42
18:15:86:HIS:CE1	85:28:33:A:H5'	2.53	0.42
27:27:12:LEU:HB2	27:27:81:MET:HB3	2.01	0.42
30:30:46:VAL:HB	30:30:71:VAL:HG22	2.01	0.42
34:34:63:VAL:HG13	34:34:66:ARG:CZ	2.49	0.42
45:AS:106:THR:HG22	45:AS:108:ASP:H	1.85	0.42
66:S6:103:ASP:H	66:S6:106:LEU:HD23	1.84	0.42
71:S3:172:VAL:HG13	71:S3:185:LYS:HG2	2.01	0.42
79:L9:47:LEU:HD13	79:L9:55:LEU:HD12	2.01	0.42
80:18:23:G:C4	80:18:24:C:C5	3.07	0.42
80:18:75:G:N2	80:18:77:A:H5''	2.28	0.42
80:18:94:G:C4	80:18:95:G:C8	3.07	0.42
80:18:374:G:H2'	80:18:375:U:H6	1.82	0.42
80:18:477:G:C2	80:18:478:G:C8	3.07	0.42
80:18:1406:G:H2'	80:18:1407:U:H6	1.83	0.42
81:v:396:MET:HB3	81:v:485:ILE:HB	2.00	0.42
85:28:699:C:H2'	85:28:700:G:H8	1.84	0.42
85:28:1633:G:H4'	85:28:1634:A:O5'	2.19	0.42
85:28:2492:C:C2	85:28:2493:G:N7	2.87	0.42
3:S2:191:VAL:HG11	3:S2:236:PHE:HA	2.00	0.42
10:L4:38:ASN:O	10:L4:42:THR:HG23	2.19	0.42
28:dd:82:VAL:HB	28:dd:86:THR:HG21	2.02	0.42
46:FF:40:LEU:HD13	46:FF:53:ILE:HD11	2.01	0.42
47:VV:82:LYS:HE2	47:VV:82:LYS:HB3	1.80	0.42
49:t:146:ARG:HA	49:t:146:ARG:HD2	1.61	0.42
55:S5:152:TRP:CH2	80:18:1221:G:H4'	2.55	0.42
59:AA:22:ALA:HB2	59:AA:69:VAL:HG13	2.00	0.42
80:18:1293:A:C5	80:18:1294:G:C8	3.07	0.42
80:18:1787:G:H2'	80:18:1788:A:C8	2.54	0.42
80:18:1820:G:H2'	80:18:1821:U:C6	2.54	0.42
81:v:394:LEU:HB3	81:v:487:THR:HG23	2.01	0.42
85:28:1569:U:H2'	85:28:1570:G:C8	2.54	0.42
85:28:2479:G:C4	85:28:2480:G:C8	3.06	0.42
7:6:51:G:H21	78:11:12:MET:CE	2.32	0.42
7:6:113:G:H2'	7:6:114:U:H6	1.83	0.42
11:L5:43:LYS:HB3	11:L5:46:THR:HB	2.00	0.42
13:L7:103:LYS:O	13:L7:107:VAL:HG23	2.20	0.42
17:14:47:ARG:HH22	17:14:69:ARG:HA	1.84	0.42
23:21:14:MET:HE1	23:21:55:LYS:HB2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:31:45:ALA:O	31:31:48:GLU:HG2	2.19	0.42
33:ee:54:LYS:HB3	85:28:443:G:H5''	2.00	0.42
53:EE:92:CYS:HB3	53:EE:102:LYS:HB3	2.01	0.42
57:II:12:VAL:HA	80:18:1397:U:O4	2.19	0.42
62:LL:27:ALA:HB1	62:LL:42:HIS:CE1	2.55	0.42
68:S9:144:ILE:HG12	80:18:824:C:C2	2.53	0.42
69:S7:6:ALA:HA	69:S7:28:LEU:HD11	2.01	0.42
80:18:299:A:H2'	80:18:300:U:H6	1.84	0.42
80:18:570:C:H2'	80:18:571:U:C6	2.54	0.42
80:18:1115:U:O3'	80:18:1116:C:H2'	2.18	0.42
80:18:1650:A:H1'	80:18:1675:A:N6	2.34	0.42
80:18:1702:G:H2'	80:18:1703:C:O4'	2.20	0.42
85:28:441:G:H2'	85:28:442:G:H8	1.83	0.42
85:28:1315:C:H2'	85:28:1316:G:H8	1.84	0.42
85:28:2397:G:C8	85:28:2399:G:C8	3.07	0.42
85:28:4357:G:H2'	85:28:4358:U:C6	2.55	0.42
85:28:4749:C:H2'	85:28:4750:G:O4'	2.19	0.42
85:28:4759:C:H2'	85:28:4760:G:O4'	2.19	0.42
3:S2:65:LYS:HA	3:S2:68:ARG:HD2	2.02	0.42
23:21:89:ILE:HG22	85:28:4300:U:H4'	2.02	0.42
55:S5:119:SER:OG	55:S5:189:ALA:HB1	2.20	0.42
65:SS:10:ARG:HG2	65:SS:11:LYS:HG2	2.00	0.42
66:S6:7:PHE:CD1	66:S6:113:ILE:HB	2.54	0.42
80:18:14:C:H2'	80:18:15:U:H6	1.81	0.42
80:18:39:A:H2'	80:18:40:A:O4'	2.20	0.42
80:18:220:U:H2'	80:18:221:A:C8	2.54	0.42
80:18:1272:C:O2'	80:18:1273:C:H5'	2.20	0.42
80:18:1389:C:H2'	80:18:1390:U:C6	2.54	0.42
80:18:1531:A:H2'	80:18:1532:C:H6	1.85	0.42
80:18:1675:A:H2'	80:18:1676:U:H6	1.84	0.42
81:v:304:ILE:HG21	81:v:336:LEU:HD13	2.01	0.42
81:v:313:ALA:HA	81:v:316:ILE:HG12	2.01	0.42
85:28:1510:G:H2'	85:28:1511:U:C6	2.54	0.42
85:28:1681:G:H2'	85:28:1682:A:C8	2.54	0.42
85:28:2418:A:C5	85:28:2419:C:C5	3.08	0.42
85:28:2610:G:H2'	85:28:2611:A:C8	2.54	0.42
6:58:56:G:H2'	6:58:57:C:O4'	2.19	0.42
6:58:71:A:H2'	26:26:50:ARG:NH1	2.35	0.42
13:L7:113:LEU:HD21	13:L7:120:THR:HG22	2.01	0.42
29:29:31:SER:HA	85:28:1463:C:H5''	2.01	0.42
31:31:70:LYS:HE2	85:28:2389:A:H5'	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:CC:65:ARG:HA	58:CC:65:ARG:HD2	1.88	0.42
61:MM:129:ARG:O	61:MM:133:ARG:HG3	2.19	0.42
65:SS:29:HIS:HB2	65:SS:32:LYS:HG3	2.02	0.42
71:S3:66:ILE:O	71:S3:70:THR:HG23	2.19	0.42
71:S3:142:LEU:HD13	71:S3:143:ARG:HG3	2.00	0.42
74:S8:8:TRP:HA	74:S8:18:ARG:HD2	2.01	0.42
80:18:943:U:C2	80:18:944:A:C8	3.08	0.42
81:v:669:VAL:HG21	81:v:707:VAL:HG22	2.01	0.42
85:28:294:G:O6	85:28:315:G:H1'	2.19	0.42
85:28:1340:C:C2	85:28:1341:U:C5	3.07	0.42
85:28:2034:G:H2'	85:28:2035:C:C6	2.55	0.42
85:28:2559:G:H2'	85:28:2560:C:H6	1.83	0.42
85:28:2647:A:H62	85:28:2686:G:H8	1.67	0.42
85:28:3795:A:H2'	85:28:3796:U:C6	2.55	0.42
85:28:4419:U:O2	85:28:4419:U:H2'	2.19	0.42
85:28:4433:G:H2'	85:28:4434:C:C6	2.54	0.42
8:L8:187:HIS:HB3	85:28:2740:U:O4'	2.20	0.42
11:L5:37:VAL:HB	11:L5:50:ARG:HD3	2.02	0.42
18:15:51:LEU:HD13	18:15:117:ASN:HB3	2.00	0.42
23:21:96:ILE:HD13	23:21:96:ILE:HA	1.81	0.42
59:AA:249:CYS:HB2	59:AA:258:ILE:HG22	2.02	0.42
60:OO:24:LEU:O	60:OO:86:LYS:HA	2.20	0.42
61:MM:39:LEU:HD23	61:MM:56:ARG:NH1	2.34	0.42
61:MM:62:ARG:HD3	80:18:1542:C:OP1	2.20	0.42
63:XX:33:LYS:HE2	63:XX:34:TYR:CZ	2.54	0.42
64:RR:5:ARG:O	73:WX:77:PRO:HD3	2.20	0.42
65:SS:111:LYS:HD2	80:18:56:G:H5'	2.02	0.42
76:GG:38:ASN:C	76:GG:69:SER:HB2	2.44	0.42
80:18:465:A:H4'	80:18:466:G:O5'	2.19	0.42
80:18:478:G:H2'	80:18:479:C:C6	2.55	0.42
81:v:504:VAL:HG11	81:v:810:PRO:HG2	2.01	0.42
84:ES:2953:C:H2'	84:ES:2954:G:H8	1.84	0.42
85:28:324:A:H2'	85:28:325:U:H6	1.84	0.42
85:28:434:A:H2'	85:28:435:A:O4'	2.19	0.42
85:28:1464:C:C2	85:28:1465:G:C8	3.08	0.42
85:28:1577:G:O2'	85:28:1612:G:H4'	2.20	0.42
85:28:1991:A:OP1	85:28:1991:A:H4'	2.20	0.42
85:28:3633:C:H2'	85:28:3634:G:C8	2.55	0.42
85:28:3654:G:H22	85:28:3817:A:H2	1.67	0.42
85:28:4235:G:C2	85:28:4236:G:C8	3.08	0.42
85:28:4951:G:C2	85:28:4952:G:C8	3.07	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L6:127:LYS:HB2	85:28:958:G:C2	2.54	0.42
37:37:4:GLY:HA3	85:28:1601:A:OP2	2.19	0.42
49:t:142:ASN:HA	49:t:146:ARG:NH1	2.32	0.42
64:RR:90:CYS:SG	64:RR:130:LEU:HD21	2.59	0.42
71:S3:99:ILE:HG12	71:S3:100:ALA:N	2.35	0.42
73:WX:103:VAL:HA	73:WX:112:ASP:HA	2.02	0.42
80:18:900:C:H2'	80:18:901:G:C8	2.55	0.42
80:18:1227:G:C2	80:18:1228:A:C8	3.07	0.42
80:18:1485:U:H2'	80:18:1486:A:O4'	2.19	0.42
80:18:1650:A:H2'	80:18:1651:A:O4'	2.20	0.42
84:ES:2942:C:C2'	84:ES:2943:C:H5'	2.49	0.42
85:28:422:C:H2'	85:28:423:G:H8	1.85	0.42
85:28:679:C:C2	85:28:680:G:C8	3.08	0.42
85:28:733:A:C4	85:28:734:G:C8	3.07	0.42
85:28:949:G:H2'	85:28:950:G:H8	1.84	0.42
85:28:2329:U:H2'	85:28:2330:G:O4'	2.19	0.42
85:28:2724:G:H5''	85:28:2725:A:OP2	2.20	0.42
85:28:2728:U:H2'	85:28:2729:C:C6	2.55	0.42
85:28:2804:C:H2'	85:28:2805:C:C6	2.55	0.42
85:28:2885:A:H2'	85:28:2886:U:H6	1.84	0.42
85:28:4564:A:H2'	85:28:4565:C:C6	2.54	0.42
1:IF:116:ARG:HH22	1:IF:158:LEU:CB	2.18	0.42
2:BB:131:HIS:HA	2:BB:134:LEU:HD12	2.01	0.42
11:L5:41:LYS:HB2	23:21:68:THR:O	2.20	0.42
15:10:190:LEU:HB3	15:10:197:VAL:HG21	2.02	0.42
16:13:58:ILE:HG23	16:13:70:VAL:HG11	2.02	0.42
19:bb:80:PHE:HA	19:bb:83:THR:HG22	2.01	0.42
22:20:28:TYR:CE1	22:20:52:LYS:HE3	2.55	0.42
33:ee:78:HIS:HB2	33:ee:85:ARG:HG3	2.01	0.42
48:s:192:VAL:O	48:s:198:ILE:HA	2.19	0.42
65:SS:13:MET:HB2	65:SS:13:MET:HE2	1.86	0.42
65:SS:45:ALA:HB1	65:SS:50:THR:O	2.20	0.42
74:S8:11:ARG:NH2	74:S8:17:LYS:HE3	2.35	0.42
80:18:155:G:C2	80:18:156:G:C8	3.08	0.42
80:18:1035:A:H2'	80:18:1036:A:C8	2.54	0.42
80:18:1230:C:H2'	80:18:1231:C:H6	1.84	0.42
81:v:304:ILE:HD13	81:v:336:LEU:HA	2.00	0.42
85:28:1592:G:C2	85:28:1593:A:C8	3.08	0.42
85:28:2555:G:H2'	85:28:2556:G:C8	2.55	0.42
85:28:2895:A:H2'	85:28:2896:G:C8	2.54	0.42
6:58:155:C:H2'	6:58:156:U:C6	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:6:55:A:C4	7:6:56:G:C8	3.08	0.42
10:L4:137:VAL:HG21	10:L4:150:LEU:HD21	2.02	0.42
14:aa:228:ARG:HG3	14:aa:283:TYR:CG	2.55	0.42
28:dd:38:MET:HA	28:dd:42:ARG:HE	1.84	0.42
43:ff:7:LYS:HE2	85:28:2875:C:H2'	2.02	0.42
45:AS:49:VAL:HG21	45:AS:62:LEU:HD13	2.01	0.42
49:t:64:ILE:HA	49:t:69:ALA:HA	2.02	0.42
52:ZZ:89:LYS:HB3	80:18:1507:G:C4	2.54	0.42
69:S7:130:LEU:HB2	69:S7:177:TYR:CE1	2.55	0.42
80:18:563:G:C2	80:18:564:A:N7	2.88	0.42
80:18:1131:G:H2'	80:18:1132:C:H6	1.85	0.42
80:18:1686:G:H2'	80:18:1687:C:H6	1.85	0.42
81:v:225:LEU:HD11	81:v:261:TRP:HB2	2.01	0.42
85:28:456:C:H2'	85:28:457:G:C8	2.54	0.42
85:28:489:C:H2'	85:28:490:C:H6	1.85	0.42
85:28:1082:C:C2'	85:28:1083:U:H5'	2.50	0.42
85:28:1199:G:C2	85:28:1200:G:N7	2.88	0.42
85:28:2465:C:H1'	85:28:3672:G:N2	2.35	0.42
85:28:3846:C:H2'	85:28:3847:C:H6	1.84	0.42
85:28:4233:A:C4	85:28:4235:G:N7	2.87	0.42
85:28:4251:A:H2'	85:28:4252:C:O4'	2.19	0.42
13:L7:215:PRO:HD3	13:L7:246:MET:HE2	2.02	0.42
14:aa:223:LEU:HA	14:aa:223:LEU:HD23	1.72	0.42
16:13:57:PRO:HG3	16:13:75:GLY:C	2.45	0.42
26:26:58:VAL:HG13	26:26:59:ARG:HG2	2.02	0.42
33:ee:33:VAL:HG23	33:ee:38:GLU:HB2	2.01	0.42
34:34:63:VAL:HG13	34:34:66:ARG:NH2	2.35	0.42
80:18:965:U:O2	80:18:1066:U:H1'	2.20	0.42
80:18:1109:C:H2'	80:18:1110:G:O4'	2.19	0.42
81:v:285:LEU:HD12	81:v:286:PRO:HD2	2.02	0.42
84:ES:3245:G:H2'	84:ES:3246:G:C8	2.55	0.42
85:28:425:U:H2'	85:28:426:A:H8	1.85	0.42
85:28:676:C:H2'	85:28:677:G:C8	2.53	0.42
85:28:1095:A:H2'	85:28:1096:C:C6	2.54	0.42
85:28:2281:U:C2	85:28:2282:A:C8	3.08	0.42
85:28:3712:A:H2'	85:28:3713:U:H5''	2.02	0.42
6:58:85:U:H5'	6:58:87:G:O4'	2.20	0.41
6:58:91:A:H2'	6:58:92:U:O4'	2.20	0.41
7:6:118:C:H2'	7:6:119:U:C6	2.55	0.41
8:L8:9:ARG:HD2	85:28:1628:C:OP2	2.20	0.41
16:13:184:MET:HG2	85:28:1482:G:H1	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:15:94:PHE:CE2	18:15:96:ARG:HB2	2.55	0.41
22:20:16:CYS:HB3	22:20:25:PRO:HG2	2.02	0.41
29:29:28:ARG:HB3	85:28:1805:A:C4	2.55	0.41
30:30:77:ASN:OD1	30:30:80:GLU:HG2	2.20	0.41
41:41:3:ALA:HB3	80:18:1842:C:OP1	2.20	0.41
45:AS:181:LEU:HA	45:AS:184:VAL:HG22	2.01	0.41
50:F:25:GLY:HA3	50:F:333:ILE:HG13	2.02	0.41
51:Q:35:LEU:HD23	51:Q:35:LEU:HA	1.90	0.41
52:ZZ:140:TYR:HE1	52:ZZ:145:CYS:HA	1.84	0.41
59:AA:173:LEU:HD22	59:AA:189:ILE:HG12	2.02	0.41
64:RR:104:GLY:O	80:18:648:A:H4'	2.20	0.41
69:S7:140:VAL:HG21	69:S7:159:ASP:HB3	2.01	0.41
78:11:57:VAL:HG12	78:11:59:SER:H	1.85	0.41
80:18:27:A:H2'	80:18:28:U:C6	2.55	0.41
83:A:102:PHE:CD1	83:A:102:PHE:N	2.88	0.41
85:28:1392:A:H2'	85:28:1393:G:C8	2.54	0.41
85:28:1490:G:H2'	85:28:1491:A:C8	2.55	0.41
85:28:1490:G:H2'	85:28:1491:A:H8	1.85	0.41
85:28:1808:C:H1'	85:28:1831:G:N2	2.35	0.41
85:28:2089:G:H1'	85:28:2090:U:OP2	2.20	0.41
85:28:2102:G:O2'	85:28:2103:A:H5'	2.20	0.41
85:28:2479:G:N3	85:28:2480:G:C8	2.88	0.41
85:28:2691:U:H2'	85:28:2692:U:C6	2.55	0.41
85:28:2897:G:H2'	85:28:2898:G:H8	1.84	0.41
85:28:4088:C:H2'	85:28:4089:G:H8	1.85	0.41
85:28:4638:U:H2'	85:28:4639:G:N3	2.34	0.41
1:IF:140:ALA:O	1:IF:144:LEU:HG	2.21	0.41
1:IF:159:PHE:O	1:IF:163:GLN:HB2	2.20	0.41
7:6:113:G:H2'	7:6:114:U:C6	2.55	0.41
14:aa:169:ALA:O	14:aa:172:GLU:HG3	2.20	0.41
19:bb:130:LYS:HB2	19:bb:133:ARG:HG2	2.02	0.41
25:cc:146:ALA:HA	25:cc:149:VAL:HG22	2.00	0.41
49:t:108:GLU:HA	49:t:111:ASN:HD21	1.85	0.41
51:Q:173:LYS:HE3	51:Q:173:LYS:HB2	1.91	0.41
59:AA:17:TRP:O	59:AA:36:ARG:HG2	2.20	0.41
68:S9:128:VAL:HG22	70:YY:104:ARG:HH22	1.85	0.41
80:18:298:G:C4	80:18:299:A:C8	3.08	0.41
80:18:1050:A:H62	80:18:1068:G:H21	1.68	0.41
80:18:1266:C:H42	80:18:1516:G:H1	1.69	0.41
80:18:1503:C:H2'	80:18:1504:U:C6	2.56	0.41
80:18:1512:C:H2'	80:18:1513:C:C6	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:18:1706:G:H2'	80:18:1707:U:C6	2.54	0.41
85:28:385:A:N3	85:28:387:G:H5''	2.35	0.41
85:28:1094:G:H2'	85:28:1095:A:H8	1.84	0.41
85:28:1895:G:H2'	85:28:1896:A:O4'	2.20	0.41
85:28:2380:G:N2	85:28:2424:G:H5''	2.35	0.41
85:28:3829:G:C2	85:28:3830:A:C8	3.07	0.41
85:28:4389:C:H2'	85:28:4390:A:H8	1.84	0.41
85:28:4889:G:H2'	85:28:4890:G:C8	2.55	0.41
14:aa:243:LEU:HD12	14:aa:243:LEU:HA	1.85	0.41
16:13:184:MET:HE2	16:13:184:MET:HB2	1.91	0.41
18:15:95:ALA:HB3	85:28:30:C:H5''	2.02	0.41
48:s:57:LYS:HB3	48:s:60:MET:HB3	2.02	0.41
60:OO:56:MET:SD	60:OO:86:LYS:HB3	2.61	0.41
62:LL:142:ARG:HE	62:LL:142:ARG:HB2	1.64	0.41
69:S7:36:LEU:HD13	69:S7:75:ILE:HD11	2.02	0.41
76:GG:94:HIS:CD2	76:GG:127:GLY:HA3	2.55	0.41
79:L9:12:ILE:H	79:L9:12:ILE:HG12	1.77	0.41
80:18:191:A:N3	80:18:191:A:H2'	2.34	0.41
80:18:221:A:H2'	80:18:222:U:H6	1.85	0.41
80:18:1279:C:H2'	80:18:1280:G:C8	2.54	0.41
81:v:831:PRO:HA	81:v:834:VAL:HB	2.01	0.41
85:28:691:C:H2'	85:28:692:A:C8	2.56	0.41
85:28:952:G:H2'	85:28:953:C:C6	2.55	0.41
85:28:1479:G:H2'	85:28:1480:C:C6	2.55	0.41
85:28:1505:C:C2	85:28:1506:G:C8	3.08	0.41
85:28:1604:G:H2'	85:28:1605:G:C8	2.55	0.41
85:28:2266:C:H4'	85:28:2267:U:O5'	2.20	0.41
85:28:2273:G:H2'	85:28:2274:C:H6	1.85	0.41
85:28:2436:U:C2	85:28:2783:A:C8	3.08	0.41
85:28:2556:G:C2	85:28:2557:G:N7	2.89	0.41
85:28:2815:A:H2'	85:28:2816:G:C8	2.55	0.41
85:28:4678:G:N2	85:28:4713:G:H1'	2.35	0.41
1:IF:78:LYS:HE2	1:IF:115:ARG:NH2	2.36	0.41
1:IF:228:PRO:HG2	1:IF:231:LEU:HD12	2.02	0.41
3:S2:183:LYS:HG3	73:WX:95:PRO:O	2.20	0.41
7:6:55:A:H2'	7:6:56:G:H8	1.85	0.41
10:L4:70:GLY:HA2	85:28:3905:A:O3'	2.20	0.41
13:L7:49:ILE:HD12	13:L7:185:CYS:HB3	2.01	0.41
13:L7:102:PRO:HD3	85:28:1876:U:O3'	2.20	0.41
13:L7:219:MET:HB3	13:L7:231:ASP:OD2	2.20	0.41
26:26:47:MET:HE1	26:26:118:ILE:HB	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:26:59:ARG:HG3	26:26:103:LYS:HD2	2.01	0.41
36:36:34:THR:HB	36:36:37:THR:HG23	2.03	0.41
65:SS:60:PHE:HB2	80:18:571:U:O3'	2.20	0.41
67:S4:68:ARG:HG2	67:S4:76:VAL:HG11	2.03	0.41
74:S8:10:LYS:HB2	74:S8:10:LYS:HE3	1.80	0.41
80:18:431:G:N3	80:18:432:G:C8	2.88	0.41
80:18:695:C:H2'	80:18:696:G:C8	2.55	0.41
80:18:1261:C:C4	80:18:1262:C:C4	3.09	0.41
85:28:516:C:H2'	85:28:517:C:C6	2.54	0.41
85:28:962:C:C2	85:28:963:G:C8	3.08	0.41
85:28:1421:G:C2	85:28:1422:G:C8	3.08	0.41
85:28:3833:C:H2'	85:28:3834:C:H6	1.85	0.41
85:28:3834:C:H2'	85:28:3835:C:H6	1.85	0.41
86:23:36:ASN:HD22	86:23:36:ASN:HA	1.71	0.41
7:6:58:A:H2'	7:6:59:G:C8	2.56	0.41
14:aa:210:ILE:HG23	14:aa:220:VAL:HG11	2.02	0.41
20:17:122:ALA:HB3	20:17:143:PRO:HG2	2.03	0.41
29:29:102:PRO:HA	29:29:109:ARG:HH22	1.85	0.41
31:31:23:ARG:HD3	31:31:25:TYR:OH	2.20	0.41
36:36:90:LEU:O	36:36:93:VAL:HG22	2.21	0.41
43:ff:13:LYS:HE3	43:ff:14:TYR:CZ	2.56	0.41
51:Q:42:THR:OG1	85:28:1428:U:H5''	2.20	0.41
60:OO:34:LYS:O	60:OO:38:ASP:HB2	2.21	0.41
69:S7:158:LEU:O	69:S7:190:PRO:HD2	2.20	0.41
75:W:35:LYS:HD3	75:W:51:TRP:CZ2	2.55	0.41
80:18:186:C:H2'	80:18:187:G:C8	2.55	0.41
80:18:479:C:H2'	80:18:480:G:C8	2.55	0.41
80:18:1390:U:C2	80:18:1391:C:C6	3.08	0.41
80:18:1716:C:H2'	80:18:1717:C:C6	2.56	0.41
80:18:1738:C:H2'	80:18:1739:C:C6	2.56	0.41
80:18:1750:C:H2'	80:18:1751:C:C6	2.56	0.41
85:28:656:C:H2'	85:28:657:C:C6	2.56	0.41
85:28:700:G:H2'	85:28:701:G:H8	1.85	0.41
85:28:1578:U:H2'	85:28:1579:C:C6	2.56	0.41
85:28:1761:G:H2'	85:28:1762:C:C6	2.55	0.41
85:28:2379:A:H2'	85:28:2380:G:O4'	2.20	0.41
85:28:2556:G:N3	85:28:2557:G:C8	2.88	0.41
85:28:3933:G:H2'	85:28:3934:G:C8	2.55	0.41
1:IF:240:GLN:HG2	1:IF:366:ARG:NH1	2.35	0.41
8:L8:117:GLU:HG2	8:L8:124:GLY:N	2.35	0.41
8:L8:199:VAL:HG21	85:28:1631:A:N7	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:L4:205:ARG:HG3	85:28:2297:G:H5'	2.02	0.41
10:L4:339:THR:HG22	10:L4:342:ARG:HH22	1.84	0.41
44:gg:113:ARG:O	44:gg:117:ILE:HG13	2.20	0.41
57:II:19:ALA:HB2	57:II:75:GLY:HA3	2.02	0.41
58:CC:86:PRO:HA	58:CC:87:PRO:HD3	1.91	0.41
67:S4:208:VAL:HB	67:S4:225:ILE:HD11	2.03	0.41
80:18:348:A:H2'	80:18:349:A:H8	1.84	0.41
80:18:1390:U:H2'	80:18:1391:C:H6	1.85	0.41
84:ES:2955:A:H2	84:ES:3239:G:H1	1.67	0.41
85:28:23:C:H2'	85:28:24:G:O4'	2.20	0.41
85:28:1311:G:H2'	85:28:1312:A:O4'	2.20	0.41
85:28:1753:G:N2	85:28:1778:C:C2	2.89	0.41
85:28:1951:G:C6	85:28:2033:A:C2	3.08	0.41
85:28:2385:U:H2'	85:28:2386:U:C6	2.56	0.41
85:28:2688:G:H2'	85:28:2689:C:C6	2.56	0.41
85:28:2750:G:H2'	85:28:2751:G:O4'	2.20	0.41
85:28:3916:G:H2'	85:28:3917:A:H8	1.83	0.41
2:BB:38:ILE:HD11	2:BB:150:THR:HG22	2.01	0.41
5:DD:128:VAL:HB	5:DD:140:PHE:HB3	2.01	0.41
6:58:28:C:H2'	6:58:29:G:H8	1.85	0.41
13:L7:180:LYS:HE3	13:L7:181:TYR:CZ	2.55	0.41
23:21:80:VAL:O	23:21:83:LYS:HG2	2.20	0.41
59:AA:127:LYS:HE2	59:AA:149:GLU:HA	2.02	0.41
59:AA:139:LYS:HG3	59:AA:140:TYR:CD2	2.56	0.41
60:OO:56:MET:HE2	60:OO:56:MET:HB2	1.97	0.41
67:S4:105:THR:HB	67:S4:245:ARG:HG2	2.02	0.41
71:S3:46:THR:HB	71:S3:84:VAL:HA	2.02	0.41
80:18:23:G:C5	80:18:24:C:C4	3.09	0.41
80:18:653:A:H2'	80:18:654:A:O4'	2.20	0.41
80:18:964:A:H2'	80:18:965:U:H6	1.86	0.41
80:18:1083:A:H4'	80:18:1085:C:C5	2.55	0.41
80:18:1221:G:C2	80:18:1222:G:C5	3.09	0.41
85:28:1301:C:H42	85:28:2316:G:H5'	1.86	0.41
85:28:1471:U:H2'	85:28:1472:C:H6	1.86	0.41
85:28:1549:G:C2	85:28:1550:G:C8	3.09	0.41
85:28:2518:G:H1'	85:28:2539:C:H1'	2.02	0.41
85:28:2557:G:H2'	85:28:2558:C:H6	1.84	0.41
85:28:2863:G:C4	85:28:2864:A:C8	3.08	0.41
85:28:3685:C:C2	85:28:3686:G:C8	3.09	0.41
85:28:4068:U:H2'	85:28:4069:U:C6	2.56	0.41
85:28:4400:G:C2	85:28:4401:G:C8	3.09	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:28:4486:C:H2'	85:28:4487:A:O4'	2.21	0.41
85:28:4685:U:H2'	85:28:4686:G:H8	1.85	0.41
2:BB:32:PHE:CG	80:18:1097:G:H4'	2.56	0.41
10:L4:142:HIS:CD2	10:L4:249:PHE:H	2.39	0.41
18:15:150:TRP:CH2	18:15:151:ILE:HG12	2.55	0.41
27:27:98:LYS:HE2	27:27:98:LYS:HB3	1.78	0.41
30:30:12:GLU:CD	30:30:12:GLU:H	2.28	0.41
46:FF:49:GLN:O	46:FF:53:ILE:HG12	2.21	0.41
52:ZZ:107:LYS:HG2	52:ZZ:117:LEU:HD11	2.03	0.41
59:AA:279:SER:O	59:AA:280:LYS:HG2	2.20	0.41
64:RR:107:ARG:CG	64:RR:110:HIS:HB3	2.51	0.41
65:SS:37:LYS:HD2	65:SS:57:VAL:O	2.21	0.41
68:S9:170:PRO:HB2	68:S9:174:LYS:HB3	2.02	0.41
71:S3:163:PRO:HA	71:S3:166:TYR:CE2	2.56	0.41
80:18:375:U:C2	80:18:376:A:C8	3.09	0.41
80:18:1328:G:H2'	80:18:1329:U:C6	2.55	0.41
80:18:1351:G:H2'	80:18:1352:G:H8	1.85	0.41
80:18:1627:C:C2	80:18:1628:C:C5	3.09	0.41
80:18:1787:G:H2'	80:18:1788:A:H8	1.85	0.41
85:28:751:G:C4	85:28:752:G:C8	3.09	0.41
85:28:952:G:H2'	85:28:953:C:H6	1.86	0.41
85:28:1196:G:H2'	85:28:1197:C:C6	2.56	0.41
85:28:1511:U:H2'	85:28:1512:G:H8	1.84	0.41
85:28:1750:G:C2	85:28:1751:A:C8	3.09	0.41
85:28:3802:U:O2'	85:28:3803:A:H5'	2.21	0.41
85:28:4346:U:H2'	85:28:4347:G:C8	2.55	0.41
85:28:4648:A:C4	85:28:4649:G:C8	3.09	0.41
3:S2:94:ILE:HD12	3:S2:162:ILE:HD11	2.03	0.41
4:PP:73:ALA:HB1	4:PP:78:ILE:HB	2.02	0.41
6:58:45:C:C2	6:58:46:G:C8	3.08	0.41
8:L8:102:LEU:HD12	8:L8:106:THR:OG1	2.21	0.41
8:L8:225:ILE:HD11	8:L8:233:ARG:HG3	2.02	0.41
10:L4:60:HIS:CE1	10:L4:100:ARG:HD3	2.47	0.41
12:L6:116:PRO:HG2	12:L6:119:TYR:CZ	2.56	0.41
13:L7:124:LEU:HD12	13:L7:124:LEU:HA	1.82	0.41
15:10:31:ILE:HG22	15:10:62:SER:HB2	2.02	0.41
16:13:92:ARG:CZ	85:28:109:G:H5'	2.50	0.41
17:14:89:THR:HG22	17:14:91:TRP:H	1.85	0.41
19:bb:81:TRP:HB2	19:bb:104:VAL:HG21	2.03	0.41
28:dd:40:HIS:HA	85:28:1675:C:H1'	2.03	0.41
30:30:91:VAL:HG12	85:28:2673:G:O2'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:40:92:THR:HG22	40:40:94:ASN:H	1.86	0.41
43:ff:49:ARG:HB2	43:ff:55:TRP:CZ3	2.56	0.41
45:AS:136:ARG:NH1	80:18:941:C:H5''	2.36	0.41
45:AS:163:GLN:O	45:AS:166:LYS:HG2	2.21	0.41
45:AS:180:ASP:O	45:AS:184:VAL:HG13	2.21	0.41
50:F:130:ALA:HB3	50:F:133:THR:OG1	2.21	0.41
54:TT:91:LEU:HD22	54:TT:96:LEU:HD12	2.03	0.41
55:S5:144:LEU:HD23	56:WW:49:PRO:HG2	2.02	0.41
57:II:18:THR:HB	57:II:75:GLY:HA2	2.03	0.41
66:S6:157:VAL:HG22	80:18:75:G:H22	1.86	0.41
68:S9:42:GLU:O	68:S9:46:VAL:HG23	2.21	0.41
73:WX:36:ARG:O	73:WX:40:VAL:HG23	2.21	0.41
78:11:161:GLU:HA	78:11:164:ARG:HG2	2.02	0.41
79:L9:40:HIS:ND1	79:L9:41:ILE:HG13	2.36	0.41
80:18:215:G:H2'	80:18:216:C:H6	1.86	0.41
80:18:319:C:H2'	80:18:320:G:C8	2.56	0.41
80:18:812:A:C4	80:18:813:A:C8	3.08	0.41
80:18:854:A:C2	80:18:855:G:C8	3.09	0.41
80:18:1266:C:C4	80:18:1517:G:N2	2.89	0.41
80:18:1385:G:C4	80:18:1386:A:C8	3.09	0.41
80:18:1395:C:H2'	80:18:1396:A:N3	2.35	0.41
80:18:1444:U:H2'	80:18:1445:U:C6	2.56	0.41
80:18:1529:C:H5'	80:18:1666:C:OP1	2.21	0.41
80:18:1590:C:H3'	80:18:1591:C:C6	2.54	0.41
80:18:1836:G:OP1	80:18:1839:U:H4'	2.21	0.41
85:28:2:G:H2'	85:28:3:C:C6	2.56	0.41
85:28:228:C:H2'	85:28:229:G:H8	1.85	0.41
85:28:262:G:N3	85:28:263:G:C8	2.89	0.41
85:28:470:A:C4	85:28:471:A:C8	3.09	0.41
85:28:1078:A:H2'	85:28:1078:A:N3	2.36	0.41
85:28:1200:G:C5	85:28:1201:U:C5	3.09	0.41
85:28:1206:C:H2'	85:28:1207:C:C6	2.56	0.41
85:28:1537:A:H2'	85:28:1538:U:C6	2.56	0.41
85:28:1594:C:O2'	85:28:1597:G:H1'	2.20	0.41
85:28:1720:C:H2'	85:28:1721:G:O4'	2.21	0.41
85:28:1874:A:H2'	85:28:1875:C:C6	2.56	0.41
85:28:1881:C:H5'	85:28:2281:U:H1'	2.03	0.41
85:28:2060:G:H2'	85:28:2061:U:C6	2.55	0.41
85:28:2359:U:H5''	85:28:2360:A:OP2	2.21	0.41
85:28:2488:C:H3'	85:28:2490:U:O4	2.21	0.41
85:28:2602:G:O4'	85:28:2742:G:H2'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:28:4400:G:C4	85:28:4401:G:C8	3.09	0.41
85:28:4459:U:H2'	85:28:4460:U:H6	1.86	0.41
85:28:4500:U:H2'	85:28:4501:U:C6	2.56	0.41
85:28:4524:G:H2'	85:28:4525:C:H6	1.86	0.41
85:28:4994:G:H2'	85:28:4995:U:C6	2.56	0.41
85:28:4997:G:H2'	85:28:4998:G:H8	1.86	0.41
9:L3:86:VAL:HG12	9:L3:201:LEU:HD12	2.03	0.41
11:L5:146:LEU:HD21	11:L5:159:VAL:CG1	2.51	0.41
14:aa:165:GLN:HA	14:aa:168:LEU:HG	2.03	0.41
18:15:184:ILE:HD12	85:28:99:A:H5''	2.03	0.41
31:31:121:ASN:C	31:31:121:ASN:HD22	2.29	0.41
35:35:96:ASN:N	35:35:96:ASN:ND2	2.68	0.41
52:ZZ:100:LEU:HD11	80:18:1285:G:H1'	2.03	0.41
66:S6:135:PRO:HG2	66:S6:144:LEU:HD22	2.03	0.41
80:18:405:G:H2'	80:18:406:U:O4'	2.21	0.41
80:18:1578:U:H5''	80:18:1579:A:N3	2.36	0.41
81:v:176:GLN:O	81:v:180:ARG:HG2	2.21	0.41
85:28:52:G:H4'	85:28:1529:G:H4'	2.03	0.41
85:28:125:C:H2'	85:28:126:C:C6	2.55	0.41
85:28:673:C:H2'	85:28:674:G:C8	2.56	0.41
85:28:1617:G:H1'	85:28:2513:A:H61	1.85	0.41
85:28:1620:U:H2'	85:28:1621:A:C8	2.56	0.41
85:28:1665:C:H2'	85:28:1666:C:H6	1.86	0.41
85:28:1862:U:H4'	85:28:4212:A:OP2	2.21	0.41
85:28:2671:C:H2'	85:28:2672:C:C6	2.56	0.41
85:28:2706:G:H2'	85:28:2708:U:H2'	2.03	0.41
85:28:3911:C:C2	85:28:3912:U:C5	3.09	0.41
85:28:3927:U:H2'	85:28:3928:A:H8	1.85	0.41
85:28:5030:U:H2'	85:28:5031:G:C8	2.53	0.41
1:IF:212:PHE:HA	1:IF:235:LEU:HD22	2.03	0.40
11:L5:146:LEU:HD22	85:28:4323:A:H2	1.86	0.40
15:10:19:LYS:HB3	15:10:26:VAL:HG21	2.02	0.40
17:14:122:ILE:HD12	19:bb:189:ILE:HG22	2.02	0.40
18:15:85:VAL:HA	42:42:49:GLY:HA2	2.03	0.40
21:19:106:LEU:HD13	21:19:138:LEU:HD21	2.02	0.40
28:dd:119:LYS:HA	28:dd:140:VAL:HG13	2.04	0.40
61:MM:86:GLY:O	80:18:1530:U:H4'	2.20	0.40
67:S4:100:ARG:HB2	67:S4:114:ILE:HD13	2.04	0.40
67:S4:123:LEU:HD11	67:S4:159:THR:HB	2.03	0.40
71:S3:100:ALA:O	71:S3:103:GLU:HG3	2.20	0.40
76:GG:121:ARG:HD2	76:GG:121:ARG:HA	1.85	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:18:616:A:C2	80:18:632:C:H1'	2.56	0.40
80:18:1137:U:O2'	80:18:1138:C:H3'	2.21	0.40
80:18:1609:C:H2'	80:18:1610:G:C8	2.56	0.40
80:18:1685:U:C4	80:18:1686:G:N7	2.88	0.40
80:18:1834:A:H2'	80:18:1834:A:N3	2.36	0.40
81:v:4:PHE:HD1	81:v:4:PHE:HA	1.76	0.40
81:v:423:THR:HG23	81:v:448:GLN:O	2.21	0.40
81:v:757:GLY:HA3	85:28:2009:A:H5'	2.03	0.40
85:28:1356:U:H2'	85:28:1357:C:C6	2.56	0.40
85:28:2647:A:H3'	85:28:2648:G:H8	1.86	0.40
85:28:3937:C:H2'	85:28:3938:G:C8	2.56	0.40
85:28:4186:A:H2'	85:28:4187:G:C8	2.55	0.40
85:28:4924:C:H2'	85:28:4925:U:C2	2.56	0.40
6:58:114:G:C4	6:58:115:G:C8	3.09	0.40
7:6:4:U:H2'	7:6:5:A:H8	1.86	0.40
7:6:60:G:N3	7:6:61:G:C8	2.89	0.40
11:L5:146:LEU:CD1	11:L5:163:LEU:HB2	2.50	0.40
21:19:93:VAL:O	21:19:97:ARG:HG2	2.21	0.40
28:dd:130:SER:OG	85:28:1396:G:H5''	2.21	0.40
44:gg:51:VAL:HG12	44:gg:117:ILE:HD12	2.04	0.40
46:FF:4:MET:HE3	46:FF:121:ARG:HG2	2.03	0.40
47:VV:12:PRO:HB3	69:S7:192:PHE:HB2	2.03	0.40
47:VV:53:VAL:HG23	47:VV:62:VAL:HG23	2.03	0.40
49:t:20:GLY:H	49:t:54:LYS:HA	1.86	0.40
59:AA:165:ILE:HD11	59:AA:177:TRP:HB2	2.02	0.40
61:MM:13:GLU:HA	61:MM:16:ARG:HD2	2.02	0.40
65:SS:76:TYR:CE2	65:SS:82:ALA:HA	2.57	0.40
65:SS:105:LYS:HE2	65:SS:105:LYS:HB2	1.96	0.40
80:18:203:G:H2'	80:18:204:G:C8	2.56	0.40
80:18:352:U:C2	80:18:353:C:C5	3.09	0.40
80:18:429:C:H2'	80:18:430:C:H6	1.86	0.40
80:18:1367:U:H2'	80:18:1368:U:H6	1.86	0.40
80:18:1671:G:H2'	80:18:1672:U:C6	2.56	0.40
80:18:1826:G:H2'	80:18:1827:U:C6	2.55	0.40
81:v:120:ARG:NH2	81:v:497:MET:HA	2.36	0.40
85:28:1370:G:H4'	85:28:1371:A:O5'	2.21	0.40
85:28:1461:C:C2	85:28:1462:A:C8	3.09	0.40
85:28:2089:G:H4'	85:28:2090:U:O5'	2.20	0.40
85:28:2529:A:O2'	85:28:2530:U:H5''	2.22	0.40
85:28:3702:A:C4	85:28:3703:G:C8	3.08	0.40
85:28:3760:A:H1'	85:28:3761:C:OP1	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:28:4273:A:H62	85:28:4335:C:N4	2.19	0.40
85:28:4642:U:H2'	85:28:4643:G:C8	2.56	0.40
1:IF:107:LEU:HD11	1:IF:386:ASN:HB2	2.03	0.40
1:IF:278:ILE:HG23	1:IF:332:THR:CG2	2.37	0.40
5:DD:55:TYR:OH	5:DD:116:CYS:HB3	2.22	0.40
6:58:130:C:H2'	6:58:131:G:C8	2.55	0.40
9:L3:175:GLN:HA	85:28:4986:G:H5'	2.03	0.40
12:L6:206:ILE:O	12:L6:209:VAL:HG12	2.21	0.40
16:13:182:LEU:HD23	36:36:7:MET:HE3	2.02	0.40
17:14:62:LEU:HD13	17:14:64:PHE:HE2	1.86	0.40
18:15:108:ARG:HB2	18:15:161:MET:HE1	2.04	0.40
66:S6:7:PHE:CZ	66:S6:9:ALA:HB3	2.56	0.40
67:S4:151:ASP:HB3	67:S4:154:ILE:HG13	2.03	0.40
73:WX:93:LEU:HD21	73:WX:128:PHE:CD1	2.56	0.40
80:18:298:G:C2	80:18:299:A:C8	3.09	0.40
80:18:457:C:C2	80:18:458:A:C8	3.09	0.40
80:18:678:U:C2	80:18:679:A:C8	3.09	0.40
80:18:877:C:C2	80:18:910:G:N2	2.90	0.40
80:18:1019:C:H2'	80:18:1020:A:O4'	2.21	0.40
80:18:1352:G:H2'	80:18:1353:A:H8	1.86	0.40
80:18:1523:C:H2'	80:18:1524:G:C8	2.55	0.40
80:18:1536:G:C2	80:18:1537:A:C5	3.10	0.40
80:18:1810:U:H2'	80:18:1811:C:C6	2.56	0.40
80:18:1834:A:C2	80:18:1836:G:C2	3.09	0.40
81:v:335:LEU:O	81:v:339:VAL:HG12	2.20	0.40
85:28:27:C:H2'	85:28:28:C:C6	2.56	0.40
85:28:86:U:H2'	85:28:87:A:C8	2.55	0.40
85:28:310:G:C4	85:28:311:G:C8	3.09	0.40
85:28:1205:G:H2'	85:28:1206:C:H6	1.87	0.40
85:28:1322:A:H1'	85:28:1324:A:OP2	2.22	0.40
85:28:1359:G:H3'	85:28:1360:G:C8	2.56	0.40
85:28:1455:G:H4'	85:28:1456:C:OP1	2.22	0.40
85:28:1469:C:C2	85:28:1470:G:C8	3.09	0.40
85:28:1589:C:H2'	85:28:1590:C:C6	2.56	0.40
85:28:2335:C:H2'	85:28:2336:G:C8	2.41	0.40
85:28:2691:U:C2	85:28:2692:U:C5	3.09	0.40
85:28:3907:G:H2'	85:28:4447:C:O2'	2.21	0.40
85:28:4174:U:H2'	85:28:4175:G:C8	2.55	0.40
2:BB:74:VAL:HG13	2:BB:121:LEU:HB3	2.03	0.40
2:BB:77:ILE:HG12	2:BB:99:ILE:HB	2.03	0.40
10:L4:83:GLY:H	85:28:368:C:H1'	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:15:158:HIS:HB3	18:15:161:MET:CG	2.52	0.40
19:bb:126:VAL:HG13	19:bb:127:VAL:HG23	2.03	0.40
19:bb:179:LYS:HD3	19:bb:179:LYS:HA	1.90	0.40
22:20:115:ALA:HB2	85:28:2060:G:N2	2.36	0.40
50:F:31:VAL:HG21	50:F:56:ILE:CG2	2.52	0.40
58:CC:64:TRP:CG	63:XX:23:VAL:HG13	2.57	0.40
64:RR:76:LYS:HB3	80:18:482:G:H5''	2.03	0.40
66:S6:136:LYS:HB2	80:18:65:C:N4	2.36	0.40
66:S6:216:ARG:NH1	67:S4:153:LEU:HD13	2.36	0.40
75:W:107:GLN:O	75:W:110:ARG:HG3	2.21	0.40
76:GG:99:ALA:H	76:GG:133:THR:HG22	1.85	0.40
80:18:4:C:H2'	80:18:5:U:C6	2.55	0.40
80:18:34:U:H2'	80:18:35:C:C6	2.57	0.40
80:18:221:A:H2'	80:18:222:U:C6	2.55	0.40
80:18:1753:C:H2'	80:18:1754:G:C8	2.57	0.40
85:28:651:C:H2'	85:28:652:G:C8	2.52	0.40
85:28:961:G:C4	85:28:962:C:C5	3.09	0.40
85:28:1304:C:H2'	85:28:1305:C:C6	2.57	0.40
85:28:1341:U:C2	85:28:1342:A:C8	3.10	0.40
85:28:1519:C:C2	85:28:1520:C:C5	3.10	0.40
85:28:2538:U:H2'	85:28:2539:C:H6	1.86	0.40
85:28:2540:C:H2'	85:28:2541:G:C8	2.56	0.40
85:28:3652:A:H2'	85:28:3653:A:C5	2.57	0.40
85:28:3896:C:H2'	85:28:3897:G:C4	2.56	0.40
85:28:4346:U:H2'	85:28:4347:G:H8	1.86	0.40
85:28:4886:C:H2'	85:28:4887:C:H6	1.87	0.40
1:IF:84:LEU:HD11	1:IF:99:LEU:HD12	2.03	0.40
6:58:28:C:C2	6:58:29:G:C8	3.10	0.40
6:58:40:A:H2'	6:58:41:A:H8	1.87	0.40
6:58:108:A:H2'	6:58:109:C:O4'	2.21	0.40
10:L4:32:ILE:HD12	10:L4:130:ALA:HB2	2.03	0.40
12:L6:269:GLN:HG2	85:28:4930:C:H5'	2.04	0.40
19:bb:169:ARG:CZ	85:28:4860:G:H5'	2.52	0.40
33:ee:106:TYR:CD1	33:ee:107:PRO:HD3	2.56	0.40
42:42:74:GLU:HG3	42:42:77:CYS:H	1.87	0.40
45:AS:136:ARG:HD2	45:AS:138:PHE:CZ	2.57	0.40
48:s:192:VAL:HB	48:s:199:TYR:HB3	2.04	0.40
59:AA:20:GLN:HG2	59:AA:69:VAL:H	1.86	0.40
66:S6:174:PRO:HB3	80:18:65:C:C6	2.57	0.40
74:S8:107:THR:OG1	74:S8:108:PRO:HD3	2.20	0.40
80:18:162:C:H5''	80:18:163:U:OP2	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:18:475:C:H1'	80:18:507:G:O2'	2.21	0.40
80:18:918:U:H2'	80:18:919:A:O4'	2.21	0.40
80:18:1689:C:H2'	80:18:1690:U:C6	2.57	0.40
81:v:301:PHE:CE1	81:v:340:MET:HE3	2.57	0.40
85:28:20:U:H3'	85:28:21:G:H8	1.86	0.40
85:28:909:G:C2	85:28:910:G:C8	3.09	0.40
85:28:1291:G:H4'	85:28:1292:C:OP1	2.22	0.40
85:28:2497:C:H2'	85:28:2498:C:H6	1.85	0.40
85:28:4483:C:C2	85:28:4484:A:C8	3.09	0.40
85:28:4647:G:C2	85:28:4648:A:C8	3.10	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	IF	338/442 (76%)	336 (99%)	2 (1%)	0	100	100
2	BB	215/217 (99%)	207 (96%)	8 (4%)	0	100	100
3	S2	219/221 (99%)	217 (99%)	2 (1%)	0	100	100
4	PP	81/83 (98%)	80 (99%)	1 (1%)	0	100	100
5	DD	139/151 (92%)	133 (96%)	6 (4%)	0	100	100
8	L8	246/248 (99%)	237 (96%)	9 (4%)	0	100	100
9	L3	392/394 (100%)	380 (97%)	12 (3%)	0	100	100
10	L4	360/362 (99%)	355 (99%)	5 (1%)	0	100	100
11	L5	291/293 (99%)	285 (98%)	6 (2%)	0	100	100
12	L6	208/291 (72%)	197 (95%)	11 (5%)	0	100	100
13	L7	223/225 (99%)	214 (96%)	8 (4%)	1 (0%)	30	59
14	aa	229/240 (95%)	224 (98%)	5 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	10	201/213 (94%)	200 (100%)	1 (0%)	0	100	100
16	13	208/210 (99%)	203 (98%)	5 (2%)	0	100	100
17	14	136/138 (99%)	134 (98%)	2 (2%)	0	100	100
18	15	201/203 (99%)	192 (96%)	9 (4%)	0	100	100
19	bb	197/199 (99%)	196 (100%)	1 (0%)	0	100	100
20	17	151/153 (99%)	151 (100%)	0	0	100	100
21	19	178/180 (99%)	174 (98%)	4 (2%)	0	100	100
22	20	174/176 (99%)	172 (99%)	2 (1%)	0	100	100
23	21	157/159 (99%)	155 (99%)	2 (1%)	0	100	100
24	22	97/99 (98%)	94 (97%)	3 (3%)	0	100	100
25	cc	116/118 (98%)	115 (99%)	1 (1%)	0	100	100
26	26	132/134 (98%)	132 (100%)	0	0	100	100
27	27	133/135 (98%)	130 (98%)	3 (2%)	0	100	100
28	dd	145/147 (99%)	137 (94%)	8 (6%)	0	100	100
29	29	100/245 (41%)	98 (98%)	2 (2%)	0	100	100
30	30	96/98 (98%)	94 (98%)	2 (2%)	0	100	100
31	31	105/107 (98%)	103 (98%)	2 (2%)	0	100	100
32	32	126/128 (98%)	124 (98%)	2 (2%)	0	100	100
33	ee	107/109 (98%)	104 (97%)	3 (3%)	0	100	100
34	34	112/114 (98%)	112 (100%)	0	0	100	100
35	35	120/122 (98%)	118 (98%)	2 (2%)	0	100	100
36	36	100/102 (98%)	98 (98%)	2 (2%)	0	100	100
37	37	84/86 (98%)	84 (100%)	0	0	100	100
38	38	67/69 (97%)	65 (97%)	2 (3%)	0	100	100
39	39	48/50 (96%)	47 (98%)	1 (2%)	0	100	100
40	40	50/52 (96%)	50 (100%)	0	0	100	100
41	41	23/25 (92%)	23 (100%)	0	0	100	100
42	42	100/104 (96%)	99 (99%)	1 (1%)	0	100	100
43	ff	89/91 (98%)	87 (98%)	2 (2%)	0	100	100
44	gg	122/124 (98%)	119 (98%)	3 (2%)	0	100	100
45	AS	211/213 (99%)	207 (98%)	4 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
46	FF	147/149 (99%)	144 (98%)	3 (2%)	0	100	100
47	VV	81/83 (98%)	80 (99%)	1 (1%)	0	100	100
48	s	194/196 (99%)	188 (97%)	6 (3%)	0	100	100
49	t	151/153 (99%)	143 (95%)	8 (5%)	0	100	100
50	F	356/358 (99%)	348 (98%)	8 (2%)	0	100	100
51	Q	185/188 (98%)	180 (97%)	5 (3%)	0	100	100
52	ZZ	66/68 (97%)	65 (98%)	1 (2%)	0	100	100
53	EE	115/132 (87%)	109 (95%)	6 (5%)	0	100	100
54	TT	73/75 (97%)	71 (97%)	2 (3%)	0	100	100
55	S5	181/191 (95%)	169 (93%)	12 (7%)	0	100	100
56	WW	60/62 (97%)	60 (100%)	0	0	100	100
57	II	140/142 (99%)	137 (98%)	3 (2%)	0	100	100
58	CC	94/96 (98%)	86 (92%)	7 (7%)	1 (1%)	11	36
59	AA	311/313 (99%)	299 (96%)	12 (4%)	0	100	100
60	OO	98/100 (98%)	97 (99%)	1 (1%)	0	100	100
61	MM	139/141 (99%)	135 (97%)	4 (3%)	0	100	100
62	LL	142/144 (99%)	135 (95%)	7 (5%)	0	100	100
63	XX	53/55 (96%)	52 (98%)	1 (2%)	0	100	100
64	RR	139/141 (99%)	134 (96%)	4 (3%)	1 (1%)	18	48
65	SS	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
66	S6	235/237 (99%)	233 (99%)	2 (1%)	0	100	100
67	S4	260/262 (99%)	256 (98%)	4 (2%)	0	100	100
68	S9	183/185 (99%)	179 (98%)	4 (2%)	0	100	100
69	S7	181/189 (96%)	178 (98%)	3 (2%)	0	100	100
70	YY	53/55 (96%)	53 (100%)	0	0	100	100
71	S3	212/214 (99%)	209 (99%)	3 (1%)	0	100	100
72	RS	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
73	WX	127/129 (98%)	123 (97%)	4 (3%)	0	100	100
74	S8	204/206 (99%)	198 (97%)	6 (3%)	0	100	100
75	W	102/121 (84%)	101 (99%)	1 (1%)	0	100	100
76	GG	133/135 (98%)	131 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
77	UU	99/101 (98%)	98 (99%)	1 (1%)	0	100	100
78	11	168/170 (99%)	164 (98%)	4 (2%)	0	100	100
79	L9	188/190 (99%)	180 (96%)	8 (4%)	0	100	100
81	v	824/857 (96%)	813 (99%)	11 (1%)	0	100	100
82	LA	45/1096 (4%)	45 (100%)	0	0	100	100
83	A	119/121 (98%)	115 (97%)	4 (3%)	0	100	100
86	23	137/139 (99%)	136 (99%)	1 (1%)	0	100	100
All	All	13074/14720 (89%)	12774 (98%)	297 (2%)	3 (0%)	100	100

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
58	CC	65	ARG
64	RR	62	PRO
13	L7	196	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	IF	286/357 (80%)	273 (96%)	13 (4%)	24	58
2	BB	180/181 (99%)	167 (93%)	13 (7%)	13	39
3	S2	187/187 (100%)	180 (96%)	7 (4%)	30	64
4	PP	67/67 (100%)	63 (94%)	4 (6%)	17	47
5	DD	130/136 (96%)	124 (95%)	6 (5%)	24	57
8	L8	190/190 (100%)	182 (96%)	8 (4%)	26	60
9	L3	342/342 (100%)	329 (96%)	13 (4%)	29	64
10	L4	302/302 (100%)	292 (97%)	10 (3%)	33	67
11	L5	247/247 (100%)	241 (98%)	6 (2%)	43	75
12	L6	190/251 (76%)	183 (96%)	7 (4%)	30	64

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
13	L7	196/196 (100%)	189 (96%)	7 (4%)	31	65
14	aa	200/205 (98%)	191 (96%)	9 (4%)	24	58
15	10	175/180 (97%)	171 (98%)	4 (2%)	44	76
16	13	175/175 (100%)	167 (95%)	8 (5%)	24	57
17	14	117/117 (100%)	111 (95%)	6 (5%)	21	53
18	15	171/171 (100%)	164 (96%)	7 (4%)	27	61
19	bb	171/171 (100%)	163 (95%)	8 (5%)	23	56
20	17	134/134 (100%)	132 (98%)	2 (2%)	57	84
21	19	159/159 (100%)	151 (95%)	8 (5%)	22	53
22	20	157/157 (100%)	150 (96%)	7 (4%)	24	58
23	21	139/139 (100%)	136 (98%)	3 (2%)	45	77
24	22	89/89 (100%)	86 (97%)	3 (3%)	32	66
25	cc	106/106 (100%)	105 (99%)	1 (1%)	70	90
26	26	124/124 (100%)	117 (94%)	7 (6%)	19	50
27	27	117/117 (100%)	114 (97%)	3 (3%)	40	73
28	dd	119/119 (100%)	117 (98%)	2 (2%)	53	82
29	29	84/184 (46%)	81 (96%)	3 (4%)	31	65
30	30	84/84 (100%)	83 (99%)	1 (1%)	63	86
31	31	98/98 (100%)	93 (95%)	5 (5%)	21	53
32	32	114/114 (100%)	108 (95%)	6 (5%)	20	52
33	ee	88/88 (100%)	83 (94%)	5 (6%)	18	49
34	34	98/98 (100%)	97 (99%)	1 (1%)	68	89
35	35	109/109 (100%)	106 (97%)	3 (3%)	38	72
36	36	86/86 (100%)	82 (95%)	4 (5%)	23	56
37	37	73/73 (100%)	71 (97%)	2 (3%)	39	73
38	38	64/64 (100%)	62 (97%)	2 (3%)	35	69
39	39	47/47 (100%)	46 (98%)	1 (2%)	47	77
40	40	48/48 (100%)	48 (100%)	0	100	100
41	41	24/24 (100%)	24 (100%)	0	100	100
42	42	90/92 (98%)	88 (98%)	2 (2%)	45	77
43	ff	74/74 (100%)	70 (95%)	4 (5%)	20	51

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
44	gg	107/108 (99%)	104 (97%)	3 (3%)	38	72
45	AS	194/194 (100%)	188 (97%)	6 (3%)	35	69
46	FF	130/130 (100%)	123 (95%)	7 (5%)	20	51
47	VV	75/75 (100%)	69 (92%)	6 (8%)	11	34
48	s	164/164 (100%)	152 (93%)	12 (7%)	13	38
49	t	126/126 (100%)	115 (91%)	11 (9%)	9	30
50	F	307/307 (100%)	293 (95%)	14 (5%)	24	57
51	Q	164/165 (99%)	162 (99%)	2 (1%)	63	86
52	ZZ	61/61 (100%)	59 (97%)	2 (3%)	33	67
53	EE	99/108 (92%)	96 (97%)	3 (3%)	36	70
54	TT	66/66 (100%)	63 (96%)	3 (4%)	24	58
55	S5	158/161 (98%)	151 (96%)	7 (4%)	25	59
56	WW	55/55 (100%)	52 (94%)	3 (6%)	19	50
57	II	117/117 (100%)	111 (95%)	6 (5%)	21	53
58	CC	87/87 (100%)	84 (97%)	3 (3%)	32	66
59	AA	272/272 (100%)	263 (97%)	9 (3%)	33	67
60	OO	92/92 (100%)	87 (95%)	5 (5%)	20	51
61	MM	111/111 (100%)	109 (98%)	2 (2%)	51	80
62	LL	125/125 (100%)	117 (94%)	8 (6%)	16	44
63	XX	48/48 (100%)	46 (96%)	2 (4%)	26	60
64	RR	113/113 (100%)	109 (96%)	4 (4%)	32	66
65	SS	107/107 (100%)	101 (94%)	6 (6%)	19	50
66	S6	207/207 (100%)	202 (98%)	5 (2%)	43	75
67	S4	224/224 (100%)	220 (98%)	4 (2%)	51	80
68	S9	161/161 (100%)	154 (96%)	7 (4%)	26	60
69	S7	165/169 (98%)	159 (96%)	6 (4%)	31	65
70	YY	46/46 (100%)	44 (96%)	2 (4%)	26	60
71	S3	177/177 (100%)	162 (92%)	15 (8%)	10	31
72	RS	119/119 (100%)	111 (93%)	8 (7%)	15	43
73	WX	112/112 (100%)	108 (96%)	4 (4%)	31	65
74	S8	178/178 (100%)	173 (97%)	5 (3%)	38	72

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
75	W	86/100 (86%)	82 (95%)	4 (5%)	23	56
76	GG	105/105 (100%)	100 (95%)	5 (5%)	23	55
77	UU	88/88 (100%)	85 (97%)	3 (3%)	32	66
78	11	143/143 (100%)	139 (97%)	4 (3%)	38	72
79	L9	169/169 (100%)	162 (96%)	7 (4%)	27	61
81	v	705/728 (97%)	667 (95%)	38 (5%)	20	51
82	LA	45/948 (5%)	41 (91%)	4 (9%)	9	28
83	A	107/107 (100%)	97 (91%)	10 (9%)	8	27
86	23	106/106 (100%)	103 (97%)	3 (3%)	38	72
All	All	11372/12581 (90%)	10903 (96%)	469 (4%)	28	61

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

Mol	Chain	Res	Type
1	IF	127	LEU
1	IF	129	LYS
1	IF	156	GLU
1	IF	199	GLN
1	IF	208	LEU
1	IF	210	SER
1	IF	246	LEU
1	IF	248	ILE
1	IF	294	LEU
1	IF	310	LEU
1	IF	349	ILE
1	IF	400	LEU
1	IF	434	VAL
2	BB	5	LEU
2	BB	44	ASP
2	BB	51	LEU
2	BB	84	GLN
2	BB	88	LEU
2	BB	136	GLU
2	BB	140	VAL
2	BB	145	ILE
2	BB	157	VAL
2	BB	159	ILE
2	BB	177	MET
2	BB	178	LEU

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Mol	Chain	Res	Type
2	BB	208	GLU
3	S2	86	LEU
3	S2	146	GLU
3	S2	165	VAL
3	S2	212	LYS
3	S2	215	MET
3	S2	227	ARG
3	S2	252	THR
4	PP	32	ILE
4	PP	51	LYS
4	PP	70	LEU
4	PP	72	LEU
5	DD	7	GLU
5	DD	12	LYS
5	DD	16	ILE
5	DD	42	LEU
5	DD	46	THR
5	DD	56	ILE
8	L8	42	LYS
8	L8	75	LEU
8	L8	101	VAL
8	L8	158	ILE
8	L8	162	ASN
8	L8	163	ARG
8	L8	165	VAL
8	L8	208	GLU
9	L3	56	ILE
9	L3	89	ILE
9	L3	94	GLU
9	L3	158	GLN
9	L3	173	LEU
9	L3	240	LEU
9	L3	246	ARG
9	L3	248	LEU
9	L3	258	HIS
9	L3	262	VAL
9	L3	314	ILE
9	L3	351	LEU
9	L3	362	LYS
10	L4	3	CYS
10	L4	49	ARG
10	L4	57	LEU

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Mol	Chain	Res	Type
10	L4	62	THR
10	L4	205	ARG
10	L4	227	ILE
10	L4	232	VAL
10	L4	285	LEU
10	L4	294	LYS
10	L4	313	VAL
11	L5	35	ARG
11	L5	56	THR
11	L5	69	ILE
11	L5	225	GLN
11	L5	249	GLU
11	L5	261	VAL
12	L6	51	VAL
12	L6	112	LEU
12	L6	166	VAL
12	L6	178	VAL
12	L6	197	VAL
12	L6	215	LEU
12	L6	217	ASP
13	L7	34	LYS
13	L7	41	LEU
13	L7	54	LYS
13	L7	97	ILE
13	L7	124	LEU
13	L7	151	GLU
13	L7	189	LEU
14	aa	159	THR
14	aa	166	ARG
14	aa	193	VAL
14	aa	199	LEU
14	aa	212	HIS
14	aa	220	VAL
14	aa	226	LEU
14	aa	237	LEU
14	aa	295	LEU
15	10	44	ASP
15	10	63	GLU
15	10	146	GLU
15	10	163	GLN
16	13	59	VAL
16	13	63	THR

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Mol	Chain	Res	Type
16	13	67	HIS
16	13	124	LEU
16	13	144	LEU
16	13	154	VAL
16	13	164	GLU
16	13	205	GLN
17	14	34	ASN
17	14	38	VAL
17	14	59	ASP
17	14	62	LEU
17	14	103	LYS
17	14	137	LYS
18	15	61	ILE
18	15	64	ILE
18	15	66	VAL
18	15	75	VAL
18	15	80	THR
18	15	151	ILE
18	15	198	LEU
19	bb	5	GLN
19	bb	7	LEU
19	bb	12	ARG
19	bb	27	VAL
19	bb	36	VAL
19	bb	113	ASP
19	bb	124	LEU
19	bb	144	GLU
20	17	69	ARG
20	17	103	GLU
21	19	15	LEU
21	19	46	LYS
21	19	50	ILE
21	19	74	ARG
21	19	106	LEU
21	19	145	LEU
21	19	149	LYS
21	19	155	LEU
22	20	1	MET
22	20	7	LEU
22	20	17	LEU
22	20	39	VAL
22	20	90	THR

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Mol	Chain	Res	Type
22	20	111	ARG
22	20	159	LEU
23	21	69	GLN
23	21	106	LEU
23	21	121	GLU
24	22	23	LEU
24	22	30	GLU
24	22	50	ASN
25	cc	147	LEU
26	26	40	GLN
26	26	55	VAL
26	26	58	VAL
26	26	79	VAL
26	26	104	VAL
26	26	119	LEU
26	26	120	GLU
27	27	54	THR
27	27	77	TYR
27	27	120	GLU
28	dd	86	THR
28	dd	103	VAL
29	29	9	THR
29	29	65	MET
29	29	104	LEU
30	30	105	ILE
31	31	26	THR
31	31	46	LEU
31	31	96	GLU
31	31	111	VAL
31	31	121	ASN
32	32	4	LEU
32	32	33	ARG
32	32	44	ARG
32	32	48	ARG
32	32	85	LEU
32	32	91	CYS
33	ee	18	LEU
33	ee	23	GLU
33	ee	33	VAL
33	ee	103	VAL
33	ee	105	LEU
34	34	60	ARG

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Mol	Chain	Res	Type
35	35	47	ILE
35	35	96	ASN
35	35	111	GLU
36	36	29	ARG
36	36	42	ASP
36	36	66	ASP
36	36	94	LEU
37	37	58	THR
37	37	83	THR
38	38	12	LEU
38	38	57	LYS
39	39	51	LEU
42	42	82	MET
42	42	85	ILE
43	ff	52	VAL
43	ff	54	ILE
43	ff	74	THR
43	ff	89	LEU
44	gg	90	LEU
44	gg	103	HIS
44	gg	119	ARG
45	AS	60	ASP
45	AS	78	GLU
45	AS	122	GLU
45	AS	134	LEU
45	AS	183	GLU
45	AS	212	VAL
46	FF	22	VAL
46	FF	45	LEU
46	FF	75	LEU
46	FF	102	LEU
46	FF	118	ILE
46	FF	119	GLU
46	FF	142	GLU
47	VV	7	LEU
47	VV	14	GLU
47	VV	29	ASN
47	VV	53	VAL
47	VV	63	LEU
47	VV	73	LEU
48	s	29	ILE
48	s	30	VAL

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Mol	Chain	Res	Type
48	s	68	HIS
48	s	94	ASP
48	s	95	LEU
48	s	126	GLN
48	s	144	THR
48	s	153	GLU
48	s	158	VAL
48	s	174	LEU
48	s	180	ILE
48	s	189	ILE
49	t	32	ILE
49	t	54	LYS
49	t	58	ILE
49	t	81	ILE
49	t	83	LYS
49	t	96	LYS
49	t	123	ARG
49	t	124	GLU
49	t	125	LEU
49	t	128	THR
49	t	146	ARG
50	F	21	TYR
50	F	51	LYS
50	F	82	VAL
50	F	131	GLN
50	F	177	PHE
50	F	190	LEU
50	F	195	ILE
50	F	209	GLN
50	F	226	VAL
50	F	287	LYS
50	F	319	PHE
50	F	350	GLN
50	F	353	GLU
50	F	354	LEU
51	Q	63	LEU
51	Q	158	THR
52	ZZ	107	LYS
52	ZZ	114	ILE
53	EE	26	LEU
53	EE	65	VAL
53	EE	122	ASP

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Mol	Chain	Res	Type
54	TT	58	LEU
54	TT	69	THR
54	TT	75	GLU
55	S5	25	THR
55	S5	59	LYS
55	S5	81	ARG
55	S5	98	GLU
55	S5	142	SER
55	S5	152	TRP
55	S5	154	LEU
56	WW	24	GLN
56	WW	28	THR
56	WW	57	THR
57	II	39	LEU
57	II	47	LEU
57	II	68	ILE
57	II	81	ILE
57	II	86	GLN
57	II	126	ARG
58	CC	32	HIS
58	CC	39	ASN
58	CC	93	THR
59	AA	17	TRP
59	AA	98	THR
59	AA	149	GLU
59	AA	198	VAL
59	AA	206	LEU
59	AA	246	TYR
59	AA	256	ILE
59	AA	257	LYS
59	AA	280	LYS
60	OO	39	LEU
60	OO	44	LYS
60	OO	46	LYS
60	OO	68	THR
60	OO	84	ILE
61	MM	16	ARG
61	MM	43	LYS
62	LL	36	VAL
62	LL	54	LYS
62	LL	75	ARG
62	LL	77	TYR

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Mol	Chain	Res	Type
62	LL	83	PHE
62	LL	98	VAL
62	LL	108	ARG
62	LL	141	ARG
63	XX	13	LYS
63	XX	50	ILE
64	RR	17	ARG
64	RR	52	LEU
64	RR	99	GLU
64	RR	107	ARG
65	SS	4	THR
65	SS	29	HIS
65	SS	44	LEU
65	SS	51	THR
65	SS	61	ARG
65	SS	110	ARG
66	S6	21	GLU
66	S6	24	LEU
66	S6	76	LEU
66	S6	146	ASN
66	S6	160	LYS
67	S4	3	ARG
67	S4	42	LEU
67	S4	156	VAL
67	S4	245	ARG
68	S9	3	VAL
68	S9	27	GLN
68	S9	59	GLU
68	S9	61	LEU
68	S9	101	LYS
68	S9	106	LEU
68	S9	131	ARG
69	S7	9	VAL
69	S7	18	GLU
69	S7	29	GLU
69	S7	31	GLU
69	S7	60	ILE
69	S7	121	THR
70	YY	107	ARG
70	YY	122	PHE
71	S3	1	MET
71	S3	4	GLN

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Mol	Chain	Res	Type
71	S3	44	THR
71	S3	45	ARG
71	S3	59	LEU
71	S3	97	CYS
71	S3	99	ILE
71	S3	109	LEU
71	S3	123	LEU
71	S3	124	ARG
71	S3	126	ILE
71	S3	142	LEU
71	S3	157	MET
71	S3	167	TYR
71	S3	175	VAL
72	RS	16	ILE
72	RS	18	GLU
72	RS	24	LEU
72	RS	31	ASN
72	RS	81	ARG
72	RS	88	VAL
72	RS	107	LYS
72	RS	123	THR
73	WX	57	ARG
73	WX	87	GLU
73	WX	103	VAL
73	WX	104	LEU
74	S8	6	ASP
74	S8	73	THR
74	S8	140	LYS
74	S8	144	LYS
74	S8	178	ARG
75	W	30	GLN
75	W	82	ILE
75	W	94	ARG
75	W	97	LYS
76	GG	52	THR
76	GG	76	LEU
76	GG	86	LYS
76	GG	98	ARG
76	GG	147	ARG
77	UU	19	GLN
77	UU	43	ASN
77	UU	46	GLU

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Mol	Chain	Res	Type
78	11	33	LEU
78	11	46	GLN
78	11	67	LYS
78	11	148	THR
79	L9	12	ILE
79	L9	20	LEU
79	L9	42	ASN
79	L9	57	VAL
79	L9	74	CYS
79	L9	141	LYS
79	L9	162	GLN
81	v	3	ASN
81	v	4	PHE
81	v	15	LYS
81	v	16	LYS
81	v	20	ARG
81	v	34	THR
81	v	75	ILE
81	v	77	LEU
81	v	99	LEU
81	v	140	GLU
81	v	164	LEU
81	v	211	THR
81	v	212	VAL
81	v	249	ARG
81	v	294	LEU
81	v	323	LEU
81	v	350	LEU
81	v	385	ILE
81	v	386	LYS
81	v	400	LYS
81	v	416	VAL
81	v	421	VAL
81	v	425	LEU
81	v	439	LYS
81	v	442	LEU
81	v	461	ILE
81	v	464	VAL
81	v	480	VAL
81	v	554	LEU
81	v	568	ILE
81	v	577	VAL

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Mol	Chain	Res	Type
81	v	729	LEU
81	v	746	LEU
81	v	773	GLU
81	v	775	GLN
81	v	776	VAL
81	v	783	VAL
81	v	800	LEU
82	LA	665	HIS
82	LA	683	LEU
82	LA	688	GLN
82	LA	690	LEU
83	A	25	LEU
83	A	37	TYR
83	A	54	HIS
83	A	60	LEU
83	A	76	VAL
83	A	85	ILE
83	A	86	LEU
83	A	96	VAL
83	A	102	PHE
83	A	126	VAL
86	23	16	ILE
86	23	18	LEU
86	23	35	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (138) such sidechains are listed below:

Mol	Chain	Res	Type
1	IF	253	GLN
1	IF	384	GLN
2	BB	9	GLN
2	BB	84	GLN
2	BB	111	GLN
2	BB	141	ASN
3	S2	113	GLN
3	S2	136	HIS
4	PP	47	ASN
5	DD	11	GLN
8	L8	22	HIS
8	L8	140	ASN
8	L8	216	HIS
9	L3	68	ASN

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Mol	Chain	Res	Type
9	L3	109	HIS
9	L3	158	GLN
9	L3	175	GLN
9	L3	179	HIS
10	L4	48	ASN
10	L4	50	GLN
10	L4	60	HIS
10	L4	178	ASN
10	L4	223	ASN
10	L4	338	ASN
10	L4	346	ASN
11	L5	195	HIS
15	10	95	HIS
16	13	67	HIS
16	13	104	ASN
16	13	149	GLN
19	bb	63	ASN
19	bb	143	HIS
19	bb	150	GLN
19	bb	184	ASN
20	17	21	ASN
20	17	25	HIS
20	17	56	GLN
20	17	75	GLN
20	17	116	HIS
20	17	118	GLN
20	17	120	ASN
20	17	137	ASN
21	19	66	ASN
21	19	143	HIS
22	20	66	GLN
23	21	98	HIS
23	21	131	GLN
24	22	17	GLN
24	22	38	ASN
25	cc	93	ASN
26	26	20	ASN
28	dd	17	HIS
28	dd	66	ASN
28	dd	85	GLN
28	dd	120	GLN
29	29	6	ASN

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Mol	Chain	Res	Type
29	29	12	GLN
29	29	27	GLN
29	29	61	ASN
32	32	52	GLN
32	32	126	ASN
34	34	112	GLN
35	35	68	ASN
35	35	96	ASN
37	37	13	ASN
37	37	66	HIS
38	38	31	ASN
40	40	64	ASN
43	ff	92	GLN
44	gg	103	HIS
46	FF	69	ASN
46	FF	101	HIS
47	VV	9	HIS
47	VV	29	ASN
48	s	42	GLN
49	t	142	ASN
49	t	147	HIS
50	F	29	ASN
50	F	113	HIS
50	F	188	HIS
50	F	213	HIS
50	F	350	GLN
51	Q	57	ASN
52	ZZ	139	HIS
54	TT	64	ASN
55	S5	51	HIS
55	S5	74	ASN
55	S5	118	ASN
55	S5	203	ASN
56	WW	24	GLN
57	II	24	HIS
58	CC	28	HIS
58	CC	32	HIS
59	AA	26	GLN
61	MM	42	HIS
61	MM	126	GLN
62	LL	19	ASN
62	LL	105	ASN

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Mol	Chain	Res	Type
64	RR	73	GLN
64	RR	97	ASN
65	SS	19	GLN
65	SS	22	GLN
65	SS	29	HIS
65	SS	112	ASN
66	S6	4	ASN
66	S6	13	GLN
66	S6	59	GLN
66	S6	110	ASN
66	S6	177	GLN
68	S9	75	ASN
68	S9	113	GLN
68	S9	154	GLN
69	S7	33	ASN
69	S7	193	GLN
72	RS	56	HIS
72	RS	93	GLN
73	WX	16	ASN
73	WX	64	ASN
74	S8	35	ASN
75	W	30	GLN
75	W	48	GLN
76	GG	94	HIS
78	11	71	HIS
79	L9	79	ASN
79	L9	140	GLN
81	v	30	HIS
81	v	219	HIS
81	v	357	HIS
81	v	365	GLN
81	v	468	ASN
81	v	535	GLN
81	v	544	HIS
81	v	750	GLN
81	v	803	ASN
81	v	807	GLN
81	v	853	ASN
82	LA	680	ASN
86	23	36	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
6	58	149/156 (95%)	22 (14%)	1 (0%)
7	6	119/120 (99%)	9 (7%)	0
80	18	1675/1698 (98%)	299 (17%)	14 (0%)
84	ES	34/5070 (0%)	7 (20%)	1 (2%)
85	28	3479/4808 (72%)	579 (16%)	48 (1%)
All	All	5456/11852 (46%)	916 (16%)	64 (1%)

All (916) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
6	58	2	G
6	58	34	U
6	58	35	C
6	58	59	A
6	58	62	A
6	58	63	U
6	58	86	U
6	58	103	A
6	58	105	C
6	58	109	C
6	58	110	U
6	58	111	U
6	58	112	G
6	58	113	C
6	58	114	G
6	58	122	G
6	58	123	U
6	58	124	U
6	58	125	C
6	58	126	C
6	58	127	U
6	58	151	G
7	6	7	G
7	6	25	G
7	6	33	U
7	6	53	U
7	6	54	A
7	6	64	G
7	6	100	A
7	6	110	G
7	6	120	U
80	18	2	A
80	18	3	C

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Mol	Chain	Res	Type
80	18	4	C
80	18	25	A
80	18	26	U
80	18	33	G
80	18	36	U
80	18	41	G
80	18	44	U
80	18	45	A
80	18	46	A
80	18	50	A
80	18	51	U
80	18	56	G
80	18	67	C
80	18	74	G
80	18	77	A
80	18	79	A
80	18	93	U
80	18	99	A
80	18	103	A
80	18	111	A
80	18	113	G
80	18	115	U
80	18	116	U
80	18	124	U
80	18	126	G
80	18	127	C
80	18	142	C
80	18	143	U
80	18	147	A
80	18	155	G
80	18	160	U
80	18	161	U
80	18	162	C
80	18	163	U
80	18	168	C
80	18	169	U
80	18	182	C
80	18	183	G
80	18	184	G
80	18	191	A
80	18	192	C
80	18	206	G

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Mol	Chain	Res	Type
80	18	292	A
80	18	294	U
80	18	307	G
80	18	308	G
80	18	309	G
80	18	312	G
80	18	319	C
80	18	330	G
80	18	339	A
80	18	340	C
80	18	350	C
80	18	351	G
80	18	360	A
80	18	362	C
80	18	364	A
80	18	368	U
80	18	369	C
80	18	377	G
80	18	385	G
80	18	386	C
80	18	399	C
80	18	400	C
80	18	408	A
80	18	409	C
80	18	418	A
80	18	435	A
80	18	448	A
80	18	450	C
80	18	451	G
80	18	452	G
80	18	465	A
80	18	466	G
80	18	467	G
80	18	472	C
80	18	473	A
80	18	474	G
80	18	487	U
80	18	492	C
80	18	496	C
80	18	500	A
80	18	517	C
80	18	525	A

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Mol	Chain	Res	Type
80	18	532	C
80	18	533	A
80	18	536	A
80	18	537	C
80	18	542	U
80	18	547	G
80	18	554	A
80	18	555	A
80	18	556	U
80	18	559	G
80	18	560	A
80	18	562	U
80	18	564	A
80	18	568	C
80	18	574	A
80	18	576	A
80	18	587	A
80	18	588	G
80	18	590	A
80	18	591	U
80	18	606	G
80	18	607	U
80	18	608	C
80	18	614	C
80	18	629	A
80	18	631	U
80	18	643	A
80	18	644	G
80	18	655	A
80	18	657	U
80	18	660	C
80	18	668	A
80	18	669	A
80	18	671	A
80	18	672	A
80	18	673	G
80	18	683	G
80	18	688	U
80	18	734	C
80	18	752	G
80	18	753	C
80	18	754	G

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Mol	Chain	Res	Type
80	18	799	U
80	18	811	A
80	18	821	G
80	18	822	U
80	18	830	A
80	18	847	A
80	18	848	U
80	18	852	G
80	18	853	C
80	18	870	A
80	18	871	U
80	18	872	A
80	18	873	G
80	18	878	G
80	18	879	C
80	18	887	U
80	18	890	U
80	18	893	U
80	18	894	G
80	18	898	U
80	18	901	G
80	18	913	A
80	18	914	U
80	18	920	A
80	18	922	A
80	18	933	G
80	18	943	U
80	18	955	A
80	18	956	G
80	18	971	G
80	18	978	G
80	18	990	A
80	18	992	A
80	18	999	G
80	18	1002	U
80	18	1023	A
80	18	1045	U
80	18	1060	A
80	18	1062	A
80	18	1083	A
80	18	1085	C
80	18	1100	A

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Mol	Chain	Res	Type
80	18	1113	A
80	18	1115	U
80	18	1116	C
80	18	1117	C
80	18	1118	C
80	18	1120	U
80	18	1131	G
80	18	1133	A
80	18	1138	C
80	18	1139	C
80	18	1150	A
80	18	1153	C
80	18	1154	U
80	18	1155	U
80	18	1158	G
80	18	1195	A
80	18	1207	G
80	18	1212	G
80	18	1215	C
80	18	1216	C
80	18	1224	G
80	18	1242	U
80	18	1251	A
80	18	1253	A
80	18	1256	G
80	18	1257	G
80	18	1259	A
80	18	1265	A
80	18	1269	G
80	18	1273	C
80	18	1274	G
80	18	1275	G
80	18	1281	G
80	18	1285	G
80	18	1286	G
80	18	1293	A
80	18	1298	G
80	18	1299	A
80	18	1300	U
80	18	1301	A
80	18	1302	G
80	18	1308	U

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Mol	Chain	Res	Type
80	18	1315	U
80	18	1316	C
80	18	1317	C
80	18	1341	C
80	18	1342	U
80	18	1343	U
80	18	1369	A
80	18	1371	U
80	18	1372	U
80	18	1374	C
80	18	1378	A
80	18	1395	C
80	18	1396	A
80	18	1397	U
80	18	1402	A
80	18	1404	U
80	18	1412	C
80	18	1428	G
80	18	1429	G
80	18	1442	U
80	18	1443	C
80	18	1454	A
80	18	1462	U
80	18	1463	U
80	18	1476	A
80	18	1477	U
80	18	1489	A
80	18	1490	G
80	18	1497	G
80	18	1498	A
80	18	1521	C
80	18	1522	A
80	18	1533	A
80	18	1536	G
80	18	1548	G
80	18	1552	G
80	18	1553	C
80	18	1556	A
80	18	1557	C
80	18	1570	G
80	18	1575	G
80	18	1578	U

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Mol	Chain	Res	Type
80	18	1579	A
80	18	1580	A
80	18	1587	G
80	18	1588	A
80	18	1600	G
80	18	1601	A
80	18	1603	G
80	18	1606	G
80	18	1621	U
80	18	1623	A
80	18	1637	A
80	18	1638	G
80	18	1648	G
80	18	1665	G
80	18	1679	A
80	18	1680	G
80	18	1683	C
80	18	1695	A
80	18	1698	C
80	18	1721	U
80	18	1722	G
80	18	1729	U
80	18	1753	C
80	18	1756	C
80	18	1757	G
80	18	1774	C
80	18	1779	G
80	18	1783	C
80	18	1784	G
80	18	1785	C
80	18	1793	A
80	18	1805	G
80	18	1823	A
80	18	1824	A
80	18	1825	A
80	18	1836	G
80	18	1838	U
80	18	1849	G
80	18	1851	A
80	18	1861	G
80	18	1862	G
80	18	1863	A

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Mol	Chain	Res	Type
80	18	1865	C
80	18	1867	U
80	18	1869	A
84	ES	2941	G
84	ES	2942	C
84	ES	2943	C
84	ES	2958	C
84	ES	3237	G
84	ES	3238	C
84	ES	3247	A
85	28	8	U
85	28	11	G
85	28	13	U
85	28	17	A
85	28	25	A
85	28	39	A
85	28	42	A
85	28	48	G
85	28	49	U
85	28	56	A
85	28	58	G
85	28	59	A
85	28	64	A
85	28	65	A
85	28	71	C
85	28	73	A
85	28	76	A
85	28	84	A
85	28	91	G
85	28	104	G
85	28	108	A
85	28	109	G
85	28	110	C
85	28	119	G
85	28	120	A
85	28	126	C
85	28	134	G
85	28	135	G
85	28	136	C
85	28	151	G
85	28	157	U
85	28	159	C

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Mol	Chain	Res	Type
85	28	171	U
85	28	172	C
85	28	173	C
85	28	200	U
85	28	201	C
85	28	202	C
85	28	203	U
85	28	209	U
85	28	216	C
85	28	218	A
85	28	220	C
85	28	224	U
85	28	233	U
85	28	234	G
85	28	237	G
85	28	245	C
85	28	246	G
85	28	265	C
85	28	266	C
85	28	276	C
85	28	280	G
85	28	297	U
85	28	306	A
85	28	309	C
85	28	310	G
85	28	315	G
85	28	316	U
85	28	334	A
85	28	340	C
85	28	350	C
85	28	362	A
85	28	363	A
85	28	386	A
85	28	387	G
85	28	406	C
85	28	407	A
85	28	410	A
85	28	412	G
85	28	413	G
85	28	414	C
85	28	440	U
85	28	449	C

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Mol	Chain	Res	Type
85	28	450	G
85	28	452	A
85	28	453	G
85	28	454	U
85	28	463	A
85	28	467	U
85	28	468	U
85	28	481	G
85	28	481(A)	C
85	28	482	G
85	28	483	G
85	28	485	C
85	28	486	C
85	28	492	U
85	28	493	G
85	28	497	G
85	28	498	C
85	28	499	G
85	28	505	G
85	28	506	C
85	28	510	U
85	28	666	G
85	28	667	A
85	28	669	C
85	28	685	C
85	28	686	A
85	28	687	U
85	28	688	U
85	28	691	C
85	28	696	C
85	28	697	G
85	28	704	C
85	28	705	G
85	28	708	G
85	28	719	C
85	28	730	G
85	28	731	G
85	28	738	C
85	28	738(A)	C
85	28	739	G
85	28	747	A
85	28	749	G

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Mol	Chain	Res	Type
85	28	758	G
85	28	914	U
85	28	915	A
85	28	916	C
85	28	917	A
85	28	918	G
85	28	923	C
85	28	925	C
85	28	926	G
85	28	929	A
85	28	931	C
85	28	932	A
85	28	933	G
85	28	934	C
85	28	935	A
85	28	935(A)	G
85	28	936	C
85	28	938	C
85	28	939	G
85	28	941	C
85	28	943	A
85	28	944	A
85	28	945	U
85	28	946	C
85	28	956	A
85	28	959	G
85	28	960	A
85	28	961	G
85	28	964	A
85	28	965	G
85	28	966	A
85	28	967	C
85	28	968	C
85	28	969	C
85	28	970	G
85	28	980	C
85	28	983	U
85	28	1070	G
85	28	1072	C
85	28	1073	G
85	28	1079	C
85	28	1081	C

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Mol	Chain	Res	Type
85	28	1083	U
85	28	1179	U
85	28	1195	G
85	28	1211	G
85	28	1212	G
85	28	1214	C
85	28	1215	C
85	28	1234	G
85	28	1235	G
85	28	1236	C
85	28	1237	C
85	28	1238	A
85	28	1239	C
85	28	1277	G
85	28	1280	C
85	28	1283	G
85	28	1284	G
85	28	1287	G
85	28	1292	C
85	28	1293	G
85	28	1296	G
85	28	1297	U
85	28	1301	C
85	28	1303	A
85	28	1304	C
85	28	1326	A
85	28	1330	A
85	28	1354	A
85	28	1358	G
85	28	1359	G
85	28	1371	A
85	28	1377	G
85	28	1379	C
85	28	1387	A
85	28	1394	G
85	28	1397	A
85	28	1398	A
85	28	1419	G
85	28	1420	A
85	28	1433	A
85	28	1435	G
85	28	1445	U

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Mol	Chain	Res	Type
85	28	1446	C
85	28	1456	C
85	28	1457	G
85	28	1482	G
85	28	1483	C
85	28	1484	G
85	28	1497	A
85	28	1498	G
85	28	1502	G
85	28	1504	G
85	28	1523	A
85	28	1534	A
85	28	1547	A
85	28	1566	C
85	28	1574	G
85	28	1578	U
85	28	1591	U
85	28	1596	U
85	28	1612	G
85	28	1613	A
85	28	1624	G
85	28	1625	G
85	28	1631	A
85	28	1633	G
85	28	1634	A
85	28	1638	A
85	28	1641	G
85	28	1654	G
85	28	1661	C
85	28	1676	C
85	28	1677	U
85	28	1726	U
85	28	1731	C
85	28	1742	A
85	28	1752	G
85	28	1755	C
85	28	1756	U
85	28	1757	U
85	28	1760	G
85	28	1761	G
85	28	1764	G
85	28	1765	A

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Mol	Chain	Res	Type
85	28	1769	G
85	28	1772	C
85	28	1773	U
85	28	1776	A
85	28	1781	U
85	28	1787	A
85	28	1804	A
85	28	1805	A
85	28	1807	C
85	28	1821	G
85	28	1822	U
85	28	1828	C
85	28	1832	C
85	28	1836	G
85	28	1837	A
85	28	1842	G
85	28	1855	G
85	28	1869	G
85	28	1883	G
85	28	1897	A
85	28	1918	U
85	28	1920	C
85	28	1921	C
85	28	1922	G
85	28	1931	C
85	28	1940	G
85	28	1948	G
85	28	1951	G
85	28	1955	G
85	28	1957	U
85	28	1958	A
85	28	1960	A
85	28	1961	G
85	28	1962	A
85	28	1976	G
85	28	1979	A
85	28	1980	U
85	28	1984	A
85	28	1985	G
85	28	1987	C
85	28	1988	G
85	28	1991	A

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Mol	Chain	Res	Type
85	28	1992	U
85	28	1993	C
85	28	1997	U
85	28	2001	G
85	28	2002	A
85	28	2003	G
85	28	2004	U
85	28	2010	A
85	28	2011	C
85	28	2025	A
85	28	2026	A
85	28	2046	G
85	28	2047	A
85	28	2048	U
85	28	2055	G
85	28	2056	G
85	28	2069	A
85	28	2084	U
85	28	2090	U
85	28	2092	G
85	28	2093	G
85	28	2094	C
85	28	2097	A
85	28	2098	G
85	28	2100	G
85	28	2102	G
85	28	2104	A
85	28	2107	A
85	28	2108	G
85	28	2109	A
85	28	2267	U
85	28	2268	A
85	28	2275	G
85	28	2279	A
85	28	2289	C
85	28	2300	A
85	28	2301	G
85	28	2306	G
85	28	2313	A
85	28	2314	G
85	28	2333	G
85	28	2348	G

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Mol	Chain	Res	Type
85	28	2351	C
85	28	2360	A
85	28	2395	A
85	28	2422	C
85	28	2425	U
85	28	2433	G
85	28	2441	C
85	28	2470	C
85	28	2471	G
85	28	2475	G
85	28	2488	C
85	28	2489	C
85	28	2490	U
85	28	2491	C
85	28	2503	G
85	28	2504	C
85	28	2505	C
85	28	2506	G
85	28	2507	A
85	28	2513	A
85	28	2529	A
85	28	2537	A
85	28	2544	G
85	28	2545	U
85	28	2546	G
85	28	2547	G
85	28	2553	A
85	28	2554	U
85	28	2566	G
85	28	2575	U
85	28	2583	C
85	28	2587	A
85	28	2627	C
85	28	2638	G
85	28	2653	C
85	28	2669	C
85	28	2686	G
85	28	2687	U
85	28	2694	G
85	28	2695	A
85	28	2696	A
85	28	2707	U

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Mol	Chain	Res	Type
85	28	2708	U
85	28	2709	C
85	28	2711	G
85	28	2712	G
85	28	2714	G
85	28	2716	C
85	28	2725	A
85	28	2726	G
85	28	2735	G
85	28	2740	U
85	28	2743	A
85	28	2760	G
85	28	2763	U
85	28	2764	A
85	28	2769	U
85	28	2787	A
85	28	2788	U
85	28	2790	U
85	28	2826	U
85	28	2842	G
85	28	2855	G
85	28	2869	U
85	28	3616	U
85	28	3625	G
85	28	3626	G
85	28	3635	A
85	28	3644	U
85	28	3646	A
85	28	3662	A
85	28	3664	G
85	28	3711	A
85	28	3712	A
85	28	3713	U
85	28	3714	G
85	28	3743	G
85	28	3748	A
85	28	3753	G
85	28	3760	A
85	28	3761	C
85	28	3773	U
85	28	3776	G
85	28	3777	G

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Mol	Chain	Res	Type
85	28	3784	A
85	28	3786	U
85	28	3810	C
85	28	3811	G
85	28	3814	U
85	28	3817	A
85	28	3819	G
85	28	3838	U
85	28	3839	G
85	28	3840	U
85	28	3877	A
85	28	3878	C
85	28	3879	G
85	28	3897	G
85	28	3901	A
85	28	3905	A
85	28	3906	A
85	28	3907	G
85	28	3908	A
85	28	3915	U
85	28	3923	A
85	28	3938	G
85	28	4073	A
85	28	4076	G
85	28	4086	G
85	28	4094	G
85	28	4116	C
85	28	4119	C
85	28	4120	U
85	28	4121	G
85	28	4122	G
85	28	4127	A
85	28	4158	C
85	28	4162	C
85	28	4163	U
85	28	4170	A
85	28	4183	G
85	28	4184	G
85	28	4191	G
85	28	4203	A
85	28	4229	U
85	28	4233	A

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Mol	Chain	Res	Type
85	28	4251	A
85	28	4253	A
85	28	4254	G
85	28	4266	G
85	28	4268	A
85	28	4273	A
85	28	4281	A
85	28	4291	G
85	28	4297	G
85	28	4305	G
85	28	4306	U
85	28	4314	C
85	28	4317	A
85	28	4330	G
85	28	4332	C
85	28	4348	A
85	28	4349	C
85	28	4354	U
85	28	4355	G
85	28	4377	G
85	28	4378	A
85	28	4380	A
85	28	4387	C
85	28	4394	A
85	28	4395	U
85	28	4419	U
85	28	4422	A
85	28	4426	C
85	28	4444	C
85	28	4448	G
85	28	4449	A
85	28	4453	C
85	28	4464	A
85	28	4466	C
85	28	4475	G
85	28	4476	C
85	28	4500	U
85	28	4512	U
85	28	4513	A
85	28	4519	C
85	28	4524	G
85	28	4548	A

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Mol	Chain	Res	Type
85	28	4549	G
85	28	4554	G
85	28	4560	C
85	28	4567	G
85	28	4570	G
85	28	4573	G
85	28	4574	U
85	28	4575	G
85	28	4586	G
85	28	4590	A
85	28	4627	U
85	28	4636	U
85	28	4656	A
85	28	4670	C
85	28	4671	C
85	28	4672	A
85	28	4677	U
85	28	4700	A
85	28	4709	U
85	28	4719	G
85	28	4720	C
85	28	4729	A
85	28	4730	C
85	28	4731	G
85	28	4732	G
85	28	4733	C
85	28	4734	A
85	28	4751	G
85	28	4754	G
85	28	4757	C
85	28	4759	C
85	28	4761	G
85	28	4765	G
85	28	4771	C
85	28	4870	G
85	28	4872	G
85	28	4875	G
85	28	4877	G
85	28	4882	U
85	28	4883	C
85	28	4885	U
85	28	4895	C

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Mol	Chain	Res	Type
85	28	4902	C
85	28	4904	G
85	28	4906	C
85	28	4910	A
85	28	4912	G
85	28	4914	G
85	28	4915	G
85	28	4918	C
85	28	4919	G
85	28	4921	C
85	28	4922	C
85	28	4923	U
85	28	4925	U
85	28	4926	C
85	28	4927	G
85	28	4928	C
85	28	4929	C
85	28	4931	G
85	28	4935	C
85	28	4937	C
85	28	4941	G
85	28	4943	A
85	28	4944	C
85	28	4948	C
85	28	4949	G
85	28	4950	U
85	28	4951	G
85	28	4960	G
85	28	4965	U
85	28	4966	A
85	28	4976	U
85	28	4979	A
85	28	4988	U
85	28	4990	C
85	28	5007	A
85	28	5017	G
85	28	5029	C
85	28	5041	G
85	28	5050	C
85	28	5053	U
85	28	5054	C
85	28	5061	A

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Mol	Chain	Res	Type
85	28	5062	G

All (64) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
6	58	124	U
80	18	110	U
80	18	291	G
80	18	434	G
80	18	465	A
80	18	642	U
80	18	752	G
80	18	870	A
80	18	1137	U
80	18	1394	G
80	18	1395	C
80	18	1520	G
80	18	1637	A
80	18	1664	A
80	18	1862	G
84	ES	3236	G
85	28	12	A
85	28	47	A
85	28	48	G
85	28	125	C
85	28	134	G
85	28	217	C
85	28	245	C
85	28	265	C
85	28	275	C
85	28	385	A
85	28	406	C
85	28	449	C
85	28	480	C
85	28	485	C
85	28	492	U
85	28	504	G
85	28	684	G
85	28	930	G
85	28	959	G
85	28	1072	C
85	28	1211	G

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Mol	Chain	Res	Type
85	28	1238	A
85	28	1291	G
85	28	1329	G
85	28	1370	G
85	28	1445	U
85	28	1455	G
85	28	1633	G
85	28	1804	A
85	28	1979	A
85	28	2046	G
85	28	2089	G
85	28	2266	C
85	28	2502	A
85	28	2546	G
85	28	2695	A
85	28	2724	G
85	28	3760	A
85	28	3876	A
85	28	3904	G
85	28	4119	C
85	28	4232	U
85	28	4448	G
85	28	4699	U
85	28	4884	G
85	28	4925	U
85	28	4936	G
85	28	4947	U

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

1 non-standard protein/DNA/RNA residue is 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	$\# Z > 2$
81	DDE	v	715	81	18,20,21	1.00	1 (5%)	17,28,30	0.95	1 (5%)

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
81	DDE	v	715	81	-	8/20/21/23	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
81	v	715	DDE	CD2-CG	2.29	1.41	1.36

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
81	v	715	DDE	CAU-CBW-CBI	-2.74	105.86	111.22

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
81	v	715	DDE	CAT-CAU-CBW-CBI
81	v	715	DDE	N-CA-CB-CG
81	v	715	DDE	CAT-CAU-CBW-NCB
81	v	715	DDE	C-CA-CB-CG
81	v	715	DDE	CA-CB-CG-CD2
81	v	715	DDE	CA-CB-CG-ND1
81	v	715	DDE	NAD-CBI-CBW-NCB
81	v	715	DDE	NAD-CBI-CBW-CAU

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 4 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	$\# Z > 2$
88	GDP	v	900	-	29,30,30	3.30	12 (41%)	45,47,47	1.89	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
88	GDP	v	900	-	-	0/16/32/32	0/3/3/3

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
88	v	900	GDP	O6-C6	9.61	1.41	1.23
88	v	900	GDP	C2'-C3'	-8.57	1.30	1.53
88	v	900	GDP	O4'-C4'	-6.19	1.31	1.45
88	v	900	GDP	C2-N2	4.68	1.45	1.34
88	v	900	GDP	PA-O3A	4.18	1.64	1.59
88	v	900	GDP	C3'-C4'	3.58	1.62	1.53
88	v	900	GDP	C6-N1	-3.42	1.32	1.38
88	v	900	GDP	C1'-N9	-3.26	1.38	1.47
88	v	900	GDP	O2'-C2'	3.15	1.50	1.43
88	v	900	GDP	C2-N1	-2.28	1.32	1.37
88	v	900	GDP	C8-N9	-2.25	1.32	1.37
88	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(°)
88	v	900	GDP	C5-C4-N3	-5.88	119.03	128.39
88	v	900	GDP	C2-N3-C4	4.78	120.53	112.30
88	v	900	GDP	N9-C4-N3	4.01	133.97	125.95
88	v	900	GDP	C6-C5-N7	2.92	135.60	130.29
88	v	900	GDP	C4-C5-N7	-2.91	106.07	110.67

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
88	v	900	GDP	C8-N7-C5	2.87	109.37	104.26
88	v	900	GDP	N9-C8-N7	-2.65	108.48	113.40
88	v	900	GDP	O4'-C1'-N9	2.62	114.30	108.36
88	v	900	GDP	O6-C6-C5	-2.50	119.94	126.53
88	v	900	GDP	C2'-C1'-N9	-2.30	106.86	113.25
88	v	900	GDP	C5-C6-N1	2.28	119.05	113.25
88	v	900	GDP	C2-N1-C6	-2.27	121.00	125.11
88	v	900	GDP	O2B-PB-O3A	2.04	111.47	104.64

There are no chirality outliers.

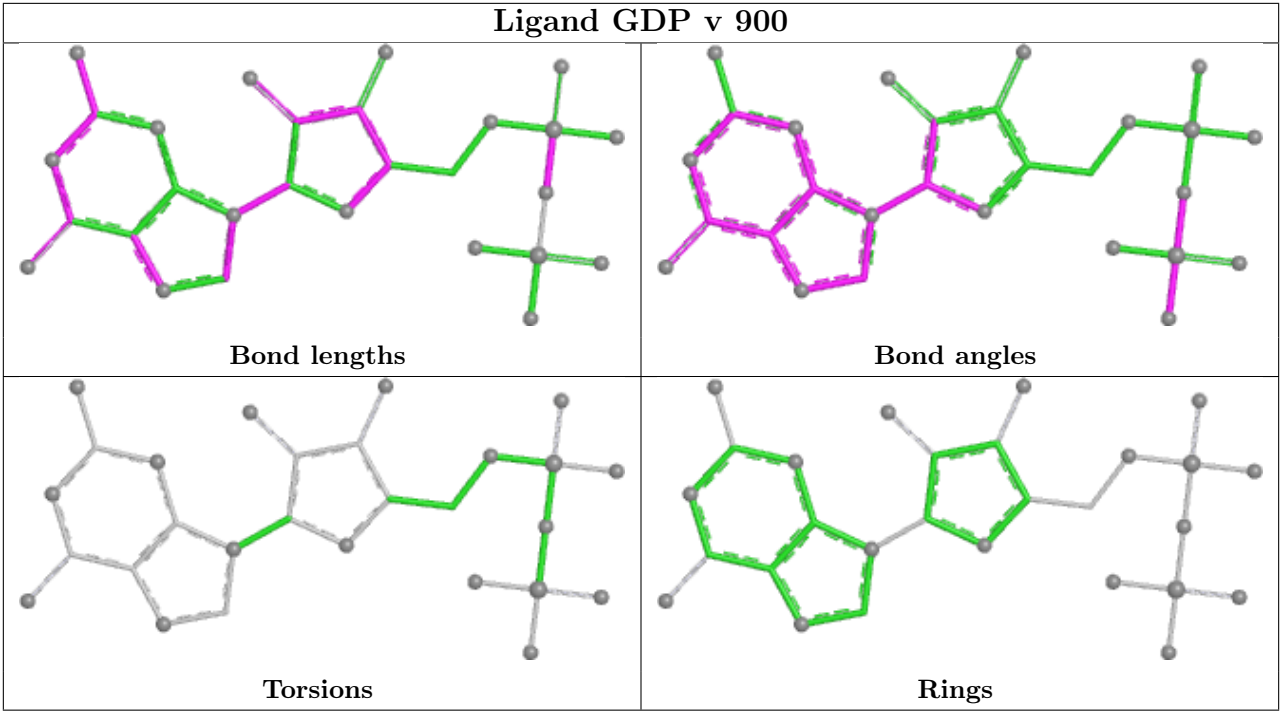
There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
88	v	900	GDP	1	0

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
80	18	8

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	18	756:C	O3'	788:G	P	20.24
1	18	697:G	O3'	729:C	P	19.25
1	18	1417:C	O3'	1423:C	P	17.98
1	18	834:C	O3'	841:G	P	16.30
1	18	745:C	O3'	749:U	P	8.18
1	18	736:C	O3'	743:U	P	7.85
1	18	225:G	O3'	287:U	P	4.33
1	18	1432:U	O3'	1438:A	P	3.60

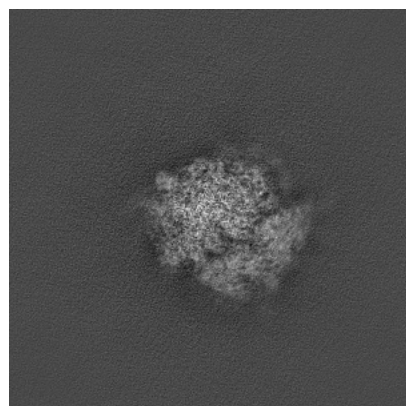
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-75740. These allow visual inspection of the internal detail of the map and identification of artifacts.

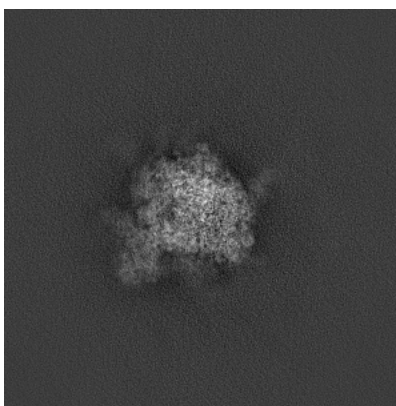
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

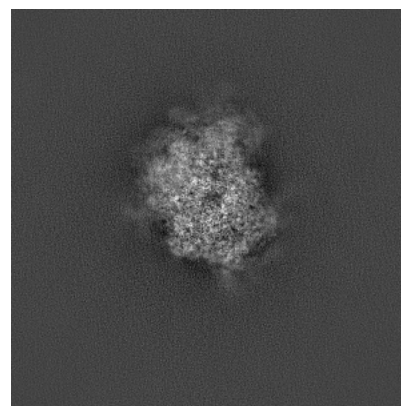
6.1.1 Primary map



X

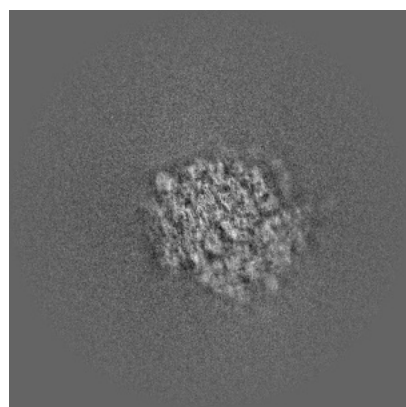


Y

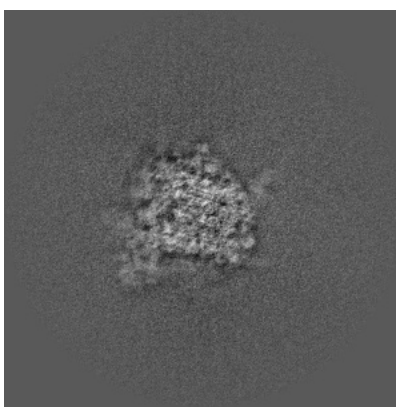


Z

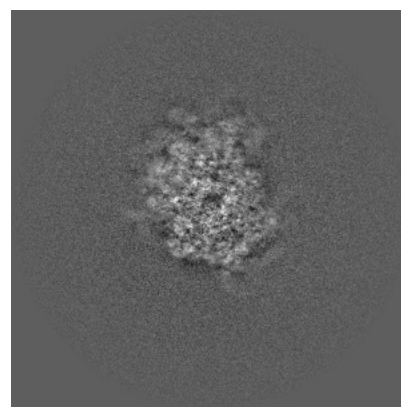
6.1.2 Raw map



X



Y

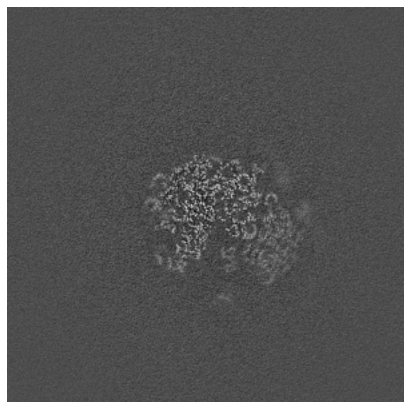


Z

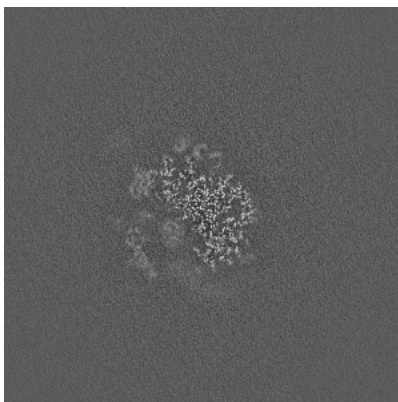
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

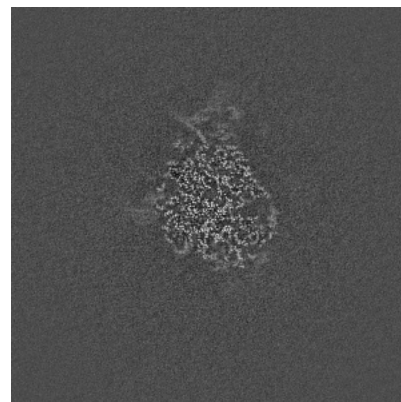
6.2.1 Primary map



X Index: 400

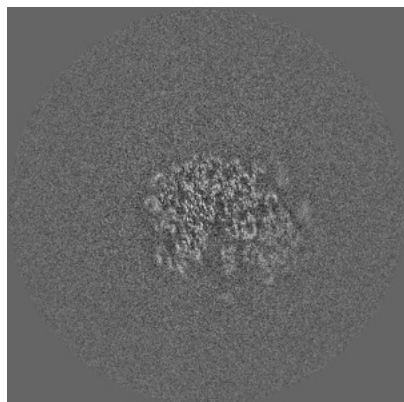


Y Index: 400

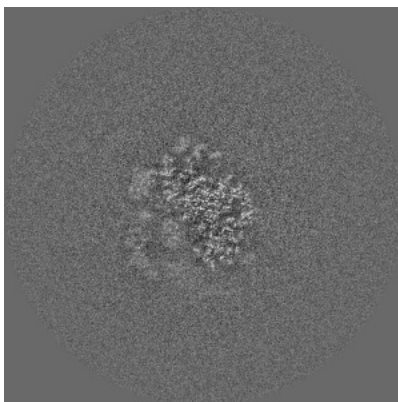


Z Index: 400

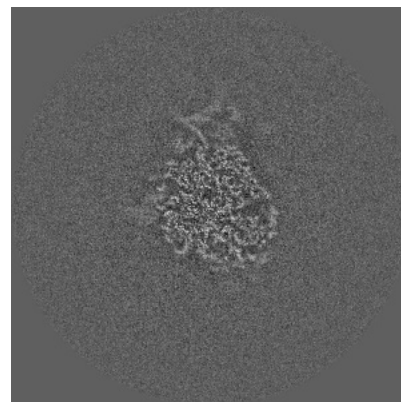
6.2.2 Raw map



X Index: 400



Y Index: 400

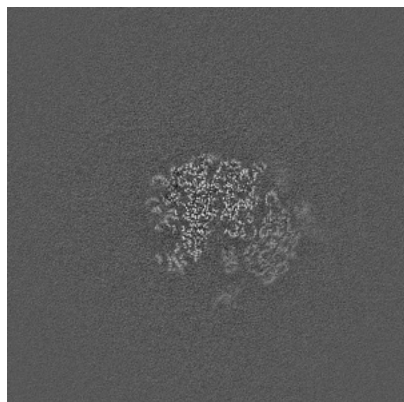


Z Index: 400

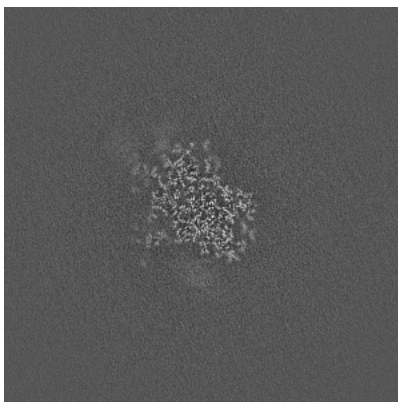
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

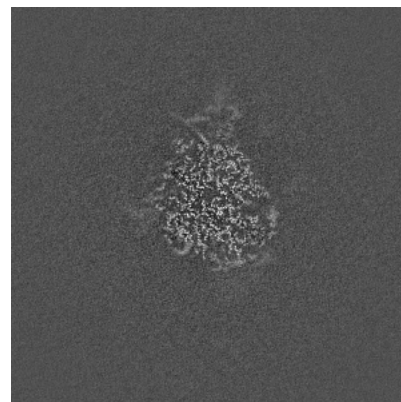
6.3.1 Primary map



X Index: 397

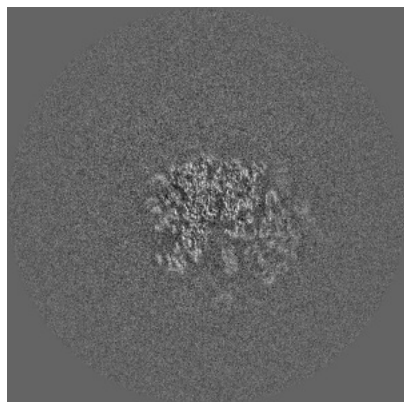


Y Index: 381

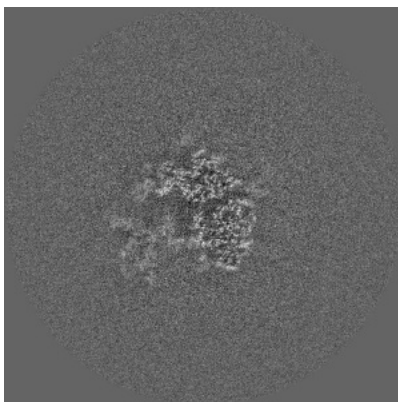


Z Index: 402

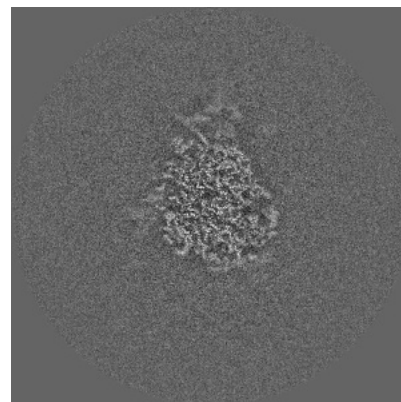
6.3.2 Raw map



X Index: 397



Y Index: 420

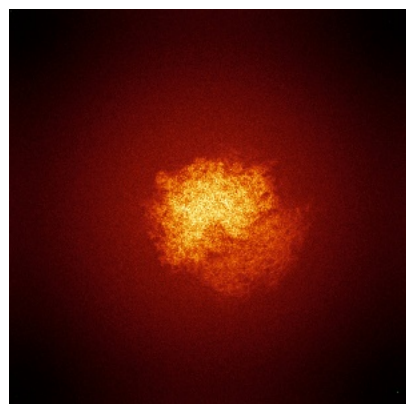


Z Index: 402

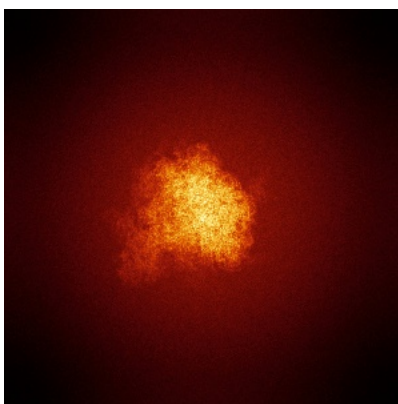
The images above show the largest variance slices of the map in three orthogonal directions.

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

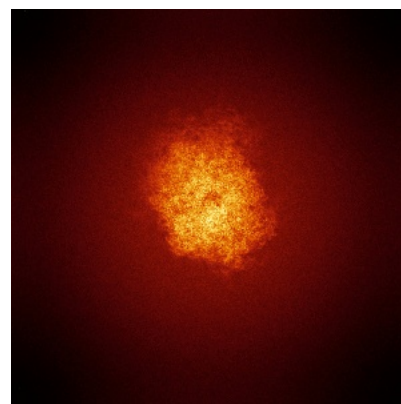
6.4.1 Primary map



X

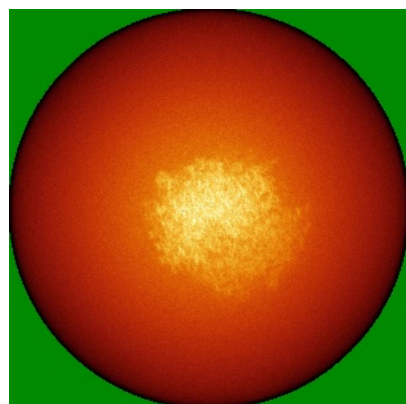


Y

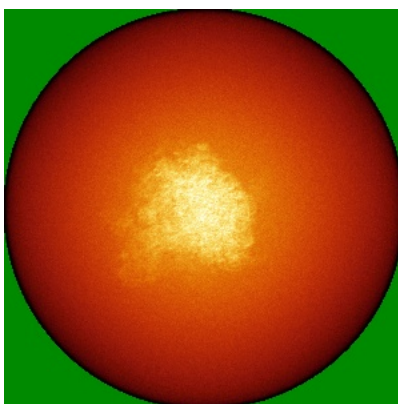


Z

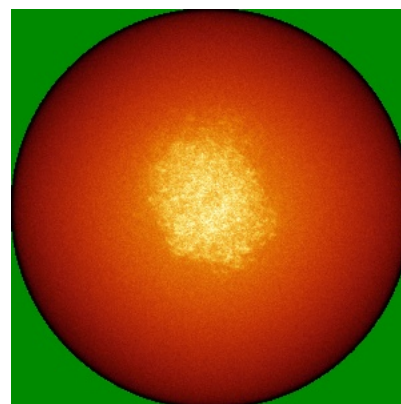
6.4.2 Raw map



X



Y

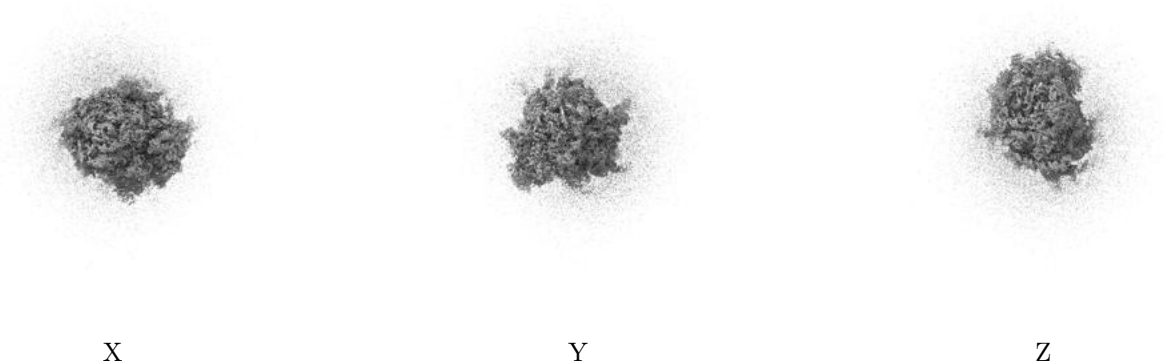


Z

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.

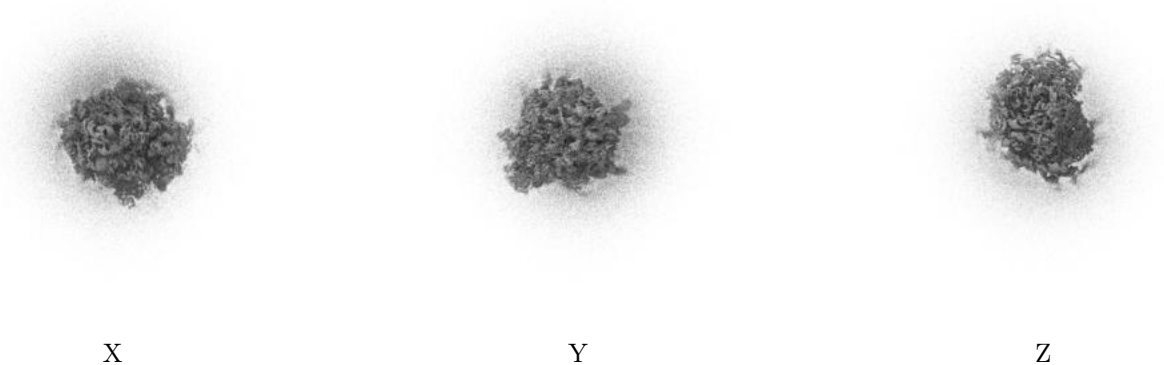
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 3.2. 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.

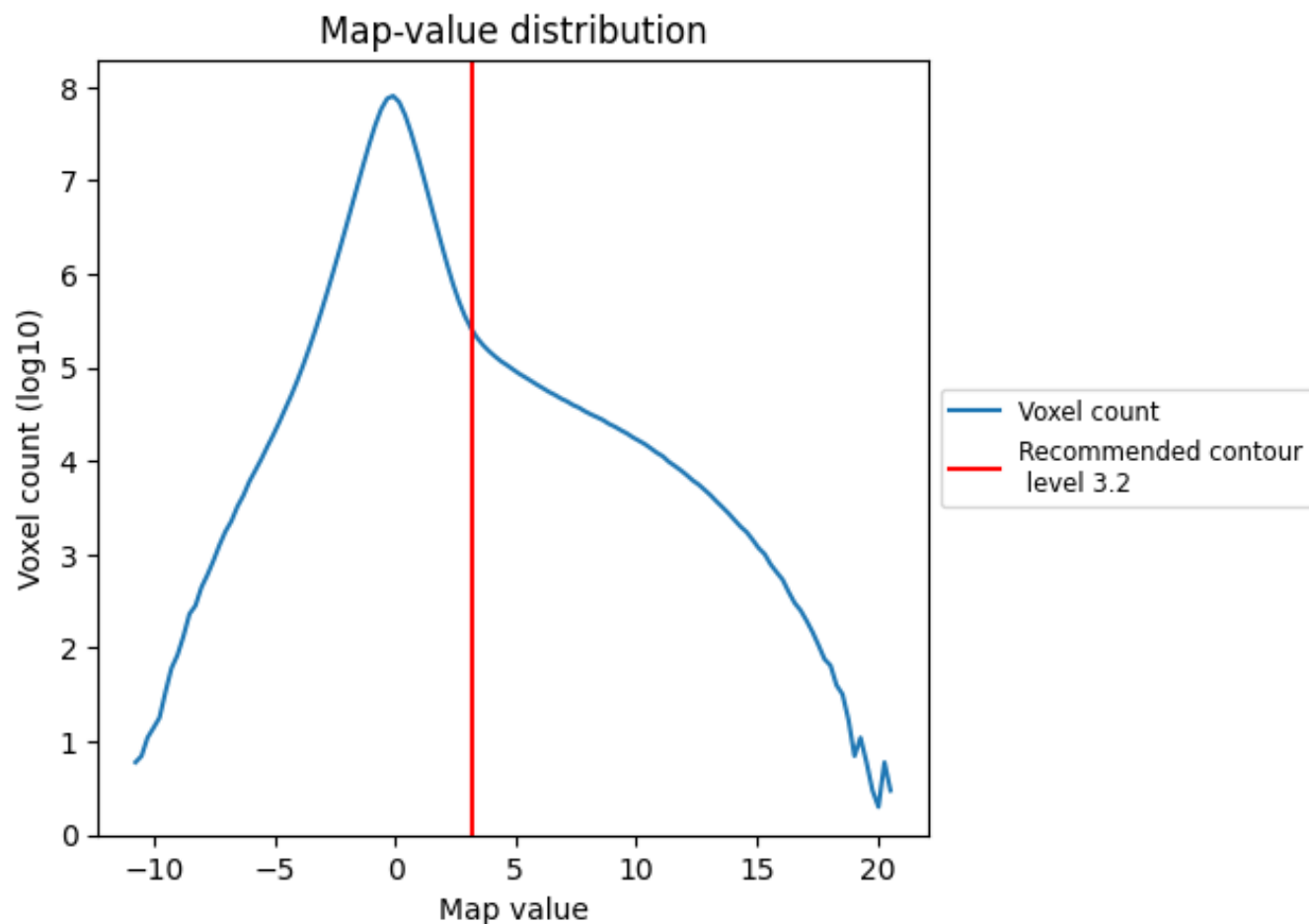
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

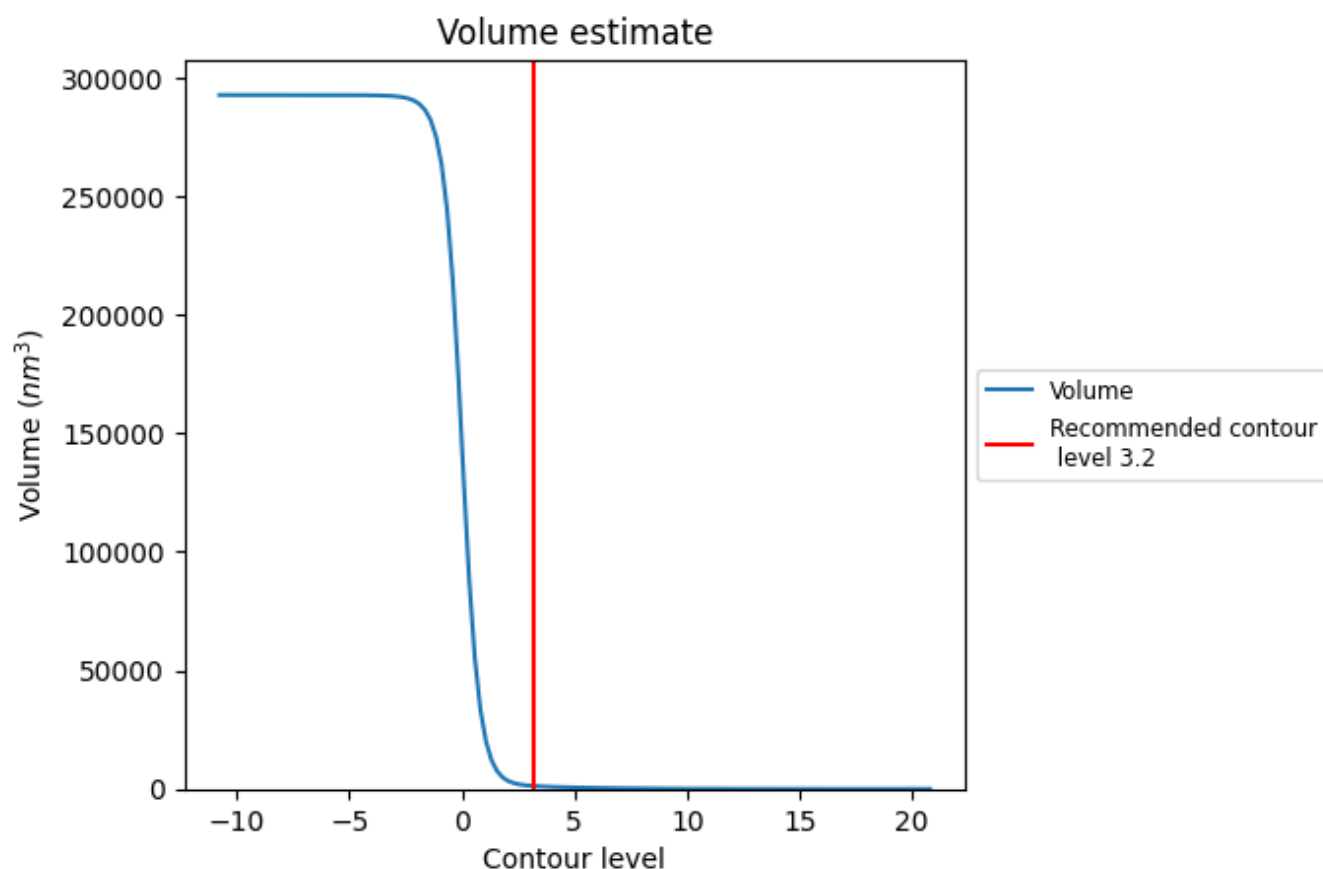
This section contains the results of statistical analysis of the map.

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.

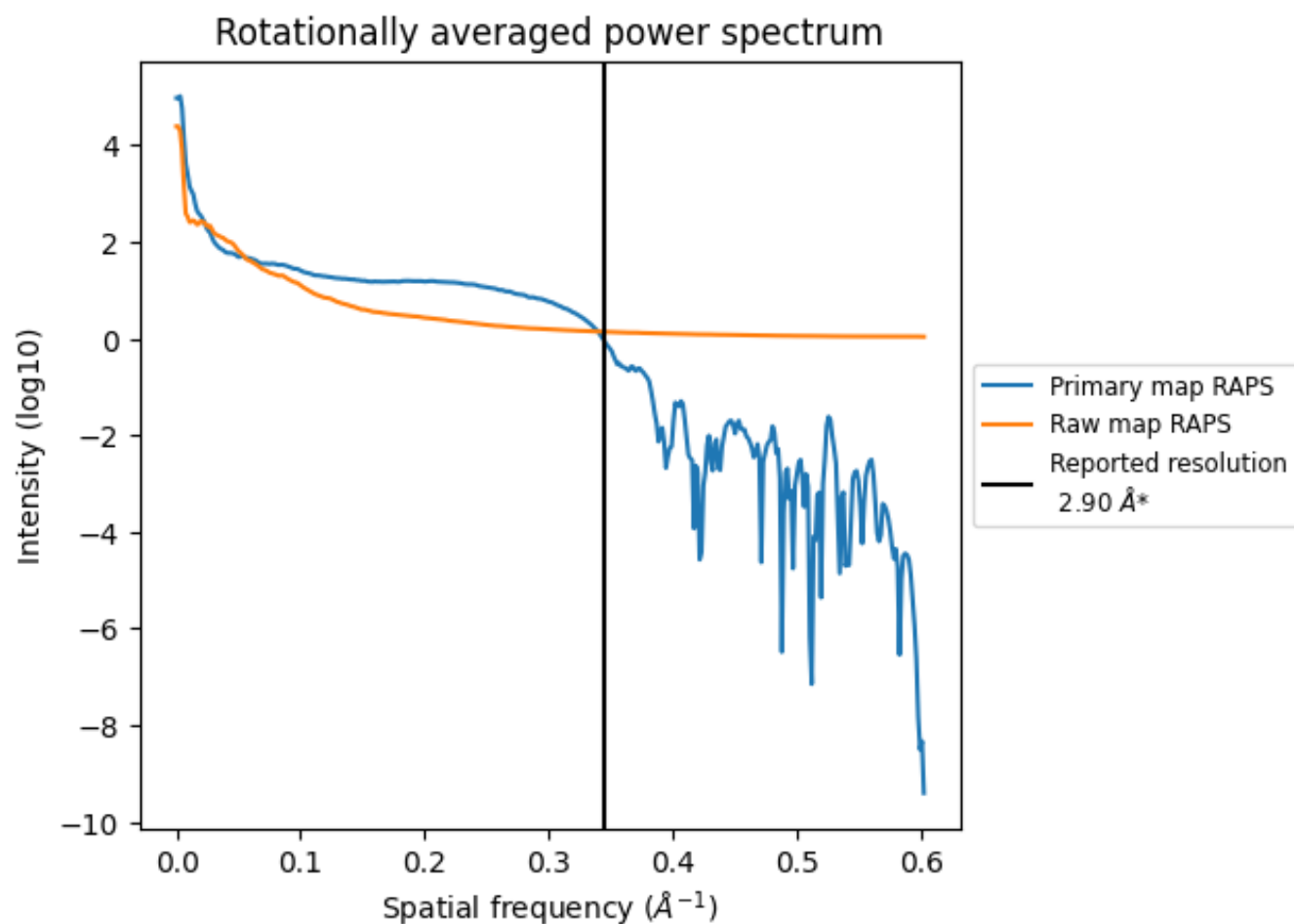
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1261 nm^3 ; this corresponds to an approximate mass of 1139 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 ⓘ

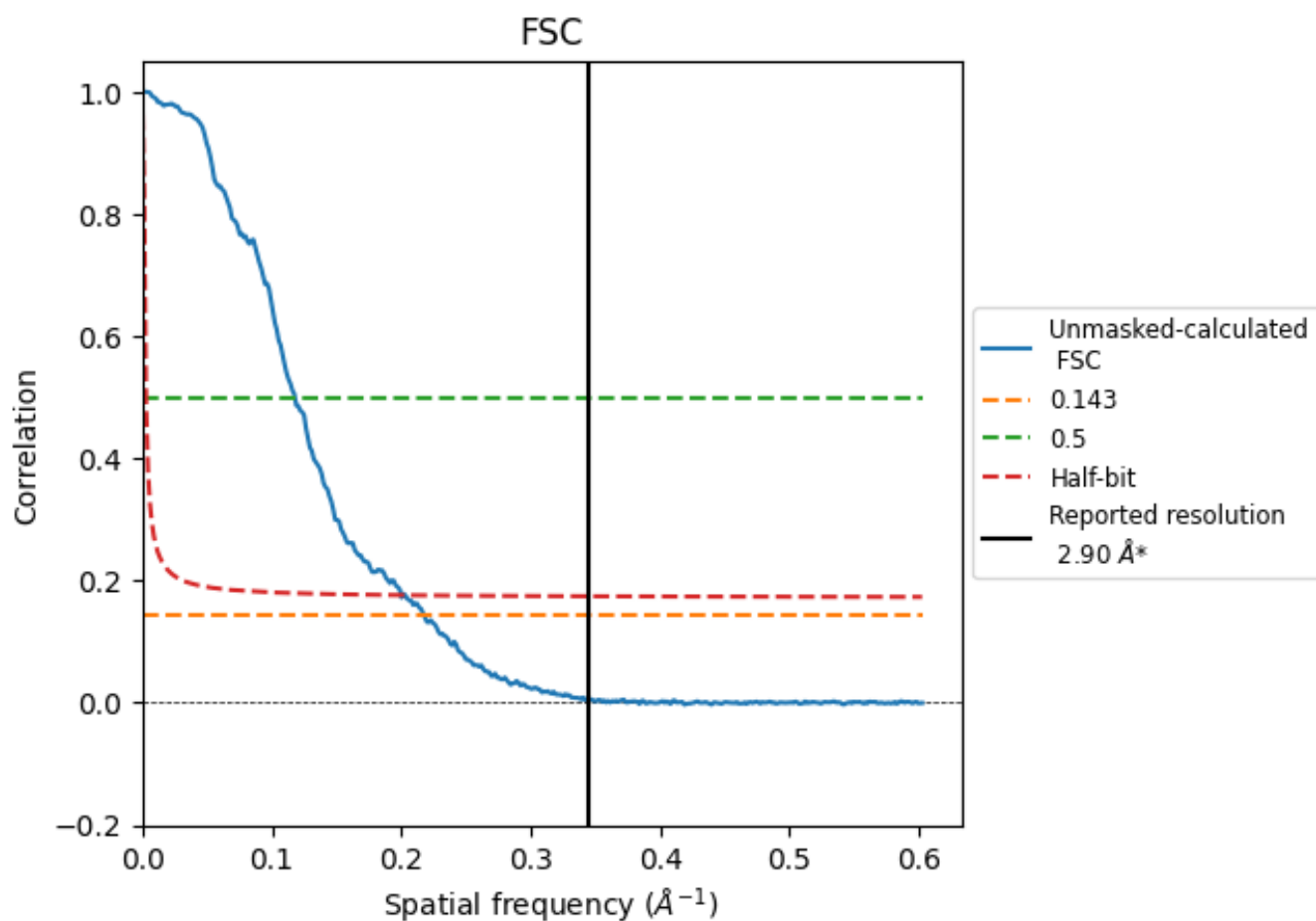


*Reported resolution corresponds to spatial frequency of 0.345 Å⁻¹

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 0.345 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

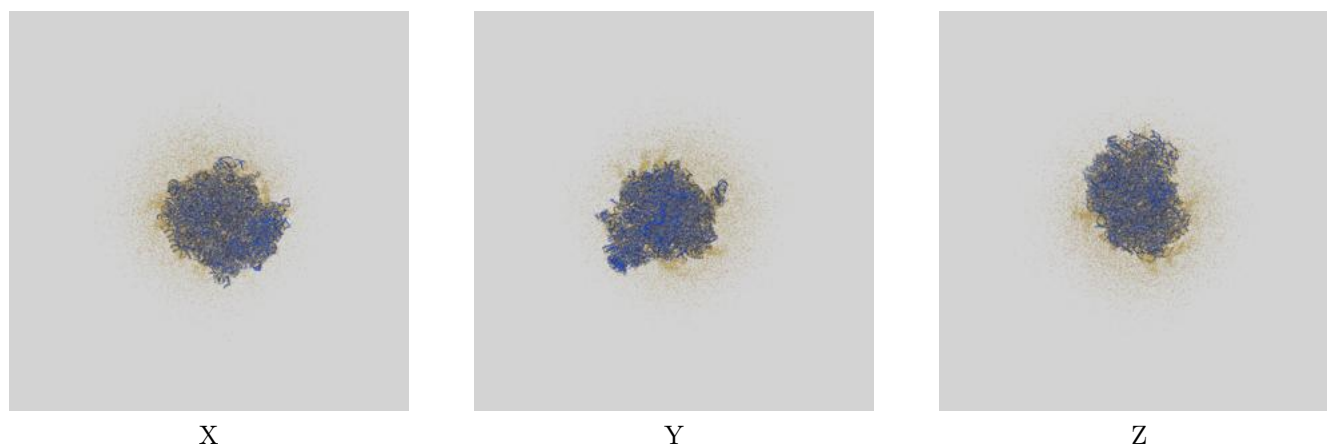
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.59	8.48	5.00

*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 4.59 differs from the reported value 2.9 by more than 10 %

9 Map-model fit [i](#)

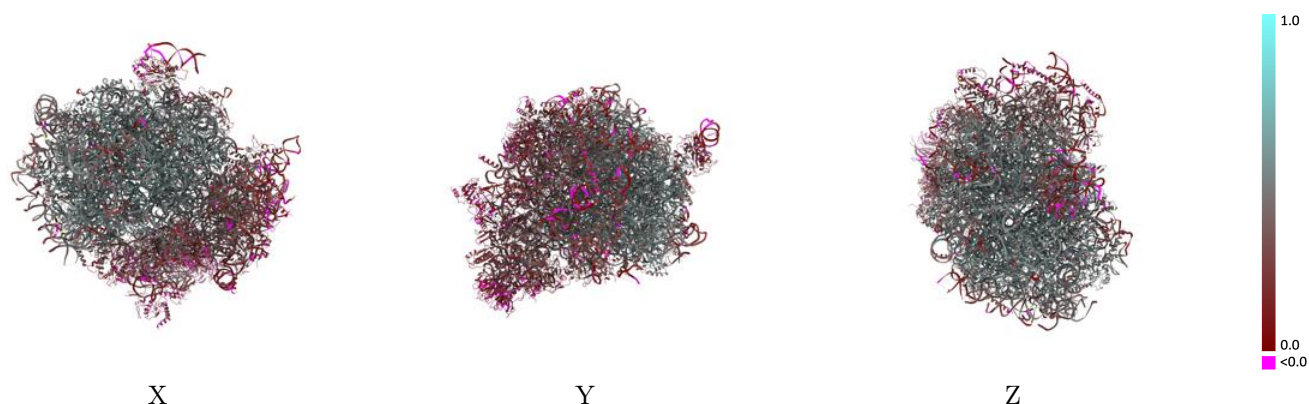
This section contains information regarding the fit between EMDB map EMD-75740 and PDB model 11JJ. Per-residue inclusion information can be found in section 3 on page 21.

9.1 Map-model overlay [i](#)



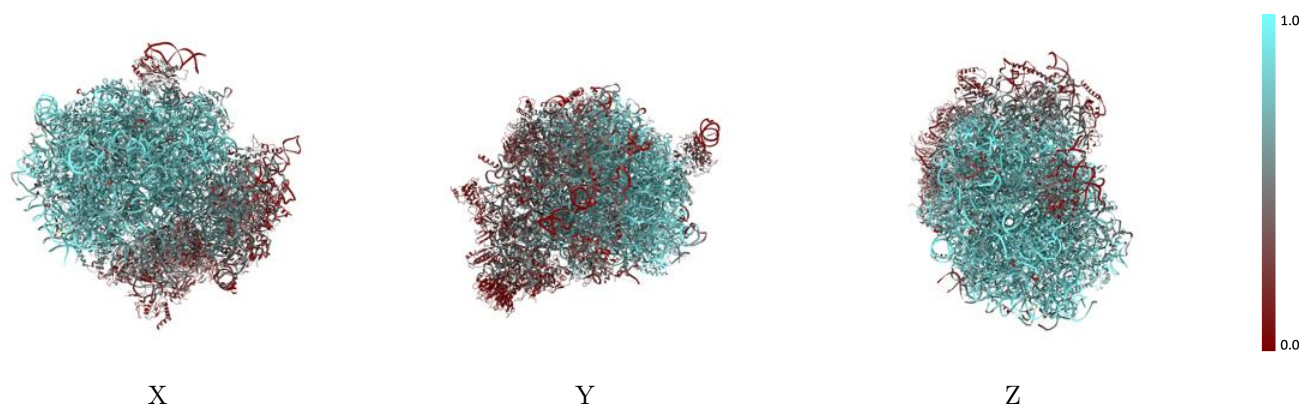
The images above show the 3D surface view of the map at the recommended contour level 3.2 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



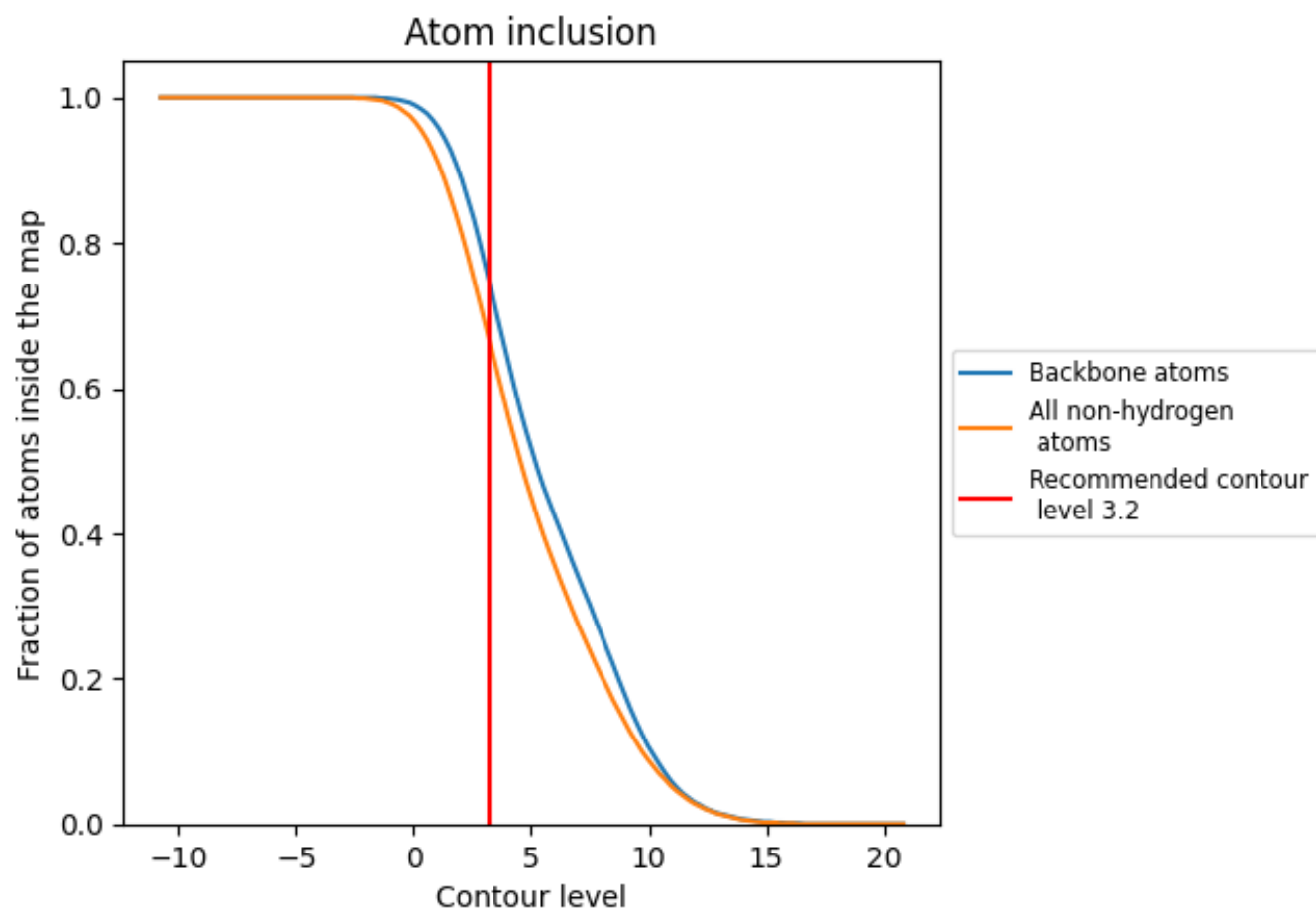
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (3.2).

9.4 Atom inclusion [i](#)



At the recommended contour level, 75% of all backbone atoms, 67% 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 (3.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6670	 0.4080
10	 0.7490	 0.4880
11	 0.6020	 0.3890
13	 0.7640	 0.4850
14	 0.7450	 0.4850
15	 0.8280	 0.5430
17	 0.7860	 0.5120
18	 0.6030	 0.3420
19	 0.6910	 0.4330
20	 0.8050	 0.5280
21	 0.7620	 0.4910
22	 0.5930	 0.3740
23	 0.7080	 0.5010
26	 0.7700	 0.4910
27	 0.7360	 0.4740
28	 0.8630	 0.4850
29	 0.6700	 0.4220
30	 0.6870	 0.4530
31	 0.7340	 0.4790
32	 0.7990	 0.5310
34	 0.7480	 0.5010
35	 0.7320	 0.4780
36	 0.7610	 0.4710
37	 0.8260	 0.5310
38	 0.6640	 0.3980
39	 0.7470	 0.4960
40	 0.7450	 0.4700
41	 0.6010	 0.4280
42	 0.7660	 0.4940
58	 0.8800	 0.5010
6	 0.9160	 0.5280
A	 0.3080	 0.2190
AA	 0.1050	 0.1450
AS	 0.4760	 0.3570
BB	 0.3090	 0.2870



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Chain	Atom inclusion	Q-score
CC	 0.2570	 0.1650
DD	 0.4560	 0.3680
EE	 0.0970	 0.1220
ES	 0.0520	 0.0560
F	 0.3330	 0.2280
FF	 0.5150	 0.3820
GG	 0.5140	 0.3690
IF	 0.4380	 0.3460
II	 0.2230	 0.2210
L3	 0.7740	 0.5130
L4	 0.7960	 0.5140
L5	 0.7250	 0.4560
L6	 0.7380	 0.4660
L7	 0.8050	 0.5220
L8	 0.8020	 0.5290
L9	 0.7210	 0.4690
LA	 0.1890	 0.2190
LL	 0.3280	 0.2330
MM	 0.2730	 0.2120
OO	 0.2130	 0.2300
PP	 0.3040	 0.2730
Q	 0.8080	 0.5280
RR	 0.4590	 0.3320
RS	 0.2560	 0.2360
S2	 0.3490	 0.3000
S3	 0.3040	 0.2600
S4	 0.2960	 0.2750
S5	 0.3190	 0.2380
S6	 0.3070	 0.2260
S7	 0.2480	 0.2370
S8	 0.4090	 0.3260
S9	 0.3250	 0.2760
SS	 0.2620	 0.2010
TT	 0.2500	 0.1950
UU	 0.5100	 0.3560
VV	 0.3410	 0.3030
W	 0.5030	 0.3490
WW	 0.2830	 0.2500
WX	 0.4140	 0.3510
XX	 0.4040	 0.2980
YY	 0.2490	 0.2060
ZZ	 0.1220	 0.1120

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Chain	Atom inclusion	Q-score
aa	 0.7120	 0.4390
bb	 0.8070	 0.5140
cc	 0.7490	 0.4890
dd	 0.8120	 0.5380
ee	 0.8230	 0.5340
ff	 0.7370	 0.4960
gg	 0.7990	 0.5110
s	 0.3910	 0.2590
t	 0.1840	 0.1360
v	 0.3680	 0.2590