



Full wwPDB EM Validation Report ⓘ

Mar 6, 2026 – 07:31 PM UTC

PDB ID : 9F9S / pdb_00009f9s
EMDB ID : EMD-50259
Title : Yeast SDD1 Disome with Mbf1
Authors : Denk, T.; Beckmann, R.
Deposited on : 2024-05-08
Resolution : 2.90 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:

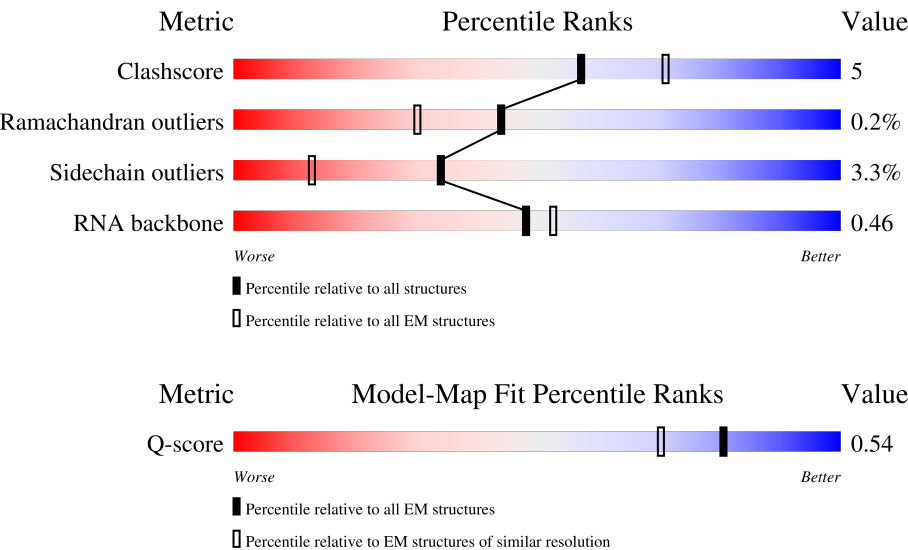
EMDB validation analysis	:	0.0.1.dev132
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
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 2.90 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



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

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

Mol	Chain	Length	Quality of chain
1	CC	233	
2	CM	41	
3	CN	151	

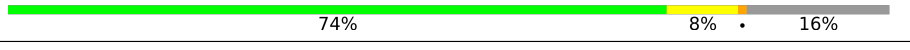
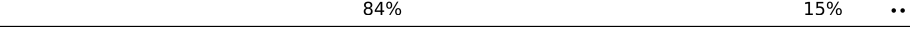
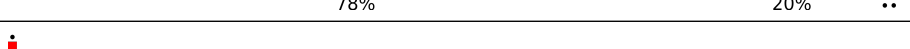
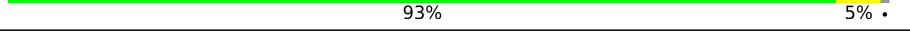
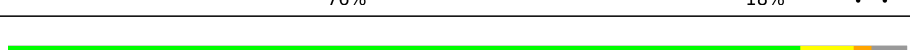
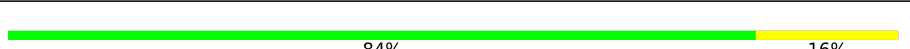
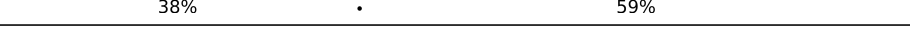
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Mol	Chain	Length	Quality of chain
4	CP	76	
5	L1	3396	
6	L2	158	
6	M2	158	
7	L3	121	
7	M3	121	
8	LA	176	
9	LB	244	
9	MB	244	
10	LC	256	
10	MC	256	
11	LD	191	
11	MD	191	
12	LE	221	
12	ME	221	
13	LF	174	
13	MF	174	
14	LG	199	
14	MG	199	
15	LH	138	
15	MH	138	
16	LI	204	
16	MI	204	
17	LJ	199	
17	MJ	199	

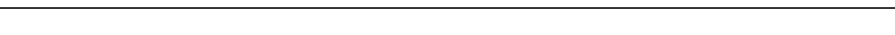
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Mol	Chain	Length	Quality of chain
18	LK	184	
18	MK	184	
19	LL	186	
19	ML	186	
20	LM	189	
20	MM	189	
21	LN	172	
21	MN	172	
22	LO	160	
22	MO	160	
23	La	137	
23	Ma	137	
24	Lb	92	
24	Mb	92	
25	Lc	106	
25	Mc	106	
26	Ld	25	
26	Md	25	
27	Le	128	
27	Me	128	
28	Lf	51	
28	Mf	51	
29	Lg	78	
29	Mg	78	
30	Lh	88	

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Mol	Chain	Length	Quality of chain
30	Mh	88	
31	Li	100	
31	Mi	100	
32	Lj	120	
32	Mj	120	
33	Lk	121	
33	Mk	121	
34	Ll	107	
34	Ml	107	
35	Lm	130	
35	Mm	130	
36	Ln	113	
36	Mn	113	
37	Lo	105	
37	Mo	105	
38	Lp	59	
38	Mp	59	
39	Lq	149	
39	Mq	149	
40	Lr	136	
40	Mr	136	
41	Ls	127	
41	Ms	127	
42	Lt	142	
42	Mt	142	

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Mol	Chain	Length	Quality of chain
43	Lu	155	
43	Mu	155	
44	Lv	121	
44	Mv	121	
45	Lw	254	
45	Mw	254	
46	Lx	387	
46	Mx	387	
47	Ly	362	
47	My	362	
48	Lz	297	
48	Mz	297	
49	R1	1800	
49	S1	1800	
50	RA	119	
50	SA	119	
51	RB	82	
51	SB	82	
52	SC	67	
53	RD	56	
53	SD	56	
54	RE	63	
54	SE	63	
55	RF	152	
55	SF	152	

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Mol	Chain	Length	Quality of chain
56	RG	319	
56	SG	319	
57	Ra	252	
57	Sa	252	
58	Rb	255	
58	Sb	255	
59	Rc	254	
59	Sc	254	
60	Rd	240	
60	Sd	240	
61	Re	261	
61	Se	261	
62	Rf	225	
62	Sf	225	
63	Rg	236	
63	Sg	236	
64	Rh	190	
64	Sh	190	
65	Ri	200	
65	Si	200	
66	Rj	197	
66	Sj	197	
67	Rk	105	
67	Sk	105	
68	Rl	156	

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Mol	Chain	Length	Quality of chain
68	Sl	156	
69	Rm	143	
69	Sm	143	
70	Rn	151	
70	Sn	151	
71	So	137	
72	Rp	142	
72	Sp	142	
73	Rq	143	
73	Sq	143	
74	Sr	136	
75	Rs	146	
75	Ss	146	
76	Rt	144	
76	St	144	
77	Ru	121	
77	Su	121	
78	Rv	87	
78	Sv	87	
79	Rw	130	
79	Sw	130	
80	Rx	145	
80	Sx	145	
81	Ry	135	
81	Sy	135	

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Mol	Chain	Length	Quality of chain
82	Rz	108	
82	Sz	108	
83	RC	67	
84	Ro	138	
85	Rr	136	
86	MA	176	
87	M1	3396	
88	DQ	77	
89	MQ	312	
90	MP	165	
91	DP	76	

2 Entry composition [i](#)

There are 95 unique types of molecules in this entry. The entry contains 406583 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 Uncharacterized protein YEL057C.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	CC	14	Total	C	N	O	S	0	0
			129	85	21	22	1		

- Molecule 2 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	CM	41	Total	C	N	O	P	0	0
			838	377	108	312	41		

- Molecule 3 is a protein called Multiprotein-bridging factor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	CN	136	Total	C	N	O	S	0	0
			1046	636	210	199	1		

- Molecule 4 is a RNA chain called tRNA P-site, stalled.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	CP	76	Total	C	N	O	P	0	0
			1621	723	290	532	76		

- Molecule 5 is a RNA chain called Saccharomyces cerevisiae S288C 25S ribosomal RNA (RDN25-1).

Mol	Chain	Residues	Atoms					AltConf	Trace
5	L1	3116	Total	C	N	O	P	0	0
			66660	29774	12025	21745	3116		

- Molecule 6 is a RNA chain called Saccharomyces cerevisiae S288C 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	L2	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

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Mol	Chain	Residues	Atoms					AltConf	Trace
6	M2	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 7 is a RNA chain called *Saccharomyces cerevisiae* S288C 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	L3	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		
7	M3	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 8 is a protein called 60S ribosomal protein L6-B.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	LA	167	Total	C	N	O	0	0
			1305	842	234	229		

- Molecule 9 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LB	222	Total	C	N	O	S	0	0
			1784	1151	324	308	1		
9	MB	222	Total	C	N	O	S	0	0
			1784	1151	324	308	1		

- Molecule 10 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LC	233	Total	C	N	O	S	0	0
			1804	1151	323	327	3		
10	MC	233	Total	C	N	O	S	0	0
			1804	1151	323	327	3		

- Molecule 11 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LD	191	Total	C	N	O	S	0	0
			1508	957	274	273	4		
11	MD	191	Total	C	N	O	S	0	0
			1518	963	274	277	4		

- Molecule 12 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LE	218	Total	C	N	O	S	0	0
			1764	1117	334	306	7		
12	ME	215	Total	C	N	O	S	0	0
			1743	1102	331	303	7		

- Molecule 13 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LF	169	Total	C	N	O	S	0	0
			1350	846	253	247	4		
13	MF	169	Total	C	N	O	S	0	0
			1353	847	253	249	4		

- Molecule 14 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	LG	193	Total	C	N	O	0	0
			1543	962	315	266		
14	MG	193	Total	C	N	O	0	0
			1543	962	315	266		

- Molecule 15 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LH	136	Total	C	N	O	S	0	0
			1053	675	199	177	2		
15	MH	136	Total	C	N	O	S	0	0
			1053	675	199	177	2		

- Molecule 16 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LI	203	Total	C	N	O	S	0	0
			1720	1077	361	281	1		
16	MI	203	Total	C	N	O	S	0	0
			1720	1077	361	281	1		

- Molecule 17 is a protein called 60S ribosomal protein L16-A.

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

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

- Molecule 18 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LK	183	Total	C	N	O		0	0
			1416	879	284	253			
18	MK	154	Total	C	N	O		0	0
			1222	761	237	224			

- Molecule 19 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LL	185	Total	C	N	O	S	0	0
			1441	908	290	241	2		
19	ML	185	Total	C	N	O	S	0	0
			1441	908	290	241	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LM	188	Total	C	N	O		0	0
			1515	932	323	260			
20	MM	176	Total	C	N	O		0	0
			1423	875	308	240			

- Molecule 21 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LN	171	Total	C	N	O	S	0	0
			1437	925	266	243	3		
21	MN	172	Total	C	N	O	S	0	0
			1445	930	267	244	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LO	159	Total	C	N	O	S	0	0
			1276	805	246	221	4		
22	MO	159	Total	C	N	O	S	0	0
			1276	805	246	221	4		

- Molecule 23 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	La	136	Total	C	N	O	S	0	0
			1003	628	189	179	7		
23	Ma	129	Total	C	N	O	S	0	0
			963	607	180	169	7		

- Molecule 24 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Lb	91	Total	C	N	O	S	0	0
			694	429	138	121	6		
24	Mb	91	Total	C	N	O	S	0	0
			694	429	138	121	6		

- Molecule 25 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Lc	103	Total	C	N	O	S	0	0
			824	517	167	135	5		
25	Mc	102	Total	C	N	O	S	0	0
			819	514	166	134	5		

- Molecule 26 is a protein called 60S ribosomal protein L41-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Ld	25	Total	C	N	O	S	0	0
			229	139	62	27	1		
26	Md	25	Total	C	N	O	S	0	0
			233	142	63	27	1		

- Molecule 27 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Le	52	Total	C	N	O	S	0	0
			417	259	86	67	5		
27	Me	52	Total	C	N	O	S	0	0
			417	259	86	67	5		

- Molecule 28 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Lf	50	Total	C	N	O	S	0	0
			436	272	97	65	2		
28	Mf	50	Total	C	N	O	S	0	0
			436	272	97	65	2		

- Molecule 29 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Lg	77	Total	C	N	O		0	0
			612	391	115	106			
29	Mg	77	Total	C	N	O		0	0
			612	391	115	106			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Lh	85	Total	C	N	O	S	0	0
			670	408	146	111	5		
30	Mh	84	Total	C	N	O	S	0	0
			665	405	145	110	5		

- Molecule 31 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Li	99	Total	C	N	O	S	0	0
			766	478	154	132	2		
31	Mi	99	Total	C	N	O	S	0	0
			771	481	156	132	2		

- Molecule 32 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Lj	119	Total	C	N	O	S	0	0
			969	615	186	167	1		
32	Mj	119	Total	C	N	O	S	0	0
			969	615	186	167	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Lk	106	Total	C	N	O	S	0	0
			836	519	171	142	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
33	Mk	109	Total	C	N	O	S	0	0
			861	533	175	149	4		

- Molecule 34 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Ll	106	Total	C	N	O	S	0	0
			850	540	165	144	1		
34	Ml	106	Total	C	N	O	S	0	0
			850	540	165	144	1		

- Molecule 35 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Lm	127	Total	C	N	O	S	0	0
			1017	644	205	167	1		
35	Mm	127	Total	C	N	O	S	0	0
			1020	647	205	167	1		

- Molecule 36 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Ln	109	Total	C	N	O	S	0	0
			876	556	167	152	1		
36	Mn	109	Total	C	N	O	S	0	0
			883	559	167	156	1		

- Molecule 37 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Lo	96	Total	C	N	O	S	0	0
			737	476	123	137	1		
37	Mo	97	Total	C	N	O	S	0	0
			742	479	124	138	1		

- Molecule 38 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	Lp	58	Total	C	N	O	0	0
			462	289	100	73		
38	Mp	58	Total	C	N	O	0	0
			462	289	100	73		

- Molecule 39 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Lq	148	Total	C	N	O	S	0	0
			1173	749	231	190	3		
39	Mq	148	Total	C	N	O	S	0	0
			1173	749	231	190	3		

- Molecule 40 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
40	Lr	135	Total	C	N	O	0	0
			1092	710	202	180		
40	Mr	135	Total	C	N	O	0	0
			1092	710	202	180		

- Molecule 41 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	Ls	125	Total	C	N	O	0	0
			984	620	191	173		
41	Ms	126	Total	C	N	O	0	0
			993	625	192	176		

- Molecule 42 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Lt	121	Total	C	N	O	S	0	0
			964	620	169	173	2		
42	Mt	120	Total	C	N	O	S	0	0
			959	617	168	172	2		

- Molecule 43 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Lu	126	Total	C	N	O	S	0	0
			836	525	165	145	1		
43	Mu	63	Total	C	N	O	S	0	0
			521	336	102	82	1		

- Molecule 44 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	Lv	100	Total	C	N	O	0	0
			796	516	131	149		
44	Mv	97	Total	C	N	O	0	0
			770	499	126	145		

- Molecule 45 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Lw	251	Total	C	N	O	S	0	0
			1899	1182	385	331	1		
45	Mw	252	Total	C	N	O	S	0	0
			1914	1191	388	334	1		

- Molecule 46 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Lx	386	Total	C	N	O	S	0	0
			3075	1950	584	533	8		
46	Mx	386	Total	C	N	O	S	0	0
			3075	1950	584	533	8		

- Molecule 47 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Ly	361	Total	C	N	O	S	0	0
			2748	1729	522	494	3		
47	My	361	Total	C	N	O	S	0	0
			2748	1729	522	494	3		

- Molecule 48 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Lz	294	Total	C	N	O	S	0	0
			2351	1484	410	455	2		
48	Mz	296	Total	C	N	O	S	0	0
			2375	1501	414	458	2		

- Molecule 49 is a RNA chain called *Saccharomyces cerevisiae* S288C 18S ribosomal RNA (RDN18-1).

Mol	Chain	Residues	Atoms					AltConf	Trace
49	S1	1771	Total	C	N	O	P	0	0
			37739	16872	6683	12413	1771		

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Mol	Chain	Residues	Atoms					AltConf	Trace
49	R1	1758	Total	C	N	O	P	0	0
			37455	16745	6624	12328	1758		

- Molecule 50 is a protein called Small ribosomal subunit protein eS26A.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	SA	97	Total	C	N	O	S	0	0
			769	475	160	129	5		
50	RA	97	Total	C	N	O	S	0	0
			769	475	160	129	5		

- Molecule 51 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	SB	81	Total	C	N	O	S	0	0
			610	382	110	113	5		
51	RB	81	Total	C	N	O	S	0	0
			610	382	110	113	5		

- Molecule 52 is a protein called Small ribosomal subunit protein eS28B.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	SC	62	Total	C	N	O	S	0	0
			486	300	95	90	1		

- Molecule 53 is a protein called Small ribosomal subunit protein uS14A.

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

- Molecule 54 is a protein called 40S ribosomal protein S30-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SE	60	Total	C	N	O	S	0	0
			472	298	97	76	1		
54	RE	48	Total	C	N	O		0	0
			385	246	77	62			

- Molecule 55 is a protein called Ubiquitin.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SF	73	Total	C	N	O	S	0	0
			556	352	105	95	4		
55	RF	72	Total	C	N	O	S	0	0
			547	347	104	92	4		

- Molecule 56 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SG	312	Total	C	N	O	S	0	0
			2383	1514	409	452	8		
56	RG	313	Total	C	N	O	S	0	0
			2403	1521	411	463	8		

- Molecule 57 is a protein called 40S ribosomal protein S0-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	Sa	206	Total	C	N	O	S	0	0
			1603	1030	284	287	2		
57	Ra	206	Total	C	N	O	S	0	0
			1583	1017	281	283	2		

- Molecule 58 is a protein called 40S ribosomal protein S1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	Sb	226	Total	C	N	O	S	0	0
			1798	1139	330	325	4		
58	Rb	216	Total	C	N	O	S	0	0
			1722	1091	312	315	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
59	Sc	216	Total	C	N	O	S	0	0
			1626	1042	287	295	2		
59	Rc	217	Total	C	N	O	S	0	0
			1635	1047	289	297	2		

- Molecule 60 is a protein called Small ribosomal subunit protein uS3.

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

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Mol	Chain	Residues	Atoms					AltConf	Trace
60	Rd	223	Total	C	N	O	S	0	0
			1734	1101	313	314	6		

- Molecule 61 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	Se	258	Total	C	N	O	S	0	0
			2056	1308	387	358	3		
61	Re	260	Total	C	N	O	S	0	0
			2068	1316	389	360	3		

- Molecule 62 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	Sf	206	Total	C	N	O	S	0	0
			1605	1005	299	298	3		
62	Rf	206	Total	C	N	O	S	0	0
			1609	1007	300	299	3		

- Molecule 63 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	Sg	228	Total	C	N	O	S	0	0
			1815	1138	351	323	3		
63	Rg	218	Total	C	N	O	S	0	0
			1755	1102	337	313	3		

- Molecule 64 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
64	Sh	184	Total	C	N	O	0	0
			1473	946	263	264		
64	Rh	185	Total	C	N	O	0	0
			1486	954	266	266		

- Molecule 65 is a protein called 40S ribosomal protein S8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	Si	187	Total	C	N	O	S	0	0
			1476	916	295	263	2		
65	Ri	188	Total	C	N	O	S	0	0
			1489	925	298	264	2		

- Molecule 66 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Sj	184	Total	C	N	O	S	0	0
			1479	935	285	258	1		
66	Rj	185	Total	C	N	O	S	0	0
			1494	943	289	261	1		

- Molecule 67 is a protein called 40S ribosomal protein S10-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	Sk	92	Total	C	N	O	S	0	0
			752	487	122	141	2		
67	Rk	92	Total	C	N	O	S	0	0
			741	478	121	140	2		

- Molecule 68 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	Sl	144	Total	C	N	O	S	0	0
			1159	742	219	195	3		
68	Rl	146	Total	C	N	O	S	0	0
			1168	747	221	197	3		

- Molecule 69 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	Sm	121	Total	C	N	O	S	0	0
			875	551	153	169	2		
69	Rm	124	Total	C	N	O	S	0	0
			890	560	156	172	2		

- Molecule 70 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	Sn	150	Total	C	N	O	S	0	0
			1192	759	224	207	2		
70	Rn	150	Total	C	N	O	S	0	0
			1192	759	224	207	2		

- Molecule 71 is a protein called 40S ribosomal protein S14-A.

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

- Molecule 72 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	Sp	117	Total	C	N	O	S	0	0
			916	583	171	155	7		
72	Rp	119	Total	C	N	O	S	0	0
			939	595	176	161	7		

- Molecule 73 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	Sq	141	Total	C	N	O		0	0
			1105	708	203	194			
73	Rq	141	Total	C	N	O		0	0
			1105	708	203	194			

- Molecule 74 is a protein called 40S ribosomal protein S17-B.

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

- Molecule 75 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	Ss	145	Total	C	N	O	S	0	0
			1192	743	237	210	2		
75	Rs	145	Total	C	N	O	S	0	0
			1192	743	237	210	2		

- Molecule 76 is a protein called 40S ribosomal protein S19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	St	143	Total	C	N	O	S	0	0
			1112	694	208	208	2		
76	Rt	143	Total	C	N	O	S	0	0
			1112	694	208	208	2		

- Molecule 77 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Su	100	Total	C	N	O	S	0	0
			797	506	144	146	1		
77	Ru	101	Total	C	N	O	S	0	0
			805	512	145	147	1		

- Molecule 78 is a protein called Small ribosomal subunit protein eS21A.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Sv	87	Total	C	N	O	S	0	0
			673	415	125	131	2		
78	Rv	87	Total	C	N	O	S	0	0
			684	420	125	137	2		

- Molecule 79 is a protein called 40S ribosomal protein S22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	Sw	129	Total	C	N	O	S	0	0
			1021	650	188	180	3		
79	Rw	129	Total	C	N	O	S	0	0
			1021	650	188	180	3		

- Molecule 80 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Sx	144	Total	C	N	O	S	0	0
			1121	708	220	191	2		
80	Rx	144	Total	C	N	O	S	0	0
			1121	708	220	191	2		

- Molecule 81 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
81	Sy	134	Total	C	N	O	0	0
			1073	676	208	189		
81	Ry	134	Total	C	N	O	0	0
			1073	676	208	189		

- Molecule 82 is a protein called 40S ribosomal protein S25-A.

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

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Mol	Chain	Residues	Atoms				AltConf	Trace
82	Rz	69	Total	C	N	O	0	0
			558	357	103	98		

- Molecule 83 is a protein called 40S ribosomal protein S28-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	RC	63	Total	C	N	O	S	0	0
			497	306	99	91	1		

- Molecule 84 is a protein called 40S ribosomal protein S14-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	Ro	128	Total	C	N	O	S	0	0
			949	582	188	176	3		

- Molecule 85 is a protein called 40S ribosomal protein S17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	Rr	125	Total	C	N	O	S	0	0
			1000	625	188	185	2		

- Molecule 86 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
86	MA	155	Total	C	N	O	S	0	0
			1230	795	221	213	1		

- Molecule 87 is a RNA chain called *Saccharomyces cerevisiae* S288C 18S ribosomal RNA (RDN18-1) with modifications.

Mol	Chain	Residues	Atoms					AltConf	Trace
87	M1	3190	Total	C	N	O	P	0	0
			68285	30524	12313	22258	3190		

- Molecule 88 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
88	DQ	77	Total	C	N	O	P	0	0
			1644	732	298	537	77		

- Molecule 89 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
89	MQ	197	Total	C	N	O	S	0	0
			1531	980	266	281	4		

- Molecule 90 is a protein called 60S ribosomal protein L12-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
90	MP	158	Total	C	N	O	S	0	0
			1196	750	216	228	2		

- Molecule 91 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
91	DP	76	Total	C	N	O	P	0	0
			1638	736	294	533	75		

- Molecule 92 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
92	CP	1	Total	Mg	0
			1	1	
92	S1	84	Total	Mg	0
			84	84	
92	Sf	1	Total	Mg	0
			1	1	
92	Sx	1	Total	Mg	0
			1	1	
92	M1	194	Total	Mg	0
			194	194	
92	MK	1	Total	Mg	0
			1	1	
92	M3	4	Total	Mg	0
			4	4	
92	M2	3	Total	Mg	0
			3	3	
92	MM	1	Total	Mg	0
			1	1	
92	Mx	1	Total	Mg	0
			1	1	
92	Ma	1	Total	Mg	0
			1	1	
92	ME	1	Total	Mg	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
92	MI	2	Total	Mg	0
			2	2	

- Molecule 93 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
93	Lb	1	Total	Zn	0
			1	1	
93	Lc	1	Total	Zn	0
			1	1	
93	Le	1	Total	Zn	0
			1	1	
93	Lh	1	Total	Zn	0
			1	1	
93	Lk	1	Total	Zn	0
			1	1	
93	SD	1	Total	Zn	0
			1	1	
93	SF	1	Total	Zn	0
			1	1	
93	RB	1	Total	Zn	0
			1	1	
93	Mk	1	Total	Zn	0
			1	1	
93	Mh	1	Total	Zn	0
			1	1	
93	Me	1	Total	Zn	0
			1	1	
93	Mc	1	Total	Zn	0
			1	1	
93	Mb	1	Total	Zn	0
			1	1	

- Molecule 94 is POTASSIUM ION (CCD ID: K) (formula: K).

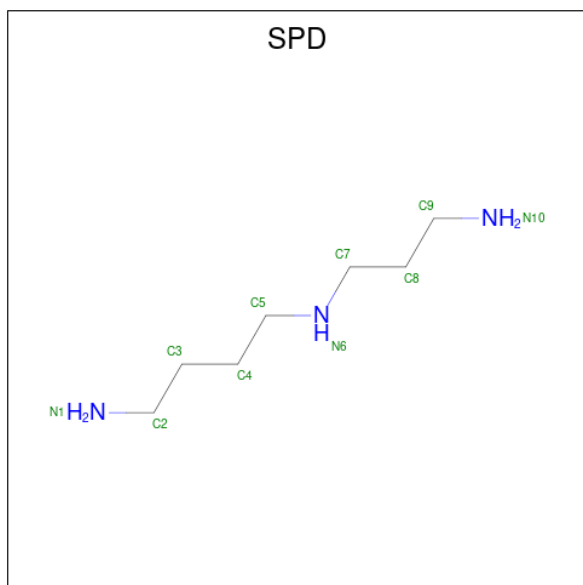
Mol	Chain	Residues	Atoms		AltConf
94	M1	11	Total	K	0
			11	11	
94	Mw	1	Total	K	0
			1	1	
94	ME	1	Total	K	0
			1	1	

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Mol	Chain	Residues	Atoms	AltConf
94	Mm	1	Total K 1 1	0
94	Mk	1	Total K 1 1	0
94	Mc	1	Total K 1 1	0

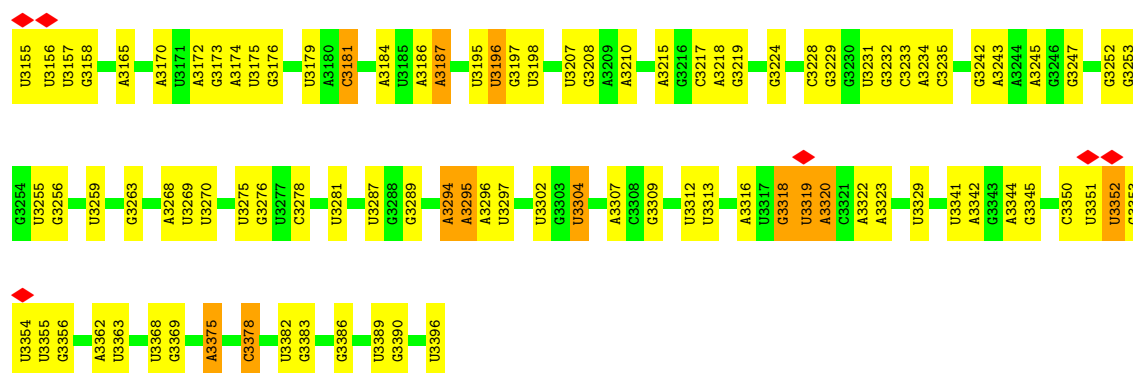
- Molecule 95 is SPERMIDINE (CCD ID: SPD) (formula: $C_7H_{19}N_3$).



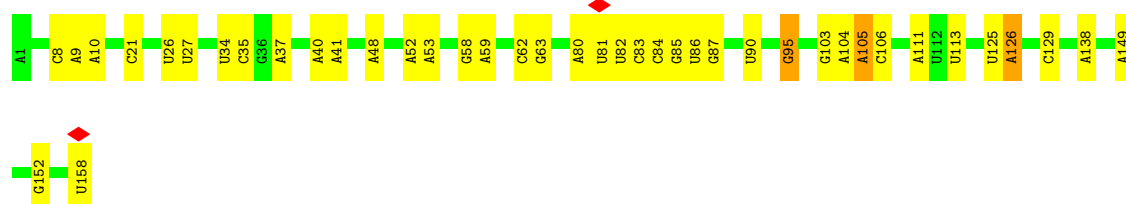
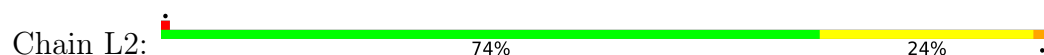
Mol	Chain	Residues	Atoms	AltConf
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95	M1	1	Total C N 10 7 3	0
95	M1	1	Total C N 10 7 3	0



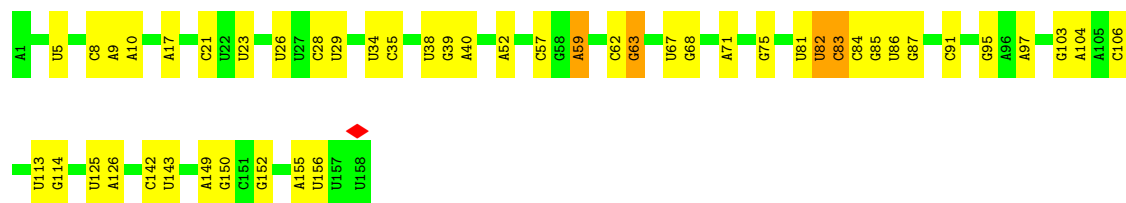
G2997	C2852	G2728	A2695	U	C2338	A2188	U	C	A1858	G1748	U1607	G1486
A3012	U2855	U2729	C2600	C	A	C2192	U	U	G1863	A1749	C1608	G1487
A3016	C2867	C2741	G2606	U	A	U2193	A	A	A2093	A1750	A1619	G1488
A3017	U2868	A2747	G2607	U	G	G2194	C2094	C	C1866	G1751	A1621	G1492
G3022	G2871	A2748	U2611	U	G	G2201	C2101	U	A1867	A1757	U1622	G1493
U3037	A2872	U2752	U2612	U	U	U2205	U2102	C	U1871	A1760	C1497	C1498
U3038	U2875	G2753	U2613	U	G	A2207	C2108	C	U1877	C1761	A1498	C1499
C3039	C2876	G2761	G2614	A	G	A2208	U2109	U	U1878	C1762	U1629	C1508
G3044	U2882	U2767	A2626	A	A	U2209	G2110	G	A1879	U1763	G1634	G1513
G3045	C2883	U2768	U2629	A	A	G2210	G2111	U	A1880	U1764	C1639	G1522
U3049	U2884	U2769	C2630	U	U	G2211	A2112	C	U1881	U1765	A1642	U1522
U3056	A2887	C2772	U2631	G	A	A2213	C2113	U	A1884	G1766	A1643	U1554
C3067	A2890	C2773	A2637	U	U	A2214	G2115	G	U1885	U1770	G1644	G1536
U3068	C2894	G2777	A2642	A	G	A2223	A2120	C	A1886	G1775	U1645	C1551
U3069	C2898	G2778	G2651	U	G	U2225	G2121	U	A1889	G1778	G1650	G1552
G3069	G2899	C2788	U2652	C	G	U2228	A2126	G	U1900	C1779	A1656	U1555
A3070	A2900	A2792	C2653	U	U	A2229	U2129	C	G1906	G1780	G1657	C1556
U3075	U2901	G2793	A2656	U	G	A2232	G2130	U	C1907	G1786	U1659	A1557
U3078	A2911	U2794	U2662	U	C	A2233	A2131	C	G1914	A1787	C1660	G1560
C3084	U2923	G2796	G2663	C	G	A2244	U2137	U	U1920	C1793	G1662	C1561
G3085	A2933	A2799	C2666	U	C	G2249	U2140	G	A1797	A1797	G1666	C1562
U3086	U2934	G2800	G2672	C	C	G2250	U2141	U	A1798	A1798	A1667	C1563
A3092	A2936	A2801	A2674	U	U	A2256	A2142	G	A1799	A1799	G1668	A1566
C3093	G2937	U2803	C2677	G	G	C2257	A2144	C	A1800	A1800	U1567	U1567
A3094	U2938	C2809	U2677	U	U	G2272	U2147	U	C1805	C1805	U1568	U1569
G3101	A2940	C2810	A2680	A	A	G2273	A2152	G	A1814	A1814	U1570	U1571
U3104	C2941	A2812	A2689	A	A	U2274	U2153	U	U1815	U1815	A1572	U1572
U3121	C2942	G2813	U2690	U	U	A2275	G2154	C	A1816	A1816	A1575	G1576
A3122	G2947	U2814	A2691	C	C	A2280	U2155	A	U1820	U1820	A1580	A1580
A3129	C2948	G2815	A2694	C	A	U2282	A2158	C	U1821	U1821	C1581	C1581
A3130	U2960	U2816	U2695	U	U	G2288	G2160	G	U1834	U1834	C1582	A1583
U3131	G2961	A2817	A2696	C	C	G2307	G2169	C	A1835	A1835	U1716	U1716
A3139	A2969	C2818	U2697	U	U	C2308	U2170	C	C1836	C1836	G1718	G1718
G3140	C2970	U2819	G2698	C	C	U2310	G2171	G	U1837	U1837	U1721	U1721
A3141	A2971	A2820	A2703	U	U	U2311	U2176	U	G1838	G1838	U1722	U1722
A3142	C2971	G2821	A2704	U	U	U2313	G2177	C	U1839	U1839	A1723	A1723
C3143	U2983	U2842	G2714	A	A	U2314	A2180	C	A1841	A1841	G1725	G1725
G2990	C2983	C2843	G2715	U	U	G2315	G2180	C	A1842	A1842	C1736	C1736
A2991	G2990	A2844	G2584	U	U	U2318	U2181	C	C1846	C1846	C1596	C1596
U2992	A2991	A2845	G2585	U	U	U2334	U2185	C	C1849	C1849	C1597	C1597
U2996	U2992	C2849	G2586	U	U	G2335	G2185	A	A1850	A1850	A1605	A1605
			G2592	U	U			A				
			A2593	U	U			A				
			C2594	U	U			A				



- Molecule 6: *Saccharomyces cerevisiae* S288C 5.8S ribosomal RNA



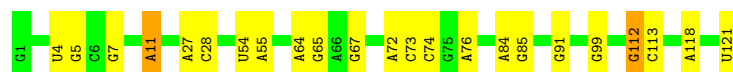
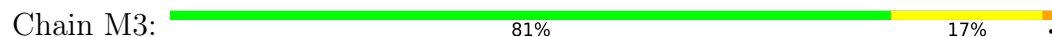
- Molecule 6: *Saccharomyces cerevisiae* S288C 5.8S ribosomal RNA



- Molecule 7: *Saccharomyces cerevisiae* S288C 5S ribosomal RNA

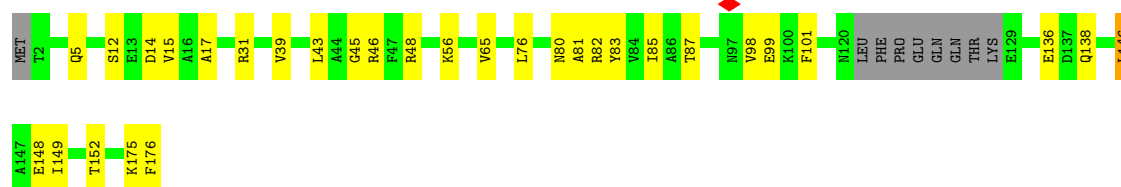


- Molecule 7: *Saccharomyces cerevisiae* S288C 5S ribosomal RNA



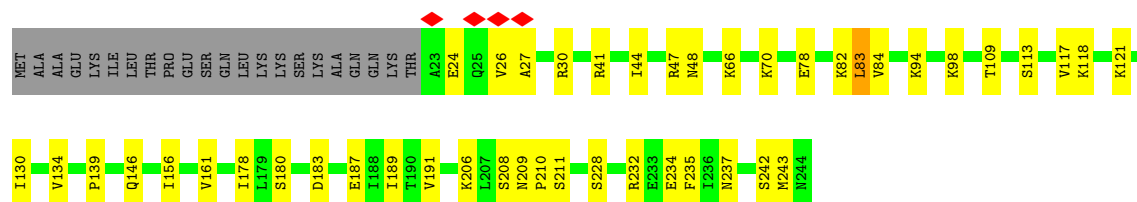
- Molecule 8: 60S ribosomal protein L6-B

Chain LA:  77% 17% 5%



- Molecule 9: 60S ribosomal protein L7-A

Chain LB:  73% 18% 9%



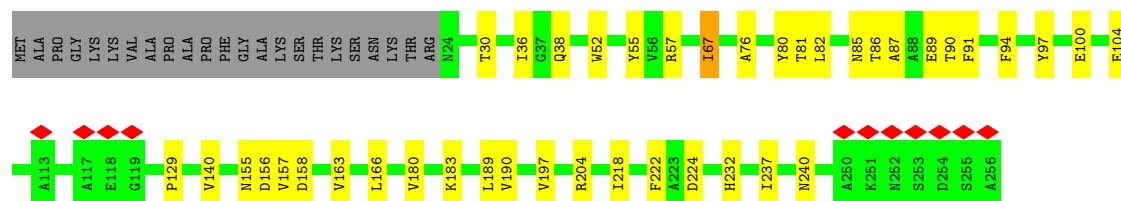
- Molecule 9: 60S ribosomal protein L7-A

Chain MB:  85% 6% 9%



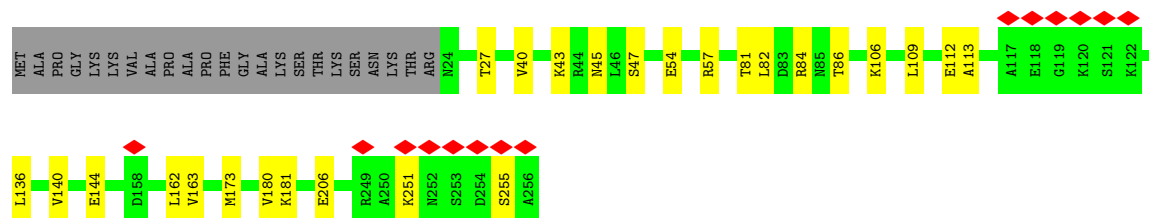
- Molecule 10: 60S ribosomal protein L8-A

Chain LC:  75% 16% 9%

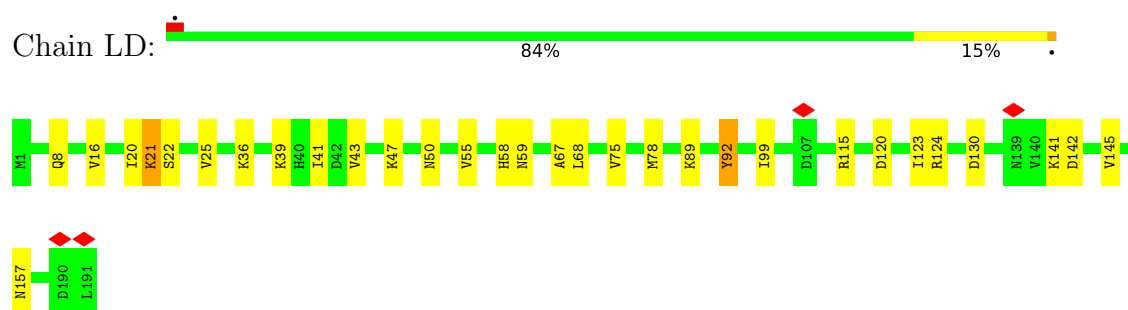


- Molecule 10: 60S ribosomal protein L8-A

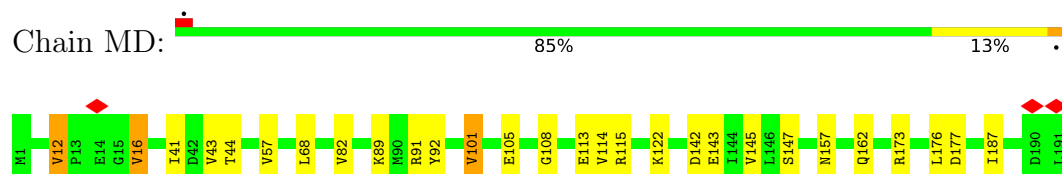
Chain MC:  81% 10% 9%



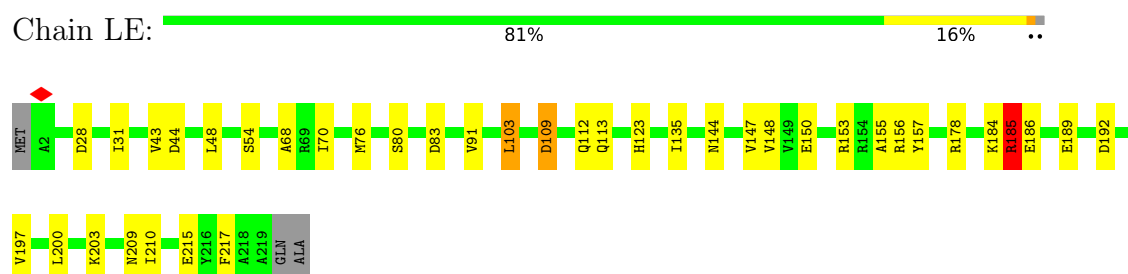
- Molecule 11: 60S ribosomal protein L9-A



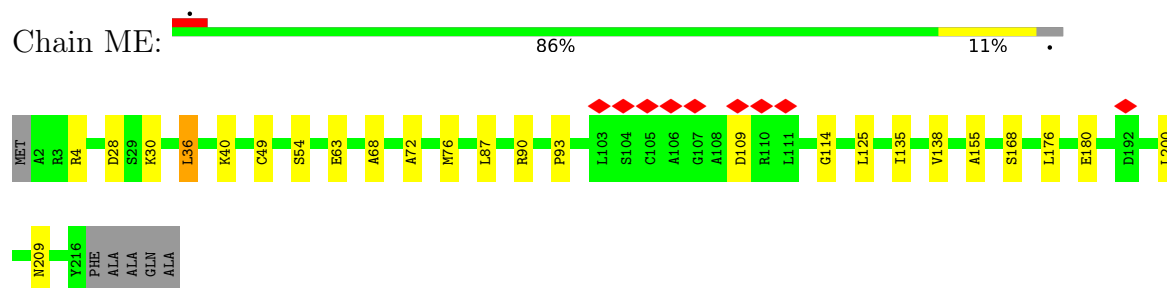
- Molecule 11: 60S ribosomal protein L9-A



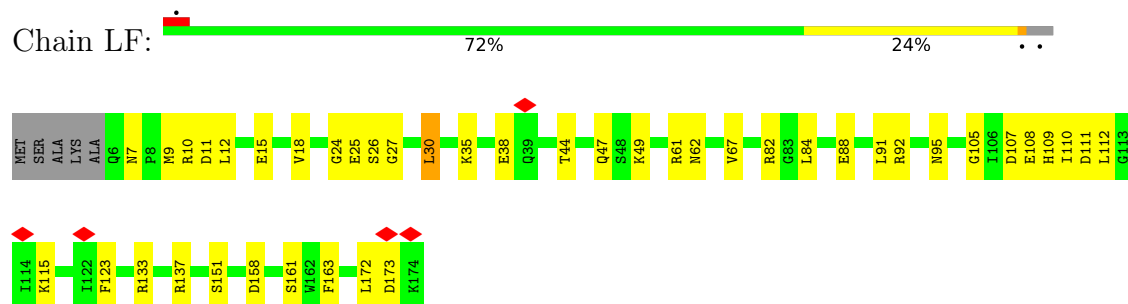
- Molecule 12: 60S ribosomal protein L10



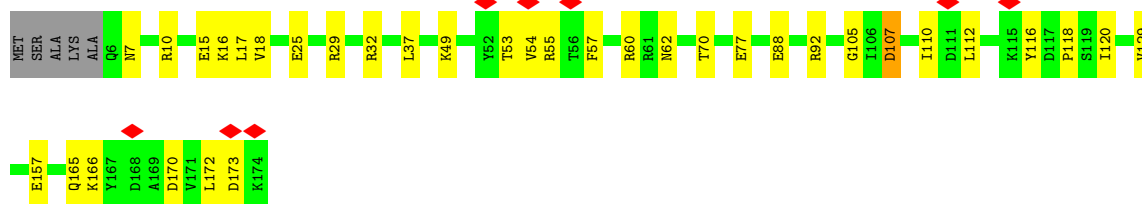
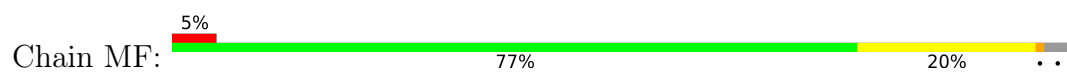
- Molecule 12: 60S ribosomal protein L10



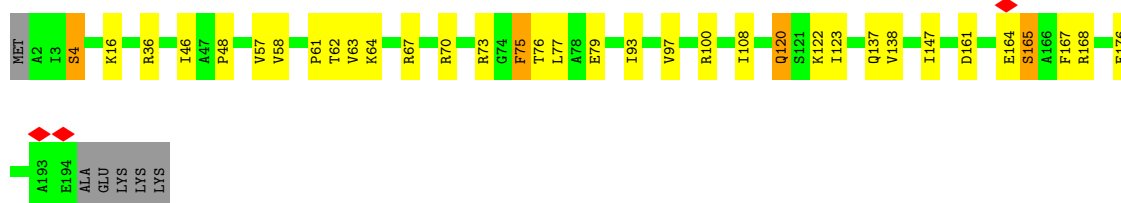
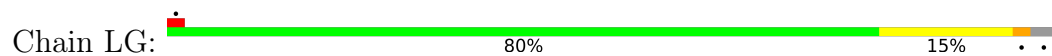
- Molecule 13: 60S ribosomal protein L11-A



- Molecule 13: 60S ribosomal protein L11-A



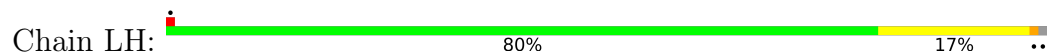
- Molecule 14: 60S ribosomal protein L13-A



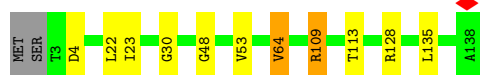
- Molecule 14: 60S ribosomal protein L13-A



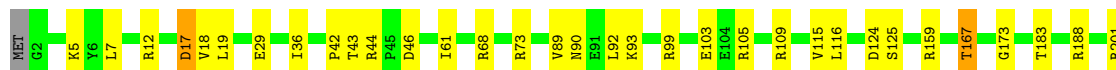
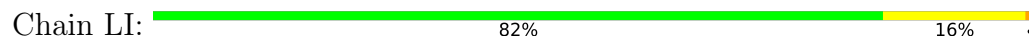
- Molecule 15: 60S ribosomal protein L14-A



- Molecule 15: 60S ribosomal protein L14-A



- Molecule 16: 60S ribosomal protein L15-A





- Molecule 16: 60S ribosomal protein L15-A

Chain MI: 87% 12%



- Molecule 17: 60S ribosomal protein L16-A

Chain LJ: 84% 14% ..



- Molecule 17: 60S ribosomal protein L16-A

Chain MJ: 87% 12% ..



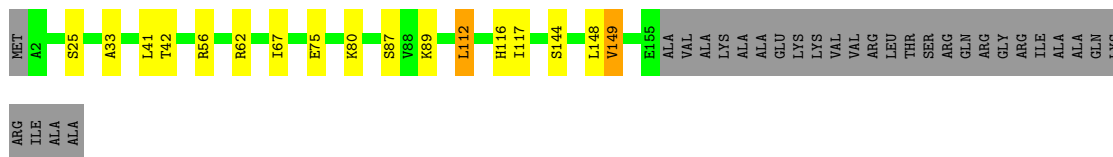
- Molecule 18: 60S ribosomal protein L17-A

Chain LK: 90% 9% ..



- Molecule 18: 60S ribosomal protein L17-A

Chain MK: 74% 8% 16%



- Molecule 19: 60S ribosomal protein L18-A

Chain LL: 84% 15% ..



- Molecule 19: 60S ribosomal protein L18-A

Chain ML:  89% 11% .



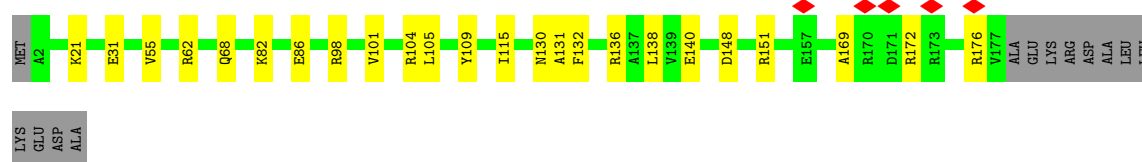
- Molecule 20: 60S ribosomal protein L19-A

Chain LM:  7% 89% 9% ..



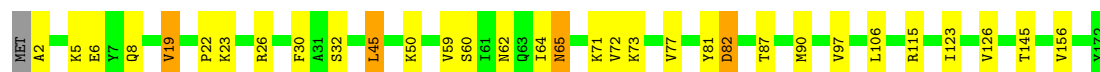
- Molecule 20: 60S ribosomal protein L19-A

Chain MM:  80% 13% 7%



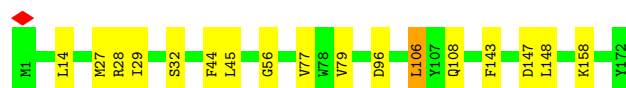
- Molecule 21: 60S ribosomal protein L20-A

Chain LN:  81% 16% ..



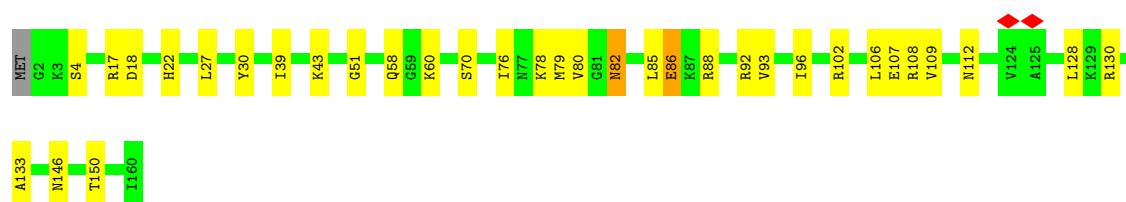
- Molecule 21: 60S ribosomal protein L20-A

Chain MN:  90% 9% .



- Molecule 22: 60S ribosomal protein L21-A

Chain LO:  78% 20% ..



- Molecule 22: 60S ribosomal protein L21-A

Chain MO:  88% 12%



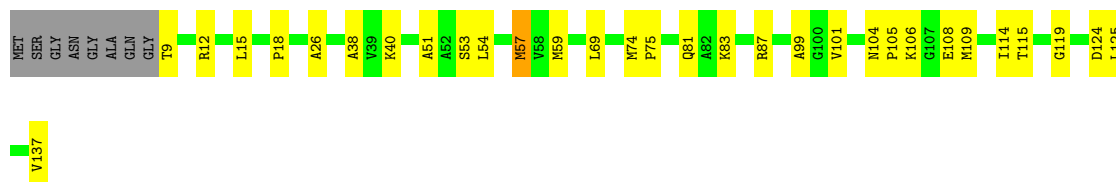
- Molecule 23: 60S ribosomal protein L23-A

Chain La:  88% 12%



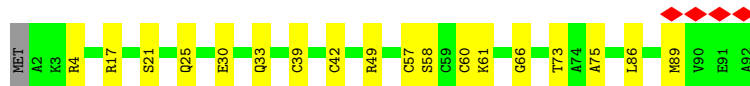
- Molecule 23: 60S ribosomal protein L23-A

Chain Ma:  72% 22% 6%



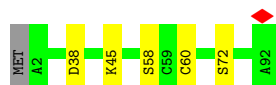
- Molecule 24: 60S ribosomal protein L43-A

Chain Lb:  79% 20%



- Molecule 24: 60S ribosomal protein L43-A

Chain Mb:  93% 5%



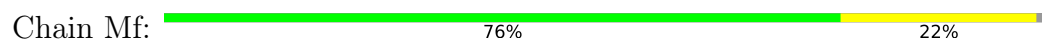
- Molecule 25: 60S ribosomal protein L42-A

Chain Lc:  76% 18%



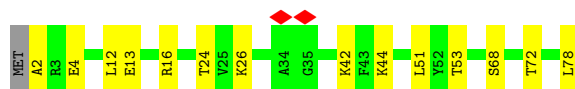
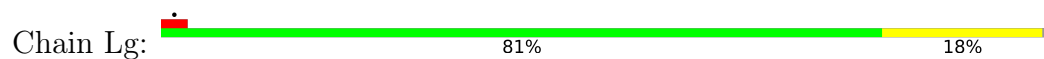
- Molecule 25: 60S ribosomal protein L42-A

Chain Mc:  89% 6%

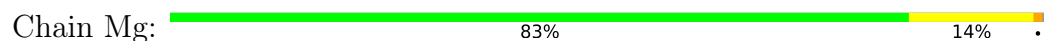




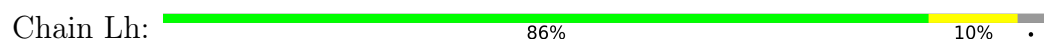
- Molecule 29: 60S ribosomal protein L38



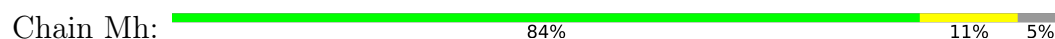
- Molecule 29: 60S ribosomal protein L38



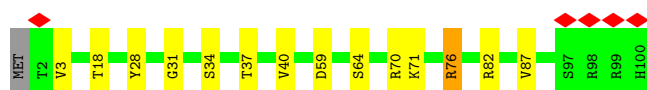
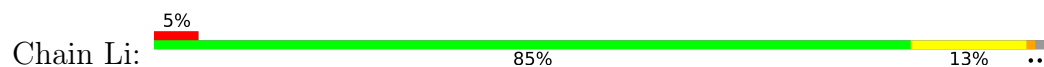
- Molecule 30: 60S ribosomal protein L37-A



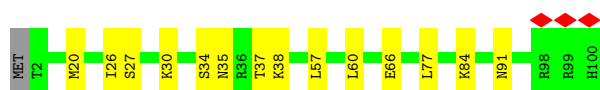
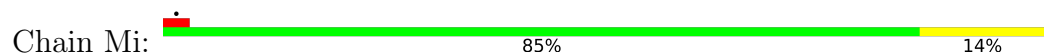
- Molecule 30: 60S ribosomal protein L37-A



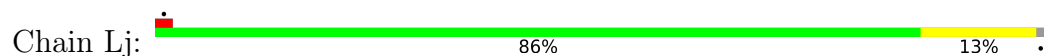
- Molecule 31: 60S ribosomal protein L36-A

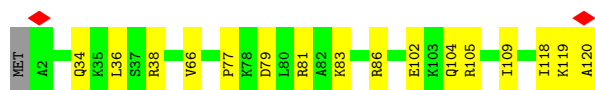


- Molecule 31: 60S ribosomal protein L36-A



- Molecule 32: 60S ribosomal protein L35-A

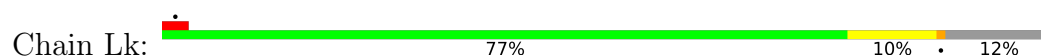




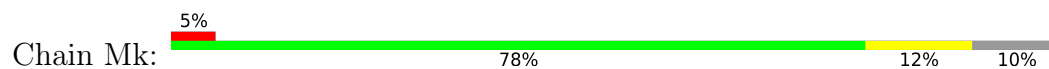
- Molecule 32: 60S ribosomal protein L35-A



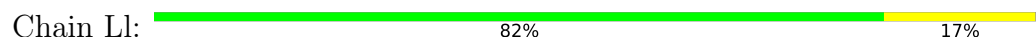
- Molecule 33: 60S ribosomal protein L34-A



- Molecule 33: 60S ribosomal protein L34-A



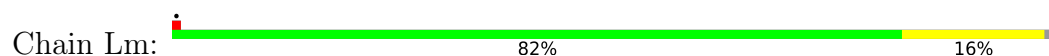
- Molecule 34: 60S ribosomal protein L33-A



- Molecule 34: 60S ribosomal protein L33-A



- Molecule 35: 60S ribosomal protein L32



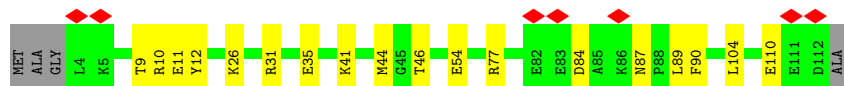
- Molecule 35: 60S ribosomal protein L32

Chain Mm:  88% 8% ..



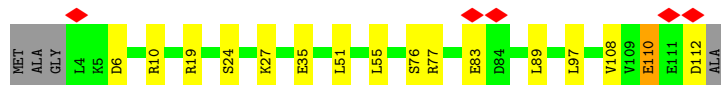
- Molecule 36: 60S ribosomal protein L31-A

Chain Ln:  81% 16% .



- Molecule 36: 60S ribosomal protein L31-A

Chain Mn:  82% 13% ..



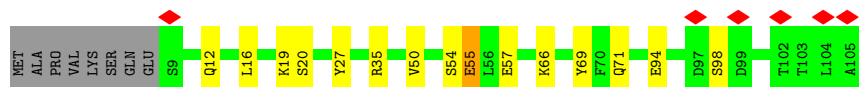
- Molecule 37: 60S ribosomal protein L30

Chain Lo:  73% 17% . 9%



- Molecule 37: 60S ribosomal protein L30

Chain Mo:  78% 13% . 8%



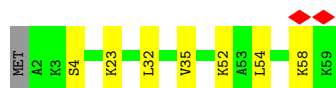
- Molecule 38: 60S ribosomal protein L29

Chain Lp:  85% 12% ..

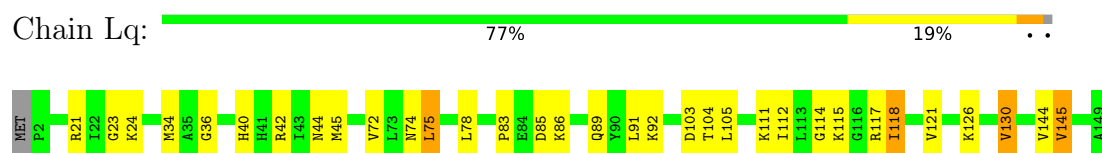


- Molecule 38: 60S ribosomal protein L29

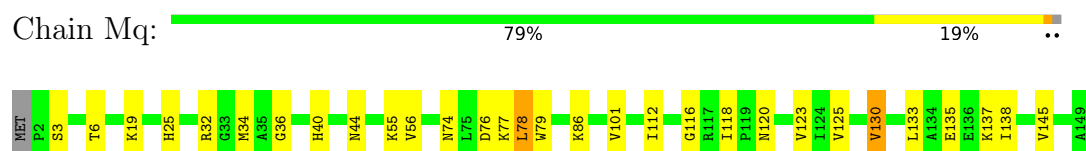
Chain Mp:  86% 12% .



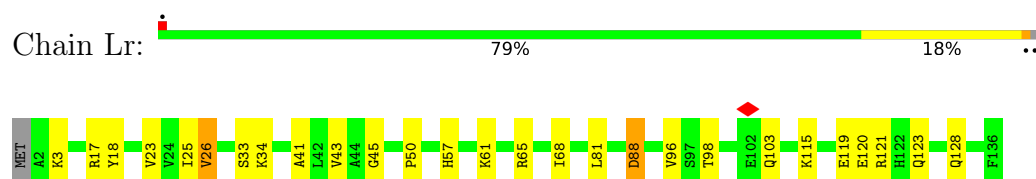
- Molecule 39: 60S ribosomal protein L28



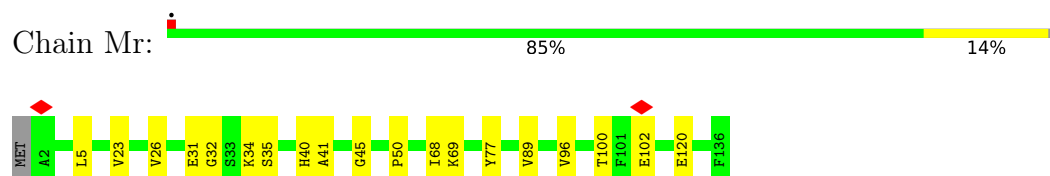
- Molecule 39: 60S ribosomal protein L28



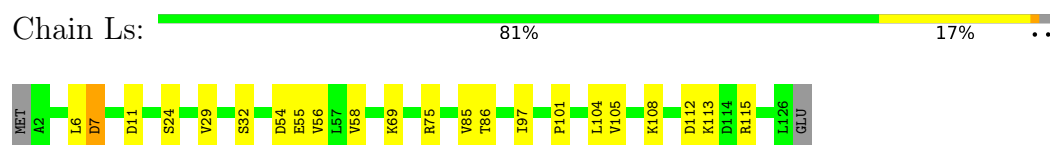
- Molecule 40: 60S ribosomal protein L27-A



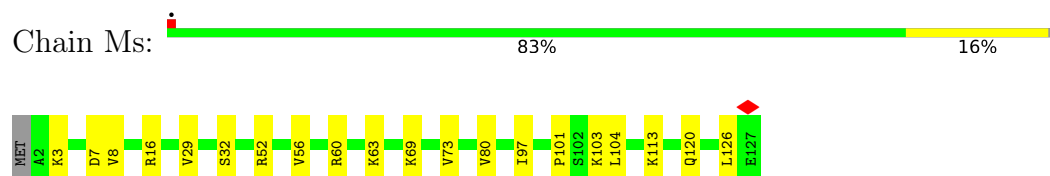
- Molecule 40: 60S ribosomal protein L27-A



- Molecule 41: 60S ribosomal protein L26-A



- Molecule 41: 60S ribosomal protein L26-A

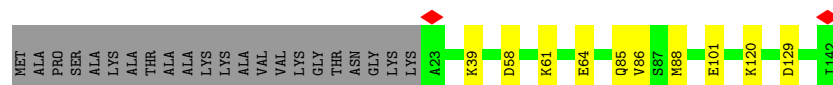
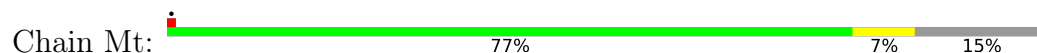


- Molecule 42: 60S ribosomal protein L25

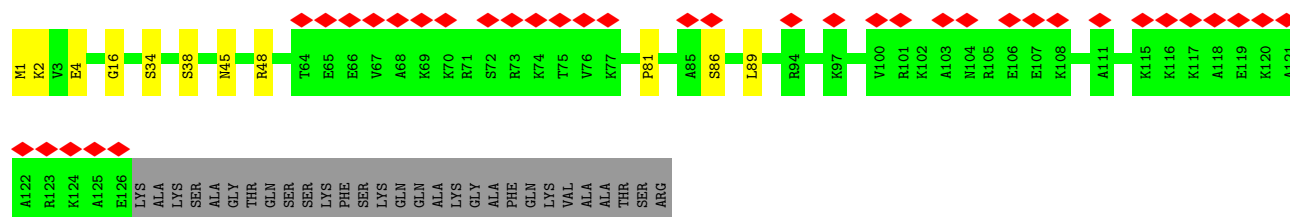
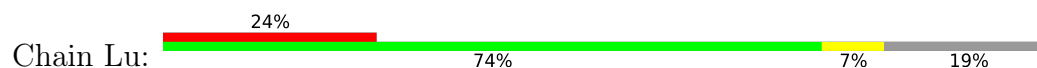




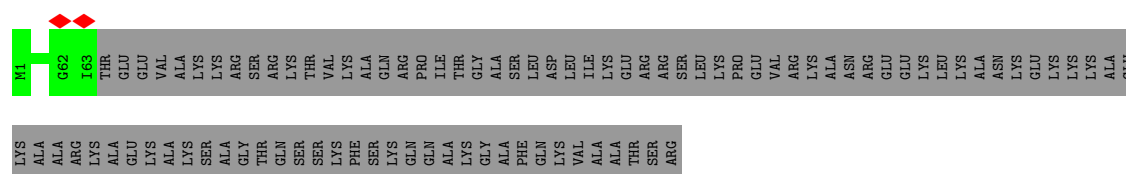
- Molecule 42: 60S ribosomal protein L25



- Molecule 43: 60S ribosomal protein L24-A



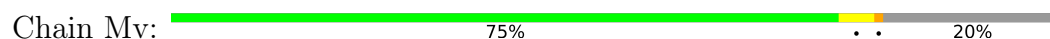
- Molecule 43: 60S ribosomal protein L24-A



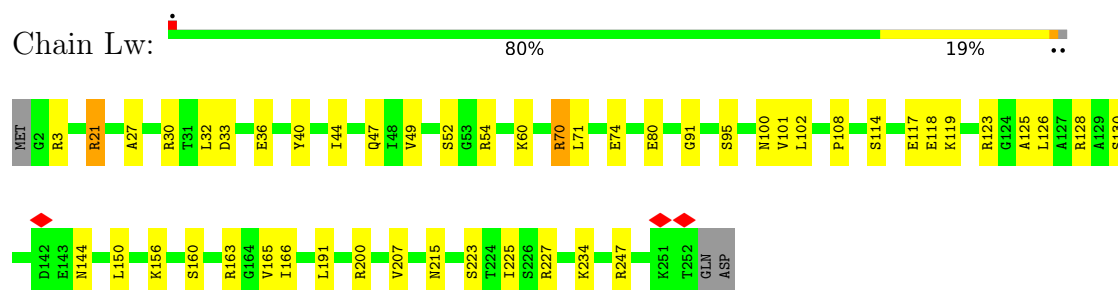
- Molecule 44: 60S ribosomal protein L22-A



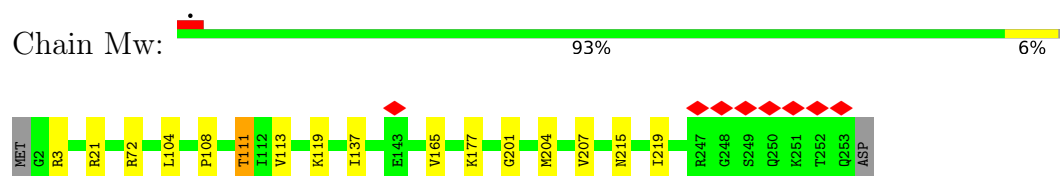
- Molecule 44: 60S ribosomal protein L22-A



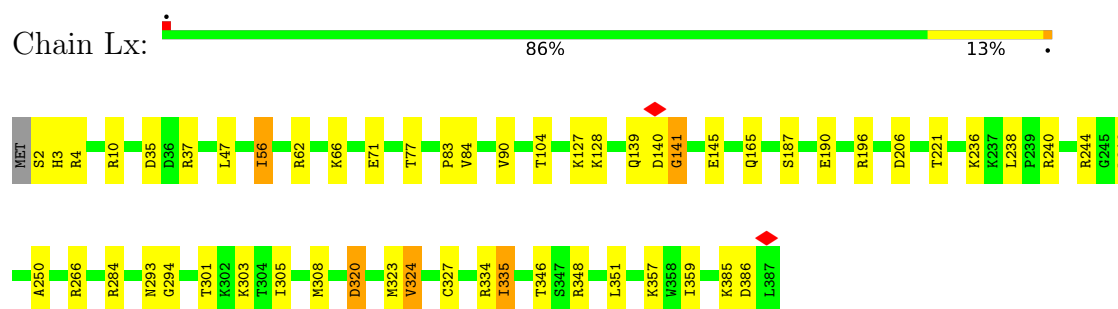
- Molecule 45: 60S ribosomal protein L2-A



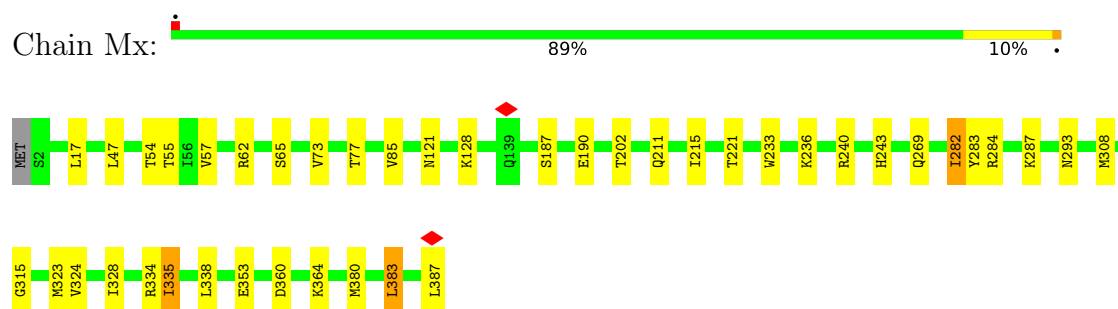
- Molecule 45: 60S ribosomal protein L2-A



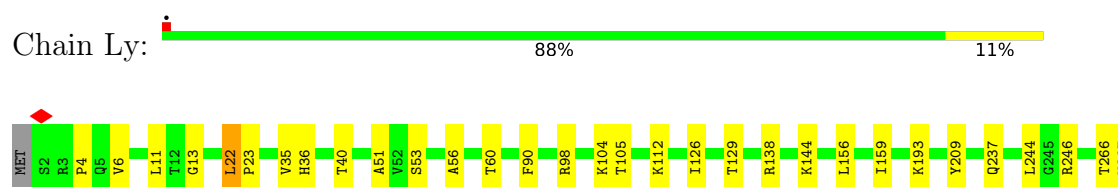
- Molecule 46: 60S ribosomal protein L3

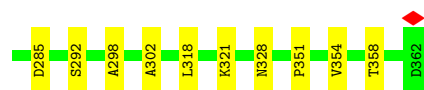


- Molecule 46: 60S ribosomal protein L3



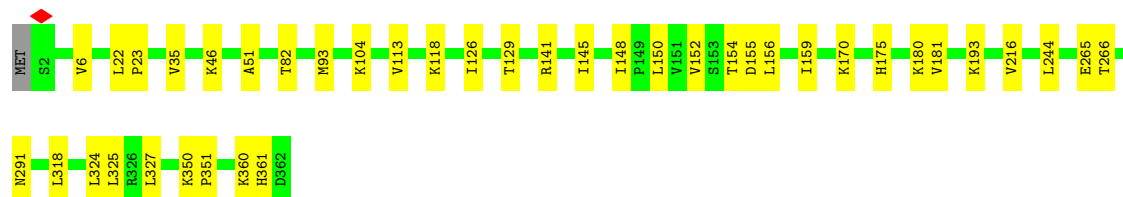
- Molecule 47: 60S ribosomal protein L4-A





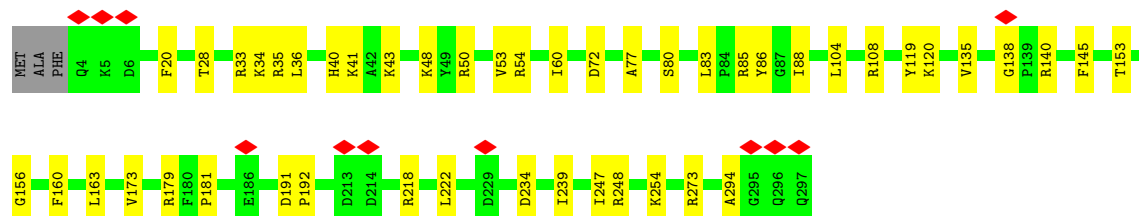
- Molecule 47: 60S ribosomal protein L4-A

Chain My: 89% 11%



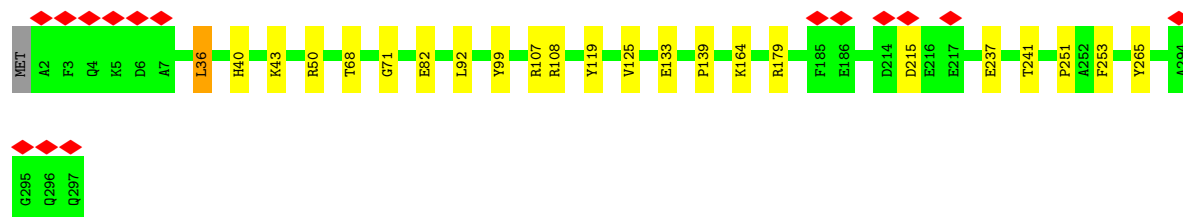
- Molecule 48: 60S ribosomal protein L5

Chain Lz: 83% 16%



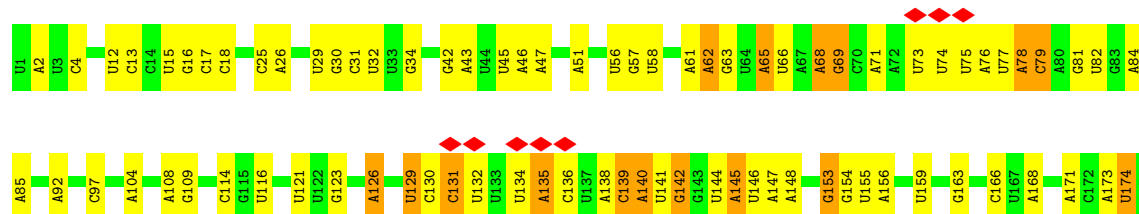
- Molecule 48: 60S ribosomal protein L5

Chain Mz: 5% 92% 7%



- Molecule 49: *Saccharomyces cerevisiae* S288C 18S ribosomal RNA (RDN18-1)

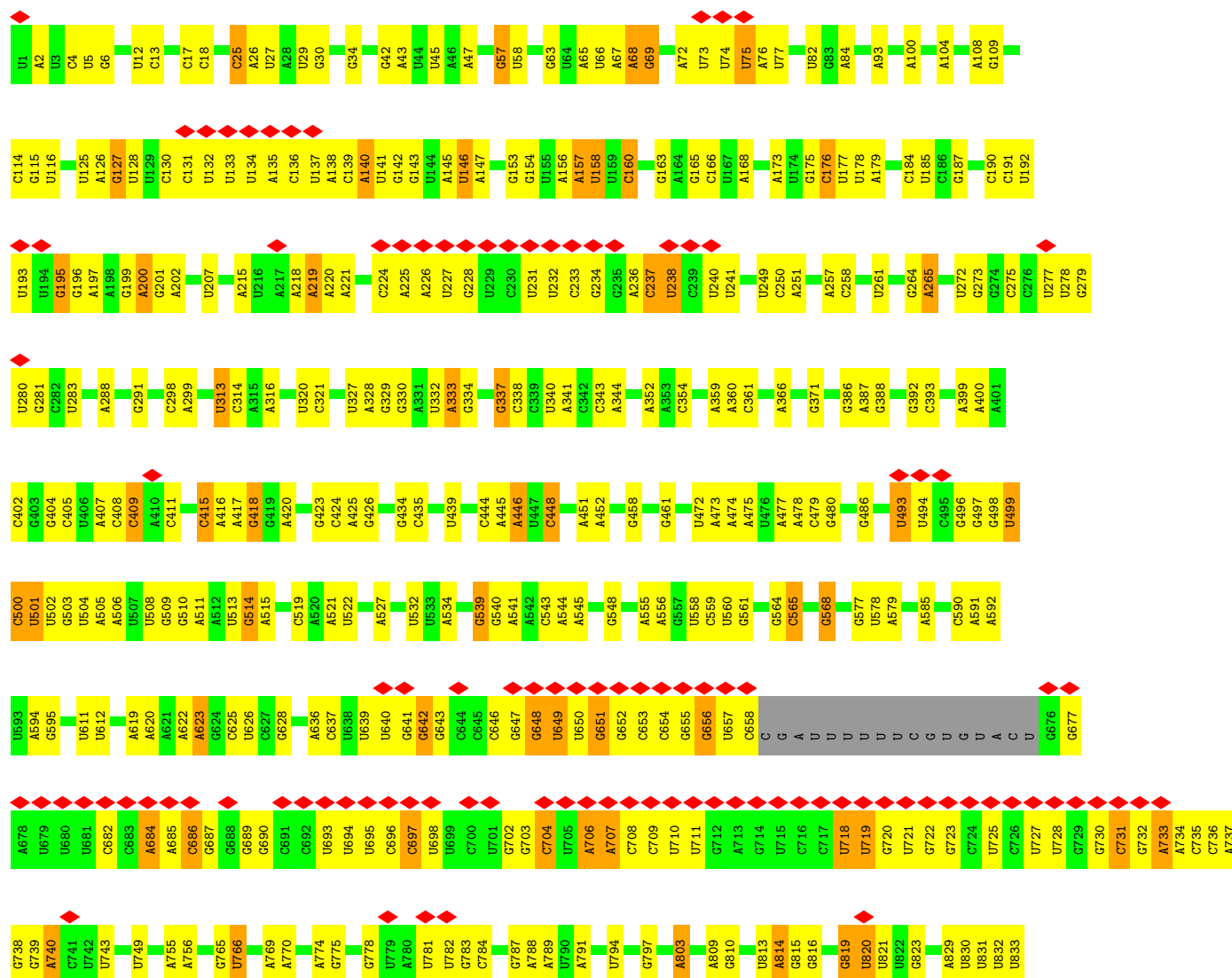
Chain S1: 5% 56% 36% 6%

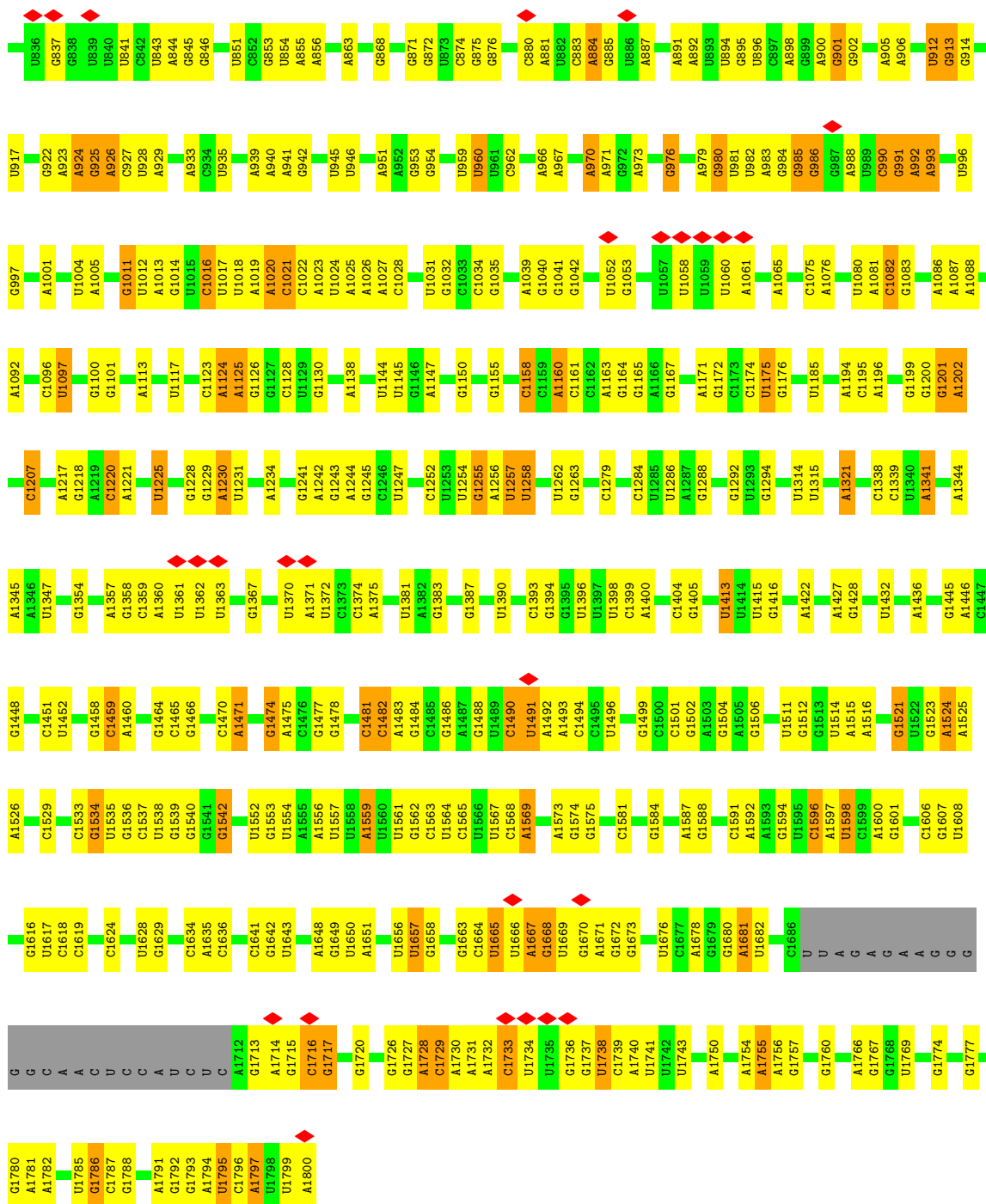


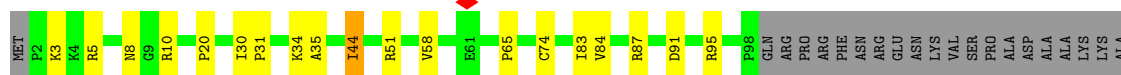




• Molecule 49: *Saccharomyces cerevisiae* S288C 18S ribosomal RNA (RDN18-1)

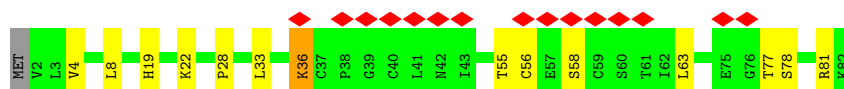
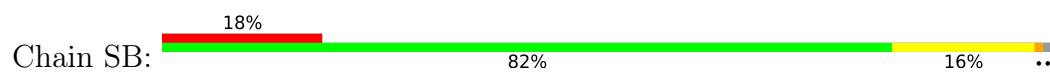




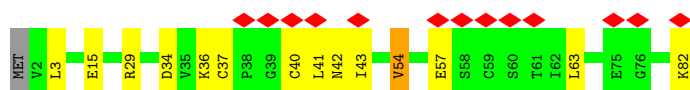
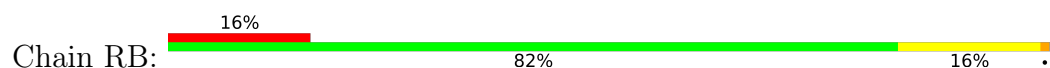


LEU

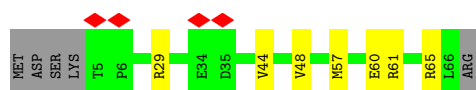
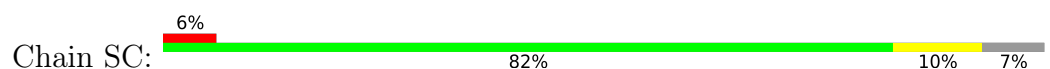
- Molecule 51: 40S ribosomal protein S27-A



- Molecule 51: 40S ribosomal protein S27-A



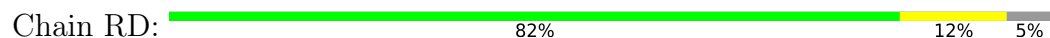
- Molecule 52: Small ribosomal subunit protein eS28B



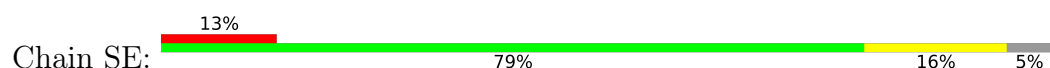
- Molecule 53: Small ribosomal subunit protein uS14A

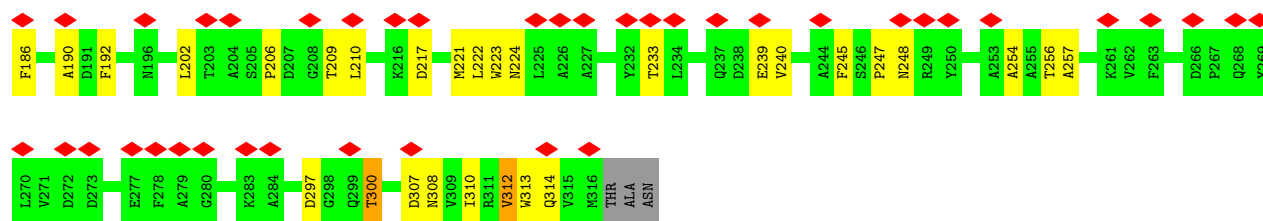


- Molecule 53: Small ribosomal subunit protein uS14A

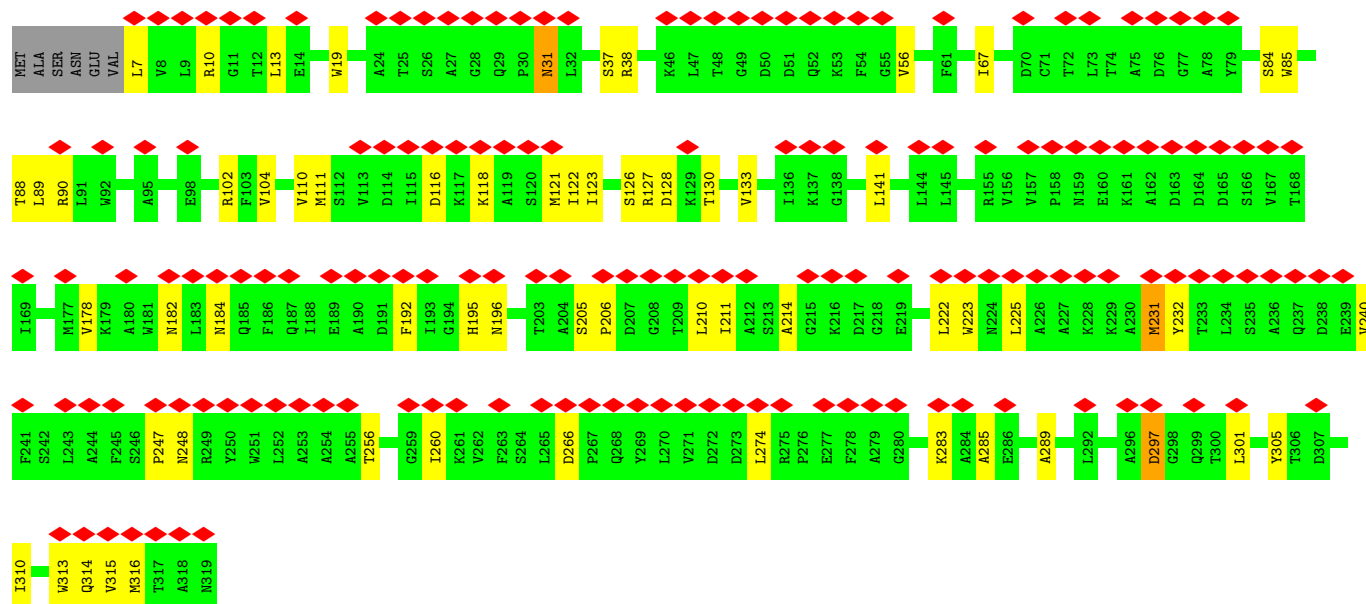
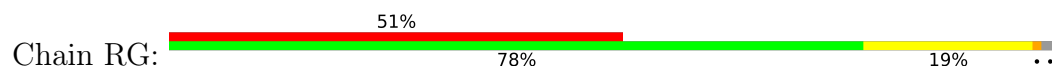


- Molecule 54: 40S ribosomal protein S30-A

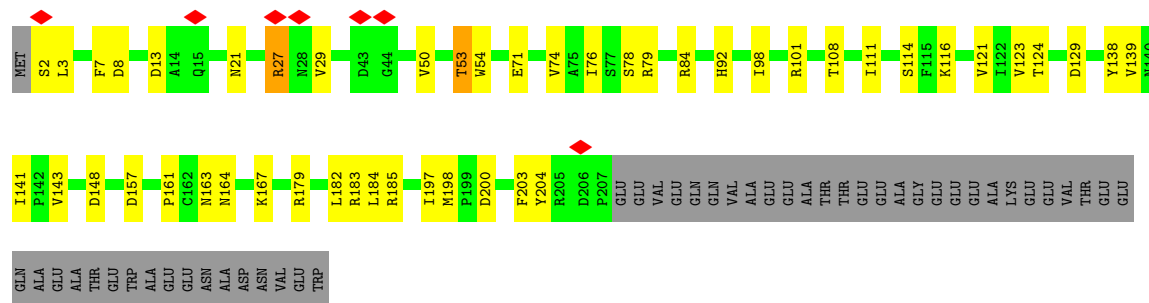




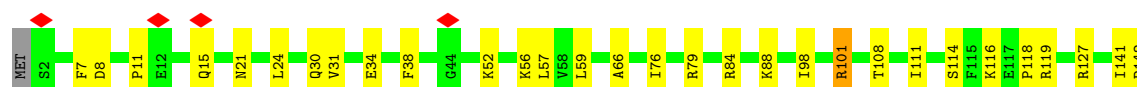
• Molecule 56: Guanine nucleotide-binding protein subunit beta-like protein



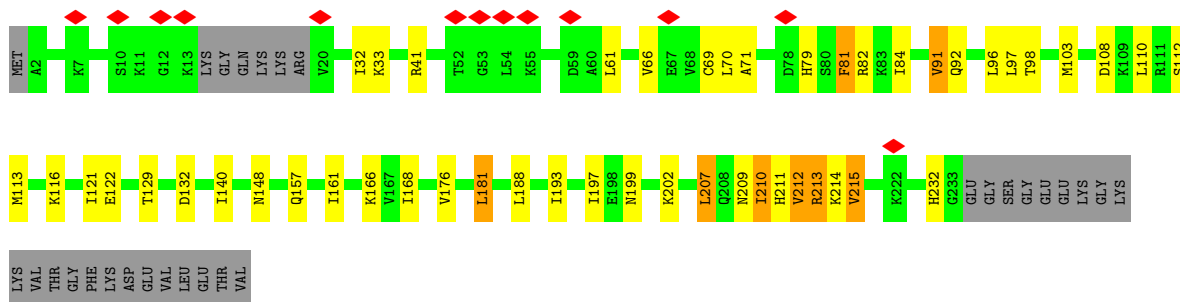
• Molecule 57: 40S ribosomal protein S0-A



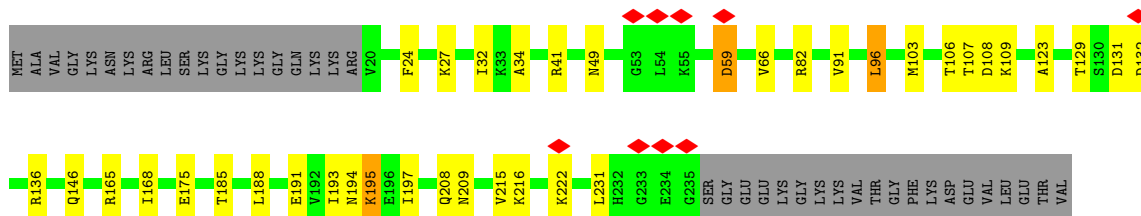
• Molecule 57: 40S ribosomal protein S0-A



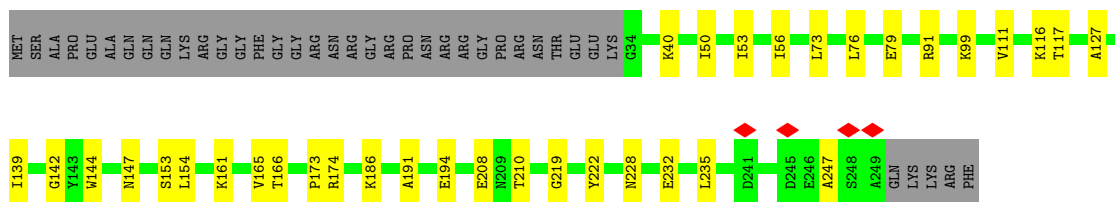
- Molecule 58: 40S ribosomal protein S1-A



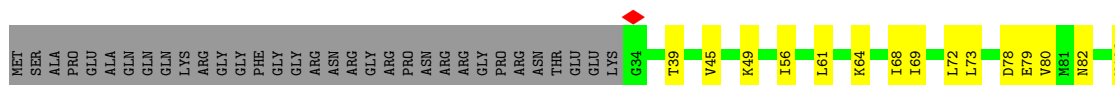
- Molecule 58: 40S ribosomal protein S1-A

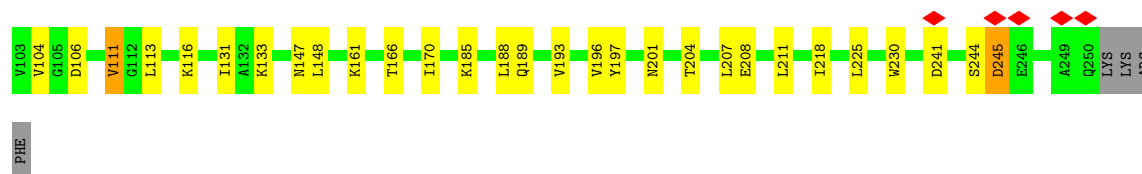


- Molecule 59: 40S ribosomal protein S2

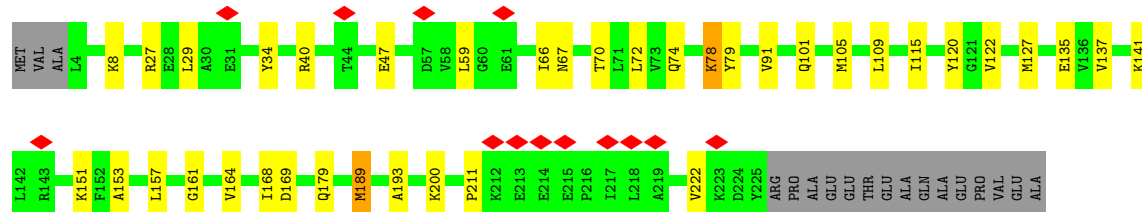
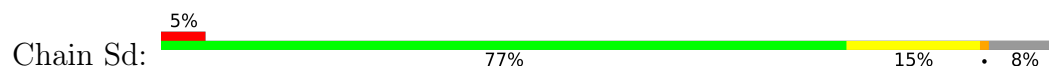


- Molecule 59: 40S ribosomal protein S2

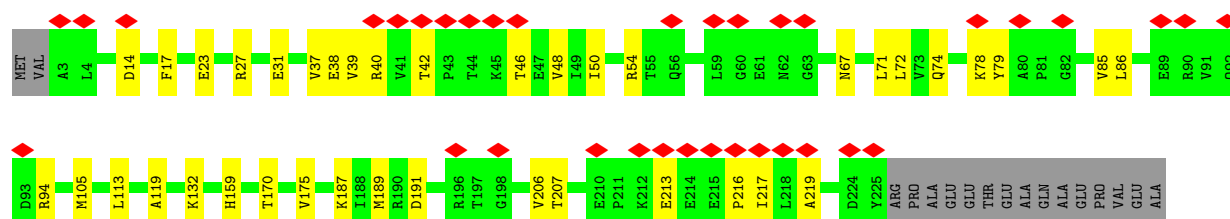
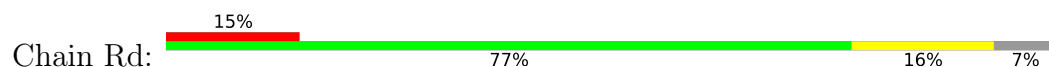




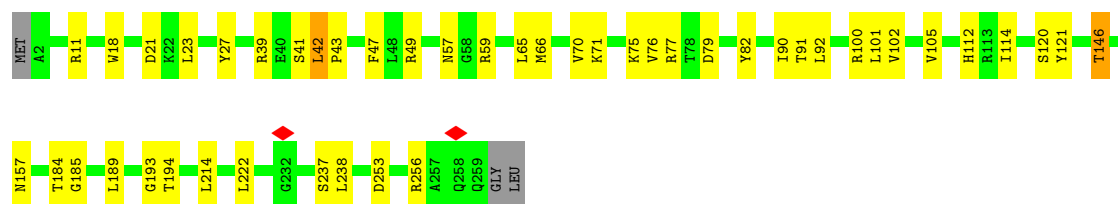
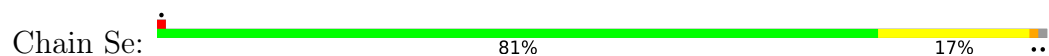
- Molecule 60: Small ribosomal subunit protein uS3



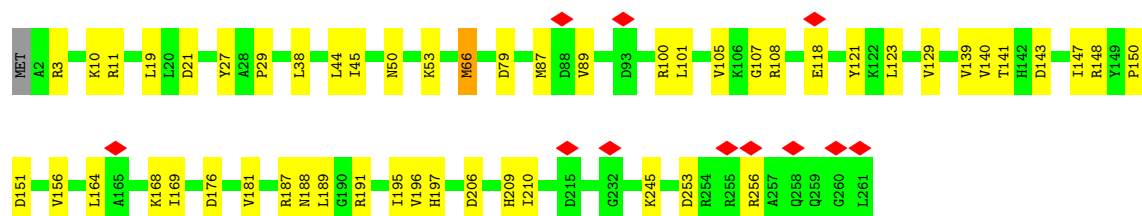
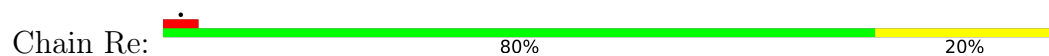
- Molecule 60: Small ribosomal subunit protein uS3



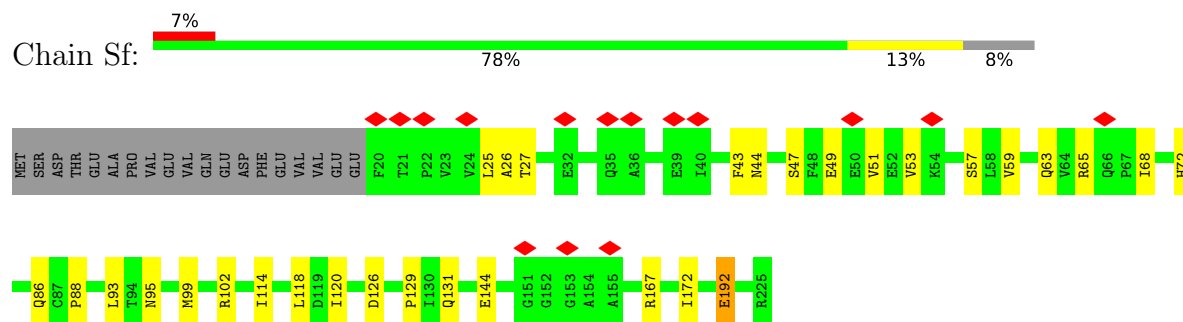
- Molecule 61: 40S ribosomal protein S4-A



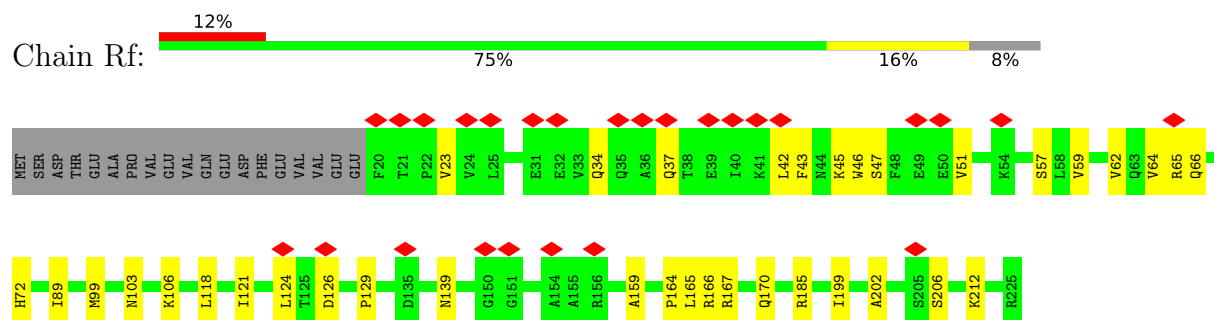
- Molecule 61: 40S ribosomal protein S4-A



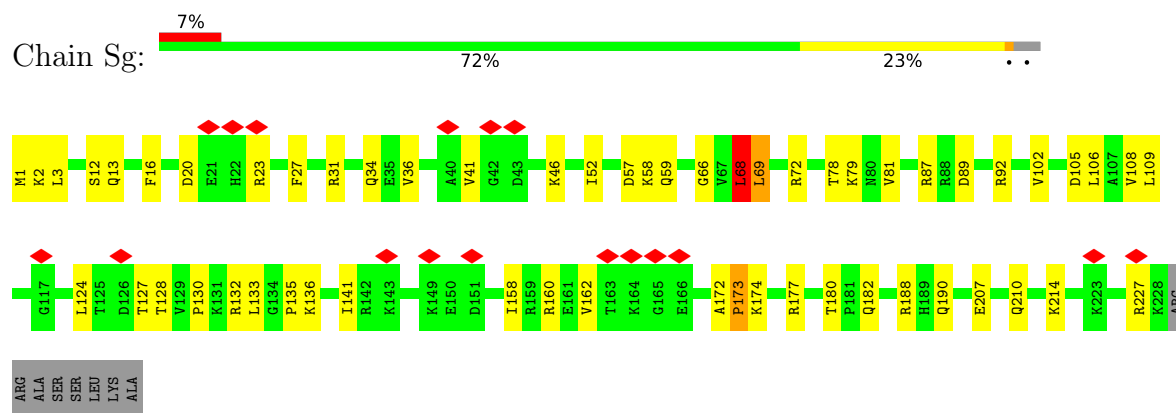
• Molecule 62: 40S ribosomal protein S5



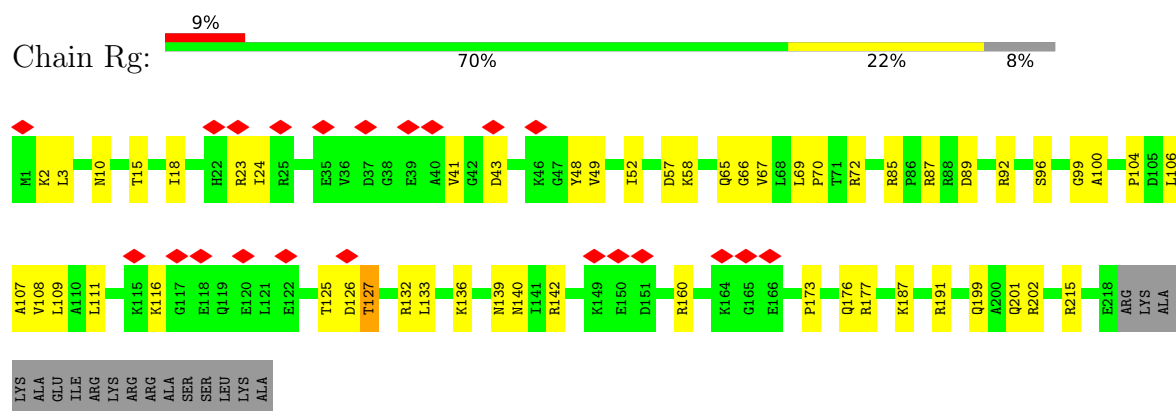
• Molecule 62: 40S ribosomal protein S5



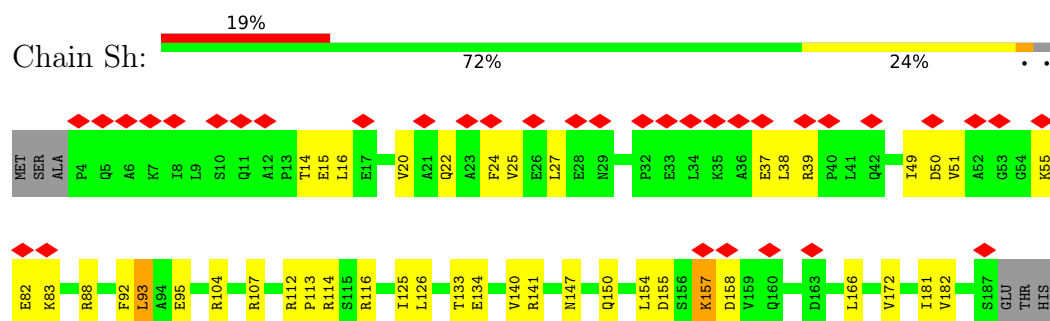
• Molecule 63: 40S ribosomal protein S6-A



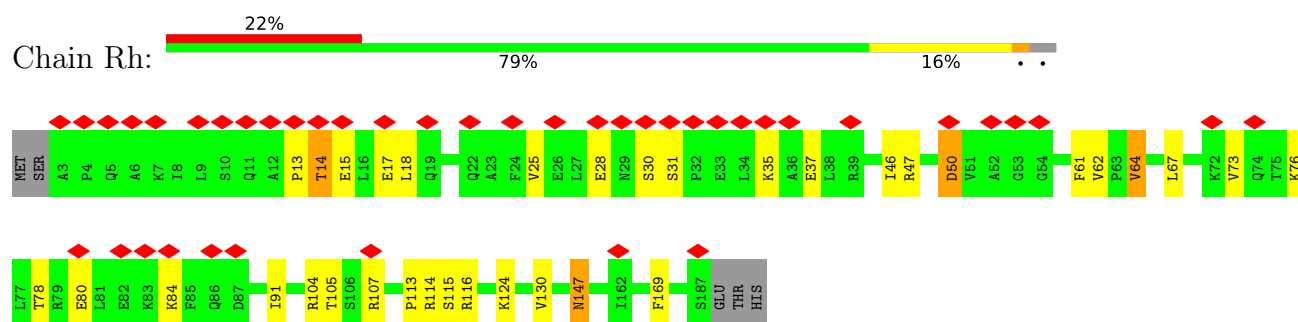
• Molecule 63: 40S ribosomal protein S6-A



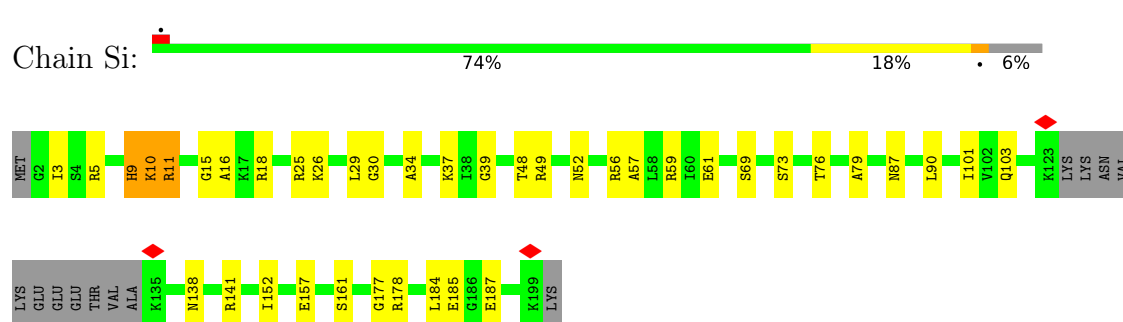
- Molecule 64: 40S ribosomal protein S7-A



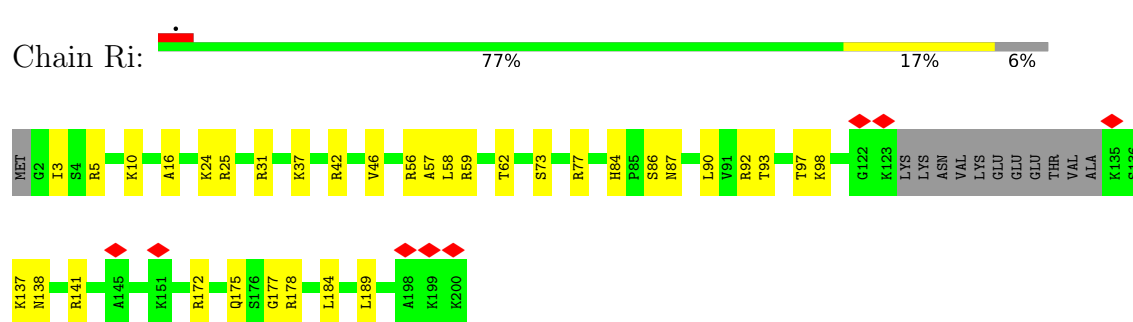
- Molecule 64: 40S ribosomal protein S7-A



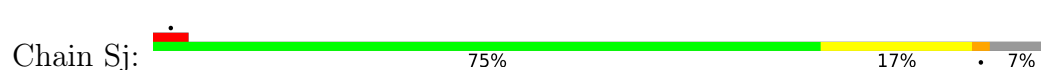
- Molecule 65: 40S ribosomal protein S8-A

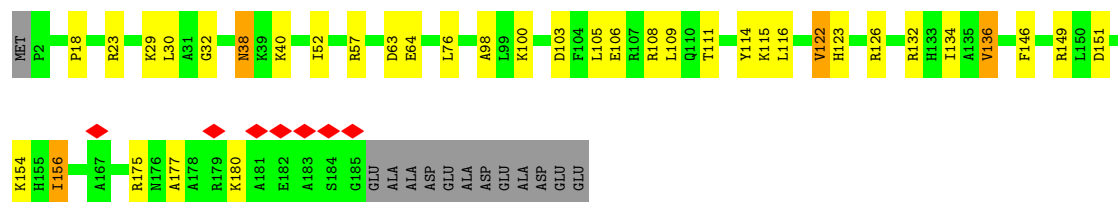


- Molecule 65: 40S ribosomal protein S8-A

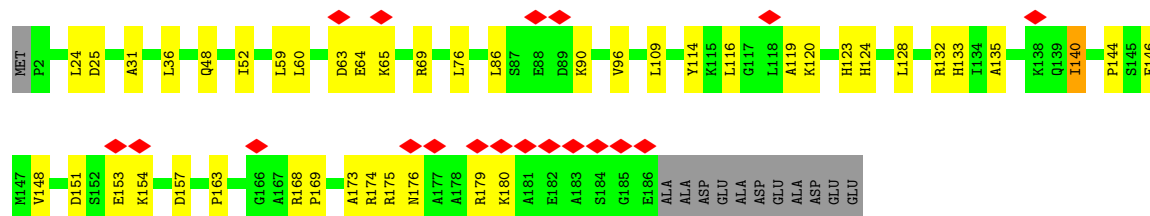
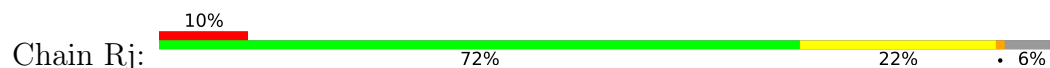


- Molecule 66: 40S ribosomal protein S9-A





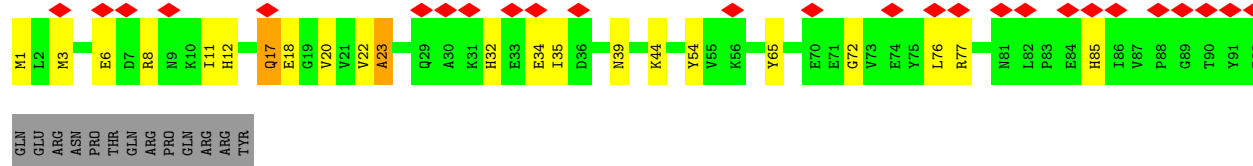
- Molecule 66: 40S ribosomal protein S9-A



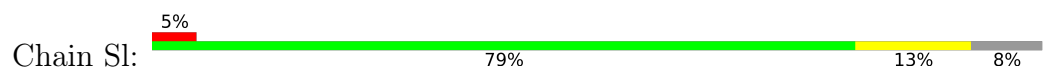
- Molecule 67: 40S ribosomal protein S10-A



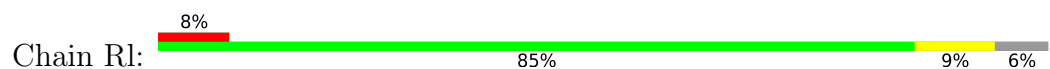
- Molecule 67: 40S ribosomal protein S10-A



- Molecule 68: 40S ribosomal protein S11-A

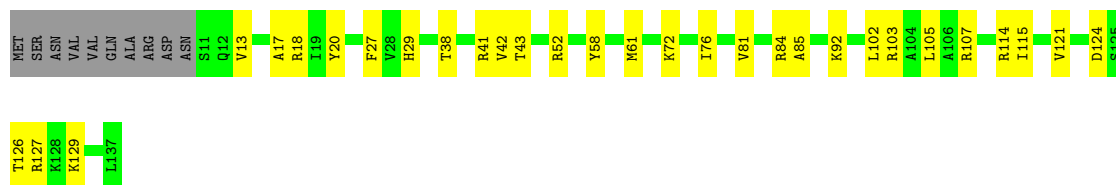


- Molecule 68: 40S ribosomal protein S11-A



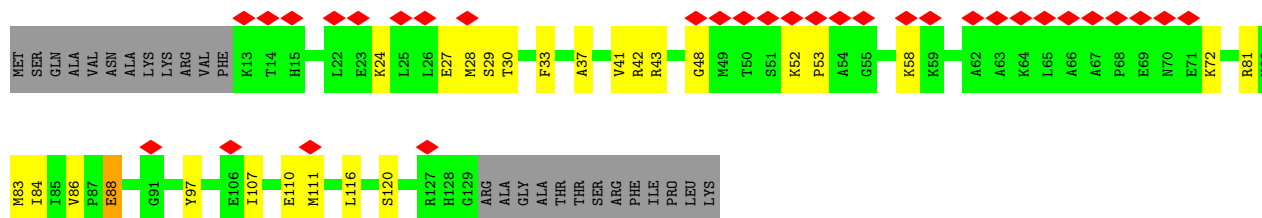


Chain So: 



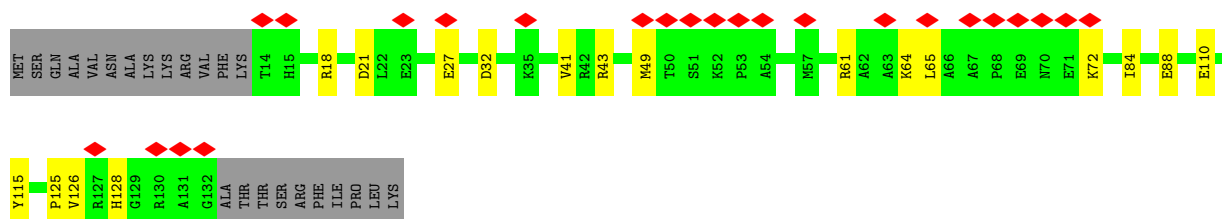
- Molecule 72: 40S ribosomal protein S15

Chain Sp: 



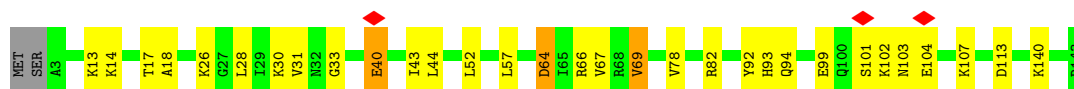
- Molecule 72: 40S ribosomal protein S15

Chain Rp: 



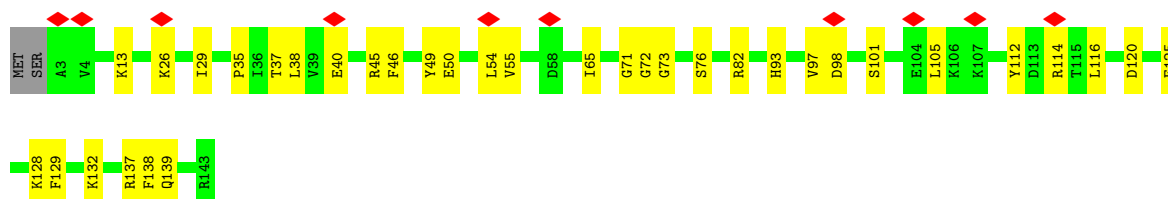
- Molecule 73: 40S ribosomal protein S16-A

Chain Sq: 

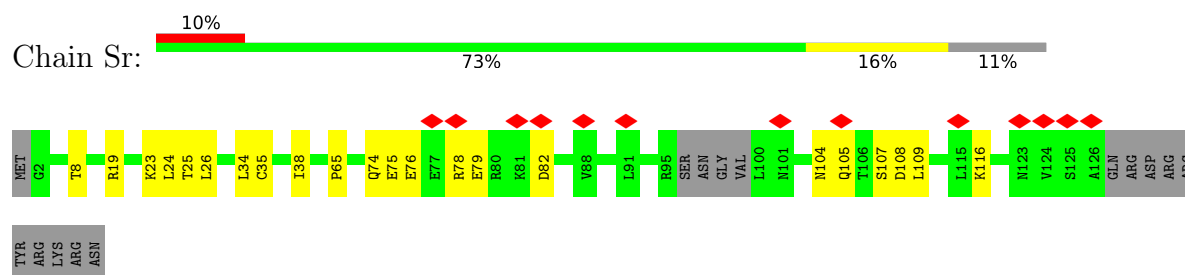


- Molecule 73: 40S ribosomal protein S16-A

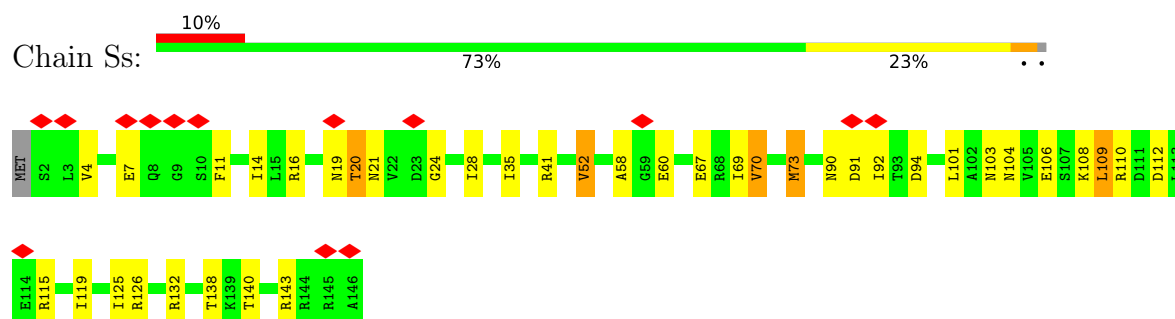
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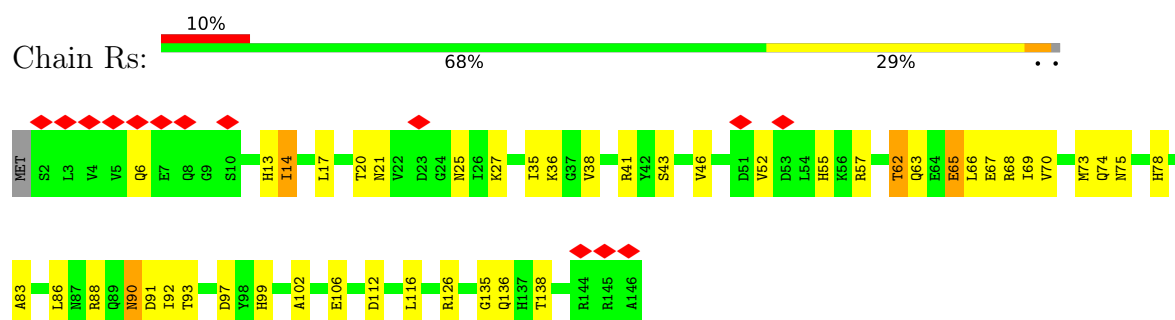
- Molecule 74: 40S ribosomal protein S17-B



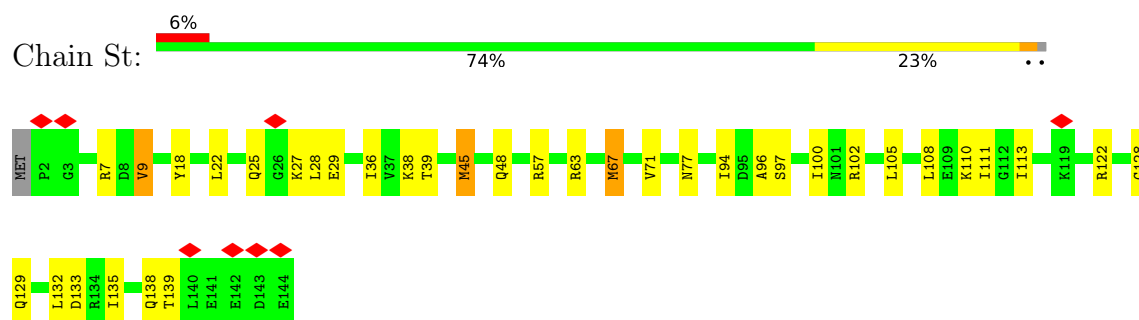
- Molecule 75: 40S ribosomal protein S18-A



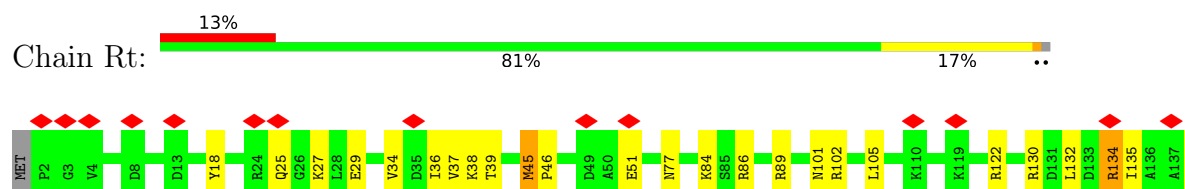
- Molecule 75: 40S ribosomal protein S18-A

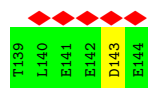


- Molecule 76: 40S ribosomal protein S19-A

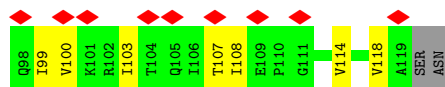


- Molecule 76: 40S ribosomal protein S19-A

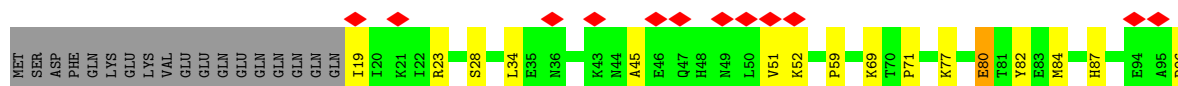




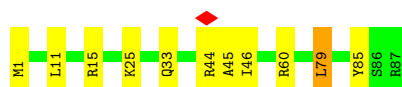
- Molecule 77: Small ribosomal subunit protein uS10



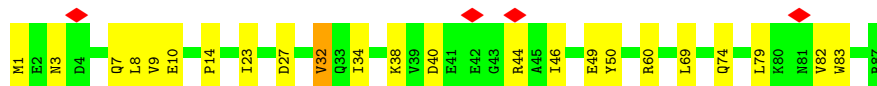
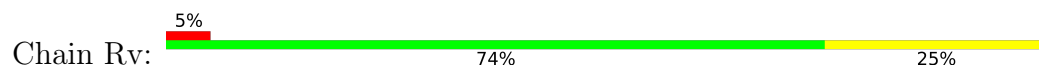
- Molecule 77: Small ribosomal subunit protein uS10



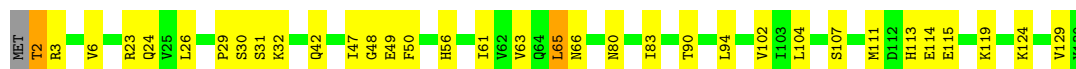
- Molecule 78: Small ribosomal subunit protein eS21A



- Molecule 78: Small ribosomal subunit protein eS21A



- Molecule 79: 40S ribosomal protein S22-A



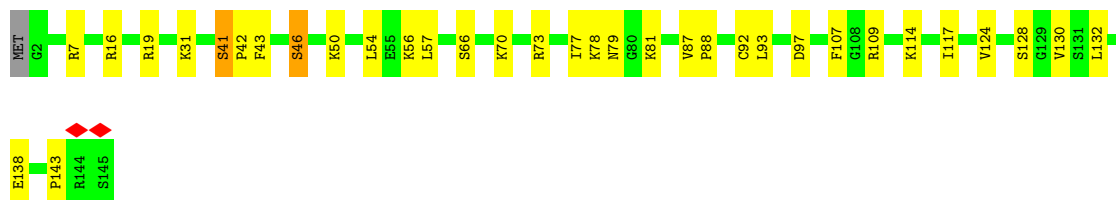
- Molecule 79: 40S ribosomal protein S22-A

Chain Rw:  86% 13% .



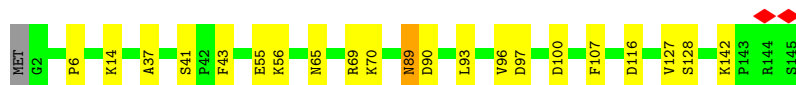
- Molecule 80: 40S ribosomal protein S23-A

Chain Sx:  76% 22% ..



- Molecule 80: 40S ribosomal protein S23-A

Chain Rx:  85% 14% ..



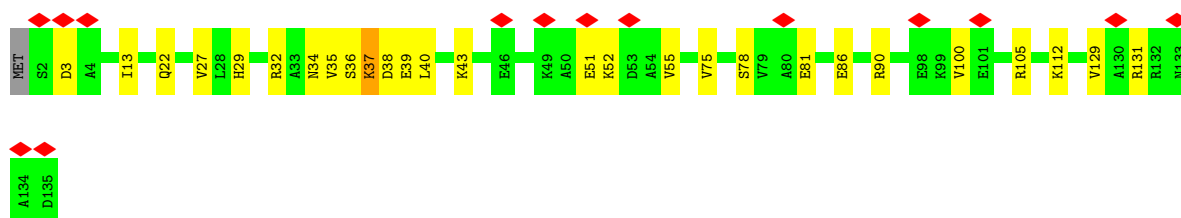
- Molecule 81: 40S ribosomal protein S24-A

Chain Sy:  84% 13% ..



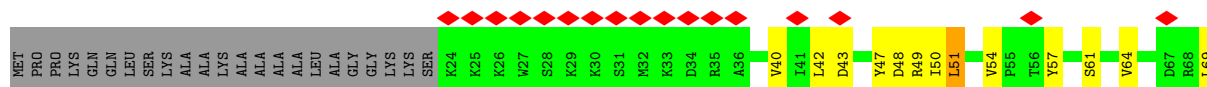
- Molecule 81: 40S ribosomal protein S24-A

Chain Ry:  10% 79% 19% ..



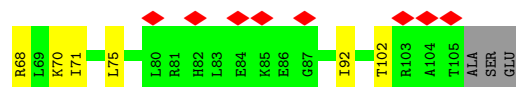
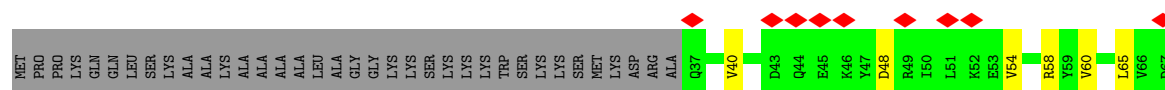
- Molecule 82: 40S ribosomal protein S25-A

Chain Sz:  19% 55% 19% 24%

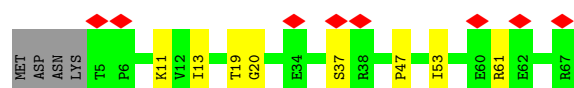
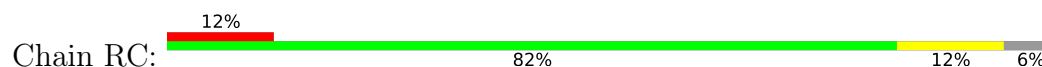




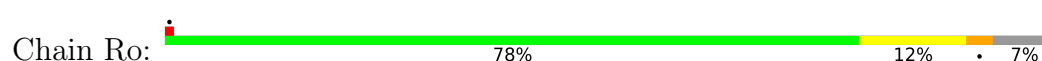
- Molecule 82: 40S ribosomal protein S25-A



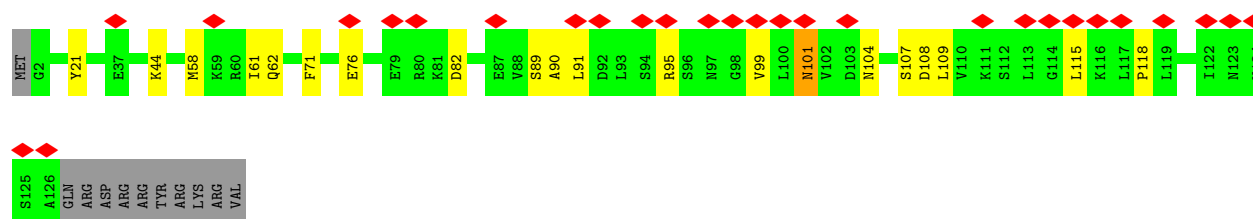
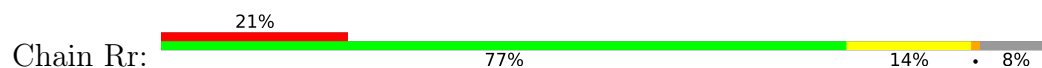
- Molecule 83: 40S ribosomal protein S28-A



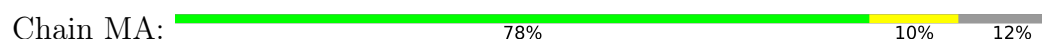
- Molecule 84: 40S ribosomal protein S14-B



- Molecule 85: 40S ribosomal protein S17-A

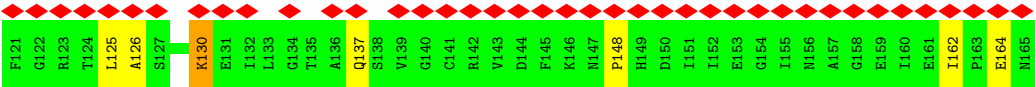


- Molecule 86: 60S ribosomal protein L6-A

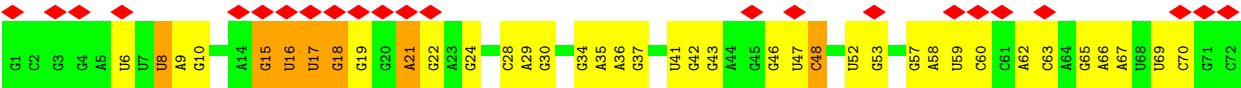




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C3092	A2936	A2801	G2677	U	G2457	U2347	A2207	A	G	G	A1696	A1697	U1570
C3096	C2942	A2678	A2679	U	A2458	A2357	A2208	A	A	U	A1571	A1572	A1571
C3097	G2943	A2679	A2679	U	U2459	A2358	U2209	U	U	C	U1705	U1705	U1572
U3121	G2945	A2808	U2683	U	A2461	A2363	A2213	A	U	A	C1574	C1574	C1573
A3122	A2946	A2812	C2684	U	A2462	A2546	A2214	A	C	A	U1716	U1716	U1574
A3130	G2947	A2813	A2689	U	U2463	A2372	G2218	C2094	C	A	U1717	U1717	A1580
U3131	C2948	A2814	A2691	U	U2464	A2373	A2219	C2095	C	C	G1829	G1829	G1576
A3142	G2951	A2815	A2691	U	G2465	G2375	A2220	C2101	C	G	U1831	U1831	A1581
C3143	C2959	A2816	A2696	U	G2466	G2376	A2223	U2102	C	C	A1842	U1724	G1582
U3155	G2960	A2817	A2697	U	G2467	G2377	A2224	A2103	C	C	U1730	U1730	A1583
U3156	C2961	U2818	A2698	U	A2468	C2383	U2225	A2107	C	G	U1737	U1737	A1587
U3157	G2966	G2828	A2704	U	C2470	U2388	A2226	G2110	C	U	G1861	U1741	A1588
U3160	A2967	C2836	A2705	U	U2471	A2394	A2229	G2111	C	C	G1863	U1742	A1589
A3168	G2968	C2844	G2714	U	U2472	G2394	A2244	U2112	C	U	A1864	U1742	G1590
U3179	C2970	A2845	G2720	U	G2473	A2397	G2253	A2113	C	A	G1878	G1748	A1593
A3180	G2972	C2852	U2724	U	G2474	A2401	U2254	C2114	C	U	A1867	A1749	C1596
U3181	C2977	U2860	A2736	U	G2475	A2402	A2255	G2122	C	G	G1879	A1750	C1597
U3182	G2983	U2861	A2747	U	C2476	A2403	G2261	U2129	C	U	U1888	G1751	A1605
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U3199	G3004	C2870	A2751	U	A2484	U2411	C2267	A2131	C	C	A1899	U1763	G1617
G3204	U3042	G2871	G2752	U	A2485	G2412	U2268	U2140	C	U	G1899	U1764	U1629
G3205	A3024	A2872	G2753	U	A2486	U2417	U2269	U2141	C	U	U1785	U1785	U1630
U3207	U3056	U2875	G2754	U	A2487	G2418	A2270	A2143	C	U	G1786	G1786	A1631
A3210	G3059	C2876	G2755	U	A2488	A2419	A2271	A2144	C	U	A1787	A1787	A1632
U3214	U3066	U2882	C2756	U	C2489	U2421	G2272	C2146	C	U	U1645	U1645	G1635
A3215	C3067	U2883	G2757	U	A2491	G2425	C2278	A2152	C	U	G1646	G1646	G1638
G3216	U3068	U2887	U2767	U	C2492	U2426	A2279	U2153	C	U	C1657	C1657	A1642
C3217	G3075	A2888	U2768	U	U2493	U2427	A2280	A2158	C	C	A1797	A1797	A1643
A3218	U3078	C2889	A2769	U	A2494	U2428	A2281	U2159	C	U	A1799	A1800	G1661
G3219	U3079	U2895	C2772	U	C2495	G2435	U2282	G2160	C	U	A1800	A1800	G1662
U3231		A2930	G2777	U	U2496	A2438	C2304	G2161	C	U	G1952	G1952	G1666
		C2931	G2778	U	U2497	A2439	G2307	G2168	C	C	G	G	A1806
			A2792	U	U2498	G2440	U2340	G2169	C	U	U	U	A1807
			G2793	U	A2500	A2441	A2313	U2170	C	U	A	A	G1668
			G2794	U	U2501	G2444	G2314	G2171	C	U	G	G	A1679
			U2795	U	A2502	A2445	G2315	U2176	C	U	U	U	A1812
			G2796	U	A2511	A2446	G2316	G2185	C	C	U	U	A1813
			A2799	U	U2514	A2447	U2335	G2188	C	C	U	U	A1814
				U	A2515	G2448	U2336	A2188	C	C	U	U	U1815
				U	G2522	G2450	U2344	U2193	C	C	U	U	
				U	A2523	G2451	A2345	G2194	C	C	U	U	
				U	A2535	G2452			C	C	U	U	
				U	A2536	U2453			C	C	U	U	
				C					A	A			



• Molecule 91: tRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	189911	Depositor
Resolution determination method	OTHER	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	43.6	Depositor
Minimum defocus (nm)	400	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	5.572	Depositor
Minimum map value	-0.178	Depositor
Average map value	0.020	Depositor
Map value standard deviation	0.125	Depositor
Recommended contour level	0.44	Depositor
Map size ($\text{\AA}$)	655.21497, 655.21497, 655.21497	wwPDB
Map dimensions	627, 627, 627	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.045, 1.045, 1.045	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: A2M, 5MC, ZN, MG, UR3, K, SPD, OMC, YYG, OMU, 1MA, OMG

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	CC	0.24	0/132	0.48	0/175
2	CM	0.21	0/927	0.40	0/1434
3	CN	0.16	0/1053	0.40	0/1414
4	CP	0.36	3/1810 (0.2%)	0.30	0/2817
5	L1	0.35	0/74617	0.38	0/116334
6	L2	0.35	0/3746	0.37	0/5832
6	M2	0.33	0/3746	0.35	0/5832
7	L3	0.29	0/2883	0.31	0/4491
7	M3	0.28	0/2883	0.30	0/4491
8	LA	0.24	0/1327	0.43	0/1791
9	LB	0.32	0/1821	0.45	0/2451
9	MB	0.28	0/1821	0.42	0/2451
10	LC	0.27	0/1836	0.53	0/2481
10	MC	0.25	0/1836	0.48	0/2481
11	LD	0.25	0/1529	0.47	0/2060
11	MD	0.24	0/1539	0.43	0/2073
12	LE	0.28	0/1801	0.50	1/2416 (0.0%)
12	ME	0.25	0/1779	0.40	0/2386
13	LF	0.26	0/1371	0.63	3/1838 (0.2%)
13	MF	0.24	0/1374	0.54	0/1842
14	LG	0.29	0/1568	0.53	0/2106
14	MG	0.28	0/1568	0.50	0/2106
15	LH	0.26	0/1068	0.41	0/1438
15	MH	0.23	0/1068	0.37	0/1438
16	LI	0.32	0/1757	0.42	0/2354
16	MI	0.31	0/1757	0.41	0/2354
17	LJ	0.30	0/1585	0.46	1/2128 (0.0%)
17	MJ	0.27	0/1585	0.45	0/2128
18	LK	0.30	0/1439	0.47	0/1938
18	MK	0.28	0/1245	0.45	0/1676
19	LL	0.30	0/1465	0.48	0/1965
19	ML	0.27	0/1465	0.44	0/1965

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
20	LM	0.27	0/1532	0.46	0/2043
20	MM	0.25	0/1440	0.49	0/1921
21	LN	0.30	0/1473	0.50	0/1980
21	MN	0.28	0/1481	0.45	0/1990
22	LO	0.30	0/1300	0.49	0/1743
22	MO	0.28	0/1300	0.48	1/1743 (0.1%)
23	La	0.29	0/1018	0.42	0/1369
23	Ma	0.28	0/978	0.46	0/1316
24	Lb	0.29	0/701	0.50	0/934
24	Mb	0.24	0/701	0.43	0/934
25	Lc	0.30	0/836	0.52	0/1104
25	Mc	0.26	0/831	0.49	0/1097
26	Ld	0.29	0/230	0.32	0/296
26	Md	0.28	0/234	0.56	0/300
27	Le	0.32	0/423	0.52	0/562
27	Me	0.24	0/423	0.35	0/562
28	Lf	0.34	0/443	0.43	0/588
28	Mf	0.31	0/443	0.64	0/588
29	Lg	0.23	0/618	0.44	0/826
29	Mg	0.24	0/618	0.48	0/826
30	Lh	0.31	0/685	0.42	0/908
30	Mh	0.33	0/680	0.51	0/901
31	Li	0.26	0/772	0.45	0/1026
31	Mi	0.24	0/778	0.49	0/1034
32	Lj	0.27	0/978	0.42	0/1301
32	Mj	0.26	0/978	0.46	0/1301
33	Lk	0.29	0/846	0.39	0/1130
33	Mk	0.27	0/871	0.40	0/1164
34	Ll	0.33	0/868	0.42	0/1168
34	Ml	0.31	0/868	0.42	0/1168
35	Lm	0.30	0/1038	0.44	0/1390
35	Mm	0.27	0/1041	0.37	0/1394
36	Ln	0.29	0/890	0.45	0/1196
36	Mn	0.28	0/897	0.58	3/1205 (0.2%)
37	Lo	0.27	0/745	0.48	0/1001
37	Mo	0.25	0/750	0.44	0/1008
38	Lp	0.29	0/473	0.65	3/629 (0.5%)
38	Mp	0.25	0/473	0.40	0/629
39	Lq	0.33	0/1204	0.59	0/1612
39	Mq	0.31	0/1204	0.52	0/1612
40	Lr	0.26	0/1118	0.48	0/1497
40	Mr	0.25	0/1118	0.48	0/1497
41	Ls	0.27	0/995	0.46	0/1329

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
41	Ms	0.26	0/1004	0.45	1/1341 (0.1%)
42	Lt	0.28	0/979	0.48	0/1321
42	Mt	0.29	0/974	0.51	0/1314
43	Lu	0.26	0/850	0.54	0/1152
43	Mu	0.24	0/533	0.43	0/707
44	Lv	0.23	0/812	0.54	0/1099
44	Mv	0.28	0/786	0.64	0/1065
45	Lw	0.32	0/1933	0.49	0/2598
45	Mw	0.29	0/1948	0.42	0/2617
46	Lx	0.31	0/3146	0.51	0/4228
46	Mx	0.27	0/3146	0.45	0/4228
47	Ly	0.31	0/2800	0.47	0/3790
47	My	0.27	0/2800	0.44	0/3790
48	Lz	0.23	0/2400	0.46	0/3239
48	Mz	0.21	0/2425	0.40	0/3271
49	R1	0.23	0/41891	0.37	0/65273
49	S1	0.28	0/42211	0.39	3/65773 (0.0%)
50	RA	0.24	0/782	0.58	0/1047
50	SA	0.30	0/782	0.66	2/1047 (0.2%)
51	RB	0.22	0/620	0.61	0/838
51	SB	0.26	0/620	0.59	1/838 (0.1%)
52	SC	0.26	0/488	0.65	0/656
53	RD	0.17	0/452	0.41	0/600
53	SD	0.24	0/452	0.47	0/600
54	RE	0.31	0/391	0.55	0/520
54	SE	0.23	0/480	0.57	0/639
55	RF	0.21	0/557	0.59	1/749 (0.1%)
55	SF	0.23	0/567	0.67	0/764
56	RG	0.14	0/2456	0.42	0/3343
56	SG	0.20	0/2436	0.56	3/3318 (0.1%)
57	Ra	0.24	0/1623	0.58	0/2222
57	Sa	0.26	0/1644	0.63	1/2249 (0.0%)
58	Rb	0.20	0/1748	0.45	0/2352
58	Sb	0.26	0/1823	0.63	1/2447 (0.0%)
59	Rc	0.22	0/1665	0.44	0/2263
59	Sc	0.29	0/1656	0.57	0/2251
60	Rd	0.21	0/1759	0.51	0/2368
60	Sd	0.21	0/1754	0.47	1/2361 (0.0%)
61	Re	0.19	0/2109	0.47	0/2839
61	Se	0.26	0/2097	0.58	1/2823 (0.0%)
62	Rf	0.20	0/1629	0.52	0/2202
62	Sf	0.23	0/1625	0.53	3/2197 (0.1%)
63	Rg	0.15	0/1779	0.43	1/2379 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
63	Sg	0.20	0/1839	0.48	1/2460 (0.0%)
64	Rh	0.20	0/1511	0.50	0/2036
64	Sh	0.25	0/1498	0.64	2/2019 (0.1%)
65	Ri	0.16	0/1514	0.34	0/2021
65	Si	0.28	0/1501	0.59	0/2006
66	Rj	0.20	0/1519	0.50	1/2035 (0.0%)
66	Sj	0.23	0/1504	0.52	0/2016
67	Rk	0.24	0/757	0.60	0/1022
67	Sk	0.34	0/769	0.93	1/1039 (0.1%)
68	Rl	0.21	0/1194	0.41	0/1610
68	Sl	0.29	0/1185	0.58	0/1598
69	Rm	0.23	0/898	0.70	1/1220 (0.1%)
69	Sm	0.29	0/883	0.90	3/1199 (0.3%)
70	Rn	0.24	0/1215	0.62	1/1638 (0.1%)
70	Sn	0.28	0/1215	0.59	0/1638
71	So	0.28	0/937	0.68	0/1261
72	Rp	0.21	0/959	0.59	1/1288 (0.1%)
72	Sp	0.28	0/936	0.71	1/1259 (0.1%)
73	Rq	0.20	0/1125	0.53	0/1510
73	Sq	0.23	0/1125	0.58	0/1510
74	Sr	0.26	0/957	0.66	1/1283 (0.1%)
75	Rs	0.23	0/1211	0.61	1/1628 (0.1%)
75	Ss	0.27	0/1211	0.65	0/1628
76	Rt	0.22	0/1130	0.59	2/1517 (0.1%)
76	St	0.28	0/1130	0.74	3/1517 (0.2%)
77	Ru	0.24	0/815	0.63	0/1102
77	Su	0.25	0/807	0.64	0/1091
78	Rv	0.24	0/693	0.58	0/935
78	Sv	0.28	0/682	0.60	0/921
79	Rw	0.24	0/1038	0.45	0/1395
79	Sw	0.28	0/1038	0.48	0/1395
80	Rx	0.23	0/1139	0.47	0/1518
80	Sx	0.28	0/1139	0.58	0/1518
81	Ry	0.20	0/1087	0.56	1/1449 (0.1%)
81	Sy	0.22	0/1087	0.54	0/1449
82	Rz	0.26	0/566	0.59	1/761 (0.1%)
82	Sz	0.25	0/661	0.70	0/888
83	RC	0.22	0/499	0.56	0/670
84	Ro	0.29	0/960	0.68	3/1290 (0.2%)
85	Rr	0.22	0/1010	0.57	0/1355
86	MA	0.24	0/1251	0.46	0/1682
87	M1	0.33	1/75384 (0.0%)	0.36	1/117530 (0.0%)
88	DQ	0.17	0/1836	0.29	0/2859

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
89	MQ	0.17	0/1558	0.48	0/2107
90	MP	0.15	0/1210	0.37	0/1627
91	DP	0.14	0/1788	0.28	0/2786
All	All	0.29	4/435297 (0.0%)	0.43	56/639512 (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
9	MB	0	1
10	LC	0	3
11	LD	0	1
13	LF	0	1
14	LG	0	2
15	LH	0	1
16	LI	0	1
17	LJ	0	1
20	LM	0	1
25	Mc	0	1
28	Mf	0	1
32	Lj	0	1
38	Lp	0	1
40	Mr	0	1
42	Lt	0	1
45	Lw	0	1
46	Lx	0	4
47	Ly	0	2
47	My	0	1
50	SA	0	1
55	SF	0	1
57	Ra	0	1
58	Sb	0	2
61	Re	0	1
61	Se	0	1
63	Sg	0	1
64	Rh	0	2
64	Sh	0	1
65	Si	0	1
67	Rk	0	1
69	Sm	0	6

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Mol	Chain	#Chirality outliers	#Planarity outliers
72	Sp	0	1
73	Rq	0	1
73	Sq	0	1
75	Rs	0	1
75	Ss	0	1
77	Ru	0	1
80	Sx	0	2
82	Rz	0	1
All	All	0	54

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	CP	34	I	C5-C6	6.44	1.52	1.39
4	CP	34	I	N3-C4	6.14	1.48	1.35
87	M1	2946	A2M	O3'-P	5.23	1.61	1.56
4	CP	34	I	C2-N3	5.17	1.46	1.35

All (56) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	Mn	110	GLU	CA-CB-CG	8.21	130.51	114.10
76	Rt	29	GLU	CA-CB-CG	7.60	129.31	114.10
70	Rn	36	GLN	CA-CB-CG	7.28	128.66	114.10
63	Rg	69	LEU	CA-CB-CG	6.81	140.15	116.30
13	LF	108	GLU	CA-C-N	6.80	134.53	121.54
13	LF	108	GLU	C-N-CA	6.80	134.53	121.54
36	Mn	110	GLU	CB-CG-CD	6.78	124.13	112.60
61	Se	193	GLY	N-CA-C	6.14	127.73	113.18
81	Ry	51	GLU	CA-CB-CG	6.12	126.34	114.10
12	LE	185	ARG	CA-CB-CG	6.08	126.25	114.10
57	Sa	27	ARG	CA-CB-CG	6.07	126.24	114.10
36	Mn	97	LEU	CA-CB-CG	5.92	137.03	116.30
62	Sf	65	ARG	CA-CB-CG	5.87	125.83	114.10
51	SB	36	LYS	CB-CG-CD	5.83	124.70	111.30
49	S1	1791	A	C2'-C3'-O3'	5.82	118.22	109.50
76	St	29	GLU	CA-CB-CG	5.81	125.72	114.10
69	Sm	68	GLU	CA-CB-CG	5.78	125.65	114.10
55	RF	107	LYS	CB-CG-CD	5.74	124.50	111.30
49	S1	322	G	C2'-C3'-O3'	5.73	118.09	109.50
38	Lp	24	PRO	CA-C-N	5.69	132.41	121.54
38	Lp	24	PRO	C-N-CA	5.69	132.41	121.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
67	Sk	31	LYS	CB-CG-CD	5.67	124.33	111.30
62	Sf	59	VAL	CA-C-N	5.59	132.21	121.54
62	Sf	59	VAL	C-N-CA	5.59	132.21	121.54
69	Rm	62	LEU	CA-CB-CG	5.57	135.79	116.30
38	Lp	25	LYS	N-CA-CB	5.56	119.89	110.49
66	Rj	65	LYS	CA-CB-CG	5.53	125.16	114.10
60	Sd	78	LYS	CA-CB-CG	5.53	125.15	114.10
72	Sp	72	LYS	CB-CG-CD	5.44	123.82	111.30
74	Sr	116	LYS	CB-CG-CD	5.44	123.82	111.30
56	SG	111	MET	CB-CG-SD	5.43	129.00	112.70
76	St	67	MET	CB-CG-SD	5.40	128.90	112.70
82	Rz	70	LYS	CB-CG-CD	5.38	123.68	111.30
84	Ro	129	LYS	CB-CG-CD	5.34	123.58	111.30
41	Ms	126	LEU	CA-CB-CG	5.34	134.98	116.30
63	Sg	69	LEU	CA-CB-CG	5.28	134.79	116.30
72	Rp	72	LYS	CA-CB-CG	5.28	124.67	114.10
84	Ro	129	LYS	CA-CB-CG	5.25	124.60	114.10
56	SG	53	LYS	CA-C-N	5.25	131.57	121.54
56	SG	53	LYS	C-N-CA	5.25	131.57	121.54
76	St	45	MET	CB-CG-SD	5.24	128.41	112.70
87	M1	406	G	O4'-C1'-N9	5.22	116.03	108.20
76	Rt	45	MET	CB-CG-SD	5.21	128.32	112.70
49	S1	322	G	P-O3'-C3'	5.20	128.00	120.20
58	Sb	210	ILE	CG1-CB-CG2	-5.20	95.11	110.70
17	LJ	187	GLU	CA-CB-CG	5.19	124.48	114.10
13	LF	88	GLU	CA-CB-CG	5.13	124.36	114.10
69	Sm	38	HIS	CA-C-N	5.13	131.33	121.54
69	Sm	38	HIS	C-N-CA	5.13	131.33	121.54
50	SA	7	SER	CA-C-N	5.12	131.32	121.54
50	SA	7	SER	C-N-CA	5.12	131.32	121.54
64	Sh	157	LYS	CA-CB-CG	5.11	124.31	114.10
75	Rs	65	GLU	CA-CB-CG	5.10	124.30	114.10
84	Ro	124	ASP	CA-CB-CG	5.09	117.69	112.60
64	Sh	157	LYS	CB-CG-CD	5.07	122.96	111.30
22	MO	127	GLN	CA-CB-CG	5.07	124.24	114.10

There are no chirality outliers.

All (54) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
10	LC	158	ASP	Peptide
10	LC	30	THR	Peptide

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Mol	Chain	Res	Type	Group
10	LC	76	ALA	Peptide
11	LD	21	LYS	Peptide
13	LF	115	LYS	Peptide
14	LG	46	ILE	Peptide
14	LG	75	PHE	Peptide
15	LH	12	TRP	Peptide
16	LI	92	LEU	Peptide
17	LJ	110	PRO	Peptide
20	LM	52	LYS	Peptide
32	Lj	83	LYS	Peptide
38	Lp	19	ASN	Peptide
42	Lt	43	ALA	Peptide
45	Lw	70	ARG	Sidechain
46	Lx	127	LYS	Peptide
46	Lx	139	GLN	Peptide
46	Lx	141	GLY	Peptide
46	Lx	3	HIS	Peptide
47	Ly	13	GLY	Peptide
47	Ly	318	LEU	Peptide
9	MB	232	ARG	Peptide
25	Mc	7	THR	Peptide
28	Mf	32	ASN	Peptide
40	Mr	102	GLU	Peptide
47	My	318	LEU	Peptide
57	Ra	184	LEU	Peptide
61	Re	195	ILE	Peptide
64	Rh	130	VAL	Peptide
64	Rh	64	VAL	Peptide
67	Rk	23	ALA	Peptide
73	Rq	40	GLU	Peptide
75	Rs	90	ASN	Peptide
77	Ru	69	LYS	Peptide
82	Rz	68	ARG	Sidechain
50	SA	9	GLY	Peptide
55	SF	144	CYS	Peptide
58	Sb	211	HIS	Peptide
58	Sb	81	PHE	Peptide
61	Se	42	LEU	Peptide
63	Sg	68	LEU	Peptide
64	Sh	64	VAL	Peptide
65	Si	9	HIS	Peptide
69	Sm	108	ARG	Peptide

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Mol	Chain	Res	Type	Group
69	Sm	110	GLY	Peptide
69	Sm	130	THR	Peptide
69	Sm	137	MET	Peptide
69	Sm	84	ASN	Peptide
69	Sm	90	LYS	Peptide
72	Sp	27	GLU	Peptide
73	Sq	40	GLU	Peptide
75	Ss	90	ASN	Peptide
80	Sx	41	SER	Peptide
80	Sx	88	PRO	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	CC	129	0	120	2	0
2	CM	838	0	421	6	0
3	CN	1046	0	1088	14	0
4	CP	1621	0	821	14	0
5	L1	66660	0	33498	364	0
6	L2	3353	0	1695	14	0
6	M2	3353	0	1695	26	0
7	L3	2579	0	1304	23	0
7	M3	2579	0	1304	9	0
8	LA	1305	0	1372	19	0
9	LB	1784	0	1862	25	0
9	MB	1784	0	1862	9	0
10	LC	1804	0	1877	25	0
10	MC	1804	0	1877	12	0
11	LD	1508	0	1572	21	0
11	MD	1518	0	1587	14	0
12	LE	1764	0	1804	24	0
12	ME	1743	0	1785	14	0
13	LF	1350	0	1381	24	0
13	MF	1353	0	1383	23	0
14	LG	1543	0	1608	22	0
14	MG	1543	0	1608	14	0
15	LH	1053	0	1149	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
15	MH	1053	0	1149	7	0
16	LI	1720	0	1779	24	0
16	MI	1720	0	1779	18	0
17	LJ	1555	0	1659	16	0
17	MJ	1555	0	1659	15	0
18	LK	1416	0	1433	9	0
18	MK	1222	0	1231	7	0
19	LL	1441	0	1543	19	0
19	ML	1441	0	1543	13	0
20	LM	1515	0	1606	17	0
20	MM	1423	0	1510	14	0
21	LN	1437	0	1475	21	0
21	MN	1445	0	1487	9	0
22	LO	1276	0	1323	25	0
22	MO	1276	0	1323	9	0
23	La	1003	0	1048	6	0
23	Ma	963	0	1015	17	0
24	Lb	694	0	735	14	0
24	Mb	694	0	734	1	0
25	Lc	824	0	888	14	0
25	Mc	819	0	886	5	0
26	Ld	229	0	273	2	0
26	Md	233	0	282	6	0
27	Le	417	0	455	2	0
27	Me	417	0	455	4	0
28	Lf	436	0	475	7	0
28	Mf	436	0	475	8	0
29	Lg	612	0	682	6	0
29	Mg	612	0	682	8	0
30	Lh	670	0	673	6	0
30	Mh	665	0	668	8	0
31	Li	766	0	844	11	0
31	Mi	771	0	849	9	0
32	Lj	969	0	1078	10	0
32	Mj	969	0	1078	6	0
33	Lk	836	0	897	8	0
33	Mk	861	0	918	11	0
34	Ll	850	0	880	12	0
34	Ml	850	0	880	8	0
35	Lm	1017	0	1081	11	0
35	Mm	1020	0	1090	7	0
36	Ln	876	0	912	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
36	Mn	883	0	918	8	0
37	Lo	737	0	792	8	0
37	Mo	742	0	797	11	0
38	Lp	462	0	491	3	0
38	Mp	462	0	491	6	0
39	Lq	1173	0	1215	27	0
39	Mq	1173	0	1215	16	0
40	Lr	1092	0	1155	14	0
40	Mr	1092	0	1155	9	0
41	Ls	984	0	1075	10	0
41	Ms	993	0	1081	13	0
42	Lt	964	0	1025	15	0
42	Mt	959	0	1023	5	0
43	Lu	836	0	706	8	0
43	Mu	521	0	551	0	0
44	Lv	796	0	812	10	0
44	Mv	770	0	780	4	0
45	Lw	1899	0	1957	32	0
45	Mw	1914	0	1981	8	0
46	Lx	3075	0	3142	35	0
46	Mx	3075	0	3142	25	0
47	Ly	2748	0	2859	27	0
47	My	2748	0	2859	22	0
48	Lz	2351	0	2294	35	0
48	Mz	2375	0	2325	15	0
49	R1	37455	0	18845	350	0
49	S1	37739	0	18987	321	0
50	RA	769	0	818	12	0
50	SA	769	0	818	11	0
51	RB	610	0	631	8	0
51	SB	610	0	633	8	0
52	SC	486	0	522	6	0
53	RD	442	0	432	6	0
53	SD	442	0	428	13	0
54	RE	385	0	431	8	0
54	SE	472	0	521	9	0
55	RF	547	0	542	7	0
55	SF	556	0	546	12	0
56	RG	2403	0	2350	41	0
56	SG	2383	0	2332	52	0
57	Ra	1583	0	1578	33	0
57	Sa	1603	0	1610	33	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
58	Rb	1722	0	1793	25	0
58	Sb	1798	0	1890	27	0
59	Rc	1635	0	1723	28	0
59	Sc	1626	0	1715	21	0
60	Rd	1734	0	1817	25	0
60	Sd	1729	0	1812	23	0
61	Re	2068	0	2154	32	0
61	Se	2056	0	2140	26	0
62	Rf	1609	0	1675	21	0
62	Sf	1605	0	1668	19	0
63	Rg	1755	0	1846	42	0
63	Sg	1815	0	1894	36	0
64	Rh	1486	0	1576	27	0
64	Sh	1473	0	1555	25	0
65	Ri	1489	0	1525	29	0
65	Si	1476	0	1501	27	0
66	Rj	1494	0	1573	31	0
66	Sj	1479	0	1556	27	0
67	Rk	741	0	691	16	0
67	Sk	752	0	719	17	0
68	Rl	1168	0	1233	7	0
68	Sl	1159	0	1225	11	0
69	Rm	890	0	887	23	0
69	Sm	875	0	878	17	0
70	Rn	1192	0	1255	18	0
70	Sn	1192	0	1255	14	0
71	So	926	0	950	23	0
72	Rp	939	0	968	13	0
72	Sp	916	0	941	17	0
73	Rq	1105	0	1166	20	0
73	Sq	1105	0	1166	18	0
74	Sr	948	0	990	14	0
75	Rs	1192	0	1222	28	0
75	Ss	1192	0	1222	26	0
76	Rt	1112	0	1124	17	0
76	St	1112	0	1124	28	0
77	Ru	805	0	874	14	0
77	Su	797	0	863	16	0
78	Rv	684	0	672	17	0
78	Sv	673	0	662	11	0
79	Rw	1021	0	1060	12	0
79	Sw	1021	0	1060	24	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
80	Rx	1121	0	1196	13	0
80	Sx	1121	0	1196	19	0
81	Ry	1073	0	1132	16	0
81	Sy	1073	0	1132	16	0
82	Rz	558	0	598	7	0
82	Sz	651	0	682	14	0
83	RC	497	0	535	6	0
84	Ro	949	0	985	14	0
85	Rr	1000	0	1063	17	0
86	MA	1230	0	1320	13	0
87	M1	68285	0	34372	359	0
88	DQ	1644	0	837	15	0
89	MQ	1531	0	1571	27	0
90	MP	1196	0	1257	20	0
91	DP	1638	0	836	12	0
92	CP	1	0	0	0	0
92	M1	194	0	0	0	0
92	M2	3	0	0	0	0
92	M3	4	0	0	0	0
92	ME	1	0	0	0	0
92	MI	2	0	0	0	0
92	MK	1	0	0	0	0
92	MM	1	0	0	0	0
92	Ma	1	0	0	0	0
92	Mx	1	0	0	0	0
92	S1	84	0	0	0	0
92	Sf	1	0	0	0	0
92	Sx	1	0	0	0	0
93	Lb	1	0	0	0	0
93	Lc	1	0	0	0	0
93	Le	1	0	0	0	0
93	Lh	1	0	0	0	0
93	Lk	1	0	0	0	0
93	Mb	1	0	0	0	0
93	Mc	1	0	0	0	0
93	Me	1	0	0	0	0
93	Mh	1	0	0	0	0
93	Mk	1	0	0	0	0
93	RB	1	0	0	0	0
93	SD	1	0	0	0	0
93	SF	1	0	0	0	0
94	M1	11	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
94	ME	1	0	0	0	0
94	Mc	1	0	0	0	0
94	Mk	1	0	0	0	0
94	Mm	1	0	0	0	0
94	Mw	1	0	0	0	0
95	M1	30	0	57	4	0
All	All	406583	0	300359	3269	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 5.

All (3269) 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)
5:L1:1018:G:H1	5:L1:1034:U:H3	1.09	0.95
87:M1:2448:G:H1	87:M1:2499:U:H3	1.15	0.95
49:S1:895:G:H1	49:S1:917:U:H3	1.08	0.92
49:R1:142:G:N1	49:R1:173:A:C2	2.36	0.91
49:R1:1588:G:H1	49:R1:1608:U:H3	0.91	0.89
49:S1:1229:G:H21	49:S1:1256:A:H62	1.17	0.89
87:M1:542:G:H1	87:M1:549:U:H3	0.89	0.88
49:R1:142:G:N1	49:R1:173:A:H2	1.70	0.87
49:S1:1588:G:H1	49:S1:1608:U:H3	1.23	0.85
49:R1:142:G:H1	49:R1:173:A:H2	0.92	0.85
49:S1:174:U:H3	49:S1:266:A:H62	1.22	0.85
87:M1:2450:G:H1	87:M1:2497:U:H3	1.28	0.81
64:Sh:37:GLU:H	64:Sh:39:ARG:HH21	1.25	0.80
49:R1:1663:G:H1	49:R1:1738:U:H3	1.30	0.79
49:S1:273:G:H1	49:S1:283:U:H3	1.30	0.79
87:M1:2679:A:H62	13:MF:55:ARG:HH22	1.31	0.79
28:Mf:28:ARG:H	28:Mf:33:ASN:HD21	1.30	0.79
81:Ry:35:VAL:HG12	81:Ry:40:LEU:HD11	1.66	0.77
49:R1:388:G:N2	49:R1:409:C:C2	2.51	0.77
70:Rn:72:MET:N	70:Rn:72:MET:SD	2.58	0.76
87:M1:824:C:H5"	45:Mw:21:ARG:HD3	1.69	0.75
49:R1:273:G:H1	49:R1:283:U:H3	1.34	0.74
54:SE:55:ARG:HH21	54:SE:58:PRO:HA	1.51	0.74
57:Ra:180:GLU:HA	57:Ra:183:ARG:HB2	1.70	0.74
58:Sb:32:ILE:HD13	58:Sb:96:LEU:HD11	1.70	0.73
49:R1:868:G:H1	49:R1:960:U:H3	1.34	0.73
17:LJ:27:LEU:HD21	17:LJ:102:LEU:HB2	1.71	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:LO:79:MET:HE1	38:Lp:21:ILE:HG21	1.71	0.72
49:R1:991:G:H1'	49:R1:1786:G:H5'	1.69	0.72
23:Ma:87:ARG:HH22	23:Ma:137:VAL:HG21	1.54	0.72
7:L3:52:G:H21	13:LF:9:MET:HE1	1.53	0.72
87:M1:2764:C:H42	88:DQ:77:A:H8	1.38	0.71
5:L1:640:U:OP1	39:Lq:21:ARG:NH2	2.23	0.71
7:L3:76:A:N3	21:LN:50:LYS:NZ	2.39	0.71
35:Lm:69:SER:HG	35:Lm:71:HIS:HD1	1.37	0.71
69:Rm:63:VAL:HG11	69:Rm:66:VAL:HG13	1.70	0.70
5:L1:95:A:H5''	39:Lq:34:MET:HB3	1.73	0.70
87:M1:2969:A:N7	45:Mw:215:ASN:ND2	2.40	0.70
87:M1:2193:U:H5'	87:M1:2194:G:H5'	1.73	0.70
49:S1:992:A:H2	49:S1:1012:U:H3	1.40	0.70
51:SB:19:HIS:HB3	51:SB:22:LYS:HG3	1.74	0.69
49:S1:636:A:H5''	79:Sw:31:SER:HB2	1.73	0.69
64:Sh:157:LYS:HD3	64:Sh:158:ASP:HB2	1.75	0.69
49:S1:699:U:H3	49:S1:739:G:H1	1.39	0.69
67:Rk:77:ARG:HH12	67:Rk:85:HIS:H	1.41	0.69
45:Lw:27:ALA:O	45:Lw:128:ARG:NH2	2.26	0.69
87:M1:394:G:H22	87:M1:397:A:H5'	1.57	0.69
49:R1:1542:G:N2	49:R1:1569:A:OP2	2.24	0.69
5:L1:1639:C:OP2	33:Lk:74:ARG:NH2	2.26	0.68
49:S1:706:A:H61	49:S1:731:C:H5''	1.58	0.68
79:Rw:4:SER:HG	49:R1:1101:G:HO2'	1.41	0.68
59:Rc:170:ILE:HB	59:Rc:197:TYR:HB2	1.75	0.68
5:L1:2147:A:OP2	45:Lw:200:ARG:NH1	2.27	0.68
61:Se:157:ASN:HD22	61:Se:222:LEU:HD11	1.59	0.68
65:Si:79:ALA:HB3	65:Si:103:GLN:HB3	1.75	0.68
49:R1:187:G:H3'	65:Ri:138:ASN:HD21	1.58	0.68
5:L1:1677:G:N7	44:Lv:74:LYS:NZ	2.42	0.67
49:S1:1236:A:H1'	55:SF:138:ARG:HH12	1.57	0.67
88:DQ:51:U:H3	88:DQ:65:G:H1	1.40	0.67
67:Sk:55:VAL:HG12	67:Sk:68:LEU:HA	1.76	0.67
63:Rg:67:VAL:HG12	63:Rg:99:GLY:HA2	1.76	0.67
87:M1:2457:G:N2	87:M1:2486:A:N1	2.40	0.67
5:L1:1846:C:OP1	5:L1:1849:C:N4	2.26	0.67
5:L1:1684:U:OP1	44:Lv:86:LYS:NZ	2.28	0.67
75:Rs:41:ARG:NH2	76:Rt:36:ILE:O	2.28	0.67
60:Rd:71:LEU:HB3	67:Rk:20:VAL:HG21	1.77	0.67
49:S1:1034:C:HO2'	79:Sw:2:THR:N	1.93	0.67
81:Ry:37:LYS:HG3	49:R1:522:U:H5''	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
87:M1:2679:A:N7	13:MF:55:ARG:NH1	2.42	0.67
76:Rt:102:ARG:NH2	49:R1:1502:G:N7	2.42	0.66
5:L1:838:G:O6	24:Lb:4:ARG:NH2	2.29	0.66
75:Ss:106:GLU:HG2	75:Ss:110:ARG:HH22	1.59	0.66
49:R1:1594:G:OP2	49:R1:1596:C:N4	2.29	0.66
9:LB:210:PRO:HD3	9:LB:243:MET:HE3	1.77	0.66
72:Sp:41:VAL:HG23	72:Sp:84:ILE:HD13	1.78	0.66
65:Si:57:ALA:HB2	65:Si:177:GLY:HA2	1.78	0.66
12:LE:217:PHE:HB3	48:Lz:294:ALA:HB1	1.77	0.66
83:RC:11:LYS:HB3	83:RC:53:ILE:HD13	1.78	0.66
9:LB:118:LYS:HG3	9:LB:191:VAL:HG11	1.78	0.65
14:LG:137:GLN:HA	32:Lj:119:LYS:HZ1	1.59	0.65
49:S1:545:A:H2'	54:SE:31:LYS:HD3	1.76	0.65
49:S1:699:U:O2	49:S1:739:G:N2	2.30	0.65
5:L1:68:C:OP2	5:L1:301:G:N2	2.29	0.65
67:Sk:82:LEU:HD22	67:Sk:83:PRO:HD2	1.78	0.65
25:Lc:2:VAL:N	25:Lc:90:HIS:O	2.30	0.65
49:S1:821:U:O4	49:S1:852:C:N3	2.29	0.65
87:M1:1132:C:H2'	87:M1:1133:A2M:H8	1.78	0.65
21:MN:14:LEU:H	21:MN:56:GLY:HA2	1.62	0.65
49:R1:329:G:H5''	65:Ri:98:LYS:HB3	1.77	0.65
58:Rb:82:ARG:NH1	58:Rb:191:GLU:OE2	2.29	0.65
5:L1:1471:U:H5''	20:LM:5:ARG:HG3	1.79	0.65
5:L1:2948:C:OP1	46:Lx:244:ARG:NH2	2.30	0.65
75:Ss:16:ARG:HH21	75:Ss:19:ASN:HA	1.61	0.65
50:RA:44:ILE:HD11	50:RA:65:PRO:HG2	1.78	0.65
39:Mq:76:ASP:HB3	39:Mq:116:GLY:HA3	1.79	0.65
5:L1:2969:A:N7	45:Lw:215:ASN:ND2	2.45	0.65
14:LG:123:ILE:HG22	32:Lj:118:ILE:HG22	1.77	0.65
49:S1:1456:C:H5''	49:S1:1457:C:H5''	1.79	0.65
51:SB:56:CYS:HG	51:SB:58:SER:HG	1.45	0.65
64:Sh:133:THR:OG1	64:Sh:134:GLU:N	2.28	0.65
49:R1:127:G:N7	63:Rg:202:ARG:NH2	2.45	0.65
5:L1:845:G:N2	5:L1:848:A:OP2	2.30	0.65
5:L1:1257:C:N3	5:L1:1261:G:N1	2.45	0.65
49:R1:142:G:O6	49:R1:173:A:N1	2.30	0.65
6:M2:156:U:OP2	10:MC:84:ARG:NH2	2.29	0.64
69:Rm:62:LEU:HD12	69:Rm:63:VAL:HG12	1.78	0.64
5:L1:860:G:OP1	24:Lb:17:ARG:NH1	2.30	0.64
49:S1:338:C:H5''	65:Si:10:LYS:HD3	1.80	0.64
69:Sm:131:ASP:HA	69:Sm:134:SER:HB2	1.77	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
75:Rs:38:VAL:HG11	75:Rs:73:MET:HE2	1.78	0.64
57:Sa:27:ARG:HD2	57:Sa:29:VAL:H	1.61	0.64
5:L1:824:C:H5''	45:Lw:21:ARG:HD3	1.78	0.64
22:LO:39:ILE:HD12	22:LO:102:ARG:HD3	1.78	0.64
49:S1:1229:G:N2	49:S1:1256:A:H62	1.92	0.64
59:Rc:78:ASP:HB3	59:Rc:104:VAL:HG12	1.80	0.64
49:R1:1774:G:N7	26:Md:4:LYS:NZ	2.45	0.64
21:LN:65:ASN:OD1	21:LN:65:ASN:N	2.31	0.64
41:Ms:3:LYS:HD3	41:Ms:8:VAL:HG23	1.80	0.64
28:Mf:20:ASN:ND2	28:Mf:42:ARG:O	2.28	0.64
16:LI:99:ARG:HB3	16:LI:167:THR:HG21	1.79	0.64
76:St:22:LEU:HD13	76:St:28:LEU:HD21	1.80	0.64
5:L1:595:G:OP2	9:LB:30:ARG:NH1	2.31	0.63
61:Se:57:ASN:HD22	61:Se:59:ARG:HE	1.46	0.63
49:R1:979:A:H62	49:R1:1021:C:H41	1.43	0.63
5:L1:2794:G:OP1	25:Lc:61:LYS:NZ	2.31	0.63
55:SF:106:TYR:HB3	55:SF:116:LYS:HA	1.81	0.63
67:Sk:28:ASN:H	67:Sk:40:LEU:HB2	1.62	0.63
17:MJ:113:ASP:OD1	17:MJ:113:ASP:N	2.29	0.63
5:L1:1940:G:H21	5:L1:3362:A:H8	1.47	0.63
82:Sz:89:ILE:HG22	82:Sz:103:ARG:HA	1.79	0.63
5:L1:829:U:H3	5:L1:895:A:H62	1.45	0.63
18:LK:18:ARG:NH2	18:LK:147:GLU:OE1	2.32	0.63
58:Sb:71:ALA:HB3	71:So:114:ARG:HH12	1.63	0.63
76:St:108:LEU:HD22	76:St:113:ILE:HG21	1.80	0.63
49:R1:298:C:H5''	61:Re:38:LEU:HD23	1.80	0.63
49:R1:988:A:N6	49:R1:1014:G:O6	2.31	0.63
49:R1:1065:A:N3	58:Rb:146:GLN:NE2	2.45	0.63
84:Ro:20:TYR:HB3	84:Ro:27:PHE:HB2	1.80	0.63
58:Sb:199:ASN:HA	58:Sb:202:LYS:HE3	1.81	0.63
49:R1:1014:G:N2	49:R1:1786:G:O2'	2.31	0.63
49:R1:1482:C:OP2	49:R1:1521:G:N2	2.32	0.63
4:CP:5:U:H3	4:CP:68:G:H1	1.47	0.63
5:L1:1257:C:N4	5:L1:1261:G:N2	2.46	0.63
52:SC:57:MET:N	52:SC:57:MET:SD	2.72	0.63
49:R1:1739:C:H2'	49:R1:1740:A:H8	1.63	0.63
5:L1:68:C:N4	5:L1:314:U:O2'	2.31	0.63
87:M1:3306:U:OP1	46:Mx:269:GLN:NE2	2.32	0.63
29:Mg:24:THR:HG23	29:Mg:44:LYS:HB2	1.81	0.63
12:LE:44:ASP:OD2	12:LE:185:ARG:NH1	2.31	0.63
19:LL:19:PRO:HB3	19:LL:53:PHE:HA	1.80	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
82:Sz:50:ILE:HG23	82:Sz:69:LEU:HD11	1.81	0.62
49:R1:649:U:H5'	64:Rh:147:ASN:HD21	1.63	0.62
49:R1:653:C:H42	49:R1:682:C:H42	1.46	0.62
49:S1:1565:C:OP1	75:Ss:41:ARG:NH1	2.32	0.62
57:Sa:84:ARG:NH1	57:Sa:203:PHE:O	2.30	0.62
58:Rb:91:VAL:HG12	58:Rb:96:LEU:HB3	1.81	0.62
46:Lx:320:ASP:OD1	46:Lx:320:ASP:N	2.33	0.62
77:Su:22:ILE:HG22	77:Su:118:VAL:HA	1.80	0.62
75:Rs:90:ASN:O	72:Rp:18:ARG:NH1	2.33	0.62
62:Rf:64:VAL:HG23	62:Rf:65:ARG:HH22	1.64	0.62
67:Rk:32:HIS:NE2	67:Rk:34:GLU:OE1	2.32	0.62
5:L1:2842:U:OP1	5:L1:2844:C:N4	2.31	0.62
49:S1:1339:C:O2'	49:S1:1341:A:N7	2.27	0.62
22:LO:82:ASN:C	22:LO:82:ASN:HD22	2.05	0.62
49:S1:1229:G:N1	69:Sm:47:GLU:OE2	2.33	0.62
51:SB:4:VAL:HG22	79:Sw:23:ARG:HD3	1.80	0.62
46:Mx:211:GLN:NE2	46:Mx:283:TYR:O	2.33	0.62
5:L1:687:U:OP2	14:LG:36:ARG:NH2	2.31	0.62
49:S1:1584:G:N2	49:S1:1611:A:OP2	2.32	0.62
57:Sa:53:THR:HG22	57:Sa:161:PRO:HG2	1.82	0.62
88:DQ:1:C:H42	88:DQ:73:A:H61	1.48	0.62
61:Se:11:ARG:NH1	61:Se:21:ASP:O	2.33	0.62
49:R1:1673:G:O2'	63:Rg:92:ARG:NH2	2.33	0.62
20:MM:31:GLU:N	20:MM:31:GLU:OE2	2.33	0.62
49:S1:1476:C:O2'	76:St:45:MET:SD	2.58	0.62
78:Sv:85:TYR:OH	79:Sw:23:ARG:NH2	2.33	0.62
62:Rf:43:PHE:HB3	62:Rf:46:TRP:HB2	1.82	0.62
89:MQ:48:ARG:NH1	89:MQ:89:THR:OG1	2.33	0.62
27:Le:78:ILE:HG21	27:Le:83:LYS:HE3	1.81	0.61
49:S1:749:U:H5''	79:Sw:83:ILE:HG12	1.81	0.61
49:S1:765:G:N2	49:S1:765:G:OP2	2.33	0.61
49:S1:1171:A:H2'	49:S1:1172:G:C8	2.35	0.61
56:RG:19:TRP:HB2	56:RG:38:ARG:HG3	1.82	0.61
58:Rb:191:GLU:OE1	58:Rb:194:ASN:ND2	2.33	0.61
58:Rb:222:LYS:NZ	87:M1:2546:C:O2'	2.33	0.61
49:S1:1610:G:OP1	62:Sf:72:HIS:NE2	2.31	0.61
61:Se:100:ARG:NH2	61:Se:121:TYR:O	2.33	0.61
49:R1:565:C:O2'	49:R1:1755:A:N6	2.33	0.61
60:Rd:105:MET:HE1	60:Rd:119:ALA:HA	1.80	0.61
49:S1:896:U:O2	71:So:41:ARG:NH1	2.32	0.61
49:S1:1502:G:N7	76:St:102:ARG:NH2	2.48	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:Sg:27:PHE:HE1	63:Sg:36:VAL:HG21	1.66	0.61
75:Ss:14:ILE:HG22	75:Ss:24:GLY:H	1.65	0.61
87:M1:627:U:H4'	87:M1:1399:A:H1'	1.82	0.61
87:M1:1301:A:H4'	87:M1:1302:A:H5''	1.80	0.61
5:L1:692:A:OP1	16:LI:201:ARG:NH2	2.34	0.61
5:L1:2433:U:H1'	16:LI:125:SER:HB2	1.82	0.61
51:RB:40:CYS:SG	51:RB:41:LEU:N	2.72	0.61
49:R1:224:C:C4	49:R1:225:A:N6	2.69	0.61
87:M1:2895:G:O2'	27:Me:100:TYR:O	2.17	0.61
49:S1:1797:A:N6	50:SA:84:VAL:O	2.33	0.61
59:Sc:165:VAL:HG11	59:Sc:210:THR:HG22	1.82	0.61
69:Sm:92:ALA:HB3	69:Sm:96:GLN:HE22	1.65	0.61
56:RG:178:VAL:HB	56:RG:192:PHE:HB2	1.81	0.61
49:S1:207:U:O2	65:Si:178:ARG:NH2	2.33	0.61
57:Sa:183:ARG:O	78:Sv:44:ARG:NH2	2.34	0.61
81:Ry:29:HIS:HB2	81:Ry:32:ARG:HB2	1.83	0.61
7:M3:64:A:N7	12:ME:209:ASN:ND2	2.48	0.61
64:Sh:50:ASP:OD1	64:Sh:56:LYS:NZ	2.33	0.61
56:RG:13:LEU:HB2	56:RG:310:ILE:HB	1.82	0.61
56:RG:231:MET:SD	56:RG:231:MET:N	2.74	0.61
49:R1:1488:G:H3'	49:R1:1515:A:H61	1.66	0.61
7:L3:31:U:H4'	48:Lz:218:ARG:HH12	1.65	0.61
77:Ru:45:ALA:O	77:Ru:52:LYS:NZ	2.34	0.61
82:Rz:40:VAL:HA	82:Rz:75:LEU:HD11	1.83	0.61
49:R1:1339:C:O2'	49:R1:1341:A:N7	2.33	0.61
51:RB:36:LYS:HZ1	51:RB:43:ILE:HD13	1.66	0.60
49:S1:123:G:H21	61:Se:146:THR:HG21	1.65	0.60
79:Rw:2:THR:N	49:R1:1034:C:HO2'	1.99	0.60
80:Sx:97:ASP:OD2	80:Sx:97:ASP:N	2.33	0.60
56:RG:111:MET:N	56:RG:111:MET:SD	2.74	0.60
87:M1:519:A:N7	47:My:360:LYS:NZ	2.48	0.60
49:R1:967:A:OP2	70:Rn:124:ARG:NH2	2.35	0.60
41:Ls:54:ASP:OD2	41:Ls:115:ARG:NH2	2.34	0.60
57:Sa:184:LEU:HD12	78:Sv:45:ALA:HB2	1.82	0.60
59:Sc:73:LEU:HD13	59:Sc:76:LEU:HD21	1.82	0.60
66:Sj:114:TYR:HB3	66:Sj:115:LYS:HE2	1.83	0.60
57:Ra:30:GLN:NE2	57:Ra:151:SER:O	2.35	0.60
87:M1:508:U:OP1	9:MB:211:SER:OG	2.20	0.60
5:L1:3092:C:O2'	5:L1:3094:A:OP2	2.19	0.60
68:Sl:33:ARG:NH2	68:Sl:48:ALA:O	2.35	0.60
49:R1:1321:A:OP2	57:Ra:101:ARG:NH2	2.33	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:R1:1552:U:OP2	72:Rp:43:ARG:NH2	2.34	0.60
5:L1:1390:A:N6	5:L1:1418:A:O2'	2.35	0.60
49:S1:931:C:H5''	58:Sb:116:LYS:HB3	1.84	0.60
53:SD:6:VAL:HA	53:SD:9:SER:HB3	1.84	0.60
75:Rs:135:GLY:HA3	49:R1:1559:A:H5''	1.82	0.60
49:R1:941:A:N3	49:R1:976:G:O2'	2.34	0.60
49:R1:1292:G:H21	57:Ra:111:ILE:HD11	1.66	0.60
60:Rd:170:THR:HG22	60:Rd:187:LYS:HG2	1.82	0.60
60:Sd:193:ALA:O	60:Sd:200:LYS:NZ	2.35	0.60
77:Su:70:THR:OG1	77:Su:72:ASN:O	2.18	0.60
80:Rx:90:ASP:HB2	54:RE:12:GLY:HA2	1.83	0.60
49:R1:926:A:N6	84:Ro:124:ASP:O	2.33	0.60
57:Ra:114:SER:O	57:Ra:116:LYS:NZ	2.35	0.60
87:M1:2452:G:H2'	87:M1:2462:A:H1'	1.83	0.60
35:Mm:31:ASN:OD1	35:Mm:31:ASN:N	2.35	0.60
49:S1:142:G:H1	49:S1:173:A:H2	1.50	0.60
49:S1:992:A:O2'	49:S1:1785:U:O2	2.20	0.60
49:R1:992:A:N7	49:R1:1777:G:O2'	2.31	0.60
87:M1:1245:A:OP1	90:MP:16:ARG:NH1	2.34	0.60
11:LD:115:ARG:HG2	11:LD:123:ILE:HD12	1.84	0.59
13:LF:49:LYS:HB3	13:LF:62:ASN:HA	1.84	0.59
13:LF:133:ARG:NH2	13:LF:158:ASP:OD2	2.33	0.59
42:Lt:31:THR:OG1	42:Lt:33:ARG:NH1	2.35	0.59
49:S1:129:U:O2'	49:S1:131:C:N4	2.34	0.59
52:SC:44:VAL:HG11	52:SC:48:VAL:HB	1.83	0.59
87:M1:1219:C:O2'	87:M1:1286:A:N1	2.32	0.59
5:L1:2177:G:OP2	45:Lw:128:ARG:NH1	2.35	0.59
49:S1:1594:G:OP2	49:S1:1596:C:N4	2.34	0.59
55:SF:142:GLY:O	55:SF:145:HIS:ND1	2.33	0.59
56:SG:217:ASP:OD2	56:SG:217:ASP:N	2.34	0.59
65:Si:39:GLY:HA2	65:Si:61:GLU:HG3	1.83	0.59
56:RG:206:PRO:HG3	56:RG:247:PRO:HA	1.84	0.59
5:L1:293:C:O3'	31:Li:76:ARG:NH1	2.34	0.59
41:Ls:112:ASP:OD2	41:Ls:113:LYS:N	2.35	0.59
53:SD:52:PHE:HB3	77:Su:82:TYR:HB3	1.84	0.59
49:R1:224:C:N4	49:R1:225:A:H62	2.00	0.59
49:R1:993:A:H62	49:R1:1011:G:H21	1.50	0.59
61:Re:253:ASP:HA	61:Re:256:ARG:HG2	1.83	0.59
49:S1:1584:G:HO2'	49:S1:1610:G:H1	1.49	0.59
5:L1:3037:U:O3'	46:Lx:348:ARG:NH2	2.36	0.59
6:L2:95:G:OP2	30:Lh:72:ARG:NH1	2.36	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:L3:7:G:OP1	48:Lz:33:ARG:NH1	2.36	0.59
87:M1:705:A:N7	39:Mq:74:ASN:ND2	2.45	0.59
87:M1:1477:A:OP1	87:M1:3075:G:O2'	2.21	0.59
49:R1:478:A:O2'	66:Rj:124:HIS:ND1	2.35	0.59
87:M1:1022:U:H3	87:M1:1030:A:H61	1.51	0.59
46:Mx:77:THR:HG21	46:Mx:328:ILE:HG12	1.85	0.59
49:S1:217:A:N1	49:S1:844:A:O2'	2.34	0.59
74:Sr:25:THR:OG1	74:Sr:26:LEU:N	2.36	0.59
49:R1:479:C:H4'	66:Rj:120:LYS:HE3	1.85	0.59
49:S1:623:A:N6	49:S1:970:A:OP1	2.35	0.59
53:RD:13:ARG:NH1	49:R1:1554:U:OP1	2.36	0.59
49:R1:224:C:N4	49:R1:225:A:N6	2.50	0.59
49:R1:1471:A:OP1	62:Rf:185:ARG:NH1	2.36	0.59
57:Ra:84:ARG:HD3	57:Ra:204:TYR:HA	1.84	0.59
5:L1:3275:U:O2'	34:Ll:99:ARG:NH1	2.36	0.59
60:Sd:105:MET:HG2	60:Sd:122:VAL:HG21	1.83	0.59
79:Rw:22:LYS:HD3	51:RB:3:LEU:HD12	1.85	0.59
49:R1:1561:U:H2'	49:R1:1562:G:H8	1.68	0.59
3:CN:93:LYS:NZ	49:R1:1262:U:O3'	2.36	0.59
5:L1:1352:A:H4'	5:L1:1353:U:H5'	1.85	0.59
5:L1:2392:C:O2'	46:Lx:266:ARG:NH2	2.29	0.59
22:LO:51:GLY:HA3	22:LO:92:ARG:HG3	1.83	0.59
47:Ly:285:ASP:OD1	47:Ly:285:ASP:N	2.36	0.59
49:R1:195:G:N7	65:Ri:141:ARG:NH1	2.50	0.59
58:Rb:123:ALA:HB2	58:Rb:165:ARG:HG2	1.85	0.59
5:L1:198:A:N3	5:L1:218:G:O2'	2.36	0.58
24:Lb:39:CYS:HB3	24:Lb:42:CYS:SG	2.43	0.58
58:Sb:108:ASP:O	58:Sb:112:SER:OG	2.21	0.58
79:Sw:23:ARG:NH1	79:Sw:24:GLN:OE1	2.36	0.58
56:RG:205:SER:HB3	56:RG:210:LEU:HB2	1.85	0.58
49:R1:1785:U:H2'	49:R1:1786:G:H8	1.68	0.58
87:M1:1322:U:O2	21:MN:108:GLN:NE2	2.36	0.58
77:Su:83:GLU:OE2	77:Su:85:ARG:NH1	2.36	0.58
55:RF:132:LEU:HD23	55:RF:139:LEU:HB3	1.85	0.58
49:R1:386:G:OP2	65:Ri:25:ARG:NH2	2.35	0.58
87:M1:126:U:OP1	16:MI:144:ARG:NH1	2.36	0.58
69:Sm:30:VAL:HA	69:Sm:33:ARG:HG2	1.84	0.58
81:Ry:105:ARG:NH2	49:R1:458:G:OP2	2.36	0.58
49:R1:871:G:H2'	49:R1:872:G:C8	2.38	0.58
49:R1:925:G:OP1	49:R1:986:G:O2'	2.20	0.58
85:Rr:89:SER:O	85:Rr:95:ARG:NH1	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
87:M1:1255:C:H4'	90:MP:130:LYS:HB3	1.83	0.58
5:L1:1682:U:O4	44:Lv:90:ARG:NH1	2.35	0.58
5:L1:3268:A:OP1	8:LA:46:ARG:NH2	2.36	0.58
50:SA:45:VAL:HB	50:SA:64:LEU:HD21	1.84	0.58
9:LB:232:ARG:HB2	9:LB:235:PHE:HB2	1.86	0.58
43:Lu:2:LYS:NZ	43:Lu:4:GLU:OE2	2.36	0.58
49:S1:967:A:OP2	70:Sn:124:ARG:NH2	2.36	0.58
65:Si:187:GLU:OE2	65:Si:187:GLU:N	2.34	0.58
82:Sz:42:LEU:HD22	82:Sz:75:LEU:HD11	1.86	0.58
49:R1:224:C:N3	49:R1:225:A:N6	2.51	0.58
49:R1:623:A:N6	49:R1:970:A:OP1	2.36	0.58
49:R1:1591:C:H2'	49:R1:1592:A:H8	1.69	0.58
60:Rd:31:GLU:O	60:Rd:54:ARG:NH2	2.36	0.58
87:M1:1390:A:N6	87:M1:1418:A:O2'	2.35	0.58
46:Mx:360:ASP:OD2	46:Mx:364:LYS:NZ	2.35	0.58
12:ME:30:LYS:HG3	12:ME:63:GLU:HG3	1.86	0.58
3:CN:69:THR:OG1	60:Rd:94:ARG:NH2	2.37	0.58
5:L1:289:A:O2'	16:LI:93:LYS:O	2.22	0.58
12:LE:184:LYS:HG2	12:LE:189:GLU:HB2	1.85	0.58
20:LM:105:LEU:HD23	20:LM:138:LEU:HD23	1.86	0.58
66:Sj:18:PRO:O	66:Sj:23:ARG:NH2	2.36	0.58
87:M1:292:U:OP2	16:MI:68:ARG:NH2	2.37	0.58
87:M1:1268:G:H21	87:M1:1273:A:H62	1.50	0.58
87:M1:3041:U:OP1	23:Ma:12:ARG:NH1	2.36	0.58
49:S1:1690:G:H2'	49:S1:1691:A:H8	1.69	0.58
56:RG:297:ASP:OD1	56:RG:297:ASP:N	2.37	0.58
63:Rg:57:ASP:HA	63:Rg:106:LEU:HA	1.85	0.58
21:MN:27:MET:HE3	21:MN:29:ILE:HD11	1.84	0.58
55:SF:133:ALA:HB3	55:SF:140:TYR:HB3	1.85	0.58
59:Sc:173:PRO:HG2	66:Sj:57:ARG:HD2	1.85	0.58
49:R1:58:U:O2'	49:R1:451:A:N3	2.36	0.58
87:M1:1018:G:OP1	87:M1:1035:G:N2	2.37	0.58
87:M1:2674:A:H5''	13:MF:105:GLY:HA3	1.86	0.58
40:Mr:31:GLU:OE1	40:Mr:31:GLU:N	2.37	0.58
5:L1:1884:A:OP1	36:Ln:31:ARG:NH2	2.37	0.58
16:LI:202:TYR:HB3	47:Ly:112:LYS:HG3	1.85	0.58
49:S1:1216:C:O2	49:S1:1446:A:N6	2.37	0.58
62:Sf:57:SER:OG	62:Sf:167:ARG:NH2	2.37	0.58
75:Ss:94:ASP:N	75:Ss:94:ASP:OD1	2.36	0.58
76:Rt:122:ARG:NH1	49:R1:1499:G:OP1	2.36	0.58
87:M1:1448:U:H2'	87:M1:1449:A2M:H8	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
87:M1:1940:G:H21	87:M1:3362:A:H8	1.52	0.58
4:CP:73:G:H5'	4:CP:74:C:H5'	1.86	0.58
64:Sh:79:ARG:HA	64:Sh:82:GLU:HG2	1.86	0.58
76:St:105:LEU:HD13	76:St:122:ARG:HD3	1.84	0.58
60:Rd:50:ILE:HD11	60:Rd:86:LEU:HD23	1.85	0.58
5:L1:426:G:OP1	35:Lm:15:LYS:NZ	2.36	0.57
46:Lx:35:ASP:OD2	46:Lx:37:ARG:NH1	2.37	0.57
91:DP:58:A:H1'	91:DP:60:C:H41	1.68	0.57
5:L1:3039:C:OP1	46:Lx:62:ARG:NH2	2.37	0.57
56:SG:17:ASN:HA	56:SG:308:ASN:HD21	1.68	0.57
59:Sc:208:GLU:OE1	59:Sc:208:GLU:N	2.37	0.57
63:Sg:20:ASP:HB3	63:Sg:23:ARG:HE	1.69	0.57
49:R1:146:U:H2'	49:R1:147:A:H8	1.69	0.57
45:Lw:33:ASP:OD1	45:Lw:33:ASP:N	2.37	0.57
55:SF:100:LEU:HD13	55:SF:103:LEU:HD11	1.85	0.57
60:Rd:67:ASN:N	60:Rd:67:ASN:OD1	2.38	0.57
20:MM:21:LYS:HE3	20:MM:55:VAL:HA	1.86	0.57
28:Mf:30:ARG:HB2	28:Mf:33:ASN:HD22	1.68	0.57
5:L1:674:G:O6	19:LL:56:LYS:NZ	2.37	0.57
45:Lw:74:GLU:OE2	45:Lw:123:ARG:NH2	2.36	0.57
49:S1:532:U:O2	81:Sy:34:ASN:ND2	2.38	0.57
52:SC:60:GLU:OE1	71:So:107:ARG:NH1	2.38	0.57
57:Sa:13:ASP:OD2	57:Sa:179:ARG:NH2	2.37	0.57
70:Sn:64:ARG:NH1	70:Sn:64:ARG:O	2.36	0.57
72:Sp:48:GLY:O	72:Sp:52:LYS:NZ	2.35	0.57
76:St:113:ILE:HD12	76:St:128:GLY:HA2	1.86	0.57
75:Rs:91:ASP:N	75:Rs:91:ASP:OD1	2.35	0.57
61:Re:19:LEU:HD11	61:Re:108:ARG:HD2	1.85	0.57
5:L1:66:A:OP2	14:LG:100:ARG:NH2	2.37	0.57
7:L3:44:C:OP2	13:LF:137:ARG:NH2	2.37	0.57
49:S1:283:U:H5''	63:Sg:188:ARG:HD3	1.86	0.57
49:S1:554:C:H1'	49:S1:555:A:H2	1.68	0.57
49:S1:867:G:OP2	70:Sn:3:ARG:NH1	2.38	0.57
81:Sy:99:LYS:NZ	81:Sy:100:VAL:O	2.37	0.57
87:M1:2763:U:O2	95:M1:3603:SPD:N10	2.38	0.57
5:L1:3050:U:O2'	43:Lu:16:GLY:O	2.23	0.57
8:LA:175:LYS:O	15:LH:117:ARG:NH2	2.37	0.57
49:S1:897:C:O2	71:So:41:ARG:NH2	2.38	0.57
49:S1:1365:C:OP1	73:Sq:66:ARG:NH2	2.37	0.57
87:M1:1261:G:O2'	87:M1:1262:G:N7	2.37	0.57
87:M1:2453:U:O4	87:M1:2484:A:N6	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
87:M1:2901:G:O2'	87:M1:3024:A:N1	2.37	0.57
88:DQ:70:C:H2'	88:DQ:71:G:H8	1.69	0.57
6:L2:58:G:O6	30:Lh:63:ARG:NH1	2.36	0.57
49:S1:399:A:OP1	65:Si:49:ARG:NH1	2.37	0.57
49:S1:1331:A:H61	60:Sd:161:GLY:HA3	1.70	0.57
62:Sf:63:GLN:NE2	62:Sf:86:GLN:OE1	2.38	0.57
21:MN:77:VAL:HG11	21:MN:106:LEU:HD22	1.86	0.57
47:Ly:35:VAL:HG21	47:Ly:244:LEU:HD21	1.87	0.57
66:Sj:151:ASP:O	66:Sj:154:LYS:NZ	2.37	0.57
87:M1:3068:U:OP2	20:MM:62:ARG:NH2	2.37	0.57
5:L1:901:G:OP1	30:Lh:13:ASN:ND2	2.35	0.57
5:L1:1814:A:H4'	5:L1:1815:U:H5'	1.87	0.57
21:LN:77:VAL:HG11	21:LN:106:LEU:HD22	1.86	0.57
82:Rz:48:ASP:OD1	82:Rz:48:ASP:N	2.36	0.57
46:Mx:353:GLU:N	46:Mx:353:GLU:OE2	2.38	0.57
13:MF:15:GLU:HG2	13:MF:16:LYS:HG2	1.86	0.57
28:Mf:43:ASN:HB3	28:Mf:46:ARG:HG3	1.86	0.57
48:Lz:80:SER:HA	48:Lz:83:LEU:HD23	1.86	0.57
48:Lz:120:LYS:O	48:Lz:248:ARG:NH2	2.30	0.57
49:S1:1680:G:H1'	49:S1:1721:A:H61	1.69	0.57
57:Sa:198:MET:HG3	57:Sa:200:ASP:H	1.70	0.57
62:Sf:126:ASP:N	62:Sf:126:ASP:OD1	2.38	0.57
79:Rw:18:GLU:HG2	79:Rw:65:LEU:HD13	1.85	0.57
19:ML:182:LYS:NZ	39:Mq:55:LYS:O	2.35	0.57
5:L1:1156:C:OP2	9:LB:94:LYS:NZ	2.37	0.56
48:Lz:77:ALA:O	48:Lz:108:ARG:NH1	2.38	0.56
78:Rv:74:GLN:NE2	78:Rv:83:TRP:O	2.38	0.56
49:R1:885:G:OP1	58:Rb:216:LYS:NZ	2.35	0.56
65:Ri:62:THR:HG22	65:Ri:77:ARG:HG2	1.87	0.56
13:MF:107:ASP:N	13:MF:107:ASP:OD1	2.38	0.56
5:L1:2568:C:O2'	5:L1:2569:A:O4'	2.22	0.56
10:LC:94:PHE:HB3	10:LC:189:LEU:HD11	1.87	0.56
49:S1:1499:G:OP1	76:St:122:ARG:NH1	2.37	0.56
69:Sm:33:ARG:HH22	69:Sm:100:TRP:HB3	1.69	0.56
49:R1:67:A:O2'	49:R1:69:G:OP1	2.23	0.56
49:R1:1171:A:H2'	49:R1:1172:G:C8	2.40	0.56
60:Rd:217:ILE:HG13	60:Rd:219:ALA:H	1.70	0.56
63:Rg:89:ASP:N	63:Rg:89:ASP:OD1	2.38	0.56
66:Rj:135:ALA:HA	66:Rj:140:ILE:HA	1.86	0.56
87:M1:2448:G:N2	87:M1:2499:U:O2	2.29	0.56
5:L1:2356:A:H61	5:L1:2983:C:H5	1.51	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L1:3215:A:OP2	15:LH:125:LYS:NZ	2.38	0.56
49:S1:190:C:N4	49:S1:191:C:O2	2.38	0.56
49:S1:472:U:O2'	49:S1:769:A:N3	2.38	0.56
56:SG:206:PRO:HG2	56:SG:247:PRO:HA	1.86	0.56
57:Sa:114:SER:O	57:Sa:114:SER:OG	2.22	0.56
67:Sk:5:LYS:O	67:Sk:9:ASN:ND2	2.38	0.56
71:So:20:TYR:HB3	71:So:27:PHE:HB2	1.87	0.56
73:Sq:99:GLU:N	73:Sq:99:GLU:OE2	2.37	0.56
76:St:135:ILE:HA	76:St:138:GLN:HB2	1.87	0.56
56:RG:121:MET:HE1	56:RG:133:VAL:HG13	1.87	0.56
49:R1:153:G:H2'	49:R1:154:G:H8	1.71	0.56
49:R1:237:C:H5''	49:R1:238:U:H5'	1.87	0.56
57:Ra:79:ARG:NH1	57:Ra:164:ASN:O	2.38	0.56
59:Rc:78:ASP:OD1	59:Rc:78:ASP:N	2.36	0.56
87:M1:289:A:O2'	16:MI:93:LYS:O	2.20	0.56
5:L1:1480:G:O2'	5:L1:1871:U:O4	2.21	0.56
45:Lw:36:GLU:OE2	45:Lw:163:ARG:NH1	2.30	0.56
49:S1:765:G:H1	66:Sj:149:ARG:HH12	1.51	0.56
49:S1:1213:G:O2'	49:S1:1244:A:N7	2.38	0.56
57:Sa:8:ASP:OD2	57:Sa:8:ASP:N	2.34	0.56
50:RA:95:ARG:HG2	49:R1:1797:A:H5'	1.88	0.56
68:Rl:78:THR:HA	68:Rl:84:ILE:HG22	1.88	0.56
73:Rq:73:GLY:H	73:Rq:76:SER:HB3	1.71	0.56
21:MN:28:ARG:NH1	47:My:361:HIS:O	2.38	0.56
46:Mx:57:VAL:HG22	46:Mx:73:VAL:HG22	1.87	0.56
8:LA:148:GLU:OE2	8:LA:148:GLU:N	2.38	0.56
12:LE:189:GLU:OE1	12:LE:189:GLU:N	2.37	0.56
28:Lf:43:ASN:HB3	28:Lf:46:ARG:HG3	1.87	0.56
51:SB:36:LYS:HA	51:SB:36:LYS:HE3	1.87	0.56
72:Sp:37:ALA:O	72:Sp:42:ARG:NH1	2.39	0.56
78:Rv:60:ARG:NH1	57:Ra:157:ASP:OD1	2.38	0.56
87:M1:45:A:H5''	95:M1:3602:SPD:H31	1.88	0.56
6:M2:83:C:H41	41:Ms:52:ARG:HH12	1.53	0.56
5:L1:47:C:H5''	14:LG:16:LYS:HG2	1.88	0.56
64:Rh:113:PRO:HG2	64:Rh:116:ARG:HG2	1.87	0.56
46:Mx:383:LEU:HB2	46:Mx:387:LEU:HD13	1.88	0.56
5:L1:1793:C:OP2	24:Lb:49:ARG:NH2	2.39	0.56
23:La:66:LYS:NZ	23:La:68:GLU:OE2	2.38	0.56
32:Lj:66:VAL:HG11	42:Lt:50:ALA:HB1	1.88	0.56
49:S1:1211:A:N3	72:Sp:97:TYR:OH	2.35	0.56
49:S1:1585:U:H3	49:S1:1611:A:H2	1.52	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:SG:172:ALA:HB2	56:SG:202:LEU:HD13	1.87	0.56
75:Ss:11:PHE:HD1	75:Ss:60:GLU:HB3	1.71	0.56
49:R1:65:A:H2	49:R1:84:A:H62	1.52	0.56
49:R1:851:U:H5''	20:MM:172:ARG:HH22	1.71	0.56
21:LN:73:LYS:NZ	21:LN:97:VAL:O	2.38	0.56
49:S1:868:G:H1	49:S1:960:U:H3	1.54	0.56
49:S1:886:U:OP1	58:Sb:214:LYS:NZ	2.33	0.56
49:S1:1499:G:H1	49:S1:1508:U:H3	1.54	0.56
78:Rv:82:VAL:HA	57:Ra:52:LYS:HD3	1.88	0.56
79:Rw:31:SER:HB3	49:R1:636:A:H5''	1.87	0.56
39:Mq:112:ILE:HB	39:Mq:130:VAL:HG23	1.88	0.56
16:MI:44:ARG:NH1	16:MI:120:TRP:O	2.39	0.56
5:L1:3068:U:OP2	20:LM:62:ARG:NH2	2.36	0.56
22:LO:86:GLU:OE1	22:LO:88:ARG:NH1	2.38	0.56
26:Ld:11:ARG:NH2	49:S1:1775:U:OP1	2.39	0.56
49:S1:1041:G:H2'	49:S1:1042:G:C8	2.41	0.56
73:Sq:64:ASP:OD1	73:Sq:64:ASP:N	2.34	0.56
48:Mz:82:GLU:OE1	48:Mz:108:ARG:NH2	2.34	0.56
9:LB:121:LYS:HB2	22:LO:133:ALA:HB3	1.87	0.56
21:LN:8:GLN:HB3	21:LN:64:ILE:HD11	1.88	0.56
75:Rs:57:ARG:NH2	49:R1:1534:G:OP1	2.39	0.56
87:M1:785:G:H5''	19:ML:92:ARG:HH22	1.71	0.56
2:CM:21:U:OP2	3:CN:67:ARG:NH1	2.35	0.55
5:L1:269:G:OP2	16:LI:44:ARG:NH2	2.38	0.55
5:L1:1419:A:H5''	47:Ly:193:LYS:HZ3	1.70	0.55
13:LF:10:ARG:NH2	13:LF:151:SER:O	2.39	0.55
53:SD:7:TRP:CD1	67:Sk:28:ASN:HD22	2.24	0.55
80:Rx:69:ARG:NH2	49:R1:568:G:N7	2.54	0.55
49:R1:156:A:C2	49:R1:415:C:O2	2.59	0.55
87:M1:1447:G:N7	18:MK:25:SER:OG	2.37	0.55
46:Mx:284:ARG:NH1	46:Mx:293:ASN:O	2.39	0.55
23:Ma:54:LEU:HD21	23:Ma:119:GLY:HA3	1.88	0.55
5:L1:358:G:N2	5:L1:361:A:OP2	2.36	0.55
10:LC:52:TRP:O	10:LC:57:ARG:NH1	2.39	0.55
49:R1:1230:A:N6	49:R1:1255:G:O2'	2.39	0.55
19:ML:152:HIS:ND1	19:ML:162:ALA:O	2.38	0.55
89:MQ:25:LEU:HG	89:MQ:191:TYR:HB3	1.87	0.55
39:Mq:76:ASP:N	39:Mq:76:ASP:OD1	2.39	0.55
16:LI:68:ARG:NH1	16:LI:124:ASP:O	2.33	0.55
24:Lb:39:CYS:CB	24:Lb:42:CYS:SG	2.94	0.55
49:S1:778:G:H1	81:Sy:10:ARG:HD3	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:SD:44:ARG:NH1	77:Su:80:GLU:OE1	2.37	0.55
57:Sa:84:ARG:NH2	74:Sr:82:ASP:O	2.36	0.55
62:Sf:25:LEU:HD22	62:Sf:26:ALA:H	1.71	0.55
77:Ru:82:TYR:HB3	53:RD:52:PHE:HB3	1.88	0.55
49:R1:158:U:O2'	49:R1:160:C:OP2	2.24	0.55
87:M1:1239:C:OP1	90:MP:90:ARG:NH2	2.40	0.55
18:MK:116:HIS:HB3	18:MK:149:VAL:HG13	1.88	0.55
5:L1:112:U:OP1	32:Lj:104:GLN:NE2	2.39	0.55
5:L1:1054:A:H5''	5:L1:2637:A:H61	1.71	0.55
13:LF:109:HIS:ND1	13:LF:123:PHE:O	2.39	0.55
41:Ls:85:VAL:HG12	41:Ls:97:ILE:HD13	1.89	0.55
47:Ly:144:LYS:H	47:Ly:144:LYS:HD2	1.71	0.55
49:S1:521:A:O2'	81:Sy:34:ASN:O	2.24	0.55
49:S1:1673:G:O6	49:S1:1728:A:N1	2.39	0.55
49:S1:1695:G:H1	49:S1:1706:C:H42	1.55	0.55
64:Rh:13:PRO:HB2	64:Rh:14:THR:HG22	1.88	0.55
73:Rq:50:GLU:OE1	73:Rq:82:ARG:NH1	2.37	0.55
17:MJ:164:SER:HG	87:M1:3181:C:HO2'	1.52	0.55
46:Mx:380:MET:HE2	46:Mx:383:LEU:HD11	1.89	0.55
5:L1:114:A:N1	5:L1:266:A:O2'	2.38	0.55
5:L1:837:A:OP2	24:Lb:4:ARG:NH1	2.38	0.55
42:Lt:82:LEU:HD11	42:Lt:135:ILE:HD11	1.89	0.55
49:S1:123:G:OP1	61:Se:77:ARG:NH2	2.39	0.55
49:S1:447:U:O2'	61:Se:27:TYR:O	2.25	0.55
63:Sg:59:GLN:OE1	63:Sg:72:ARG:NH1	2.39	0.55
75:Ss:112:ASP:OD1	75:Ss:115:ARG:NH1	2.35	0.55
56:RG:196:ASN:ND2	60:Rd:216:PRO:O	2.39	0.55
49:R1:69:G:H1	49:R1:82:U:H3	1.53	0.55
49:R1:1117:U:OP1	26:Md:21:ARG:NH1	2.39	0.55
49:R1:1681:A:N6	49:R1:1720:G:O2'	2.39	0.55
64:Rh:80:GLU:O	64:Rh:84:LYS:NZ	2.39	0.55
67:Rk:17:GLN:HE21	67:Rk:18:GLU:HG2	1.71	0.55
68:Rl:2:SER:OG	68:Rl:116:ARG:NH1	2.40	0.55
84:Ro:81:VAL:HG21	84:Ro:102:LEU:HD13	1.87	0.55
5:L1:627:U:H2'	5:L1:628:A:C8	2.41	0.55
9:LB:48:ASN:ND2	47:Ly:328:ASN:OD1	2.40	0.55
12:LE:150:GLU:OE2	12:LE:153:ARG:NE	2.36	0.55
15:LH:13:ARG:NH1	15:LH:65:LEU:O	2.39	0.55
17:LJ:61:ALA:HA	17:LJ:70:PRO:HD2	1.88	0.55
24:Lb:30:GLU:HA	24:Lb:33:GLN:HG2	1.87	0.55
35:Lm:96:ILE:HG21	35:Lm:105:ARG:HG2	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:Ls:7:ASP:OD1	41:Ls:7:ASP:N	2.38	0.55
41:Ls:55:GLU:OE2	41:Ls:69:LYS:NZ	2.40	0.55
49:S1:1553:G:N7	72:Sp:43:ARG:NH2	2.50	0.55
80:Rx:6:PRO:HG3	80:Rx:14:LYS:HG2	1.88	0.55
49:R1:511:A:H5'	66:Rj:173:ALA:HB2	1.89	0.55
5:L1:1295:G:O2'	21:LN:115:ARG:NH1	2.40	0.55
13:LF:92:ARG:HA	13:LF:172:LEU:HB2	1.87	0.55
69:Sm:130:THR:OG1	69:Sm:131:ASP:N	2.38	0.55
81:Sy:10:ARG:HB2	81:Sy:24:VAL:HG23	1.87	0.55
49:R1:1553:G:O6	72:Rp:43:ARG:NH1	2.40	0.55
87:M1:664:U:H2'	87:M1:665:A:C8	2.42	0.55
87:M1:1661:G:H2'	87:M1:1662:G:C8	2.42	0.55
87:M1:2767:U:O2'	25:Mc:30:ALA:O	2.20	0.55
89:MQ:135:PHE:HB2	89:MQ:172:LEU:HD13	1.89	0.55
5:L1:2792:A:H5'	25:Lc:84:THR:HG21	1.89	0.55
8:LA:56:LYS:NZ	8:LA:101:PHE:O	2.40	0.55
19:LL:147:ARG:HB2	19:LL:150:VAL:HG23	1.89	0.55
46:Lx:140:ASP:OD1	46:Lx:141:GLY:N	2.38	0.55
49:S1:69:G:H1	49:S1:82:U:H3	1.55	0.55
49:S1:400:A:H5''	65:Si:25:ARG:HA	1.89	0.55
56:SG:221:MET:SD	56:SG:223:TRP:NE1	2.80	0.55
77:Su:33:GLN:N	77:Su:33:GLN:OE1	2.40	0.55
81:Ry:37:LYS:HA	81:Ry:40:LEU:HD13	1.88	0.55
49:R1:29:U:H2'	49:R1:30:G:H8	1.72	0.55
49:R1:1254:U:OP2	69:Rm:46:ARG:NH2	2.38	0.55
65:Ri:86:SER:HA	68:Rl:11:ARG:HH21	1.72	0.55
84:Ro:99:GLN:HA	84:Ro:99:GLN:NE2	2.21	0.55
15:LH:116:GLU:HG2	17:LJ:197:LEU:HD22	1.88	0.55
42:Lt:115:ARG:HD3	42:Lt:121:LYS:HE3	1.89	0.55
49:S1:1672:G:H2'	49:S1:1673:G:C8	2.42	0.55
56:SG:115:ILE:HD11	56:SG:119:ALA:HA	1.89	0.55
81:Ry:3:ASP:OD1	81:Ry:3:ASP:N	2.40	0.55
61:Re:148:ARG:NH2	63:Rg:201:GLN:OE1	2.40	0.55
73:Rq:37:THR:O	73:Rq:45:ARG:NH1	2.40	0.55
6:M2:81:U:H5''	6:M2:82:U:H5'	1.88	0.55
18:LK:47:TYR:OH	18:LK:57:ALA:O	2.22	0.55
41:Ls:29:VAL:O	41:Ls:32:SER:OG	2.24	0.55
68:Sl:27:THR:O	68:Sl:30:ARG:NH1	2.38	0.55
76:St:39:THR:HA	76:St:100:ILE:HD13	1.89	0.55
55:RF:106:TYR:HE2	69:Rm:78:LEU:HD11	1.72	0.55
56:RG:266:ASP:N	56:RG:266:ASP:OD1	2.40	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:Rc:82:ASN:HB2	59:Rc:207:LEU:HD22	1.89	0.55
12:ME:36:LEU:HD11	12:ME:87:LEU:HD23	1.89	0.55
3:CN:112:ASP:N	3:CN:112:ASP:OD1	2.39	0.54
5:L1:2600:C:OP1	16:LI:93:LYS:NZ	2.39	0.54
7:L3:28:C:OP1	13:LF:137:ARG:NH1	2.36	0.54
14:LG:76:THR:O	14:LG:79:GLU:N	2.37	0.54
49:R1:814:A:O2'	49:R1:816:G:OP2	2.25	0.54
87:M1:1261:G:OP2	87:M1:1261:G:N2	2.40	0.54
87:M1:3042:U:OP2	87:M1:3092:C:N4	2.34	0.54
5:L1:595:G:H1	5:L1:609:G:H5''	1.72	0.54
8:LA:146:LEU:HA	8:LA:149:ILE:HB	1.89	0.54
16:LI:5:LYS:HG3	31:LI:40:VAL:HG11	1.90	0.54
49:S1:871:G:H2'	49:S1:872:G:C8	2.42	0.54
57:Sa:167:LYS:NZ	57:Sa:204:TYR:O	2.41	0.54
54:RE:31:LYS:HD3	49:R1:545:A:H2'	1.87	0.54
66:Rj:157:ASP:OD2	66:Rj:157:ASP:N	2.38	0.54
69:Rm:131:ASP:HA	69:Rm:134:SER:HB2	1.89	0.54
87:M1:361:A:O3'	30:Mh:45:ARG:NH2	2.40	0.54
5:L1:715:A:H5''	39:Lq:115:LYS:HA	1.90	0.54
5:L1:993:G:OP1	22:LO:43:LYS:NZ	2.41	0.54
14:LG:75:PHE:H	14:LG:97:VAL:HA	1.72	0.54
40:Lr:17:ARG:NH2	40:Lr:18:TYR:OH	2.40	0.54
49:S1:587:C:OP1	54:SE:26:LYS:NZ	2.39	0.54
55:SF:121:CYS:SG	55:SF:122:SER:N	2.80	0.54
81:Ry:86:GLU:OE2	81:Ry:90:ARG:NH1	2.41	0.54
49:R1:175:G:H21	49:R1:176:C:H41	1.54	0.54
49:S1:346:G:H5'	68:Sl:79:LYS:HD3	1.89	0.54
49:S1:556:A:H5'	54:SE:56:MET:HE3	1.90	0.54
49:R1:207:U:O2	65:Ri:178:ARG:NH1	2.40	0.54
87:M1:1095:U:H4'	87:M1:1096:U:H5'	1.89	0.54
87:M1:2213:A:H2'	87:M1:2214:A:C8	2.42	0.54
40:Lr:115:LYS:NZ	40:Lr:119:GLU:OE1	2.40	0.54
45:Lw:3:ARG:HB2	45:Lw:207:VAL:HG22	1.90	0.54
73:Sq:44:LEU:HB3	73:Sq:78:VAL:HG11	1.89	0.54
79:Rw:68:ARG:HA	59:Rc:225:LEU:HD22	1.90	0.54
81:Ry:112:LYS:NZ	49:R1:57:G:OP1	2.40	0.54
3:CN:89:ARG:NH2	49:R1:1263:G:O2'	2.40	0.54
5:L1:76:G:O2'	14:LG:100:ARG:NH1	2.35	0.54
5:L1:728:G:H5''	19:LL:43:PRO:HB2	1.90	0.54
26:Ld:21:ARG:NH2	49:S1:1118:G:OP1	2.38	0.54
78:Rv:38:LYS:HD3	78:Rv:49:GLU:HB3	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:RG:38:ARG:HA	56:RG:67:ILE:HG23	1.89	0.54
39:Mq:44:ASN:ND2	14:MG:4:SER:O	2.41	0.54
49:S1:1487:A:OP2	60:Sd:8:LYS:NZ	2.41	0.54
49:R1:258:C:O2	65:Ri:178:ARG:NH1	2.41	0.54
59:Rc:79:GLU:N	59:Rc:79:GLU:OE2	2.40	0.54
64:Rh:147:ASN:OD1	64:Rh:147:ASN:N	2.40	0.54
87:M1:3211:C:OP2	15:MH:109:ARG:NH2	2.40	0.54
10:LC:82:LEU:HB3	10:LC:87:ALA:HB2	1.90	0.54
48:Lz:160:PHE:HA	48:Lz:163:LEU:HB3	1.90	0.54
49:S1:154:G:OP1	63:Sg:2:LYS:NZ	2.38	0.54
49:S1:1147:A:OP1	59:Sc:91:ARG:NH1	2.40	0.54
55:SF:123:ASN:ND2	55:SF:144:CYS:SG	2.80	0.54
59:Sc:142:GLY:N	59:Sc:153:SER:O	2.34	0.54
49:R1:788:A:OP2	61:Re:108:ARG:NH2	2.41	0.54
87:M1:1646:G:O2'	87:M1:1808:G:N2	2.37	0.54
5:L1:3070:A:OP1	20:LM:62:ARG:NH1	2.41	0.54
49:S1:1102:G:OP2	80:Sx:7:ARG:NH1	2.35	0.54
56:SG:110:VAL:HA	56:SG:126:SER:HA	1.88	0.54
87:M1:269:G:H5''	16:MI:14:LYS:HE2	1.90	0.54
87:M1:2453:U:O4	87:M1:2485:A:N6	2.40	0.54
20:MM:98:ARG:NH2	20:MM:130:ASN:OD1	2.41	0.54
89:MQ:75:LYS:NZ	89:MQ:196:VAL:O	2.41	0.54
10:MC:109:LEU:HA	10:MC:112:GLU:HB3	1.89	0.54
4:CP:56:C:OP1	13:LF:61:ARG:NH1	2.41	0.54
5:L1:542:G:N1	5:L1:550:A:C6	2.76	0.54
5:L1:1119:C:H2'	5:L1:1120:A:H8	1.73	0.54
5:L1:1334:U:H5''	9:LB:206:LYS:HB3	1.90	0.54
49:S1:1171:A:H2'	49:S1:1172:G:H8	1.73	0.54
49:S1:1229:G:H21	49:S1:1256:A:N6	1.98	0.54
74:Sr:35:CYS:HA	74:Sr:38:ILE:HG22	1.89	0.54
79:Sw:2:THR:OG1	79:Sw:3:ARG:N	2.40	0.54
81:Ry:38:ASP:O	81:Ry:52:LYS:NZ	2.41	0.54
56:RG:211:ILE:HD11	56:RG:225:LEU:HD23	1.89	0.54
72:Rp:32:ASP:N	72:Rp:32:ASP:OD1	2.33	0.54
87:M1:2899:C:O2'	87:M1:2901:G:OP2	2.22	0.54
44:Mv:25:ASN:O	44:Mv:25:ASN:ND2	2.37	0.54
10:MC:45:ASN:OD1	10:MC:47:SER:OG	2.22	0.54
40:Mr:50:PRO:HD3	40:Mr:68:ILE:HG12	1.90	0.54
11:LD:36:LYS:HB2	11:LD:78:MET:HE1	1.90	0.53
11:LD:120:ASP:OD2	11:LD:124:ARG:NH2	2.41	0.53
21:LN:5:LYS:NZ	21:LN:32:SER:O	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:S1:386:G:OP2	65:Si:25:ARG:NH2	2.40	0.53
56:SG:248:ASN:ND2	56:SG:297:ASP:O	2.40	0.53
60:Sd:67:ASN:O	60:Sd:70:THR:OG1	2.25	0.53
49:R1:177:U:O2'	63:Rg:191:ARG:NH1	2.41	0.53
87:M1:2792:A:H2'	87:M1:2793:OMG:H8	1.73	0.53
21:MN:27:MET:HE1	21:MN:44:PHE:HB2	1.89	0.53
5:L1:89:A:OP2	19:LL:171:LYS:NZ	2.41	0.53
5:L1:591:G:N2	5:L1:612:U:OP1	2.39	0.53
10:LC:100:GLU:HG2	10:LC:104:GLU:HG3	1.89	0.53
11:LD:92:TYR:HB3	11:LD:99:ILE:HD12	1.90	0.53
33:Lk:90:ILE:HD13	40:Lr:81:LEU:HD22	1.90	0.53
39:Lq:21:ARG:O	39:Lq:24:LYS:NZ	2.41	0.53
49:S1:1534:G:OP2	82:Sz:74:SER:OG	2.20	0.53
50:SA:79:ILE:HG12	50:SA:85:ARG:HA	1.90	0.53
66:Sj:109:LEU:HB2	66:Sj:146:PHE:HB3	1.90	0.53
81:Ry:131:ARG:NH1	49:R1:153:G:OP2	2.41	0.53
64:Rh:115:SER:OG	64:Rh:116:ARG:NH1	2.40	0.53
87:M1:981:U:HO2'	87:M1:1105:A:HO2'	1.57	0.53
87:M1:1029:G:H2'	87:M1:1030:A:H8	1.72	0.53
87:M1:1367:G:N2	87:M1:1368:U:O4	2.42	0.53
6:M2:67:U:H5''	30:Mh:85:LYS:HB2	1.89	0.53
32:Lj:102:GLU:OE2	32:Lj:105:ARG:NH2	2.40	0.53
36:Ln:46:THR:HG21	36:Ln:90:PHE:HA	1.89	0.53
49:S1:1009:U:OP2	71:So:129:LYS:NZ	2.41	0.53
49:S1:1681:A:H8	63:Sg:66:GLY:HA3	1.73	0.53
73:Sq:28:LEU:HD12	73:Sq:30:LYS:HE3	1.90	0.53
49:R1:313:U:O4	49:R1:1130:G:O2'	2.26	0.53
49:R1:651:G:H2'	49:R1:652:G:C8	2.44	0.53
49:R1:803:A:O2'	64:Rh:104:ARG:NH1	2.41	0.53
87:M1:2489:C:H3'	87:M1:2490:C:H2'	1.89	0.53
18:MK:33:ALA:HB1	18:MK:117:ILE:HG12	1.90	0.53
5:L1:2584:G:O2'	10:LC:240:ASN:OD1	2.26	0.53
46:Lx:187:SER:OG	46:Lx:190:GLU:OE1	2.25	0.53
49:S1:1159:C:O2'	73:Sq:140:LYS:NZ	2.41	0.53
56:SG:54:PHE:HE1	56:SG:312:VAL:HG21	1.72	0.53
56:SG:221:MET:HB3	56:SG:233:THR:HG23	1.90	0.53
58:Sb:212:VAL:HG13	58:Sb:213:ARG:H	1.73	0.53
61:Se:120:SER:O	61:Se:120:SER:OG	2.26	0.53
76:Rt:77:ASN:OD1	76:Rt:101:ASN:ND2	2.41	0.53
56:RG:240:VAL:HA	56:RG:256:THR:HA	1.90	0.53
87:M1:1799:A:H2'	87:M1:1800:A:C8	2.44	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
88:DQ:51:U:O4	88:DQ:65:G:O6	2.27	0.53
47:My:141:ARG:HD2	47:My:180:LYS:HB2	1.90	0.53
5:L1:3375:A:O2'	5:L1:3378:C:OP2	2.26	0.53
72:Sp:81:ARG:NH2	72:Sp:120:SER:O	2.40	0.53
82:Sz:95:HIS:ND1	82:Sz:96:SER:O	2.41	0.53
49:R1:142:G:C6	49:R1:173:A:N1	2.76	0.53
49:R1:1257:U:O2'	49:R1:1258:U:O4'	2.27	0.53
57:Ra:84:ARG:NH1	85:Rr:82:ASP:O	2.41	0.53
86:MA:62:THR:HG21	86:MA:78:ARG:HD2	1.90	0.53
33:Mk:41:ARG:O	33:Mk:43:LYS:NZ	2.39	0.53
5:L1:2890:A:O2'	5:L1:2933:A:N3	2.39	0.53
9:LB:47:ARG:NH1	9:LB:183:ASP:OD2	2.42	0.53
14:LG:67:ARG:HD2	39:Lq:105:LEU:HD22	1.91	0.53
18:LK:122:ALA:HB3	18:LK:143:PRO:HB2	1.91	0.53
49:S1:736:C:H2'	49:S1:737:A:H8	1.73	0.53
56:SG:109:ASP:HB2	56:SG:127:ARG:HD2	1.91	0.53
58:Sb:69:CYS:SG	71:So:114:ARG:NH1	2.82	0.53
53:RD:19:ARG:NH1	49:R1:1597:A:OP1	2.42	0.53
85:Rr:82:ASP:OD1	85:Rr:82:ASP:N	2.31	0.53
41:Ms:7:ASP:OD1	41:Ms:7:ASP:N	2.34	0.53
5:L1:1245:A:N6	5:L1:1272:C:O2'	2.39	0.53
5:L1:2213:A:H2'	5:L1:2214:A:C8	2.44	0.53
79:Sw:31:SER:OG	79:Sw:32:LYS:N	2.41	0.53
49:R1:493:U:H2'	49:R1:494:U:H2'	1.91	0.53
49:R1:1387:G:N7	85:Rr:44:LYS:NZ	2.52	0.53
61:Re:21:ASP:N	61:Re:21:ASP:OD1	2.39	0.53
61:Re:141:THR:OG1	61:Re:143:ASP:OD1	2.24	0.53
20:MM:148:ASP:OD1	20:MM:151:ARG:NH2	2.41	0.53
24:Lb:39:CYS:HB2	24:Lb:57:CYS:SG	2.48	0.53
39:Lq:72:VAL:HG12	39:Lq:111:LYS:HB3	1.91	0.53
49:S1:154:G:OP2	81:Sy:131:ARG:NH2	2.42	0.53
49:S1:334:G:O6	65:Si:5:ARG:NH2	2.41	0.53
49:S1:1060:U:H3'	49:S1:1061:A:H5''	1.90	0.53
80:Rx:90:ASP:N	80:Rx:90:ASP:OD1	2.41	0.53
73:Rq:125:GLU:OE2	73:Rq:128:LYS:NZ	2.42	0.53
5:L1:1661:G:H2'	5:L1:1662:G:C8	2.44	0.53
34:Ll:39:GLN:OE1	34:Ll:39:GLN:N	2.42	0.53
49:S1:159:U:O2'	63:Sg:87:ARG:NH1	2.42	0.53
70:Sn:87:ASP:N	70:Sn:87:ASP:OD1	2.42	0.53
79:Rw:87:GLU:N	79:Rw:87:GLU:OE2	2.42	0.53
49:R1:486:G:H1	49:R1:501:U:H3	1.57	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:R1:959:U:H5''	70:Rn:14:SER:HB2	1.91	0.53
87:M1:2697:A:H2'	87:M1:2698:G:C8	2.44	0.53
6:M2:40:A:OP2	6:M2:103:G:N1	2.40	0.53
23:Ma:38:ALA:HB3	23:Ma:59:MET:HB2	1.90	0.53
10:MC:140:VAL:HG21	16:MI:3:ALA:HB2	1.91	0.53
9:LB:234:GLU:O	9:LB:237:ASN:ND2	2.42	0.53
10:LC:189:LEU:HD23	10:LC:190:VAL:HG13	1.91	0.53
23:La:24:ASN:ND2	23:La:97:ASP:OD2	2.41	0.53
60:Sd:164:VAL:HG13	60:Sd:168:ILE:HD12	1.90	0.53
66:Sj:136:VAL:HA	66:Sj:156:ILE:HG22	1.91	0.53
77:Su:22:ILE:HD11	77:Su:93:LEU:HD12	1.91	0.53
80:Sx:54:LEU:HD12	80:Sx:73:ARG:HG2	1.91	0.53
75:Rs:36:LYS:NZ	49:R1:1567:U:O3'	2.41	0.53
49:R1:1665:U:O4'	49:R1:1733:C:N4	2.42	0.53
58:Rb:24:PHE:HZ	84:Ro:39:ILE:HA	1.74	0.53
17:MJ:161:LYS:NZ	87:M1:3182:G:O3'	2.42	0.53
87:M1:627:U:H2'	87:M1:628:A:C8	2.43	0.53
31:Mi:66:GLU:OE2	31:Mi:91:ASN:ND2	2.41	0.53
5:L1:1650:G:O3'	45:Lw:70:ARG:NH2	2.43	0.52
5:L1:1925:U:O2'	5:L1:1927:G:N7	2.42	0.52
12:LE:83:ASP:OD1	12:LE:83:ASP:N	2.41	0.52
12:LE:215:GLU:OE1	12:LE:215:GLU:N	2.42	0.52
33:Lk:22:VAL:HG12	33:Lk:30:LEU:HD22	1.91	0.52
37:Lo:43:ILE:HB	37:Lo:90:VAL:HG13	1.91	0.52
65:Si:187:GLU:OE1	68:Sl:21:ASN:ND2	2.41	0.52
69:Rm:33:ARG:NH2	69:Rm:100:TRP:O	2.41	0.52
85:Rr:21:TYR:OH	85:Rr:62:GLN:NE2	2.43	0.52
13:MF:92:ARG:HA	13:MF:172:LEU:HB2	1.91	0.52
34:Mi:39:GLN:OE1	34:Mi:39:GLN:N	2.40	0.52
58:Sb:33:LYS:O	58:Sb:98:THR:OG1	2.25	0.52
75:Rs:35:ILE:HG23	75:Rs:102:ALA:HB2	1.91	0.52
77:Ru:28:SER:HB3	77:Ru:34:LEU:HD22	1.90	0.52
49:R1:1175:U:H2'	49:R1:1176:G:H8	1.74	0.52
87:M1:40:A:OP1	95:M1:3603:SPD:N1	2.42	0.52
30:Mh:14:LYS:HE3	28:Mf:51:ILE:HD11	1.89	0.52
5:L1:577:C:O2'	5:L1:579:G:OP1	2.27	0.52
5:L1:1257:C:N4	5:L1:1261:G:H22	2.07	0.52
59:Sc:40:LYS:HD3	59:Sc:247:ALA:HB1	1.90	0.52
72:Sp:107:ILE:HA	72:Sp:111:MET:HE2	1.90	0.52
80:Sx:109:ARG:HG3	80:Sx:114:LYS:HA	1.90	0.52
76:Rt:89:ARG:NH1	49:R1:1562:G:OP1	2.39	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:R1:591:A:H2'	49:R1:592:A:C8	2.45	0.52
49:R1:647:G:H1	49:R1:687:G:H1	1.56	0.52
49:R1:844:A:H2'	49:R1:845:G:H8	1.75	0.52
49:R1:1474:G:H2'	49:R1:1475:A:C8	2.44	0.52
58:Rb:27:LYS:NZ	58:Rb:49:ASN:OD1	2.40	0.52
62:Rf:42:LEU:HD22	62:Rf:47:SER:HA	1.89	0.52
63:Rg:126:ASP:N	63:Rg:126:ASP:OD1	2.37	0.52
87:M1:982:C:H5''	38:Mp:23:LYS:HD3	1.91	0.52
45:Mw:3:ARG:HB2	45:Mw:207:VAL:HG22	1.91	0.52
90:MP:13:LEU:HD22	90:MP:62:LEU:HD12	1.92	0.52
5:L1:1080:A:OP2	48:Lz:140:ARG:NH2	2.42	0.52
61:Se:71:LYS:HG3	61:Se:91:THR:HB	1.90	0.52
66:Sj:106:GLU:O	66:Sj:111:THR:OG1	2.25	0.52
69:Sm:103:LEU:HD11	69:Sm:115:VAL:HG23	1.90	0.52
49:R1:225:A:C6	49:R1:837:G:N1	2.78	0.52
87:M1:2425:G:OP2	16:MI:90:ASN:ND2	2.39	0.52
23:Ma:81:GLN:HG2	23:Ma:83:LYS:H	1.74	0.52
48:Mz:215:ASP:N	48:Mz:215:ASP:OD1	2.42	0.52
5:L1:2514:U:OP2	5:L1:2586:G:N2	2.42	0.52
5:L1:2767:U:O2'	25:Lc:30:ALA:O	2.24	0.52
7:L3:107:C:OP2	12:LE:203:LYS:NZ	2.43	0.52
36:Ln:10:ARG:NH1	36:Ln:12:TYR:OH	2.42	0.52
49:S1:1564:U:OP1	76:St:38:LYS:NZ	2.37	0.52
72:Sp:88:GLU:OE2	72:Sp:88:GLU:N	2.42	0.52
75:Ss:140:THR:HA	75:Ss:143:ARG:HH21	1.75	0.52
83:RC:53:ILE:HG22	62:Rf:57:SER:HB3	1.91	0.52
57:Ra:119:ARG:NH1	59:Rc:241:ASP:OD2	2.43	0.52
17:MJ:121:PRO:HA	17:MJ:124:LEU:HD12	1.92	0.52
87:M1:2219:A:H2'	87:M1:2220:A2M:H8	1.90	0.52
10:MC:54:GLU:HG2	10:MC:57:ARG:HH21	1.74	0.52
36:Mn:10:ARG:HG2	36:Mn:108:VAL:HG22	1.92	0.52
69:Rm:81:ASP:N	69:Rm:81:ASP:OD1	2.42	0.52
85:Rr:108:ASP:OD2	85:Rr:108:ASP:N	2.39	0.52
87:M1:2815:OMG:N2	87:M1:2818:U:O2	2.41	0.52
46:Mx:85:VAL:HG22	46:Mx:202:THR:HG22	1.90	0.52
5:L1:638:C:OP1	35:Lm:21:HIS:NE2	2.26	0.52
7:L3:28:C:H5''	13:LF:137:ARG:HG2	1.90	0.52
23:La:18:PRO:HA	23:La:51:ALA:HA	1.92	0.52
49:S1:68:A:N6	63:Sg:132:ARG:O	2.41	0.52
52:SC:57:MET:HG2	62:Sf:144:GLU:HG3	1.91	0.52
65:Si:11:ARG:NH1	65:Si:15:GLY:O	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:R1:992:A:H5''	49:R1:993:A:H8	1.75	0.52
87:M1:2960:C:H2'	87:M1:2961:G:C8	2.44	0.52
5:L1:2812:C:H2'	5:L1:2813:A:C8	2.45	0.52
36:Ln:31:ARG:NH1	36:Ln:35:GLU:OE2	2.43	0.52
66:Sj:100:LYS:HB3	66:Sj:103:ASP:H	1.75	0.52
80:Rx:41:SER:OG	80:Rx:43:PHE:O	2.28	0.52
55:RF:130:VAL:HG11	55:RF:143:LYS:HB2	1.92	0.52
56:RG:37:SER:OG	56:RG:38:ARG:N	2.43	0.52
49:R1:474:A:H5''	66:Rj:144:PRO:HD2	1.91	0.52
59:Rc:45:VAL:HG21	59:Rc:68:ILE:HG23	1.91	0.52
64:Rh:14:THR:H	64:Rh:17:GLU:HG3	1.74	0.52
87:M1:714:G:HO2'	87:M1:753:C:HO2'	1.56	0.52
87:M1:2270:A:H2'	87:M1:2271:A:C8	2.45	0.52
87:M1:3343:G:O2'	87:M1:3362:A:N6	2.42	0.52
18:MK:62:ARG:NH1	6:M2:5:U:OP2	2.43	0.52
5:L1:664:U:H2'	5:L1:665:A:C8	2.45	0.52
5:L1:1477:A:OP1	5:L1:3075:G:O2'	2.25	0.52
5:L1:1778:G:O2'	5:L1:1780:G:OP2	2.28	0.52
24:Lb:86:LEU:HD13	45:Lw:108:PRO:HG2	1.91	0.52
49:S1:647:G:H22	49:S1:687:G:H1	1.58	0.52
76:St:135:ILE:O	76:St:139:THR:OG1	2.25	0.52
75:Rs:106:GLU:HG3	13:MF:118:PRO:HG3	1.92	0.52
78:Rv:23:ILE:HG12	59:Rc:225:LEU:HD12	1.91	0.52
55:RF:140:TYR:OH	49:R1:1234:A:N3	2.37	0.52
49:R1:25:C:HO2'	49:R1:366:A:HO2'	1.51	0.52
49:R1:156:A:N1	49:R1:415:C:O2	2.43	0.52
34:Ml:49:ILE:HG23	34:Ml:100:ILE:HG13	1.92	0.52
25:Mc:7:THR:O	25:Mc:22:GLN:NE2	2.43	0.52
5:L1:1656:A:OP2	33:Lk:37:LYS:NZ	2.42	0.52
5:L1:2112:U:H4'	5:L1:2113:A:H5'	1.91	0.52
5:L1:2899:C:O2'	5:L1:2901:G:OP2	2.25	0.52
31:Li:64:SER:O	31:Li:64:SER:OG	2.27	0.52
49:S1:1785:U:H2'	49:S1:1786:G:H8	1.75	0.52
53:SD:40:ARG:NH2	77:Su:71:PRO:O	2.43	0.52
68:Sl:143:SER:O	68:Sl:143:SER:OG	2.22	0.52
49:R1:257:A:H1'	65:Ri:73:SER:HB2	1.92	0.52
49:R1:327:U:O2	68:Rl:11:ARG:NH1	2.43	0.52
57:Ra:198:MET:HE1	85:Rr:89:SER:HB2	1.91	0.52
19:ML:89:ASP:OD1	19:ML:90:ASP:N	2.43	0.52
19:ML:175:ALA:HB2	39:Mq:56:VAL:HG22	1.91	0.52
11:MD:91:ARG:HD2	11:MD:143:GLU:HB2	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:Mq:19:LYS:HG2	39:Mq:25:HIS:HB2	1.91	0.52
5:L1:618:C:OP1	18:LK:173:ARG:NH2	2.42	0.51
5:L1:3329:U:H5''	46:Lx:308:MET:HE2	1.91	0.51
39:Lq:85:ASP:OD2	39:Lq:85:ASP:N	2.36	0.51
49:S1:1237:G:H2'	49:S1:1238:A:H8	1.74	0.51
66:Sj:108:ARG:HH22	66:Sj:126:ARG:HH21	1.58	0.51
72:Sp:81:ARG:NH1	72:Sp:97:TYR:O	2.40	0.51
63:Rg:67:VAL:H	63:Rg:100:ALA:HB2	1.76	0.51
89:MQ:51:VAL:HG22	89:MQ:87:VAL:HG22	1.91	0.51
90:MP:11:LYS:HB3	90:MP:64:ILE:HB	1.92	0.51
5:L1:765:C:N4	14:LG:176:GLU:OE1	2.43	0.51
5:L1:1432:C:O2'	5:L1:1434:G:OP2	2.27	0.51
5:L1:1786:G:H2'	5:L1:1787:A:C8	2.45	0.51
28:Lf:25:GLN:OE1	28:Lf:28:ARG:NH1	2.43	0.51
49:S1:1504:G:N3	49:S1:1563:C:O2'	2.43	0.51
56:SG:148:ASN:OD1	56:SG:148:ASN:N	2.41	0.51
66:Sj:108:ARG:HB2	66:Sj:111:THR:HG23	1.92	0.51
70:Sn:29:SER:OG	70:Sn:31:GLU:OE1	2.27	0.51
74:Sr:24:LEU:HB3	74:Sr:34:LEU:HD21	1.92	0.51
79:Sw:90:THR:HG23	79:Sw:94:LEU:HD12	1.91	0.51
75:Rs:88:ARG:NH1	75:Rs:112:ASP:OD2	2.41	0.51
80:Rx:89:ASN:OD1	80:Rx:89:ASN:N	2.42	0.51
53:RD:44:ARG:NH2	49:R1:1279:C:O3'	2.43	0.51
62:Rf:164:PRO:HA	62:Rf:167:ARG:HD3	1.91	0.51
64:Rh:14:THR:OG1	64:Rh:15:GLU:N	2.41	0.51
87:M1:129:U:H2'	87:M1:130:A:C8	2.46	0.51
87:M1:2864:A:H5''	12:ME:114:GLY:HA2	1.92	0.51
89:MQ:104:ARG:HD2	89:MQ:184:GLY:HA3	1.91	0.51
47:My:126:ILE:O	47:My:129:THR:OG1	2.27	0.51
13:MF:7:ASN:HB3	13:MF:10:ARG:HB2	1.90	0.51
5:L1:744:A:H1'	19:LL:141:ARG:HE	1.76	0.51
8:LA:31:ARG:NE	34:Ll:107:ILE:O	2.40	0.51
49:S1:1321:A:OP2	57:Sa:101:ARG:NH2	2.43	0.51
63:Sg:68:LEU:HB3	63:Sg:69:LEU:HG	1.92	0.51
64:Sh:58:LEU:HG	64:Sh:88:ARG:HD2	1.91	0.51
68:Sl:100:TYR:OH	79:Sw:80:ASN:ND2	2.43	0.51
56:RG:182:ASN:ND2	56:RG:184:ASN:OD1	2.43	0.51
49:R1:854:U:O4	49:R1:855:A:N6	2.43	0.51
40:Mr:34:LYS:HD3	40:Mr:35:SER:H	1.74	0.51
11:MD:57:VAL:HG23	11:MD:68:LEU:HD13	1.92	0.51
5:L1:1257:C:C4	5:L1:1261:G:N2	2.78	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:LG:57:VAL:HG23	14:LG:147:ILE:HD12	1.91	0.51
53:SD:39:CYS:SG	53:SD:42:CYS:HB2	2.50	0.51
49:R1:250:C:H2'	49:R1:251:A:H8	1.75	0.51
73:Rq:54:LEU:HD21	73:Rq:112:TYR:HB3	1.92	0.51
87:M1:1389:G:H5''	35:Mm:101:SER:HB3	1.92	0.51
87:M1:1437:OMC:HM22	47:My:93:MET:HG3	1.92	0.51
87:M1:1899:G:O2'	87:M1:2334:U:O4	2.24	0.51
18:MK:67:ILE:HD11	18:MK:80:LYS:HB3	1.91	0.51
20:MM:101:VAL:HG12	20:MM:104:ARG:HH12	1.76	0.51
40:Mr:23:VAL:HG12	40:Mr:45:GLY:HA3	1.92	0.51
5:L1:541:U:O4	5:L1:542:G:O6	2.29	0.51
19:LL:125:ASP:OD2	19:LL:125:ASP:N	2.37	0.51
56:SG:9:LEU:O	56:SG:10:ARG:NH1	2.43	0.51
79:Sw:80:ASN:OD1	79:Sw:124:LYS:NZ	2.35	0.51
76:Rt:37:VAL:HG12	76:Rt:39:THR:H	1.75	0.51
49:R1:126:A:H62	49:R1:291:G:H21	1.59	0.51
49:R1:163:G:N2	49:R1:163:G:OP2	2.37	0.51
49:R1:1591:C:H2'	49:R1:1592:A:C8	2.45	0.51
72:Rp:61:ARG:NH1	72:Rp:88:GLU:OE2	2.44	0.51
87:M1:2129:U:H2'	87:M1:2130:G:C8	2.45	0.51
87:M1:2269:U:H2'	87:M1:2270:A:H2	1.75	0.51
87:M1:2836:C:H5	87:M1:2852:C:H42	1.59	0.51
90:MP:65:GLN:O	90:MP:68:GLN:NE2	2.40	0.51
5:L1:769:G:O2'	14:LG:168:ARG:NH1	2.40	0.51
5:L1:1634:G:N7	40:Lr:17:ARG:NH1	2.59	0.51
8:LA:99:GLU:OE1	8:LA:99:GLU:N	2.40	0.51
22:LO:106:LEU:HA	22:LO:109:VAL:HG12	1.93	0.51
29:Lg:12:LEU:HD11	29:Lg:68:SER:HB3	1.92	0.51
49:S1:590:C:OP1	54:SE:43:ARG:NH1	2.40	0.51
49:S1:1474:G:H2'	49:S1:1475:A:C8	2.45	0.51
57:Sa:74:VAL:HB	57:Sa:121:VAL:HG12	1.92	0.51
49:R1:992:A:O2'	49:R1:1785:U:O2	2.21	0.51
63:Rg:48:TYR:HE1	63:Rg:116:LYS:HG3	1.75	0.51
17:MJ:178:VAL:HG22	15:MH:135:LEU:HD11	1.93	0.51
87:M1:2261:G:O2'	87:M1:2262:A:N7	2.41	0.51
16:MI:192:LYS:O	16:MI:196:THR:OG1	2.29	0.51
2:CM:22:U:O2'	3:CN:22:ARG:NH2	2.43	0.51
5:L1:571:U:H2'	5:L1:572:A:H8	1.75	0.51
19:LL:30:VAL:O	19:LL:34:THR:OG1	2.24	0.51
49:S1:1776:A:H2'	49:S1:1777:G:C8	2.46	0.51
50:RA:51:ARG:HH21	83:RC:37:SER:HB3	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:R1:200:A:H2'	49:R1:201:G:C8	2.46	0.51
49:R1:343:C:H2'	49:R1:344:A:H8	1.75	0.51
5:L1:1236:G:N1	5:L1:1244:A:OP1	2.44	0.51
7:L3:64:A:N7	12:LE:209:ASN:ND2	2.53	0.51
39:Lq:104:THR:HG21	39:Lq:112:ILE:HD11	1.93	0.51
65:Si:138:ASN:HA	65:Si:141:ARG:HH11	1.75	0.51
65:Si:157:GLU:N	65:Si:157:GLU:OE1	2.44	0.51
79:Rw:57:ARG:NH2	70:Rn:16:ILE:O	2.36	0.51
57:Ra:127:ARG:NH2	57:Ra:150:ASP:O	2.44	0.51
64:Rh:31:SER:O	64:Rh:35:LYS:NZ	2.44	0.51
64:Rh:64:VAL:HG23	64:Rh:67:LEU:HB2	1.93	0.51
5:L1:533:A:O2'	5:L1:535:G:OP2	2.29	0.51
5:L1:598:A:OP1	9:LB:41:ARG:NH1	2.44	0.51
19:LL:36:LEU:O	19:LL:40:THR:OG1	2.28	0.51
32:Lj:34:GLN:OE1	32:Lj:38:ARG:NH2	2.44	0.51
49:S1:1727:G:H2'	49:S1:1728:A:C8	2.45	0.51
56:SG:126:SER:OG	56:SG:127:ARG:N	2.43	0.51
57:Sa:79:ARG:NH2	57:Sa:164:ASN:O	2.40	0.51
75:Ss:20:THR:HG21	75:Ss:35:ILE:HG23	1.93	0.51
77:Su:37:VAL:HG13	77:Su:107:THR:HB	1.93	0.51
49:R1:797:G:O2'	68:Rl:69:LYS:NZ	2.41	0.51
49:R1:1465:C:OP1	73:Rq:139:GLN:NE2	2.44	0.51
66:Rj:128:LEU:HD22	66:Rj:133:HIS:HD2	1.76	0.51
85:Rr:58:MET:HA	85:Rr:61:ILE:HB	1.91	0.51
87:M1:351:A:N6	28:Mf:37:TYR:O	2.39	0.51
13:MF:18:VAL:HG13	13:MF:70:THR:HG22	1.92	0.51
5:L1:406:G:OP1	5:L1:1415:U:O2'	2.27	0.51
5:L1:649:A:OP2	5:L1:2868:U:O2'	2.29	0.51
5:L1:655:C:H2'	5:L1:656:A:H8	1.76	0.51
46:Lx:301:THR:HG23	46:Lx:303:LYS:HG2	1.93	0.51
49:S1:1591:C:H2'	49:S1:1592:A:H8	1.75	0.51
66:Sj:114:TYR:HD1	66:Sj:122:VAL:HG13	1.75	0.51
49:R1:1124:A:H2'	49:R1:1125:A:C8	2.46	0.51
49:R1:1413:U:O2'	49:R1:1416:G:OP1	2.26	0.51
60:Rd:14:ASP:OD2	60:Rd:14:ASP:N	2.36	0.51
61:Re:87:MET:HE1	61:Re:123:LEU:HD12	1.92	0.51
87:M1:112:U:OP1	32:Mj:104:GLN:NE2	2.41	0.51
87:M1:1349:G:H5'	47:My:291:ASN:HD21	1.76	0.51
5:L1:655:C:H2'	5:L1:656:A:C8	2.45	0.50
13:LF:30:LEU:HD11	13:LF:47:GLN:HG2	1.92	0.50
49:S1:29:U:H2'	49:S1:30:G:H8	1.77	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:S1:1691:A:H2'	49:S1:1692:G:H8	1.74	0.50
63:Sg:52:ILE:HG23	63:Sg:109:LEU:HD11	1.91	0.50
67:Sk:14:TYR:CD2	67:Sk:35:ILE:HD11	2.45	0.50
81:Ry:13:ILE:HG23	81:Ry:22:GLN:HG3	1.91	0.50
49:R1:337:G:O2'	65:Ri:10:LYS:NZ	2.33	0.50
49:R1:647:G:H22	49:R1:687:G:H1	1.58	0.50
49:R1:926:A:H4'	49:R1:1016:C:H5'	1.93	0.50
58:Rb:34:ALA:HB3	58:Rb:41:ARG:HA	1.93	0.50
59:Rc:185:LYS:NZ	59:Rc:189:GLN:OE1	2.44	0.50
65:Ri:87:ASN:HB3	65:Ri:90:LEU:HG	1.93	0.50
73:Rq:132:LYS:HG3	73:Rq:138:PHE:HE1	1.76	0.50
87:M1:394:G:N1	87:M1:397:A:OP2	2.42	0.50
89:MQ:159:VAL:HG21	89:MQ:165:VAL:HG22	1.94	0.50
90:MP:104:ILE:HG23	90:MP:108:GLU:HB3	1.93	0.50
5:L1:541:U:C4	5:L1:542:G:O6	2.63	0.50
5:L1:2550:U:O4'	10:LC:38:GLN:NE2	2.45	0.50
13:LF:26:SER:OG	13:LF:27:GLY:N	2.44	0.50
20:LM:176:ARG:NH2	49:S1:852:C:OP1	2.42	0.50
49:S1:1175:U:H2'	49:S1:1176:G:H8	1.76	0.50
49:S1:1797:A:H5'	50:SA:95:ARG:HG2	1.93	0.50
63:Sg:57:ASP:HA	63:Sg:106:LEU:HA	1.92	0.50
80:Sx:92:CYS:HB3	80:Sx:132:LEU:HD11	1.92	0.50
82:Rz:54:VAL:HG13	82:Rz:60:VAL:HG11	1.93	0.50
56:RG:90:ARG:HH21	56:RG:102:ARG:HD3	1.75	0.50
49:R1:1484:G:H21	49:R1:1606:C:H1'	1.76	0.50
12:ME:176:LEU:HD22	12:ME:180:GLU:HG2	1.92	0.50
37:Mo:57:GLU:OE2	37:Mo:69:TYR:OH	2.20	0.50
5:L1:1838:G:H5''	5:L1:1839:A:H5'	1.93	0.50
5:L1:2137:U:OP2	5:L1:2142:A:N6	2.37	0.50
5:L1:2680:A:H2	13:LF:24:GLY:HA2	1.77	0.50
6:L2:53:A:OP1	28:Lf:19:GLN:NE2	2.38	0.50
8:LA:80:ASN:HB3	8:LA:83:TYR:HD2	1.74	0.50
40:Lr:33:SER:OG	40:Lr:34:LYS:N	2.43	0.50
49:S1:1791:A:H3'	50:SA:8:ASN:HB3	1.94	0.50
56:SG:240:VAL:HA	56:SG:256:THR:HA	1.92	0.50
68:Sl:101:GLU:OE1	80:Sx:16:ARG:NH2	2.44	0.50
49:R1:393:C:OP1	49:R1:1673:G:N1	2.45	0.50
66:Rj:116:LEU:HD11	66:Rj:153:GLU:HB3	1.94	0.50
70:Rn:29:SER:OG	70:Rn:30:SER:N	2.42	0.50
87:M1:370:U:H4'	87:M1:404:G:H5'	1.92	0.50
6:M2:71:A:O2'	41:Ms:52:ARG:NH1	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L1:107:A:O2'	5:L1:324:A:N3	2.44	0.50
11:LD:89:LYS:HG2	11:LD:145:VAL:HG22	1.92	0.50
22:LO:30:TYR:O	48:Lz:41:LYS:NZ	2.39	0.50
24:Lb:66:GLY:HA2	45:Lw:80:GLU:HG3	1.94	0.50
49:S1:66:U:H5''	63:Sg:173:PRO:HA	1.93	0.50
49:S1:1504:G:OP1	76:St:97:SER:OG	2.23	0.50
56:SG:223:TRP:HZ3	60:Sd:222:VAL:HG22	1.76	0.50
60:Sd:137:VAL:HG22	60:Sd:151:LYS:HG3	1.94	0.50
65:Si:3:ILE:O	65:Si:30:GLY:N	2.43	0.50
69:Sm:29:LYS:O	69:Sm:33:ARG:NE	2.37	0.50
70:Sn:132:VAL:HG23	70:Sn:134:VAL:HG13	1.94	0.50
79:Sw:30:SER:O	79:Sw:30:SER:OG	2.26	0.50
80:Rx:97:ASP:N	80:Rx:100:ASP:OD2	2.45	0.50
49:R1:125:U:OP1	63:Rg:201:GLN:NE2	2.37	0.50
49:R1:532:U:OP1	66:Rj:132:ARG:NH2	2.44	0.50
11:MD:101:VAL:HB	11:MD:114:VAL:HG22	1.93	0.50
5:L1:297:G:O6	16:LI:12:ARG:NH1	2.39	0.50
5:L1:1455:U:H1'	36:Ln:26:LYS:HE3	1.93	0.50
5:L1:2960:C:H2'	5:L1:2961:G:C8	2.47	0.50
5:L1:3186:A:N6	11:LD:58:HIS:O	2.33	0.50
44:Lv:58:GLU:OE1	44:Lv:60:GLY:N	2.43	0.50
49:S1:513:U:H2'	49:S1:514:G:C8	2.47	0.50
61:Se:18:TRP:NE1	61:Se:41:SER:O	2.42	0.50
63:Sg:31:ARG:H	63:Sg:34:GLN:HG3	1.76	0.50
66:Sj:38:ASN:HB2	66:Sj:40:LYS:H	1.75	0.50
73:Sq:103:ASN:O	73:Sq:107:LYS:NZ	2.37	0.50
49:R1:1483:A:H4'	73:Rq:71:GLY:HA2	1.94	0.50
60:Rd:38:GLU:N	60:Rd:38:GLU:OE1	2.45	0.50
87:M1:26:A:N3	87:M1:328:U:O2'	2.41	0.50
6:L2:8:C:H2'	6:L2:9:A:C8	2.46	0.50
9:LB:66:LYS:NZ	9:LB:78:GLU:OE2	2.43	0.50
49:S1:123:G:OP1	61:Se:75:LYS:NZ	2.45	0.50
49:S1:1003:A:O2'	49:S1:1005:A:N7	2.43	0.50
49:S1:1081:A:O2'	49:S1:1083:G:N7	2.43	0.50
59:Sc:147:ASN:OD1	59:Sc:147:ASN:N	2.42	0.50
65:Si:69:SER:OG	65:Si:185:GLU:OE1	2.23	0.50
68:Sl:78:THR:HA	68:Sl:84:ILE:HG22	1.93	0.50
82:Sz:49:ARG:HG2	82:Sz:69:LEU:HD13	1.93	0.50
49:R1:564:G:N2	49:R1:577:G:OP1	2.40	0.50
49:R1:1474:G:H2'	49:R1:1475:A:H8	1.76	0.50
87:M1:2476:C:H2'	87:M1:2477:G:H4'	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:MH:23:ILE:O	15:MH:30:GLY:N	2.45	0.50
5:L1:567:G:H2'	5:L1:568:G:C8	2.46	0.50
7:L3:73:C:H41	21:LN:19:VAL:HG11	1.77	0.50
10:LC:157:VAL:HG21	10:LC:163:VAL:HG21	1.92	0.50
11:LD:22:SER:OG	11:LD:39:LYS:NZ	2.44	0.50
16:LI:42:PRO:HD3	16:LI:61:ILE:HG13	1.92	0.50
22:LO:60:LYS:HB3	22:LO:76:ILE:HD12	1.93	0.50
42:Lt:67:ILE:HD12	42:Lt:121:LYS:HG3	1.93	0.50
49:S1:17:C:O2'	49:S1:1137:A:N1	2.36	0.50
49:S1:1381:U:H4'	77:Su:59:PRO:HG3	1.92	0.50
49:S1:1628:U:H2'	49:S1:1629:G:C8	2.46	0.50
49:S1:1690:G:H2'	49:S1:1691:A:C8	2.47	0.50
56:SG:177:MET:HE1	56:SG:179:LYS:HG3	1.94	0.50
75:Rs:86:LEU:HG	75:Rs:97:ASP:HB3	1.93	0.50
49:R1:330:G:OP2	65:Ri:172:ARG:NH1	2.45	0.50
49:R1:590:C:H2'	49:R1:591:A:H8	1.77	0.50
49:R1:1201:G:H21	49:R1:1600:A:H5'	1.76	0.50
59:Rc:245:ASP:N	59:Rc:245:ASP:OD1	2.38	0.50
87:M1:348:A:N3	87:M1:352:A:O2'	2.44	0.50
87:M1:358:G:N2	87:M1:361:A:OP2	2.39	0.50
89:MQ:38:MET:HA	89:MQ:41:VAL:HB	1.94	0.50
45:Mw:201:GLY:HA2	45:Mw:204:MET:HG3	1.94	0.50
46:Mx:47:LEU:HD22	46:Mx:335:ILE:HD11	1.94	0.50
5:L1:2656:A:H4'	25:Lc:98:LYS:HD2	1.93	0.50
5:L1:2674:A:H5''	13:LF:105:GLY:HA3	1.94	0.50
10:LC:97:TYR:HE1	10:LC:204:ARG:HE	1.60	0.50
32:Lj:77:PRO:HG2	42:Lt:50:ALA:HB2	1.94	0.50
49:S1:990:C:H5''	71:So:129:LYS:HB3	1.94	0.50
49:S1:1220:C:H2'	49:S1:1221:A:H8	1.77	0.50
56:SG:14:GLU:N	56:SG:14:GLU:OE1	2.44	0.50
56:SG:209:THR:OG1	56:SG:224:ASN:OD1	2.30	0.50
61:Se:79:ASP:HB3	61:Se:82:TYR:HB2	1.94	0.50
63:Sg:12:SER:OG	63:Sg:124:LEU:O	2.29	0.50
75:Ss:7:GLU:HB3	82:Sz:43:ASP:HA	1.93	0.50
49:R1:200:A:H2'	49:R1:201:G:H8	1.77	0.50
87:M1:1572:U:O4	87:M1:1574:C:N4	2.44	0.50
87:M1:3343:G:H21	87:M1:3362:A:H2	1.60	0.50
48:Mz:68:THR:OG1	48:Mz:71:GLY:O	2.25	0.50
41:Ms:101:PRO:HA	41:Ms:104:LEU:HD12	1.94	0.50
4:CP:63:U:H2'	4:CP:64:G:H8	1.77	0.50
5:L1:1261:G:N2	5:L1:1261:G:OP2	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L1:1553:U:H4'	5:L1:1554:U:H5'	1.94	0.50
35:Lm:91:THR:HG22	35:Lm:92:TYR:CD1	2.47	0.50
49:S1:903:U:O2'	49:S1:905:A:N7	2.32	0.50
59:Sc:79:GLU:HG2	59:Sc:186:LYS:HE3	1.94	0.50
49:R1:65:A:OP1	63:Rg:176:GLN:NE2	2.41	0.50
49:R1:560:U:H2'	49:R1:561:G:H8	1.77	0.50
49:R1:990:C:H2'	49:R1:991:G:C8	2.47	0.50
59:Rc:56:ILE:HG23	59:Rc:61:LEU:HB2	1.94	0.50
63:Rg:70:PRO:HA	63:Rg:99:GLY:HA3	1.94	0.50
64:Rh:17:GLU:OE2	64:Rh:46:ILE:N	2.44	0.50
87:M1:549:U:H2'	87:M1:550:A:H8	1.76	0.50
87:M1:1147:G:OP1	35:Mm:47:ARG:NH1	2.44	0.50
46:Mx:215:ILE:HD12	46:Mx:338:LEU:HB3	1.94	0.50
48:Mz:108:ARG:HG2	48:Mz:251:PRO:HB2	1.94	0.50
13:MF:49:LYS:HB3	13:MF:62:ASN:HA	1.93	0.50
5:L1:294:U:P	31:Li:76:ARG:HH12	2.35	0.49
11:LD:47:LYS:HB2	15:LH:7:VAL:HB	1.93	0.49
14:LG:165:SER:O	14:LG:167:PHE:N	2.45	0.49
49:S1:502:U:H2'	49:S1:503:G:H8	1.75	0.49
80:Sx:41:SER:O	80:Sx:41:SER:OG	2.29	0.49
81:Ry:34:ASN:ND2	49:R1:521:A:N3	2.60	0.49
49:R1:1739:C:H2'	49:R1:1740:A:C8	2.45	0.49
85:Rr:62:GLN:N	85:Rr:62:GLN:OE1	2.45	0.49
17:MJ:75:ALA:HB3	17:MJ:78:ARG:HG2	1.94	0.49
87:M1:2727:A:OP2	87:M1:2728:G:N2	2.44	0.49
39:Mq:133:LEU:HG	39:Mq:137:LYS:HD2	1.94	0.49
5:L1:662:U:H2'	5:L1:663:C:C6	2.47	0.49
5:L1:1717:U:H2'	5:L1:1718:G:C8	2.47	0.49
6:L2:126:A:O2'	6:L2:129:C:N4	2.44	0.49
29:Lg:2:ALA:N	29:Lg:51:LEU:O	2.45	0.49
62:Sf:118:LEU:HD22	62:Sf:129:PRO:HB2	1.93	0.49
75:Ss:28:ILE:HA	75:Ss:58:ALA:HB2	1.93	0.49
56:RG:214:ALA:HB1	56:RG:240:VAL:HG11	1.95	0.49
49:R1:68:A:OP1	63:Rg:160:ARG:NH2	2.41	0.49
49:R1:895:G:H21	84:Ro:38:THR:HG21	1.77	0.49
49:R1:1727:G:O6	49:R1:1728:A:N6	2.44	0.49
62:Rf:139:ASN:ND2	62:Rf:202:ALA:O	2.46	0.49
87:M1:2160:G:H2'	87:M1:2161:G:C8	2.47	0.49
47:My:35:VAL:HG21	47:My:244:LEU:HD21	1.93	0.49
32:Mj:118:ILE:HG22	32:Mj:120:ALA:H	1.78	0.49
5:L1:1114:U:OP1	39:Lq:23:GLY:N	2.43	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:LC:87:ALA:HA	10:LC:90:THR:HG22	1.94	0.49
15:LH:23:ILE:HA	15:LH:63:VAL:HG12	1.94	0.49
35:Lm:95:GLU:OE1	35:Lm:120:THR:OG1	2.27	0.49
45:Lw:32:LEU:HD13	45:Lw:163:ARG:HD3	1.94	0.49
49:S1:1178:G:H5'	49:S1:1190:C:H42	1.77	0.49
60:Sd:157:LEU:HA	60:Sd:189:MET:HE2	1.94	0.49
62:Sf:26:ALA:HB2	73:Sq:26:LYS:HG3	1.94	0.49
63:Sg:23:ARG:NH1	63:Sg:41:VAL:O	2.40	0.49
79:Sw:47:ILE:HG22	79:Sw:65:LEU:HD23	1.93	0.49
78:Rv:3:ASN:HD21	78:Rv:7:GLN:HB3	1.77	0.49
49:R1:1014:G:N2	49:R1:1786:G:HO2'	2.09	0.49
87:M1:1003:A:N1	87:M1:1049:C:O2'	2.41	0.49
87:M1:2768:U:H2'	87:M1:2769:A:H8	1.77	0.49
89:MQ:104:ARG:NH2	89:MQ:182:THR:O	2.45	0.49
40:Mr:5:LEU:HD11	37:Mo:35:ARG:HD2	1.94	0.49
11:MD:173:ARG:NH1	27:Me:125:LYS:O	2.40	0.49
5:L1:591:G:O2'	8:LA:17:ALA:O	2.28	0.49
5:L1:1019:G:H1	5:L1:1033:U:H3	1.60	0.49
37:Lo:30:THR:HG23	37:Lo:91:SER:HB2	1.94	0.49
48:Lz:135:VAL:HG23	48:Lz:138:GLY:HA3	1.95	0.49
49:S1:1175:U:H2'	49:S1:1176:G:C8	2.47	0.49
49:S1:1356:U:H2'	49:S1:1357:A:H8	1.77	0.49
50:SA:83:ILE:HG22	50:SA:84:VAL:HG13	1.93	0.49
58:Sb:41:ARG:NH1	66:Rj:154:LYS:O	2.45	0.49
62:Sf:63:GLN:HB3	62:Sf:88:PRO:HA	1.93	0.49
68:Sl:36:LYS:NZ	68:Sl:62:GLY:O	2.46	0.49
69:Sm:61:VAL:HB	69:Sm:121:VAL:HB	1.95	0.49
81:Sy:86:GLU:OE2	81:Sy:90:ARG:NH1	2.46	0.49
55:RF:105:TYR:O	55:RF:118:ARG:NH2	2.41	0.49
67:Rk:54:TYR:HD2	67:Rk:72:GLY:HA2	1.77	0.49
88:DQ:10:G:H2'	88:DQ:11:A:H8	1.77	0.49
14:MG:62:THR:O	14:MG:64:LYS:N	2.45	0.49
5:L1:77:A:OP2	14:LG:73:ARG:NH1	2.46	0.49
5:L1:1799:A:H2'	5:L1:1800:A:C8	2.47	0.49
5:L1:2772:C:H4'	5:L1:2773:C:H5'	1.94	0.49
12:LE:54:SER:HB3	12:LE:135:ILE:HD11	1.94	0.49
12:LE:153:ARG:NH1	12:LE:157:TYR:OH	2.46	0.49
23:La:128:ARG:O	23:La:132:ASN:ND2	2.46	0.49
49:S1:61:A:O2'	49:S1:62:A:O4'	2.30	0.49
49:S1:712:G:O6	49:S1:726:C:O2'	2.30	0.49
52:SC:61:ARG:HH22	71:So:58:TYR:HB2	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
81:Sy:53:ASP:OD2	81:Sy:53:ASP:N	2.46	0.49
49:R1:704:C:N4	49:R1:735:C:O2	2.45	0.49
49:R1:1482:C:O2'	73:Rq:72:GLY:O	2.30	0.49
58:Rb:175:GLU:HG3	58:Rb:193:ILE:HD11	1.94	0.49
60:Rd:213:GLU:OE1	60:Rd:213:GLU:N	2.39	0.49
63:Rg:139:ASN:HA	63:Rg:142:ARG:HB2	1.94	0.49
65:Ri:42:ARG:HG3	65:Ri:58:LEU:HB2	1.94	0.49
87:M1:38:U:H4'	39:Mq:32:ARG:HD2	1.95	0.49
87:M1:1717:U:H2'	87:M1:1718:G:C8	2.47	0.49
5:L1:94:G:H2'	5:L1:95:A:C8	2.47	0.49
5:L1:2697:A:H2'	5:L1:2698:G:C8	2.47	0.49
17:LJ:74:ARG:HG3	17:LJ:145:VAL:HG23	1.93	0.49
49:S1:1481:C:OP1	76:St:63:ARG:NH2	2.41	0.49
60:Sd:135:GLU:HG3	60:Sd:153:ALA:HB2	1.95	0.49
72:Sp:52:LYS:HD3	72:Sp:53:PRO:HD3	1.94	0.49
75:Ss:106:GLU:HA	75:Ss:109:LEU:HB2	1.93	0.49
56:RG:31:ASN:OD1	56:RG:31:ASN:N	2.39	0.49
57:Ra:11:PRO:HG3	85:Rr:115:LEU:HD13	1.94	0.49
58:Rb:208:GLN:HG3	58:Rb:209:ASN:HB2	1.95	0.49
61:Re:181:VAL:HG21	61:Re:210:ILE:HD12	1.94	0.49
87:M1:3016:A:H2'	87:M1:3017:A:C8	2.48	0.49
89:MQ:37:GLN:NE2	89:MQ:183:PHE:O	2.41	0.49
5:L1:1757:A:OP1	44:Lv:94:ARG:NH2	2.35	0.49
5:L1:2799:A:O2'	39:Lq:42:ARG:NH1	2.45	0.49
36:Ln:54:GLU:N	36:Ln:54:GLU:OE2	2.44	0.49
49:S1:257:A:H1'	65:Si:73:SER:HB2	1.94	0.49
75:Ss:67:GLU:HA	75:Ss:70:VAL:HG22	1.94	0.49
87:M1:651:G:O2'	87:M1:1435:A:OP1	2.29	0.49
87:M1:3160:U:H3	87:M1:3290:G:H1	1.60	0.49
23:Ma:18:PRO:HA	23:Ma:51:ALA:HA	1.93	0.49
5:L1:528:U:H2'	5:L1:529:A:C8	2.48	0.49
5:L1:544:C:H2'	5:L1:547:G:H1	1.77	0.49
5:L1:1015:U:O2	5:L1:1017:C:O2'	2.31	0.49
5:L1:2585:G:O6	42:Lt:27:ARG:NH2	2.37	0.49
49:S1:29:U:H2'	49:S1:30:G:C8	2.48	0.49
70:Sn:142:GLU:N	70:Sn:142:GLU:OE1	2.46	0.49
80:Sx:46:SER:OG	80:Sx:78:LYS:NZ	2.46	0.49
54:RE:37:ARG:HD2	66:Rj:123:HIS:CG	2.48	0.49
49:R1:939:A:H2'	49:R1:940:A:C8	2.47	0.49
49:R1:1230:A:H2	49:R1:1255:G:H21	1.59	0.49
49:R1:1727:G:H3'	49:R1:1728:A:H5''	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:Rr:104:ASN:O	85:Rr:107:SER:OG	2.30	0.49
87:M1:1134:G:O2'	87:M1:2642:A:N3	2.42	0.49
87:M1:1385:C:OP1	47:My:141:ARG:NH2	2.45	0.49
4:CP:30:G:OP1	49:S1:1462:G:O2'	2.29	0.49
5:L1:1348:U:OP2	19:LL:38:ARG:NH2	2.45	0.49
11:LD:41:ILE:HD11	11:LD:67:ALA:HB1	1.95	0.49
39:Lq:89:GLN:OE1	39:Lq:89:GLN:N	2.39	0.49
45:Lw:225:ILE:HG21	45:Lw:234:LYS:HA	1.94	0.49
46:Lx:284:ARG:NH1	46:Lx:293:ASN:O	2.45	0.49
49:S1:146:U:H2'	49:S1:147:A:H8	1.77	0.49
49:S1:733:A:N3	49:S1:736:C:N4	2.61	0.49
59:Sc:50:ILE:HG21	59:Sc:56:ILE:HD11	1.95	0.49
64:Sh:150:GLN:HB2	64:Sh:181:ILE:HG22	1.95	0.49
49:R1:637:C:O2	64:Rh:114:ARG:NH1	2.36	0.49
87:M1:655:C:H2'	87:M1:656:A:C8	2.47	0.49
87:M1:3294:A:OP1	46:Mx:128:LYS:NZ	2.41	0.49
19:ML:147:ARG:HB2	19:ML:150:VAL:HG23	1.93	0.49
36:Mn:51:LEU:HB3	36:Mn:55:LEU:HD23	1.95	0.49
5:L1:1740:U:H4'	5:L1:1741:A:H5'	1.95	0.49
11:LD:8:GLN:HG3	11:LD:68:LEU:HD22	1.95	0.49
41:Ls:101:PRO:HA	41:Ls:104:LEU:HD12	1.93	0.49
58:Sb:61:LEU:HD13	58:Sb:96:LEU:HD22	1.94	0.49
77:Ru:23:ARG:NH2	49:R1:1347:U:OP2	2.40	0.49
77:Ru:99:ILE:O	77:Ru:102:ARG:NH1	2.46	0.49
49:R1:1220:C:H2'	49:R1:1221:A:H8	1.77	0.49
49:R1:1477:G:H2'	49:R1:1478:G:H8	1.78	0.49
57:Ra:15:GLN:OE1	57:Ra:15:GLN:N	2.38	0.49
61:Re:11:ARG:NH1	61:Re:21:ASP:O	2.46	0.49
87:M1:36:C:OP2	16:MI:83:LYS:NZ	2.33	0.49
87:M1:1258:U:OP1	89:MQ:42:ARG:NH1	2.46	0.49
87:M1:2376:G:H2'	87:M1:2377:G:C8	2.48	0.49
5:L1:1696:A:H2'	5:L1:1697:A:C8	2.48	0.48
9:LB:24:GLU:HG2	9:LB:26:VAL:HG22	1.94	0.48
49:S1:861:U:O2'	79:Sw:56:HIS:O	2.31	0.48
49:S1:953:G:H2'	49:S1:954:G:C8	2.48	0.48
49:S1:1555:A:N6	53:SD:14:TYR:OH	2.40	0.48
51:RB:82:LYS:HZ2	70:Rn:25:TRP:HE3	1.61	0.48
56:RG:231:MET:HG2	56:RG:232:TYR:HD2	1.78	0.48
49:R1:334:G:O6	65:Ri:5:ARG:NH2	2.43	0.48
49:R1:1158:C:O2'	49:R1:1581:C:OP2	2.31	0.48
58:Rb:59:ASP:OD2	58:Rb:59:ASP:N	2.35	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
66:Rj:59:LEU:HD22	66:Rj:69:ARG:HA	1.95	0.48
87:M1:663:OMC:HM21	47:My:104:LYS:HB2	1.95	0.48
87:M1:900:G:H1'	87:M1:1589:A:N6	2.27	0.48
87:M1:3023:U:H2'	87:M1:3024:A:H8	1.77	0.48
32:Mj:15:GLU:OE2	32:Mj:15:GLU:N	2.44	0.48
5:L1:1119:C:H2'	5:L1:1120:A:C8	2.48	0.48
5:L1:2193:U:H5'	5:L1:2194:G:H5'	1.95	0.48
5:L1:3322:A:H2'	5:L1:3323:A:C8	2.48	0.48
49:S1:250:C:H2'	49:S1:251:A:H8	1.79	0.48
60:Sd:74:GLN:NE2	60:Sd:79:TYR:O	2.46	0.48
60:Sd:141:LYS:O	60:Sd:179:GLN:NE2	2.46	0.48
61:Se:70:VAL:HG12	61:Se:92:LEU:HG	1.95	0.48
64:Sh:49:ILE:HG13	64:Sh:172:VAL:HG22	1.95	0.48
72:Sp:29:SER:OG	72:Sp:30:THR:N	2.46	0.48
49:R1:472:U:O2'	49:R1:769:A:N3	2.42	0.48
49:R1:1041:G:H2'	49:R1:1042:G:C8	2.48	0.48
49:R1:1713:G:H2'	49:R1:1714:A:H8	1.79	0.48
63:Rg:10:ASN:ND2	63:Rg:127:THR:O	2.46	0.48
87:M1:3322:A:H2'	87:M1:3323:A:C8	2.47	0.48
6:M2:29:U:H5''	14:MG:27:ASP:HB3	1.95	0.48
91:DP:28:C:H2'	91:DP:29:A:H8	1.78	0.48
12:LE:76:MET:HE2	12:LE:148:VAL:HA	1.95	0.48
16:LI:17:ASP:OD1	16:LI:17:ASP:N	2.44	0.48
36:Ln:44:MET:O	36:Ln:77:ARG:NH1	2.46	0.48
49:S1:142:G:N7	63:Sg:177:ARG:NH2	2.61	0.48
49:S1:554:C:H1'	49:S1:555:A:C2	2.48	0.48
57:Sa:139:VAL:HG13	57:Sa:141:ILE:HD12	1.94	0.48
74:Sr:75:GLU:HA	74:Sr:78:ARG:HG2	1.94	0.48
74:Sr:79:GLU:HA	74:Sr:82:ASP:HB3	1.94	0.48
49:R1:706:A:O2'	49:R1:707:A:O4'	2.31	0.48
58:Rb:131:ASP:N	58:Rb:131:ASP:OD1	2.46	0.48
87:M1:1262:G:H2'	87:M1:1264:G:H1'	1.95	0.48
90:MP:110:ILE:HD11	90:MP:125:LEU:HD13	1.96	0.48
46:Mx:221:THR:O	46:Mx:334:ARG:NH1	2.44	0.48
14:MG:129:ASN:N	14:MG:129:ASN:OD1	2.47	0.48
91:DP:52:U:H2'	91:DP:53:G:H8	1.78	0.48
5:L1:86:G:O2'	5:L1:98:G:O6	2.27	0.48
5:L1:2357:A:H2'	5:L1:2358:A:C8	2.48	0.48
11:LD:50:ASN:ND2	15:LH:4:ASP:OD2	2.46	0.48
19:LL:95:GLU:N	19:LL:95:GLU:OE2	2.46	0.48
22:LO:93:VAL:HG11	48:Lz:41:LYS:HD2	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:Sb:82:ARG:NH2	58:Sb:188:LEU:O	2.47	0.48
76:St:105:LEU:HD23	76:St:108:LEU:HD12	1.95	0.48
56:RG:289:ALA:HA	56:RG:305:TYR:HA	1.95	0.48
49:R1:168:A:OP1	63:Rg:140:ASN:ND2	2.40	0.48
49:R1:177:U:O2	63:Rg:191:ARG:NH2	2.46	0.48
49:R1:273:G:O6	49:R1:283:U:O4	2.30	0.48
87:M1:2469:G:H1	87:M1:2476:C:H42	1.61	0.48
87:M1:2552:C:N4	37:Mo:54:SER:OG	2.46	0.48
19:ML:148:GLU:OE2	19:ML:151:ARG:NH1	2.47	0.48
89:MQ:130:PRO:HG3	89:MQ:145:ILE:HG21	1.95	0.48
90:MP:85:LEU:HD22	90:MP:102:GLY:HA3	1.95	0.48
22:MO:8:ARG:O	22:MO:11:THR:OG1	2.25	0.48
5:L1:565:U:H2'	5:L1:566:G:H8	1.76	0.48
8:LA:136:GLU:N	8:LA:136:GLU:OE1	2.44	0.48
49:S1:1316:G:HO2'	49:S1:1401:A:HO2'	1.60	0.48
56:SG:210:LEU:HD21	56:SG:222:LEU:HD21	1.94	0.48
57:Sa:50:VAL:HG22	74:Sr:109:LEU:HD21	1.96	0.48
65:Si:26:LYS:HG2	65:Si:29:LEU:HD23	1.96	0.48
75:Rs:62:THR:OG1	75:Rs:63:GLN:N	2.45	0.48
56:RG:260:ILE:HB	56:RG:274:LEU:HB2	1.96	0.48
49:R1:697:C:H2'	49:R1:733:A:H61	1.78	0.48
87:M1:542:G:O6	87:M1:549:U:O4	2.31	0.48
39:Mq:34:MET:HE3	39:Mq:34:MET:HB3	1.72	0.48
5:L1:426:G:H5'	35:Lm:50:ILE:HG22	1.95	0.48
5:L1:900:G:H1'	5:L1:1589:A:N6	2.28	0.48
10:LC:224:ASP:OD1	10:LC:224:ASP:N	2.42	0.48
33:Lk:79:SER:OG	33:Lk:80:ARG:NH1	2.44	0.48
49:S1:594:A:OP2	66:Sj:38:ASN:ND2	2.46	0.48
49:S1:1436:A:OP2	60:Sd:27:ARG:NH2	2.32	0.48
56:SG:74:THR:HG22	56:SG:115:ILE:HG12	1.95	0.48
62:Sf:43:PHE:HD2	62:Sf:44:ASN:H	1.61	0.48
73:Sq:82:ARG:NH1	73:Sq:113:ASP:OD2	2.39	0.48
80:Rx:56:LYS:NZ	80:Rx:96:VAL:O	2.46	0.48
49:R1:65:A:O5'	63:Rg:136:LYS:NZ	2.43	0.48
58:Rb:106:THR:HG23	58:Rb:109:LYS:H	1.78	0.48
87:M1:1239:C:O2'	90:MP:97:ASN:OD1	2.28	0.48
87:M1:1572:U:H2'	87:M1:1573:G:C8	2.48	0.48
87:M1:2160:G:H2'	87:M1:2161:G:H8	1.79	0.48
41:Ms:56:VAL:HG21	41:Ms:104:LEU:HD13	1.96	0.48
5:L1:1899:G:O2'	5:L1:2334:U:O4	2.27	0.48
31:Li:70:ARG:HG3	31:Li:87:VAL:HG21	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:Lx:323:MET:HE1	46:Lx:359:ILE:HD13	1.95	0.48
49:S1:1307:U:H3	49:S1:1318:G:H21	1.62	0.48
57:Sa:157:ASP:OD1	78:Sv:60:ARG:NH1	2.46	0.48
77:Ru:102:ARG:H	77:Ru:102:ARG:HD3	1.78	0.48
50:RA:3:LYS:NZ	50:RA:8:ASN:OD1	2.46	0.48
49:R1:646:C:H2'	49:R1:647:G:C8	2.49	0.48
49:R1:1533:C:H4'	49:R1:1539:G:C6	2.48	0.48
69:Rm:70:ASN:OD1	69:Rm:70:ASN:N	2.46	0.48
86:MA:45:GLY:O	86:MA:48:ARG:NH1	2.46	0.48
48:Mz:119:TYR:OH	48:Mz:139:PRO:O	2.26	0.48
37:Mo:16:LEU:HB3	37:Mo:98:SER:HB2	1.94	0.48
3:CN:7:ASN:OD1	3:CN:7:ASN:N	2.47	0.48
5:L1:1279:C:H2'	5:L1:1280:C:C6	2.49	0.48
12:LE:48:LEU:HD12	12:LE:178:ARG:HH22	1.78	0.48
49:S1:153:G:H5'	81:Sy:131:ARG:HH12	1.78	0.48
49:S1:163:G:OP2	49:S1:163:G:N2	2.44	0.48
56:SG:48:THR:OG1	56:SG:50:ASP:OD1	2.30	0.48
79:Sw:6:VAL:HG23	79:Sw:29:PRO:HD2	1.96	0.48
80:Sx:130:VAL:HG21	80:Sx:143:PRO:HD3	1.95	0.48
49:R1:648:G:H21	64:Rh:147:ASN:ND2	2.11	0.48
49:R1:1081:A:O2'	49:R1:1083:G:N7	2.43	0.48
49:R1:1524:A:H2'	49:R1:1525:A:C8	2.49	0.48
87:M1:1696:A:H2'	87:M1:1697:A:C8	2.48	0.48
87:M1:2552:C:H2'	37:Mo:50:VAL:HG11	1.94	0.48
25:Mc:8:ARG:HA	25:Mc:8:ARG:HD2	1.71	0.48
5:L1:2228:A:H2'	5:L1:2229:A:C8	2.49	0.48
5:L1:3318:G:O2'	5:L1:3320:A:OP2	2.31	0.48
51:SB:55:THR:HA	51:SB:63:LEU:HB2	1.96	0.48
75:Rs:14:ILE:HD11	75:Rs:21:ASN:HB3	1.94	0.48
76:Rt:130:ARG:HG3	76:Rt:134:ARG:HH21	1.79	0.48
49:R1:29:U:H2'	49:R1:30:G:C8	2.49	0.48
49:R1:142:G:H5''	63:Rg:139:ASN:HD21	1.79	0.48
49:R1:791:A:OP1	61:Re:187:ARG:NH2	2.38	0.48
63:Rg:52:ILE:HG23	63:Rg:109:LEU:HD21	1.95	0.48
70:Rn:105:ASN:OD1	70:Rn:105:ASN:N	2.47	0.48
87:M1:549:U:H2'	87:M1:550:A:C8	2.49	0.48
5:L1:31:C:OP2	16:LI:188:ARG:NH1	2.37	0.48
5:L1:282:G:O2'	5:L1:283:G:OP2	2.28	0.48
5:L1:689:U:O4	47:Ly:209:TYR:OH	2.29	0.48
5:L1:3295:A:H2'	5:L1:3296:A:C8	2.49	0.48
25:Lc:10:THR:OG1	25:Lc:11:TYR:N	2.45	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:Lw:36:GLU:HG3	45:Lw:91:GLY:HA2	1.95	0.48
46:Lx:303:LYS:NZ	46:Lx:359:ILE:O	2.46	0.48
49:S1:1198:G:OP1	49:S1:1199:G:O2'	2.31	0.48
49:S1:1477:G:H2'	49:S1:1478:G:H8	1.79	0.48
65:Si:87:ASN:HB3	65:Si:90:LEU:HG	1.94	0.48
74:Sr:108:ASP:OD1	74:Sr:108:ASP:N	2.47	0.48
76:Rt:39:THR:OG1	49:R1:1478:G:OP1	2.31	0.48
49:R1:590:C:H2'	49:R1:591:A:C8	2.49	0.48
49:R1:1667:A:H5''	49:R1:1668:G:C2	2.49	0.48
57:Ra:88:LYS:HZ3	57:Ra:201:LEU:HG	1.78	0.48
87:M1:1033:U:H2'	87:M1:1034:U:C6	2.49	0.48
13:MF:157:GLU:N	13:MF:157:GLU:OE2	2.46	0.48
5:L1:1724:U:H1'	5:L1:1725:C:C6	2.48	0.47
5:L1:2129:U:H2'	5:L1:2130:G:C8	2.48	0.47
11:LD:59:ASN:OD1	15:LH:41:GLN:NE2	2.47	0.47
49:S1:78:A:H2'	49:S1:79:C:C6	2.49	0.47
49:S1:900:A:OP1	71:So:43:THR:OG1	2.29	0.47
57:Sa:121:VAL:HG23	57:Sa:143:VAL:HG23	1.95	0.47
63:Sg:78:THR:OG1	63:Sg:79:LYS:N	2.47	0.47
49:R1:12:U:H2'	49:R1:13:C:C6	2.49	0.47
49:R1:984:G:C2	49:R1:985:G:H1'	2.49	0.47
49:R1:1490:C:H4'	49:R1:1491:U:H5'	1.96	0.47
59:Rc:116:LYS:HB2	59:Rc:131:ILE:HD12	1.95	0.47
87:M1:216:G:OP1	41:Ms:16:ARG:NH1	2.44	0.47
87:M1:655:C:H2'	87:M1:656:A:H8	1.78	0.47
87:M1:2218:G:H2'	87:M1:2219:A:H8	1.78	0.47
5:L1:1657:C:O2'	5:L1:1797:A:OP2	2.22	0.47
5:L1:2338:C:OP1	46:Lx:236:LYS:NZ	2.34	0.47
5:L1:3208:G:OP2	15:LH:102:LYS:NZ	2.45	0.47
8:LA:82:ARG:NH2	34:Ll:106:ASN:OD1	2.47	0.47
15:LH:94:TRP:O	15:LH:97:SER:OG	2.31	0.47
22:LO:108:ARG:O	22:LO:112:ASN:N	2.45	0.47
48:Lz:83:LEU:HB3	48:Lz:88:ILE:HB	1.96	0.47
49:S1:1673:G:H1	49:S1:1728:A:H2	1.56	0.47
58:Sb:121:ILE:HG12	58:Sb:161:ILE:HG23	1.95	0.47
79:Sw:102:VAL:HB	79:Sw:113:HIS:HB3	1.97	0.47
49:R1:225:A:N1	49:R1:837:G:C2	2.82	0.47
49:R1:1786:G:OP2	84:Ro:133:ARG:NH1	2.47	0.47
87:M1:894:G:H4'	87:M1:895:A:H5'	1.96	0.47
87:M1:1786:G:H2'	87:M1:1787:A:C8	2.49	0.47
5:L1:13:A:H5''	5:L1:13:A:H8	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L1:1522:U:OP2	42:Lt:121:LYS:NZ	2.46	0.47
5:L1:2815:G:N2	5:L1:2818:U:O2	2.46	0.47
7:L3:73:C:N3	21:LN:23:LYS:NZ	2.60	0.47
37:Lo:74:ASN:OD1	37:Lo:74:ASN:N	2.40	0.47
40:Lr:88:ASP:OD2	40:Lr:121:ARG:NH2	2.46	0.47
49:S1:407:A:H2'	49:S1:408:C:C6	2.49	0.47
57:Sa:163:ASN:OD1	57:Sa:163:ASN:N	2.46	0.47
60:Sd:59:LEU:HD23	60:Sd:66:ILE:HG21	1.95	0.47
61:Se:21:ASP:OD1	61:Se:21:ASP:N	2.46	0.47
76:Rt:51:GLU:N	76:Rt:51:GLU:OE2	2.47	0.47
57:Ra:21:ASN:HB3	57:Ra:24:LEU:HD23	1.96	0.47
65:Ri:172:ARG:HE	65:Ri:175:GLN:HG3	1.80	0.47
69:Rm:91:VAL:HG21	69:Rm:97:LEU:HD12	1.95	0.47
73:Rq:120:ASP:N	73:Rq:120:ASP:OD1	2.47	0.47
87:M1:1596:C:H2'	87:M1:1597:C:C6	2.49	0.47
89:MQ:127:GLY:HA2	89:MQ:149:THR:HA	1.97	0.47
5:L1:399:A:O2'	5:L1:403:C:O2'	2.30	0.47
5:L1:3044:G:H2'	5:L1:3045:G:C8	2.50	0.47
16:LI:103:GLU:HG2	16:LI:115:VAL:HG11	1.96	0.47
29:Lg:13:GLU:OE2	29:Lg:16:ARG:NH1	2.42	0.47
49:S1:428:A:N3	49:S1:440:U:O2'	2.44	0.47
49:S1:487:G:H2'	49:S1:488:G:C8	2.50	0.47
53:SD:19:ARG:NE	53:SD:32:ARG:HH12	2.13	0.47
57:Sa:71:GLU:OE2	57:Sa:71:GLU:N	2.40	0.47
65:Si:37:LYS:HB2	65:Si:59:ARG:HG3	1.97	0.47
75:Rs:138:THR:OG1	49:R1:1459:C:OP2	2.25	0.47
49:R1:201:G:H2'	49:R1:202:A:C8	2.49	0.47
49:R1:895:G:H1	49:R1:917:U:H3	1.62	0.47
49:R1:979:A:H5'	49:R1:1787:C:H1'	1.96	0.47
59:Rc:161:LYS:HG3	59:Rc:166:THR:HG22	1.96	0.47
65:Ri:138:ASN:HA	65:Ri:141:ARG:HE	1.80	0.47
70:Rn:4:MET:HE1	70:Rn:121:ARG:HG3	1.96	0.47
87:M1:799:G:O2'	14:MG:18:TRP:NE1	2.41	0.47
87:M1:2736:A:OP1	22:MO:92:ARG:NH1	2.46	0.47
87:M1:3016:A:H2'	87:M1:3017:A:H8	1.80	0.47
11:MD:113:GLU:OE1	11:MD:115:ARG:NH1	2.47	0.47
16:LI:173:GLY:O	16:LI:183:THR:OG1	2.32	0.47
46:Lx:346:THR:HA	46:Lx:351:LEU:HD21	1.95	0.47
49:S1:126:A:H8	49:S1:204:G:H21	1.61	0.47
62:Sf:25:LEU:HD13	62:Sf:27:THR:H	1.79	0.47
63:Sg:2:LYS:HB3	63:Sg:108:VAL:HG22	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:Sh:14:THR:OG1	64:Sh:15:GLU:N	2.45	0.47
64:Sh:38:LEU:H	64:Sh:39:ARG:NH2	2.12	0.47
80:Sx:41:SER:O	80:Sx:43:PHE:N	2.48	0.47
49:R1:1357:A:H2'	49:R1:1358:G:C8	2.50	0.47
49:R1:1588:G:O6	49:R1:1608:U:O4	2.31	0.47
57:Ra:98:ILE:HD11	57:Ra:116:LYS:HE3	1.95	0.47
87:M1:2768:U:H2'	87:M1:2769:A:C8	2.49	0.47
5:L1:63:A:N3	5:L1:78:U:O2'	2.39	0.47
5:L1:2703:A:N6	48:Lz:28:THR:O	2.43	0.47
7:L3:1:G:O3'	48:Lz:273:ARG:NH2	2.47	0.47
17:LJ:12:LYS:HA	17:LJ:40:GLU:HB2	1.96	0.47
46:Lx:37:ARG:HD2	46:Lx:187:SER:H	1.79	0.47
58:Sb:32:ILE:HD12	58:Sb:66:VAL:HG21	1.95	0.47
62:Sf:63:GLN:HE21	62:Sf:86:GLN:HA	1.79	0.47
65:Si:48:THR:OG1	65:Si:52:ASN:O	2.31	0.47
56:RG:210:LEU:HD12	56:RG:222:LEU:HD12	1.97	0.47
49:R1:686:C:H2'	49:R1:687:G:H8	1.80	0.47
57:Ra:7:PHE:HA	57:Ra:191:ARG:HH21	1.79	0.47
66:Rj:176:ASN:OD1	66:Rj:179:ARG:NH1	2.47	0.47
73:Rq:46:PHE:HA	73:Rq:49:TYR:HB2	1.96	0.47
87:M1:2185:G:H5'	45:Mw:219:ILE:HD11	1.97	0.47
87:M1:3155:U:H5'	87:M1:3156:U:H4'	1.95	0.47
87:M1:3285:C:H2'	87:M1:3286:G:H8	1.78	0.47
87:M1:3324:C:OP1	36:Mn:19:ARG:NH1	2.37	0.47
47:My:113:VAL:HB	47:My:118:LYS:HE2	1.96	0.47
35:Mm:96:ILE:HG21	35:Mm:105:ARG:HG2	1.97	0.47
33:Mk:3:GLN:HB3	33:Mk:30:LEU:HD12	1.96	0.47
5:L1:3016:A:H2'	5:L1:3017:A:H8	1.79	0.47
35:Lm:86:THR:HG23	35:Lm:115:LEU:HD22	1.97	0.47
47:Ly:156:LEU:HD12	47:Ly:159:ILE:HD12	1.97	0.47
49:S1:97:C:O2	49:S1:425:A:O2'	2.32	0.47
49:S1:1020:A:OP1	70:Sn:106:ARG:NH1	2.43	0.47
49:S1:1459:C:OP1	75:Ss:126:ARG:NH2	2.47	0.47
49:S1:1641:C:H2'	49:S1:1642:G:C8	2.50	0.47
64:Sh:155:ASP:OD1	64:Sh:155:ASP:N	2.46	0.47
69:Sm:34:THR:HA	69:Sm:37:VAL:HB	1.96	0.47
79:Rw:41:MET:HG2	79:Rw:129:VAL:HG11	1.96	0.47
54:RE:3:LYS:HE3	49:R1:1754:A:H2'	1.97	0.47
49:R1:1035:G:OP1	70:Rn:2:GLY:N	2.47	0.47
49:R1:1147:A:O2'	49:R1:1636:C:OP2	2.28	0.47
87:M1:2167:A:H2'	87:M1:2168:A:C8	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
87:M1:2218:G:H2'	87:M1:2219:A:C8	2.50	0.47
6:M2:149:A:H2'	6:M2:150:G:C8	2.50	0.47
11:MD:147:SER:HB3	11:MD:187:ILE:HD11	1.96	0.47
14:MG:47:ALA:HB3	14:MG:49:ARG:HD3	1.97	0.47
15:MH:4:ASP:OD1	15:MH:4:ASP:N	2.40	0.47
5:L1:873:C:H3'	5:L1:874:U:H4'	1.97	0.47
5:L1:1134:G:O2'	5:L1:2642:A:N3	2.44	0.47
5:L1:1196:C:OP1	5:L1:1309:U:O2'	2.29	0.47
10:LC:82:LEU:HG	10:LC:86:THR:HG23	1.96	0.47
13:LF:82:ARG:HB3	13:LF:112:LEU:HD22	1.95	0.47
31:Li:34:SER:H	31:Li:37:THR:HG22	1.80	0.47
76:St:25:GLN:HG3	76:St:27:LYS:HG2	1.96	0.47
80:Sx:50:LYS:HB3	80:Sx:77:ILE:HD12	1.96	0.47
49:R1:264:G:H5''	49:R1:265:A:H5'	1.96	0.47
49:R1:392:G:OP1	65:Ri:24:LYS:NZ	2.45	0.47
49:R1:1650:U:H2'	49:R1:1651:A:C8	2.49	0.47
58:Rb:129:THR:OG1	58:Rb:131:ASP:OD1	2.30	0.47
87:M1:110:G:OP2	14:MG:73:ARG:NH2	2.39	0.47
87:M1:567:G:H2'	87:M1:568:G:C8	2.50	0.47
88:DQ:16:C:OP2	88:DQ:17:C:N4	2.48	0.47
89:MQ:141:VAL:HA	89:MQ:156:VAL:HG21	1.97	0.47
32:Mj:5:LYS:HB2	32:Mj:8:GLU:HG2	1.97	0.47
5:L1:417:A:H2'	5:L1:418:A:C8	2.49	0.47
5:L1:675:C:O2'	5:L1:679:U:OP1	2.32	0.47
5:L1:1367:G:N2	5:L1:1368:U:O4	2.45	0.47
45:Lw:144:ASN:HB2	45:Lw:160:SER:HB2	1.97	0.47
49:S1:639:U:OP1	64:Sh:112:ARG:NH2	2.48	0.47
49:S1:924:A:H2'	49:S1:925:G:C8	2.49	0.47
49:S1:1341:A:H1'	56:SG:65:SER:HB3	1.97	0.47
49:S1:1674:C:OP1	63:Sg:92:ARG:NH1	2.42	0.47
56:RG:10:ARG:HH12	56:RG:314:GLN:HB3	1.79	0.47
49:R1:992:A:H2	49:R1:1012:U:H3	1.62	0.47
61:Re:147:ILE:HG21	61:Re:169:ILE:HG13	1.97	0.47
84:Ro:81:VAL:HG13	84:Ro:115:ILE:HG13	1.96	0.47
87:M1:3291:G:H2'	87:M1:3292:A:H8	1.79	0.47
89:MQ:144:LYS:HE2	89:MQ:151:GLU:HB3	1.97	0.47
21:MN:143:PHE:HA	21:MN:148:LEU:HD11	1.97	0.47
46:Mx:284:ARG:HB3	46:Mx:323:MET:HG2	1.97	0.47
35:Mm:75:LEU:HD12	35:Mm:95:GLU:HB3	1.96	0.47
5:L1:760:G:O2'	5:L1:770:G:N2	2.41	0.47
20:LM:8:LYS:NZ	20:LM:22:VAL:O	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:Lq:91:LEU:HD23	39:Lq:121:VAL:HG21	1.97	0.47
49:S1:354:C:H5''	65:Si:16:ALA:HB2	1.97	0.47
56:SG:7:LEU:HB3	56:SG:313:TRP:HB3	1.97	0.47
56:SG:300:THR:HG22	56:SG:314:GLN:HB2	1.97	0.47
75:Rs:92:ILE:HG23	75:Rs:93:THR:HG23	1.96	0.47
49:R1:418:G:O2'	63:Rg:72:ARG:NH2	2.45	0.47
49:R1:766:U:H3	49:R1:770:A:H62	1.62	0.47
49:R1:1081:A:N3	49:R1:1082:C:N4	2.63	0.47
87:M1:2714:G:H8	87:M1:2751:G:H2'	1.80	0.47
87:M1:2812:C:H2'	87:M1:2813:A:C8	2.50	0.47
6:M2:83:C:H2'	6:M2:85:G:H21	1.79	0.47
34:Ml:14:LEU:HD11	34:Ml:31:LYS:HB2	1.96	0.47
5:L1:776:U:OP1	38:Lp:41:ARG:NH1	2.38	0.46
11:LD:20:ILE:HG12	11:LD:25:VAL:HG13	1.97	0.46
17:LJ:27:LEU:O	17:LJ:101:ARG:NH1	2.48	0.46
34:Ll:37:THR:HG22	34:Ll:39:GLN:H	1.79	0.46
49:S1:205:U:H2'	49:S1:206:A:H8	1.79	0.46
49:S1:898:A:N1	49:S1:911:U:O2'	2.44	0.46
49:S1:1591:C:H2'	49:S1:1592:A:C8	2.50	0.46
49:S1:1791:A:O2'	49:S1:1792:G:OP2	2.33	0.46
77:Su:26:LEU:HD12	77:Su:114:VAL:HG22	1.97	0.46
57:Ra:179:ARG:HH11	57:Ra:183:ARG:HH22	1.63	0.46
84:Ro:82:LYS:HZ2	84:Ro:118:VAL:HG11	1.80	0.46
87:M1:1258:U:N3	87:M1:1261:G:OP2	2.38	0.46
87:M1:3379:C:H4'	46:Mx:315:GLY:HA2	1.96	0.46
6:M2:59:A:O2'	42:Mt:61:LYS:NZ	2.36	0.46
42:Mt:58:ASP:OD1	42:Mt:58:ASP:N	2.41	0.46
6:L2:9:A:H2'	6:L2:10:A:C8	2.50	0.46
6:L2:103:G:OP2	6:L2:105:A:O2'	2.24	0.46
10:LC:86:THR:HA	10:LC:89:GLU:HG3	1.97	0.46
49:S1:565:C:O3'	80:Sx:66:SER:OG	2.33	0.46
49:S1:956:C:OP1	49:S1:1072:C:O2'	2.32	0.46
57:Sa:7:PHE:O	57:Sa:54:TRP:NE1	2.39	0.46
59:Sc:139:ILE:HG13	59:Sc:191:ALA:HB1	1.96	0.46
67:Sk:54:TYR:O	67:Sk:69:THR:OG1	2.32	0.46
71:So:92:LYS:HD3	71:So:121:VAL:HG22	1.98	0.46
77:Su:40:ASN:HA	77:Su:43:LYS:HG2	1.98	0.46
77:Su:62:VAL:HG13	77:Su:83:GLU:HG3	1.96	0.46
82:Sz:48:ASP:HA	82:Sz:51:LEU:HD23	1.97	0.46
87:M1:209:A:O2'	87:M1:211:A:OP2	2.33	0.46
87:M1:1094:U:OP1	22:MO:116:ARG:NH2	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
87:M1:2720:G:OP1	19:ML:180:ARG:NH1	2.48	0.46
87:M1:2792:A:H2'	87:M1:2793:OMG:C8	2.49	0.46
87:M1:2960:C:H2'	87:M1:2961:G:H8	1.81	0.46
6:M2:8:C:H2'	6:M2:9:A:C8	2.50	0.46
90:MP:85:LEU:HD23	90:MP:104:ILE:HG13	1.98	0.46
39:Mq:3:SER:O	39:Mq:6:THR:OG1	2.29	0.46
15:MH:48:GLY:HA3	15:MH:53:VAL:HB	1.97	0.46
5:L1:1722:U:OP1	20:LM:100:ARG:NH1	2.49	0.46
5:L1:2108:C:H1'	5:L1:3344:A:C8	2.50	0.46
5:L1:3198:U:H1'	11:LD:21:LYS:HB2	1.97	0.46
9:LB:208:SER:OG	9:LB:209:ASN:N	2.48	0.46
19:LL:89:ASP:OD2	19:LL:90:ASP:N	2.49	0.46
23:La:10:LYS:HB2	23:La:125:LEU:HD22	1.97	0.46
49:S1:444:C:OP2	81:Sy:108:ARG:NH2	2.45	0.46
49:S1:1606:C:H2'	49:S1:1607:G:C8	2.50	0.46
50:SA:33:ASP:OD1	50:SA:33:ASP:N	2.49	0.46
56:SG:18:GLY:N	56:SG:308:ASN:OD1	2.49	0.46
56:SG:60:SER:O	73:Sq:94:GLN:NE2	2.48	0.46
69:Sm:58:LEU:HD23	69:Sm:125:ASN:H	1.81	0.46
71:So:29:HIS:HB3	71:So:41:ARG:HG3	1.97	0.46
71:So:81:VAL:HG11	71:So:102:LEU:HD23	1.96	0.46
77:Su:44:ASN:HA	77:Su:47:GLN:HE21	1.80	0.46
75:Rs:27:LYS:HE3	75:Rs:55:HIS:HA	1.97	0.46
78:Rv:40:ASP:OD1	78:Rv:40:ASP:N	2.45	0.46
58:Rb:168:ILE:HG12	58:Rb:197:ILE:HD12	1.98	0.46
63:Rg:132:ARG:HG3	63:Rg:133:LEU:HG	1.96	0.46
66:Rj:52:ILE:HG23	66:Rj:76:LEU:HD11	1.98	0.46
67:Rk:32:HIS:HB2	67:Rk:39:ASN:HB2	1.95	0.46
69:Rm:137:MET:H	69:Rm:137:MET:HE3	1.79	0.46
86:MA:17:ALA:O	87:M1:591:G:O2'	2.30	0.46
87:M1:1096:U:OP2	22:MO:116:ARG:NH1	2.48	0.46
87:M1:1553:U:H4'	87:M1:1554:U:H5'	1.97	0.46
87:M1:2812:C:H2'	87:M1:2813:A:H8	1.79	0.46
47:My:265:GLU:HG2	47:My:266:THR:HG23	1.97	0.46
23:Ma:106:LYS:HE2	23:Ma:106:LYS:HB2	1.73	0.46
12:ME:109:ASP:OD1	12:ME:109:ASP:N	2.45	0.46
13:MF:53:THR:HG22	13:MF:60:ARG:HA	1.97	0.46
31:Mi:35:ASN:HA	31:Mi:38:LYS:HB2	1.98	0.46
5:L1:952:A:H5''	38:Lp:15:LYS:HD3	1.97	0.46
5:L1:1863:G:N1	5:L1:1866:C:OP2	2.31	0.46
7:L3:81:U:H2'	7:L3:82:G:H8	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:LF:25:GLU:OE2	13:LF:25:GLU:N	2.49	0.46
39:Lq:130:VAL:HG21	39:Lq:145:VAL:HG21	1.98	0.46
43:Lu:1:MET:HE3	43:Lu:1:MET:HB3	1.79	0.46
47:Ly:90:PHE:O	47:Ly:98:ARG:NH1	2.49	0.46
49:S1:1294:G:O2'	57:Sa:108:THR:OG1	2.32	0.46
57:Sa:92:HIS:HB3	57:Sa:182:LEU:HD11	1.98	0.46
67:Sk:3:MET:SD	67:Sk:7:ASP:HB2	2.54	0.46
75:Ss:73:MET:HE2	75:Ss:73:MET:HB2	1.80	0.46
49:R1:224:C:H2'	49:R1:225:A:C8	2.50	0.46
59:Rc:69:ILE:O	59:Rc:73:LEU:N	2.48	0.46
59:Rc:113:LEU:HD11	59:Rc:211:LEU:HB3	1.97	0.46
61:Re:206:ASP:N	61:Re:206:ASP:OD2	2.49	0.46
87:M1:1203:A:H2'	87:M1:1204:A:C8	2.50	0.46
87:M1:1914:G:O2'	20:MM:82:LYS:O	2.28	0.46
47:My:156:LEU:HD12	47:My:159:ILE:HD12	1.97	0.46
11:MD:89:LYS:HG2	11:MD:145:VAL:HG22	1.98	0.46
29:Mg:10:GLN:HA	29:Mg:13:GLU:HG2	1.98	0.46
3:CN:13:ARG:HG2	54:RE:49:LEU:HD21	1.97	0.46
5:L1:1203:A:H2'	5:L1:1204:A:C8	2.50	0.46
5:L1:1596:C:H2'	5:L1:1597:C:C6	2.51	0.46
73:Sq:52:LEU:HD23	73:Sq:57:LEU:HD21	1.98	0.46
51:RB:54:VAL:HG13	51:RB:63:LEU:HB2	1.97	0.46
55:RF:92:LYS:H	55:RF:92:LYS:HG3	1.51	0.46
49:R1:656:G:O2'	49:R1:657:U:O4'	2.32	0.46
59:Rc:111:VAL:HG21	59:Rc:218:ILE:HD12	1.97	0.46
84:Ro:99:GLN:HA	84:Ro:99:GLN:HE21	1.80	0.46
17:MJ:16:VAL:HG23	17:MJ:80:PHE:HD1	1.80	0.46
87:M1:585:A:H5''	34:MI:70:LYS:HD2	1.96	0.46
87:M1:792:G:H2'	87:M1:793:C:C6	2.50	0.46
87:M1:960:U:H4'	87:M1:963:G:C2	2.51	0.46
87:M1:2897:A:H5''	27:Me:125:LYS:HB2	1.98	0.46
87:M1:3295:A:H2'	87:M1:3296:A:C8	2.51	0.46
20:MM:109:TYR:HB3	20:MM:115:ILE:HG12	1.97	0.46
5:L1:1764:U:OP2	20:LM:43:LYS:NZ	2.31	0.46
5:L1:2115:G:H22	5:L1:2120:A:H1'	1.80	0.46
5:L1:2575:G:H2'	5:L1:2576:G:H8	1.81	0.46
5:L1:3352:U:O2'	65:Si:161:SER:O	2.27	0.46
9:LB:130:ILE:HD12	9:LB:134:VAL:HG11	1.96	0.46
22:LO:70:SER:OG	22:LO:92:ARG:NH1	2.47	0.46
40:Lr:57:HIS:HB3	40:Lr:61:LYS:HB3	1.97	0.46
47:Ly:53:SER:HB3	47:Ly:56:ALA:HB2	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:S1:199:G:H2'	49:S1:200:A:C8	2.50	0.46
49:S1:234:G:C2	49:S1:235:G:H1'	2.49	0.46
63:Sg:105:ASP:OD1	63:Sg:105:ASP:N	2.46	0.46
72:Sp:24:LYS:HE2	72:Sp:24:LYS:HB2	1.73	0.46
81:Sy:26:ASP:OD1	81:Sy:26:ASP:N	2.47	0.46
75:Rs:83:ALA:HA	75:Rs:86:LEU:HD23	1.97	0.46
51:RB:42:ASN:ND2	51:RB:57:GLU:OE2	2.42	0.46
59:Rc:106:ASP:OD1	59:Rc:106:ASP:N	2.38	0.46
61:Re:100:ARG:NH1	61:Re:118:GLU:OE1	2.49	0.46
87:M1:528:U:H2'	87:M1:529:A:H8	1.81	0.46
41:Ms:60:ARG:HB2	41:Ms:103:LYS:HB3	1.96	0.46
36:Mn:77:ARG:HD2	36:Mn:89:LEU:HD13	1.97	0.46
35:Mm:63:THR:HA	35:Mm:66:LEU:HD22	1.97	0.46
16:MI:68:ARG:NH1	16:MI:124:ASP:O	2.36	0.46
16:MI:104:GLU:OE1	16:MI:108:ARG:NH1	2.48	0.46
5:L1:3121:U:H1'	5:L1:3122:A:H5''	1.97	0.46
10:LC:80:TYR:OH	10:LC:232:HIS:NE2	2.30	0.46
12:LE:48:LEU:HA	12:LE:178:ARG:HH22	1.81	0.46
14:LG:4:SER:O	39:Lq:44:ASN:ND2	2.48	0.46
37:Lo:80:ALA:O	70:Sn:151:ASN:ND2	2.48	0.46
45:Lw:52:SER:HB3	45:Lw:191:LEU:HD22	1.97	0.46
49:S1:742:U:O2	64:Sh:107:ARG:NH2	2.49	0.46
49:S1:804:A:C8	79:Sw:107:SER:HA	2.50	0.46
49:S1:1374:C:H2'	49:S1:1375:A:H8	1.80	0.46
49:S1:1753:A:H2'	49:S1:1754:A:C8	2.51	0.46
64:Sh:20:VAL:O	64:Sh:24:PHE:N	2.42	0.46
81:Ry:36:SER:O	81:Ry:38:ASP:N	2.49	0.46
50:RA:91:ASP:N	50:RA:91:ASP:OD1	2.49	0.46
56:RG:89:LEU:HD21	56:RG:110:VAL:HG11	1.98	0.46
49:R1:93:A:H1'	61:Re:3:ARG:HB3	1.98	0.46
49:R1:513:U:H2'	49:R1:514:G:C8	2.51	0.46
49:R1:991:G:H22	49:R1:1013:A:H62	1.63	0.46
61:Re:107:GLY:HA2	61:Re:189:LEU:HG	1.98	0.46
66:Rj:25:ASP:OD1	66:Rj:25:ASP:N	2.47	0.46
69:Rm:60:VAL:HG22	69:Rm:122:VAL:HG22	1.98	0.46
86:MA:131:LYS:HB3	86:MA:131:LYS:HE2	1.83	0.46
87:M1:528:U:H2'	87:M1:529:A:C8	2.50	0.46
46:Mx:62:ARG:HD2	46:Mx:65:SER:HB2	1.97	0.46
10:MC:81:THR:HG21	10:MC:181:LYS:HG3	1.97	0.46
16:MI:138:GLN:HA	16:MI:143:ARG:HH11	1.81	0.46
5:L1:705:A:N7	39:Lq:74:ASN:ND2	2.59	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L1:1244:A:O2'	5:L1:1247:U:OP1	2.26	0.46
5:L1:3255:U:H2'	5:L1:3256:G:H8	1.81	0.46
6:L2:21:C:OP1	47:Ly:193:LYS:NZ	2.31	0.46
11:LD:75:VAL:HA	11:LD:78:MET:HG2	1.98	0.46
22:LO:82:ASN:C	22:LO:82:ASN:ND2	2.73	0.46
49:S1:514:G:H2'	49:S1:515:A:H8	1.81	0.46
49:S1:939:A:H2'	49:S1:940:A:C8	2.51	0.46
71:So:126:THR:OG1	71:So:127:ARG:N	2.48	0.46
79:Rw:90:THR:O	79:Rw:94:LEU:HB2	2.16	0.46
50:RA:30:ILE:HD13	50:RA:74:CYS:HA	1.98	0.46
49:R1:1175:U:H2'	49:R1:1176:G:C8	2.51	0.46
49:R1:1481:C:O2'	49:R1:1482:C:O5'	2.30	0.46
64:Rh:62:VAL:HG12	64:Rh:64:VAL:H	1.81	0.46
84:Ro:18:ARG:NH2	84:Ro:31:THR:OG1	2.42	0.46
87:M1:1232:C:H2'	87:M1:1233:G:C8	2.51	0.46
48:Mz:36:LEU:HD22	48:Mz:50:ARG:HG2	1.98	0.46
14:MG:117:LYS:HE3	14:MG:117:LYS:HB2	1.69	0.46
5:L1:3309:G:H1'	18:LK:69:ARG:HD2	1.97	0.46
50:SA:39:MET:HE2	50:SA:39:MET:HB2	1.70	0.46
61:Se:184:THR:O	61:Se:184:THR:OG1	2.25	0.46
67:Sk:73:VAL:HG13	67:Sk:77:ARG:HH22	1.81	0.46
69:Sm:70:ASN:OD1	69:Sm:70:ASN:N	2.49	0.46
71:So:17:ALA:HB3	71:So:81:VAL:HA	1.97	0.46
71:So:84:ARG:NH1	71:So:85:ALA:O	2.49	0.46
56:RG:84:SER:OG	56:RG:85:TRP:N	2.49	0.46
49:R1:856:A:N6	64:Rh:115:SER:O	2.49	0.46
49:R1:1713:G:H2'	49:R1:1714:A:C8	2.51	0.46
60:Rd:37:VAL:HG12	60:Rd:50:ILE:HA	1.98	0.46
62:Rf:103:ASN:HA	62:Rf:106:LYS:HD2	1.98	0.46
87:M1:1570:U:N3	87:M1:1572:U:O2'	2.49	0.46
19:ML:82:VAL:HB	19:ML:139:ILE:HD13	1.98	0.46
5:L1:2232:A:H2'	5:L1:2233:A:C8	2.50	0.46
5:L1:3231:U:H2'	5:L1:3232:G:H8	1.81	0.46
42:Lt:105:VAL:HG11	42:Lt:126:LEU:HD13	1.97	0.46
45:Lw:70:ARG:CZ	45:Lw:71:LEU:H	2.29	0.46
56:SG:124:SER:HG	56:SG:134:TRP:HE1	1.62	0.46
75:Rs:70:VAL:O	75:Rs:74:GLN:HG2	2.16	0.46
81:Ry:39:GLU:O	81:Ry:43:LYS:N	2.44	0.46
82:Rz:58:ARG:HE	62:Rf:124:LEU:HA	1.81	0.46
82:Rz:71:ILE:HG12	82:Rz:75:LEU:HD13	1.98	0.46
49:R1:371:G:N2	49:R1:612:U:O2	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:R1:1020:A:N6	49:R1:1021:C:O2	2.49	0.46
65:Ri:90:LEU:HA	65:Ri:93:THR:HG22	1.98	0.46
87:M1:400:G:H4'	87:M1:401:U:H5''	1.96	0.46
87:M1:1907:C:O2	46:Mx:240:ARG:NH2	2.49	0.46
87:M1:2795:U:OP2	25:Mc:63:LYS:HG2	2.16	0.46
87:M1:2991:A:O2'	87:M1:3309:G:N7	2.49	0.46
10:MC:251:LYS:O	10:MC:255:SER:OG	2.34	0.46
13:MF:77:GLU:OE1	13:MF:77:GLU:N	2.47	0.46
91:DP:15:G:O6	91:DP:48:C:O2	2.34	0.46
5:L1:26:A:N3	5:L1:328:U:O2'	2.47	0.45
5:L1:559:A:O2'	15:LH:84:LYS:NZ	2.43	0.45
6:L2:26:U:O2'	47:Ly:51:ALA:O	2.33	0.45
6:L2:149:A:N3	10:LC:55:TYR:OH	2.46	0.45
9:LB:178:ILE:HD11	9:LB:187:GLU:HG3	1.98	0.45
21:LN:26:ARG:NH1	22:LO:150:THR:OG1	2.47	0.45
27:Le:98:LYS:HE2	27:Le:120:GLN:HG3	1.97	0.45
39:Lq:118:ILE:HD12	39:Lq:118:ILE:HA	1.79	0.45
46:Lx:47:LEU:HD22	46:Lx:335:ILE:HD11	1.97	0.45
49:S1:1592:A:H2'	49:S1:1593:A:H8	1.81	0.45
49:S1:1693:A:H2'	49:S1:1694:A:H8	1.81	0.45
76:St:77:ASN:HA	76:St:96:ALA:HB3	1.98	0.45
80:Sx:79:ASN:HB2	80:Sx:81:LYS:HG2	1.96	0.45
76:Rt:45:MET:HE3	76:Rt:46:PRO:HD2	1.97	0.45
49:R1:1404:C:H2'	49:R1:1405:G:H8	1.81	0.45
49:R1:1488:G:O2'	49:R1:1494:C:O2	2.26	0.45
58:Rb:107:THR:OG1	84:Ro:116:GLU:OE2	2.34	0.45
62:Rf:72:HIS:O	73:Rq:114:ARG:NH1	2.46	0.45
66:Rj:132:ARG:HB3	66:Rj:140:ILE:HD11	1.97	0.45
66:Rj:153:GLU:OE2	66:Rj:153:GLU:N	2.35	0.45
67:Rk:11:ILE:HA	67:Rk:35:ILE:HD13	1.98	0.45
86:MA:8:LYS:HZ1	87:M1:1353:U:H2'	1.80	0.45
87:M1:1765:U:H2'	87:M1:1766:G:C8	2.51	0.45
87:M1:2281:A2M:H8	87:M1:2281:A2M:H2'	1.72	0.45
37:Mo:71:GLN:OE1	37:Mo:71:GLN:N	2.38	0.45
2:CM:41:A:H2'	49:S1:1634:C:H41	1.80	0.45
5:L1:1667:A:H2'	5:L1:1668:G:C8	2.51	0.45
5:L1:3181:C:OP2	17:LJ:171:LYS:NZ	2.42	0.45
5:L1:3304:U:O3'	46:Lx:334:ARG:NH2	2.48	0.45
9:LB:84:VAL:HG23	9:LB:117:VAL:HB	1.97	0.45
11:LD:92:TYR:CD1	11:LD:142:ASP:HB2	2.51	0.45
14:LG:161:ASP:OD1	14:LG:161:ASP:N	2.37	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:S1:108:A:H2'	49:S1:109:G:C8	2.51	0.45
49:S1:200:A:H2'	49:S1:201:G:C8	2.52	0.45
49:S1:381:C:O2'	49:S1:755:A:N1	2.46	0.45
49:S1:805:U:O4	64:Sh:104:ARG:NH2	2.46	0.45
49:S1:1488:G:H3'	49:S1:1515:A:H61	1.80	0.45
66:Sj:52:ILE:HG23	66:Sj:76:LEU:HD11	1.98	0.45
75:Ss:52:VAL:HG21	75:Ss:69:ILE:HD11	1.99	0.45
75:Ss:101:LEU:H	75:Ss:104:ASN:HB2	1.80	0.45
76:St:67:MET:HA	76:St:67:MET:HE3	1.96	0.45
80:Sx:57:LEU:HD11	80:Sx:73:ARG:HB2	1.99	0.45
77:Ru:77:LYS:NZ	49:R1:1195:C:OP1	2.37	0.45
58:Rb:129:THR:OG1	58:Rb:131:ASP:O	2.34	0.45
63:Rg:10:ASN:ND2	63:Rg:125:THR:O	2.49	0.45
67:Rk:32:HIS:CE1	67:Rk:35:ILE:H	2.34	0.45
72:Rp:41:VAL:HG13	72:Rp:84:ILE:HD13	1.98	0.45
87:M1:1015:U:O2	87:M1:1028:U:O2'	2.29	0.45
87:M1:2546:C:H2'	87:M1:2547:A:C8	2.51	0.45
89:MQ:16:ARG:HH22	89:MQ:19:LEU:HD22	1.81	0.45
5:L1:1551:C:O2'	5:L1:2170:U:O2'	2.34	0.45
5:L1:2392:C:HO2'	46:Lx:266:ARG:HH22	1.57	0.45
6:L2:95:G:O2'	30:Lh:81:GLY:O	2.27	0.45
10:LC:85:ASN:OD1	10:LC:86:THR:N	2.49	0.45
15:LH:15:VAL:HG12	15:LH:38:ILE:HD11	1.97	0.45
49:S1:32:U:O2'	49:S1:594:A:N1	2.50	0.45
49:S1:1691:A:H2'	49:S1:1692:G:C8	2.51	0.45
60:Sd:211:PRO:HD3	74:Sr:19:ARG:HD3	1.97	0.45
62:Sf:47:SER:OG	62:Sf:49:GLU:OE1	2.35	0.45
49:R1:642:G:H2'	49:R1:643:G:C8	2.51	0.45
49:R1:891:A:H2'	49:R1:892:A:C8	2.51	0.45
49:R1:1664:C:H2'	49:R1:1665:U:H4'	1.99	0.45
60:Rd:191:ASP:OD1	60:Rd:191:ASP:N	2.49	0.45
87:M1:13:A:H4'	42:Mt:39:LYS:HG2	1.98	0.45
87:M1:1824:U:O2'	29:Mg:17:ARG:NH1	2.49	0.45
87:M1:2724:OMU:HM23	87:M1:2724:OMU:H1'	1.69	0.45
7:M3:84:A:H2'	7:M3:85:G:C8	2.51	0.45
6:M2:9:A:H2'	6:M2:10:A:C8	2.51	0.45
10:MC:109:LEU:O	10:MC:113:ALA:N	2.36	0.45
10:MC:162:LEU:HD23	16:MI:7:LEU:HD11	1.97	0.45
38:Mp:52:LYS:HE2	38:Mp:52:LYS:HB3	1.80	0.45
5:L1:1244:A:N6	5:L1:1271:A:OP1	2.49	0.45
7:L3:53:U:O2'	7:L3:55:A:N7	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:LA:39:VAL:O	8:LA:87:THR:OG1	2.30	0.45
18:LK:182:ILE:HD12	18:LK:182:ILE:HA	1.86	0.45
19:LL:39:ARG:HH12	47:Ly:302:ALA:HB2	1.80	0.45
37:Lo:17:VAL:HG11	37:Lo:92:ILE:HD12	1.98	0.45
43:Lu:86:SER:O	43:Lu:89:LEU:N	2.50	0.45
45:Lw:40:TYR:HA	45:Lw:91:GLY:HA3	1.99	0.45
48:Lz:85:ARG:NH2	48:Lz:86:TYR:OH	2.49	0.45
49:S1:68:A:H5'	63:Sg:160:ARG:HH12	1.80	0.45
49:S1:219:A:OP1	63:Sg:227:ARG:NH1	2.48	0.45
49:S1:1169:G:N1	49:S1:1575:G:OP2	2.38	0.45
54:RE:31:LYS:NZ	49:R1:544:A:O2'	2.48	0.45
49:R1:980:G:N2	49:R1:1020:A:H61	2.14	0.45
49:R1:1175:U:H3	49:R1:1464:G:H1	1.65	0.45
61:Re:79:ASP:OD1	61:Re:79:ASP:N	2.39	0.45
66:Rj:168:ARG:HD3	66:Rj:174:ARG:HH11	1.80	0.45
87:M1:266:A:H2'	31:Mi:30:LYS:HE3	1.98	0.45
87:M1:1799:A:H2'	87:M1:1800:A:H8	1.81	0.45
87:M1:2669:G:H2'	87:M1:2670:G:H8	1.80	0.45
41:Ms:69:LYS:HB3	41:Ms:69:LYS:HE3	1.66	0.45
91:DP:28:C:H2'	91:DP:29:A:C8	2.51	0.45
2:CM:38:C:H2'	2:CM:39:G:H8	1.81	0.45
17:LJ:121:PRO:HA	17:LJ:124:LEU:HD12	1.99	0.45
34:Ll:32:ILE:HG23	34:Ll:100:ILE:HD12	1.99	0.45
49:S1:12:U:H2'	49:S1:13:C:C6	2.52	0.45
49:S1:166:C:O2'	63:Sg:133:LEU:O	2.35	0.45
53:SD:19:ARG:HD3	53:SD:32:ARG:HH22	1.81	0.45
59:Sc:219:GLY:O	78:Sv:25:LYS:NZ	2.38	0.45
66:Sj:177:ALA:HA	66:Sj:180:LYS:HE3	1.97	0.45
80:Rx:93:LEU:HD21	54:RE:8:LEU:HD23	1.98	0.45
49:R1:195:G:O6	65:Ri:137:LYS:NZ	2.45	0.45
49:R1:1164:G:H2'	49:R1:1165:G:C8	2.51	0.45
49:R1:1729:C:H4'	65:Ri:3:ILE:HG22	1.97	0.45
87:M1:498:A:O2'	87:M1:3273:A:N1	2.49	0.45
89:MQ:74:GLU:HA	89:MQ:77:LEU:HG	1.98	0.45
47:My:82:THR:O	47:My:82:THR:OG1	2.35	0.45
12:ME:49:CYS:HB3	12:ME:168:SER:HB3	1.98	0.45
29:Mg:3:ARG:HE	29:Mg:3:ARG:HB3	1.58	0.45
5:L1:1079:A:H4'	48:Lz:140:ARG:O	2.16	0.45
5:L1:1157:G:O2'	5:L1:1169:A:N3	2.46	0.45
5:L1:1486:G:H21	33:Lk:6:THR:HG22	1.82	0.45
5:L1:1659:U:H2'	5:L1:1660:C:C6	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L1:3016:A:H2'	5:L1:3017:A:C8	2.52	0.45
7:L3:112:G:H2'	7:L3:113:C:C6	2.51	0.45
33:Lk:90:ILE:HG22	33:Lk:94:LEU:HD22	1.99	0.45
45:Lw:47:GLN:HG3	45:Lw:49:VAL:HG13	1.99	0.45
49:S1:194:U:H2'	49:S1:195:G:H4'	1.99	0.45
49:S1:502:U:H2'	49:S1:503:G:C8	2.51	0.45
49:R1:992:A:H5''	49:R1:993:A:C8	2.51	0.45
60:Rd:14:ASP:HA	60:Rd:17:PHE:HB3	1.98	0.45
65:Ri:184:LEU:HB3	65:Ri:189:LEU:HB2	1.99	0.45
84:Ro:42:VAL:HG23	84:Ro:46:MET:HE2	1.98	0.45
87:M1:1245:A:N7	87:M1:1271:A:O2'	2.41	0.45
6:M2:68:G:OP2	30:Mh:85:LYS:NZ	2.46	0.45
46:Mx:236:LYS:HE2	46:Mx:236:LYS:HB2	1.83	0.45
41:Ms:73:VAL:HG13	41:Ms:80:VAL:HG12	1.99	0.45
5:L1:993:G:N3	5:L1:2637:A:H2'	2.32	0.45
5:L1:1920:U:O2'	5:L1:1932:A:N7	2.43	0.45
5:L1:2525:G:O2'	5:L1:2526:C:OP2	2.32	0.45
5:L1:3038:U:OP1	46:Lx:348:ARG:NH1	2.50	0.45
5:L1:3319:U:O2'	5:L1:3320:A:OP1	2.35	0.45
17:LJ:189:ASP:OD2	17:LJ:189:ASP:N	2.49	0.45
49:S1:1471:A:H62	49:S1:1538:U:H3	1.65	0.45
50:SA:30:ILE:HD13	50:SA:74:CYS:HA	1.98	0.45
56:SG:45:TRP:HA	56:SG:57:PRO:HA	1.99	0.45
56:SG:239:GLU:O	56:SG:257:ALA:N	2.48	0.45
69:Sm:42:ALA:HB3	69:Sm:122:VAL:HB	1.99	0.45
76:St:18:TYR:HD1	76:St:135:ILE:HD13	1.82	0.45
78:Sv:15:ARG:NH1	78:Sv:33:GLN:OE1	2.49	0.45
79:Sw:50:PHE:HB3	79:Sw:63:VAL:HG13	1.99	0.45
62:Rf:166:ARG:HH12	62:Rf:170:GLN:HE21	1.64	0.45
63:Rg:2:LYS:HB3	63:Rg:108:VAL:HG12	1.99	0.45
63:Rg:23:ARG:NH1	63:Rg:41:VAL:O	2.50	0.45
63:Rg:58:LYS:NZ	63:Rg:104:PRO:O	2.44	0.45
64:Rh:91:ILE:HG21	64:Rh:169:PHE:HE1	1.82	0.45
66:Rj:109:LEU:HB2	66:Rj:146:PHE:HB3	1.99	0.45
67:Rk:12:HIS:HB3	67:Rk:76:LEU:HD11	1.98	0.45
87:M1:1718:G:H2'	87:M1:1719:G:C8	2.52	0.45
7:M3:4:U:H2'	7:M3:5:G:H8	1.81	0.45
44:Mv:38:ILE:HG23	44:Mv:50:LEU:HD11	1.98	0.45
5:L1:117:U:O2'	5:L1:119:U:OP2	2.32	0.45
5:L1:1805:C:H2'	5:L1:1806:A:H8	1.81	0.45
5:L1:3184:A:N3	5:L1:3187:A:O2'	2.43	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L1:3233:C:H2'	5:L1:3234:A:C8	2.52	0.45
40:Lr:26:VAL:HG21	40:Lr:96:VAL:HB	1.98	0.45
47:Ly:126:ILE:O	47:Ly:129:THR:OG1	2.31	0.45
49:S1:448:C:OP2	61:Se:49:ARG:NH1	2.34	0.45
49:S1:598:U:H2'	49:S1:599:A:H8	1.81	0.45
49:S1:1173:C:OP1	75:Ss:132:ARG:NH2	2.45	0.45
49:S1:1292:G:H21	57:Sa:111:ILE:HD11	1.81	0.45
56:SG:175:ASP:OD1	56:SG:175:ASP:N	2.42	0.45
60:Sd:78:LYS:HE2	60:Sd:78:LYS:N	2.32	0.45
76:Rt:102:ARG:NH1	49:R1:1501:C:OP2	2.46	0.45
78:Rv:50:TYR:HE1	57:Ra:66:ALA:HB1	1.82	0.45
56:RG:116:ASP:OD1	56:RG:116:ASP:N	2.49	0.45
49:R1:653:C:H42	49:R1:682:C:N4	2.15	0.45
49:R1:894:U:H2'	49:R1:895:G:C8	2.52	0.45
49:R1:1483:A:H2'	49:R1:1484:G:C8	2.52	0.45
58:Rb:103:MET:HB3	58:Rb:215:VAL:HG22	1.98	0.45
61:Re:188:ASN:HB3	61:Re:191:ARG:HD3	1.99	0.45
69:Rm:89:ILE:HB	69:Rm:140:PHE:HE1	1.81	0.45
17:MJ:46:GLU:HG3	17:MJ:48:PHE:H	1.81	0.45
17:MJ:60:LYS:NZ	87:M1:1307:G:OP1	2.46	0.45
87:M1:1061:A:H4'	22:MO:102:ARG:HD2	1.99	0.45
87:M1:1666:G:H2'	87:M1:1667:A:C8	2.52	0.45
87:M1:1667:A:H2'	87:M1:1668:G:C8	2.52	0.45
6:M2:57:C:OP2	30:Mh:68:LYS:NZ	2.50	0.45
41:Ms:29:VAL:O	41:Ms:32:SER:OG	2.31	0.45
5:L1:307:A:H2'	5:L1:308:A:C8	2.51	0.45
13:LF:110:ILE:H	13:LF:110:ILE:HG12	1.51	0.45
16:LI:183:THR:OG1	16:LI:183:THR:O	2.32	0.45
21:LN:82:ASP:OD1	21:LN:82:ASP:N	2.50	0.45
25:Lc:68:VAL:HG13	25:Lc:85:LEU:HB2	1.98	0.45
49:S1:486:G:N2	49:S1:501:U:O2	2.50	0.45
49:S1:615:A:O2'	49:S1:621:A:N1	2.45	0.45
49:S1:1160:A:H2'	49:S1:1161:C:C6	2.51	0.45
49:S1:1434:U:H4'	53:SD:24:CYS:HB2	1.99	0.45
55:SF:149:LYS:HA	55:SF:149:LYS:HD3	1.79	0.45
56:SG:156:VAL:HG12	56:SG:169:ILE:HG22	1.99	0.45
57:Sa:182:LEU:HD23	57:Sa:182:LEU:HA	1.82	0.45
59:Sc:232:GLU:OE1	59:Sc:232:GLU:N	2.39	0.45
56:RG:285:ALA:HB1	49:R1:1393:C:H5''	1.99	0.45
49:R1:156:A:H2'	49:R1:157:A:O4'	2.16	0.45
63:Rg:58:LYS:HA	63:Rg:107:ALA:HB2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
68:Rl:83:THR:HG22	68:Rl:110:HIS:HA	1.98	0.45
86:MA:5:LYS:NZ	87:M1:1423:C:O2'	2.50	0.45
87:M1:127:G:H2'	87:M1:128:G:H8	1.82	0.45
87:M1:1054:A:H5''	87:M1:2637:A:H61	1.82	0.45
87:M1:1737:U:O2	33:Mk:52:GLN:NE2	2.49	0.45
48:Mz:99:TYR:HE2	48:Mz:164:LYS:HG3	1.82	0.45
28:Mf:28:ARG:N	28:Mf:33:ASN:HD21	2.06	0.45
5:L1:19:U:H2'	5:L1:20:A:C8	2.52	0.45
5:L1:631:U:H2'	5:L1:632:G:C8	2.52	0.45
5:L1:994:G:N2	5:L1:995:U:O4	2.40	0.45
5:L1:1378:U:H2'	5:L1:1379:G:H8	1.83	0.45
17:LJ:127:LEU:HD22	21:LN:156:VAL:HG13	1.99	0.45
17:LJ:138:LEU:HD12	17:LJ:138:LEU:HA	1.83	0.45
21:LN:81:TYR:CE1	21:LN:90:MET:HE3	2.52	0.45
34:Ll:19:SER:OG	34:Ll:20:LYS:N	2.49	0.45
49:S1:477:A:H2'	49:S1:478:A:H8	1.80	0.45
59:Sc:194:GLU:OE1	59:Sc:194:GLU:N	2.42	0.45
61:Se:90:ILE:HD12	61:Se:101:LEU:HD21	1.99	0.45
64:Sh:22:GLN:HA	64:Sh:25:VAL:HG12	1.97	0.45
67:Sk:3:MET:HB2	67:Sk:41:TYR:CZ	2.52	0.45
76:St:27:LYS:O	76:St:110:LYS:NZ	2.50	0.45
79:Sw:111:MET:HE2	79:Sw:111:MET:HB3	1.72	0.45
56:RG:126:SER:OG	56:RG:127:ARG:N	2.50	0.45
49:R1:140:A:OP2	63:Rg:187:LYS:NZ	2.47	0.45
49:R1:225:A:N6	49:R1:837:G:N1	2.65	0.45
49:R1:340:U:H2'	49:R1:341:A:H8	1.82	0.45
49:R1:1477:G:H2'	49:R1:1478:G:C8	2.52	0.45
61:Re:100:ARG:NH2	61:Re:121:TYR:O	2.47	0.45
70:Rn:28:LEU:HD13	70:Rn:29:SER:HB3	1.99	0.45
73:Rq:55:VAL:HG11	73:Rq:105:LEU:HD23	1.97	0.45
73:Rq:114:ARG:H	73:Rq:116:LEU:HD12	1.82	0.45
86:MA:97:ASN:OD1	86:MA:97:ASN:N	2.43	0.45
87:M1:1250:G:H2'	87:M1:1251:A:C8	2.52	0.45
87:M1:1828:A:H2'	87:M1:1829:G:C8	2.52	0.45
87:M1:2417:OMU:HM23	87:M1:2417:OMU:H1'	1.61	0.45
23:Ma:109:MET:HE2	23:Ma:109:MET:HB3	1.85	0.45
37:Mo:27:TYR:OH	37:Mo:55:GLU:OE1	2.30	0.45
8:LA:76:LEU:N	8:LA:138:GLN:OE1	2.50	0.44
14:LG:62:THR:O	14:LG:64:LYS:N	2.50	0.44
14:LG:122:LYS:O	32:Lj:120:ALA:N	2.50	0.44
56:SG:180:ALA:HB3	56:SG:190:ALA:HB3	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:Sb:70:LEU:HD13	58:Sb:84:ILE:HG13	2.00	0.44
58:Sb:168:ILE:HG12	58:Sb:197:ILE:HD12	1.99	0.44
56:RG:88:THR:HG22	56:RG:104:VAL:HG12	1.98	0.44
60:Rd:72:LEU:HD22	67:Rk:65:TYR:HD1	1.82	0.44
60:Rd:74:GLN:NE2	60:Rd:79:TYR:O	2.50	0.44
67:Rk:6:GLU:N	67:Rk:6:GLU:OE2	2.48	0.44
87:M1:2094:C:H2'	87:M1:2095:G:H8	1.82	0.44
87:M1:3329:U:H5''	46:Mx:308:MET:HE2	1.99	0.44
5:L1:1108:U:H2'	5:L1:1109:U:C6	2.52	0.44
11:LD:41:ILE:HD12	11:LD:41:ILE:HA	1.88	0.44
47:Ly:11:LEU:HD21	47:Ly:156:LEU:HB2	1.99	0.44
49:S1:15:U:H2'	49:S1:16:G:O4'	2.18	0.44
49:S1:31:C:O2'	49:S1:547:U:OP1	2.34	0.44
49:S1:637:C:O2	64:Sh:114:ARG:NH2	2.39	0.44
49:S1:1220:C:H2'	49:S1:1221:A:C8	2.53	0.44
49:S1:1297:G:N2	49:S1:1300:A:OP2	2.42	0.44
58:Sb:207:LEU:O	58:Sb:210:ILE:HD11	2.17	0.44
61:Se:100:ARG:HG2	61:Se:102:VAL:HG13	1.99	0.44
63:Sg:180:THR:HG22	63:Sg:182:GLN:H	1.83	0.44
69:Sm:29:LYS:HB2	69:Sm:29:LYS:HE2	1.85	0.44
70:Sn:106:ARG:HE	70:Sn:106:ARG:HB3	1.70	0.44
49:R1:5:U:OP2	59:Rc:204:THR:OG1	2.35	0.44
49:R1:446:A:N6	49:R1:461:G:H21	2.16	0.44
49:R1:642:G:H2'	49:R1:643:G:H8	1.82	0.44
49:R1:1164:G:H2'	49:R1:1165:G:H8	1.81	0.44
57:Ra:56:LYS:HZ2	57:Ra:158:VAL:HG23	1.82	0.44
59:Rc:73:LEU:HD23	59:Rc:73:LEU:HA	1.90	0.44
61:Re:151:ASP:OD1	63:Rg:215:ARG:NH2	2.50	0.44
69:Rm:90:LYS:HA	69:Rm:90:LYS:HE2	2.00	0.44
87:M1:1718:G:H2'	87:M1:1719:G:H8	1.82	0.44
18:MK:56:ARG:NH2	18:MK:75:GLU:OE2	2.43	0.44
6:M2:57:C:H4'	6:M2:63:G:N7	2.32	0.44
15:LH:38:ILE:HG12	15:LH:44:VAL:HG12	1.99	0.44
21:LN:6:GLU:HG3	21:LN:30:PHE:CE2	2.52	0.44
43:Lu:81:PRO:HB2	63:Sg:130:PRO:HB3	1.99	0.44
46:Lx:294:GLY:HA2	46:Lx:359:ILE:HD12	2.00	0.44
49:S1:58:U:OP1	49:S1:456:A:O2'	2.32	0.44
54:SE:33:ARG:HE	66:Sj:123:HIS:HD2	1.65	0.44
56:SG:123:ILE:HG21	56:SG:169:ILE:HG21	2.00	0.44
60:Sd:109:LEU:HD22	60:Sd:115:ILE:HD13	2.00	0.44
63:Sg:3:LEU:N	63:Sg:16:PHE:O	2.49	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:Sn:119:GLU:HG3	70:Sn:141:TYR:HE2	1.82	0.44
73:Sq:99:GLU:HA	73:Sq:102:LYS:HB2	1.99	0.44
74:Sr:65:PRO:HB3	74:Sr:74:GLN:HE22	1.82	0.44
78:Sv:79:LEU:HD12	78:Sv:79:LEU:HA	1.83	0.44
49:R1:340:U:H2'	49:R1:341:A:C8	2.52	0.44
49:R1:1294:G:O2'	49:R1:1321:A:N1	2.48	0.44
49:R1:1728:A:O2'	49:R1:1729:C:O4'	2.31	0.44
64:Rh:37:GLU:HG3	64:Rh:73:VAL:HG11	1.99	0.44
69:Rm:63:VAL:HB	69:Rm:119:SER:HB2	1.99	0.44
73:Rq:98:ASP:O	73:Rq:101:SER:OG	2.29	0.44
85:Rr:99:VAL:HG22	85:Rr:118:PRO:HB2	1.99	0.44
87:M1:2103:U:H2'	87:M1:2104:A:C8	2.53	0.44
88:DQ:72:C:H2'	88:DQ:73:A:H8	1.81	0.44
42:Mt:86:VAL:HG23	42:Mt:120:LYS:HB3	1.98	0.44
9:MB:130:ILE:HD12	9:MB:134:VAL:HG11	1.99	0.44
39:Mq:77:LYS:O	39:Mq:79:TRP:N	2.51	0.44
29:Mg:33:LYS:HE3	29:Mg:33:LYS:HB3	1.65	0.44
5:L1:643:U:O2'	5:L1:1153:A:N1	2.45	0.44
5:L1:1203:A:N3	5:L1:2855:U:O2'	2.42	0.44
5:L1:1666:G:H2'	5:L1:1667:A:C8	2.53	0.44
5:L1:1798:A:H2'	5:L1:1799:A:C8	2.53	0.44
5:L1:2947:G:N3	46:Lx:250:ALA:HB1	2.33	0.44
12:LE:44:ASP:OD1	12:LE:44:ASP:N	2.50	0.44
34:Ll:16:TYR:OH	34:Ll:89:LEU:O	2.26	0.44
42:Lt:90:ALA:O	42:Lt:120:LYS:NZ	2.50	0.44
48:Lz:85:ARG:HH12	48:Lz:254:LYS:H	1.66	0.44
49:S1:821:U:N3	49:S1:852:C:O2	2.42	0.44
54:SE:40:TYR:CG	66:Sj:32:GLY:HA3	2.52	0.44
56:SG:88:THR:HG22	56:SG:104:VAL:HG23	1.99	0.44
59:Sc:161:LYS:HG3	59:Sc:166:THR:HG22	1.98	0.44
63:Sg:102:VAL:HG13	63:Sg:106:LEU:HD12	1.99	0.44
56:RG:121:MET:HE2	56:RG:123:ILE:HG23	1.99	0.44
56:RG:301:LEU:HG	56:RG:313:TRP:HB2	1.98	0.44
49:R1:508:U:H2'	49:R1:509:G:H8	1.82	0.44
61:Re:66:MET:HE3	61:Re:66:MET:HB3	1.87	0.44
87:M1:307:A:H2'	87:M1:308:A:C8	2.53	0.44
87:M1:1083:G:H2'	87:M1:1084:A:C8	2.52	0.44
87:M1:2619:OMG:HM23	87:M1:2619:OMG:H1'	1.72	0.44
19:LL:71:LEU:HD22	19:LL:99:THR:HG21	2.00	0.44
46:Lx:56:ILE:HD13	46:Lx:56:ILE:HA	1.79	0.44
48:Lz:50:ARG:NH1	48:Lz:72:ASP:OD2	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:Lz:247:ILE:HD13	48:Lz:247:ILE:HA	1.90	0.44
49:S1:92:A:N6	63:Sg:89:ASP:OD2	2.46	0.44
49:S1:1237:G:H2'	49:S1:1238:A:C8	2.52	0.44
49:S1:1474:G:H2'	49:S1:1475:A:H8	1.82	0.44
49:S1:1553:G:N1	49:S1:1556:A:OP2	2.50	0.44
49:S1:1689:A:H2'	49:S1:1690:G:C8	2.52	0.44
53:SD:7:TRP:HD1	67:Sk:28:ASN:HD22	1.64	0.44
66:Sj:63:ASP:OD1	66:Sj:64:GLU:N	2.51	0.44
73:Sq:92:TYR:HD2	73:Sq:93:HIS:HD2	1.66	0.44
76:St:94:ILE:HD12	76:St:94:ILE:HA	1.84	0.44
82:Sz:91:PRO:HB3	82:Sz:101:TYR:HE2	1.83	0.44
77:Ru:19:ILE:HG22	77:Ru:96:PRO:HD3	1.99	0.44
77:Ru:80:GLU:OE2	53:RD:54:LYS:NZ	2.40	0.44
49:R1:166:C:O2'	63:Rg:133:LEU:O	2.35	0.44
69:Rm:140:PHE:O	69:Rm:143:GLN:NE2	2.51	0.44
70:Rn:100:LYS:HE3	70:Rn:100:LYS:HB3	1.78	0.44
73:Rq:129:PHE:O	73:Rq:137:ARG:NH1	2.46	0.44
86:MA:31:ARG:NH2	34:Ml:107:ILE:O	2.45	0.44
87:M1:2469:G:H21	87:M1:2488:A:H8	1.64	0.44
87:M1:3186:A:N3	11:MD:44:THR:OG1	2.50	0.44
11:MD:12:VAL:HG23	11:MD:16:VAL:HB	2.00	0.44
13:MF:170:ASP:OD1	13:MF:170:ASP:N	2.50	0.44
37:Mo:55:GLU:HG3	33:Mk:90:ILE:HG21	2.00	0.44
33:Mk:47:CYS:HB3	33:Mk:84:CYS:SG	2.58	0.44
5:L1:82:C:H4'	16:LI:204:LYS:HE2	1.98	0.44
5:L1:138:U:H2'	5:L1:139:G:H8	1.81	0.44
9:LB:211:SER:H	9:LB:242:SER:HB2	1.83	0.44
41:Ls:24:SER:O	41:Ls:75:ARG:NH1	2.51	0.44
56:SG:144:LEU:HD11	56:SG:186:PHE:HB3	2.00	0.44
56:SG:178:VAL:HB	56:SG:192:PHE:HB2	1.99	0.44
56:SG:206:PRO:HD3	56:SG:245:PHE:HB3	2.00	0.44
79:Sw:30:SER:HB2	79:Sw:61:ILE:HG13	1.99	0.44
75:Rs:126:ARG:NH1	49:R1:1459:C:OP1	2.36	0.44
56:RG:314:GLN:HB3	56:RG:316:MET:HE1	2.00	0.44
49:R1:1628:U:H2'	49:R1:1629:G:C8	2.52	0.44
60:Rd:132:LYS:HB3	60:Rd:189:MET:HG2	1.99	0.44
61:Re:168:LYS:HA	61:Re:168:LYS:HD3	1.84	0.44
66:Rj:114:TYR:HA	66:Rj:119:ALA:HB3	1.99	0.44
70:Rn:101:HIS:HA	70:Rn:104:ARG:HH21	1.83	0.44
85:Rr:21:TYR:HB2	85:Rr:71:PHE:HB2	1.99	0.44
17:MJ:187:GLU:OE2	17:MJ:187:GLU:N	2.49	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
87:M1:47:C:H5''	14:Mg:16:LYS:HG2	2.00	0.44
87:M1:94:G:H2'	87:M1:95:A:C8	2.52	0.44
87:M1:247:C:H2'	87:M1:248:U:O4'	2.18	0.44
87:M1:1750:A:OP1	29:Mg:44:LYS:NZ	2.39	0.44
6:M2:21:C:OP1	47:My:193:LYS:NZ	2.40	0.44
33:Mk:3:GLN:HE22	33:Mk:29:ILE:HB	1.83	0.44
2:CM:38:C:H2'	2:CM:39:G:C8	2.52	0.44
5:L1:1194:G:H2'	5:L1:1195:A:C8	2.52	0.44
5:L1:1364:C:H5''	19:LL:3:ILE:HD13	2.00	0.44
10:LC:81:THR:OG1	10:LC:82:LEU:N	2.51	0.44
10:LC:140:VAL:HG22	10:LC:166:LEU:HD21	1.98	0.44
12:LE:80:SER:OG	12:LE:144:ASN:ND2	2.51	0.44
61:Se:112:HIS:NE2	61:Se:237:SER:O	2.51	0.44
81:Ry:55:VAL:HG12	81:Ry:75:VAL:HG22	1.99	0.44
57:Ra:8:ASP:OD2	57:Ra:8:ASP:N	2.51	0.44
87:M1:118:U:O2	87:M1:121:A:H5''	2.18	0.44
87:M1:1035:G:H2'	87:M1:1036:A:H8	1.80	0.44
87:M1:1108:U:H2'	87:M1:1109:U:C6	2.53	0.44
87:M1:1176:C:H2'	87:M1:1177:G:N2	2.33	0.44
47:My:170:LYS:HG3	47:My:175:HIS:HB2	1.99	0.44
11:MD:92:TYR:HB2	11:MD:142:ASP:HB3	1.99	0.44
12:ME:93:PRO:HB2	12:ME:125:LEU:HB3	2.00	0.44
32:Mj:49:LYS:HD3	32:Mj:49:LYS:HA	1.80	0.44
3:CN:102:LYS:HE2	3:CN:102:LYS:HB3	1.75	0.44
5:L1:20:A:H2'	5:L1:21:G:C8	2.52	0.44
5:L1:277:G:H5''	25:Lc:49:GLY:HA2	1.99	0.44
5:L1:1253:U:N3	5:L1:1264:G:OP1	2.49	0.44
5:L1:1423:C:O2'	8:LA:5:GLN:OE1	2.29	0.44
5:L1:2357:A:H2'	5:L1:2358:A:H8	1.83	0.44
5:L1:2940:A:N7	46:Lx:2:SER:N	2.65	0.44
16:LI:73:ARG:HB3	16:LI:89:VAL:HG13	2.00	0.44
17:LJ:51:LYS:HE2	17:LJ:144:SER:HB2	1.99	0.44
36:Ln:77:ARG:HD2	36:Ln:89:LEU:HD13	2.00	0.44
43:Lu:45:ASN:HB3	43:Lu:48:ARG:HG3	2.00	0.44
49:S1:918:U:H4'	71:So:18:ARG:HD3	1.99	0.44
59:Sc:116:LYS:HG2	59:Sc:127:ALA:HB3	1.99	0.44
72:Sp:28:MET:N	72:Sp:28:MET:SD	2.91	0.44
76:Rt:38:LYS:NZ	49:R1:1564:U:OP1	2.40	0.44
78:Rv:14:PRO:HG2	78:Rv:23:ILE:HD12	2.00	0.44
50:RA:8:ASN:HB3	49:R1:1791:A:H5''	2.00	0.44
56:RG:121:MET:HE3	56:RG:122:ILE:N	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:R1:577:G:N3	91:DP:35:A:O2'	2.46	0.44
49:R1:924:A:H2'	49:R1:925:G:C8	2.53	0.44
61:Re:10:LYS:HA	61:Re:27:TYR:HA	1.99	0.44
62:Rf:62:VAL:HG13	62:Rf:89:ILE:HG21	2.00	0.44
87:M1:728:G:H5''	19:ML:43:PRO:HB2	2.00	0.44
87:M1:1112:A:OP1	14:MG:5:LYS:NZ	2.49	0.44
87:M1:1493:G:O6	28:Mf:2:ALA:N	2.50	0.44
87:M1:3231:U:H2'	87:M1:3232:G:H8	1.83	0.44
6:M2:142:C:OP1	16:MI:38:ARG:NH1	2.51	0.44
88:DQ:72:C:H2'	88:DQ:73:A:C8	2.53	0.44
89:MQ:60:ARG:HB3	89:MQ:64:ARG:HH22	1.82	0.44
22:MO:120:LYS:HE3	22:MO:120:LYS:HB2	1.71	0.44
4:CP:68:G:H2'	4:CP:69:G:H8	1.82	0.44
5:L1:531:G:H2'	5:L1:532:A:C8	2.53	0.44
5:L1:671:U:H2'	5:L1:672:A:C8	2.53	0.44
5:L1:835:G:O2'	5:L1:857:G:N2	2.34	0.44
5:L1:1084:A:H2'	5:L1:1085:A:C8	2.53	0.44
5:L1:1836:C:O2'	5:L1:1842:A:N1	2.46	0.44
5:L1:3252:G:H2'	5:L1:3253:G:C8	2.53	0.44
11:LD:141:LYS:HB2	11:LD:141:LYS:HE2	1.66	0.44
18:LK:129:THR:HG22	18:LK:131:ARG:HD2	1.99	0.44
39:Lq:83:PRO:HG2	39:Lq:86:LYS:HD3	1.99	0.44
45:Lw:100:ASN:HB2	45:Lw:166:ILE:HD12	2.00	0.44
47:Ly:193:LYS:HB2	47:Ly:193:LYS:HE3	1.82	0.44
49:S1:183:U:H2'	49:S1:184:C:H6	1.83	0.44
49:S1:199:G:H2'	49:S1:200:A:H8	1.82	0.44
49:S1:209:U:H2'	49:S1:210:A:C8	2.52	0.44
49:S1:553:G:H3'	49:S1:554:C:H2'	2.00	0.44
55:SF:106:TYR:HE1	55:SF:131:PHE:HZ	1.66	0.44
60:Sd:101:GLN:HG3	60:Sd:122:VAL:HG13	2.00	0.44
75:Rs:52:VAL:HG21	75:Rs:69:ILE:HD11	2.00	0.44
56:RG:128:ASP:OD1	56:RG:130:THR:OG1	2.33	0.44
56:RG:248:ASN:ND2	56:RG:297:ASP:O	2.49	0.44
49:R1:1641:C:H2'	49:R1:1642:G:C8	2.53	0.44
62:Rf:64:VAL:H	62:Rf:65:ARG:NH1	2.16	0.44
64:Rh:13:PRO:HA	64:Rh:14:THR:HA	1.69	0.44
65:Ri:92:ARG:NH1	87:M1:2107:A:O3'	2.47	0.44
67:Rk:77:ARG:NH2	67:Rk:85:HIS:O	2.51	0.44
68:Rl:109:VAL:HG12	68:Rl:137:PHE:HB2	1.99	0.44
72:Rp:27:GLU:OE2	72:Rp:27:GLU:N	2.48	0.44
87:M1:1062:A:H5''	87:M1:1063:G:H5'	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:My:325:LEU:O	9:MB:41:ARG:NH2	2.50	0.44
5:L1:284:A:OP2	25:Lc:41:ARG:NH1	2.45	0.43
5:L1:847:A:H61	49:S1:972:G:H1'	1.83	0.43
14:LG:138:VAL:HG13	32:Lj:119:LYS:HE3	1.99	0.43
16:LI:116:LEU:O	16:LI:159:ARG:NH2	2.51	0.43
20:LM:21:LYS:HA	20:LM:53:LYS:HD2	2.00	0.43
39:Lq:34:MET:HE2	39:Lq:45:MET:HE1	1.98	0.43
40:Lr:3:LYS:H	40:Lr:3:LYS:HG2	1.67	0.43
48:Lz:53:VAL:O	48:Lz:54:ARG:NH1	2.43	0.43
49:S1:520:A:H2	81:Sy:34:ASN:HD21	1.66	0.43
49:S1:560:U:H2'	49:S1:561:G:H8	1.83	0.43
49:S1:849:C:H2'	49:S1:850:A:H8	1.82	0.43
56:SG:37:SER:OG	56:SG:38:ARG:N	2.51	0.43
59:Sc:174:ARG:HB3	66:Sj:98:ALA:HB2	1.99	0.43
75:Rs:17:LEU:HD21	75:Rs:66:LEU:HD22	2.00	0.43
49:R1:75:U:O2'	49:R1:76:A:O4'	2.34	0.43
49:R1:329:G:H2'	49:R1:330:G:H8	1.82	0.43
63:Rg:85:ARG:O	63:Rg:87:ARG:NH1	2.51	0.43
64:Rh:50:ASP:OD1	64:Rh:50:ASP:N	2.35	0.43
87:M1:656:A:H2'	87:M1:657:A:C8	2.53	0.43
87:M1:821:U:H2'	87:M1:822:G:H8	1.83	0.43
87:M1:1182:A:OP2	21:MN:158:LYS:NZ	2.50	0.43
87:M1:2795:U:OP1	25:Mc:62:ALA:N	2.46	0.43
13:MF:173:ASP:OD1	13:MF:173:ASP:N	2.52	0.43
4:CP:58:A:O2'	4:CP:60:U:OP2	2.26	0.43
5:L1:1662:G:H22	5:L1:1787:A:H2	1.66	0.43
5:L1:2653:C:P	25:Lc:89:LYS:HG3	2.58	0.43
5:L1:3067:C:H3'	20:LM:62:ARG:HH22	1.83	0.43
48:Lz:48:LYS:HG2	48:Lz:145:PHE:HE2	1.83	0.43
48:Lz:156:GLY:HA2	48:Lz:181:PRO:HD3	2.00	0.43
49:S1:1296:A:OP1	57:Sa:138:TYR:OH	2.28	0.43
51:SB:33:LEU:HD23	51:SB:81:ARG:HA	1.99	0.43
65:Si:34:ALA:HB2	65:Si:56:ARG:HD3	2.00	0.43
66:Sj:105:LEU:HB2	66:Sj:108:ARG:HD2	2.00	0.43
81:Sy:7:ILE:HG22	81:Sy:27:VAL:HG13	2.00	0.43
75:Rs:43:SER:HA	75:Rs:46:VAL:HG22	2.00	0.43
75:Rs:65:GLU:HA	75:Rs:68:ARG:HB2	1.99	0.43
49:R1:976:G:H22	49:R1:1027:A:H2	1.65	0.43
49:R1:1716:C:H2'	49:R1:1717:G:H8	1.83	0.43
57:Ra:38:PHE:HE2	85:Rr:109:LEU:HA	1.83	0.43
58:Rb:231:LEU:HD12	58:Rb:231:LEU:HA	1.85	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:Rh:105:THR:O	64:Rh:107:ARG:NE	2.43	0.43
87:M1:897:U:H2'	87:M1:898:OMU:H6	2.00	0.43
87:M1:1493:G:OP2	87:M1:1493:G:N2	2.49	0.43
87:M1:1560:G:O2'	87:M1:1561:G:O4'	2.35	0.43
87:M1:1597:C:H5'	87:M1:1696:A:H1'	2.00	0.43
87:M1:2679:A:H62	13:MF:55:ARG:NH2	2.09	0.43
6:M2:26:U:O2'	47:My:51:ALA:O	2.36	0.43
26:Md:8:LYS:HD3	26:Md:12:ARG:NH2	2.33	0.43
26:Md:25:LYS:HD3	26:Md:25:LYS:HA	1.76	0.43
5:L1:799:G:H2'	5:L1:801:A:H62	1.82	0.43
12:LE:153:ARG:HG3	12:LE:156:ARG:HH21	1.83	0.43
37:Lo:66:LYS:NZ	37:Lo:103:THR:O	2.48	0.43
42:Lt:25:LYS:O	42:Lt:27:ARG:NH1	2.51	0.43
49:S1:78:A:O2'	63:Sg:172:ALA:O	2.35	0.43
49:S1:537:G:OP2	66:Sj:175:ARG:NH2	2.35	0.43
49:S1:844:A:H2'	49:S1:845:G:H8	1.81	0.43
75:Ss:41:ARG:NH2	76:St:36:ILE:O	2.51	0.43
81:Sy:98:GLU:OE1	81:Sy:98:GLU:N	2.52	0.43
82:Sz:43:ASP:O	82:Sz:47:TYR:N	2.49	0.43
83:RC:61:ARG:NH1	62:Rf:159:ALA:O	2.40	0.43
49:R1:221:A:OP2	49:R1:832:U:O2'	2.36	0.43
49:R1:1738:U:H2'	49:R1:1739:C:C6	2.53	0.43
49:R1:1755:A:O2'	49:R1:1756:A:N7	2.51	0.43
87:M1:156:G:OP2	31:Mi:27:SER:OG	2.36	0.43
87:M1:1129:A:H2'	87:M1:1130:A:C8	2.53	0.43
87:M1:1679:A:OP1	44:Mv:94:ARG:NH2	2.49	0.43
87:M1:2882:U:H2'	87:M1:2883:U:C6	2.53	0.43
89:MQ:45:LEU:HD13	89:MQ:49:ALA:HB3	1.99	0.43
90:MP:46:ILE:HG12	90:MP:60:VAL:HG11	2.00	0.43
30:Mh:43:LYS:HB2	30:Mh:43:LYS:HE3	1.87	0.43
5:L1:1807:G:O2'	5:L1:2559:U:O4	2.34	0.43
9:LB:156:ILE:HD13	9:LB:161:VAL:HB	2.00	0.43
15:LH:105:GLN:OE1	15:LH:109:ARG:NH2	2.44	0.43
20:LM:173:ARG:NH1	20:LM:173:ARG:HA	2.32	0.43
34:Ll:53:TYR:CZ	34:Ll:65:ARG:HB2	2.53	0.43
46:Lx:221:THR:O	46:Lx:334:ARG:NH1	2.51	0.43
49:S1:1253:U:H5''	55:SF:130:VAL:HG23	1.99	0.43
49:S1:1260:U:H2'	49:S1:1261:G:H8	1.83	0.43
77:Ru:59:PRO:HG3	49:R1:1381:U:H4'	2.00	0.43
49:R1:1225:U:O2	49:R1:1230:A:O2'	2.30	0.43
60:Rd:23:GLU:OE2	60:Rd:27:ARG:NH2	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:Rf:206:SER:O	62:Rf:212:LYS:NZ	2.37	0.43
65:Ri:57:ALA:HB2	65:Ri:177:GLY:HA2	2.00	0.43
66:Rj:31:ALA:HA	66:Rj:36:LEU:HD12	2.00	0.43
66:Rj:175:ARG:HG2	66:Rj:179:ARG:HE	1.83	0.43
69:Rm:73:LYS:H	69:Rm:73:LYS:HG2	1.62	0.43
87:M1:2966:G:H2'	87:M1:2967:A:C8	2.53	0.43
46:Mx:17:LEU:HD21	46:Mx:233:TRP:HH2	1.84	0.43
23:Ma:40:LYS:HG3	23:Ma:57:MET:HG2	2.00	0.43
48:Mz:40:HIS:HB3	48:Mz:43:LYS:HG3	2.00	0.43
4:CP:22:C:OP2	4:CP:46:A:N6	2.49	0.43
4:CP:63:U:H2'	4:CP:64:G:C8	2.54	0.43
5:L1:629:U:H2'	5:L1:630:A:C8	2.53	0.43
5:L1:992:A:H5''	22:LO:43:LYS:HD2	1.99	0.43
5:L1:1751:G:H5'	29:Lg:26:LYS:HE2	2.00	0.43
5:L1:2883:U:H2'	5:L1:2884:C:C6	2.53	0.43
19:LL:122:ILE:HG23	19:LL:126:GLN:HB2	2.00	0.43
42:Lt:57:LEU:HD12	42:Lt:57:LEU:HA	1.92	0.43
42:Lt:88:MET:HE3	42:Lt:88:MET:HB3	1.76	0.43
63:Sg:135:PRO:HB2	63:Sg:141:ILE:HG12	2.00	0.43
64:Sh:141:ARG:NH2	79:Sw:49:GLU:OE2	2.51	0.43
66:Sj:149:ARG:N	66:Sj:149:ARG:HD2	2.34	0.43
71:So:13:VAL:HG12	71:So:76:ILE:HD13	1.99	0.43
81:Ry:78:SER:O	81:Ry:81:GLU:N	2.41	0.43
49:R1:1597:A:O2'	49:R1:1598:U:O5'	2.36	0.43
57:Ra:179:ARG:O	57:Ra:183:ARG:N	2.47	0.43
59:Rc:188:LEU:HD13	59:Rc:196:VAL:HG11	2.01	0.43
62:Rf:34:GLN:HA	62:Rf:37:GLN:HE21	1.83	0.43
73:Rq:35:PRO:HD2	73:Rq:38:LEU:HD22	2.00	0.43
87:M1:1246:G:O2'	87:M1:1263:A:O2'	2.26	0.43
87:M1:1336:U:H2'	87:M1:1337:A:H8	1.82	0.43
87:M1:1490:A:O2'	30:Mh:12:HIS:O	2.34	0.43
87:M1:1805:C:H2'	87:M1:1806:A:H8	1.83	0.43
87:M1:2103:U:H2'	87:M1:2104:A:H8	1.83	0.43
87:M1:2477:G:N2	87:M1:2478:C:O4'	2.52	0.43
88:DQ:10:G:H2'	88:DQ:11:A:C8	2.52	0.43
37:Mo:12:GLN:OE1	37:Mo:12:GLN:N	2.48	0.43
14:MG:104:ARG:HA	31:Mi:20:MET:HB2	2.01	0.43
2:CM:28:U:O4	52:SC:65:ARG:NH1	2.51	0.43
5:L1:243:G:H2'	5:L1:244:G:H8	1.84	0.43
5:L1:1492:G:N7	28:Lf:2:ALA:N	2.67	0.43
58:Sb:97:LEU:HB3	58:Sb:232:HIS:CE1	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:Rx:37:ALA:O	80:Rx:41:SER:OG	2.27	0.43
49:R1:1556:A:OP1	72:Rp:115:TYR:OH	2.30	0.43
49:R1:1676:U:H1'	49:R1:1726:G:N2	2.33	0.43
62:Rf:118:LEU:HD22	62:Rf:129:PRO:HB2	2.01	0.43
65:Ri:84:HIS:NE2	65:Ri:97:THR:OG1	2.42	0.43
69:Rm:80:ASN:HA	69:Rm:86:VAL:HG13	2.00	0.43
87:M1:612:U:H2'	87:M1:613:G:H8	1.84	0.43
87:M1:643:U:O2'	87:M1:1153:A:N1	2.41	0.43
87:M1:1110:U:H2'	87:M1:1111:U:C6	2.54	0.43
46:Mx:187:SER:O	46:Mx:190:GLU:N	2.49	0.43
46:Mx:282:ILE:HA	46:Mx:324:VAL:HA	2.01	0.43
44:Mv:38:ILE:H	44:Mv:38:ILE:HD12	1.83	0.43
34:Mi:31:LYS:NZ	34:Mi:78:SER:O	2.52	0.43
5:L1:1098:A:O2'	22:LO:130:ARG:O	2.32	0.43
5:L1:2185:G:O2'	5:L1:2314:U:OP2	2.32	0.43
5:L1:2376:G:H2'	5:L1:2377:G:C8	2.53	0.43
5:L1:3022:G:O2'	5:L1:3031:G:O6	2.35	0.43
12:LE:43:VAL:HG21	12:LE:197:VAL:HB	2.01	0.43
12:LE:70:ILE:HD13	12:LE:70:ILE:HA	1.89	0.43
41:Ls:55:GLU:HB2	41:Ls:108:LYS:HB2	2.00	0.43
49:S1:1345:A:N6	49:S1:1377:U:O2'	2.51	0.43
49:S1:1374:C:H2'	49:S1:1375:A:C8	2.54	0.43
49:S1:1673:G:C6	49:S1:1728:A:N1	2.86	0.43
60:Sd:127:MET:HE3	60:Sd:127:MET:HB3	1.87	0.43
75:Rs:86:LEU:HD13	75:Rs:99:HIS:HB2	2.01	0.43
78:Rv:32:VAL:HG13	57:Ra:142:PRO:HG3	2.00	0.43
79:Rw:83:ILE:HB	49:R1:749:U:H5''	2.01	0.43
49:R1:108:A:H2'	49:R1:109:G:C8	2.54	0.43
67:Rk:22:VAL:HG23	67:Rk:23:ALA:H	1.83	0.43
89:MQ:12:PHE:HE1	89:MQ:58:MET:HE2	1.83	0.43
23:Ma:57:MET:HE3	23:Ma:75:PRO:HB3	2.01	0.43
41:Ms:63:LYS:HE3	41:Ms:97:ILE:HD12	1.99	0.43
11:MD:105:GLU:HG3	11:MD:108:GLY:HA2	2.00	0.43
15:MH:22:LEU:HB3	15:MH:64:VAL:HG13	2.00	0.43
5:L1:1110:U:H2'	5:L1:1111:U:C6	2.53	0.43
5:L1:1497:C:H2'	5:L1:1498:A:H8	1.84	0.43
20:LM:30:SER:OG	20:LM:31:GLU:OE1	2.28	0.43
22:LO:30:TYR:CZ	48:Lz:34:LYS:HE2	2.54	0.43
29:Lg:44:LYS:HG2	29:Lg:53:THR:HG23	2.00	0.43
40:Lr:25:ILE:HG23	40:Lr:41:ALA:HB1	2.01	0.43
49:S1:135:A:H4'	49:S1:136:C:H5'	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:S1:190:C:H2'	49:S1:191:C:H4'	2.01	0.43
49:S1:895:G:H2'	49:S1:896:U:C6	2.54	0.43
49:S1:1340:U:H5''	49:S1:1341:A:H5''	2.01	0.43
55:SF:107:LYS:NZ	55:SF:109:ASP:HB2	2.34	0.43
59:Sc:222:TYR:OH	78:Sv:11:LEU:O	2.28	0.43
67:Sk:6:GLU:HA	67:Sk:9:ASN:HD21	1.82	0.43
76:Rt:105:LEU:HD13	76:Rt:122:ARG:HD2	2.01	0.43
77:Ru:87:HIS:ND1	49:R1:1383:G:OP1	2.51	0.43
69:Rm:116:VAL:HG22	69:Rm:117:GLY:H	1.84	0.43
72:Rp:41:VAL:HG13	72:Rp:84:ILE:HG21	2.01	0.43
87:M1:417:A:H2'	87:M1:418:A:C8	2.53	0.43
87:M1:421:G:O6	87:M1:2383:C:O2'	2.33	0.43
6:M2:142:C:H2'	6:M2:143:U:C6	2.54	0.43
5:L1:544:C:O2'	5:L1:548:G:N2	2.52	0.43
5:L1:2354:C:OP1	18:LK:86:LYS:NZ	2.42	0.43
5:L1:2423:U:H2'	5:L1:2424:A:C8	2.54	0.43
5:L1:2424:A:OP1	16:LI:90:ASN:ND2	2.37	0.43
5:L1:2768:U:H2'	5:L1:2769:A:H8	1.82	0.43
5:L1:2812:C:H2'	5:L1:2813:A:H8	1.84	0.43
8:LA:45:GLY:O	8:LA:48:ARG:NH1	2.48	0.43
14:LG:61:PRO:HD3	14:LG:70:ARG:HH21	1.84	0.43
40:Lr:103:GLN:OE1	40:Lr:103:GLN:N	2.52	0.43
45:Lw:95:SER:O	45:Lw:100:ASN:ND2	2.39	0.43
49:S1:388:G:OP1	49:S1:423:G:O2'	2.23	0.43
49:S1:407:A:H2'	49:S1:408:C:H6	1.84	0.43
49:S1:558:U:OP2	54:SE:55:ARG:NH1	2.52	0.43
49:S1:1466:G:O2'	49:S1:1602:C:OP1	2.34	0.43
64:Sh:50:ASP:HA	64:Sh:56:LYS:HZ1	1.84	0.43
70:Sn:33:VAL:HG21	70:Sn:66:ILE:HG21	2.01	0.43
78:Rv:46:ILE:H	78:Rv:46:ILE:HD12	1.83	0.43
50:RA:30:ILE:HG12	50:RA:35:ALA:HB2	2.00	0.43
49:R1:143:G:O6	63:Rg:177:ARG:NH2	2.52	0.43
49:R1:1525:A:H2'	49:R1:1526:A:C8	2.54	0.43
59:Rc:208:GLU:H	59:Rc:208:GLU:CD	2.27	0.43
61:Re:89:VAL:HG21	61:Re:164:LEU:HD11	2.00	0.43
69:Rm:45:LEU:HB3	69:Rm:120:VAL:HG21	2.01	0.43
87:M1:436:A:H2'	87:M1:437:G:H8	1.84	0.43
87:M1:1257:C:H42	87:M1:1261:G:N2	2.16	0.43
90:MP:126:ALA:N	90:MP:164:GLU:OE2	2.52	0.43
36:Mn:6:ASP:OD1	36:Mn:6:ASP:N	2.49	0.43
24:Mb:38:ASP:HA	24:Mb:45:LYS:HA	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L1:22:G:H5''	30:Lh:43:LYS:HG2	2.00	0.43
5:L1:89:A:N7	19:LL:171:LYS:NZ	2.67	0.43
5:L1:411:U:H2'	5:L1:412:G:H8	1.84	0.43
5:L1:2176:U:OP1	45:Lw:54:ARG:NH2	2.40	0.43
5:L1:2419:A:H2'	5:L1:2420:C:C6	2.54	0.43
8:LA:43:LEU:HD21	8:LA:85:ILE:HD12	2.01	0.43
22:LO:80:VAL:HG21	22:LO:85:LEU:HD12	2.00	0.43
28:Lf:30:ARG:HE	28:Lf:30:ARG:HB2	1.61	0.43
47:Ly:321:LYS:HB2	47:Ly:321:LYS:HE2	1.72	0.43
49:S1:532:U:OP1	66:Sj:132:ARG:NH2	2.52	0.43
49:S1:836:U:H2'	49:S1:837:G:C8	2.54	0.43
49:S1:1680:G:H1'	49:S1:1721:A:N6	2.33	0.43
51:SB:28:PRO:HG3	70:Sn:17:PRO:HG3	2.00	0.43
60:Sd:29:LEU:HB2	60:Sd:34:TYR:HB2	2.00	0.43
61:Se:39:ARG:HD2	61:Se:39:ARG:HA	1.68	0.43
65:Si:152:ILE:H	65:Si:152:ILE:HG12	1.65	0.43
81:Sy:56:SER:N	81:Sy:74:LEU:O	2.45	0.43
49:R1:225:A:N1	49:R1:837:G:N1	2.67	0.43
59:Rc:147:ASN:OD1	59:Rc:147:ASN:N	2.43	0.43
66:Rj:163:PRO:HB3	66:Rj:169:PRO:HA	1.99	0.43
70:Rn:72:MET:O	70:Rn:76:LYS:N	2.36	0.43
87:M1:45:A:O2'	87:M1:95:A:N1	2.45	0.43
87:M1:1920:U:O2'	87:M1:1932:A:N7	2.43	0.43
87:M1:2662:G:H2'	87:M1:2663:G:C8	2.54	0.43
87:M1:2683:U:H2'	87:M1:2684:C:C6	2.54	0.43
23:Ma:74:MET:HB3	23:Ma:74:MET:HE2	1.79	0.43
11:MD:177:ASP:OD1	11:MD:177:ASP:N	2.51	0.43
12:ME:72:ALA:O	12:ME:76:MET:HG3	2.19	0.43
3:CN:65:VAL:HG12	60:Rd:113:LEU:HD22	2.01	0.42
5:L1:1307:G:OP1	17:LJ:60:LYS:NZ	2.51	0.42
9:LB:70:LYS:HB3	47:Ly:351:PRO:HB3	2.01	0.42
24:Lb:73:THR:HG22	24:Lb:75:ALA:H	1.84	0.42
31:Li:71:LYS:HD2	31:Li:71:LYS:HA	1.80	0.42
45:Lw:60:LYS:HE2	45:Lw:60:LYS:HB2	1.84	0.42
45:Lw:119:LYS:HE3	45:Lw:119:LYS:HB2	1.84	0.42
46:Lx:71:GLU:OE2	46:Lx:357:LYS:NZ	2.40	0.42
49:S1:1592:A:H2'	49:S1:1593:A:C8	2.54	0.42
49:S1:1611:A:O2'	62:Sf:95:ASN:O	2.36	0.42
57:Sa:2:SER:OG	57:Sa:3:LEU:N	2.52	0.42
59:Sc:144:TRP:CE2	59:Sc:173:PRO:HG3	2.54	0.42
62:Sf:51:VAL:HA	62:Sf:131:GLN:HG2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
76:Rt:143:ASP:OD1	76:Rt:143:ASP:N	2.49	0.42
79:Rw:68:ARG:HD3	59:Rc:230:TRP:CE2	2.54	0.42
80:Rx:128:SER:OG	80:Rx:142:LYS:NZ	2.41	0.42
49:R1:853:G:OP2	20:MM:176:ARG:NH2	2.51	0.42
65:Ri:37:LYS:HB2	65:Ri:59:ARG:HG3	2.00	0.42
70:Rn:91:LEU:HB3	70:Rn:122:ILE:HG12	2.00	0.42
87:M1:294:U:H4'	31:Mi:77:LEU:HD23	2.01	0.42
87:M1:873:C:H3'	87:M1:874:U:H4'	2.01	0.42
87:M1:3121:U:H1'	87:M1:3122:A:H5''	2.00	0.42
7:M3:118:A:H5''	48:Mz:253:PHE:CZ	2.54	0.42
89:MQ:48:ARG:HH21	89:MQ:95:GLU:HG3	1.83	0.42
12:ME:68:ALA:HB1	12:ME:155:ALA:HB1	2.01	0.42
32:Mj:79:ASP:OD2	32:Mj:79:ASP:N	2.40	0.42
27:Me:98:LYS:HG3	27:Me:118:THR:HG21	2.00	0.42
5:L1:297:G:OP2	5:L1:297:G:N2	2.38	0.42
5:L1:1562:C:H2'	5:L1:1563:C:C6	2.54	0.42
5:L1:2152:A:H2'	5:L1:2153:U:H6	1.84	0.42
5:L1:3085:G:OP1	43:Lu:34:SER:OG	2.29	0.42
16:LI:36:ILE:HD11	16:LI:105:ARG:HB3	2.00	0.42
21:LN:71:LYS:HE3	21:LN:73:LYS:HD2	2.00	0.42
53:SD:53:ASN:OD1	53:SD:53:ASN:N	2.52	0.42
56:SG:53:LYS:HE2	56:SG:53:LYS:HB2	1.89	0.42
62:Sf:120:ILE:HG13	82:Sz:100:ILE:HD13	2.01	0.42
75:Ss:106:GLU:OE2	75:Ss:106:GLU:N	2.44	0.42
82:Sz:61:SER:H	82:Sz:64:VAL:HB	1.83	0.42
78:Rv:79:LEU:HD11	57:Ra:59:LEU:HD22	2.01	0.42
50:RA:44:ILE:HD12	84:Ro:115:ILE:HG22	2.01	0.42
49:R1:328:A:N3	65:Ri:86:SER:OG	2.46	0.42
59:Rc:49:LYS:HA	59:Rc:49:LYS:HD3	1.74	0.42
67:Rk:3:MET:HE2	67:Rk:8:ARG:HG2	2.02	0.42
87:M1:985:U:H2'	87:M1:986:U:H6	1.84	0.42
87:M1:1010:G:H5''	12:ME:40:LYS:HE3	2.01	0.42
87:M1:1019:G:H2'	87:M1:1020:G:H8	1.84	0.42
87:M1:1194:G:H2'	87:M1:1195:A:C8	2.54	0.42
87:M1:1861:G:O2'	87:M1:3066:U:OP1	2.28	0.42
7:M3:112:G:H2'	7:M3:113:C:C6	2.54	0.42
89:MQ:16:ARG:NH2	89:MQ:20:GLU:OE2	2.51	0.42
22:MO:57:TYR:CG	22:MO:89:LEU:HD21	2.54	0.42
10:MC:82:LEU:HD22	10:MC:86:THR:HB	2.01	0.42
39:Mq:36:GLY:HA3	39:Mq:40:HIS:CE1	2.54	0.42
38:Mp:54:LEU:HD23	38:Mp:54:LEU:HA	1.82	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L1:411:U:H2'	5:L1:412:G:C8	2.55	0.42
5:L1:1150:A:O2'	34:L1:21:ARG:NH2	2.50	0.42
5:L1:1336:U:H2'	5:L1:1337:A:H8	1.84	0.42
5:L1:1369:A:OP1	39:Lq:21:ARG:NH1	2.53	0.42
5:L1:2724:U:OP1	22:LO:78:LYS:NZ	2.49	0.42
5:L1:3302:U:H3	5:L1:3312:U:H3	1.66	0.42
7:L3:11:A:N1	7:L3:67:G:O2'	2.46	0.42
10:LC:156:ASP:HB2	10:LC:183:LYS:HG2	2.01	0.42
21:LN:60:SER:OG	21:LN:62:ASN:OD1	2.36	0.42
25:Lc:77:CYS:SG	25:Lc:79:THR:OG1	2.71	0.42
31:Li:59:ASP:N	31:Li:59:ASP:OD2	2.52	0.42
40:Lr:50:PRO:HD3	40:Lr:68:ILE:HD13	2.01	0.42
43:Lu:34:SER:O	43:Lu:38:SER:OG	2.29	0.42
46:Lx:238:LEU:HB2	46:Lx:246:LEU:HB2	2.00	0.42
48:Lz:119:TYR:OH	48:Lz:140:ARG:N	2.53	0.42
49:S1:905:A:H5''	71:So:52:ARG:HD3	2.00	0.42
66:Sj:30:LEU:HD23	66:Sj:30:LEU:HA	1.89	0.42
72:Sp:58:LYS:HA	72:Sp:58:LYS:HD3	1.83	0.42
80:Rx:65:ASN:ND2	80:Rx:116:ASP:OD2	2.49	0.42
49:R1:332:U:OP1	65:Ri:56:ARG:NH2	2.50	0.42
49:R1:874:C:H2'	49:R1:875:G:C8	2.54	0.42
49:R1:883:C:H2'	49:R1:884:A:H8	1.83	0.42
49:R1:1656:U:H5''	49:R1:1657:U:H5''	2.01	0.42
60:Rd:132:LYS:HE2	60:Rd:191:ASP:HB3	2.01	0.42
66:Rj:146:PHE:HD2	66:Rj:148:VAL:HG12	1.84	0.42
87:M1:1019:G:H1	87:M1:1033:U:H3	1.66	0.42
87:M1:1616:U:H2'	87:M1:1617:G:C8	2.54	0.42
10:MC:43:LYS:HD3	10:MC:43:LYS:HA	1.79	0.42
16:MI:183:THR:HG22	16:MI:187:ARG:HB2	2.01	0.42
26:Md:2:ARG:HB3	26:Md:5:TRP:CD1	2.54	0.42
3:CN:37:ARG:HD3	66:Rj:120:LYS:HB2	2.01	0.42
5:L1:1307:G:H4'	5:L1:1308:A:H5'	2.01	0.42
5:L1:1748:G:OP2	29:Lg:42:LYS:NZ	2.45	0.42
37:Lo:53:LYS:O	37:Lo:57:GLU:HG3	2.19	0.42
49:S1:1120:U:H2'	49:S1:1121:C:C6	2.54	0.42
49:S1:1486:G:N2	49:S1:1522:U:O4	2.53	0.42
49:S1:1645:G:H1	49:S1:1755:A:H2	1.65	0.42
56:SG:69:GLN:N	56:SG:83:ALA:O	2.49	0.42
61:Se:185:GLY:H	61:Se:189:LEU:HD13	1.84	0.42
62:Sf:102:ARG:H	62:Sf:102:ARG:HG3	1.64	0.42
69:Sm:139:HIS:O	69:Sm:143:GLN:NE2	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
72:Sp:33:PHE:HD1	72:Sp:86:VAL:HG23	1.84	0.42
75:Ss:108:LYS:HA	75:Ss:108:LYS:HD2	1.81	0.42
80:Rx:70:LYS:HB3	80:Rx:93:LEU:HD22	2.00	0.42
49:R1:5:U:H2'	49:R1:6:G:H8	1.84	0.42
49:R1:153:G:H2'	49:R1:154:G:C8	2.52	0.42
49:R1:393:C:H4'	49:R1:1673:G:C2	2.54	0.42
61:Re:139:VAL:HG13	61:Re:150:PRO:HG3	2.00	0.42
69:Rm:97:LEU:HD22	69:Rm:118:ALA:HB1	2.00	0.42
85:Rr:101:ASN:OD1	85:Rr:101:ASN:N	2.42	0.42
88:DQ:69:C:H2'	88:DQ:70:C:C6	2.54	0.42
21:MN:147:ASP:OD1	21:MN:147:ASP:N	2.51	0.42
47:My:350:LYS:HG3	47:My:351:PRO:HD2	2.01	0.42
23:Ma:15:LEU:HD23	23:Ma:53:SER:HB3	2.01	0.42
40:Mr:41:ALA:HB2	40:Mr:77:TYR:HE1	1.85	0.42
34:ML:12:LYS:HD3	34:ML:12:LYS:HA	1.82	0.42
5:L1:1245:A:H62	5:L1:1272:C:HO2'	1.65	0.42
5:L1:1513:G:OP1	20:LM:5:ARG:NH2	2.52	0.42
5:L1:1621:A:H2'	5:L1:1622:U:C6	2.55	0.42
5:L1:2223:A:H2'	5:L1:2224:A:C8	2.54	0.42
12:LE:109:ASP:HA	12:LE:112:GLN:HB2	2.02	0.42
49:S1:386:G:H2'	49:S1:387:A:C8	2.54	0.42
49:S1:1579:U:H2'	49:S1:1580:C:C6	2.55	0.42
57:Sa:76:ILE:HB	57:Sa:123:VAL:HG12	2.01	0.42
57:Sa:184:LEU:O	78:Sv:44:ARG:NH1	2.53	0.42
63:Sg:68:LEU:HD22	63:Sg:68:LEU:HA	1.78	0.42
74:Sr:75:GLU:OE1	74:Sr:75:GLU:N	2.50	0.42
76:St:9:VAL:HG21	76:St:139:THR:HB	2.00	0.42
77:Su:103:ILE:H	77:Su:103:ILE:HD12	1.84	0.42
76:Rt:25:GLN:OE1	76:Rt:27:LYS:HG3	2.20	0.42
56:RG:211:ILE:HB	56:RG:223:TRP:HB2	2.02	0.42
56:RG:315:VAL:C	56:RG:316:MET:HE3	2.44	0.42
49:R1:17:C:H2'	49:R1:18:C:C6	2.54	0.42
49:R1:953:G:H2'	49:R1:954:G:C8	2.55	0.42
57:Ra:118:PRO:HG2	57:Ra:141:ILE:HD13	2.02	0.42
61:Re:197:HIS:HB3	61:Re:209:HIS:HB2	2.00	0.42
62:Rf:66:GLN:OE1	62:Rf:66:GLN:N	2.40	0.42
66:Rj:63:ASP:OD2	66:Rj:64:GLU:N	2.52	0.42
87:M1:629:U:H2'	87:M1:630:A:C8	2.54	0.42
87:M1:791:A:H2'	87:M1:792:G:C8	2.55	0.42
7:M3:121:U:OP2	48:Mz:265:TYR:OH	2.32	0.42
88:DQ:68:C:H2'	88:DQ:69:C:C6	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:MM:169:ALA:HA	20:MM:172:ARG:HH11	1.83	0.42
45:Mw:108:PRO:O	45:Mw:111:THR:OG1	2.30	0.42
90:MP:137:GLN:HB2	90:MP:148:PRO:HB2	2.00	0.42
22:MO:139:ARG:HG2	9:MB:77:VAL:HB	2.01	0.42
9:MB:178:ILE:HD11	9:MB:187:GLU:HG3	2.01	0.42
33:Mk:86:LYS:O	33:Mk:90:ILE:HD12	2.19	0.42
3:CN:75:LYS:HB2	3:CN:120:PRO:HD2	2.00	0.42
3:CN:94:MET:HE1	3:CN:99:LEU:HB2	2.02	0.42
5:L1:3196:U:O2	5:L1:3197:G:N1	2.52	0.42
7:L3:4:U:H2'	7:L3:5:G:H8	1.83	0.42
9:LB:27:ALA:HA	9:LB:30:ARG:HB3	2.00	0.42
13:LF:173:ASP:N	13:LF:173:ASP:OD1	2.52	0.42
21:LN:77:VAL:HG13	21:LN:126:VAL:HG22	2.02	0.42
48:Lz:60:ILE:HB	48:Lz:80:SER:HB3	2.00	0.42
49:S1:1307:U:H3	49:S1:1318:G:N2	2.17	0.42
55:SF:107:LYS:HZ2	55:SF:109:ASP:HB2	1.85	0.42
56:SG:54:PHE:CD1	56:SG:312:VAL:HG11	2.55	0.42
56:SG:307:ASP:OD1	56:SG:307:ASP:N	2.35	0.42
65:Si:101:ILE:HD12	65:Si:184:LEU:HD11	2.02	0.42
82:Sz:70:LYS:HB3	82:Sz:70:LYS:HE3	1.80	0.42
49:R1:1393:C:H2'	49:R1:1394:G:H8	1.84	0.42
61:Re:101:LEU:HD23	61:Re:101:LEU:HA	1.88	0.42
61:Re:129:VAL:HG22	61:Re:139:VAL:HG12	2.02	0.42
64:Rh:30:SER:OG	64:Rh:31:SER:N	2.52	0.42
69:Rm:89:ILE:HG23	69:Rm:90:LYS:H	1.84	0.42
72:Rp:110:GLU:OE1	72:Rp:110:GLU:N	2.53	0.42
87:M1:422:A:C2	87:M1:2363:A:H4'	2.55	0.42
87:M1:1863:G:N1	87:M1:1866:C:OP2	2.36	0.42
87:M1:2357:A:H2'	87:M1:2358:A:C8	2.55	0.42
20:MM:136:ARG:O	20:MM:140:GLU:HG2	2.20	0.42
23:Ma:26:ALA:HB2	23:Ma:99:ALA:HB1	2.01	0.42
23:Ma:57:MET:HE1	23:Ma:105:PRO:HA	2.00	0.42
9:MB:84:VAL:HG23	9:MB:117:VAL:HB	2.02	0.42
14:MG:116:LEU:O	14:MG:120:GLN:NE2	2.44	0.42
36:Mn:112:ASP:N	36:Mn:112:ASP:OD1	2.50	0.42
35:Mm:126:LEU:HD12	35:Mm:126:LEU:HA	1.86	0.42
5:L1:714:G:O2'	5:L1:753:C:O2'	2.33	0.42
5:L1:1497:C:H2'	5:L1:1498:A:C8	2.54	0.42
5:L1:1666:G:H2'	5:L1:1667:A:H8	1.83	0.42
5:L1:2389:C:H2'	5:L1:2390:A:C8	2.55	0.42
6:L2:27:U:H4'	47:Ly:51:ALA:HB3	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:LB:178:ILE:HG23	9:LB:183:ASP:HB3	2.01	0.42
10:LC:91:PHE:HE1	10:LC:180:VAL:HG21	1.85	0.42
13:LF:10:ARG:H	13:LF:10:ARG:HG2	1.74	0.42
21:LN:2:ALA:HB3	21:LN:32:SER:HB2	2.02	0.42
24:Lb:89:MET:HE2	24:Lb:89:MET:HB2	1.94	0.42
35:Lm:3:SER:OG	35:Lm:4:LEU:N	2.52	0.42
39:Lq:75:LEU:HB2	39:Lq:114:GLY:HA2	2.02	0.42
49:S1:258:C:O2	65:Si:178:ARG:NH1	2.49	0.42
57:Sa:124:THR:O	57:Sa:164:ASN:ND2	2.52	0.42
74:Sr:104:ASN:O	74:Sr:107:SER:OG	2.37	0.42
77:Su:97:VAL:HA	77:Su:100:VAL:HB	2.01	0.42
79:Sw:42:GLN:NE2	79:Sw:48:GLY:O	2.38	0.42
80:Sx:70:LYS:HD2	80:Sx:93:LEU:HD12	2.00	0.42
49:R1:891:A:H2'	49:R1:892:A:H8	1.84	0.42
49:R1:895:G:H2'	49:R1:896:U:C6	2.55	0.42
49:R1:1144:U:H2'	49:R1:1145:U:C6	2.55	0.42
49:R1:1160:A:H2'	49:R1:1161:C:C6	2.53	0.42
86:MA:43:LEU:HD11	86:MA:85:ILE:HG13	2.01	0.42
86:MA:100:LYS:NZ	86:MA:137:ASP:OD1	2.46	0.42
17:MJ:54:TYR:OH	17:MJ:73:PHE:O	2.37	0.42
87:M1:831:G:O2'	87:M1:1864:A:N3	2.47	0.42
87:M1:1232:C:O2'	89:MQ:36:GLN:OE1	2.24	0.42
87:M1:2101:C:H2'	87:M1:2102:U:C6	2.55	0.42
87:M1:2462:A:H5'	87:M1:2463:G:H2'	2.01	0.42
87:M1:3066:U:H2'	87:M1:3067:C:C6	2.55	0.42
38:Mp:32:LEU:HD22	38:Mp:35:VAL:HG21	2.01	0.42
5:L1:170:G:H2'	5:L1:171:G:C8	2.55	0.42
5:L1:1029:G:H2'	5:L1:1030:A:H8	1.84	0.42
5:L1:1343:A:H2'	5:L1:1344:G:C8	2.54	0.42
5:L1:1799:A:H2'	5:L1:1800:A:H8	1.84	0.42
11:LD:130:ASP:OD1	11:LD:130:ASP:N	2.53	0.42
12:LE:68:ALA:HB1	12:LE:155:ALA:HB1	2.01	0.42
41:Ls:108:LYS:HE3	41:Ls:108:LYS:HB3	1.88	0.42
44:Lv:18:ASP:HB3	44:Lv:104:ARG:HG3	2.00	0.42
45:Lw:30:ARG:O	45:Lw:163:ARG:NH1	2.37	0.42
49:S1:139:C:H4'	49:S1:140:A:H5'	2.02	0.42
56:SG:96:THR:O	56:SG:96:THR:OG1	2.35	0.42
56:SG:111:MET:HA	56:SG:111:MET:HE3	2.02	0.42
67:Sk:5:LYS:HA	67:Sk:5:LYS:HD3	1.87	0.42
71:So:72:LYS:HE2	71:So:72:LYS:HB2	1.71	0.42
74:Sr:23:LYS:HD3	74:Sr:23:LYS:HA	1.88	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:Sx:31:LYS:HB2	80:Sx:31:LYS:HE3	1.66	0.42
78:Rv:27:ASP:OD1	78:Rv:27:ASP:N	2.46	0.42
56:RG:283:LYS:HE2	56:RG:283:LYS:HB2	1.83	0.42
49:R1:739:G:C2	49:R1:740:A:H1'	2.55	0.42
49:R1:1617:U:H2'	49:R1:1618:C:C6	2.55	0.42
49:R1:1681:A:H1'	63:Rg:66:GLY:HA2	2.01	0.42
61:Re:176:ASP:OD1	61:Re:176:ASP:N	2.51	0.42
87:M1:407:A:C2	6:M2:17:A:H1'	2.54	0.42
87:M1:631:U:H2'	87:M1:632:G:C8	2.55	0.42
87:M1:1704:A:H2'	87:M1:1705:U:C6	2.55	0.42
90:MP:82:ILE:HA	90:MP:85:LEU:HD12	2.02	0.42
91:DP:18:G:H1'	91:DP:57:G:H22	1.85	0.42
5:L1:821:U:H2'	5:L1:822:G:H8	1.85	0.42
5:L1:2631:U:OP2	22:LO:4:SER:OG	2.37	0.42
5:L1:3044:G:H2'	5:L1:3045:G:H8	1.84	0.42
8:LA:31:ARG:NH1	8:LA:81:ALA:O	2.32	0.42
9:LB:83:LEU:HD13	9:LB:139:PRO:HD2	2.02	0.42
21:LN:22:PRO:O	22:LO:146:ASN:ND2	2.49	0.42
46:Lx:385:LYS:H	46:Lx:385:LYS:HG3	1.68	0.42
49:S1:751:G:H2'	49:S1:752:A:H8	1.84	0.42
49:S1:1477:G:H2'	49:S1:1478:G:C8	2.55	0.42
56:SG:36:ALA:HB2	56:SG:71:CYS:HB3	2.01	0.42
58:Sb:91:VAL:HA	58:Sb:96:LEU:HA	2.01	0.42
58:Sb:132:ASP:OD1	58:Sb:132:ASP:N	2.53	0.42
61:Se:100:ARG:HB2	61:Se:114:ILE:HD13	2.02	0.42
64:Sh:55:LYS:HE2	64:Sh:55:LYS:N	2.34	0.42
78:Rv:1:MET:N	78:Rv:10:GLU:OE1	2.44	0.42
49:R1:991:G:N7	49:R1:1011:G:N1	2.66	0.42
57:Ra:57:LEU:HG	57:Ra:177:LEU:HD13	2.01	0.42
73:Rq:13:LYS:O	73:Rq:76:SER:OG	2.33	0.42
87:M1:53:G:OP2	30:Mh:48:ASN:ND2	2.39	0.42
87:M1:1011:A:H2'	87:M1:1012:G:H8	1.84	0.42
87:M1:1255:C:H2'	87:M1:1256:G:C8	2.54	0.42
87:M1:1448:U:H2'	87:M1:1449:A2M:C8	2.50	0.42
7:M3:118:A:H5''	48:Mz:253:PHE:HZ	1.85	0.42
46:Mx:54:THR:OG1	46:Mx:55:THR:N	2.51	0.42
23:Ma:124:ASP:OD1	23:Ma:124:ASP:N	2.52	0.42
13:MF:17:LEU:HD13	13:MF:129:VAL:HG22	2.01	0.42
4:CP:70:G:H2'	4:CP:71:A:H8	1.85	0.42
6:L2:40:A:H2'	6:L2:41:A:C8	2.54	0.42
7:L3:77:G:C4	21:LN:50:LYS:HE3	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:L3:81:U:H2'	7:L3:82:G:C8	2.54	0.42
39:Lq:86:LYS:HA	39:Lq:89:GLN:HE22	1.85	0.42
39:Lq:103:ASP:HA	39:Lq:126:LYS:HB2	2.02	0.42
49:S1:705:U:O2'	49:S1:706:A:O5'	2.34	0.42
49:S1:884:A:H2'	49:S1:885:G:C8	2.54	0.42
49:S1:1477:G:H5'	76:St:45:MET:SD	2.60	0.42
49:S1:1776:A:H2'	49:S1:1777:G:H8	1.82	0.42
58:Sb:113:MET:HG2	58:Sb:209:ASN:ND2	2.35	0.42
64:Sh:140:VAL:HG22	64:Sh:150:GLN:HG3	2.02	0.42
68:Sl:33:ARG:NH1	68:Sl:53:TYR:O	2.53	0.42
80:Sx:56:LYS:HE2	80:Sx:93:LEU:HD22	2.01	0.42
50:RA:10:ARG:HH21	50:RA:34:LYS:HG2	1.85	0.42
56:RG:7:LEU:HD13	56:RG:315:VAL:HB	2.02	0.42
49:R1:1087:A:H2'	49:R1:1088:A:C8	2.55	0.42
49:R1:1587:A:H2'	49:R1:1588:G:H8	1.84	0.42
63:Rg:43:ASP:OD1	63:Rg:43:ASP:N	2.51	0.42
63:Rg:199:GLN:HG2	63:Rg:202:ARG:HH12	1.84	0.42
66:Rj:90:LYS:HA	66:Rj:90:LYS:HD3	1.82	0.42
87:M1:785:G:OP2	19:ML:63:SER:OG	2.32	0.42
87:M1:1011:A:H2'	87:M1:1012:G:C8	2.55	0.42
87:M1:2427:U:H2'	87:M1:2428:U:C6	2.55	0.42
87:M1:2440:G:H2'	87:M1:2441:A:C8	2.55	0.42
87:M1:2499:U:H2'	87:M1:2500:A:O4'	2.20	0.42
20:MM:105:LEU:HD23	20:MM:138:LEU:HD23	2.02	0.42
89:MQ:139:LEU:HD12	89:MQ:172:LEU:HD22	2.00	0.42
90:MP:116:MET:O	90:MP:120:SER:OG	2.26	0.42
33:Mk:90:ILE:HD12	33:Mk:90:ILE:H	1.85	0.42
5:L1:2741:C:O2'	25:Lc:20:HIS:ND1	2.47	0.41
5:L1:2748:A:C2	48:Lz:35:ARG:HB2	2.54	0.41
7:L3:1:G:O2'	48:Lz:273:ARG:NH2	2.53	0.41
10:LC:155:ASN:OD1	10:LC:155:ASN:N	2.53	0.41
23:La:71:LYS:HE2	23:La:71:LYS:HB3	1.82	0.41
40:Lr:23:VAL:HG12	40:Lr:45:GLY:HA3	2.02	0.41
46:Lx:83:PRO:O	46:Lx:165:GLN:NE2	2.46	0.41
49:S1:480:G:H1	49:S1:508:U:H3	1.68	0.41
49:S1:808:U:H2'	49:S1:809:A:C8	2.55	0.41
49:S1:1486:G:H2'	49:S1:1487:A:C8	2.55	0.41
59:Sc:99:LYS:HG3	59:Sc:117:THR:HG22	2.02	0.41
63:Sg:46:LYS:HA	63:Sg:46:LYS:HD2	1.84	0.41
67:Sk:17:GLN:OE1	67:Sk:17:GLN:N	2.45	0.41
78:Sv:25:LYS:HB3	78:Sv:25:LYS:HE3	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
79:Sw:115:GLU:OE1	79:Sw:119:LYS:NZ	2.50	0.41
81:Sy:14:SER:HA	81:Sy:21:LYS:HG3	2.02	0.41
59:Rc:69:ILE:HD11	59:Rc:133:LYS:HB3	2.02	0.41
66:Rj:180:LYS:HA	66:Rj:180:LYS:HD3	1.80	0.41
67:Rk:1:MET:HE2	67:Rk:44:LYS:HB2	2.01	0.41
87:M1:155:G:H21	31:Mi:26:ILE:HD11	1.85	0.41
87:M1:1033:U:O2'	87:M1:1034:U:OP1	2.33	0.41
19:ML:71:LEU:HD22	19:ML:99:THR:HG21	2.02	0.41
23:Ma:104:ASN:OD1	23:Ma:108:GLU:N	2.42	0.41
40:Mr:32:GLY:HA2	40:Mr:40:HIS:CE1	2.55	0.41
38:Mp:58:LYS:HD3	38:Mp:58:LYS:HA	1.87	0.41
16:MI:17:ASP:OD1	16:MI:17:ASP:N	2.52	0.41
91:DP:66:A:H2'	91:DP:67:A:C8	2.55	0.41
5:L1:271:C:O2	31:Li:82:ARG:NH2	2.38	0.41
5:L1:2352:A:H5''	18:LK:83:TRP:O	2.20	0.41
22:LO:17:ARG:HG2	22:LO:22:HIS:HA	2.02	0.41
22:LO:96:ILE:HD13	22:LO:96:ILE:HA	1.88	0.41
44:Lv:58:GLU:OE1	44:Lv:59:ASP:N	2.53	0.41
47:Ly:138:ARG:NH1	47:Ly:138:ARG:HB3	2.35	0.41
49:S1:250:C:H2'	49:S1:251:A:C8	2.55	0.41
49:S1:454:U:C4	61:Se:66:MET:HE1	2.55	0.41
49:S1:1517:U:H5''	49:S1:1518:C:H5	1.85	0.41
49:S1:1531:G:N2	76:St:48:GLN:OE1	2.43	0.41
49:S1:1534:G:O2'	49:S1:1535:U:O2	2.27	0.41
60:Sd:40:ARG:HB2	60:Sd:47:GLU:HG3	2.02	0.41
61:Se:42:LEU:HG	61:Se:47:PHE:HB2	2.03	0.41
63:Sg:214:LYS:HE3	63:Sg:214:LYS:HB3	1.80	0.41
67:Sk:24:LYS:HG2	67:Sk:63:TYR:CE1	2.55	0.41
74:Sr:76:GLU:HA	74:Sr:79:GLU:HG3	2.02	0.41
76:St:132:LEU:HD23	76:St:132:LEU:HA	1.88	0.41
82:Sz:57:TYR:O	82:Sz:103:ARG:NH1	2.53	0.41
51:RB:15:GLU:O	51:RB:29:ARG:NH2	2.48	0.41
49:R1:1255:G:O6	69:Rm:46:ARG:NE	2.46	0.41
49:R1:1288:G:OP1	49:R1:1624:C:O2'	2.37	0.41
57:Ra:198:MET:HE3	57:Ra:200:ASP:HB2	2.02	0.41
72:Rp:49:MET:HE2	72:Rp:49:MET:HA	2.01	0.41
17:MJ:39:GLU:HG2	17:MJ:40:GLU:HG2	2.02	0.41
87:M1:507:U:H2'	87:M1:508:U:C6	2.55	0.41
87:M1:1044:U:OP1	12:ME:90:ARG:NH2	2.50	0.41
87:M1:1277:C:H2'	87:M1:1278:A:H8	1.85	0.41
87:M1:1281:G:H5'	89:MQ:55:LYS:HG2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
87:M1:1456:A:N1	87:M1:1476:G:O2'	2.50	0.41
87:M1:1615:C:H2'	87:M1:1616:U:C6	2.56	0.41
87:M1:1695:U:O2'	87:M1:1749:A:N1	2.45	0.41
87:M1:1798:A:H2'	87:M1:1799:A:C8	2.55	0.41
87:M1:3204:C:H2'	87:M1:3205:G:C8	2.56	0.41
40:Mr:26:VAL:HG11	40:Mr:96:VAL:HB	2.00	0.41
31:Mi:34:SER:O	31:Mi:37:THR:N	2.52	0.41
91:DP:16:U:H4'	91:DP:17:U:H5	1.85	0.41
4:CP:69:G:H2'	4:CP:70:G:H8	1.85	0.41
5:L1:129:U:H2'	5:L1:130:A:C8	2.55	0.41
5:L1:299:G:C4	31:Li:31:GLY:HA3	2.55	0.41
5:L1:1877:U:H5''	5:L1:1878:G:O4'	2.20	0.41
10:LC:67:ILE:HG23	10:LC:237:ILE:HB	2.02	0.41
10:LC:82:LEU:HD13	10:LC:222:PHE:HE2	1.85	0.41
10:LC:218:ILE:HD13	10:LC:218:ILE:HA	1.86	0.41
11:LD:50:ASN:HD21	15:LH:4:ASP:HB2	1.85	0.41
14:LG:48:PRO:HA	14:LG:137:GLN:HB3	2.02	0.41
39:Lq:74:ASN:OD1	39:Lq:115:LYS:HB2	2.21	0.41
49:S1:1524:A:H2'	49:S1:1525:A:C8	2.55	0.41
58:Sb:166:LYS:HE3	58:Sb:166:LYS:HB2	1.80	0.41
67:Sk:24:LYS:HG2	67:Sk:63:TYR:HE1	1.85	0.41
75:Rs:75:ASN:HB3	75:Rs:78:HIS:ND1	2.35	0.41
49:R1:445:A:H2'	49:R1:446:A:H8	1.84	0.41
49:R1:689:G:H2'	49:R1:690:G:C8	2.55	0.41
49:R1:809:A:H2'	49:R1:810:G:C8	2.55	0.41
49:R1:843:U:H2'	49:R1:844:A:C8	2.55	0.41
49:R1:1231:U:H3	49:R1:1254:U:H3	1.67	0.41
49:R1:1374:C:H2'	49:R1:1375:A:H8	1.84	0.41
49:R1:1504:G:N3	49:R1:1563:C:O2'	2.46	0.41
73:Rq:29:ILE:HG23	73:Rq:65:ILE:HB	2.03	0.41
73:Rq:93:HIS:HA	73:Rq:97:VAL:HG22	2.01	0.41
87:M1:1831:U:O2'	6:M2:114:G:OP1	2.26	0.41
87:M1:2611:U:H2'	87:M1:2612:U:C6	2.56	0.41
87:M1:2945:G:O2'	87:M1:2948:OMC:OP2	2.37	0.41
87:M1:3291:G:H2'	87:M1:3292:A:C8	2.55	0.41
19:ML:92:ARG:HG2	39:Mq:76:ASP:HB2	2.03	0.41
20:MM:130:ASN:O	20:MM:132:PHE:N	2.53	0.41
48:Mz:237:GLU:O	48:Mz:241:THR:OG1	2.31	0.41
9:MB:82:LYS:HB2	9:MB:82:LYS:HE3	1.76	0.41
13:MF:54:VAL:HG12	13:MF:55:ARG:HD2	2.01	0.41
1:CC:7:ASP:OD2	1:CC:10:ILE:HG13	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:CP:76:A:N1	5:L1:2819:A:O2'	2.49	0.41
5:L1:1622:U:H2'	5:L1:1623:G:H8	1.85	0.41
8:LA:176:PHE:O	15:LH:113:THR:OG1	2.33	0.41
13:LF:35:LYS:HA	13:LF:38:GLU:HB2	2.01	0.41
42:Lt:105:VAL:HG21	42:Lt:135:ILE:HD13	2.02	0.41
49:S1:17:C:H2'	49:S1:18:C:H6	1.85	0.41
49:S1:187:G:N1	49:S1:197:A:N1	2.68	0.41
49:S1:1650:U:H2'	49:S1:1651:A:C8	2.55	0.41
50:SA:44:ILE:HG23	50:SA:45:VAL:HG23	2.03	0.41
51:SB:4:VAL:HG13	79:Sw:23:ARG:NH1	2.36	0.41
58:Sb:79:HIS:HB3	58:Sb:82:ARG:HD3	2.01	0.41
64:Sh:126:LEU:HD12	64:Sh:126:LEU:HA	1.92	0.41
76:Rt:84:LYS:HG2	76:Rt:86:ARG:HG2	2.01	0.41
49:R1:219:A:N6	49:R1:843:U:O2	2.53	0.41
49:R1:472:U:H2'	49:R1:473:A:H8	1.86	0.41
49:R1:591:A:H5''	66:Rj:24:LEU:HD13	2.02	0.41
49:R1:625:C:H2'	49:R1:626:U:C6	2.55	0.41
49:R1:1097:U:O4	59:Rc:201:ASN:ND2	2.53	0.41
49:R1:1511:U:H2'	49:R1:1512:G:H8	1.84	0.41
67:Rk:44:LYS:HA	67:Rk:44:LYS:HD3	1.72	0.41
70:Rn:16:ILE:HG23	70:Rn:62:GLN:HE22	1.85	0.41
87:M1:309:U:OP1	31:Mi:84:LYS:NZ	2.46	0.41
87:M1:1024:G:H21	87:M1:1027:A:H8	1.69	0.41
87:M1:1119:C:H2'	87:M1:1120:A:H8	1.86	0.41
87:M1:1748:G:OP2	29:Mg:42:LYS:NZ	2.46	0.41
87:M1:1764:U:H3'	87:M1:1765:U:H4'	2.02	0.41
87:M1:2152:A:H2'	87:M1:2153:U:H6	1.85	0.41
7:M3:11:A:N1	7:M3:67:G:O2'	2.50	0.41
89:MQ:126:THR:OG1	89:MQ:127:GLY:N	2.53	0.41
90:MP:44:GLU:HG3	90:MP:48:LYS:HE2	2.02	0.41
37:Mo:54:SER:HB3	33:Mk:94:LEU:HD13	2.02	0.41
5:L1:1721:U:OP2	20:LM:124:TYR:OH	2.29	0.41
24:Lb:21:SER:O	24:Lb:25:GLN:HG3	2.21	0.41
39:Lq:117:ARG:HD3	39:Lq:117:ARG:HA	1.86	0.41
48:Lz:153:THR:HG23	48:Lz:160:PHE:HZ	1.85	0.41
48:Lz:191:ASP:HA	48:Lz:192:PRO:HD3	1.93	0.41
49:S1:144:U:H2'	49:S1:145:A:C8	2.56	0.41
49:S1:1010:C:H2'	49:S1:1011:G:O4'	2.20	0.41
49:S1:1114:G:O2'	49:S1:1130:G:O6	2.30	0.41
49:S1:1247:U:H2'	49:S1:1248:C:C6	2.55	0.41
64:Sh:77:LEU:HD12	64:Sh:92:PHE:HZ	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
66:Sj:116:LEU:HD23	66:Sj:156:ILE:HD11	2.01	0.41
75:Ss:14:ILE:HD13	75:Ss:21:ASN:OD1	2.20	0.41
82:Rz:75:LEU:H	82:Rz:75:LEU:HD12	1.85	0.41
49:R1:1001:A:OP1	88:DQ:39:A:O2'	2.34	0.41
58:Rb:82:ARG:NH2	58:Rb:188:LEU:O	2.53	0.41
60:Rd:40:ARG:NH1	60:Rd:40:ARG:HA	2.35	0.41
60:Rd:78:LYS:HD2	60:Rd:78:LYS:HA	1.76	0.41
64:Rh:76:LYS:HB2	64:Rh:76:LYS:HE2	1.75	0.41
17:MJ:59:ARG:NH2	87:M1:1307:G:OP2	2.43	0.41
87:M1:1547:G:OP1	16:MI:108:ARG:NH2	2.51	0.41
87:M1:2946:A2M:HM'3	87:M1:2946:A2M:H1'	1.93	0.41
6:M2:8:C:H2'	6:M2:9:A:H8	1.85	0.41
88:DQ:6:G:H2'	88:DQ:7:G:C8	2.55	0.41
48:Mz:133:GLU:H	48:Mz:133:GLU:HG3	1.70	0.41
13:MF:110:ILE:HG21	13:MF:116:TYR:HA	2.01	0.41
3:CN:103:ILE:HG13	3:CN:105:GLU:HB3	2.02	0.41
5:L1:402:A:OP1	28:Lf:36:ARG:NH2	2.53	0.41
5:L1:800:G:O6	47:Ly:104:LYS:NZ	2.48	0.41
5:L1:986:U:OP1	9:LB:98:LYS:NZ	2.42	0.41
5:L1:1900:A:O2'	5:L1:1906:G:N7	2.47	0.41
5:L1:2244:A:O2'	45:Lw:223:SER:OG	2.26	0.41
9:LB:44:ILE:HG12	9:LB:180:SER:HB3	2.03	0.41
19:LL:176:ARG:HG3	19:LL:183:GLY:HA3	2.02	0.41
20:LM:31:GLU:OE1	20:LM:31:GLU:N	2.54	0.41
35:Lm:81:ASP:OD2	35:Lm:81:ASP:N	2.52	0.41
49:S1:17:C:H2'	49:S1:18:C:C6	2.55	0.41
49:S1:890:C:H2'	49:S1:891:A:H8	1.85	0.41
68:Sl:116:ARG:H	68:Sl:116:ARG:HD3	1.86	0.41
72:Sp:110:GLU:HB3	75:Ss:119:ILE:HD13	2.01	0.41
75:Ss:106:GLU:HG2	75:Ss:110:ARG:NH2	2.33	0.41
56:RG:133:VAL:O	56:RG:141:LEU:N	2.54	0.41
49:R1:142:G:C2	49:R1:173:A:H2	2.35	0.41
49:R1:199:G:O2'	49:R1:200:A:H8	2.03	0.41
49:R1:730:G:H21	49:R1:731:C:H5''	1.86	0.41
63:Rg:3:LEU:HD22	63:Rg:111:LEU:HD11	2.02	0.41
64:Rh:25:VAL:HA	64:Rh:28:GLU:HB3	2.02	0.41
64:Rh:35:LYS:H	64:Rh:35:LYS:HG2	1.68	0.41
87:M1:1046:A:H2'	87:M1:1049:C:C5	2.55	0.41
90:MP:126:ALA:HA	90:MP:162:ILE:HG13	2.02	0.41
11:MD:41:ILE:HG22	11:MD:43:VAL:HG13	2.02	0.41
5:L1:632:G:H21	34:Ll:23:ASN:HD21	1.69	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:L3:71:G:H2'	7:L3:72:A:C8	2.55	0.41
8:LA:14:ASP:OD2	8:LA:15:VAL:N	2.54	0.41
12:LE:192:ASP:N	12:LE:192:ASP:OD1	2.54	0.41
14:LG:120:GLN:HE21	14:LG:120:GLN:HB2	1.70	0.41
15:LH:3:THR:OG1	15:LH:4:ASP:N	2.53	0.41
36:Ln:110:GLU:H	36:Ln:110:GLU:HG3	1.72	0.41
49:S1:591:A:H2'	49:S1:592:A:C8	2.55	0.41
49:S1:598:U:H2'	49:S1:599:A:C8	2.56	0.41
49:S1:704:C:H42	49:S1:734:A:H61	1.67	0.41
49:S1:1217:A:H5'	67:Sk:1:MET:HE2	2.01	0.41
49:S1:1362:U:O2'	49:S1:1363:U:O2	2.32	0.41
62:Sf:93:LEU:HD12	62:Sf:172:ILE:HG23	2.02	0.41
53:RD:36:LEU:HD12	53:RD:36:LEU:HA	1.93	0.41
49:R1:912:U:OP1	49:R1:913:G:O2'	2.29	0.41
49:R1:1681:A:H8	63:Rg:65:GLN:HG3	1.84	0.41
61:Re:105:VAL:HG21	61:Re:245:LYS:H	1.85	0.41
72:Rp:64:LYS:HA	72:Rp:64:LYS:HD3	1.75	0.41
87:M1:1119:C:H2'	87:M1:1120:A:C8	2.56	0.41
87:M1:1632:A:OP1	40:Mr:69:LYS:NZ	2.53	0.41
87:M1:1785:U:H2'	87:M1:1786:G:C8	2.56	0.41
87:M1:1807:G:O2'	87:M1:2559:U:O4	2.35	0.41
87:M1:2440:G:H2'	87:M1:2441:A:H8	1.86	0.41
6:M2:85:G:OP2	41:Ms:113:LYS:NZ	2.53	0.41
47:My:155:ASP:N	47:My:155:ASP:OD2	2.50	0.41
10:MC:144:GLU:HA	10:MC:173:MET:HE2	2.03	0.41
13:MF:10:ARG:HE	13:MF:10:ARG:HB3	1.74	0.41
36:Mn:83:GLU:H	36:Mn:83:GLU:HG2	1.72	0.41
1:CC:16:LYS:HD2	1:CC:16:LYS:HA	1.79	0.41
5:L1:121:A:C2	10:LC:129:PRO:HB3	2.56	0.41
5:L1:985:U:H2'	5:L1:986:U:H6	1.86	0.41
5:L1:1018:G:O6	5:L1:1034:U:O4	2.38	0.41
5:L1:2592:G:H4'	5:L1:2594:C:C2	2.55	0.41
5:L1:2611:U:H2'	5:L1:2612:U:C6	2.55	0.41
5:L1:2767:U:H2'	5:L1:2768:U:C6	2.56	0.41
12:LE:103:LEU:HD13	12:LE:103:LEU:HA	1.96	0.41
13:LF:91:LEU:HD23	13:LF:95:ASN:HD22	1.85	0.41
44:Lv:101:ASN:HA	44:Lv:103:TYR:CZ	2.56	0.41
45:Lw:117:GLU:HA	45:Lw:125:ALA:HB3	2.02	0.41
49:S1:340:U:H2'	49:S1:341:A:C8	2.56	0.41
72:Sp:83:MET:HB3	72:Sp:116:LEU:HD12	2.03	0.41
76:St:105:LEU:HA	76:St:108:LEU:HB2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:Sx:138:GLU:N	80:Sx:138:GLU:OE1	2.53	0.41
77:Ru:84:MET:HE3	77:Ru:84:MET:HB2	1.93	0.41
51:RB:34:ASP:OD1	51:RB:34:ASP:N	2.53	0.41
83:RC:47:PRO:HG2	62:Rf:165:LEU:HD23	2.03	0.41
49:R1:420:A:OP1	63:Rg:96:SER:OG	2.37	0.41
49:R1:448:C:H5'	61:Re:29:PRO:HA	2.02	0.41
61:Re:50:ASN:O	61:Re:53:LYS:NZ	2.53	0.41
86:MA:20:LYS:HD3	86:MA:20:LYS:HA	1.82	0.41
86:MA:34:LEU:HD13	86:MA:34:LEU:HA	1.97	0.41
17:MJ:12:LYS:HA	17:MJ:40:GLU:HB2	2.03	0.41
87:M1:92:G:C8	95:M1:3603:SPD:H72	2.56	0.41
87:M1:158:G:H2'	87:M1:159:A:H8	1.85	0.41
87:M1:821:U:H2'	87:M1:822:G:C8	2.56	0.41
87:M1:1635:G:N2	87:M1:1638:A:OP2	2.39	0.41
87:M1:2228:A:H2'	87:M1:2229:A:C8	2.56	0.41
87:M1:2561:A:H2'	87:M1:2562:A:H8	1.86	0.41
89:MQ:14:LYS:HD2	89:MQ:14:LYS:HA	1.85	0.41
9:MB:236:ILE:HD12	9:MB:236:ILE:HA	1.97	0.41
13:MF:29:ARG:HD2	13:MF:32:ARG:HH22	1.86	0.41
13:MF:165:GLN:OE1	13:MF:166:LYS:N	2.54	0.41
91:DP:8:U:O2'	91:DP:21:A:N1	2.45	0.41
5:L1:1219:C:H4'	5:L1:1223:A:H5'	2.03	0.41
5:L1:1622:U:H2'	5:L1:1623:G:C8	2.56	0.41
5:L1:2154:U:H2'	5:L1:2155:G:C8	2.56	0.41
5:L1:2274:U:H2'	5:L1:2275:A:C8	2.56	0.41
5:L1:2413:A:H2'	5:L1:2414:G:H8	1.85	0.41
5:L1:2662:G:H2'	5:L1:2663:G:C8	2.56	0.41
16:LI:5:LYS:HE3	16:LI:5:LYS:HB2	1.89	0.41
20:LM:162:ARG:NH2	49:S1:815:G:N3	2.69	0.41
30:Lh:66:TYR:OH	30:Lh:73:ARG:NH2	2.54	0.41
42:Lt:86:VAL:HG11	42:Lt:95:ILE:HD11	2.03	0.41
45:Lw:150:LEU:HD11	45:Lw:156:LYS:HD2	2.03	0.41
46:Lx:206:ASP:OD1	46:Lx:206:ASP:N	2.54	0.41
47:Ly:22:LEU:HA	47:Ly:23:PRO:HD3	1.91	0.41
47:Ly:237:GLN:O	47:Ly:246:ARG:HD3	2.20	0.41
47:Ly:266:THR:HG23	47:Ly:267:VAL:HG13	2.03	0.41
48:Lz:104:LEU:HD13	48:Lz:247:ILE:HD12	2.02	0.41
48:Lz:153:THR:HG22	48:Lz:179:ARG:HD2	2.03	0.41
48:Lz:239:ILE:HD13	48:Lz:239:ILE:HA	1.88	0.41
49:S1:65:A:H2	49:S1:84:A:H62	1.68	0.41
49:S1:85:A:N3	49:S1:148:A:O2'	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:S1:227:U:H2'	49:S1:228:G:H8	1.86	0.41
49:S1:934:C:N3	49:S1:1077:C:H4'	2.36	0.41
49:S1:1344:A:H2'	49:S1:1345:A:C8	2.56	0.41
49:S1:1393:C:H2'	49:S1:1394:G:H8	1.85	0.41
49:S1:1701:A:H2'	49:S1:1702:A:C8	2.56	0.41
49:S1:1732:A:H2'	49:S1:1733:C:C6	2.56	0.41
56:SG:13:LEU:HB2	56:SG:310:ILE:HB	2.03	0.41
56:SG:248:ASN:OD1	56:SG:248:ASN:N	2.47	0.41
57:Sa:185:ARG:C	78:Sv:44:ARG:HH12	2.28	0.41
58:Sb:181:LEU:HD22	58:Sb:181:LEU:HA	1.87	0.41
59:Sc:228:ASN:C	59:Sc:228:ASN:HD22	2.29	0.41
60:Sd:115:ILE:H	60:Sd:115:ILE:HG12	1.74	0.41
64:Sh:113:PRO:HG2	64:Sh:116:ARG:HD3	2.03	0.41
69:Sm:32:LEU:HB3	69:Sm:33:ARG:HH21	1.85	0.41
73:Sq:31:VAL:HA	73:Sq:67:VAL:HG22	2.03	0.41
75:Rs:41:ARG:HD3	49:R1:1565:C:OP1	2.21	0.41
54:RE:7:SER:O	54:RE:7:SER:OG	2.37	0.41
49:R1:405:C:O2'	63:Rg:92:ARG:O	2.35	0.41
49:R1:508:U:H2'	49:R1:509:G:C8	2.55	0.41
49:R1:628:G:H21	49:R1:971:A:H62	1.68	0.41
49:R1:718:U:H2'	49:R1:719:U:H5	1.86	0.41
49:R1:884:A:H5'	58:Rb:136:ARG:CZ	2.51	0.41
49:R1:1220:C:H2'	49:R1:1221:A:C8	2.56	0.41
57:Ra:59:LEU:HD23	57:Ra:158:VAL:HG21	2.03	0.41
60:Rd:39:VAL:HG22	60:Rd:48:VAL:HG22	2.03	0.41
66:Rj:86:LEU:HD12	66:Rj:86:LEU:HA	1.97	0.41
86:MA:8:LYS:NZ	87:M1:1354:G:O4'	2.47	0.41
87:M1:127:G:H2'	87:M1:128:G:C8	2.56	0.41
87:M1:544:C:O2	87:M1:547:G:N2	2.54	0.41
87:M1:1101:G:H1'	9:MB:105:LEU:HD23	2.03	0.41
87:M1:1534:A:H2'	87:M1:1535:A:C8	2.56	0.41
87:M1:2747:A:H2'	87:M1:2748:A:C8	2.56	0.41
87:M1:3214:U:OP2	15:MH:128:ARG:NH1	2.54	0.41
87:M1:3233:C:H2'	87:M1:3234:A:C8	2.56	0.41
6:M2:63:G:H22	6:M2:97:A:H2	1.68	0.41
45:Mw:119:LYS:HE3	45:Mw:119:LYS:HB2	1.97	0.41
23:Ma:101:VAL:HG11	23:Ma:114:ILE:HD12	2.03	0.41
13:MF:32:ARG:HD2	13:MF:120:ILE:HA	2.02	0.41
5:L1:1420:C:OP2	47:Ly:193:LYS:NZ	2.49	0.41
5:L1:1688:U:H2'	5:L1:1689:U:C6	2.56	0.41
5:L1:2747:A:H2'	5:L1:2748:A:C8	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L1:3296:A:H2'	5:L1:3297:U:H6	1.86	0.41
15:LH:66:THR:HA	15:LH:99:TRP:HZ3	1.86	0.41
16:LI:7:LEU:HD12	16:LI:46:ASP:HB3	2.02	0.41
16:LI:19:LEU:HD23	16:LI:19:LEU:HA	1.90	0.41
20:LM:173:ARG:HA	20:LM:173:ARG:HH11	1.86	0.41
39:Lq:36:GLY:HA3	39:Lq:40:HIS:CE1	2.56	0.41
39:Lq:89:GLN:HA	39:Lq:92:LYS:HE3	2.03	0.41
39:Lq:105:LEU:HA	39:Lq:105:LEU:HD23	1.87	0.41
46:Lx:196:ARG:HA	46:Lx:196:ARG:HD2	1.81	0.41
46:Lx:305:ILE:HD11	46:Lx:359:ILE:HG21	2.03	0.41
48:Lz:40:HIS:HB3	48:Lz:43:LYS:HE2	2.03	0.41
49:S1:1132:A:H2'	49:S1:1133:A:H8	1.86	0.41
49:S1:1479:A:OP1	76:St:57:ARG:NE	2.48	0.41
49:S1:1610:G:N7	73:Sq:14:LYS:NZ	2.68	0.41
56:SG:240:VAL:HG21	56:SG:254:ALA:HB1	2.03	0.41
69:Sm:91:VAL:HG11	69:Sm:97:LEU:HD22	2.03	0.41
73:Sq:13:LYS:HD2	73:Sq:13:LYS:HA	1.77	0.41
77:Ru:110:PRO:HA	60:Rd:40:ARG:HH12	1.86	0.41
78:Rv:34:ILE:HD13	78:Rv:34:ILE:HA	1.89	0.41
49:R1:126:A:H62	49:R1:291:G:N2	2.18	0.41
49:R1:539:G:H21	49:R1:540:G:H1	1.68	0.41
58:Rb:32:ILE:HD13	58:Rb:66:VAL:HG21	2.03	0.41
62:Rf:121:ILE:HG23	62:Rf:199:ILE:HD11	2.03	0.41
64:Rh:47:ARG:HG3	64:Rh:61:PHE:HE2	1.86	0.41
85:Rr:76:GLU:OE1	85:Rr:76:GLU:N	2.37	0.41
87:M1:791:A:H2'	87:M1:792:G:H8	1.85	0.41
87:M1:1254:C:H2'	87:M1:1255:C:C6	2.56	0.41
87:M1:1450:OMG:HM23	87:M1:1450:OMG:H1'	1.93	0.41
48:Mz:107:ARG:HB3	48:Mz:251:PRO:HG3	2.03	0.41
11:MD:122:LYS:HE3	11:MD:122:LYS:HB2	1.91	0.41
29:Mg:74:LYS:HA	29:Mg:74:LYS:HD3	1.86	0.41
91:DP:42:G:H2'	91:DP:43:G:H8	1.86	0.41
4:CP:62:C:H2'	4:CP:63:U:H6	1.86	0.40
5:L1:616:G:H2'	5:L1:617:G:C8	2.56	0.40
5:L1:1945:A:H2'	5:L1:1946:A:C8	2.55	0.40
5:L1:2882:U:H2'	5:L1:2883:U:C6	2.56	0.40
5:L1:3084:C:H2'	5:L1:3085:G:O4'	2.21	0.40
6:L2:37:A:OP2	32:Lj:86:ARG:HD2	2.20	0.40
7:L3:3:U:H2'	7:L3:4:U:C6	2.57	0.40
21:LN:45:LEU:HD23	21:LN:45:LEU:HA	1.88	0.40
37:Lo:10:ILE:HG12	37:Lo:68:TYR:HE1	1.85	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:S1:156:A:O2'	49:S1:416:A:N6	2.54	0.40
49:S1:312:A:N6	49:S1:352:A:N3	2.68	0.40
49:S1:886:U:O2'	71:So:121:VAL:O	2.39	0.40
49:S1:1433:G:N1	53:SD:45:GLU:OE2	2.47	0.40
49:S1:1681:A:N6	49:S1:1720:G:O2'	2.50	0.40
63:Sg:58:LYS:HE3	63:Sg:58:LYS:HB2	1.89	0.40
70:Sn:146:ALA:HA	70:Sn:149:LEU:HB3	2.02	0.40
76:St:7:ARG:HG2	76:St:67:MET:HE1	2.01	0.40
75:Rs:67:GLU:HA	75:Rs:70:VAL:HG22	2.02	0.40
78:Rv:9:VAL:O	78:Rv:10:GLU:HG2	2.20	0.40
50:RA:5:ARG:NH2	49:R1:1795:U:OP2	2.54	0.40
49:R1:333:A:OP1	65:Ri:31:ARG:NH2	2.54	0.40
49:R1:354:C:H5''	65:Ri:16:ALA:HB2	2.03	0.40
49:R1:499:U:HO2'	49:R1:500:C:C5'	2.33	0.40
49:R1:819:G:N2	49:R1:820:U:O4	2.41	0.40
49:R1:1470:C:OP1	49:R1:1540:G:O2'	2.38	0.40
49:R1:1648:A:H2'	49:R1:1649:G:C8	2.56	0.40
63:Rg:18:ILE:HG13	63:Rg:24:ILE:HD11	2.02	0.40
66:Rj:60:LEU:HA	66:Rj:60:LEU:HD23	1.88	0.40
70:Rn:146:ALA:HA	70:Rn:149:LEU:HD12	2.02	0.40
72:Rp:21:ASP:OD1	72:Rp:21:ASP:N	2.53	0.40
17:MJ:170:LYS:HB3	17:MJ:170:LYS:HE2	1.68	0.40
87:M1:1225:A:H3'	87:M1:1226:G:H8	1.85	0.40
87:M1:1437:OMC:HM23	87:M1:1437:OMC:H1'	1.82	0.40
87:M1:2344:U:H2'	87:M1:2345:A:C8	2.56	0.40
18:MK:41:LEU:HD12	18:MK:112:LEU:HB3	2.02	0.40
12:ME:54:SER:HB2	12:ME:135:ILE:HD11	2.02	0.40
14:MG:182:ILE:HD12	14:MG:182:ILE:HA	1.91	0.40
4:CP:70:G:H2'	4:CP:71:A:C8	2.56	0.40
5:L1:1219:C:O2'	5:L1:1286:A:N1	2.52	0.40
5:L1:1907:C:O2	46:Lx:240:ARG:NH2	2.53	0.40
5:L1:3294:A:H2'	5:L1:3295:A:O4'	2.21	0.40
11:LD:41:ILE:HG23	11:LD:43:VAL:HG13	2.04	0.40
25:Lc:15:LYS:HE2	25:Lc:15:LYS:HB3	1.91	0.40
40:Lr:23:VAL:HB	40:Lr:43:VAL:HB	2.02	0.40
45:Lw:102:LEU:HD13	45:Lw:166:ILE:HD11	2.04	0.40
45:Lw:114:SER:N	45:Lw:165:VAL:O	2.52	0.40
46:Lx:77:THR:HG23	46:Lx:324:VAL:HG13	2.01	0.40
47:Ly:36:HIS:O	47:Ly:40:THR:HG23	2.21	0.40
48:Lz:54:ARG:HD3	48:Lz:54:ARG:HA	1.91	0.40
49:S1:953:G:H2'	49:S1:954:G:H8	1.85	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:S1:1145:U:H5	49:S1:1633:A:N1	2.20	0.40
49:S1:1564:U:H2'	49:S1:1565:C:C6	2.56	0.40
56:SG:54:PHE:HD1	56:SG:312:VAL:HG11	1.86	0.40
57:Sa:78:SER:OG	57:Sa:129:ASP:OD1	2.27	0.40
57:Sa:98:ILE:HD11	57:Sa:116:LYS:HZ3	1.87	0.40
64:Sh:93:LEU:HD12	64:Sh:125:ILE:HD13	2.04	0.40
73:Sq:101:SER:O	73:Sq:104:GLU:HG3	2.21	0.40
75:Ss:125:ILE:H	75:Ss:125:ILE:HG12	1.67	0.40
82:Rz:58:ARG:NH2	62:Rf:126:ASP:OD1	2.54	0.40
55:RF:92:LYS:HD3	49:R1:1247:U:H4'	2.04	0.40
49:R1:66:U:C5	63:Rg:173:PRO:HG3	2.56	0.40
57:Ra:76:ILE:HD13	57:Ra:98:ILE:HB	2.02	0.40
58:Rb:195:LYS:HA	58:Rb:195:LYS:HD2	1.82	0.40
87:M1:113:C:OP1	16:MI:147:ARG:NE	2.53	0.40
87:M1:663:OMC:HM23	87:M1:663:OMC:H1'	1.89	0.40
87:M1:863:C:H2'	87:M1:864:G:O4'	2.21	0.40
87:M1:945:C:H2'	87:M1:946:U:C6	2.56	0.40
87:M1:1117:G:OP1	38:Mp:4:SER:HB2	2.21	0.40
87:M1:1486:G:H21	33:Mk:6:THR:HG22	1.86	0.40
87:M1:1793:C:OP1	45:Mw:177:LYS:NZ	2.54	0.40
87:M1:2444:C:H3'	87:M1:2445:A:H8	1.85	0.40
87:M1:3294:A:H2'	87:M1:3295:A:O4'	2.20	0.40
90:MP:50:THR:HA	90:MP:53:PHE:HD2	1.85	0.40
39:Mq:125:VAL:HG21	39:Mq:138:ILE:HD13	2.02	0.40
5:L1:541:U:H2'	5:L1:542:G:C8	2.56	0.40
5:L1:1238:C:N4	5:L1:1245:A:OP2	2.55	0.40
5:L1:2155:G:O2'	45:Lw:227:ARG:NH2	2.52	0.40
5:L1:2836:C:H5	5:L1:2852:C:H42	1.68	0.40
7:L3:107:C:H2'	7:L3:108:A:H8	1.86	0.40
12:LE:144:ASN:OD1	12:LE:147:VAL:HB	2.22	0.40
24:Lb:61:LYS:HE2	24:Lb:61:LYS:N	2.36	0.40
25:Lc:8:ARG:HH11	25:Lc:10:THR:HB	1.86	0.40
28:Lf:9:ILE:HD13	28:Lf:9:ILE:HA	1.90	0.40
44:Lv:86:LYS:HA	44:Lv:86:LYS:HD3	2.01	0.40
46:Lx:62:ARG:HG2	46:Lx:348:ARG:NH1	2.36	0.40
48:Lz:234:ASP:OD1	48:Lz:234:ASP:N	2.54	0.40
49:S1:647:G:N2	49:S1:687:G:H22	2.20	0.40
58:Sb:103:MET:HB3	58:Sb:215:VAL:HG13	2.03	0.40
58:Sb:129:THR:HG22	58:Sb:176:VAL:HG13	2.03	0.40
58:Sb:140:ILE:N	58:Sb:212:VAL:O	2.54	0.40
61:Se:23:LEU:HD13	61:Se:23:LEU:HA	1.96	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:R1:651:G:N1	49:R1:684:A:N7	2.70	0.40
49:R1:962:C:H5''	70:Rn:72:MET:HE3	2.03	0.40
87:M1:184:U:H2'	87:M1:185:C:C6	2.57	0.40
87:M1:1035:G:H2'	87:M1:1036:A:C8	2.55	0.40
87:M1:2828:G:O2'	12:ME:4:ARG:NH2	2.43	0.40
87:M1:3175:U:OP1	34:Ml:10:LYS:NZ	2.44	0.40
6:M2:28:C:H2'	6:M2:29:U:C6	2.56	0.40
90:MP:32:ILE:HG22	90:MP:37:LEU:HB2	2.02	0.40
48:Mz:179:ARG:HA	48:Mz:179:ARG:HD3	1.73	0.40
42:Mt:64:GLU:OE1	42:Mt:85:GLN:NE2	2.55	0.40
36:Mn:24:SER:HB2	36:Mn:27:LYS:HG3	2.03	0.40
33:Mk:58:ARG:HA	33:Mk:58:ARG:HD2	1.79	0.40
5:L1:1181:U:O4	17:LJ:21:SER:OG	2.35	0.40
5:L1:1493:G:OP2	5:L1:1493:G:N2	2.47	0.40
5:L1:1498:A:H2'	5:L1:1499:C:C6	2.56	0.40
5:L1:2180:G:H2'	5:L1:2181:C:C6	2.56	0.40
5:L1:2883:U:H2'	5:L1:2884:C:H6	1.86	0.40
13:LF:84:LEU:HD11	13:LF:163:PHE:HZ	1.86	0.40
17:LJ:25:LYS:HA	17:LJ:25:LYS:HD2	1.76	0.40
31:Li:28:TYR:HD1	31:Li:28:TYR:HA	1.79	0.40
35:Lm:109:LEU:O	35:Lm:113:LYS:HD3	2.22	0.40
49:S1:895:G:H21	71:So:38:THR:HG21	1.86	0.40
54:SE:44:PHE:CE2	66:Sj:29:LYS:HG2	2.57	0.40
56:SG:124:SER:OG	56:SG:134:TRP:NE1	2.40	0.40
63:Sg:136:LYS:HE3	63:Sg:174:LYS:HB2	2.04	0.40
73:Sq:18:ALA:HB2	73:Sq:69:VAL:HG13	2.03	0.40
80:Sx:19:ARG:HA	80:Sx:19:ARG:HD3	1.76	0.40
75:Rs:92:ILE:HD12	75:Rs:92:ILE:HA	1.89	0.40
76:Rt:18:TYR:CD1	76:Rt:135:ILE:HG13	2.56	0.40
77:Ru:106:ILE:HG13	77:Ru:107:THR:HG23	2.03	0.40
78:Rv:44:ARG:HA	78:Rv:44:ARG:HD3	1.90	0.40
50:RA:20:PRO:HA	50:RA:31:PRO:HA	2.04	0.40
49:R1:219:A:C6	49:R1:843:U:H1'	2.57	0.40
49:R1:386:G:H2'	49:R1:387:A:C8	2.57	0.40
49:R1:739:G:H2'	49:R1:740:A:H4'	2.04	0.40
49:R1:884:A:H2'	49:R1:885:G:C8	2.56	0.40
49:R1:901:G:H3'	49:R1:902:G:C8	2.55	0.40
59:Rc:64:LYS:HD3	59:Rc:64:LYS:HA	1.79	0.40
70:Rn:136:PRO:HG2	70:Rn:139:TRP:HD1	1.86	0.40
87:M1:2930:A:H2'	87:M1:2931:C:C6	2.56	0.40
87:M1:3096:C:H2'	87:M1:3097:C:C6	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:M3:27:A:H2'	7:M3:28:C:C6	2.56	0.40
88:DQ:5:G:H2'	88:DQ:6:G:H8	1.86	0.40
22:MO:13:TYR:HA	22:MO:16:GLN:HG3	2.02	0.40
47:My:22:LEU:HA	47:My:23:PRO:HD3	1.86	0.40
47:My:145:ILE:HD11	47:My:150:LEU:HD22	2.02	0.40
26:Md:23:ARG:HB2	26:Md:23:ARG:HH11	1.87	0.40
91:DP:52:U:H2'	91:DP:53:G:C8	2.57	0.40
5:L1:1063:G:C6	22:LO:109:VAL:HG23	2.56	0.40
5:L1:2389:C:H2'	5:L1:2390:A:H8	1.87	0.40
13:LF:7:ASN:OD1	13:LF:7:ASN:N	2.53	0.40
13:LF:12:LEU:HD23	13:LF:12:LEU:HA	1.88	0.40
17:LJ:54:TYR:OH	17:LJ:73:PHE:O	2.37	0.40
19:LL:133:LYS:HE3	47:Ly:298:ALA:HB1	2.03	0.40
33:Lk:67:LYS:O	33:Lk:71:THR:OG1	2.34	0.40
34:Ll:16:TYR:HD2	34:Ll:23:ASN:HD22	1.69	0.40
44:Lv:97:SER:HA	44:Lv:103:TYR:HA	2.04	0.40
49:S1:523:G:H22	49:S1:527:A:H3'	1.87	0.40
49:S1:869:A:H61	49:S1:958:U:H3	1.69	0.40
49:S1:1382:A:O2'	49:S1:1383:G:OP1	2.33	0.40
49:S1:1484:G:H21	49:S1:1606:C:H1'	1.86	0.40
49:S1:1556:A:H4'	49:S1:1557:U:H5	1.87	0.40
49:S1:1761:U:H1'	49:S1:1762:A:N7	2.37	0.40
50:SA:48:ALA:O	71:So:103:ARG:NH1	2.55	0.40
56:SG:42:LEU:HB2	56:SG:61:PHE:HB2	2.04	0.40
60:Sd:78:LYS:HE2	60:Sd:78:LYS:H	1.86	0.40
61:Se:253:ASP:HA	61:Se:256:ARG:NH2	2.37	0.40
62:Sf:192:GLU:H	62:Sf:192:GLU:HG2	1.71	0.40
63:Sg:207:GLU:O	63:Sg:210:GLN:NE2	2.54	0.40
75:Ss:103:ASN:OD1	75:Ss:103:ASN:N	2.55	0.40
83:RC:19:THR:OG1	83:RC:20:GLY:N	2.54	0.40
49:R1:250:C:H2'	49:R1:251:A:C8	2.55	0.40
49:R1:1202:A:H1'	49:R1:1207:C:H42	1.87	0.40
49:R1:1787:C:H2'	49:R1:1788:G:C8	2.56	0.40
57:Ra:182:LEU:HD23	57:Ra:182:LEU:HA	1.96	0.40
64:Rh:124:LYS:HD3	64:Rh:124:LYS:HA	1.96	0.40
69:Rm:125:ASN:OD1	69:Rm:126:TRP:N	2.54	0.40
85:Rr:89:SER:OG	85:Rr:90:ALA:N	2.54	0.40
87:M1:170:G:H2'	87:M1:171:G:C8	2.56	0.40
87:M1:629:U:H2'	87:M1:630:A:H8	1.86	0.40
87:M1:1083:G:H2'	87:M1:1084:A:H8	1.87	0.40
87:M1:2948:OMC:H5'	46:Mx:243:HIS:HB3	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:My:152:VAL:HG11	47:My:156:LEU:HD22	2.04	0.40
37:Mo:66:LYS:H	37:Mo:66:LYS:HG2	1.65	0.40
14:MG:139:LEU:HD13	14:MG:139:LEU:HA	1.96	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	CC	12/233 (5%)	11 (92%)	1 (8%)	0	100	100
3	CN	132/151 (87%)	130 (98%)	2 (2%)	0	100	100
8	LA	163/176 (93%)	153 (94%)	10 (6%)	0	100	100
9	LB	220/244 (90%)	208 (94%)	12 (6%)	0	100	100
9	MB	220/244 (90%)	213 (97%)	7 (3%)	0	100	100
10	LC	231/256 (90%)	215 (93%)	16 (7%)	0	100	100
10	MC	231/256 (90%)	221 (96%)	10 (4%)	0	100	100
11	LD	189/191 (99%)	175 (93%)	14 (7%)	0	100	100
11	MD	189/191 (99%)	176 (93%)	13 (7%)	0	100	100
12	LE	216/221 (98%)	206 (95%)	10 (5%)	0	100	100
12	ME	213/221 (96%)	202 (95%)	11 (5%)	0	100	100
13	LF	167/174 (96%)	151 (90%)	16 (10%)	0	100	100
13	MF	167/174 (96%)	153 (92%)	14 (8%)	0	100	100
14	LG	191/199 (96%)	173 (91%)	16 (8%)	2 (1%)	12	39
14	MG	191/199 (96%)	173 (91%)	17 (9%)	1 (0%)	24	54
15	LH	134/138 (97%)	125 (93%)	9 (7%)	0	100	100
15	MH	134/138 (97%)	128 (96%)	6 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
16	LI	201/204 (98%)	191 (95%)	10 (5%)	0	100	100
16	MI	201/204 (98%)	187 (93%)	14 (7%)	0	100	100
17	LJ	195/199 (98%)	188 (96%)	5 (3%)	2 (1%)	12	39
17	MJ	195/199 (98%)	191 (98%)	4 (2%)	0	100	100
18	LK	181/184 (98%)	171 (94%)	10 (6%)	0	100	100
18	MK	152/184 (83%)	149 (98%)	3 (2%)	0	100	100
19	LL	183/186 (98%)	171 (93%)	12 (7%)	0	100	100
19	ML	183/186 (98%)	177 (97%)	6 (3%)	0	100	100
20	LM	186/189 (98%)	181 (97%)	4 (2%)	1 (0%)	24	54
20	MM	174/189 (92%)	169 (97%)	4 (2%)	1 (1%)	21	51
21	LN	169/172 (98%)	163 (96%)	6 (4%)	0	100	100
21	MN	170/172 (99%)	159 (94%)	11 (6%)	0	100	100
22	LO	157/160 (98%)	148 (94%)	9 (6%)	0	100	100
22	MO	157/160 (98%)	148 (94%)	9 (6%)	0	100	100
23	La	134/137 (98%)	132 (98%)	2 (2%)	0	100	100
23	Ma	127/137 (93%)	123 (97%)	4 (3%)	0	100	100
24	Lb	89/92 (97%)	82 (92%)	7 (8%)	0	100	100
24	Mb	89/92 (97%)	84 (94%)	5 (6%)	0	100	100
25	Lc	101/106 (95%)	96 (95%)	5 (5%)	0	100	100
25	Mc	100/106 (94%)	93 (93%)	7 (7%)	0	100	100
26	Ld	23/25 (92%)	23 (100%)	0	0	100	100
26	Md	23/25 (92%)	23 (100%)	0	0	100	100
27	Le	50/128 (39%)	49 (98%)	1 (2%)	0	100	100
27	Me	50/128 (39%)	50 (100%)	0	0	100	100
28	Lf	48/51 (94%)	46 (96%)	2 (4%)	0	100	100
28	Mf	48/51 (94%)	41 (85%)	7 (15%)	0	100	100
29	Lg	75/78 (96%)	74 (99%)	1 (1%)	0	100	100
29	Mg	75/78 (96%)	69 (92%)	6 (8%)	0	100	100
30	Lh	83/88 (94%)	80 (96%)	3 (4%)	0	100	100
30	Mh	82/88 (93%)	75 (92%)	7 (8%)	0	100	100
31	Li	97/100 (97%)	92 (95%)	5 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
31	Mi	97/100 (97%)	86 (89%)	11 (11%)	0	100	100
32	Lj	117/120 (98%)	115 (98%)	2 (2%)	0	100	100
32	Mj	117/120 (98%)	109 (93%)	8 (7%)	0	100	100
33	Lk	104/121 (86%)	100 (96%)	4 (4%)	0	100	100
33	Mk	107/121 (88%)	105 (98%)	2 (2%)	0	100	100
34	Ll	104/107 (97%)	99 (95%)	5 (5%)	0	100	100
34	Ml	104/107 (97%)	100 (96%)	4 (4%)	0	100	100
35	Lm	125/130 (96%)	121 (97%)	4 (3%)	0	100	100
35	Mm	125/130 (96%)	124 (99%)	1 (1%)	0	100	100
36	Ln	107/113 (95%)	97 (91%)	10 (9%)	0	100	100
36	Mn	107/113 (95%)	98 (92%)	8 (8%)	1 (1%)	14	41
37	Lo	94/105 (90%)	94 (100%)	0	0	100	100
37	Mo	95/105 (90%)	94 (99%)	1 (1%)	0	100	100
38	Lp	56/59 (95%)	46 (82%)	10 (18%)	0	100	100
38	Mp	56/59 (95%)	51 (91%)	5 (9%)	0	100	100
39	Lq	146/149 (98%)	124 (85%)	21 (14%)	1 (1%)	18	48
39	Mq	146/149 (98%)	133 (91%)	12 (8%)	1 (1%)	18	48
40	Lr	133/136 (98%)	123 (92%)	10 (8%)	0	100	100
40	Mr	133/136 (98%)	124 (93%)	9 (7%)	0	100	100
41	Ls	123/127 (97%)	119 (97%)	4 (3%)	0	100	100
41	Ms	124/127 (98%)	119 (96%)	5 (4%)	0	100	100
42	Lt	119/142 (84%)	112 (94%)	6 (5%)	1 (1%)	16	44
42	Mt	118/142 (83%)	112 (95%)	6 (5%)	0	100	100
43	Lu	124/155 (80%)	115 (93%)	9 (7%)	0	100	100
43	Mu	61/155 (39%)	61 (100%)	0	0	100	100
44	Lv	98/121 (81%)	91 (93%)	7 (7%)	0	100	100
44	Mv	95/121 (78%)	86 (90%)	9 (10%)	0	100	100
45	Lw	249/254 (98%)	227 (91%)	22 (9%)	0	100	100
45	Mw	250/254 (98%)	239 (96%)	11 (4%)	0	100	100
46	Lx	384/387 (99%)	356 (93%)	26 (7%)	2 (0%)	24	54
46	Mx	384/387 (99%)	365 (95%)	19 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
47	Ly	359/362 (99%)	331 (92%)	26 (7%)	2 (1%)	21	51
47	My	359/362 (99%)	340 (95%)	19 (5%)	0	100	100
48	Lz	292/297 (98%)	277 (95%)	14 (5%)	1 (0%)	36	65
48	Mz	294/297 (99%)	278 (95%)	16 (5%)	0	100	100
50	RA	95/119 (80%)	82 (86%)	13 (14%)	0	100	100
50	SA	95/119 (80%)	83 (87%)	10 (10%)	2 (2%)	5	21
51	RB	79/82 (96%)	69 (87%)	10 (13%)	0	100	100
51	SB	79/82 (96%)	67 (85%)	12 (15%)	0	100	100
52	SC	60/67 (90%)	58 (97%)	2 (3%)	0	100	100
53	RD	51/56 (91%)	50 (98%)	1 (2%)	0	100	100
53	SD	51/56 (91%)	49 (96%)	2 (4%)	0	100	100
54	RE	46/63 (73%)	45 (98%)	1 (2%)	0	100	100
54	SE	58/63 (92%)	52 (90%)	6 (10%)	0	100	100
55	RF	68/152 (45%)	53 (78%)	15 (22%)	0	100	100
55	SF	71/152 (47%)	50 (70%)	21 (30%)	0	100	100
56	RG	311/319 (98%)	297 (96%)	14 (4%)	0	100	100
56	SG	310/319 (97%)	282 (91%)	28 (9%)	0	100	100
57	Ra	204/252 (81%)	173 (85%)	30 (15%)	1 (0%)	24	54
57	Sa	204/252 (81%)	181 (89%)	23 (11%)	0	100	100
58	Rb	214/255 (84%)	201 (94%)	13 (6%)	0	100	100
58	Sb	222/255 (87%)	194 (87%)	26 (12%)	2 (1%)	14	41
59	Rc	215/254 (85%)	208 (97%)	7 (3%)	0	100	100
59	Sc	214/254 (84%)	203 (95%)	11 (5%)	0	100	100
60	Rd	221/240 (92%)	207 (94%)	14 (6%)	0	100	100
60	Sd	220/240 (92%)	211 (96%)	9 (4%)	0	100	100
61	Re	258/261 (99%)	239 (93%)	18 (7%)	1 (0%)	30	59
61	Se	256/261 (98%)	230 (90%)	25 (10%)	1 (0%)	30	59
62	Rf	204/225 (91%)	186 (91%)	18 (9%)	0	100	100
62	Sf	204/225 (91%)	190 (93%)	14 (7%)	0	100	100
63	Rg	216/236 (92%)	204 (94%)	12 (6%)	0	100	100
63	Sg	226/236 (96%)	210 (93%)	14 (6%)	2 (1%)	14	41

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
64	Rh	183/190 (96%)	169 (92%)	14 (8%)	0	100	100
64	Sh	182/190 (96%)	169 (93%)	13 (7%)	0	100	100
65	Ri	184/200 (92%)	178 (97%)	6 (3%)	0	100	100
65	Si	183/200 (92%)	162 (88%)	19 (10%)	2 (1%)	11	36
66	Rj	183/197 (93%)	166 (91%)	17 (9%)	0	100	100
66	Sj	182/197 (92%)	164 (90%)	18 (10%)	0	100	100
67	Rk	90/105 (86%)	73 (81%)	17 (19%)	0	100	100
67	Sk	90/105 (86%)	79 (88%)	11 (12%)	0	100	100
68	Rl	144/156 (92%)	135 (94%)	9 (6%)	0	100	100
68	Sl	142/156 (91%)	129 (91%)	13 (9%)	0	100	100
69	Rm	122/143 (85%)	101 (83%)	21 (17%)	0	100	100
69	Sm	119/143 (83%)	90 (76%)	27 (23%)	2 (2%)	7	26
70	Rn	148/151 (98%)	137 (93%)	11 (7%)	0	100	100
70	Sn	148/151 (98%)	139 (94%)	9 (6%)	0	100	100
71	So	125/137 (91%)	108 (86%)	16 (13%)	1 (1%)	16	44
72	Rp	117/142 (82%)	102 (87%)	14 (12%)	1 (1%)	14	41
72	Sp	115/142 (81%)	103 (90%)	12 (10%)	0	100	100
73	Rq	139/143 (97%)	129 (93%)	10 (7%)	0	100	100
73	Sq	139/143 (97%)	126 (91%)	12 (9%)	1 (1%)	18	48
74	Sr	117/136 (86%)	111 (95%)	6 (5%)	0	100	100
75	Rs	143/146 (98%)	125 (87%)	18 (13%)	0	100	100
75	Ss	143/146 (98%)	128 (90%)	13 (9%)	2 (1%)	9	30
76	Rt	141/144 (98%)	132 (94%)	9 (6%)	0	100	100
76	St	141/144 (98%)	126 (89%)	15 (11%)	0	100	100
77	Ru	99/121 (82%)	90 (91%)	8 (8%)	1 (1%)	12	39
77	Su	98/121 (81%)	91 (93%)	7 (7%)	0	100	100
78	Rv	85/87 (98%)	79 (93%)	6 (7%)	0	100	100
78	Sv	85/87 (98%)	73 (86%)	12 (14%)	0	100	100
79	Rw	127/130 (98%)	122 (96%)	5 (4%)	0	100	100
79	Sw	127/130 (98%)	119 (94%)	8 (6%)	0	100	100
80	Rx	142/145 (98%)	133 (94%)	9 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
80	Sx	142/145 (98%)	123 (87%)	18 (13%)	1 (1%)	18	48
81	Ry	132/135 (98%)	122 (92%)	9 (7%)	1 (1%)	16	44
81	Sy	132/135 (98%)	123 (93%)	9 (7%)	0	100	100
82	Rz	67/108 (62%)	63 (94%)	4 (6%)	0	100	100
82	Sz	80/108 (74%)	69 (86%)	11 (14%)	0	100	100
83	RC	61/67 (91%)	58 (95%)	3 (5%)	0	100	100
84	Ro	126/138 (91%)	106 (84%)	20 (16%)	0	100	100
85	Rr	123/136 (90%)	116 (94%)	7 (6%)	0	100	100
86	MA	151/176 (86%)	140 (93%)	11 (7%)	0	100	100
89	MQ	195/312 (62%)	189 (97%)	6 (3%)	0	100	100
90	MP	156/165 (94%)	146 (94%)	10 (6%)	0	100	100
All	All	22304/24622 (91%)	20726 (93%)	1541 (7%)	37 (0%)	44	72

All (37) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
17	LJ	111	PRO
50	SA	84	VAL
65	Si	10	LYS
14	MG	63	VAL
14	LG	63	VAL
39	Lq	78	LEU
42	Lt	44	PRO
46	Lx	4	ARG
69	Sm	131	ASP
75	Ss	91	ASP
81	Ry	37	LYS
46	Lx	128	LYS
48	Lz	20	PHE
63	Sg	173	PRO
39	Mq	78	LEU
61	Se	43	PRO
63	Sg	68	LEU
72	Rp	125	PRO
20	MM	131	ALA
14	LG	77	LEU
17	LJ	110	PRO
47	Ly	4	PRO

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Mol	Chain	Res	Type
50	SA	9	GLY
69	Sm	109	GLU
71	So	124	ASP
77	Ru	71	PRO
20	LM	53	LYS
47	Ly	292	SER
58	Sb	213	ARG
65	Si	9	HIS
36	Mn	110	GLU
57	Ra	31	VAL
73	Sq	33	GLY
75	Ss	92	ILE
58	Sb	212	VAL
80	Sx	42	PRO
61	Re	196	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	CC	13/215 (6%)	12 (92%)	1 (8%)	12	35
3	CN	112/123 (91%)	111 (99%)	1 (1%)	70	90
8	LA	138/155 (89%)	133 (96%)	5 (4%)	31	65
9	LB	186/205 (91%)	179 (96%)	7 (4%)	29	64
9	MB	186/205 (91%)	184 (99%)	2 (1%)	65	88
10	LC	187/208 (90%)	184 (98%)	3 (2%)	55	83
10	MC	187/208 (90%)	180 (96%)	7 (4%)	30	64
11	LD	168/171 (98%)	164 (98%)	4 (2%)	43	75
11	MD	171/171 (100%)	164 (96%)	7 (4%)	27	61
12	LE	185/187 (99%)	174 (94%)	11 (6%)	18	48
12	ME	184/187 (98%)	180 (98%)	4 (2%)	45	77
13	LF	146/150 (97%)	137 (94%)	9 (6%)	16	46

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
13	MF	147/150 (98%)	141 (96%)	6 (4%)	27	61
14	LG	154/159 (97%)	147 (96%)	7 (4%)	24	58
14	MG	154/159 (97%)	152 (99%)	2 (1%)	61	86
15	LH	107/109 (98%)	105 (98%)	2 (2%)	50	79
15	MH	107/109 (98%)	104 (97%)	3 (3%)	38	72
16	LI	175/176 (99%)	169 (97%)	6 (3%)	32	66
16	MI	175/176 (99%)	170 (97%)	5 (3%)	37	71
17	LJ	160/162 (99%)	157 (98%)	3 (2%)	50	79
17	MJ	160/162 (99%)	157 (98%)	3 (2%)	50	79
18	LK	138/146 (94%)	133 (96%)	5 (4%)	31	65
18	MK	125/146 (86%)	118 (94%)	7 (6%)	19	50
19	LL	150/151 (99%)	147 (98%)	3 (2%)	48	78
19	ML	150/151 (99%)	148 (99%)	2 (1%)	61	86
20	LM	152/154 (99%)	149 (98%)	3 (2%)	48	78
20	MM	143/154 (93%)	141 (99%)	2 (1%)	59	85
21	LN	155/156 (99%)	146 (94%)	9 (6%)	18	49
21	MN	156/156 (100%)	151 (97%)	5 (3%)	34	68
22	LO	136/137 (99%)	129 (95%)	7 (5%)	21	53
22	MO	136/137 (99%)	129 (95%)	7 (5%)	21	53
23	La	104/105 (99%)	99 (95%)	5 (5%)	23	55
23	Ma	101/105 (96%)	96 (95%)	5 (5%)	22	53
24	Lb	71/72 (99%)	69 (97%)	2 (3%)	38	72
24	Mb	71/72 (99%)	68 (96%)	3 (4%)	26	60
25	Lc	87/91 (96%)	80 (92%)	7 (8%)	11	34
25	Mc	87/91 (96%)	84 (97%)	3 (3%)	32	66
26	Ld	22/23 (96%)	20 (91%)	2 (9%)	9	28
26	Md	23/23 (100%)	22 (96%)	1 (4%)	26	60
27	Le	47/116 (40%)	46 (98%)	1 (2%)	47	77
27	Me	47/116 (40%)	47 (100%)	0	100	100
28	Lf	45/46 (98%)	44 (98%)	1 (2%)	45	77
28	Mf	45/46 (98%)	45 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
29	Lg	68/69 (99%)	64 (94%)	4 (6%)	18	48
29	Mg	68/69 (99%)	64 (94%)	4 (6%)	18	48
30	Lh	69/71 (97%)	67 (97%)	2 (3%)	37	71
30	Mh	69/71 (97%)	66 (96%)	3 (4%)	26	60
31	Li	80/82 (98%)	77 (96%)	3 (4%)	29	64
31	Mi	81/82 (99%)	79 (98%)	2 (2%)	42	74
32	Lj	104/105 (99%)	100 (96%)	4 (4%)	29	64
32	Mj	104/105 (99%)	103 (99%)	1 (1%)	68	89
33	Lk	91/103 (88%)	88 (97%)	3 (3%)	33	67
33	Mk	94/103 (91%)	92 (98%)	2 (2%)	47	77
34	Ll	90/91 (99%)	87 (97%)	3 (3%)	33	67
34	Ml	90/91 (99%)	88 (98%)	2 (2%)	45	77
35	Lm	108/111 (97%)	105 (97%)	3 (3%)	38	72
35	Mm	109/111 (98%)	106 (97%)	3 (3%)	38	72
36	Ln	92/97 (95%)	86 (94%)	6 (6%)	15	44
36	Mn	94/97 (97%)	92 (98%)	2 (2%)	47	77
37	Lo	81/88 (92%)	75 (93%)	6 (7%)	13	38
37	Mo	81/88 (92%)	77 (95%)	4 (5%)	22	54
38	Lp	46/47 (98%)	43 (94%)	3 (6%)	15	44
38	Mp	46/47 (98%)	46 (100%)	0	100	100
39	Lq	118/119 (99%)	113 (96%)	5 (4%)	26	60
39	Mq	118/119 (99%)	109 (92%)	9 (8%)	12	36
40	Lr	115/116 (99%)	108 (94%)	7 (6%)	17	46
40	Mr	115/116 (99%)	112 (97%)	3 (3%)	40	73
41	Ls	108/110 (98%)	101 (94%)	7 (6%)	15	44
41	Ms	109/110 (99%)	108 (99%)	1 (1%)	70	90
42	Lt	104/118 (88%)	101 (97%)	3 (3%)	37	71
42	Mt	104/118 (88%)	101 (97%)	3 (3%)	37	71
43	Lu	56/129 (43%)	56 (100%)	0	100	100
43	Mu	55/129 (43%)	55 (100%)	0	100	100
44	Lv	87/107 (81%)	85 (98%)	2 (2%)	44	76

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
44	Mv	84/107 (78%)	81 (96%)	3 (4%)	31	65
45	Lw	190/196 (97%)	183 (96%)	7 (4%)	30	64
45	Mw	193/196 (98%)	187 (97%)	6 (3%)	35	69
46	Lx	319/323 (99%)	307 (96%)	12 (4%)	29	64
46	Mx	320/323 (99%)	315 (98%)	5 (2%)	55	83
47	Ly	288/289 (100%)	282 (98%)	6 (2%)	47	77
47	My	288/289 (100%)	280 (97%)	8 (3%)	38	72
48	Lz	241/245 (98%)	238 (99%)	3 (1%)	63	86
48	Mz	244/245 (100%)	241 (99%)	3 (1%)	63	86
50	RA	83/101 (82%)	78 (94%)	5 (6%)	17	47
50	SA	83/101 (82%)	81 (98%)	2 (2%)	43	75
51	RB	70/71 (99%)	68 (97%)	2 (3%)	37	71
51	SB	70/71 (99%)	67 (96%)	3 (4%)	26	60
52	SC	55/60 (92%)	54 (98%)	1 (2%)	51	80
53	RD	47/49 (96%)	46 (98%)	1 (2%)	47	77
53	SD	47/49 (96%)	46 (98%)	1 (2%)	47	77
54	RE	41/54 (76%)	41 (100%)	0	100	100
54	SE	50/54 (93%)	49 (98%)	1 (2%)	48	78
55	RF	55/135 (41%)	52 (94%)	3 (6%)	19	50
55	SF	56/135 (42%)	52 (93%)	4 (7%)	13	40
56	RG	255/262 (97%)	249 (98%)	6 (2%)	43	75
56	SG	250/262 (95%)	247 (99%)	3 (1%)	63	86
57	Ra	165/210 (79%)	161 (98%)	4 (2%)	43	75
57	Sa	170/210 (81%)	166 (98%)	4 (2%)	43	75
58	Rb	192/224 (86%)	186 (97%)	6 (3%)	35	69
58	Sb	200/224 (89%)	189 (94%)	11 (6%)	19	50
59	Rc	176/205 (86%)	167 (95%)	9 (5%)	21	53
59	Sc	175/205 (85%)	171 (98%)	4 (2%)	44	76
60	Rd	182/195 (93%)	175 (96%)	7 (4%)	29	64
60	Sd	182/195 (93%)	177 (97%)	5 (3%)	39	73
61	Re	221/222 (100%)	216 (98%)	5 (2%)	44	76

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
61	Se	220/222 (99%)	213 (97%)	7 (3%)	34	68
62	Rf	173/191 (91%)	168 (97%)	5 (3%)	37	71
62	Sf	172/191 (90%)	167 (97%)	5 (3%)	37	71
63	Rg	187/201 (93%)	184 (98%)	3 (2%)	55	83
63	Sg	189/201 (94%)	180 (95%)	9 (5%)	23	55
64	Rh	165/170 (97%)	160 (97%)	5 (3%)	36	70
64	Sh	163/170 (96%)	152 (93%)	11 (7%)	15	43
65	Ri	150/161 (93%)	149 (99%)	1 (1%)	76	92
65	Si	148/161 (92%)	145 (98%)	3 (2%)	48	78
66	Rj	158/166 (95%)	154 (98%)	4 (2%)	42	74
66	Sj	156/166 (94%)	151 (97%)	5 (3%)	34	68
67	Rk	73/98 (74%)	72 (99%)	1 (1%)	59	85
67	Sk	77/98 (79%)	71 (92%)	6 (8%)	11	35
68	Rl	129/137 (94%)	125 (97%)	4 (3%)	35	69
68	Sl	129/137 (94%)	124 (96%)	5 (4%)	28	63
69	Rm	88/119 (74%)	86 (98%)	2 (2%)	44	76
69	Sm	88/119 (74%)	83 (94%)	5 (6%)	18	49
70	Rn	127/128 (99%)	123 (97%)	4 (3%)	35	69
70	Sn	127/128 (99%)	117 (92%)	10 (8%)	11	34
71	So	91/105 (87%)	87 (96%)	4 (4%)	25	59
72	Rp	98/118 (83%)	95 (97%)	3 (3%)	35	69
72	Sp	95/118 (80%)	94 (99%)	1 (1%)	65	88
73	Rq	117/119 (98%)	116 (99%)	1 (1%)	70	90
73	Sq	117/119 (98%)	112 (96%)	5 (4%)	26	60
74	Sr	101/124 (82%)	99 (98%)	2 (2%)	48	78
75	Rs	128/129 (99%)	120 (94%)	8 (6%)	16	45
75	Ss	128/129 (99%)	121 (94%)	7 (6%)	19	50
76	Rt	115/116 (99%)	111 (96%)	4 (4%)	32	66
76	St	115/116 (99%)	110 (96%)	5 (4%)	26	60
77	Ru	94/114 (82%)	92 (98%)	2 (2%)	47	77
77	Su	93/114 (82%)	87 (94%)	6 (6%)	15	44

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
78	Rv	74/74 (100%)	71 (96%)	3 (4%)	27	61
78	Sv	71/74 (96%)	68 (96%)	3 (4%)	26	60
79	Rw	110/111 (99%)	107 (97%)	3 (3%)	39	73
79	Sw	110/111 (99%)	103 (94%)	7 (6%)	16	44
80	Rx	119/120 (99%)	115 (97%)	4 (3%)	32	66
80	Sx	119/120 (99%)	113 (95%)	6 (5%)	22	53
81	Ry	112/113 (99%)	109 (97%)	3 (3%)	39	73
81	Sy	112/113 (99%)	108 (96%)	4 (4%)	31	65
82	Rz	61/89 (68%)	58 (95%)	3 (5%)	22	54
82	Sz	67/89 (75%)	63 (94%)	4 (6%)	17	47
83	RC	56/60 (93%)	55 (98%)	1 (2%)	51	80
84	Ro	97/105 (92%)	92 (95%)	5 (5%)	21	52
85	Rr	113/124 (91%)	111 (98%)	2 (2%)	51	80
86	MA	133/153 (87%)	131 (98%)	2 (2%)	57	84
89	MQ	167/254 (66%)	162 (97%)	5 (3%)	36	70
90	MP	129/136 (95%)	126 (98%)	3 (2%)	44	76
All	All	18800/20698 (91%)	18181 (97%)	619 (3%)	34	67

All (619) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	CC	14	ARG
3	CN	38	GLN
8	LA	12	SER
8	LA	65	VAL
8	LA	98	VAL
8	LA	146	LEU
8	LA	152	THR
9	LB	82	LYS
9	LB	83	LEU
9	LB	109	THR
9	LB	113	SER
9	LB	146	GLN
9	LB	189	ILE
9	LB	228	SER
10	LC	36	ILE

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Mol	Chain	Res	Type
10	LC	67	ILE
10	LC	197	VAL
11	LD	16	VAL
11	LD	55	VAL
11	LD	92	TYR
11	LD	157	ASN
12	LE	28	ASP
12	LE	31	ILE
12	LE	91	VAL
12	LE	103	LEU
12	LE	109	ASP
12	LE	113	GLN
12	LE	123	HIS
12	LE	185	ARG
12	LE	186	GLU
12	LE	200	LEU
12	LE	210	ILE
13	LF	11	ASP
13	LF	15	GLU
13	LF	18	VAL
13	LF	30	LEU
13	LF	44	THR
13	LF	67	VAL
13	LF	107	ASP
13	LF	111	ASP
13	LF	161	SER
14	LG	4	SER
14	LG	58	VAL
14	LG	93	ILE
14	LG	108	ILE
14	LG	120	GLN
14	LG	164	GLU
14	LG	165	SER
15	LH	107	GLU
15	LH	116	GLU
16	LI	17	ASP
16	LI	18	VAL
16	LI	29	GLU
16	LI	43	THR
16	LI	109	ARG
16	LI	167	THR
17	LJ	84	LEU

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Mol	Chain	Res	Type
17	LJ	129	LEU
17	LJ	136	THR
18	LK	9	THR
18	LK	29	THR
18	LK	54	HIS
18	LK	144	SER
18	LK	182	ILE
19	LL	3	ILE
19	LL	21	SER
19	LL	100	THR
20	LM	6	THR
20	LM	31	GLU
20	LM	133	LYS
21	LN	19	VAL
21	LN	45	LEU
21	LN	59	VAL
21	LN	65	ASN
21	LN	72	VAL
21	LN	82	ASP
21	LN	87	THR
21	LN	123	ILE
21	LN	145	THR
22	LO	18	ASP
22	LO	27	LEU
22	LO	58	GLN
22	LO	82	ASN
22	LO	86	GLU
22	LO	107	GLU
22	LO	128	LEU
23	La	37	ILE
23	La	73	VAL
23	La	81	GLN
23	La	112	SER
23	La	135	VAL
24	Lb	58	SER
24	Lb	60	CYS
25	Lc	10	THR
25	Lc	35	LEU
25	Lc	57	VAL
25	Lc	68	VAL
25	Lc	71	ARG
25	Lc	80	ARG

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Mol	Chain	Res	Type
25	Lc	98	LYS
26	Ld	15	ARG
26	Ld	20	VAL
27	Le	85	LEU
28	Lf	47	THR
29	Lg	4	GLU
29	Lg	24	THR
29	Lg	72	THR
29	Lg	78	LEU
30	Lh	46	SER
30	Lh	82	SER
31	Li	3	VAL
31	Li	18	THR
31	Li	76	ARG
32	Lj	36	LEU
32	Lj	79	ASP
32	Lj	81	ARG
32	Lj	109	ILE
33	Lk	17	SER
33	Lk	36	LYS
33	Lk	94	LEU
34	Ll	56	SER
34	Ll	59	VAL
34	Ll	67	MET
35	Lm	14	THR
35	Lm	31	ASN
35	Lm	41	VAL
36	Ln	9	THR
36	Ln	11	GLU
36	Ln	41	LYS
36	Ln	84	ASP
36	Ln	87	ASN
36	Ln	104	LEU
37	Lo	20	SER
37	Lo	24	THR
37	Lo	61	MET
37	Lo	63	SER
37	Lo	90	VAL
37	Lo	98	SER
38	Lp	19	ASN
38	Lp	35	VAL
38	Lp	54	LEU

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Mol	Chain	Res	Type
39	Lq	75	LEU
39	Lq	118	ILE
39	Lq	130	VAL
39	Lq	144	VAL
39	Lq	145	VAL
40	Lr	26	VAL
40	Lr	65	ARG
40	Lr	88	ASP
40	Lr	98	THR
40	Lr	120	GLU
40	Lr	123	GLN
40	Lr	128	GLN
41	Ls	6	LEU
41	Ls	7	ASP
41	Ls	11	ASP
41	Ls	56	VAL
41	Ls	58	VAL
41	Ls	86	THR
41	Ls	105	VAL
42	Lt	31	THR
42	Lt	37	THR
42	Lt	135	ILE
44	Lv	56	VAL
44	Lv	102	GLU
45	Lw	21	ARG
45	Lw	44	ILE
45	Lw	101	VAL
45	Lw	118	GLU
45	Lw	126	LEU
45	Lw	130	SER
45	Lw	247	ARG
46	Lx	10	ARG
46	Lx	56	ILE
46	Lx	66	LYS
46	Lx	84	VAL
46	Lx	90	VAL
46	Lx	104	THR
46	Lx	145	GLU
46	Lx	320	ASP
46	Lx	324	VAL
46	Lx	327	CYS
46	Lx	335	ILE

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Mol	Chain	Res	Type
46	Lx	386	ASP
47	Ly	6	VAL
47	Ly	22	LEU
47	Ly	60	THR
47	Ly	105	THR
47	Ly	354	VAL
47	Ly	358	THR
48	Lz	36	LEU
48	Lz	173	VAL
48	Lz	222	LEU
50	SA	51	ARG
50	SA	58	VAL
51	SB	8	LEU
51	SB	77	THR
51	SB	78	SER
52	SC	29	ARG
53	SD	8	PHE
54	SE	4	VAL
55	SF	98	VAL
55	SF	117	LEU
55	SF	135	HIS
55	SF	147	VAL
56	SG	58	VAL
56	SG	300	THR
56	SG	312	VAL
57	Sa	21	ASN
57	Sa	53	THR
57	Sa	148	ASP
57	Sa	197	ILE
58	Sb	81	PHE
58	Sb	91	VAL
58	Sb	92	GLN
58	Sb	110	LEU
58	Sb	122	GLU
58	Sb	148	ASN
58	Sb	157	GLN
58	Sb	181	LEU
58	Sb	193	ILE
58	Sb	207	LEU
58	Sb	215	VAL
59	Sc	53	ILE
59	Sc	111	VAL

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Mol	Chain	Res	Type
59	Sc	154	LEU
59	Sc	235	LEU
60	Sd	72	LEU
60	Sd	91	VAL
60	Sd	120	TYR
60	Sd	169	ASP
60	Sd	189	MET
61	Se	65	LEU
61	Se	76	VAL
61	Se	105	VAL
61	Se	146	THR
61	Se	194	THR
61	Se	214	LEU
61	Se	238	LEU
62	Sf	53	VAL
62	Sf	68	ILE
62	Sf	99	MET
62	Sf	114	ILE
62	Sf	192	GLU
63	Sg	1	MET
63	Sg	13	GLN
63	Sg	68	LEU
63	Sg	81	VAL
63	Sg	127	THR
63	Sg	128	THR
63	Sg	158	ILE
63	Sg	162	VAL
63	Sg	190	GLN
64	Sh	16	LEU
64	Sh	27	LEU
64	Sh	51	VAL
64	Sh	77	LEU
64	Sh	83	LYS
64	Sh	93	LEU
64	Sh	95	GLU
64	Sh	147	ASN
64	Sh	154	LEU
64	Sh	166	LEU
64	Sh	182	VAL
65	Si	11	ARG
65	Si	18	ARG
65	Si	76	THR

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Mol	Chain	Res	Type
66	Sj	38	ASN
66	Sj	122	VAL
66	Sj	134	ILE
66	Sj	136	VAL
66	Sj	156	ILE
67	Sk	8	ARG
67	Sk	15	LEU
67	Sk	35	ILE
67	Sk	63	TYR
67	Sk	78	GLU
67	Sk	80	LEU
68	Sl	61	THR
68	Sl	63	LEU
68	Sl	74	THR
68	Sl	109	VAL
68	Sl	124	THR
69	Sm	66	VAL
69	Sm	71	ILE
69	Sm	81	ASP
69	Sm	86	VAL
69	Sm	103	LEU
70	Sn	27	LYS
70	Sn	28	LEU
70	Sn	29	SER
70	Sn	38	VAL
70	Sn	52	VAL
70	Sn	62	GLN
70	Sn	80	LEU
70	Sn	84	ILE
70	Sn	119	GLU
70	Sn	134	VAL
71	So	42	VAL
71	So	61	MET
71	So	105	LEU
71	So	115	ILE
72	Sp	88	GLU
73	Sq	17	THR
73	Sq	40	GLU
73	Sq	43	ILE
73	Sq	64	ASP
73	Sq	69	VAL
74	Sr	8	THR

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Mol	Chain	Res	Type
74	Sr	105	GLN
75	Ss	4	VAL
75	Ss	20	THR
75	Ss	52	VAL
75	Ss	70	VAL
75	Ss	73	MET
75	Ss	109	LEU
75	Ss	138	THR
76	St	9	VAL
76	St	71	VAL
76	St	111	ILE
76	St	129	GLN
76	St	133	ASP
77	Su	26	LEU
77	Su	27	THR
77	Su	28	SER
77	Su	70	THR
77	Su	99	ILE
77	Su	108	ILE
78	Sv	1	MET
78	Sv	46	ILE
78	Sv	79	LEU
79	Sw	2	THR
79	Sw	26	LEU
79	Sw	65	LEU
79	Sw	66	ASN
79	Sw	104	LEU
79	Sw	114	GLU
79	Sw	129	VAL
80	Sx	46	SER
80	Sx	87	VAL
80	Sx	107	PHE
80	Sx	117	ILE
80	Sx	124	VAL
80	Sx	128	SER
81	Sy	7	ILE
81	Sy	17	LEU
81	Sy	24	VAL
81	Sy	51	GLU
82	Sz	40	VAL
82	Sz	51	LEU
82	Sz	54	VAL

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Mol	Chain	Res	Type
82	Sz	75	LEU
75	Rs	6	GLN
75	Rs	13	HIS
75	Rs	14	ILE
75	Rs	20	THR
75	Rs	25	ASN
75	Rs	62	THR
75	Rs	116	LEU
75	Rs	136	GLN
76	Rt	34	VAL
76	Rt	132	LEU
76	Rt	134	ARG
76	Rt	138	GLN
77	Ru	51	VAL
77	Ru	80	GLU
78	Rv	8	LEU
78	Rv	32	VAL
78	Rv	69	LEU
79	Rw	25	VAL
79	Rw	93	LEU
79	Rw	98	GLN
80	Rx	55	GLU
80	Rx	89	ASN
80	Rx	107	PHE
80	Rx	127	VAL
81	Ry	27	VAL
81	Ry	100	VAL
81	Ry	129	VAL
82	Rz	65	LEU
82	Rz	92	ILE
82	Rz	102	THR
50	RA	44	ILE
50	RA	58	VAL
50	RA	83	ILE
50	RA	84	VAL
50	RA	87	ARG
51	RB	37	CYS
51	RB	54	VAL
83	RC	13	ILE
53	RD	39	CYS
55	RF	98	VAL
55	RF	147	VAL

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Mol	Chain	Res	Type
55	RF	150	VAL
56	RG	31	ASN
56	RG	56	VAL
56	RG	118	LYS
56	RG	195	HIS
56	RG	231	MET
56	RG	297	ASP
57	Ra	34	GLU
57	Ra	101	ARG
57	Ra	108	THR
57	Ra	180	GLU
58	Rb	59	ASP
58	Rb	96	LEU
58	Rb	108	ASP
58	Rb	132	ASP
58	Rb	185	THR
58	Rb	195	LYS
59	Rc	39	THR
59	Rc	72	LEU
59	Rc	80	VAL
59	Rc	102	VAL
59	Rc	111	VAL
59	Rc	148	LEU
59	Rc	193	VAL
59	Rc	244	SER
59	Rc	245	ASP
60	Rd	42	THR
60	Rd	46	THR
60	Rd	85	VAL
60	Rd	159	HIS
60	Rd	175	VAL
60	Rd	206	VAL
60	Rd	207	THR
61	Re	44	LEU
61	Re	45	ILE
61	Re	66	MET
61	Re	140	VAL
61	Re	156	VAL
62	Rf	23	VAL
62	Rf	45	LYS
62	Rf	51	VAL
62	Rf	59	VAL

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Mol	Chain	Res	Type
62	Rf	99	MET
63	Rg	15	THR
63	Rg	49	VAL
63	Rg	127	THR
64	Rh	14	THR
64	Rh	18	LEU
64	Rh	50	ASP
64	Rh	78	THR
64	Rh	147	ASN
65	Ri	46	VAL
66	Rj	48	GLN
66	Rj	96	VAL
66	Rj	140	ILE
66	Rj	151	ASP
67	Rk	17	GLN
68	Rl	6	THR
68	Rl	7	VAL
68	Rl	21	ASN
68	Rl	140	VAL
69	Rm	61	VAL
69	Rm	86	VAL
70	Rn	37	ILE
70	Rn	46	THR
70	Rn	52	VAL
70	Rn	105	ASN
84	Ro	42	VAL
84	Ro	79	VAL
84	Ro	81	VAL
84	Ro	99	GLN
84	Ro	132	ARG
72	Rp	65	LEU
72	Rp	126	VAL
72	Rp	128	HIS
73	Rq	26	LYS
85	Rr	91	LEU
85	Rr	101	ASN
86	MA	59	GLU
86	MA	98	VAL
17	MJ	14	HIS
17	MJ	99	LEU
17	MJ	126	VAL
18	MK	42	THR

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Mol	Chain	Res	Type
18	MK	87	SER
18	MK	89	LYS
18	MK	112	LEU
18	MK	144	SER
18	MK	148	LEU
18	MK	149	VAL
19	ML	127	LEU
19	ML	173	GLU
20	MM	68	GLN
20	MM	86	GLU
89	MQ	58	MET
89	MQ	60	ARG
89	MQ	114	VAL
89	MQ	158	VAL
89	MQ	159	VAL
21	MN	32	SER
21	MN	45	LEU
21	MN	79	VAL
21	MN	96	ASP
21	MN	106	LEU
45	Mw	72	ARG
45	Mw	104	LEU
45	Mw	111	THR
45	Mw	113	VAL
45	Mw	137	ILE
45	Mw	165	VAL
90	MP	32	ILE
90	MP	116	MET
90	MP	130	LYS
22	MO	27	LEU
22	MO	79	MET
22	MO	103	GLN
22	MO	106	LEU
22	MO	118	GLU
22	MO	128	LEU
22	MO	157	GLU
46	Mx	121	ASN
46	Mx	282	ILE
46	Mx	287	LYS
46	Mx	335	ILE
46	Mx	383	LEU
44	Mv	20	SER

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Mol	Chain	Res	Type
44	Mv	47	VAL
44	Mv	50	LEU
47	My	6	VAL
47	My	46	LYS
47	My	148	ILE
47	My	154	THR
47	My	181	VAL
47	My	216	VAL
47	My	324	LEU
47	My	327	LEU
23	Ma	9	THR
23	Ma	57	MET
23	Ma	69	LEU
23	Ma	115	THR
23	Ma	125	LEU
48	Mz	36	LEU
48	Mz	92	LEU
48	Mz	125	VAL
42	Mt	88	MET
42	Mt	101	GLU
42	Mt	129	ASP
9	MB	45	LEU
9	MB	165	ASP
41	Ms	120	GLN
10	MC	27	THR
10	MC	40	VAL
10	MC	106	LYS
10	MC	136	LEU
10	MC	163	VAL
10	MC	180	VAL
10	MC	206	GLU
40	Mr	89	VAL
40	Mr	100	THR
40	Mr	120	GLU
11	MD	12	VAL
11	MD	16	VAL
11	MD	82	VAL
11	MD	101	VAL
11	MD	157	ASN
11	MD	162	GLN
11	MD	176	LEU
39	Mq	78	LEU

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Mol	Chain	Res	Type
39	Mq	86	LYS
39	Mq	101	VAL
39	Mq	118	ILE
39	Mq	120	ASN
39	Mq	123	VAL
39	Mq	130	VAL
39	Mq	135	GLU
39	Mq	145	VAL
12	ME	28	ASP
12	ME	36	LEU
12	ME	138	VAL
12	ME	200	LEU
13	MF	25	GLU
13	MF	37	LEU
13	MF	57	PHE
13	MF	88	GLU
13	MF	107	ASP
13	MF	112	LEU
37	Mo	19	LYS
37	Mo	20	SER
37	Mo	55	GLU
37	Mo	94	GLU
14	MG	5	LYS
14	MG	24	VAL
36	Mn	35	GLU
36	Mn	76	SER
15	MH	64	VAL
15	MH	109	ARG
15	MH	113	THR
35	Mm	23	ASP
35	Mm	31	ASN
35	Mm	67	SER
16	MI	17	ASP
16	MI	43	THR
16	MI	64	VAL
16	MI	135	VAL
16	MI	155	VAL
34	MI	49	ILE
34	MI	67	MET
33	Mk	64	THR
33	Mk	65	VAL
32	Mj	37	SER

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Mol	Chain	Res	Type
31	Mi	57	LEU
31	Mi	60	LEU
30	Mh	67	LEU
30	Mh	75	LYS
30	Mh	82	SER
29	Mg	8	ILE
29	Mg	24	THR
29	Mg	65	LEU
29	Mg	72	THR
26	Md	13	LEU
25	Mc	2	VAL
25	Mc	8	ARG
25	Mc	26	THR
24	Mb	58	SER
24	Mb	60	CYS
24	Mb	72	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (164) such sidechains are listed below:

Mol	Chain	Res	Type
3	CN	24	ASN
8	LA	172	HIS
9	LB	37	ASN
9	LB	166	ASN
10	LC	33	ASN
11	LD	37	ASN
11	LD	64	HIS
11	LD	96	HIS
11	LD	102	ASN
13	LF	68	HIS
13	LF	90	GLN
13	LF	95	ASN
14	LG	99	HIS
15	LH	41	GLN
15	LH	56	GLN
16	LI	15	GLN
17	LJ	182	ASN
18	LK	72	GLN
18	LK	133	HIS
19	LL	126	GLN
20	LM	141	HIS
20	LM	166	ASN

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Mol	Chain	Res	Type
22	LO	98	HIS
22	LO	134	GLN
25	Lc	47	GLN
25	Lc	102	GLN
29	Lg	10	GLN
29	Lg	76	ASN
30	Lh	57	HIS
30	Lh	76	ASN
32	Lj	16	GLN
32	Lj	59	ASN
32	Lj	99	GLN
33	Lk	33	GLN
36	Ln	56	ASN
36	Ln	57	GLN
38	Lp	6	ASN
38	Lp	19	ASN
38	Lp	43	HIS
40	Lr	57	HIS
40	Lr	122	HIS
44	Lv	87	ASN
45	Lw	86	GLN
45	Lw	97	ASN
45	Lw	205	ASN
46	Lx	121	ASN
46	Lx	139	GLN
46	Lx	184	ASN
46	Lx	198	HIS
46	Lx	224	HIS
47	Ly	87	GLN
50	SA	69	ASN
54	SE	17	GLN
58	Sb	95	ASN
59	Sc	199	GLN
60	Sd	92	GLN
60	Sd	101	GLN
60	Sd	165	ASN
61	Se	57	ASN
62	Sf	63	GLN
63	Sg	182	GLN
64	Sh	11	GLN
64	Sh	42	GLN
64	Sh	180	GLN

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Mol	Chain	Res	Type
65	Si	119	GLN
66	Sj	38	ASN
66	Sj	124	HIS
67	Sk	9	ASN
69	Sm	139	HIS
70	Sn	105	ASN
73	Sq	103	ASN
74	Sr	105	GLN
75	Ss	8	GLN
75	Ss	137	HIS
76	St	12	GLN
76	St	70	GLN
76	St	138	GLN
77	Su	87	HIS
77	Su	105	GLN
78	Sv	29	HIS
79	Sw	12	ASN
80	Sx	28	ASN
81	Sy	34	ASN
82	Sz	37	GLN
75	Rs	6	GLN
75	Rs	136	GLN
77	Ru	105	GLN
79	Rw	39	GLN
50	RA	25	ASN
51	RB	9	HIS
51	RB	51	GLN
83	RC	51	ASN
53	RD	53	ASN
55	RF	145	HIS
56	RG	187	GLN
56	RG	200	ASN
56	RG	268	GLN
57	Ra	168	HIS
58	Rb	74	GLN
60	Rd	162	GLN
60	Rd	165	ASN
61	Re	57	ASN
61	Re	67	GLN
61	Re	69	HIS
61	Re	223	ASN
62	Rf	37	GLN

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Mol	Chain	Res	Type
62	Rf	122	ASN
63	Rg	119	GLN
63	Rg	189	HIS
64	Rh	11	GLN
64	Rh	19	GLN
64	Rh	174	ASN
65	Ri	35	ASN
65	Ri	52	ASN
65	Ri	64	ASN
66	Rj	139	GLN
67	Rk	13	GLN
68	RI	14	GLN
68	RI	138	ASN
70	Rn	58	HIS
73	Rq	139	GLN
85	Rr	29	GLN
17	MJ	50	ASN
18	MK	50	GLN
19	ML	126	GLN
89	MQ	98	ASN
89	MQ	189	GLN
21	MN	65	ASN
45	Mw	132	ASN
45	Mw	250	GLN
90	MP	105	GLN
46	Mx	224	HIS
46	Mx	243	HIS
44	Mv	88	GLN
44	Mv	101	ASN
47	My	9	HIS
47	My	260	GLN
48	Mz	4	GLN
48	Mz	32	GLN
48	Mz	206	GLN
9	MB	64	GLN
10	MC	95	ASN
40	Mr	29	HIS
40	Mr	78	ASN
11	MD	51	GLN
11	MD	163	GLN
39	Mq	11	HIS
39	Mq	38	GLN

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Mol	Chain	Res	Type
39	Mq	44	ASN
38	Mp	45	HIS
13	MF	90	GLN
13	MF	150	ASN
14	MG	19	GLN
36	Mn	15	ASN
16	MI	138	GLN
33	Mk	3	GLN
32	Mj	59	ASN
32	Mj	99	GLN
32	Mj	113	GLN
30	Mh	69	HIS
28	Mf	33	ASN
28	Mf	43	ASN
25	Mc	3	ASN
25	Mc	23	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	CM	40/41 (97%)	17 (42%)	1 (2%)
4	CP	73/76 (96%)	10 (13%)	0
49	R1	1755/1800 (97%)	474 (27%)	26 (1%)
49	S1	1768/1800 (98%)	462 (26%)	37 (2%)
5	L1	3111/3396 (91%)	584 (18%)	33 (1%)
6	L2	157/158 (99%)	26 (16%)	1 (0%)
6	M2	157/158 (99%)	24 (15%)	0
7	L3	120/121 (99%)	13 (10%)	1 (0%)
7	M3	120/121 (99%)	11 (9%)	1 (0%)
87	M1	3185/3396 (93%)	507 (15%)	14 (0%)
88	DQ	76/77 (98%)	13 (17%)	0
91	DP	75/76 (98%)	26 (34%)	1 (1%)
All	All	10637/11220 (94%)	2167 (20%)	115 (1%)

All (2167) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	CM	2	U
2	CM	7	U
2	CM	14	U
2	CM	15	U

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Mol	Chain	Res	Type
2	CM	16	U
2	CM	17	U
2	CM	19	U
2	CM	21	U
2	CM	22	U
2	CM	23	U
2	CM	24	U
2	CM	25	U
2	CM	26	U
2	CM	30	U
2	CM	31	U
2	CM	35	C
2	CM	38	C
4	CP	16	U
4	CP	17	G
4	CP	19	U
4	CP	24	G
4	CP	42	G
4	CP	47	U
4	CP	48	U
4	CP	58	A
4	CP	73	G
4	CP	76	A
5	L1	6	A
5	L1	12	A
5	L1	13	A
5	L1	14	U
5	L1	18	G
5	L1	26	A
5	L1	40	A
5	L1	43	A
5	L1	49	A
5	L1	58	G
5	L1	59	G
5	L1	60	A
5	L1	65	A
5	L1	66	A
5	L1	67	A
5	L1	75	G
5	L1	92	G
5	L1	109	A
5	L1	110	G

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Mol	Chain	Res	Type
5	L1	111	C
5	L1	116	A
5	L1	120	G
5	L1	121	A
5	L1	122	A
5	L1	133	U
5	L1	135	C
5	L1	136	G
5	L1	148	G
5	L1	156	G
5	L1	157	A
5	L1	165	A
5	L1	166	C
5	L1	172	G
5	L1	173	G
5	L1	187	A
5	L1	190	U
5	L1	191	U
5	L1	200	C
5	L1	206	G
5	L1	210	U
5	L1	211	A
5	L1	213	A
5	L1	218	G
5	L1	219	A
5	L1	220	G
5	L1	234	G
5	L1	240	U
5	L1	241	G
5	L1	243	G
5	L1	245	U
5	L1	249	U
5	L1	252	U
5	L1	269	G
5	L1	283	G
5	L1	286	U
5	L1	290	G
5	L1	291	C
5	L1	295	A
5	L1	298	U
5	L1	305	U
5	L1	323	A

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Mol	Chain	Res	Type
5	L1	329	U
5	L1	338	A
5	L1	339	C
5	L1	350	C
5	L1	376	G
5	L1	390	G
5	L1	398	A
5	L1	401	U
5	L1	402	A
5	L1	403	C
5	L1	406	G
5	L1	407	A
5	L1	421	G
5	L1	422	A
5	L1	429	U
5	L1	498	A
5	L1	510	G
5	L1	518	G
5	L1	521	A
5	L1	523	A
5	L1	535	G
5	L1	546	C
5	L1	547	G
5	L1	552	G
5	L1	555	U
5	L1	557	A
5	L1	558	U
5	L1	559	A
5	L1	578	A
5	L1	579	G
5	L1	597	G
5	L1	600	G
5	L1	604	G
5	L1	609	G
5	L1	610	G
5	L1	611	A
5	L1	620	U
5	L1	621	A
5	L1	622	A
5	L1	637	C
5	L1	638	C
5	L1	649	A

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Mol	Chain	Res	Type
5	L1	660	A
5	L1	677	A
5	L1	681	U
5	L1	683	U
5	L1	689	U
5	L1	705	A
5	L1	712	G
5	L1	715	A
5	L1	716	A
5	L1	719	U
5	L1	720	A
5	L1	727	G
5	L1	764	U
5	L1	765	C
5	L1	767	U
5	L1	776	U
5	L1	777	U
5	L1	780	A
5	L1	781	G
5	L1	785	G
5	L1	786	A
5	L1	799	G
5	L1	802	C
5	L1	806	A
5	L1	817	A
5	L1	830	A
5	L1	846	A
5	L1	847	A
5	L1	849	C
5	L1	861	C
5	L1	869	G
5	L1	874	U
5	L1	879	U
5	L1	890	C
5	L1	896	A
5	L1	897	U
5	L1	907	G
5	L1	908	G
5	L1	909	G
5	L1	914	A
5	L1	916	G
5	L1	917	A

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Mol	Chain	Res	Type
5	L1	920	A
5	L1	921	A
5	L1	923	C
5	L1	924	G
5	L1	925	A
5	L1	932	U
5	L1	937	G
5	L1	944	C
5	L1	959	C
5	L1	960	U
5	L1	962	A
5	L1	981	U
5	L1	982	C
5	L1	984	G
5	L1	991	G
5	L1	994	G
5	L1	1000	C
5	L1	1001	G
5	L1	1002	A
5	L1	1010	G
5	L1	1015	U
5	L1	1017	C
5	L1	1018	G
5	L1	1020	G
5	L1	1024	G
5	L1	1036	A
5	L1	1037	C
5	L1	1047	A
5	L1	1049	C
5	L1	1064	A
5	L1	1065	A
5	L1	1072	G
5	L1	1081	U
5	L1	1087	G
5	L1	1093	A
5	L1	1094	U
5	L1	1095	U
5	L1	1097	G
5	L1	1098	A
5	L1	1103	A
5	L1	1104	G
5	L1	1117	G

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Mol	Chain	Res	Type
5	L1	1129	A
5	L1	1131	G
5	L1	1135	A
5	L1	1144	U
5	L1	1150	A
5	L1	1153	A
5	L1	1155	C
5	L1	1159	A
5	L1	1178	G
5	L1	1179	A
5	L1	1180	A
5	L1	1181	U
5	L1	1186	G
5	L1	1192	C
5	L1	1193	A
5	L1	1196	C
5	L1	1201	C
5	L1	1202	A
5	L1	1206	G
5	L1	1208	U
5	L1	1217	A
5	L1	1222	G
5	L1	1225	A
5	L1	1227	C
5	L1	1230	G
5	L1	1232	C
5	L1	1233	G
5	L1	1235	U
5	L1	1236	G
5	L1	1240	A
5	L1	1241	U
5	L1	1243	G
5	L1	1245	A
5	L1	1246	G
5	L1	1248	C
5	L1	1251	A
5	L1	1253	U
5	L1	1254	C
5	L1	1258	U
5	L1	1262	G
5	L1	1263	A
5	L1	1264	G

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Mol	Chain	Res	Type
5	L1	1265	U
5	L1	1269	U
5	L1	1270	A
5	L1	1271	A
5	L1	1272	C
5	L1	1274	A
5	L1	1278	A
5	L1	1279	C
5	L1	1285	G
5	L1	1286	A
5	L1	1287	A
5	L1	1295	G
5	L1	1305	U
5	L1	1309	U
5	L1	1313	G
5	L1	1331	U
5	L1	1348	U
5	L1	1349	G
5	L1	1351	U
5	L1	1352	A
5	L1	1354	G
5	L1	1355	A
5	L1	1356	U
5	L1	1357	G
5	L1	1386	A
5	L1	1391	C
5	L1	1392	G
5	L1	1399	A
5	L1	1400	G
5	L1	1419	A
5	L1	1431	G
5	L1	1434	G
5	L1	1437	C
5	L1	1443	G
5	L1	1446	A
5	L1	1450	G
5	L1	1469	C
5	L1	1477	A
5	L1	1481	A
5	L1	1482	A
5	L1	1483	G
5	L1	1484	U

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Mol	Chain	Res	Type
5	L1	1488	G
5	L1	1508	C
5	L1	1536	G
5	L1	1555	U
5	L1	1556	C
5	L1	1557	A
5	L1	1560	G
5	L1	1562	C
5	L1	1563	C
5	L1	1566	A
5	L1	1567	U
5	L1	1568	U
5	L1	1569	U
5	L1	1572	U
5	L1	1575	A
5	L1	1576	G
5	L1	1580	A
5	L1	1582	C
5	L1	1583	A
5	L1	1587	A
5	L1	1588	A
5	L1	1589	A
5	L1	1590	G
5	L1	1593	A
5	L1	1605	A
5	L1	1607	U
5	L1	1608	C
5	L1	1619	A
5	L1	1629	U
5	L1	1639	C
5	L1	1642	A
5	L1	1643	A
5	L1	1645	U
5	L1	1677	G
5	L1	1683	A
5	L1	1716	U
5	L1	1717	U
5	L1	1724	U
5	L1	1725	C
5	L1	1736	G
5	L1	1741	A
5	L1	1750	A

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Mol	Chain	Res	Type
5	L1	1751	G
5	L1	1760	A
5	L1	1764	U
5	L1	1765	U
5	L1	1766	G
5	L1	1770	G
5	L1	1775	G
5	L1	1780	G
5	L1	1797	A
5	L1	1814	A
5	L1	1816	A
5	L1	1820	U
5	L1	1821	U
5	L1	1834	U
5	L1	1835	A
5	L1	1839	A
5	L1	1840	U
5	L1	1842	A
5	L1	1846	C
5	L1	1849	C
5	L1	1850	A
5	L1	1858	A
5	L1	1866	C
5	L1	1867	A
5	L1	1880	U
5	L1	1881	A
5	L1	1886	A
5	L1	1893	A
5	L1	1899	G
5	L1	1906	G
5	L1	1914	G
5	L1	1952	G
5	L1	1953	G
5	L1	1954	G
5	L1	2094	C
5	L1	2101	C
5	L1	2102	U
5	L1	2110	G
5	L1	2111	G
5	L1	2112	U
5	L1	2113	A
5	L1	2121	G

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Mol	Chain	Res	Type
5	L1	2122	G
5	L1	2126	A
5	L1	2131	A
5	L1	2140	U
5	L1	2144	A
5	L1	2158	A
5	L1	2160	G
5	L1	2169	G
5	L1	2171	G
5	L1	2176	U
5	L1	2184	U
5	L1	2188	A
5	L1	2192	C
5	L1	2201	G
5	L1	2205	U
5	L1	2206	G
5	L1	2207	A
5	L1	2209	U
5	L1	2210	G
5	L1	2223	A
5	L1	2225	U
5	L1	2249	G
5	L1	2250	G
5	L1	2256	A
5	L1	2257	C
5	L1	2272	G
5	L1	2273	G
5	L1	2280	A
5	L1	2281	A
5	L1	2282	U
5	L1	2288	G
5	L1	2307	G
5	L1	2308	C
5	L1	2310	U
5	L1	2313	A
5	L1	2314	U
5	L1	2315	G
5	L1	2318	U
5	L1	2334	U
5	L1	2335	G
5	L1	2364	G
5	L1	2372	A

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Mol	Chain	Res	Type
5	L1	2373	A
5	L1	2374	C
5	L1	2375	G
5	L1	2385	G
5	L1	2388	U
5	L1	2393	G
5	L1	2394	G
5	L1	2397	A
5	L1	2402	A
5	L1	2403	G
5	L1	2404	A
5	L1	2411	U
5	L1	2419	A
5	L1	2435	G
5	L1	2514	U
5	L1	2515	A
5	L1	2522	G
5	L1	2526	C
5	L1	2531	C
5	L1	2532	U
5	L1	2548	C
5	L1	2549	G
5	L1	2550	U
5	L1	2552	C
5	L1	2555	G
5	L1	2561	A
5	L1	2569	A
5	L1	2570	U
5	L1	2571	U
5	L1	2572	C
5	L1	2573	G
5	L1	2585	G
5	L1	2593	A
5	L1	2594	C
5	L1	2595	A
5	L1	2606	G
5	L1	2607	G
5	L1	2614	G
5	L1	2626	A
5	L1	2629	U
5	L1	2651	G
5	L1	2652	U

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Mol	Chain	Res	Type
5	L1	2656	A
5	L1	2666	C
5	L1	2672	G
5	L1	2674	A
5	L1	2677	G
5	L1	2689	A
5	L1	2691	A
5	L1	2694	A
5	L1	2696	A
5	L1	2704	A
5	L1	2714	G
5	L1	2719	U
5	L1	2728	G
5	L1	2729	U
5	L1	2752	U
5	L1	2753	G
5	L1	2761	G
5	L1	2772	C
5	L1	2777	G
5	L1	2778	G
5	L1	2788	C
5	L1	2796	G
5	L1	2799	A
5	L1	2800	G
5	L1	2801	A
5	L1	2803	A
5	L1	2809	C
5	L1	2810	C
5	L1	2814	G
5	L1	2815	G
5	L1	2817	A
5	L1	2818	U
5	L1	2821	C
5	L1	2842	U
5	L1	2844	C
5	L1	2845	A
5	L1	2849	C
5	L1	2867	C
5	L1	2871	G
5	L1	2872	A
5	L1	2875	U
5	L1	2876	C

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Mol	Chain	Res	Type
5	L1	2887	A
5	L1	2894	C
5	L1	2898	G
5	L1	2899	C
5	L1	2911	A
5	L1	2923	U
5	L1	2935	U
5	L1	2936	A
5	L1	2938	G
5	L1	2941	A
5	L1	2942	C
5	L1	2947	G
5	L1	2948	C
5	L1	2971	A
5	L1	2983	C
5	L1	2990	G
5	L1	2992	U
5	L1	2996	U
5	L1	2997	G
5	L1	3012	A
5	L1	3039	C
5	L1	3049	A
5	L1	3056	U
5	L1	3078	U
5	L1	3086	A
5	L1	3092	C
5	L1	3101	G
5	L1	3104	U
5	L1	3122	A
5	L1	3129	A
5	L1	3130	A
5	L1	3131	U
5	L1	3139	A
5	L1	3140	G
5	L1	3142	A
5	L1	3143	C
5	L1	3151	U
5	L1	3154	C
5	L1	3155	U
5	L1	3156	U
5	L1	3157	U
5	L1	3158	G

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Mol	Chain	Res	Type
5	L1	3165	A
5	L1	3170	A
5	L1	3172	A
5	L1	3173	G
5	L1	3174	A
5	L1	3175	U
5	L1	3176	G
5	L1	3179	U
5	L1	3181	C
5	L1	3187	A
5	L1	3195	U
5	L1	3196	U
5	L1	3207	U
5	L1	3210	A
5	L1	3217	C
5	L1	3218	A
5	L1	3219	G
5	L1	3224	G
5	L1	3229	G
5	L1	3235	C
5	L1	3242	G
5	L1	3243	A
5	L1	3245	A
5	L1	3247	G
5	L1	3259	U
5	L1	3263	G
5	L1	3270	U
5	L1	3276	G
5	L1	3278	C
5	L1	3281	U
5	L1	3287	U
5	L1	3289	G
5	L1	3294	A
5	L1	3295	A
5	L1	3304	U
5	L1	3307	A
5	L1	3313	U
5	L1	3316	A
5	L1	3318	G
5	L1	3319	U
5	L1	3320	A
5	L1	3341	U

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Mol	Chain	Res	Type
5	L1	3342	A
5	L1	3345	G
5	L1	3351	U
5	L1	3352	U
5	L1	3353	G
5	L1	3354	U
5	L1	3355	U
5	L1	3356	G
5	L1	3363	U
5	L1	3368	U
5	L1	3369	G
5	L1	3375	A
5	L1	3378	C
5	L1	3382	U
5	L1	3383	G
5	L1	3386	G
5	L1	3389	U
5	L1	3390	G
5	L1	3396	U
6	L2	34	U
6	L2	35	C
6	L2	48	A
6	L2	52	A
6	L2	59	A
6	L2	62	C
6	L2	63	G
6	L2	80	A
6	L2	81	U
6	L2	82	U
6	L2	83	C
6	L2	84	C
6	L2	86	U
6	L2	87	G
6	L2	90	U
6	L2	95	G
6	L2	104	A
6	L2	105	A
6	L2	106	C
6	L2	111	A
6	L2	113	U
6	L2	125	U
6	L2	126	A

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Mol	Chain	Res	Type
6	L2	138	A
6	L2	152	G
6	L2	158	U
7	L3	7	G
7	L3	11	A
7	L3	33	U
7	L3	53	U
7	L3	54	U
7	L3	55	A
7	L3	65	G
7	L3	77	G
7	L3	91	G
7	L3	99	G
7	L3	102	A
7	L3	112	G
7	L3	121	U
49	S1	2	A
49	S1	4	C
49	S1	25	C
49	S1	26	A
49	S1	34	G
49	S1	42	G
49	S1	43	A
49	S1	45	U
49	S1	46	A
49	S1	47	A
49	S1	51	A
49	S1	56	U
49	S1	57	G
49	S1	62	A
49	S1	63	G
49	S1	65	A
49	S1	68	A
49	S1	69	G
49	S1	71	A
49	S1	73	U
49	S1	74	U
49	S1	75	U
49	S1	76	A
49	S1	78	A
49	S1	79	C
49	S1	81	G

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Mol	Chain	Res	Type
49	S1	104	A
49	S1	114	C
49	S1	116	U
49	S1	121	U
49	S1	126	A
49	S1	129	U
49	S1	130	C
49	S1	131	C
49	S1	132	U
49	S1	134	U
49	S1	135	A
49	S1	138	A
49	S1	140	A
49	S1	141	U
49	S1	142	G
49	S1	145	A
49	S1	153	G
49	S1	155	U
49	S1	168	A
49	S1	171	A
49	S1	174	U
49	S1	176	C
49	S1	178	U
49	S1	179	A
49	S1	180	A
49	S1	185	U
49	S1	186	C
49	S1	187	G
49	S1	188	A
49	S1	191	C
49	S1	193	U
49	S1	195	G
49	S1	216	U
49	S1	218	A
49	S1	224	C
49	S1	225	A
49	S1	227	U
49	S1	228	G
49	S1	229	U
49	S1	230	C
49	S1	232	U
49	S1	233	C

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Mol	Chain	Res	Type
49	S1	234	G
49	S1	235	G
49	S1	240	U
49	S1	241	U
49	S1	250	C
49	S1	257	A
49	S1	260	U
49	S1	261	U
49	S1	265	A
49	S1	272	U
49	S1	274	G
49	S1	276	C
49	S1	277	U
49	S1	278	U
49	S1	279	G
49	S1	280	U
49	S1	281	G
49	S1	287	G
49	S1	299	A
49	S1	314	C
49	S1	316	A
49	S1	320	U
49	S1	322	G
49	S1	323	A
49	S1	330	G
49	S1	334	G
49	S1	337	G
49	S1	338	C
49	S1	352	A
49	S1	353	A
49	S1	359	A
49	S1	361	C
49	S1	373	G
49	S1	388	G
49	S1	390	G
49	S1	399	A
49	S1	400	A
49	S1	401	A
49	S1	402	C
49	S1	404	G
49	S1	416	A
49	S1	417	A

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Mol	Chain	Res	Type
49	S1	418	G
49	S1	419	G
49	S1	423	G
49	S1	424	C
49	S1	425	A
49	S1	426	G
49	S1	428	A
49	S1	434	G
49	S1	437	A
49	S1	439	U
49	S1	444	C
49	S1	445	A
49	S1	446	A
49	S1	448	C
49	S1	455	C
49	S1	459	G
49	S1	460	A
49	S1	468	A
49	S1	471	A
49	S1	477	A
49	S1	483	A
49	S1	485	A
49	S1	487	G
49	S1	489	C
49	S1	491	C
49	S1	492	A
49	S1	493	U
49	S1	494	U
49	S1	496	G
49	S1	498	G
49	S1	499	U
49	S1	500	C
49	S1	502	U
49	S1	505	A
49	S1	506	A
49	S1	507	U
49	S1	510	G
49	S1	511	A
49	S1	527	A
49	S1	534	A
49	S1	538	A
49	S1	539	G

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Mol	Chain	Res	Type
49	S1	540	G
49	S1	541	A
49	S1	542	A
49	S1	543	C
49	S1	544	A
49	S1	546	U
49	S1	555	A
49	S1	556	A
49	S1	557	G
49	S1	558	U
49	S1	559	C
49	S1	565	C
49	S1	568	G
49	S1	579	A
49	S1	580	A
49	S1	582	U
49	S1	583	C
49	S1	594	A
49	S1	595	G
49	S1	606	A
49	S1	609	U
49	S1	610	G
49	S1	611	U
49	S1	619	A
49	S1	620	A
49	S1	621	A
49	S1	622	A
49	S1	623	A
49	S1	624	G
49	S1	629	U
49	S1	630	A
49	S1	639	U
49	S1	640	U
49	S1	641	G
49	S1	643	G
49	S1	645	C
49	S1	650	U
49	S1	651	G
49	S1	653	C
49	S1	654	C
49	S1	655	G
49	S1	656	G

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Mol	Chain	Res	Type
49	S1	657	U
49	S1	677	G
49	S1	680	U
49	S1	681	U
49	S1	687	G
49	S1	694	U
49	S1	696	C
49	S1	697	C
49	S1	698	U
49	S1	699	U
49	S1	700	C
49	S1	702	G
49	S1	703	G
49	S1	704	C
49	S1	705	U
49	S1	706	A
49	S1	707	A
49	S1	708	C
49	S1	709	C
49	S1	710	U
49	S1	711	U
49	S1	712	G
49	S1	713	A
49	S1	714	G
49	S1	728	U
49	S1	729	G
49	S1	730	G
49	S1	732	G
49	S1	733	A
49	S1	734	A
49	S1	738	G
49	S1	741	C
49	S1	742	U
49	S1	743	U
49	S1	745	U
49	S1	753	A
49	S1	765	G
49	S1	766	U
49	S1	767	U
49	S1	771	A
49	S1	774	A
49	S1	775	G

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Mol	Chain	Res	Type
49	S1	778	G
49	S1	779	U
49	S1	780	A
49	S1	781	U
49	S1	782	U
49	S1	783	G
49	S1	787	G
49	S1	789	A
49	S1	812	A
49	S1	813	U
49	S1	814	A
49	S1	815	G
49	S1	816	G
49	S1	819	G
49	S1	820	U
49	S1	821	U
49	S1	823	G
49	S1	824	G
49	S1	832	U
49	S1	833	U
49	S1	835	U
49	S1	838	G
49	S1	840	U
49	S1	841	U
49	S1	846	G
49	S1	852	C
49	S1	855	A
49	S1	856	A
49	S1	857	U
49	S1	863	A
49	S1	899	G
49	S1	901	G
49	S1	902	G
49	S1	912	U
49	S1	913	G
49	S1	914	G
49	S1	921	U
49	S1	929	A
49	S1	933	A
49	S1	934	C
49	S1	935	U
49	S1	942	G

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Mol	Chain	Res	Type
49	S1	945	U
49	S1	960	U
49	S1	966	A
49	S1	970	A
49	S1	988	A
49	S1	992	A
49	S1	993	A
49	S1	1004	U
49	S1	1005	A
49	S1	1012	U
49	S1	1023	A
49	S1	1024	U
49	S1	1026	A
49	S1	1028	C
49	S1	1032	G
49	S1	1039	A
49	S1	1053	G
49	S1	1058	U
49	S1	1060	U
49	S1	1061	A
49	S1	1076	A
49	S1	1082	C
49	S1	1092	A
49	S1	1093	A
49	S1	1096	C
49	S1	1098	U
49	S1	1100	G
49	S1	1101	G
49	S1	1109	G
49	S1	1138	A
49	S1	1150	G
49	S1	1158	C
49	S1	1159	C
49	S1	1160	A
49	S1	1164	G
49	S1	1167	G
49	S1	1170	G
49	S1	1182	U
49	S1	1185	U
49	S1	1194	A
49	S1	1196	A
49	S1	1199	G

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Mol	Chain	Res	Type
49	S1	1200	G
49	S1	1202	A
49	S1	1207	C
49	S1	1216	C
49	S1	1217	A
49	S1	1218	G
49	S1	1227	A
49	S1	1229	G
49	S1	1241	G
49	S1	1243	G
49	S1	1244	A
49	S1	1245	G
49	S1	1246	C
49	S1	1252	C
49	S1	1256	A
49	S1	1257	U
49	S1	1274	C
49	S1	1275	A
49	S1	1285	U
49	S1	1286	U
49	S1	1291	G
49	S1	1301	U
49	S1	1307	U
49	S1	1314	U
49	S1	1316	G
49	S1	1318	G
49	S1	1321	A
49	S1	1322	A
49	S1	1325	A
49	S1	1337	A
49	S1	1344	A
49	S1	1345	A
49	S1	1346	A
49	S1	1348	A
49	S1	1349	G
49	S1	1361	U
49	S1	1363	U
49	S1	1364	G
49	S1	1367	G
49	S1	1370	U
49	S1	1371	A
49	S1	1373	C

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Mol	Chain	Res	Type
49	S1	1381	U
49	S1	1382	A
49	S1	1383	G
49	S1	1389	C
49	S1	1390	U
49	S1	1398	U
49	S1	1399	C
49	S1	1400	A
49	S1	1402	G
49	S1	1410	A
49	S1	1414	U
49	S1	1425	A
49	S1	1427	A
49	S1	1431	C
49	S1	1432	U
49	S1	1433	G
49	S1	1436	A
49	S1	1444	A
49	S1	1445	G
49	S1	1446	A
49	S1	1447	C
49	S1	1459	C
49	S1	1466	G
49	S1	1468	U
49	S1	1469	A
49	S1	1471	A
49	S1	1472	C
49	S1	1479	A
49	S1	1486	G
49	S1	1490	C
49	S1	1491	U
49	S1	1492	A
49	S1	1493	A
49	S1	1496	U
49	S1	1503	A
49	S1	1506	G
49	S1	1514	U
49	S1	1516	A
49	S1	1517	U
49	S1	1518	C
49	S1	1521	G
49	S1	1523	G

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Mol	Chain	Res	Type
49	S1	1524	A
49	S1	1528	U
49	S1	1535	U
49	S1	1536	G
49	S1	1537	C
49	S1	1540	G
49	S1	1543	A
49	S1	1554	U
49	S1	1556	A
49	S1	1558	U
49	S1	1559	A
49	S1	1570	A
49	S1	1572	G
49	S1	1573	A
49	S1	1574	G
49	S1	1575	G
49	S1	1576	A
49	S1	1577	A
49	S1	1583	A
49	S1	1584	G
49	S1	1585	U
49	S1	1590	G
49	S1	1601	G
49	S1	1607	G
49	S1	1611	A
49	S1	1616	G
49	S1	1622	G
49	S1	1631	A
49	S1	1634	C
49	S1	1635	A
49	S1	1636	C
49	S1	1637	C
49	S1	1657	U
49	S1	1658	G
49	S1	1682	U
49	S1	1688	U
49	S1	1697	G
49	S1	1701	A
49	S1	1703	C
49	S1	1709	C
49	S1	1715	G
49	S1	1716	C

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Mol	Chain	Res	Type
49	S1	1717	G
49	S1	1760	G
49	S1	1762	A
49	S1	1766	A
49	S1	1767	G
49	S1	1769	U
49	S1	1780	G
49	S1	1782	A
49	S1	1783	C
49	S1	1791	A
49	S1	1792	G
49	S1	1793	G
49	S1	1794	A
49	S1	1795	U
49	S1	1796	C
49	S1	1799	U
49	R1	2	A
49	R1	4	C
49	R1	25	C
49	R1	26	A
49	R1	27	U
49	R1	34	G
49	R1	42	G
49	R1	43	A
49	R1	45	U
49	R1	47	A
49	R1	57	G
49	R1	63	G
49	R1	68	A
49	R1	69	G
49	R1	72	A
49	R1	73	U
49	R1	74	U
49	R1	75	U
49	R1	77	U
49	R1	100	A
49	R1	104	A
49	R1	114	C
49	R1	115	G
49	R1	116	U
49	R1	127	G
49	R1	128	U

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Mol	Chain	Res	Type
49	R1	131	C
49	R1	132	U
49	R1	133	U
49	R1	134	U
49	R1	135	A
49	R1	136	C
49	R1	137	U
49	R1	138	A
49	R1	140	A
49	R1	141	U
49	R1	145	A
49	R1	146	U
49	R1	157	A
49	R1	158	U
49	R1	160	C
49	R1	165	G
49	R1	176	C
49	R1	178	U
49	R1	179	A
49	R1	184	C
49	R1	185	U
49	R1	190	C
49	R1	191	C
49	R1	192	U
49	R1	193	U
49	R1	195	G
49	R1	196	G
49	R1	197	A
49	R1	200	A
49	R1	215	A
49	R1	218	A
49	R1	219	A
49	R1	220	A
49	R1	226	A
49	R1	227	U
49	R1	228	G
49	R1	231	U
49	R1	232	U
49	R1	233	C
49	R1	234	G
49	R1	236	A
49	R1	237	C

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Mol	Chain	Res	Type
49	R1	238	U
49	R1	240	U
49	R1	241	U
49	R1	249	U
49	R1	261	U
49	R1	265	A
49	R1	272	U
49	R1	275	C
49	R1	277	U
49	R1	278	U
49	R1	279	G
49	R1	280	U
49	R1	281	G
49	R1	288	A
49	R1	299	A
49	R1	313	U
49	R1	314	C
49	R1	316	A
49	R1	320	U
49	R1	321	C
49	R1	333	A
49	R1	337	G
49	R1	338	C
49	R1	352	A
49	R1	359	A
49	R1	360	A
49	R1	361	C
49	R1	399	A
49	R1	400	A
49	R1	402	C
49	R1	404	G
49	R1	407	A
49	R1	409	C
49	R1	411	C
49	R1	415	C
49	R1	416	A
49	R1	417	A
49	R1	418	G
49	R1	423	G
49	R1	424	C
49	R1	425	A
49	R1	426	G

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Mol	Chain	Res	Type
49	R1	434	G
49	R1	435	C
49	R1	439	U
49	R1	444	C
49	R1	446	A
49	R1	448	C
49	R1	452	A
49	R1	475	A
49	R1	477	A
49	R1	480	G
49	R1	493	U
49	R1	496	G
49	R1	497	G
49	R1	498	G
49	R1	499	U
49	R1	500	C
49	R1	502	U
49	R1	503	G
49	R1	504	U
49	R1	505	A
49	R1	506	A
49	R1	510	G
49	R1	514	G
49	R1	515	A
49	R1	519	C
49	R1	527	A
49	R1	534	A
49	R1	539	G
49	R1	541	A
49	R1	543	C
49	R1	548	G
49	R1	555	A
49	R1	556	A
49	R1	558	U
49	R1	559	C
49	R1	565	C
49	R1	568	G
49	R1	578	U
49	R1	579	A
49	R1	585	A
49	R1	594	A
49	R1	595	G

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Mol	Chain	Res	Type
49	R1	611	U
49	R1	619	A
49	R1	620	A
49	R1	622	A
49	R1	623	A
49	R1	639	U
49	R1	640	U
49	R1	642	G
49	R1	648	G
49	R1	649	U
49	R1	650	U
49	R1	651	G
49	R1	654	C
49	R1	655	G
49	R1	656	G
49	R1	658	C
49	R1	677	G
49	R1	684	A
49	R1	685	A
49	R1	686	C
49	R1	693	U
49	R1	694	U
49	R1	695	U
49	R1	696	C
49	R1	697	C
49	R1	698	U
49	R1	702	G
49	R1	703	G
49	R1	704	C
49	R1	706	A
49	R1	707	A
49	R1	708	C
49	R1	709	C
49	R1	710	U
49	R1	711	U
49	R1	718	U
49	R1	719	U
49	R1	721	U
49	R1	722	G
49	R1	723	G
49	R1	725	U
49	R1	727	U

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Mol	Chain	Res	Type
49	R1	728	U
49	R1	731	C
49	R1	732	G
49	R1	733	A
49	R1	734	A
49	R1	736	C
49	R1	737	A
49	R1	738	G
49	R1	740	A
49	R1	743	U
49	R1	755	A
49	R1	756	A
49	R1	765	G
49	R1	766	U
49	R1	774	A
49	R1	775	G
49	R1	778	G
49	R1	781	U
49	R1	782	U
49	R1	783	G
49	R1	784	C
49	R1	787	G
49	R1	789	A
49	R1	794	U
49	R1	803	A
49	R1	813	U
49	R1	814	A
49	R1	815	G
49	R1	819	G
49	R1	820	U
49	R1	821	U
49	R1	823	G
49	R1	829	A
49	R1	830	U
49	R1	831	U
49	R1	833	U
49	R1	841	U
49	R1	846	G
49	R1	863	A
49	R1	876	G
49	R1	880	C
49	R1	881	A

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Mol	Chain	Res	Type
49	R1	884	A
49	R1	887	A
49	R1	898	A
49	R1	900	A
49	R1	901	G
49	R1	905	A
49	R1	906	A
49	R1	912	U
49	R1	913	G
49	R1	914	G
49	R1	922	G
49	R1	923	A
49	R1	924	A
49	R1	925	G
49	R1	926	A
49	R1	927	C
49	R1	928	U
49	R1	929	A
49	R1	933	A
49	R1	935	U
49	R1	942	G
49	R1	945	U
49	R1	946	U
49	R1	951	A
49	R1	960	U
49	R1	966	A
49	R1	970	A
49	R1	973	A
49	R1	976	G
49	R1	980	G
49	R1	981	U
49	R1	982	U
49	R1	983	A
49	R1	985	G
49	R1	986	G
49	R1	990	C
49	R1	991	G
49	R1	992	A
49	R1	993	A
49	R1	996	U
49	R1	997	G
49	R1	1004	U

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Mol	Chain	Res	Type
49	R1	1005	A
49	R1	1011	G
49	R1	1016	C
49	R1	1017	U
49	R1	1018	U
49	R1	1019	A
49	R1	1020	A
49	R1	1021	C
49	R1	1022	C
49	R1	1023	A
49	R1	1024	U
49	R1	1025	A
49	R1	1026	A
49	R1	1028	C
49	R1	1031	U
49	R1	1032	G
49	R1	1039	A
49	R1	1040	G
49	R1	1052	U
49	R1	1053	G
49	R1	1058	U
49	R1	1060	U
49	R1	1061	A
49	R1	1075	C
49	R1	1076	A
49	R1	1080	U
49	R1	1082	C
49	R1	1086	A
49	R1	1092	A
49	R1	1096	C
49	R1	1097	U
49	R1	1100	G
49	R1	1113	A
49	R1	1123	C
49	R1	1124	A
49	R1	1125	A
49	R1	1126	G
49	R1	1128	C
49	R1	1138	A
49	R1	1150	G
49	R1	1155	G
49	R1	1158	C

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Mol	Chain	Res	Type
49	R1	1160	A
49	R1	1163	A
49	R1	1167	G
49	R1	1174	C
49	R1	1175	U
49	R1	1185	U
49	R1	1194	A
49	R1	1196	A
49	R1	1199	G
49	R1	1200	G
49	R1	1201	G
49	R1	1202	A
49	R1	1207	C
49	R1	1217	A
49	R1	1218	G
49	R1	1220	C
49	R1	1225	U
49	R1	1228	G
49	R1	1229	G
49	R1	1230	A
49	R1	1241	G
49	R1	1242	A
49	R1	1243	G
49	R1	1244	A
49	R1	1245	G
49	R1	1252	C
49	R1	1255	G
49	R1	1256	A
49	R1	1257	U
49	R1	1258	U
49	R1	1284	C
49	R1	1286	U
49	R1	1314	U
49	R1	1315	U
49	R1	1321	A
49	R1	1338	C
49	R1	1341	A
49	R1	1344	A
49	R1	1345	A
49	R1	1354	G
49	R1	1359	C
49	R1	1360	A

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Mol	Chain	Res	Type
49	R1	1361	U
49	R1	1362	U
49	R1	1363	U
49	R1	1367	G
49	R1	1370	U
49	R1	1371	A
49	R1	1372	U
49	R1	1390	U
49	R1	1396	U
49	R1	1398	U
49	R1	1399	C
49	R1	1400	A
49	R1	1413	U
49	R1	1415	U
49	R1	1422	A
49	R1	1427	A
49	R1	1428	G
49	R1	1432	U
49	R1	1436	A
49	R1	1445	G
49	R1	1446	A
49	R1	1448	G
49	R1	1452	U
49	R1	1458	G
49	R1	1459	C
49	R1	1460	A
49	R1	1466	G
49	R1	1471	A
49	R1	1474	G
49	R1	1481	C
49	R1	1482	C
49	R1	1486	G
49	R1	1490	C
49	R1	1491	U
49	R1	1492	A
49	R1	1493	A
49	R1	1496	U
49	R1	1506	G
49	R1	1514	U
49	R1	1516	A
49	R1	1521	G
49	R1	1523	G

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Mol	Chain	Res	Type
49	R1	1524	A
49	R1	1529	C
49	R1	1534	G
49	R1	1536	G
49	R1	1537	C
49	R1	1538	U
49	R1	1542	G
49	R1	1557	U
49	R1	1559	A
49	R1	1569	A
49	R1	1574	G
49	R1	1575	G
49	R1	1584	G
49	R1	1596	C
49	R1	1598	U
49	R1	1601	G
49	R1	1607	G
49	R1	1616	G
49	R1	1619	C
49	R1	1634	C
49	R1	1635	A
49	R1	1643	U
49	R1	1657	U
49	R1	1658	G
49	R1	1665	U
49	R1	1666	U
49	R1	1667	A
49	R1	1668	G
49	R1	1669	U
49	R1	1670	G
49	R1	1671	A
49	R1	1672	G
49	R1	1678	A
49	R1	1680	G
49	R1	1681	A
49	R1	1682	U
49	R1	1715	G
49	R1	1716	C
49	R1	1717	G
49	R1	1728	A
49	R1	1729	C
49	R1	1730	A

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Mol	Chain	Res	Type
49	R1	1731	A
49	R1	1732	A
49	R1	1733	C
49	R1	1734	U
49	R1	1736	G
49	R1	1737	G
49	R1	1738	U
49	R1	1741	U
49	R1	1743	U
49	R1	1750	A
49	R1	1755	A
49	R1	1757	G
49	R1	1760	G
49	R1	1766	A
49	R1	1767	G
49	R1	1769	U
49	R1	1780	G
49	R1	1781	A
49	R1	1782	A
49	R1	1786	G
49	R1	1792	G
49	R1	1793	G
49	R1	1794	A
49	R1	1795	U
49	R1	1796	C
49	R1	1797	A
49	R1	1799	U
49	R1	1800	A
87	M1	4	U
87	M1	6	A
87	M1	21	G
87	M1	26	A
87	M1	40	A
87	M1	43	A
87	M1	49	A
87	M1	59	G
87	M1	60	A
87	M1	65	A
87	M1	66	A
87	M1	86	G
87	M1	92	G
87	M1	99	A

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Mol	Chain	Res	Type
87	M1	110	G
87	M1	111	C
87	M1	116	A
87	M1	117	U
87	M1	122	A
87	M1	135	C
87	M1	136	G
87	M1	147	U
87	M1	156	G
87	M1	157	A
87	M1	174	C
87	M1	190	U
87	M1	200	C
87	M1	211	A
87	M1	219	A
87	M1	220	G
87	M1	241	G
87	M1	243	G
87	M1	249	U
87	M1	251	G
87	M1	252	U
87	M1	269	G
87	M1	286	U
87	M1	295	A
87	M1	305	U
87	M1	329	U
87	M1	337	G
87	M1	349	A
87	M1	374	A
87	M1	376	G
87	M1	398	A
87	M1	401	U
87	M1	402	A
87	M1	403	C
87	M1	420	G
87	M1	421	G
87	M1	422	A
87	M1	521	A
87	M1	532	A
87	M1	533	A
87	M1	534	U
87	M1	545	U

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Mol	Chain	Res	Type
87	M1	548	G
87	M1	555	U
87	M1	557	A
87	M1	558	U
87	M1	559	A
87	M1	560	G
87	M1	592	A
87	M1	602	A
87	M1	607	A
87	M1	611	A
87	M1	620	U
87	M1	621	A
87	M1	636	C
87	M1	649	A2M
87	M1	660	A
87	M1	677	A
87	M1	678	G
87	M1	680	G
87	M1	681	U
87	M1	691	A
87	M1	705	A
87	M1	712	G
87	M1	715	A
87	M1	719	U
87	M1	758	C
87	M1	763	G
87	M1	766	U
87	M1	767	U
87	M1	776	U
87	M1	781	G
87	M1	785	G
87	M1	786	A
87	M1	817	A2M
87	M1	830	A
87	M1	849	C
87	M1	861	C
87	M1	869	G
87	M1	874	U
87	M1	879	U
87	M1	880	G
87	M1	896	A
87	M1	907	G

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Mol	Chain	Res	Type
87	M1	908	OMG
87	M1	914	A
87	M1	916	G
87	M1	917	A
87	M1	921	A
87	M1	923	C
87	M1	924	G
87	M1	925	A
87	M1	937	G
87	M1	938	C
87	M1	944	C
87	M1	953	G
87	M1	959	C
87	M1	960	U
87	M1	961	C
87	M1	964	G
87	M1	980	A
87	M1	982	C
87	M1	993	G
87	M1	995	U
87	M1	1000	C
87	M1	1015	U
87	M1	1017	C
87	M1	1018	G
87	M1	1023	C
87	M1	1026	A
87	M1	1027	A
87	M1	1028	U
87	M1	1029	G
87	M1	1032	C
87	M1	1034	U
87	M1	1036	A
87	M1	1037	C
87	M1	1047	A
87	M1	1064	A
87	M1	1066	G
87	M1	1072	G
87	M1	1081	U
87	M1	1083	G
87	M1	1087	G
87	M1	1096	U
87	M1	1097	G

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Mol	Chain	Res	Type
87	M1	1098	A
87	M1	1103	A
87	M1	1104	G
87	M1	1117	G
87	M1	1131	G
87	M1	1143	A
87	M1	1144	U
87	M1	1153	A
87	M1	1159	A
87	M1	1178	G
87	M1	1179	A
87	M1	1180	A
87	M1	1181	U
87	M1	1182	A
87	M1	1191	U
87	M1	1193	A
87	M1	1196	C
87	M1	1201	C
87	M1	1208	U
87	M1	1209	G
87	M1	1222	G
87	M1	1231	A
87	M1	1235	U
87	M1	1236	G
87	M1	1237	G
87	M1	1244	A
87	M1	1245	A
87	M1	1246	G
87	M1	1249	G
87	M1	1253	U
87	M1	1254	C
87	M1	1257	C
87	M1	1258	U
87	M1	1262	G
87	M1	1263	A
87	M1	1264	G
87	M1	1265	U
87	M1	1272	C
87	M1	1275	C
87	M1	1281	G
87	M1	1284	C
87	M1	1285	G

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Mol	Chain	Res	Type
87	M1	1286	A
87	M1	1287	A
87	M1	1302	A
87	M1	1307	G
87	M1	1308	A
87	M1	1309	U
87	M1	1313	G
87	M1	1330	A
87	M1	1345	G
87	M1	1348	U
87	M1	1349	G
87	M1	1351	U
87	M1	1352	A
87	M1	1353	U
87	M1	1355	A
87	M1	1356	U
87	M1	1357	G
87	M1	1386	A
87	M1	1391	C
87	M1	1392	G
87	M1	1399	A
87	M1	1400	G
87	M1	1418	A
87	M1	1421	G
87	M1	1425	U
87	M1	1434	G
87	M1	1437	OMC
87	M1	1446	A
87	M1	1450	OMG
87	M1	1469	C
87	M1	1481	A
87	M1	1483	G
87	M1	1484	U
87	M1	1487	G
87	M1	1496	C
87	M1	1502	C
87	M1	1508	C
87	M1	1525	G
87	M1	1536	G
87	M1	1539	A
87	M1	1555	U
87	M1	1556	C

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Mol	Chain	Res	Type
87	M1	1560	G
87	M1	1561	G
87	M1	1562	C
87	M1	1563	C
87	M1	1566	A
87	M1	1568	U
87	M1	1569	U
87	M1	1571	A
87	M1	1572	U
87	M1	1573	G
87	M1	1575	A
87	M1	1580	A
87	M1	1581	C
87	M1	1583	A
87	M1	1587	A
87	M1	1589	A
87	M1	1590	G
87	M1	1593	A
87	M1	1605	A
87	M1	1629	U
87	M1	1630	U
87	M1	1642	A
87	M1	1643	A
87	M1	1645	U
87	M1	1657	C
87	M1	1683	A
87	M1	1688	U
87	M1	1716	U
87	M1	1724	U
87	M1	1730	G
87	M1	1741	A
87	M1	1742	U
87	M1	1750	A
87	M1	1751	G
87	M1	1759	C
87	M1	1762	C
87	M1	1763	U
87	M1	1765	U
87	M1	1769	G
87	M1	1775	G
87	M1	1780	G
87	M1	1797	A

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Mol	Chain	Res	Type
87	M1	1808	G
87	M1	1812	G
87	M1	1813	A
87	M1	1815	U
87	M1	1816	A
87	M1	1817	G
87	M1	1821	U
87	M1	1842	A
87	M1	1858	A
87	M1	1866	C
87	M1	1867	A
87	M1	1878	G
87	M1	1879	A
87	M1	1880	U
87	M1	1893	A
87	M1	1899	G
87	M1	1906	G
87	M1	2102	U
87	M1	2110	G
87	M1	2111	G
87	M1	2112	U
87	M1	2114	C
87	M1	2122	G
87	M1	2131	A
87	M1	2140	U
87	M1	2144	A
87	M1	2146	C
87	M1	2158	A
87	M1	2168	A
87	M1	2169	G
87	M1	2170	U
87	M1	2171	G
87	M1	2176	U
87	M1	2188	A
87	M1	2207	A
87	M1	2209	U
87	M1	2223	A
87	M1	2225	U
87	M1	2244	A
87	M1	2254	U
87	M1	2267	C
87	M1	2268	U

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Mol	Chain	Res	Type
87	M1	2269	U
87	M1	2271	A
87	M1	2273	G
87	M1	2281	A2M
87	M1	2282	U
87	M1	2304	C
87	M1	2307	G
87	M1	2310	U
87	M1	2313	A
87	M1	2315	G
87	M1	2334	U
87	M1	2335	G
87	M1	2336	U
87	M1	2363	A
87	M1	2372	A
87	M1	2373	A
87	M1	2374	C
87	M1	2375	G
87	M1	2388	U
87	M1	2393	G
87	M1	2394	G
87	M1	2397	A
87	M1	2401	A
87	M1	2402	A
87	M1	2403	G
87	M1	2404	A
87	M1	2411	U
87	M1	2412	G
87	M1	2418	G
87	M1	2419	A
87	M1	2435	G
87	M1	2438	A
87	M1	2444	C
87	M1	2447	A
87	M1	2450	G
87	M1	2453	U
87	M1	2454	G
87	M1	2459	A
87	M1	2460	U
87	M1	2461	A
87	M1	2462	A
87	M1	2464	U

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Mol	Chain	Res	Type
87	M1	2465	G
87	M1	2466	G
87	M1	2467	G
87	M1	2468	A
87	M1	2470	C
87	M1	2471	U
87	M1	2472	U
87	M1	2474	G
87	M1	2475	G
87	M1	2476	C
87	M1	2477	G
87	M1	2478	C
87	M1	2479	C
87	M1	2480	A
87	M1	2488	A
87	M1	2489	C
87	M1	2490	C
87	M1	2492	C
87	M1	2493	U
87	M1	2494	A
87	M1	2495	C
87	M1	2496	C
87	M1	2499	U
87	M1	2501	U
87	M1	2511	A
87	M1	2514	U
87	M1	2515	A
87	M1	2522	G
87	M1	2523	A
87	M1	2552	C
87	M1	2554	A
87	M1	2555	G
87	M1	2560	C
87	M1	2561	A
87	M1	2569	A
87	M1	2570	U
87	M1	2571	U
87	M1	2572	C
87	M1	2573	G
87	M1	2585	G
87	M1	2593	A
87	M1	2606	G

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Mol	Chain	Res	Type
87	M1	2607	G
87	M1	2614	G
87	M1	2651	G
87	M1	2652	U
87	M1	2656	A
87	M1	2672	G
87	M1	2674	A
87	M1	2677	G
87	M1	2678	A
87	M1	2689	A
87	M1	2691	A
87	M1	2696	A
87	M1	2704	A
87	M1	2705	A
87	M1	2714	G
87	M1	2728	G
87	M1	2753	G
87	M1	2755	C
87	M1	2772	C
87	M1	2777	G
87	M1	2778	G
87	M1	2793	OMG
87	M1	2795	U
87	M1	2796	G
87	M1	2799	A
87	M1	2800	G
87	M1	2801	A
87	M1	2802	A
87	M1	2808	A
87	M1	2809	C
87	M1	2810	C
87	M1	2814	G
87	M1	2817	A
87	M1	2844	C
87	M1	2845	A
87	M1	2860	U
87	M1	2861	U
87	M1	2871	G
87	M1	2872	A
87	M1	2875	U
87	M1	2876	C
87	M1	2887	A

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Mol	Chain	Res	Type
87	M1	2889	C
87	M1	2899	C
87	M1	2914	G
87	M1	2922	OMG
87	M1	2935	U
87	M1	2936	A
87	M1	2942	C
87	M1	2943	G
87	M1	2947	G
87	M1	2951	G
87	M1	2971	A
87	M1	2972	G
87	M1	2977	G
87	M1	2983	C
87	M1	2990	G
87	M1	2996	U
87	M1	2997	G
87	M1	3012	A
87	M1	3049	A
87	M1	3056	U
87	M1	3059	G
87	M1	3078	U
87	M1	3080	G
87	M1	3092	C
87	M1	3122	A
87	M1	3130	A
87	M1	3131	U
87	M1	3142	A
87	M1	3143	C
87	M1	3153	U
87	M1	3154	C
87	M1	3155	U
87	M1	3156	U
87	M1	3157	U
87	M1	3168	A
87	M1	3170	A
87	M1	3172	A
87	M1	3173	G
87	M1	3176	G
87	M1	3179	U
87	M1	3181	C
87	M1	3187	A

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Mol	Chain	Res	Type
87	M1	3199	G
87	M1	3207	U
87	M1	3210	A
87	M1	3216	G
87	M1	3217	C
87	M1	3218	A
87	M1	3219	G
87	M1	3243	A
87	M1	3247	G
87	M1	3273	A
87	M1	3276	G
87	M1	3277	U
87	M1	3278	C
87	M1	3281	U
87	M1	3294	A
87	M1	3303	G
87	M1	3304	U
87	M1	3313	U
87	M1	3316	A
87	M1	3320	A
87	M1	3341	U
87	M1	3345	G
87	M1	3351	U
87	M1	3352	U
87	M1	3353	G
87	M1	3369	G
87	M1	3378	C
87	M1	3382	U
87	M1	3386	G
87	M1	3389	U
87	M1	3390	G
7	M3	7	G
7	M3	11	A
7	M3	54	U
7	M3	55	A
7	M3	65	G
7	M3	73	C
7	M3	74	C
7	M3	76	A
7	M3	91	G
7	M3	99	G
7	M3	112	G

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Mol	Chain	Res	Type
6	M2	23	U
6	M2	34	U
6	M2	35	C
6	M2	38	U
6	M2	39	G
6	M2	52	A
6	M2	59	A
6	M2	62	C
6	M2	63	G
6	M2	75	G
6	M2	82	U
6	M2	83	C
6	M2	84	C
6	M2	86	U
6	M2	87	G
6	M2	91	C
6	M2	95	G
6	M2	104	A
6	M2	106	C
6	M2	113	U
6	M2	125	U
6	M2	126	A
6	M2	152	G
6	M2	155	A
88	DQ	8	U
88	DQ	10	G
88	DQ	18	C
88	DQ	19	G
88	DQ	20	G
88	DQ	21	U
88	DQ	22	A
88	DQ	48	U
88	DQ	49	C
88	DQ	56	U
88	DQ	62	C
88	DQ	63	C
88	DQ	77	A
91	DP	6	U
91	DP	8	U
91	DP	9	A
91	DP	10	G
91	DP	15	G

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Mol	Chain	Res	Type
91	DP	16	U
91	DP	17	U
91	DP	18	G
91	DP	19	G
91	DP	21	A
91	DP	22	G
91	DP	24	G
91	DP	30	G
91	DP	34	G
91	DP	36	A
91	DP	41	U
91	DP	46	G
91	DP	47	U
91	DP	48	C
91	DP	59	U
91	DP	62	A
91	DP	63	C
91	DP	65	G
91	DP	70	C
91	DP	74	C
91	DP	75	C

All (115) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	CM	21	U
5	L1	13	A
5	L1	65	A
5	L1	239	G
5	L1	282	G
5	L1	406	G
5	L1	588	G
5	L1	637	C
5	L1	715	A
5	L1	763	G
5	L1	846	A
5	L1	916	G
5	L1	1064	A
5	L1	1097	G
5	L1	1355	A
5	L1	1554	U
5	L1	1562	C

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Mol	Chain	Res	Type
5	L1	1607	U
5	L1	1716	U
5	L1	1815	U
5	L1	1820	U
5	L1	2101	C
5	L1	2112	U
5	L1	2525	G
5	L1	2875	U
5	L1	3121	U
5	L1	3140	G
5	L1	3218	A
5	L1	3228	C
5	L1	3269	U
5	L1	3319	U
5	L1	3350	C
5	L1	3351	U
5	L1	3375	A
6	L2	85	G
7	L3	52	G
49	S1	68	A
49	S1	77	U
49	S1	139	C
49	S1	141	U
49	S1	278	U
49	S1	280	U
49	S1	313	U
49	S1	322	G
49	S1	352	A
49	S1	387	A
49	S1	400	A
49	S1	539	G
49	S1	541	A
49	S1	555	A
49	S1	609	U
49	S1	639	U
49	S1	640	U
49	S1	705	U
49	S1	711	U
49	S1	765	G
49	S1	819	G
49	S1	928	U
49	S1	1023	A

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Mol	Chain	Res	Type
49	S1	1226	A
49	S1	1256	A
49	S1	1273	G
49	S1	1274	C
49	S1	1344	A
49	S1	1382	A
49	S1	1430	U
49	S1	1471	A
49	S1	1573	A
49	S1	1584	G
49	S1	1615	C
49	S1	1633	A
49	S1	1636	C
49	S1	1791	A
49	R1	73	U
49	R1	130	C
49	R1	132	U
49	R1	139	C
49	R1	218	A
49	R1	240	U
49	R1	278	U
49	R1	408	C
49	R1	417	A
49	R1	501	U
49	R1	503	G
49	R1	555	A
49	R1	641	G
49	R1	685	A
49	R1	720	G
49	R1	721	U
49	R1	829	A
49	R1	924	A
49	R1	1244	A
49	R1	1255	G
49	R1	1344	A
49	R1	1451	C
49	R1	1481	C
49	R1	1535	U
49	R1	1568	C
49	R1	1573	A
87	M1	601	U
87	M1	619	A

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Mol	Chain	Res	Type
87	M1	873	C
87	M1	916	G
87	M1	1033	U
87	M1	1562	C
87	M1	2101	C
87	M1	2253	G
87	M1	2372	A
87	M1	2487	U
87	M1	2500	A
87	M1	2792	A
87	M1	2971	A
87	M1	3121	U
7	M3	72	A
91	DP	69	U

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
87	A2M	M1	2220	87	22,25,26	3.56	10 (45%)	30,36,39	3.86	13 (43%)
87	OMG	M1	2793	87	23,26,27	0.64	0	32,38,41	0.51	0
87	OMG	M1	2288	87	23,26,27	0.61	0	32,38,41	0.59	0
87	A2M	M1	1133	92,87	22,25,26	3.56	10 (45%)	30,36,39	3.77	14 (46%)
87	OMU	M1	2921	87	19,22,23	3.00	8 (42%)	25,31,34	1.86	5 (20%)
87	OMC	M1	663	87	19,22,23	0.67	0	25,31,34	0.94	1 (4%)
87	OMC	M1	2948	87	19,22,23	0.66	0	25,31,34	0.95	2 (8%)
87	OMU	M1	898	87	19,22,23	2.92	8 (42%)	25,31,34	1.80	5 (20%)
87	OMU	M1	2729	87	19,22,23	2.91	7 (36%)	25,31,34	1.93	5 (20%)
87	OMG	M1	2791	87	23,26,27	0.55	0	32,38,41	0.54	0
87	OMC	M1	650	92,87	19,22,23	0.73	1 (5%)	25,31,34	0.73	0
87	A2M	M1	876	87	22,25,26	3.52	10 (45%)	30,36,39	3.89	13 (43%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
87	OMG	M1	2619	87	23,26,27	0.57	0	32,38,41	0.50	0
87	OMC	M1	2959	87	19,22,23	0.66	0	25,31,34	0.83	1 (4%)
87	A2M	M1	2281	87	22,25,26	3.47	10 (45%)	30,36,39	3.82	14 (46%)
87	5MC	M1	2278	92,87	19,22,23	0.75	1 (5%)	26,32,35	1.05	2 (7%)
87	OMC	M1	2337	87	19,22,23	0.70	0	25,31,34	0.74	0
87	OMU	M1	2347	87	19,22,23	3.02	7 (36%)	25,31,34	1.90	5 (20%)
87	1MA	M1	2142	92,87	21,25,26	0.71	0	30,37,40	0.92	2 (6%)
87	OMG	M1	2815	87	23,26,27	0.59	0	32,38,41	0.54	0
87	UR3	M1	2634	87	19,22,23	3.04	8 (42%)	26,32,35	1.76	4 (15%)
87	OMG	M1	908	87	23,26,27	0.55	0	32,38,41	0.63	0
87	A2M	M1	2640	87	22,25,26	3.52	10 (45%)	30,36,39	3.84	14 (46%)
87	5MC	M1	2870	94,87	19,22,23	0.84	1 (5%)	26,32,35	0.78	0
87	A2M	M1	2256	87	22,25,26	3.55	10 (45%)	30,36,39	4.09	16 (53%)
87	A2M	M1	649	87	22,25,26	3.46	10 (45%)	30,36,39	3.89	15 (50%)
87	1MA	M1	645	92,87	21,25,26	0.66	0	30,37,40	0.77	1 (3%)
87	A2M	M1	807	87	22,25,26	3.55	10 (45%)	30,36,39	4.03	13 (43%)
87	OMG	M1	1450	87	23,26,27	0.59	0	32,38,41	0.50	0
87	OMU	M1	1888	87	19,22,23	2.98	8 (42%)	25,31,34	1.91	5 (20%)
87	OMG	M1	805	87	23,26,27	0.60	0	32,38,41	0.67	1 (3%)
87	A2M	M1	1449	92,87	22,25,26	3.55	10 (45%)	30,36,39	3.86	13 (43%)
87	OMU	M1	2417	87	19,22,23	2.83	7 (36%)	25,31,34	1.90	5 (20%)
87	A2M	M1	2946	92,87	22,25,26	3.46	10 (45%)	30,36,39	3.77	14 (46%)
87	OMG	M1	867	94,87	23,26,27	0.62	0	32,38,41	0.58	0
87	OMU	M1	2724	87	19,22,23	2.93	8 (42%)	25,31,34	1.82	5 (20%)
87	A2M	M1	817	92,87	22,25,26	3.58	10 (45%)	30,36,39	3.89	13 (43%)
91	YYG	DP	37	91	38,42,43	0.67	0	45,62,65	1.31	7 (15%)
87	OMC	M1	1437	92,87	19,22,23	0.69	0	25,31,34	1.03	1 (4%)
87	OMG	M1	2922	91,87	23,26,27	0.57	0	32,38,41	0.46	0
87	OMC	M1	2197	94,87	19,22,23	0.72	1 (5%)	25,31,34	0.67	0
87	A2M	M1	2280	87	22,25,26	3.52	10 (45%)	30,36,39	3.81	13 (43%)
87	OMU	M1	2421	87	19,22,23	2.85	7 (36%)	25,31,34	1.96	5 (20%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
87	A2M	M1	2220	87	-	1/9/27/28	0/3/3/3
87	OMG	M1	2793	87	-	0/9/27/28	0/3/3/3
87	OMG	M1	2288	87	-	0/9/27/28	0/3/3/3
87	A2M	M1	1133	92,87	-	0/9/27/28	0/3/3/3
87	OMU	M1	2921	87	-	0/9/27/28	0/2/2/2
87	OMC	M1	663	87	-	0/9/27/28	0/2/2/2
87	OMC	M1	2948	87	-	0/9/27/28	0/2/2/2
87	OMU	M1	898	87	-	0/9/27/28	0/2/2/2
87	OMU	M1	2729	87	-	0/9/27/28	0/2/2/2
87	OMG	M1	2791	87	-	0/9/27/28	0/3/3/3
87	OMC	M1	650	92,87	-	0/9/27/28	0/2/2/2
87	A2M	M1	876	87	-	0/9/27/28	0/3/3/3
87	OMG	M1	2619	87	-	3/9/27/28	0/3/3/3
87	OMC	M1	2959	87	-	0/9/27/28	0/2/2/2
87	A2M	M1	2281	87	-	2/9/27/28	0/3/3/3
87	5MC	M1	2278	92,87	-	2/7/25/26	0/2/2/2
87	OMC	M1	2337	87	-	0/9/27/28	0/2/2/2
87	OMU	M1	2347	87	-	1/9/27/28	0/2/2/2
87	1MA	M1	2142	92,87	-	0/7/25/26	0/3/3/3
87	OMG	M1	2815	87	-	0/9/27/28	0/3/3/3
87	UR3	M1	2634	87	-	0/7/25/26	0/2/2/2
87	OMG	M1	908	87	-	0/9/27/28	0/3/3/3
87	A2M	M1	2640	87	-	0/9/27/28	0/3/3/3
87	5MC	M1	2870	94,87	-	3/7/25/26	0/2/2/2
87	A2M	M1	2256	87	-	2/9/27/28	0/3/3/3
87	A2M	M1	649	87	-	2/9/27/28	0/3/3/3
87	1MA	M1	645	92,87	-	0/7/25/26	0/3/3/3
87	A2M	M1	807	87	-	1/9/27/28	0/3/3/3
87	OMG	M1	1450	87	-	2/9/27/28	0/3/3/3
87	OMU	M1	1888	87	-	0/9/27/28	0/2/2/2
87	OMG	M1	805	87	-	0/9/27/28	0/3/3/3
87	A2M	M1	1449	92,87	-	0/9/27/28	0/3/3/3
87	OMU	M1	2417	87	-	1/9/27/28	0/2/2/2
87	A2M	M1	2946	92,87	-	1/9/27/28	0/3/3/3
87	OMG	M1	867	94,87	-	0/9/27/28	0/3/3/3
87	OMU	M1	2724	87	-	1/9/27/28	0/2/2/2
87	A2M	M1	817	92,87	-	2/9/27/28	0/3/3/3
91	YYG	DP	37	91	-	7/24/42/43	0/4/4/4
87	OMC	M1	1437	92,87	-	2/9/27/28	0/2/2/2
87	OMG	M1	2922	91,87	-	3/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
87	OMC	M1	2197	94,87	-	4/9/27/28	0/2/2/2
87	A2M	M1	2280	87	-	2/9/27/28	0/3/3/3
87	OMU	M1	2421	87	-	0/9/27/28	0/2/2/2

All (192) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
87	M1	817	A2M	C2'-C1'	-9.31	1.30	1.53
87	M1	1449	A2M	C2'-C1'	-9.05	1.30	1.53
87	M1	2220	A2M	C2'-C1'	-9.05	1.30	1.53
87	M1	2256	A2M	C2'-C1'	-9.00	1.31	1.53
87	M1	2640	A2M	C2'-C1'	-8.99	1.31	1.53
87	M1	2281	A2M	C2'-C1'	-8.99	1.31	1.53
87	M1	1133	A2M	C2'-C1'	-8.97	1.31	1.53
87	M1	876	A2M	C2'-C1'	-8.90	1.31	1.53
87	M1	807	A2M	C2'-C1'	-8.86	1.31	1.53
87	M1	649	A2M	C2'-C1'	-8.79	1.31	1.53
87	M1	2280	A2M	O4'-C1'	8.74	1.62	1.42
87	M1	2220	A2M	O4'-C1'	8.72	1.62	1.42
87	M1	1449	A2M	O4'-C1'	8.70	1.62	1.42
87	M1	2280	A2M	C2'-C1'	-8.69	1.31	1.53
87	M1	1133	A2M	O4'-C1'	8.67	1.62	1.42
87	M1	876	A2M	O4'-C1'	8.67	1.62	1.42
87	M1	2946	A2M	C2'-C1'	-8.64	1.31	1.53
87	M1	2640	A2M	O4'-C1'	8.61	1.61	1.42
87	M1	2946	A2M	O4'-C1'	8.61	1.61	1.42
87	M1	817	A2M	O4'-C1'	8.47	1.61	1.42
87	M1	2256	A2M	O4'-C1'	8.41	1.61	1.42
87	M1	807	A2M	O4'-C1'	8.36	1.61	1.42
87	M1	649	A2M	O4'-C1'	8.33	1.61	1.42
87	M1	2281	A2M	O4'-C1'	7.99	1.60	1.42
87	M1	2634	UR3	C2-N1	7.40	1.48	1.38
87	M1	2347	OMU	C2-N1	7.37	1.50	1.38
87	M1	2921	OMU	C2-N1	6.96	1.49	1.38
87	M1	1888	OMU	C2-N1	6.90	1.49	1.38
87	M1	807	A2M	O4'-C4'	-6.87	1.29	1.45
87	M1	817	A2M	O4'-C4'	-6.80	1.29	1.45
87	M1	2921	OMU	C2-N3	6.70	1.49	1.38
87	M1	1888	OMU	C2-N3	6.67	1.49	1.38
87	M1	2347	OMU	C2-N3	6.67	1.49	1.38
87	M1	2280	A2M	O4'-C4'	-6.63	1.30	1.45
87	M1	898	OMU	C2-N1	6.61	1.48	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
87	M1	2724	OMU	C2-N3	6.60	1.49	1.38
87	M1	2729	OMU	C2-N1	6.60	1.48	1.38
87	M1	1449	A2M	O4'-C4'	-6.59	1.30	1.45
87	M1	2724	OMU	C2-N1	6.59	1.48	1.38
87	M1	1133	A2M	O4'-C4'	-6.57	1.30	1.45
87	M1	2634	UR3	C6-C5	6.56	1.50	1.35
87	M1	2421	OMU	C2-N3	6.54	1.49	1.38
87	M1	876	A2M	O4'-C4'	-6.54	1.30	1.45
87	M1	2281	A2M	O4'-C4'	-6.51	1.30	1.45
87	M1	898	OMU	C2-N3	6.51	1.49	1.38
87	M1	2729	OMU	C2-N3	6.48	1.49	1.38
87	M1	2417	OMU	C2-N3	6.47	1.49	1.38
87	M1	2220	A2M	O4'-C4'	-6.47	1.30	1.45
87	M1	649	A2M	O4'-C4'	-6.46	1.30	1.45
87	M1	2256	A2M	O4'-C4'	-6.44	1.30	1.45
87	M1	2640	A2M	O4'-C4'	-6.44	1.30	1.45
87	M1	2421	OMU	C2-N1	6.43	1.48	1.38
87	M1	2946	A2M	O4'-C4'	-6.36	1.30	1.45
87	M1	2417	OMU	C2-N1	6.26	1.48	1.38
87	M1	2724	OMU	C6-C5	5.57	1.48	1.35
87	M1	898	OMU	C6-C5	5.54	1.47	1.35
87	M1	2921	OMU	C6-C5	5.46	1.47	1.35
87	M1	1888	OMU	C6-C5	5.41	1.47	1.35
87	M1	2421	OMU	C6-C5	5.35	1.47	1.35
87	M1	2729	OMU	C6-C5	5.32	1.47	1.35
87	M1	2347	OMU	C6-C5	5.30	1.47	1.35
87	M1	2634	UR3	C2-N3	5.28	1.49	1.39
87	M1	2417	OMU	C6-C5	5.28	1.47	1.35
87	M1	2220	A2M	C6-N6	4.37	1.45	1.34
87	M1	2256	A2M	C6-N6	4.37	1.45	1.34
87	M1	876	A2M	C6-N6	4.31	1.45	1.34
87	M1	2280	A2M	C6-N6	4.30	1.45	1.34
87	M1	807	A2M	C6-N6	4.26	1.45	1.34
87	M1	1449	A2M	C6-N6	4.18	1.44	1.34
87	M1	2640	A2M	C6-N6	4.16	1.44	1.34
87	M1	649	A2M	C6-N6	4.14	1.44	1.34
87	M1	1133	A2M	C6-N6	4.13	1.44	1.34
87	M1	817	A2M	C6-N6	4.12	1.44	1.34
87	M1	2921	OMU	C4-N3	4.08	1.45	1.38
87	M1	2946	A2M	C6-N6	4.08	1.44	1.34
87	M1	2281	A2M	C5-C4	-3.98	1.32	1.39
87	M1	2724	OMU	C4-N3	3.81	1.45	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
87	M1	2347	OMU	C4-N3	3.79	1.45	1.38
87	M1	1888	OMU	C4-N3	3.77	1.45	1.38
87	M1	2281	A2M	C6-N6	3.77	1.43	1.34
87	M1	2634	UR3	O2-C2	-3.75	1.15	1.22
87	M1	2729	OMU	C4-N3	3.74	1.45	1.38
87	M1	2256	A2M	O2'-C2'	3.56	1.51	1.42
87	M1	2729	OMU	O4-C4	-3.53	1.17	1.24
87	M1	898	OMU	C4-N3	3.49	1.44	1.38
87	M1	2417	OMU	C4-N3	3.49	1.44	1.38
87	M1	2634	UR3	C6-N1	3.49	1.46	1.38
87	M1	807	A2M	C5-C4	-3.48	1.32	1.39
87	M1	2421	OMU	C4-N3	3.47	1.44	1.38
87	M1	2280	A2M	C5-C4	-3.45	1.32	1.39
87	M1	817	A2M	C5-C4	-3.43	1.33	1.39
87	M1	2347	OMU	O4-C4	-3.41	1.17	1.24
87	M1	2640	A2M	C5-C4	-3.39	1.33	1.39
87	M1	2256	A2M	C5-C4	-3.38	1.33	1.39
87	M1	898	OMU	O4-C4	-3.36	1.18	1.24
87	M1	2417	OMU	O4-C4	-3.36	1.18	1.24
87	M1	2946	A2M	C5-C4	-3.35	1.33	1.39
87	M1	1133	A2M	C5-C4	-3.34	1.33	1.39
87	M1	2220	A2M	C5-C4	-3.28	1.33	1.39
87	M1	1449	A2M	C5-C4	-3.26	1.33	1.39
87	M1	876	A2M	C5-C4	-3.26	1.33	1.39
87	M1	2421	OMU	O4-C4	-3.25	1.18	1.24
87	M1	1888	OMU	O4-C4	-3.25	1.18	1.24
87	M1	2921	OMU	O4-C4	-3.21	1.18	1.24
87	M1	649	A2M	C5-C4	-3.18	1.33	1.39
87	M1	2724	OMU	O4-C4	-3.16	1.18	1.24
87	M1	1133	A2M	O3'-C3'	-3.12	1.35	1.43
87	M1	2220	A2M	O3'-C3'	-3.11	1.35	1.43
87	M1	2220	A2M	O2'-C2'	3.07	1.50	1.42
87	M1	876	A2M	O3'-C3'	-3.07	1.35	1.43
87	M1	807	A2M	C8-N9	-3.01	1.32	1.37
87	M1	1888	OMU	O2-C2	-3.01	1.17	1.23
87	M1	2640	A2M	O3'-C3'	-3.00	1.35	1.43
87	M1	1449	A2M	O3'-C3'	-2.97	1.35	1.43
87	M1	817	A2M	C8-N9	-2.96	1.32	1.37
87	M1	807	A2M	O2'-C2'	2.96	1.49	1.42
87	M1	2640	A2M	O2'-C2'	2.95	1.49	1.42
87	M1	649	A2M	O2'-C2'	2.95	1.49	1.42
87	M1	2256	A2M	O3'-C3'	-2.94	1.35	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
87	M1	1133	A2M	O2'-C2'	2.94	1.49	1.42
87	M1	2946	A2M	O2'-C2'	2.94	1.49	1.42
87	M1	649	A2M	O3'-C3'	-2.94	1.35	1.43
87	M1	2417	OMU	O2-C2	-2.93	1.17	1.23
87	M1	2280	A2M	O3'-C3'	-2.91	1.35	1.43
87	M1	1449	A2M	C8-N9	-2.89	1.32	1.37
87	M1	2729	OMU	O2-C2	-2.89	1.17	1.23
87	M1	2634	UR3	C4-N3	2.88	1.46	1.40
87	M1	2280	A2M	O2'-C2'	2.87	1.49	1.42
87	M1	1449	A2M	O2'-C2'	2.86	1.49	1.42
87	M1	807	A2M	O3'-C3'	-2.85	1.35	1.43
87	M1	2256	A2M	C8-N9	-2.84	1.32	1.37
87	M1	898	OMU	O2-C2	-2.84	1.18	1.23
87	M1	2421	OMU	O2-C2	-2.81	1.18	1.23
87	M1	2281	A2M	C4-N9	-2.80	1.31	1.37
87	M1	2724	OMU	O2-C2	-2.80	1.18	1.23
87	M1	2921	OMU	O2-C2	-2.77	1.18	1.23
87	M1	2281	A2M	O3'-C3'	-2.76	1.36	1.43
87	M1	2921	OMU	C6-N1	2.74	1.44	1.38
87	M1	649	A2M	C8-N9	-2.74	1.32	1.37
87	M1	2220	A2M	C8-N9	-2.71	1.32	1.37
87	M1	2946	A2M	C5-N7	-2.71	1.34	1.39
87	M1	898	OMU	C6-N1	2.71	1.44	1.38
87	M1	2347	OMU	C6-N1	2.71	1.44	1.38
87	M1	2347	OMU	O2-C2	-2.71	1.18	1.23
87	M1	1133	A2M	C8-N9	-2.71	1.32	1.37
87	M1	876	A2M	O2'-C2'	2.70	1.49	1.42
87	M1	2946	A2M	O3'-C3'	-2.70	1.36	1.43
87	M1	2634	UR3	O4-C4	-2.68	1.17	1.23
87	M1	1888	OMU	C6-N1	2.67	1.44	1.38
87	M1	817	A2M	O2'-C2'	2.67	1.49	1.42
87	M1	2640	A2M	C8-N9	-2.66	1.33	1.37
87	M1	817	A2M	C5-N7	-2.65	1.34	1.39
87	M1	817	A2M	C4-N9	-2.63	1.32	1.37
87	M1	1449	A2M	C5-N7	-2.62	1.34	1.39
87	M1	876	A2M	C8-N9	-2.60	1.33	1.37
87	M1	817	A2M	O3'-C3'	-2.59	1.36	1.43
87	M1	2281	A2M	O2'-C2'	2.59	1.49	1.42
87	M1	1133	A2M	C5-N7	-2.58	1.34	1.39
87	M1	807	A2M	C4-N9	-2.57	1.32	1.37
87	M1	2724	OMU	C6-N1	2.56	1.44	1.38
87	M1	1133	A2M	C4-N9	-2.56	1.32	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
87	M1	2256	A2M	C4-N9	-2.55	1.32	1.37
87	M1	2281	A2M	C5-N7	-2.53	1.34	1.39
87	M1	2280	A2M	C5-N7	-2.52	1.34	1.39
87	M1	649	A2M	C5-N7	-2.52	1.34	1.39
87	M1	876	A2M	C5-N7	-2.51	1.34	1.39
87	M1	2729	OMU	C6-N1	2.50	1.44	1.38
87	M1	2417	OMU	C6-N1	2.50	1.44	1.38
87	M1	2281	A2M	C8-N9	-2.48	1.33	1.37
87	M1	649	A2M	C4-N9	-2.48	1.32	1.37
87	M1	2946	A2M	C8-N9	-2.45	1.33	1.37
87	M1	2280	A2M	C8-N9	-2.41	1.33	1.37
87	M1	807	A2M	C5-N7	-2.37	1.34	1.39
87	M1	2421	OMU	C6-N1	2.37	1.43	1.38
87	M1	2640	A2M	C5-N7	-2.37	1.34	1.39
87	M1	2220	A2M	C5-N7	-2.36	1.34	1.39
87	M1	2634	UR3	C5-C4	2.33	1.49	1.43
87	M1	2640	A2M	C4-N9	-2.33	1.32	1.37
87	M1	2220	A2M	C4-N9	-2.31	1.32	1.37
87	M1	876	A2M	C4-N9	-2.26	1.33	1.37
87	M1	2278	5MC	C4-N3	-2.24	1.30	1.34
87	M1	650	OMC	C4-N3	-2.22	1.30	1.34
87	M1	2870	5MC	C4-N3	-2.22	1.30	1.34
87	M1	898	OMU	C5-C4	2.22	1.48	1.43
87	M1	1449	A2M	C4-N9	-2.18	1.33	1.37
87	M1	1888	OMU	C5-C4	2.12	1.48	1.43
87	M1	2946	A2M	C4-N9	-2.12	1.33	1.37
87	M1	2197	OMC	C4-N3	-2.11	1.30	1.34
87	M1	2256	A2M	C5-N7	-2.11	1.35	1.39
87	M1	2280	A2M	C4-N9	-2.11	1.33	1.37
87	M1	2724	OMU	C5-C4	2.03	1.48	1.43
87	M1	2921	OMU	C5-C4	2.02	1.48	1.43

All (227) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
87	M1	807	A2M	C1'-N9-C8	-9.94	105.03	127.09
87	M1	2256	A2M	C1'-N9-C8	-9.80	105.33	127.09
87	M1	1449	A2M	C1'-N9-C8	-9.67	105.63	127.09
87	M1	2640	A2M	C1'-N9-C8	-9.52	105.96	127.09
87	M1	876	A2M	C1'-N9-C8	-9.48	106.06	127.09
87	M1	2220	A2M	C1'-N9-C8	-9.43	106.16	127.09
87	M1	649	A2M	C1'-N9-C8	-9.36	106.32	127.09

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
87	M1	817	A2M	N6-C6-N1	-9.19	97.91	118.38
87	M1	2280	A2M	C1'-N9-C8	-9.12	106.85	127.09
87	M1	876	A2M	N6-C6-N1	-9.05	98.22	118.38
87	M1	649	A2M	N6-C6-N1	-9.01	98.31	118.38
87	M1	2281	A2M	N6-C6-N1	-8.99	98.35	118.38
87	M1	817	A2M	C1'-N9-C8	-8.98	107.16	127.09
87	M1	807	A2M	N6-C6-N1	-8.92	98.51	118.38
87	M1	1133	A2M	C1'-N9-C8	-8.92	107.31	127.09
87	M1	2946	A2M	C1'-N9-C8	-8.91	107.32	127.09
87	M1	1449	A2M	N6-C6-N1	-8.78	98.81	118.38
87	M1	2280	A2M	N6-C6-N1	-8.75	98.88	118.38
87	M1	2640	A2M	N6-C6-N1	-8.73	98.93	118.38
87	M1	2256	A2M	N6-C6-N1	-8.68	99.03	118.38
87	M1	2220	A2M	N6-C6-N1	-8.67	99.06	118.38
87	M1	2946	A2M	N6-C6-N1	-8.65	99.11	118.38
87	M1	2256	A2M	C4-N9-C8	8.23	114.38	105.74
87	M1	1133	A2M	N6-C6-N1	-8.21	100.09	118.38
87	M1	2281	A2M	C1'-N9-C8	-8.10	109.12	127.09
87	M1	807	A2M	C4-N9-C8	8.06	114.20	105.74
87	M1	2256	A2M	N9-C8-N7	-7.54	103.23	113.94
87	M1	807	A2M	N9-C8-N7	-7.32	103.55	113.94
87	M1	817	A2M	C4-N9-C8	7.26	113.37	105.74
87	M1	2281	A2M	C4-N9-C8	7.24	113.34	105.74
87	M1	817	A2M	N9-C8-N7	-7.08	103.90	113.94
87	M1	2220	A2M	C4-N9-C8	7.02	113.11	105.74
87	M1	2281	A2M	N9-C8-N7	-7.01	103.98	113.94
87	M1	649	A2M	C4-N9-C8	6.87	112.95	105.74
87	M1	1133	A2M	C4-N9-C8	6.76	112.84	105.74
87	M1	2640	A2M	C4-N9-C8	6.66	112.73	105.74
87	M1	649	A2M	N9-C8-N7	-6.62	104.54	113.94
87	M1	1449	A2M	C4-N9-C1'	6.61	142.10	126.63
87	M1	876	A2M	N9-C8-N7	-6.60	104.57	113.94
87	M1	2220	A2M	N9-C8-N7	-6.59	104.58	113.94
87	M1	2280	A2M	N9-C8-N7	-6.55	104.65	113.94
87	M1	876	A2M	C4-N9-C8	6.54	112.61	105.74
87	M1	2640	A2M	N9-C8-N7	-6.39	104.87	113.94
87	M1	2280	A2M	C4-N9-C8	6.36	112.41	105.74
87	M1	876	A2M	C4-N9-C1'	6.28	141.33	126.63
87	M1	2640	A2M	C4-N9-C1'	6.27	141.29	126.63
87	M1	1133	A2M	N9-C8-N7	-6.26	105.05	113.94
87	M1	1449	A2M	C4-N9-C8	6.21	112.26	105.74
87	M1	649	A2M	C5-C6-N6	6.19	138.60	123.29

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
87	M1	817	A2M	C5-C6-N6	6.17	138.57	123.29
87	M1	876	A2M	C5-C6-N6	6.12	138.45	123.29
87	M1	2946	A2M	N9-C8-N7	-6.12	105.25	113.94
87	M1	2421	OMU	C4-N3-C2	-6.12	119.01	126.61
87	M1	2729	OMU	C4-N3-C2	-6.05	119.10	126.61
87	M1	807	A2M	C4-N9-C1'	6.04	140.75	126.63
87	M1	2946	A2M	C4-N9-C1'	6.03	140.74	126.63
87	M1	2280	A2M	C4-N9-C1'	6.03	140.74	126.63
87	M1	649	A2M	C4-N9-C1'	6.03	140.73	126.63
87	M1	2220	A2M	C4-N9-C1'	6.02	140.72	126.63
87	M1	1449	A2M	N9-C8-N7	-6.02	105.40	113.94
87	M1	2634	UR3	C4-N3-C2	-6.00	119.75	124.58
87	M1	807	A2M	C5-C6-N6	5.94	137.98	123.29
87	M1	2417	OMU	C4-N3-C2	-5.90	119.28	126.61
87	M1	2946	A2M	C4-N9-C8	5.88	111.91	105.74
87	M1	1449	A2M	C5-C6-N6	5.86	137.80	123.29
87	M1	1888	OMU	C4-N3-C2	-5.85	119.35	126.61
87	M1	817	A2M	N3-C2-N1	-5.85	119.73	128.58
87	M1	2256	A2M	C4-N9-C1'	5.83	140.28	126.63
87	M1	1133	A2M	N3-C2-N1	-5.83	119.75	128.58
87	M1	2220	A2M	N3-C2-N1	-5.82	119.77	128.58
87	M1	649	A2M	N3-C2-N1	-5.82	119.78	128.58
87	M1	2220	A2M	C5-C6-N6	5.80	137.64	123.29
87	M1	807	A2M	N3-C2-N1	-5.79	119.81	128.58
87	M1	2256	A2M	C5-C6-N6	5.79	137.61	123.29
87	M1	2640	A2M	C5-C6-N6	5.76	137.55	123.29
87	M1	2280	A2M	C5-C6-N6	5.75	137.51	123.29
87	M1	2946	A2M	C5-C6-N6	5.74	137.49	123.29
87	M1	2281	A2M	N3-C2-N1	-5.71	119.94	128.58
87	M1	2256	A2M	N3-C2-N1	-5.70	119.96	128.58
87	M1	2921	OMU	C4-N3-C2	-5.69	119.55	126.61
87	M1	2347	OMU	C4-N3-C2	-5.68	119.56	126.61
87	M1	1449	A2M	N3-C2-N1	-5.68	119.98	128.58
87	M1	1133	A2M	C4-N9-C1'	5.65	139.84	126.63
87	M1	2640	A2M	N3-C2-N1	-5.61	120.09	128.58
87	M1	2281	A2M	C5-C6-N6	5.60	137.16	123.29
87	M1	876	A2M	N3-C2-N1	-5.59	120.12	128.58
87	M1	2280	A2M	N3-C2-N1	-5.57	120.15	128.58
87	M1	898	OMU	C4-N3-C2	-5.54	119.74	126.61
87	M1	817	A2M	C4-N9-C1'	5.47	139.42	126.63
87	M1	1133	A2M	C5-C6-N6	5.40	136.65	123.29
87	M1	2724	OMU	C4-N3-C2	-5.39	119.92	126.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
87	M1	2946	A2M	N3-C2-N1	-5.39	120.43	128.58
87	M1	2946	A2M	C5-C4-N3	-4.72	120.22	126.72
87	M1	1449	A2M	N3-C4-N9	4.72	135.19	127.17
87	M1	1449	A2M	C5-C4-N3	-4.67	120.29	126.72
87	M1	2280	A2M	C5-C4-N3	-4.66	120.30	126.72
87	M1	2281	A2M	C4-N9-C1'	4.56	137.31	126.63
87	M1	2946	A2M	N3-C4-N9	4.55	134.91	127.17
87	M1	2280	A2M	N3-C4-N9	4.55	134.91	127.17
87	M1	2640	A2M	N3-C4-N9	4.53	134.87	127.17
87	M1	2220	A2M	N3-C4-N9	4.42	134.68	127.17
87	M1	2640	A2M	C5-C4-N3	-4.40	120.66	126.72
87	M1	1133	A2M	C2'-C1'-N9	-4.35	106.59	113.75
87	M1	876	A2M	C5-C4-N3	-4.33	120.76	126.72
87	M1	1133	A2M	N3-C4-N9	4.32	134.51	127.17
87	M1	876	A2M	N3-C4-N9	4.25	134.39	127.17
87	M1	807	A2M	N3-C4-N9	4.23	134.35	127.17
87	M1	649	A2M	N3-C4-N9	4.21	134.32	127.17
87	M1	2281	A2M	N3-C4-N9	4.21	134.32	127.17
87	M1	2256	A2M	N3-C4-N9	4.16	134.25	127.17
87	M1	1888	OMU	N3-C2-N1	4.16	120.31	114.89
87	M1	2421	OMU	N3-C2-N1	4.16	120.30	114.89
87	M1	2281	A2M	O4'-C1'-N9	4.13	116.02	108.09
87	M1	2220	A2M	C5-C4-N3	-4.12	121.04	126.72
87	M1	817	A2M	N3-C4-N9	4.11	134.15	127.17
87	M1	898	OMU	N3-C2-N1	4.11	120.24	114.89
87	M1	649	A2M	C5-C4-N3	-4.10	121.07	126.72
87	M1	2634	UR3	C5-C4-N3	4.06	120.39	115.04
87	M1	817	A2M	C5-C4-N3	-4.05	121.14	126.72
87	M1	2417	OMU	N3-C2-N1	4.04	120.15	114.89
87	M1	2347	OMU	C5-C4-N3	4.01	120.42	114.80
87	M1	2724	OMU	N3-C2-N1	4.00	120.10	114.89
87	M1	2729	OMU	N3-C2-N1	3.97	120.06	114.89
87	M1	2729	OMU	C5-C4-N3	3.95	120.34	114.80
87	M1	2281	A2M	C5-C4-N3	-3.95	121.27	126.72
87	M1	2417	OMU	C5-C4-N3	3.93	120.31	114.80
87	M1	1133	A2M	C5-C4-N3	-3.89	121.36	126.72
87	M1	2921	OMU	N3-C2-N1	3.87	119.93	114.89
87	M1	2921	OMU	C5-C4-N3	3.87	120.22	114.80
87	M1	2256	A2M	O2'-C2'-C1'	3.86	116.31	108.99
87	M1	2421	OMU	C5-C4-N3	3.81	120.14	114.80
87	M1	898	OMU	C5-C4-N3	3.78	120.09	114.80
87	M1	1888	OMU	C5-C4-N3	3.75	120.06	114.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
87	M1	2256	A2M	C5-C4-N3	-3.73	121.58	126.72
87	M1	2256	A2M	C5-N7-C8	3.69	109.25	103.45
87	M1	817	A2M	C5-N7-C8	3.66	109.21	103.45
87	M1	2347	OMU	N3-C2-N1	3.65	119.64	114.89
87	M1	807	A2M	C5-C4-N3	-3.63	121.71	126.72
87	M1	807	A2M	C5-N7-C8	3.56	109.04	103.45
87	M1	2280	A2M	C2-N3-C4	3.55	120.49	111.83
87	M1	1449	A2M	C2-N3-C4	3.54	120.47	111.83
87	M1	2724	OMU	C5-C4-N3	3.53	119.75	114.80
87	M1	876	A2M	C5-N7-C8	3.52	108.98	103.45
87	M1	817	A2M	C2-N3-C4	3.49	120.36	111.83
87	M1	2281	A2M	C4'-O4'-C1'	-3.46	101.82	109.47
87	M1	2640	A2M	C2-N3-C4	3.46	120.28	111.83
87	M1	876	A2M	C2-N3-C4	3.42	120.19	111.83
87	M1	649	A2M	C2-N3-C4	3.42	120.19	111.83
87	M1	2220	A2M	C2-N3-C4	3.41	120.16	111.83
87	M1	2946	A2M	C2-N3-C4	3.40	120.14	111.83
87	M1	2280	A2M	C5-N7-C8	3.40	108.79	103.45
87	M1	2281	A2M	C2-N3-C4	3.39	120.12	111.83
87	M1	649	A2M	C5-N7-C8	3.39	108.77	103.45
87	M1	2256	A2M	C2-N3-C4	3.32	119.94	111.83
87	M1	2347	OMU	O4-C4-C5	-3.32	119.44	125.16
91	DP	37	YYG	C3-N3-C4	3.31	129.53	123.11
87	M1	807	A2M	C2-N3-C4	3.28	119.85	111.83
87	M1	1133	A2M	C2-N3-C4	3.28	119.84	111.83
87	M1	2220	A2M	C5-N7-C8	3.20	108.48	103.45
91	DP	37	YYG	C5-C4-N3	-3.19	121.40	123.99
87	M1	2921	OMU	O4-C4-C5	-3.19	119.66	125.16
87	M1	2281	A2M	C5-N7-C8	3.15	108.40	103.45
87	M1	2946	A2M	C5-N7-C8	3.13	108.37	103.45
87	M1	2640	A2M	C5-N7-C8	3.12	108.35	103.45
87	M1	1449	A2M	C5-N7-C8	3.10	108.33	103.45
87	M1	2946	A2M	O4'-C1'-N9	3.07	113.99	108.09
87	M1	2417	OMU	O4-C4-C5	-3.01	119.97	125.16
87	M1	1133	A2M	O4'-C1'-N9	2.99	113.83	108.09
91	DP	37	YYG	C3-N3-C2	-2.96	114.33	120.32
87	M1	2729	OMU	O4-C4-C5	-2.95	120.07	125.16
87	M1	2142	1MA	N1-C6-N6	2.95	127.11	119.71
87	M1	2421	OMU	O4-C4-C5	-2.94	120.09	125.16
87	M1	1133	A2M	C5-N7-C8	2.94	108.07	103.45
87	M1	2948	OMC	C1'-N1-C2	2.88	124.81	118.44
91	DP	37	YYG	C2-N1-C12	-2.85	104.82	109.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
91	DP	37	YYG	O6-C6-N1	2.81	123.88	119.87
87	M1	2281	A2M	C5-C6-N1	2.75	124.49	117.51
87	M1	2347	OMU	C1'-N1-C2	2.74	122.50	117.59
87	M1	2724	OMU	O4-C4-C5	-2.73	120.46	125.16
87	M1	1888	OMU	O4-C4-C5	-2.72	120.47	125.16
87	M1	1437	OMC	C1'-N1-C2	2.70	124.40	118.44
91	DP	37	YYG	N3-C2-N2	-2.68	122.92	126.62
87	M1	898	OMU	O4-C4-C5	-2.63	120.62	125.16
87	M1	2417	OMU	O2-C2-N1	-2.61	119.40	122.80
87	M1	2634	UR3	C6-N1-C2	-2.59	119.68	121.80
87	M1	2256	A2M	CM'-O2'-C2'	2.59	121.11	114.47
87	M1	2220	A2M	O4'-C1'-N9	2.57	113.03	108.09
91	DP	37	YYG	N9-C4-N3	2.52	133.53	129.45
87	M1	2421	OMU	O2-C2-N1	-2.48	119.56	122.80
87	M1	2256	A2M	O4'-C1'-C2'	-2.48	102.32	106.59
87	M1	2278	5MC	C1'-N1-C6	-2.43	117.14	121.15
87	M1	817	A2M	C2'-C1'-N9	2.40	117.71	113.75
87	M1	2280	A2M	C5-C6-N1	2.40	123.61	117.51
87	M1	2724	OMU	O2-C2-N1	-2.39	119.69	122.80
87	M1	2280	A2M	C4'-O4'-C1'	-2.37	104.23	109.47
87	M1	2640	A2M	C5-C6-N1	2.37	123.52	117.51
87	M1	807	A2M	C5-C6-N1	2.36	123.51	117.51
87	M1	876	A2M	C2'-C1'-N9	-2.36	109.86	113.75
87	M1	817	A2M	C5-C6-N1	2.36	123.50	117.51
87	M1	1449	A2M	O4'-C1'-N9	2.34	112.59	108.09
87	M1	645	1MA	N1-C6-N6	2.33	125.56	119.71
87	M1	2946	A2M	C5-C6-N1	2.32	123.40	117.51
87	M1	1449	A2M	C5-C6-N1	2.31	123.39	117.51
87	M1	2256	A2M	C5-C6-N1	2.30	123.36	117.51
87	M1	876	A2M	C5-C6-N1	2.29	123.33	117.51
87	M1	2220	A2M	C5-C6-N1	2.28	123.30	117.51
87	M1	2634	UR3	C1'-N1-C2	2.26	120.75	117.04
87	M1	1133	A2M	C5-C6-N1	2.26	123.25	117.51
87	M1	2278	5MC	C1'-N1-C2	2.26	123.43	118.44
87	M1	805	OMG	C2'-C1'-N9	-2.21	110.04	114.24
87	M1	649	A2M	C2'-C1'-N9	-2.21	110.12	113.75
87	M1	2640	A2M	O4'-C1'-N9	2.20	112.32	108.09
87	M1	649	A2M	C5-C6-N1	2.20	123.09	117.51
87	M1	2729	OMU	O2-C2-N1	-2.19	119.94	122.80
87	M1	2948	OMC	C1'-N1-C6	-2.17	116.13	120.78
87	M1	2256	A2M	C4'-O4'-C1'	-2.16	104.71	109.47
87	M1	649	A2M	O4'-C1'-N9	2.14	112.20	108.09

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
87	M1	663	OMC	C1'-N1-C2	2.12	123.11	118.44
87	M1	1888	OMU	O2-C2-N1	-2.09	120.07	122.80
87	M1	649	A2M	C3'-C2'-C1'	2.09	106.80	102.81
87	M1	807	A2M	C4'-O4'-C1'	-2.08	104.88	109.47
87	M1	2946	A2M	O4'-C4'-C3'	-2.07	101.04	105.15
87	M1	2142	1MA	C6-C5-N7	-2.06	128.52	132.16
87	M1	898	OMU	O2-C2-N1	-2.05	120.13	122.80
87	M1	2959	OMC	C1'-N1-C2	2.04	122.94	118.44
87	M1	2921	OMU	O2-C2-N1	-2.04	120.14	122.80
87	M1	2640	A2M	C2'-C1'-N9	-2.04	110.40	113.75

There are no chirality outliers.

All (42) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
87	M1	1437	OMC	C1'-C2'-O2'-CM2
87	M1	1450	OMG	O4'-C4'-C5'-O5'
87	M1	2220	A2M	C1'-C2'-O2'-CM'
87	M1	2256	A2M	C1'-C2'-O2'-CM'
87	M1	2417	OMU	C1'-C2'-O2'-CM2
87	M1	2619	OMG	C1'-C2'-O2'-CM2
87	M1	2724	OMU	C1'-C2'-O2'-CM2
87	M1	2946	A2M	C1'-C2'-O2'-CM'
91	DP	37	YYG	N20-C21-O23-C24
91	DP	37	YYG	O22-C21-O23-C24
91	DP	37	YYG	C15-C16-O18-C19
87	M1	2197	OMC	C2'-C1'-N1-C6
87	M1	2280	A2M	O4'-C4'-C5'-O5'
87	M1	2922	OMG	O4'-C4'-C5'-O5'
87	M1	2278	5MC	O4'-C4'-C5'-O5'
87	M1	2281	A2M	O4'-C4'-C5'-O5'
91	DP	37	YYG	O17-C16-O18-C19
91	DP	37	YYG	O23-C21-N20-C15
87	M1	2197	OMC	C2'-C1'-N1-C2
87	M1	1450	OMG	C3'-C4'-C5'-O5'
87	M1	2281	A2M	C3'-C4'-C5'-O5'
91	DP	37	YYG	O22-C21-N20-C15
87	M1	2280	A2M	C3'-C4'-C5'-O5'
87	M1	2922	OMG	C3'-C4'-C5'-O5'
87	M1	2278	5MC	C3'-C4'-C5'-O5'
87	M1	2870	5MC	C2'-C1'-N1-C6
87	M1	2197	OMC	O4'-C1'-N1-C6

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Mol	Chain	Res	Type	Atoms
87	M1	2870	5MC	O4'-C1'-N1-C6
87	M1	649	A2M	C4'-C5'-O5'-P
87	M1	2197	OMC	O4'-C1'-N1-C2
87	M1	817	A2M	C4'-C5'-O5'-P
87	M1	2619	OMG	C3'-C4'-C5'-O5'
91	DP	37	YYG	C12-C13-C14-C15
87	M1	649	A2M	C1'-C2'-O2'-CM'
87	M1	2256	A2M	C4'-C5'-O5'-P
87	M1	2922	OMG	C3'-C2'-O2'-CM2
87	M1	2870	5MC	O4'-C1'-N1-C2
87	M1	807	A2M	O4'-C1'-N9-C8
87	M1	1437	OMC	O4'-C4'-C5'-O5'
87	M1	2347	OMU	C3'-C4'-C5'-O5'
87	M1	2619	OMG	O4'-C4'-C5'-O5'
87	M1	817	A2M	O4'-C4'-C5'-O5'

There are no ring outliers.

15 monomers are involved in 20 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
87	M1	2220	A2M	1	0
87	M1	2793	OMG	2	0
87	M1	1133	A2M	1	0
87	M1	663	OMC	2	0
87	M1	2948	OMC	2	0
87	M1	898	OMU	1	0
87	M1	2619	OMG	1	0
87	M1	2281	A2M	1	0
87	M1	2815	OMG	1	0
87	M1	1450	OMG	1	0
87	M1	1449	A2M	2	0
87	M1	2417	OMU	1	0
87	M1	2946	A2M	1	0
87	M1	2724	OMU	1	0
87	M1	1437	OMC	2	0

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 327 ligands modelled in this entry, 324 are monoatomic - leaving 3 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
95	SPD	M1	3603	-	9,9,9	0.31	0	8,8,8	0.32	0
95	SPD	M1	3604	-	9,9,9	0.28	0	8,8,8	0.40	0
95	SPD	M1	3602	-	9,9,9	0.28	0	8,8,8	0.29	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
95	SPD	M1	3603	-	-	3/7/7/7	-
95	SPD	M1	3604	-	-	3/7/7/7	-
95	SPD	M1	3602	-	-	1/7/7/7	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
95	M1	3604	SPD	C8-C7-N6-C5
95	M1	3603	SPD	N1-C2-C3-C4
95	M1	3603	SPD	C2-C3-C4-C5
95	M1	3604	SPD	C2-C3-C4-C5
95	M1	3603	SPD	C7-C8-C9-N10
95	M1	3604	SPD	C4-C5-N6-C7
95	M1	3602	SPD	C8-C7-N6-C5

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
95	M1	3603	SPD	3	0
95	M1	3602	SPD	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

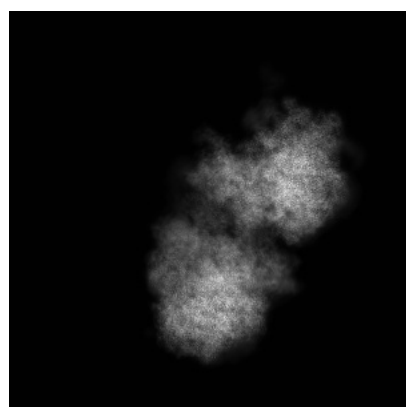
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-50259. These allow visual inspection of the internal detail of the map and identification of artifacts.

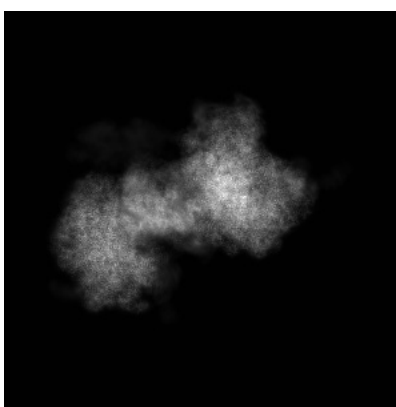
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

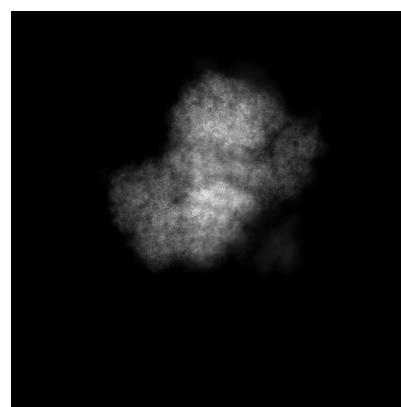
6.1.1 Primary map



X



Y

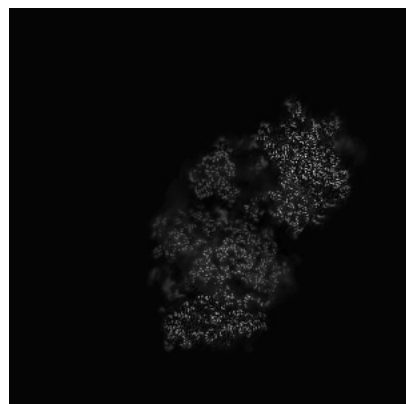


Z

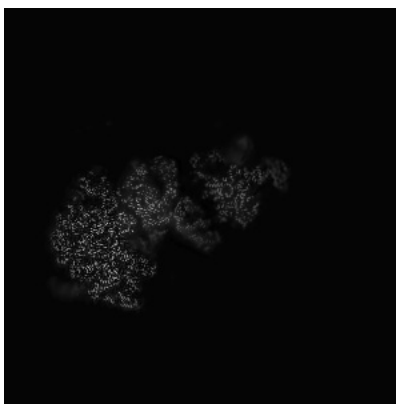
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

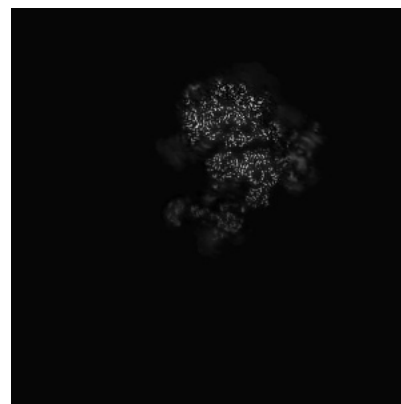
6.2.1 Primary map



X Index: 313



Y Index: 313

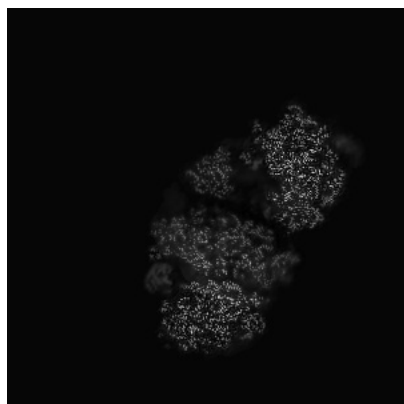


Z Index: 313

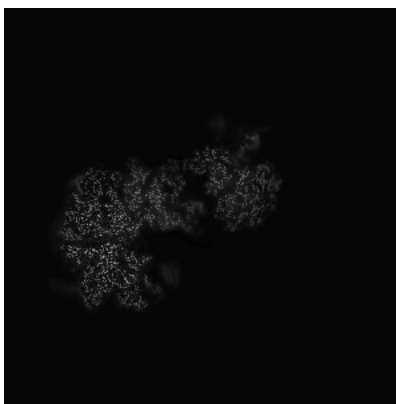
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

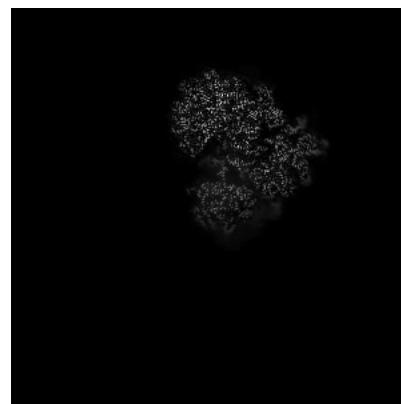
6.3.1 Primary map



X Index: 303



Y Index: 330

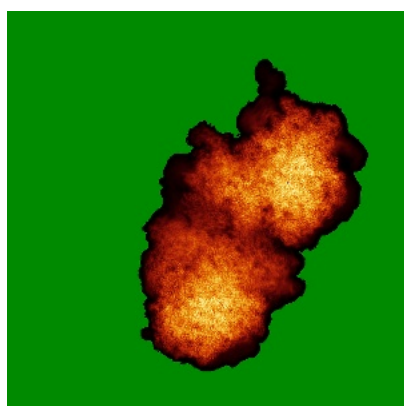


Z Index: 372

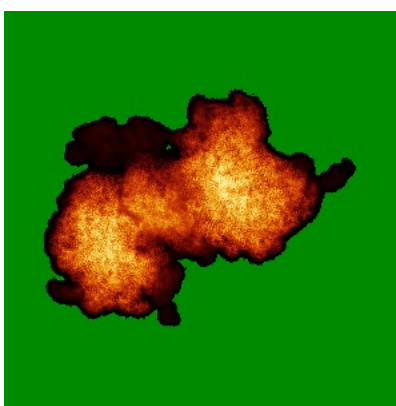
The images above show the largest variance slices of the map in three orthogonal directions.

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

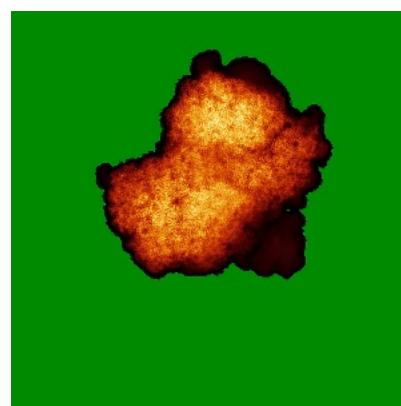
6.4.1 Primary map



X



Y

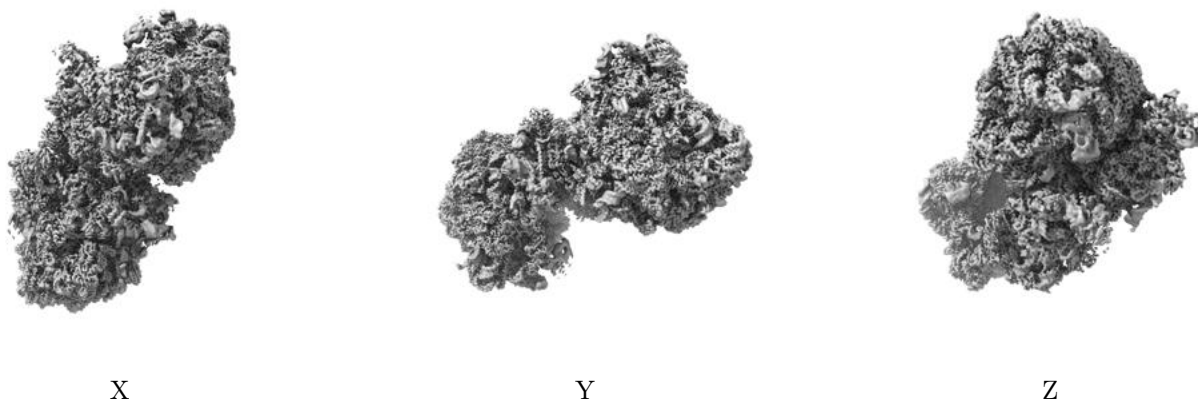


Z

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 0.44. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

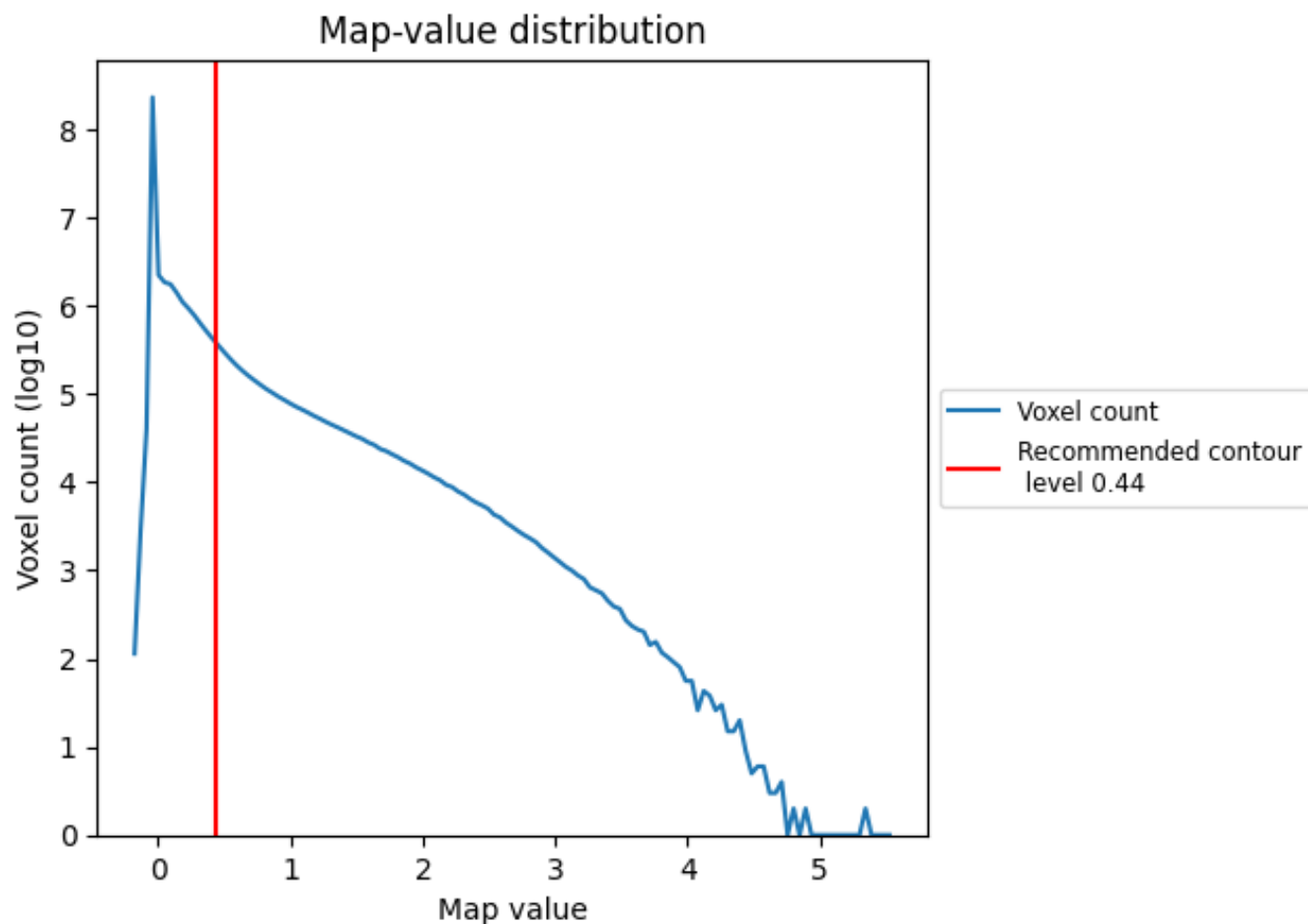
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

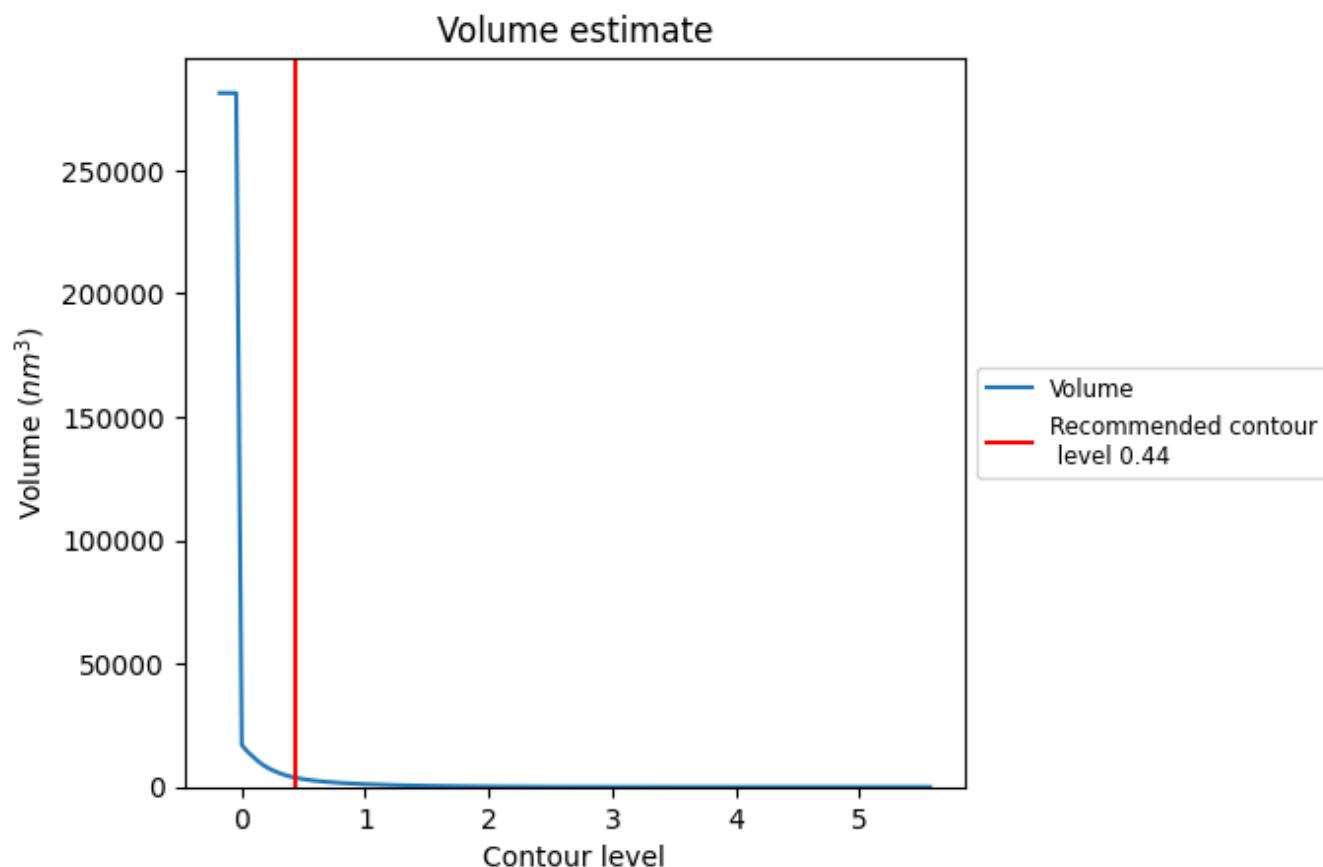
This section contains the results of statistical analysis of the map.

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.

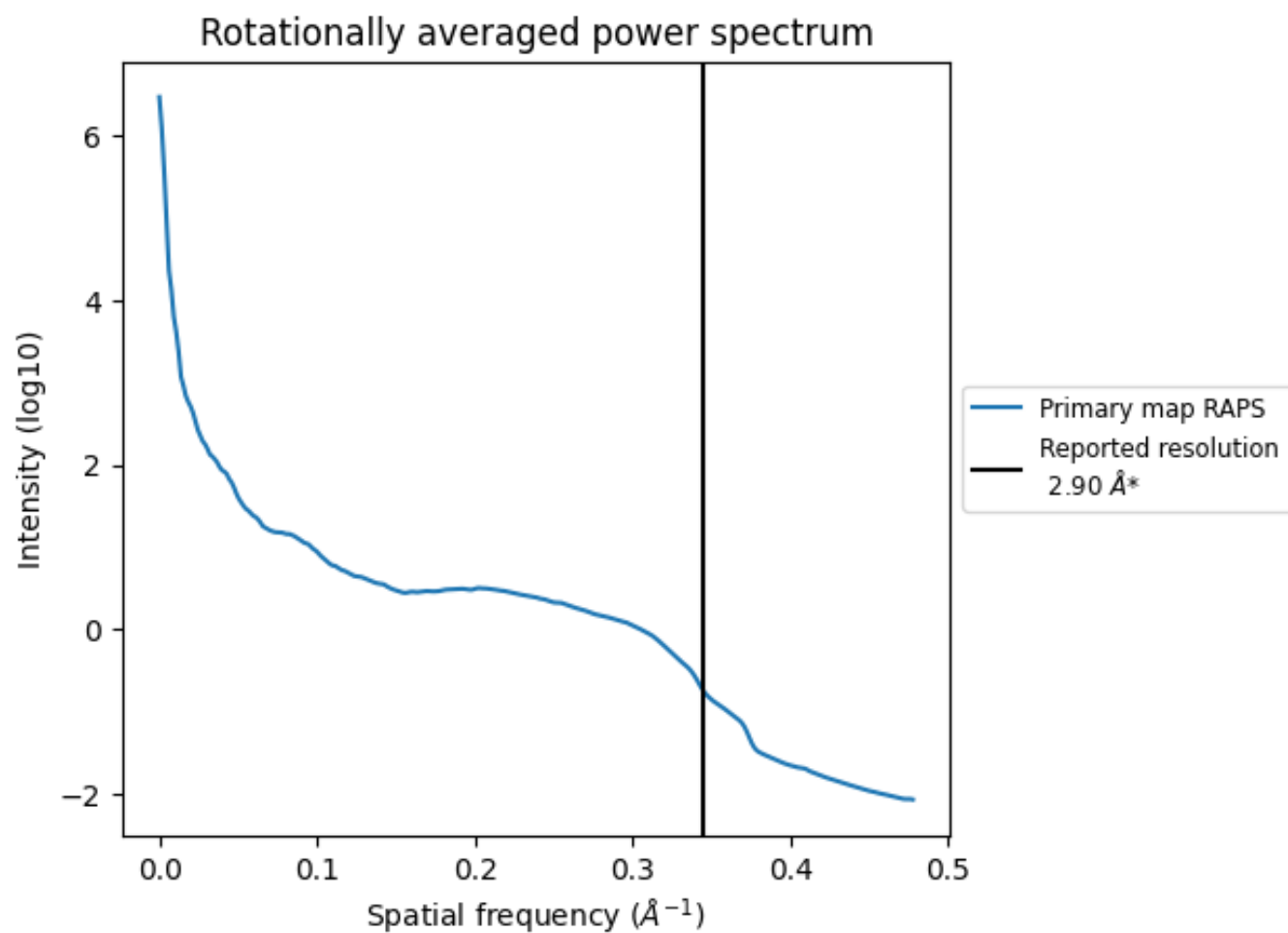
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3730 nm^3 ; this corresponds to an approximate mass of 3369 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ



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

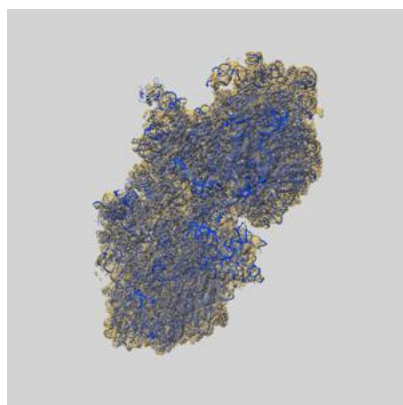
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

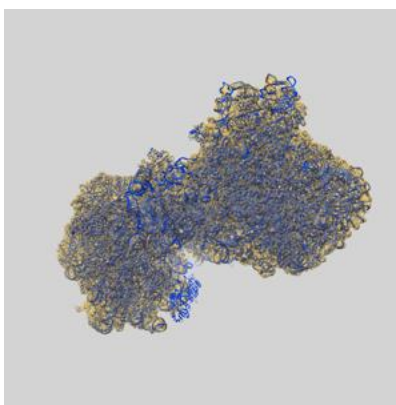
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-50259 and PDB model 9F9S. Per-residue inclusion information can be found in section [3](#) on page [29](#).

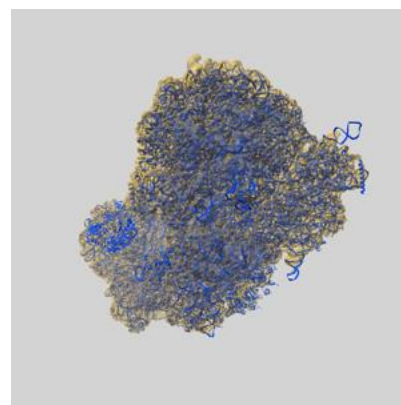
9.1 Map-model overlay [i](#)



X



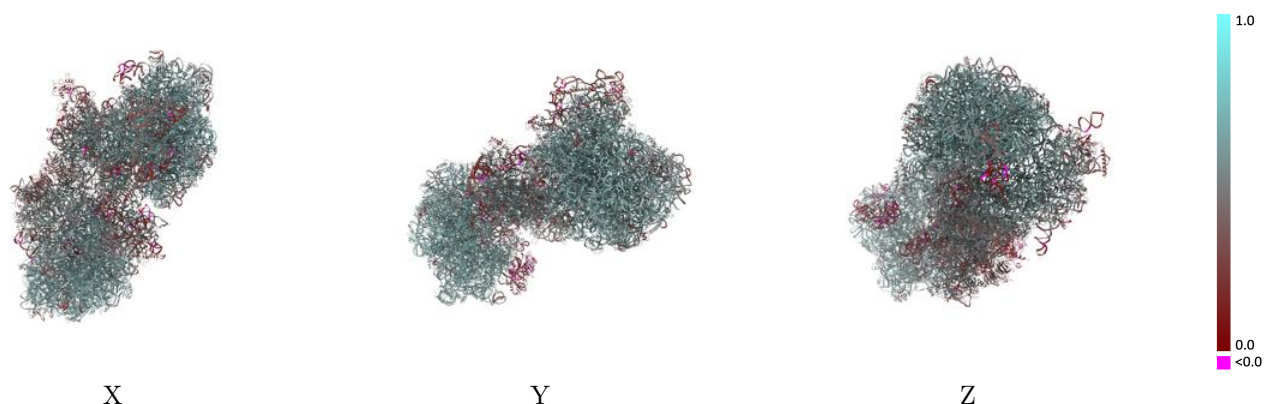
Y



Z

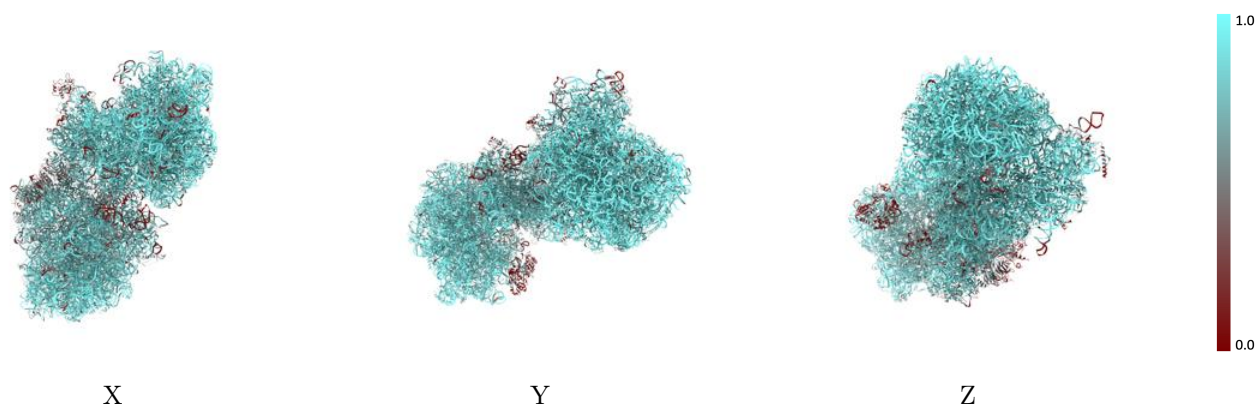
The images above show the 3D surface view of the map at the recommended contour level 0.44 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



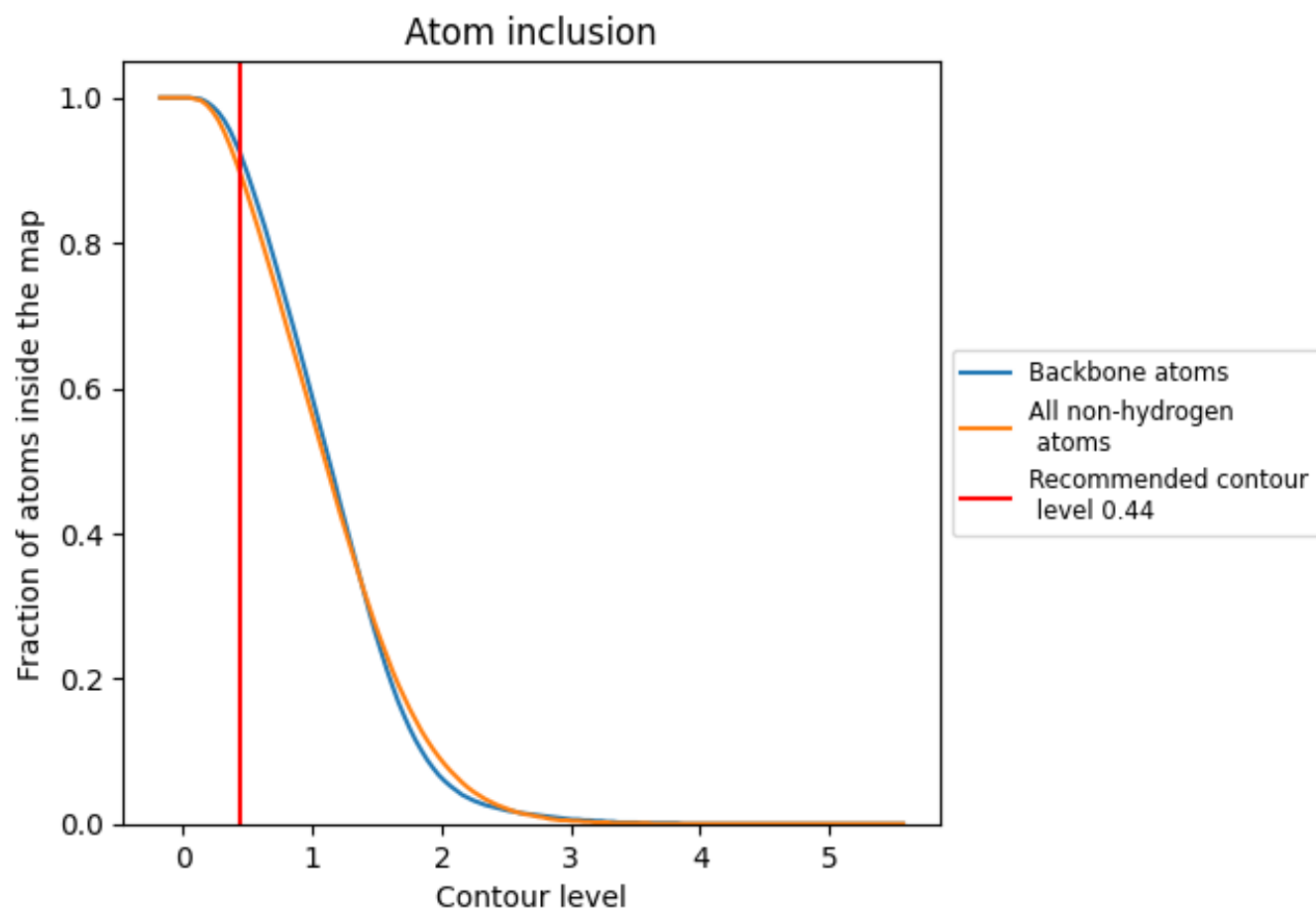
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.44).

9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 90% 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 (0.44) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8970	 0.5400
CC	 0.9590	 0.5410
CM	 0.7410	 0.4200
CN	 0.7350	 0.4190
CP	 0.9150	 0.4080
DP	 0.5840	 0.3000
DQ	 0.8320	 0.3620
L1	 0.9700	 0.5780
L2	 0.9780	 0.6010
L3	 0.9930	 0.5740
LA	 0.9190	 0.5220
LB	 0.9590	 0.5860
LC	 0.8560	 0.5130
LD	 0.9140	 0.5420
LE	 0.9100	 0.5550
LF	 0.8290	 0.4730
LG	 0.9210	 0.5680
LH	 0.9520	 0.5560
LI	 0.9930	 0.6230
LJ	 0.9680	 0.5970
LK	 0.9560	 0.6060
LL	 0.9770	 0.5990
LM	 0.8660	 0.5520
LN	 0.9530	 0.5840
LO	 0.9420	 0.5750
La	 0.9350	 0.5950
Lb	 0.9300	 0.5960
Lc	 0.9380	 0.5810
Ld	 0.9860	 0.6140
Le	 0.9280	 0.5680
Lf	 0.9810	 0.6260
Lg	 0.8830	 0.5210
Lh	 0.9940	 0.6260
Li	 0.8990	 0.5420
Lj	 0.9410	 0.5710



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Chain	Atom inclusion	Q-score
Lk	 0.9240	 0.5810
Ll	 0.9900	 0.6200
Lm	 0.9760	 0.6100
Ln	 0.9020	 0.5650
Lo	 0.8850	 0.5570
Lp	 0.9270	 0.5400
Lq	 0.9510	 0.5940
Lr	 0.9120	 0.5500
Ls	 0.9630	 0.5870
Lt	 0.9460	 0.5670
Lu	 0.7240	 0.4730
Lv	 0.8720	 0.4970
Lw	 0.9720	 0.6150
Lx	 0.9540	 0.5890
Ly	 0.9610	 0.5870
Lz	 0.8620	 0.5020
M1	 0.9580	 0.5960
M2	 0.9840	 0.6280
M3	 0.9940	 0.6080
MA	 0.9220	 0.5750
MB	 0.9640	 0.6240
MC	 0.8440	 0.5670
MD	 0.9230	 0.5830
ME	 0.9090	 0.6030
MF	 0.8270	 0.5030
MG	 0.9240	 0.6000
MH	 0.9540	 0.5930
MI	 0.9850	 0.6600
MJ	 0.9700	 0.6290
MK	 0.9760	 0.6510
ML	 0.9800	 0.6360
MM	 0.9040	 0.5790
MN	 0.9590	 0.6190
MO	 0.9550	 0.6160
MP	 0.0240	 0.0980
MQ	 0.1020	 0.1700
Ma	 0.9680	 0.6250
Mb	 0.9580	 0.6300
Mc	 0.9380	 0.6180
Md	 0.9430	 0.5880
Me	 0.9430	 0.6070
Mf	 0.9830	 0.6400

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Chain	Atom inclusion	Q-score
Mg	 0.8660	 0.5590
Mh	 0.9980	 0.6600
Mi	 0.8950	 0.5720
Mj	 0.9420	 0.5970
Mk	 0.9050	 0.6200
ML	 0.9850	 0.6610
Mm	 0.9710	 0.6390
Mn	 0.9110	 0.5900
Mo	 0.8510	 0.5690
Mp	 0.9430	 0.5890
Mq	 0.9690	 0.6370
Mr	 0.8870	 0.5780
Ms	 0.9710	 0.6160
Mt	 0.9530	 0.6130
Mu	 0.9430	 0.6150
Mv	 0.8810	 0.5320
Mw	 0.9590	 0.6420
Mx	 0.9650	 0.6250
My	 0.9650	 0.6260
Mz	 0.8580	 0.5390
R1	 0.8920	 0.4830
RA	 0.9260	 0.5700
RB	 0.7380	 0.5050
RC	 0.7070	 0.4550
RD	 0.9290	 0.5460
RE	 0.7990	 0.4710
RF	 0.3350	 0.2440
RG	 0.4030	 0.3360
Ra	 0.8030	 0.4990
Rb	 0.7870	 0.5340
Rc	 0.8760	 0.5540
Rd	 0.6730	 0.4540
Re	 0.7810	 0.4810
Rf	 0.6890	 0.4390
Rg	 0.7280	 0.4120
Rh	 0.6050	 0.4160
Ri	 0.8280	 0.4570
Rj	 0.7860	 0.4660
Rk	 0.6120	 0.4190
Rl	 0.8300	 0.5010
Rm	 0.1910	 0.2300
Rn	 0.8680	 0.5280

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Chain	Atom inclusion	Q-score
Ro	 0.8890	 0.5600
Rp	 0.6740	 0.4390
Rq	 0.7220	 0.4430
Rr	 0.6490	 0.4220
Rs	 0.7280	 0.4570
Rt	 0.7110	 0.4360
Ru	 0.6100	 0.3840
Rv	 0.8010	 0.5210
Rw	 0.9490	 0.5810
Rx	 0.9250	 0.5650
Ry	 0.7210	 0.4250
Rz	 0.5680	 0.4300
S1	 0.9150	 0.5010
SA	 0.9650	 0.5730
SB	 0.7570	 0.4950
SC	 0.8310	 0.4860
SD	 0.9240	 0.5240
SE	 0.7700	 0.4520
SF	 0.2870	 0.2220
SG	 0.5650	 0.3430
Sa	 0.8150	 0.4860
Sb	 0.7960	 0.5110
Sc	 0.9140	 0.5480
Sd	 0.7660	 0.4560
Se	 0.8940	 0.5200
Sf	 0.7810	 0.4550
Sg	 0.7910	 0.4380
Sh	 0.6500	 0.4400
Si	 0.9180	 0.5520
Sj	 0.8660	 0.4920
Sk	 0.6640	 0.3720
Sl	 0.9010	 0.5640
Sm	 0.2030	 0.1860
Sn	 0.8820	 0.5440
So	 0.9340	 0.5440
Sp	 0.6250	 0.3830
Sq	 0.8180	 0.4670
Sr	 0.7540	 0.4590
Ss	 0.7620	 0.4140
St	 0.7800	 0.4090
Su	 0.7060	 0.4080
Sv	 0.8320	 0.5090

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Chain	Atom inclusion	Q-score
Sw	 0.9560	 0.5730
Sx	 0.9320	 0.5700
Sy	 0.8290	 0.4550
Sz	 0.5950	 0.3370