Full wwPDB EM Validation Report ⓘ

Nov 2, 2026 – 03:37 PM JST

PDB ID	:	9XJ6 / pdb_00009xj6
EMDB ID	:	EMD-66929
Title	:	Portimine A-bound human translating ribosome - P/P-E/E State
Authors	:	Wang, Y.; Zhang, Y.; Gao, N.
Deposited on	:	2025-11-04
Resolution	:	2.78 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

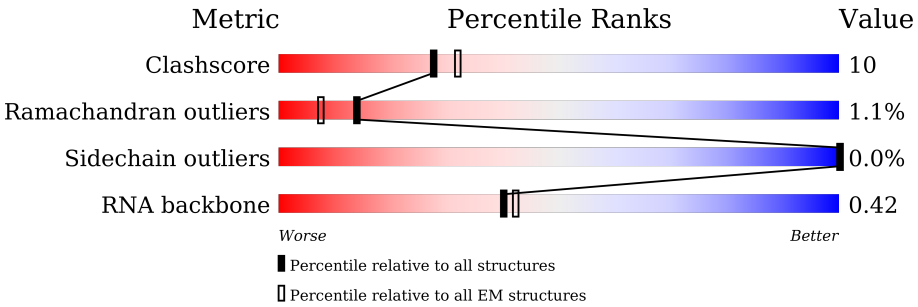
EMDB validation analysis	:	0.0.1.dev133
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4-5-2 with Phenix2.2
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using 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)	:	2.51

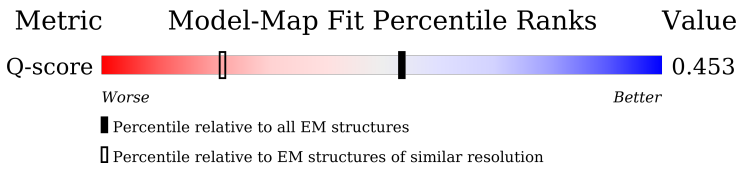
1 Overall quality at a glance

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

The reported resolution of this entry is 2.78 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	10754 (2.28 - 3.28)

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 <=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	L5	5070	19% 39% 27% 8% 26%
2	L7	121	75% 21%
3	L8	157	11% 61% 30% 8%

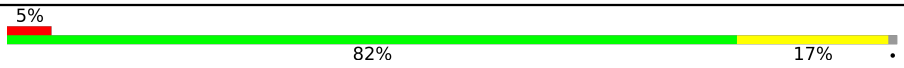
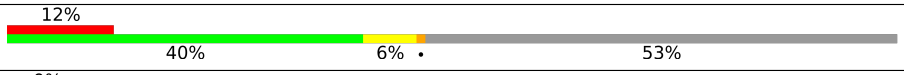
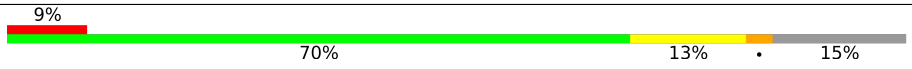
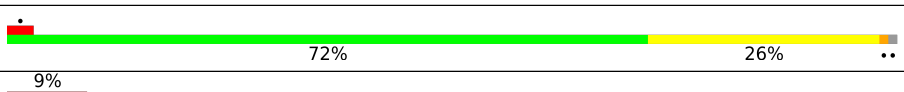
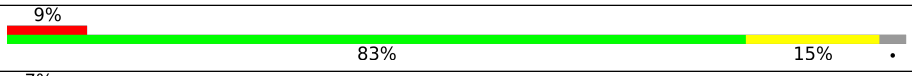
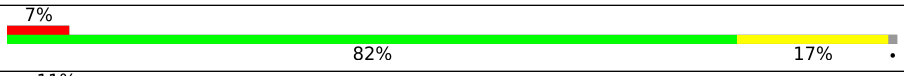
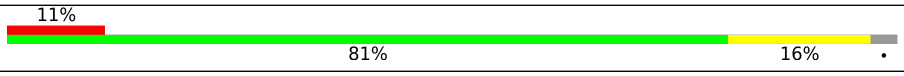
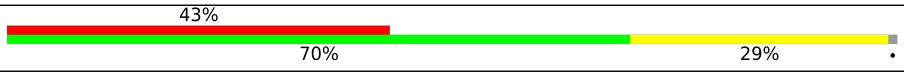
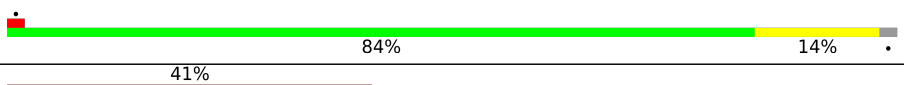
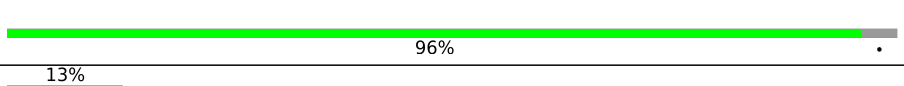
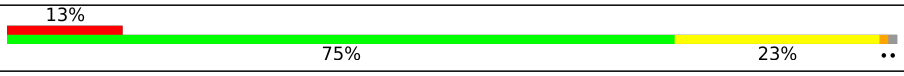
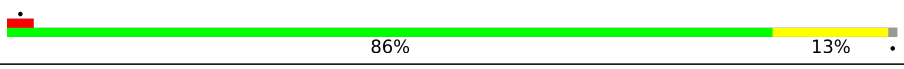
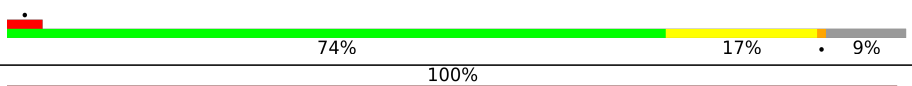
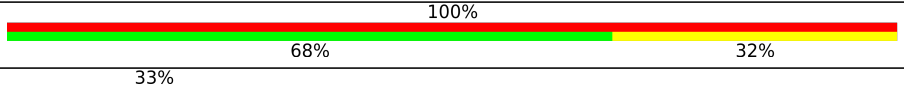
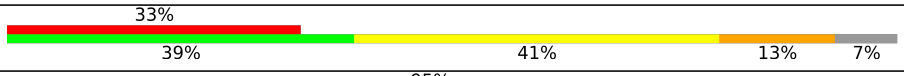
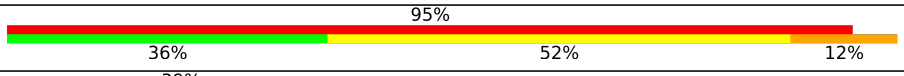
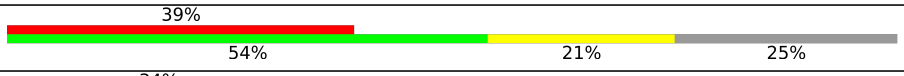
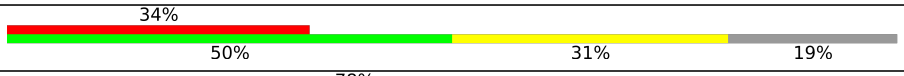
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Mol	Chain	Length	Quality of chain
4	LA	257	77% 19%
5	LB	403	5% 82% 17%
6	LC	427	5% 67% 19% 14%
7	LD	297	14% 75% 23%
8	LE	288	20% 61% 21% 16%
9	LF	248	6% 71% 19% 9%
10	LG	266	17% 75% 15% 9%
11	LH	192	14% 81% 18%
12	LI	214	18% 75% 24%
13	LJ	178	38% 72% 26%
14	LL	211	12% 80% 18%
15	LM	215	6% 49% 15% 35%
16	LN	204	82% 18%
17	LO	203	86% 13%
18	LP	184	72% 11% 17%
19	LQ	188	85% 14%
20	LR	196	16% 74% 21% 5%
21	LS	176	78% 21%
22	LT	160	12% 84% 16%
23	LU	128	42% 59% 20% 21%
24	LV	140	76% 17% 6%
25	LW	157	41% 56% 20% 21%
26	LX	156	5% 60% 16% 23%
27	LY	145	6% 74% 18% 8%
28	LZ	136	7% 77% 22%

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Mol	Chain	Length	Quality of chain
29	La	148	
30	Lb	159	
31	Lc	115	
32	Ld	125	
33	Le	135	
34	Lf	110	
35	Lg	117	
36	Lh	123	
37	Li	105	
38	Lj	97	
39	Lk	70	
40	Ll	51	
41	Lm	128	
42	Ln	25	
43	Lo	106	
44	Lp	92	
45	Lr	137	
46	Lz	217	
47	S2	1869	
48	S6	75	
49	SA	295	
50	SB	264	
51	SD	243	
52	SE	263	
53	SF	204	

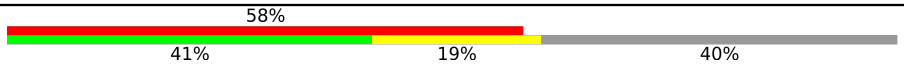
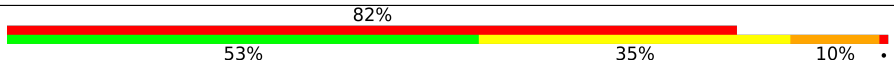
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Mol	Chain	Length	Quality of chain
54	SH	193	77% 64% 33%
55	SI	208	55% 68% 30%
56	SK	165	58% 36% 23% 41%
57	SL	158	42% 71% 26%
58	SP	145	66% 35% 30% 33%
59	SQ	146	86% 67% 33%
60	SR	135	81% 64% 33%
61	SS	152	89% 57% 41%
62	ST	145	89% 75% 23%
63	SU	119	68% 56% 30% 13%
64	SV	83	53% 83% 16%
65	SX	143	27% 69% 29%
66	Sa	115	22% 70% 23% 7%
67	Sc	69	77% 62% 30% 7%
68	Sd	56	55% 57% 38% 5%
69	Sf	156	46% 32% 12% 54%
70	Sg	317	99% 61% 36%
71	SC	293	23% 54% 22% 24%
72	SG	249	84% 62% 33% 5%
73	SJ	194	71% 66% 29% 5%
74	SM	132	92% 67% 25% 8%
75	SN	151	22% 70% 28%
76	SO	151	22% 54% 38% 7%
77	SW	130	19% 72% 28%
78	SY	133	92% 65% 34%

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Mol	Chain	Length	Quality of chain
79	SZ	125	
80	Sb	84	
81	Se	59	
82	Pt	77	

2 Entry composition (i)

There are 85 unique types of molecules in this entry. The entry contains 220451 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 RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	L5	3776	80184	35672	14597	26140	3775	0	0

- Molecule 2 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	L7	120	2558	1141	456	842	119	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	L8	156	3314	1480	585	1094	155	0	0

- Molecule 4 is a protein called Large ribosomal subunit protein uL2.

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

- Molecule 5 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	LB	402	3238	2060	608	556	14	0	0

- Molecule 6 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	LC	367	2919	1835	582	488	14	0	0

- Molecule 7 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	LD	293	Total	C	N	O	S	0	0
			2382	1507	434	427	14		

- Molecule 8 is a protein called Large ribosomal subunit protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LE	242	Total	C	N	O	S	0	0
			1958	1257	372	325	4		

- Molecule 9 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LF	225	Total	C	N	O	S	0	0
			1870	1202	358	301	9		

- Molecule 10 is a protein called Large ribosomal subunit protein eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LG	241	Total	C	N	O	S	0	0
			1927	1228	371	324	4		

- Molecule 11 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LH	190	Total	C	N	O	S	0	0
			1518	956	284	272	6		

- Molecule 12 is a protein called Ribosomal protein uL16-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LI	213	Total	C	N	O	S	0	0
			1711	1082	329	285	15		

- Molecule 13 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LJ	176	Total	C	N	O	S	0	0
			1410	888	263	253	6		

- Molecule 14 is a protein called Large ribosomal subunit protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LL	210	Total	C	N	O	S	0	0
			1701	1064	352	281	4		

- Molecule 15 is a protein called Large ribosomal subunit protein eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LM	139	Total	C	N	O	S	0	0
			1138	730	218	183	7		

- Molecule 16 is a protein called Large ribosomal subunit protein eL15.

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

- Molecule 17 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LO	201	Total	C	N	O	S	0	0
			1650	1063	321	261	5		

- Molecule 18 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LP	153	Total	C	N	O	S	0	0
			1242	776	241	216	9		

- Molecule 19 is a protein called Large ribosomal subunit protein eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LQ	187	Total	C	N	O	S	0	0
			1513	944	314	250	5		

- Molecule 20 is a protein called Large ribosomal subunit protein eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LR	187	Total	C	N	O	S	0	0
			1566	971	336	250	9		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LS	175	Total	C	N	O	S	0	0
			1453	925	283	235	10		

- Molecule 22 is a protein called Large ribosomal subunit protein eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LT	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	LU	101	Total	C	N	O	S	0	0
			825	529	144	150	2		

- Molecule 24 is a protein called Large ribosomal subunit protein uL14.

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

- Molecule 25 is a protein called Large ribosomal subunit protein eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LW	124	Total	C	N	O	S	0	0
			1015	634	207	170	4		

- Molecule 26 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LX	120	Total	C	N	O	S	0	0
			985	630	185	169	1		

- Molecule 27 is a protein called Large ribosomal subunit protein uL24.

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

- Molecule 28 is a protein called Large ribosomal subunit protein eL27.

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

- Molecule 29 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	La	147	Total	C	N	O	S	0	0
			1162	736	237	186	3		

- Molecule 30 is a protein called Large ribosomal subunit protein eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Lb	75	Total	C	N	O	S	0	0
			610	378	130	99	3		

- Molecule 31 is a protein called Large ribosomal subunit protein eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Lc	98	Total	C	N	O	S	0	0
			764	485	135	138	6		

- Molecule 32 is a protein called Large ribosomal subunit protein eL31.

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

- Molecule 33 is a protein called Large ribosomal subunit protein eL32.

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

- Molecule 34 is a protein called Large ribosomal subunit protein eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Lf	109	Total	C	N	O	S	0	0
			876	555	174	144	3		

- Molecule 35 is a protein called Large ribosomal subunit protein eL34.

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

- Molecule 36 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Lh	122	Total	C	N	O	S	0	0
			1015	641	205	168	1		

- Molecule 37 is a protein called Large ribosomal subunit protein eL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Li	102	Total	C	N	O	S	0	0
			832	521	177	129	5		

- Molecule 38 is a protein called Large ribosomal subunit protein eL37.

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

- Molecule 39 is a protein called Large ribosomal subunit protein eL38.

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

- Molecule 40 is a protein called Large ribosomal subunit protein eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Ll	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 41 is a protein called Ubiquitin-ribosomal protein eL40 fusion protein.

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

- Molecule 42 is a protein called Small ribosomal subunit protein eS32.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Ln	24	Total	C	N	O	S	0	0
			230	139	62	26	3		

- Molecule 43 is a protein called Large ribosomal subunit protein eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Lo	105	Total	C	N	O	S	0	0
			862	542	175	139	6		

- Molecule 44 is a protein called Large ribosomal subunit protein eL43.

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

- Molecule 45 is a protein called Large ribosomal subunit protein eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Lr	125	Total	C	N	O	S	0	0
			1002	622	207	168	5		

- Molecule 46 is a protein called Large ribosomal subunit protein uL1.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Lz	217	Total	C	N	O	S	0	0
			1741	1113	312	307	9		

- Molecule 47 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	S2	1742	Total	C	N	O	P	0	0
			36900	16458	6595	12106	1741		

- Molecule 48 is a RNA chain called HUMAN INITIATOR MET-TRNA-I.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	S6	75	Total	C	N	O	P	0	0
			1604	717	298	515	74		

- Molecule 49 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	SA	222	Total	C	N	O	S	0	0
			1747	1109	306	324	8		

- Molecule 50 is a protein called Small ribosomal subunit protein eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	SB	214	Total	C	N	O	S	0	0
			1738	1103	310	311	14		

- Molecule 51 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	SD	227	Total	C	N	O	S	0	0
			1765	1125	317	315	8		

- Molecule 52 is a protein called Small ribosomal subunit protein eS4, X isoform.

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

- Molecule 53 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	SF	191	Total	C	N	O	S	0	0
			1509	943	286	273	7		

- Molecule 54 is a protein called Small ribosomal subunit protein eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SH	189	Total	C	N	O	S	0	0
			1521	969	280	271	1		

- Molecule 55 is a protein called Small ribosomal subunit protein eS8.

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

- Molecule 56 is a protein called Small ribosomal subunit protein eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SK	98	Total	C	N	O	S	0	0
			827	539	148	134	6		

- Molecule 57 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SL	153	Total	C	N	O	S	0	0
			1247	793	234	214	6		

- Molecule 58 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SP	97	Total	C	N	O	S	0	0
			804	505	155	138	6		

- Molecule 59 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SQ	146	Total	C	N	O	S	0	0
			1158	736	218	200	4		

- Molecule 60 is a protein called Small ribosomal subunit protein eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SR	132	Total	C	N	O	S	0	0
			1072	673	199	195	5		

- Molecule 61 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SS	150	Total	C	N	O	S	0	0
			1235	776	250	208	1		

- Molecule 62 is a protein called Small ribosomal subunit protein eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	ST	143	Total	C	N	O	S	0	0
			1112	697	214	198	3		

- Molecule 63 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	SU	104	Total	C	N	O	S	0	0
			821	514	155	148	4		

- Molecule 64 is a protein called Small ribosomal subunit protein eS21.

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

- Molecule 65 is a protein called Small ribosomal subunit protein uS12.

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

- Molecule 66 is a protein called Small ribosomal subunit protein eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Sa	107	Total	C	N	O	S	0	0
			847	528	176	138	5		

- Molecule 67 is a protein called Small ribosomal subunit protein eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	Sc	64	Total	C	N	O	S	0	0
			506	308	102	94	2		

- Molecule 68 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	Sd	53	Total	C	N	O	S	0	0
			445	278	90	72	5		

- Molecule 69 is a protein called Ubiquitin.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	Sf	71	Total	C	N	O	S	0	0
			581	367	109	98	7		

- Molecule 70 is a protein called Small ribosomal subunit protein RACK1.

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

- Molecule 71 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	SC	222	Total	C	N	O	S	0	0
			1725	1115	298	302	10		

- Molecule 72 is a protein called Small ribosomal subunit protein eS6.

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

- Molecule 73 is a protein called Small ribosomal subunit protein uS4.

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

- Molecule 74 is a protein called Small ribosomal subunit protein eS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	SM	122	Total	C	N	O	S	0	0
			952	596	169	179	8		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SM	52	GLN	LEU	conflict	UNP P25398
SM	69	LEU	CYS	conflict	UNP P25398
SM	99	ASN	LYS	conflict	UNP P25398

- Molecule 75 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	SN	150	Total	C	N	O	S	0	0
			1208	773	229	205	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
76	SO	140	Total	C	N	O	S	0	0
			1049	642	204	197	6		

- Molecule 77 is a protein called Small ribosomal subunit protein uS8.

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

- Molecule 78 is a protein called Small ribosomal subunit protein eS24.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	SY	131	Total	C	N	O	S	0	0
			1065	673	209	178	5		

- Molecule 79 is a protein called Small ribosomal subunit protein eS25.

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

- Molecule 80 is a protein called Small ribosomal subunit protein eS27.

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

- Molecule 81 is a protein called Small ribosomal subunit protein eS30.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	Se	58	Total	C	N	O	S	0	0
			459	284	100	74	1		

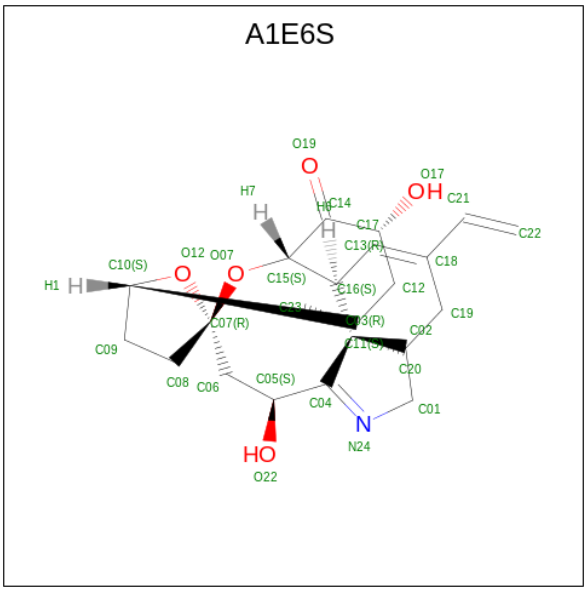
- Molecule 82 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
82	Pt	77	Total	C	N	O	P	S	0	0
			1646	734	298	536	77	1		

- Molecule 83 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	AltConf
83	L5	146	Total Mg 146 146	0
83	L7	7	Total Mg 7 7	0
83	L8	5	Total Mg 5 5	0
83	LA	1	Total Mg 1 1	0
83	LH	1	Total Mg 1 1	0
83	LN	1	Total Mg 1 1	0
83	LP	1	Total Mg 1 1	0
83	LQ	1	Total Mg 1 1	0
83	LV	1	Total Mg 1 1	0
83	Le	1	Total Mg 1 1	0
83	Ll	1	Total Mg 1 1	0
83	S2	66	Total Mg 66 66	0
83	S6	7	Total Mg 7 7	0

- Molecule 84 is (1R,3S,8R,13S,14S,16R,18S,19S)-11-ethenyl-3,16-dihydroxy-18-methyl-22,23-dioxa-5-azapentacyclo[12.7.1.11,19.04,8.08,13]tricosa-4,11-dien-15-one (CCD ID: A1E6S) (formula: $C_{23}H_{31}NO_5$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
84	L5	1	Total	C	N	O	0
			29	23	1	5	

- Molecule 85 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
85	Lg	1	Total	Zn	0
			1	1	
85	Lj	1	Total	Zn	0
			1	1	
85	Lm	1	Total	Zn	0
			1	1	
85	Lo	1	Total	Zn	0
			1	1	
85	Lp	1	Total	Zn	0
			1	1	
85	Sa	1	Total	Zn	0
			1	1	

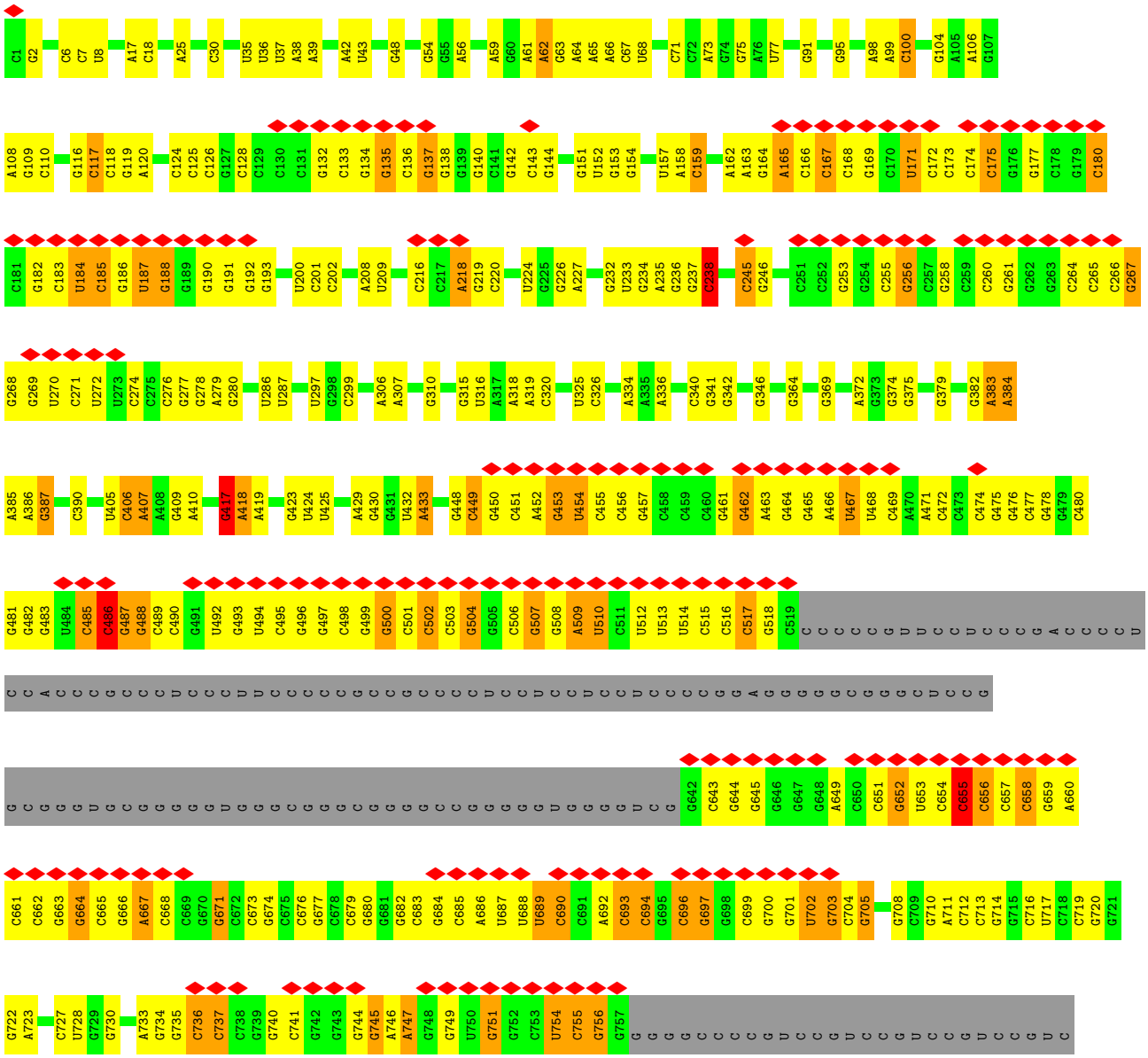
3 Residue-property plots (i)

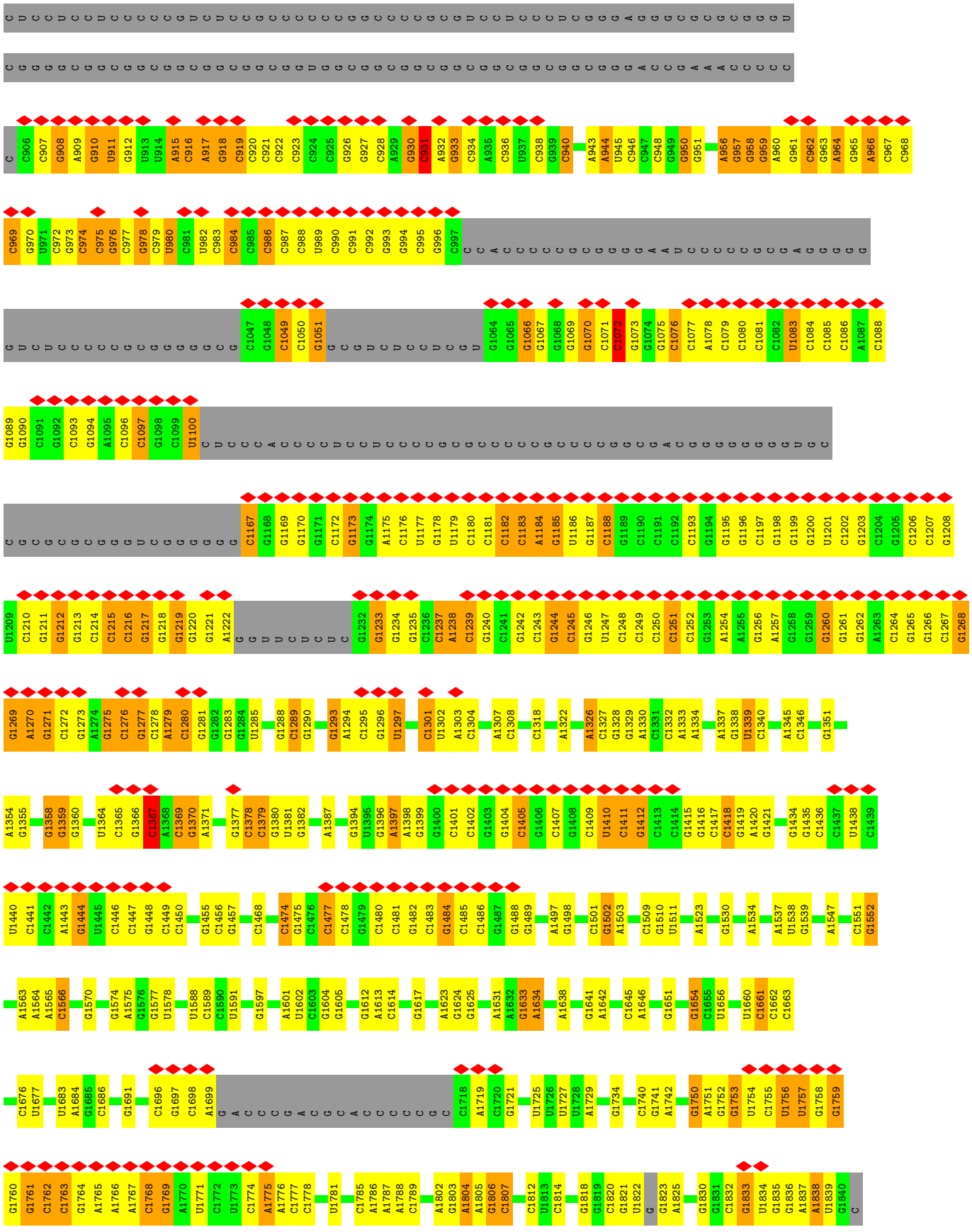
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

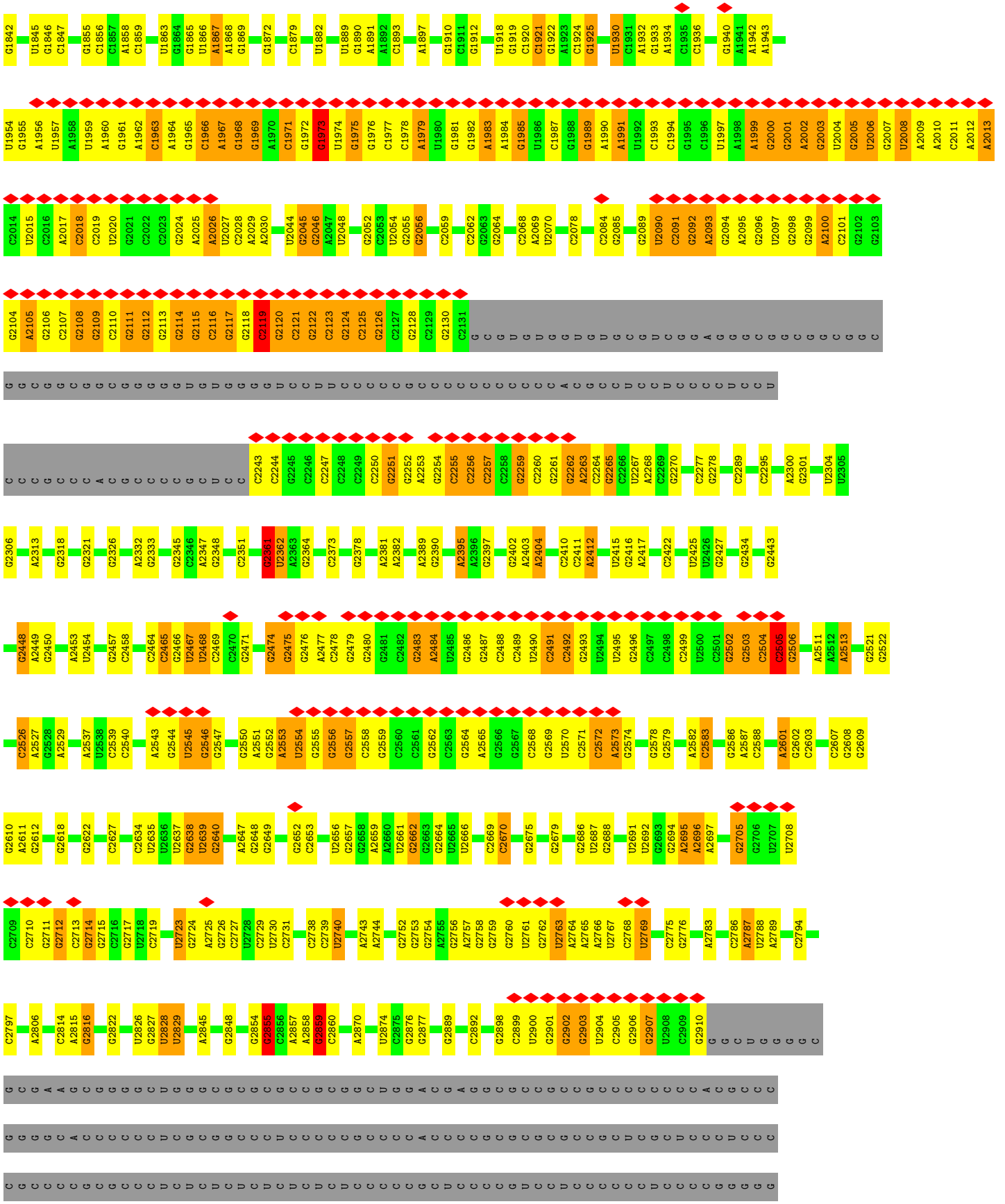
- Molecule 1: 28S ribosomal RNA

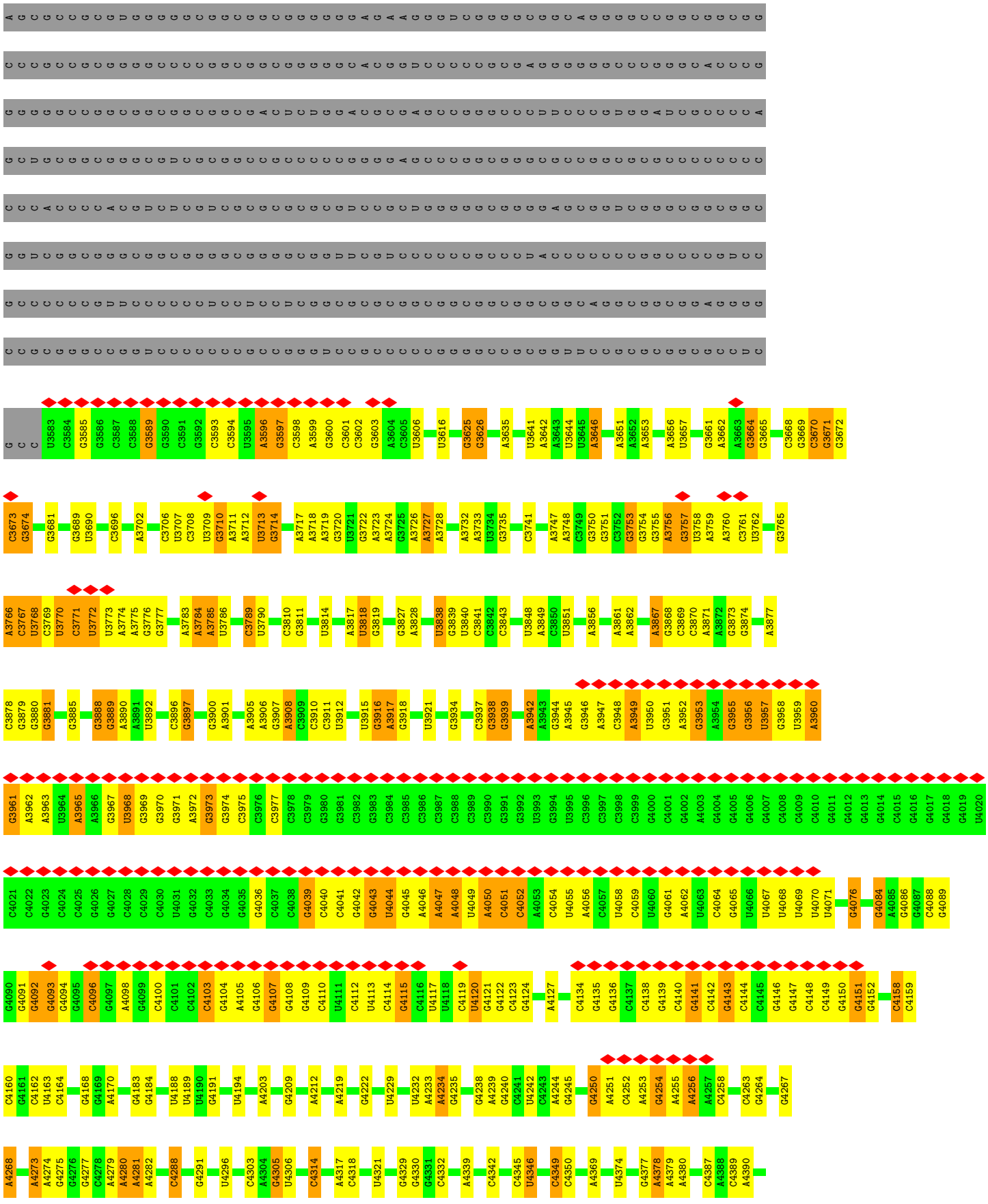
Chain L5:

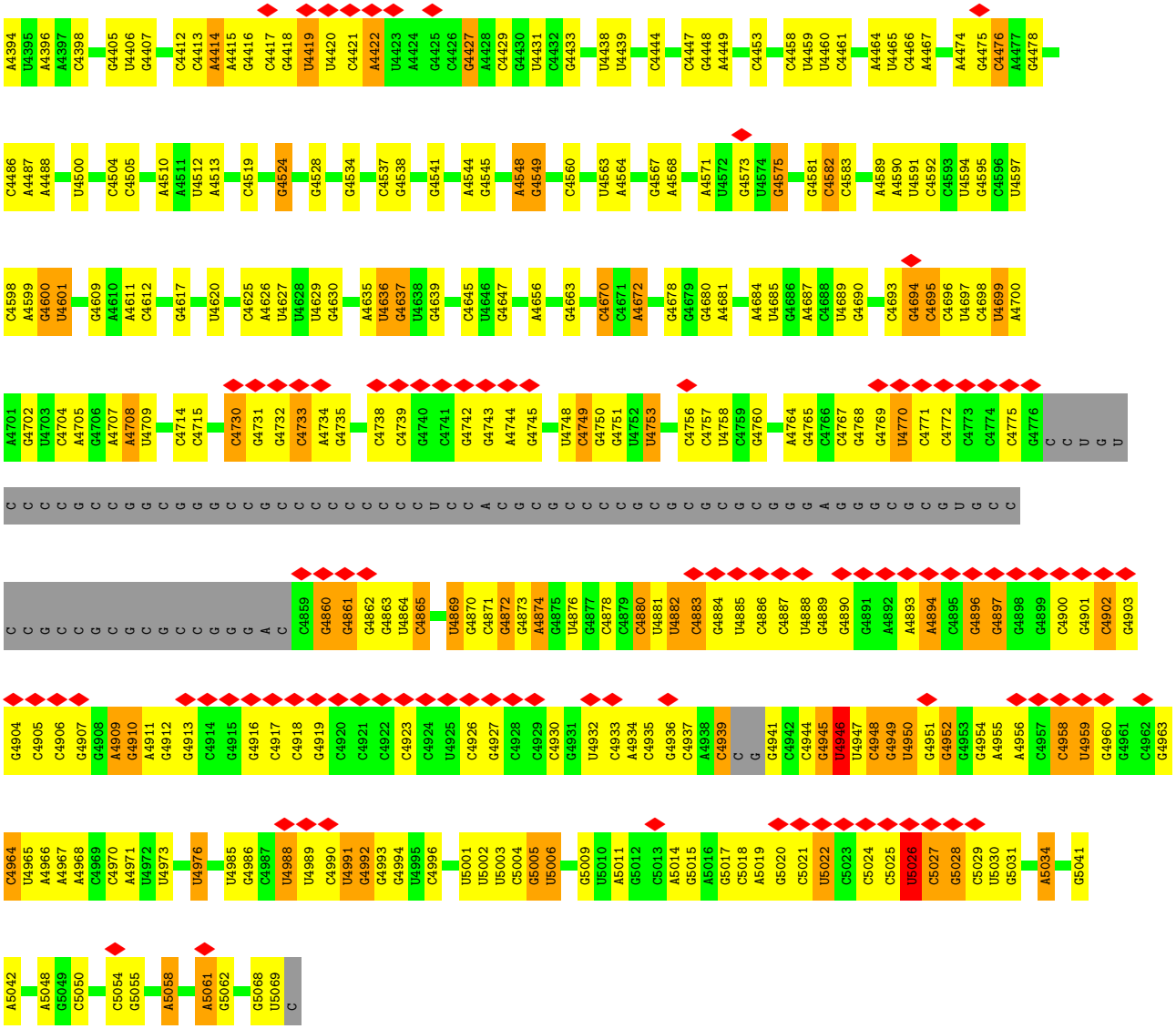








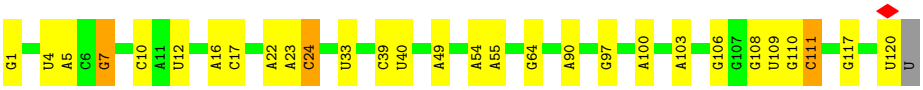




• Molecule 2: 5S ribosomal RNA

Chain L7:

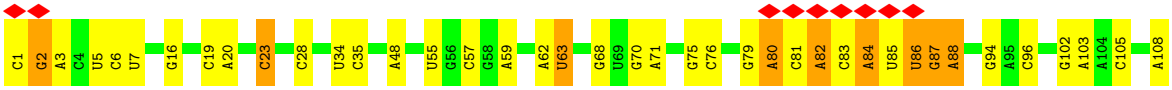


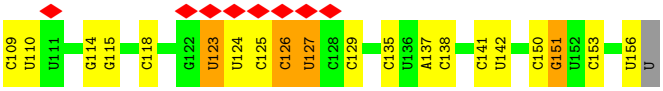


• Molecule 3: 5.8S ribosomal RNA

Chain L8:



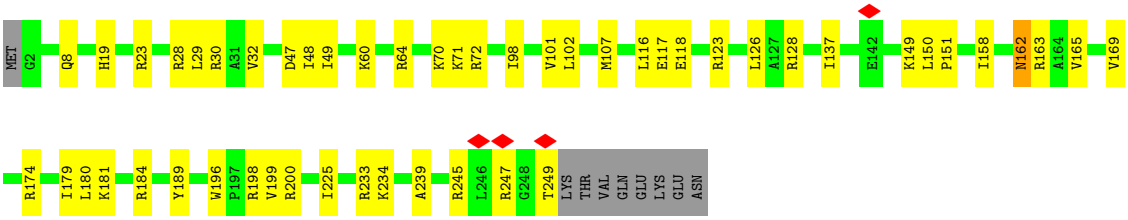




• Molecule 4: Large ribosomal subunit protein uL2

Chain LA:

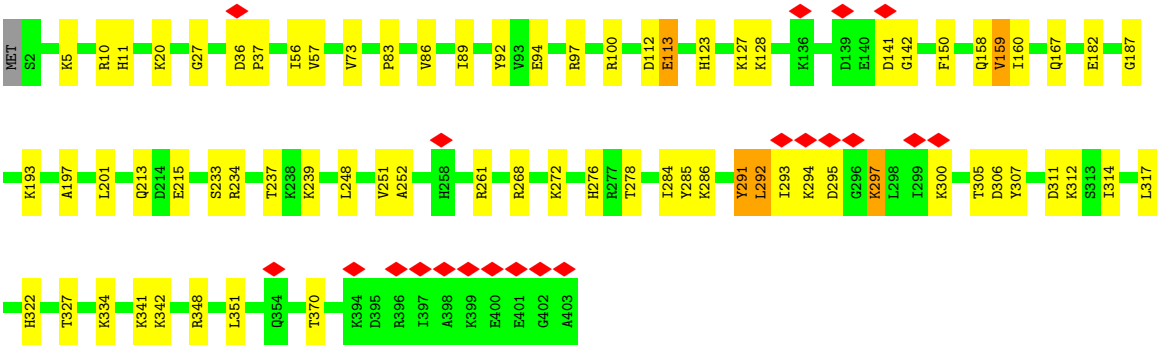




• Molecule 5: Large ribosomal subunit protein uL3

Chain LB:

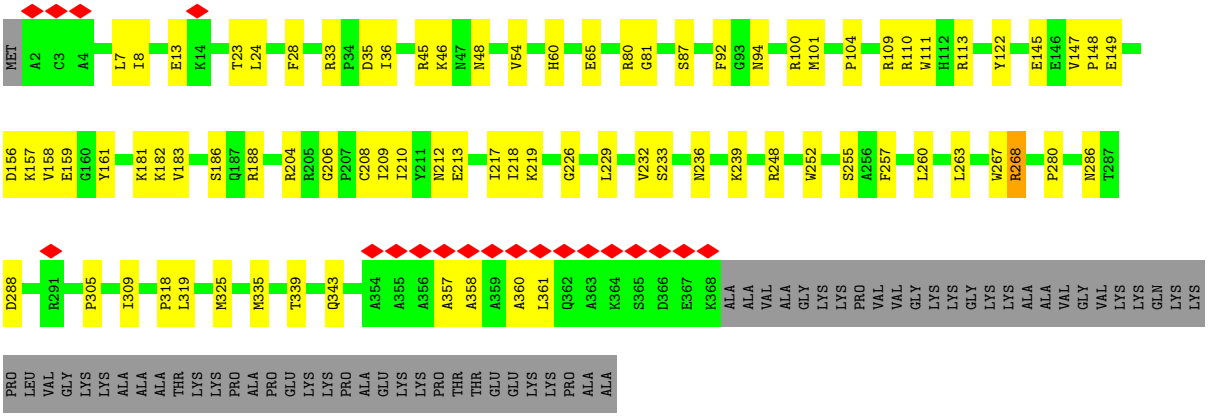




• Molecule 6: Large ribosomal subunit protein uL4

Chain LC:

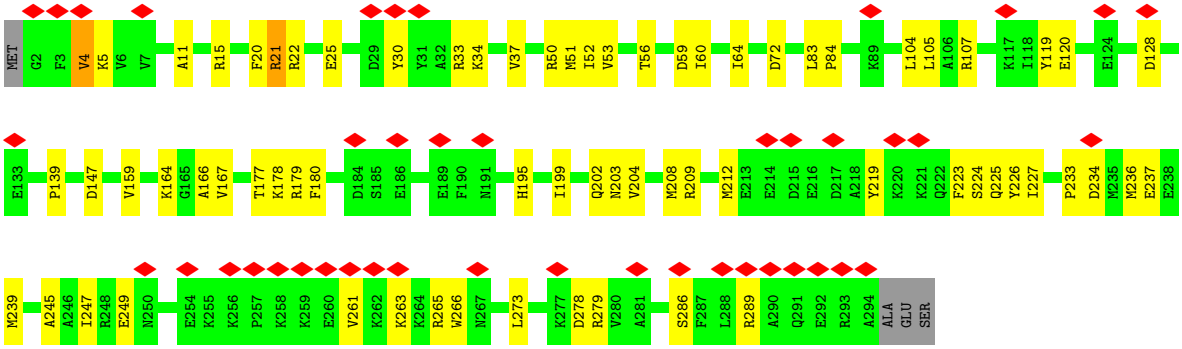




• Molecule 7: Large ribosomal subunit protein uL18

Chain LD:

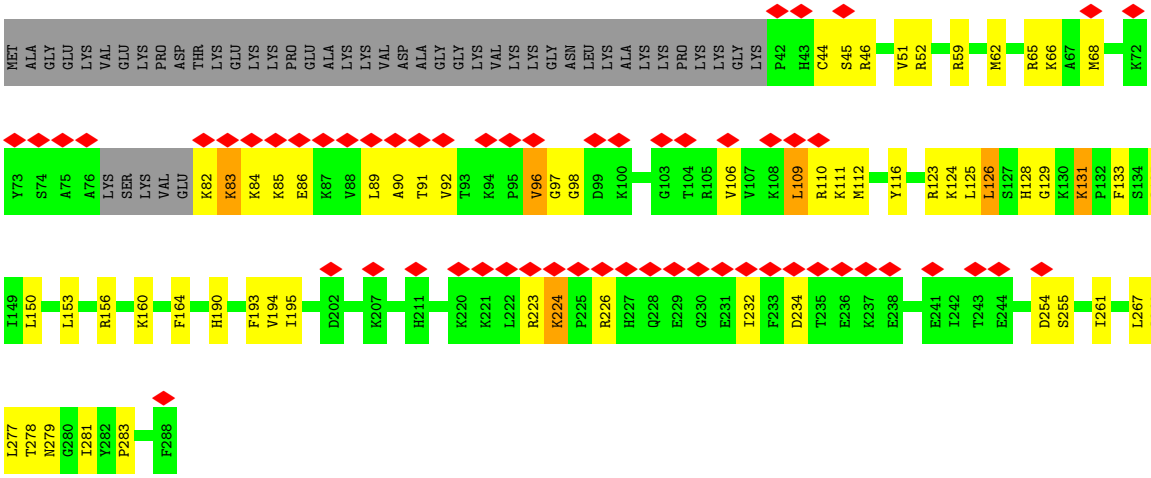




• Molecule 8: Large ribosomal subunit protein eL6

Chain LE:

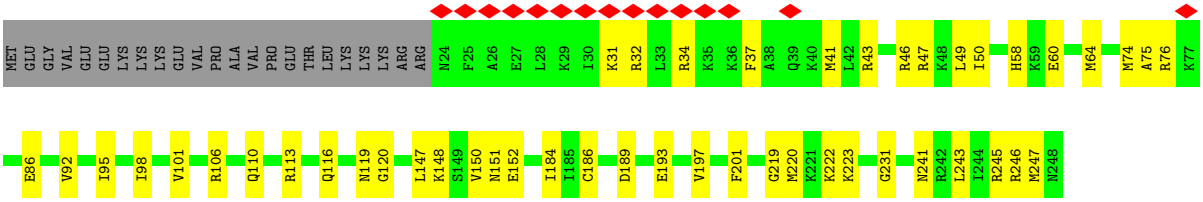




• Molecule 9: Large ribosomal subunit protein uL30

Chain LF:

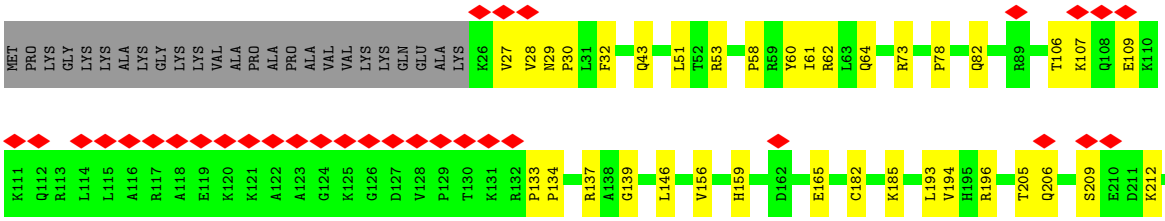


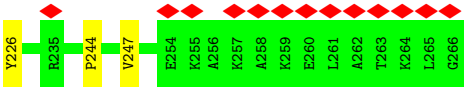


• Molecule 10: Large ribosomal subunit protein eL8

Chain LG:



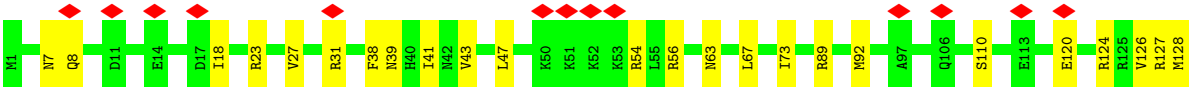


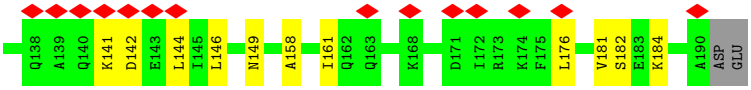


• Molecule 11: Large ribosomal subunit protein uL6

Chain LH:



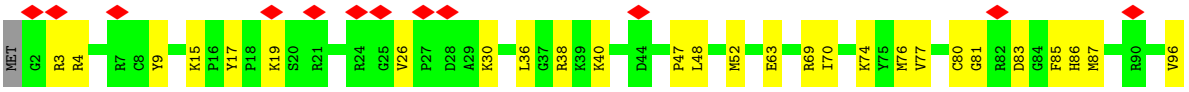


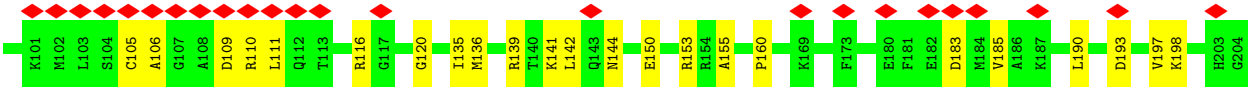


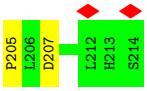
• Molecule 12: Ribosomal protein uL16-like

Chain LI:





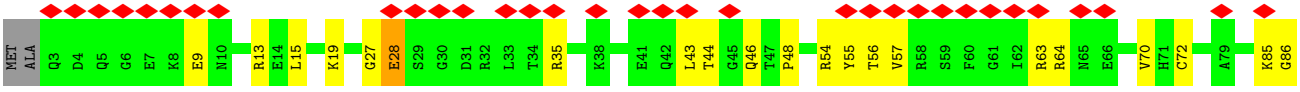


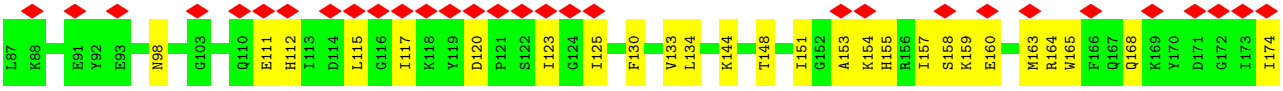


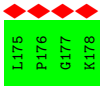
• Molecule 13: Large ribosomal subunit protein uL5

Chain LJ:





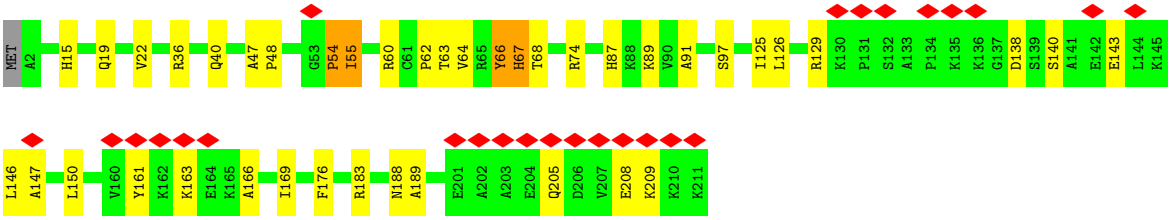




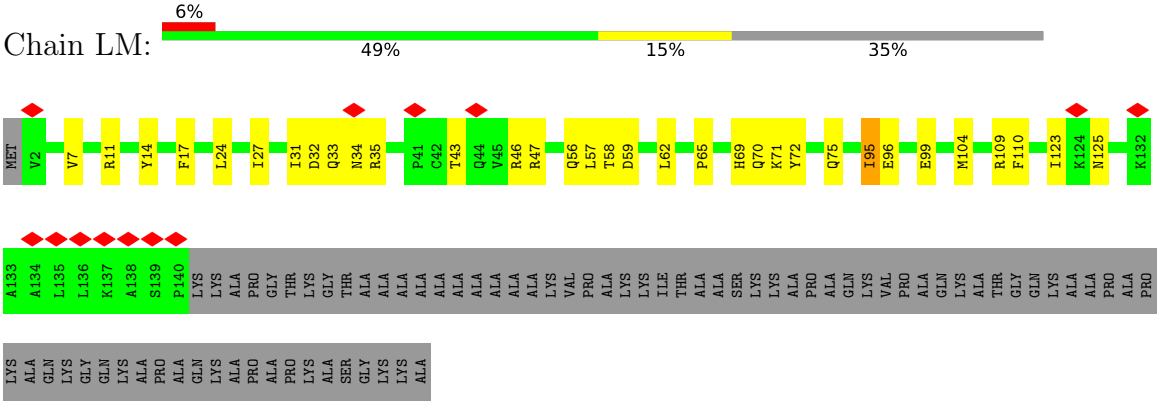
• Molecule 14: Large ribosomal subunit protein eL13

Chain LL:

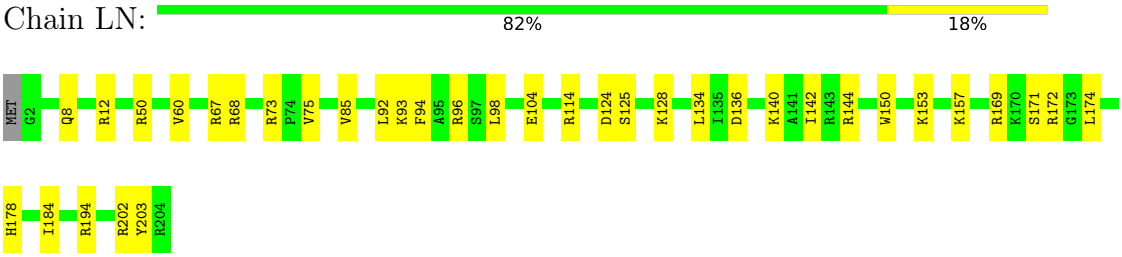




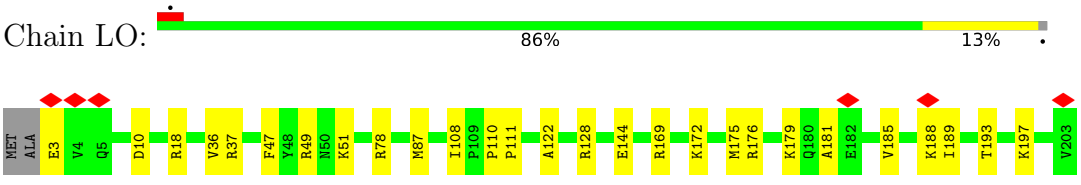
• Molecule 15: Large ribosomal subunit protein eL14



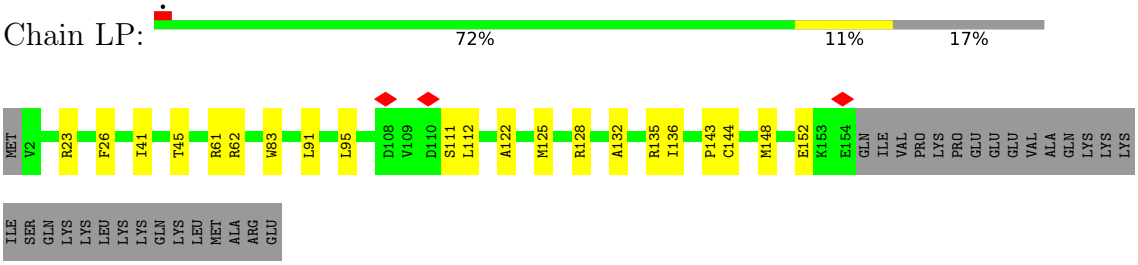
• Molecule 16: Large ribosomal subunit protein eL15



• Molecule 17: Large ribosomal subunit protein uL13

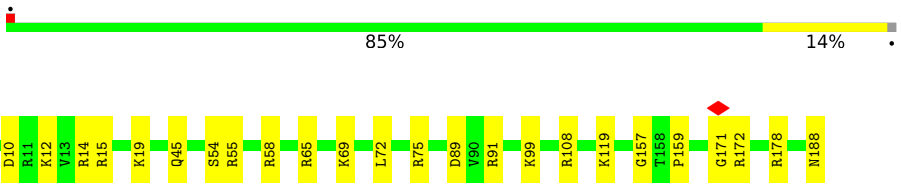


• Molecule 18: Large ribosomal subunit protein uL22



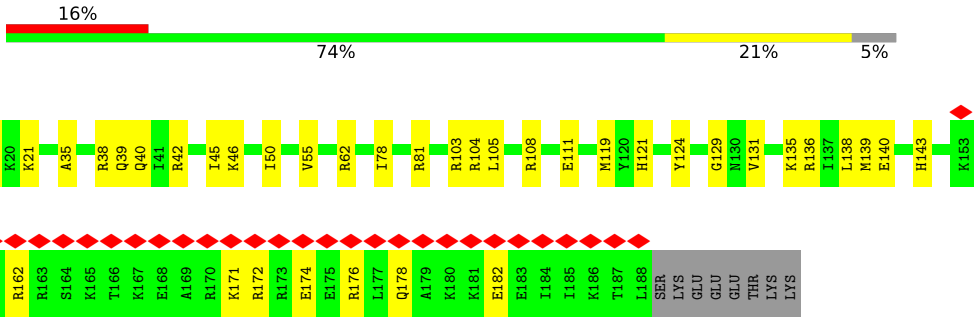
• Molecule 19: Large ribosomal subunit protein eL18

Chain LQ:



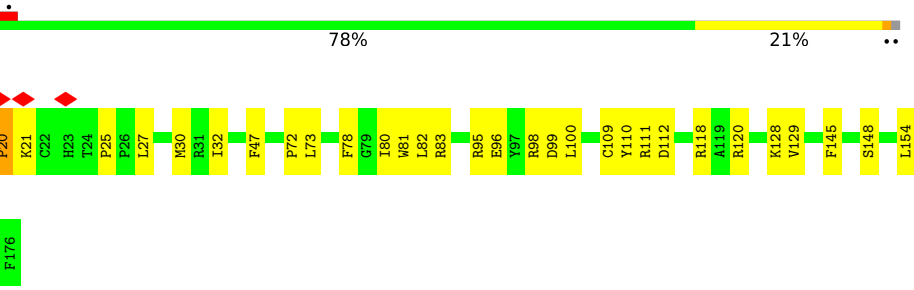
• Molecule 20: Large ribosomal subunit protein eL19

Chain LR:



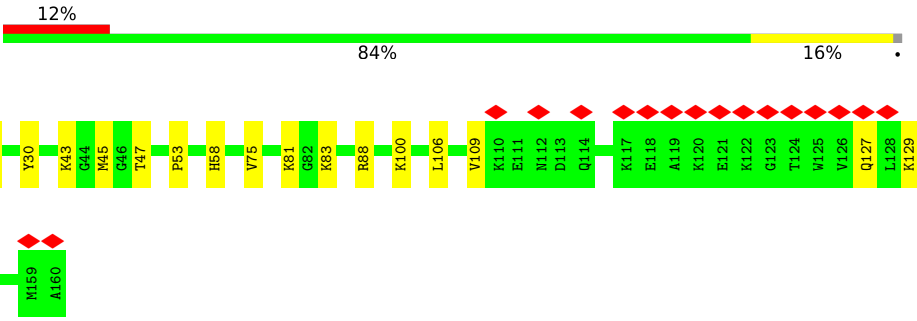
• Molecule 21: Large ribosomal subunit protein eL20

Chain LS:



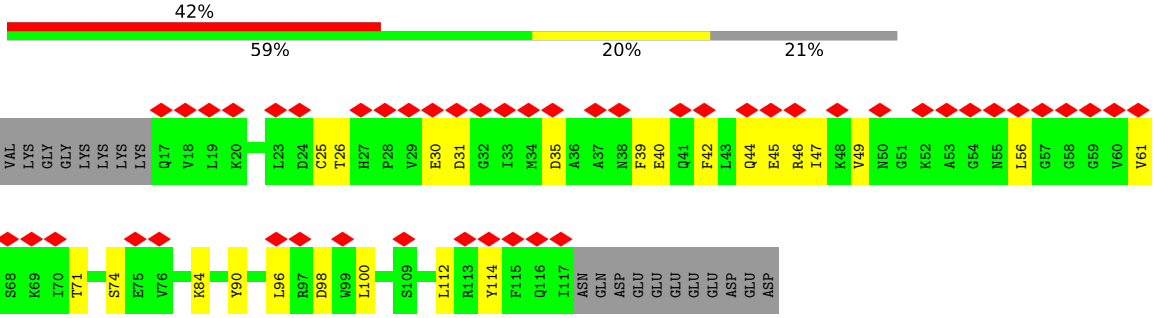
• Molecule 22: Large ribosomal subunit protein eL21

Chain LT:



• Molecule 23: Large ribosomal subunit protein eL22

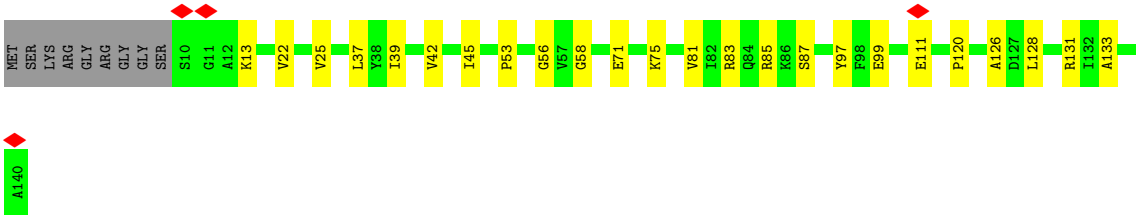
Chain LU:



• Molecule 24: Large ribosomal subunit protein uL14

Chain LV:

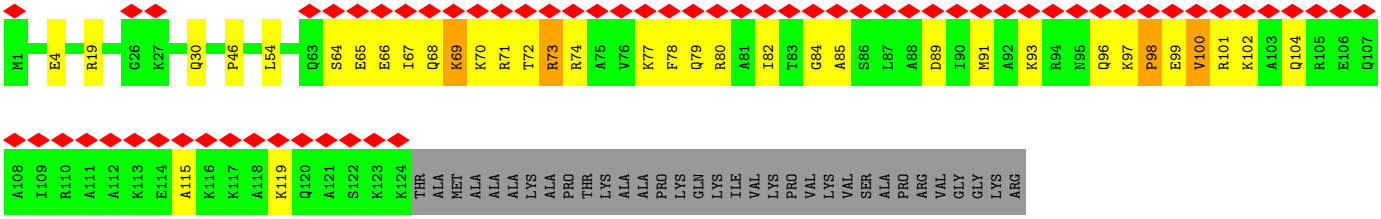




• Molecule 25: Large ribosomal subunit protein eL24

Chain LW:

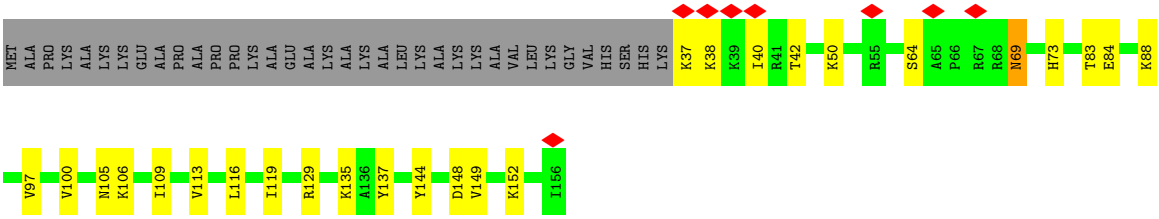




• Molecule 26: Large ribosomal subunit protein uL23

Chain LX:

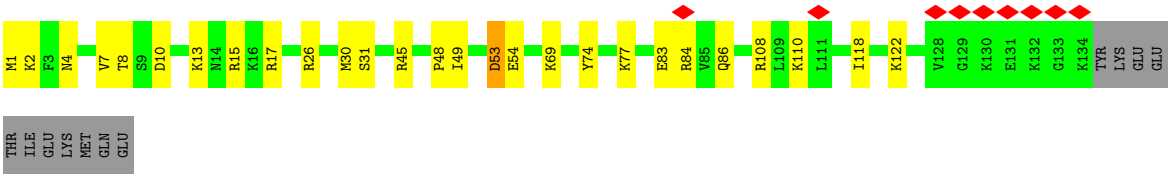




• Molecule 27: Large ribosomal subunit protein uL24

Chain LY:

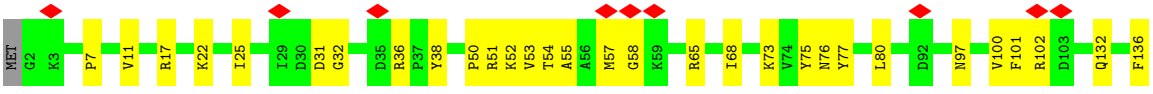




• Molecule 28: Large ribosomal subunit protein eL27

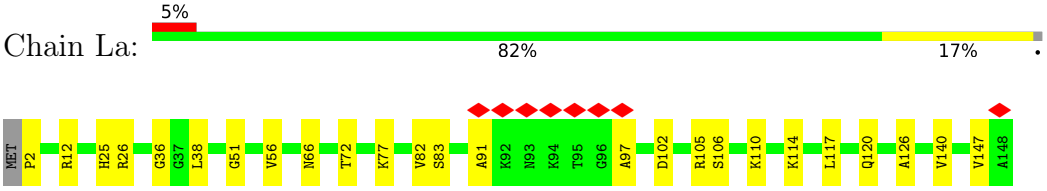
Chain LZ:





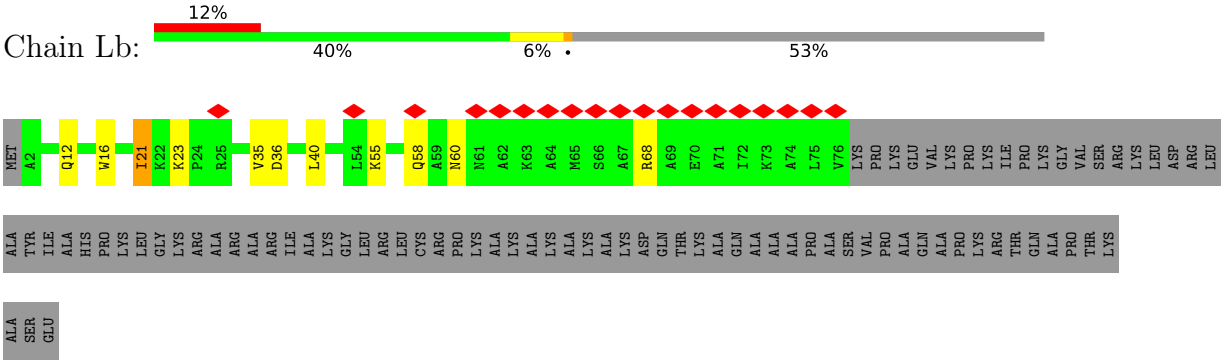
• Molecule 29: Large ribosomal subunit protein uL15

Chain La:



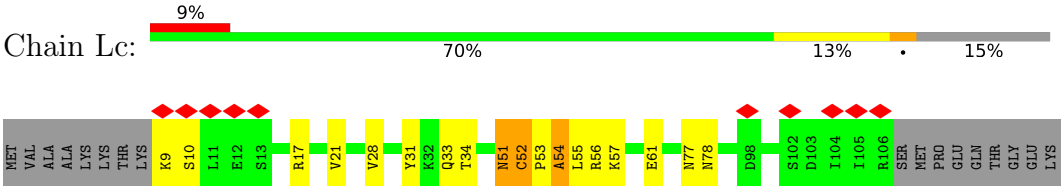
• Molecule 30: Large ribosomal subunit protein eL29

Chain Lb:



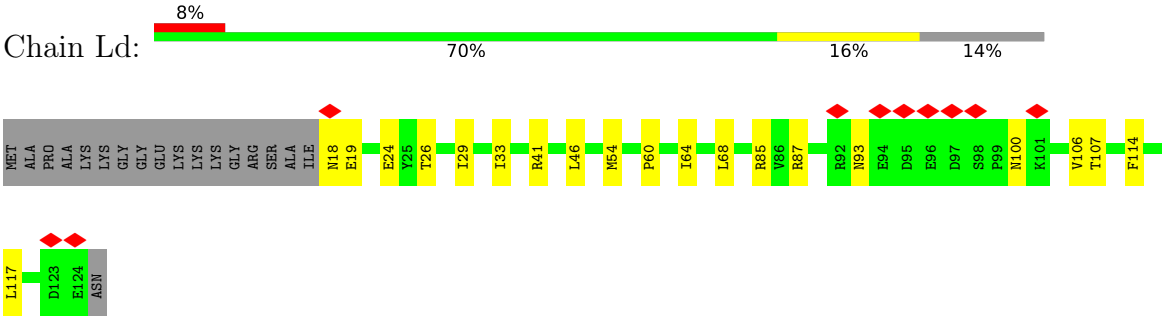
• Molecule 31: Large ribosomal subunit protein eL30

Chain Lc:



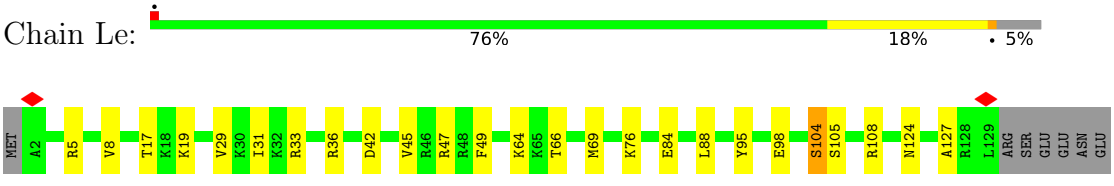
• Molecule 32: Large ribosomal subunit protein eL31

Chain Ld:



• Molecule 33: Large ribosomal subunit protein eL32

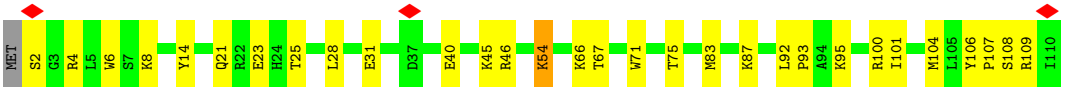
Chain Le:



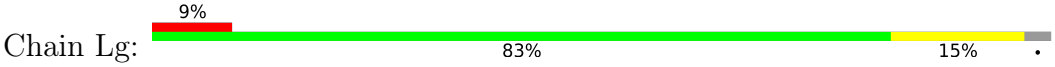
• Molecule 34: Large ribosomal subunit protein eL33

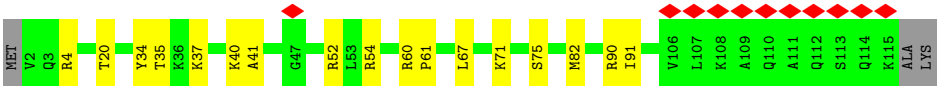
Chain Lf:



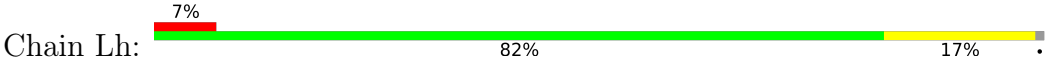


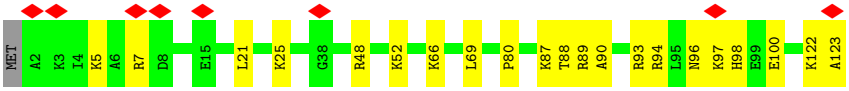
• Molecule 35: Large ribosomal subunit protein eL34



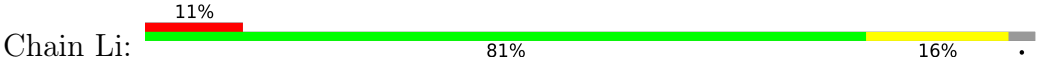


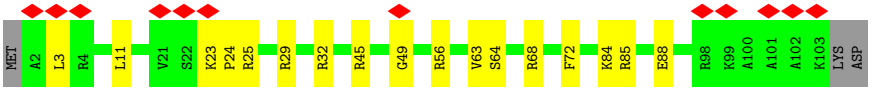
• Molecule 36: Large ribosomal subunit protein uL29





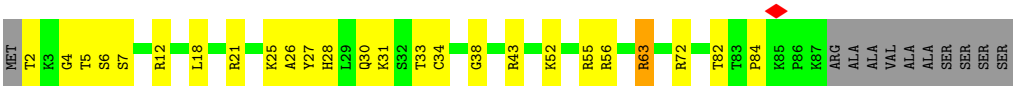
• Molecule 37: Large ribosomal subunit protein eL36





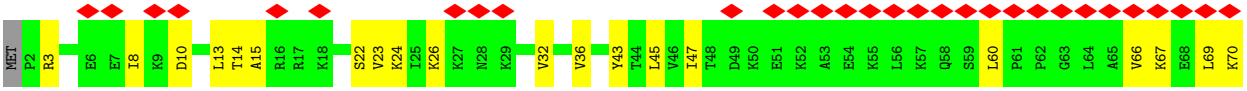
• Molecule 38: Large ribosomal subunit protein eL37



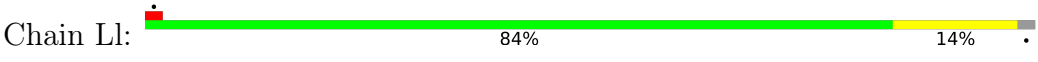


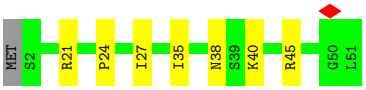
• Molecule 39: Large ribosomal subunit protein eL38



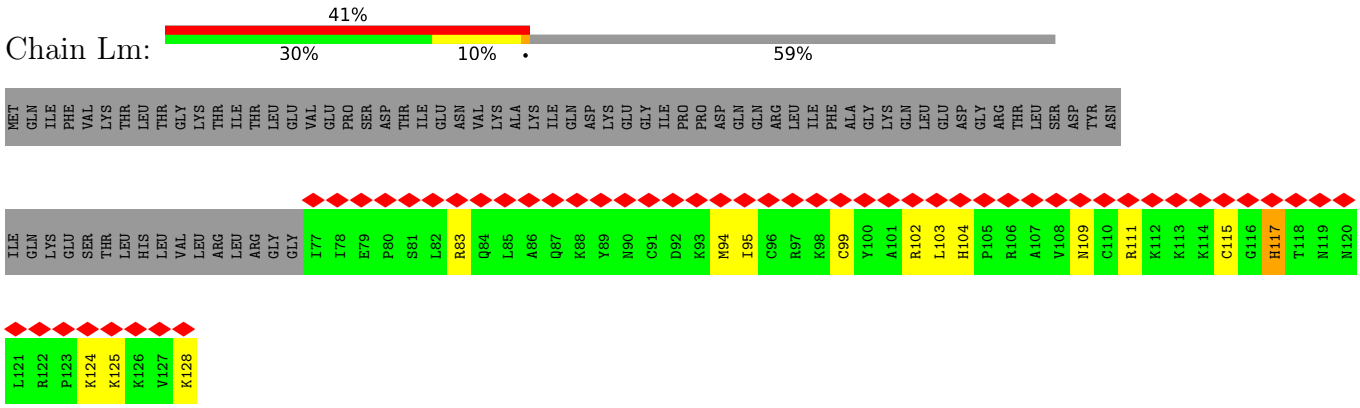


• Molecule 40: Large ribosomal subunit protein eL39

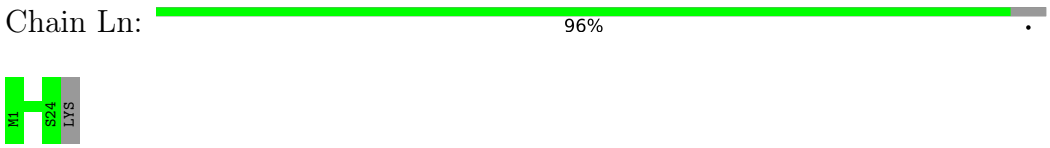




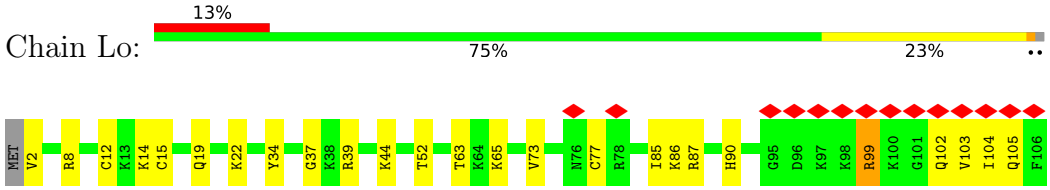
• Molecule 41: Ubiquitin-ribosomal protein eL40 fusion protein



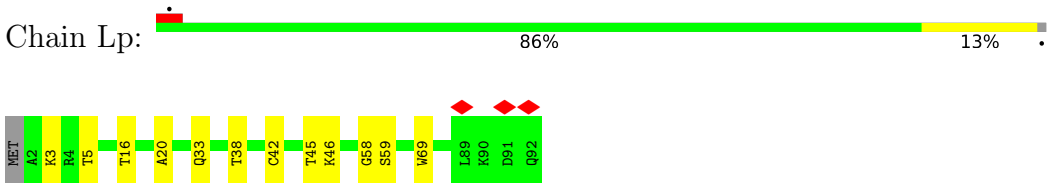
• Molecule 42: Small ribosomal subunit protein eS32



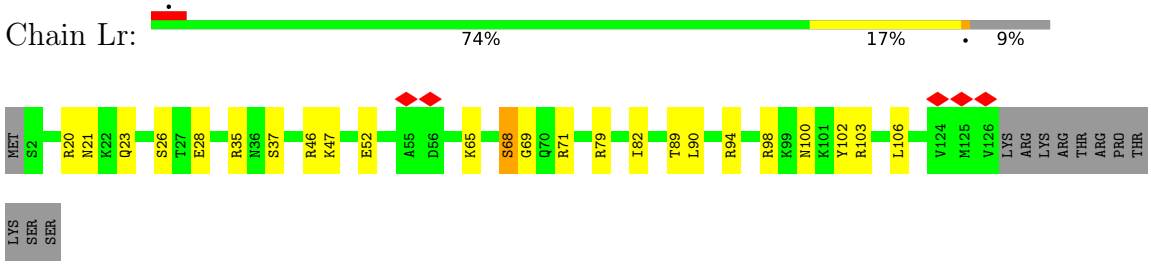
• Molecule 43: Large ribosomal subunit protein eL42



• Molecule 44: Large ribosomal subunit protein eL43



• Molecule 45: Large ribosomal subunit protein eL28



• Molecule 46: Large ribosomal subunit protein uL1

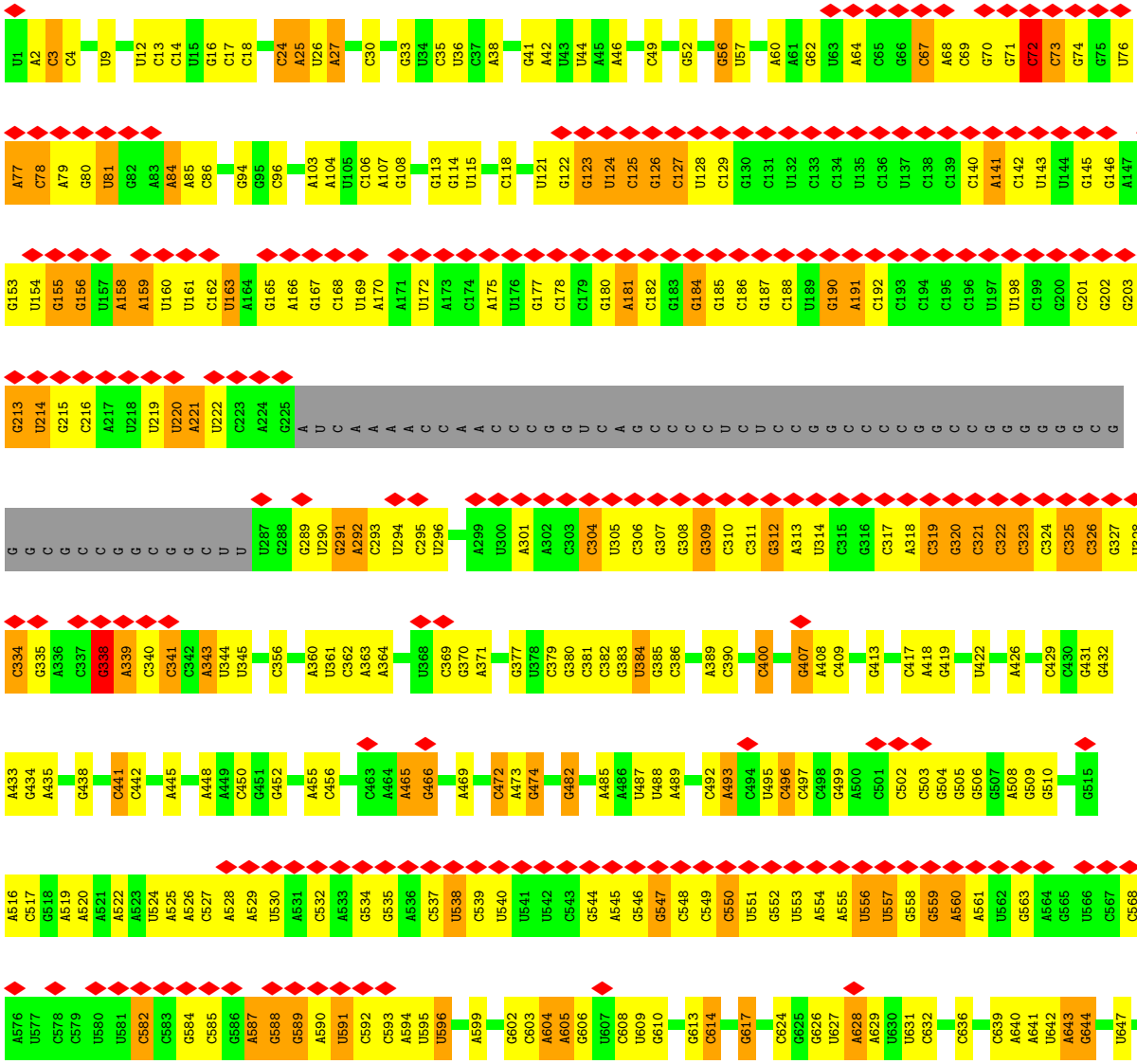


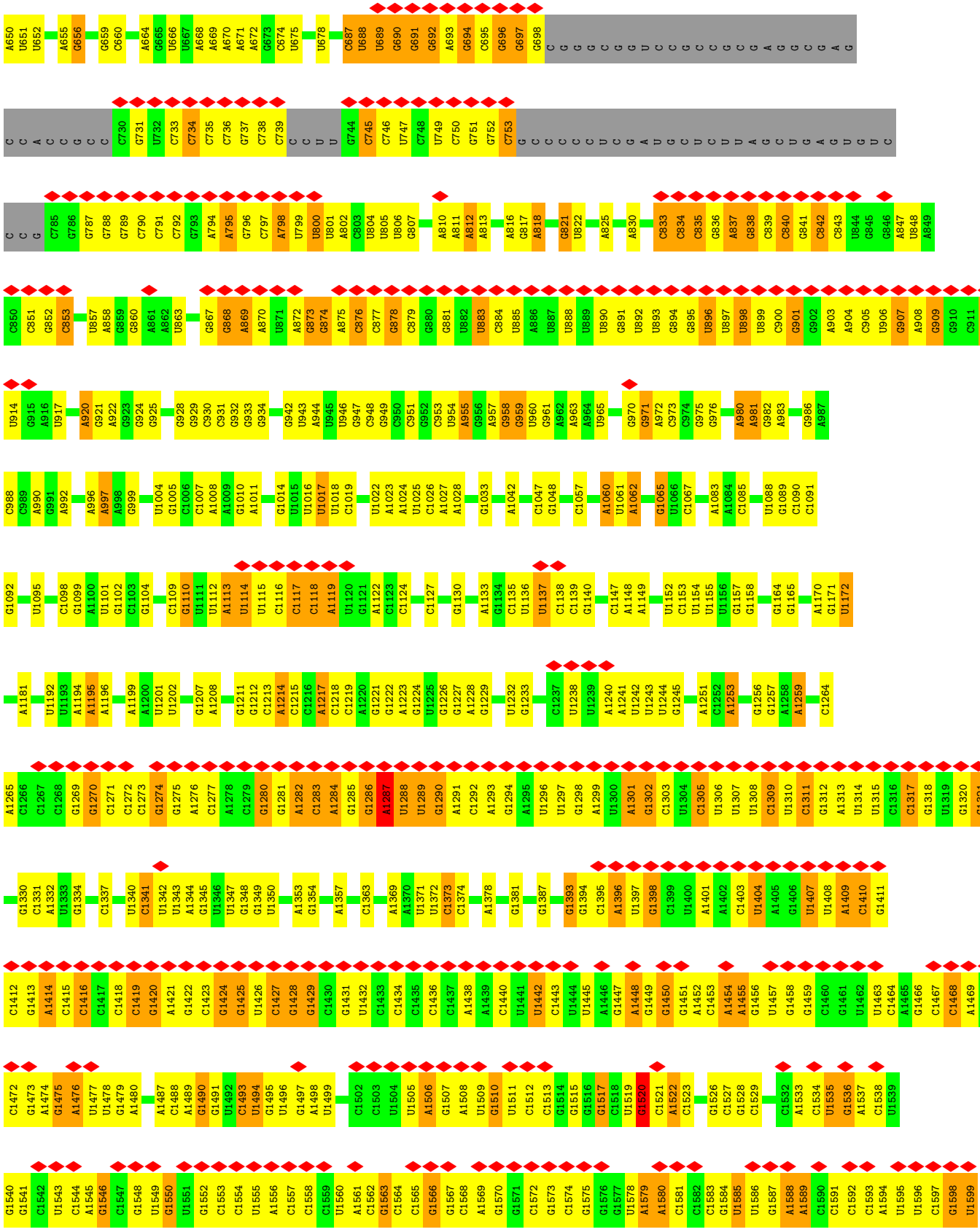


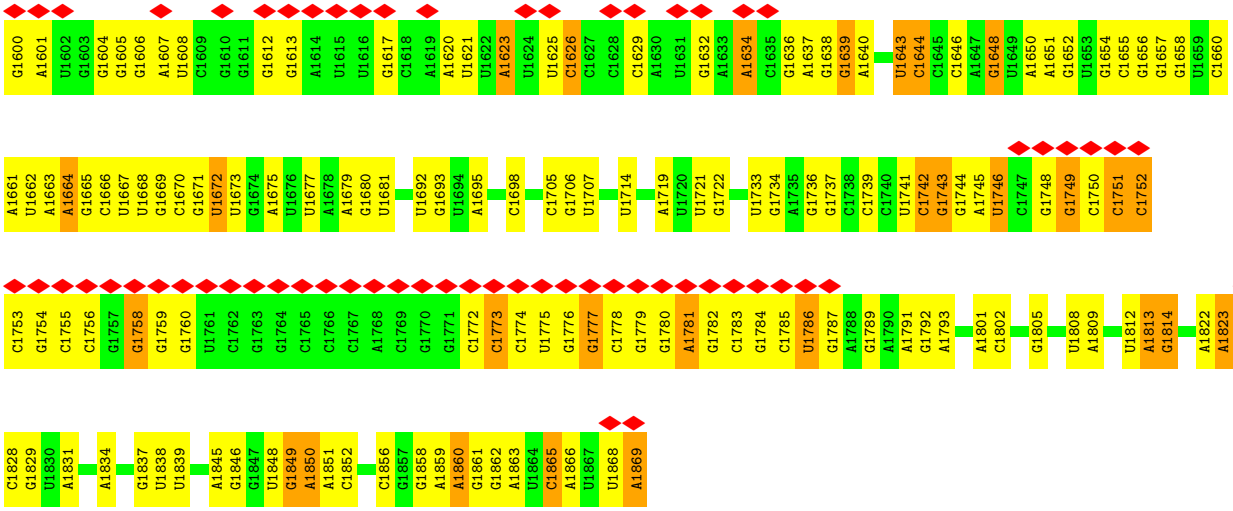
• Molecule 47: 18S ribosomal RNA

Chain S2:



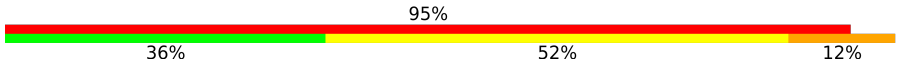


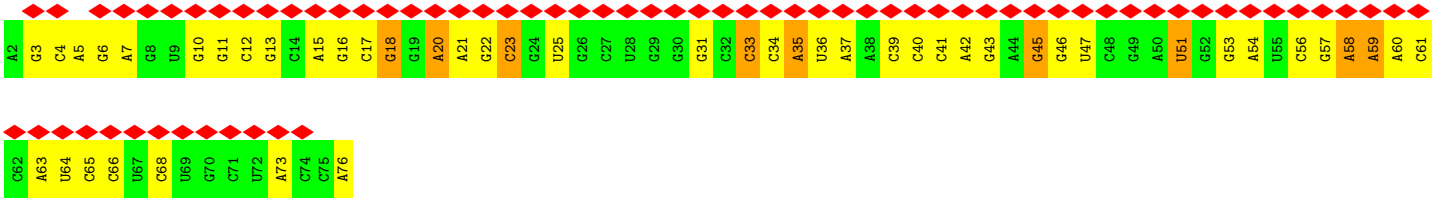




• Molecule 48: HUMAN INITIATOR MET-TRNA-I

Chain S6:

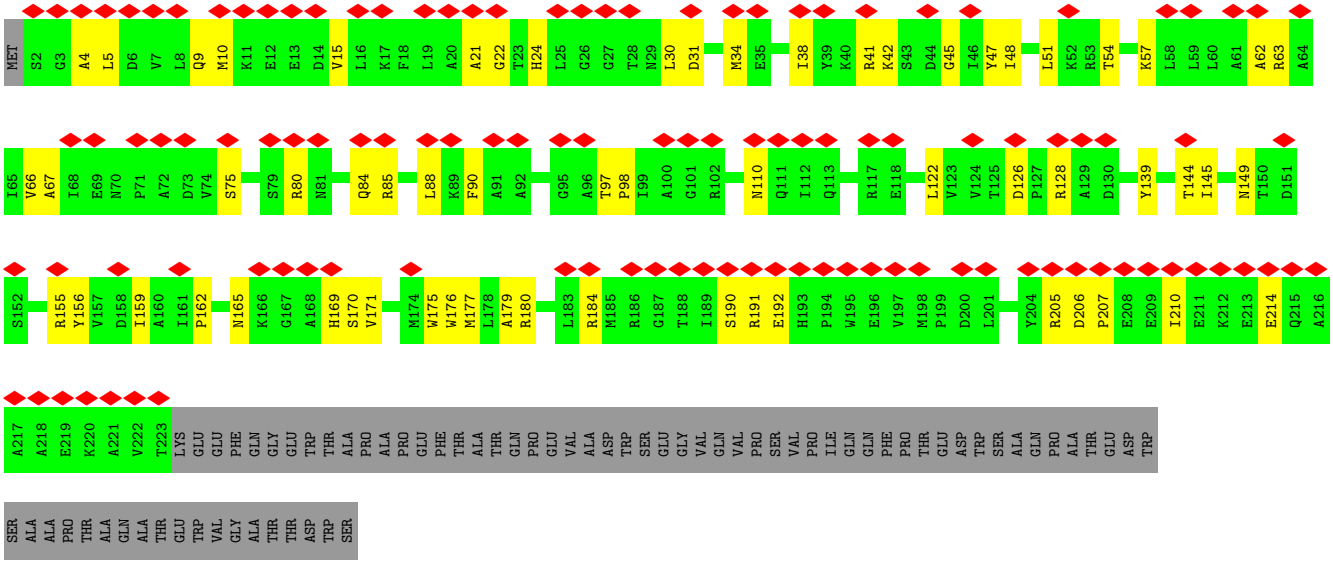




• Molecule 49: Small ribosomal subunit protein uS2

Chain SA:

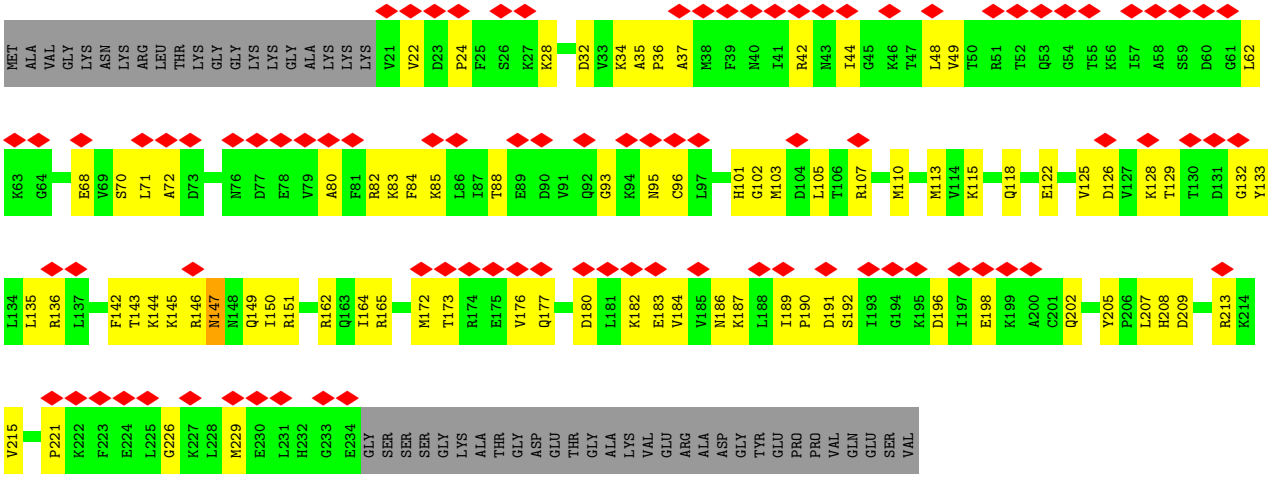




• Molecule 50: Small ribosomal subunit protein eS1

Chain SB:

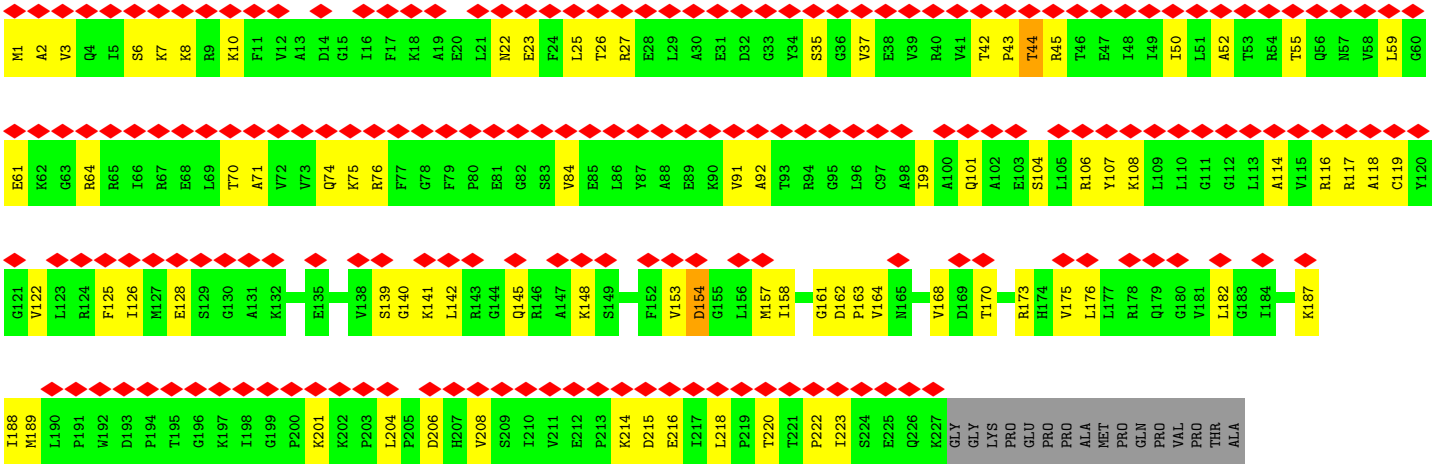




• Molecule 51: Small ribosomal subunit protein uS3

Chain SD:

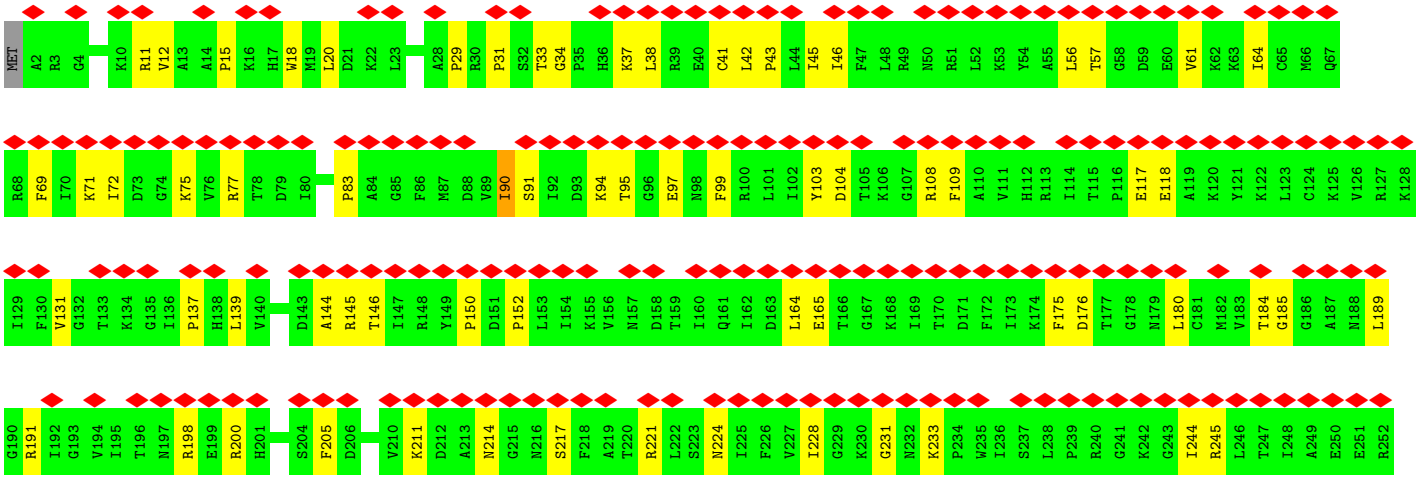


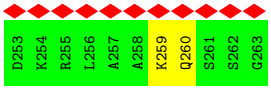


• Molecule 52: Small ribosomal subunit protein eS4, X isoform

Chain SE:



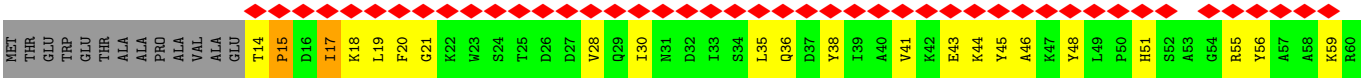


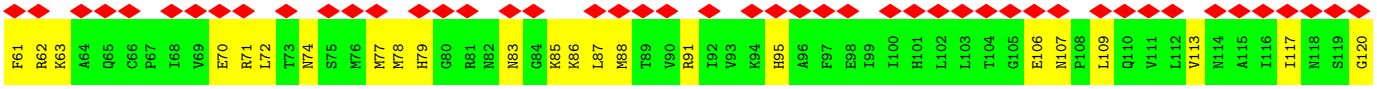


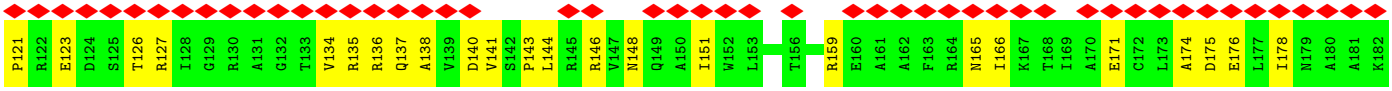
• Molecule 53: Small ribosomal subunit protein uS7

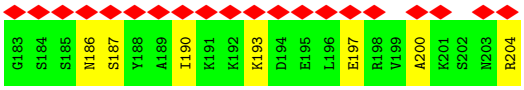
Chain SF:







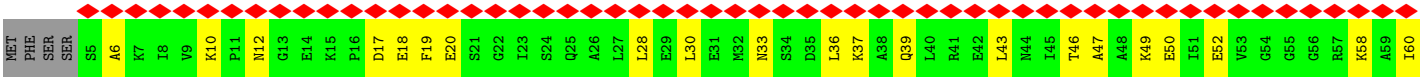


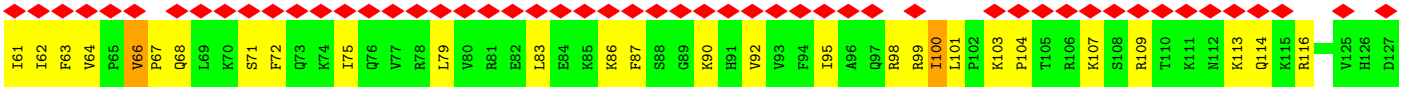


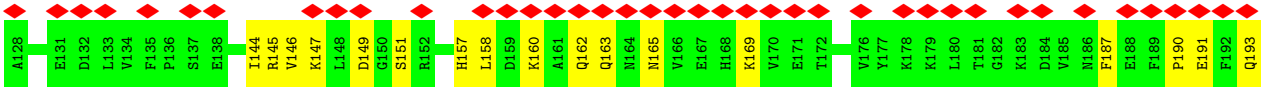
• Molecule 54: Small ribosomal subunit protein eS7

Chain SH:





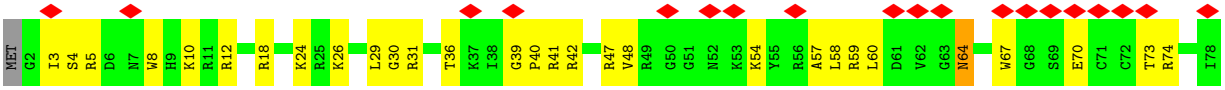


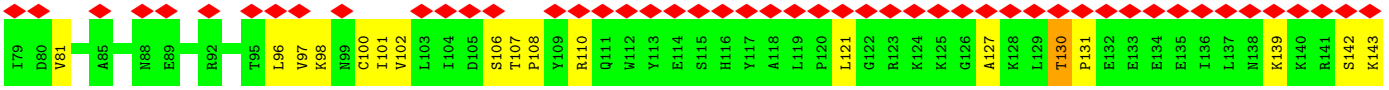


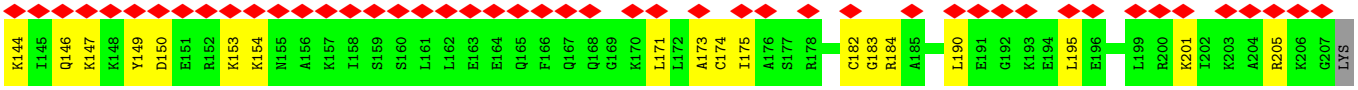
• Molecule 55: Small ribosomal subunit protein eS8

Chain SI:



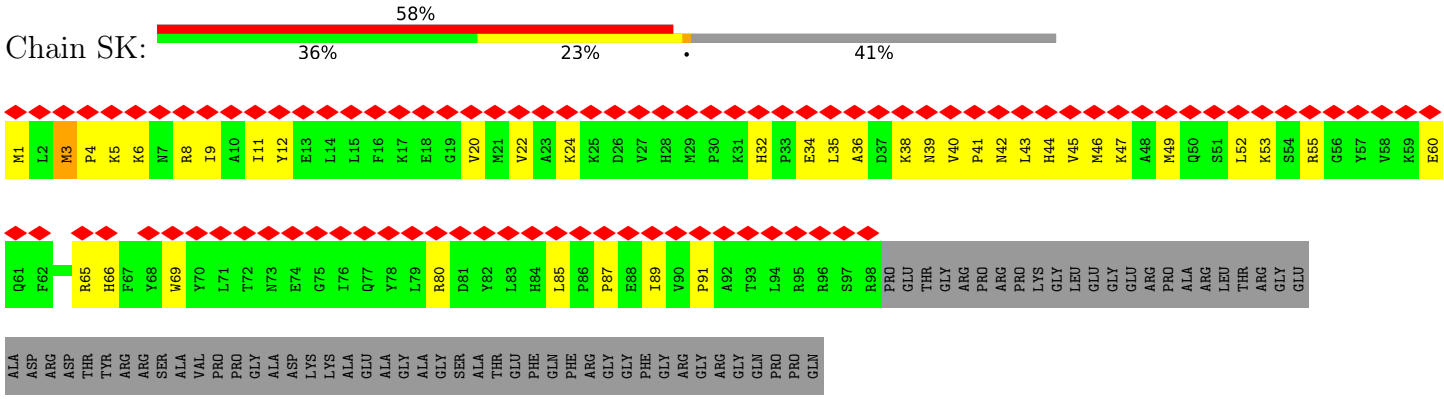






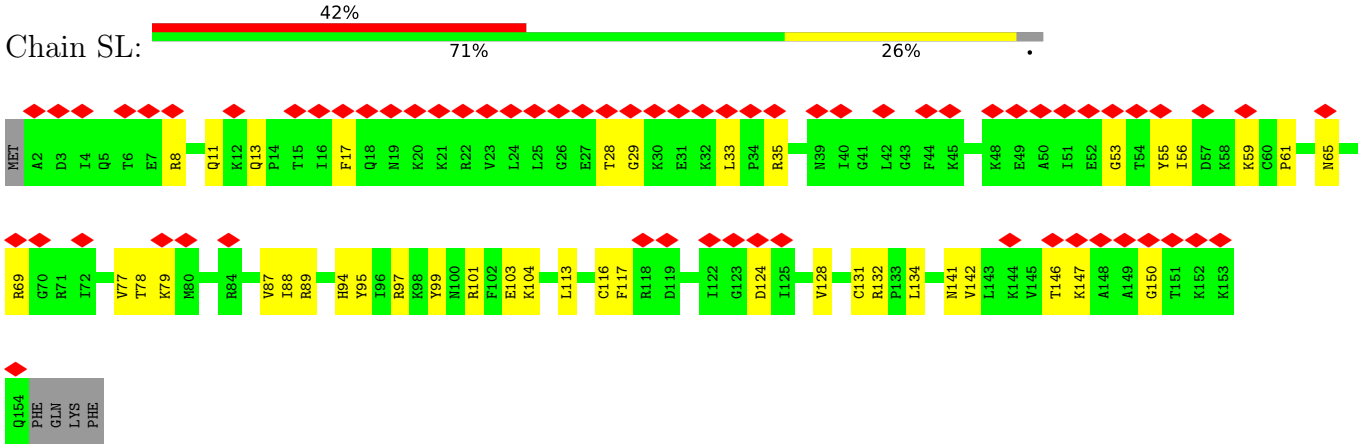
• Molecule 56: Small ribosomal subunit protein eS10

Chain SK:



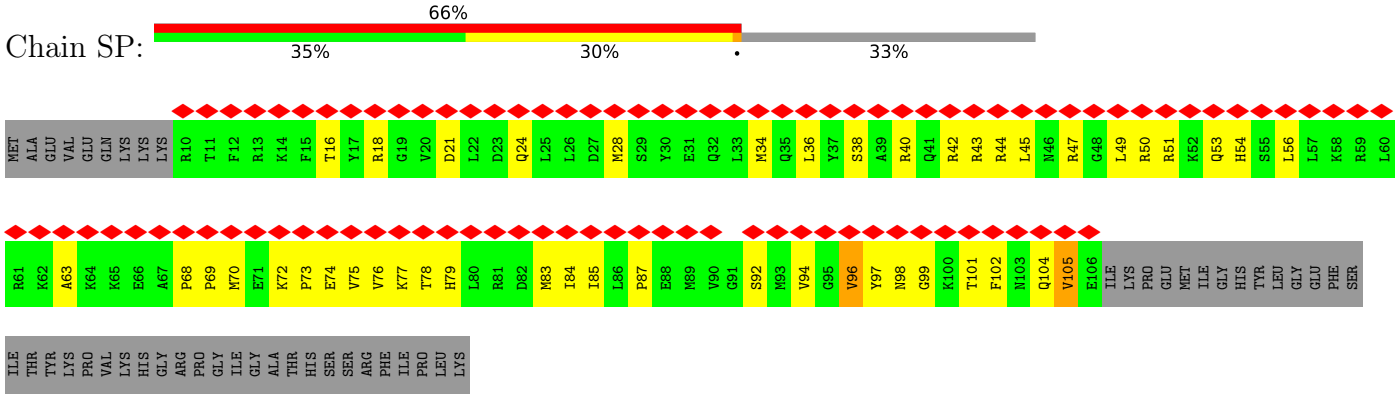
• Molecule 57: Small ribosomal subunit protein uS17

Chain SL:



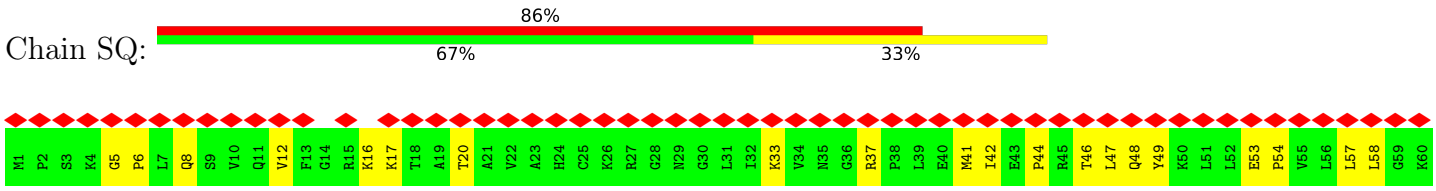
• Molecule 58: Small ribosomal subunit protein uS19

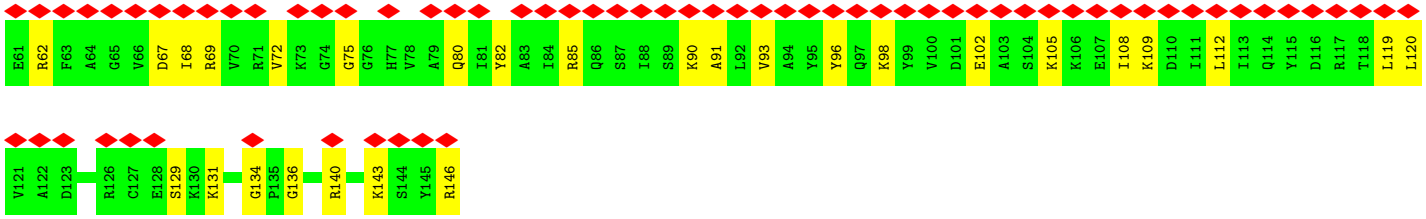
Chain SP:



• Molecule 59: Small ribosomal subunit protein uS9

Chain SQ:

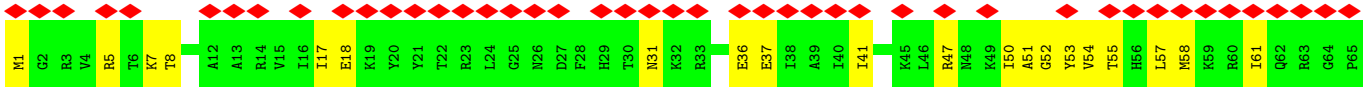


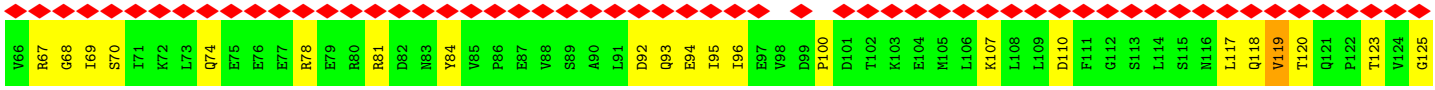


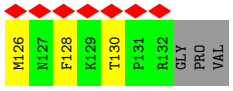
• Molecule 60: Small ribosomal subunit protein eS17

Chain SR:





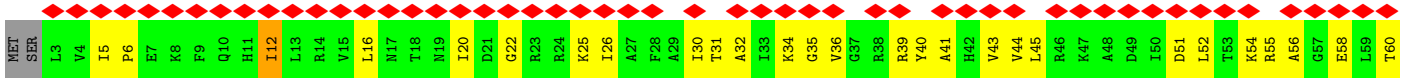


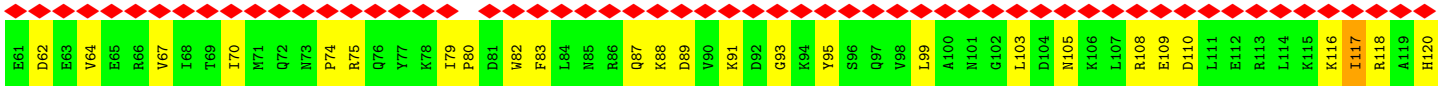


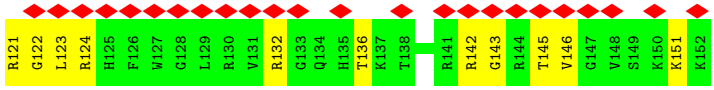
• Molecule 61: Small ribosomal subunit protein uS13

Chain SS:



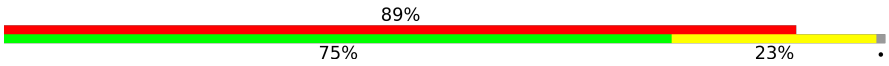


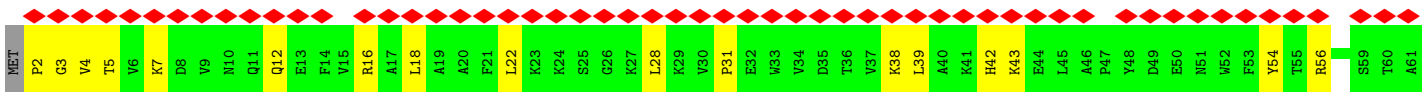


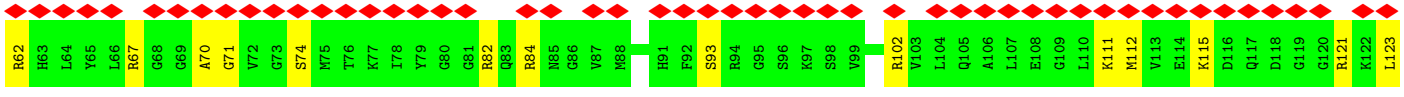


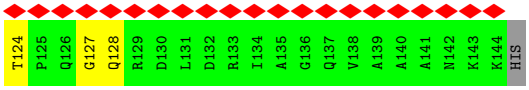
• Molecule 62: Small ribosomal subunit protein eS19

Chain ST:







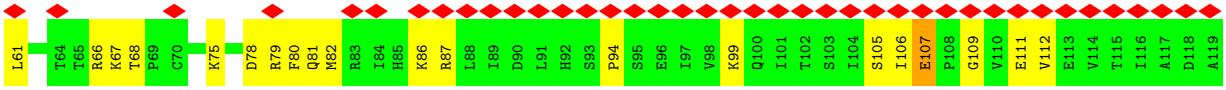


• Molecule 63: Small ribosomal subunit protein uS10

Chain SU:



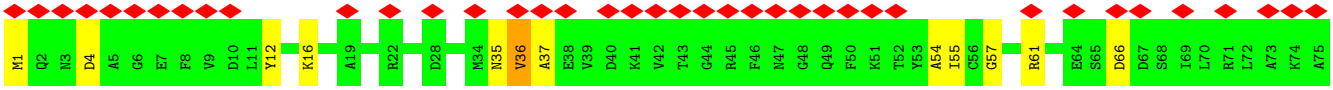


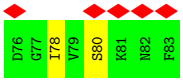


• Molecule 64: Small ribosomal subunit protein eS21

Chain SV:



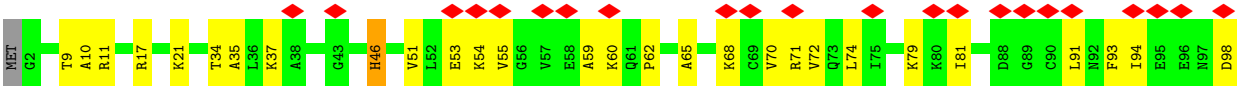


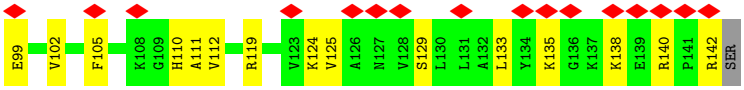


• Molecule 65: Small ribosomal subunit protein uS12

Chain SX:



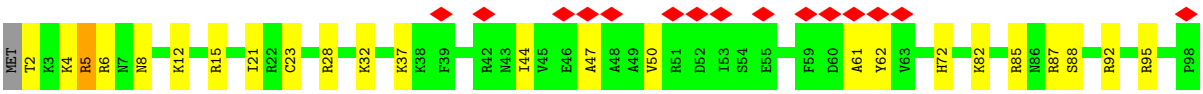


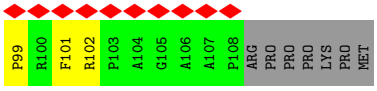


• Molecule 66: Small ribosomal subunit protein eS26

Chain Sa:

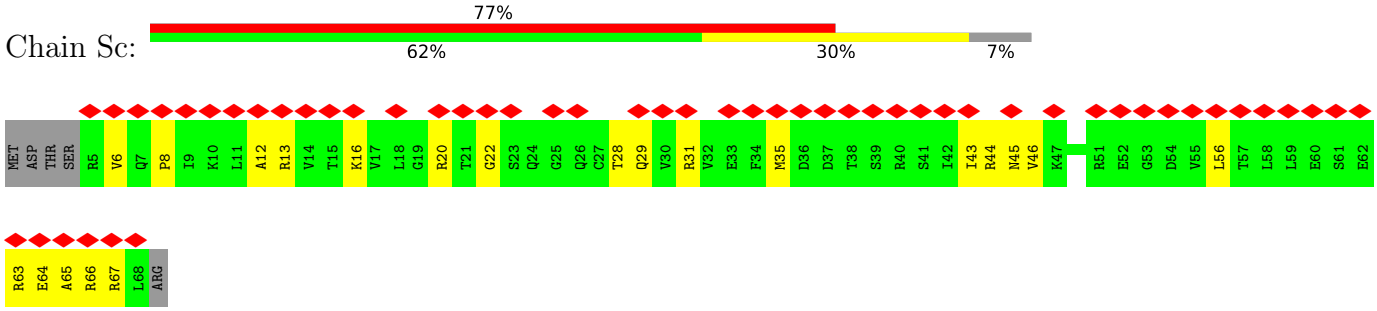






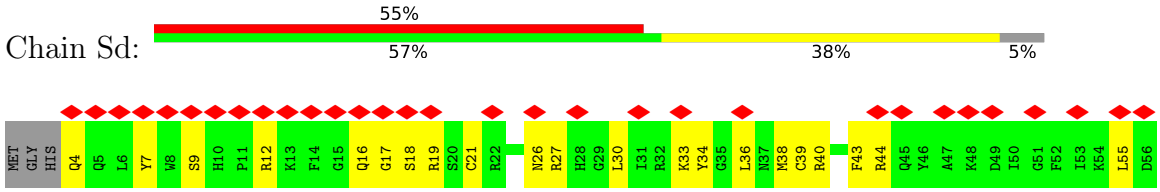
• Molecule 67: Small ribosomal subunit protein eS28

Chain Sc:



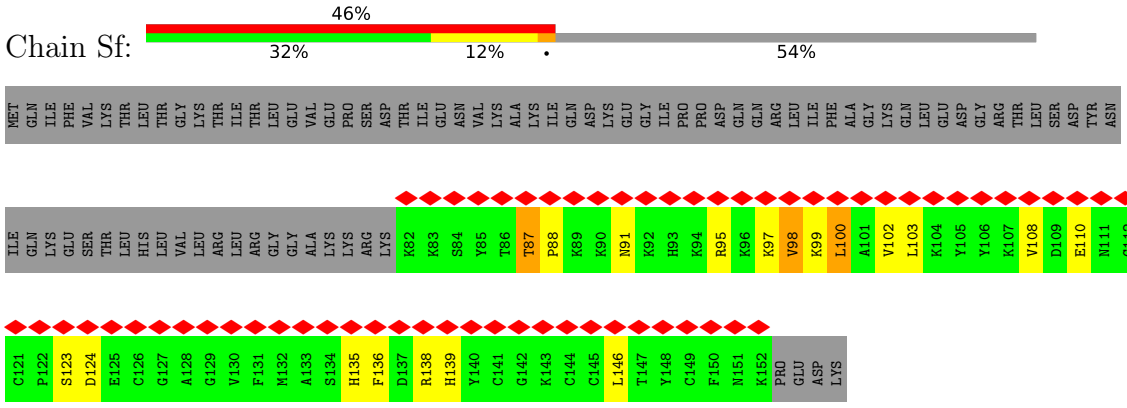
• Molecule 68: Small ribosomal subunit protein uS14

Chain Sd:



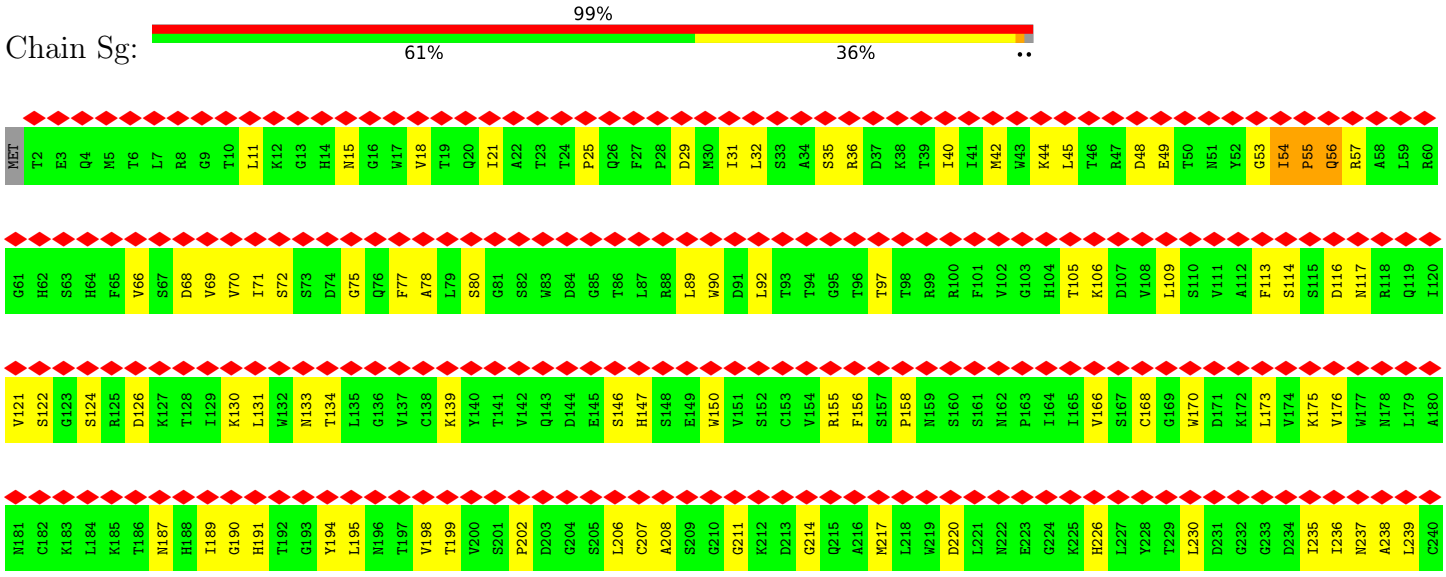
• Molecule 69: Ubiquitin

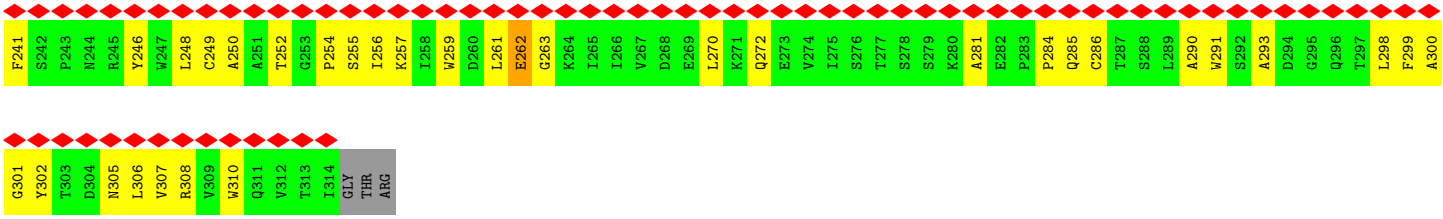
Chain Sf:



• Molecule 70: Small ribosomal subunit protein RACK1

Chain Sg:

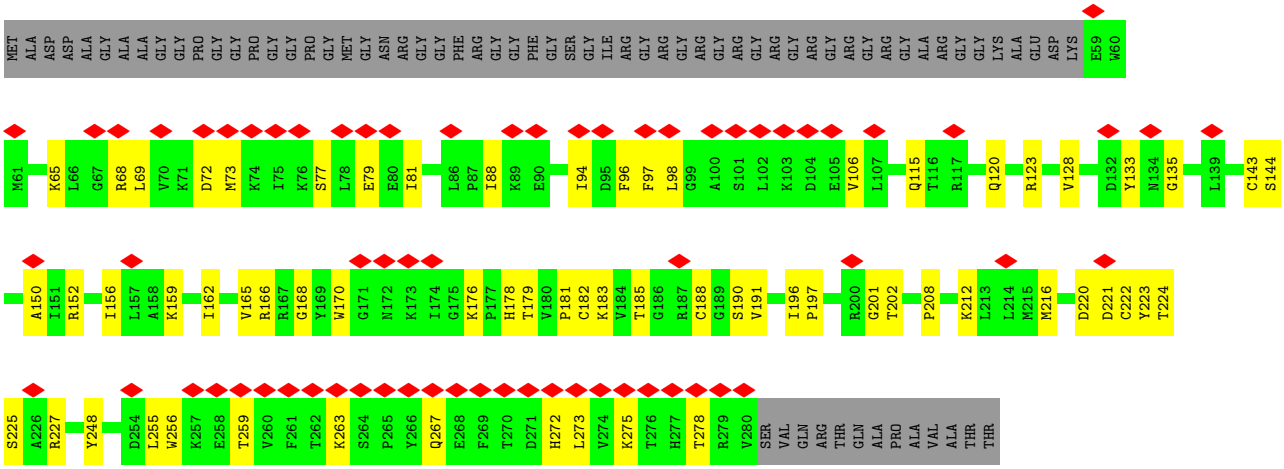




• Molecule 71: Small ribosomal subunit protein uS5

Chain SC:

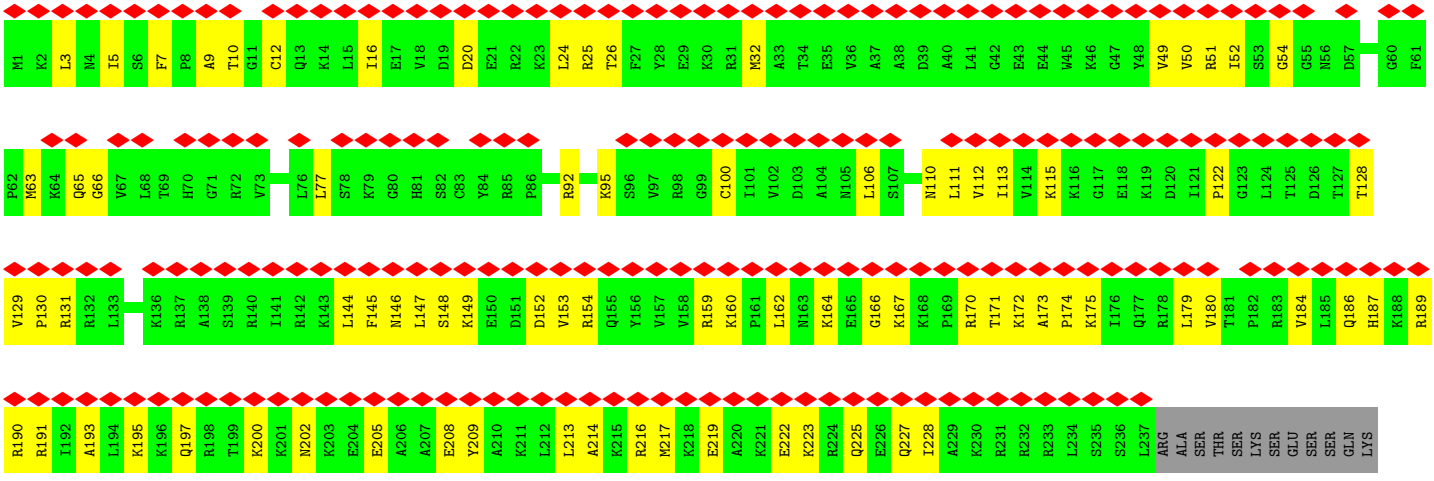




• Molecule 72: Small ribosomal subunit protein eS6

Chain SG:





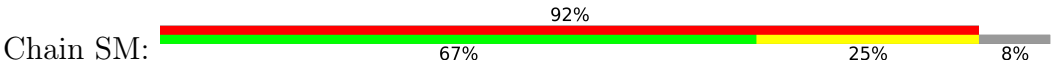
• Molecule 73: Small ribosomal subunit protein uS4

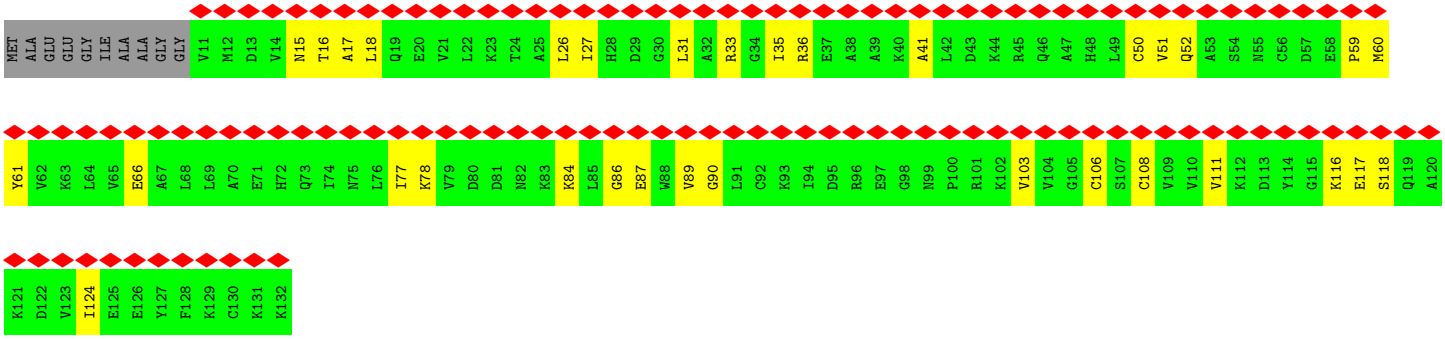
Chain SJ:





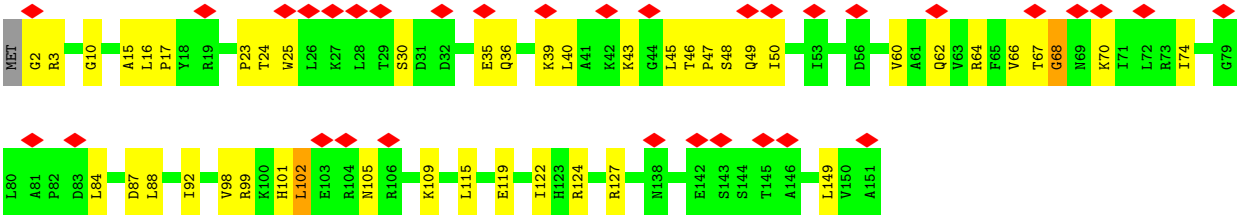
• Molecule 74: Small ribosomal subunit protein eS12





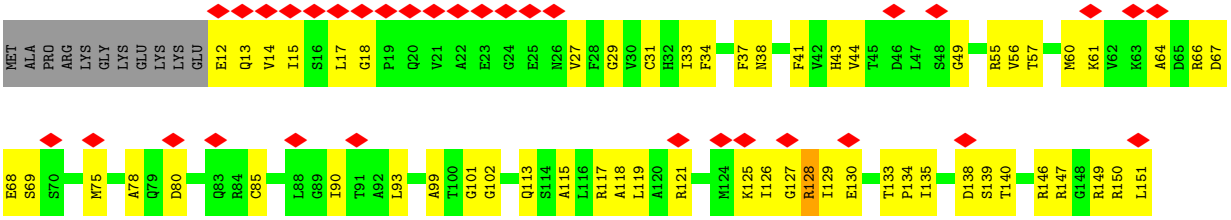
• Molecule 75: Small ribosomal subunit protein uS15





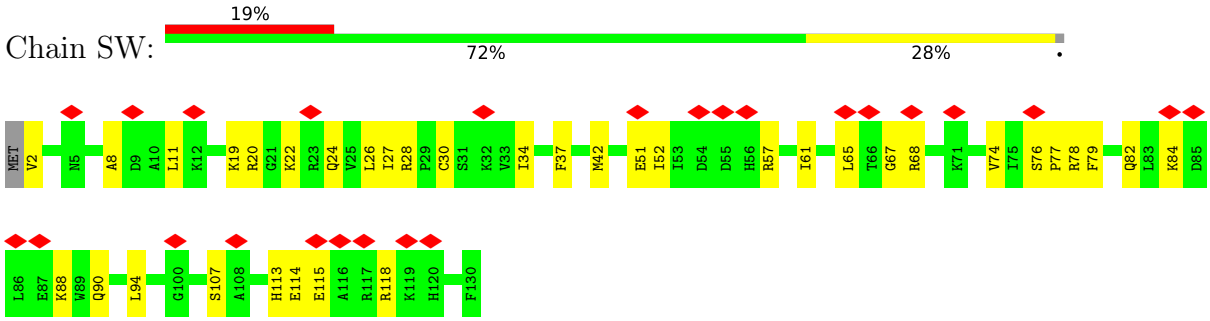
• Molecule 76: Small ribosomal subunit protein uS11





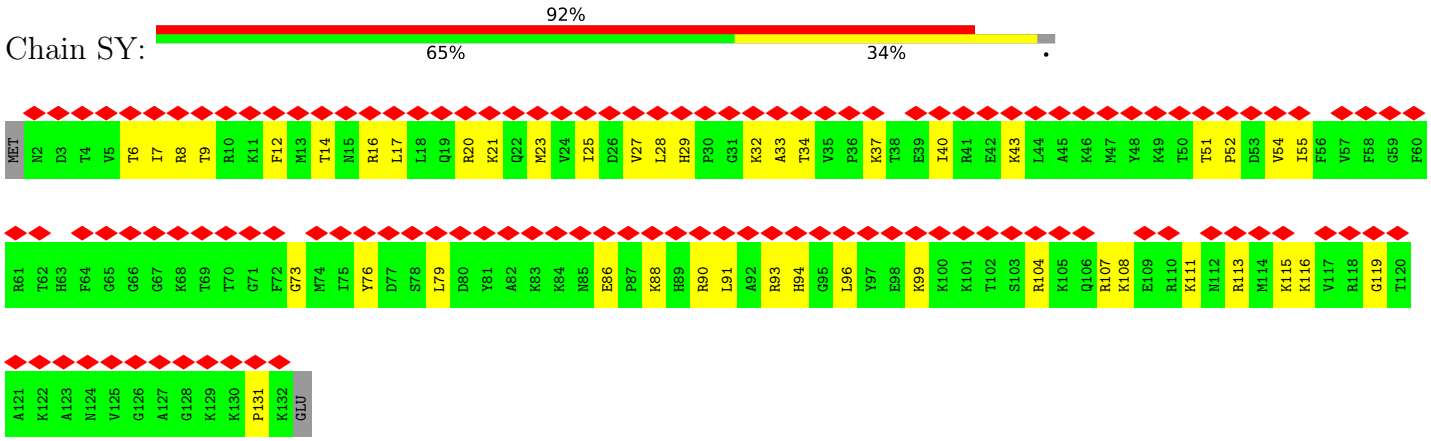
• Molecule 77: Small ribosomal subunit protein uS8

Chain SW:



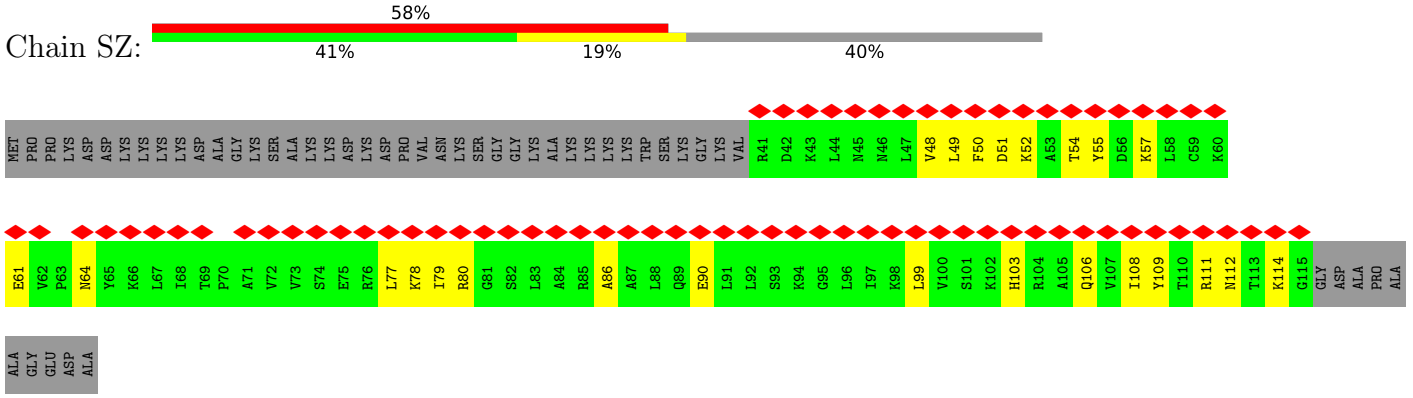
• Molecule 78: Small ribosomal subunit protein eS24

Chain SY:



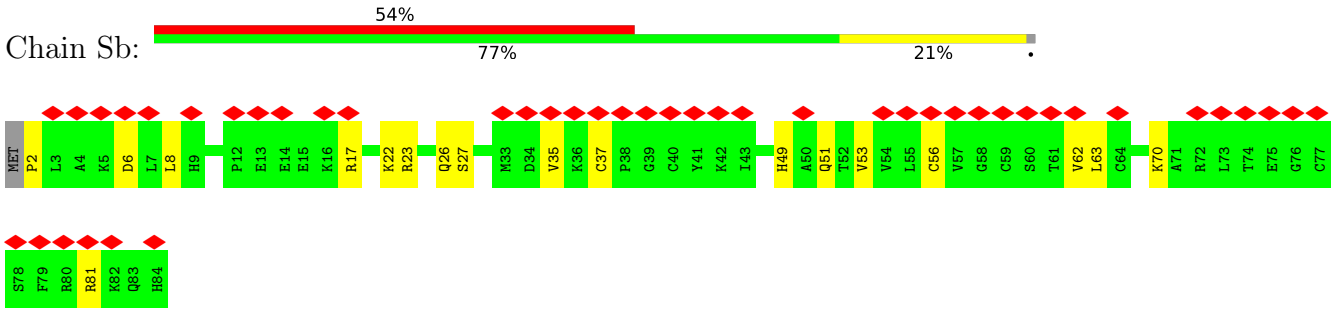
• Molecule 79: Small ribosomal subunit protein eS25

Chain SZ:



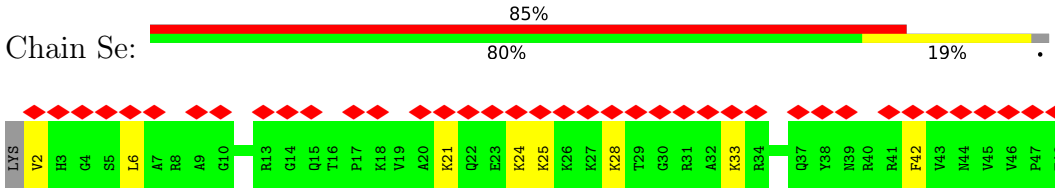
• Molecule 80: Small ribosomal subunit protein eS27

Chain Sb:



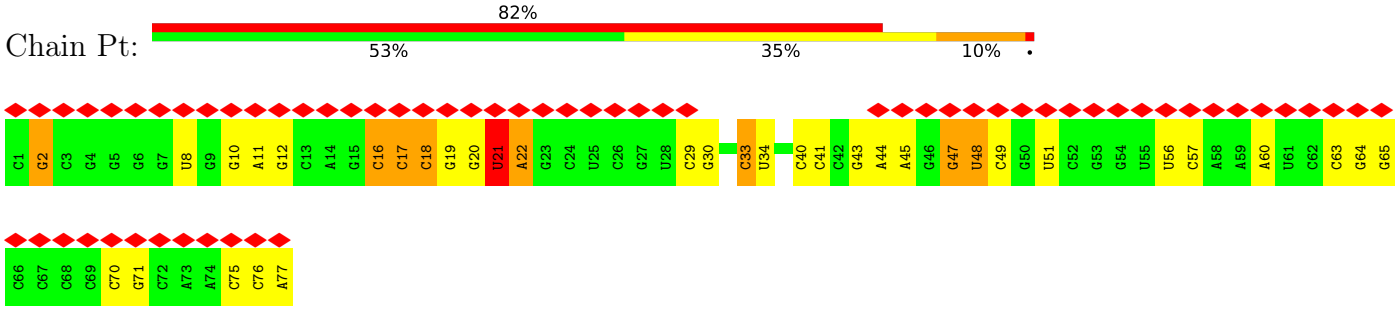
• Molecule 81: Small ribosomal subunit protein eS30

Chain Se:



• Molecule 82: P-site tRNA

Chain Pt:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	46205	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 ($e^-/Å^2$)	60	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	3.895	Depositor
Minimum map value	-1.561	Depositor
Average map value	0.009	Depositor
Map value standard deviation	0.141	Depositor
Recommended contour level	0.5	Depositor
Map size (Å)	456.0, 456.0, 456.0	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.95, 0.95, 0.95	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: OMC, G7M, H2U, A1E6S, MG, ZN, 4SU, PSU

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	L5	0.33	0/89645	0.78	54/139764 (0.0%)
2	L7	0.29	0/2858	0.70	0/4455
3	L8	0.33	0/3701	0.75	0/5766
4	LA	0.22	0/1936	0.58	0/2596
5	LB	0.19	0/3306	0.53	0/4424
6	LC	0.21	0/2973	0.57	1/3992 (0.0%)
7	LD	0.18	0/2428	0.48	0/3252
8	LE	0.22	0/1996	0.67	4/2673 (0.1%)
9	LF	0.20	0/1905	0.47	0/2539
10	LG	0.18	0/1960	0.50	1/2637 (0.0%)
11	LH	0.20	0/1537	0.54	0/2066
12	LI	0.18	0/1751	0.49	0/2340
13	LJ	0.17	0/1433	0.48	0/1915
14	LL	0.20	0/1732	0.56	2/2315 (0.1%)
15	LM	0.20	0/1161	0.59	2/1554 (0.1%)
16	LN	0.22	0/1746	0.51	0/2338
17	LO	0.19	0/1682	0.46	0/2250
18	LP	0.22	0/1268	0.55	1/1701 (0.1%)
19	LQ	0.20	0/1537	0.50	0/2052
20	LR	0.17	0/1582	0.47	0/2091
21	LS	0.40	2/1493 (0.1%)	0.67	3/2003 (0.1%)
22	LT	0.21	0/1326	0.48	0/1770
23	LU	0.18	0/839	0.53	1/1126 (0.1%)
24	LV	0.21	0/993	0.56	0/1332
25	LW	0.22	0/1030	0.63	4/1364 (0.3%)
26	LX	0.20	0/1002	0.49	0/1345
27	LY	0.22	0/1132	0.52	0/1504
28	LZ	0.17	0/1130	0.45	0/1507
29	La	0.19	0/1191	0.52	0/1591
30	Lb	0.17	0/620	0.50	0/819
31	Lc	0.20	0/774	0.50	0/1038
32	Ld	0.21	0/903	0.51	0/1216

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	Le	0.22	0/1071	0.58	1/1429 (0.1%)
34	Lf	0.20	0/895	0.52	0/1198
35	Lg	0.20	0/916	0.52	0/1220
36	Lh	0.19	0/1023	0.52	0/1351
37	Li	0.17	0/843	0.50	0/1115
38	Lj	0.21	0/720	0.56	0/952
39	Lk	0.20	0/575	0.54	0/761
40	Ll	0.18	0/454	0.49	0/599
41	Lm	0.16	0/435	0.41	0/575
42	Ln	0.17	0/231	0.54	0/294
43	Lo	0.16	0/875	0.48	0/1153
44	Lp	0.18	0/718	0.52	0/953
45	Lr	0.19	0/1017	0.59	1/1364 (0.1%)
46	Lz	0.16	0/1769	0.52	0/2371
47	S2	0.24	0/41243	0.73	26/64257 (0.0%)
48	S6	0.18	0/1795	0.61	0/2798
49	SA	0.17	0/1784	0.52	1/2424 (0.0%)
50	SB	0.20	0/1765	0.54	1/2362 (0.0%)
51	SD	0.21	0/1793	0.56	1/2414 (0.0%)
52	SE	0.18	0/2118	0.47	0/2849
53	SF	0.19	0/1531	0.58	1/2059 (0.0%)
54	SH	0.22	0/1544	0.57	0/2068
55	SI	0.17	0/1715	0.48	0/2287
56	SK	0.26	0/851	0.56	0/1147
57	SL	0.17	0/1268	0.43	0/1696
58	SP	0.20	0/815	0.63	0/1087
59	SQ	0.18	0/1177	0.50	0/1575
60	SR	0.19	0/1086	0.60	0/1457
61	SS	0.15	0/1253	0.44	0/1676
62	ST	0.16	0/1131	0.51	0/1515
63	SU	0.19	0/831	0.53	0/1115
64	SV	0.15	0/643	0.41	0/860
65	SX	0.16	0/1116	0.50	0/1490
66	Sa	0.18	0/862	0.53	1/1156 (0.1%)
67	Sc	0.20	0/508	0.56	0/680
68	Sd	0.19	0/455	0.53	0/603
69	Sf	0.18	0/593	0.55	0/786
70	Sg	0.17	0/2493	0.50	0/3394
71	SC	0.18	0/1762	0.49	0/2381
72	SG	0.18	0/1946	0.50	0/2590
73	SJ	0.16	0/1550	0.52	0/2069
74	SM	0.16	0/962	0.53	0/1290
75	SN	0.18	0/1232	0.49	1/1656 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
76	SO	0.20	0/1062	0.56	0/1425
77	SW	0.18	0/1051	0.51	0/1406
78	SY	0.21	0/1083	0.54	0/1438
79	SZ	0.13	0/604	0.45	0/810
80	Sb	0.16	0/665	0.44	0/891
81	Se	0.20	0/465	0.56	0/612
82	Pt	0.28	0/1722	0.74	0/2682
All	All	0.26	2/236586 (0.0%)	0.68	107/347675 (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
8	LE	0	1
14	LL	0	1
49	SA	0	1
70	Sg	0	1
All	All	0	4

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
21	LS	20	PRO	CG-CD	-11.18	1.12	1.50
21	LS	20	PRO	N-CD	5.97	1.56	1.47

All (107) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
21	LS	20	PRO	N-CD-CG	-13.37	83.15	103.20
21	LS	20	PRO	CA-N-CD	-11.89	95.35	112.00
1	L5	654	C	C6-N1-C2	-9.16	116.64	120.30
1	L5	486	C	C2-N1-C1'	8.11	127.72	118.80
1	L5	486	C	N1-C2-O2	8.07	123.74	118.90
1	L5	654	C	C6-N1-C1'	8.04	130.44	120.80
14	LL	54	PRO	CA-C-N	7.82	135.78	121.70
14	LL	54	PRO	C-N-CA	7.82	135.78	121.70
47	S2	694	G	O4'-C1'-N9	7.81	113.97	108.50
21	LS	20	PRO	CA-CB-CG	-7.69	89.88	104.50
1	L5	175	C	N3-C2-O2	-7.53	116.63	121.90
47	S2	1016	U	C2-N1-C1'	7.31	126.47	117.70

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Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	L5	931	C	C2-N1-C1'	7.22	126.74	118.80
1	L5	3771	C	C6-N1-C2	-7.18	117.43	120.30
51	SD	3	VAL	N-CA-C	-7.10	106.97	113.71
1	L5	5026	U	C2-N1-C1'	6.93	126.02	117.70
18	LP	91	LEU	N-CA-C	-6.86	106.11	114.75
47	S2	1022	U	C2-N1-C1'	6.59	125.61	117.70
47	S2	1453	C	C2-N1-C1'	6.53	125.98	118.80
25	LW	69	LYS	CA-C-N	6.46	133.32	121.70
25	LW	69	LYS	C-N-CA	6.46	133.32	121.70
1	L5	931	C	N1-C2-O2	6.43	122.76	118.90
47	S2	1016	U	N1-C2-O2	6.41	127.29	122.80
1	L5	1367	C	C2-N1-C1'	6.40	125.84	118.80
1	L5	1973	G	O4'-C1'-N9	6.40	112.98	108.50
1	L5	2505	C	N1-C2-O2	6.34	122.70	118.90
47	S2	1453	C	N1-C2-O2	6.30	122.68	118.90
1	L5	5026	U	N1-C2-O2	6.30	127.21	122.80
1	L5	100	C	C2-N1-C1'	6.28	125.70	118.80
47	S2	951	C	N3-C2-O2	-6.27	117.51	121.90
1	L5	486	C	N3-C2-O2	-6.25	117.53	121.90
1	L5	653	U	C6-N1-C2	-6.22	117.27	121.00
1	L5	1367	C	N1-C2-O2	6.15	122.59	118.90
49	SA	170	SER	N-CA-C	-6.12	107.04	114.75
1	L5	3771	C	C2-N1-C1'	6.07	125.48	118.80
1	L5	245	C	C2-N1-C1'	6.07	125.47	118.80
1	L5	4753	U	O5'-C5'-C4'	6.02	114.21	109.40
1	L5	417	G	O4'-C1'-N9	5.93	112.94	108.20
47	S2	124	U	N1-C1'-C2'	5.88	118.47	112.00
47	S2	128	U	O5'-C5'-C4'	5.88	114.10	109.40
1	L5	654	C	N1-C2-N3	5.82	123.28	119.20
47	S2	72	C	O5'-C5'-C4'	5.80	114.04	109.40
75	SN	102	LEU	N-CA-C	-5.80	107.44	114.75
47	S2	1117	C	C2-N1-C1'	5.80	125.18	118.80
1	L5	486	C	C6-N1-C1'	-5.75	113.90	120.80
47	S2	1287	A	O4'-C1'-N9	-5.74	104.48	108.50
1	L5	5026	U	N3-C2-O2	-5.71	118.20	122.20
47	S2	123	G	N3-C4-N9	5.70	129.42	126.00
53	SF	41	VAL	N-CA-C	-5.70	107.73	113.20
25	LW	98	PRO	CA-C-N	5.69	131.95	121.70
25	LW	98	PRO	C-N-CA	5.69	131.95	121.70
47	S2	951	C	C2-N3-C4	-5.67	117.06	119.90
1	L5	4749	C	C2-N1-C1'	5.65	125.01	118.80
1	L5	2054	U	O5'-C5'-C4'	5.64	113.91	109.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	L5	1072	C	C2-N1-C1'	5.61	124.97	118.80
1	L5	654	C	C2-N1-C1'	-5.58	112.66	118.80
45	Lr	100	ASN	N-CA-C	-5.58	107.72	114.75
6	LC	268	ARG	CA-CB-CG	5.57	125.23	114.10
1	L5	245	C	N1-C2-O2	5.56	122.24	118.90
1	L5	653	U	N3-C4-C5	-5.54	111.27	114.60
47	S2	1172	U	C2-N1-C1'	5.53	124.33	117.70
1	L5	2859	G	O4'-C1'-N9	5.53	112.62	108.20
47	S2	647	U	C2-N1-C1'	5.51	124.31	117.70
1	L5	18	C	N1-C2-O2	5.49	122.19	118.90
1	L5	175	C	N1-C2-O2	5.45	122.17	118.90
1	L5	4976	U	O5'-C5'-C4'	5.43	113.75	109.40
1	L5	653	U	O5'-C5'-C4'	5.40	113.72	109.40
47	S2	1016	U	N3-C2-O2	-5.40	118.42	122.20
1	L5	3771	C	C5-C6-N1	5.39	123.70	121.00
47	S2	1118	C	C2-N1-C1'	5.37	124.70	118.80
47	S2	1520	G	C4-N9-C1'	5.36	133.46	126.50
1	L5	2855	G	O5'-C5'-C4'	5.34	113.67	109.40
23	LU	67	LYS	CB-CA-C	-5.33	110.45	116.63
1	L5	2410	C	C2-N1-C1'	5.32	124.65	118.80
1	L5	4946	U	C2-N1-C1'	5.32	124.08	117.70
33	Le	45	VAL	N-CA-C	-5.32	107.24	111.81
47	S2	338	G	N1-C6-O6	-5.31	116.71	119.90
66	Sa	101	PHE	CB-CA-C	-5.30	110.03	117.23
15	LM	95	ILE	CA-C-N	5.28	131.62	121.54
15	LM	95	ILE	C-N-CA	5.28	131.62	121.54
1	L5	1654	G	O5'-C5'-C4'	5.26	113.61	109.40
1	L5	18	C	N3-C2-O2	-5.23	118.24	121.90
50	SB	36	PRO	CA-N-CD	-5.19	104.74	112.00
1	L5	4946	U	N3-C2-O2	-5.17	118.58	122.20
1	L5	4946	U	N1-C2-O2	5.17	126.42	122.80
47	S2	1453	C	N3-C2-O2	-5.16	118.29	121.90
1	L5	2361	G	P-O3'-C3'	5.16	125.89	119.70
1	L5	2119	C	P-O3'-C3'	5.16	125.89	119.70
1	L5	1367	C	N3-C2-O2	-5.15	118.30	121.90
47	S2	624	C	N1-C2-O2	5.13	121.98	118.90
8	LE	83	LYS	CA-C-N	5.12	130.91	121.70
8	LE	83	LYS	C-N-CA	5.12	130.91	121.70
47	S2	125	C	N3-C4-N4	-5.12	114.42	118.00
8	LE	96	VAL	CA-C-N	5.10	130.88	121.70
8	LE	96	VAL	C-N-CA	5.10	130.88	121.70
1	L5	931	C	C6-N1-C1'	-5.09	114.69	120.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
10	LG	165	GLU	N-CA-C	-5.07	108.36	114.75
1	L5	655	C	N1-C2-O2	5.07	121.94	118.90
1	L5	238	C	O5'-C5'-C4'	5.07	113.45	109.40
1	L5	4930	C	N1-C2-O2	5.06	121.94	118.90
47	S2	338	G	C5-C6-O6	5.04	131.62	128.60
1	L5	2505	C	N3-C2-O2	-5.04	118.38	121.90
1	L5	4447	C	C6-N1-C1'	5.03	126.84	120.80
1	L5	1097	C	C2-N3-C4	-5.02	117.39	119.90
1	L5	1238	A	P-O3'-C3'	5.02	125.72	119.70
47	S2	1057	C	C2-N1-C1'	5.02	124.32	118.80
47	S2	951	C	N1-C2-N3	5.00	122.70	119.20

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
8	LE	224	LYS	Peptide
14	LL	66	TYR	Peptide
49	SA	31	ASP	Peptide
70	Sg	54	ILE	Peptide

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	L5	80184	0	40395	1068	0
2	L7	2558	0	1296	15	0
3	L8	3314	0	1683	37	0
4	LA	1898	0	1993	39	0
5	LB	3238	0	3376	52	0
6	LC	2919	0	3092	65	0
7	LD	2382	0	2410	51	0
8	LE	1958	0	2126	57	0
9	LF	1870	0	1996	43	0
10	LG	1927	0	2074	28	0
11	LH	1518	0	1601	26	0
12	LI	1711	0	1748	35	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	LJ	1410	0	1441	39	0
14	LL	1701	0	1818	32	0
15	LM	1138	0	1204	30	0
16	LN	1701	0	1749	29	0
17	LO	1650	0	1794	24	0
18	LP	1242	0	1269	12	0
19	LQ	1513	0	1628	19	0
20	LR	1566	0	1729	30	0
21	LS	1453	0	1490	31	0
22	LT	1298	0	1366	17	0
23	LU	825	0	850	17	0
24	LV	979	0	1039	16	0
25	LW	1015	0	1079	32	0
26	LX	985	0	1066	23	0
27	LY	1115	0	1205	20	0
28	LZ	1107	0	1182	19	0
29	La	1162	0	1213	24	0
30	Lb	610	0	650	9	0
31	Lc	764	0	804	11	0
32	Ld	888	0	930	14	0
33	Le	1053	0	1147	23	0
34	Lf	876	0	912	23	0
35	Lg	906	0	1000	17	0
36	Lh	1015	0	1148	19	0
37	Li	832	0	917	13	0
38	Lj	705	0	738	23	0
39	Lk	569	0	637	14	0
40	Ll	444	0	483	6	0
41	Lm	429	0	466	13	0
42	Ln	230	0	276	0	0
43	Lo	862	0	931	17	0
44	Lp	708	0	756	9	0
45	Lr	1002	0	1068	19	0
46	Lz	1741	0	1854	52	0
47	S2	36900	0	18595	617	0
48	S6	1604	0	816	32	0
49	SA	1747	0	1751	45	0
50	SB	1738	0	1809	63	0
51	SD	1765	0	1865	60	0
52	SE	2076	0	2177	53	0
53	SF	1509	0	1563	72	0
54	SH	1521	0	1616	61	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
55	SI	1686	0	1772	51	0
56	SK	827	0	854	34	0
57	SL	1247	0	1323	28	0
58	SP	804	0	841	37	0
59	SQ	1158	0	1232	34	0
60	SR	1072	0	1130	39	0
61	SS	1235	0	1309	46	0
62	ST	1112	0	1146	26	0
63	SU	821	0	883	29	0
64	SV	636	0	637	14	0
65	SX	1098	0	1167	29	0
66	Sa	847	0	894	17	0
67	Sc	506	0	536	13	0
68	Sd	445	0	442	21	0
69	Sf	581	0	597	20	0
70	Sg	2436	0	2393	86	0
71	SC	1725	0	1813	46	0
72	SG	1923	0	2089	68	0
73	SJ	1525	0	1640	47	0
74	SM	952	0	983	21	0
75	SN	1208	0	1294	34	0
76	SO	1049	0	1073	48	0
77	SW	1034	0	1080	30	0
78	SY	1065	0	1142	36	0
79	SZ	598	0	656	19	0
80	Sb	651	0	672	16	0
81	Se	459	0	503	9	0
82	Pt	1646	0	842	20	0
83	L5	146	0	0	0	0
83	L7	7	0	0	0	0
83	L8	5	0	0	0	0
83	LA	1	0	0	0	0
83	LH	1	0	0	0	0
83	LN	1	0	0	0	0
83	LP	1	0	0	0	0
83	LQ	1	0	0	0	0
83	LV	1	0	0	0	0
83	Le	1	0	0	0	0
83	Ll	1	0	0	0	0
83	S2	66	0	0	0	0
83	S6	7	0	0	0	0
84	L5	29	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
85	Lg	1	0	0	0	0
85	Lj	1	0	0	0	0
85	Lm	1	0	0	0	0
85	Lo	1	0	0	0	0
85	Lp	1	0	0	0	0
85	Sa	1	0	0	0	0
All	All	220451	0	162764	3588	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 10.

All (3588) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:184:U:H3	1:L5:253:G:H1	1.04	1.02
25:LW:69:LYS:H	25:LW:70:LYS:HB2	1.23	0.99
1:L5:2552:G:H21	1:L5:2765:A:H62	1.01	0.96
48:S6:11:G:H1	48:S6:25:U:H3	1.04	0.94
7:LD:104:LEU:HB2	7:LD:247:ILE:HD11	1.49	0.94
1:L5:3710:G:N2	1:L5:3741:C:N3	2.18	0.92
35:Lg:60:ARG:HD3	35:Lg:61:PRO:HD2	1.54	0.90
70:Sg:170:TRP:HB2	70:Sg:194:TYR:HB2	1.53	0.90
47:S2:321:C:O2	47:S2:330:G:N2	2.05	0.89
1:L5:1985:G:H1	1:L5:2013:A:H62	1.20	0.88
1:L5:2638:G:H1	1:L5:2697:A:H61	1.18	0.87
1:L5:751:G:H22	1:L5:912:G:H1	1.21	0.87
1:L5:4768:G:H5'	17:LO:176:ARG:HD3	1.55	0.87
76:SO:14:VAL:H	76:SO:15:ILE:HA	1.41	0.85
1:L5:2552:G:N2	1:L5:2765:A:H62	1.75	0.84
7:LD:4:VAL:HG12	7:LD:5:LYS:H	1.41	0.84
1:L5:957:G:N2	1:L5:959:G:O6	2.09	0.84
47:S2:1398:G:H1	47:S2:1448:A:H2	1.25	0.84
47:S2:506:G:OP1	78:SY:108:LYS:NZ	2.11	0.84
54:SH:144:ILE:HG23	77:SW:52:ILE:HG23	1.59	0.84
1:L5:1234:G:H2'	1:L5:1235:G:H8	1.42	0.84
6:LC:358:ALA:HA	6:LC:361:LEU:HB3	1.60	0.83
1:L5:4748:U:H3	1:L5:4952:G:H1	1.26	0.83
61:SS:142:ARG:HE	61:SS:143:GLY:H	1.26	0.83
1:L5:1077:C:N3	1:L5:1234:G:N2	2.28	0.82
1:L5:1405:C:N3	1:L5:1412:G:N1	2.27	0.81
1:L5:4947:U:HO2'	34:Lf:2:SER:N	1.77	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:1405:C:O2	1:L5:1412:G:N2	2.13	0.81
47:S2:114:G:HO2'	47:S2:382:C:HO2'	1.28	0.80
71:SC:183:LYS:HG3	71:SC:196:ILE:HG22	1.63	0.80
76:SO:57:THR:H	76:SO:60:MET:HE3	1.45	0.80
65:SX:51:VAL:HA	65:SX:72:VAL:HG12	1.61	0.80
1:L5:3942:A:H61	1:L5:4071:U:H3	1.27	0.79
1:L5:4076:G:OP1	10:LG:73:ARG:NH1	2.16	0.79
56:SK:24:LYS:O	56:SK:42:ASN:ND2	2.15	0.79
76:SO:61:LYS:HZ1	76:SO:80:ASP:HB2	1.48	0.79
81:Se:28:LYS:O	81:Se:33:LYS:NZ	2.14	0.79
1:L5:418:A:OP2	3:L8:16:G:N2	2.17	0.78
1:L5:2552:G:H21	1:L5:2765:A:N6	1.81	0.78
51:SD:99:ILE:HG23	51:SD:173:ARG:HH21	1.47	0.78
55:SI:48:VAL:HG11	55:SI:54:LYS:HD3	1.65	0.78
1:L5:2114:G:O2'	1:L5:2115:G:N7	2.16	0.78
65:SX:68:LYS:HG2	65:SX:91:LEU:HD22	1.64	0.78
1:L5:4047:A:N6	48:S6:56:C:H42	1.80	0.78
14:LL:54:PRO:HA	14:LL:55:ILE:HG22	1.64	0.78
24:LV:111:GLU:OE1	24:LV:131:ARG:NH1	2.17	0.78
47:S2:694:G:N7	47:S2:696:G:N2	2.31	0.78
50:SB:24:PRO:O	50:SB:28:LYS:NZ	2.17	0.78
55:SI:57:ALA:HB1	55:SI:60:LEU:HD11	1.65	0.78
1:L5:159:C:H5'	37:Li:25:ARG:HH21	1.49	0.78
47:S2:1508:A:N6	47:S2:1510:G:O6	2.17	0.78
47:S2:535:G:H22	47:S2:548:C:H42	1.31	0.78
1:L5:4047:A:N6	48:S6:56:C:N4	2.32	0.77
11:LH:41:ILE:HG12	11:LH:73:ILE:HD11	1.66	0.77
47:S2:594:A:H4'	47:S2:595:U:H5'	1.66	0.77
47:S2:1563:G:N2	47:S2:1572:C:O2	2.14	0.77
15:LM:95:ILE:O	15:LM:96:GLU:HG3	1.84	0.77
6:LC:65:GLU:HB2	6:LC:80:ARG:HD2	1.66	0.76
53:SF:63:LYS:HE2	53:SF:71:ARG:HH12	1.49	0.76
1:L5:1242:G:H1	1:L5:1269:G:H21	1.34	0.76
53:SF:95:HIS:HD2	79:SZ:106:GLN:HE21	1.31	0.76
1:L5:1218:G:H2'	1:L5:1219:G:H4'	1.66	0.76
1:L5:1351:G:OP1	6:LC:33:ARG:NH1	2.19	0.76
70:Sg:173:LEU:HD22	70:Sg:189:ILE:HA	1.68	0.76
5:LB:305:THR:HG22	5:LB:307:TYR:H	1.51	0.76
70:Sg:106:LYS:HB2	70:Sg:126:ASP:HB3	1.68	0.75
47:S2:1222:G:H5"	53:SF:78:MET:HE1	1.68	0.75
21:LS:30:MET:HE3	21:LS:32:ILE:HD11	1.68	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:SE:139:LEU:HD23	52:SE:150:PRO:HB3	1.68	0.75
1:L5:1740:C:O2	1:L5:1786:A:N6	2.19	0.75
32:Ld:93:ASN:ND2	32:Ld:100:ASN:O	2.18	0.75
49:SA:205:ARG:HB2	49:SA:210:ILE:HG21	1.67	0.75
53:SF:18:LYS:HG2	53:SF:46:ALA:HB3	1.68	0.75
11:LH:7:ASN:HD21	11:LH:56:ARG:HD2	1.52	0.75
47:S2:150:A:OP2	47:S2:151:C:N4	2.17	0.75
71:SC:202:THR:OG1	71:SC:221:ASP:OD2	2.03	0.75
1:L5:1370:G:H4'	1:L5:1371:A:H5'	1.68	0.75
3:L8:102:G:H4'	38:Lj:21:ARG:HG2	1.69	0.75
10:LG:205:THR:HG22	10:LG:206:GLN:H	1.50	0.75
33:Le:66:THR:HA	33:Le:69:MET:HE3	1.67	0.75
47:S2:331:C:N4	72:SG:186:GLN:OE1	2.20	0.75
1:L5:708:G:N2	1:L5:1289:C:O2	2.14	0.75
70:Sg:18:VAL:HA	70:Sg:35:SER:HA	1.68	0.75
1:L5:728:U:H5"	9:LF:76:ARG:HD2	1.67	0.74
25:LW:82:ILE:HG21	72:SG:130:PRO:HG2	1.69	0.74
47:S2:1858:G:OP2	76:SO:146:ARG:NH2	2.20	0.74
1:L5:1866:U:O2'	1:L5:1867:A:O5'	2.04	0.74
8:LE:66:LYS:NZ	8:LE:68:MET:SD	2.60	0.74
47:S2:745:C:H5'	54:SH:107:LYS:HG2	1.69	0.74
70:Sg:230:LEU:HB3	70:Sg:259:TRP:HZ3	1.52	0.74
1:L5:6:C:O2	3:L8:151:G:N2	2.15	0.74
1:L5:1963:C:H2'	1:L5:1964:A:H8	1.50	0.74
1:L5:4894:A:OP1	15:LM:125:ASN:ND2	2.19	0.74
18:LP:23:ARG:NH1	18:LP:125:MET:SD	2.60	0.74
7:LD:177:THR:O	7:LD:179:ARG:N	2.21	0.74
7:LD:261:VAL:HG12	7:LD:263:LYS:H	1.52	0.74
22:LT:142:ARG:NH1	22:LT:143:THR:O	2.20	0.74
13:LJ:56:THR:HB	13:LJ:57:VAL:HG22	1.69	0.74
1:L5:455:C:N3	33:Le:5:ARG:NH1	2.35	0.74
23:LU:40:GLU:O	23:LU:44:GLN:NE2	2.20	0.74
72:SG:3:LEU:HD13	72:SG:5:ILE:HG13	1.66	0.74
2:L7:7:G:OP1	7:LD:33:ARG:NH1	2.20	0.74
47:S2:122:G:OP1	52:SE:75:LYS:NZ	2.19	0.74
53:SF:45:TYR:H	53:SF:46:ALA:HA	1.52	0.74
47:S2:311:C:H4'	47:S2:339:A:H4'	1.70	0.73
61:SS:6:PRO:HG2	61:SS:58:GLU:HB2	1.70	0.73
75:SN:30:SER:HB2	75:SN:67:THR:HG22	1.70	0.73
12:LI:190:LEU:HD13	12:LI:197:VAL:HG21	1.70	0.73
1:L5:126:C:H42	1:L5:142:G:H1	1.34	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:1371:A:N6	3:L8:28:C:O2'	2.21	0.73
1:L5:4635:A:H2	1:L5:4663:G:H21	1.35	0.73
1:L5:4906:C:H2'	1:L5:4907:G:H8	1.54	0.73
17:LO:193:THR:HG22	17:LO:197:LYS:HE2	1.70	0.73
47:S2:384:U:O4	55:SI:5:ARG:NH2	2.22	0.73
1:L5:517:C:H41	1:L5:645:G:H21	1.35	0.73
1:L5:1176:C:N3	1:L5:1183:C:N4	2.36	0.73
1:L5:1763:C:N4	1:L5:1769:G:O6	2.20	0.73
47:S2:150:A:N7	47:S2:168:C:N4	2.35	0.73
47:S2:1024:A:OP2	75:SN:124:ARG:NH2	2.22	0.73
58:SP:40:ARG:HE	58:SP:84:ILE:HG22	1.53	0.73
47:S2:691:G:H3'	47:S2:692:G:H5"	1.70	0.73
61:SS:30:ILE:HG22	61:SS:36:VAL:HG11	1.71	0.73
65:SX:55:VAL:HG11	81:Se:2:VAL:HG22	1.70	0.73
1:L5:3706:C:O2'	4:LA:239:ALA:O	2.07	0.72
1:L5:746:A:H61	1:L5:915:A:H3'	1.53	0.72
1:L5:4992:G:H2'	1:L5:4993:G:C8	2.24	0.72
4:LA:29:LEU:O	4:LA:123:ARG:NH1	2.22	0.72
4:LA:150:LEU:HD12	4:LA:151:PRO:HD2	1.71	0.72
44:Lp:42:CYS:SG	44:Lp:59:SER:OG	2.47	0.72
53:SF:71:ARG:NH2	53:SF:148:ASN:OD1	2.23	0.72
19:LQ:12:LYS:HB2	19:LQ:14:ARG:HH11	1.55	0.72
52:SE:56:LEU:HD23	52:SE:57:THR:HG23	1.69	0.72
8:LE:96:VAL:N	8:LE:97:GLY:HA2	2.04	0.72
1:L5:1985:G:N2	1:L5:2005:G:O6	2.23	0.72
22:LT:43:LYS:O	22:LT:58:HIS:ND1	2.21	0.72
61:SS:25:LYS:HA	61:SS:55:ARG:HA	1.72	0.72
1:L5:966:A:N6	1:L5:2253:A:OP2	2.22	0.72
1:L5:2119:C:H4'	1:L5:2120:G:H4'	1.71	0.72
1:L5:2578:G:N7	28:LZ:17:ARG:NH1	2.37	0.72
1:L5:453:G:H1	1:L5:1294:A:H8	1.35	0.72
1:L5:3717:A:H2'	1:L5:3718:A:C8	2.25	0.72
47:S2:1786:U:N3	47:S2:1787:G:N7	2.38	0.72
1:L5:2559:G:H1	1:L5:2568:C:H42	1.38	0.71
3:L8:85:U:H2'	3:L8:86:U:H4'	1.73	0.71
50:SB:125:VAL:HG21	50:SB:172:MET:HG3	1.72	0.71
54:SH:104:PRO:HB3	54:SH:107:LYS:HB2	1.72	0.71
1:L5:2789:A:O2'	40:Ll:45:ARG:NH2	2.22	0.71
7:LD:51:MET:HE3	7:LD:105:LEU:HD23	1.73	0.71
49:SA:205:ARG:NH1	49:SA:214:GLU:OE2	2.22	0.71
1:L5:2901:G:N7	1:L5:2902:G:N2	2.38	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:S2:1274:G:H21	69:Sf:97:LYS:HE2	1.55	0.71
54:SH:63:PHE:HA	54:SH:95:ILE:O	1.90	0.71
7:LD:209:ARG:NH1	7:LD:234:ASP:OD2	2.23	0.71
1:L5:4939:C:OP1	8:LE:156:ARG:NH1	2.21	0.71
47:S2:30:C:O2'	47:S2:596:U:OP1	2.07	0.71
47:S2:122:G:H4'	52:SE:145:ARG:HG3	1.73	0.71
47:S2:1387:G:N2	51:SD:206:ASP:OD1	2.24	0.71
49:SA:38:ILE:HD11	49:SA:47:TYR:HB3	1.72	0.71
47:S2:363:A:N6	47:S2:400:C:O2'	2.24	0.71
82:Pt:51:U:H3	82:Pt:65:G:H1	1.37	0.71
1:L5:268:G:H2'	1:L5:269:G:H8	1.56	0.71
13:LJ:164:ARG:O	13:LJ:168:GLN:NE2	2.24	0.71
52:SE:205:PHE:HE2	52:SE:221:ARG:HB3	1.54	0.71
47:S2:1823:A:OP1	65:SX:60:LYS:NZ	2.23	0.70
73:SJ:83:ARG:CZ	73:SJ:150:ARG:HD3	2.20	0.70
51:SD:7:LYS:HD3	51:SD:10:LYS:HE3	1.73	0.70
58:SP:104:GLN:HG2	58:SP:105:VAL:HG23	1.73	0.70
78:SY:23:MET:HB2	78:SY:73:GLY:HA3	1.72	0.70
60:SR:107:LYS:HA	60:SR:110:ASP:HB3	1.73	0.70
1:L5:2845:A:H61	1:L5:3843:C:H42	1.36	0.70
48:S6:51:U:H3	48:S6:63:A:H61	1.37	0.70
13:LJ:43:LEU:HB2	13:LJ:117:ILE:HD11	1.74	0.70
13:LJ:46:GLN:HE22	13:LJ:72:CYS:HB2	1.55	0.70
45:Lr:26:SER:OG	45:Lr:28:GLU:OE1	2.06	0.70
52:SE:18:TRP:HB3	52:SE:20:LEU:HD23	1.73	0.70
1:L5:1208:G:N2	9:LF:74:MET:SD	2.64	0.70
1:L5:2555:G:H22	1:L5:2572:C:H42	1.40	0.70
47:S2:1373:C:H5'	60:SR:7:LYS:HE3	1.74	0.70
47:S2:1468:C:H2'	47:S2:1469:A:C8	2.25	0.70
1:L5:509:A:N6	29:La:102:ASP:O	2.25	0.70
47:S2:980:A:H2'	47:S2:981:A:C8	2.27	0.70
47:S2:1199:A:OP1	66:Sa:2:THR:OG1	2.10	0.70
47:S2:1398:G:O6	47:S2:1448:A:N1	2.25	0.70
47:S2:1749:G:N2	47:S2:1786:U:O2	2.25	0.70
76:SO:147:ARG:HD2	76:SO:150:ARG:HD3	1.72	0.70
75:SN:16:LEU:HD12	75:SN:17:PRO:HD2	1.73	0.70
1:L5:472:C:H42	1:L5:682:G:H22	1.37	0.70
1:L5:2758:G:O2'	1:L5:2764:A:N3	2.21	0.70
29:La:72:THR:HG22	29:La:110:LYS:HB3	1.72	0.70
47:S2:1658:G:OP2	47:S2:1660:C:N4	2.25	0.70
53:SF:123:GLU:HG3	53:SF:200:ALA:HB2	1.74	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:SK:32:HIS:H	56:SK:41:PRO:HA	1.55	0.70
1:L5:218:A:N1	6:LC:181:LYS:NZ	2.38	0.69
3:L8:115:G:N2	3:L8:135:C:O2	2.20	0.69
15:LM:123:ILE:HD11	17:LO:189:ILE:HD13	1.73	0.69
62:ST:12:GLN:O	62:ST:16:ARG:NH1	2.25	0.69
1:L5:2638:G:N2	1:L5:2697:A:N1	2.29	0.69
1:L5:4933:C:H2'	1:L5:4934:A:C8	2.26	0.69
1:L5:2256:C:OP1	9:LF:32:ARG:NH1	2.24	0.69
47:S2:1285:G:N2	74:SM:87:GLU:OE2	2.25	0.69
1:L5:4730:C:OP2	1:L5:4965:U:O2'	2.10	0.69
1:L5:1436:C:H5"	1:L5:2119:C:H42	1.57	0.69
1:L5:4369:A:H5"	43:Lo:65:LYS:HD2	1.72	0.69
37:Li:45:ARG:NH1	37:Li:49:GLY:O	2.23	0.69
1:L5:2003:G:H1'	1:L5:2004:U:H5	1.57	0.69
1:L5:4966:A:OP1	5:LB:128:LYS:NZ	2.21	0.69
25:LW:69:LYS:N	25:LW:70:LYS:HB2	2.03	0.69
76:SO:34:PHE:HB3	76:SO:41:PHE:HB2	1.75	0.69
1:L5:1178:G:H4'	7:LD:289:ARG:HE	1.58	0.69
7:LD:20:PHE:O	7:LD:22:ARG:N	2.26	0.69
61:SS:44:VAL:HG13	61:SS:70:ILE:HG13	1.75	0.69
1:L5:128:C:O2	1:L5:140:G:N2	2.19	0.69
1:L5:917:A:O4'	1:L5:918:G:N2	2.26	0.69
47:S2:1605:G:OP1	62:ST:84:ARG:NH1	2.25	0.69
5:LB:57:VAL:HG22	5:LB:73:VAL:HG12	1.73	0.69
27:LY:2:LYS:HD2	27:LY:7:VAL:HG23	1.74	0.69
47:S2:338:G:N7	47:S2:339:A:N6	2.41	0.69
47:S2:1753:C:O2'	47:S2:1780:G:N2	2.25	0.69
68:Sd:7:TYR:HE1	69:Sf:146:LEU:HB3	1.57	0.69
24:LV:87:SER:OG	25:LW:19:ARG:NH2	2.25	0.69
47:S2:220:U:O4	47:S2:221:A:N6	2.25	0.69
1:L5:237:G:O2'	1:L5:238:C:OP1	2.12	0.68
1:L5:4047:A:H62	48:S6:56:C:N4	1.89	0.68
46:Lz:142:GLU:HG2	46:Lz:144:MET:HG2	1.74	0.68
50:SB:107:ARG:NH1	76:SO:133:THR:O	2.25	0.68
67:Sc:44:ARG:HA	67:Sc:65:ALA:HB3	1.73	0.68
3:L8:5:U:OP2	18:LP:62:ARG:NH1	2.26	0.68
50:SB:122:GLU:O	50:SB:165:ARG:NH1	2.26	0.68
63:SU:17:ILE:HG12	63:SU:94:PRO:HB3	1.75	0.68
12:LI:80:CYS:SG	12:LI:144:ASN:ND2	2.66	0.68
47:S2:852:G:N2	47:S2:852:G:OP2	2.26	0.68
1:L5:712:C:H42	1:L5:956:A:H61	1.41	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:2416:G:N2	1:L5:2427:G:N7	2.38	0.68
2:L7:39:C:O2'	13:LJ:46:GLN:OE1	2.08	0.68
47:S2:317:C:H2'	47:S2:318:A:H8	1.58	0.68
50:SB:88:THR:OG1	50:SB:96:CYS:SG	2.50	0.68
13:LJ:86:GLY:HA3	13:LJ:130:PHE:HE2	1.58	0.68
1:L5:2669:C:O2'	1:L5:2670:C:O5'	2.12	0.68
1:L5:4905:C:H2'	1:L5:4906:C:C6	2.29	0.68
5:LB:83:PRO:O	5:LB:167:GLN:NE2	2.26	0.68
11:LH:92:MET:HE3	11:LH:158:ALA:HB1	1.74	0.68
5:LB:92:TYR:HB2	5:LB:159:VAL:HG13	1.75	0.68
1:L5:1661:C:O2'	33:Le:36:ARG:NH1	2.27	0.68
1:L5:2601:A:N6	1:L5:2744:A:OP2	2.27	0.68
33:Le:19:LYS:HD3	33:Le:33:ARG:HH12	1.59	0.68
1:L5:1921:C:O2	21:LS:160:ARG:NE	2.25	0.68
1:L5:4419:U:OP1	1:L5:4421:C:N4	2.27	0.68
11:LH:110:SER:OG	11:LH:127:ARG:NH1	2.24	0.68
58:SP:44:ARG:HH22	58:SP:53:GLN:HE22	1.41	0.68
61:SS:26:ILE:HD11	61:SS:52:LEU:HA	1.75	0.68
1:L5:165:A:H61	1:L5:270:U:H3	1.41	0.68
76:SO:67:ASP:O	76:SO:69:SER:N	2.27	0.68
1:L5:2898:G:OP2	20:LR:135:LYS:NZ	2.26	0.67
5:LB:10:ARG:NH1	5:LB:11:HIS:O	2.27	0.67
47:S2:1122:A:H4'	50:SB:205:TYR:CD1	2.29	0.67
53:SF:127:ARG:HB3	53:SF:137:GLN:HB2	1.76	0.67
59:SQ:62:ARG:O	59:SQ:96:TYR:OH	2.12	0.67
1:L5:2098:G:O3'	1:L5:2259:G:N2	2.27	0.67
1:L5:2117:G:H4'	9:LF:49:LEU:HD22	1.77	0.67
1:L5:2478:C:H2'	1:L5:2479:G:H8	1.58	0.67
1:L5:1925:G:OP1	15:LM:33:GLN:NE2	2.21	0.67
3:L8:96:C:H5"	36:Lh:66:LYS:HD2	1.77	0.67
47:S2:345:U:OP1	52:SE:37:LYS:NZ	2.26	0.67
56:SK:4:PRO:HD2	56:SK:8:ARG:HE	1.59	0.67
1:L5:1301:C:H2'	33:Le:17:THR:HG21	1.75	0.67
1:L5:3598:C:H2'	1:L5:3599:A:H8	1.59	0.67
1:L5:4047:A:N7	48:S6:56:C:C4	2.61	0.67
21:LS:95:ARG:NH1	21:LS:112:ASP:OD2	2.27	0.67
53:SF:186:ASN:OD1	53:SF:187:SER:N	2.27	0.67
65:SX:53:GLU:HB2	65:SX:71:ARG:HG2	1.75	0.67
47:S2:981:A:H2'	47:S2:982:G:C8	2.29	0.67
75:SN:35:GLU:HB3	75:SN:39:LYS:NZ	2.10	0.67
1:L5:2562:G:N2	1:L5:2565:A:OP2	2.27	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:LC:319:LEU:H	6:LC:325:MET:HE2	1.60	0.67
47:S2:1353:A:OP1	49:SA:139:TYR:OH	2.11	0.67
60:SR:126:MET:HB2	60:SR:128:PHE:HD1	1.58	0.67
64:SV:1:MET:HE1	71:SC:168:GLY:HA2	1.77	0.67
73:SJ:37:LEU:HD11	73:SJ:106:LEU:HD11	1.76	0.67
47:S2:1287:A:C5	47:S2:1314:U:C4	2.82	0.67
66:Sa:4:LYS:HG2	66:Sa:5:ARG:HG3	1.77	0.67
74:SM:17:ALA:HB1	74:SM:124:ILE:HG21	1.76	0.67
70:Sg:147:HIS:HE1	70:Sg:173:LEU:HB2	1.59	0.67
72:SG:205:GLU:HA	72:SG:208:GLU:HG2	1.77	0.67
1:L5:2583:C:N4	35:Lg:75:SER:OG	2.28	0.67
47:S2:127:C:H1'	47:S2:129:C:H5'	1.76	0.67
47:S2:1707:U:O2'	47:S2:1849:G:N2	2.28	0.67
47:S2:1778:C:H2'	47:S2:1779:G:C8	2.29	0.67
1:L5:3625:G:O2'	1:L5:3626:G:OP1	2.13	0.66
48:S6:11:G:N2	48:S6:25:U:O2	2.26	0.66
51:SD:61:GLU:HG2	51:SD:64:ARG:HB3	1.77	0.66
55:SI:81:VAL:HG22	55:SI:102:VAL:HG12	1.77	0.66
1:L5:4949:G:N2	1:L5:4950:U:H2'	2.10	0.66
16:LN:96:ARG:NH2	16:LN:104:GLU:OE1	2.27	0.66
61:SS:31:THR:HA	61:SS:36:VAL:HG13	1.76	0.66
1:L5:471:A:N6	1:L5:683:C:O2	2.19	0.66
47:S2:1348:G:H22	47:S2:1381:G:H22	1.42	0.66
53:SF:134:VAL:HG12	53:SF:135:ARG:HG2	1.77	0.66
69:Sf:88:PRO:O	69:Sf:91:ASN:ND2	2.28	0.66
15:LM:70:GLN:O	15:LM:72:TYR:N	2.28	0.66
46:Lz:56:LYS:HG2	46:Lz:152:LYS:HD3	1.78	0.66
82:Pt:29:C:H2'	82:Pt:30:G:H8	1.61	0.66
76:SO:61:LYS:NZ	76:SO:80:ASP:HB2	2.09	0.66
1:L5:4635:A:H8	1:L5:5048:A:H61	1.43	0.66
51:SD:153:VAL:HG22	51:SD:154:ASP:H	1.59	0.66
66:Sa:62:TYR:OH	76:SO:128:ARG:O	2.07	0.66
1:L5:4043:G:OP2	1:L5:4045:G:N2	2.29	0.66
25:LW:98:PRO:HA	25:LW:99:GLU:HB3	1.77	0.66
47:S2:1091:C:HO2'	77:SW:2:VAL:N	1.93	0.66
1:L5:1186:U:H2'	1:L5:1187:G:C8	2.30	0.66
49:SA:88:LEU:HD23	49:SA:98:PRO:HB2	1.77	0.66
72:SG:171:THR:HG22	72:SG:172:LYS:H	1.61	0.66
1:L5:2090:U:N3	1:L5:2262:G:N7	2.43	0.66
52:SE:11:ARG:HH21	52:SE:20:LEU:HB3	1.60	0.66
1:L5:1242:G:O6	1:L5:1268:G:N2	2.27	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:LH:7:ASN:ND2	11:LH:56:ARG:HD2	2.11	0.66
43:Lo:44:LYS:HE3	43:Lo:52:THR:HB	1.78	0.66
1:L5:1485:C:O2	1:L5:4349:C:O2'	2.14	0.65
5:LB:94:GLU:HG2	5:LB:158:GLN:HE21	1.60	0.65
76:SO:126:ILE:HG22	76:SO:127:GLY:H	1.61	0.65
77:SW:27:ILE:HG12	77:SW:61:ILE:HB	1.77	0.65
1:L5:994:G:N2	1:L5:1049:C:O2	2.29	0.65
47:S2:1253:A:OP2	47:S2:1526:G:N2	2.24	0.65
47:S2:1623:A:H62	61:SS:132:ARG:HH21	1.44	0.65
52:SE:72:ILE:HB	52:SE:77:ARG:HG3	1.79	0.65
1:L5:188:G:N2	1:L5:190:G:N7	2.44	0.65
5:LB:213:GLN:HE22	5:LB:286:LYS:HA	1.62	0.65
16:LN:150:TRP:HA	16:LN:153:LYS:HE2	1.76	0.65
47:S2:1613:G:OP1	61:SS:88:LYS:NZ	2.28	0.65
14:LL:66:TYR:O	14:LL:68:THR:N	2.28	0.65
1:L5:268:G:H2'	1:L5:269:G:C8	2.32	0.65
10:LG:209:SER:HA	10:LG:212:LYS:HE3	1.78	0.65
47:S2:1493:C:O2'	47:S2:1499:U:O4	2.13	0.65
75:SN:35:GLU:HB3	75:SN:39:LYS:HZ1	1.61	0.65
1:L5:1216:C:N4	1:L5:1217:G:O6	2.29	0.65
49:SA:9:GLN:HG3	49:SA:10:MET:H	1.62	0.65
49:SA:122:LEU:HB2	49:SA:144:THR:HG22	1.78	0.65
1:L5:2910:G:H1'	1:L5:3585:G:H22	1.61	0.65
63:SU:60:THR:HG23	63:SU:81:GLN:HE22	1.61	0.65
47:S2:837:A:H2'	47:S2:838:G:H4'	1.78	0.65
55:SI:139:LYS:NZ	55:SI:149:TYR:OH	2.30	0.65
72:SG:213:LEU:HG	72:SG:217:MET:HE1	1.77	0.65
1:L5:2056:G:O2'	17:LO:18:ARG:NH2	2.30	0.65
1:L5:4047:A:C5	48:S6:56:C:N3	2.65	0.65
1:L5:4991:U:H2'	1:L5:4992:G:C8	2.32	0.65
47:S2:556:U:O2'	47:S2:558:G:OP2	2.15	0.65
47:S2:1347:U:H2'	47:S2:1348:G:C8	2.32	0.65
47:S2:1488:C:O2'	47:S2:1490:G:OP2	2.14	0.65
72:SG:160:LYS:H	72:SG:172:LYS:HG2	1.61	0.65
78:SY:90:ARG:HA	78:SY:93:ARG:HG2	1.79	0.65
1:L5:2486:G:H2'	1:L5:2487:G:H8	1.62	0.64
1:L5:4765:G:H22	1:L5:4869:U:H3	1.43	0.64
67:Sc:13:ARG:HB3	67:Sc:35:MET:HG2	1.80	0.64
1:L5:2612:G:H1	1:L5:2727:C:H42	1.45	0.64
47:S2:325:C:H4'	47:S2:327:G:H22	1.61	0.64
73:SJ:38:ARG:HG2	73:SJ:39:ASN:H	1.62	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:3961:G:H1'	1:L5:4048:A:H61	1.63	0.64
12:LI:185:VAL:HG22	12:LI:190:LEU:HD11	1.79	0.64
37:Li:23:LYS:HG2	37:Li:24:PRO:HD2	1.79	0.64
47:S2:332:G:O6	72:SG:190:ARG:NH2	2.30	0.64
49:SA:57:LYS:HZ1	49:SA:159:ILE:HG23	1.63	0.64
54:SH:83:LEU:HD11	54:SH:92:VAL:HG11	1.78	0.64
73:SJ:97:ILE:HA	73:SJ:100:LEU:HD13	1.79	0.64
1:L5:2395:A:N3	1:L5:2806:A:O2'	2.31	0.64
1:L5:4620:U:OP2	1:L5:4670:C:N4	2.26	0.64
51:SD:106:ARG:HG2	51:SD:175:VAL:HG12	1.80	0.64
1:L5:4699:U:C4	1:L5:4702:G:O6	2.51	0.64
25:LW:85:ALA:H	72:SG:129:VAL:HG13	1.62	0.64
47:S2:1499:U:H4'	51:SD:176:LEU:HD13	1.78	0.64
51:SD:74:GLN:NE2	51:SD:84:VAL:O	2.30	0.64
53:SF:126:THR:HA	53:SF:136:ARG:HE	1.63	0.64
1:L5:1804:A:N6	1:L5:1833:G:O4'	2.31	0.64
1:L5:4274:A:H2'	1:L5:4275:G:H8	1.63	0.64
3:L8:86:U:H5'	36:Lh:5:LYS:HE3	1.79	0.64
22:LT:137:GLU:CD	22:LT:138:ALA:H	2.06	0.64
45:Lr:52:GLU:OE2	45:Lr:79:ARG:NH2	2.30	0.64
60:SR:126:MET:HB2	60:SR:128:PHE:CD1	2.32	0.64
52:SE:103:TYR:HA	52:SE:109:PHE:HA	1.78	0.64
62:ST:124:THR:HG23	62:ST:127:GLY:H	1.62	0.64
75:SN:23:PRO:O	75:SN:25:TRP:N	2.30	0.64
1:L5:1656:U:OP2	29:La:26:ARG:NH2	2.31	0.64
47:S2:186:C:H2'	47:S2:187:G:H8	1.63	0.64
68:Sd:7:TYR:HE2	68:Sd:9:SER:HB2	1.61	0.64
1:L5:2543:A:H2'	1:L5:2546:G:H21	1.63	0.64
1:L5:3689:G:O2'	1:L5:3818:U:OP2	2.15	0.64
13:LJ:15:LEU:HD21	13:LJ:134:LEU:HD13	1.80	0.64
1:L5:975:C:OP1	9:LF:47:ARG:NH2	2.29	0.63
47:S2:613:G:N2	47:S2:626:G:OP1	2.29	0.63
54:SH:101:LEU:HD12	54:SH:116:ARG:HG3	1.80	0.63
73:SJ:30:LYS:HB3	81:Se:42:PHE:HE2	1.62	0.63
1:L5:374:G:OP2	38:Lj:56:ARG:NH2	2.32	0.63
62:ST:42:HIS:NE2	62:ST:82:ARG:O	2.32	0.63
64:SV:36:VAL:HG12	64:SV:37:ALA:H	1.61	0.63
1:L5:1963:C:H2'	1:L5:1964:A:C8	2.33	0.63
13:LJ:159:LYS:O	13:LJ:163:MET:HG2	1.99	0.63
47:S2:996:A:O2'	47:S2:997:A:H8	1.82	0.63
47:S2:1348:G:H22	47:S2:1381:G:N2	1.97	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:S2:1455:A:OP1	60:SR:5:ARG:NH2	2.32	0.63
47:S2:1608:U:O4	47:S2:1632:G:N2	2.31	0.63
1:L5:4279:A:H5'	1:L5:4281:A:H1'	1.81	0.63
47:S2:1407:U:H2'	47:S2:1408:U:C6	2.34	0.63
72:SG:5:ILE:HG12	72:SG:111:LEU:HB3	1.79	0.63
72:SG:214:ALA:HA	72:SG:217:MET:HE2	1.80	0.63
73:SJ:107:GLU:O	73:SJ:112:THR:OG1	2.15	0.63
1:L5:1075:G:C2	1:L5:1076:C:H1'	2.34	0.63
7:LD:219:TYR:HE2	7:LD:227:ILE:HD11	1.63	0.63
61:SS:124:ARG:HH21	61:SS:151:LYS:HE2	1.63	0.63
1:L5:1405:C:N4	1:L5:1412:G:O6	2.32	0.63
7:LD:208:MET:HE2	7:LD:233:PRO:HG3	1.79	0.63
25:LW:79:GLN:HA	25:LW:80:ARG:HB3	1.79	0.63
59:SQ:72:VAL:HG11	59:SQ:80:GLN:HB2	1.80	0.63
73:SJ:4:ALA:HB3	73:SJ:5:ARG:HA	1.79	0.63
78:SY:7:ILE:HG12	78:SY:27:VAL:HG22	1.80	0.63
1:L5:191:G:H2'	1:L5:192:G:H8	1.63	0.63
1:L5:3599:A:H2'	1:L5:3600:G:C8	2.34	0.63
1:L5:4314:C:O2'	30:Lb:36:ASP:OD2	2.15	0.63
47:S2:121:U:H5'	52:SE:77:ARG:HH12	1.64	0.63
1:L5:689:U:H2'	1:L5:690:C:C6	2.34	0.63
1:L5:3717:A:H2'	1:L5:3718:A:H8	1.64	0.63
1:L5:4947:U:O2'	34:Lf:2:SER:N	2.32	0.63
71:SC:68:ARG:NH2	71:SC:272:HIS:O	2.32	0.63
74:SM:35:ILE:HD11	74:SM:108:CYS:HB2	1.80	0.63
1:L5:4274:A:H2'	1:L5:4275:G:C8	2.34	0.63
14:LL:189:ALA:HA	37:Li:11:LEU:HD13	1.79	0.63
32:Ld:29:ILE:HG23	32:Ld:33:ILE:HD13	1.79	0.63
47:S2:570:C:O2'	78:SY:34:THR:O	2.15	0.63
47:S2:1455:A:H2'	47:S2:1456:G:H8	1.64	0.63
77:SW:76:SER:HB2	77:SW:77:PRO:HD3	1.79	0.63
82:Pt:21:H2U:H52	82:Pt:60:A:H61	1.62	0.63
1:L5:746:A:H5'	21:LS:148:SER:HB2	1.79	0.62
27:LY:83:GLU:OE1	27:LY:84:ARG:NH1	2.32	0.62
50:SB:71:LEU:HD22	50:SB:82:ARG:HG3	1.81	0.62
52:SE:69:PHE:CE1	78:SY:17:LEU:HD22	2.34	0.62
62:ST:18:LEU:HB2	62:ST:62:ARG:HH21	1.64	0.62
6:LC:212:ASN:OD1	6:LC:213:GLU:N	2.32	0.62
9:LF:98:ILE:HD12	9:LF:101:VAL:HG21	1.79	0.62
47:S2:1347:U:H2'	47:S2:1348:G:H8	1.64	0.62
1:L5:1307:A:H2'	1:L5:1308:C:C6	2.35	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:4242:U:H3	1:L5:4281:A:H2	1.44	0.62
44:Lp:33:GLN:HG3	44:Lp:69:TRP:HD1	1.64	0.62
47:S2:522:A:H4'	73:SJ:131:ARG:HH12	1.64	0.62
47:S2:1354:G:N2	47:S2:1357:A:OP2	2.26	0.62
55:SI:73:THR:O	55:SI:74:ARG:NE	2.30	0.62
1:L5:2122:G:H4'	9:LF:41:MET:HE2	1.82	0.62
1:L5:3896:C:O2'	1:L5:3897:G:O4'	2.18	0.62
19:LQ:172:ARG:NH1	29:La:56:VAL:O	2.32	0.62
49:SA:41:ARG:HH11	49:SA:47:TYR:HE1	1.46	0.62
1:L5:969:C:N3	1:L5:2256:C:N4	2.47	0.62
1:L5:1645:C:OP1	6:LC:80:ARG:NH2	2.31	0.62
23:LU:42:PHE:HD2	23:LU:46:ARG:HD3	1.64	0.62
47:S2:94:G:HO2'	47:S2:508:A:HO2'	1.46	0.62
60:SR:18:GLU:HA	60:SR:70:SER:HB2	1.81	0.62
63:SU:26:SER:HB2	63:SU:32:LEU:HD22	1.81	0.62
1:L5:508:G:N1	1:L5:510:U:O4	2.32	0.62
1:L5:2556:G:H2'	1:L5:2557:G:C8	2.34	0.62
7:LD:107:ARG:NH2	7:LD:120:GLU:O	2.33	0.62
25:LW:71:ARG:HG2	25:LW:72:THR:HG23	1.82	0.62
25:LW:74:ARG:HD3	47:S2:1781:A:H62	1.65	0.62
47:S2:1122:A:H4'	50:SB:205:TYR:HD1	1.64	0.62
47:S2:1419:C:H4'	47:S2:1420:G:OP1	2.00	0.62
70:Sg:29:ASP:HB3	70:Sg:45:LEU:HB2	1.81	0.62
3:L8:86:U:OP2	36:Lh:7:ARG:NH1	2.32	0.62
9:LF:220:MET:HE1	9:LF:223:LYS:HG3	1.80	0.62
47:S2:1010:G:H2'	47:S2:1011:A:H8	1.64	0.62
1:L5:1367:C:O2'	1:L5:1370:G:O2'	2.16	0.62
49:SA:4:ALA:H	49:SA:5:LEU:HA	1.64	0.62
1:L5:190:G:H2'	1:L5:191:G:C8	2.35	0.62
1:L5:978:G:H2'	1:L5:979:C:O4'	1.99	0.62
1:L5:1088:C:H2'	1:L5:1089:G:C8	2.34	0.62
27:LY:54:GLU:HA	27:LY:69:LYS:HA	1.81	0.62
43:Lo:15:CYS:SG	43:Lo:19:GLN:NE2	2.73	0.62
67:Sc:16:LYS:HE3	67:Sc:31:ARG:HH21	1.64	0.62
1:L5:135:G:OP2	36:Lh:87:LYS:NZ	2.30	0.62
1:L5:1924:C:OP1	15:LM:34:ASN:ND2	2.33	0.62
1:L5:4044:U:O2'	1:L5:4045:G:N7	2.33	0.62
20:LR:103:ARG:NH1	20:LR:124:TYR:OH	2.33	0.62
54:SH:87:PHE:HE2	54:SH:90:LYS:HD2	1.65	0.62
61:SS:120:HIS:O	61:SS:122:GLY:N	2.32	0.62
70:Sg:40:ILE:HD12	70:Sg:90:TRP:HE1	1.64	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:3755:G:N2	1:L5:3770:U:O2	2.33	0.61
1:L5:3873:G:H2'	1:L5:3874:G:C8	2.36	0.61
47:S2:126:G:OP2	72:SG:195:LYS:HG2	2.00	0.61
47:S2:988:C:O2'	50:SB:118:GLN:O	2.18	0.61
72:SG:24:LEU:O	72:SG:26:THR:N	2.33	0.61
20:LR:39:GLN:HA	20:LR:42:ARG:HB2	1.81	0.61
52:SE:75:LYS:O	52:SE:77:ARG:N	2.32	0.61
82:Pt:70:C:H2'	82:Pt:71:G:H8	1.65	0.61
1:L5:4906:C:H2'	1:L5:4907:G:C8	2.35	0.61
4:LA:30:ARG:O	4:LA:163:ARG:NH2	2.34	0.61
9:LF:116:GLN:HG2	9:LF:119:ASN:HD21	1.65	0.61
46:Lz:45:LYS:HD2	46:Lz:47:LYS:HE2	1.82	0.61
77:SW:115:GLU:HA	77:SW:118:ARG:HG2	1.82	0.61
16:LN:184:ILE:HG23	16:LN:194:ARG:HH22	1.64	0.61
25:LW:74:ARG:NH2	47:S2:1779:G:N7	2.49	0.61
46:Lz:70:ASP:O	46:Lz:73:HIS:ND1	2.26	0.61
50:SB:37:ALA:HA	50:SB:42:ARG:HH12	1.65	0.61
1:L5:267:G:H2'	1:L5:268:G:C8	2.34	0.61
1:L5:4770:U:N3	1:L5:4863:G:O6	2.34	0.61
2:L7:55:A:O2'	13:LJ:151:ILE:O	2.18	0.61
47:S2:322:C:O2'	47:S2:323:C:OP1	2.19	0.61
47:S2:317:C:H2'	47:S2:318:A:C8	2.35	0.61
47:S2:1242:U:O2	47:S2:1517:G:O2'	2.13	0.61
47:S2:1419:C:H42	47:S2:1429:G:H1	1.47	0.61
1:L5:126:C:N3	1:L5:142:G:N2	2.45	0.61
1:L5:1332:C:H2'	1:L5:1333:A:H8	1.64	0.61
19:LQ:157:GLY:O	19:LQ:188:ASN:ND2	2.33	0.61
47:S2:551:U:H3'	47:S2:552:G:H8	1.66	0.61
71:SC:182:CYS:SG	71:SC:183:LYS:N	2.73	0.61
1:L5:106:A:H1'	1:L5:336:A:H8	1.65	0.61
17:LO:36:VAL:HG21	17:LO:108:ILE:HD12	1.83	0.61
50:SB:144:LYS:HB2	50:SB:208:HIS:HB3	1.83	0.61
61:SS:40:TYR:HA	61:SS:43:VAL:HG12	1.82	0.61
1:L5:489:C:H42	1:L5:664:G:H1	1.47	0.61
1:L5:1502:G:H22	29:La:77:LYS:NZ	1.99	0.61
1:L5:137:G:H5'	36:Lh:96:ASN:HD21	1.64	0.61
47:S2:1589:A:N6	47:S2:1672:U:O2'	2.33	0.61
49:SA:10:MET:HE2	49:SA:15:VAL:HG12	1.82	0.61
1:L5:734:G:H5"	15:LM:70:GLN:OE1	2.01	0.60
1:L5:1185:G:H2'	1:L5:1186:U:C6	2.36	0.60
1:L5:2763:U:H2'	1:L5:2764:A:C8	2.36	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:S2:885:U:H3	47:S2:901:G:H1	1.49	0.60
70:Sg:75:GLY:HA3	70:Sg:92:LEU:HD22	1.83	0.60
1:L5:723:A:H2	1:L5:943:A:N1	1.99	0.60
1:L5:1921:C:C4	15:LM:17:PHE:HB3	2.36	0.60
6:LC:210:ILE:HD12	6:LC:252:TRP:NE1	2.17	0.60
14:LL:125:ILE:HD11	36:Lh:122:LYS:HE3	1.83	0.60
47:S2:1736:G:H2'	47:S2:1737:G:C8	2.36	0.60
56:SK:46:MET:SD	56:SK:47:LYS:HG2	2.40	0.60
73:SJ:136:ARG:HA	73:SJ:141:VAL:HA	1.82	0.60
1:L5:2486:G:H2'	1:L5:2487:G:C8	2.36	0.60
6:LC:319:LEU:HD12	6:LC:325:MET:HE1	1.83	0.60
8:LE:84:LYS:HB2	8:LE:85:LYS:HB3	1.83	0.60
47:S2:1065:G:OP1	76:SO:149:ARG:NH1	2.33	0.60
47:S2:1677:U:H5"	53:SF:148:ASN:HD21	1.66	0.60
56:SK:80:ARG:HA	56:SK:85:LEU:HD12	1.84	0.60
1:L5:2806:A:H1'	35:Lg:4:ARG:HD2	1.84	0.60
5:LB:291:TYR:O	5:LB:292:LEU:HD23	2.02	0.60
47:S2:606:G:H5"	81:Se:56:ASN:HB3	1.83	0.60
47:S2:1469:A:OP1	53:SF:59:LYS:NZ	2.33	0.60
1:L5:5004:C:H2'	1:L5:5005:G:O4'	2.01	0.60
53:SF:140:ASP:HB3	67:Sc:46:VAL:HG12	1.84	0.60
63:SU:33:GLU:OE2	63:SU:87:ARG:NH2	2.30	0.60
78:SY:54:VAL:HB	78:SY:76:TYR:HB2	1.83	0.60
1:L5:346:G:O2'	1:L5:1367:C:N4	2.23	0.60
1:L5:2647:A:H62	1:L5:2686:G:H8	1.49	0.60
1:L5:4047:A:C5	48:S6:56:C:C4	2.89	0.60
7:LD:286:SER:O	7:LD:289:ARG:HG2	2.01	0.60
47:S2:69:C:H2'	47:S2:70:G:O4'	2.02	0.60
74:SM:52:GLN:HE22	74:SM:66:GLU:HB3	1.66	0.60
1:L5:958:G:H21	8:LE:125:LEU:HD23	1.66	0.60
64:SV:12:TYR:HB3	71:SC:79:GLU:OE2	2.02	0.60
82:Pt:16:C:OP2	82:Pt:18:C:O2'	2.19	0.60
1:L5:744:G:H2'	1:L5:745:G:C8	2.37	0.60
1:L5:1933:G:H2'	1:L5:1934:A:C8	2.36	0.60
1:L5:3751:G:H21	1:L5:3775:A:H8	1.48	0.60
1:L5:3783:A:H2	1:L5:3790:U:H3	1.49	0.60
7:LD:128:ASP:O	7:LD:164:LYS:NZ	2.32	0.60
34:Lf:25:THR:HG22	34:Lf:87:LYS:HD3	1.84	0.60
47:S2:656:G:O2'	71:SC:227:ARG:NH1	2.34	0.60
59:SQ:102:GLU:HG3	59:SQ:105:LYS:HE3	1.84	0.60
67:Sc:29:GLN:HG2	67:Sc:45:ASN:HB3	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:Sg:214:GLY:HA2	70:Sg:236:ILE:HG13	1.83	0.60
70:Sg:250:ALA:HB3	70:Sg:257:LYS:HE3	1.84	0.60
1:L5:4594:U:H2'	1:L5:4595:G:H8	1.66	0.60
20:LR:159:ALA:HB2	20:LR:162:ARG:HH21	1.66	0.60
51:SD:141:LYS:HE3	51:SD:145:GLN:HA	1.83	0.60
1:L5:2477:A:H2'	1:L5:2478:C:C6	2.37	0.60
46:Lz:25:ARG:NH2	46:Lz:210:MET:O	2.35	0.60
47:S2:1452:A:N6	47:S2:1473:G:O2'	2.34	0.60
47:S2:1743:G:H21	47:S2:1791:A:H62	1.49	0.60
52:SE:175:PHE:HE1	52:SE:198:ARG:HH21	1.50	0.60
68:Sd:7:TYR:CE2	68:Sd:9:SER:HB2	2.37	0.60
1:L5:2453:A:N7	1:L5:2467:U:O2	2.35	0.59
1:L5:2723:U:N3	1:L5:2724:G:O6	2.35	0.59
4:LA:247:ARG:NH1	4:LA:249:THR:O	2.35	0.59
46:Lz:60:ARG:H	46:Lz:171:HIS:HD2	1.50	0.59
53:SF:43:GLU:HB3	53:SF:44:LYS:HA	1.83	0.59
53:SF:171:GLU:HA	53:SF:174:ALA:HB3	1.84	0.59
62:ST:70:ALA:HB1	62:ST:74:SER:HB3	1.83	0.59
17:LO:3:GLU:N	34:Lf:31:GLU:OE1	2.34	0.59
46:Lz:204:LEU:O	46:Lz:215:ARG:HA	2.03	0.59
60:SR:94:GLU:HA	60:SR:96:ILE:HG12	1.84	0.59
70:Sg:207:CYS:SG	70:Sg:208:ALA:N	2.75	0.59
72:SG:144:LEU:HB2	72:SG:147:LEU:H	1.65	0.59
78:SY:6:THR:HG22	78:SY:28:LEU:HB3	1.84	0.59
1:L5:2378:G:N2	1:L5:2381:A:OP2	2.35	0.59
1:L5:3965:A:H61	1:L5:4040:C:P	2.25	0.59
1:L5:4748:U:O4	1:L5:4952:G:O6	2.19	0.59
15:LM:104:MET:HE3	15:LM:109:ARG:HG2	1.84	0.59
47:S2:860:G:N2	77:SW:107:SER:OG	2.35	0.59
47:S2:1495:G:O2'	68:Sd:26:ASN:OD1	2.15	0.59
47:S2:1669:G:OP1	63:SU:79:ARG:NH2	2.32	0.59
48:S6:58:A:O2'	48:S6:60:A:OP2	2.20	0.59
52:SE:31:PRO:HB3	52:SE:43:PRO:HB3	1.84	0.59
1:L5:2106:G:N1	1:L5:2126:G:N7	2.51	0.59
1:L5:3773:U:O2'	1:L5:3774:A:H2'	2.03	0.59
1:L5:4250:G:OP1	13:LJ:98:ASN:ND2	2.35	0.59
47:S2:1629:C:OP1	61:SS:39:ARG:NE	2.29	0.59
61:SS:35:GLY:HA3	61:SS:99:LEU:HG	1.84	0.59
1:L5:2848:G:O2'	1:L5:3838:U:O4	2.18	0.59
17:LO:128:ARG:NH2	21:LS:162:GLN:OE1	2.36	0.59
47:S2:1288:U:O4	47:S2:1309:C:N4	2.29	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:SB:34:LYS:HG3	50:SB:42:ARG:HG3	1.85	0.59
1:L5:1240:G:N7	1:L5:1271:G:O2'	2.30	0.59
14:LL:150:LEU:HG	36:Lh:123:ALA:HB3	1.84	0.59
16:LN:68:ARG:NH1	16:LN:124:ASP:O	2.31	0.59
44:Lp:38:THR:HA	44:Lp:45:THR:HA	1.82	0.59
47:S2:555:A:H8	47:S2:556:U:H4'	1.68	0.59
54:SH:18:GLU:O	54:SH:20:GLU:N	2.35	0.59
63:SU:49:LYS:O	63:SU:51:LYS:N	2.31	0.59
82:Pt:21:H2U:H52	82:Pt:60:A:N6	2.17	0.59
1:L5:1266:G:H3'	1:L5:2121:C:H42	1.67	0.59
1:L5:1380:G:O2'	1:L5:1382:G:O6	2.17	0.59
1:L5:2448:G:H2'	1:L5:2449:A:C8	2.38	0.59
1:L5:2458:C:OP1	16:LN:67:ARG:NH2	2.36	0.59
10:LG:244:PRO:HA	10:LG:247:VAL:HG22	1.85	0.59
25:LW:66:GLU:HB2	25:LW:67:ILE:HG13	1.85	0.59
47:S2:77:A:OP2	72:SG:154:ARG:NH1	2.36	0.59
47:S2:155:G:N2	47:S2:163:U:O2	2.35	0.59
47:S2:928:G:H2'	47:S2:929:G:C8	2.37	0.59
54:SH:103:LYS:HG3	54:SH:116:ARG:HH22	1.66	0.59
73:SJ:4:ALA:N	73:SJ:5:ARG:HB2	2.18	0.59
5:LB:215:GLU:HB2	5:LB:284:ILE:HD12	1.85	0.59
20:LR:105:LEU:HD22	20:LR:135:LYS:HG3	1.85	0.59
21:LS:20:PRO:HD2	21:LS:21:LYS:H	1.67	0.59
29:La:36:GLY:O	29:La:38:LEU:N	2.35	0.59
73:SJ:4:ALA:H	73:SJ:5:ARG:HE	1.51	0.59
1:L5:703:G:N2	1:L5:705:G:OP1	2.35	0.59
1:L5:1217:G:H2'	1:L5:1218:G:C8	2.37	0.59
1:L5:4134:C:H2'	1:L5:4135:G:H8	1.67	0.59
5:LB:94:GLU:HG2	5:LB:158:GLN:NE2	2.18	0.59
44:Lp:46:LYS:HD2	44:Lp:59:SER:HB3	1.85	0.59
47:S2:931:C:H2'	47:S2:932:G:C8	2.38	0.59
47:S2:948:C:H2'	47:S2:949:G:H8	1.68	0.59
49:SA:145:ILE:HG22	49:SA:159:ILE:HB	1.83	0.59
51:SD:70:THR:O	51:SD:74:GLN:HG2	2.02	0.59
53:SF:56:TYR:OH	53:SF:70:GLU:OE1	2.21	0.59
1:L5:1441:C:OP1	1:L5:2109:G:O2'	2.20	0.59
1:L5:4745:G:H1	1:L5:4955:A:H2	1.50	0.59
7:LD:236:MET:HB2	7:LD:239:MET:HE2	1.84	0.59
74:SM:26:LEU:HD12	74:SM:27:ILE:HG23	1.85	0.59
1:L5:1076:C:O2'	1:L5:1235:G:N2	2.35	0.58
1:L5:1502:G:H22	29:La:77:LYS:HZ3	1.51	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:1761:G:H1	1:L5:1768:C:H42	1.51	0.58
8:LE:112:MET:SD	45:Lr:94:ARG:NH2	2.76	0.58
12:LI:52:MET:HE1	12:LI:155:ALA:HB3	1.85	0.58
47:S2:798:A:N6	47:S2:801:U:O5'	2.34	0.58
61:SS:64:VAL:HA	61:SS:67:VAL:HG22	1.85	0.58
1:L5:2562:G:O2'	1:L5:2564:G:N7	2.31	0.58
1:L5:3772:U:H3'	1:L5:3773:U:C6	2.38	0.58
1:L5:5061:A:H61	5:LB:127:LYS:NZ	2.01	0.58
49:SA:184:ARG:HB3	49:SA:191:ARG:HH21	1.68	0.58
70:Sg:70:VAL:HG11	70:Sg:113:PHE:HB3	1.84	0.58
47:S2:216:C:H41	47:S2:309:G:H1	1.51	0.58
47:S2:873:G:H21	54:SH:114:GLN:HE22	1.51	0.58
48:S6:16:G:N3	48:S6:20:A:N6	2.51	0.58
76:SO:44:VAL:HG11	76:SO:85:CYS:SG	2.43	0.58
1:L5:457:G:H22	1:L5:699:C:H42	1.49	0.58
1:L5:1351:G:O6	19:LQ:55:ARG:NH2	2.36	0.58
1:L5:2318:G:N2	1:L5:2321:G:OP2	2.29	0.58
1:L5:2611:A:H5'	1:L5:2688:G:H4'	1.84	0.58
1:L5:4537:C:H2'	1:L5:4538:G:H8	1.67	0.58
1:L5:4905:C:H2'	1:L5:4906:C:H6	1.68	0.58
25:LW:89:ASP:HB3	25:LW:91:MET:SD	2.42	0.58
47:S2:304:C:O2'	47:S2:309:G:N7	2.36	0.58
47:S2:312:G:H5'	47:S2:313:A:H5'	1.84	0.58
47:S2:1520:G:OP1	61:SS:136:THR:N	2.36	0.58
47:S2:1535:U:O2'	53:SF:88:MET:SD	2.59	0.58
55:SI:42:ARG:HG3	55:SI:58:LEU:HB2	1.86	0.58
58:SP:43:ARG:HH21	58:SP:47:ARG:NH2	2.02	0.58
59:SQ:129:SER:O	59:SQ:131:LYS:NZ	2.35	0.58
64:SV:16:LYS:H	71:SC:259:THR:HG21	1.67	0.58
1:L5:696:C:H5"	1:L5:697:G:H5'	1.86	0.58
1:L5:1264:C:H2'	1:L5:1265:G:C8	2.39	0.58
1:L5:1279:A:H3'	1:L5:1280:C:C6	2.39	0.58
1:L5:2028:C:H2'	1:L5:2029:A:H8	1.67	0.58
47:S2:114:G:OP1	57:SL:69:ARG:NH1	2.36	0.58
47:S2:842:C:H2'	47:S2:843:C:C6	2.38	0.58
47:S2:913:A:OP2	54:SH:99:ARG:NH2	2.37	0.58
51:SD:201:LYS:O	51:SD:201:LYS:HD2	2.03	0.58
54:SH:158:LEU:HD21	54:SH:187:PHE:HD1	1.68	0.58
57:SL:128:VAL:HG12	57:SL:142:VAL:HA	1.85	0.58
77:SW:65:LEU:HD12	77:SW:67:GLY:H	1.67	0.58
1:L5:957:G:O2'	1:L5:958:G:OP2	2.17	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:3960:A:N6	1:L5:4045:G:O2'	2.36	0.58
1:L5:1197:C:H2'	1:L5:1198:G:C8	2.39	0.58
1:L5:3722:G:OP2	37:Li:68:ARG:NH2	2.36	0.58
1:L5:4114:C:H2'	1:L5:4115:G:H21	1.68	0.58
6:LC:35:ASP:OD1	6:LC:36:ILE:N	2.37	0.58
47:S2:1808:U:H2'	47:S2:1809:A:H8	1.69	0.58
1:L5:956:A:H4'	1:L5:957:G:OP2	2.04	0.58
1:L5:2478:C:H2'	1:L5:2479:G:C8	2.38	0.58
1:L5:2694:G:H4'	1:L5:2695:A:H5'	1.85	0.58
1:L5:3653:A:H5"	4:LA:179:ILE:HD11	1.84	0.58
1:L5:4893:A:OP1	17:LO:188:LYS:NZ	2.37	0.58
20:LR:9:ARG:HA	20:LR:19:LYS:HE3	1.86	0.58
53:SF:186:ASN:H	53:SF:190:ILE:HD11	1.69	0.58
1:L5:2907:G:H1'	1:L5:3589:G:H22	1.69	0.58
10:LG:58:PRO:O	10:LG:60:TYR:N	2.36	0.58
19:LQ:65:ARG:O	19:LQ:69:LYS:HG2	2.04	0.58
34:Lf:54:LYS:O	34:Lf:66:LYS:NZ	2.25	0.58
47:S2:527:C:H2'	47:S2:528:A:H8	1.67	0.58
47:S2:1414:A:N7	47:S2:1416:C:O2'	2.34	0.58
47:S2:1544:C:O2'	59:SQ:75:GLY:O	2.19	0.58
59:SQ:12:VAL:HG21	59:SQ:91:ALA:HA	1.86	0.58
70:Sg:272:GLN:HG3	70:Sg:308:ARG:HH22	1.69	0.58
1:L5:943:A:OP1	9:LF:245:ARG:NH2	2.36	0.57
1:L5:4911:A:OP1	5:LB:97:ARG:NH2	2.36	0.57
21:LS:160:ARG:HD3	21:LS:160:ARG:H	1.69	0.57
70:Sg:78:ALA:O	70:Sg:90:TRP:N	2.33	0.57
77:SW:22:LYS:HA	80:Sb:2:PRO:HB3	1.86	0.57
1:L5:755:C:H2'	1:L5:756:G:H8	1.69	0.57
1:L5:4084:G:O6	4:LA:72:ARG:NH2	2.35	0.57
47:S2:305:U:O4	55:SI:184:ARG:NE	2.35	0.57
47:S2:896:U:O4	47:S2:898:U:N3	2.37	0.57
47:S2:1629:C:H5'	61:SS:39:ARG:HH21	1.69	0.57
70:Sg:290:ALA:HB3	70:Sg:299:PHE:HB2	1.84	0.57
1:L5:382:G:N1	1:L5:385:A:OP2	2.37	0.57
1:L5:2411:C:O2'	1:L5:2526:C:O2	2.21	0.57
13:LJ:111:GLU:HB2	13:LJ:125:ILE:HD11	1.86	0.57
26:LX:129:ARG:HD3	26:LX:135:LYS:HD2	1.85	0.57
30:Lb:55:LYS:HA	30:Lb:58:GLN:HG2	1.85	0.57
47:S2:636:C:OP2	81:Se:21:LYS:NZ	2.36	0.57
60:SR:95:ILE:H	60:SR:96:ILE:HA	1.69	0.57
70:Sg:235:ILE:O	70:Sg:252:THR:HA	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
76:SO:117:ARG:HE	76:SO:121:ARG:HH21	1.51	0.57
1:L5:713:C:H2'	1:L5:714:G:H8	1.68	0.57
1:L5:969:C:O2'	8:LE:123:ARG:NH1	2.37	0.57
1:L5:4091:G:H2'	1:L5:4092:G:C8	2.39	0.57
1:L5:4431:U:H5"	12:LI:160:PRO:HG3	1.85	0.57
8:LE:136:HIS:O	8:LE:138:ARG:NH1	2.37	0.57
35:Lg:20:THR:HG21	35:Lg:34:TYR:CD1	2.39	0.57
51:SD:76:ARG:HH21	56:SK:66:HIS:CE1	2.21	0.57
75:SN:60:VAL:HG23	75:SN:66:VAL:HG21	1.86	0.57
1:L5:1266:G:N2	1:L5:1268:G:O5'	2.38	0.57
1:L5:3651:A:OP2	4:LA:200:ARG:NH1	2.37	0.57
46:Lz:87:ILE:HA	46:Lz:90:LEU:HD13	1.86	0.57
47:S2:3:C:O2	73:SJ:18:ARG:NH2	2.20	0.57
47:S2:697:G:OP2	47:S2:734:C:O2'	2.22	0.57
47:S2:1758:G:O2'	47:S2:1774:C:N4	2.37	0.57
75:SN:39:LYS:HB3	75:SN:43:LYS:NZ	2.18	0.57
75:SN:101:HIS:NE2	75:SN:105:ASN:OD1	2.32	0.57
1:L5:192:G:H2'	1:L5:193:G:H8	1.69	0.57
1:L5:1233:G:H3'	1:L5:1234:G:C8	2.40	0.57
1:L5:2090:U:H4'	6:LC:305:PRO:HD2	1.86	0.57
1:L5:3673:C:O2'	1:L5:3674:G:OP1	2.18	0.57
3:L8:55:U:H3	3:L8:62:A:H2	1.50	0.57
7:LD:219:TYR:CE2	7:LD:227:ILE:HD11	2.40	0.57
32:Ld:64:ILE:HG13	32:Ld:68:LEU:HD23	1.87	0.57
35:Lg:82:MET:HE1	35:Lg:90:ARG:HD2	1.85	0.57
37:Li:63:VAL:O	37:Li:64:SER:OG	2.22	0.57
47:S2:655:A:H4'	47:S2:656:G:H5'	1.86	0.57
54:SH:104:PRO:HG2	54:SH:113:LYS:HG2	1.86	0.57
70:Sg:147:HIS:CE1	70:Sg:173:LEU:HB2	2.39	0.57
76:SO:17:LEU:HD23	76:SO:18:GLY:N	2.19	0.57
78:SY:88:LYS:HE3	78:SY:99:LYS:HG2	1.86	0.57
14:LL:87:HIS:CE1	14:LL:89:LYS:HB2	2.40	0.57
24:LV:13:LYS:HD2	24:LV:128:LEU:HD11	1.84	0.57
47:S2:96:C:H1'	47:S2:474:G:H5'	1.87	0.57
47:S2:1311:C:H2'	47:S2:1312:G:H8	1.68	0.57
48:S6:33:C:OP1	53:SF:136:ARG:NH1	2.38	0.57
56:SK:41:PRO:HG2	56:SK:43:LEU:HB3	1.87	0.57
1:L5:1418:C:N4	1:L5:1419:G:O6	2.38	0.57
1:L5:2475:G:N3	26:LX:50:LYS:NZ	2.40	0.57
1:L5:3870:C:H4'	5:LB:261:ARG:NH1	2.20	0.57
47:S2:1736:G:H2'	47:S2:1737:G:H8	1.67	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:SQ:146:ARG:NH2	82:Pt:34:U:O2	2.37	0.57
1:L5:165:A:N6	1:L5:270:U:H3	2.03	0.57
1:L5:456:C:H2'	1:L5:457:G:C8	2.40	0.57
1:L5:1100:U:H2'	1:L5:1167:C:C5	2.40	0.57
1:L5:2007:G:H1'	1:L5:2008:U:H5	1.69	0.57
1:L5:3784:A:O2'	1:L5:3785:A:OP1	2.22	0.57
8:LE:83:LYS:N	8:LE:84:LYS:HB3	2.20	0.57
41:Lm:109:ASN:HD21	41:Lm:117:HIS:HB3	1.69	0.57
47:S2:1606:G:HO2'	47:S2:1607:A:H8	1.53	0.57
71:SC:81:ILE:HG21	71:SC:88:ILE:HD11	1.85	0.57
4:LA:28:ARG:HE	4:LA:123:ARG:HD3	1.70	0.57
47:S2:16:G:H2'	47:S2:17:C:C6	2.40	0.57
47:S2:958:G:O2'	47:S2:959:G:O5'	2.22	0.57
48:S6:10:G:H21	48:S6:45:G:H3'	1.70	0.57
53:SF:123:GLU:OE2	53:SF:197:GLU:HA	2.04	0.57
1:L5:2503:G:H3'	1:L5:2504:C:H4'	1.87	0.56
1:L5:4698:C:H5	41:Lm:125:LYS:HZ1	1.52	0.56
1:L5:4991:U:H2'	1:L5:4992:G:H8	1.68	0.56
13:LJ:63:ARG:NH1	43:Lo:103:VAL:HG11	2.20	0.56
47:S2:942:G:H2'	47:S2:943:U:C6	2.39	0.56
53:SF:143:PRO:HA	53:SF:146:ARG:HG2	1.87	0.56
61:SS:39:ARG:HD3	62:ST:38:LYS:HD3	1.87	0.56
67:Sc:20:ARG:HD2	67:Sc:28:THR:HG22	1.87	0.56
1:L5:1802:A:N3	22:LT:130:ARG:NH2	2.53	0.56
5:LB:89:ILE:HD11	5:LB:150:PHE:HE1	1.69	0.56
7:LD:209:ARG:HA	7:LD:212:MET:HE2	1.86	0.56
13:LJ:144:LYS:O	13:LJ:148:THR:OG1	2.22	0.56
13:LJ:157:ILE:HG22	13:LJ:159:LYS:H	1.70	0.56
14:LL:126:LEU:N	14:LL:138:ASP:OD2	2.27	0.56
36:Lh:96:ASN:O	36:Lh:98:HIS:N	2.38	0.56
43:Lo:22:LYS:HE2	43:Lo:73:VAL:HG12	1.86	0.56
50:SB:49:VAL:HG11	50:SB:62:LEU:HD21	1.86	0.56
53:SF:144:LEU:O	53:SF:148:ASN:HB2	2.05	0.56
53:SF:204:ARG:HE	67:Sc:63:ARG:HB3	1.69	0.56
72:SG:66:GLY:N	72:SG:100:CYS:SG	2.77	0.56
1:L5:167:C:N4	1:L5:268:G:O6	2.38	0.56
1:L5:1483:C:O2'	1:L5:1484:G:O4'	2.21	0.56
1:L5:2115:G:N2	1:L5:2117:G:OP2	2.32	0.56
1:L5:3594:C:O2'	1:L5:3597:G:N3	2.34	0.56
1:L5:3641:U:OP2	1:L5:3646:A:N6	2.39	0.56
1:L5:3888:G:O2'	1:L5:3889:G:OP1	2.23	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:4537:C:H2'	1:L5:4538:G:C8	2.40	0.56
2:L7:49:A:H5"	7:LD:224:SER:HB2	1.87	0.56
4:LA:101:VAL:HG22	4:LA:165:VAL:HG22	1.86	0.56
4:LA:102:LEU:HB2	4:LA:107:MET:HE3	1.87	0.56
4:LA:162:ASN:HD22	4:LA:162:ASN:C	2.12	0.56
6:LC:60:HIS:NE2	6:LC:100:ARG:HD3	2.21	0.56
6:LC:318:PRO:O	6:LC:319:LEU:HB2	2.05	0.56
8:LE:89:LEU:N	8:LE:90:ALA:HA	2.20	0.56
9:LF:31:LYS:HA	9:LF:34:ARG:HH11	1.70	0.56
12:LI:48:LEU:HD11	12:LI:142:LEU:HD23	1.87	0.56
13:LJ:55:TYR:O	13:LJ:56:THR:OG1	2.17	0.56
38:Lj:34:CYS:SG	38:Lj:38:GLY:N	2.78	0.56
47:S2:67:C:H42	72:SG:164:LYS:HE2	1.70	0.56
47:S2:525:A:N6	47:S2:588:G:H22	2.03	0.56
47:S2:1285:G:H5'	74:SM:106:CYS:HB2	1.85	0.56
48:S6:53:G:H2'	48:S6:54:A:H8	1.69	0.56
51:SD:142:LEU:HB2	51:SD:148:LYS:HB3	1.86	0.56
58:SP:101:THR:HB	58:SP:102:PHE:HB3	1.87	0.56
63:SU:47:ASN:HA	63:SU:48:LEU:HB2	1.86	0.56
70:Sg:238:ALA:O	70:Sg:250:ALA:HA	2.05	0.56
72:SG:172:LYS:HG3	72:SG:174:PRO:HD3	1.87	0.56
75:SN:39:LYS:HB3	75:SN:43:LYS:HZ1	1.70	0.56
79:SZ:77:LEU:HD22	79:SZ:79:ILE:HB	1.86	0.56
1:L5:482:G:H2'	1:L5:483:G:C8	2.40	0.56
1:L5:664:G:N2	1:L5:667:A:N6	2.54	0.56
1:L5:1332:C:H2'	1:L5:1333:A:C8	2.41	0.56
1:L5:2001:G:H2'	1:L5:2002:A:H4'	1.87	0.56
1:L5:2786:C:H5"	1:L5:2787:A:H5'	1.87	0.56
6:LC:260:LEU:HA	6:LC:263:LEU:HB3	1.87	0.56
8:LE:86:GLU:H	8:LE:89:LEU:HD12	1.71	0.56
23:LU:96:LEU:HG	23:LU:100:LEU:HD22	1.88	0.56
47:S2:589:G:N3	47:S2:591:U:N3	2.53	0.56
47:S2:1221:G:H2'	47:S2:1222:G:C8	2.40	0.56
58:SP:16:THR:OG1	58:SP:21:ASP:OD1	2.24	0.56
59:SQ:47:LEU:O	59:SQ:49:TYR:N	2.38	0.56
59:SQ:136:GLY:O	59:SQ:140:ARG:NH2	2.38	0.56
73:SJ:28:GLU:HG3	73:SJ:43:VAL:HG11	1.86	0.56
74:SM:50:CYS:SG	74:SM:51:VAL:N	2.69	0.56
1:L5:736:C:H2'	1:L5:737:C:H4'	1.88	0.56
1:L5:4734:A:H2'	1:L5:4735:G:C8	2.40	0.56
21:LS:20:PRO:HD2	21:LS:21:LYS:N	2.18	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:LY:54:GLU:OE1	27:LY:54:GLU:N	2.36	0.56
47:S2:1536:G:H22	47:S2:1597:C:H42	1.52	0.56
52:SE:95:THR:OG1	52:SE:97:GLU:OE1	2.23	0.56
1:L5:466:A:H2'	1:L5:467:U:O4'	2.06	0.56
1:L5:4184:G:H5'	4:LA:233:ARG:HB2	1.88	0.56
33:Le:88:LEU:HD22	33:Le:95:TYR:CE2	2.41	0.56
47:S2:878:G:N3	47:S2:909:G:N2	2.54	0.56
47:S2:1452:A:C6	47:S2:1475:G:C6	2.93	0.56
47:S2:1834:A:H2	47:S2:1837:G:H1	1.53	0.56
49:SA:54:THR:HG22	49:SA:162:PRO:HG2	1.88	0.56
54:SH:64:VAL:HG12	54:SH:66:VAL:H	1.69	0.56
59:SQ:58:LEU:HD21	59:SQ:112:LEU:HD11	1.88	0.56
62:ST:22:LEU:HD12	62:ST:28:LEU:HD12	1.86	0.56
62:ST:39:LEU:HD23	62:ST:43:LYS:HZ1	1.71	0.56
76:SO:57:THR:N	76:SO:60:MET:HE3	2.20	0.56
1:L5:462:G:H2'	1:L5:463:A:H8	1.69	0.56
1:L5:497:G:N2	1:L5:657:C:N3	2.54	0.56
1:L5:4715:C:H5"	5:LB:278:THR:HG21	1.88	0.56
13:LJ:63:ARG:HH12	43:Lo:103:VAL:HG11	1.71	0.56
47:S2:1004:U:H2'	47:S2:1005:G:H8	1.70	0.56
47:S2:1311:C:H2'	47:S2:1312:G:C8	2.40	0.56
49:SA:180:ARG:O	49:SA:184:ARG:HG2	2.06	0.56
51:SD:170:THR:HG22	51:SD:187:LYS:HG3	1.86	0.56
56:SK:5:LYS:NZ	69:Sf:99:LYS:HE2	2.21	0.56
70:Sg:133:ASN:HD21	70:Sg:139:LYS:HB2	1.70	0.56
73:SJ:12:THR:HG22	73:SJ:45:ARG:HG3	1.87	0.56
73:SJ:30:LYS:HB3	81:Se:42:PHE:CE2	2.40	0.56
1:L5:62:A:N3	1:L5:77:U:O2'	2.37	0.56
1:L5:464:G:N2	1:L5:465:G:O6	2.39	0.56
1:L5:474:C:H2'	1:L5:475:G:C8	2.40	0.56
1:L5:755:C:H1'	11:LH:54:ARG:HH22	1.70	0.56
1:L5:1260:G:H2'	1:L5:1261:G:C8	2.40	0.56
1:L5:2028:C:H2'	1:L5:2029:A:C8	2.40	0.56
1:L5:3656:A:H2'	1:L5:3657:U:H6	1.71	0.56
14:LL:205:GLN:HA	14:LL:208:GLU:HB2	1.87	0.56
25:LW:85:ALA:HB3	72:SG:129:VAL:HG22	1.87	0.56
29:La:91:ALA:HB2	29:La:120:GLN:HG3	1.87	0.56
31:Lc:51:ASN:ND2	31:Lc:77:ASN:OD1	2.37	0.56
47:S2:1777:G:H2'	47:S2:1778:C:C2	2.40	0.56
61:SS:120:HIS:HB3	61:SS:123:LEU:HB2	1.88	0.56
1:L5:993:G:N1	1:L5:1051:G:OP1	2.35	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:1093:C:H2'	1:L5:1094:G:C8	2.41	0.56
1:L5:1307:A:H2'	1:L5:1308:C:H6	1.69	0.56
1:L5:1396:G:O2'	1:L5:1468:C:O2'	2.23	0.56
1:L5:4076:G:H5'	10:LG:73:ARG:HH11	1.70	0.56
5:LB:237:THR:HG21	5:LB:251:VAL:HG22	1.88	0.56
6:LC:218:ILE:HA	6:LC:229:LEU:HD13	1.88	0.56
9:LF:75:ALA:HB2	22:LT:140:PHE:HE1	1.70	0.56
33:Le:88:LEU:HD22	33:Le:95:TYR:HE2	1.70	0.56
47:S2:67:C:H5	72:SG:162:LEU:HD23	1.70	0.56
47:S2:149:A:N7	47:S2:169:U:O2	2.39	0.56
47:S2:614:C:O2'	47:S2:626:G:N2	2.38	0.56
73:SJ:169:ARG:NH1	73:SJ:170:PRO:O	2.38	0.56
80:Sb:23:ARG:NH1	80:Sb:27:SER:O	2.39	0.56
1:L5:1173:G:H1	1:L5:1188:C:H2'	1.69	0.56
1:L5:4149:C:H2'	1:L5:4150:G:H8	1.70	0.56
1:L5:4303:C:H2'	1:L5:4305:G:C8	2.41	0.56
47:S2:639:C:H2'	47:S2:640:A:H8	1.70	0.56
47:S2:1656:G:H2'	47:S2:1657:G:H8	1.71	0.56
50:SB:172:MET:O	50:SB:176:VAL:HG12	2.06	0.56
55:SI:150:ASP:O	55:SI:154:LYS:NZ	2.39	0.56
1:L5:3596:A:H4'	20:LR:143:HIS:CG	2.41	0.55
1:L5:3732:A:H2'	1:L5:3733:A:C8	2.41	0.55
43:Lo:2:VAL:N	43:Lo:90:HIS:O	2.40	0.55
47:S2:190:G:O2'	47:S2:209:A:N6	2.39	0.55
47:S2:1705:C:H2'	47:S2:1706:G:C8	2.41	0.55
79:SZ:51:ASP:OD1	79:SZ:52:LYS:N	2.37	0.55
1:L5:1100:U:H3	1:L5:1195:G:H1	1.53	0.55
1:L5:1277:G:C2	1:L5:1278:C:C4	2.95	0.55
1:L5:4093:G:H3'	1:L5:4094:G:H8	1.71	0.55
11:LH:182:SER:HB2	41:Lm:83:ARG:HH12	1.71	0.55
19:LQ:12:LYS:HB2	19:LQ:14:ARG:NH1	2.20	0.55
47:S2:1287:A:C6	47:S2:1314:U:C4	2.94	0.55
47:S2:1693:G:N2	47:S2:1834:A:H8	2.05	0.55
52:SE:231:GLY:O	52:SE:233:LYS:N	2.36	0.55
59:SQ:109:LYS:HZ1	59:SQ:120:LEU:HD13	1.72	0.55
1:L5:1069:G:OP2	8:LE:65:ARG:NH2	2.39	0.55
1:L5:1378:C:H3'	1:L5:1379:C:C5'	2.35	0.55
1:L5:2764:A:H2'	1:L5:2765:A:C8	2.41	0.55
6:LC:319:LEU:HD21	9:LF:152:GLU:HG3	1.89	0.55
8:LE:46:ARG:HA	8:LE:65:ARG:HH12	1.71	0.55
47:S2:688:U:H4'	47:S2:689:U:O5'	2.05	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:SU:67:LYS:HB2	63:SU:78:ASP:HB2	1.88	0.55
68:Sd:33:LYS:HG3	68:Sd:34:TYR:CD2	2.42	0.55
1:L5:976:G:H3'	1:L5:977:C:H6	1.72	0.55
27:LY:53:ASP:HB3	27:LY:108:ARG:O	2.07	0.55
38:Lj:27:TYR:HA	38:Lj:34:CYS:HA	1.87	0.55
39:Lk:24:LYS:HZ2	39:Lk:69:LEU:HB2	1.72	0.55
52:SE:185:GLY:H	52:SE:189:LEU:HB3	1.70	0.55
53:SF:17:ILE:HG23	53:SF:18:LYS:H	1.72	0.55
60:SR:128:PHE:HD2	60:SR:130:THR:H	1.54	0.55
70:Sg:105:THR:OG1	70:Sg:126:ASP:OD2	2.24	0.55
78:SY:52:PRO:HA	78:SY:55:ILE:HD13	1.89	0.55
80:Sb:35:VAL:HG22	80:Sb:37:CYS:H	1.70	0.55
1:L5:1974:U:H4'	1:L5:1975:G:H5'	1.89	0.55
1:L5:4149:C:H2'	1:L5:4150:G:C8	2.42	0.55
11:LH:128:MET:HE1	11:LH:146:LEU:HD22	1.88	0.55
47:S2:106:C:H2'	47:S2:107:A:H8	1.70	0.55
65:SX:9:THR:O	65:SX:11:ARG:N	2.39	0.55
82:Pt:48:U:H4'	82:Pt:49:C:H5'	1.88	0.55
1:L5:1966:C:H2'	1:L5:1967:A:H8	1.71	0.55
1:L5:2550:G:C2	1:L5:2551:A:C8	2.94	0.55
11:LH:23:ARG:HE	11:LH:39:ASN:HA	1.71	0.55
11:LH:92:MET:HB2	11:LH:144:LEU:HB2	1.87	0.55
31:Lc:53:PRO:O	31:Lc:55:LEU:N	2.39	0.55
39:Lk:24:LYS:NZ	39:Lk:69:LEU:HB2	2.22	0.55
47:S2:867:G:H2'	47:S2:868:G:C8	2.42	0.55
47:S2:953:C:O2	76:SO:55:ARG:NH2	2.39	0.55
53:SF:35:LEU:HD22	53:SF:117:ILE:HD13	1.89	0.55
54:SH:10:LYS:HE2	54:SH:12:ASN:HD21	1.72	0.55
55:SI:190:LEU:HB3	55:SI:195:LEU:HB2	1.88	0.55
57:SL:79:LYS:HB2	57:SL:87:VAL:HG12	1.88	0.55
77:SW:51:GLU:HG3	80:Sb:8:LEU:HD11	1.87	0.55
1:L5:956:A:H3'	1:L5:957:G:C8	2.41	0.55
1:L5:1552:G:H2'	1:L5:1574:G:H22	1.71	0.55
8:LE:44:CYS:SG	8:LE:45:SER:N	2.80	0.55
11:LH:141:LYS:HD2	11:LH:142:ASP:N	2.22	0.55
21:LS:173:ASN:OD1	21:LS:174:THR:N	2.39	0.55
47:S2:983:A:H2	76:SO:139:SER:HB3	1.71	0.55
47:S2:1010:G:H2'	47:S2:1011:A:C8	2.41	0.55
47:S2:1127:C:H4'	80:Sb:17:ARG:HD2	1.89	0.55
47:S2:1562:C:H2'	47:S2:1563:G:C8	2.41	0.55
77:SW:30:CYS:HA	77:SW:34:ILE:HD11	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:3598:C:H2'	1:L5:3599:A:C8	2.41	0.55
1:L5:4767:C:O2'	1:L5:4874:A:N6	2.39	0.55
47:S2:1213:C:O2'	47:S2:1214:A:H5'	2.07	0.55
57:SL:61:PRO:HG3	57:SL:141:ASN:ND2	2.22	0.55
69:Sf:87:THR:HB	69:Sf:91:ASN:HD21	1.72	0.55
76:SO:17:LEU:HD23	76:SO:18:GLY:H	1.72	0.55
81:Se:24:LYS:HG3	81:Se:25:LYS:HG3	1.88	0.55
1:L5:973:G:N7	1:L5:974:C:N4	2.53	0.55
1:L5:1251:C:H1'	1:L5:1260:G:H1	1.72	0.55
1:L5:1552:G:O2'	1:L5:1575:A:N6	2.40	0.55
1:L5:1879:C:O2'	1:L5:1891:A:N3	2.40	0.55
1:L5:1985:G:H1	1:L5:2013:A:N6	1.98	0.55
1:L5:4124:G:O2'	4:LA:64:ARG:NH2	2.38	0.55
1:L5:4252:C:OP2	1:L5:4253:A:O2'	2.25	0.55
6:LC:183:VAL:HG22	6:LC:204:ARG:HB2	1.88	0.55
6:LC:210:ILE:HB	6:LC:252:TRP:CD1	2.41	0.55
9:LF:243:LEU:O	9:LF:247:MET:HG3	2.06	0.55
21:LS:80:ILE:HG12	21:LS:129:VAL:HG23	1.87	0.55
22:LT:127:GLN:NE2	22:LT:129:LYS:O	2.37	0.55
47:S2:1468:C:H2'	47:S2:1469:A:H8	1.67	0.55
50:SB:103:MET:HG2	50:SB:215:VAL:HG12	1.88	0.55
50:SB:189:ILE:HB	50:SB:190:PRO:HD3	1.88	0.55
51:SD:214:LYS:HG3	51:SD:215:ASP:HB2	1.89	0.55
53:SF:95:HIS:CD2	79:SZ:106:GLN:HE21	2.20	0.55
71:SC:221:ASP:OD1	71:SC:222:CYS:N	2.39	0.55
1:L5:287:U:O2	16:LN:93:LYS:HE3	2.07	0.55
1:L5:3719:A:H2'	1:L5:3720:G:C8	2.41	0.55
1:L5:4233:A:O2'	1:L5:4234:A:H2'	2.07	0.55
24:LV:45:ILE:HG21	24:LV:53:PRO:HB3	1.89	0.55
29:La:117:LEU:HD23	29:La:140:VAL:HG21	1.89	0.55
47:S2:106:C:OP1	47:S2:431:G:O2'	2.21	0.55
47:S2:857:U:H2'	47:S2:858:A:C8	2.42	0.55
50:SB:226:GLY:HA2	50:SB:229:MET:HG2	1.89	0.55
53:SF:91:ARG:HH11	79:SZ:103:HIS:HE1	1.55	0.55
70:Sg:15:ASN:O	70:Sg:305:ASN:ND2	2.40	0.55
82:Pt:29:C:H2'	82:Pt:30:G:C8	2.42	0.55
1:L5:1410:U:O2'	1:L5:1411:C:O5'	2.23	0.54
1:L5:3772:U:H5'	1:L5:3773:U:OP2	2.06	0.54
1:L5:4232:U:O4	43:Lo:8:ARG:NH2	2.40	0.54
7:LD:21:ARG:O	7:LD:25:GLU:HG2	2.07	0.54
12:LI:135:ILE:HG22	12:LI:136:MET:HG3	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:LN:184:ILE:O	16:LN:194:ARG:NH2	2.39	0.54
46:Lz:20:GLY:O	46:Lz:23:ARG:NE	2.39	0.54
47:S2:1060:A:O2'	47:S2:1062:A:N7	2.29	0.54
47:S2:1221:G:H2'	47:S2:1222:G:H8	1.71	0.54
48:S6:20:A:H62	48:S6:59:A:H61	1.55	0.54
70:Sg:158:PRO:HG2	70:Sg:202:PRO:HB3	1.89	0.54
72:SG:159:ARG:HB3	72:SG:172:LYS:HB3	1.89	0.54
1:L5:1177:U:OP1	7:LD:279:ARG:NH2	2.40	0.54
1:L5:1758:G:OP2	1:L5:1768:C:N4	2.41	0.54
1:L5:4100:C:N4	1:L5:4109:G:H22	2.05	0.54
5:LB:300:LYS:HG2	5:LB:311:ASP:OD1	2.07	0.54
12:LI:38:ARG:HG3	12:LI:83:ASP:HB2	1.89	0.54
23:LU:35:ASP:OD1	23:LU:90:TYR:OH	2.24	0.54
47:S2:1135:C:H2'	47:S2:1136:U:C6	2.42	0.54
82:Pt:70:C:H2'	82:Pt:71:G:C8	2.41	0.54
1:L5:727:C:OP1	9:LF:76:ARG:NH2	2.35	0.54
1:L5:2815:A:H2'	1:L5:2816:G:C8	2.43	0.54
3:L8:141:C:H2'	3:L8:142:U:C6	2.42	0.54
14:LL:161:TYR:HE2	29:La:105:ARG:HH21	1.54	0.54
35:Lg:41:ALA:O	35:Lg:52:ARG:NH1	2.39	0.54
46:Lz:100:VAL:HG23	46:Lz:102:LYS:HG2	1.89	0.54
47:S2:1014:G:N2	80:Sb:51:GLN:OE1	2.40	0.54
71:SC:166:ARG:HD3	71:SC:181:PRO:HG3	1.90	0.54
1:L5:713:C:H2'	1:L5:714:G:C8	2.41	0.54
1:L5:4904:G:H2'	1:L5:4905:C:C6	2.42	0.54
6:LC:101:MET:HE3	6:LC:104:PRO:HA	1.89	0.54
34:Lf:46:ARG:H	34:Lf:107:PRO:HG2	1.72	0.54
41:Lm:95:ILE:HD13	41:Lm:102:ARG:HA	1.88	0.54
47:S2:525:A:H2'	47:S2:526:A:C8	2.43	0.54
47:S2:527:C:H2'	47:S2:528:A:C8	2.43	0.54
47:S2:863:U:O2'	77:SW:78:ARG:NH1	2.40	0.54
56:SK:60:GLU:HB3	56:SK:69:TRP:HA	1.89	0.54
60:SR:17:ILE:HD11	60:SR:54:VAL:HG13	1.90	0.54
72:SG:209:TYR:HB3	72:SG:214:ALA:HB2	1.89	0.54
1:L5:106:A:H1'	1:L5:336:A:C8	2.42	0.54
1:L5:1956:A:C5	1:L5:1957:U:H1'	2.42	0.54
1:L5:1969:G:N2	1:L5:1999:A:N3	2.56	0.54
1:L5:3959:U:O2'	1:L5:3960:A:N3	2.40	0.54
4:LA:32:VAL:HG22	4:LA:163:ARG:HH12	1.72	0.54
9:LF:219:GLY:O	9:LF:246:ARG:NH2	2.41	0.54
24:LV:126:ALA:HB1	24:LV:133:ALA:HB2	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:S2:1664:A:H3'	47:S2:1666:C:H41	1.71	0.54
48:S6:10:G:O2'	48:S6:11:G:N7	2.40	0.54
48:S6:13:G:H1	48:S6:23:C:H42	1.56	0.54
1:L5:666:G:H1'	45:Lr:46:ARG:HH12	1.73	0.54
1:L5:711:A:H1'	8:LE:136:HIS:CE1	2.43	0.54
1:L5:2295:C:O2'	6:LC:45:ARG:NH2	2.41	0.54
47:S2:1284:A:O2'	74:SM:33:ARG:NE	2.41	0.54
47:S2:1550:G:H3'	47:S2:1579:A:H61	1.72	0.54
1:L5:911:U:H2'	1:L5:912:G:C8	2.43	0.54
1:L5:2705:G:O6	20:LR:46:LYS:NZ	2.38	0.54
1:L5:4238:G:H2'	1:L5:4239:A:C8	2.42	0.54
47:S2:639:C:H2'	47:S2:640:A:C8	2.43	0.54
47:S2:1113:A:N6	47:S2:1119:A:N1	2.55	0.54
55:SI:36:THR:HG22	55:SI:57:ALA:O	2.08	0.54
77:SW:77:PRO:HG2	77:SW:79:PHE:CZ	2.43	0.54
3:L8:86:U:C5	36:Lh:7:ARG:HB3	2.42	0.54
7:LD:30:TYR:CD2	22:LT:24:VAL:HG11	2.43	0.54
7:LD:223:PHE:HB3	7:LD:226:TYR:HB2	1.90	0.54
8:LE:131:LYS:HE2	8:LE:135:GLN:HB3	1.90	0.54
8:LE:277:LEU:HA	8:LE:281:ILE:HD11	1.89	0.54
12:LI:111:LEU:HD11	82:Pt:2:G:O4'	2.08	0.54
32:Ld:18:ASN:OD1	32:Ld:19:GLU:N	2.40	0.54
62:ST:115:LYS:HZ2	62:ST:121:ARG:HD3	1.72	0.54
72:SG:51:ARG:HH21	72:SG:112:VAL:HG11	1.72	0.54
1:L5:1085:C:O2	1:L5:1213:G:N2	2.38	0.54
1:L5:1750:G:H5'	12:LI:40:LYS:HE3	1.90	0.54
1:L5:2889:G:H21	1:L5:5034:A:H8	1.54	0.54
8:LE:277:LEU:HD11	8:LE:283:PRO:HG3	1.89	0.54
25:LW:96:GLN:O	25:LW:104:GLN:NE2	2.39	0.54
27:LY:30:MET:HE2	27:LY:49:ILE:HD11	1.88	0.54
38:Lj:2:THR:O	38:Lj:7:SER:OG	2.21	0.54
47:S2:465:A:H4'	47:S2:466:G:O5'	2.07	0.54
53:SF:91:ARG:HD2	79:SZ:103:HIS:CE1	2.43	0.54
63:SU:81:GLN:HG2	68:Sd:55:LEU:HD12	1.90	0.54
1:L5:717:U:H3	1:L5:951:G:H1	1.56	0.54
1:L5:2108:G:H3'	1:L5:2109:G:C8	2.43	0.54
1:L5:3720:G:H22	1:L5:3733:A:H2	1.56	0.54
1:L5:4636:U:OP1	32:Ld:41:ARG:NH2	2.41	0.54
1:L5:5030:U:C2	1:L5:5031:G:C8	2.96	0.54
4:LA:137:ILE:HD11	4:LA:149:LYS:HB2	1.90	0.54
15:LM:96:GLU:HA	15:LM:99:GLU:HB2	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:Le:76:LYS:HD2	33:Le:98:GLU:OE2	2.08	0.54
47:S2:213:G:O2'	47:S2:214:U:OP1	2.25	0.54
47:S2:1287:A:C5	47:S2:1314:U:O4	2.61	0.54
47:S2:1537:A:H5"	62:ST:84:ARG:HH22	1.72	0.54
47:S2:1583:C:H5"	47:S2:1584:G:H2'	1.89	0.54
52:SE:152:PRO:HD2	72:SG:216:ARG:HG2	1.89	0.54
66:Sa:99:PRO:O	66:Sa:102:ARG:NH1	2.35	0.54
74:SM:31:LEU:HB3	74:SM:33:ARG:HH11	1.72	0.54
1:L5:454:U:H1'	1:L5:455:C:C5	2.43	0.53
1:L5:1177:U:C2	1:L5:1178:G:N7	2.75	0.53
1:L5:1602:U:OP1	38:Lj:2:THR:OG1	2.19	0.53
14:LL:36:ARG:O	14:LL:40:GLN:HG3	2.08	0.53
27:LY:53:ASP:OD2	27:LY:110:LYS:N	2.40	0.53
46:Lz:54:ARG:HD3	46:Lz:149:ASP:HA	1.89	0.53
47:S2:326:C:OP1	47:S2:327:G:N2	2.41	0.53
47:S2:873:G:H2'	47:S2:874:G:H8	1.73	0.53
47:S2:1393:G:H2'	47:S2:1394:G:C8	2.43	0.53
53:SF:175:ASP:OD1	53:SF:176:GLU:N	2.41	0.53
54:SH:162:GLN:OE1	54:SH:165:ASN:ND2	2.36	0.53
77:SW:24:GLN:NE2	80:Sb:6:ASP:HA	2.23	0.53
1:L5:1084:C:H2'	1:L5:1085:C:C6	2.43	0.53
7:LD:50:ARG:NH2	7:LD:72:ASP:OD2	2.41	0.53
8:LE:135:GLN:OE1	8:LE:135:GLN:N	2.41	0.53
21:LS:99:ASP:OD1	21:LS:100:LEU:N	2.39	0.53
27:LY:31:SER:HA	27:LY:48:PRO:HA	1.89	0.53
45:Lr:65:LYS:O	45:Lr:102:TYR:OH	2.19	0.53
51:SD:7:LYS:HA	51:SD:10:LYS:HE3	1.90	0.53
53:SF:59:LYS:HE3	53:SF:61:PHE:HD2	1.74	0.53
54:SH:145:ARG:NH1	77:SW:51:GLU:OE2	2.37	0.53
76:SO:64:ALA:O	76:SO:66:ARG:N	2.40	0.53
1:L5:132:G:C2	1:L5:133:C:H1'	2.43	0.53
1:L5:651:C:H2'	1:L5:652:G:C8	2.43	0.53
1:L5:978:G:C6	1:L5:1277:G:C2	2.96	0.53
5:LB:160:ILE:HD11	5:LB:193:LYS:HB3	1.91	0.53
47:S2:206:G:H2'	47:S2:207:G:C8	2.43	0.53
47:S2:1282:A:H2	47:S2:1287:A:H5'	1.73	0.53
54:SH:165:ASN:O	54:SH:169:LYS:NZ	2.41	0.53
59:SQ:12:VAL:HG11	59:SQ:90:LYS:HG3	1.90	0.53
76:SO:31:CYS:HB2	76:SO:93:LEU:HD12	1.91	0.53
1:L5:99:A:H2'	1:L5:100:C:O2	2.08	0.53
1:L5:4594:U:H2'	1:L5:4595:G:C8	2.44	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:4600:G:O2'	1:L5:4601:U:O5'	2.26	0.53
1:L5:4635:A:O2'	1:L5:4637:G:OP1	2.26	0.53
1:L5:4904:G:H2'	1:L5:4905:C:H6	1.74	0.53
7:LD:202:GLN:NE2	7:LD:237:GLU:OE1	2.41	0.53
13:LJ:35:ARG:HG2	13:LJ:123:ILE:HA	1.90	0.53
26:LX:69:ASN:HD22	26:LX:69:ASN:C	2.11	0.53
47:S2:104:A:OP1	55:SI:12:ARG:NH1	2.41	0.53
47:S2:913:A:H1'	54:SH:66:VAL:HG11	1.90	0.53
47:S2:975:G:H2'	47:S2:976:G:C8	2.44	0.53
52:SE:34:GLY:HA3	52:SE:83:PRO:HG3	1.90	0.53
68:Sd:7:TYR:CE1	69:Sf:146:LEU:HB3	2.41	0.53
73:SJ:19:PRO:O	73:SJ:24:ARG:NH2	2.42	0.53
1:L5:383:A:O2'	1:L5:384:A:H8	1.92	0.53
1:L5:509:A:N1	29:La:106:SER:OG	2.38	0.53
1:L5:746:A:H2	1:L5:916:C:H5	1.55	0.53
1:L5:3702:A:O2'	1:L5:3774:A:OP1	2.22	0.53
1:L5:3848:U:H2'	1:L5:3849:A:H8	1.74	0.53
1:L5:4413:C:H41	1:L5:4429:C:H41	1.56	0.53
25:LW:115:ALA:O	25:LW:119:LYS:HG2	2.07	0.53
27:LY:83:GLU:O	27:LY:86:GLN:NE2	2.40	0.53
29:La:82:VAL:HG13	29:La:83:SER:H	1.74	0.53
43:Lo:34:TYR:O	43:Lo:39:ARG:NH1	2.42	0.53
47:S2:62:G:O2'	47:S2:172:U:OP1	2.26	0.53
55:SI:39:GLY:HA3	55:SI:59:ARG:HD2	1.88	0.53
78:SY:86:GLU:OE2	78:SY:90:ARG:HD2	2.07	0.53
1:L5:1397:A:C8	29:La:114:LYS:HD2	2.43	0.53
1:L5:2025:A:N3	1:L5:2026:A:H1'	2.24	0.53
1:L5:2468:U:O2'	1:L5:2506:G:N2	2.41	0.53
6:LC:209:ILE:HB	6:LC:229:LEU:HD23	1.90	0.53
34:Lf:28:LEU:HD22	34:Lf:101:ILE:HD11	1.90	0.53
46:Lz:25:ARG:HH22	46:Lz:210:MET:HG3	1.74	0.53
47:S2:12:U:H2'	47:S2:13:C:C6	2.43	0.53
74:SM:59:PRO:O	74:SM:60:MET:HG3	2.08	0.53
1:L5:1075:G:N2	1:L5:1235:G:H22	2.07	0.53
1:L5:4903:G:H2'	1:L5:4904:G:H8	1.74	0.53
2:L7:23:A:HO2'	2:L7:24:C:H6	1.56	0.53
5:LB:233:SER:O	5:LB:272:LYS:NZ	2.39	0.53
5:LB:314:ILE:O	5:LB:314:ILE:HG13	2.09	0.53
33:Le:104:SER:OG	33:Le:105:SER:N	2.32	0.53
47:S2:67:C:N3	72:SG:164:LYS:NZ	2.46	0.53
47:S2:560:A:H2'	47:S2:561:A:C8	2.44	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:S2:872:A:O2'	47:S2:873:G:H8	1.91	0.53
47:S2:1033:G:OP1	75:SN:109:LYS:NZ	2.28	0.53
47:S2:1228:A:H2'	47:S2:1229:G:C8	2.44	0.53
47:S2:1280:G:H22	47:S2:1317:C:H41	1.54	0.53
52:SE:15:PRO:HD2	52:SE:18:TRP:CE3	2.44	0.53
1:L5:509:A:H2'	14:LL:163:LYS:NZ	2.24	0.53
4:LA:29:LEU:H	4:LA:123:ARG:HB3	1.74	0.53
47:S2:493:A:H1'	47:S2:574:A:H5'	1.90	0.53
47:S2:1467:C:H2'	47:S2:1468:C:C6	2.44	0.53
47:S2:1588:A:O2'	47:S2:1589:A:O5'	2.21	0.53
56:SK:9:ILE:HA	56:SK:12:TYR:HD1	1.74	0.53
69:Sf:108:VAL:HG23	69:Sf:110:GLU:H	1.72	0.53
75:SN:62:GLN:O	75:SN:66:VAL:HG23	2.09	0.53
1:L5:2695:A:H4'	1:L5:2696:A:O5'	2.09	0.53
1:L5:4124:G:N2	10:LG:43:GLN:O	2.42	0.53
19:LQ:89:ASP:OD2	19:LQ:91:ARG:NH2	2.35	0.53
20:LR:39:GLN:HB2	20:LR:42:ARG:HH21	1.74	0.53
34:Lf:40:GLU:O	34:Lf:109:ARG:NH2	2.41	0.53
47:S2:148:U:H2'	47:S2:149:A:H8	1.73	0.53
47:S2:155:G:H2'	47:S2:156:G:C8	2.44	0.53
47:S2:1102:G:OP1	50:SB:151:ARG:NH2	2.41	0.53
49:SA:21:ALA:HB1	49:SA:169:HIS:O	2.09	0.53
55:SI:8:TRP:HA	55:SI:18:ARG:HH21	1.73	0.53
63:SU:49:LYS:C	63:SU:51:LYS:H	2.17	0.53
65:SX:54:LYS:HG3	81:Se:6:LEU:HD11	1.91	0.53
70:Sg:217:MET:HE2	70:Sg:226:HIS:NE2	2.23	0.53
1:L5:687:U:H2'	1:L5:688:U:O4'	2.08	0.53
1:L5:4575:G:O2'	1:L5:5069:U:OP1	2.25	0.53
4:LA:117:GLU:O	4:LA:158:ILE:HD11	2.09	0.53
6:LC:23:THR:OG1	6:LC:24:LEU:N	2.40	0.53
7:LD:59:ASP:OD2	7:LD:60:ILE:N	2.41	0.53
9:LF:86:GLU:OE2	22:LT:136:ARG:NH1	2.42	0.53
9:LF:148:LYS:HA	9:LF:151:ASN:HB2	1.90	0.53
11:LH:184:LYS:HZ1	41:Lm:128:LYS:HA	1.74	0.53
47:S2:1109:C:O2'	47:S2:1110:G:H8	1.91	0.53
69:Sf:138:ARG:NH2	69:Sf:139:HIS:O	2.41	0.53
70:Sg:72:SER:HB2	70:Sg:113:PHE:HE2	1.74	0.53
1:L5:271:C:H2'	1:L5:272:U:C6	2.44	0.52
1:L5:1942:A:H2'	1:L5:1943:A:C8	2.44	0.52
1:L5:4069:U:H2'	1:L5:4070:U:C6	2.44	0.52
1:L5:4860:G:H2'	1:L5:4861:G:C8	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:4874:A:N3	17:LO:175:MET:HG2	2.24	0.52
1:L5:4909:A:O2'	1:L5:4910:G:O5'	2.25	0.52
11:LH:120:GLU:HG2	11:LH:124:ARG:HH12	1.74	0.52
22:LT:75:VAL:HG22	22:LT:88:ARG:HD3	1.90	0.52
25:LW:46:PRO:HB2	25:LW:54:LEU:HD12	1.90	0.52
47:S2:145:G:H2'	47:S2:146:G:C8	2.45	0.52
47:S2:482:G:N1	47:S2:485:A:OP2	2.40	0.52
47:S2:842:C:H2'	47:S2:843:C:H6	1.73	0.52
47:S2:1244:U:H2'	47:S2:1245:G:H8	1.74	0.52
50:SB:183:GLU:O	50:SB:187:LYS:HG2	2.09	0.52
55:SI:100:CYS:SG	55:SI:175:ILE:HD13	2.48	0.52
59:SQ:6:PRO:HG2	59:SQ:8:GLN:HE22	1.74	0.52
59:SQ:112:LEU:HD23	59:SQ:119:LEU:HD23	1.90	0.52
65:SX:53:GLU:O	65:SX:70:VAL:HG23	2.09	0.52
78:SY:9:THR:HG22	78:SY:25:ILE:HA	1.91	0.52
6:LC:357:ALA:O	6:LC:360:ALA:N	2.42	0.52
11:LH:7:ASN:OD1	11:LH:8:GLN:N	2.43	0.52
16:LN:136:ASP:O	16:LN:142:ILE:HD11	2.09	0.52
35:Lg:67:LEU:HD11	35:Lg:71:LYS:HD2	1.91	0.52
47:S2:496:C:H2'	47:S2:497:C:C6	2.44	0.52
47:S2:1109:C:HO2'	47:S2:1110:G:H8	1.55	0.52
49:SA:75:SER:HA	49:SA:97:THR:HB	1.90	0.52
49:SA:80:ARG:O	49:SA:84:GLN:HG3	2.09	0.52
51:SD:35:SER:HB2	51:SD:52:ALA:HA	1.91	0.52
53:SF:45:TYR:H	53:SF:46:ALA:CA	2.21	0.52
1:L5:911:U:H2'	1:L5:912:G:H8	1.74	0.52
1:L5:1477:C:H2'	1:L5:1478:C:O4'	2.10	0.52
1:L5:1866:U:O2'	1:L5:1867:A:O4'	2.26	0.52
1:L5:3719:A:H2'	1:L5:3720:G:H8	1.74	0.52
1:L5:4645:C:OP2	20:LR:62:ARG:NH2	2.43	0.52
5:LB:322:HIS:O	5:LB:342:LYS:NZ	2.42	0.52
6:LC:252:TRP:HE3	6:LC:257:PHE:HD1	1.56	0.52
18:LP:95:LEU:HD23	18:LP:148:MET:HE1	1.90	0.52
47:S2:168:C:OP1	72:SG:131:ARG:NH1	2.39	0.52
47:S2:558:G:H2'	47:S2:559:G:C8	2.44	0.52
47:S2:925:G:H1	47:S2:1017:U:H3	1.56	0.52
47:S2:1098:C:H2'	47:S2:1099:G:C8	2.44	0.52
53:SF:77:MET:HE2	53:SF:86:LYS:HB2	1.89	0.52
55:SI:36:THR:OG1	55:SI:96:LEU:O	2.26	0.52
57:SL:77:VAL:HA	57:SL:88:ILE:HG22	1.90	0.52
74:SM:51:VAL:HG23	74:SM:77:ILE:HB	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:168:C:O2	1:L5:268:G:N1	2.43	0.52
1:L5:279:A:OP2	16:LN:8:GLN:NE2	2.42	0.52
1:L5:1752:G:H2'	1:L5:1753:G:O4'	2.09	0.52
1:L5:1839:U:H5"	9:LF:113:ARG:HD2	1.90	0.52
1:L5:3599:A:H2'	1:L5:3600:G:H8	1.75	0.52
6:LC:8:ILE:HD11	6:LC:257:PHE:CZ	2.44	0.52
9:LF:31:LYS:HA	9:LF:34:ARG:NH1	2.24	0.52
12:LI:3:ARG:NH2	12:LI:63:GLU:OE2	2.42	0.52
17:LO:47:PHE:HZ	17:LO:144:GLU:HG3	1.75	0.52
47:S2:1102:G:H22	47:S2:1130:G:N2	2.08	0.52
54:SH:144:ILE:HG23	77:SW:52:ILE:CG2	2.36	0.52
77:SW:90:GLN:HB2	77:SW:94:LEU:HD12	1.91	0.52
1:L5:182:G:N2	1:L5:255:C:O2	2.39	0.52
1:L5:1072:C:H42	1:L5:1239:C:N4	2.08	0.52
1:L5:1577:G:O4'	4:LA:181:LYS:NZ	2.43	0.52
1:L5:1872:G:O2'	1:L5:4219:A:N3	2.38	0.52
1:L5:2557:G:H2'	1:L5:2558:C:C6	2.45	0.52
1:L5:3766:A:H5"	47:S2:1849:G:O6	2.10	0.52
8:LE:160:LYS:HG2	8:LE:274:VAL:HG12	1.91	0.52
23:LU:44:GLN:HG3	23:LU:56:LEU:HD21	1.91	0.52
32:Ld:54:MET:HG2	32:Ld:60:PRO:HA	1.91	0.52
47:S2:1869:A:H1'	50:SB:115:LYS:HG2	1.90	0.52
1:L5:943:A:H3'	9:LF:148:LYS:HD2	1.92	0.52
1:L5:1358:G:O2'	1:L5:1359:G:H5"	2.08	0.52
1:L5:4281:A:H2'	1:L5:4282:A:H2'	1.91	0.52
1:L5:4902:C:H2'	1:L5:4903:G:H8	1.74	0.52
17:LO:172:LYS:HG2	17:LO:176:ARG:NH1	2.25	0.52
25:LW:93:LYS:HG3	72:SG:145:PHE:H	1.74	0.52
32:Ld:24:GLU:OE2	32:Ld:87:ARG:HG2	2.10	0.52
47:S2:1340:U:H3'	47:S2:1341:C:H2'	1.91	0.52
70:Sg:69:VAL:HG23	70:Sg:80:SER:HB3	1.91	0.52
76:SO:126:ILE:HG22	76:SO:127:GLY:N	2.24	0.52
1:L5:61:A:O2'	16:LN:172:ARG:NH2	2.43	0.52
1:L5:126:C:N4	1:L5:142:G:H1	2.05	0.52
1:L5:704:C:H2'	1:L5:705:G:H8	1.74	0.52
1:L5:3754:G:H2'	1:L5:3755:G:C8	2.43	0.52
1:L5:4874:A:C2	17:LO:175:MET:HG2	2.45	0.52
32:Ld:26:THR:HB	32:Ld:85:ARG:HH11	1.75	0.52
47:S2:1112:U:H2'	47:S2:1113:A:H4'	1.91	0.52
47:S2:1563:G:H5"	62:ST:121:ARG:HH21	1.73	0.52
49:SA:63:ARG:HG2	64:SV:37:ALA:HB3	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:SH:52:GLU:HA	54:SH:58:LYS:HA	1.92	0.52
61:SS:51:ASP:OD1	61:SS:51:ASP:N	2.42	0.52
70:Sg:114:SER:OG	70:Sg:116:ASP:OD1	2.23	0.52
70:Sg:256:ILE:HB	70:Sg:270:LEU:HB3	1.90	0.52
76:SO:102:GLY:H	76:SO:134:PRO:HG2	1.73	0.52
82:Pt:22:A:N6	82:Pt:47:G7M:O2'	2.42	0.52
1:L5:983:C:H2'	1:L5:984:C:O4'	2.10	0.52
1:L5:1246:G:H2'	1:L5:1247:U:C6	2.44	0.52
1:L5:2539:C:H2'	1:L5:2540:C:C6	2.45	0.52
1:L5:3727:A:H2'	1:L5:3728:A:C8	2.45	0.52
1:L5:4993:G:H22	1:L5:5058:A:H2	1.56	0.52
11:LH:92:MET:HE2	11:LH:181:VAL:HB	1.91	0.52
28:LZ:31:ASP:OD1	28:LZ:32:GLY:N	2.43	0.52
36:Lh:48:ARG:O	36:Lh:52:LYS:HG2	2.10	0.52
47:S2:1428:G:H5"	59:SQ:33:LYS:HE2	1.90	0.52
56:SK:34:GLU:O	56:SK:36:ALA:N	2.43	0.52
70:Sg:117:ASN:O	70:Sg:134:THR:OG1	2.22	0.52
78:SY:25:ILE:HG21	78:SY:40:ILE:HD11	1.92	0.52
80:Sb:23:ARG:HH11	80:Sb:27:SER:HB2	1.74	0.52
1:L5:499:G:N2	1:L5:656:C:N3	2.58	0.52
1:L5:502:C:H5'	1:L5:504:G:H5"	1.92	0.52
1:L5:3967:G:H22	1:L5:4056:A:H1'	1.74	0.52
1:L5:5005:G:O2'	1:L5:5006:U:O5'	2.25	0.52
8:LE:223:ARG:HB3	8:LE:224:LYS:HA	1.92	0.52
51:SD:37:VAL:HG12	51:SD:50:ILE:HA	1.90	0.52
54:SH:64:VAL:HG13	54:SH:72:PHE:CE2	2.45	0.52
56:SK:1:MET:HE3	56:SK:44:HIS:H	1.75	0.52
1:L5:1378:C:H3'	1:L5:1379:C:H5'	1.90	0.52
1:L5:1447:C:C2	1:L5:1448:G:C8	2.97	0.52
1:L5:2767:U:O2'	1:L5:2769:U:O4'	2.27	0.52
6:LC:232:VAL:O	6:LC:233:SER:OG	2.25	0.52
15:LM:14:TYR:HD2	15:LM:56:GLN:HE21	1.57	0.52
46:Lz:90:LEU:HD23	46:Lz:124:LEU:HD11	1.92	0.52
47:S2:876:C:H2'	47:S2:878:G:H4'	1.92	0.52
47:S2:986:G:O4'	76:SO:138:ASP:HB2	2.10	0.52
47:S2:1285:G:O2'	47:S2:1286:G:H5'	2.10	0.52
57:SL:99:TYR:O	57:SL:101:ARG:N	2.43	0.52
61:SS:41:ALA:O	61:SS:45:LEU:HG	2.10	0.52
1:L5:973:G:N2	1:L5:1283:G:O4'	2.42	0.51
1:L5:1265:G:O3'	1:L5:2112:G:N2	2.43	0.51
1:L5:1761:G:H21	1:L5:1762:C:H41	1.57	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:1925:G:P	15:LM:33:GLN:HE22	2.30	0.51
1:L5:2669:C:O2'	1:L5:2670:C:O4'	2.28	0.51
34:Lf:75:THR:HG21	34:Lf:87:LYS:HG2	1.90	0.51
39:Lk:10:ASP:HA	39:Lk:13:LEU:HG	1.92	0.51
46:Lz:37:SER:HB3	46:Lz:203:ALA:HB3	1.92	0.51
47:S2:1008:A:H1'	75:SN:101:HIS:ND1	2.25	0.51
47:S2:1130:G:H4'	75:SN:10:GLY:HA2	1.92	0.51
47:S2:1562:C:H5"	62:ST:71:GLY:HA3	1.92	0.51
57:SL:55:TYR:OH	57:SL:116:CYS:SG	2.69	0.51
60:SR:17:ILE:HD12	60:SR:57:LEU:HD23	1.90	0.51
66:Sa:23:CYS:HB3	66:Sa:28:ARG:H	1.75	0.51
75:SN:46:THR:HG22	75:SN:49:GLN:OE1	2.10	0.51
75:SN:87:ASP:OD1	75:SN:87:ASP:N	2.43	0.51
82:Pt:63:C:H2'	82:Pt:64:G:H8	1.74	0.51
1:L5:4670:C:O2'	1:L5:4672:A:OP2	2.25	0.51
1:L5:5061:A:H61	5:LB:127:LYS:HZ2	1.58	0.51
9:LF:197:VAL:O	9:LF:201:PHE:HB2	2.10	0.51
9:LF:222:LYS:HB3	9:LF:231:GLY:HA2	1.91	0.51
23:LU:64:GLU:HB3	23:LU:71:THR:HB	1.92	0.51
47:S2:127:C:O2'	47:S2:184:G:N1	2.40	0.51
47:S2:1677:U:H5"	53:SF:148:ASN:ND2	2.23	0.51
75:SN:99:ARG:NH2	75:SN:119:GLU:OE2	2.42	0.51
75:SN:102:LEU:HD22	75:SN:115:LEU:HD13	1.91	0.51
80:Sb:56:CYS:HB3	80:Sb:63:LEU:HD22	1.93	0.51
1:L5:433:A:C2	1:L5:3867:A:H4'	2.45	0.51
1:L5:462:G:H2'	1:L5:463:A:C8	2.44	0.51
1:L5:517:C:N4	1:L5:644:G:O6	2.43	0.51
1:L5:4238:G:H2'	1:L5:4239:A:H8	1.73	0.51
8:LE:44:CYS:SG	8:LE:46:ARG:NH1	2.83	0.51
9:LF:60:GLU:O	9:LF:64:MET:HG3	2.10	0.51
47:S2:921:G:C2	80:Sb:22:LYS:HD3	2.45	0.51
47:S2:1344:A:H4'	47:S2:1345:G:H5'	1.91	0.51
50:SB:83:LYS:NZ	76:SO:130:GLU:OE2	2.35	0.51
60:SR:58:MET:HA	60:SR:61:ILE:HG12	1.91	0.51
61:SS:12:ILE:O	61:SS:22:GLY:N	2.39	0.51
64:SV:4:ASP:N	64:SV:4:ASP:OD1	2.42	0.51
65:SX:98:ASP:OD1	65:SX:99:GLU:N	2.43	0.51
1:L5:976:G:H1	1:L5:1278:C:H42	1.58	0.51
1:L5:4548:A:H5"	1:L5:4549:G:H5'	1.91	0.51
1:L5:4694:G:OP1	1:L5:4694:G:N2	2.29	0.51
3:L8:23:C:OP1	27:LY:15:ARG:NH1	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:LB:348:ARG:HH12	5:LB:351:LEU:HD22	1.75	0.51
13:LJ:85:LYS:HG2	13:LJ:115:LEU:HD22	1.91	0.51
24:LV:71:GLU:O	24:LV:75:LYS:NZ	2.38	0.51
32:Ld:60:PRO:HD2	32:Ld:100:ASN:HD21	1.76	0.51
40:Ll:24:PRO:HG2	40:Ll:27:ILE:HG12	1.91	0.51
47:S2:1706:G:HO2'	47:S2:1850:A:HO2'	1.54	0.51
52:SE:198:ARG:HD2	52:SE:200:ARG:HE	1.76	0.51
1:L5:216:C:OP1	1:L5:220:C:H5'	2.11	0.51
1:L5:464:G:H2'	1:L5:465:G:N7	2.26	0.51
1:L5:2815:A:H2'	1:L5:2816:G:H8	1.74	0.51
1:L5:2900:U:H2'	1:L5:2901:G:C8	2.45	0.51
1:L5:4439:U:O2'	12:LI:105:CYS:SG	2.68	0.51
1:L5:5027:C:H4'	1:L5:5028:G:C5'	2.41	0.51
7:LD:52:ILE:HA	7:LD:147:ASP:HB3	1.93	0.51
23:LU:42:PHE:CD2	23:LU:46:ARG:HD3	2.45	0.51
47:S2:216:C:N4	47:S2:309:G:H1	2.09	0.51
47:S2:1287:A:N6	47:S2:1312:G:O2'	2.42	0.51
48:S6:15:A:H2'	48:S6:16:G:C8	2.45	0.51
51:SD:122:VAL:O	51:SD:126:ILE:HG12	2.11	0.51
52:SE:11:ARG:NH2	52:SE:20:LEU:HB3	2.25	0.51
59:SQ:105:LYS:HA	59:SQ:108:ILE:HG22	1.91	0.51
62:ST:39:LEU:HD23	62:ST:43:LYS:NZ	2.25	0.51
73:SJ:58:ARG:O	73:SJ:62:THR:HG23	2.11	0.51
1:L5:2758:G:H2'	1:L5:2759:G:C8	2.46	0.51
8:LE:83:LYS:HB2	8:LE:84:LYS:HA	1.92	0.51
25:LW:98:PRO:HA	25:LW:99:GLU:CB	2.41	0.51
35:Lg:37:LYS:HB3	35:Lg:60:ARG:HH21	1.76	0.51
43:Lo:63:THR:O	43:Lo:87:ARG:NH2	2.42	0.51
47:S2:1289:U:H5"	69:Sf:95:ARG:HD3	1.91	0.51
47:S2:1421:A:N6	47:S2:1424:G:N7	2.59	0.51
54:SH:37:LYS:O	54:SH:39:GLN:N	2.44	0.51
55:SI:149:TYR:HB3	55:SI:153:LYS:NZ	2.26	0.51
59:SQ:98:LYS:O	70:Sg:57:ARG:NH2	2.44	0.51
68:Sd:39:CYS:SG	68:Sd:40:ARG:N	2.84	0.51
1:L5:1338:G:H22	29:La:25:HIS:CD2	2.29	0.51
1:L5:1551:C:H2'	1:L5:1552:G:O4'	2.10	0.51
1:L5:2474:G:N2	1:L5:2502:G:H2'	2.26	0.51
1:L5:2900:U:H2'	1:L5:2901:G:H8	1.75	0.51
1:L5:4280:A:OP1	7:LD:30:TYR:OH	2.22	0.51
2:L7:4:U:H2'	2:L7:5:A:H8	1.76	0.51
5:LB:86:VAL:HG12	5:LB:201:LEU:HD12	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:LE:254:ASP:OD1	8:LE:255:SER:N	2.43	0.51
36:Lh:90:ALA:O	36:Lh:94:ARG:HG2	2.10	0.51
47:S2:407:G:O6	65:SX:37:LYS:NZ	2.44	0.51
47:S2:868:G:O2'	47:S2:869:A:OP1	2.28	0.51
47:S2:1095:U:O2'	77:SW:20:ARG:NH2	2.43	0.51
47:S2:1458:G:H2'	47:S2:1459:G:H8	1.75	0.51
47:S2:1822:A:N1	47:S2:1823:A:N6	2.58	0.51
68:Sd:12:ARG:O	68:Sd:18:SER:OG	2.20	0.51
70:Sg:248:LEU:HD23	70:Sg:259:TRP:O	2.11	0.51
72:SG:77:LEU:HD12	72:SG:95:LYS:HB2	1.92	0.51
1:L5:166:C:H2'	1:L5:167:C:C6	2.46	0.51
1:L5:493:G:H2'	1:L5:494:U:C6	2.46	0.51
6:LC:210:ILE:HD12	6:LC:252:TRP:HE1	1.74	0.51
12:LI:30:LYS:HG3	12:LI:63:GLU:HB3	1.92	0.51
39:Lk:8:ILE:HD13	39:Lk:45:LEU:HD11	1.92	0.51
46:Lz:70:ASP:OD2	46:Lz:115:SER:OG	2.25	0.51
46:Lz:73:HIS:HD2	46:Lz:144:MET:SD	2.33	0.51
46:Lz:105:LYS:HB3	46:Lz:133:LYS:HD2	1.93	0.51
47:S2:691:G:H3'	47:S2:692:G:C5'	2.41	0.51
47:S2:852:G:H22	47:S2:853:C:H42	1.57	0.51
47:S2:857:U:H2'	47:S2:858:A:H8	1.74	0.51
54:SH:46:THR:HB	54:SH:63:PHE:HB2	1.93	0.51
55:SI:57:ALA:HB2	55:SI:183:GLY:HA2	1.92	0.51
70:Sg:230:LEU:HB3	70:Sg:259:TRP:CZ3	2.40	0.51
1:L5:325:U:H2'	1:L5:326:C:C6	2.46	0.51
1:L5:1645:C:P	6:LC:80:ARG:HH22	2.34	0.51
1:L5:3910:C:H2'	1:L5:3911:C:C6	2.46	0.51
1:L5:5028:G:H2'	1:L5:5029:C:H6	1.76	0.51
3:L8:79:G:H2'	3:L8:80:A:C4	2.46	0.51
25:LW:77:LYS:HB3	25:LW:78:PHE:HB3	1.93	0.51
47:S2:496:C:H5'	52:SE:29:PRO:HA	1.93	0.51
56:SK:5:LYS:HZ1	69:Sf:99:LYS:HE2	1.76	0.51
59:SQ:67:ASP:OD1	59:SQ:68:ILE:N	2.42	0.51
79:SZ:111:ARG:HH12	79:SZ:114:LYS:HG2	1.76	0.51
1:L5:1683:U:H2'	1:L5:1684:A:H8	1.76	0.51
1:L5:2457:G:H21	1:L5:3672:G:N2	2.09	0.51
9:LF:106:ARG:O	9:LF:110:GLN:HG2	2.11	0.51
16:LN:60:VAL:HG23	16:LN:134:LEU:HB2	1.92	0.51
46:Lz:34:LEU:N	46:Lz:167:VAL:O	2.44	0.51
47:S2:17:C:O2'	47:S2:1194:A:N1	2.44	0.51
47:S2:1428:G:H2'	47:S2:1429:G:C8	2.47	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:S2:1578:U:H1'	51:SD:6:SER:HB3	1.93	0.51
48:S6:5:A:H2'	48:S6:6:G:H8	1.76	0.51
50:SB:198:GLU:O	50:SB:202:GLN:HG2	2.11	0.51
53:SF:70:GLU:OE2	53:SF:74:ASN:ND2	2.44	0.51
1:L5:1100:U:H2'	1:L5:1167:C:H5	1.76	0.50
1:L5:1175:A:H2'	1:L5:1176:C:C6	2.45	0.50
1:L5:2527:A:OP2	20:LR:38:ARG:NH1	2.42	0.50
1:L5:4112:C:H2'	1:L5:4113:U:O4'	2.11	0.50
10:LG:78:PRO:O	10:LG:82:GLN:HG3	2.11	0.50
10:LG:193:LEU:HD12	10:LG:194:VAL:HG23	1.93	0.50
13:LJ:9:GLU:O	13:LJ:13:ARG:HB2	2.12	0.50
51:SD:157:MET:HA	51:SD:189:MET:HE3	1.92	0.50
55:SI:67:TRP:CD1	55:SI:70:GLU:H	2.29	0.50
55:SI:174:CYS:HB2	55:SI:190:LEU:HD11	1.93	0.50
63:SU:25:THR:HG22	63:SU:86:LYS:HG2	1.93	0.50
70:Sg:35:SER:O	70:Sg:66:VAL:HB	2.11	0.50
70:Sg:206:LEU:HD22	70:Sg:220:ASP:HA	1.93	0.50
1:L5:986:C:O2	1:L5:1067:G:N1	2.34	0.50
1:L5:2555:G:C2	1:L5:2573:A:C6	3.00	0.50
1:L5:3765:G:O2'	47:S2:1849:G:O6	2.26	0.50
7:LD:203:ASN:OD1	7:LD:204:VAL:N	2.43	0.50
14:LL:19:GLN:HA	14:LL:22:VAL:HG13	1.94	0.50
23:LU:42:PHE:HE1	23:LU:90:TYR:HD2	1.59	0.50
24:LV:22:VAL:O	24:LV:39:ILE:C	2.54	0.50
28:LZ:76:ASN:OD1	28:LZ:77:TYR:N	2.44	0.50
47:S2:552:G:H2'	47:S2:553:U:C6	2.47	0.50
47:S2:1625:U:H2'	47:S2:1626:C:C6	2.46	0.50
47:S2:1651:A:H2'	47:S2:1652:G:H8	1.75	0.50
50:SB:143:THR:HB	50:SB:205:TYR:HE2	1.76	0.50
54:SH:10:LYS:HE3	54:SH:46:THR:O	2.11	0.50
55:SI:67:TRP:HD1	55:SI:70:GLU:H	1.58	0.50
60:SR:92:ASP:OD2	60:SR:93:GLN:NE2	2.44	0.50
70:Sg:21:ILE:HB	70:Sg:290:ALA:HB2	1.91	0.50
73:SJ:18:ARG:HD2	73:SJ:21:GLU:HG2	1.92	0.50
1:L5:159:C:H5'	37:Li:25:ARG:NH2	2.24	0.50
1:L5:664:G:N2	1:L5:667:A:C6	2.79	0.50
1:L5:1085:C:H2'	1:L5:1086:C:C6	2.46	0.50
1:L5:4088:C:H2'	1:L5:4089:G:H8	1.75	0.50
6:LC:92:PHE:O	6:LC:100:ARG:NH2	2.45	0.50
7:LD:245:ALA:O	7:LD:249:GLU:HG3	2.11	0.50
47:S2:71:G:O2'	47:S2:72:C:OP1	2.29	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:S2:107:A:H2'	47:S2:108:G:C8	2.46	0.50
47:S2:319:C:H3'	47:S2:320:G:C8	2.47	0.50
55:SI:201:LYS:HE3	57:SL:8:ARG:O	2.11	0.50
71:SC:94:ILE:HD11	71:SC:98:LEU:HD12	1.94	0.50
78:SY:37:LYS:HA	78:SY:40:ILE:HG22	1.93	0.50
1:L5:137:G:H4'	36:Lh:98:HIS:CD2	2.45	0.50
1:L5:2005:G:H22	1:L5:2015:U:H1'	1.77	0.50
1:L5:3970:G:H2'	1:L5:3971:G:H8	1.76	0.50
1:L5:3971:G:H21	1:L5:4050:A:H62	1.60	0.50
1:L5:4734:A:H2'	1:L5:4735:G:H8	1.77	0.50
1:L5:4768:G:P	1:L5:4874:A:H61	2.34	0.50
1:L5:4967:A:H2'	1:L5:4968:A:C8	2.46	0.50
7:LD:177:THR:C	7:LD:179:ARG:H	2.20	0.50
22:LT:106:LEU:HA	22:LT:109:VAL:HG12	1.93	0.50
43:Lo:99:ARG:HB3	43:Lo:102:GLN:HB2	1.92	0.50
50:SB:132:GLY:HA3	50:SB:221:PRO:HG3	1.94	0.50
66:Sa:88:SER:O	66:Sa:92:ARG:HG3	2.12	0.50
1:L5:480:C:H2'	1:L5:481:G:C8	2.46	0.50
47:S2:167:G:O3'	72:SG:131:ARG:NH2	2.40	0.50
47:S2:221:A:N6	47:S2:301:A:H61	2.09	0.50
47:S2:1579:A:H4'	47:S2:1581:C:H5	1.77	0.50
51:SD:22:ASN:O	51:SD:26:THR:OG1	2.22	0.50
52:SE:137:PRO:HB2	52:SE:150:PRO:HD2	1.93	0.50
58:SP:40:ARG:HH21	58:SP:84:ILE:HG22	1.75	0.50
60:SR:81:ARG:HA	60:SR:84:TYR:CE2	2.47	0.50
77:SW:11:LEU:HD21	77:SW:37:PHE:CZ	2.46	0.50
1:L5:406:C:O2'	1:L5:407:A:OP1	2.29	0.50
1:L5:472:C:N4	1:L5:682:G:H22	2.07	0.50
1:L5:2108:G:H3'	1:L5:2109:G:H8	1.77	0.50
1:L5:4092:G:C2	1:L5:4093:G:C2	3.00	0.50
1:L5:4591:U:H2'	1:L5:4592:C:C6	2.46	0.50
1:L5:4903:G:H2'	1:L5:4904:G:C8	2.47	0.50
3:L8:137:A:H2'	3:L8:138:C:C6	2.47	0.50
15:LM:11:ARG:HB3	15:LM:27:ILE:HD12	1.94	0.50
15:LM:31:ILE:HG22	21:LS:98:ARG:HE	1.77	0.50
26:LX:64:SER:HB3	36:Lh:80:PRO:HG2	1.93	0.50
31:Lc:28:VAL:HG21	31:Lc:33:GLN:HG2	1.93	0.50
47:S2:168:C:P	72:SG:131:ARG:HH12	2.34	0.50
47:S2:604:A:H2'	47:S2:605:A:C8	2.46	0.50
47:S2:609:U:H2'	47:S2:610:G:H8	1.75	0.50
47:S2:1297:U:H2'	47:S2:1298:G:H2'	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:673:C:H2'	1:L5:674:G:C8	2.47	0.50
1:L5:1088:C:H2'	1:L5:1089:G:H8	1.74	0.50
6:LC:182:LYS:HD2	6:LC:204:ARG:HG3	1.94	0.50
47:S2:331:C:OP1	72:SG:197:GLN:NE2	2.44	0.50
47:S2:1410:C:H2'	47:S2:1411:G:H8	1.77	0.50
47:S2:1657:G:H1	47:S2:1667:U:H3	1.60	0.50
55:SI:57:ALA:HB1	55:SI:60:LEU:CD1	2.40	0.50
57:SL:104:LYS:O	65:SX:11:ARG:NH2	2.44	0.50
70:Sg:131:LEU:HD23	70:Sg:139:LYS:HB3	1.94	0.50
73:SJ:65:GLU:HA	73:SJ:70:ARG:HD3	1.94	0.50
80:Sb:53:VAL:HG13	80:Sb:62:VAL:HG21	1.94	0.50
1:L5:1248:C:H2'	1:L5:1249:C:C6	2.46	0.50
1:L5:4107:G:H2'	1:L5:4108:G:H8	1.76	0.50
8:LE:133:PHE:HA	8:LE:136:HIS:HD2	1.76	0.50
47:S2:371:A:OP2	55:SI:10:LYS:HB2	2.12	0.50
47:S2:1289:U:O2'	69:Sf:98:VAL:HG22	2.11	0.50
50:SB:28:LYS:HD3	50:SB:48:LEU:HD21	1.94	0.50
50:SB:126:ASP:OD1	50:SB:136:ARG:HG2	2.12	0.50
55:SI:97:VAL:HG13	55:SI:98:LYS:H	1.77	0.50
72:SG:164:LYS:HD2	72:SG:167:LYS:H	1.77	0.50
79:SZ:111:ARG:HG2	79:SZ:112:ASN:H	1.77	0.50
1:L5:75:G:H3'	14:LL:74:ARG:HD2	1.94	0.50
1:L5:664:G:H21	1:L5:667:A:N6	2.10	0.50
1:L5:1271:G:N3	1:L5:1271:G:H2'	2.27	0.50
10:LG:194:VAL:O	10:LG:196:ARG:N	2.45	0.50
12:LI:183:ASP:N	12:LI:183:ASP:OD1	2.44	0.50
47:S2:85:A:H2'	47:S2:86:C:H6	1.76	0.50
47:S2:794:A:H2'	47:S2:795:A:H4'	1.93	0.50
47:S2:1458:G:H2'	47:S2:1459:G:C8	2.47	0.50
47:S2:1692:U:H2'	47:S2:1693:G:C8	2.46	0.50
52:SE:94:LYS:HD3	78:SY:16:ARG:HG2	1.94	0.50
1:L5:696:C:H4'	1:L5:697:G:H8	1.76	0.49
1:L5:930:G:H4'	1:L5:931:C:O5'	2.12	0.49
1:L5:2001:G:N2	1:L5:2003:G:O6	2.45	0.49
1:L5:5026:U:O3'	1:L5:5028:G:H5"	2.12	0.49
6:LC:212:ASN:HD21	6:LC:255:SER:HB3	1.76	0.49
6:LC:335:MET:HE2	9:LF:58:HIS:CD2	2.47	0.49
28:LZ:136:PHE:HB2	35:Lg:91:ILE:HG12	1.94	0.49
47:S2:817:G:H2'	47:S2:818:A:H5"	1.94	0.49
54:SH:43:LEU:HD23	54:SH:72:PHE:CE1	2.47	0.49
55:SI:59:ARG:C	55:SI:60:LEU:HD12	2.37	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
77:SW:8:ALA:HA	77:SW:74:VAL:HG11	1.94	0.49
78:SY:20:ARG:HB3	78:SY:76:TYR:CD1	2.47	0.49
1:L5:137:G:H2'	1:L5:138:G:H8	1.77	0.49
1:L5:516:C:H42	1:L5:645:G:H22	1.59	0.49
1:L5:1176:C:H2'	1:L5:1177:U:C6	2.47	0.49
1:L5:2858:A:O2'	1:L5:2859:G:H8	1.94	0.49
1:L5:3723:A:H2'	1:L5:3724:A:H8	1.78	0.49
1:L5:4098:A:H2	1:L5:4112:C:H42	1.60	0.49
10:LG:218:LEU:O	10:LG:222:ILE:HG12	2.11	0.49
27:LY:74:TYR:CE2	27:LY:77:LYS:HE2	2.47	0.49
46:Lz:128:LEU:O	46:Lz:134:PHE:HB2	2.12	0.49
47:S2:114:G:O2'	47:S2:382:C:O2'	2.11	0.49
47:S2:329:G:N7	72:SG:189:ARG:NH1	2.58	0.49
47:S2:1606:G:H22	47:S2:1632:G:H2'	1.77	0.49
49:SA:67:ALA:HB2	64:SV:36:VAL:O	2.12	0.49
56:SK:35:LEU:HD23	56:SK:40:VAL:HG21	1.94	0.49
1:L5:1552:G:H2'	1:L5:1574:G:N2	2.27	0.49
1:L5:3651:A:H5'	4:LA:199:VAL:HG12	1.93	0.49
3:L8:87:G:O2'	3:L8:88:A:H8	1.94	0.49
28:LZ:50:PRO:HD3	28:LZ:68:ILE:HG12	1.94	0.49
45:Lr:21:ASN:O	45:Lr:23:GLN:N	2.37	0.49
47:S2:191:A:H62	47:S2:209:A:H1'	1.77	0.49
47:S2:1228:A:O2'	47:S2:1634:A:N3	2.31	0.49
47:S2:1283:C:O2	47:S2:1286:G:O2'	2.30	0.49
50:SB:182:LYS:O	50:SB:186:ASN:ND2	2.46	0.49
53:SF:106:GLU:HG2	53:SF:107:ASN:H	1.77	0.49
65:SX:59:ALA:HB3	65:SX:65:ALA:H	1.78	0.49
65:SX:74:LEU:HD23	65:SX:81:ILE:HD13	1.93	0.49
1:L5:1069:G:H2'	1:L5:1070:G:C8	2.47	0.49
1:L5:1271:G:N2	1:L5:2122:G:H5"	2.28	0.49
1:L5:2267:U:OP1	45:Lr:37:SER:OG	2.28	0.49
1:L5:4880:C:N4	1:L5:4881:U:O4	2.45	0.49
47:S2:799:U:H2'	47:S2:800:U:C6	2.47	0.49
47:S2:895:G:H2'	47:S2:896:U:H4'	1.94	0.49
47:S2:1099:G:H22	47:S2:1133:A:H2	1.58	0.49
70:Sg:77:PHE:HB3	70:Sg:89:LEU:HD11	1.93	0.49
1:L5:751:G:N2	1:L5:912:G:H1	2.00	0.49
1:L5:1633:G:H5'	1:L5:1634:A:OP1	2.13	0.49
1:L5:2666:U:OP2	20:LR:124:TYR:OH	2.29	0.49
1:L5:4467:A:O2'	1:L5:4510:A:N3	2.42	0.49
6:LC:113:ARG:HH11	6:LC:113:ARG:HG3	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:LC:252:TRP:HE3	6:LC:257:PHE:CD1	2.30	0.49
12:LI:76:MET:O	12:LI:77:VAL:HB	2.12	0.49
19:LQ:15:ARG:HH12	19:LQ:19:LYS:HB2	1.77	0.49
21:LS:20:PRO:CD	21:LS:21:LYS:H	2.25	0.49
33:Le:42:ASP:HA	33:Le:47:ARG:HH21	1.76	0.49
46:Lz:29:LEU:HD11	46:Lz:171:HIS:HB3	1.94	0.49
47:S2:381:C:H2'	47:S2:382:C:C6	2.48	0.49
47:S2:1421:A:N1	47:S2:1427:C:O2'	2.46	0.49
52:SE:164:LEU:HD12	52:SE:165:GLU:HB2	1.95	0.49
57:SL:35:ARG:HD2	57:SL:53:GLY:O	2.12	0.49
78:SY:91:LEU:HD11	78:SY:96:LEU:HD11	1.95	0.49
1:L5:1443:A:N1	1:L5:1444:G:N2	2.61	0.49
1:L5:2611:A:H2'	1:L5:2612:G:C8	2.47	0.49
1:L5:3767:C:O2'	1:L5:3768:U:OP1	2.25	0.49
4:LA:174:ARG:HA	44:Lp:69:TRP:CZ3	2.48	0.49
47:S2:442:C:O4'	72:SG:92:ARG:NH1	2.45	0.49
47:S2:678:U:OP2	47:S2:1026:C:N4	2.46	0.49
47:S2:1152:U:O2'	77:SW:19:LYS:NZ	2.36	0.49
47:S2:1217:A:H2'	47:S2:1218:C:C6	2.48	0.49
47:S2:1549:U:OP1	68:Sd:34:TYR:OH	2.23	0.49
54:SH:75:ILE:O	54:SH:79:LEU:N	2.45	0.49
65:SX:60:LYS:HB3	65:SX:62:PRO:HD2	1.95	0.49
1:L5:137:G:H5'	36:Lh:96:ASN:ND2	2.27	0.49
1:L5:1070:G:O6	8:LE:46:ARG:NH2	2.45	0.49
1:L5:1604:G:H2'	1:L5:1605:G:C8	2.48	0.49
1:L5:2757:A:H2'	1:L5:2758:G:C8	2.48	0.49
1:L5:2845:A:H61	1:L5:3843:C:N4	2.06	0.49
1:L5:4765:G:N2	1:L5:4869:U:H3	2.11	0.49
21:LS:16:CYS:HB3	21:LS:25:PRO:HG2	1.94	0.49
47:S2:24:C:OP1	73:SJ:11:LYS:NZ	2.38	0.49
47:S2:104:A:H62	47:S2:356:C:H5	1.60	0.49
47:S2:125:C:H5"	47:S2:126:G:H5"	1.95	0.49
47:S2:800:U:H2'	47:S2:801:U:O4'	2.13	0.49
47:S2:1565:C:H2'	47:S2:1566:G:O4'	2.12	0.49
70:Sg:44:LYS:HB2	70:Sg:53:GLY:HA2	1.94	0.49
72:SG:223:LYS:O	72:SG:227:GLN:HG2	2.11	0.49
1:L5:463:A:H3'	1:L5:464:G:C8	2.48	0.49
1:L5:962:C:H3'	1:L5:2264:C:N4	2.28	0.49
1:L5:4611:A:H2'	1:L5:4612:C:H6	1.78	0.49
6:LC:145:GLU:H	6:LC:145:GLU:CD	2.21	0.49
8:LE:89:LEU:H	8:LE:90:ALA:HA	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:LE:123:ARG:O	8:LE:124:LYS:HG2	2.12	0.49
11:LH:63:ASN:O	11:LH:67:LEU:HB2	2.13	0.49
15:LM:69:HIS:ND1	15:LM:69:HIS:O	2.45	0.49
47:S2:77:A:H2'	47:S2:78:C:O4'	2.12	0.49
47:S2:294:U:N3	57:SL:65:ASN:OD1	2.45	0.49
47:S2:946:U:H2'	47:S2:947:G:H8	1.78	0.49
47:S2:1592:C:H5'	53:SF:87:LEU:HD23	1.94	0.49
47:S2:1651:A:H1'	53:SF:83:ASN:OD1	2.13	0.49
47:S2:1808:U:H2'	47:S2:1809:A:C8	2.47	0.49
49:SA:85:ARG:HG2	49:SA:88:LEU:HD12	1.94	0.49
52:SE:45:ILE:HG13	52:SE:61:VAL:HG21	1.94	0.49
53:SF:85:LYS:O	53:SF:87:LEU:N	2.35	0.49
58:SP:85:ILE:HG22	58:SP:87:PRO:HD3	1.95	0.49
58:SP:98:ASN:H	58:SP:99:GLY:C	2.20	0.49
59:SQ:82:TYR:HA	59:SQ:85:ARG:HG2	1.95	0.49
67:Sc:6:VAL:HG13	67:Sc:8:PRO:HD3	1.95	0.49
1:L5:4134:C:H2'	1:L5:4135:G:C8	2.47	0.49
6:LC:54:VAL:HG11	6:LC:101:MET:HE2	1.93	0.49
9:LF:95:ILE:O	9:LF:223:LYS:HE2	2.12	0.49
10:LG:61:ILE:HA	10:LG:64:GLN:HG2	1.95	0.49
26:LX:69:ASN:O	26:LX:69:ASN:ND2	2.40	0.49
39:Lk:66:VAL:HB	39:Lk:67:LYS:HB3	1.94	0.49
47:S2:1562:C:H2'	47:S2:1563:G:H8	1.78	0.49
47:S2:1746:U:H4'	72:SG:65:GLN:NE2	2.27	0.49
54:SH:49:LYS:NZ	54:SH:61:ILE:HD11	2.28	0.49
70:Sg:121:VAL:HG23	70:Sg:156:PHE:CZ	2.48	0.49
78:SY:16:ARG:HD3	78:SY:16:ARG:H	1.78	0.49
1:L5:71:C:H1'	14:LL:62:PRO:O	2.12	0.49
1:L5:2116:C:H5"	9:LF:49:LEU:HD13	1.94	0.49
1:L5:4149:C:OP2	28:LZ:58:GLY:HA3	2.12	0.49
1:L5:4541:G:N2	1:L5:4544:A:OP2	2.35	0.49
6:LC:109:ARG:O	6:LC:111:TRP:N	2.46	0.49
17:LO:51:LYS:HE3	17:LO:144:GLU:HB3	1.94	0.49
28:LZ:53:VAL:O	28:LZ:57:MET:HE1	2.12	0.49
43:Lo:105:GLN:HB3	82:Pt:57:C:C4	2.48	0.49
46:Lz:157:PHE:HB3	46:Lz:167:VAL:HB	1.94	0.49
47:S2:1828:C:H2'	47:S2:1829:G:C8	2.47	0.49
53:SF:127:ARG:H	53:SF:136:ARG:HB3	1.77	0.49
59:SQ:134:GLY:N	59:SQ:140:ARG:HE	2.10	0.49
66:Sa:12:LYS:O	66:Sa:15:ARG:NH2	2.46	0.49
1:L5:1563:A:H4'	75:SN:127:ARG:HH22	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:1866:U:O2'	1:L5:1867:A:H8	1.96	0.48
1:L5:2029:A:H2'	1:L5:2030:A:C8	2.48	0.48
1:L5:2078:C:OP1	33:Le:64:LYS:HG2	2.13	0.48
1:L5:3713:U:H4'	1:L5:3714:G:OP2	2.13	0.48
1:L5:3944:G:H2'	1:L5:3945:A:C8	2.48	0.48
5:LB:89:ILE:HG21	5:LB:197:ALA:HB1	1.95	0.48
12:LI:77:VAL:HA	12:LI:81:GLY:O	2.13	0.48
16:LN:94:PHE:CE2	16:LN:96:ARG:HB2	2.48	0.48
18:LP:122:ALA:HB3	18:LP:143:PRO:HB2	1.95	0.48
24:LV:22:VAL:O	24:LV:39:ILE:O	2.30	0.48
25:LW:84:GLY:HA2	72:SG:131:ARG:O	2.13	0.48
40:Ll:21:ARG:O	40:Ll:38:ASN:ND2	2.46	0.48
47:S2:604:A:H4'	47:S2:605:A:OP1	2.12	0.48
47:S2:1158:G:H5"	77:SW:76:SER:OG	2.13	0.48
47:S2:1226:G:H22	47:S2:1639:G:H5'	1.78	0.48
47:S2:1606:G:O2'	47:S2:1607:A:O4'	2.31	0.48
47:S2:1845:A:H2'	47:S2:1846:G:C8	2.48	0.48
53:SF:165:ASN:OD1	53:SF:166:ILE:N	2.46	0.48
63:SU:31:SER:O	63:SU:34:LYS:HG3	2.13	0.48
76:SO:85:CYS:HB3	76:SO:90:ILE:HD11	1.94	0.48
1:L5:1237:C:H5"	8:LE:59:ARG:HB2	1.94	0.48
1:L5:1280:C:O2'	1:L5:1281:G:H2'	2.13	0.48
1:L5:1803:G:C6	22:LT:109:VAL:HG23	2.48	0.48
1:L5:4458:C:H2'	1:L5:4459:U:C6	2.48	0.48
1:L5:4767:C:O3'	1:L5:4874:A:N6	2.46	0.48
6:LC:7:LEU:HD13	6:LC:23:THR:HA	1.95	0.48
6:LC:157:LYS:O	6:LC:157:LYS:HD3	2.12	0.48
8:LE:261:ILE:HG23	8:LE:267:LEU:HD22	1.95	0.48
16:LN:8:GLN:HG3	16:LN:50:ARG:NH2	2.28	0.48
16:LN:98:LEU:HD23	16:LN:128:LYS:HD2	1.94	0.48
21:LS:109:CYS:O	21:LS:110:TYR:HB2	2.14	0.48
47:S2:505:G:H5'	78:SY:107:ARG:HH22	1.77	0.48
47:S2:1407:U:H2'	47:S2:1408:U:H6	1.78	0.48
47:S2:1476:A:H1'	60:SR:1:MET:O	2.13	0.48
50:SB:49:VAL:HG21	50:SB:62:LEU:HD22	1.95	0.48
51:SD:222:PRO:HB3	70:Sg:190:GLY:O	2.13	0.48
72:SG:3:LEU:HD11	72:SG:16:ILE:HB	1.96	0.48
72:SG:50:VAL:HG12	72:SG:113:ILE:HD13	1.95	0.48
1:L5:487:G:H2'	1:L5:488:G:O4'	2.13	0.48
1:L5:516:C:N4	1:L5:645:G:H22	2.11	0.48
1:L5:977:C:H2'	1:L5:978:G:C8	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:2000:G:H8	1:L5:2018:C:H1'	1.78	0.48
1:L5:4103:C:H2'	1:L5:4105:A:C6	2.48	0.48
1:L5:4735:G:H1	1:L5:4964:C:H42	1.61	0.48
3:L8:123:U:O2'	3:L8:126:C:N4	2.32	0.48
10:LG:106:THR:HG22	10:LG:107:LYS:N	2.28	0.48
12:LI:47:PRO:HD2	12:LI:141:LYS:HA	1.96	0.48
12:LI:110:ARG:HG3	12:LI:111:LEU:HD12	1.94	0.48
13:LJ:154:LYS:HG3	13:LJ:155:HIS:H	1.78	0.48
35:Lg:20:THR:HB	35:Lg:34:TYR:HA	1.95	0.48
38:Lj:52:LYS:O	38:Lj:56:ARG:HG3	2.12	0.48
47:S2:664:A:O2'	47:S2:670:A:N1	2.39	0.48
54:SH:87:PHE:CE2	54:SH:90:LYS:HD2	2.46	0.48
54:SH:191:GLU:HG3	54:SH:193:GLN:H	1.78	0.48
71:SC:188:CYS:SG	71:SC:191:VAL:HB	2.53	0.48
73:SJ:78:LEU:HD13	73:SJ:92:MET:HG3	1.95	0.48
1:L5:495:C:H2'	1:L5:496:G:C8	2.47	0.48
1:L5:702:U:H1'	33:Le:5:ARG:HH22	1.78	0.48
1:L5:1339:U:H2'	1:L5:1340:C:C6	2.47	0.48
7:LD:56:THR:OG1	7:LD:59:ASP:O	2.27	0.48
23:LU:61:VAL:HG12	23:LU:74:SER:HA	1.94	0.48
27:LY:8:THR:HG22	27:LY:10:ASP:H	1.78	0.48
43:Lo:12:CYS:SG	43:Lo:19:GLN:HB2	2.54	0.48
46:Lz:47:LYS:HD2	46:Lz:197:ASN:HD21	1.79	0.48
47:S2:165:G:OP2	47:S2:165:G:N2	2.47	0.48
47:S2:1147:C:OP1	66:Sa:6:ARG:NH1	2.46	0.48
47:S2:1213:C:H2'	47:S2:1214:A:C8	2.47	0.48
47:S2:1623:A:N6	61:SS:132:ARG:HH21	2.10	0.48
63:SU:31:SER:O	63:SU:35:VAL:HG23	2.12	0.48
70:Sg:32:LEU:HD23	70:Sg:42:MET:HB3	1.94	0.48
71:SC:256:TRP:CZ3	77:SW:68:ARG:HD3	2.48	0.48
74:SM:86:GLY:C	74:SM:106:CYS:H	2.21	0.48
1:L5:461:G:H2'	1:L5:461:G:N3	2.29	0.48
1:L5:1333:A:H2'	1:L5:1334:A:C8	2.48	0.48
1:L5:2539:C:H2'	1:L5:2540:C:H6	1.79	0.48
8:LE:232:ILE:O	8:LE:232:ILE:HG13	2.13	0.48
11:LH:31:ARG:HD2	11:LH:149:ASN:OD1	2.14	0.48
46:Lz:139:THR:HG23	46:Lz:141:ASN:H	1.77	0.48
47:S2:959:G:H2'	47:S2:960:U:C6	2.49	0.48
47:S2:982:G:H2'	47:S2:983:A:H8	1.79	0.48
47:S2:1322:G:H2'	47:S2:1323:U:O4'	2.14	0.48
47:S2:1693:G:H21	47:S2:1834:A:H8	1.58	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:Sg:191:HIS:ND1	70:Sg:195:LEU:HD21	2.29	0.48
71:SC:201:GLY:O	73:SJ:54:ARG:NH2	2.47	0.48
1:L5:135:G:N2	36:Lh:100:GLU:OE2	2.47	0.48
1:L5:2763:U:H2'	1:L5:2764:A:H8	1.77	0.48
1:L5:3656:A:H2'	1:L5:3657:U:C6	2.48	0.48
1:L5:3937:C:H2'	1:L5:3938:G:N2	2.29	0.48
1:L5:4934:A:N6	1:L5:4935:C:H41	2.12	0.48
3:L8:3:A:H4'	18:LP:61:ARG:NH1	2.29	0.48
3:L8:19:C:H2'	3:L8:20:A:C8	2.48	0.48
6:LC:36:ILE:HG21	6:LC:122:TYR:HD2	1.79	0.48
8:LE:51:VAL:O	8:LE:51:VAL:HG13	2.13	0.48
8:LE:153:LEU:HD11	8:LE:195:ILE:HG13	1.93	0.48
21:LS:118:ARG:O	21:LS:120:ARG:NH1	2.46	0.48
46:Lz:25:ARG:NH2	46:Lz:210:MET:HG3	2.28	0.48
46:Lz:116:LEU:HD23	46:Lz:120:ILE:HB	1.96	0.48
47:S2:203:G:OP2	55:SI:147:LYS:NZ	2.46	0.48
50:SB:105:LEU:HD12	50:SB:213:ARG:HA	1.95	0.48
50:SB:118:GLN:NE2	50:SB:142:PHE:HB3	2.28	0.48
53:SF:91:ARG:HD2	79:SZ:103:HIS:HE1	1.78	0.48
55:SI:139:LYS:HG3	55:SI:149:TYR:HE2	1.78	0.48
59:SQ:44:PRO:HG2	59:SQ:47:LEU:H	1.78	0.48
61:SS:116:LYS:O	61:SS:117:ILE:HG22	2.13	0.48
63:SU:22:ILE:HD11	63:SU:112:VAL:HG13	1.95	0.48
65:SX:17:ARG:O	65:SX:21:LYS:HG3	2.13	0.48
67:Sc:31:ARG:HB3	67:Sc:43:ILE:HD13	1.95	0.48
73:SJ:118:GLY:O	73:SJ:120:ALA:N	2.45	0.48
1:L5:1866:U:O2'	1:L5:1867:A:C8	2.66	0.48
1:L5:1867:A:H2'	1:L5:1868:A:C8	2.48	0.48
1:L5:2607:C:H2'	1:L5:2608:G:H8	1.79	0.48
1:L5:3880:G:O2'	1:L5:3881:G:C8	2.67	0.48
1:L5:3973:G:H2'	1:L5:3974:G:C8	2.49	0.48
3:L8:94:G:C6	38:Lj:84:PRO:HB3	2.48	0.48
5:LB:27:GLY:HA2	5:LB:276:HIS:CD2	2.49	0.48
47:S2:582:C:O4'	78:SY:33:ALA:HB2	2.13	0.48
47:S2:1584:G:H4'	47:S2:1585:U:H3'	1.95	0.48
47:S2:1648:G:N2	47:S2:1675:A:OP2	2.47	0.48
61:SS:124:ARG:NH2	61:SS:151:LYS:HE2	2.29	0.48
66:Sa:44:ILE:O	76:SO:113:GLN:NE2	2.44	0.48
70:Sg:254:PRO:O	70:Sg:272:GLN:NE2	2.39	0.48
71:SC:178:HIS:HB2	71:SC:220:ASP:HB3	1.95	0.48
74:SM:116:LYS:O	74:SM:118:SER:N	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:192:G:H2'	1:L5:193:G:C8	2.49	0.48
1:L5:492:U:O4	1:L5:662:C:N3	2.47	0.48
1:L5:2123:C:H3'	9:LF:37:PHE:CE1	2.49	0.48
1:L5:4114:C:H2'	1:L5:4115:G:N2	2.28	0.48
1:L5:4967:A:H2'	1:L5:4968:A:H8	1.78	0.48
4:LA:19:HIS:O	4:LA:23:ARG:NH2	2.47	0.48
35:Lg:60:ARG:CD	35:Lg:61:PRO:HD2	2.34	0.48
47:S2:1593:C:H2'	47:S2:1594:A:H8	1.79	0.48
47:S2:1860:A:H3'	66:Sa:8:ASN:HB3	1.95	0.48
52:SE:97:GLU:HG3	52:SE:99:PHE:CE1	2.48	0.48
70:Sg:246:TYR:CZ	70:Sg:261:LEU:HD12	2.49	0.48
1:L5:224:U:O2	6:LC:219:LYS:HE2	2.14	0.48
1:L5:1177:U:N3	1:L5:1178:G:N7	2.61	0.48
1:L5:2006:U:H4'	41:Lm:104:HIS:HB3	1.96	0.48
1:L5:3767:C:HO2'	1:L5:3768:U:P	2.35	0.48
1:L5:4288:C:O2'	1:L5:4321:U:OP1	2.32	0.48
1:L5:4948:C:O2'	1:L5:4949:G:OP1	2.31	0.48
13:LJ:15:LEU:HD22	13:LJ:165:TRP:CG	2.49	0.48
41:Lm:94:MET:HG3	41:Lm:103:LEU:HB2	1.96	0.48
46:Lz:54:ARG:HH11	46:Lz:152:LYS:HD2	1.78	0.48
47:S2:804:U:H2'	47:S2:805:U:H6	1.79	0.48
47:S2:1334:G:H5'	51:SD:140:GLY:HA2	1.96	0.48
47:S2:1675:A:O2'	53:SF:77:MET:SD	2.67	0.48
58:SP:34:MET:SD	58:SP:45:LEU:HD22	2.54	0.48
61:SS:60:THR:OG1	61:SS:62:ASP:OD1	2.23	0.48
63:SU:61:LEU:HB2	63:SU:82:MET:HB3	1.95	0.48
69:Sf:118:ARG:HG2	69:Sf:119:ARG:H	1.79	0.48
73:SJ:63:LEU:HD22	73:SJ:70:ARG:HB2	1.96	0.48
1:L5:185:C:O2'	1:L5:187:U:O2'	2.24	0.48
1:L5:976:G:H1	1:L5:1278:C:N4	2.11	0.48
1:L5:2000:G:C8	1:L5:2018:C:H1'	2.49	0.48
1:L5:3753:G:H22	1:L5:3771:C:H1'	1.78	0.48
1:L5:4114:C:H5'	1:L5:4115:G:C2	2.49	0.48
11:LH:92:MET:SD	11:LH:161:ILE:HD11	2.53	0.48
47:S2:524:U:O4	73:SJ:38:ARG:NH2	2.45	0.48
47:S2:1546:G:H1'	47:S2:1670:C:O2'	2.13	0.48
48:S6:6:G:H1	48:S6:68:C:H42	1.61	0.48
49:SA:206:ASP:O	49:SA:210:ILE:HG12	2.13	0.48
50:SB:129:THR:HG22	50:SB:133:TYR:O	2.14	0.48
51:SD:23:GLU:OE1	51:SD:27:ARG:NH1	2.47	0.48
1:L5:226:G:OP2	27:LY:1:MET:N	2.34	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:507:G:H2'	1:L5:508:G:C8	2.49	0.47
1:L5:3861:A:H2'	1:L5:3862:A:C8	2.49	0.47
1:L5:4958:C:N4	1:L5:4959:U:O4	2.47	0.47
1:L5:5028:G:H2'	1:L5:5029:C:C6	2.49	0.47
16:LN:8:GLN:HE22	16:LN:12:ARG:NH2	2.12	0.47
47:S2:1466:G:H2'	47:S2:1467:C:C6	2.49	0.47
50:SB:68:GLU:HG3	50:SB:85:LYS:HD2	1.96	0.47
51:SD:42:THR:OG1	51:SD:45:ARG:O	2.31	0.47
52:SE:104:ASP:OD1	52:SE:108:ARG:N	2.38	0.47
53:SF:138:ALA:HB3	53:SF:204:ARG:HA	1.96	0.47
62:ST:115:LYS:HZ2	62:ST:121:ARG:HH11	1.62	0.47
72:SG:164:LYS:HG2	72:SG:166:GLY:H	1.78	0.47
1:L5:3949:A:H2'	1:L5:3950:U:C6	2.49	0.47
7:LD:50:ARG:NH1	7:LD:147:ASP:OD2	2.47	0.47
10:LG:106:THR:HG22	10:LG:107:LYS:H	1.78	0.47
12:LI:205:PRO:HB2	12:LI:207:ASP:OD1	2.13	0.47
47:S2:1801:A:H2'	47:S2:1802:C:C6	2.49	0.47
49:SA:171:VAL:O	49:SA:175:TRP:HD1	1.97	0.47
50:SB:70:SER:OG	76:SO:128:ARG:NH1	2.46	0.47
55:SI:142:SER:HA	55:SI:146:GLN:HG2	1.96	0.47
60:SR:95:ILE:N	60:SR:96:ILE:HA	2.30	0.47
62:ST:111:LYS:O	62:ST:112:MET:HE2	2.13	0.47
63:SU:25:THR:OG1	63:SU:111:GLU:OE1	2.29	0.47
66:Sa:82:LYS:HD2	66:Sa:85:ARG:HH12	1.79	0.47
68:Sd:4:GLN:HG3	69:Sf:97:LYS:HA	1.95	0.47
72:SG:7:PHE:CE2	72:SG:9:ALA:HB3	2.49	0.47
1:L5:116:G:H2'	1:L5:117:C:C6	2.49	0.47
1:L5:5026:U:H4'	1:L5:5028:G:O4'	2.14	0.47
5:LB:293:ILE:HA	5:LB:297:LYS:HA	1.95	0.47
9:LF:43:ARG:O	9:LF:47:ARG:HG2	2.14	0.47
13:LJ:120:ASP:HB3	13:LJ:123:ILE:HG12	1.97	0.47
20:LR:136:ARG:O	20:LR:140:GLU:HG2	2.15	0.47
38:Lj:31:LYS:HG3	38:Lj:33:THR:HG22	1.95	0.47
47:S2:26:U:H2'	47:S2:27:A:H8	1.78	0.47
47:S2:1272:C:H2'	47:S2:1273:C:O4'	2.13	0.47
47:S2:1409:A:H2'	47:S2:1410:C:O4'	2.14	0.47
50:SB:71:LEU:HD13	50:SB:84:PHE:CE1	2.49	0.47
51:SD:8:LYS:NZ	63:SU:59:LYS:HD3	2.29	0.47
53:SF:113:VAL:O	53:SF:117:ILE:HG12	2.15	0.47
53:SF:175:ASP:HA	53:SF:178:ILE:HG12	1.96	0.47
57:SL:33:LEU:HD12	57:SL:33:LEU:O	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:SU:107:GLU:O	63:SU:109:GLY:N	2.46	0.47
72:SG:63:MET:HE1	72:SG:106:LEU:HD22	1.95	0.47
1:L5:162:A:H2'	1:L5:163:A:C8	2.49	0.47
1:L5:666:G:H1'	45:Lr:46:ARG:NH1	2.29	0.47
1:L5:711:A:H1'	8:LE:136:HIS:ND1	2.29	0.47
1:L5:1683:U:H2'	1:L5:1684:A:C8	2.50	0.47
1:L5:2474:G:H2'	1:L5:2502:G:N2	2.30	0.47
1:L5:4194:U:O2'	12:LI:116:ARG:NH2	2.47	0.47
5:LB:239:LYS:HG3	5:LB:248:LEU:HD13	1.95	0.47
8:LE:150:LEU:HB3	8:LE:194:VAL:CG2	2.45	0.47
26:LX:148:ASP:OD1	26:LX:149:VAL:N	2.47	0.47
34:Lf:45:LYS:NZ	34:Lf:108:SER:HA	2.29	0.47
45:Lr:68:SER:OG	45:Lr:69:GLY:N	2.45	0.47
52:SE:144:ALA:C	52:SE:145:ARG:HD2	2.39	0.47
52:SE:205:PHE:CE2	52:SE:221:ARG:HB3	2.42	0.47
53:SF:72:LEU:HB2	53:SF:151:ILE:HD11	1.97	0.47
55:SI:201:LYS:O	55:SI:205:ARG:HG2	2.14	0.47
58:SP:38:SER:HB2	58:SP:42:ARG:HB3	1.96	0.47
71:SC:133:TYR:CD2	71:SC:216:MET:HA	2.48	0.47
1:L5:2845:A:N6	1:L5:3843:C:H42	2.10	0.47
1:L5:3870:C:H2'	1:L5:3871:A:H8	1.78	0.47
1:L5:3880:G:O2'	1:L5:3881:G:H8	1.96	0.47
1:L5:4158:C:H2'	1:L5:4159:C:C6	2.50	0.47
1:L5:5029:C:H2'	1:L5:5030:U:C6	2.49	0.47
7:LD:64:ILE:HG13	7:LD:105:LEU:HD21	1.96	0.47
45:Lr:47:LYS:HD2	45:Lr:102:TYR:CE1	2.49	0.47
47:S2:692:G:H4'	47:S2:692:G:OP1	2.14	0.47
47:S2:1510:G:H2'	47:S2:1511:U:C6	2.49	0.47
47:S2:1541:G:P	62:ST:56:ARG:HH21	2.37	0.47
50:SB:173:THR:HG23	50:SB:177:GLN:OE1	2.13	0.47
56:SK:89:ILE:O	56:SK:91:PRO:HD3	2.14	0.47
70:Sg:35:SER:OG	70:Sg:36:ARG:N	2.47	0.47
70:Sg:53:GLY:HA3	70:Sg:54:ILE:HA	1.60	0.47
70:Sg:78:ALA:HB3	70:Sg:90:TRP:HB2	1.95	0.47
75:SN:40:LEU:HD12	75:SN:45:LEU:HD12	1.95	0.47
76:SO:14:VAL:HG11	76:SO:17:LEU:C	2.39	0.47
82:Pt:11:A:H2'	82:Pt:12:G:C8	2.50	0.47
1:L5:423:G:H2'	1:L5:424:U:C6	2.50	0.47
1:L5:944:A:N7	9:LF:147:LEU:HD21	2.29	0.47
1:L5:1570:G:N7	44:Lp:3:LYS:NZ	2.63	0.47
1:L5:3756:A:N6	1:L5:3757:G:C2	2.82	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:4988:U:OP2	5:LB:123:HIS:ND1	2.40	0.47
11:LH:89:ARG:HA	11:LH:146:LEU:O	2.15	0.47
41:Lm:109:ASN:ND2	41:Lm:117:HIS:HB3	2.29	0.47
45:Lr:47:LYS:HB2	45:Lr:103:ARG:HG3	1.96	0.47
47:S2:674:C:H2'	47:S2:675:U:C6	2.50	0.47
47:S2:1219:C:H42	47:S2:1646:C:H41	1.61	0.47
47:S2:1259:A:N6	47:S2:1519:U:O5'	2.47	0.47
47:S2:1302:G:N2	47:S2:1305:C:OP2	2.47	0.47
47:S2:1865:C:O2	66:Sa:92:ARG:HB3	2.15	0.47
51:SD:164:VAL:O	51:SD:168:VAL:HG22	2.14	0.47
1:L5:1075:G:N1	1:L5:1076:C:O2	2.48	0.47
1:L5:1183:C:O2	1:L5:1184:A:N6	2.48	0.47
1:L5:1242:G:O6	1:L5:1269:G:O2'	2.33	0.47
1:L5:1488:G:OP1	14:LL:183:ARG:NH2	2.48	0.47
1:L5:1768:C:H4'	1:L5:1769:G:C8	2.50	0.47
1:L5:1837:A:H2'	1:L5:1838:A:C8	2.49	0.47
1:L5:1863:U:OP1	12:LI:15:LYS:HG3	2.14	0.47
1:L5:1921:C:H1'	21:LS:160:ARG:HG3	1.95	0.47
1:L5:1972:G:N2	1:L5:1973:G:H21	2.13	0.47
1:L5:4135:G:H2'	1:L5:4136:G:H8	1.80	0.47
1:L5:4768:G:H2'	1:L5:4769:G:C8	2.49	0.47
1:L5:4882:U:O2'	1:L5:4883:C:H5'	2.15	0.47
1:L5:4896:G:H2'	1:L5:4897:G:C8	2.49	0.47
16:LN:140:LYS:O	16:LN:144:ARG:HG2	2.15	0.47
34:Lf:25:THR:HG22	34:Lf:87:LYS:CD	2.45	0.47
36:Lh:21:LEU:O	36:Lh:25:LYS:HG2	2.15	0.47
38:Lj:2:THR:HG22	38:Lj:4:GLY:H	1.80	0.47
46:Lz:92:LYS:HA	46:Lz:97:LYS:HG2	1.97	0.47
46:Lz:114:GLU:OE1	46:Lz:114:GLU:N	2.48	0.47
47:S2:143:U:N3	72:SG:184:VAL:HG11	2.30	0.47
47:S2:599:A:H2'	47:S2:606:G:H21	1.79	0.47
47:S2:642:U:P	73:SJ:39:ASN:HB2	2.55	0.47
47:S2:694:G:N7	47:S2:696:G:C2	2.82	0.47
47:S2:1092:G:OP1	75:SN:2:GLY:N	2.48	0.47
47:S2:1478:U:H2'	47:S2:1479:G:C8	2.50	0.47
47:S2:1536:G:H22	47:S2:1597:C:N4	2.10	0.47
47:S2:1677:U:OP1	53:SF:71:ARG:NH2	2.47	0.47
47:S2:1748:G:C6	47:S2:1787:G:C6	3.02	0.47
47:S2:1755:C:O2'	47:S2:1777:G:N2	2.48	0.47
50:SB:102:GLY:HA2	50:SB:215:VAL:HG13	1.96	0.47
51:SD:55:THR:O	51:SD:59:LEU:HD13	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:SU:60:THR:HG23	63:SU:81:GLN:NE2	2.29	0.47
70:Sg:173:LEU:HB3	70:Sg:175:LYS:HE3	1.97	0.47
71:SC:135:GLY:O	71:SC:165:VAL:N	2.47	0.47
72:SG:170:ARG:HG3	72:SG:171:THR:O	2.15	0.47
73:SJ:4:ALA:H	73:SJ:5:ARG:NE	2.11	0.47
75:SN:47:PRO:HA	75:SN:50:ILE:HB	1.96	0.47
1:L5:151:G:O6	10:LG:139:GLY:HA3	2.14	0.47
1:L5:1830:G:O3'	30:Lb:68:ARG:NH1	2.48	0.47
1:L5:2415:U:H2'	1:L5:2416:G:C8	2.50	0.47
1:L5:4487:A:O2'	1:L5:4708:A:N1	2.43	0.47
8:LE:91:THR:HG22	8:LE:92:VAL:HG22	1.97	0.47
8:LE:97:GLY:N	8:LE:98:GLY:HA3	2.30	0.47
13:LJ:27:GLY:O	13:LJ:28:GLU:HG3	2.15	0.47
13:LJ:55:TYR:CD2	13:LJ:56:THR:HG23	2.50	0.47
14:LL:63:THR:HG22	14:LL:64:VAL:N	2.30	0.47
17:LO:185:VAL:O	17:LO:189:ILE:HG12	2.14	0.47
29:La:82:VAL:HG13	29:La:83:SER:N	2.30	0.47
47:S2:17:C:H2'	47:S2:18:C:H6	1.80	0.47
47:S2:1321:G:H3'	47:S2:1322:G:C8	2.48	0.47
47:S2:1536:G:H1	47:S2:1597:C:N4	2.13	0.47
47:S2:1759:G:N2	47:S2:1760:G:O6	2.48	0.47
58:SP:36:LEU:C	58:SP:38:SER:H	2.23	0.47
60:SR:37:GLU:OE1	70:Sg:150:TRP:NE1	2.32	0.47
61:SS:74:PRO:HG2	61:SS:75:ARG:HD2	1.95	0.47
61:SS:105:ASN:OD1	61:SS:108:ARG:NH2	2.47	0.47
63:SU:66:ARG:HH21	63:SU:75:LYS:HG2	1.79	0.47
65:SX:105:PHE:CD2	65:SX:112:VAL:HG21	2.49	0.47
67:Sc:29:GLN:HE22	67:Sc:67:ARG:H	1.61	0.47
1:L5:658:C:H2'	1:L5:659:G:C8	2.50	0.47
1:L5:1085:C:H2'	1:L5:1086:C:H6	1.79	0.47
1:L5:2120:G:H2'	1:L5:2121:C:O4'	2.14	0.47
1:L5:3668:C:H5'	4:LA:8:GLN:O	2.15	0.47
1:L5:4094:G:N1	1:L5:4114:C:O2	2.45	0.47
1:L5:4096:C:N4	1:L5:4115:G:OP2	2.48	0.47
1:L5:4136:G:N2	1:L5:4149:C:H1'	2.30	0.47
3:L8:2:G:H2'	3:L8:3:A:O4'	2.14	0.47
3:L8:94:G:OP2	38:Lj:72:ARG:NH2	2.48	0.47
5:LB:37:PRO:HA	5:LB:187:GLY:O	2.15	0.47
5:LB:285:TYR:CE2	5:LB:334:LYS:HB2	2.50	0.47
6:LC:156:ASP:C	6:LC:158:VAL:H	2.22	0.47
47:S2:1692:U:H2'	47:S2:1693:G:H8	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:SS:22:GLY:HA2	61:SS:56:ALA:HB3	1.96	0.47
81:Se:50:GLY:O	81:Se:53:LYS:HG2	2.15	0.47
1:L5:157:U:O2'	1:L5:158:A:C5	2.68	0.47
1:L5:455:C:C4	33:Le:5:ARG:NH1	2.83	0.47
1:L5:486:C:O2	1:L5:486:C:H2'	2.15	0.47
1:L5:1264:C:H2'	1:L5:1265:G:H8	1.80	0.47
1:L5:1266:G:H1'	1:L5:2111:G:H4'	1.97	0.47
1:L5:1563:A:H4'	75:SN:127:ARG:NH2	2.30	0.47
1:L5:1601:A:OP1	38:Lj:5:THR:OG1	2.31	0.47
1:L5:2661:U:O2'	1:L5:2662:G:O5'	2.33	0.47
1:L5:3707:U:H2'	1:L5:3708:C:C6	2.50	0.47
1:L5:4188:U:H2'	1:L5:4189:U:C6	2.50	0.47
1:L5:4916:G:H2'	1:L5:4917:C:C6	2.50	0.47
2:L7:1:G:O5'	7:LD:265:ARG:NE	2.48	0.47
3:L8:6:C:H2'	3:L8:7:U:H6	1.80	0.47
8:LE:153:LEU:HD13	34:Lf:106:TYR:HA	1.97	0.47
10:LG:137:ARG:HG3	10:LG:146:LEU:HD11	1.96	0.47
11:LH:38:PHE:O	11:LH:41:ILE:HG22	2.15	0.47
15:LM:7:VAL:HG13	15:LM:27:ILE:HD13	1.97	0.47
26:LX:100:VAL:HG21	26:LX:109:ILE:CD1	2.45	0.47
28:LZ:53:VAL:HG13	28:LZ:54:THR:H	1.81	0.47
35:Lg:20:THR:HG22	35:Lg:35:THR:H	1.80	0.47
47:S2:72:C:H1'	47:S2:73:C:H2'	1.97	0.47
47:S2:535:G:N2	47:S2:548:C:H42	2.05	0.47
47:S2:1601:A:O2'	47:S2:1604:G:O6	2.33	0.47
51:SD:99:ILE:H	51:SD:99:ILE:HD12	1.80	0.47
54:SH:6:ALA:HB2	54:SH:28:LEU:HD21	1.97	0.47
58:SP:70:MET:O	58:SP:72:LYS:HG2	2.15	0.47
62:ST:42:HIS:HD2	62:ST:93:SER:HB2	1.80	0.47
76:SO:149:ARG:NH2	76:SO:151:LEU:HD21	2.29	0.47
1:L5:383:A:O2'	1:L5:384:A:C8	2.68	0.46
1:L5:492:U:N3	1:L5:662:C:C2	2.83	0.46
1:L5:1072:C:H42	1:L5:1239:C:H42	1.60	0.46
1:L5:2760:G:O2'	1:L5:2762:G:N2	2.47	0.46
1:L5:3753:G:H22	1:L5:3771:C:H6	1.62	0.46
1:L5:4164:C:OP2	10:LG:62:ARG:NH1	2.48	0.46
7:LD:33:ARG:O	7:LD:37:VAL:HB	2.14	0.46
22:LT:45:MET:HE2	22:LT:47:THR:HB	1.97	0.46
23:LU:39:PHE:HA	23:LU:90:TYR:CE2	2.51	0.46
24:LV:85:ARG:NH1	24:LV:99:GLU:O	2.48	0.46
58:SP:78:THR:OG1	58:SP:96:VAL:N	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:260:C:H2'	1:L5:261:G:C8	2.50	0.46
1:L5:307:A:N3	1:L5:310:G:O2'	2.45	0.46
1:L5:1865:G:OP1	12:LI:120:GLY:N	2.47	0.46
1:L5:2493:G:O2'	3:L8:127:U:OP1	2.27	0.46
1:L5:3770:U:H2'	1:L5:3771:C:O4'	2.16	0.46
5:LB:293:ILE:HD12	5:LB:297:LYS:HB3	1.97	0.46
34:Lf:8:LYS:HB3	34:Lf:100:ARG:NH1	2.30	0.46
47:S2:380:G:N1	47:S2:383:G:OP2	2.25	0.46
47:S2:690:G:H2'	47:S2:691:G:C8	2.51	0.46
47:S2:955:A:H61	47:S2:971:G:H1'	1.81	0.46
47:S2:1756:C:H42	47:S2:1776:G:H1	1.63	0.46
49:SA:30:LEU:HD22	49:SA:34:MET:HB2	1.97	0.46
51:SD:218:LEU:HG	51:SD:220:THR:HG23	1.97	0.46
56:SK:45:VAL:HB	56:SK:49:MET:HE1	1.96	0.46
58:SP:18:ARG:HH21	61:SS:93:GLY:HA3	1.80	0.46
71:SC:152:ARG:O	71:SC:156:ILE:HD12	2.16	0.46
73:SJ:150:ARG:HB2	73:SJ:153:SER:OG	2.15	0.46
1:L5:668:C:OP1	45:Lr:69:GLY:HA2	2.16	0.46
1:L5:733:A:C8	1:L5:734:G:C8	3.04	0.46
1:L5:746:A:C2	1:L5:916:C:H5	2.33	0.46
1:L5:1244:G:H1'	1:L5:1245:C:C2	2.49	0.46
1:L5:2465:C:H2'	1:L5:2466:G:O4'	2.14	0.46
1:L5:2611:A:H2'	1:L5:2612:G:H8	1.81	0.46
1:L5:4406:U:C2	1:L5:4407:G:C8	3.04	0.46
3:L8:75:G:OP2	27:LY:74:TYR:OH	2.33	0.46
4:LA:47:ASP:OD1	4:LA:48:ILE:N	2.49	0.46
6:LC:24:LEU:HD21	6:LC:28:PHE:HB2	1.96	0.46
13:LJ:54:ARG:NH1	13:LJ:55:TYR:HB3	2.30	0.46
15:LM:32:ASP:HB2	21:LS:145:PHE:CZ	2.51	0.46
25:LW:68:GLN:H	25:LW:70:LYS:HB2	1.80	0.46
28:LZ:22:LYS:NZ	28:LZ:132:GLN:O	2.49	0.46
38:Lj:26:ALA:O	38:Lj:34:CYS:HB2	2.16	0.46
47:S2:85:A:H1'	47:S2:150:A:H1'	1.96	0.46
47:S2:883:U:H2'	47:S2:884:C:C6	2.50	0.46
47:S2:1164:G:O2'	47:S2:1165:G:H5'	2.15	0.46
47:S2:1607:A:N6	47:S2:1632:G:O2'	2.48	0.46
50:SB:28:LYS:CD	50:SB:48:LEU:HD21	2.46	0.46
54:SH:68:GLN:HG2	54:SH:72:PHE:CE2	2.51	0.46
62:ST:123:LEU:HD22	62:ST:128:GLN:OE1	2.16	0.46
68:Sd:30:LEU:HD12	68:Sd:38:MET:O	2.14	0.46
1:L5:319:A:H1'	1:L5:3726:A:H8	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:2579:G:N2	1:L5:2582:A:OP2	2.39	0.46
1:L5:4504:C:H2'	1:L5:4505:C:C6	2.51	0.46
1:L5:4597:U:H2'	1:L5:4598:C:O4'	2.15	0.46
12:LI:109:ASP:HA	12:LI:110:ARG:HA	1.62	0.46
17:LO:181:ALA:O	17:LO:185:VAL:HG12	2.14	0.46
18:LP:111:SER:OG	18:LP:152:GLU:HB2	2.15	0.46
19:LQ:159:PRO:HD3	19:LQ:188:ASN:OD1	2.16	0.46
37:Li:56:ARG:HD2	37:Li:72:PHE:CZ	2.50	0.46
41:Lm:104:HIS:HD2	41:Lm:111:ARG:HH21	1.63	0.46
46:Lz:14:VAL:HG23	46:Lz:15:ARG:HG2	1.97	0.46
47:S2:986:G:N2	76:SO:135:ILE:HD12	2.31	0.46
50:SB:180:ASP:O	50:SB:184:VAL:HG23	2.15	0.46
52:SE:191:ARG:HE	52:SE:245:ARG:HD2	1.79	0.46
53:SF:120:GLY:HA3	53:SF:146:ARG:HE	1.80	0.46
57:SL:13:GLN:NE2	57:SL:35:ARG:HH21	2.12	0.46
59:SQ:37:ARG:HD3	59:SQ:41:MET:HE2	1.96	0.46
1:L5:153:G:H2'	1:L5:154:G:H8	1.80	0.46
1:L5:962:C:H42	1:L5:2255:C:N4	2.13	0.46
1:L5:1077:C:C4	1:L5:1234:G:N2	2.83	0.46
1:L5:1474:C:H2'	1:L5:1475:G:O4'	2.16	0.46
1:L5:1510:G:H2'	1:L5:1511:U:C6	2.51	0.46
1:L5:1978:C:H41	1:L5:1979:A:H2	1.63	0.46
8:LE:46:ARG:HB3	8:LE:62:MET:HE3	1.98	0.46
8:LE:86:GLU:HB2	8:LE:89:LEU:HD12	1.96	0.46
9:LF:116:GLN:HG2	9:LF:119:ASN:ND2	2.28	0.46
10:LG:58:PRO:HD2	10:LG:61:ILE:HD11	1.96	0.46
20:LR:171:LYS:HA	20:LR:174:GLU:HG2	1.97	0.46
47:S2:118:C:H1'	47:S2:445:A:C6	2.51	0.46
47:S2:123:G:C5	47:S2:124:U:C4	3.04	0.46
47:S2:640:A:H2'	47:S2:641:A:C8	2.51	0.46
47:S2:906:U:H2'	47:S2:907:G:C8	2.50	0.46
47:S2:1408:U:H1'	47:S2:1442:U:O4	2.16	0.46
47:S2:1419:C:N4	47:S2:1429:G:H1	2.13	0.46
47:S2:1656:G:H1	47:S2:1668:U:H3	1.62	0.46
47:S2:1813:A:O2'	47:S2:1814:G:OP1	2.33	0.46
52:SE:191:ARG:HH21	52:SE:245:ARG:HD2	1.80	0.46
54:SH:67:PRO:HG2	54:SH:68:GLN:OE1	2.15	0.46
65:SX:94:ILE:HA	65:SX:125:VAL:HG21	1.97	0.46
65:SX:140:ARG:HH22	65:SX:142:ARG:HH11	1.63	0.46
72:SG:51:ARG:O	72:SG:112:VAL:HG12	2.16	0.46
1:L5:480:C:H2'	1:L5:481:G:H8	1.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:1076:C:O2	1:L5:1235:G:N1	2.49	0.46
1:L5:2056:G:OP1	1:L5:2056:G:H4'	2.16	0.46
1:L5:2464:C:HO2'	1:L5:2465:C:H6	1.63	0.46
1:L5:4256:A:N6	13:LJ:57:VAL:HG11	2.31	0.46
1:L5:4970:C:C2	1:L5:4971:A:C8	3.04	0.46
1:L5:5015:G:O2'	1:L5:5034:A:N6	2.49	0.46
10:LG:106:THR:HB	10:LG:109:GLU:OE1	2.16	0.46
21:LS:82:LEU:HD21	21:LS:109:CYS:SG	2.56	0.46
28:LZ:11:VAL:HG11	28:LZ:80:LEU:HB3	1.96	0.46
33:Le:84:GLU:CD	45:Lr:20:ARG:HH22	2.23	0.46
47:S2:921:G:C5	77:SW:28:ARG:HD2	2.51	0.46
47:S2:1201:U:H2'	47:S2:1202:U:C6	2.50	0.46
49:SA:10:MET:HE1	49:SA:51:LEU:HB3	1.98	0.46
52:SE:211:LYS:HD3	52:SE:217:SER:HB2	1.98	0.46
54:SH:83:LEU:O	54:SH:86:LYS:HG3	2.15	0.46
55:SI:110:ARG:NE	55:SI:121:LEU:O	2.42	0.46
57:SL:94:HIS:N	57:SL:103:GLU:O	2.47	0.46
57:SL:95:TYR:HE2	57:SL:97:ARG:HE	1.63	0.46
58:SP:40:ARG:NH2	58:SP:83:MET:HB2	2.30	0.46
70:Sg:254:PRO:HA	70:Sg:285:GLN:HA	1.97	0.46
71:SC:123:ARG:NH2	71:SC:143:CYS:O	2.46	0.46
1:L5:417:G:H1'	1:L5:418:A:OP2	2.16	0.46
1:L5:456:C:H2'	1:L5:457:G:H8	1.79	0.46
1:L5:1756:U:C5	1:L5:1776:A:H1'	2.51	0.46
1:L5:1759:G:H2'	1:L5:1760:G:H8	1.80	0.46
1:L5:2854:G:H2'	1:L5:2855:G:H5"	1.98	0.46
1:L5:3641:U:H5	1:L5:3646:A:N7	2.14	0.46
1:L5:3723:A:H2'	1:L5:3724:A:C8	2.51	0.46
1:L5:4093:G:C2	1:L5:4094:G:C5	3.04	0.46
1:L5:4474:A:H2'	1:L5:4476:C:H5"	1.97	0.46
1:L5:4993:G:H2'	1:L5:4994:G:H8	1.81	0.46
2:L7:4:U:H2'	2:L7:5:A:C8	2.50	0.46
18:LP:112:LEU:HD23	18:LP:152:GLU:HB3	1.98	0.46
34:Lf:4:ARG:O	34:Lf:6:TRP:N	2.47	0.46
47:S2:123:G:C6	47:S2:124:U:C4	3.04	0.46
47:S2:158:A:H2'	47:S2:159:A:C8	2.51	0.46
47:S2:557:U:H2'	47:S2:558:G:C8	2.50	0.46
48:S6:12:C:H2'	48:S6:13:G:C8	2.51	0.46
50:SB:128:LYS:NZ	50:SB:132:GLY:O	2.49	0.46
53:SF:19:LEU:HG	53:SF:48:TYR:HE1	1.80	0.46
1:L5:54:G:OP1	38:Lj:43:ARG:NH1	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:1270:A:N7	1:L5:1271:G:O2'	2.49	0.46
1:L5:1954:U:H2'	1:L5:1955:G:O4'	2.16	0.46
1:L5:2738:C:O2'	1:L5:2740:U:O2	2.34	0.46
14:LL:161:TYR:HE2	29:La:105:ARG:NH2	2.14	0.46
21:LS:20:PRO:CD	21:LS:21:LYS:N	2.79	0.46
33:Le:47:ARG:HD2	33:Le:49:PHE:HE2	1.80	0.46
33:Le:108:ARG:HH22	33:Le:124:ASN:ND2	2.14	0.46
53:SF:77:MET:CE	53:SF:86:LYS:HB2	2.46	0.46
1:L5:3970:G:H1'	1:L5:4052:C:H42	1.81	0.46
1:L5:4861:G:OP1	17:LO:169:ARG:HD3	2.16	0.46
14:LL:47:ALA:HB3	14:LL:48:PRO:HD3	1.97	0.46
23:LU:42:PHE:CE1	23:LU:90:TYR:HD2	2.34	0.46
40:Ll:21:ARG:HH12	40:Ll:24:PRO:HD3	1.81	0.46
47:S2:319:C:H3'	47:S2:320:G:H8	1.81	0.46
47:S2:643:A:H4'	47:S2:644:G:H5'	1.96	0.46
47:S2:1232:U:H2'	47:S2:1233:G:H8	1.81	0.46
47:S2:1573:G:H2'	47:S2:1574:C:O4'	2.15	0.46
50:SB:71:LEU:HB2	50:SB:82:ARG:HB2	1.98	0.46
58:SP:104:GLN:O	58:SP:105:VAL:HB	2.15	0.46
60:SR:67:ARG:HA	60:SR:68:GLY:HA2	1.58	0.46
60:SR:100:PRO:HG3	60:SR:118:GLN:HB2	1.98	0.46
62:ST:28:LEU:HD22	62:ST:54:TYR:CE1	2.51	0.46
70:Sg:31:ILE:HG12	70:Sg:45:LEU:HD11	1.97	0.46
71:SC:208:PRO:O	71:SC:212:LYS:HG3	2.16	0.46
72:SG:197:GLN:HA	72:SG:200:LYS:HG2	1.98	0.46
1:L5:483:G:N2	1:L5:671:G:H22	2.13	0.46
1:L5:1293:G:H3'	1:L5:1294:A:C2	2.51	0.46
1:L5:4159:C:H2'	1:L5:4160:C:C6	2.51	0.46
1:L5:4704:C:H2'	1:L5:4705:A:C8	2.51	0.46
6:LC:208:CYS:HB2	6:LC:248:ARG:HE	1.80	0.46
7:LD:119:TYR:OH	7:LD:139:PRO:O	2.22	0.46
24:LV:83:ARG:NH1	24:LV:120:PRO:O	2.37	0.46
25:LW:78:PHE:HD2	25:LW:79:GLN:HB2	1.81	0.46
47:S2:538:U:H5"	47:S2:546:G:C4	2.50	0.46
47:S2:795:A:N7	54:SH:109:ARG:NH2	2.63	0.46
47:S2:840:C:H5'	47:S2:841:G:H5"	1.98	0.46
47:S2:975:G:O2'	76:SO:49:GLY:O	2.31	0.46
47:S2:1679:A:H4'	47:S2:1680:G:C8	2.51	0.46
49:SA:5:LEU:HD21	64:SV:80:SER:HB2	1.97	0.46
49:SA:126:ASP:OD2	49:SA:128:ARG:HB3	2.16	0.46
53:SF:19:LEU:HD11	59:SQ:49:TYR:OH	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:SF:140:ASP:OD1	53:SF:141:VAL:N	2.49	0.46
55:SI:107:THR:OG1	55:SI:108:PRO:HD3	2.16	0.46
58:SP:51:ARG:O	58:SP:54:HIS:N	2.41	0.46
60:SR:50:ILE:O	60:SR:54:VAL:HG23	2.15	0.46
61:SS:20:ILE:HG13	61:SS:32:ALA:HB3	1.98	0.46
62:ST:42:HIS:ND1	62:ST:43:LYS:HG3	2.31	0.46
1:L5:449:C:H4'	1:L5:449:C:OP1	2.14	0.45
1:L5:704:C:H2'	1:L5:705:G:C8	2.50	0.45
1:L5:1084:C:H2'	1:L5:1085:C:H6	1.80	0.45
1:L5:3789:C:H2'	1:L5:3790:U:C5	2.51	0.45
1:L5:4135:G:H2'	1:L5:4136:G:C8	2.51	0.45
1:L5:4698:C:OP1	41:Lm:125:LYS:NZ	2.37	0.45
1:L5:5029:C:H2'	1:L5:5030:U:H6	1.80	0.45
9:LF:98:ILE:HG23	9:LF:98:ILE:O	2.15	0.45
14:LL:55:ILE:HD12	14:LL:55:ILE:HA	1.88	0.45
15:LM:33:GLN:C	15:LM:35:ARG:H	2.24	0.45
17:LO:185:VAL:HG22	17:LO:188:LYS:HB2	1.98	0.45
21:LS:154:LEU:HB3	21:LS:157:ARG:HD3	1.97	0.45
34:Lf:46:ARG:HD2	34:Lf:106:TYR:OH	2.16	0.45
47:S2:555:A:C8	47:S2:556:U:H4'	2.50	0.45
51:SD:104:SER:HA	51:SD:107:TYR:CZ	2.51	0.45
53:SF:59:LYS:HB3	53:SF:62:ARG:HD3	1.98	0.45
54:SH:158:LEU:HD21	54:SH:187:PHE:CD1	2.48	0.45
56:SK:8:ARG:HD2	56:SK:45:VAL:HG12	1.98	0.45
57:SL:146:THR:O	57:SL:146:THR:HG22	2.16	0.45
61:SS:34:LYS:HB3	61:SS:103:LEU:HD21	1.98	0.45
70:Sg:175:LYS:NZ	70:Sg:187:ASN:HB3	2.31	0.45
71:SC:255:LEU:O	71:SC:256:TRP:HB2	2.15	0.45
78:SY:29:HIS:ND1	78:SY:29:HIS:O	2.49	0.45
1:L5:948:C:H5"	8:LE:51:VAL:HG21	1.97	0.45
1:L5:2899:C:H2'	1:L5:2900:U:C6	2.51	0.45
1:L5:4158:C:H2'	1:L5:4159:C:H6	1.81	0.45
3:L8:3:A:O2'	18:LP:61:ARG:HD2	2.17	0.45
3:L8:82:A:H62	3:L8:84:A:H5'	1.81	0.45
9:LF:247:MET:HE2	9:LF:247:MET:HB3	1.84	0.45
34:Lf:21:GLN:NE2	34:Lf:23:GLU:OE2	2.49	0.45
51:SD:125:PHE:HA	51:SD:128:GLU:HG2	1.97	0.45
52:SE:18:TRP:CD1	52:SE:46:ILE:HD13	2.51	0.45
66:Sa:47:ALA:O	66:Sa:50:VAL:HG12	2.16	0.45
79:SZ:50:PHE:HB2	79:SZ:55:TYR:CE1	2.50	0.45
1:L5:62:A:H5'	16:LN:174:LEU:HD13	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:325:U:H2'	1:L5:326:C:H6	1.81	0.45
1:L5:465:G:H2'	1:L5:466:A:C8	2.51	0.45
1:L5:676:C:H2'	1:L5:677:G:C8	2.52	0.45
1:L5:699:C:H2'	1:L5:700:G:C8	2.51	0.45
1:L5:1367:C:O2'	1:L5:1369:C:OP2	2.28	0.45
1:L5:2120:G:HO2'	1:L5:2121:C:P	2.38	0.45
1:L5:2858:A:O2'	1:L5:2859:G:O5'	2.34	0.45
1:L5:3908:A:H2'	1:L5:3908:A:N3	2.30	0.45
1:L5:4088:C:H2'	1:L5:4089:G:C8	2.51	0.45
7:LD:11:ALA:O	7:LD:15:ARG:HG2	2.16	0.45
13:LJ:44:THR:HG22	13:LJ:46:GLN:HG3	1.98	0.45
14:LL:146:LEU:HA	14:LL:147:ALA:HB3	1.97	0.45
14:LL:205:GLN:HB3	14:LL:209:LYS:HG3	1.98	0.45
15:LM:72:TYR:HA	15:LM:75:GLN:HG2	1.98	0.45
23:LU:25:CYS:HB3	23:LU:112:LEU:HD13	1.99	0.45
47:S2:210:U:H2'	47:S2:211:G:C8	2.51	0.45
47:S2:310:C:H2'	47:S2:311:C:C6	2.52	0.45
47:S2:493:A:H61	47:S2:510:G:H1'	1.81	0.45
47:S2:1673:U:OP2	59:SQ:17:LYS:HE2	2.17	0.45
48:S6:3:G:H2'	48:S6:4:C:C6	2.52	0.45
58:SP:49:LEU:O	58:SP:50:ARG:HG3	2.16	0.45
1:L5:1185:G:H1'	7:LD:278:ASP:OD2	2.16	0.45
1:L5:1370:G:OP1	6:LC:48:ASN:ND2	2.37	0.45
19:LQ:54:SER:O	19:LQ:58:ARG:HG2	2.17	0.45
26:LX:148:ASP:O	26:LX:152:LYS:HG3	2.17	0.45
33:Le:19:LYS:HD3	33:Le:33:ARG:NH1	2.28	0.45
47:S2:344:U:H2'	47:S2:345:U:C6	2.51	0.45
47:S2:948:C:H2'	47:S2:949:G:C8	2.49	0.45
53:SF:56:TYR:HA	53:SF:62:ARG:HH21	1.81	0.45
58:SP:75:VAL:O	58:SP:77:LYS:N	2.49	0.45
71:SC:224:THR:HG22	71:SC:225:SER:H	1.82	0.45
72:SG:209:TYR:O	72:SG:214:ALA:N	2.49	0.45
76:SO:57:THR:HG22	76:SO:60:MET:CE	2.46	0.45
1:L5:418:A:N6	3:L8:16:G:H1'	2.31	0.45
1:L5:1187:G:H2'	1:L5:1188:C:C2	2.51	0.45
1:L5:4422:A:N3	1:L5:4427:G:N1	2.62	0.45
20:LR:78:ILE:HD13	20:LR:81:ARG:NH1	2.32	0.45
22:LT:83:LYS:HE3	22:LT:83:LYS:HB2	1.83	0.45
38:Lj:27:TYR:HD1	38:Lj:34:CYS:HB3	1.80	0.45
45:Lr:103:ARG:NH2	45:Lr:106:LEU:HD11	2.31	0.45
47:S2:207:G:H3'	47:S2:208:G:H5"	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:S2:606:G:N3	47:S2:606:G:H2'	2.31	0.45
49:SA:149:ASN:HB2	49:SA:165:ASN:OD1	2.16	0.45
54:SH:104:PRO:HA	54:SH:107:LYS:HD2	1.99	0.45
55:SI:64:ASN:O	55:SI:64:ASN:ND2	2.45	0.45
71:SC:263:LYS:HE2	71:SC:263:LYS:HB3	1.80	0.45
72:SG:50:VAL:HB	72:SG:111:LEU:HD11	1.98	0.45
72:SG:187:HIS:O	72:SG:191:ARG:HG3	2.17	0.45
73:SJ:32:ILE:HD11	73:SJ:40:LYS:HG2	1.99	0.45
74:SM:16:THR:HG21	74:SM:84:LYS:HE2	1.98	0.45
76:SO:78:ALA:HB1	76:SO:119:LEU:HG	1.97	0.45
1:L5:173:C:H2'	1:L5:174:C:O4'	2.16	0.45
1:L5:2130:G:H22	1:L5:2243:C:N4	2.14	0.45
1:L5:2495:U:H2'	1:L5:2496:G:C8	2.51	0.45
6:LC:267:TRP:NE1	6:LC:280:PRO:O	2.37	0.45
12:LI:193:ASP:OD2	12:LI:198:LYS:HB2	2.16	0.45
19:LQ:7:HIS:HB2	19:LQ:10:ASP:OD1	2.17	0.45
27:LY:54:GLU:H	27:LY:54:GLU:CD	2.25	0.45
39:Lk:66:VAL:HA	39:Lk:67:LYS:HA	1.71	0.45
46:Lz:29:LEU:HD13	46:Lz:173:LYS:HD2	1.99	0.45
46:Lz:155:ILE:HD12	46:Lz:167:VAL:HG21	1.98	0.45
47:S2:321:C:N3	47:S2:322:C:N4	2.64	0.45
47:S2:322:C:HO2'	47:S2:323:C:P	2.39	0.45
47:S2:334:C:H2'	47:S2:335:G:H8	1.80	0.45
47:S2:753:C:OP1	47:S2:792:C:O2'	2.26	0.45
47:S2:835:C:H3'	78:SY:8:ARG:HH21	1.82	0.45
47:S2:1226:G:N2	47:S2:1639:G:H5'	2.32	0.45
47:S2:1528:G:H2'	47:S2:1529:C:C6	2.52	0.45
47:S2:1779:G:H2'	47:S2:1780:G:C8	2.52	0.45
51:SD:101:GLN:HG2	51:SD:126:ILE:HD11	1.99	0.45
56:SK:6:LYS:HD2	69:Sf:103:LEU:O	2.17	0.45
58:SP:53:GLN:O	58:SP:56:LEU:HB2	2.15	0.45
60:SR:36:GLU:OE2	60:SR:47:ARG:NH1	2.35	0.45
65:SX:110:HIS:ND1	65:SX:111:ALA:N	2.65	0.45
73:SJ:46:VAL:HA	73:SJ:49:THR:HG22	1.99	0.45
76:SO:117:ARG:HE	76:SO:121:ARG:NH2	2.14	0.45
78:SY:54:VAL:HG13	78:SY:79:LEU:HD23	1.99	0.45
1:L5:1774:C:H2'	1:L5:1775:A:O4'	2.17	0.45
1:L5:1971:C:H5"	1:L5:2001:G:N2	2.32	0.45
1:L5:2361:G:O2'	1:L5:2362:U:P	2.75	0.45
1:L5:2483:G:H2'	1:L5:2484:A:H5"	1.99	0.45
1:L5:2486:G:N2	1:L5:2493:G:H1	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:3949:A:H2'	1:L5:3950:U:H6	1.82	0.45
1:L5:4896:G:H2'	1:L5:4897:G:H8	1.82	0.45
8:LE:278:THR:O	8:LE:281:ILE:HG12	2.16	0.45
20:LR:129:GLY:O	20:LR:131:VAL:HG23	2.16	0.45
20:LR:159:ALA:HA	20:LR:162:ARG:HE	1.80	0.45
24:LV:42:VAL:HG13	24:LV:45:ILE:HG13	1.99	0.45
26:LX:97:VAL:HG22	26:LX:137:TYR:CD1	2.51	0.45
26:LX:100:VAL:HG21	26:LX:109:ILE:HD12	1.99	0.45
31:Lc:31:TYR:HA	31:Lc:34:THR:HG22	1.99	0.45
47:S2:381:C:H2'	47:S2:382:C:H6	1.80	0.45
51:SD:139:SER:O	51:SD:182:LEU:HB2	2.17	0.45
52:SE:184:THR:HA	52:SE:189:LEU:HB2	1.99	0.45
54:SH:98:ARG:O	54:SH:100:ILE:N	2.48	0.45
64:SV:35:ASN:ND2	71:SC:267:GLN:OE1	2.50	0.45
65:SX:135:LYS:HE2	65:SX:135:LYS:HB3	1.71	0.45
67:Sc:12:ALA:O	67:Sc:56:LEU:N	2.49	0.45
1:L5:979:C:H5"	1:L5:980:U:OP1	2.16	0.45
1:L5:1448:G:H2'	1:L5:1449:C:H6	1.82	0.45
1:L5:3848:U:H2'	1:L5:3849:A:C8	2.51	0.45
1:L5:3856:A:H5"	18:LP:83:TRP:O	2.17	0.45
1:L5:4524:G:C2	5:LB:252:ALA:HB1	2.52	0.45
14:LL:140:SER:HA	14:LL:143:GLU:HB3	1.98	0.45
15:LM:32:ASP:OD1	15:LM:33:GLN:N	2.49	0.45
28:LZ:53:VAL:HG13	28:LZ:54:THR:N	2.32	0.45
39:Lk:3:ARG:HH11	39:Lk:3:ARG:HG3	1.82	0.45
47:S2:810:A:N7	47:S2:851:C:N4	2.65	0.45
47:S2:1088:U:H4'	47:S2:1089:G:OP2	2.17	0.45
47:S2:1232:U:H2'	47:S2:1233:G:C8	2.52	0.45
47:S2:1280:G:H22	47:S2:1317:C:N4	2.14	0.45
47:S2:1398:G:C6	47:S2:1448:A:N1	2.85	0.45
47:S2:1866:A:H5'	66:Sa:95:ARG:HG2	1.99	0.45
50:SB:72:ALA:HB2	50:SB:80:ALA:HB2	1.98	0.45
50:SB:149:GLN:HE21	50:SB:151:ARG:HB2	1.81	0.45
51:SD:161:GLY:O	51:SD:164:VAL:HG12	2.17	0.45
52:SE:38:LEU:HA	52:SE:41:CYS:SG	2.57	0.45
54:SH:103:LYS:HG3	54:SH:116:ARG:NH2	2.31	0.45
76:SO:12:GLU:N	76:SO:14:VAL:HA	2.32	0.45
1:L5:663:G:N2	1:L5:664:G:N7	2.65	0.45
1:L5:1488:G:C2	1:L5:1489:G:C4	3.05	0.45
1:L5:2638:G:H1	1:L5:2697:A:N6	2.00	0.45
4:LA:126:LEU:HD13	4:LA:150:LEU:CD1	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:Lj:28:HIS:CE1	38:Lj:30:GLN:HB3	2.52	0.45
41:Lm:99:CYS:HB2	41:Lm:115:CYS:HB3	1.99	0.45
47:S2:106:C:H2'	47:S2:107:A:C8	2.50	0.45
47:S2:122:G:O6	47:S2:343:A:C6	2.70	0.45
47:S2:546:G:C5	47:S2:547:G:H1'	2.52	0.45
47:S2:1114:U:H3	47:S2:1119:A:H61	1.63	0.45
47:S2:1227:G:H2'	47:S2:1227:G:N3	2.31	0.45
47:S2:1270:G:O2'	47:S2:1301:A:N6	2.41	0.45
47:S2:1588:A:HO2'	47:S2:1589:A:P	2.39	0.45
49:SA:51:LEU:O	49:SA:54:THR:OG1	2.32	0.45
53:SF:127:ARG:NH2	67:Sc:22:GLY:O	2.50	0.45
54:SH:58:LYS:O	54:SH:90:LYS:HB3	2.17	0.45
55:SI:40:PRO:HD2	55:SI:59:ARG:HE	1.82	0.45
70:Sg:48:ASP:OD1	70:Sg:49:GLU:N	2.48	0.45
70:Sg:257:LYS:HD3	70:Sg:259:TRP:CD2	2.52	0.45
1:L5:515:C:H2'	1:L5:516:C:O4'	2.16	0.45
1:L5:4239:A:H2'	1:L5:4240:G:C8	2.53	0.45
1:L5:4273:A:H2'	1:L5:4274:A:C8	2.52	0.45
1:L5:4345:C:H2'	1:L5:4346:U:C6	2.51	0.45
2:L7:49:A:OP1	7:LD:225:GLN:HB2	2.17	0.45
25:LW:64:SER:OG	25:LW:65:GLU:N	2.50	0.45
39:Lk:15:ALA:HB1	39:Lk:60:LEU:HD21	1.99	0.45
47:S2:1047:C:H2'	47:S2:1048:G:O4'	2.17	0.45
49:SA:4:ALA:H	49:SA:5:LEU:CA	2.29	0.45
53:SF:14:THR:HA	53:SF:15:PRO:HA	1.79	0.45
55:SI:97:VAL:HG13	55:SI:98:LYS:N	2.32	0.45
58:SP:84:ILE:HD11	61:SS:117:ILE:HG21	1.98	0.45
66:Sa:87:ARG:HE	66:Sa:92:ARG:HA	1.82	0.45
68:Sd:17:GLY:HA2	68:Sd:27:ARG:HG2	1.99	0.45
73:SJ:3:VAL:HB	73:SJ:5:ARG:HB2	1.99	0.45
73:SJ:77:LEU:HA	73:SJ:80:ARG:HE	1.81	0.45
1:L5:456:C:H42	1:L5:701:G:H21	1.65	0.44
1:L5:755:C:N4	1:L5:908:G:H1	2.15	0.44
1:L5:1086:C:C2	1:L5:1212:G:N2	2.85	0.44
1:L5:1449:C:H2'	1:L5:1450:C:C6	2.52	0.44
1:L5:2411:C:H2'	1:L5:2412:A:H8	1.82	0.44
1:L5:2476:G:C6	1:L5:2502:G:N1	2.85	0.44
1:L5:3861:A:H2'	1:L5:3862:A:H8	1.82	0.44
10:LG:27:VAL:HG23	10:LG:28:VAL:HG22	1.99	0.44
14:LL:54:PRO:HA	14:LL:55:ILE:CG2	2.42	0.44
15:LM:24:LEU:O	15:LM:43:THR:HG21	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:LV:56:GLY:O	24:LV:81:VAL:HG21	2.17	0.44
38:Lj:2:THR:HB	38:Lj:6:SER:OG	2.17	0.44
46:Lz:59:PRO:HB2	46:Lz:61:PRO:HD2	1.99	0.44
46:Lz:120:ILE:HG13	46:Lz:124:LEU:HD22	1.99	0.44
47:S2:508:A:H3'	47:S2:509:G:H8	1.81	0.44
47:S2:1644:C:OP1	59:SQ:143:LYS:N	2.45	0.44
51:SD:204:LEU:C	51:SD:206:ASP:H	2.25	0.44
53:SF:59:LYS:HE3	53:SF:61:PHE:CD2	2.52	0.44
55:SI:130:THR:HB	55:SI:131:PRO:HD3	1.98	0.44
72:SG:152:ASP:OD1	72:SG:153:VAL:N	2.49	0.44
75:SN:62:GLN:HG3	75:SN:64:ARG:HG2	2.00	0.44
75:SN:70:LYS:O	75:SN:74:ILE:HG13	2.17	0.44
1:L5:63:G:OP2	16:LN:169:ARG:NH2	2.29	0.44
1:L5:716:C:H2'	1:L5:717:U:C6	2.52	0.44
1:L5:2029:A:H2'	1:L5:2030:A:H8	1.81	0.44
8:LE:82:LYS:N	8:LE:84:LYS:HD3	2.32	0.44
9:LF:148:LYS:O	9:LF:152:GLU:OE1	2.36	0.44
10:LG:51:LEU:C	10:LG:53:ARG:H	2.24	0.44
11:LH:120:GLU:HG2	11:LH:124:ARG:NH1	2.31	0.44
19:LQ:99:LYS:NZ	19:LQ:119:LYS:HD2	2.32	0.44
25:LW:66:GLU:HA	25:LW:67:ILE:HA	1.58	0.44
26:LX:113:VAL:HG12	26:LX:119:ILE:HG21	1.98	0.44
34:Lf:6:TRP:CZ3	34:Lf:8:LYS:HG2	2.52	0.44
46:Lz:80:VAL:HG13	46:Lz:147:LYS:HE2	1.98	0.44
47:S2:1101:U:H2'	47:S2:1102:G:C8	2.51	0.44
47:S2:1749:G:H2'	47:S2:1750:C:C2	2.52	0.44
47:S2:1849:G:O2'	47:S2:1850:A:O5'	2.32	0.44
52:SE:72:ILE:HD12	52:SE:90:ILE:HG12	1.99	0.44
57:SL:11:GLN:HB2	57:SL:56:ILE:HD11	1.99	0.44
71:SC:72:ASP:OD2	71:SC:272:HIS:ND1	2.46	0.44
77:SW:113:HIS:NE2	77:SW:114:GLU:OE2	2.50	0.44
1:L5:919:C:C2	15:LM:65:PRO:HG3	2.52	0.44
1:L5:2557:G:N2	1:L5:2571:C:H1'	2.32	0.44
1:L5:2652:G:N2	44:Lp:58:GLY:O	2.51	0.44
1:L5:3747:A:N7	4:LA:245:ARG:HG3	2.32	0.44
1:L5:4680:G:H2'	1:L5:4681:A:C8	2.53	0.44
5:LB:36:ASP:N	5:LB:36:ASP:OD1	2.50	0.44
5:LB:295:ASP:OD1	5:LB:295:ASP:N	2.48	0.44
12:LI:4:ARG:HD2	12:LI:9:TYR:OH	2.18	0.44
16:LN:124:ASP:OD1	16:LN:125:SER:N	2.47	0.44
28:LZ:52:LYS:HD3	28:LZ:54:THR:HG23	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:Lf:93:PRO:C	34:Lf:95:LYS:H	2.25	0.44
47:S2:14:C:OP1	71:SC:190:SER:OG	2.35	0.44
47:S2:71:G:H3'	47:S2:72:C:H5"	1.98	0.44
47:S2:812:A:O2'	52:SE:12:VAL:O	2.32	0.44
47:S2:1286:G:C2	47:S2:1312:G:H2'	2.52	0.44
47:S2:1792:G:H2'	47:S2:1793:A:H8	1.81	0.44
49:SA:45:GLY:HA3	60:SR:126:MET:HE1	1.98	0.44
49:SA:156:TYR:OH	64:SV:61:ARG:NH1	2.50	0.44
51:SD:75:LYS:NZ	56:SK:22:VAL:HG22	2.31	0.44
54:SH:18:GLU:OE1	54:SH:19:PHE:N	2.47	0.44
61:SS:87:GLN:HA	61:SS:95:TYR:CD1	2.52	0.44
70:Sg:113:PHE:CZ	70:Sg:117:ASN:HA	2.52	0.44
70:Sg:195:LEU:HA	70:Sg:211:GLY:HA3	1.99	0.44
71:SC:106:VAL:HG23	71:SC:128:VAL:HG22	1.99	0.44
76:SO:14:VAL:N	76:SO:15:ILE:HA	2.12	0.44
1:L5:125:C:H2'	1:L5:126:C:H6	1.83	0.44
1:L5:3973:G:H21	1:L5:4051:C:H5'	1.82	0.44
1:L5:5002:U:H2'	1:L5:5003:U:C6	2.52	0.44
3:L8:6:C:H2'	3:L8:7:U:C6	2.53	0.44
5:LB:306:ASP:OD1	5:LB:306:ASP:N	2.49	0.44
7:LD:236:MET:CB	7:LD:239:MET:HE2	2.45	0.44
9:LF:50:ILE:HD12	9:LF:186:CYS:HB3	1.98	0.44
12:LI:105:CYS:HA	12:LI:106:ALA:HA	1.67	0.44
24:LV:87:SER:HG	25:LW:19:ARG:HH21	1.60	0.44
25:LW:77:LYS:HA	25:LW:78:PHE:HA	1.85	0.44
27:LY:4:ASN:HB3	27:LY:7:VAL:HG22	1.99	0.44
28:LZ:51:ARG:HB2	28:LZ:65:ARG:HG2	1.99	0.44
39:Lk:45:LEU:HD21	39:Lk:47:ILE:HG23	2.00	0.44
46:Lz:163:LEU:HG	46:Lz:164:CYS:SG	2.58	0.44
47:S2:26:U:H2'	47:S2:27:A:C8	2.52	0.44
47:S2:1285:G:O6	74:SM:90:GLY:HA3	2.18	0.44
50:SB:32:ASP:OD2	50:SB:34:LYS:NZ	2.48	0.44
52:SE:214:ASN:HB2	52:SE:244:ILE:HD11	1.98	0.44
53:SF:18:LYS:HE3	53:SF:48:TYR:HA	1.99	0.44
55:SI:40:PRO:HG2	55:SI:59:ARG:HH21	1.82	0.44
57:SL:28:THR:HA	57:SL:29:GLY:HA2	1.79	0.44
60:SR:119:VAL:HA	60:SR:120:THR:HA	1.57	0.44
60:SR:125:GLY:HA3	60:SR:126:MET:HE2	2.00	0.44
70:Sg:300:ALA:HB3	70:Sg:310:TRP:HZ3	1.83	0.44
71:SC:170:TRP:HD1	71:SC:197:PRO:HB2	1.82	0.44
73:SJ:2:PRO:O	73:SJ:3:VAL:HG22	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
82:Pt:64:G:H2'	82:Pt:65:G:H8	1.83	0.44
1:L5:180:C:O2	1:L5:256:G:N2	2.41	0.44
1:L5:485:C:H5	1:L5:664:G:C5	2.35	0.44
1:L5:1195:G:H2'	1:L5:1196:G:C8	2.52	0.44
1:L5:2480:G:O6	1:L5:2499:C:N4	2.51	0.44
1:L5:2730:U:H2'	1:L5:2731:C:C6	2.53	0.44
1:L5:4148:C:H2'	1:L5:4149:C:O4'	2.17	0.44
7:LD:266:TRP:CD1	7:LD:266:TRP:H	2.36	0.44
8:LE:268:GLN:O	8:LE:272:ARG:HG3	2.17	0.44
9:LF:46:ARG:O	9:LF:50:ILE:HG12	2.18	0.44
13:LJ:63:ARG:HD3	13:LJ:64:ARG:N	2.32	0.44
15:LM:58:THR:HG22	15:LM:59:ASP:N	2.33	0.44
17:LO:10:ASP:OD1	17:LO:37:ARG:NH2	2.50	0.44
23:LU:26:THR:O	23:LU:30:GLU:HG2	2.17	0.44
34:Lf:6:TRP:HZ3	34:Lf:8:LYS:HG2	1.81	0.44
66:Sa:37:LYS:HG2	66:Sa:72:HIS:ND1	2.33	0.44
69:Sf:135:HIS:CG	69:Sf:136:PHE:N	2.85	0.44
70:Sg:166:VAL:HG12	70:Sg:176:VAL:HG22	2.00	0.44
75:SN:36:GLN:O	75:SN:40:LEU:HD23	2.17	0.44
75:SN:92:ILE:HD13	75:SN:122:ILE:HD13	1.99	0.44
78:SY:94:HIS:NE2	78:SY:96:LEU:HD23	2.33	0.44
82:Pt:33:OMC:H1'	82:Pt:33:OMC:HM23	1.56	0.44
1:L5:659:G:H2'	1:L5:660:A:H8	1.81	0.44
1:L5:1281:G:OP1	8:LE:52:ARG:NH1	2.49	0.44
1:L5:1449:C:H2'	1:L5:1450:C:H6	1.81	0.44
1:L5:1662:C:H2'	1:L5:1663:C:C6	2.53	0.44
1:L5:1757:U:O2'	1:L5:1758:G:N3	2.47	0.44
1:L5:2265:G:H5"	45:Lr:35:ARG:HH22	1.82	0.44
1:L5:2552:G:H22	1:L5:2766:A:N6	2.15	0.44
1:L5:4253:A:H5'	1:L5:4254:G:C8	2.53	0.44
1:L5:4256:A:H62	13:LJ:57:VAL:HG11	1.82	0.44
6:LC:206:GLY:HA3	6:LC:226:GLY:O	2.17	0.44
8:LE:84:LYS:O	8:LE:89:LEU:HD13	2.17	0.44
13:LJ:9:GLU:HG2	13:LJ:13:ARG:NH1	2.33	0.44
19:LQ:3:VAL:HG12	19:LQ:5:ILE:HG23	2.00	0.44
47:S2:80:G:H2'	47:S2:81:U:C6	2.53	0.44
47:S2:126:G:C5	72:SG:195:LYS:HE3	2.52	0.44
47:S2:875:A:H2'	47:S2:876:C:C6	2.53	0.44
47:S2:1522:A:OP1	61:SS:145:THR:OG1	2.27	0.44
47:S2:1594:A:C2	47:S2:1595:U:C5	3.06	0.44
47:S2:1598:G:H3'	79:SZ:80:ARG:HG3	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:S2:1777:G:C4	47:S2:1778:C:N3	2.85	0.44
54:SH:147:LYS:O	54:SH:149:ASP:N	2.51	0.44
55:SI:26:LYS:HD2	55:SI:29:LEU:HD23	1.99	0.44
62:ST:2:PRO:HA	62:ST:3:GLY:HA3	1.61	0.44
65:SX:46:HIS:HA	65:SX:102:VAL:O	2.18	0.44
70:Sg:291:TRP:CH2	70:Sg:298:LEU:HB2	2.53	0.44
72:SG:10:THR:HB	72:SG:128:THR:OG1	2.17	0.44
76:SO:75:MET:HG3	76:SO:118:ALA:HB2	2.00	0.44
1:L5:1398:A:N3	1:L5:1419:G:N2	2.62	0.44
1:L5:1509:C:H5"	29:La:2:PRO:HD3	1.99	0.44
5:LB:112:ASP:O	5:LB:113:GLU:HB2	2.17	0.44
9:LF:184:ILE:HD11	9:LF:193:GLU:HG2	1.99	0.44
30:Lb:35:VAL:HB	30:Lb:40:LEU:HD21	1.99	0.44
37:Li:85:ARG:HA	37:Li:88:GLU:HG2	1.99	0.44
47:S2:17:C:H2'	47:S2:18:C:C6	2.52	0.44
47:S2:143:U:O4	72:SG:180:VAL:HA	2.17	0.44
47:S2:305:U:N3	55:SI:182:CYS:O	2.51	0.44
47:S2:821:G:N2	73:SJ:83:ARG:HH22	2.16	0.44
47:S2:1005:G:OP2	50:SB:162:ARG:NH2	2.37	0.44
47:S2:1472:C:H3'	47:S2:1473:G:H8	1.83	0.44
50:SB:146:ARG:CZ	50:SB:146:ARG:HA	2.47	0.44
52:SE:64:ILE:HG23	52:SE:69:PHE:CE1	2.52	0.44
55:SI:142:SER:O	55:SI:144:LYS:N	2.51	0.44
58:SP:42:ARG:HG2	58:SP:43:ARG:N	2.32	0.44
58:SP:78:THR:HG21	58:SP:97:TYR:HB2	1.99	0.44
64:SV:36:VAL:HG12	64:SV:37:ALA:N	2.31	0.44
76:SO:29:GLY:O	76:SO:93:LEU:HB2	2.17	0.44
78:SY:104:ARG:HA	78:SY:107:ARG:HB3	1.99	0.44
82:Pt:40:C:H2'	82:Pt:41:C:C6	2.53	0.44
1:L5:269:G:H2'	1:L5:270:U:H6	1.83	0.44
1:L5:702:U:OP1	33:Le:8:VAL:HG23	2.18	0.44
1:L5:972:C:N3	1:L5:1283:G:N7	2.66	0.44
1:L5:1182:C:H5'	1:L5:1183:C:O4'	2.17	0.44
1:L5:3597:G:H2'	1:L5:3598:C:C6	2.52	0.44
1:L5:3911:C:H2'	1:L5:3912:U:C6	2.53	0.44
1:L5:3955:G:H4'	1:L5:3956:G:OP2	2.14	0.44
13:LJ:112:HIS:CE1	13:LJ:125:ILE:HD12	2.53	0.44
17:LO:122:ALA:HB2	21:LS:162:GLN:HB3	1.99	0.44
31:Lc:9:LYS:HA	31:Lc:10:SER:HA	1.74	0.44
47:S2:38:A:H5"	73:SJ:5:ARG:HD2	1.99	0.44
47:S2:84:A:O2'	78:SY:119:GLY:O	2.34	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:S2:380:G:H5”	55:SI:31:ARG:NH1	2.33	0.44
47:S2:1454:A:N6	60:SR:1:MET:HE1	2.33	0.44
47:S2:1560:U:H2’	47:S2:1561:A:H8	1.81	0.44
48:S6:42:A:H2’	48:S6:43:G:C8	2.53	0.44
53:SF:121:PRO:HA	53:SF:193:LYS:HE2	1.99	0.44
56:SK:1:MET:HE3	56:SK:44:HIS:N	2.33	0.44
57:SL:35:ARG:NH2	57:SL:55:TYR:O	2.51	0.44
70:Sg:241:PHE:CE1	70:Sg:248:LEU:HB3	2.53	0.44
71:SC:77:SER:HA	71:SC:97:PHE:CD1	2.53	0.44
74:SM:35:ILE:HG21	74:SM:61:TYR:HE1	1.83	0.44
76:SO:27:VAL:HG23	76:SO:90:ILE:HG22	2.00	0.44
76:SO:43:HIS:HA	76:SO:55:ARG:HA	1.99	0.44
78:SY:29:HIS:ND1	78:SY:32:LYS:O	2.46	0.44
82:Pt:44:A:H2’	82:Pt:45:A:C8	2.53	0.44
1:L5:35:U:H5’	1:L5:36:U:OP2	2.18	0.44
1:L5:1200:G:H2’	1:L5:1201:U:C6	2.52	0.44
1:L5:1806:G:H2’	1:L5:1807:C:C6	2.53	0.44
1:L5:4342:C:O3’	43:Lo:37:GLY:HA3	2.18	0.44
18:LP:128:ARG:NH2	18:LP:136:ILE:HD13	2.31	0.44
27:LY:118:ILE:O	27:LY:122:LYS:HG2	2.17	0.44
32:Ld:87:ARG:HB2	32:Ld:107:THR:OG1	2.18	0.44
45:Lr:82:ILE:HG21	45:Lr:89:THR:HG23	2.00	0.44
47:S2:57:U:O2’	47:S2:499:G:N3	2.50	0.44
47:S2:221:A:N6	47:S2:301:A:N6	2.65	0.44
47:S2:301:A:N3	55:SI:73:THR:HG21	2.32	0.44
47:S2:982:G:H2’	47:S2:983:A:C8	2.52	0.44
47:S2:1733:U:H2’	47:S2:1734:G:O4’	2.18	0.44
49:SA:42:LYS:HB2	49:SA:48:ILE:HD11	1.99	0.44
50:SB:129:THR:HG21	50:SB:133:TYR:HB2	2.00	0.44
52:SE:71:LYS:HG3	52:SE:91:SER:HB2	1.98	0.44
52:SE:180:LEU:HD12	52:SE:228:ILE:HG13	1.99	0.44
54:SH:145:ARG:HD3	77:SW:51:GLU:OE2	2.18	0.44
61:SS:117:ILE:HG13	61:SS:118:ARG:H	1.82	0.44
67:Sc:64:GLU:HG2	67:Sc:66:ARG:HB2	2.00	0.44
70:Sg:191:HIS:NE2	70:Sg:217:MET:HG2	2.33	0.44
74:SM:31:LEU:HD11	74:SM:111:VAL:HA	1.99	0.44
78:SY:14:THR:HA	78:SY:21:LYS:HA	1.99	0.44
79:SZ:77:LEU:HD23	79:SZ:78:LYS:N	2.33	0.44
1:L5:475:G:H2’	1:L5:476:G:C8	2.53	0.43
1:L5:969:C:H1’	1:L5:970:G:C4	2.53	0.43
1:L5:1401:C:H2’	1:L5:1402:C:O4’	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:2263:A:O2'	1:L5:2264:C:O5'	2.35	0.43
1:L5:2475:G:H4'	1:L5:2476:G:C8	2.52	0.43
1:L5:3601:C:H2'	1:L5:3602:C:O4'	2.18	0.43
1:L5:3938:G:H4'	1:L5:3939:G:O5'	2.16	0.43
1:L5:3946:G:N2	1:L5:4068:U:O2	2.51	0.43
1:L5:4414:A:C8	1:L5:4422:A:N1	2.86	0.43
1:L5:5061:A:H4'	1:L5:5062:G:H5"	2.00	0.43
6:LC:159:GLU:HA	6:LC:217:ILE:HB	2.00	0.43
20:LR:108:ARG:HA	20:LR:111:GLU:HG2	2.00	0.43
25:LW:96:GLN:HG3	25:LW:101:ARG:HH12	1.82	0.43
33:Le:124:ASN:OD1	33:Le:124:ASN:N	2.51	0.43
37:Li:23:LYS:HD3	37:Li:24:PRO:O	2.18	0.43
46:Lz:60:ARG:H	46:Lz:171:HIS:CD2	2.32	0.43
47:S2:67:C:C5	72:SG:162:LEU:HD23	2.53	0.43
47:S2:1593:C:N4	47:S2:1594:A:H62	2.16	0.43
47:S2:1834:A:H2	47:S2:1837:G:N1	2.16	0.43
50:SB:118:GLN:HE21	50:SB:142:PHE:HB3	1.82	0.43
57:SL:11:GLN:OE1	57:SL:11:GLN:N	2.50	0.43
59:SQ:41:MET:HE1	62:ST:7:LYS:O	2.17	0.43
61:SS:52:LEU:HD23	61:SS:52:LEU:H	1.83	0.43
77:SW:82:GLN:HG3	77:SW:84:LYS:HG2	1.99	0.43
1:L5:173:C:H42	1:L5:264:C:H1'	1.83	0.43
1:L5:933:G:H2'	1:L5:940:C:H41	1.82	0.43
1:L5:1083:U:H1'	1:L5:1217:G:H22	1.84	0.43
1:L5:2622:G:OP2	23:LU:84:LYS:NZ	2.50	0.43
1:L5:4742:G:H2'	1:L5:4743:G:H8	1.83	0.43
1:L5:4885:U:C4	1:L5:4886:C:C2	3.06	0.43
1:L5:4903:G:C6	1:L5:4919:G:C6	3.06	0.43
6:LC:81:GLY:O	6:LC:87:SER:OG	2.31	0.43
14:LL:63:THR:HG21	29:La:66:ASN:HB3	1.99	0.43
21:LS:72:PRO:HG2	21:LS:73:LEU:HD12	2.00	0.43
24:LV:58:GLY:H	24:LV:81:VAL:HG23	1.84	0.43
46:Lz:93:LEU:O	46:Lz:93:LEU:HD23	2.18	0.43
47:S2:379:C:O2	55:SI:5:ARG:NH1	2.51	0.43
47:S2:795:A:H62	54:SH:109:ARG:HH22	1.65	0.43
47:S2:1004:U:H2'	47:S2:1005:G:C8	2.51	0.43
47:S2:1404:U:N3	47:S2:1580:A:OP1	2.51	0.43
47:S2:1751:C:C5	47:S2:1752:C:H1'	2.53	0.43
49:SA:176:TRP:CZ3	49:SA:177:MET:HE2	2.52	0.43
52:SE:117:GLU:O	52:SE:118:GLU:HG2	2.18	0.43
56:SK:65:ARG:NH2	68:Sd:21:CYS:O	2.47	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
66:Sa:21:ILE:HD13	66:Sa:32:LYS:HG3	2.00	0.43
70:Sg:249:CYS:HA	70:Sg:257:LYS:O	2.18	0.43
72:SG:225:GLN:HA	72:SG:228:ILE:HG22	1.99	0.43
73:SJ:106:LEU:HD12	73:SJ:109:ARG:HE	1.83	0.43
76:SO:12:GLU:HG3	76:SO:13:GLN:HG3	2.00	0.43
76:SO:102:GLY:N	76:SO:134:PRO:HG2	2.33	0.43
1:L5:744:G:H2'	1:L5:745:G:H8	1.81	0.43
1:L5:747:A:H62	1:L5:916:C:H42	1.66	0.43
1:L5:1890:G:O2'	1:L5:1891:A:H5'	2.19	0.43
1:L5:1912:G:N2	17:LO:87:MET:HE2	2.32	0.43
1:L5:3910:C:H2'	1:L5:3911:C:H6	1.81	0.43
5:LB:351:LEU:HD23	5:LB:351:LEU:H	1.83	0.43
9:LF:147:LEU:O	9:LF:150:VAL:HG22	2.18	0.43
46:Lz:49:PHE:HZ	46:Lz:190:LEU:HB3	1.83	0.43
47:S2:816:A:H2'	47:S2:817:G:O4'	2.19	0.43
47:S2:929:G:N2	47:S2:1104:G:H4'	2.34	0.43
47:S2:1155:U:OP1	71:SC:185:THR:OG1	2.19	0.43
47:S2:1287:A:C6	47:S2:1314:U:O4	2.72	0.43
47:S2:1656:G:H2'	47:S2:1657:G:C8	2.52	0.43
47:S2:1781:A:O2'	47:S2:1782:G:N7	2.45	0.43
61:SS:36:VAL:HG23	61:SS:40:TYR:HD2	1.82	0.43
70:Sg:25:PRO:HA	70:Sg:293:ALA:HB2	2.00	0.43
70:Sg:44:LYS:N	70:Sg:55:PRO:O	2.51	0.43
70:Sg:254:PRO:HB3	70:Sg:284:PRO:HG2	2.01	0.43
71:SC:94:ILE:HG21	71:SC:159:LYS:HB3	1.99	0.43
73:SJ:111:GLN:NE2	73:SJ:127:ARG:HB2	2.34	0.43
78:SY:111:LYS:O	78:SY:115:LYS:HG2	2.19	0.43
79:SZ:50:PHE:HA	79:SZ:54:THR:OG1	2.18	0.43
1:L5:158:A:H5"	1:L5:159:C:H2'	2.01	0.43
1:L5:162:A:H2'	1:L5:163:A:H8	1.83	0.43
1:L5:208:A:N6	1:L5:233:U:H5	2.16	0.43
1:L5:269:G:H2'	1:L5:270:U:C6	2.54	0.43
1:L5:1326:A:H2'	1:L5:1327:C:C6	2.54	0.43
1:L5:2104:G:H2'	1:L5:2105:A:H5'	2.01	0.43
1:L5:2326:G:H5'	33:Le:127:ALA:HB1	1.99	0.43
1:L5:2434:G:O3'	26:LX:83:THR:HG21	2.17	0.43
1:L5:3956:G:O2'	1:L5:3957:U:OP2	2.30	0.43
3:L8:1:C:H5"	3:L8:2:G:H21	1.84	0.43
5:LB:312:LYS:HE3	5:LB:370:THR:OG1	2.18	0.43
7:LD:34:LYS:HE2	22:LT:30:TYR:CZ	2.53	0.43
8:LE:83:LYS:H	8:LE:84:LYS:HB3	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:LE:109:LEU:O	8:LE:110:ARG:HG2	2.18	0.43
8:LE:190:HIS:HB3	8:LE:193:PHE:HD1	1.83	0.43
12:LI:83:ASP:OD1	12:LI:83:ASP:N	2.50	0.43
16:LN:184:ILE:HG23	16:LN:194:ARG:NH2	2.31	0.43
21:LS:109:CYS:C	21:LS:111:ARG:H	2.26	0.43
25:LW:73:ARG:NE	47:S2:1781:A:H61	2.16	0.43
30:Lb:23:LYS:HE3	30:Lb:23:LYS:HB3	1.79	0.43
34:Lf:14:TYR:OH	34:Lf:92:LEU:O	2.31	0.43
47:S2:377:G:H5'	55:SI:98:LYS:HD2	1.99	0.43
47:S2:525:A:H2'	47:S2:526:A:H8	1.81	0.43
50:SB:93:GLY:O	50:SB:95:ASN:ND2	2.51	0.43
50:SB:135:LEU:HD12	50:SB:215:VAL:HG22	2.00	0.43
50:SB:208:HIS:CE1	50:SB:209:ASP:HB2	2.53	0.43
72:SG:189:ARG:O	72:SG:193:ALA:HB2	2.18	0.43
76:SO:37:PHE:O	76:SO:38:ASN:HB2	2.18	0.43
1:L5:492:U:C4	1:L5:662:C:N3	2.86	0.43
1:L5:1271:G:H22	1:L5:2122:G:H5"	1.84	0.43
1:L5:2026:A:H2'	1:L5:2027:U:H6	1.83	0.43
1:L5:2124:G:O2'	1:L5:2125:C:OP1	2.32	0.43
1:L5:2373:C:H5'	32:Ld:46:LEU:HD23	2.00	0.43
1:L5:2691:U:C2	1:L5:2692:U:C5	3.06	0.43
1:L5:2902:G:H3'	1:L5:2903:G:H5'	2.00	0.43
1:L5:4267:G:H5'	1:L5:4268:A:OP2	2.18	0.43
2:L7:108:G:OP1	7:LD:273:LEU:HD12	2.19	0.43
5:LB:56:ILE:O	5:LB:73:VAL:HA	2.19	0.43
17:LO:110:PRO:N	17:LO:111:PRO:HD2	2.33	0.43
27:LY:13:LYS:O	27:LY:17:ARG:HD3	2.18	0.43
47:S2:291:G:H4'	47:S2:292:A:C8	2.54	0.43
47:S2:804:U:H2'	47:S2:805:U:C6	2.53	0.43
47:S2:1222:G:H2'	47:S2:1223:A:C8	2.54	0.43
47:S2:1228:A:H2'	47:S2:1229:G:H8	1.82	0.43
47:S2:1286:G:N1	47:S2:1312:G:H2'	2.34	0.43
51:SD:114:ALA:HB3	51:SD:117:ARG:HG2	2.00	0.43
56:SK:8:ARG:HA	56:SK:11:ILE:HG12	2.01	0.43
70:Sg:168:CYS:HB3	70:Sg:198:VAL:HB	2.01	0.43
70:Sg:261:LEU:O	70:Sg:263:GLY:N	2.52	0.43
1:L5:238:C:OP2	27:LY:45:ARG:NH2	2.52	0.43
1:L5:485:C:H5	1:L5:664:G:N7	2.17	0.43
1:L5:1247:U:H2'	1:L5:1248:C:C6	2.54	0.43
1:L5:1786:A:H2'	1:L5:1789:C:C5	2.54	0.43
1:L5:4629:U:C2	1:L5:4630:G:C8	3.07	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:4996:C:H4'	32:Ld:26:THR:HG23	1.98	0.43
2:L7:10:C:C4	7:LD:20:PHE:HD1	2.36	0.43
5:LB:291:TYR:CE2	5:LB:327:THR:HG22	2.53	0.43
9:LF:241:ASN:O	9:LF:245:ARG:HG3	2.18	0.43
31:Lc:52:CYS:HA	31:Lc:53:PRO:HD3	1.83	0.43
31:Lc:57:LYS:O	31:Lc:61:GLU:HG3	2.18	0.43
46:Lz:186:ALA:O	46:Lz:190:LEU:HG	2.18	0.43
47:S2:1369:A:OP1	60:SR:1:MET:HA	2.18	0.43
47:S2:1643:U:O2'	47:S2:1644:C:O5'	2.34	0.43
50:SB:85:LYS:HB2	50:SB:101:HIS:HB3	2.01	0.43
53:SF:28:VAL:HG23	53:SF:109:LEU:HD22	2.01	0.43
56:SK:39:ASN:HB3	56:SK:40:VAL:H	1.67	0.43
58:SP:101:THR:HA	58:SP:102:PHE:HA	1.76	0.43
1:L5:910:G:H2'	1:L5:911:U:C6	2.54	0.43
1:L5:1220:G:O6	1:L5:1221:G:N1	2.52	0.43
1:L5:1966:C:H2'	1:L5:1967:A:C8	2.52	0.43
1:L5:2091:C:OP2	1:L5:2257:C:H1'	2.19	0.43
1:L5:2491:C:H2'	1:L5:2492:C:C6	2.54	0.43
1:L5:2504:C:H2'	1:L5:2505:C:H5"	2.00	0.43
1:L5:3917:A:H2'	1:L5:3918:G:H8	1.83	0.43
3:L8:57:C:H4'	3:L8:63:U:C5	2.54	0.43
6:LC:335:MET:HE2	9:LF:58:HIS:HD2	1.83	0.43
23:LU:42:PHE:HA	23:LU:45:GLU:CD	2.43	0.43
26:LX:105:ASN:OD1	26:LX:106:LYS:N	2.52	0.43
34:Lf:106:TYR:O	34:Lf:108:SER:N	2.52	0.43
47:S2:1467:C:OP1	60:SR:1:MET:HG2	2.19	0.43
47:S2:1680:G:H2'	47:S2:1681:U:C6	2.53	0.43
47:S2:1801:A:H2'	47:S2:1802:C:H6	1.84	0.43
50:SB:164:ILE:HD13	50:SB:207:LEU:HD21	2.00	0.43
51:SD:215:ASP:CG	51:SD:216:GLU:H	2.27	0.43
54:SH:17:ASP:OD1	54:SH:17:ASP:N	2.50	0.43
63:SU:80:PHE:HD1	68:Sd:43:PHE:HE2	1.67	0.43
70:Sg:89:LEU:O	70:Sg:97:THR:HA	2.19	0.43
72:SG:32:MET:HA	72:SG:52:ILE:HG13	2.01	0.43
73:SJ:80:ARG:O	73:SJ:83:ARG:HB3	2.19	0.43
76:SO:99:ALA:O	76:SO:101:GLY:N	2.51	0.43
79:SZ:99:LEU:HD13	79:SZ:109:TYR:CE1	2.54	0.43
1:L5:673:C:H2'	1:L5:674:G:H8	1.83	0.43
1:L5:740:G:H2'	1:L5:741:C:C6	2.54	0.43
1:L5:1197:C:H2'	1:L5:1198:G:H8	1.82	0.43
1:L5:2059:C:O2'	21:LS:118:ARG:NH1	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:4093:G:H3'	1:L5:4094:G:C8	2.51	0.43
1:L5:4263:C:H2'	1:L5:4264:G:O4'	2.18	0.43
1:L5:4893:A:C2	1:L5:4894:A:H1'	2.54	0.43
8:LE:234:ASP:OD1	8:LE:234:ASP:N	2.51	0.43
11:LH:41:ILE:HG23	11:LH:43:VAL:HG22	2.00	0.43
12:LI:19:LYS:HD3	12:LI:26:VAL:HG21	2.01	0.43
14:LL:176:PHE:HD1	37:Li:3:LEU:HD22	1.84	0.43
47:S2:77:A:H2	72:SG:179:LEU:HD21	1.82	0.43
47:S2:943:U:C2	47:S2:944:A:C8	3.07	0.43
47:S2:1101:U:H2'	47:S2:1102:G:H8	1.84	0.43
47:S2:1320:G:C4	47:S2:1321:G:H1'	2.53	0.43
47:S2:1387:G:H22	51:SD:206:ASP:CG	2.26	0.43
48:S6:64:U:H2'	48:S6:65:C:C6	2.54	0.43
50:SB:144:LYS:HG2	50:SB:145:LYS:O	2.18	0.43
51:SD:162:ASP:N	51:SD:163:PRO:HD2	2.34	0.43
58:SP:92:SER:C	58:SP:104:GLN:HE22	2.25	0.43
60:SR:51:ALA:O	60:SR:55:THR:HG23	2.18	0.43
65:SX:124:LYS:HA	65:SX:129:SER:HA	2.00	0.43
65:SX:133:LEU:HD12	65:SX:138:LYS:HB2	2.01	0.43
72:SG:202:ASN:O	72:SG:205:GLU:HG2	2.19	0.43
1:L5:710:G:H2'	1:L5:711:A:C8	2.54	0.43
1:L5:2093:A:OP1	1:L5:2095:A:H2'	2.19	0.43
1:L5:2828:U:O2'	1:L5:2829:U:OP1	2.34	0.43
1:L5:4378:A:O2'	1:L5:4379:A:H2'	2.18	0.43
1:L5:4581:G:H4'	5:LB:182:GLU:OE2	2.19	0.43
1:L5:4864:U:H2'	1:L5:4865:C:C6	2.53	0.43
8:LE:128:HIS:HB3	8:LE:129:GLY:H	1.60	0.43
21:LS:78:PHE:O	21:LS:96:GLU:HA	2.19	0.43
38:Lj:63:ARG:HD2	38:Lj:63:ARG:HA	1.79	0.43
47:S2:818:A:OP1	73:SJ:80:ARG:NH2	2.51	0.43
47:S2:924:G:H1	47:S2:1018:U:H3	1.66	0.43
47:S2:1290:G:O5'	69:Sf:98:VAL:HG23	2.18	0.43
47:S2:1395:C:H3'	47:S2:1396:A:H5"	2.00	0.43
47:S2:1845:A:H2'	47:S2:1846:G:H8	1.83	0.43
50:SB:142:PHE:HB2	50:SB:209:ASP:HB3	2.00	0.43
53:SF:44:LYS:H	53:SF:46:ALA:HB2	1.83	0.43
53:SF:78:MET:HB2	53:SF:159:ARG:CZ	2.48	0.43
57:SL:124:ASP:HB2	57:SL:147:LYS:HB3	2.01	0.43
58:SP:68:PRO:HA	58:SP:69:PRO:HD3	1.92	0.43
60:SR:31:ASN:HD21	60:SR:55:THR:HG22	1.84	0.43
61:SS:40:TYR:HD1	61:SS:83:PHE:HE2	1.65	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:Sg:252:THR:O	70:Sg:255:SER:OG	2.26	0.43
79:SZ:48:VAL:HG12	79:SZ:80:ARG:HB2	2.00	0.43
1:L5:375:G:O6	38:Lj:56:ARG:NH1	2.51	0.43
1:L5:1213:G:C6	1:L5:1215:C:C4	3.07	0.43
1:L5:2656:U:H2'	1:L5:2657:G:O4'	2.19	0.43
1:L5:3968:U:O3'	46:Lz:160:LYS:HG2	2.19	0.43
1:L5:4568:A:P	5:LB:20:LYS:HB2	2.59	0.43
1:L5:4932:U:H2'	1:L5:4933:C:C6	2.53	0.43
6:LC:339:THR:O	6:LC:343:GLN:HG2	2.18	0.43
16:LN:114:ARG:HH12	16:LN:157:LYS:HG2	1.84	0.43
47:S2:520:A:O2'	47:S2:825:A:N3	2.43	0.43
47:S2:801:U:C2	47:S2:802:A:C8	3.06	0.43
47:S2:1396:A:N7	47:S2:1450:G:C6	2.87	0.43
47:S2:1741:U:H2'	47:S2:1742:C:O4'	2.19	0.43
48:S6:53:G:H2'	48:S6:54:A:C8	2.52	0.43
51:SD:71:ALA:HB3	56:SK:20:VAL:HG11	2.00	0.43
51:SD:116:ARG:HA	51:SD:119:CYS:SG	2.59	0.43
52:SE:42:LEU:HD13	52:SE:109:PHE:HD2	1.84	0.43
58:SP:73:PRO:HB2	58:SP:74:GLU:HB2	2.01	0.43
60:SR:5:ARG:NH1	60:SR:53:TYR:HD1	2.17	0.43
61:SS:109:GLU:OE1	61:SS:109:GLU:N	2.52	0.43
63:SU:35:VAL:HG22	63:SU:105:SER:OG	2.19	0.43
70:Sg:54:ILE:HA	70:Sg:55:PRO:HA	1.83	0.43
71:SC:73:MET:HG2	71:SC:96:PHE:HZ	1.84	0.43
72:SG:54:GLY:O	72:SG:110:ASN:HB2	2.18	0.43
1:L5:37:U:H2'	1:L5:38:A:O4'	2.18	0.42
1:L5:369:G:N2	1:L5:372:A:OP2	2.41	0.42
1:L5:495:C:H2'	1:L5:496:G:H8	1.84	0.42
1:L5:497:G:H1	1:L5:656:C:H42	1.65	0.42
1:L5:1265:G:H22	1:L5:2111:G:H1'	1.84	0.42
1:L5:1410:U:HO2'	1:L5:1411:C:P	2.42	0.42
1:L5:1768:C:H4'	1:L5:1769:G:H8	1.84	0.42
1:L5:2263:A:C8	1:L5:2265:G:C8	3.07	0.42
1:L5:3956:G:HO2'	1:L5:3957:U:P	2.41	0.42
1:L5:4687:A:OP2	41:Lm:125:LYS:HE2	2.18	0.42
1:L5:4872:G:C2	21:LS:170:LYS:NZ	2.87	0.42
6:LC:65:GLU:OE1	6:LC:80:ARG:NE	2.45	0.42
10:LG:133:PRO:HA	10:LG:134:PRO:HD3	1.89	0.42
13:LJ:19:LYS:HB3	13:LJ:133:VAL:CG1	2.49	0.42
15:LM:47:ARG:HH12	15:LM:69:HIS:HA	1.83	0.42
20:LR:105:LEU:HD23	20:LR:138:LEU:HD23	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:LS:81:TRP:CE3	21:LS:128:LYS:HG3	2.54	0.42
28:LZ:97:ASN:O	28:LZ:100:VAL:HG12	2.19	0.42
45:Lr:94:ARG:O	45:Lr:98:ARG:HG2	2.19	0.42
46:Lz:120:ILE:O	46:Lz:124:LEU:HB2	2.19	0.42
47:S2:339:A:C6	47:S2:341:C:N4	2.86	0.42
47:S2:389:A:H2'	47:S2:390:C:H6	1.83	0.42
47:S2:602:G:H3'	47:S2:603:C:H2'	2.01	0.42
47:S2:628:A:N6	51:SD:145:GLN:HG2	2.34	0.42
48:S6:18:G:N2	48:S6:57:G:H2'	2.34	0.42
50:SB:191:ASP:OD1	50:SB:191:ASP:N	2.50	0.42
51:SD:101:GLN:O	51:SD:104:SER:OG	2.35	0.42
56:SK:80:ARG:HG3	56:SK:85:LEU:HB2	2.01	0.42
65:SX:105:PHE:HD2	65:SX:112:VAL:HG11	1.84	0.42
70:Sg:68:ASP:OD1	70:Sg:69:VAL:N	2.51	0.42
1:L5:722:G:H2'	1:L5:723:A:C8	2.54	0.42
1:L5:990:C:H41	1:L5:1050:C:H42	1.67	0.42
1:L5:1206:C:H2'	1:L5:1207:C:C6	2.54	0.42
1:L5:1265:G:N2	1:L5:2111:G:O3'	2.52	0.42
1:L5:1332:C:H5"	33:Le:29:VAL:HG23	2.02	0.42
1:L5:1482:G:O6	14:LL:188:ASN:ND2	2.52	0.42
1:L5:1818:G:OP2	1:L5:1818:G:N2	2.31	0.42
1:L5:1930:U:OP2	17:LO:49:ARG:HD2	2.19	0.42
1:L5:2411:C:H2'	1:L5:2412:A:C8	2.54	0.42
1:L5:4389:C:H2'	1:L5:4390:A:C8	2.54	0.42
1:L5:5022:U:H3	1:L5:5028:G:N2	2.17	0.42
4:LA:28:ARG:HH21	4:LA:123:ARG:CD	2.32	0.42
13:LJ:54:ARG:O	13:LJ:64:ARG:HD3	2.18	0.42
13:LJ:85:LYS:HE3	13:LJ:115:LEU:HB3	2.01	0.42
19:LQ:178:ARG:N	29:La:51:GLY:HA2	2.34	0.42
47:S2:49:C:H2'	47:S2:472:C:H41	1.84	0.42
47:S2:122:G:C2	47:S2:123:G:C5	3.07	0.42
47:S2:219:U:H2'	47:S2:220:U:O4'	2.20	0.42
47:S2:432:G:H2'	47:S2:433:A:C8	2.54	0.42
47:S2:947:G:H2'	47:S2:948:C:H6	1.85	0.42
47:S2:1321:G:C8	47:S2:1322:G:C4	3.07	0.42
47:S2:1450:G:C4	47:S2:1451:G:C8	3.07	0.42
49:SA:62:ALA:O	49:SA:66:VAL:HG23	2.19	0.42
49:SA:155:ARG:HG2	49:SA:156:TYR:CD1	2.54	0.42
50:SB:192:SER:O	50:SB:196:ASP:HB2	2.18	0.42
53:SF:19:LEU:HG	53:SF:48:TYR:CE1	2.53	0.42
53:SF:30:ILE:HG12	53:SF:113:VAL:HG11	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:SP:98:ASN:HB2	58:SP:99:GLY:HA3	2.01	0.42
71:SC:65:LYS:HD3	71:SC:273:LEU:HD22	2.00	0.42
71:SC:168:GLY:N	71:SC:179:THR:O	2.46	0.42
1:L5:483:G:N2	1:L5:671:G:H1	2.17	0.42
1:L5:655:C:OP1	6:LC:268:ARG:NH1	2.52	0.42
1:L5:688:U:H2'	1:L5:689:U:C5	2.53	0.42
1:L5:1327:C:H2'	1:L5:1328:G:C8	2.55	0.42
1:L5:4232:U:H4'	1:L5:4233:A:O4'	2.19	0.42
1:L5:4733:C:H2'	1:L5:4734:A:H5'	1.99	0.42
3:L8:19:C:H2'	3:L8:20:A:H8	1.84	0.42
4:LA:128:ARG:HA	4:LA:169:VAL:HG21	2.02	0.42
13:LJ:158:SER:C	13:LJ:160:GLU:H	2.26	0.42
28:LZ:101:PHE:O	28:LZ:102:ARG:HG2	2.19	0.42
47:S2:617:G:OP2	65:SX:68:LYS:NZ	2.36	0.42
47:S2:980:A:HO2'	47:S2:981:A:P	2.42	0.42
47:S2:1136:U:H2'	47:S2:1137:U:C6	2.54	0.42
47:S2:1490:G:H2'	47:S2:1491:G:C8	2.54	0.42
47:S2:1585:U:H3	62:ST:67:ARG:HH22	1.66	0.42
54:SH:68:GLN:HB2	54:SH:71:SER:OG	2.20	0.42
54:SH:101:LEU:HB2	54:SH:116:ARG:HD3	2.01	0.42
55:SI:41:ARG:HA	55:SI:59:ARG:O	2.19	0.42
58:SP:24:GLN:O	58:SP:28:MET:HG2	2.19	0.42
63:SU:67:LYS:HA	68:Sd:44:ARG:NH1	2.34	0.42
68:Sd:19:ARG:HG3	68:Sd:30:LEU:CD2	2.49	0.42
70:Sg:146:SER:O	70:Sg:147:HIS:ND1	2.53	0.42
71:SC:166:ARG:HB2	71:SC:248:TYR:CD1	2.54	0.42
76:SO:125:LYS:HD3	76:SO:125:LYS:HA	1.78	0.42
1:L5:184:U:O4	1:L5:253:G:O6	2.37	0.42
1:L5:477:C:H2'	1:L5:478:G:C8	2.54	0.42
1:L5:492:U:N3	1:L5:662:C:O2	2.53	0.42
1:L5:688:U:OP1	8:LE:111:LYS:NZ	2.52	0.42
1:L5:1410:U:O4	1:L5:1814:C:H5"	2.20	0.42
1:L5:1858:A:H2'	1:L5:1859:C:H6	1.84	0.42
1:L5:2557:G:H22	1:L5:2571:C:H1'	1.84	0.42
1:L5:2583:C:N4	35:Lg:75:SER:HG	2.18	0.42
1:L5:3600:G:H2'	1:L5:3601:C:C6	2.54	0.42
1:L5:3708:C:H2'	1:L5:3710:G:C8	2.54	0.42
1:L5:3956:G:O2'	1:L5:3957:U:P	2.77	0.42
1:L5:4106:G:N2	1:L5:4107:G:H21	2.18	0.42
1:L5:4418:G:H2'	1:L5:4421:C:H42	1.84	0.42
1:L5:5020:G:C6	1:L5:5021:C:C4	3.08	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L7:12:U:O3'	2:L7:109:U:O2'	2.30	0.42
4:LA:32:VAL:HG22	4:LA:163:ARG:NH1	2.34	0.42
4:LA:117:GLU:HB2	4:LA:162:ASN:HB2	2.01	0.42
5:LB:234:ARG:NH1	5:LB:268:ARG:O	2.51	0.42
6:LC:46:LYS:HD2	6:LC:113:ARG:HD2	2.02	0.42
10:LG:156:VAL:HG22	10:LG:182:CYS:SG	2.60	0.42
11:LH:18:ILE:HG22	11:LH:27:VAL:HA	1.99	0.42
12:LI:150:GLU:OE2	12:LI:153:ARG:HD3	2.19	0.42
23:LU:47:ILE:HG22	23:LU:49:VAL:HG23	2.01	0.42
25:LW:96:GLN:C	25:LW:104:GLN:HE22	2.25	0.42
25:LW:100:VAL:HB	25:LW:102:LYS:HG3	2.01	0.42
26:LX:119:ILE:HG13	26:LX:144:TYR:CE2	2.54	0.42
41:Lm:95:ILE:HG12	41:Lm:124:LYS:HB2	2.02	0.42
47:S2:920:A:O2'	47:S2:922:A:O5'	2.36	0.42
47:S2:1195:A:H2'	47:S2:1196:A:H8	1.85	0.42
47:S2:1349:G:H2'	47:S2:1350:U:C6	2.54	0.42
47:S2:1410:C:N4	47:S2:1411:G:O6	2.52	0.42
51:SD:1:MET:SD	51:SD:2:ALA:N	2.93	0.42
51:SD:91:VAL:HG12	51:SD:92:ALA:O	2.20	0.42
54:SH:47:ALA:O	54:SH:62:ILE:HA	2.19	0.42
54:SH:157:HIS:HB3	54:SH:190:PRO:HG3	2.01	0.42
74:SM:18:LEU:HD23	74:SM:124:ILE:HD11	2.02	0.42
1:L5:320:C:OP1	37:Li:84:LYS:NZ	2.49	0.42
1:L5:497:G:H22	1:L5:656:C:H42	1.66	0.42
1:L5:735:G:H2'	1:L5:736:C:C6	2.53	0.42
1:L5:922:C:H2'	1:L5:923:C:C6	2.55	0.42
1:L5:1846:G:H2'	1:L5:1847:C:C6	2.54	0.42
1:L5:2100:A:H3'	1:L5:2101:C:C6	2.54	0.42
1:L5:2464:C:O2'	1:L5:2465:C:H6	2.01	0.42
1:L5:2475:G:C2	26:LX:50:LYS:HD2	2.54	0.42
1:L5:3681:G:N2	4:LA:118:GLU:OE2	2.52	0.42
1:L5:4412:C:C2	1:L5:4413:C:O2	2.73	0.42
1:L5:4582:C:H2'	1:L5:4583:C:O4'	2.19	0.42
1:L5:4625:C:O2'	1:L5:4626:A:H5'	2.19	0.42
1:L5:5015:G:H21	1:L5:5034:A:H2	1.64	0.42
2:L7:110:G:H2'	2:L7:111:C:C6	2.55	0.42
9:LF:184:ILE:HA	9:LF:189:ASP:OD1	2.18	0.42
10:LG:222:ILE:HG23	10:LG:226:TYR:HD2	1.85	0.42
15:LM:110:PHE:O	15:LM:110:PHE:CD2	2.72	0.42
26:LX:37:LYS:HA	26:LX:38:LYS:HA	1.58	0.42
26:LX:69:ASN:C	26:LX:69:ASN:ND2	2.75	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:Li:29:ARG:O	37:Li:32:ARG:HD3	2.19	0.42
40:Ll:27:ILE:HG21	40:Ll:35:ILE:HD11	2.01	0.42
47:S2:1650:A:H2'	47:S2:1651:A:O4'	2.20	0.42
51:SD:175:VAL:HG22	51:SD:182:LEU:O	2.19	0.42
55:SI:4:SER:OG	55:SI:24:LYS:HD3	2.20	0.42
55:SI:101:ILE:HA	55:SI:173:ALA:O	2.20	0.42
56:SK:40:VAL:N	56:SK:41:PRO:HD3	2.35	0.42
56:SK:53:LYS:HE3	56:SK:60:GLU:HG2	2.00	0.42
58:SP:40:ARG:NE	58:SP:84:ILE:HG22	2.28	0.42
58:SP:98:ASN:N	58:SP:99:GLY:O	2.52	0.42
70:Sg:286:CYS:HB3	70:Sg:302:TYR:CE1	2.54	0.42
1:L5:169:G:N2	1:L5:171:U:H3	2.17	0.42
1:L5:319:A:H1'	1:L5:3726:A:C8	2.55	0.42
1:L5:987:C:H2'	1:L5:988:C:C6	2.55	0.42
1:L5:1251:C:H1'	1:L5:1260:G:N1	2.35	0.42
1:L5:2045:G:O2'	1:L5:2046:G:H5"	2.20	0.42
1:L5:2634:C:H2'	1:L5:2635:U:C6	2.54	0.42
1:L5:3664:G:H2'	1:L5:3665:G:H8	1.85	0.42
1:L5:4141:G:H4'	1:L5:4143:G:O6	2.19	0.42
1:L5:4486:C:H2'	1:L5:4487:A:O4'	2.19	0.42
1:L5:4945:G:N2	34:Lf:67:THR:O	2.53	0.42
1:L5:5001:U:H5"	5:LB:317:LEU:HD23	2.01	0.42
6:LC:94:ASN:HA	6:LC:100:ARG:O	2.18	0.42
7:LD:164:LYS:HA	7:LD:167:VAL:HG22	2.02	0.42
15:LM:62:LEU:HD23	15:LM:62:LEU:HA	1.91	0.42
16:LN:202:ARG:HH21	16:LN:203:TYR:HE1	1.67	0.42
18:LP:26:PHE:HA	18:LP:144:CYS:SG	2.59	0.42
24:LV:25:VAL:HA	24:LV:37:LEU:O	2.20	0.42
28:LZ:73:LYS:HD3	28:LZ:75:TYR:CZ	2.54	0.42
46:Lz:29:LEU:HG	46:Lz:171:HIS:ND1	2.34	0.42
47:S2:155:G:H1	47:S2:162:C:N4	2.17	0.42
47:S2:872:A:HO2'	47:S2:873:G:H8	1.66	0.42
47:S2:1373:C:C5'	60:SR:7:LYS:HE3	2.47	0.42
47:S2:1493:C:H5"	47:S2:1494:U:H5'	2.01	0.42
51:SD:168:VAL:HA	51:SD:188:ILE:O	2.20	0.42
51:SD:208:VAL:HG13	60:SR:41:ILE:HG22	2.02	0.42
53:SF:18:LYS:HE2	53:SF:46:ALA:HB3	2.01	0.42
54:SH:33:ASN:HB2	54:SH:36:LEU:HB2	2.01	0.42
55:SI:3:ILE:O	55:SI:30:GLY:N	2.52	0.42
58:SP:84:ILE:HG23	58:SP:85:ILE:HG12	2.01	0.42
59:SQ:93:VAL:HG22	59:SQ:108:ILE:HG23	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:ST:18:LEU:HB2	62:ST:62:ARG:NH2	2.32	0.42
75:SN:46:THR:HG23	75:SN:48:SER:H	1.84	0.42
75:SN:67:THR:OG1	75:SN:68:GLY:N	2.49	0.42
1:L5:921:C:H2'	1:L5:922:C:H6	1.84	0.42
1:L5:958:G:O2'	1:L5:959:G:OP1	2.32	0.42
1:L5:1297:U:O2	1:L5:1297:U:H2'	2.19	0.42
1:L5:3602:C:H2'	1:L5:3603:G:C8	2.54	0.42
1:L5:3726:A:O2'	1:L5:3727:A:O4'	2.37	0.42
6:LC:148:PRO:O	6:LC:149:GLU:C	2.62	0.42
6:LC:188:ARG:HH12	6:LC:204:ARG:HH21	1.68	0.42
12:LI:17:TYR:O	12:LI:96:VAL:HG12	2.20	0.42
21:LS:15:ARG:HB3	21:LS:27:LEU:HD13	2.01	0.42
31:Lc:17:ARG:O	31:Lc:21:VAL:HG23	2.20	0.42
43:Lo:85:ILE:HG22	43:Lo:86:LYS:H	1.84	0.42
46:Lz:50:SER:HB2	46:Lz:138:LEU:HD13	2.02	0.42
46:Lz:89:ALA:HB1	46:Lz:92:LYS:HE2	2.01	0.42
47:S2:332:G:C2	47:S2:333:G:C8	3.07	0.42
47:S2:1273:C:H5'	47:S2:1274:G:OP1	2.20	0.42
47:S2:1536:G:H2'	47:S2:1537:A:H8	1.83	0.42
49:SA:90:PHE:CD1	49:SA:179:ALA:HB2	2.54	0.42
53:SF:19:LEU:O	53:SF:21:GLY:N	2.52	0.42
53:SF:55:ARG:HD3	53:SF:55:ARG:H	1.84	0.42
57:SL:59:LYS:HG2	57:SL:134:LEU:HD11	2.01	0.42
59:SQ:16:LYS:HG2	59:SQ:82:TYR:HB2	2.01	0.42
60:SR:68:GLY:HA3	60:SR:69:ILE:HA	1.69	0.42
69:Sf:123:SER:OG	69:Sf:124:ASP:N	2.53	0.42
71:SC:115:GLN:OE1	71:SC:120:GLN:NE2	2.52	0.42
73:SJ:21:GLU:C	73:SJ:23:SER:H	2.27	0.42
75:SN:15:ALA:HB1	80:Sb:26:GLN:HG2	2.00	0.42
1:L5:1246:G:H2'	1:L5:1247:U:H6	1.85	0.42
1:L5:1355:G:OP1	19:LQ:108:ARG:NH2	2.37	0.42
1:L5:2610:G:H2'	1:L5:2611:A:C8	2.55	0.42
1:L5:3870:C:H2'	1:L5:3871:A:C8	2.54	0.42
4:LA:189:TYR:CD2	4:LA:196:TRP:HB2	2.55	0.42
20:LR:172:ARG:O	20:LR:176:ARG:HG3	2.19	0.42
30:Lb:12:GLN:HB3	30:Lb:16:TRP:CZ3	2.55	0.42
39:Lk:10:ASP:O	39:Lk:14:THR:HG23	2.20	0.42
47:S2:587:A:H2	47:S2:589:G:H1	1.68	0.42
47:S2:688:U:H2'	54:SH:103:LYS:HD3	2.01	0.42
47:S2:1522:A:H1'	61:SS:146:VAL:HG22	2.01	0.42
47:S2:1679:A:H4'	47:S2:1680:G:H8	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:SD:44:THR:OG1	51:SD:45:ARG:N	2.52	0.42
57:SL:147:LYS:HE3	57:SL:150:GLY:HA3	2.02	0.42
65:SX:34:THR:O	65:SX:37:LYS:N	2.49	0.42
71:SC:65:LYS:O	71:SC:69:LEU:HD23	2.20	0.42
72:SG:197:GLN:O	72:SG:200:LYS:HG2	2.20	0.42
1:L5:1367:C:H1'	1:L5:1371:A:OP1	2.19	0.42
1:L5:1588:U:H2'	1:L5:1589:C:C6	2.55	0.42
1:L5:1740:C:H2'	1:L5:1785:C:H42	1.84	0.42
1:L5:3948:C:H3'	1:L5:3949:A:C8	2.55	0.42
7:LD:83:LEU:N	7:LD:84:PRO:HD3	2.34	0.42
8:LE:62:MET:HA	8:LE:65:ARG:HB3	2.01	0.42
13:LJ:153:ALA:HA	13:LJ:154:LYS:HA	1.72	0.42
20:LR:45:ILE:HD13	20:LR:50:ILE:HB	2.01	0.42
36:Lh:88:THR:C	36:Lh:90:ALA:H	2.27	0.42
39:Lk:36:VAL:HG23	39:Lk:43:TYR:HB2	2.00	0.42
46:Lz:120:ILE:HG23	46:Lz:121:PRO:HD3	2.02	0.42
47:S2:344:U:H2'	47:S2:345:U:H6	1.84	0.42
47:S2:455:A:H2'	47:S2:456:C:C6	2.55	0.42
47:S2:1563:G:H2'	47:S2:1564:C:C6	2.54	0.42
63:SU:66:ARG:NH1	63:SU:68:THR:OG1	2.51	0.42
1:L5:497:G:H1	1:L5:656:C:N4	2.17	0.42
1:L5:936:C:N3	15:LM:46:ARG:HG3	2.34	0.42
1:L5:1245:C:H1'	1:L5:2111:G:C6	2.55	0.42
1:L5:1447:C:H2'	1:L5:1448:G:H8	1.83	0.42
1:L5:1565:A:C5	1:L5:1566:C:H1'	2.55	0.42
1:L5:2695:A:H5"	39:Lk:26:LYS:HE3	2.01	0.42
1:L5:3681:G:O2'	4:LA:126:LEU:HA	2.20	0.42
1:L5:4151:G:H2'	1:L5:4152:G:H8	1.84	0.42
1:L5:4916:G:C2	1:L5:4917:C:C2	3.08	0.42
10:LG:29:ASN:OD1	10:LG:30:PRO:HD2	2.20	0.42
11:LH:126:VAL:HG11	11:LH:161:ILE:HG22	2.02	0.42
17:LO:78:ARG:HA	17:LO:78:ARG:HD2	1.92	0.42
27:LY:26:ARG:O	27:LY:30:MET:HG3	2.19	0.42
30:Lb:60:ASN:C	30:Lb:60:ASN:HD22	2.24	0.42
31:Lc:77:ASN:OD1	31:Lc:78:ASN:N	2.52	0.42
39:Lk:22:SER:OG	39:Lk:23:VAL:N	2.53	0.42
44:Lp:3:LYS:C	44:Lp:5:THR:H	2.27	0.42
46:Lz:113:SER:OG	46:Lz:114:GLU:N	2.53	0.42
47:S2:946:U:C2	47:S2:947:G:C8	3.08	0.42
47:S2:1443:C:H4'	59:SQ:20:THR:HG21	2.02	0.42
47:S2:1751:C:N4	47:S2:1781:A:N7	2.63	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:SE:189:LEU:H	52:SE:245:ARG:HH22	1.67	0.42
54:SH:50:GLU:OE2	54:SH:60:ILE:HD12	2.20	0.42
58:SP:40:ARG:CZ	58:SP:83:MET:HB2	2.50	0.42
60:SR:36:GLU:OE1	60:SR:36:GLU:N	2.45	0.42
63:SU:80:PHE:HD1	68:Sd:43:PHE:CE2	2.38	0.42
64:SV:54:ALA:O	64:SV:55:ILE:HD13	2.20	0.42
65:SX:93:PHE:CE1	65:SX:133:LEU:HB3	2.55	0.42
65:SX:105:PHE:CD2	65:SX:112:VAL:HG11	2.55	0.42
70:Sg:237:ASN:HD22	70:Sg:237:ASN:C	2.27	0.42
70:Sg:239:LEU:HD13	70:Sg:250:ALA:HB2	2.02	0.42
79:SZ:57:LYS:HE2	79:SZ:77:LEU:HD11	2.01	0.42
1:L5:385:A:N3	1:L5:387:G:H5"	2.35	0.41
1:L5:463:A:H2'	1:L5:464:G:O4'	2.20	0.41
1:L5:499:G:H2'	1:L5:500:G:H5"	2.01	0.41
1:L5:693:C:H2'	1:L5:694:C:C6	2.55	0.41
1:L5:1327:C:H2'	1:L5:1328:G:H8	1.85	0.41
1:L5:1845:U:H2'	1:L5:1846:G:H8	1.85	0.41
1:L5:1963:C:O4'	1:L5:2027:U:O2'	2.38	0.41
1:L5:2404:A:H1'	38:Lj:12:ARG:HH11	1.84	0.41
8:LE:148:THR:HG22	8:LE:164:PHE:HB3	2.02	0.41
10:LG:32:PHE:CE2	28:LZ:55:ALA:HB2	2.55	0.41
12:LI:70:ILE:HG22	12:LI:74:LYS:HE2	2.02	0.41
14:LL:60:ARG:NH2	14:LL:67:HIS:O	2.53	0.41
30:Lb:16:TRP:HD1	30:Lb:21:ILE:HD11	1.85	0.41
47:S2:1124:C:H5"	50:SB:150:ILE:HG12	2.00	0.41
47:S2:1598:G:N2	47:S2:1599:U:O4	2.31	0.41
48:S6:65:C:H2'	48:S6:66:C:C6	2.55	0.41
50:SB:35:ALA:HB2	50:SB:44:ILE:HD11	2.02	0.41
53:SF:51:HIS:CE1	59:SQ:82:TYR:OH	2.73	0.41
61:SS:5:ILE:HG21	61:SS:54:LYS:HE3	2.01	0.41
75:SN:98:VAL:HG12	75:SN:115:LEU:HD12	2.01	0.41
1:L5:509:A:H5"	29:La:82:VAL:O	2.20	0.41
1:L5:974:C:H4'	1:L5:975:C:OP1	2.20	0.41
1:L5:1066:G:C2	1:L5:1067:G:C8	3.08	0.41
1:L5:1333:A:H2'	1:L5:1334:A:H8	1.84	0.41
1:L5:1806:G:H2'	1:L5:1807:C:H6	1.84	0.41
1:L5:1962:A:H8	1:L5:2024:G:H21	1.68	0.41
1:L5:2714:G:C2	1:L5:2715:G:N7	2.88	0.41
1:L5:2898:G:OP1	20:LR:104:ARG:NH2	2.50	0.41
1:L5:4039:G:H2'	1:L5:4040:C:C6	2.55	0.41
1:L5:4233:A:C5	1:L5:4235:G:C8	3.08	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:LC:236:ASN:HB3	6:LC:239:LYS:HB2	2.03	0.41
6:LC:286:ASN:O	6:LC:288:ASP:N	2.52	0.41
13:LJ:48:PRO:HB2	13:LJ:70:VAL:HG22	2.02	0.41
25:LW:97:LYS:H	72:SG:146:ASN:CG	2.26	0.41
47:S2:345:U:H1'	52:SE:33:THR:HG23	2.01	0.41
47:S2:883:U:H2'	47:S2:884:C:H6	1.85	0.41
47:S2:1424:G:H2'	47:S2:1425:G:C8	2.55	0.41
47:S2:1664:A:H2'	47:S2:1666:C:C5	2.55	0.41
47:S2:1758:G:H2'	47:S2:1759:G:O4'	2.19	0.41
47:S2:1848:U:N3	47:S2:1850:A:OP2	2.53	0.41
48:S6:5:A:H2'	48:S6:6:G:C8	2.55	0.41
49:SA:4:ALA:N	49:SA:5:LEU:HA	2.33	0.41
51:SD:43:PRO:O	51:SD:44:THR:OG1	2.36	0.41
56:SK:38:LYS:NZ	69:Sf:103:LEU:HD11	2.35	0.41
68:Sd:16:GLN:HG2	68:Sd:27:ARG:HB3	2.02	0.41
72:SG:51:ARG:NH2	72:SG:112:VAL:HG11	2.35	0.41
77:SW:26:LEU:HA	77:SW:61:ILE:O	2.19	0.41
79:SZ:50:PHE:HB2	79:SZ:55:TYR:CD1	2.55	0.41
1:L5:125:C:H2'	1:L5:126:C:C6	2.55	0.41
1:L5:499:G:H1	1:L5:656:C:N4	2.18	0.41
1:L5:1979:A:C6	1:L5:1983:A:H5"	2.54	0.41
1:L5:2505:C:H4'	1:L5:2506:G:O5'	2.21	0.41
1:L5:4460:U:H2'	1:L5:4461:C:H6	1.85	0.41
4:LA:181:LYS:HD3	4:LA:184:ARG:NH1	2.36	0.41
5:LB:141:ASP:OD1	5:LB:142:GLY:N	2.53	0.41
7:LD:51:MET:HE1	7:LD:166:ALA:HB2	2.01	0.41
7:LD:195:HIS:CE1	7:LD:199:ILE:HD11	2.55	0.41
8:LE:116:TYR:HE2	45:Lr:90:LEU:HD23	1.85	0.41
10:LG:209:SER:CA	10:LG:212:LYS:HE3	2.47	0.41
12:LI:85:PHE:CE2	12:LI:87:MET:HE3	2.54	0.41
23:LU:31:ASP:OD2	23:LU:114:TYR:OH	2.16	0.41
28:LZ:7:PRO:HA	28:LZ:25:ILE:HG22	2.02	0.41
43:Lo:104:ILE:HA	43:Lo:105:GLN:HA	1.70	0.41
48:S6:60:A:P	48:S6:61:C:H41	2.43	0.41
51:SD:25:LEU:HD13	51:SD:50:ILE:HD12	2.02	0.41
52:SE:185:GLY:HA3	52:SE:224:ASN:CG	2.45	0.41
54:SH:30:LEU:HD21	54:SH:79:LEU:CD1	2.50	0.41
54:SH:114:GLN:HG3	54:SH:114:GLN:O	2.20	0.41
56:SK:52:LEU:HA	56:SK:55:ARG:HG2	2.01	0.41
57:SL:113:LEU:HG	57:SL:117:PHE:CZ	2.55	0.41
57:SL:132:ARG:O	57:SL:134:LEU:N	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:SV:66:ASP:OD1	64:SV:66:ASP:N	2.52	0.41
70:Sg:11:LEU:H	70:Sg:306:LEU:HD11	1.85	0.41
70:Sg:109:LEU:H	70:Sg:124:SER:HA	1.85	0.41
71:SC:196:ILE:CG1	71:SC:223:TYR:HB2	2.50	0.41
75:SN:88:LEU:O	75:SN:92:ILE:HG12	2.19	0.41
76:SO:33:ILE:HD11	76:SO:115:ALA:HB3	2.03	0.41
78:SY:7:ILE:HB	78:SY:43:LYS:HD2	2.03	0.41
1:L5:964:A:N1	1:L5:2251:G:O2'	2.50	0.41
1:L5:1972:G:N3	1:L5:1972:G:H2'	2.36	0.41
1:L5:2094:G:H3'	1:L5:2095:A:H8	1.84	0.41
1:L5:4413:C:N4	1:L5:4429:C:H41	2.17	0.41
1:L5:4714:C:H4'	5:LB:351:LEU:HD11	2.03	0.41
3:L8:81:C:O3'	3:L8:87:G:H5"	2.20	0.41
4:LA:49:ILE:HD13	4:LA:60:LYS:HE3	2.02	0.41
5:LB:341:LYS:O	5:LB:342:LYS:HB2	2.20	0.41
15:LM:11:ARG:HG2	15:LM:57:LEU:HD22	2.02	0.41
32:Ld:114:PHE:HA	32:Ld:117:LEU:HD12	2.02	0.41
35:Lg:20:THR:HG21	35:Lg:34:TYR:HD1	1.82	0.41
35:Lg:37:LYS:HB3	35:Lg:60:ARG:NH2	2.35	0.41
46:Lz:42:ASP:O	46:Lz:45:LYS:HG2	2.19	0.41
47:S2:441:C:H2'	47:S2:442:C:C6	2.55	0.41
47:S2:602:G:OP2	47:S2:603:C:O2'	2.26	0.41
47:S2:912:C:H4'	47:S2:913:A:OP2	2.20	0.41
47:S2:1273:C:C2	47:S2:1506:A:H2	2.38	0.41
47:S2:1285:G:OP1	74:SM:89:VAL:HG11	2.21	0.41
50:SB:110:MET:HE3	50:SB:113:MET:HE3	2.01	0.41
56:SK:80:ARG:NH2	56:SK:87:PRO:HA	2.35	0.41
60:SR:52:GLY:O	60:SR:55:THR:OG1	2.38	0.41
60:SR:74:GLN:O	60:SR:78:ARG:NE	2.52	0.41
70:Sg:155:ARG:NH1	70:Sg:199:THR:OG1	2.53	0.41
71:SC:144:SER:HB2	71:SC:150:ALA:HB2	2.02	0.41
1:L5:124:C:OP1	16:LN:144:ARG:HD2	2.21	0.41
1:L5:429:A:H2'	1:L5:430:G:C8	2.56	0.41
1:L5:2003:G:H1'	1:L5:2004:U:C5	2.45	0.41
1:L5:2347:A:C6	33:Le:31:ILE:HD11	2.56	0.41
1:L5:2474:G:C6	1:L5:2502:G:C6	3.08	0.41
1:L5:4689:U:H2'	1:L5:4690:G:O4'	2.20	0.41
3:L8:80:A:H2'	3:L8:81:C:O4'	2.21	0.41
7:LD:53:VAL:HB	7:LD:159:VAL:HG23	2.02	0.41
7:LD:236:MET:HA	7:LD:239:MET:HG2	2.01	0.41
9:LF:92:VAL:O	9:LF:120:GLY:HA2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:LI:86:HIS:HB3	12:LI:139:ARG:HE	1.85	0.41
14:LL:166:ALA:HB1	29:La:97:ALA:O	2.20	0.41
20:LR:7:GLN:NE2	20:LR:35:ALA:O	2.47	0.41
22:LT:17:ARG:NH1	22:LT:45:MET:HG3	2.35	0.41
30:Lb:16:TRP:CD1	30:Lb:21:ILE:HD11	2.55	0.41
47:S2:24:C:O2'	47:S2:25:A:H8	2.04	0.41
47:S2:35:C:H2'	47:S2:36:U:C6	2.55	0.41
47:S2:56:G:OP1	78:SY:111:LYS:NZ	2.53	0.41
47:S2:85:A:H2'	47:S2:86:C:C6	2.54	0.41
47:S2:141:A:O2'	47:S2:178:C:N3	2.39	0.41
47:S2:1192:U:OP2	65:SX:119:ARG:NH2	2.53	0.41
47:S2:1760:G:N1	47:S2:1773:C:H5'	2.35	0.41
57:SL:78:THR:HG21	57:SL:89:ARG:HG3	2.01	0.41
71:SC:123:ARG:HH21	71:SC:144:SER:HA	1.86	0.41
78:SY:113:ARG:NH2	78:SY:131:PRO:HB3	2.36	0.41
80:Sb:81:ARG:HG3	80:Sb:81:ARG:O	2.20	0.41
1:L5:756:G:N3	1:L5:756:G:H2'	2.35	0.41
1:L5:1510:G:H2'	1:L5:1511:U:H6	1.85	0.41
1:L5:2402:G:C2	1:L5:2403:A:C8	3.09	0.41
1:L5:2477:A:O2'	1:L5:2478:C:O4'	2.28	0.41
1:L5:2573:A:N6	1:L5:2574:G:N3	2.69	0.41
1:L5:2695:A:H1'	1:L5:2696:A:OP2	2.20	0.41
1:L5:2712:G:H2'	1:L5:2713:C:O4'	2.20	0.41
1:L5:3971:G:N2	1:L5:4050:A:H62	2.19	0.41
1:L5:4911:A:OP2	5:LB:100:ARG:NH1	2.53	0.41
4:LA:196:TRP:O	4:LA:198:ARG:N	2.53	0.41
20:LR:178:GLN:O	20:LR:182:GLU:HG3	2.20	0.41
22:LT:100:LYS:N	22:LT:100:LYS:HD2	2.34	0.41
24:LV:87:SER:HA	24:LV:97:TYR:HB3	2.03	0.41
26:LX:64:SER:HB2	36:Lh:69:LEU:HD21	2.01	0.41
26:LX:83:THR:HG22	26:LX:84:GLU:N	2.36	0.41
26:LX:84:GLU:O	26:LX:88:LYS:HG2	2.20	0.41
47:S2:180:G:O2'	47:S2:181:A:N3	2.53	0.41
47:S2:553:U:H2'	47:S2:554:A:C8	2.56	0.41
47:S2:687:C:O2'	54:SH:103:LYS:HD2	2.21	0.41
47:S2:1311:C:H5"	74:SM:36:ARG:HD3	2.02	0.41
47:S2:1651:A:H2'	47:S2:1652:G:C8	2.53	0.41
50:SB:136:ARG:O	50:SB:215:VAL:HA	2.20	0.41
54:SH:146:VAL:HG12	77:SW:42:MET:HE1	2.03	0.41
63:SU:106:ILE:O	63:SU:107:GLU:HB3	2.19	0.41
68:Sd:36:LEU:HD21	68:Sd:43:PHE:CD1	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
72:SG:172:LYS:HD2	72:SG:173:ALA:H	1.85	0.41
73:SJ:63:LEU:HD23	73:SJ:64:ASP:O	2.21	0.41
77:SW:57:ARG:NH1	80:Sb:26:GLN:OE1	2.54	0.41
79:SZ:61:GLU:O	79:SZ:64:ASN:ND2	2.44	0.41
80:Sb:63:LEU:HD23	80:Sb:63:LEU:H	1.85	0.41
1:L5:679:C:H2'	1:L5:680:G:C8	2.56	0.41
1:L5:1198:G:H2'	1:L5:1199:G:C8	2.55	0.41
1:L5:1370:G:H22	6:LC:239:LYS:NZ	2.19	0.41
1:L5:1398:A:O3'	1:L5:1399:G:H8	2.04	0.41
1:L5:2583:C:OP1	35:Lg:54:ARG:HB2	2.21	0.41
1:L5:3959:U:O2'	1:L5:3960:A:O4'	2.39	0.41
10:LG:159:HIS:HB2	10:LG:185:LYS:HA	2.03	0.41
16:LN:73:ARG:HG2	16:LN:75:VAL:HG13	2.02	0.41
19:LQ:172:ARG:O	19:LQ:172:ARG:HG2	2.19	0.41
26:LX:73:HIS:HB3	26:LX:116:LEU:HD23	2.02	0.41
32:Ld:68:LEU:HD22	32:Ld:106:VAL:O	2.20	0.41
35:Lg:40:LYS:HB3	35:Lg:40:LYS:HE2	1.82	0.41
47:S2:311:C:H4'	47:S2:339:A:H5"	2.01	0.41
47:S2:568:C:H2'	47:S2:569:A:H8	1.86	0.41
47:S2:1109:C:N3	60:SR:123:THR:OG1	2.52	0.41
47:S2:1426:U:C4	47:S2:1427:C:H1'	2.56	0.41
47:S2:1451:G:O2'	47:S2:1474:A:N6	2.54	0.41
47:S2:1671:G:H2'	47:S2:1672:U:C6	2.55	0.41
52:SE:42:LEU:HG	52:SE:46:ILE:HD11	2.02	0.41
54:SH:60:ILE:HG23	54:SH:92:VAL:HG23	2.03	0.41
54:SH:147:LYS:HG2	54:SH:151:SER:HB3	2.02	0.41
54:SH:160:LYS:HD2	54:SH:163:GLN:OE1	2.19	0.41
58:SP:77:LYS:HA	58:SP:78:THR:HB	2.03	0.41
62:ST:31:PRO:HG3	62:ST:102:ARG:HG2	2.01	0.41
63:SU:27:ARG:HD3	63:SU:82:MET:HE2	2.03	0.41
1:L5:43:U:OP1	16:LN:85:VAL:HG23	2.21	0.41
1:L5:173:C:OP1	14:LL:129:ARG:NH1	2.54	0.41
1:L5:931:C:O2	1:L5:931:C:H2'	2.20	0.41
1:L5:1275:G:H2'	1:L5:1276:C:C6	2.56	0.41
1:L5:1436:C:H5"	1:L5:2119:C:N4	2.30	0.41
1:L5:1660:U:H2'	29:La:12:ARG:HG3	2.02	0.41
1:L5:1823:G:H2'	1:L5:1825:A:C8	2.55	0.41
1:L5:2120:G:O2'	1:L5:2121:C:OP1	2.32	0.41
1:L5:2553:A:H4'	1:L5:2554:U:O4'	2.21	0.41
1:L5:4239:A:H2'	1:L5:4240:G:H8	1.86	0.41
1:L5:4684:A:H2'	1:L5:4685:U:O4'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:4699:U:C4	1:L5:4702:G:C6	3.09	0.41
5:LB:294:LYS:HG3	5:LB:295:ASP:OD1	2.21	0.41
12:LI:36:LEU:HD11	12:LI:69:ARG:NH1	2.35	0.41
20:LR:21:LYS:HE3	20:LR:55:VAL:HA	2.03	0.41
46:Lz:212:LYS:HE2	46:Lz:212:LYS:HB2	1.91	0.41
47:S2:182:C:H2'	47:S2:184:G:C8	2.55	0.41
47:S2:422:U:O2'	47:S2:652:U:OP1	2.38	0.41
47:S2:1113:A:N3	47:S2:1113:A:H2'	2.36	0.41
47:S2:1373:C:H2'	47:S2:1374:C:C6	2.56	0.41
47:S2:1457:U:H2'	47:S2:1458:G:C8	2.56	0.41
48:S6:64:U:H2'	48:S6:65:C:H6	1.84	0.41
49:SA:41:ARG:NH1	49:SA:47:TYR:HE1	2.16	0.41
51:SD:43:PRO:HG2	63:SU:99:LYS:NZ	2.36	0.41
51:SD:158:ILE:HG12	51:SD:189:MET:HE1	2.03	0.41
52:SE:146:THR:HG23	52:SE:146:THR:O	2.20	0.41
52:SE:259:LYS:HG3	52:SE:260:GLN:HG2	2.03	0.41
53:SF:15:PRO:HD3	59:SQ:57:LEU:HG	2.03	0.41
57:SL:131:CYS:SG	57:SL:132:ARG:N	2.92	0.41
70:Sg:71:ILE:HD11	70:Sg:75:GLY:HA2	2.02	0.41
70:Sg:261:LEU:HB3	70:Sg:262:GLU:H	1.68	0.41
71:SC:166:ARG:HB2	71:SC:248:TYR:CE1	2.56	0.41
72:SG:209:TYR:HB3	72:SG:214:ALA:CB	2.49	0.41
79:SZ:86:ALA:O	79:SZ:90:GLU:HG2	2.21	0.41
1:L5:7:C:H2'	1:L5:8:U:C6	2.56	0.41
1:L5:95:G:H5'	14:LL:15:HIS:HE1	1.86	0.41
1:L5:299:C:O3'	16:LN:171:SER:HA	2.21	0.41
1:L5:318:A:H2'	1:L5:319:A:C8	2.56	0.41
1:L5:509:A:H2'	14:LL:163:LYS:HZ2	1.84	0.41
1:L5:933:G:H2'	1:L5:940:C:C5	2.55	0.41
1:L5:973:G:C8	1:L5:974:C:N4	2.89	0.41
1:L5:1089:G:H2'	1:L5:1090:G:C8	2.56	0.41
1:L5:1100:U:O2	1:L5:1195:G:N2	2.53	0.41
1:L5:1968:G:H8	1:L5:1968:G:OP2	2.04	0.41
1:L5:2361:G:H1'	1:L5:2362:U:H5	1.85	0.41
1:L5:2545:U:H5'	1:L5:2546:G:O5'	2.21	0.41
1:L5:3916:G:H2'	1:L5:3917:A:C8	2.56	0.41
1:L5:3952:A:H2'	1:L5:3953:G:C8	2.56	0.41
1:L5:4041:C:O2'	46:Lz:98:LYS:HD3	2.20	0.41
1:L5:4113:U:H3'	1:L5:4114:C:H5"	2.03	0.41
1:L5:4120:U:H1'	31:Lc:54:ALA:HB1	2.01	0.41
1:L5:4151:G:H2'	1:L5:4152:G:C8	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:4563:U:C2	1:L5:4564:A:C8	3.09	0.41
1:L5:4765:G:H1	1:L5:4869:U:H3	1.67	0.41
2:L7:16:A:H2'	2:L7:17:C:C6	2.56	0.41
2:L7:108:G:H2'	2:L7:109:U:C6	2.55	0.41
3:L8:70:G:H1'	3:L8:88:A:N6	2.35	0.41
4:LA:98:ILE:HD12	4:LA:98:ILE:H	1.85	0.41
6:LC:13:GLU:OE2	6:LC:161:TYR:OH	2.30	0.41
6:LC:23:THR:O	6:LC:24:LEU:HB2	2.20	0.41
8:LE:109:LEU:C	8:LE:111:LYS:H	2.29	0.41
13:LJ:55:TYR:HD1	13:LJ:64:ARG:HD2	1.85	0.41
13:LJ:56:THR:HA	13:LJ:57:VAL:HA	1.80	0.41
18:LP:41:ILE:O	18:LP:45:THR:HG23	2.21	0.41
19:LQ:171:GLY:O	19:LQ:172:ARG:HB3	2.20	0.41
40:Ll:38:ASN:O	40:Ll:40:LYS:N	2.52	0.41
43:Lo:14:LYS:HE2	43:Lo:77:CYS:SG	2.61	0.41
46:Lz:21:ASN:N	46:Lz:176:ASP:OD2	2.53	0.41
47:S2:289:G:H2'	47:S2:290:U:C6	2.56	0.41
47:S2:333:G:C6	47:S2:334:C:C5	3.09	0.41
47:S2:389:A:H2'	47:S2:390:C:C6	2.54	0.41
47:S2:445:A:H5"	55:SI:47:ARG:NH2	2.36	0.41
47:S2:693:A:H2'	47:S2:696:G:O6	2.21	0.41
47:S2:833:C:O2'	47:S2:834:C:OP1	2.38	0.41
47:S2:1223:A:OP2	53:SF:79:HIS:NE2	2.54	0.41
47:S2:1535:U:H5'	47:S2:1536:G:C8	2.55	0.41
47:S2:1596:U:H2'	47:S2:1597:C:C6	2.55	0.41
47:S2:1617:G:N1	47:S2:1620:A:OP2	2.54	0.41
47:S2:1667:U:H2'	47:S2:1668:U:C6	2.55	0.41
47:S2:1785:C:O2'	47:S2:1786:U:O4'	2.38	0.41
48:S6:6:G:H2'	48:S6:7:A:H8	1.86	0.41
49:SA:176:TRP:HZ3	49:SA:177:MET:HE2	1.85	0.41
49:SA:184:ARG:HH11	49:SA:191:ARG:HG3	1.86	0.41
49:SA:206:ASP:HA	49:SA:207:PRO:HD3	1.97	0.41
51:SD:108:LYS:HE3	51:SD:118:ALA:HA	2.02	0.41
52:SE:176:ASP:OD2	52:SE:176:ASP:N	2.54	0.41
54:SH:43:LEU:HD23	54:SH:72:PHE:CD1	2.56	0.41
69:Sf:135:HIS:CG	69:Sf:136:PHE:H	2.39	0.41
70:Sg:122:SER:OG	70:Sg:130:LYS:O	2.34	0.41
70:Sg:257:LYS:HG2	70:Sg:259:TRP:NE1	2.36	0.41
72:SG:49:VAL:HG12	72:SG:115:LYS:HB2	2.03	0.41
72:SG:219:GLU:HG2	72:SG:222:GLU:HB2	2.03	0.41
73:SJ:111:GLN:NE2	73:SJ:127:ARG:HD2	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
75:SN:46:THR:OG1	75:SN:47:PRO:HD2	2.21	0.41
78:SY:113:ARG:HA	78:SY:116:LYS:NZ	2.36	0.41
1:L5:1280:C:H2'	1:L5:1281:G:H3'	2.03	0.41
1:L5:1965:G:H4'	1:L5:4695:C:O2'	2.20	0.41
1:L5:3772:U:H2'	1:L5:3773:U:O4'	2.21	0.41
1:L5:4275:G:H4'	22:LT:12:ARG:HH21	1.86	0.41
1:L5:4504:C:H2'	1:L5:4505:C:H6	1.84	0.41
1:L5:4894:A:H5'	15:LM:125:ASN:HD21	1.86	0.41
3:L8:94:G:N3	38:Lj:82:THR:HG23	2.36	0.41
6:LC:60:HIS:CE1	6:LC:100:ARG:HD3	2.55	0.41
11:LH:47:LEU:HD23	11:LH:47:LEU:HA	1.86	0.41
20:LR:135:LYS:HG2	20:LR:139:MET:HE3	2.03	0.41
20:LR:156:ALA:O	20:LR:160:GLU:HG3	2.21	0.41
21:LS:30:MET:HE1	21:LS:47:PHE:HB2	2.02	0.41
26:LX:40:ILE:O	26:LX:42:THR:HG23	2.20	0.41
29:La:126:ALA:O	29:La:147:VAL:HG22	2.22	0.41
45:Lr:71:ARG:NH1	45:Lr:71:ARG:HB2	2.36	0.41
46:Lz:210:MET:O	46:Lz:210:MET:HG3	2.21	0.41
47:S2:419:G:O2'	77:SW:88:LYS:HE3	2.20	0.41
47:S2:806:U:C2	47:S2:807:G:C8	3.08	0.41
47:S2:1534:C:O2	47:S2:1598:G:N2	2.54	0.41
47:S2:1540:G:C6	47:S2:1594:A:N6	2.89	0.41
47:S2:1742:C:H2'	47:S2:1743:G:O4'	2.21	0.41
55:SI:42:ARG:HH21	55:SI:59:ARG:NH2	2.19	0.41
55:SI:106:SER:HB3	55:SI:171:LEU:HG	2.02	0.41
63:SU:47:ASN:OD1	63:SU:47:ASN:N	2.54	0.41
71:SC:77:SER:HA	71:SC:97:PHE:CE1	2.56	0.41
71:SC:133:TYR:CE2	71:SC:216:MET:HA	2.56	0.41
1:L5:68:U:OP1	16:LN:178:HIS:ND1	2.39	0.40
1:L5:499:G:H1	1:L5:656:C:H42	1.69	0.40
1:L5:950:G:H2'	1:L5:951:G:C8	2.56	0.40
1:L5:1276:C:N4	1:L5:1277:G:C5	2.89	0.40
1:L5:1537:A:H2'	1:L5:1538:U:C6	2.56	0.40
1:L5:2119:C:H4'	1:L5:2120:G:C4'	2.47	0.40
1:L5:2555:G:H1	1:L5:2572:C:H42	1.69	0.40
1:L5:2602:G:H2'	1:L5:2603:C:C6	2.56	0.40
1:L5:3772:U:OP1	1:L5:3772:U:H4'	2.16	0.40
1:L5:4860:G:O2'	1:L5:4861:G:P	2.79	0.40
6:LC:147:VAL:HG12	6:LC:148:PRO:O	2.21	0.40
25:LW:4:GLU:HB3	25:LW:30:GLN:NE2	2.35	0.40
31:Lc:53:PRO:HG2	31:Lc:56:ARG:NH1	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:Lf:71:TRP:HZ3	34:Lf:104:MET:HE3	1.85	0.40
38:Lj:18:LEU:HA	38:Lj:25:LYS:HA	2.03	0.40
47:S2:122:G:H2'	47:S2:123:G:H8	1.85	0.40
47:S2:549:C:C2	47:S2:550:C:H1'	2.56	0.40
47:S2:1350:U:O2'	49:SA:110:ASN:OD1	2.29	0.40
47:S2:1859:A:O2'	47:S2:1860:A:H5'	2.21	0.40
48:S6:33:C:H2'	48:S6:35:A:OP2	2.21	0.40
50:SB:71:LEU:HD21	50:SB:189:ILE:HG23	2.03	0.40
50:SB:72:ALA:HB3	76:SO:128:ARG:HH12	1.85	0.40
50:SB:146:ARG:O	50:SB:147:ASN:HB2	2.21	0.40
51:SD:162:ASP:C	51:SD:162:ASP:OD1	2.64	0.40
58:SP:78:THR:OG1	58:SP:79:HIS:N	2.54	0.40
70:Sg:72:SER:HB2	70:Sg:113:PHE:CE2	2.55	0.40
73:SJ:50:LEU:HA	73:SJ:53:ILE:HG22	2.02	0.40
78:SY:12:PHE:HD1	78:SY:23:MET:SD	2.44	0.40
1:L5:364:G:O6	38:Lj:55:ARG:NH2	2.54	0.40
1:L5:383:A:O2'	1:L5:384:A:O5'	2.36	0.40
1:L5:2759:G:O2'	1:L5:2762:G:N2	2.52	0.40
1:L5:2759:G:O2'	1:L5:2763:U:O2	2.30	0.40
1:L5:2876:G:C8	44:Lp:16:THR:HG22	2.56	0.40
1:L5:3827:G:H3'	1:L5:3828:A:H5"	2.03	0.40
1:L5:4146:G:H2'	1:L5:4147:G:C8	2.56	0.40
1:L5:4244:A:H2'	1:L5:4245:G:O4'	2.21	0.40
1:L5:4887:C:H6	1:L5:4887:C:H2'	1.64	0.40
1:L5:5018:C:H2'	1:L5:5019:A:C8	2.56	0.40
4:LA:225:ILE:HG12	4:LA:234:LYS:HA	2.02	0.40
7:LD:180:PHE:HB3	7:LD:195:HIS:CD2	2.57	0.40
16:LN:92:LEU:C	16:LN:93:LYS:HG3	2.46	0.40
20:LR:38:ARG:C	20:LR:40:GLN:H	2.29	0.40
28:LZ:36:ARG:HG3	28:LZ:38:TYR:CZ	2.56	0.40
47:S2:873:G:H21	54:SH:114:GLN:NE2	2.18	0.40
47:S2:1025:U:OP1	47:S2:1090:C:O2'	2.39	0.40
47:S2:1113:A:H3'	47:S2:1114:U:H5'	2.04	0.40
47:S2:1288:U:H1'	47:S2:1312:G:C2	2.57	0.40
47:S2:1445:U:H1'	47:S2:1580:A:H61	1.86	0.40
49:SA:22:GLY:C	49:SA:24:HIS:H	2.30	0.40
56:SK:11:ILE:HD11	56:SK:40:VAL:HG23	2.03	0.40
58:SP:63:ALA:HB3	58:SP:74:GLU:OE2	2.21	0.40
59:SQ:53:GLU:HB2	59:SQ:54:PRO:HD3	2.02	0.40
61:SS:89:ASP:O	61:SS:91:LYS:N	2.55	0.40
64:SV:57:GLY:O	64:SV:61:ARG:HG3	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
68:Sd:36:LEU:HD21	68:Sd:43:PHE:CE1	2.56	0.40
71:SC:224:THR:HG22	71:SC:225:SER:N	2.35	0.40
75:SN:84:LEU:HD21	75:SN:149:LEU:HD21	2.04	0.40
78:SY:20:ARG:HD3	78:SY:76:TYR:CZ	2.56	0.40
1:L5:701:G:O2'	33:Le:5:ARG:NH2	2.55	0.40
1:L5:754:U:H2'	1:L5:755:C:C6	2.57	0.40
1:L5:970:G:N2	8:LE:126:LEU:HD21	2.36	0.40
1:L5:1266:G:H5'	1:L5:2112:G:N2	2.36	0.40
1:L5:1345:A:H2'	1:L5:1346:C:C6	2.57	0.40
1:L5:1662:C:H2'	1:L5:1663:C:H6	1.87	0.40
1:L5:2094:G:H3'	1:L5:2095:A:C8	2.56	0.40
1:L5:2521:G:H5'	1:L5:2640:G:H1'	2.04	0.40
1:L5:3951:G:C2	1:L5:4061:G:C6	3.09	0.40
1:L5:4405:G:O2'	12:LI:4:ARG:NH2	2.55	0.40
1:L5:5005:G:H1'	1:L5:5042:A:H61	1.86	0.40
19:LQ:72:LEU:HD12	19:LQ:75:ARG:NH1	2.35	0.40
19:LQ:178:ARG:H	29:La:51:GLY:HA2	1.85	0.40
26:LX:119:ILE:HD12	26:LX:149:VAL:HG11	2.03	0.40
36:Lh:89:ARG:HG3	36:Lh:93:ARG:NH1	2.37	0.40
46:Lz:11:TYR:HB3	46:Lz:216:LEU:HA	2.03	0.40
47:S2:957:A:O2'	47:S2:958:G:O5'	2.39	0.40
47:S2:1018:U:H2'	47:S2:1019:C:C6	2.56	0.40
49:SA:190:SER:C	49:SA:192:GLU:H	2.30	0.40
51:SD:206:ASP:OD1	60:SR:8:THR:HG21	2.21	0.40
56:SK:3:MET:HG3	56:SK:4:PRO:HD3	2.04	0.40
59:SQ:44:PRO:C	59:SQ:46:THR:H	2.29	0.40
60:SR:117:LEU:HG	60:SR:119:VAL:HG23	2.03	0.40
61:SS:80:PRO:HB3	61:SS:82:TRP:NE1	2.36	0.40
61:SS:110:ASP:OD1	61:SS:110:ASP:N	2.53	0.40
70:Sg:301:GLY:HA2	70:Sg:307:VAL:HG22	2.03	0.40
71:SC:275:LYS:HD2	71:SC:275:LYS:HA	1.90	0.40
1:L5:1617:G:H1'	1:L5:2513:A:N6	2.36	0.40
1:L5:2092:G:O2'	1:L5:2093:A:O5'	2.36	0.40
1:L5:3670:C:O2'	1:L5:3671:G:C8	2.73	0.40
1:L5:3755:G:H2'	1:L5:3756:A:C4	2.57	0.40
1:L5:3937:C:H1'	16:LN:125:SER:HB2	2.02	0.40
1:L5:4946:U:O2	1:L5:4946:U:H2'	2.20	0.40
1:L5:4992:G:H2'	1:L5:4993:G:H8	1.79	0.40
1:L5:5001:U:H4'	5:LB:317:LEU:HB3	2.04	0.40
4:LA:70:LYS:HG3	4:LA:71:LYS:N	2.37	0.40
6:LC:186:SER:HB2	6:LC:204:ARG:HG2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:LH:176:LEU:HD12	11:LH:176:LEU:O	2.22	0.40
17:LO:175:MET:HE3	17:LO:179:LYS:HG3	2.02	0.40
20:LR:119:MET:HE3	20:LR:119:MET:HB2	1.97	0.40
47:S2:1007:C:H2'	47:S2:1008:A:C8	2.56	0.40
47:S2:1429:G:OP1	59:SQ:69:ARG:HD2	2.22	0.40
47:S2:1495:G:H2'	47:S2:1496:U:C6	2.57	0.40
51:SD:76:ARG:NH2	56:SK:66:HIS:CE1	2.88	0.40
56:SK:42:ASN:OD1	56:SK:46:MET:HB3	2.22	0.40
61:SS:74:PRO:HA	61:SS:79:ILE:HB	2.04	0.40
70:Sg:191:HIS:HE2	70:Sg:217:MET:HG2	1.85	0.40
72:SG:148:SER:HA	72:SG:149:LYS:HA	1.81	0.40
73:SJ:37:LEU:HB3	73:SJ:38:ARG:H	1.68	0.40
73:SJ:107:GLU:OE2	73:SJ:116:LYS:NZ	2.54	0.40
1:L5:286:U:H2'	1:L5:287:U:C6	2.56	0.40
1:L5:385:A:H1'	1:L5:386:A:H5"	2.04	0.40
1:L5:1989:G:N1	1:L5:1991:A:N1	2.70	0.40
1:L5:2639:U:H2'	1:L5:2694:G:H1	1.86	0.40
1:L5:2664:G:OP2	20:LR:121:HIS:ND1	2.43	0.40
1:L5:2696:A:H5'	39:Lk:70:LYS:HD2	2.03	0.40
1:L5:3868:G:N2	1:L5:3900:G:O2'	2.54	0.40
1:L5:4416:G:H2'	1:L5:4417:C:C6	2.55	0.40
14:LL:54:PRO:HB3	14:LL:97:SER:HB3	2.03	0.40
15:LM:32:ASP:HB2	21:LS:145:PHE:CE1	2.57	0.40
47:S2:222:U:H5"	57:SL:17:PHE:CG	2.56	0.40
47:S2:559:G:OP2	47:S2:559:G:H8	2.04	0.40
47:S2:946:U:H2'	47:S2:947:G:C8	2.56	0.40
47:S2:1706:G:H2'	47:S2:1707:U:H6	1.86	0.40
53:SF:36:GLN:C	53:SF:38:TYR:H	2.29	0.40
69:Sf:98:VAL:HG13	69:Sf:100:LEU:HD12	2.04	0.40
70:Sg:44:LYS:HG3	70:Sg:56:GLN:HB2	2.04	0.40
73:SJ:75:ASN:C	73:SJ:75:ASN:HD22	2.28	0.40
74:SM:15:ASN:HB3	74:SM:78:LYS:O	2.22	0.40
78:SY:7:ILE:HD13	78:SY:40:ILE:HD12	2.04	0.40
80:Sb:49:HIS:HD1	80:Sb:70:LYS:HA	1.87	0.40
82:Pt:17:C:H5"	82:Pt:18:C:H3'	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
4	LA	246/257 (96%)	224 (91%)	20 (8%)	2 (1%)	16 40
5	LB	400/403 (99%)	366 (92%)	28 (7%)	6 (2%)	8 25
6	LC	365/427 (86%)	318 (87%)	45 (12%)	2 (0%)	24 52
7	LD	291/297 (98%)	270 (93%)	18 (6%)	3 (1%)	12 35
8	LE	238/288 (83%)	197 (83%)	35 (15%)	6 (2%)	4 14
9	LF	223/248 (90%)	210 (94%)	13 (6%)	0	100 100
10	LG	239/266 (90%)	215 (90%)	24 (10%)	0	100 100
11	LH	188/192 (98%)	171 (91%)	17 (9%)	0	100 100
12	LI	211/214 (99%)	196 (93%)	15 (7%)	0	100 100
13	LJ	174/178 (98%)	157 (90%)	15 (9%)	2 (1%)	11 32
14	LL	208/211 (99%)	188 (90%)	16 (8%)	4 (2%)	6 19
15	LM	137/215 (64%)	121 (88%)	15 (11%)	1 (1%)	18 44
16	LN	201/204 (98%)	190 (94%)	11 (6%)	0	100 100
17	LO	199/203 (98%)	188 (94%)	11 (6%)	0	100 100
18	LP	151/184 (82%)	138 (91%)	11 (7%)	2 (1%)	9 28
19	LQ	185/188 (98%)	176 (95%)	9 (5%)	0	100 100
20	LR	185/196 (94%)	180 (97%)	5 (3%)	0	100 100
21	LS	173/176 (98%)	153 (88%)	19 (11%)	1 (1%)	21 47
22	LT	157/160 (98%)	148 (94%)	7 (4%)	2 (1%)	9 28
23	LU	99/128 (77%)	91 (92%)	7 (7%)	1 (1%)	12 35
24	LV	129/140 (92%)	117 (91%)	12 (9%)	0	100 100
25	LW	122/157 (78%)	104 (85%)	16 (13%)	2 (2%)	7 23
26	LX	118/156 (76%)	112 (95%)	6 (5%)	0	100 100
27	LY	132/145 (91%)	124 (94%)	7 (5%)	1 (1%)	16 40
28	LZ	133/136 (98%)	117 (88%)	16 (12%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
29	La	145/148 (98%)	126 (87%)	19 (13%)	0	100 100
30	Lb	73/159 (46%)	66 (90%)	6 (8%)	1 (1%)	9 26
31	Lc	96/115 (84%)	88 (92%)	5 (5%)	3 (3%)	3 10
32	Ld	105/125 (84%)	97 (92%)	8 (8%)	0	100 100
33	Le	126/135 (93%)	113 (90%)	12 (10%)	1 (1%)	16 40
34	Lf	107/110 (97%)	98 (92%)	7 (6%)	2 (2%)	6 19
35	Lg	112/117 (96%)	108 (96%)	4 (4%)	0	100 100
36	Lh	120/123 (98%)	113 (94%)	6 (5%)	1 (1%)	16 40
37	Li	100/105 (95%)	93 (93%)	7 (7%)	0	100 100
38	Lj	84/97 (87%)	75 (89%)	8 (10%)	1 (1%)	10 30
39	Lk	67/70 (96%)	58 (87%)	8 (12%)	1 (2%)	8 25
40	Ll	48/51 (94%)	45 (94%)	3 (6%)	0	100 100
41	Lm	50/128 (39%)	48 (96%)	1 (2%)	1 (2%)	6 18
42	Ln	22/25 (88%)	20 (91%)	2 (9%)	0	100 100
43	Lo	102/106 (96%)	96 (94%)	5 (5%)	1 (1%)	12 35
44	Lp	89/92 (97%)	80 (90%)	8 (9%)	1 (1%)	11 32
45	Lr	123/137 (90%)	108 (88%)	14 (11%)	1 (1%)	16 40
46	Lz	215/217 (99%)	190 (88%)	25 (12%)	0	100 100
49	SA	220/295 (75%)	199 (90%)	21 (10%)	0	100 100
50	SB	212/264 (80%)	187 (88%)	23 (11%)	2 (1%)	14 37
51	SD	225/243 (93%)	195 (87%)	27 (12%)	3 (1%)	9 28
52	SE	260/263 (99%)	229 (88%)	29 (11%)	2 (1%)	16 40
53	SF	189/204 (93%)	158 (84%)	28 (15%)	3 (2%)	7 23
54	SH	187/193 (97%)	162 (87%)	23 (12%)	2 (1%)	11 32
55	SI	204/208 (98%)	175 (86%)	26 (13%)	3 (2%)	8 25
56	SK	96/165 (58%)	82 (85%)	13 (14%)	1 (1%)	12 35
57	SL	151/158 (96%)	138 (91%)	13 (9%)	0	100 100
58	SP	95/145 (66%)	61 (64%)	30 (32%)	4 (4%)	2 6
59	SQ	144/146 (99%)	124 (86%)	17 (12%)	3 (2%)	5 17
60	SR	130/135 (96%)	116 (89%)	13 (10%)	1 (1%)	16 40
61	SS	148/152 (97%)	126 (85%)	18 (12%)	4 (3%)	4 12

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
62	ST	141/145 (97%)	123 (87%)	16 (11%)	2 (1%)	9 26
63	SU	102/119 (86%)	90 (88%)	10 (10%)	2 (2%)	6 18
64	SV	81/83 (98%)	70 (86%)	9 (11%)	2 (2%)	4 14
65	SX	139/143 (97%)	124 (89%)	11 (8%)	4 (3%)	3 11
66	Sa	103/115 (90%)	85 (82%)	16 (16%)	2 (2%)	6 19
67	Sc	62/69 (90%)	47 (76%)	15 (24%)	0	100 100
68	Sd	51/56 (91%)	48 (94%)	3 (6%)	0	100 100
69	Sf	69/156 (44%)	53 (77%)	12 (17%)	4 (6%)	1 3
70	Sg	311/317 (98%)	272 (88%)	35 (11%)	4 (1%)	9 28
71	SC	220/293 (75%)	201 (91%)	16 (7%)	3 (1%)	9 26
72	SG	235/249 (94%)	205 (87%)	25 (11%)	5 (2%)	5 17
73	SJ	183/194 (94%)	165 (90%)	15 (8%)	3 (2%)	7 23
74	SM	120/132 (91%)	99 (82%)	18 (15%)	3 (2%)	4 14
75	SN	148/151 (98%)	139 (94%)	6 (4%)	3 (2%)	6 18
76	SO	138/151 (91%)	109 (79%)	24 (17%)	5 (4%)	2 8
77	SW	127/130 (98%)	119 (94%)	8 (6%)	0	100 100
78	SY	129/133 (97%)	117 (91%)	11 (8%)	1 (1%)	16 40
79	SZ	73/125 (58%)	61 (84%)	10 (14%)	2 (3%)	4 12
80	Sb	81/84 (96%)	70 (86%)	11 (14%)	0	100 100
81	Se	56/59 (95%)	49 (88%)	7 (12%)	0	100 100
All	All	11518/12904 (89%)	10291 (89%)	1105 (10%)	122 (1%)	14 32

All (122) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	LB	113	GLU
7	LD	21	ARG
8	LE	131	LYS
14	LL	91	ALA
33	Le	104	SER
43	Lo	99	ARG
44	Lp	20	ALA
50	SB	147	ASN
53	SF	15	PRO
54	SH	66	VAL

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Mol	Chain	Res	Type
55	SI	130	THR
56	SK	3	MET
58	SP	94	VAL
59	SQ	42	ILE
59	SQ	48	GLN
61	SS	117	ILE
61	SS	121	ARG
62	ST	4	VAL
62	ST	5	THR
63	SU	50	VAL
63	SU	107	GLU
65	SX	10	ALA
65	SX	35	ALA
70	Sg	56	GLN
72	SG	25	ARG
72	SG	122	PRO
73	SJ	3	VAL
73	SJ	8	VAL
75	SN	24	THR
76	SO	68	GLU
4	LA	116	LEU
5	LB	159	VAL
5	LB	292	LEU
5	LB	297	LYS
7	LD	4	VAL
7	LD	178	LYS
8	LE	106	VAL
8	LE	226	ARG
14	LL	67	HIS
18	LP	132	ALA
21	LS	83	ARG
22	LT	81	LYS
31	Lc	51	ASN
36	Lh	97	LYS
45	Lr	68	SER
53	SF	17	ILE
58	SP	76	VAL
58	SP	105	VAL
60	SR	119	VAL
61	SS	12	ILE
64	SV	78	ILE
69	Sf	100	LEU

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Mol	Chain	Res	Type
70	Sg	281	ALA
71	SC	278	THR
74	SM	117	GLU
4	LA	180	LEU
6	LC	110	ARG
8	LE	279	ASN
15	LM	71	LYS
31	Lc	52	CYS
31	Lc	54	ALA
34	Lf	83	MET
38	Lj	63	ARG
51	SD	223	ILE
53	SF	20	PHE
55	SI	143	LYS
64	SV	36	VAL
65	SX	79	LYS
66	Sa	61	ALA
72	SG	20	ASP
74	SM	41	ALA
76	SO	128	ARG
5	LB	5	LYS
5	LB	291	TYR
6	LC	309	ILE
8	LE	126	LEU
25	LW	73	ARG
41	Lm	117	HIS
51	SD	44	THR
52	SE	131	VAL
69	Sf	98	VAL
69	Sf	102	VAL
73	SJ	122	SER
75	SN	3	ARG
76	SO	56	VAL
76	SO	129	ILE
8	LE	109	LEU
13	LJ	28	GLU
13	LJ	174	ILE
14	LL	55	ILE
14	LL	169	ILE
18	LP	135	ARG
22	LT	53	PRO
30	Lb	21	ILE

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Mol	Chain	Res	Type
39	Lk	32	VAL
50	SB	22	VAL
54	SH	100	ILE
61	SS	16	LEU
65	SX	46	HIS
66	Sa	5	ARG
70	Sg	262	GLU
72	SG	12	CYS
74	SM	103	VAL
75	SN	68	GLY
76	SO	140	THR
78	SY	51	THR
23	LU	98	ASP
27	LY	53	ASP
34	Lf	54	LYS
51	SD	154	ASP
55	SI	127	ALA
72	SG	175	LYS
79	SZ	49	LEU
79	SZ	108	ILE
52	SE	90	ILE
71	SC	162	ILE
71	SC	176	LYS
25	LW	100	VAL
58	SP	96	VAL
70	Sg	55	PRO
69	Sf	87	THR
59	SQ	5	GLY

5.3.2 Protein sidechains (i)

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
4	LA	190/199 (96%)	189 (100%)	1 (0%)	81 92
5	LB	348/349 (100%)	348 (100%)	0	100 100
6	LC	305/348 (88%)	305 (100%)	0	100 100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	LD	246/250 (98%)	246 (100%)	0	100	100
8	LE	215/252 (85%)	215 (100%)	0	100	100
9	LF	194/215 (90%)	194 (100%)	0	100	100
10	LG	203/223 (91%)	203 (100%)	0	100	100
11	LH	169/171 (99%)	169 (100%)	0	100	100
12	LI	180/181 (99%)	180 (100%)	0	100	100
13	LJ	148/149 (99%)	148 (100%)	0	100	100
14	LL	176/177 (99%)	176 (100%)	0	100	100
15	LM	118/161 (73%)	118 (100%)	0	100	100
16	LN	171/172 (99%)	171 (100%)	0	100	100
17	LO	173/174 (99%)	173 (100%)	0	100	100
18	LP	134/163 (82%)	134 (100%)	0	100	100
19	LQ	164/165 (99%)	163 (99%)	1 (1%)	78	91
20	LR	166/175 (95%)	166 (100%)	0	100	100
21	LS	156/157 (99%)	156 (100%)	0	100	100
22	LT	139/140 (99%)	139 (100%)	0	100	100
23	LU	91/115 (79%)	91 (100%)	0	100	100
24	LV	101/107 (94%)	101 (100%)	0	100	100
25	LW	103/126 (82%)	103 (100%)	0	100	100
26	LX	108/133 (81%)	107 (99%)	1 (1%)	70	87
27	LY	124/135 (92%)	124 (100%)	0	100	100
28	LZ	117/118 (99%)	117 (100%)	0	100	100
29	La	120/121 (99%)	120 (100%)	0	100	100
30	Lb	63/126 (50%)	63 (100%)	0	100	100
31	Lc	83/97 (86%)	83 (100%)	0	100	100
32	Ld	98/110 (89%)	98 (100%)	0	100	100
33	Le	114/121 (94%)	114 (100%)	0	100	100
34	Lf	88/89 (99%)	88 (100%)	0	100	100
35	Lg	98/100 (98%)	98 (100%)	0	100	100
36	Lh	109/110 (99%)	109 (100%)	0	100	100
37	Li	86/89 (97%)	86 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
38	Lj	73/80 (91%)	73 (100%)	0	100	100
39	Lk	64/65 (98%)	64 (100%)	0	100	100
40	Ll	47/48 (98%)	47 (100%)	0	100	100
41	Lm	48/116 (41%)	48 (100%)	0	100	100
42	Ln	23/24 (96%)	23 (100%)	0	100	100
43	Lo	93/94 (99%)	93 (100%)	0	100	100
44	Lp	74/75 (99%)	74 (100%)	0	100	100
45	Lr	109/121 (90%)	109 (100%)	0	100	100
46	Lz	195/196 (100%)	195 (100%)	0	100	100
49	SA	184/243 (76%)	184 (100%)	0	100	100
50	SB	195/231 (84%)	195 (100%)	0	100	100
51	SD	190/202 (94%)	190 (100%)	0	100	100
52	SE	224/225 (100%)	224 (100%)	0	100	100
53	SF	161/170 (95%)	161 (100%)	0	100	100
54	SH	169/173 (98%)	169 (100%)	0	100	100
55	SI	178/180 (99%)	177 (99%)	1 (1%)	78	91
56	SK	89/136 (65%)	89 (100%)	0	100	100
57	SL	137/142 (96%)	137 (100%)	0	100	100
58	SP	87/130 (67%)	87 (100%)	0	100	100
59	SQ	121/121 (100%)	121 (100%)	0	100	100
60	SR	120/122 (98%)	120 (100%)	0	100	100
61	SS	130/132 (98%)	130 (100%)	0	100	100
62	ST	113/115 (98%)	113 (100%)	0	100	100
63	SU	94/107 (88%)	94 (100%)	0	100	100
64	SV	67/67 (100%)	67 (100%)	0	100	100
65	SX	113/115 (98%)	113 (100%)	0	100	100
66	Sa	90/98 (92%)	90 (100%)	0	100	100
67	Sc	57/62 (92%)	57 (100%)	0	100	100
68	Sd	47/49 (96%)	47 (100%)	0	100	100
69	Sf	64/140 (46%)	64 (100%)	0	100	100
70	Sg	272/275 (99%)	272 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
71	SC	188/225 (84%)	188 (100%)	0	100	100
72	SG	207/218 (95%)	207 (100%)	0	100	100
73	SJ	161/168 (96%)	161 (100%)	0	100	100
74	SM	104/108 (96%)	104 (100%)	0	100	100
75	SN	130/131 (99%)	130 (100%)	0	100	100
76	SO	110/119 (92%)	110 (100%)	0	100	100
77	SW	112/113 (99%)	112 (100%)	0	100	100
78	SY	113/115 (98%)	113 (100%)	0	100	100
79	SZ	66/103 (64%)	66 (100%)	0	100	100
80	Sb	75/76 (99%)	75 (100%)	0	100	100
81	Se	47/48 (98%)	47 (100%)	0	100	100
All	All	10039/10996 (91%)	10035 (100%)	4 (0%)	100	100

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	LA	162	ASN
19	LQ	45	GLN
26	LX	69	ASN
55	SI	64	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (102) such sidechains are listed below:

Mol	Chain	Res	Type
4	LA	215	ASN
5	LB	213	GLN
6	LC	43	ASN
6	LC	116	ASN
6	LC	119	GLN
6	LC	329	ASN
7	LD	195	HIS
8	LE	191	GLN
8	LE	227	HIS
9	LF	116	GLN
9	LF	119	ASN
9	LF	192	HIS
9	LF	206	ASN

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Mol	Chain	Res	Type
9	LF	239	GLN
10	LG	43	GLN
11	LH	40	HIS
11	LH	102	ASN
12	LI	166	HIS
12	LI	213	HIS
13	LJ	168	GLN
14	LL	13	HIS
14	LL	15	HIS
16	LN	8	GLN
16	LN	32	GLN
16	LN	86	HIS
17	LO	42	ASN
17	LO	143	HIS
18	LP	97	ASN
19	LQ	7	HIS
20	LR	141	HIS
20	LR	178	GLN
23	LU	27	HIS
25	LW	104	GLN
26	LX	57	GLN
26	LX	69	ASN
26	LX	108	GLN
27	LY	20	ASN
27	LY	96	HIS
28	LZ	132	GLN
29	La	40	HIS
29	La	60	HIS
29	La	62	HIS
29	La	89	ASN
30	Lb	49	HIS
32	Ld	34	HIS
33	Le	23	HIS
33	Le	80	HIS
34	Lf	20	ASN
34	Lf	56	ASN
35	Lg	100	GLN
40	Ll	4	HIS
41	Lm	104	HIS
41	Lm	120	ASN
43	Lo	51	GLN
46	Lz	21	ASN

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Mol	Chain	Res	Type
46	Lz	119	GLN
46	Lz	143	ASN
50	SB	43	ASN
50	SB	95	ASN
50	SB	101	HIS
50	SB	118	GLN
50	SB	149	GLN
50	SB	202	GLN
50	SB	208	HIS
51	SD	165	ASN
52	SE	36	HIS
52	SE	216	ASN
52	SE	224	ASN
53	SF	51	HIS
53	SF	95	HIS
53	SF	137	GLN
54	SH	25	GLN
54	SH	114	GLN
54	SH	164	ASN
55	SI	84	ASN
55	SI	146	GLN
56	SK	66	HIS
56	SK	73	ASN
57	SL	13	GLN
57	SL	18	GLN
59	SQ	8	GLN
60	SR	56	HIS
62	ST	126	GLN
64	SV	35	ASN
65	SX	20	GLN
65	SX	26	GLN
65	SX	73	GLN
65	SX	92	ASN
70	Sg	51	ASN
70	Sg	133	ASN
70	Sg	147	HIS
70	Sg	162	ASN
72	SG	155	GLN
73	SJ	75	ASN
74	SM	15	ASN
74	SM	52	GLN
74	SM	82	ASN

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Mol	Chain	Res	Type
74	SM	119	GLN
76	SO	32	HIS
77	SW	120	HIS
79	SZ	46	ASN
79	SZ	103	HIS

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	L5	3707/5070 (73%)	1041 (28%)	47 (1%)
2	L7	119/121 (98%)	15 (12%)	0
3	L8	155/157 (98%)	34 (21%)	1 (0%)
47	S2	1714/1869 (91%)	567 (33%)	22 (1%)
48	S6	74/75 (98%)	23 (31%)	2 (2%)
82	Pt	76/77 (98%)	14 (18%)	0
All	All	5845/7369 (79%)	1694 (28%)	72 (1%)

All (1694) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	L5	2	G
1	L5	17	A
1	L5	25	A
1	L5	30	C
1	L5	39	A
1	L5	42	A
1	L5	48	G
1	L5	56	A
1	L5	59	A
1	L5	62	A
1	L5	64	A
1	L5	65	A
1	L5	66	A
1	L5	67	C
1	L5	73	A
1	L5	91	G
1	L5	98	A
1	L5	104	G
1	L5	108	A
1	L5	109	G
1	L5	110	C

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Mol	Chain	Res	Type
1	L5	117	C
1	L5	118	C
1	L5	119	G
1	L5	120	A
1	L5	134	G
1	L5	135	G
1	L5	136	C
1	L5	137	G
1	L5	143	C
1	L5	144	G
1	L5	152	U
1	L5	159	C
1	L5	164	G
1	L5	165	A
1	L5	167	C
1	L5	171	U
1	L5	172	C
1	L5	175	C
1	L5	177	G
1	L5	180	C
1	L5	183	C
1	L5	184	U
1	L5	185	C
1	L5	186	G
1	L5	187	U
1	L5	188	G
1	L5	200	U
1	L5	202	C
1	L5	209	U
1	L5	218	A
1	L5	219	G
1	L5	227	A
1	L5	232	G
1	L5	234	G
1	L5	235	A
1	L5	236	G
1	L5	238	C
1	L5	245	C
1	L5	246	G
1	L5	256	G
1	L5	258	G
1	L5	265	C

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Mol	Chain	Res	Type
1	L5	266	C
1	L5	267	G
1	L5	274	C
1	L5	276	C
1	L5	277	G
1	L5	278	G
1	L5	280	G
1	L5	297	U
1	L5	306	A
1	L5	315	G
1	L5	316	U
1	L5	334	A
1	L5	340	C
1	L5	341	G
1	L5	342	G
1	L5	379	G
1	L5	383	A
1	L5	384	A
1	L5	387	G
1	L5	390	C
1	L5	405	U
1	L5	406	C
1	L5	407	A
1	L5	409	G
1	L5	410	A
1	L5	417	G
1	L5	418	A
1	L5	419	A
1	L5	425	U
1	L5	432	U
1	L5	433	A
1	L5	448	G
1	L5	449	C
1	L5	450	G
1	L5	451	C
1	L5	452	A
1	L5	453	G
1	L5	454	U
1	L5	462	G
1	L5	467	U
1	L5	468	U
1	L5	469	C

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Mol	Chain	Res	Type
1	L5	485	C
1	L5	486	C
1	L5	487	G
1	L5	488	G
1	L5	490	C
1	L5	498	C
1	L5	500	G
1	L5	501	C
1	L5	502	C
1	L5	503	C
1	L5	504	G
1	L5	506	C
1	L5	507	G
1	L5	509	A
1	L5	510	U
1	L5	512	U
1	L5	513	U
1	L5	514	U
1	L5	517	C
1	L5	518	G
1	L5	643	C
1	L5	649	A
1	L5	652	G
1	L5	655	C
1	L5	656	C
1	L5	658	C
1	L5	661	C
1	L5	664	G
1	L5	665	C
1	L5	667	A
1	L5	671	G
1	L5	684	G
1	L5	685	C
1	L5	686	A
1	L5	689	U
1	L5	690	C
1	L5	692	A
1	L5	694	C
1	L5	696	C
1	L5	697	G
1	L5	702	U
1	L5	703	G

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Mol	Chain	Res	Type
1	L5	705	G
1	L5	719	C
1	L5	720	G
1	L5	730	G
1	L5	736	C
1	L5	737	C
1	L5	745	G
1	L5	747	A
1	L5	749	G
1	L5	751	G
1	L5	754	U
1	L5	755	C
1	L5	756	G
1	L5	907	C
1	L5	908	G
1	L5	909	A
1	L5	910	G
1	L5	911	U
1	L5	915	A
1	L5	916	C
1	L5	917	A
1	L5	918	G
1	L5	919	C
1	L5	920	C
1	L5	926	G
1	L5	927	G
1	L5	928	C
1	L5	930	G
1	L5	931	C
1	L5	932	A
1	L5	933	G
1	L5	934	C
1	L5	938	C
1	L5	940	C
1	L5	944	A
1	L5	945	U
1	L5	946	C
1	L5	950	G
1	L5	957	G
1	L5	958	G
1	L5	959	G
1	L5	960	A

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Mol	Chain	Res	Type
1	L5	961	G
1	L5	962	C
1	L5	963	G
1	L5	964	A
1	L5	965	G
1	L5	966	A
1	L5	967	C
1	L5	968	C
1	L5	969	C
1	L5	974	C
1	L5	975	C
1	L5	976	G
1	L5	978	G
1	L5	980	U
1	L5	982	U
1	L5	984	C
1	L5	986	C
1	L5	989	U
1	L5	991	C
1	L5	992	C
1	L5	995	C
1	L5	996	G
1	L5	1049	C
1	L5	1051	G
1	L5	1066	G
1	L5	1070	G
1	L5	1071	C
1	L5	1072	C
1	L5	1073	G
1	L5	1076	C
1	L5	1078	A
1	L5	1079	C
1	L5	1080	C
1	L5	1081	C
1	L5	1083	U
1	L5	1096	C
1	L5	1097	C
1	L5	1100	U
1	L5	1167	C
1	L5	1169	G
1	L5	1170	G
1	L5	1172	C

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Mol	Chain	Res	Type
1	L5	1173	G
1	L5	1179	U
1	L5	1180	C
1	L5	1181	C
1	L5	1182	C
1	L5	1183	C
1	L5	1184	A
1	L5	1185	G
1	L5	1188	C
1	L5	1193	C
1	L5	1202	C
1	L5	1203	G
1	L5	1210	C
1	L5	1211	G
1	L5	1212	G
1	L5	1214	C
1	L5	1215	C
1	L5	1216	C
1	L5	1217	G
1	L5	1219	G
1	L5	1222	A
1	L5	1233	G
1	L5	1237	C
1	L5	1238	A
1	L5	1239	C
1	L5	1243	C
1	L5	1244	G
1	L5	1245	C
1	L5	1250	C
1	L5	1251	C
1	L5	1252	C
1	L5	1254	A
1	L5	1256	G
1	L5	1257	A
1	L5	1260	G
1	L5	1262	G
1	L5	1267	C
1	L5	1268	G
1	L5	1269	G
1	L5	1270	A
1	L5	1271	G
1	L5	1272	C

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Mol	Chain	Res	Type
1	L5	1273	G
1	L5	1275	G
1	L5	1276	C
1	L5	1277	G
1	L5	1279	A
1	L5	1280	C
1	L5	1285	U
1	L5	1288	G
1	L5	1289	C
1	L5	1290	G
1	L5	1293	G
1	L5	1295	C
1	L5	1296	G
1	L5	1297	U
1	L5	1301	C
1	L5	1302	U
1	L5	1303	A
1	L5	1304	C
1	L5	1318	C
1	L5	1322	A
1	L5	1326	A
1	L5	1330	A
1	L5	1337	A
1	L5	1339	U
1	L5	1354	A
1	L5	1358	G
1	L5	1359	G
1	L5	1360	G
1	L5	1364	U
1	L5	1365	C
1	L5	1366	G
1	L5	1367	C
1	L5	1369	C
1	L5	1370	G
1	L5	1377	G
1	L5	1378	C
1	L5	1379	C
1	L5	1381	U
1	L5	1387	A
1	L5	1394	G
1	L5	1397	A
1	L5	1404	G

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Mol	Chain	Res	Type
1	L5	1405	C
1	L5	1407	C
1	L5	1409	C
1	L5	1410	U
1	L5	1411	C
1	L5	1412	G
1	L5	1415	G
1	L5	1416	G
1	L5	1417	C
1	L5	1418	C
1	L5	1420	A
1	L5	1421	G
1	L5	1434	G
1	L5	1435	G
1	L5	1438	U
1	L5	1440	U
1	L5	1444	G
1	L5	1446	C
1	L5	1456	C
1	L5	1457	G
1	L5	1474	C
1	L5	1477	C
1	L5	1480	C
1	L5	1481	C
1	L5	1484	G
1	L5	1486	C
1	L5	1497	A
1	L5	1498	G
1	L5	1501	C
1	L5	1502	G
1	L5	1503	A
1	L5	1523	A
1	L5	1530	G
1	L5	1534	A
1	L5	1539	G
1	L5	1547	A
1	L5	1552	G
1	L5	1564	A
1	L5	1566	C
1	L5	1578	U
1	L5	1591	U
1	L5	1597	G

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Mol	Chain	Res	Type
1	L5	1612	G
1	L5	1613	A
1	L5	1614	C
1	L5	1623	A
1	L5	1624	G
1	L5	1625	G
1	L5	1631	A
1	L5	1633	G
1	L5	1634	A
1	L5	1638	A
1	L5	1641	G
1	L5	1642	A
1	L5	1646	A
1	L5	1651	G
1	L5	1654	G
1	L5	1661	C
1	L5	1676	C
1	L5	1677	U
1	L5	1686	C
1	L5	1691	G
1	L5	1696	C
1	L5	1697	G
1	L5	1698	C
1	L5	1699	A
1	L5	1719	A
1	L5	1721	G
1	L5	1725	U
1	L5	1727	U
1	L5	1729	A
1	L5	1734	G
1	L5	1741	G
1	L5	1742	A
1	L5	1750	G
1	L5	1751	A
1	L5	1753	G
1	L5	1754	U
1	L5	1755	C
1	L5	1756	U
1	L5	1757	U
1	L5	1759	G
1	L5	1761	G
1	L5	1762	C

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Mol	Chain	Res	Type
1	L5	1763	C
1	L5	1764	G
1	L5	1765	A
1	L5	1766	A
1	L5	1767	A
1	L5	1768	C
1	L5	1769	G
1	L5	1771	U
1	L5	1775	A
1	L5	1777	C
1	L5	1778	C
1	L5	1781	U
1	L5	1787	A
1	L5	1788	A
1	L5	1804	A
1	L5	1805	A
1	L5	1806	G
1	L5	1807	C
1	L5	1812	C
1	L5	1820	C
1	L5	1821	G
1	L5	1822	U
1	L5	1832	C
1	L5	1833	G
1	L5	1834	U
1	L5	1835	G
1	L5	1836	G
1	L5	1838	A
1	L5	1842	G
1	L5	1855	G
1	L5	1856	C
1	L5	1867	A
1	L5	1869	G
1	L5	1882	U
1	L5	1889	U
1	L5	1893	C
1	L5	1897	A
1	L5	1910	G
1	L5	1918	U
1	L5	1919	G
1	L5	1920	C
1	L5	1921	C

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Mol	Chain	Res	Type
1	L5	1922	G
1	L5	1925	G
1	L5	1930	U
1	L5	1932	A
1	L5	1936	C
1	L5	1940	G
1	L5	1959	U
1	L5	1960	A
1	L5	1961	G
1	L5	1963	C
1	L5	1966	C
1	L5	1967	A
1	L5	1968	G
1	L5	1969	G
1	L5	1971	C
1	L5	1973	G
1	L5	1975	G
1	L5	1976	G
1	L5	1977	C
1	L5	1979	A
1	L5	1981	G
1	L5	1982	G
1	L5	1983	A
1	L5	1984	A
1	L5	1985	G
1	L5	1987	C
1	L5	1989	G
1	L5	1990	A
1	L5	1991	A
1	L5	1993	C
1	L5	1994	C
1	L5	1997	U
1	L5	1999	A
1	L5	2000	G
1	L5	2001	G
1	L5	2002	A
1	L5	2003	G
1	L5	2005	G
1	L5	2006	U
1	L5	2008	U
1	L5	2009	A
1	L5	2010	A

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Mol	Chain	Res	Type
1	L5	2011	C
1	L5	2012	A
1	L5	2013	A
1	L5	2017	A
1	L5	2018	C
1	L5	2019	C
1	L5	2020	U
1	L5	2026	A
1	L5	2044	U
1	L5	2045	G
1	L5	2046	G
1	L5	2048	U
1	L5	2052	G
1	L5	2055	G
1	L5	2056	G
1	L5	2062	C
1	L5	2064	G
1	L5	2069	A
1	L5	2070	U
1	L5	2084	C
1	L5	2085	G
1	L5	2089	G
1	L5	2090	U
1	L5	2091	C
1	L5	2092	G
1	L5	2093	A
1	L5	2096	G
1	L5	2097	U
1	L5	2099	G
1	L5	2100	A
1	L5	2105	A
1	L5	2107	C
1	L5	2108	G
1	L5	2109	G
1	L5	2110	C
1	L5	2111	G
1	L5	2112	G
1	L5	2113	G
1	L5	2114	G
1	L5	2115	G
1	L5	2116	C
1	L5	2117	G

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Mol	Chain	Res	Type
1	L5	2118	G
1	L5	2119	C
1	L5	2120	G
1	L5	2121	C
1	L5	2122	G
1	L5	2123	C
1	L5	2124	G
1	L5	2125	C
1	L5	2126	G
1	L5	2128	G
1	L5	2244	C
1	L5	2247	C
1	L5	2250	C
1	L5	2251	G
1	L5	2252	G
1	L5	2254	G
1	L5	2255	C
1	L5	2256	C
1	L5	2257	C
1	L5	2259	G
1	L5	2260	C
1	L5	2261	G
1	L5	2262	G
1	L5	2263	A
1	L5	2265	G
1	L5	2268	A
1	L5	2270	G
1	L5	2277	C
1	L5	2278	G
1	L5	2289	C
1	L5	2300	A
1	L5	2301	G
1	L5	2304	U
1	L5	2306	G
1	L5	2313	A
1	L5	2332	A
1	L5	2333	G
1	L5	2345	G
1	L5	2348	G
1	L5	2351	C
1	L5	2361	G
1	L5	2362	U

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Mol	Chain	Res	Type
1	L5	2364	G
1	L5	2382	A
1	L5	2390	G
1	L5	2395	A
1	L5	2397	G
1	L5	2404	A
1	L5	2412	A
1	L5	2417	A
1	L5	2422	C
1	L5	2425	U
1	L5	2443	G
1	L5	2448	G
1	L5	2450	G
1	L5	2454	U
1	L5	2465	C
1	L5	2468	U
1	L5	2469	C
1	L5	2471	G
1	L5	2474	G
1	L5	2475	G
1	L5	2483	G
1	L5	2484	A
1	L5	2488	C
1	L5	2489	C
1	L5	2490	U
1	L5	2491	C
1	L5	2492	C
1	L5	2502	G
1	L5	2503	G
1	L5	2504	C
1	L5	2505	C
1	L5	2506	G
1	L5	2511	A
1	L5	2513	A
1	L5	2522	G
1	L5	2526	C
1	L5	2529	A
1	L5	2537	A
1	L5	2544	G
1	L5	2545	U
1	L5	2546	G
1	L5	2547	G

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Mol	Chain	Res	Type
1	L5	2553	A
1	L5	2554	U
1	L5	2556	G
1	L5	2557	G
1	L5	2569	G
1	L5	2570	U
1	L5	2572	C
1	L5	2573	A
1	L5	2583	C
1	L5	2586	G
1	L5	2587	A
1	L5	2588	C
1	L5	2601	A
1	L5	2609	G
1	L5	2618	G
1	L5	2627	C
1	L5	2637	U
1	L5	2638	G
1	L5	2640	G
1	L5	2648	G
1	L5	2649	G
1	L5	2653	C
1	L5	2659	A
1	L5	2662	G
1	L5	2670	C
1	L5	2675	G
1	L5	2679	G
1	L5	2687	U
1	L5	2696	A
1	L5	2705	G
1	L5	2708	U
1	L5	2710	C
1	L5	2711	G
1	L5	2712	G
1	L5	2714	G
1	L5	2717	G
1	L5	2719	C
1	L5	2723	U
1	L5	2725	A
1	L5	2726	G
1	L5	2729	C
1	L5	2739	C

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Mol	Chain	Res	Type
1	L5	2740	U
1	L5	2743	A
1	L5	2752	G
1	L5	2753	G
1	L5	2754	G
1	L5	2756	G
1	L5	2761	U
1	L5	2763	U
1	L5	2768	C
1	L5	2769	U
1	L5	2776	G
1	L5	2783	A
1	L5	2787	A
1	L5	2788	U
1	L5	2794	C
1	L5	2797	C
1	L5	2814	C
1	L5	2816	G
1	L5	2822	G
1	L5	2826	U
1	L5	2827	G
1	L5	2828	U
1	L5	2829	U
1	L5	2855	G
1	L5	2857	A
1	L5	2859	G
1	L5	2860	C
1	L5	2870	A
1	L5	2874	U
1	L5	2877	G
1	L5	2892	C
1	L5	2902	G
1	L5	2903	G
1	L5	2904	U
1	L5	2905	C
1	L5	2906	G
1	L5	2907	G
1	L5	3589	G
1	L5	3593	C
1	L5	3596	A
1	L5	3597	G
1	L5	3606	U

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Mol	Chain	Res	Type
1	L5	3616	U
1	L5	3625	G
1	L5	3626	G
1	L5	3635	A
1	L5	3642	A
1	L5	3644	U
1	L5	3646	A
1	L5	3661	G
1	L5	3662	A
1	L5	3664	G
1	L5	3669	G
1	L5	3670	C
1	L5	3671	G
1	L5	3673	C
1	L5	3674	G
1	L5	3690	U
1	L5	3696	C
1	L5	3709	U
1	L5	3710	G
1	L5	3711	A
1	L5	3712	A
1	L5	3713	U
1	L5	3714	G
1	L5	3727	A
1	L5	3735	G
1	L5	3748	A
1	L5	3750	G
1	L5	3753	G
1	L5	3756	A
1	L5	3757	G
1	L5	3758	U
1	L5	3759	A
1	L5	3760	A
1	L5	3761	C
1	L5	3762	U
1	L5	3766	A
1	L5	3767	C
1	L5	3768	U
1	L5	3769	C
1	L5	3770	U
1	L5	3772	U
1	L5	3776	G

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Mol	Chain	Res	Type
1	L5	3777	G
1	L5	3785	A
1	L5	3786	U
1	L5	3789	C
1	L5	3811	G
1	L5	3814	U
1	L5	3817	A
1	L5	3818	U
1	L5	3819	G
1	L5	3838	U
1	L5	3839	G
1	L5	3840	U
1	L5	3841	C
1	L5	3851	U
1	L5	3867	A
1	L5	3869	C
1	L5	3877	A
1	L5	3878	C
1	L5	3879	G
1	L5	3881	G
1	L5	3885	G
1	L5	3889	G
1	L5	3890	A
1	L5	3892	U
1	L5	3897	G
1	L5	3901	A
1	L5	3905	A
1	L5	3906	A
1	L5	3907	G
1	L5	3908	A
1	L5	3915	U
1	L5	3916	G
1	L5	3917	A
1	L5	3921	U
1	L5	3934	G
1	L5	3938	G
1	L5	3939	G
1	L5	3942	A
1	L5	3947	A
1	L5	3949	A
1	L5	3953	G
1	L5	3956	G

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Mol	Chain	Res	Type
1	L5	3957	U
1	L5	3958	G
1	L5	3960	A
1	L5	3961	G
1	L5	3962	A
1	L5	3963	A
1	L5	3965	A
1	L5	3968	U
1	L5	3969	G
1	L5	3972	A
1	L5	3973	G
1	L5	3975	C
1	L5	3977	C
1	L5	4036	G
1	L5	4039	G
1	L5	4042	G
1	L5	4043	G
1	L5	4044	U
1	L5	4046	A
1	L5	4047	A
1	L5	4048	A
1	L5	4049	U
1	L5	4050	A
1	L5	4051	C
1	L5	4052	C
1	L5	4054	C
1	L5	4055	U
1	L5	4058	U
1	L5	4059	C
1	L5	4062	A
1	L5	4064	C
1	L5	4065	G
1	L5	4067	U
1	L5	4076	G
1	L5	4084	G
1	L5	4086	G
1	L5	4092	G
1	L5	4093	G
1	L5	4096	C
1	L5	4103	C
1	L5	4104	G
1	L5	4107	G

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Mol	Chain	Res	Type
1	L5	4110	C
1	L5	4115	G
1	L5	4117	U
1	L5	4119	C
1	L5	4120	U
1	L5	4121	G
1	L5	4122	G
1	L5	4123	C
1	L5	4127	A
1	L5	4138	C
1	L5	4139	G
1	L5	4140	C
1	L5	4141	G
1	L5	4142	C
1	L5	4143	G
1	L5	4144	C
1	L5	4151	G
1	L5	4158	C
1	L5	4162	C
1	L5	4163	U
1	L5	4168	G
1	L5	4170	A
1	L5	4183	G
1	L5	4191	G
1	L5	4203	A
1	L5	4209	G
1	L5	4212	A
1	L5	4222	G
1	L5	4229	U
1	L5	4234	A
1	L5	4250	G
1	L5	4251	A
1	L5	4254	G
1	L5	4255	A
1	L5	4256	A
1	L5	4258	C
1	L5	4268	A
1	L5	4273	A
1	L5	4277	G
1	L5	4280	A
1	L5	4281	A
1	L5	4288	C

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Mol	Chain	Res	Type
1	L5	4291	G
1	L5	4296	U
1	L5	4305	G
1	L5	4306	U
1	L5	4314	C
1	L5	4317	A
1	L5	4318	C
1	L5	4329	G
1	L5	4330	G
1	L5	4332	C
1	L5	4339	A
1	L5	4346	U
1	L5	4349	C
1	L5	4350	C
1	L5	4374	U
1	L5	4377	G
1	L5	4378	A
1	L5	4380	A
1	L5	4387	C
1	L5	4394	A
1	L5	4396	A
1	L5	4398	C
1	L5	4414	A
1	L5	4415	A
1	L5	4419	U
1	L5	4420	U
1	L5	4422	A
1	L5	4427	G
1	L5	4433	G
1	L5	4438	U
1	L5	4444	C
1	L5	4448	G
1	L5	4449	A
1	L5	4453	C
1	L5	4464	A
1	L5	4465	U
1	L5	4466	C
1	L5	4475	G
1	L5	4476	C
1	L5	4478	G
1	L5	4488	A
1	L5	4500	U

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Mol	Chain	Res	Type
1	L5	4512	U
1	L5	4513	A
1	L5	4519	C
1	L5	4524	G
1	L5	4528	G
1	L5	4534	G
1	L5	4545	G
1	L5	4548	A
1	L5	4549	G
1	L5	4560	C
1	L5	4567	G
1	L5	4571	A
1	L5	4573	G
1	L5	4575	G
1	L5	4582	C
1	L5	4589	A
1	L5	4590	A
1	L5	4599	A
1	L5	4600	G
1	L5	4601	U
1	L5	4609	G
1	L5	4617	G
1	L5	4627	U
1	L5	4636	U
1	L5	4637	G
1	L5	4639	G
1	L5	4647	G
1	L5	4656	A
1	L5	4670	C
1	L5	4672	A
1	L5	4678	G
1	L5	4693	C
1	L5	4694	G
1	L5	4695	C
1	L5	4696	C
1	L5	4697	U
1	L5	4699	U
1	L5	4700	A
1	L5	4707	A
1	L5	4708	A
1	L5	4709	U
1	L5	4730	C

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Mol	Chain	Res	Type
1	L5	4732	G
1	L5	4733	C
1	L5	4738	C
1	L5	4739	C
1	L5	4744	A
1	L5	4749	C
1	L5	4750	G
1	L5	4751	G
1	L5	4753	U
1	L5	4756	C
1	L5	4757	C
1	L5	4758	U
1	L5	4760	G
1	L5	4764	A
1	L5	4770	U
1	L5	4771	C
1	L5	4772	C
1	L5	4775	C
1	L5	4860	G
1	L5	4861	G
1	L5	4862	G
1	L5	4865	C
1	L5	4869	U
1	L5	4870	G
1	L5	4871	C
1	L5	4872	G
1	L5	4873	G
1	L5	4874	A
1	L5	4876	U
1	L5	4878	C
1	L5	4880	C
1	L5	4882	U
1	L5	4883	C
1	L5	4884	G
1	L5	4888	U
1	L5	4890	G
1	L5	4894	A
1	L5	4896	G
1	L5	4897	G
1	L5	4900	C
1	L5	4901	G
1	L5	4902	C

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Mol	Chain	Res	Type
1	L5	4909	A
1	L5	4910	G
1	L5	4912	G
1	L5	4913	G
1	L5	4918	C
1	L5	4923	C
1	L5	4926	C
1	L5	4927	G
1	L5	4936	G
1	L5	4937	C
1	L5	4939	C
1	L5	4941	G
1	L5	4944	C
1	L5	4945	G
1	L5	4946	U
1	L5	4949	G
1	L5	4950	U
1	L5	4951	G
1	L5	4952	G
1	L5	4954	G
1	L5	4956	A
1	L5	4958	C
1	L5	4959	U
1	L5	4960	G
1	L5	4963	G
1	L5	4964	C
1	L5	4973	U
1	L5	4976	U
1	L5	4985	U
1	L5	4986	G
1	L5	4988	U
1	L5	4989	U
1	L5	4990	C
1	L5	4991	U
1	L5	4992	G
1	L5	5006	U
1	L5	5009	G
1	L5	5011	A
1	L5	5014	A
1	L5	5017	G
1	L5	5022	U
1	L5	5024	C

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Mol	Chain	Res	Type
1	L5	5025	C
1	L5	5026	U
1	L5	5027	C
1	L5	5028	G
1	L5	5034	A
1	L5	5041	G
1	L5	5050	C
1	L5	5054	C
1	L5	5055	G
1	L5	5058	A
1	L5	5061	A
1	L5	5068	G
2	L7	7	G
2	L7	22	A
2	L7	24	C
2	L7	33	U
2	L7	40	U
2	L7	54	A
2	L7	64	G
2	L7	90	A
2	L7	97	G
2	L7	100	A
2	L7	103	A
2	L7	106	G
2	L7	111	C
2	L7	117	G
2	L7	120	U
3	L8	2	G
3	L8	23	C
3	L8	34	U
3	L8	35	C
3	L8	48	A
3	L8	59	A
3	L8	63	U
3	L8	68	G
3	L8	71	A
3	L8	76	C
3	L8	80	A
3	L8	82	A
3	L8	83	C
3	L8	84	A
3	L8	86	U

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Mol	Chain	Res	Type
3	L8	87	G
3	L8	88	A
3	L8	103	A
3	L8	105	C
3	L8	108	A
3	L8	109	C
3	L8	110	U
3	L8	114	G
3	L8	118	C
3	L8	123	U
3	L8	124	U
3	L8	125	C
3	L8	126	C
3	L8	127	U
3	L8	129	C
3	L8	150	C
3	L8	151	G
3	L8	153	C
3	L8	156	U
47	S2	2	A
47	S2	3	C
47	S2	4	C
47	S2	9	U
47	S2	25	A
47	S2	27	A
47	S2	33	G
47	S2	41	G
47	S2	42	A
47	S2	44	U
47	S2	46	A
47	S2	52	G
47	S2	56	G
47	S2	60	A
47	S2	64	A
47	S2	67	C
47	S2	68	A
47	S2	72	C
47	S2	73	C
47	S2	74	G
47	S2	76	U
47	S2	77	A
47	S2	78	C

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Mol	Chain	Res	Type
47	S2	79	A
47	S2	81	U
47	S2	84	A
47	S2	103	A
47	S2	113	G
47	S2	115	U
47	S2	126	G
47	S2	127	C
47	S2	140	C
47	S2	141	A
47	S2	142	C
47	S2	148	U
47	S2	151	C
47	S2	153	G
47	S2	154	U
47	S2	155	G
47	S2	156	G
47	S2	158	A
47	S2	159	A
47	S2	160	U
47	S2	161	U
47	S2	163	U
47	S2	166	A
47	S2	170	A
47	S2	175	A
47	S2	177	G
47	S2	181	A
47	S2	184	G
47	S2	185	G
47	S2	188	C
47	S2	190	G
47	S2	191	A
47	S2	192	C
47	S2	198	U
47	S2	201	C
47	S2	202	G
47	S2	208	G
47	S2	209	A
47	S2	210	U
47	S2	211	G
47	S2	214	U
47	S2	215	G

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Mol	Chain	Res	Type
47	S2	220	U
47	S2	221	A
47	S2	291	G
47	S2	292	A
47	S2	293	C
47	S2	295	C
47	S2	296	U
47	S2	304	C
47	S2	306	C
47	S2	307	G
47	S2	308	G
47	S2	309	G
47	S2	312	G
47	S2	314	U
47	S2	319	C
47	S2	320	G
47	S2	321	C
47	S2	322	C
47	S2	323	C
47	S2	324	C
47	S2	325	C
47	S2	326	C
47	S2	328	U
47	S2	329	G
47	S2	330	G
47	S2	334	C
47	S2	338	G
47	S2	339	A
47	S2	340	C
47	S2	341	C
47	S2	343	A
47	S2	360	A
47	S2	361	U
47	S2	362	C
47	S2	364	A
47	S2	369	C
47	S2	370	G
47	S2	384	U
47	S2	385	G
47	S2	386	C
47	S2	400	C
47	S2	407	G

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Mol	Chain	Res	Type
47	S2	408	A
47	S2	409	C
47	S2	413	G
47	S2	418	A
47	S2	426	A
47	S2	429	C
47	S2	434	G
47	S2	435	A
47	S2	438	G
47	S2	441	C
47	S2	448	A
47	S2	450	C
47	S2	452	G
47	S2	465	A
47	S2	466	G
47	S2	469	A
47	S2	472	C
47	S2	473	A
47	S2	474	G
47	S2	482	G
47	S2	487	U
47	S2	488	U
47	S2	489	A
47	S2	492	C
47	S2	493	A
47	S2	495	U
47	S2	496	C
47	S2	502	C
47	S2	503	C
47	S2	504	G
47	S2	516	A
47	S2	517	C
47	S2	519	A
47	S2	529	A
47	S2	530	U
47	S2	532	C
47	S2	534	G
47	S2	537	C
47	S2	538	U
47	S2	539	C
47	S2	540	U
47	S2	544	G

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Mol	Chain	Res	Type
47	S2	545	A
47	S2	547	G
47	S2	550	C
47	S2	556	U
47	S2	557	U
47	S2	559	G
47	S2	560	A
47	S2	563	G
47	S2	574	A
47	S2	575	A
47	S2	582	C
47	S2	584	G
47	S2	585	C
47	S2	587	A
47	S2	588	G
47	S2	589	G
47	S2	590	A
47	S2	591	U
47	S2	592	C
47	S2	593	C
47	S2	596	U
47	S2	604	A
47	S2	605	A
47	S2	608	C
47	S2	614	C
47	S2	617	G
47	S2	627	U
47	S2	628	A
47	S2	629	A
47	S2	631	U
47	S2	632	C
47	S2	643	A
47	S2	644	G
47	S2	650	A
47	S2	651	U
47	S2	656	G
47	S2	659	G
47	S2	660	C
47	S2	666	U
47	S2	668	A
47	S2	669	A
47	S2	671	A

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Mol	Chain	Res	Type
47	S2	672	A
47	S2	687	C
47	S2	688	U
47	S2	689	U
47	S2	690	G
47	S2	691	G
47	S2	692	G
47	S2	695	C
47	S2	696	G
47	S2	697	G
47	S2	698	G
47	S2	731	G
47	S2	733	C
47	S2	734	C
47	S2	735	C
47	S2	736	C
47	S2	737	G
47	S2	738	C
47	S2	739	C
47	S2	745	C
47	S2	746	C
47	S2	747	U
47	S2	749	U
47	S2	750	C
47	S2	751	G
47	S2	752	G
47	S2	753	C
47	S2	787	G
47	S2	788	G
47	S2	789	G
47	S2	790	C
47	S2	791	C
47	S2	795	A
47	S2	796	G
47	S2	797	C
47	S2	798	A
47	S2	800	U
47	S2	811	A
47	S2	812	A
47	S2	813	A
47	S2	818	A
47	S2	821	G

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Mol	Chain	Res	Type
47	S2	822	U
47	S2	830	A
47	S2	834	C
47	S2	835	C
47	S2	836	G
47	S2	837	A
47	S2	838	G
47	S2	839	C
47	S2	840	C
47	S2	842	C
47	S2	847	A
47	S2	848	U
47	S2	853	C
47	S2	869	A
47	S2	870	A
47	S2	873	G
47	S2	874	G
47	S2	876	C
47	S2	877	C
47	S2	878	G
47	S2	879	C
47	S2	881	G
47	S2	883	U
47	S2	888	U
47	S2	890	U
47	S2	891	G
47	S2	892	U
47	S2	893	U
47	S2	894	G
47	S2	896	U
47	S2	897	U
47	S2	898	U
47	S2	899	U
47	S2	900	C
47	S2	901	G
47	S2	903	A
47	S2	904	A
47	S2	905	C
47	S2	907	G
47	S2	908	A
47	S2	909	G
47	S2	913	A

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Mol	Chain	Res	Type
47	S2	914	U
47	S2	917	U
47	S2	920	A
47	S2	930	C
47	S2	933	G
47	S2	934	G
47	S2	954	U
47	S2	955	A
47	S2	958	G
47	S2	959	G
47	S2	961	G
47	S2	963	A
47	S2	965	U
47	S2	970	G
47	S2	971	G
47	S2	972	A
47	S2	973	C
47	S2	981	A
47	S2	990	A
47	S2	992	A
47	S2	997	A
47	S2	999	G
47	S2	1017	U
47	S2	1023	A
47	S2	1027	A
47	S2	1028	A
47	S2	1042	A
47	S2	1060	A
47	S2	1062	A
47	S2	1065	G
47	S2	1067	C
47	S2	1083	A
47	S2	1085	C
47	S2	1110	G
47	S2	1113	A
47	S2	1114	U
47	S2	1115	U
47	S2	1116	C
47	S2	1117	C
47	S2	1118	C
47	S2	1119	A
47	S2	1138	C

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Mol	Chain	Res	Type
47	S2	1139	C
47	S2	1140	G
47	S2	1148	A
47	S2	1149	A
47	S2	1153	C
47	S2	1154	U
47	S2	1157	G
47	S2	1170	A
47	S2	1171	G
47	S2	1172	U
47	S2	1181	A
47	S2	1195	A
47	S2	1207	G
47	S2	1208	A
47	S2	1211	G
47	S2	1212	G
47	S2	1214	A
47	S2	1215	C
47	S2	1217	A
47	S2	1224	G
47	S2	1238	U
47	S2	1240	A
47	S2	1241	A
47	S2	1243	U
47	S2	1251	A
47	S2	1253	A
47	S2	1256	G
47	S2	1257	G
47	S2	1259	A
47	S2	1264	C
47	S2	1265	A
47	S2	1269	G
47	S2	1270	G
47	S2	1271	C
47	S2	1274	G
47	S2	1275	G
47	S2	1276	A
47	S2	1277	C
47	S2	1280	G
47	S2	1281	G
47	S2	1282	A
47	S2	1283	C

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Mol	Chain	Res	Type
47	S2	1284	A
47	S2	1286	G
47	S2	1287	A
47	S2	1288	U
47	S2	1289	U
47	S2	1290	G
47	S2	1291	A
47	S2	1292	C
47	S2	1294	G
47	S2	1296	U
47	S2	1299	A
47	S2	1301	A
47	S2	1302	G
47	S2	1303	C
47	S2	1305	C
47	S2	1306	U
47	S2	1307	U
47	S2	1308	U
47	S2	1309	C
47	S2	1310	U
47	S2	1311	C
47	S2	1313	A
47	S2	1315	U
47	S2	1317	C
47	S2	1318	G
47	S2	1321	G
47	S2	1324	G
47	S2	1330	G
47	S2	1331	C
47	S2	1332	A
47	S2	1337	C
47	S2	1341	C
47	S2	1342	U
47	S2	1343	U
47	S2	1363	C
47	S2	1371	U
47	S2	1372	U
47	S2	1373	C
47	S2	1378	A
47	S2	1393	G
47	S2	1396	A
47	S2	1397	U

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Mol	Chain	Res	Type
47	S2	1398	G
47	S2	1401	A
47	S2	1403	C
47	S2	1404	U
47	S2	1407	U
47	S2	1409	A
47	S2	1410	C
47	S2	1412	C
47	S2	1413	G
47	S2	1414	A
47	S2	1415	C
47	S2	1416	C
47	S2	1418	C
47	S2	1419	C
47	S2	1420	G
47	S2	1422	G
47	S2	1423	C
47	S2	1424	G
47	S2	1425	G
47	S2	1427	C
47	S2	1428	G
47	S2	1429	G
47	S2	1431	G
47	S2	1432	U
47	S2	1434	C
47	S2	1436	C
47	S2	1438	A
47	S2	1440	C
47	S2	1442	U
47	S2	1447	G
47	S2	1448	A
47	S2	1449	G
47	S2	1450	G
47	S2	1454	A
47	S2	1455	A
47	S2	1463	U
47	S2	1464	C
47	S2	1468	C
47	S2	1471	C
47	S2	1475	G
47	S2	1476	A
47	S2	1477	U

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Mol	Chain	Res	Type
47	S2	1480	A
47	S2	1487	A
47	S2	1489	A
47	S2	1490	G
47	S2	1493	C
47	S2	1494	U
47	S2	1497	G
47	S2	1498	A
47	S2	1505	U
47	S2	1506	A
47	S2	1507	G
47	S2	1509	U
47	S2	1510	G
47	S2	1512	C
47	S2	1513	C
47	S2	1515	G
47	S2	1517	G
47	S2	1520	G
47	S2	1521	C
47	S2	1522	A
47	S2	1523	C
47	S2	1527	C
47	S2	1533	A
47	S2	1535	U
47	S2	1536	G
47	S2	1538	C
47	S2	1543	U
47	S2	1545	A
47	S2	1546	G
47	S2	1548	G
47	S2	1550	G
47	S2	1552	G
47	S2	1553	C
47	S2	1554	C
47	S2	1555	U
47	S2	1556	A
47	S2	1557	C
47	S2	1558	C
47	S2	1563	G
47	S2	1566	G
47	S2	1567	G
47	S2	1568	C

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Mol	Chain	Res	Type
47	S2	1569	A
47	S2	1570	G
47	S2	1575	G
47	S2	1579	A
47	S2	1580	A
47	S2	1585	U
47	S2	1586	U
47	S2	1587	G
47	S2	1588	A
47	S2	1589	A
47	S2	1591	C
47	S2	1598	G
47	S2	1599	U
47	S2	1600	G
47	S2	1612	G
47	S2	1621	U
47	S2	1623	A
47	S2	1626	C
47	S2	1634	A
47	S2	1636	G
47	S2	1637	A
47	S2	1638	G
47	S2	1639	G
47	S2	1640	A
47	S2	1643	U
47	S2	1644	C
47	S2	1648	G
47	S2	1654	G
47	S2	1655	C
47	S2	1661	A
47	S2	1662	U
47	S2	1663	A
47	S2	1665	G
47	S2	1672	U
47	S2	1695	A
47	S2	1698	C
47	S2	1714	U
47	S2	1719	A
47	S2	1721	U
47	S2	1722	G
47	S2	1739	C
47	S2	1742	C

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Mol	Chain	Res	Type
47	S2	1743	G
47	S2	1744	G
47	S2	1745	A
47	S2	1746	U
47	S2	1749	G
47	S2	1751	C
47	S2	1752	C
47	S2	1754	G
47	S2	1758	G
47	S2	1772	C
47	S2	1773	C
47	S2	1775	U
47	S2	1777	G
47	S2	1781	A
47	S2	1783	C
47	S2	1784	G
47	S2	1786	U
47	S2	1789	G
47	S2	1805	G
47	S2	1812	U
47	S2	1813	A
47	S2	1814	G
47	S2	1823	A
47	S2	1824	A
47	S2	1825	A
47	S2	1826	G
47	S2	1831	A
47	S2	1838	U
47	S2	1839	U
47	S2	1849	G
47	S2	1850	A
47	S2	1851	A
47	S2	1852	C
47	S2	1856	C
47	S2	1861	G
47	S2	1862	G
47	S2	1863	A
47	S2	1865	C
47	S2	1868	U
47	S2	1869	A
48	S6	17	C
48	S6	18	G

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Mol	Chain	Res	Type
48	S6	20	A
48	S6	21	A
48	S6	22	G
48	S6	23	C
48	S6	31	G
48	S6	33	C
48	S6	34	C
48	S6	35	A
48	S6	36	U
48	S6	37	A
48	S6	39	C
48	S6	40	C
48	S6	41	C
48	S6	45	G
48	S6	46	G
48	S6	47	U
48	S6	51	U
48	S6	58	A
48	S6	59	A
48	S6	73	A
48	S6	76	A
82	Pt	2	G
82	Pt	10	G
82	Pt	16	C
82	Pt	17	C
82	Pt	18	C
82	Pt	19	G
82	Pt	20	G
82	Pt	21	H2U
82	Pt	22	A
82	Pt	43	G
82	Pt	48	U
82	Pt	75	C
82	Pt	76	C
82	Pt	77	A

All (72) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	L5	201	C
1	L5	406	C
1	L5	417	G

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Mol	Chain	Res	Type
1	L5	693	C
1	L5	930	G
1	L5	931	C
1	L5	956	A
1	L5	958	G
1	L5	974	C
1	L5	1072	C
1	L5	1238	A
1	L5	1329	G
1	L5	1359	G
1	L5	1410	U
1	L5	1455	G
1	L5	1633	G
1	L5	2068	C
1	L5	2096	G
1	L5	2119	C
1	L5	2120	G
1	L5	2124	G
1	L5	2361	G
1	L5	2389	A
1	L5	2467	U
1	L5	2639	U
1	L5	2695	A
1	L5	2775	C
1	L5	2828	U
1	L5	3625	G
1	L5	3673	C
1	L5	3713	U
1	L5	3767	C
1	L5	3784	A
1	L5	3810	C
1	L5	3888	G
1	L5	3955	G
1	L5	3956	G
1	L5	4419	U
1	L5	4600	G
1	L5	4731	G
1	L5	4860	G
1	L5	4889	G
1	L5	4909	A
1	L5	4948	C
1	L5	4991	U

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Mol	Chain	Res	Type
1	L5	5005	G
1	L5	5027	C
3	L8	87	G
47	S2	24	C
47	S2	141	A
47	S2	213	G
47	S2	322	C
47	S2	417	C
47	S2	465	A
47	S2	604	A
47	S2	668	A
47	S2	688	U
47	S2	795	A
47	S2	833	C
47	S2	868	G
47	S2	912	C
47	S2	980	A
47	S2	1061	U
47	S2	1137	U
47	S2	1293	A
47	S2	1419	C
47	S2	1664	A
47	S2	1813	A
47	S2	1823	A
47	S2	1860	A
48	S6	33	C
48	S6	34	C

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
82	H2U	Pt	21	82	18,21,22	0.45	0	21,30,33	1.04	1 (4%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
82	4SU	Pt	8	82	18,21,22	4.29	8 (44%)	26,30,33	2.21	5 (19%)
82	OMC	Pt	33	47,82	19,22,23	0.54	0	26,31,34	0.78	1 (3%)
82	PSU	Pt	56	82	18,21,22	1.13	1 (5%)	22,30,33	1.73	4 (18%)
82	G7M	Pt	47	82	23,26,27	2.93	8 (34%)	35,39,42	2.18	10 (28%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
82	H2U	Pt	21	82	-	3/7/38/39	0/2/2/2
82	4SU	Pt	8	82	-	1/7/25/26	0/2/2/2
82	OMC	Pt	33	47,82	-	1/9/27/28	0/2/2/2
82	PSU	Pt	56	82	-	0/7/25/26	0/2/2/2
82	G7M	Pt	47	82	-	0/7/25/26	0/3/3/3

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
82	Pt	8	4SU	C2-N1	9.22	1.53	1.38
82	Pt	8	4SU	C4-N3	8.58	1.46	1.37
82	Pt	8	4SU	C2-N3	7.06	1.50	1.38
82	Pt	47	G7M	C2-N2	6.93	1.50	1.34
82	Pt	8	4SU	C5-C4	6.86	1.51	1.42
82	Pt	8	4SU	C6-C5	6.49	1.50	1.35
82	Pt	47	G7M	C2-N3	6.45	1.48	1.33
82	Pt	47	G7M	C4-N3	6.10	1.48	1.34
82	Pt	47	G7M	C5-N7	-4.92	1.33	1.39
82	Pt	8	4SU	C4-S4	-4.31	1.60	1.68
82	Pt	47	G7M	C5-C6	4.06	1.54	1.43
82	Pt	56	PSU	C6-C5	3.75	1.39	1.35
82	Pt	47	G7M	C6-N1	2.80	1.44	1.38
82	Pt	47	G7M	C2-N1	2.64	1.44	1.37
82	Pt	8	4SU	C6-N1	2.63	1.44	1.38
82	Pt	47	G7M	O6-C6	-2.52	1.18	1.23
82	Pt	8	4SU	O2-C2	-2.49	1.18	1.23

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
82	Pt	8	4SU	C4-N3-C2	-7.76	119.80	127.34
82	Pt	47	G7M	CN7-N7-C5	5.99	134.21	126.77
82	Pt	8	4SU	C5-C4-N3	5.33	119.64	114.69
82	Pt	47	G7M	CN7-N7-C8	-4.57	117.79	124.84
82	Pt	56	PSU	C4-N3-C2	-4.51	119.83	126.34
82	Pt	47	G7M	C2-N3-C4	4.41	120.15	112.30
82	Pt	56	PSU	N1-C2-N3	4.37	120.08	115.13
82	Pt	47	G7M	C5-C4-N3	-4.18	120.14	128.15
82	Pt	47	G7M	C5-C6-N1	3.96	120.06	111.79
82	Pt	8	4SU	N3-C2-N1	3.83	119.97	114.89
82	Pt	47	G7M	O6-C6-C5	-3.54	120.08	128.06
82	Pt	8	4SU	C5-C4-S4	-3.50	119.96	124.47
82	Pt	21	H2U	C5-C4-N3	-3.11	113.16	116.65
82	Pt	47	G7M	C2-N1-C6	-3.06	119.53	125.10
82	Pt	47	G7M	N9-C4-N3	3.03	132.01	125.94
82	Pt	47	G7M	C1'-N9-C4	-2.95	117.73	126.50
82	Pt	56	PSU	O2-C2-N1	-2.51	120.03	122.79
82	Pt	33	OMC	C1'-N1-C2	2.27	123.49	118.42
82	Pt	47	G7M	C1'-N9-C8	2.21	134.18	126.74
82	Pt	8	4SU	O2-C2-N1	-2.17	119.91	122.79
82	Pt	56	PSU	C6-N1-C2	-2.16	120.47	122.68

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
82	Pt	21	H2U	C3'-C4'-C5'-O5'
82	Pt	33	OMC	C1'-C2'-O2'-CM2
82	Pt	21	H2U	O4'-C4'-C5'-O5'
82	Pt	21	H2U	C4'-C5'-O5'-P
82	Pt	8	4SU	O4'-C4'-C5'-O5'

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
82	Pt	21	H2U	2	0
82	Pt	33	OMC	1	0
82	Pt	47	G7M	1	0

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 246 ligands modelled in this entry, 245 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	$\#\|Z\| > 2$
84	A1E6S	L5	5245	-	26,33,33	5.20	13 (50%)	12,52,52	2.11	4 (33%)

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
84	A1E6S	L5	5245	-	-	3/7/76/76	0/3/5/5

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
84	L5	5245	A1E6S	C17-C18	23.09	1.52	1.33
84	L5	5245	A1E6S	C11-C10	5.87	1.59	1.53
84	L5	5245	A1E6S	C12-C11	4.63	1.61	1.54
84	L5	5245	A1E6S	C03-C04	-4.27	1.46	1.50
84	L5	5245	A1E6S	C16-C17	3.79	1.56	1.50
84	L5	5245	A1E6S	C12-C13	3.63	1.59	1.53
84	L5	5245	A1E6S	O19-C14	-3.54	1.15	1.21
84	L5	5245	A1E6S	C03-C16	3.24	1.60	1.55
84	L5	5245	A1E6S	O12-C07	3.21	1.48	1.43
84	L5	5245	A1E6S	O12-C10	3.04	1.50	1.43
84	L5	5245	A1E6S	O17-C13	-2.62	1.37	1.42
84	L5	5245	A1E6S	O22-C05	-2.12	1.38	1.42
84	L5	5245	A1E6S	C19-C18	2.02	1.53	1.50

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
84	L5	5245	A1E6S	C02-C03-C04	5.47	108.28	100.64
84	L5	5245	A1E6S	O12-C10-C09	-2.54	100.17	104.01
84	L5	5245	A1E6S	C19-C20-C03	2.46	116.03	112.02
84	L5	5245	A1E6S	C07-O12-C10	2.06	112.28	107.71

There are no chirality outliers.

All (3) torsion outliers are listed below:

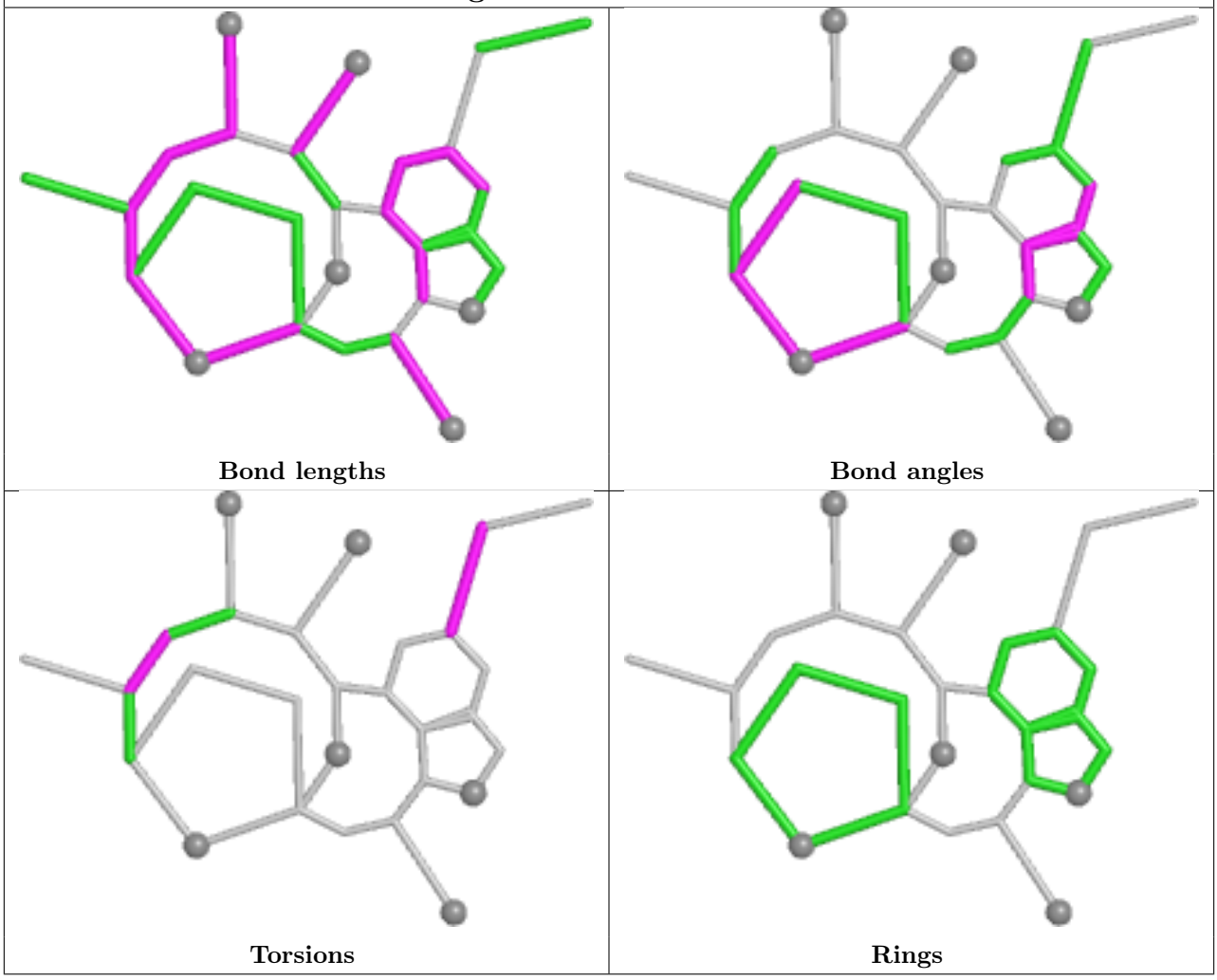
Mol	Chain	Res	Type	Atoms
84	L5	5245	A1E6S	C17-C18-C21-C22
84	L5	5245	A1E6S	C19-C18-C21-C22
84	L5	5245	A1E6S	C10-C11-C12-C13

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 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.

Ligand A1E6S L5 5245



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
43	Lo	1
66	Sa	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	Lo	105:GLN	C	106:PHE	N	6.09

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	Sa	99:PRO	C	100:ARG	N	3.64

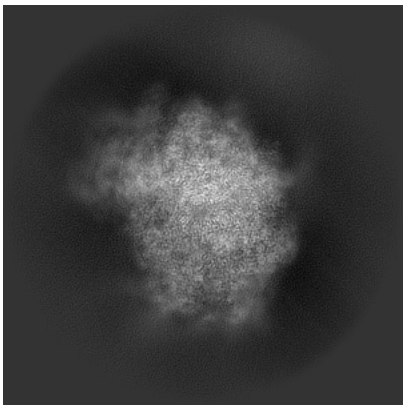
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-66929. These allow visual inspection of the internal detail of the map and identification of artifacts.

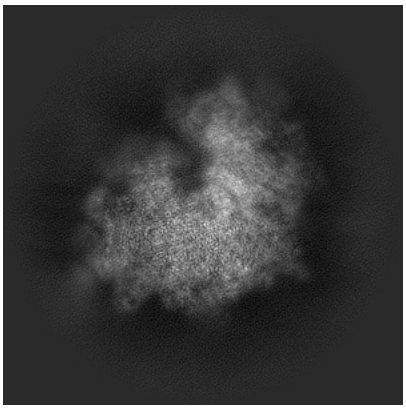
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

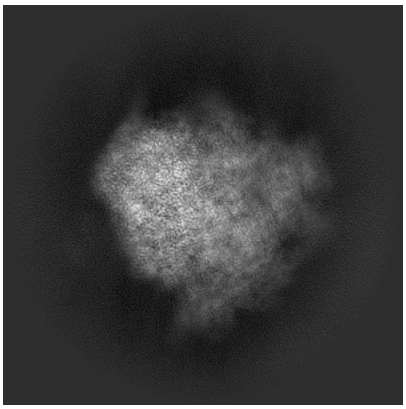
6.1.1 Primary map



X

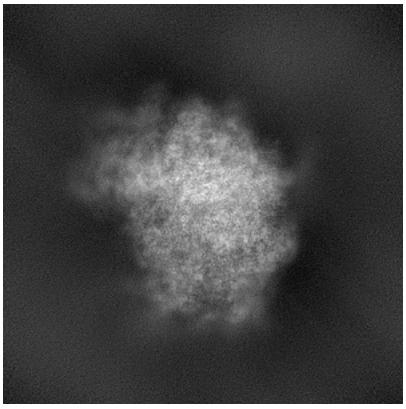


Y

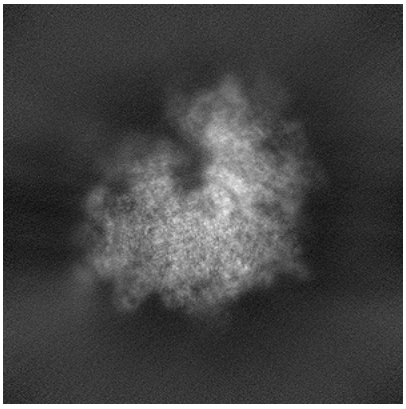


Z

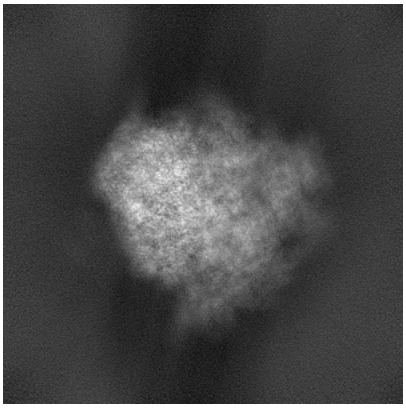
6.1.2 Raw map



X



Y

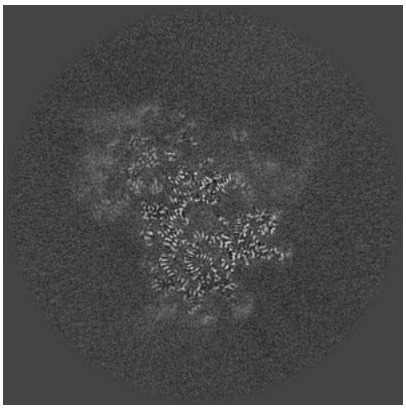


Z

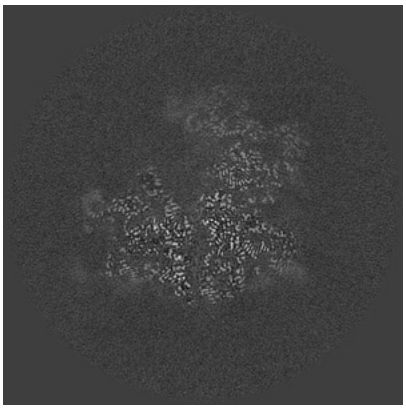
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

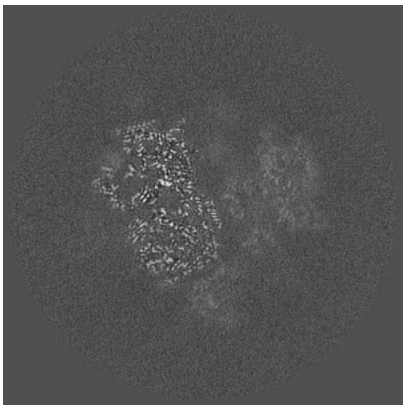
6.2.1 Primary map



X Index: 240

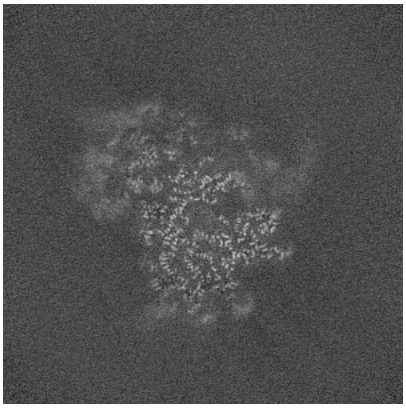


Y Index: 240

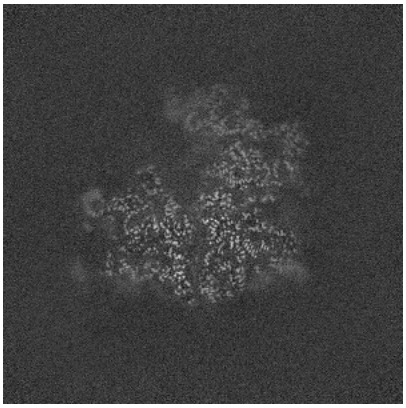


Z Index: 240

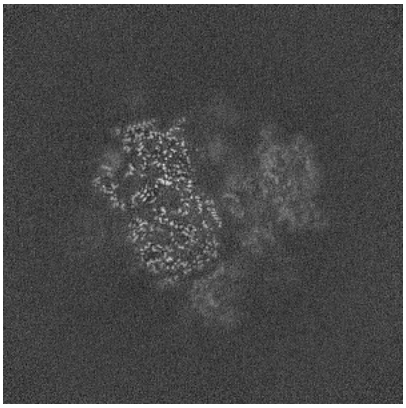
6.2.2 Raw map



X Index: 240



Y Index: 240

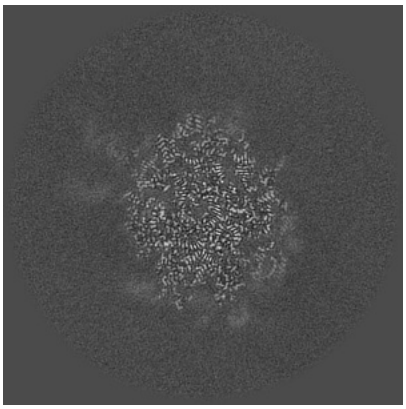


Z Index: 240

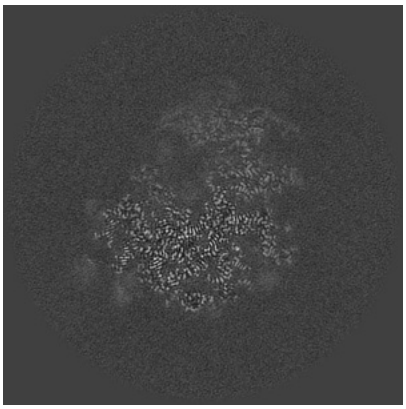
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

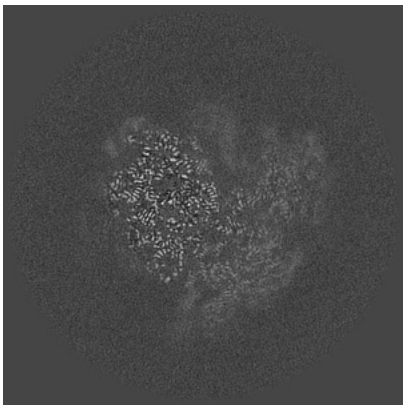
6.3.1 Primary map



X Index: 212

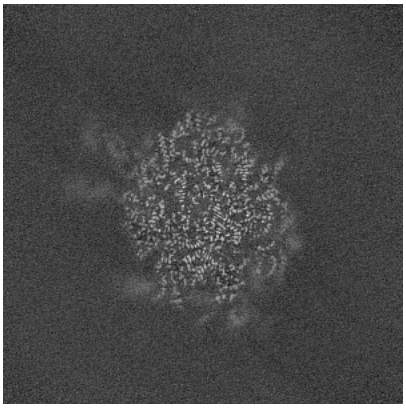


Y Index: 254

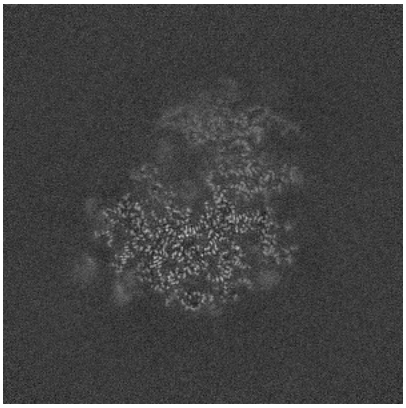


Z Index: 263

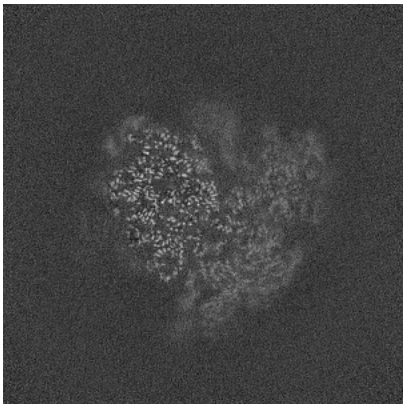
6.3.2 Raw map



X Index: 211



Y Index: 254

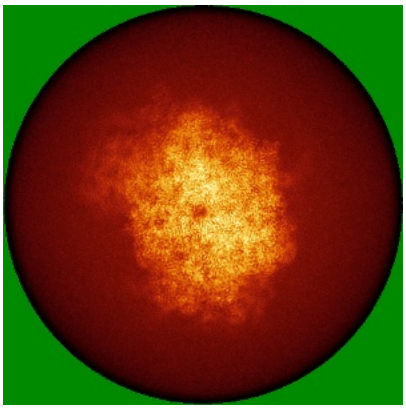


Z Index: 263

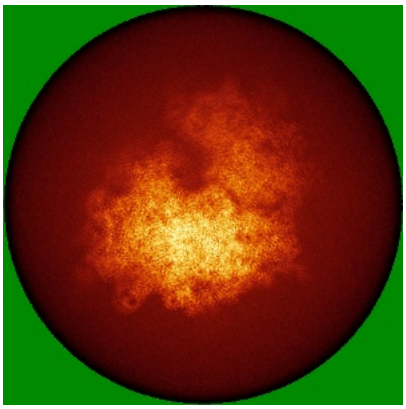
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

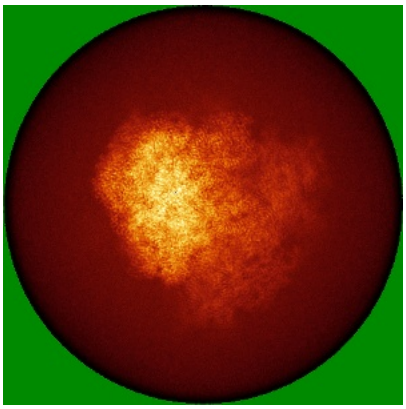
6.4.1 Primary map



X

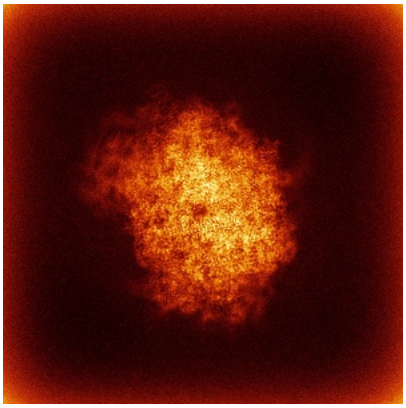


Y

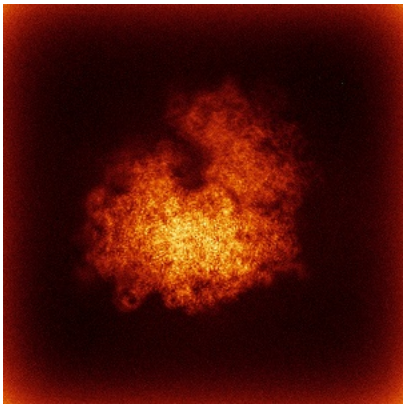


Z

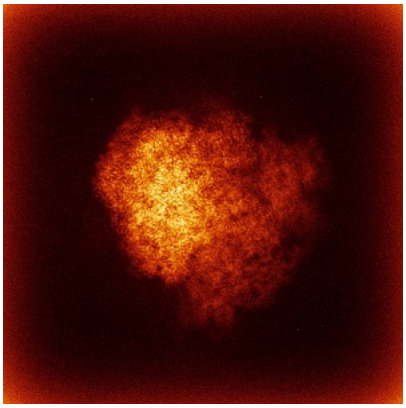
6.4.2 Raw map



X



Y

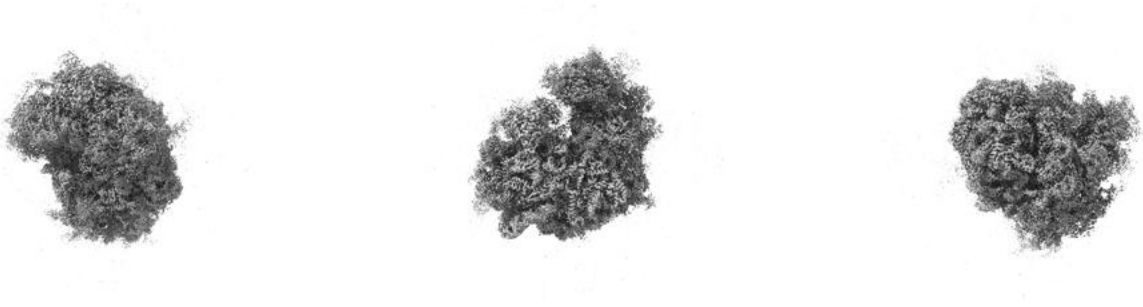


Z

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



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.5. 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



X Y Z

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.

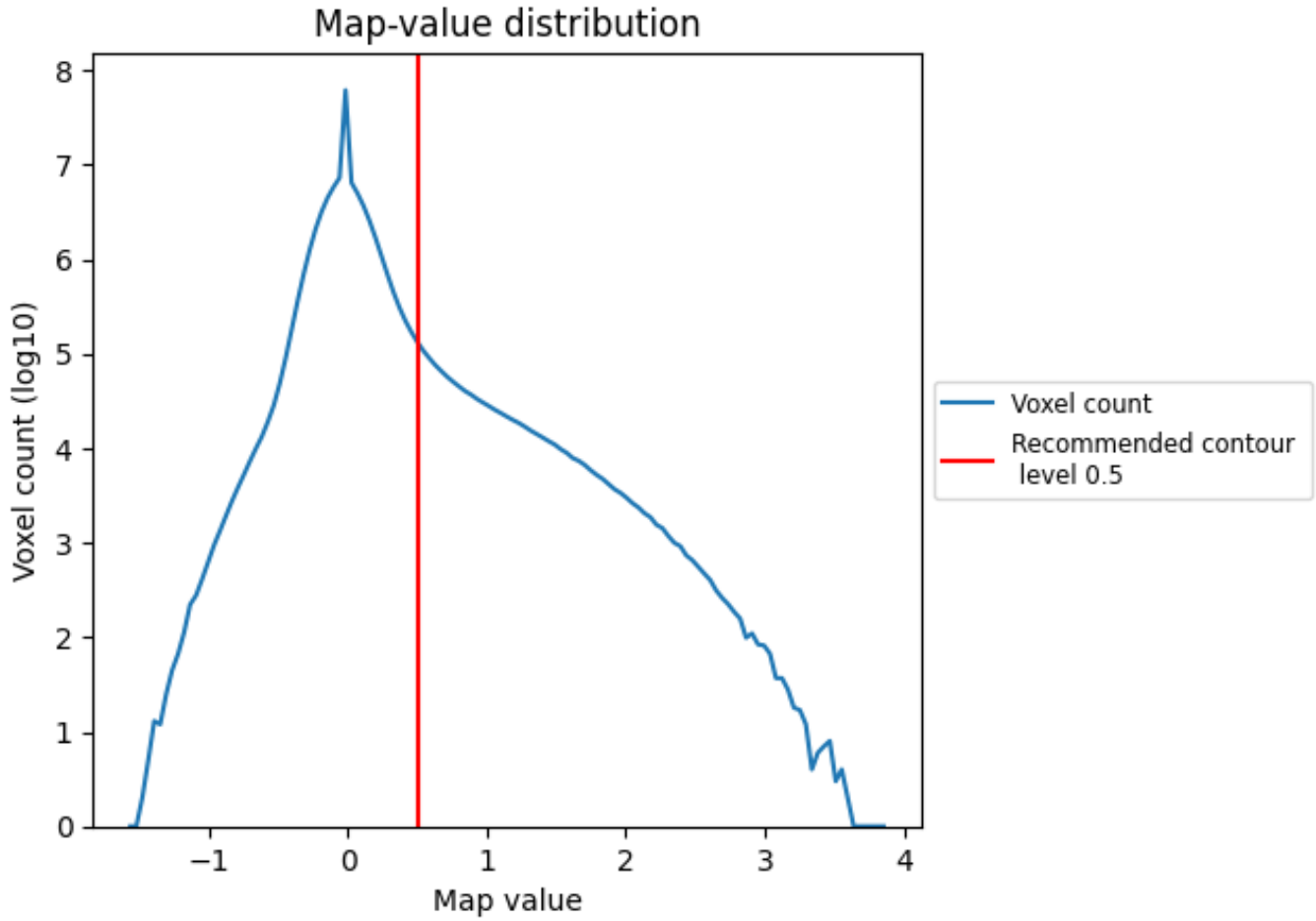
6.6 Mask visualisation (i)

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

7 Map analysis

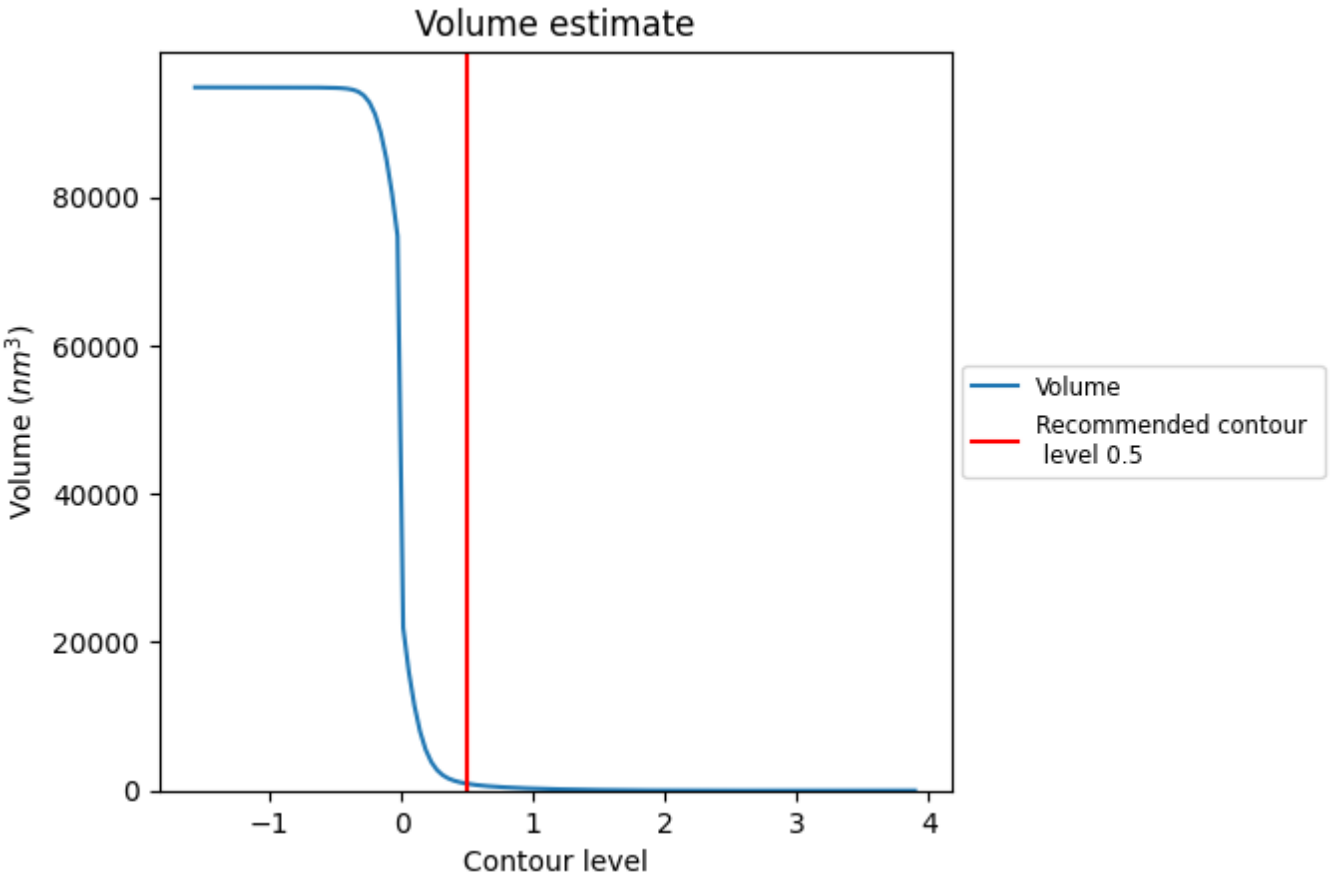
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

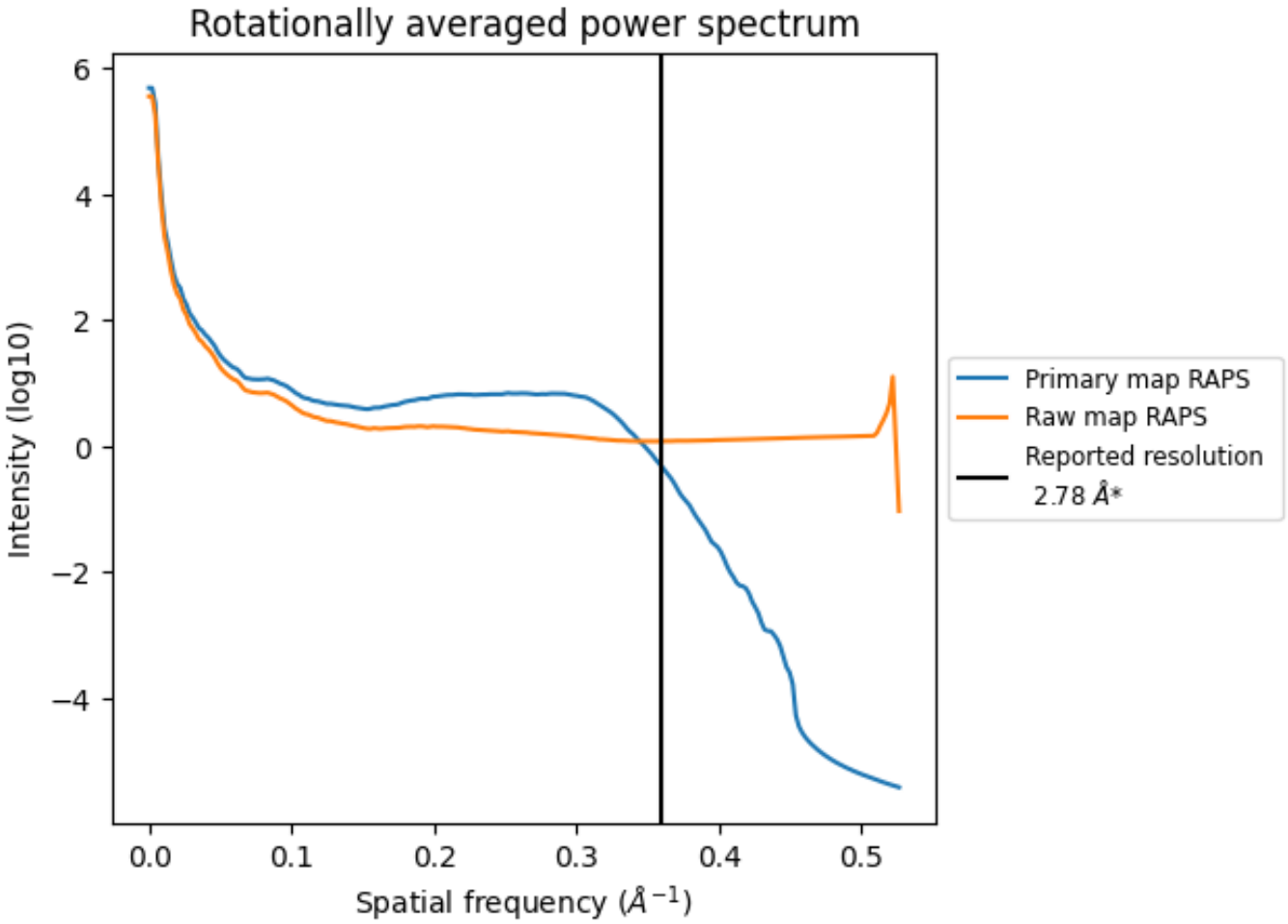
7.2 Volume estimate



The volume at the recommended contour level is 930 nm^3; this corresponds to an approximate mass of 840 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 (i)

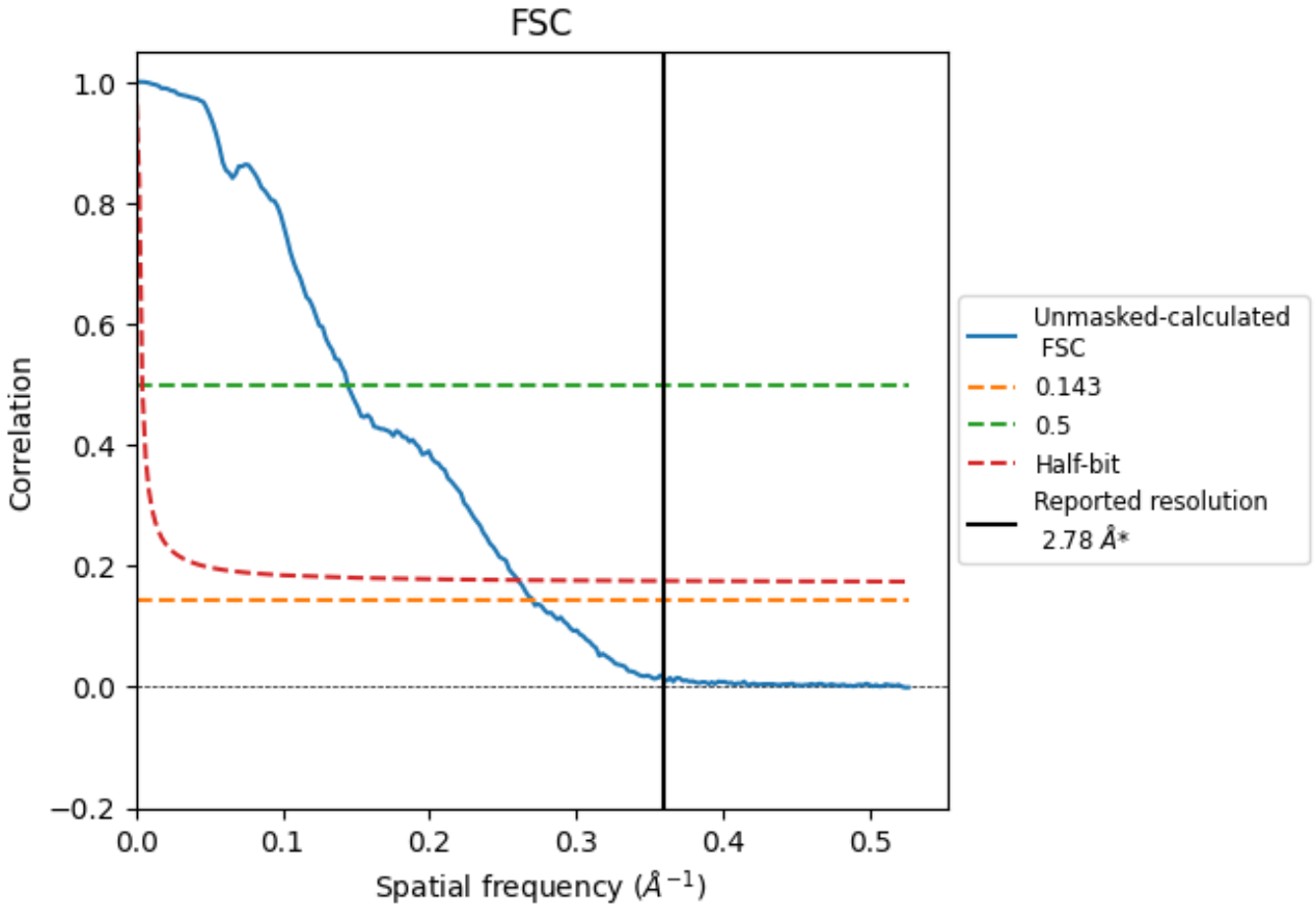


*Reported resolution corresponds to spatial frequency of 0.360 Å^{-1}

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.360 Å^{-1}

8.2 Resolution estimates (i)

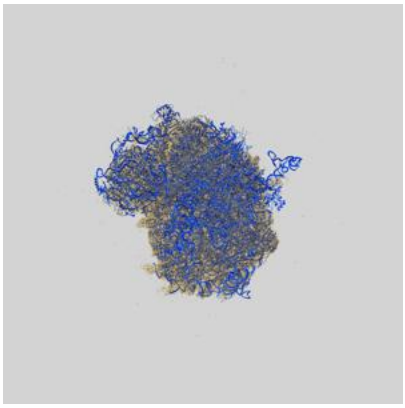
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.78	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.70	6.93	3.84

*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 3.70 differs from the reported value 2.78 by more than 10 %

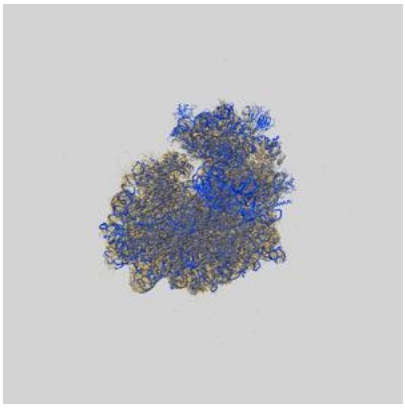
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-66929 and PDB model 9XJ6. Per-residue inclusion information can be found in section 3 on page 21.

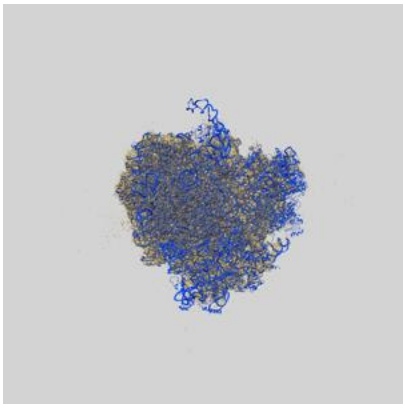
9.1 Map-model overlay



X



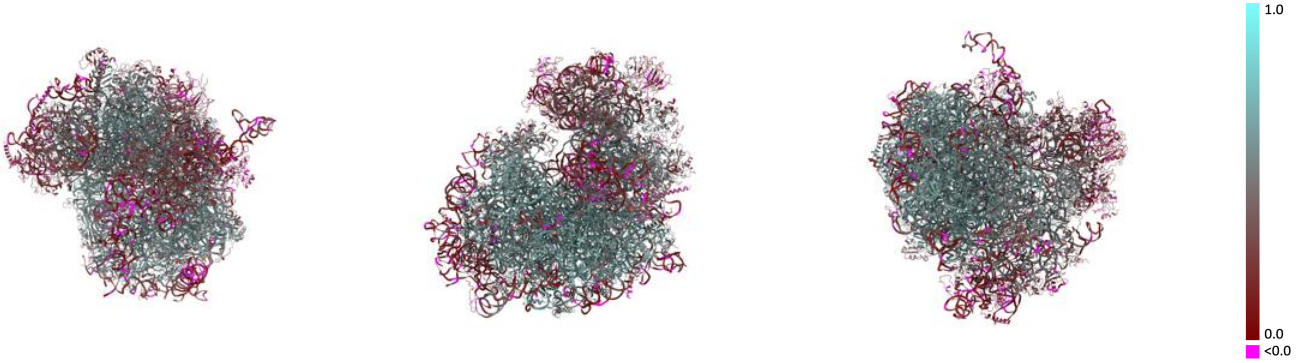
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.5 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.

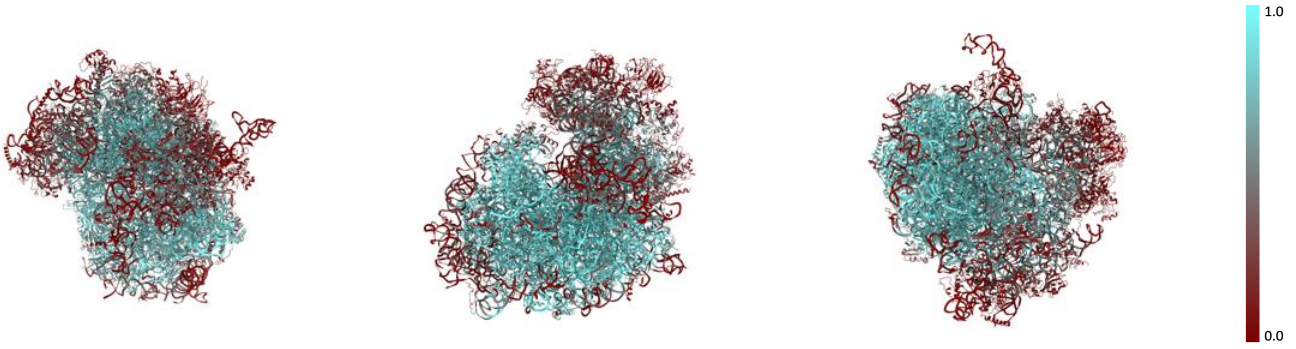
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according 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.

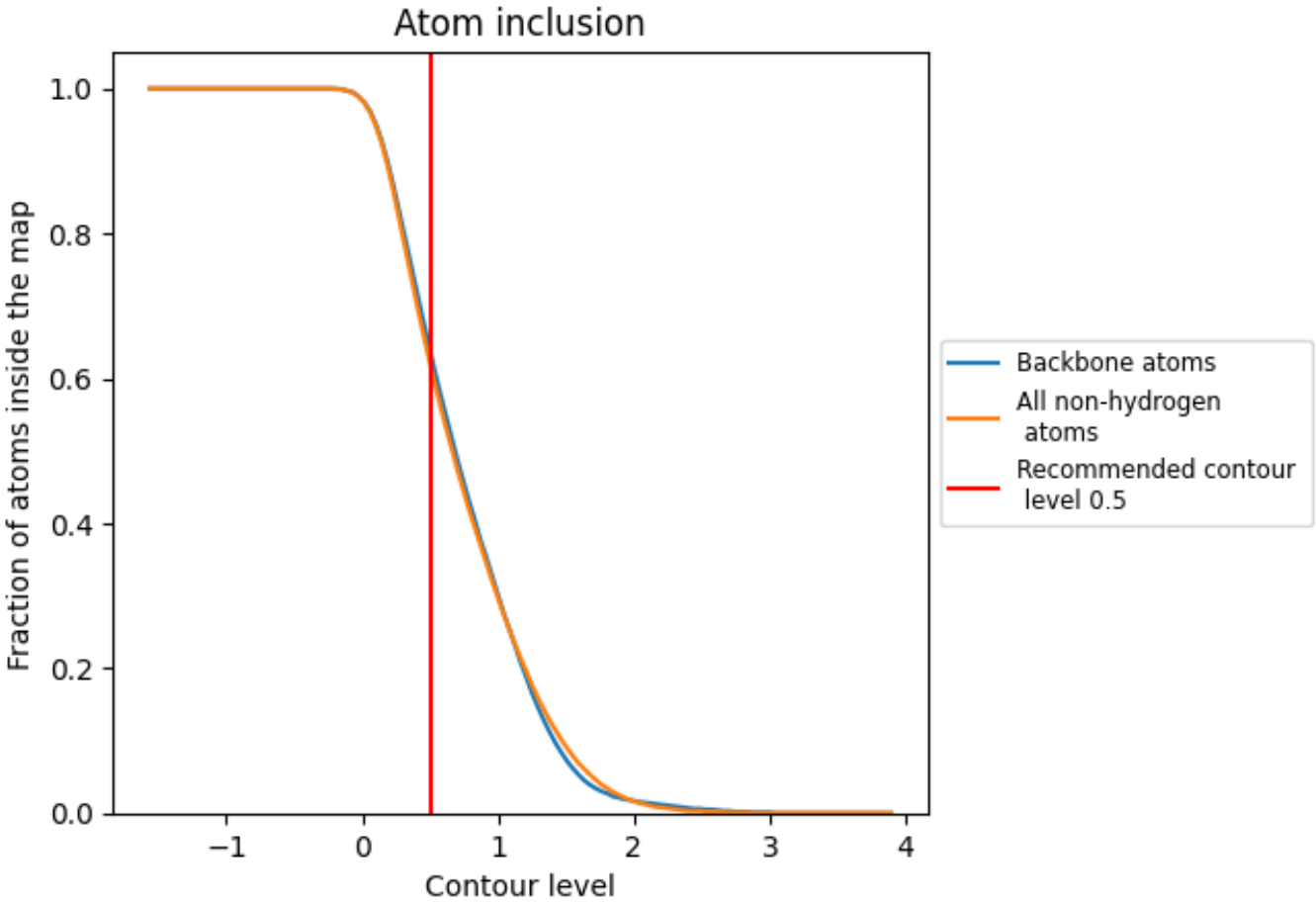
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.5).

9.4 Atom inclusion (i)



At the recommended contour level, 64% of all backbone atoms, 62% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6200	0.4530
L5	0.7290	0.4800
L7	0.9340	0.5950
L8	0.8810	0.5770
LA	0.9000	0.6010
LB	0.8180	0.5730
LC	0.8320	0.5710
LD	0.6960	0.5090
LE	0.6010	0.4510
LF	0.8390	0.5830
LG	0.6870	0.5070
LH	0.6520	0.5130
LI	0.6420	0.4920
LJ	0.4980	0.4290
LL	0.7570	0.5490
LM	0.7320	0.5300
LN	0.9230	0.6200
LO	0.8500	0.5960
LP	0.8670	0.5980
LQ	0.8900	0.6040
LR	0.6970	0.5060
LS	0.8340	0.5730
LT	0.7860	0.5630
LU	0.3990	0.4000
LV	0.8120	0.5870
LW	0.4290	0.3540
LX	0.7960	0.5600
LY	0.7780	0.5620
LZ	0.7240	0.5430
La	0.8770	0.6020
Lb	0.6890	0.5170
Lc	0.7300	0.5220
Ld	0.7790	0.5480
Le	0.8640	0.5990
Lf	0.8950	0.6050



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Chain	Atom inclusion	Q-score
Lg	0.7860	0.5610
Lh	0.7780	0.5650
Li	0.7180	0.5290
Lj	0.9140	0.6040
Lk	0.5100	0.4490
Ll	0.8440	0.5850
Lm	0.0020	0.0930
Ln	0.8710	0.6010
Lo	0.7560	0.5460
Lp	0.8140	0.5620
Lr	0.8450	0.5840
Lz	0.0040	0.0980
Pt	0.1910	0.2830
S2	0.5650	0.3940
S6	0.1070	0.1690
SA	0.3810	0.4470
SB	0.4600	0.4540
SC	0.5160	0.4730
SD	0.1890	0.3120
SE	0.2470	0.3670
SF	0.2120	0.3010
SG	0.1480	0.2550
SH	0.2080	0.3350
SI	0.3690	0.4000
SJ	0.3040	0.3910
SK	0.0680	0.1980
SL	0.4560	0.4570
SM	0.0010	0.0810
SN	0.6000	0.5110
SO	0.5660	0.4650
SP	0.0710	0.1620
SQ	0.1880	0.3120
SR	0.1900	0.3130
SS	0.1640	0.2820
ST	0.1440	0.2790
SU	0.2070	0.2980
SV	0.3910	0.4380
SW	0.6010	0.5230
SX	0.5600	0.4610
SY	0.1570	0.2950
SZ	0.1000	0.2200
Sa	0.6200	0.4810

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Chain	Atom inclusion	Q-score
Sb	0.3910	0.4260
Sc	0.2180	0.3190
Sd	0.3230	0.3440
Se	0.2090	0.2650
Sf	0.0020	0.1030
Sg	0.0240	0.2050