



Full wwPDB EM Validation Report ⓘ

Mar 20, 2026 – 03:13 AM UTC

PDB ID : 6T7T / pdb_00006t7t
EMDB ID : EMD-10397
Title : Structure of yeast 80S ribosome stalled on poly(A) tract.
Authors : Tesina, P.; Buschauer, R.; Cheng, J.; Berninghausen, O.; Becker, R.; Beckmann, R.
Deposited on : 2019-10-23
Resolution : 3.10 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

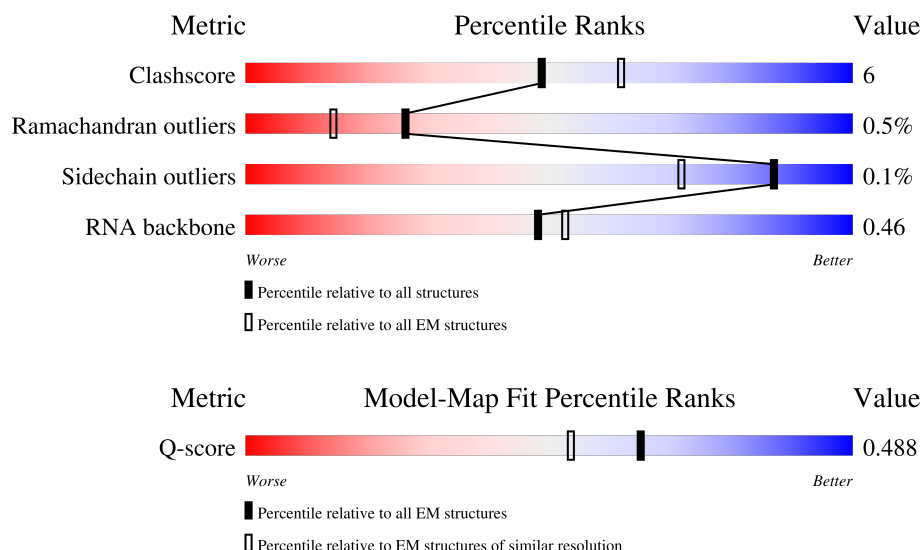
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.10 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	14724 (2.60 - 3.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	LA	251	
2	SA	206	
3	LB	386	

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Mol	Chain	Length	Quality of chain
4	SB	232	
5	C2	1771	
6	SP	117	
7	SC	216	
8	SD	222	
9	SE	258	
10	SF	206	
11	SG	228	
12	SH	184	
13	SI	187	
14	SJ	184	
15	SK	92	
16	SL	144	
17	SM	121	
18	SN	150	
19	SO	127	
20	SQ	141	
21	SR	125	
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23	ST	143	
24	SU	100	
25	SV	87	
26	SW	129	
27	SX	144	
28	SY	134	

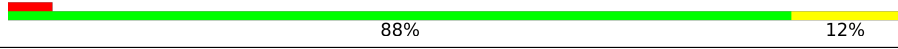
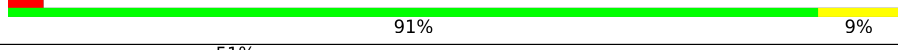
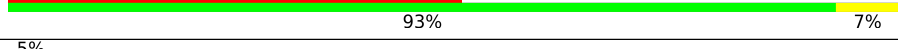
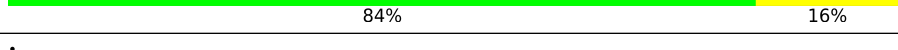
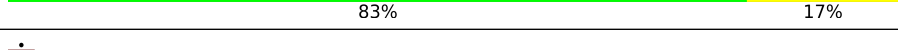
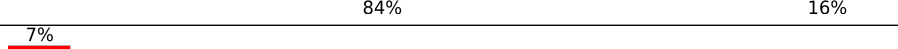
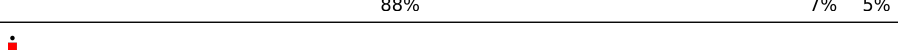
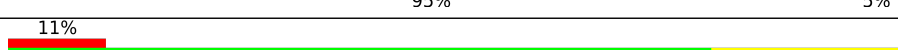
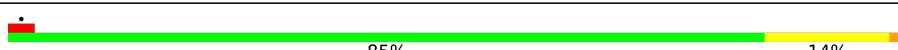
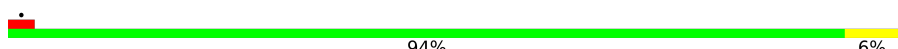
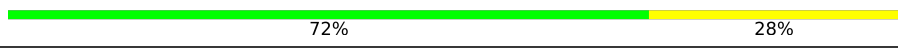
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Mol	Chain	Length	Quality of chain
29	SZ	82	
30	Sa	97	
31	Sb	81	
32	Sd	53	
33	Se	60	
34	Sf	73	
35	Sg	312	
36	Sc	63	
37	C4	121	
38	C3	158	
39	LC	361	
40	LD	294	
41	LE	175	
42	LF	222	
43	LG	233	
44	LH	191	
45	LI	218	
46	LJ	169	
47	LL	193	
48	LM	136	
49	LN	203	
50	LO	197	
51	LP	183	
52	LQ	185	
53	LR	188	

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Mol	Chain	Length	Quality of chain
54	LS	171	
55	LT	159	
56	LU	100	
57	LV	136	
58	LW	126	
59	LX	121	
60	LY	125	
61	LZ	135	
62	La	148	
63	Lb	58	
64	Lc	96	
65	Ld	109	
66	Le	127	
67	Lf	106	
68	Lg	112	
69	Lh	119	
70	Li	99	
71	Lj	85	
72	Lk	77	
73	Ll	50	
74	Lm	52	
75	Ln	25	
76	Lo	103	
77	Lp	91	
78	C1	3184	

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Mol	Chain	Length	Quality of chain
79	5	11	45% 55%
80	6	76	5% 51% 39% 9%
80	7	76	97% 61% 28% 12%
81	A	4	50% 25% 50% 25%

2 Entry composition

There are 81 unique types of molecules in this entry. The entry contains 202869 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	LA	251	Total	C	N	O	S	0	0
			1899	1182	385	331	1		

- Molecule 2 is a protein called 40S ribosomal protein S0-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	SA	206	Total	C	N	O	S	0	0
			1603	1030	284	287	2		

- Molecule 3 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	LB	386	Total	C	N	O	S	0	0
			3075	1950	584	533	8		

- Molecule 4 is a protein called 40S ribosomal protein S1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	SB	226	Total	C	N	O	S	0	0
			1798	1139	330	325	4		

- Molecule 5 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	C2	1771	Total	C	N	O	P	0	0
			37604	16807	6624	12402	1771		

- Molecule 6 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	SP	117	Total	C	N	O	S	0	0
			916	583	171	155	7		

- Molecule 7 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	SC	216	Total	C	N	O	S	0	0
			1626	1042	287	295	2		

- Molecule 8 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	SD	222	Total	C	N	O	S	0	0
			1729	1098	312	313	6		

- Molecule 9 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	SE	258	Total	C	N	O	S	0	0
			2056	1308	387	358	3		

- Molecule 10 is a protein called Rps5p.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	SF	206	Total	C	N	O	S	0	0
			1605	1005	299	298	3		

- Molecule 11 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	SG	228	Total	C	N	O	S	0	0
			1815	1138	351	323	3		

- Molecule 12 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	SH	184	Total	C	N	O	0	0
			1473	946	263	264		

- Molecule 13 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	SI	187	Total	C	N	O	S	0	0
			1476	916	295	263	2		

- Molecule 14 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	SJ	184	Total	C	N	O	S	0	0
			1479	935	285	258	1		

- Molecule 15 is a protein called 40S ribosomal protein S10-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	SK	92	Total	C	N	O	S	0	0
			752	487	122	141	2		

- Molecule 16 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	SL	144	Total	C	N	O	S	0	0
			1159	742	219	195	3		

- Molecule 17 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	SM	121	Total	C	N	O	S	0	0
			875	551	153	169	2		

- Molecule 18 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	SN	150	Total	C	N	O	S	0	0
			1192	759	224	207	2		

- Molecule 19 is a protein called 40S ribosomal protein S14-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	SO	127	Total	C	N	O	S	0	0
			926	569	185	169	3		

- Molecule 20 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	SQ	141	Total	C	N	O	0	0
			1105	708	203	194		

- Molecule 21 is a protein called 40S ribosomal protein S17-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	SR	121	Total	C	N	O	S	0	0
			948	596	179	171	2		

- Molecule 22 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	SS	145	Total	C	N	O	S	0	0
			1192	743	237	210	2		

- Molecule 23 is a protein called 40S ribosomal protein S19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	ST	143	Total	C	N	O	S	0	0
			1112	694	208	208	2		

- Molecule 24 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	SU	100	Total	C	N	O	S	0	0
			797	506	144	146	1		

- Molecule 25 is a protein called 40S ribosomal protein S21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	SV	87	Total	C	N	O	S	0	0
			673	415	125	131	2		

- Molecule 26 is a protein called 40S ribosomal protein S22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	SW	129	Total	C	N	O	S	0	0
			1021	650	188	180	3		

- Molecule 27 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	SX	144	Total	C	N	O	S	0	0
			1121	708	220	191	2		

- Molecule 28 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	SY	134	Total	C	N	O	0	0
			1073	676	208	189		

- Molecule 29 is a protein called 40S ribosomal protein S25-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	SZ	82	Total	C	N	O	0	0
			651	416	123	112		

- Molecule 30 is a protein called 40S ribosomal protein S26-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Sa	97	Total	C	N	O	S	0	0
			769	475	160	129	5		

- Molecule 31 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Sb	81	Total	C	N	O	S	0	0
			610	382	110	113	5		

- Molecule 32 is a protein called 40S ribosomal protein S29-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Sd	53	Total	C	N	O	S	0	0
			442	274	92	72	4		

- Molecule 33 is a protein called 40S ribosomal protein S30-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Se	60	Total	C	N	O	S	0	0
			472	298	97	76	1		

- Molecule 34 is a protein called Ubiquitin-40S ribosomal protein S31.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Sf	73	Total	C	N	O	S	0	0
			556	352	105	95	4		

- Molecule 35 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Sg	312	Total	C	N	O	S	0	0
			2383	1514	409	452	8		

- Molecule 36 is a protein called 40S ribosomal protein S28-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Sc	63	Total	C	N	O	S	0	0
			491	303	96	91	1		

- Molecule 37 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	C4	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 38 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	C3	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 39 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	LC	361	Total	C	N	O	S	0	0
			2748	1729	522	494	3		

- Molecule 40 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	LD	294	Total	C	N	O	S	0	0
			2351	1484	410	455	2		

- Molecule 41 is a protein called 60S ribosomal protein L6-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	LE	167	Total	C	N	O	S	0	0
			1305	841	234	229	1		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LE	146	ILE	LEU	conflict	UNP P05739
LE	173	MET	LEU	conflict	UNP P05739

- Molecule 42 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	LF	222	Total	C	N	O	S	0	0
			1784	1151	324	308	1		

- Molecule 43 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	LG	233	Total	C	N	O	S	0	0
			1804	1151	323	327	3		

- Molecule 44 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	LH	191	Total	C	N	O	S	0	0
			1508	957	274	273	4		

- Molecule 45 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	LI	218	Total	C	N	O	S	0	0
			1764	1117	334	306	7		

- Molecule 46 is a protein called 60S ribosomal protein L11-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	LJ	169	Total	C	N	O	S	0	0
			1350	846	253	247	4		

- Molecule 47 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
47	LL	193	Total	C	N	O	0	0
			1543	962	315	266		

- Molecule 48 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	LM	136	Total	C	N	O	S	0	0
			1053	675	199	177	2		

- Molecule 49 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	LN	203	Total	C	N	O	S	0	0
			1720	1077	361	281	1		

- Molecule 50 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	LO	197	Total	C	N	O	S	197	0
			1555	1003	289	262	1		

- Molecule 51 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	LP	183	Total	C	N	O		0	0
			1416	879	284	253			

- Molecule 52 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	LQ	185	Total	C	N	O	S	0	0
			1441	908	290	241	2		

- Molecule 53 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	LR	188	Total	C	N	O		0	0
			1515	932	323	260			

- Molecule 54 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	LS	171	Total	C	N	O	S	0	0
			1437	925	266	243	3		

- Molecule 55 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	LT	159	Total	C	N	O	S	0	0
			1276	805	246	221	4		

- Molecule 56 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	LU	100	Total	C	N	O	S	0	0
			796	516	131	149			

- Molecule 57 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	LV	136	Total	C	N	O	S	0	0
			1003	628	189	179	7		

- Molecule 58 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	LW	126	Total	C	N	O	S	0	0
			836	525	165	145	1		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LW	104	GLN	ASN	conflict	UNP P04449
LW	109	GLN	LEU	conflict	UNP P04449
LW	112	ASP	ASN	conflict	UNP P04449
LW	119	ALA	GLU	conflict	UNP P04449

- Molecule 59 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	LX	121	Total	C	N	O	S	0	0
			964	620	169	173	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
60	LY	125	Total	C	N	O	S	0	0
			984	620	191	173			

- Molecule 61 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
61	LZ	135	Total	C	N	O	0	0
			1092	710	202	180		

- Molecule 62 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	La	148	Total	C	N	O	S	0	0
			1173	749	231	190	3		

- Molecule 63 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
63	Lb	58	Total	C	N	O	0	0
			462	289	100	73		

- Molecule 64 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	Lc	96	Total	C	N	O	S	0	0
			737	476	123	137	1		

- Molecule 65 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	Ld	109	Total	C	N	O	S	0	0
			876	556	167	152	1		

- Molecule 66 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Le	127	Total	C	N	O	S	0	0
			1017	644	205	167	1		

- Molecule 67 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	Lf	106	Total	C	N	O	S	0	0
			850	540	165	144	1		

- Molecule 68 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	Lg	112	Total	C	N	O	S	0	0
			880	545	179	152	4		

- Molecule 69 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	Lh	119	Total	C	N	O	S	0	0
			969	615	186	167	1		

- Molecule 70 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	Li	99	Total	C	N	O	S	0	0
			766	478	154	132	2		

- Molecule 71 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	Lj	85	Total	C	N	O	S	0	0
			670	408	146	111	5		

- Molecule 72 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms				AltConf	Trace
72	Lk	77	Total	C	N	O	0	0
			612	391	115	106		

- Molecule 73 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	Ll	50	Total	C	N	O	S	0	0
			436	272	97	65	2		

- Molecule 74 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	Lm	52	Total	C	N	O	S	0	0
			417	259	86	67	5		

- Molecule 75 is a protein called 60S ribosomal protein L41-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	Ln	25	Total	C	N	O	S	0	0
			229	139	62	27	1		

- Molecule 76 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Lo	103	Total	C	N	O	S	0	0
			824	517	167	135	5		

- Molecule 77 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Lp	91	Total	C	N	O	S	0	0
			694	429	138	121	6		

- Molecule 78 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	C1	3184	Total	C	N	O	P	0	0
			68091	30415	12259	22233	3184		

- Molecule 79 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	5	11	Total	C	N	O	P	0	0
			242	110	55	66	11		

- Molecule 80 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	7	76	Total	C	N	O	P	0	0
			1616	721	281	538	76		
80	6	76	Total	C	N	O	P	0	0
			1616	721	281	538	76		

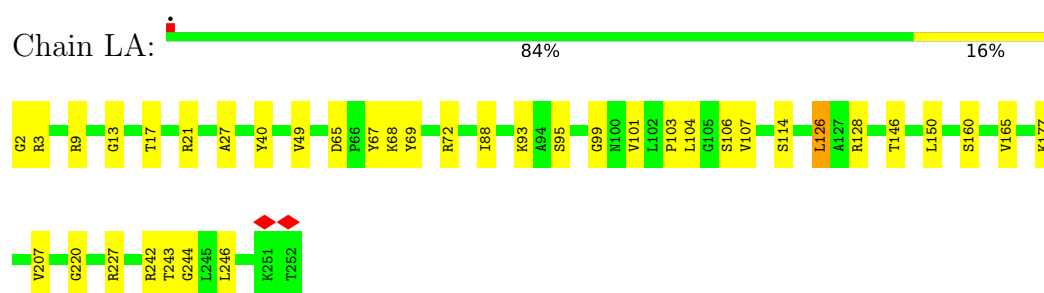
- Molecule 81 is a protein called nascent chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
81	A	4	Total	C	N	O	1	0
			41	27	9	5		

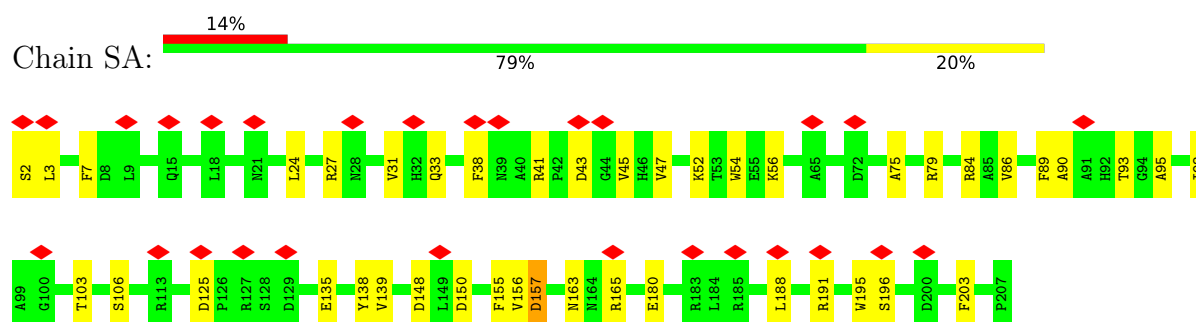
3 Residue-property plots [i](#)

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.

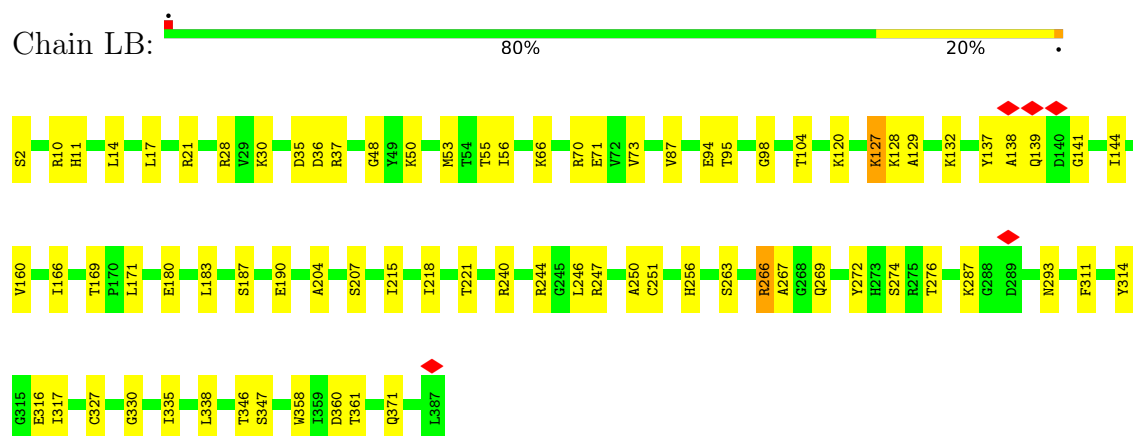
- Molecule 1: 60S ribosomal protein L2-A



- Molecule 2: 40S ribosomal protein S0-A

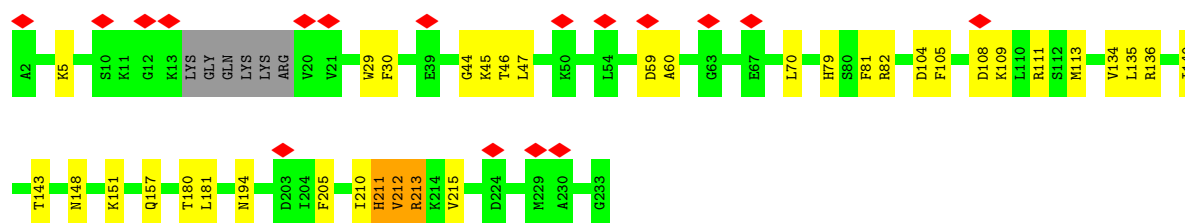


- Molecule 3: 60S ribosomal protein L3



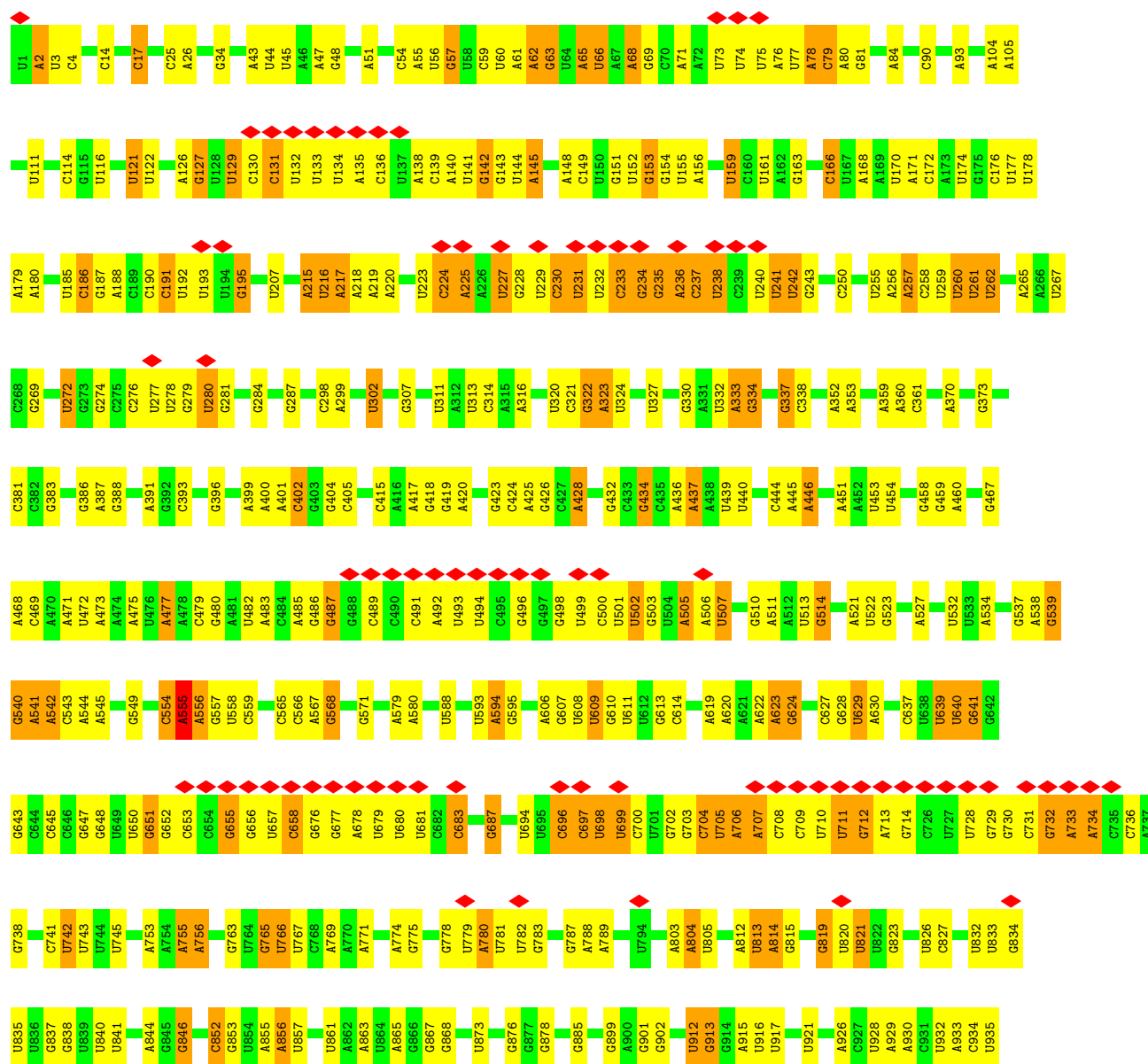
- Molecule 4: 40S ribosomal protein S1-A

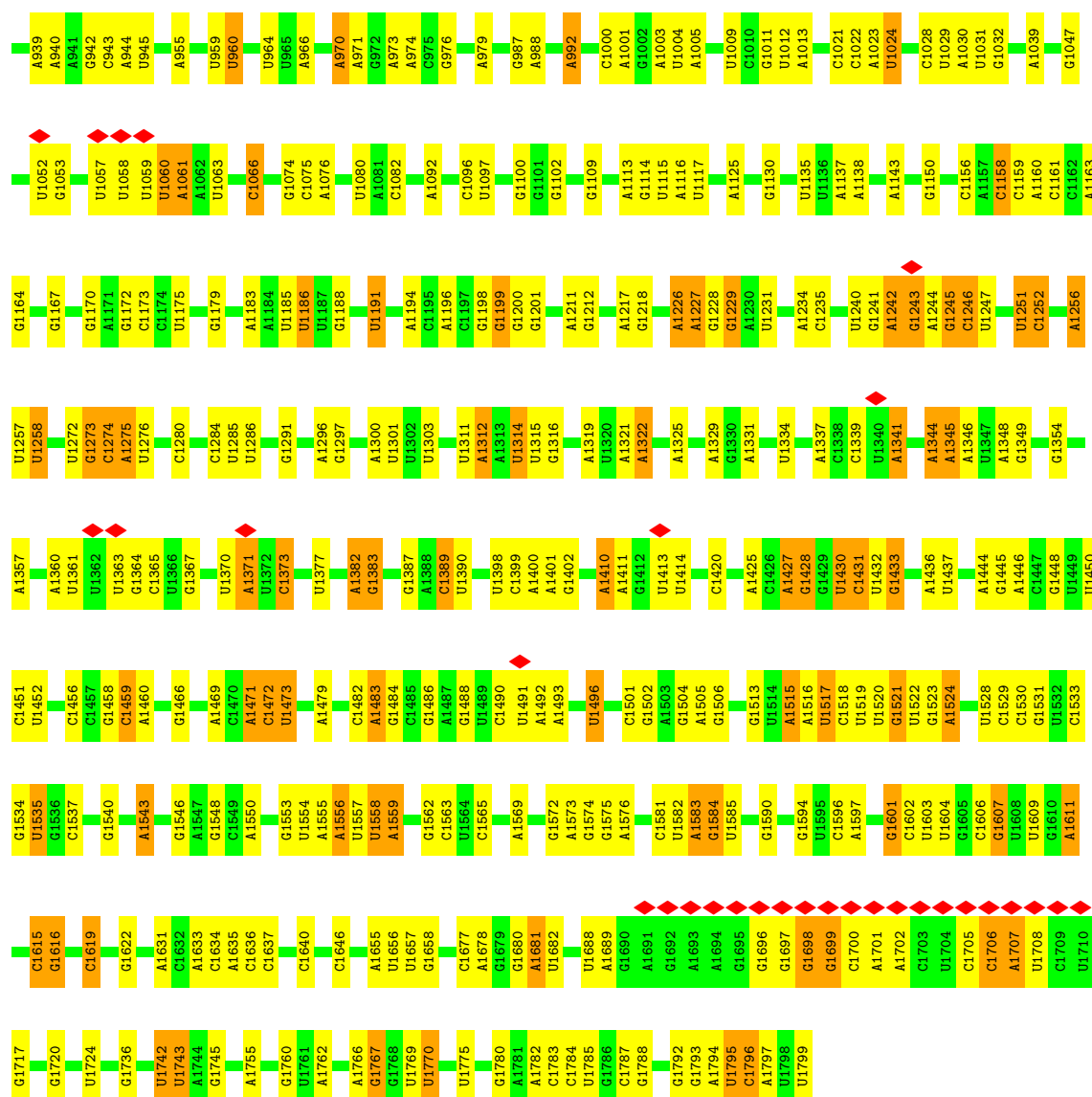
Chain SB: 



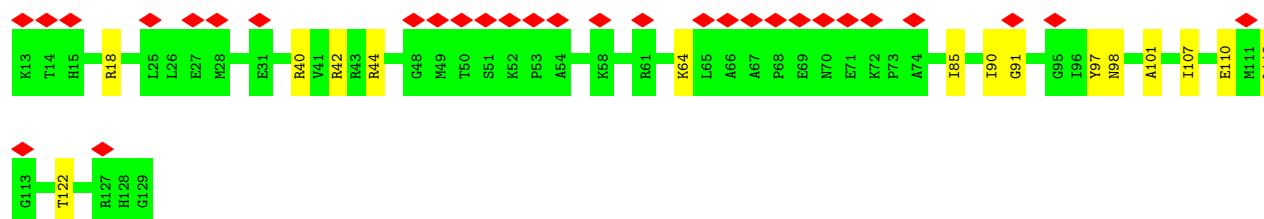
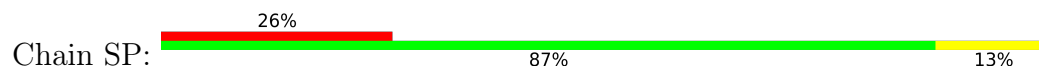
• Molecule 5: 18S rRNA

Chain C2: 

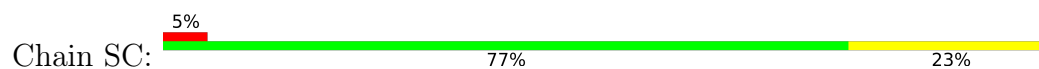


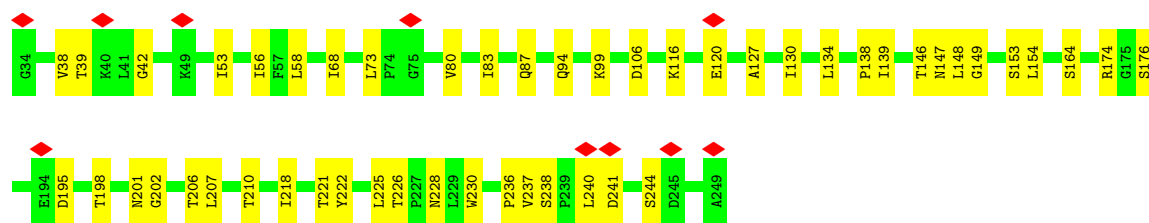


• Molecule 6: 40S ribosomal protein S15

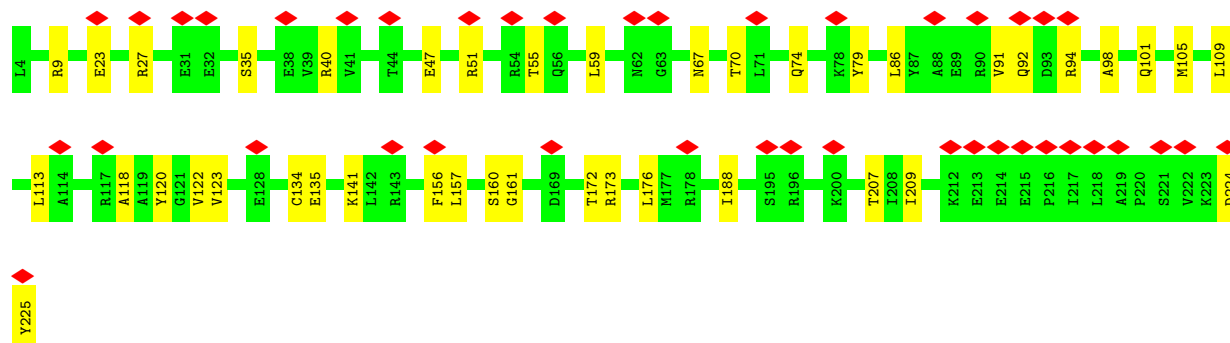
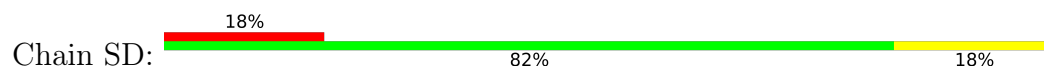


• Molecule 7: 40S ribosomal protein S2

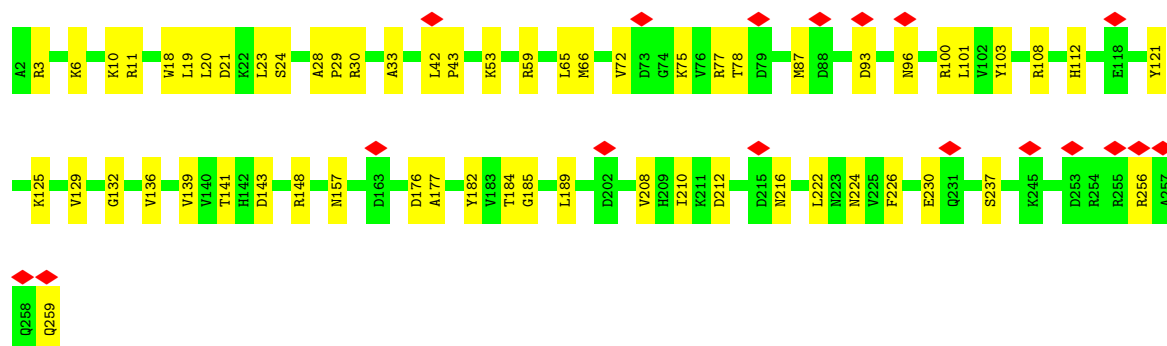
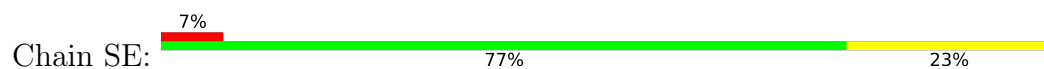




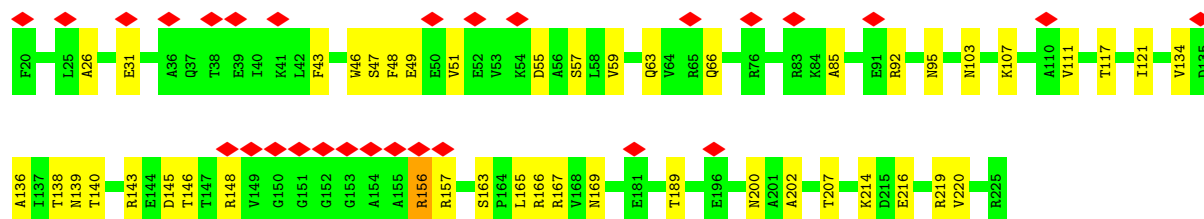
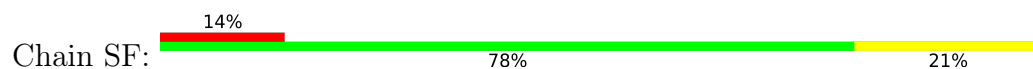
• Molecule 8: 40S ribosomal protein S3



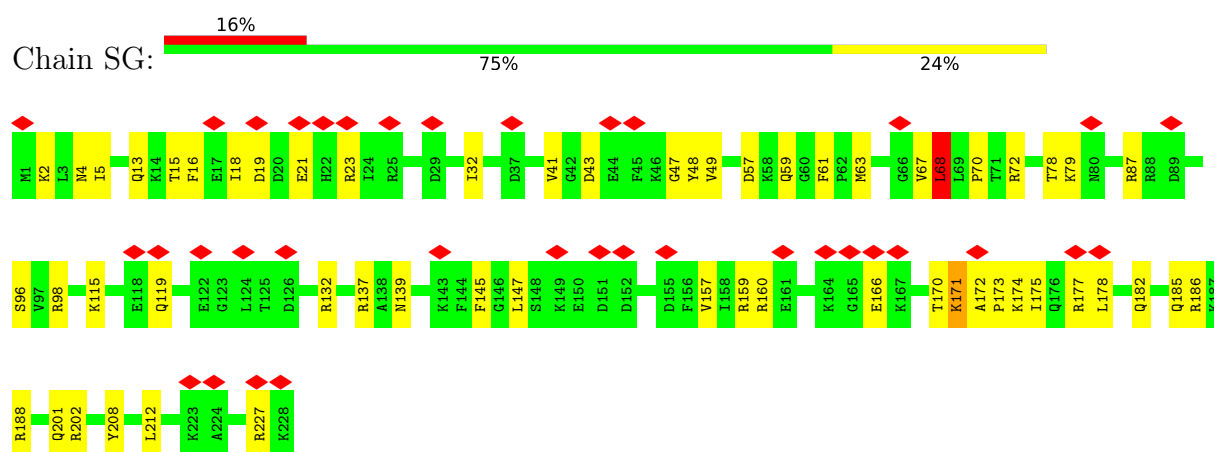
• Molecule 9: 40S ribosomal protein S4-A



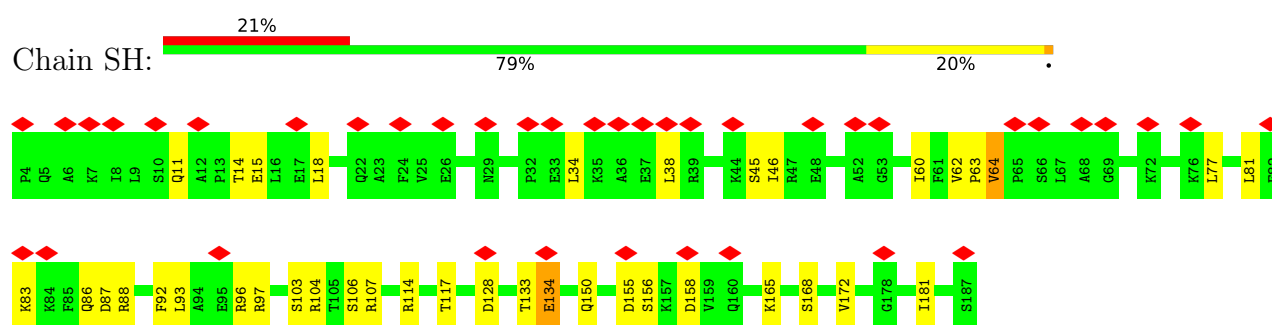
• Molecule 10: Rps5p



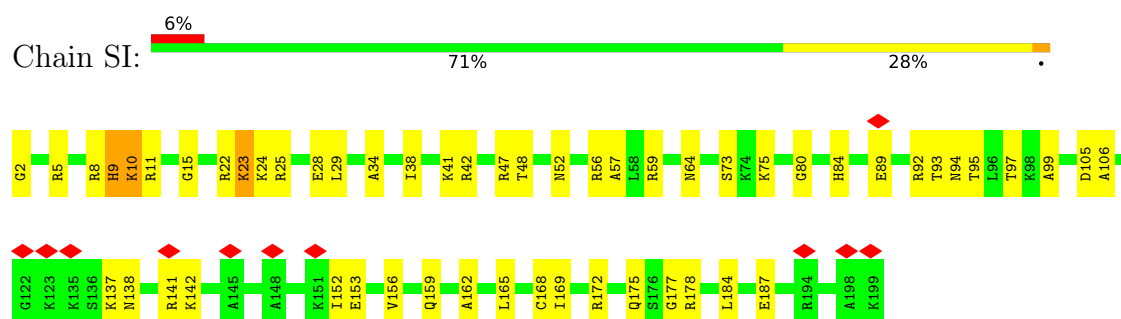
• Molecule 11: 40S ribosomal protein S6-A



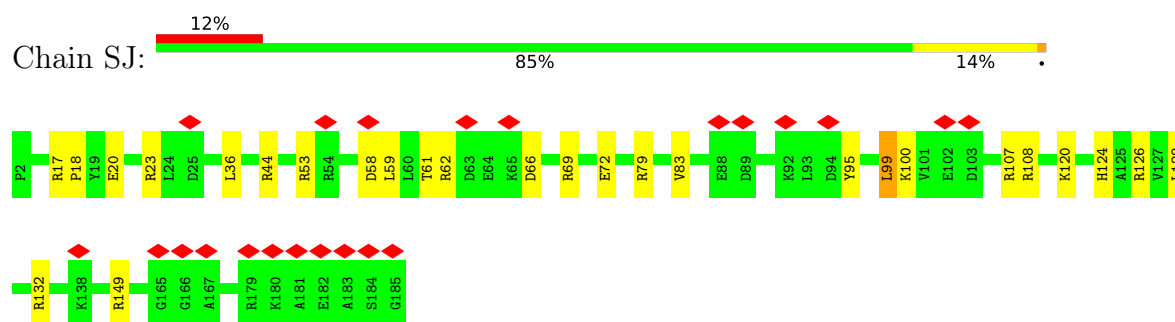
- Molecule 12: 40S ribosomal protein S7-A



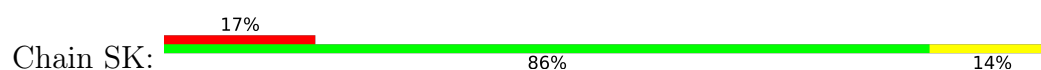
- Molecule 13: 40S ribosomal protein S8

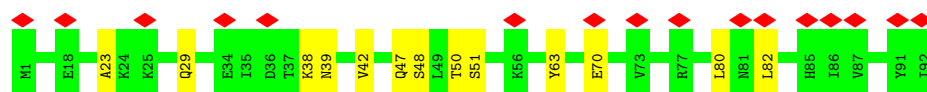


- Molecule 14: 40S ribosomal protein S9-A

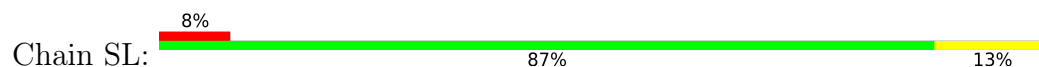


- Molecule 15: 40S ribosomal protein S10-A

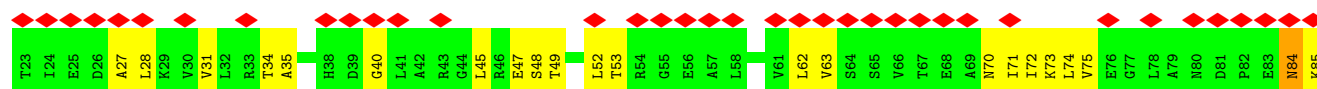
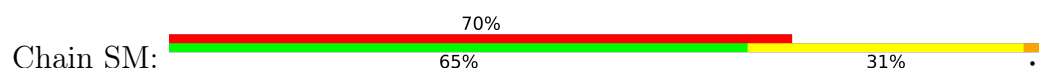




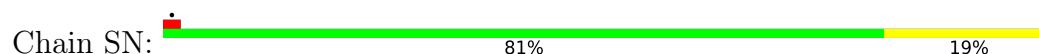
- Molecule 16: 40S ribosomal protein S11-A



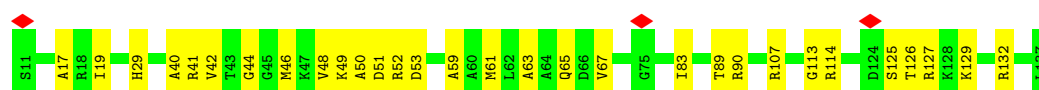
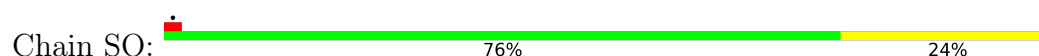
- Molecule 17: 40S ribosomal protein S12



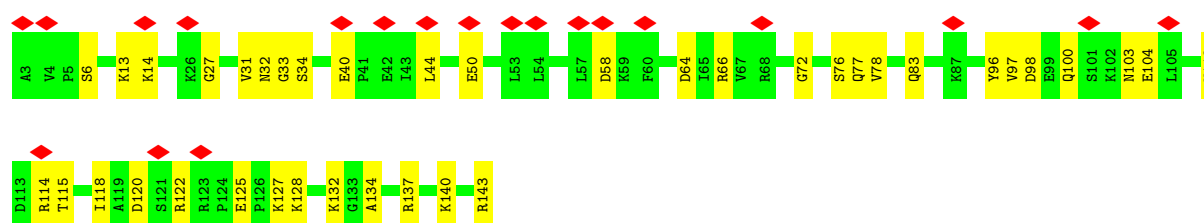
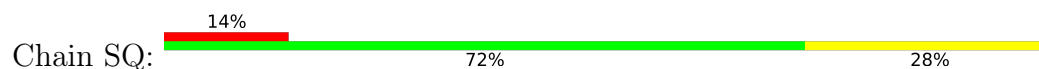
- Molecule 18: 40S ribosomal protein S13



- Molecule 19: 40S ribosomal protein S14-B

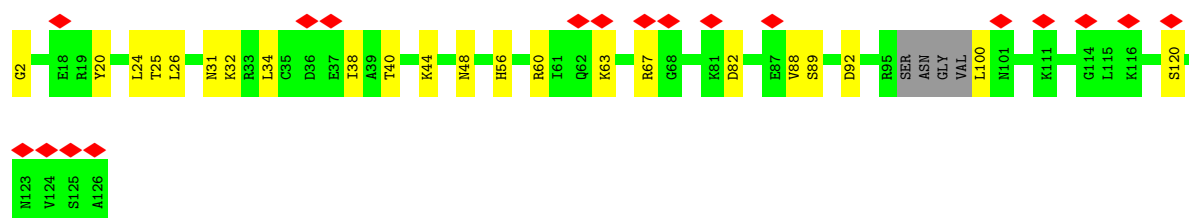


- Molecule 20: 40S ribosomal protein S16-A



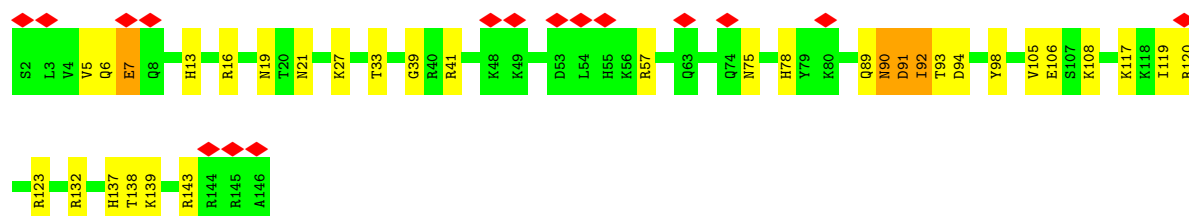
- Molecule 21: 40S ribosomal protein S17-B

Chain SR: 



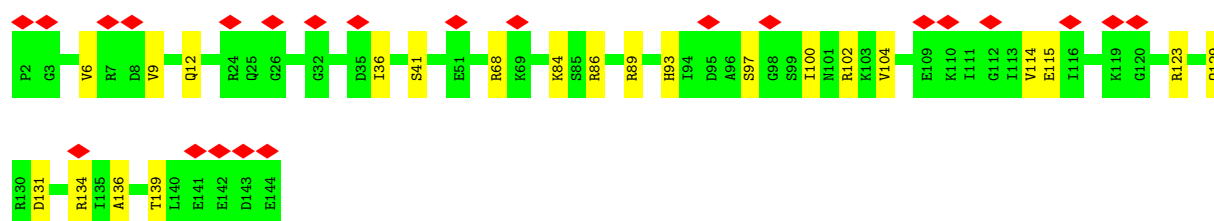
- Molecule 22: 40S ribosomal protein S18-A

Chain SS: 



- Molecule 23: 40S ribosomal protein S19-A

Chain ST: 



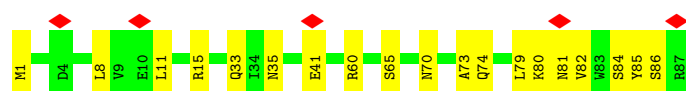
- Molecule 24: 40S ribosomal protein S20

Chain SU: 



- Molecule 25: 40S ribosomal protein S21-A

Chain SV: 

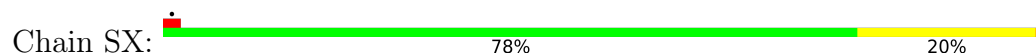


- Molecule 26: 40S ribosomal protein S22-A

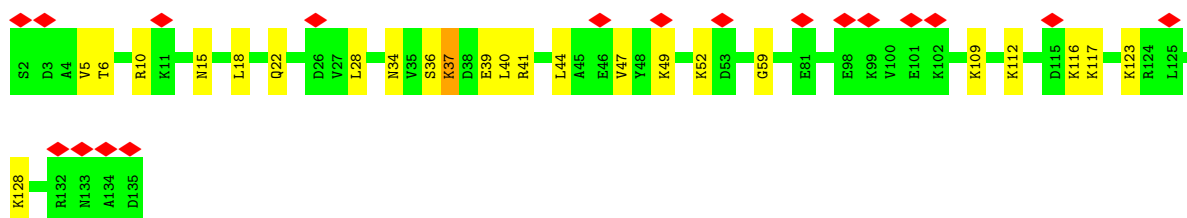
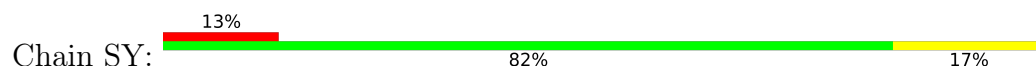
Chain SW: 



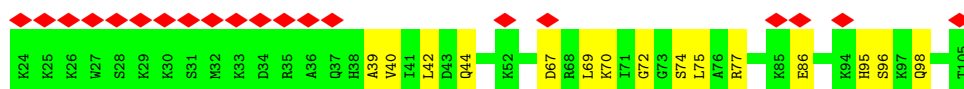
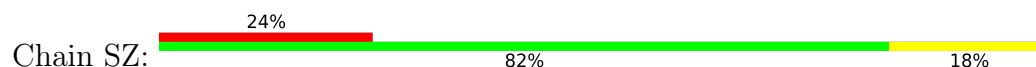
- Molecule 27: 40S ribosomal protein S23-A



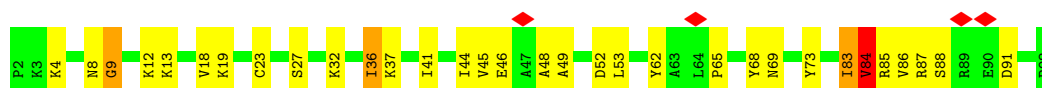
- Molecule 28: 40S ribosomal protein S24-A



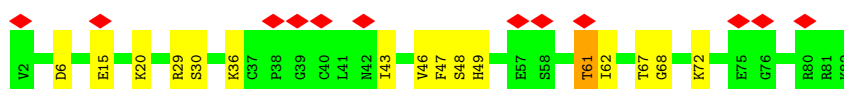
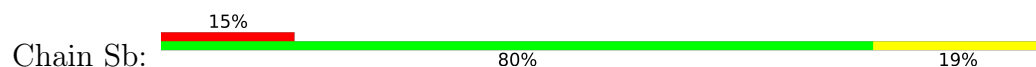
- Molecule 29: 40S ribosomal protein S25-A



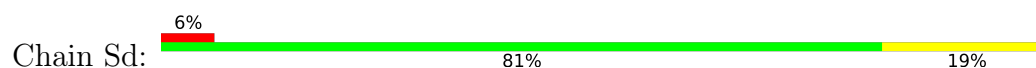
- Molecule 30: 40S ribosomal protein S26-B



- Molecule 31: 40S ribosomal protein S27-A

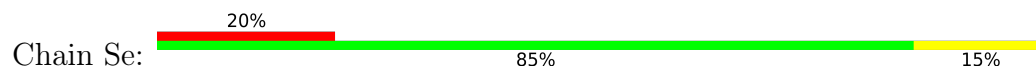


- Molecule 32: 40S ribosomal protein S29-A

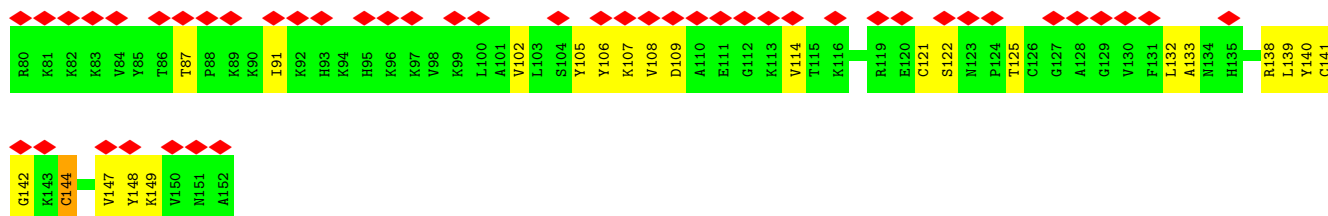




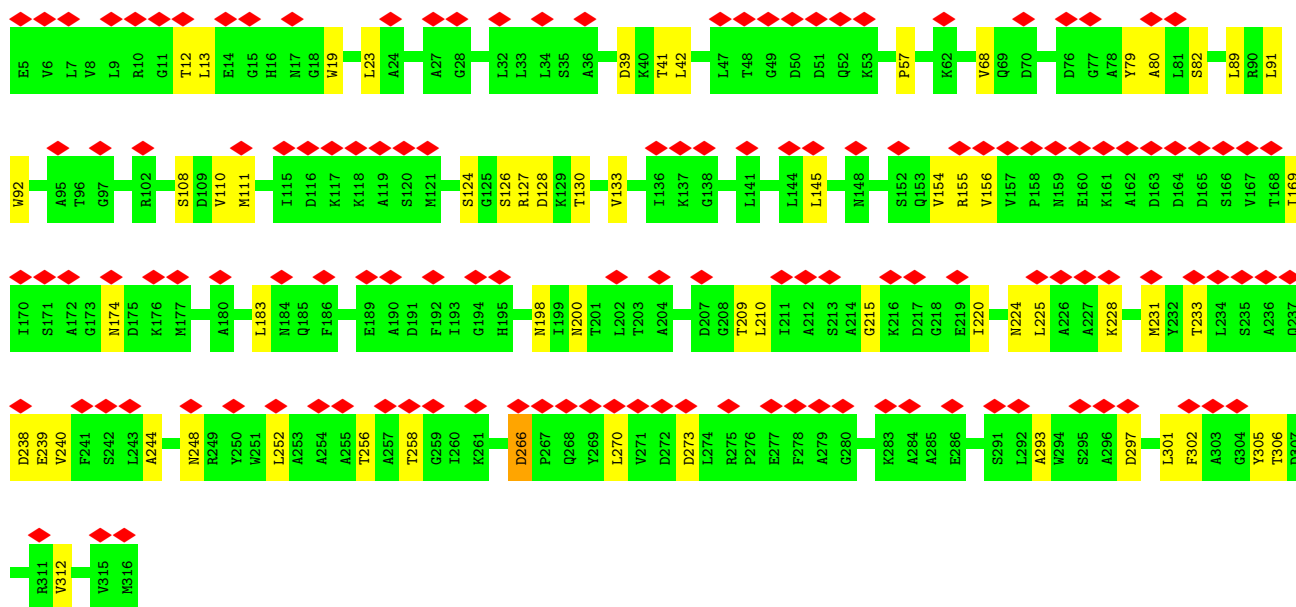
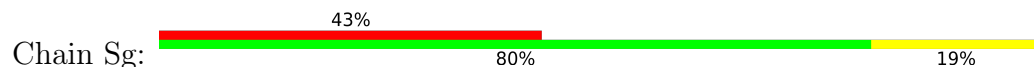
- Molecule 33: 40S ribosomal protein S30-A



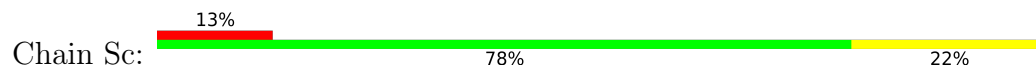
- Molecule 34: Ubiquitin-40S ribosomal protein S31

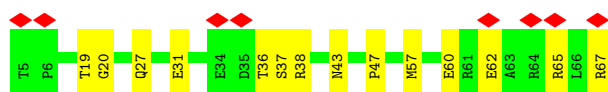


- Molecule 35: Guanine nucleotide-binding protein subunit beta-like protein



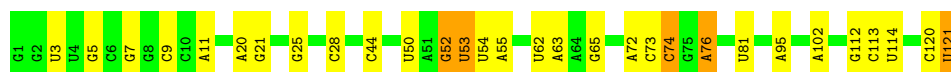
- Molecule 36: 40S ribosomal protein S28-A





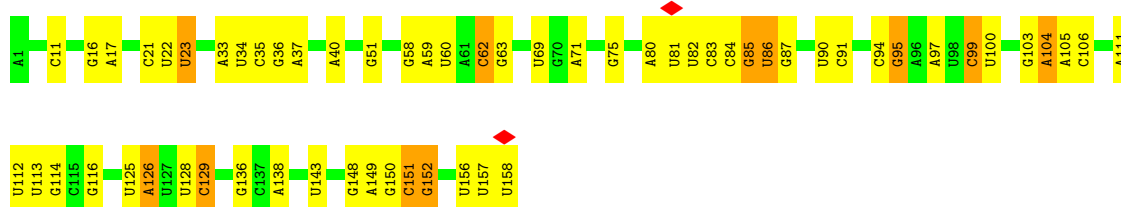
• Molecule 37: 5S rRNA

Chain C4: 75% 21% .



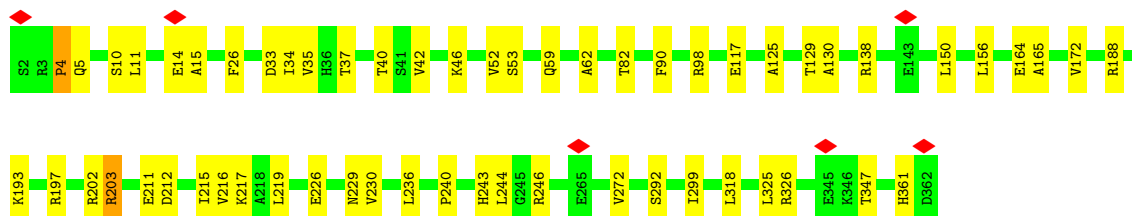
• Molecule 38: 5.8S rRNA

Chain C3: 62% 31% 7% .



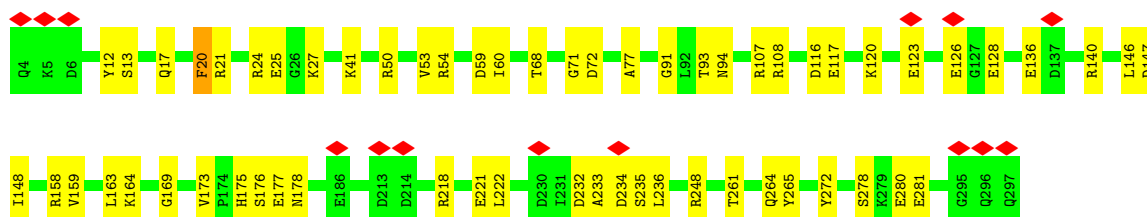
• Molecule 39: 60S ribosomal protein L4-A

Chain LC: 84% 16% .



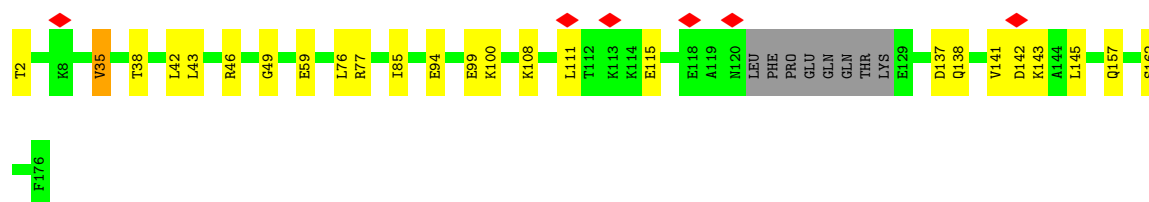
• Molecule 40: 60S ribosomal protein L5

Chain LD: 5% 80% 20% .

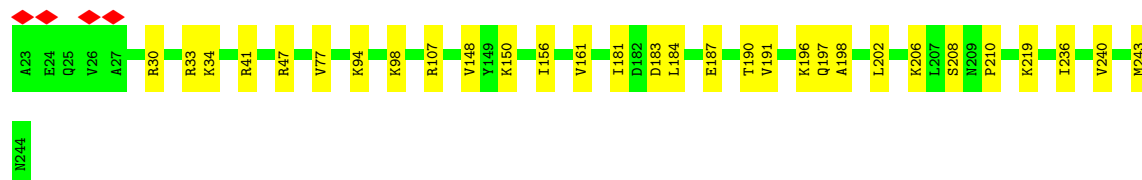


• Molecule 41: 60S ribosomal protein L6-B

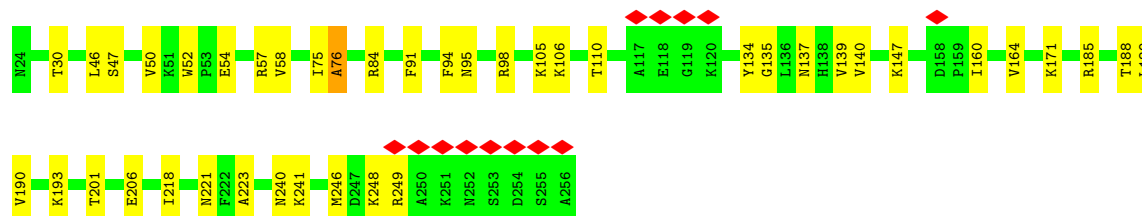
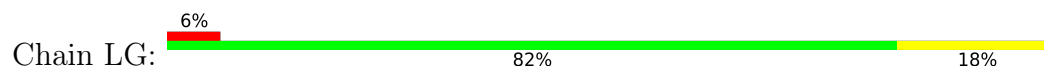
Chain LE: 81% 14% 5% .



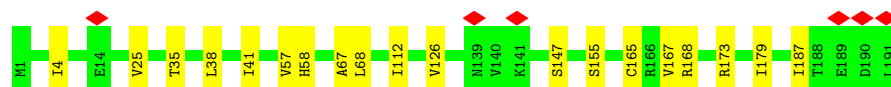
- Molecule 42: 60S ribosomal protein L7-A



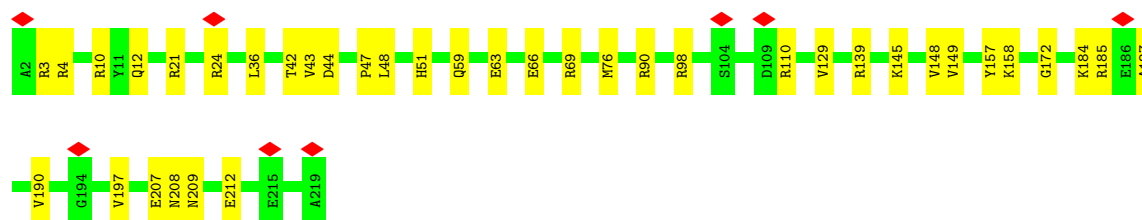
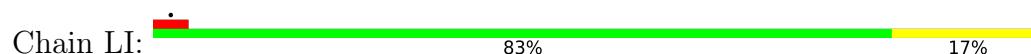
- Molecule 43: 60S ribosomal protein L8-A



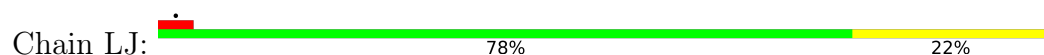
- Molecule 44: 60S ribosomal protein L9-A

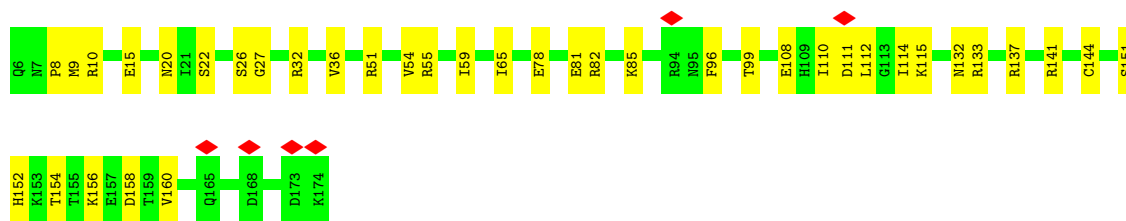


- Molecule 45: 60S ribosomal protein L10



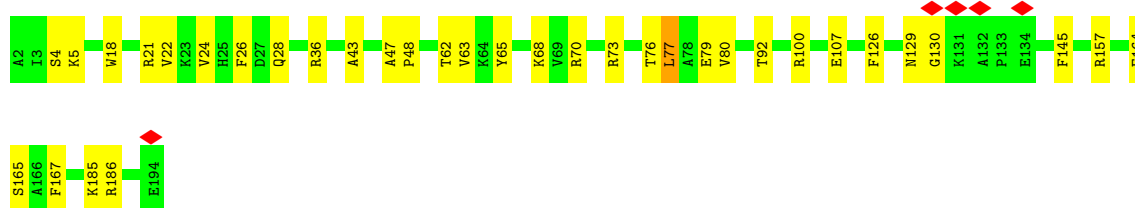
- Molecule 46: 60S ribosomal protein L11-B





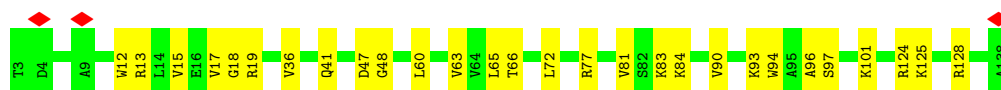
- Molecule 47: 60S ribosomal protein L13-A

Chain LL: 82% 18%



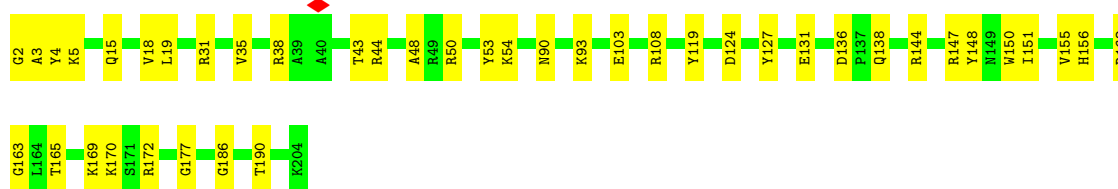
- Molecule 48: 60S ribosomal protein L14-A

Chain LM: 79% 21%



- Molecule 49: 60S ribosomal protein L15-A

Chain LN: 79% 21%



- Molecule 50: 60S ribosomal protein L16-A

Chain LO: 87% 12%

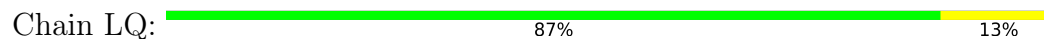


- Molecule 51: 60S ribosomal protein L17-A

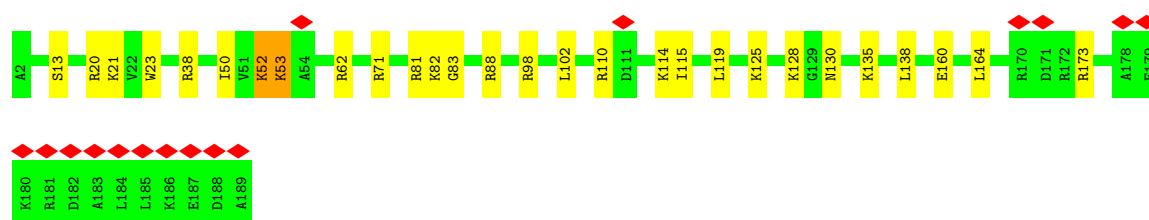
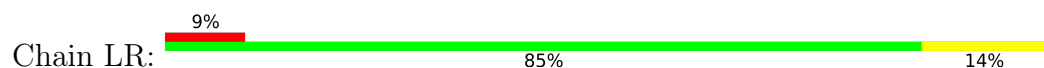
Chain LP: 7% 87% 13%



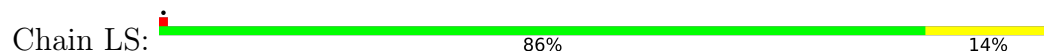
- Molecule 52: 60S ribosomal protein L18-A



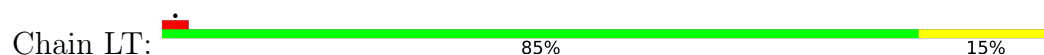
- Molecule 53: 60S ribosomal protein L19-A



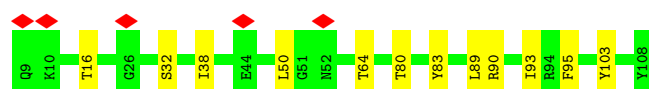
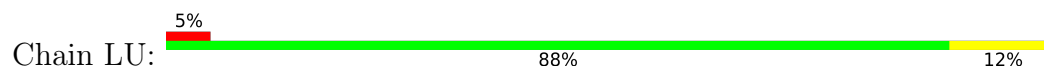
- Molecule 54: 60S ribosomal protein L20-A



- Molecule 55: 60S ribosomal protein L21-A



- Molecule 56: 60S ribosomal protein L22-A

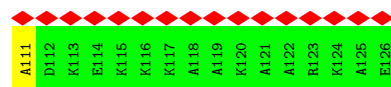
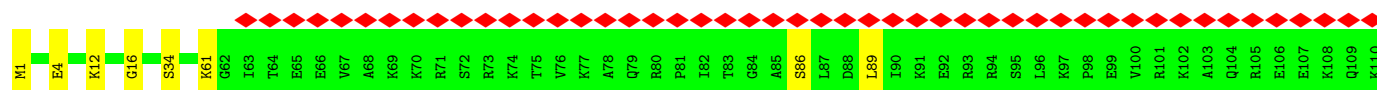


- Molecule 57: 60S ribosomal protein L23-A

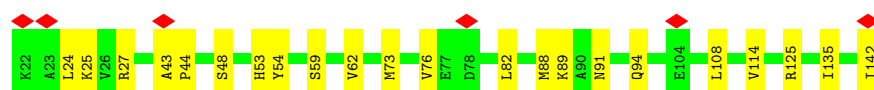
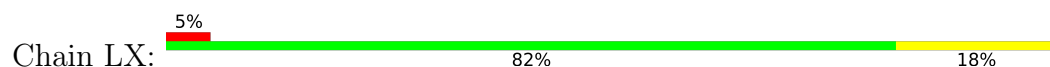




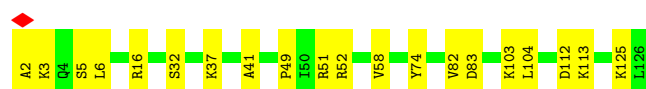
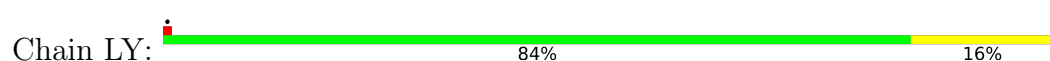
- Molecule 58: 60S ribosomal protein L24-A



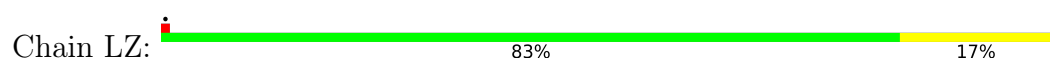
- Molecule 59: 60S ribosomal protein L25



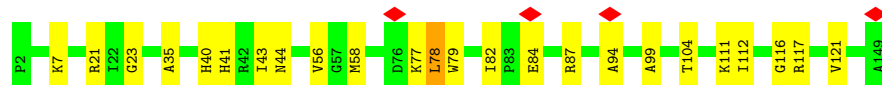
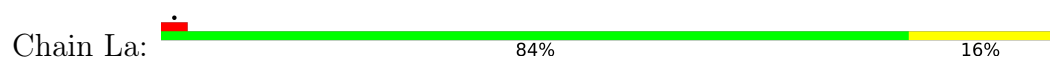
- Molecule 60: 60S ribosomal protein L26-A



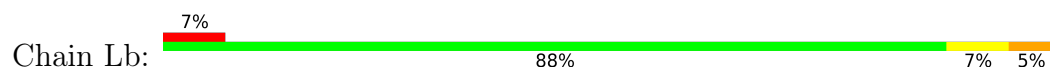
- Molecule 61: 60S ribosomal protein L27-A

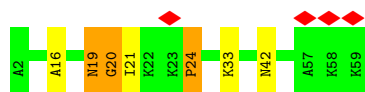


- Molecule 62: 60S ribosomal protein L28



- Molecule 63: 60S ribosomal protein L29

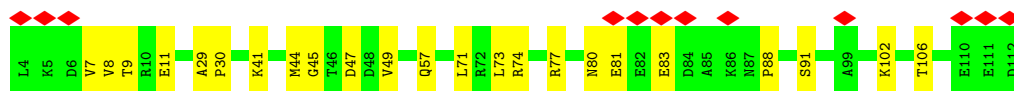
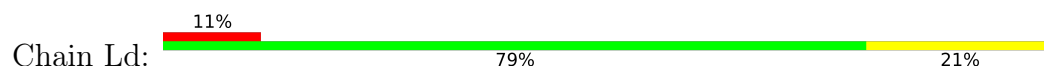




- Molecule 64: 60S ribosomal protein L30



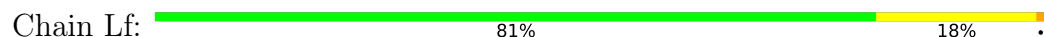
- Molecule 65: 60S ribosomal protein L31-A



- Molecule 66: 60S ribosomal protein L32



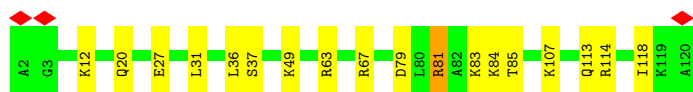
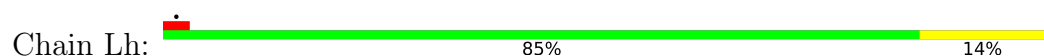
- Molecule 67: 60S ribosomal protein L33-A



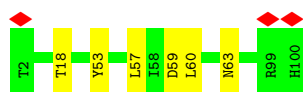
- Molecule 68: 60S ribosomal protein L34-A



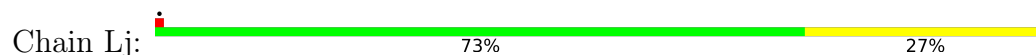
- Molecule 69: 60S ribosomal protein L35-A



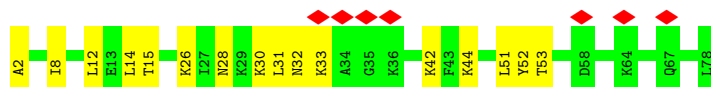
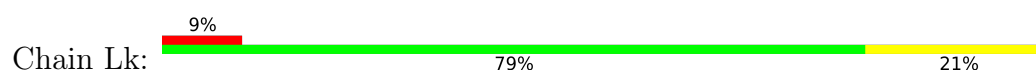
- Molecule 70: 60S ribosomal protein L36-A



- Molecule 71: 60S ribosomal protein L37-A



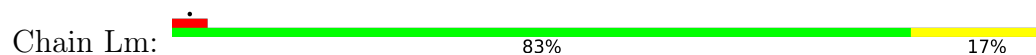
- Molecule 72: 60S ribosomal protein L38



- Molecule 73: 60S ribosomal protein L39



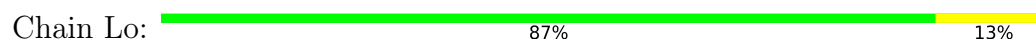
- Molecule 74: Ubiquitin-60S ribosomal protein L40



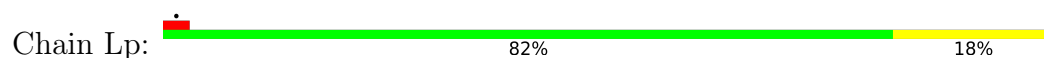
- Molecule 75: 60S ribosomal protein L41-A



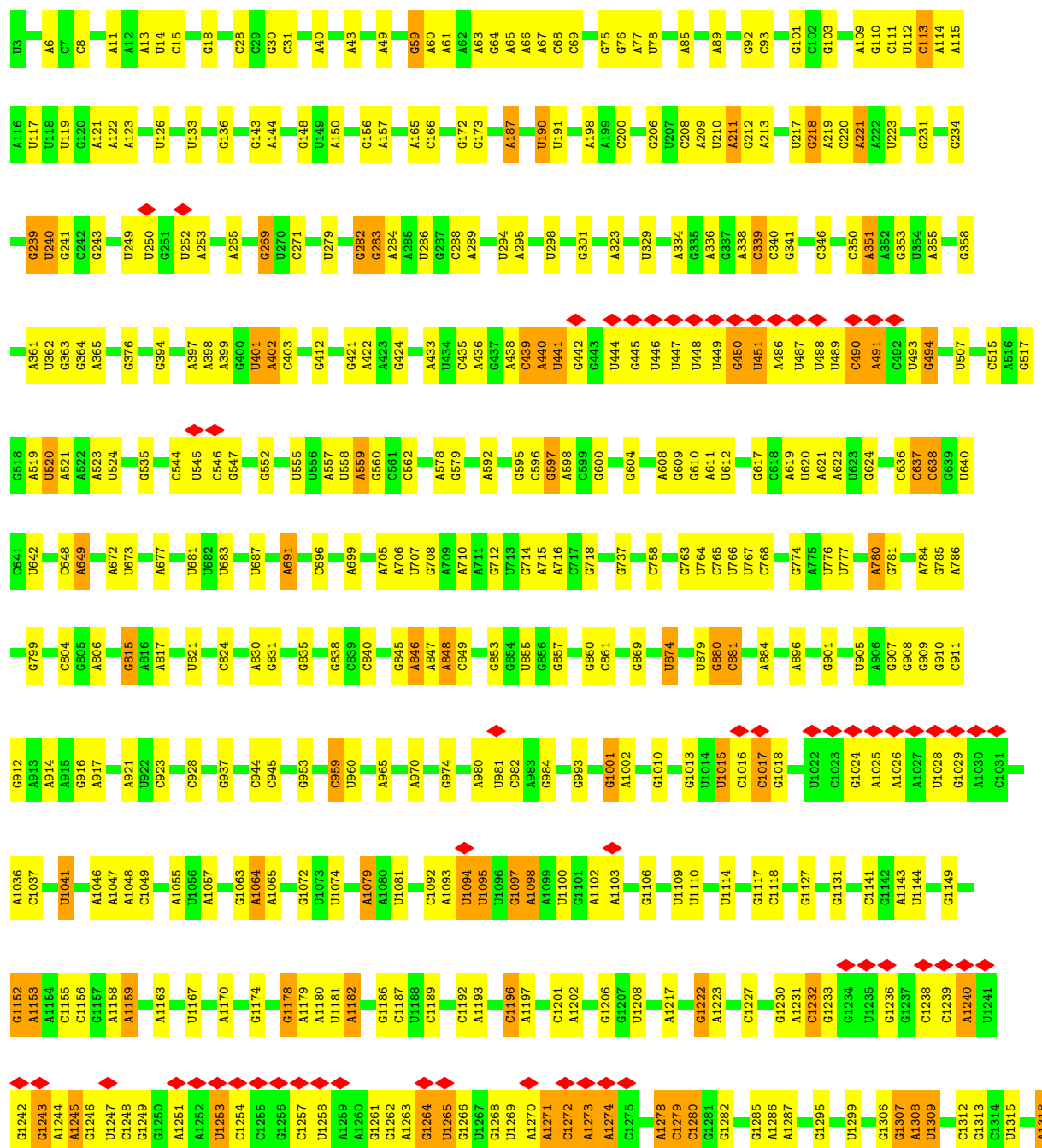
- Molecule 76: 60S ribosomal protein L42-A



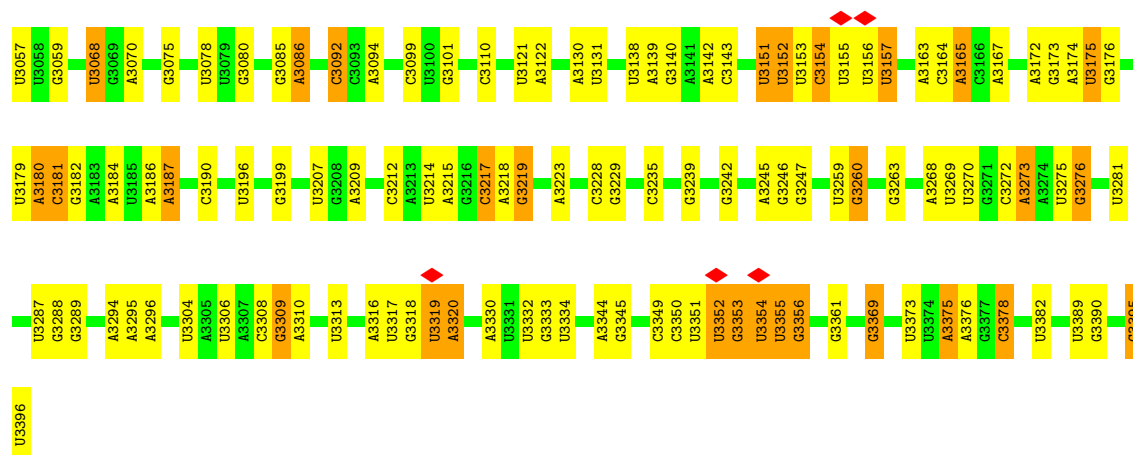
• Molecule 77: 60S ribosomal protein L43-A



• Molecule 78: 25S rRNA

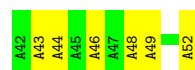


A2911	G2800	G2672	U2550	U2434	G2311	U2184	G1935	U1815	C1693	U1567	G1443	G1319
G2912	A2801	A2673	U2551	G2435	A2312	G2185	U1935	A1816	U1694	U1568	G1444	C1320
G2913	A2802	G2674	C2552	U2436	C2313	G2186	C1943	U1817	A1695	U1569	G1445	U1321
G2914	A2803	G2675	U2553	U2314	G2315	A2188	G1949	U1818	A1696	U1570	A1446	U1322
G2918	C2810	G2676	A2554	A2438	G2323	C2192	G1952	U1819	U1702	U1571	U1452	U1323
G2918	C2810	G2677	G2555	A2439	G2324	C2192	G1953	U1820	U1703	U1572	U1452	U1325
U2923	G2814	U2681	G2556	G2442	G2325	A2198	G1954	U1821	A1704	G1573	U1455	A1330
C2929	A2817	U2688	A2557	A2443	C2326	G2206	U1955	C1822	U1717	C1574	U1470	U1331
U2933	U2818	A2689	C2560	C2444	C2333	A2207	U1956	U1831	U1720	A1575	U1470	U1334
A2934	C2821	G2690	G2564	U2446	U2334	A2208	C2094	U1834	U1721	G1576	G1473	G1345
U2935	G2828	A2694	C2568	U2447	U2335	U2209	C2094	A1835	U1722	A1580	A1474	G1345
A2936	A2695	A2696	A2569	G2448	A2355	G2210	C2101	U1840	A1723	C1581	A1477	U1348
G2937	G2834	A2696	U2570	A2449	A2356	G2221	U102	A1841	U1724	C1582	A1477	U1349
G2938	U2703	U2704	G2571	G2450	A2357	A2222	U2103	A1842	C1725	A1583	G1480	A1350
G2939	A2704	G2451	C2572	G2451	A2104	A2223	A2104	A1843	A1729	A1588	G1481	U1351
A2940	A2705	G2452	C2573	G2452	C2360	A2224	A2107	C1844	A1736	A1589	A1482	A1352
A2941	A2838	G2452	G2574	G2452	A2361	U2225	A2107	G1846	U1737	C1596	G1483	U1353
C2942	U2842	U2717	G2580	U2493	C2362	G2231	G2111	A1847	U1737	C1597	G1493	G1354
G2943	U2843	U2718	U2581	U2493	C2366	G2236	U2112	C1848	A1741	A1603	U1494	A1355
U2944	C2844	U2719	C2582	A2494	A2373	G2245	A2113	C1849	U1742	G1604	C1497	U1356
G2945	A2845	U2722	C2583	C2495	A2374	C2246	C2114	A1850	G1743	U1607	C1505	U1357
A2946	U2846	A2727	G2584	C2496	G2374	C2246	G2115	A1858	G1748	C1608	C1508	A1373
G2947	A2847	G2728	G2585	U2497	G2375	G2246	G2116	A1859	A1749	U1613	U1523	G1383
C2948	U2848	U2729	G2586	U2498	G2377	G2249	G2117	A1864	A1750	U1620	A1524	U1384
U2971	C2852	C2737	A2593	U2499	C2382	A2255	G2121	A1865	G1751	G1624	G1525	C1385
G2972	U2860	C2742	C2594	A2500	C2383	A2256	G2122	A1866	A1760	U1629	C1527	G1386
G2972	U2861	C2742	A2595	U2501	G2388	C2257	U2129	A1867	C1761	U1630	U1533	G1389
G2973	C2852	U2752	C2600	A2502	U2388	U2258	G2130	G1872	G1762	C1631	A1534	C1390
C2983	U2860	G2753	G2606	U2506	C2392	A2259	A2131	G1875	U1763	C1632	A1535	C1391
U2989	C2867	G2754	G2607	C2507	G2393	G2261	U2137	U1880	U1764	C1633	G1536	G1392
G2990	U2868	C2755	G2614	C2507	G2394	G2272	A2138	U1886	G1770	G1634	G1542	A1399
A2991	C2867	C2755	G2614	U2514	A2397	G2273	A2139	A1887	G1771	G1635	G1543	G1400
U2996	U2875	G2764	G2618	A2515	A2398	U2274	A2142	G1889	U1772	A1638	G1547	G1404
G2997	A2872	U2767	G2619	A2522	A2399	U2274	A2143	U1894	G1775	C1639	U1547	A1407
C3002	G2877	U2768	G2625	G2523	G2400	A2279	A2144	A1895	G1778	A1642	U1554	A1418
A3008	A2887	A2769	C2625	A2524	A2401	A2280	A2144	A1896	C1779	A1643	U1555	A1419
G3009	U2888	G2770	C2625	G2525	A2402	A2281	A2144	G1897	G1780	G1644	C1556	G1420
A3012	C2889	G2770	C2625	G2526	G2403	U2282	G2161	U1906	G1794	U1645	A1557	G1421
A3021	A2890	G2777	U2631	C2526	A2404	U2282	G2161	C1907	U1795	G1658	A1558	U1428
G3030	C2894	G2778	A2635	A2529	U2411	G2288	U2153	G1914	A1797	G1661	G1561	G1429
A2895	A2895	A2780	G2645	G2530	G2412	U2292	A2158	U1930	C1802	G1662	C1562	C1432
A2897	A2897	U2781	G2645	C2531	C2415	U2292	U2159	A1930	G1812	G1677	C1563	A1433
U3041	G2898	G2786	G2648	U2532	C2415	A2295	G2160	U1931	A1813	U1682	U1564	G1434
G3043	C2899	G2786	G2648	G2533	A2419	A2303	G2161	A1932	A1814	U1683	A1566	C1437
A3046	A2900	G2794	U2652	U2537	A2419	A2303	G2169	G1914	G1802	U1683	A1566	C1437
U3050	G2901	U2795	A2656	U2538	C2422	G2307	U2170	U1930	G1812	U1683	A1566	C1437
	A2901	G2796	A2657	C2539	U2423	A2309	A2178	A1930	A1813	U1683	A1566	C1437
	G2908	A2799	G2658	A2540	A2424	U2310	C2181	A1932	A1814	U1683	A1566	C1437
				U2542	A2424	U2310	C2181	A1932	A1814	U1683	A1566	C1437
				U2544	A2424	U2310	C2181	A1932	A1814	U1683	A1566	C1437
				A2547	A2424	U2310	C2181	A1932	A1814	U1683	A1566	C1437
				C2548	A2424	U2310	C2181	A1932	A1814	U1683	A1566	C1437
				G2549	A2424	U2310	C2181	A1932	A1814	U1683	A1566	C1437



- Molecule 79: mRNA

Chain 5: 45% 55%



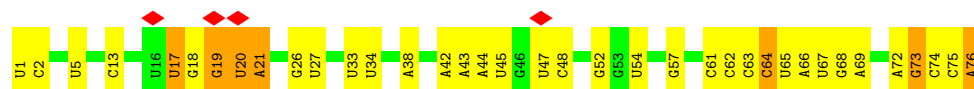
- Molecule 80: tRNA

Chain 7: 97% 61% 28% 12%



- Molecule 80: tRNA

Chain 6: 5% 51% 39% 9%



- Molecule 81: nascent chain

Chain A: 25% 50% 25%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	229084	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	2.5	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.533	Depositor
Minimum map value	-0.254	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.017	Depositor
Recommended contour level	0.045	Depositor
Map size ($\text{\AA}$)	433.6, 433.6, 433.6	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.084, 1.084, 1.084	Depositor

5 Model quality

5.1 Standard geometry

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	LA	0.59	0/1933	0.67	0/2598
2	SA	0.28	0/1644	0.48	0/2249
3	LB	0.55	0/3146	0.60	0/4228
4	SB	0.36	0/1823	0.61	0/2447
5	C2	0.28	0/42053	0.40	1/65522 (0.0%)
6	SP	0.24	0/936	0.49	0/1259
7	SC	0.35	0/1656	0.52	0/2251
8	SD	0.26	0/1754	0.51	0/2361
9	SE	0.31	0/2097	0.55	0/2823
10	SF	0.28	0/1625	0.54	0/2197
11	SG	0.28	0/1839	0.54	0/2460
12	SH	0.27	0/1498	0.55	0/2019
13	SI	0.37	0/1501	0.62	1/2006 (0.0%)
14	SJ	0.29	0/1504	0.55	0/2016
15	SK	0.22	0/769	0.47	0/1039
16	SL	0.39	0/1185	0.54	0/1598
17	SM	0.25	0/883	0.69	0/1199
18	SN	0.38	0/1215	0.58	0/1638
19	SO	0.38	0/937	0.63	0/1261
20	SQ	0.28	0/1125	0.54	0/1510
21	SR	0.25	0/957	0.56	0/1283
22	SS	0.27	0/1211	0.55	0/1628
23	ST	0.26	0/1130	0.48	0/1517
24	SU	0.28	0/807	0.50	0/1091
25	SV	0.31	0/682	0.64	1/921 (0.1%)
26	SW	0.39	0/1038	0.58	1/1395 (0.1%)
27	SX	0.39	0/1139	0.57	0/1518
28	SY	0.27	0/1087	0.54	0/1449
29	SZ	0.26	0/661	0.51	0/888
30	Sa	0.43	1/782 (0.1%)	0.75	0/1047
31	Sb	0.32	0/620	0.59	0/838
32	Sd	0.28	0/452	0.48	0/600
33	Se	0.26	0/480	0.49	0/639
34	Sf	0.22	0/567	0.58	0/764

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	Sg	0.22	0/2436	0.52	0/3318
36	Sc	0.29	0/493	0.55	0/663
37	C4	0.36	0/2883	0.38	0/4491
38	C3	0.40	0/3746	0.42	0/5832
39	LC	0.53	0/2800	0.58	0/3790
40	LD	0.41	0/2400	0.55	0/3239
41	LE	0.40	0/1327	0.59	1/1790 (0.1%)
42	LF	0.55	0/1821	0.60	0/2451
43	LG	0.43	0/1836	0.59	0/2481
44	LH	0.41	0/1529	0.51	0/2060
45	LI	0.49	0/1801	0.58	0/2416
46	LJ	0.39	0/1371	0.59	0/1838
47	LL	0.51	0/1568	0.61	0/2106
48	LM	0.44	0/1068	0.58	0/1438
49	LN	0.60	0/1757	0.62	1/2354 (0.0%)
50	LO	0.55	0/1585	0.58	0/2128
51	LP	0.54	0/1439	0.59	0/1938
52	LQ	0.56	1/1465 (0.1%)	0.58	0/1965
53	LR	0.47	0/1532	0.59	0/2043
54	LS	0.49	0/1473	0.57	1/1980 (0.1%)
55	LT	0.53	0/1300	0.58	0/1743
56	LU	0.34	0/812	0.50	0/1099
57	LV	0.54	0/1018	0.55	0/1369
58	LW	0.40	0/850	0.50	0/1152
59	LX	0.45	0/979	0.54	0/1321
60	LY	0.47	0/995	0.57	0/1329
61	LZ	0.41	0/1118	0.57	0/1497
62	La	0.56	0/1204	0.63	0/1612
63	Lb	0.45	0/473	0.64	0/629
64	Lc	0.43	0/745	0.54	0/1001
65	Ld	0.49	0/890	0.57	0/1196
66	Le	0.51	0/1038	0.54	0/1390
67	Lf	0.60	0/868	0.67	1/1168 (0.1%)
68	Lg	0.51	0/890	0.54	0/1189
69	Lh	0.45	0/978	0.58	0/1301
70	Li	0.41	0/772	0.58	0/1026
71	Lj	0.61	0/685	0.63	0/908
72	Lk	0.38	0/618	0.55	0/826
73	Ll	0.57	0/443	0.65	0/588
74	Lm	0.48	0/423	0.50	0/562
75	Ln	0.52	0/230	0.75	0/296
76	Lo	0.48	0/836	0.60	0/1104
77	Lp	0.51	0/701	0.58	0/934

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
78	C1	0.41	0/76214	0.43	0/118821
79	5	0.27	0/274	0.33	0/425
80	6	0.48	0/1804	0.41	0/2809
80	7	0.16	0/1804	0.37	0/2809
81	A	0.35	0/39	0.97	0/45
All	All	0.39	2/218067 (0.0%)	0.48	8/320729 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
3	LB	0	3
4	SB	0	4
9	SE	0	1
11	SG	0	1
12	SH	0	1
13	SI	0	1
14	SJ	0	1
16	SL	0	1
17	SM	0	4
19	SO	0	1
20	SQ	0	2
22	SS	0	1
26	SW	0	1
27	SX	0	1
29	SZ	0	1
30	Sa	0	3
31	Sb	0	1
34	Sf	0	1
39	LC	0	1
43	LG	0	2
48	LM	0	1
50	LO	0	1
53	LR	0	1
59	LX	0	1
60	LY	0	1
61	LZ	0	1
62	La	0	1
63	Lb	0	3
69	Lh	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
81	A	0	2
All	All	0	45

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
52	LQ	41	ASP	C-N	5.05	1.39	1.33
30	Sa	12	LYS	CA-CB	-5.01	1.46	1.53

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	SW	28	ARG	C-N-CD	-7.70	103.67	120.60
54	LS	140	VAL	N-CA-C	-6.13	106.97	112.12
25	SV	41	GLU	N-CA-CB	-5.84	107.51	114.17
67	Lf	21	ARG	N-CA-C	5.58	119.66	112.41
13	SI	80	GLY	N-CA-C	5.47	118.56	110.63
49	LN	177	GLY	N-CA-C	5.24	117.68	110.56
5	C2	555	A	C2'-C3'-O3'	5.20	117.31	109.50
41	LE	35	VAL	N-CA-C	-5.17	104.95	109.19

There are no chirality outliers.

All (45) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
81	A	176	LYS	Mainchain
3	LB	127	LYS	Peptide
3	LB	139	GLN	Peptide
3	LB	141	GLY	Peptide
39	LC	318	LEU	Peptide
43	LG	30	THR	Peptide
43	LG	76	ALA	Peptide
48	LM	12	TRP	Peptide
50	LO	110[A]	PRO	Peptide
53	LR	52	LYS	Peptide
59	LX	43	ALA	Peptide
60	LY	51	ARG	Peptide
61	LZ	58	GLY	Peptide
62	La	116	GLY	Peptide
63	Lb	19	ASN	Peptide
63	Lb	20	GLY	Peptide

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Mol	Chain	Res	Type	Group
63	Lb	24	PRO	Peptide
69	Lh	83	LYS	Peptide
4	SB	151	LYS	Peptide
4	SB	211	HIS	Peptide
4	SB	44	GLY	Peptide
4	SB	81	PHE	Peptide
9	SE	42	LEU	Peptide
11	SG	68	LEU	Peptide
12	SH	64	VAL	Peptide
13	SI	9	HIS	Peptide
14	SJ	99	LEU	Peptide
16	SL	4	GLU	Peptide
17	SM	110	GLY	Peptide
17	SM	128	ALA	Peptide
17	SM	130	THR	Peptide
17	SM	84	ASN	Peptide
19	SO	90	ARG	Peptide
20	SQ	33	GLY	Peptide
20	SQ	40	GLU	Peptide
22	SS	90	ASN	Peptide
26	SW	54	ASP	Peptide
27	SX	41	SER	Peptide
29	SZ	67	ASP	Peptide
30	Sa	36	ILE	Peptide
30	Sa	84	VAL	Peptide
30	Sa	9	GLY	Peptide
31	Sb	61	THR	Peptide
34	Sf	144	CYS	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	LA	1899	0	1957	31	0
2	SA	1603	0	1610	27	0
3	LB	3075	0	3142	62	0
4	SB	1798	0	1890	24	0
5	C2	37604	0	18919	405	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	SP	916	0	941	12	0
7	SC	1626	0	1715	35	0
8	SD	1729	0	1812	33	0
9	SE	2056	0	2140	39	0
10	SF	1605	0	1669	32	0
11	SG	1815	0	1894	48	0
12	SH	1473	0	1555	27	0
13	SI	1476	0	1501	44	0
14	SJ	1479	0	1556	19	0
15	SK	752	0	719	7	0
16	SL	1159	0	1225	14	0
17	SM	875	0	878	26	0
18	SN	1192	0	1255	20	0
19	SO	926	0	950	21	0
20	SQ	1105	0	1166	29	0
21	SR	948	0	990	18	0
22	SS	1192	0	1222	28	0
23	ST	1112	0	1124	18	0
24	SU	797	0	863	12	0
25	SV	673	0	662	15	0
26	SW	1021	0	1060	9	0
27	SX	1121	0	1196	24	0
28	SY	1073	0	1132	22	0
29	SZ	651	0	682	13	0
30	Sa	769	0	818	22	0
31	Sb	610	0	633	11	0
32	Sd	442	0	432	12	0
33	Se	472	0	521	6	0
34	Sf	556	0	549	19	0
35	Sg	2383	0	2332	40	0
36	Sc	491	0	524	10	0
37	C4	2579	0	1304	17	0
38	C3	3353	0	1695	36	0
39	LC	2748	0	2859	44	0
40	LD	2351	0	2294	42	0
41	LE	1305	0	1370	18	0
42	LF	1784	0	1862	25	0
43	LG	1804	0	1877	28	0
44	LH	1508	0	1572	15	0
45	LI	1764	0	1804	26	0
46	LJ	1350	0	1381	29	0
47	LL	1543	0	1608	28	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
48	LM	1053	0	1149	21	0
49	LN	1720	0	1779	33	0
50	LO	1555	0	1659	20	0
51	LP	1416	0	1433	20	0
52	LQ	1441	0	1543	20	0
53	LR	1515	0	1606	24	0
54	LS	1437	0	1475	20	0
55	LT	1276	0	1323	18	0
56	LU	796	0	812	8	0
57	LV	1003	0	1048	8	0
58	LW	836	0	709	9	0
59	LX	964	0	1025	16	0
60	LY	984	0	1075	14	0
61	LZ	1092	0	1155	16	0
62	La	1173	0	1215	18	0
63	Lb	462	0	491	8	0
64	Lc	737	0	792	5	0
65	Ld	876	0	912	15	0
66	Le	1017	0	1081	14	0
67	Lf	850	0	880	14	0
68	Lg	880	0	945	14	0
69	Lh	969	0	1078	15	0
70	Li	766	0	844	4	0
71	Lj	670	0	677	22	0
72	Lk	612	0	682	12	0
73	Ll	436	0	475	12	0
74	Lm	417	0	459	9	0
75	Ln	229	0	273	6	0
76	Lo	824	0	892	9	0
77	Lp	694	0	738	11	0
78	C1	68091	0	34216	507	0
79	5	242	0	122	1	0
80	6	1616	0	815	36	0
80	7	1616	0	816	12	0
81	A	41	0	56	18	0
All	All	202869	0	149110	1946	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

All (1946) 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)
80:6:76:A:H4'	81:A:177[A]:LYS:HG3	1.16	1.10
78:C1:2258:U:O2'	78:C1:2259:A:O5'	1.69	1.10
46:LJ:55:ARG:NH1	80:6:20:U:OP1	1.87	1.06
44:LH:41:ILE:HD11	44:LH:67:ALA:HB1	1.35	1.05
80:6:76:A:C4'	81:A:177[A]:LYS:HG3	1.86	1.05
78:C1:2258:U:O2'	78:C1:2259:A:C5'	2.07	1.02
5:C2:227:U:N3	5:C2:235:G:O6	1.99	0.95
78:C1:2258:U:H2'	78:C1:2259:A:H8	1.33	0.94
78:C1:2258:U:C2'	78:C1:2259:A:H8	1.82	0.92
45:LI:110:ARG:NH1	80:6:75:C:OP2	2.02	0.92
80:6:73:G:H5'	80:6:74:C:H5'	1.51	0.91
5:C2:227:U:C4	5:C2:235:G:O6	2.23	0.91
78:C1:2258:U:H2'	78:C1:2259:A:C8	2.06	0.90
3:LB:215:ILE:HD12	3:LB:338:LEU:HD12	1.52	0.90
78:C1:3349:C:O2	78:C1:3356:G:N2	2.05	0.90
35:Sg:220:ILE:O	35:Sg:233:THR:HA	1.72	0.90
37:C4:76:A:O2'	54:LS:50:LYS:NZ	2.04	0.89
5:C2:142:G:N7	11:SG:177:ARG:NH2	2.22	0.88
78:C1:2101:C:O2'	78:C1:2102:U:O5'	1.92	0.88
80:6:76:A:OP1	81:A:177[A]:LYS:HD2	1.73	0.87
5:C2:826:U:O4	5:C2:846:G:O6	1.93	0.87
58:LW:4:GLU:O	58:LW:12:LYS:HA	1.75	0.87
80:6:76:A:H4'	81:A:177[A]:LYS:CG	2.03	0.87
73:LI:21:ARG:NH1	73:LI:22:PRO:O	2.08	0.87
5:C2:704:C:H42	5:C2:734:A:N6	1.73	0.86
53:LR:62:ARG:NH1	78:C1:3068:U:OP2	2.08	0.86
54:LS:108:GLN:NE2	78:C1:1322:U:O2	2.07	0.86
35:Sg:156:VAL:HG12	35:Sg:169:ILE:HG22	1.56	0.86
44:LH:168:ARG:NH2	78:C1:2894:C:OP2	2.08	0.86
5:C2:1496:U:HO2'	5:C2:1519:U:HO2'	1.09	0.86
54:LS:22:PRO:O	55:LT:146:ASN:ND2	2.08	0.86
5:C2:1135:U:OP2	27:SX:121:ARG:NH2	2.10	0.84
78:C1:2531:C:N4	78:C1:2548:C:O2	2.10	0.84
5:C2:521:A:N3	28:SY:34:ASN:ND2	2.25	0.84
5:C2:1563:C:OP1	23:ST:84:LYS:NZ	2.10	0.84
4:SB:136:ARG:O	4:SB:215:VAL:HA	1.76	0.84
48:LM:60:LEU:HD13	54:LS:152:LEU:HD11	1.58	0.84
1:LA:65:ASP:OD2	1:LA:72:ARG:NH1	2.12	0.83
43:LG:241:LYS:NZ	78:C1:2526:C:O2	2.10	0.83
11:SG:32:ILE:HD11	11:SG:63:MET:HE3	1.61	0.83
18:SN:99:ARG:NH2	18:SN:119:GLU:OE2	2.12	0.83
67:Lf:21:ARG:NH2	78:C1:1149:G:OP2	2.12	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C2:61:A:O2'	5:C2:62:A:O4'	1.97	0.82
78:C1:3092:C:O2'	78:C1:3094:A:OP2	1.96	0.82
5:C2:227:U:O4	5:C2:235:G:O6	1.96	0.82
5:C2:1646:C:H4'	78:C1:2258:U:O4	1.79	0.82
5:C2:1198:G:OP1	5:C2:1199:G:O2'	1.97	0.82
50:LO:85[A]:ARG:NH2	78:C1:2383:C:OP2	2.13	0.82
73:Ll:27:ILE:O	73:Ll:33:ASN:ND2	2.13	0.82
78:C1:2899:C:O2'	78:C1:2901:G:OP2	1.97	0.82
50:LO:164[A]:SER:HG	78:C1:3181:C:HO2'	1.17	0.82
30:Sa:32:LYS:O	30:Sa:37:LYS:NZ	2.12	0.81
78:C1:441:U:OP2	78:C1:490:C:N4	2.13	0.81
1:LA:220:GLY:O	78:C1:2245:C:O2'	1.96	0.81
49:LN:169:LYS:NZ	78:C1:64:G:OP2	2.12	0.81
80:6:17:U:O2'	80:6:57:G:N2	2.13	0.81
81:A:175:LYS:HD3	81:A:175:LYS:N	1.95	0.81
68:Lg:59:PRO:O	78:C1:1802:C:O2'	1.98	0.81
5:C2:1472:C:C2	5:C2:1534:G:N2	2.48	0.81
78:C1:2323:G:O2'	78:C1:2325:G:OP2	1.98	0.81
39:LC:117:GLU:OE2	78:C1:673:U:O2'	1.99	0.81
4:SB:30:PHE:O	4:SB:45:LYS:HA	1.81	0.81
5:C2:1339:C:O2'	5:C2:1341:A:N7	2.13	0.81
38:C3:100:U:O2'	59:LX:89:LYS:NZ	2.13	0.81
9:SE:141:THR:OG1	9:SE:143:ASP:OD1	1.98	0.81
43:LG:147:LYS:O	43:LG:201:THR:OG1	1.99	0.81
53:LR:88:ARG:O	78:C1:1779:C:N4	2.14	0.81
5:C2:656:G:O6	5:C2:679:U:C2	2.34	0.80
61:LZ:135:ARG:O	78:C1:2555:G:N2	2.14	0.80
5:C2:1584:G:N2	5:C2:1611:A:OP2	2.13	0.80
35:Sg:42:LEU:HD11	35:Sg:68:VAL:HG11	1.61	0.80
5:C2:219:A:OP1	11:SG:227:ARG:NH2	2.15	0.80
5:C2:992:A:O2'	5:C2:1785:U:O2	1.99	0.80
73:Ll:20:ASN:ND2	73:Ll:42:ARG:O	2.14	0.80
78:C1:2258:U:O2'	78:C1:2259:A:O4'	2.00	0.80
38:C3:104:A:OP1	71:Lj:21:ARG:NH2	2.14	0.80
78:C1:1231:A:O2'	78:C1:1261:G:O2'	1.99	0.80
13:Sl:162:ALA:O	78:C1:3352:U:O2'	2.00	0.80
55:LT:99:SER:OG	55:LT:101:CYS:SG	2.40	0.80
19:SO:17:ALA:O	19:SO:29:HIS:O	2.00	0.80
55:LT:71:SER:OG	55:LT:91:LEU:O	1.99	0.79
5:C2:1022:C:O2'	5:C2:1125:A:N1	2.15	0.79
5:C2:1116:A:OP1	75:Ln:17:ARG:NH2	2.16	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C2:1787:C:OP1	19:SO:127:ARG:NH2	2.16	0.79
38:C3:95:G:OP2	71:Lj:72:ARG:NH1	2.16	0.79
42:LF:98:LYS:NZ	78:C1:1057:A:OP1	2.15	0.79
62:La:21:ARG:NH2	78:C1:640:U:OP1	2.15	0.79
5:C2:322:G:O2'	5:C2:323:A:OP2	2.00	0.79
5:C2:623:A:N6	5:C2:970:A:OP1	2.14	0.79
78:C1:2404:A:C2	81:A:174:ALA:HB3	2.17	0.79
5:C2:1558:U:OP2	5:C2:1559:A:O2'	2.01	0.79
5:C2:623:A:O2'	5:C2:624:G:OP1	2.01	0.79
78:C1:649:A:OP2	78:C1:2868:U:O2'	2.01	0.79
5:C2:959:U:OP2	31:Sb:20:LYS:NZ	2.15	0.78
61:LZ:22:LYS:NZ	61:LZ:129:TRP:O	2.17	0.78
5:C2:704:C:N4	5:C2:734:A:H61	1.82	0.78
73:Ll:2:ALA:N	78:C1:1493:G:O6	2.16	0.78
78:C1:1348:U:O2	78:C1:1349:G:N2	2.17	0.78
47:LL:126:PHE:O	69:Lh:114:ARG:NH2	2.16	0.78
51:LP:141:SER:OG	78:C1:2355:G:OP1	2.01	0.78
53:LR:62:ARG:NH2	78:C1:3070:A:OP1	2.16	0.78
61:LZ:17:ARG:NH1	78:C1:1634:G:N7	2.30	0.78
10:SF:148:ARG:NH2	80:7:32:C:O2'	2.17	0.78
61:LZ:67:LYS:NZ	78:C1:1630:U:OP1	2.17	0.78
80:7:58:A:O2'	80:7:60:C:OP2	2.02	0.78
37:C4:28:C:OP1	46:LJ:137:ARG:NH1	2.16	0.78
66:Le:98:HIS:O	66:Le:125:ARG:NH2	2.16	0.78
5:C2:227:U:O4	5:C2:230:C:N4	2.17	0.78
5:C2:629:U:O4	5:C2:970:A:N7	2.17	0.78
46:LJ:99:THR:O	46:LJ:154:THR:OG1	2.01	0.78
54:LS:161:LYS:NZ	78:C1:3209:A:OP2	2.17	0.78
5:C2:337:G:O2'	13:SI:10:LYS:NZ	2.17	0.77
38:C3:136:G:OP1	59:LX:48:SER:OG	2.00	0.77
5:C2:1227:A:OP1	5:C2:1229:G:O2'	2.03	0.77
27:SX:42:PRO:O	27:SX:79:ASN:ND2	2.18	0.77
30:Sa:83:ILE:O	30:Sa:85:ARG:N	2.16	0.77
5:C2:819:G:C6	5:C2:853:G:C2	2.72	0.77
5:C2:1173:C:OP1	22:SS:132:ARG:NH2	2.17	0.77
5:C2:1611:A:OP1	10:SF:107:LYS:NZ	2.16	0.77
78:C1:339:C:OP1	78:C1:1380:G:O2'	2.02	0.77
80:7:10:G:N2	80:7:25:C:O2	2.17	0.77
50:LO:27[A]:LEU:O	50:LO:101[A]:ARG:NH1	2.17	0.77
78:C1:282:G:O2'	78:C1:283:G:OP2	2.03	0.77
5:C2:1534:G:O2'	5:C2:1535:U:O2	2.02	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
78:C1:1239:C:O2	78:C1:1249:G:N2	2.15	0.77
9:SE:185:GLY:H	9:SE:189:LEU:HD13	1.51	0.76
39:LC:98:ARG:NH2	78:C1:804:C:OP1	2.18	0.76
5:C2:428:A:N3	5:C2:440:U:O2'	2.17	0.76
13:SI:89:GLU:OE2	13:SI:92:ARG:NH2	2.17	0.76
62:La:58:MET:SD	78:C1:2786:G:N2	2.54	0.76
80:6:19:G:O2'	80:6:21:A:OP1	2.04	0.76
1:LA:69:TYR:OH	78:C1:2557:A:OP1	2.01	0.76
45:LI:209:ASN:O	45:LI:212:GLU:O	2.03	0.76
5:C2:154:G:O6	28:SY:128:LYS:NZ	2.18	0.76
34:Sf:125:THR:OG1	34:Sf:144:CYS:SG	2.43	0.76
38:C3:126:A:O2'	38:C3:128:U:OP2	2.03	0.76
43:LG:52:TRP:O	43:LG:57:ARG:NH1	2.18	0.76
48:LM:125:LYS:NZ	78:C1:3215:A:OP2	2.18	0.76
63:Lb:19:ASN:ND2	78:C1:970:A:OP2	2.18	0.76
78:C1:2307:G:O2'	78:C1:2310:U:OP2	2.04	0.76
5:C2:142:G:OP2	11:SG:139:ASN:ND2	2.19	0.76
61:LZ:64:LYS:NZ	78:C1:1812:G:N7	2.33	0.76
78:C1:221:A:O2'	78:C1:223:U:OP2	2.04	0.76
5:C2:1009:U:OP2	19:SO:129:LYS:NZ	2.19	0.76
39:LC:325:LEU:O	42:LF:41:ARG:NH2	2.19	0.76
5:C2:383:G:OP1	9:SE:6:LYS:NZ	2.18	0.76
5:C2:477:A:OP2	33:Se:28:LYS:NZ	2.19	0.76
78:C1:117:U:O2'	78:C1:119:U:OP2	2.00	0.76
5:C2:487:G:C6	5:C2:501:U:N3	2.54	0.76
42:LF:210:PRO:O	78:C1:1167:U:O2'	2.04	0.76
49:LN:31:ARG:NH1	49:LN:124:ASP:OD2	2.19	0.76
74:Lm:125:LYS:NZ	78:C1:2847:A:O4'	2.18	0.76
76:Lo:13:LYS:NZ	78:C1:2717:U:O3'	2.19	0.76
78:C1:439:C:O2'	78:C1:440:A:OP1	2.05	0.75
81:A:175:LYS:HD3	81:A:175:LYS:H	1.48	0.75
5:C2:159:U:O2'	11:SG:87:ARG:NH1	2.19	0.75
5:C2:272:U:O2	5:C2:284:G:N2	2.20	0.75
5:C2:539:G:O2'	5:C2:540:G:O5'	2.03	0.75
71:Lj:2:GLY:N	78:C1:2138:A:HO2'	1.84	0.75
3:LB:244:ARG:NH2	78:C1:2948:C:OP1	2.20	0.75
9:SE:100:ARG:NH2	9:SE:121:TYR:O	2.19	0.75
48:LM:128:ARG:NH1	78:C1:3214:U:OP2	2.20	0.75
5:C2:1615:C:O2'	5:C2:1616:G:OP2	2.05	0.75
53:LR:125:LYS:NZ	78:C1:840:C:O3'	2.20	0.75
16:SL:16:GLN:NE2	16:SL:61:THR:OG1	2.20	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C2:1594:G:OP2	5:C2:1596:C:N4	2.19	0.75
71:Lj:13:ASN:ND2	78:C1:901:G:OP1	2.18	0.75
80:6:76:A:OP1	81:A:177[A]:LYS:CD	2.34	0.75
5:C2:151:G:N3	11:SG:13:GLN:NE2	2.35	0.75
5:C2:1548:G:O2'	22:SS:89:GLN:NE2	2.20	0.75
22:SS:16:ARG:NH2	22:SS:19:ASN:OD1	2.20	0.75
49:LN:5:LYS:NZ	78:C1:265:A:O2'	2.18	0.75
5:C2:656:G:O6	5:C2:679:U:O2	2.05	0.74
5:C2:704:C:H42	5:C2:734:A:H61	1.34	0.74
10:SF:92:ARG:NH2	10:SF:169:ASN:OD1	2.19	0.74
5:C2:1550:A:OP2	6:SP:42:ARG:NH2	2.20	0.74
24:SU:80:GLU:OE1	32:Sd:44:ARG:NH1	2.20	0.74
55:LT:4:SER:OG	78:C1:2631:U:OP2	2.05	0.74
55:LT:119:ALA:HB3	55:LT:126:VAL:HG13	1.69	0.74
1:LA:27:ALA:O	1:LA:128:ARG:NH2	2.20	0.74
5:C2:235:G:O2'	5:C2:236:A:O5'	2.05	0.74
78:C1:2568:C:O2'	78:C1:2569:A:O4'	2.04	0.74
5:C2:230:C:O2	5:C2:236:A:N6	2.20	0.74
40:LD:77:ALA:O	40:LD:108:ARG:NH1	2.20	0.74
45:LI:66:GLU:OE1	45:LI:69:ARG:NH2	2.21	0.74
5:C2:44:U:OP2	5:C2:437:A:N6	2.21	0.74
8:SD:209:ILE:O	21:SR:20:TYR:OH	2.05	0.74
27:SX:102:VAL:HG12	27:SX:127:VAL:HG12	1.70	0.74
43:LG:137:ASN:OD1	49:LN:3:ALA:N	2.20	0.74
52:LQ:123:THR:OG1	52:LQ:125:ASP:OD1	2.05	0.74
49:LN:155:VAL:O	49:LN:162:ARG:NH2	2.21	0.74
54:LS:12:ARG:NH1	54:LS:57:GLU:OE2	2.19	0.74
76:Lo:30:ALA:O	78:C1:2767:U:O2'	2.05	0.74
78:C1:2842:U:OP1	78:C1:2844:C:N4	2.20	0.74
5:C2:68:A:OP1	11:SG:171:LYS:NZ	2.20	0.74
5:C2:705:U:O2'	5:C2:706:A:O5'	2.04	0.74
52:LQ:40:THR:OG1	52:LQ:45:ASN:OD1	2.05	0.74
5:C2:235:G:N7	5:C2:834:G:N2	2.36	0.74
46:LJ:15:GLU:OE2	46:LJ:132:ASN:ND2	2.20	0.74
61:LZ:56:LYS:NZ	78:C1:2574:G:OP2	2.20	0.74
61:LZ:69:LYS:NZ	78:C1:1632:A:OP1	2.21	0.74
5:C2:487:G:N1	5:C2:501:U:C2	2.56	0.73
47:LL:4:SER:O	62:La:44:ASN:ND2	2.21	0.73
80:7:46:G:O2'	80:7:47:U:OP1	2.05	0.73
5:C2:1297:G:N2	5:C2:1300:A:OP2	2.19	0.73
22:SS:91:ASP:OD2	22:SS:108:LYS:NZ	2.20	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:Sc:27:GLN:OE1	36:Sc:43:ASN:ND2	2.21	0.73
78:C1:1243:G:HO2'	78:C1:1271:A:HO2'	1.33	0.73
78:C1:1243:G:O2'	78:C1:1271:A:O2'	2.04	0.73
5:C2:1459:C:OP2	22:SS:138:THR:OG1	2.05	0.73
11:SG:160:ARG:O	11:SG:170:THR:C	2.32	0.73
60:LY:2:ALA:N	78:C1:212:G:OP2	2.21	0.73
27:SX:96:VAL:HG12	27:SX:127:VAL:HG11	1.69	0.73
74:Lm:100:TYR:O	78:C1:2895:G:O2'	2.06	0.73
3:LB:35:ASP:OD2	3:LB:37:ARG:NH1	2.22	0.73
43:LG:95:ASN:OD1	43:LG:98:ARG:NH2	2.21	0.73
50:LO:74[A]:ARG:NH1	78:C1:3008:A:OP2	2.21	0.73
67:Lf:57:LYS:NZ	78:C1:433:A:OP2	2.20	0.73
78:C1:198:A:N3	78:C1:218:G:O2'	2.22	0.73
27:SX:111:GLY:O	27:SX:121:ARG:NH1	2.21	0.73
78:C1:1015:U:O2'	78:C1:1017:C:OP2	2.07	0.73
5:C2:186:C:OP2	13:SI:142:LYS:NZ	2.21	0.73
7:SC:236:PRO:O	25:SV:33:GLN:NE2	2.21	0.73
48:LM:84:LYS:NZ	78:C1:559:A:O2'	2.22	0.73
4:SB:111:ARG:NH2	5:C2:930:A:N3	2.36	0.73
5:C2:207:U:O2	13:SI:178:ARG:NH1	2.21	0.73
5:C2:704:C:N3	5:C2:734:A:N1	2.36	0.73
2:SA:103:THR:O	2:SA:106:SER:OG	2.05	0.72
5:C2:979:A:N3	5:C2:1775:U:O2'	2.21	0.72
5:C2:1784:C:H41	75:Ln:5:TRP:HH2	1.36	0.72
7:SC:222:TYR:OH	25:SV:11:LEU:O	2.06	0.72
55:LT:88:ARG:O	78:C1:2722:U:O2'	2.05	0.72
73:Ll:42:ARG:NH2	78:C1:1494:U:OP1	2.22	0.72
77:Lp:46:THR:OG1	77:Lp:57:CYS:SG	2.47	0.72
78:C1:2282:U:OP1	78:C1:2973:G:O2'	2.06	0.72
8:SD:94:ARG:O	8:SD:101:GLN:NE2	2.22	0.72
78:C1:2258:U:O2'	78:C1:2259:A:H8	1.73	0.72
5:C2:1504:G:OP1	23:ST:97:SER:OG	2.07	0.72
78:C1:68:C:OP2	78:C1:301:G:N2	2.22	0.72
3:LB:28:ARG:NH2	78:C1:3140:G:N7	2.38	0.72
78:C1:2945:G:O2'	78:C1:2948:C:OP2	2.04	0.72
78:C1:3154:C:N3	78:C1:3157:U:O4	2.22	0.72
5:C2:1767:G:OP1	5:C2:1770:U:O2'	2.06	0.71
45:LI:190:VAL:HG13	45:LI:197:VAL:HG21	1.71	0.71
78:C1:2525:G:O2'	78:C1:2526:C:OP2	2.02	0.71
4:SB:113:MET:HE1	4:SB:211:HIS:HB2	1.71	0.71
38:C3:126:A:O2'	38:C3:129:C:N4	2.22	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:LZ:55:LYS:NZ	78:C1:2564:G:OP2	2.17	0.71
78:C1:2185:G:O2'	78:C1:2314:U:OP2	2.08	0.71
5:C2:930:A:OP1	30:Sa:32:LYS:NZ	2.17	0.71
64:Lc:30:THR:HG23	64:Lc:91:SER:HB2	1.73	0.71
3:LB:10:ARG:NH1	3:LB:263:SER:O	2.23	0.71
5:C2:944:A:OP2	30:Sa:19:LYS:NZ	2.23	0.71
5:C2:1371:A:O2'	5:C2:1373:C:OP1	2.07	0.71
5:C2:1382:A:O2'	5:C2:1383:G:OP1	2.08	0.71
13:SI:2:GLY:O	13:SI:24:LYS:NZ	2.17	0.71
65:Ld:41:LYS:NZ	65:Ld:47:ASP:OD1	2.17	0.71
5:C2:742:U:O2	12:SH:107:ARG:NH2	2.21	0.71
43:LG:240:ASN:OD1	78:C1:2584:G:O2'	2.09	0.71
53:LR:98:ARG:NH2	53:LR:130:ASN:OD1	2.23	0.71
5:C2:1502:G:N7	23:ST:102:ARG:NH2	2.39	0.71
8:SD:74:GLN:NE2	8:SD:79:TYR:O	2.24	0.71
12:SH:14:THR:OG1	12:SH:15:GLU:OE2	2.08	0.71
28:SY:5:VAL:O	28:SY:28:LEU:O	2.07	0.71
47:LL:36:ARG:NH2	78:C1:687:U:OP2	2.23	0.71
3:LB:256:HIS:O	78:C1:2940:A:O2'	2.06	0.71
5:C2:68:A:N6	11:SG:132:ARG:O	2.24	0.71
5:C2:861:U:OP1	18:SN:64:ARG:NH2	2.23	0.71
57:LV:81:GLN:O	57:LV:98:ASN:ND2	2.22	0.71
78:C1:2258:U:C2'	78:C1:2259:A:C8	2.66	0.71
10:SF:200:ASN:ND2	10:SF:207:THR:OG1	2.24	0.71
35:Sg:248:ASN:ND2	35:Sg:297:ASP:O	2.23	0.71
38:C3:21:C:OP1	39:LC:193:LYS:NZ	2.13	0.71
78:C1:3375:A:O2'	78:C1:3378:C:OP2	2.09	0.71
5:C2:1387:G:N7	21:SR:44:LYS:NZ	2.38	0.71
76:Lo:34:SER:OG	76:Lo:35:LEU:O	2.07	0.71
5:C2:473:A:OP1	14:SJ:44:ARG:NH1	2.23	0.71
7:SC:120:GLU:OE1	8:SD:120:TYR:OH	2.09	0.71
61:LZ:28:PRO:O	61:LZ:29:HIS:ND1	2.23	0.71
3:LB:246:LEU:N	78:C1:1889:G:OP1	2.24	0.70
41:LE:35:VAL:O	41:LE:38:THR:OG1	2.09	0.70
50:LO:128[A]:ARG:NH2	78:C1:1318:A:OP1	2.24	0.70
78:C1:1015:U:O2	78:C1:1017:C:O2'	2.08	0.70
69:Lh:81:ARG:NH1	69:Lh:81:ARG:O	2.24	0.70
78:C1:1253:U:N3	78:C1:1264:G:OP1	2.25	0.70
5:C2:704:C:N4	5:C2:732:G:O2'	2.24	0.70
5:C2:868:G:N2	18:SN:48:SER:OG	2.23	0.70
78:C1:1695:U:O2'	78:C1:1749:A:N1	2.23	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:SB:5:LYS:NZ	19:SO:51:ASP:OD2	2.25	0.70
5:C2:467:G:O2'	5:C2:469:C:OP2	2.05	0.70
5:C2:486:G:O6	5:C2:502:U:O4	2.09	0.70
5:C2:391:A:OP2	13:SI:23:LYS:NZ	2.22	0.70
43:LG:171:LYS:NZ	43:LG:223:ALA:O	2.25	0.70
68:Lg:74:ARG:NH2	78:C1:1639:C:OP2	2.23	0.70
78:C1:2618:G:N2	78:C1:2645:G:OP1	2.24	0.70
5:C2:1601:G:OP1	23:ST:86:ARG:NH2	2.25	0.70
22:SS:16:ARG:NH1	46:LJ:111:ASP:OD1	2.24	0.70
46:LJ:133:ARG:NH2	46:LJ:158:ASP:OD2	2.24	0.69
67:Lf:87:ASN:ND2	78:C1:624:G:OP1	2.23	0.69
11:SG:47:GLY:O	11:SG:115:LYS:NZ	2.24	0.69
14:SJ:36:LEU:HD21	14:SJ:108:ARG:HH12	1.56	0.69
77:Lp:17:ARG:NH1	78:C1:860:G:OP1	2.25	0.69
5:C2:59:C:O2'	5:C2:60:U:O4'	2.09	0.69
5:C2:1706:C:O2'	5:C2:1707:A:O4'	2.06	0.69
20:SQ:31:VAL:N	20:SQ:34:SER:O	2.25	0.69
33:Se:38:LEU:O	33:Se:41:THR:OG1	2.09	0.69
80:6:5:U:H3	80:6:68:G:H1	1.39	0.69
5:C2:45:U:O2	5:C2:434:G:O2'	2.10	0.69
5:C2:696:C:OP2	5:C2:697:C:N4	2.24	0.69
52:LQ:38:ARG:NH2	78:C1:1348:U:OP2	2.26	0.69
78:C1:1566:A:N1	78:C1:1571:A:N6	2.41	0.69
9:SE:129:VAL:HG12	9:SE:139:VAL:HG12	1.74	0.69
2:SA:84:ARG:NH2	21:SR:82:ASP:O	2.26	0.69
5:C2:332:U:OP2	13:SI:175:GLN:NE2	2.25	0.69
45:LI:21:ARG:O	45:LI:24:ARG:NH2	2.25	0.69
38:C3:143:U:OP1	49:LN:38:ARG:NH2	2.24	0.69
61:LZ:48:ARG:NH2	78:C1:1631:C:OP2	2.26	0.69
28:SY:41:ARG:NH2	28:SY:52:LYS:O	2.25	0.69
35:Sg:108:SER:OG	35:Sg:128:ASP:N	2.26	0.69
13:SI:106:ALA:HB2	13:SI:165:LEU:HG	1.74	0.68
16:SL:93:TYR:OH	16:SL:98:ASN:OD1	2.11	0.68
49:LN:147:ARG:NE	78:C1:113:C:OP1	2.24	0.68
5:C2:55:A:OP1	28:SY:112:LYS:NZ	2.21	0.68
47:LL:145:PHE:HE1	69:Lh:118:ILE:HD11	1.57	0.68
13:SI:5:ARG:NH1	13:SI:29:LEU:O	2.27	0.68
5:C2:143:G:OP2	11:SG:139:ASN:ND2	2.26	0.68
5:C2:479:C:O3'	14:SJ:120:LYS:NZ	2.27	0.68
58:LW:16:GLY:O	78:C1:3050:U:O2'	2.06	0.68
5:C2:1231:U:O2'	5:C2:1258:U:O2'	2.12	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:SR:100:LEU:O	21:SR:120:SER:N	2.26	0.68
22:SS:16:ARG:NE	46:LJ:108:GLU:OE2	2.26	0.68
49:LN:93:LYS:NZ	78:C1:2600:C:OP1	2.26	0.68
69:Lh:107:LYS:NZ	78:C1:112:U:OP1	2.27	0.68
3:LB:66:LYS:O	3:LB:70:ARG:NH1	2.27	0.68
5:C2:486:G:C6	5:C2:502:U:C4	2.82	0.68
13:SI:47:ARG:NH2	13:SI:48:THR:O	2.27	0.68
44:LH:57:VAL:HG23	44:LH:68:LEU:HD12	1.76	0.68
47:LL:73:ARG:NH2	78:C1:77:A:OP2	2.25	0.68
5:C2:1585:U:OP1	20:SQ:125:GLU:N	2.27	0.68
10:SF:216:GLU:OE1	10:SF:219:ARG:NH1	2.26	0.68
25:SV:73:ALA:HB3	25:SV:79:LEU:HD12	1.76	0.68
51:LP:182:ILE:HD11	78:C1:3217:C:C2	2.28	0.68
5:C2:1582:U:O2'	5:C2:1583:A:OP2	2.11	0.67
50:LO:87[A]:MET:HE2	78:C1:1174:G:N2	2.08	0.67
49:LN:4:TYR:OH	78:C1:148:G:OP2	2.07	0.67
3:LB:187:SER:O	3:LB:190:GLU:N	2.26	0.67
5:C2:129:U:O2'	5:C2:131:C:N4	2.25	0.67
40:LD:126:GLU:N	40:LD:126:GLU:OE1	2.27	0.67
42:LF:94:LYS:NZ	78:C1:1156:C:OP2	2.26	0.67
78:C1:3306:U:O2'	78:C1:3308:C:OP2	2.03	0.67
6:SP:18:ARG:NH1	22:SS:90:ASN:OD1	2.28	0.67
36:Sc:31:GLU:OE2	36:Sc:37:SER:N	2.26	0.67
5:C2:819:G:C5	5:C2:853:G:C2	2.82	0.67
5:C2:1275:A:N3	8:SD:141:LYS:NZ	2.38	0.67
46:LJ:20:ASN:ND2	78:C1:2681:U:O2	2.27	0.67
5:C2:637:C:O2	12:SH:114:ARG:NH1	2.28	0.67
42:LF:30:ARG:NH2	78:C1:595:G:OP2	2.27	0.67
27:SX:69:ARG:NH2	27:SX:116:ASP:OD2	2.28	0.67
47:LL:129:ASN:OD1	47:LL:130:GLY:N	2.28	0.67
78:C1:441:U:N3	78:C1:493:U:O2'	2.28	0.67
5:C2:545:A:O4'	5:C2:594:A:N6	2.28	0.67
22:SS:92:ILE:HG23	22:SS:93:THR:HG23	1.77	0.67
38:C3:149:A:H61	78:C1:8:C:N4	1.92	0.67
53:LR:71:ARG:NH1	78:C1:2101:C:OP2	2.28	0.67
5:C2:765:G:O6	14:SJ:149:ARG:NH2	2.27	0.67
52:LQ:2:GLY:N	78:C1:1159:A:OP1	2.28	0.67
78:C1:449:U:O2'	78:C1:450:G:N2	2.28	0.67
78:C1:2514:U:OP2	78:C1:2586:G:N2	2.27	0.67
52:LQ:16:ARG:NH1	78:C1:672:A:OP1	2.28	0.66
67:Lf:49:ILE:HD11	67:Lf:71:VAL:HG22	1.76	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
78:C1:2875:U:H5	81:A:177[B]:LYS:HG2	1.59	0.66
51:LP:171:ARG:NH1	78:C1:3276:G:N7	2.43	0.66
65:Ld:102:LYS:NZ	78:C1:3373:U:OP2	2.18	0.66
78:C1:959:C:O2	78:C1:2614:G:O2'	2.13	0.66
78:C1:1244:A:O2'	78:C1:1247:U:OP1	2.10	0.66
5:C2:1387:G:H21	5:C2:1410:A:H61	1.42	0.66
50:LO:110[A]:PRO:O	50:LO:112[A]:TYR:N	2.27	0.66
5:C2:1677:C:H42	5:C2:1724:U:H3	1.42	0.66
78:C1:2537:U:O2'	78:C1:2538:U:O5'	2.10	0.66
5:C2:555:A:O2'	5:C2:556:A:O4'	2.12	0.66
22:SS:117:LYS:O	22:SS:120:ARG:NH2	2.29	0.66
55:LT:9:SER:O	55:LT:55:LYS:NZ	2.25	0.66
74:Lm:114:LYS:O	78:C1:1299:U:O2'	2.14	0.66
5:C2:1430:U:O2'	5:C2:1431:C:OP1	2.09	0.66
24:SU:20:ILE:N	24:SU:94:GLU:OE1	2.29	0.66
66:Le:81:ASP:O	66:Le:84:THR:OG1	2.14	0.66
5:C2:1211:A:N3	6:SP:97:TYR:OH	2.26	0.65
45:LI:209:ASN:O	45:LI:212:GLU:C	2.40	0.65
52:LQ:21:SER:OG	78:C1:673:U:OP1	2.12	0.65
1:LA:146:THR:HG1	1:LA:160:SER:HG	1.42	0.65
5:C2:487:G:C2	5:C2:501:U:C2	2.84	0.65
38:C3:60:U:OP1	59:LX:54:TYR:OH	2.13	0.65
72:Lk:14:LEU:HD21	72:Lk:52:TYR:CD2	2.31	0.65
12:SH:133:THR:OG1	12:SH:134:GLU:N	2.23	0.65
40:LD:117:GLU:OE1	40:LD:117:GLU:N	2.29	0.65
5:C2:1681:A:N6	5:C2:1720:G:O2'	2.30	0.65
9:SE:11:ARG:NH2	9:SE:21:ASP:O	2.30	0.65
14:SJ:59:LEU:HD22	14:SJ:69:ARG:HA	1.79	0.65
29:SZ:95:HIS:ND1	29:SZ:96:SER:O	2.30	0.65
38:C3:97:A:OP1	69:Lh:67:ARG:NH2	2.24	0.65
51:LP:62:ARG:NH1	78:C1:412:G:OP1	2.28	0.65
5:C2:1472:C:O2	5:C2:1534:G:N2	2.28	0.65
35:Sg:200:ASN:ND2	35:Sg:239:GLU:OE1	2.29	0.65
5:C2:1450:U:O2'	32:Sd:7:TRP:O	2.11	0.65
2:SA:56:LYS:NZ	25:SV:70:ASN:OD1	2.29	0.65
5:C2:475:A:OP1	14:SJ:126:ARG:NH1	2.30	0.65
5:C2:514:G:C5	5:C2:537:G:N2	2.65	0.65
5:C2:1303:U:O2'	5:C2:1322:A:OP2	2.15	0.65
78:C1:1196:C:OP1	78:C1:1309:U:O2'	2.12	0.65
5:C2:63:G:O2'	5:C2:170:U:OP1	2.15	0.65
9:SE:256:ARG:O	9:SE:259:GLN:NE2	2.30	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:LQ:37:ALA:O	52:LQ:46:LYS:NZ	2.29	0.65
67:Lf:16:TYR:OH	67:Lf:89:LEU:O	2.09	0.65
2:SA:188:LEU:HD21	2:SA:195:TRP:CD1	2.32	0.65
22:SS:75:ASN:OD1	22:SS:78:HIS:ND1	2.29	0.65
56:LU:90:ARG:NH1	78:C1:1682:U:O4	2.30	0.64
5:C2:1534:G:OP2	29:SZ:74:SER:OG	2.08	0.64
11:SG:160:ARG:O	11:SG:170:THR:O	2.16	0.64
24:SU:70:THR:O	32:Sd:40:ARG:NH1	2.31	0.64
28:SY:6:THR:HG23	28:SY:28:LEU:HB2	1.80	0.64
78:C1:1724:U:O2'	78:C1:1725:C:OP2	2.11	0.64
21:SR:60:ARG:O	21:SR:63:LYS:O	2.14	0.64
34:Sf:102:VAL:O	34:Sf:105:TYR:OH	2.15	0.64
78:C1:1596:C:O2'	78:C1:1696:A:N3	2.26	0.64
5:C2:1795:U:OP2	30:Sa:4:LYS:NZ	2.31	0.64
13:SI:99:ALA:N	13:SI:169:ILE:O	2.30	0.64
65:Ld:11:GLU:OE2	65:Ld:74:ARG:NH2	2.31	0.64
78:C1:239:G:O2'	78:C1:240:U:OP1	2.14	0.64
78:C1:2568:C:O2'	78:C1:2569:A:O5'	2.16	0.64
42:LF:208:SER:OG	42:LF:243:MET:O	2.14	0.64
67:Lf:19:SER:HB2	78:C1:1330:A:OP1	1.96	0.64
3:LB:10:ARG:NH2	3:LB:11:HIS:O	2.31	0.64
78:C1:1565:G:C2	78:C1:1575:A:C6	2.86	0.64
78:C1:2295:A:N3	78:C1:2929:C:O2'	2.30	0.64
4:SB:157:GLN:NE2	5:C2:1047:G:OP1	2.31	0.64
74:Lm:94:SER:OG	74:Lm:104:PRO:O	2.16	0.64
4:SB:212:VAL:HG13	4:SB:213:ARG:H	1.62	0.64
5:C2:974:A:O3'	18:SN:112:LYS:NZ	2.31	0.63
5:C2:1387:G:OP1	21:SR:32:LYS:NZ	2.19	0.63
5:C2:1227:A:N6	5:C2:1256:A:O2'	2.31	0.63
5:C2:1603:U:OP2	20:SQ:132:LYS:NZ	2.26	0.63
35:Sg:224:ASN:O	35:Sg:228:LYS:N	2.31	0.63
39:LC:37:THR:O	39:LC:40:THR:OG1	2.15	0.63
40:LD:232:ASP:O	40:LD:235:SER:OG	2.16	0.63
68:Lg:95:ILE:HD11	78:C1:2555:G:N7	2.13	0.63
5:C2:1546:G:OP1	22:SS:123:ARG:NH2	2.30	0.63
30:Sa:45:VAL:HG23	30:Sa:46:GLU:H	1.63	0.63
34:Sf:141:CYS:SG	34:Sf:142:GLY:N	2.72	0.63
53:LR:38:ARG:NH1	78:C1:1603:A:OP1	2.31	0.63
78:C1:3349:C:N3	78:C1:3356:G:N1	2.47	0.63
2:SA:156:VAL:HG12	2:SA:157:ASP:O	1.98	0.63
5:C2:707:A:N6	5:C2:733:A:OP1	2.31	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C2:396:G:N1	5:C2:399:A:OP2	2.32	0.63
48:LM:77:ARG:NH2	78:C1:524:U:OP1	2.31	0.63
16:SL:2:SER:O	16:SL:3:THR:OG1	2.15	0.63
38:C3:94:C:OP1	71:Lj:75:LYS:NZ	2.30	0.63
40:LD:20:PHE:O	40:LD:24:ARG:NH2	2.32	0.63
41:LE:49:GLY:O	41:LE:162:SER:OG	2.17	0.63
51:LP:57:ALA:HB2	51:LP:72:GLN:OE1	1.98	0.63
13:SI:11:ARG:NH1	13:SI:15:GLY:O	2.30	0.63
39:LC:46:LYS:NZ	78:C1:691:A:OP1	2.32	0.63
40:LD:128:GLU:O	40:LD:164:LYS:NZ	2.31	0.63
55:LT:37:GLY:N	55:LT:64:VAL:O	2.30	0.63
67:Lf:26:ASN:OD1	67:Lf:88:ASN:ND2	2.31	0.63
73:Ll:37:TYR:O	78:C1:351:A:N6	2.31	0.63
39:LC:150:LEU:HD21	39:LC:172:VAL:CG1	2.29	0.63
45:LI:207:GLU:OE1	45:LI:208:ASN:ND2	2.32	0.63
5:C2:260:U:O2	13:SI:41:LYS:NZ	2.24	0.62
5:C2:826:U:C4	5:C2:846:G:O6	2.52	0.62
28:SY:5:VAL:C	28:SY:28:LEU:O	2.41	0.62
10:SF:43:PHE:N	10:SF:46:TRP:O	2.29	0.62
39:LC:62:ALA:HB3	39:LC:90:PHE:CE2	2.34	0.62
3:LB:221:THR:OG1	78:C1:3046:A:O3'	2.18	0.62
5:C2:487:G:N1	5:C2:501:U:N3	2.47	0.62
7:SC:218:ILE:O	7:SC:221:THR:OG1	2.13	0.62
34:Sf:121:CYS:SG	34:Sf:122:SER:N	2.72	0.62
60:LY:41:ALA:O	60:LY:125:LYS:NZ	2.32	0.62
78:C1:69:C:HO2'	78:C1:101:G:HO2'	1.42	0.62
20:SQ:6:SER:N	20:SQ:96:TYR:OH	2.32	0.62
21:SR:89:SER:O	21:SR:92:ASP:N	2.31	0.62
43:LG:193:LYS:NZ	78:C1:144:A:OP1	2.17	0.62
73:Ll:45:ARG:NH2	78:C1:1848:G:N7	2.47	0.62
78:C1:1477:A:OP1	78:C1:3075:G:O2'	2.15	0.62
78:C1:2258:U:O2'	78:C1:2259:A:C4'	2.47	0.62
5:C2:152:U:O2'	11:SG:15:THR:HG23	1.99	0.62
5:C2:1755:A:O2'	78:C1:2256:A:N6	2.33	0.62
7:SC:73:LEU:HD13	7:SC:106:ASP:OD2	2.00	0.62
10:SF:107:LYS:O	10:SF:111:VAL:HG23	2.00	0.62
25:SV:15:ARG:NH1	25:SV:33:GLN:OE1	2.33	0.62
5:C2:1553:G:N1	5:C2:1556:A:OP2	2.31	0.62
38:C3:11:C:O3'	51:LP:3:ARG:NH1	2.33	0.62
41:LE:42:LEU:O	41:LE:49:GLY:N	2.33	0.62
54:LS:158:LYS:NZ	78:C1:1182:A:OP1	2.20	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C2:1075:C:O2'	30:Sa:13:LYS:O	2.17	0.61
9:SE:212:ASP:OD1	9:SE:216:ASN:N	2.32	0.61
13:SI:153:GLU:OE2	13:SI:156:VAL:N	2.33	0.61
44:LH:173:ARG:NH1	74:Lm:125:LYS:O	2.33	0.61
3:LB:250:ALA:HB1	78:C1:2947:G:N3	2.14	0.61
53:LR:115:ILE:HG13	53:LR:119:LEU:HD23	1.80	0.61
71:Lj:31:LYS:NZ	78:C1:815:G:OP2	2.32	0.61
5:C2:477:A:O3'	33:Se:33:ARG:NH2	2.33	0.61
5:C2:656:G:C6	5:C2:679:U:O2	2.53	0.61
48:LM:83:LYS:NZ	78:C1:560:G:OP1	2.26	0.61
77:Lp:4:ARG:NH2	78:C1:855:U:O4	2.34	0.61
11:SG:182:GLN:NE2	11:SG:185:GLN:OE1	2.34	0.61
5:C2:566:C:OP2	27:SX:66:SER:OG	2.17	0.61
5:C2:1179:G:H21	5:C2:1460:A:H62	1.49	0.61
5:C2:1117:U:OP1	75:Ln:21:ARG:NH2	2.34	0.61
11:SG:160:ARG:N	11:SG:170:THR:O	2.33	0.61
35:Sg:154:VAL:O	35:Sg:155:ARG:NH1	2.33	0.61
38:C3:71:A:O2'	60:LY:52:ARG:NH2	2.34	0.61
5:C2:235:G:N2	5:C2:236:A:H62	1.98	0.61
5:C2:867:G:OP2	18:SN:3:ARG:NH1	2.34	0.61
14:SJ:58:ASP:O	14:SJ:61:THR:OG1	2.15	0.61
76:Lo:41:ARG:NH1	78:C1:284:A:OP2	2.33	0.61
6:SP:85:ILE:HG22	6:SP:112:LEU:HD23	1.82	0.61
14:SJ:20:GLU:N	14:SJ:20:GLU:OE2	2.34	0.60
21:SR:60:ARG:O	21:SR:63:LYS:C	2.44	0.60
42:LF:34:LYS:NZ	78:C1:596:C:OP2	2.20	0.60
78:C1:648:C:O2	78:C1:2374:C:O2'	2.17	0.60
7:SC:153:SER:OG	7:SC:154:LEU:N	2.33	0.60
27:SX:56:LYS:O	27:SX:57:LEU:HD23	2.00	0.60
63:Lb:16:ALA:O	63:Lb:20:GLY:CA	2.50	0.60
66:Le:23:ASP:OD2	78:C1:424:G:O2'	2.18	0.60
78:C1:2255:A:H5'	78:C1:2261:G:H22	1.67	0.60
3:LB:218:ILE:CG1	3:LB:276:THR:HG23	2.31	0.60
4:SB:194:ASN:ND2	4:SB:210:ILE:O	2.34	0.60
5:C2:241:U:O2'	5:C2:242:U:O4'	2.20	0.60
5:C2:1401:A:OP1	21:SR:56:HIS:NE2	2.34	0.60
8:SD:172:THR:O	8:SD:173:ARG:NH1	2.34	0.60
46:LJ:55:ARG:CZ	80:6:20:U:OP1	2.49	0.60
15:SK:23:ALA:O	15:SK:63:TYR:C	2.45	0.60
78:C1:28:C:O2'	78:C1:61:A:N3	2.33	0.60
3:LB:269:GLN:NE2	78:C1:3306:U:OP1	2.35	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
78:C1:1778:G:O2'	78:C1:1780:G:OP2	2.18	0.60
20:SQ:50:GLU:OE2	20:SQ:112:TYR:OH	2.11	0.60
51:LP:80:LYS:NZ	78:C1:2388:U:O3'	2.35	0.60
5:C2:256:A:N3	13:SI:73:SER:OG	2.32	0.59
41:LE:76:LEU:N	41:LE:138:GLN:OE1	2.34	0.59
47:LL:76:THR:O	47:LL:79:GLU:N	2.34	0.59
72:Lk:26:LYS:NZ	78:C1:1750:A:O5'	2.35	0.59
10:SF:63:GLN:NE2	10:SF:66:GLN:OE1	2.35	0.59
38:C3:151:C:H5	59:LX:24:LEU:HD11	1.66	0.59
53:LR:115:ILE:HD11	53:LR:119:LEU:HG	1.83	0.59
5:C2:224:C:O2'	5:C2:225:A:OP1	2.17	0.59
49:LN:144:ARG:NH1	78:C1:126:U:OP1	2.35	0.59
5:C2:514:G:N7	5:C2:537:G:N2	2.50	0.59
8:SD:92:GLN:OE1	8:SD:92:GLN:N	2.35	0.59
35:Sg:238:ASP:OD2	35:Sg:258:THR:OG1	2.15	0.59
40:LD:41:LYS:HE2	55:LT:93:VAL:HG11	1.84	0.59
46:LJ:112:LEU:O	46:LJ:114:ILE:HD12	2.01	0.59
47:LL:18:TRP:O	47:LL:21:ARG:C	2.45	0.59
78:C1:1189:C:N3	78:C1:1315:U:O2	2.35	0.59
5:C2:1411:A:OP1	20:SQ:114:ARG:NH2	2.36	0.59
5:C2:1529:C:O2	23:ST:12:GLN:NE2	2.35	0.59
39:LC:150:LEU:HD21	39:LC:172:VAL:HG11	1.84	0.59
49:LN:15:GLN:NE2	78:C1:294:U:OP2	2.36	0.59
78:C1:2257:C:H2'	78:C1:2258:U:C6	2.37	0.59
5:C2:68:A:OP1	11:SG:160:ARG:NH2	2.36	0.59
5:C2:640:U:O2'	5:C2:641:G:OP1	2.19	0.59
5:C2:853:G:OP2	53:LR:173:ARG:NH2	2.35	0.59
5:C2:1245:G:O2'	5:C2:1247:U:OP2	2.19	0.59
5:C2:237:C:O2'	5:C2:238:U:O5'	2.19	0.59
6:SP:18:ARG:NH1	22:SS:90:ASN:O	2.35	0.59
11:SG:43:ASP:O	11:SG:119:GLN:NE2	2.35	0.59
43:LG:185:ARG:O	43:LG:188:THR:OG1	2.20	0.59
48:LM:19:ARG:NH2	48:LM:66:THR:O	2.36	0.59
48:LM:96:ALA:O	48:LM:101:LYS:NZ	2.21	0.59
78:C1:3344:A:H2	78:C1:3361:G:H21	1.46	0.59
13:SI:84:HIS:NE2	13:SI:97:THR:OG1	2.34	0.59
38:C3:16:G:O2'	38:C3:17:A:OP2	2.19	0.59
78:C1:824:C:O2'	78:C1:1534:A:N3	2.34	0.59
80:7:7:U:O2'	80:7:49:A:O4'	2.20	0.59
39:LC:164:GLU:OE1	39:LC:164:GLU:N	2.35	0.59
46:LJ:133:ARG:NH1	46:LJ:152:HIS:O	2.35	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:LD:17:GLN:O	78:C1:2688:U:N3	2.33	0.59
42:LF:33:ARG:NH1	78:C1:596:C:OP1	2.36	0.59
49:LN:54:LYS:NZ	78:C1:114:A:OP1	2.36	0.59
78:C1:1639:C:O2'	78:C1:1737:U:O2'	2.20	0.59
78:C1:2273:G:O2'	78:C1:2311:G:O6	2.16	0.59
5:C2:190:C:N4	5:C2:191:C:O2	2.36	0.58
5:C2:1755:A:C2'	78:C1:2256:A:N6	2.66	0.58
37:C4:121:U:OP2	40:LD:265:TYR:OH	2.20	0.58
69:Lh:63:ARG:NH2	69:Lh:79:ASP:O	2.36	0.58
78:C1:1693:C:HO2'	78:C1:1772:U:HO2'	1.50	0.58
5:C2:1755:A:H2'	78:C1:2256:A:H62	1.68	0.58
7:SC:146:THR:O	7:SC:148:LEU:N	2.35	0.58
78:C1:2258:U:O2'	78:C1:2259:A:C8	2.56	0.58
1:LA:242:ARG:NH2	1:LA:243:THR:O	2.36	0.58
5:C2:1678:A:OP1	13:SI:59:ARG:NH1	2.36	0.58
43:LG:91:PHE:O	43:LG:95:ASN:ND2	2.35	0.58
68:Lg:74:ARG:NH2	78:C1:1638:A:OP1	2.27	0.58
78:C1:1245:A:N6	78:C1:1272:C:O2'	2.35	0.58
78:C1:2257:C:O2'	78:C1:2258:U:H5'	2.03	0.58
4:SB:70:LEU:HD23	4:SB:79:HIS:HB3	1.84	0.58
40:LD:123:GLU:OE1	40:LD:123:GLU:N	2.35	0.58
59:LX:91:ASN:N	59:LX:94:GLN:OE1	2.35	0.58
24:SU:106:ILE:HG13	24:SU:107:THR:HG23	1.84	0.58
27:SX:41:SER:O	27:SX:43:PHE:N	2.36	0.58
78:C1:187:A:N3	78:C1:208:C:O2'	2.33	0.58
5:C2:505:A:O2'	5:C2:507:U:OP1	2.15	0.58
10:SF:49:GLU:OE1	10:SF:49:GLU:N	2.36	0.58
56:LU:32:SER:OG	56:LU:83:TYR:OH	2.09	0.58
62:La:117:ARG:NH2	78:C1:718:G:OP1	2.37	0.58
78:C1:3344:A:C2	78:C1:3361:G:N2	2.64	0.58
5:C2:1300:A:OP1	7:SC:99:LYS:NZ	2.36	0.58
9:SE:157:ASN:ND2	9:SE:222:LEU:HD21	2.19	0.58
66:Le:95:GLU:OE2	66:Le:120:THR:OG1	2.21	0.58
78:C1:2393:G:O2'	78:C1:2394:G:OP2	2.19	0.58
5:C2:819:G:C5	5:C2:853:G:N2	2.72	0.58
39:LC:211:GLU:N	39:LC:211:GLU:OE1	2.37	0.58
5:C2:765:G:O2'	5:C2:766:U:O5'	2.19	0.58
10:SF:139:ASN:O	10:SF:214:LYS:NZ	2.20	0.58
39:LC:361:HIS:O	54:LS:28:ARG:NH2	2.34	0.58
40:LD:146:LEU:HD11	40:LD:163:LEU:HD12	1.84	0.58
43:LG:246:MET:SD	43:LG:249:ARG:NH2	2.75	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:LW:86:SER:O	58:LW:89:LEU:N	2.37	0.58
62:La:23:GLY:N	78:C1:1114:U:OP1	2.35	0.58
78:C1:1524:A:O2'	78:C1:1526:U:OP2	2.17	0.58
78:C1:1565:G:N3	78:C1:1575:A:N1	2.52	0.58
2:SA:89:PHE:O	2:SA:93:THR:OG1	2.21	0.57
15:SK:29:GLN:OE1	15:SK:39:ASN:ND2	2.36	0.57
22:SS:94:ASP:OD2	22:SS:98:TYR:OH	2.09	0.57
39:LC:326:ARG:NE	78:C1:596:C:O2	2.37	0.57
41:LE:77:ARG:NH2	78:C1:3273:A:OP2	2.35	0.57
69:Lh:12:LYS:NZ	69:Lh:20:GLN:OE1	2.36	0.57
4:SB:148:ASN:OD1	5:C2:1066:C:O2'	2.20	0.57
5:C2:1172:G:O2'	5:C2:1543:A:O2'	2.22	0.57
9:SE:21:ASP:OD1	9:SE:24:SER:OG	2.22	0.57
9:SE:23:LEU:O	9:SE:24:SER:OG	2.21	0.57
52:LQ:171:LYS:NZ	78:C1:89:A:OP2	2.25	0.57
56:LU:80:THR:HG21	56:LU:95:PHE:HD2	1.69	0.57
72:Lk:32:ASN:OD1	72:Lk:33:LYS:N	2.37	0.57
78:C1:2875:U:C5	81:A:177[B]:LYS:HG2	2.38	0.57
3:LB:132:LYS:NZ	78:C1:3151:U:OP2	2.32	0.57
5:C2:307:G:OP1	16:SL:90:TYR:OH	2.21	0.57
42:LF:150:LYS:NZ	78:C1:507:U:OP1	2.37	0.57
42:LF:196:LYS:NZ	78:C1:1100:U:OP2	2.36	0.57
5:C2:1427:A:O2'	5:C2:1428:G:OP2	2.16	0.57
49:LN:43:THR:OG1	49:LN:131:GLU:OE2	2.15	0.57
72:Lk:42:LYS:NZ	78:C1:1748:G:OP2	2.38	0.57
78:C1:1819:U:O2'	78:C1:1820:U:OP1	2.20	0.57
5:C2:1274:C:O2'	5:C2:1275:A:OP2	2.19	0.57
5:C2:1471:A:O2'	5:C2:1472:C:OP1	2.18	0.57
35:Sg:200:ASN:ND2	35:Sg:240:VAL:O	2.37	0.57
5:C2:1482:C:O2'	20:SQ:72:GLY:O	2.19	0.57
8:SD:105:MET:HG2	8:SD:122:VAL:HG21	1.85	0.57
19:SO:126:THR:OG1	19:SO:127:ARG:N	2.36	0.57
24:SU:71:PRO:O	32:Sd:40:ARG:NH2	2.37	0.57
27:SX:47:SER:OG	27:SX:48:HIS:ND1	2.32	0.57
41:LE:108:LYS:NZ	78:C1:617:G:OP1	2.38	0.57
5:C2:1562:G:OP1	23:ST:89:ARG:NH2	2.35	0.57
43:LG:248:LYS:NZ	78:C1:2529:A:OP1	2.37	0.57
53:LR:102:LEU:HD22	53:LR:138:LEU:HD13	1.86	0.57
5:C2:804:A:N3	26:SW:105:THR:HG22	2.20	0.57
8:SD:91:VAL:HG22	8:SD:92:GLN:O	2.03	0.57
38:C3:149:A:H61	78:C1:8:C:H42	1.52	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:LG:160:ILE:O	43:LG:164:VAL:HG13	2.05	0.57
5:C2:1183:A:N6	6:SP:122:THR:O	2.37	0.57
5:C2:1555:A:O3'	6:SP:44:ARG:NH1	2.38	0.57
19:SO:61:MET:SD	19:SO:65:GLN:NE2	2.78	0.57
43:LG:106:LYS:O	43:LG:110:THR:HG23	2.05	0.57
80:7:36:U:O2'	80:7:37:A:OP1	2.16	0.57
23:ST:136:ALA:O	23:ST:139:THR:OG1	2.22	0.57
40:LD:173:VAL:O	40:LD:175:HIS:ND1	2.37	0.57
42:LF:47:ARG:NH1	42:LF:183:ASP:OD2	2.37	0.57
46:LJ:81:GLU:OE1	46:LJ:85:LYS:NZ	2.38	0.57
1:LA:227:ARG:NH1	78:C1:2161:G:O3'	2.37	0.56
5:C2:1513:G:O2'	5:C2:1515:A:N3	2.29	0.56
6:SP:64:LYS:NZ	6:SP:90:ILE:O	2.38	0.56
5:C2:1486:G:N2	5:C2:1522:U:O4	2.38	0.56
42:LF:107:ARG:NH2	42:LF:202:LEU:O	2.38	0.56
54:LS:68:HIS:O	54:LS:73:LYS:NZ	2.39	0.56
5:C2:1272:U:O2'	5:C2:1275:A:OP1	2.16	0.56
14:SJ:83:VAL:O	14:SJ:107:ARG:NE	2.39	0.56
40:LD:93:THR:O	40:LD:158:ARG:NH1	2.37	0.56
41:LE:2:THR:OG1	66:Le:81:ASP:OD2	2.18	0.56
43:LG:206:GLU:OE1	43:LG:206:GLU:N	2.38	0.56
49:LN:119:TYR:OH	49:LN:131:GLU:OE1	2.06	0.56
52:LQ:178:ARG:NH2	78:C1:780:A:OP1	2.37	0.56
53:LR:110:ARG:NH1	78:C1:1720:U:OP1	2.38	0.56
59:LX:88:MET:HE1	59:LX:114:VAL:HG22	1.86	0.56
78:C1:63:A:N3	78:C1:78:U:O2'	2.35	0.56
78:C1:362:U:O2'	78:C1:928:C:O2'	2.05	0.56
78:C1:1223:A:OP2	78:C1:1285:G:N2	2.39	0.56
5:C2:257:A:N3	13:SI:64:ASN:ND2	2.53	0.56
25:SV:74:GLN:NE2	25:SV:80:LYS:O	2.38	0.56
38:C3:150:G:O2'	38:C3:152:G:OP1	2.16	0.56
53:LR:83:GLY:N	78:C1:1864:A:OP1	2.36	0.56
62:La:104:THR:HG21	62:La:112:ILE:HD11	1.87	0.56
71:Lj:24:ARG:NH2	78:C1:362:U:O4	2.38	0.56
2:SA:31:VAL:HG12	2:SA:33:GLN:H	1.71	0.56
5:C2:588:U:O2	33:Se:57:ASN:ND2	2.39	0.56
5:C2:1502:G:N2	5:C2:1505:A:OP2	2.28	0.56
11:SG:175:ILE:HB	11:SG:178:LEU:HD22	1.88	0.56
13:SI:22:ARG:NH1	13:SI:28:GLU:OE1	2.38	0.56
34:Sf:148:TYR:O	34:Sf:149:LYS:NZ	2.26	0.56
40:LD:146:LEU:HD11	40:LD:163:LEU:CD1	2.35	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C2:821:U:O4	5:C2:852:C:N3	2.39	0.56
8:SD:209:ILE:HD12	21:SR:38:ILE:O	2.05	0.56
9:SE:208:VAL:HG13	9:SE:210:ILE:HD11	1.88	0.56
38:C3:99:C:OP1	59:LX:53:HIS:NE2	2.31	0.56
44:LH:25:VAL:O	44:LH:35:THR:OG1	2.11	0.56
50:LO:83[A]:ALA:O	78:C1:1312:C:O2'	2.23	0.56
66:Le:36:LYS:NZ	78:C1:945:C:OP1	2.38	0.56
78:C1:2206:G:H21	78:C1:2207:A:H61	1.53	0.56
5:C2:1459:C:O2'	22:SS:138:THR:O	2.10	0.56
5:C2:1473:U:O2'	10:SF:103:ASN:ND2	2.37	0.56
27:SX:57:LEU:HD11	27:SX:73:ARG:HG2	1.86	0.56
39:LC:35:VAL:HG21	39:LC:244:LEU:HD21	1.88	0.56
46:LJ:78:GLU:OE2	46:LJ:82:ARG:NE	2.39	0.56
78:C1:1624:G:O6	78:C1:1819:U:O4	2.23	0.56
5:C2:647:G:N2	5:C2:687:G:H22	2.04	0.56
9:SE:103:TYR:O	9:SE:182:TYR:OH	2.24	0.56
4:SB:59:ASP:OD1	4:SB:60:ALA:N	2.39	0.56
4:SB:180:THR:OG1	4:SB:181:LEU:N	2.36	0.56
5:C2:939:A:OP1	18:SN:114:ARG:NH2	2.39	0.56
80:6:76:A:C5'	81:A:177[A]:LYS:HG3	2.36	0.56
5:C2:765:G:H21	5:C2:765:G:P	2.28	0.55
7:SC:53:ILE:HD13	7:SC:73:LEU:HD11	1.88	0.55
9:SE:18:TRP:HE3	9:SE:20:LEU:HD11	1.71	0.55
3:LB:266:ARG:NH2	78:C1:2392:C:O2'	2.36	0.55
5:C2:540:G:C2	5:C2:542:A:N6	2.74	0.55
5:C2:1030:A:OP2	30:Sa:8:ASN:ND2	2.38	0.55
61:LZ:10:VAL:O	61:LZ:83:THR:OG1	2.09	0.55
78:C1:2374:C:N4	78:C1:2941:A:O4'	2.39	0.55
10:SF:85:ALA:HB2	10:SF:165:LEU:HD11	1.88	0.55
36:Sc:62:GLU:OE1	36:Sc:62:GLU:N	2.39	0.55
60:LY:3:LYS:NZ	78:C1:336:A:OP1	2.38	0.55
78:C1:1231:A:HO2'	78:C1:1278:A:H61	1.54	0.55
5:C2:554:C:N4	5:C2:571:G:O6	2.39	0.55
9:SE:132:GLY:N	9:SE:136:VAL:O	2.38	0.55
40:LD:120:LYS:O	40:LD:248:ARG:NH2	2.39	0.55
55:LT:101:CYS:SG	55:LT:102:ARG:N	2.79	0.55
78:C1:1189:C:C4	78:C1:1315:U:O2	2.59	0.55
5:C2:195:G:N7	13:SI:137:LYS:NZ	2.43	0.55
5:C2:1558:U:O2'	5:C2:1559:A:OP2	2.21	0.55
44:LH:155:SER:OG	78:C1:3110:C:O3'	2.25	0.55
5:C2:1755:A:C2'	78:C1:2256:A:H62	2.18	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:SQ:134:ALA:O	20:SQ:137:ARG:NH2	2.40	0.55
42:LF:219:LYS:N	78:C1:1170:A:OP1	2.39	0.55
55:LT:43:LYS:NZ	78:C1:993:G:OP1	2.39	0.55
3:LB:180:GLU:OE2	78:C1:3002:C:O2'	2.10	0.55
9:SE:19:LEU:HD11	9:SE:108:ARG:HD2	1.89	0.55
40:LD:91:GLY:O	40:LD:94:ASN:ND2	2.40	0.55
60:LY:82:VAL:HG12	60:LY:83:ASP:O	2.07	0.55
78:C1:884:A:OP2	78:C1:2139:A:N6	2.40	0.55
78:C1:921:A:N6	78:C1:1846:C:OP2	2.39	0.55
78:C1:1244:A:O2'	78:C1:1249:G:O6	2.25	0.55
5:C2:1114:G:O2'	5:C2:1130:G:O6	2.22	0.55
37:C4:52:G:H21	46:LJ:9:MET:HE1	1.72	0.55
38:C3:156:U:OP2	43:LG:84:ARG:NH2	2.40	0.55
54:LS:77:VAL:HG13	54:LS:126:VAL:HG22	1.89	0.55
77:Lp:2:ALA:N	78:C1:853:G:O6	2.40	0.55
78:C1:1268:G:O2'	78:C1:1269:U:O2	2.24	0.55
38:C3:23:U:OP1	60:LY:16:ARG:NE	2.40	0.55
40:LD:232:ASP:N	40:LD:232:ASP:OD1	2.39	0.55
50:LO:176[A]:LYS:NZ	78:C1:3190:C:O3'	2.38	0.55
41:LE:2:THR:N	78:C1:1385:C:HO2'	2.05	0.55
47:LL:145:PHE:CE1	69:Lh:118:ILE:HD11	2.41	0.55
5:C2:1334:U:O2'	24:SU:85:ARG:NH2	2.38	0.54
5:C2:1483:A:N3	5:C2:1607:G:O2'	2.34	0.54
23:ST:115:GLU:OE2	23:ST:123:ARG:NH1	2.41	0.54
26:SW:15:ASN:ND2	26:SW:72:CYS:O	2.40	0.54
39:LC:10:SER:OG	39:LC:11:LEU:N	2.39	0.54
40:LD:136:GLU:N	40:LD:136:GLU:OE1	2.40	0.54
1:LA:177:LYS:HB2	77:Lp:29:LEU:HD13	1.88	0.54
3:LB:94:GLU:OE1	3:LB:94:GLU:N	2.40	0.54
3:LB:358:TRP:CG	58:LW:1:MET:HE1	2.42	0.54
11:SG:23:ARG:NH2	11:SG:41:VAL:O	2.40	0.54
78:C1:2794:G:O2'	78:C1:2795:U:OP2	2.23	0.54
1:LA:21:ARG:NH1	78:C1:824:C:OP1	2.41	0.54
3:LB:267:ALA:O	78:C1:2989:U:O2'	2.25	0.54
5:C2:298:C:O3'	9:SE:30:ARG:NH1	2.40	0.54
5:C2:1228:G:OP2	17:SM:119:SER:OG	2.13	0.54
13:SI:187:GLU:N	13:SI:187:GLU:OE1	2.38	0.54
38:C3:114:G:OP1	78:C1:1831:U:O2'	2.17	0.54
48:LM:94:TRP:O	48:LM:97:SER:OG	2.23	0.54
78:C1:2540:A:N3	78:C1:2541:U:N3	2.55	0.54
81:A:176:LYS:N	81:A:176:LYS:HD2	2.23	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:SY:15:ASN:OD1	28:SY:18:LEU:N	2.40	0.54
34:Sf:138:ARG:C	34:Sf:139:LEU:HD12	2.32	0.54
46:LJ:141:ARG:NH2	46:LJ:144:CYS:O	2.40	0.54
50:LO:87[A]:MET:HE2	78:C1:1174:G:H21	1.73	0.54
78:C1:1480:G:N1	78:C1:1872:C:OP2	2.41	0.54
78:C1:3164:C:HO2'	78:C1:3165:A:P	2.30	0.54
47:LL:92:THR:O	69:Lh:113:GLN:NE2	2.40	0.54
72:Lk:51:LEU:N	78:C1:1613:A:OP1	2.39	0.54
78:C1:2890:A:N1	78:C1:2913:C:N3	2.55	0.54
20:SQ:125:GLU:OE1	20:SQ:128:LYS:NZ	2.40	0.54
52:LQ:95:GLU:OE1	52:LQ:95:GLU:N	2.39	0.54
5:C2:259:U:OP1	13:SI:75:LYS:NZ	2.37	0.54
5:C2:819:G:O6	5:C2:853:G:C6	2.60	0.54
5:C2:865:A:OP1	26:SW:3:ARG:NH2	2.41	0.54
5:C2:1529:C:OP1	29:SZ:95:HIS:NE2	2.41	0.54
11:SG:21:GLU:OE1	11:SG:21:GLU:N	2.41	0.54
35:Sg:89:LEU:HD11	35:Sg:124:SER:CB	2.37	0.54
65:Ld:80:ASN:OD1	65:Ld:81:GLU:N	2.40	0.54
80:6:62:C:H2'	80:6:63:C:C6	2.41	0.54
14:SJ:18:PRO:O	14:SJ:23:ARG:NH2	2.41	0.54
26:SW:2:THR:OG1	26:SW:3:ARG:N	2.39	0.54
48:LM:124:ARG:NH2	78:C1:3212:C:OP2	2.40	0.54
69:Lh:84:LYS:O	69:Lh:85:THR:HG23	2.08	0.54
39:LC:272:VAL:HG22	78:C1:696:C:OP1	2.08	0.54
71:Lj:5:THR:OG1	78:C1:884:A:OP1	2.22	0.54
77:Lp:8:VAL:O	77:Lp:11:THR:OG1	2.26	0.54
20:SQ:120:ASP:OD2	20:SQ:122:ARG:NH2	2.41	0.54
66:Le:80:LYS:NZ	78:C1:1386:A:OP1	2.39	0.54
78:C1:2695:A:O2'	78:C1:2696:A:O5'	2.20	0.54
78:C1:2890:A:H61	78:C1:2913:C:H42	1.55	0.54
5:C2:334:G:O6	13:SI:5:ARG:NH2	2.40	0.53
5:C2:1565:C:OP1	22:SS:41:ARG:NH1	2.40	0.53
10:SF:134:VAL:O	10:SF:138:THR:HG23	2.09	0.53
50:LO:121[A]:PRO:HA	50:LO:124[A]:LEU:HD12	1.88	0.53
3:LB:87:VAL:O	3:LB:87:VAL:HG23	2.08	0.53
5:C2:105:A:O3'	13:SI:8:ARG:NH1	2.41	0.53
5:C2:647:G:H22	5:C2:687:G:H22	1.55	0.53
5:C2:1451:C:OP1	32:Sd:12:ARG:NH2	2.39	0.53
12:SH:155:ASP:OD1	12:SH:156:SER:N	2.39	0.53
13:SI:162:ALA:HA	78:C1:3352:U:H2'	1.90	0.53
40:LD:281:GLU:N	40:LD:281:GLU:OE1	2.39	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
78:C1:2434:U:O4	78:C1:2595:A:N1	2.41	0.53
49:LN:170:LYS:NZ	78:C1:288:C:OP1	2.40	0.53
72:Lk:14:LEU:HD21	72:Lk:52:TYR:CG	2.43	0.53
5:C2:1186:U:OP2	5:C2:1456:C:O2'	2.14	0.53
6:SP:98:ASN:OD1	6:SP:101:ALA:N	2.42	0.53
24:SU:99:ILE:HD12	24:SU:102:ARG:HD3	1.90	0.53
26:SW:31:SER:H	26:SW:34:ILE:HD12	1.74	0.53
66:Le:21:HIS:NE2	78:C1:638:C:OP1	2.41	0.53
5:C2:327:U:O3'	16:SL:14:GLN:NE2	2.37	0.53
35:Sg:89:LEU:HD21	35:Sg:110:VAL:HG11	1.90	0.53
38:C3:95:G:O2'	71:Lj:81:GLY:O	2.21	0.53
44:LH:57:VAL:CG2	44:LH:68:LEU:HD12	2.38	0.53
66:Le:89:THR:HG22	66:Le:117:ILE:HG12	1.90	0.53
76:Lo:45:ARG:NH2	78:C1:279:U:O4	2.35	0.53
78:C1:1268:G:N2	78:C1:1269:U:O4	2.41	0.53
5:C2:623:A:H3'	5:C2:624:G:C5'	2.38	0.53
14:SJ:59:LEU:HD21	14:SJ:72:GLU:OE2	2.08	0.53
17:SM:31:VAL:HA	17:SM:34:THR:HG22	1.90	0.53
78:C1:2400:G:N7	78:C1:2401:A:N6	2.56	0.53
5:C2:57:G:OP2	28:SY:116:LYS:NZ	2.38	0.53
5:C2:451:A:N6	5:C2:453:U:O2	2.42	0.53
5:C2:1483:A:OP2	5:C2:1521:G:N2	2.32	0.53
7:SC:240:LEU:O	7:SC:244:SER:OG	2.24	0.53
18:SN:26:PHE:CE2	18:SN:66:ILE:HD12	2.43	0.53
3:LB:50:LYS:NZ	3:LB:330:GLY:O	2.18	0.53
5:C2:1387:G:N2	5:C2:1410:A:H61	2.06	0.53
8:SD:70:THR:HG23	8:SD:86:LEU:HD22	1.91	0.53
41:LE:43:LEU:HD21	41:LE:85:ILE:HD11	1.90	0.53
65:Ld:29:ALA:HB3	65:Ld:30:PRO:HD3	1.90	0.53
67:Lf:22:VAL:CG1	67:Lf:23:ASN:N	2.71	0.53
78:C1:2495:C:O2'	78:C1:2496:C:OP1	2.20	0.53
80:7:48:C:O2'	80:7:49:A:OP1	2.24	0.53
3:LB:250:ALA:HB1	78:C1:2947:G:C2	2.44	0.53
11:SG:57:ASP:OD1	11:SG:61:PHE:N	2.42	0.53
5:C2:1188:G:O2'	5:C2:1430:U:OP1	2.26	0.53
5:C2:1433:G:O4'	32:Sd:41:GLN:NE2	2.42	0.53
50:LO:151[A]:ASP:OD1	50:LO:152[A]:VAL:N	2.42	0.53
60:LY:58:VAL:HG22	60:LY:104:LEU:HD23	1.90	0.53
5:C2:163:G:OP2	5:C2:163:G:N2	2.41	0.52
5:C2:1436:A:OP2	8:SD:27:ARG:NH2	2.39	0.52
7:SC:206:THR:O	7:SC:210:THR:HG23	2.08	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:Sf:107:LYS:NZ	34:Sf:109:ASP:OD1	2.41	0.52
35:Sg:156:VAL:HG12	35:Sg:169:ILE:CG2	2.32	0.52
41:LE:111:LEU:HD11	41:LE:115:GLU:CB	2.39	0.52
45:LI:110:ARG:O	80:6:74:C:N4	2.34	0.52
55:LT:71:SER:OG	55:LT:72:VAL:N	2.42	0.52
5:C2:1365:C:OP1	20:SQ:66:ARG:NH1	2.42	0.52
5:C2:1445:G:C5	34:Sf:91:ILE:HD11	2.44	0.52
47:LL:186:ARG:NH2	78:C1:768:C:OP1	2.42	0.52
48:LM:77:ARG:O	48:LM:81:VAL:HG23	2.09	0.52
78:C1:3057:U:H5'	78:C1:3086:A:H61	1.74	0.52
5:C2:148:A:H62	5:C2:166:C:N4	2.07	0.52
5:C2:284:G:N7	11:SG:188:ARG:NH1	2.56	0.52
26:SW:24:GLN:OE1	26:SW:24:GLN:N	2.42	0.52
52:LQ:148:GLU:N	52:LQ:148:GLU:OE2	2.42	0.52
55:LT:109:VAL:HG13	78:C1:1063:G:N1	2.23	0.52
69:Lh:81:ARG:N	69:Lh:81:ARG:HH11	2.07	0.52
77:Lp:41:PHE:O	78:C1:1729:A:N6	2.43	0.52
5:C2:121:U:H1'	9:SE:33:ALA:HB3	1.91	0.52
11:SG:174:LYS:O	11:SG:175:ILE:HD13	2.10	0.52
17:SM:97:LEU:HD23	17:SM:118:ALA:O	2.09	0.52
18:SN:119:GLU:O	18:SN:123:HIS:ND1	2.42	0.52
36:Sc:31:GLU:OE2	36:Sc:36:THR:OG1	2.22	0.52
45:LI:76:MET:SD	45:LI:148:VAL:HG12	2.50	0.52
47:LL:107:GLU:OE1	47:LL:107:GLU:N	2.41	0.52
56:LU:16:THR:HG22	56:LU:64:THR:HG22	1.92	0.52
78:C1:1257:C:N3	78:C1:1261:G:N1	2.56	0.52
7:SC:138:PRO:O	7:SC:139:ILE:HD13	2.09	0.52
47:LL:100:ARG:NH2	78:C1:76:G:O2'	2.42	0.52
51:LP:127:ARG:NH1	78:C1:1508:C:OP1	2.39	0.52
80:6:68:G:H2'	80:6:69:A:C8	2.45	0.52
45:LI:10:ARG:O	45:LI:59:GLN:N	2.41	0.52
78:C1:1178:G:H2'	78:C1:1179:A:C8	2.44	0.52
1:LA:13:GLY:O	1:LA:17:THR:HG23	2.10	0.52
5:C2:230:C:O2'	5:C2:231:U:O5'	2.28	0.52
5:C2:486:G:N1	5:C2:502:U:C4	2.77	0.52
39:LC:156:LEU:O	39:LC:215:ILE:HD13	2.09	0.52
62:La:84:GLU:N	62:La:84:GLU:OE2	2.43	0.52
78:C1:1562:C:O2'	78:C1:1563:C:O5'	2.17	0.52
5:C2:819:G:C4	5:C2:853:G:N2	2.78	0.52
5:C2:1175:U:OP2	22:SS:137:HIS:ND1	2.43	0.52
27:SX:68:ILE:O	27:SX:70:LYS:NZ	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27: SX:141: GLU: N	27: SX:141: GLU: OE2	2.43	0.52
64: Lc:99: ASP: OD1	64: Lc:99: ASP: N	2.42	0.52
5: C2:1656: U: HO2'	78: C1:2292: U: HO2'	1.58	0.52
9: SE:125: LYS: NZ	9: SE:222: LEU: O	2.37	0.52
45: LI:3: ARG: NH1	45: LI:63: GLU: OE2	2.41	0.52
78: C1:439: C: O2'	78: C1:494: G: N2	2.40	0.52
1: LA:9: ARG: NH1	78: C1:911: C: O5'	2.42	0.52
3: LB:35: ASP: OD1	3: LB:36: ASP: N	2.43	0.52
5: C2:655: G: N3	5: C2:678: A: N6	2.58	0.52
39: LC:229: ASN: OD1	39: LC:230: VAL: N	2.42	0.52
53: LR:23: TRP: NE1	78: C1:1473: G: O3'	2.41	0.52
63: Lb:21: ILE: HG22	63: Lb:21: ILE: O	2.09	0.52
65: Ld:83: GLU: OE1	65: Ld:83: GLU: N	2.43	0.52
73: Ll:10: LYS: NZ	78: C1:1834: U: OP2	2.34	0.52
1: LA:126: LEU: HD13	1: LA:150: LEU: HD21	1.92	0.51
7: SC:195: ASP: OD1	7: SC:195: ASP: N	2.42	0.51
66: Le:2: ALA: N	78: C1:439: C: OP1	2.42	0.51
78: C1:845: G: N2	78: C1:848: A: OP2	2.44	0.51
78: C1:1349: G: O2'	78: C1:1350: A: O4'	2.28	0.51
80: 7:10: G: N1	80: 7:25: C: N3	2.55	0.51
5: C2:1387: G: H21	5: C2:1410: A: N6	2.07	0.51
17: SM:62: LEU: HD23	17: SM:63: VAL: O	2.11	0.51
30: Sa:52: ASP: OD1	36: Sc:38: ARG: NH1	2.43	0.51
1: LA:65: ASP: OD1	1: LA:67: TYR: N	2.42	0.51
3: LB:218: ILE: HG12	3: LB:276: THR: HG23	1.93	0.51
5: C2:1158: C: O2'	5: C2:1581: C: OP2	2.24	0.51
6: SP:91: GLY: N	6: SP:107: ILE: O	2.42	0.51
35: Sg:302: PHE: HD1	35: Sg:312: VAL: HG12	1.76	0.51
40: LD:12: TYR: OH	78: C1:2688: U: OP1	2.28	0.51
73: Ll:48: LYS: NZ	78: C1:1843: C: OP1	2.43	0.51
5: C2:1553: G: O6	6: SP:40: ARG: NH2	2.41	0.51
5: C2:1797: A: N6	30: Sa:84: VAL: O	2.43	0.51
17: SM:45: LEU: O	17: SM:49: THR: HG23	2.09	0.51
20: SQ:13: LYS: HG3	20: SQ:14: LYS: H	1.75	0.51
30: Sa:46: GLU: OE1	30: Sa:48: ALA: N	2.42	0.51
39: LC:299: ILE: HG23	52: LQ:39: ARG: HE	1.75	0.51
40: LD:218: ARG: O	40: LD:222: LEU: HD23	2.09	0.51
69: Lh:36: LEU: HD12	69: Lh:37: SER: N	2.25	0.51
71: Lj:45: ARG: NH2	78: C1:361: A: O3'	2.43	0.51
78: C1:3349: C: C2	78: C1:3356: G: N2	2.75	0.51
7: SC:241: ASP: OD2	25: SV:35: ASN: ND2	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:SK:48:SER:O	15:SK:51:SER:OG	2.20	0.51
27:SX:131:SER:O	27:SX:134:ALA:N	2.44	0.51
31:Sb:67:THR:HG22	31:Sb:68:GLY:H	1.75	0.51
45:LI:158:LYS:NZ	78:C1:2852:C:N3	2.58	0.51
47:LL:62:THR:O	47:LL:65:TYR:N	2.42	0.51
3:LB:360:ASP:OD1	3:LB:371:GLN:NE2	2.43	0.51
5:C2:1344:A:O2'	5:C2:1345:A:OP1	2.23	0.51
8:SD:113:LEU:HD23	8:SD:118:ALA:HB2	1.92	0.51
9:SE:182:TYR:N	9:SE:226:PHE:O	2.35	0.51
13:SI:168:CYS:HB2	13:SI:184:LEU:HD11	1.93	0.51
18:SN:16:ILE:O	26:SW:57:ARG:NH2	2.42	0.51
23:ST:131:ASP:OD1	23:ST:134:ARG:NH2	2.42	0.51
47:LL:18:TRP:O	47:LL:22:VAL:HG23	2.10	0.51
55:LT:118:GLU:OE2	55:LT:122:GLN:NE2	2.44	0.51
78:C1:1001:G:O2'	78:C1:1041:U:OP2	2.28	0.51
78:C1:2727:A:OP2	78:C1:2728:G:N2	2.42	0.51
5:C2:1163:A:O3'	10:SF:166:ARG:NH2	2.44	0.51
13:SI:138:ASN:OD1	13:SI:141:ARG:NH2	2.44	0.51
52:LQ:36:LEU:O	52:LQ:40:THR:OG1	2.28	0.51
59:LX:88:MET:HE1	59:LX:114:VAL:CG2	2.40	0.51
3:LB:166:ILE:O	3:LB:169:THR:OG1	2.21	0.51
5:C2:1125:A:OP1	75:Ln:18:ARG:NH1	2.44	0.51
20:SQ:100:GLN:OE1	20:SQ:100:GLN:N	2.42	0.51
49:LN:18:VAL:HG13	49:LN:19:LEU:HD12	1.93	0.51
49:LN:90:ASN:ND2	78:C1:2424:A:OP1	2.44	0.51
59:LX:82:LEU:HD11	59:LX:135:ILE:HD11	1.93	0.51
65:Ld:57:GLN:OE1	78:C1:1474:A:O2'	2.25	0.51
5:C2:960:U:OP2	18:SN:14:SER:OG	2.25	0.51
12:SH:62:VAL:HG22	12:SH:93:LEU:O	2.11	0.51
17:SM:130:THR:OG1	17:SM:131:ASP:N	2.43	0.51
19:SO:129:LYS:O	30:Sa:27:SER:OG	2.27	0.51
38:C3:149:A:N6	78:C1:8:C:H42	2.08	0.51
49:LN:93:LYS:O	78:C1:289:A:O2'	2.29	0.51
49:LN:103:GLU:OE1	49:LN:165:THR:HG21	2.11	0.51
52:LQ:69:ARG:NH1	78:C1:784:A:OP2	2.41	0.51
78:C1:2500:A:O2'	78:C1:2501:U:OP1	2.28	0.51
5:C2:235:G:C5	5:C2:834:G:N2	2.79	0.51
5:C2:1245:G:O2'	5:C2:1246:C:O5'	2.29	0.51
5:C2:1533:C:OP2	29:SZ:77:ARG:NH1	2.41	0.51
27:SX:41:SER:O	27:SX:41:SER:OG	2.26	0.51
29:SZ:39:ALA:O	29:SZ:72:GLY:N	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:Sa:18:VAL:O	30:Sa:18:VAL:HG12	2.11	0.51
39:LC:82:THR:HG21	78:C1:364:G:O2'	2.11	0.51
43:LG:105:LYS:NZ	78:C1:123:A:OP1	2.37	0.51
50:LO:126[A]:VAL:O	54:LS:154:HIS:NE2	2.41	0.51
78:C1:67:A:N6	78:C1:271:C:O2'	2.44	0.51
78:C1:1432:C:O2'	78:C1:1434:G:OP2	2.29	0.51
78:C1:3355:U:HO2'	78:C1:3356:G:P	2.34	0.51
5:C2:567:A:OP1	27:SX:70:LYS:NZ	2.43	0.50
9:SE:112:HIS:NE2	9:SE:237:SER:OG	2.43	0.50
56:LU:103:TYR:OH	78:C1:1677:G:OP2	2.27	0.50
70:Li:59:ASP:OD1	70:Li:60:LEU:N	2.44	0.50
5:C2:1501:C:OP2	23:ST:102:ARG:NH1	2.41	0.50
8:SD:118:ALA:O	8:SD:122:VAL:HG23	2.10	0.50
39:LC:326:ARG:NH1	78:C1:608:A:O3'	2.45	0.50
5:C2:1312:A:N7	21:SR:2:GLY:N	2.59	0.50
11:SG:145:PHE:HB3	11:SG:147:LEU:HD21	1.94	0.50
39:LC:203:ARG:HB2	39:LC:203:ARG:CZ	2.40	0.50
78:C1:1244:A:N6	78:C1:1271:A:OP1	2.43	0.50
80:6:76:A:C3'	81:A:177[A]:LYS:HG3	2.39	0.50
20:SQ:64:ASP:OD1	20:SQ:64:ASP:N	2.42	0.50
78:C1:394:G:N1	78:C1:397:A:OP2	2.42	0.50
10:SF:55:ASP:O	10:SF:59:VAL:HG23	2.11	0.50
15:SK:70:GLU:OE1	15:SK:70:GLU:N	2.42	0.50
16:SL:57:LYS:O	16:SL:138:ASN:ND2	2.45	0.50
22:SS:139:LYS:O	22:SS:143:ARG:NH2	2.45	0.50
34:Sf:108:VAL:HG22	34:Sf:114:VAL:HG12	1.92	0.50
54:LS:115:ARG:NH2	78:C1:1320:C:O2	2.44	0.50
55:LT:84:TYR:HE1	63:Lb:21:ILE:HG22	1.77	0.50
81:A:174:ALA:HB1	81:A:175:LYS:HE2	1.93	0.50
3:LB:274:SER:OG	78:C1:3139:A:OP1	2.28	0.50
5:C2:381:C:OP1	9:SE:10:LYS:NZ	2.41	0.50
5:C2:1705:C:O3'	5:C2:1706:C:O4'	2.29	0.50
19:SO:42:VAL:HG13	19:SO:63:ALA:HB1	1.93	0.50
40:LD:278:SER:OG	40:LD:280:GLU:OE1	2.29	0.50
57:LV:14:SER:O	57:LV:81:GLN:NE2	2.44	0.50
61:LZ:9:LYS:NZ	61:LZ:83:THR:O	2.34	0.50
1:LA:88:ILE:HG23	1:LA:99:GLY:O	2.12	0.50
3:LB:71:GLU:OE1	3:LB:71:GLU:N	2.45	0.50
5:C2:327:U:OP2	16:SL:57:LYS:NZ	2.28	0.50
5:C2:522:U:OP1	28:SY:37:LYS:NZ	2.43	0.50
5:C2:1389:C:OP1	21:SR:48:ASN:ND2	2.41	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:SH:168:SER:O	12:SH:172:VAL:HG23	2.12	0.50
42:LF:190:THR:O	42:LF:190:THR:OG1	2.28	0.50
54:LS:19:VAL:O	54:LS:19:VAL:HG13	2.12	0.50
57:LV:10:LYS:NZ	57:LV:56:ASP:OD1	2.31	0.50
4:SB:140:ILE:HG22	4:SB:212:VAL:O	2.12	0.50
5:C2:819:G:C6	5:C2:853:G:N1	2.80	0.50
5:C2:1484:G:H21	5:C2:1606:C:H1'	1.77	0.50
12:SH:15:GLU:OE2	12:SH:15:GLU:N	2.45	0.50
20:SQ:31:VAL:HG12	20:SQ:32:ASN:ND2	2.27	0.50
28:SY:39:GLU:OE1	28:SY:39:GLU:N	2.42	0.50
35:Sg:293:ALA:O	35:Sg:301:LEU:HD12	2.11	0.50
40:LD:68:THR:OG1	40:LD:71:GLY:O	2.29	0.50
43:LG:50:VAL:HG21	59:LX:27:ARG:HD2	1.94	0.50
71:Lj:2:GLY:N	78:C1:2138:A:O2'	2.43	0.50
74:Lm:114:LYS:NZ	78:C1:2908:G:O2'	2.45	0.50
5:C2:144:U:O4	11:SG:137:ARG:NH1	2.41	0.49
5:C2:322:G:HO2'	5:C2:323:A:P	2.29	0.49
27:SX:130:VAL:O	27:SX:130:VAL:HG12	2.11	0.49
39:LC:62:ALA:HB3	39:LC:90:PHE:CD2	2.47	0.49
80:6:62:C:H2'	80:6:63:C:H6	1.76	0.49
2:SA:188:LEU:HD21	2:SA:195:TRP:CG	2.46	0.49
3:LB:53:MET:HE1	3:LB:327:CYS:SG	2.52	0.49
3:LB:274:SER:HG	78:C1:3139:A:P	2.34	0.49
5:C2:233:C:O2'	5:C2:234:G:N2	2.36	0.49
38:C3:33:A:H2'	78:C1:59:G:H2'	1.93	0.49
38:C3:75:G:OP2	60:LY:74:TYR:OH	2.26	0.49
40:LD:50:ARG:NH1	40:LD:72:ASP:OD2	2.44	0.49
1:LA:103:PRO:O	1:LA:106:SER:OG	2.28	0.49
3:LB:48:GLY:O	3:LB:335:ILE:HD12	2.12	0.49
5:C2:912:U:OP1	5:C2:913:G:O2'	2.18	0.49
17:SM:98:GLY:O	17:SM:101:ALA:C	2.55	0.49
35:Sg:12:THR:O	35:Sg:13:LEU:HD23	2.12	0.49
41:LE:94:GLU:OE1	41:LE:94:GLU:N	2.44	0.49
52:LQ:148:GLU:HA	52:LQ:151:ARG:HG3	1.93	0.49
60:LY:103:LYS:NZ	78:C1:217:U:O2	2.41	0.49
71:Lj:56:ARG:NH2	78:C1:363:G:OP2	2.45	0.49
78:C1:1064:A:N1	78:C1:1092:C:N3	2.59	0.49
78:C1:2258:U:O2'	78:C1:2259:A:H5'	2.05	0.49
5:C2:628:G:H2'	78:C1:846:A:N3	2.27	0.49
5:C2:976:G:N2	5:C2:1024:U:OP2	2.45	0.49
5:C2:992:A:OP2	5:C2:1011:G:N1	2.41	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C2:1235:C:N3	34:Sf:138:ARG:NH1	2.60	0.49
5:C2:1452:U:OP1	32:Sd:10:HIS:ND1	2.40	0.49
7:SC:176:SER:OG	14:SJ:53:ARG:NH1	2.45	0.49
40:LD:148:ILE:HG22	40:LD:159:VAL:HG21	1.93	0.49
49:LN:50:ARG:NH1	78:C1:115:A:O4'	2.43	0.49
5:C2:813:U:O2'	5:C2:814:A:OP2	2.26	0.49
5:C2:1102:G:OP2	27:SX:7:ARG:NH1	2.40	0.49
7:SC:225:LEU:HD21	7:SC:230:TRP:CD1	2.47	0.49
11:SG:59:GLN:OE1	11:SG:72:ARG:NH1	2.43	0.49
40:LD:177:GLU:OE1	40:LD:177:GLU:N	2.44	0.49
78:C1:451:U:N3	78:C1:486:A:C6	2.81	0.49
2:SA:156:VAL:O	25:SV:65:SER:OG	2.30	0.49
5:C2:217:A:N1	5:C2:844:A:O2'	2.39	0.49
5:C2:987:G:N2	5:C2:1013:A:OP1	2.42	0.49
40:LD:107:ARG:NH1	40:LD:120:LYS:O	2.45	0.49
55:LT:130:ARG:NE	78:C1:1098:A:OP1	2.41	0.49
80:7:9:A:O2'	80:7:10:G:N7	2.43	0.49
5:C2:1515:A:O2'	5:C2:1517:U:OP2	2.30	0.49
12:SH:114:ARG:O	12:SH:117:THR:HG22	2.13	0.49
13:SI:57:ALA:HB2	13:SI:177:GLY:HA2	1.93	0.49
20:SQ:97:VAL:HG12	20:SQ:98:ASP:H	1.77	0.49
31:Sb:67:THR:HG22	31:Sb:68:GLY:N	2.28	0.49
38:C3:103:G:OP2	38:C3:105:A:O2'	2.30	0.49
40:LD:59:ASP:OD1	40:LD:60:ILE:N	2.45	0.49
4:SB:104:ASP:OD1	4:SB:105:PHE:N	2.45	0.49
5:C2:959:U:OP1	31:Sb:30:SER:OG	2.26	0.49
8:SD:40:ARG:NH1	8:SD:47:GLU:OE2	2.46	0.49
45:LI:42:THR:OG1	45:LI:43:VAL:N	2.46	0.49
65:Ld:41:LYS:O	65:Ld:45:GLY:N	2.45	0.49
5:C2:1521:G:O6	23:ST:68:ARG:NH2	2.43	0.49
7:SC:38:VAL:O	7:SC:39:THR:HG23	2.12	0.49
31:Sb:15:GLU:O	31:Sb:29:ARG:NH2	2.46	0.49
47:LL:164:GLU:OE1	47:LL:164:GLU:N	2.45	0.49
47:LL:165:SER:O	47:LL:167:PHE:N	2.37	0.49
49:LN:124:ASP:OD1	49:LN:127:TYR:N	2.41	0.49
49:LN:136:ASP:OD1	49:LN:138:GLN:N	2.45	0.49
3:LB:215:ILE:HD12	3:LB:338:LEU:CD1	2.36	0.49
5:C2:148:A:N6	5:C2:166:C:C4	2.81	0.49
25:SV:84:SER:OG	25:SV:86:SER:O	2.30	0.49
58:LW:34:SER:OG	78:C1:3085:G:OP1	2.25	0.49
67:Lf:49:ILE:HD11	67:Lf:71:VAL:CG2	2.40	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:Li:59:ASP:O	70:Li:63:ASN:ND2	2.46	0.49
78:C1:1016:C:O2'	78:C1:1028:U:O4'	2.29	0.49
78:C1:1624:G:O6	78:C1:1819:U:C4	2.66	0.49
80:7:15:G:H22	80:7:48:C:H42	1.60	0.49
8:SD:67:ASN:O	8:SD:70:THR:OG1	2.29	0.48
31:Sb:36:LYS:HG3	31:Sb:43:ILE:HG22	1.95	0.48
47:LL:43:ALA:O	47:LL:47:ALA:HA	2.12	0.48
2:SA:7:PHE:O	2:SA:54:TRP:NE1	2.42	0.48
2:SA:52:LYS:HG2	25:SV:82:VAL:HG22	1.94	0.48
5:C2:629:U:C5	78:C1:846:A:C6	3.00	0.48
10:SF:143:ARG:NH1	36:Sc:57:MET:SD	2.86	0.48
17:SM:35:ALA:O	17:SM:40:GLY:N	2.46	0.48
65:Ld:8:VAL:HG22	65:Ld:9:THR:N	2.28	0.48
68:Lg:4:ARG:NH2	78:C1:1483:G:O6	2.44	0.48
78:C1:1016:C:N4	78:C1:2672:G:OP2	2.46	0.48
78:C1:1064:A:N6	78:C1:1092:C:C2	2.81	0.48
78:C1:1639:C:HO2'	78:C1:1737:U:HO2'	1.54	0.48
5:C2:1534:G:OP1	22:SS:57:ARG:NH2	2.46	0.48
5:C2:1597:A:OP2	32:Sd:32:ARG:NH1	2.44	0.48
12:SH:45:SER:OG	12:SH:46:ILE:N	2.46	0.48
17:SM:70:ASN:OD1	17:SM:71:ILE:N	2.46	0.48
24:SU:96:PRO:O	24:SU:100:VAL:HG23	2.13	0.48
29:SZ:44:GLN:O	29:SZ:44:GLN:NE2	2.46	0.48
35:Sg:305:TYR:O	35:Sg:308:ASN:N	2.44	0.48
50:LO:117[A]:ARG:NH2	78:C1:3182:G:OP1	2.44	0.48
60:LY:112:ASP:OD1	60:LY:113:LYS:N	2.46	0.48
62:La:77:LYS:O	62:La:79:TRP:N	2.46	0.48
70:Li:53:TYR:O	70:Li:57:LEU:HD23	2.13	0.48
78:C1:1761:C:O2'	78:C1:1763:U:OP2	2.29	0.48
78:C1:2137:U:OP2	78:C1:2142:A:N6	2.39	0.48
78:C1:2991:A:O2'	78:C1:3309:G:N7	2.44	0.48
1:LA:101:VAL:O	1:LA:101:VAL:HG12	2.13	0.48
5:C2:153:G:H4'	11:SG:15:THR:HG21	1.95	0.48
5:C2:472:U:O2'	5:C2:769:A:N3	2.40	0.48
39:LC:4:PRO:O	39:LC:5:GLN:HG2	2.13	0.48
65:Ld:80:ASN:N	65:Ld:88:PRO:O	2.47	0.48
7:SC:58:LEU:O	25:SV:15:ARG:NE	2.45	0.48
12:SH:34:LEU:HB2	12:SH:38:LEU:HD23	1.93	0.48
13:SI:153:GLU:OE2	13:SI:156:VAL:HG23	2.12	0.48
35:Sg:244:ALA:O	35:Sg:252:LEU:HD12	2.13	0.48
37:C4:5:G:OP2	40:LD:27:LYS:NZ	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:LC:203:ARG:HH21	39:LC:240:PRO:HG2	1.78	0.48
78:C1:880:G:O2'	78:C1:881:C:OP1	2.30	0.48
80:6:20:U:H5'	80:6:21:A:OP1	2.12	0.48
3:LB:361:THR:N	3:LB:371:GLN:OE1	2.45	0.48
4:SB:136:ARG:NH1	5:C2:885:G:OP1	2.46	0.48
4:SB:210:ILE:O	4:SB:210:ILE:HG22	2.13	0.48
5:C2:827:C:N3	5:C2:846:G:C6	2.82	0.48
5:C2:917:U:O2'	19:SO:29:HIS:NE2	2.46	0.48
8:SD:123:VAL:HG23	8:SD:134:CYS:HB3	1.95	0.48
9:SE:65:LEU:HD23	9:SE:78:THR:HA	1.95	0.48
18:SN:22:ALA:HB1	18:SN:23:PRO:HA	1.96	0.48
34:Sf:133:ALA:HB3	34:Sf:140:TYR:HB3	1.95	0.48
41:LE:99:GLU:OE1	41:LE:99:GLU:N	2.45	0.48
46:LJ:114:ILE:O	46:LJ:114:ILE:HG22	2.12	0.48
78:C1:1261:G:O2'	78:C1:1278:A:N6	2.42	0.48
78:C1:1306:G:O6	78:C1:2366:C:O2'	2.29	0.48
78:C1:3154:C:C2	78:C1:3157:U:N3	2.82	0.48
78:C1:3154:C:O2	78:C1:3157:U:N3	2.46	0.48
10:SF:163:SER:OG	36:Sc:47:PRO:O	2.17	0.48
11:SG:166:GLU:OE2	11:SG:166:GLU:N	2.45	0.48
18:SN:56:ASP:OD1	18:SN:57:ALA:N	2.47	0.48
19:SO:107:ARG:NH1	36:Sc:60:GLU:OE2	2.46	0.48
53:LR:135:LYS:NZ	78:C1:1949:G:OP2	2.39	0.48
62:La:111:LYS:NZ	78:C1:714:G:N7	2.52	0.48
78:C1:220:G:C6	78:C1:1389:G:C2	3.01	0.48
78:C1:2258:U:O2'	78:C1:2259:A:P	2.72	0.48
3:LB:127:LYS:O	3:LB:129:ALA:N	2.46	0.48
5:C2:302:U:OP1	13:SI:22:ARG:NH2	2.41	0.48
8:SD:55:THR:O	8:SD:59:LEU:HD23	2.14	0.48
17:SM:48:SER:O	17:SM:52:LEU:HD23	2.14	0.48
29:SZ:39:ALA:N	29:SZ:70:LYS:O	2.41	0.48
39:LC:165:ALA:HB1	39:LC:219:LEU:HD21	1.96	0.48
48:LM:13:ARG:NH1	48:LM:65:LEU:O	2.47	0.48
51:LP:122:ALA:HB1	51:LP:123:PRO:HD2	1.95	0.48
78:C1:1307:G:O2'	78:C1:1308:A:OP2	2.23	0.48
81:A:175:LYS:N	81:A:175:LYS:CD	2.73	0.48
5:C2:698:U:H2'	5:C2:699:U:O4'	2.13	0.48
5:C2:1655:A:N6	5:C2:1745:G:O2'	2.46	0.48
11:SG:5:ILE:HD12	11:SG:16:PHE:CD1	2.49	0.48
13:SI:48:THR:OG1	13:SI:52:ASN:O	2.18	0.48
30:Sa:41:ILE:HG23	30:Sa:68:TYR:CE1	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:Sg:79:TYR:HB3	35:Sg:91:LEU:HD11	1.96	0.48
41:LE:141:VAL:O	41:LE:145:LEU:HD23	2.14	0.48
46:LJ:22:SER:O	78:C1:2676:A:N6	2.47	0.48
51:LP:25:SER:OG	51:LP:28:ASN:ND2	2.44	0.48
76:Lo:80:ARG:NE	78:C1:2769:A:O3'	2.47	0.48
78:C1:2875:U:C5	81:A:177[B]:LYS:HE3	2.49	0.48
78:C1:3319:U:O2'	78:C1:3320:A:OP1	2.27	0.48
5:C2:258:C:O2	13:SI:178:ARG:NH2	2.43	0.48
5:C2:916:U:O4	19:SO:41:ARG:NH1	2.47	0.48
8:SD:207:THR:HB	21:SR:40:THR:HG22	1.95	0.48
31:Sb:48:SER:OG	31:Sb:49:HIS:ND1	2.45	0.48
53:LR:114:LYS:NZ	78:C1:2093:A:N1	2.61	0.48
66:Le:118:LYS:NZ	78:C1:438:A:OP1	2.40	0.48
78:C1:3154:C:N3	78:C1:3157:U:C4	2.82	0.48
22:SS:41:ARG:NH2	23:ST:36:ILE:O	2.47	0.47
30:Sa:49:ALA:O	30:Sa:53:LEU:HD23	2.14	0.47
43:LG:134:TYR:CG	43:LG:190:VAL:HG21	2.50	0.47
57:LV:6:ALA:HB1	57:LV:125:LEU:HD11	1.96	0.47
67:Lf:13:HIS:O	67:Lf:95:GLY:N	2.47	0.47
78:C1:340:C:H2'	78:C1:341:G:O4'	2.13	0.47
3:LB:2:SER:N	78:C1:2940:A:OP2	2.47	0.47
9:SE:72:VAL:N	9:SE:75:LYS:O	2.39	0.47
28:SY:36:SER:OG	28:SY:39:GLU:OE1	2.32	0.47
35:Sg:111:MET:SD	35:Sg:127:ARG:NH2	2.87	0.47
37:C4:81:U:O2'	78:C1:1055:A:N3	2.46	0.47
39:LC:125:ALA:O	39:LC:129:THR:HG23	2.14	0.47
40:LD:53:VAL:O	40:LD:54:ARG:NH1	2.47	0.47
78:C1:1273:A:O2'	78:C1:1274:A:OP1	2.30	0.47
1:LA:3:ARG:HG3	1:LA:207:VAL:HG22	1.96	0.47
4:SB:30:PHE:O	4:SB:45:LYS:CA	2.59	0.47
5:C2:623:A:H3'	5:C2:624:G:H5''	1.95	0.47
39:LC:26:PHE:CD1	39:LC:130:ALA:HB2	2.48	0.47
73:Ll:25:GLN:OE1	73:Ll:28:ARG:NE	2.48	0.47
78:C1:3353:G:H3'	78:C1:3354:U:O4'	2.15	0.47
5:C2:765:G:HO2'	5:C2:766:U:P	2.37	0.47
5:C2:1234:A:HO2'	34:Sf:140:TYR:HH	1.55	0.47
5:C2:1273:G:H4'	5:C2:1274:C:H3'	1.94	0.47
13:SI:93:THR:OG1	13:SI:95:THR:OG1	2.28	0.47
42:LF:206:LYS:NZ	78:C1:1334:U:OP1	2.39	0.47
48:LM:90:VAL:O	48:LM:93:LYS:N	2.48	0.47
60:LY:5:SER:OG	60:LY:6:LEU:N	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C2:154:G:OP1	11:SG:2:LYS:NZ	2.47	0.47
37:C4:62:U:O4	37:C4:63:A:N6	2.47	0.47
50:LO:171[A]:LYS:NZ	78:C1:3180:A:OP1	2.28	0.47
53:LR:81:ARG:NH2	78:C1:2104:A:OP2	2.46	0.47
56:LU:89:LEU:HB3	56:LU:93:ILE:HD12	1.97	0.47
63:Lb:42:ASN:ND2	78:C1:1074:U:O2'	2.47	0.47
77:Lp:75:ALA:O	77:Lp:79:VAL:HG23	2.15	0.47
5:C2:241:U:O2'	5:C2:242:U:O5'	2.33	0.47
17:SM:73:LYS:CG	34:Sf:108:VAL:HG11	2.44	0.47
27:SX:98:GLU:N	27:SX:100:ASP:OD2	2.48	0.47
53:LR:128:LYS:NZ	78:C1:1724:U:OP1	2.47	0.47
78:C1:3355:U:O2'	78:C1:3356:G:O5'	2.23	0.47
5:C2:122:U:O3'	9:SE:77:ARG:NH2	2.48	0.47
5:C2:148:A:N6	5:C2:166:C:N4	2.62	0.47
5:C2:215:A:H2'	5:C2:216:U:O4'	2.14	0.47
5:C2:415:C:O2	5:C2:418:G:C6	2.67	0.47
5:C2:514:G:N7	5:C2:537:G:C2	2.83	0.47
5:C2:568:G:N7	27:SX:69:ARG:NH1	2.62	0.47
5:C2:1533:C:OP1	22:SS:27:LYS:NZ	2.40	0.47
12:SH:77:LEU:O	12:SH:81:LEU:HD23	2.14	0.47
40:LD:21:ARG:NH1	40:LD:25:GLU:OE2	2.47	0.47
40:LD:234:ASP:OD1	40:LD:234:ASP:N	2.47	0.47
42:LF:184:LEU:CD1	42:LF:198:ALA:HB1	2.44	0.47
47:LL:28:GLN:NE2	78:C1:683:U:OP2	2.46	0.47
48:LM:17:VAL:HG13	48:LM:36:VAL:O	2.14	0.47
48:LM:60:LEU:HA	48:LM:63:VAL:HG22	1.95	0.47
68:Lg:41:ARG:O	68:Lg:43:LYS:NZ	2.37	0.47
68:Lg:95:ILE:HG22	78:C1:2553:U:C5	2.50	0.47
78:C1:209:A:O2'	78:C1:211:A:OP2	2.32	0.47
78:C1:444:U:O4	78:C1:491:A:N6	2.48	0.47
78:C1:1863:G:N1	78:C1:1866:C:OP2	2.39	0.47
2:SA:31:VAL:HG23	2:SA:150:ASP:HA	1.97	0.47
3:LB:316:GLU:OE2	3:LB:316:GLU:N	2.48	0.47
5:C2:628:G:H2'	78:C1:846:A:C2	2.49	0.47
7:SC:87:GLN:NE2	7:SC:94:GLN:OE1	2.48	0.47
15:SK:38:LYS:O	15:SK:42:VAL:HG23	2.15	0.47
29:SZ:42:LEU:HD23	29:SZ:42:LEU:H	1.79	0.47
53:LR:13:SER:OG	53:LR:38:ARG:NH2	2.48	0.47
53:LR:160:GLU:O	53:LR:164:LEU:HD23	2.15	0.47
69:Lh:27:GLU:O	69:Lh:31:LEU:HD13	2.15	0.47
78:C1:637:C:O2'	78:C1:638:C:O5'	2.19	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
78:C1:2258:U:C2'	78:C1:2259:A:O5'	2.62	0.47
4:SB:143:THR:HG22	4:SB:205:PHE:CE2	2.49	0.47
5:C2:66:U:O2	11:SG:160:ARG:NE	2.43	0.47
18:SN:151:ASN:OD1	64:Lc:15:ALA:HB2	2.15	0.47
37:C4:11:A:N6	40:LD:13:SER:O	2.45	0.47
45:LI:184:LYS:O	45:LI:187:ALA:C	2.58	0.47
78:C1:835:G:O2'	78:C1:857:G:N2	2.42	0.47
78:C1:2704:A:O2'	78:C1:2705:A:O5'	2.30	0.47
5:C2:627:C:H2'	5:C2:628:G:O4'	2.15	0.47
10:SF:136:ALA:O	10:SF:140:THR:HG22	2.15	0.47
21:SR:25:THR:O	21:SR:31:ASN:ND2	2.45	0.47
29:SZ:40:VAL:C	29:SZ:75:LEU:HD11	2.40	0.47
35:Sg:39:ASP:OD1	35:Sg:41:THR:OG1	2.28	0.47
38:C3:22:U:O4	78:C1:341:G:O2'	2.33	0.47
39:LC:347:THR:O	78:C1:520:U:N3	2.48	0.47
44:LH:155:SER:CB	78:C1:3110:C:HO2'	2.27	0.47
78:C1:1858:A:HO2'	78:C1:1859:A:P	2.38	0.47
4:SB:108:ASP:OD1	4:SB:109:LYS:N	2.48	0.46
5:C2:1482:C:O2'	20:SQ:77:GLN:NE2	2.48	0.46
11:SG:49:VAL:HG12	11:SG:115:LYS:HB3	1.96	0.46
11:SG:78:THR:OG1	11:SG:79:LYS:N	2.47	0.46
18:SN:6:SER:OG	18:SN:7:ALA:N	2.48	0.46
20:SQ:44:LEU:HB3	20:SQ:78:VAL:HG11	1.97	0.46
24:SU:40:ASN:OD1	24:SU:41:ILE:N	2.48	0.46
35:Sg:209:THR:HG23	35:Sg:210:LEU:HG	1.97	0.46
41:LE:142:ASP:OD1	41:LE:143:LYS:N	2.48	0.46
45:LI:47:PRO:O	45:LI:172:GLY:N	2.48	0.46
71:Lj:55:ARG:NH1	78:C1:353:G:O6	2.48	0.46
75:Ln:19:LYS:O	75:Ln:22:ALA:HB3	2.16	0.46
78:C1:1693:C:O2'	78:C1:1772:U:O2'	2.21	0.46
5:C2:486:G:O6	5:C2:502:U:C4	2.66	0.46
5:C2:1280:C:OP1	32:Sd:44:ARG:NH2	2.44	0.46
16:SL:8:GLN:NE2	16:SL:14:GLN:O	2.47	0.46
38:C3:36:G:N2	38:C3:37:A:N1	2.59	0.46
39:LC:212:ASP:OD2	39:LC:216:VAL:HG22	2.16	0.46
42:LF:148:VAL:HG12	42:LF:181:ILE:HD11	1.97	0.46
46:LJ:26:SER:OG	46:LJ:27:GLY:N	2.46	0.46
47:LL:68:LYS:NZ	78:C1:699:A:O5'	2.48	0.46
53:LR:82:LYS:O	78:C1:1914:G:O2'	2.30	0.46
66:Le:78:ASN:OD1	66:Le:78:ASN:N	2.46	0.46
66:Le:80:LYS:O	66:Le:84:THR:HG23	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:LB:10:ARG:HH11	3:LB:14:LEU:HD21	1.80	0.46
8:SD:70:THR:CG2	8:SD:86:LEU:HD22	2.46	0.46
19:SO:113:GLY:O	19:SO:114:ARG:C	2.59	0.46
35:Sg:220:ILE:O	35:Sg:233:THR:CA	2.55	0.46
43:LG:47:SER:OG	78:C1:2585:G:N7	2.32	0.46
46:LJ:32:ARG:O	46:LJ:36:VAL:HG23	2.15	0.46
55:LT:124:VAL:O	55:LT:124:VAL:HG12	2.15	0.46
68:Lg:79:SER:OG	68:Lg:80:ARG:NH1	2.48	0.46
5:C2:79:C:OP1	11:SG:159:ARG:NH2	2.46	0.46
5:C2:420:A:OP1	11:SG:96:SER:OG	2.17	0.46
11:SG:208:TYR:CE2	11:SG:212:LEU:HD11	2.51	0.46
14:SJ:124:HIS:CE1	14:SJ:128:LEU:HD11	2.50	0.46
45:LI:51:HIS:HD2	55:LT:160:ILE:HD12	1.79	0.46
62:La:7:LYS:NZ	78:C1:1373:A:OP2	2.42	0.46
68:Lg:95:ILE:HG22	78:C1:2553:U:C4	2.51	0.46
5:C2:1311:U:N3	5:C2:1314:U:OP2	2.41	0.46
7:SC:42:GLY:CA	7:SC:68:ILE:HD11	2.44	0.46
22:SS:21:ASN:ND2	46:LJ:108:GLU:OE2	2.48	0.46
37:C4:50:U:O2'	40:LD:221:GLU:O	2.26	0.46
59:LX:59:SER:HA	59:LX:62:VAL:HG22	1.98	0.46
72:Lk:30:LYS:O	72:Lk:31:LEU:HD22	2.15	0.46
80:6:72:A:H2'	80:6:73:G:O4'	2.15	0.46
47:LL:24:VAL:HG11	47:LL:26:PHE:CZ	2.50	0.46
48:LM:128:ARG:NH2	78:C1:3260:G:OP2	2.48	0.46
50:LO:39[A]:GLU:OE1	50:LO:39[A]:GLU:N	2.44	0.46
62:La:82:ILE:O	62:La:87:ARG:NH2	2.48	0.46
78:C1:93:C:OP2	78:C1:2764:C:O2'	2.28	0.46
5:C2:227:U:C4	5:C2:230:C:N4	2.84	0.46
5:C2:628:G:H21	5:C2:971:A:H62	1.62	0.46
5:C2:1251:U:O2'	5:C2:1252:C:OP1	2.29	0.46
5:C2:1488:G:H3'	5:C2:1515:A:H61	1.80	0.46
47:LL:68:LYS:HZ1	78:C1:699:A:P	2.39	0.46
72:Lk:26:LYS:NZ	72:Lk:28:ASN:OD1	2.48	0.46
78:C1:401:U:O2'	78:C1:402:A:OP1	2.28	0.46
12:SH:63:PRO:O	12:SH:64:VAL:HG12	2.16	0.46
16:SL:118:GLN:N	16:SL:121:ASP:OD2	2.49	0.46
5:C2:955:A:OP1	18:SN:3:ARG:NE	2.48	0.46
5:C2:1060:U:H3'	5:C2:1061:A:H5''	1.97	0.46
7:SC:116:LYS:HG2	7:SC:127:ALA:HB3	1.98	0.46
12:SH:64:VAL:O	12:SH:64:VAL:HG22	2.16	0.46
13:SI:34:ALA:HB2	13:SI:56:ARG:CD	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:Sa:85:ARG:HG3	30:Sa:86:VAL:H	1.80	0.46
54:LS:148:LEU:HD12	54:LS:149:LYS:N	2.30	0.46
71:Lj:53:ALA:O	71:Lj:57:HIS:ND1	2.48	0.46
78:C1:358:G:N2	78:C1:361:A:OP2	2.41	0.46
78:C1:1264:G:N2	78:C1:1265:U:O4	2.47	0.46
78:C1:1906:G:O2'	78:C1:1907:C:OP2	2.29	0.46
80:6:1:U:H2'	80:6:2:C:H6	1.81	0.46
3:LB:160:VAL:CG2	3:LB:183:LEU:HD11	2.45	0.46
9:SE:148:ARG:NH2	11:SG:201:GLN:OE1	2.48	0.46
47:LL:70:ARG:NH2	78:C1:103:G:OP1	2.49	0.46
54:LS:77:VAL:HG11	54:LS:106:LEU:HD13	1.98	0.46
71:Lj:11:ARG:NH2	78:C1:1844:C:O2'	2.49	0.46
4:SB:46:THR:C	4:SB:47:LEU:HD12	2.40	0.45
5:C2:261:U:O2'	5:C2:262:U:O5'	2.33	0.45
34:Sf:121:CYS:HB2	34:Sf:132:LEU:HD21	1.97	0.45
39:LC:188:ARG:NE	39:LC:197:ARG:O	2.48	0.45
46:LJ:110:ILE:HG23	46:LJ:115:LYS:O	2.15	0.45
3:LB:144:ILE:H	3:LB:144:ILE:HD12	1.81	0.45
5:C2:629:U:C5	5:C2:630:A:C8	3.04	0.45
5:C2:1445:G:N2	34:Sf:87:THR:HG23	2.31	0.45
5:C2:1530:C:OP2	29:SZ:96:SER:OG	2.29	0.45
5:C2:1640:C:N4	79:5:48:A:OP1	2.49	0.45
22:SS:5:VAL:O	29:SZ:42:LEU:HD21	2.16	0.45
68:Lg:8:ARG:NH2	78:C1:1597:C:OP1	2.44	0.45
77:Lp:58:SER:O	77:Lp:61:LYS:NZ	2.33	0.45
78:C1:831:G:O2'	78:C1:1864:A:N3	2.43	0.45
78:C1:1222:G:O2'	78:C1:1285:G:N2	2.45	0.45
78:C1:3153:U:O2'	78:C1:3154:C:O4'	2.31	0.45
78:C1:3184:A:N3	78:C1:3187:A:O2'	2.46	0.45
2:SA:84:ARG:NH1	2:SA:203:PHE:O	2.43	0.45
5:C2:487:G:C2	5:C2:501:U:O2	2.68	0.45
5:C2:1524:A:O3'	23:ST:93:HIS:ND1	2.49	0.45
18:SN:151:ASN:CG	64:Lc:15:ALA:HB2	2.42	0.45
20:SQ:143:ARG:NH2	80:6:33:U:C6	2.84	0.45
38:C3:40:A:OP2	38:C3:103:G:N1	2.42	0.45
80:6:68:G:H2'	80:6:69:A:H8	1.80	0.45
3:LB:171:LEU:HD21	3:LB:314:TYR:CE1	2.51	0.45
3:LB:221:THR:O	3:LB:272:TYR:N	2.49	0.45
4:SB:134:VAL:O	4:SB:135:LEU:HD23	2.17	0.45
5:C2:159:U:HO2'	11:SG:87:ARG:NH1	2.12	0.45
5:C2:446:A:OP1	9:SE:59:ARG:NH1	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:SD:156:PHE:C	8:SD:157:LEU:HD12	2.41	0.45
9:SE:87:MET:N	9:SE:101:LEU:O	2.49	0.45
13:SI:152:ILE:HG13	13:SI:153:GLU:H	1.82	0.45
25:SV:1:MET:O	25:SV:8:LEU:HD12	2.16	0.45
35:Sg:19:TRP:CD2	35:Sg:306:THR:HG22	2.52	0.45
35:Sg:80:ALA:O	35:Sg:91:LEU:HD12	2.17	0.45
45:LI:44:ASP:OD1	45:LI:185:ARG:NE	2.50	0.45
45:LI:157:TYR:OH	78:C1:1206:G:OP1	2.20	0.45
48:LM:15:VAL:HG22	48:LM:65:LEU:HD21	1.98	0.45
65:Ld:11:GLU:O	65:Ld:106:THR:OG1	2.18	0.45
78:C1:1481:A:O2'	78:C1:1858:A:O2'	2.30	0.45
5:C2:149:C:N3	5:C2:166:C:N4	2.64	0.45
5:C2:269:G:N7	11:SG:186:ARG:NH2	2.64	0.45
5:C2:658:C:O2	5:C2:676:G:N2	2.50	0.45
5:C2:788:A:OP2	9:SE:108:ARG:NH1	2.46	0.45
5:C2:1240:U:N3	5:C2:1243:G:OP2	2.48	0.45
10:SF:146:THR:HG21	10:SF:220:VAL:HG12	1.98	0.45
53:LR:23:TRP:O	53:LR:50:ILE:HG23	2.16	0.45
78:C1:1523:U:OP1	78:C1:1607:U:N3	2.45	0.45
5:C2:458:G:OP1	28:SY:109:LYS:NZ	2.41	0.45
10:SF:31:GLU:OE1	10:SF:31:GLU:N	2.44	0.45
10:SF:117:THR:HG22	10:SF:121:ILE:CD1	2.47	0.45
17:SM:84:ASN:O	17:SM:86:VAL:HG22	2.17	0.45
19:SO:48:VAL:HG22	19:SO:49:LYS:H	1.81	0.45
33:Se:14:VAL:O	33:Se:17:GLN:N	2.49	0.45
34:Sf:147:VAL:HG13	34:Sf:147:VAL:O	2.16	0.45
35:Sg:240:VAL:HA	35:Sg:256:THR:HG22	1.99	0.45
47:LL:77:LEU:HA	47:LL:80:VAL:HG22	1.99	0.45
50:LO:12[A]:LYS:NZ	78:C1:3184:A:OP2	2.30	0.45
78:C1:1482:A:OP1	78:C1:1866:C:O2'	2.28	0.45
5:C2:3:U:O2	14:SJ:17:ARG:NH1	2.46	0.45
7:SC:226:THR:HG23	7:SC:228:ASN:OD1	2.15	0.45
16:SL:102:LYS:O	27:SX:13:ARG:NH2	2.47	0.45
45:LI:12:GLN:NE2	45:LI:129:VAL:O	2.49	0.45
63:Lb:16:ALA:O	63:Lb:20:GLY:HA2	2.16	0.45
76:Lo:77:CYS:SG	76:Lo:79:THR:OG1	2.61	0.45
3:LB:251:CYS:SG	78:C1:2943:G:N2	2.90	0.45
5:C2:402:C:OP1	9:SE:3:ARG:NH2	2.50	0.45
5:C2:545:A:N1	5:C2:593:U:O2'	2.48	0.45
12:SH:83:LYS:O	12:SH:86:GLN:NE2	2.50	0.45
44:LH:58:HIS:O	78:C1:3186:A:N6	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:LL:157:ARG:O	62:La:99:ALA:N	2.47	0.45
78:C1:3152:U:OP2	78:C1:3395:G:N1	2.45	0.45
2:SA:2:SER:OG	2:SA:3:LEU:N	2.46	0.45
2:SA:24:LEU:O	2:SA:163:ASN:ND2	2.50	0.45
3:LB:14:LEU:O	78:C1:3009:G:O2'	2.30	0.45
3:LB:287:LYS:O	3:LB:293:ASN:ND2	2.50	0.45
9:SE:19:LEU:HD11	9:SE:108:ARG:CD	2.47	0.45
26:SW:6:VAL:HG23	26:SW:29:PRO:HD2	1.99	0.45
45:LI:36:LEU:HD21	45:LI:69:ARG:HD3	1.98	0.45
80:6:52:G:O6	80:6:63:C:N4	2.50	0.45
5:C2:393:C:OP2	13:SI:2:GLY:N	2.50	0.45
5:C2:711:U:O2'	5:C2:712:G:OP2	2.31	0.45
5:C2:1001:A:H5'	80:6:38:A:O3'	2.17	0.45
5:C2:1159:C:O2'	20:SQ:140:LYS:NZ	2.50	0.45
38:C3:151:C:N4	78:C1:2585:G:O5'	2.50	0.45
43:LG:54:GLU:O	43:LG:58:VAL:HG23	2.17	0.45
43:LG:75:ILE:O	43:LG:76:ALA:HB3	2.17	0.45
59:LX:73:MET:HE2	59:LX:142:ILE:C	2.42	0.45
71:Lj:29:VAL:O	71:Lj:32:LYS:NZ	2.33	0.45
5:C2:755:A:HO2'	5:C2:756:A:P	2.38	0.44
5:C2:1596:C:OP1	32:Sd:16:LYS:NZ	2.49	0.44
9:SE:53:LYS:O	28:SY:22:GLN:NE2	2.50	0.44
10:SF:157:ARG:HH22	80:7:31:G:H21	1.65	0.44
35:Sg:133:VAL:HG11	35:Sg:183:LEU:HD11	1.99	0.44
35:Sg:215:GLY:O	35:Sg:240:VAL:HG12	2.17	0.44
38:C3:149:A:N6	78:C1:8:C:N4	2.61	0.44
41:LE:157:GLN:OE1	41:LE:157:GLN:N	2.47	0.44
47:LL:18:TRP:O	47:LL:21:ARG:O	2.35	0.44
49:LN:48:ALA:HB1	49:LN:53:TYR:HB2	1.98	0.44
49:LN:48:ALA:HB1	49:LN:53:TYR:CB	2.47	0.44
52:LQ:42:ALA:HB3	52:LQ:45:ASN:OD1	2.17	0.44
76:Lo:21:THR:HG22	76:Lo:22:GLN:N	2.32	0.44
1:LA:243:THR:HG22	1:LA:244:GLY:N	2.31	0.44
3:LB:21:ARG:NH2	78:C1:3309:G:O6	2.44	0.44
5:C2:127:G:O6	11:SG:202:ARG:NH2	2.50	0.44
5:C2:523:G:OP2	28:SY:37:LYS:NZ	2.50	0.44
5:C2:1329:A:OP2	8:SD:160:SER:OG	2.33	0.44
5:C2:1563:C:O3'	23:ST:41:SER:OG	2.35	0.44
10:SF:57:SER:OG	10:SF:167:ARG:NH2	2.49	0.44
35:Sg:266:ASP:OD1	35:Sg:266:ASP:N	2.40	0.44
35:Sg:270:LEU:HD21	35:Sg:273:ASP:HB2	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:LE:100:LYS:NZ	41:LE:137:ASP:OD1	2.50	0.44
42:LF:197:GLN:OE1	42:LF:197:GLN:N	2.47	0.44
51:LP:181:ARG:NH2	78:C1:3268:A:OP1	2.49	0.44
54:LS:148:LEU:HD11	54:LS:150:PHE:HD2	1.81	0.44
71:Lj:58:THR:OG1	71:Lj:59:THR:N	2.51	0.44
78:C1:1141:C:O2'	78:C1:1153:A:N3	2.44	0.44
5:C2:607:G:OP2	5:C2:613:G:N1	2.50	0.44
7:SC:38:VAL:O	7:SC:38:VAL:HG13	2.18	0.44
9:SE:184:THR:N	9:SE:224:ASN:O	2.45	0.44
15:SK:80:LEU:HB2	15:SK:82:LEU:HD23	2.00	0.44
35:Sg:41:THR:C	35:Sg:42:LEU:HD12	2.43	0.44
50:LO:8[A]:VAL:O	50:LO:118[A]:VAL:HG22	2.17	0.44
59:LX:73:MET:HA	59:LX:76:VAL:HG12	1.99	0.44
78:C1:451:U:C2	78:C1:486:A:C6	3.05	0.44
78:C1:2875:U:C6	81:A:177[B]:LYS:HE3	2.53	0.44
1:LA:95:SER:N	78:C1:2551:U:O4	2.45	0.44
3:LB:358:TRP:CD1	58:LW:1:MET:HE1	2.53	0.44
5:C2:144:U:H2'	5:C2:145:A:O4'	2.16	0.44
5:C2:523:G:OP1	28:SY:59:GLY:N	2.50	0.44
5:C2:647:G:H22	5:C2:687:G:H1	1.66	0.44
5:C2:1226:A:H61	17:SM:114:LYS:CB	2.30	0.44
5:C2:1681:A:H2	5:C2:1720:G:H21	1.64	0.44
11:SG:157:VAL:HG11	11:SG:172:ALA:HB1	1.98	0.44
22:SS:57:ARG:HE	29:SZ:40:VAL:HG21	1.82	0.44
35:Sg:23:LEU:HB2	35:Sg:293:ALA:HB2	2.00	0.44
52:LQ:177:GLY:O	52:LQ:186:VAL:N	2.48	0.44
1:LA:65:ASP:OD1	1:LA:68:LYS:N	2.51	0.44
4:SB:29:TRP:CE3	4:SB:47:LEU:HD11	2.53	0.44
20:SQ:58:ASP:N	20:SQ:58:ASP:OD1	2.51	0.44
23:ST:100:ILE:O	23:ST:104:VAL:HG23	2.18	0.44
44:LH:147:SER:OG	44:LH:187:ILE:HD11	2.18	0.44
51:LP:47:TYR:OH	51:LP:57:ALA:O	2.20	0.44
17:SM:34:THR:HG21	17:SM:128:ALA:HB2	2.00	0.44
36:Sc:65:ARG:NH2	36:Sc:67:ARG:O	2.50	0.44
39:LC:59:GLN:OE1	71:Lj:55:ARG:NH2	2.50	0.44
42:LF:41:ARG:NH1	78:C1:597:G:O3'	2.51	0.44
46:LJ:96:PHE:CD2	46:LJ:160:VAL:HG12	2.52	0.44
52:LQ:158:HIS:H	52:LQ:186:VAL:HG11	1.82	0.44
78:C1:2116:G:OP1	78:C1:2118:C:N4	2.51	0.44
78:C1:3353:G:H3'	78:C1:3354:U:C4'	2.47	0.44
2:SA:41:ARG:N	2:SA:45:VAL:O	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:LB:247:ARG:NH1	78:C1:1888:U:OP1	2.51	0.44
11:SG:48:TYR:OH	11:SG:119:GLN:O	2.25	0.44
12:SH:14:THR:C	12:SH:18:LEU:HD12	2.43	0.44
17:SM:53:THR:HG21	34:Sf:106:TYR:OH	2.18	0.44
27:SX:91:GLY:O	27:SX:94:ASN:ND2	2.51	0.44
42:LF:187:GLU:O	42:LF:191:VAL:HA	2.17	0.44
54:LS:12:ARG:HE	54:LS:22:PRO:HD2	1.83	0.44
78:C1:2206:G:H21	78:C1:2207:A:N6	2.14	0.44
5:C2:229:U:C4	5:C2:236:A:N6	2.85	0.44
5:C2:1584:G:O2'	5:C2:1585:U:OP2	2.31	0.44
5:C2:1611:A:O2'	10:SF:95:ASN:O	2.33	0.44
7:SC:148:LEU:HD21	14:SJ:95:TYR:CZ	2.53	0.44
10:SF:145:ASP:OD1	10:SF:146:THR:N	2.47	0.44
13:SI:34:ALA:HB2	13:SI:56:ARG:HD2	1.99	0.44
13:SI:105:ASP:O	13:SI:106:ALA:HB3	2.18	0.44
19:SO:42:VAL:HG23	19:SO:46:MET:HE2	2.00	0.44
24:SU:92:ASP:O	24:SU:93:LEU:HD22	2.18	0.44
56:LU:50:LEU:HD23	56:LU:50:LEU:H	1.83	0.44
78:C1:1279:C:H2'	78:C1:1280:C:O4'	2.17	0.44
78:C1:2129:U:O2'	78:C1:2144:A:N3	2.49	0.44
1:LA:190:ARG:NH1	1:LA:191:LEU:HD21	2.33	0.44
2:SA:138:TYR:OH	5:C2:1296:A:OP1	2.31	0.44
3:LB:346:THR:OG1	3:LB:347:SER:N	2.51	0.44
5:C2:1382:A:HO2'	5:C2:1383:G:P	2.32	0.44
5:C2:1742:U:O2'	5:C2:1743:U:OP1	2.34	0.44
13:SI:159:GLN:HB3	13:SI:165:LEU:HD23	1.99	0.44
20:SQ:100:GLN:NE2	35:Sg:57:PRO:O	2.51	0.44
39:LC:138:ARG:HE	39:LC:243:HIS:HB2	1.82	0.44
42:LF:184:LEU:HD11	42:LF:198:ALA:HB1	2.00	0.44
61:LZ:24:VAL:HG22	61:LZ:25:ILE:O	2.18	0.44
76:Lo:2:VAL:N	76:Lo:90:HIS:O	2.50	0.44
78:C1:2452:G:H2'	78:C1:2494:A:H61	1.83	0.44
78:C1:2837:A:OP2	78:C1:2845:A:N6	2.49	0.44
1:LA:93:LYS:NZ	78:C1:2547:A:O3'	2.51	0.43
5:C2:652:G:N2	5:C2:683:C:OP2	2.51	0.43
5:C2:1097:U:O4	7:SC:201:ASN:ND2	2.50	0.43
5:C2:1191:U:C2	80:6:34:U:H5'	2.53	0.43
5:C2:1609:U:OP2	20:SQ:14:LYS:NZ	2.37	0.43
8:SD:134:CYS:SG	8:SD:135:GLU:N	2.91	0.43
11:SG:70:PRO:HA	11:SG:98:ARG:HH22	1.82	0.43
18:SN:5:HIS:HD2	18:SN:121:ARG:HE	1.66	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:Sa:36:ILE:HG22	30:Sa:73:TYR:H	1.83	0.43
37:C4:21:G:H4'	40:LD:272:TYR:OH	2.17	0.43
40:LD:54:ARG:NH2	40:LD:147:ASP:OD1	2.42	0.43
54:LS:113:ARG:NH2	78:C1:1187:C:OP1	2.51	0.43
68:Lg:81:CYS:O	68:Lg:85:VAL:HG23	2.18	0.43
78:C1:1232:C:C4	78:C1:1261:G:N2	2.86	0.43
78:C1:1562:C:HO2'	78:C1:1563:C:C5'	2.28	0.43
2:SA:90:ALA:HA	2:SA:95:ALA:HB3	2.00	0.43
5:C2:1319:A:OP2	21:SR:67:ARG:NH1	2.52	0.43
7:SC:130:ILE:O	7:SC:134:LEU:HD23	2.18	0.43
8:SD:224:ASP:OD1	8:SD:225:TYR:N	2.51	0.43
25:SV:73:ALA:CB	25:SV:79:LEU:HD12	2.46	0.43
43:LG:140:VAL:HG11	49:LN:2:GLY:O	2.19	0.43
48:LM:77:ARG:NH1	78:C1:562:C:OP2	2.48	0.43
78:C1:1635:G:N2	78:C1:1638:A:OP2	2.49	0.43
78:C1:2101:C:HO2'	78:C1:2102:U:P	2.32	0.43
5:C2:486:G:C6	5:C2:502:U:O4	2.68	0.43
22:SS:6:GLN:O	22:SS:7:GLU:HG2	2.18	0.43
35:Sg:174:ASN:OD1	35:Sg:198:ASN:ND2	2.51	0.43
61:LZ:89:VAL:HG23	61:LZ:89:VAL:O	2.18	0.43
81:A:174:ALA:O	81:A:176:LYS:HD2	2.18	0.43
3:LB:311:PHE:CD2	3:LB:317:ILE:HD11	2.54	0.43
5:C2:513:U:H2'	5:C2:514:G:C8	2.52	0.43
9:SE:28:ALA:HB1	9:SE:29:PRO:CD	2.48	0.43
10:SF:156:ARG:NH1	19:SO:53:ASP:OD1	2.47	0.43
35:Sg:82:SER:OG	35:Sg:92:TRP:NE1	2.41	0.43
37:C4:3:U:O2'	37:C4:25:G:N3	2.51	0.43
51:LP:107:LEU:HD23	51:LP:152:GLU:HG3	2.00	0.43
72:Lk:8:ILE:O	72:Lk:12:LEU:HD23	2.18	0.43
78:C1:1635:G:N1	78:C1:1638:A:OP2	2.44	0.43
80:6:44:A:H2'	80:6:45:U:O4'	2.19	0.43
80:6:64:C:H2'	80:6:65:U:C6	2.53	0.43
1:LA:191:LEU:HD12	78:C1:1794:G:H4'	1.99	0.43
1:LA:246:LEU:HD12	78:C1:2153:U:OP1	2.19	0.43
5:C2:215:A:O2'	5:C2:216:U:OP1	2.32	0.43
5:C2:629:U:C5	78:C1:846:A:C5	3.07	0.43
19:SO:89:THR:HG22	19:SO:125:SER:OG	2.18	0.43
59:LX:108:LEU:N	59:LX:125:ARG:O	2.48	0.43
65:Ld:49:VAL:HG22	65:Ld:91:SER:HB2	2.00	0.43
78:C1:1222:G:O2'	78:C1:1285:G:N1	2.44	0.43
78:C1:1240:A:H61	78:C1:1244:A:C5'	2.31	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
78:C1:2877:G:O2'	78:C1:2923:U:O2'	2.36	0.43
17:SM:71:ILE:O	17:SM:75:VAL:HG23	2.18	0.43
17:SM:133:LEU:HA	17:SM:136:ILE:HG22	1.99	0.43
28:SY:6:THR:CG2	28:SY:28:LEU:HB2	2.48	0.43
30:Sa:44:ILE:HD12	30:Sa:65:PRO:HG2	2.00	0.43
38:C3:62:C:OP1	69:Lh:49:LYS:NZ	2.51	0.43
38:C3:94:C:P	71:Lj:75:LYS:HZ1	2.40	0.43
78:C1:1046:A:O2'	78:C1:1048:A:OP2	2.24	0.43
5:C2:65:A:H2	5:C2:84:A:H62	1.65	0.43
5:C2:78:A:C6	11:SG:178:LEU:HD23	2.53	0.43
10:SF:47:SER:OG	10:SF:48:PHE:N	2.52	0.43
18:SN:76:LYS:HA	18:SN:81:ALA:HB2	2.01	0.43
31:Sb:61:THR:O	31:Sb:62:ILE:HG12	2.18	0.43
36:Sc:19:THR:HG22	36:Sc:20:GLY:N	2.34	0.43
43:LG:94:PHE:CB	43:LG:189:LEU:HD11	2.49	0.43
50:LO:85[A]:ARG:NH1	78:C1:2382:G:OP1	2.52	0.43
71:Lj:21:ARG:NH2	71:Lj:41:ALA:O	2.40	0.43
78:C1:401:U:H3'	78:C1:402:A:C5'	2.49	0.43
78:C1:451:U:C4	78:C1:486:A:N1	2.86	0.43
80:6:66:A:H2'	80:6:67:U:O4'	2.19	0.43
3:LB:73:VAL:HG11	57:LV:90:GLY:HA3	2.00	0.43
5:C2:386:G:OP2	13:SI:25:ARG:NH2	2.52	0.43
5:C2:454:U:H5'	9:SE:66:MET:HE3	2.00	0.43
5:C2:878:G:OP1	5:C2:943:C:O2'	2.28	0.43
10:SF:121:ILE:HG22	10:SF:121:ILE:O	2.18	0.43
17:SM:27:ALA:O	17:SM:31:VAL:HG13	2.19	0.43
17:SM:62:LEU:HD12	17:SM:75:VAL:HG11	2.00	0.43
28:SY:40:LEU:O	28:SY:44:LEU:HD13	2.18	0.43
39:LC:52:VAL:HG22	39:LC:53:SER:H	1.83	0.43
40:LD:233:ALA:O	40:LD:236:LEU:N	2.52	0.43
51:LP:167:ARG:C	51:LP:168:LEU:HD22	2.44	0.43
68:Lg:71:THR:HG22	68:Lg:72:VAL:N	2.34	0.43
70:Li:18:THR:HG23	70:Li:18:THR:O	2.19	0.43
72:Lk:12:LEU:O	72:Lk:15:THR:OG1	2.28	0.43
78:C1:905:U:O2'	78:C1:910:G:O3'	2.34	0.43
1:LA:40:TYR:OH	78:C1:2551:U:O2	2.31	0.43
1:LA:104:LEU:HA	1:LA:107:VAL:HG22	2.01	0.43
2:SA:38:PHE:N	2:SA:47:VAL:O	2.48	0.43
2:SA:148:ASP:OD2	2:SA:165:ARG:NH1	2.52	0.43
39:LC:82:THR:HG22	78:C1:365:A:H1'	2.00	0.43
42:LF:77:VAL:HG22	54:LS:59:VAL:HA	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:LN:44:ARG:NH2	78:C1:269:G:OP2	2.46	0.43
53:LR:20:ARG:NE	78:C1:1875:G:N7	2.67	0.43
5:C2:1240:U:O2'	5:C2:1242:A:N7	2.44	0.43
5:C2:1420:C:OP1	32:Sd:54:LYS:NZ	2.51	0.43
6:SP:110:GLU:HG2	22:SS:119:ILE:HD11	2.01	0.43
30:Sa:88:SER:OG	30:Sa:91:ASP:OD1	2.26	0.43
37:C4:20:A:H2'	37:C4:21:G:O4'	2.18	0.43
40:LD:116:ASP:OD1	40:LD:117:GLU:N	2.50	0.43
52:LQ:125:ASP:OD1	52:LQ:125:ASP:N	2.49	0.43
78:C1:3042:U:OP2	78:C1:3092:C:N4	2.44	0.43
8:SD:105:MET:CG	8:SD:122:VAL:HG21	2.49	0.42
12:SH:87:ASP:O	12:SH:88:ARG:NH1	2.47	0.42
19:SO:50:ALA:HB1	19:SO:52:ARG:HG2	2.00	0.42
48:LM:18:GLY:HA2	48:LM:72:LEU:HD12	2.01	0.42
71:Lj:17:THR:OG1	71:Lj:18:LEU:N	2.52	0.42
78:C1:3163:A:N6	78:C1:3288:G:O6	2.51	0.42
5:C2:614:C:OP1	27:SX:3:LYS:NZ	2.45	0.42
8:SD:105:MET:O	8:SD:109:LEU:HD13	2.18	0.42
12:SH:60:ILE:HD12	12:SH:92:PHE:CE1	2.54	0.42
15:SK:47:GLN:O	15:SK:50:THR:OG1	2.34	0.42
21:SR:26:LEU:HD12	21:SR:26:LEU:N	2.35	0.42
26:SW:105:THR:OG1	26:SW:126:LEU:HD11	2.18	0.42
30:Sa:23:CYS:O	30:Sa:27:SER:N	2.52	0.42
61:LZ:13:VAL:O	61:LZ:20:GLY:N	2.52	0.42
78:C1:2890:A:H61	78:C1:2913:C:N4	2.17	0.42
2:SA:75:ALA:O	2:SA:98:ILE:N	2.49	0.42
17:SM:91:VAL:HG22	17:SM:92:ALA:H	1.84	0.42
39:LC:33:ASP:OD1	39:LC:34:ILE:N	2.51	0.42
59:LX:25:LYS:HE2	59:LX:27:ARG:HH11	1.83	0.42
68:Lg:61:GLN:HA	68:Lg:64:THR:HG22	2.00	0.42
78:C1:435:C:H2'	78:C1:436:A:C8	2.54	0.42
80:7:35:U:O2'	80:7:36:U:O5'	2.30	0.42
5:C2:763:G:OP2	14:SJ:79:ARG:NH1	2.52	0.42
10:SF:51:VAL:O	10:SF:51:VAL:HG12	2.19	0.42
38:C3:58:G:N7	71:Lj:63:ARG:NH2	2.64	0.42
40:LD:261:THR:HG1	40:LD:264:GLN:CD	2.19	0.42
44:LH:4:ILE:HG22	48:LM:41:GLN:OE1	2.19	0.42
51:LP:71:ALA:HB2	78:C1:3310:A:OP1	2.19	0.42
72:Lk:44:LYS:HG2	72:Lk:53:THR:HG23	2.00	0.42
78:C1:2434:U:O4	78:C1:2595:A:C2	2.72	0.42
7:SC:53:ILE:HA	7:SC:56:ILE:HD12	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:SN:35:GLU:HA	18:SN:38:VAL:HG12	2.02	0.42
21:SR:34:LEU:O	21:SR:38:ILE:HG22	2.19	0.42
23:ST:6:VAL:HA	23:ST:9:VAL:HG12	2.00	0.42
39:LC:226:GLU:OE1	39:LC:246:ARG:NH1	2.50	0.42
44:LH:167:VAL:HG12	44:LH:168:ARG:N	2.34	0.42
46:LJ:10:ARG:NH2	46:LJ:151:SER:O	2.45	0.42
49:LN:44:ARG:NH1	78:C1:269:G:OP2	2.50	0.42
50:LO:72[A]:HIS:ND1	78:C1:3008:A:OP1	2.50	0.42
63:Lb:33:LYS:NZ	78:C1:2722:U:OP1	2.37	0.42
64:Lc:50:VAL:HG21	78:C1:2553:U:O4'	2.19	0.42
65:Ld:71:LEU:HD23	65:Ld:73:LEU:HD21	2.00	0.42
1:LA:2:GLY:N	78:C1:2415:C:OP1	2.53	0.42
2:SA:79:ARG:NH1	2:SA:125:ASP:OD2	2.53	0.42
3:LB:14:LEU:HA	3:LB:17:LEU:HD13	2.01	0.42
5:C2:1063:U:OP1	31:Sb:72:LYS:NZ	2.53	0.42
10:SF:189:THR:HG21	29:SZ:98:GLN:OE1	2.19	0.42
12:SH:103:SER:O	12:SH:106:SER:OG	2.35	0.42
41:LE:59:GLU:OE1	41:LE:59:GLU:N	2.51	0.42
46:LJ:54:VAL:HG12	46:LJ:59:ILE:CG1	2.50	0.42
57:LV:45:ARG:NE	78:C1:3043:C:OP1	2.49	0.42
78:C1:249:U:O2	78:C1:250:U:N3	2.53	0.42
78:C1:1094:U:H1'	78:C1:1095:U:O5'	2.19	0.42
3:LB:247:ARG:N	78:C1:1889:G:OP1	2.40	0.42
5:C2:1775:U:OP1	75:Ln:11:ARG:NH1	2.44	0.42
17:SM:108:ARG:O	17:SM:110:GLY:N	2.52	0.42
19:SO:44:GLY:HA2	19:SO:59:ALA:HB1	2.00	0.42
25:SV:85:TYR:O	31:Sb:6:ASP:N	2.52	0.42
37:C4:72:A:O2'	37:C4:74:C:OP1	2.21	0.42
44:LH:112:ILE:N	44:LH:126:VAL:O	2.43	0.42
78:C1:444:U:C4	78:C1:491:A:C6	3.08	0.42
78:C1:2221:G:N2	78:C1:2224:A:OP2	2.44	0.42
2:SA:75:ALA:HB1	2:SA:86:VAL:HB	2.02	0.42
3:LB:55:THR:HG22	3:LB:56:ILE:H	1.84	0.42
3:LB:204:ALA:O	3:LB:207:SER:OG	2.22	0.42
5:C2:159:U:OP2	28:SY:117:LYS:NZ	2.42	0.42
17:SM:28:LEU:HA	17:SM:31:VAL:HG22	2.02	0.42
20:SQ:103:ASN:OD1	20:SQ:104:GLU:N	2.53	0.42
31:Sb:46:VAL:HG12	31:Sb:47:PHE:O	2.20	0.42
37:C4:52:G:O2'	37:C4:53:U:OP1	2.35	0.42
37:C4:52:G:N2	46:LJ:9:MET:HE1	2.33	0.42
62:La:78:LEU:HD23	62:La:78:LEU:O	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
68:Lg:95:ILE:HD11	78:C1:2555:G:C5	2.54	0.42
78:C1:401:U:HO2'	78:C1:402:A:P	2.41	0.42
4:SB:215:VAL:O	4:SB:215:VAL:HG13	2.20	0.42
5:C2:639:U:OP1	12:SH:117:THR:OG1	2.37	0.42
5:C2:780:A:N1	28:SY:10:ARG:NH2	2.68	0.42
5:C2:1000:C:N4	5:C2:1003:A:OP2	2.50	0.42
16:SL:27:THR:HG22	16:SL:28:SER:N	2.35	0.42
24:SU:40:ASN:HA	24:SU:43:LYS:HG2	2.02	0.42
35:Sg:126:SER:OG	35:Sg:127:ARG:N	2.52	0.42
35:Sg:130:THR:HG22	35:Sg:145:LEU:CD2	2.50	0.42
49:LN:148:TYR:O	49:LN:151:ILE:HG22	2.20	0.42
78:C1:1404:G:N2	78:C1:1407:A:OP2	2.48	0.42
78:C1:1445:U:OP2	78:C1:1446:A:O2'	2.22	0.42
2:SA:180:GLU:OE2	2:SA:191:ARG:NH2	2.52	0.42
4:SB:180:THR:HG1	4:SB:181:LEU:H	1.68	0.42
5:C2:14:C:OP1	7:SC:164:SER:OG	2.33	0.42
5:C2:821:U:C4	5:C2:852:C:N3	2.88	0.42
8:SD:23:GLU:OE1	32:Sd:46:LYS:NZ	2.48	0.42
9:SE:176:ASP:OD1	9:SE:177:ALA:N	2.53	0.42
20:SQ:13:LYS:HG2	20:SQ:76:SER:HA	2.00	0.42
24:SU:33:GLN:OE1	24:SU:33:GLN:N	2.52	0.42
39:LC:14:GLU:OE1	39:LC:14:GLU:N	2.43	0.42
40:LD:176:SER:OG	40:LD:178:ASN:OD1	2.38	0.42
44:LH:38:LEU:O	44:LH:41:ILE:HG22	2.19	0.42
66:Le:96:ILE:HG21	66:Le:105:ARG:HG2	2.02	0.42
73:Ll:34:THR:HG22	73:Ll:34:THR:O	2.20	0.42
74:Lm:79:GLU:OE1	74:Lm:79:GLU:N	2.52	0.42
78:C1:444:U:C4	78:C1:491:A:N6	2.88	0.42
78:C1:1152:G:OP2	78:C1:1152:G:N2	2.44	0.42
2:SA:27:ARG:NH2	2:SA:43:ASP:O	2.50	0.41
11:SG:18:ILE:HG22	11:SG:19:ASP:O	2.20	0.41
16:SL:37:ASN:OD1	16:SL:37:ASN:N	2.53	0.41
43:LG:94:PHE:HB3	43:LG:189:LEU:HD11	2.02	0.41
45:LI:4:ARG:NH1	78:C1:2828:G:O2'	2.53	0.41
46:LJ:156:LYS:O	46:LJ:160:VAL:HG13	2.20	0.41
49:LN:163:GLY:O	49:LN:172:ARG:NH1	2.44	0.41
51:LP:107:LEU:HD23	51:LP:152:GLU:CG	2.50	0.41
53:LR:21:LYS:O	53:LR:53:LYS:HB2	2.19	0.41
1:LA:114:SER:N	1:LA:165:VAL:O	2.50	0.41
5:C2:805:U:O4	12:SH:104:ARG:NH1	2.53	0.41
8:SD:176:LEU:HD12	8:SD:176:LEU:N	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:SH:11:GLN:NE2	12:SH:11:GLN:O	2.53	0.41
14:SJ:62:ARG:NE	14:SJ:66:ASP:OD2	2.42	0.41
27:SX:93:LEU:HA	27:SX:96:VAL:HG22	2.01	0.41
39:LC:14:GLU:HG2	39:LC:15:ALA:N	2.35	0.41
43:LG:218:ILE:O	43:LG:221:ASN:N	2.53	0.41
49:LN:150:TRP:O	49:LN:156:HIS:ND1	2.53	0.41
51:LP:23:ARG:NH1	78:C1:1505:C:OP2	2.49	0.41
58:LW:61:LYS:NZ	78:C1:3369:G:OP2	2.50	0.41
59:LX:108:LEU:HD23	59:LX:125:ARG:HD3	2.00	0.41
63:Lb:16:ALA:O	63:Lb:20:GLY:HA3	2.20	0.41
65:Ld:44:MET:O	65:Ld:77:ARG:NH1	2.53	0.41
78:C1:2333:C:H2'	78:C1:2334:U:O4'	2.20	0.41
3:LB:240:ARG:NH2	78:C1:874:U:OP2	2.54	0.41
5:C2:17:C:O2'	5:C2:1137:A:N1	2.49	0.41
5:C2:1604:U:OP2	20:SQ:127:LYS:NZ	2.48	0.41
7:SC:201:ASN:OD1	7:SC:202:GLY:N	2.54	0.41
39:LC:202:ARG:NE	78:C1:1384:U:OP2	2.47	0.41
40:LD:107:ARG:NH1	40:LD:169:GLY:O	2.47	0.41
49:LN:186:GLY:O	49:LN:190:THR:HG23	2.21	0.41
51:LP:122:ALA:HB1	51:LP:123:PRO:CD	2.50	0.41
67:Lf:10:LYS:NZ	78:C1:3175:U:OP1	2.47	0.41
5:C2:1191:U:O2	80:6:34:U:H5'	2.21	0.41
5:C2:1229:G:N1	17:SM:47:GLU:OE1	2.53	0.41
11:SG:68:LEU:HD23	11:SG:68:LEU:HA	1.97	0.41
16:SL:2:SER:OG	16:SL:3:THR:N	2.48	0.41
17:SM:62:LEU:HD11	17:SM:72:ILE:HG23	2.02	0.41
17:SM:97:LEU:HD11	17:SM:121:VAL:CG2	2.50	0.41
20:SQ:83:GLN:NE2	20:SQ:118:ILE:O	2.53	0.41
34:Sf:91:ILE:HD12	34:Sf:91:ILE:H	1.85	0.41
42:LF:236:ILE:O	42:LF:240:VAL:HG23	2.19	0.41
78:C1:1906:G:HO2'	78:C1:1907:C:P	2.44	0.41
78:C1:2876:C:H2'	78:C1:2877:G:O4'	2.20	0.41
5:C2:1275:A:H62	5:C2:1431:C:H42	1.68	0.41
5:C2:1345:A:N6	5:C2:1377:U:O2'	2.54	0.41
30:Sa:69:ASN:OD1	30:Sa:69:ASN:N	2.52	0.41
33:Se:30:PRO:HB2	33:Se:34:ALA:HB3	2.03	0.41
40:LD:140:ARG:O	78:C1:1079:A:H4'	2.20	0.41
45:LI:190:VAL:CG1	45:LI:197:VAL:HG21	2.47	0.41
49:LN:108:ARG:NH2	78:C1:1547:G:OP1	2.48	0.41
74:Lm:122:ARG:NH1	74:Lm:123:PRO:O	2.54	0.41
78:C1:494:G:C2	78:C1:619:A:N1	2.89	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
78:C1:2208:A:H2	78:C1:2236:G:H22	1.68	0.41
78:C1:2360:C:O2'	78:C1:2362:C:OP2	2.28	0.41
78:C1:2754:G:O2'	78:C1:2755:C:OP1	2.33	0.41
3:LB:95:THR:OG1	3:LB:98:GLY:N	2.53	0.41
5:C2:149:C:O3'	28:SY:123:LYS:NZ	2.52	0.41
5:C2:280:U:O4	58:LW:111:ALA:N	2.54	0.41
5:C2:415:C:O2	5:C2:418:G:O6	2.38	0.41
5:C2:1161:C:H1'	5:C2:1619:C:H42	1.85	0.41
9:SE:230:GLU:OE1	9:SE:230:GLU:N	2.53	0.41
12:SH:96:ARG:NH1	12:SH:128:ASP:OD2	2.52	0.41
22:SS:105:VAL:HG23	22:SS:106:GLU:N	2.36	0.41
23:ST:114:VAL:HG13	23:ST:123:ARG:O	2.20	0.41
35:Sg:89:LEU:HD11	35:Sg:124:SER:HB2	2.02	0.41
39:LC:82:THR:HG23	78:C1:355:A:H61	1.84	0.41
39:LC:203:ARG:CZ	78:C1:1383:G:H5''	2.50	0.41
41:LE:46:ARG:NH1	78:C1:3268:A:OP1	2.41	0.41
49:LN:35:VAL:HG23	78:C1:1543:G:OP1	2.20	0.41
52:LQ:174:ARG:O	62:La:56:VAL:HG21	2.21	0.41
62:La:43:ILE:HD12	78:C1:965:A:C2	2.55	0.41
77:Lp:18:TYR:O	77:Lp:22:LEU:HD12	2.21	0.41
80:6:61:C:H2'	80:6:62:C:C6	2.55	0.41
2:SA:135:GLU:O	2:SA:139:VAL:HG12	2.21	0.41
5:C2:2:A:O2'	7:SC:198:THR:O	2.38	0.41
5:C2:54:C:O2'	5:C2:459:G:N7	2.48	0.41
8:SD:98:ALA:HB2	8:SD:188:ILE:HD12	2.02	0.41
12:SH:150:GLN:HB2	12:SH:181:ILE:HG22	2.01	0.41
42:LF:156:ILE:HD12	42:LF:161:VAL:HB	2.02	0.41
43:LG:46:LEU:O	43:LG:50:VAL:HG23	2.20	0.41
45:LI:24:ARG:NH1	78:C1:2648:G:OP1	2.54	0.41
47:LL:47:ALA:HB3	47:LL:48:PRO:HD3	2.02	0.41
61:LZ:86:THR:HG22	61:LZ:87:LEU:N	2.36	0.41
72:Lk:2:ALA:N	72:Lk:51:LEU:O	2.54	0.41
78:C1:1493:G:OP2	78:C1:1493:G:N2	2.49	0.41
78:C1:3332:U:H2'	78:C1:3333:G:O4'	2.20	0.41
1:LA:192:LYS:NZ	78:C1:2181:C:OP1	2.47	0.41
5:C2:856:A:OP2	12:SH:97:ARG:NH2	2.54	0.41
5:C2:1698:G:O2'	5:C2:1699:G:O5'	2.25	0.41
11:SG:32:ILE:HD11	11:SG:63:MET:CE	2.40	0.41
14:SJ:20:GLU:OE1	14:SJ:23:ARG:NE	2.41	0.41
21:SR:88:VAL:O	21:SR:89:SER:OG	2.32	0.41
58:LW:4:GLU:O	58:LW:12:LYS:CA	2.59	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:LY:37:LYS:HZ1	78:C1:190:U:P	2.43	0.41
78:C1:1109:U:H2'	78:C1:1110:U:O4'	2.21	0.41
78:C1:1189:C:N3	78:C1:1315:U:C2	2.89	0.41
80:6:54:U:O5'	80:6:54:U:H6	2.03	0.41
3:LB:137:TYR:CE1	3:LB:144:ILE:HG21	2.56	0.41
3:LB:218:ILE:HG13	3:LB:276:THR:HG23	2.02	0.41
5:C2:152:U:O2	11:SG:4:ASN:ND2	2.53	0.41
5:C2:608:U:O2'	5:C2:609:U:OP2	2.32	0.41
5:C2:651:G:O6	5:C2:652:G:N1	2.53	0.41
5:C2:827:C:N4	5:C2:846:G:O6	2.54	0.41
5:C2:852:C:H2'	5:C2:853:G:O4'	2.21	0.41
5:C2:1357:A:N3	23:ST:129:GLN:NE2	2.60	0.41
7:SC:207:LEU:H	7:SC:207:LEU:HD12	1.86	0.41
7:SC:237:VAL:HG22	7:SC:238:SER:H	1.86	0.41
8:SD:105:MET:SD	8:SD:118:ALA:HB1	2.61	0.41
9:SE:96:ASN:ND2	9:SE:96:ASN:O	2.54	0.41
12:SH:92:PHE:C	12:SH:93:LEU:HD22	2.46	0.41
12:SH:165:LYS:O	12:SH:168:SER:OG	2.34	0.41
16:SL:63:LEU:H	16:SL:63:LEU:HD23	1.86	0.41
18:SN:87:ASP:OD1	18:SN:88:LEU:N	2.54	0.41
19:SO:40:ALA:HB1	19:SO:67:VAL:HG12	2.03	0.41
22:SS:33:THR:HG22	22:SS:39:GLY:C	2.45	0.41
35:Sg:224:ASN:HB3	35:Sg:231:MET:HE3	2.01	0.41
37:C4:113:C:H2'	37:C4:114:U:O4'	2.21	0.41
44:LH:165:CYS:SG	44:LH:179:ILE:HD12	2.61	0.41
45:LI:98:ARG:NH2	78:C1:1127:G:OP2	2.43	0.41
45:LI:145:LYS:O	45:LI:149:VAL:HG23	2.20	0.41
46:LJ:65:ILE:HD11	78:C1:2681:U:H5'	2.03	0.41
51:LP:71:ALA:HB2	78:C1:3310:A:P	2.61	0.41
57:LV:104:ASN:OD1	57:LV:108:GLU:N	2.54	0.41
65:Ld:7:VAL:O	65:Ld:7:VAL:HG13	2.20	0.41
67:Lf:2:ALA:N	78:C1:3219:G:N7	2.69	0.41
67:Lf:56:SER:O	67:Lf:63:LYS:NZ	2.50	0.41
78:C1:821:U:O2'	78:C1:912:G:OP1	2.32	0.41
78:C1:1097:G:O2'	78:C1:1098:A:OP2	2.37	0.41
78:C1:1661:G:H2'	78:C1:1662:G:C8	2.56	0.41
80:6:64:C:H2'	80:6:65:U:H6	1.86	0.41
20:SQ:83:GLN:NE2	20:SQ:115:THR:O	2.47	0.41
43:LG:135:GLY:O	43:LG:139:VAL:HG23	2.21	0.41
46:LJ:51:ARG:N	78:C1:2681:U:OP1	2.54	0.41
54:LS:2:ALA:HB2	78:C1:1324:U:OP1	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:LY:32:SER:HA	60:LY:49:PRO:HA	2.02	0.41
62:La:35:ALA:O	62:La:41:HIS:ND1	2.43	0.41
62:La:94:ALA:HA	62:La:121:VAL:HG23	2.02	0.41
80:6:26:G:C5	80:6:27:U:C5	3.08	0.41
3:LB:30:LYS:HZ2	78:C1:3138:U:P	2.43	0.40
5:C2:333:A:O2'	5:C2:334:G:O5'	2.31	0.40
5:C2:1331:A:H61	8:SD:161:GLY:HA3	1.86	0.40
5:C2:1615:C:HO2'	5:C2:1616:G:P	2.34	0.40
8:SD:35:SER:OG	8:SD:51:ARG:O	2.33	0.40
39:LC:216:VAL:HG23	39:LC:217:LYS:N	2.36	0.40
42:LF:41:ARG:NH1	78:C1:598:A:OP1	2.54	0.40
74:Lm:79:GLU:O	74:Lm:82:LEU:N	2.54	0.40
5:C2:532:U:OP1	14:SJ:132:ARG:NH2	2.54	0.40
5:C2:540:G:O2'	5:C2:541:A:H3'	2.21	0.40
5:C2:1490:C:OP1	8:SD:9:ARG:NH1	2.46	0.40
5:C2:1788:G:H3'	19:SO:132:ARG:HH12	1.86	0.40
10:SF:26:ALA:HB3	20:SQ:27:GLY:C	2.46	0.40
13:SI:172:ARG:HE	13:SI:175:GLN:HG3	1.85	0.40
39:LC:42:VAL:HG13	39:LC:236:LEU:HD21	2.03	0.40
45:LI:48:LEU:O	45:LI:139:ARG:HA	2.21	0.40
48:LM:47:ASP:OD1	48:LM:48:GLY:N	2.54	0.40
73:LI:36:ARG:NH2	78:C1:401:U:O2'	2.54	0.40
78:C1:220:G:C6	78:C1:1389:G:N1	2.90	0.40
2:SA:155:PHE:N	25:SV:60:ARG:O	2.48	0.40
5:C2:486:G:N1	5:C2:502:U:N3	2.69	0.40
5:C2:1678:A:OP2	13:SI:42:ARG:NH1	2.52	0.40
7:SC:80:VAL:CG2	7:SC:83:ILE:HD11	2.51	0.40
7:SC:149:GLY:O	7:SC:174:ARG:NH2	2.55	0.40
10:SF:139:ASN:ND2	10:SF:202:ALA:O	2.54	0.40
51:LP:5:GLY:N	51:LP:147:GLU:OE2	2.51	0.40
60:LY:5:SER:C	60:LY:6:LEU:HD22	2.46	0.40
78:C1:1064:A:N1	78:C1:1092:C:C4	2.89	0.40
78:C1:2375:G:O2'	78:C1:2377:G:OP2	2.24	0.40
80:6:18:G:H4'	80:6:19:G:O5'	2.21	0.40
1:LA:49:VAL:C	77:Lp:54:ILE:HD11	2.46	0.40
5:C2:1796:C:OP1	30:Sa:87:ARG:NE	2.55	0.40
7:SC:218:ILE:HA	7:SC:221:THR:HG23	2.03	0.40
9:SE:93:ASP:OD1	9:SE:93:ASP:N	2.55	0.40
17:SM:74:LEU:HD22	34:Sf:108:VAL:HG21	2.04	0.40
35:Sg:209:THR:O	35:Sg:225:LEU:HD23	2.22	0.40
37:C4:44:C:P	46:LJ:137:ARG:HH21	2.44	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:C3:85:G:O2'	38:C3:86:U:O5'	2.37	0.40
47:LL:185:LYS:NZ	78:C1:2781:U:O3'	2.53	0.40
56:LU:38:ILE:HG23	56:LU:50:LEU:HD11	2.03	0.40
69:Lh:118:ILE:HG23	69:Lh:118:ILE:O	2.20	0.40
78:C1:706:A:H2'	78:C1:707:U:O4'	2.21	0.40
1:LA:146:THR:OG1	1:LA:160:SER:OG	2.14	0.40
3:LB:120:LYS:N	78:C1:3296:A:OP1	2.48	0.40
3:LB:137:TYR:O	3:LB:138:ALA:HB3	2.21	0.40
5:C2:629:U:O4	5:C2:970:A:C5	2.74	0.40
5:C2:655:G:N3	5:C2:678:A:C6	2.90	0.40
5:C2:821:U:N3	5:C2:852:C:O2	2.53	0.40
13:SI:38:ILE:HD12	13:SI:94:ASN:HB3	2.03	0.40
19:SO:19:ILE:HB	19:SO:83:ILE:HD12	2.03	0.40
28:SY:47:VAL:O	28:SY:49:LYS:NZ	2.38	0.40
57:LV:12:ARG:NH1	78:C1:3041:U:OP1	2.49	0.40
62:La:104:THR:HG21	62:La:112:ILE:CD1	2.50	0.40
67:Lf:18:ARG:HB2	67:Lf:22:VAL:O	2.21	0.40
80:6:52:G:N1	80:6:63:C:N3	2.69	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	LA	249/251 (99%)	231 (93%)	17 (7%)	1 (0%)	30	61
2	SA	204/206 (99%)	182 (89%)	20 (10%)	2 (1%)	12	41
3	LB	384/386 (100%)	347 (90%)	36 (9%)	1 (0%)	36	67
4	SB	222/232 (96%)	192 (86%)	27 (12%)	3 (1%)	9	34
6	SP	115/117 (98%)	101 (88%)	14 (12%)	0	100	100
7	SC	214/216 (99%)	197 (92%)	16 (8%)	1 (0%)	24	57

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	SD	220/222 (99%)	211 (96%)	9 (4%)	0	100	100
9	SE	256/258 (99%)	233 (91%)	22 (9%)	1 (0%)	30	61
10	SF	204/206 (99%)	183 (90%)	21 (10%)	0	100	100
11	SG	226/228 (99%)	204 (90%)	18 (8%)	4 (2%)	6	28
12	SH	182/184 (99%)	161 (88%)	19 (10%)	2 (1%)	11	39
13	SI	183/187 (98%)	165 (90%)	15 (8%)	3 (2%)	7	30
14	SJ	182/184 (99%)	165 (91%)	15 (8%)	2 (1%)	11	39
15	SK	90/92 (98%)	77 (86%)	13 (14%)	0	100	100
16	SL	142/144 (99%)	128 (90%)	14 (10%)	0	100	100
17	SM	119/121 (98%)	79 (66%)	35 (29%)	5 (4%)	2	13
18	SN	148/150 (99%)	134 (90%)	13 (9%)	1 (1%)	18	49
19	SO	125/127 (98%)	111 (89%)	14 (11%)	0	100	100
20	SQ	139/141 (99%)	122 (88%)	17 (12%)	0	100	100
21	SR	117/125 (94%)	107 (92%)	9 (8%)	1 (1%)	14	44
22	SS	143/145 (99%)	129 (90%)	10 (7%)	4 (3%)	4	20
23	ST	141/143 (99%)	126 (89%)	15 (11%)	0	100	100
24	SU	98/100 (98%)	90 (92%)	8 (8%)	0	100	100
25	SV	85/87 (98%)	72 (85%)	12 (14%)	1 (1%)	10	37
26	SW	127/129 (98%)	116 (91%)	11 (9%)	0	100	100
27	SX	142/144 (99%)	119 (84%)	22 (16%)	1 (1%)	18	49
28	SY	132/134 (98%)	120 (91%)	11 (8%)	1 (1%)	16	47
29	SZ	80/82 (98%)	67 (84%)	12 (15%)	1 (1%)	9	35
30	Sa	95/97 (98%)	72 (76%)	19 (20%)	4 (4%)	2	13
31	Sb	79/81 (98%)	71 (90%)	8 (10%)	0	100	100
32	Sd	51/53 (96%)	49 (96%)	2 (4%)	0	100	100
33	Se	58/60 (97%)	50 (86%)	8 (14%)	0	100	100
34	Sf	71/73 (97%)	47 (66%)	24 (34%)	0	100	100
35	Sg	310/312 (99%)	281 (91%)	29 (9%)	0	100	100
36	Sc	61/63 (97%)	57 (93%)	4 (7%)	0	100	100
39	LC	359/361 (99%)	332 (92%)	25 (7%)	2 (1%)	21	52
40	LD	292/294 (99%)	273 (94%)	18 (6%)	1 (0%)	36	67

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
41	LE	163/175 (93%)	147 (90%)	16 (10%)	0	100	100
42	LF	220/222 (99%)	209 (95%)	11 (5%)	0	100	100
43	LG	231/233 (99%)	209 (90%)	22 (10%)	0	100	100
44	LH	189/191 (99%)	172 (91%)	17 (9%)	0	100	100
45	LI	216/218 (99%)	205 (95%)	11 (5%)	0	100	100
46	LJ	167/169 (99%)	146 (87%)	20 (12%)	1 (1%)	21	52
47	LL	191/193 (99%)	164 (86%)	24 (13%)	3 (2%)	7	30
48	LM	134/136 (98%)	121 (90%)	13 (10%)	0	100	100
49	LN	201/203 (99%)	185 (92%)	16 (8%)	0	100	100
50	LO	195/197 (99%)	185 (95%)	8 (4%)	2 (1%)	12	41
51	LP	181/183 (99%)	166 (92%)	15 (8%)	0	100	100
52	LQ	183/185 (99%)	169 (92%)	14 (8%)	0	100	100
53	LR	186/188 (99%)	179 (96%)	5 (3%)	2 (1%)	11	39
54	LS	169/171 (99%)	162 (96%)	7 (4%)	0	100	100
55	LT	157/159 (99%)	143 (91%)	14 (9%)	0	100	100
56	LU	98/100 (98%)	90 (92%)	8 (8%)	0	100	100
57	LV	134/136 (98%)	124 (92%)	10 (8%)	0	100	100
58	LW	124/126 (98%)	109 (88%)	15 (12%)	0	100	100
59	LX	119/121 (98%)	109 (92%)	9 (8%)	1 (1%)	16	47
60	LY	123/125 (98%)	117 (95%)	6 (5%)	0	100	100
61	LZ	133/135 (98%)	118 (89%)	15 (11%)	0	100	100
62	La	146/148 (99%)	121 (83%)	23 (16%)	2 (1%)	9	34
63	Lb	56/58 (97%)	48 (86%)	7 (12%)	1 (2%)	6	28
64	Lc	94/96 (98%)	90 (96%)	4 (4%)	0	100	100
65	Ld	107/109 (98%)	95 (89%)	12 (11%)	0	100	100
66	Le	125/127 (98%)	117 (94%)	8 (6%)	0	100	100
67	Lf	104/106 (98%)	102 (98%)	2 (2%)	0	100	100
68	Lg	110/112 (98%)	107 (97%)	3 (3%)	0	100	100
69	Lh	117/119 (98%)	108 (92%)	9 (8%)	0	100	100
70	Li	97/99 (98%)	89 (92%)	8 (8%)	0	100	100
71	Lj	83/85 (98%)	78 (94%)	5 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
72	Lk	75/77 (97%)	74 (99%)	1 (1%)	0	100	100
73	Ll	48/50 (96%)	43 (90%)	5 (10%)	0	100	100
74	Lm	50/52 (96%)	47 (94%)	3 (6%)	0	100	100
75	Ln	23/25 (92%)	23 (100%)	0	0	100	100
76	Lo	101/103 (98%)	94 (93%)	7 (7%)	0	100	100
77	Lp	89/91 (98%)	83 (93%)	6 (7%)	0	100	100
81	A	2/4 (50%)	1 (50%)	1 (50%)	0	100	100
All	All	10986/11162 (98%)	9950 (91%)	982 (9%)	54 (0%)	26	57

All (54) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
11	SG	68	LEU
13	SI	10	LYS
30	Sa	84	VAL
50	LO	111[A]	PRO
62	La	78	LEU
1	LA	126	LEU
3	LB	128	LYS
4	SB	212	VAL
9	SE	43	PRO
14	SJ	99	LEU
17	SM	130	THR
18	SN	28	LEU
21	SR	24	LEU
22	SS	91	ASP
47	LL	63	VAL
50	LO	110[A]	PRO
59	LX	44	PRO
2	SA	196	SER
4	SB	213	ARG
12	SH	158	ASP
14	SJ	100	LYS
30	Sa	62	TYR
39	LC	292	SER
40	LD	20	PHE
62	La	40	HIS
12	SH	134	GLU
13	SI	9	HIS
13	SI	23	LYS

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Mol	Chain	Res	Type
17	SM	109	GLU
17	SM	126	TRP
25	SV	81	ASN
28	SY	37	LYS
47	LL	5	LYS
47	LL	77	LEU
63	Lb	24	PRO
2	SA	157	ASP
4	SB	82	ARG
7	SC	147	ASN
11	SG	171	LYS
11	SG	173	PRO
17	SM	90	LYS
22	SS	7	GLU
29	SZ	69	LEU
30	Sa	9	GLY
39	LC	4	PRO
53	LR	52	LYS
53	LR	53	LYS
17	SM	85	LYS
22	SS	13	HIS
11	SG	67	VAL
22	SS	92	ILE
27	SX	42	PRO
46	LJ	8	PRO
30	Sa	83	ILE

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	LA	190/193 (98%)	190 (100%)	0	100	100
2	SA	170/173 (98%)	170 (100%)	0	100	100
3	LB	320/322 (99%)	318 (99%)	2 (1%)	78	83
4	SB	200/205 (98%)	200 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	SP	95/98 (97%)	95 (100%)	0	100	100
7	SC	175/175 (100%)	175 (100%)	0	100	100
8	SD	182/182 (100%)	182 (100%)	0	100	100
9	SE	220/220 (100%)	220 (100%)	0	100	100
10	SF	172/173 (99%)	171 (99%)	1 (1%)	78	83
11	SG	189/195 (97%)	189 (100%)	0	100	100
12	SH	163/165 (99%)	163 (100%)	0	100	100
13	SI	148/149 (99%)	148 (100%)	0	100	100
14	SJ	156/157 (99%)	156 (100%)	0	100	100
15	SK	77/85 (91%)	77 (100%)	0	100	100
16	SL	129/129 (100%)	129 (100%)	0	100	100
17	SM	88/98 (90%)	88 (100%)	0	100	100
18	SN	127/127 (100%)	127 (100%)	0	100	100
19	SO	91/96 (95%)	91 (100%)	0	100	100
20	SQ	117/117 (100%)	117 (100%)	0	100	100
21	SR	101/113 (89%)	101 (100%)	0	100	100
22	SS	128/128 (100%)	128 (100%)	0	100	100
23	ST	115/115 (100%)	115 (100%)	0	100	100
24	SU	93/93 (100%)	93 (100%)	0	100	100
25	SV	71/74 (96%)	71 (100%)	0	100	100
26	SW	110/110 (100%)	110 (100%)	0	100	100
27	SX	119/119 (100%)	119 (100%)	0	100	100
28	SY	112/112 (100%)	112 (100%)	0	100	100
29	SZ	67/73 (92%)	66 (98%)	1 (2%)	57	75
30	Sa	83/83 (100%)	83 (100%)	0	100	100
31	Sb	70/70 (100%)	70 (100%)	0	100	100
32	Sd	47/47 (100%)	47 (100%)	0	100	100
33	Se	50/51 (98%)	50 (100%)	0	100	100
34	Sf	56/64 (88%)	56 (100%)	0	100	100
35	Sg	250/257 (97%)	249 (100%)	1 (0%)	84	86
36	Sc	55/56 (98%)	55 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
39	LC	288/288 (100%)	287 (100%)	1 (0%)	86	87
40	LD	241/243 (99%)	241 (100%)	0	100	100
41	LE	138/154 (90%)	138 (100%)	0	100	100
42	LF	186/186 (100%)	186 (100%)	0	100	100
43	LG	187/191 (98%)	187 (100%)	0	100	100
44	LH	168/171 (98%)	168 (100%)	0	100	100
45	LI	185/185 (100%)	184 (100%)	1 (0%)	81	85
46	LJ	146/147 (99%)	146 (100%)	0	100	100
47	LL	154/154 (100%)	154 (100%)	0	100	100
48	LM	107/107 (100%)	107 (100%)	0	100	100
49	LN	175/175 (100%)	175 (100%)	0	100	100
50	LO	160/160 (100%)	159 (99%)	1 (1%)	78	83
51	LP	138/145 (95%)	138 (100%)	0	100	100
52	LQ	150/150 (100%)	150 (100%)	0	100	100
53	LR	152/153 (99%)	152 (100%)	0	100	100
54	LS	155/155 (100%)	155 (100%)	0	100	100
55	LT	136/136 (100%)	136 (100%)	0	100	100
56	LU	87/87 (100%)	87 (100%)	0	100	100
57	LV	104/104 (100%)	104 (100%)	0	100	100
58	LW	56/107 (52%)	56 (100%)	0	100	100
59	LX	104/105 (99%)	104 (100%)	0	100	100
60	LY	108/108 (100%)	108 (100%)	0	100	100
61	LZ	115/115 (100%)	115 (100%)	0	100	100
62	La	118/118 (100%)	118 (100%)	0	100	100
63	Lb	46/46 (100%)	46 (100%)	0	100	100
64	Lc	81/81 (100%)	81 (100%)	0	100	100
65	Ld	92/96 (96%)	92 (100%)	0	100	100
66	Le	108/109 (99%)	108 (100%)	0	100	100
67	Lf	90/90 (100%)	89 (99%)	1 (1%)	65	78
68	Lg	95/95 (100%)	95 (100%)	0	100	100
69	Lh	104/104 (100%)	103 (99%)	1 (1%)	68	79

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
70	Li	80/81 (99%)	80 (100%)	0	100	100
71	Lj	69/69 (100%)	69 (100%)	0	100	100
72	Lk	68/68 (100%)	68 (100%)	0	100	100
73	Ll	45/45 (100%)	45 (100%)	0	100	100
74	Lm	47/47 (100%)	47 (100%)	0	100	100
75	Ln	22/23 (96%)	22 (100%)	0	100	100
76	Lo	87/88 (99%)	87 (100%)	0	100	100
77	Lp	71/71 (100%)	71 (100%)	0	100	100
81	A	4/3 (133%)	0	4 (100%)	0	0
All	All	9203/9384 (98%)	9189 (100%)	14 (0%)	87	89

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	LB	104	THR
3	LB	266	ARG
10	SF	156	ARG
29	SZ	86	GLU
35	Sg	266	ASP
39	LC	203	ARG
45	LI	90	ARG
50	LO	34[A]	VAL
67	Lf	20	LYS
69	Lh	81	ARG
81	A	175	LYS
81	A	176	LYS
81	A	177[A]	LYS
81	A	177[B]	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (90) such sidechains are listed below:

Mol	Chain	Res	Type
1	LA	79	ASN
1	LA	139	HIS
1	LA	218	HIS
2	SA	163	ASN
3	LB	182	GLN
3	LB	259	HIS

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Mol	Chain	Res	Type
3	LB	293	ASN
4	SB	79	HIS
6	SP	70	ASN
7	SC	199	GLN
8	SD	162	GLN
9	SE	153	ASN
9	SE	157	ASN
9	SE	224	ASN
10	SF	103	ASN
10	SF	139	ASN
10	SF	200	ASN
10	SF	224	ASN
11	SG	189	HIS
11	SG	190	GLN
11	SG	197	ASN
12	SH	89	HIS
12	SH	108	GLN
14	SJ	112	GLN
14	SJ	139	GLN
14	SJ	155	HIS
15	SK	9	ASN
16	SL	110	HIS
18	SN	49	GLN
18	SN	105	ASN
19	SO	65	GLN
19	SO	80	HIS
20	SQ	77	GLN
22	SS	89	GLN
27	SX	21	ASN
27	SX	79	ASN
27	SX	89	ASN
28	SY	31	ASN
28	SY	63	GLN
30	Sa	94	ASN
31	Sb	5	GLN
34	Sf	134	ASN
35	Sg	69	GLN
35	Sg	148	ASN
35	Sg	198	ASN
35	Sg	237	GLN
35	Sg	288	HIS
36	Sc	27	GLN

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Mol	Chain	Res	Type
36	Sc	43	ASN
39	LC	58	HIS
39	LC	291	ASN
39	LC	311	HIS
40	LD	90	HIS
42	LF	186	HIS
44	LH	5	GLN
44	LH	157	ASN
44	LH	169	ASN
45	LI	73	ASN
46	LJ	68	HIS
47	LL	114	GLN
49	LN	138	GLN
49	LN	182	ASN
51	LP	28	ASN
51	LP	96	GLN
51	LP	145	HIS
52	LQ	5	HIS
53	LR	66	HIS
53	LR	150	GLN
54	LS	68	HIS
54	LS	74	ASN
55	LT	5	HIS
55	LT	22	HIS
55	LT	131	GLN
57	LV	7	GLN
57	LV	98	ASN
60	LY	120	GLN
61	LZ	106	GLN
61	LZ	122	HIS
62	La	14	HIS
62	La	49	HIS
62	La	64	GLN
63	Lb	7	HIS
63	Lb	42	ASN
65	Ld	17	HIS
66	Le	26	HIS
66	Le	104	ASN
68	Lg	108	GLN
73	Ll	20	ASN
73	Ll	43	ASN
76	Lo	82	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
37	C4	120/121 (99%)	14 (11%)	1 (0%)
38	C3	157/158 (99%)	35 (22%)	2 (1%)
5	C2	1768/1771 (99%)	525 (29%)	54 (3%)
78	C1	3180/3184 (99%)	669 (21%)	44 (1%)
79	5	10/11 (90%)	5 (50%)	0
80	6	75/76 (98%)	12 (16%)	0
80	7	75/76 (98%)	22 (29%)	4 (5%)
All	All	5385/5397 (99%)	1282 (23%)	105 (1%)

All (1282) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
5	C2	2	A
5	C2	4	C
5	C2	17	C
5	C2	25	C
5	C2	26	A
5	C2	34	G
5	C2	43	A
5	C2	47	A
5	C2	48	G
5	C2	51	A
5	C2	56	U
5	C2	57	G
5	C2	62	A
5	C2	63	G
5	C2	65	A
5	C2	66	U
5	C2	68	A
5	C2	69	G
5	C2	71	A
5	C2	73	U
5	C2	74	U
5	C2	75	U
5	C2	76	A
5	C2	78	A
5	C2	79	C
5	C2	80	A
5	C2	81	G
5	C2	90	C
5	C2	93	A

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Mol	Chain	Res	Type
5	C2	104	A
5	C2	111	U
5	C2	114	C
5	C2	116	U
5	C2	121	U
5	C2	126	A
5	C2	127	G
5	C2	129	U
5	C2	130	C
5	C2	131	C
5	C2	132	U
5	C2	133	U
5	C2	134	U
5	C2	135	A
5	C2	136	C
5	C2	138	A
5	C2	140	A
5	C2	141	U
5	C2	142	G
5	C2	145	A
5	C2	153	G
5	C2	155	U
5	C2	156	A
5	C2	159	U
5	C2	161	U
5	C2	166	C
5	C2	168	A
5	C2	171	A
5	C2	172	C
5	C2	174	U
5	C2	176	C
5	C2	178	U
5	C2	179	A
5	C2	180	A
5	C2	185	U
5	C2	186	C
5	C2	187	G
5	C2	188	A
5	C2	191	C
5	C2	192	U
5	C2	193	U
5	C2	195	G

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Mol	Chain	Res	Type
5	C2	216	U
5	C2	217	A
5	C2	218	A
5	C2	220	A
5	C2	223	U
5	C2	225	A
5	C2	227	U
5	C2	228	G
5	C2	230	C
5	C2	231	U
5	C2	232	U
5	C2	233	C
5	C2	234	G
5	C2	235	G
5	C2	236	A
5	C2	237	C
5	C2	238	U
5	C2	240	U
5	C2	241	U
5	C2	242	U
5	C2	243	G
5	C2	250	C
5	C2	255	U
5	C2	257	A
5	C2	260	U
5	C2	261	U
5	C2	262	U
5	C2	265	A
5	C2	267	U
5	C2	272	U
5	C2	274	G
5	C2	276	C
5	C2	277	U
5	C2	278	U
5	C2	279	G
5	C2	280	U
5	C2	281	G
5	C2	287	G
5	C2	299	A
5	C2	302	U
5	C2	311	U
5	C2	314	C

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Mol	Chain	Res	Type
5	C2	316	A
5	C2	320	U
5	C2	321	C
5	C2	322	G
5	C2	323	A
5	C2	324	U
5	C2	330	G
5	C2	333	A
5	C2	334	G
5	C2	337	G
5	C2	338	C
5	C2	352	A
5	C2	353	A
5	C2	359	A
5	C2	360	A
5	C2	361	C
5	C2	370	A
5	C2	373	G
5	C2	388	G
5	C2	400	A
5	C2	401	A
5	C2	402	C
5	C2	404	G
5	C2	405	C
5	C2	417	A
5	C2	419	G
5	C2	423	G
5	C2	424	C
5	C2	425	A
5	C2	426	G
5	C2	428	A
5	C2	432	G
5	C2	434	G
5	C2	436	A
5	C2	437	A
5	C2	439	U
5	C2	444	C
5	C2	445	A
5	C2	446	A
5	C2	460	A
5	C2	468	A
5	C2	471	A

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Mol	Chain	Res	Type
5	C2	477	A
5	C2	480	G
5	C2	482	U
5	C2	483	A
5	C2	485	A
5	C2	487	G
5	C2	489	C
5	C2	491	C
5	C2	492	A
5	C2	493	U
5	C2	494	U
5	C2	496	G
5	C2	498	G
5	C2	499	U
5	C2	500	C
5	C2	502	U
5	C2	503	G
5	C2	505	A
5	C2	506	A
5	C2	507	U
5	C2	510	G
5	C2	511	A
5	C2	514	G
5	C2	527	A
5	C2	534	A
5	C2	538	A
5	C2	539	G
5	C2	540	G
5	C2	541	A
5	C2	542	A
5	C2	543	C
5	C2	544	A
5	C2	549	G
5	C2	554	C
5	C2	555	A
5	C2	556	A
5	C2	557	G
5	C2	558	U
5	C2	559	C
5	C2	565	C
5	C2	568	G
5	C2	579	A

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Mol	Chain	Res	Type
5	C2	580	A
5	C2	594	A
5	C2	595	G
5	C2	606	A
5	C2	609	U
5	C2	610	G
5	C2	611	U
5	C2	619	A
5	C2	620	A
5	C2	622	A
5	C2	623	A
5	C2	624	G
5	C2	629	U
5	C2	639	U
5	C2	640	U
5	C2	641	G
5	C2	643	G
5	C2	645	C
5	C2	648	G
5	C2	650	U
5	C2	651	G
5	C2	653	C
5	C2	655	G
5	C2	657	U
5	C2	658	C
5	C2	677	G
5	C2	680	U
5	C2	681	U
5	C2	683	C
5	C2	687	G
5	C2	694	U
5	C2	696	C
5	C2	697	C
5	C2	698	U
5	C2	699	U
5	C2	700	C
5	C2	702	G
5	C2	703	G
5	C2	704	C
5	C2	705	U
5	C2	706	A
5	C2	707	A

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Mol	Chain	Res	Type
5	C2	708	C
5	C2	709	C
5	C2	710	U
5	C2	711	U
5	C2	712	G
5	C2	713	A
5	C2	714	G
5	C2	728	U
5	C2	729	G
5	C2	730	G
5	C2	731	C
5	C2	732	G
5	C2	733	A
5	C2	734	A
5	C2	736	C
5	C2	738	G
5	C2	741	C
5	C2	742	U
5	C2	743	U
5	C2	745	U
5	C2	753	A
5	C2	756	A
5	C2	765	G
5	C2	766	U
5	C2	767	U
5	C2	771	A
5	C2	774	A
5	C2	775	G
5	C2	778	G
5	C2	779	U
5	C2	780	A
5	C2	781	U
5	C2	782	U
5	C2	783	G
5	C2	787	G
5	C2	789	A
5	C2	804	A
5	C2	812	A
5	C2	813	U
5	C2	814	A
5	C2	815	G
5	C2	819	G

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Mol	Chain	Res	Type
5	C2	820	U
5	C2	821	U
5	C2	823	G
5	C2	832	U
5	C2	833	U
5	C2	835	U
5	C2	837	G
5	C2	838	G
5	C2	840	U
5	C2	841	U
5	C2	846	G
5	C2	852	C
5	C2	855	A
5	C2	856	A
5	C2	857	U
5	C2	863	A
5	C2	873	U
5	C2	876	G
5	C2	899	G
5	C2	901	G
5	C2	902	G
5	C2	912	U
5	C2	913	G
5	C2	915	A
5	C2	921	U
5	C2	926	A
5	C2	928	U
5	C2	929	A
5	C2	932	U
5	C2	933	A
5	C2	934	C
5	C2	935	U
5	C2	940	A
5	C2	942	G
5	C2	945	U
5	C2	960	U
5	C2	964	U
5	C2	966	A
5	C2	970	A
5	C2	973	A
5	C2	988	A
5	C2	992	A

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Mol	Chain	Res	Type
5	C2	1004	U
5	C2	1005	A
5	C2	1012	U
5	C2	1021	C
5	C2	1023	A
5	C2	1024	U
5	C2	1028	C
5	C2	1029	U
5	C2	1031	U
5	C2	1032	G
5	C2	1039	A
5	C2	1052	U
5	C2	1053	G
5	C2	1057	U
5	C2	1058	U
5	C2	1059	U
5	C2	1060	U
5	C2	1061	A
5	C2	1066	C
5	C2	1074	G
5	C2	1076	A
5	C2	1080	U
5	C2	1082	C
5	C2	1092	A
5	C2	1096	C
5	C2	1100	G
5	C2	1109	G
5	C2	1113	A
5	C2	1115	U
5	C2	1138	A
5	C2	1143	A
5	C2	1150	G
5	C2	1156	C
5	C2	1158	C
5	C2	1160	A
5	C2	1164	G
5	C2	1167	G
5	C2	1170	G
5	C2	1185	U
5	C2	1186	U
5	C2	1191	U
5	C2	1194	A

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Mol	Chain	Res	Type
5	C2	1196	A
5	C2	1199	G
5	C2	1200	G
5	C2	1201	G
5	C2	1212	G
5	C2	1217	A
5	C2	1218	G
5	C2	1227	A
5	C2	1229	G
5	C2	1241	G
5	C2	1242	A
5	C2	1243	G
5	C2	1244	A
5	C2	1245	G
5	C2	1246	C
5	C2	1251	U
5	C2	1252	C
5	C2	1256	A
5	C2	1257	U
5	C2	1258	U
5	C2	1274	C
5	C2	1275	A
5	C2	1276	U
5	C2	1284	C
5	C2	1285	U
5	C2	1286	U
5	C2	1291	G
5	C2	1301	U
5	C2	1312	A
5	C2	1314	U
5	C2	1315	U
5	C2	1316	G
5	C2	1321	A
5	C2	1322	A
5	C2	1325	A
5	C2	1337	A
5	C2	1341	A
5	C2	1344	A
5	C2	1345	A
5	C2	1346	A
5	C2	1348	A
5	C2	1349	G

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Mol	Chain	Res	Type
5	C2	1354	G
5	C2	1360	A
5	C2	1361	U
5	C2	1363	U
5	C2	1364	G
5	C2	1367	G
5	C2	1370	U
5	C2	1371	A
5	C2	1373	C
5	C2	1382	A
5	C2	1383	G
5	C2	1389	C
5	C2	1390	U
5	C2	1398	U
5	C2	1399	C
5	C2	1400	A
5	C2	1402	G
5	C2	1410	A
5	C2	1413	U
5	C2	1414	U
5	C2	1425	A
5	C2	1427	A
5	C2	1428	G
5	C2	1431	C
5	C2	1432	U
5	C2	1433	G
5	C2	1437	U
5	C2	1444	A
5	C2	1446	A
5	C2	1448	G
5	C2	1458	G
5	C2	1459	C
5	C2	1466	G
5	C2	1469	A
5	C2	1472	C
5	C2	1473	U
5	C2	1479	A
5	C2	1483	A
5	C2	1491	U
5	C2	1492	A
5	C2	1493	A
5	C2	1496	U

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Mol	Chain	Res	Type
5	C2	1506	G
5	C2	1515	A
5	C2	1516	A
5	C2	1517	U
5	C2	1518	C
5	C2	1520	U
5	C2	1521	G
5	C2	1523	G
5	C2	1524	A
5	C2	1528	U
5	C2	1531	G
5	C2	1535	U
5	C2	1537	C
5	C2	1540	G
5	C2	1543	A
5	C2	1554	U
5	C2	1557	U
5	C2	1558	U
5	C2	1559	A
5	C2	1569	A
5	C2	1572	G
5	C2	1573	A
5	C2	1574	G
5	C2	1575	G
5	C2	1576	A
5	C2	1583	A
5	C2	1584	G
5	C2	1590	G
5	C2	1601	G
5	C2	1602	C
5	C2	1607	G
5	C2	1611	A
5	C2	1616	G
5	C2	1619	C
5	C2	1622	G
5	C2	1631	A
5	C2	1634	C
5	C2	1635	A
5	C2	1637	C
5	C2	1657	U
5	C2	1658	G
5	C2	1681	A

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Mol	Chain	Res	Type
5	C2	1682	U
5	C2	1688	U
5	C2	1689	A
5	C2	1696	G
5	C2	1697	G
5	C2	1698	G
5	C2	1699	G
5	C2	1700	C
5	C2	1701	A
5	C2	1702	A
5	C2	1706	C
5	C2	1707	A
5	C2	1708	U
5	C2	1715	G
5	C2	1716	C
5	C2	1717	G
5	C2	1736	G
5	C2	1742	U
5	C2	1743	U
5	C2	1760	G
5	C2	1762	A
5	C2	1766	A
5	C2	1767	G
5	C2	1769	U
5	C2	1770	U
5	C2	1780	G
5	C2	1782	A
5	C2	1783	C
5	C2	1792	G
5	C2	1793	G
5	C2	1794	A
5	C2	1795	U
5	C2	1796	C
5	C2	1799	U
37	C4	7	G
37	C4	9	C
37	C4	53	U
37	C4	54	U
37	C4	55	A
37	C4	65	G
37	C4	73	C
37	C4	74	C

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Mol	Chain	Res	Type
37	C4	76	A
37	C4	95	A
37	C4	102	A
37	C4	112	G
37	C4	120	C
37	C4	121	U
38	C3	23	U
38	C3	34	U
38	C3	35	C
38	C3	51	G
38	C3	59	A
38	C3	62	C
38	C3	63	G
38	C3	69	U
38	C3	80	A
38	C3	81	U
38	C3	82	U
38	C3	83	C
38	C3	84	C
38	C3	85	G
38	C3	86	U
38	C3	87	G
38	C3	90	U
38	C3	91	C
38	C3	95	G
38	C3	99	C
38	C3	104	A
38	C3	106	C
38	C3	111	A
38	C3	112	U
38	C3	113	U
38	C3	116	G
38	C3	125	U
38	C3	126	A
38	C3	129	C
38	C3	138	A
38	C3	148	G
38	C3	151	C
38	C3	152	G
38	C3	157	U
38	C3	158	U
78	C1	6	A

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Mol	Chain	Res	Type
78	C1	11	A
78	C1	13	A
78	C1	14	U
78	C1	15	C
78	C1	18	G
78	C1	30	G
78	C1	31	C
78	C1	40	A
78	C1	43	A
78	C1	49	A
78	C1	59	G
78	C1	60	A
78	C1	65	A
78	C1	66	A
78	C1	75	G
78	C1	85	A
78	C1	92	G
78	C1	109	A
78	C1	110	G
78	C1	111	C
78	C1	113	C
78	C1	121	A
78	C1	122	A
78	C1	133	U
78	C1	136	G
78	C1	143	G
78	C1	150	A
78	C1	156	G
78	C1	157	A
78	C1	165	A
78	C1	166	C
78	C1	172	G
78	C1	173	G
78	C1	187	A
78	C1	190	U
78	C1	191	U
78	C1	200	C
78	C1	206	G
78	C1	210	U
78	C1	211	A
78	C1	213	A
78	C1	218	G

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Mol	Chain	Res	Type
78	C1	219	A
78	C1	221	A
78	C1	231	G
78	C1	234	G
78	C1	240	U
78	C1	241	G
78	C1	243	G
78	C1	252	U
78	C1	253	A
78	C1	269	G
78	C1	283	G
78	C1	286	U
78	C1	295	A
78	C1	298	U
78	C1	323	A
78	C1	329	U
78	C1	334	A
78	C1	338	A
78	C1	339	C
78	C1	346	C
78	C1	350	C
78	C1	351	A
78	C1	376	G
78	C1	398	A
78	C1	399	A
78	C1	401	U
78	C1	402	A
78	C1	403	C
78	C1	421	G
78	C1	422	A
78	C1	439	C
78	C1	440	A
78	C1	441	U
78	C1	442	G
78	C1	445	G
78	C1	446	U
78	C1	447	U
78	C1	448	U
78	C1	450	G
78	C1	451	U
78	C1	487	U
78	C1	488	U

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Mol	Chain	Res	Type
78	C1	489	U
78	C1	490	C
78	C1	491	A
78	C1	494	G
78	C1	515	C
78	C1	517	G
78	C1	519	A
78	C1	520	U
78	C1	521	A
78	C1	523	A
78	C1	535	G
78	C1	544	C
78	C1	545	U
78	C1	546	C
78	C1	547	G
78	C1	552	G
78	C1	555	U
78	C1	557	A
78	C1	558	U
78	C1	559	A
78	C1	578	A
78	C1	579	G
78	C1	592	A
78	C1	597	G
78	C1	600	G
78	C1	604	G
78	C1	609	G
78	C1	610	G
78	C1	611	A
78	C1	612	U
78	C1	620	U
78	C1	621	A
78	C1	622	A
78	C1	636	C
78	C1	637	C
78	C1	638	C
78	C1	642	U
78	C1	649	A
78	C1	677	A
78	C1	681	U
78	C1	691	A
78	C1	705	A

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Mol	Chain	Res	Type
78	C1	708	G
78	C1	710	A
78	C1	712	G
78	C1	715	A
78	C1	716	A
78	C1	737	G
78	C1	758	C
78	C1	763	G
78	C1	764	U
78	C1	765	C
78	C1	766	U
78	C1	767	U
78	C1	774	G
78	C1	776	U
78	C1	777	U
78	C1	780	A
78	C1	781	G
78	C1	785	G
78	C1	786	A
78	C1	799	G
78	C1	806	A
78	C1	815	G
78	C1	817	A
78	C1	830	A
78	C1	838	G
78	C1	846	A
78	C1	847	A
78	C1	848	A
78	C1	849	C
78	C1	861	C
78	C1	869	G
78	C1	874	U
78	C1	879	U
78	C1	881	C
78	C1	896	A
78	C1	907	G
78	C1	908	G
78	C1	909	G
78	C1	914	A
78	C1	916	G
78	C1	917	A
78	C1	923	C

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Mol	Chain	Res	Type
78	C1	937	G
78	C1	944	C
78	C1	953	G
78	C1	959	C
78	C1	960	U
78	C1	974	G
78	C1	980	A
78	C1	981	U
78	C1	982	C
78	C1	984	G
78	C1	1001	G
78	C1	1002	A
78	C1	1010	G
78	C1	1013	G
78	C1	1015	U
78	C1	1017	C
78	C1	1018	G
78	C1	1024	G
78	C1	1025	A
78	C1	1026	A
78	C1	1029	G
78	C1	1036	A
78	C1	1037	C
78	C1	1041	U
78	C1	1047	A
78	C1	1049	C
78	C1	1064	A
78	C1	1065	A
78	C1	1072	G
78	C1	1079	A
78	C1	1081	U
78	C1	1093	A
78	C1	1094	U
78	C1	1095	U
78	C1	1097	G
78	C1	1098	A
78	C1	1102	A
78	C1	1103	A
78	C1	1106	G
78	C1	1117	G
78	C1	1118	C
78	C1	1131	G

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Mol	Chain	Res	Type
78	C1	1143	A
78	C1	1144	U
78	C1	1152	G
78	C1	1153	A
78	C1	1155	C
78	C1	1158	A
78	C1	1159	A
78	C1	1163	A
78	C1	1178	G
78	C1	1180	A
78	C1	1181	U
78	C1	1182	A
78	C1	1186	G
78	C1	1192	C
78	C1	1193	A
78	C1	1196	C
78	C1	1197	A
78	C1	1201	C
78	C1	1202	A
78	C1	1208	U
78	C1	1217	A
78	C1	1222	G
78	C1	1227	C
78	C1	1230	G
78	C1	1232	C
78	C1	1233	G
78	C1	1236	G
78	C1	1238	C
78	C1	1240	A
78	C1	1242	G
78	C1	1243	G
78	C1	1245	A
78	C1	1246	G
78	C1	1248	C
78	C1	1251	A
78	C1	1253	U
78	C1	1254	C
78	C1	1258	U
78	C1	1262	G
78	C1	1263	A
78	C1	1264	G
78	C1	1265	U

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Mol	Chain	Res	Type
78	C1	1266	G
78	C1	1270	A
78	C1	1271	A
78	C1	1272	C
78	C1	1274	A
78	C1	1278	A
78	C1	1279	C
78	C1	1280	C
78	C1	1282	G
78	C1	1286	A
78	C1	1287	A
78	C1	1295	G
78	C1	1307	G
78	C1	1308	A
78	C1	1309	U
78	C1	1313	G
78	C1	1318	A
78	C1	1325	U
78	C1	1330	A
78	C1	1331	U
78	C1	1345	G
78	C1	1348	U
78	C1	1349	G
78	C1	1351	U
78	C1	1352	A
78	C1	1353	U
78	C1	1356	U
78	C1	1357	G
78	C1	1380	G
78	C1	1386	A
78	C1	1391	C
78	C1	1392	G
78	C1	1399	A
78	C1	1400	G
78	C1	1418	A
78	C1	1419	A
78	C1	1421	G
78	C1	1428	A
78	C1	1429	G
78	C1	1434	G
78	C1	1437	C
78	C1	1443	G

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Mol	Chain	Res	Type
78	C1	1445	U
78	C1	1446	A
78	C1	1452	A
78	C1	1455	U
78	C1	1470	U
78	C1	1477	A
78	C1	1482	A
78	C1	1483	G
78	C1	1497	C
78	C1	1508	C
78	C1	1523	U
78	C1	1527	C
78	C1	1533	U
78	C1	1536	G
78	C1	1542	G
78	C1	1555	U
78	C1	1556	C
78	C1	1557	A
78	C1	1558	A
78	C1	1559	A
78	C1	1560	G
78	C1	1562	C
78	C1	1563	C
78	C1	1566	A
78	C1	1568	U
78	C1	1569	U
78	C1	1572	U
78	C1	1574	C
78	C1	1575	A
78	C1	1576	G
78	C1	1580	A
78	C1	1581	C
78	C1	1582	C
78	C1	1583	A
78	C1	1588	A
78	C1	1589	A
78	C1	1596	C
78	C1	1604	G
78	C1	1607	U
78	C1	1608	C
78	C1	1613	A
78	C1	1620	U

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Mol	Chain	Res	Type
78	C1	1629	U
78	C1	1631	C
78	C1	1632	A
78	C1	1639	C
78	C1	1642	A
78	C1	1643	A
78	C1	1645	U
78	C1	1658	G
78	C1	1683	A
78	C1	1702	U
78	C1	1704	A
78	C1	1717	U
78	C1	1722	U
78	C1	1725	C
78	C1	1736	G
78	C1	1741	A
78	C1	1743	G
78	C1	1750	A
78	C1	1751	G
78	C1	1760	A
78	C1	1765	U
78	C1	1766	G
78	C1	1770	G
78	C1	1775	G
78	C1	1780	G
78	C1	1796	G
78	C1	1797	A
78	C1	1813	A
78	C1	1814	A
78	C1	1816	A
78	C1	1817	G
78	C1	1819	U
78	C1	1820	U
78	C1	1821	U
78	C1	1822	C
78	C1	1835	A
78	C1	1840	U
78	C1	1841	A
78	C1	1842	A
78	C1	1846	C
78	C1	1849	C
78	C1	1850	A

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Mol	Chain	Res	Type
78	C1	1866	C
78	C1	1867	A
78	C1	1880	U
78	C1	1886	A
78	C1	1889	G
78	C1	1893	A
78	C1	1895	A
78	C1	1897	G
78	C1	1906	G
78	C1	1930	A
78	C1	1932	A
78	C1	1935	G
78	C1	1943	C
78	C1	1952	G
78	C1	1953	G
78	C1	1954	G
78	C1	1955	U
78	C1	2094	C
78	C1	2101	C
78	C1	2102	U
78	C1	2107	A
78	C1	2111	G
78	C1	2112	U
78	C1	2113	A
78	C1	2114	C
78	C1	2121	G
78	C1	2122	G
78	C1	2131	A
78	C1	2139	A
78	C1	2142	A
78	C1	2149	A
78	C1	2158	A
78	C1	2160	G
78	C1	2169	G
78	C1	2170	U
78	C1	2178	A
78	C1	2184	U
78	C1	2188	A
78	C1	2192	C
78	C1	2198	A
78	C1	2206	G
78	C1	2207	A

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Mol	Chain	Res	Type
78	C1	2209	U
78	C1	2210	G
78	C1	2223	A
78	C1	2225	U
78	C1	2231	C
78	C1	2246	G
78	C1	2249	G
78	C1	2255	A
78	C1	2256	A
78	C1	2257	C
78	C1	2258	U
78	C1	2259	A
78	C1	2272	G
78	C1	2273	G
78	C1	2274	U
78	C1	2279	A
78	C1	2281	A
78	C1	2282	U
78	C1	2288	G
78	C1	2303	A
78	C1	2307	G
78	C1	2309	A
78	C1	2310	U
78	C1	2313	A
78	C1	2314	U
78	C1	2315	G
78	C1	2334	U
78	C1	2336	U
78	C1	2357	A
78	C1	2373	A
78	C1	2374	C
78	C1	2375	G
78	C1	2388	U
78	C1	2393	G
78	C1	2397	A
78	C1	2398	A
78	C1	2402	A
78	C1	2403	G
78	C1	2404	A
78	C1	2411	U
78	C1	2412	G
78	C1	2419	A

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Mol	Chain	Res	Type
78	C1	2422	C
78	C1	2435	G
78	C1	2437	G
78	C1	2439	A
78	C1	2445	A
78	C1	2446	U
78	C1	2447	A
78	C1	2448	G
78	C1	2452	G
78	C1	2496	C
78	C1	2498	U
78	C1	2499	U
78	C1	2501	U
78	C1	2502	A
78	C1	2506	U
78	C1	2507	C
78	C1	2515	A
78	C1	2522	G
78	C1	2524	A
78	C1	2526	C
78	C1	2531	C
78	C1	2533	G
78	C1	2537	U
78	C1	2538	U
78	C1	2539	C
78	C1	2540	A
78	C1	2541	U
78	C1	2542	U
78	C1	2543	U
78	C1	2544	U
78	C1	2547	A
78	C1	2549	G
78	C1	2552	C
78	C1	2554	A
78	C1	2555	G
78	C1	2560	C
78	C1	2561	A
78	C1	2569	A
78	C1	2570	U
78	C1	2571	U
78	C1	2572	C
78	C1	2573	G

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Mol	Chain	Res	Type
78	C1	2580	A
78	C1	2582	C
78	C1	2585	G
78	C1	2593	A
78	C1	2594	C
78	C1	2606	G
78	C1	2607	G
78	C1	2614	G
78	C1	2619	G
78	C1	2625	C
78	C1	2635	A
78	C1	2652	U
78	C1	2656	A
78	C1	2658	G
78	C1	2674	A
78	C1	2677	G
78	C1	2689	A
78	C1	2690	G
78	C1	2694	A
78	C1	2696	A
78	C1	2703	A
78	C1	2704	A
78	C1	2719	U
78	C1	2728	G
78	C1	2729	U
78	C1	2737	C
78	C1	2742	C
78	C1	2752	U
78	C1	2753	G
78	C1	2770	G
78	C1	2777	G
78	C1	2778	G
78	C1	2780	A
78	C1	2796	G
78	C1	2799	A
78	C1	2800	G
78	C1	2801	A
78	C1	2803	A
78	C1	2810	C
78	C1	2814	G
78	C1	2817	A
78	C1	2818	U

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Mol	Chain	Res	Type
78	C1	2821	C
78	C1	2834	G
78	C1	2838	A
78	C1	2842	U
78	C1	2845	A
78	C1	2847	A
78	C1	2849	C
78	C1	2860	U
78	C1	2867	C
78	C1	2871	G
78	C1	2872	A
78	C1	2875	U
78	C1	2876	C
78	C1	2887	A
78	C1	2889	C
78	C1	2894	C
78	C1	2897	A
78	C1	2898	G
78	C1	2899	C
78	C1	2911	A
78	C1	2914	G
78	C1	2918	G
78	C1	2923	U
78	C1	2933	A
78	C1	2935	U
78	C1	2936	A
78	C1	2938	G
78	C1	2941	A
78	C1	2942	C
78	C1	2945	G
78	C1	2947	G
78	C1	2971	A
78	C1	2983	C
78	C1	2990	G
78	C1	2996	U
78	C1	2997	G
78	C1	3012	A
78	C1	3021	A
78	C1	3030	G
78	C1	3046	A
78	C1	3059	G
78	C1	3068	U

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Mol	Chain	Res	Type
78	C1	3078	U
78	C1	3080	G
78	C1	3086	A
78	C1	3092	C
78	C1	3099	C
78	C1	3101	G
78	C1	3122	A
78	C1	3130	A
78	C1	3131	U
78	C1	3142	A
78	C1	3143	C
78	C1	3151	U
78	C1	3152	U
78	C1	3154	C
78	C1	3155	U
78	C1	3156	U
78	C1	3157	U
78	C1	3165	A
78	C1	3167	A
78	C1	3172	A
78	C1	3173	G
78	C1	3174	A
78	C1	3175	U
78	C1	3176	G
78	C1	3179	U
78	C1	3180	A
78	C1	3181	C
78	C1	3187	A
78	C1	3196	U
78	C1	3199	G
78	C1	3207	U
78	C1	3217	C
78	C1	3218	A
78	C1	3219	G
78	C1	3223	A
78	C1	3229	G
78	C1	3235	C
78	C1	3239	G
78	C1	3242	G
78	C1	3245	A
78	C1	3246	G
78	C1	3247	G

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Mol	Chain	Res	Type
78	C1	3259	U
78	C1	3260	G
78	C1	3263	G
78	C1	3270	U
78	C1	3272	C
78	C1	3273	A
78	C1	3276	G
78	C1	3281	U
78	C1	3287	U
78	C1	3289	G
78	C1	3294	A
78	C1	3295	A
78	C1	3304	U
78	C1	3309	G
78	C1	3313	U
78	C1	3316	A
78	C1	3317	U
78	C1	3318	G
78	C1	3319	U
78	C1	3320	A
78	C1	3330	A
78	C1	3334	U
78	C1	3345	G
78	C1	3351	U
78	C1	3352	U
78	C1	3353	G
78	C1	3354	U
78	C1	3355	U
78	C1	3356	G
78	C1	3369	G
78	C1	3375	A
78	C1	3376	A
78	C1	3378	C
78	C1	3382	U
78	C1	3389	U
78	C1	3390	G
78	C1	3395	G
78	C1	3396	U
79	5	43	A
79	5	44	A
79	5	46	A
79	5	49	A

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Mol	Chain	Res	Type
79	5	52	A
80	7	10	G
80	7	16	U
80	7	17	U
80	7	18	G
80	7	19	G
80	7	20	U
80	7	24	G
80	7	28	U
80	7	31	G
80	7	33	U
80	7	34	U
80	7	36	U
80	7	37	A
80	7	38	A
80	7	43	A
80	7	45	U
80	7	46	G
80	7	47	U
80	7	48	C
80	7	49	A
80	7	73	G
80	7	76	A
80	6	13	C
80	6	17	U
80	6	19	G
80	6	20	U
80	6	21	A
80	6	42	A
80	6	43	A
80	6	47	U
80	6	48	C
80	6	64	C
80	6	73	G
80	6	76	A

All (105) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
5	C2	68	A
5	C2	77	U
5	C2	139	C

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Mol	Chain	Res	Type
5	C2	141	U
5	C2	177	U
5	C2	215	A
5	C2	224	C
5	C2	235	G
5	C2	237	C
5	C2	261	U
5	C2	278	U
5	C2	280	U
5	C2	313	U
5	C2	322	G
5	C2	352	A
5	C2	387	A
5	C2	400	A
5	C2	539	G
5	C2	541	A
5	C2	555	A
5	C2	609	U
5	C2	639	U
5	C2	640	U
5	C2	705	U
5	C2	711	U
5	C2	755	A
5	C2	765	G
5	C2	803	A
5	C2	813	U
5	C2	819	G
5	C2	912	U
5	C2	928	U
5	C2	1023	A
5	C2	1226	A
5	C2	1245	G
5	C2	1251	U
5	C2	1256	A
5	C2	1273	G
5	C2	1274	C
5	C2	1344	A
5	C2	1382	A
5	C2	1427	A
5	C2	1430	U
5	C2	1471	A
5	C2	1556	A

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Mol	Chain	Res	Type
5	C2	1558	U
5	C2	1573	A
5	C2	1601	G
5	C2	1615	C
5	C2	1633	A
5	C2	1636	C
5	C2	1680	G
5	C2	1681	A
5	C2	1742	U
37	C4	52	G
38	C3	85	G
38	C3	125	U
78	C1	13	A
78	C1	65	A
78	C1	239	G
78	C1	282	G
78	C1	439	C
78	C1	545	U
78	C1	637	C
78	C1	763	G
78	C1	846	A
78	C1	880	G
78	C1	916	G
78	C1	1064	A
78	C1	1094	U
78	C1	1097	G
78	C1	1273	A
78	C1	1307	G
78	C1	1352	A
78	C1	1355	A
78	C1	1554	U
78	C1	1562	C
78	C1	1607	U
78	C1	1815	U
78	C1	1819	U
78	C1	1820	U
78	C1	2112	U
78	C1	2255	A
78	C1	2256	A
78	C1	2257	C
78	C1	2258	U
78	C1	2495	C

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Mol	Chain	Res	Type
78	C1	2500	A
78	C1	2501	U
78	C1	2525	G
78	C1	2537	U
78	C1	2541	U
78	C1	3121	U
78	C1	3218	A
78	C1	3228	C
78	C1	3269	U
78	C1	3275	U
78	C1	3316	A
78	C1	3319	U
78	C1	3350	C
78	C1	3351	U
80	7	35	U
80	7	36	U
80	7	37	A
80	7	46	G

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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
78	C1	3
5	C2	2
13	SI	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C1	1955:U	O3'	2093:A	P	26.47
1	SI	123:LYS	C	135:LYS	N	20.93
1	C1	2452:G	O3'	2492:C	P	17.29
1	C2	658:C	O3'	676:G	P	16.25
1	C2	714:G	O3'	726:C	P	10.98
1	C1	451:U	O3'	486:A	P	10.24

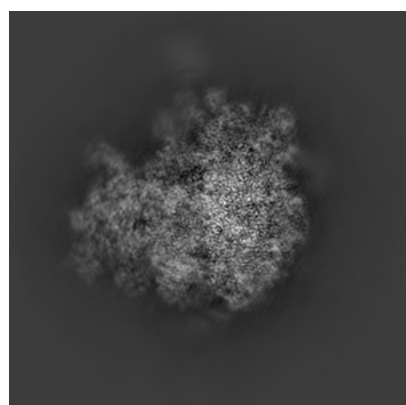
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10397. These allow visual inspection of the internal detail of the map and identification of artifacts.

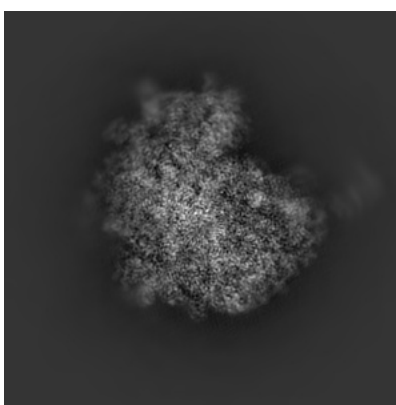
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

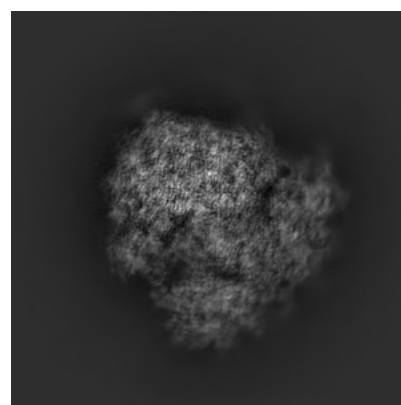
6.1.1 Primary map



X



Y

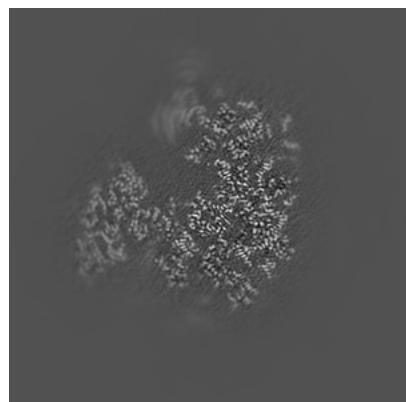


Z

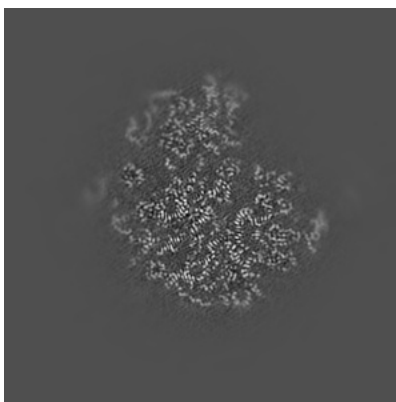
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

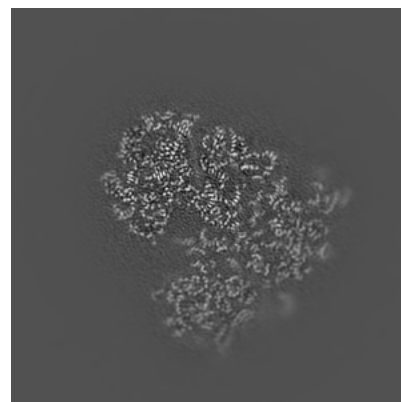
6.2.1 Primary map



X Index: 200



Y Index: 200

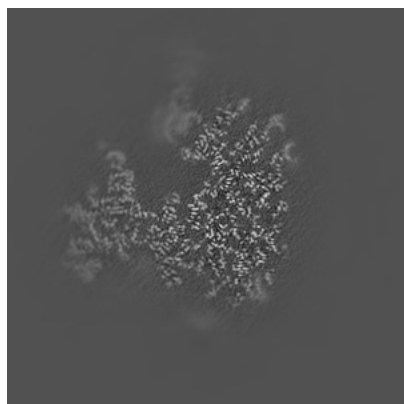


Z Index: 200

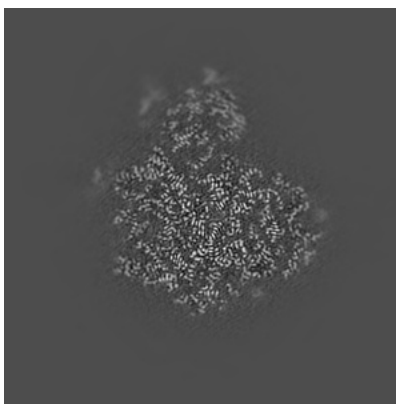
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

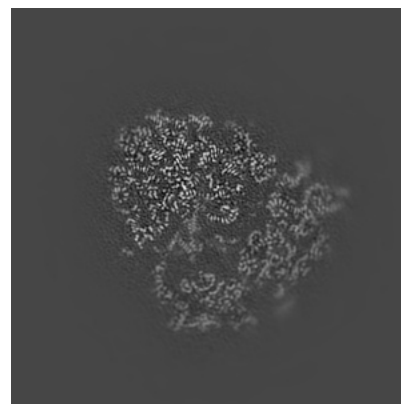
6.3.1 Primary map



X Index: 207



Y Index: 215

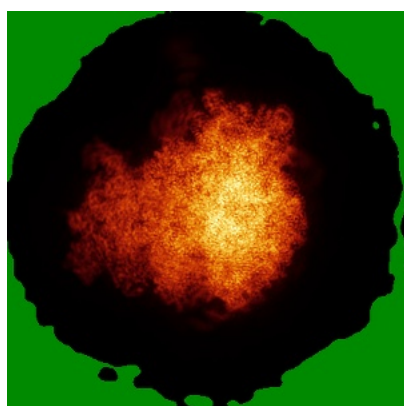


Z Index: 210

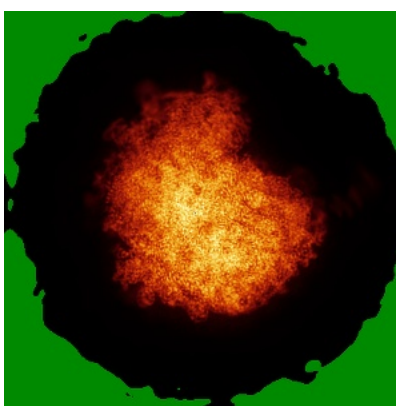
The images above show the largest variance slices of the map in three orthogonal directions.

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

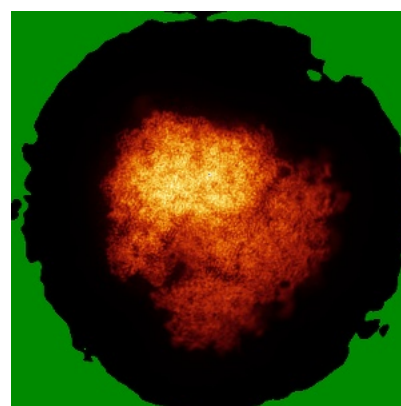
6.4.1 Primary map



X



Y

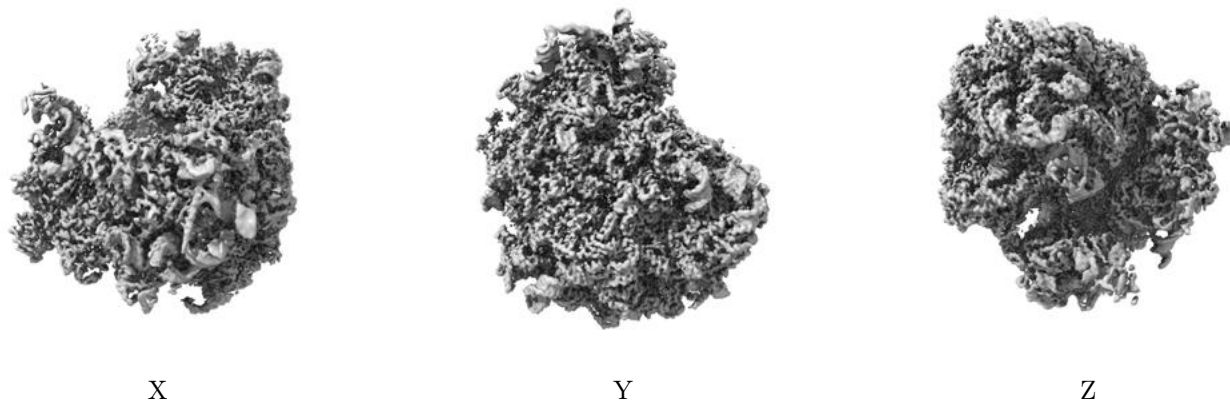


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.045. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

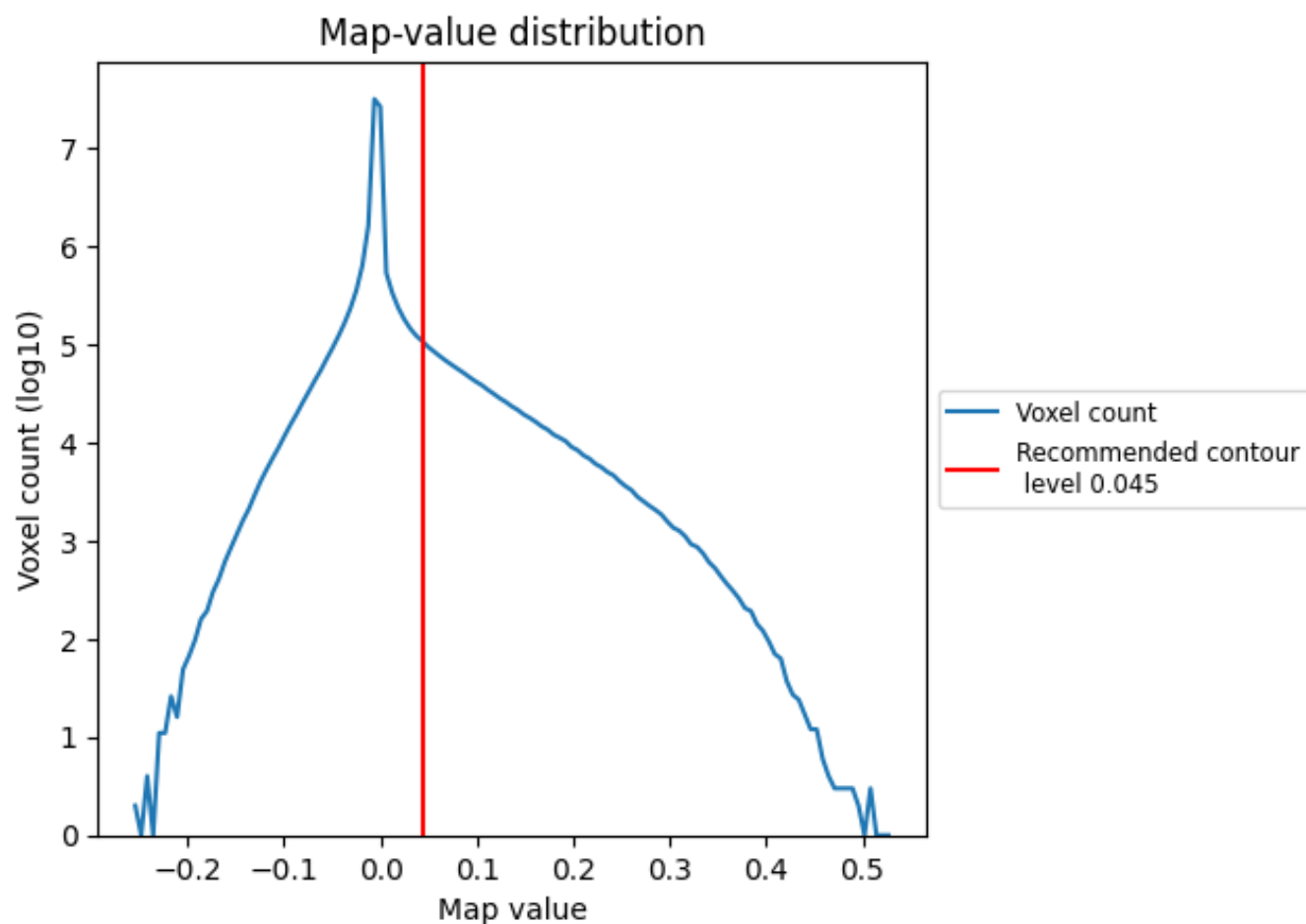
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

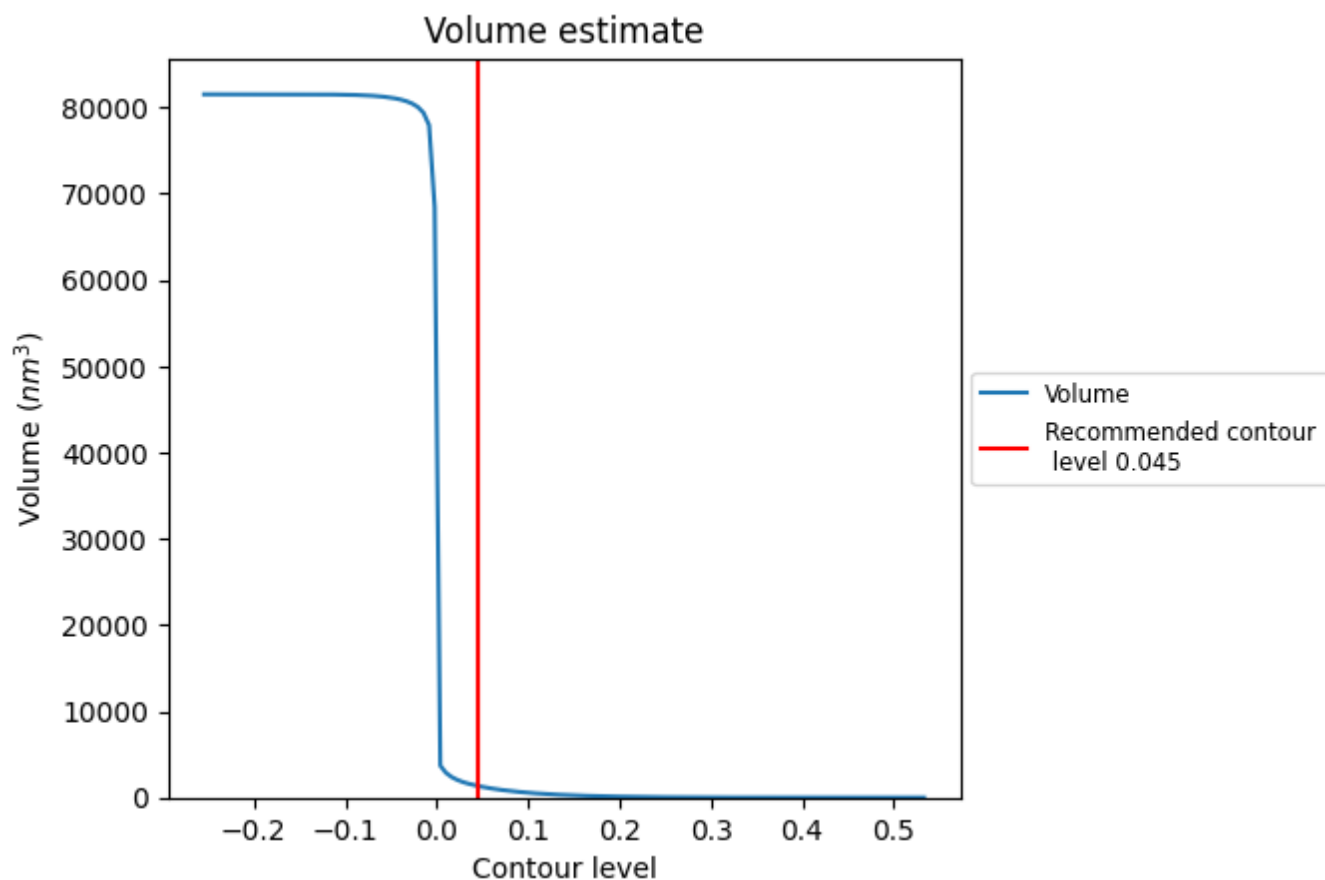
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

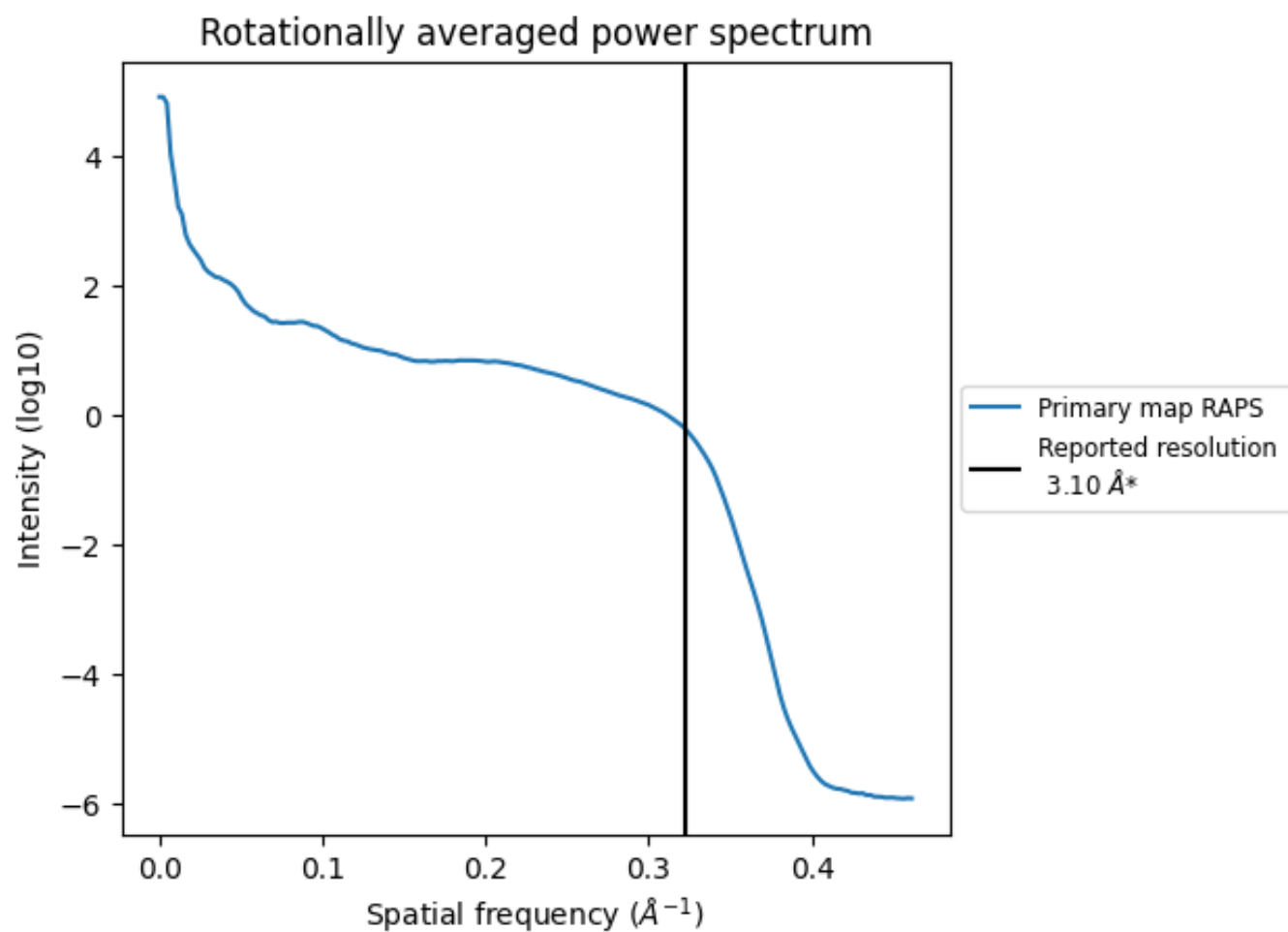
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1348 nm³; this corresponds to an approximate mass of 1218 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

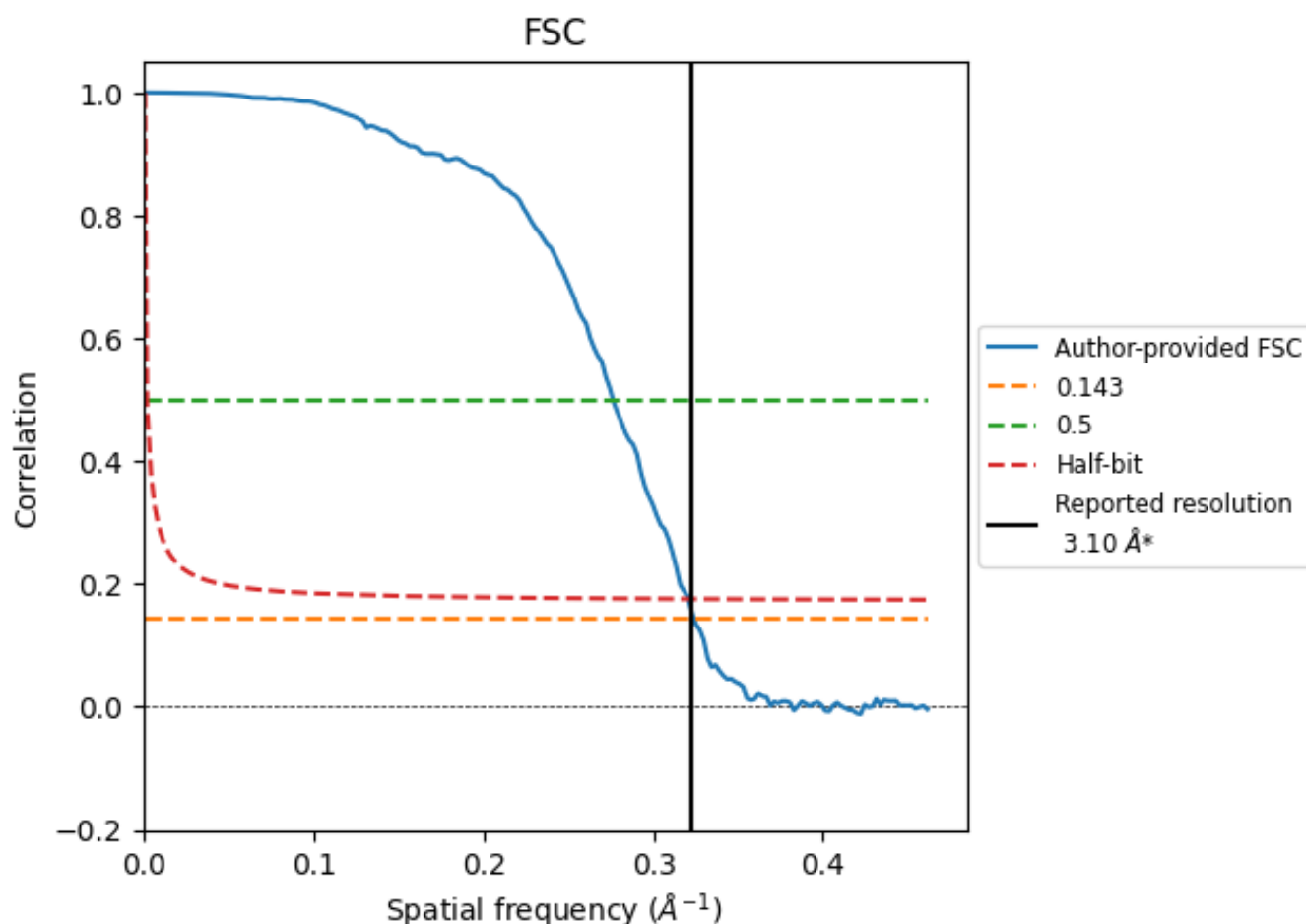


*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

8.2 Resolution estimates [i](#)

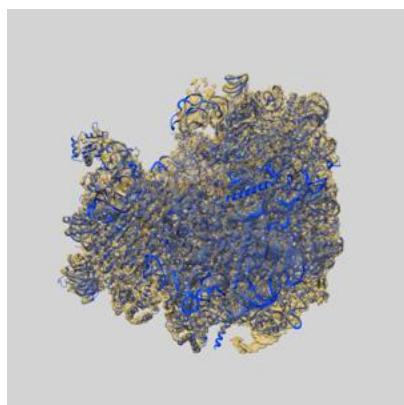
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.09	3.62	3.12
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

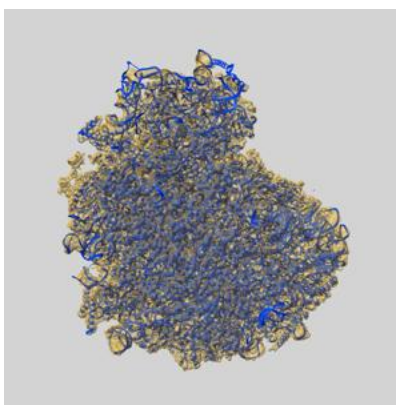
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-10397 and PDB model 6T7T. Per-residue inclusion information can be found in section [3](#) on page [19](#).

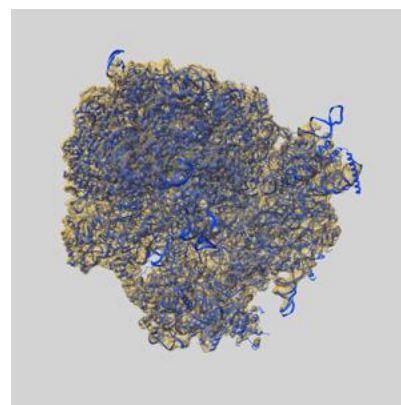
9.1 Map-model overlay [i](#)



X



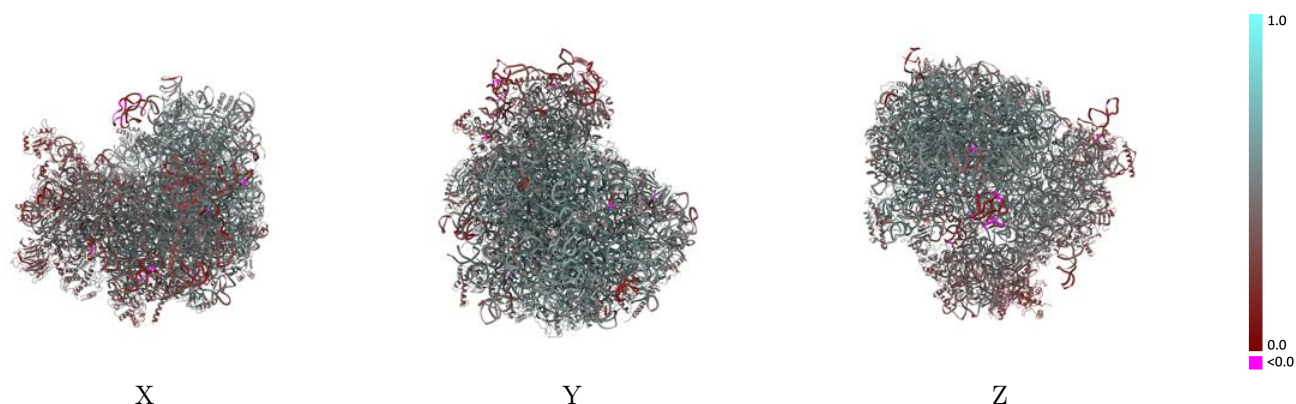
Y



Z

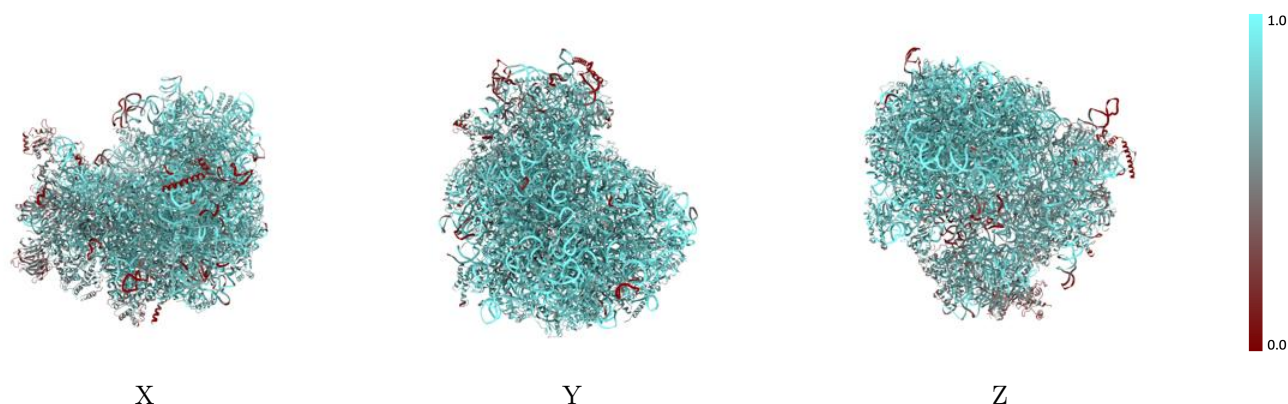
The images above show the 3D surface view of the map at the recommended contour level 0.045 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



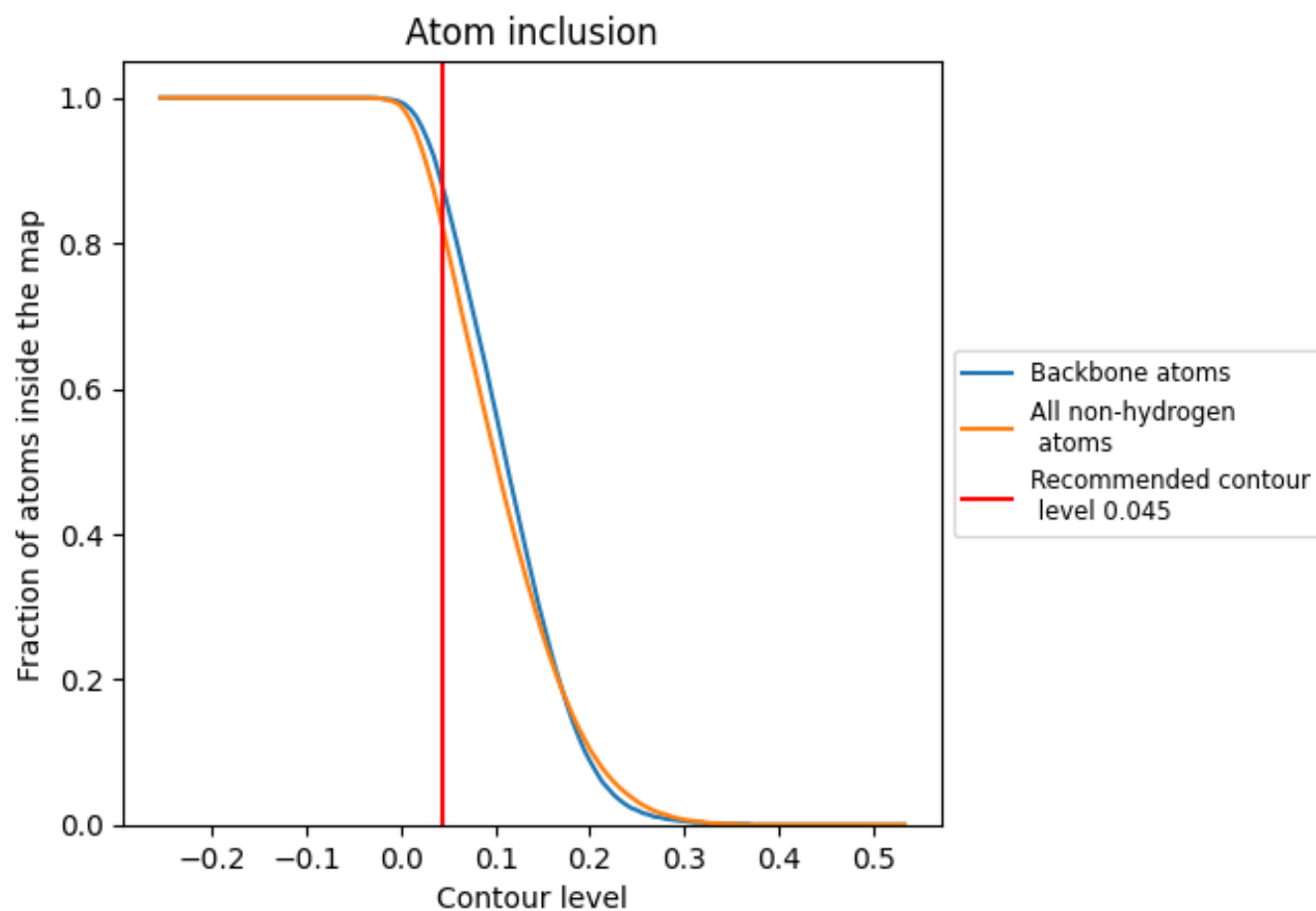
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.045).

9.4 Atom inclusion ⓘ



At the recommended contour level, 87% of all backbone atoms, 82% 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 (0.045) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8180	 0.4880
5	 0.8430	 0.5060
6	 0.8900	 0.4990
7	 0.0310	 0.2020
A	 0.5310	 0.5220
C1	 0.9240	 0.5340
C2	 0.8580	 0.4450
C3	 0.9440	 0.5450
C4	 0.9610	 0.5380
LA	 0.8470	 0.5610
LB	 0.8530	 0.5390
LC	 0.8250	 0.5300
LD	 0.7700	 0.4760
LE	 0.7730	 0.4820
LF	 0.8270	 0.5200
LG	 0.7430	 0.4690
LH	 0.7820	 0.5080
LI	 0.7920	 0.5190
LJ	 0.7440	 0.4700
LL	 0.8080	 0.5200
LM	 0.8110	 0.5020
LN	 0.8640	 0.5640
LO	 0.8360	 0.5370
LP	 0.8150	 0.5320
LQ	 0.8500	 0.5470
LR	 0.7380	 0.4850
LS	 0.8290	 0.5370
LT	 0.8270	 0.5460
LU	 0.7150	 0.4460
LV	 0.8110	 0.5470
LW	 0.4960	 0.4240
LX	 0.7730	 0.5030
LY	 0.7870	 0.5040
LZ	 0.7710	 0.4760
La	 0.8500	 0.5500



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Chain	Atom inclusion	Q-score
Lb	 0.7740	 0.5080
Lc	 0.7670	 0.4810
Ld	 0.7690	 0.5160
Le	 0.8300	 0.5490
Lf	 0.8770	 0.5640
Lg	 0.7870	 0.5170
Lh	 0.7760	 0.4820
Li	 0.7610	 0.4920
Lj	 0.8790	 0.5590
Lk	 0.6860	 0.4610
Ll	 0.8510	 0.5480
Lm	 0.7940	 0.5330
Ln	 0.7310	 0.5130
Lo	 0.8160	 0.5350
Lp	 0.7760	 0.5390
SA	 0.6320	 0.4080
SB	 0.6650	 0.4520
SC	 0.6860	 0.4600
SD	 0.5490	 0.3990
SE	 0.6530	 0.4390
SF	 0.6160	 0.3990
SG	 0.6210	 0.3900
SH	 0.5790	 0.3820
SI	 0.7250	 0.4780
SJ	 0.6370	 0.4120
SK	 0.5460	 0.3440
SL	 0.7350	 0.5000
SM	 0.2570	 0.2250
SN	 0.7330	 0.4700
SO	 0.7310	 0.4770
SP	 0.5700	 0.3820
SQ	 0.6130	 0.4130
SR	 0.6050	 0.3810
SS	 0.6240	 0.3970
ST	 0.5910	 0.3820
SU	 0.5520	 0.3820
SV	 0.6600	 0.4370
SW	 0.7330	 0.4850
SX	 0.7270	 0.5050
SY	 0.6160	 0.3820
SZ	 0.5140	 0.3660
Sa	 0.7670	 0.4950

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Chain	Atom inclusion	Q-score
Sb	 0.6670	 0.4460
Sc	 0.6030	 0.4290
Sd	 0.7490	 0.4550
Se	 0.6010	 0.4280
Sf	 0.3330	 0.2360
Sg	 0.4430	 0.3320