



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 09:43 AM UTC

PDB ID : 7Z3O / pdb_00007z3o
EMDB ID : EMD-14480
Title : Cryo-EM structure of the ribosome-associated RAC complex on the 80S ribosome - RAC-2 conformation
Authors : Kisonaite, M.; Wild, K.; Sinning, I.
Deposited on : 2022-03-02
Resolution : 3.30 Å(reported)
Based on initial model : 7OLC

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
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

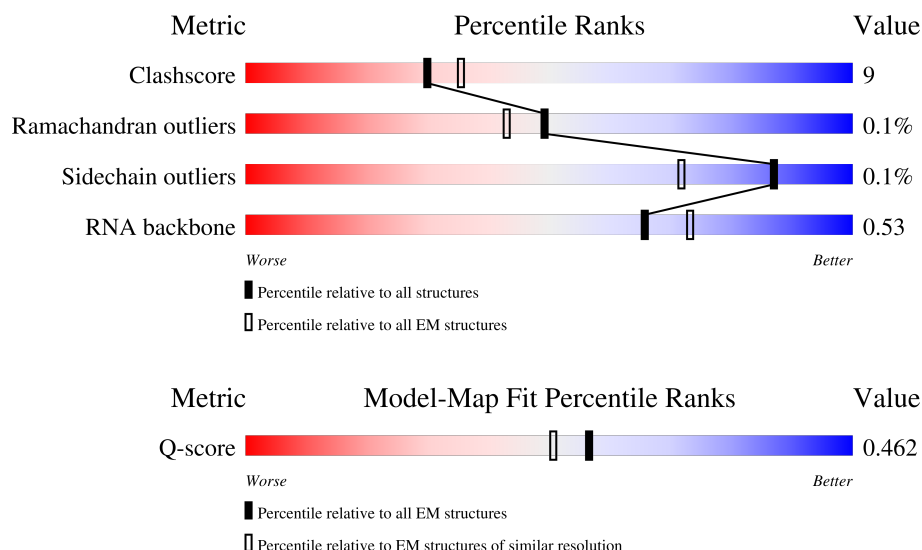
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.30 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	15087 (2.80 - 3.80)

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	1	3337	
2	2	1796	
3	3	120	

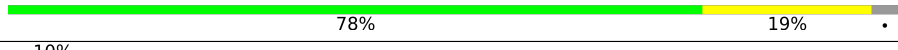
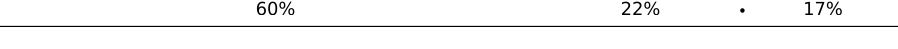
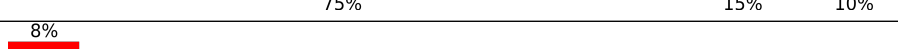
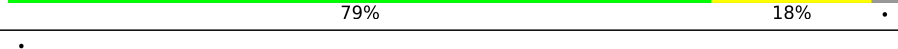
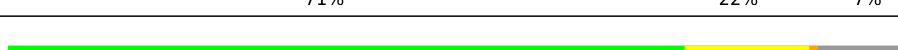
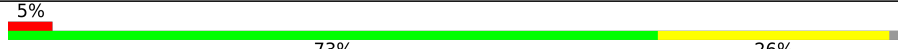
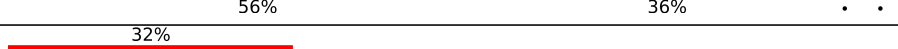
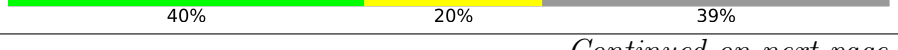
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Mol	Chain	Length	Quality of chain
4	4	156	
5	A	316	
6	B	302	
7	C	446	
8	D	578	
9	LA	254	
10	LB	392	
11	LC	365	
12	LD	304	
13	LE	200	
14	LF	249	
15	LG	262	
16	LH	192	
17	LI	219	
18	LJ	173	
19	LK	165	
20	LL	213	
21	LM	142	
22	LN	203	
23	LO	204	
24	LP	187	
25	LQ	213	
26	LR	192	
27	LS	174	
28	LT	160	

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Mol	Chain	Length	Quality of chain
29	LU	127	
30	LV	139	
31	LW	161	
32	LX	156	
33	LY	138	
34	LZ	135	
35	La	149	
36	Lb	65	
37	Lc	108	
38	Ld	120	
39	Le	131	
40	Lf	109	
41	Lg	119	
42	Lh	126	
43	Li	110	
44	Lj	95	
45	Lk	81	
46	Ll	51	
47	Lm	128	
48	Ln	25	
48	Lr	25	
49	Lo	106	
50	Lp	92	
51	Lq	147	
52	Ls	312	

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Mol	Chain	Length	Quality of chain
53	NC	27	 93%
54	SA	285	 50% 23% 27%
55	SB	255	 61% 30% 9%
56	SC	263	 52% 30% 18%
57	SD	254	 53% 31% 16%
58	SE	264	 63% 36%
59	SF	212	 7% 56% 38% 6%
60	SG	239	 59% 38%
61	SH	203	 62% 34%
62	SI	202	 73% 27%
63	SJ	190	 56% 38% 6%
64	SK	159	 25% 31% 44%
65	SL	161	 70% 22% 7%
66	SM	144	 54% 46% 35% 18%
67	SN	151	 68% 31%
68	SO	150	 65% 25% 10%
69	SP	153	 11% 46% 29% 25%
70	SQ	143	 6% 61% 36%
71	SR	143	 52% 37% 10%
72	SS	156	 54% 34% 12%
73	ST	153	 53% 40% 7%
74	SU	116	 64% 25% 11%
75	SV	98	 63% 24% 12%
76	SW	130	 72% 27%
77	SX	145	 73% 25%

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Mol	Chain	Length	Quality of chain
78	SY	136	
79	SZ	99	
80	Sa	119	
81	Sb	82	
82	Sc	68	
83	Sd	56	
84	Se	62	
85	Sf	154	

2 Entry composition

There are 88 unique types of molecules in this entry. The entry contains 213449 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 26S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	3191	Total	C	N	O	P	0	0
			68242	30465	12334	22252	3191		

- Molecule 2 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	1765	Total	C	N	O	P	0	0
			37637	16817	6705	12350	1765		

- Molecule 3 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	119	Total	C	N	O	P	0	0
			2535	1132	453	831	119		

- Molecule 4 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	156	Total	C	N	O	P	0	0
			3319	1484	589	1090	156		

- Molecule 5 is a protein called Putative guanine nucleotide-binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	A	312	Total	C	N	O	S	0	0
			2438	1534	424	468	12		

- Molecule 6 is a protein called HABP4_PA1-RBP1 domain-containing protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	B	31	Total	C	N	O	0	0
			243	144	49	50		

- Molecule 7 is a protein called Putative ribosome associated protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	C	444	Total	C	N	O	S	0	0
			3566	2218	661	683	4		

- Molecule 8 is a protein called Putative heat shock protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	D	519	Total	C	N	O	S	0	0
			3942	2470	689	780	3		

- Molecule 9 is a protein called 60S ribosomal protein L2-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LA	252	Total	C	N	O	S	0	0
			1925	1203	385	334	3		

- Molecule 10 is a protein called 60S ribosomal protein L3-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LB	387	Total	C	N	O	S	0	0
			3088	1964	576	535	13		

- Molecule 11 is a protein called 60S ribosomal protein L4-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LC	363	Total	C	N	O	S	0	0
			2758	1741	527	481	9		

- Molecule 12 is a protein called 60S ribosomal protein l5-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LD	300	Total	C	N	O	S	0	0
			2440	1545	431	461	3		

- Molecule 13 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LE	194	Total	C	N	O	S	0	0
			1518	974	274	267	3		

- Molecule 14 is a protein called 60S ribosomal protein l7-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LF	247	Total	C	N	O	S	0	0
			2017	1294	376	344	3		

- Molecule 15 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LG	235	Total	C	N	O	S	0	0
			1900	1218	351	326	5		

- Molecule 16 is a protein called uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LH	191	Total	C	N	O	S	0	0
			1505	955	269	275	6		

- Molecule 17 is a protein called 60S ribosomal protein L10-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LI	217	Total	C	N	O	S	0	0
			1760	1109	343	299	9		

- Molecule 18 is a protein called Putative ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LJ	167	Total	C	N	O	S	0	0
			1367	854	268	239	6		

- Molecule 19 is a protein called 60S ribosomal protein L12-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LK	155	Total	C	N	O	S	0	0
			762	452	155	155			

- Molecule 20 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LL	209	Total	C	N	O	S	0	0
			1666	1037	340	287	2		

- Molecule 21 is a protein called 60S ribosomal protein L14-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LM	141	Total	C	N	O	S	0	0
			1125	714	216	194	1		

- Molecule 22 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LN	202	Total	C	N	O	S	0	0
			1703	1062	360	277	4		

- Molecule 23 is a protein called 60S ribosomal protein L16-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LO	203	Total	C	N	O	S	0	0
			1613	1036	305	267	5		

- Molecule 24 is a protein called 60S ribosomal protein l17-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LP	186	Total	C	N	O	S	0	0
			1472	912	295	262	3		

- Molecule 25 is a protein called Ribosomal protein L18-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LQ	183	Total	C	N	O	S	0	0
			1481	935	306	238	2		

- Molecule 26 is a protein called Ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LR	184	Total	C	N	O	S	0	0
			1506	928	324	249	5		

- Molecule 27 is a protein called 60S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LS	173	Total	C	N	O	S	0	0
			1425	917	266	238	4		

- Molecule 28 is a protein called 60S ribosomal protein l21-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LT	158	Total	C	N	O	S	0	0
			1266	803	246	215	2		

- Molecule 29 is a protein called 60S ribosomal protein L22-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LU	104	Total	C	N	O	S	0	0
			842	547	146	148	1		

- Molecule 30 is a protein called 60S ribosomal protein l23-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	LV	135	Total	C	N	O	S	0	0
			994	633	185	169	7		

- Molecule 31 is a protein called eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	LW	133	Total	C	N	O	S	0	0
			1075	667	221	185	2		

- Molecule 32 is a protein called 60S ribosomal protein L25-like protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	LX	121	Total	C	N	O	0	0
			965	620	175	170		

- Molecule 33 is a protein called 60S ribosomal protein L26-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	LY	134	Total	C	N	O	S	0	0
			1065	664	215	184	2		

- Molecule 34 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	LZ	135	Total	C	N	O	S	0	0
			1111	713	207	187	4		

- Molecule 35 is a protein called 60S ribosomal protein L28-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	La	148	Total	C	N	O	S	0	0
			1180	745	239	194	2		

- Molecule 36 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Lb	62	Total	C	N	O	S	0	0
			508	310	112	86			

- Molecule 37 is a protein called 60S ribosomal protein l30-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Lc	97	Total	C	N	O	S	0	0
			722	458	125	134	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Ld	119	Total	C	N	O	S	0	0
			965	607	188	168	2		

- Molecule 39 is a protein called 60S ribosomal protein L32-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Le	124	Total	C	N	O	S	0	0
			1001	629	205	161	6		

- Molecule 40 is a protein called 60S ribosomal protein l33-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Lf	107	Total	C	N	O	S	0	0
			853	540	170	142	1		

- Molecule 41 is a protein called Ribosomal protein l34-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Lg	112	Total	C	N	O	S	0	0
			891	554	181	152	4		

- Molecule 42 is a protein called Dolichyl-diphosphooligosaccharide--protein glycotransferase.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	Lh	122	Total	C	N	O	0	0
			1003	637	198	168		

- Molecule 43 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Li	102	Total	C	N	O	S	0	0
			836	515	184	136	1		

- Molecule 44 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Lj	86	Total	C	N	O	S	0	0
			684	418	152	109	5		

- Molecule 45 is a protein called eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Lk	80	Total	C	N	O	S	0	0
			658	415	126	115	2		

- Molecule 46 is a protein called Ribosomal protein eL39.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	Ll	50	Total	C	N	O	0	0
			435	275	97	63		

- Molecule 47 is a protein called Putative ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Lm	52	Total	C	N	O	S	0	0
			418	261	86	65	6		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Lm	1	MET	SER	conflict	UNP G0S8G4
Lm	2	GLN	ARG	conflict	UNP G0S8G4

- Molecule 48 is a protein called 60S ribosomal protein L41-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Ln	24	Total	C	N	O	S	0	0
			224	136	61	26	1		
48	Lr	24	Total	C	N	O	S	0	0
			224	136	61	26	1		

- Molecule 49 is a protein called 60S ribosomal protein L44-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	Lo	104	Total	C	N	O	S	0	0
			822	520	161	136	5		

- Molecule 50 is a protein called 60S ribosomal protein L43-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Lp	91	Total	C	N	O	S	0	0
			697	430	138	123	6		

- Molecule 51 is a protein called Putative 60S ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	Lq	141	Total	C	N	O		0	0
			1083	678	215	190			

- Molecule 52 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	Ls	189	Total	C	N	O	S	0	0
			1449	927	250	265	7		

- Molecule 53 is a protein called Nascent chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	NC	27	Total	C	N	O		0	0
			135	81	27	27			

- Molecule 54 is a protein called 40S ribosomal protein S0.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SA	208	Total	C	N	O	S	0	0
			1641	1051	289	295	6		

- Molecule 55 is a protein called 40S ribosomal protein S1.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SB	232	Total	C	N	O	S	0	0
			1871	1190	351	325	5		

- Molecule 56 is a protein called 40S ribosomal protein S2-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SC	216	Total	C	N	O	S	0	0
			1672	1074	294	301	3		

- Molecule 57 is a protein called 40S ribosomal protein S3-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SD	214	Total	C	N	O	S	0	0
			1688	1068	307	305	8		

- Molecule 58 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SE	261	Total	C	N	O	S	0	0
			2072	1314	389	362	7		

- Molecule 59 is a protein called 40S ribosomal protein s5-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SF	199	Total	C	N	O	S	0	0
			1557	971	294	285	7		

- Molecule 60 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SG	232	Total	C	N	O	S	0	0
			1875	1171	376	323	5		

- Molecule 61 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SH	195	Total	C	N	O		0	0
			1562	983	300	279			

- Molecule 62 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	SI	201	Total	C	N	O	S	0	0
			1621	1009	330	281	1		

- Molecule 63 is a protein called 40S ribosomal protein s9-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	SJ	179	Total	C	N	O	S	0	0
			1466	933	290	241	2		

- Molecule 64 is a protein called 40S ribosomal protein s10-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	SK	89	Total	C	N	O	S	0	0
			742	487	124	129	2		

- Molecule 65 is a protein called 40S ribosomal protein S11-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	SL	150	Total	C	N	O	S	0	0
			1222	780	236	201	5		

- Molecule 66 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	SM	118	Total	C	N	O	S	0	0
			923	577	167	171	8		

- Molecule 67 is a protein called 40S ribosomal protein S13-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	SN	150	Total	C	N	O	S	0	0
			1182	756	220	205	1		

- Molecule 68 is a protein called 40S ribosomal protein S14-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	SO	135	Total	C	N	O	S	0	0
			1002	614	199	184	5		

- Molecule 69 is a protein called 40S ribosomal protein s15-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	SP	115	Total	C	N	O	S	0	0
			917	583	172	159	3		

- Molecule 70 is a protein called 40S ribosomal protein S16-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	SQ	138	Total	C	N	O	S	0	0
			1081	693	202	184	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
71	SR	128	Total	C	N	O	S	0	0
			1045	657	190	195	3		

- Molecule 72 is a protein called Putative ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	SS	137	Total	C	N	O	S	0	0
			1118	699	222	196	1		

- Molecule 73 is a protein called 40S ribosomal protein S19-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	ST	142	Total	C	N	O	S	0	0
			1117	694	221	201	1		

- Molecule 74 is a protein called 40S ribosomal protein S20-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	SU	103	Total	C	N	O	S	0	0
			819	517	150	148	4		

- Molecule 75 is a protein called 40S ribosomal protein S21-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	SV	86	Total	C	N	O	S	0	0
			664	408	124	128	4		

- Molecule 76 is a protein called 40S ribosomal protein S22-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	SW	129	Total	C	N	O	S	0	0
			1037	659	195	178	5		

- Molecule 77 is a protein called 40S ribosomal protein s23-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	SX	142	Total	C	N	O	S	0	0
			1099	694	215	188	2		

- Molecule 78 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	SY	132	Total	C	N	O	S	0	0
			1061	668	209	182	2		

- Molecule 79 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	SZ	69	Total	C	N	O	S	0	0
			546	345	101	98	2		

- Molecule 80 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Sa	104	Total	C	N	O	S	0	0
			839	518	177	137	7		

- Molecule 81 is a protein called Ribosomal protein s27-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	Sb	81	Total	C	N	O	S	0	0
			611	386	111	107	7		

- Molecule 82 is a protein called 40S ribosomal protein S28-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	Sc	61	Total	C	N	O	S	0	0
			484	298	97	88	1		

- Molecule 83 is a protein called Ribosomal protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	Sd	52	Total	C	N	O	S	0	0
			419	261	84	70	4		

- Molecule 84 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms				AltConf	Trace
84	Se	40	Total	C	N	O	0	0
			322	202	67	53		

- Molecule 85 is a protein called 40S ribosomal protein S27a-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	Sf	73	Total	C	N	O	S	0	0
			604	382	115	101	6		

- Molecule 86 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
86	1	366	Total	Mg	0
			366	366	
86	2	80	Total	Mg	0
			80	80	
86	3	7	Total	Mg	0
			7	7	
86	4	9	Total	Mg	0
			9	9	
86	D	1	Total	Mg	0
			1	1	
86	LC	1	Total	Mg	0
			1	1	
86	LN	3	Total	Mg	0
			3	3	
86	LP	1	Total	Mg	0
			1	1	
86	LV	1	Total	Mg	0
			1	1	
86	LW	1	Total	Mg	0
			1	1	
86	Lb	1	Total	Mg	0
			1	1	
86	Lo	1	Total	Mg	0
			1	1	

- # ATP

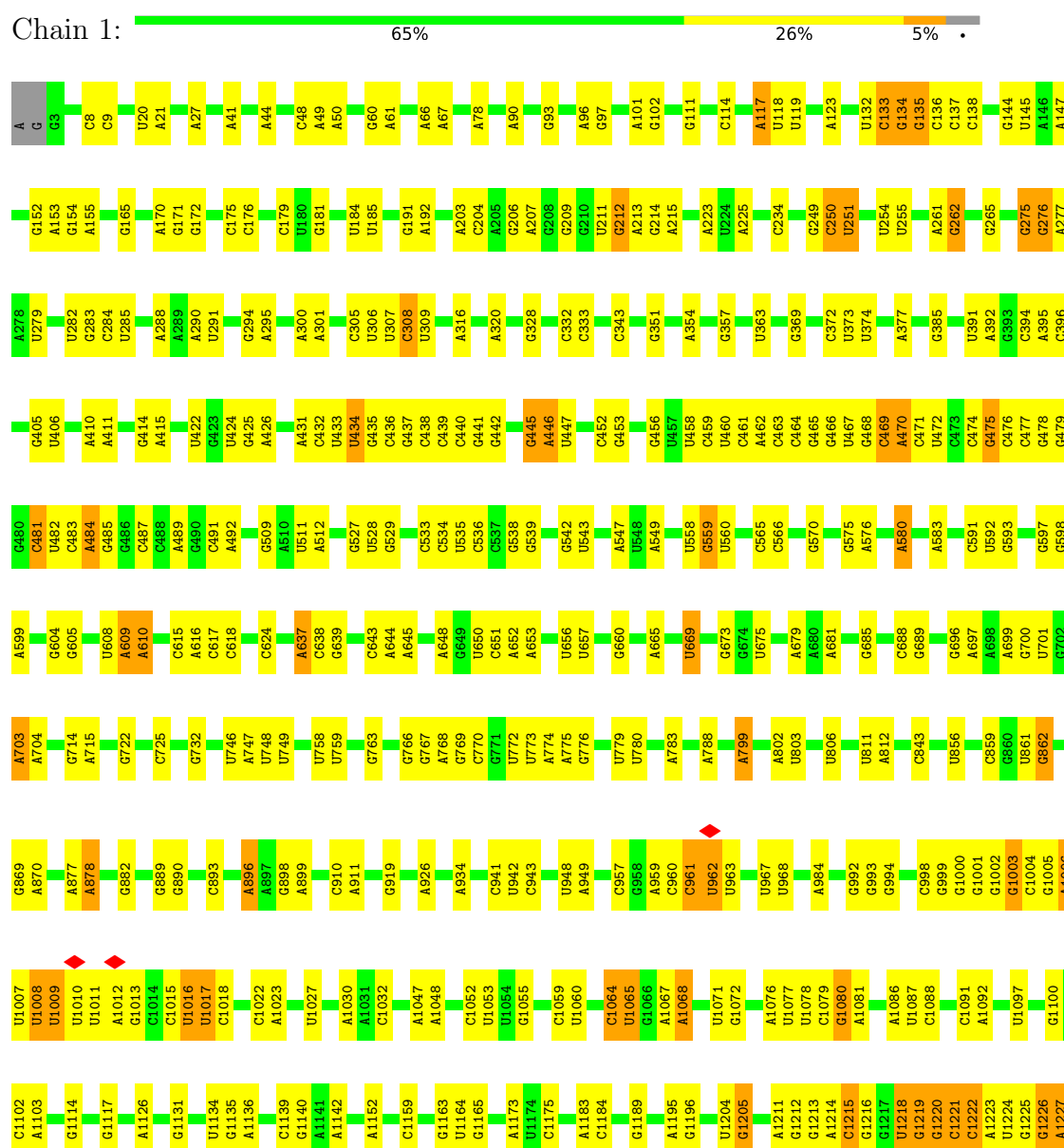
- Molecule 88 is ZINC ION (CCD ID: ZN) (formula: Zn).



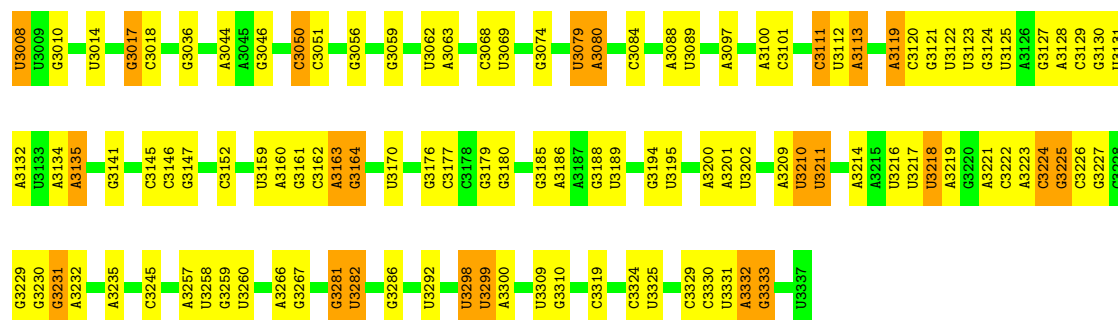
3 Residue-property plots

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

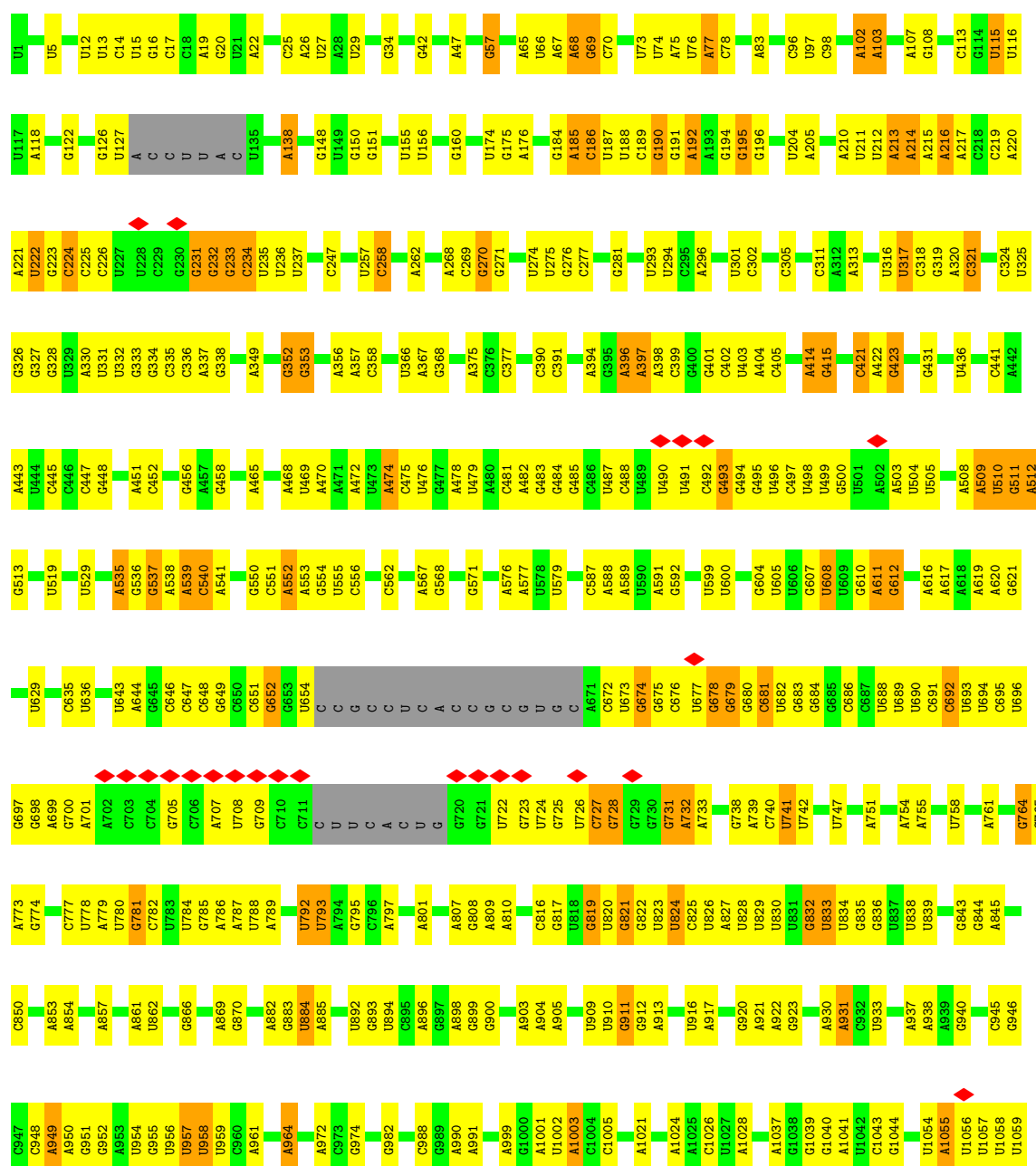
• Molecule 1: 26S rRNA

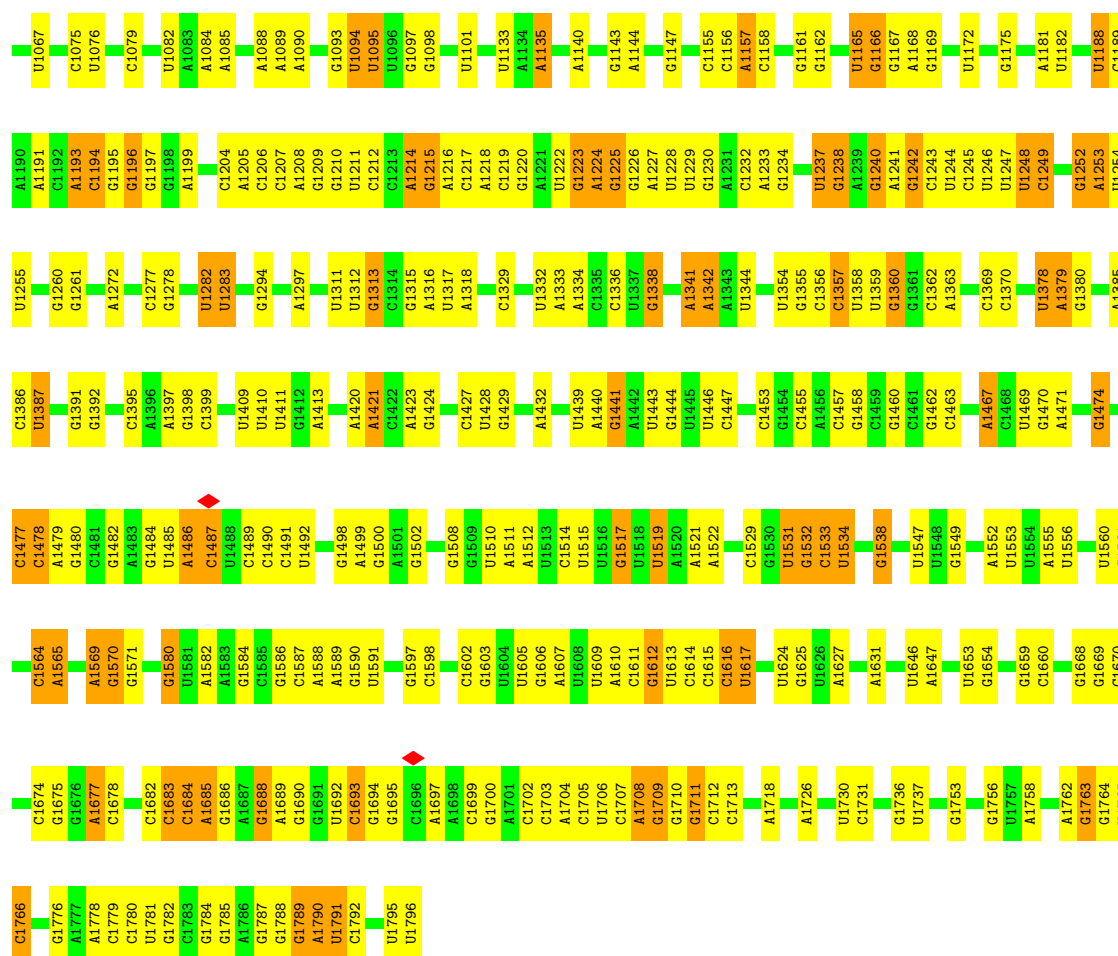


C2830	U2676	G2533	A	U2389	U2133	G	G	A1863	G1749	G1615	G1485	C1323	A1228
A2831	G2679	G2534	◆	U2390	G2134	G	G	A1866	G1750	A1618	C1491	U1324	G1229
C2840	G2687	G2535		G2391	U2139	C	C	A1867	U1752	G1751	C1491	A1331	U1230
U2842	U2688	G2536		A2393	A2141	U	U	A1876	G1758	A1622	U1495	G1332	G1232
C2843		G2537	◆	U2396	G2148	C	C	G1879	C1759	G1623	U1506	A1333	G1233
A2846	G2704	G2538		G2400	U2149	G	U	G1886	G1760	C1624	U1516	A1335	C1237
G2854	A2707	G2539		G2405	U2151	C	A	C1887	C1761	U1625	U1516	C1336	C1238
C2858	G2710	A2552		C2406	G2166	G	C	A1888	C1763	G1632	G1530	A1337	U1239
U2863	U2711	G2553		C2407	C2167	U	C	A1893	G1766	G1633	G1530	U1339	
U2868	G2712	G2554		C2408	U2168	C	G	C1906	A1767	G1634	U1537	A1242	A1243
C2713	G2713	G2555		U2409	G2169	G	G	G1907	C1768	G1635	U1538	A1244	G1244
C2714	C2714	G2556		A2410	A2170	A	A	C1921	U1770	A1636	C1539	A1246	G1245
U2882	G2719	G2557		G2411	A2171	C	C	U1922	A1777	G1641	A1541	U1247	U1248
U2894	G2720	G2558		U	U2172	U	C	G1929	A1778	G1642	A1542	G1249	G1249
A2895	A2721	G2559		G	G2173	G	G	U1932	U1779	G1643	G1544	U1252	U1252
A2900	U2726	G2560		U	A2176	C	C	G1933	U1780	G1644	G1545	A1253	A1253
G2904	A2727	G2561		A	A2177	C	G	G1934	C1782	C1651	G1546	A1254	C1254
A2905	G2729	A2585		A	G2181	C	C	C1935	G1792	U1668	G1552	C1255	C1255
G2906	U2730	A2601		U	A2182	C	G	A1936	A1793	U1669	U1553	G1387	C1260
C2907	C2731	A2602		A	G2183	C	C	C1937	U1794	C1670	G1554	A1390	C1261
C2919	C2732	U2611		G	A2184	C	C	U1938	U1795	U1671	C1555	U1401	C1262
G2920	G2736	U2612		C	G2185	C	C	G1939	A1796	C1673	U1560	A1402	C1263
U2921	A2737	A2615		U	A2192	C	C	U1940	U1797	A1676	G1561	U1264	U1264
C2922	G2755	A2616		G	A2207	C	C	U1941	U1798	A1677	U1562	C1265	C1265
G2923		G2617		U	G2212	C	U	G	U1799	C1677	C1267	G1404	C1266
A2926	A2758	G2621		A	G2216	C	C	C	U1800	U1685	A1567	G1417	G1267
G2927	G2759	G2622		C	U2217	C	C	U	U1801	A1695	A1568	G1420	G1268
A2930	A2760	G2623		U	A2218	C	A	U	G1812	A1696	A1569	G1420	G1272
G2931	A2763	C2633		C	A2219	C	C	C	G1813	C1697	G1570	G1433	A1277
C2932		A2633		U	C2220	C	C	C	C1818	U1702	G1571	U1442	G1278
C2942	C2769	G2636		G	U2221	C	C	C	A1819	G1703	A1574	U1442	G1290
U2945	A2776	U2642		C	A2222	C	C	C	U1820	U1704	C1577	A1291	A1291
A2946	U2777	C2643		C	U2237	C	C	C	A1821	C1705	G1578	U1292	U1292
C2960	G2783	A2648		C	C2228	C	A	A	A1822	G1727	A1582	A1450	G1296
G2966		G2649		U	U2232	C	U	C	C1826	G1730	A1585	U1454	C1297
A2970	U2788	A2516		G	G2235	C	C	C	U1829	A1731	U1586	G1455	U1298
U2974	G2798	G2517		A	G2236	C	A	C	A1830	C1739	U1587	G1458	C1299
C2975	C2803	G2518		A	U2242	C	C	U	A1838	A1740	C1588	A1464	A1300
A2804	A2804	A2521		U	A2243	C	C	G	G1843	C1741	G1597	A1464	A1301
C2983		G2524		C	U2244	C	C	C	G1846	U1742	G1598	C1306	C1306
U3005	A2823	U2666		C	U2245	C	U	C	U1743	C1744	A1599	A1313	A1313
A3006	U2824	C2667		A	G2123	C	A	C	G1858	U1745	U1609	U1314	U1314
A3007	U2828	G2673		U	G2124	C	C	C	U1859	U1746	G1610	G1476	C1319
					G2132	C	A	A	U1860	U1747	C1611	G1320	G1320



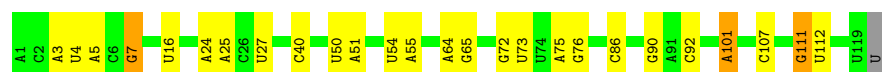
• Molecule 2: 18S rRNA





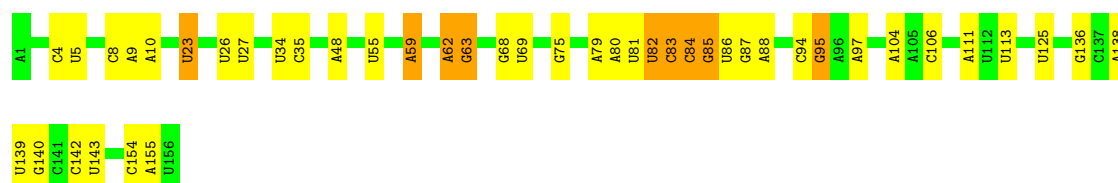
- Molecule 3: 5S rRNA

Chain 3: 78% 19% ..



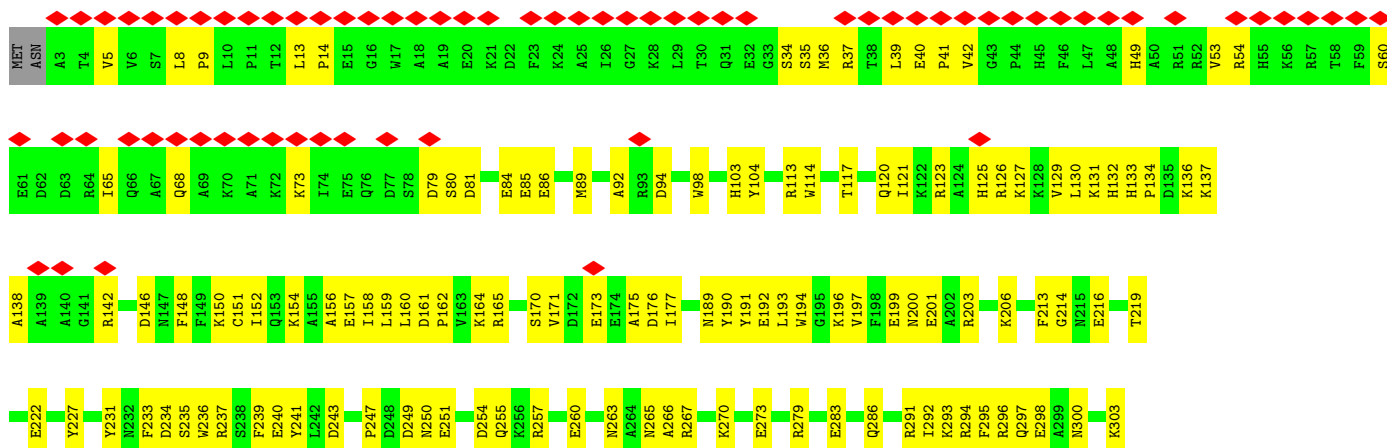
- Molecule 4: 5.8S rRNA

Chain 4: 72% 22% 6%

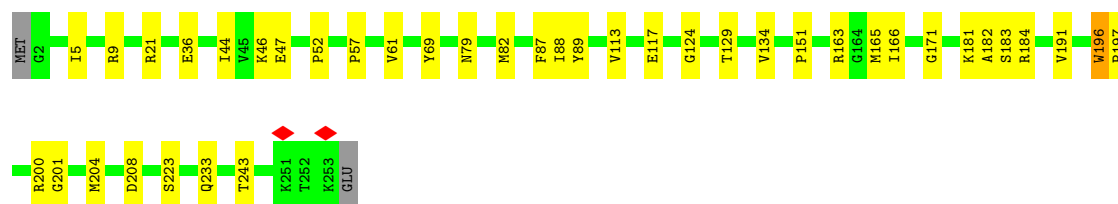


- Molecule 5: Putative guanine nucleotide-binding protein

Chain A: 13% 63% 36%

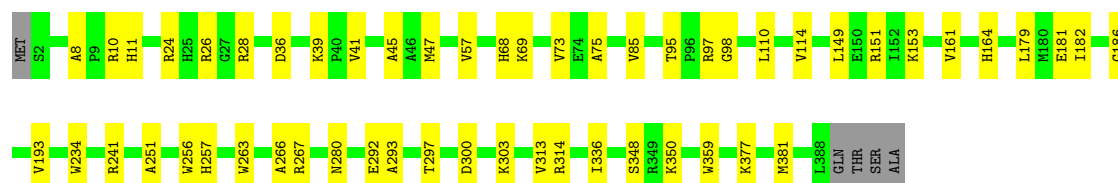


Chain LA:  83% 15% .



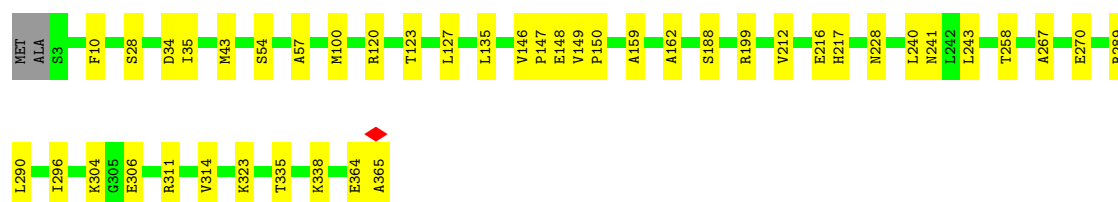
- Molecule 10: 60S ribosomal protein L3-like protein

Chain LB:  85% 14% .



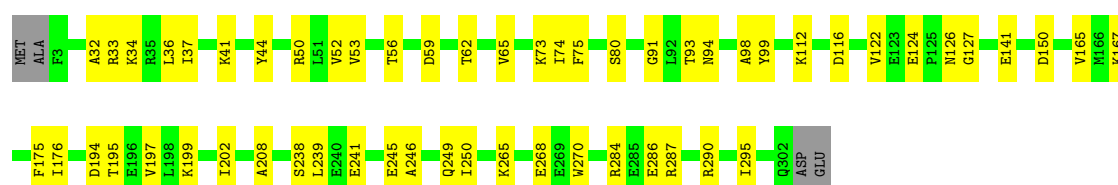
- Molecule 11: 60S ribosomal protein L4-like protein

Chain LC:  88% 12% .



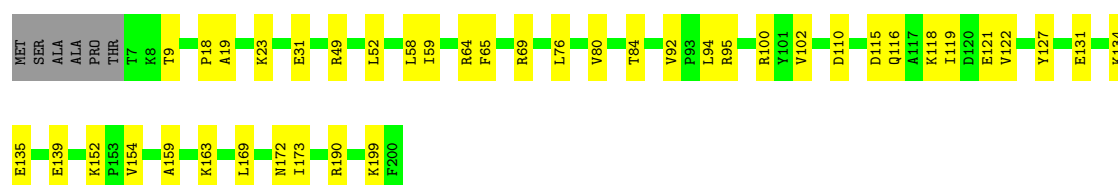
- Molecule 12: 60S ribosomal protein l5-like protein

Chain LD:  80% 18% .



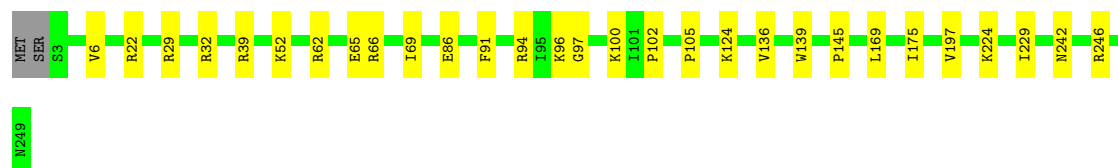
- Molecule 13: 60S ribosomal protein L6

Chain LE:  76% 20% .



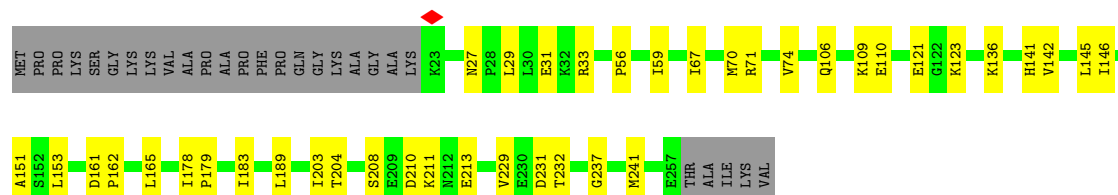
- Molecule 14: 60S ribosomal protein l7-like protein

Chain LF:  88% 12%



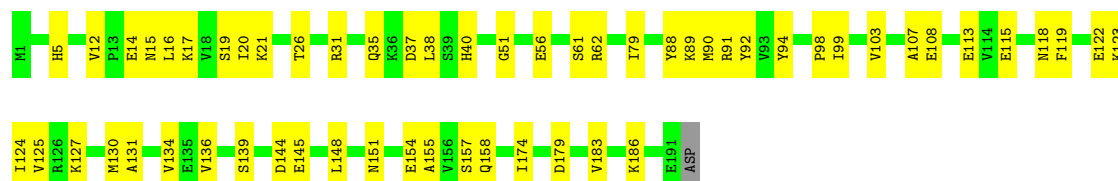
- Molecule 15: 60S ribosomal protein L8

Chain LG:  74% 15% 10%



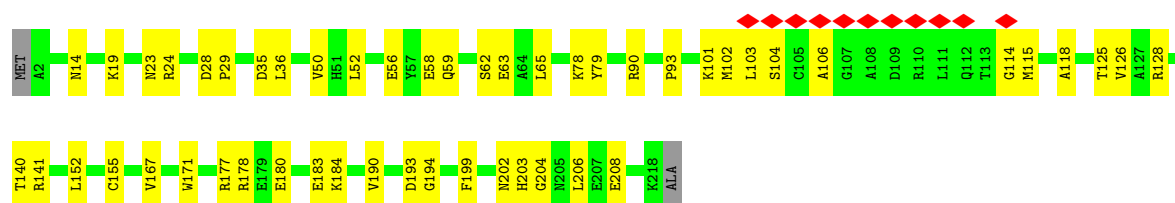
- Molecule 16: uL6

Chain LH:  70% 30%



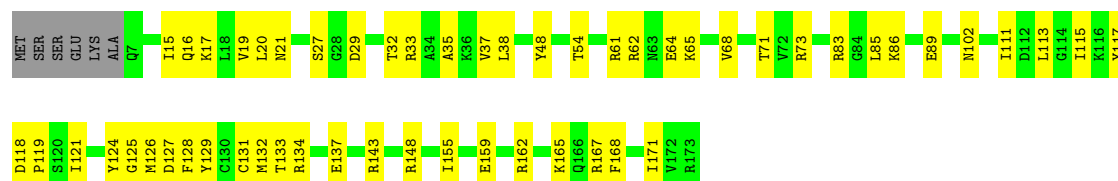
- Molecule 17: 60S ribosomal protein L10-like protein

Chain LI:  5% 76% 23%

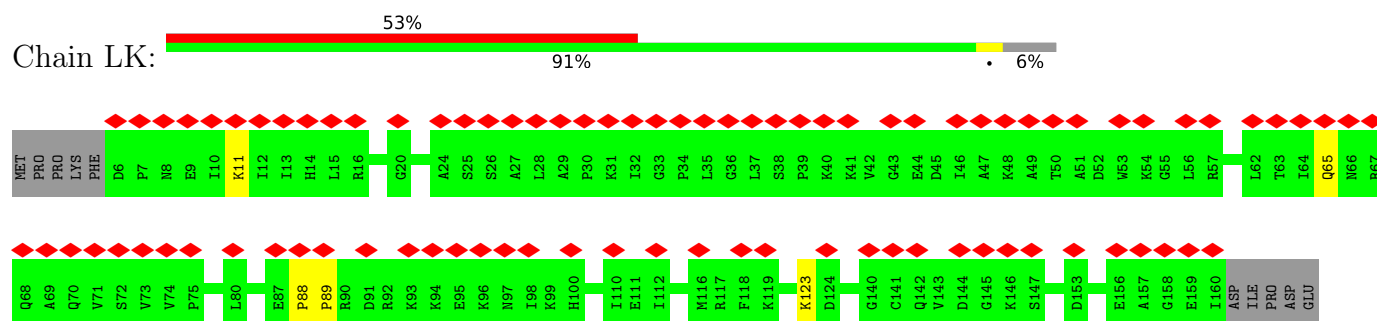


- Molecule 18: Putative ribosomal protein

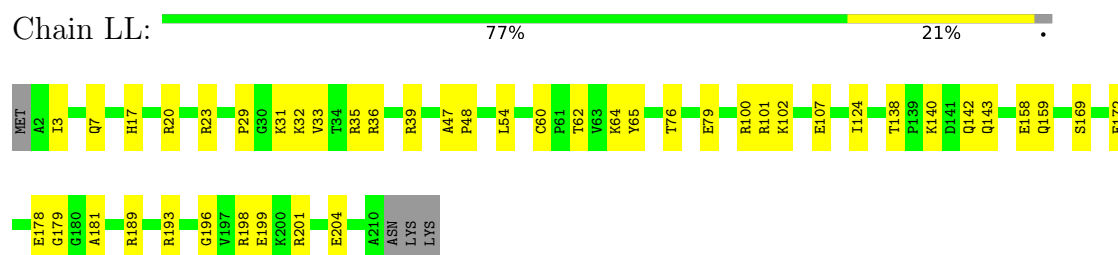
Chain LJ:  65% 31%



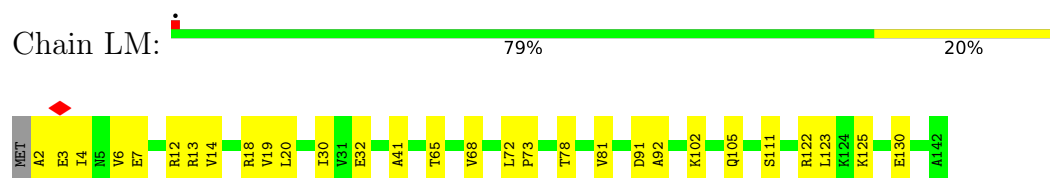
- Molecule 19: 60S ribosomal protein L12-like protein



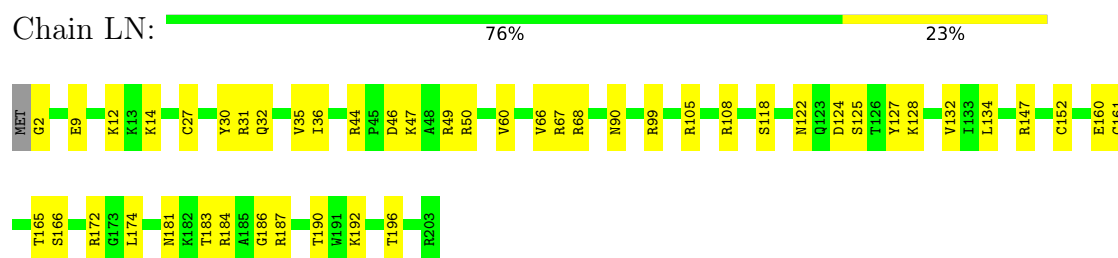
- Molecule 20: 60S ribosomal protein L13



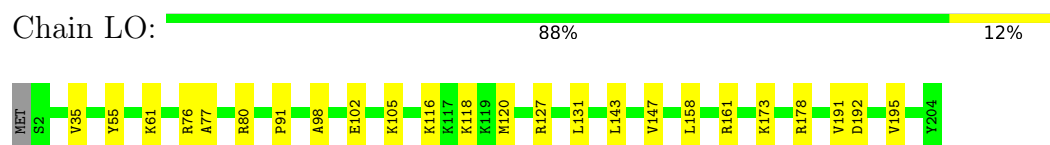
- Molecule 21: 60S ribosomal protein L14-like protein



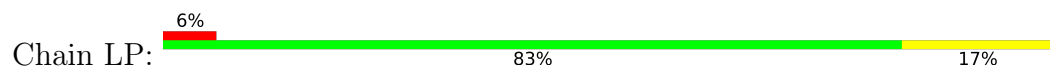
- Molecule 22: Ribosomal protein L15

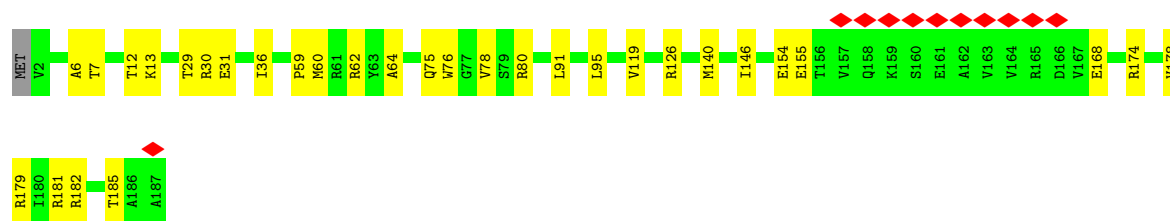


- Molecule 23: 60S ribosomal protein L16-like protein



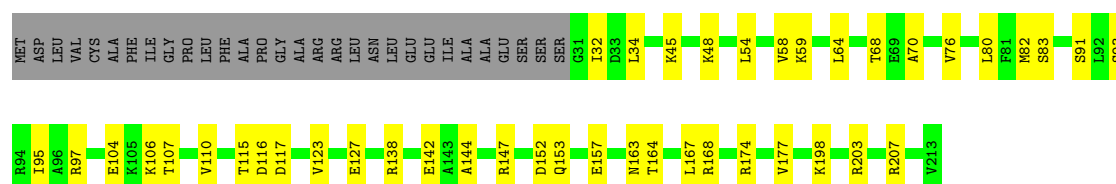
- Molecule 24: 60S ribosomal protein l17-like protein





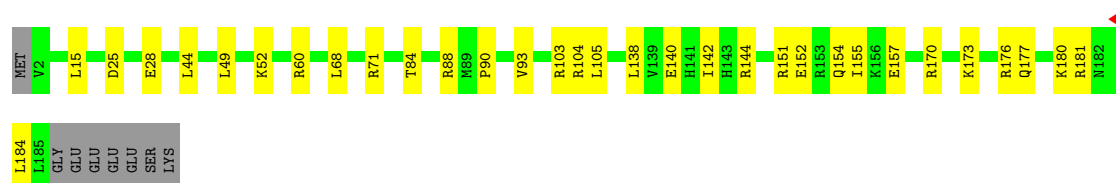
- Molecule 25: Ribosomal protein L18-like protein

Chain LQ: 66% 20% 14%



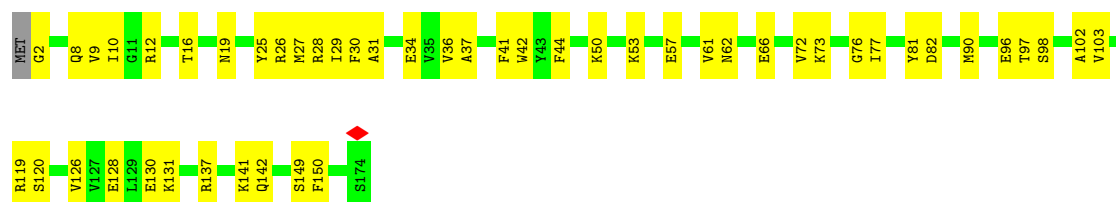
- Molecule 26: Ribosomal protein L19

Chain LR: 79% 17% .



- Molecule 27: 60S ribosomal protein L20

Chain LS: 71% 28% .



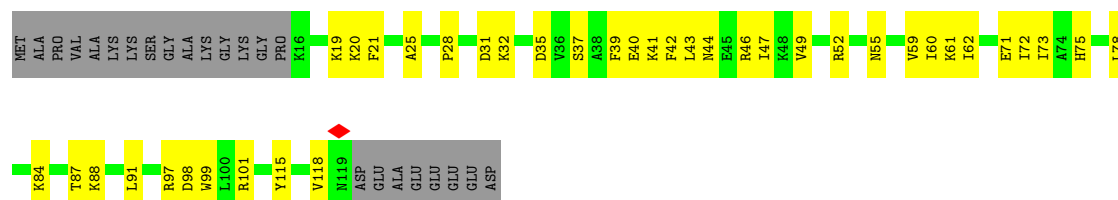
- Molecule 28: 60S ribosomal protein L21-like protein

Chain LT: 87% 12% .



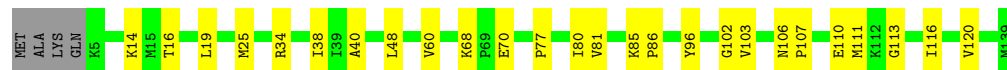
- Molecule 29: 60S ribosomal protein L22-like protein

Chain LU: 51% 31% 18%



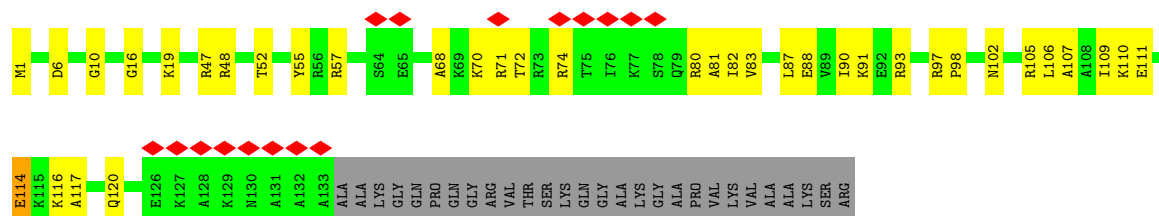
- Molecule 30: 60S ribosomal protein l23-like protein

Chain LV: 78% 19%



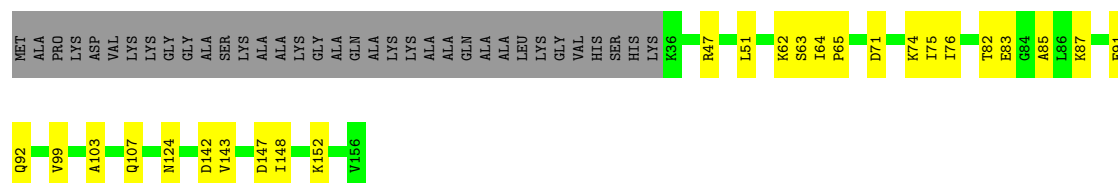
- Molecule 31: eL24

Chain LW: 10% 60% 22% 17%



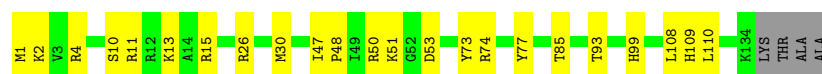
- Molecule 32: 60S ribosomal protein L25-like protein

Chain LX: 62% 16% 22%



- Molecule 33: 60S ribosomal protein L26-like protein

Chain LY: 80% 17%



- Molecule 34: 60S ribosomal protein L27

Chain LZ: 76% 24%





- Molecule 35: 60S ribosomal protein L28-like protein

Chain La: 80% 19% .



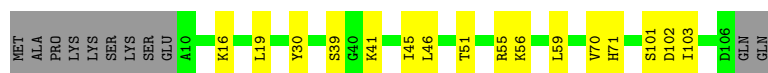
- Molecule 36: 60S ribosomal protein L29

Chain Lb: 74% 22% 5%



- Molecule 37: 60S ribosomal protein l30-like protein

Chain Lc: 75% 15% 10%



- Molecule 38: Putative 60S ribosomal protein

Chain Ld: 8% 75% 24% .



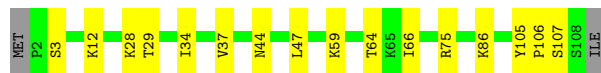
- Molecule 39: 60S ribosomal protein L32-like protein

Chain Le: 88% 7% 5%



- Molecule 40: 60S ribosomal protein l33-like protein

Chain Lf: 83% 15% .



- Molecule 41: Ribosomal protein l34-like protein

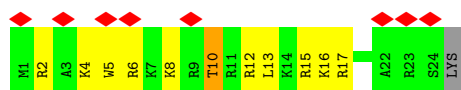
Chain Lg: 75% 19% 6%

Chain Ln: 



- Molecule 48: 60S ribosomal protein L41-A

Chain Lr: 



- Molecule 49: 60S ribosomal protein L44-like protein

Chain Lo: 



- Molecule 50: 60S ribosomal protein L43-like protein

Chain Lp: 



- Molecule 51: Putative 60S ribosomal protein

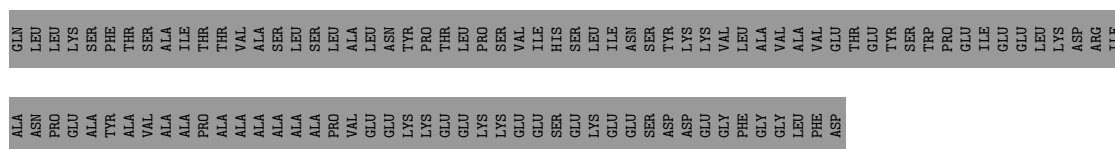
Chain Lq: 



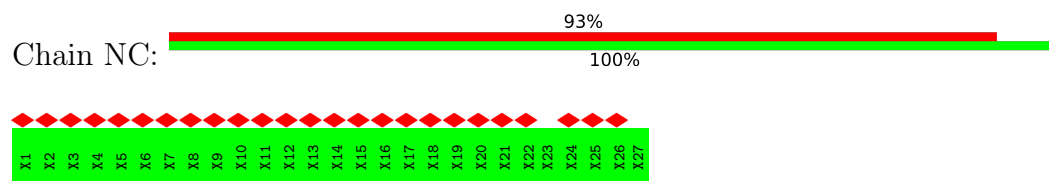
- Molecule 52: 60S acidic ribosomal protein P0

Chain Ls: 

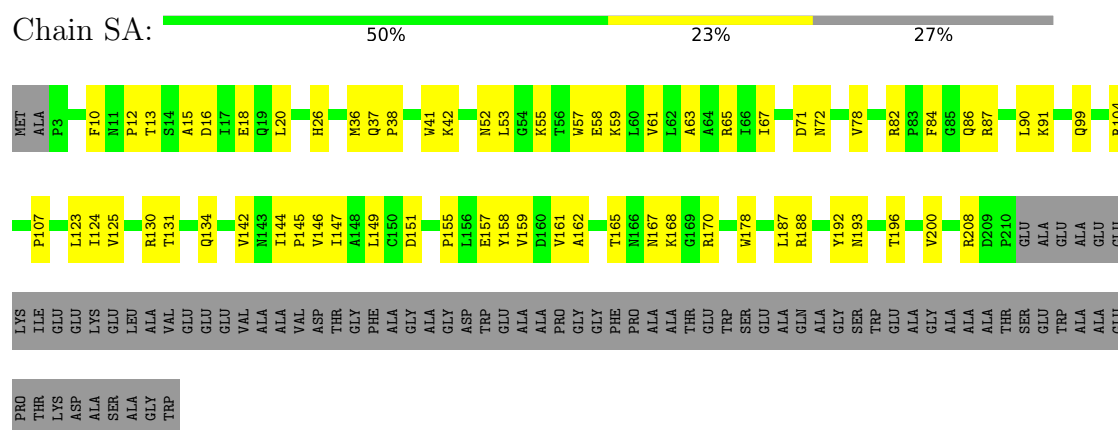




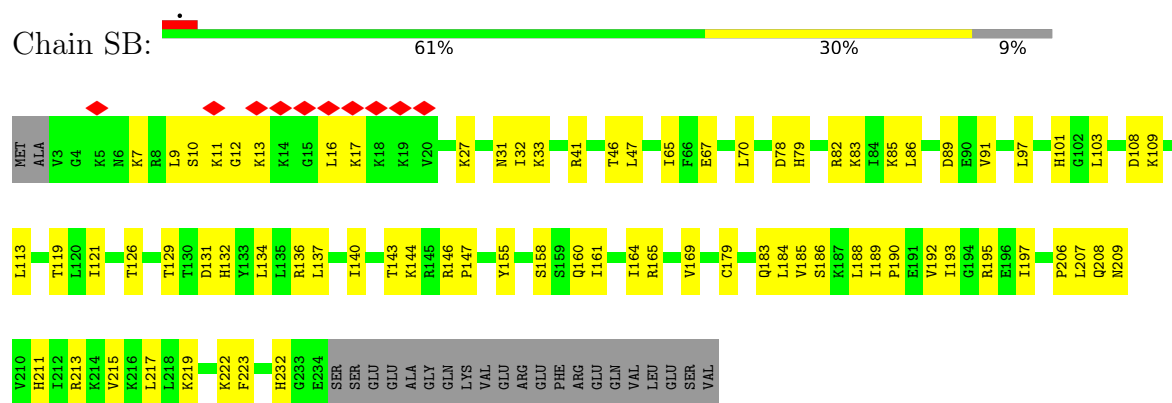
- Molecule 53: Nascent chain



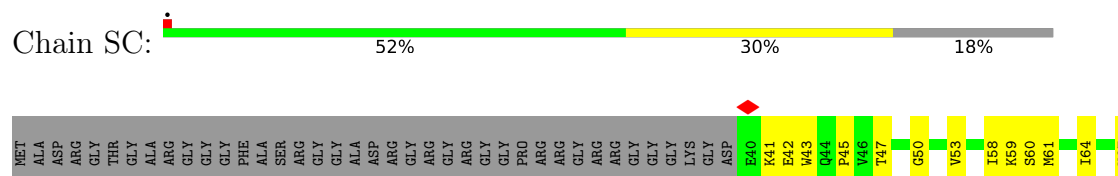
- Molecule 54: 40S ribosomal protein S0

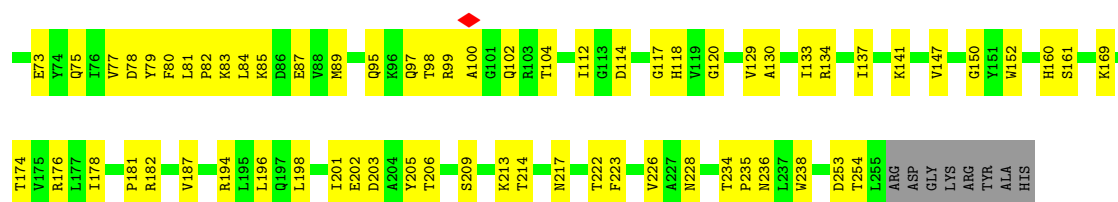


- Molecule 55: 40S ribosomal protein S1

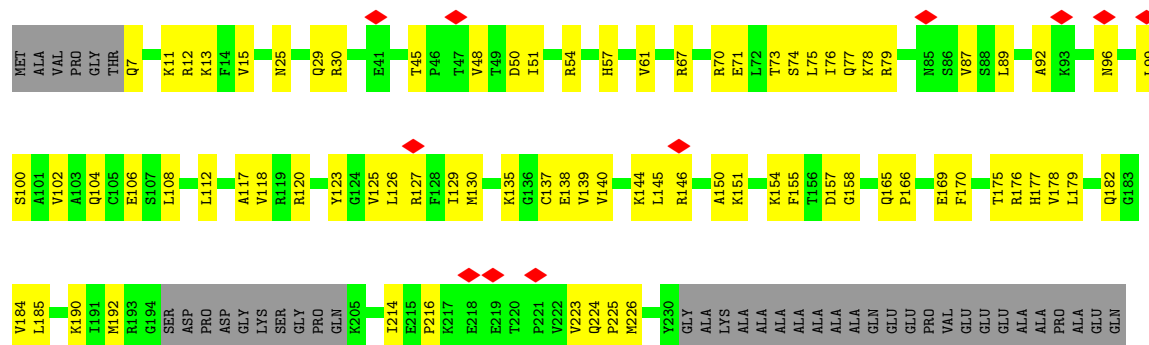


- Molecule 56: 40S ribosomal protein S2-like protein

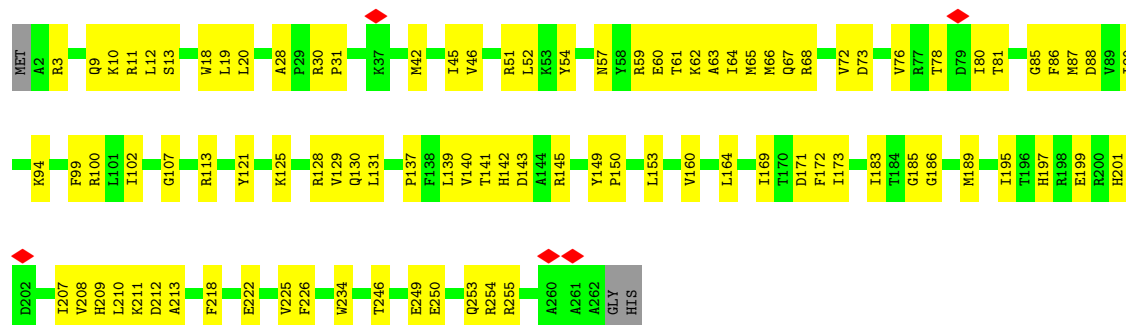




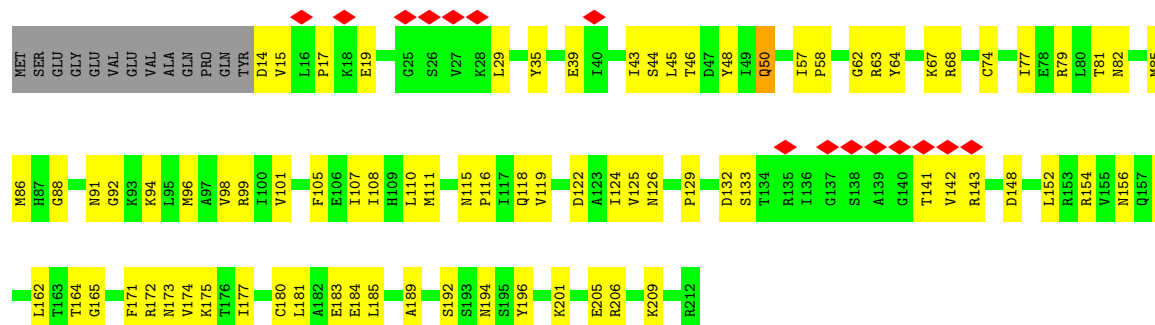
- Molecule 57: 40S ribosomal protein S3-like protein



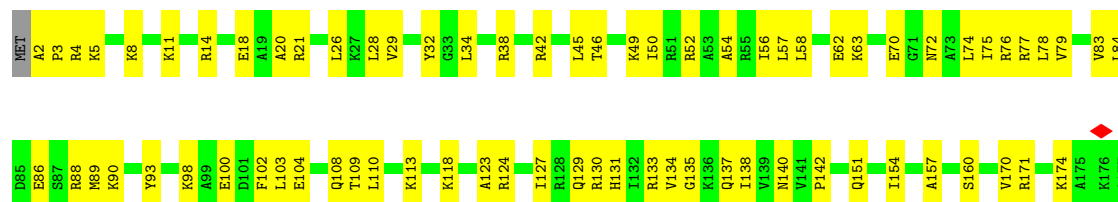
- Molecule 58: 40S ribosomal protein S4



- Molecule 59: 40S ribosomal protein s5-like protein



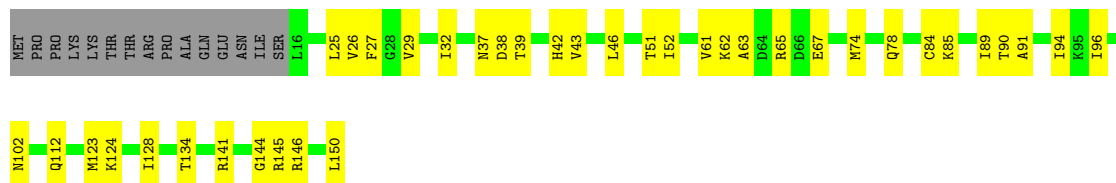
Chain SG: 59% 38% 3%





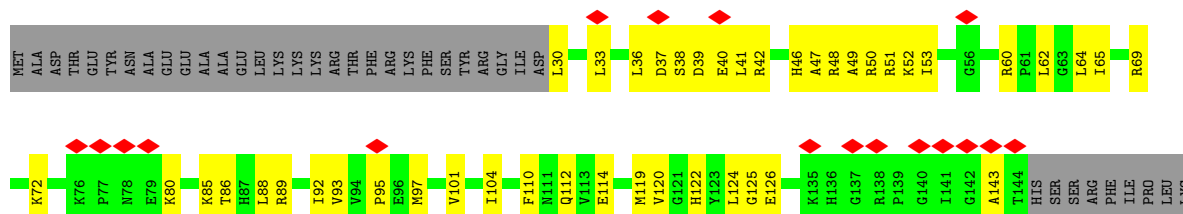
- Molecule 68: 40S ribosomal protein S14-like protein

Chain SO: 65% 25% 10%



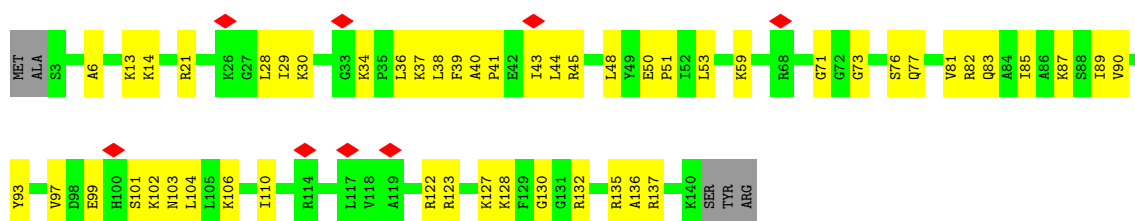
- Molecule 69: 40S ribosomal protein s15-like protein

Chain SP: 11% 46% 29% 25%



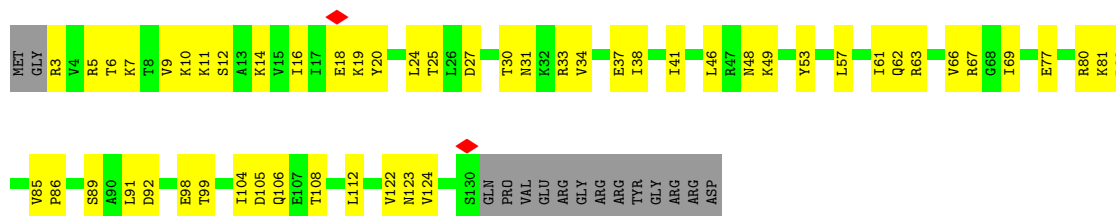
- Molecule 70: 40S ribosomal protein S16-like protein

Chain SQ: 6% 61% 36% .

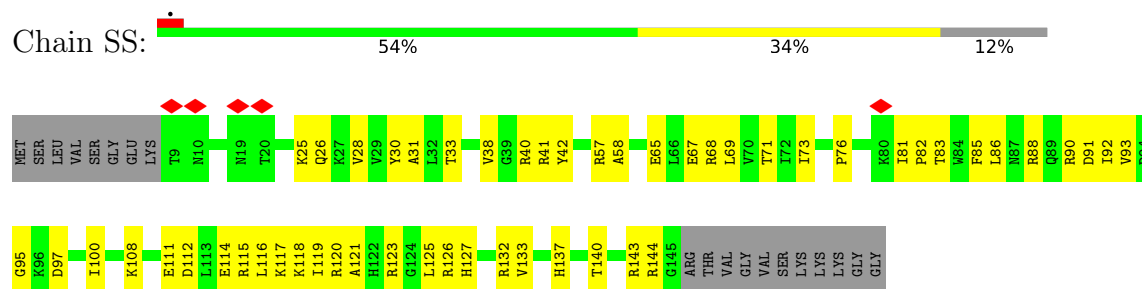


- Molecule 71: 40S ribosomal protein S17-like protein

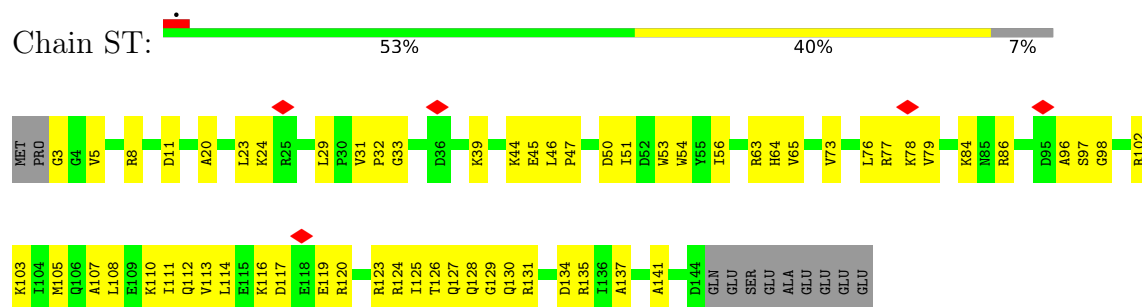
Chain SR: 52% 37% 10%



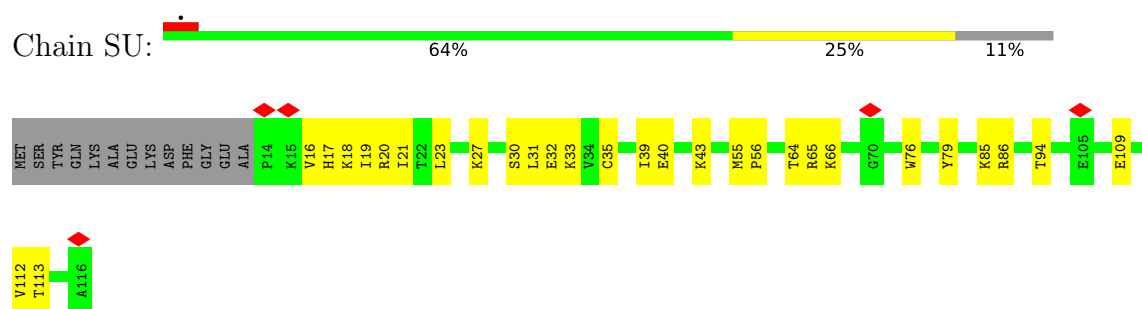
- Molecule 72: Putative ribosomal protein



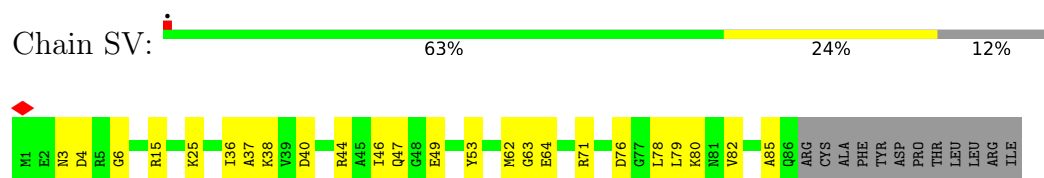
- Molecule 73: 40S ribosomal protein S19-like protein



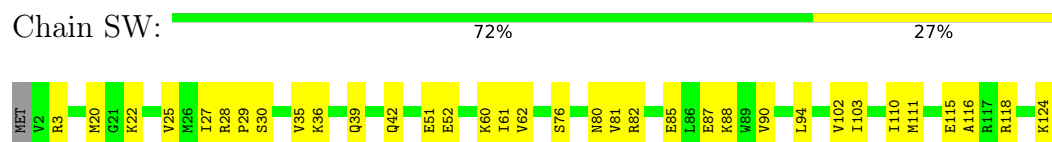
- Molecule 74: 40S ribosomal protein S20-like protein



- Molecule 75: 40S ribosomal protein S21-like protein

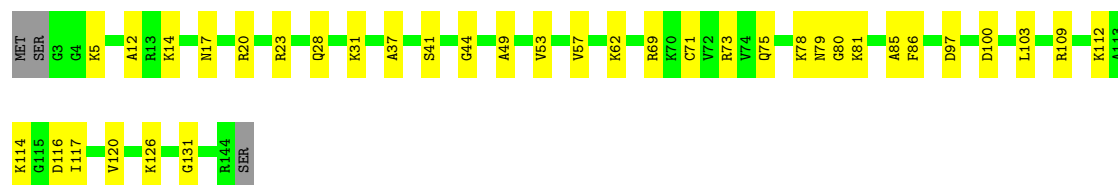


- Molecule 76: 40S ribosomal protein S22-like protein

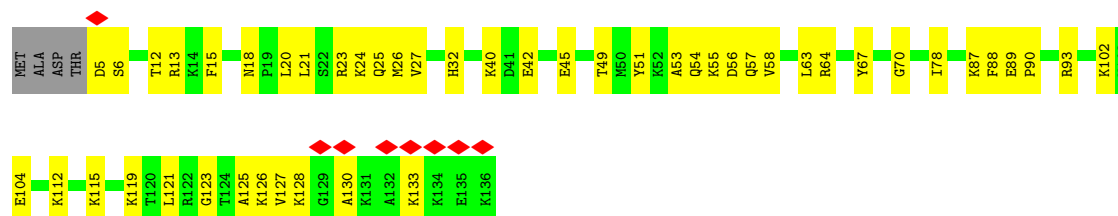


- Molecule 77: 40S ribosomal protein s23-like protein

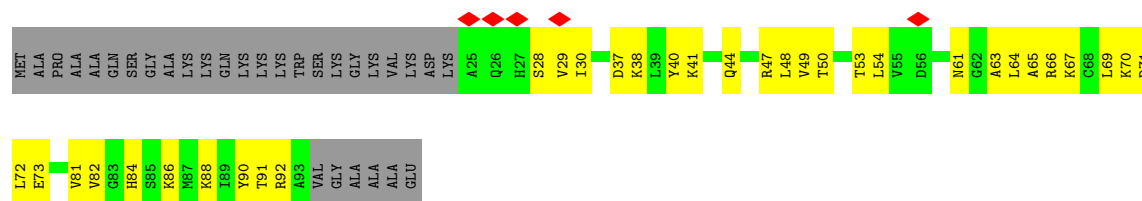




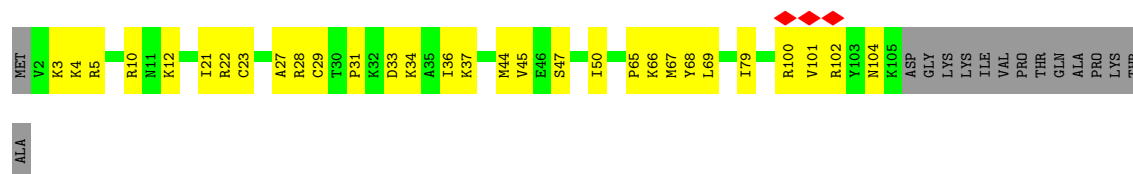
- Molecule 78: 40S ribosomal protein S24



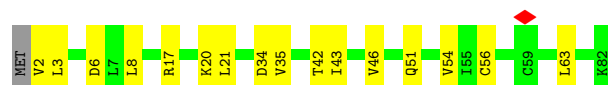
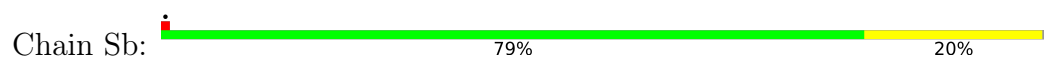
- Molecule 79: 40S ribosomal protein S25



- Molecule 80: 40S ribosomal protein S26

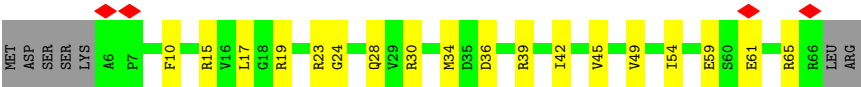


- Molecule 81: Ribosomal protein s27-like protein



- Molecule 82: 40S ribosomal protein S28-like protein





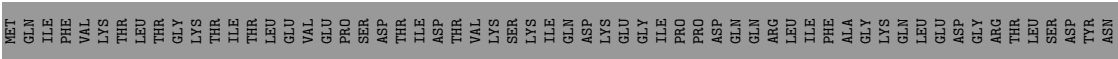
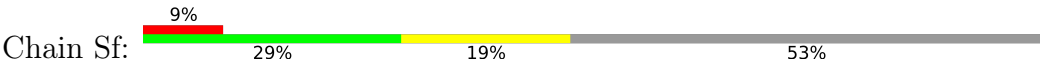
• Molecule 83: Ribosomal protein uS14



• Molecule 84: 40S ribosomal protein S30



• Molecule 85: 40S ribosomal protein S27a-like protein



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	284425	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	39.4	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	23.126	Depositor
Minimum map value	-11.480	Depositor
Average map value	-0.006	Depositor
Map value standard deviation	0.885	Depositor
Recommended contour level	2	Depositor
Map size ($\text{\AA}$)	534.60004, 534.60004, 534.60004	wwPDB
Map dimensions	486, 486, 486	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.1, 1.1, 1.1	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: OMG, ATP, SAC, ZN, MG

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	1	0.14	0/76339	0.32	1/119028 (0.0%)
2	2	0.12	0/42095	0.31	0/65600
3	3	0.13	0/2833	0.29	0/4413
4	4	0.13	0/3710	0.31	0/5778
5	A	0.14	0/2495	0.46	0/3390
6	B	0.17	0/242	0.55	0/314
7	C	0.18	0/3624	0.49	0/4860
8	D	0.15	0/4002	0.42	0/5437
9	LA	0.15	0/1964	0.43	0/2641
10	LB	0.14	0/3156	0.38	0/4238
11	LC	0.14	0/2815	0.38	0/3795
12	LD	0.15	0/2487	0.41	0/3341
13	LE	0.16	0/1547	0.42	0/2081
14	LF	0.17	0/2055	0.42	0/2758
15	LG	0.14	0/1929	0.41	0/2579
16	LH	0.18	0/1525	0.52	0/2050
17	LI	0.14	0/1797	0.45	0/2413
18	LJ	0.19	0/1389	0.50	0/1856
19	LK	0.13	0/761	0.41	0/1056
20	LL	0.16	0/1695	0.45	0/2276
21	LM	0.16	0/1144	0.43	0/1539
22	LN	0.16	0/1740	0.40	0/2332
23	LO	0.18	0/1638	0.47	0/2197
24	LP	0.14	0/1495	0.41	0/2014
25	LQ	0.16	0/1507	0.42	0/2017
26	LR	0.21	0/1525	0.53	0/2028
27	LS	0.16	0/1460	0.37	0/1965
28	LT	0.16	0/1292	0.39	0/1738
29	LU	0.20	0/855	0.58	0/1144
30	LV	0.14	0/1012	0.44	0/1361
31	LW	0.22	0/1088	0.56	2/1443 (0.1%)
32	LX	0.17	0/981	0.52	0/1324

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	LY	0.15	0/1079	0.41	0/1443
34	LZ	0.16	0/1134	0.43	0/1519
35	La	0.14	0/1212	0.36	0/1627
36	Lb	0.17	0/518	0.45	0/684
37	Lc	0.19	0/731	0.45	0/983
38	Ld	0.18	0/979	0.49	0/1308
39	Le	0.13	0/1019	0.33	0/1358
40	Lf	0.17	0/874	0.37	0/1176
41	Lg	0.17	0/904	0.42	0/1210
42	Lh	0.19	0/1014	0.48	0/1349
43	Li	0.19	0/844	0.53	0/1115
44	Lj	0.19	0/697	0.46	0/922
45	Lk	0.21	0/666	0.58	0/884
46	Ll	0.15	0/445	0.39	0/593
47	Lm	0.13	0/424	0.41	0/561
48	Ln	0.37	0/225	0.83	0/289
48	Lr	0.37	0/225	0.83	0/289
49	Lo	0.14	0/835	0.38	0/1105
50	Lp	0.16	0/705	0.43	0/940
51	Lq	0.15	0/1101	0.38	0/1482
52	Ls	0.16	0/1477	0.50	0/1995
54	SA	0.17	0/1683	0.48	0/2299
55	SB	0.16	0/1900	0.47	0/2551
56	SC	0.22	0/1703	0.54	0/2303
57	SD	0.19	0/1712	0.51	0/2299
58	SE	0.16	0/2112	0.48	0/2842
59	SF	0.20	0/1578	0.56	0/2130
60	SG	0.17	0/1906	0.48	0/2547
61	SH	0.17	0/1587	0.49	0/2140
62	SI	0.17	0/1654	0.51	0/2213
63	SJ	0.18	0/1489	0.52	0/1993
64	SK	0.22	0/764	0.62	0/1038
65	SL	0.18	0/1249	0.50	1/1678 (0.1%)
66	SM	0.20	0/934	0.62	0/1255
67	SN	0.19	0/1205	0.52	0/1627
68	SO	0.16	0/1014	0.53	0/1361
69	SP	0.21	0/932	0.63	0/1248
70	SQ	0.19	0/1098	0.53	0/1472
71	SR	0.23	0/1060	0.62	0/1424
72	SS	0.18	0/1133	0.56	0/1520
73	ST	0.17	0/1137	0.45	0/1533
74	SU	0.18	0/828	0.51	0/1112
75	SV	0.23	0/671	0.63	1/900 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	SW	0.18	0/1055	0.54	0/1416
77	SX	0.16	0/1116	0.48	0/1489
78	SY	0.18	0/1075	0.51	0/1431
79	SZ	0.18	0/550	0.49	0/736
80	Sa	0.16	0/852	0.43	0/1136
81	Sb	0.14	0/623	0.49	0/843
82	Sc	0.15	0/487	0.50	0/653
83	Sd	0.22	0/427	0.57	0/570
84	Se	0.22	0/325	0.64	0/427
85	Sf	0.12	0/614	0.38	0/813
All	All	0.15	0/227778	0.39	5/332837 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
65	SL	79	ARG	CB-CG-CD	8.16	130.07	111.30
75	SV	63	GLY	N-CA-C	5.56	123.55	115.32
1	1	1205	G	O4'-C1'-N9	5.29	116.14	108.20
31	LW	114	GLU	N-CA-CB	5.21	117.87	110.16
31	LW	114	GLU	CA-CB-CG	5.10	124.31	114.10

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	68242	0	34371	545	0
2	2	37637	0	18965	542	0
3	3	2535	0	1284	16	0
4	4	3319	0	1678	25	0
5	A	2438	0	2385	85	0
6	B	243	0	237	18	0
7	C	3566	0	3558	160	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	D	3942	0	3967	137	0
9	LA	1925	0	1999	29	0
10	LB	3088	0	3206	38	0
11	LC	2758	0	2883	32	0
12	LD	2440	0	2431	38	0
13	LE	1518	0	1619	33	0
14	LF	2017	0	2130	24	0
15	LG	1900	0	2066	25	0
16	LH	1505	0	1581	45	0
17	LI	1760	0	1798	40	0
18	LJ	1367	0	1405	44	0
19	LK	762	0	362	2	0
20	LL	1666	0	1756	33	0
21	LM	1125	0	1198	29	0
22	LN	1703	0	1767	37	0
23	LO	1613	0	1706	22	0
24	LP	1472	0	1518	23	0
25	LQ	1481	0	1596	32	0
26	LR	1506	0	1603	36	0
27	LS	1425	0	1484	37	0
28	LT	1266	0	1328	14	0
29	LU	842	0	890	31	0
30	LV	994	0	1055	21	0
31	LW	1075	0	1146	38	0
32	LX	965	0	1050	22	0
33	LY	1065	0	1156	23	0
34	LZ	1111	0	1181	21	0
35	La	1180	0	1203	22	0
36	Lb	508	0	526	11	0
37	Lc	722	0	766	10	0
38	Ld	965	0	1028	19	0
39	Le	1001	0	1070	7	0
40	Lf	853	0	880	15	0
41	Lg	891	0	958	21	0
42	Lh	1003	0	1116	19	0
43	Li	836	0	915	18	0
44	Lj	684	0	712	13	0
45	Lk	658	0	721	15	0
46	Ll	435	0	473	9	0
47	Lm	418	0	459	5	0
48	Ln	224	0	271	4	0
48	Lr	224	0	271	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
49	Lo	822	0	891	7	0
50	Lp	697	0	737	9	0
51	Lq	1083	0	1140	9	0
52	Ls	1449	0	1488	45	0
53	NC	135	0	33	0	0
54	SA	1641	0	1650	49	0
55	SB	1871	0	1989	60	0
56	SC	1672	0	1777	62	0
57	SD	1688	0	1750	68	0
58	SE	2072	0	2155	77	0
59	SF	1557	0	1608	76	0
60	SG	1875	0	1983	85	0
61	SH	1562	0	1641	52	0
62	SI	1621	0	1645	46	0
63	SJ	1466	0	1582	53	0
64	SK	742	0	738	44	0
65	SL	1222	0	1289	30	0
66	SM	923	0	946	44	0
67	SN	1182	0	1264	34	0
68	SO	1002	0	1034	33	0
69	SP	917	0	978	43	0
70	SQ	1081	0	1151	49	0
71	SR	1045	0	1083	46	0
72	SS	1118	0	1172	49	0
73	ST	1117	0	1133	51	0
74	SU	819	0	895	30	0
75	SV	664	0	662	20	0
76	SW	1037	0	1076	33	0
77	SX	1099	0	1169	26	0
78	SY	1061	0	1150	43	0
79	SZ	546	0	591	33	0
80	Sa	839	0	891	29	0
81	Sb	611	0	633	16	0
82	Sc	484	0	513	15	0
83	Sd	419	0	418	32	0
84	Se	322	0	365	9	0
85	Sf	604	0	640	28	0
86	1	366	0	0	0	0
86	2	80	0	0	0	0
86	3	7	0	0	0	0
86	4	9	0	0	0	0
86	D	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
86	LC	1	0	0	0	0
86	LN	3	0	0	0	0
86	LP	1	0	0	0	0
86	LV	1	0	0	0	0
86	LW	1	0	0	0	0
86	Lb	1	0	0	0	0
86	Lo	1	0	0	0	0
87	D	31	0	12	2	0
88	Lg	1	0	0	0	0
88	Lj	1	0	0	0	0
88	Lm	1	0	0	0	0
88	Lo	1	0	0	0	0
88	Lp	1	0	0	0	0
88	Sa	1	0	0	0	0
88	Sb	1	0	0	0	0
88	Sd	1	0	0	0	0
All	All	213449	0	161600	3391	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 9.

All (3391) 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)
52:Ls:57:THR:HG23	52:Ls:60:ARG:HB2	1.46	0.97
60:SG:170:LYS:HE3	60:SG:171:PRO:HD2	1.44	0.97
16:LH:130:MET:HE1	16:LH:136:VAL:HG21	1.49	0.94
2:2:77:A:N3	60:SG:177:ARG:NH2	2.16	0.93
75:SV:40:ASP:HB3	75:SV:46:ILE:HD11	1.47	0.92
2:2:1467:A:H62	2:2:1534:U:H3	1.13	0.91
2:2:485:G:H1	2:2:496:U:H3	1.15	0.89
2:2:1787:G:OP2	80:Sa:10:ARG:NH2	2.06	0.88
7:C:296:ARG:HH12	29:LU:118:VAL:HG11	1.39	0.87
2:2:1675:G:H21	2:2:1718:A:H62	1.19	0.87
57:SD:123:TYR:HB3	57:SD:127:ARG:HH12	1.38	0.87
63:SJ:171:ARG:HH12	63:SJ:174:LYS:HD2	1.39	0.86
72:SS:88:ARG:HD3	72:SS:108:LYS:HZ1	1.39	0.86
63:SJ:131:HIS:HD2	63:SJ:160:SER:HB2	1.40	0.86
7:C:157:GLU:O	7:C:164:LYS:NZ	2.07	0.86
71:SR:77:GLU:OE1	71:SR:80:ARG:NH2	2.09	0.86
61:SH:50:VAL:HG23	61:SH:69:PRO:HD3	1.56	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:824:U:H3	2:2:844:G:H1	1.25	0.85
2:2:1143:G:O3'	56:SC:99:ARG:NH2	2.10	0.85
1:1:1000:G:H1	1:1:1017:U:H3	1.18	0.84
56:SC:43:TRP:CZ3	56:SC:45:PRO:HA	2.11	0.84
2:2:476:U:H4'	63:SJ:118:LYS:HE3	1.59	0.84
61:SH:23:GLU:HA	61:SH:26:ILE:HG12	1.60	0.84
58:SE:212:ASP:OD1	58:SE:213:ALA:N	2.10	0.84
76:SW:90:VAL:HG23	76:SW:94:LEU:HD12	1.59	0.83
78:SY:23:ARG:HE	78:SY:25:GLN:HE21	1.23	0.83
7:C:319:GLU:HA	7:C:322:ARG:HD2	1.61	0.83
1:1:1222:C:H2'	1:1:1223:A:H8	1.43	0.82
2:2:539:A:N1	84:Se:28:LYS:NZ	2.27	0.82
2:2:1277:C:O3'	74:SU:66:LYS:NZ	2.13	0.82
2:2:475:C:H5'	84:Se:33:ARG:HH22	1.44	0.81
74:SU:55:MET:HG2	74:SU:85:LYS:HB3	1.62	0.81
55:SB:78:ASP:OD1	55:SB:79:HIS:ND1	2.15	0.80
57:SD:54:ARG:HH12	57:SD:92:ALA:HB3	1.46	0.80
7:C:293:LYS:HA	7:C:296:ARG:HD2	1.63	0.80
78:SY:123:GLY:O	78:SY:128:LYS:NZ	2.13	0.80
67:SN:142:GLU:OE2	67:SN:145:THR:OG1	1.99	0.80
70:SQ:38:LEU:HD11	73:ST:11:ASP:HA	1.63	0.80
80:Sa:67:MET:HE3	80:Sa:69:LEU:HD23	1.64	0.80
34:LZ:80:MET:HE2	41:Lg:91:ILE:HD12	1.64	0.79
63:SJ:129:GLN:OE1	63:SJ:131:HIS:ND1	2.15	0.79
1:1:675:U:OP2	20:LL:36:ARG:NH2	2.14	0.79
2:2:219:C:O2	2:2:835:G:N2	2.14	0.79
8:D:53:TYR:HE1	8:D:58:GLU:HG3	1.48	0.79
28:LT:68:THR:HG22	28:LT:69:LYS:H	1.46	0.79
1:1:1242:A:N3	1:1:1263:C:O2'	2.16	0.79
2:2:508:A:H5''	63:SJ:171:ARG:HD3	1.64	0.79
70:SQ:28:LEU:HD21	70:SQ:30:LYS:HE2	1.64	0.79
58:SE:100:ARG:NH2	58:SE:121:TYR:O	2.14	0.79
21:LM:12:ARG:HB3	21:LM:18:ARG:HH12	1.48	0.78
2:2:850:C:H5''	26:LR:176:ARG:HH12	1.48	0.78
69:SP:69:ARG:NH2	69:SP:97:MET:SD	2.56	0.78
1:1:961:C:H3'	1:1:962:U:H4'	1.66	0.78
66:SM:32:GLY:HA2	66:SM:35:LYS:HE2	1.65	0.78
9:LA:196:TRP:HB3	9:LA:197:PRO:HD3	1.63	0.78
57:SD:73:THR:HG22	57:SD:89:LEU:HD23	1.66	0.77
54:SA:124:ILE:HB	54:SA:146:VAL:HG12	1.65	0.77
2:2:1355:G:O2'	73:ST:134:ASP:OD2	2.02	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:SD:117:ALA:HB3	57:SD:120:ARG:HD3	1.66	0.77
31:LW:88:GLU:HA	31:LW:91:LYS:HE2	1.67	0.77
1:1:262:G:H5''	22:LN:14:LYS:HE2	1.65	0.76
2:2:1181:A:HO2'	2:2:1206:C:HO2'	1.32	0.76
18:LJ:167:ARG:HG2	18:LJ:168:PHE:CD2	2.20	0.76
18:LJ:126:MET:HE3	18:LJ:128:PHE:HE1	1.50	0.76
56:SC:47:THR:HG23	56:SC:50:GLY:H	1.48	0.76
18:LJ:19:VAL:HG22	18:LJ:71:THR:HG22	1.68	0.76
2:2:898:A:H3'	2:2:899:G:H21	1.50	0.76
2:2:959:U:H5''	67:SN:71:ILE:HG21	1.68	0.76
11:LC:335:THR:HA	11:LC:338:LYS:HG2	1.67	0.76
55:SB:137:LEU:HG	55:SB:215:VAL:HG22	1.68	0.76
55:SB:164:ILE:HG12	55:SB:207:LEU:HD11	1.66	0.76
59:SF:152:LEU:HD23	59:SF:156:ASN:HD21	1.49	0.76
1:1:2621:G:H2'	1:1:2622:G:C8	2.21	0.76
1:1:3160:A:OP2	21:LM:125:LYS:NZ	2.19	0.76
57:SD:15:VAL:HG11	83:Sd:34:TYR:HB3	1.66	0.75
2:2:761:A:OP1	63:SJ:77:ARG:NH2	2.19	0.75
83:Sd:21:CYS:SG	83:Sd:24:CYS:HB3	2.25	0.75
1:1:2387:A:OP1	22:LN:90:ASN:ND2	2.19	0.75
2:2:700:G:N2	2:2:731:G:O2'	2.17	0.75
8:D:209:VAL:HG22	8:D:349:ILE:HD11	1.68	0.75
52:Ls:19:LEU:HD11	52:Ls:64:LYS:HZ1	1.51	0.75
57:SD:112:LEU:HD21	57:SD:118:VAL:HA	1.67	0.75
7:C:98:TRP:HA	7:C:154:LYS:HZ2	1.52	0.75
37:Lc:16:LYS:NZ	37:Lc:102:ASP:OD1	2.19	0.75
56:SC:41:LYS:NZ	56:SC:42:GLU:O	2.20	0.75
11:LC:149:VAL:HG13	11:LC:150:PRO:HD3	1.68	0.75
39:Le:88:MET:HG3	51:Lq:36:THR:HA	1.69	0.75
2:2:510:U:H5'	63:SJ:129:GLN:HE21	1.51	0.74
7:C:297:GLN:NE2	29:LU:31:ASP:O	2.20	0.74
52:Ls:159:VAL:HG11	52:Ls:165:VAL:HG22	1.69	0.74
70:SQ:40:ALA:HB3	70:SQ:45:ARG:HD2	1.68	0.74
21:LM:130:GLU:HG2	23:LO:191:VAL:HG21	1.68	0.74
1:1:1338:A:O2'	25:LQ:59:LYS:NZ	2.19	0.74
60:SG:221:GLU:O	60:SG:225:GLN:NE2	2.19	0.74
12:LD:53:VAL:HG12	12:LD:62:THR:HG22	1.69	0.74
7:C:37:ARG:HH22	8:D:447:GLU:HB3	1.50	0.74
63:SJ:32:TYR:OH	63:SJ:100:GLU:OE2	2.05	0.73
2:2:276:G:N7	31:LW:116:LYS:NZ	2.35	0.73
2:2:1580:G:N2	2:2:1607:A:OP2	2.16	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:4:8:C:H2'	4:4:9:A:H8	1.54	0.73
37:Lc:16:LYS:HE3	37:Lc:103:ILE:HD13	1.70	0.73
2:2:1247:U:O2'	85:Sf:135:MET:SD	2.46	0.73
79:SZ:69:LEU:HD12	79:SZ:90:TYR:HD2	1.52	0.73
1:1:2500:U:H3'	1:1:2501:U:H4'	1.70	0.73
27:LS:96:GLU:OE2	27:LS:102:ALA:N	2.22	0.73
59:SF:67:LYS:HG3	59:SF:68:ARG:H	1.54	0.73
59:SF:115:ASN:HB3	59:SF:118:GLN:HG2	1.71	0.73
2:2:629:U:OP1	65:SL:107:LYS:NZ	2.21	0.73
2:2:681:C:O2'	76:SW:118:ARG:NH1	2.21	0.73
5:A:242:SER:OG	5:A:245:ARG:O	2.04	0.73
2:2:903:A:H5''	68:SO:65:ARG:HG2	1.70	0.73
21:LM:102:LYS:HG2	21:LM:105:GLN:HE21	1.53	0.73
60:SG:167:GLU:HG3	60:SG:169:LYS:HE2	1.70	0.73
66:SM:47:LEU:HA	66:SM:50:ALA:HB3	1.69	0.73
2:2:485:G:N2	2:2:496:U:O2	2.19	0.73
57:SD:100:SER:O	57:SD:104:GLN:NE2	2.21	0.73
2:2:1397:A:O3'	71:SR:5:ARG:NH1	2.21	0.72
60:SG:64:LYS:HB2	60:SG:97:VAL:HG11	1.70	0.72
55:SB:27:LYS:HD2	55:SB:47:LEU:HD21	1.71	0.72
2:2:57:G:OP2	78:SY:119:LYS:NZ	2.22	0.72
2:2:801:A:N3	61:SH:110:ARG:NH1	2.38	0.72
7:C:35:SER:O	8:D:422:HIS:N	2.21	0.72
71:SR:57:LEU:O	71:SR:61:ILE:HG13	1.89	0.72
12:LD:75:PHE:O	12:LD:112:LYS:NZ	2.23	0.72
26:LR:140:GLU:HG2	26:LR:144:ARG:HH12	1.54	0.72
60:SG:167:GLU:HG2	60:SG:169:LYS:H	1.55	0.72
80:Sa:45:VAL:HG23	80:Sa:50:ILE:HD13	1.71	0.72
6:B:134:ASP:O	57:SD:120:ARG:NH2	2.23	0.72
13:LE:19:ALA:HB3	13:LE:23:LYS:HG2	1.72	0.72
22:LN:46:ASP:OD1	22:LN:47:LYS:N	2.22	0.72
65:SL:79:ARG:NH1	65:SL:125:GLY:O	2.22	0.72
70:SQ:36:LEU:O	70:SQ:45:ARG:NH2	2.18	0.72
2:2:691:C:H4'	2:2:692:C:H5'	1.69	0.72
8:D:317:GLU:OE1	8:D:321:ARG:NH2	2.22	0.72
52:Ls:67:MET:HE1	52:Ls:69:ASP:HB3	1.71	0.72
80:Sa:10:ARG:HH12	80:Sa:31:PRO:HG2	1.54	0.71
2:2:219:C:N3	2:2:835:G:N1	2.31	0.71
64:SK:21:MET:HB2	64:SK:64:TYR:HB2	1.72	0.71
1:1:1876:A:H61	1:1:2302:C:H42	1.38	0.71
73:ST:116:LYS:HE3	73:ST:123:ARG:HE	1.54	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:LA:36:GLU:OE2	9:LA:163:ARG:NH1	2.22	0.71
55:SB:190:PRO:HG2	55:SB:192:VAL:HG23	1.71	0.71
70:SQ:99:GLU:HB2	70:SQ:102:LYS:HE3	1.71	0.71
1:1:117:A:OP2	22:LN:2:GLY:N	2.23	0.71
30:LV:106:ASN:ND2	30:LV:110:GLU:OE2	2.20	0.71
14:LF:124:LYS:HD3	14:LF:197:VAL:HG11	1.72	0.71
1:1:2577:G:C5	17:LI:115:MET:HE1	2.24	0.71
68:SO:112:GLN:HE22	80:Sa:45:VAL:HG12	1.56	0.71
2:2:1675:G:N2	2:2:1718:A:H62	1.88	0.71
5:A:99:ARG:NH1	5:A:135:LEU:O	2.23	0.71
58:SE:63:ALA:O	58:SE:67:GLN:NE2	2.24	0.71
4:4:55:U:H3	4:4:62:A:H2	1.37	0.71
8:D:351:SER:HA	8:D:386:PRO:HB3	1.71	0.71
2:2:866:G:H1	2:2:958:U:H3	1.36	0.70
7:C:138:ALA:HA	7:C:142:ARG:HB2	1.72	0.70
18:LJ:111:ILE:HG12	18:LJ:117:TYR:HB2	1.71	0.70
30:LV:77:PRO:HG2	30:LV:107:PRO:HD3	1.73	0.70
32:LX:91:GLU:HG2	32:LX:92:GLN:HG3	1.71	0.70
2:2:955:G:N2	81:Sb:51:GLN:OE1	2.24	0.70
8:D:347:GLU:HG2	8:D:373:ARG:HB3	1.73	0.70
62:SI:141:SER:HA	62:SI:144:LYS:HZ3	1.55	0.70
28:LT:48:VAL:HG21	28:LT:94:GLU:HG2	1.72	0.70
50:Lp:51:ALA:HB3	50:Lp:54:ILE:HD13	1.74	0.70
57:SD:67:ARG:HD2	64:SK:88:THR:HG22	1.74	0.70
15:LG:31:GLU:OE2	15:LG:33:ARG:NH1	2.25	0.70
69:SP:104:ILE:HD12	69:SP:124:LEU:HD21	1.71	0.70
82:Sc:34:MET:HE1	82:Sc:54:ILE:HG23	1.72	0.70
2:2:1441:G:N2	85:Sf:87:THR:O	2.25	0.70
8:D:15:VAL:HG12	8:D:152:SER:HB2	1.74	0.70
26:LR:28:GLU:HG3	26:LR:49:LEU:HD13	1.73	0.70
64:SK:15:LEU:HD22	64:SK:21:MET:HE3	1.72	0.70
2:2:1446:U:O2'	83:Sd:7:TRP:O	2.07	0.70
66:SM:108:ARG:HE	66:SM:109:GLU:N	1.89	0.70
17:LI:14:ASN:O	17:LI:128:ARG:NH2	2.25	0.70
54:SA:157:GLU:HG3	54:SA:158:TYR:HD1	1.56	0.70
31:LW:87:LEU:HD23	31:LW:90:ILE:HD11	1.73	0.70
1:1:2266:A:OP1	48:Ln:23:ARG:NH1	2.25	0.69
7:C:240:GLU:HG3	7:C:267:ARG:HD3	1.72	0.69
12:LD:91:GLY:O	12:LD:94:ASN:ND2	2.25	0.69
52:Ls:74:GLU:HA	52:Ls:77:LEU:HG	1.72	0.69
1:1:291:U:OP2	43:Li:42:GLN:NE2	2.25	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:961:A:OP2	67:SN:70:LYS:NZ	2.25	0.69
7:C:126:ARG:HE	7:C:130:LEU:HD21	1.57	0.69
65:SL:76:LEU:HD12	65:SL:93:ARG:NH1	2.08	0.69
1:1:2477:U:OP1	15:LG:71:ARG:NH1	2.26	0.69
68:SO:84:CYS:HB2	68:SO:89:ILE:HD11	1.72	0.69
79:SZ:40:TYR:O	79:SZ:44:GLN:NE2	2.23	0.69
1:1:1337:G:N2	1:1:1339:U:O2'	2.25	0.69
2:2:333:G:O6	62:SI:5:ARG:NH1	2.25	0.69
18:LJ:15:ILE:HG13	18:LJ:132:MET:HE1	1.74	0.69
66:SM:108:ARG:HE	66:SM:109:GLU:H	1.38	0.69
1:1:206:G:OP2	33:LY:1:MET:N	2.24	0.69
57:SD:67:ARG:NH1	64:SK:87:ALA:O	2.25	0.69
65:SL:71:ILE:HD11	65:SL:131:GLY:HA3	1.75	0.69
1:1:1582:A:N6	32:LX:83:GLU:OE2	2.26	0.69
2:2:487:U:H3	2:2:494:G:H1	1.41	0.69
2:2:1510:U:O2	57:SD:12:ARG:NH2	2.25	0.69
6:B:141:ILE:HD11	56:SC:89:MET:HE1	1.74	0.69
7:C:171:VAL:HG21	7:C:241:TYR:HB3	1.75	0.69
8:D:384:LEU:HD13	8:D:392:ARG:HH12	1.57	0.69
30:LV:81:VAL:HB	30:LV:120:VAL:HG23	1.75	0.69
64:SK:79:HIS:HB3	66:SM:39:MET:HE3	1.75	0.69
65:SL:79:ARG:HE	65:SL:127:MET:HE3	1.58	0.69
71:SR:46:LEU:HA	71:SR:49:LYS:HG2	1.74	0.69
1:1:3068:C:O2'	16:LH:157:SER:OG	2.10	0.69
18:LJ:86:LYS:HA	18:LJ:86:LYS:HE3	1.75	0.69
33:LY:1:MET:HE3	33:LY:2:LYS:H	1.57	0.68
4:4:83:C:H41	33:LY:50:ARG:HH22	1.41	0.68
64:SK:75:ARG:NH2	64:SK:81:PRO:O	2.26	0.68
75:SV:62:MET:HG2	75:SV:64:GLU:OE1	1.94	0.68
8:D:427:ILE:HB	8:D:444:ILE:HB	1.76	0.68
16:LH:19:SER:HG	16:LH:26:THR:HG1	1.39	0.68
1:1:357:G:OP2	44:Lj:52:LYS:NZ	2.27	0.68
1:1:2518:G:OP1	9:LA:69:TYR:OH	2.12	0.68
2:2:1357:C:HO2'	73:ST:3:GLY:N	1.91	0.68
13:LE:119:ILE:HA	13:LE:122:VAL:HG12	1.75	0.68
39:Le:96:GLU:OE1	39:Le:121:THR:OG1	2.10	0.68
2:2:1709:G:OP1	31:LW:71:ARG:NH2	2.26	0.68
18:LJ:20:LEU:HD11	18:LJ:38:LEU:HD11	1.74	0.68
38:Ld:96:LYS:HG3	38:Ld:97:LEU:HD12	1.76	0.68
43:Li:44:LYS:HA	43:Li:47:GLN:HG3	1.76	0.68
60:SG:67:VAL:HG13	60:SG:99:GLY:HA2	1.76	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:LY:30:MET:HE1	33:LY:74:ARG:HA	1.74	0.68
1:1:1001:G:H1	1:1:1016:U:H3	1.42	0.68
15:LG:106:GLN:NE2	15:LG:110:GLU:OE2	2.26	0.68
52:Ls:98:GLU:HA	52:Ls:101:LEU:HD13	1.75	0.68
27:LS:27:MET:HE3	27:LS:29:ILE:HD11	1.75	0.68
76:SW:88:LYS:HA	76:SW:88:LYS:HE3	1.75	0.68
1:1:1641:G:H2'	1:1:1642:G:C8	2.29	0.67
2:2:1214:A:O4'	64:SK:42:LYS:NZ	2.25	0.67
7:C:89:MET:HE3	7:C:92:ALA:HA	1.76	0.67
1:1:2960:C:O2'	10:LB:181:GLU:OE2	2.10	0.67
20:LL:169:SER:OG	20:LL:172:GLU:OE1	2.11	0.67
58:SE:42:MET:HE3	58:SE:46:VAL:HG13	1.76	0.67
74:SU:40:GLU:HA	74:SU:43:LYS:HG2	1.76	0.67
1:1:2407:C:H2'	1:1:2408:A:C8	2.29	0.67
1:1:2730:U:OP2	1:1:2731:C:N4	2.27	0.67
2:2:1582:A:OP1	70:SQ:132:ARG:N	2.26	0.67
2:2:1611:C:OP1	59:SF:68:ARG:NH2	2.27	0.67
55:SB:78:ASP:OD1	55:SB:79:HIS:N	2.27	0.67
67:SN:47:PRO:HA	67:SN:50:ILE:HG12	1.77	0.67
6:B:135:GLU:HA	57:SD:120:ARG:NH2	2.10	0.67
23:LO:127:ARG:HG3	23:LO:131:LEU:HD12	1.75	0.67
24:LP:12:THR:HG23	24:LP:13:LYS:HD3	1.77	0.67
65:SL:80:VAL:HG12	65:SL:126:ASP:H	1.59	0.67
70:SQ:6:ALA:HB1	70:SQ:21:ARG:HE	1.59	0.67
2:2:474:A:O2'	84:Se:33:ARG:NH2	2.28	0.67
2:2:1517:G:O2'	2:2:1519:U:OP2	2.12	0.67
7:C:35:SER:OG	7:C:37:ARG:NH1	2.28	0.67
18:LJ:159:GLU:OE1	18:LJ:162:ARG:NH1	2.28	0.67
1:1:1469:G:H21	41:Lg:7:THR:HG22	1.58	0.67
2:2:1391:G:H2'	2:2:1392:G:C8	2.30	0.67
72:SS:25:LYS:HZ2	79:SZ:29:VAL:H	1.43	0.67
2:2:103:A:OP2	2:2:305:C:N4	2.28	0.67
70:SQ:83:GLN:HG3	70:SQ:87:LYS:HZ1	1.60	0.67
80:Sa:23:CYS:HB3	80:Sa:28:ARG:H	1.60	0.67
20:LL:62:THR:HG21	35:La:66:ASN:HD22	1.60	0.67
55:SB:79:HIS:CD2	55:SB:82:ARG:HH21	2.11	0.67
67:SN:52:VAL:HG23	67:SN:55:ARG:HH21	1.57	0.67
1:1:1238:C:H2'	1:1:1239:G:H8	1.58	0.66
2:2:1363:A:O2'	73:ST:8:ARG:NH1	2.28	0.66
7:C:171:VAL:HG22	7:C:239:PHE:HA	1.76	0.66
27:LS:130:GLU:HG2	27:LS:131:LYS:HG2	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
65:SL:79:ARG:NE	65:SL:127:MET:HE3	2.10	0.66
2:2:747:U:OP1	76:SW:82:ARG:NH1	2.28	0.66
58:SE:80:ILE:HG13	58:SE:81:THR:HG23	1.76	0.66
64:SK:78:LEU:HD12	64:SK:80:LEU:H	1.60	0.66
76:SW:111:MET:HB2	76:SW:115:GLU:OE1	1.95	0.66
1:1:377:A:H5''	7:C:257:ARG:HH12	1.59	0.66
2:2:643:U:H2'	2:2:644:A:H8	1.59	0.66
2:2:1144:A:OP1	56:SC:99:ARG:NH1	2.27	0.66
60:SG:74:ARG:HD2	60:SG:96:SER:HB3	1.78	0.66
73:ST:77:ARG:HD3	73:ST:98:GLY:HA2	1.76	0.66
1:1:275:G:O2'	1:1:276:G:OP2	2.11	0.66
7:C:254:ASP:OD1	7:C:255:GLN:N	2.29	0.66
1:1:2410:A:N6	1:1:2463:A:N3	2.43	0.66
2:2:469:U:H2'	2:2:470:A:H8	1.61	0.66
26:LR:25:ASP:HB3	26:LR:28:GLU:OE2	1.95	0.66
26:LR:138:LEU:O	26:LR:142:ILE:HD12	1.94	0.66
54:SA:38:PRO:O	54:SA:55:LYS:NZ	2.28	0.66
73:ST:126:THR:HG23	73:ST:129:GLY:H	1.60	0.66
8:D:548:GLU:OE2	8:D:550:THR:OG1	2.14	0.66
17:LI:93:PRO:HB2	17:LI:125:THR:HG22	1.77	0.66
65:SL:43:VAL:HG13	65:SL:65:PHE:CE1	2.31	0.66
2:2:331:U:O4	62:SI:5:ARG:NH2	2.28	0.66
54:SA:82:ARG:HA	54:SA:82:ARG:NH1	2.11	0.66
1:1:1248:U:H2'	1:1:1249:G:C8	2.31	0.66
2:2:643:U:H2'	2:2:644:A:C8	2.31	0.66
58:SE:45:ILE:HG13	58:SE:61:THR:HG21	1.77	0.66
71:SR:5:ARG:HB2	71:SR:9:VAL:HG21	1.78	0.66
77:SX:17:ASN:OD1	77:SX:20:ARG:NH2	2.29	0.66
5:A:217:MET:SD	5:A:219:TRP:NE1	2.65	0.66
10:LB:313:VAL:HG12	10:LB:314:ARG:HG3	1.78	0.66
16:LH:115:GLU:OE2	16:LH:125:VAL:HG22	1.96	0.66
44:Lj:21:ARG:NH2	44:Lj:37:CYS:O	2.28	0.66
54:SA:87:ARG:O	54:SA:91:LYS:HG2	1.96	0.66
60:SG:21:GLU:OE1	60:SG:25:ARG:NE	2.29	0.66
61:SH:154:GLU:HA	76:SW:42:GLN:HE21	1.61	0.66
2:2:1215:G:N2	2:2:1440:A:OP2	2.30	0.65
4:4:95:G:OP2	44:Lj:72:ARG:NH1	2.29	0.65
5:A:43:TRP:HA	5:A:55:PRO:HA	1.78	0.65
9:LA:61:VAL:HG11	9:LA:88:ILE:HD11	1.78	0.65
25:LQ:107:THR:HB	25:LQ:164:THR:HG22	1.78	0.65
1:1:2524:G:OP2	34:LZ:54:ARG:NH1	2.28	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:1677:A:H1'	60:SG:66:GLY:HA2	1.77	0.65
64:SK:5:LYS:HB3	64:SK:9:LYS:NZ	2.10	0.65
72:SS:117:LYS:HZ3	72:SS:125:LEU:HD23	1.61	0.65
83:Sd:33:LYS:HD3	83:Sd:33:LYS:N	2.09	0.65
10:LB:36:ASP:OD2	10:LB:39:LYS:NZ	2.29	0.65
10:LB:41:VAL:HG12	10:LB:186:GLY:HA3	1.78	0.65
56:SC:235:PRO:HA	56:SC:238:TRP:NE1	2.11	0.65
2:2:115:U:O2'	2:2:330:A:N3	2.26	0.65
11:LC:148:GLU:HG3	11:LC:150:PRO:HD2	1.79	0.65
16:LH:139:SER:HB3	16:LH:145:GLU:HB3	1.79	0.65
58:SE:9:GLN:HB2	58:SE:30:ARG:HD3	1.78	0.65
65:SL:31:ARG:HB2	65:SL:34:LYS:HB2	1.77	0.65
12:LD:245:GLU:O	12:LD:249:GLN:NE2	2.30	0.65
29:LU:20:LYS:NZ	29:LU:71:GLU:OE2	2.27	0.65
31:LW:52:THR:HG23	31:LW:55:TYR:H	1.61	0.65
71:SR:24:LEU:HB2	71:SR:31:ASN:HD22	1.60	0.65
1:1:1226:G:N3	1:1:1253:A:O2'	2.30	0.65
1:1:2993:C:O2	16:LH:123:LYS:NZ	2.27	0.65
2:2:816:C:OP1	61:SH:119:LYS:NZ	2.29	0.65
57:SD:25:ASN:O	57:SD:29:GLN:NE2	2.29	0.65
2:2:1101:U:OP1	77:SX:14:LYS:NZ	2.30	0.65
2:2:1688:G:H2'	2:2:1689:A:C8	2.31	0.65
57:SD:13:LYS:NZ	74:SU:109:GLU:OE1	2.30	0.65
58:SE:57:ASN:O	58:SE:61:THR:OG1	2.11	0.65
77:SX:97:ASP:N	77:SX:100:ASP:OD2	2.29	0.65
2:2:66:U:H1'	60:SG:174:LYS:HE2	1.78	0.65
55:SB:144:LYS:HB3	55:SB:206:PRO:HB2	1.79	0.65
59:SF:175:LYS:NZ	59:SF:180:CYS:SG	2.70	0.65
78:SY:42:GLU:HA	78:SY:45:GLU:HG2	1.78	0.65
78:SY:121:LEU:HD12	78:SY:128:LYS:HE3	1.78	0.65
5:A:87:LEU:HB3	5:A:101:PHE:HB2	1.79	0.64
66:SM:31:LYS:HD2	66:SM:100:TRP:HB3	1.79	0.64
1:1:1221:C:H3'	1:1:1222:C:H5''	1.79	0.64
1:1:1863:A:OP1	38:Ld:42:LYS:NZ	2.29	0.64
2:2:529:U:OP1	63:SJ:130:ARG:NH2	2.30	0.64
38:Ld:41:ILE:HD11	38:Ld:67:VAL:HG11	1.78	0.64
54:SA:65:ARG:NH2	75:SV:37:ALA:O	2.31	0.64
62:SI:81:VAL:HG12	62:SI:102:VAL:HG12	1.77	0.64
74:SU:79:TYR:HB3	83:Sd:52:PHE:HB3	1.79	0.64
1:1:2355:C:O2'	10:LB:267:ARG:NH2	2.29	0.64
32:LX:103:ALA:HA	32:LX:107:GLN:HE21	1.61	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
69:SP:49:ALA:HA	69:SP:52:LYS:NZ	2.12	0.64
70:SQ:83:GLN:HG3	70:SQ:87:LYS:NZ	2.12	0.64
2:2:1484:G:O2'	2:2:1490:C:O2	2.15	0.64
1:1:806:U:H5''	9:LA:21:ARG:HD3	1.80	0.64
1:1:1796:A:H2'	1:1:1797:A:C8	2.32	0.64
44:Lj:39:TYR:HB3	44:Lj:40:PRO:HD3	1.79	0.64
67:SN:87:ASP:OD1	67:SN:88:LEU:N	2.29	0.64
74:SU:55:MET:HE3	74:SU:85:LYS:HB2	1.80	0.64
1:1:1887:C:O2	10:LB:241:ARG:NH2	2.31	0.64
18:LJ:33:ARG:HD2	18:LJ:121:ILE:HA	1.79	0.64
29:LU:49:VAL:HB	29:LU:55:ASN:HB3	1.78	0.64
2:2:1692:U:H2'	2:2:1693:C:C6	2.33	0.64
8:D:306:ASP:OD1	8:D:307:PHE:N	2.30	0.64
22:LN:68:ARG:NH1	22:LN:124:ASP:O	2.31	0.64
64:SK:36:ARG:NE	64:SK:38:LEU:HD21	2.12	0.64
1:1:1222:C:H2'	1:1:1223:A:C8	2.30	0.64
1:1:1229:G:N2	1:1:1249:G:OP2	2.30	0.64
2:2:29:U:O3'	77:SX:126:LYS:NZ	2.26	0.64
13:LE:131:GLU:O	13:LE:135:GLU:HG3	1.98	0.64
67:SN:60:ILE:H	67:SN:60:ILE:HD12	1.61	0.64
1:1:1578:G:OP2	41:Lg:32:ARG:NH2	2.31	0.64
58:SE:86:PHE:CD2	58:SE:87:MET:HG2	2.32	0.64
69:SP:64:LEU:HD22	69:SP:88:LEU:HD21	1.79	0.64
71:SR:104:ILE:HG12	71:SR:122:VAL:HG11	1.78	0.64
18:LJ:16:GLN:OE1	18:LJ:17:LYS:HG2	1.99	0.63
26:LR:170:ARG:HH21	26:LR:173:LYS:HD2	1.62	0.63
34:LZ:102:GLU:OE2	34:LZ:105:GLN:HG3	1.98	0.63
70:SQ:41:PRO:HG2	70:SQ:44:LEU:HB2	1.79	0.63
1:1:1242:A:N6	52:Ls:53:MET:SD	2.70	0.63
1:1:1748:C:OP2	45:Lk:74:ARG:NH1	2.31	0.63
2:2:916:U:H2'	2:2:917:A:C8	2.34	0.63
7:C:113:ARG:HD2	7:C:175:ALA:HB2	1.79	0.63
7:C:131:LYS:HD2	7:C:132:HIS:CE1	2.32	0.63
14:LF:86:GLU:OE2	28:LT:136:ARG:N	2.32	0.63
69:SP:39:ASP:O	69:SP:42:ARG:HG2	1.98	0.63
64:SK:14:TYR:CD2	64:SK:21:MET:HE1	2.33	0.63
2:2:1067:U:H4'	81:Sb:17:ARG:HE	1.63	0.63
54:SA:52:ASN:HD22	54:SA:55:LYS:HE3	1.62	0.63
63:SJ:18:GLU:OE1	63:SJ:21:ARG:N	2.28	0.63
64:SK:5:LYS:HB3	64:SK:9:LYS:HZ3	1.62	0.63
66:SM:61:MET:HA	66:SM:87:PRO:HB2	1.79	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:811:U:H3	1:1:877:A:N6	1.96	0.63
1:1:3046:G:OP1	10:LB:314:ARG:NH1	2.31	0.63
54:SA:71:ASP:OD1	54:SA:72:ASN:N	2.30	0.63
85:Sf:120:GLU:OE2	85:Sf:123:ASN:ND2	2.31	0.63
7:C:13:LEU:HD12	7:C:14:PRO:HD2	1.81	0.63
40:Lf:44:ASN:HA	40:Lf:47:LEU:HD23	1.79	0.63
56:SC:81:LEU:HB3	56:SC:84:LEU:HD21	1.80	0.63
74:SU:27:LYS:HZ2	74:SU:30:SER:H	1.44	0.63
1:1:1796:A:H2'	1:1:1797:A:H8	1.63	0.63
11:LC:216:GLU:OE2	11:LC:217:HIS:ND1	2.32	0.63
31:LW:80:ARG:NH2	60:SG:131:LYS:H	1.96	0.63
59:SF:152:LEU:HD23	59:SF:156:ASN:ND2	2.13	0.63
62:SI:22:ARG:HD2	62:SI:25:ARG:HE	1.61	0.63
67:SN:29:THR:HG23	67:SN:32:GLN:H	1.64	0.63
65:SL:104:ARG:HG3	77:SX:12:ALA:HB2	1.80	0.63
2:2:67:A:O2'	2:2:69:G:OP1	2.17	0.62
2:2:723:G:C5	2:2:724:U:H1'	2.34	0.62
3:3:40:C:O2	18:LJ:73:ARG:NH1	2.31	0.62
58:SE:141:THR:HG22	58:SE:145:ARG:HB2	1.81	0.62
2:2:893:G:H2'	2:2:894:U:C6	2.35	0.62
2:2:352:G:H2'	2:2:353:G:H8	1.65	0.62
2:2:1484:G:H3'	2:2:1511:A:H61	1.64	0.62
4:4:23:U:OP1	33:LY:15:ARG:NH1	2.32	0.62
13:LE:139:GLU:HG2	13:LE:152:LYS:HE2	1.80	0.62
16:LH:98:PRO:O	16:LH:118:ASN:ND2	2.32	0.62
58:SE:59:ARG:HH12	78:SY:90:PRO:HB3	1.63	0.62
2:2:1082:U:OP1	56:SC:169:LYS:NZ	2.31	0.62
58:SE:160:VAL:HG21	58:SE:169:ILE:HD12	1.81	0.62
62:SI:176:ARG:HE	62:SI:179:GLN:HG3	1.64	0.62
72:SS:111:GLU:O	72:SS:115:ARG:HG2	1.99	0.62
1:1:320:A:OP1	20:LL:23:ARG:NH2	2.33	0.62
1:1:2974:A:H2'	1:1:2975:G:H8	1.64	0.62
16:LH:14:GLU:OE2	21:LM:2:ALA:N	2.32	0.62
63:SJ:62:GLU:HG3	63:SJ:63:LYS:HG2	1.80	0.62
2:2:1467:A:N6	2:2:1534:U:H3	1.94	0.62
11:LC:365:ALA:HB3	27:LS:28:ARG:HD2	1.82	0.62
27:LS:73:LYS:NZ	27:LS:97:THR:O	2.32	0.62
52:Ls:37:GLN:HE21	52:Ls:185:MET:HE2	1.65	0.62
1:1:1219:G:H5''	1:1:1228:A:H1'	1.82	0.62
1:1:2100:U:OP2	1:1:2105:A:N6	2.31	0.62
2:2:648:C:H2'	2:2:649:G:C8	2.35	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:C:337:GLU:HA	7:C:340:LYS:HE3	1.79	0.62
60:SG:221:GLU:OE1	60:SG:225:GLN:NE2	2.33	0.62
68:SO:123:MET:HE3	68:SO:124:LYS:H	1.64	0.62
1:1:405:G:OP1	24:LP:62:ARG:NH1	2.32	0.62
11:LC:159:ALA:HB3	11:LC:162:ALA:HB2	1.80	0.62
47:Lm:79:GLU:OE2	47:Lm:81:SER:OG	2.08	0.62
69:SP:49:ALA:HA	69:SP:52:LYS:HZ3	1.65	0.62
2:2:188:U:OP2	2:2:189:C:N4	2.31	0.62
2:2:648:C:H2'	2:2:649:G:H8	1.65	0.62
5:A:10:THR:HG22	5:A:308:ARG:HG3	1.82	0.62
8:D:50:ILE:HD13	8:D:65:LYS:HA	1.81	0.62
57:SD:75:LEU:HD12	64:SK:63:TYR:HD1	1.63	0.62
1:1:957:C:H5''	25:LQ:82:MET:HE2	1.82	0.62
7:C:156:ALA:O	7:C:160:LEU:HB2	2.00	0.62
55:SB:160:GLN:O	55:SB:164:ILE:HD12	1.99	0.62
59:SF:177:ILE:HA	59:SF:180:CYS:HB3	1.81	0.62
66:SM:51:SER:HA	66:SM:54:LEU:HG	1.82	0.62
66:SM:83:GLU:OE1	85:Sf:114:ILE:HD12	1.99	0.62
1:1:2058:A:OP1	62:SI:202:LYS:NZ	2.33	0.61
3:3:4:U:H2'	3:3:5:A:H8	1.65	0.61
22:LN:31:ARG:NH1	22:LN:124:ASP:OD2	2.33	0.61
55:SB:129:THR:OG1	55:SB:131:ASP:OD1	2.17	0.61
72:SS:41:ARG:NH1	73:ST:47:PRO:HD3	2.15	0.61
2:2:1758:A:OP2	6:B:98:LYS:NZ	2.27	0.61
52:Ls:121:VAL:HG23	52:Ls:158:LEU:HD11	1.82	0.61
55:SB:158:SER:HA	55:SB:161:ILE:HD12	1.82	0.61
62:SI:36:THR:OG1	62:SI:96:LEU:O	2.18	0.61
25:LQ:152:ASP:OD2	25:LQ:153:GLN:N	2.33	0.61
27:LS:27:MET:HE1	27:LS:44:PHE:HB2	1.82	0.61
63:SJ:4:ARG:HH11	63:SJ:4:ARG:HA	1.64	0.61
80:Sa:44:MET:HG3	80:Sa:65:PRO:HG2	1.82	0.61
2:2:922:A:H2'	2:2:923:G:C8	2.35	0.61
35:La:149:ALA:HB2	43:Li:16:LEU:HA	1.82	0.61
63:SJ:140:ASN:ND2	78:SY:67:TYR:OH	2.33	0.61
81:Sb:56:CYS:HB2	81:Sb:63:LEU:HD11	1.83	0.61
2:2:673:U:H2'	2:2:674:G:C8	2.35	0.61
4:4:75:G:OP2	33:LY:73:TYR:OH	2.17	0.61
6:B:135:GLU:HA	57:SD:120:ARG:HH22	1.65	0.61
11:LC:306:GLU:OE2	14:LF:29:ARG:NH1	2.34	0.61
16:LH:31:ARG:NH1	16:LH:151:ASN:OD1	2.32	0.61
18:LJ:126:MET:HE3	18:LJ:128:PHE:CE1	2.34	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:SB:184:LEU:HD23	55:SB:188:LEU:HD11	1.83	0.61
69:SP:39:ASP:OD1	69:SP:40:GLU:N	2.32	0.61
83:Sd:45:GLU:HG2	83:Sd:46:LYS:HG3	1.82	0.61
1:1:575:G:H2'	1:1:576:A:H8	1.66	0.61
1:1:1196:G:OP1	27:LS:137:ARG:NH1	2.33	0.61
1:1:3050:C:O2	30:LV:14:LYS:NZ	2.29	0.61
63:SJ:4:ARG:HA	63:SJ:4:ARG:NH1	2.15	0.61
68:SO:32:ILE:HB	68:SO:96:ILE:HG22	1.83	0.61
85:Sf:119:ARG:HH21	85:Sf:150:PHE:HZ	1.46	0.61
56:SC:253:ASP:OD1	56:SC:254:THR:N	2.32	0.61
83:Sd:26:HIS:O	83:Sd:30:LEU:HD21	2.01	0.61
2:2:1590:G:H5''	83:Sd:33:LYS:HZ1	1.66	0.61
7:C:206:LYS:NZ	7:C:234:ASP:OD1	2.17	0.61
18:LJ:61:ARG:NH1	49:Lo:105:VAL:O	2.34	0.61
7:C:243:ASP:OD2	7:C:267:ARG:NH2	2.34	0.61
72:SS:76:PRO:HB2	72:SS:81:ILE:HD11	1.82	0.61
79:SZ:69:LEU:HD12	79:SZ:90:TYR:CD2	2.35	0.61
1:1:1464:A:O2'	1:1:1838:A:N3	2.30	0.61
2:2:1294:G:N2	2:2:1297:A:OP2	2.31	0.61
2:2:1421:A:H4'	56:SC:100:ALA:HB1	1.81	0.61
7:C:292:ILE:O	7:C:296:ARG:HG2	2.01	0.61
8:D:328:ASN:HD21	8:D:363:ASN:HD21	1.49	0.61
44:Lj:60:GLY:HA2	44:Lj:64:MET:HE3	1.82	0.61
67:SN:29:THR:OG1	67:SN:31:GLU:OE1	2.19	0.61
2:2:1054:U:H2'	2:2:1055:A:C8	2.36	0.60
2:2:1223:G:O2'	2:2:1253:A:N6	2.29	0.60
5:A:251:ALA:HB2	5:A:289:LEU:HD11	1.83	0.60
15:LG:151:ALA:HA	15:LG:204:THR:HG22	1.82	0.60
28:LT:81:LYS:O	28:LT:82:HIS:ND1	2.34	0.60
1:1:1265:G:H4'	52:Ls:83:ASN:HB2	1.82	0.60
1:1:1695:A:H4'	1:1:1696:A:H5'	1.82	0.60
2:2:1710:G:H2'	2:2:1711:G:H1'	1.83	0.60
2:2:1791:U:H3'	80:Sa:5:ARG:HH21	1.66	0.60
5:A:193:GLY:N	5:A:213:ASP:OD1	2.34	0.60
62:SI:100:ALA:HB3	62:SI:173:ILE:HD13	1.82	0.60
64:SK:32:GLU:HG2	64:SK:33:ILE:HG13	1.81	0.60
66:SM:95:LYS:O	66:SM:117:ASN:ND2	2.34	0.60
66:SM:104:CYS:HA	66:SM:113:ARG:HH21	1.65	0.60
5:A:62:HIS:ND1	5:A:84:ASP:OD2	2.33	0.60
24:LP:64:ALA:O	24:LP:80:ARG:NH1	2.35	0.60
41:Lg:109:GLN:NE2	41:Lg:110:SER:OG	2.35	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:SD:123:TYR:HB3	57:SD:127:ARG:NH1	2.12	0.60
60:SG:3:LEU:HD13	60:SG:109:LEU:HB2	1.83	0.60
66:SM:31:LYS:HZ2	66:SM:100:TRP:CG	2.19	0.60
66:SM:94:GLY:HA2	66:SM:97:LEU:HB2	1.83	0.60
5:A:246:TYR:CE1	5:A:261:LEU:HB2	2.35	0.60
63:SJ:90:LYS:HB2	63:SJ:93:TYR:HD2	1.66	0.60
72:SS:30:TYR:HE1	72:SS:40:ARG:HG3	1.66	0.60
2:2:1380:G:H4'	74:SU:32:GLU:OE2	2.01	0.60
2:2:1467:A:N7	2:2:1534:U:O4	2.34	0.60
10:LB:153:LYS:HG2	10:LB:193:VAL:HG21	1.83	0.60
29:LU:40:GLU:OE2	29:LU:44:ASN:ND2	2.33	0.60
71:SR:5:ARG:NH2	71:SR:53:TYR:OH	2.34	0.60
1:1:643:C:H2'	1:1:644:A:H8	1.66	0.60
1:1:2679:G:P	25:LQ:207:ARG:HH22	2.24	0.60
2:2:1498:G:N7	73:ST:102:ARG:NH2	2.45	0.60
8:D:389:LEU:HD23	8:D:392:ARG:NH2	2.16	0.60
8:D:450:VAL:HB	8:D:451:PRO:CD	2.32	0.60
14:LF:91:PHE:HB2	14:LF:145:PRO:HG3	1.81	0.60
7:C:161:ASP:HB3	7:C:164:LYS:HG2	1.82	0.60
12:LD:295:ILE:HG13	17:LI:206:LEU:HD21	1.84	0.60
42:Lh:33:GLN:NE2	42:Lh:37:GLN:HE22	1.99	0.60
49:Lo:38:GLN:OE1	49:Lo:41:ARG:NH2	2.34	0.60
60:SG:120:ASP:OD1	60:SG:121:ILE:N	2.35	0.60
68:SO:38:ASP:OD1	68:SO:39:THR:N	2.34	0.60
1:1:681:A:H5''	11:LC:43:MET:HE3	1.82	0.60
2:2:1695:G:O6	7:C:362:ARG:NH1	2.35	0.60
22:LN:192:LYS:O	22:LN:196:THR:HG23	2.02	0.60
55:SB:121:ILE:HD12	55:SB:161:ILE:HG23	1.84	0.60
66:SM:27:LEU:H	66:SM:30:LEU:HD23	1.67	0.60
75:SV:80:LYS:O	75:SV:82:VAL:HG23	2.02	0.60
5:A:28:PRO:O	5:A:47:ARG:NH2	2.34	0.60
5:A:147:HIS:CD2	5:A:169:GLY:HA3	2.37	0.60
84:Se:41:THR:HA	84:Se:45:VAL:HG22	1.83	0.60
1:1:1727:G:H21	45:Lk:2:PRO:HG2	1.66	0.60
33:LY:30:MET:HE2	33:LY:77:TYR:HA	1.83	0.60
73:ST:53:TRP:HA	73:ST:56:ILE:HG12	1.83	0.60
2:2:1538:G:N2	2:2:1565:A:OP2	2.35	0.59
13:LE:122:VAL:HG23	13:LE:127:TYR:CE2	2.36	0.59
52:Ls:19:LEU:HA	52:Ls:88:PHE:CE2	2.37	0.59
69:SP:89:ARG:HE	69:SP:125:GLY:HA3	1.67	0.59
72:SS:26:GLN:HE22	72:SS:31:ALA:HA	1.67	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:452:C:H2'	1:1:453:G:H8	1.67	0.59
1:1:2176:A:H2'	1:1:2177:A:C8	2.37	0.59
1:1:2923:G:N2	1:1:2926:A:OP2	2.32	0.59
28:LT:51:GLY:HA3	28:LT:92:ARG:HG3	1.84	0.59
70:SQ:34:LYS:HD2	70:SQ:39:PHE:HB2	1.84	0.59
1:1:1387:G:N2	1:1:1390:A:OP2	2.31	0.59
1:1:2396:U:H1'	22:LN:125:SER:HB3	1.85	0.59
1:1:2919:C:H2'	1:1:2920:G:H8	1.67	0.59
9:LA:57:PRO:HB3	50:Lp:54:ILE:HD11	1.84	0.59
34:LZ:32:THR:OG1	34:LZ:34:SER:O	2.20	0.59
65:SL:79:ARG:HH11	65:SL:125:GLY:C	2.09	0.59
2:2:1519:U:O5'	73:ST:78:LYS:NZ	2.33	0.59
57:SD:11:LYS:HE3	83:Sd:34:TYR:HE1	1.67	0.59
57:SD:45:THR:OG1	57:SD:48:VAL:O	2.17	0.59
60:SG:35:GLU:OE2	60:SG:51:ARG:NH1	2.36	0.59
62:SI:142:VAL:HA	62:SI:145:LYS:HG2	1.85	0.59
72:SS:116:LEU:HA	72:SS:119:ILE:HG22	1.83	0.59
75:SV:46:ILE:HB	75:SV:49:GLU:OE2	2.01	0.59
1:1:308:C:OP1	20:LL:102:LYS:NZ	2.33	0.59
1:1:732:G:OP1	36:Lb:44:ARG:NH1	2.35	0.59
1:1:1704:U:H1'	1:1:1705:C:C6	2.37	0.59
2:2:1095:U:P	56:SC:176:ARG:HH12	2.24	0.59
11:LC:241:ASN:OD1	11:LC:243:LEU:N	2.35	0.59
30:LV:111:MET:HE1	30:LV:116:ILE:HD11	1.84	0.59
55:SB:209:ASN:OD1	55:SB:211:HIS:ND1	2.35	0.59
59:SF:107:ILE:HG22	59:SF:111:MET:HE1	1.84	0.59
71:SR:6:THR:HG22	71:SR:7:LYS:H	1.68	0.59
1:1:2673:G:H8	1:1:2710:G:H2'	1.68	0.59
7:C:35:SER:N	8:D:422:HIS:O	2.36	0.59
60:SG:39:ASP:O	60:SG:46:LYS:NZ	2.35	0.59
62:SI:36:THR:HG21	62:SI:177:PRO:HB2	1.85	0.59
62:SI:141:SER:HA	62:SI:144:LYS:NZ	2.17	0.59
62:SI:172:ILE:HG12	62:SI:188:LEU:HD23	1.84	0.59
64:SK:31:HIS:CE1	64:SK:37:ASN:H	2.21	0.59
64:SK:36:ARG:HE	64:SK:38:LEU:HD21	1.66	0.59
76:SW:111:MET:HG3	76:SW:116:ALA:HB2	1.84	0.59
1:1:2123:G:H2'	1:1:2124:G:H8	1.68	0.59
1:1:3008:U:O2'	31:LW:16:GLY:O	2.21	0.59
2:2:65:A:H2	2:2:83:A:H62	1.51	0.59
2:2:1429:G:O2'	83:Sd:24:CYS:SG	2.60	0.59
9:LA:117:GLU:HG2	9:LA:124:GLY:H	1.67	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:LV:106:ASN:OD1	30:LV:107:PRO:HD2	2.03	0.59
54:SA:87:ARG:NH2	71:SR:82:ASP:O	2.35	0.59
60:SG:102:VAL:HG23	60:SG:106:LEU:HD21	1.84	0.59
69:SP:69:ARG:HH21	69:SP:72:LYS:NZ	2.01	0.59
76:SW:103:ILE:HD11	76:SW:129:PHE:HE1	1.68	0.59
1:1:1876:A:H61	1:1:2302:C:N4	2.01	0.59
1:1:2623:C:OP2	18:LJ:143:ARG:NH1	2.36	0.59
1:1:3185:G:O6	10:LB:151:ARG:NH1	2.35	0.59
5:A:32:LEU:HD12	5:A:71:ILE:HG12	1.85	0.59
5:A:150:TRP:HH2	71:SR:34:VAL:HG22	1.66	0.59
5:A:279:LYS:HD2	5:A:280:LYS:HG2	1.85	0.59
18:LJ:29:ASP:HA	18:LJ:32:THR:HG22	1.84	0.59
76:SW:20:MET:HE3	76:SW:22:LYS:NZ	2.18	0.59
76:SW:80:ASN:OD1	76:SW:124:LYS:NZ	2.35	0.59
2:2:916:U:H2'	2:2:917:A:H8	1.67	0.59
2:2:1529:C:OP2	79:SZ:66:ARG:NH2	2.27	0.59
31:LW:107:ALA:O	31:LW:110:LYS:HG3	2.02	0.59
59:SF:122:ASP:HA	59:SF:125:VAL:HG12	1.83	0.59
1:1:2064:C:H2'	1:1:2065:U:C6	2.38	0.59
2:2:588:A:H2'	2:2:589:A:C8	2.38	0.59
2:2:1169:G:OP1	72:SS:144:ARG:NH1	2.35	0.59
29:LU:37:SER:HB2	29:LU:41:LYS:NZ	2.18	0.59
5:A:36:ARG:HA	5:A:65:ILE:HG13	1.84	0.58
52:Ls:19:LEU:HD11	52:Ls:64:LYS:NZ	2.18	0.58
68:SO:26:VAL:HG23	68:SO:89:ILE:HA	1.84	0.58
75:SV:36:ILE:HG21	75:SV:78:LEU:HD21	1.85	0.58
1:1:1290:G:H5'	23:LO:61:LYS:HE3	1.85	0.58
1:1:1758:G:O2'	1:1:1760:G:OP2	2.18	0.58
2:2:503:A:H2'	2:2:504:U:C6	2.37	0.58
18:LJ:35:ALA:HB2	18:LJ:68:VAL:HG21	1.84	0.58
20:LL:181:ALA:HB1	35:La:147:LEU:HD21	1.85	0.58
45:Lk:53:ASP:OD1	45:Lk:54:LYS:N	2.36	0.58
55:SB:129:THR:OG1	55:SB:131:ASP:O	2.21	0.58
1:1:811:U:H3	1:1:877:A:H61	1.51	0.58
2:2:1484:G:OP2	57:SD:11:LYS:NZ	2.21	0.58
5:A:54:TYR:OH	70:SQ:103:ASN:OD1	2.21	0.58
5:A:199:THR:HG21	5:A:240:VAL:HA	1.85	0.58
8:D:332:GLU:HA	8:D:335:VAL:HG12	1.84	0.58
22:LN:118:SER:HB3	22:LN:132:VAL:HG22	1.84	0.58
24:LP:30:ARG:NH1	24:LP:31:GLU:OE2	2.37	0.58
35:La:82:VAL:O	35:La:87:ARG:NH1	2.37	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:SA:41:TRP:O	54:SA:42:LYS:HD3	2.03	0.58
57:SD:157:ASP:OD1	57:SD:158:GLY:N	2.35	0.58
74:SU:55:MET:HE3	74:SU:85:LYS:CB	2.33	0.58
80:Sa:47:SER:HA	80:Sa:50:ILE:HG12	1.85	0.58
2:2:956:U:OP2	81:Sb:20:LYS:NZ	2.33	0.58
2:2:1602:C:H2'	2:2:1603:G:C8	2.38	0.58
80:Sa:10:ARG:NH1	80:Sa:31:PRO:HG2	2.18	0.58
1:1:3010:G:OP1	31:LW:19:LYS:NZ	2.32	0.58
2:2:118:A:H1'	2:2:394:A:C5	2.37	0.58
7:C:148:PHE:O	7:C:152:ILE:HD12	2.04	0.58
27:LS:12:ARG:NH2	27:LS:57:GLU:OE2	2.33	0.58
59:SF:62:GLY:HA3	59:SF:64:TYR:CE1	2.38	0.58
64:SK:40:VAL:O	64:SK:44:LEU:HG	2.03	0.58
70:SQ:81:VAL:O	70:SQ:85:ILE:HG12	2.02	0.58
1:1:2176:A:H2'	1:1:2177:A:H8	1.67	0.58
8:D:290:ARG:HH22	8:D:356:ASN:HB3	1.67	0.58
27:LS:31:ALA:HB1	27:LS:36:VAL:HG23	1.85	0.58
45:Lk:51:ASP:OD1	45:Lk:52:SER:N	2.35	0.58
61:SH:7:ASN:HA	61:SH:16:ARG:HH12	1.68	0.58
67:SN:60:ILE:HG23	67:SN:66:VAL:HG21	1.84	0.58
72:SS:57:ARG:HG3	79:SZ:29:VAL:HG21	1.84	0.58
74:SU:21:ILE:HG22	74:SU:112:VAL:HA	1.84	0.58
2:2:1549:G:N1	2:2:1552:A:OP2	2.37	0.58
7:C:173:GLU:HG3	7:C:175:ALA:H	1.69	0.58
34:LZ:65:SER:HB2	34:LZ:121:TYR:HE2	1.69	0.58
59:SF:45:LEU:HG	59:SF:125:VAL:HG23	1.85	0.58
62:SI:137:LYS:NZ	62:SI:143:GLU:OE2	2.36	0.58
2:2:5:U:H3'	56:SC:213:LYS:NZ	2.18	0.58
2:2:233:G:O2'	2:2:234:C:OP1	2.20	0.58
5:A:57:ARG:HH22	5:A:94:THR:HA	1.69	0.58
1:1:1818:C:H5''	1:1:1819:A:H5'	1.86	0.58
2:2:1764:G:OP2	6:B:98:LYS:NZ	2.37	0.58
8:D:53:TYR:CE1	8:D:58:GLU:HG3	2.36	0.58
8:D:247:LYS:O	8:D:250:ILE:HG22	2.04	0.58
11:LC:365:ALA:HB3	27:LS:28:ARG:HH11	1.69	0.58
63:SJ:133:ARG:NH1	63:SJ:135:GLY:O	2.37	0.58
76:SW:20:MET:HE3	76:SW:22:LYS:HZ2	1.67	0.58
2:2:499:U:H2'	2:2:500:G:C8	2.39	0.58
4:4:8:C:H2'	4:4:9:A:C8	2.38	0.58
26:LR:173:LYS:HG2	26:LR:177:GLN:HE22	1.68	0.58
55:SB:108:ASP:OD1	55:SB:109:LYS:N	2.37	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:SH:36:ASN:OD1	61:SH:37:THR:N	2.36	0.58
1:1:1599:A:H5'	48:Lr:15:ARG:NH1	2.18	0.57
2:2:321:C:OP1	65:SL:138:LYS:NZ	2.34	0.57
2:2:709:G:H1	2:2:722:U:H3	1.50	0.57
7:C:36:MET:HE2	7:C:68:GLN:O	2.04	0.57
7:C:65:ILE:HD13	8:D:416:ALA:HA	1.86	0.57
15:LG:161:ASP:HB3	15:LG:162:PRO:HD3	1.86	0.57
21:LM:18:ARG:HE	21:LM:68:VAL:HG22	1.69	0.57
31:LW:80:ARG:NH2	31:LW:81:ALA:O	2.37	0.57
66:SM:65:ASN:O	66:SM:74:LYS:NZ	2.37	0.57
73:ST:23:LEU:HD11	73:ST:29:LEU:HD11	1.85	0.57
7:C:37:ARG:NH2	8:D:447:GLU:HB3	2.18	0.57
7:C:340:LYS:HA	7:C:343:ARG:HG2	1.86	0.57
16:LH:17:LYS:NZ	21:LM:3:GLU:O	2.25	0.57
52:Ls:12:PHE:HB3	52:Ls:16:LYS:HZ1	1.69	0.57
56:SC:97:GLN:OE1	56:SC:102:GLN:NE2	2.37	0.57
2:2:66:U:OP2	60:SG:136:LYS:NZ	2.37	0.57
16:LH:17:LYS:HZ3	21:LM:3:GLU:HG3	1.69	0.57
18:LJ:134:ARG:HG3	18:LJ:155:ILE:HD11	1.86	0.57
56:SC:61:MET:HE2	56:SC:81:LEU:HD11	1.86	0.57
83:Sd:10:ARG:HE	83:Sd:11:PRO:HD2	1.70	0.57
1:1:1001:G:H2'	1:1:1002:G:C8	2.39	0.57
1:1:1228:A:H2'	1:1:1255:C:H4'	1.87	0.57
1:1:3119:A:H61	1:1:3226:C:H42	1.49	0.57
2:2:701:A:N6	2:2:731:G:H1'	2.19	0.57
54:SA:55:LYS:HA	54:SA:58:GLU:OE2	2.03	0.57
72:SS:114:GLU:HG2	72:SS:118:LYS:NZ	2.19	0.57
75:SV:71:ARG:HG2	75:SV:71:ARG:HH11	1.68	0.57
5:A:292:SER:OG	5:A:294:ASP:OD1	2.20	0.57
10:LB:24:ARG:HH21	10:LB:28:ARG:HB2	1.68	0.57
24:LP:182:ARG:HA	24:LP:185:THR:HG22	1.86	0.57
1:1:1243:A:H1'	1:1:1263:C:H1'	1.85	0.57
2:2:1354:U:H2'	2:2:1355:G:C8	2.40	0.57
7:C:296:ARG:HH22	29:LU:118:VAL:HG12	1.70	0.57
56:SC:129:VAL:O	56:SC:133:ILE:HD12	2.05	0.57
58:SE:99:PHE:HE1	58:SE:113:ARG:HD3	1.69	0.57
59:SF:158:ALA:O	59:SF:162:LEU:HD23	2.03	0.57
62:SI:162:LYS:O	62:SI:165:GLU:HG3	2.04	0.57
63:SJ:28:LEU:HD12	63:SJ:103:LEU:HD23	1.85	0.57
1:1:1635:G:N2	1:1:1781:U:O4	2.36	0.57
3:3:76:G:N2	3:3:101:A:OP2	2.36	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:LI:101:LYS:HZ1	17:LI:103:LEU:H	1.50	0.57
66:SM:52:LYS:HD3	85:Sf:129:GLY:HA3	1.85	0.57
70:SQ:128:LYS:HD2	74:SU:76:TRP:HB2	1.86	0.57
1:1:2063:A:H5'	26:LR:71:ARG:HH12	1.70	0.57
1:1:2919:C:H2'	1:1:2920:G:C8	2.39	0.57
2:2:833:U:H2'	2:2:834:U:C6	2.40	0.57
7:C:49:HIS:O	7:C:53:VAL:HG23	2.03	0.57
8:D:389:LEU:HD23	8:D:392:ARG:HH22	1.68	0.57
20:LL:76:THR:OG1	20:LL:79:GLU:OE1	2.23	0.57
21:LM:72:LEU:HD12	21:LM:73:PRO:HD2	1.87	0.57
31:LW:57:ARG:HG3	31:LW:57:ARG:HH11	1.69	0.57
38:Ld:5:GLN:O	38:Ld:9:ARG:HG3	2.04	0.57
45:Lk:56:GLU:N	45:Lk:56:GLU:OE2	2.36	0.57
67:SN:69:ASN:HB3	67:SN:74:ILE:HD11	1.87	0.57
80:Sa:100:ARG:O	80:Sa:102:ARG:NH1	2.38	0.57
1:1:1744:C:H3'	1:1:1745:U:H5''	1.86	0.57
1:1:1929:G:OP1	26:LR:104:ARG:NH1	2.38	0.57
2:2:707:A:H2'	2:2:708:U:H6	1.69	0.57
2:2:909:U:H1'	2:2:913:A:H1'	1.87	0.57
8:D:207:ILE:HD11	8:D:349:ILE:HG23	1.86	0.57
13:LE:110:ASP:O	13:LE:172:ASN:ND2	2.37	0.57
54:SA:78:VAL:HG12	54:SA:125:VAL:HB	1.87	0.57
56:SC:160:HIS:HB2	56:SC:202:GLU:OE1	2.04	0.57
1:1:464:C:H2'	1:1:465:G:H8	1.69	0.57
7:C:364:LEU:O	7:C:368:VAL:HG23	2.05	0.57
30:LV:34:ARG:HH11	30:LV:34:ARG:HG3	1.70	0.57
1:1:2495:U:H2'	1:1:2496:G:H8	1.70	0.56
2:2:1587:C:H2'	2:2:1588:A:H8	1.70	0.56
2:2:1646:U:H2'	2:2:1647:A:C8	2.40	0.56
2:2:1785:G:OP2	68:SO:145:ARG:NH2	2.37	0.56
6:B:130:ALA:HA	6:B:133:LYS:NZ	2.20	0.56
8:D:216:ARG:HG3	8:D:238:TYR:CE1	2.40	0.56
52:Ls:40:GLU:OE1	52:Ls:103:ASN:ND2	2.38	0.56
76:SW:87:GLU:HA	76:SW:90:VAL:HG12	1.87	0.56
5:A:101:PHE:CE1	5:A:136:GLY:HA2	2.40	0.56
11:LC:34:ASP:OD1	11:LC:35:ILE:N	2.37	0.56
24:LP:168:GLU:OE1	24:LP:179:ARG:NH1	2.37	0.56
25:LQ:203:ARG:O	35:La:51:GLY:HA2	2.05	0.56
32:LX:82:THR:H	32:LX:85:ALA:HB3	1.71	0.56
54:SA:130:ARG:HH21	54:SA:155:PRO:HD3	1.69	0.56
57:SD:165:GLN:N	57:SD:166:PRO:HD2	2.20	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:SF:181:LEU:HD12	59:SF:184:GLU:OE2	2.05	0.56
64:SK:28:GLU:OE1	83:Sd:8:ASN:ND2	2.38	0.56
73:ST:111:ILE:HG23	73:ST:113:VAL:HG23	1.86	0.56
1:1:434:U:H2'	1:1:435:G:C8	2.41	0.56
1:1:1333:A:H2'	1:1:1335:A:H5''	1.87	0.56
1:1:1530:G:OP1	22:LN:108:ARG:NH2	2.32	0.56
1:1:2666:U:H2'	1:1:2667:C:C6	2.40	0.56
2:2:777:C:H41	78:SY:13:ARG:HH12	1.54	0.56
2:2:784:U:H2'	2:2:785:G:H8	1.70	0.56
2:2:853:A:OP1	61:SH:12:ASN:ND2	2.38	0.56
33:LY:50:ARG:HG2	33:LY:51:LYS:H	1.70	0.56
34:LZ:88:LEU:HD11	34:LZ:120:ARG:HD3	1.88	0.56
61:SH:44:LEU:HA	61:SH:47:LEU:HD23	1.86	0.56
61:SH:62:LYS:HE2	61:SH:94:ARG:HD2	1.86	0.56
66:SM:69:GLU:CD	66:SM:70:GLU:H	2.11	0.56
71:SR:105:ASP:O	71:SR:108:THR:OG1	2.20	0.56
73:ST:65:VAL:HG11	73:ST:114:LEU:HD22	1.87	0.56
79:SZ:69:LEU:HG	79:SZ:88:LYS:HE2	1.86	0.56
82:Sc:45:VAL:HG11	82:Sc:49:VAL:HG21	1.85	0.56
1:1:652:A:H2'	1:1:653:A:C8	2.41	0.56
1:1:1506:U:O2'	32:LX:124:ASN:ND2	2.38	0.56
2:2:1133:U:O4	77:SX:112:LYS:NZ	2.31	0.56
7:C:8:LEU:HD22	8:D:439:LYS:HE3	1.86	0.56
7:C:358:LYS:O	7:C:361:LYS:HG3	2.05	0.56
16:LH:107:ALA:O	16:LH:108:GLU:HG3	2.06	0.56
21:LM:19:VAL:O	21:LM:65:THR:OG1	2.24	0.56
21:LM:30:ILE:HD13	21:LM:41:ALA:HB2	1.88	0.56
68:SO:27:PHE:CD1	68:SO:91:ALA:HB3	2.41	0.56
78:SY:15:PHE:HZ	78:SY:24:LYS:HD2	1.69	0.56
85:Sf:121:CYS:O	85:Sf:123:ASN:ND2	2.38	0.56
1:1:1022:C:H2'	1:1:1023:A:C8	2.40	0.56
1:1:1541:A:H1'	32:LX:47:ARG:HG2	1.87	0.56
2:2:19:A:OP1	77:SX:109:ARG:NH1	2.39	0.56
2:2:150:G:H2'	2:2:151:G:H8	1.71	0.56
2:2:834:U:H2'	2:2:835:G:H8	1.69	0.56
5:A:24:SER:C	5:A:25:MET:HE2	2.29	0.56
64:SK:5:LYS:HA	64:SK:5:LYS:HE3	1.87	0.56
2:2:1193:A:OP2	2:2:1460:G:N2	2.37	0.56
2:2:1354:U:H2'	2:2:1355:G:H8	1.70	0.56
2:2:1378:U:H4'	2:2:1379:A:OP1	2.04	0.56
2:2:1606:G:H4'	59:SF:94:LYS:HZ3	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A:218:LEU:HD11	5:A:228:TYR:CE1	2.41	0.56
57:SD:144:LYS:O	57:SD:144:LYS:HD2	2.05	0.56
59:SF:132:ASP:OD1	59:SF:133:SER:N	2.39	0.56
66:SM:86:ILE:HG23	66:SM:88:LEU:HD23	1.88	0.56
8:D:58:GLU:OE1	8:D:137:ARG:NE	2.34	0.56
15:LG:178:ILE:HD12	15:LG:179:PRO:HD2	1.88	0.56
20:LL:196:GLY:O	20:LL:199:GLU:HG3	2.06	0.56
31:LW:102:ASN:HD22	31:LW:105:ARG:NH2	2.03	0.56
70:SQ:50:GLU:HA	70:SQ:53:LEU:HG	1.87	0.56
2:2:77:A:H2'	2:2:78:C:C6	2.41	0.56
2:2:204:U:H2'	2:2:205:A:H8	1.71	0.56
2:2:741:U:O2	61:SH:115:ARG:NH1	2.39	0.56
2:2:1547:U:O4	69:SP:48:ARG:NH2	2.39	0.56
32:LX:147:ASP:OD1	32:LX:148:ILE:N	2.39	0.56
45:Lk:5:VAL:HG23	45:Lk:47:LEU:HD13	1.86	0.56
60:SG:2:LYS:HB2	60:SG:108:VAL:HG22	1.88	0.56
73:ST:31:VAL:HG12	73:ST:33:GLY:H	1.70	0.56
1:1:261:A:C5	22:LN:12:LYS:HD2	2.41	0.56
1:1:878:A:OP1	9:LA:183:SER:OG	2.14	0.56
2:2:1616:C:O2'	2:2:1617:U:OP1	2.24	0.56
6:B:89:ARG:HH11	6:B:90:ARG:H	1.54	0.56
8:D:112:ILE:HD11	8:D:125:LEU:HD12	1.86	0.56
26:LR:144:ARG:HG3	26:LR:144:ARG:HH11	1.71	0.56
52:Ls:93:LEU:HA	52:Ls:96:VAL:HG12	1.87	0.56
57:SD:135:LYS:HD2	57:SD:192:MET:HE2	1.86	0.56
79:SZ:61:ASN:HB3	79:SZ:64:LEU:HD13	1.87	0.56
85:Sf:133:ALA:HB1	85:Sf:135:MET:HE3	1.88	0.56
1:1:1252:U:H1'	1:1:1255:C:H5	1.70	0.56
2:2:1491:C:H42	2:2:1508:G:H1	1.52	0.56
8:D:450:VAL:HB	8:D:451:PRO:HD3	1.87	0.56
10:LB:57:VAL:HG22	10:LB:73:VAL:HG22	1.87	0.56
13:LE:49:ARG:HB2	13:LE:52:LEU:HD13	1.87	0.56
18:LJ:133:THR:HG22	18:LJ:134:ARG:N	2.21	0.56
54:SA:193:ASN:HB3	54:SA:196:THR:HG22	1.88	0.56
60:SG:177:ARG:NE	60:SG:177:ARG:HA	2.21	0.56
7:C:279:ARG:HG2	7:C:279:ARG:HH11	1.71	0.55
56:SC:60:SER:OG	56:SC:61:MET:SD	2.63	0.55
76:SW:62:VAL:HG11	81:Sb:8:LEU:HD21	1.88	0.55
83:Sd:22:ARG:HB2	83:Sd:38:ILE:HG22	1.88	0.55
1:1:3298:U:O2'	1:1:3299:U:OP1	2.24	0.55
2:2:921:A:H2'	2:2:922:A:C8	2.41	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:LW:70:LYS:HB2	31:LW:74:ARG:HH21	1.71	0.55
52:Ls:48:GLN:NE2	52:Ls:90:ASN:OD1	2.28	0.55
79:SZ:49:VAL:HG23	79:SZ:54:LEU:HD21	1.87	0.55
1:1:101:A:H3'	1:1:102:G:H21	1.71	0.55
1:1:1577:C:OP1	41:Lg:32:ARG:NH1	2.38	0.55
1:1:2513:C:OP1	41:Lg:103:LYS:NZ	2.38	0.55
2:2:257:U:H3'	2:2:258:C:H5'	1.87	0.55
7:C:360:ASN:HD21	7:C:404:ALA:HB2	1.70	0.55
16:LH:113:GLU:HG3	16:LH:127:LYS:NZ	2.21	0.55
26:LR:15:LEU:HD13	26:LR:52:LYS:HB2	1.89	0.55
30:LV:38:ILE:HD12	30:LV:60:VAL:HG21	1.87	0.55
54:SA:26:HIS:HB3	54:SA:53:LEU:HD21	1.89	0.55
57:SD:125:VAL:O	57:SD:129:ILE:HG12	2.06	0.55
1:1:192:A:N3	1:1:212:G:O2'	2.38	0.55
1:1:434:U:H2'	1:1:435:G:H8	1.72	0.55
1:1:2227:U:H2'	1:1:2228:C:H6	1.69	0.55
2:2:224:C:H2'	2:2:225:C:C6	2.41	0.55
14:LF:29:ARG:O	14:LF:32:ARG:HG2	2.06	0.55
18:LJ:33:ARG:NH2	18:LJ:124:TYR:OH	2.40	0.55
27:LS:9:VAL:HG12	27:LS:61:VAL:HG23	1.87	0.55
58:SE:59:ARG:NH1	78:SY:90:PRO:HB3	2.21	0.55
1:1:604:G:H2'	1:1:605:G:C8	2.41	0.55
1:1:701:U:OP1	43:Li:18:ARG:NH2	2.38	0.55
1:1:1064:C:H4'	1:1:1065:U:H5	1.71	0.55
2:2:1157:A:H2'	2:2:1158:C:C6	2.41	0.55
6:B:134:ASP:C	57:SD:120:ARG:HH22	2.14	0.55
7:C:307:ARG:O	7:C:311:GLU:HG2	2.05	0.55
17:LI:208:GLU:OE1	17:LI:208:GLU:N	2.28	0.55
55:SB:126:THR:HG22	55:SB:136:ARG:HE	1.71	0.55
58:SE:145:ARG:NH1	58:SE:145:ARG:HA	2.21	0.55
1:1:2538:G:OP2	1:1:2539:A:O2'	2.19	0.55
1:1:2552:A:H4'	1:1:2553:C:O5'	2.05	0.55
2:2:1336:C:O2'	2:2:1338:G:N7	2.35	0.55
7:C:39:LEU:HD22	8:D:228:MET:HE2	1.88	0.55
17:LI:171:TRP:HE3	17:LI:178:ARG:HG3	1.71	0.55
24:LP:29:THR:HG21	24:LP:146:ILE:HD11	1.87	0.55
43:Li:11:VAL:O	43:Li:28:ARG:NH2	2.31	0.55
52:Ls:92:ASP:O	52:Ls:95:GLU:HG3	2.07	0.55
59:SF:85:MET:HE1	59:SF:94:LYS:NZ	2.22	0.55
63:SJ:170:VAL:HG13	63:SJ:171:ARG:HH11	1.71	0.55
64:SK:2:LEU:HA	64:SK:8:ARG:HH12	1.70	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
75:SV:38:LYS:HG3	75:SV:49:GLU:HG2	1.88	0.55
78:SY:18:ASN:HD21	78:SY:21:LEU:HD23	1.71	0.55
1:1:1016:U:H2'	1:1:1017:U:C6	2.42	0.55
1:1:2064:C:O2'	1:1:2065:U:OP1	2.25	0.55
1:1:2900:A:OP2	10:LB:257:HIS:ND1	2.40	0.55
2:2:1462:G:O2'	2:2:1598:C:OP1	2.24	0.55
12:LD:98:ALA:HB1	12:LD:165:VAL:HG23	1.88	0.55
21:LM:13:ARG:HH12	27:LS:150:PHE:C	2.14	0.55
58:SE:10:LYS:O	58:SE:13:SER:OG	2.24	0.55
60:SG:84:TYR:OH	60:SG:91:GLU:OE2	2.23	0.55
1:1:136:C:OP1	15:LG:109:LYS:NZ	2.39	0.55
1:1:1907:G:C8	50:Lp:16:THR:HG22	2.42	0.55
2:2:1199:A:N6	2:2:1453:C:OP1	2.37	0.55
5:A:192:THR:OG1	5:A:213:ASP:OD1	2.21	0.55
9:LA:134:VAL:HG12	9:LA:151:PRO:HD3	1.87	0.55
21:LM:20:LEU:HD11	21:LM:30:ILE:HD11	1.88	0.55
29:LU:97:ARG:HH11	29:LU:97:ARG:HG2	1.72	0.55
47:Lm:79:GLU:OE2	47:Lm:82:LEU:N	2.37	0.55
67:SN:49:GLN:HA	67:SN:52:VAL:HG12	1.89	0.55
71:SR:104:ILE:HG12	71:SR:122:VAL:CG1	2.37	0.55
73:ST:32:PRO:HG3	73:ST:103:LYS:HD2	1.87	0.55
1:1:1262:C:H2'	1:1:1263:C:C6	2.41	0.55
1:1:3123:U:H2'	1:1:3124:G:H8	1.72	0.55
2:2:57:G:OP1	78:SY:115:LYS:NZ	2.31	0.55
21:LM:91:ASP:OD1	21:LM:92:ALA:N	2.39	0.55
31:LW:80:ARG:HG2	31:LW:81:ALA:H	1.71	0.55
36:Lb:47:LEU:HA	36:Lb:50:THR:HG22	1.88	0.55
39:Le:88:MET:HA	39:Le:88:MET:HE2	1.87	0.55
55:SB:134:LEU:HB3	55:SB:219:LYS:HG3	1.87	0.55
57:SD:145:LEU:O	57:SD:146:ARG:HG2	2.07	0.55
61:SH:37:THR:OG1	61:SH:39:ASP:OD1	2.23	0.55
65:SL:91:ILE:HD11	65:SL:112:LEU:HD23	1.88	0.55
85:Sf:107:LYS:HD3	85:Sf:108:VAL:H	1.72	0.55
2:2:1207:C:H2'	2:2:1208:A:H8	1.72	0.55
8:D:204:ASP:HA	8:D:224:SER:O	2.06	0.55
29:LU:21:PHE:HB2	29:LU:72:ILE:HB	1.89	0.55
32:LX:71:ASP:O	32:LX:75:ILE:HG12	2.06	0.55
56:SC:182:ARG:HA	56:SC:203:ASP:OD2	2.06	0.55
62:SI:189:GLU:N	62:SI:192:GLU:OE2	2.39	0.55
74:SU:64:THR:OG1	83:Sd:40:ARG:NH1	2.39	0.55
77:SX:86:PHE:HB2	77:SX:120:VAL:HG11	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:351:G:N2	1:1:354:A:OP2	2.36	0.54
1:1:2727:U:H2'	1:1:2728:A:H8	1.71	0.54
8:D:129:GLU:OE2	8:D:133:ARG:NE	2.37	0.54
17:LI:62:SER:HA	17:LI:65:LEU:HD12	1.89	0.54
76:SW:27:ILE:HB	76:SW:61:ILE:HB	1.89	0.54
79:SZ:70:LYS:O	79:SZ:73:GLU:HG3	2.07	0.54
81:Sb:2:VAL:HG12	81:Sb:3:LEU:HD23	1.90	0.54
1:1:478:G:H2'	1:1:479:G:H8	1.72	0.54
1:1:1139:C:OP2	14:LF:100:LYS:NZ	2.40	0.54
2:2:70:C:H5''	60:SG:165:LYS:HE3	1.90	0.54
2:2:404:A:H2'	2:2:405:C:H6	1.71	0.54
2:2:694:U:H2'	2:2:695:C:C6	2.43	0.54
2:2:1386:C:H2'	2:2:1387:U:H4'	1.89	0.54
9:LA:201:GLY:HA2	9:LA:204:MET:HG3	1.88	0.54
26:LR:170:ARG:HA	26:LR:170:ARG:CZ	2.37	0.54
29:LU:62:ILE:HA	29:LU:72:ILE:HD13	1.89	0.54
31:LW:102:ASN:HD22	31:LW:105:ARG:HH22	1.54	0.54
61:SH:123:PRO:HD2	61:SH:126:ARG:HD2	1.88	0.54
1:1:604:G:H2'	1:1:605:G:H8	1.73	0.54
5:A:210:GLY:HA3	5:A:236:ILE:HD11	1.89	0.54
7:C:265:ASN:OD1	7:C:266:ALA:N	2.40	0.54
8:D:53:TYR:HB2	8:D:74:ASN:HB3	1.90	0.54
8:D:245:LEU:HD21	8:D:323:VAL:HG21	1.90	0.54
16:LH:12:VAL:HG11	21:LM:4:ILE:HD11	1.88	0.54
49:Lo:103:ALA:O	49:Lo:104:LEU:HD22	2.07	0.54
56:SC:61:MET:SD	56:SC:61:MET:N	2.80	0.54
58:SE:129:VAL:HG12	58:SE:139:LEU:HB3	1.88	0.54
63:SJ:26:LEU:HA	63:SJ:29:VAL:HG12	1.88	0.54
73:ST:112:GLN:HB3	73:ST:128:GLN:HE22	1.72	0.54
77:SX:75:GLN:NE2	77:SX:80:GLY:HA2	2.22	0.54
78:SY:13:ARG:O	78:SY:27:VAL:HG12	2.07	0.54
1:1:2218:A:HO2'	2:2:1753:G:HO2'	1.55	0.54
2:2:403:U:H2'	2:2:404:A:H8	1.72	0.54
2:2:1420:A:OP2	57:SD:154:LYS:NZ	2.41	0.54
7:C:331:ALA:O	7:C:334:GLU:HG2	2.07	0.54
8:D:405:GLU:O	8:D:409:ILE:HD12	2.08	0.54
31:LW:93:ARG:HH21	60:SG:156:TYR:HA	1.73	0.54
44:Lj:29:ASN:O	44:Lj:32:LYS:NZ	2.25	0.54
55:SB:184:LEU:O	55:SB:188:LEU:HD12	2.06	0.54
61:SH:91:PHE:HB2	61:SH:94:ARG:NH2	2.23	0.54
72:SS:83:THR:OG1	72:SS:97:ASP:OD2	2.21	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
83:Sd:49:ASP:OD1	83:Sd:50:ILE:N	2.41	0.54
1:1:425:G:H2'	1:1:426:A:C8	2.42	0.54
1:1:452:C:H2'	1:1:453:G:C8	2.41	0.54
1:1:617:C:H2'	1:1:618:C:C6	2.43	0.54
1:1:1766:G:H2'	1:1:1767:A:C8	2.43	0.54
1:1:2842:U:H2'	1:1:2843:C:C6	2.43	0.54
2:2:892:U:H2'	2:2:893:G:C8	2.43	0.54
2:2:1313:G:H5'	71:SR:7:LYS:HD3	1.90	0.54
2:2:1703:C:H2'	2:2:1704:A:C8	2.43	0.54
3:3:7:G:OP1	12:LD:33:ARG:NH1	2.40	0.54
3:3:16:U:OP1	18:LJ:148:ARG:NH1	2.41	0.54
7:C:347:LYS:O	7:C:351:GLU:HG2	2.07	0.54
20:LL:158:GLU:OE2	20:LL:159:GLN:HG2	2.07	0.54
30:LV:68:LYS:NZ	30:LV:70:GLU:OE2	2.38	0.54
2:2:784:U:H2'	2:2:785:G:C8	2.42	0.54
4:4:9:A:H2'	4:4:10:A:H8	1.72	0.54
16:LH:90:MET:HG2	16:LH:183:VAL:HA	1.90	0.54
24:LP:78:VAL:HG12	24:LP:80:ARG:H	1.72	0.54
58:SE:11:ARG:HH12	58:SE:20:LEU:HD12	1.73	0.54
71:SR:6:THR:HG22	71:SR:7:LYS:N	2.22	0.54
1:1:1879:G:O2'	1:1:2297:U:O4	2.20	0.54
2:2:327:G:OP2	62:SI:176:ARG:NH1	2.40	0.54
2:2:1359:U:H4'	2:2:1360:G:C2	2.42	0.54
8:D:208:VAL:HB	8:D:348:VAL:HG22	1.90	0.54
8:D:472:VAL:HG21	8:D:529:ILE:HG23	1.90	0.54
56:SC:196:LEU:HD22	56:SC:201:ILE:HG21	1.88	0.54
61:SH:165:ASP:OD1	61:SH:166:GLU:N	2.40	0.54
65:SL:7:VAL:HG13	65:SL:8:GLN:HG2	1.89	0.54
69:SP:33:LEU:HD13	69:SP:36:LEU:HD22	1.88	0.54
71:SR:34:VAL:O	71:SR:38:ILE:HG22	2.07	0.54
72:SS:120:ARG:HG2	72:SS:125:LEU:HD21	1.89	0.54
1:1:688:C:H2'	1:1:689:G:H8	1.72	0.54
1:1:1067:A:H4'	12:LD:44:TYR:CE2	2.42	0.54
1:1:1290:G:N3	23:LO:61:LYS:HE2	2.22	0.54
1:1:1464:A:O2'	1:1:1838:A:H1'	2.07	0.54
1:1:2332:G:H2'	1:1:2333:G:C8	2.43	0.54
1:1:3332:A:O2'	1:1:3333:G:OP1	2.22	0.54
5:A:22:ALA:HB3	5:A:32:LEU:HB2	1.89	0.54
22:LN:124:ASP:OD1	22:LN:125:SER:N	2.36	0.54
45:Lk:12:ILE:HG22	45:Lk:16:ARG:NE	2.23	0.54
1:1:3299:U:H2'	1:1:3300:A:H8	1.73	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:66:U:O2	60:SG:160:ARG:NH1	2.41	0.54
2:2:1675:G:H21	2:2:1718:A:N6	1.98	0.54
7:C:154:LYS:O	7:C:158:ILE:HG12	2.08	0.54
8:D:197:ARG:HD3	8:D:384:LEU:HD11	1.90	0.54
28:LT:100:ARG:HB3	28:LT:103:GLU:OE1	2.07	0.54
31:LW:80:ARG:CZ	60:SG:130:PRO:HA	2.38	0.54
67:SN:40:LEU:HD13	67:SN:53:ILE:HD11	1.90	0.54
78:SY:125:ALA:HA	78:SY:128:LYS:HE2	1.90	0.54
1:1:644:A:H2'	1:1:645:A:C8	2.43	0.54
2:2:862:U:H5''	76:SW:28:ARG:HH21	1.74	0.54
2:2:1277:C:H2'	2:2:1278:G:C8	2.43	0.54
5:A:59:LEU:O	5:A:60:HIS:ND1	2.40	0.54
31:LW:111:GLU:HA	31:LW:114:GLU:CD	2.33	0.54
57:SD:175:THR:O	57:SD:176:ARG:NH1	2.38	0.54
59:SF:85:MET:HE1	59:SF:94:LYS:HZ1	1.72	0.54
82:Sc:15:ARG:NH1	82:Sc:30:ARG:HH22	2.06	0.54
1:1:779:U:H2'	1:1:780:U:C6	2.43	0.53
1:1:967:U:H2'	1:1:968:U:H6	1.74	0.53
1:1:1091:C:H2'	1:1:1092:A:H8	1.73	0.53
1:1:1222:C:H4'	1:1:1222:C:OP1	2.08	0.53
1:1:1637:C:O2'	1:1:1777:A:OP2	2.23	0.53
2:2:537:G:N2	2:2:539:A:N7	2.56	0.53
2:2:1511:A:O2'	2:2:1514:C:N4	2.42	0.53
2:2:1609:U:OP1	59:SF:79:ARG:NH2	2.41	0.53
2:2:1709:G:H2'	2:2:1710:G:O4'	2.08	0.53
11:LC:149:VAL:CG1	11:LC:150:PRO:HD3	2.36	0.53
15:LG:74:VAL:HB	15:LG:237:GLY:HA3	1.89	0.53
18:LJ:133:THR:HG21	18:LJ:137:GLU:HG2	1.90	0.53
29:LU:60:ILE:HA	29:LU:73:ILE:O	2.08	0.53
73:ST:114:LEU:HD13	73:ST:123:ARG:HB3	1.89	0.53
82:Sc:23:ARG:NE	82:Sc:23:ARG:HA	2.23	0.53
1:1:747:A:O2'	20:LL:198:ARG:NH2	2.41	0.53
1:1:2495:U:H2'	1:1:2496:G:C8	2.42	0.53
1:1:2726:U:H2'	1:1:2727:U:C6	2.42	0.53
2:2:468:A:H5''	63:SJ:8:LYS:HE2	1.89	0.53
6:B:130:ALA:HA	6:B:133:LYS:HZ2	1.72	0.53
8:D:385:ASN:HB3	8:D:388:GLU:HB2	1.90	0.53
14:LF:105:PRO:HB3	14:LF:136:VAL:HG12	1.90	0.53
22:LN:152:CYS:HB2	42:Lh:97:LEU:HD11	1.90	0.53
71:SR:5:ARG:HG2	71:SR:10:LYS:HZ2	1.72	0.53
72:SS:86:LEU:HD12	72:SS:97:ASP:HB3	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1779:A:H2'	1:1:1780:A:H8	1.74	0.53
16:LH:99:ILE:HG22	16:LH:119:PHE:HA	1.90	0.53
34:LZ:75:ASN:OD1	34:LZ:76:TYR:N	2.41	0.53
34:LZ:105:GLN:HA	34:LZ:108:GLU:HG3	1.90	0.53
38:Ld:4:THR:HA	38:Ld:7:LYS:HG2	1.90	0.53
45:Lk:77:ARG:NH1	45:Lk:79:SER:OG	2.42	0.53
1:1:1597:G:P	48:Lr:5:TRP:HH2	2.32	0.53
1:1:2227:U:H2'	1:1:2228:C:C6	2.43	0.53
5:A:33:SER:HG	5:A:43:TRP:HE1	1.57	0.53
7:C:161:ASP:H	7:C:164:LYS:NZ	2.05	0.53
18:LJ:48:TYR:CD2	18:LJ:65:LYS:HD3	2.44	0.53
38:Ld:57:VAL:HG12	38:Ld:99:SER:OG	2.09	0.53
57:SD:224:GLN:HB3	57:SD:225:PRO:HD3	1.90	0.53
58:SE:131:LEU:HA	58:SE:137:PRO:HA	1.91	0.53
59:SF:43:ILE:HG13	59:SF:44:SER:H	1.74	0.53
61:SH:62:LYS:HG3	61:SH:94:ARG:HG3	1.90	0.53
68:SO:94:ILE:HD11	68:SO:128:ILE:HD12	1.90	0.53
74:SU:20:ARG:HG2	74:SU:20:ARG:HH11	1.73	0.53
2:2:148:G:H22	2:2:160:G:H1	1.56	0.53
2:2:494:G:H2'	2:2:495:G:H8	1.72	0.53
2:2:1477:C:O2'	2:2:1478:C:O5'	2.23	0.53
60:SG:198:ARG:NE	60:SG:201:GLN:HE22	2.07	0.53
61:SH:166:GLU:OE1	61:SH:196:PRO:HG2	2.09	0.53
62:SI:110:ARG:O	62:SI:114:GLU:HG2	2.09	0.53
1:1:1727:G:N2	45:Lk:2:PRO:HG2	2.23	0.53
2:2:98:C:OP2	2:2:375:A:O2'	2.23	0.53
2:2:1166:G:N1	2:2:1571:G:OP2	2.41	0.53
8:D:420:MET:HE2	8:D:450:VAL:HG13	1.90	0.53
10:LB:95:THR:HG23	10:LB:97:ARG:H	1.73	0.53
14:LF:39:ARG:HG2	14:LF:39:ARG:HH11	1.73	0.53
14:LF:65:GLU:O	14:LF:69:ILE:HG13	2.09	0.53
25:LQ:123:VAL:HG23	25:LQ:144:ALA:HB2	1.91	0.53
69:SP:37:ASP:OD1	69:SP:40:GLU:HG2	2.07	0.53
72:SS:82:PRO:HG2	72:SS:85:PHE:HB2	1.91	0.53
72:SS:91:ASP:OD1	72:SS:92:ILE:N	2.41	0.53
76:SW:94:LEU:HD11	76:SW:102:VAL:HG23	1.89	0.53
1:1:673:G:OP1	20:LL:39:ARG:NH2	2.36	0.53
2:2:1195:G:OP1	2:2:1196:G:O2'	2.18	0.53
30:LV:106:ASN:HD22	30:LV:110:GLU:CD	2.15	0.53
40:Lf:105:TYR:HB2	40:Lf:106:PRO:HD3	1.91	0.53
44:Lj:14:LYS:HZ1	46:Ll:51:LEU:HD21	1.74	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:Ls:126:THR:OG1	52:Ls:150:ILE:O	2.22	0.53
85:Sf:121:CYS:HB3	85:Sf:146:LEU:HD13	1.89	0.53
2:2:1519:U:H6	73:ST:78:LYS:HZ1	1.55	0.53
10:LB:10:ARG:NH1	10:LB:11:HIS:O	2.42	0.53
30:LV:68:LYS:HG2	30:LV:70:GLU:OE1	2.09	0.53
58:SE:64:ILE:HG23	78:SY:20:LEU:HD21	1.91	0.53
1:1:993:G:H2'	1:1:994:G:C8	2.43	0.53
1:1:1782:C:OP1	48:Lr:2:ARG:NH2	2.42	0.53
2:2:1569:A:H4'	2:2:1570:G:OP2	2.09	0.53
5:A:236:ILE:HG22	5:A:252:THR:HG22	1.90	0.53
16:LH:15:ASN:O	16:LH:15:ASN:ND2	2.41	0.53
16:LH:136:VAL:HG22	16:LH:148:LEU:HD23	1.91	0.53
71:SR:62:GLN:HG3	71:SR:63:ARG:NH1	2.24	0.53
1:1:1599:A:H5'	48:Lr:15:ARG:CZ	2.39	0.53
1:1:3084:C:H1'	16:LH:158:GLN:HE22	1.74	0.53
2:2:1470:G:H2'	2:2:1471:A:H8	1.74	0.53
12:LD:208:ALA:HB2	12:LD:239:LEU:HD21	1.89	0.53
2:2:824:U:H2'	2:2:825:C:C6	2.44	0.52
2:2:931:A:OP2	80:Sa:37:LYS:NZ	2.31	0.52
2:2:1480:G:H21	2:2:1602:C:H1'	1.75	0.52
8:D:186:GLU:HB2	8:D:390:GLN:HG2	1.90	0.52
54:SA:130:ARG:HG2	54:SA:130:ARG:HH11	1.74	0.52
59:SF:165:GLY:HA2	59:SF:196:TYR:HD2	1.74	0.52
62:SI:101:VAL:HG22	62:SI:172:ILE:CD1	2.39	0.52
67:SN:114:ARG:O	67:SN:118:ILE:HG12	2.09	0.52
72:SS:67:GLU:O	72:SS:71:THR:HG23	2.09	0.52
78:SY:53:ALA:HB1	78:SY:57:GLN:HE21	1.73	0.52
78:SY:87:LYS:HD2	78:SY:87:LYS:O	2.09	0.52
1:1:2320:A:H2'	1:1:2321:A:C8	2.44	0.52
2:2:301:U:OP1	65:SL:141:ARG:NH1	2.42	0.52
2:2:1189:C:O2'	70:SQ:137:ARG:NH2	2.42	0.52
12:LD:175:PHE:O	12:LD:176:ILE:HD13	2.09	0.52
23:LO:77:ALA:HB3	23:LO:80:ARG:HG2	1.91	0.52
23:LO:120:MET:HE2	23:LO:120:MET:HA	1.90	0.52
73:ST:114:LEU:HB2	73:ST:124:ARG:O	2.09	0.52
76:SW:82:ARG:HB2	76:SW:85:GLU:OE1	2.08	0.52
2:2:231:G:H2'	2:2:232:G:C8	2.44	0.52
2:2:421:C:O2'	2:2:423:G:OP1	2.23	0.52
2:2:1443:U:OP1	85:Sf:83:LYS:NZ	2.30	0.52
8:D:426:ALA:HB2	8:D:446:PRO:HG3	1.91	0.52
35:La:93:GLY:O	35:La:96:LYS:NZ	2.39	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:Lj:84:LYS:HE2	44:Lj:84:LYS:HA	1.91	0.52
78:SY:87:LYS:HG3	78:SY:88:PHE:CE1	2.44	0.52
1:1:261:A:OP1	22:LN:50:ARG:NH1	2.42	0.52
1:1:766:G:C8	25:LQ:93:SER:HB3	2.44	0.52
2:2:1095:U:OP2	56:SC:176:ARG:NH1	2.36	0.52
2:2:1329:C:O2'	57:SD:165:GLN:NE2	2.42	0.52
13:LE:115:ASP:OD1	13:LE:116:GLN:N	2.42	0.52
56:SC:130:ALA:O	56:SC:134:ARG:NH1	2.42	0.52
64:SK:42:LYS:HA	64:SK:45:GLN:HG3	1.92	0.52
76:SW:51:GLU:HG3	81:Sb:8:LEU:HD11	1.91	0.52
1:1:203:A:N3	11:LC:228:ASN:ND2	2.57	0.52
1:1:2906:G:C2	10:LB:251:ALA:HB1	2.45	0.52
2:2:539:A:O2'	2:2:540:C:O5'	2.26	0.52
2:2:1428:U:H4'	2:2:1429:G:H5''	1.91	0.52
2:2:1580:G:C8	70:SQ:122:ARG:HB3	2.45	0.52
10:LB:377:LYS:O	10:LB:381:MET:HB2	2.10	0.52
12:LD:284:ARG:HA	12:LD:284:ARG:HH11	1.74	0.52
24:LP:36:ILE:HG13	24:LP:36:ILE:O	2.10	0.52
33:LY:50:ARG:HG2	33:LY:51:LYS:N	2.24	0.52
55:SB:189:ILE:HG13	55:SB:190:PRO:HD3	1.90	0.52
57:SD:150:ALA:C	57:SD:151:LYS:HD3	2.34	0.52
63:SJ:38:ARG:O	63:SJ:42:ARG:HG3	2.10	0.52
69:SP:47:ALA:HA	69:SP:50:ARG:HE	1.75	0.52
72:SS:143:ARG:O	72:SS:144:ARG:HD2	2.08	0.52
74:SU:39:ILE:O	74:SU:43:LYS:HG2	2.10	0.52
79:SZ:54:LEU:HD12	79:SZ:65:ALA:HB1	1.91	0.52
1:1:1003:G:H2'	1:1:1004:C:C6	2.44	0.52
1:1:2149:U:OP2	9:LA:200:ARG:NH1	2.42	0.52
2:2:483:G:H22	2:2:498:U:H3	1.55	0.52
2:2:1144:A:H5'	56:SC:99:ARG:HH22	1.74	0.52
21:LM:14:VAL:HG12	27:LS:150:PHE:O	2.10	0.52
27:LS:82:ASP:HB2	27:LS:120:SER:HB2	1.92	0.52
29:LU:59:VAL:O	29:LU:75:HIS:ND1	2.43	0.52
54:SA:149:LEU:HD23	54:SA:165:THR:HG21	1.92	0.52
58:SE:153:LEU:HD11	58:SE:172:PHE:CZ	2.45	0.52
60:SG:11:GLY:O	60:SG:129:HIS:ND1	2.42	0.52
60:SG:152:ASP:OD2	60:SG:155:LYS:HG2	2.09	0.52
61:SH:10:ALA:HA	61:SH:48:GLN:OE1	2.09	0.52
61:SH:164:LEU:HD21	61:SH:193:PHE:HD1	1.72	0.52
77:SX:69:ARG:HG3	77:SX:117:ILE:HG12	1.91	0.52
1:1:2314:U:H2'	1:1:2315:A:H8	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2465:U:H2'	1:1:2466:G:C8	2.45	0.52
2:2:107:A:H2'	2:2:108:G:C8	2.44	0.52
2:2:469:U:O2'	2:2:768:A:N3	2.42	0.52
29:LU:61:LYS:O	29:LU:72:ILE:HA	2.10	0.52
35:La:100:PRO:HG2	35:La:123:VAL:HG23	1.92	0.52
52:Ls:173:LEU:HD12	52:Ls:178:ILE:HG23	1.92	0.52
58:SE:171:ASP:OD1	58:SE:172:PHE:N	2.39	0.52
63:SJ:11:LYS:HG2	63:SJ:45:LEU:HD12	1.91	0.52
64:SK:72:ASP:OD1	64:SK:73:TYR:N	2.43	0.52
64:SK:86:PRO:HA	64:SK:89:HIS:HB3	1.92	0.52
72:SS:28:VAL:HG12	72:SS:58:ALA:HA	1.90	0.52
1:1:2320:A:H2'	1:1:2321:A:H8	1.73	0.52
2:2:999:A:N7	6:B:89:ARG:NH2	2.50	0.52
5:A:268:ASP:OD1	5:A:269:GLU:N	2.43	0.52
7:C:260:GLU:HA	7:C:263:ASN:HD21	1.74	0.52
23:LO:178:ARG:NE	23:LO:178:ARG:HA	2.23	0.52
35:La:75:ILE:HD11	35:La:118:LEU:HD22	1.91	0.52
52:Ls:106:LYS:HE2	52:Ls:179:SER:HB2	1.91	0.52
55:SB:13:LYS:H	55:SB:13:LYS:HD2	1.75	0.52
59:SF:67:LYS:HG3	59:SF:68:ARG:N	2.21	0.52
60:SG:165:LYS:HG3	60:SG:166:GLY:H	1.74	0.52
61:SH:57:VAL:HG21	61:SH:178:THR:HA	1.91	0.52
71:SR:24:LEU:HB2	71:SR:31:ASN:ND2	2.25	0.52
1:1:78:A:H5'	20:LL:100:ARG:NH1	2.24	0.52
6:B:129:GLU:O	6:B:132:LEU:HG	2.10	0.52
16:LH:26:THR:HG22	16:LH:35:GLN:OE1	2.09	0.52
20:LL:124:ILE:HG22	42:Lh:122:ALA:O	2.09	0.52
22:LN:35:VAL:HG12	22:LN:36:ILE:HG13	1.92	0.52
25:LQ:174:ARG:HB3	25:LQ:177:VAL:HG23	1.92	0.52
35:La:75:ILE:HG22	35:La:115:LYS:H	1.75	0.52
52:Ls:12:PHE:HB3	52:Ls:16:LYS:NZ	2.25	0.52
61:SH:86:GLU:HA	61:SH:89:LYS:HG2	1.91	0.52
77:SX:53:VAL:HG12	77:SX:100:ASP:H	1.74	0.52
1:1:285:U:OP2	22:LN:68:ARG:NH2	2.43	0.52
1:1:1006:A:H2'	1:1:1008:U:H5''	1.92	0.52
1:1:2974:A:H2'	1:1:2975:G:C8	2.45	0.52
4:4:136:G:OP1	32:LX:62:LYS:NZ	2.43	0.52
5:A:159:ASN:HB2	5:A:161:GLN:OE1	2.08	0.52
7:C:322:ARG:HA	7:C:325:LYS:HD2	1.92	0.52
12:LD:246:ALA:O	12:LD:250:ILE:HG12	2.10	0.52
24:LP:119:VAL:HG22	24:LP:146:ILE:HG12	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:Li:71:ARG:HD3	43:Li:103:ILE:HD11	1.91	0.52
55:SB:146:ARG:HD3	55:SB:147:PRO:HD2	1.92	0.52
67:SN:4:LEU:HD11	67:SN:124:ARG:NH2	2.24	0.52
78:SY:5:ASP:OD1	78:SY:6:SER:N	2.40	0.52
81:Sb:35:VAL:HG21	81:Sb:63:LEU:HD23	1.92	0.52
1:1:2405:G:H2'	1:1:2406:A:H8	1.75	0.51
2:2:1355:G:H2'	2:2:1356:C:C6	2.45	0.51
3:3:4:U:H2'	3:3:5:A:C8	2.44	0.51
7:C:400:ALA:HA	7:C:403:ILE:HD12	1.92	0.51
27:LS:28:ARG:O	27:LS:29:ILE:HD13	2.10	0.51
34:LZ:41:LEU:HD22	34:LZ:73:VAL:HG22	1.92	0.51
48:Ln:8:LYS:HE2	48:Ln:12:ARG:NH2	2.26	0.51
48:Lr:8:LYS:HE2	48:Lr:12:ARG:NH2	2.26	0.51
55:SB:89:ASP:HB3	55:SB:223:PHE:HE1	1.74	0.51
57:SD:117:ALA:CB	57:SD:120:ARG:HD3	2.38	0.51
71:SR:66:VAL:HG13	71:SR:69:ILE:HD13	1.91	0.51
72:SS:69:LEU:O	72:SS:73:ILE:HG12	2.09	0.51
84:Se:27:LYS:HD3	84:Se:27:LYS:N	2.25	0.51
1:1:1227:A:O5'	1:1:1254:A:O2'	2.22	0.51
1:1:2058:A:H2'	1:1:2059:A:C8	2.44	0.51
1:1:2148:G:O2'	1:1:2277:U:OP2	2.29	0.51
2:2:835:G:H2'	2:2:836:G:H8	1.75	0.51
9:LA:113:VAL:HG12	9:LA:166:ILE:HD13	1.92	0.51
16:LH:16:LEU:HD21	16:LH:79:ILE:HG23	1.91	0.51
18:LJ:133:THR:HG22	18:LJ:134:ARG:H	1.76	0.51
31:LW:97:ARG:HG3	31:LW:98:PRO:HD2	1.92	0.51
56:SC:98:THR:HG22	56:SC:99:ARG:H	1.74	0.51
58:SE:246:THR:N	58:SE:249:GLU:OE2	2.42	0.51
60:SG:211:TYR:HA	60:SG:214:ILE:HG22	1.92	0.51
61:SH:160:LEU:HB3	61:SH:191:VAL:HG22	1.92	0.51
62:SI:125:ARG:HH12	62:SI:132:VAL:HG13	1.75	0.51
66:SM:33:VAL:HG22	66:SM:132:GLU:HB3	1.91	0.51
70:SQ:34:LYS:HD3	70:SQ:38:LEU:HB2	1.92	0.51
74:SU:31:LEU:HD21	74:SU:86:ARG:HB2	1.91	0.51
79:SZ:50:THR:O	79:SZ:54:LEU:HG	2.10	0.51
1:1:209:G:OP1	33:LY:11:ARG:NH1	2.41	0.51
1:1:558:U:H2'	1:1:559:G:N2	2.25	0.51
1:1:2405:G:H1	1:1:2468:U:H3	1.56	0.51
1:1:2574:G:H2'	1:1:2575:C:H6	1.76	0.51
1:1:2719:C:N3	49:Lo:63:LYS:NZ	2.58	0.51
2:2:535:A:H5'	2:2:540:C:C5	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:707:A:H2'	2:2:708:U:C6	2.45	0.51
3:3:86:C:O2'	27:LS:119:ARG:NH1	2.42	0.51
31:LW:88:GLU:HA	31:LW:91:LYS:CE	2.37	0.51
38:Ld:12:ILE:HG12	38:Ld:85:ARG:NH2	2.25	0.51
41:Lg:20:ARG:HG3	41:Lg:20:ARG:HH11	1.74	0.51
55:SB:134:LEU:HB2	55:SB:219:LYS:HE3	1.92	0.51
58:SE:254:ARG:HH11	58:SE:255:ARG:HH12	1.57	0.51
66:SM:47:LEU:HD13	66:SM:73:TYR:HE1	1.75	0.51
69:SP:52:LYS:HZ1	69:SP:92:ILE:HD13	1.75	0.51
71:SR:41:ILE:HD11	71:SR:46:LEU:HG	1.92	0.51
1:1:1373:A:N6	1:1:1401:A:O2'	2.43	0.51
1:1:2390:U:H2'	1:1:2391:U:C6	2.45	0.51
15:LG:208:SER:HA	15:LG:211:LYS:HE3	1.92	0.51
68:SO:141:ARG:HH12	80:Sa:27:ALA:HB2	1.76	0.51
69:SP:69:ARG:HE	69:SP:72:LYS:HZ1	1.57	0.51
72:SS:114:GLU:O	72:SS:118:LYS:HD3	2.11	0.51
82:Sc:17:LEU:HD12	82:Sc:17:LEU:O	2.10	0.51
84:Se:43:ARG:O	84:Se:44:PHE:HD1	1.93	0.51
1:1:223:A:OP2	33:LY:4:ARG:NH1	2.39	0.51
1:1:2369:C:H2'	1:1:2370:C:C6	2.46	0.51
2:2:414:A:H4'	2:2:415:G:O5'	2.10	0.51
4:4:154:C:H2'	4:4:155:A:C8	2.46	0.51
12:LD:99:TYR:HE2	12:LD:167:LYS:HG3	1.76	0.51
17:LI:193:ASP:OD2	17:LI:194:GLY:N	2.43	0.51
56:SC:59:LYS:HE2	56:SC:59:LYS:HA	1.92	0.51
62:SI:137:LYS:NZ	62:SI:139:SER:O	2.44	0.51
65:SL:39:TRP:O	65:SL:66:THR:HG22	2.11	0.51
65:SL:49:THR:HA	65:SL:65:PHE:CE2	2.45	0.51
85:Sf:118:ARG:NE	85:Sf:132:MET:O	2.42	0.51
1:1:309:U:O2'	43:Li:39:LYS:NZ	2.41	0.51
1:1:656:U:H2'	1:1:657:U:C6	2.46	0.51
1:1:660:G:OP2	25:LQ:83:SER:OG	2.28	0.51
2:2:920:G:H2'	2:2:921:A:C8	2.46	0.51
12:LD:32:ALA:O	12:LD:36:LEU:HD13	2.11	0.51
14:LF:94:ARG:NH2	14:LF:97:GLY:O	2.41	0.51
25:LQ:110:VAL:HG22	25:LQ:167:LEU:HB2	1.93	0.51
63:SJ:104:GLU:O	63:SJ:109:THR:OG1	2.27	0.51
69:SP:62:LEU:HA	69:SP:65:ILE:HG22	1.92	0.51
76:SW:30:SER:HB3	76:SW:61:ILE:HG12	1.93	0.51
1:1:1027:U:OP1	17:LI:90:ARG:NH2	2.37	0.51
1:1:1213:G:H3'	1:1:1214:A:H8	1.76	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:539:A:O2'	2:2:540:C:H3'	2.11	0.51
2:2:920:G:H2'	2:2:921:A:H8	1.76	0.51
2:2:974:G:N1	2:2:1021:A:O2'	2.36	0.51
5:A:235:GLU:O	5:A:253:ALA:N	2.44	0.51
46:Ll:27:ILE:O	46:Ll:33:ASN:ND2	2.43	0.51
57:SD:150:ALA:O	57:SD:151:LYS:HD3	2.10	0.51
66:SM:31:LYS:HG3	66:SM:35:LYS:HZ3	1.76	0.51
69:SP:89:ARG:HA	69:SP:124:LEU:HD22	1.93	0.51
70:SQ:29:ILE:HG22	70:SQ:36:LEU:HD21	1.91	0.51
2:2:683:G:H2'	2:2:684:G:H8	1.75	0.51
2:2:1067:U:H4'	81:Sb:17:ARG:NE	2.25	0.51
2:2:1219:C:H2'	2:2:1220:G:C8	2.45	0.51
2:2:1790:A:N3	80:Sa:79:ILE:HD11	2.26	0.51
7:C:126:ARG:O	7:C:130:LEU:HG	2.10	0.51
8:D:555:THR:C	8:D:557:LEU:H	2.18	0.51
11:LC:267:ALA:HA	11:LC:270:GLU:HG2	1.93	0.51
20:LL:107:GLU:OE1	20:LL:107:GLU:N	2.43	0.51
26:LR:180:LYS:HD2	26:LR:181:ARG:HE	1.74	0.51
27:LS:16:THR:HG23	27:LS:19:ASN:H	1.75	0.51
71:SR:11:LYS:O	71:SR:14:LYS:HG3	2.11	0.51
77:SX:57:VAL:HG23	77:SX:71:CYS:SG	2.51	0.51
1:1:1615:G:N2	1:1:1618:A:OP2	2.42	0.51
2:2:1469:U:C6	59:SF:177:ILE:HD13	2.46	0.51
7:C:85:GLU:HG3	7:C:86:GLU:H	1.74	0.51
8:D:158:PRO:HD2	8:D:161:PHE:CE2	2.45	0.51
17:LI:152:LEU:HA	17:LI:155:CYS:SG	2.51	0.51
20:LL:76:THR:HG22	20:LL:101:ARG:HB3	1.93	0.51
20:LL:124:ILE:HD11	20:LL:138:THR:HG21	1.93	0.51
20:LL:142:GLN:OE1	20:LL:142:GLN:N	2.44	0.51
59:SF:192:SER:OG	59:SF:194:ASN:OD1	2.18	0.51
1:1:769:G:H2'	1:1:770:C:C6	2.46	0.51
1:1:2064:C:H2'	1:1:2065:U:H6	1.74	0.51
2:2:835:G:H2'	2:2:836:G:C8	2.46	0.51
2:2:1098:G:H5''	76:SW:76:SER:HB3	1.92	0.51
4:4:9:A:H2'	4:4:10:A:C8	2.45	0.51
5:A:5:LEU:HD12	5:A:310:TRP:HB3	1.92	0.51
5:A:64:HIS:ND1	5:A:65:ILE:HG22	2.26	0.51
5:A:291:TRP:CE2	5:A:298:LEU:HD21	2.46	0.51
39:Le:82:ASP:OD1	51:Lq:30:ARG:NH2	2.44	0.51
59:SF:201:LYS:O	59:SF:205:GLU:HG2	2.11	0.51
64:SK:67:THR:HG22	64:SK:69:ALA:H	1.76	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
78:SY:45:GLU:O	78:SY:49:THR:HG23	2.10	0.51
81:Sb:46:VAL:HG23	81:Sb:54:VAL:HG21	1.92	0.51
83:Sd:21:CYS:HB3	83:Sd:25:THR:N	2.26	0.51
85:Sf:120:GLU:HA	85:Sf:132:MET:HE1	1.92	0.51
1:1:1076:A:OP1	28:LT:120:LYS:NZ	2.35	0.50
2:2:1479:A:H2	2:2:1603:G:H1'	1.76	0.50
2:2:1531:U:H4'	2:2:1532:G:O5'	2.11	0.50
5:A:29:ASN:HA	5:A:45:LEU:HB2	1.93	0.50
7:C:270:LYS:O	7:C:273:GLU:HG3	2.11	0.50
57:SD:78:LYS:NZ	64:SK:20:VAL:O	2.33	0.50
78:SY:89:GLU:OE2	78:SY:93:ARG:NH1	2.35	0.50
1:1:250:C:O2'	1:1:251:U:OP1	2.28	0.50
1:1:2468:U:H2'	1:1:2469:U:C6	2.46	0.50
1:1:2704:G:N2	1:1:2707:A:OP2	2.38	0.50
2:2:219:C:H2'	2:2:220:A:C8	2.45	0.50
2:2:510:U:H5'	63:SJ:129:GLN:NE2	2.24	0.50
2:2:1474:G:OP1	73:ST:44:LYS:HE2	2.12	0.50
5:A:64:HIS:CE1	5:A:65:ILE:HG22	2.46	0.50
7:C:300:ASN:HA	7:C:303:LYS:NZ	2.25	0.50
7:C:307:ARG:O	7:C:310:ARG:HG2	2.11	0.50
9:LA:44:ILE:HG12	9:LA:87:PHE:HE2	1.76	0.50
25:LQ:116:ASP:OD1	25:LQ:117:ASP:N	2.45	0.50
42:Lh:23:ILE:O	42:Lh:27:LEU:HD23	2.11	0.50
42:Lh:34:LEU:HD22	42:Lh:49:ILE:HD11	1.92	0.50
51:Lq:35:LEU:O	51:Lq:36:THR:OG1	2.22	0.50
54:SA:192:TYR:HA	75:SV:44:ARG:HH21	1.76	0.50
56:SC:194:ARG:HH21	56:SC:198:LEU:HD21	1.77	0.50
59:SF:98:VAL:HG13	70:SQ:43:ILE:HG12	1.93	0.50
70:SQ:135:ARG:HG2	70:SQ:136:ALA:H	1.76	0.50
1:1:993:G:H2'	1:1:994:G:H8	1.76	0.50
1:1:1239:G:H4'	19:LK:123:LYS:HA	1.93	0.50
8:D:278:ARG:HH11	8:D:278:ARG:HG3	1.75	0.50
17:LI:190:VAL:HG22	17:LI:199:PHE:HD1	1.76	0.50
33:LY:53:ASP:HB3	33:LY:109:HIS:H	1.76	0.50
39:Le:92:THR:HG1	39:Le:93:TYR:HD2	1.57	0.50
40:Lf:34:ILE:HB	40:Lf:37:VAL:CG2	2.42	0.50
52:Ls:61:ARG:O	52:Ls:65:THR:HG23	2.11	0.50
77:SX:23:ARG:HG2	77:SX:23:ARG:HH11	1.76	0.50
1:1:859:C:O2'	1:1:862:G:O2'	2.26	0.50
1:1:1059:C:H2'	1:1:1060:U:C6	2.46	0.50
1:1:2400:G:H1	1:1:2473:U:H3	1.60	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2503:C:H4'	1:1:2504:G:H8	1.76	0.50
26:LR:154:GLN:HA	26:LR:157:GLU:HG3	1.94	0.50
55:SB:9:LEU:HD23	55:SB:9:LEU:H	1.76	0.50
60:SG:78:SER:OG	60:SG:79:GLU:N	2.45	0.50
66:SM:107:ASP:OD1	66:SM:108:ARG:N	2.44	0.50
79:SZ:71:ASP:OD1	79:SZ:72:LEU:N	2.45	0.50
82:Sc:19:ARG:HD3	82:Sc:24:GLY:O	2.11	0.50
2:2:150:G:H2'	2:2:151:G:C8	2.46	0.50
2:2:1219:C:H2'	2:2:1220:G:H8	1.76	0.50
2:2:1252:G:O2'	2:2:1253:A:O5'	2.27	0.50
7:C:94:ASP:OD2	7:C:148:PHE:HB2	2.12	0.50
20:LL:32:LYS:O	20:LL:36:ARG:HG3	2.11	0.50
24:LP:59:PRO:HD3	24:LP:76:TRP:NE1	2.27	0.50
52:Ls:48:GLN:NE2	52:Ls:89:THR:OG1	2.37	0.50
57:SD:79:ARG:HD2	64:SK:22:VAL:HG11	1.93	0.50
1:1:2679:G:OP1	25:LQ:207:ARG:NH2	2.44	0.50
2:2:1229:U:H2'	2:2:1230:G:C8	2.47	0.50
12:LD:199:LYS:O	12:LD:202:ILE:HG22	2.11	0.50
20:LL:47:ALA:HB3	20:LL:48:PRO:HD3	1.94	0.50
24:LP:154:GLU:HG2	24:LP:155:GLU:H	1.76	0.50
29:LU:43:LEU:O	29:LU:47:ILE:HD12	2.11	0.50
30:LV:16:THR:HG21	30:LV:85:LYS:NZ	2.27	0.50
37:Lc:101:SER:OG	37:Lc:102:ASP:N	2.42	0.50
47:Lm:79:GLU:OE2	47:Lm:82:LEU:HG	2.12	0.50
59:SF:105:PHE:HD2	59:SF:116:PRO:HB2	1.76	0.50
61:SH:134:ALA:HA	61:SH:137:THR:HG22	1.94	0.50
2:2:937:A:H2'	2:2:938:A:C8	2.47	0.50
2:2:1379:A:OP1	74:SU:56:PRO:HA	2.11	0.50
7:C:293:LYS:HA	7:C:296:ARG:CD	2.37	0.50
11:LC:364:GLU:OE1	27:LS:26:ARG:NH1	2.45	0.50
14:LF:62:ARG:HG2	14:LF:62:ARG:HH11	1.76	0.50
23:LO:76:ARG:NH1	23:LO:147:VAL:O	2.45	0.50
29:LU:25:ALA:HB1	29:LU:28:PRO:HG2	1.94	0.50
30:LV:16:THR:HG21	30:LV:85:LYS:HZ2	1.76	0.50
32:LX:103:ALA:HA	32:LX:107:GLN:NE2	2.27	0.50
35:La:82:VAL:HG13	35:La:87:ARG:HB2	1.93	0.50
58:SE:195:ILE:HD13	58:SE:210:LEU:HG	1.93	0.50
58:SE:250:GLU:O	58:SE:253:GLN:NE2	2.27	0.50
60:SG:73:VAL:HG23	60:SG:75:LEU:HD11	1.94	0.50
61:SH:40:LEU:O	61:SH:44:LEU:HG	2.12	0.50
80:Sa:12:LYS:HB2	80:Sa:33:ASP:OD2	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:171:G:H2'	1:1:172:G:H8	1.76	0.50
1:1:696:G:N2	1:1:699:A:OP2	2.44	0.50
1:1:1632:G:H2'	1:1:1633:G:H8	1.77	0.50
2:2:404:A:H2'	2:2:405:C:C6	2.47	0.50
2:2:1218:A:OP1	64:SK:50:ARG:NH1	2.40	0.50
8:D:53:TYR:CE2	8:D:114:ASP:HB3	2.47	0.50
16:LH:131:ALA:O	16:LH:134:VAL:HG22	2.12	0.50
17:LI:23:ASN:C	17:LI:24:ARG:HD3	2.36	0.50
18:LJ:118:ASP:OD1	18:LJ:119:PRO:HD2	2.11	0.50
29:LU:39:PHE:O	29:LU:43:LEU:HD13	2.12	0.50
56:SC:213:LYS:HE2	56:SC:213:LYS:HA	1.93	0.50
57:SD:54:ARG:NH1	57:SD:92:ALA:HB3	2.21	0.50
59:SF:206:ARG:HG2	59:SF:206:ARG:HH11	1.76	0.50
70:SQ:122:ARG:C	70:SQ:123:ARG:HD3	2.37	0.50
71:SR:30:THR:O	71:SR:34:VAL:HG23	2.11	0.50
72:SS:92:ILE:HG13	72:SS:93:VAL:H	1.77	0.50
79:SZ:66:ARG:HG2	79:SZ:88:LYS:NZ	2.26	0.50
1:1:20:U:H2'	1:1:21:A:C8	2.47	0.50
1:1:1213:G:H3'	1:1:1214:A:C8	2.47	0.50
1:1:1702:U:OP2	26:LR:103:ARG:NH1	2.45	0.50
2:2:1272:A:H62	2:2:1427:C:H42	1.60	0.50
2:2:1669:G:H2'	2:2:1670:C:C6	2.47	0.50
7:C:133:HIS:HE2	8:D:93:THR:HA	1.77	0.50
8:D:443:ILE:HG23	8:D:456:VAL:HG13	1.94	0.50
12:LD:34:LYS:HE2	28:LT:30:TYR:CZ	2.47	0.50
12:LD:286:GLU:O	12:LD:290:ARG:HG3	2.12	0.50
13:LE:76:LEU:HB2	13:LE:80:VAL:HG23	1.94	0.50
17:LI:190:VAL:HG22	17:LI:199:PHE:CD1	2.46	0.50
18:LJ:133:THR:CG2	18:LJ:137:GLU:HG2	2.42	0.50
31:LW:82:ILE:H	31:LW:82:ILE:HD12	1.77	0.50
55:SB:129:THR:HB	55:SB:179:CYS:O	2.12	0.50
59:SF:129:PRO:O	59:SF:154:ARG:HG3	2.11	0.50
62:SI:163:GLN:NE2	62:SI:170:TYR:HD2	2.10	0.50
66:SM:135:VAL:HA	66:SM:138:ASN:ND2	2.26	0.50
74:SU:27:LYS:NZ	74:SU:30:SER:H	2.10	0.50
1:1:1480:C:O2'	1:1:1582:A:N3	2.42	0.49
1:1:1876:A:N6	1:1:2302:C:H42	2.08	0.49
1:1:2460:C:H2'	1:1:2461:C:C6	2.47	0.49
3:3:107:C:OP2	17:LI:203:HIS:NE2	2.44	0.49
7:C:206:LYS:HD3	7:C:236:TRP:CZ2	2.47	0.49
7:C:320:GLU:HA	7:C:323:LEU:HD12	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:D:225:ARG:HH22	8:D:230:THR:HG21	1.77	0.49
15:LG:145:LEU:HD13	15:LG:204:THR:HG21	1.93	0.49
16:LH:5:HIS:NE2	16:LH:56:GLU:OE2	2.45	0.49
26:LR:140:GLU:HG2	26:LR:144:ARG:NH1	2.25	0.49
29:LU:37:SER:HB2	29:LU:41:LYS:HZ3	1.76	0.49
33:LY:26:ARG:HG2	33:LY:77:TYR:HE1	1.77	0.49
43:Li:14:THR:HG23	43:Li:21:ASN:HB3	1.94	0.49
49:Lo:15:LYS:O	49:Lo:15:LYS:HD3	2.12	0.49
56:SC:84:LEU:HB3	56:SC:112:ILE:HD11	1.94	0.49
56:SC:187:VAL:O	56:SC:206:THR:OG1	2.26	0.49
60:SG:148:SER:N	60:SG:151:ASP:OD2	2.33	0.49
2:2:1457:C:H2'	2:2:1458:G:C8	2.47	0.49
5:A:201:SER:OG	5:A:203:ASP:OD1	2.26	0.49
7:C:42:VAL:HB	8:D:229:TYR:OH	2.12	0.49
8:D:117:GLU:HB2	8:D:120:ALA:HB2	1.92	0.49
20:LL:178:GLU:HG2	20:LL:179:GLY:N	2.27	0.49
32:LX:63:SER:HB2	42:Lh:71:LEU:HD23	1.92	0.49
33:LY:1:MET:HE3	33:LY:2:LYS:N	2.24	0.49
46:Li:24:PRO:HG2	46:Li:27:ILE:HG12	1.94	0.49
48:Lr:2:ARG:HD3	48:Lr:5:TRP:NE1	2.27	0.49
66:SM:71:GLU:OE1	66:SM:75:LYS:NZ	2.42	0.49
68:SO:29:VAL:HG12	68:SO:46:LEU:H	1.76	0.49
68:SO:85:LYS:HA	68:SO:85:LYS:HE2	1.94	0.49
73:ST:20:ALA:O	73:ST:24:LYS:HG2	2.11	0.49
1:1:1290:G:C2	23:LO:61:LYS:HE2	2.47	0.49
2:2:281:G:O6	60:SG:191:ARG:NH2	2.46	0.49
2:2:892:U:H2'	2:2:893:G:H8	1.77	0.49
2:2:1317:U:H3'	54:SA:104:ARG:HH22	1.78	0.49
2:2:1606:G:O3'	59:SF:94:LYS:NZ	2.45	0.49
2:2:1695:G:N7	7:C:362:ARG:HG2	2.27	0.49
5:A:156:PHE:CD1	5:A:165:ILE:HD11	2.46	0.49
7:C:355:ASN:OD1	7:C:356:ALA:N	2.45	0.49
16:LH:88:TYR:CZ	16:LH:186:LYS:HG2	2.47	0.49
17:Li:177:ARG:N	17:Li:180:GLU:OE2	2.44	0.49
26:LR:90:PRO:HG2	26:LR:93:VAL:HG12	1.94	0.49
26:LR:180:LYS:CD	26:LR:181:ARG:HH21	2.25	0.49
29:LU:101:ARG:HD2	29:LU:115:TYR:HE1	1.76	0.49
65:SL:78:GLY:O	65:SL:127:MET:HA	2.11	0.49
66:SM:96:GLN:NE2	66:SM:96:GLN:O	2.43	0.49
1:1:425:G:H2'	1:1:426:A:H8	1.77	0.49
1:1:440:C:H2'	1:1:441:G:C8	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1306:C:H4'	27:LS:2:GLY:HA2	1.94	0.49
1:1:2370:C:H2'	1:1:2371:U:H6	1.78	0.49
2:2:22:A:H4'	63:SJ:14:ARG:HA	1.95	0.49
2:2:1589:A:H2'	2:2:1590:G:H8	1.77	0.49
7:C:161:ASP:H	7:C:164:LYS:HZ2	1.59	0.49
8:D:84:GLY:HA3	8:D:165:GLN:HA	1.94	0.49
17:LI:101:LYS:NZ	17:LI:103:LEU:H	2.10	0.49
36:Lb:5:LYS:NZ	36:Lb:8:SER:HB2	2.27	0.49
56:SC:87:GLU:OE1	56:SC:194:ARG:NH2	2.45	0.49
57:SD:50:ASP:O	57:SD:51:ILE:HD13	2.13	0.49
63:SJ:45:LEU:O	63:SJ:49:LYS:HG2	2.12	0.49
65:SL:49:THR:HA	65:SL:65:PHE:HE2	1.77	0.49
76:SW:25:VAL:O	76:SW:62:VAL:HA	2.13	0.49
77:SX:79:ASN:OD1	77:SX:81:LYS:HG2	2.12	0.49
79:SZ:40:TYR:C	79:SZ:44:GLN:HE22	2.17	0.49
1:1:652:A:H2'	1:1:653:A:H8	1.76	0.49
2:2:1355:G:H4'	73:ST:130:GLN:HE22	1.78	0.49
10:LB:110:LEU:HD12	10:LB:114:VAL:HG21	1.94	0.49
22:LN:66:VAL:O	22:LN:127:TYR:HA	2.12	0.49
25:LQ:106:LYS:HG2	25:LQ:163:ASN:OD1	2.13	0.49
59:SF:39:GLU:OE2	59:SF:118:GLN:HA	2.12	0.49
78:SY:55:LYS:O	78:SY:58:VAL:HG22	2.13	0.49
78:SY:130:ALA:O	78:SY:133:LYS:NZ	2.45	0.49
81:Sb:20:LYS:HG3	81:Sb:21:LEU:HD23	1.93	0.49
1:1:307:U:H2'	1:1:308:C:C6	2.46	0.49
1:1:768:A:N6	25:LQ:115:THR:HG21	2.26	0.49
1:1:2823:A:H5''	17:LI:114:GLY:HA2	1.94	0.49
1:1:3176:G:H2'	1:1:3177:C:C6	2.48	0.49
2:2:195:G:H2'	2:2:196:G:H8	1.77	0.49
2:2:391:C:H42	2:2:398:A:H62	1.61	0.49
2:2:519:U:H5''	78:SY:40:LYS:HE3	1.95	0.49
2:2:866:G:OP1	67:SN:121:ARG:NH1	2.44	0.49
2:2:1693:C:H2'	2:2:1694:G:C8	2.47	0.49
5:A:59:LEU:HD13	5:A:90:TRP:CD2	2.47	0.49
7:C:311:GLU:HA	7:C:314:GLU:CD	2.37	0.49
56:SC:222:THR:O	56:SC:226:VAL:HG23	2.11	0.49
58:SE:129:VAL:HG12	58:SE:139:LEU:CB	2.42	0.49
59:SF:85:MET:HG3	59:SF:85:MET:O	2.12	0.49
70:SQ:135:ARG:HG2	70:SQ:136:ALA:N	2.28	0.49
72:SS:112:ASP:HA	72:SS:115:ARG:HD3	1.94	0.49
1:1:768:A:H62	25:LQ:115:THR:HG21	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:402:C:O2'	60:SG:92:ARG:O	2.25	0.49
2:2:1693:C:H2'	2:2:1694:G:H8	1.77	0.49
8:D:81:ASP:OD1	8:D:82:ILE:HG13	2.12	0.49
9:LA:181:LYS:HB2	9:LA:184:ARG:HG3	1.95	0.49
10:LB:297:THR:HG23	10:LB:300:ASP:H	1.77	0.49
11:LC:289:ARG:HG2	11:LC:289:ARG:HH11	1.77	0.49
16:LH:19:SER:OG	16:LH:26:THR:OG1	2.18	0.49
30:LV:19:LEU:HD21	30:LV:80:ILE:HD13	1.95	0.49
44:Lj:39:TYR:HD2	44:Lj:40:PRO:HD3	1.77	0.49
56:SC:120:GLY:HA2	56:SC:223:PHE:CE2	2.46	0.49
56:SC:120:GLY:HA2	56:SC:223:PHE:HE2	1.78	0.49
73:ST:108:LEU:O	73:ST:111:ILE:HG22	2.12	0.49
73:ST:117:ASP:OD2	73:ST:120:ARG:HG2	2.13	0.49
78:SY:15:PHE:CZ	78:SY:24:LYS:HD2	2.47	0.49
1:1:1159:C:H4'	23:LO:91:PRO:HD3	1.95	0.49
2:2:204:U:H2'	2:2:205:A:C8	2.47	0.49
2:2:948:C:H2'	2:2:949:A:C8	2.47	0.49
2:2:1222:U:H3'	2:2:1223:G:C8	2.48	0.49
4:4:83:C:H41	33:LY:50:ARG:NH2	2.10	0.49
7:C:85:GLU:HG3	7:C:86:GLU:N	2.28	0.49
7:C:427:VAL:HG21	7:C:441:ILE:HG21	1.93	0.49
13:LE:119:ILE:HA	13:LE:122:VAL:CG1	2.40	0.49
18:LJ:165:LYS:NZ	18:LJ:171:ILE:HA	2.28	0.49
34:LZ:71:ILE:HD11	34:LZ:95:ILE:HG21	1.93	0.49
46:Ll:15:LYS:O	46:Ll:19:GLN:HG2	2.13	0.49
48:Ln:2:ARG:HD3	48:Ln:5:TRP:NE1	2.27	0.49
57:SD:214:ILE:O	71:SR:20:TYR:OH	2.27	0.49
59:SF:86:MET:HE1	59:SF:164:THR:HA	1.95	0.49
69:SP:69:ARG:HE	69:SP:72:LYS:NZ	2.11	0.49
10:LB:85:VAL:HB	10:LB:164:HIS:NE2	2.28	0.49
10:LB:293:ALA:HB2	10:LB:303:LYS:HG3	1.94	0.49
23:LO:161:ARG:HG2	23:LO:161:ARG:HH11	1.76	0.49
52:Ls:5:SER:HB3	52:Ls:8:LYS:HB3	1.95	0.49
58:SE:63:ALA:C	58:SE:67:GLN:HE22	2.21	0.49
58:SE:183:ILE:HD11	58:SE:218:PHE:CE1	2.48	0.49
61:SH:104:ILE:HG22	61:SH:131:VAL:HG11	1.95	0.49
62:SI:125:ARG:O	62:SI:125:ARG:HD2	2.13	0.49
66:SM:79:ALA:HB1	85:Sf:114:ILE:HD11	1.94	0.49
73:ST:5:VAL:HG21	73:ST:141:ALA:HB2	1.95	0.49
73:ST:45:GLU:HG2	73:ST:46:LEU:HG	1.95	0.49
1:1:3068:C:H2'	1:1:3069:U:C6	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:3329:C:OP2	38:Ld:8:GLN:NE2	2.42	0.49
2:2:456:G:OP1	78:SY:112:LYS:NZ	2.37	0.49
2:2:1386:C:H5'	71:SR:49:LYS:HZ2	1.77	0.49
5:A:35:SER:OG	5:A:36:ARG:N	2.44	0.49
7:C:37:ARG:NH1	8:D:422:HIS:HB2	2.27	0.49
40:Lf:34:ILE:HB	40:Lf:37:VAL:HG21	1.95	0.49
42:Lh:19:GLU:OE1	42:Lh:19:GLU:N	2.33	0.49
50:Lp:85:ARG:O	50:Lp:89:ILE:HG12	2.11	0.49
54:SA:82:ARG:HA	54:SA:82:ARG:HH11	1.78	0.49
56:SC:117:GLY:HA2	56:SC:147:VAL:HG22	1.95	0.49
60:SG:49:ILE:HG12	60:SG:115:LYS:HB3	1.94	0.49
60:SG:71:ASN:OD1	60:SG:72:ARG:N	2.40	0.49
69:SP:95:PRO:HD3	69:SP:120:VAL:HG23	1.94	0.49
1:1:147:A:P	22:LN:147:ARG:HH22	2.36	0.48
1:1:1211:A:H2'	1:1:1212:G:C8	2.48	0.48
1:1:1779:A:H2'	1:1:1780:A:C8	2.48	0.48
2:2:825:C:H2'	2:2:826:U:C6	2.48	0.48
2:2:1199:A:H1'	2:2:1204:C:H42	1.77	0.48
2:2:1354:U:H4'	73:ST:127:GLN:OE1	2.13	0.48
2:2:1790:A:OP2	80:Sa:4:LYS:NZ	2.44	0.48
10:LB:47:MET:HE2	10:LB:336:ILE:HD11	1.94	0.48
13:LE:84:THR:HB	13:LE:94:LEU:HA	1.94	0.48
22:LN:165:THR:HG22	22:LN:166:SER:N	2.28	0.48
44:Lj:39:TYR:CD2	44:Lj:40:PRO:HD3	2.48	0.48
51:Lq:139:ARG:HB3	51:Lq:140:ARG:NH2	2.27	0.48
54:SA:123:LEU:O	54:SA:124:ILE:HD13	2.13	0.48
56:SC:174:THR:OG1	56:SC:209:SER:HB2	2.13	0.48
66:SM:34:LEU:HB2	66:SM:43:LEU:HD12	1.95	0.48
73:ST:107:ALA:HA	73:ST:110:LYS:NZ	2.27	0.48
74:SU:65:ARG:HG2	74:SU:76:TRP:CZ3	2.48	0.48
1:1:481:C:H2'	1:1:482:U:C6	2.48	0.48
1:1:615:C:H2'	1:1:616:A:C8	2.48	0.48
1:1:725:C:O2	25:LQ:168:ARG:NH1	2.46	0.48
1:1:2167:C:H2'	1:1:2168:U:C6	2.48	0.48
1:1:2566:G:OP1	9:LA:233:GLN:NE2	2.33	0.48
2:2:945:C:H2'	2:2:946:G:H8	1.78	0.48
2:2:1278:G:P	74:SU:66:LYS:HZ1	2.34	0.48
5:A:108:VAL:HG12	5:A:124:SER:HB2	1.94	0.48
7:C:316:LYS:O	7:C:319:GLU:HG2	2.14	0.48
8:D:50:ILE:HG13	8:D:77:ALA:HB2	1.95	0.48
8:D:247:LYS:HA	8:D:250:ILE:HG22	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:LG:27:ASN:OD1	15:LG:29:LEU:HD23	2.13	0.48
31:LW:68:ALA:O	31:LW:72:THR:HG23	2.13	0.48
57:SD:140:VAL:HG22	57:SD:154:LYS:HG2	1.95	0.48
62:SI:126:GLN:O	62:SI:129:GLN:NE2	2.44	0.48
69:SP:85:LYS:HB3	69:SP:110:PHE:CZ	2.48	0.48
80:Sa:68:TYR:O	80:Sa:69:LEU:HD22	2.13	0.48
1:1:2227:U:O2'	1:1:2228:C:OP1	2.28	0.48
1:1:2406:A:H2'	1:1:2407:C:C6	2.47	0.48
1:1:2615:A:C8	1:1:2617:G:C8	3.01	0.48
1:1:3079:U:H1'	1:1:3080:A:H5''	1.94	0.48
2:2:66:U:OP2	60:SG:177:ARG:HB2	2.13	0.48
2:2:1369:C:H4'	2:2:1370:C:H5''	1.95	0.48
7:C:49:HIS:CE1	8:D:450:VAL:HG11	2.49	0.48
7:C:133:HIS:CE1	8:D:92:PRO:HG2	2.48	0.48
7:C:231:TYR:OH	7:C:286:GLN:OE1	2.27	0.48
7:C:260:GLU:HA	7:C:263:ASN:ND2	2.28	0.48
7:C:441:ILE:HD11	7:C:444:LEU:HG	1.95	0.48
17:LI:193:ASP:CG	17:LI:194:GLY:H	2.20	0.48
22:LN:183:THR:HG22	22:LN:187:ARG:HB2	1.95	0.48
73:ST:50:ASP:O	73:ST:53:TRP:HE3	1.96	0.48
77:SX:73:ARG:HH11	77:SX:73:ARG:HG3	1.76	0.48
1:1:1338:A:H4'	1:1:1339:U:O5'	2.14	0.48
1:1:1447:G:N2	1:1:1450:A:OP2	2.46	0.48
1:1:3179:G:H2'	1:1:3180:G:H8	1.77	0.48
1:1:3231:G:H2'	1:1:3232:A:C8	2.48	0.48
1:1:3281:G:O2'	1:1:3282:U:OP1	2.31	0.48
2:2:469:U:H2'	2:2:470:A:C8	2.46	0.48
2:2:1094:U:H4'	2:2:1095:U:O5'	2.13	0.48
2:2:1244:U:H5'	85:Sf:90:LYS:HD2	1.96	0.48
5:A:33:SER:OG	5:A:43:TRP:NE1	2.38	0.48
7:C:231:TYR:HE1	7:C:283:GLU:OE1	1.97	0.48
18:LJ:54:THR:HG23	18:LJ:61:ARG:HA	1.94	0.48
30:LV:103:VAL:HG21	30:LV:111:MET:HE2	1.96	0.48
37:Lc:55:ARG:O	37:Lc:59:LEU:HD23	2.13	0.48
55:SB:67:GLU:OE1	55:SB:83:LYS:NZ	2.47	0.48
55:SB:217:LEU:HD23	55:SB:217:LEU:H	1.78	0.48
59:SF:205:GLU:O	59:SF:209:LYS:HG2	2.14	0.48
63:SJ:75:ILE:HD11	63:SJ:89:MET:HA	1.95	0.48
1:1:580:A:N6	1:1:598:G:H1'	2.28	0.48
1:1:1260:C:H2'	1:1:1261:A:C8	2.47	0.48
1:1:3298:U:H2'	1:1:3299:U:C6	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:1397:A:H4'	71:SR:5:ARG:HH12	1.78	0.48
8:D:272:ARG:NH1	8:D:301:LEU:O	2.42	0.48
8:D:332:GLU:O	8:D:336:LYS:HG2	2.14	0.48
31:LW:48:ARG:HG3	31:LW:48:ARG:HH11	1.79	0.48
40:Lf:47:LEU:HD11	40:Lf:75:ARG:HA	1.95	0.48
56:SC:81:LEU:HB3	56:SC:84:LEU:CD2	2.42	0.48
61:SH:173:ASP:OD1	61:SH:174:TYR:N	2.46	0.48
73:ST:107:ALA:HA	73:ST:110:LYS:HZ3	1.79	0.48
79:SZ:81:VAL:HG23	79:SZ:82:VAL:H	1.79	0.48
1:1:467:U:H2'	1:1:468:G:C8	2.49	0.48
1:1:2405:G:H2'	1:1:2406:A:C8	2.48	0.48
1:1:2945:U:H2'	1:1:2946:A:H8	1.78	0.48
2:2:1556:U:O4	69:SP:48:ARG:NH2	2.41	0.48
2:2:1710:G:OP2	31:LW:70:LYS:NZ	2.47	0.48
9:LA:79:ASN:OD1	9:LA:165:MET:HE3	2.14	0.48
11:LC:311:ARG:HH21	11:LC:314:VAL:HB	1.79	0.48
13:LE:58:LEU:HD13	13:LE:102:VAL:HG13	1.94	0.48
18:LJ:21:ASN:OD1	18:LJ:127:ASP:HB3	2.13	0.48
54:SA:107:PRO:HB3	54:SA:134:GLN:HE21	1.78	0.48
67:SN:30:PRO:HA	67:SN:33:VAL:HG12	1.96	0.48
69:SP:89:ARG:HE	69:SP:125:GLY:CA	2.27	0.48
85:Sf:134:SER:HA	85:Sf:139:GLN:HG3	1.95	0.48
1:1:1260:C:H2'	1:1:1261:A:H8	1.79	0.48
1:1:2633:A:N6	18:LJ:125:GLY:O	2.46	0.48
52:Ls:133:THR:O	52:Ls:137:GLN:HG2	2.13	0.48
60:SG:32:MET:HG3	60:SG:100:CYS:HB2	1.95	0.48
66:SM:135:VAL:HA	66:SM:138:ASN:HD21	1.79	0.48
70:SQ:73:GLY:N	70:SQ:76:SER:OG	2.32	0.48
71:SR:98:GLU:HG2	71:SR:99:THR:N	2.28	0.48
73:ST:119:GLU:OE2	73:ST:120:ARG:NE	2.46	0.48
2:2:12:U:H2'	2:2:13:U:C6	2.48	0.48
2:2:499:U:H2'	2:2:500:G:H8	1.77	0.48
5:A:20:SER:OG	5:A:67:SER:O	2.28	0.48
7:C:40:GLU:HB2	8:D:229:TYR:CE2	2.49	0.48
54:SA:63:ALA:O	54:SA:67:ILE:HG12	2.14	0.48
57:SD:108:LEU:HD13	57:SD:125:VAL:HG21	1.95	0.48
58:SE:85:GLY:N	58:SE:88:ASP:OD2	2.26	0.48
60:SG:214:ILE:HD12	60:SG:217:LYS:HD3	1.96	0.48
74:SU:40:GLU:HA	74:SU:43:LYS:CG	2.42	0.48
1:1:1323:C:H2'	1:1:1324:U:C6	2.49	0.48
1:1:3179:G:H2'	1:1:3180:G:C8	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:1332:U:H2'	2:2:1333:A:H8	1.79	0.48
2:2:1591:U:P	83:Sd:33:LYS:NZ	2.86	0.48
2:2:1609:U:H2'	2:2:1610:A:N3	2.28	0.48
15:LG:210:ASP:OD1	15:LG:210:ASP:N	2.46	0.48
38:Ld:15:VAL:HA	38:Ld:85:ARG:O	2.13	0.48
54:SA:178:TRP:HE1	54:SA:200:VAL:HG23	1.78	0.48
55:SB:31:ASN:OD1	55:SB:32:ILE:N	2.47	0.48
55:SB:222:LYS:HE2	55:SB:222:LYS:HA	1.96	0.48
62:SI:140:LYS:HA	62:SI:143:GLU:OE1	2.13	0.48
71:SR:91:LEU:HD12	71:SR:92:ASP:N	2.28	0.48
83:Sd:10:ARG:NE	83:Sd:11:PRO:HD2	2.28	0.48
1:1:2307:U:H2'	1:1:2308:A:H8	1.78	0.48
1:1:2471:U:H2'	1:1:2472:U:H6	1.79	0.48
2:2:195:G:H2'	2:2:196:G:C8	2.49	0.48
2:2:443:A:P	58:SE:59:ARG:HH21	2.37	0.48
2:2:479:U:H3	2:2:503:A:H2	1.61	0.48
2:2:1683:C:H2'	2:2:1684:C:C6	2.49	0.48
2:2:1685:A:H2'	2:2:1686:G:O4'	2.14	0.48
9:LA:46:LYS:HG3	9:LA:47:GLU:HG3	1.96	0.48
12:LD:268:GLU:OE1	12:LD:268:GLU:N	2.35	0.48
24:LP:126:ARG:HD3	24:LP:140:MET:HE1	1.95	0.48
25:LQ:152:ASP:OD2	25:LQ:153:GLN:HG3	2.13	0.48
35:La:75:ILE:HG12	35:La:118:LEU:HD13	1.95	0.48
37:Lc:51:THR:HG23	37:Lc:56:LYS:HE2	1.96	0.48
52:Ls:133:THR:HG21	52:Ls:145:ILE:HD11	1.96	0.48
56:SC:228:ASN:OD1	75:SV:25:LYS:NZ	2.46	0.48
75:SV:4:ASP:OD1	75:SV:4:ASP:N	2.47	0.48
1:1:802:A:H2'	1:1:803:U:C6	2.48	0.47
1:1:1016:U:O2'	1:1:1017:U:OP1	2.31	0.47
1:1:2115:A:H2'	1:1:2116:U:H6	1.78	0.47
2:2:1224:A:O2'	2:2:1225:G:OP2	2.31	0.47
5:A:54:TYR:CD1	5:A:55:PRO:HD2	2.49	0.47
5:A:68:ASP:OD1	5:A:69:CYS:N	2.47	0.47
8:D:58:GLU:HB3	8:D:137:ARG:HH21	1.79	0.47
8:D:352:GLY:O	8:D:355:SER:HB2	2.14	0.47
26:LR:105:LEU:HD23	26:LR:138:LEU:HD23	1.96	0.47
28:LT:68:THR:HG22	28:LT:69:LYS:N	2.21	0.47
34:LZ:8:ARG:HB3	34:LZ:24:ILE:HD12	1.96	0.47
37:Lc:46:LEU:HD22	37:Lc:71:HIS:HB3	1.96	0.47
52:Ls:63:LEU:HA	52:Ls:66:PHE:CD2	2.48	0.47
56:SC:214:THR:HG22	56:SC:217:ASN:H	1.78	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:SD:179:LEU:HD13	57:SD:184:VAL:HG22	1.95	0.47
58:SE:128:ARG:HG2	58:SE:140:VAL:HG12	1.95	0.47
63:SJ:170:VAL:HG13	63:SJ:171:ARG:HD2	1.96	0.47
65:SL:43:VAL:HG13	65:SL:65:PHE:HE1	1.74	0.47
72:SS:90:ARG:HA	72:SS:95:GLY:HA3	1.95	0.47
1:1:265:G:H1'	43:Li:91:ARG:HH12	1.79	0.47
1:1:910:C:H2'	1:1:911:A:C8	2.50	0.47
1:1:2389:U:H2'	1:1:2390:U:C6	2.48	0.47
2:2:758:U:OP1	63:SJ:5:LYS:NZ	2.29	0.47
2:2:884:U:O2'	68:SO:134:THR:O	2.32	0.47
2:2:956:U:O2'	2:2:958:U:OP2	2.28	0.47
2:2:1216:A:O2'	64:SK:46:SER:HA	2.14	0.47
11:LC:127:LEU:HD11	11:LC:240:LEU:HD12	1.97	0.47
20:LL:7:GLN:O	35:La:49:HIS:NE2	2.47	0.47
26:LR:170:ARG:NH2	26:LR:173:LYS:HD2	2.29	0.47
29:LU:19:LYS:NZ	29:LU:78:LEU:H	2.12	0.47
36:Lb:28:ARG:HG2	36:Lb:29:TYR:CD1	2.48	0.47
55:SB:9:LEU:HD12	55:SB:12:GLY:HA2	1.96	0.47
56:SC:85:LYS:O	56:SC:112:ILE:HD12	2.14	0.47
64:SK:16:PHE:O	64:SK:85:VAL:HG12	2.15	0.47
65:SL:6:THR:HG23	65:SL:9:SER:HB3	1.97	0.47
76:SW:3:ARG:HG2	76:SW:3:ARG:HH11	1.79	0.47
1:1:481:C:H2'	1:1:482:U:H6	1.79	0.47
1:1:2270:G:O2'	1:1:2273:U:OP2	2.32	0.47
2:2:652:G:H1	2:2:673:U:H3	1.60	0.47
2:2:697:G:H2'	2:2:698:G:H8	1.78	0.47
5:A:33:SER:HG	5:A:43:TRP:NE1	2.12	0.47
8:D:222:LEU:HD12	8:D:229:TYR:HB2	1.96	0.47
8:D:410:GLU:OE2	8:D:414:HIS:NE2	2.47	0.47
10:LB:45:ALA:HB3	10:LB:182:ILE:HG12	1.97	0.47
12:LD:238:SER:HA	12:LD:241:GLU:OE2	2.15	0.47
14:LF:242:ASN:O	14:LF:246:ARG:HG2	2.14	0.47
24:LP:6:ALA:O	24:LP:7:THR:OG1	2.29	0.47
55:SB:140:ILE:HG21	55:SB:213:ARG:HD3	1.96	0.47
72:SS:114:GLU:HA	72:SS:117:LYS:HB3	1.96	0.47
72:SS:120:ARG:O	72:SS:120:ARG:HD2	2.15	0.47
57:SD:12:ARG:O	57:SD:15:VAL:HG12	2.14	0.47
57:SD:57:HIS:O	57:SD:61:VAL:HG23	2.14	0.47
65:SL:150:ARG:HH11	65:SL:150:ARG:HA	1.78	0.47
67:SN:35:GLU:HA	67:SN:38:CYS:SG	2.55	0.47
68:SO:27:PHE:HD1	68:SO:91:ALA:HB3	1.78	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:643:C:H2'	1:1:644:A:C8	2.47	0.47
1:1:1921:C:H2'	1:1:1922:U:C6	2.50	0.47
1:1:2642:U:H2'	1:1:2643:C:C6	2.49	0.47
2:2:1193:A:H4'	2:2:1194:C:O5'	2.14	0.47
2:2:1479:A:C2	2:2:1603:G:H1'	2.49	0.47
2:2:1492:U:H4'	2:2:1515:U:O2'	2.14	0.47
5:A:159:ASN:ND2	5:A:203:ASP:O	2.48	0.47
8:D:363:ASN:O	8:D:367:ILE:HG12	2.13	0.47
10:LB:161:VAL:O	10:LB:181:GLU:HA	2.14	0.47
13:LE:199:LYS:HE2	21:LM:111:SER:HA	1.97	0.47
55:SB:119:THR:HB	55:SB:143:THR:HG23	1.95	0.47
1:1:145:U:P	22:LN:49:ARG:HH22	2.37	0.47
1:1:2181:G:H2'	1:1:2182:A:H8	1.80	0.47
1:1:3161:G:H8	40:Lf:3:SER:HB3	1.79	0.47
2:2:786:A:C5	58:SE:19:LEU:HD11	2.50	0.47
2:2:1193:A:O3'	70:SQ:135:ARG:NH2	2.47	0.47
8:D:24:ASN:ND2	8:D:46:GLN:HB3	2.30	0.47
8:D:52:SER:OG	8:D:71:ASN:ND2	2.38	0.47
8:D:320:ALA:O	8:D:323:VAL:HG22	2.14	0.47
8:D:349:ILE:HG22	8:D:375:LEU:HB2	1.97	0.47
13:LE:31:GLU:HA	51:Lq:109:GLN:HE22	1.78	0.47
18:LJ:102:ASN:OD1	18:LJ:131:CYS:HA	2.14	0.47
20:LL:29:PRO:O	20:LL:33:VAL:HG23	2.14	0.47
22:LN:30:TYR:C	22:LN:32:GLN:H	2.23	0.47
22:LN:181:ASN:OD1	22:LN:184:ARG:NH2	2.47	0.47
43:Li:99:LEU:HA	43:Li:102:ILE:HG22	1.97	0.47
50:Lp:79:MET:HA	50:Lp:82:THR:HG22	1.95	0.47
57:SD:126:LEU:O	57:SD:130:MET:HG2	2.14	0.47
58:SE:65:MET:HB3	58:SE:78:THR:HA	1.97	0.47
69:SP:65:ILE:O	69:SP:69:ARG:HG2	2.15	0.47
1:1:154:G:H2'	1:1:155:A:H8	1.79	0.47
1:1:439:C:H2'	1:1:440:C:C6	2.50	0.47
1:1:967:U:H2'	1:1:968:U:C6	2.49	0.47
1:1:2392:G:H2'	1:1:2393:A:H8	1.79	0.47
1:1:3202:U:OP1	21:LM:122:ARG:NH2	2.45	0.47
2:2:834:U:H2'	2:2:835:G:C8	2.47	0.47
2:2:893:G:H21	68:SO:51:THR:HG21	1.78	0.47
2:2:1232:C:H4'	85:Sf:145:HIS:NE2	2.30	0.47
2:2:1470:G:H2'	2:2:1471:A:C8	2.49	0.47
21:LM:18:ARG:NE	21:LM:68:VAL:HG22	2.29	0.47
27:LS:73:LYS:HD3	27:LS:128:GLU:OE2	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:La:85:ASP:OD1	35:La:86:VAL:N	2.46	0.47
41:Lg:46:GLY:N	41:Lg:80:SER:O	2.44	0.47
52:Ls:61:ARG:NH1	52:Ls:62:ALA:HB2	2.29	0.47
55:SB:7:LYS:HE3	55:SB:10:SER:HA	1.96	0.47
58:SE:183:ILE:HD11	58:SE:218:PHE:HE1	1.80	0.47
61:SH:153:LYS:O	76:SW:42:GLN:NE2	2.48	0.47
67:SN:70:LYS:O	67:SN:74:ILE:HG12	2.14	0.47
68:SO:61:VAL:HG22	68:SO:63:ALA:H	1.79	0.47
76:SW:28:ARG:HB3	76:SW:29:PRO:HD3	1.95	0.47
77:SX:69:ARG:HB3	77:SX:86:PHE:HE1	1.79	0.47
77:SX:71:CYS:HB2	77:SX:85:ALA:O	2.14	0.47
78:SY:58:VAL:HG12	78:SY:78:ILE:HD12	1.97	0.47
80:Sa:21:ILE:O	80:Sa:29:CYS:HA	2.15	0.47
1:1:2469:U:H2'	1:1:2470:U:C6	2.50	0.47
2:2:138:A:N6	60:SG:190:LYS:HD2	2.30	0.47
2:2:1624:U:H2'	2:2:1625:G:H8	1.80	0.47
7:C:151:CYS:O	7:C:154:LYS:HG2	2.14	0.47
7:C:191:TYR:HA	7:C:213:PHE:HE2	1.80	0.47
8:D:81:ASP:OD1	8:D:82:ILE:N	2.48	0.47
13:LE:59:ILE:HG13	13:LE:69:ARG:HG2	1.96	0.47
14:LF:229:ILE:HG23	27:LS:36:VAL:HG12	1.96	0.47
16:LH:94:TYR:HA	16:LH:179:ASP:OD1	2.15	0.47
18:LJ:33:ARG:O	18:LJ:37:VAL:HG23	2.14	0.47
58:SE:141:THR:CG2	58:SE:145:ARG:HB2	2.43	0.47
66:SM:70:GLU:HG3	66:SM:73:TYR:H	1.80	0.47
70:SQ:13:LYS:HG3	70:SQ:14:LYS:H	1.80	0.47
71:SR:25:THR:HG23	71:SR:27:ASP:H	1.80	0.47
78:SY:26:MET:HE1	78:SY:51:TYR:CE1	2.49	0.47
1:1:775:A:H2'	1:1:776:G:H8	1.80	0.47
1:1:1476:G:OP2	1:1:1476:G:N2	2.41	0.47
1:1:1762:U:H2'	1:1:1763:C:C6	2.50	0.47
12:LD:65:VAL:HG12	12:LD:74:ILE:HD13	1.96	0.47
24:LP:154:GLU:OE1	24:LP:154:GLU:N	2.48	0.47
26:LR:181:ARG:HH22	26:LR:184:LEU:HD13	1.80	0.47
37:Lc:30:TYR:CE1	37:Lc:55:ARG:HD2	2.49	0.47
41:Lg:75:ARG:NH2	41:Lg:82:CYS:O	2.48	0.47
55:SB:11:LYS:HZ2	55:SB:17:LYS:HE2	1.80	0.47
58:SE:18:TRP:HB3	58:SE:20:LEU:HD23	1.97	0.47
58:SE:100:ARG:HB3	58:SE:102:ILE:HD11	1.97	0.47
62:SI:137:LYS:HZ3	62:SI:143:GLU:CD	2.22	0.47
72:SS:30:TYR:O	72:SS:33:THR:OG1	2.33	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:491:C:H2'	1:1:492:A:H8	1.79	0.47
1:1:509:G:OP2	1:1:509:G:N2	2.31	0.47
1:1:1001:G:H2'	1:1:1002:G:H8	1.78	0.47
1:1:2469:U:H2'	1:1:2470:U:H6	1.80	0.47
2:2:1215:G:H1	2:2:1440:A:H2'	1.79	0.47
5:A:31:LEU:O	5:A:42:ILE:HD12	2.14	0.47
7:C:125:HIS:O	7:C:129:VAL:HG23	2.15	0.47
8:D:214:GLY:O	8:D:241:HIS:HB2	2.15	0.47
17:LI:52:LEU:HB2	17:LI:152:LEU:HD12	1.97	0.47
17:LI:101:LYS:HG2	17:LI:104:SER:HB3	1.97	0.47
51:Lq:31:ASP:OD1	51:Lq:32:ALA:N	2.49	0.47
59:SF:119:VAL:HG23	59:SF:189:ALA:HB2	1.97	0.47
60:SG:135:PRO:HB2	60:SG:141:ILE:HD13	1.96	0.47
60:SG:198:ARG:CZ	60:SG:201:GLN:HE22	2.28	0.47
68:SO:102:ASN:HB3	68:SO:141:ARG:HD3	1.96	0.47
71:SR:34:VAL:O	71:SR:37:GLU:HG3	2.14	0.47
72:SS:126:ARG:NE	72:SS:132:ARG:O	2.48	0.47
1:1:1017:U:H2'	1:1:1018:C:H6	1.80	0.46
1:1:1673:C:O2'	1:1:1752:U:O2'	2.33	0.46
1:1:3068:C:HO2'	16:LH:157:SER:HG	1.56	0.46
2:2:493:G:H2'	2:2:494:G:H8	1.79	0.46
2:2:742:U:OP1	61:SH:116:ASN:ND2	2.48	0.46
2:2:792:U:H1'	2:2:793:U:OP2	2.15	0.46
2:2:1161:G:H2'	2:2:1162:G:H8	1.79	0.46
4:4:94:C:H5''	44:Lj:76:ASN:HD21	1.80	0.46
8:D:274:LEU:CD1	8:D:278:ARG:HH12	2.28	0.46
12:LD:41:LYS:HB2	28:LT:68:THR:O	2.15	0.46
12:LD:50:ARG:HB2	12:LD:65:VAL:CG2	2.44	0.46
17:LI:202:ASN:O	17:LI:203:HIS:ND1	2.48	0.46
25:LQ:104:GLU:H	25:LQ:104:GLU:CD	2.23	0.46
54:SA:208:ARG:HE	71:SR:81:LYS:HE2	1.79	0.46
58:SE:208:VAL:HG21	58:SE:225:VAL:HG11	1.96	0.46
62:SI:37:ARG:HG2	62:SI:37:ARG:HH11	1.79	0.46
73:ST:50:ASP:OD1	73:ST:51:ILE:N	2.49	0.46
79:SZ:50:THR:HG23	79:SZ:53:THR:H	1.79	0.46
79:SZ:63:ALA:O	79:SZ:67:LYS:HG2	2.15	0.46
1:1:2730:U:O2'	1:1:2731:C:O4'	2.31	0.46
2:2:853:A:O2'	2:2:854:A:H3'	2.16	0.46
2:2:1693:C:N4	7:C:362:ARG:HH21	2.13	0.46
4:4:82:U:H5'	4:4:83:C:H5'	1.96	0.46
5:A:99:ARG:HD2	5:A:99:ARG:HA	1.77	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A:131:LEU:HD12	5:A:140:TYR:HB3	1.95	0.46
7:C:146:ASP:O	7:C:150:LYS:HG3	2.15	0.46
7:C:330:ARG:O	7:C:333:LYS:HG3	2.15	0.46
8:D:157:ILE:O	8:D:185:SER:HA	2.15	0.46
14:LF:52:LYS:HB2	14:LF:52:LYS:HE2	1.77	0.46
24:LP:182:ARG:HH11	24:LP:182:ARG:HG2	1.79	0.46
48:Lr:6:ARG:O	48:Lr:10:THR:HG22	2.16	0.46
52:Ls:100:ILE:O	52:Ls:185:MET:HG3	2.16	0.46
59:SF:50:GLN:HG2	59:SF:74:CYS:N	2.30	0.46
61:SH:33:LEU:HD12	61:SH:40:LEU:HD22	1.96	0.46
62:SI:119:GLN:NE2	62:SI:150:PHE:CD1	2.83	0.46
81:Sb:42:THR:HG22	81:Sb:43:ILE:N	2.30	0.46
1:1:300:A:H2'	1:1:301:A:H8	1.79	0.46
1:1:1067:A:H2'	1:1:1068:A:C8	2.51	0.46
1:1:2477:U:H5	15:LG:241:MET:HE1	1.80	0.46
1:1:3194:G:H2'	1:1:3195:U:C6	2.49	0.46
2:2:781:G:H2'	2:2:782:C:H6	1.79	0.46
2:2:820:U:H2'	2:2:821:G:H5''	1.96	0.46
2:2:1043:C:H2'	2:2:1044:G:H8	1.80	0.46
2:2:1478:C:O2'	70:SQ:77:GLN:NE2	2.48	0.46
2:2:1479:A:H2'	2:2:1480:G:C8	2.50	0.46
2:2:1547:U:OP2	69:SP:51:ARG:NH1	2.48	0.46
2:2:1689:A:H2'	2:2:1690:G:C8	2.50	0.46
7:C:219:THR:HG23	7:C:222:GLU:H	1.81	0.46
7:C:327:ALA:O	7:C:330:ARG:HG3	2.16	0.46
7:C:424:LYS:HA	7:C:427:VAL:HG12	1.97	0.46
8:D:423:VAL:HB	8:D:448:THR:HG23	1.97	0.46
10:LB:68:HIS:CD2	10:LB:69:LYS:HG3	2.50	0.46
25:LQ:138:ARG:O	25:LQ:142:GLU:HG3	2.15	0.46
32:LX:142:ASP:OD2	32:LX:143:VAL:N	2.48	0.46
52:Ls:15:LEU:CD1	52:Ls:16:LYS:HD3	2.45	0.46
55:SB:33:LYS:HA	55:SB:41:ARG:O	2.16	0.46
56:SC:50:GLY:O	56:SC:53:VAL:HG12	2.15	0.46
59:SF:63:ARG:HH22	70:SQ:122:ARG:HG3	1.81	0.46
59:SF:99:ARG:NH2	79:SZ:86:LYS:HE3	2.31	0.46
61:SH:9:ILE:HD11	61:SH:15:SER:OG	2.16	0.46
64:SK:74:LEU:HD23	64:SK:78:LEU:HD23	1.97	0.46
69:SP:38:SER:HA	69:SP:41:LEU:HG	1.96	0.46
69:SP:93:VAL:HG11	69:SP:119:MET:SD	2.55	0.46
82:Sc:28:GLN:HE21	82:Sc:42:ILE:HG21	1.80	0.46
84:Se:38:LEU:HD21	84:Se:42:ARG:NH2	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:609:A:H4'	1:1:610:A:O5'	2.14	0.46
1:1:1173:A:H2'	1:1:1173:A:N3	2.29	0.46
1:1:1597:G:OP1	48:Lr:5:TRP:HH2	1.98	0.46
1:1:1745:U:H4'	1:1:1745:U:OP1	2.15	0.46
2:2:607:G:O2'	2:2:610:G:O2'	2.21	0.46
2:2:957:U:H5''	67:SN:15:ALA:O	2.16	0.46
2:2:1199:A:H1'	2:2:1204:C:N4	2.30	0.46
2:2:1591:U:OP1	83:Sd:33:LYS:NZ	2.45	0.46
5:A:217:MET:HG2	5:A:218:LEU:N	2.31	0.46
7:C:364:LEU:HD22	7:C:395:ILE:HD11	1.97	0.46
8:D:71:ASN:OD1	8:D:75:THR:OG1	2.33	0.46
8:D:228:MET:HE3	8:D:229:TYR:O	2.14	0.46
42:Lh:6:LYS:HD3	42:Lh:6:LYS:N	2.30	0.46
56:SC:95:GLN:OE1	56:SC:104:THR:HG22	2.16	0.46
58:SE:86:PHE:CE2	58:SE:87:MET:HE2	2.50	0.46
58:SE:125:LYS:H	58:SE:226:PHE:HE1	1.62	0.46
65:SL:137:SER:OG	65:SL:138:LYS:N	2.48	0.46
1:1:282:U:H2'	1:1:283:G:H8	1.79	0.46
1:1:893:C:OP2	9:LA:9:ARG:HD2	2.15	0.46
1:1:1004:C:H2'	1:1:1005:G:H8	1.81	0.46
1:1:1135:G:N2	1:1:1183:A:H61	2.13	0.46
1:1:2227:U:HO2'	1:1:2228:C:P	2.38	0.46
2:2:786:A:C4	58:SE:19:LEU:HD11	2.50	0.46
2:2:817:G:O2'	2:2:819:G:OP2	2.33	0.46
4:4:26:U:H2'	4:4:27:U:C6	2.50	0.46
8:D:186:GLU:HG2	8:D:187:PRO:HD3	1.97	0.46
8:D:206:ILE:HB	8:D:345:VAL:HA	1.97	0.46
13:LE:159:ALA:O	13:LE:163:LYS:HG3	2.15	0.46
22:LN:165:THR:HG22	22:LN:166:SER:H	1.79	0.46
27:LS:137:ARG:HA	27:LS:137:ARG:HD3	1.71	0.46
42:Lh:17:LYS:HG3	42:Lh:63:ILE:HD11	1.98	0.46
52:Ls:95:GLU:OE1	52:Ls:99:LYS:NZ	2.40	0.46
57:SD:96:ASN:ND2	57:SD:99:LEU:HD23	2.30	0.46
58:SE:128:ARG:HG3	58:SE:130:GLN:OE1	2.15	0.46
59:SF:82:ASN:HA	59:SF:85:MET:HE2	1.97	0.46
61:SH:87:LEU:HD22	61:SH:96:VAL:HG21	1.96	0.46
68:SO:61:VAL:HG11	68:SO:67:GLU:HA	1.97	0.46
69:SP:69:ARG:HH21	69:SP:72:LYS:HZ1	1.64	0.46
72:SS:90:ARG:O	72:SS:90:ARG:HD3	2.15	0.46
1:1:300:A:H2'	1:1:301:A:C8	2.50	0.46
1:1:533:C:H2'	1:1:534:C:C6	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1248:U:O2	1:1:1260:C:H1'	2.16	0.46
1:1:3211:U:C4	13:LE:64:ARG:NH1	2.84	0.46
2:2:397:A:H5''	62:SI:25:ARG:HA	1.98	0.46
2:2:496:U:H2'	2:2:497:C:C6	2.51	0.46
5:A:234:ASP:OD1	5:A:252:THR:HB	2.15	0.46
7:C:431:VAL:HA	7:C:436:LEU:O	2.14	0.46
8:D:87:PHE:O	8:D:90:VAL:HG22	2.15	0.46
17:LI:177:ARG:HB2	17:LI:180:GLU:OE1	2.15	0.46
32:LX:152:LYS:HA	32:LX:152:LYS:HD3	1.80	0.46
35:La:73:ILE:HB	35:La:109:TYR:CD2	2.50	0.46
37:Lc:45:ILE:HG13	37:Lc:70:VAL:HG23	1.98	0.46
54:SA:130:ARG:NH2	54:SA:155:PRO:HD3	2.30	0.46
59:SF:108:ILE:HD11	59:SF:116:PRO:HB3	1.97	0.46
61:SH:144:GLU:OE1	67:SN:21:ASN:ND2	2.47	0.46
63:SJ:110:LEU:HD12	63:SJ:151:GLN:HE22	1.80	0.46
67:SN:29:THR:O	67:SN:32:GLN:HG2	2.16	0.46
67:SN:39:LYS:O	67:SN:43:LYS:HG2	2.16	0.46
69:SP:62:LEU:O	69:SP:65:ILE:HG22	2.14	0.46
72:SS:116:LEU:O	72:SS:119:ILE:HG22	2.16	0.46
77:SX:28:GLN:OE1	77:SX:28:GLN:N	2.46	0.46
79:SZ:38:LYS:HE2	79:SZ:41:LYS:NZ	2.30	0.46
1:1:90:A:N7	25:LQ:198:LYS:NZ	2.64	0.46
1:1:135:G:H2'	1:1:136:C:C6	2.50	0.46
1:1:638:C:H2'	1:1:639:G:C8	2.51	0.46
1:1:896:A:C2	9:LA:204:MET:HE2	2.51	0.46
1:1:1052:C:H2'	1:1:1053:U:H6	1.81	0.46
1:1:1126:A:H5'	1:1:1351:U:H1'	1.98	0.46
1:1:1140:G:O2'	1:1:1152:A:N3	2.49	0.46
1:1:1843:G:N1	1:1:1846:C:OP2	2.47	0.46
1:1:3332:A:HO2'	1:1:3333:G:P	2.37	0.46
2:2:222:U:O2	2:2:832:G:O6	2.34	0.46
2:2:551:C:N4	2:2:568:G:O6	2.49	0.46
2:2:1781:U:H2'	2:2:1782:G:H8	1.80	0.46
3:3:27:U:OP2	12:LD:56:THR:OG1	2.33	0.46
7:C:126:ARG:HH21	7:C:130:LEU:HD21	1.81	0.46
8:D:228:MET:HE3	8:D:229:TYR:H	1.81	0.46
21:LM:78:THR:HA	21:LM:81:VAL:HG12	1.98	0.46
31:LW:110:LYS:O	31:LW:114:GLU:OE1	2.33	0.46
39:Le:68:MET:HG2	39:Le:72:HIS:O	2.15	0.46
48:Ln:6:ARG:O	48:Ln:10:THR:HG22	2.16	0.46
57:SD:73:THR:HB	57:SD:87:VAL:HG23	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:SF:152:LEU:O	59:SF:156:ASN:ND2	2.49	0.46
63:SJ:18:GLU:OE2	63:SJ:20:ALA:HB3	2.16	0.46
71:SR:5:ARG:O	71:SR:10:LYS:NZ	2.48	0.46
71:SR:6:THR:CG2	71:SR:7:LYS:H	2.27	0.46
77:SX:126:LYS:HG2	77:SX:131:GLY:HA2	1.98	0.46
85:Sf:107:LYS:O	85:Sf:114:ILE:HG23	2.15	0.46
85:Sf:119:ARG:NH1	85:Sf:121:CYS:SG	2.88	0.46
1:1:333:C:OP2	11:LC:199:ARG:NH1	2.43	0.46
1:1:477:C:H2'	1:1:478:G:C8	2.50	0.46
1:1:669:U:O2'	1:1:685:G:O6	2.34	0.46
1:1:1215:C:H2'	1:1:1216:G:C8	2.51	0.46
2:2:231:G:H2'	2:2:232:G:H8	1.81	0.46
2:2:535:A:H5'	2:2:540:C:H5	1.81	0.46
7:C:190:TYR:HD2	7:C:191:TYR:CD1	2.34	0.46
7:C:227:TYR:O	7:C:231:TYR:HD2	1.98	0.46
8:D:274:LEU:HD13	8:D:278:ARG:HH12	1.80	0.46
10:LB:359:TRP:HB3	31:LW:1:MET:HE1	1.98	0.46
14:LF:102:PRO:HB2	14:LF:105:PRO:HD2	1.96	0.46
15:LG:213:GLU:H	15:LG:213:GLU:CD	2.23	0.46
17:LI:50:VAL:HG12	17:LI:167:VAL:HG22	1.97	0.46
18:LJ:113:LEU:HD23	18:LJ:113:LEU:H	1.81	0.46
38:Ld:20:TYR:CD1	38:Ld:83:ILE:HD12	2.51	0.46
57:SD:138:GLU:OE1	57:SD:138:GLU:N	2.49	0.46
71:SR:108:THR:O	71:SR:112:LEU:HG	2.16	0.46
78:SY:32:HIS:ND1	78:SY:70:GLY:O	2.48	0.46
1:1:2369:C:H2'	1:1:2370:C:H6	1.81	0.46
2:2:352:G:H2'	2:2:353:G:C8	2.49	0.46
2:2:608:U:H5''	77:SX:5:LYS:NZ	2.30	0.46
2:2:777:C:N4	78:SY:13:ARG:HH12	2.13	0.46
2:2:824:U:H2'	2:2:825:C:H6	1.80	0.46
7:C:316:LYS:HA	7:C:319:GLU:HG2	1.98	0.46
8:D:188:ALA:HA	8:D:191:VAL:HG22	1.98	0.46
13:LE:65:PHE:CD1	13:LE:92:VAL:HG22	2.51	0.46
16:LH:92:TYR:HB2	16:LH:144:ASP:OD1	2.15	0.46
16:LH:113:GLU:HG3	16:LH:127:LYS:HZ2	1.81	0.46
18:LJ:33:ARG:NE	18:LJ:121:ILE:O	2.48	0.46
26:LR:173:LYS:O	26:LR:176:ARG:HG2	2.16	0.46
34:LZ:8:ARG:HD3	34:LZ:8:ARG:HA	1.72	0.46
55:SB:192:VAL:HA	55:SB:195:ARG:NH1	2.31	0.46
59:SF:96:MET:O	59:SF:99:ARG:HG2	2.16	0.46
61:SH:177:ASP:OD1	61:SH:178:THR:N	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:SQ:101:SER:O	70:SQ:104:LEU:HG	2.15	0.46
1:1:644:A:H2'	1:1:645:A:H8	1.81	0.46
1:1:1255:C:H3'	1:1:1256:A:H8	1.81	0.46
1:1:1676:A:H2'	1:1:1677:A:C8	2.50	0.46
1:1:3161:G:C8	40:Lf:3:SER:HB3	2.50	0.46
2:2:635:C:N3	61:SH:124:ARG:NH2	2.64	0.46
2:2:1205:A:H5''	2:2:1206:C:OP2	2.16	0.46
2:2:1282:U:H1'	2:2:1283:U:OP2	2.16	0.46
2:2:1706:U:H2'	2:2:1707:C:C6	2.51	0.46
4:4:59:A:O2'	32:LX:74:LYS:NZ	2.48	0.46
5:A:245:ARG:HB2	5:A:247:TRP:CE3	2.51	0.46
7:C:117:THR:O	7:C:121:ILE:HG12	2.15	0.46
7:C:214:GLY:O	7:C:291:ARG:NH2	2.48	0.46
15:LG:142:VAL:O	15:LG:146:ILE:HG13	2.16	0.46
18:LJ:165:LYS:HZ2	18:LJ:171:ILE:HA	1.81	0.46
21:LM:123:LEU:HD22	23:LO:195:VAL:HG13	1.97	0.46
24:LP:59:PRO:HD3	24:LP:76:TRP:CD1	2.51	0.46
31:LW:6:ASP:HB3	31:LW:10:GLY:H	1.81	0.46
54:SA:10:PHE:O	54:SA:57:TRP:NE1	2.37	0.46
54:SA:12:PRO:HD3	54:SA:57:TRP:CD1	2.51	0.46
54:SA:99:GLN:OE1	54:SA:99:GLN:N	2.49	0.46
56:SC:152:TRP:CZ2	56:SC:181:PRO:HG3	2.50	0.46
56:SC:178:ILE:HB	56:SC:205:TYR:HB2	1.96	0.46
73:ST:105:MET:HE1	73:ST:123:ARG:HH11	1.80	0.46
78:SY:102:LYS:HG3	78:SY:104:GLU:OE1	2.16	0.46
79:SZ:67:LYS:HE2	79:SZ:70:LYS:NZ	2.30	0.46
1:1:2621:G:O2'	1:1:2622:G:OP1	2.28	0.45
2:2:20:G:H5'	2:2:568:G:C8	2.51	0.45
2:2:884:U:C2	2:2:885:A:C8	3.04	0.45
2:2:1485:U:OP2	2:2:1511:A:N6	2.49	0.45
2:2:1624:U:H2'	2:2:1625:G:C8	2.51	0.45
2:2:1781:U:OP2	68:SO:146:ARG:NH2	2.45	0.45
5:A:157:SER:HG	5:A:164:VAL:H	1.57	0.45
7:C:415:VAL:HG12	7:C:418:GLU:H	1.81	0.45
8:D:67:PHE:HD1	8:D:70:ARG:HH21	1.63	0.45
8:D:241:HIS:CE1	8:D:243:ILE:HB	2.51	0.45
41:Lg:107:LYS:C	41:Lg:107:LYS:HD3	2.41	0.45
57:SD:138:GLU:CD	57:SD:190:LYS:HB2	2.41	0.45
59:SF:110:LEU:HB3	79:SZ:48:LEU:HD21	1.98	0.45
82:Sc:15:ARG:HH11	82:Sc:30:ARG:NH2	2.14	0.45
1:1:1212:G:H2'	1:1:1213:G:C8	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:225:C:H2'	2:2:226:C:C6	2.51	0.45
2:2:1669:G:H2'	2:2:1670:C:H6	1.80	0.45
6:B:146:LYS:HD2	6:B:147:LYS:HG3	1.98	0.45
7:C:54:ARG:NH1	8:D:412:SER:OG	2.50	0.45
8:D:29:HIS:CG	8:D:30:THR:H	2.34	0.45
8:D:430:VAL:HB	8:D:470:LYS:HG3	1.97	0.45
12:LD:194:ASP:OD2	12:LD:197:VAL:HG23	2.15	0.45
16:LH:89:LYS:HB3	16:LH:145:GLU:OE1	2.16	0.45
17:LI:184:LYS:HG2	17:LI:190:VAL:HG23	1.98	0.45
20:LL:3:ILE:H	20:LL:3:ILE:HD12	1.80	0.45
57:SD:137:CYS:SG	57:SD:138:GLU:N	2.89	0.45
59:SF:115:ASN:OD1	59:SF:116:PRO:HD2	2.15	0.45
59:SF:141:THR:HG22	59:SF:142:VAL:H	1.81	0.45
64:SK:59:TRP:CD2	83:Sd:23:VAL:HG12	2.51	0.45
65:SL:79:ARG:NE	65:SL:127:MET:CE	2.76	0.45
78:SY:54:GLN:CD	78:SY:56:ASP:H	2.24	0.45
79:SZ:91:THR:OG1	79:SZ:92:ARG:N	2.49	0.45
1:1:2245:U:OP1	1:1:2932:G:O2'	2.28	0.45
1:1:2726:U:H2'	1:1:2727:U:H6	1.82	0.45
2:2:270:G:H2'	2:2:271:G:H8	1.81	0.45
2:2:696:U:H2'	2:2:697:G:C8	2.51	0.45
2:2:869:A:H2'	2:2:870:G:C8	2.51	0.45
2:2:930:A:OP2	55:SB:155:TYR:OH	2.23	0.45
2:2:1075:C:H2'	2:2:1076:U:C6	2.51	0.45
2:2:1341:A:H2'	2:2:1342:A:C8	2.51	0.45
2:2:1446:U:H2'	2:2:1447:C:C6	2.51	0.45
2:2:1560:U:H2'	2:2:1561:C:C6	2.51	0.45
7:C:424:LYS:HE2	7:C:445:VAL:HA	1.98	0.45
8:D:248:VAL:HG23	8:D:249:LEU:HD22	1.98	0.45
20:LL:201:ARG:O	20:LL:204:GLU:HG3	2.15	0.45
25:LQ:32:ILE:HG23	25:LQ:34:LEU:HG	1.97	0.45
29:LU:62:ILE:O	29:LU:62:ILE:HG22	2.17	0.45
42:Lh:32:SER:O	42:Lh:36:ILE:HG12	2.17	0.45
52:Ls:19:LEU:HA	52:Ls:88:PHE:HE2	1.79	0.45
52:Ls:22:TYR:HB2	52:Ls:88:PHE:HD2	1.81	0.45
55:SB:109:LYS:O	55:SB:113:LEU:HD23	2.16	0.45
73:ST:77:ARG:NE	73:ST:96:ALA:O	2.49	0.45
76:SW:81:VAL:HG22	76:SW:82:ARG:O	2.16	0.45
1:1:478:G:H2'	1:1:479:G:C8	2.49	0.45
1:1:2056:A:O2'	1:1:2057:C:OP2	2.30	0.45
2:2:1223:G:HO2'	2:2:1253:A:H61	1.60	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:1606:G:H4'	59:SF:92:GLY:HA2	1.97	0.45
2:2:1705:C:H2'	2:2:1706:U:C6	2.52	0.45
7:C:5:VAL:HA	8:D:457:HIS:HB2	1.97	0.45
25:LQ:153:GLN:O	25:LQ:157:GLU:HG3	2.15	0.45
33:LY:10:SER:OG	33:LY:13:LYS:HB2	2.16	0.45
40:Lf:28:LYS:HB2	40:Lf:28:LYS:HE2	1.81	0.45
43:Li:17:ILE:HA	43:Li:22:LYS:HB2	1.99	0.45
52:Ls:129:GLU:CD	52:Ls:130:PRO:HD2	2.41	0.45
58:SE:199:GLU:OE1	58:SE:207:ILE:HB	2.17	0.45
58:SE:254:ARG:NH1	58:SE:255:ARG:HH12	2.14	0.45
65:SL:140:VAL:C	65:SL:141:ARG:HD2	2.42	0.45
1:1:410:A:H2'	1:1:411:A:C8	2.52	0.45
1:1:1017:U:H2'	1:1:1018:C:C6	2.51	0.45
1:1:1244:G:H4'	1:1:1261:A:C2	2.52	0.45
1:1:1932:G:O6	1:1:2058:A:N6	2.49	0.45
1:1:2092:U:H2'	1:1:2093:G:C8	2.52	0.45
1:1:2471:U:H2'	1:1:2472:U:C6	2.52	0.45
1:1:3056:G:OP1	10:LB:280:ASN:ND2	2.44	0.45
1:1:3159:U:H1'	13:LE:190:ARG:NH1	2.32	0.45
2:2:682:U:H5'	76:SW:118:ARG:HH12	1.81	0.45
2:2:1708:A:H2'	2:2:1709:G:H8	1.81	0.45
2:2:1784:G:OP2	68:SO:145:ARG:NH1	2.48	0.45
4:4:139:U:H2'	4:4:140:G:H8	1.81	0.45
7:C:392:ASP:O	7:C:396:THR:HG23	2.16	0.45
13:LE:100:ARG:O	40:Lf:107:SER:OG	2.27	0.45
16:LH:122:GLU:HG3	16:LH:124:ILE:H	1.82	0.45
18:LJ:54:THR:OG1	18:LJ:62:ARG:HG3	2.16	0.45
24:LP:95:LEU:HD23	24:LP:95:LEU:HA	1.84	0.45
42:Lh:19:GLU:O	42:Lh:23:ILE:HG12	2.16	0.45
58:SE:60:GLU:O	58:SE:64:ILE:HG12	2.16	0.45
61:SH:85:ARG:C	61:SH:89:LYS:HZ2	2.24	0.45
62:SI:117:TYR:HB3	62:SI:119:GLN:NE2	2.32	0.45
63:SJ:29:VAL:HG23	63:SJ:34:LEU:HB2	1.97	0.45
63:SJ:54:ALA:O	63:SJ:58:LEU:HD23	2.17	0.45
72:SS:100:ILE:HG13	72:SS:108:LYS:NZ	2.31	0.45
76:SW:52:GLU:HA	76:SW:60:LYS:O	2.17	0.45
80:Sa:66:LYS:HB3	80:Sa:68:TYR:CE2	2.52	0.45
80:Sa:67:MET:HE3	80:Sa:69:LEU:CD2	2.43	0.45
1:1:474:C:H2'	1:1:475:G:C8	2.52	0.45
1:1:1229:G:C4	1:1:1247:C:H2'	2.52	0.45
1:1:3111:C:N4	1:1:3113:A:H1'	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:857:A:C6	67:SN:73:ARG:HD3	2.52	0.45
2:2:1242:G:H21	85:Sf:93:HIS:CD2	2.34	0.45
2:2:1521:A:H2'	2:2:1522:A:O4'	2.17	0.45
2:2:1789:G:O6	80:Sa:34:LYS:NZ	2.50	0.45
5:A:118:ARG:HH12	5:A:133:ASN:HB2	1.81	0.45
7:C:41:PRO:O	8:D:182:GLN:NE2	2.34	0.45
7:C:176:ASP:OD1	7:C:176:ASP:N	2.50	0.45
8:D:350:MET:HG3	8:D:355:SER:OG	2.17	0.45
20:LL:158:GLU:CD	20:LL:159:GLN:HG2	2.42	0.45
26:LR:44:LEU:HD22	26:LR:49:LEU:HD12	1.99	0.45
39:Le:68:MET:HB2	39:Le:69:PRO:HD2	1.99	0.45
52:Ls:142:PRO:HD2	52:Ls:156:ILE:HG13	1.98	0.45
52:Ls:143:THR:HG22	52:Ls:152:ILE:HG13	1.98	0.45
54:SA:84:PHE:HE2	54:SA:170:ARG:HB2	1.80	0.45
63:SJ:127:ILE:HG21	63:SJ:142:PRO:HA	1.97	0.45
77:SX:49:ALA:O	77:SX:103:LEU:HD12	2.17	0.45
1:1:637:A:H2'	1:1:638:C:C6	2.51	0.45
1:1:769:G:H2'	1:1:770:C:H6	1.81	0.45
1:1:869:G:H2'	1:1:870:A:C8	2.51	0.45
1:1:1228:A:H5'	1:1:1230:U:OP2	2.17	0.45
1:1:3231:G:H2'	1:1:3232:A:H8	1.80	0.45
2:2:1244:U:H5''	85:Sf:91:ILE:O	2.17	0.45
2:2:1341:A:H4'	2:2:1342:A:OP1	2.16	0.45
8:D:93:THR:HG23	8:D:94:HIS:H	1.81	0.45
8:D:314:LEU:HD23	8:D:315:ARG:HH12	1.81	0.45
19:LK:11:LYS:HA	19:LK:65:GLN:O	2.17	0.45
32:LX:82:THR:O	32:LX:85:ALA:N	2.50	0.45
55:SB:11:LYS:NZ	55:SB:16:LEU:O	2.49	0.45
55:SB:89:ASP:HB3	55:SB:223:PHE:CE1	2.51	0.45
60:SG:95:LYS:HG3	60:SG:96:SER:H	1.80	0.45
63:SJ:137:GLN:OE1	63:SJ:138:ILE:N	2.50	0.45
66:SM:72:ALA:HA	66:SM:75:LYS:NZ	2.32	0.45
69:SP:36:LEU:HD12	69:SP:36:LEU:HA	1.88	0.45
74:SU:20:ARG:O	74:SU:113:THR:OG1	2.31	0.45
83:Sd:33:LYS:O	83:Sd:36:LEU:HG	2.16	0.45
84:Se:43:ARG:O	84:Se:44:PHE:CD1	2.69	0.45
1:1:328:G:OP2	33:LY:13:LYS:NZ	2.34	0.45
1:1:1059:C:C6	36:Lb:42:ASN:ND2	2.85	0.45
1:1:1744:C:H3'	1:1:1745:U:C5'	2.46	0.45
1:1:1799:U:H5'	48:Lr:13:LEU:HD13	1.98	0.45
1:1:1939:U:H3	1:1:2045:G:H22	1.63	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:964:A:P	67:SN:124:ARG:HH21	2.40	0.45
2:2:1054:U:O2	2:2:1055:A:N6	2.49	0.45
2:2:1432:A:OP2	57:SD:30:ARG:NH2	2.50	0.45
8:D:50:ILE:HG23	8:D:64:ALA:HB3	1.99	0.45
10:LB:8:ALA:HB2	30:LV:48:LEU:HD12	1.98	0.45
10:LB:164:HIS:HB3	10:LB:179:LEU:HD12	1.99	0.45
14:LF:62:ARG:O	14:LF:66:ARG:HG2	2.17	0.45
20:LL:31:LYS:O	20:LL:35:ARG:HG3	2.17	0.45
54:SA:13:THR:OG1	54:SA:16:ASP:OD2	2.28	0.45
62:SI:117:TYR:HB3	62:SI:119:GLN:CD	2.42	0.45
63:SJ:86:GLU:H	63:SJ:86:GLU:CD	2.25	0.45
66:SM:79:ALA:HA	66:SM:82:GLN:HE22	1.82	0.45
73:ST:112:GLN:HB3	73:ST:128:GLN:NE2	2.31	0.45
74:SU:66:LYS:HG3	83:Sd:44:ARG:NH2	2.31	0.45
76:SW:36:LYS:HB3	76:SW:110:ILE:HD11	1.98	0.45
1:1:469:C:H1'	1:1:470:A:C6	2.52	0.45
1:1:1619:C:OP2	41:Lg:75:ARG:NH2	2.50	0.45
1:1:2676:U:O3'	49:Lo:13:LYS:NZ	2.49	0.45
2:2:552:A:N3	2:2:587:C:O2'	2.46	0.45
2:2:883:G:H2'	2:2:884:U:C6	2.52	0.45
2:2:1580:G:H22	2:2:1607:A:P	2.36	0.45
6:B:127:GLU:OE1	6:B:127:GLU:N	2.49	0.45
7:C:34:SER:HA	8:D:424:THR:H	1.82	0.45
8:D:49:THR:HG23	8:D:134:TYR:CE2	2.52	0.45
55:SB:85:LYS:HB2	55:SB:101:HIS:HB3	1.98	0.45
56:SC:98:THR:HG22	56:SC:99:ARG:N	2.31	0.45
59:SF:124:ILE:HG13	59:SF:125:VAL:N	2.32	0.45
62:SI:110:ARG:HG3	62:SI:121:LEU:HD21	1.97	0.45
63:SJ:83:VAL:HG21	63:SJ:102:PHE:CD1	2.52	0.45
66:SM:97:LEU:HA	66:SM:100:TRP:CE3	2.52	0.45
70:SQ:87:LYS:HA	70:SQ:90:VAL:HG22	1.98	0.45
70:SQ:93:TYR:HA	70:SQ:97:VAL:HG12	1.99	0.45
75:SV:64:GLU:OE1	75:SV:64:GLU:N	2.50	0.45
79:SZ:66:ARG:HG2	79:SZ:88:LYS:HZ2	1.82	0.45
1:1:615:C:H2'	1:1:616:A:H8	1.81	0.45
1:1:2389:U:H2'	1:1:2390:U:H6	1.81	0.45
2:2:483:G:H1	2:2:498:U:H3	1.64	0.45
2:2:751:A:H2	2:2:795:G:H22	1.65	0.45
2:2:797:A:H4'	58:SE:201:HIS:NE2	2.32	0.45
2:2:1500:G:OP1	73:ST:97:SER:OG	2.35	0.45
2:2:1580:G:O2'	2:2:1606:G:O6	2.30	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:C:343:ARG:NH1	7:C:344:GLU:OE2	2.50	0.45
13:LE:23:LYS:HD2	14:LF:6:VAL:HG21	1.99	0.45
14:LF:22:ARG:HG2	14:LF:22:ARG:HH11	1.82	0.45
15:LG:67:ILE:HA	15:LG:70:MET:HG2	1.99	0.45
25:LQ:68:THR:HG22	25:LQ:70:ALA:H	1.82	0.45
34:LZ:51:LYS:O	34:LZ:64:ARG:NH1	2.49	0.45
58:SE:222:GLU:O	58:SE:225:VAL:HG22	2.17	0.45
58:SE:255:ARG:NE	58:SE:255:ARG:HA	2.32	0.45
59:SF:180:CYS:O	59:SF:183:GLU:HG3	2.17	0.45
70:SQ:106:LYS:O	70:SQ:110:ILE:HG12	2.16	0.45
71:SR:18:GLU:OE2	71:SR:19:LYS:HG3	2.16	0.45
71:SR:106:GLN:HA	71:SR:124:VAL:HG11	1.99	0.45
72:SS:114:GLU:HG2	72:SS:118:LYS:HZ3	1.81	0.45
73:ST:63:ARG:HD3	73:ST:64:HIS:HD2	1.82	0.45
74:SU:23:LEU:O	74:SU:85:LYS:HA	2.17	0.45
75:SV:78:LEU:O	75:SV:79:LEU:HD23	2.17	0.45
1:1:372:C:H2'	1:1:373:U:H6	1.82	0.44
2:2:1028:A:OP1	80:Sa:3:LYS:NZ	2.34	0.44
2:2:1165:U:HO2'	2:2:1166:G:P	2.39	0.44
2:2:1168:A:H2'	2:2:1169:G:H8	1.81	0.44
2:2:1207:C:H2'	2:2:1208:A:C8	2.51	0.44
2:2:1211:U:H2'	2:2:1212:C:C6	2.52	0.44
2:2:1233:A:H2'	2:2:1234:G:C8	2.52	0.44
7:C:73:LYS:HA	7:C:73:LYS:HD2	1.84	0.44
7:C:293:LYS:O	7:C:296:ARG:HG3	2.16	0.44
8:D:109:VAL:HG12	8:D:126:THR:HA	1.98	0.44
8:D:216:ARG:HG3	8:D:238:TYR:HE1	1.81	0.44
8:D:373:ARG:HE	8:D:374:ILE:N	2.15	0.44
11:LC:34:ASP:OD1	11:LC:35:ILE:HG13	2.17	0.44
12:LD:59:ASP:OD1	12:LD:80:SER:HB2	2.17	0.44
17:LI:35:ASP:C	17:LI:36:LEU:HD12	2.42	0.44
17:LI:171:TRP:CE3	17:LI:178:ARG:HG3	2.51	0.44
35:La:15:VAL:O	35:La:16:SER:OG	2.31	0.44
50:Lp:10:ILE:HG22	50:Lp:27:LYS:HG3	1.98	0.44
55:SB:103:LEU:HD13	55:SB:188:LEU:HD22	1.99	0.44
55:SB:113:LEU:HD13	55:SB:113:LEU:HA	1.79	0.44
58:SE:19:LEU:HB3	58:SE:51:ARG:HH22	1.82	0.44
60:SG:43:PRO:HA	60:SG:46:LYS:HE2	2.00	0.44
61:SH:33:LEU:HA	61:SH:36:ASN:OD1	2.17	0.44
61:SH:127:THR:O	61:SH:131:VAL:HG13	2.17	0.44
64:SK:60:GLN:HE22	83:Sd:23:VAL:C	2.23	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
69:SP:65:ILE:HD12	69:SP:97:MET:CE	2.47	0.44
1:1:934:A:C2	1:1:1097:U:H4'	2.52	0.44
2:2:391:C:C4'	60:SG:92:ARG:HH12	2.30	0.44
2:2:722:U:H2'	2:2:723:G:C8	2.52	0.44
2:2:1315:G:H2'	2:2:1316:A:C8	2.52	0.44
8:D:23:SER:HB2	87:D:601:ATP:O1B	2.17	0.44
8:D:388:GLU:HB3	8:D:392:ARG:HE	1.82	0.44
10:LB:263:TRP:CD1	10:LB:263:TRP:H	2.35	0.44
10:LB:348:SER:C	10:LB:350:LYS:H	2.25	0.44
16:LH:21:LYS:HA	21:LM:7:GLU:OE1	2.17	0.44
30:LV:111:MET:HG2	30:LV:113:GLY:H	1.80	0.44
41:Lg:74:GLN:OE1	41:Lg:74:GLN:HA	2.17	0.44
54:SA:157:GLU:HG3	54:SA:158:TYR:CD1	2.46	0.44
59:SF:125:VAL:HG13	59:SF:126:ASN:OD1	2.17	0.44
62:SI:3:ILE:H	62:SI:3:ILE:HD12	1.82	0.44
62:SI:201:HIS:ND1	62:SI:201:HIS:O	2.50	0.44
68:SO:42:HIS:HE2	68:SO:51:THR:HG22	1.82	0.44
69:SP:101:VAL:HA	69:SP:112:GLN:HE22	1.81	0.44
70:SQ:82:ARG:HG2	70:SQ:82:ARG:HH11	1.82	0.44
1:1:171:G:H2'	1:1:172:G:C8	2.53	0.44
1:1:3186:A:N7	23:LO:158:LEU:HD21	2.33	0.44
2:2:138:A:H61	60:SG:190:LYS:HD2	1.83	0.44
2:2:646:C:H2'	2:2:647:C:C6	2.52	0.44
2:2:1549:G:H4'	83:Sd:14:TYR:CE1	2.53	0.44
2:2:1684:C:H2'	2:2:1685:A:C8	2.53	0.44
2:2:1736:G:H2'	2:2:1737:U:C6	2.53	0.44
5:A:81:ALA:HB1	5:A:108:VAL:HG23	2.00	0.44
7:C:80:SER:O	7:C:84:GLU:HG2	2.17	0.44
7:C:170:SER:OG	7:C:237:ARG:HG3	2.17	0.44
7:C:227:TYR:O	7:C:231:TYR:CD2	2.70	0.44
17:LI:63:GLU:OE1	17:LI:63:GLU:N	2.46	0.44
20:LL:60:CYS:HB2	20:LL:65:TYR:O	2.17	0.44
27:LS:34:GLU:HA	27:LS:37:ALA:HB3	1.99	0.44
29:LU:87:THR:O	29:LU:91:LEU:HD23	2.16	0.44
34:LZ:30:GLN:OE1	34:LZ:30:GLN:N	2.47	0.44
52:Ls:65:THR:HG21	52:Ls:77:LEU:HD21	1.98	0.44
58:SE:189:MET:HE2	58:SE:189:MET:HA	2.00	0.44
62:SI:65:PHE:HA	62:SI:185:GLY:O	2.17	0.44
63:SJ:52:ARG:O	63:SJ:56:ILE:HG12	2.17	0.44
72:SS:65:GLU:O	72:SS:69:LEU:HG	2.16	0.44
75:SV:53:TYR:OH	75:SV:76:ASP:OD2	2.34	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
82:Sc:28:GLN:NE2	82:Sc:65:ARG:O	2.51	0.44
1:1:2184:G:N7	43:Li:76:LYS:NZ	2.64	0.44
1:1:3218:U:C2	40:Lf:64:THR:HG22	2.52	0.44
2:2:78:C:H5'	60:SG:175:ALA:HB3	2.00	0.44
2:2:390:C:H2'	2:2:391:C:C6	2.52	0.44
2:2:1144:A:P	56:SC:99:ARG:HH22	2.39	0.44
2:2:1602:C:H2'	2:2:1603:G:H8	1.82	0.44
8:D:157:ILE:HD13	8:D:183:LEU:HD13	1.98	0.44
22:LN:186:GLY:O	22:LN:190:THR:HG23	2.18	0.44
26:LR:25:ASP:HB3	26:LR:28:GLU:CD	2.43	0.44
29:LU:101:ARG:HB3	29:LU:115:TYR:CE1	2.53	0.44
58:SE:197:HIS:CE1	58:SE:209:HIS:HD2	2.35	0.44
72:SS:140:THR:O	72:SS:140:THR:HG22	2.17	0.44
1:1:290:A:H3'	43:Li:42:GLN:HE22	1.83	0.44
2:2:151:G:N2	60:SG:60:GLY:O	2.44	0.44
2:2:191:G:O2'	2:2:192:A:H8	2.00	0.44
2:2:1175:G:H21	69:SP:143:ALA:HB2	1.82	0.44
2:2:1237:U:N3	2:2:1240:G:OP2	2.31	0.44
7:C:117:THR:O	7:C:120:GLN:HG2	2.17	0.44
7:C:189:ASN:HB3	7:C:192:GLU:CG	2.47	0.44
7:C:189:ASN:HB3	7:C:192:GLU:HG3	1.99	0.44
26:LR:68:LEU:HD13	26:LR:71:ARG:HD2	2.00	0.44
29:LU:98:ASP:OD1	29:LU:99:TRP:N	2.50	0.44
54:SA:59:LYS:NZ	54:SA:162:ALA:O	2.51	0.44
56:SC:58:ILE:HG21	56:SC:64:ILE:HD11	1.99	0.44
56:SC:67:HIS:HA	75:SV:15:ARG:HH21	1.81	0.44
58:SE:11:ARG:O	58:SE:12:LEU:HB2	2.18	0.44
59:SF:173:ASN:HD22	59:SF:175:LYS:HE3	1.83	0.44
72:SS:132:ARG:HD3	72:SS:133:VAL:H	1.83	0.44
76:SW:51:GLU:HB2	76:SW:62:VAL:CG1	2.46	0.44
78:SY:64:ARG:HE	78:SY:64:ARG:HB3	1.68	0.44
1:1:3135:A:OP2	23:LO:173:LYS:NZ	2.43	0.44
2:2:587:C:H2'	2:2:588:A:H8	1.82	0.44
2:2:882:A:H2'	2:2:883:G:C8	2.53	0.44
2:2:1222:U:H3'	2:2:1223:G:H8	1.82	0.44
5:A:121:VAL:HG22	5:A:156:PHE:CE2	2.53	0.44
5:A:217:MET:HE3	5:A:219:TRP:CD1	2.53	0.44
7:C:360:ASN:ND2	7:C:404:ALA:HB2	2.31	0.44
8:D:266:ASP:HB3	8:D:269:GLU:OE1	2.18	0.44
8:D:350:MET:HG3	8:D:355:SER:CB	2.47	0.44
17:LI:102:MET:O	17:LI:106:ALA:HB3	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:LN:160:GLU:HG2	22:LN:161:CYS:N	2.32	0.44
31:LW:80:ARG:NH2	60:SG:130:PRO:HA	2.33	0.44
31:LW:83:VAL:HB	60:SG:130:PRO:HB2	1.99	0.44
58:SE:141:THR:OG1	58:SE:142:HIS:N	2.50	0.44
61:SH:11:ALA:HA	61:SH:16:ARG:HD2	2.00	0.44
70:SQ:41:PRO:O	70:SQ:45:ARG:HG2	2.18	0.44
70:SQ:73:GLY:O	70:SQ:76:SER:OG	2.19	0.44
82:Sc:36:ASP:OD2	82:Sc:39:ARG:HG2	2.18	0.44
1:1:250:C:H2'	1:1:251:U:H6	1.83	0.44
1:1:405:G:H2'	1:1:406:U:C6	2.52	0.44
1:1:436:C:H2'	1:1:437:G:C8	2.53	0.44
1:1:535:U:H2'	1:1:536:C:H5''	1.99	0.44
1:1:1812:C:H2'	1:1:1813:G:H8	1.83	0.44
1:1:2854:G:O2'	47:Lm:100:TYR:O	2.35	0.44
1:1:3017:G:H2'	1:1:3018:C:C6	2.53	0.44
2:2:68:A:OP1	60:SG:174:LYS:NZ	2.51	0.44
2:2:293:U:H2'	2:2:294:U:C6	2.53	0.44
2:2:568:G:H5''	77:SX:114:LYS:NZ	2.33	0.44
2:2:921:A:H2'	2:2:922:A:H8	1.81	0.44
2:2:972:A:O3'	67:SN:112:LYS:NZ	2.51	0.44
2:2:1144:A:H5'	56:SC:99:ARG:NH2	2.32	0.44
2:2:1248:U:HO2'	2:2:1249:C:H6	1.60	0.44
3:3:50:U:C2	3:3:51:A:C8	3.06	0.44
4:4:68:G:H2'	4:4:69:U:H6	1.83	0.44
7:C:94:ASP:CG	7:C:148:PHE:HB2	2.43	0.44
7:C:406:LEU:HA	7:C:409:LYS:HD2	2.00	0.44
8:D:298:VAL:HB	8:D:301:LEU:HD21	1.98	0.44
12:LD:116:ASP:OD1	12:LD:116:ASP:N	2.46	0.44
15:LG:136:LYS:HD2	15:LG:141:HIS:HE1	1.83	0.44
18:LJ:89:GLU:HG3	18:LJ:89:GLU:O	2.17	0.44
23:LO:55:TYR:CE1	23:LO:147:VAL:HG11	2.52	0.44
36:Lb:60:GLY:H	36:Lb:62:ARG:NH1	2.15	0.44
46:Ll:20:ASN:ND2	46:Ll:42:ARG:O	2.50	0.44
55:SB:183:GLN:O	55:SB:186:SER:OG	2.32	0.44
59:SF:29:LEU:HD22	59:SF:35:TYR:H	1.82	0.44
66:SM:61:MET:HE3	66:SM:123:VAL:CG2	2.47	0.44
82:Sc:15:ARG:HH11	82:Sc:30:ARG:HH22	1.65	0.44
1:1:701:U:P	43:Li:18:ARG:HH22	2.39	0.44
1:1:2966:G:O6	1:1:3097:A:N6	2.51	0.44
2:2:1646:U:H2'	2:2:1647:A:H8	1.83	0.44
3:3:3:A:H2'	3:3:4:U:C6	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:C:233:PHE:HE2	7:C:235:SER:HB2	1.81	0.44
7:C:340:LYS:O	7:C:344:GLU:HG2	2.18	0.44
8:D:342:PRO:O	8:D:345:VAL:HG12	2.18	0.44
12:LD:93:THR:O	12:LD:93:THR:HG22	2.18	0.44
17:LI:28:ASP:OD1	17:LI:29:PRO:HD2	2.17	0.44
18:LJ:83:ARG:HE	18:LJ:113:LEU:HD12	1.83	0.44
55:SB:97:LEU:HB3	55:SB:232:HIS:CD2	2.53	0.44
56:SC:79:TYR:HD1	56:SC:80:PHE:CD1	2.36	0.44
56:SC:133:ILE:O	56:SC:137:ILE:HG13	2.16	0.44
58:SE:107:GLY:HA2	58:SE:189:MET:HB3	2.00	0.44
59:SF:77:ILE:H	59:SF:77:ILE:HD12	1.82	0.44
59:SF:141:THR:HG22	59:SF:142:VAL:N	2.33	0.44
70:SQ:37:LYS:NZ	73:ST:11:ASP:HB2	2.33	0.44
75:SV:47:GLN:H	75:SV:47:GLN:CD	2.26	0.44
75:SV:79:LEU:O	75:SV:80:LYS:HD3	2.17	0.44
78:SY:23:ARG:HE	78:SY:25:GLN:NE2	2.03	0.44
1:1:542:G:H2'	1:1:543:U:C6	2.53	0.44
1:1:766:G:N2	25:LQ:97:ARG:HE	2.16	0.44
1:1:1570:G:C2	1:1:1571:G:C8	3.06	0.44
2:2:78:C:H1'	60:SG:177:ARG:CZ	2.46	0.44
2:2:115:U:H2'	2:2:116:U:C6	2.53	0.44
2:2:352:G:O2'	2:2:353:G:OP1	2.31	0.44
2:2:396:A:H4'	58:SE:3:ARG:HG3	2.00	0.44
2:2:1410:U:H5''	71:SR:3:ARG:CZ	2.48	0.44
8:D:386:PRO:HA	8:D:389:LEU:HG	1.99	0.44
12:LD:194:ASP:O	12:LD:195:THR:OG1	2.27	0.44
20:LL:140:LYS:HA	20:LL:143:GLN:HG3	1.99	0.44
35:La:112:LEU:HD22	35:La:125:VAL:HG11	2.00	0.44
43:Li:83:LYS:HD2	43:Li:89:PHE:HD2	1.83	0.44
57:SD:139:VAL:HG22	57:SD:155:PHE:HB2	2.00	0.44
60:SG:163:GLN:HB3	60:SG:171:PRO:HB3	2.00	0.44
60:SG:181:LEU:O	60:SG:186:ARG:NH1	2.51	0.44
62:SI:61:ASP:OD2	62:SI:61:ASP:N	2.51	0.44
63:SJ:57:LEU:HD11	63:SJ:70:GLU:HG3	1.98	0.44
63:SJ:72:ASN:HA	63:SJ:75:ILE:HG22	2.00	0.44
71:SR:89:SER:OG	71:SR:91:LEU:HG	2.18	0.44
84:Se:25:GLU:OE1	84:Se:26:LYS:N	2.51	0.44
1:1:262:G:OP2	22:LN:44:ARG:NH2	2.37	0.43
1:1:2166:U:H2'	1:1:2167:C:C6	2.52	0.43
2:2:509:A:H2'	2:2:510:U:C6	2.53	0.43
2:2:821:G:H2'	2:2:822:G:O4'	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:909:U:C4	55:SB:9:LEU:HD21	2.52	0.43
2:2:1674:C:H2'	2:2:1675:G:O4'	2.18	0.43
4:4:139:U:H2'	4:4:140:G:C8	2.53	0.43
6:B:135:GLU:CA	57:SD:120:ARG:HH22	2.30	0.43
8:D:93:THR:HG23	8:D:94:HIS:N	2.32	0.43
18:LJ:132:MET:O	18:LJ:133:THR:OG1	2.36	0.43
31:LW:6:ASP:HB3	31:LW:10:GLY:N	2.32	0.43
32:LX:142:ASP:OD2	32:LX:143:VAL:HG23	2.18	0.43
41:Lg:52:LEU:HD11	41:Lg:80:SER:H	1.83	0.43
42:Lh:24:LEU:O	42:Lh:28:LYS:HG3	2.18	0.43
54:SA:12:PRO:HB3	54:SA:57:TRP:CD2	2.53	0.43
56:SC:130:ALA:C	56:SC:134:ARG:HH12	2.26	0.43
57:SD:71:GLU:O	57:SD:74:SER:OG	2.30	0.43
59:SF:88:GLY:O	59:SF:91:ASN:ND2	2.45	0.43
59:SF:148:ASP:OD1	82:Sc:45:VAL:HA	2.17	0.43
60:SG:7:HIS:HB2	60:SG:124:LEU:HD21	2.00	0.43
77:SX:28:GLN:HA	77:SX:31:LYS:HE3	2.00	0.43
81:Sb:34:ASP:HB2	81:Sb:43:ILE:HG23	2.00	0.43
1:1:135:G:H2'	1:1:136:C:H6	1.82	0.43
1:1:1530:G:OP1	22:LN:105:ARG:NH1	2.51	0.43
1:1:1739:C:H2'	1:1:1740:A:H8	1.82	0.43
1:1:2065:U:H2'	1:1:2066:U:C6	2.53	0.43
2:2:788:U:H2'	2:2:789:A:H8	1.84	0.43
2:2:832:G:O2'	2:2:833:U:OP1	2.36	0.43
2:2:1232:C:N3	85:Sf:138:ARG:NH1	2.66	0.43
2:2:1730:U:H2'	2:2:1731:C:C6	2.53	0.43
5:A:91:GLU:OE1	5:A:93:SER:OG	2.23	0.43
8:D:66:ASN:O	8:D:70:ARG:NH2	2.51	0.43
8:D:353:GLY:H	87:D:601:ATP:PA	2.41	0.43
17:LI:115:MET:O	17:LI:118:ALA:HB2	2.18	0.43
17:LI:180:GLU:HA	17:LI:183:GLU:HG3	2.00	0.43
25:LQ:127:GLU:OE2	25:LQ:147:ARG:HB2	2.19	0.43
30:LV:25:MET:HE1	30:LV:80:ILE:HG12	2.00	0.43
33:LY:47:ILE:HD12	33:LY:48:PRO:HD2	2.00	0.43
51:Lq:24:ARG:O	51:Lq:25:THR:OG1	2.30	0.43
55:SB:91:VAL:O	55:SB:91:VAL:HG13	2.17	0.43
56:SC:234:THR:OG1	56:SC:236:ASN:OD1	2.19	0.43
58:SE:62:LYS:O	58:SE:66:MET:HG2	2.18	0.43
64:SK:2:LEU:CA	64:SK:8:ARG:HH12	2.30	0.43
66:SM:32:GLY:HA2	66:SM:35:LYS:CE	2.43	0.43
69:SP:92:ILE:HD12	69:SP:122:HIS:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
73:ST:105:MET:HE1	73:ST:123:ARG:NH1	2.33	0.43
74:SU:65:ARG:HG2	74:SU:76:TRP:CH2	2.53	0.43
1:1:133:C:H5''	1:1:134:G:C4	2.53	0.43
1:1:249:G:H2'	1:1:250:C:H6	1.83	0.43
1:1:445:G:O2'	1:1:446:A:H5'	2.18	0.43
1:1:1244:G:OP2	1:1:1244:G:N2	2.42	0.43
1:1:1323:C:H2'	1:1:1324:U:H6	1.84	0.43
2:2:96:C:H2'	2:2:97:U:C6	2.52	0.43
2:2:102:A:H4'	2:2:103:A:O5'	2.18	0.43
2:2:188:U:O2'	2:2:190:G:O6	2.25	0.43
2:2:678:G:O2'	2:2:679:G:OP1	2.34	0.43
2:2:823:U:O2'	2:2:824:U:H6	2.01	0.43
2:2:1357:C:O2'	73:ST:3:GLY:N	2.49	0.43
2:2:1498:G:O6	73:ST:102:ARG:NH1	2.51	0.43
4:4:4:C:H2'	4:4:5:U:C6	2.53	0.43
5:A:108:VAL:HA	5:A:124:SER:HA	1.99	0.43
7:C:189:ASN:O	7:C:192:GLU:HG3	2.19	0.43
7:C:279:ARG:HG2	7:C:279:ARG:NH1	2.32	0.43
13:LE:122:VAL:HG23	13:LE:127:TYR:CD2	2.53	0.43
15:LG:67:ILE:O	15:LG:71:ARG:HG2	2.18	0.43
23:LO:118:LYS:HG3	23:LO:120:MET:HE3	2.01	0.43
45:Lk:10:LYS:O	45:Lk:14:ILE:HG12	2.18	0.43
55:SB:10:SER:OG	55:SB:11:LYS:N	2.51	0.43
59:SF:79:ARG:NH2	59:SF:156:ASN:OD1	2.51	0.43
61:SH:155:ASP:OD1	61:SH:156:GLY:N	2.51	0.43
63:SJ:134:VAL:HG22	63:SJ:154:ILE:HG13	2.01	0.43
78:SY:63:LEU:HD23	78:SY:63:LEU:H	1.83	0.43
1:1:483:C:H2'	1:1:484:A:C8	2.53	0.43
1:1:948:U:H2'	1:1:949:A:H8	1.84	0.43
1:1:1002:G:H2'	1:1:1003:G:H4'	2.00	0.43
1:1:2535:G:H2'	1:1:2536:C:C6	2.54	0.43
2:2:481:C:H2'	2:2:482:A:C8	2.54	0.43
2:2:607:G:H2'	2:2:611:A:C8	2.54	0.43
2:2:777:C:H2'	2:2:778:U:H2'	2.00	0.43
2:2:1039:G:H2'	2:2:1040:G:C8	2.53	0.43
2:2:1363:A:H5'	70:SQ:30:LYS:NZ	2.33	0.43
5:A:30:MET:HE1	5:A:71:ILE:HD13	2.00	0.43
7:C:191:TYR:HE2	7:C:216:GLU:HA	1.83	0.43
14:LF:39:ARG:HG2	14:LF:39:ARG:NH1	2.34	0.43
16:LH:35:GLN:OE1	16:LH:35:GLN:HA	2.18	0.43
27:LS:76:GLY:C	27:LS:77:ILE:HD13	2.43	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:LU:84:LYS:HE2	29:LU:88:LYS:HE3	2.00	0.43
32:LX:87:LYS:HG2	32:LX:91:GLU:OE2	2.18	0.43
35:La:59:ARG:HH22	49:Lo:38:GLN:NE2	2.16	0.43
38:Ld:12:ILE:HG12	38:Ld:85:ARG:HH22	1.84	0.43
54:SA:147:ILE:HG23	54:SA:161:VAL:HB	1.99	0.43
56:SC:78:ASP:OD1	56:SC:78:ASP:N	2.46	0.43
62:SI:37:ARG:HG2	62:SI:37:ARG:NH1	2.33	0.43
67:SN:103:GLU:HA	67:SN:106:ARG:HH12	1.83	0.43
72:SS:127:HIS:CG	72:SS:133:VAL:HG11	2.53	0.43
1:1:491:C:H2'	1:1:492:A:C8	2.54	0.43
1:1:1668:U:H2'	1:1:1669:U:C6	2.53	0.43
1:1:2462:U:H2'	1:1:2463:A:H4'	2.00	0.43
2:2:826:U:O4	2:2:827:A:N6	2.52	0.43
5:A:67:SER:HB3	5:A:83:TRP:HE1	1.84	0.43
5:A:159:ASN:HA	5:A:160:PRO:HD3	1.84	0.43
7:C:126:ARG:NE	7:C:130:LEU:HD21	2.29	0.43
7:C:427:VAL:O	7:C:431:VAL:HG23	2.18	0.43
18:LJ:115:ILE:O	18:LJ:115:ILE:HG22	2.18	0.43
20:LL:189:ARG:O	20:LL:193:ARG:HG3	2.18	0.43
22:LN:66:VAL:HG12	22:LN:67:ARG:N	2.34	0.43
27:LS:81:TYR:CE1	27:LS:90:MET:HE3	2.52	0.43
58:SE:141:THR:HG23	58:SE:143:ASP:H	1.84	0.43
58:SE:153:LEU:HD23	60:SG:218:ARG:HH12	1.83	0.43
58:SE:211:LYS:HD3	58:SE:212:ASP:O	2.19	0.43
59:SF:171:PHE:CD2	59:SF:172:ARG:HG3	2.53	0.43
59:SF:173:ASN:OD1	59:SF:174:VAL:N	2.52	0.43
63:SJ:108:GLN:HE22	63:SJ:124:ARG:HG3	1.83	0.43
68:SO:112:GLN:NE2	80:Sa:45:VAL:HG12	2.30	0.43
72:SS:117:LYS:NZ	72:SS:125:LEU:HD23	2.32	0.43
77:SX:62:LYS:HG2	77:SX:116:ASP:O	2.18	0.43
1:1:96:A:H5''	35:La:34:MET:CB	2.48	0.43
1:1:1643:C:H2'	1:1:1644:G:H8	1.83	0.43
1:1:1741:C:H1'	1:1:1743:U:OP1	2.19	0.43
1:1:1769:G:H2'	1:1:1770:U:H6	1.83	0.43
2:2:16:G:H21	2:2:1135:A:H62	1.65	0.43
2:2:331:U:H2'	2:2:332:U:H6	1.84	0.43
2:2:1143:G:H2'	2:2:1144:A:C8	2.53	0.43
2:2:1217:C:H2'	2:2:1218:A:C8	2.54	0.43
5:A:107:ASP:OD1	5:A:107:ASP:N	2.50	0.43
7:C:60:SER:HB3	8:D:416:ALA:HB3	2.01	0.43
7:C:296:ARG:HG2	7:C:296:ARG:H	1.63	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:D:453:ARG:HA	8:D:551:ILE:O	2.19	0.43
11:LC:10:PHE:CZ	11:LC:147:PRO:HB2	2.53	0.43
22:LN:68:ARG:HD2	22:LN:128:LYS:HD2	2.00	0.43
26:LR:152:GLU:OE1	26:LR:152:GLU:N	2.50	0.43
26:LR:170:ARG:HA	26:LR:170:ARG:NE	2.34	0.43
30:LV:40:ALA:O	30:LV:60:VAL:HG23	2.18	0.43
34:LZ:114:LYS:HE3	34:LZ:118:GLU:OE2	2.19	0.43
55:SB:11:LYS:HZ2	55:SB:17:LYS:HA	1.84	0.43
58:SE:52:LEU:HD11	58:SE:99:PHE:HE2	1.83	0.43
58:SE:145:ARG:HA	58:SE:145:ARG:HH11	1.84	0.43
62:SI:36:THR:HG22	62:SI:57:ALA:O	2.17	0.43
71:SR:20:TYR:CE2	71:SR:38:ILE:HD11	2.54	0.43
73:ST:131:ARG:HH21	73:ST:135:ARG:HH21	1.67	0.43
77:SX:37:ALA:HA	77:SX:41:SER:HB2	2.00	0.43
81:Sb:2:VAL:O	81:Sb:3:LEU:HB2	2.17	0.43
1:1:1000:G:N2	1:1:1017:U:O2	2.37	0.43
1:1:2544:G:H2'	1:1:2544:G:N3	2.33	0.43
1:1:3007:A:C6	10:LB:75:ALA:HB2	2.54	0.43
2:2:487:U:H2'	2:2:488:C:C6	2.54	0.43
2:2:1084:A:H2'	2:2:1085:A:C8	2.53	0.43
2:2:1614:C:H1'	2:2:1615:C:H5	1.84	0.43
4:4:142:C:H2'	4:4:143:U:C6	2.53	0.43
5:A:245:ARG:HB2	5:A:247:TRP:CZ3	2.54	0.43
8:D:241:HIS:ND1	8:D:243:ILE:HB	2.34	0.43
9:LA:5:ILE:HG22	9:LA:208:ASP:O	2.19	0.43
15:LG:123:LYS:HB2	15:LG:123:LYS:HE2	1.81	0.43
16:LH:174:ILE:HD12	47:Lm:90:ASN:HB2	2.00	0.43
21:LM:102:LYS:O	21:LM:105:GLN:HG3	2.19	0.43
31:LW:111:GLU:HA	31:LW:114:GLU:OE1	2.19	0.43
42:Lh:18:GLU:HG2	42:Lh:19:GLU:N	2.34	0.43
42:Lh:89:LEU:HB3	42:Lh:93:LEU:HD23	2.00	0.43
55:SB:132:HIS:HB3	55:SB:219:LYS:NZ	2.34	0.43
56:SC:82:PRO:O	56:SC:83:LYS:HG2	2.19	0.43
68:SO:145:ARG:HG3	80:Sa:29:CYS:SG	2.58	0.43
72:SS:132:ARG:HD3	72:SS:133:VAL:N	2.34	0.43
79:SZ:29:VAL:O	79:SZ:64:LEU:HD11	2.18	0.43
81:Sb:17:ARG:NH1	81:Sb:17:ARG:HG2	2.33	0.43
85:Sf:80:ARG:C	85:Sf:81:LYS:HD3	2.43	0.43
1:1:2512:U:C2	9:LA:89:TYR:HE2	2.37	0.43
1:1:3062:U:H2'	1:1:3063:A:H8	1.83	0.43
2:2:301:U:H2'	2:2:302:C:C6	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:1398:G:H2'	2:2:1399:C:C6	2.54	0.43
3:3:64:A:H8	17:LI:204:GLY:O	2.02	0.43
7:C:380:SER:O	7:C:383:THR:HG22	2.18	0.43
57:SD:67:ARG:NH1	57:SD:70:ARG:HD2	2.34	0.43
57:SD:79:ARG:HD2	64:SK:22:VAL:CG1	2.49	0.43
59:SF:46:THR:C	59:SF:48:TYR:H	2.27	0.43
61:SH:151:ARG:HA	76:SW:51:GLU:OE1	2.19	0.43
71:SR:12:SER:O	71:SR:16:ILE:HG12	2.19	0.43
72:SS:123:ARG:O	72:SS:127:HIS:HD2	2.01	0.43
73:ST:73:VAL:O	73:ST:77:ARG:HG2	2.19	0.43
1:1:1545:G:H2'	1:1:1546:G:H8	1.84	0.43
1:1:2602:A:H5'	36:Lb:6:ASN:ND2	2.34	0.43
2:2:681:C:H2'	2:2:682:U:C6	2.54	0.43
2:2:1161:G:H2'	2:2:1162:G:C8	2.54	0.43
2:2:1260:G:H2'	2:2:1261:G:O4'	2.19	0.43
5:A:41:ILE:HD12	5:A:58:ARG:HG3	2.01	0.43
7:C:136:LYS:HE2	7:C:137:LYS:HE3	2.00	0.43
7:C:251:GLU:HG2	8:D:259:LYS:HG3	2.01	0.43
8:D:315:ARG:NE	8:D:315:ARG:HA	2.34	0.43
8:D:328:ASN:ND2	8:D:363:ASN:HD21	2.15	0.43
15:LG:121:GLU:OE1	15:LG:123:LYS:NZ	2.47	0.43
16:LH:37:ASP:O	16:LH:38:LEU:HD23	2.19	0.43
20:LL:64:LYS:HD2	35:La:69:TRP:CD1	2.54	0.43
30:LV:86:PRO:HA	30:LV:96:TYR:HB3	2.00	0.43
37:Lc:39:SER:HB2	37:Lc:41:LYS:NZ	2.34	0.43
45:Lk:71:VAL:HG13	45:Lk:71:VAL:O	2.18	0.43
70:SQ:59:LYS:O	70:SQ:93:TYR:OH	2.36	0.43
1:1:191:G:H21	1:1:212:G:H21	1.66	0.43
1:1:1300:A:O2'	1:1:1301:A:H3'	2.19	0.43
1:1:1560:U:O3'	1:1:1561:G:N2	2.41	0.43
1:1:3221:A:O2'	1:1:3222:C:H6	2.02	0.43
2:2:724:U:O2	2:2:724:U:H2'	2.19	0.43
2:2:838:U:H2'	2:2:839:U:H6	1.84	0.43
2:2:1584:G:N1	2:2:1605:U:N3	2.67	0.43
4:4:97:A:OP1	42:Lh:68:ARG:NH2	2.52	0.43
7:C:295:PHE:HA	7:C:298:GLU:OE1	2.18	0.43
10:LB:149:LEU:O	10:LB:153:LYS:HG3	2.19	0.43
12:LD:73:LYS:HA	12:LD:73:LYS:HD2	1.89	0.43
15:LG:229:VAL:HA	15:LG:232:THR:HG22	2.00	0.43
22:LN:66:VAL:HG12	22:LN:67:ARG:H	1.84	0.43
43:Li:32:LYS:NZ	43:Li:33:GLU:CD	2.76	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:Ls:64:LYS:HA	52:Ls:64:LYS:HD2	1.86	0.43
59:SF:43:ILE:HD12	59:SF:43:ILE:HA	1.93	0.43
60:SG:185:GLN:O	60:SG:188:GLN:HG2	2.19	0.43
63:SJ:76:ARG:HA	63:SJ:79:VAL:HG12	2.01	0.43
64:SK:37:ASN:O	64:SK:41:ILE:HG12	2.19	0.43
66:SM:98:GLY:O	66:SM:101:ALA:N	2.52	0.43
1:1:223:A:P	33:LY:4:ARG:HH12	2.41	0.42
1:1:250:C:H2'	1:1:251:U:C6	2.54	0.42
1:1:1117:G:O2'	1:1:2601:A:N3	2.39	0.42
2:2:14:C:H2'	2:2:15:U:C6	2.54	0.42
2:2:950:A:H5''	67:SN:94:LYS:NZ	2.34	0.42
5:A:7:LEU:HG	5:A:310:TRP:CH2	2.53	0.42
5:A:59:LEU:C	5:A:60:HIS:ND1	2.77	0.42
13:LE:64:ARG:HH22	24:LP:181:ARG:NE	2.17	0.42
13:LE:118:LYS:HD2	13:LE:121:GLU:OE2	2.19	0.42
27:LS:9:VAL:HG21	27:LS:41:PHE:HB2	2.00	0.42
29:LU:19:LYS:NZ	29:LU:78:LEU:O	2.46	0.42
33:LY:53:ASP:HB2	33:LY:108:LEU:HA	2.01	0.42
38:Ld:37:ALA:H	38:Ld:72:ILE:HG23	1.84	0.42
41:Lg:21:THR:HB	41:Lg:33:VAL:CG1	2.49	0.42
59:SF:173:ASN:ND2	59:SF:175:LYS:HG2	2.34	0.42
60:SG:30:LYS:HD3	60:SG:30:LYS:HA	1.83	0.42
60:SG:32:MET:HE2	60:SG:32:MET:HB3	1.93	0.42
78:SY:126:LYS:HD2	78:SY:127:VAL:N	2.33	0.42
1:1:528:U:C2	1:1:529:G:C8	3.07	0.42
1:1:1260:C:C2	1:1:1261:A:C8	3.06	0.42
1:1:1345:G:H2'	1:1:1346:A:C8	2.54	0.42
1:1:3152:C:N4	21:LM:102:LYS:NZ	2.68	0.42
2:2:781:G:H2'	2:2:782:C:C6	2.53	0.42
2:2:1245:C:H2'	2:2:1246:U:C6	2.54	0.42
2:2:1587:C:H2'	2:2:1588:A:C8	2.51	0.42
8:D:86:ASP:O	8:D:90:VAL:HG13	2.20	0.42
8:D:167:ALA:HA	8:D:170:ILE:HG22	2.00	0.42
8:D:256:GLU:O	8:D:260:LYS:HG3	2.19	0.42
8:D:364:PHE:HD1	8:D:368:PHE:HE1	1.66	0.42
20:LL:76:THR:N	20:LL:79:GLU:OE2	2.47	0.42
26:LR:144:ARG:HG3	26:LR:144:ARG:NH1	2.34	0.42
32:LX:63:SER:HB2	42:Lh:71:LEU:CD2	2.50	0.42
32:LX:64:ILE:HD12	32:LX:65:PRO:HD2	2.01	0.42
32:LX:76:ILE:HD13	32:LX:99:VAL:HG12	2.01	0.42
34:LZ:59:ALA:O	34:LZ:62:GLU:HG3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:Lh:37:GLN:OE1	42:Lh:37:GLN:N	2.52	0.42
46:Ll:18:LYS:HE3	46:Ll:18:LYS:HB2	1.81	0.42
52:Ls:106:LYS:O	52:Ls:106:LYS:HD3	2.19	0.42
55:SB:193:ILE:O	55:SB:197:ILE:HG12	2.20	0.42
60:SG:39:ASP:OD2	60:SG:46:LYS:HA	2.19	0.42
60:SG:187:LEU:O	60:SG:191:ARG:HG3	2.19	0.42
63:SJ:133:ARG:HD3	63:SJ:157:ALA:HA	2.01	0.42
66:SM:60:HIS:HB3	66:SM:126:TRP:CH2	2.54	0.42
72:SS:38:VAL:HG23	72:SS:42:TYR:HD2	1.84	0.42
73:ST:84:LYS:NZ	73:ST:86:ARG:HA	2.34	0.42
78:SY:112:LYS:O	78:SY:115:LYS:HG3	2.19	0.42
79:SZ:50:THR:HG22	79:SZ:53:THR:HG23	2.01	0.42
79:SZ:81:VAL:HG23	79:SZ:82:VAL:N	2.34	0.42
1:1:306:U:H2'	1:1:307:U:C6	2.54	0.42
1:1:438:C:H2'	1:1:439:C:H6	1.84	0.42
1:1:468:G:OP2	1:1:468:G:H8	2.02	0.42
1:1:2221:U:C2	1:1:2222:A:C8	3.07	0.42
1:1:2307:U:H2'	1:1:2308:A:C8	2.54	0.42
1:1:2336:A:N3	1:1:2783:G:O2'	2.40	0.42
1:1:2392:G:H2'	1:1:2393:A:C8	2.54	0.42
1:1:2468:U:H2'	1:1:2469:U:H6	1.84	0.42
1:1:2470:U:H2'	1:1:2471:U:H6	1.84	0.42
1:1:2904:G:O2'	1:1:2907:C:OP2	2.37	0.42
1:1:3129:C:OP1	40:Lf:12:LYS:NZ	2.38	0.42
2:2:481:C:H2'	2:2:482:A:H8	1.83	0.42
2:2:904:A:H2'	2:2:905:A:C8	2.54	0.42
2:2:1560:U:H2'	2:2:1561:C:H6	1.84	0.42
7:C:36:MET:O	7:C:36:MET:HE3	2.19	0.42
7:C:114:TRP:CE2	7:C:203:ARG:HD3	2.55	0.42
9:LA:44:ILE:HG12	9:LA:87:PHE:CE2	2.53	0.42
16:LH:20:ILE:HG12	21:LM:6:VAL:HG12	2.00	0.42
22:LN:9:GLU:HA	22:LN:9:GLU:OE2	2.19	0.42
27:LS:30:PHE:CE2	27:LS:103:VAL:HG21	2.54	0.42
36:Lb:36:ASP:OD1	36:Lb:37:PRO:HD2	2.19	0.42
59:SF:67:LYS:CG	59:SF:68:ARG:H	2.27	0.42
60:SG:41:LEU:HD22	60:SG:45:TRP:CD2	2.55	0.42
61:SH:95:HIS:CE1	61:SH:175:ARG:HD2	2.55	0.42
63:SJ:2:ALA:HB3	63:SJ:3:PRO:HD3	2.01	0.42
63:SJ:109:THR:O	63:SJ:113:LYS:HG2	2.19	0.42
64:SK:55:THR:HG22	64:SK:56:GLN:N	2.34	0.42
66:SM:96:GLN:NE2	66:SM:96:GLN:C	2.77	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
67:SN:99:ARG:NH2	67:SN:119:GLU:OE2	2.52	0.42
69:SP:80:LYS:HD2	69:SP:80:LYS:HA	1.83	0.42
73:ST:65:VAL:HG12	73:ST:125:ILE:HG23	2.02	0.42
74:SU:19:ILE:H	74:SU:19:ILE:HD12	1.84	0.42
1:1:211:U:H4'	33:LY:99:HIS:CD2	2.55	0.42
1:1:2207:A:O2'	9:LA:223:SER:OG	2.25	0.42
1:1:2636:G:H2'	1:1:2636:G:N3	2.34	0.42
1:1:2841:U:H2'	1:1:2842:U:C6	2.55	0.42
1:1:3134:A:C4	23:LO:116:LYS:HA	2.54	0.42
2:2:1479:A:H4'	70:SQ:71:GLY:HA2	2.01	0.42
2:2:1590:G:H5''	83:Sd:33:LYS:NZ	2.33	0.42
6:B:89:ARG:NH1	6:B:90:ARG:HB2	2.34	0.42
12:LD:284:ARG:HD2	12:LD:287:ARG:NH1	2.34	0.42
25:LQ:48:LYS:HE2	25:LQ:48:LYS:HB2	1.93	0.42
25:LQ:64:LEU:HD23	25:LQ:64:LEU:HA	1.95	0.42
25:LQ:91:SER:O	25:LQ:95:ILE:HG13	2.19	0.42
26:LR:151:ARG:O	26:LR:155:ILE:HG12	2.19	0.42
31:LW:106:LEU:O	31:LW:109:ILE:HG22	2.19	0.42
54:SA:123:LEU:HD12	54:SA:145:PRO:O	2.19	0.42
55:SB:144:LYS:HB2	55:SB:208:GLN:H	1.84	0.42
58:SE:149:TYR:N	58:SE:150:PRO:HD3	2.34	0.42
59:SF:99:ARG:HH21	79:SZ:84:HIS:CE1	2.37	0.42
69:SP:65:ILE:HD12	69:SP:97:MET:HE2	2.01	0.42
76:SW:35:VAL:O	76:SW:39:GLN:HG3	2.19	0.42
1:1:575:G:H2'	1:1:576:A:C8	2.50	0.42
1:1:948:U:H2'	1:1:949:A:C8	2.54	0.42
1:1:1080:G:H8	28:LT:128:LEU:HD11	1.85	0.42
1:1:1506:U:HO2'	32:LX:124:ASN:ND2	2.18	0.42
1:1:2503:C:H4'	1:1:2504:G:O5'	2.19	0.42
1:1:2642:U:H2'	1:1:2643:C:H6	1.83	0.42
1:1:3209:A:C5	13:LE:154:VAL:HG21	2.55	0.42
2:2:12:U:H2'	2:2:13:U:H6	1.84	0.42
2:2:447:C:H2'	2:2:448:G:C8	2.54	0.42
2:2:882:A:H2'	2:2:883:G:H8	1.84	0.42
5:A:209:SER:OG	5:A:217:MET:HE2	2.20	0.42
5:A:217:MET:HA	5:A:229:SER:OG	2.19	0.42
8:D:430:VAL:HG22	8:D:529:ILE:HD13	2.02	0.42
15:LG:153:LEU:HB3	15:LG:203:ILE:HG22	2.01	0.42
16:LH:12:VAL:HG12	16:LH:51:GLY:O	2.20	0.42
24:LP:60:MET:HE3	24:LP:60:MET:HB3	1.87	0.42
27:LS:142:GLN:HE21	27:LS:142:GLN:HB3	1.69	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:SB:70:LEU:HD11	55:SB:189:ILE:HG22	2.01	0.42
55:SB:119:THR:HB	55:SB:143:THR:CG2	2.49	0.42
60:SG:64:LYS:NZ	60:SG:83:CYS:H	2.18	0.42
62:SI:129:GLN:OE1	62:SI:132:VAL:HG11	2.19	0.42
62:SI:189:GLU:HA	62:SI:193:LEU:HB2	2.01	0.42
65:SL:116:VAL:HG23	65:SL:144:VAL:HG21	2.01	0.42
77:SX:44:GLY:H	77:SX:78:LYS:NZ	2.18	0.42
78:SY:12:THR:O	78:SY:13:ARG:HD3	2.20	0.42
1:1:714:G:N1	1:1:725:C:OP2	2.46	0.42
1:1:1016:U:H2'	1:1:1017:U:H6	1.82	0.42
1:1:2574:G:H2'	1:1:2575:C:C6	2.54	0.42
1:1:2622:G:H5''	18:LJ:143:ARG:NH1	2.35	0.42
2:2:1238:G:H4'	69:SP:86:THR:HA	2.01	0.42
2:2:1385:A:H5''	71:SR:48:ASN:ND2	2.35	0.42
2:2:1763:G:OP1	2:2:1766:C:H4'	2.18	0.42
7:C:37:ARG:NH1	8:D:447:GLU:OE1	2.46	0.42
7:C:162:PRO:HA	7:C:165:ARG:HG2	2.01	0.42
7:C:219:THR:HG22	7:C:222:GLU:HG3	2.02	0.42
8:D:422:HIS:HA	8:D:448:THR:O	2.19	0.42
12:LD:122:VAL:C	12:LD:124:GLU:H	2.25	0.42
13:LE:116:GLN:OE1	13:LE:119:ILE:HD11	2.20	0.42
14:LF:96:LYS:HB3	14:LF:139:TRP:HD1	1.85	0.42
22:LN:27:CYS:HB2	22:LN:122:ASN:ND2	2.35	0.42
34:LZ:104:SER:HA	34:LZ:107:GLU:OE1	2.20	0.42
42:Lh:54:LYS:O	42:Lh:58:ARG:HG3	2.19	0.42
57:SD:67:ARG:HH12	57:SD:70:ARG:HD2	1.84	0.42
57:SD:216:PRO:HB3	71:SR:20:TYR:HE1	1.84	0.42
69:SP:80:LYS:HZ1	69:SP:114:GLU:CD	2.26	0.42
70:SQ:40:ALA:HB2	70:SQ:48:LEU:HD11	2.02	0.42
72:SS:126:ARG:HD3	72:SS:133:VAL:HA	2.01	0.42
74:SU:66:LYS:HA	83:Sd:44:ARG:HH21	1.84	0.42
82:Sc:59:GLU:OE2	82:Sc:61:GLU:HB2	2.19	0.42
1:1:650:U:H2'	1:1:651:C:C6	2.54	0.42
1:1:2100:U:H5	1:1:2105:A:N7	2.17	0.42
1:1:2115:A:H2'	1:1:2116:U:C6	2.54	0.42
1:1:2181:G:H2'	1:1:2182:A:C8	2.54	0.42
1:1:3119:A:H2'	1:1:3120:C:C6	2.54	0.42
1:1:3163:A:H4'	1:1:3164:G:O5'	2.20	0.42
2:2:738:G:H2'	2:2:739:A:C8	2.55	0.42
2:2:1591:U:P	83:Sd:33:LYS:HZ1	2.42	0.42
2:2:1659:G:H2'	2:2:1660:C:C6	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A:161:GLN:HG2	5:A:162:ASN:N	2.35	0.42
8:D:397:GLN:O	8:D:401:ILE:HG12	2.18	0.42
9:LA:171:GLY:O	50:Lp:68:ALA:HB2	2.20	0.42
13:LE:100:ARG:HA	13:LE:100:ARG:HD3	1.87	0.42
13:LE:169:LEU:O	13:LE:173:ILE:HG13	2.20	0.42
16:LH:103:VAL:O	16:LH:103:VAL:HG13	2.18	0.42
22:LN:60:VAL:CG2	22:LN:134:LEU:HB2	2.49	0.42
27:LS:66:GLU:HG3	27:LS:98:SER:HB2	2.02	0.42
29:LU:98:ASP:CG	29:LU:99:TRP:CD1	2.97	0.42
31:LW:117:ALA:HA	31:LW:120:GLN:OE1	2.19	0.42
54:SA:61:VAL:O	54:SA:65:ARG:HG3	2.20	0.42
58:SE:94:LYS:HD2	78:SY:20:LEU:HA	2.00	0.42
64:SK:7:ASP:OD1	64:SK:8:ARG:N	2.53	0.42
65:SL:38:ARG:NH2	65:SL:58:TYR:O	2.34	0.42
85:Sf:131:PHE:C	85:Sf:132:MET:HG3	2.44	0.42
1:1:137:C:H2'	1:1:138:C:C6	2.55	0.42
1:1:462:A:H2'	1:1:463:C:C6	2.55	0.42
1:1:1476:G:O2'	46:Ll:13:LEU:HD22	2.19	0.42
1:1:1670:C:H2'	1:1:1671:U:C6	2.55	0.42
1:1:1769:G:H2'	1:1:1770:U:C6	2.55	0.42
2:2:122:G:O2'	58:SE:145:ARG:NH1	2.35	0.42
2:2:194:G:N3	2:2:195:G:C8	2.88	0.42
2:2:213:A:H3'	2:2:214:A:H5''	2.02	0.42
2:2:844:G:H2'	2:2:845:A:H8	1.84	0.42
2:2:1217:C:H2'	2:2:1218:A:H8	1.84	0.42
2:2:1477:C:HO2'	2:2:1478:C:P	2.40	0.42
8:D:341:ASP:CG	8:D:342:PRO:HD2	2.45	0.42
10:LB:95:THR:HG22	10:LB:98:GLY:O	2.19	0.42
11:LC:120:ARG:HA	11:LC:123:THR:HG22	2.01	0.42
15:LG:231:ASP:OD1	15:LG:232:THR:N	2.52	0.42
36:Lb:44:ARG:HH11	36:Lb:44:ARG:HG3	1.85	0.42
50:Lp:38:THR:HA	50:Lp:45:ASN:HA	2.01	0.42
58:SE:72:VAL:HG12	58:SE:90:ILE:HG23	2.02	0.42
71:SR:33:ARG:HD3	71:SR:33:ARG:HA	1.76	0.42
74:SU:16:VAL:HG12	74:SU:18:LYS:HD3	2.01	0.42
75:SV:85:ALA:HB1	81:Sb:6:ASP:H	1.85	0.42
78:SY:5:ASP:CG	78:SY:6:SER:H	2.24	0.42
85:Sf:108:VAL:HG23	85:Sf:114:ILE:HG12	2.00	0.42
1:1:773:U:H2'	1:1:774:A:C8	2.55	0.42
1:1:1052:C:H2'	1:1:1053:U:C6	2.54	0.42
1:1:1574:A:OP2	41:Lg:37:LYS:NZ	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2840:C:H2'	1:1:2841:U:C6	2.55	0.42
1:1:3210:U:OP1	13:LE:95:ARG:HD3	2.20	0.42
2:2:317:U:H2'	2:2:318:C:C6	2.55	0.42
2:2:727:C:H2'	2:2:728:G:C8	2.55	0.42
2:2:808:G:C6	61:SH:121:LYS:NZ	2.87	0.42
2:2:1209:G:H2'	2:2:1210:G:H8	1.85	0.42
2:2:1334:A:P	70:SQ:123:ARG:HH22	2.42	0.42
2:2:1668:G:H2'	2:2:1669:G:C8	2.55	0.42
3:3:24:A:H2'	3:3:25:A:C8	2.55	0.42
4:4:84:C:H3'	4:4:85:G:O4'	2.20	0.42
4:4:84:C:C5	4:4:85:G:H1'	2.55	0.42
5:A:248:LEU:HD22	5:A:259:PHE:HD2	1.85	0.42
7:C:81:ASP:OD1	7:C:81:ASP:N	2.53	0.42
7:C:200:ASN:C	7:C:200:ASN:HD22	2.28	0.42
8:D:71:ASN:HB2	8:D:74:ASN:HB2	2.02	0.42
10:LB:292:GLU:OE1	10:LB:292:GLU:N	2.50	0.42
12:LD:52:VAL:HG12	12:LD:150:ASP:HB3	2.01	0.42
12:LD:126:ASN:OD1	12:LD:127:GLY:N	2.52	0.42
16:LH:91:ARG:HD2	16:LH:145:GLU:OE2	2.20	0.42
28:LT:24:GLN:OE1	28:LT:25:ILE:N	2.53	0.42
32:LX:51:LEU:HD23	32:LX:51:LEU:H	1.85	0.42
41:Lg:16:THR:O	41:Lg:18:SER:N	2.53	0.42
58:SE:73:ASP:HA	58:SE:164:LEU:HD11	2.01	0.42
58:SE:149:TYR:HD2	60:SG:211:TYR:CG	2.38	0.42
61:SH:140:VAL:HG12	61:SH:179:TYR:CE2	2.55	0.42
63:SJ:74:LEU:O	63:SJ:78:LEU:HD23	2.20	0.42
69:SP:42:ARG:HH22	69:SP:53:ILE:C	2.27	0.42
79:SZ:47:ARG:C	79:SZ:48:LEU:HD22	2.45	0.42
1:1:441:G:H2'	1:1:442:G:H8	1.85	0.42
1:1:882:G:H1'	1:1:1569:A:N6	2.35	0.42
1:1:1059:C:H2'	1:1:1060:U:H6	1.83	0.42
1:1:2063:A:H5'	26:LR:71:ARG:HH22	1.84	0.42
2:2:327:G:H2'	2:2:328:G:C8	2.55	0.42
2:2:336:C:H2'	2:2:337:A:H8	1.85	0.42
2:2:478:A:H2'	2:2:479:U:H6	1.84	0.42
2:2:1333:A:O2'	70:SQ:123:ARG:NH2	2.53	0.42
5:A:219:TRP:CH2	5:A:226:HIS:HB2	2.54	0.42
7:C:296:ARG:NH1	29:LU:118:VAL:HG11	2.20	0.42
8:D:222:LEU:HD13	8:D:231:ILE:HA	2.02	0.42
11:LC:54:SER:HB3	11:LC:57:ALA:HB2	2.02	0.42
34:LZ:60:ARG:O	34:LZ:64:ARG:HG3	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:Lq:139:ARG:HB3	51:Lq:140:ARG:HH22	1.85	0.42
54:SA:15:ALA:O	54:SA:18:GLU:HB3	2.20	0.42
58:SE:185:GLY:N	58:SE:189:MET:HE1	2.35	0.42
59:SF:50:GLN:HE21	59:SF:50:GLN:HB2	1.69	0.42
59:SF:57:ILE:HG13	59:SF:58:PRO:HD2	2.01	0.42
59:SF:110:LEU:HD23	59:SF:110:LEU:HA	1.77	0.42
63:SJ:123:ALA:O	63:SJ:127:ILE:HG13	2.20	0.42
64:SK:41:ILE:HG13	64:SK:42:LYS:N	2.35	0.42
67:SN:129:TYR:HA	67:SN:132:VAL:HG12	2.02	0.42
68:SO:37:ASN:O	68:SO:67:GLU:HG3	2.19	0.42
70:SQ:50:GLU:CD	70:SQ:51:PRO:HD3	2.44	0.42
72:SS:65:GLU:HA	72:SS:68:ARG:HG2	2.01	0.42
73:ST:116:LYS:CE	73:ST:123:ARG:HE	2.29	0.42
1:1:1319:C:H2'	1:1:1320:G:H8	1.85	0.41
1:1:2141:A:H5''	9:LA:129:THR:HG21	2.02	0.41
1:1:2242:A:N7	1:1:2251:G:C8	2.88	0.41
2:2:78:C:H1'	60:SG:177:ARG:NE	2.35	0.41
2:2:293:U:H2'	2:2:294:U:H6	1.84	0.41
2:2:391:C:H4'	60:SG:92:ARG:HH12	1.84	0.41
2:2:1710:G:H2'	2:2:1711:G:C1'	2.48	0.41
5:A:185:GLN:HG2	5:A:186:THR:N	2.35	0.41
7:C:193:LEU:HA	7:C:196:LYS:NZ	2.35	0.41
7:C:294:ARG:O	7:C:298:GLU:OE1	2.38	0.41
12:LD:33:ARG:HG2	28:LT:27:LEU:HD21	2.02	0.41
17:LI:59:GLN:HB3	17:LI:126:VAL:HG21	2.02	0.41
23:LO:35:VAL:HG22	23:LO:105:LYS:HB2	2.02	0.41
26:LR:84:THR:O	26:LR:88:ARG:HG3	2.19	0.41
27:LS:10:ILE:HA	27:LS:25:TYR:O	2.19	0.41
45:Lk:38:VAL:O	45:Lk:44:LEU:HD12	2.20	0.41
54:SA:52:ASN:ND2	54:SA:55:LYS:HE3	2.34	0.41
54:SA:167:ASN:C	54:SA:168:LYS:HD2	2.45	0.41
57:SD:75:LEU:HD22	64:SK:20:VAL:HG21	2.02	0.41
59:SF:17:PRO:HB2	59:SF:19:GLU:HG2	2.02	0.41
60:SG:57:ASP:HA	60:SG:106:LEU:HA	2.02	0.41
60:SG:175:ALA:HA	60:SG:176:PRO:HD3	1.69	0.41
85:Sf:140:TYR:HA	85:Sf:146:LEU:O	2.20	0.41
1:1:2577:G:O2'	1:1:2824:U:OP1	2.33	0.41
2:2:324:C:H2'	2:2:325:U:C6	2.55	0.41
2:2:607:G:C8	2:2:611:A:H1'	2.56	0.41
2:2:654:U:O2	2:2:672:C:H1'	2.20	0.41
2:2:807:A:C6	2:2:808:G:C6	3.08	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:951:G:H2'	2:2:952:G:H8	1.85	0.41
2:2:1167:G:C2	2:2:1168:A:C8	3.07	0.41
2:2:1564:C:H4'	2:2:1565:A:O5'	2.19	0.41
3:3:75:A:N3	27:LS:50:LYS:NZ	2.66	0.41
5:A:64:HIS:CG	5:A:65:ILE:H	2.39	0.41
7:C:297:GLN:HE22	29:LU:32:LYS:C	2.28	0.41
12:LD:41:LYS:HD3	12:LD:41:LYS:HA	1.86	0.41
17:LI:78:LYS:HE2	17:LI:79:TYR:CE2	2.55	0.41
22:LN:172:ARG:HB2	22:LN:174:LEU:HD13	2.02	0.41
26:LR:181:ARG:HH12	26:LR:184:LEU:HD13	1.85	0.41
50:Lp:89:ILE:HG13	50:Lp:90:THR:N	2.35	0.41
54:SA:187:LEU:HD12	54:SA:188:ARG:HG3	2.02	0.41
55:SB:65:ILE:HA	55:SB:86:LEU:O	2.20	0.41
58:SE:52:LEU:HB3	58:SE:54:TYR:CD2	2.55	0.41
58:SE:66:MET:HE3	58:SE:66:MET:HA	2.03	0.41
61:SH:47:LEU:HD12	61:SH:76:PHE:CD2	2.54	0.41
63:SJ:171:ARG:CZ	63:SJ:171:ARG:HA	2.50	0.41
69:SP:126:GLU:OE2	72:SS:121:ALA:HB1	2.20	0.41
1:1:372:C:H2'	1:1:373:U:C6	2.55	0.41
1:1:799:A:H8	44:Lj:15:THR:HG1	1.61	0.41
1:1:1237:C:H2'	1:1:1238:C:C6	2.56	0.41
1:1:2642:U:H1'	18:LJ:129:TYR:CE2	2.55	0.41
1:1:2648:A:H2'	1:1:2648:A:N3	2.35	0.41
1:1:3111:C:C4	1:1:3113:A:H1'	2.56	0.41
1:1:3145:C:C2	23:LO:178:ARG:NH2	2.88	0.41
2:2:216:A:H2'	2:2:217:A:C8	2.55	0.41
2:2:403:U:H2'	2:2:404:A:C8	2.53	0.41
2:2:443:A:N1	2:2:458:G:O2'	2.46	0.41
2:2:484:G:H2'	2:2:485:G:H8	1.85	0.41
2:2:1703:C:H2'	2:2:1704:A:H8	1.83	0.41
2:2:1780:C:H2'	2:2:1781:U:C6	2.55	0.41
7:C:200:ASN:HB3	7:C:201:GLU:OE2	2.20	0.41
7:C:395:ILE:HA	7:C:398:ILE:HG22	2.02	0.41
7:C:406:LEU:HD12	7:C:409:LYS:HB2	2.02	0.41
8:D:271:PRO:HA	8:D:274:LEU:HG	2.01	0.41
11:LC:304:LYS:HA	14:LF:32:ARG:NH2	2.34	0.41
12:LD:265:LYS:HB2	12:LD:270:TRP:CE2	2.55	0.41
13:LE:9:THR:O	13:LE:18:PRO:HD2	2.20	0.41
13:LE:163:LYS:HB3	13:LE:163:LYS:HE3	1.84	0.41
14:LF:169:LEU:HD23	14:LF:175:ILE:HD11	2.01	0.41
15:LG:183:ILE:HG21	15:LG:189:LEU:HD21	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:LH:113:GLU:OE1	16:LH:113:GLU:N	2.53	0.41
16:LH:154:GLU:HG2	16:LH:155:ALA:N	2.36	0.41
17:LI:56:GLU:HB2	17:LI:58:GLU:OE2	2.20	0.41
25:LQ:45:LYS:NZ	25:LQ:45:LYS:HB2	2.35	0.41
25:LQ:54:LEU:O	25:LQ:58:VAL:HG23	2.19	0.41
25:LQ:76:VAL:O	25:LQ:80:LEU:HD23	2.20	0.41
28:LT:107:ARG:HH12	28:LT:108:ARG:HA	1.86	0.41
31:LW:93:ARG:NH2	60:SG:156:TYR:HA	2.34	0.41
35:La:6:SER:OG	35:La:8:THR:HG22	2.20	0.41
52:Ls:51:VAL:HG12	52:Ls:87:VAL:HG13	2.02	0.41
59:SF:98:VAL:O	59:SF:101:VAL:HG12	2.19	0.41
60:SG:137:ARG:O	60:SG:141:ILE:HG12	2.20	0.41
61:SH:154:GLU:HA	76:SW:42:GLN:NE2	2.32	0.41
1:1:1469:G:N2	41:Lg:7:THR:HG22	2.32	0.41
1:1:1610:G:H1	1:1:1792:G:H2'	1.85	0.41
1:1:3216:U:C4	40:Lf:66:ILE:HD11	2.55	0.41
2:2:732:A:H3'	2:2:733:A:H8	1.85	0.41
2:2:1028:A:P	80:Sa:3:LYS:HZ3	2.39	0.41
2:2:1245:C:H2'	2:2:1246:U:H6	1.85	0.41
2:2:1462:G:H2'	2:2:1463:C:C6	2.55	0.41
8:D:27:ILE:HG13	8:D:38:ILE:HB	2.02	0.41
10:LB:359:TRP:CB	31:LW:1:MET:HE1	2.49	0.41
18:LJ:85:LEU:HA	18:LJ:85:LEU:HD23	1.79	0.41
33:LY:110:LEU:HD23	33:LY:110:LEU:HA	1.94	0.41
36:Lb:33:LYS:HE3	36:Lb:33:LYS:HB3	1.78	0.41
36:Lb:60:GLY:H	36:Lb:62:ARG:HH12	1.69	0.41
38:Ld:108:ASN:HA	38:Ld:109:PRO:HD3	1.88	0.41
54:SA:82:ARG:HD3	54:SA:131:THR:HG21	2.02	0.41
56:SC:81:LEU:O	56:SC:84:LEU:HD23	2.19	0.41
57:SD:102:VAL:O	57:SD:106:GLU:OE1	2.37	0.41
59:SF:184:GLU:HG2	59:SF:185:LEU:HD22	2.02	0.41
66:SM:61:MET:HE3	66:SM:123:VAL:HG22	2.01	0.41
66:SM:63:VAL:HA	66:SM:89:ILE:O	2.20	0.41
67:SN:83:ASP:OD1	67:SN:84:ILE:N	2.53	0.41
70:SQ:127:LYS:HB2	70:SQ:130:GLY:O	2.19	0.41
72:SS:25:LYS:HA	79:SZ:29:VAL:HG11	2.02	0.41
75:SV:3:ASN:OD1	75:SV:6:GLY:N	2.50	0.41
78:SY:42:GLU:HA	78:SY:45:GLU:CG	2.49	0.41
80:Sa:101:VAL:HG12	80:Sa:104:ASN:H	1.86	0.41
83:Sd:21:CYS:SG	83:Sd:24:CYS:CB	3.04	0.41
1:1:8:C:H2'	1:1:9:C:H6	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:254:U:H2'	1:1:255:U:O4'	2.20	0.41
1:1:438:C:H2'	1:1:439:C:C6	2.56	0.41
1:1:1152:A:H4'	14:LF:224:LYS:HE2	2.02	0.41
2:2:816:C:O2'	2:2:817:G:H5'	2.20	0.41
2:2:1005:C:H5'	68:SO:150:LEU:HD12	2.03	0.41
2:2:1606:G:C3'	59:SF:94:LYS:HZ3	2.33	0.41
2:2:1612:G:H2'	2:2:1613:U:C6	2.56	0.41
3:3:111:G:H2'	3:3:112:U:C6	2.54	0.41
7:C:37:ARG:HH22	8:D:447:GLU:CB	2.27	0.41
7:C:158:ILE:HG13	7:C:159:LEU:HG	2.02	0.41
7:C:328:GLU:OE2	7:C:332:ARG:NE	2.49	0.41
7:C:358:LYS:O	7:C:362:ARG:HD3	2.21	0.41
31:LW:47:ARG:NH1	31:LW:47:ARG:HB2	2.36	0.41
40:Lf:29:THR:HG22	40:Lf:86:LYS:HZ3	1.86	0.41
41:Lg:20:ARG:HG3	41:Lg:20:ARG:NH1	2.35	0.41
42:Lh:71:LEU:HD12	42:Lh:71:LEU:HA	1.79	0.41
45:Lk:14:ILE:O	45:Lk:17:ARG:HG3	2.20	0.41
56:SC:43:TRP:CZ3	56:SC:73:GLU:OE1	2.74	0.41
58:SE:68:ARG:HB3	58:SE:76:VAL:HG21	2.01	0.41
59:SF:77:ILE:O	59:SF:81:THR:HG23	2.19	0.41
60:SG:185:GLN:HA	60:SG:188:GLN:CD	2.45	0.41
63:SJ:46:THR:O	63:SJ:50:ILE:HG13	2.21	0.41
70:SQ:89:ILE:HD11	70:SQ:93:TYR:CZ	2.56	0.41
74:SU:30:SER:O	74:SU:33:LYS:HG3	2.19	0.41
76:SW:52:GLU:HG2	76:SW:52:GLU:O	2.20	0.41
1:1:48:C:OP2	1:1:49:A:O2'	2.25	0.41
1:1:441:G:H2'	1:1:442:G:C8	2.55	0.41
1:1:1218:U:N3	1:1:1220:G:O4'	2.54	0.41
1:1:1587:U:O2'	1:1:1588:C:P	2.78	0.41
1:1:2221:U:H2'	1:1:2222:A:H8	1.85	0.41
1:1:2577:G:N7	17:LI:115:MET:HE1	2.36	0.41
2:2:539:A:H2'	2:2:539:A:N3	2.35	0.41
2:2:698:G:H2'	2:2:699:A:C8	2.56	0.41
2:2:723:G:C4	2:2:724:U:H1'	2.56	0.41
2:2:1194:C:P	70:SQ:135:ARG:HH22	2.44	0.41
7:C:154:LYS:HA	7:C:157:GLU:CD	2.45	0.41
11:LC:100:MET:HE3	11:LC:100:MET:HB2	1.92	0.41
14:LF:62:ARG:HA	14:LF:65:GLU:OE1	2.20	0.41
17:LI:19:LYS:HE3	17:LI:19:LYS:HB2	1.85	0.41
17:LI:140:THR:OG1	17:LI:141:ARG:N	2.51	0.41
24:LP:91:LEU:HD23	24:LP:91:LEU:HA	1.88	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:LS:77:ILE:HD12	27:LS:126:VAL:HG22	2.02	0.41
27:LS:137:ARG:O	27:LS:141:LYS:HG3	2.21	0.41
33:LY:85:THR:HG23	33:LY:93:THR:HB	2.02	0.41
54:SA:16:ASP:O	54:SA:20:LEU:HD23	2.20	0.41
56:SC:77:VAL:HG21	56:SC:141:LYS:HB3	2.03	0.41
56:SC:114:ASP:OD2	56:SC:118:HIS:ND1	2.53	0.41
56:SC:150:GLY:N	56:SC:161:SER:O	2.48	0.41
57:SD:223:VAL:HG22	57:SD:225:PRO:HD2	2.02	0.41
58:SE:9:GLN:OE1	58:SE:28:ALA:HB3	2.20	0.41
58:SE:140:VAL:HA	58:SE:145:ARG:O	2.21	0.41
58:SE:186:GLY:O	58:SE:189:MET:HE3	2.20	0.41
60:SG:198:ARG:HA	60:SG:201:GLN:OE1	2.21	0.41
62:SI:63:GLY:HA3	62:SI:183:ALA:O	2.21	0.41
64:SK:10:ALA:O	64:SK:13:GLU:HG3	2.21	0.41
73:ST:5:VAL:HG23	73:ST:137:ALA:HB1	2.00	0.41
79:SZ:28:SER:OG	79:SZ:30:ILE:O	2.37	0.41
82:Sc:39:ARG:NE	82:Sc:39:ARG:HA	2.35	0.41
1:1:147:A:OP2	22:LN:147:ARG:NH2	2.52	0.41
1:1:2370:C:H2'	1:1:2371:U:C6	2.55	0.41
1:1:2945:U:C2	1:1:2946:A:C8	3.09	0.41
2:2:503:A:H2'	2:2:504:U:H6	1.86	0.41
2:2:1188:U:O2'	2:2:1189:C:O4'	2.29	0.41
2:2:1362:C:H2'	2:2:1363:A:C8	2.56	0.41
2:2:1477:C:H4'	2:2:1478:C:OP1	2.19	0.41
2:2:1531:U:O2'	2:2:1532:G:OP2	2.30	0.41
4:4:63:G:H22	4:4:97:A:H2	1.68	0.41
7:C:154:LYS:HA	7:C:157:GLU:OE2	2.21	0.41
11:LC:28:SER:O	51:Lq:3:ASN:ND2	2.54	0.41
11:LC:212:VAL:O	11:LC:258:THR:HG23	2.21	0.41
21:LM:13:ARG:HH22	27:LS:149:SER:C	2.29	0.41
27:LS:8:GLN:HG2	27:LS:62:ASN:HB2	2.03	0.41
62:SI:125:ARG:NH1	62:SI:131:GLN:H	2.19	0.41
64:SK:57:PHE:CZ	64:SK:60:GLN:HA	2.55	0.41
74:SU:17:HIS:ND1	74:SU:94:THR:OG1	2.53	0.41
78:SY:23:ARG:NE	78:SY:25:GLN:HE21	2.04	0.41
1:1:1071:U:C2	1:1:1072:G:C8	3.09	0.41
1:1:3079:U:H4'	1:1:3080:A:OP1	2.21	0.41
2:2:366:U:O2'	2:2:368:G:OP2	2.38	0.41
2:2:508:A:C5'	63:SJ:171:ARG:HD3	2.43	0.41
2:2:764:G:H2'	2:2:764:G:N3	2.36	0.41
2:2:1395:C:O2	71:SR:67:ARG:NH2	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:1413:A:O3'	70:SQ:127:LYS:NZ	2.51	0.41
5:A:85:LYS:HE3	5:A:105:THR:C	2.46	0.41
24:LP:75:GLN:NE2	24:LP:76:TRP:CE2	2.85	0.41
31:LW:102:ASN:ND2	31:LW:105:ARG:HH22	2.16	0.41
41:Lg:26:THR:HG22	41:Lg:30:GLN:H	1.85	0.41
46:Ll:15:LYS:HA	46:Ll:15:LYS:HD2	1.84	0.41
52:Ls:19:LEU:HD12	52:Ls:20:GLU:N	2.35	0.41
60:SG:105:ASP:OD2	60:SG:106:LEU:N	2.53	0.41
67:SN:3:ARG:HG2	67:SN:3:ARG:HH11	1.85	0.41
68:SO:43:VAL:HG13	68:SO:52:ILE:HB	2.02	0.41
68:SO:74:MET:O	68:SO:78:GLN:HG2	2.20	0.41
72:SS:41:ARG:NH1	73:ST:39:LYS:HD3	2.36	0.41
79:SZ:67:LYS:HE2	79:SZ:70:LYS:HZ3	1.85	0.41
83:Sd:41:GLN:H	83:Sd:41:GLN:CD	2.27	0.41
1:1:175:C:H2'	1:1:176:C:C6	2.56	0.41
1:1:294:G:H2'	1:1:295:A:C8	2.56	0.41
1:1:305:C:H2'	1:1:306:U:C6	2.56	0.41
1:1:533:C:H2'	1:1:534:C:H6	1.85	0.41
1:1:773:U:H2'	1:1:774:A:H8	1.85	0.41
1:1:962:U:H2'	1:1:963:U:C6	2.56	0.41
1:1:1442:U:C1'	38:Ld:64:ASN:HD22	2.33	0.41
1:1:1454:U:H2'	1:1:1455:G:H8	1.85	0.41
1:1:1782:C:H5''	48:Lr:2:ARG:NH1	2.36	0.41
1:1:2058:A:H2'	1:1:2059:A:H8	1.85	0.41
1:1:2920:G:H2'	1:1:2921:U:C6	2.56	0.41
2:2:185:A:H2'	2:2:186:C:O4'	2.20	0.41
2:2:235:U:OP2	2:2:832:G:O2'	2.31	0.41
2:2:414:A:H5'	2:2:415:G:C4	2.56	0.41
2:2:550:G:OP2	2:2:551:C:O2'	2.30	0.41
2:2:599:U:H2'	2:2:600:U:C6	2.55	0.41
2:2:843:G:H2'	2:2:844:G:H8	1.86	0.41
2:2:1001:A:H1'	2:2:1003:A:N7	2.35	0.41
2:2:1040:G:H2'	2:2:1041:A:H8	1.86	0.41
2:2:1172:U:OP2	72:SS:137:HIS:ND1	2.54	0.41
2:2:1467:A:H5'	59:SF:171:PHE:HE2	1.86	0.41
2:2:1486:A:H2'	2:2:1487:C:H4'	2.03	0.41
2:2:1533:C:H5''	2:2:1534:U:OP1	2.21	0.41
3:3:24:A:H2'	3:3:25:A:H8	1.86	0.41
5:A:23:THR:HG21	5:A:292:SER:HA	2.02	0.41
5:A:25:MET:HE2	5:A:25:MET:N	2.36	0.41
5:A:79:LEU:HD21	5:A:87:LEU:HD21	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A:195:ILE:HA	5:A:211:GLY:HA3	2.03	0.41
7:C:79:ASP:OD1	7:C:123:ARG:NH2	2.50	0.41
7:C:196:LYS:O	7:C:199:GLU:HG3	2.21	0.41
7:C:391:VAL:O	7:C:395:ILE:HG13	2.20	0.41
10:LB:234:TRP:CD1	10:LB:266:ALA:HB1	2.55	0.41
12:LD:33:ARG:O	12:LD:37:ILE:HG12	2.21	0.41
16:LH:40:HIS:CD2	16:LH:40:HIS:H	2.39	0.41
29:LU:35:ASP:OD2	29:LU:37:SER:OG	2.33	0.41
29:LU:42:PHE:O	29:LU:46:ARG:HG2	2.20	0.41
29:LU:52:ARG:NH1	29:LU:55:ASN:HA	2.36	0.41
30:LV:25:MET:HE2	30:LV:102:GLY:HA3	2.03	0.41
34:LZ:49:PRO:HD3	34:LZ:67:ILE:HG13	2.02	0.41
44:Lj:39:TYR:CB	44:Lj:40:PRO:HD3	2.49	0.41
46:Ll:28:ARG:NH1	46:Ll:36:ARG:O	2.53	0.41
52:Ls:189:GLN:OE1	52:Ls:193:GLN:N	2.52	0.41
54:SA:37:GLN:N	54:SA:38:PRO:HD2	2.36	0.41
55:SB:32:ILE:HD11	55:SB:46:THR:HB	2.02	0.41
55:SB:165:ARG:O	55:SB:169:VAL:HG23	2.21	0.41
57:SD:7:GLN:HE21	57:SD:7:GLN:HB3	1.76	0.41
58:SE:31:PRO:HA	58:SE:81:THR:HB	2.02	0.41
59:SF:43:ILE:HG22	82:Sc:10:PHE:CE2	2.56	0.41
59:SF:63:ARG:HH12	70:SQ:122:ARG:HD2	1.85	0.41
60:SG:64:LYS:O	60:SG:100:CYS:HB3	2.21	0.41
60:SG:163:GLN:CB	60:SG:171:PRO:HB3	2.51	0.41
60:SG:167:GLU:OE1	60:SG:167:GLU:N	2.53	0.41
62:SI:81:VAL:HG22	62:SI:94:ASN:OD1	2.20	0.41
65:SL:79:ARG:CZ	65:SL:127:MET:HE3	2.51	0.41
66:SM:80:LEU:HA	66:SM:83:GLU:CD	2.46	0.41
67:SN:54:LEU:HD13	67:SN:60:ILE:HB	2.03	0.41
68:SO:61:VAL:HG22	68:SO:62:LYS:N	2.36	0.41
68:SO:144:GLY:O	80:Sa:22:ARG:NH2	2.54	0.41
69:SP:60:ARG:HH21	69:SP:88:LEU:HD23	1.86	0.41
69:SP:124:LEU:HD23	69:SP:124:LEU:C	2.46	0.41
74:SU:35:CYS:O	74:SU:39:ILE:HG23	2.21	0.41
75:SV:71:ARG:HG2	75:SV:71:ARG:NH1	2.34	0.41
80:Sa:4:LYS:HE2	80:Sa:5:ARG:HH12	1.86	0.41
1:1:3329:C:O2'	1:1:3330:C:H5'	2.21	0.41
2:2:696:U:H2'	2:2:697:G:H8	1.86	0.41
2:2:899:G:H2'	2:2:900:G:C8	2.56	0.41
2:2:911:G:C6	55:SB:13:LYS:HD3	2.55	0.41
7:C:134:PRO:O	7:C:138:ALA:HB3	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:D:126:THR:O	8:D:130:ILE:HG12	2.21	0.41
8:D:244:ALA:O	8:D:248:VAL:HG13	2.21	0.41
11:LC:290:LEU:O	11:LC:296:ILE:HD12	2.20	0.41
13:LE:118:LYS:HA	13:LE:121:GLU:OE2	2.21	0.41
27:LS:42:TRP:CD1	27:LS:53:LYS:HD2	2.56	0.41
34:LZ:87:GLU:C	34:LZ:88:LEU:HD22	2.45	0.41
38:Ld:87:ARG:HG3	38:Ld:87:ARG:HH11	1.85	0.41
41:Lg:93:ALA:O	41:Lg:97:GLU:HG2	2.21	0.41
54:SA:36:MET:HE2	54:SA:151:ASP:O	2.21	0.41
56:SC:75:GLN:HA	56:SC:78:ASP:OD1	2.21	0.41
59:SF:143:ARG:CZ	68:SO:65:ARG:HH12	2.34	0.41
61:SH:33:LEU:H	61:SH:33:LEU:HD23	1.86	0.41
61:SH:81:GLN:O	61:SH:85:ARG:HD3	2.20	0.41
61:SH:112:ALA:O	61:SH:113:ARG:HG3	2.21	0.41
63:SJ:84:LEU:HD21	63:SJ:88:ARG:O	2.21	0.41
68:SO:25:LEU:HB2	68:SO:90:THR:OG1	2.21	0.41
69:SP:30:LEU:HG	72:SS:93:VAL:HG21	2.03	0.41
85:Sf:96:LYS:HE3	85:Sf:96:LYS:HB3	1.92	0.41
1:1:8:C:H2'	1:1:9:C:C6	2.57	0.40
1:1:424:U:H2'	1:1:425:G:C8	2.56	0.40
1:1:772:U:H2'	1:1:773:U:H6	1.85	0.40
1:1:1102:C:H2'	1:1:1103:A:H8	1.86	0.40
1:1:1298:U:H4'	1:1:1300:A:O4'	2.21	0.40
5:A:121:VAL:HG12	5:A:131:LEU:HD23	2.03	0.40
5:A:218:LEU:HD11	5:A:228:TYR:CD1	2.56	0.40
7:C:9:PRO:O	8:D:431:SER:OG	2.38	0.40
7:C:103:HIS:C	7:C:104:TYR:HD1	2.30	0.40
8:D:207:ILE:HA	8:D:347:GLU:O	2.21	0.40
8:D:207:ILE:HD12	8:D:347:GLU:O	2.21	0.40
10:LB:256:TRP:CD1	10:LB:256:TRP:C	2.99	0.40
11:LC:323:LYS:HE2	11:LC:323:LYS:HB2	1.86	0.40
12:LD:141:GLU:OE1	12:LD:141:GLU:N	2.55	0.40
17:LI:23:ASN:O	17:LI:24:ARG:HD3	2.20	0.40
23:LO:143:LEU:O	23:LO:147:VAL:HG23	2.21	0.40
24:LP:174:ARG:O	24:LP:178:VAL:HG23	2.21	0.40
34:LZ:91:LEU:O	34:LZ:91:LEU:HD12	2.21	0.40
52:Ls:21:GLU:HG3	52:Ls:22:TYR:CD1	2.56	0.40
55:SB:185:VAL:HA	55:SB:188:LEU:CD1	2.51	0.40
56:SC:169:LYS:HB2	56:SC:174:THR:HG22	2.04	0.40
57:SD:223:VAL:O	57:SD:226:MET:HE1	2.21	0.40
60:SG:167:GLU:HG2	60:SG:169:LYS:HG3	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:SK:38:LEU:H	64:SK:38:LEU:HD23	1.85	0.40
1:1:284:C:H2'	1:1:285:U:C6	2.56	0.40
1:1:373:U:H2'	1:1:374:U:C6	2.57	0.40
1:1:465:G:H2'	1:1:466:G:C8	2.56	0.40
1:1:1008:U:H2'	1:1:1009:U:H5'	2.03	0.40
1:1:1246:A:N3	1:1:1246:A:H2'	2.36	0.40
1:1:1643:C:H2'	1:1:1644:G:C8	2.56	0.40
1:1:1932:G:C6	1:1:2058:A:C6	3.10	0.40
1:1:2123:G:H2'	1:1:2124:G:C8	2.54	0.40
1:1:2207:A:O4'	9:LA:243:THR:HG21	2.21	0.40
1:1:3224:C:H4'	1:1:3225:G:OP1	2.21	0.40
1:1:3266:A:H2'	1:1:3267:G:H8	1.85	0.40
5:A:200:ILE:HG12	5:A:207:CYS:SG	2.61	0.40
6:B:89:ARG:HG2	6:B:90:ARG:N	2.36	0.40
7:C:79:ASP:O	7:C:127:LYS:NZ	2.54	0.40
7:C:79:ASP:CG	7:C:123:ARG:HH22	2.28	0.40
7:C:249:ASP:OD1	7:C:250:ASN:N	2.54	0.40
9:LA:82:MET:HE2	9:LA:82:MET:HB3	1.91	0.40
11:LC:188:SER:O	11:LC:188:SER:OG	2.38	0.40
13:LE:131:GLU:HA	13:LE:134:LYS:HZ3	1.85	0.40
16:LH:61:SER:OG	16:LH:62:ARG:N	2.55	0.40
16:LH:92:TYR:HD2	16:LH:144:ASP:OD1	2.04	0.40
21:LM:102:LYS:HA	21:LM:105:GLN:HG3	2.02	0.40
31:LW:87:LEU:HA	31:LW:90:ILE:HG12	2.03	0.40
38:Ld:18:ARG:HB2	38:Ld:20:TYR:CE1	2.57	0.40
38:Ld:59:LEU:HD12	38:Ld:63:LEU:HD23	2.03	0.40
38:Ld:83:ILE:HG12	38:Ld:101:VAL:HG12	2.02	0.40
41:Lg:16:THR:C	41:Lg:18:SER:H	2.29	0.40
54:SA:55:LYS:O	54:SA:59:LYS:HG2	2.22	0.40
54:SA:159:VAL:O	54:SA:159:VAL:HG23	2.21	0.40
57:SD:144:LYS:HE2	57:SD:182:GLN:HB2	2.03	0.40
60:SG:116:GLN:OE1	60:SG:117:GLY:N	2.52	0.40
60:SG:147:LEU:HD12	60:SG:151:ASP:CB	2.51	0.40
62:SI:188:LEU:HB2	62:SI:192:GLU:OE2	2.20	0.40
64:SK:14:TYR:HA	64:SK:17:ARG:HE	1.87	0.40
64:SK:56:GLN:HA	64:SK:56:GLN:OE1	2.21	0.40
66:SM:80:LEU:HA	66:SM:83:GLU:OE1	2.21	0.40
68:SO:123:MET:HE3	68:SO:124:LYS:N	2.35	0.40
79:SZ:37:ASP:O	79:SZ:41:LYS:HG2	2.20	0.40
83:Sd:22:ARG:NE	83:Sd:36:LEU:O	2.52	0.40
1:1:425:G:C5'	40:Lf:59:LYS:HZ1	2.35	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:426:A:OP2	40:Lf:59:LYS:NZ	2.31	0.40
1:1:439:C:H2'	1:1:440:C:H6	1.86	0.40
1:1:1267:C:H2'	1:1:1268:G:C4	2.56	0.40
1:1:1893:A:N3	1:1:2083:G:H2'	2.37	0.40
1:1:2727:U:H2'	1:1:2728:A:C8	2.54	0.40
1:1:3224:C:H2'	1:1:3225:G:C8	2.56	0.40
2:2:352:G:HO2'	2:2:353:G:P	2.41	0.40
2:2:512:A:H2'	2:2:513:G:O4'	2.21	0.40
2:2:1277:C:H2'	2:2:1278:G:H8	1.84	0.40
2:2:1334:A:O5'	70:SQ:123:ARG:NH2	2.48	0.40
7:C:177:ILE:HD11	7:C:197:VAL:HA	2.03	0.40
7:C:247:PRO:HB2	7:C:249:ASP:OD1	2.22	0.40
7:C:361:LYS:O	7:C:365:ARG:HG2	2.20	0.40
9:LA:182:ALA:HB1	9:LA:196:TRP:HH2	1.87	0.40
11:LC:146:VAL:HA	11:LC:147:PRO:HD3	1.96	0.40
18:LJ:27:SER:HB2	18:LJ:65:LYS:O	2.21	0.40
20:LL:17:HIS:HB3	20:LL:20:ARG:HH11	1.86	0.40
22:LN:99:ARG:NH1	22:LN:118:SER:O	2.55	0.40
37:Lc:19:LEU:HD23	37:Lc:101:SER:HB2	2.03	0.40
38:Ld:33:PHE:HB3	38:Ld:73:LYS:HG2	2.03	0.40
45:Lk:67:GLN:OE1	45:Lk:67:GLN:HA	2.22	0.40
52:Ls:67:MET:HB2	52:Ls:67:MET:HE2	1.84	0.40
54:SA:86:GLN:O	54:SA:90:LEU:HD23	2.20	0.40
57:SD:169:GLU:HG2	57:SD:170:PHE:N	2.37	0.40
57:SD:178:VAL:HG13	57:SD:185:LEU:HB2	2.03	0.40
59:SF:14:ASP:OD1	59:SF:15:VAL:N	2.46	0.40
59:SF:171:PHE:CE2	59:SF:172:ARG:HG3	2.56	0.40
60:SG:136:LYS:NZ	60:SG:177:ARG:HB2	2.37	0.40
60:SG:149:LYS:HE3	60:SG:149:LYS:HB3	1.83	0.40
61:SH:5:SER:OG	61:SH:28:GLY:HA2	2.22	0.40
66:SM:80:LEU:HD23	66:SM:83:GLU:OE1	2.22	0.40
66:SM:96:GLN:C	66:SM:96:GLN:HE21	2.29	0.40
72:SS:116:LEU:HD12	72:SS:119:ILE:HG21	2.03	0.40
1:1:703:A:H3'	35:La:115:LYS:HG3	2.04	0.40
1:1:1742:U:C4	1:1:1743:U:H1'	2.56	0.40
1:1:2376:A:H2'	1:1:2377:G:H8	1.86	0.40
1:1:3005:U:O2'	1:1:3006:A:H5'	2.22	0.40
1:1:3124:G:O2'	1:1:3125:U:H5'	2.21	0.40
2:2:511:G:O2'	2:2:512:A:H5'	2.22	0.40
2:2:612:G:O4'	2:2:612:G:OP1	2.40	0.40
2:2:854:A:N6	61:SH:102:ARG:HG2	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:1232:C:H2'	2:2:1233:A:C8	2.57	0.40
2:2:1244:U:OP1	85:Sf:92:LYS:HD2	2.20	0.40
7:C:194:TRP:O	7:C:197:VAL:HG22	2.21	0.40
9:LA:52:PRO:HB2	9:LA:191:VAL:HG21	2.03	0.40
10:LB:24:ARG:HH12	10:LB:26:ARG:NH2	2.19	0.40
15:LG:56:PRO:HG2	15:LG:59:ILE:HD12	2.03	0.40
20:LL:54:LEU:HD12	20:LL:54:LEU:HA	1.93	0.40
23:LO:98:ALA:O	23:LO:102:GLU:HG2	2.21	0.40
23:LO:191:VAL:HG23	23:LO:192:ASP:N	2.36	0.40
26:LR:180:LYS:HD2	26:LR:181:ARG:HH21	1.86	0.40
26:LR:180:LYS:HD3	26:LR:181:ARG:HH21	1.85	0.40
35:La:133:GLU:OE1	35:La:136:ARG:NE	2.54	0.40
43:Li:77:ARG:HG3	43:Li:77:ARG:HH11	1.86	0.40
52:Ls:144:LYS:HE3	52:Ls:144:LYS:HB2	1.89	0.40
57:SD:130:MET:HE2	57:SD:130:MET:HA	2.03	0.40
58:SE:173:ILE:HD11	58:SE:234:TRP:CZ3	2.56	0.40
61:SH:47:LEU:HD12	61:SH:76:PHE:CE2	2.55	0.40
61:SH:175:ARG:O	61:SH:178:THR:OG1	2.37	0.40
62:SI:69:SER:HB2	65:SL:24:LYS:HG3	2.02	0.40
62:SI:175:SER:OG	62:SI:176:ARG:N	2.55	0.40
63:SJ:98:LYS:NZ	63:SJ:100:GLU:H	2.18	0.40
65:SL:30:THR:O	65:SL:37:ARG:NH2	2.54	0.40
66:SM:85:LYS:HA	66:SM:85:LYS:HD3	1.88	0.40
69:SP:46:HIS:CE1	69:SP:48:ARG:HB2	2.56	0.40
71:SR:85:VAL:HA	71:SR:86:PRO:HD3	1.98	0.40
73:ST:76:LEU:HA	73:ST:79:VAL:HB	2.02	0.40
83:Sd:26:HIS:NE2	83:Sd:28:ALA:HB3	2.37	0.40
1:1:565:C:H2'	1:1:566:C:C6	2.56	0.40
1:1:1651:C:O3'	26:LR:60:ARG:NH1	2.55	0.40
1:1:2065:U:H2'	1:1:2066:U:H6	1.87	0.40
1:1:2470:U:H2'	1:1:2471:U:C6	2.57	0.40
2:2:316:U:H1'	2:2:320:A:C4	2.56	0.40
2:2:954:U:C2	2:2:955:G:C8	3.09	0.40
2:2:1232:C:H2'	2:2:1233:A:H8	1.87	0.40
5:A:193:GLY:H	5:A:213:ASP:CG	2.29	0.40
6:B:132:LEU:HD12	6:B:133:LYS:N	2.36	0.40
11:LC:135:LEU:HD23	11:LC:135:LEU:HA	1.95	0.40
16:LH:17:LYS:NZ	21:LM:3:GLU:HG3	2.34	0.40
18:LJ:61:ARG:N	18:LJ:64:GLU:OE2	2.30	0.40
21:LM:32:GLU:HG2	27:LS:72:VAL:HG11	2.04	0.40
26:LR:181:ARG:NE	26:LR:181:ARG:HA	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:Li:95:LYS:HD3	43:Li:95:LYS:HA	1.90	0.40
45:Lk:77:ARG:NH1	45:Lk:80:SER:O	2.55	0.40
54:SA:142:VAL:HG23	54:SA:144:ILE:CD1	2.52	0.40
57:SD:76:ILE:HG13	57:SD:77:GLN:N	2.36	0.40
60:SG:63:MET:HG3	60:SG:99:GLY:O	2.22	0.40
60:SG:87:ARG:O	60:SG:88:ARG:HG3	2.21	0.40
67:SN:111:SER:HA	67:SN:114:ARG:HG2	2.03	0.40
71:SR:122:VAL:HG12	71:SR:123:ASN:N	2.36	0.40
73:ST:32:PRO:HD2	73:ST:54:TRP:CH2	2.56	0.40
78:SY:26:MET:HE1	78:SY:51:TYR:HE1	1.85	0.40
80:Sa:36:ILE:O	80:Sa:36:ILE:HG13	2.21	0.40
83:Sd:38:ILE:HD11	83:Sd:43:PHE:HD1	1.86	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	A	310/316 (98%)	293 (94%)	17 (6%)	0	100	100
6	B	27/302 (9%)	26 (96%)	1 (4%)	0	100	100
7	C	442/446 (99%)	428 (97%)	14 (3%)	0	100	100
8	D	511/578 (88%)	497 (97%)	12 (2%)	2 (0%)	30	60
9	LA	250/254 (98%)	237 (95%)	12 (5%)	1 (0%)	30	60
10	LB	385/392 (98%)	363 (94%)	22 (6%)	0	100	100
11	LC	361/365 (99%)	345 (96%)	16 (4%)	0	100	100
12	LD	298/304 (98%)	290 (97%)	8 (3%)	0	100	100
13	LE	192/200 (96%)	174 (91%)	18 (9%)	0	100	100
14	LF	245/249 (98%)	238 (97%)	7 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	LG	233/262 (89%)	224 (96%)	8 (3%)	1 (0%)	30	60
16	LH	189/192 (98%)	183 (97%)	6 (3%)	0	100	100
17	LI	215/219 (98%)	199 (93%)	16 (7%)	0	100	100
18	LJ	165/173 (95%)	160 (97%)	5 (3%)	0	100	100
19	LK	153/165 (93%)	132 (86%)	19 (12%)	2 (1%)	9	35
20	LL	207/213 (97%)	200 (97%)	7 (3%)	0	100	100
21	LM	139/142 (98%)	134 (96%)	5 (4%)	0	100	100
22	LN	200/203 (98%)	192 (96%)	8 (4%)	0	100	100
23	LO	201/204 (98%)	195 (97%)	6 (3%)	0	100	100
24	LP	184/187 (98%)	175 (95%)	9 (5%)	0	100	100
25	LQ	181/213 (85%)	175 (97%)	6 (3%)	0	100	100
26	LR	182/192 (95%)	177 (97%)	5 (3%)	0	100	100
27	LS	171/174 (98%)	165 (96%)	6 (4%)	0	100	100
28	LT	156/160 (98%)	152 (97%)	4 (3%)	0	100	100
29	LU	102/127 (80%)	101 (99%)	1 (1%)	0	100	100
30	LV	133/139 (96%)	131 (98%)	2 (2%)	0	100	100
31	LW	131/161 (81%)	131 (100%)	0	0	100	100
32	LX	119/156 (76%)	113 (95%)	6 (5%)	0	100	100
33	LY	132/138 (96%)	129 (98%)	3 (2%)	0	100	100
34	LZ	133/135 (98%)	130 (98%)	3 (2%)	0	100	100
35	La	146/149 (98%)	137 (94%)	9 (6%)	0	100	100
36	Lb	60/65 (92%)	59 (98%)	1 (2%)	0	100	100
37	Lc	95/108 (88%)	95 (100%)	0	0	100	100
38	Ld	117/120 (98%)	115 (98%)	2 (2%)	0	100	100
39	Le	122/131 (93%)	118 (97%)	4 (3%)	0	100	100
40	Lf	105/109 (96%)	98 (93%)	7 (7%)	0	100	100
41	Lg	110/119 (92%)	104 (94%)	6 (6%)	0	100	100
42	Lh	120/126 (95%)	117 (98%)	3 (2%)	0	100	100
43	Li	100/110 (91%)	95 (95%)	5 (5%)	0	100	100
44	Lj	84/95 (88%)	80 (95%)	3 (4%)	1 (1%)	10	37
45	Lk	78/81 (96%)	77 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
46	Ll	48/51 (94%)	46 (96%)	2 (4%)	0	100	100
47	Lm	50/128 (39%)	50 (100%)	0	0	100	100
48	Ln	22/25 (88%)	22 (100%)	0	0	100	100
48	Lr	22/25 (88%)	22 (100%)	0	0	100	100
49	Lo	102/106 (96%)	99 (97%)	3 (3%)	0	100	100
50	Lp	89/92 (97%)	82 (92%)	7 (8%)	0	100	100
51	Lq	139/147 (95%)	135 (97%)	4 (3%)	0	100	100
52	Ls	187/312 (60%)	184 (98%)	3 (2%)	0	100	100
54	SA	206/285 (72%)	192 (93%)	14 (7%)	0	100	100
55	SB	230/255 (90%)	216 (94%)	14 (6%)	0	100	100
56	SC	214/263 (81%)	207 (97%)	7 (3%)	0	100	100
57	SD	210/254 (83%)	198 (94%)	12 (6%)	0	100	100
58	SE	259/264 (98%)	246 (95%)	13 (5%)	0	100	100
59	SF	197/212 (93%)	187 (95%)	10 (5%)	0	100	100
60	SG	230/239 (96%)	222 (96%)	8 (4%)	0	100	100
61	SH	193/203 (95%)	185 (96%)	8 (4%)	0	100	100
62	SI	199/202 (98%)	195 (98%)	4 (2%)	0	100	100
63	SJ	177/190 (93%)	172 (97%)	5 (3%)	0	100	100
64	SK	87/159 (55%)	86 (99%)	1 (1%)	0	100	100
65	SL	148/161 (92%)	145 (98%)	3 (2%)	0	100	100
66	SM	116/144 (81%)	104 (90%)	12 (10%)	0	100	100
67	SN	148/151 (98%)	146 (99%)	2 (1%)	0	100	100
68	SO	133/150 (89%)	124 (93%)	9 (7%)	0	100	100
69	SP	113/153 (74%)	106 (94%)	7 (6%)	0	100	100
70	SQ	136/143 (95%)	128 (94%)	8 (6%)	0	100	100
71	SR	126/143 (88%)	124 (98%)	2 (2%)	0	100	100
72	SS	135/156 (86%)	124 (92%)	11 (8%)	0	100	100
73	ST	140/153 (92%)	134 (96%)	6 (4%)	0	100	100
74	SU	101/116 (87%)	97 (96%)	4 (4%)	0	100	100
75	SV	84/98 (86%)	82 (98%)	2 (2%)	0	100	100
76	SW	127/130 (98%)	118 (93%)	9 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
77	SX	140/145 (97%)	132 (94%)	8 (6%)	0	100	100
78	SY	130/136 (96%)	128 (98%)	2 (2%)	0	100	100
79	SZ	67/99 (68%)	67 (100%)	0	0	100	100
80	Sa	102/119 (86%)	99 (97%)	3 (3%)	0	100	100
81	Sb	79/82 (96%)	75 (95%)	4 (5%)	0	100	100
82	Sc	59/68 (87%)	56 (95%)	3 (5%)	0	100	100
83	Sd	50/56 (89%)	48 (96%)	2 (4%)	0	100	100
84	Se	38/62 (61%)	37 (97%)	1 (3%)	0	100	100
85	Sf	71/154 (46%)	64 (90%)	7 (10%)	0	100	100
All	All	12588/14205 (89%)	12068 (96%)	513 (4%)	7 (0%)	49	75

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	D	450	VAL
19	LK	88	PRO
44	Lj	39	TYR
15	LG	165	LEU
8	D	556	ASP
19	LK	89	PRO
9	LA	196	TRP

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	
5	A	271/274 (99%)	271 (100%)	0	100	100
6	B	22/224 (10%)	22 (100%)	0	100	100
7	C	363/367 (99%)	363 (100%)	0	100	100
8	D	427/474 (90%)	427 (100%)	0	100	100
9	LA	196/198 (99%)	196 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	LB	327/331 (99%)	327 (100%)	0	100	100
11	LC	284/285 (100%)	284 (100%)	0	100	100
12	LD	250/253 (99%)	250 (100%)	0	100	100
13	LE	162/166 (98%)	162 (100%)	0	100	100
14	LF	213/215 (99%)	213 (100%)	0	100	100
15	LG	203/222 (91%)	203 (100%)	0	100	100
16	LH	168/169 (99%)	168 (100%)	0	100	100
17	LI	182/183 (100%)	182 (100%)	0	100	100
18	LJ	145/150 (97%)	145 (100%)	0	100	100
20	LL	172/176 (98%)	172 (100%)	0	100	100
21	LM	116/117 (99%)	116 (100%)	0	100	100
22	LN	179/180 (99%)	179 (100%)	0	100	100
23	LO	161/162 (99%)	161 (100%)	0	100	100
24	LP	151/152 (99%)	151 (100%)	0	100	100
25	LQ	155/178 (87%)	155 (100%)	0	100	100
26	LR	153/160 (96%)	153 (100%)	0	100	100
27	LS	153/154 (99%)	153 (100%)	0	100	100
28	LT	134/135 (99%)	134 (100%)	0	100	100
29	LU	92/108 (85%)	92 (100%)	0	100	100
30	LV	99/102 (97%)	99 (100%)	0	100	100
31	LW	107/125 (86%)	107 (100%)	0	100	100
32	LX	108/129 (84%)	108 (100%)	0	100	100
33	LY	117/119 (98%)	117 (100%)	0	100	100
34	LZ	121/121 (100%)	121 (100%)	0	100	100
35	La	121/122 (99%)	121 (100%)	0	100	100
36	Lb	53/55 (96%)	53 (100%)	0	100	100
37	Lc	78/88 (89%)	78 (100%)	0	100	100
38	Ld	104/105 (99%)	104 (100%)	0	100	100
39	Le	107/114 (94%)	107 (100%)	0	100	100
40	Lf	88/90 (98%)	88 (100%)	0	100	100
41	Lg	97/102 (95%)	97 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
42	Lh	109/112 (97%)	109 (100%)	0	100	100
43	Li	86/93 (92%)	86 (100%)	0	100	100
44	Lj	70/78 (90%)	70 (100%)	0	100	100
45	Lk	76/77 (99%)	76 (100%)	0	100	100
46	Ll	45/46 (98%)	45 (100%)	0	100	100
47	Lm	47/115 (41%)	47 (100%)	0	100	100
48	Ln	22/23 (96%)	18 (82%)	4 (18%)	2	8
48	Lr	22/23 (96%)	18 (82%)	4 (18%)	2	8
49	Lo	88/90 (98%)	88 (100%)	0	100	100
50	Lp	73/74 (99%)	73 (100%)	0	100	100
51	Lq	109/112 (97%)	109 (100%)	0	100	100
52	Ls	155/255 (61%)	155 (100%)	0	100	100
54	SA	178/225 (79%)	178 (100%)	0	100	100
55	SB	203/223 (91%)	203 (100%)	0	100	100
56	SC	181/206 (88%)	181 (100%)	0	100	100
57	SD	182/206 (88%)	181 (100%)	1 (0%)	81	83
58	SE	219/221 (99%)	219 (100%)	0	100	100
59	SF	167/178 (94%)	166 (99%)	1 (1%)	78	81
60	SG	198/204 (97%)	198 (100%)	0	100	100
61	SH	169/177 (96%)	169 (100%)	0	100	100
62	SI	163/164 (99%)	163 (100%)	0	100	100
63	SJ	154/162 (95%)	154 (100%)	0	100	100
64	SK	77/126 (61%)	77 (100%)	0	100	100
65	SL	133/143 (93%)	133 (100%)	0	100	100
66	SM	101/121 (84%)	100 (99%)	1 (1%)	68	76
67	SN	129/130 (99%)	129 (100%)	0	100	100
68	SO	102/117 (87%)	102 (100%)	0	100	100
69	SP	99/132 (75%)	99 (100%)	0	100	100
70	SQ	111/115 (96%)	111 (100%)	0	100	100
71	SR	119/131 (91%)	119 (100%)	0	100	100
72	SS	120/135 (89%)	120 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
73	ST	114/124 (92%)	114 (100%)	0	100	100
74	SU	93/103 (90%)	93 (100%)	0	100	100
75	SV	69/80 (86%)	69 (100%)	0	100	100
76	SW	112/113 (99%)	112 (100%)	0	100	100
77	SX	113/116 (97%)	113 (100%)	0	100	100
78	SY	112/115 (97%)	112 (100%)	0	100	100
79	SZ	60/80 (75%)	60 (100%)	0	100	100
80	Sa	91/103 (88%)	91 (100%)	0	100	100
81	Sb	70/71 (99%)	70 (100%)	0	100	100
82	Sc	54/61 (88%)	54 (100%)	0	100	100
83	Sd	43/46 (94%)	43 (100%)	0	100	100
84	Se	34/51 (67%)	34 (100%)	0	100	100
85	Sf	66/139 (48%)	66 (100%)	0	100	100
All	All	10617/11721 (91%)	10606 (100%)	11 (0%)	87	90

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
48	Ln	4	LYS
48	Ln	10	THR
48	Ln	16	LYS
48	Ln	17	ARG
48	Lr	4	LYS
48	Lr	10	THR
48	Lr	16	LYS
48	Lr	17	ARG
57	SD	177	HIS
59	SF	50	GLN
66	SM	96	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (101) such sidechains are listed below:

Mol	Chain	Res	Type
5	A	44	ASN
5	A	119	GLN
5	A	147	HIS

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Mol	Chain	Res	Type
5	A	159	ASN
5	A	226	HIS
7	C	275	ASN
7	C	297	GLN
7	C	360	ASN
8	D	62	GLN
8	D	85	GLN
8	D	241	HIS
8	D	252	HIS
8	D	363	ASN
9	LA	250	GLN
10	LB	260	HIS
10	LB	372	GLN
11	LC	115	ASN
11	LC	141	HIS
11	LC	203	HIS
12	LD	81	HIS
12	LD	90	HIS
12	LD	249	GLN
14	LF	99	ASN
14	LF	242	ASN
17	LI	55	ASN
17	LI	198	GLN
18	LJ	63	ASN
20	LL	103	ASN
21	LM	105	GLN
22	LN	87	GLN
22	LN	91	GLN
22	LN	123	GLN
24	LP	34	GLN
24	LP	116	HIS
25	LQ	98	ASN
25	LQ	179	HIS
26	LR	3	ASN
28	LT	22	HIS
28	LT	146	ASN
31	LW	102	ASN
32	LX	107	GLN
35	La	14	HIS
35	La	66	ASN
36	Lb	12	GLN
39	Le	21	HIS

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Mol	Chain	Res	Type
39	Le	50	ASN
40	Lf	79	ASN
41	Lg	109	GLN
42	Lh	33	GLN
42	Lh	64	ASN
43	Li	42	GLN
44	Lj	29	ASN
45	Lk	28	ASN
46	Ll	4	HIS
46	Ll	43	HIS
49	Lo	82	GLN
51	Lq	43	HIS
52	Ls	32	ASN
54	SA	52	ASN
55	SB	21	GLN
56	SC	44	GLN
57	SD	7	GLN
57	SD	224	GLN
58	SE	67	GLN
58	SE	142	HIS
58	SE	209	HIS
59	SF	50	GLN
59	SF	145	GLN
59	SF	187	ASN
60	SG	13	GLN
60	SG	201	GLN
60	SG	225	GLN
61	SH	81	GLN
62	SI	116	HIS
62	SI	179	GLN
63	SJ	121	HIS
63	SJ	140	ASN
66	SM	40	HIS
66	SM	96	GLN
71	SR	31	ASN
72	SS	21	ASN
72	SS	26	GLN
72	SS	87	ASN
72	SS	127	HIS
73	ST	49	GLN
73	ST	130	GLN
75	SV	50	ASN

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Mol	Chain	Res	Type
76	SW	42	GLN
76	SW	44	HIS
78	SY	25	GLN
78	SY	109	GLN
79	SZ	80	GLN
80	Sa	43	ASN
80	Sa	94	ASN
81	Sb	65	GLN
82	Sc	28	GLN
83	Sd	26	HIS
85	Sf	93	HIS
85	Sf	123	ASN
85	Sf	136	GLN
85	Sf	139	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	3188/3337 (95%)	522 (16%)	51 (1%)
2	2	1761/1796 (98%)	332 (18%)	35 (1%)
3	3	118/120 (98%)	9 (7%)	1 (0%)
4	4	155/156 (99%)	24 (15%)	2 (1%)
All	All	5222/5409 (96%)	887 (16%)	89 (1%)

All (887) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	27	A
1	1	41	A
1	1	44	A
1	1	50	A
1	1	60	G
1	1	61	A
1	1	66	A
1	1	67	A
1	1	93	G
1	1	97	G
1	1	111	G
1	1	114	C
1	1	117	A
1	1	118	U

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Mol	Chain	Res	Type
1	1	119	U
1	1	123	A
1	1	132	U
1	1	133	C
1	1	134	G
1	1	135	G
1	1	144	G
1	1	152	G
1	1	153	A
1	1	165	G
1	1	170	A
1	1	179	C
1	1	181	G
1	1	184	U
1	1	185	U
1	1	204	C
1	1	207	A
1	1	212	G
1	1	213	A
1	1	214	G
1	1	215	A
1	1	225	A
1	1	234	C
1	1	251	U
1	1	262	G
1	1	276	G
1	1	277	A
1	1	279	U
1	1	288	A
1	1	308	C
1	1	316	A
1	1	332	C
1	1	343	C
1	1	363	U
1	1	369	G
1	1	385	G
1	1	391	U
1	1	392	A
1	1	394	C
1	1	395	A
1	1	396	C
1	1	414	G

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Mol	Chain	Res	Type
1	1	415	A
1	1	422	U
1	1	432	C
1	1	433	U
1	1	434	U
1	1	445	G
1	1	446	A
1	1	447	U
1	1	456	G
1	1	458	U
1	1	460	U
1	1	461	C
1	1	469	C
1	1	470	A
1	1	471	C
1	1	472	U
1	1	475	G
1	1	476	C
1	1	481	C
1	1	485	G
1	1	487	C
1	1	489	A
1	1	511	U
1	1	512	A
1	1	527	G
1	1	538	G
1	1	539	G
1	1	547	A
1	1	549	A
1	1	559	G
1	1	560	U
1	1	570	G
1	1	580	A
1	1	583	A
1	1	591	C
1	1	592	U
1	1	593	G
1	1	597	G
1	1	599	A
1	1	608	U
1	1	609	A
1	1	610	A

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Mol	Chain	Res	Type
1	1	624	C
1	1	637	A
1	1	648	A
1	1	665	A
1	1	669	U
1	1	679	A
1	1	697	A
1	1	700	G
1	1	703	A
1	1	704	A
1	1	715	A
1	1	722	G
1	1	746	U
1	1	748	U
1	1	749	U
1	1	758	U
1	1	759	U
1	1	763	G
1	1	767	G
1	1	783	A
1	1	788	A
1	1	799	A
1	1	812	A
1	1	843	C
1	1	856	U
1	1	861	U
1	1	862	G
1	1	878	A
1	1	889	G
1	1	890	G
1	1	896	A
1	1	898	G
1	1	899	A
1	1	919	G
1	1	926	A
1	1	941	C
1	1	942	U
1	1	943	C
1	1	959	A
1	1	960	C
1	1	961	C
1	1	962	U

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Mol	Chain	Res	Type
1	1	984	A
1	1	992	G
1	1	998	C
1	1	999	G
1	1	1003	G
1	1	1006	A
1	1	1007	U
1	1	1008	U
1	1	1009	U
1	1	1010	U
1	1	1011	U
1	1	1012	A
1	1	1013	G
1	1	1015	C
1	1	1017	U
1	1	1030	A
1	1	1032	C
1	1	1047	A
1	1	1048	A
1	1	1055	G
1	1	1064	C
1	1	1065	U
1	1	1068	A
1	1	1077	U
1	1	1078	U
1	1	1079	C
1	1	1080	G
1	1	1081	A
1	1	1086	A
1	1	1087	U
1	1	1088	C
1	1	1100	G
1	1	1114	G
1	1	1131	G
1	1	1134	U
1	1	1136	A
1	1	1142	A
1	1	1163	G
1	1	1164	U
1	1	1165	G
1	1	1175	C
1	1	1184	C

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Mol	Chain	Res	Type
1	1	1189	G
1	1	1195	A
1	1	1204	U
1	1	1205	G
1	1	1215	C
1	1	1218	U
1	1	1219	G
1	1	1220	G
1	1	1221	C
1	1	1222	C
1	1	1224	U
1	1	1225	G
1	1	1226	G
1	1	1227	A
1	1	1228	A
1	1	1229	G
1	1	1231	C
1	1	1233	G
1	1	1245	G
1	1	1246	A
1	1	1247	C
1	1	1248	U
1	1	1264	U
1	1	1268	G
1	1	1272	G
1	1	1278	G
1	1	1290	G
1	1	1291	A
1	1	1292	U
1	1	1296	G
1	1	1313	A
1	1	1314	U
1	1	1331	A
1	1	1332	G
1	1	1333	A
1	1	1335	A
1	1	1336	C
1	1	1337	G
1	1	1339	U
1	1	1369	A
1	1	1382	A
1	1	1383	G

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Mol	Chain	Res	Type
1	1	1402	A
1	1	1404	G
1	1	1417	G
1	1	1420	C
1	1	1433	G
1	1	1458	G
1	1	1464	A
1	1	1465	A
1	1	1466	G
1	1	1485	G
1	1	1491	C
1	1	1495	U
1	1	1506	U
1	1	1516	U
1	1	1537	U
1	1	1538	U
1	1	1539	C
1	1	1540	A
1	1	1543	G
1	1	1545	G
1	1	1552	G
1	1	1554	G
1	1	1555	C
1	1	1560	U
1	1	1561	G
1	1	1562	U
1	1	1563	G
1	1	1567	A
1	1	1585	A
1	1	1587	U
1	1	1588	C
1	1	1609	U
1	1	1611	C
1	1	1619	C
1	1	1622	A
1	1	1623	A
1	1	1624	C
1	1	1625	U
1	1	1637	C
1	1	1685	U
1	1	1696	A
1	1	1697	C

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Mol	Chain	Res	Type
1	1	1704	U
1	1	1727	G
1	1	1730	A
1	1	1731	G
1	1	1740	A
1	1	1741	C
1	1	1742	U
1	1	1745	U
1	1	1746	G
1	1	1748	C
1	1	1750	G
1	1	1760	G
1	1	1777	A
1	1	1794	A
1	1	1796	A
1	1	1797	A
1	1	1798	U
1	1	1799	U
1	1	1800	C
1	1	1801	U
1	1	1819	A
1	1	1820	U
1	1	1821	A
1	1	1822	A
1	1	1826	C
1	1	1829	C
1	1	1830	A
1	1	1858	G
1	1	1859	A
1	1	1860	U
1	1	1866	A
1	1	1886	G
1	1	1887	C
1	1	1888	A
1	1	1906	C
1	1	1933	G
1	1	1934	G
1	1	1935	C
1	1	1936	A
1	1	1937	C
1	1	1938	G
1	1	1939	U

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Mol	Chain	Res	Type
1	1	1941	G
1	1	2045	G
1	1	2046	C
1	1	2047	G
1	1	2048	U
1	1	2051	G
1	1	2054	U
1	1	2055	A
1	1	2063	A
1	1	2065	U
1	1	2076	A
1	1	2084	G
1	1	2085	G
1	1	2094	A
1	1	2107	A
1	1	2121	A
1	1	2132	G
1	1	2133	U
1	1	2134	G
1	1	2139	U
1	1	2151	A
1	1	2168	U
1	1	2170	A
1	1	2171	A
1	1	2172	U
1	1	2173	G
1	1	2192	A
1	1	2207	A
1	1	2212	G
1	1	2216	G
1	1	2219	A
1	1	2221	U
1	1	2228	C
1	1	2233	A
1	1	2235	G
1	1	2236	G
1	1	2242	A
1	1	2244	A
1	1	2248	C
1	1	2251	G
1	1	2270	G
1	1	2273	U

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Mol	Chain	Res	Type
1	1	2276	A
1	1	2278	G
1	1	2281	U
1	1	2297	U
1	1	2299	U
1	1	2335	A
1	1	2336	A
1	1	2337	C
1	1	2338	G
1	1	2339	G
1	1	2356	G
1	1	2360	A
1	1	2364	A
1	1	2365	A
1	1	2366	G
1	1	2367	A
1	1	2374	U
1	1	2382	A
1	1	2409	U
1	1	2410	A
1	1	2414	G
1	1	2459	U
1	1	2460	C
1	1	2463	A
1	1	2464	U
1	1	2465	U
1	1	2474	A
1	1	2477	U
1	1	2478	A
1	1	2487	A
1	1	2488	G
1	1	2489	C
1	1	2492	G
1	1	2498	A
1	1	2501	U
1	1	2502	G
1	1	2503	C
1	1	2504	G
1	1	2505	U
1	1	2506	C
1	1	2508	A
1	1	2510	C

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Mol	Chain	Res	Type
1	1	2513	C
1	1	2516	G
1	1	2521	A
1	1	2529	U
1	1	2530	C
1	1	2531	G
1	1	2532	C
1	1	2533	G
1	1	2543	G
1	1	2544	G
1	1	2552	A
1	1	2553	C
1	1	2565	G
1	1	2566	G
1	1	2573	G
1	1	2578	OMG
1	1	2585	A
1	1	2611	U
1	1	2615	A
1	1	2622	G
1	1	2633	A
1	1	2636	G
1	1	2648	A
1	1	2650	A
1	1	2653	A
1	1	2655	A
1	1	2663	A
1	1	2673	G
1	1	2687	G
1	1	2688	U
1	1	2711	U
1	1	2712	G
1	1	2714	C
1	1	2721	A
1	1	2731	C
1	1	2732	C
1	1	2736	G
1	1	2737	A
1	1	2755	G
1	1	2758	A
1	1	2759	G
1	1	2760	A

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Mol	Chain	Res	Type
1	1	2763	A
1	1	2769	C
1	1	2776	A
1	1	2777	U
1	1	2778	A
1	1	2788	U
1	1	2798	G
1	1	2803	C
1	1	2804	A
1	1	2828	U
1	1	2830	G
1	1	2831	A
1	1	2846	A
1	1	2858	C
1	1	2863	U
1	1	2882	U
1	1	2894	U
1	1	2895	A
1	1	2906	G
1	1	2930	A
1	1	2942	C
1	1	2970	A
1	1	3007	A
1	1	3008	U
1	1	3014	U
1	1	3017	G
1	1	3036	G
1	1	3044	A
1	1	3050	C
1	1	3051	C
1	1	3059	G
1	1	3074	G
1	1	3080	A
1	1	3088	A
1	1	3089	U
1	1	3100	A
1	1	3101	C
1	1	3111	C
1	1	3112	U
1	1	3113	A
1	1	3119	A
1	1	3122	U

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Mol	Chain	Res	Type
1	1	3127	G
1	1	3128	A
1	1	3130	G
1	1	3131	U
1	1	3132	A
1	1	3135	A
1	1	3141	G
1	1	3146	C
1	1	3147	G
1	1	3162	C
1	1	3163	A
1	1	3164	G
1	1	3170	U
1	1	3188	G
1	1	3189	U
1	1	3200	A
1	1	3201	A
1	1	3211	U
1	1	3214	A
1	1	3217	U
1	1	3218	U
1	1	3219	A
1	1	3223	A
1	1	3225	G
1	1	3227	G
1	1	3229	G
1	1	3230	G
1	1	3231	G
1	1	3235	A
1	1	3245	C
1	1	3257	A
1	1	3258	U
1	1	3259	G
1	1	3260	U
1	1	3282	U
1	1	3286	G
1	1	3292	U
1	1	3299	U
1	1	3309	U
1	1	3310	G
1	1	3319	C
1	1	3324	C

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Mol	Chain	Res	Type
1	1	3325	U
1	1	3331	U
1	1	3332	A
1	1	3333	G
2	2	17	C
2	2	25	C
2	2	26	A
2	2	27	U
2	2	34	G
2	2	42	G
2	2	47	A
2	2	57	G
2	2	68	A
2	2	69	G
2	2	73	U
2	2	74	U
2	2	75	A
2	2	76	U
2	2	77	A
2	2	103	A
2	2	113	C
2	2	115	U
2	2	126	G
2	2	127	U
2	2	138	A
2	2	155	U
2	2	156	U
2	2	174	U
2	2	175	G
2	2	176	A
2	2	184	G
2	2	185	A
2	2	186	C
2	2	187	U
2	2	190	G
2	2	192	A
2	2	195	G
2	2	210	A
2	2	212	U
2	2	213	A
2	2	214	A
2	2	215	A

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Mol	Chain	Res	Type
2	2	216	A
2	2	221	A
2	2	222	U
2	2	223	G
2	2	224	C
2	2	231	G
2	2	232	G
2	2	234	C
2	2	236	U
2	2	237	U
2	2	247	C
2	2	258	C
2	2	262	A
2	2	268	A
2	2	269	C
2	2	270	G
2	2	274	U
2	2	275	U
2	2	277	C
2	2	296	A
2	2	311	C
2	2	313	A
2	2	317	U
2	2	319	G
2	2	321	C
2	2	326	G
2	2	334	G
2	2	335	C
2	2	338	G
2	2	349	A
2	2	353	G
2	2	356	A
2	2	357	A
2	2	358	C
2	2	367	A
2	2	377	C
2	2	396	A
2	2	397	A
2	2	399	C
2	2	401	G
2	2	414	A
2	2	415	G

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Mol	Chain	Res	Type
2	2	421	C
2	2	422	A
2	2	423	G
2	2	431	G
2	2	436	U
2	2	441	C
2	2	445	C
2	2	451	A
2	2	452	C
2	2	465	A
2	2	472	A
2	2	474	A
2	2	490	U
2	2	491	U
2	2	492	C
2	2	493	G
2	2	505	U
2	2	510	U
2	2	511	G
2	2	512	A
2	2	535	A
2	2	536	G
2	2	537	G
2	2	538	A
2	2	539	A
2	2	540	C
2	2	541	A
2	2	552	A
2	2	553	A
2	2	554	G
2	2	555	U
2	2	556	C
2	2	562	C
2	2	567	A
2	2	571	G
2	2	576	A
2	2	577	A
2	2	579	U
2	2	591	A
2	2	592	G
2	2	604	G
2	2	605	U

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Mol	Chain	Res	Type
2	2	608	U
2	2	611	A
2	2	612	G
2	2	616	A
2	2	617	A
2	2	619	A
2	2	620	A
2	2	621	G
2	2	636	U
2	2	651	C
2	2	652	G
2	2	674	G
2	2	675	G
2	2	676	C
2	2	677	U
2	2	678	G
2	2	679	G
2	2	680	G
2	2	681	C
2	2	686	C
2	2	688	U
2	2	689	U
2	2	690	U
2	2	692	C
2	2	693	U
2	2	705	G
2	2	725	G
2	2	726	U
2	2	727	C
2	2	728	G
2	2	731	G
2	2	732	A
2	2	741	U
2	2	754	A
2	2	755	A
2	2	764	G
2	2	765	C
2	2	773	A
2	2	774	G
2	2	779	A
2	2	780	U
2	2	781	G

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Mol	Chain	Res	Type
2	2	787	A
2	2	792	U
2	2	793	U
2	2	809	A
2	2	810	A
2	2	819	G
2	2	821	G
2	2	824	U
2	2	828	U
2	2	829	U
2	2	830	U
2	2	832	G
2	2	833	U
2	2	861	A
2	2	884	U
2	2	896	A
2	2	910	U
2	2	911	G
2	2	912	G
2	2	931	A
2	2	933	U
2	2	940	G
2	2	949	A
2	2	957	U
2	2	958	U
2	2	964	A
2	2	982	G
2	2	988	C
2	2	990	A
2	2	991	A
2	2	1002	U
2	2	1003	A
2	2	1024	A
2	2	1026	C
2	2	1037	A
2	2	1055	A
2	2	1056	U
2	2	1057	U
2	2	1058	U
2	2	1059	U
2	2	1079	C
2	2	1088	A

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Mol	Chain	Res	Type
2	2	1089	A
2	2	1090	A
2	2	1093	G
2	2	1094	U
2	2	1095	U
2	2	1097	G
2	2	1135	A
2	2	1140	A
2	2	1147	G
2	2	1155	C
2	2	1156	C
2	2	1157	A
2	2	1166	G
2	2	1182	U
2	2	1188	U
2	2	1191	A
2	2	1193	A
2	2	1194	C
2	2	1196	G
2	2	1197	G
2	2	1214	A
2	2	1215	G
2	2	1223	G
2	2	1225	G
2	2	1226	G
2	2	1227	A
2	2	1228	U
2	2	1237	U
2	2	1238	G
2	2	1240	G
2	2	1241	A
2	2	1242	G
2	2	1243	C
2	2	1248	U
2	2	1249	C
2	2	1252	G
2	2	1253	A
2	2	1254	U
2	2	1255	U
2	2	1282	U
2	2	1283	U
2	2	1311	U

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Mol	Chain	Res	Type
2	2	1312	U
2	2	1313	G
2	2	1318	A
2	2	1338	G
2	2	1341	A
2	2	1342	A
2	2	1344	U
2	2	1357	C
2	2	1358	U
2	2	1360	G
2	2	1379	A
2	2	1387	U
2	2	1409	U
2	2	1411	U
2	2	1421	A
2	2	1423	A
2	2	1424	G
2	2	1439	U
2	2	1441	G
2	2	1444	G
2	2	1455	C
2	2	1467	A
2	2	1474	G
2	2	1478	C
2	2	1482	G
2	2	1486	A
2	2	1487	C
2	2	1489	C
2	2	1499	A
2	2	1502	G
2	2	1512	A
2	2	1517	G
2	2	1519	U
2	2	1532	G
2	2	1533	C
2	2	1534	U
2	2	1538	G
2	2	1553	U
2	2	1555	A
2	2	1564	C
2	2	1565	A
2	2	1570	G

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Mol	Chain	Res	Type
2	2	1580	G
2	2	1586	G
2	2	1597	G
2	2	1612	G
2	2	1617	U
2	2	1627	A
2	2	1631	A
2	2	1653	U
2	2	1654	G
2	2	1677	A
2	2	1678	C
2	2	1682	C
2	2	1683	C
2	2	1684	C
2	2	1685	A
2	2	1688	G
2	2	1693	C
2	2	1697	A
2	2	1699	C
2	2	1700	G
2	2	1702	C
2	2	1708	A
2	2	1709	G
2	2	1711	G
2	2	1712	C
2	2	1713	C
2	2	1726	A
2	2	1756	G
2	2	1762	A
2	2	1763	G
2	2	1765	U
2	2	1766	C
2	2	1776	G
2	2	1778	A
2	2	1779	C
2	2	1788	G
2	2	1789	G
2	2	1790	A
2	2	1791	U
2	2	1792	C
2	2	1795	U
2	2	1796	U

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Mol	Chain	Res	Type
3	3	7	G
3	3	54	U
3	3	55	A
3	3	65	G
3	3	73	U
3	3	90	G
3	3	92	C
3	3	101	A
3	3	111	G
4	4	23	U
4	4	34	U
4	4	35	C
4	4	48	A
4	4	59	A
4	4	62	A
4	4	63	G
4	4	79	A
4	4	80	A
4	4	81	U
4	4	82	U
4	4	83	C
4	4	84	C
4	4	85	G
4	4	86	U
4	4	87	G
4	4	88	A
4	4	95	G
4	4	104	A
4	4	106	C
4	4	111	A
4	4	113	U
4	4	125	U
4	4	138	A

All (89) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	133	C
1	1	250	C
1	1	275	G
1	1	431	A
1	1	459	C

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Mol	Chain	Res	Type
1	1	469	C
1	1	484	A
1	1	609	A
1	1	703	A
1	1	746	U
1	1	898	G
1	1	960	C
1	1	1009	U
1	1	1012	A
1	1	1016	U
1	1	1047	A
1	1	1219	G
1	1	1224	U
1	1	1226	G
1	1	1246	A
1	1	1267	C
1	1	1277	A
1	1	1290	G
1	1	1338	A
1	1	1587	U
1	1	1741	C
1	1	1796	A
1	1	2064	C
1	1	2075	U
1	1	2167	C
1	1	2172	U
1	1	2220	C
1	1	2227	U
1	1	2232	U
1	1	2502	G
1	1	2503	C
1	1	2532	C
1	1	2552	A
1	1	2621	G
1	1	2731	C
1	1	3074	G
1	1	3079	U
1	1	3121	G
1	1	3163	A
1	1	3210	U
1	1	3224	C
1	1	3230	G

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Mol	Chain	Res	Type
1	1	3258	U
1	1	3281	G
1	1	3298	U
1	1	3332	A
2	2	75	A
2	2	102	A
2	2	184	G
2	2	211	U
2	2	231	G
2	2	233	G
2	2	269	C
2	2	352	G
2	2	414	A
2	2	509	A
2	2	539	A
2	2	552	A
2	2	555	U
2	2	604	G
2	2	676	C
2	2	678	G
2	2	740	C
2	2	754	A
2	2	792	U
2	2	832	G
2	2	1094	U
2	2	1165	U
2	2	1193	A
2	2	1224	A
2	2	1241	A
2	2	1252	G
2	2	1282	U
2	2	1341	A
2	2	1378	U
2	2	1477	C
2	2	1531	U
2	2	1564	C
2	2	1569	A
2	2	1616	C
2	2	1653	U
3	3	72	G
4	4	86	U
4	4	87	G

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

2 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	$\# Z > 2$
23	SAC	LO	2	23	7,8,9	1.00	0	7,9,11	0.99	0
1	OMG	1	2578	1	23,26,27	0.47	0	32,38,41	0.49	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
23	SAC	LO	2	23	-	2/7/8/10	-
1	OMG	1	2578	1	-	2/9/27/28	0/3/3/3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
23	LO	2	SAC	N-CA-CB-OG
23	LO	2	SAC	C-CA-CB-OG
1	1	2578	OMG	O4'-C4'-C5'-O5'
1	1	2578	OMG	C3'-C4'-C5'-O5'

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 481 ligands modelled in this entry, 480 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
87	ATP	D	601	86	32,33,33	0.27	0	48,52,52	0.27	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
87	ATP	D	601	86	-	5/22/38/38	0/3/3/3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (5) torsion outliers are listed below:

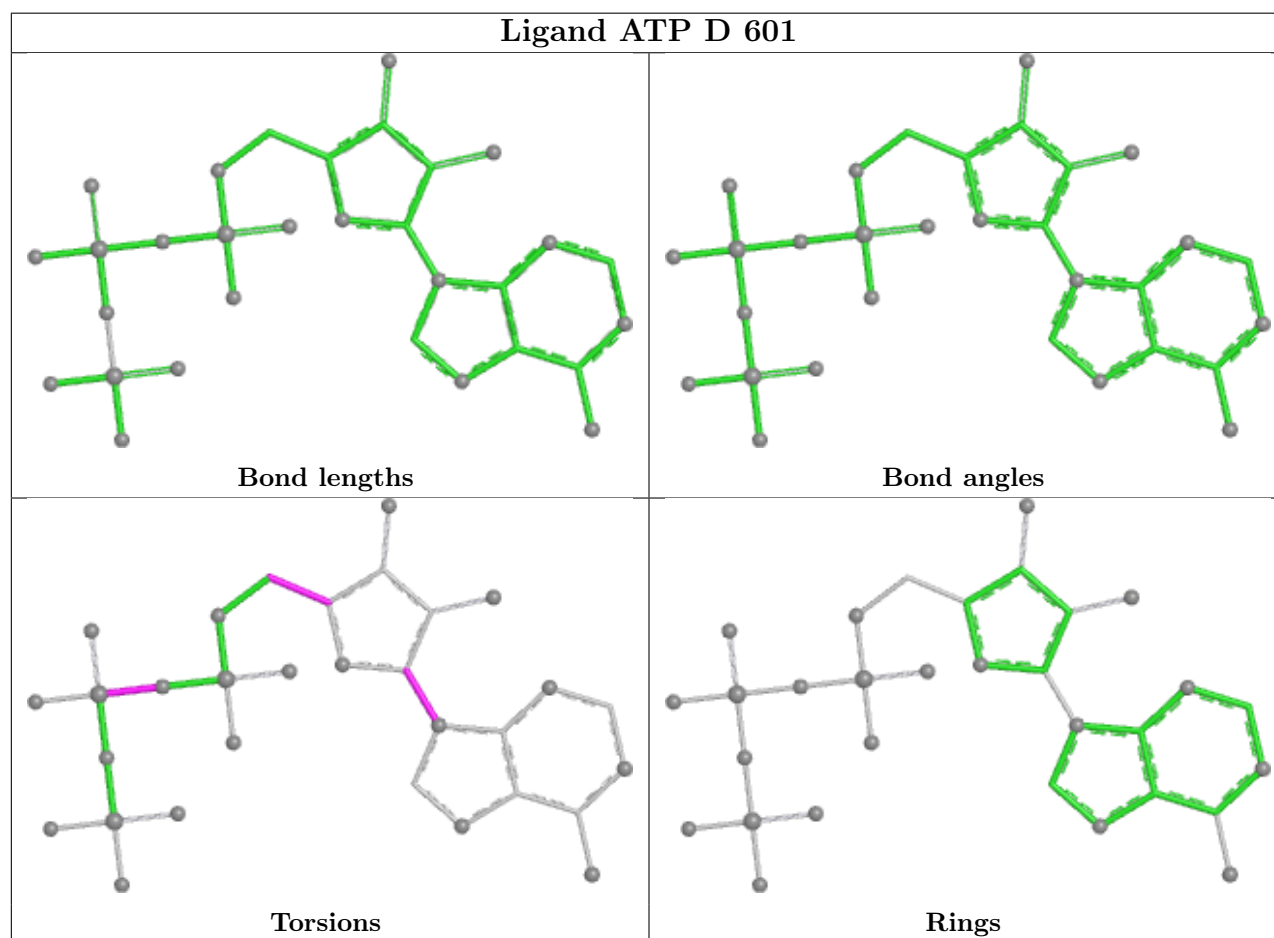
Mol	Chain	Res	Type	Atoms
87	D	601	ATP	C3'-C4'-C5'-O5'
87	D	601	ATP	PA-O3A-PB-O2B
87	D	601	ATP	C2'-C1'-N9-C8
87	D	601	ATP	O4'-C4'-C5'-O5'
87	D	601	ATP	PA-O3A-PB-O1B

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
87	D	601	ATP	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

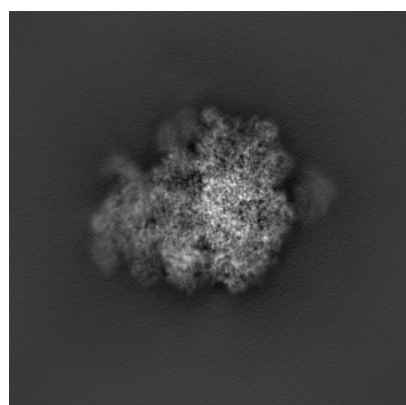
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14480. These allow visual inspection of the internal detail of the map and identification of artifacts.

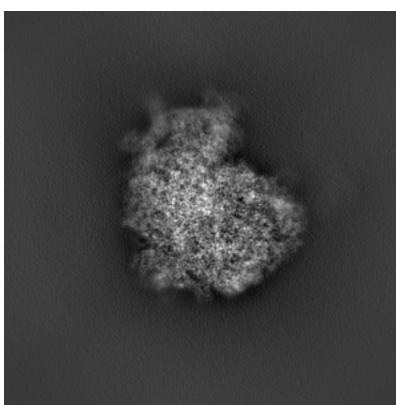
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

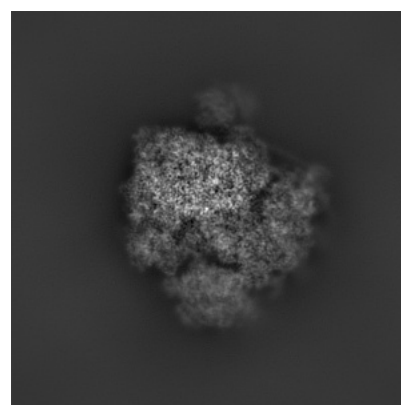
6.1.1 Primary map



X



Y

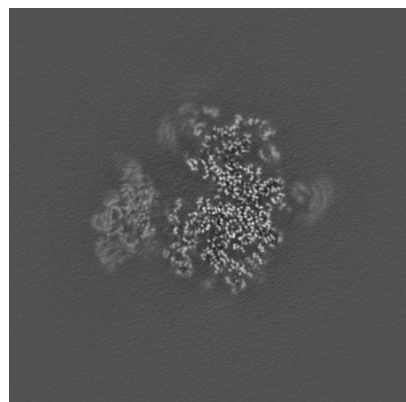


Z

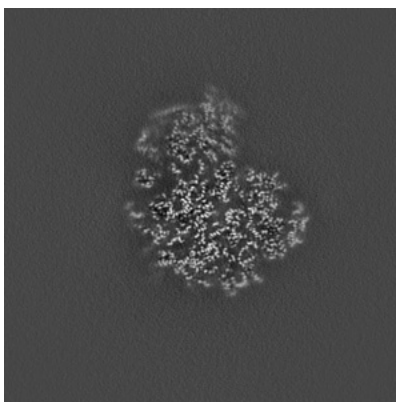
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

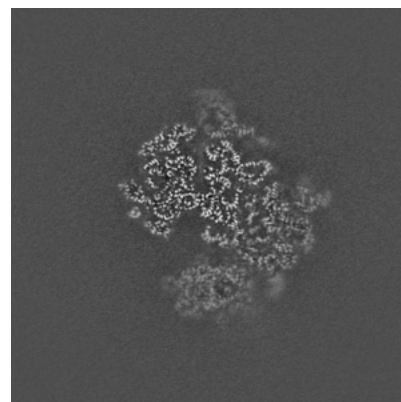
6.2.1 Primary map



X Index: 243



Y Index: 243

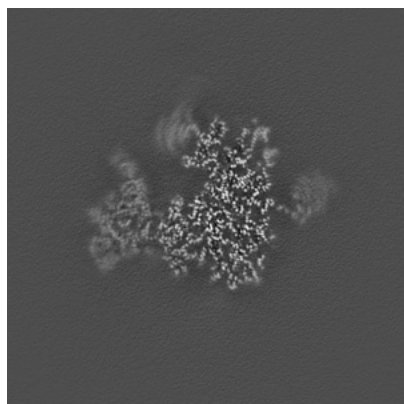


Z Index: 243

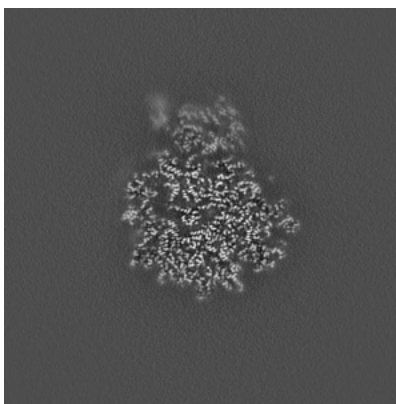
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

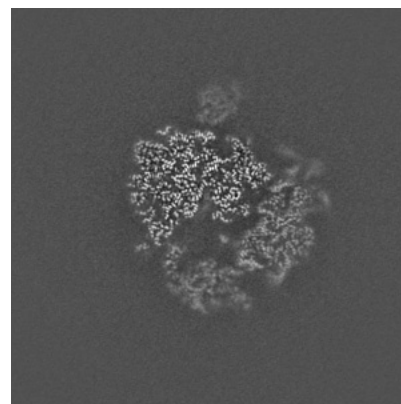
6.3.1 Primary map



X Index: 253



Y Index: 267

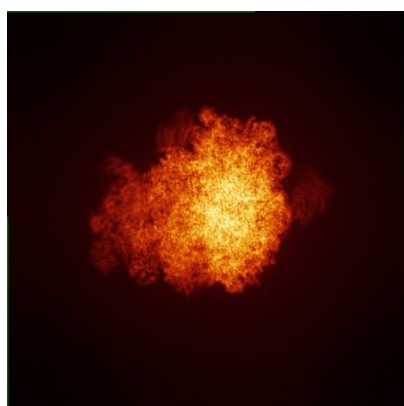


Z Index: 258

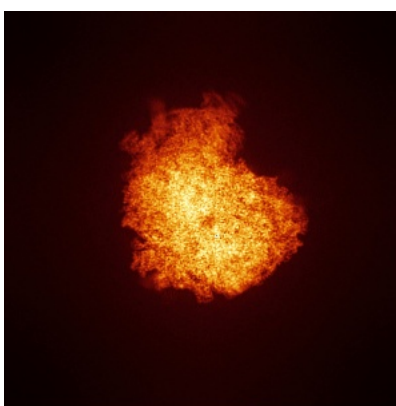
The images above show the largest variance slices of the map in three orthogonal directions.

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

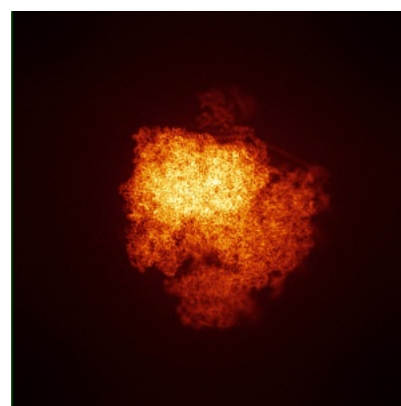
6.4.1 Primary map



X



Y

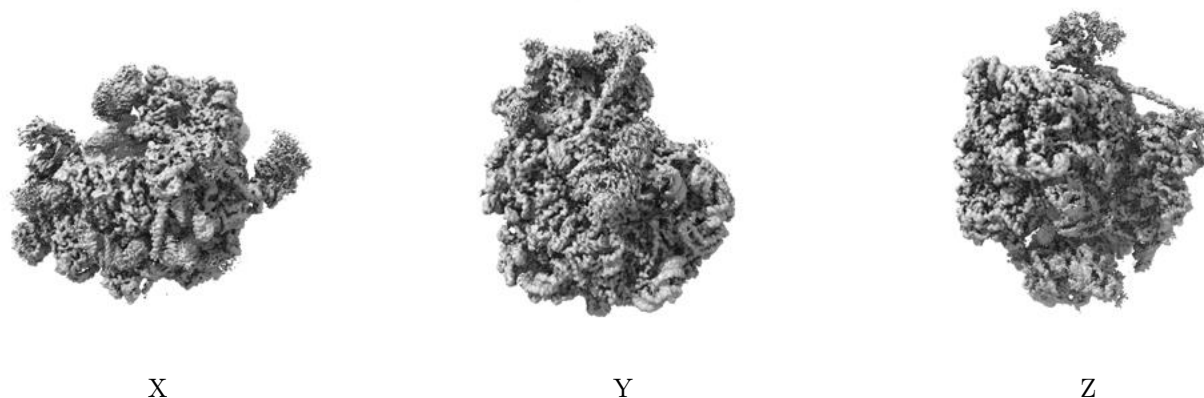


Z

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

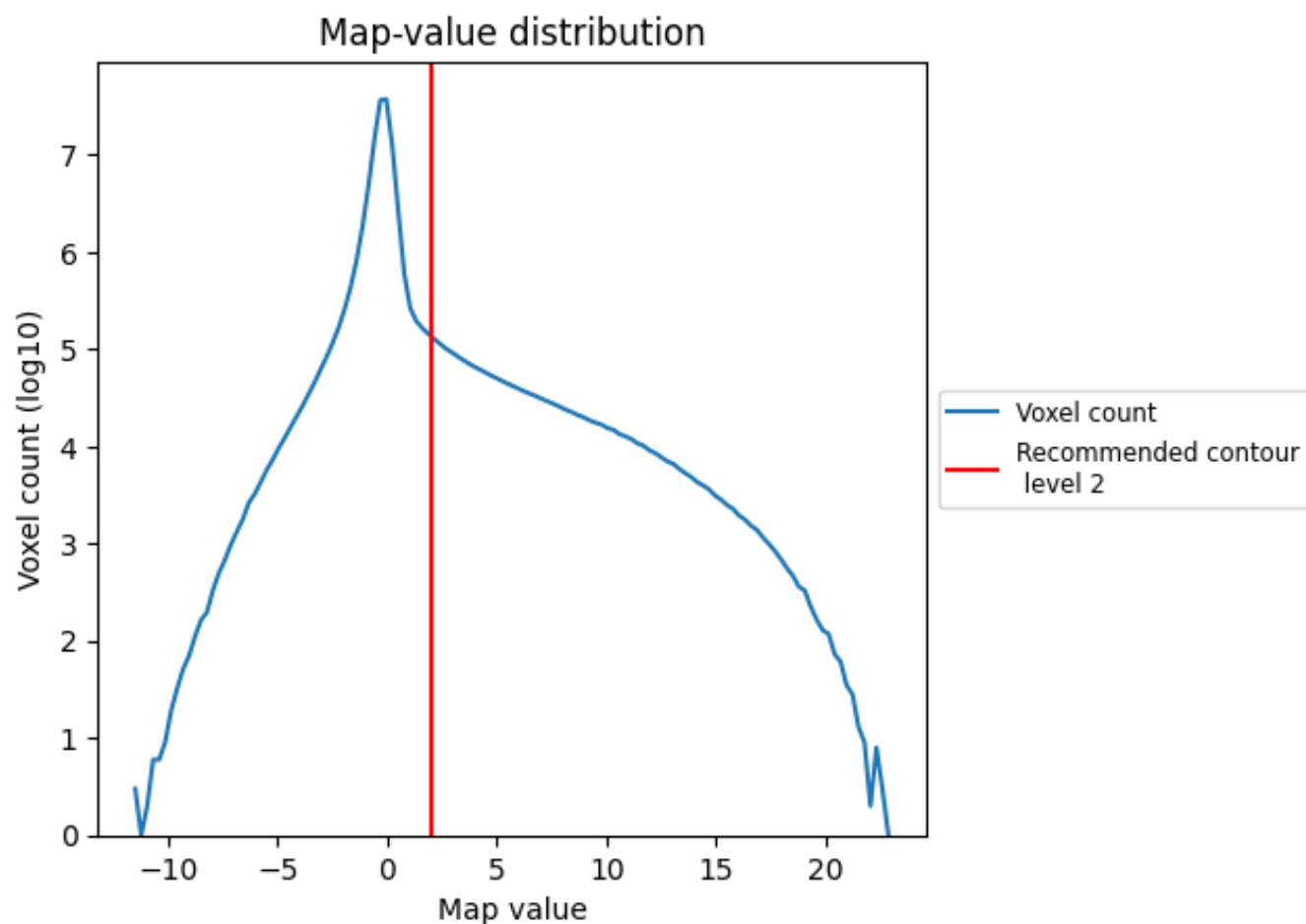
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

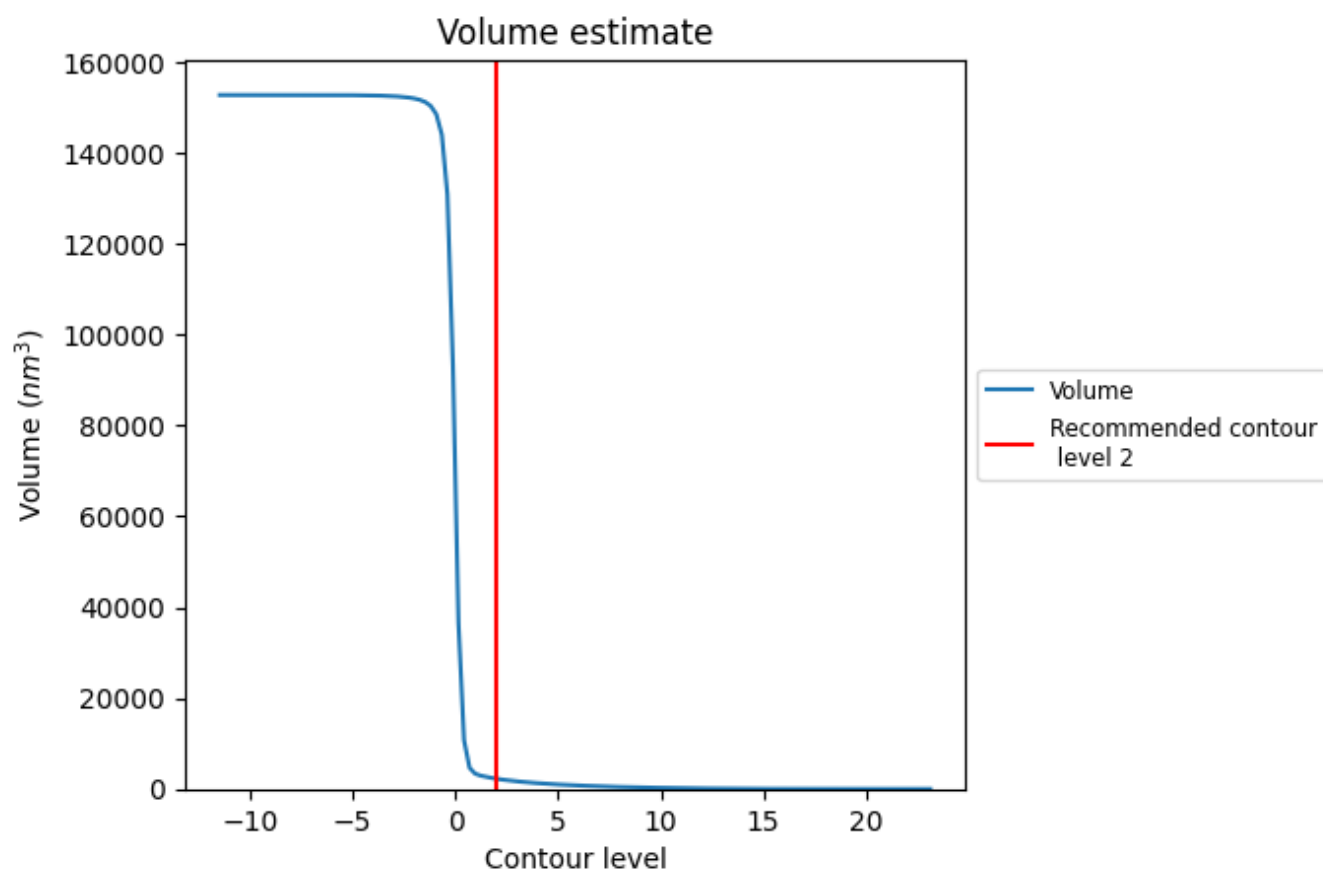
This section contains the results of statistical analysis of the map.

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.

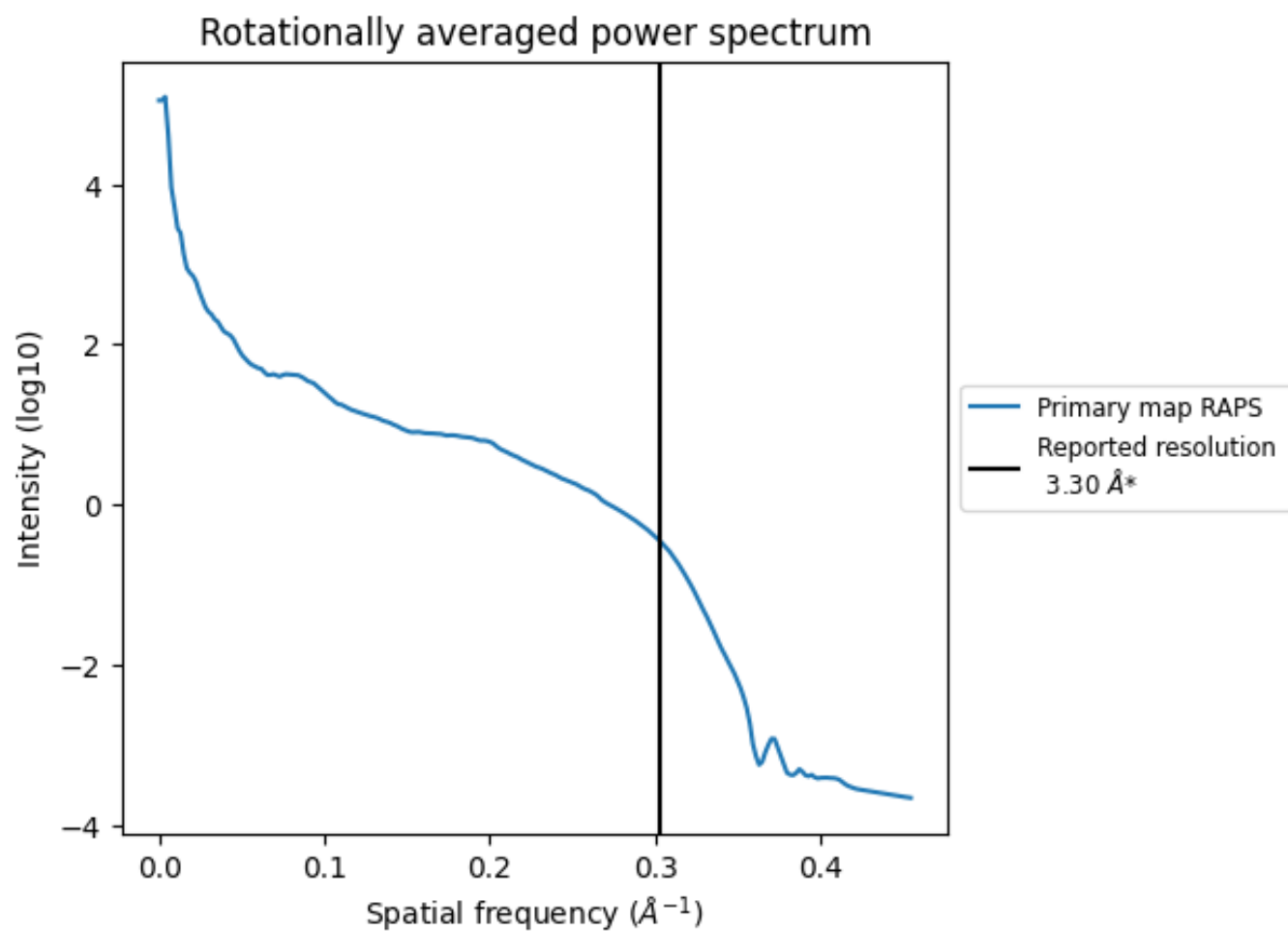
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2245 nm³; this corresponds to an approximate mass of 2028 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 ⓘ

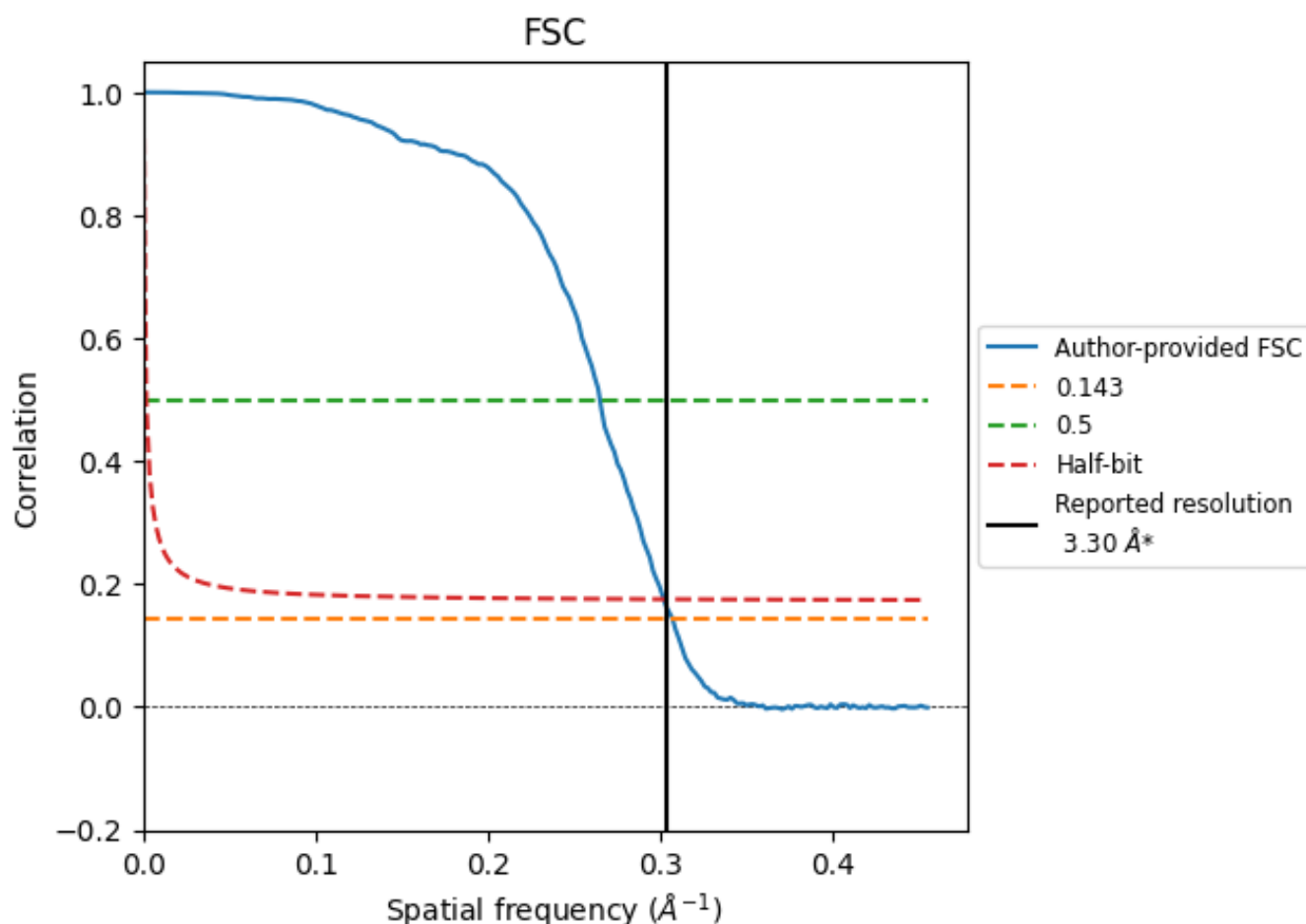


*Reported resolution corresponds to spatial frequency of 0.303 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.303 Å⁻¹

8.2 Resolution estimates [i](#)

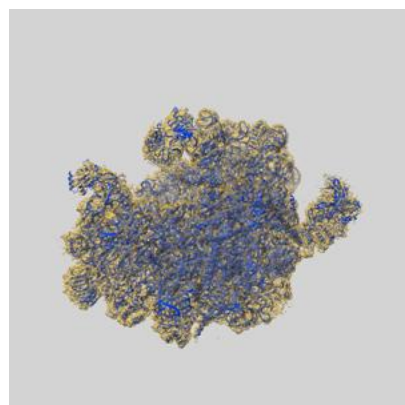
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	3.26	3.78	3.31
Unmasked-calculated*	-	-	-

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

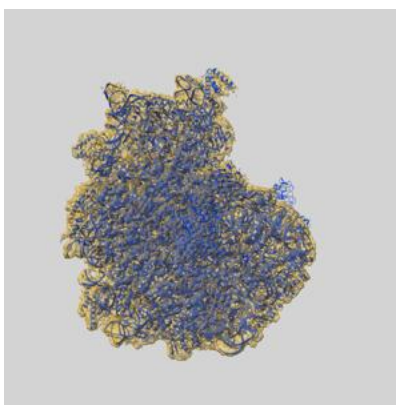
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-14480 and PDB model 7Z3O. Per-residue inclusion information can be found in section [3](#) on page [21](#).

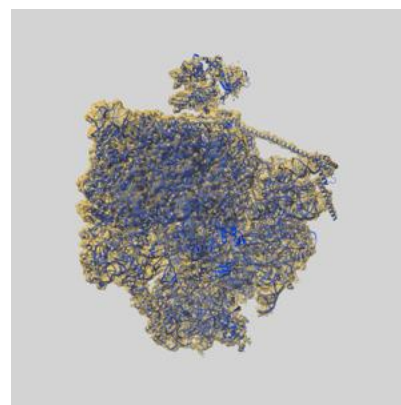
9.1 Map-model overlay [i](#)



X



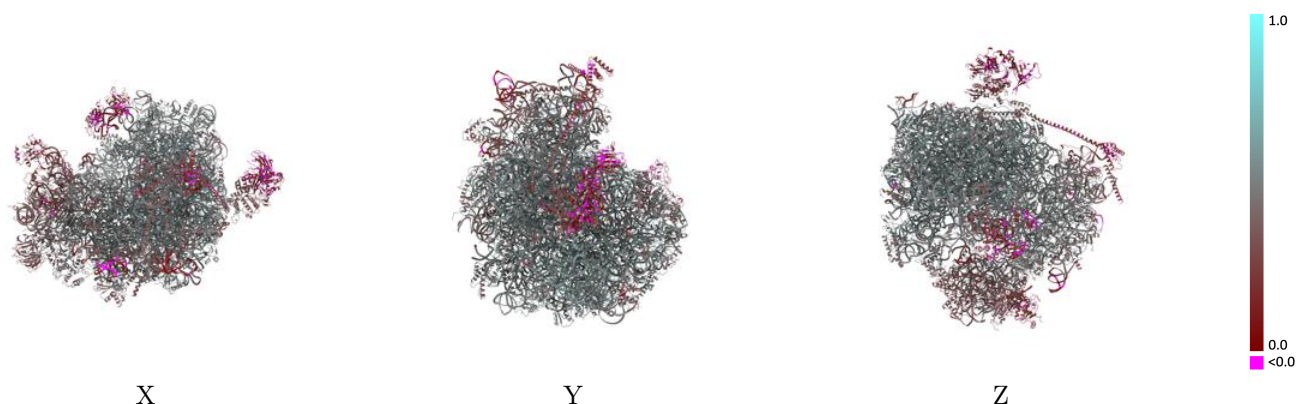
Y



Z

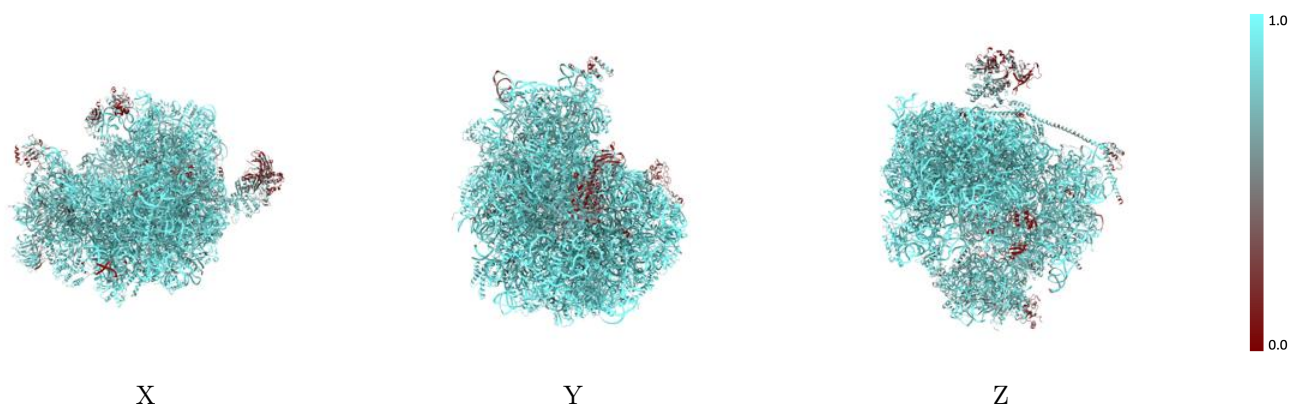
The images above show the 3D surface view of the map at the recommended contour level 2.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



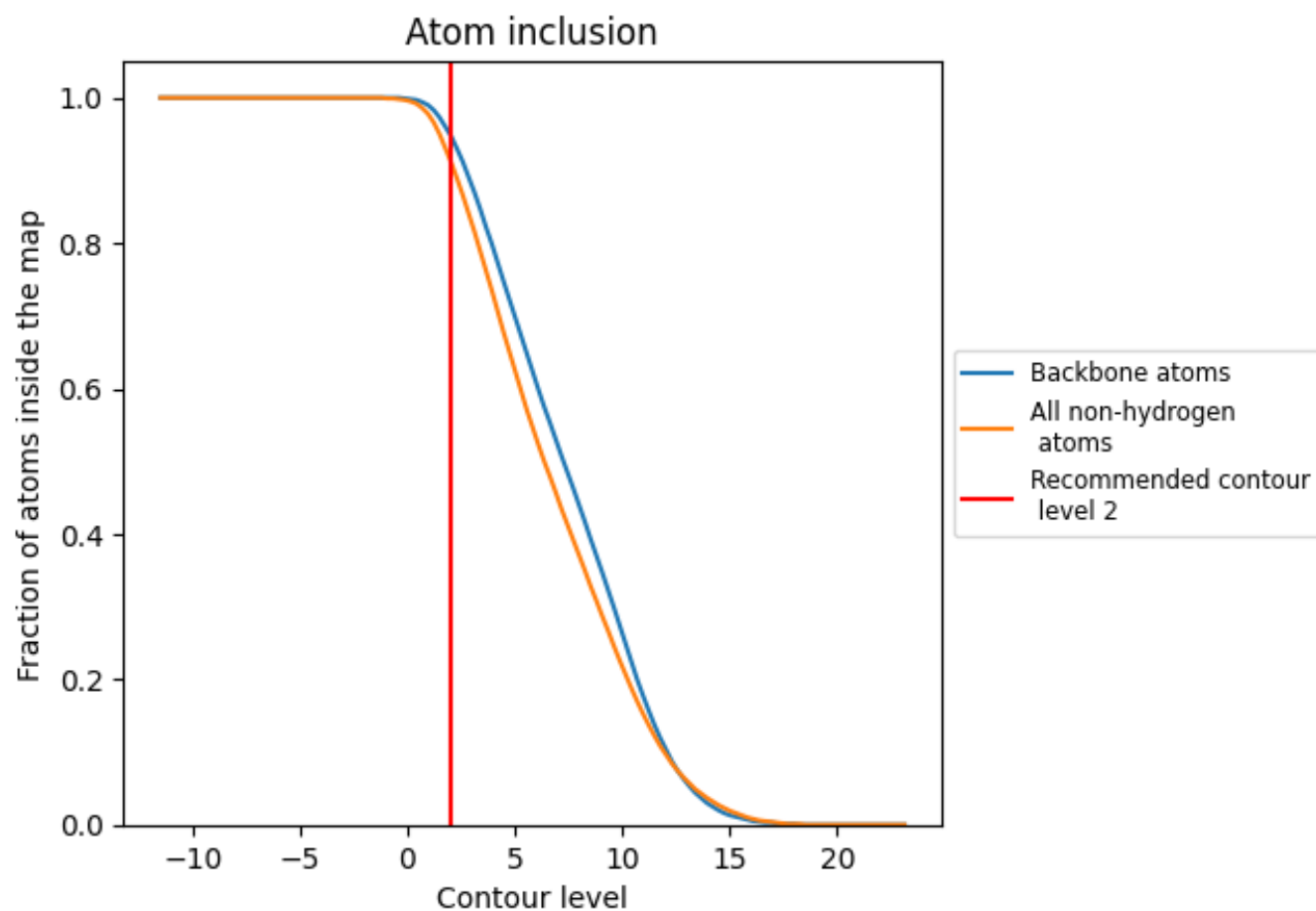
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2).

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 91% 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 (2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9140	 0.4620
1	 0.9880	 0.5080
2	 0.9510	 0.4360
3	 0.9980	 0.5100
4	 0.9950	 0.5170
A	 0.7170	 0.3140
B	 0.4770	 0.3630
C	 0.6170	 0.2520
D	 0.4680	 0.1790
LA	 0.9250	 0.5420
LB	 0.9540	 0.5310
LC	 0.9440	 0.5300
LD	 0.9340	 0.4740
LE	 0.9260	 0.4760
LF	 0.9360	 0.5110
LG	 0.9270	 0.4970
LH	 0.9340	 0.4900
LI	 0.9080	 0.5030
LJ	 0.9180	 0.4420
LK	 0.4400	 0.1350
LL	 0.9560	 0.5180
LM	 0.9290	 0.4960
LN	 0.9530	 0.5500
LO	 0.9480	 0.5130
LP	 0.8870	 0.5030
LQ	 0.9500	 0.5400
LR	 0.9240	 0.5020
LS	 0.9430	 0.5260
LT	 0.9400	 0.5140
LU	 0.9090	 0.4580
LV	 0.9370	 0.5310
LW	 0.7970	 0.3950
LX	 0.9280	 0.5070
LY	 0.9640	 0.5190
LZ	 0.9430	 0.5100



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Chain	Atom inclusion	Q-score
La	 0.9540	 0.5430
Lb	 0.9170	 0.4880
Lc	 0.9270	 0.4980
Ld	 0.8530	 0.4950
Le	 0.9430	 0.5430
Lf	 0.9390	 0.5400
Lg	 0.9370	 0.5280
Lh	 0.9290	 0.4920
Li	 0.9060	 0.4760
Lj	 0.9510	 0.5530
Lk	 0.8820	 0.4560
Ll	 0.9300	 0.5270
Lm	 0.9430	 0.5150
Ln	 0.8520	 0.4730
Lo	 0.9530	 0.5340
Lp	 0.9050	 0.5190
Lq	 0.9490	 0.5240
Lr	 0.5960	 0.2870
Ls	 0.3250	 0.1470
NC	 0.1260	 0.3880
SA	 0.9020	 0.4520
SB	 0.8580	 0.4510
SC	 0.8750	 0.4610
SD	 0.7540	 0.3640
SE	 0.8600	 0.4640
SF	 0.7550	 0.3620
SG	 0.8870	 0.4130
SH	 0.8690	 0.4260
SI	 0.8800	 0.4630
SJ	 0.8530	 0.4350
SK	 0.8160	 0.3240
SL	 0.8560	 0.4990
SM	 0.3060	 0.1880
SN	 0.8760	 0.4700
SO	 0.9090	 0.4740
SP	 0.7420	 0.2980
SQ	 0.7450	 0.3470
SR	 0.8360	 0.3960
SS	 0.7820	 0.3100
ST	 0.7960	 0.3260
SU	 0.7630	 0.3490
SV	 0.8960	 0.4610

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Chain	Atom inclusion	Q-score
SW	 0.9030	 0.4890
SX	 0.8760	 0.4770
SY	 0.8670	 0.4190
SZ	 0.7790	 0.3090
Sa	 0.9080	 0.4830
Sb	 0.8900	 0.4730
Sc	 0.8120	 0.4170
Sd	 0.8060	 0.3710
Se	 0.9070	 0.4650
Sf	 0.6990	 0.1840