



Full wwPDB EM Validation Report ⓘ

Sep 6, 2026 – 06:50 PM EDT

PDB ID : 11HG / pdb_000011hg
EMDB ID : EMD-75689
Title : Rabbit 80S with eEF2,CCDC124,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 : 2026-02-24
Resolution : 2.90 Å(reported)
Based on initial models : 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

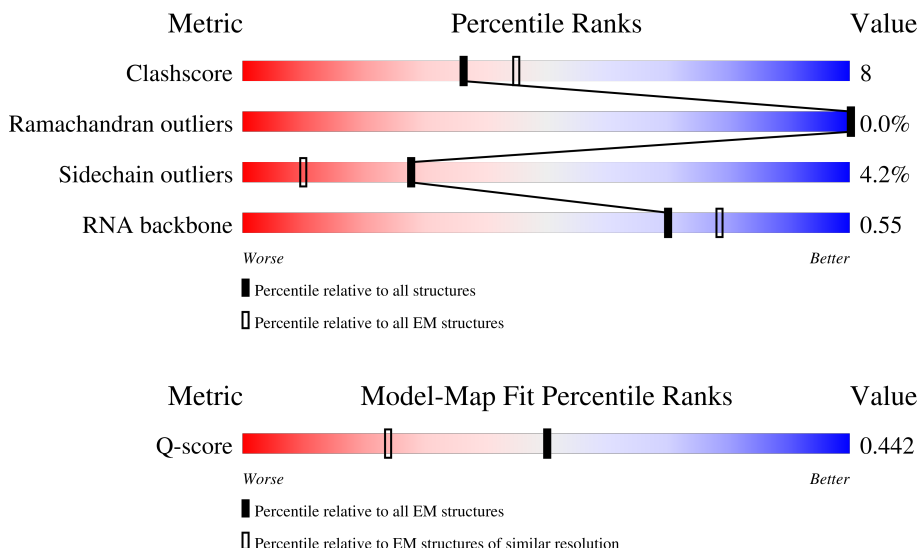
1 Overall quality at a glance

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.



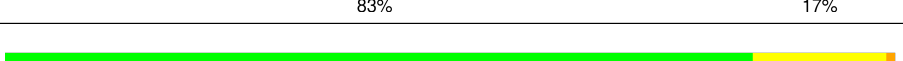
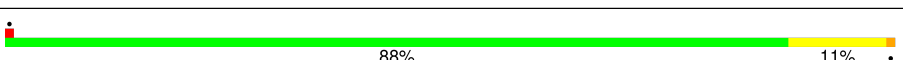
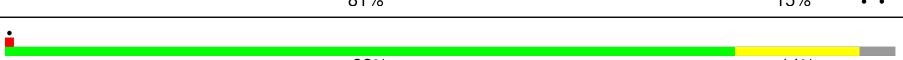
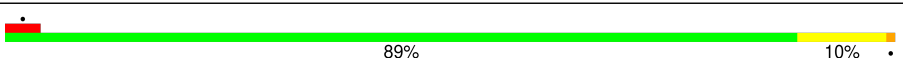
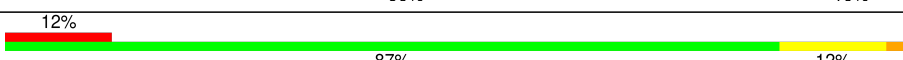
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13054 (2.40 - 3.40)

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	BB	217	
2	S2	221	
3	PP	83	

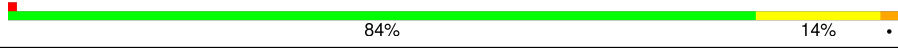
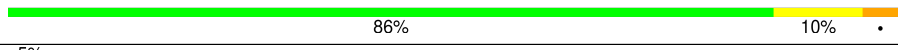
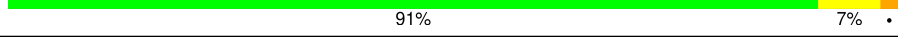
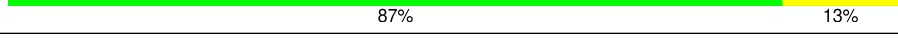
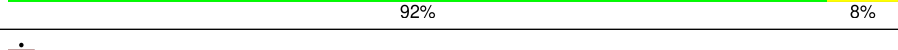
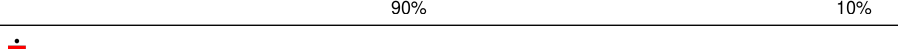
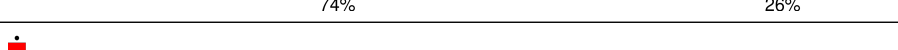
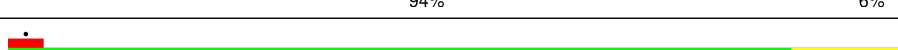
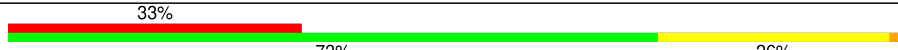
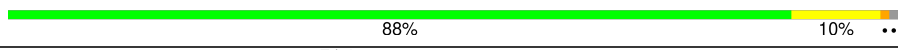
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Mol	Chain	Length	Quality of chain
4	DD	151	
5	58	156	
6	6	120	
7	L8	248	
8	L3	394	
9	L4	362	
10	L5	293	
11	L6	251	
12	L7	225	
13	aa	240	
14	10	213	
15	13	211	
16	14	138	
17	15	203	
18	bb	199	
19	17	153	
20	19	180	
21	20	176	
22	21	159	
23	22	99	
24	cc	118	
25	26	134	
26	27	135	
27	dd	147	
28	29	245	

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Mol	Chain	Length	Quality of chain
29	30	98	
30	31	107	
31	32	128	
32	ee	109	
33	34	114	
34	35	122	
35	36	102	
36	37	86	
37	38	69	
38	39	50	
39	40	52	
40	41	25	
41	42	104	
42	ff	91	
43	gg	124	
44	AS	213	
45	FF	149	
46	VV	83	
47	s	196	
48	t	153	
49	F	358	
50	Q	188	
51	ZZ	68	
52	EE	117	
53	TT	75	

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Mol	Chain	Length	Quality of chain
54	S5	191	
55	WW	62	
56	II	142	
57	CC	96	
58	AA	313	
59	OO	100	
60	MM	141	
61	LL	144	
62	XX	55	
63	RR	143	
64	SS	124	
65	S6	237	
66	S4	262	
67	S9	185	
68	S7	189	
69	YY	55	
70	S3	214	
71	RS	132	
72	WX	129	
73	S8	206	
74	W	121	
75	GG	136	
76	UU	101	
77	11	170	
78	L9	190	

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Mol	Chain	Length	Quality of chain
79	18	1688	14% 44% 49% 6%
80	v	857	23% 78% 18%
81	LA	1096	95%
82	CE	223	24% 31% 67%
83	A	121	29% 79% 19%
84	ES	5070	99%
85	28	4808	37% 31% 5% 27%
86	23	140	6% 84% 16%

2 Entry composition

There are 88 unique types of molecules in this entry. The entry contains 221973 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 40S_SA_C domain-containing protein.

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

- Molecule 2 is a protein called 40S ribosomal protein S2.

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

- Molecule 3 is a protein called eS21.

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

- Molecule 4 is a protein called Small ribosomal subunit protein uS17.

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

- Molecule 5 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	58	151	Total	C	N	O	P	0	0
			3208	1432	564	1062	150		

- Molecule 6 is a RNA chain called 5S rRNA.

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

- Molecule 7 is a protein called 60S ribosomal protein L8.

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

- Molecule 8 is a protein called 60S ribosomal protein L3.

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

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

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

- Molecule 10 is a protein called 60S ribosomal protein L5.

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

- Molecule 11 is a protein called Large ribosomal subunit protein eL6.

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

- Molecule 12 is a protein called 60S ribosomal protein L7.

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

- Molecule 13 is a protein called Large ribosomal subunit protein eL8.

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

- Molecule 14 is a protein called Ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	10	205	Total	C	N	O	S	0	0
			1664	1056	321	274	13		

- Molecule 15 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	13	210	Total	C	N	O	S	0	0
			1702	1065	354	279	4		

- Molecule 16 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	14	138	Total	C	N	O	S	0	0
			1137	727	221	182	7		

- Molecule 17 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	15	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 18 is a protein called Large ribosomal subunit protein uL13.

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

- Molecule 19 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	17	153	Total	C	N	O	S	0	0
			1242	777	241	215	9		

- Molecule 20 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	19	180	Total	C	N	O	S	0	0
			1508	933	328	238	9		

- Molecule 21 is a protein called Large ribosomal subunit protein eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	20	176	Total	C	N	O	S	0	0
			1462	930	285	236	11		

- Molecule 22 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	21	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 23 is a protein called Large ribosomal subunit protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	22	99	Total	C	N	O	S	0	0
			809	519	141	147	2		

- Molecule 24 is a protein called Large ribosomal subunit protein uL23.

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

- Molecule 25 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	26	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 26 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	27	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 27 is a protein called 60S ribosomal protein L27a.

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

- Molecule 28 is a protein called Large ribosomal subunit protein eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	29	104	Total	C	N	O	S	0	0
			848	527	189	129	3		

- Molecule 29 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	30	98	Total	C	N	O	S	0	0
			761	481	134	140	6		

- Molecule 30 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	31	107	Total	C	N	O	S	0	0
			888	560	171	155	2		

- Molecule 31 is a protein called Large ribosomal subunit protein eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	32	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 32 is a protein called Large ribosomal subunit protein eL33.

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

- Molecule 33 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	34	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

- Molecule 34 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	35	122	Total	C	N	O	S	0	0
			1013	640	204	168	1		

- Molecule 35 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	36	102	Total	C	N	O	S	0	0
			830	520	176	129	5		

- Molecule 36 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	37	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 37 is a protein called Large ribosomal subunit protein eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	38	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

- Molecule 38 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	39	50	Total	C	N	O	S	0	0
			447	286	96	64	1		

- Molecule 39 is a protein called Large ribosomal subunit protein eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	40	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 40 is a protein called eL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	41	25	Total	C	N	O	S	0	0
			239	145	64	27	3		

- Molecule 41 is a protein called eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	42	104	Total	C	N	O	S	0	0
			851	533	174	138	6		

- Molecule 42 is a protein called 60S ribosomal protein L37a.

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

- Molecule 43 is a protein called 60S ribosomal protein L28.

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

- Molecule 44 is a protein called 40S ribosomal protein S3a.

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

- Molecule 45 is a protein called 40S ribosomal protein S13.

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

- Molecule 46 is a protein called 40S ribosomal protein S27.

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

- Molecule 47 is a protein called 60S acidic ribosomal protein P0.

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

- Molecule 48 is a protein called uL11.

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

- Molecule 49 is a protein called Proliferation-associated protein 2G4.

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

- Molecule 50 is a protein called Large ribosomal subunit protein eL18.

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

- Molecule 51 is a protein called 40S ribosomal protein S27a.

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

- Molecule 52 is a protein called 40S ribosomal protein S12.

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

- Molecule 53 is a protein called 40S ribosomal protein S25.

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

- Molecule 54 is a protein called Small ribosomal subunit protein uS7.

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

- Molecule 55 is a protein called 40S ribosomal protein S28.

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

- Molecule 56 is a protein called Small ribosomal subunit protein uS9.

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

- Molecule 57 is a protein called 40S ribosomal protein S10.

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

- Molecule 58 is a protein called Receptor of activated protein C kinase 1.

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

- Molecule 59 is a protein called 40S ribosomal protein S20.

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

- Molecule 60 is a protein called Small ribosomal subunit protein eS19.

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

- Molecule 61 is a protein called 40S ribosomal protein S18.

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

- Molecule 62 is a protein called 40S ribosomal protein S29.

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

- Molecule 63 is a protein called uS12.

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

- Molecule 64 is a protein called 40S ribosomal protein S24.

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

- Molecule 65 is a protein called 40S ribosomal protein S6.

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

- Molecule 66 is a protein called 40S ribosomal protein S4.

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

- Molecule 67 is a protein called 40S ribosomal protein S9.

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

- Molecule 68 is a protein called Small ribosomal subunit protein eS7.

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

- Molecule 69 is a protein called 40S ribosomal protein S30.

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

- Molecule 70 is a protein called Small ribosomal subunit protein uS3.

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

- Molecule 71 is a protein called 40S ribosomal protein S17.

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

- Molecule 72 is a protein called 40S ribosomal protein S15a.

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

- Molecule 73 is a protein called 40S ribosomal protein S8.

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

- Molecule 74 is a protein called Ribosomal protein L24.

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

- Molecule 75 is a protein called Small ribosomal subunit protein uS11.

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

- Molecule 76 is a protein called eS26.

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

- Molecule 77 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	11	170	Total	C	N	O	S	0	0
			1362	861	254	241	6		

- Molecule 78 is a protein called 60S ribosomal protein L9.

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

- Molecule 79 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	18	1688	Total	C	N	O	P	0	0
			36043	16088	6476	11792	1687		

- Molecule 80 is a protein called Elongation factor 2.

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

- Molecule 81 is a protein called La-related protein 1.

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

- Molecule 82 is a protein called Coiled-coil domain-containing protein 124.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	CE	73	Total	C	N	O	S	0	0
			613	369	122	121	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		

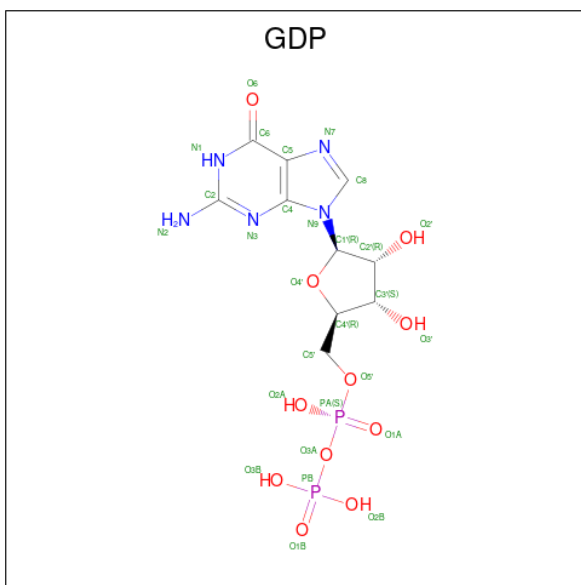
- Molecule 86 is a protein called Ribosomal protein L23.

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) (labeled as "Ligand of Interest" by depositor).

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) (labeled as "Ligand of Interest" by depositor).

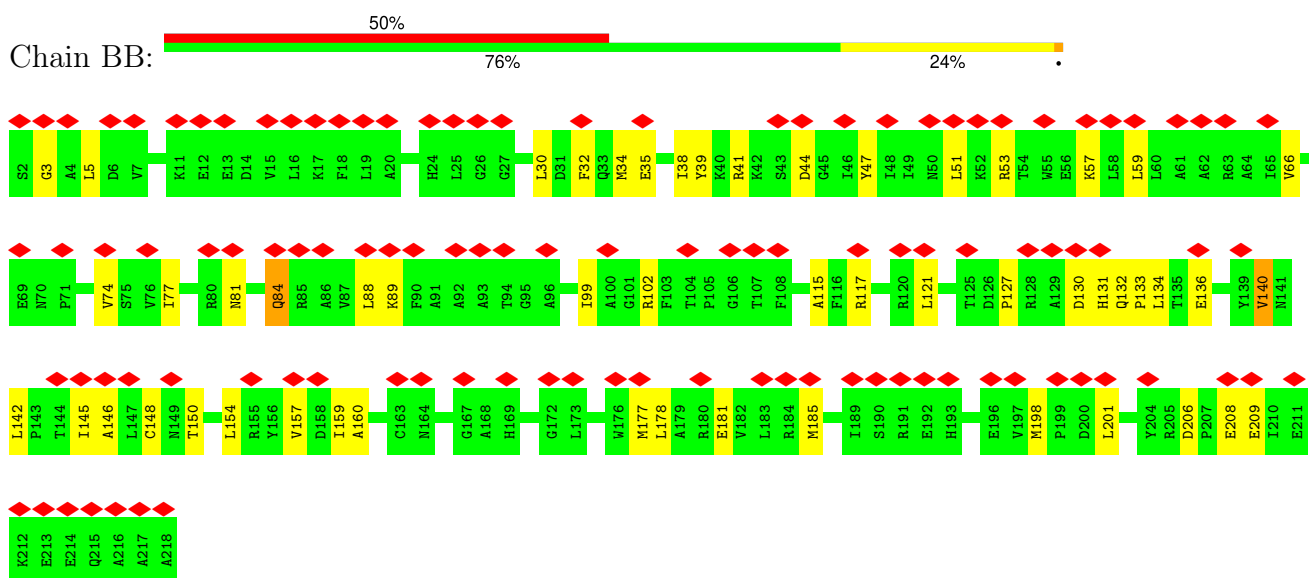


Mol	Chain	Residues	Atoms					AltConf
88	v	1	Total	C	N	O	P	0
			28	10	5	11	2	

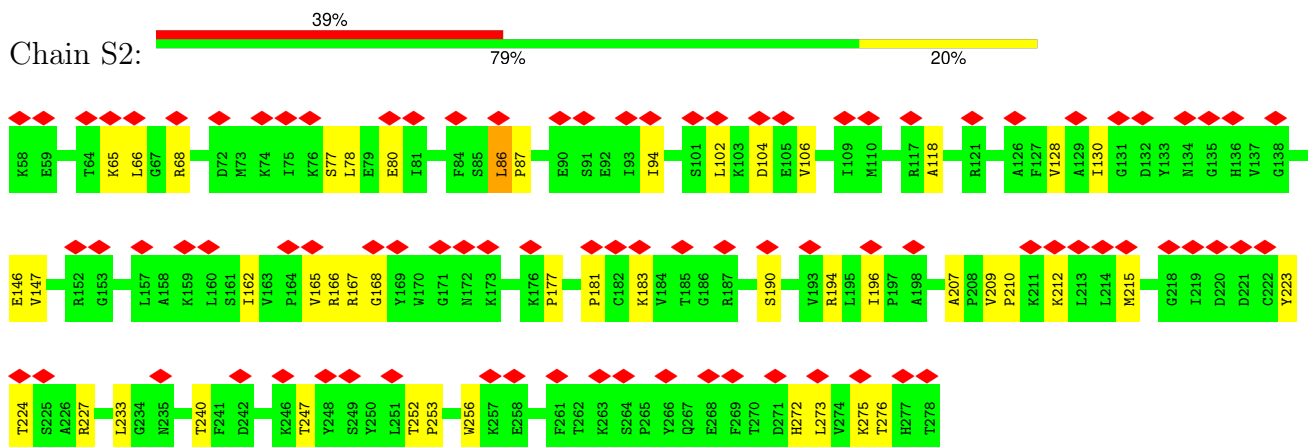
3 Residue-property plots

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

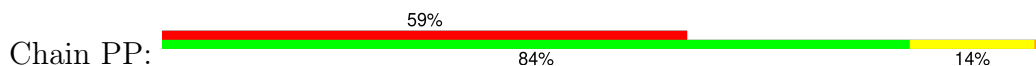
- Molecule 1: 40S_SA_C domain-containing protein

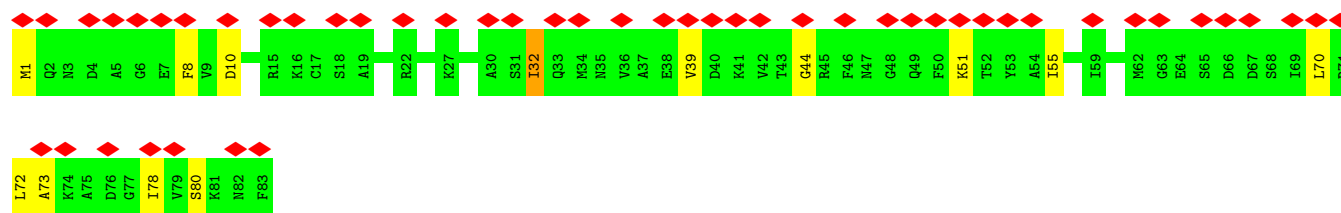


- Molecule 2: 40S ribosomal protein S2

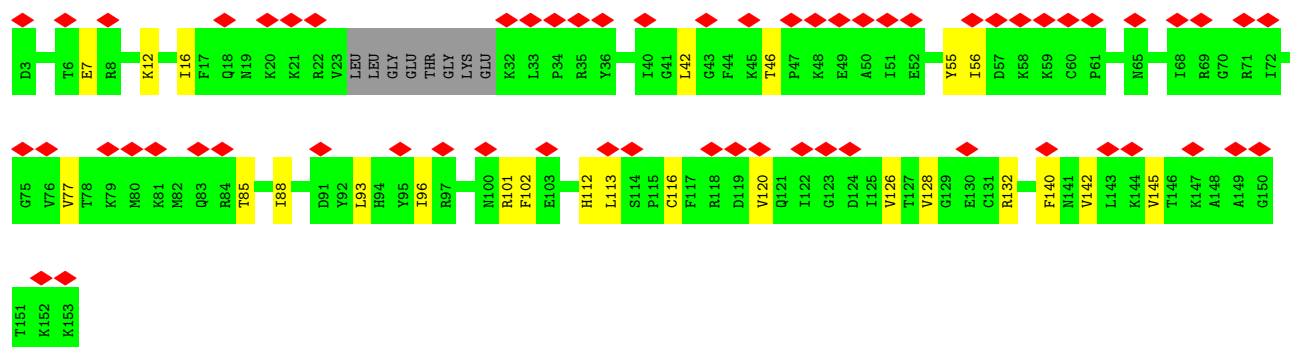
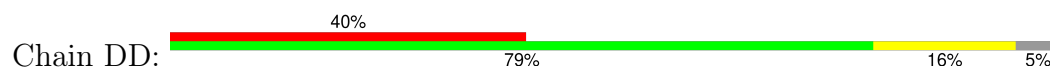


- Molecule 3: eS21

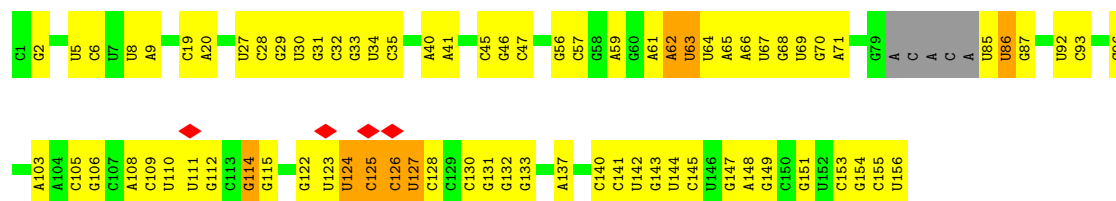




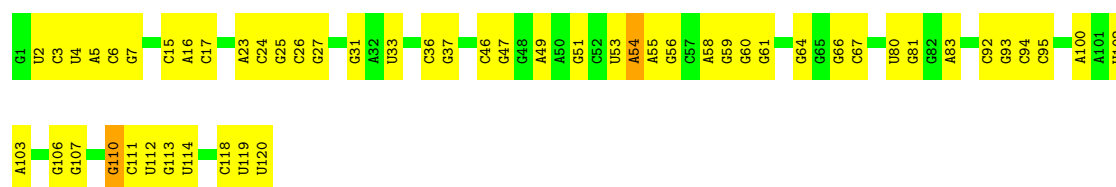
• Molecule 4: Small ribosomal subunit protein uS17



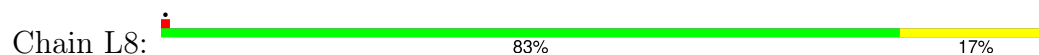
• Molecule 5: 5.8S rRNA

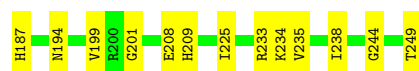


• Molecule 6: 5S rRNA



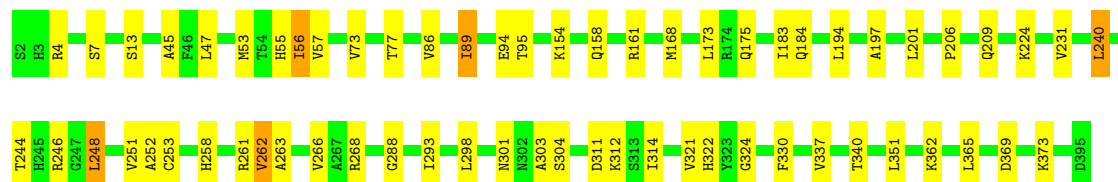
• Molecule 7: 60S ribosomal protein L8





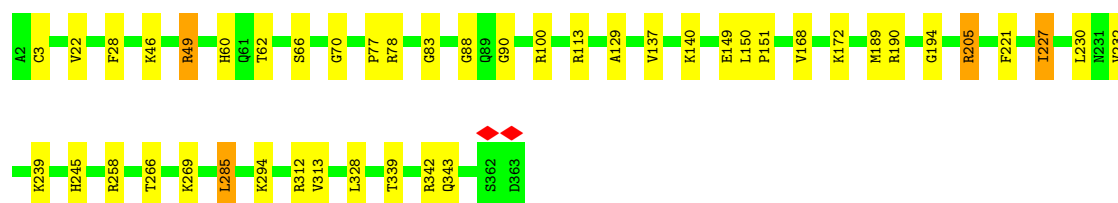
• Molecule 8: 60S ribosomal protein L3

Chain L3: 84% 15%



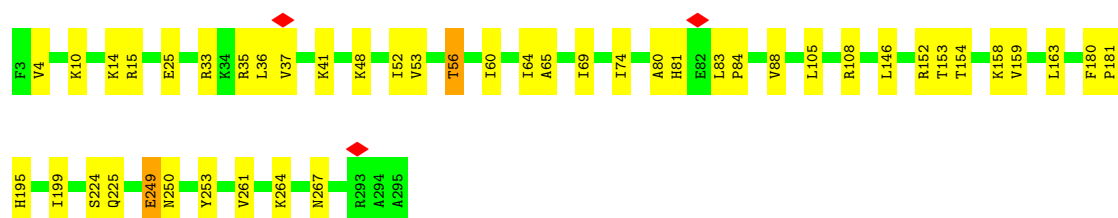
• Molecule 9: 60S ribosomal protein L4

Chain L4: 88% 11%



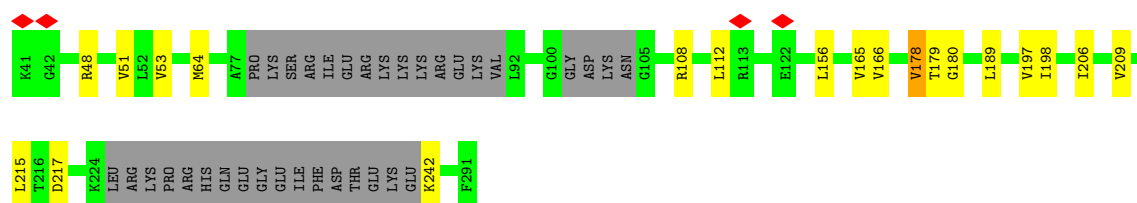
• Molecule 10: 60S ribosomal protein L5

Chain L5: 85% 15%



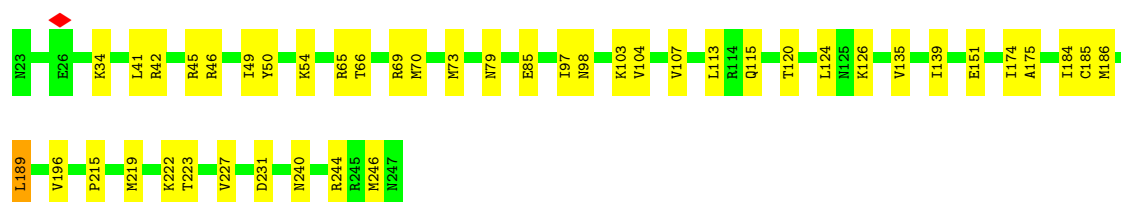
• Molecule 11: Large ribosomal subunit protein eL6

Chain L6: 78% 8% 14%

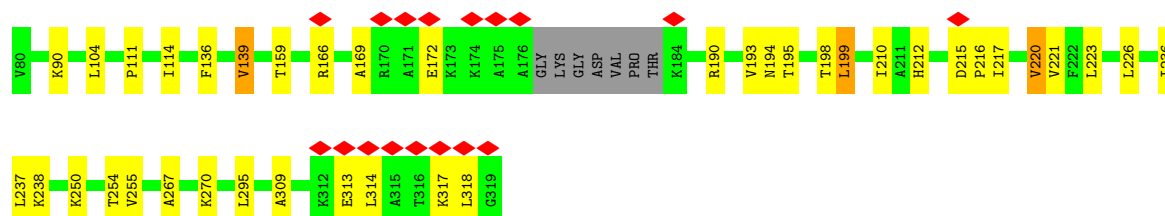
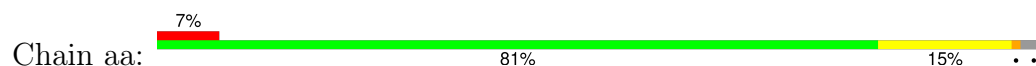


• Molecule 12: 60S ribosomal protein L7

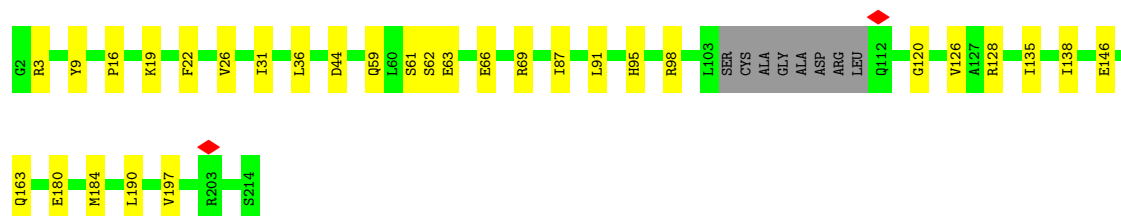
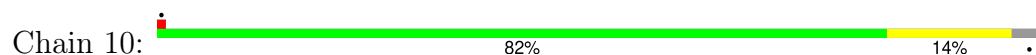
Chain L7: 80% 19%



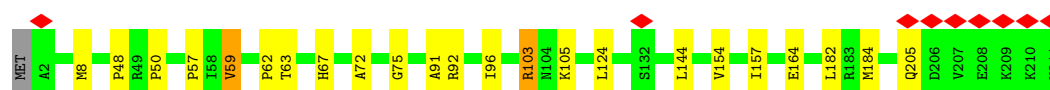
- Molecule 13: Large ribosomal subunit protein eL8



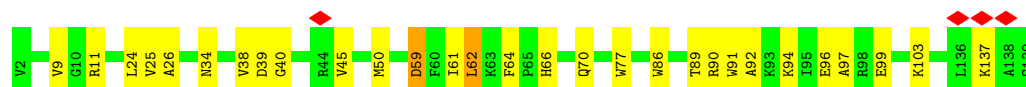
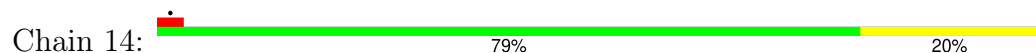
- Molecule 14: Ribosomal protein L10



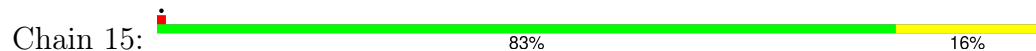
- Molecule 15: 60S ribosomal protein L13

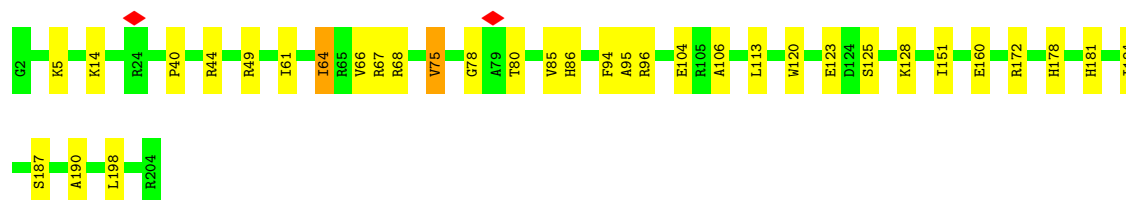


- Molecule 16: 60S ribosomal protein L14



- Molecule 17: 60S ribosomal protein L15





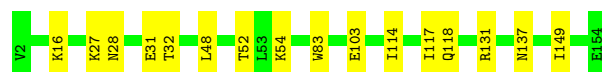
- Molecule 18: Large ribosomal subunit protein uL13

Chain bb: 79% 20% .



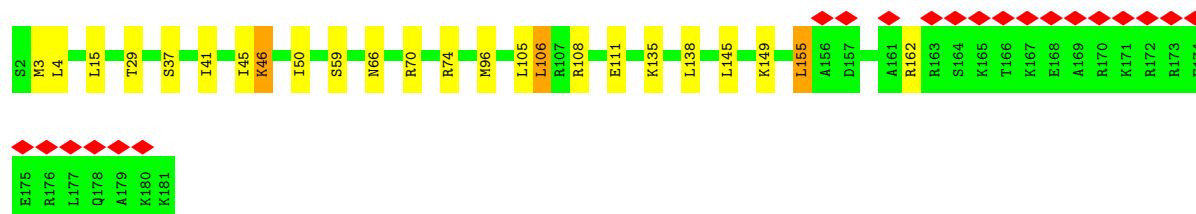
- Molecule 19: 60S ribosomal protein L17

Chain 17: 90% 10% .



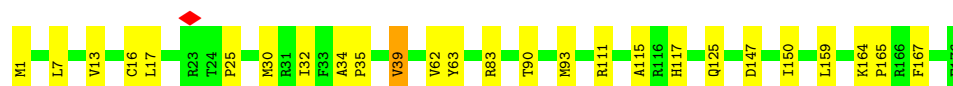
- Molecule 20: 60S ribosomal protein L19

Chain 19: 12% 87% 12% .



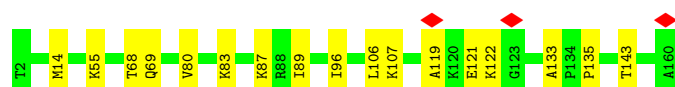
- Molecule 21: Large ribosomal subunit protein eL20

Chain 20: 85% 14% .



- Molecule 22: 60S ribosomal protein L21

Chain 21: 89% 11% .

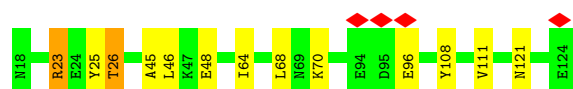


- | |
|-----|
| GLY | LYS | PRO | LYS | ALA | GLN | ALA | ALA | GLN | LYS | PRO | LYS | ALA | GLN | ALA | ALA | GLN | GLN | GLN | GLN | THR | LYS | PRO | PRO | LYS | ALA | ALA | ALA | VAL | VAL | PRO | PRO | PRO | GLN | ALA | ALA | GLY | ALA | GLN | PRO | PRO | PRO | LYS | ALA | LYS | ALA | ALA |
|-----|

• Molecule 29: 60S ribosomal protein L30

Chain 30:  87% 12%

• Molecule 30: 60S ribosomal protein L31

Chain 31:  88% 10%

• Molecule 31: Large ribosomal subunit protein eL32

Chain 32:  84% 14%

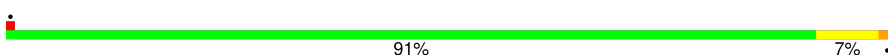
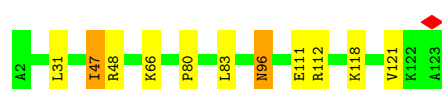
• Molecule 32: Large ribosomal subunit protein eL33

Chain ee:  86% 10%

• Molecule 33: 60S ribosomal protein L34

Chain 34:  5% 90% 9%

• Molecule 34: 60S ribosomal protein L35

Chain 35:  91% 7%

• Molecule 35: 60S ribosomal protein L36

Chain 36:  87% 13%



- Molecule 36: 60S ribosomal protein L37

Chain 37: 92% 8%



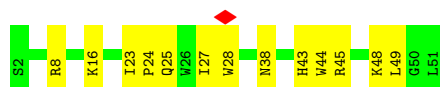
- Molecule 37: Large ribosomal subunit protein eL38

Chain 38: 90% 10%



- Molecule 38: 60S ribosomal protein L39

Chain 39: 74% 26%



- Molecule 39: Large ribosomal subunit protein eL40

Chain 40: 94% 6%



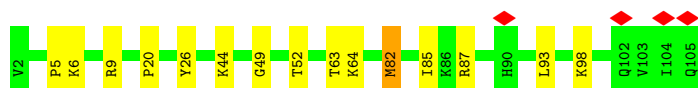
- Molecule 40: eL41

Chain 41: 88% 12%



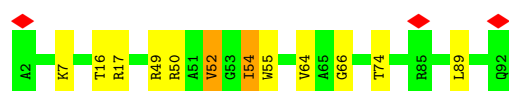
- Molecule 41: eL42

Chain 42: 86% 13%



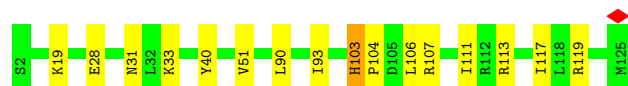
- Molecule 42: 60S ribosomal protein L37a

Chain ff:  87% 11% .



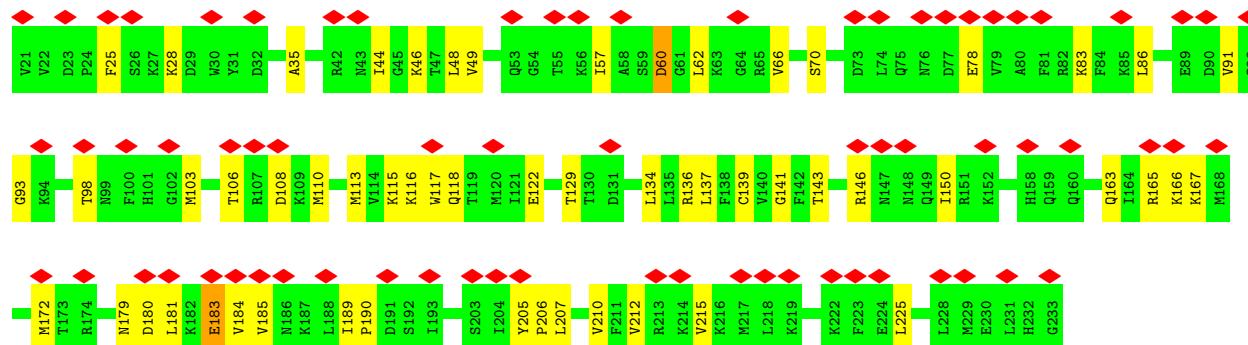
- Molecule 43: 60S ribosomal protein L28

Chain gg:  87% 12% .



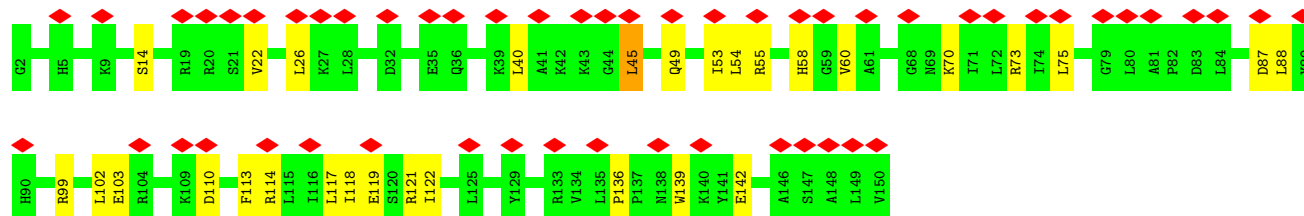
- Molecule 44: 40S ribosomal protein S3a

Chain AS:  33% 73% 26% .



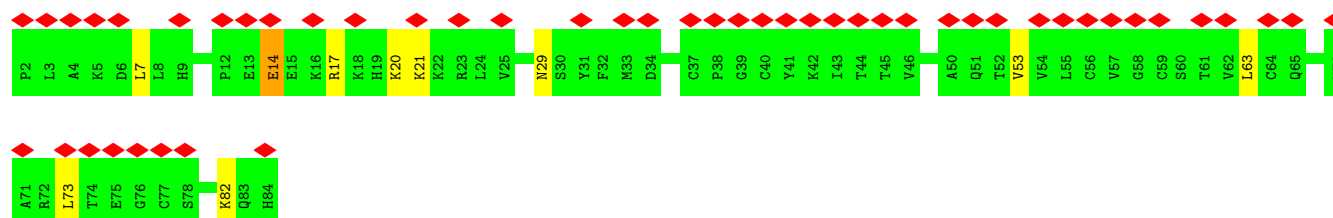
- Molecule 45: 40S ribosomal protein S13

Chain FF:  36% 80% 19% .

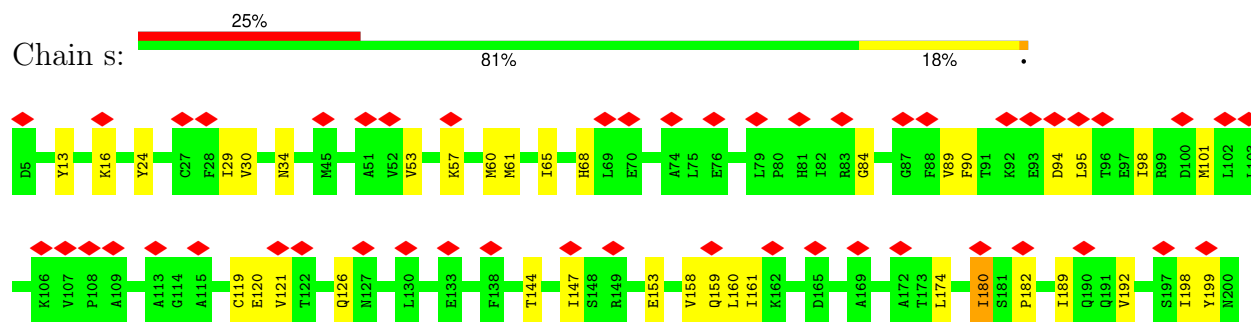


- Molecule 46: 40S ribosomal protein S27

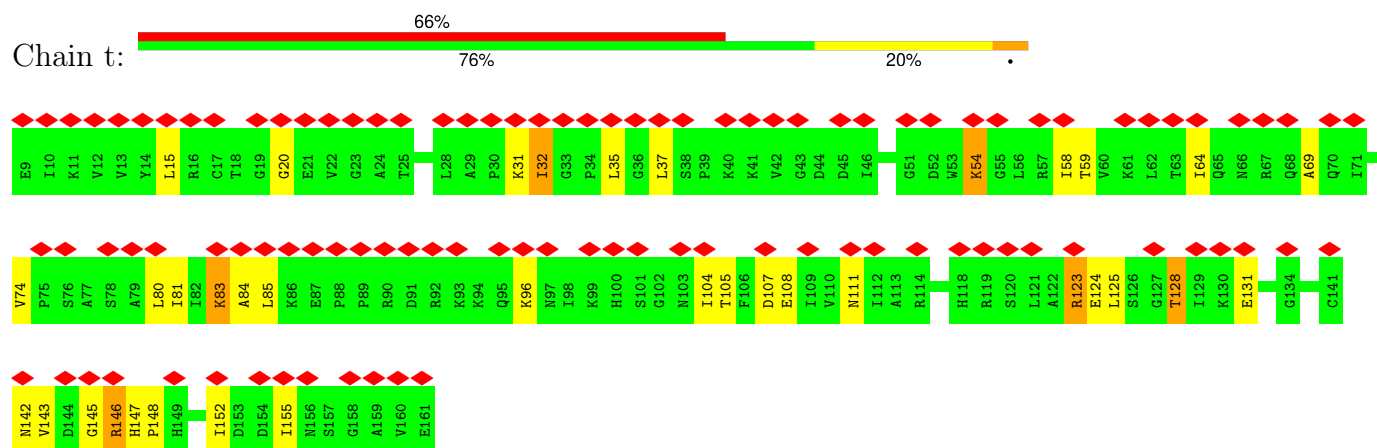
Chain VV:  59% 88% 11% .



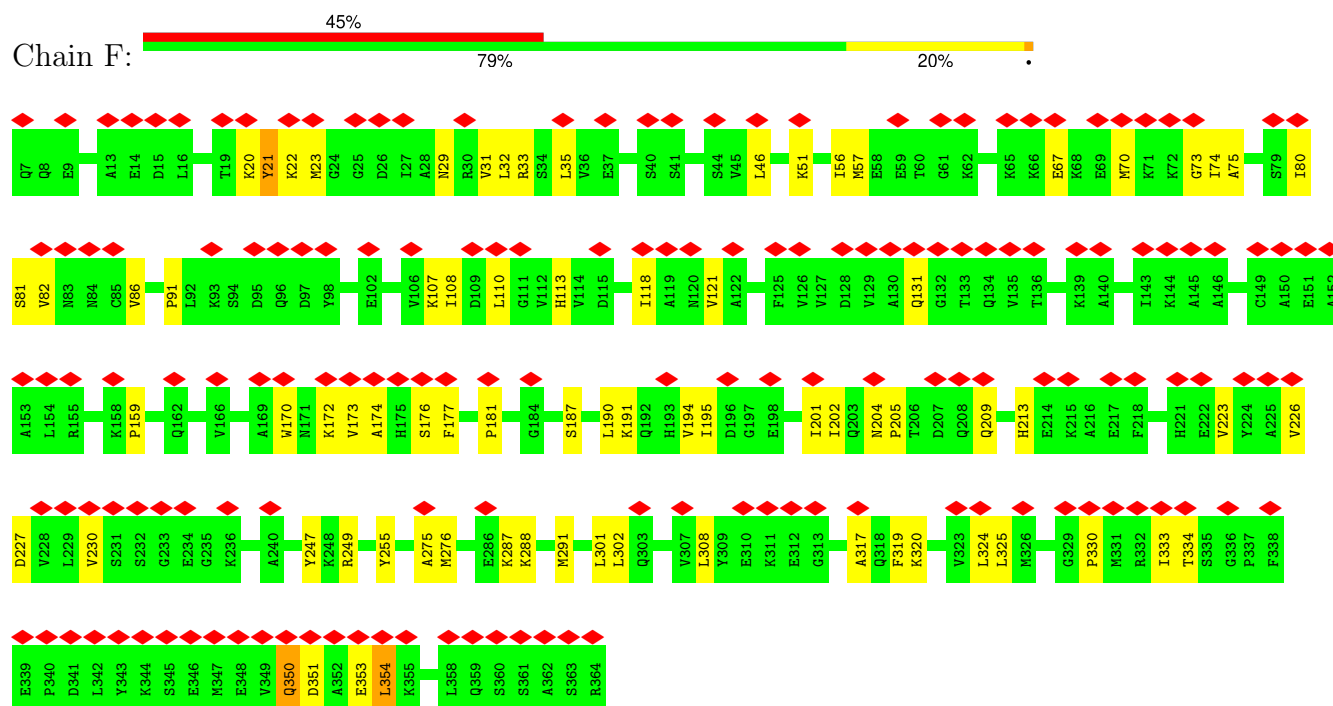
- Molecule 47: 60S acidic ribosomal protein P0



- Molecule 48: uL11



- Molecule 49: Proliferation-associated protein 2G4



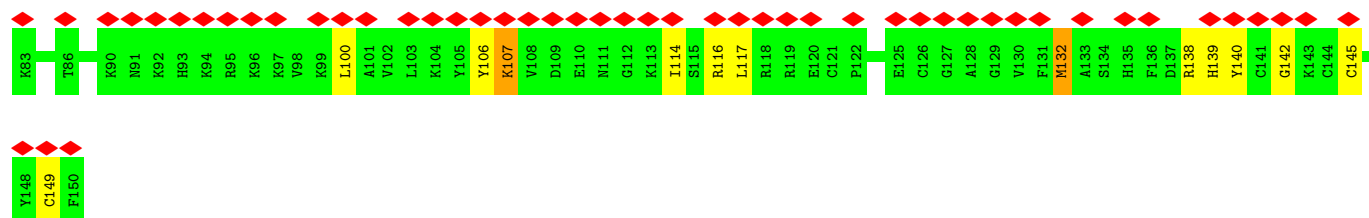
- Molecule 50: Large ribosomal subunit protein eL18

Chain Q:  88% 10% ..



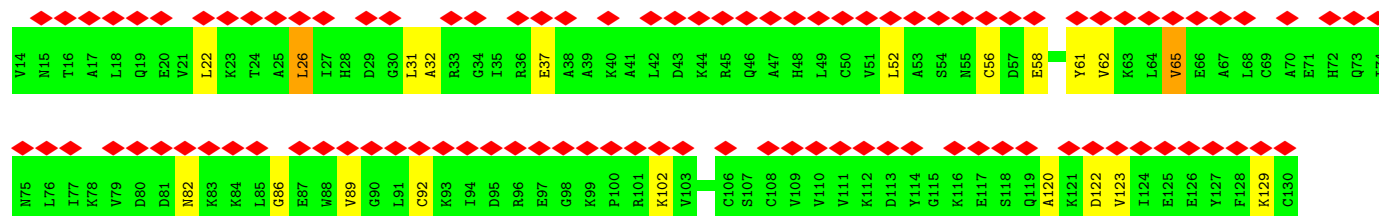
- Molecule 51: 40S ribosomal protein S27a

Chain ZZ:  74% 81% 16% .



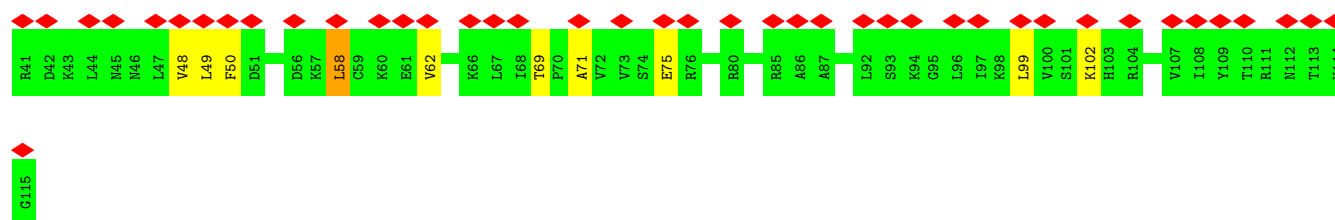
- Molecule 52: 40S ribosomal protein S12

Chain EE:  84% 83% 15% .



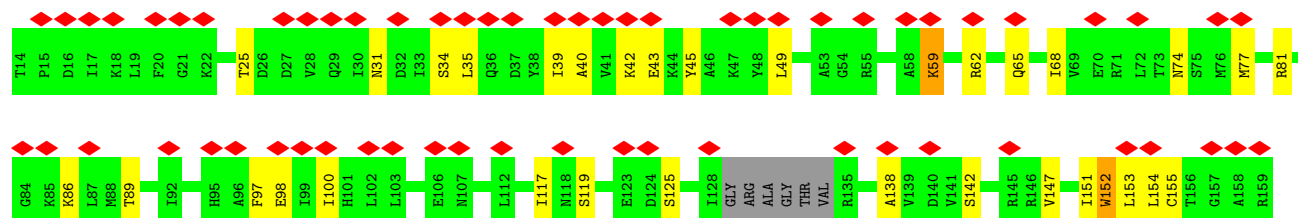
- Molecule 53: 40S ribosomal protein S25

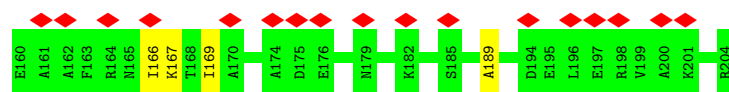
Chain TT:  56% 87% 12% .



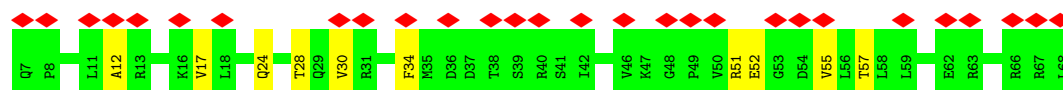
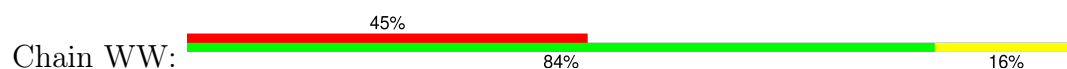
- Molecule 54: Small ribosomal subunit protein uS7

Chain S5:  41% 77% 18% ..

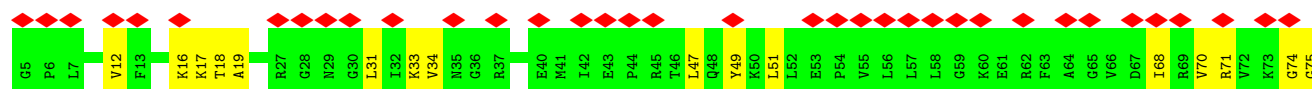
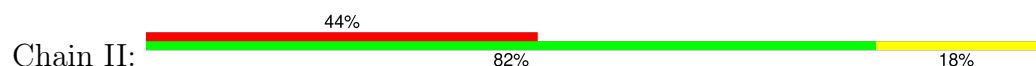




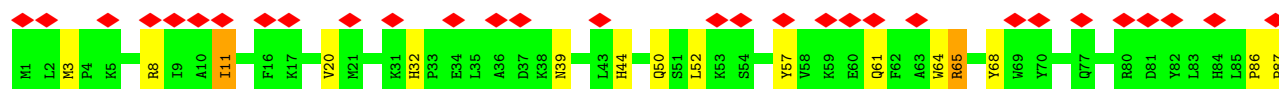
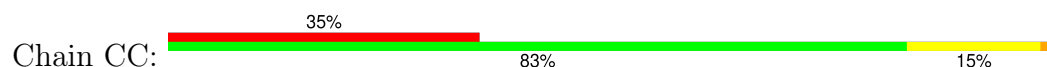
- Molecule 55: 40S ribosomal protein S28



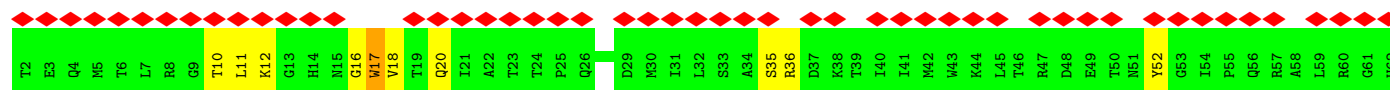
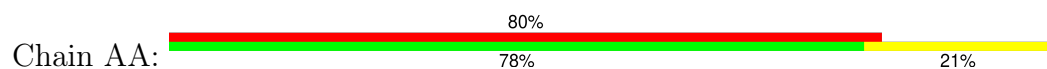
- Molecule 56: Small ribosomal subunit protein uS9

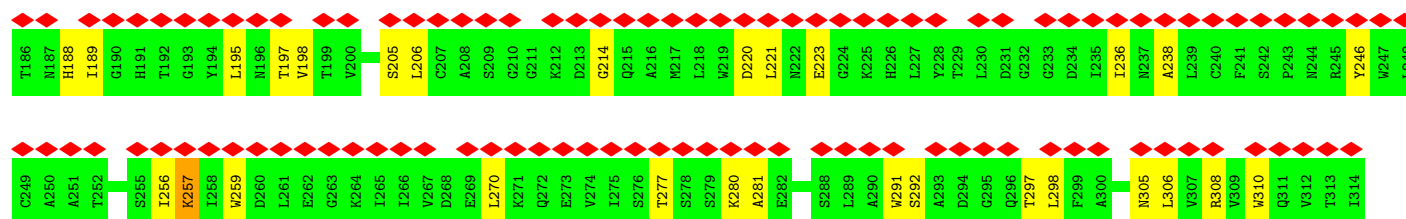


- Molecule 57: 40S ribosomal protein S10

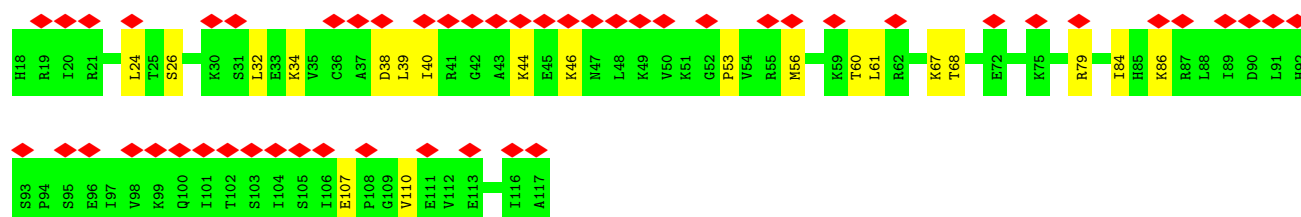
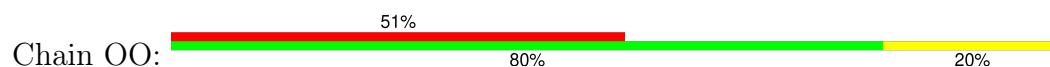


- Molecule 58: Receptor of activated protein C kinase 1

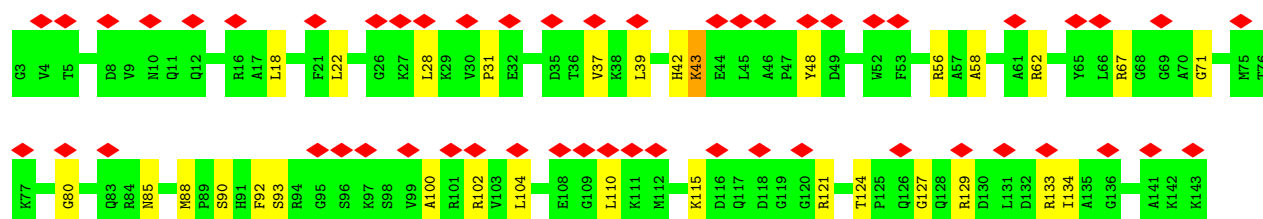
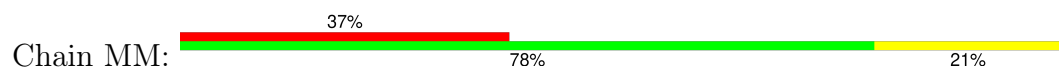




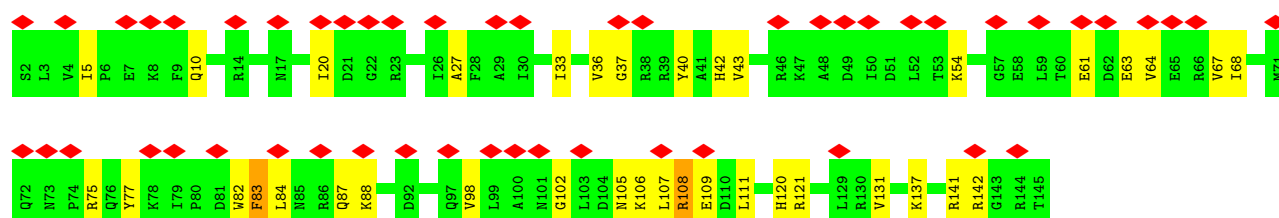
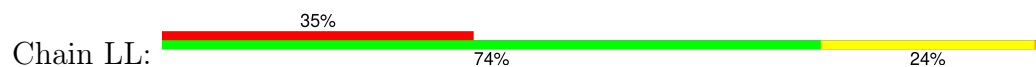
• Molecule 59: 40S ribosomal protein S20



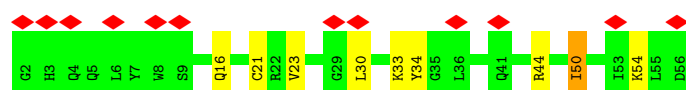
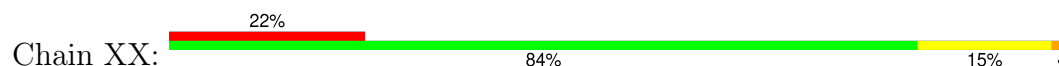
• Molecule 60: Small ribosomal subunit protein eS19



• Molecule 61: 40S ribosomal protein S18

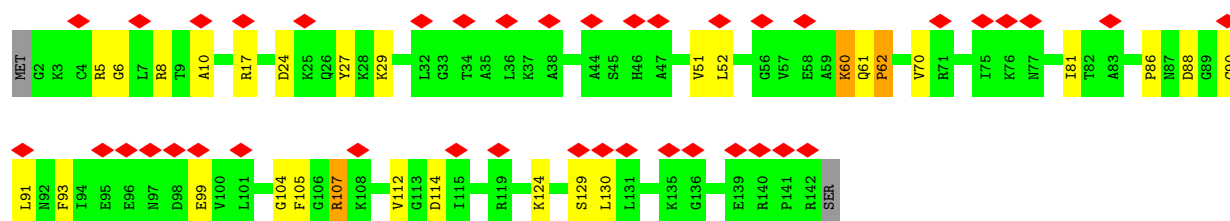


• Molecule 62: 40S ribosomal protein S29



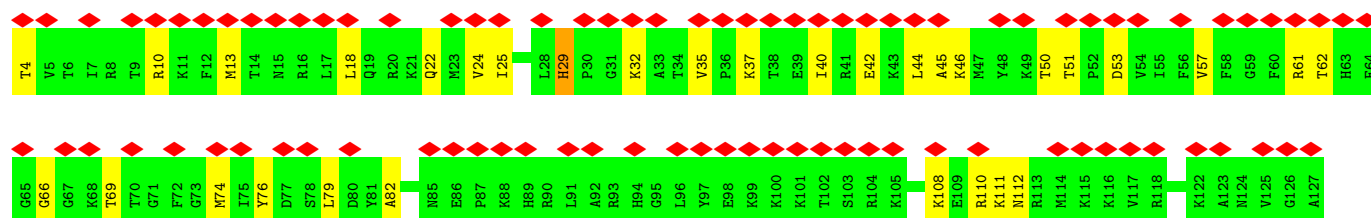
• Molecule 63: uS12

Chain RR: 



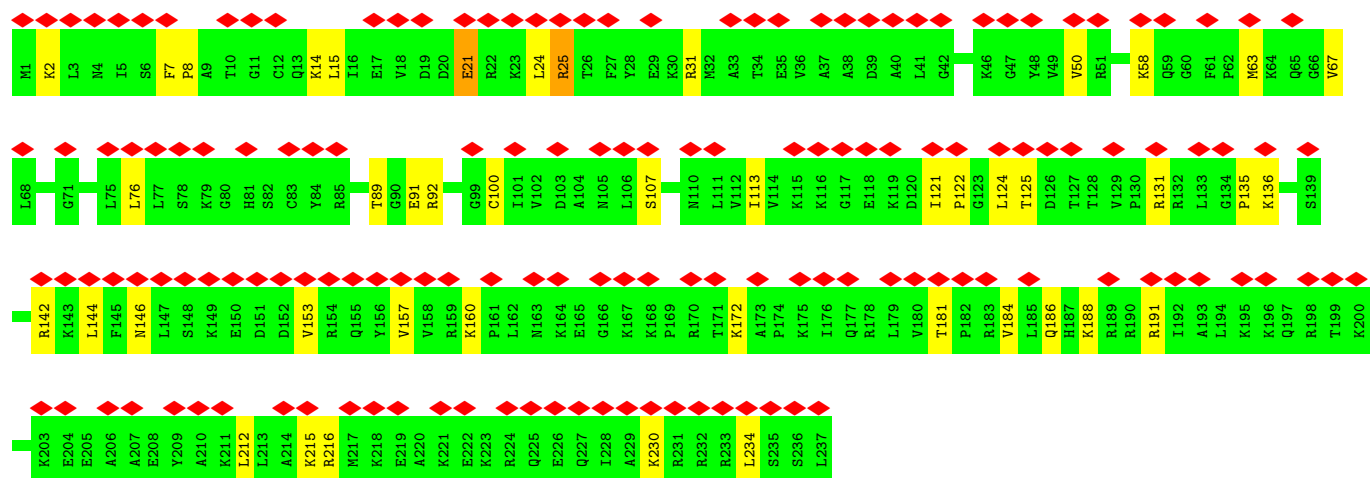
• Molecule 64: 40S ribosomal protein S24

Chain SS: 



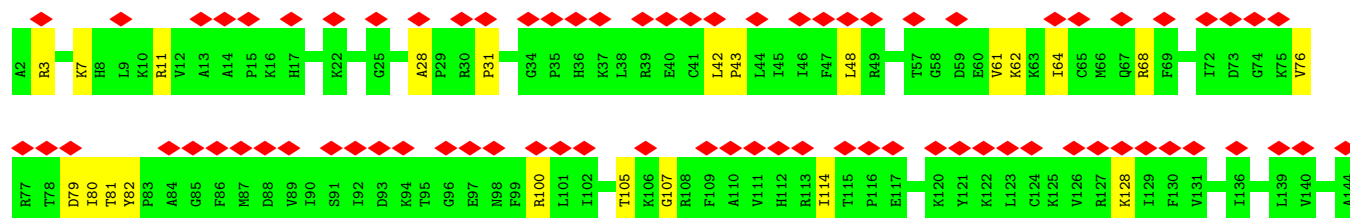
• Molecule 65: 40S ribosomal protein S6

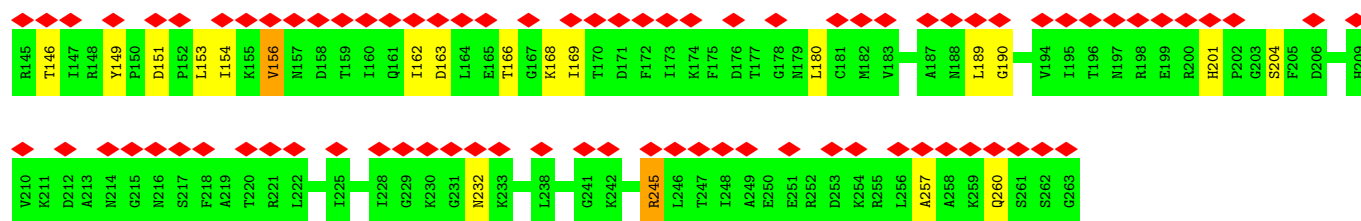
Chain S6: 



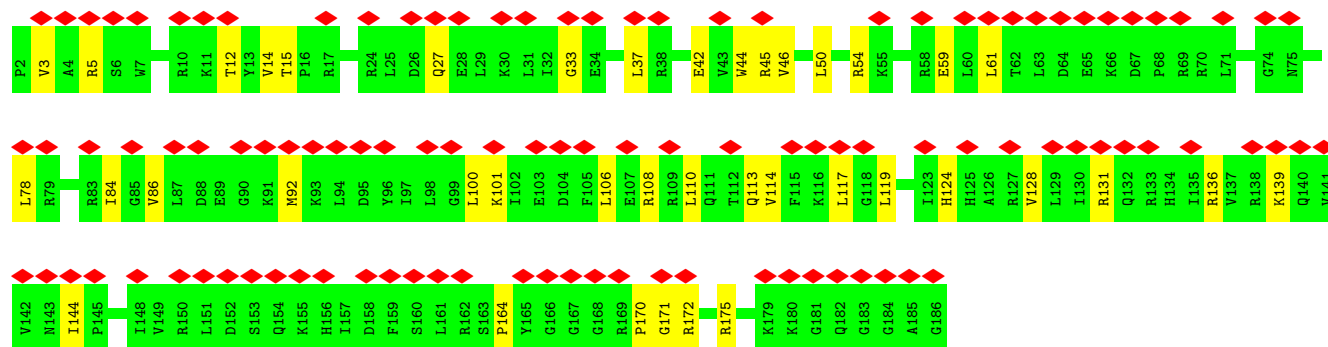
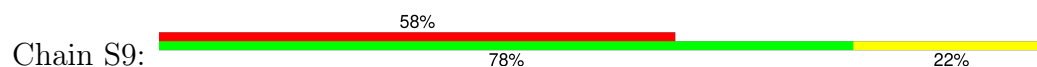
• Molecule 66: 40S ribosomal protein S4

Chain S4: 

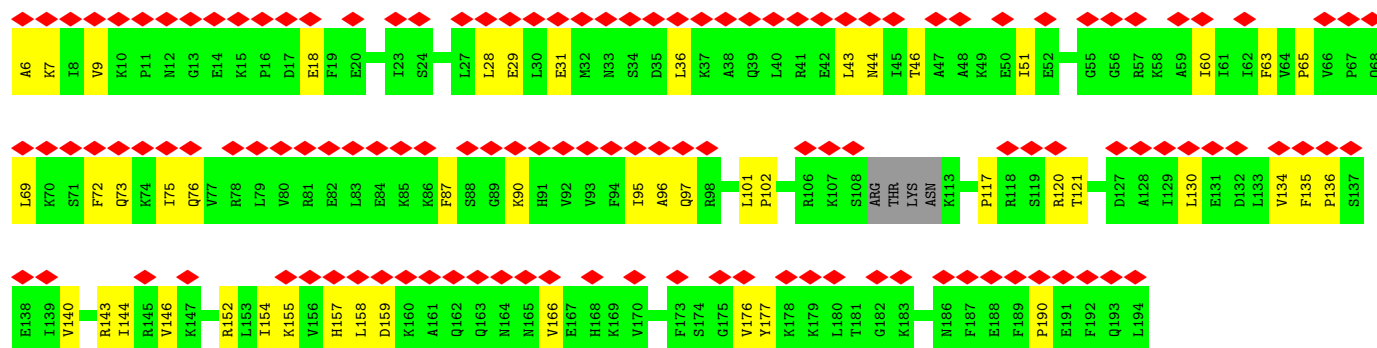
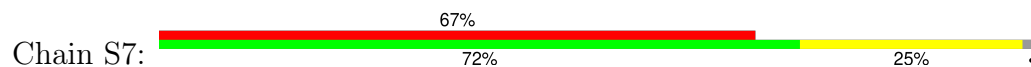




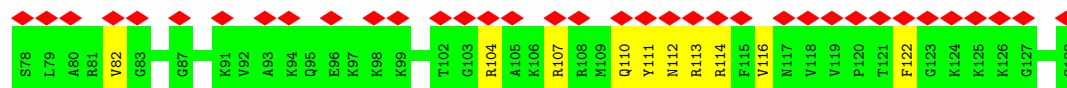
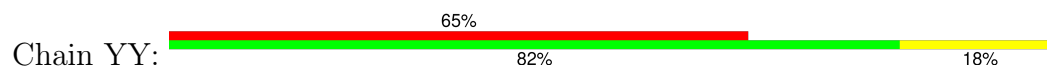
• Molecule 67: 40S ribosomal protein S9



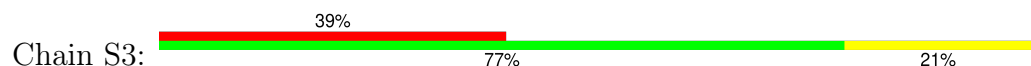
• Molecule 68: Small ribosomal subunit protein eS7

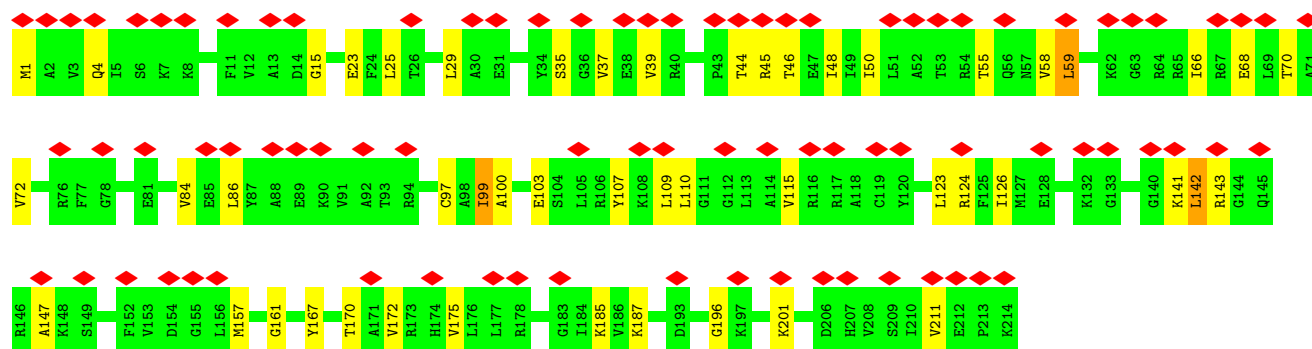


• Molecule 69: 40S ribosomal protein S30



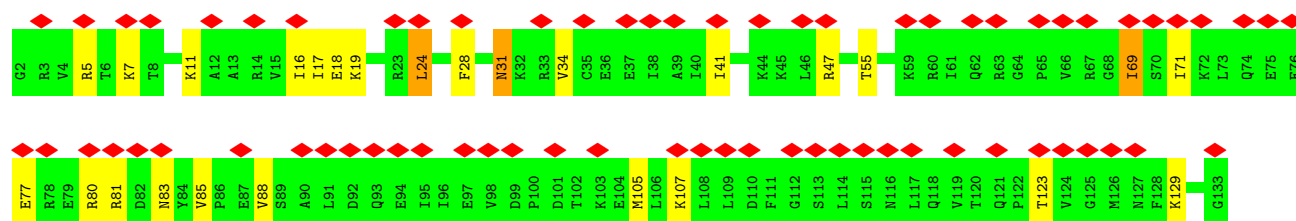
• Molecule 70: Small ribosomal subunit protein uS3





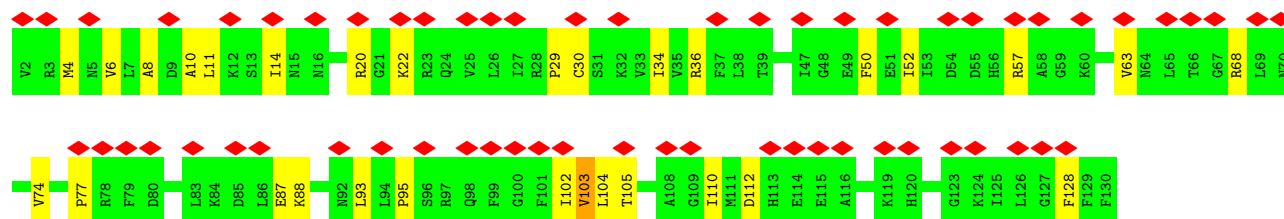
• Molecule 71: 40S ribosomal protein S17

Chain RS:



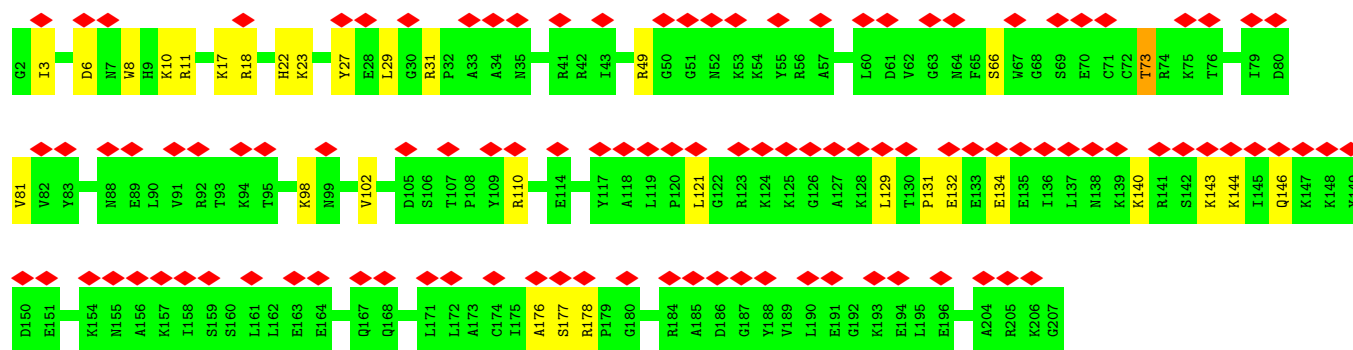
• Molecule 72: 40S ribosomal protein S15a

Chain WX:

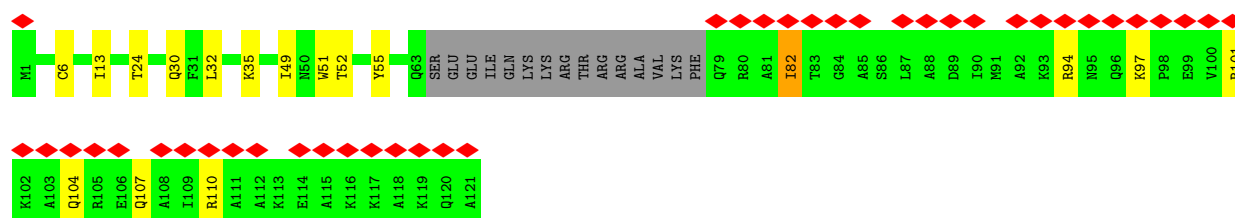
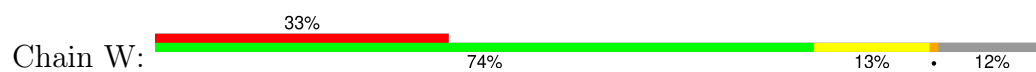


• Molecule 73: 40S ribosomal protein S8

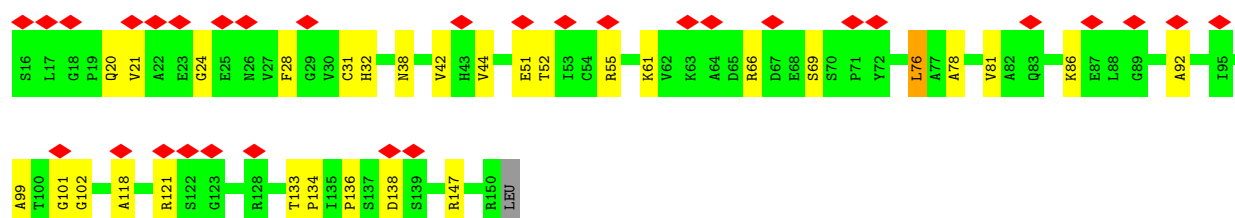
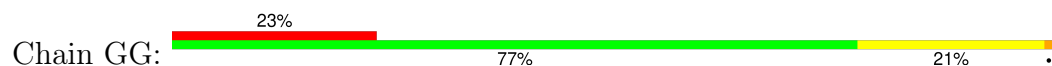
Chain S8:



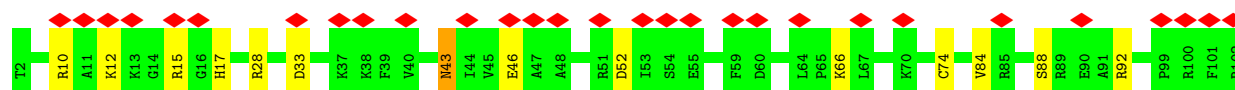
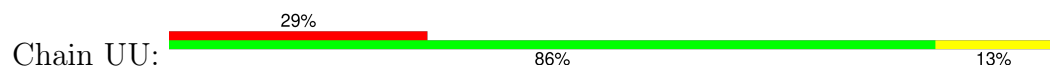
• Molecule 74: Ribosomal protein L24



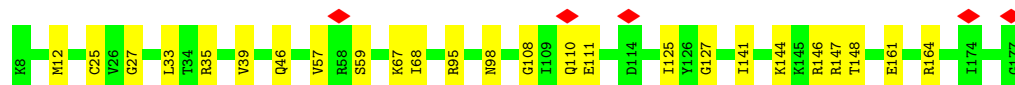
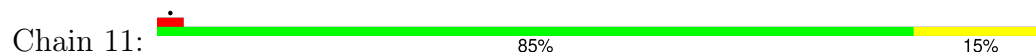
- Molecule 75: Small ribosomal subunit protein uS11



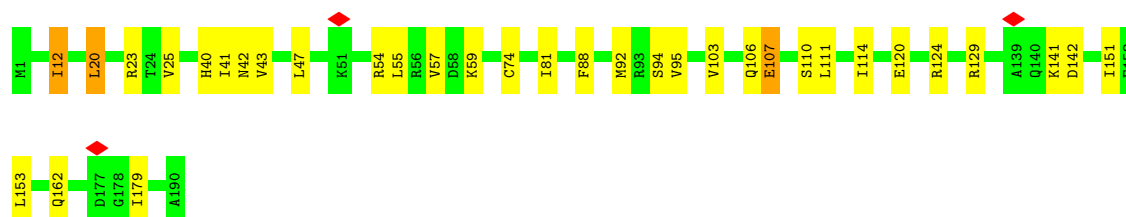
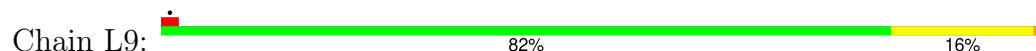
- Molecule 76: eS26



- Molecule 77: 60S ribosomal protein L11

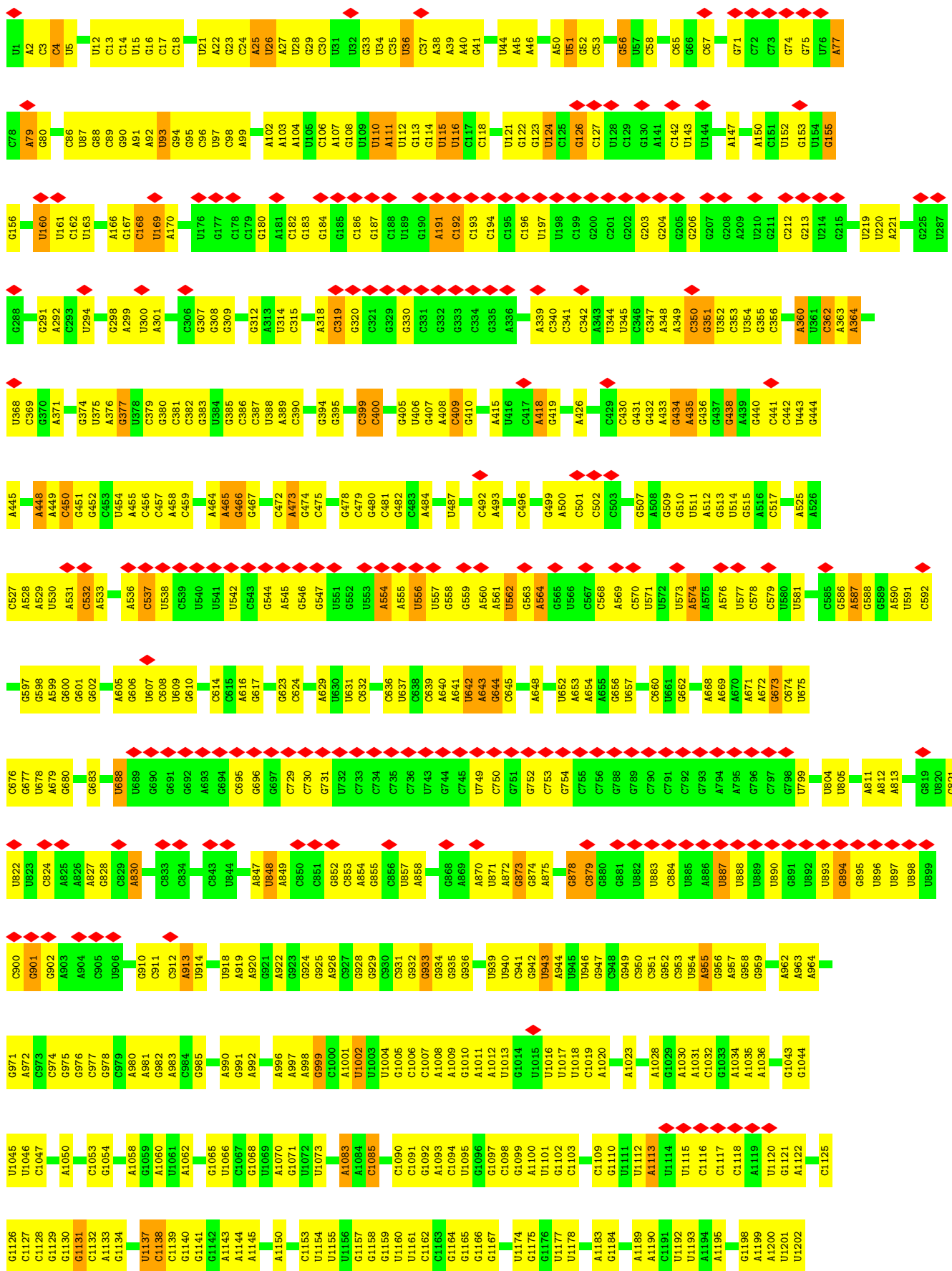


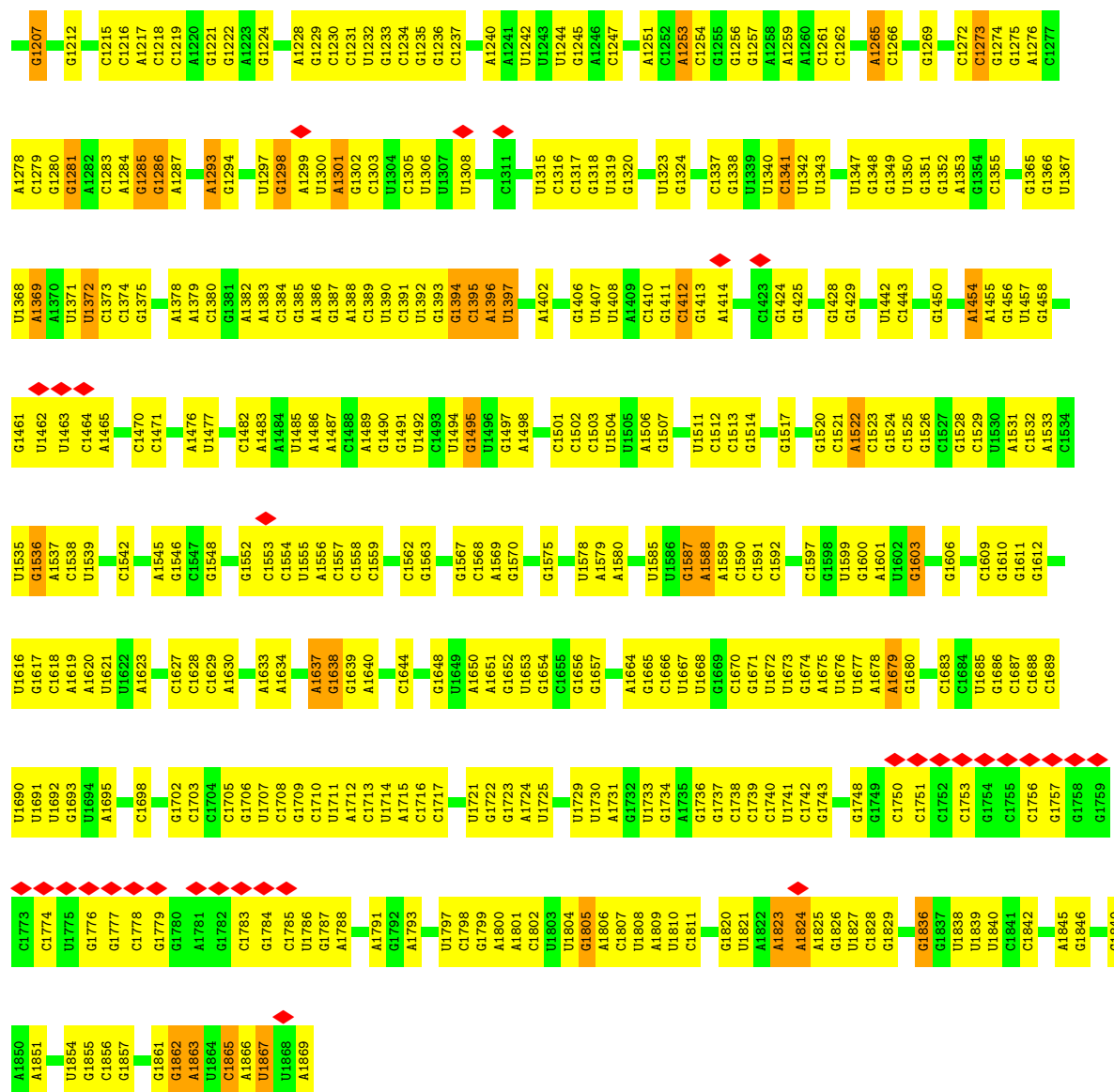
- Molecule 78: 60S ribosomal protein L9



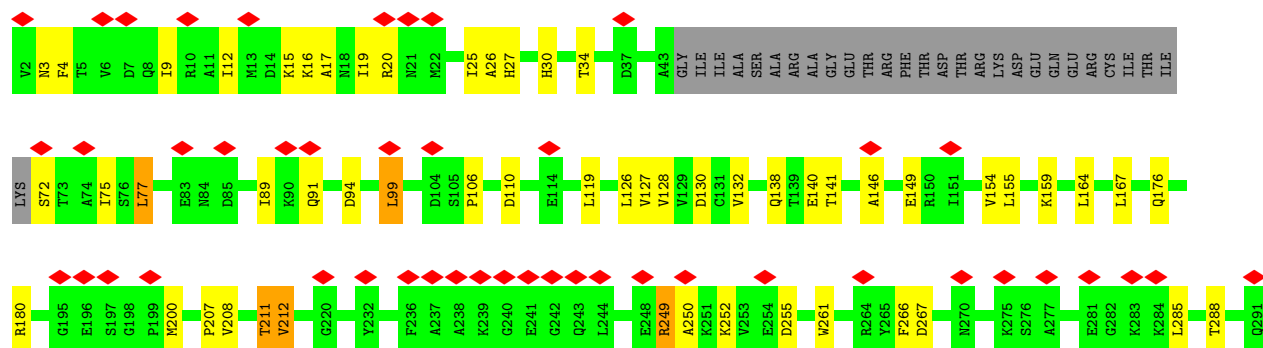
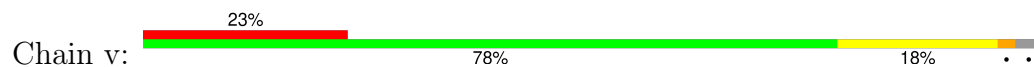
- Molecule 79: 18S rRNA

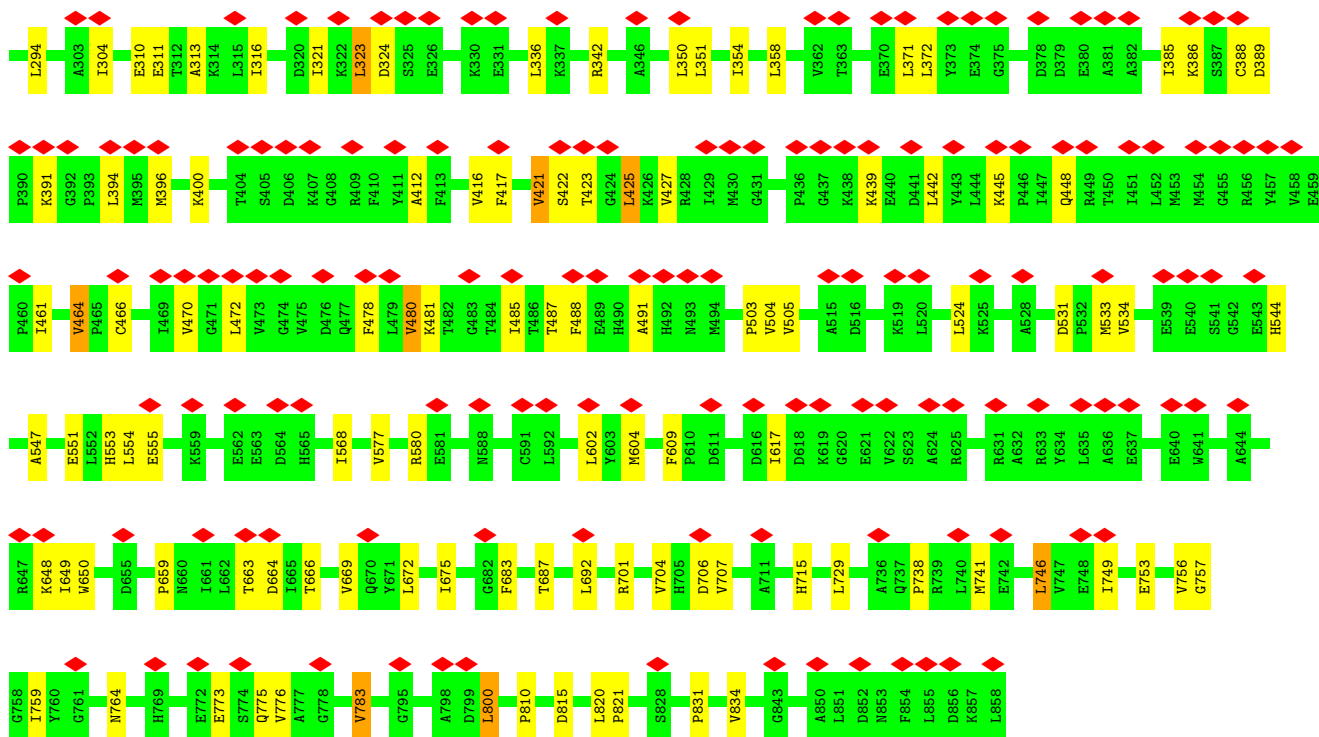




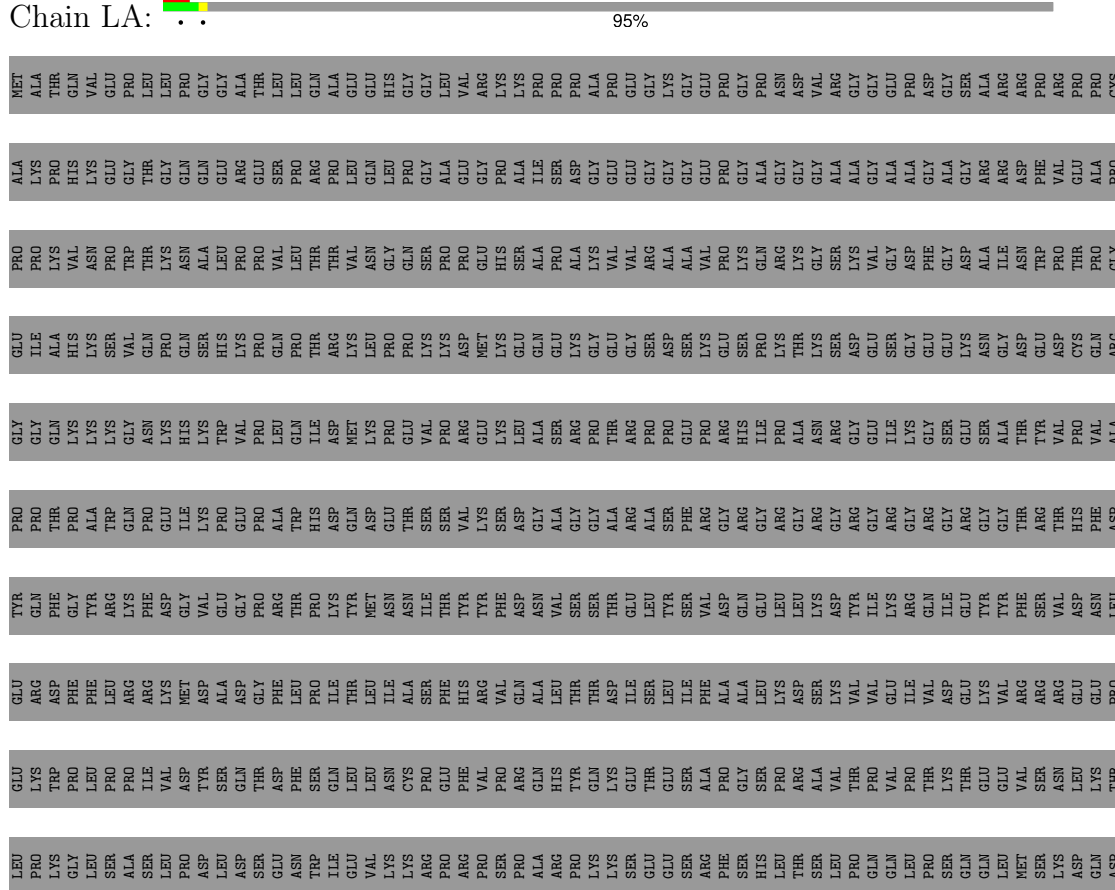


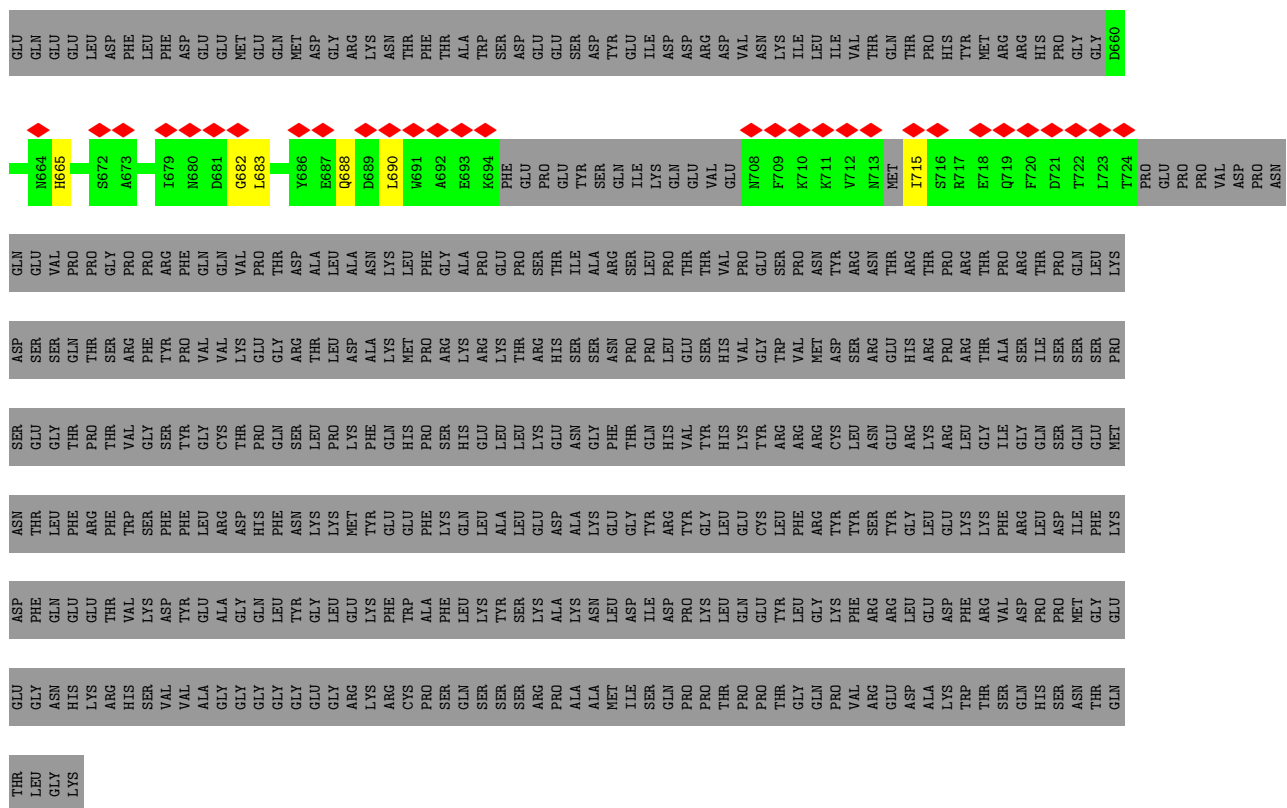
• Molecule 80: Elongation factor 2



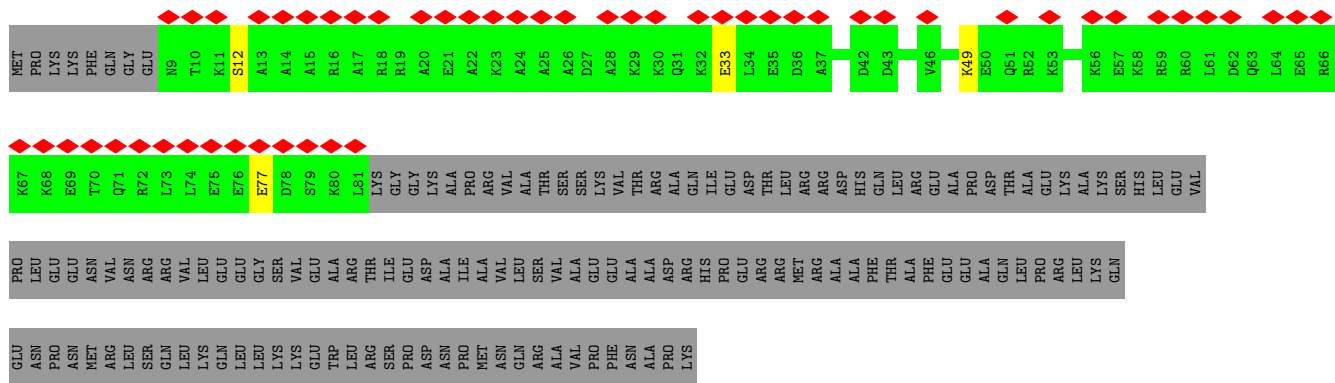


- Molecule 81: La-related protein 1

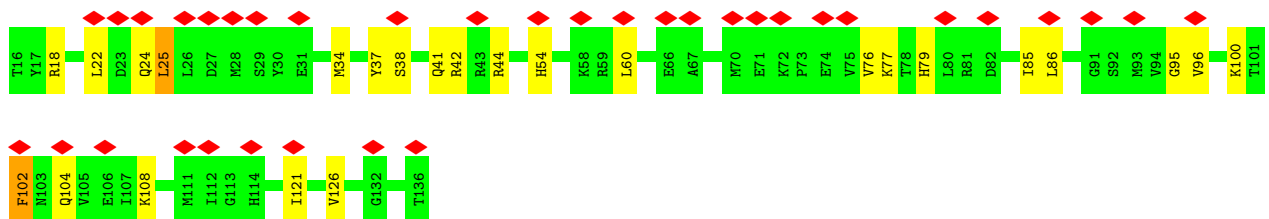
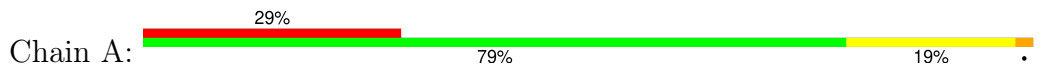
Chain LA: 



- Molecule 82: Coiled-coil domain-containing protein 124



- Molecule 83: Small ribosomal subunit protein uS19



Chain ES:

99%



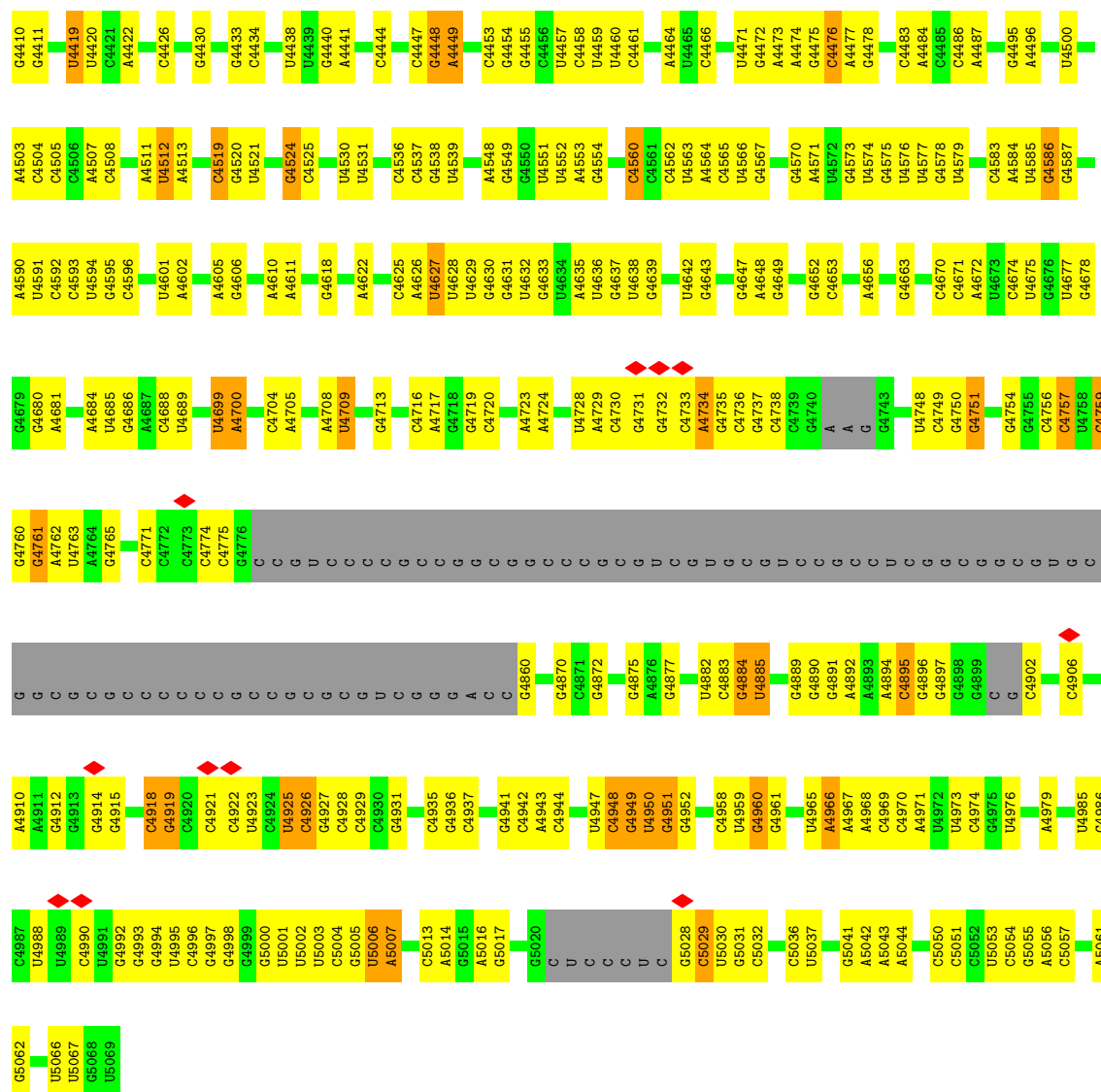




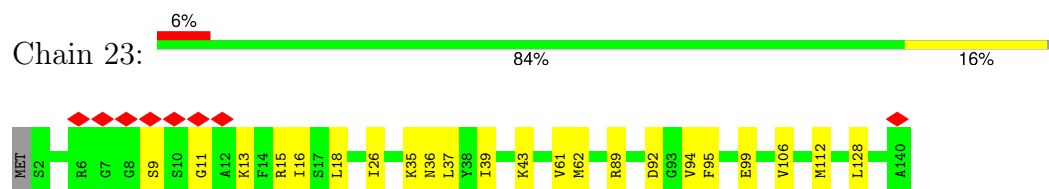








• Molecule 86: Ribosomal protein L23



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	8501	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	26.920	Depositor
Minimum map value	-14.119	Depositor
Average map value	0.004	Depositor
Map value standard deviation	1.115	Depositor
Recommended contour level	3.3	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: ZN, GDP, DDE

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	BB	0.13	0/1747	0.34	0/2374
2	S2	0.13	0/1753	0.31	0/2369
3	PP	0.12	0/643	0.28	0/860
4	DD	0.12	0/1195	0.32	0/1597
5	58	0.13	0/3581	0.29	0/5577
6	6	0.13	0/2858	0.26	0/4455
7	L8	0.13	0/1936	0.32	0/2596
8	L3	0.13	0/3240	0.33	0/4339
9	L4	0.12	0/2937	0.31	0/3946
10	L5	0.13	0/2437	0.32	0/3264
11	L6	0.13	0/1762	0.32	0/2362
12	L7	0.12	0/1911	0.28	0/2549
13	aa	0.14	0/1910	0.33	0/2569
14	10	0.12	0/1702	0.29	0/2272
15	13	0.12	0/1733	0.30	0/2316
16	14	0.14	0/1158	0.33	0/1547
17	15	0.13	0/1746	0.32	0/2338
18	bb	0.13	0/1662	0.31	0/2222
19	17	0.13	0/1268	0.33	0/1700
20	19	0.13	0/1524	0.29	0/2013
21	20	0.13	0/1501	0.28	0/2012
22	21	0.11	0/1326	0.27	0/1770
23	22	0.13	0/823	0.35	0/1104
24	cc	0.12	0/984	0.30	0/1323
25	26	0.12	0/1132	0.31	0/1504
26	27	0.12	0/1130	0.30	0/1507
27	dd	0.13	0/1191	0.33	0/1590
28	29	0.12	0/861	0.29	0/1138
29	30	0.12	0/771	0.27	0/1034
30	31	0.14	0/903	0.33	0/1216
31	32	0.12	0/1071	0.32	0/1429
32	ee	0.13	0/895	0.33	0/1198

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	34	0.13	0/916	0.33	0/1220
34	35	0.12	0/1021	0.31	0/1348
35	36	0.12	0/841	0.29	0/1112
36	37	0.12	0/720	0.34	0/952
37	38	0.11	0/575	0.28	0/761
38	39	0.13	0/459	0.29	0/608
39	40	0.12	0/435	0.28	0/575
40	41	0.13	0/240	0.26	0/305
41	42	0.13	0/864	0.30	0/1140
42	ff	0.12	0/718	0.34	0/953
43	gg	0.12	0/1006	0.29	0/1349
44	AS	0.14	0/1756	0.34	0/2350
45	FF	0.15	0/1226	0.36	0/1649
46	VV	0.13	0/665	0.30	0/891
47	s	0.14	0/1530	0.37	0/2064
48	t	0.16	0/1174	0.43	0/1582
49	F	0.25	1/2845 (0.0%)	0.33	0/3828
50	Q	0.12	0/1538	0.36	0/2054
51	ZZ	0.13	0/567	0.35	0/753
52	EE	0.15	0/918	0.36	0/1233
53	TT	0.29	1/604 (0.2%)	0.39	0/810
54	S5	0.14	0/1492	0.36	0/2005
55	WW	0.11	0/490	0.29	0/656
56	II	0.14	0/1146	0.35	0/1534
57	CC	0.16	0/834	0.41	0/1125
58	AA	0.13	0/2493	0.33	0/3394
59	OO	0.13	0/805	0.33	0/1081
60	MM	0.13	0/1115	0.33	0/1493
61	LL	0.14	0/1208	0.39	0/1618
62	XX	0.12	0/470	0.33	0/623
63	RR	0.13	0/1116	0.35	0/1490
64	SS	0.13	0/1028	0.31	0/1366
65	S6	0.13	0/1946	0.35	1/2590 (0.0%)
66	S4	0.27	1/2118 (0.0%)	0.35	0/2849
67	S9	0.13	0/1550	0.32	0/2069
68	S7	0.13	0/1510	0.34	0/2022
69	YY	0.13	0/447	0.34	0/587
70	S3	0.14	0/1688	0.34	0/2269
71	RS	0.13	0/1082	0.35	0/1452
72	WX	0.14	0/1051	0.34	0/1406
73	S8	0.13	0/1715	0.32	0/2287
74	W	0.13	0/873	0.31	0/1158
75	GG	0.13	0/1020	0.35	0/1369

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	UU	0.12	0/828	0.30	0/1109
77	11	0.12	0/1385	0.31	0/1852
78	L9	0.13	0/1535	0.33	0/2063
79	18	0.13	0/40302	0.31	0/62804
80	v	0.14	0/6577	0.33	0/8883
81	LA	0.12	0/426	0.31	0/568
82	CE	0.16	0/616	0.30	0/812
83	A	0.14	0/1001	0.35	0/1339
84	ES	0.16	0/844	0.40	0/1314
85	28	0.14	0/84014	0.31	0/131028
86	23	0.13	0/1048	0.32	0/1402
All	All	0.14	3/237682 (0.0%)	0.32	1/347244 (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
47	s	0	1
63	RR	0	1
All	All	0	2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
49	F	204	ASN	C-O	10.96	1.29	1.23
66	S4	149	TYR	C-O	-9.98	1.19	1.23
53	TT	62	VAL	CA-CB	6.34	1.57	1.54

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
65	S6	67	VAL	N-CA-C	-6.02	107.99	113.71

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
63	RR	60	LYS	Peptide
47	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	BB	1710	0	1708	27	0
2	S2	1716	0	1806	29	0
3	PP	636	0	637	6	0
4	DD	1175	0	1249	13	0
5	58	3208	0	1629	60	0
6	6	2558	0	1296	38	0
7	L8	1898	0	1993	28	0
8	L3	3172	0	3310	36	0
9	L4	2883	0	3053	27	0
10	L5	2391	0	2424	31	0
11	L6	1729	0	1887	12	0
12	L7	1875	0	1995	29	0
13	aa	1879	0	2027	23	0
14	10	1664	0	1712	17	0
15	13	1702	0	1820	14	0
16	14	1137	0	1211	14	0
17	15	1701	0	1749	21	0
18	bb	1630	0	1778	23	0
19	17	1242	0	1274	10	0
20	19	1508	0	1664	14	0
21	20	1462	0	1508	15	0
22	21	1298	0	1366	11	0
23	22	809	0	833	6	0
24	cc	967	0	1040	12	0
25	26	1115	0	1205	10	0
26	27	1107	0	1182	13	0
27	dd	1162	0	1209	16	0
28	29	848	0	920	6	0
29	30	761	0	794	8	0
30	31	888	0	930	7	0
31	32	1053	0	1147	13	0
32	ee	876	0	912	11	0
33	34	906	0	1000	8	0
34	35	1013	0	1147	8	0
35	36	830	0	916	6	0
36	37	705	0	738	4	0
37	38	569	0	637	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	39	447	0	480	11	0
39	40	429	0	469	3	0
40	41	239	0	289	3	0
41	42	851	0	924	9	0
42	ff	708	0	758	8	0
43	gg	990	0	1044	9	0
44	AS	1729	0	1803	35	0
45	FF	1202	0	1289	16	0
46	VV	651	0	672	3	0
47	s	1507	0	1564	15	0
48	t	1160	0	1218	24	0
49	F	2798	0	2809	41	0
50	Q	1514	0	1634	15	0
51	ZZ	555	0	567	8	0
52	EE	908	0	939	11	0
53	TT	598	0	656	5	0
54	S5	1471	0	1522	21	0
55	WW	488	0	514	4	0
56	II	1128	0	1195	16	0
57	CC	810	0	836	12	0
58	AA	2436	0	2393	36	0
59	OO	795	0	862	11	0
60	MM	1097	0	1132	18	0
61	LL	1190	0	1249	23	0
62	XX	459	0	452	9	0
63	RR	1098	0	1167	19	0
64	SS	1011	0	1083	18	0
65	S6	1923	0	2089	27	0
66	S4	2076	0	2177	23	0
67	S9	1525	0	1640	23	0
68	S7	1488	0	1582	24	0
69	YY	443	0	492	6	0
70	S3	1662	0	1760	27	0
71	RS	1068	0	1121	15	0
72	WX	1034	0	1080	20	0
73	S8	1686	0	1772	20	0
74	W	860	0	903	10	0
75	GG	1007	0	1028	20	0
76	UU	814	0	865	12	0
77	11	1362	0	1399	14	0
78	L9	1516	0	1597	16	0
79	18	36043	0	18202	676	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
80	v	6470	0	6548	75	0
81	LA	421	0	405	2	0
82	CE	613	0	625	2	0
83	A	983	0	1030	11	0
84	ES	756	0	384	21	0
85	28	75105	0	37942	1216	0
86	23	1034	0	1097	12	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	221973	0	168976	3002	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

All (3002) 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)
79:18:639:C:H2'	79:18:640:A:H8	1.33	0.91
85:28:2492:C:H2'	85:28:2493:G:H8	1.36	0.91
79:18:730:C:H2'	79:18:731:G:C8	2.07	0.88
79:18:677:G:H21	79:18:1028:A:H62	1.21	0.87
85:28:2478:C:H2'	85:28:2479:G:H8	1.38	0.86
61:LL:37:GLY:H	79:18:1630:A:H5''	1.41	0.85
85:28:4949:G:H4'	85:28:4950:U:H5'	1.57	0.84
79:18:1410:C:H2'	79:18:1411:G:H8	1.42	0.84
85:28:3717:A:H2'	85:28:3718:A:H8	1.40	0.83
85:28:3751:G:H21	85:28:3775:A:H8	1.22	0.83
85:28:2457:G:H21	85:28:3672:G:H21	1.26	0.83
79:18:957:A:H3'	79:18:958:G:H21	1.42	0.82
85:28:2492:C:H2'	85:28:2493:G:C8	2.14	0.82
85:28:2486:G:H2'	85:28:2487:G:C8	2.14	0.82
57:CC:64:TRP:HB3	62:XX:23:VAL:HA	1.62	0.81
79:18:639:C:H2'	79:18:640:A:C8	2.15	0.81
85:28:4992:G:H2'	85:28:4993:G:C8	2.15	0.81
85:28:2411:C:H2'	85:28:2412:A:H8	1.46	0.80
85:28:4618:G:H5''	86:23:15:ARG:HB3	1.62	0.80
85:28:1538:U:H2'	85:28:1539:G:H8	1.45	0.80
5:58:85:U:H5''	5:58:86:U:H3'	1.65	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
79:18:1536:G:H2'	79:18:1537:A:H8	1.48	0.79
79:18:1004:U:H2'	79:18:1005:G:H8	1.48	0.79
79:18:1776:G:H2'	79:18:1777:G:H8	1.47	0.79
85:28:1970:A:H5''	85:28:1971:U:H5'	1.65	0.79
51:ZZ:132:MET:HG3	51:ZZ:139:HIS:HB3	1.64	0.79
78:L9:43:VAL:HG12	78:L9:59:LYS:HD3	1.66	0.78
85:28:2745:A:H2'	85:28:2746:A:H8	1.48	0.78
79:18:1486:A:H2'	79:18:1487:A:H8	1.45	0.78
85:28:2335:C:H2'	85:28:2336:G:H8	1.48	0.78
85:28:3717:A:H2'	85:28:3718:A:C8	2.19	0.78
85:28:1198:G:H2'	85:28:1199:G:C8	2.19	0.78
85:28:2478:C:H2'	85:28:2479:G:C8	2.19	0.77
79:18:530:U:H2'	79:18:531:A:H8	1.49	0.77
85:28:1327:C:H2'	85:28:1328:G:H8	1.50	0.77
79:18:116:U:H3	79:18:347:G:H1	1.30	0.77
52:EE:32:ALA:HB1	52:EE:37:GLU:HB3	1.66	0.77
79:18:730:C:H2'	79:18:731:G:H8	1.50	0.76
79:18:1221:G:H2'	79:18:1222:G:H8	1.50	0.76
79:18:1711:U:H2'	79:18:1712:A:H8	1.50	0.76
85:28:4967:A:H2'	85:28:4968:A:H8	1.47	0.76
17:15:125:SER:HB3	85:28:3937:C:H1'	1.66	0.76
85:28:1857:C:H2'	85:28:1858:A:H8	1.49	0.76
85:28:2744:A:H2'	85:28:2745:A:C8	2.19	0.76
79:18:1101:U:H2'	79:18:1102:G:H8	1.51	0.76
79:18:1670:C:H2'	79:18:1671:G:C8	2.20	0.76
85:28:2477:A:H2'	85:28:2478:C:C6	2.21	0.76
80:v:17:ALA:HB3	80:v:94:ASP:HB2	1.66	0.76
1:BB:66:VAL:HG21	1:BB:185:MET:HB3	1.66	0.75
85:28:1332:C:H2'	85:28:1333:A:H8	1.47	0.75
33:34:60:ARG:HG3	33:34:61:PRO:HD2	1.69	0.75
79:18:941:C:H2'	79:18:942:G:C8	2.22	0.75
85:28:1769:G:H2'	85:28:1770:A:C8	2.21	0.75
80:v:354:ILE:HG23	80:v:358:LEU:HD12	1.69	0.75
79:18:1098:C:H2'	79:18:1099:G:C8	2.22	0.74
85:28:1169:G:H2'	85:28:1170:G:H8	1.50	0.74
67:S9:5:ARG:HD3	79:18:38:A:H5''	1.69	0.74
79:18:511:U:H2'	79:18:512:A:H8	1.51	0.74
80:v:604:MET:HE3	80:v:704:VAL:HG12	1.68	0.73
66:S4:201:HIS:HB3	66:S4:204:SER:HB3	1.69	0.73
85:28:1461:C:H2'	85:28:1462:A:H8	1.52	0.73
79:18:1711:U:H2'	79:18:1712:A:C8	2.23	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
79:18:894:G:H2'	79:18:895:G:H8	1.54	0.73
58:AA:87:LEU:HB2	58:AA:101:PHE:HB2	1.69	0.73
85:28:4537:C:H2'	85:28:4538:G:H8	1.54	0.73
68:S7:134:VAL:HG13	68:S7:166:VAL:HG21	1.71	0.72
79:18:1144:A:H5'	79:18:1355:C:H41	1.54	0.72
79:18:1244:U:H2'	79:18:1245:G:H8	1.54	0.72
79:18:640:A:H2'	79:18:641:A:C8	2.23	0.72
79:18:1007:C:H2'	79:18:1008:A:C8	2.24	0.72
85:28:3868:G:H22	85:28:3900:G:H1'	1.54	0.72
85:28:4319:C:H2'	85:28:4320:G:H8	1.53	0.72
21:20:147:ASP:HB3	21:20:150:ILE:HB	1.69	0.72
65:S6:58:LYS:HA	65:S6:107:SER:HB2	1.72	0.72
79:18:1776:G:H2'	79:18:1777:G:C8	2.25	0.72
80:v:267:ASP:HA	80:v:285:LEU:HD11	1.72	0.72
79:18:24:C:H2'	79:18:25:A:C8	2.25	0.72
85:28:2480:G:H2'	85:28:2481:G:C8	2.24	0.72
74:W:101:ARG:HA	74:W:104:GLN:HG2	1.71	0.72
79:18:1410:C:H2'	79:18:1411:G:C8	2.24	0.72
80:v:77:LEU:HD21	80:v:351:LEU:HD21	1.72	0.72
85:28:2448:G:H2'	85:28:2449:A:C8	2.25	0.71
85:28:1306:C:H2'	85:28:1307:A:H8	1.53	0.71
80:v:531:ASP:HB3	80:v:534:VAL:HG22	1.72	0.71
84:ES:3238:C:H2'	84:ES:3239:G:H8	1.55	0.71
85:28:4967:A:H2'	85:28:4968:A:C8	2.25	0.71
66:S4:107:GLY:HA2	66:S4:189:LEU:HD23	1.71	0.71
85:28:1414:C:H2'	85:28:1415:G:C8	2.24	0.71
46:VV:14:GLU:HA	46:VV:17:ARG:HD3	1.72	0.71
75:GG:21:VAL:HG22	75:GG:24:GLY:H	1.55	0.71
85:28:963:G:HO2'	85:28:964:A:H8	1.38	0.71
85:28:4274:A:H2'	85:28:4275:G:H8	1.56	0.71
50:Q:67:ILE:HD12	50:Q:96:PRO:HD2	1.73	0.71
70:S3:196:GLY:HA3	70:S3:201:LYS:HE3	1.72	0.71
79:18:1486:A:H2'	79:18:1487:A:C8	2.26	0.70
79:18:1536:G:H2'	79:18:1537:A:C8	2.27	0.70
85:28:1942:A:H2'	85:28:1943:A:C8	2.25	0.70
13:aa:111:PRO:HD2	13:aa:114:ILE:HD12	1.73	0.70
85:28:2707:U:H3'	85:28:2708:U:H5''	1.73	0.70
85:28:4134:C:H2'	85:28:4135:G:H8	1.56	0.70
85:28:4321:U:H2'	85:28:4322:G:C8	2.26	0.70
63:RR:61:GLN:HB3	63:RR:62:PRO:HD3	1.74	0.70
66:S4:163:ASP:HB3	66:S4:166:THR:HG22	1.71	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:28:2520:C:H2'	85:28:2521:G:H8	1.55	0.70
66:S4:11:ARG:HA	66:S4:28:ALA:HB2	1.73	0.70
19:17:118:GLN:HE22	85:28:423:G:H21	1.36	0.70
79:18:58:C:H5''	79:18:499:G:H21	1.55	0.70
79:18:1010:G:H2'	79:18:1011:A:C8	2.27	0.70
24:cc:93:ASN:HB3	24:cc:95:THR:HG23	1.74	0.70
49:F:190:LEU:HB2	49:F:223:VAL:HG23	1.74	0.70
79:18:300:U:H2'	79:18:301:A:C8	2.27	0.70
85:28:4896:G:H2'	85:28:4897:G:H8	1.56	0.70
85:28:1086:C:H2'	85:28:1087:A:H8	1.57	0.70
85:28:1344:C:H2'	85:28:1345:A:H8	1.54	0.69
66:S4:146:THR:HB	79:18:123:G:H1'	1.74	0.69
80:v:464:VAL:HG11	80:v:470:VAL:HG11	1.74	0.69
7:L8:234:LYS:HG2	7:L8:238:ILE:HD12	1.72	0.69
79:18:126:G:H21	79:18:180:G:H21	1.40	0.69
79:18:640:A:H2'	79:18:641:A:H8	1.55	0.69
84:ES:3239:G:H2'	84:ES:3240:A:H8	1.57	0.69
85:28:1327:C:H2'	85:28:1328:G:C8	2.27	0.69
85:28:2607:C:H2'	85:28:2608:G:H8	1.56	0.69
84:ES:2946:G:H2'	84:ES:2947:G:C8	2.28	0.69
85:28:4761:G:H2'	85:28:4762:A:H8	1.56	0.69
57:CC:61:GLN:HB3	57:CC:68:TYR:HB2	1.75	0.69
49:F:159:PRO:HD3	49:F:325:LEU:HD11	1.75	0.69
79:18:941:C:H2'	79:18:942:G:H8	1.58	0.69
85:28:1193:C:H2'	85:28:1194:G:C8	2.28	0.69
20:19:162:ARG:HB3	79:18:873:G:H5'	1.74	0.68
49:F:57:MET:HE3	49:F:74:ILE:HG13	1.74	0.68
80:v:488:PHE:HB3	80:v:491:ALA:HB2	1.74	0.68
79:18:75:G:H21	79:18:77:A:H5''	1.59	0.68
79:18:122:G:H2'	79:18:123:G:H8	1.58	0.68
85:28:710:G:H2'	85:28:711:A:H8	1.57	0.68
79:18:1101:U:H2'	79:18:1102:G:C8	2.28	0.68
66:S4:31:PRO:HG3	66:S4:43:PRO:HG3	1.75	0.68
79:18:389:A:H2'	79:18:390:C:C6	2.28	0.68
49:F:57:MET:HE1	49:F:73:GLY:HA2	1.74	0.68
79:18:1424:G:H2'	79:18:1425:G:H8	1.58	0.68
85:28:1198:G:H2'	85:28:1199:G:H8	1.57	0.68
79:18:1010:G:H2'	79:18:1011:A:H8	1.59	0.68
64:SS:108:LYS:HD3	79:18:53:C:H4'	1.75	0.68
85:28:1197:C:H2'	85:28:1198:G:C8	2.29	0.68
47:s:13:TYR:HA	47:s:16:LYS:HG2	1.75	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
79:18:981:A:H2'	79:18:982:G:C8	2.28	0.67
85:28:2486:G:H2'	85:28:2487:G:H8	1.59	0.67
31:32:90:MET:HG3	43:gg:33:LYS:HA	1.76	0.67
45:FF:136:PRO:HG2	45:FF:139:TRP:HB2	1.76	0.67
78:L9:12:ILE:HG22	78:L9:81:ILE:HD11	1.76	0.67
85:28:2411:C:H2'	85:28:2412:A:C8	2.30	0.67
85:28:2485:U:H2'	85:28:2486:G:C8	2.29	0.67
85:28:4992:G:H2'	85:28:4993:G:H8	1.59	0.67
57:CC:64:TRP:HE1	70:S3:23:GLU:HG2	1.60	0.67
79:18:110:U:H2'	79:18:111:A:C8	2.28	0.67
85:28:3848:U:H2'	85:28:3849:A:H8	1.59	0.67
10:L5:4:VAL:HG11	85:28:4247:G:H5''	1.76	0.67
49:F:29:ASN:HD21	49:F:334:THR:HA	1.59	0.67
49:F:176:SER:HB3	49:F:350:GLN:H	1.60	0.67
85:28:4274:A:H2'	85:28:4275:G:C8	2.28	0.67
26:27:103:ASP:HB3	26:27:106:LEU:HB2	1.75	0.67
69:YY:113:ARG:HG3	69:YY:114:ARG:HG3	1.77	0.67
70:S3:37:VAL:HG12	70:S3:50:ILE:HA	1.75	0.67
10:L5:83:LEU:HB3	10:L5:88:VAL:HB	1.77	0.67
79:18:874:G:H2'	79:18:875:A:H8	1.60	0.67
85:28:1669:A:H4'	85:28:1685:G:N2	2.09	0.67
85:28:1683:U:H2'	85:28:1684:A:C8	2.30	0.67
85:28:4239:A:H2'	85:28:4240:G:C8	2.30	0.67
79:18:1221:G:H2'	79:18:1222:G:C8	2.28	0.67
85:28:2015:U:H2'	85:28:2016:C:H6	1.60	0.67
11:L6:165:VAL:HG13	11:L6:180:GLY:N	2.09	0.66
14:10:87:ILE:HG12	14:10:138:ILE:HG12	1.78	0.66
49:F:255:TYR:HB3	49:F:301:LEU:HD21	1.75	0.66
79:18:14:C:H2'	79:18:15:U:C6	2.30	0.66
85:28:1503:A:H1'	85:28:1504:G:C8	2.30	0.66
79:18:1692:U:H2'	79:18:1693:G:C8	2.30	0.66
5:58:67:U:H2'	5:58:68:G:H8	1.59	0.66
26:27:59:LYS:HA	26:27:62:ILE:HB	1.77	0.66
85:28:1512:G:H2'	85:28:1513:U:H6	1.61	0.66
85:28:3684:G:H2'	85:28:3685:C:C6	2.30	0.66
60:MM:124:THR:HG23	60:MM:127:GLY:H	1.60	0.66
85:28:1190:C:H2'	85:28:1191:C:C6	2.31	0.66
44:AS:110:MET:HA	44:AS:113:MET:HE2	1.78	0.66
75:GG:61:LYS:HB3	75:GG:76:LEU:HD12	1.76	0.66
79:18:1705:C:H2'	79:18:1706:G:C8	2.31	0.66
85:28:3610:A:H2'	85:28:3611:A:H8	1.61	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:28:175:C:H2'	85:28:176:G:H8	1.61	0.66
85:28:1414:C:H2'	85:28:1415:G:H8	1.60	0.66
85:28:1683:U:H2'	85:28:1684:A:H8	1.61	0.66
85:28:1769:G:H2'	85:28:1770:A:H8	1.60	0.66
42:ff:17:ARG:HH22	85:28:1578:U:H5''	1.60	0.66
58:AA:17:TRP:HA	58:AA:305:ASN:HA	1.76	0.66
7:L8:137:ILE:HD11	7:L8:149:LYS:HB3	1.78	0.65
50:Q:78:LYS:HG2	50:Q:137:VAL:HG23	1.78	0.65
79:18:28:U:H2'	79:18:29:G:H8	1.60	0.65
85:28:4239:A:H2'	85:28:4240:G:H8	1.61	0.65
53:TT:48:VAL:HG23	53:TT:49:LEU:HG	1.78	0.65
80:v:746:LEU:HB2	80:v:815:ASP:HB2	1.78	0.65
79:18:1125:C:H2'	79:18:1126:G:H8	1.61	0.65
79:18:1198:G:H2'	79:18:1199:A:C8	2.32	0.65
85:28:2413:U:H2'	85:28:2414:G:H8	1.61	0.65
85:28:2845:A:H61	85:28:3843:C:H42	1.42	0.65
85:28:3893:C:H2'	85:28:3894:A:H8	1.62	0.65
31:32:104:SER:HB2	85:28:2303:C:H5''	1.77	0.65
85:28:1344:C:H2'	85:28:1345:A:C8	2.32	0.65
11:L6:165:VAL:HG11	11:L6:178:VAL:HG13	1.79	0.65
85:28:1093:C:H2'	85:28:1094:G:H8	1.62	0.65
63:RR:24:ASP:HB3	63:RR:27:TYR:HB3	1.79	0.65
68:S7:144:ILE:HB	72:WX:52:ILE:HB	1.79	0.65
85:28:1332:C:H2'	85:28:1333:A:C8	2.30	0.65
85:28:3721:U:H2'	85:28:3722:G:H8	1.62	0.65
17:15:14:LYS:HE2	85:28:280:G:H5''	1.79	0.64
36:37:33:THR:HG22	36:37:40:PRO:HG2	1.79	0.64
84:ES:2943:C:H2'	84:ES:2944:G:H8	1.62	0.64
85:28:4260:U:H2'	85:28:4261:C:C6	2.32	0.64
85:28:3893:C:H2'	85:28:3894:A:C8	2.32	0.64
16:14:40:GLY:HA3	16:14:45:VAL:HB	1.79	0.64
85:28:983:U:H2'	85:28:984:C:C6	2.33	0.64
24:cc:83:THR:HG21	85:28:2434:G:H4'	1.79	0.64
50:Q:178:ARG:HA	50:Q:184:ARG:HB3	1.78	0.64
79:18:152:U:H2'	79:18:153:G:C8	2.32	0.64
85:28:3598:C:H2'	85:28:3599:A:C8	2.33	0.64
79:18:894:G:H2'	79:18:895:G:C8	2.31	0.64
79:18:1125:C:H2'	79:18:1126:G:C8	2.33	0.64
79:18:1854:U:H2'	79:18:1855:G:H8	1.62	0.64
85:28:3911:C:H2'	85:28:3912:U:H6	1.63	0.64
5:58:19:C:H2'	5:58:20:A:C8	2.33	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:15:67:ARG:HD2	85:28:2458:C:H5''	1.80	0.64
79:18:121:U:H2'	79:18:122:G:C8	2.33	0.64
85:28:3598:C:H2'	85:28:3599:A:H8	1.63	0.64
49:F:333:ILE:HG23	49:F:334:THR:HG23	1.80	0.64
67:S9:136:ARG:HE	67:S9:139:LYS:HA	1.63	0.64
79:18:374:G:H2'	79:18:375:U:C6	2.33	0.64
85:28:1358:G:N2	85:28:1381:U:O4	2.31	0.64
79:18:389:A:H2'	79:18:390:C:H6	1.62	0.63
79:18:1217:A:H2'	79:18:1218:C:C6	2.33	0.63
79:18:1845:A:H2'	79:18:1846:G:C8	2.32	0.63
85:28:1942:A:H2'	85:28:1943:A:H8	1.63	0.63
1:BB:34:MET:HE3	1:BB:154:LEU:HD11	1.79	0.63
5:58:19:C:H2'	5:58:20:A:H8	1.63	0.63
78:L9:94:SER:HB3	78:L9:142:ASP:HB3	1.80	0.63
8:L3:13:SER:HB2	85:28:4622:A:H4'	1.80	0.63
68:S7:143:ARG:HB2	68:S7:155:LYS:HB2	1.79	0.63
79:18:928:G:H1	79:18:1013:U:H3	1.46	0.63
85:28:2480:G:H2'	85:28:2481:G:H8	1.63	0.63
85:28:3619:G:H22	85:28:3624:A:H1'	1.63	0.63
85:28:3917:A:H2'	85:28:3918:G:H8	1.63	0.63
27:dd:36:GLY:HA2	27:dd:39:HIS:HB2	1.79	0.63
84:ES:2945:C:H2'	84:ES:2946:G:H8	1.63	0.63
49:F:118:ILE:HG13	49:F:195:ILE:HG22	1.81	0.63
85:28:1402:C:H2'	85:28:1403:G:C8	2.34	0.63
2:S2:167:ARG:HB2	2:S2:177:PRO:HB2	1.81	0.63
23:22:28:PRO:HB2	23:22:34:MET:HG2	1.79	0.63
70:S3:35:SER:HA	70:S3:99:ILE:HG13	1.81	0.63
79:18:454:U:H2'	79:18:455:A:H8	1.64	0.63
79:18:804:U:H2'	79:18:805:U:C6	2.33	0.63
85:28:4504:C:H2'	85:28:4505:C:C6	2.33	0.63
72:WX:6:VAL:HG12	72:WX:34:ILE:HD11	1.81	0.63
85:28:4774:C:H2'	85:28:4775:C:C6	2.34	0.63
79:18:677:G:N2	79:18:1028:A:H62	1.96	0.63
80:v:119:LEU:HD21	80:v:146:ALA:HA	1.79	0.63
84:ES:2943:C:H2'	84:ES:2944:G:C8	2.34	0.63
79:18:106:C:H2'	79:18:107:A:H8	1.62	0.62
79:18:729:C:H2'	79:18:730:C:C6	2.34	0.62
79:18:940:U:H3	79:18:1002:U:H3	1.45	0.62
85:28:1503:A:H4'	85:28:1504:G:H5'	1.81	0.62
85:28:4095:G:H22	85:28:4113:U:H3	1.47	0.62
85:28:517:C:H2'	85:28:518:G:H8	1.63	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:13:62:PRO:HG3	85:28:74:G:H1'	1.81	0.62
70:S3:70:THR:HG22	70:S3:86:LEU:HD13	1.80	0.62
85:28:3736:A:H2'	85:28:3737:A:H8	1.63	0.62
49:F:187:SER:HB3	49:F:201:ILE:HB	1.81	0.62
4:DD:126:VAL:HG22	4:DD:145:VAL:HG22	1.81	0.62
79:18:878:G:C2	79:18:879:C:H1'	2.35	0.62
85:28:3736:A:H2'	85:28:3737:A:C8	2.34	0.62
85:28:4680:G:H2'	85:28:4681:A:C8	2.35	0.62
79:18:1714:U:H2'	79:18:1715:A:C8	2.34	0.62
15:13:8:MET:HG3	50:Q:166:TYR:HB3	1.82	0.62
17:15:104:GLU:HA	17:15:160:GLU:HG3	1.82	0.62
68:S7:46:THR:HG23	68:S7:65:PRO:HG3	1.82	0.62
85:28:1382:G:H2'	85:28:1383:G:H8	1.65	0.62
85:28:1984:A:H2'	85:28:2011:C:H5'	1.80	0.62
85:28:3910:C:H2'	85:28:3911:C:H6	1.65	0.62
2:S2:102:LEU:HD21	2:S2:130:ILE:HD11	1.81	0.62
9:L4:60:HIS:HE1	9:L4:100:ARG:HD3	1.64	0.62
55:WW:12:ALA:HA	55:WW:34:PHE:HA	1.81	0.62
75:GG:101:GLY:HA3	75:GG:134:PRO:HG2	1.82	0.62
85:28:233:U:H2'	85:28:234:G:C8	2.35	0.62
85:28:1307:A:H2'	85:28:1308:C:H6	1.65	0.62
12:L7:46:ARG:NH1	85:28:976:C:H5''	2.15	0.61
63:RR:91:LEU:HB3	69:YY:82:VAL:HG21	1.82	0.61
79:18:1128:C:H2'	79:18:1129:G:H8	1.63	0.61
85:28:2745:A:H2'	85:28:2746:A:C8	2.34	0.61
85:28:5030:U:H2'	85:28:5031:G:H8	1.65	0.61
44:AS:86:LEU:HB3	44:AS:98:THR:HB	1.81	0.61
79:18:1845:A:H2'	79:18:1846:G:H8	1.65	0.61
84:ES:3244:U:H2'	84:ES:3245:G:H8	1.63	0.61
85:28:1093:C:H2'	85:28:1094:G:C8	2.35	0.61
85:28:1073:G:H1	85:28:1238:A:H2	1.47	0.61
85:28:1326:A:H2'	85:28:1327:C:C6	2.36	0.61
80:v:72:SER:HB3	80:v:106:PRO:HD3	1.82	0.61
85:28:469:C:H2'	85:28:470:A:H8	1.65	0.61
85:28:1341:U:H2'	85:28:1342:A:H8	1.64	0.61
58:AA:197:THR:HG21	58:AA:238:ALA:HA	1.82	0.61
59:OO:40:ILE:HD11	59:OO:53:PRO:HG3	1.83	0.61
79:18:441:C:H41	79:18:448:A:H1'	1.66	0.61
85:28:651:C:H2'	85:28:652:G:H8	1.64	0.61
85:28:1857:C:H2'	85:28:1858:A:C8	2.33	0.61
85:28:3664:G:H2'	85:28:3665:G:H8	1.66	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:28:3848:U:H2'	85:28:3849:A:C8	2.35	0.61
25:26:30:MET:HB3	25:26:101:PRO:HG2	1.83	0.61
79:18:874:G:H2'	79:18:875:A:C8	2.36	0.61
83:A:34:MET:HB3	83:A:42:ARG:HG3	1.81	0.61
85:28:93:G:H2'	85:28:94:A:C8	2.36	0.61
85:28:4993:G:H2'	85:28:4994:G:H8	1.66	0.61
85:28:440:U:H2'	85:28:441:G:H8	1.65	0.61
85:28:2607:C:H2'	85:28:2608:G:C8	2.35	0.61
28:29:3:LYS:HD3	85:28:4194:U:H3'	1.83	0.61
85:28:1964:A:C8	85:28:1965:G:C8	2.89	0.61
85:28:3861:A:H2'	85:28:3862:A:H8	1.64	0.61
74:W:24:THR:HG23	86:23:99:GLU:HB3	1.82	0.61
79:18:418:A:H3'	79:18:419:G:H8	1.64	0.61
85:28:1358:G:C2	85:28:1381:U:O4	2.53	0.61
85:28:1749:A:H2'	85:28:1750:G:H8	1.66	0.61
85:28:4448:G:H5''	85:28:4449:A:H5''	1.83	0.61
54:S5:39:ILE:HG23	54:S5:68:ILE:HG21	1.83	0.61
68:S7:157:HIS:HB3	68:S7:190:PRO:HG3	1.83	0.60
79:18:382:C:H2'	79:18:383:G:H8	1.65	0.60
79:18:952:G:H2'	79:18:953:C:C6	2.35	0.60
85:28:3910:C:H2'	85:28:3911:C:C6	2.36	0.60
79:18:1797:U:H2'	79:18:1798:C:C6	2.37	0.60
79:18:556:U:H2'	79:18:557:U:H6	1.66	0.60
80:v:666:THR:HG22	80:v:706:ASP:HA	1.83	0.60
85:28:1338:G:H4'	85:28:1339:U:H6	1.66	0.60
85:28:4637:G:H2'	85:28:4638:U:C6	2.37	0.60
48:t:80:LEU:HA	48:t:83:LYS:HG2	1.82	0.60
57:CC:64:TRP:NE1	70:S3:23:GLU:HG2	2.15	0.60
73:S8:110:ARG:HG3	73:S8:121:LEU:HB3	1.83	0.60
27:dd:21:ARG:HG3	85:28:2282:A:H4'	1.82	0.60
61:LL:84:LEU:HB2	61:LL:87:GLN:HG2	1.84	0.60
85:28:1307:A:H2'	85:28:1308:C:C6	2.35	0.60
29:30:105:ILE:HD12	29:30:106:ARG:HG3	1.82	0.60
44:AS:189:ILE:HB	44:AS:190:PRO:HD3	1.82	0.60
79:18:1004:U:H2'	79:18:1005:G:C8	2.34	0.60
4:DD:77:VAL:HA	4:DD:88:ILE:HG22	1.84	0.60
19:17:114:ILE:HD11	19:17:117:ILE:HB	1.84	0.60
79:18:381:C:H2'	79:18:382:C:C6	2.37	0.60
84:ES:3238:C:H2'	84:ES:3239:G:C8	2.36	0.60
85:28:1169:G:H2'	85:28:1170:G:C8	2.36	0.60
85:28:1436:C:H42	85:28:1448:G:H1	1.49	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:S2:190:SER:HB2	79:18:1143:A:H5'	1.83	0.60
44:AS:141:GLY:HA2	44:AS:210:VAL:HG22	1.84	0.60
76:UU:12:LYS:HG3	76:UU:15:ARG:HB2	1.82	0.60
85:28:4970:C:C2	85:28:4971:A:C8	2.89	0.60
5:58:148:A:H2'	5:58:149:G:C8	2.36	0.60
8:L3:240:LEU:HB3	8:L3:244:THR:HG21	1.84	0.60
65:S6:14:LYS:HB2	65:S6:124:LEU:HD11	1.84	0.60
67:S9:164:PRO:HG3	79:18:561:A:H5''	1.83	0.60
79:18:318:A:H3'	79:18:319:C:H5''	1.84	0.60
85:28:1461:C:H2'	85:28:1462:A:C8	2.34	0.60
85:28:1204:C:H2'	85:28:1205:G:H8	1.66	0.60
13:aa:139:VAL:HG11	13:aa:238:LYS:HD2	1.84	0.59
27:dd:38:MET:HA	27:dd:42:ARG:HE	1.67	0.59
79:18:115:U:H2'	79:18:116:U:C6	2.37	0.59
14:10:61:SER:HA	14:10:126:VAL:HG23	1.83	0.59
16:14:96:GLU:HA	16:14:99:GLU:HG2	1.85	0.59
44:AS:91:VAL:HG12	44:AS:93:GLY:H	1.67	0.59
79:18:912:C:H3'	79:18:913:A:H5''	1.83	0.59
85:28:1512:G:H2'	85:28:1513:U:C6	2.37	0.59
5:58:65:A:H2'	5:58:66:A:H8	1.67	0.59
8:L3:56:ILE:O	8:L3:73:VAL:HA	2.02	0.59
17:15:75:VAL:HG23	17:15:78:GLY:HA2	1.85	0.59
79:18:107:A:H2'	79:18:108:G:C8	2.37	0.59
85:28:2640:G:H2'	85:28:2641:A:H8	1.66	0.59
19:17:118:GLN:NE2	85:28:423:G:H21	2.00	0.59
79:18:1736:G:H2'	79:18:1737:G:C8	2.38	0.59
3:PP:32:ILE:HD12	3:PP:55:ILE:HB	1.83	0.59
53:TT:71:ALA:HB1	54:S5:167:LYS:HA	1.84	0.59
78:L9:107:GLU:HG3	78:L9:110:SER:HB2	1.83	0.59
65:S6:50:VAL:HG12	65:S6:113:ILE:HD13	1.85	0.59
66:S4:162:ILE:HG22	66:S4:169:ILE:HA	1.85	0.59
79:18:16:G:H2'	79:18:17:C:C6	2.38	0.59
79:18:556:U:H2'	79:18:557:U:C6	2.37	0.59
83:A:22:LEU:HA	83:A:25:LEU:HD23	1.85	0.59
85:28:1317:U:H2'	85:28:1318:C:C6	2.37	0.59
85:28:4344:U:H2'	85:28:4345:C:C6	2.38	0.59
74:W:104:GLN:O	74:W:107:GLN:HG3	2.02	0.59
79:18:1007:C:H2'	79:18:1008:A:H8	1.68	0.59
79:18:1008:A:H2'	79:18:1009:A:C8	2.38	0.59
85:28:4091:G:H2'	85:28:4092:G:H8	1.67	0.59
26:27:54:THR:H	26:27:57:MET:HE2	1.67	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
79:18:1714:U:H2'	79:18:1715:A:H8	1.68	0.59
8:L3:224:LYS:HG2	8:L3:340:THR:HB	1.85	0.59
12:L7:227:VAL:HA	21:20:39:VAL:HG12	1.85	0.59
71:RS:28:PHE:HA	71:RS:55:THR:HG21	1.85	0.59
79:18:1008:A:H2'	79:18:1009:A:H8	1.67	0.59
80:v:266:PHE:HB2	80:v:288:THR:HG22	1.83	0.59
85:28:2409:U:H4'	85:28:2428:A:H4'	1.85	0.59
85:28:4458:C:H2'	85:28:4459:U:C6	2.38	0.59
79:18:1513:C:H2'	79:18:1514:G:H8	1.68	0.59
85:28:1298:C:H2'	85:28:1299:G:H8	1.67	0.59
85:28:1524:A:H61	85:28:1651:G:H22	1.51	0.59
60:MM:71:GLY:HA3	79:18:1562:C:H5''	1.84	0.58
85:28:1088:C:H2'	85:28:1089:G:H8	1.67	0.58
85:28:4319:C:H2'	85:28:4320:G:C8	2.37	0.58
73:S8:29:LEU:HD13	79:18:448:A:H62	1.67	0.58
78:L9:120:GLU:HG2	85:28:4611:A:H2	1.69	0.58
79:18:112:U:H2'	79:18:115:U:H5	1.68	0.58
80:v:692:LEU:HD11	80:v:738:PRO:HB2	1.84	0.58
85:28:2413:U:H2'	85:28:2414:G:C8	2.38	0.58
85:28:4080:C:H2'	85:28:4081:G:H8	1.69	0.58
8:L3:56:ILE:HD12	8:L3:365:LEU:HD22	1.86	0.58
15:13:59:VAL:HG22	85:28:74:G:H5'	1.86	0.58
79:18:121:U:H2'	79:18:122:G:H8	1.68	0.58
79:18:1545:A:H2'	79:18:1546:G:C8	2.37	0.58
85:28:300:A:H2'	85:28:301:G:H8	1.68	0.58
85:28:713:C:H2'	85:28:714:G:H8	1.68	0.58
85:28:907:C:H2'	85:28:908:G:H8	1.68	0.58
85:28:1893:C:H1'	85:28:1937:C:O2	2.03	0.58
85:28:2870:A:H2'	85:28:2871:A:H8	1.68	0.58
79:18:1382:A:H2'	79:18:1383:A:C8	2.37	0.58
85:28:2528:G:H4'	85:28:2783:A:H4'	1.86	0.58
50:Q:59:PRO:HG3	50:Q:143:ARG:HA	1.85	0.58
84:ES:2945:C:H2'	84:ES:2946:G:C8	2.37	0.58
4:DD:93:LEU:HB3	4:DD:102:PHE:HB3	1.86	0.58
10:L5:64:ILE:HG13	10:L5:105:LEU:HD21	1.85	0.58
11:L6:156:LEU:HD11	11:L6:198:ILE:HG13	1.85	0.58
18:bb:185:VAL:HG22	18:bb:188:LYS:HB3	1.85	0.58
49:F:80:ILE:HG12	49:F:108:ILE:HG12	1.85	0.58
79:18:314:U:H2'	79:18:315:C:C6	2.39	0.58
13:aa:136:PHE:HB3	13:aa:212:HIS:HB2	1.85	0.58
79:18:514:U:H2'	79:18:515:G:O4'	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
79:18:1280:G:H2'	79:18:1281:G:C8	2.39	0.58
85:28:679:C:H2'	85:28:680:G:H8	1.69	0.58
76:UU:43:ASN:HA	76:UU:66:LYS:HA	1.84	0.58
79:18:93:U:H2'	79:18:94:G:O4'	2.04	0.58
85:28:667:A:H5''	85:28:668:C:H5	1.69	0.58
85:28:3911:C:H2'	85:28:3912:U:C6	2.38	0.58
85:28:3916:G:H2'	85:28:3917:A:C8	2.38	0.58
67:S9:172:ARG:HH12	79:18:586:G:H3'	1.69	0.58
79:18:418:A:H3'	79:18:419:G:C8	2.39	0.58
79:18:1777:G:H2'	79:18:1778:C:H6	1.68	0.58
72:WX:88:LYS:HE2	79:18:419:G:H4'	1.86	0.58
79:18:1201:U:H2'	79:18:1202:U:C6	2.39	0.58
84:ES:3244:U:H2'	84:ES:3245:G:C8	2.39	0.58
85:28:3796:U:H2'	85:28:3797:C:C6	2.38	0.58
85:28:4537:C:H2'	85:28:4538:G:C8	2.37	0.58
85:28:4736:C:H2'	85:28:4737:G:H8	1.69	0.58
86:23:9:SER:HB2	86:23:128:LEU:HD12	1.86	0.58
56:II:12:VAL:HG21	56:II:91:ALA:HA	1.86	0.57
65:S6:2:LYS:HB3	65:S6:15:LEU:HD11	1.86	0.57
67:S9:108:ARG:HA	67:S9:113:GLN:HE21	1.69	0.57
79:18:79:A:H3'	79:18:80:G:H8	1.69	0.57
85:28:2521:G:H2'	85:28:2522:G:H8	1.68	0.57
85:28:3684:G:H2'	85:28:3685:C:H6	1.68	0.57
2:S2:78:LEU:HD23	2:S2:78:LEU:H	1.69	0.57
25:26:11:ARG:HG3	85:28:229:G:H5''	1.85	0.57
58:AA:128:THR:HG22	58:AA:143:GLN:HA	1.86	0.57
68:S7:51:ILE:HD11	68:S7:176:VAL:HG22	1.85	0.57
79:18:1494:U:H4'	79:18:1495:G:H5''	1.86	0.57
79:18:1801:A:H2'	79:18:1802:C:H6	1.67	0.57
85:28:4577:U:H2'	85:28:4578:G:H8	1.69	0.57
49:F:202:ILE:HG12	49:F:205:PRO:HB3	1.86	0.57
49:F:351:ASP:HB3	49:F:354:LEU:HD21	1.86	0.57
58:AA:10:THR:HB	58:AA:306:LEU:HD11	1.85	0.57
80:v:649:ILE:HG22	80:v:663:THR:HG22	1.86	0.57
85:28:2566:G:H2'	85:28:2567:G:C8	2.39	0.57
85:28:4232:U:H4'	85:28:4233:A:O5'	2.04	0.57
85:28:5006:U:H4'	85:28:5007:A:H5'	1.86	0.57
5:58:153:C:H2'	5:58:154:G:H8	1.70	0.57
29:30:38:ILE:HG21	29:30:63:TYR:HB3	1.85	0.57
79:18:1130:G:C8	79:18:1131:G:C8	2.93	0.57
79:18:1382:A:H2'	79:18:1383:A:H8	1.69	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:28:3932:U:H2'	85:28:3933:G:H8	1.69	0.57
85:28:4260:U:H2'	85:28:4261:C:H6	1.68	0.57
47:s:180:ILE:HG12	47:s:182:PRO:HD3	1.85	0.57
79:18:643:A:H4'	79:18:644:G:H5'	1.86	0.57
85:28:2373:C:H2'	85:28:2374:A:H8	1.68	0.57
85:28:2706:G:H2'	85:28:2708:U:H5'	1.85	0.57
9:L4:343:GLN:HG2	85:28:724:C:H1'	1.85	0.57
26:27:46:ILE:HD11	26:27:49:TYR:HA	1.86	0.57
73:S8:129:LEU:HG	73:S8:131:PRO:HD2	1.86	0.57
79:18:1737:G:H1	79:18:1797:U:H3	1.53	0.57
79:18:1801:A:H2'	79:18:1802:C:C6	2.40	0.57
80:v:820:LEU:HD12	80:v:821:PRO:HD2	1.86	0.57
85:28:673:C:H2'	85:28:674:G:H8	1.69	0.57
85:28:1505:C:H2'	85:28:1506:G:H8	1.69	0.57
2:S2:166:ARG:HB3	2:S2:247:THR:HB	1.86	0.57
9:L4:190:ARG:HD2	9:L4:194:GLY:HA3	1.87	0.57
32:ee:54:LYS:HE2	85:28:4748:U:H5''	1.87	0.57
44:AS:25:PHE:HA	44:AS:28:LYS:HG2	1.87	0.57
79:18:1637:A:H4'	79:18:1638:G:O5'	2.04	0.57
85:28:2493:G:H2'	85:28:2494:U:H6	1.69	0.57
85:28:4577:U:H2'	85:28:4578:G:C8	2.39	0.57
18:bb:60:LYS:HE2	85:28:2046:G:H5'	1.87	0.57
79:18:931:C:H2'	79:18:932:G:C8	2.39	0.57
85:28:2568:C:H2'	85:28:2569:G:C8	2.40	0.57
85:28:2568:C:H2'	85:28:2569:G:H8	1.69	0.57
60:MM:42:HIS:HB3	60:MM:93:SER:HB3	1.85	0.57
75:GG:31:CYS:HB3	75:GG:44:VAL:HG22	1.87	0.57
79:18:942:G:H2'	79:18:943:U:C6	2.40	0.57
85:28:163:A:H2'	85:28:164:G:H8	1.68	0.57
85:28:922:C:H2'	85:28:922(A):G:H8	1.70	0.57
85:28:4173:G:H2'	85:28:4174:U:C6	2.40	0.57
15:13:62:PRO:O	85:28:71:C:H1'	2.05	0.57
48:t:146:ARG:HB3	48:t:148:PRO:HD2	1.86	0.57
65:S6:121:ILE:HD12	65:S6:122:PRO:HD2	1.85	0.57
68:S7:87:PHE:HB3	68:S7:90:LYS:HD3	1.86	0.57
79:18:528:A:H2'	79:18:529:A:H8	1.69	0.57
79:18:1337:C:H2'	79:18:1338:G:H8	1.69	0.57
79:18:1347:U:H2'	79:18:1348:G:N3	2.19	0.57
79:18:1633:A:H2'	79:18:1634:A:C8	2.40	0.57
85:28:134:G:H4'	85:28:135:G:O5'	2.05	0.57
85:28:3845:A:H2'	85:28:3846:C:H6	1.70	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:28:4471:U:H2'	85:28:4472:G:H8	1.70	0.57
9:L4:78:ARG:HB3	9:L4:88:GLY:HA2	1.85	0.56
11:L6:108:ARG:HD2	85:28:470:A:H1'	1.87	0.56
85:28:3648:A:H1'	85:28:3785:A:N6	2.20	0.56
85:28:4174:U:H2'	85:28:4175:G:H8	1.70	0.56
38:39:24:PRO:HG2	38:39:27:ILE:HG12	1.87	0.56
63:RR:51:VAL:HG22	63:RR:70:VAL:HG11	1.87	0.56
78:L9:114:ILE:HB	78:L9:124:ARG:HG3	1.86	0.56
79:18:219:U:H2'	79:18:220:U:C6	2.40	0.56
85:28:423:G:H2'	85:28:424:U:C6	2.40	0.56
85:28:1329:G:C2	85:28:3865:A:H1'	2.39	0.56
85:28:1341:U:H2'	85:28:1342:A:C8	2.41	0.56
12:L7:104:VAL:HG13	12:L7:135:VAL:HG12	1.87	0.56
68:S7:144:ILE:HG12	68:S7:154:ILE:HG13	1.87	0.56
74:W:52:THR:HG23	74:W:55:TYR:H	1.70	0.56
79:18:1854:U:H2'	79:18:1855:G:C8	2.41	0.56
85:28:2521:G:H5'	85:28:2640:G:H1'	1.88	0.56
85:28:3727:A:H2'	85:28:3728:A:C8	2.40	0.56
85:28:4344:U:H2'	85:28:4345:C:H6	1.70	0.56
6:6:49:A:H5''	10:L5:224:SER:HB3	1.88	0.56
6:6:110:G:H2'	6:6:111:C:C6	2.40	0.56
54:S5:153:LEU:HB3	54:S5:189:ALA:HA	1.87	0.56
79:18:963:A:H2'	79:18:964:A:C8	2.39	0.56
85:28:710:G:H2'	85:28:711:A:C8	2.38	0.56
85:28:2496:G:H2'	85:28:2497:C:C6	2.41	0.56
2:S2:86:LEU:HD13	2:S2:87:PRO:HD2	1.87	0.56
5:58:106:G:H4'	5:58:137:A:H5'	1.87	0.56
32:ee:7:CYS:HB2	32:ee:103:VAL:HG23	1.86	0.56
53:TT:49:LEU:HB3	61:LL:5:ILE:HG12	1.87	0.56
85:28:478:G:H2'	85:28:479:G:H8	1.71	0.56
85:28:1538:U:H2'	85:28:1539:G:C8	2.35	0.56
85:28:4635:A:H2	85:28:4663:G:H21	1.52	0.56
21:20:13:VAL:HG23	21:20:62:VAL:HB	1.87	0.56
48:t:85:LEU:HD21	48:t:104:ILE:HB	1.86	0.56
56:II:103:ALA:O	56:II:106:LYS:HG3	2.06	0.56
58:AA:172:LYS:HA	58:AA:195:LEU:HG	1.88	0.56
79:18:1692:U:H2'	79:18:1693:G:H8	1.68	0.56
85:28:265:C:H4'	85:28:266:C:OP2	2.05	0.56
85:28:1504:G:H2'	85:28:1505:C:C6	2.40	0.56
85:28:1749:A:H2'	85:28:1750:G:C8	2.40	0.56
85:28:2844:A:O2'	85:28:4631:G:H4'	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:28:3606:U:H2'	85:28:3607:U:C6	2.40	0.56
85:28:3870:C:H2'	85:28:3871:A:H8	1.71	0.56
18:bb:5:GLN:HG2	18:bb:6:VAL:HG23	1.87	0.56
37:38:26:LYS:HE3	37:38:28:ASN:HB3	1.87	0.56
49:F:31:VAL:HG21	49:F:56:ILE:HG22	1.86	0.56
79:18:545:A:H2'	79:18:546:G:C8	2.40	0.56
79:18:1121:G:C2	79:18:1122:A:C8	2.94	0.56
79:18:1228:A:H2'	79:18:1229:G:C8	2.40	0.56
79:18:1228:A:H2'	79:18:1229:G:H8	1.71	0.56
79:18:1457:U:H2'	79:18:1458:G:H8	1.71	0.56
85:28:448:G:H3'	85:28:449:C:H5''	1.86	0.56
18:bb:125:LYS:HG3	18:bb:129:LEU:HD12	1.86	0.56
80:v:602:LEU:HB3	80:v:604:MET:HE1	1.88	0.56
85:28:4563:U:H2'	85:28:4564:A:H8	1.71	0.56
85:28:4594:U:H2'	85:28:4595:G:H8	1.71	0.56
85:28:4629:U:C2	85:28:4630:G:C8	2.94	0.56
85:28:4884:G:H2'	85:28:4885:U:O4'	2.06	0.56
34:35:31:LEU:HB3	34:35:47:ILE:HG22	1.87	0.56
79:18:1633:A:H2'	79:18:1634:A:H8	1.71	0.56
85:28:268:G:H2'	85:28:269:G:H8	1.71	0.56
85:28:1760:G:O6	85:28:1773:U:O2	2.23	0.56
85:28:4699:U:H1'	85:28:4700:A:H5''	1.87	0.56
1:BB:198:MET:HB3	71:RS:85:VAL:HG11	1.87	0.56
58:AA:205:SER:HA	58:AA:221:LEU:HB2	1.87	0.56
79:18:382:C:H2'	79:18:383:G:C8	2.41	0.56
79:18:974:C:H2'	79:18:975:G:H8	1.70	0.56
85:28:462:G:H2'	85:28:463:A:C8	2.41	0.56
85:28:2080:U:H2'	85:28:2081:C:C6	2.41	0.56
85:28:2412:A:H2'	85:28:2413:U:C6	2.41	0.56
85:28:2457:G:H21	85:28:3672:G:N2	2.01	0.56
85:28:2540:C:H2'	85:28:2541:G:H8	1.71	0.56
85:28:3606:U:H2'	85:28:3607:U:H6	1.71	0.56
85:28:4948:C:H2'	85:28:4949:G:N2	2.21	0.56
4:DD:101:ARG:HB2	63:RR:10:ALA:HB2	1.89	0.55
71:RS:41:ILE:HG21	71:RS:47:ARG:HB2	1.88	0.55
79:18:1279:C:H2'	79:18:1280:G:H8	1.71	0.55
79:18:1616:U:H2'	79:18:1617:G:C8	2.41	0.55
80:v:617:ILE:HD12	80:v:659:PRO:HA	1.88	0.55
85:28:418:A:H4'	85:28:2311:C:H5'	1.88	0.55
85:28:1770:A:H2'	85:28:1771:U:C6	2.40	0.55
11:L6:48:ARG:HB2	11:L6:64:MET:HE1	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
79:18:1035:A:H2'	79:18:1036:A:H8	1.71	0.55
79:18:1413:G:H2'	79:18:1414:A:H8	1.71	0.55
84:ES:2953:C:H2'	84:ES:2954:G:C8	2.41	0.55
12:L7:126:LYS:HB2	22:21:133:ALA:HB3	1.88	0.55
51:ZZ:140:TYR:CE1	51:ZZ:145:CYS:HA	2.41	0.55
53:TT:99:LEU:HD21	53:TT:102:LYS:HB2	1.87	0.55
75:GG:78:ALA:HB3	75:GG:118:ALA:HB3	1.87	0.55
79:18:1424:G:H2'	79:18:1425:G:C8	2.41	0.55
85:28:922:C:H2'	85:28:922(A):G:C8	2.41	0.55
85:28:3720:G:H22	85:28:3733:A:H2	1.53	0.55
85:28:3721:U:H2'	85:28:3722:G:C8	2.41	0.55
85:28:3933:G:H2'	85:28:3934:G:H8	1.70	0.55
85:28:4070:U:H2'	85:28:4071:U:C6	2.41	0.55
85:28:4601:U:H2'	85:28:4602:A:H8	1.71	0.55
4:DD:132:ARG:HD3	79:18:114:G:H5'	1.88	0.55
49:F:227:ASP:HB3	49:F:320:LYS:HD3	1.89	0.55
85:28:1669:A:H4'	85:28:1685:G:H22	1.69	0.55
6:6:66:G:H5'	10:L5:10:LYS:HG3	1.88	0.55
38:39:45:ARG:NH2	85:28:2796:G:H5'	2.22	0.55
43:gg:19:LYS:HG3	85:28:2337:C:H4'	1.89	0.55
54:S5:34:SER:HA	55:WW:55:VAL:HB	1.88	0.55
79:18:479:C:C2	79:18:480:G:C8	2.95	0.55
79:18:1511:U:H2'	79:18:1512:C:C6	2.41	0.55
85:28:426:A:H2'	85:28:427:A:H8	1.71	0.55
5:58:8:U:H2'	5:58:9:A:H8	1.71	0.55
41:42:98:LYS:HE3	85:28:4233:A:H4'	1.89	0.55
56:II:74:GLY:HA2	79:18:1545:A:H4'	1.88	0.55
64:SS:108:LYS:HB3	79:18:53:C:H5''	1.87	0.55
73:S8:81:VAL:HG22	73:S8:102:VAL:HG12	1.89	0.55
79:18:96:C:H2'	79:18:97:U:C6	2.41	0.55
79:18:1183:A:H2'	79:18:1184:G:H8	1.71	0.55
79:18:1470:C:H2'	79:18:1471:C:H6	1.71	0.55
80:v:580:ARG:HB2	80:v:741:MET:HB2	1.89	0.55
85:28:1338:G:H4'	85:28:1339:U:C6	2.41	0.55
85:28:4238:G:H2'	85:28:4239:A:H8	1.71	0.55
17:15:187:SER:H	17:15:190:ALA:HB3	1.70	0.55
44:AS:179:ASN:HB3	44:AS:183:GLU:HB2	1.89	0.55
79:18:1301:A:H2'	79:18:1303:C:O2	2.07	0.55
85:28:233:U:H2'	85:28:234:G:H8	1.70	0.55
85:28:2078:C:H2'	85:28:2079:G:C8	2.42	0.55
85:28:3739:C:C2	85:28:3740:G:C8	2.95	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:28:4591:U:H2'	85:28:4592:C:C6	2.42	0.55
5:58:67:U:H2'	5:58:68:G:C8	2.40	0.55
18:bb:157:GLU:HA	18:bb:160:ARG:HG2	1.89	0.55
20:19:41:ILE:O	20:19:45:ILE:HG12	2.07	0.55
26:27:11:VAL:HG11	26:27:80:LEU:HB3	1.88	0.55
79:18:35:C:H2'	79:18:36:U:C6	2.40	0.55
79:18:1159:G:H2'	79:18:1160:U:H6	1.72	0.55
85:28:4642:U:H2'	85:28:4643:G:H8	1.70	0.55
45:FF:99:ARG:O	45:FF:103:GLU:HG2	2.07	0.55
61:LL:121:ARG:HG3	61:LL:131:VAL:HG21	1.89	0.55
85:28:2521:G:H2'	85:28:2522:G:C8	2.42	0.55
85:28:2683:C:H2'	85:28:2684:C:C6	2.41	0.55
85:28:3845:A:H2'	85:28:3846:C:C6	2.42	0.55
85:28:4563:U:C2	85:28:4564:A:C8	2.95	0.55
85:28:5028:G:H2'	85:28:5029:C:O4'	2.07	0.55
15:13:50:PRO:HG3	34:35:121:VAL:HG22	1.88	0.55
21:20:13:VAL:HG22	21:20:63:TYR:HB3	1.89	0.55
24:cc:93:ASN:ND2	85:28:2533:C:H5'	2.21	0.55
79:18:1828:C:H2'	79:18:1829:G:C8	2.42	0.55
85:28:1340:C:H2'	85:28:1341:U:C6	2.42	0.55
85:28:1727:U:H2'	85:28:1728:U:C6	2.42	0.55
85:28:4398:C:H2'	85:28:4399:U:H6	1.71	0.55
85:28:4578:G:H2'	85:28:4579:U:C6	2.42	0.55
85:28:4716:C:H2'	85:28:4717:A:H8	1.72	0.55
20:19:46:LYS:HE3	85:28:2710:C:H41	1.71	0.54
79:18:122:G:H2'	79:18:123:G:C8	2.41	0.54
85:28:1867:A:H2'	85:28:1868:A:C8	2.43	0.54
85:28:2539:C:H2'	85:28:2540:C:C6	2.42	0.54
48:t:142:ASN:HA	48:t:146:ARG:HH11	1.73	0.54
79:18:387:C:H2'	79:18:388:U:C6	2.42	0.54
79:18:432:G:H2'	79:18:433:A:H8	1.72	0.54
5:58:8:U:H2'	5:58:9:A:C8	2.43	0.54
9:L4:140:LYS:HE3	9:L4:245:HIS:HB2	1.87	0.54
79:18:857:U:H2'	79:18:858:A:C8	2.42	0.54
79:18:957:A:H3'	79:18:958:G:N2	2.18	0.54
80:v:30:HIS:CE1	80:v:130:ASP:H	2.26	0.54
85:28:4458:C:H2'	85:28:4459:U:H6	1.73	0.54
2:S2:207:ALA:HB2	79:18:4:C:H4'	1.89	0.54
13:aa:317:LYS:HG2	44:AS:225:LEU:HB3	1.88	0.54
17:15:40:PRO:HG3	85:28:8:U:H5''	1.88	0.54
47:s:121:VAL:HG13	47:s:182:PRO:HG2	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:s:160:LEU:HG	47:s:161:ILE:HG23	1.89	0.54
71:RS:17:ILE:HD13	71:RS:24:LEU:HD23	1.90	0.54
73:S8:66:SER:HA	73:S8:73:THR:HB	1.90	0.54
85:28:1504:G:H2'	85:28:1505:C:H6	1.72	0.54
85:28:2608:G:H2'	85:28:2609:G:H8	1.72	0.54
85:28:2689:C:H2'	85:28:2690:C:H6	1.71	0.54
5:58:70:G:H22	5:58:87:G:H1'	1.71	0.54
5:58:147:G:H2'	5:58:148:A:H8	1.72	0.54
14:10:16:PRO:HA	14:10:95:HIS:CD2	2.42	0.54
48:t:108:GLU:HA	48:t:111:ASN:ND2	2.22	0.54
66:S4:62:LYS:HE2	79:18:502:C:H4'	1.88	0.54
79:18:29:G:H2'	79:18:30:C:C6	2.42	0.54
58:AA:162:ASN:HB3	58:AA:164:ILE:HD12	1.88	0.54
67:S9:50:LEU:O	67:S9:54:ARG:HG3	2.07	0.54
79:18:674:C:H2'	79:18:675:U:C6	2.43	0.54
79:18:1365:G:H2'	79:18:1366:G:H8	1.72	0.54
85:28:1593:A:H5''	85:28:2839:U:H5''	1.89	0.54
85:28:2555:G:H2'	85:28:2556:G:H8	1.72	0.54
85:28:2858:A:H2'	85:28:2859:G:H8	1.70	0.54
85:28:2890:C:H2'	85:28:2891:U:C6	2.43	0.54
85:28:3861:A:H2'	85:28:3862:A:C8	2.42	0.54
85:28:4092:G:H2'	85:28:4093:G:H8	1.72	0.54
85:28:4188:U:H2'	85:28:4189:U:C6	2.42	0.54
85:28:4704:C:H2'	85:28:4705:A:H8	1.73	0.54
4:DD:113:LEU:HD21	4:DD:120:VAL:HG21	1.90	0.54
31:32:100:ALA:HB3	31:32:103:VAL:HG23	1.90	0.54
65:S6:131:ARG:HG3	74:W:82:ILE:HG22	1.90	0.54
66:S4:48:LEU:HD23	66:S4:61:VAL:HG22	1.90	0.54
79:18:126:G:H21	79:18:180:G:N2	2.04	0.54
79:18:354:U:H2'	79:18:355:G:C8	2.43	0.54
79:18:509:G:H2'	79:18:510:G:H8	1.72	0.54
79:18:935:G:H2'	79:18:936:G:H8	1.73	0.54
85:28:1348:U:H2'	85:28:1349:G:H8	1.72	0.54
5:58:144:U:H2'	5:58:145:C:C6	2.43	0.54
12:L7:42:ARG:O	12:L7:46:ARG:HG2	2.08	0.54
73:S8:177:SER:HB3	79:18:220:U:H5'	1.89	0.54
79:18:479:C:H2'	79:18:480:G:H8	1.72	0.54
79:18:1058:A:C8	82:CE:12:SER:HB3	2.43	0.54
85:28:676:C:H2'	85:28:677:G:H8	1.73	0.54
85:28:4996:C:C2	85:28:4997:G:C8	2.96	0.54
52:EE:56:CYS:SG	52:EE:82:ASN:HB2	2.48	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:CC:8:ARG:O	57:CC:11:ILE:HG12	2.08	0.54
79:18:530:U:H3	79:18:554:A:H61	1.55	0.54
79:18:1395:C:H4'	79:18:1396:A:OP1	2.08	0.54
85:28:517:C:H2'	85:28:518:G:C8	2.43	0.54
85:28:1450:C:H2'	85:28:1451:G:C8	2.42	0.54
85:28:2292:C:H2'	85:28:2293:U:C6	2.43	0.54
85:28:2292:C:H2'	85:28:2293:U:H6	1.73	0.54
85:28:3610:A:H2'	85:28:3611:A:C8	2.42	0.54
85:28:4948:C:H2'	85:28:4949:G:H21	1.73	0.54
4:DD:85:THR:HG22	4:DD:112:HIS:HA	1.89	0.53
15:13:91:ALA:HB1	15:13:96:ILE:HB	1.89	0.53
43:gg:28:GLU:HB2	43:gg:31:ASN:HB2	1.90	0.53
58:AA:270:LEU:HB3	58:AA:310:TRP:CZ2	2.43	0.53
59:OO:24:LEU:HB3	59:OO:32:LEU:HD11	1.90	0.53
75:GG:121:ARG:HD3	76:UU:52:ASP:HB2	1.90	0.53
79:18:848:U:H2'	79:18:849:A:H8	1.73	0.53
79:18:1232:U:H2'	79:18:1233:G:H8	1.73	0.53
85:28:4163:U:H5'	85:28:4164:C:H5''	1.90	0.53
7:L8:90:CYS:HB3	7:L8:101:VAL:HG13	1.89	0.53
9:L4:78:ARG:HA	9:L4:90:GLY:HA2	1.90	0.53
66:S4:166:THR:HG23	66:S4:168:LYS:H	1.73	0.53
73:S8:27:TYR:HB2	79:18:381:C:H41	1.73	0.53
79:18:89:C:H2'	79:18:90:G:C8	2.42	0.53
79:18:186:C:H2'	79:18:187:G:H8	1.73	0.53
80:v:412:ALA:HB3	80:v:472:LEU:H	1.73	0.53
85:28:1340:C:H2'	85:28:1341:U:H6	1.73	0.53
85:28:2566:G:H2'	85:28:2567:G:H8	1.72	0.53
85:28:2684:C:H2'	85:28:2685:C:C6	2.43	0.53
85:28:4238:G:H2'	85:28:4239:A:C8	2.43	0.53
85:28:4704:C:H2'	85:28:4705:A:C8	2.44	0.53
9:L4:339:THR:HG22	9:L4:342:ARG:NH2	2.23	0.53
14:10:98:ARG:HB3	14:10:120:GLY:HA3	1.90	0.53
24:cc:77:ILE:HD12	24:cc:116:LEU:HD12	1.88	0.53
58:AA:79:LEU:HB2	58:AA:113:PHE:CZ	2.42	0.53
59:OO:26:SER:HB3	59:OO:32:LEU:HB2	1.90	0.53
74:W:13:ILE:HD11	74:W:32:LEU:HB2	1.90	0.53
79:18:107:A:H2'	79:18:108:G:H8	1.73	0.53
79:18:949:G:H2'	79:18:950:C:C6	2.42	0.53
79:18:982:G:H2'	79:18:983:A:H8	1.73	0.53
79:18:1017:U:H2'	79:18:1018:U:H6	1.73	0.53
79:18:1590:C:H3'	79:18:1591:C:H6	1.72	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:28:1088:C:H2'	85:28:1089:G:C8	2.43	0.53
85:28:1468:C:H2'	85:28:1469:C:H6	1.73	0.53
85:28:1558:A:H2'	85:28:1559:G:H8	1.73	0.53
85:28:3732:A:H2'	85:28:3733:A:H8	1.73	0.53
85:28:4993:G:H2'	85:28:4994:G:C8	2.42	0.53
27:dd:72:THR:HG22	27:dd:110:LYS:HB3	1.90	0.53
27:dd:100:ILE:HG13	27:dd:123:ILE:HB	1.90	0.53
61:LL:63:GLU:O	61:LL:67:VAL:HG23	2.09	0.53
79:18:17:C:H2'	79:18:18:C:H6	1.74	0.53
79:18:1337:C:H2'	79:18:1338:G:C8	2.43	0.53
79:18:1690:U:H2'	79:18:1691:U:H6	1.74	0.53
80:v:252:LYS:HA	80:v:255:ASP:OD2	2.08	0.53
80:v:323:LEU:HD13	80:v:324:ASP:H	1.73	0.53
85:28:1346:C:H2'	85:28:1347:G:H8	1.74	0.53
85:28:1420:A:H4'	85:28:1421:G:H5'	1.91	0.53
85:28:2634:C:H2'	85:28:2635:U:H6	1.73	0.53
45:FF:14:SER:HB2	79:18:1016:U:H5''	1.90	0.53
73:S8:49:ARG:HD3	79:18:381:C:C5	2.43	0.53
79:18:1283:C:H4'	79:18:1287:A:H5'	1.90	0.53
85:28:287:U:H2'	85:28:288:G:C8	2.44	0.53
85:28:674:G:H2'	85:28:675:C:H6	1.73	0.53
85:28:2414:G:H2'	85:28:2415:U:H6	1.74	0.53
85:28:2895:A:H2'	85:28:2896:G:C8	2.43	0.53
85:28:3871:A:H2'	85:28:3872:A:C8	2.44	0.53
85:28:3873:G:H2'	85:28:3874:G:C8	2.43	0.53
8:L3:263:ALA:HB3	8:L3:266:VAL:HG23	1.91	0.53
59:OO:26:SER:HB2	59:OO:110:VAL:HG13	1.91	0.53
79:18:925:G:H1	79:18:1017:U:H3	1.55	0.53
79:18:996:A:H2'	79:18:997:A:C8	2.43	0.53
79:18:1102:G:H2'	79:18:1103:C:C6	2.43	0.53
79:18:1318:G:H2'	79:18:1319:U:C6	2.44	0.53
80:v:503:PRO:HD3	80:v:533:MET:HE2	1.91	0.53
83:A:77:LYS:HE2	83:A:79:HIS:CE1	2.43	0.53
85:28:440:U:H2'	85:28:441:G:C8	2.43	0.53
85:28:2373:C:H2'	85:28:2374:A:C8	2.44	0.53
9:L4:168:VAL:O	9:L4:172:LYS:HG2	2.08	0.53
24:cc:76:ILE:HA	24:cc:101:ASP:HB2	1.90	0.53
41:42:63:THR:HG21	41:42:87:ARG:HB3	1.91	0.53
49:F:107:LYS:HD3	49:F:317:ALA:HA	1.90	0.53
50:Q:181:ARG:HB2	50:Q:184:ARG:HB2	1.89	0.53
79:18:430:C:C2	79:18:431:G:C8	2.97	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
79:18:949:G:H2'	79:18:950:C:H6	1.74	0.53
85:28:1204:C:H2'	85:28:1205:G:C8	2.43	0.53
85:28:1494:U:H2'	85:28:1495:G:H8	1.74	0.53
85:28:2633:U:H2'	85:28:2634:C:H6	1.74	0.53
85:28:2676:A:C4	85:28:2677:G:C8	2.97	0.53
85:28:3697:U:H5''	85:28:3698:G:H5'	1.91	0.53
8:L3:53:MET:HG2	8:L3:77:THR:HG22	1.91	0.53
16:14:26:ALA:HB2	16:14:77:TRP:HZ3	1.74	0.53
20:19:66:ASN:O	20:19:70:ARG:HG2	2.09	0.53
41:42:5:PRO:HD3	85:28:4232:U:C2	2.43	0.53
79:18:1035:A:C4	79:18:1036:A:C8	2.97	0.53
79:18:1140:G:H2'	79:18:1141:G:H8	1.72	0.53
79:18:1708:C:H2'	79:18:1709:G:H8	1.73	0.53
85:28:2483:G:H1	85:28:2495:U:H3	1.55	0.53
85:28:3732:A:H2'	85:28:3733:A:C8	2.44	0.53
85:28:4894:A:H5''	85:28:4895:C:H2'	1.90	0.53
7:L8:21:LYS:HG2	85:28:1541:C:H5''	1.90	0.53
9:L4:77:PRO:O	9:L4:90:GLY:HA2	2.09	0.53
79:18:26:U:H2'	79:18:27:A:H8	1.73	0.53
79:18:1323:U:H2'	79:18:1324:G:C8	2.44	0.53
79:18:1558:C:H2'	79:18:1559:C:C6	2.44	0.53
85:28:496:G:H2'	85:28:497:G:H5'	1.90	0.53
85:28:4399:U:C2	85:28:4400:G:C8	2.97	0.53
5:58:64:U:C2	5:58:65:A:C8	2.97	0.53
11:L6:165:VAL:HG13	11:L6:180:GLY:H	1.72	0.53
12:L7:175:ALA:HB1	85:28:2102:G:C8	2.44	0.53
58:AA:11:LEU:HD21	58:AA:52:TYR:HB3	1.90	0.53
64:SS:66:GLY:HA2	79:18:581:U:H4'	1.90	0.53
79:18:1687:C:H2'	79:18:1688:C:H6	1.74	0.53
85:28:245:C:H4'	85:28:246:G:O5'	2.09	0.53
85:28:677:G:H2'	85:28:678:C:H6	1.72	0.53
85:28:2078:C:H2'	85:28:2079:G:H8	1.74	0.53
85:28:4756:C:H5'	85:28:4757:C:OP1	2.09	0.53
7:L8:194:ASN:HB2	85:28:1539:G:H4'	1.90	0.52
52:EE:52:LEU:HD13	52:EE:65:VAL:HG11	1.91	0.52
52:EE:86:GLY:O	52:EE:89:VAL:HG12	2.09	0.52
79:18:1189:A:H2'	79:18:1190:A:H8	1.75	0.52
79:18:1537:A:H2'	79:18:1538:C:C6	2.44	0.52
85:28:460:C:H2'	85:28:461:G:H8	1.73	0.52
5:58:130:C:H2'	5:58:131:G:H8	1.73	0.52
10:L5:37:VAL:HG23	10:L5:48:LYS:O	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:L5:65:ALA:HB2	10:L5:74:ILE:HD13	1.92	0.52
48:t:123:ARG:NH1	48:t:123:ARG:HA	2.24	0.52
56:II:140:ARG:HB2	79:18:1644:C:H4'	1.90	0.52
79:18:5:U:O2'	79:18:602:G:H4'	2.08	0.52
79:18:89:C:H2'	79:18:90:G:H8	1.74	0.52
79:18:110:U:H2'	79:18:111:A:H8	1.71	0.52
79:18:925:G:C2	79:18:926:A:C8	2.97	0.52
85:28:33:A:H3'	85:28:47:A:H61	1.73	0.52
85:28:423:G:H2'	85:28:424:U:H6	1.73	0.52
85:28:1195:G:H2'	85:28:1196:G:H8	1.72	0.52
85:28:1591:U:OP1	85:28:1592:G:H5'	2.08	0.52
85:28:2093:G:H22	85:28:2262:G:H1	1.57	0.52
85:28:2478:C:C2	85:28:2479:G:N7	2.78	0.52
85:28:2539:C:H2'	85:28:2540:C:H6	1.74	0.52
85:28:2699:C:H2'	85:28:2700:G:H8	1.74	0.52
2:S2:65:LYS:HD3	2:S2:273:LEU:HD13	1.90	0.52
12:L7:85:GLU:HB2	22:21:135:PRO:HB3	1.90	0.52
17:15:49:ARG:HH12	85:28:152:U:P	2.32	0.52
18:bb:168:TYR:CE2	18:bb:172:LYS:HD2	2.44	0.52
49:F:46:LEU:HB3	49:F:91:PRO:HG2	1.91	0.52
79:18:1823:A:C5	79:18:1824:A:H1'	2.44	0.52
85:28:456:C:H2'	85:28:457:G:H8	1.74	0.52
85:28:1333:A:H2'	85:28:1334:A:C8	2.44	0.52
85:28:4091:G:H2'	85:28:4092:G:C8	2.44	0.52
85:28:4343:U:H2'	85:28:4344:U:C6	2.44	0.52
1:BB:132:GLN:HB3	1:BB:133:PRO:HD3	1.91	0.52
5:58:70:G:N2	5:58:87:G:H1'	2.24	0.52
26:27:59:LYS:HE2	85:28:4148:C:H5''	1.91	0.52
40:41:2:ARG:HD3	40:41:5:TRP:CD1	2.44	0.52
54:S5:169:ILE:HG12	79:18:1535:U:C5	2.44	0.52
79:18:729:C:H2'	79:18:730:C:H6	1.73	0.52
79:18:1798:C:H2'	79:18:1799:G:O4'	2.09	0.52
85:28:2465:C:H2'	85:28:2466:G:O4'	2.09	0.52
85:28:2704:C:H2'	85:28:2705:G:O4'	2.09	0.52
85:28:3607:U:H2'	85:28:3608:A:H8	1.75	0.52
27:dd:98:ALA:HB2	27:dd:121:PRO:HB2	1.92	0.52
54:S5:97:PHE:HA	54:S5:100:ILE:HD12	1.90	0.52
79:18:573:U:H2'	79:18:574:A:H5''	1.90	0.52
79:18:1670:C:H2'	79:18:1671:G:H8	1.72	0.52
85:28:1339:U:H2'	85:28:1340:C:C6	2.45	0.52
6:6:2:U:H2'	6:6:3:C:H6	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:6:26:C:H5''	10:L5:56:THR:HG21	1.91	0.52
37:38:2:PRO:HB2	85:28:2692:U:O2	2.10	0.52
79:18:544:G:C2	79:18:545:A:C5	2.97	0.52
80:v:159:LYS:HG2	88:v:900:GDP:C6	2.44	0.52
84:ES:2946:G:H2'	84:ES:2947:G:H8	1.72	0.52
85:28:1236:C:H2'	85:28:1238:A:C8	2.44	0.52
65:S6:142:ARG:HG2	65:S6:153:VAL:HG11	1.90	0.52
79:18:1144:A:H2'	79:18:1145:A:C8	2.44	0.52
79:18:1240:A:C4	83:A:100:LYS:HD2	2.44	0.52
79:18:1523:C:H2'	79:18:1524:G:H8	1.74	0.52
79:18:1748:G:H1	79:18:1786:U:H3	1.57	0.52
85:28:162:A:H2'	85:28:163:A:C8	2.45	0.52
6:6:6:C:H4'	10:L5:52:ILE:HD13	1.91	0.52
9:L4:312:ARG:HB3	85:28:2274:C:H5'	1.90	0.52
27:dd:29:PRO:HA	85:28:1654:G:H5''	1.91	0.52
44:AS:103:MET:HE3	44:AS:215:VAL:HG23	1.92	0.52
69:YY:112:ASN:HA	69:YY:116:VAL:HG12	1.91	0.52
79:18:528:A:H2'	79:18:529:A:C8	2.44	0.52
79:18:910:G:H2'	79:18:911:C:C6	2.45	0.52
79:18:1350:U:C2	79:18:1351:G:C8	2.98	0.52
79:18:1501:C:H2'	79:18:1502:C:H6	1.74	0.52
79:18:1627:C:H2'	79:18:1628:C:C6	2.45	0.52
85:28:247:G:H2'	85:28:248:C:H6	1.74	0.52
85:28:1958:A:H4'	85:28:1962:A:H1'	1.90	0.52
85:28:3719:A:C4	85:28:3720:G:C8	2.97	0.52
85:28:4459:U:H2'	85:28:4460:U:C6	2.44	0.52
2:S2:196:ILE:HB	2:S2:223:TYR:HB2	1.92	0.52
79:18:21:U:H2'	79:18:22:A:C8	2.45	0.52
85:28:175:C:H2'	85:28:176:G:C8	2.43	0.52
85:28:270:U:H2'	85:28:271:C:H6	1.75	0.52
85:28:2544:G:H5''	85:28:2545:U:H5	1.75	0.52
85:28:2743:A:H2'	85:28:2744:A:C8	2.44	0.52
14:10:16:PRO:HA	14:10:95:HIS:HD2	1.75	0.52
79:18:409:C:H2'	79:18:410:G:H8	1.75	0.52
79:18:1092:G:H2'	79:18:1093:A:H8	1.75	0.52
80:v:138:GLN:HA	80:v:141:THR:HG22	1.91	0.52
85:28:714:G:H2'	85:28:715:G:H8	1.75	0.52
85:28:1345:A:H2'	85:28:1346:C:C6	2.45	0.52
85:28:1933:G:H2'	85:28:1934:A:C8	2.45	0.52
85:28:2560:C:H42	85:28:2567:G:H1	1.57	0.52
85:28:4652:G:H2'	85:28:4653:C:H6	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:28:4716:C:H2'	85:28:4717:A:C8	2.45	0.52
85:28:4889:G:H2'	85:28:4890:G:H8	1.74	0.52
57:CC:20:VAL:HG21	70:S3:72:VAL:HG22	1.90	0.51
58:AA:174:VAL:HB	58:AA:188:HIS:HB2	1.91	0.51
64:SS:35:VAL:HG21	64:SS:40:ILE:HD11	1.93	0.51
66:S4:79:ASP:HB3	66:S4:82:TYR:HB2	1.92	0.51
79:18:677:G:H21	79:18:1028:A:N6	2.00	0.51
85:28:1505:C:H2'	85:28:1506:G:C8	2.44	0.51
85:28:1527:A:H2'	85:28:1528:U:C6	2.45	0.51
85:28:2556:G:H2'	85:28:2557:G:H8	1.75	0.51
85:28:4320:G:H2'	85:28:4321:U:C6	2.45	0.51
85:28:4357:G:H2'	85:28:4358:U:H6	1.76	0.51
5:58:70:G:H5''	25:26:27:ARG:CZ	2.40	0.51
18:bb:54:TYR:CD1	18:bb:145:VAL:HG21	2.46	0.51
41:42:6:LYS:HG2	41:42:93:LEU:HB3	1.92	0.51
77:11:108:GLY:HA3	85:28:4251:A:H5''	1.91	0.51
79:18:102:A:H4'	79:18:104:A:C8	2.45	0.51
79:18:481:C:H2'	79:18:482:G:C8	2.44	0.51
79:18:511:U:H2'	79:18:512:A:C8	2.37	0.51
85:28:674:G:H2'	85:28:675:C:C6	2.46	0.51
85:28:734:G:C2	85:28:735:G:C8	2.98	0.51
85:28:3726:A:H2'	85:28:3727:A:C8	2.45	0.51
7:L8:14:SER:H	7:L8:17:ARG:HG3	1.76	0.51
7:L8:183:GLY:HA2	85:28:1613:A:H5''	1.92	0.51
7:L8:233:ARG:HB2	85:28:4184:G:H5'	1.93	0.51
26:27:38:TYR:HB3	85:28:2656:U:H5''	1.91	0.51
44:AS:46:LYS:HE3	75:GG:20:GLN:HB2	1.92	0.51
44:AS:48:LEU:HD23	44:AS:48:LEU:H	1.75	0.51
60:MM:37:VAL:HG23	79:18:1567:G:H4'	1.91	0.51
79:18:440:G:H2'	79:18:441:C:O4'	2.10	0.51
79:18:1609:C:H2'	79:18:1610:G:H8	1.75	0.51
79:18:1808:U:H2'	79:18:1809:A:H8	1.75	0.51
85:28:158:A:H5''	85:28:159:C:H2'	1.92	0.51
85:28:2277:C:H2'	85:28:2278:G:C8	2.45	0.51
85:28:2726:G:H2'	85:28:2727:C:C6	2.45	0.51
85:28:4578:G:H2'	85:28:4579:U:H6	1.74	0.51
85:28:4685:U:H2'	85:28:4686:G:C8	2.45	0.51
16:14:25:VAL:HG11	16:14:50:MET:HE1	1.91	0.51
58:AA:12:LYS:HB3	58:AA:306:LEU:HD13	1.93	0.51
79:18:344:U:H2'	79:18:345:U:C6	2.46	0.51
79:18:509:G:H2'	79:18:510:G:C8	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:v:524:LEU:HD21	80:v:544:HIS:HB3	1.93	0.51
85:28:3719:A:H2'	85:28:3720:G:H8	1.75	0.51
5:58:65:A:H2'	5:58:66:A:C8	2.46	0.51
11:L6:53:VAL:HG11	85:28:947:C:H5''	1.93	0.51
30:31:26:THR:HG23	85:28:4996:C:H4'	1.91	0.51
32:ee:45:LYS:HD2	32:ee:105:LEU:HA	1.92	0.51
60:MM:100:ALA:O	60:MM:104:LEU:HG	2.11	0.51
79:18:28:U:H2'	79:18:29:G:C8	2.45	0.51
79:18:656:G:H5'	79:18:662:G:N2	2.25	0.51
79:18:1131:G:H2'	79:18:1132:C:C6	2.46	0.51
79:18:1511:U:H2'	79:18:1512:C:H6	1.74	0.51
79:18:1823:A:N7	79:18:1824:A:H1'	2.26	0.51
85:28:1329:G:H2'	85:28:3865:A:H5'	1.91	0.51
85:28:2859:G:H2'	85:28:2860:C:H6	1.74	0.51
85:28:4208:U:H2'	85:28:4209:G:H8	1.75	0.51
5:58:47:C:H1'	5:58:61:A:H2'	1.93	0.51
45:FF:26:LEU:HD21	45:FF:60:VAL:HG12	1.92	0.51
72:WX:105:THR:HB	72:WX:110:ILE:HG12	1.92	0.51
76:UU:17:HIS:HB3	79:18:999:G:C8	2.45	0.51
79:18:192:C:H2'	79:18:193:C:H6	1.74	0.51
85:28:164:G:H2'	85:28:165:A:H8	1.76	0.51
5:58:144:U:H2'	5:58:145:C:H6	1.76	0.51
13:aa:250:LYS:HB3	85:28:6:C:H5''	1.92	0.51
23:22:84:LYS:HG3	23:22:102:VAL:HG11	1.92	0.51
79:18:192:C:H2'	79:18:193:C:C6	2.46	0.51
79:18:1174:U:H2'	79:18:1175:G:H8	1.75	0.51
79:18:1244:U:H2'	79:18:1245:G:C8	2.40	0.51
85:28:50:C:C2	85:28:51:A:C8	2.99	0.51
85:28:956:A:H1'	85:28:2076:G:H5''	1.93	0.51
85:28:2079:G:H2'	85:28:2080:U:C6	2.46	0.51
85:28:2858:A:H2'	85:28:2859:G:C8	2.45	0.51
85:28:4173:G:H2'	85:28:4174:U:H6	1.76	0.51
85:28:5004:C:H2'	85:28:5005:G:O4'	2.10	0.51
2:S2:168:GLY:HA2	3:PP:1:MET:HE1	1.93	0.51
19:17:16:LYS:HG2	19:17:149:ILE:HG12	1.92	0.51
33:34:66:ARG:HD3	85:28:2539:C:H5''	1.93	0.51
44:AS:129:THR:HB	44:AS:180:ASP:HA	1.93	0.51
67:S9:86:VAL:HG12	67:S9:100:LEU:HD11	1.92	0.51
70:S3:99:ILE:H	70:S3:99:ILE:HD13	1.75	0.51
79:18:431:G:C2	79:18:432:G:C8	2.99	0.51
79:18:1839:U:H2'	79:18:1840:U:C6	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:v:110:ASP:HB3	80:v:553:HIS:HB2	1.93	0.51
80:v:154:VAL:HG12	80:v:211:THR:HG22	1.93	0.51
80:v:445:LYS:HG3	80:v:478:PHE:CZ	2.46	0.51
85:28:734:G:H1	85:28:929:A:H62	1.59	0.51
85:28:3769:C:H2'	85:28:3770:U:C6	2.46	0.51
10:L5:60:ILE:HB	10:L5:80:ALA:HB2	1.93	0.51
22:21:87:LYS:NZ	85:28:4305:G:H22	2.09	0.51
25:26:89:LYS:HG2	25:26:90:ALA:H	1.76	0.51
66:S4:80:ILE:HG23	66:S4:81:THR:HG23	1.92	0.51
79:18:126:G:N2	79:18:180:G:H21	2.07	0.51
85:28:424:U:H2'	85:28:425:U:H6	1.76	0.51
85:28:1645:C:H2'	85:28:1646:A:C8	2.45	0.51
85:28:2376:A:H2'	85:28:2377:C:C6	2.46	0.51
85:28:3707:U:H2'	85:28:3708:C:C6	2.46	0.51
85:28:3917:A:H2'	85:28:3918:G:C8	2.44	0.51
85:28:4273:A:H2'	85:28:4274:A:C8	2.46	0.51
85:28:4356:G:C2	85:28:4357:G:C8	2.99	0.51
1:BB:32:PHE:HA	1:BB:35:GLU:HG3	1.93	0.51
18:bb:54:TYR:HD1	18:bb:145:VAL:HG21	1.76	0.51
77:11:141:ILE:HG23	77:11:144:LYS:HE2	1.93	0.51
79:18:152:U:H2'	79:18:153:G:H8	1.76	0.51
79:18:454:U:H2'	79:18:455:A:C8	2.46	0.51
79:18:1006:C:H2'	79:18:1007:C:C6	2.45	0.51
79:18:1030:A:H2'	79:18:1031:A:H8	1.76	0.51
79:18:1031:A:H2'	79:18:1032:C:C6	2.46	0.51
79:18:1207:G:P	79:18:1207:G:H8	2.34	0.51
85:28:1684:A:C4	85:28:1685:G:C8	2.99	0.51
85:28:2417:A:C4	85:28:2418:A:C8	2.98	0.51
85:28:2591:A:H2'	85:28:2592:U:C6	2.45	0.51
85:28:3722:G:H2'	85:28:3723:A:H8	1.75	0.51
85:28:4507:A:H2'	85:28:4508:C:C6	2.46	0.51
85:28:4563:U:H2'	85:28:4564:A:C8	2.45	0.51
51:ZZ:138:ARG:HB2	51:ZZ:149:CYS:HA	1.93	0.50
73:S8:98:LYS:HB3	79:18:377:G:H5'	1.93	0.50
79:18:394:G:C2	79:18:395:G:C8	2.99	0.50
80:v:89:ILE:HG13	80:v:91:GLN:H	1.76	0.50
85:28:262:G:H2'	85:28:263:G:H8	1.76	0.50
85:28:4178:A:H2'	85:28:4179:G:C8	2.46	0.50
85:28:4383:U:H2'	85:28:4384:U:C6	2.46	0.50
85:28:4538:G:H2'	85:28:4539:U:C6	2.47	0.50
2:S2:66:LEU:HD12	2:S2:86:LEU:HD12	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:S3:115:VAL:HG11	70:S3:142:LEU:HD21	1.93	0.50
70:S3:141:LYS:HA	70:S3:147:ALA:HA	1.92	0.50
79:18:455:A:H2'	79:18:456:C:C6	2.46	0.50
85:28:653:C:H2'	85:28:654:C:H6	1.76	0.50
85:28:2293:U:H2'	85:28:2294:G:C8	2.46	0.50
85:28:2412:A:H2'	85:28:2413:U:H6	1.76	0.50
85:28:2640:G:H2'	85:28:2641:A:C8	2.45	0.50
85:28:2682:G:H2'	85:28:2683:C:C6	2.46	0.50
85:28:4925:U:H1'	85:28:4926:C:OP2	2.11	0.50
2:S2:166:ARG:HG2	2:S2:181:PRO:HG3	1.94	0.50
28:29:4:SER:HB2	85:28:1855:G:OP1	2.10	0.50
54:S5:40:ALA:HB1	54:S5:45:TYR:CD2	2.46	0.50
70:S3:107:TYR:HA	70:S3:110:LEU:HB2	1.92	0.50
79:18:12:U:H2'	79:18:13:C:C6	2.46	0.50
79:18:123:G:H3'	79:18:124:U:H5''	1.94	0.50
79:18:441:C:H2'	79:18:442:C:H6	1.76	0.50
79:18:1740:C:H2'	79:18:1741:U:C6	2.47	0.50
84:ES:2947:G:H1	84:ES:3247:A:H2	1.54	0.50
85:28:162:A:H2'	85:28:163:A:H8	1.75	0.50
85:28:223:G:H4'	85:28:225:G:N7	2.25	0.50
85:28:433:A:C2	85:28:3867:A:H4'	2.46	0.50
85:28:2425:U:H5'	85:28:2426:U:H5	1.76	0.50
10:L5:146:LEU:HD22	85:28:4323:A:H2	1.75	0.50
14:10:22:PHE:CZ	85:28:1788:A:H2'	2.46	0.50
24:cc:71:LEU:HG	24:cc:76:ILE:HG22	1.92	0.50
45:FF:87:ASP:HB3	79:18:924:G:H21	1.75	0.50
52:EE:26:LEU:HD12	52:EE:31:LEU:HD21	1.93	0.50
53:TT:50:PHE:CZ	53:TT:58:LEU:HD13	2.46	0.50
61:LL:102:GLY:HA2	61:LL:105:ASN:HB2	1.94	0.50
79:18:409:C:H2'	79:18:410:G:C8	2.47	0.50
79:18:749:U:H2'	79:18:750:C:C6	2.46	0.50
85:28:1458:C:C2	85:28:1459:A:C8	2.99	0.50
85:28:1846:G:H2'	85:28:1847:C:H6	1.76	0.50
85:28:1973:G:OP2	85:28:1974:U:H3'	2.11	0.50
85:28:2075:G:H2'	85:28:2076:G:H8	1.77	0.50
85:28:4228:G:H5''	85:28:4229:U:O4'	2.12	0.50
85:28:4503:A:H2'	85:28:4504:C:H6	1.77	0.50
45:FF:110:ASP:O	45:FF:114:ARG:HG2	2.11	0.50
48:t:143:VAL:C	48:t:145:GLY:H	2.19	0.50
66:S4:257:ALA:HA	66:S4:260:GLN:HG3	1.94	0.50
68:S7:146:VAL:HG22	68:S7:152:ARG:HG2	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
79:18:212:C:H2'	79:18:213:G:C8	2.46	0.50
79:18:1232:U:H2'	79:18:1233:G:C8	2.46	0.50
79:18:1656:G:C2	79:18:1657:G:C8	2.99	0.50
85:28:1298:C:H2'	85:28:1299:G:C8	2.45	0.50
85:28:2293:U:H2'	85:28:2294:G:H8	1.77	0.50
85:28:4688:C:H2'	85:28:4689:U:C6	2.46	0.50
50:Q:53:MET:HB3	50:Q:57:ASN:HB2	1.93	0.50
56:II:104:SER:HA	56:II:107:GLU:HG3	1.93	0.50
68:S7:73:GLN:HA	68:S7:76:GLN:HG2	1.93	0.50
85:28:64:A:H1'	85:28:76:A:H1'	1.92	0.50
85:28:2290:C:C2	85:28:2291:G:C8	2.99	0.50
5:58:141:C:H2'	5:58:142:U:C6	2.47	0.50
6:6:59:G:H4'	10:L5:267:ASN:HD21	1.76	0.50
7:L8:24:LYS:HG3	7:L8:49:ILE:HD12	1.93	0.50
56:II:51:LEU:HD21	56:II:81:ILE:HG13	1.94	0.50
79:18:570:C:H2'	79:18:571:U:C6	2.47	0.50
79:18:1305:C:H2'	79:18:1306:U:C6	2.47	0.50
85:28:1199:G:H2'	85:28:1200:G:H8	1.76	0.50
85:28:1333:A:H2'	85:28:1334:A:H8	1.75	0.50
85:28:2845:A:H61	85:28:3843:C:N4	2.10	0.50
85:28:3707:U:H2'	85:28:3708:C:H6	1.77	0.50
10:L5:108:ARG:CZ	10:L5:253:TYR:HB2	2.42	0.50
12:L7:103:LYS:O	12:L7:107:VAL:HG23	2.12	0.50
20:19:108:ARG:HA	20:19:111:GLU:HG2	1.93	0.50
25:26:100:HIS:CD2	85:28:231:U:H4'	2.46	0.50
85:28:161:G:H2'	85:28:162:A:H8	1.76	0.50
85:28:163:A:H2'	85:28:164:G:C8	2.47	0.50
85:28:3832:U:H2'	85:28:3833:C:H6	1.77	0.50
85:28:4258:C:H2'	85:28:4259:C:H6	1.77	0.50
85:28:4586:G:C2	85:28:4587:G:C8	3.00	0.50
85:28:4760:G:H2'	85:28:4761:G:O4'	2.12	0.50
5:58:5:U:H2'	5:58:6:C:C6	2.46	0.50
7:L8:125:LYS:HB3	85:28:3681:G:C6	2.47	0.50
7:L8:209:HIS:CE1	7:L8:235:VAL:HG11	2.47	0.50
12:L7:70:MET:HA	12:L7:73:MET:HE2	1.94	0.50
60:MM:42:HIS:CD2	60:MM:43:LYS:HG2	2.47	0.50
70:S3:59:LEU:HA	70:S3:66:ILE:HG13	1.93	0.50
79:18:51:U:H2'	79:18:52:G:H8	1.77	0.50
79:18:438:G:H8	79:18:1800:A:H4'	1.77	0.50
79:18:1058:A:H8	82:CE:12:SER:HB3	1.75	0.50
79:18:1065:G:H2'	79:18:1066:U:C6	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
79:18:1407:U:H2'	79:18:1408:U:H6	1.77	0.50
79:18:1537:A:H2'	79:18:1538:C:H6	1.76	0.50
79:18:1653:U:H2'	79:18:1654:G:C8	2.47	0.50
84:ES:3239:G:H2'	84:ES:3240:A:C8	2.43	0.50
85:28:222:C:H2'	85:28:223:G:O4'	2.12	0.50
85:28:287:U:H2'	85:28:288:G:H8	1.77	0.50
85:28:1090:G:H2'	85:28:1091:C:C6	2.47	0.50
85:28:1463:C:H2'	85:28:1464:C:C6	2.47	0.50
85:28:1528:U:H2'	85:28:1529:G:C8	2.47	0.50
85:28:1804:A:H4'	85:28:1805:A:O5'	2.10	0.50
85:28:1875:C:H2'	85:28:1876:U:C6	2.47	0.50
85:28:4595:G:H2'	85:28:4596:C:C6	2.46	0.50
2:S2:147:VAL:HB	81:LA:682:GLY:HA3	1.94	0.49
5:58:124:U:H4'	5:58:125:C:O5'	2.10	0.49
8:L3:303:ALA:HB3	8:L3:312:LYS:HG3	1.93	0.49
23:22:62:SER:HB3	23:22:73:THR:HG23	1.94	0.49
29:30:29:LEU:HD23	29:30:94:LEU:HD13	1.94	0.49
63:RR:107:ARG:HB2	63:RR:112:VAL:HG22	1.94	0.49
85:28:1072:C:C2	85:28:1073:G:C8	3.00	0.49
85:28:1315:C:H2'	85:28:1316:G:H8	1.76	0.49
85:28:1676:C:H41	85:28:4378:A:H5''	1.77	0.49
85:28:2610:G:H2'	85:28:2611:A:H8	1.75	0.49
85:28:3611:A:H2	85:28:5016:A:H8	1.60	0.49
85:28:4346:U:H2'	85:28:4347:G:H8	1.76	0.49
2:S2:65:LYS:HA	2:S2:68:ARG:HD2	1.94	0.49
17:15:64:ILE:HG21	17:15:106:ALA:HB2	1.94	0.49
41:42:64:LYS:HD2	85:28:4370:G:H5''	1.93	0.49
54:S5:35:LEU:HD23	54:S5:35:LEU:H	1.77	0.49
58:AA:173:LEU:HD22	58:AA:189:ILE:HG12	1.94	0.49
71:RS:5:ARG:NH2	79:18:1454:A:H5'	2.27	0.49
74:W:6:CYS:HB2	74:W:13:ILE:HD11	1.95	0.49
79:18:991:G:C6	79:18:1134:G:H4'	2.47	0.49
10:L5:152:ARG:HG3	10:L5:154:THR:HG23	1.94	0.49
12:L7:49:ILE:HD12	12:L7:185:CYS:HB3	1.94	0.49
12:L7:184:ILE:HG21	85:28:2102:G:C6	2.47	0.49
17:15:172:ARG:HG2	85:28:29:G:H5''	1.94	0.49
18:bb:26:GLN:HG3	21:20:167:PHE:HZ	1.77	0.49
31:32:90:MET:HE2	31:32:90:MET:HA	1.94	0.49
32:ee:47:CYS:HB3	32:ee:103:VAL:HG12	1.94	0.49
44:AS:35:ALA:HB2	44:AS:44:ILE:HD11	1.93	0.49
45:FF:55:ARG:HE	79:18:1017:U:H5'	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:F:191:LYS:HB2	49:F:194:VAL:HB	1.95	0.49
54:S5:125:SER:HA	54:S5:138:ALA:HA	1.95	0.49
67:S9:42:GLU:HA	67:S9:45:ARG:HB3	1.94	0.49
79:18:350:C:C2	79:18:351:G:C8	3.00	0.49
79:18:1128:C:H2'	79:18:1129:G:C8	2.47	0.49
79:18:1627:C:H2'	79:18:1628:C:H6	1.76	0.49
79:18:1750:C:H2'	79:18:1751:C:H6	1.77	0.49
80:v:310:GLU:HG2	80:v:311:GLU:N	2.26	0.49
85:28:1306:C:H2'	85:28:1307:A:C8	2.41	0.49
85:28:2402:G:C2	85:28:2403:A:C8	3.00	0.49
85:28:3607:U:H2'	85:28:3608:A:C8	2.47	0.49
85:28:4495:G:C2	85:28:4496:A:N7	2.80	0.49
5:58:5:U:H2'	5:58:6:C:H6	1.77	0.49
13:aa:195:THR:O	13:aa:199:LEU:HG	2.11	0.49
58:AA:292:SER:HB2	58:AA:297:THR:HB	1.93	0.49
60:MM:22:LEU:HB3	60:MM:28:LEU:HD11	1.95	0.49
68:S7:36:LEU:HD22	68:S7:75:ILE:HD11	1.93	0.49
76:UU:17:HIS:HB3	79:18:999:G:N7	2.26	0.49
79:18:166:A:C6	79:18:167:G:N7	2.80	0.49
79:18:1017:U:H2'	79:18:1018:U:C6	2.48	0.49
85:28:673:C:C2	85:28:674:G:C8	3.01	0.49
85:28:1094:G:H1	85:28:1202:C:H42	1.61	0.49
85:28:4178:A:H2'	85:28:4179:G:H8	1.77	0.49
85:28:5002:U:H2'	85:28:5003:U:H6	1.76	0.49
13:aa:139:VAL:HG23	13:aa:236:ILE:HG22	1.95	0.49
13:aa:317:LYS:HE3	44:AS:225:LEU:HB2	1.95	0.49
19:17:54:LYS:HA	19:17:83:TRP:CD1	2.47	0.49
63:RR:60:LYS:HB2	63:RR:114:ASP:OD1	2.12	0.49
79:18:87:U:C2	79:18:88:G:C8	3.01	0.49
79:18:1126:G:H2'	79:18:1127:C:C6	2.47	0.49
85:28:125:C:H2'	85:28:126:C:H6	1.76	0.49
85:28:325:U:H2'	85:28:326:C:C6	2.47	0.49
85:28:4244:A:H2'	85:28:4245:G:O4'	2.12	0.49
4:DD:96:ILE:HD12	63:RR:10:ALA:HB1	1.95	0.49
8:L3:55:HIS:HB2	8:L3:369:ASP:HB2	1.95	0.49
44:AS:146:ARG:HD3	44:AS:206:PRO:HG3	1.95	0.49
47:s:98:ILE:HG13	47:s:101:MET:HE3	1.93	0.49
67:S9:117:LEU:HD23	67:S9:119:LEU:HD11	1.95	0.49
79:18:812:A:C5	79:18:813:A:C8	3.00	0.49
79:18:1189:A:H2'	79:18:1190:A:C8	2.47	0.49
79:18:1739:C:H2'	79:18:1740:C:C6	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:28:1824:G:H2'	85:28:1825:A:C8	2.47	0.49
85:28:2308:A:H4'	85:28:2334:C:H4'	1.94	0.49
85:28:2683:C:H2'	85:28:2684:C:H6	1.77	0.49
85:28:3930:U:H2'	85:28:3931:C:C6	2.47	0.49
26:27:51:ARG:HB2	26:27:65:ARG:HG3	1.93	0.49
48:t:59:THR:HG23	48:t:74:VAL:HB	1.94	0.49
79:18:441:C:H2'	79:18:442:C:C6	2.47	0.49
79:18:600:G:C2	79:18:601:G:C8	3.00	0.49
79:18:1457:U:H2'	79:18:1458:G:C8	2.48	0.49
79:18:1712:A:H2'	79:18:1713:C:H6	1.78	0.49
85:28:734:G:H1	85:28:929:A:N6	2.11	0.49
5:58:65:A:C4	5:58:66:A:C8	3.01	0.49
14:10:91:LEU:HD12	14:10:135:ILE:HG23	1.95	0.49
79:18:17:C:H2'	79:18:18:C:C6	2.48	0.49
79:18:354:U:H2'	79:18:355:G:H8	1.78	0.49
79:18:1365:G:H2'	79:18:1366:G:C8	2.48	0.49
85:28:58:G:H4'	85:28:59:A:H4'	1.95	0.49
85:28:699:C:H2'	85:28:700:G:H8	1.77	0.49
85:28:2404:A:H61	85:28:2787:A:H61	1.59	0.49
85:28:3770:U:H2'	85:28:3771:C:C6	2.47	0.49
85:28:4208:U:H2'	85:28:4209:G:C8	2.48	0.49
85:28:4406:U:C2	85:28:4407:G:C8	3.00	0.49
6:6:3:C:H2'	6:6:4:U:H6	1.76	0.49
6:6:23:A:H2'	6:6:24:C:C6	2.48	0.49
58:AA:154:VAL:HG12	58:AA:167:SER:HB2	1.95	0.49
77:11:110:GLN:HG2	77:11:111:GLU:HG2	1.95	0.49
79:18:15:U:H2'	79:18:16:G:O4'	2.13	0.49
79:18:37:C:H2'	79:18:38:A:O4'	2.13	0.49
79:18:1348:G:C8	79:18:1349:G:C8	3.01	0.49
79:18:1482:C:H2'	79:18:1483:A:O4'	2.13	0.49
79:18:1706:G:H2'	79:18:1707:U:H6	1.76	0.49
84:ES:3242:U:H2'	84:ES:3243:C:C6	2.48	0.49
85:28:271:C:H2'	85:28:272:U:H6	1.77	0.49
85:28:1617:G:H1'	85:28:2513:A:N6	2.28	0.49
85:28:1662:C:H2'	85:28:1663:C:C6	2.47	0.49
85:28:2780:C:H2'	85:28:2781:G:H8	1.78	0.49
85:28:4460:U:H2'	85:28:4461:C:H6	1.77	0.49
85:28:5003:U:H2'	85:28:5004:C:C6	2.47	0.49
6:6:36:C:H2'	6:6:37:G:C8	2.47	0.49
8:L3:321:VAL:HG12	8:L3:322:HIS:HD1	1.78	0.49
15:13:182:LEU:HD23	35:36:7:MET:HE3	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:t:128:THR:HA	48:t:131:GLU:HG2	1.94	0.49
50:Q:67:ILE:HD13	50:Q:98:LEU:HD11	1.95	0.49
63:RR:86:PRO:HG2	63:RR:130:LEU:HD22	1.94	0.49
79:18:356:C:O2	79:18:356:C:H2'	2.13	0.49
79:18:1651:A:H2'	79:18:1652:G:H8	1.78	0.49
85:28:1398:A:H61	85:28:1419:G:H2'	1.78	0.49
85:28:2080:U:H2'	85:28:2081:C:H6	1.78	0.49
85:28:2895:A:H2'	85:28:2896:G:H8	1.77	0.49
1:BB:201:LEU:HD11	71:RS:83:ASN:HA	1.95	0.48
8:L3:57:VAL:HG22	8:L3:73:VAL:HG12	1.95	0.48
49:F:174:ALA:HB2	49:F:181:PRO:HD3	1.94	0.48
60:MM:85:ASN:HB2	60:MM:88:MET:HB2	1.95	0.48
61:LL:40:TYR:HA	61:LL:43:VAL:HG22	1.93	0.48
79:18:1101:U:C2	79:18:1102:G:N7	2.81	0.48
79:18:1159:G:H2'	79:18:1160:U:C6	2.48	0.48
79:18:1199:A:H2'	79:18:1200:A:C8	2.48	0.48
79:18:1688:C:H2'	79:18:1689:C:C6	2.48	0.48
85:28:1565:A:C5	85:28:1566:C:H1'	2.48	0.48
85:28:5042:A:C4	85:28:5043:A:C8	3.01	0.48
2:S2:104:ASP:HB3	2:S2:130:ILE:HG13	1.95	0.48
47:s:34:ASN:HA	85:28:1968:G:O2'	2.12	0.48
78:L9:129:ARG:HG2	78:L9:153:LEU:HD22	1.95	0.48
79:18:1673:U:H2'	79:18:1674:G:O4'	2.13	0.48
80:v:208:VAL:HG12	80:v:261:TRP:HB3	1.95	0.48
85:28:490:C:H2'	85:28:491:G:C8	2.48	0.48
85:28:654:C:H2'	85:28:655:C:H6	1.78	0.48
85:28:1564:A:H2'	85:28:1565:A:C8	2.48	0.48
85:28:1804:A:H5''	85:28:1806:G:C8	2.49	0.48
85:28:2870:A:H2'	85:28:2871:A:C8	2.48	0.48
85:28:3855:C:H2'	85:28:3856:A:H8	1.78	0.48
85:28:4552:U:H2'	85:28:4553:A:C8	2.49	0.48
85:28:4593:C:H2'	85:28:4594:U:H6	1.76	0.48
85:28:4973:U:H2'	85:28:4974:C:C6	2.48	0.48
8:L3:261:ARG:HB2	18:bb:64:THR:HG21	1.94	0.48
10:L5:33:ARG:HA	10:L5:36:LEU:HB2	1.95	0.48
10:L5:53:VAL:HB	10:L5:159:VAL:HG13	1.95	0.48
49:F:75:ALA:HB1	49:F:118:ILE:HG23	1.96	0.48
56:II:31:LEU:HD21	56:II:33:LYS:HE3	1.95	0.48
79:18:319:C:H4'	79:18:319:C:OP1	2.11	0.48
79:18:1628:C:H2'	79:18:1629:C:H6	1.79	0.48
85:28:684:G:H5'	85:28:685:C:OP2	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:28:2602:G:H2'	85:28:2603:C:C6	2.48	0.48
85:28:3870:C:H2'	85:28:3871:A:C8	2.49	0.48
85:28:3920:U:H2'	85:28:3921:U:C6	2.48	0.48
85:28:4400:G:C6	85:28:4401:G:N7	2.81	0.48
85:28:5031:G:H2'	85:28:5032:C:C6	2.48	0.48
2:S2:106:VAL:HG22	2:S2:128:VAL:HG22	1.95	0.48
5:58:127:U:H2'	5:58:128:C:O4'	2.12	0.48
8:L3:301:ASN:HB3	8:L3:311:ASP:HA	1.94	0.48
9:L4:230:LEU:HD11	9:L4:239:LYS:HB2	1.95	0.48
62:XX:21:CYS:HA	62:XX:30:LEU:HD11	1.95	0.48
79:18:644:G:H2'	79:18:645:C:C6	2.47	0.48
79:18:1712:A:H2'	79:18:1713:C:C6	2.48	0.48
80:v:26:ALA:HB2	80:v:128:VAL:HB	1.96	0.48
85:28:271:C:H2'	85:28:272:U:C6	2.49	0.48
85:28:422:C:H2'	85:28:423:G:H8	1.79	0.48
85:28:1192:C:H2'	85:28:1193:C:C6	2.48	0.48
85:28:1308:C:H2'	85:28:1309:C:C6	2.48	0.48
85:28:1739:G:H2'	85:28:1740:C:C6	2.47	0.48
85:28:1802:A:H5''	85:28:1803:G:H5'	1.93	0.48
85:28:2561:C:H42	85:28:2566:G:H1	1.61	0.48
85:28:3654:G:H22	85:28:3817:A:H2	1.61	0.48
85:28:3769:C:H2'	85:28:3770:U:H6	1.79	0.48
30:31:64:ILE:HD11	85:28:2373:C:H4'	1.95	0.48
41:42:9:ARG:HA	41:42:20:PRO:HA	1.94	0.48
44:AS:48:LEU:HG	75:GG:51:GLU:HG2	1.95	0.48
47:s:57:LYS:HB3	47:s:60:MET:HB3	1.94	0.48
58:AA:18:VAL:HA	58:AA:35:SER:HA	1.94	0.48
58:AA:277:THR:HB	58:AA:281:ALA:HB3	1.95	0.48
79:18:574:A:H2'	79:18:574:A:N3	2.29	0.48
79:18:1102:G:H2'	79:18:1103:C:H6	1.79	0.48
79:18:1253:A:H4'	79:18:1254:C:H5''	1.96	0.48
79:18:1667:U:H2'	79:18:1668:U:C6	2.49	0.48
80:v:389:ASP:HB2	80:v:391:LYS:HE3	1.95	0.48
80:v:683:PHE:O	80:v:687:THR:HG22	2.14	0.48
85:28:1191:C:H2'	85:28:1192:C:H6	1.79	0.48
85:28:1744:U:C2	85:28:1745:G:C8	3.01	0.48
85:28:4584:A:H2'	85:28:4585:U:O4'	2.12	0.48
85:28:4594:U:C2	85:28:4595:G:C8	3.01	0.48
85:28:4708:A:N3	85:28:4709:U:H5'	2.29	0.48
85:28:5043:A:H2'	85:28:5044:A:C8	2.49	0.48
14:10:31:ILE:HG22	14:10:62:SER:HB2	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:27:51:ARG:HD2	26:27:65:ARG:HD2	1.95	0.48
31:32:35:TRP:CZ2	31:32:56:PRO:HD2	2.49	0.48
42:ff:7:LYS:HE2	85:28:2875:C:H2'	1.95	0.48
59:OO:67:LYS:HB3	79:18:1337:C:H4'	1.95	0.48
66:S4:7:LYS:HB2	79:18:93:U:O2'	2.13	0.48
79:18:26:U:H2'	79:18:27:A:C8	2.49	0.48
79:18:348:A:H2'	79:18:349:A:C8	2.49	0.48
79:18:673:G:H2'	79:18:674:C:C6	2.49	0.48
79:18:677:G:H2'	79:18:678:U:C6	2.49	0.48
79:18:1198:G:H2'	79:18:1199:A:H8	1.78	0.48
85:28:478:G:H2'	85:28:479:G:C8	2.48	0.48
85:28:711:A:H2'	85:28:712:C:C6	2.48	0.48
85:28:1557:C:H2'	85:28:1558:A:C8	2.49	0.48
85:28:2689:C:H2'	85:28:2690:C:C6	2.48	0.48
85:28:4254:G:H2'	85:28:4254:G:N3	2.28	0.48
2:S2:272:HIS:HA	2:S2:275:LYS:HG2	1.96	0.48
6:6:83:A:H4'	12:L7:223:THR:HB	1.95	0.48
10:L5:181:PRO:HG2	10:L5:195:HIS:HD2	1.79	0.48
17:15:5:LYS:NZ	35:36:37:THR:HG22	2.28	0.48
26:27:95:VAL:HG12	26:27:110:ALA:HA	1.95	0.48
32:ee:106:TYR:CD1	32:ee:107:PRO:HD3	2.49	0.48
61:LL:137:LYS:HE2	79:18:1234:C:N4	2.28	0.48
79:18:379:C:H2'	79:18:380:G:C8	2.49	0.48
79:18:958:G:H2'	79:18:959:G:O4'	2.13	0.48
80:v:551:GLU:O	80:v:555:GLU:HG2	2.14	0.48
85:28:648:G:H2'	85:28:649:A:H8	1.79	0.48
85:28:2589:C:C2	85:28:2590:G:C8	3.02	0.48
6:6:2:U:H2'	6:6:3:C:C6	2.49	0.48
44:AS:57:ILE:HB	44:AS:60:ASP:HB3	1.95	0.48
61:LL:108:ARG:NH1	61:LL:109:GLU:HA	2.29	0.48
73:S8:22:HIS:HB3	79:18:433:A:H5''	1.95	0.48
79:18:220:U:H2'	79:18:221:A:H8	1.78	0.48
79:18:349:A:H2'	79:18:350:C:C6	2.49	0.48
79:18:482:G:N2	79:18:484:A:H3'	2.28	0.48
79:18:1092:G:C2	79:18:1093:A:N7	2.81	0.48
79:18:1230:C:H2'	79:18:1231:C:C6	2.48	0.48
79:18:1347:U:H3'	79:18:1348:G:H21	1.79	0.48
85:28:469:C:H2'	85:28:470:A:C8	2.46	0.48
85:28:4345:C:H2'	85:28:4346:U:H6	1.78	0.48
85:28:4605:A:H2'	85:28:4606:G:O4'	2.14	0.48
85:28:4737:G:H2'	85:28:4738:C:C6	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:28:4890:G:H2'	85:28:4891:G:H8	1.78	0.48
7:L8:244:GLY:HA3	85:28:3746:A:H5''	1.96	0.48
7:L8:249:THR:HG22	79:18:1044:G:C8	2.49	0.48
19:17:28:ASN:O	19:17:32:THR:HG22	2.14	0.48
38:39:8:ARG:H	38:39:8:ARG:HD2	1.79	0.48
49:F:21:TYR:CD1	49:F:324:LEU:HD21	2.49	0.48
49:F:121:VAL:HB	49:F:334:THR:HB	1.95	0.48
52:EE:22:LEU:HD21	52:EE:89:VAL:HB	1.96	0.48
70:S3:161:GLY:CA	79:18:1388:A:H61	2.27	0.48
75:GG:99:ALA:N	75:GG:133:THR:HG22	2.29	0.48
79:18:1031:A:H2'	79:18:1032:C:H6	1.79	0.48
85:28:1846:G:H2'	85:28:1847:C:C6	2.49	0.48
85:28:2079:G:H2'	85:28:2080:U:H6	1.78	0.48
5:58:132:G:H2'	5:58:133:G:H8	1.79	0.48
6:6:15:C:H2'	6:6:16:A:H8	1.79	0.48
6:6:16:A:H2'	6:6:17:C:C6	2.49	0.48
24:cc:87:MET:HG3	49:F:291:MET:HE1	1.95	0.48
30:31:68:LEU:HA	30:31:108:TYR:HB2	1.96	0.48
79:18:557:U:H2'	79:18:558:G:C8	2.49	0.48
85:28:519:C:H2'	85:28:520:U:C6	2.49	0.48
85:28:4400:G:C2	85:28:4401:G:C8	3.02	0.48
6:6:112:U:H2'	6:6:113:G:H8	1.79	0.47
9:L4:28:PHE:HA	9:L4:129:ALA:HA	1.96	0.47
9:L4:221:PHE:HB3	9:L4:227:ILE:HG21	1.96	0.47
44:AS:115:LYS:H	44:AS:118:GLN:NE2	2.11	0.47
61:LL:120:HIS:HD2	83:A:121:ILE:HG22	1.79	0.47
67:S9:164:PRO:HB3	67:S9:170:PRO:HA	1.96	0.47
68:S7:69:LEU:HD13	68:S7:96:ALA:HB2	1.96	0.47
79:18:1297:U:H2'	79:18:1298:G:H2'	1.96	0.47
79:18:1568:C:H2'	79:18:1569:A:C8	2.48	0.47
79:18:1628:C:H2'	79:18:1629:C:C6	2.48	0.47
79:18:1839:U:H2'	79:18:1840:U:H6	1.79	0.47
85:28:1447:C:H2'	85:28:1448:G:H8	1.79	0.47
85:28:1463:C:H2'	85:28:1464:C:H6	1.78	0.47
85:28:1831:G:H2'	85:28:1832:C:O4'	2.14	0.47
85:28:4737:G:H2'	85:28:4738:C:H6	1.79	0.47
85:28:4970:C:H2'	85:28:4971:A:H8	1.77	0.47
85:28:5043:A:H2'	85:28:5044:A:H8	1.79	0.47
2:S2:272:HIS:O	2:S2:276:THR:HG22	2.15	0.47
4:DD:101:ARG:HD2	63:RR:6:GLY:O	2.14	0.47
9:L4:339:THR:HA	9:L4:342:ARG:HB3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L7:79:ASN:HA	22:21:143:THR:HG22	1.96	0.47
66:S4:189:LEU:HD12	66:S4:190:GLY:H	1.79	0.47
68:S7:63:PHE:HB3	68:S7:97:GLN:HB2	1.95	0.47
79:18:160:U:H3'	79:18:161:U:H5''	1.96	0.47
79:18:478:G:H2'	79:18:479:C:C6	2.50	0.47
79:18:900:C:H2'	79:18:901:G:C8	2.50	0.47
79:18:901:G:H2'	79:18:902:G:H8	1.78	0.47
79:18:1384:C:C2	79:18:1385:G:C8	3.02	0.47
85:28:2744:A:H2'	85:28:2745:A:H8	1.75	0.47
85:28:4130:C:H2'	85:28:4131:G:H8	1.79	0.47
85:28:4346:U:H2'	85:28:4347:G:C8	2.48	0.47
8:L3:45:ALA:HB3	8:L3:183:ILE:HG23	1.96	0.47
8:L3:161:ARG:HG2	8:L3:184:GLN:HA	1.97	0.47
13:aa:215:ASP:HB2	13:aa:216:PRO:HD3	1.96	0.47
16:14:89:THR:HG22	16:14:91:TRP:H	1.79	0.47
49:F:32:LEU:HA	49:F:35:LEU:HG	1.97	0.47
58:AA:64:HIS:HB3	58:AA:83:TRP:HB2	1.96	0.47
60:MM:48:TYR:HB2	79:18:1539:U:H1'	1.95	0.47
73:S8:129:LEU:HD23	73:S8:132:GLU:H	1.79	0.47
79:18:939:U:H2'	79:18:940:U:C6	2.48	0.47
83:A:38:SER:HB3	83:A:41:GLN:OE1	2.15	0.47
85:28:1077:C:C4	85:28:1078:A:N7	2.83	0.47
85:28:1447:C:H2'	85:28:1448:G:C8	2.49	0.47
85:28:2051:C:H2'	85:28:2052:G:O4'	2.14	0.47
85:28:3690:U:H2'	85:28:3691:G:O4'	2.13	0.47
85:28:4235:G:C2	85:28:4236:G:C8	3.03	0.47
1:BB:39:TYR:CE2	71:RS:105:MET:HB3	2.49	0.47
27:dd:35:ALA:HB2	85:28:38:A:H5''	1.97	0.47
46:VV:20:LYS:HG3	46:VV:21:LYS:HG2	1.96	0.47
60:MM:18:LEU:HD13	60:MM:134:ILE:HD13	1.97	0.47
60:MM:67:ARG:HD3	79:18:1587:G:N7	2.29	0.47
61:LL:88:LYS:HG2	83:A:18:ARG:HD3	1.96	0.47
68:S7:7:LYS:HB3	68:S7:44:ASN:HA	1.96	0.47
79:18:569:A:H2'	79:18:570:C:C6	2.50	0.47
80:v:669:VAL:HG21	80:v:707:VAL:HG22	1.96	0.47
85:28:270:U:H2'	85:28:271:C:C6	2.48	0.47
85:28:731:G:C6	85:28:932:A:C4	3.02	0.47
85:28:2547:G:H2'	85:28:2548:C:C6	2.49	0.47
85:28:4454:G:H2'	85:28:4455:G:H8	1.80	0.47
24:cc:140:LEU:HD11	24:cc:149:VAL:HG21	1.96	0.47
41:42:44:LYS:HE3	41:42:52:THR:HB	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
65:S6:131:ARG:HB3	79:18:168:C:O2'	2.15	0.47
77:11:127:GLY:HA3	85:28:4251:A:C2	2.50	0.47
79:18:527:C:H2'	79:18:528:A:H8	1.79	0.47
79:18:1112:U:H2'	79:18:1113:A:C8	2.50	0.47
79:18:1278:A:C6	79:18:1320:G:C6	3.02	0.47
79:18:1531:A:H2'	79:18:1532:C:C6	2.49	0.47
79:18:1687:C:H2'	79:18:1688:C:C6	2.49	0.47
85:28:60:A:C4	85:28:61:A:C8	3.03	0.47
85:28:490:C:H2'	85:28:491:G:H8	1.79	0.47
85:28:2749:C:H2'	85:28:2750:G:C8	2.49	0.47
85:28:4734:A:H1'	85:28:4735:G:C8	2.49	0.47
17:15:120:TRP:HZ2	17:15:123:GLU:HG2	1.80	0.47
34:35:112:ARG:HG2	85:28:173:C:H1'	1.96	0.47
38:39:23:ILE:HG23	38:39:38:ASN:HB2	1.97	0.47
38:39:43:HIS:HE2	85:28:2429:A:H5''	1.79	0.47
65:S6:2:LYS:HD2	65:S6:15:LEU:HD21	1.96	0.47
75:GG:78:ALA:O	75:GG:81:VAL:HG12	2.15	0.47
78:L9:20:LEU:HB3	78:L9:25:VAL:HG12	1.96	0.47
79:18:22:A:C2	79:18:23:G:C8	3.03	0.47
79:18:928:G:H2'	79:18:929:G:C8	2.49	0.47
79:18:1046:U:H2'	79:18:1047:C:C6	2.49	0.47
80:v:503:PRO:HB2	80:v:547:ALA:HB1	1.96	0.47
85:28:652:G:H2'	85:28:653:C:H6	1.79	0.47
85:28:1346:C:H2'	85:28:1347:G:C8	2.49	0.47
85:28:2633:U:H2'	85:28:2634:C:C6	2.50	0.47
85:28:2635:U:C4	85:28:2636:U:C4	3.02	0.47
85:28:3904:G:H1'	85:28:3905:A:OP1	2.13	0.47
85:28:4197:G:C4	85:28:4198:G:C8	3.02	0.47
85:28:4266:G:H2'	85:28:4266:G:N3	2.30	0.47
85:28:5031:G:H2'	85:28:5032:C:H6	1.79	0.47
86:23:13:LYS:HB2	86:23:128:LEU:HD21	1.95	0.47
5:58:142:U:C2	5:58:143:G:C8	3.02	0.47
6:6:51:G:H21	77:11:12:MET:HE3	1.80	0.47
7:L8:116:LEU:HA	7:L8:164:ALA:HB2	1.97	0.47
12:L7:222:LYS:HE3	85:28:1907:A:H4'	1.97	0.47
16:14:9:VAL:HG11	16:14:66:HIS:HA	1.96	0.47
17:15:86:HIS:CE1	85:28:33:A:H5'	2.49	0.47
54:S5:31:ASN:HB2	54:S5:117:ILE:HD13	1.97	0.47
58:AA:214:GLY:HA2	58:AA:236:ILE:HG12	1.96	0.47
61:LL:43:VAL:HG11	61:LL:83:PHE:CZ	2.49	0.47
79:18:14:C:H2'	79:18:15:U:H6	1.76	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
79:18:23:G:C4	79:18:24:C:C5	3.02	0.47
79:18:319:C:H2'	79:18:320:G:H8	1.80	0.47
79:18:399:C:H3'	79:18:400:C:H5'	1.95	0.47
79:18:465:A:H5''	79:18:466:G:C4	2.49	0.47
79:18:527:C:H2'	79:18:528:A:C8	2.50	0.47
79:18:1174:U:H2'	79:18:1175:G:C8	2.50	0.47
79:18:1236:G:H2'	79:18:1237:C:C6	2.49	0.47
85:28:20:U:H3'	85:28:21:G:H8	1.79	0.47
85:28:153:G:H2'	85:28:154:G:H8	1.79	0.47
85:28:673:C:H2'	85:28:674:G:C8	2.48	0.47
85:28:1170:G:H2'	85:28:1171:G:H8	1.79	0.47
85:28:1201:U:H2'	85:28:1202:C:C6	2.50	0.47
85:28:1662:C:H2'	85:28:1663:C:H6	1.79	0.47
85:28:2106:G:C6	85:28:2108:G:N7	2.83	0.47
85:28:2555:G:C2	85:28:2556:G:C5	3.02	0.47
85:28:2708:U:O2'	85:28:2709:C:H5'	2.14	0.47
85:28:2815:A:C4	85:28:2816:G:C8	3.02	0.47
85:28:3685:C:C2	85:28:3686:G:C8	3.03	0.47
85:28:3784:A:O2'	85:28:3785:A:H3'	2.15	0.47
85:28:4134:C:H2'	85:28:4135:G:C8	2.45	0.47
85:28:4189:U:H2'	85:28:4190:U:O4'	2.14	0.47
85:28:4433:G:H2'	85:28:4434:C:H6	1.80	0.47
85:28:4440:G:C4	85:28:4441:A:C8	3.02	0.47
85:28:4508:C:N3	85:28:4512:U:H5	2.13	0.47
85:28:4551:U:H2'	85:28:4552:U:C6	2.50	0.47
6:6:80:U:C2	6:6:81:G:C8	3.03	0.47
8:L3:324:GLY:HA2	85:28:5051:C:H4'	1.97	0.47
16:14:86:TRP:CE2	16:14:92:ALA:HB2	2.49	0.47
22:21:119:ALA:HA	22:21:122:LYS:HB2	1.97	0.47
58:AA:16:GLY:HA3	58:AA:36:ARG:HB2	1.96	0.47
67:S9:12:THR:O	67:S9:45:ARG:HA	2.14	0.47
79:18:828:G:N2	79:18:830:A:H1'	2.30	0.47
79:18:933:G:H1'	79:18:1001:A:H5'	1.96	0.47
79:18:1591:C:H2'	79:18:1592:C:C6	2.49	0.47
80:v:759:ILE:HG13	80:v:800:LEU:HD21	1.97	0.47
85:28:733:A:C4	85:28:734:G:C8	3.03	0.47
85:28:1957:U:O2'	85:28:1958:A:H5'	2.14	0.47
85:28:2732:G:H2'	85:28:2733:C:C6	2.50	0.47
85:28:3753:G:H2'	85:28:3754:G:H8	1.80	0.47
85:28:3834:C:H2'	85:28:3835:C:H6	1.80	0.47
85:28:4996:C:H2'	85:28:4997:G:H8	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:PP:39:VAL:HG22	3:PP:44:GLY:HA2	1.97	0.47
5:58:27:U:H2'	5:58:28:C:H6	1.80	0.47
5:58:32:C:H2'	5:58:33:G:O4'	2.15	0.47
5:58:40:A:H2'	5:58:41:A:H8	1.80	0.47
11:L6:165:VAL:HG12	11:L6:178:VAL:HG22	1.96	0.47
12:L7:215:PRO:HD3	12:L7:246:MET:HE2	1.97	0.47
19:17:83:TRP:O	85:28:3856:A:H5''	2.15	0.47
66:S4:180:LEU:HG	66:S4:232:ASN:HA	1.97	0.47
67:S9:33:GLY:HA3	69:YY:111:TYR:CD1	2.49	0.47
79:18:1034:A:C4	79:18:1035:A:C8	3.02	0.47
79:18:1166:G:H2'	79:18:1167:G:H8	1.80	0.47
79:18:1372:U:H2'	79:18:1373:C:O4'	2.15	0.47
79:18:1491:G:H2'	79:18:1492:U:C6	2.50	0.47
79:18:1528:G:H2'	79:18:1529:C:C6	2.49	0.47
84:ES:3245:G:H2'	84:ES:3246:G:H8	1.80	0.47
85:28:652:G:H2'	85:28:653:C:C6	2.50	0.47
85:28:2477:A:H2'	85:28:2478:C:C5	2.49	0.47
85:28:2502:A:H4'	85:28:2503:G:OP2	2.15	0.47
85:28:2538:U:H2'	85:28:2539:C:C6	2.50	0.47
85:28:3762:U:H2'	85:28:3763:A:O4'	2.14	0.47
85:28:3829:G:C2	85:28:3830:A:C8	3.02	0.47
85:28:4092:G:H2'	85:28:4093:G:C8	2.49	0.47
85:28:4625:C:O2'	85:28:4626:A:H5'	2.15	0.47
85:28:4652:G:H2'	85:28:4653:C:C6	2.50	0.47
5:58:140:C:H2'	5:58:141:C:H6	1.79	0.47
5:58:147:G:H2'	5:58:148:A:C8	2.49	0.47
8:L3:301:ASN:HB2	8:L3:304:SER:HB2	1.96	0.47
18:bb:62:MET:HG2	18:bb:65:ASN:H	1.80	0.47
38:39:16:LYS:HG3	38:39:49:LEU:HD11	1.97	0.47
45:FF:70:LYS:HG2	45:FF:73:ARG:HD2	1.96	0.47
51:ZZ:140:TYR:CE2	51:ZZ:142:GLY:HA2	2.50	0.47
58:AA:10:THR:HG22	58:AA:308:ARG:HB3	1.98	0.47
62:XX:33:LYS:HE2	62:XX:34:TYR:CZ	2.50	0.47
79:18:112:U:H2'	79:18:115:U:C5	2.49	0.47
79:18:168:C:H2'	79:18:169:U:H5'	1.96	0.47
79:18:432:G:H2'	79:18:433:A:C8	2.50	0.47
79:18:475:C:H1'	79:18:507:G:HO2'	1.80	0.47
80:v:648:LYS:HB3	80:v:664:ASP:HB3	1.96	0.47
85:28:178:C:H2'	85:28:179:G:C8	2.49	0.47
85:28:299:C:H2'	85:28:300:A:C8	2.50	0.47
85:28:951:G:H2'	85:28:952:G:H8	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:28:970:G:H2'	85:28:971:U:O4'	2.15	0.47
85:28:1750:G:C2	85:28:1751:A:C8	3.03	0.47
85:28:2682:G:H2'	85:28:2683:C:H6	1.80	0.47
85:28:4349:C:H3'	85:28:4350:C:H5'	1.97	0.47
85:28:4419:U:C4	85:28:4420:U:C5	3.03	0.47
85:28:5002:U:H2'	85:28:5003:U:C6	2.50	0.47
5:58:67:U:C2	5:58:68:G:C8	3.03	0.46
61:LL:64:VAL:O	61:LL:68:ILE:HG12	2.15	0.46
68:S7:117:PRO:HG2	68:S7:120:ARG:HD3	1.97	0.46
72:WX:11:LEU:HD12	72:WX:74:VAL:HB	1.98	0.46
79:18:531:A:H3'	79:18:532:C:H5''	1.97	0.46
79:18:577:U:H2'	79:18:578:C:H6	1.80	0.46
79:18:976:G:H2'	79:18:977:C:O4'	2.16	0.46
79:18:1126:G:H2'	79:18:1127:C:H6	1.80	0.46
85:28:86:U:H2'	85:28:87:A:H8	1.80	0.46
85:28:1566:C:H2'	85:28:1567:U:H6	1.80	0.46
85:28:1965:G:H2'	85:28:1966:C:C6	2.50	0.46
85:28:2034:G:H2'	85:28:2035:C:C6	2.50	0.46
85:28:2894:A:H2'	85:28:2895:A:C8	2.50	0.46
85:28:3932:U:H2'	85:28:3933:G:C8	2.49	0.46
8:L3:231:VAL:HG21	8:L3:251:VAL:HG23	1.97	0.46
13:aa:223:LEU:HD12	13:aa:254:THR:HG21	1.97	0.46
39:40:56:LEU:HB3	78:L9:95:VAL:HG22	1.97	0.46
44:AS:139:CYS:HB3	44:AS:172:MET:HE3	1.98	0.46
51:ZZ:107:LYS:HG2	51:ZZ:117:LEU:HD11	1.96	0.46
56:II:34:VAL:HG12	56:II:70:VAL:HB	1.96	0.46
57:CC:50:GLN:HE22	79:18:1276:A:H4'	1.78	0.46
60:MM:18:LEU:HB3	60:MM:58:ALA:HB1	1.96	0.46
79:18:1352:G:H2'	79:18:1353:A:H8	1.79	0.46
79:18:1597:C:H4'	79:18:1603:G:C6	2.51	0.46
85:28:1582:U:C2	85:28:1583:A:C8	3.04	0.46
85:28:1664:U:H2'	85:28:1665:C:C6	2.51	0.46
85:28:3637:U:O4	85:28:3651:A:H2	1.98	0.46
86:23:89:ARG:HB2	86:23:95:PHE:CE2	2.51	0.46
5:58:30:U:H2'	5:58:31:G:H8	1.80	0.46
7:L8:49:ILE:HD13	7:L8:60:LYS:HE3	1.95	0.46
8:L3:262:VAL:HG21	8:L3:268:ARG:NH1	2.30	0.46
14:10:3:ARG:NH2	85:28:4430:G:H5'	2.30	0.46
15:13:72:ALA:HA	15:13:157:ILE:HD12	1.97	0.46
21:20:83:ARG:HB3	21:20:125:GLN:HB2	1.98	0.46
27:dd:89:ASN:HA	27:dd:92:LYS:HG2	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
65:S6:63:MET:HE3	65:S6:100:CYS:HA	1.98	0.46
65:S6:136:LYS:HB2	79:18:65:C:N4	2.30	0.46
71:RS:77:GLU:HA	71:RS:80:ARG:HG2	1.96	0.46
76:UU:28:ARG:HD3	76:UU:74:CYS:SG	2.55	0.46
79:18:155:G:C2	79:18:156:G:C8	3.03	0.46
79:18:636:C:H2'	79:18:637:U:O4'	2.14	0.46
79:18:1160:U:H2'	79:18:1161:U:H6	1.80	0.46
79:18:1826:G:H2'	79:18:1827:U:C6	2.49	0.46
85:28:164:G:H2'	85:28:165:A:C8	2.51	0.46
85:28:424:U:H2'	85:28:425:U:C6	2.50	0.46
85:28:950:G:H2'	85:28:951:G:H8	1.80	0.46
85:28:1505:C:C2	85:28:1506:G:C8	3.03	0.46
85:28:2479:G:C4	85:28:2480:G:C8	3.02	0.46
85:28:2567:G:H2'	85:28:2568:C:H6	1.80	0.46
85:28:2664:G:H4'	85:28:2677:G:H4'	1.97	0.46
85:28:4968:A:H2'	85:28:4969:C:C6	2.50	0.46
5:58:27:U:H2'	5:58:28:C:C6	2.51	0.46
13:aa:104:LEU:HD11	85:28:4086:G:C4	2.51	0.46
20:19:4:LEU:HD11	20:19:29:THR:HG23	1.96	0.46
32:ee:46:ARG:HD2	32:ee:106:TYR:OH	2.15	0.46
47:s:57:LYS:HD2	85:28:2020:U:H5'	1.98	0.46
51:ZZ:106:TYR:CE2	51:ZZ:116:ARG:HG2	2.50	0.46
58:AA:220:ASP:HB3	58:AA:223:GLU:O	2.15	0.46
61:LL:27:ALA:HB1	61:LL:42:HIS:CE1	2.51	0.46
77:11:146:ARG:HG2	77:11:147:ARG:HG2	1.97	0.46
79:18:642:U:H4'	79:18:643:A:OP1	2.14	0.46
79:18:1035:A:H2'	79:18:1036:A:C8	2.49	0.46
79:18:1349:G:H2'	79:18:1350:U:C6	2.51	0.46
79:18:1455:A:H2'	79:18:1456:G:H8	1.80	0.46
85:28:713:C:H2'	85:28:714:G:C8	2.50	0.46
85:28:726:G:H2'	85:28:727:C:C6	2.51	0.46
85:28:1472:C:H2'	85:28:1473:U:C6	2.50	0.46
85:28:2386:U:C2	85:28:2387:G:C8	3.03	0.46
85:28:2634:C:C2	85:28:2635:U:C5	3.04	0.46
85:28:3633:C:H2'	85:28:3634:G:C8	2.50	0.46
85:28:3927:U:H2'	85:28:3928:A:H8	1.80	0.46
85:28:4460:U:H2'	85:28:4461:C:C6	2.50	0.46
8:L3:373:LYS:HE2	85:28:4627:U:H4'	1.97	0.46
14:10:19:LYS:HB3	14:10:26:VAL:HG21	1.96	0.46
19:17:131:ARG:HG3	19:17:137:ASN:ND2	2.31	0.46
21:20:16:CYS:HB3	21:20:25:PRO:HG2	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:ee:23:GLU:H	32:ee:23:GLU:CD	2.24	0.46
65:S6:230:LYS:O	65:S6:234:LEU:HG	2.15	0.46
78:L9:88:PHE:CE2	78:L9:151:ILE:HB	2.50	0.46
79:18:350:C:N3	79:18:351:G:C8	2.84	0.46
79:18:848:U:O2	79:18:849:A:C8	2.68	0.46
79:18:1006:C:H2'	79:18:1007:C:H6	1.80	0.46
79:18:1177:U:H2'	79:18:1178:U:C6	2.51	0.46
79:18:1375:G:H5'	79:18:1464:C:O2	2.15	0.46
79:18:1412:C:C2	79:18:1413:G:C8	3.04	0.46
79:18:1686:G:H2'	79:18:1687:C:C6	2.50	0.46
85:28:311:G:H2'	85:28:312:G:H8	1.80	0.46
85:28:317:A:C2	85:28:4361:U:H1'	2.50	0.46
85:28:2771:G:H2'	85:28:2772:C:O4'	2.15	0.46
85:28:2832:A:C4	85:28:2833:A:C8	3.04	0.46
85:28:3890:A:N7	85:28:4571:A:H1'	2.31	0.46
85:28:4089:G:H2'	85:28:4090:G:H8	1.80	0.46
85:28:4968:A:H2'	85:28:4969:C:H6	1.81	0.46
1:BB:59:LEU:HD22	1:BB:181:GLU:HG2	1.98	0.46
4:DD:55:TYR:OH	4:DD:116:CYS:HB3	2.16	0.46
5:58:141:C:H2'	5:58:142:U:H6	1.81	0.46
13:aa:210:ILE:HA	13:aa:254:THR:HG22	1.97	0.46
68:S7:101:LEU:HD13	68:S7:120:ARG:HG2	1.98	0.46
79:18:443:U:H2'	79:18:444:G:C8	2.51	0.46
79:18:1609:C:H2'	79:18:1610:G:C8	2.50	0.46
80:v:9:ILE:HA	80:v:12:ILE:HG22	1.97	0.46
80:v:126:LEU:HA	80:v:154:VAL:HG23	1.96	0.46
85:28:1519:C:H2'	85:28:1520:C:C6	2.51	0.46
85:28:1958:A:C4'	85:28:1962:A:H1'	2.46	0.46
85:28:2556:G:C2	85:28:2557:G:N7	2.84	0.46
85:28:3787:G:H1'	85:28:3789:C:N4	2.31	0.46
85:28:4233:A:C8	85:28:4235:G:C8	3.03	0.46
85:28:4503:A:H2'	85:28:4504:C:C6	2.50	0.46
85:28:4637:G:H2'	85:28:4638:U:H6	1.78	0.46
85:28:4951:G:C2	85:28:4952:G:C8	3.03	0.46
1:BB:148:CYS:SG	1:BB:160:ALA:HB1	2.56	0.46
10:L5:153:THR:HG21	85:28:4323:A:C6	2.50	0.46
12:L7:240:ASN:O	12:L7:244:ARG:HG2	2.16	0.46
38:39:25:GLN:HG3	38:39:28:TRP:CZ2	2.51	0.46
47:s:24:TYR:CG	47:s:90:PHE:HB3	2.50	0.46
49:F:32:LEU:HD12	49:F:110:LEU:HD21	1.96	0.46
61:LL:82:TRP:CD1	61:LL:82:TRP:H	2.32	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:SS:62:THR:HA	64:SS:69:THR:HG22	1.97	0.46
75:GG:28:PHE:HA	75:GG:92:ALA:HB3	1.98	0.46
79:18:479:C:H2'	79:18:480:G:C8	2.50	0.46
79:18:1588:A:H2'	79:18:1589:A:C8	2.51	0.46
80:v:132:VAL:HG13	80:v:167:LEU:HD11	1.98	0.46
80:v:480:VAL:HG13	80:v:481:LYS:H	1.81	0.46
85:28:1348:U:H2'	85:28:1349:G:C8	2.51	0.46
85:28:1382:G:N3	85:28:1383:G:C8	2.83	0.46
85:28:1460:C:H2'	85:28:1461:C:H6	1.81	0.46
85:28:1578:U:H2'	85:28:1579:C:C6	2.51	0.46
85:28:1829:G:H2'	85:28:1830:G:C8	2.51	0.46
85:28:2016:C:C2	85:28:2017:A:C8	3.03	0.46
85:28:2542:G:H2'	85:28:2543:A:C8	2.50	0.46
85:28:2557:G:H2'	85:28:2558:C:H6	1.79	0.46
85:28:3768:U:H2'	85:28:3769:C:H6	1.81	0.46
85:28:4524:G:H2'	85:28:4525:C:H6	1.81	0.46
1:BB:131:HIS:HA	1:BB:134:LEU:HD12	1.97	0.46
2:S2:256:TRP:CE2	72:WX:68:ARG:HB3	2.51	0.46
7:L8:28:ARG:HD3	7:L8:123:ARG:HD3	1.98	0.46
12:L7:50:TYR:CD1	85:28:1237:C:H2'	2.50	0.46
20:19:105:LEU:HD22	20:19:135:LYS:HG3	1.98	0.46
31:32:108:ARG:HD3	31:32:127:ALA:HB3	1.98	0.46
44:AS:165:ARG:HD2	79:18:1004:U:OP1	2.15	0.46
48:t:152:ILE:HD12	48:t:155:ILE:HD12	1.98	0.46
58:AA:270:LEU:HD22	58:AA:310:TRP:CE3	2.50	0.46
70:S3:66:ILE:O	70:S3:70:THR:HG23	2.15	0.46
79:18:299:A:H2'	79:18:300:U:H6	1.81	0.46
79:18:512:A:C2	79:18:513:G:C8	3.04	0.46
79:18:953:C:H2'	79:18:954:U:O4'	2.16	0.46
79:18:1367:U:H2'	79:18:1368:U:C6	2.51	0.46
79:18:1501:C:H2'	79:18:1502:C:C6	2.51	0.46
80:v:313:ALA:HA	80:v:316:ILE:HG12	1.98	0.46
85:28:1359:G:H3'	85:28:1360:G:C8	2.51	0.46
85:28:1590:C:H4'	85:28:2857:A:H5'	1.98	0.46
85:28:2634:C:H2'	85:28:2635:U:C6	2.49	0.46
85:28:4389:C:H2'	85:28:4390:A:H8	1.80	0.46
86:23:11:GLY:H	86:23:128:LEU:HD13	1.81	0.46
6:6:55:A:H2'	6:6:56:G:H8	1.80	0.46
9:L4:189:MET:HE3	85:28:2333:G:N7	2.31	0.46
49:F:181:PRO:HA	49:F:230:VAL:HA	1.97	0.46
51:ZZ:100:LEU:HD11	79:18:1285:G:H1'	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:EE:52:LEU:HD11	52:EE:62:VAL:HG23	1.97	0.46
65:S6:7:PHE:HD1	65:S6:8:PRO:HD2	1.80	0.46
72:WX:8:ALA:HA	72:WX:74:VAL:HG11	1.97	0.46
73:S8:8:TRP:HA	73:S8:18:ARG:HD2	1.98	0.46
79:18:676:C:H2'	79:18:677:G:O4'	2.15	0.46
79:18:1161:U:H2'	79:18:1162:C:C6	2.51	0.46
79:18:1393:G:H2'	79:18:1394:G:C8	2.51	0.46
79:18:1461:G:H1'	79:18:1465:A:N6	2.30	0.46
85:28:221:C:H2'	85:28:222:C:C6	2.51	0.46
85:28:1199:G:C2	85:28:1200:G:C5	3.04	0.46
85:28:1291:G:H2'	85:28:1292:C:C6	2.51	0.46
85:28:1421:G:C2	85:28:1422:G:C8	3.04	0.46
85:28:1972:G:C4	85:28:1995:G:N2	2.84	0.46
85:28:2499:C:H2'	85:28:2500:U:C6	2.51	0.46
85:28:2885:A:H2'	85:28:2886:U:C6	2.51	0.46
9:L4:149:GLU:HG2	9:L4:151:PRO:HD2	1.97	0.46
16:14:39:ASP:OD2	16:14:70:GLN:HG2	2.16	0.46
18:bb:188:LYS:HD3	85:28:4892:A:H5''	1.97	0.46
24:cc:80:PRO:HA	24:cc:98:PHE:HA	1.98	0.46
45:FF:113:PHE:CE2	45:FF:117:LEU:HD11	2.51	0.46
76:UU:84:VAL:HB	79:18:1866:A:N6	2.30	0.46
79:18:434:G:H2'	79:18:435:A:C8	2.51	0.46
79:18:883:U:H2'	79:18:884:C:C6	2.51	0.46
79:18:1413:G:H2'	79:18:1414:A:C8	2.51	0.46
79:18:1610:G:H2'	79:18:1611:G:C8	2.51	0.46
80:v:304:ILE:HD13	80:v:336:LEU:HA	1.97	0.46
85:28:426:A:H2'	85:28:427:A:C8	2.51	0.46
85:28:516:C:H2'	85:28:517:C:H6	1.81	0.46
85:28:2421:G:OP2	85:28:2828:U:H1'	2.16	0.46
85:28:2610:G:H2'	85:28:2611:A:C8	2.51	0.46
85:28:3832:U:H2'	85:28:3833:C:C6	2.51	0.46
85:28:3933:G:H2'	85:28:3934:G:C8	2.50	0.46
85:28:4345:C:H2'	85:28:4346:U:C6	2.51	0.46
85:28:4477:A:C4	85:28:4478:G:C8	3.04	0.46
7:L8:83:HIS:HB3	42:ff:64:VAL:HG22	1.98	0.45
61:LL:107:LEU:O	61:LL:111:LEU:HG	2.16	0.45
73:S8:23:LYS:HD2	79:18:448:A:H3'	1.99	0.45
79:18:98:C:H2'	79:18:426:A:H4'	1.97	0.45
79:18:348:A:H2'	79:18:349:A:H8	1.79	0.45
79:18:673:G:H2'	79:18:674:C:H6	1.82	0.45
79:18:887:U:O2	79:18:887:U:H2'	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
79:18:1094:C:H2'	79:18:1095:U:C6	2.51	0.45
79:18:1137:U:O2'	79:18:1138:C:H3'	2.16	0.45
79:18:1688:C:H2'	79:18:1689:C:H6	1.81	0.45
79:18:1733:U:H2'	79:18:1734:G:O4'	2.16	0.45
79:18:1806:A:H2'	79:18:1807:C:C6	2.51	0.45
85:28:263:G:H2'	85:28:264:C:C6	2.51	0.45
85:28:1212:G:H2'	85:28:1213:G:C8	2.51	0.45
85:28:1963:C:C2	85:28:1964:A:C2	3.04	0.45
85:28:2000:G:H4'	85:28:2017:A:C2	2.52	0.45
85:28:2281:U:C2	85:28:2282:A:C8	3.04	0.45
85:28:2385:U:H2'	85:28:2386:U:H6	1.81	0.45
85:28:2689:C:C2	85:28:2690:C:C5	3.03	0.45
85:28:2893:U:H2'	85:28:2894:A:H8	1.80	0.45
8:L3:154:LYS:HG3	8:L3:194:LEU:HD23	1.98	0.45
18:bb:169:ARG:CZ	85:28:4860:G:H5'	2.46	0.45
79:18:106:C:H2'	79:18:107:A:C8	2.49	0.45
79:18:449:A:O2'	79:18:450:C:H4'	2.16	0.45
79:18:501:C:H2'	79:18:502:C:H5''	1.99	0.45
79:18:896:U:H2'	79:18:897:U:C6	2.52	0.45
79:18:980:A:H2'	79:18:981:A:C8	2.51	0.45
85:28:1687:U:H2'	85:28:1688:G:C8	2.51	0.45
85:28:2358:G:H2'	85:28:2359:U:O4'	2.16	0.45
85:28:2520:C:H2'	85:28:2521:G:C8	2.44	0.45
85:28:2555:G:H2'	85:28:2556:G:C8	2.51	0.45
85:28:2690:C:C4	85:28:2691:U:C4	3.05	0.45
85:28:2815:A:H2'	85:28:2816:G:H8	1.80	0.45
3:PP:8:PHE:CZ	3:PP:10:ASP:HB2	2.52	0.45
6:6:55:A:C4	6:6:56:G:C8	3.05	0.45
18:bb:26:GLN:HG3	21:20:167:PHE:CZ	2.52	0.45
24:cc:72:ASP:O	24:cc:76:ILE:HG23	2.17	0.45
67:S9:84:ILE:HG13	67:S9:86:VAL:HG23	1.97	0.45
77:11:25:CYS:HB3	85:28:4252:C:H42	1.81	0.45
79:18:89:C:O2'	79:18:499:G:H5''	2.16	0.45
79:18:934:G:C2	79:18:935:G:C8	3.03	0.45
84:ES:2953:C:H2'	84:ES:2954:G:H8	1.81	0.45
85:28:233:U:C2'	85:28:234:G:C8	2.99	0.45
85:28:275:C:H2'	85:28:276:C:C6	2.51	0.45
85:28:1988:G:C2	85:28:1989:G:C8	3.04	0.45
85:28:2295:C:H2'	85:28:2296:G:H8	1.81	0.45
85:28:2587:A:H5''	85:28:2588:C:C5	2.51	0.45
85:28:2623:A:H2'	85:28:2624:G:H8	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:28:2858:A:H2'	85:28:2859:G:O4'	2.16	0.45
12:L7:115:GLN:HG3	50:Q:3:VAL:HG12	1.97	0.45
41:42:26:TYR:HB2	41:42:82:MET:HE1	1.98	0.45
64:SS:53:ASP:HB3	64:SS:79:LEU:HD13	1.99	0.45
65:S6:21:GLU:O	65:S6:25:ARG:HD3	2.16	0.45
65:S6:135:PRO:HG2	65:S6:144:LEU:HD22	1.98	0.45
71:RS:31:ASN:HA	71:RS:34:VAL:HB	1.97	0.45
72:WX:103:VAL:HA	72:WX:112:ASP:HA	1.99	0.45
73:S8:11:ARG:NH2	73:S8:17:LYS:HE3	2.31	0.45
79:18:854:A:C2	79:18:855:G:C8	3.05	0.45
79:18:950:C:H2'	79:18:951:C:H6	1.80	0.45
79:18:1531:A:H2'	79:18:1532:C:H6	1.82	0.45
79:18:1591:C:H2'	79:18:1592:C:H6	1.80	0.45
85:28:1199:G:C2	85:28:1200:G:N7	2.85	0.45
85:28:1315:C:H2'	85:28:1316:G:C8	2.51	0.45
85:28:2264:C:H2'	85:28:2265:G:O4'	2.15	0.45
85:28:2629:C:H2'	85:28:2630:U:O4'	2.15	0.45
85:28:4638:U:H2'	85:28:4639:G:N3	2.30	0.45
5:58:130:C:H2'	5:58:131:G:C8	2.51	0.45
17:15:178:HIS:HA	17:15:181:HIS:NE2	2.31	0.45
44:AS:163:GLN:O	44:AS:167:LYS:HG2	2.17	0.45
67:S9:42:GLU:O	67:S9:46:VAL:HG23	2.16	0.45
70:S3:211:VAL:HG12	81:LA:715:ILE:HG13	1.98	0.45
79:18:1043:G:N2	79:18:1073:U:C4	2.85	0.45
79:18:1351:G:H2'	79:18:1352:G:H8	1.81	0.45
85:28:460:C:H2'	85:28:461:G:C8	2.51	0.45
85:28:1479:G:H2'	85:28:1480:C:C6	2.51	0.45
85:28:1664:U:H2'	85:28:1665:C:H6	1.82	0.45
85:28:2413:U:C2	85:28:2414:G:C8	3.05	0.45
85:28:2457:G:H2'	85:28:2458:C:C6	2.52	0.45
85:28:3722:G:H2'	85:28:3723:A:C8	2.52	0.45
49:F:113:HIS:CE1	49:F:276:MET:HG3	2.52	0.45
63:RR:88:ASP:HB2	79:18:617:G:H4'	1.99	0.45
79:18:458:A:H2'	79:18:459:C:C6	2.52	0.45
79:18:493:A:C8	79:18:574:A:H8	2.34	0.45
79:18:1090:C:H2'	79:18:1091:C:H6	1.82	0.45
79:18:1272:C:O2'	79:18:1273:C:H5'	2.17	0.45
79:18:1554:C:H2'	79:18:1555:U:C5	2.51	0.45
85:28:1592:G:C2	85:28:1593:A:C8	3.05	0.45
85:28:2588:C:H5''	85:28:2589:C:H5''	1.99	0.45
85:28:2885:A:H2'	85:28:2886:U:H6	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:28:3846:C:H2'	85:28:3847:C:H6	1.81	0.45
1:BB:206:ASP:HB3	1:BB:209:GLU:HG3	1.98	0.45
2:S2:210:PRO:HB3	2:S2:240:THR:HG21	1.99	0.45
21:20:93:MET:HE1	21:20:117:HIS:CE1	2.52	0.45
22:21:89:ILE:HG22	85:28:4300:U:H4'	1.99	0.45
30:31:70:LYS:HE2	85:28:2389:A:H5'	1.99	0.45
36:37:3:LYS:HB3	85:28:3642:A:C4	2.51	0.45
47:s:84:GLY:C	85:28:2021:G:H4'	2.41	0.45
48:t:105:THR:HG22	48:t:108:GLU:CD	2.41	0.45
49:F:20:LYS:O	49:F:23:MET:HG2	2.16	0.45
50:Q:63:LEU:O	50:Q:67:ILE:HG12	2.16	0.45
59:OO:79:ARG:H	62:XX:54:LYS:HE3	1.81	0.45
61:LL:108:ARG:HH11	61:LL:109:GLU:HA	1.82	0.45
64:SS:37:LYS:HD2	64:SS:57:VAL:O	2.17	0.45
79:18:456:C:H2'	79:18:457:C:H6	1.81	0.45
79:18:609:U:H2'	79:18:610:G:H8	1.81	0.45
79:18:1109:C:H2'	79:18:1110:G:O4'	2.17	0.45
85:28:1206:C:H2'	85:28:1207:C:H6	1.82	0.45
85:28:2404:A:H61	85:28:2787:A:N6	2.14	0.45
85:28:2553:A:H2	85:28:2765:A:H62	1.62	0.45
85:28:2556:G:N3	85:28:2557:G:C8	2.85	0.45
85:28:5030:U:H2'	85:28:5031:G:C8	2.49	0.45
6:6:102:U:C2	6:6:103:A:C8	3.05	0.45
14:10:59:GLN:HG2	14:10:128:ARG:HB3	1.99	0.45
27:dd:24:LYS:HE2	27:dd:24:LYS:HB2	1.74	0.45
31:32:22:ARG:HG3	31:32:36:ARG:H	1.81	0.45
33:34:5:LEU:HD21	33:34:30:ILE:HG22	1.98	0.45
48:t:83:LYS:HG3	48:t:84:ALA:N	2.31	0.45
50:Q:69:LYS:HD2	85:28:1458:C:H5''	1.97	0.45
54:S5:39:ILE:HG23	54:S5:68:ILE:HD13	1.98	0.45
57:CC:52:LEU:HB3	57:CC:57:TYR:HB2	1.98	0.45
66:S4:128:LYS:HA	66:S4:156:VAL:HG13	1.99	0.45
70:S3:39:VAL:HA	70:S3:48:ILE:HG22	1.98	0.45
72:WX:36:ARG:HB2	72:WX:110:ILE:HD12	1.99	0.45
79:18:946:U:H2'	79:18:947:G:C8	2.52	0.45
79:18:1395:C:H2'	79:18:1396:A:C2	2.51	0.45
79:18:1723:G:H2'	79:18:1724:A:H8	1.81	0.45
80:v:609:PHE:CE1	80:v:701:ARG:HB2	2.51	0.45
85:28:489:C:H2'	85:28:490:C:C6	2.51	0.45
85:28:4174:U:H2'	85:28:4175:G:C8	2.51	0.45
85:28:4307:A:H2'	85:28:4308:C:H6	1.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:28:4504:C:H2'	85:28:4505:C:H6	1.82	0.45
85:28:5055:G:H2'	85:28:5056:A:H8	1.82	0.45
2:S2:118:ALA:HB2	79:18:1486:A:H4'	1.99	0.45
8:L3:253:CYS:SG	85:28:4521:U:H1'	2.57	0.45
17:15:85:VAL:HA	41:42:49:GLY:HA2	1.99	0.45
48:t:104:ILE:HG23	48:t:143:VAL:HG22	1.99	0.45
65:S6:186:GLN:HE22	79:18:318:A:H61	1.65	0.45
72:WX:50:PHE:HB3	72:WX:63:VAL:HG13	1.99	0.45
79:18:563:G:C2	79:18:564:A:N7	2.85	0.45
79:18:1090:C:H2'	79:18:1091:C:C6	2.52	0.45
80:v:425:LEU:HD12	80:v:427:VAL:HG13	1.99	0.45
83:A:95:GLY:HA2	83:A:104:GLN:HA	1.98	0.45
85:28:272:U:H2'	85:28:273:U:C6	2.52	0.45
85:28:679:C:C2	85:28:680:G:C8	3.05	0.45
85:28:751:G:C4	85:28:752:G:C8	3.05	0.45
85:28:1298:C:C2	85:28:1299:G:C8	3.05	0.45
85:28:1569:U:H2'	85:28:1570:G:C8	2.52	0.45
85:28:1732:C:O2'	85:28:1733:G:H5'	2.17	0.45
85:28:4130:C:H2'	85:28:4131:G:C8	2.52	0.45
85:28:4198:G:H2'	85:28:4199:C:H6	1.82	0.45
85:28:4685:U:H2'	85:28:4686:G:H8	1.81	0.45
7:L8:187:HIS:HB3	85:28:2740:U:O4'	2.17	0.45
9:L4:113:ARG:HG3	85:28:1508:A:OP1	2.17	0.45
68:S7:140:VAL:HG21	68:S7:159:ASP:HB3	1.99	0.45
79:18:203:G:H2'	79:18:204:G:C8	2.51	0.45
80:v:757:GLY:HA3	85:28:2009:A:H5'	1.99	0.45
85:28:969:C:H42	85:28:2095:A:H61	1.64	0.45
85:28:978:C:H2'	85:28:979:G:H8	1.82	0.45
85:28:1195:G:N3	85:28:1196:G:C8	2.85	0.45
85:28:1895:G:H2'	85:28:1896:A:O4'	2.17	0.45
85:28:2479:G:H2'	85:28:2480:G:H8	1.82	0.45
85:28:2540:C:H2'	85:28:2541:G:C8	2.51	0.45
85:28:4152:G:H2'	85:28:4153:C:C6	2.52	0.45
85:28:4407:G:H2'	85:28:4408:G:H8	1.82	0.45
5:58:40:A:H2'	5:58:41:A:C8	2.51	0.44
30:31:45:ALA:O	30:31:48:GLU:HG2	2.17	0.44
32:ee:54:LYS:HB3	85:28:443:G:H5''	1.99	0.44
36:37:12:ARG:HH11	85:28:2404:A:H1'	1.82	0.44
48:t:146:ARG:HA	48:t:146:ARG:HD2	1.58	0.44
58:AA:173:LEU:HB2	58:AA:175:LYS:HZ2	1.82	0.44
60:MM:62:ARG:HD3	79:18:1542:C:OP1	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:RR:90:CYS:SG	63:RR:130:LEU:HD21	2.57	0.44
79:18:431:G:N3	79:18:432:G:C8	2.85	0.44
79:18:918:U:H2'	79:18:919:A:O4'	2.17	0.44
79:18:1019:C:H2'	79:18:1020:A:O4'	2.17	0.44
79:18:1671:G:H2'	79:18:1672:U:H6	1.82	0.44
79:18:1730:U:C2	79:18:1731:A:C8	3.05	0.44
84:ES:3245:G:H2'	84:ES:3246:G:C8	2.53	0.44
85:28:1350:C:H2'	85:28:1351:G:C8	2.52	0.44
85:28:1475:G:H2'	85:28:1476:C:C6	2.52	0.44
85:28:4197:G:H2'	85:28:4198:G:H8	1.82	0.44
85:28:4594:U:H2'	85:28:4595:G:C8	2.51	0.44
85:28:4960:G:H2'	85:28:4961:G:C8	2.52	0.44
85:28:5066:U:H2'	85:28:5067:U:C6	2.52	0.44
9:L4:22:VAL:HG22	9:L4:258:ARG:NH1	2.32	0.44
12:L7:174:ILE:HD13	12:L7:189:LEU:HD12	1.99	0.44
18:bb:130:LYS:HB2	18:bb:133:ARG:HG2	2.00	0.44
29:30:64:ALA:HB1	29:30:69:THR:O	2.16	0.44
43:gg:104:PRO:O	43:gg:107:ARG:HG2	2.17	0.44
45:FF:88:LEU:HD11	45:FF:122:ILE:HG23	1.99	0.44
48:t:105:THR:HG23	48:t:107:ASP:H	1.82	0.44
61:LL:20:ILE:HD11	61:LL:33:ILE:HD11	1.99	0.44
63:RR:124:LYS:HA	63:RR:129:SER:HA	1.97	0.44
79:18:219:U:H2'	79:18:220:U:H6	1.81	0.44
79:18:943:U:C2	79:18:944:A:C8	3.06	0.44
79:18:1217:A:H2'	79:18:1218:C:H6	1.79	0.44
79:18:1340:U:H2'	79:18:1341:C:C5	2.53	0.44
79:18:1689:C:H2'	79:18:1690:U:H6	1.82	0.44
79:18:1862:G:H4'	79:18:1863:A:OP1	2.17	0.44
85:28:25:A:C8	85:28:341:G:C8	3.05	0.44
85:28:27:C:H2'	85:28:28:C:H6	1.81	0.44
85:28:149:A:H5''	85:28:151:G:O4'	2.17	0.44
85:28:1932:A:H2'	85:28:1933:G:C8	2.52	0.44
85:28:1964:A:H2'	85:28:1965:G:O4'	2.16	0.44
85:28:3896:C:H2'	85:28:3897:G:C4	2.52	0.44
85:28:4069:U:H2'	85:28:4070:U:H6	1.82	0.44
85:28:4263:C:H2'	85:28:4264:G:O4'	2.17	0.44
1:BB:81:ASN:HA	1:BB:84:GLN:HE22	1.83	0.44
5:58:28:C:H2'	5:58:29:G:H8	1.82	0.44
5:58:96:C:H5''	34:35:66:LYS:HG2	1.99	0.44
6:6:46:C:OP1	10:L5:158:LYS:HG3	2.18	0.44
7:L8:47:ASP:HA	7:L8:84:THR:HG22	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:L3:86:VAL:HG12	8:L3:201:LEU:HD12	2.00	0.44
34:35:80:PRO:HD2	34:35:83:LEU:HD12	2.00	0.44
38:39:44:TRP:CZ3	38:39:45:ARG:HD3	2.53	0.44
44:AS:49:VAL:HG21	44:AS:62:LEU:HD13	1.98	0.44
48:t:20:GLY:H	48:t:54:LYS:HA	1.82	0.44
59:OO:56:MET:SD	59:OO:86:LYS:HB3	2.58	0.44
65:S6:7:PHE:CD1	65:S6:113:ILE:HB	2.52	0.44
65:S6:181:THR:HG23	65:S6:184:VAL:H	1.82	0.44
73:S8:10:LYS:HB2	79:18:371:A:OP2	2.18	0.44
79:18:1743:G:H21	79:18:1791:A:H62	1.65	0.44
85:28:677:G:H2'	85:28:678:C:C6	2.51	0.44
85:28:963:G:N3	85:28:964:A:C8	2.85	0.44
85:28:2478:C:C2	85:28:2479:G:C8	3.06	0.44
85:28:2671:C:H2'	85:28:2672:C:C6	2.52	0.44
85:28:2863:G:C4	85:28:2864:A:C8	3.05	0.44
85:28:3702:A:C4	85:28:3703:G:C8	3.04	0.44
85:28:4407:G:H1'	85:28:4438:U:C2	2.52	0.44
12:L7:46:ARG:HH11	85:28:976:C:H5''	1.79	0.44
29:30:105:ILE:H	29:30:105:ILE:HG13	1.53	0.44
43:gg:51:VAL:HG12	43:gg:117:ILE:HD12	2.00	0.44
51:ZZ:140:TYR:HE1	51:ZZ:145:CYS:HA	1.81	0.44
58:AA:165:ILE:HD11	58:AA:177:TRP:HB2	1.99	0.44
59:OO:34:LYS:O	59:OO:38:ASP:HB2	2.18	0.44
67:S9:144:ILE:HG12	79:18:824:C:C2	2.52	0.44
73:S8:31:ARG:HE	79:18:380:G:H5''	1.82	0.44
79:18:464:A:H3'	79:18:465:A:H5'	1.99	0.44
79:18:1261:C:C4	79:18:1262:C:C4	3.06	0.44
79:18:1562:C:H2'	79:18:1563:G:H8	1.83	0.44
79:18:1709:G:H2'	79:18:1710:C:H6	1.81	0.44
79:18:1739:C:H2'	79:18:1740:C:H6	1.81	0.44
79:18:1742:C:H2'	79:18:1743:G:O4'	2.18	0.44
85:28:269:G:H2'	85:28:270:U:H6	1.81	0.44
85:28:987:C:H2'	85:28:988:C:H6	1.82	0.44
85:28:1557:C:H2'	85:28:1558:A:H8	1.82	0.44
85:28:1558:A:H2'	85:28:1559:G:C8	2.52	0.44
85:28:1730:U:H2'	85:28:1731:C:C6	2.53	0.44
85:28:1792:U:H2'	85:28:1793:A:O4'	2.18	0.44
85:28:1862:U:H4'	85:28:4212:A:OP2	2.18	0.44
85:28:2479:G:N3	85:28:2480:G:C8	2.85	0.44
85:28:3916:G:H2'	85:28:3917:A:H8	1.79	0.44
85:28:4565:C:H2'	85:28:4566:U:H6	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:28:4678:G:N2	85:28:4713:G:H1'	2.33	0.44
4:DD:102:PHE:H	63:RR:8:ARG:HA	1.82	0.44
6:6:118:C:H2'	6:6:119:U:C6	2.52	0.44
7:L8:3:ARG:HD3	85:28:1628:C:H42	1.82	0.44
12:L7:65:ARG:CZ	85:28:1210:C:H41	2.31	0.44
17:15:95:ALA:HB3	85:28:30:C:H5''	1.99	0.44
20:19:70:ARG:HH22	85:28:2810:U:H5''	1.81	0.44
25:26:59:ARG:HG3	25:26:103:LYS:HD2	1.98	0.44
35:36:74:LYS:HA	35:36:83:ALA:HB2	1.99	0.44
49:F:249:ARG:HB3	49:F:275:ALA:HA	1.99	0.44
60:MM:39:LEU:HD23	60:MM:56:ARG:NH1	2.32	0.44
68:S7:102:PRO:HA	79:18:688:U:C5	2.53	0.44
72:WX:30:CYS:HA	72:WX:34:ILE:HD12	1.99	0.44
80:v:249:ARG:HG3	80:v:250:ALA:N	2.32	0.44
80:v:749:ILE:O	80:v:783:VAL:HA	2.17	0.44
85:28:396:A:H2'	85:28:397:G:C8	2.53	0.44
85:28:676:C:H2'	85:28:677:G:C8	2.51	0.44
85:28:1690:C:H2'	85:28:1691:G:O4'	2.18	0.44
85:28:2011:C:C2	85:28:2012:A:C8	3.06	0.44
85:28:2329:U:H2'	85:28:2330:G:O4'	2.17	0.44
85:28:2499:C:H2'	85:28:2500:U:H6	1.83	0.44
85:28:3626:G:C6	85:28:3836:A:C2	3.06	0.44
85:28:3664:G:C2	85:28:3665:G:N7	2.86	0.44
1:BB:30:LEU:HD21	1:BB:35:GLU:HG2	1.98	0.44
1:BB:127:PRO:HG3	1:BB:146:ALA:HB1	1.99	0.44
5:58:153:C:H2'	5:58:154:G:C8	2.52	0.44
9:L4:328:LEU:HB3	12:L7:186:MET:HG3	1.98	0.44
14:10:190:LEU:HB3	14:10:197:VAL:HG21	1.99	0.44
18:bb:80:PHE:HA	18:bb:83:THR:HG22	1.99	0.44
21:20:35:PRO:HD2	21:20:39:VAL:HG21	1.99	0.44
29:30:38:ILE:HD13	29:30:43:ALA:HB3	1.98	0.44
44:AS:70:SER:HA	44:AS:83:LYS:HG2	1.99	0.44
45:FF:54:LEU:HD23	45:FF:58:HIS:ND1	2.33	0.44
55:WW:51:ARG:HG2	55:WW:52:GLU:H	1.81	0.44
56:II:71:ARG:CZ	79:18:1407:U:H4'	2.48	0.44
63:RR:90:CYS:HA	63:RR:93:PHE:CD1	2.52	0.44
63:RR:105:PHE:HB3	63:RR:112:VAL:HG21	2.00	0.44
74:W:49:ILE:O	74:W:52:THR:HG22	2.17	0.44
79:18:23:G:C5	79:18:24:C:C4	3.06	0.44
79:18:1676:U:C4	79:18:1677:U:C5	3.06	0.44
80:v:421:VAL:HA	80:v:425:LEU:HG	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:28:211:G:C2	85:28:212:A:C8	3.06	0.44
85:28:221:C:H2'	85:28:222:C:H6	1.82	0.44
85:28:470:A:C4	85:28:471:A:C8	3.05	0.44
85:28:1808:C:H1'	85:28:1831:G:N2	2.32	0.44
85:28:2804:C:H2'	85:28:2805:C:C6	2.53	0.44
5:58:28:C:C2	5:58:29:G:C8	3.06	0.44
5:58:92:U:H2'	5:58:93:C:O4'	2.17	0.44
6:6:58:A:H2'	6:6:59:G:H8	1.81	0.44
10:L5:15:ARG:CZ	85:28:1743:A:H1'	2.47	0.44
13:aa:267:ALA:HA	13:aa:270:LYS:HG2	1.99	0.44
14:10:9:TYR:HE1	85:28:1866:U:H5'	1.82	0.44
16:14:24:LEU:HD11	16:14:86:TRP:CG	2.53	0.44
20:19:3:MET:HG2	85:28:2385:U:H4'	2.00	0.44
65:S6:216:ARG:NH1	66:S4:153:LEU:HD13	2.32	0.44
75:GG:42:VAL:HG11	75:GG:81:VAL:HG11	1.99	0.44
79:18:1266:C:C4	79:18:1517:G:N2	2.86	0.44
79:18:1650:A:H2'	79:18:1651:A:O4'	2.17	0.44
80:v:504:VAL:HG11	80:v:810:PRO:HG2	1.98	0.44
85:28:1382:G:C2	85:28:1383:G:N7	2.86	0.44
85:28:1545:G:H2'	85:28:1546:C:C6	2.53	0.44
85:28:2089:G:H4'	85:28:2090:U:O5'	2.17	0.44
1:BB:130:ASP:C	1:BB:133:PRO:HD2	2.43	0.44
1:BB:140:VAL:HB	1:BB:142:LEU:HG	2.00	0.44
6:6:60:G:C2	6:6:61:G:C8	3.06	0.44
10:L5:146:LEU:HD22	85:28:4323:A:C2	2.52	0.44
26:27:50:PRO:HD3	26:27:68:ILE:HD13	1.98	0.44
44:AS:207:LEU:HD12	44:AS:210:VAL:HG21	1.99	0.44
58:AA:12:LYS:H	58:AA:12:LYS:HD3	1.83	0.44
64:SS:22:GLN:HB3	64:SS:74:MET:HG3	1.99	0.44
69:YY:110:GLN:HA	69:YY:113:ARG:HG2	2.00	0.44
79:18:186:C:H2'	79:18:187:G:C8	2.52	0.44
79:18:537:C:H2'	79:18:538:U:C6	2.51	0.44
79:18:1485:U:H2'	79:18:1486:A:O4'	2.18	0.44
79:18:1666:C:H2'	79:18:1667:U:C6	2.53	0.44
85:28:299:C:H2'	85:28:300:A:H8	1.83	0.44
85:28:1095:A:H2'	85:28:1096:C:C6	2.53	0.44
85:28:1514:U:H2'	85:28:1515:A:C8	2.53	0.44
85:28:1519:C:H2'	85:28:1520:C:H6	1.83	0.44
85:28:1951:G:C6	85:28:2033:A:C2	3.05	0.44
5:58:140:C:H2'	5:58:141:C:C6	2.52	0.44
7:L8:183:GLY:CA	85:28:1613:A:H5''	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:bb:85:ARG:HG3	18:bb:99:LEU:HD11	1.99	0.44
28:29:43:MET:HE2	28:29:43:MET:HB3	1.89	0.44
31:32:35:TRP:HH2	31:32:55:MET:HG2	1.83	0.44
60:MM:31:PRO:HG3	60:MM:102:ARG:HG2	1.99	0.44
66:S4:151:ASP:HB3	66:S4:154:ILE:HG13	1.99	0.44
77:11:27:GLY:HA2	77:11:68:ILE:HB	1.99	0.44
77:11:111:GLU:HB2	77:11:125:ILE:HD11	1.99	0.44
79:18:39:A:H2'	79:18:40:A:O4'	2.18	0.44
85:28:1334:A:H2'	85:28:1335:G:H8	1.82	0.44
85:28:1350:C:H2'	85:28:1351:G:H8	1.83	0.44
85:28:1402:C:H2'	85:28:1403:G:H8	1.80	0.44
85:28:1720:C:H2'	85:28:1721:G:O4'	2.18	0.44
85:28:1797:G:H2'	85:28:1798:G:H8	1.83	0.44
85:28:2380:G:N2	85:28:2424:G:H5''	2.33	0.44
85:28:3768:U:H2'	85:28:3769:C:C6	2.53	0.44
85:28:3851:U:H2'	85:28:3852:A:O4'	2.18	0.44
85:28:4889:G:H2'	85:28:4890:G:C8	2.53	0.44
4:DD:128:VAL:HB	4:DD:140:PHE:HB3	1.99	0.43
6:6:51:G:H21	77:11:12:MET:CE	2.31	0.43
8:L3:4:ARG:HD2	8:L3:7:SER:HA	1.99	0.43
12:L7:45:ARG:O	12:L7:49:ILE:HG12	2.17	0.43
13:aa:90:LYS:HG3	85:28:4127:A:C2	2.53	0.43
27:dd:76:ASP:HB2	27:dd:115:GLY:HA3	1.99	0.43
33:34:60:ARG:HB3	33:34:63:VAL:HG23	2.00	0.43
34:35:47:ILE:HG13	34:35:48:ARG:N	2.31	0.43
39:40:99:LYS:HG3	85:28:4474:A:H5'	2.00	0.43
49:F:170:TRP:HA	49:F:173:VAL:HG22	2.00	0.43
54:S5:59:LYS:HB3	54:S5:62:ARG:HB2	1.99	0.43
56:II:12:VAL:HA	79:18:1397:U:O4	2.18	0.43
58:AA:142:VAL:HG11	58:AA:145:GLU:HB3	1.99	0.43
62:XX:50:ILE:HG13	70:S3:15:GLY:C	2.43	0.43
64:SS:45:ALA:HB1	64:SS:50:THR:O	2.18	0.43
67:S9:128:VAL:HG22	69:YY:104:ARG:HH22	1.83	0.43
76:UU:92:ARG:HB3	79:18:1865:C:O2	2.17	0.43
79:18:375:U:C2	79:18:376:A:C8	3.06	0.43
79:18:537:C:H2'	79:18:538:U:C5	2.53	0.43
79:18:1293:A:C5	79:18:1294:G:C8	3.06	0.43
79:18:1716:C:H2'	79:18:1717:C:H6	1.83	0.43
80:v:388:CYS:HB2	80:v:466:CYS:SG	2.58	0.43
85:28:93:G:H2'	85:28:94:A:H8	1.82	0.43
85:28:1077:C:C2	85:28:1078:A:C8	3.06	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:28:2688:G:H2'	85:28:2689:C:C6	2.53	0.43
85:28:2893:U:H2'	85:28:2894:A:C8	2.53	0.43
85:28:4638:U:C2	85:28:4639:G:C2	3.06	0.43
86:23:43:LYS:HE2	86:23:62:MET:SD	2.57	0.43
2:S2:183:LYS:HG3	72:WX:95:PRO:O	2.18	0.43
8:L3:56:ILE:HA	8:L3:56:ILE:HD13	1.72	0.43
13:aa:194:ASN:O	13:aa:198:THR:HG23	2.18	0.43
22:21:107:LYS:HE3	22:21:107:LYS:HB3	1.88	0.43
33:34:70:THR:HG21	85:28:2588:C:H41	1.82	0.43
36:37:4:GLY:HA3	85:28:1601:A:OP2	2.18	0.43
44:AS:150:ILE:HD13	71:RS:129:LYS:HB2	2.00	0.43
49:F:29:ASN:O	49:F:33:ARG:HG2	2.18	0.43
65:S6:91:GLU:HG2	65:S6:92:ARG:N	2.33	0.43
66:S4:105:THR:HB	66:S4:245:ARG:HG2	2.00	0.43
74:W:35:LYS:HD3	74:W:51:TRP:CZ2	2.53	0.43
76:UU:84:VAL:HG12	79:18:1867:U:C4	2.53	0.43
79:18:375:U:H2'	79:18:376:A:C8	2.54	0.43
79:18:465:A:H4'	79:18:466:G:O5'	2.18	0.43
79:18:493:A:H1'	79:18:574:A:O5'	2.18	0.43
79:18:677:G:H2'	79:18:678:U:H6	1.83	0.43
79:18:974:C:H2'	79:18:975:G:C8	2.53	0.43
79:18:1369:A:H8	79:18:1369:A:OP1	2.01	0.43
80:v:19:ILE:HD12	80:v:99:LEU:HB3	2.00	0.43
85:28:12:A:H5'	85:28:13:U:OP2	2.18	0.43
85:28:441:G:H2'	85:28:442:G:H8	1.82	0.43
85:28:1753:G:N2	85:28:1778:C:C2	2.86	0.43
85:28:2397:G:C8	85:28:2399:G:C8	3.06	0.43
85:28:2662:G:H2'	85:28:2663:G:C8	2.53	0.43
85:28:4251:A:H2'	85:28:4252:C:O4'	2.18	0.43
85:28:4448:G:H4'	85:28:4449:A:OP2	2.18	0.43
1:BB:102:ARG:HA	1:BB:102:ARG:HD2	1.65	0.43
8:L3:175:GLN:HA	85:28:4986:G:H5'	2.00	0.43
9:L4:83:GLY:H	85:28:368:C:H1'	1.83	0.43
13:aa:309:ALA:O	13:aa:313:GLU:HG2	2.17	0.43
65:S6:89:THR:HG22	79:18:91:A:H61	1.83	0.43
65:S6:172:LYS:HE2	79:18:65:C:H4'	1.99	0.43
67:S9:144:ILE:HG21	79:18:824:C:H1'	2.00	0.43
79:18:298:G:C4	79:18:299:A:C8	3.06	0.43
79:18:353:C:H2'	79:18:354:U:C6	2.53	0.43
79:18:363:A:H4'	79:18:364:A:H4'	1.99	0.43
80:v:764:ASN:HB3	85:28:4419:U:H1'	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:v:831:PRO:HA	80:v:834:VAL:HB	1.99	0.43
85:28:962:C:C2	85:28:963:G:C8	3.05	0.43
85:28:973:C:H2'	85:28:974:G:H8	1.83	0.43
85:28:1464:C:C2	85:28:1465:G:C8	3.07	0.43
85:28:1510:G:H2'	85:28:1511:U:C6	2.53	0.43
85:28:2310:C:H2'	85:28:2311:C:C6	2.53	0.43
85:28:2335:C:H2'	85:28:2336:G:C8	2.40	0.43
85:28:2735:G:C2	85:28:2736:G:C8	3.07	0.43
85:28:2864:A:H2'	85:28:2865:U:C6	2.53	0.43
85:28:4357:G:H2'	85:28:4358:U:C6	2.54	0.43
85:28:4647:G:C2	85:28:4648:A:C8	3.06	0.43
85:28:4995:U:H2'	85:28:4996:C:C6	2.52	0.43
3:PP:73:ALA:HB1	3:PP:78:ILE:HB	1.99	0.43
6:6:3:C:H2'	6:6:4:U:C6	2.54	0.43
14:10:66:GLU:CD	14:10:69:ARG:HH21	2.27	0.43
16:14:90:ARG:O	16:14:94:LYS:HG2	2.17	0.43
27:dd:55:LYS:HD3	85:28:92:C:C2	2.52	0.43
33:34:26:PRO:HA	85:28:2639:U:H1'	2.00	0.43
56:II:16:LYS:HG3	56:II:17:LYS:H	1.83	0.43
64:SS:42:GLU:O	64:SS:46:LYS:HG3	2.18	0.43
67:S9:110:LEU:O	67:S9:114:VAL:HG23	2.19	0.43
77:11:57:VAL:HG12	77:11:59:SER:H	1.83	0.43
79:18:609:U:H2'	79:18:610:G:C8	2.53	0.43
79:18:1702:G:H2'	79:18:1703:C:O4'	2.19	0.43
80:v:27:HIS:HB3	80:v:30:HIS:CE1	2.54	0.43
85:28:385:A:H4'	85:28:386:A:OP1	2.18	0.43
85:28:432:U:H4'	85:28:433:A:H5''	1.99	0.43
85:28:1465:G:C2	85:28:1466:G:C8	3.06	0.43
85:28:1490:G:H2'	85:28:1491:A:H8	1.83	0.43
85:28:1633:G:H4'	85:28:1634:A:O5'	2.18	0.43
85:28:1964:A:H2'	85:28:1965:G:H8	1.83	0.43
85:28:2386:U:H2'	85:28:2387:G:H8	1.83	0.43
85:28:2699:C:H2'	85:28:2700:G:C8	2.53	0.43
6:6:4:U:H2'	6:6:5:A:H8	1.83	0.43
6:6:106:G:C4	6:6:107:G:C8	3.06	0.43
15:13:57:PRO:HG3	15:13:75:GLY:C	2.44	0.43
18:bb:84:VAL:HG11	18:bb:102:LEU:HD22	2.00	0.43
21:20:164:LYS:HB3	21:20:165:PRO:HD3	2.00	0.43
30:31:70:LYS:HG3	85:28:2389:A:H4'	2.00	0.43
44:AS:66:VAL:HA	44:AS:86:LEU:O	2.17	0.43
56:II:18:THR:HB	56:II:75:GLY:HA2	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:AA:108:VAL:HA	58:AA:124:SER:HA	2.01	0.43
64:SS:29:HIS:HB2	64:SS:32:LYS:HG3	2.01	0.43
79:18:493:A:C8	79:18:574:A:C8	3.07	0.43
79:18:1618:C:H2'	79:18:1619:A:C8	2.54	0.43
79:18:1677:U:C2	79:18:1678:A:C8	3.06	0.43
79:18:1686:G:H2'	79:18:1687:C:H6	1.83	0.43
84:ES:2949:U:H2'	84:ES:2950:G:C8	2.53	0.43
85:28:651:C:H2'	85:28:652:G:C8	2.50	0.43
85:28:653:C:H2'	85:28:654:C:C6	2.54	0.43
85:28:679:C:H2'	85:28:680:G:C8	2.49	0.43
85:28:1594:C:O2'	85:28:1597:G:H1'	2.18	0.43
85:28:1959:U:H1'	85:28:1961:G:N3	2.33	0.43
85:28:1962:A:C2	85:28:1963:C:C6	3.06	0.43
85:28:2357:G:C2	85:28:2358:G:C5	3.07	0.43
85:28:5013:C:H4'	85:28:5014:A:H5''	2.00	0.43
7:L8:199:VAL:HG21	85:28:1631:A:N7	2.34	0.43
10:L5:249:GLU:HG3	10:L5:250:ASN:N	2.34	0.43
31:32:29:VAL:HB	85:28:1332:C:H5''	2.00	0.43
47:s:53:VAL:HA	47:s:89:VAL:HA	2.00	0.43
49:F:288:LYS:HB2	49:F:288:LYS:HE3	1.68	0.43
70:S3:68:GLU:O	70:S3:72:VAL:HG23	2.18	0.43
75:GG:102:GLY:C	75:GG:136:PRO:HG3	2.44	0.43
78:L9:47:LEU:HD13	78:L9:55:LEU:HD12	2.00	0.43
79:18:150:A:H62	79:18:168:C:H42	1.66	0.43
79:18:1650:A:H1'	79:18:1675:A:N6	2.33	0.43
80:v:422:SER:H	80:v:425:LEU:HD23	1.84	0.43
85:28:48:G:H1'	85:28:49:U:OP2	2.19	0.43
85:28:1461:C:C2	85:28:1462:A:C8	3.07	0.43
85:28:1490:G:H2'	85:28:1491:A:C8	2.54	0.43
85:28:1884:C:H2'	85:28:1885:G:H8	1.83	0.43
85:28:2492:C:C2	85:28:2493:G:N7	2.87	0.43
85:28:4082:G:H2'	85:28:4083:U:C6	2.53	0.43
1:BB:41:ARG:HB2	1:BB:47:TYR:CE1	2.54	0.43
2:S2:253:PRO:HA	2:S2:256:TRP:CE2	2.54	0.43
5:58:30:U:H2'	5:58:31:G:C8	2.53	0.43
9:L4:137:VAL:HG21	9:L4:150:LEU:HD21	2.01	0.43
12:L7:66:THR:O	12:L7:70:MET:HG2	2.19	0.43
33:34:6:THR:HG22	85:28:2400:G:H21	1.84	0.43
44:AS:106:THR:HG22	44:AS:108:ASP:H	1.84	0.43
54:S5:152:TRP:CH2	79:18:1221:G:H4'	2.54	0.43
79:18:1144:A:H5'	79:18:1355:C:N4	2.30	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:28:299:C:C2	85:28:300:A:C8	3.07	0.43
85:28:1681:G:H2'	85:28:1682:A:C8	2.54	0.43
85:28:2056:G:C8	85:28:2058:G:C8	3.06	0.43
85:28:2897:G:H2'	85:28:2898:G:H8	1.83	0.43
85:28:3794:C:H2'	85:28:3795:A:H8	1.84	0.43
85:28:4985:U:H2'	85:28:4986:G:H8	1.83	0.43
6:6:31:G:C6	6:6:47:G:C6	3.07	0.43
8:L3:168:MET:HE3	8:L3:175:GLN:NE2	2.32	0.43
14:10:36:LEU:HD23	14:10:69:ARG:HH11	1.83	0.43
48:t:54:LYS:O	48:t:54:LYS:HG2	2.19	0.43
48:t:146:ARG:HE	48:t:147:HIS:H	1.67	0.43
50:Q:173:LYS:HE3	50:Q:173:LYS:HB2	1.89	0.43
60:MM:129:ARG:O	60:MM:133:ARG:HG3	2.19	0.43
65:S6:188:LYS:O	65:S6:191:ARG:HG2	2.19	0.43
72:WX:93:LEU:HD21	72:WX:128:PHE:CD1	2.54	0.43
79:18:1525:C:H2'	79:18:1526:G:H8	1.84	0.43
79:18:1787:G:H2'	79:18:1788:A:H8	1.83	0.43
80:v:394:LEU:HB3	80:v:487:THR:HG23	2.01	0.43
85:28:283:G:H2'	85:28:284:G:H8	1.83	0.43
85:28:324:A:H2'	85:28:325:U:H6	1.84	0.43
85:28:1340:C:C2	85:28:1341:U:C5	3.07	0.43
85:28:2505:C:H1'	85:28:2506:G:C8	2.54	0.43
85:28:5001:U:H2'	85:28:5002:U:O4'	2.18	0.43
86:23:92:ASP:OD1	86:23:94:VAL:HG22	2.19	0.43
7:L8:201:GLY:HA3	7:L8:209:HIS:CE1	2.54	0.43
11:L6:242:LYS:HB2	11:L6:242:LYS:HE2	1.80	0.43
20:19:96:MET:SD	85:28:2607:C:H5''	2.59	0.43
42:ff:49:ARG:HB2	42:ff:55:TRP:CZ3	2.54	0.43
52:EE:120:ALA:HA	52:EE:123:VAL:HG12	1.99	0.43
56:II:104:SER:HA	56:II:107:GLU:CG	2.48	0.43
63:RR:5:ARG:O	72:WX:77:PRO:HD3	2.19	0.43
70:S3:142:LEU:HD13	70:S3:143:ARG:HG3	2.00	0.43
79:18:79:A:C8	79:18:80:G:C8	3.07	0.43
79:18:1201:U:H2'	79:18:1202:U:H6	1.82	0.43
79:18:1221:G:C2	79:18:1222:G:C5	3.07	0.43
85:28:125:C:H2'	85:28:126:C:C6	2.53	0.43
85:28:952:G:H2'	85:28:953:C:H6	1.84	0.43
85:28:1577:G:O2'	85:28:1612:G:H4'	2.19	0.43
85:28:1956:A:O2'	85:28:1957:U:H5'	2.19	0.43
85:28:2015:U:H2'	85:28:2016:C:C6	2.46	0.43
85:28:2078:C:C2	85:28:2079:G:C8	3.07	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:28:2317:C:H2'	85:28:2318:G:C8	2.54	0.43
85:28:2446:C:H2'	85:28:2447:U:C6	2.54	0.43
85:28:4378:A:O2'	85:28:4379:A:H2'	2.19	0.43
85:28:4389:C:H2'	85:28:4390:A:C8	2.54	0.43
85:28:4486:C:H2'	85:28:4487:A:O4'	2.19	0.43
1:BB:38:ILE:HD11	1:BB:150:THR:HG22	1.99	0.43
5:58:148:A:H2'	5:58:149:G:H8	1.83	0.43
5:58:155:C:H2'	5:58:156:U:C6	2.54	0.43
8:L3:89:ILE:HG21	8:L3:197:ALA:HB1	2.01	0.43
9:L4:205:ARG:HG3	85:28:2297:G:H5'	2.00	0.43
10:L5:41:LYS:HB2	22:21:68:THR:O	2.19	0.43
19:17:48:LEU:O	19:17:52:THR:HG23	2.19	0.43
20:19:37:SER:O	20:19:41:ILE:HG12	2.19	0.43
43:gg:113:ARG:O	43:gg:117:ILE:HG13	2.18	0.43
44:AS:181:LEU:O	44:AS:185:VAL:HG23	2.19	0.43
49:F:247:TYR:HB3	49:F:302:LEU:HB3	2.00	0.43
58:AA:257:LYS:HD2	58:AA:259:TRP:CZ2	2.54	0.43
61:LL:142:ARG:HE	61:LL:142:ARG:HB2	1.63	0.43
70:S3:170:THR:HB	70:S3:187:LYS:HG2	2.01	0.43
75:GG:38:ASN:C	75:GG:69:SER:HB2	2.43	0.43
78:L9:106:GLN:HB2	78:L9:111:LEU:HB3	2.00	0.43
79:18:71:G:C8	79:18:79:A:C6	3.07	0.43
79:18:678:U:C2	79:18:679:A:C8	3.07	0.43
80:v:155:LEU:O	80:v:212:VAL:HA	2.19	0.43
85:28:434:A:H2'	85:28:435:A:O4'	2.18	0.43
85:28:1370:G:H4'	85:28:1371:A:O5'	2.19	0.43
85:28:2730:U:H2'	85:28:2731:C:C6	2.54	0.43
85:28:2894:A:H2'	85:28:2895:A:H8	1.83	0.43
8:L3:252:ALA:HB3	85:28:4457:U:H1'	2.01	0.42
16:14:11:ARG:NH2	16:14:61:ILE:HD11	2.34	0.42
16:14:62:LEU:HD13	16:14:64:PHE:HE2	1.84	0.42
38:39:44:TRP:CH2	38:39:45:ARG:HD3	2.54	0.42
49:F:202:ILE:HB	49:F:213:HIS:CD2	2.53	0.42
59:OO:34:LYS:HD3	59:OO:107:GLU:HG3	2.00	0.42
65:S6:157:VAL:HG22	79:18:75:G:H22	1.84	0.42
75:GG:55:ARG:HH12	79:18:954:U:H1'	1.83	0.42
79:18:220:U:C2	79:18:221:A:C8	3.06	0.42
79:18:430:C:H2'	79:18:431:G:H8	1.83	0.42
79:18:935:G:H2'	79:18:936:G:C8	2.53	0.42
79:18:1387:G:C2	79:18:1388:A:H1'	2.54	0.42
79:18:1590:C:H3'	79:18:1591:C:C6	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
79:18:1787:G:H2'	79:18:1788:A:C8	2.54	0.42
85:28:134:G:OP1	85:28:134:G:H2'	2.19	0.42
85:28:254:G:H2'	85:28:255:C:C6	2.54	0.42
85:28:678:C:H2'	85:28:679:C:H6	1.83	0.42
85:28:962:C:H2'	85:28:963:G:C8	2.53	0.42
85:28:1617:G:H1'	85:28:2513:A:H61	1.84	0.42
85:28:1920:C:H3'	85:28:1921:C:H5''	2.00	0.42
85:28:2538:U:H2'	85:28:2539:C:H6	1.83	0.42
85:28:2640:G:N3	85:28:2641:A:C8	2.86	0.42
2:S2:209:VAL:HG21	2:S2:233:LEU:HD11	2.01	0.42
9:L4:66:SER:HA	9:L4:77:PRO:HA	2.01	0.42
11:L6:156:LEU:HD13	32:ee:105:LEU:HD13	2.00	0.42
14:10:180:GLU:O	14:10:184:MET:HG3	2.19	0.42
22:21:80:VAL:O	22:21:83:LYS:HG2	2.19	0.42
25:26:59:ARG:HB2	25:26:103:LYS:HB3	2.02	0.42
26:27:98:LYS:HE2	26:27:98:LYS:HB3	1.77	0.42
27:dd:82:VAL:HB	27:dd:86:THR:HG21	2.01	0.42
70:S3:99:ILE:HG12	70:S3:100:ALA:N	2.34	0.42
72:WX:20:ARG:HG2	72:WX:22:LYS:HE2	2.01	0.42
78:L9:92:MET:HE2	78:L9:179:ILE:HG22	2.01	0.42
79:18:191:A:N3	79:18:191:A:H2'	2.33	0.42
79:18:1011:A:H2'	79:18:1012:A:C8	2.53	0.42
79:18:1856:C:H2'	79:18:1857:G:H8	1.84	0.42
80:v:149:GLU:HA	80:v:371:LEU:HD13	2.01	0.42
83:A:108:LYS:HD3	83:A:108:LYS:HA	1.86	0.42
85:28:228:C:H2'	85:28:229:G:H8	1.84	0.42
85:28:262:G:N3	85:28:263:G:C8	2.87	0.42
85:28:691:C:H2'	85:28:692:A:C8	2.54	0.42
85:28:2060:G:H2'	85:28:2061:U:C6	2.54	0.42
85:28:3803:A:C2	85:28:3804:G:C8	3.06	0.42
85:28:4356:G:N3	85:28:4357:G:C8	2.87	0.42
5:58:71:A:H2'	25:26:50:ARG:NH1	2.34	0.42
5:58:108:A:H2'	5:58:109:C:O4'	2.19	0.42
15:13:184:MET:HG2	85:28:1482:G:H1	1.84	0.42
21:20:30:MET:HE3	21:20:32:ILE:HD11	2.01	0.42
42:ff:16:THR:HG22	85:28:2876:G:N7	2.34	0.42
45:FF:117:LEU:O	45:FF:121:ARG:HG3	2.18	0.42
47:s:192:VAL:HB	47:s:199:TYR:HB3	2.01	0.42
48:t:35:LEU:HD11	48:t:37:LEU:HB2	2.02	0.42
77:11:95:ARG:HB2	77:11:98:ASN:OD1	2.20	0.42
79:18:34:U:H5'	79:18:564:A:H4'	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
79:18:86:C:H1'	79:18:170:A:N1	2.34	0.42
79:18:111:A:H2'	79:18:112:U:C6	2.54	0.42
79:18:652:U:H2'	79:18:653:A:C8	2.54	0.42
79:18:1083:A:H4'	79:18:1085:C:C5	2.54	0.42
79:18:1406:G:H2'	79:18:1407:U:H6	1.84	0.42
85:28:648:G:H2'	85:28:649:A:C8	2.55	0.42
85:28:930:G:H2'	85:28:931:C:O4'	2.18	0.42
85:28:1191:C:H2'	85:28:1192:C:C6	2.54	0.42
85:28:1633:G:H5'	85:28:1634:A:OP1	2.19	0.42
85:28:1673:U:H2'	85:28:1674:C:H6	1.85	0.42
85:28:2611:A:O5'	85:28:2688:G:H4'	2.20	0.42
85:28:2678:A:H2'	85:28:2679:G:H8	1.84	0.42
85:28:3907:G:H2'	85:28:4447:C:O2'	2.19	0.42
85:28:4088:C:H2'	85:28:4089:G:H8	1.84	0.42
85:28:4122:G:C6	85:28:4123:C:C4	3.07	0.42
2:S2:77:SER:O	2:S2:80:GLU:HG2	2.19	0.42
2:S2:256:TRP:CD2	72:WX:68:ARG:HD3	2.54	0.42
7:L8:9:ARG:HD2	85:28:1628:C:OP2	2.20	0.42
8:L3:293:ILE:HA	8:L3:298:LEU:HA	2.02	0.42
9:L4:70:GLY:HA2	85:28:3905:A:O3'	2.18	0.42
10:L5:146:LEU:CD1	10:L5:163:LEU:HB2	2.49	0.42
10:L5:264:LYS:HE3	10:L5:264:LYS:HB2	1.90	0.42
15:13:103:ARG:HH22	85:28:73:A:N6	2.18	0.42
16:14:97:ALA:HB2	18:bb:203:VAL:HB	2.01	0.42
20:19:59:SER:HA	85:28:2634:C:H5'	2.00	0.42
26:27:11:VAL:CG1	26:27:80:LEU:HB3	2.48	0.42
32:ee:33:VAL:HG23	32:ee:38:GLU:HB2	2.01	0.42
47:s:120:GLU:HG3	47:s:159:GLN:HE22	1.83	0.42
48:t:32:ILE:HG22	48:t:37:LEU:HB3	2.01	0.42
49:F:22:LYS:HE2	49:F:22:LYS:HB3	1.93	0.42
49:F:67:GLU:O	49:F:70:MET:HG2	2.20	0.42
54:S5:74:ASN:HD21	54:S5:86:LYS:HE3	1.84	0.42
57:CC:3:MET:HE3	57:CC:44:HIS:HB3	2.01	0.42
71:RS:105:MET:HE2	71:RS:105:MET:HB2	1.95	0.42
78:L9:40:HIS:ND1	78:L9:41:ILE:HG13	2.34	0.42
79:18:94:G:C4	79:18:95:G:C8	3.07	0.42
79:18:887:U:H2'	79:18:888:U:H5''	2.01	0.42
79:18:1369:A:OP1	79:18:1369:A:C8	2.72	0.42
79:18:1389:C:H2'	79:18:1390:U:C6	2.54	0.42
79:18:1536:G:C2	79:18:1537:A:C5	3.08	0.42
80:v:372:LEU:HD22	80:v:417:PHE:CZ	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:28:324:A:H2'	85:28:325:U:C6	2.54	0.42
85:28:489:C:H2'	85:28:490:C:H6	1.84	0.42
85:28:2266:C:H4'	85:28:2267:U:O5'	2.19	0.42
85:28:4293:U:N3	85:28:4294:C:C5	2.87	0.42
85:28:4565:C:H2'	85:28:4566:U:C6	2.55	0.42
1:BB:32:PHE:CG	79:18:1097:G:H4'	2.55	0.42
5:58:45:C:C2	5:58:46:G:C8	3.07	0.42
5:58:126:C:HO2'	5:58:127:U:H5	1.67	0.42
13:aa:223:LEU:HA	13:aa:223:LEU:HD23	1.71	0.42
17:15:94:PHE:CE2	17:15:96:ARG:HB2	2.55	0.42
20:19:155:LEU:HD13	20:19:155:LEU:HA	1.88	0.42
21:20:164:LYS:HE2	21:20:164:LYS:HB2	1.90	0.42
29:30:77:ASN:OD1	29:30:80:GLU:HG2	2.20	0.42
45:FF:113:PHE:O	45:FF:117:LEU:HG	2.20	0.42
58:AA:139:LYS:HG3	58:AA:140:TYR:CD2	2.54	0.42
64:SS:10:ARG:HB3	64:SS:24:VAL:HB	2.01	0.42
64:SS:18:LEU:HD13	66:S4:64:ILE:HD11	2.01	0.42
64:SS:111:LYS:HD2	79:18:56:G:H5'	2.01	0.42
79:18:351:G:C2	79:18:352:U:C6	3.07	0.42
85:28:152:U:C2	85:28:153:G:C8	3.08	0.42
85:28:1341:U:C2	85:28:1342:A:C8	3.08	0.42
85:28:1586:G:C2	85:28:1608:G:C5	3.08	0.42
85:28:2647:A:H62	85:28:2686:G:H8	1.67	0.42
85:28:4400:G:C4	85:28:4401:G:C8	3.07	0.42
42:ff:50:ARG:HB3	42:ff:54:ILE:HD13	2.02	0.42
48:t:142:ASN:HB2	48:t:145:GLY:C	2.43	0.42
49:F:81:SER:HB2	49:F:107:LYS:HE2	2.02	0.42
70:S3:46:THR:HB	70:S3:84:VAL:HA	2.01	0.42
73:S8:143:LYS:HA	73:S8:146:GLN:HB3	2.02	0.42
77:11:161:GLU:HA	77:11:164:ARG:HG2	2.01	0.42
79:18:298:G:C2	79:18:299:A:C8	3.07	0.42
79:18:382:C:C2	79:18:383:G:N7	2.87	0.42
79:18:433:A:H2'	79:18:434:G:C8	2.54	0.42
79:18:616:A:C2	79:18:632:C:H1'	2.54	0.42
79:18:997:A:H2'	79:18:998:A:C8	2.54	0.42
79:18:1140:G:H2'	79:18:1141:G:C8	2.52	0.42
80:v:396:MET:HB3	80:v:485:ILE:HB	2.01	0.42
85:28:959:G:H4'	85:28:960:A:O5'	2.18	0.42
85:28:1078:A:H2'	85:28:1078:A:N3	2.34	0.42
85:28:1239:C:H4'	85:28:1244:G:P	2.59	0.42
85:28:1392:A:H2'	85:28:1393:G:C8	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:28:2385:U:H2'	85:28:2386:U:C6	2.55	0.42
85:28:2454:U:C2	85:28:2455:G:C8	3.07	0.42
85:28:2627:C:H41	85:28:4649:G:H1	1.68	0.42
85:28:2697:A:C2	85:28:2698:G:C8	3.08	0.42
85:28:4068:U:H2'	85:28:4069:U:C6	2.54	0.42
85:28:4273:A:H62	85:28:4335:C:N4	2.16	0.42
86:23:39:ILE:HG12	86:23:61:VAL:HG11	2.02	0.42
1:BB:53:ARG:O	1:BB:57:LYS:HG2	2.20	0.42
1:BB:77:ILE:HG12	1:BB:99:ILE:HB	2.02	0.42
6:6:59:G:H2'	6:6:60:G:H8	1.85	0.42
9:L4:285:LEU:HD22	9:L4:285:LEU:HA	1.92	0.42
12:L7:98:ASN:OD1	85:28:1897:A:H5''	2.19	0.42
12:L7:219:MET:HB3	12:L7:231:ASP:OD2	2.20	0.42
37:38:32:VAL:HG11	37:38:53:ALA:HB1	2.01	0.42
58:AA:20:GLN:HG2	58:AA:69:VAL:H	1.84	0.42
75:GG:121:ARG:HD2	75:GG:121:ARG:HA	1.83	0.42
79:18:27:A:H2'	79:18:28:U:C6	2.55	0.42
79:18:193:C:H2'	79:18:194:C:H6	1.85	0.42
79:18:1385:G:C4	79:18:1386:A:C8	3.08	0.42
79:18:1391:C:H2'	79:18:1392:U:C6	2.55	0.42
80:v:207:PRO:HG2	80:v:261:TRP:CE2	2.54	0.42
85:28:123:C:H2'	85:28:124:C:H6	1.85	0.42
85:28:1170:G:H2'	85:28:1171:G:C8	2.55	0.42
85:28:1528:U:H2'	85:28:1529:G:H8	1.84	0.42
85:28:1588:U:H2'	85:28:1589:C:C6	2.55	0.42
85:28:1933:G:H8	85:28:1933:G:O5'	2.03	0.42
85:28:2374:A:H2'	85:28:2375:A:H8	1.84	0.42
85:28:4343:U:H2'	85:28:4344:U:H6	1.83	0.42
85:28:4595:G:H2'	85:28:4596:C:H6	1.85	0.42
85:28:4648:A:C4	85:28:4649:G:C8	3.08	0.42
86:23:36:ASN:HD22	86:23:36:ASN:HA	1.70	0.42
18:bb:47:PHE:HA	18:bb:136:ALA:HB2	2.02	0.42
19:17:27:LYS:O	19:17:31:GLU:HG2	2.19	0.42
31:32:89:LEU:HD13	31:32:118:LEU:HD22	2.02	0.42
43:gg:93:ILE:HD11	43:gg:111:ILE:HA	2.01	0.42
48:t:108:GLU:HA	48:t:111:ASN:HD21	1.85	0.42
65:S6:212:LEU:HD12	65:S6:215:LYS:HD3	2.01	0.42
68:S7:43:LEU:HD23	68:S7:72:PHE:CE1	2.55	0.42
73:S8:129:LEU:HD22	73:S8:134:GLU:HB2	2.02	0.42
79:18:92:A:H5'	79:18:93:U:C5	2.55	0.42
79:18:639:C:C2	79:18:640:A:N7	2.88	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
84:ES:2942:C:C2'	84:ES:2943:C:H5'	2.50	0.42
85:28:233:U:H6	85:28:2304:U:C4	2.37	0.42
85:28:262:G:C2	85:28:263:G:C8	3.08	0.42
85:28:294:G:O6	85:28:315:G:H1'	2.19	0.42
85:28:385:A:N3	85:28:387:G:H5''	2.34	0.42
85:28:949:G:H2'	85:28:950:G:H8	1.83	0.42
85:28:1673:U:H2'	85:28:1674:C:C6	2.54	0.42
85:28:1958:A:H5''	85:28:1962:A:O2'	2.19	0.42
85:28:4674:C:H2'	85:28:4675:U:C6	2.54	0.42
85:28:5036:C:H2'	85:28:5037:U:C6	2.54	0.42
1:BB:34:MET:HE2	1:BB:34:MET:HA	2.01	0.42
5:58:114:G:C4	5:58:115:G:C8	3.08	0.42
6:6:60:G:N3	6:6:61:G:C8	2.87	0.42
11:L6:179:THR:OG1	11:L6:189:LEU:HD23	2.19	0.42
25:26:47:MET:HE1	25:26:118:ILE:HB	2.02	0.42
42:ff:52:VAL:HG21	85:28:2739:C:H4'	2.02	0.42
44:AS:136:ARG:NH1	79:18:941:C:H5''	2.35	0.42
45:FF:49:GLN:O	45:FF:53:ILE:HG12	2.20	0.42
54:S5:147:VAL:O	54:S5:151:ILE:HG13	2.20	0.42
72:WX:10:ALA:O	72:WX:14:ILE:HG13	2.20	0.42
79:18:341:C:H2'	79:18:342:C:C6	2.55	0.42
79:18:578:C:C2	79:18:579:C:C6	3.07	0.42
79:18:1284:A:OP1	79:18:1286:G:H5'	2.20	0.42
80:v:324:ASP:HB3	80:v:342:ARG:HH12	1.84	0.42
85:28:758:G:H2'	85:28:759:G:O4'	2.20	0.42
85:28:1445:U:H2'	85:28:1446:C:C6	2.55	0.42
85:28:1737:A:C4	85:28:1738:A:C8	3.08	0.42
85:28:1874:A:H2'	85:28:1875:C:C6	2.54	0.42
85:28:2479:G:C2	85:28:2480:G:C8	3.08	0.42
85:28:2602:G:O4'	85:28:2742:G:H2'	2.20	0.42
85:28:2837:U:N3	85:28:2838:G:C8	2.88	0.42
85:28:3734:U:H2'	85:28:3735:G:O4'	2.20	0.42
85:28:3760:A:H1'	85:28:3761:C:OP1	2.20	0.42
85:28:4562:C:H2'	85:28:4563:U:H6	1.84	0.42
85:28:4610:A:C4	85:28:4611:A:C8	3.08	0.42
40:41:2:ARG:HD3	40:41:5:TRP:NE1	2.35	0.42
47:s:192:VAL:O	47:s:198:ILE:HA	2.19	0.42
75:GG:32:HIS:CD2	79:18:975:G:H4'	2.55	0.42
75:GG:66:ARG:HB3	79:18:962:A:H5''	2.01	0.42
78:L9:12:ILE:HG12	78:L9:54:ARG:HA	2.02	0.42
79:18:92:A:H5'	79:18:93:U:H5	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
79:18:1018:U:H2'	79:18:1019:C:C6	2.55	0.42
79:18:1675:A:H2'	79:18:1676:U:H6	1.84	0.42
79:18:1738:C:H2'	79:18:1739:C:C6	2.55	0.42
80:v:200:MET:HE2	80:v:200:MET:HB2	1.99	0.42
84:ES:2955:A:H2	84:ES:3239:G:H1	1.65	0.42
85:28:318:A:H2'	85:28:319:A:C8	2.55	0.42
85:28:1216:C:C4	85:28:1217:G:N7	2.88	0.42
85:28:1511:U:H2'	85:28:1512:G:H8	1.84	0.42
85:28:1527:A:H2'	85:28:1528:U:H6	1.83	0.42
85:28:2556:G:C2	85:28:2557:G:C5	3.07	0.42
85:28:2724:G:H5''	85:28:2725:A:OP2	2.20	0.42
85:28:3696:C:H2'	85:28:3697:U:O4'	2.20	0.42
85:28:3737:A:C4	85:28:3738:G:C8	3.08	0.42
85:28:4068:U:H2'	85:28:4069:U:H6	1.85	0.42
85:28:4300:U:H2'	85:28:4301:U:C6	2.55	0.42
85:28:4642:U:H2'	85:28:4643:G:C8	2.51	0.42
85:28:4750:G:H2'	85:28:4751:G:C8	2.55	0.42
85:28:4941:G:O2'	85:28:4942:C:H5'	2.20	0.42
85:28:5056:A:H2'	85:28:5057:C:C6	2.55	0.42
86:23:26:ILE:HG12	86:23:37:LEU:HB3	2.02	0.42
2:S2:94:ILE:HD12	2:S2:162:ILE:HD11	2.02	0.41
2:S2:253:PRO:HA	2:S2:256:TRP:CD1	2.56	0.41
6:6:67:C:OP1	10:L5:14:LYS:HG2	2.19	0.41
12:L7:69:ARG:O	12:L7:73:MET:HG3	2.20	0.41
13:aa:190:ARG:O	13:aa:255:VAL:HA	2.20	0.41
18:bb:81:TRP:HB2	18:bb:104:VAL:HG21	2.02	0.41
32:ee:28:LEU:HG	32:ee:101:ILE:HD11	2.01	0.41
35:36:34:THR:HB	35:36:37:THR:HG23	2.02	0.41
38:39:48:LYS:HD2	38:39:48:LYS:HA	1.72	0.41
46:VV:82:LYS:HE2	46:VV:82:LYS:HB3	1.83	0.41
50:Q:12:LYS:HG2	85:28:2082:G:H5''	2.01	0.41
67:S9:15:THR:HG22	67:S9:44:TRP:CZ3	2.55	0.41
72:WX:93:LEU:HB3	72:WX:102:ILE:HD11	2.02	0.41
79:18:4:C:H2'	79:18:5:U:C6	2.54	0.41
79:18:23:G:C5	79:18:24:C:C5	3.08	0.41
79:18:695:C:H2'	79:18:696:G:C8	2.55	0.41
79:18:1804:U:H2'	79:18:1805:G:O4'	2.19	0.41
79:18:1810:U:H2'	79:18:1811:C:C6	2.55	0.41
80:v:176:GLN:O	80:v:180:ARG:HG2	2.20	0.41
85:28:48:G:H4'	85:28:49:U:O5'	2.20	0.41
85:28:963:G:C2	85:28:964:A:C8	3.08	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:28:963:G:O2'	85:28:964:A:H8	1.99	0.41
85:28:1205:G:H2'	85:28:1206:C:H6	1.85	0.41
85:28:1604:G:H2'	85:28:1605:G:C8	2.55	0.41
85:28:4081:G:H2'	85:28:4082:G:H8	1.84	0.41
85:28:4419:U:N3	85:28:4420:U:C6	2.88	0.41
85:28:4419:U:O2	85:28:4419:U:H2'	2.19	0.41
85:28:4958:C:H2'	85:28:4959:U:C6	2.55	0.41
5:58:56:G:H2'	5:58:57:C:O4'	2.20	0.41
5:58:153:C:H5'	13:aa:238:LYS:HE2	2.00	0.41
17:15:68:ARG:HG2	17:15:128:LYS:HG3	2.01	0.41
23:22:19:LEU:HD12	23:22:77:PRO:HA	2.00	0.41
50:Q:158:THR:HG22	50:Q:161:SER:HB3	2.01	0.41
52:EE:58:GLU:HB3	52:EE:61:TYR:HB3	2.02	0.41
70:S3:172:VAL:HG13	70:S3:185:LYS:HG2	2.02	0.41
73:S8:10:LYS:HB2	73:S8:10:LYS:HE3	1.81	0.41
79:18:360:A:C2	79:18:362:C:H2'	2.55	0.41
79:18:896:U:H2'	79:18:897:U:N1	2.36	0.41
79:18:1043:G:H2'	79:18:1044:G:O4'	2.20	0.41
79:18:1265:A:H5''	79:18:1266:C:OP2	2.20	0.41
79:18:1724:A:H2'	79:18:1725:U:C6	2.55	0.41
79:18:1856:C:H2'	79:18:1857:G:C8	2.55	0.41
85:28:424:U:C2	85:28:425:U:C5	3.08	0.41
85:28:1200:G:C5	85:28:1201:U:C5	3.08	0.41
85:28:1460:C:H2'	85:28:1461:C:C6	2.54	0.41
85:28:1468:C:H2'	85:28:1469:C:C6	2.54	0.41
85:28:1948:G:H2'	85:28:1949:U:C6	2.55	0.41
85:28:1991:A:OP1	85:28:1991:A:H4'	2.21	0.41
85:28:2436:U:C2	85:28:2783:A:C8	3.07	0.41
85:28:2735:G:N3	85:28:2736:G:C8	2.88	0.41
85:28:3720:G:C2	85:28:3721:U:C6	3.08	0.41
85:28:3911:C:C2	85:28:3912:U:C5	3.08	0.41
85:28:4200:G:C4	85:28:4201:G:C8	3.07	0.41
1:BB:3:GLY:HA2	3:PP:80:SER:OG	2.20	0.41
7:L8:80:GLU:HG3	42:ff:66:GLY:HA2	2.02	0.41
7:L8:132:ASN:OD1	85:28:3682:A:H5''	2.21	0.41
11:L6:206:ILE:O	11:L6:209:VAL:HG12	2.19	0.41
21:20:34:ALA:HB1	21:20:39:VAL:CG2	2.50	0.41
27:dd:40:HIS:HA	85:28:1675:C:H1'	2.02	0.41
33:34:56:VAL:HG13	33:34:72:LYS:HA	2.01	0.41
35:36:70:LEU:HD22	35:36:87:ARG:NH1	2.35	0.41
35:36:90:LEU:O	35:36:93:VAL:HG22	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:gg:33:LYS:HD2	43:gg:40:TYR:CE1	2.55	0.41
56:II:81:ILE:O	56:II:84:ILE:HG12	2.20	0.41
59:OO:67:LYS:HG2	62:XX:44:ARG:HH12	1.85	0.41
74:W:107:GLN:O	74:W:110:ARG:HG3	2.20	0.41
79:18:75:G:N2	79:18:77:A:H5''	2.29	0.41
79:18:475:C:H1'	79:18:507:G:O2'	2.20	0.41
80:v:464:VAL:HG21	80:v:470:VAL:HB	2.02	0.41
85:28:919:C:H2'	85:28:920:C:H6	1.85	0.41
85:28:1537:A:H2'	85:28:1538:U:C6	2.55	0.41
85:28:2518:G:H1'	85:28:2539:C:H1'	2.02	0.41
85:28:2724:G:H4'	85:28:2725:A:OP1	2.20	0.41
85:28:3834:C:H2'	85:28:3835:C:C6	2.55	0.41
85:28:3857:G:H2'	85:28:3858:C:C6	2.56	0.41
85:28:4175:G:H2'	85:28:4176:C:H6	1.85	0.41
85:28:4576:U:H2'	85:28:4577:U:C6	2.55	0.41
85:28:4997:G:H2'	85:28:4998:G:H8	1.85	0.41
85:28:5055:G:H2'	85:28:5056:A:C8	2.55	0.41
6:6:113:G:H2'	6:6:114:U:H6	1.85	0.41
10:L5:81:HIS:O	10:L5:84:PRO:HD2	2.21	0.41
10:L5:195:HIS:CE1	10:L5:199:ILE:HD11	2.55	0.41
57:CC:86:PRO:HA	57:CC:87:PRO:HD3	1.91	0.41
64:SS:29:HIS:HE1	64:SS:69:THR:HG23	1.86	0.41
66:S4:68:ARG:HG2	66:S4:76:VAL:HG11	2.02	0.41
71:RS:11:LYS:HB3	71:RS:11:LYS:HE2	1.86	0.41
72:WX:6:VAL:CG1	72:WX:29:PRO:HB2	2.50	0.41
79:18:405:G:H2'	79:18:406:U:O4'	2.20	0.41
79:18:1820:G:H2'	79:18:1821:U:C6	2.55	0.41
80:v:666:THR:HB	80:v:669:VAL:HB	2.02	0.41
83:A:102:PHE:CD1	83:A:102:PHE:N	2.89	0.41
85:28:284:G:H2'	85:28:285:G:H8	1.85	0.41
85:28:1461:C:C2	85:28:1462:A:N7	2.89	0.41
85:28:4628:U:C2	85:28:4629:U:C5	3.09	0.41
1:BB:74:VAL:HG13	1:BB:121:LEU:HB3	2.02	0.41
7:L8:15:VAL:HG21	85:28:1628:C:H5''	2.01	0.41
7:L8:225:ILE:HD11	7:L8:233:ARG:HG3	2.02	0.41
8:L3:206:PRO:HD2	8:L3:209:GLN:HG3	2.02	0.41
8:L3:240:LEU:HB2	8:L3:248:LEU:HA	2.03	0.41
31:32:33:ARG:H	31:32:33:ARG:HD2	1.85	0.41
45:FF:40:LEU:HD13	45:FF:53:ILE:HD11	2.02	0.41
58:AA:17:TRP:O	58:AA:36:ARG:HG2	2.21	0.41
60:MM:115:LYS:HA	60:MM:121:ARG:HG2	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
79:18:34:U:H2'	79:18:35:C:C6	2.56	0.41
79:18:118:C:H1'	79:18:445:A:C5	2.56	0.41
79:18:399:C:H5	79:18:680:G:H5''	1.85	0.41
79:18:640:A:C2	79:18:641:A:C5	3.08	0.41
79:18:950:C:H2'	79:18:951:C:C6	2.56	0.41
79:18:1367:U:H2'	79:18:1368:U:H6	1.85	0.41
79:18:1396:A:N7	79:18:1450:G:N2	2.68	0.41
85:28:86:U:H2'	85:28:87:A:C8	2.55	0.41
85:28:121:A:H5'	85:28:122:U:OP2	2.20	0.41
85:28:268:G:H2'	85:28:269:G:C8	2.54	0.41
85:28:1201:U:H2'	85:28:1202:C:H6	1.85	0.41
85:28:1693:U:H2'	85:28:1694:C:O4'	2.19	0.41
85:28:1884:C:H4'	85:28:2070:U:C4	2.55	0.41
85:28:2359:U:H5''	85:28:2360:A:OP2	2.20	0.41
85:28:4235:G:C6	85:28:4236:G:N7	2.88	0.41
85:28:4564:A:H2'	85:28:4565:C:C6	2.55	0.41
85:28:4759:C:H2'	85:28:4760:G:O4'	2.20	0.41
85:28:4995:U:H2'	85:28:4996:C:H6	1.85	0.41
6:6:58:A:H2'	6:6:59:G:C8	2.56	0.41
12:L7:113:LEU:HD21	12:L7:120:THR:HG22	2.03	0.41
15:13:105:LYS:HE2	15:13:105:LYS:HB3	1.86	0.41
18:bb:126:VAL:HG13	18:bb:127:VAL:HG23	2.02	0.41
22:21:96:ILE:HD13	22:21:96:ILE:HA	1.81	0.41
23:22:23:LEU:HB3	23:22:110:TYR:HB2	2.03	0.41
28:29:28:ARG:HB3	85:28:1805:A:C4	2.55	0.41
30:31:23:ARG:HD3	30:31:25:TYR:OH	2.21	0.41
49:F:325:LEU:HD13	49:F:330:PRO:HB3	2.03	0.41
57:CC:64:TRP:CD1	62:XX:23:VAL:HG13	2.55	0.41
65:S6:7:PHE:CD2	65:S6:125:THR:HG22	2.56	0.41
75:GG:138:ASP:OD2	79:18:985:G:H1'	2.21	0.41
76:UU:12:LYS:HE3	76:UU:12:LYS:HB3	1.90	0.41
77:11:35:ARG:O	77:11:39:VAL:HG23	2.21	0.41
79:18:155:G:N3	79:18:156:G:C8	2.89	0.41
79:18:577:U:H2'	79:18:578:C:C6	2.55	0.41
79:18:1192:U:H2'	79:18:1193:U:C6	2.56	0.41
79:18:1218:C:H2'	79:18:1219:C:C6	2.56	0.41
79:18:1503:C:H2'	79:18:1504:U:C6	2.56	0.41
79:18:1639:G:H2'	79:18:1640:A:C8	2.56	0.41
80:v:753:GLU:HA	80:v:756:VAL:HG23	2.02	0.41
85:28:1373:A:C2	85:28:1374:G:C8	3.09	0.41
85:28:2611:A:H2'	85:28:2612:G:C8	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:28:2815:A:H2'	85:28:2816:G:C8	2.55	0.41
85:28:4474:A:H2'	85:28:4476:C:O5'	2.21	0.41
85:28:4519:C:OP1	85:28:4520:G:H5''	2.21	0.41
85:28:5000:G:C2	85:28:5051:C:C2	3.08	0.41
5:58:62:A:H4'	5:58:63:U:O5'	2.21	0.41
6:6:60:G:H2'	6:6:61:G:H8	1.85	0.41
9:L4:266:THR:HG22	9:L4:269:LYS:HB3	2.02	0.41
14:10:59:GLN:HA	14:10:128:ARG:HA	2.02	0.41
16:14:11:ARG:NH1	16:14:59:ASP:HA	2.35	0.41
38:39:45:ARG:HA	38:39:45:ARG:HD2	1.67	0.41
44:AS:116:LYS:HG2	44:AS:117:TRP:CD2	2.55	0.41
47:s:61:MET:O	47:s:65:ILE:HG12	2.20	0.41
49:F:86:VAL:HB	49:F:308:LEU:HB2	2.02	0.41
54:S5:45:TYR:CE1	54:S5:65:GLN:HB2	2.56	0.41
58:AA:291:TRP:CE2	58:AA:298:LEU:HD13	2.55	0.41
61:LL:102:GLY:O	61:LL:106:LYS:HG2	2.21	0.41
64:SS:13:MET:HB2	64:SS:13:MET:HE2	1.88	0.41
70:S3:161:GLY:HA3	79:18:1388:A:H61	1.84	0.41
72:WX:4:MET:SD	79:18:1159:G:H1'	2.60	0.41
73:S8:176:ALA:HB3	79:18:220:U:H4'	2.02	0.41
75:GG:99:ALA:H	75:GG:133:THR:HG22	1.85	0.41
79:18:812:A:C4	79:18:813:A:C8	3.08	0.41
79:18:955:A:C2	79:18:972:A:C6	3.09	0.41
80:v:25:ILE:O	80:v:127:VAL:HA	2.20	0.41
80:v:650:TRP:HZ2	80:v:672:LEU:HD21	1.86	0.41
85:28:99:A:H2'	85:28:100:C:O2	2.21	0.41
85:28:456:C:H2'	85:28:457:G:C8	2.55	0.41
85:28:705:G:H2'	85:28:706:C:C6	2.55	0.41
85:28:750:U:C2	85:28:751:G:C8	3.09	0.41
85:28:1423:U:H2'	85:28:1424:G:H8	1.85	0.41
85:28:1469:C:C2	85:28:1470:G:C8	3.09	0.41
85:28:1552:G:H1'	85:28:1575:A:N6	2.36	0.41
85:28:2529:A:O2'	85:28:2530:U:H5''	2.21	0.41
85:28:2587:A:H5''	85:28:2588:C:C4	2.56	0.41
85:28:3785:A:C6	85:28:4536:C:H1'	2.54	0.41
85:28:3786:U:O2	85:28:3814:U:H4'	2.20	0.41
85:28:3923:A:H2'	85:28:3924:C:C6	2.55	0.41
85:28:4918:C:H2'	85:28:4919:G:C8	2.55	0.41
9:L4:46:LYS:HA	9:L4:49:ARG:HD3	2.02	0.41
27:dd:85:GLN:NE2	85:28:508:G:H21	2.19	0.41
43:gg:103:HIS:CD2	43:gg:106:LEU:HD22	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:EE:129:LYS:HE3	52:EE:129:LYS:HB3	1.89	0.41
59:OO:61:LEU:HD23	62:XX:34:TYR:CD2	2.55	0.41
61:LL:61:GLU:O	61:LL:64:VAL:HG22	2.21	0.41
67:S9:124:HIS:O	67:S9:128:VAL:HG23	2.21	0.41
70:S3:25:LEU:HG	70:S3:29:LEU:HD12	2.03	0.41
78:L9:23:ARG:HH22	85:28:4763:U:H5''	1.85	0.41
79:18:430:C:H2'	79:18:431:G:C8	2.56	0.41
79:18:587:A:H5'	79:18:592:C:H41	1.86	0.41
79:18:695:C:H2'	79:18:696:G:H8	1.85	0.41
79:18:827:A:C6	79:18:828:G:C5	3.08	0.41
85:28:161:G:H2'	85:28:162:A:C8	2.55	0.41
85:28:325:U:H2'	85:28:326:C:H6	1.86	0.41
85:28:1304:C:H2'	85:28:1305:C:C6	2.56	0.41
85:28:1620:U:H2'	85:28:1621:A:C8	2.56	0.41
85:28:1672:U:H2'	85:28:1673:U:C6	2.56	0.41
85:28:2488:C:H3'	85:28:2490:U:O4	2.21	0.41
85:28:2559:G:H2'	85:28:2560:C:H6	1.84	0.41
85:28:2750:G:H2'	85:28:2751:G:O4'	2.20	0.41
85:28:2757:A:O2'	85:28:2758:G:H5'	2.21	0.41
85:28:3633:C:H2'	85:28:3634:G:H8	1.86	0.41
85:28:4081:G:H2'	85:28:4082:G:C8	2.55	0.41
85:28:4174:U:C2	85:28:4175:G:C8	3.08	0.41
85:28:4459:U:H2'	85:28:4460:U:H6	1.86	0.41
86:23:106:VAL:HG12	86:23:112:MET:HA	2.03	0.41
1:BB:115:ALA:O	1:BB:117:ARG:HG2	2.21	0.41
5:58:68:G:C5	5:58:69:U:C5	3.09	0.41
6:6:94:C:H2'	6:6:95:C:H6	1.86	0.41
8:L3:252:ALA:HB1	85:28:4524:G:C2	2.56	0.41
10:L5:180:PHE:HB3	10:L5:195:HIS:CD2	2.56	0.41
12:L7:135:VAL:O	12:L7:139:ILE:HG12	2.20	0.41
13:aa:217:ILE:O	13:aa:221:VAL:HG13	2.21	0.41
18:bb:149:TYR:OH	85:28:4583:C:H5''	2.21	0.41
21:20:115:ALA:HB2	85:28:2060:G:N2	2.36	0.41
24:cc:148:ASP:O	24:cc:152:LYS:HD3	2.21	0.41
28:29:102:PRO:HA	28:29:109:ARG:HH22	1.86	0.41
31:32:35:TRP:CH2	31:32:55:MET:HG2	2.56	0.41
44:AS:62:LEU:HD23	44:AS:91:VAL:HG21	2.02	0.41
44:AS:137:LEU:HG	44:AS:215:VAL:HG22	2.03	0.41
44:AS:181:LEU:HA	44:AS:184:VAL:HG22	2.01	0.41
49:F:172:LYS:HB3	49:F:354:LEU:HD22	2.03	0.41
54:S5:42:LYS:HG2	54:S5:43:GLU:HB3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:S5:166:ILE:HG13	79:18:1599:U:N3	2.36	0.41
56:II:19:ALA:HB2	56:II:75:GLY:HA3	2.03	0.41
66:S4:100:ARG:HB2	66:S4:114:ILE:HD13	2.03	0.41
67:S9:37:LEU:HD23	67:S9:42:GLU:HG3	2.03	0.41
68:S7:130:LEU:HB2	68:S7:177:TYR:CE1	2.56	0.41
79:18:436:G:H5''	79:18:473:A:H62	1.85	0.41
79:18:457:C:C2	79:18:458:A:C8	3.08	0.41
79:18:598:G:H2'	79:18:599:A:H8	1.86	0.41
79:18:854:A:N3	79:18:855:G:C8	2.89	0.41
79:18:934:G:N3	79:18:935:G:C8	2.89	0.41
79:18:1050:A:H62	79:18:1068:G:H21	1.69	0.41
79:18:1070:A:H2'	79:18:1071:G:O4'	2.20	0.41
79:18:1351:G:C2	79:18:1352:G:N7	2.89	0.41
79:18:1413:G:C4	79:18:1414:A:C8	3.09	0.41
79:18:1678:A:H2'	79:18:1679:A:H5'	2.03	0.41
79:18:1687:C:C2	79:18:1688:C:C5	3.09	0.41
79:18:1706:G:H2'	79:18:1707:U:C6	2.54	0.41
79:18:1723:G:H2'	79:18:1724:A:C8	2.56	0.41
80:v:423:THR:HG23	80:v:448:GLN:O	2.21	0.41
85:28:223:G:H4'	85:28:225:G:C8	2.56	0.41
85:28:247:G:H2'	85:28:248:C:C6	2.54	0.41
85:28:1359:G:H3'	85:28:1360:G:H8	1.84	0.41
85:28:1494:U:H2'	85:28:1495:G:C8	2.54	0.41
85:28:1549:G:C2	85:28:1550:G:C8	3.09	0.41
85:28:1589:C:H2'	85:28:1590:C:C6	2.55	0.41
85:28:1744:U:H2'	85:28:1745:G:H8	1.86	0.41
85:28:2732:G:H2'	85:28:2733:C:H6	1.86	0.41
85:28:4233:A:C4	85:28:4235:G:N7	2.88	0.41
85:28:4723:A:H2'	85:28:4724:A:C8	2.55	0.41
85:28:4728:U:H4'	85:28:4966:A:H1'	2.01	0.41
13:aa:210:ILE:HG23	13:aa:220:VAL:HG11	2.03	0.41
23:22:24:ASP:HB3	23:22:69:LYS:HG3	2.03	0.41
39:40:69:ILE:HD12	85:28:4473:A:H5''	2.03	0.41
40:41:3:ALA:HB3	79:18:1842:C:OP1	2.21	0.41
48:t:15:LEU:HD11	48:t:31:LYS:HE3	2.03	0.41
48:t:64:ILE:HA	48:t:69:ALA:HA	2.03	0.41
55:WW:17:VAL:HG23	55:WW:30:VAL:HG22	2.03	0.41
60:MM:80:GLY:HA3	60:MM:92:PHE:HE1	1.85	0.41
62:XX:16:GLN:CD	62:XX:16:GLN:H	2.29	0.41
68:S7:6:ALA:HA	68:S7:28:LEU:HD11	2.03	0.41
70:S3:55:THR:O	70:S3:58:VAL:HG22	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
79:18:653:A:H2'	79:18:654:A:O4'	2.20	0.41
79:18:1053:C:H2'	79:18:1054:G:H8	1.86	0.41
79:18:1506:A:H4'	79:18:1507:G:H3'	2.03	0.41
85:28:22:G:H2'	85:28:23:C:C6	2.56	0.41
85:28:272:U:H2'	85:28:273:U:H6	1.86	0.41
85:28:2273:G:H2'	85:28:2274:C:H6	1.86	0.41
85:28:2503:G:H2'	85:28:2504:C:C1'	2.51	0.41
85:28:3860:A:H61	85:28:4560:C:H5	1.67	0.41
85:28:3927:U:H2'	85:28:3928:A:C8	2.55	0.41
85:28:4215:C:C2	85:28:4216:G:C8	3.09	0.41
85:28:4433:G:H2'	85:28:4434:C:C6	2.56	0.41
85:28:5043:A:C4	85:28:5044:A:C8	3.09	0.41
6:6:27:G:N2	6:6:54:A:N6	2.70	0.40
13:aa:169:ALA:O	13:aa:172:GLU:HG3	2.21	0.40
24:cc:146:ALA:HA	24:cc:149:VAL:HG22	2.01	0.40
44:AS:163:GLN:O	44:AS:166:LYS:HG2	2.21	0.40
52:EE:92:CYS:HB3	52:EE:102:LYS:HB3	2.03	0.40
54:S5:77:MET:HB3	54:S5:89:THR:HG21	2.03	0.40
58:AA:36:ARG:O	58:AA:65:PHE:HA	2.22	0.40
61:LL:10:GLN:H	61:LL:10:GLN:HG2	1.76	0.40
64:SS:76:TYR:CE2	64:SS:82:ALA:HA	2.56	0.40
67:S9:78:LEU:HB3	67:S9:92:MET:CG	2.51	0.40
71:RS:69:ILE:HG23	71:RS:71:ILE:HG23	2.03	0.40
76:UU:10:ARG:HB2	76:UU:33:ASP:OD2	2.21	0.40
79:18:196:C:H2'	79:18:197:U:C6	2.56	0.40
79:18:220:U:H2'	79:18:221:A:C8	2.55	0.40
79:18:1228:A:C2	79:18:1229:G:C5	3.09	0.40
79:18:1230:C:H2'	79:18:1231:C:H6	1.85	0.40
79:18:1379:A:H2'	79:18:1380:C:C6	2.56	0.40
79:18:1390:U:C2	79:18:1391:C:C6	3.08	0.40
85:28:263:G:C6	85:28:264:C:N4	2.89	0.40
85:28:275:C:H4'	85:28:276:C:OP1	2.21	0.40
85:28:441:G:H2'	85:28:442:G:C8	2.56	0.40
85:28:726:G:H2'	85:28:727:C:H6	1.86	0.40
85:28:956:A:N6	85:28:1283:G:H1'	2.36	0.40
85:28:1468:C:C2	85:28:1469:C:C5	3.09	0.40
85:28:1735:U:C2	85:28:1736:A:C8	3.09	0.40
85:28:1779:U:H2'	85:28:1780:A:H8	1.86	0.40
85:28:2102:G:O2'	85:28:2103:A:H5'	2.22	0.40
85:28:3698:G:O6	85:28:3816:A:H5''	2.21	0.40
85:28:4562:C:H2'	85:28:4563:U:C6	2.55	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:28:5000:G:H2'	85:28:5001:U:O4'	2.21	0.40
1:BB:89:LYS:HD3	1:BB:201:LEU:HG	2.03	0.40
6:6:92:C:H2'	6:6:93:G:H8	1.86	0.40
8:L3:252:ALA:HB1	85:28:4524:G:N3	2.36	0.40
15:13:48:PRO:HG3	34:35:118:LYS:HE3	2.03	0.40
29:30:91:VAL:HG12	85:28:2673:G:O2'	2.21	0.40
34:35:96:ASN:N	34:35:96:ASN:ND2	2.68	0.40
57:CC:65:ARG:HA	57:CC:65:ARG:HD2	1.84	0.40
68:S7:63:PHE:HA	68:S7:95:ILE:O	2.21	0.40
71:RS:19:LYS:HD3	71:RS:19:LYS:HA	1.96	0.40
79:18:407:G:H2'	79:18:407:G:N3	2.36	0.40
79:18:431:G:H2'	79:18:432:G:H8	1.87	0.40
79:18:562:U:H3	79:18:587:A:H62	1.68	0.40
79:18:1235:G:H5'	79:18:1247:C:H42	1.86	0.40
79:18:1522:A:H5'	79:18:1523:C:OP2	2.21	0.40
79:18:1611:G:H2'	79:18:1612:G:H8	1.86	0.40
79:18:1620:A:OP1	83:A:44:ARG:HD3	2.21	0.40
79:18:1708:C:C2	79:18:1709:G:C8	3.09	0.40
79:18:1739:C:C2	79:18:1740:C:C5	3.09	0.40
85:28:153:G:N3	85:28:154:G:C8	2.89	0.40
85:28:516:C:H2'	85:28:517:C:C6	2.55	0.40
85:28:909:G:C2	85:28:910:G:C8	3.09	0.40
85:28:922(B):C:H3'	85:28:923:C:H5''	2.04	0.40
85:28:952:G:H2'	85:28:953:C:C6	2.56	0.40
85:28:2089:G:H1'	85:28:2090:U:OP2	2.21	0.40
85:28:2519:U:H1'	85:28:2520:C:C6	2.56	0.40
85:28:3718:A:H2'	85:28:3719:A:H8	1.87	0.40
85:28:4291:G:C8	85:28:4328:G:C4	3.09	0.40
85:28:4410:G:C2	85:28:4411:G:C8	3.10	0.40
85:28:4632:U:H2'	85:28:4633:G:O4'	2.20	0.40
85:28:4684:A:H2'	85:28:4685:U:O4'	2.21	0.40
5:58:132:G:H2'	5:58:133:G:C8	2.56	0.40
5:58:141:C:H5'	17:15:113:LEU:HD11	2.02	0.40
10:L5:36:LEU:HD23	10:L5:36:LEU:HA	1.95	0.40
17:15:184:ILE:HD12	85:28:99:A:H5''	2.03	0.40
22:21:14:MET:HE1	22:21:55:LYS:HB2	2.03	0.40
31:32:44:ARG:H	31:32:44:ARG:HG3	1.57	0.40
58:AA:150:TRP:HB2	58:AA:170:TRP:HB2	2.04	0.40
63:RR:104:GLY:O	79:18:648:A:H4'	2.20	0.40
67:S9:171:GLY:O	67:S9:175:ARG:HG3	2.22	0.40
68:S7:135:PHE:CG	68:S7:136:PRO:HD3	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
68:S7:158:LEU:O	68:S7:190:PRO:HD2	2.21	0.40
70:S3:100:ALA:O	70:S3:103:GLU:HG3	2.21	0.40
71:RS:7:LYS:O	71:RS:11:LYS:HG2	2.21	0.40
76:UU:88:SER:O	76:UU:92:ARG:HG3	2.21	0.40
79:18:597:G:H2'	79:18:598:G:O4'	2.22	0.40
79:18:623:G:C2	79:18:624:C:C6	3.10	0.40
79:18:1716:C:H2'	79:18:1717:C:C6	2.57	0.40
85:28:318:A:H2'	85:28:319:A:H8	1.86	0.40
85:28:656:C:H2'	85:28:657:C:C6	2.57	0.40
85:28:920:C:H2'	85:28:921:C:H6	1.86	0.40
85:28:1206:C:H2'	85:28:1207:C:C6	2.57	0.40
85:28:1912:G:C6	85:28:2057:A:C2	3.09	0.40
85:28:2299:G:C2	85:28:2336:G:C5	3.09	0.40
85:28:2654:C:H2'	85:28:2655:C:H6	1.86	0.40
85:28:4092:G:C4	85:28:4093:G:C8	3.10	0.40
85:28:4483:C:C2	85:28:4484:A:C8	3.09	0.40
2:S2:194:ARG:O	2:S2:224:THR:HA	2.21	0.40
4:DD:126:VAL:HG13	4:DD:142:VAL:HG13	2.03	0.40
8:L3:288:GLY:HA3	8:L3:330:PHE:CE1	2.56	0.40
10:L5:53:VAL:HG11	10:L5:159:VAL:HA	2.02	0.40
13:aa:314:LEU:O	13:aa:318:LEU:HB2	2.21	0.40
25:26:119:LEU:HD13	25:26:119:LEU:HA	1.95	0.40
27:dd:57:GLY:HA3	50:Q:172:ARG:HD2	2.03	0.40
49:F:57:MET:HE2	49:F:57:MET:HA	2.02	0.40
63:RR:29:LYS:HE3	63:RR:29:LYS:HB3	1.88	0.40
64:SS:25:ILE:HG13	64:SS:57:VAL:HG13	2.04	0.40
65:S6:31:ARG:HG2	65:S6:100:CYS:SG	2.61	0.40
79:18:24:C:C2	79:18:25:A:N7	2.89	0.40
79:18:24:C:H4'	79:18:415:A:H4'	2.04	0.40
79:18:1137:U:H4'	79:18:1138:C:OP1	2.22	0.40
79:18:1164:G:O2'	79:18:1165:G:H5'	2.21	0.40
79:18:1365:G:C2	79:18:1366:G:C5	3.09	0.40
79:18:1545:A:C2	79:18:1671:G:H1'	2.57	0.40
79:18:1685:U:C4	79:18:1686:G:N7	2.89	0.40
79:18:1836:G:OP1	79:18:1839:U:H4'	2.21	0.40
85:28:2:G:H2'	85:28:3:C:C6	2.57	0.40
85:28:228:C:H2'	85:28:229:G:C8	2.56	0.40
85:28:229:G:H2'	85:28:230:G:C8	2.56	0.40
85:28:2292:C:C2	85:28:2293:U:C5	3.09	0.40
85:28:2556:G:C2	85:28:2557:G:C8	3.10	0.40
85:28:2817:C:H2'	85:28:2818:C:C6	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:28:4089:G:H2'	85:28:4090:G:C8	2.56	0.40
85:28:4158:C:H2'	85:28:4159:C:C6	2.56	0.40
85:28:4177:C:C2	85:28:4178:A:C8	3.10	0.40
85:28:4401:G:H2'	85:28:4402:C:H6	1.86	0.40
85:28:4511:A:H2'	85:28:4512:U:O4'	2.21	0.40
85:28:4749:C:H2'	85:28:4750:G:O4'	2.21	0.40
8:L3:77:THR:HG21	8:L3:337:VAL:HG22	2.04	0.40
15:13:92:ARG:CZ	85:28:109:G:H5'	2.51	0.40
17:15:44:ARG:HH12	85:28:280:G:P	2.45	0.40
20:19:106:LEU:HD13	20:19:138:LEU:HD21	2.03	0.40
28:29:31:SER:HA	85:28:1463:C:H5''	2.03	0.40
44:AS:143:THR:HB	44:AS:205:TYR:CE1	2.56	0.40
45:FF:45:LEU:HD12	45:FF:45:LEU:HA	1.74	0.40
54:S5:49:LEU:HG	56:II:49:TYR:HB2	2.04	0.40
54:S5:119:SER:OG	54:S5:189:ALA:HB1	2.22	0.40
61:LL:82:TRP:CD1	79:18:1567:G:C6	3.10	0.40
79:18:52:G:H2'	79:18:53:C:C6	2.57	0.40
79:18:1512:C:H2'	79:18:1513:C:C6	2.57	0.40
85:28:981:U:H2'	85:28:982:C:C6	2.56	0.40
85:28:1216:C:C2	85:28:1217:G:C8	3.09	0.40
85:28:1311:G:H2'	85:28:1312:A:O4'	2.22	0.40
85:28:1384:C:C2	85:28:1385:G:C8	3.09	0.40
85:28:1745:G:C2	85:28:1746:A:C8	3.10	0.40
85:28:2007:G:H21	85:28:2012:A:H62	1.69	0.40
85:28:2294:G:H2'	85:28:2295:C:C6	2.56	0.40
85:28:2503:G:N2	85:28:4084:G:C8	2.89	0.40
85:28:2728:U:H2'	85:28:2729:C:C6	2.57	0.40
85:28:4340:U:C4	85:28:4341:C:C5	3.10	0.40
85:28:4530:U:H2'	85:28:4531:U:H2'	2.02	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	BB	215/217 (99%)	208 (97%)	7 (3%)	0	100	100
2	S2	219/221 (99%)	217 (99%)	2 (1%)	0	100	100
3	PP	81/83 (98%)	80 (99%)	1 (1%)	0	100	100
4	DD	139/151 (92%)	132 (95%)	7 (5%)	0	100	100
7	L8	246/248 (99%)	239 (97%)	7 (3%)	0	100	100
8	L3	392/394 (100%)	379 (97%)	13 (3%)	0	100	100
9	L4	360/362 (99%)	354 (98%)	6 (2%)	0	100	100
10	L5	291/293 (99%)	285 (98%)	6 (2%)	0	100	100
11	L6	208/251 (83%)	199 (96%)	9 (4%)	0	100	100
12	L7	223/225 (99%)	214 (96%)	8 (4%)	1 (0%)	30	59
13	aa	229/240 (95%)	224 (98%)	5 (2%)	0	100	100
14	10	201/213 (94%)	200 (100%)	1 (0%)	0	100	100
15	13	208/211 (99%)	202 (97%)	6 (3%)	0	100	100
16	14	136/138 (99%)	134 (98%)	2 (2%)	0	100	100
17	15	201/203 (99%)	193 (96%)	8 (4%)	0	100	100
18	bb	197/199 (99%)	196 (100%)	1 (0%)	0	100	100
19	17	151/153 (99%)	151 (100%)	0	0	100	100
20	19	178/180 (99%)	175 (98%)	3 (2%)	0	100	100
21	20	174/176 (99%)	172 (99%)	2 (1%)	0	100	100
22	21	157/159 (99%)	156 (99%)	1 (1%)	0	100	100
23	22	97/99 (98%)	94 (97%)	3 (3%)	0	100	100
24	cc	116/118 (98%)	115 (99%)	1 (1%)	0	100	100
25	26	132/134 (98%)	132 (100%)	0	0	100	100
26	27	133/135 (98%)	129 (97%)	4 (3%)	0	100	100
27	dd	145/147 (99%)	138 (95%)	7 (5%)	0	100	100
28	29	100/245 (41%)	98 (98%)	2 (2%)	0	100	100
29	30	96/98 (98%)	95 (99%)	1 (1%)	0	100	100
30	31	105/107 (98%)	103 (98%)	2 (2%)	0	100	100
31	32	126/128 (98%)	124 (98%)	2 (2%)	0	100	100
32	ee	107/109 (98%)	103 (96%)	4 (4%)	0	100	100
33	34	112/114 (98%)	112 (100%)	0	0	100	100
34	35	120/122 (98%)	118 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
35	36	100/102 (98%)	99 (99%)	1 (1%)	0	100	100
36	37	84/86 (98%)	84 (100%)	0	0	100	100
37	38	67/69 (97%)	66 (98%)	1 (2%)	0	100	100
38	39	48/50 (96%)	47 (98%)	1 (2%)	0	100	100
39	40	50/52 (96%)	50 (100%)	0	0	100	100
40	41	23/25 (92%)	23 (100%)	0	0	100	100
41	42	102/104 (98%)	101 (99%)	1 (1%)	0	100	100
42	ff	89/91 (98%)	86 (97%)	3 (3%)	0	100	100
43	gg	122/124 (98%)	119 (98%)	3 (2%)	0	100	100
44	AS	211/213 (99%)	207 (98%)	4 (2%)	0	100	100
45	FF	147/149 (99%)	145 (99%)	2 (1%)	0	100	100
46	VV	81/83 (98%)	79 (98%)	2 (2%)	0	100	100
47	s	194/196 (99%)	188 (97%)	6 (3%)	0	100	100
48	t	151/153 (99%)	143 (95%)	8 (5%)	0	100	100
49	F	356/358 (99%)	349 (98%)	7 (2%)	0	100	100
50	Q	185/188 (98%)	181 (98%)	4 (2%)	0	100	100
51	ZZ	66/68 (97%)	65 (98%)	1 (2%)	0	100	100
52	EE	115/117 (98%)	109 (95%)	6 (5%)	0	100	100
53	TT	73/75 (97%)	69 (94%)	4 (6%)	0	100	100
54	S5	181/191 (95%)	168 (93%)	13 (7%)	0	100	100
55	WW	60/62 (97%)	60 (100%)	0	0	100	100
56	II	140/142 (99%)	137 (98%)	3 (2%)	0	100	100
57	CC	94/96 (98%)	86 (92%)	7 (7%)	1 (1%)	11	36
58	AA	311/313 (99%)	297 (96%)	14 (4%)	0	100	100
59	OO	98/100 (98%)	97 (99%)	1 (1%)	0	100	100
60	MM	139/141 (99%)	135 (97%)	4 (3%)	0	100	100
61	LL	142/144 (99%)	136 (96%)	6 (4%)	0	100	100
62	XX	53/55 (96%)	52 (98%)	1 (2%)	0	100	100
63	RR	139/143 (97%)	135 (97%)	3 (2%)	1 (1%)	18	48
64	SS	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
65	S6	235/237 (99%)	234 (100%)	1 (0%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
66	S4	260/262 (99%)	257 (99%)	3 (1%)	0	100	100
67	S9	183/185 (99%)	179 (98%)	4 (2%)	0	100	100
68	S7	181/189 (96%)	178 (98%)	3 (2%)	0	100	100
69	YY	53/55 (96%)	53 (100%)	0	0	100	100
70	S3	212/214 (99%)	209 (99%)	3 (1%)	0	100	100
71	RS	130/132 (98%)	126 (97%)	4 (3%)	0	100	100
72	WX	127/129 (98%)	123 (97%)	4 (3%)	0	100	100
73	S8	204/206 (99%)	199 (98%)	5 (2%)	0	100	100
74	W	102/121 (84%)	101 (99%)	1 (1%)	0	100	100
75	GG	133/136 (98%)	131 (98%)	2 (2%)	0	100	100
76	UU	99/101 (98%)	98 (99%)	1 (1%)	0	100	100
77	11	168/170 (99%)	166 (99%)	2 (1%)	0	100	100
78	L9	188/190 (99%)	181 (96%)	7 (4%)	0	100	100
80	v	824/857 (96%)	809 (98%)	15 (2%)	0	100	100
81	LA	45/1096 (4%)	45 (100%)	0	0	100	100
82	CE	71/223 (32%)	71 (100%)	0	0	100	100
83	A	119/121 (98%)	116 (98%)	3 (2%)	0	100	100
86	23	137/140 (98%)	137 (100%)	0	0	100	100
All	All	12809/14451 (89%)	12518 (98%)	288 (2%)	3 (0%)	100	100

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
63	RR	62	PRO
57	CC	65	ARG
12	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	BB	180/181 (99%)	167 (93%)	13 (7%)	13	39
2	S2	187/187 (100%)	180 (96%)	7 (4%)	30	64
3	PP	67/67 (100%)	63 (94%)	4 (6%)	17	47
4	DD	130/136 (96%)	124 (95%)	6 (5%)	24	57
7	L8	190/190 (100%)	182 (96%)	8 (4%)	26	60
8	L3	342/342 (100%)	327 (96%)	15 (4%)	25	59
9	L4	302/302 (100%)	293 (97%)	9 (3%)	36	70
10	L5	247/247 (100%)	240 (97%)	7 (3%)	38	72
11	L6	190/223 (85%)	183 (96%)	7 (4%)	30	64
12	L7	196/196 (100%)	189 (96%)	7 (4%)	31	65
13	aa	200/205 (98%)	191 (96%)	9 (4%)	24	58
14	10	175/180 (97%)	171 (98%)	4 (2%)	44	76
15	13	175/176 (99%)	166 (95%)	9 (5%)	21	53
16	14	117/117 (100%)	111 (95%)	6 (5%)	21	53
17	15	171/171 (100%)	164 (96%)	7 (4%)	27	61
18	bb	171/171 (100%)	163 (95%)	8 (5%)	23	56
19	17	134/134 (100%)	133 (99%)	1 (1%)	76	92
20	19	159/159 (100%)	151 (95%)	8 (5%)	22	53
21	20	157/157 (100%)	150 (96%)	7 (4%)	24	58
22	21	139/139 (100%)	136 (98%)	3 (2%)	45	77
23	22	89/89 (100%)	86 (97%)	3 (3%)	32	66
24	cc	106/106 (100%)	105 (99%)	1 (1%)	70	90
25	26	124/124 (100%)	117 (94%)	7 (6%)	19	50
26	27	117/117 (100%)	114 (97%)	3 (3%)	40	73
27	dd	119/119 (100%)	117 (98%)	2 (2%)	53	82
28	29	84/184 (46%)	82 (98%)	2 (2%)	43	75
29	30	84/84 (100%)	82 (98%)	2 (2%)	43	75
30	31	98/98 (100%)	92 (94%)	6 (6%)	17	46
31	32	114/114 (100%)	108 (95%)	6 (5%)	20	52
32	ee	88/88 (100%)	83 (94%)	5 (6%)	18	49
33	34	98/98 (100%)	97 (99%)	1 (1%)	68	89
34	35	109/109 (100%)	106 (97%)	3 (3%)	38	72

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
35	36	86/86 (100%)	82 (95%)	4 (5%)	23	56
36	37	73/73 (100%)	71 (97%)	2 (3%)	39	73
37	38	64/64 (100%)	62 (97%)	2 (3%)	35	69
38	39	47/47 (100%)	47 (100%)	0	100	100
39	40	48/48 (100%)	48 (100%)	0	100	100
40	41	24/24 (100%)	24 (100%)	0	100	100
41	42	92/92 (100%)	90 (98%)	2 (2%)	45	77
42	ff	74/74 (100%)	70 (95%)	4 (5%)	20	51
43	gg	107/108 (99%)	104 (97%)	3 (3%)	38	72
44	AS	194/194 (100%)	188 (97%)	6 (3%)	35	69
45	FF	130/130 (100%)	123 (95%)	7 (5%)	20	51
46	VV	75/75 (100%)	69 (92%)	6 (8%)	11	34
47	s	164/164 (100%)	151 (92%)	13 (8%)	11	34
48	t	126/126 (100%)	115 (91%)	11 (9%)	9	30
49	F	307/307 (100%)	295 (96%)	12 (4%)	28	63
50	Q	164/165 (99%)	162 (99%)	2 (1%)	63	86
51	ZZ	61/61 (100%)	58 (95%)	3 (5%)	22	54
52	EE	99/99 (100%)	96 (97%)	3 (3%)	36	70
53	TT	66/66 (100%)	63 (96%)	3 (4%)	24	58
54	S5	158/161 (98%)	150 (95%)	8 (5%)	21	53
55	WW	55/55 (100%)	52 (94%)	3 (6%)	19	50
56	II	117/117 (100%)	112 (96%)	5 (4%)	26	60
57	CC	87/87 (100%)	84 (97%)	3 (3%)	32	66
58	AA	272/272 (100%)	263 (97%)	9 (3%)	33	67
59	OO	92/92 (100%)	86 (94%)	6 (6%)	15	44
60	MM	111/111 (100%)	108 (97%)	3 (3%)	39	73
61	LL	125/125 (100%)	117 (94%)	8 (6%)	16	44
62	XX	48/48 (100%)	47 (98%)	1 (2%)	47	77
63	RR	113/115 (98%)	108 (96%)	5 (4%)	25	59
64	SS	107/107 (100%)	100 (94%)	7 (6%)	15	44
65	S6	207/207 (100%)	201 (97%)	6 (3%)	37	71

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
66	S4	224/224 (100%)	220 (98%)	4 (2%)	51	80
67	S9	161/161 (100%)	153 (95%)	8 (5%)	22	53
68	S7	165/169 (98%)	159 (96%)	6 (4%)	31	65
69	YY	46/46 (100%)	44 (96%)	2 (4%)	26	60
70	S3	177/177 (100%)	162 (92%)	15 (8%)	10	31
71	RS	119/119 (100%)	110 (92%)	9 (8%)	12	36
72	WX	112/112 (100%)	108 (96%)	4 (4%)	31	65
73	S8	178/178 (100%)	172 (97%)	6 (3%)	32	66
74	W	86/100 (86%)	82 (95%)	4 (5%)	23	56
75	GG	105/106 (99%)	101 (96%)	4 (4%)	29	64
76	UU	88/88 (100%)	86 (98%)	2 (2%)	44	76
77	11	143/143 (100%)	139 (97%)	4 (3%)	38	72
78	L9	169/169 (100%)	160 (95%)	9 (5%)	20	52
80	v	705/728 (97%)	664 (94%)	41 (6%)	18	49
81	LA	45/948 (5%)	41 (91%)	4 (9%)	9	28
82	CE	62/190 (33%)	59 (95%)	3 (5%)	23	55
83	A	107/107 (100%)	96 (90%)	11 (10%)	7	23
86	23	106/107 (99%)	103 (97%)	3 (3%)	38	72
All	All	11150/12382 (90%)	10678 (96%)	472 (4%)	28	60

All (472) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	BB	5	LEU
1	BB	44	ASP
1	BB	51	LEU
1	BB	84	GLN
1	BB	88	LEU
1	BB	136	GLU
1	BB	140	VAL
1	BB	145	ILE
1	BB	157	VAL
1	BB	159	ILE
1	BB	177	MET
1	BB	178	LEU
1	BB	208	GLU

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Mol	Chain	Res	Type
2	S2	86	LEU
2	S2	146	GLU
2	S2	165	VAL
2	S2	212	LYS
2	S2	215	MET
2	S2	227	ARG
2	S2	252	THR
3	PP	32	ILE
3	PP	51	LYS
3	PP	70	LEU
3	PP	72	LEU
4	DD	7	GLU
4	DD	12	LYS
4	DD	16	ILE
4	DD	42	LEU
4	DD	46	THR
4	DD	56	ILE
7	L8	42	LYS
7	L8	75	LEU
7	L8	101	VAL
7	L8	158	ILE
7	L8	162	ASN
7	L8	163	ARG
7	L8	165	VAL
7	L8	208	GLU
8	L3	47	LEU
8	L3	56	ILE
8	L3	89	ILE
8	L3	94	GLU
8	L3	95	THR
8	L3	158	GLN
8	L3	173	LEU
8	L3	240	LEU
8	L3	246	ARG
8	L3	248	LEU
8	L3	258	HIS
8	L3	262	VAL
8	L3	314	ILE
8	L3	351	LEU
8	L3	362	LYS
9	L4	3	CYS
9	L4	49	ARG

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Mol	Chain	Res	Type
9	L4	62	THR
9	L4	205	ARG
9	L4	227	ILE
9	L4	232	VAL
9	L4	285	LEU
9	L4	294	LYS
9	L4	313	VAL
10	L5	25	GLU
10	L5	35	ARG
10	L5	56	THR
10	L5	69	ILE
10	L5	225	GLN
10	L5	249	GLU
10	L5	261	VAL
11	L6	51	VAL
11	L6	112	LEU
11	L6	166	VAL
11	L6	178	VAL
11	L6	197	VAL
11	L6	215	LEU
11	L6	217	ASP
12	L7	34	LYS
12	L7	41	LEU
12	L7	54	LYS
12	L7	97	ILE
12	L7	124	LEU
12	L7	151	GLU
12	L7	189	LEU
13	aa	139	VAL
13	aa	159	THR
13	aa	166	ARG
13	aa	193	VAL
13	aa	199	LEU
13	aa	220	VAL
13	aa	226	LEU
13	aa	237	LEU
13	aa	295	LEU
14	10	44	ASP
14	10	63	GLU
14	10	146	GLU
14	10	163	GLN
15	13	59	VAL

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Mol	Chain	Res	Type
15	13	63	THR
15	13	67	HIS
15	13	103	ARG
15	13	124	LEU
15	13	144	LEU
15	13	154	VAL
15	13	164	GLU
15	13	205	GLN
16	14	34	ASN
16	14	38	VAL
16	14	59	ASP
16	14	62	LEU
16	14	103	LYS
16	14	137	LYS
17	15	61	ILE
17	15	64	ILE
17	15	66	VAL
17	15	75	VAL
17	15	80	THR
17	15	151	ILE
17	15	198	LEU
18	bb	5	GLN
18	bb	7	LEU
18	bb	12	ARG
18	bb	27	VAL
18	bb	72	HIS
18	bb	113	ASP
18	bb	124	LEU
18	bb	144	GLU
19	17	103	GLU
20	19	15	LEU
20	19	46	LYS
20	19	50	ILE
20	19	74	ARG
20	19	106	LEU
20	19	145	LEU
20	19	149	LYS
20	19	155	LEU
21	20	1	MET
21	20	7	LEU
21	20	17	LEU
21	20	39	VAL

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Mol	Chain	Res	Type
21	20	90	THR
21	20	111	ARG
21	20	159	LEU
22	21	69	GLN
22	21	106	LEU
22	21	121	GLU
23	22	23	LEU
23	22	30	GLU
23	22	50	ASN
24	cc	147	LEU
25	26	8	THR
25	26	40	GLN
25	26	55	VAL
25	26	79	VAL
25	26	104	VAL
25	26	119	LEU
25	26	120	GLU
26	27	54	THR
26	27	77	TYR
26	27	120	GLU
27	dd	86	THR
27	dd	103	VAL
28	29	9	THR
28	29	104	LEU
29	30	101	ASP
29	30	105	ILE
30	31	23	ARG
30	31	26	THR
30	31	46	LEU
30	31	96	GLU
30	31	111	VAL
30	31	121	ASN
31	32	4	LEU
31	32	33	ARG
31	32	44	ARG
31	32	48	ARG
31	32	85	LEU
31	32	91	CYS
32	ee	18	LEU
32	ee	23	GLU
32	ee	33	VAL
32	ee	103	VAL

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Mol	Chain	Res	Type
32	ee	105	LEU
33	34	60	ARG
34	35	47	ILE
34	35	96	ASN
34	35	111	GLU
35	36	29	ARG
35	36	42	ASP
35	36	66	ASP
35	36	94	LEU
36	37	58	THR
36	37	83	THR
37	38	12	LEU
37	38	57	LYS
41	42	82	MET
41	42	85	ILE
42	ff	52	VAL
42	ff	54	ILE
42	ff	74	THR
42	ff	89	LEU
43	gg	90	LEU
43	gg	103	HIS
43	gg	119	ARG
44	AS	60	ASP
44	AS	78	GLU
44	AS	122	GLU
44	AS	134	LEU
44	AS	183	GLU
44	AS	212	VAL
45	FF	22	VAL
45	FF	45	LEU
45	FF	75	LEU
45	FF	102	LEU
45	FF	118	ILE
45	FF	119	GLU
45	FF	142	GLU
46	VV	7	LEU
46	VV	14	GLU
46	VV	29	ASN
46	VV	53	VAL
46	VV	63	LEU
46	VV	73	LEU
47	s	29	ILE

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Mol	Chain	Res	Type
47	s	30	VAL
47	s	68	HIS
47	s	94	ASP
47	s	95	LEU
47	s	126	GLN
47	s	144	THR
47	s	147	ILE
47	s	153	GLU
47	s	158	VAL
47	s	174	LEU
47	s	180	ILE
47	s	189	ILE
48	t	32	ILE
48	t	54	LYS
48	t	58	ILE
48	t	81	ILE
48	t	83	LYS
48	t	96	LYS
48	t	123	ARG
48	t	124	GLU
48	t	125	LEU
48	t	128	THR
48	t	146	ARG
49	F	21	TYR
49	F	51	LYS
49	F	82	VAL
49	F	131	GLN
49	F	177	PHE
49	F	209	GLN
49	F	226	VAL
49	F	287	LYS
49	F	319	PHE
49	F	350	GLN
49	F	353	GLU
49	F	354	LEU
50	Q	63	LEU
50	Q	158	THR
51	ZZ	107	LYS
51	ZZ	114	ILE
51	ZZ	132	MET
52	EE	26	LEU
52	EE	65	VAL

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Mol	Chain	Res	Type
52	EE	122	ASP
53	TT	58	LEU
53	TT	69	THR
53	TT	75	GLU
54	S5	25	THR
54	S5	59	LYS
54	S5	81	ARG
54	S5	98	GLU
54	S5	142	SER
54	S5	152	TRP
54	S5	154	LEU
54	S5	155	CYS
55	WW	24	GLN
55	WW	28	THR
55	WW	57	THR
56	II	47	LEU
56	II	68	ILE
56	II	81	ILE
56	II	86	GLN
56	II	126	ARG
57	CC	11	ILE
57	CC	32	HIS
57	CC	39	ASN
58	AA	17	TRP
58	AA	98	THR
58	AA	149	GLU
58	AA	198	VAL
58	AA	206	LEU
58	AA	246	TYR
58	AA	256	ILE
58	AA	257	LYS
58	AA	280	LYS
59	OO	39	LEU
59	OO	44	LYS
59	OO	46	LYS
59	OO	60	THR
59	OO	68	THR
59	OO	84	ILE
60	MM	43	LYS
60	MM	90	SER
60	MM	110	LEU
61	LL	36	VAL

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Mol	Chain	Res	Type
61	LL	54	LYS
61	LL	75	ARG
61	LL	77	TYR
61	LL	83	PHE
61	LL	98	VAL
61	LL	108	ARG
61	LL	141	ARG
62	XX	50	ILE
63	RR	17	ARG
63	RR	52	LEU
63	RR	81	ILE
63	RR	99	GLU
63	RR	107	ARG
64	SS	4	THR
64	SS	29	HIS
64	SS	44	LEU
64	SS	51	THR
64	SS	61	ARG
64	SS	110	ARG
64	SS	112	ASN
65	S6	21	GLU
65	S6	24	LEU
65	S6	25	ARG
65	S6	76	LEU
65	S6	146	ASN
65	S6	160	LYS
66	S4	3	ARG
66	S4	42	LEU
66	S4	156	VAL
66	S4	245	ARG
67	S9	3	VAL
67	S9	14	VAL
67	S9	27	GLN
67	S9	59	GLU
67	S9	61	LEU
67	S9	101	LYS
67	S9	106	LEU
67	S9	131	ARG
68	S7	9	VAL
68	S7	18	GLU
68	S7	29	GLU
68	S7	31	GLU

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Mol	Chain	Res	Type
68	S7	60	ILE
68	S7	121	THR
69	YY	107	ARG
69	YY	122	PHE
70	S3	1	MET
70	S3	4	GLN
70	S3	44	THR
70	S3	45	ARG
70	S3	59	LEU
70	S3	97	CYS
70	S3	99	ILE
70	S3	109	LEU
70	S3	123	LEU
70	S3	124	ARG
70	S3	126	ILE
70	S3	142	LEU
70	S3	157	MET
70	S3	167	TYR
70	S3	175	VAL
71	RS	16	ILE
71	RS	18	GLU
71	RS	24	LEU
71	RS	31	ASN
71	RS	69	ILE
71	RS	81	ARG
71	RS	88	VAL
71	RS	107	LYS
71	RS	123	THR
72	WX	57	ARG
72	WX	87	GLU
72	WX	103	VAL
72	WX	104	LEU
73	S8	3	ILE
73	S8	6	ASP
73	S8	73	THR
73	S8	140	LYS
73	S8	144	LYS
73	S8	178	ARG
74	W	30	GLN
74	W	82	ILE
74	W	94	ARG
74	W	97	LYS

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Mol	Chain	Res	Type
75	GG	52	THR
75	GG	76	LEU
75	GG	86	LYS
75	GG	147	ARG
76	UU	43	ASN
76	UU	46	GLU
77	11	33	LEU
77	11	46	GLN
77	11	67	LYS
77	11	148	THR
78	L9	12	ILE
78	L9	20	LEU
78	L9	42	ASN
78	L9	57	VAL
78	L9	74	CYS
78	L9	103	VAL
78	L9	107	GLU
78	L9	141	LYS
78	L9	162	GLN
80	v	3	ASN
80	v	4	PHE
80	v	15	LYS
80	v	16	LYS
80	v	20	ARG
80	v	34	THR
80	v	75	ILE
80	v	77	LEU
80	v	99	LEU
80	v	140	GLU
80	v	164	LEU
80	v	211	THR
80	v	212	VAL
80	v	249	ARG
80	v	294	LEU
80	v	321	ILE
80	v	323	LEU
80	v	350	LEU
80	v	385	ILE
80	v	386	LYS
80	v	400	LYS
80	v	416	VAL
80	v	421	VAL

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Mol	Chain	Res	Type
80	v	425	LEU
80	v	439	LYS
80	v	442	LEU
80	v	461	ILE
80	v	464	VAL
80	v	480	VAL
80	v	505	VAL
80	v	554	LEU
80	v	568	ILE
80	v	577	VAL
80	v	675	ILE
80	v	729	LEU
80	v	746	LEU
80	v	773	GLU
80	v	775	GLN
80	v	776	VAL
80	v	783	VAL
80	v	800	LEU
81	LA	665	HIS
81	LA	683	LEU
81	LA	688	GLN
81	LA	690	LEU
82	CE	33	GLU
82	CE	49	LYS
82	CE	77	GLU
83	A	24	GLN
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 (141) such sidechains are listed below:

Mol	Chain	Res	Type
1	BB	9	GLN
1	BB	84	GLN
1	BB	111	GLN
1	BB	141	ASN
2	S2	113	GLN
2	S2	136	HIS
4	DD	11	GLN
4	DD	112	HIS
7	L8	22	HIS
7	L8	83	HIS
7	L8	216	HIS
8	L3	109	HIS
8	L3	123	HIS
8	L3	158	GLN
8	L3	175	GLN
8	L3	184	GLN
8	L3	204	GLN
8	L3	258	HIS
9	L4	50	GLN
9	L4	60	HIS
9	L4	178	ASN
9	L4	317	ASN
9	L4	338	ASN
9	L4	346	ASN
10	L5	195	HIS
10	L5	198	HIS
14	10	95	HIS
15	13	149	GLN
16	14	20	HIS
17	15	109	HIS
18	bb	26	GLN
18	bb	143	HIS
18	bb	150	GLN
18	bb	167	HIS
18	bb	184	ASN
19	17	21	ASN
19	17	25	HIS
19	17	28	ASN
19	17	56	GLN
19	17	75	GLN
19	17	116	HIS
19	17	118	GLN
19	17	120	ASN

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Mol	Chain	Res	Type
19	17	137	ASN
20	19	66	ASN
20	19	143	HIS
21	20	66	GLN
21	20	156	HIS
22	21	98	HIS
22	21	131	GLN
23	22	17	GLN
23	22	38	ASN
24	cc	93	ASN
25	26	20	ASN
25	26	61	HIS
27	dd	66	ASN
27	dd	85	GLN
27	dd	120	GLN
28	29	6	ASN
28	29	27	GLN
28	29	61	ASN
30	31	116	ASN
33	34	28	ASN
33	34	112	GLN
34	35	68	ASN
34	35	96	ASN
36	37	13	ASN
36	37	66	HIS
37	38	31	ASN
39	40	64	ASN
42	ff	92	GLN
43	gg	103	HIS
45	FF	69	ASN
45	FF	101	HIS
46	VV	9	HIS
46	VV	29	ASN
47	s	68	HIS
47	s	71	ASN
47	s	72	ASN
48	t	97	ASN
48	t	137	GLN
48	t	142	ASN
48	t	147	HIS
49	F	29	ASN
49	F	113	HIS

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Mol	Chain	Res	Type
49	F	147	HIS
49	F	213	HIS
49	F	303	GLN
49	F	350	GLN
50	Q	57	ASN
51	ZZ	139	HIS
53	TT	64	ASN
54	S5	51	HIS
54	S5	74	ASN
54	S5	118	ASN
54	S5	148	ASN
54	S5	203	ASN
55	WW	29	GLN
57	CC	28	HIS
57	CC	32	HIS
58	AA	26	GLN
60	MM	42	HIS
60	MM	126	GLN
61	LL	105	ASN
63	RR	73	GLN
64	SS	19	GLN
64	SS	22	GLN
64	SS	29	HIS
64	SS	112	ASN
65	S6	4	ASN
65	S6	13	GLN
65	S6	59	GLN
65	S6	110	ASN
66	S4	112	HIS
67	S9	75	ASN
67	S9	113	GLN
67	S9	154	GLN
67	S9	177	ASN
68	S7	33	ASN
68	S7	193	GLN
71	RS	56	HIS
72	WX	64	ASN
72	WX	70	ASN
73	S8	7	ASN
73	S8	167	GLN
74	W	48	GLN
75	GG	94	HIS

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Mol	Chain	Res	Type
77	11	23	ASN
77	11	71	HIS
78	L9	79	ASN
78	L9	140	GLN
80	v	27	HIS
80	v	30	HIS
80	v	108	HIS
80	v	357	HIS
80	v	535	GLN
80	v	803	ASN
80	v	807	GLN
80	v	853	ASN
81	LA	680	ASN
86	23	36	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
5	58	149/156 (95%)	20 (13%)	1 (0%)
6	6	119/120 (99%)	9 (7%)	0
79	18	1675/1688 (99%)	300 (17%)	14 (0%)
84	ES	34/5070 (0%)	7 (20%)	1 (2%)
85	28	3479/4808 (72%)	581 (16%)	48 (1%)
All	All	5456/11842 (46%)	917 (16%)	64 (1%)

All (917) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
5	58	2	G
5	58	34	U
5	58	35	C
5	58	59	A
5	58	62	A
5	58	63	U
5	58	86	U
5	58	103	A
5	58	105	C
5	58	110	U
5	58	111	U
5	58	112	G
5	58	114	G

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Mol	Chain	Res	Type
5	58	122	G
5	58	123	U
5	58	124	U
5	58	125	C
5	58	126	C
5	58	127	U
5	58	151	G
6	6	7	G
6	6	25	G
6	6	33	U
6	6	53	U
6	6	54	A
6	6	64	G
6	6	100	A
6	6	110	G
6	6	120	U
79	18	2	A
79	18	3	C
79	18	4	C
79	18	25	A
79	18	26	U
79	18	33	G
79	18	36	U
79	18	41	G
79	18	44	U
79	18	45	A
79	18	46	A
79	18	50	A
79	18	51	U
79	18	56	G
79	18	67	C
79	18	74	G
79	18	77	A
79	18	79	A
79	18	93	U
79	18	99	A
79	18	103	A
79	18	111	A
79	18	113	G
79	18	115	U
79	18	116	U
79	18	124	U

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Mol	Chain	Res	Type
79	18	126	G
79	18	127	C
79	18	142	C
79	18	143	U
79	18	147	A
79	18	155	G
79	18	160	U
79	18	162	C
79	18	163	U
79	18	168	C
79	18	169	U
79	18	182	C
79	18	183	G
79	18	184	G
79	18	191	A
79	18	192	C
79	18	206	G
79	18	292	A
79	18	294	U
79	18	307	G
79	18	308	G
79	18	309	G
79	18	312	G
79	18	319	C
79	18	330	G
79	18	339	A
79	18	340	C
79	18	350	C
79	18	351	G
79	18	360	A
79	18	362	C
79	18	364	A
79	18	368	U
79	18	369	C
79	18	377	G
79	18	385	G
79	18	386	C
79	18	399	C
79	18	400	C
79	18	408	A
79	18	409	C
79	18	418	A

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Mol	Chain	Res	Type
79	18	435	A
79	18	438	G
79	18	448	A
79	18	450	C
79	18	451	G
79	18	452	G
79	18	465	A
79	18	466	G
79	18	467	G
79	18	472	C
79	18	473	A
79	18	474	G
79	18	487	U
79	18	492	C
79	18	496	C
79	18	500	A
79	18	517	C
79	18	525	A
79	18	532	C
79	18	533	A
79	18	536	A
79	18	537	C
79	18	542	U
79	18	547	G
79	18	554	A
79	18	555	A
79	18	556	U
79	18	559	G
79	18	560	A
79	18	562	U
79	18	564	A
79	18	568	C
79	18	574	A
79	18	576	A
79	18	587	A
79	18	588	G
79	18	590	A
79	18	591	U
79	18	605	A
79	18	606	G
79	18	607	U
79	18	608	C

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Mol	Chain	Res	Type
79	18	614	C
79	18	629	A
79	18	631	U
79	18	643	A
79	18	644	G
79	18	657	U
79	18	660	C
79	18	668	A
79	18	669	A
79	18	671	A
79	18	672	A
79	18	673	G
79	18	683	G
79	18	688	U
79	18	752	G
79	18	753	C
79	18	754	G
79	18	799	U
79	18	811	A
79	18	821	G
79	18	822	U
79	18	830	A
79	18	847	A
79	18	848	U
79	18	852	G
79	18	853	C
79	18	870	A
79	18	871	U
79	18	872	A
79	18	873	G
79	18	878	G
79	18	879	C
79	18	887	U
79	18	890	U
79	18	893	U
79	18	894	G
79	18	898	U
79	18	901	G
79	18	913	A
79	18	914	U
79	18	920	A
79	18	922	A

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Mol	Chain	Res	Type
79	18	933	G
79	18	943	U
79	18	955	A
79	18	956	G
79	18	971	G
79	18	978	G
79	18	990	A
79	18	992	A
79	18	999	G
79	18	1002	U
79	18	1023	A
79	18	1045	U
79	18	1060	A
79	18	1062	A
79	18	1083	A
79	18	1085	C
79	18	1100	A
79	18	1113	A
79	18	1115	U
79	18	1116	C
79	18	1117	C
79	18	1118	C
79	18	1120	U
79	18	1131	G
79	18	1133	A
79	18	1138	C
79	18	1139	C
79	18	1150	A
79	18	1153	C
79	18	1154	U
79	18	1155	U
79	18	1157	G
79	18	1158	G
79	18	1195	A
79	18	1207	G
79	18	1212	G
79	18	1215	C
79	18	1216	C
79	18	1224	G
79	18	1242	U
79	18	1251	A
79	18	1253	A

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Mol	Chain	Res	Type
79	18	1256	G
79	18	1257	G
79	18	1259	A
79	18	1265	A
79	18	1269	G
79	18	1273	C
79	18	1274	G
79	18	1275	G
79	18	1281	G
79	18	1285	G
79	18	1286	G
79	18	1293	A
79	18	1298	G
79	18	1299	A
79	18	1300	U
79	18	1301	A
79	18	1302	G
79	18	1308	U
79	18	1315	U
79	18	1316	C
79	18	1317	C
79	18	1341	C
79	18	1342	U
79	18	1343	U
79	18	1369	A
79	18	1371	U
79	18	1372	U
79	18	1374	C
79	18	1378	A
79	18	1395	C
79	18	1396	A
79	18	1397	U
79	18	1402	A
79	18	1412	C
79	18	1428	G
79	18	1429	G
79	18	1442	U
79	18	1443	C
79	18	1454	A
79	18	1462	U
79	18	1463	U
79	18	1476	A

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Mol	Chain	Res	Type
79	18	1477	U
79	18	1489	A
79	18	1490	G
79	18	1495	G
79	18	1497	G
79	18	1498	A
79	18	1521	C
79	18	1522	A
79	18	1533	A
79	18	1536	G
79	18	1548	G
79	18	1552	G
79	18	1553	C
79	18	1556	A
79	18	1557	C
79	18	1570	G
79	18	1575	G
79	18	1578	U
79	18	1579	A
79	18	1580	A
79	18	1585	U
79	18	1587	G
79	18	1588	A
79	18	1600	G
79	18	1601	A
79	18	1603	G
79	18	1606	G
79	18	1621	U
79	18	1623	A
79	18	1637	A
79	18	1638	G
79	18	1648	G
79	18	1665	G
79	18	1679	A
79	18	1680	G
79	18	1683	C
79	18	1695	A
79	18	1698	C
79	18	1721	U
79	18	1722	G
79	18	1729	U
79	18	1753	C

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Mol	Chain	Res	Type
79	18	1756	C
79	18	1757	G
79	18	1774	C
79	18	1779	G
79	18	1783	C
79	18	1784	G
79	18	1785	C
79	18	1793	A
79	18	1805	G
79	18	1823	A
79	18	1824	A
79	18	1825	A
79	18	1836	G
79	18	1838	U
79	18	1849	G
79	18	1851	A
79	18	1861	G
79	18	1862	G
79	18	1863	A
79	18	1865	C
79	18	1867	U
79	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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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	496	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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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	978	C
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
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	1285	U
85	28	1287	G
85	28	1292	C
85	28	1293	G

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Mol	Chain	Res	Type
85	28	1296	G
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	1414	C
85	28	1419	G
85	28	1420	A
85	28	1433	A
85	28	1435	G
85	28	1445	U
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	1516	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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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	2703	G
85	28	2707	U
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

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Mol	Chain	Res	Type
85	28	2826	U
85	28	2842	G
85	28	2855	G
85	28	2869	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	3729	U
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
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	3839	G
85	28	3840	U
85	28	3860	A
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

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Mol	Chain	Res	Type
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
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	4377	G

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
85	28	4902	C
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	4943	A

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Mol	Chain	Res	Type
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	5006	U
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
85	28	5062	G

All (64) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
5	58	124	U
79	18	110	U
79	18	291	G
79	18	434	G
79	18	465	A
79	18	642	U
79	18	752	G
79	18	870	A
79	18	1137	U
79	18	1394	G
79	18	1395	C
79	18	1520	G
79	18	1637	A
79	18	1664	A
79	18	1862	G
84	ES	3236	G

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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	$\# Z > 2$
80	DDE	v	715	80	18,20,21	1.03	1 (5%)	17,28,30	0.85	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
80	DDE	v	715	80	-	9/20/21/23	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
80	v	715	DDE	CD2-CG	2.57	1.41	1.36

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
80	v	715	DDE	CAU-CBW-CBI	-2.29	106.75	111.22

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
80	v	715	DDE	C-CA-CB-CG
80	v	715	DDE	NAD-CBI-CBW-CAU
80	v	715	DDE	CAT-CAU-CBW-CBI
80	v	715	DDE	CAT-CAU-CBW-NCB
80	v	715	DDE	OAG-CBI-CBW-CAU
80	v	715	DDE	CA-CB-CG-ND1
80	v	715	DDE	CA-CB-CG-CD2
80	v	715	DDE	N-CA-CB-CG
80	v	715	DDE	CE1-CAT-CAU-CBW

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	3.49	12 (41%)	45,47,47	1.89	12 (26%)

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	9.57	1.41	1.23
88	v	900	GDP	C2'-C3'	-8.18	1.31	1.53
88	v	900	GDP	O4'-C4'	-6.89	1.29	1.45
88	v	900	GDP	O4'-C1'	5.72	1.55	1.42
88	v	900	GDP	C2-N2	4.69	1.45	1.34
88	v	900	GDP	C1'-N9	-4.29	1.35	1.47
88	v	900	GDP	PA-O3A	4.22	1.64	1.59
88	v	900	GDP	C3'-C4'	3.55	1.62	1.53
88	v	900	GDP	C6-N1	-3.33	1.32	1.38
88	v	900	GDP	O2'-C2'	3.02	1.50	1.43
88	v	900	GDP	C8-N9	-2.18	1.32	1.37
88	v	900	GDP	C2-N1	-2.07	1.32	1.37

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
88	v	900	GDP	C5-C4-N3	-6.03	118.79	128.39
88	v	900	GDP	C2-N3-C4	5.04	120.98	112.30
88	v	900	GDP	N9-C4-N3	4.17	134.29	125.95
88	v	900	GDP	C8-N7-C5	2.92	109.46	104.26
88	v	900	GDP	C4-C5-N7	-2.91	106.06	110.67
88	v	900	GDP	C6-C5-N7	2.83	135.44	130.29
88	v	900	GDP	N9-C8-N7	-2.61	108.55	113.40
88	v	900	GDP	C3'-C2'-C1'	2.45	106.09	101.46
88	v	900	GDP	O6-C6-C5	-2.42	120.14	126.53
88	v	900	GDP	C2-N1-C6	-2.31	120.92	125.11
88	v	900	GDP	C4'-O4'-C1'	-2.31	104.37	109.47
88	v	900	GDP	C5-C6-N1	2.28	119.07	113.25

There are no chirality outliers.

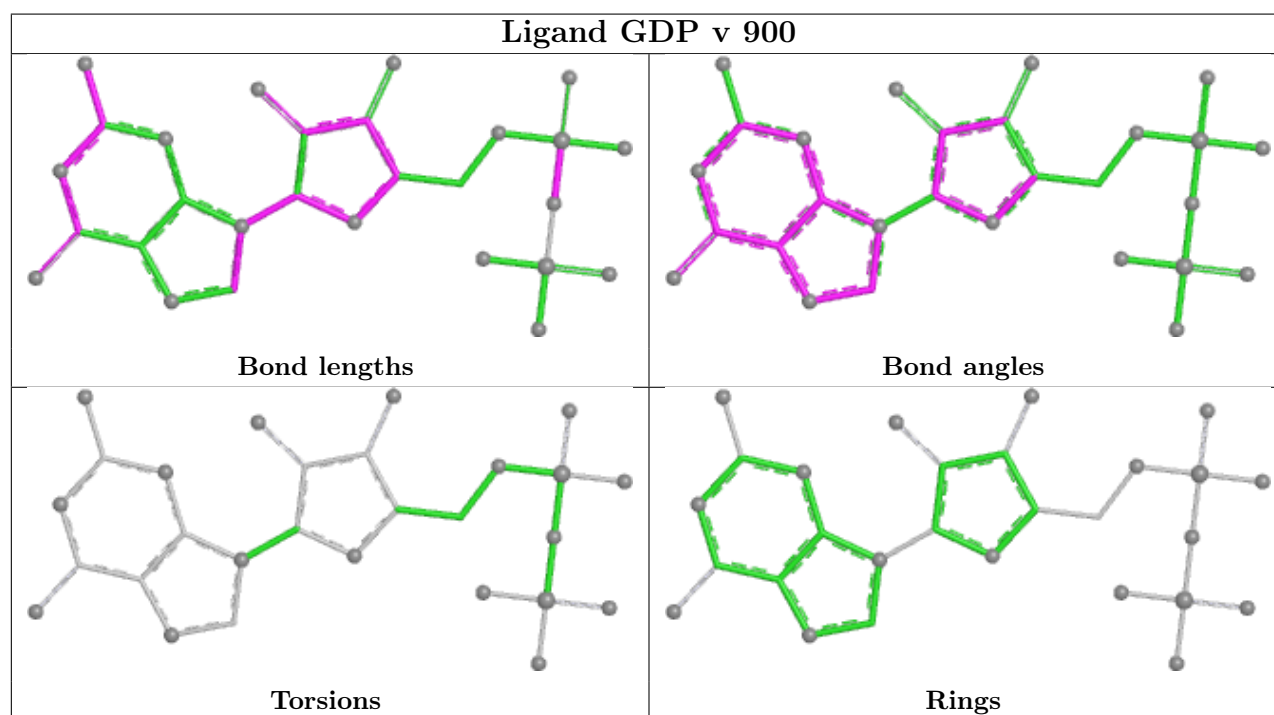
There are no torsion outliers.

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 [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
79	18	12

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	20.22
1	18	697:G	O3'	729:C	P	19.25
1	18	1417:C	O3'	1423:C	P	17.97
1	18	321:C	O3'	329:G	P	16.66
1	18	1759:G	O3'	1773:C	P	16.39
1	18	834:C	O3'	841:G	P	16.28
1	18	130:G	O3'	141:A	P	15.80
1	18	547:G	O3'	551:U	P	13.14
1	18	745:C	O3'	749:U	P	8.25
1	18	736:C	O3'	743:U	P	7.88
1	18	225:G	O3'	287:U	P	4.28
1	18	1432:U	O3'	1438:A	P	3.64

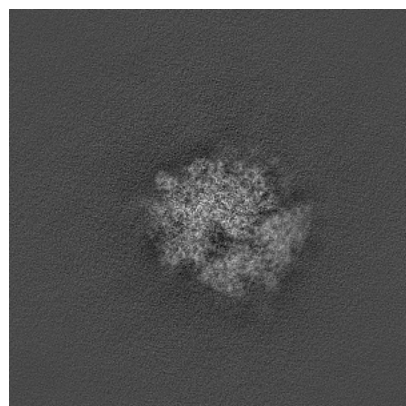
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-75689. These allow visual inspection of the internal detail of the map and identification of artifacts.

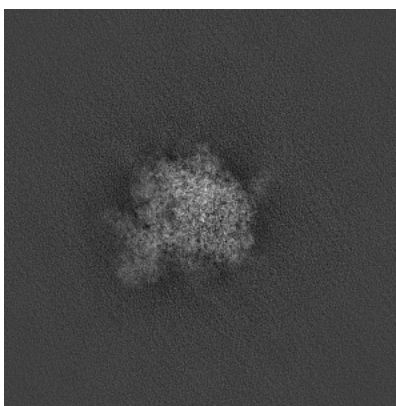
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

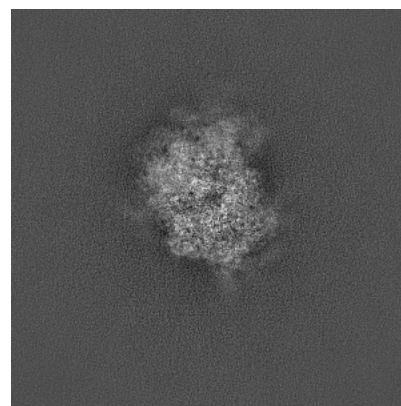
6.1.1 Primary map



X

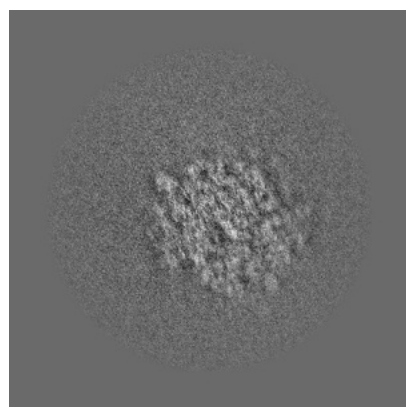


Y

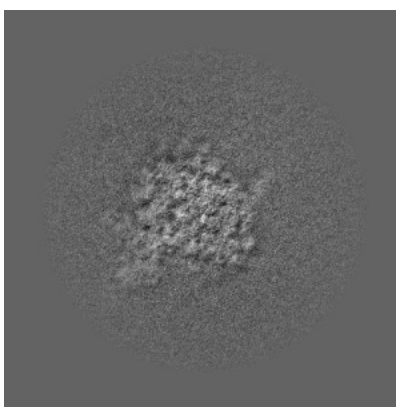


Z

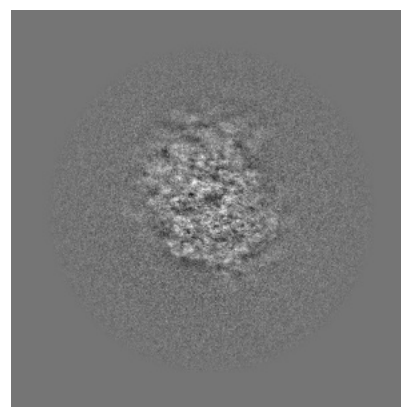
6.1.2 Raw map



X



Y

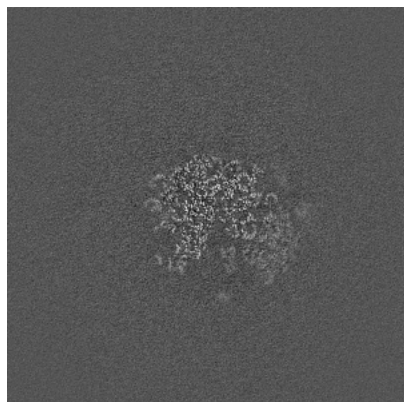


Z

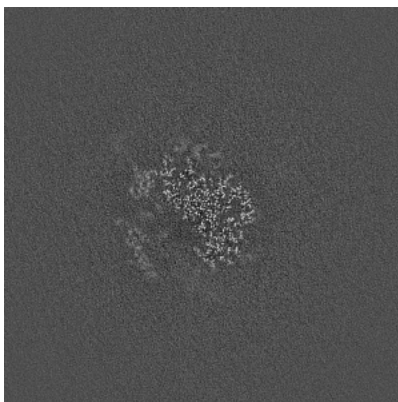
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

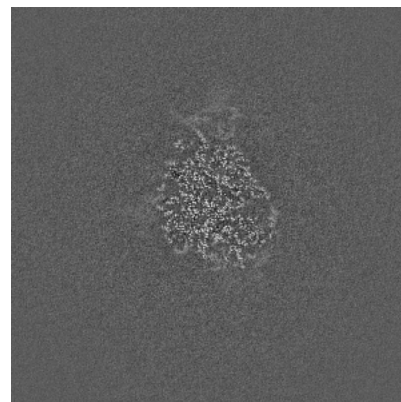
6.2.1 Primary map



X Index: 400

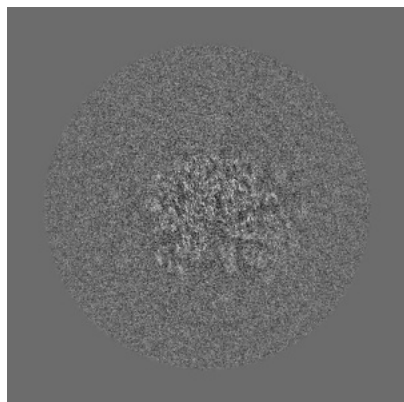


Y Index: 400

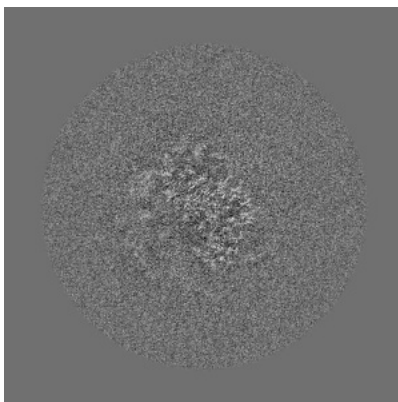


Z Index: 400

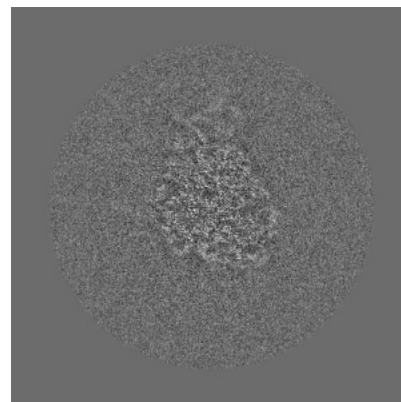
6.2.2 Raw map



X Index: 400



Y Index: 400

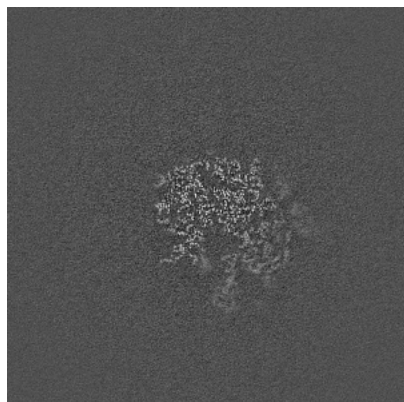


Z Index: 400

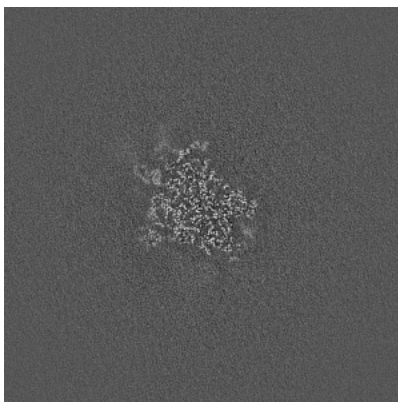
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

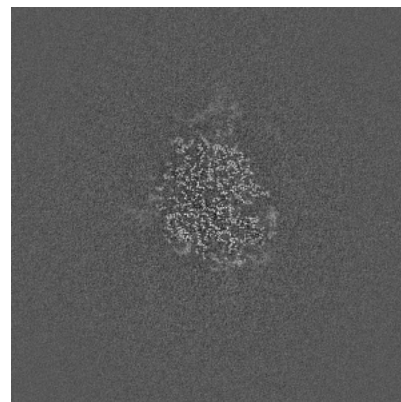
6.3.1 Primary map



X Index: 385

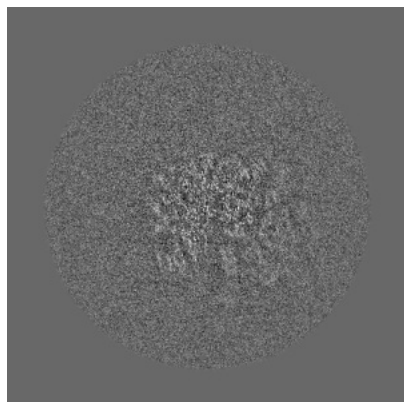


Y Index: 376

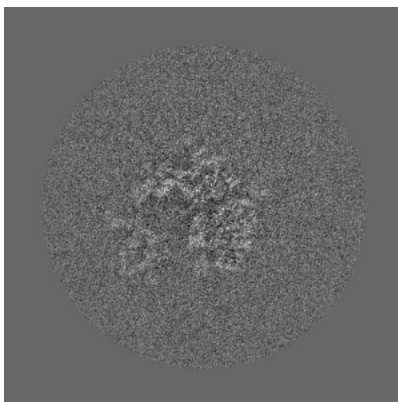


Z Index: 403

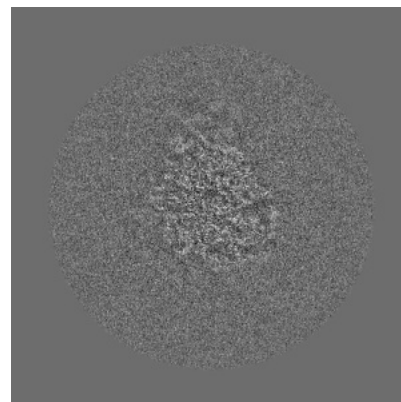
6.3.2 Raw map



X Index: 396



Y Index: 420

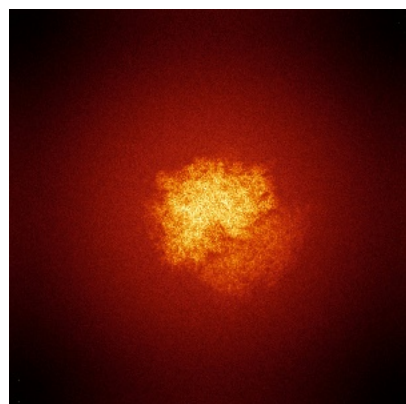


Z Index: 402

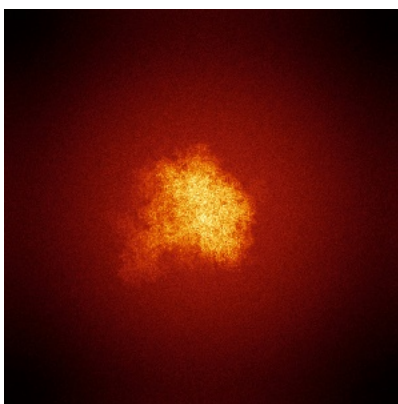
The images above show the largest variance slices of the map in three orthogonal directions.

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

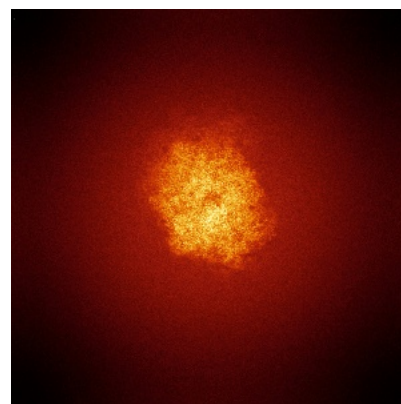
6.4.1 Primary map



X

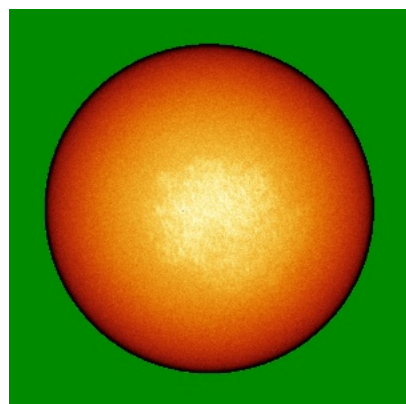


Y

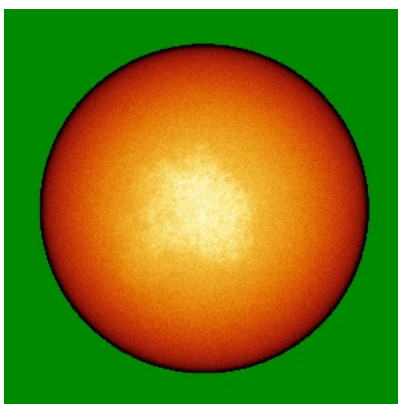


Z

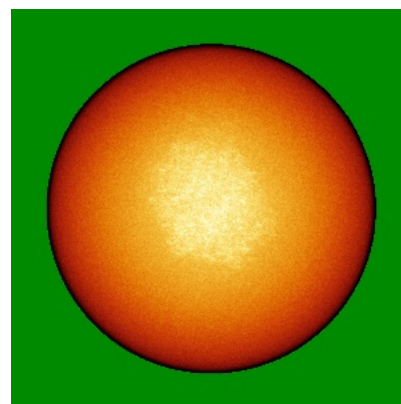
6.4.2 Raw map



X



Y

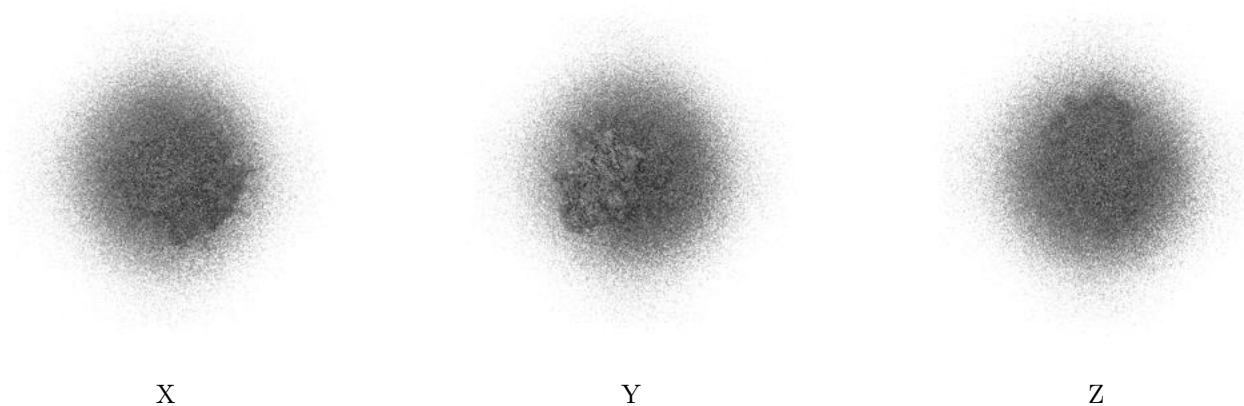


Z

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.

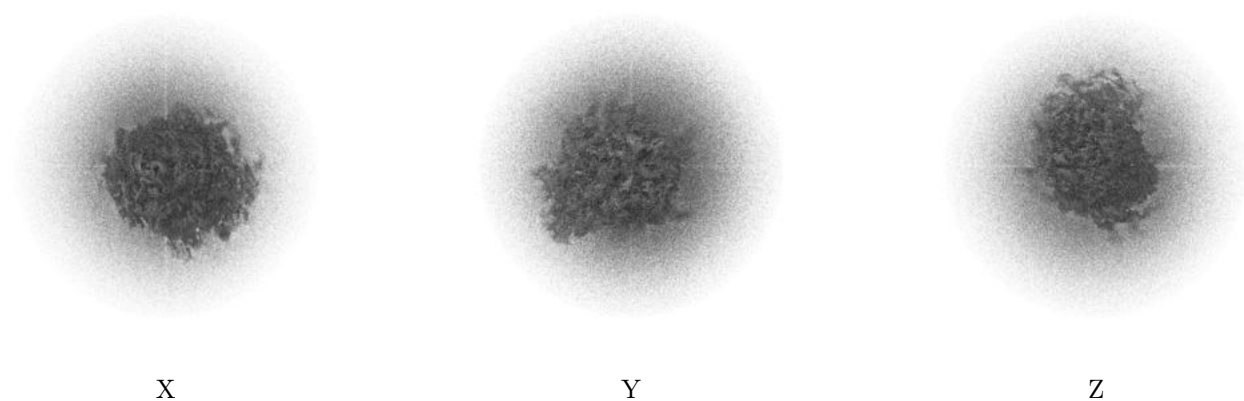
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 3.3. 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.

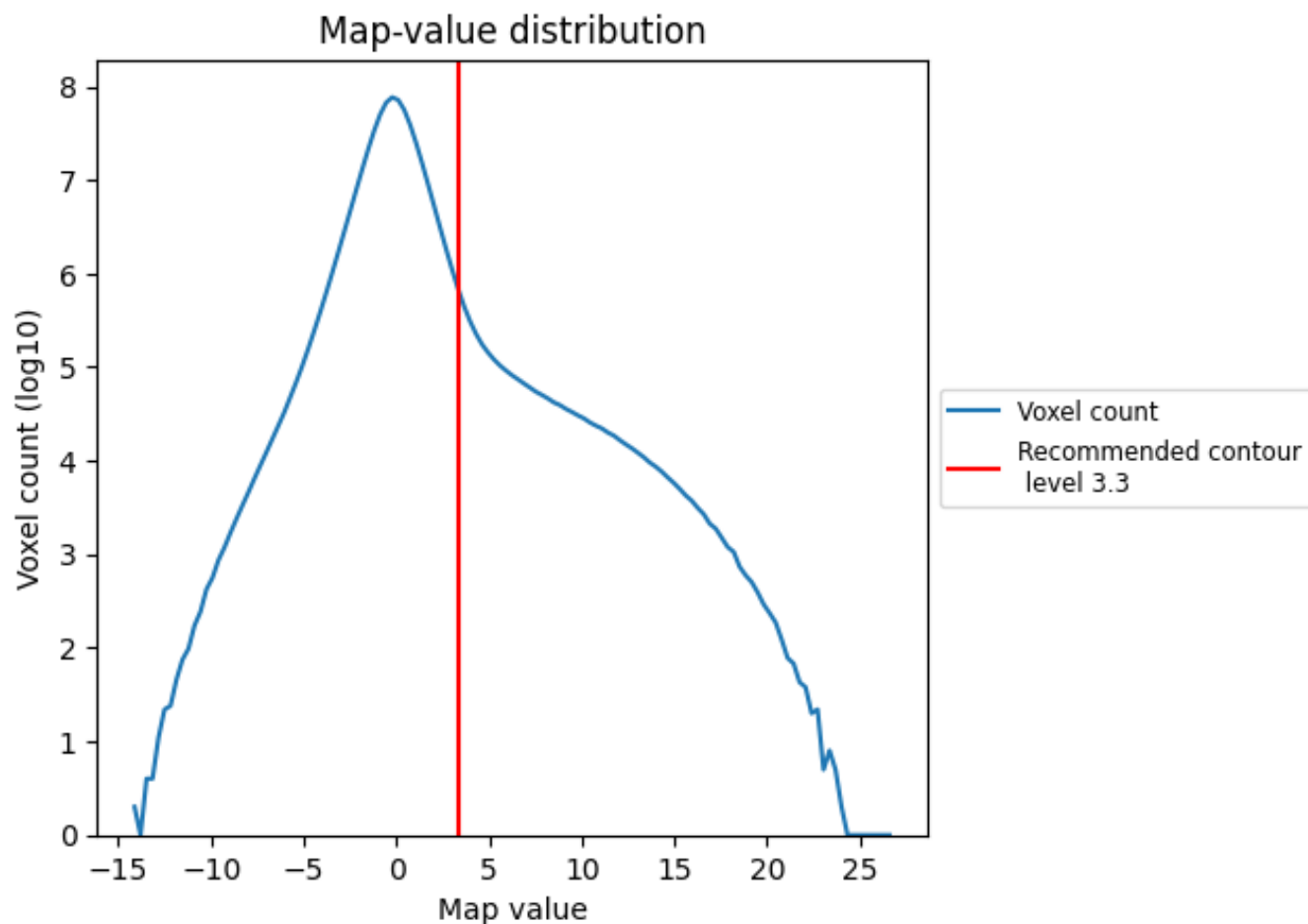
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

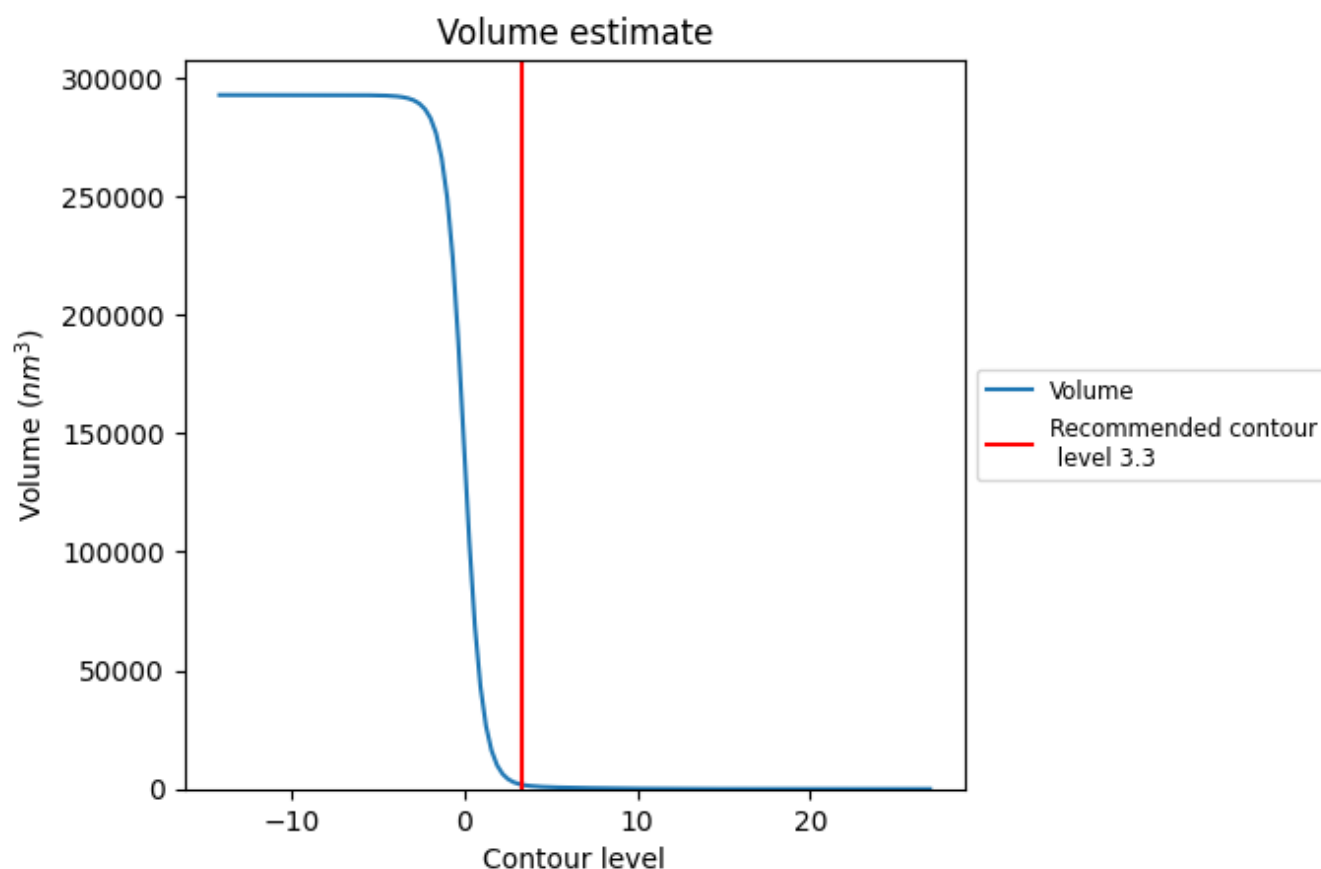
This section contains the results of statistical analysis of the map.

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.

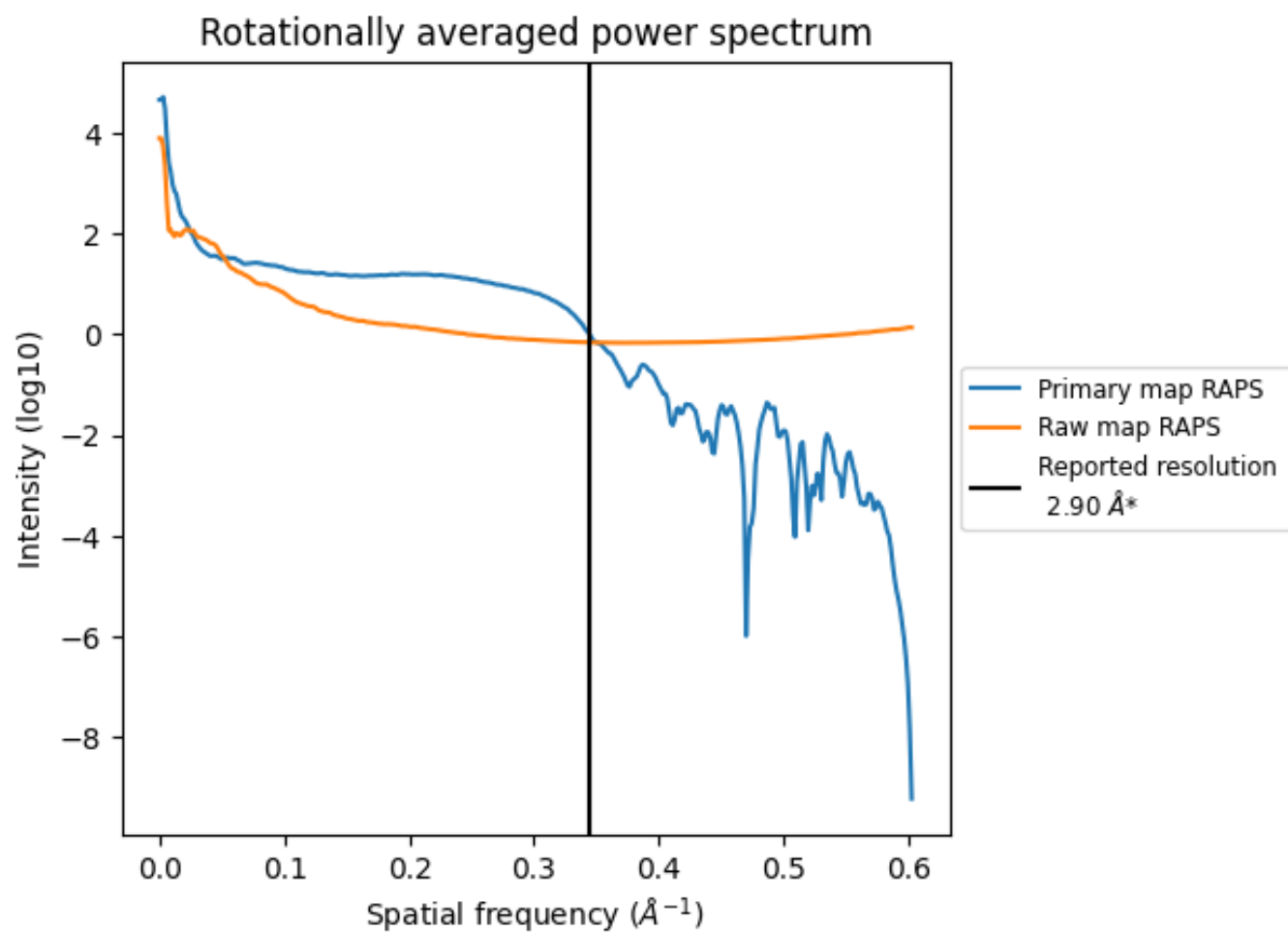
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1898 nm^3 ; this corresponds to an approximate mass of 1715 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 ⓘ

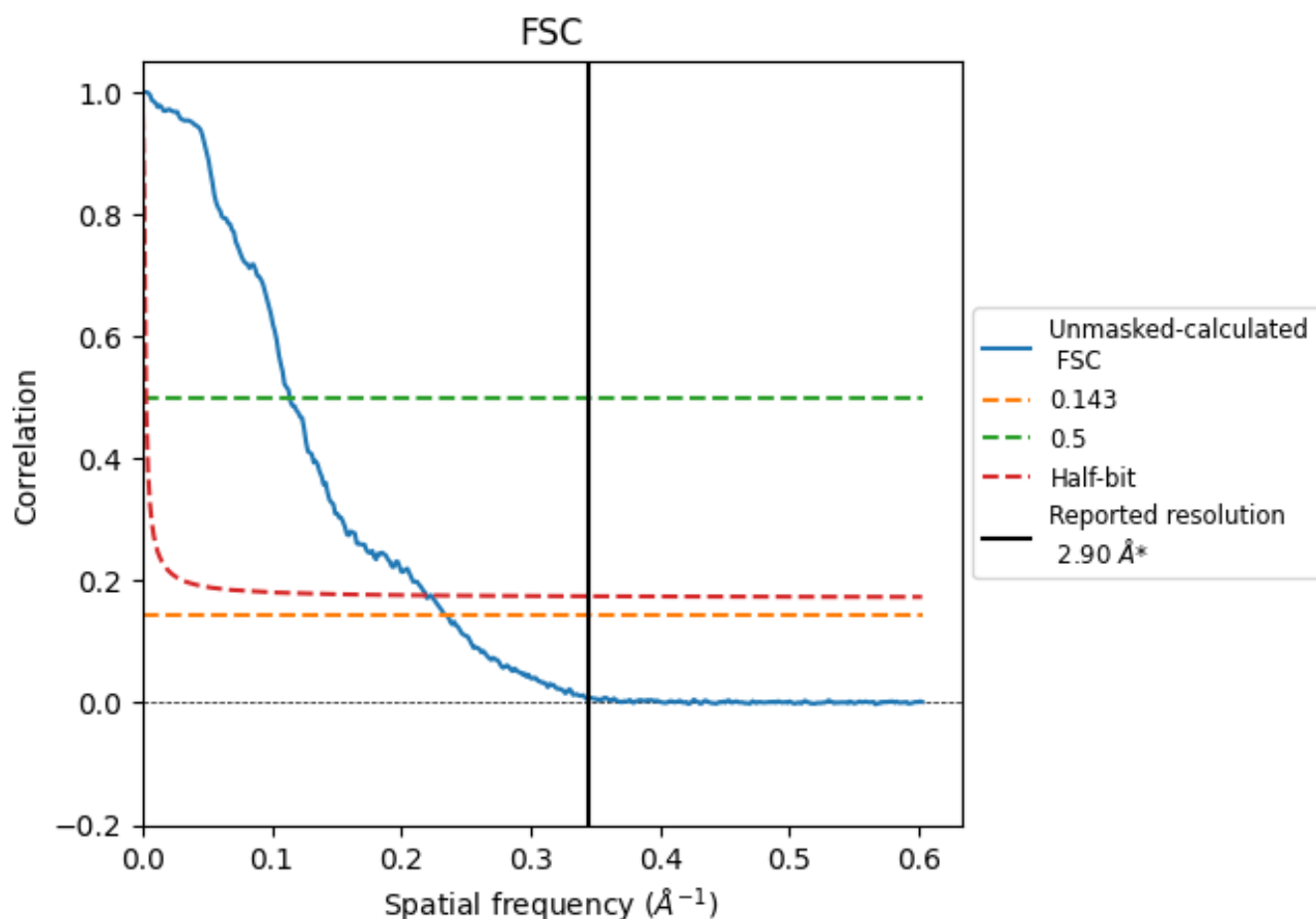


*Reported resolution corresponds to spatial frequency of 0.345 Å⁻¹

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](#)

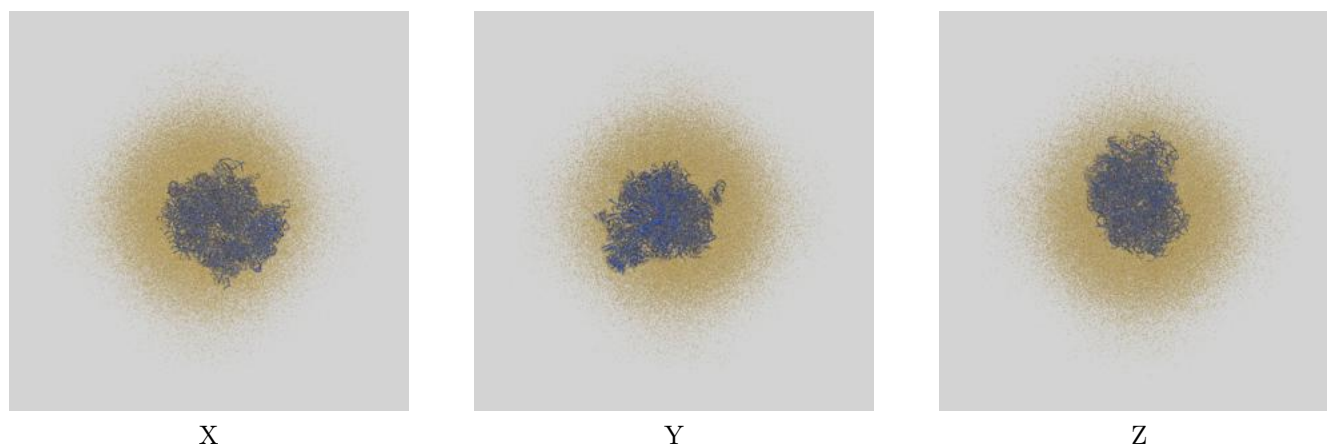
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.25	8.78	4.56

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

9 Map-model fit [i](#)

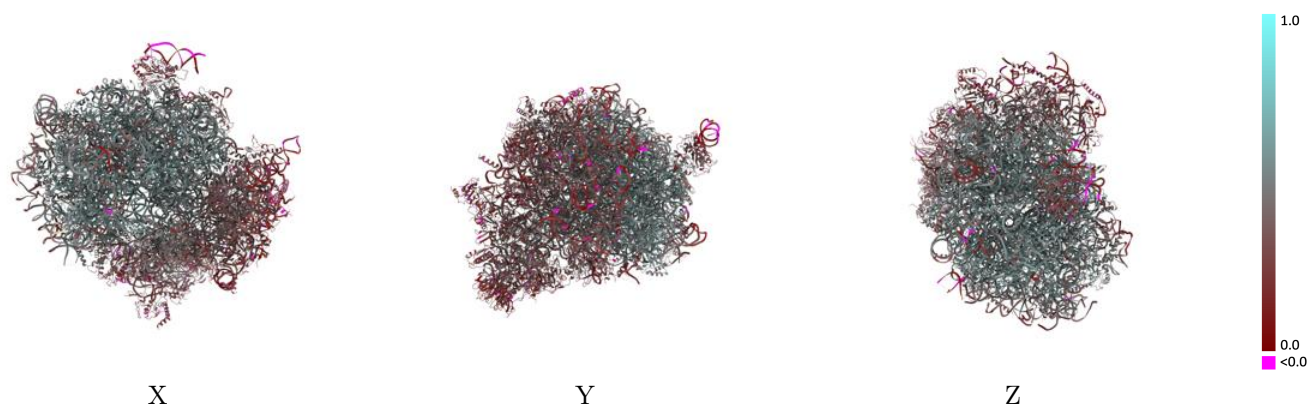
This section contains information regarding the fit between EMDB map EMD-75689 and PDB model 11HG. Per-residue inclusion information can be found in section [3](#) on page [21](#).

9.1 Map-model overlay [i](#)



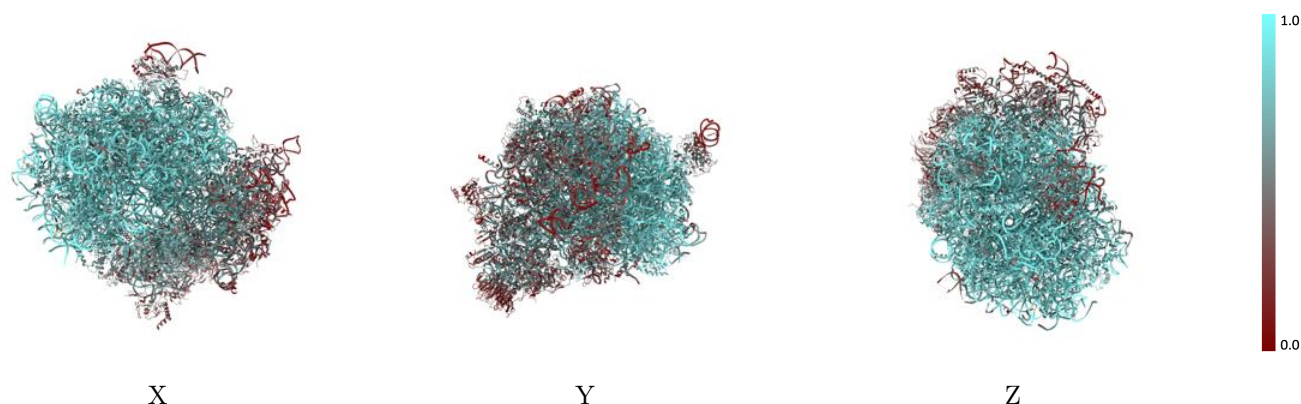
The images above show the 3D surface view of the map at the recommended contour level 3.3 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



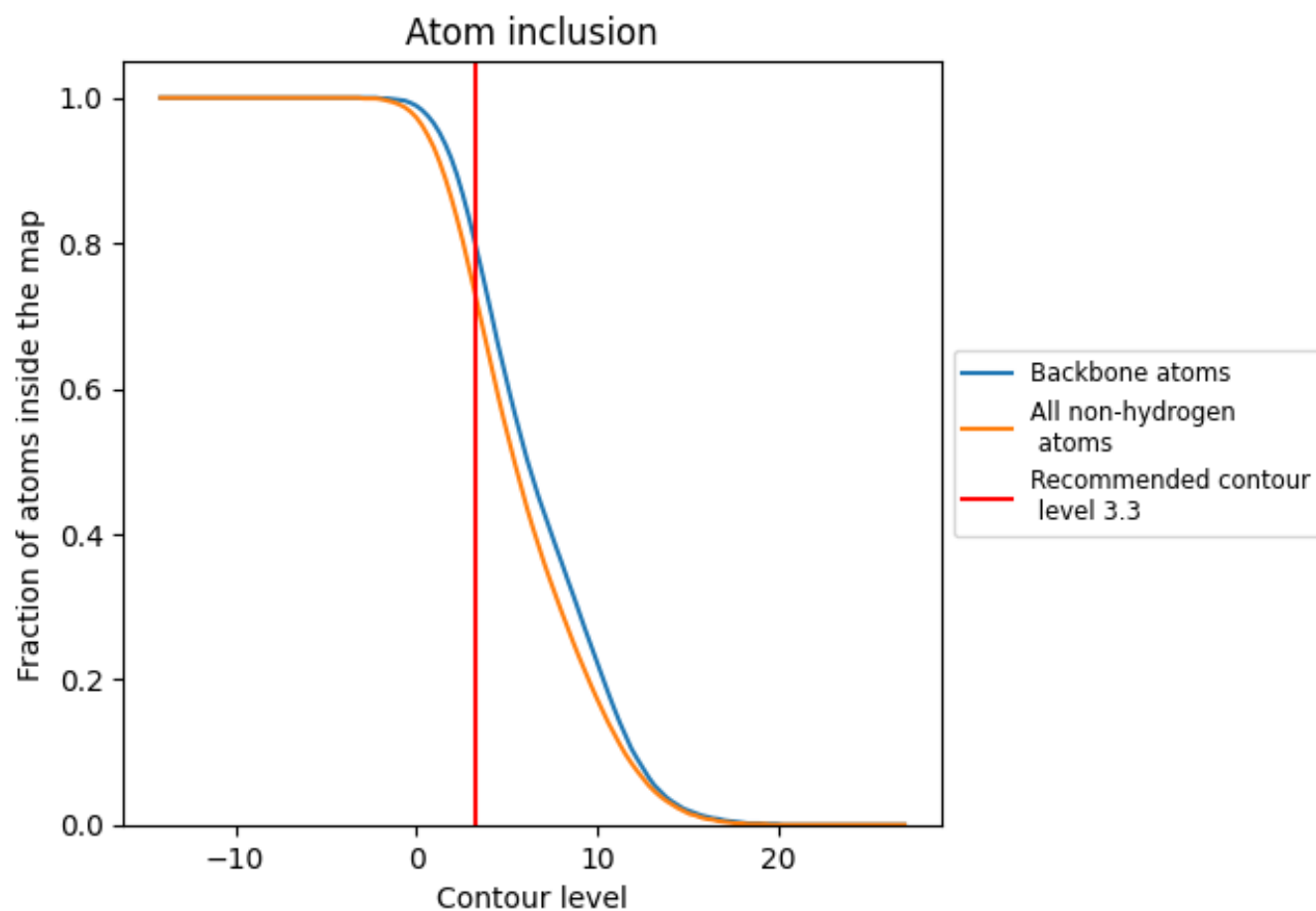
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (3.3).

9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 72% 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 (3.3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7230	 0.4420
10	 0.8140	 0.5240
11	 0.7250	 0.4540
13	 0.8000	 0.5120
14	 0.8250	 0.5140
15	 0.8640	 0.5650
17	 0.8380	 0.5420
18	 0.6610	 0.3730
19	 0.7440	 0.4780
20	 0.8520	 0.5420
21	 0.8160	 0.5180
22	 0.6880	 0.4230
23	 0.7780	 0.5200
26	 0.8120	 0.5180
27	 0.8040	 0.5130
28	 0.8810	 0.5040
29	 0.7470	 0.4800
30	 0.7750	 0.5000
31	 0.7880	 0.4920
32	 0.8610	 0.5550
34	 0.7950	 0.5160
35	 0.7850	 0.5110
36	 0.8140	 0.5100
37	 0.8650	 0.5570
38	 0.7200	 0.4570
39	 0.8240	 0.5260
40	 0.7850	 0.5060
41	 0.7250	 0.4510
42	 0.7880	 0.5150
58	 0.8940	 0.5170
6	 0.9330	 0.5430
A	 0.5330	 0.3280
AA	 0.2430	 0.2290
AS	 0.4930	 0.3670
BB	 0.4030	 0.3340



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Chain	Atom inclusion	Q-score
CC	 0.4730	 0.3120
CE	 0.3390	 0.2980
DD	 0.4610	 0.3730
EE	 0.2460	 0.2150
ES	 0.1350	 0.0620
F	 0.4420	 0.3130
FF	 0.4890	 0.3710
GG	 0.5780	 0.3760
II	 0.4330	 0.3240
L3	 0.8210	 0.5340
L4	 0.8560	 0.5420
L5	 0.8010	 0.4940
L6	 0.8140	 0.5000
L7	 0.8310	 0.5440
L8	 0.8390	 0.5540
L9	 0.7890	 0.5050
LA	 0.3300	 0.2710
LL	 0.4910	 0.3030
MM	 0.4490	 0.3120
OO	 0.4160	 0.3240
PP	 0.3760	 0.2930
Q	 0.8580	 0.5540
RR	 0.5270	 0.3710
RS	 0.3830	 0.3070
S2	 0.4600	 0.3460
S3	 0.4530	 0.3200
S4	 0.3340	 0.2970
S5	 0.4600	 0.3230
S6	 0.3410	 0.2710
S7	 0.3210	 0.2960
S8	 0.4190	 0.3440
S9	 0.3690	 0.3000
SS	 0.3050	 0.2670
TT	 0.3840	 0.2960
UU	 0.5430	 0.3760
VV	 0.3870	 0.3380
W	 0.5580	 0.3860
WW	 0.4210	 0.3170
WX	 0.4450	 0.3590
XX	 0.5740	 0.3960
YY	 0.3500	 0.2870
ZZ	 0.2830	 0.2210

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Chain	Atom inclusion	Q-score
aa	 0.7630	 0.4810
bb	 0.8520	 0.5370
cc	 0.7960	 0.5150
dd	 0.8530	 0.5580
ee	 0.8400	 0.5460
ff	 0.7950	 0.5120
gg	 0.8340	 0.5330
s	 0.5250	 0.3450
t	 0.3210	 0.2140
v	 0.5600	 0.3700