



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 04:38 AM UTC

PDB ID : 7Z3N / pdb_00007z3n
EMDB ID : EMD-14479
Title : Cryo-EM structure of the ribosome-associated RAC complex on the 80S ribosome - RAC-1 conformation
Authors : Kisonaite, M.; Wild, K.; Sinning, I.
Deposited on : 2022-03-02
Resolution : 3.20 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:

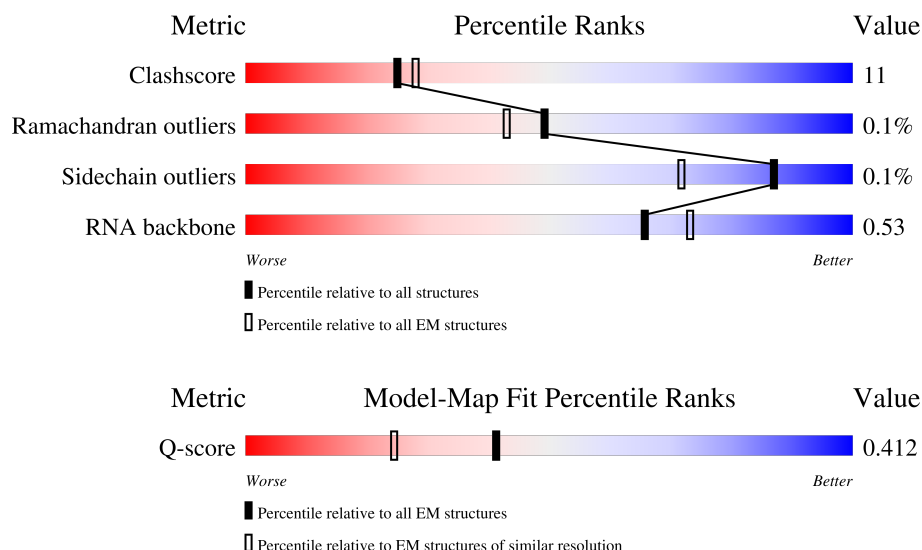
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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

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

The reported resolution of this entry is 3.20 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	15020 (2.70 - 3.70)

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	

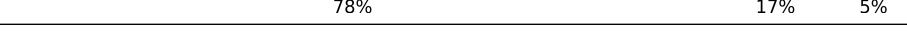
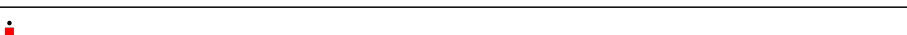
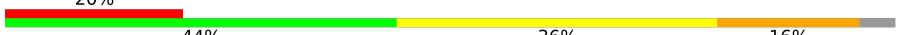
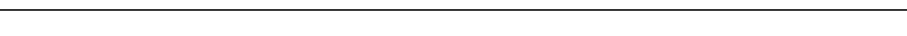
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Mol	Chain	Length	Quality of chain
4	4	156	
5	A	316	
6	B	302	
7	C	446	
8	D	578	
9	LA	254	
10	LB	392	
11	LC	365	
12	LD	304	
13	LE	200	
14	LF	249	
15	LG	262	
16	LH	192	
17	LI	219	
18	LJ	173	
19	LK	165	
20	LL	213	
21	LM	142	
22	LN	203	
23	LO	204	
24	LP	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	
54	SA	285	
55	SB	255	
56	SC	263	
57	SD	254	
58	SE	264	
59	SF	212	
60	SG	239	
61	SH	203	
62	SI	202	
63	SJ	190	
64	SK	159	
65	SL	161	
66	SM	144	
67	SN	151	
68	SO	150	
69	SP	153	
70	SQ	143	
71	SR	143	
72	SS	156	
73	ST	153	
74	SU	116	
75	SV	98	
76	SW	130	
77	SX	145	

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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 213543 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	1772	Total	C	N	O	P	0	0
			37781	16882	6728	12399	1772		

- 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
			3548	2211	661	672	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	102	Total	C	N	O	S	0	0
			827	538	143	145	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).

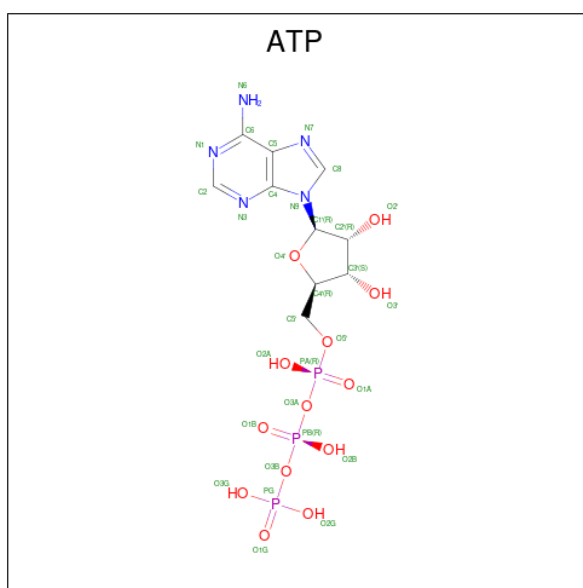
Mol	Chain	Residues	Atoms		AltConf
86	1	360	Total	Mg	0
			360	360	
86	2	66	Total	Mg	0
			66	66	
86	3	6	Total	Mg	0
			6	6	
86	4	10	Total	Mg	0
			10	10	
86	D	1	Total	Mg	0
			1	1	
86	LB	1	Total	Mg	0
			1	1	
86	LC	1	Total	Mg	0
			1	1	
86	LI	1	Total	Mg	0
			1	1	
86	LJ	1	Total	Mg	0
			1	1	
86	LN	1	Total	Mg	0
			1	1	
86	LP	1	Total	Mg	0
			1	1	
86	LV	1	Total	Mg	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
86	LW	1	Total	Mg	0
			1	1	
86	Lb	1	Total	Mg	0
			1	1	
86	SN	1	Total	Mg	0
			1	1	
86	SO	1	Total	Mg	0
			1	1	
86	SQ	1	Total	Mg	0
			1	1	

- Molecule 87 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).



Mol	Chain	Residues	Atoms					AltConf
87	D	1	Total	C	N	O	P	0
			31	10	5	13	3	

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

Mol	Chain	Residues	Atoms		AltConf
88	Lg	1	Total	Zn	0
			1	1	
88	Lj	1	Total	Zn	0
			1	1	
88	Lm	1	Total	Zn	0
			1	1	

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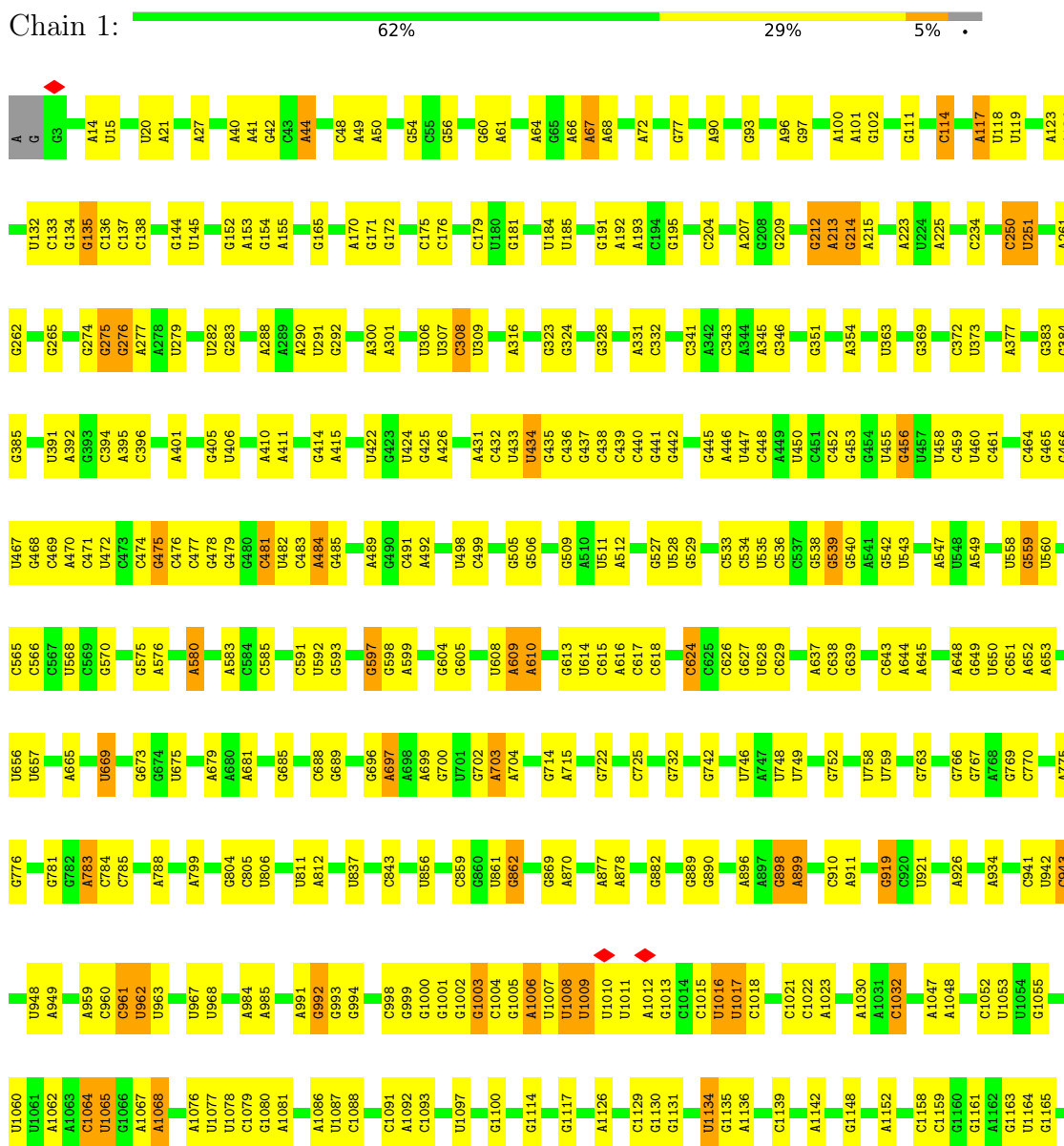
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Mol	Chain	Residues	Atoms		AltConf
88	Lo	1	Total 1	Zn 1	0
88	Lp	1	Total 1	Zn 1	0
88	Sa	1	Total 1	Zn 1	0
88	Sb	1	Total 1	Zn 1	0
88	Sd	1	Total 1	Zn 1	0

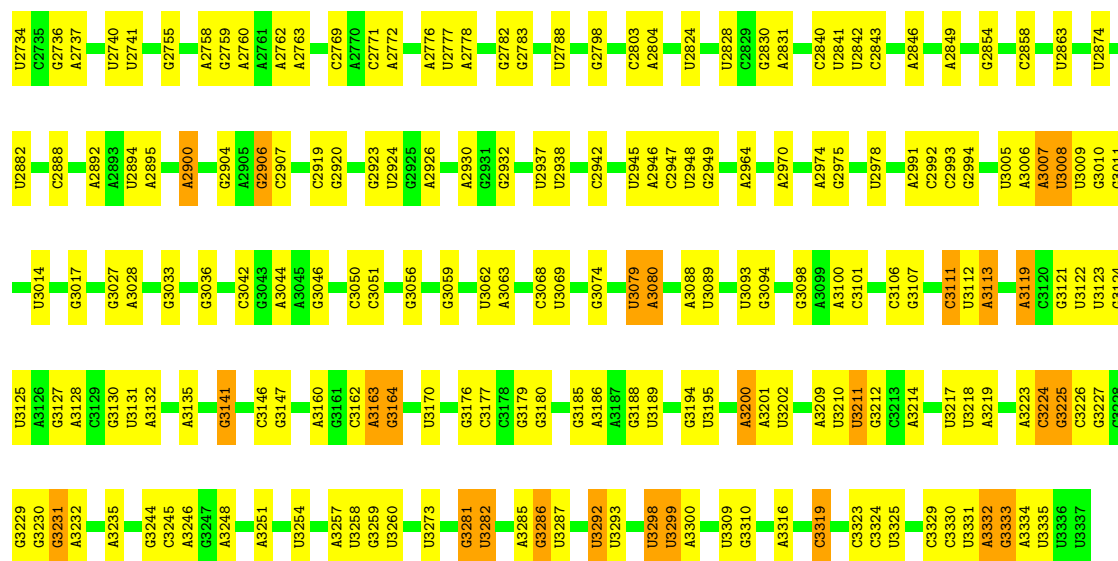
3 Residue-property plots

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.

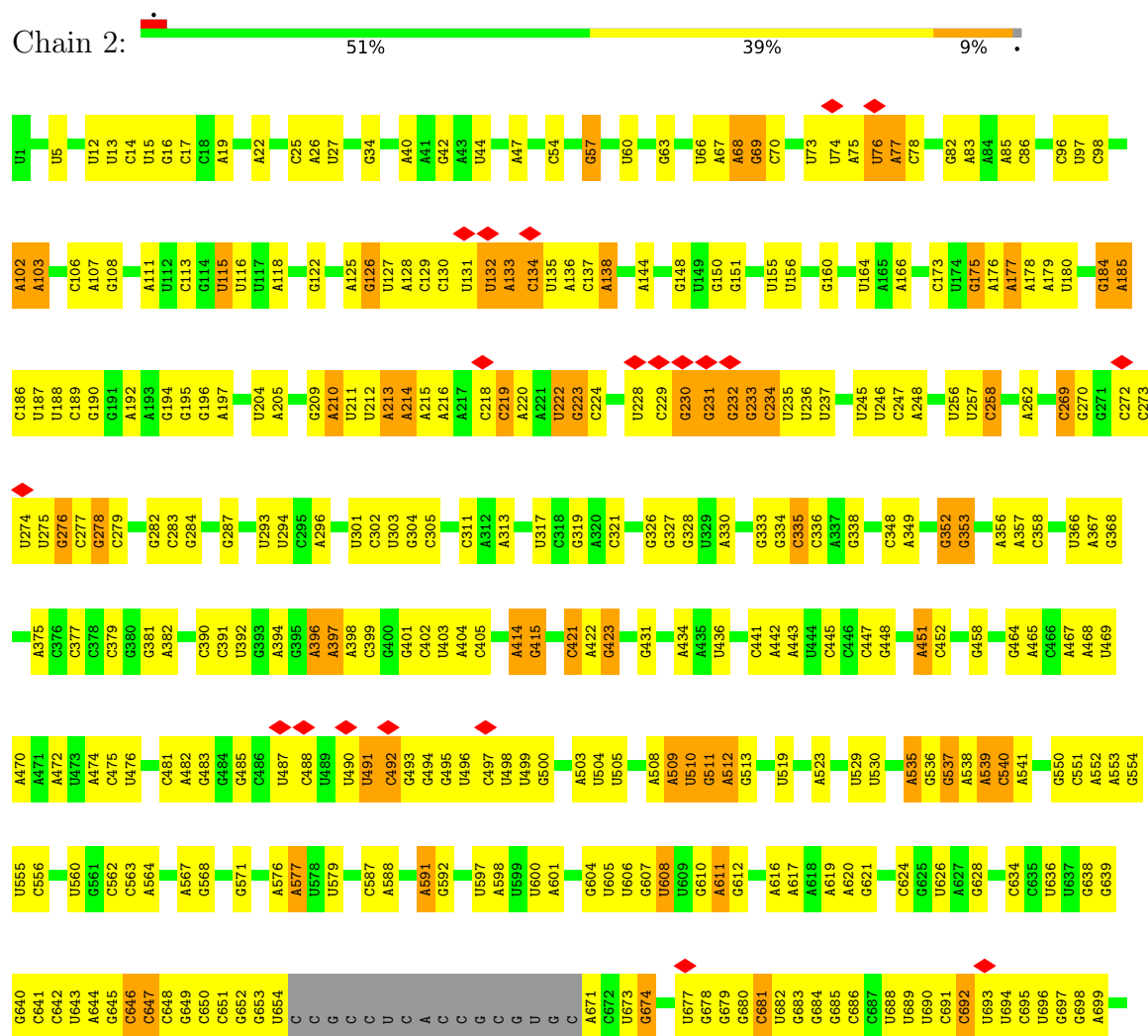
• Molecule 1: 26S rRNA

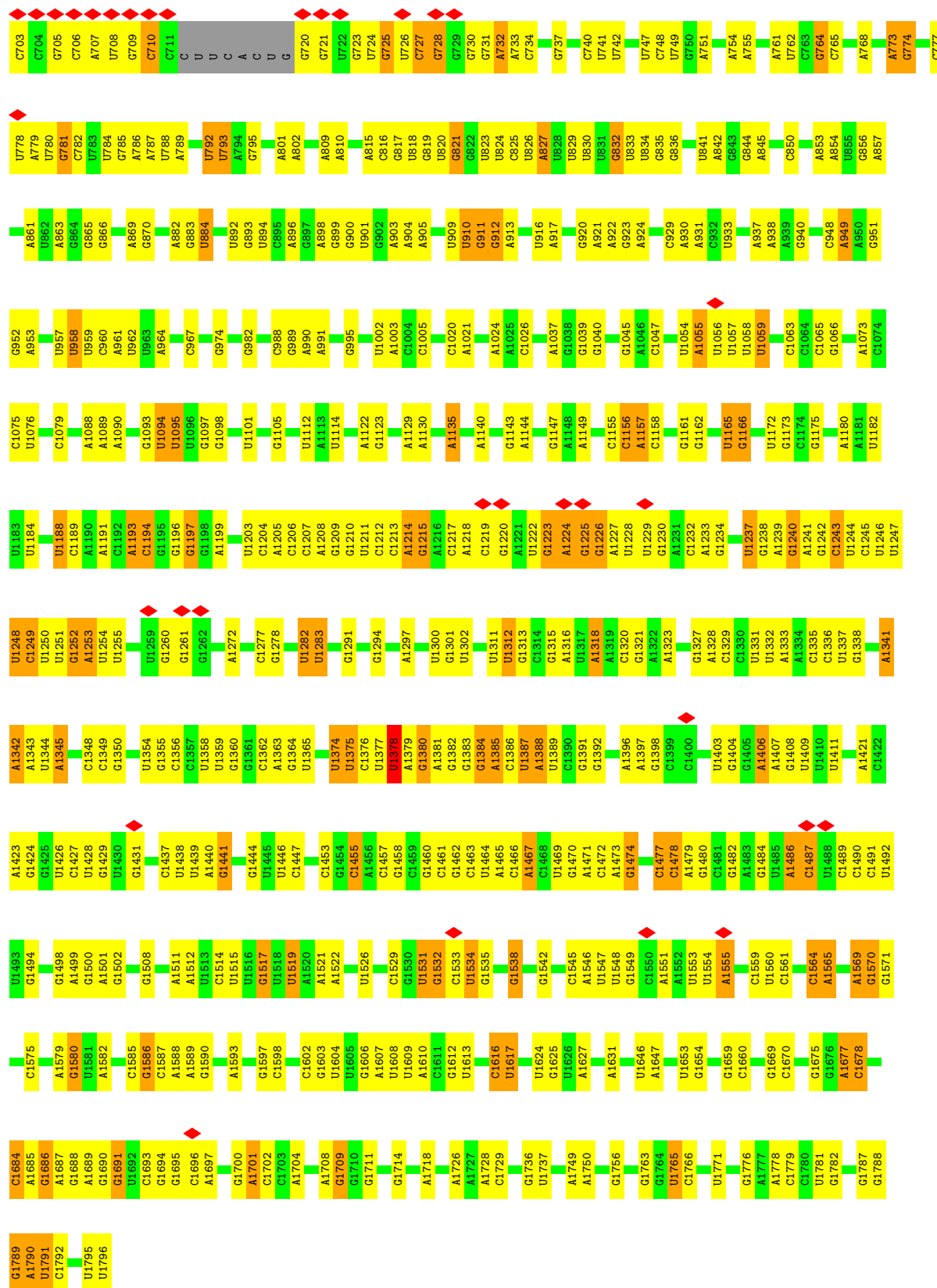






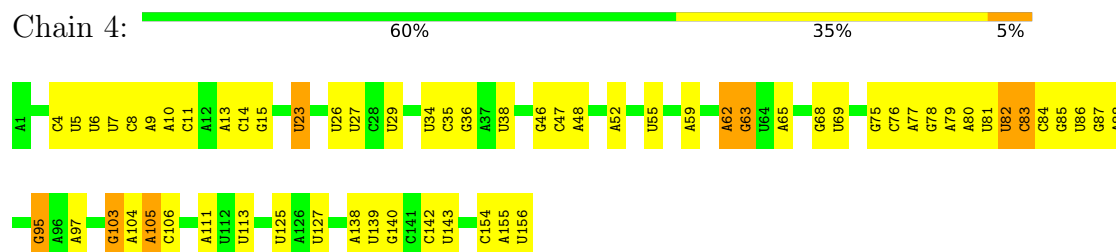
• Molecule 2: 18S rRNA



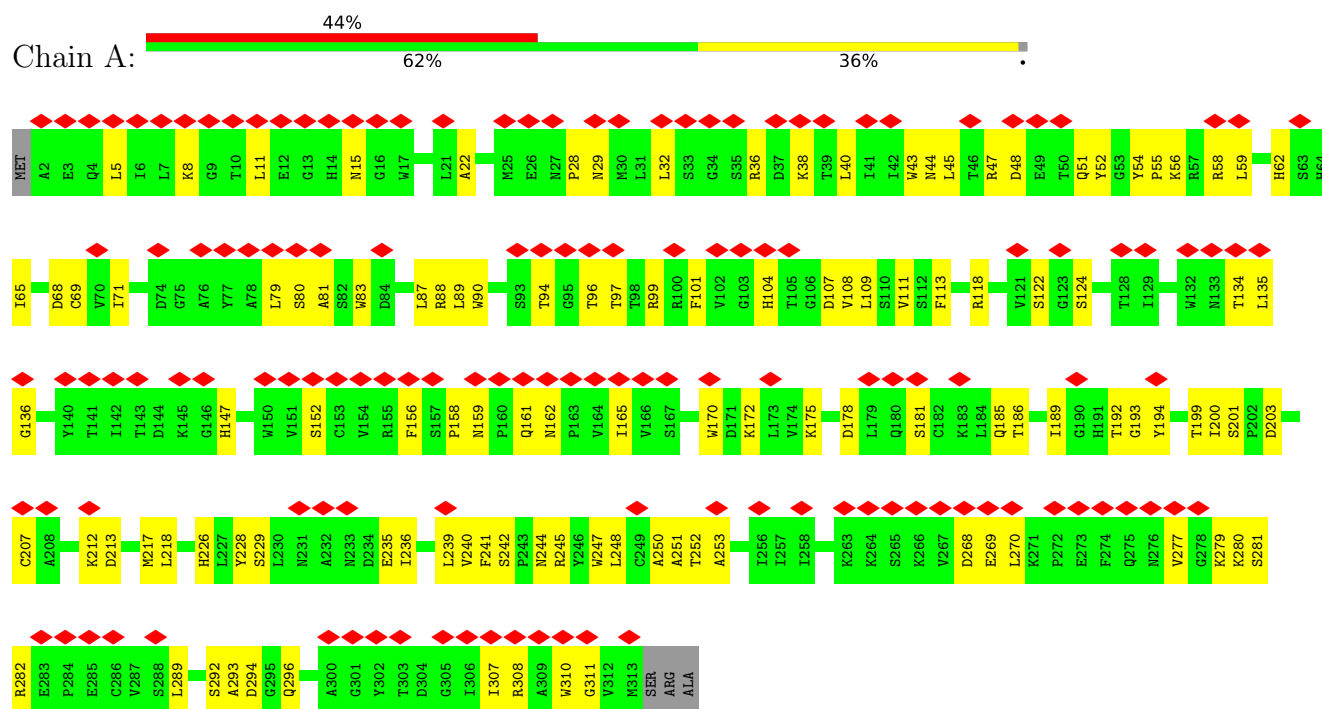


• Molecule 3: 5S rRNA

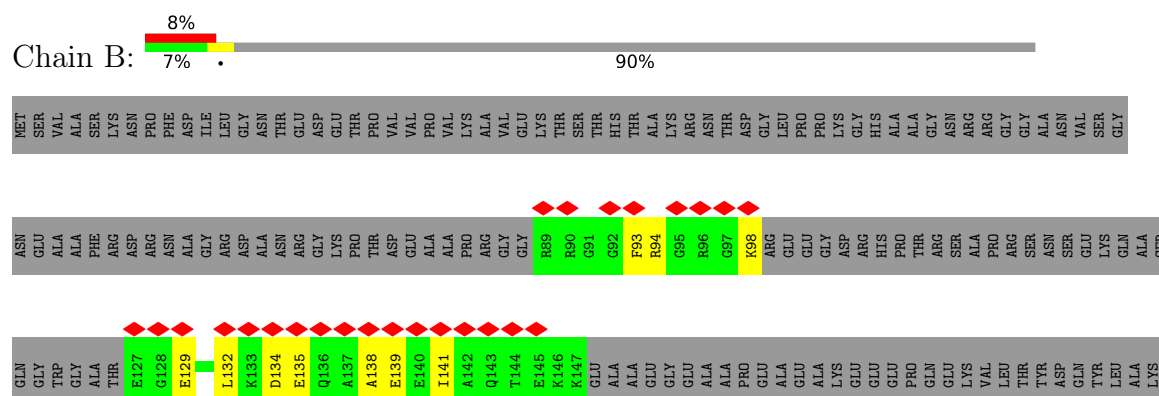
- Molecule 4: 5.8S rRNA



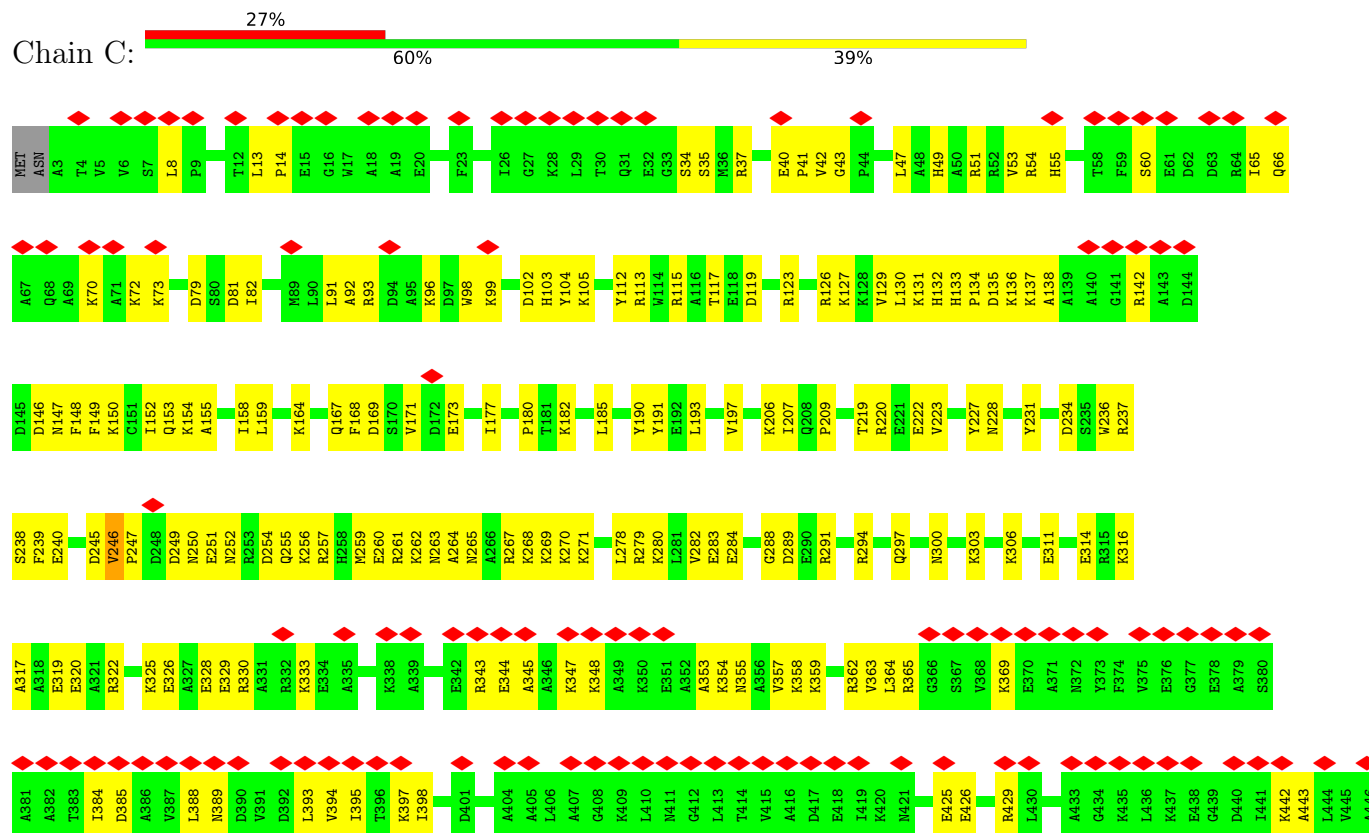
- Molecule 5: Putative guanine nucleotide-binding protein



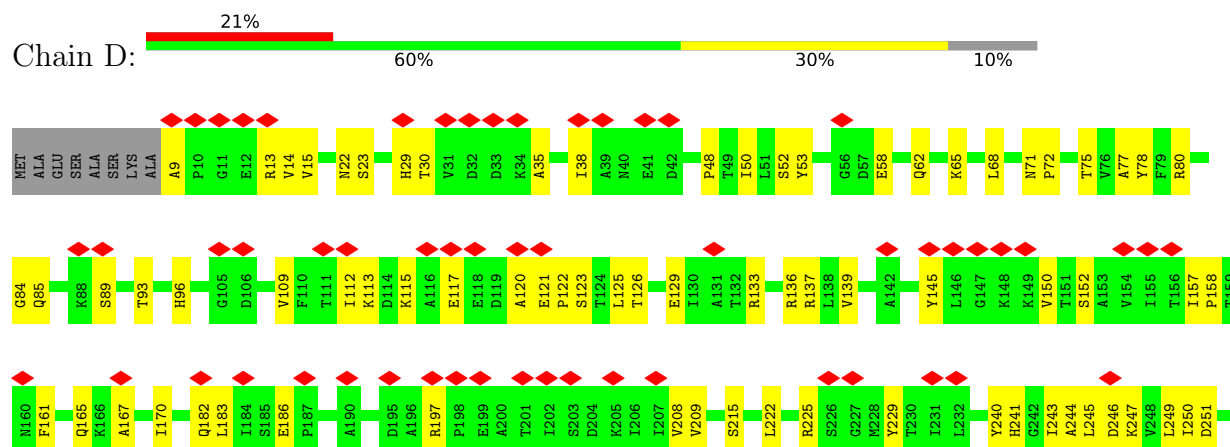
- Molecule 6: HABP4_PA1-RBP1 domain-containing protein

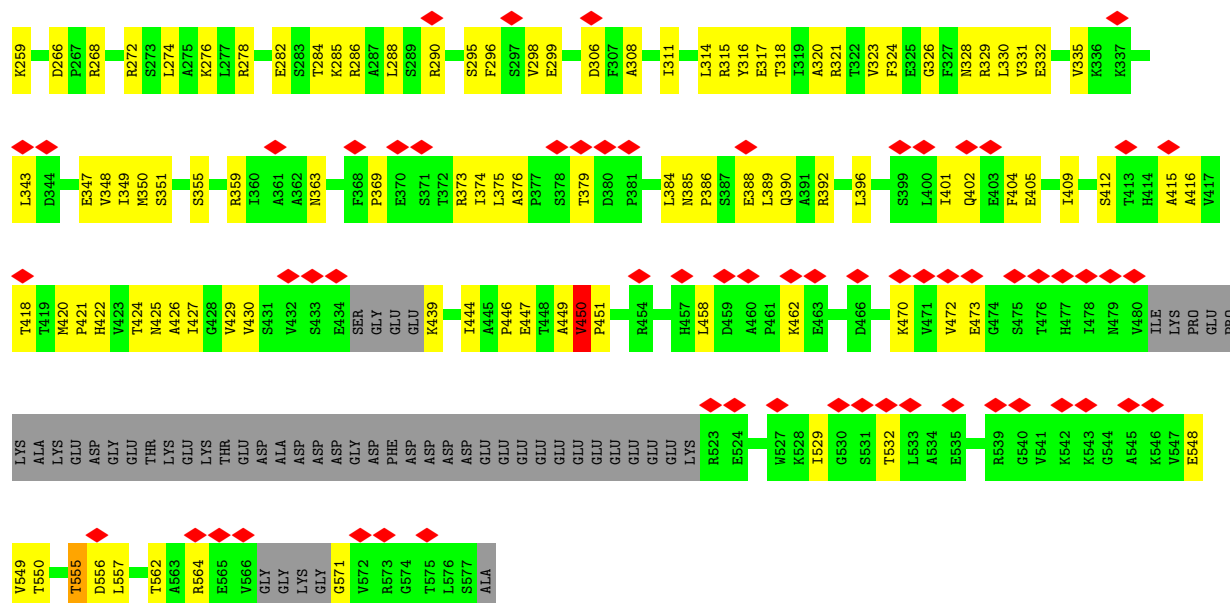


- Molecule 7: Putative ribosome associated protein



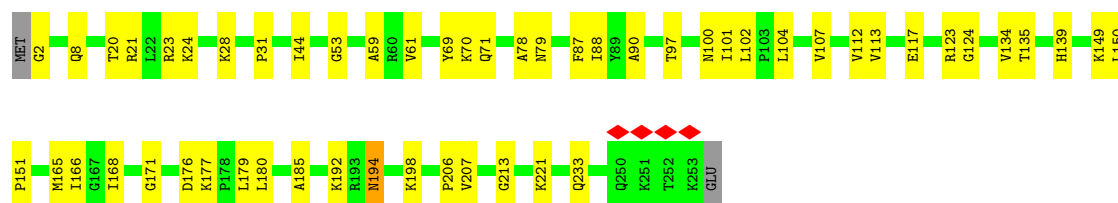
- Molecule 8: Putative heat shock protein





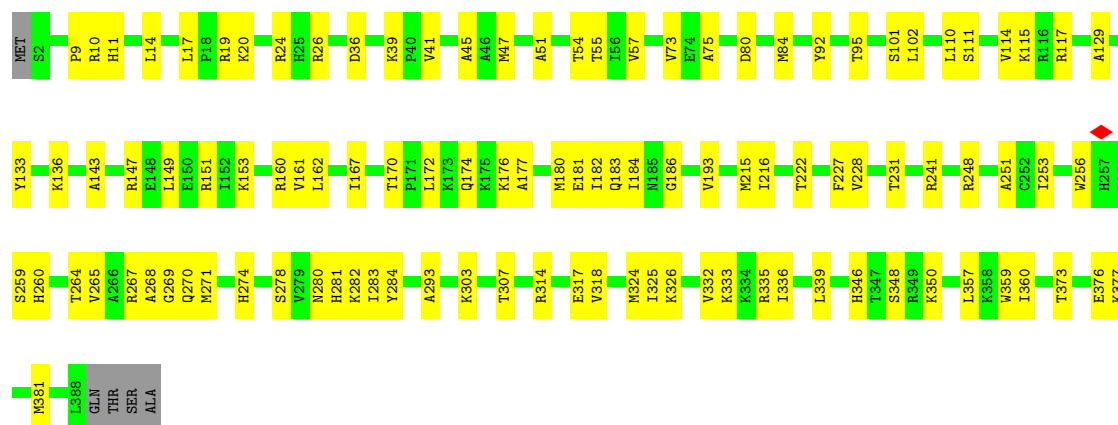
• Molecule 9: 60S ribosomal protein L2-like protein

Chain LA: 78% 21%



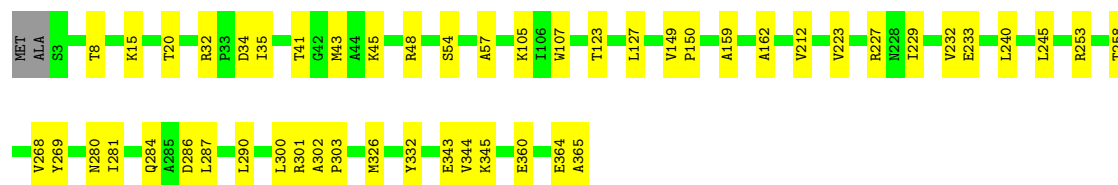
• Molecule 10: 60S ribosomal protein L3-like protein

Chain LB: 72% 27%



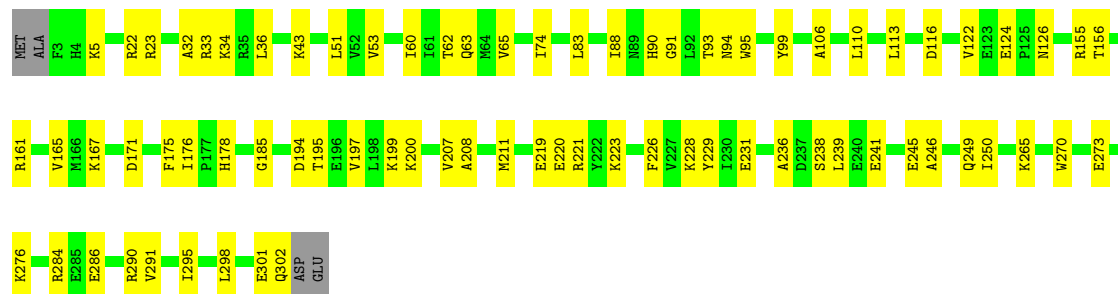
• Molecule 11: 60S ribosomal protein L4-like protein

Chain LC: 86% 14%



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

Chain LD: 74% 25% .



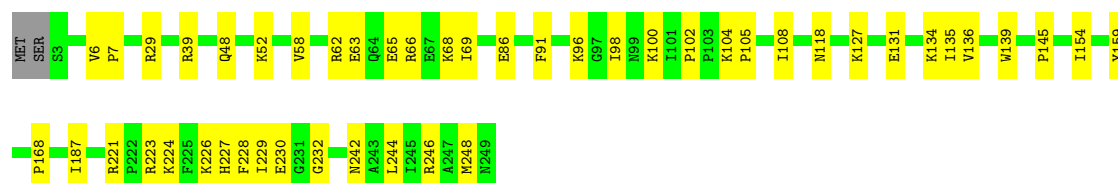
- Molecule 13: 60S ribosomal protein L6

Chain LE: 73% 24% .



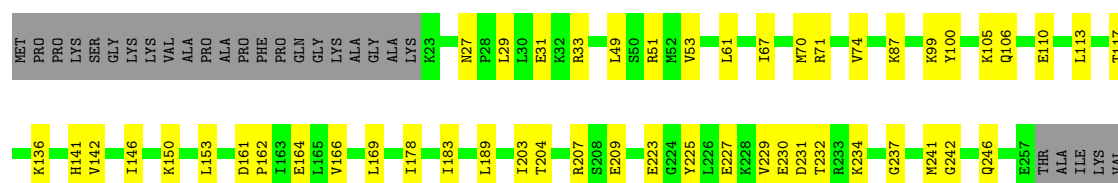
- Molecule 14: 60S ribosomal protein l7-like protein

Chain LF: 80% 19% .



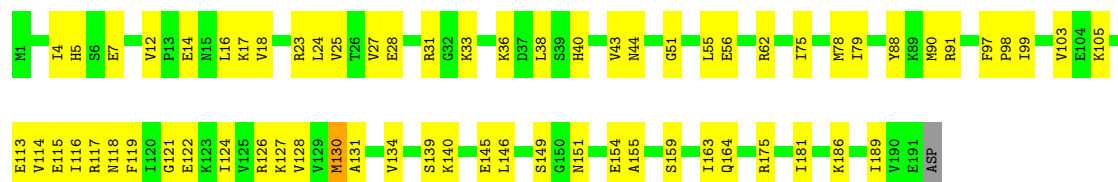
- Molecule 15: 60S ribosomal protein L8

Chain LG: 71% 19% 10%



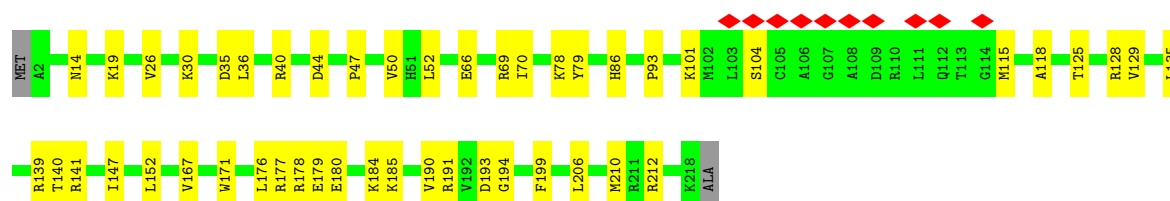
- Molecule 16: uL6

Chain LH: 



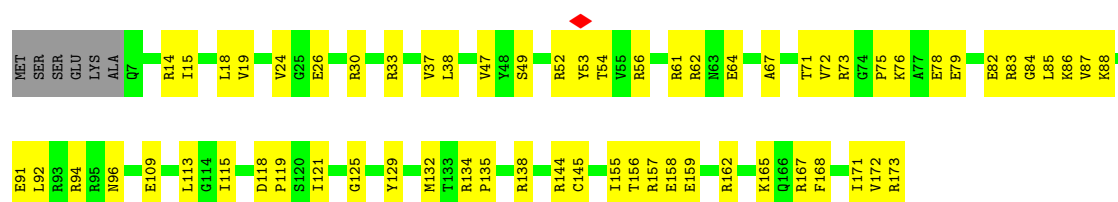
- Molecule 17: 60S ribosomal protein L10-like protein

Chain LI: 



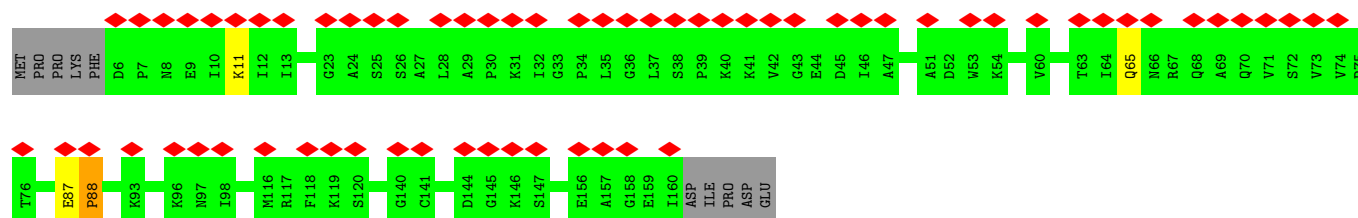
- Molecule 18: Putative ribosomal protein

Chain LJ: 



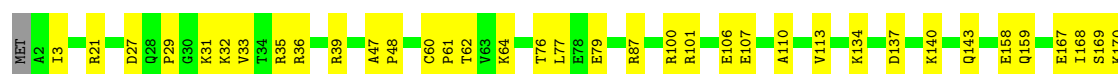
- Molecule 19: 60S ribosomal protein L12-like protein

Chain LK: 



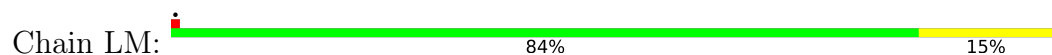
- Molecule 20: 60S ribosomal protein L13

Chain LL: 





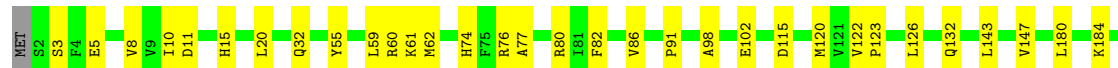
- Molecule 21: 60S ribosomal protein L14-like protein



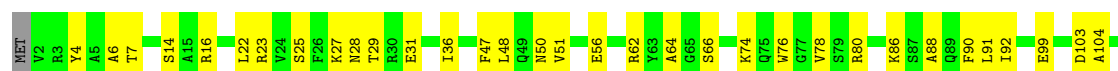
- Molecule 22: Ribosomal protein L15



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



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



- Molecule 25: Ribosomal protein L18-like protein





- Molecule 26: Ribosomal protein L19

Chain LR: 71% 24%



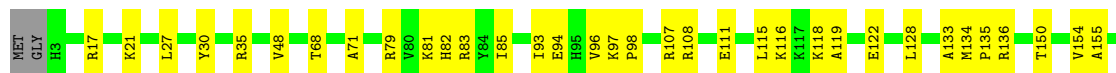
- Molecule 27: 60S ribosomal protein L20

Chain LS: 74% 26%



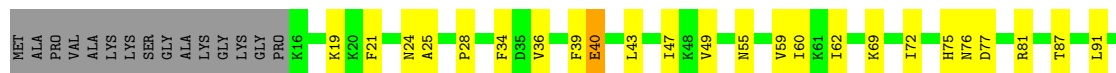
- Molecule 28: 60S ribosomal protein l21-like protein

Chain LT: 78% 21%



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

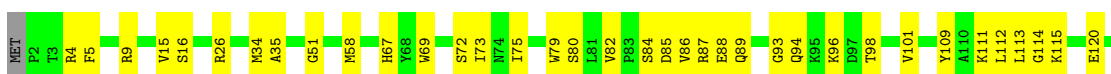
Chain LU: 57% 23% 20%



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

Chain LV: 83% 14%







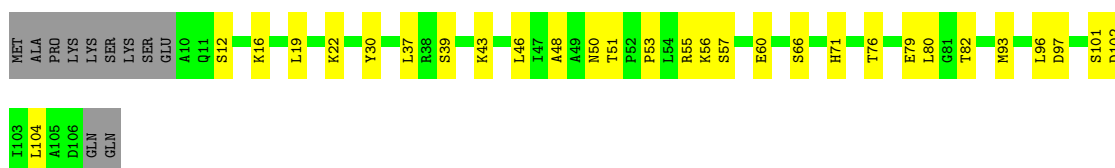
- Molecule 36: 60S ribosomal protein L29

Chain Lb: 78% 17% 5%



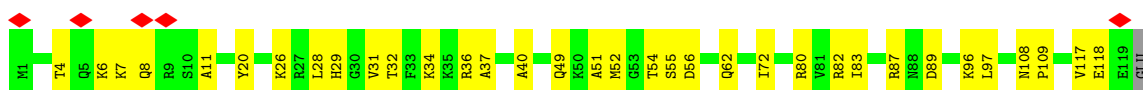
- Molecule 37: 60S ribosomal protein l30-like protein

Chain Lc: 63% 27% 10%



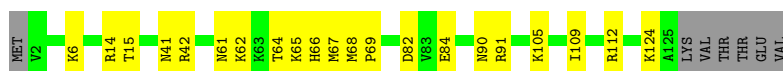
- Molecule 38: Putative 60S ribosomal protein

Chain Ld: 71% 28% .



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

Chain Le: 79% 16% 5%



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

Chain Lf: 78% 20% .



- Molecule 41: Ribosomal protein l34-like protein

Chain Lg: 66% 28% 6%



- Molecule 42: Dolichyl-diphosphooligosaccharide--protein glycotransferase

- Molecule 43: 60S ribosomal protein L36

- Molecule 44: Ribosomal protein L37

- Molecule 45: eL38

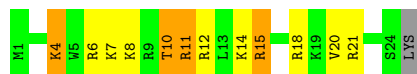
- Molecule 46: Ribosomal protein eL39

- Molecule 47: Putative ribosomal protein

WORLDWIDE
PDB
PROTEIN DATA BANK

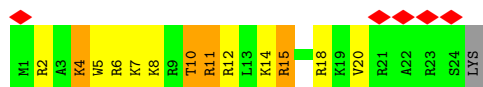
- Molecule 48: 60S ribosomal protein L41-A

Chain Ln:  48% 32% 16% .



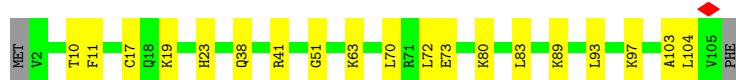
- Molecule 48: 60S ribosomal protein L41-A

Chain Lr:  20% 44% 36% 16% .



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

Chain Lo:  80% 18% .



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

Chain Lp:  73% 26% .

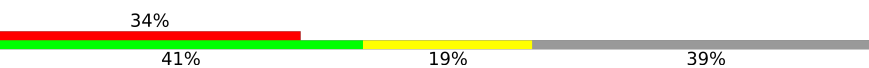


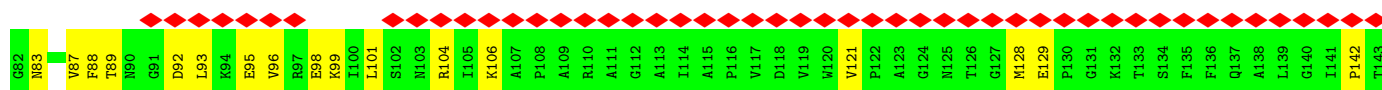
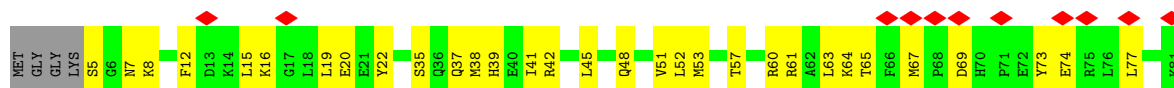
- Molecule 51: Putative 60S ribosomal protein

Chain Lq:  69% 27% .

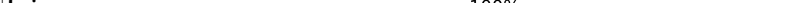


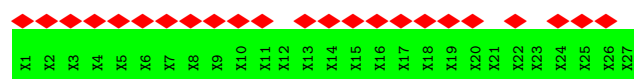
- Molecule 52: 60S acidic ribosomal protein P0

Chain Ls:  34% 41% 19% 39%

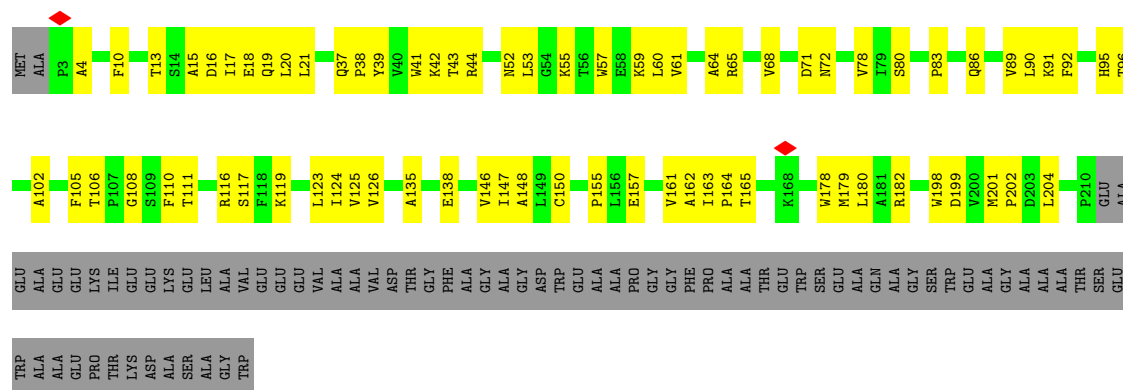


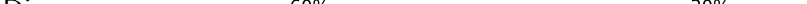


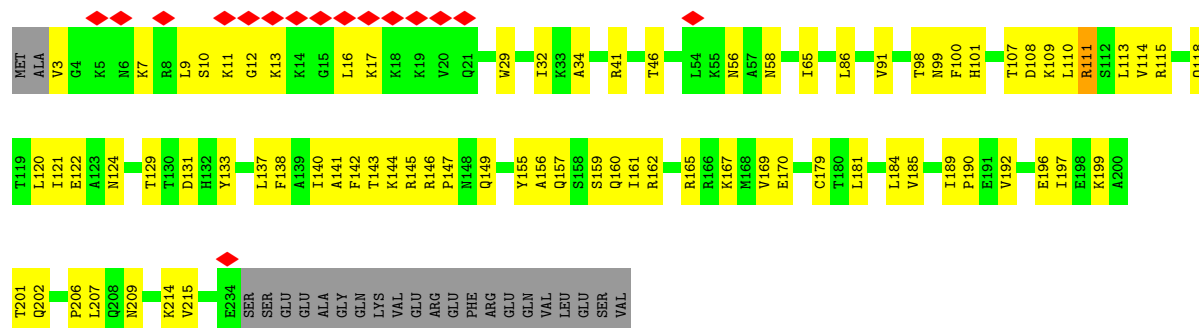
Chain NC:  85% 100%

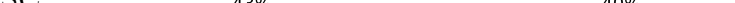


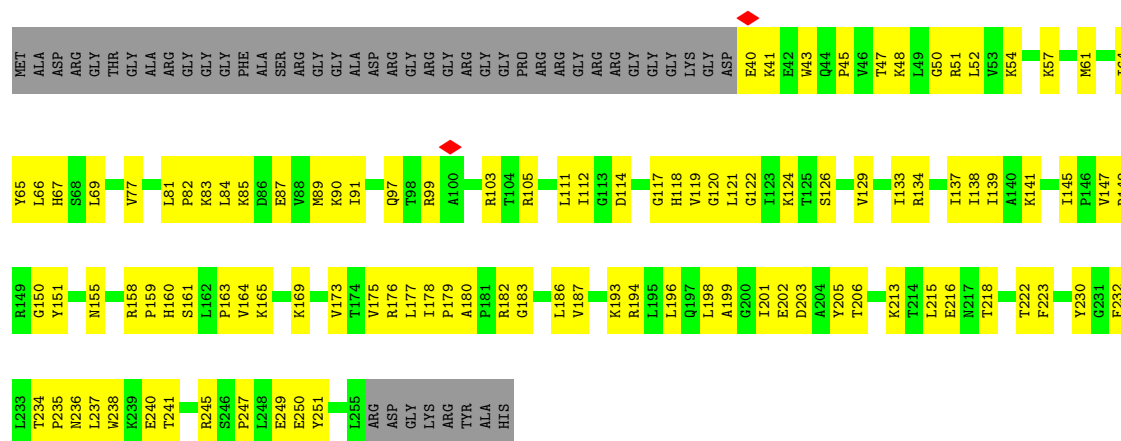
Chain SA:



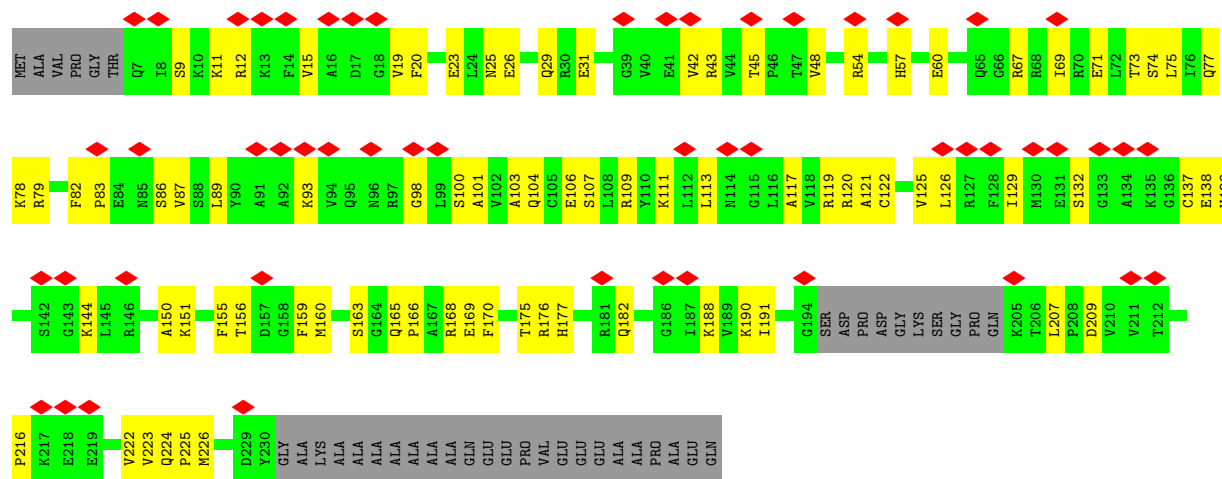
Chain SB: 



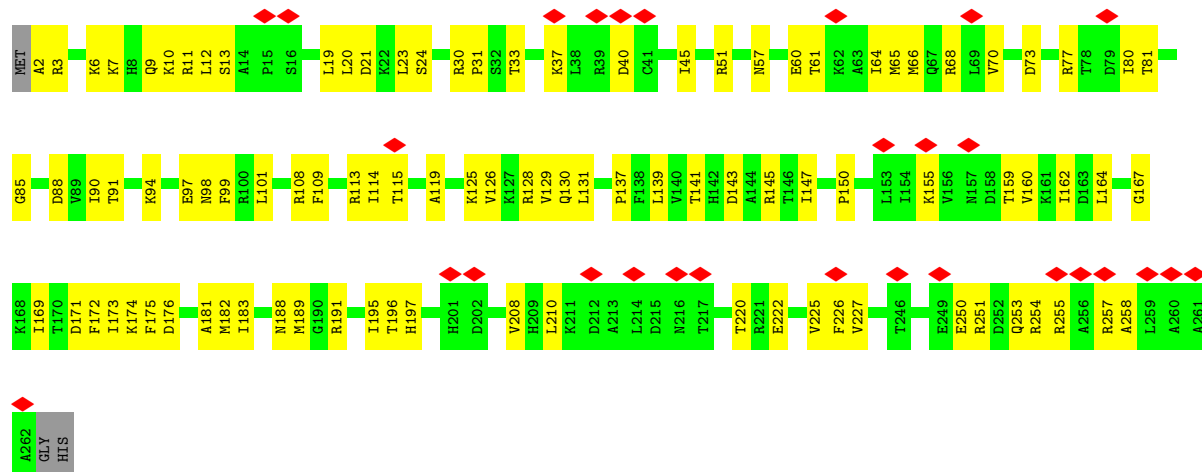
Chain SC: 



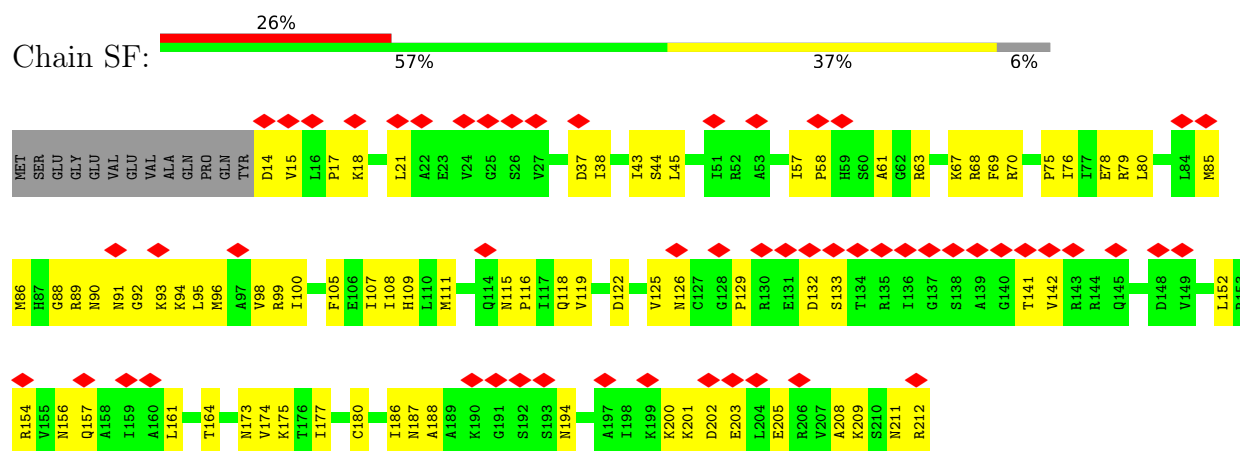
• Molecule 57: 40S ribosomal protein S3-like protein



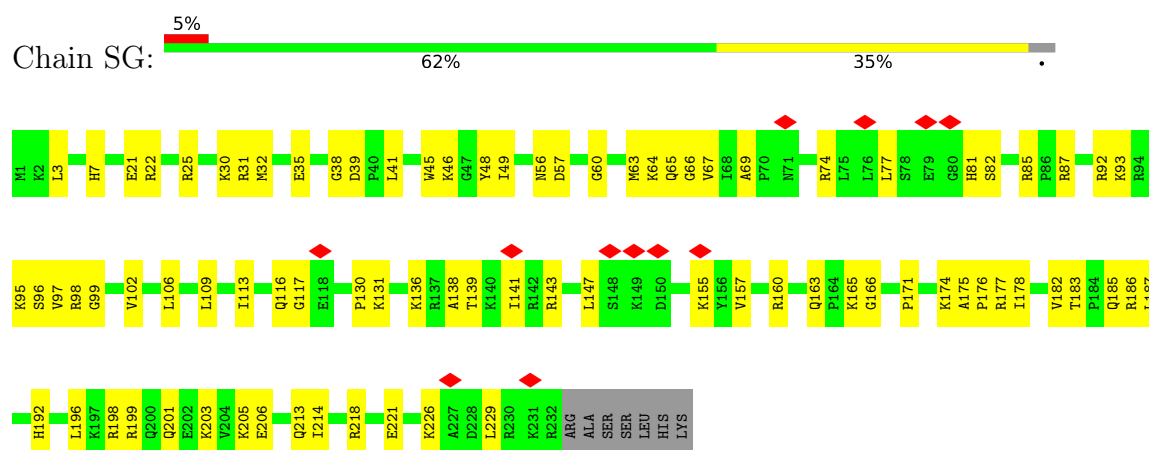
• Molecule 58: 40S ribosomal protein S4



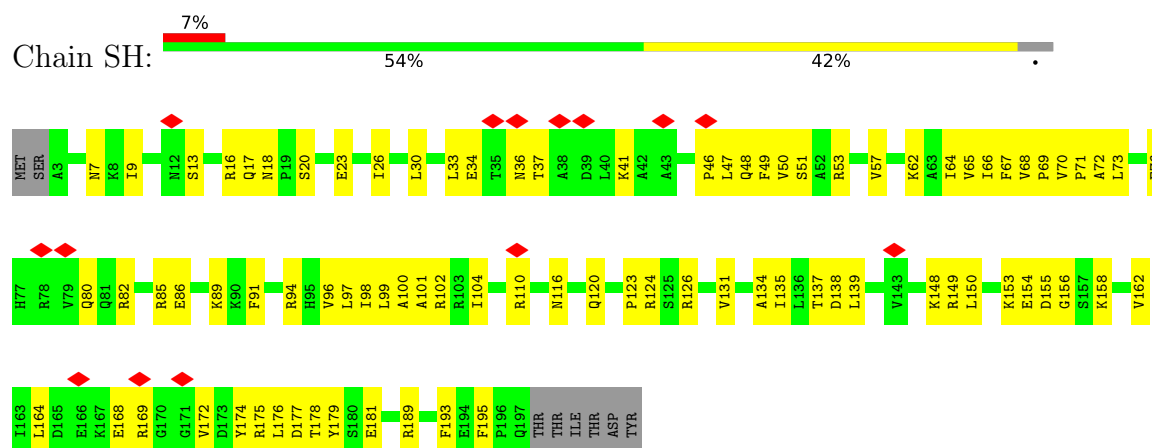
- Molecule 59: 40S ribosomal protein s5-like protein



- Molecule 60: 40S ribosomal protein S6



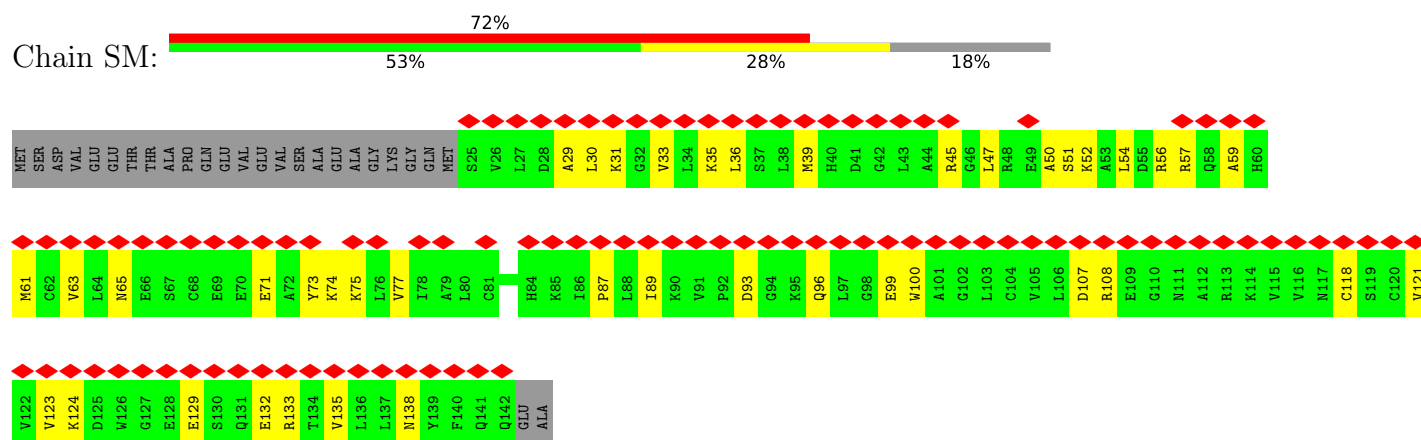
- Molecule 61: 40S ribosomal protein S7



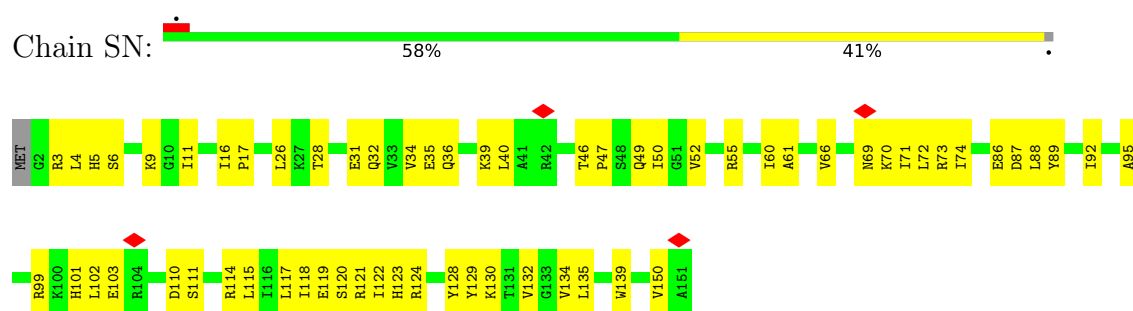
- Molecule 62: 40S ribosomal protein S8



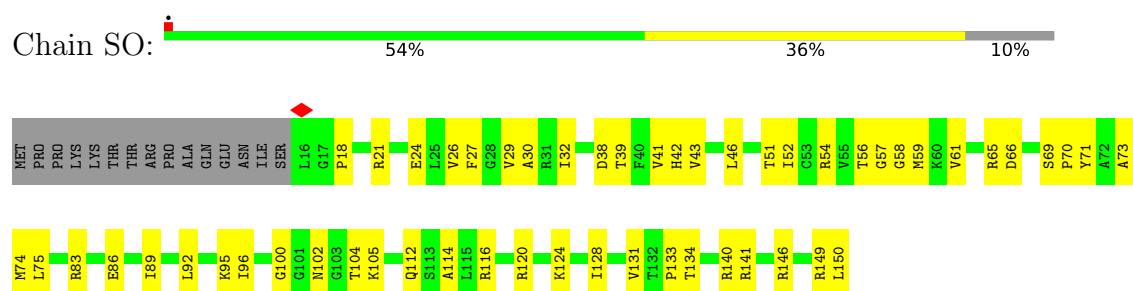
- Molecule 66: 40S ribosomal protein S12



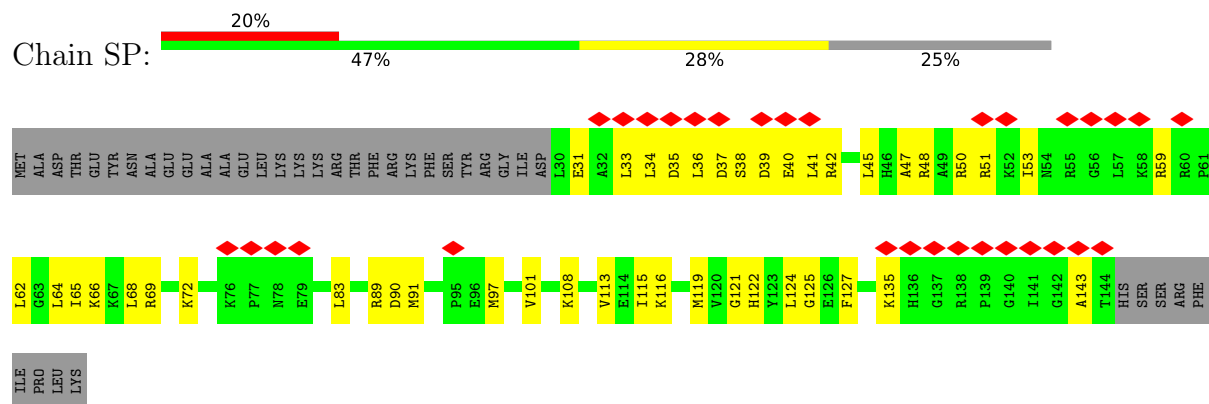
- Molecule 67: 40S ribosomal protein S13-like protein



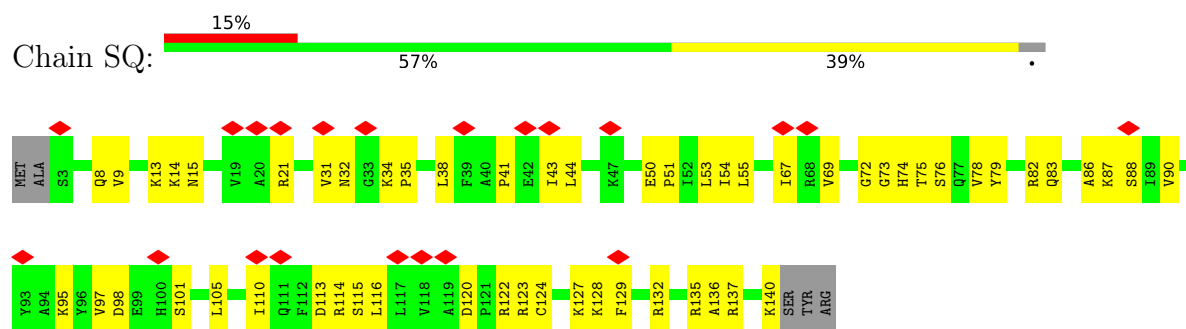
- Molecule 68: 40S ribosomal protein S14-like protein



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



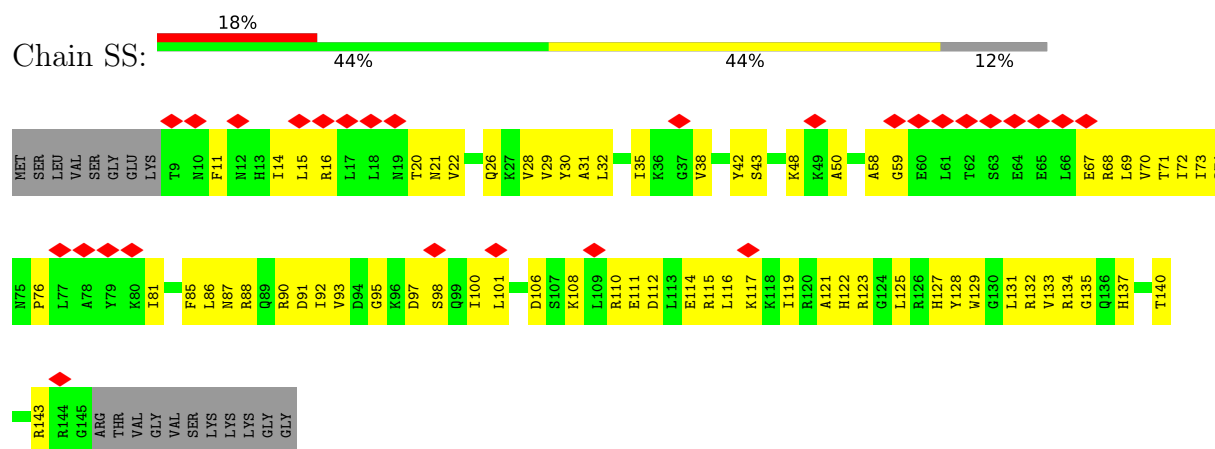
- Molecule 70: 40S ribosomal protein S16-like protein



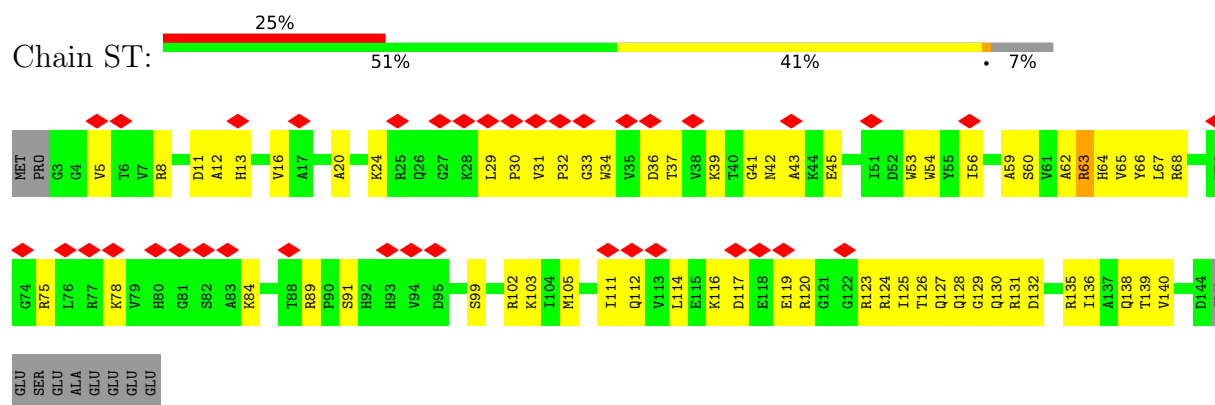
- Molecule 71: 40S ribosomal protein S17-like protein



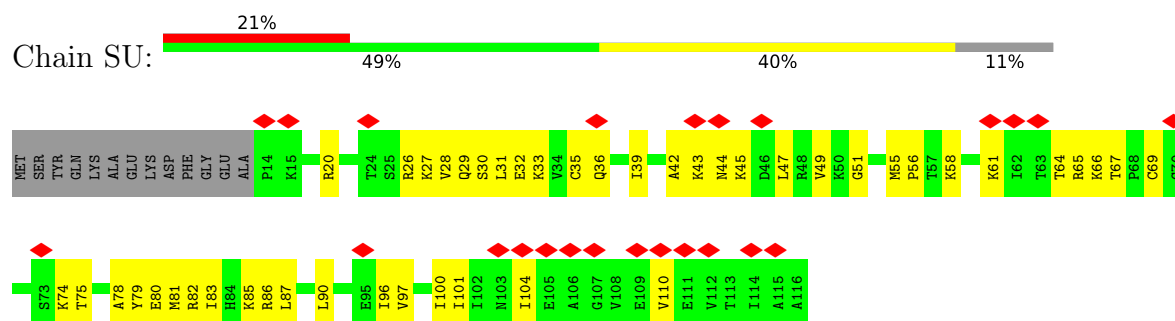
- Molecule 72: Putative ribosomal protein



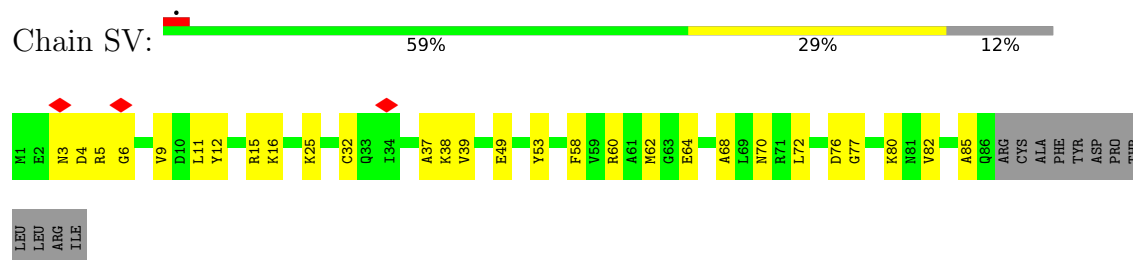
- Molecule 73: 40S ribosomal protein S19-like protein



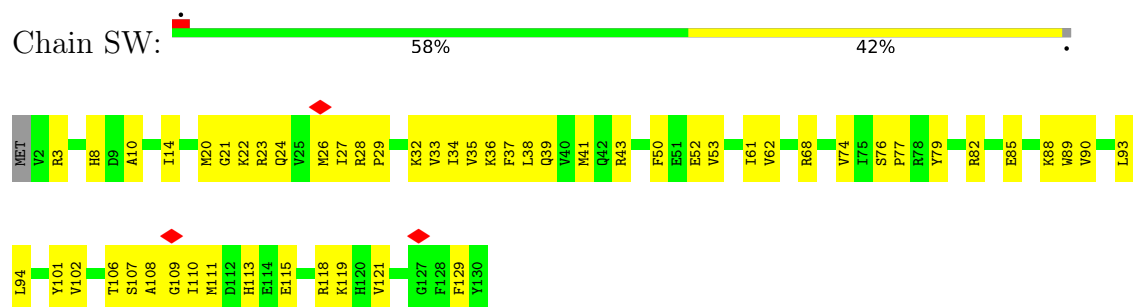
- Molecule 74: 40S ribosomal protein S20-like protein



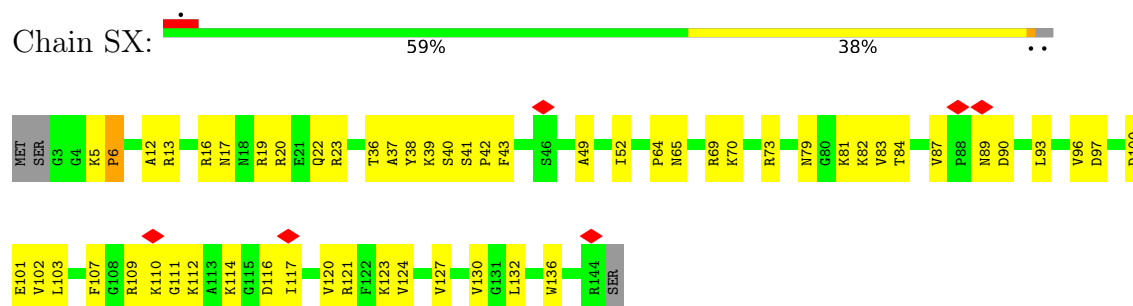
- Molecule 75: 40S ribosomal protein S21-like protein



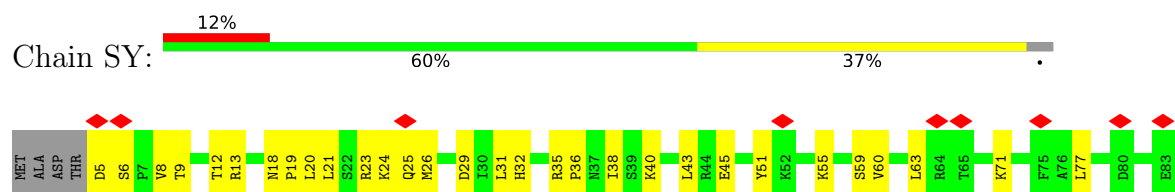
- Molecule 76: 40S ribosomal protein S22-like protein

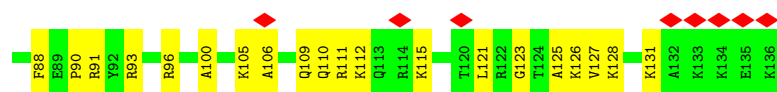


- Molecule 77: 40S ribosomal protein s23-like protein

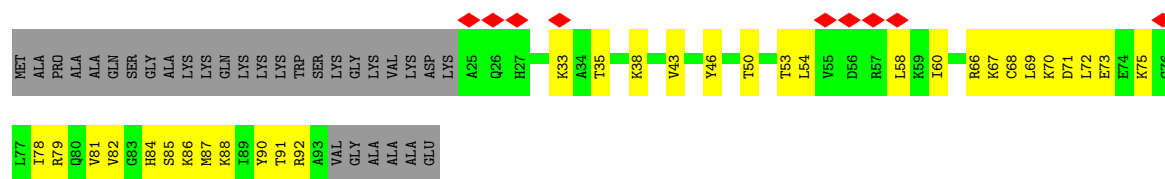


- Molecule 78: 40S ribosomal protein S24

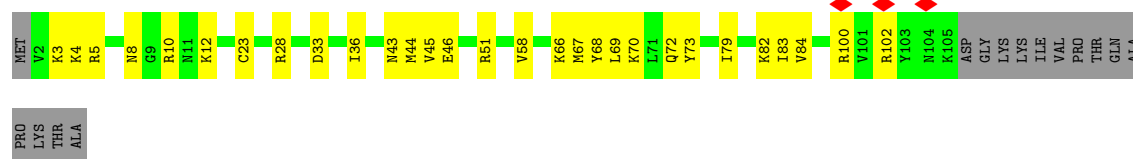




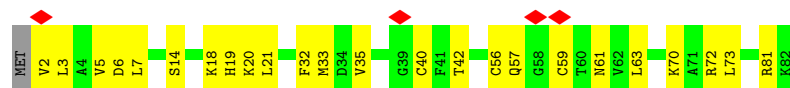
- Molecule 79: 40S ribosomal protein S25



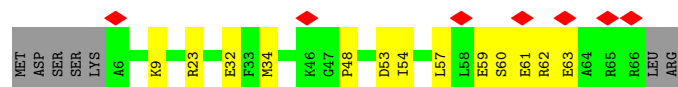
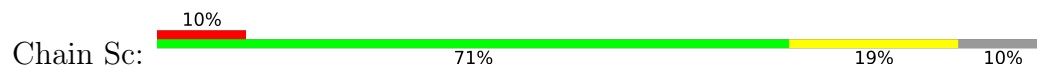
- Molecule 80: 40S ribosomal protein S26



- Molecule 81: Ribosomal protein s27-like protein

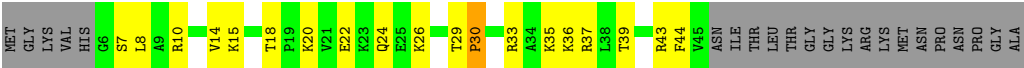


- Molecule 82: 40S ribosomal protein S28-like protein

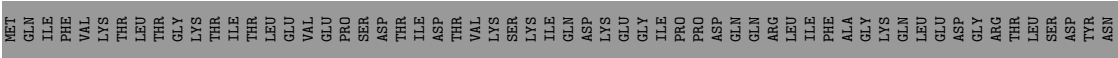
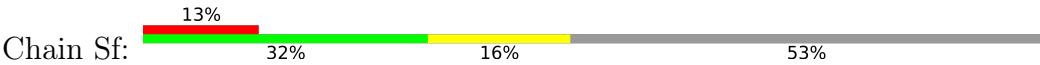


- Molecule 83: Ribosomal protein uS14





• Molecule 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	305951	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	25.266	Depositor
Minimum map value	-11.982	Depositor
Average map value	-0.007	Depositor
Map value standard deviation	0.913	Depositor
Recommended contour level	1.8	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: SAC, MG, ZN, OMG, ATP

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	0.11	0/76339	0.29	0/119028
2	2	0.12	0/42256	0.32	1/65852 (0.0%)
3	3	0.10	0/2833	0.28	0/4413
4	4	0.10	0/3710	0.31	0/5778
5	A	0.17	0/2495	0.51	0/3390
6	B	0.13	0/242	0.36	0/314
7	C	0.20	0/3606	0.52	0/4836
8	D	0.17	0/4002	0.48	1/5437 (0.0%)
9	LA	0.11	0/1964	0.39	0/2641
10	LB	0.12	0/3156	0.40	0/4238
11	LC	0.13	0/2815	0.37	0/3795
12	LD	0.15	0/2487	0.44	0/3341
13	LE	0.16	0/1547	0.44	0/2081
14	LF	0.16	0/2055	0.43	0/2758
15	LG	0.14	0/1929	0.43	0/2579
16	LH	0.15	0/1525	0.45	1/2050 (0.0%)
17	LI	0.13	0/1797	0.39	0/2413
18	LJ	0.19	0/1389	0.56	1/1856 (0.1%)
19	LK	0.12	0/761	0.40	0/1056
20	LL	0.14	0/1695	0.41	0/2276
21	LM	0.13	0/1144	0.39	0/1539
22	LN	0.13	0/1740	0.39	0/2332
23	LO	0.15	0/1638	0.46	0/2197
24	LP	0.16	0/1495	0.45	0/2014
25	LQ	0.11	0/1507	0.37	0/2017
26	LR	0.18	0/1525	0.48	0/2028
27	LS	0.13	0/1460	0.37	0/1965
28	LT	0.14	0/1292	0.38	0/1738
29	LU	0.21	0/840	0.55	1/1123 (0.1%)
30	LV	0.13	0/1012	0.40	0/1361
31	LW	0.17	0/1088	0.47	0/1443
32	LX	0.17	0/981	0.50	0/1324

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	LY	0.16	0/1079	0.43	0/1443
34	LZ	0.14	0/1134	0.44	0/1519
35	La	0.13	0/1212	0.40	0/1627
36	Lb	0.16	0/518	0.53	0/684
37	Lc	0.17	0/731	0.45	0/983
38	Ld	0.17	0/979	0.47	0/1308
39	Le	0.12	0/1019	0.37	0/1358
40	Lf	0.15	0/874	0.40	0/1176
41	Lg	0.16	0/904	0.43	0/1210
42	Lh	0.19	0/1014	0.51	0/1349
43	Li	0.19	0/844	0.51	0/1115
44	Lj	0.17	0/697	0.47	0/922
45	Lk	0.18	0/666	0.56	1/884 (0.1%)
46	Ll	0.11	0/445	0.34	0/593
47	Lm	0.16	0/424	0.53	0/561
48	Ln	0.38	0/225	0.90	0/289
48	Lr	0.39	0/225	0.90	0/289
49	Lo	0.12	0/835	0.37	0/1105
50	Lp	0.13	0/705	0.43	0/940
51	Lq	0.13	0/1101	0.40	0/1482
52	Ls	0.15	0/1477	0.47	0/1995
54	SA	0.21	0/1683	0.57	0/2299
55	SB	0.20	0/1900	0.55	1/2551 (0.0%)
56	SC	0.20	0/1703	0.55	0/2303
57	SD	0.20	0/1712	0.57	0/2299
58	SE	0.17	0/2112	0.51	0/2842
59	SF	0.20	0/1578	0.53	0/2130
60	SG	0.19	0/1906	0.47	0/2547
61	SH	0.19	0/1587	0.53	0/2140
62	SI	0.16	0/1654	0.48	0/2213
63	SJ	0.20	0/1489	0.59	1/1993 (0.1%)
64	SK	0.19	0/764	0.55	0/1038
65	SL	0.14	0/1249	0.41	0/1678
66	SM	0.20	0/934	0.57	0/1255
67	SN	0.20	0/1205	0.57	0/1627
68	SO	0.17	0/1014	0.52	0/1361
69	SP	0.19	0/932	0.55	0/1248
70	SQ	0.17	0/1098	0.52	0/1472
71	SR	0.24	0/1060	0.71	0/1424
72	SS	0.18	0/1133	0.53	0/1520
73	ST	0.23	0/1137	0.60	1/1533 (0.1%)
74	SU	0.17	0/828	0.55	0/1112
75	SV	0.15	0/671	0.47	0/900

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	SW	0.20	0/1055	0.57	0/1416
77	SX	0.45	1/1116 (0.1%)	0.80	3/1489 (0.2%)
78	SY	0.17	0/1075	0.51	0/1431
79	SZ	0.16	0/550	0.52	0/736
80	Sa	0.13	0/852	0.39	0/1136
81	Sb	0.15	0/623	0.47	0/843
82	Sc	0.16	0/487	0.44	0/653
83	Sd	0.15	0/427	0.54	0/570
84	Se	0.60	1/325 (0.3%)	1.04	3/427 (0.7%)
85	Sf	0.11	0/614	0.34	0/813
All	All	0.14	2/227906 (0.0%)	0.39	15/333044 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
77	SX	6	PRO	CG-CD	-12.56	1.08	1.50
84	Se	30	PRO	CG-CD	-8.85	1.20	1.50

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
77	SX	6	PRO	N-CD-CG	-15.07	80.59	103.20
84	Se	30	PRO	CA-N-CD	-10.75	96.95	112.00
84	Se	30	PRO	N-CD-CG	-10.19	87.91	103.20
77	SX	6	PRO	CA-CB-CG	-8.70	87.97	104.50
73	ST	63	ARG	CB-CG-CD	7.46	128.45	111.30
77	SX	6	PRO	CA-N-CD	-6.89	102.35	112.00
63	SJ	52	ARG	CA-CB-CG	6.43	126.97	114.10
84	Se	30	PRO	CA-CB-CG	-6.05	93.00	104.50
8	D	450	VAL	CG1-CB-CG2	-5.80	98.04	110.80
18	LJ	109	GLU	CB-CA-C	5.64	120.03	109.71
45	Lk	13	GLU	CA-CB-CG	5.30	124.69	114.10
55	SB	111	ARG	CB-CG-CD	5.17	123.18	111.30
29	LU	40	GLU	N-CA-CB	5.15	117.78	110.16
2	2	1378	U	C2'-C3'-O3'	5.14	117.22	109.50
16	LH	130	MET	CB-CG-SD	5.02	127.75	112.70

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	600	0
2	2	37781	0	19038	612	0
3	3	2535	0	1284	28	0
4	4	3319	0	1678	39	0
5	A	2438	0	2385	102	0
6	B	243	0	237	9	0
7	C	3548	0	3547	151	0
8	D	3942	0	3967	135	0
9	LA	1925	0	1999	38	0
10	LB	3088	0	3206	77	0
11	LC	2758	0	2883	41	0
12	LD	2440	0	2431	59	0
13	LE	1518	0	1619	40	0
14	LF	2017	0	2130	40	0
15	LG	1900	0	2066	34	0
16	LH	1505	0	1581	47	0
17	LI	1760	0	1798	32	0
18	LJ	1367	0	1405	51	0
19	LK	762	0	362	2	0
20	LL	1666	0	1756	33	0
21	LM	1125	0	1198	19	0
22	LN	1703	0	1767	52	0
23	LO	1613	0	1706	23	0
24	LP	1472	0	1518	43	0
25	LQ	1481	0	1596	37	0
26	LR	1506	0	1603	36	0
27	LS	1425	0	1484	38	0
28	LT	1266	0	1328	27	0
29	LU	827	0	875	23	0
30	LV	994	0	1055	14	0
31	LW	1075	0	1146	21	0
32	LX	965	0	1050	23	0
33	LY	1065	0	1156	25	0
34	LZ	1111	0	1181	28	0
35	La	1180	0	1203	44	0
36	Lb	508	0	526	10	0
37	Lc	722	0	766	23	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	Ld	965	0	1028	26	0
39	Le	1001	0	1070	16	0
40	Lf	853	0	880	14	0
41	Lg	891	0	958	27	0
42	Lh	1003	0	1116	26	0
43	Li	836	0	915	25	0
44	Lj	684	0	712	17	0
45	Lk	658	0	721	19	0
46	Ll	435	0	473	7	0
47	Lm	418	0	459	12	0
48	Ln	224	0	271	12	0
48	Lr	224	0	271	17	0
49	Lo	822	0	891	16	0
50	Lp	697	0	737	18	0
51	Lq	1083	0	1140	29	0
52	Ls	1449	0	1488	57	0
53	NC	135	0	33	0	0
54	SA	1641	0	1650	67	0
55	SB	1871	0	1989	60	0
56	SC	1672	0	1777	89	0
57	SD	1688	0	1750	73	0
58	SE	2072	0	2155	84	0
59	SF	1557	0	1608	63	0
60	SG	1875	0	1983	69	0
61	SH	1562	0	1641	69	0
62	SI	1621	0	1645	66	0
63	SJ	1466	0	1582	70	0
64	SK	742	0	738	46	0
65	SL	1222	0	1289	25	0
66	SM	923	0	946	37	0
67	SN	1182	0	1264	59	0
68	SO	1002	0	1034	47	0
69	SP	917	0	978	37	0
70	SQ	1081	0	1151	50	0
71	SR	1045	0	1083	67	0
72	SS	1118	0	1172	58	0
73	ST	1117	0	1133	62	0
74	SU	819	0	895	48	0
75	SV	664	0	662	26	0
76	SW	1037	0	1076	47	0
77	SX	1099	0	1169	54	0
78	SY	1061	0	1150	45	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
79	SZ	546	0	591	28	0
80	Sa	839	0	891	27	0
81	Sb	611	0	633	24	0
82	Sc	484	0	513	14	0
83	Sd	419	0	418	28	0
84	Se	322	0	365	23	0
85	Sf	604	0	640	18	0
86	1	360	0	0	0	0
86	2	66	0	0	0	0
86	3	6	0	0	0	0
86	4	10	0	0	0	0
86	D	1	0	0	0	0
86	LB	1	0	0	0	0
86	LC	1	0	0	0	0
86	LI	1	0	0	0	0
86	LJ	1	0	0	0	0
86	LN	1	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	SN	1	0	0	0	0
86	SO	1	0	0	0	0
86	SQ	1	0	0	0	0
87	D	31	0	12	1	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	213543	0	161647	3930	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 11.

All (3930) 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)
7:C:246:VAL:CG2	7:C:259:MET:HE3	1.56	1.32
7:C:246:VAL:HG22	7:C:247:PRO:HD2	1.15	1.12
7:C:246:VAL:HG21	7:C:259:MET:CE	1.83	1.09
7:C:249:ASP:CG	8:D:259:LYS:HE2	1.79	1.08
7:C:246:VAL:HG21	7:C:259:MET:HE3	1.31	1.05
7:C:249:ASP:OD1	8:D:259:LYS:HE2	1.55	1.04
2:2:485:G:H1	2:2:496:U:H3	1.06	1.04
2:2:1467:A:N6	2:2:1534:U:H3	1.59	1.00
54:SA:83:PRO:HA	54:SA:86:GLN:HE22	1.29	0.98
71:SR:109:LYS:HG2	71:SR:113:LYS:HZ3	1.31	0.96
2:2:900:G:H21	2:2:905:A:H62	0.97	0.93
1:1:1000:G:H1	1:1:1017:U:H3	1.11	0.92
73:ST:29:LEU:HD23	73:ST:30:PRO:HD2	1.55	0.89
55:SB:107:THR:HB	55:SB:111:ARG:HH12	1.37	0.89
44:Lj:39:TYR:HB3	44:Lj:40:PRO:HD3	1.54	0.89
74:SU:27:LYS:HZ2	74:SU:30:SER:HB3	1.36	0.89
78:SY:23:ARG:HD2	78:SY:77:LEU:HD11	1.55	0.88
7:C:249:ASP:OD2	8:D:259:LYS:HG2	1.75	0.87
2:2:1388:A:H61	2:2:1403:U:H3	1.23	0.86
2:2:245:U:O3'	65:SL:41:LYS:NZ	2.09	0.86
7:C:246:VAL:HG23	7:C:259:MET:HE3	1.56	0.85
74:SU:64:THR:HG23	83:Sd:44:ARG:HH21	1.39	0.85
63:SJ:131:HIS:HD2	63:SJ:160:SER:HB2	1.40	0.85
8:D:450:VAL:HG23	8:D:451:PRO:HD3	1.59	0.85
2:2:681:C:H4'	76:SW:118:ARG:HH22	1.42	0.85
2:2:1580:G:N2	2:2:1607:A:OP2	2.10	0.85
5:A:189:ILE:HD12	57:SD:222:VAL:HG23	1.56	0.85
1:1:568:U:OP1	14:LF:246:ARG:NH2	2.10	0.83
1:1:1876:A:H61	1:1:2302:C:H42	1.22	0.83
65:SL:127:MET:HB3	65:SL:148:LEU:HB2	1.61	0.83
7:C:246:VAL:CG2	7:C:247:PRO:HD2	2.04	0.83
2:2:900:G:N2	2:2:905:A:H62	1.75	0.83
55:SB:115:ARG:HB2	55:SB:118:GLN:HE22	1.42	0.83
2:2:475:C:OP1	84:Se:37:ARG:NH1	2.11	0.83
56:SC:178:ILE:HB	56:SC:205:TYR:HB2	1.59	0.83
2:2:643:U:H2'	2:2:644:A:H8	1.43	0.82
7:C:191:TYR:HD1	7:C:291:ARG:HH21	1.26	0.82
55:SB:107:THR:HB	55:SB:111:ARG:NH1	1.95	0.82
55:SB:146:ARG:HB3	55:SB:149:GLN:HG3	1.61	0.82
54:SA:124:ILE:HB	54:SA:146:VAL:HG12	1.61	0.82
57:SD:109:ARG:HH21	57:SD:176:ARG:HB3	1.45	0.82
2:2:850:C:H5''	26:LR:176:ARG:HH12	1.44	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
65:SL:106:GLU:OE1	77:SX:13:ARG:NH2	2.11	0.81
74:SU:45:LYS:HG3	74:SU:47:LEU:HD13	1.62	0.81
74:SU:61:LYS:HD2	74:SU:78:ALA:HB1	1.60	0.81
2:2:900:G:H21	2:2:905:A:N6	1.76	0.81
2:2:391:C:H42	2:2:398:A:H62	1.25	0.81
2:2:1189:C:O2'	70:SQ:137:ARG:NH2	2.13	0.81
2:2:961:A:OP2	67:SN:70:LYS:NZ	2.14	0.81
63:SJ:57:LEU:HD11	63:SJ:67:ARG:HA	1.61	0.81
56:SC:120:GLY:HA2	56:SC:223:PHE:HE2	1.45	0.81
37:Lc:79:GLU:HA	37:Lc:82:THR:HG22	1.63	0.80
4:4:46:G:OP2	46:Ll:15:LYS:NZ	2.15	0.80
52:Ls:15:LEU:HB3	52:Ls:60:ARG:HH21	1.44	0.80
2:2:1467:A:H62	2:2:1534:U:H3	0.82	0.80
5:A:11:LEU:HD22	5:A:43:TRP:HZ2	1.47	0.80
76:SW:27:ILE:HB	76:SW:61:ILE:HB	1.62	0.80
1:1:732:G:OP1	36:Lb:44:ARG:NH1	2.15	0.79
2:2:1387:U:OP2	71:SR:49:LYS:NZ	2.16	0.79
52:Ls:98:GLU:HA	52:Ls:101:LEU:HD13	1.63	0.79
44:Lj:20:ARG:NH2	44:Lj:39:TYR:OH	2.16	0.79
1:1:3330:C:OP2	38:Ld:6:LYS:NZ	2.15	0.79
7:C:246:VAL:CG2	7:C:259:MET:CE	2.41	0.79
32:LX:91:GLU:HG2	32:LX:92:GLN:HG3	1.62	0.79
1:1:675:U:OP2	20:LL:36:ARG:NH2	2.16	0.79
1:1:1876:A:H61	1:1:2302:C:N4	1.81	0.79
5:A:236:ILE:HA	5:A:252:THR:HA	1.65	0.79
61:SH:23:GLU:HA	61:SH:26:ILE:HG12	1.65	0.78
5:A:199:THR:HG21	5:A:240:VAL:HA	1.63	0.78
79:SZ:72:LEU:HG	79:SZ:75:LYS:HE3	1.65	0.78
2:2:327:G:OP2	62:SI:176:ARG:NH1	2.16	0.78
48:Lr:8:LYS:HE3	48:Lr:12:ARG:HH12	1.48	0.78
70:SQ:31:VAL:HG23	70:SQ:67:ILE:HD11	1.65	0.78
2:2:761:A:OP1	63:SJ:77:ARG:NH2	2.16	0.78
56:SC:183:GLY:HA3	63:SJ:51:ARG:HH12	1.47	0.78
1:1:291:U:OP2	43:Li:42:GLN:NE2	2.16	0.78
5:A:11:LEU:HB2	5:A:307:ILE:HB	1.64	0.78
16:LH:4:ILE:HG22	16:LH:5:HIS:HD2	1.48	0.78
2:2:747:U:OP1	76:SW:82:ARG:NH2	2.16	0.78
2:2:1114:U:OP1	48:Ln:21:ARG:NH2	2.15	0.78
51:Lq:54:ILE:HB	51:Lq:114:ARG:HD3	1.66	0.78
24:LP:168:GLU:HB2	24:LP:171:LEU:HD21	1.65	0.77
48:Ln:8:LYS:HE3	48:Ln:12:ARG:HH12	1.48	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
77:SX:69:ARG:HG3	77:SX:117:ILE:HG22	1.66	0.77
1:1:2621:G:H2'	1:1:2622:G:C8	2.20	0.77
56:SC:165:LYS:HG3	56:SC:179:PRO:HD2	1.66	0.77
58:SE:128:ARG:NH1	58:SE:129:VAL:O	2.16	0.77
63:SJ:129:GLN:OE1	63:SJ:131:HIS:ND1	2.18	0.77
2:2:1542:G:OP1	72:SS:123:ARG:NH2	2.17	0.77
7:C:280:LYS:NZ	7:C:284:GLU:OE2	2.18	0.77
9:LA:180:LEU:HD22	50:Lp:26:VAL:HG21	1.67	0.77
71:SR:36:ASP:CG	71:SR:47:ARG:HE	1.93	0.77
57:SD:73:THR:HG22	57:SD:89:LEU:HD23	1.67	0.77
2:2:898:A:H3'	2:2:899:G:H21	1.47	0.77
7:C:250:ASN:O	7:C:252:ASN:N	2.17	0.77
78:SY:121:LEU:HD13	78:SY:128:LYS:HG3	1.65	0.77
51:Lq:10:TRP:O	51:Lq:14:ARG:HB2	1.84	0.76
54:SA:59:LYS:NZ	54:SA:162:ALA:O	2.16	0.76
55:SB:137:LEU:HD13	55:SB:215:VAL:HG22	1.67	0.76
1:1:2978:U:O2	1:1:2992:C:N4	2.18	0.76
10:LB:51:ALA:O	10:LB:333:LYS:NZ	2.17	0.76
52:Ls:15:LEU:HD13	52:Ls:60:ARG:HE	1.51	0.76
78:SY:126:LYS:HD2	78:SY:127:VAL:HG13	1.68	0.76
5:A:242:SER:OG	5:A:245:ARG:O	2.04	0.76
2:2:1771:U:O4	48:Ln:4:LYS:NZ	2.19	0.75
2:2:824:U:H3	2:2:844:G:H1	1.32	0.75
74:SU:64:THR:OG1	83:Sd:40:ARG:NH1	2.19	0.75
77:SX:102:VAL:HG12	77:SX:127:VAL:HG12	1.68	0.75
2:2:1112:U:O3'	48:Ln:14:LYS:NZ	2.19	0.75
22:LN:9:GLU:HG3	43:Li:53:ILE:HG21	1.69	0.75
52:Ls:96:VAL:HG23	52:Ls:99:LYS:HD3	1.68	0.75
54:SA:86:GLN:HG3	54:SA:102:ALA:HB1	1.67	0.75
55:SB:138:PHE:HD2	55:SB:214:LYS:HG2	1.51	0.75
13:LE:50:LYS:O	13:LE:53:GLN:NE2	2.18	0.75
55:SB:196:GLU:HA	55:SB:199:LYS:HG2	1.69	0.75
2:2:111:A:O2'	65:SL:72:ARG:NH2	2.18	0.75
59:SF:45:LEU:HD13	59:SF:125:VAL:HG23	1.68	0.75
57:SD:165:GLN:HB2	57:SD:168:ARG:HH21	1.50	0.75
58:SE:94:LYS:HZ2	78:SY:19:PRO:HG2	1.52	0.74
65:SL:138:LYS:HG3	65:SL:139:THR:HG23	1.69	0.74
72:SS:132:ARG:HH21	72:SS:133:VAL:HG22	1.52	0.74
66:SM:61:MET:HA	66:SM:87:PRO:HB2	1.68	0.74
2:2:648:C:H2'	2:2:649:G:H8	1.52	0.74
61:SH:154:GLU:O	76:SW:43:ARG:NH2	2.20	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:SI:100:ALA:HB3	62:SI:173:ILE:HD12	1.69	0.74
77:SX:109:ARG:HB2	77:SX:114:LYS:HE3	1.68	0.74
52:Ls:57:THR:HB	52:Ls:60:ARG:HB3	1.69	0.74
61:SH:73:LEU:HD12	61:SH:100:ALA:HB2	1.70	0.74
35:La:84:SER:HA	35:La:87:ARG:HG2	1.68	0.74
1:1:1599:A:H5'	48:Lr:15:ARG:HH12	1.50	0.74
15:LG:230:GLU:O	15:LG:234:LYS:NZ	2.21	0.74
1:1:1222:C:H2'	1:1:1223:A:H8	1.52	0.73
1:1:1242:A:N3	1:1:1263:C:O2'	2.20	0.73
35:La:101:VAL:HG12	35:La:124:VAL:HB	1.70	0.73
45:Lk:51:ASP:OD2	45:Lk:54:LYS:NZ	2.20	0.73
7:C:54:ARG:NH1	8:D:412:SER:OG	2.21	0.73
1:1:1337:G:N2	1:1:1339:U:O2'	2.21	0.73
8:D:555:THR:C	8:D:557:LEU:H	1.96	0.73
15:LG:161:ASP:HB3	15:LG:162:PRO:HD3	1.68	0.73
2:2:643:U:H2'	2:2:644:A:C8	2.24	0.73
13:LE:19:ALA:HB3	13:LE:23:LYS:HG2	1.69	0.73
1:1:1614:G:OP1	34:LZ:106:ARG:NH1	2.21	0.73
20:LL:140:LYS:HA	20:LL:143:GLN:HG3	1.69	0.73
52:Ls:159:VAL:HG11	52:Ls:165:VAL:HG22	1.70	0.73
71:SR:10:LYS:HB3	71:SR:14:LYS:HZ3	1.51	0.73
2:2:485:G:N2	2:2:496:U:O2	2.19	0.73
4:4:8:C:H2'	4:4:9:A:H8	1.54	0.73
2:2:390:C:O2'	60:SG:92:ARG:NH2	2.21	0.73
73:ST:29:LEU:HD22	73:ST:54:TRP:CH2	2.23	0.73
8:D:209:VAL:HG22	8:D:349:ILE:HD11	1.71	0.73
56:SC:235:PRO:HA	56:SC:238:TRP:NE1	2.03	0.73
60:SG:64:LYS:HB2	60:SG:97:VAL:HG11	1.68	0.73
66:SM:61:MET:HE2	66:SM:123:VAL:HG23	1.71	0.73
2:2:706:C:H2'	2:2:707:A:C8	2.24	0.72
47:Lm:88:LYS:HZ2	47:Lm:89:PHE:HE1	1.37	0.72
64:SK:67:THR:HG23	64:SK:70:GLY:H	1.54	0.72
66:SM:93:ASP:HB3	66:SM:96:GLN:HE22	1.53	0.72
67:SN:35:GLU:OE1	67:SN:39:LYS:NZ	2.21	0.72
73:ST:116:LYS:HD2	73:ST:117:ASP:H	1.52	0.72
38:Ld:11:ALA:O	38:Ld:87:ARG:NH2	2.22	0.72
56:SC:155:ASN:ND2	75:SV:3:ASN:O	2.22	0.72
74:SU:65:ARG:O	83:Sd:44:ARG:NH2	2.23	0.72
2:2:77:A:O2'	60:SG:177:ARG:NH2	2.22	0.72
45:Lk:8:ILE:HD11	45:Lk:58:LEU:HD12	1.71	0.72
57:SD:79:ARG:HD2	64:SK:22:VAL:HG11	1.71	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2489:C:N3	15:LG:51:ARG:NH1	2.36	0.72
8:D:186:GLU:O	8:D:390:GLN:NE2	2.22	0.72
22:LN:68:ARG:NH1	22:LN:124:ASP:O	2.23	0.72
28:LT:48:VAL:HG11	28:LT:94:GLU:HG2	1.70	0.72
62:SI:156:VAL:HG21	62:SI:160:LEU:HD22	1.69	0.72
1:1:961:C:H3'	1:1:962:U:H4'	1.72	0.72
1:1:1701:U:O4	26:LR:128:LYS:NZ	2.21	0.72
2:2:175:G:H1'	60:SG:198:ARG:HH22	1.55	0.72
69:SP:91:MET:HE3	69:SP:124:LEU:HD12	1.71	0.72
5:A:58:ARG:HH22	70:SQ:95:LYS:HD3	1.54	0.72
5:A:158:PRO:HD3	5:A:200:ILE:HD12	1.71	0.72
54:SA:178:TRP:HZ3	54:SA:202:PRO:HG3	1.54	0.72
74:SU:101:ILE:HD11	74:SU:110:VAL:HG21	1.70	0.72
1:1:3141:G:OP1	16:LH:23:ARG:NH1	2.22	0.72
22:LN:9:GLU:HG2	43:Li:53:ILE:HD13	1.72	0.72
2:2:691:C:H4'	2:2:692:C:H5'	1.71	0.72
63:SJ:133:ARG:NH1	63:SJ:135:GLY:O	2.22	0.72
7:C:249:ASP:CG	8:D:259:LYS:CE	2.61	0.71
8:D:350:MET:HB3	8:D:355:SER:HB3	1.72	0.71
34:LZ:94:VAL:HG23	34:LZ:95:ILE:HD12	1.71	0.71
56:SC:66:LEU:O	75:SV:15:ARG:NH1	2.23	0.71
27:LS:80:ARG:NH2	28:LT:154:VAL:O	2.22	0.71
68:SO:38:ASP:OD1	68:SO:39:THR:N	2.23	0.71
2:2:1560:U:OP1	73:ST:39:LYS:NZ	2.23	0.71
7:C:246:VAL:HG21	7:C:259:MET:HE2	1.70	0.71
47:Lm:79:GLU:OE2	47:Lm:81:SER:OG	2.07	0.71
1:1:223:A:H5''	33:LY:3:VAL:HG12	1.73	0.71
8:D:426:ALA:HB2	8:D:446:PRO:HG3	1.73	0.71
18:LJ:33:ARG:NH1	18:LJ:121:ILE:O	2.24	0.71
24:LP:23:ARG:O	24:LP:86:LYS:NZ	2.22	0.71
1:1:1410:U:OP2	35:La:4:ARG:NH2	2.23	0.71
1:1:806:U:H5''	9:LA:21:ARG:HD3	1.72	0.71
1:1:1265:G:H4'	52:Ls:83:ASN:HB2	1.72	0.71
5:A:65:ILE:HG23	5:A:83:TRP:CE3	2.25	0.71
83:Sd:45:GLU:HG2	83:Sd:46:LYS:HG3	1.70	0.71
2:2:1606:G:H4'	59:SF:94:LYS:HZ1	1.56	0.70
58:SE:9:GLN:HB2	58:SE:30:ARG:HD3	1.71	0.70
7:C:149:PHE:O	7:C:153:GLN:NE2	2.24	0.70
4:4:55:U:H3	4:4:62:A:H2	1.39	0.70
72:SS:88:ARG:HH21	72:SS:91:ASP:HA	1.56	0.70
8:D:22:ASN:OD1	8:D:23:SER:N	2.23	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:4:83:C:H41	33:LY:50:ARG:HH22	1.40	0.70
48:Lr:10:THR:O	48:Lr:14:LYS:HG2	1.92	0.70
62:SI:137:LYS:NZ	62:SI:139:SER:O	2.24	0.70
5:A:88:ARG:NH1	5:A:89:LEU:O	2.24	0.70
8:D:251:ASP:OD1	8:D:268:ARG:NH2	2.22	0.70
63:SJ:84:LEU:HD12	63:SJ:97:LEU:HD21	1.74	0.70
67:SN:95:ALA:O	67:SN:99:ARG:HG3	1.92	0.70
1:1:1226:G:N3	1:1:1253:A:O2'	2.25	0.70
52:Ls:15:LEU:HD23	52:Ls:19:LEU:HD23	1.74	0.70
66:SM:47:LEU:HA	66:SM:50:ALA:HB3	1.73	0.70
75:SV:53:TYR:OH	75:SV:76:ASP:OD2	2.10	0.70
78:SY:123:GLY:O	78:SY:128:LYS:NZ	2.22	0.70
1:1:2924:U:O2	9:LA:221:LYS:NZ	2.24	0.69
7:C:123:ARG:HH12	7:C:126:ARG:HD2	1.57	0.69
48:Ln:10:THR:O	48:Ln:14:LYS:HG2	1.92	0.69
76:SW:22:LYS:HZ1	81:Sb:3:LEU:HD13	1.57	0.69
80:Sa:3:LYS:NZ	80:Sa:8:ASN:OD1	2.24	0.69
80:Sa:70:LYS:HE2	80:Sa:72:GLN:HE21	1.57	0.69
1:1:2728:A:H5''	49:Lo:80:LYS:HD2	1.74	0.69
2:2:509:A:OP1	63:SJ:171:ARG:NH1	2.25	0.69
56:SC:61:MET:HB3	56:SC:65:TYR:HE1	1.56	0.69
57:SD:100:SER:O	57:SD:104:GLN:NE2	2.25	0.69
1:1:1582:A:N6	32:LX:83:GLU:OE2	2.24	0.69
2:2:1059:U:O2	81:Sb:72:ARG:NH1	2.24	0.69
5:A:11:LEU:HD22	5:A:43:TRP:CZ2	2.28	0.69
2:2:1272:A:H62	2:2:1427:C:H42	1.39	0.69
58:SE:250:GLU:OE2	58:SE:254:ARG:NE	2.26	0.69
73:ST:12:ALA:O	73:ST:16:VAL:HG13	1.91	0.69
2:2:551:C:N4	2:2:568:G:O6	2.24	0.69
8:D:53:TYR:HE1	8:D:58:GLU:HG3	1.57	0.69
1:1:1387:G:N2	1:1:1390:A:OP2	2.24	0.69
16:LH:90:MET:HE3	16:LH:146:LEU:HD23	1.74	0.69
66:SM:65:ASN:O	66:SM:74:LYS:NZ	2.26	0.69
1:1:90:A:OP2	25:LQ:198:LYS:NZ	2.26	0.69
1:1:1922:U:O2'	1:1:3286:G:O2'	2.09	0.69
1:1:2516:G:N2	34:LZ:134:ARG:O	2.24	0.69
37:Lc:46:LEU:HD23	37:Lc:71:HIS:HB3	1.74	0.69
54:SA:78:VAL:HG12	54:SA:125:VAL:HB	1.74	0.69
54:SA:83:PRO:HA	54:SA:86:GLN:NE2	2.07	0.69
59:SF:173:ASN:HD22	59:SF:175:LYS:NZ	1.89	0.69
2:2:1224:A:H3'	66:SM:45:ARG:HH21	1.58	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1929:G:OP1	26:LR:104:ARG:NH1	2.26	0.69
8:D:52:SER:OG	8:D:71:ASN:ND2	2.25	0.69
8:D:450:VAL:CG2	8:D:451:PRO:HD3	2.24	0.68
60:SG:67:VAL:HG13	60:SG:99:GLY:HA2	1.74	0.68
2:2:150:G:N2	60:SG:56:ASN:OD1	2.26	0.68
74:SU:85:LYS:HZ3	74:SU:87:LEU:HD13	1.59	0.68
80:Sa:83:ILE:HG22	80:Sa:84:VAL:HG23	1.76	0.68
7:C:191:TYR:HE1	7:C:291:ARG:HE	1.41	0.68
12:LD:91:GLY:O	12:LD:94:ASN:ND2	2.27	0.68
64:SK:32:GLU:HG2	64:SK:33:ILE:HG12	1.75	0.68
2:2:1294:G:N2	2:2:1297:A:OP2	2.24	0.68
3:3:86:C:O2'	27:LS:119:ARG:NH2	2.26	0.68
16:LH:31:ARG:NH1	16:LH:151:ASN:OD1	2.27	0.68
50:Lp:85:ARG:HG2	50:Lp:85:ARG:HH11	1.59	0.68
2:2:1391:G:H2'	2:2:1392:G:C8	2.28	0.68
7:C:51:ARG:O	7:C:55:HIS:ND1	2.24	0.68
8:D:115:LYS:NZ	8:D:123:SER:OG	2.25	0.68
57:SD:117:ALA:HB3	57:SD:120:ARG:HD2	1.75	0.68
59:SF:126:ASN:ND2	59:SF:188:ALA:O	2.22	0.68
67:SN:28:THR:HG23	67:SN:32:GLN:HE21	1.58	0.68
70:SQ:38:LEU:HD11	73:ST:11:ASP:HA	1.76	0.68
2:2:115:U:O2'	2:2:330:A:N3	2.23	0.68
2:2:510:U:OP1	63:SJ:129:GLN:NE2	2.27	0.68
1:1:1692:G:N2	1:1:1712:U:O4	2.20	0.68
2:2:1143:G:H2'	2:2:1144:A:C8	2.29	0.67
57:SD:45:THR:OG1	57:SD:48:VAL:O	2.10	0.67
66:SM:59:ALA:HA	66:SM:124:LYS:HE2	1.75	0.67
2:2:392:U:H3	2:2:396:A:H62	1.40	0.67
1:1:2063:A:H5'	26:LR:71:ARG:HH12	1.59	0.67
2:2:866:G:H1	2:2:958:U:H3	1.41	0.67
7:C:207:ILE:HG22	7:C:209:PRO:HD2	1.76	0.67
16:LH:98:PRO:O	16:LH:118:ASN:ND2	2.28	0.67
65:SL:101:LYS:HE2	65:SL:102:TYR:HE1	1.59	0.67
77:SX:109:ARG:HG3	77:SX:112:LYS:HG3	1.74	0.67
2:2:1123:G:H5'	48:Ln:11:ARG:HD3	1.76	0.67
2:2:1498:G:N7	73:ST:102:ARG:NH2	2.40	0.67
54:SA:39:TYR:HD1	54:SA:55:LYS:HD3	1.58	0.67
1:1:2524:G:OP2	34:LZ:54:ARG:NH1	2.28	0.67
55:SB:121:ILE:HD11	55:SB:161:ILE:HD12	1.75	0.67
8:D:555:THR:O	8:D:557:LEU:N	2.28	0.67
10:LB:228:VAL:HG21	10:LB:271:MET:HE2	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
68:SO:26:VAL:HG23	68:SO:89:ILE:HD12	1.77	0.67
73:ST:16:VAL:HG12	73:ST:63:ARG:NE	2.10	0.67
9:LA:194:ASN:O	9:LA:194:ASN:ND2	2.27	0.67
7:C:239:PHE:CD2	7:C:270:LYS:HD3	2.30	0.67
8:D:133:ARG:HG2	8:D:136:ARG:HH21	1.60	0.67
76:SW:90:VAL:HG13	76:SW:94:LEU:HD12	1.77	0.67
84:Se:33:ARG:O	84:Se:36:LYS:HG3	1.95	0.67
78:SY:91:ARG:HH22	78:SY:100:ALA:HB3	1.59	0.67
7:C:92:ALA:O	7:C:93:ARG:HG3	1.95	0.66
9:LA:97:THR:OG1	9:LA:100:ASN:ND2	2.28	0.66
15:LG:150:LYS:O	15:LG:204:THR:OG1	2.10	0.66
15:LG:223:GLU:HA	15:LG:227:GLU:HG2	1.76	0.66
66:SM:36:LEU:HA	66:SM:39:MET:HG2	1.77	0.66
1:1:275:G:O2'	1:1:276:G:OP2	2.11	0.66
2:2:70:C:H5''	60:SG:165:LYS:HE3	1.75	0.66
62:SI:78:ILE:HD11	62:SI:102:VAL:HB	1.76	0.66
1:1:2500:U:H3'	1:1:2501:U:H4'	1.77	0.66
2:2:801:A:N3	61:SH:110:ARG:NH1	2.42	0.66
2:2:1386:C:H4'	71:SR:48:ASN:HB3	1.77	0.66
56:SC:182:ARG:O	63:SJ:51:ARG:NH2	2.28	0.66
61:SH:57:VAL:HG21	61:SH:178:THR:HA	1.78	0.66
65:SL:85:MET:HE2	65:SL:88:THR:HB	1.77	0.66
78:SY:106:ALA:O	78:SY:111:ARG:NH1	2.29	0.66
2:2:905:A:N3	2:2:995:G:O2'	2.27	0.66
7:C:133:HIS:HD2	7:C:135:ASP:HB2	1.59	0.66
9:LA:134:VAL:HG12	9:LA:151:PRO:HD3	1.77	0.66
34:LZ:21:LYS:NZ	34:LZ:128:TRP:O	2.26	0.66
44:Lj:52:LYS:O	44:Lj:56:ARG:HG2	1.96	0.66
54:SA:52:ASN:HB3	54:SA:55:LYS:HG2	1.77	0.66
10:LB:57:VAL:HG22	10:LB:73:VAL:HG22	1.77	0.66
24:LP:64:ALA:O	24:LP:80:ARG:NH1	2.29	0.66
48:Ln:8:LYS:HE3	48:Ln:12:ARG:NH1	2.11	0.66
68:SO:43:VAL:HG13	68:SO:52:ILE:HB	1.78	0.66
2:2:1678:C:H5'	60:SG:65:GLN:HE21	1.60	0.66
11:LC:365:ALA:HB3	27:LS:28:ARG:HD2	1.76	0.66
5:A:217:MET:SD	5:A:229:SER:OG	2.54	0.66
27:LS:155:ARG:NH1	27:LS:174:SER:OG	2.29	0.66
41:Lg:75:ARG:NH2	41:Lg:82:CYS:O	2.29	0.66
2:2:476:U:H4'	63:SJ:118:LYS:HE3	1.78	0.66
56:SC:67:HIS:HA	75:SV:15:ARG:HH12	1.60	0.66
60:SG:85:ARG:O	60:SG:87:ARG:NH1	2.25	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1599:A:H5'	48:Lr:15:ARG:NH1	2.09	0.66
2:2:257:U:OP2	62:SI:41:LYS:NZ	2.26	0.66
2:2:1484:G:O2'	2:2:1490:C:O2	2.14	0.66
12:LD:60:ILE:HD11	12:LD:93:THR:HG23	1.77	0.66
13:LE:132:LYS:HG2	13:LE:136:LYS:HD2	1.77	0.66
18:LJ:19:VAL:HG22	18:LJ:71:THR:HG22	1.76	0.66
57:SD:67:ARG:HD2	64:SK:88:THR:HG22	1.76	0.66
2:2:66:U:H1'	60:SG:174:LYS:HE2	1.78	0.65
2:2:1223:G:O2'	2:2:1253:A:N6	2.29	0.65
2:2:1517:G:O2'	2:2:1519:U:OP2	2.13	0.65
8:D:113:LYS:HE3	8:D:120:ALA:HB3	1.78	0.65
59:SF:177:ILE:HA	59:SF:180:CYS:HB3	1.78	0.65
64:SK:75:ARG:HD2	64:SK:81:PRO:HA	1.77	0.65
14:LF:242:ASN:O	14:LF:246:ARG:HG2	1.95	0.65
22:LN:46:ASP:OD1	22:LN:47:LYS:N	2.29	0.65
56:SC:235:PRO:HA	56:SC:238:TRP:CD1	2.32	0.65
63:SJ:167:PRO:O	63:SJ:172:ARG:NH1	2.27	0.65
2:2:1484:G:H3'	2:2:1511:A:H61	1.61	0.65
9:LA:61:VAL:HG11	9:LA:88:ILE:HD11	1.78	0.65
44:Lj:39:TYR:HB3	44:Lj:40:PRO:CD	2.26	0.65
45:Lk:7:ASP:OD1	45:Lk:10:LYS:NZ	2.30	0.65
57:SD:67:ARG:NH1	64:SK:87:ALA:O	2.30	0.65
73:ST:126:THR:HG23	73:ST:129:GLY:H	1.60	0.65
2:2:1690:G:H2'	2:2:1691:G:C8	2.31	0.65
5:A:87:LEU:HB3	5:A:101:PHE:HB2	1.78	0.65
56:SC:105:ARG:HH21	56:SC:126:SER:HA	1.61	0.65
74:SU:64:THR:HG23	83:Sd:44:ARG:NH2	2.11	0.65
2:2:1143:G:O3'	56:SC:99:ARG:NH1	2.30	0.65
7:C:98:TRP:CD1	7:C:99:LYS:HD3	2.31	0.65
52:Ls:22:TYR:HD2	52:Ls:88:PHE:HB3	1.60	0.65
72:SS:111:GLU:HG3	72:SS:115:ARG:HH21	1.60	0.65
35:La:79:TRP:O	35:La:87:ARG:NH1	2.28	0.65
52:Ls:16:LYS:NZ	52:Ls:64:LYS:HE3	2.12	0.65
63:SJ:75:ILE:HG22	63:SJ:94:VAL:HG11	1.78	0.65
69:SP:116:LYS:H	69:SP:119:MET:HE2	1.62	0.65
1:1:377:A:H4'	7:C:261:ARG:NH2	2.11	0.65
1:1:1221:C:H3'	1:1:1222:C:H5''	1.79	0.65
2:2:126:G:H22	2:2:175:G:H3'	1.62	0.65
2:2:391:C:N4	2:2:398:A:H62	1.95	0.65
23:LO:11:ASP:O	23:LO:15:HIS:NE2	2.29	0.65
1:1:56:G:OP1	44:Lj:43:LYS:NZ	2.30	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:3287:U:OP2	62:SI:92:ARG:NE	2.23	0.65
10:LB:161:VAL:O	10:LB:181:GLU:HA	1.96	0.65
71:SR:5:ARG:HB2	71:SR:9:VAL:HG11	1.77	0.65
1:1:1248:U:H2'	1:1:1249:G:C8	2.32	0.65
15:LG:242:GLY:O	15:LG:246:GLN:NE2	2.29	0.65
54:SA:71:ASP:OD1	54:SA:72:ASN:N	2.30	0.65
59:SF:122:ASP:HA	59:SF:125:VAL:HG12	1.79	0.65
1:1:114:C:OP1	22:LN:147:ARG:NH1	2.30	0.65
2:2:1095:U:P	56:SC:176:ARG:HH22	2.19	0.65
2:2:1606:G:H4'	59:SF:94:LYS:NZ	2.12	0.65
14:LF:98:ILE:HG13	25:LQ:31:GLY:HA3	1.78	0.65
34:LZ:102:GLU:OE2	34:LZ:105:GLN:HG3	1.97	0.65
43:Li:53:ILE:HA	43:Li:56:VAL:HG12	1.77	0.65
60:SG:218:ARG:NE	60:SG:221:GLU:OE2	2.28	0.65
63:SJ:51:ARG:HG2	63:SJ:55:ARG:NH2	2.12	0.65
85:Sf:105:TYR:OH	85:Sf:118:ARG:NH2	2.30	0.65
2:2:231:G:H2'	2:2:232:G:C8	2.33	0.64
16:LH:17:LYS:NZ	21:LM:3:GLU:O	2.29	0.64
49:Lo:10:THR:HG22	49:Lo:11:PHE:H	1.63	0.64
69:SP:39:ASP:OD1	69:SP:40:GLU:N	2.30	0.64
70:SQ:110:ILE:HG13	70:SQ:114:ARG:HA	1.77	0.64
1:1:2949:G:H5'	10:LB:20:LYS:HD2	1.80	0.64
2:2:333:G:O6	62:SI:5:ARG:NH1	2.29	0.64
8:D:343:LEU:HD23	8:D:369:PRO:HG3	1.78	0.64
20:LL:62:THR:HG23	20:LL:64:LYS:O	1.97	0.64
32:LX:103:ALA:HA	32:LX:107:GLN:HE21	1.62	0.64
81:Sb:59:CYS:SG	81:Sb:61:ASN:ND2	2.70	0.64
56:SC:43:TRP:O	56:SC:54:LYS:NZ	2.31	0.64
66:SM:56:ARG:HH21	66:SM:57:ARG:HD3	1.63	0.64
2:2:336:C:OP1	62:SI:10:LYS:NZ	2.30	0.64
56:SC:186:LEU:HB2	56:SC:193:LYS:HE3	1.77	0.64
59:SF:202:ASP:HA	59:SF:205:GLU:OE1	1.97	0.64
62:SI:137:LYS:NZ	62:SI:143:GLU:OE2	2.24	0.64
2:2:76:U:O2'	60:SG:155:LYS:NZ	2.31	0.64
10:LB:54:THR:HG22	10:LB:55:THR:H	1.61	0.64
52:Ls:61:ARG:HA	52:Ls:64:LYS:HD3	1.79	0.64
54:SA:59:LYS:HZ3	54:SA:163:ILE:HD13	1.62	0.64
54:SA:60:LEU:HD11	54:SA:180:LEU:HD13	1.79	0.64
55:SB:138:PHE:CD2	55:SB:214:LYS:HG2	2.33	0.64
79:SZ:54:LEU:HG	79:SZ:58:LEU:HD22	1.77	0.64
1:1:1876:A:N6	1:1:2302:C:H42	1.92	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:78:C:O4'	60:SG:177:ARG:NH2	2.31	0.64
7:C:177:ILE:HD11	7:C:197:VAL:HG22	1.80	0.64
8:D:384:LEU:HD13	8:D:392:ARG:HH12	1.61	0.64
55:SB:108:ASP:OD1	55:SB:109:LYS:N	2.31	0.64
68:SO:96:ILE:O	68:SO:131:VAL:N	2.27	0.64
73:ST:29:LEU:HG	73:ST:111:ILE:HD11	1.80	0.64
2:2:1546:A:H8	69:SP:51:ARG:HH22	1.43	0.64
8:D:328:ASN:HD21	8:D:363:ASN:HD21	1.45	0.64
2:2:607:G:O2'	2:2:610:G:O2'	2.15	0.64
5:A:88:ARG:HH22	5:A:97:THR:HA	1.62	0.64
25:LQ:109:VAL:HB	25:LQ:166:LEU:HD23	1.80	0.64
61:SH:150:LEU:HD21	61:SH:158:LYS:HD3	1.80	0.64
64:SK:28:GLU:OE1	83:Sd:8:ASN:ND2	2.30	0.64
1:1:1635:G:N2	1:1:1781:U:O4	2.31	0.64
2:2:352:G:H2'	2:2:353:G:H8	1.63	0.64
26:LR:44:LEU:HD22	26:LR:49:LEU:HD22	1.80	0.64
58:SE:80:ILE:HG13	58:SE:81:THR:HG23	1.80	0.64
78:SY:18:ASN:HD21	78:SY:21:LEU:HB3	1.62	0.64
3:3:44:C:H4'	12:LD:155:ARG:HH12	1.63	0.64
58:SE:94:LYS:HZ3	78:SY:20:LEU:N	1.96	0.64
59:SF:67:LYS:HG3	59:SF:68:ARG:H	1.62	0.64
2:2:469:U:H2'	2:2:470:A:H8	1.63	0.63
3:3:7:G:OP1	12:LD:33:ARG:NH1	2.31	0.63
10:LB:153:LYS:HG2	10:LB:193:VAL:HG11	1.80	0.63
48:Lr:8:LYS:HE3	48:Lr:12:ARG:NH1	2.11	0.63
54:SA:10:PHE:HZ	75:SV:39:VAL:HG21	1.61	0.63
54:SA:86:GLN:O	54:SA:90:LEU:HG	1.97	0.63
55:SB:122:GLU:HG3	55:SB:140:ILE:HD13	1.79	0.63
1:1:2352:C:H5''	24:LP:66:SER:HA	1.80	0.63
4:4:38:U:H5'	42:Lh:83:LEU:HD21	1.78	0.63
18:LJ:24:VAL:HG21	18:LJ:30:ARG:HG2	1.80	0.63
2:2:1538:G:N2	2:2:1565:A:OP2	2.31	0.63
10:LB:110:LEU:HD12	10:LB:114:VAL:HG21	1.81	0.63
34:LZ:83:ARG:NH1	41:Lg:98:GLU:OE1	2.31	0.63
62:SI:22:ARG:HD2	62:SI:25:ARG:HE	1.63	0.63
2:2:151:G:N2	60:SG:60:GLY:O	2.27	0.63
51:Lq:34:ASN:ND2	51:Lq:43:HIS:O	2.32	0.63
1:1:1238:C:H2'	1:1:1239:G:H8	1.62	0.63
5:A:99:ARG:NH1	5:A:135:LEU:O	2.32	0.63
11:LC:229:ILE:HG23	11:LC:232:VAL:HB	1.80	0.63
15:LG:31:GLU:OE2	15:LG:33:ARG:NH1	2.32	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:LQ:152:ASP:OD1	25:LQ:153:GLN:N	2.32	0.63
55:SB:133:TYR:HE2	55:SB:181:LEU:HD11	1.63	0.63
60:SG:64:LYS:HZ2	60:SG:82:SER:H	1.44	0.63
60:SG:182:VAL:HA	60:SG:186:ARG:HH21	1.63	0.63
69:SP:68:LEU:HD12	69:SP:97:MET:HE2	1.80	0.63
70:SQ:83:GLN:NE2	70:SQ:115:SER:O	2.27	0.63
76:SW:106:THR:HG23	76:SW:108:ALA:H	1.63	0.63
8:D:548:GLU:OE2	8:D:550:THR:OG1	2.16	0.63
10:LB:36:ASP:OD2	10:LB:39:LYS:NZ	2.32	0.63
58:SE:251:ARG:HD3	58:SE:254:ARG:NH2	2.14	0.63
71:SR:9:VAL:HG23	71:SR:50:ILE:HG22	1.80	0.63
1:1:2355:C:O2'	10:LB:267:ARG:NH2	2.31	0.63
3:3:4:U:H2'	3:3:5:A:H8	1.63	0.63
61:SH:64:ILE:HD11	61:SH:96:VAL:HG22	1.81	0.63
62:SI:175:SER:HB3	62:SI:184:ASP:H	1.63	0.63
65:SL:30:THR:O	65:SL:37:ARG:NH2	2.32	0.63
70:SQ:128:LYS:NZ	74:SU:75:THR:OG1	2.22	0.63
78:SY:25:GLN:OE1	78:SY:25:GLN:N	2.32	0.63
5:A:54:TYR:CD1	5:A:55:PRO:HD2	2.34	0.63
74:SU:49:VAL:HG22	74:SU:90:LEU:HD11	1.80	0.63
1:1:1887:C:O2	10:LB:241:ARG:NH2	2.32	0.62
2:2:608:U:H5''	77:SX:5:LYS:HE3	1.80	0.62
2:2:922:A:H2'	2:2:923:G:C8	2.34	0.62
13:LE:28:TYR:OH	51:Lq:112:VAL:HG22	1.99	0.62
17:LI:93:PRO:HB2	17:LI:125:THR:HG22	1.81	0.62
1:1:1796:A:H2'	1:1:1797:A:C8	2.34	0.62
2:2:1431:G:N7	64:SK:25:LYS:NZ	2.46	0.62
39:Le:82:ASP:OD1	51:Lq:30:ARG:NH2	2.31	0.62
57:SD:11:LYS:HG2	57:SD:12:ARG:HD3	1.82	0.62
69:SP:72:LYS:NZ	69:SP:97:MET:SD	2.71	0.62
5:A:88:ARG:HD2	5:A:90:TRP:NE1	2.14	0.62
61:SH:150:LEU:HB3	76:SW:52:GLU:OE2	1.99	0.62
1:1:1796:A:H2'	1:1:1797:A:H8	1.63	0.62
58:SE:131:LEU:HA	58:SE:137:PRO:HA	1.81	0.62
68:SO:61:VAL:HG21	68:SO:66:ASP:HB3	1.81	0.62
1:1:1229:G:N2	1:1:1249:G:OP2	2.32	0.62
1:1:1347:G:H5''	25:LQ:32:ILE:HD13	1.81	0.62
2:2:176:A:H2'	2:2:177:A:C8	2.33	0.62
5:A:212:LYS:HG3	5:A:235:GLU:HG3	1.80	0.62
58:SE:174:LYS:HD3	58:SE:175:PHE:N	2.15	0.62
61:SH:168:GLU:OE2	61:SH:172:VAL:HG12	1.98	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
71:SR:10:LYS:HB3	71:SR:14:LYS:NZ	2.14	0.62
1:1:209:G:OP1	33:LY:11:ARG:NH1	2.32	0.62
1:1:2100:U:OP2	1:1:2105:A:N6	2.32	0.62
1:1:2148:G:O2'	1:1:2277:U:OP2	2.18	0.62
1:1:2601:A:O2'	36:Lb:6:ASN:ND2	2.33	0.62
2:2:1467:A:N7	2:2:1534:U:O4	2.32	0.62
12:LD:208:ALA:HB2	12:LD:239:LEU:HD21	1.80	0.62
16:LH:14:GLU:OE2	21:LM:2:ALA:N	2.32	0.62
45:Lk:10:LYS:HA	45:Lk:13:GLU:OE2	1.99	0.62
67:SN:102:LEU:HD21	67:SN:115:LEU:HD22	1.80	0.62
69:SP:113:VAL:HG21	69:SP:127:PHE:HD2	1.63	0.62
76:SW:115:GLU:O	76:SW:118:ARG:HG2	1.99	0.62
77:SX:19:ARG:HG3	77:SX:23:ARG:HD2	1.82	0.62
1:1:1641:G:H2'	1:1:1642:G:C8	2.35	0.62
2:2:587:C:OP1	84:Se:43:ARG:NH2	2.33	0.62
8:D:80:ARG:NH2	87:D:601:ATP:O3G	2.32	0.62
52:Ls:19:LEU:HD12	52:Ls:20:GLU:HG2	1.82	0.62
56:SC:48:LYS:HE2	56:SC:51:ARG:HH21	1.65	0.62
57:SD:207:LEU:HD23	57:SD:209:ASP:H	1.63	0.62
72:SS:76:PRO:HB2	72:SS:81:ILE:HD11	1.81	0.62
8:D:197:ARG:HD3	8:D:384:LEU:HD11	1.81	0.62
1:1:2410:A:N6	1:1:2463:A:N3	2.47	0.62
2:2:391:C:H42	2:2:398:A:N6	1.95	0.62
2:2:696:U:H2'	2:2:697:G:H8	1.64	0.62
27:LS:96:GLU:OE2	27:LS:102:ALA:N	2.33	0.62
54:SA:39:TYR:OH	75:SV:70:ASN:ND2	2.33	0.62
54:SA:42:LYS:NZ	54:SA:43:THR:O	2.33	0.62
72:SS:116:LEU:HA	72:SS:119:ILE:HG12	1.80	0.62
7:C:113:ARG:NH2	7:C:173:GLU:O	2.33	0.62
10:LB:111:SER:O	10:LB:115:LYS:HG3	2.00	0.62
26:LR:138:LEU:O	26:LR:142:ILE:HD12	1.99	0.62
58:SE:45:ILE:HG13	58:SE:61:THR:HG21	1.82	0.62
84:Se:14:VAL:O	84:Se:18:THR:OG1	2.16	0.62
1:1:405:G:OP1	24:LP:62:ARG:NH1	2.31	0.61
10:LB:20:LYS:HE2	10:LB:20:LYS:HA	1.81	0.61
2:2:1587:C:H2'	2:2:1588:A:H8	1.65	0.61
8:D:245:LEU:HD11	8:D:323:VAL:HG11	1.82	0.61
18:LJ:91:GLU:OE2	18:LJ:173:ARG:HG2	2.00	0.61
32:LX:64:ILE:HD12	32:LX:65:PRO:HD2	1.82	0.61
84:Se:43:ARG:HG3	84:Se:44:PHE:CD1	2.35	0.61
5:A:32:LEU:HD12	5:A:71:ILE:HG12	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:LR:42:ARG:HA	26:LR:45:VAL:HG12	1.82	0.61
77:SX:64:PRO:HD2	77:SX:65:ASN:H	1.66	0.61
82:Sc:53:ASP:OD1	82:Sc:54:ILE:N	2.33	0.61
1:1:1758:G:O2'	1:1:1760:G:OP2	2.16	0.61
2:2:953:A:OP1	67:SN:3:ARG:NH2	2.33	0.61
37:Lc:19:LEU:HD22	37:Lc:101:SER:HB2	1.82	0.61
59:SF:173:ASN:HD22	59:SF:175:LYS:HZ3	1.48	0.61
59:SF:209:LYS:HD3	59:SF:212:ARG:HD2	1.82	0.61
72:SS:26:GLN:HE22	72:SS:31:ALA:HA	1.66	0.61
74:SU:66:LYS:HA	83:Sd:44:ARG:HH12	1.64	0.61
2:2:1193:A:H3'	70:SQ:135:ARG:HH22	1.64	0.61
2:2:1500:G:N3	2:2:1559:C:O2'	2.32	0.61
8:D:133:ARG:HA	8:D:136:ARG:HE	1.66	0.61
54:SA:178:TRP:CZ3	54:SA:202:PRO:HG3	2.34	0.61
67:SN:4:LEU:HD11	67:SN:124:ARG:HH12	1.65	0.61
1:1:15:U:O3'	32:LX:55:ARG:NH2	2.34	0.61
2:2:857:A:C6	67:SN:73:ARG:HD2	2.36	0.61
2:2:1547:U:O4	69:SP:48:ARG:NH2	2.32	0.61
7:C:13:LEU:HD12	7:C:14:PRO:HD2	1.82	0.61
7:C:103:HIS:HB2	7:C:168:PHE:HE2	1.66	0.61
10:LB:231:THR:OG1	10:LB:248:ARG:NH2	2.34	0.61
58:SE:65:MET:HE2	58:SE:77:ARG:O	2.01	0.61
2:2:1175:G:H21	69:SP:143:ALA:HB2	1.65	0.61
7:C:47:LEU:HD23	8:D:404:PHE:HE2	1.66	0.61
7:C:237:ARG:O	7:C:271:LYS:NZ	2.32	0.61
10:LB:253:ILE:HG23	10:LB:265:VAL:HG11	1.83	0.61
18:LJ:15:ILE:HD13	18:LJ:132:MET:HE1	1.82	0.61
2:2:1321:G:H5'	54:SA:116:ARG:NH1	2.16	0.61
11:LC:287:LEU:HD23	25:LQ:56:LEU:HG	1.82	0.61
18:LJ:14:ARG:HH12	18:LJ:135:PRO:HD3	1.66	0.61
33:LY:71:SER:OG	33:LY:80:HIS:ND1	2.26	0.61
48:Ln:15:ARG:HA	48:Ln:18:ARG:HG2	1.82	0.61
71:SR:31:ASN:HA	71:SR:34:VAL:HG22	1.82	0.61
2:2:276:G:N7	31:LW:116:LYS:NZ	2.48	0.61
5:A:5:LEU:HD12	5:A:310:TRP:HB3	1.83	0.61
16:LH:28:GLU:HB3	16:LH:33:LYS:HG3	1.82	0.61
20:LL:181:ALA:HB1	35:La:147:LEU:HD21	1.82	0.61
1:1:2666:U:H2'	1:1:2667:C:C6	2.36	0.61
1:1:2730:U:OP2	1:1:2731:C:N4	2.33	0.61
68:SO:102:ASN:HB3	68:SO:141:ARG:HG3	1.82	0.61
82:Sc:62:ARG:HD3	82:Sc:63:GLU:H	1.66	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2476:U:H4'	15:LG:241:MET:HE1	1.82	0.60
2:2:98:C:OP2	2:2:375:A:O2'	2.14	0.60
3:3:44:C:O2'	12:LD:155:ARG:NH2	2.34	0.60
5:A:245:ARG:HH11	5:A:247:TRP:HB2	1.66	0.60
7:C:265:ASN:HA	7:C:268:LYS:HZ2	1.66	0.60
28:LT:134:MET:HE3	28:LT:135:PRO:HD2	1.83	0.60
52:Ls:38:MET:SD	52:Ls:39:HIS:ND1	2.73	0.60
57:SD:216:PRO:HG2	71:SR:19:LYS:HD2	1.83	0.60
1:1:1064:C:H4'	1:1:1065:U:H5	1.65	0.60
1:1:1578:G:OP2	41:Lg:32:ARG:NH2	2.33	0.60
37:Lc:12:SER:O	37:Lc:16:LYS:HG3	2.01	0.60
63:SJ:108:GLN:HE22	63:SJ:124:ARG:HG3	1.65	0.60
2:2:606:U:O3'	77:SX:19:ARG:NH2	2.34	0.60
4:4:75:G:OP2	33:LY:73:TYR:OH	2.18	0.60
12:LD:295:ILE:HD11	17:LI:206:LEU:HD11	1.83	0.60
32:LX:104:ASN:OD1	32:LX:107:GLN:HG2	2.00	0.60
34:LZ:2:LYS:NZ	37:Lc:39:SER:O	2.33	0.60
54:SA:15:ALA:O	54:SA:19:GLN:HG2	2.01	0.60
58:SE:94:LYS:NZ	78:SY:19:PRO:HG2	2.14	0.60
76:SW:88:LYS:HA	76:SW:88:LYS:HE3	1.83	0.60
1:1:1076:A:OP1	28:LT:116:LYS:NZ	2.35	0.60
1:1:2919:C:H2'	1:1:2920:G:H8	1.66	0.60
1:1:3160:A:OP2	21:LM:125:LYS:NZ	2.31	0.60
1:1:3212:G:N1	13:LE:135:GLU:OE2	2.34	0.60
2:2:727:C:H2'	2:2:728:G:C8	2.35	0.60
2:2:1215:G:N2	2:2:1440:A:OP2	2.34	0.60
7:C:146:ASP:HB3	7:C:150:LYS:NZ	2.16	0.60
7:C:254:ASP:OD1	7:C:255:GLN:N	2.34	0.60
31:LW:80:ARG:NH2	31:LW:81:ALA:O	2.34	0.60
34:LZ:65:SER:HB2	34:LZ:121:TYR:HE2	1.66	0.60
2:2:19:A:OP1	77:SX:109:ARG:NH1	2.34	0.60
2:2:893:G:H2'	2:2:894:U:C6	2.37	0.60
35:La:120:GLU:OE1	35:La:120:GLU:N	2.32	0.60
58:SE:125:LYS:HE2	58:SE:226:PHE:HA	1.82	0.60
60:SG:21:GLU:OE1	60:SG:25:ARG:HD3	2.02	0.60
58:SE:11:ARG:HH21	58:SE:20:LEU:HD12	1.66	0.60
59:Sf:187:ASN:ND2	59:Sf:194:ASN:OD1	2.31	0.60
62:SI:110:ARG:O	62:SI:114:GLU:HG2	2.02	0.60
69:SP:68:LEU:HB3	69:SP:97:MET:HE2	1.83	0.60
85:Sf:121:CYS:O	85:Sf:123:ASN:ND2	2.35	0.60
1:1:2705:A:N7	12:LD:156:THR:HG21	2.16	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
71:SR:110:ASP:HA	71:SR:113:LYS:HE2	1.83	0.60
1:1:2874:U:OP1	30:LV:47:ARG:NH2	2.35	0.60
2:2:231:G:H2'	2:2:232:G:H8	1.67	0.60
5:A:43:TRP:HD1	5:A:45:LEU:HD22	1.66	0.60
7:C:123:ARG:HG3	7:C:127:LYS:HE3	1.84	0.60
60:SG:74:ARG:HD2	60:SG:96:SER:HB3	1.83	0.60
2:2:1582:A:OP1	70:SQ:132:ARG:N	2.34	0.60
2:2:1709:G:OP2	31:LW:70:LYS:NZ	2.35	0.60
5:A:292:SER:OG	5:A:294:ASP:OD1	2.19	0.60
12:LD:194:ASP:HB3	12:LD:197:VAL:HG12	1.81	0.60
48:Lr:15:ARG:HA	48:Lr:18:ARG:HG2	1.82	0.60
71:SR:52:GLY:O	71:SR:56:HIS:ND1	2.33	0.60
73:ST:31:VAL:HG12	73:ST:33:GLY:H	1.66	0.60
83:Sd:26:HIS:CE1	83:Sd:28:ALA:HB3	2.36	0.60
1:1:124:A:OP2	15:LG:105:LYS:NZ	2.28	0.60
1:1:688:C:H2'	1:1:689:G:H8	1.67	0.60
2:2:85:A:HO2'	2:2:144:A:HO2'	1.50	0.60
2:2:1199:A:N6	2:2:1453:C:OP1	2.34	0.60
52:Ls:121:VAL:HG23	52:Ls:158:LEU:HD11	1.84	0.60
63:SJ:39:GLU:HA	63:SJ:42:ARG:HG2	1.84	0.60
1:1:1196:G:OP1	27:LS:137:ARG:NH1	2.35	0.59
2:2:1690:G:H2'	2:2:1691:G:H8	1.65	0.59
8:D:462:LYS:H	8:D:462:LYS:HD2	1.67	0.59
32:LX:100:ASP:OD1	32:LX:101:VAL:N	2.34	0.59
34:LZ:110:LYS:HA	34:LZ:113:VAL:HG12	1.84	0.59
38:Ld:54:THR:HG23	38:Ld:56:ASP:H	1.66	0.59
63:SJ:86:GLU:HA	63:SJ:89:MET:HE3	1.83	0.59
68:SO:70:PRO:HB2	82:Sc:62:ARG:HH22	1.67	0.59
2:2:683:G:H2'	2:2:684:G:C8	2.37	0.59
21:LM:123:LEU:HD12	23:LO:195:VAL:HG13	1.84	0.59
31:LW:80:ARG:NH2	60:SG:131:LYS:H	2.00	0.59
56:SC:164:VAL:HG21	56:SC:232:PHE:HD2	1.67	0.59
2:2:884:U:O2'	68:SO:134:THR:O	2.20	0.59
13:LE:84:THR:HB	13:LE:94:LEU:HA	1.84	0.59
22:LN:113:LEU:HB2	22:LN:134:LEU:HD12	1.84	0.59
26:LR:185:LEU:HD21	61:SH:46:PRO:HG3	1.84	0.59
58:SE:253:GLN:NE2	58:SE:254:ARG:HG3	2.18	0.59
2:2:1193:A:OP2	2:2:1460:G:N2	2.33	0.59
2:2:1320:C:O2'	54:SA:116:ARG:NH1	2.33	0.59
8:D:351:SER:HA	8:D:386:PRO:HB3	1.83	0.59
9:LA:2:GLY:HA2	9:LA:207:VAL:HG23	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:Lb:36:ASP:OD1	36:Lb:39:PHE:HB3	2.02	0.59
62:SI:103:GLN:OE1	62:SI:168:ARG:HD2	2.01	0.59
77:SX:69:ARG:O	77:SX:70:LYS:HG2	2.03	0.59
83:Sd:26:HIS:HE1	83:Sd:28:ALA:HB3	1.66	0.59
1:1:1506:U:O2'	32:LX:124:ASN:ND2	2.35	0.59
2:2:103:A:OP2	2:2:305:C:N4	2.34	0.59
8:D:422:HIS:HA	8:D:449:ALA:HA	1.82	0.59
55:SB:144:LYS:HE3	55:SB:206:PRO:HB3	1.85	0.59
71:SR:92:ASP:O	71:SR:96:ASN:ND2	2.35	0.59
2:2:304:G:OP1	65:SL:108:ARG:NH1	2.33	0.59
15:LG:106:GLN:NE2	15:LG:110:GLU:OE2	2.35	0.59
24:LP:115:LYS:HB2	24:LP:151:THR:HG22	1.84	0.59
7:C:35:SER:OG	7:C:37:ARG:NH1	2.34	0.59
56:SC:158:ARG:NH1	56:SC:159:PRO:O	2.35	0.59
65:SL:79:ARG:NH2	65:SL:127:MET:SD	2.76	0.59
1:1:575:G:H2'	1:1:576:A:H8	1.68	0.59
1:1:2974:A:H2'	1:1:2975:G:H8	1.67	0.59
2:2:638:G:H1'	61:SH:189:ARG:HH12	1.68	0.59
7:C:246:VAL:HG22	7:C:259:MET:HE3	1.76	0.59
61:SH:36:ASN:OD1	61:SH:37:THR:N	2.35	0.59
1:1:811:U:H3	1:1:877:A:N6	2.01	0.59
1:1:2621:G:O2'	1:1:2622:G:OP1	2.21	0.59
22:LN:192:LYS:O	22:LN:196:THR:HG23	2.03	0.59
32:LX:71:ASP:O	32:LX:75:ILE:HG12	2.02	0.59
46:Ll:28:ARG:HH22	46:Ll:36:ARG:HA	1.68	0.59
55:SB:133:TYR:CE2	55:SB:181:LEU:HD11	2.38	0.59
61:SH:123:PRO:HD2	61:SH:126:ARG:HD2	1.85	0.59
67:SN:36:GLN:HA	67:SN:39:LYS:HZ2	1.68	0.59
70:SQ:75:THR:HA	70:SQ:78:VAL:HG12	1.83	0.59
72:SS:112:ASP:HA	72:SS:115:ARG:HG2	1.84	0.59
76:SW:94:LEU:HD11	76:SW:102:VAL:HG23	1.83	0.59
1:1:2923:G:N2	1:1:2926:A:OP2	2.28	0.59
2:2:607:G:H2'	2:2:611:A:C8	2.38	0.59
7:C:206:LYS:HA	7:C:236:TRP:CH2	2.38	0.59
18:LJ:82:GLU:O	18:LJ:86:LYS:HG2	2.03	0.59
18:LJ:92:LEU:O	18:LJ:172:VAL:HA	2.03	0.59
24:LP:114:ILE:HD13	24:LP:150:LEU:HD21	1.84	0.59
35:La:75:ILE:HG12	35:La:114:GLY:HA2	1.83	0.59
40:Lf:71:GLY:HA3	40:Lf:87:PHE:CD1	2.37	0.59
68:SO:83:ARG:NH1	68:SO:86:GLU:OE2	2.36	0.59
1:1:1581:U:OP2	26:LR:38:ARG:HD2	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:443:A:N1	2:2:458:G:O2'	2.35	0.58
2:2:893:G:H21	68:SO:51:THR:HG21	1.68	0.58
2:2:1787:G:HO2'	2:2:1789:G:H8	1.51	0.58
6:B:129:GLU:HA	6:B:132:LEU:HD13	1.84	0.58
8:D:58:GLU:O	8:D:137:ARG:NH2	2.36	0.58
8:D:285:LYS:HD2	8:D:286:ARG:HE	1.67	0.58
32:LX:105:LYS:NZ	32:LX:123:ILE:O	2.35	0.58
64:SK:85:VAL:HG22	64:SK:87:ALA:H	1.67	0.58
70:SQ:79:TYR:HA	70:SQ:82:ARG:HG2	1.85	0.58
1:1:101:A:H3'	1:1:102:G:H21	1.68	0.58
1:1:2949:G:H4'	10:LB:20:LYS:HZ2	1.68	0.58
2:2:1341:A:H2'	2:2:1342:A:C8	2.39	0.58
8:D:222:LEU:HD12	8:D:229:TYR:HB2	1.85	0.58
8:D:425:ASN:ND2	8:D:473:GLU:OE1	2.36	0.58
59:SF:85:MET:HE1	59:SF:94:LYS:HZ3	1.67	0.58
69:SP:64:LEU:HD11	69:SP:91:MET:HE1	1.85	0.58
77:SX:89:ASN:OD1	77:SX:90:ASP:N	2.36	0.58
1:1:2407:C:H2'	1:1:2408:A:C8	2.38	0.58
10:LB:222:THR:O	10:LB:335:ARG:NH1	2.35	0.58
57:SD:25:ASN:O	57:SD:29:GLN:NE2	2.36	0.58
62:SI:38:ILE:HD13	62:SI:94:ASN:OD1	2.02	0.58
1:1:351:G:N2	1:1:354:A:OP2	2.33	0.58
1:1:2949:G:H4'	10:LB:20:LYS:NZ	2.19	0.58
2:2:1542:G:N2	72:SS:87:ASN:OD1	2.36	0.58
2:2:1675:G:H21	2:2:1718:A:H62	1.49	0.58
15:LG:74:VAL:HB	15:LG:237:GLY:HA3	1.85	0.58
69:SP:116:LYS:HE3	69:SP:116:LYS:HA	1.86	0.58
77:SX:109:ARG:HB3	77:SX:121:ARG:NH1	2.18	0.58
1:1:643:C:H2'	1:1:644:A:H8	1.68	0.58
1:1:1152:A:H4'	14:LF:224:LYS:HD3	1.86	0.58
1:1:3286:G:H5''	62:SI:92:ARG:CZ	2.34	0.58
5:A:36:ARG:HA	5:A:65:ILE:HG13	1.85	0.58
8:D:450:VAL:HG23	8:D:451:PRO:CD	2.33	0.58
13:LE:110:ASP:O	13:LE:172:ASN:ND2	2.35	0.58
13:LE:131:GLU:O	13:LE:135:GLU:HG2	2.03	0.58
40:Lf:38:ASP:OD1	40:Lf:39:ASP:N	2.36	0.58
45:Lk:10:LYS:HA	45:Lk:13:GLU:CD	2.27	0.58
68:SO:32:ILE:HG22	68:SO:41:VAL:HG23	1.85	0.58
1:1:464:C:H2'	1:1:465:G:H8	1.68	0.58
2:2:834:U:H2'	2:2:835:G:H8	1.68	0.58
7:C:222:GLU:N	7:C:222:GLU:OE1	2.35	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:LL:32:LYS:O	20:LL:36:ARG:HG3	2.03	0.58
39:Le:84:GLU:OE2	39:Le:112:ARG:NE	2.35	0.58
41:Lg:20:ARG:HG3	41:Lg:20:ARG:HH11	1.69	0.58
56:SC:173:VAL:HG11	56:SC:218:THR:HA	1.85	0.58
67:SN:16:ILE:HD12	67:SN:17:PRO:HD2	1.84	0.58
2:2:654:U:H2'	2:2:671:A:H2	1.69	0.58
30:LV:111:MET:HE1	30:LV:116:ILE:HD11	1.86	0.58
56:SC:77:VAL:HG21	56:SC:141:LYS:HB3	1.84	0.58
64:SK:14:TYR:O	64:SK:18:GLU:HG3	2.04	0.58
1:1:1695:A:H4'	1:1:1696:A:H5'	1.85	0.58
1:1:2495:U:H2'	1:1:2496:G:H8	1.69	0.58
2:2:1677:A:H1'	60:SG:66:GLY:HA2	1.85	0.58
9:LA:117:GLU:HG2	9:LA:124:GLY:H	1.69	0.58
18:LJ:75:PRO:HA	18:LJ:78:GLU:HG3	1.86	0.58
29:LU:59:VAL:HG13	29:LU:60:ILE:HG12	1.86	0.58
34:LZ:32:THR:OG1	34:LZ:34:SER:O	2.21	0.58
47:Lm:88:LYS:NZ	47:Lm:89:PHE:HE1	2.00	0.58
1:1:68:A:O2'	1:1:308:C:O2	2.22	0.58
1:1:1727:G:H21	45:Lk:2:PRO:HG2	1.69	0.58
1:1:3008:U:O2'	31:LW:16:GLY:O	2.21	0.58
18:LJ:144:ARG:HH11	18:LJ:145:CYS:HB2	1.68	0.58
48:Ln:7:LYS:HG2	48:Ln:11:ARG:HH22	1.68	0.58
48:Lr:7:LYS:HG2	48:Lr:11:ARG:HH22	1.68	0.58
62:SI:175:SER:HB2	62:SI:184:ASP:HB2	1.85	0.58
64:SK:48:GLN:NE2	64:SK:55:THR:HB	2.19	0.58
72:SS:29:VAL:O	72:SS:43:SER:OG	2.17	0.58
1:1:377:A:H4'	7:C:261:ARG:HH22	1.68	0.58
5:A:147:HIS:CE1	5:A:175:LYS:HE3	2.39	0.58
8:D:389:LEU:HD23	8:D:392:ARG:NH2	2.19	0.58
51:Lq:104:ARG:HB3	51:Lq:107:LEU:HD12	1.85	0.58
54:SA:15:ALA:HA	54:SA:18:GLU:OE2	2.03	0.58
83:Sd:21:CYS:HB3	83:Sd:24:CYS:O	2.02	0.58
1:1:1022:C:OP2	12:LD:5:LYS:NZ	2.37	0.57
1:1:2978:U:H2'	1:1:2991:A:H61	1.68	0.57
2:2:696:U:H2'	2:2:697:G:C8	2.39	0.57
2:2:833:U:H2'	2:2:834:U:H6	1.69	0.57
2:2:833:U:H2'	2:2:834:U:C6	2.39	0.57
7:C:99:LYS:NZ	7:C:245:ASP:OD2	2.35	0.57
14:LF:91:PHE:HB2	14:LF:145:PRO:HG3	1.86	0.57
24:LP:116:HIS:NE2	24:LP:147:GLU:OE2	2.36	0.57
52:Ls:128:MET:HG2	52:Ls:129:GLU:H	1.69	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:SB:190:PRO:HG2	55:SB:192:VAL:HG23	1.85	0.57
57:SD:165:GLN:N	57:SD:166:PRO:HD2	2.19	0.57
1:1:1067:A:OP1	28:LT:35:ARG:NH1	2.35	0.57
1:1:1599:A:C5'	48:Lr:15:ARG:HH22	2.17	0.57
2:2:1101:U:OP2	77:SX:6:PRO:HD3	2.03	0.57
2:2:1349:C:H2'	2:2:1350:G:C8	2.38	0.57
8:D:429:VAL:HG11	8:D:458:LEU:HD11	1.86	0.57
16:LH:91:ARG:HE	47:Lm:82:LEU:HD21	1.69	0.57
79:SZ:69:LEU:HD12	79:SZ:90:TYR:HD2	1.69	0.57
1:1:1766:G:H2'	1:1:1767:A:C8	2.39	0.57
2:2:1343:A:OP2	2:2:1345:A:N6	2.30	0.57
16:LH:12:VAL:HG11	21:LM:4:ILE:HD11	1.86	0.57
18:LJ:75:PRO:O	18:LJ:78:GLU:HG3	2.04	0.57
26:LR:68:LEU:HD13	26:LR:71:ARG:HD2	1.86	0.57
52:Ls:61:ARG:O	52:Ls:65:THR:HG23	2.04	0.57
56:SC:103:ARG:HH12	56:SC:105:ARG:HG2	1.69	0.57
69:SP:65:ILE:HG23	69:SP:69:ARG:NH2	2.20	0.57
74:SU:61:LYS:HD3	74:SU:79:TYR:O	2.04	0.57
2:2:784:U:H2'	2:2:785:G:H8	1.69	0.57
2:2:1461:C:H5''	70:SQ:136:ALA:HB3	1.86	0.57
14:LF:102:PRO:HB2	14:LF:105:PRO:HD2	1.84	0.57
18:LJ:94:ARG:HH21	18:LJ:157:ARG:HH12	1.51	0.57
27:LS:31:ALA:HB1	27:LS:36:VAL:HG23	1.87	0.57
34:LZ:114:LYS:O	34:LZ:118:GLU:HG2	2.05	0.57
45:Lk:3:GLN:HE21	45:Lk:45:TYR:HE1	1.52	0.57
62:SI:40:PRO:HG2	62:SI:59:ARG:NH1	2.19	0.57
63:SJ:104:GLU:HG3	63:SJ:105:ARG:HG2	1.86	0.57
65:SL:38:ARG:NH2	65:SL:58:TYR:O	2.31	0.57
78:SY:12:THR:HB	78:SY:26:MET:SD	2.43	0.57
81:Sb:2:VAL:HG12	81:Sb:3:LEU:HD23	1.85	0.57
1:1:1720:A:O2'	41:Lg:39:ARG:NH2	2.38	0.57
2:2:1384:G:H21	2:2:1407:A:H61	1.53	0.57
9:LA:176:ASP:OD1	9:LA:177:LYS:N	2.36	0.57
40:Lf:44:ASN:HA	40:Lf:47:LEU:HD23	1.85	0.57
52:Ls:38:MET:HA	52:Ls:41:ILE:HG22	1.86	0.57
58:SE:141:THR:HG22	58:SE:145:ARG:HB2	1.85	0.57
61:SH:30:LEU:O	61:SH:34:GLU:HG3	2.05	0.57
61:SH:149:ARG:HE	76:SW:53:VAL:HG23	1.70	0.57
69:SP:83:LEU:HA	69:SP:101:VAL:HG23	1.86	0.57
73:ST:65:VAL:HG13	73:ST:125:ILE:HD11	1.87	0.57
2:2:1781:U:OP2	68:SO:146:ARG:NH2	2.36	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:C:362:ARG:HA	7:C:365:ARG:HD2	1.87	0.57
8:D:317:GLU:HG2	8:D:324:PHE:HE2	1.69	0.57
2:2:948:C:O2'	67:SN:101:HIS:ND1	2.37	0.57
10:LB:259:SER:O	10:LB:260:HIS:ND1	2.37	0.57
54:SA:16:ASP:OD1	54:SA:182:ARG:NH2	2.38	0.57
61:SH:86:GLU:HA	61:SH:89:LYS:HG2	1.86	0.57
2:2:869:A:H2'	2:2:870:G:C8	2.39	0.57
2:2:1491:C:H42	2:2:1508:G:H1	1.53	0.57
2:2:1616:C:O2'	2:2:1617:U:OP1	2.23	0.57
4:4:156:U:OP1	15:LG:87:LYS:NZ	2.32	0.57
8:D:284:THR:HG21	8:D:296:PHE:CD2	2.39	0.57
43:Li:17:ILE:HA	43:Li:22:LYS:HB2	1.85	0.57
61:SH:41:LYS:HE2	61:SH:41:LYS:HA	1.85	0.57
63:SJ:111:VAL:HG21	63:SJ:127:ILE:HD11	1.86	0.57
67:SN:61:ALA:HB2	81:Sb:32:PHE:HZ	1.70	0.57
2:2:219:C:H2'	2:2:220:A:C8	2.40	0.57
2:2:256:U:O4'	62:SI:182:ARG:NH2	2.37	0.57
2:2:1328:A:N6	57:SD:163:SER:OG	2.36	0.57
7:C:136:LYS:HE2	7:C:137:LYS:HE3	1.87	0.57
7:C:394:VAL:O	7:C:398:ILE:HG12	2.05	0.57
22:LN:115:VAL:HG21	22:LN:160:GLU:HB3	1.87	0.57
44:Lj:21:ARG:NH1	44:Lj:37:CYS:SG	2.75	0.57
63:SJ:173:LYS:HA	63:SJ:176:LYS:HE3	1.86	0.57
64:SK:21:MET:HE2	64:SK:64:TYR:HB2	1.87	0.57
71:SR:101:MET:HE1	71:SR:123:ASN:HD22	1.70	0.57
72:SS:69:LEU:O	72:SS:73:ILE:HG12	2.05	0.57
2:2:648:C:H2'	2:2:649:G:C8	2.37	0.57
5:A:236:ILE:HG13	5:A:252:THR:HG22	1.85	0.57
8:D:347:GLU:OE1	8:D:349:ILE:HG23	2.05	0.57
29:LU:43:LEU:HD23	29:LU:47:ILE:HD11	1.86	0.57
71:SR:74:GLN:O	71:SR:77:GLU:HG2	2.05	0.57
74:SU:27:LYS:NZ	74:SU:30:SER:HB3	2.13	0.57
81:Sb:14:SER:O	81:Sb:18:LYS:NZ	2.37	0.57
1:1:2495:U:H2'	1:1:2496:G:C8	2.39	0.56
1:1:3007:A:N3	10:LB:55:THR:OG1	2.38	0.56
1:1:3299:U:H2'	1:1:3300:A:H8	1.70	0.56
2:2:825:C:H2'	2:2:826:U:H6	1.70	0.56
2:2:1047:C:H5''	81:Sb:70:LYS:HE2	1.87	0.56
2:2:1291:G:H1	2:2:1300:U:H3	1.54	0.56
9:LA:59:ALA:HB2	9:LA:78:ALA:HB2	1.87	0.56
42:Lh:32:SER:O	42:Lh:36:ILE:HG12	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:Lk:31:THR:O	45:Lk:50:LYS:NZ	2.38	0.56
45:Lk:53:ASP:OD1	45:Lk:54:LYS:N	2.37	0.56
60:SG:69:ALA:O	60:SG:98:ARG:NH1	2.38	0.56
68:SO:112:GLN:HE22	80:Sa:45:VAL:HA	1.70	0.56
80:Sa:100:ARG:O	80:Sa:102:ARG:NH1	2.38	0.56
1:1:1366:G:N2	51:Lq:16:TYR:OH	2.38	0.56
2:2:494:G:H2'	2:2:495:G:H8	1.69	0.56
7:C:60:SER:HB3	8:D:416:ALA:HB3	1.87	0.56
10:LB:9:PRO:HD3	30:LV:47:ARG:HH22	1.70	0.56
12:LD:65:VAL:HG12	12:LD:74:ILE:HD13	1.87	0.56
15:LG:166:VAL:HA	15:LG:169:LEU:HD23	1.86	0.56
43:Li:63:GLU:HA	43:Li:66:VAL:HG12	1.87	0.56
1:1:309:U:O2'	43:Li:39:LYS:NZ	2.35	0.56
1:1:1060:U:O3'	12:LD:43:LYS:NZ	2.39	0.56
2:2:930:A:OP2	55:SB:155:TYR:OH	2.19	0.56
2:2:1207:C:H2'	2:2:1208:A:H8	1.70	0.56
7:C:133:HIS:CD2	7:C:135:ASP:HB2	2.39	0.56
7:C:138:ALA:HA	7:C:142:ARG:HB2	1.87	0.56
7:C:182:LYS:HG3	7:C:185:LEU:H	1.69	0.56
8:D:243:ILE:HG22	8:D:247:LYS:NZ	2.20	0.56
8:D:376:ALA:HB3	8:D:379:THR:HG22	1.87	0.56
10:LB:170:THR:HG23	10:LB:172:LEU:H	1.70	0.56
10:LB:215:MET:HG2	10:LB:346:HIS:CE1	2.40	0.56
14:LF:39:ARG:HH11	14:LF:39:ARG:HG3	1.70	0.56
17:LI:14:ASN:O	17:LI:128:ARG:NH2	2.38	0.56
26:LR:15:LEU:HD13	26:LR:52:LYS:HB2	1.88	0.56
35:La:85:ASP:OD1	35:La:86:VAL:N	2.37	0.56
56:SC:120:GLY:HA2	56:SC:223:PHE:CE2	2.33	0.56
60:SG:35:GLU:OE2	60:SG:49:ILE:HB	2.05	0.56
61:SH:174:TYR:HD2	61:SH:175:ARG:HH12	1.52	0.56
64:SK:21:MET:HB2	64:SK:64:TYR:HB2	1.88	0.56
64:SK:22:VAL:HA	64:SK:62:TYR:O	2.06	0.56
77:SX:96:VAL:HG22	77:SX:127:VAL:HG11	1.87	0.56
78:SY:109:GLN:NE2	78:SY:110:GLN:HG2	2.19	0.56
79:SZ:43:VAL:HA	79:SZ:46:TYR:CD2	2.41	0.56
79:SZ:78:ILE:HG21	79:SZ:90:TYR:HB3	1.87	0.56
1:1:2477:U:OP1	15:LG:71:ARG:NH1	2.38	0.56
1:1:2552:A:H4'	1:1:2553:C:O5'	2.03	0.56
2:2:644:A:H2'	2:2:645:G:C8	2.39	0.56
13:LE:28:TYR:OH	51:Lq:112:VAL:O	2.24	0.56
18:LJ:49:SER:HB3	18:LJ:67:ALA:HB3	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:Lj:14:LYS:HZ1	46:Ll:51:LEU:HD21	1.70	0.56
63:SJ:42:ARG:HH11	63:SJ:42:ARG:HG3	1.71	0.56
1:1:652:A:H2'	1:1:653:A:C8	2.41	0.56
1:1:1117:G:O2'	1:1:2601:A:N3	2.37	0.56
1:1:1480:C:O2'	1:1:1582:A:N3	2.36	0.56
1:1:2919:C:H2'	1:1:2920:G:C8	2.40	0.56
2:2:66:U:O2	60:SG:160:ARG:NH1	2.39	0.56
2:2:683:G:H2'	2:2:684:G:H8	1.69	0.56
2:2:1441:G:N2	85:Sf:87:THR:O	2.37	0.56
2:2:1701:A:H2'	2:2:1702:C:C6	2.39	0.56
5:A:43:TRP:CZ3	5:A:55:PRO:HD3	2.41	0.56
10:LB:160:ARG:HA	10:LB:183:GLN:HA	1.87	0.56
25:LQ:116:ASP:OD1	25:LQ:117:ASP:N	2.38	0.56
26:LR:37:SER:O	26:LR:41:ILE:HG12	2.06	0.56
37:Lc:56:LYS:O	37:Lc:60:GLU:HG3	2.06	0.56
55:SB:3:VAL:N	68:SO:58:GLY:O	2.38	0.56
59:SF:119:VAL:HG21	59:SF:186:ILE:HD13	1.86	0.56
1:1:192:A:N3	1:1:212:G:O2'	2.37	0.56
1:1:434:U:H2'	1:1:435:G:C8	2.41	0.56
1:1:1021:C:H5''	12:LD:5:LYS:HE2	1.86	0.56
1:1:1222:C:H2'	1:1:1223:A:C8	2.38	0.56
2:2:1156:C:O2'	70:SQ:137:ARG:NH1	2.39	0.56
2:2:1765:U:OP1	6:B:98:LYS:NZ	2.32	0.56
4:4:8:C:H2'	4:4:9:A:C8	2.39	0.56
7:C:260:GLU:OE2	7:C:267:ARG:NH1	2.39	0.56
20:LL:31:LYS:O	20:LL:35:ARG:HG3	2.06	0.56
29:LU:24:ASN:HA	29:LU:69:LYS:HG2	1.88	0.56
57:SD:83:PRO:O	57:SD:86:SER:OG	2.19	0.56
72:SS:86:LEU:HD12	72:SS:97:ASP:HB3	1.87	0.56
74:SU:55:MET:SD	74:SU:56:PRO:HD2	2.46	0.56
79:SZ:79:ARG:NH1	79:SZ:92:ARG:O	2.38	0.56
81:Sb:19:HIS:HE1	81:Sb:21:LEU:HD13	1.69	0.56
2:2:1384:G:H2'	2:2:1385:A:H8	1.69	0.56
5:A:268:ASP:OD1	5:A:269:GLU:N	2.39	0.56
7:C:49:HIS:O	7:C:53:VAL:HG23	2.05	0.56
44:Lj:84:LYS:HG3	44:Lj:85:GLY:H	1.69	0.56
52:Ls:16:LYS:HZ3	52:Ls:64:LYS:HE3	1.68	0.56
55:SB:115:ARG:HB2	55:SB:118:GLN:NE2	2.18	0.56
63:SJ:26:LEU:HA	63:SJ:29:VAL:HG12	1.86	0.56
70:SQ:35:PRO:HG2	70:SQ:38:LEU:HD23	1.86	0.56
75:SV:85:ALA:HB1	81:Sb:6:ASP:H	1.71	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:48:C:OP2	1:1:49:A:O2'	2.21	0.56
1:1:1632:G:H2'	1:1:1633:G:H8	1.70	0.56
5:A:199:THR:OG1	5:A:239:LEU:O	2.22	0.56
21:LM:130:GLU:HG2	23:LO:191:VAL:HG21	1.87	0.56
24:LP:22:LEU:HD22	24:LP:146:ILE:HD13	1.87	0.56
24:LP:182:ARG:HA	24:LP:185:THR:HG22	1.87	0.56
37:Lc:51:THR:HG23	37:Lc:56:LYS:HG2	1.86	0.56
57:SD:103:ALA:HA	57:SD:106:GLU:OE2	2.05	0.56
60:SG:39:ASP:O	60:SG:46:LYS:NZ	2.37	0.56
60:SG:93:LYS:HZ2	60:SG:95:LYS:HG2	1.71	0.56
68:SO:42:HIS:ND1	68:SO:54:ARG:HB2	2.21	0.56
71:SR:30:THR:O	71:SR:34:VAL:HG13	2.05	0.56
74:SU:45:LYS:HE2	74:SU:96:ILE:HD11	1.86	0.56
76:SW:22:LYS:HA	76:SW:22:LYS:HE3	1.88	0.56
79:SZ:54:LEU:HB3	79:SZ:60:ILE:HD11	1.88	0.56
82:Sc:9:LYS:CE	82:Sc:60:SER:HB3	2.36	0.56
13:LE:194:LYS:HD2	13:LE:197:LEU:HD21	1.88	0.56
45:Lk:39:ARG:HD2	45:Lk:40:CYS:O	2.06	0.56
52:Ls:12:PHE:O	52:Ls:16:LYS:HG2	2.05	0.56
54:SA:18:GLU:HA	54:SA:21:LEU:HD23	1.86	0.56
55:SB:118:GLN:HB2	55:SB:143:THR:OG1	2.05	0.56
66:SM:51:SER:HA	66:SM:54:LEU:HG	1.85	0.56
83:Sd:53:VAL:HG22	83:Sd:54:LYS:H	1.71	0.56
1:1:20:U:H2'	1:1:21:A:C8	2.41	0.56
1:1:3212:G:N7	13:LE:136:LYS:NZ	2.53	0.56
2:2:1391:G:H5'	5:A:277:VAL:HB	1.88	0.56
14:LF:118:ASN:OD1	14:LF:248:MET:HE1	2.06	0.56
29:LU:21:PHE:HB2	29:LU:72:ILE:HB	1.88	0.56
56:SC:105:ARG:HH11	56:SC:105:ARG:HG3	1.71	0.56
1:1:1704:U:H1'	1:1:1705:C:C6	2.42	0.55
1:1:1818:C:H5''	1:1:1819:A:H5'	1.88	0.55
1:1:3298:U:O2'	1:1:3299:U:OP1	2.23	0.55
2:2:1546:A:H5''	69:SP:51:ARG:NH2	2.21	0.55
14:LF:65:GLU:O	14:LF:69:ILE:HG13	2.06	0.55
59:SF:88:GLY:O	59:SF:91:ASN:ND2	2.38	0.55
62:SI:67:TRP:CD1	62:SI:187:ILE:HD11	2.41	0.55
62:SI:87:ASN:OD1	62:SI:89:GLU:N	2.39	0.55
79:SZ:66:ARG:HG2	79:SZ:88:LYS:NZ	2.22	0.55
2:2:607:G:HO2'	2:2:610:G:HO2'	1.54	0.55
3:3:76:G:N2	3:3:101:A:OP2	2.38	0.55
8:D:332:GLU:HA	8:D:335:VAL:HG12	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:LD:273:GLU:HA	12:LD:276:LYS:NZ	2.22	0.55
27:LS:136:LYS:O	27:LS:141:LYS:NZ	2.39	0.55
54:SA:59:LYS:NZ	54:SA:163:ILE:HD13	2.21	0.55
56:SC:148:ARG:HD3	56:SC:163:PRO:HG3	1.88	0.55
68:SO:116:ARG:NH1	80:Sa:46:GLU:OE2	2.33	0.55
70:SQ:34:LYS:NZ	73:ST:8:ARG:HG3	2.21	0.55
77:SX:37:ALA:O	77:SX:41:SER:OG	2.19	0.55
79:SZ:35:THR:HA	79:SZ:38:LYS:NZ	2.21	0.55
1:1:681:A:H5''	11:LC:43:MET:HE3	1.88	0.55
1:1:3254:U:H5'	10:LB:176:LYS:HD3	1.87	0.55
5:A:279:LYS:HD2	5:A:280:LYS:HG2	1.88	0.55
8:D:564:ARG:HG2	8:D:571:GLY:HA3	1.88	0.55
13:LE:28:TYR:CZ	51:Lq:116:SER:HB3	2.41	0.55
14:LF:229:ILE:HG23	27:LS:36:VAL:HG12	1.88	0.55
56:SC:61:MET:HB3	56:SC:65:TYR:CE1	2.40	0.55
64:SK:48:GLN:HE21	64:SK:64:TYR:HD1	1.50	0.55
1:1:307:U:H2'	1:1:308:C:C6	2.41	0.55
1:1:2120:G:C5	9:LA:150:LEU:HD23	2.42	0.55
2:2:1479:A:H4'	70:SQ:72:GLY:H	1.70	0.55
2:2:1678:C:H5'	60:SG:65:GLN:NE2	2.20	0.55
41:Lg:46:GLY:N	41:Lg:80:SER:O	2.35	0.55
45:Lk:36:PHE:CE2	45:Lk:58:LEU:HD22	2.41	0.55
52:Ls:22:TYR:HB2	52:Ls:88:PHE:HD2	1.70	0.55
58:SE:60:GLU:O	58:SE:64:ILE:HG12	2.06	0.55
67:SN:49:GLN:HA	67:SN:52:VAL:HG12	1.88	0.55
72:SS:28:VAL:HG12	72:SS:58:ALA:HA	1.88	0.55
84:Se:7:SER:HB3	84:Se:10:ARG:NH2	2.21	0.55
1:1:477:C:H2'	1:1:478:G:H8	1.72	0.55
4:4:154:C:H2'	4:4:155:A:C8	2.41	0.55
7:C:40:GLU:HB2	8:D:229:TYR:CE2	2.41	0.55
7:C:131:LYS:HG3	7:C:132:HIS:CD2	2.42	0.55
9:LA:112:VAL:HG22	50:Lp:79:MET:HE2	1.88	0.55
13:LE:25:GLN:HG3	13:LE:28:TYR:HB3	1.89	0.55
24:LP:103:ASP:OD1	24:LP:104:ALA:N	2.39	0.55
56:SC:187:VAL:O	56:SC:206:THR:OG1	2.22	0.55
74:SU:74:LYS:HE3	74:SU:74:LYS:HA	1.88	0.55
1:1:434:U:H2'	1:1:435:G:H8	1.72	0.55
1:1:509:G:OP2	1:1:509:G:N2	2.28	0.55
1:1:2117:U:H2'	1:1:2118:G:H8	1.71	0.55
2:2:421:C:O2'	2:2:423:G:OP1	2.19	0.55
7:C:129:VAL:O	7:C:133:HIS:HB2	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:D:243:ILE:HG22	8:D:247:LYS:HZ3	1.72	0.55
56:SC:194:ARG:HH21	56:SC:198:LEU:HD21	1.72	0.55
57:SD:109:ARG:NH2	57:SD:177:HIS:O	2.40	0.55
61:SH:9:ILE:O	61:SH:48:GLN:NE2	2.39	0.55
70:SQ:50:GLU:HG2	70:SQ:51:PRO:HD3	1.87	0.55
71:SR:24:LEU:HD21	71:SR:31:ASN:HD22	1.71	0.55
72:SS:116:LEU:HD21	72:SS:121:ALA:HB3	1.89	0.55
2:2:710:C:O2	2:2:721:G:N2	2.31	0.55
11:LC:34:ASP:OD1	11:LC:35:ILE:N	2.40	0.55
21:LM:72:LEU:HD12	21:LM:73:PRO:HD2	1.87	0.55
60:SG:203:LYS:O	60:SG:206:GLU:HG3	2.06	0.55
61:SH:102:ARG:NH2	61:SH:138:ASP:OD2	2.38	0.55
65:SL:7:VAL:HG13	65:SL:8:GLN:HG2	1.89	0.55
69:SP:72:LYS:HD3	69:SP:97:MET:HE1	1.89	0.55
73:ST:45:GLU:N	73:ST:45:GLU:OE1	2.39	0.55
1:1:2405:G:H2'	1:1:2406:A:H8	1.72	0.55
2:2:598:A:OP2	77:SX:110:LYS:NZ	2.32	0.55
2:2:824:U:H2'	2:2:825:C:C6	2.41	0.55
2:2:841:U:H2'	2:2:842:A:C8	2.41	0.55
2:2:1166:G:N1	2:2:1571:G:OP2	2.40	0.55
3:3:40:C:O2	18:LJ:73:ARG:NH1	2.38	0.55
11:LC:159:ALA:HB3	11:LC:162:ALA:HB2	1.88	0.55
29:LU:81:ARG:HH11	29:LU:81:ARG:HG3	1.71	0.55
44:Lj:84:LYS:HE2	44:Lj:84:LYS:HA	1.89	0.55
72:SS:100:ILE:HG12	72:SS:108:LYS:HD3	1.87	0.55
1:1:467:U:H2'	1:1:468:G:C8	2.42	0.55
1:1:3123:U:H2'	1:1:3124:G:H8	1.71	0.55
2:2:499:U:H2'	2:2:500:G:C8	2.41	0.55
2:2:1462:G:O2'	2:2:1598:C:OP1	2.24	0.55
7:C:146:ASP:HB3	7:C:150:LYS:HZ3	1.72	0.55
9:LA:20:THR:HA	9:LA:23:ARG:HD2	1.87	0.55
16:LH:130:MET:CE	16:LH:159:SER:HB2	2.37	0.55
17:LI:177:ARG:HB3	17:LI:180:GLU:OE1	2.07	0.55
55:SB:99:ASN:OD1	55:SB:100:PHE:N	2.29	0.55
67:SN:60:ILE:H	67:SN:60:ILE:HD12	1.70	0.55
73:ST:102:ARG:NE	73:ST:103:LYS:HZ1	2.05	0.55
74:SU:81:MET:CE	83:Sd:52:PHE:HD1	2.20	0.55
1:1:697:A:OP1	25:LQ:206:ARG:NH2	2.40	0.55
2:2:1214:A:H4'	64:SK:42:LYS:HE3	1.89	0.55
14:LF:86:GLU:OE2	28:LT:136:ARG:N	2.40	0.55
42:Lh:110:LYS:O	42:Lh:114:THR:HG23	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:SD:73:THR:HB	57:SD:87:VAL:HG23	1.89	0.55
63:SJ:131:HIS:CD2	63:SJ:160:SER:HB2	2.31	0.55
72:SS:114:GLU:HA	72:SS:117:LYS:HB3	1.89	0.55
2:2:834:U:H2'	2:2:835:G:C8	2.42	0.54
2:2:1380:G:H2'	2:2:1381:A:C8	2.41	0.54
2:2:1465:A:H2'	2:2:1466:C:C6	2.42	0.54
14:LF:105:PRO:HA	14:LF:108:ILE:HG22	1.89	0.54
25:LQ:174:ARG:HB3	25:LQ:177:VAL:HG23	1.89	0.54
34:LZ:8:ARG:HB3	34:LZ:24:ILE:HD12	1.88	0.54
67:SN:99:ARG:NH1	67:SN:119:GLU:OE2	2.40	0.54
82:Sc:62:ARG:HD3	82:Sc:63:GLU:N	2.22	0.54
2:2:510:U:H5'	63:SJ:129:GLN:HG2	1.88	0.54
15:LG:33:ARG:HH11	15:LG:33:ARG:HG3	1.71	0.54
25:LQ:107:THR:HB	25:LQ:164:THR:HG22	1.89	0.54
25:LQ:108:VAL:HG12	25:LQ:165:LEU:HD11	1.89	0.54
56:SC:230:TYR:HB2	75:SV:25:LYS:NZ	2.22	0.54
78:SY:23:ARG:HH11	78:SY:23:ARG:HG3	1.72	0.54
1:1:2064:C:O2'	1:1:2065:U:OP1	2.25	0.54
1:1:3332:A:O2'	1:1:3333:G:OP1	2.21	0.54
7:C:8:LEU:HD22	8:D:439:LYS:HE3	1.88	0.54
7:C:42:VAL:HB	8:D:229:TYR:OH	2.07	0.54
9:LA:179:LEU:HD13	9:LA:185:ALA:HB2	1.89	0.54
11:LC:149:VAL:CG1	11:LC:150:PRO:HD3	2.38	0.54
28:LT:108:ARG:HA	28:LT:111:GLU:OE2	2.08	0.54
30:LV:123:GLU:OE1	30:LV:123:GLU:N	2.41	0.54
60:SG:157:VAL:HG11	60:SG:178:ILE:HD11	1.88	0.54
61:SH:53:ARG:O	61:SH:65:VAL:N	2.32	0.54
77:SX:13:ARG:HA	77:SX:16:ARG:NH1	2.21	0.54
77:SX:36:THR:OG1	77:SX:40:SER:OG	2.15	0.54
1:1:1744:C:H3'	1:1:1745:U:H5''	1.89	0.54
1:1:2667:C:H2'	1:1:2668:C:H6	1.73	0.54
2:2:841:U:H2'	2:2:842:A:H8	1.72	0.54
2:2:1105:G:H1	77:SX:22:GLN:NE2	2.04	0.54
7:C:91:LEU:HD11	7:C:105:LYS:HZ2	1.72	0.54
13:LE:119:ILE:HD12	13:LE:119:ILE:H	1.72	0.54
52:Ls:67:MET:HE1	52:Ls:69:ASP:HB3	1.90	0.54
54:SA:92:PHE:O	54:SA:96:THR:HG22	2.08	0.54
58:SE:171:ASP:OD1	58:SE:172:PHE:N	2.36	0.54
75:SV:64:GLU:HG2	81:Sb:3:LEU:HG	1.89	0.54
84:Se:43:ARG:O	84:Se:44:PHE:HD1	1.91	0.54
1:1:1702:U:OP1	26:LR:100:ARG:NE	2.39	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2673:G:H8	1:1:2710:G:H2'	1.72	0.54
2:2:451:A:C4	58:SE:66:MET:HE2	2.42	0.54
2:2:697:G:H2'	2:2:698:G:C8	2.43	0.54
8:D:15:VAL:HG12	8:D:152:SER:HB2	1.87	0.54
10:LB:373:THR:HG23	10:LB:376:GLU:H	1.72	0.54
18:LJ:56:ARG:HA	18:LJ:56:ARG:CZ	2.38	0.54
22:LN:136:ASP:O	22:LN:142:ILE:HG21	2.07	0.54
51:Lq:5:SER:O	51:Lq:9:ILE:HG13	2.06	0.54
2:2:133:A:H2'	2:2:134:C:H4'	1.89	0.54
2:2:335:C:H5''	62:SI:10:LYS:HE3	1.88	0.54
2:2:468:A:H1'	63:SJ:6:TYR:HD2	1.72	0.54
2:2:503:A:H2'	2:2:504:U:C6	2.43	0.54
2:2:1494:G:OP1	73:ST:75:ARG:NE	2.41	0.54
5:A:118:ARG:HA	5:A:134:THR:HB	1.90	0.54
7:C:343:ARG:HB3	7:C:347:LYS:NZ	2.22	0.54
58:SE:2:ALA:O	58:SE:3:ARG:HG2	2.07	0.54
59:SF:92:GLY:HA2	59:SF:94:LYS:NZ	2.22	0.54
61:SH:20:SER:N	61:SH:23:GLU:OE2	2.37	0.54
73:ST:62:ALA:HA	73:ST:65:VAL:HG12	1.90	0.54
85:Sf:117:LEU:HG	85:Sf:118:ARG:HG3	1.90	0.54
1:1:452:C:H2'	1:1:453:G:H8	1.72	0.54
1:1:2719:C:N3	49:Lo:63:LYS:NZ	2.55	0.54
1:1:3119:A:H61	1:1:3226:C:H42	1.56	0.54
2:2:784:U:H2'	2:2:785:G:C8	2.42	0.54
20:LL:76:THR:OG1	20:LL:79:GLU:OE1	2.26	0.54
25:LQ:68:THR:HG22	25:LQ:70:ALA:H	1.70	0.54
29:LU:76:ASN:OD1	29:LU:77:ASP:N	2.39	0.54
30:LV:103:VAL:HG21	30:LV:111:MET:HE2	1.90	0.54
63:SJ:37:LYS:HE2	63:SJ:41:TRP:CH2	2.43	0.54
63:SJ:121:HIS:HD2	84:Se:33:ARG:NH2	2.05	0.54
65:SL:106:GLU:CD	77:SX:13:ARG:HH21	2.13	0.54
73:ST:13:HIS:O	73:ST:16:VAL:HG22	2.07	0.54
2:2:210:A:H4'	65:SL:31:ARG:HH22	1.72	0.54
2:2:742:U:OP1	61:SH:116:ASN:ND2	2.41	0.54
2:2:1184:U:H3	2:2:1197:G:H1	1.55	0.54
10:LB:41:VAL:HG12	10:LB:186:GLY:HA3	1.88	0.54
14:LF:223:ARG:HD3	14:LF:226:LYS:HE3	1.90	0.54
18:LJ:134:ARG:HG3	18:LJ:155:ILE:HD11	1.89	0.54
49:Lo:38:GLN:OE1	49:Lo:41:ARG:NH2	2.41	0.54
69:SP:135:LYS:HA	69:SP:135:LYS:HE3	1.90	0.54
71:SR:29:GLU:HA	71:SR:32:LYS:NZ	2.23	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1022:C:H2'	1:1:1023:A:C8	2.43	0.54
2:2:1356:C:OP1	73:ST:131:ARG:NH1	2.41	0.54
2:2:1396:A:H1'	71:SR:67:ARG:HH22	1.72	0.54
2:2:1477:C:HO2'	2:2:1478:C:P	2.31	0.54
2:2:1511:A:O2'	2:2:1514:C:N4	2.41	0.54
4:4:23:U:OP1	33:LY:15:ARG:NH1	2.41	0.54
7:C:65:ILE:HD13	8:D:416:ALA:HA	1.90	0.54
7:C:385:ASP:O	7:C:389:ASN:ND2	2.40	0.54
8:D:311:ILE:HD11	8:D:315:ARG:HG2	1.90	0.54
12:LD:126:ASN:HA	12:LD:199:LYS:HE2	1.90	0.54
23:LO:76:ARG:NH1	23:LO:147:VAL:O	2.41	0.54
34:LZ:41:LEU:HD22	34:LZ:73:VAL:HG22	1.90	0.54
62:SI:67:TRP:CG	62:SI:187:ILE:HD11	2.43	0.54
64:SK:72:ASP:OD1	64:SK:73:TYR:N	2.41	0.54
67:SN:114:ARG:O	67:SN:118:ILE:HD12	2.07	0.54
1:1:627:G:OP1	39:Le:41:ASN:ND2	2.39	0.54
2:2:921:A:H2'	2:2:922:A:C8	2.43	0.54
8:D:317:GLU:HG3	8:D:359:ARG:HG3	1.88	0.54
12:LD:219:GLU:HB3	12:LD:223:LYS:HE3	1.90	0.54
16:LH:44:ASN:ND2	16:LH:56:GLU:OE2	2.41	0.54
40:Lf:51:VAL:HG23	40:Lf:102:ILE:HD13	1.89	0.54
44:Lj:64:MET:HE1	44:Lj:67:LEU:HD22	1.89	0.54
52:Ls:22:TYR:HB2	52:Ls:88:PHE:CD2	2.43	0.54
67:SN:4:LEU:HD11	67:SN:124:ARG:NH1	2.22	0.54
70:SQ:34:LYS:HA	70:SQ:34:LYS:HE3	1.90	0.54
2:2:1548:U:O2'	2:2:1593:A:N3	2.36	0.53
12:LD:208:ALA:HB1	12:LD:236:ALA:HB1	1.90	0.53
14:LF:221:ARG:NH2	14:LF:232:GLY:O	2.38	0.53
56:SC:64:ILE:HG23	56:SC:69:LEU:HG	1.89	0.53
56:SC:117:GLY:HA2	56:SC:147:VAL:HG12	1.90	0.53
58:SE:11:ARG:NH2	58:SE:21:ASP:OD1	2.41	0.53
61:SH:34:GLU:HA	61:SH:41:LYS:NZ	2.24	0.53
65:SL:79:ARG:HB2	65:SL:92:ARG:CG	2.38	0.53
71:SR:17:ILE:HD13	71:SR:57:LEU:HD22	1.90	0.53
77:SX:73:ARG:HH22	77:SX:82:LYS:HB3	1.72	0.53
1:1:1001:G:H2'	1:1:1002:G:C8	2.42	0.53
2:2:246:U:H5	65:SL:39:TRP:CZ2	2.27	0.53
2:2:892:U:H2'	2:2:893:G:C8	2.43	0.53
2:2:1143:G:H4'	56:SC:99:ARG:NH2	2.22	0.53
8:D:276:LYS:HZ3	8:D:299:GLU:N	2.06	0.53
13:LE:141:ALA:HA	13:LE:144:LYS:NZ	2.23	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:Ls:93:LEU:HA	52:Ls:96:VAL:HG12	1.90	0.53
57:SD:224:GLN:HB3	57:SD:225:PRO:HD3	1.90	0.53
68:SO:66:ASP:OD1	68:SO:69:SER:OG	2.21	0.53
71:SR:12:SER:O	71:SR:16:ILE:HG12	2.08	0.53
79:SZ:66:ARG:HG2	79:SZ:88:LYS:HZ1	1.73	0.53
1:1:1228:A:H2'	1:1:1255:C:H4'	1.91	0.53
1:1:1747:U:P	45:Lk:74:ARG:HH12	2.32	0.53
1:1:1843:G:N1	1:1:1846:C:OP2	2.30	0.53
1:1:2123:G:H2'	1:1:2124:G:H8	1.74	0.53
1:1:3046:G:OP1	10:LB:314:ARG:NH1	2.40	0.53
2:2:223:G:H8	2:2:223:G:OP1	1.91	0.53
2:2:974:G:N1	2:2:1021:A:O2'	2.33	0.53
2:2:1349:C:H2'	2:2:1350:G:H8	1.74	0.53
2:2:1470:G:H2'	2:2:1471:A:H8	1.73	0.53
2:2:1602:C:H2'	2:2:1603:G:C8	2.43	0.53
4:4:9:A:H2'	4:4:10:A:H8	1.73	0.53
12:LD:53:VAL:HG12	12:LD:62:THR:HG22	1.89	0.53
12:LD:185:GLY:HA3	12:LD:197:VAL:HG11	1.89	0.53
43:Li:46:THR:HA	43:Li:49:VAL:HG12	1.90	0.53
1:1:452:C:H2'	1:1:453:G:C8	2.43	0.53
2:2:1569:A:H4'	2:2:1570:G:OP2	2.08	0.53
12:LD:273:GLU:HA	12:LD:276:LYS:HZ3	1.72	0.53
25:LQ:153:GLN:O	25:LQ:157:GLU:HG3	2.07	0.53
59:SF:68:ARG:HE	59:SF:69:PHE:HE1	1.55	0.53
61:SH:53:ARG:N	61:SH:65:VAL:O	2.39	0.53
2:2:1688:G:H3'	2:2:1689:A:H8	1.73	0.53
3:3:4:U:H2'	3:3:5:A:C8	2.41	0.53
7:C:246:VAL:HG22	7:C:247:PRO:CD	2.10	0.53
10:LB:115:LYS:HE2	10:LB:129:ALA:HB3	1.90	0.53
17:LI:176:LEU:HD21	17:LI:180:GLU:HG2	1.91	0.53
20:LL:169:SER:HA	35:La:98:THR:HG23	1.91	0.53
23:LO:55:TYR:CE2	23:LO:147:VAL:HG11	2.43	0.53
26:LR:105:LEU:HD23	26:LR:138:LEU:HD23	1.90	0.53
30:LV:87:TRP:HE1	30:LV:89:ARG:HH12	1.56	0.53
37:Lc:43:LYS:HD2	37:Lc:104:LEU:HD21	1.89	0.53
58:SE:162:ILE:HD11	58:SE:167:GLY:HA2	1.89	0.53
2:2:60:U:N3	2:2:63:G:OP1	2.30	0.53
2:2:1551:A:O2'	69:SP:90:ASP:OD2	2.19	0.53
5:A:159:ASN:HB3	5:A:161:GLN:OE1	2.08	0.53
7:C:193:LEU:O	7:C:197:VAL:HG23	2.09	0.53
24:LP:126:ARG:HE	24:LP:140:MET:HE1	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:La:80:SER:HA	35:La:87:ARG:HH12	1.74	0.53
37:Lc:101:SER:OG	37:Lc:102:ASP:N	2.39	0.53
56:SC:177:LEU:HD11	56:SC:196:LEU:HD11	1.91	0.53
63:SJ:13:PRO:HG3	63:SJ:21:ARG:HH12	1.74	0.53
67:SN:99:ARG:HA	67:SN:102:LEU:HG	1.91	0.53
85:Sf:121:CYS:HB2	85:Sf:132:MET:HE3	1.90	0.53
1:1:331:A:OP1	11:LC:48:ARG:NH2	2.41	0.53
1:1:1219:G:H5''	1:1:1228:A:H1'	1.89	0.53
2:2:694:U:H2'	2:2:695:C:C6	2.44	0.53
8:D:22:ASN:ND2	8:D:215:SER:HB3	2.24	0.53
8:D:472:VAL:HG21	8:D:529:ILE:HG23	1.91	0.53
9:LA:31:PRO:HB3	9:LA:123:ARG:HH21	1.73	0.53
16:LH:99:ILE:HG22	16:LH:119:PHE:HA	1.91	0.53
22:LN:39:ALA:HB3	22:LN:61:ILE:HG23	1.90	0.53
40:Lf:16:LEU:HD11	40:Lf:33:LYS:HB2	1.91	0.53
49:Lo:17:CYS:O	49:Lo:19:LYS:NZ	2.26	0.53
51:Lq:131:LYS:NZ	51:Lq:132:LYS:O	2.42	0.53
57:SD:78:LYS:NZ	64:SK:20:VAL:O	2.40	0.53
58:SE:251:ARG:HB3	58:SE:255:ARG:HH22	1.73	0.53
59:SF:109:HIS:HB2	59:SF:116:PRO:HG3	1.90	0.53
63:SJ:121:HIS:CD2	84:Se:33:ARG:NH2	2.77	0.53
71:SR:46:LEU:HA	71:SR:49:LYS:HG2	1.90	0.53
77:SX:127:VAL:O	77:SX:130:VAL:HG22	2.09	0.53
1:1:1126:A:H5'	1:1:1351:U:H1'	1.91	0.53
1:1:1242:A:N6	52:Ls:53:MET:SD	2.81	0.53
2:2:802:A:C8	76:SW:107:SER:HA	2.44	0.53
2:2:1354:U:H2'	2:2:1355:G:C8	2.44	0.53
2:2:1397:A:H5''	71:SR:5:ARG:HH12	1.74	0.53
5:A:235:GLU:O	5:A:253:ALA:N	2.42	0.53
7:C:98:TRP:HZ3	7:C:154:LYS:HB3	1.73	0.53
7:C:426:GLU:HA	7:C:429:ARG:HE	1.74	0.53
12:LD:32:ALA:O	12:LD:36:LEU:HD13	2.08	0.53
18:LJ:113:LEU:HD23	18:LJ:113:LEU:H	1.73	0.53
36:Lb:43:HIS:HD1	36:Lb:47:LEU:HD23	1.74	0.53
40:Lf:71:GLY:HA3	40:Lf:87:PHE:HD1	1.74	0.53
54:SA:59:LYS:NZ	54:SA:163:ILE:HA	2.23	0.53
58:SE:174:LYS:HD2	58:SE:176:ASP:HB2	1.91	0.53
64:SK:13:GLU:HB2	64:SK:17:ARG:NH1	2.24	0.53
72:SS:132:ARG:HE	72:SS:133:VAL:H	1.54	0.53
85:Sf:134:SER:HA	85:Sf:139:GLN:HG3	1.91	0.53
7:C:252:ASN:O	7:C:256:LYS:NZ	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:LE:150:GLN:OE1	13:LE:150:GLN:N	2.42	0.53
17:LI:47:PRO:O	17:LI:178:ARG:NH2	2.42	0.53
17:LI:115:MET:O	17:LI:115:MET:HG2	2.08	0.53
32:LX:145:ALA:HA	32:LX:148:ILE:HG22	1.91	0.53
55:SB:120:LEU:HD23	55:SB:120:LEU:H	1.74	0.53
59:SF:92:GLY:HA2	59:SF:94:LYS:HZ1	1.72	0.53
60:SG:45:TRP:HA	60:SG:48:TYR:HD2	1.74	0.53
63:SJ:51:ARG:HG2	63:SJ:55:ARG:CZ	2.39	0.53
63:SJ:90:LYS:HB2	63:SJ:93:TYR:HD2	1.74	0.53
1:1:1779:A:H2'	1:1:1780:A:H8	1.74	0.53
1:1:2538:G:OP2	1:1:2539:A:O2'	2.23	0.53
2:2:1277:C:H2'	2:2:1278:G:C8	2.44	0.53
2:2:1467:A:N6	2:2:1534:U:N3	2.33	0.53
8:D:318:THR:HA	8:D:321:ARG:HG3	1.91	0.53
12:LD:83:LEU:HD22	12:LD:88:ILE:HD12	1.90	0.53
25:LQ:177:VAL:HA	25:LQ:180:PHE:CD2	2.44	0.53
31:LW:123:LYS:O	31:LW:126:GLU:HG3	2.09	0.53
1:1:1139:C:OP2	14:LF:100:LYS:NZ	2.42	0.52
1:1:1615:G:N2	1:1:1618:A:OP2	2.42	0.52
2:2:164:U:O2'	60:SG:136:LYS:HG3	2.09	0.52
2:2:786:A:OP2	58:SE:108:ARG:NH2	2.32	0.52
2:2:1580:G:O2'	2:2:1606:G:O6	2.23	0.52
6:B:135:GLU:OE1	6:B:138:ALA:N	2.43	0.52
7:C:294:ARG:O	7:C:297:GLN:HG3	2.10	0.52
28:LT:119:ALA:HA	28:LT:122:GLU:HG3	1.91	0.52
29:LU:34:PHE:HZ	29:LU:39:PHE:CD2	2.27	0.52
67:SN:3:ARG:CG	67:SN:6:SER:HB2	2.39	0.52
68:SO:120:ARG:NE	82:Sc:61:GLU:HG3	2.24	0.52
1:1:649:G:OP2	1:1:649:G:N2	2.30	0.52
1:1:811:U:H3	1:1:877:A:H61	1.56	0.52
1:1:1599:A:H5'	48:Lr:15:ARG:HH22	1.74	0.52
1:1:2406:A:H2'	1:1:2407:C:C6	2.45	0.52
2:2:684:G:H2'	2:2:685:G:H8	1.75	0.52
2:2:788:U:H2'	2:2:789:A:H8	1.72	0.52
2:2:1575:C:H5''	70:SQ:140:LYS:HE3	1.91	0.52
3:3:98:G:H4'	14:LF:134:LYS:NZ	2.25	0.52
5:A:107:ASP:N	5:A:107:ASP:OD1	2.42	0.52
15:LG:225:TYR:O	15:LG:229:VAL:HG22	2.08	0.52
16:LH:43:VAL:HG21	16:LH:55:LEU:HD12	1.90	0.52
16:LH:149:SER:HB2	16:LH:189:ILE:HD11	1.90	0.52
23:LO:10:ILE:HD11	27:LS:165:PHE:HE1	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:Ld:82:ARG:HH12	38:Ld:117:VAL:HG11	1.73	0.52
54:SA:65:ARG:HH21	75:SV:38:LYS:HA	1.73	0.52
59:SF:132:ASP:OD1	59:SF:133:SER:N	2.41	0.52
1:1:2110:A:H5''	9:LA:198:LYS:O	2.10	0.52
2:2:67:A:O2'	2:2:69:G:OP1	2.25	0.52
2:2:560:U:H3	2:2:577:A:H62	1.58	0.52
5:A:212:LYS:HA	5:A:235:GLU:HG2	1.92	0.52
8:D:282:GLU:HG2	8:D:285:LYS:HE3	1.91	0.52
22:LN:118:SER:HB3	22:LN:132:VAL:HG22	1.90	0.52
52:Ls:51:VAL:HG12	52:Ls:87:VAL:HG22	1.90	0.52
55:SB:157:GLN:O	55:SB:161:ILE:HG12	2.08	0.52
56:SC:160:HIS:HB2	56:SC:202:GLU:OE2	2.09	0.52
83:Sd:21:CYS:HB2	83:Sd:30:LEU:HD11	1.90	0.52
1:1:2307:U:H2'	1:1:2308:A:H8	1.73	0.52
2:2:1144:A:H5'	56:SC:99:ARG:NH1	2.25	0.52
2:2:1545:C:OP1	69:SP:50:ARG:NH2	2.42	0.52
7:C:168:PHE:HA	7:C:171:VAL:HG12	1.91	0.52
7:C:393:LEU:O	7:C:397:LYS:HG2	2.09	0.52
18:LJ:83:ARG:HH21	18:LJ:113:LEU:HD12	1.74	0.52
33:LY:50:ARG:HG2	33:LY:51:LYS:H	1.74	0.52
83:Sd:10:ARG:HE	83:Sd:11:PRO:HD2	1.73	0.52
1:1:1193:U:OP1	16:LH:62:ARG:NH2	2.42	0.52
2:2:892:U:H2'	2:2:893:G:H8	1.75	0.52
2:2:911:G:C6	55:SB:13:LYS:HD3	2.45	0.52
4:4:83:C:H41	33:LY:50:ARG:NH2	2.08	0.52
5:A:88:ARG:HH12	5:A:97:THR:HA	1.75	0.52
11:LC:284:GLN:HE22	11:LC:286:ASP:HB3	1.75	0.52
23:LO:20:LEU:HD13	23:LO:122:VAL:HG11	1.91	0.52
24:LP:48:LEU:HD22	24:LP:92:ILE:HD11	1.92	0.52
25:LQ:47:PRO:HD3	25:LQ:81:PHE:HE1	1.74	0.52
34:LZ:75:ASN:OD1	34:LZ:76:TYR:N	2.43	0.52
71:SR:20:TYR:HD2	71:SR:23:ARG:HE	1.57	0.52
1:1:2409:U:H5'	43:Li:72:ASN:HD21	1.75	0.52
1:1:2632:A:OP1	18:LJ:96:ASN:ND2	2.43	0.52
2:2:673:U:H2'	2:2:674:G:C8	2.44	0.52
2:2:916:U:H2'	2:2:917:A:C8	2.45	0.52
4:4:13:A:C1'	24:LP:120:ASN:HD21	2.23	0.52
7:C:326:GLU:O	7:C:330:ARG:NE	2.41	0.52
11:LC:364:GLU:OE2	28:LT:150:THR:OG1	2.27	0.52
31:LW:87:LEU:HD12	31:LW:88:GLU:N	2.25	0.52
41:Lg:93:ALA:O	41:Lg:97:GLU:HG2	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:SD:150:ALA:C	57:SD:151:LYS:HD3	2.34	0.52
58:SE:251:ARG:NH1	58:SE:254:ARG:HH22	2.08	0.52
63:SJ:62:GLU:HG3	63:SJ:63:LYS:HG2	1.91	0.52
63:SJ:98:LYS:HD2	63:SJ:100:GLU:H	1.74	0.52
71:SR:71:PHE:CZ	71:SR:74:GLN:HB2	2.45	0.52
78:SY:24:LYS:O	78:SY:77:LEU:HD12	2.10	0.52
78:SY:29:ASP:OD1	78:SY:71:LYS:NZ	2.42	0.52
80:Sa:68:TYR:O	80:Sa:69:LEU:HD23	2.10	0.52
1:1:1333:A:H2'	1:1:1335:A:H5''	1.92	0.52
1:1:1782:C:OP1	48:Lr:2:ARG:NH2	2.43	0.52
1:1:2176:A:H2'	1:1:2177:A:C8	2.45	0.52
2:2:204:U:H2'	2:2:205:A:H8	1.74	0.52
20:LL:189:ARG:O	20:LL:193:ARG:HG3	2.09	0.52
68:SO:140:ARG:NH1	68:SO:141:ARG:O	2.42	0.52
1:1:1674:U:O3'	41:Lg:25:LYS:NZ	2.42	0.52
1:1:2159:C:O2'	1:1:2233:A:N3	2.37	0.52
1:1:2369:C:H2'	1:1:2370:C:C6	2.45	0.52
2:2:844:G:H2'	2:2:845:A:H8	1.75	0.52
2:2:1646:U:H2'	2:2:1647:A:C8	2.45	0.52
7:C:365:ARG:O	7:C:369:LYS:HG2	2.10	0.52
20:LL:106:GLU:OE2	43:Li:29:ARG:HD2	2.10	0.52
25:LQ:110:VAL:HG22	25:LQ:167:LEU:HB2	1.92	0.52
1:1:450:U:O4	1:1:468:G:N2	2.43	0.52
1:1:1091:C:H2'	1:1:1092:A:H8	1.75	0.52
1:1:1541:A:O2'	32:LX:47:ARG:HD3	2.10	0.52
2:2:210:A:O3'	65:SL:31:ARG:NH2	2.42	0.52
2:2:1157:A:H2'	2:2:1158:C:C6	2.45	0.52
8:D:244:ALA:HA	8:D:247:LYS:HE2	1.92	0.52
10:LB:149:LEU:O	10:LB:153:LYS:HG3	2.10	0.52
16:LH:23:ARG:HH11	16:LH:23:ARG:HG3	1.74	0.52
43:Li:70:LEU:HD21	43:Li:100:GLN:HG2	1.92	0.52
57:SD:31:GLU:OE1	64:SK:56:GLN:NE2	2.33	0.52
59:SF:200:LYS:O	59:SF:203:GLU:HG3	2.10	0.52
61:SH:17:GLN:OE1	61:SH:18:ASN:ND2	2.43	0.52
72:SS:73:ILE:HG22	72:SS:101:LEU:HD21	1.91	0.52
73:ST:89:ARG:HH11	73:ST:89:ARG:HG3	1.74	0.52
1:1:1476:G:N2	1:1:1476:G:OP2	2.36	0.52
1:1:2058:A:H2'	1:1:2059:A:C8	2.44	0.52
2:2:937:A:H2'	2:2:938:A:C8	2.45	0.52
2:2:1312:U:H1'	71:SR:4:VAL:HG21	1.91	0.52
2:2:1609:U:H2'	2:2:1610:A:N3	2.25	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:1695:G:N7	7:C:365:ARG:NH1	2.58	0.52
16:LH:131:ALA:O	16:LH:134:VAL:HG22	2.09	0.52
27:LS:80:ARG:HB3	27:LS:122:HIS:HB2	1.93	0.52
36:Lb:28:ARG:HG2	36:Lb:29:TYR:CD1	2.45	0.52
43:Li:99:LEU:HA	43:Li:102:ILE:HG22	1.91	0.52
55:SB:197:ILE:O	55:SB:201:THR:HG22	2.10	0.52
57:SD:75:LEU:HD11	64:SK:63:TYR:CD1	2.45	0.52
60:SG:64:LYS:HZ1	60:SG:81:HIS:HB3	1.75	0.52
63:SJ:56:ILE:O	63:SJ:59:THR:HG22	2.10	0.52
67:SN:120:SER:O	67:SN:124:ARG:HG3	2.10	0.52
71:SR:75:GLU:HA	71:SR:78:ARG:HH11	1.75	0.52
77:SX:36:THR:O	77:SX:40:SER:N	2.34	0.52
83:Sd:10:ARG:NE	83:Sd:11:PRO:HD2	2.25	0.52
1:1:1222:C:H4'	1:1:1222:C:OP1	2.10	0.51
2:2:19:A:P	77:SX:109:ARG:HH12	2.32	0.51
2:2:403:U:H2'	2:2:404:A:H8	1.76	0.51
2:2:1479:A:H2	2:2:1603:G:H1'	1.75	0.51
5:A:40:LEU:O	5:A:59:LEU:HB2	2.10	0.51
5:A:59:LEU:HB3	5:A:90:TRP:CH2	2.44	0.51
15:LG:67:ILE:O	15:LG:71:ARG:HG2	2.09	0.51
45:Lk:13:GLU:HA	45:Lk:16:ARG:HG2	1.93	0.51
58:SE:19:LEU:HB3	58:SE:51:ARG:HH22	1.74	0.51
58:SE:145:ARG:NH1	58:SE:145:ARG:HA	2.25	0.51
60:SG:192:HIS:CE1	60:SG:196:LEU:HD21	2.45	0.51
65:SL:79:ARG:HB2	65:SL:92:ARG:HG3	1.92	0.51
1:1:250:C:O2'	1:1:251:U:OP1	2.26	0.51
1:1:478:G:H2'	1:1:479:G:H8	1.75	0.51
1:1:1267:C:H2'	1:1:1268:G:C4	2.46	0.51
1:1:2900:A:OP2	10:LB:256:TRP:HB3	2.09	0.51
2:2:483:G:H22	2:2:498:U:H3	1.58	0.51
2:2:697:G:H2'	2:2:698:G:H8	1.75	0.51
2:2:856:G:OP2	2:2:856:G:N2	2.32	0.51
8:D:13:ARG:NH2	8:D:402:GLN:O	2.42	0.51
22:LN:139:HIS:O	22:LN:142:ILE:HG22	2.11	0.51
59:SF:43:ILE:HG13	59:SF:44:SER:H	1.75	0.51
64:SK:71:LEU:HD12	64:SK:74:LEU:HD11	1.92	0.51
72:SS:91:ASP:OD1	72:SS:92:ILE:N	2.44	0.51
74:SU:42:ALA:O	74:SU:45:LYS:HG2	2.11	0.51
76:SW:85:GLU:HB2	76:SW:88:LYS:HG2	1.93	0.51
1:1:306:U:H2'	1:1:307:U:C6	2.45	0.51
2:2:1428:U:H4'	2:2:1429:G:H5''	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:1677:A:O2'	60:SG:31:ARG:NH1	2.43	0.51
4:4:65:A:OP1	42:Lh:58:ARG:NH1	2.40	0.51
16:LH:103:VAL:HG23	16:LH:114:VAL:HG22	1.92	0.51
30:LV:111:MET:HG2	30:LV:113:GLY:H	1.75	0.51
32:LX:116:TYR:O	32:LX:118:ILE:HG23	2.09	0.51
35:La:34:MET:HA	35:La:34:MET:HE3	1.92	0.51
35:La:112:LEU:HD22	35:La:125:VAL:HG11	1.92	0.51
41:Lg:72:THR:HG22	41:Lg:73:VAL:H	1.74	0.51
54:SA:80:SER:HB3	54:SA:89:VAL:HG21	1.93	0.51
55:SB:34:ALA:HB3	55:SB:41:ARG:HA	1.92	0.51
56:SC:40:GLU:OE1	56:SC:41:LYS:HG2	2.10	0.51
59:SF:96:MET:O	59:SF:100:ILE:HG12	2.10	0.51
63:SJ:121:HIS:CD2	84:Se:37:ARG:HH21	2.29	0.51
1:1:1262:C:H2'	1:1:1263:C:C6	2.45	0.51
1:1:3254:U:O5'	10:LB:174:GLN:NE2	2.43	0.51
2:2:257:U:H3'	2:2:258:C:H5'	1.92	0.51
2:2:1094:U:O2'	56:SC:176:ARG:NH2	2.43	0.51
8:D:422:HIS:CD2	8:D:449:ALA:HB2	2.44	0.51
12:LD:99:TYR:HE2	12:LD:167:LYS:HG3	1.75	0.51
21:LM:19:VAL:O	21:LM:65:THR:OG1	2.28	0.51
27:LS:81:TYR:CZ	27:LS:90:MET:HE3	2.44	0.51
41:Lg:104:LYS:O	41:Lg:107:LYS:HG3	2.11	0.51
49:Lo:10:THR:HG22	49:Lo:11:PHE:N	2.24	0.51
52:Ls:16:LYS:HZ2	52:Ls:63:LEU:HD11	1.76	0.51
56:SC:196:LEU:HD12	56:SC:201:ILE:HG21	1.92	0.51
57:SD:101:ALA:HB2	57:SD:191:ILE:HG22	1.91	0.51
58:SE:160:VAL:HG21	58:SE:169:ILE:HD12	1.92	0.51
66:SM:135:VAL:HA	66:SM:138:ASN:ND2	2.25	0.51
1:1:624:C:O2	1:1:2340:G:O2'	2.24	0.51
1:1:993:G:OP1	17:LI:40:ARG:NH1	2.41	0.51
1:1:1410:U:H5	35:La:4:ARG:HE	1.57	0.51
1:1:2268:G:OP2	1:1:2268:G:N2	2.37	0.51
2:2:487:U:H3	2:2:494:G:H1	1.58	0.51
2:2:751:A:H2	2:2:795:G:H22	1.58	0.51
2:2:1385:A:H5'	71:SR:48:ASN:HD21	1.75	0.51
2:2:1479:A:C2	2:2:1603:G:H1'	2.45	0.51
16:LH:97:PHE:CD2	16:LH:121:GLY:HA3	2.46	0.51
26:LR:90:PRO:HG2	26:LR:93:VAL:HG12	1.92	0.51
26:LR:105:LEU:HD22	26:LR:135:LYS:HD2	1.93	0.51
37:Lc:43:LYS:NZ	37:Lc:97:ASP:HA	2.25	0.51
43:Li:14:THR:O	43:Li:25:LYS:NZ	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:Lq:133:LEU:HD23	51:Lq:136:ALA:HB3	1.92	0.51
54:SA:64:ALA:O	54:SA:68:VAL:HG23	2.11	0.51
57:SD:139:VAL:HG22	57:SD:155:PHE:HB2	1.92	0.51
68:SO:21:ARG:NH1	68:SO:24:GLU:OE1	2.44	0.51
80:Sa:4:LYS:HE2	80:Sa:5:ARG:HH12	1.76	0.51
1:1:962:U:H2'	1:1:963:U:C6	2.46	0.51
1:1:993:G:H2'	1:1:994:G:C8	2.46	0.51
1:1:1016:U:H2'	1:1:1017:U:C6	2.46	0.51
1:1:2176:A:H2'	1:1:2177:A:H8	1.75	0.51
2:2:638:G:H1'	61:SH:189:ARG:NH1	2.25	0.51
3:3:108:C:H2'	3:3:109:G:H8	1.75	0.51
10:LB:161:VAL:HB	10:LB:184:ILE:HD11	1.91	0.51
14:LF:131:GLU:O	14:LF:135:ILE:HG12	2.11	0.51
22:LN:124:ASP:OD1	22:LN:125:SER:N	2.37	0.51
29:LU:25:ALA:C	29:LU:28:PRO:HD2	2.36	0.51
29:LU:94:MET:HA	29:LU:94:MET:HE3	1.93	0.51
42:Lh:68:ARG:HD2	42:Lh:85:LEU:HD21	1.93	0.51
55:SB:13:LYS:H	55:SB:13:LYS:HD2	1.76	0.51
55:SB:185:VAL:O	55:SB:189:ILE:HD12	2.10	0.51
57:SD:144:LYS:HZ3	57:SD:182:GLN:HG3	1.76	0.51
71:SR:18:GLU:O	71:SR:72:LYS:NZ	2.39	0.51
72:SS:48:LYS:HG2	73:ST:36:ASP:OD1	2.10	0.51
1:1:2167:C:H2'	1:1:2168:U:C6	2.46	0.51
1:1:2227:U:H2'	1:1:2228:C:C6	2.46	0.51
1:1:2518:G:OP1	9:LA:69:TYR:OH	2.17	0.51
2:2:1355:G:H5'	73:ST:127:GLN:HE22	1.76	0.51
2:2:1453:C:H4'	72:SS:137:HIS:CD2	2.46	0.51
2:2:1529:C:OP2	79:SZ:66:ARG:NH2	2.32	0.51
5:A:294:ASP:O	5:A:296:GLN:NE2	2.44	0.51
11:LC:8:THR:HA	11:LC:20:THR:HG22	1.93	0.51
12:LD:286:GLU:O	12:LD:290:ARG:HG3	2.11	0.51
15:LG:27:ASN:OD1	15:LG:29:LEU:HD23	2.11	0.51
15:LG:153:LEU:HB3	15:LG:203:ILE:HG22	1.92	0.51
18:LJ:85:LEU:HD12	18:LJ:168:PHE:CD2	2.45	0.51
24:LP:36:ILE:HG13	24:LP:36:ILE:O	2.10	0.51
27:LS:81:TYR:CZ	27:LS:88:HIS:HB2	2.46	0.51
36:Lb:43:HIS:ND1	36:Lb:47:LEU:HD23	2.26	0.51
42:Lh:107:GLU:HA	42:Lh:110:LYS:HG2	1.93	0.51
49:Lo:103:ALA:O	49:Lo:104:LEU:HD22	2.11	0.51
52:Ls:106:LYS:HE2	52:Ls:179:SER:HB2	1.93	0.51
71:SR:36:ASP:CG	71:SR:47:ARG:NE	2.65	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
72:SS:111:GLU:HA	72:SS:114:GLU:OE2	2.11	0.51
73:ST:136:ILE:O	73:ST:140:VAL:HG12	2.11	0.51
79:SZ:43:VAL:HA	79:SZ:46:TYR:HD2	1.76	0.51
81:Sb:56:CYS:HB3	81:Sb:63:LEU:HD11	1.92	0.51
1:1:643:C:H2'	1:1:644:A:C8	2.46	0.51
1:1:1409:C:H3'	35:La:4:ARG:HH21	1.76	0.51
2:2:825:C:H2'	2:2:826:U:C6	2.46	0.51
2:2:1149:A:H5''	80:Sa:82:LYS:HE2	1.92	0.51
5:A:36:ARG:O	5:A:36:ARG:HD3	2.10	0.51
12:LD:228:LYS:O	12:LD:231:GLU:HG3	2.11	0.51
31:LW:111:GLU:HA	31:LW:114:GLU:CD	2.35	0.51
34:LZ:45:ILE:HG23	34:LZ:67:ILE:HG23	1.92	0.51
54:SA:39:TYR:HD1	54:SA:55:LYS:CD	2.24	0.51
57:SD:188:LYS:HB3	57:SD:190:LYS:NZ	2.26	0.51
58:SE:65:MET:HG3	58:SE:68:ARG:NH2	2.26	0.51
67:SN:36:GLN:HA	67:SN:39:LYS:NZ	2.25	0.51
71:SR:77:GLU:HB2	71:SR:81:LYS:HE3	1.93	0.51
1:1:3209:A:OP1	13:LE:64:ARG:NH2	2.42	0.51
2:2:118:A:H1'	2:2:394:A:C6	2.46	0.51
5:A:104:HIS:NE2	5:A:122:SER:OG	2.36	0.51
7:C:249:ASP:OD2	8:D:259:LYS:CG	2.54	0.51
17:LI:19:LYS:HD2	17:LI:26:VAL:HG11	1.93	0.51
20:LL:178:GLU:HG2	20:LL:179:GLY:N	2.26	0.51
24:LP:4:TYR:CZ	24:LP:16:ARG:HD3	2.46	0.51
28:LT:93:ILE:HA	28:LT:96:VAL:HG12	1.93	0.51
43:Li:60:ALA:HB3	43:Li:63:GLU:HG3	1.93	0.51
55:SB:144:LYS:HB3	55:SB:206:PRO:HB2	1.93	0.51
57:SD:109:ARG:O	57:SD:113:LEU:HD23	2.11	0.51
64:SK:13:GLU:HB2	64:SK:17:ARG:HH12	1.76	0.51
66:SM:52:LYS:HD3	85:Sf:129:GLY:HA3	1.93	0.51
71:SR:23:ARG:HH12	71:SR:34:VAL:HG21	1.76	0.51
72:SS:68:ARG:NH1	72:SS:72:ILE:HD11	2.26	0.51
76:SW:89:TRP:O	76:SW:93:LEU:HD23	2.11	0.51
1:1:117:A:OP2	22:LN:2:GLY:N	2.44	0.51
1:1:2320:A:H2'	1:1:2321:A:H8	1.76	0.51
1:1:2465:U:H2'	1:1:2466:G:C8	2.46	0.51
2:2:352:G:H2'	2:2:353:G:C8	2.43	0.51
2:2:865:G:H1	2:2:959:U:H3	1.59	0.51
2:2:1224:A:H1'	2:2:1226:G:C4	2.46	0.51
2:2:1498:G:O6	73:ST:102:ARG:NH1	2.43	0.51
2:2:1781:U:H2'	2:2:1782:G:H8	1.76	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A:109:LEU:HD23	5:A:152:SER:O	2.11	0.51
7:C:278:LEU:O	7:C:282:VAL:HG23	2.10	0.51
7:C:317:ALA:HA	7:C:320:GLU:HG2	1.93	0.51
24:LP:50:ASN:HB3	24:LP:56:GLU:OE1	2.11	0.51
57:SD:138:GLU:OE2	57:SD:190:LYS:HB2	2.10	0.51
57:SD:165:GLN:HB2	57:SD:168:ARG:NH2	2.23	0.51
58:SE:139:LEU:HD23	58:SE:147:ILE:O	2.11	0.51
66:SM:135:VAL:HA	66:SM:138:ASN:HD21	1.76	0.51
1:1:3293:U:O2	62:SI:168:ARG:NH2	2.43	0.50
2:2:1075:C:H2'	2:2:1076:U:C6	2.46	0.50
7:C:279:ARG:O	7:C:283:GLU:HG2	2.11	0.50
44:Lj:51:GLU:CD	44:Lj:55:ARG:HH21	2.19	0.50
55:SB:86:LEU:HB3	55:SB:98:THR:HG21	1.93	0.50
62:SI:42:ARG:O	62:SI:43:ILE:HD13	2.11	0.50
77:SX:127:VAL:HG13	77:SX:132:LEU:HD21	1.93	0.50
78:SY:59:SER:OG	78:SY:77:LEU:HB3	2.11	0.50
1:1:617:C:H2'	1:1:618:C:C6	2.47	0.50
1:1:1907:G:C8	50:Lp:16:THR:HG22	2.46	0.50
1:1:2064:C:H2'	1:1:2065:U:C6	2.46	0.50
8:D:35:ALA:HB2	8:D:396:LEU:HG	1.93	0.50
8:D:282:GLU:O	8:D:285:LYS:HG3	2.11	0.50
14:LF:29:ARG:NH1	14:LF:29:ARG:HB2	2.26	0.50
22:LN:84:PRO:HA	22:LN:87:GLN:NE2	2.27	0.50
26:LR:81:ARG:HE	26:LR:88:ARG:NH1	2.09	0.50
27:LS:80:ARG:HH21	28:LT:155:ALA:C	2.19	0.50
27:LS:82:ASP:HB2	27:LS:120:SER:HB2	1.93	0.50
29:LU:25:ALA:O	29:LU:28:PRO:HD2	2.12	0.50
52:Ls:16:LYS:NZ	52:Ls:63:LEU:HD11	2.26	0.50
54:SA:201:MET:HE1	71:SR:85:VAL:HG13	1.93	0.50
58:SE:94:LYS:HZ1	78:SY:20:LEU:HG	1.75	0.50
68:SO:73:ALA:HB1	68:SO:114:ALA:HB2	1.93	0.50
69:SP:113:VAL:HG21	69:SP:127:PHE:CD2	2.45	0.50
74:SU:45:LYS:NZ	74:SU:100:ILE:HD13	2.26	0.50
74:SU:81:MET:HE3	83:Sd:52:PHE:HD1	1.76	0.50
75:SV:58:PHE:O	75:SV:62:MET:HG3	2.12	0.50
76:SW:102:VAL:O	76:SW:113:HIS:N	2.43	0.50
1:1:265:G:H1'	43:Li:91:ARG:HH12	1.77	0.50
1:1:696:G:N2	1:1:699:A:OP2	2.38	0.50
1:1:3185:G:O6	10:LB:151:ARG:NH1	2.44	0.50
2:2:913:A:H61	68:SO:54:ARG:HH12	1.58	0.50
2:2:1233:A:H2'	2:2:1234:G:C8	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A:193:GLY:N	5:A:213:ASP:OD1	2.43	0.50
7:C:262:LYS:HA	7:C:265:ASN:OD1	2.11	0.50
8:D:284:THR:HG21	8:D:296:PHE:HD2	1.76	0.50
57:SD:75:LEU:HD22	64:SK:20:VAL:HG11	1.93	0.50
60:SG:165:LYS:HG3	60:SG:166:GLY:H	1.76	0.50
61:SH:34:GLU:O	61:SH:41:LYS:HD2	2.11	0.50
63:SJ:101:ASP:O	63:SJ:104:GLU:HG2	2.11	0.50
67:SN:87:ASP:OD1	67:SN:88:LEU:N	2.44	0.50
70:SQ:50:GLU:HA	70:SQ:53:LEU:HG	1.92	0.50
1:1:477:C:H2'	1:1:478:G:C8	2.46	0.50
6:B:141:ILE:HD11	56:SC:89:MET:CE	2.41	0.50
7:C:442:LYS:HG3	7:C:443:ALA:H	1.76	0.50
8:D:112:ILE:HD11	8:D:125:LEU:HD12	1.93	0.50
12:LD:246:ALA:O	12:LD:250:ILE:HG12	2.12	0.50
54:SA:44:ARG:NH2	71:SR:127:VAL:O	2.45	0.50
58:SE:128:ARG:CZ	58:SE:130:GLN:HB3	2.41	0.50
60:SG:22:ARG:HA	60:SG:25:ARG:HG2	1.93	0.50
61:SH:76:PHE:O	61:SH:80:GLN:HG2	2.10	0.50
69:SP:42:ARG:HD2	69:SP:53:ILE:HB	1.93	0.50
71:SR:5:ARG:HE	71:SR:10:LYS:HD3	1.76	0.50
78:SY:5:ASP:OD1	78:SY:6:SER:N	2.42	0.50
1:1:1148:G:OP1	40:Lf:86:LYS:NZ	2.45	0.50
1:1:1447:G:N2	1:1:1450:A:OP2	2.42	0.50
1:1:2245:U:OP1	1:1:2932:G:O2'	2.24	0.50
1:1:3027:G:C2	1:1:3028:A:C8	2.99	0.50
1:1:3141:G:C8	21:LM:9:THR:HG22	2.46	0.50
2:2:381:G:H2'	2:2:382:A:C8	2.47	0.50
10:LB:19:ARG:O	10:LB:20:LYS:HE2	2.12	0.50
11:LC:300:LEU:HD21	25:LQ:67:ARG:NH2	2.25	0.50
20:LL:64:LYS:HD2	35:La:69:TRP:CD1	2.47	0.50
24:LP:47:PHE:O	24:LP:51:VAL:HG23	2.12	0.50
25:LQ:51:ASN:HB3	25:LQ:54:LEU:HB3	1.93	0.50
25:LQ:92:LEU:HD12	25:LQ:116:ASP:HA	1.94	0.50
42:Lh:34:LEU:HG	42:Lh:37:GLN:HE21	1.75	0.50
56:SC:103:ARG:HH11	56:SC:103:ARG:HG2	1.76	0.50
56:SC:133:ILE:O	56:SC:137:ILE:HG13	2.12	0.50
66:SM:33:VAL:HG13	66:SM:133:ARG:NH2	2.27	0.50
67:SN:73:ARG:HG2	67:SN:73:ARG:HH11	1.77	0.50
72:SS:92:ILE:HG13	72:SS:93:VAL:H	1.77	0.50
79:SZ:35:THR:HA	79:SZ:38:LYS:HZ2	1.76	0.50
1:1:2533:G:P	34:LZ:55:ARG:HH21	2.34	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:708:U:H2'	2:2:709:G:C8	2.47	0.50
4:4:9:A:H2'	4:4:10:A:C8	2.46	0.50
7:C:117:THR:OG1	7:C:119:ASP:OD1	2.26	0.50
20:LL:47:ALA:HB3	20:LL:48:PRO:HD3	1.94	0.50
24:LP:47:PHE:CE1	24:LP:56:GLU:HG3	2.47	0.50
24:LP:99:GLU:OE2	24:LP:109:THR:OG1	2.21	0.50
29:LU:59:VAL:HA	29:LU:75:HIS:HD2	1.76	0.50
34:LZ:80:MET:HE3	41:Lg:91:ILE:HD12	1.94	0.50
54:SA:16:ASP:O	54:SA:20:LEU:HD23	2.12	0.50
74:SU:26:ARG:NH2	74:SU:81:MET:HB3	2.27	0.50
78:SY:8:VAL:HG12	78:SY:32:HIS:HA	1.94	0.50
84:Se:43:ARG:C	84:Se:44:PHE:HD1	2.20	0.50
1:1:3007:A:C6	10:LB:75:ALA:HB2	2.47	0.50
2:2:66:U:H6	60:SG:136:LYS:HZ2	1.60	0.50
2:2:626:U:OP2	2:2:967:C:N4	2.45	0.50
2:2:1054:U:H2'	2:2:1055:A:C8	2.47	0.50
3:3:86:C:OP1	14:LF:223:ARG:NH1	2.45	0.50
5:A:59:LEU:HD23	5:A:90:TRP:CE3	2.46	0.50
12:LD:113:LEU:O	12:LD:113:LEU:HD23	2.11	0.50
30:LV:88:LYS:HD2	30:LV:94:PHE:CZ	2.47	0.50
35:La:73:ILE:HB	35:La:109:TYR:CD2	2.46	0.50
38:Ld:4:THR:O	38:Ld:7:LYS:HG2	2.12	0.50
57:SD:175:THR:O	57:SD:176:ARG:NH1	2.39	0.50
65:SL:39:TRP:CZ2	65:SL:41:LYS:HE2	2.46	0.50
69:SP:37:ASP:OD1	69:SP:40:GLU:HG3	2.11	0.50
69:SP:38:SER:HA	69:SP:41:LEU:HG	1.94	0.50
69:SP:62:LEU:HA	69:SP:65:ILE:HG22	1.94	0.50
72:SS:42:TYR:HD1	72:SS:85:PHE:HE2	1.60	0.50
77:SX:19:ARG:O	77:SX:23:ARG:HG3	2.11	0.50
80:Sa:43:ASN:OD1	80:Sa:66:LYS:NZ	2.44	0.50
1:1:425:G:H2'	1:1:426:A:C8	2.46	0.50
1:1:1338:A:H4'	1:1:1339:U:O5'	2.12	0.50
1:1:2703:U:H2'	1:1:2704:G:C8	2.47	0.50
1:1:2906:G:C2	10:LB:251:ALA:HB1	2.47	0.50
1:1:2964:A:H62	1:1:3098:G:H21	1.58	0.50
2:2:724:U:H5''	2:2:725:G:C8	2.46	0.50
7:C:300:ASN:O	7:C:303:LYS:HG2	2.12	0.50
15:LG:142:VAL:O	15:LG:146:ILE:HG13	2.11	0.50
31:LW:89:VAL:HA	31:LW:92:GLU:OE2	2.12	0.50
47:Lm:104:PRO:HD3	47:Lm:111:ARG:HH21	1.76	0.50
55:SB:113:LEU:HB3	55:SB:142:PHE:CE2	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:SF:37:ASP:O	59:SF:118:GLN:NE2	2.45	0.50
60:SG:3:LEU:HD13	60:SG:109:LEU:HB2	1.93	0.50
64:SK:73:TYR:O	64:SK:76:GLU:HG3	2.11	0.50
66:SM:36:LEU:HA	66:SM:39:MET:CG	2.42	0.50
1:1:615:C:H2'	1:1:616:A:C8	2.46	0.50
1:1:2181:G:H2'	1:1:2182:A:H8	1.77	0.50
2:2:176:A:H2'	2:2:177:A:H8	1.77	0.50
2:2:1315:G:H2'	2:2:1316:A:C8	2.47	0.50
8:D:84:GLY:HA3	8:D:165:GLN:HA	1.94	0.50
26:LR:24:LEU:HD23	26:LR:32:ILE:HG21	1.93	0.50
27:LS:8:GLN:HG2	27:LS:62:ASN:HB2	1.94	0.50
30:LV:77:PRO:HG2	30:LV:107:PRO:HD3	1.94	0.50
40:Lf:29:THR:HG22	40:Lf:86:LYS:HD3	1.94	0.50
52:Ls:60:ARG:O	52:Ls:63:LEU:HG	2.11	0.50
78:SY:18:ASN:ND2	78:SY:21:LEU:HB3	2.26	0.50
1:1:72:A:P	35:La:67:HIS:HE2	2.35	0.49
2:2:681:C:H2'	2:2:682:U:C6	2.47	0.49
2:2:1332:U:H2'	2:2:1333:A:C8	2.47	0.49
5:A:28:PRO:O	5:A:47:ARG:NH2	2.45	0.49
7:C:206:LYS:HG3	7:C:234:ASP:O	2.12	0.49
10:LB:10:ARG:NH1	10:LB:11:HIS:O	2.45	0.49
16:LH:122:GLU:HG3	16:LH:124:ILE:H	1.76	0.49
28:LT:83:ARG:HD2	28:LT:85:ILE:HD11	1.93	0.49
31:LW:47:ARG:HH12	31:LW:58:GLN:HG3	1.77	0.49
31:LW:81:ALA:HB1	31:LW:90:ILE:HD13	1.94	0.49
42:Lh:6:LYS:HE2	42:Lh:51:ASP:OD1	2.12	0.49
58:SE:145:ARG:HA	58:SE:145:ARG:HH11	1.76	0.49
68:SO:131:VAL:HG12	68:SO:131:VAL:O	2.12	0.49
73:ST:102:ARG:CZ	73:ST:103:LYS:HZ1	2.24	0.49
84:Se:7:SER:HB3	84:Se:10:ARG:HH22	1.76	0.49
1:1:67:A:N3	22:LN:176:LYS:NZ	2.55	0.49
1:1:604:G:H2'	1:1:605:G:C8	2.47	0.49
1:1:615:C:H2'	1:1:616:A:H8	1.77	0.49
1:1:1215:C:H2'	1:1:1216:G:C8	2.47	0.49
1:1:1607:U:H2'	1:1:1794:A:H62	1.77	0.49
1:1:2662:A:OP2	12:LD:23:ARG:NH2	2.35	0.49
1:1:3251:A:OP1	24:LP:74:LYS:NZ	2.37	0.49
2:2:1455:C:H5'	72:SS:131:LEU:HD21	1.93	0.49
2:2:1579:A:O2'	59:SF:63:ARG:NH2	2.45	0.49
8:D:347:GLU:OE2	8:D:375:LEU:HG	2.11	0.49
10:LB:117:ARG:CZ	10:LB:176:LYS:HE2	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:SE:99:PHE:HE1	58:SE:113:ARG:HD3	1.78	0.49
59:SF:89:ARG:O	59:SF:93:LYS:NZ	2.45	0.49
72:SS:15:LEU:HB2	72:SS:22:VAL:HG22	1.93	0.49
73:ST:64:HIS:O	73:ST:68:ARG:HG3	2.12	0.49
77:SX:37:ALA:HA	77:SX:41:SER:HB3	1.94	0.49
1:1:1599:A:H5'	48:Lr:15:ARG:NH2	2.27	0.49
1:1:1813:G:O2'	46:Ll:3:SER:O	2.30	0.49
1:1:2227:U:H2'	1:1:2228:C:H6	1.75	0.49
2:2:414:A:H4'	2:2:415:G:O5'	2.11	0.49
2:2:634:C:OP2	76:SW:32:LYS:NZ	2.45	0.49
2:2:1519:U:O4	73:ST:68:ARG:NH1	2.45	0.49
5:A:88:ARG:NH2	5:A:97:THR:HA	2.27	0.49
8:D:389:LEU:HD23	8:D:392:ARG:HH22	1.76	0.49
8:D:415:ALA:HA	8:D:418:THR:HG22	1.94	0.49
11:LC:54:SER:HB3	11:LC:57:ALA:HB2	1.94	0.49
11:LC:123:THR:O	11:LC:127:LEU:HD23	2.13	0.49
15:LG:164:GLU:OE1	15:LG:164:GLU:N	2.46	0.49
23:LO:98:ALA:O	23:LO:102:GLU:HG2	2.13	0.49
30:LV:30:ASN:HD21	30:LV:114:SER:HG	1.54	0.49
32:LX:82:THR:H	32:LX:85:ALA:HB3	1.78	0.49
35:La:72:SER:HB2	35:La:113:LEU:HD13	1.94	0.49
55:SB:9:LEU:HD13	55:SB:12:GLY:HA2	1.94	0.49
59:SF:105:PHE:HA	59:SF:108:ILE:HG12	1.94	0.49
1:1:328:G:OP2	33:LY:13:LYS:NZ	2.31	0.49
1:1:481:C:H2'	1:1:482:U:C6	2.47	0.49
1:1:656:U:H2'	1:1:657:U:C6	2.47	0.49
1:1:2611:U:O3'	49:Lo:89:LYS:NZ	2.45	0.49
1:1:3231:G:H2'	1:1:3232:A:C8	2.47	0.49
2:2:788:U:H2'	2:2:789:A:C8	2.46	0.49
2:2:1203:U:OP2	2:2:1204:C:O2'	2.24	0.49
8:D:109:VAL:HG12	8:D:126:THR:HA	1.94	0.49
11:LC:303:PRO:HA	25:LQ:67:ARG:NH1	2.28	0.49
12:LD:53:VAL:HG11	12:LD:165:VAL:HG11	1.93	0.49
13:LE:119:ILE:HA	13:LE:122:VAL:HG12	1.92	0.49
16:LH:91:ARG:NH1	16:LH:145:GLU:OE1	2.45	0.49
17:LI:78:LYS:HG2	17:LI:79:TYR:CD1	2.47	0.49
59:SF:208:ALA:O	59:SF:212:ARG:HG3	2.13	0.49
72:SS:11:PHE:CE1	72:SS:59:GLY:HA3	2.46	0.49
76:SW:41:MET:HE1	76:SW:129:PHE:CD1	2.48	0.49
1:1:20:U:H4'	22:LN:138:ASN:HD21	1.77	0.49
1:1:1906:C:OP2	50:Lp:7:LYS:NZ	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2396:U:H1'	22:LN:125:SER:HB3	1.94	0.49
1:1:2840:C:H2'	1:1:2841:U:C6	2.48	0.49
2:2:213:A:H3'	2:2:214:A:H5''	1.95	0.49
2:2:219:C:H2'	2:2:220:A:H8	1.77	0.49
2:2:634:C:OP1	76:SW:32:LYS:HG3	2.12	0.49
2:2:1143:G:H4'	56:SC:99:ARG:HH22	1.78	0.49
2:2:1161:G:H2'	2:2:1162:G:H8	1.77	0.49
2:2:1224:A:H4'	2:2:1225:G:H5'	1.94	0.49
7:C:34:SER:HA	8:D:424:THR:H	1.77	0.49
10:LB:24:ARG:HH12	10:LB:26:ARG:NH2	2.10	0.49
18:LJ:158:GLU:O	18:LJ:162:ARG:HG3	2.13	0.49
20:LL:76:THR:N	20:LL:79:GLU:OE2	2.45	0.49
23:LO:143:LEU:O	23:LO:147:VAL:HG23	2.12	0.49
24:LP:171:LEU:HD13	24:LP:175:GLN:HE21	1.78	0.49
28:LT:17:ARG:NH2	28:LT:21:LYS:O	2.46	0.49
28:LT:79:ARG:HG2	28:LT:79:ARG:HH11	1.76	0.49
42:Lh:23:ILE:O	42:Lh:27:LEU:HD23	2.13	0.49
58:SE:31:PRO:HA	58:SE:81:THR:HB	1.95	0.49
64:SK:11:ILE:O	64:SK:15:LEU:HG	2.13	0.49
69:SP:121:GLY:O	69:SP:122:HIS:ND1	2.43	0.49
71:SR:44:LYS:O	71:SR:47:ARG:HB3	2.12	0.49
75:SV:4:ASP:OD1	75:SV:4:ASP:N	2.45	0.49
1:1:96:A:H5''	35:La:34:MET:HB2	1.95	0.49
1:1:2468:U:H2'	1:1:2469:U:C6	2.47	0.49
1:1:3202:U:OP1	21:LM:122:ARG:NH2	2.43	0.49
2:2:921:A:H2'	2:2:922:A:H8	1.76	0.49
2:2:1684:C:H2'	2:2:1685:A:C8	2.47	0.49
7:C:344:GLU:O	7:C:348:LYS:HG2	2.12	0.49
11:LC:280:ASN:OD1	11:LC:281:ILE:N	2.46	0.49
31:LW:80:ARG:HG2	31:LW:81:ALA:H	1.78	0.49
39:Le:61:ASN:OD1	39:Le:62:LYS:N	2.45	0.49
56:SC:121:LEU:HD22	56:SC:223:PHE:CD2	2.48	0.49
57:SD:54:ARG:HH22	57:SD:93:LYS:C	2.21	0.49
59:SF:67:LYS:HB3	59:SF:70:ARG:HG2	1.95	0.49
68:SO:100:GLY:HA3	68:SO:133:PRO:HG2	1.94	0.49
72:SS:38:VAL:HG23	72:SS:42:TYR:HD2	1.77	0.49
74:SU:35:CYS:O	74:SU:39:ILE:HG12	2.12	0.49
1:1:1464:A:O2'	1:1:1838:A:H1'	2.11	0.49
2:2:634:C:O2	61:SH:124:ARG:NH1	2.45	0.49
2:2:1554:U:H4'	72:SS:135:GLY:H	1.78	0.49
15:LG:183:ILE:HG21	15:LG:189:LEU:HD21	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:LJ:54:THR:OG1	18:LJ:62:ARG:HG2	2.13	0.49
18:LJ:167:ARG:HG2	18:LJ:168:PHE:HD1	1.77	0.49
21:LM:104:LEU:HA	21:LM:107:GLU:HG2	1.94	0.49
28:LT:115:LEU:HA	28:LT:118:LYS:HG2	1.94	0.49
54:SA:147:ILE:HG23	54:SA:161:VAL:HB	1.95	0.49
63:SJ:104:GLU:O	63:SJ:109:THR:OG1	2.29	0.49
67:SN:89:TYR:CE1	67:SN:150:VAL:HA	2.48	0.49
72:SS:90:ARG:HA	72:SS:95:GLY:HA3	1.95	0.49
73:ST:29:LEU:HD22	73:ST:54:TRP:HH2	1.77	0.49
1:1:1006:A:H2'	1:1:1008:U:H5''	1.94	0.49
1:1:2247:C:N4	1:1:2271:C:O4'	2.45	0.49
1:1:2332:G:H2'	1:1:2333:G:C8	2.48	0.49
1:1:2574:G:H2'	1:1:2575:C:H6	1.78	0.49
1:1:2974:A:H2'	1:1:2975:G:C8	2.48	0.49
1:1:3316:A:C2	1:1:3319:C:H5''	2.48	0.49
2:2:1332:U:H2'	2:2:1333:A:H8	1.77	0.49
2:2:1374:U:O2'	2:2:1377:U:O4	2.31	0.49
18:LJ:167:ARG:HG2	18:LJ:168:PHE:CD1	2.46	0.49
20:LL:196:GLY:O	20:LL:199:GLU:HG3	2.12	0.49
23:LO:3:SER:OG	23:LO:5:GLU:OE2	2.26	0.49
37:Lc:43:LYS:NZ	37:Lc:96:LEU:O	2.44	0.49
38:Ld:51:ALA:O	38:Ld:52:MET:HE2	2.13	0.49
56:SC:129:VAL:O	56:SC:133:ILE:HG12	2.13	0.49
57:SD:223:VAL:HG22	57:SD:225:PRO:HD2	1.94	0.49
58:SE:174:LYS:HD3	58:SE:175:PHE:H	1.77	0.49
60:SG:63:MET:HG3	60:SG:99:GLY:O	2.13	0.49
79:SZ:81:VAL:HG23	79:SZ:82:VAL:H	1.78	0.49
1:1:1577:C:OP1	41:Lg:32:ARG:NH1	2.45	0.49
1:1:1879:G:O2'	1:1:2297:U:O4	2.24	0.49
1:1:2669:C:H2'	1:1:2670:C:C6	2.48	0.49
1:1:3009:U:H2'	1:1:3010:G:H8	1.78	0.49
2:2:77:A:H2'	2:2:78:C:C6	2.48	0.49
2:2:222:U:O2'	2:2:223:G:P	2.70	0.49
2:2:916:U:H2'	2:2:917:A:H8	1.77	0.49
8:D:85:GLN:NE2	8:D:89:SER:O	2.46	0.49
12:LD:197:VAL:HA	12:LD:200:LYS:HG2	1.94	0.49
24:LP:88:ALA:O	24:LP:92:ILE:HG12	2.13	0.49
24:LP:154:GLU:HG2	24:LP:155:GLU:H	1.77	0.49
37:Lc:53:PRO:HA	37:Lc:56:LYS:HG3	1.95	0.49
51:Lq:64:ILE:HG22	51:Lq:80:THR:HG22	1.95	0.49
55:SB:157:GLN:O	55:SB:160:GLN:HG2	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:SD:43:ARG:HH22	74:SU:104:ILE:HG23	1.78	0.49
60:SG:139:THR:O	60:SG:143:ARG:HD3	2.13	0.49
61:SH:13:SER:HB2	61:SH:50:VAL:HG23	1.95	0.49
61:SH:68:VAL:HB	61:SH:99:LEU:O	2.13	0.49
64:SK:48:GLN:CD	64:SK:53:VAL:HG13	2.37	0.49
71:SR:29:GLU:HA	71:SR:32:LYS:HZ3	1.78	0.49
73:ST:105:MET:HE1	73:ST:123:ARG:HH11	1.77	0.49
1:1:506:G:H5''	11:LC:345:LYS:HE3	1.94	0.49
1:1:1260:C:H2'	1:1:1261:A:H8	1.78	0.49
1:1:1762:U:H2'	1:1:1763:C:C6	2.47	0.49
1:1:2577:G:O2'	1:1:2824:U:OP1	2.27	0.49
2:2:929:C:O2	55:SB:120:LEU:HD21	2.13	0.49
2:2:1161:G:H2'	2:2:1162:G:C8	2.48	0.49
5:A:218:LEU:HD21	5:A:228:TYR:CZ	2.47	0.49
7:C:343:ARG:HB3	7:C:347:LYS:HZ2	1.78	0.49
8:D:117:GLU:HG2	8:D:120:ALA:HB2	1.95	0.49
8:D:430:VAL:HB	8:D:470:LYS:HG3	1.93	0.49
59:SF:99:ARG:NH2	79:SZ:86:LYS:HE2	2.28	0.49
61:SH:7:ASN:HA	61:SH:16:ARG:HH12	1.77	0.49
64:SK:4:PRO:HD2	64:SK:8:ARG:NH2	2.28	0.49
67:SN:89:TYR:OH	67:SN:150:VAL:O	2.25	0.49
69:SP:31:GLU:O	69:SP:34:LEU:HD23	2.13	0.49
72:SS:16:ARG:HD2	72:SS:20:THR:O	2.13	0.49
73:ST:5:VAL:HG22	73:ST:138:GLN:HG3	1.95	0.49
80:Sa:51:ARG:NE	80:Sa:51:ARG:HA	2.28	0.49
1:1:135:G:H2'	1:1:136:C:C6	2.47	0.48
1:1:440:C:H2'	1:1:441:G:C8	2.47	0.48
2:2:519:U:H5''	78:SY:40:LYS:HE3	1.93	0.48
2:2:824:U:H2'	2:2:825:C:H6	1.77	0.48
3:3:62:U:O3'	12:LD:290:ARG:NH1	2.46	0.48
7:C:227:TYR:OH	7:C:289:ASP:OD2	2.30	0.48
7:C:311:GLU:O	7:C:314:GLU:HG3	2.12	0.48
8:D:93:THR:O	8:D:96:HIS:ND1	2.45	0.48
23:LO:8:VAL:HG23	23:LO:120:MET:HG3	1.95	0.48
29:LU:62:ILE:HD13	29:LU:72:ILE:HD12	1.94	0.48
47:Lm:79:GLU:OE2	47:Lm:82:LEU:HG	2.13	0.48
52:Ls:92:ASP:O	52:Ls:95:GLU:HG3	2.13	0.48
56:SC:150:GLY:N	56:SC:161:SER:O	2.46	0.48
56:SC:234:THR:OG1	56:SC:236:ASN:OD1	2.16	0.48
57:SD:156:THR:OG1	57:SD:160:MET:HE3	2.12	0.48
58:SE:141:THR:HG23	58:SE:143:ASP:H	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:SF:152:LEU:O	59:SF:156:ASN:ND2	2.46	0.48
61:SH:57:VAL:HG23	61:SH:181:GLU:HB2	1.95	0.48
66:SM:129:GLU:HB3	66:SM:133:ARG:NH1	2.27	0.48
70:SQ:127:LYS:NZ	70:SQ:129:PHE:HB2	2.27	0.48
72:SS:11:PHE:HE1	72:SS:59:GLY:HA3	1.79	0.48
76:SW:28:ARG:HB3	76:SW:29:PRO:HD3	1.95	0.48
1:1:1062:A:C2	12:LD:113:LEU:HD21	2.48	0.48
1:1:1373:A:N6	1:1:1401:A:O2'	2.46	0.48
2:2:86:C:O2'	2:2:166:A:N1	2.40	0.48
2:2:150:G:H2'	2:2:151:G:C8	2.48	0.48
2:2:233:G:O2'	2:2:234:C:OP1	2.26	0.48
2:2:366:U:O2'	2:2:368:G:OP2	2.31	0.48
2:2:1219:C:H2'	2:2:1220:G:C8	2.48	0.48
7:C:126:ARG:O	7:C:130:LEU:HG	2.12	0.48
12:LD:175:PHE:O	12:LD:176:ILE:HD13	2.13	0.48
56:SC:230:TYR:HB2	75:SV:25:LYS:HZ2	1.78	0.48
65:SL:39:TRP:O	65:SL:66:THR:HG22	2.13	0.48
73:ST:20:ALA:O	73:ST:24:LYS:HG2	2.12	0.48
1:1:703:A:H3'	35:La:115:LYS:HG3	1.95	0.48
3:3:3:A:H2'	3:3:4:U:C6	2.48	0.48
4:4:36:G:N7	42:Lh:91:ARG:HD3	2.28	0.48
5:A:189:ILE:HD12	57:SD:222:VAL:CG2	2.36	0.48
7:C:66:GLN:O	7:C:70:LYS:HG3	2.12	0.48
31:LW:63:ILE:HG22	31:LW:64:SER:N	2.28	0.48
33:LY:50:ARG:HG2	33:LY:51:LYS:N	2.28	0.48
42:Lh:19:GLU:HB2	42:Lh:22:LYS:HE3	1.95	0.48
59:SF:17:PRO:O	59:SF:21:LEU:HG	2.13	0.48
59:SF:107:ILE:HG22	59:SF:111:MET:HE1	1.96	0.48
64:SK:21:MET:O	64:SK:63:TYR:HA	2.13	0.48
73:ST:42:ASN:O	73:ST:84:LYS:NZ	2.37	0.48
73:ST:114:LEU:HB3	73:ST:125:ILE:HD13	1.95	0.48
74:SU:43:LYS:HD2	74:SU:44:ASN:N	2.29	0.48
1:1:673:G:OP1	20:LL:39:ARG:NH2	2.38	0.48
1:1:2356:G:H4'	10:LB:253:ILE:HD12	1.93	0.48
2:2:1232:C:O2	85:Sf:138:ARG:NE	2.46	0.48
4:4:52:A:C4	46:Ll:23:ILE:HG22	2.49	0.48
8:D:386:PRO:HA	8:D:389:LEU:HG	1.95	0.48
18:LJ:132:MET:HA	18:LJ:132:MET:HE2	1.95	0.48
33:LY:54:GLU:HB2	33:LY:107:LYS:HB3	1.95	0.48
60:SG:98:ARG:HE	60:SG:106:LEU:HD11	1.78	0.48
61:SH:134:ALA:HA	61:SH:137:THR:HG22	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:SJ:121:HIS:CD2	84:Se:37:ARG:NH2	2.81	0.48
75:SV:80:LYS:O	75:SV:82:VAL:HG13	2.13	0.48
1:1:1213:G:H3'	1:1:1214:A:H8	1.79	0.48
1:1:3056:G:OP1	10:LB:280:ASN:ND2	2.41	0.48
2:2:44:U:OP2	2:2:434:A:N6	2.46	0.48
2:2:1687:A:H2'	2:2:1688:G:C8	2.48	0.48
27:LS:73:LYS:NZ	27:LS:97:THR:O	2.47	0.48
55:SB:129:THR:OG1	55:SB:131:ASP:O	2.24	0.48
56:SC:169:LYS:HA	56:SC:173:VAL:O	2.13	0.48
57:SD:9:SER:OG	57:SD:12:ARG:HG2	2.13	0.48
68:SO:30:ALA:HB2	68:SO:92:LEU:HD23	1.95	0.48
70:SQ:50:GLU:O	70:SQ:54:ILE:HG12	2.13	0.48
1:1:213:A:HO2'	1:1:214:G:H21	1.56	0.48
1:1:323:G:C2	1:1:324:G:C8	3.02	0.48
1:1:1573:A:OP1	41:Lg:61:ARG:NH1	2.47	0.48
1:1:2064:C:H2'	1:1:2065:U:H6	1.78	0.48
2:2:16:G:H21	2:2:1135:A:H62	1.62	0.48
2:2:1252:G:O2'	2:2:1253:A:O5'	2.26	0.48
2:2:1375:U:H1'	70:SQ:8:GLN:CD	2.39	0.48
5:A:217:MET:HE1	5:A:226:HIS:ND1	2.29	0.48
5:A:239:LEU:HD11	5:A:248:LEU:HG	1.94	0.48
9:LA:117:GLU:OE2	9:LA:123:ARG:N	2.38	0.48
10:LB:359:TRP:O	10:LB:360:ILE:HD13	2.14	0.48
25:LQ:152:ASP:OD1	25:LQ:153:GLN:HG3	2.13	0.48
35:La:87:ARG:HG3	35:La:88:GLU:N	2.29	0.48
55:SB:156:ALA:HB3	55:SB:161:ILE:HD11	1.94	0.48
57:SD:69:ILE:O	57:SD:73:THR:HG23	2.14	0.48
57:SD:125:VAL:O	57:SD:129:ILE:HG12	2.13	0.48
62:SI:98:LYS:HD2	62:SI:176:ARG:HH11	1.78	0.48
63:SJ:72:ASN:HA	63:SJ:75:ILE:HG12	1.95	0.48
76:SW:119:LYS:O	76:SW:121:VAL:HG23	2.13	0.48
1:1:64:A:H5''	22:LN:174:LEU:HD21	1.95	0.48
1:1:481:C:H2'	1:1:482:U:H6	1.79	0.48
1:1:2405:G:H2'	1:1:2406:A:C8	2.48	0.48
1:1:3292:U:OP2	62:SI:124:ARG:NH2	2.46	0.48
2:2:1239:A:O2'	69:SP:59:ARG:NH1	2.42	0.48
2:2:1686:G:H2'	2:2:1687:A:C8	2.49	0.48
16:LH:139:SER:O	16:LH:140:LYS:HE2	2.14	0.48
17:LI:52:LEU:HB2	17:LI:152:LEU:HD12	1.94	0.48
52:Ls:104:ARG:NH2	52:Ls:182:THR:O	2.47	0.48
61:SH:67:PHE:HB3	61:SH:101:ALA:HB2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
67:SN:130:LYS:NZ	67:SN:139:TRP:O	2.38	0.48
70:SQ:8:GLN:HB2	70:SQ:21:ARG:NH2	2.29	0.48
77:SX:107:PHE:CE1	77:SX:123:LYS:HB3	2.49	0.48
81:Sb:33:MET:HE1	81:Sb:73:LEU:HD11	1.95	0.48
2:2:988:C:O4'	68:SO:140:ARG:NH2	2.47	0.48
2:2:1463:C:H2'	2:2:1464:U:C6	2.48	0.48
7:C:37:ARG:NH2	8:D:447:GLU:HB2	2.28	0.48
7:C:180:PRO:HB3	7:C:197:VAL:HG21	1.95	0.48
17:LI:86:HIS:HB3	17:LI:139:ARG:HG2	1.96	0.48
21:LM:14:VAL:HG12	27:LS:150:PHE:O	2.14	0.48
21:LM:104:LEU:O	21:LM:108:ARG:HG3	2.14	0.48
38:Ld:4:THR:O	38:Ld:8:GLN:HG2	2.14	0.48
59:SF:157:GLN:O	59:SF:161:LEU:HD23	2.14	0.48
61:SH:99:LEU:HD11	61:SH:139:LEU:HD13	1.96	0.48
69:SP:66:LYS:N	69:SP:69:ARG:HH21	2.12	0.48
71:SR:41:ILE:HD11	71:SR:46:LEU:HB2	1.95	0.48
73:ST:59:ALA:CB	73:ST:63:ARG:NH1	2.77	0.48
75:SV:38:LYS:HG3	75:SV:49:GLU:OE1	2.14	0.48
76:SW:8:HIS:HB2	76:SW:74:VAL:HG11	1.95	0.48
77:SX:41:SER:OG	77:SX:43:PHE:O	2.31	0.48
77:SX:83:VAL:HG22	77:SX:84:THR:H	1.79	0.48
77:SX:107:PHE:HD2	77:SX:114:LYS:HG2	1.79	0.48
1:1:1875:A:O2'	1:1:3011:G:H4'	2.14	0.48
1:1:2270:G:O2'	1:1:2273:U:OP2	2.30	0.48
2:2:1237:U:N3	2:2:1240:G:OP2	2.28	0.48
5:A:11:LEU:HD21	5:A:52:TYR:HB3	1.95	0.48
5:A:28:PRO:HB3	5:A:293:ALA:HB3	1.96	0.48
5:A:244:ASN:ND2	5:A:296:GLN:HE21	2.12	0.48
7:C:134:PRO:O	7:C:138:ALA:HB2	2.14	0.48
12:LD:116:ASP:OD1	12:LD:116:ASP:N	2.47	0.48
29:LU:49:VAL:HB	29:LU:55:ASN:HB3	1.94	0.48
29:LU:98:ASP:OD1	29:LU:99:TRP:N	2.47	0.48
37:Lc:19:LEU:HA	37:Lc:22:LYS:HG2	1.96	0.48
40:Lf:56:ARG:HG2	40:Lf:66:ILE:CD1	2.44	0.48
42:Lh:99:LYS:HE2	42:Lh:99:LYS:HA	1.95	0.48
61:SH:91:PHE:HB2	61:SH:94:ARG:NH2	2.29	0.48
62:SI:42:ARG:CZ	62:SI:59:ARG:HH21	2.26	0.48
63:SJ:13:PRO:HG3	63:SJ:21:ARG:NH1	2.29	0.48
68:SO:120:ARG:HE	82:Sc:61:GLU:HG3	1.78	0.48
71:SR:32:LYS:O	71:SR:47:ARG:NH2	2.47	0.48
73:ST:34:TRP:O	73:ST:37:THR:HG22	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
74:SU:61:LYS:NZ	74:SU:80:GLU:HB3	2.28	0.48
74:SU:85:LYS:NZ	74:SU:87:LEU:HB2	2.29	0.48
1:1:425:G:H2'	1:1:426:A:H8	1.78	0.48
1:1:1243:A:OP1	52:Ls:7:ASN:ND2	2.47	0.48
2:2:1098:G:H5''	76:SW:76:SER:HB3	1.96	0.48
2:2:1531:U:H4'	2:2:1532:G:O5'	2.14	0.48
3:3:108:C:H5''	12:LD:284:ARG:NH1	2.29	0.48
5:A:43:TRP:HA	5:A:55:PRO:HA	1.96	0.48
8:D:68:LEU:HD13	8:D:75:THR:HG21	1.96	0.48
9:LA:102:LEU:HD21	9:LA:166:ILE:HD11	1.95	0.48
38:Ld:4:THR:HA	38:Ld:7:LYS:HE3	1.96	0.48
41:Lg:77:TYR:HB3	41:Lg:81:ARG:HG3	1.96	0.48
56:SC:82:PRO:HG2	56:SC:83:LYS:HZ2	1.79	0.48
56:SC:124:LYS:NZ	56:SC:126:SER:HB3	2.29	0.48
64:SK:42:LYS:HG3	64:SK:45:GLN:HE21	1.79	0.48
73:ST:16:VAL:HB	73:ST:63:ARG:NH2	2.29	0.48
78:SY:9:THR:CG2	78:SY:31:LEU:HB2	2.44	0.48
1:1:261:A:C5	22:LN:12:LYS:HD2	2.48	0.47
1:1:491:C:H2'	1:1:492:A:H8	1.78	0.47
1:1:1016:U:O2'	1:1:1017:U:OP1	2.31	0.47
2:2:397:A:H5''	62:SI:25:ARG:HA	1.96	0.47
2:2:777:C:N4	78:SY:13:ARG:HH12	2.11	0.47
2:2:866:G:P	67:SN:121:ARG:HH12	2.37	0.47
7:C:155:ALA:O	7:C:159:LEU:HD13	2.13	0.47
7:C:354:LYS:O	7:C:358:LYS:HE3	2.14	0.47
16:LH:25:VAL:HG11	16:LH:36:LYS:HE2	1.96	0.47
23:LO:32:GLN:OE1	40:Lf:14:ARG:NH1	2.32	0.47
29:LU:24:ASN:HD22	29:LU:111:GLU:HG2	1.77	0.47
40:Lf:105:TYR:HB2	40:Lf:106:PRO:HD3	1.96	0.47
54:SA:41:TRP:CD1	71:SR:111:LEU:HD11	2.49	0.47
67:SN:32:GLN:O	67:SN:35:GLU:HG3	2.13	0.47
73:ST:53:TRP:HA	73:ST:56:ILE:HG22	1.95	0.47
85:Sf:100:LEU:HG	85:Sf:103:LEU:HB2	1.96	0.47
1:1:1596:U:H2'	1:1:1597:G:H8	1.79	0.47
1:1:2369:C:H2'	1:1:2370:C:H6	1.79	0.47
1:1:2503:C:H4'	1:1:2504:G:H8	1.79	0.47
2:2:1272:A:H62	2:2:1427:C:N4	2.11	0.47
6:B:141:ILE:HD13	56:SC:87:GLU:OE2	2.15	0.47
8:D:158:PRO:HD2	8:D:161:PHE:CE2	2.49	0.47
12:LD:291:VAL:O	12:LD:295:ILE:HG12	2.14	0.47
20:LL:77:LEU:HD13	20:LL:87:ARG:HH21	1.78	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:LP:29:THR:HG23	24:LP:119:VAL:HG11	1.96	0.47
41:Lg:92:ARG:O	41:Lg:96:ILE:HG12	2.14	0.47
45:Lk:58:LEU:HD23	45:Lk:62:LEU:HD23	1.96	0.47
57:SD:75:LEU:HD11	64:SK:63:TYR:CE1	2.49	0.47
62:SI:37:ARG:O	62:SI:59:ARG:HA	2.14	0.47
73:ST:59:ALA:HB1	73:ST:63:ARG:NH1	2.29	0.47
76:SW:109:GLY:O	76:SW:111:MET:HE1	2.14	0.47
80:Sa:12:LYS:HB2	80:Sa:33:ASP:OD2	2.12	0.47
81:Sb:81:ARG:HG2	81:Sb:81:ARG:HH11	1.79	0.47
1:1:609:A:H4'	1:1:610:A:O5'	2.13	0.47
1:1:993:G:H2'	1:1:994:G:H8	1.79	0.47
2:2:282:G:OP1	60:SG:199:ARG:NH2	2.47	0.47
2:2:899:G:H2'	2:2:900:G:C8	2.49	0.47
2:2:1790:A:OP2	80:Sa:4:LYS:NZ	2.46	0.47
5:A:101:PHE:CE1	5:A:136:GLY:HA2	2.49	0.47
7:C:43:GLY:O	7:C:47:LEU:HD13	2.13	0.47
16:LH:139:SER:OG	16:LH:145:GLU:HB2	2.13	0.47
17:LI:190:VAL:HG22	17:LI:199:PHE:CD1	2.50	0.47
24:LP:25:SER:OG	24:LP:28:ASN:HB2	2.13	0.47
36:Lb:47:LEU:HA	36:Lb:50:THR:HG22	1.96	0.47
44:Lj:51:GLU:OE2	44:Lj:55:ARG:NH2	2.47	0.47
50:Lp:79:MET:HA	50:Lp:82:THR:HG22	1.96	0.47
58:SE:188:ASN:OD1	58:SE:191:ARG:HG3	2.14	0.47
77:SX:97:ASP:N	77:SX:100:ASP:OD2	2.39	0.47
1:1:3079:U:H1'	1:1:3080:A:H5''	1.96	0.47
2:2:732:A:H3'	2:2:733:A:H8	1.79	0.47
2:2:1180:A:C8	69:SP:108:LYS:HE3	2.49	0.47
3:3:16:U:H2'	3:3:17:A:C8	2.49	0.47
4:4:68:G:H2'	4:4:69:U:H6	1.78	0.47
16:LH:175:ARG:NH2	47:Lm:127:LEU:HD13	2.30	0.47
24:LP:27:LYS:O	24:LP:31:GLU:HG2	2.14	0.47
39:Le:65:LYS:HE3	39:Le:66:HIS:CE1	2.49	0.47
41:Lg:99:GLN:HA	41:Lg:102:VAL:HG12	1.97	0.47
48:Lr:4:LYS:HE2	48:Lr:4:LYS:HB3	1.37	0.47
55:SB:29:TRP:CE2	68:SO:18:PRO:HD3	2.50	0.47
55:SB:110:LEU:O	55:SB:114:VAL:HG23	2.15	0.47
59:SF:173:ASN:OD1	59:SF:174:VAL:N	2.47	0.47
61:SH:162:VAL:HG12	61:SH:164:LEU:HD22	1.95	0.47
67:SN:70:LYS:O	67:SN:74:ILE:HG12	2.14	0.47
68:SO:71:TYR:HA	68:SO:74:MET:HG2	1.96	0.47
70:SQ:41:PRO:HG2	70:SQ:44:LEU:HB2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
71:SR:6:THR:O	71:SR:10:LYS:HG2	2.14	0.47
77:SX:79:ASN:OD1	77:SX:81:LYS:HG2	2.15	0.47
78:SY:112:LYS:O	78:SY:115:LYS:HG3	2.15	0.47
79:SZ:67:LYS:HA	79:SZ:70:LYS:HG2	1.95	0.47
1:1:377:A:H5'	7:C:257:ARG:HH12	1.78	0.47
1:1:1000:G:N2	1:1:1017:U:O2	2.30	0.47
2:2:597:U:H2'	2:2:598:A:H8	1.80	0.47
2:2:1521:A:HO2'	2:2:1585:C:HO2'	1.62	0.47
3:3:6:C:OP2	12:LD:22:ARG:NH2	2.47	0.47
6:B:134:ASP:OD2	57:SD:120:ARG:NE	2.48	0.47
7:C:326:GLU:C	7:C:330:ARG:HE	2.23	0.47
12:LD:298:LEU:HA	12:LD:301:GLU:OE1	2.14	0.47
26:LR:122:GLU:O	26:LR:126:LEU:HD23	2.14	0.47
55:SB:56:ASN:ND2	55:SB:58:ASN:OD1	2.48	0.47
63:SJ:29:VAL:HG23	63:SJ:34:LEU:HB2	1.94	0.47
66:SM:107:ASP:OD1	66:SM:108:ARG:N	2.47	0.47
67:SN:119:GLU:O	67:SN:123:HIS:ND1	2.40	0.47
72:SS:67:GLU:O	72:SS:71:THR:HG23	2.14	0.47
79:SZ:70:LYS:O	79:SZ:73:GLU:HG3	2.14	0.47
1:1:652:A:H2'	1:1:653:A:H8	1.78	0.47
1:1:2117:U:H2'	1:1:2118:G:C8	2.49	0.47
1:1:3231:G:H2'	1:1:3232:A:H8	1.78	0.47
2:2:392:U:O4	2:2:396:A:N7	2.47	0.47
2:2:1180:A:N3	2:2:1207:C:O2'	2.41	0.47
2:2:1222:U:H3'	2:2:1223:G:C8	2.50	0.47
2:2:1245:C:C2	2:2:1246:U:C5	3.03	0.47
7:C:123:ARG:O	7:C:127:LYS:HG3	2.14	0.47
7:C:364:LEU:HD21	7:C:395:ILE:HD13	1.96	0.47
8:D:286:ARG:O	8:D:290:ARG:HG2	2.14	0.47
12:LD:220:GLU:HA	12:LD:223:LYS:HD2	1.96	0.47
12:LD:226:PHE:HB3	12:LD:229:TYR:HB2	1.97	0.47
22:LN:121:VAL:HG21	22:LN:131:GLU:HG2	1.97	0.47
39:Le:90:ASN:OD1	39:Le:91:ARG:HG3	2.15	0.47
54:SA:91:LYS:NZ	54:SA:204:LEU:O	2.48	0.47
57:SD:119:ARG:HE	57:SD:155:PHE:HZ	1.62	0.47
66:SM:31:LYS:HB3	66:SM:35:LYS:NZ	2.30	0.47
82:Sc:9:LYS:HE2	82:Sc:60:SER:HB3	1.96	0.47
1:1:604:G:H2'	1:1:605:G:H8	1.80	0.47
1:1:1932:G:O6	1:1:2058:A:N6	2.47	0.47
1:1:2227:U:O2'	1:1:2228:C:OP1	2.29	0.47
1:1:2460:C:H2'	1:1:2461:C:C6	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:3176:G:H2'	1:1:3177:C:C6	2.50	0.47
2:2:68:A:OP1	60:SG:160:ARG:NH2	2.47	0.47
2:2:107:A:H2'	2:2:108:G:C8	2.49	0.47
2:2:148:G:N2	2:2:160:G:H22	2.12	0.47
2:2:177:A:H2'	2:2:178:A:C8	2.50	0.47
2:2:510:U:O4	63:SJ:169:ARG:NH2	2.47	0.47
2:2:893:G:N2	68:SO:51:THR:HG21	2.29	0.47
2:2:920:G:H2'	2:2:921:A:H8	1.78	0.47
2:2:1467:A:N6	2:2:1534:U:C2	2.82	0.47
2:2:1470:G:H2'	2:2:1471:A:C8	2.49	0.47
5:A:44:ASN:OD1	5:A:56:LYS:HB2	2.14	0.47
7:C:265:ASN:HD22	7:C:269:LYS:HZ1	1.62	0.47
8:D:157:ILE:HD13	8:D:183:LEU:HD13	1.96	0.47
9:LA:28:LYS:HB3	9:LA:123:ARG:HB3	1.96	0.47
11:LC:301:ARG:HG2	11:LC:302:ALA:H	1.80	0.47
18:LJ:54:THR:HG23	18:LJ:61:ARG:HA	1.97	0.47
20:LL:167:GLU:OE2	35:La:98:THR:HG22	2.15	0.47
24:LP:171:LEU:CD1	24:LP:175:GLN:HE21	2.27	0.47
32:LX:96:VAL:HG22	32:LX:136:PHE:CD1	2.49	0.47
35:La:149:ALA:HB2	43:Li:16:LEU:HA	1.97	0.47
38:Ld:29:HIS:C	38:Ld:29:HIS:CD2	2.93	0.47
39:Le:84:GLU:CD	39:Le:112:ARG:HE	2.22	0.47
49:Lo:70:LEU:HD13	49:Lo:72:LEU:HD21	1.95	0.47
55:SB:65:ILE:HD12	55:SB:101:HIS:CD2	2.49	0.47
59:SF:75:PRO:HB2	59:SF:78:GLU:OE1	2.14	0.47
60:SG:77:LEU:HD12	60:SG:95:LYS:HB2	1.96	0.47
61:SH:62:LYS:HE2	61:SH:94:ARG:HD2	1.96	0.47
71:SR:28:PHE:HA	71:SR:31:ASN:OD1	2.13	0.47
73:ST:60:SER:HA	73:ST:63:ARG:CZ	2.44	0.47
74:SU:66:LYS:HA	83:Sd:44:ARG:NH1	2.30	0.47
75:SV:11:LEU:HD22	75:SV:12:TYR:HD1	1.80	0.47
77:SX:93:LEU:HD22	84:Se:8:LEU:HD11	1.97	0.47
78:SY:13:ARG:O	78:SY:26:MET:HG3	2.15	0.47
1:1:869:G:H2'	1:1:870:A:C8	2.50	0.47
1:1:1003:G:H2'	1:1:1004:C:C6	2.49	0.47
1:1:1643:C:H2'	1:1:1644:G:H8	1.80	0.47
2:2:57:G:OP1	78:SY:115:LYS:NZ	2.48	0.47
2:2:328:G:H21	62:SI:5:ARG:HD2	1.79	0.47
2:2:499:U:H2'	2:2:500:G:H8	1.79	0.47
2:2:1282:U:H1'	2:2:1283:U:OP2	2.15	0.47
2:2:1588:A:H2'	2:2:1589:A:H8	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:D:328:ASN:O	8:D:331:VAL:HG12	2.14	0.47
16:LH:113:GLU:HG3	16:LH:127:LYS:NZ	2.29	0.47
18:LJ:61:ARG:N	18:LJ:64:GLU:OE2	2.34	0.47
27:LS:6:GLU:OE2	27:LS:28:ARG:NH2	2.47	0.47
27:LS:142:GLN:HG3	27:LS:143:LEU:HD22	1.96	0.47
55:SB:11:LYS:HZ2	55:SB:17:LYS:HE2	1.80	0.47
56:SC:97:GLN:HE22	56:SC:99:ARG:HH22	1.62	0.47
58:SE:115:THR:O	58:SE:119:ALA:HB2	2.14	0.47
60:SG:138:ALA:O	60:SG:141:ILE:HG22	2.14	0.47
62:SI:108:PRO:O	62:SI:111:GLN:HG3	2.14	0.47
77:SX:42:PRO:HB3	77:SX:81:LYS:NZ	2.30	0.47
78:SY:128:LYS:HD2	78:SY:131:LYS:HZ3	1.79	0.47
79:SZ:50:THR:O	79:SZ:53:THR:OG1	2.32	0.47
1:1:2370:C:H2'	1:1:2371:U:H6	1.80	0.47
1:1:2842:U:H2'	1:1:2843:C:C6	2.50	0.47
1:1:2948:U:O2'	10:LB:268:ALA:O	2.27	0.47
2:2:14:C:H2'	2:2:15:U:C6	2.49	0.47
8:D:296:PHE:O	8:D:308:ALA:HA	2.14	0.47
10:LB:377:LYS:O	10:LB:381:MET:HB2	2.15	0.47
18:LJ:52:ARG:HH21	18:LJ:53:TYR:HD1	1.63	0.47
21:LM:78:THR:HA	21:LM:81:VAL:HG12	1.96	0.47
22:LN:80:THR:OG1	22:LN:87:GLN:HG3	2.15	0.47
30:LV:86:PRO:HA	30:LV:96:TYR:HB3	1.97	0.47
38:Ld:20:TYR:O	38:Ld:80:ARG:HD3	2.15	0.47
39:Le:124:LYS:HE2	39:Le:124:LYS:HA	1.97	0.47
48:Ln:4:LYS:HB3	48:Ln:4:LYS:HE2	1.37	0.47
52:Ls:65:THR:HB	52:Ls:74:GLU:HB3	1.96	0.47
54:SA:105:PHE:HZ	54:SA:110:PHE:CE2	2.33	0.47
56:SC:134:ARG:O	56:SC:138:ILE:HG12	2.15	0.47
56:SC:180:ALA:HB3	56:SC:203:ASP:HB3	1.97	0.47
57:SD:98:GLY:HA3	57:SD:132:SER:OG	2.15	0.47
68:SO:27:PHE:C	68:SO:89:ILE:HD11	2.40	0.47
74:SU:66:LYS:HA	83:Sd:44:ARG:HH22	1.80	0.47
85:Sf:118:ARG:NH1	85:Sf:134:SER:H	2.13	0.47
1:1:2842:U:H2'	1:1:2843:C:H6	1.79	0.47
2:2:853:A:O2'	2:2:854:A:H3'	2.15	0.47
2:2:1207:C:H2'	2:2:1208:A:C8	2.48	0.47
2:2:1404:G:O2'	5:A:15:ASN:OD1	2.31	0.47
5:A:170:TRP:HA	5:A:194:TYR:HB2	1.96	0.47
7:C:47:LEU:HD21	8:D:401:ILE:HG22	1.96	0.47
7:C:190:TYR:OH	7:C:288:GLY:HA3	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:C:291:ARG:O	7:C:294:ARG:HG3	2.15	0.47
10:LB:14:LEU:HD22	10:LB:17:LEU:HD13	1.97	0.47
22:LN:99:ARG:NH1	22:LN:118:SER:O	2.48	0.47
25:LQ:123:VAL:HG23	25:LQ:144:ALA:HB2	1.97	0.47
33:LY:53:ASP:HB3	33:LY:109:HIS:H	1.80	0.47
35:La:94:GLN:HA	35:La:96:LYS:HZ1	1.80	0.47
36:Lb:6:ASN:OD1	36:Lb:7:SER:N	2.48	0.47
39:Le:64:THR:HA	39:Le:67:MET:SD	2.55	0.47
54:SA:13:THR:OG1	54:SA:16:ASP:OD2	2.30	0.47
54:SA:20:LEU:HD12	54:SA:53:LEU:HD12	1.97	0.47
57:SD:26:GLU:HG3	64:SK:59:TRP:HE1	1.80	0.47
62:SI:77:ARG:HH21	62:SI:79:ILE:HA	1.80	0.47
71:SR:82:ASP:OD1	71:SR:82:ASP:N	2.47	0.47
1:1:1545:G:H2'	1:1:1546:G:H8	1.80	0.46
2:2:402:C:O2'	60:SG:92:ARG:O	2.30	0.46
2:2:815:A:O4'	61:SH:120:GLN:NE2	2.47	0.46
5:A:8:LYS:NZ	5:A:311:GLY:O	2.48	0.46
7:C:126:ARG:HA	7:C:129:VAL:HG12	1.98	0.46
7:C:231:TYR:HD2	38:Ld:11:ALA:HB1	1.80	0.46
8:D:384:LEU:HD13	8:D:392:ARG:NH1	2.30	0.46
8:D:472:VAL:HG12	8:D:532:THR:HG23	1.98	0.46
12:LD:33:ARG:HG2	28:LT:27:LEU:HD21	1.97	0.46
16:LH:103:VAL:O	16:LH:103:VAL:HG13	2.15	0.46
22:LN:17:ASP:OD1	22:LN:18:VAL:N	2.48	0.46
22:LN:104:GLU:OE1	22:LN:161:CYS:HB3	2.15	0.46
37:Lc:50:ASN:OD1	37:Lc:76:THR:OG1	2.17	0.46
70:SQ:87:LYS:HA	70:SQ:90:VAL:HG22	1.96	0.46
71:SR:37:GLU:HG2	71:SR:38:ILE:HG23	1.97	0.46
72:SS:116:LEU:HG	72:SS:119:ILE:HD11	1.97	0.46
1:1:702:G:N7	35:La:111:LYS:HE2	2.29	0.46
1:1:837:U:H4'	26:LR:95:TRP:CZ3	2.50	0.46
1:1:3068:C:H2'	1:1:3069:U:C6	2.50	0.46
2:2:150:G:H2'	2:2:151:G:H8	1.80	0.46
2:2:1469:U:C6	59:SF:177:ILE:HD13	2.48	0.46
2:2:1519:U:O5'	73:ST:78:LYS:NZ	2.48	0.46
3:3:31:G:O2'	12:LD:221:ARG:NH2	2.48	0.46
8:D:427:ILE:HB	8:D:444:ILE:HB	1.97	0.46
16:LH:130:MET:HE3	16:LH:159:SER:HB2	1.97	0.46
26:LR:139:VAL:HG22	26:LR:143:HIS:CE1	2.49	0.46
39:Le:105:LYS:O	39:Le:109:ILE:HG13	2.15	0.46
43:Li:13:ARG:HD2	43:Li:23:GLY:HA3	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:Lk:10:LYS:O	45:Lk:14:ILE:HG12	2.16	0.46
52:Ls:12:PHE:HA	52:Ls:60:ARG:NH2	2.30	0.46
58:SE:222:GLU:O	58:SE:225:VAL:HG22	2.15	0.46
61:SH:68:VAL:CG1	61:SH:76:PHE:HE2	2.28	0.46
1:1:154:G:H2'	1:1:155:A:H8	1.80	0.46
1:1:3042:C:O2'	1:1:3273:U:OP1	2.25	0.46
2:2:12:U:H2'	2:2:13:U:C6	2.49	0.46
2:2:644:A:H2'	2:2:645:G:H8	1.79	0.46
2:2:853:A:HO2'	2:2:854:A:H3'	1.80	0.46
2:2:1687:A:H2'	2:2:1688:G:H8	1.80	0.46
5:A:29:ASN:HA	5:A:45:LEU:HB2	1.96	0.46
8:D:385:ASN:HB3	8:D:388:GLU:HB2	1.97	0.46
22:LN:14:LYS:HA	22:LN:19:VAL:HG11	1.97	0.46
42:Lh:16:ASN:ND2	42:Lh:19:GLU:OE2	2.48	0.46
56:SC:122:GLY:HA3	56:SC:139:ILE:HG13	1.97	0.46
58:SE:251:ARG:HB3	58:SE:255:ARG:NH2	2.30	0.46
62:SI:188:LEU:O	62:SI:193:LEU:HD12	2.14	0.46
63:SJ:12:VAL:HG22	63:SJ:41:TRP:HZ3	1.79	0.46
74:SU:55:MET:HG2	74:SU:85:LYS:HD2	1.98	0.46
1:1:135:G:H2'	1:1:136:C:H6	1.79	0.46
1:1:468:G:OP2	1:1:468:G:H8	1.98	0.46
1:1:483:C:H2'	1:1:484:A:C8	2.50	0.46
1:1:781:G:H2'	1:1:783:A:H62	1.80	0.46
1:1:1173:A:H2'	1:1:1173:A:N3	2.29	0.46
1:1:1454:U:H2'	1:1:1455:G:H8	1.79	0.46
1:1:1812:C:H2'	1:1:1813:G:H8	1.79	0.46
1:1:2523:G:H2'	1:1:2524:G:H8	1.79	0.46
2:2:40:A:H62	2:2:464:G:H21	1.64	0.46
2:2:923:G:H2'	2:2:924:A:C8	2.51	0.46
2:2:1331:U:O2'	74:SU:82:ARG:NH2	2.48	0.46
8:D:373:ARG:HE	8:D:374:ILE:H	1.63	0.46
11:LC:41:THR:O	11:LC:45:LYS:NZ	2.32	0.46
26:LR:38:ARG:O	26:LR:42:ARG:HG2	2.16	0.46
56:SC:119:VAL:CG2	56:SC:199:ALA:HA	2.46	0.46
61:SH:70:VAL:HG23	61:SH:71:PRO:HD3	1.97	0.46
62:SI:57:ALA:HB2	62:SI:181:GLY:HA2	1.97	0.46
63:SJ:8:LYS:HD2	63:SJ:10:TYR:CE1	2.51	0.46
64:SK:14:TYR:CE1	64:SK:18:GLU:HG2	2.50	0.46
76:SW:10:ALA:O	76:SW:14:ILE:HG13	2.16	0.46
76:SW:82:ARG:HB2	76:SW:85:GLU:OE1	2.15	0.46
80:Sa:10:ARG:HD2	80:Sa:12:LYS:HB3	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:436:C:H2'	1:1:437:G:C8	2.50	0.46
2:2:118:A:H1'	2:2:394:A:C5	2.51	0.46
2:2:600:U:H2'	2:2:601:A:H8	1.80	0.46
2:2:1005:C:H5'	68:SO:150:LEU:HD12	1.98	0.46
7:C:345:ALA:HA	7:C:348:LYS:HE3	1.96	0.46
10:LB:162:LEU:HD23	10:LB:181:GLU:HB3	1.97	0.46
29:LU:19:LYS:NZ	29:LU:77:ASP:HA	2.31	0.46
30:LV:87:TRP:HE1	30:LV:89:ARG:NH1	2.14	0.46
33:LY:122:LYS:O	33:LY:126:GLU:OE1	2.33	0.46
43:Li:28:ARG:HH11	43:Li:28:ARG:HG3	1.80	0.46
52:Ls:37:GLN:HG2	52:Ls:185:MET:HE2	1.97	0.46
52:Ls:142:PRO:HD2	52:Ls:156:ILE:HG13	1.97	0.46
56:SC:48:LYS:O	56:SC:52:LEU:HD23	2.15	0.46
56:SC:161:SER:HA	56:SC:201:ILE:HD11	1.97	0.46
57:SD:129:ILE:HG21	57:SD:137:CYS:HB3	1.97	0.46
59:SF:152:LEU:HD11	82:Sc:48:PRO:HD2	1.98	0.46
62:SI:141:SER:HA	62:SI:144:LYS:NZ	2.30	0.46
76:SW:21:GLY:O	76:SW:23:ARG:NH1	2.48	0.46
1:1:1260:C:H2'	1:1:1261:A:C8	2.50	0.46
2:2:844:G:H2'	2:2:845:A:C8	2.51	0.46
5:A:79:LEU:HD21	5:A:87:LEU:HD21	1.97	0.46
7:C:104:TYR:OH	7:C:169:ASP:OD1	2.15	0.46
8:D:9:ALA:O	8:D:13:ARG:HG3	2.16	0.46
17:LI:66:GLU:O	17:LI:70:ILE:HG13	2.15	0.46
20:LL:3:ILE:H	20:LL:3:ILE:HD12	1.81	0.46
38:Ld:32:THR:HG22	38:Ld:34:LYS:H	1.81	0.46
41:Lg:97:GLU:O	41:Lg:101:ILE:HG12	2.16	0.46
56:SC:240:GLU:OE1	56:SC:241:THR:N	2.44	0.46
58:SE:254:ARG:O	58:SE:257:ARG:HD3	2.15	0.46
59:SF:175:LYS:HE2	59:SF:180:CYS:SG	2.55	0.46
63:SJ:13:PRO:CG	63:SJ:21:ARG:HH12	2.29	0.46
63:SJ:89:MET:O	63:SJ:90:LYS:HD2	2.16	0.46
76:SW:24:GLN:HG3	81:Sb:7:LEU:HD22	1.98	0.46
82:Sc:59:GLU:OE2	82:Sc:62:ARG:N	2.41	0.46
84:Se:24:GLN:OE1	84:Se:26:LYS:HE3	2.15	0.46
1:1:1702:U:OP2	26:LR:103:ARG:NH1	2.49	0.46
2:2:835:G:H2'	2:2:836:G:H8	1.81	0.46
2:2:923:G:H2'	2:2:924:A:H8	1.81	0.46
2:2:1063:C:H4'	55:SB:149:GLN:HG2	1.97	0.46
2:2:1165:U:HO2'	2:2:1166:G:P	2.38	0.46
2:2:1323:A:H5''	57:SD:159:PHE:CE1	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:C:180:PRO:HG3	7:C:197:VAL:HG21	1.98	0.46
17:LI:147:ILE:HD12	17:LI:147:ILE:H	1.80	0.46
28:LT:68:THR:OG1	28:LT:71:ALA:O	2.33	0.46
31:LW:3:THR:OG1	31:LW:13:ILE:O	2.31	0.46
31:LW:80:ARG:NH2	60:SG:130:PRO:HA	2.31	0.46
32:LX:67:GLU:CD	32:LX:68:PRO:HD2	2.40	0.46
42:Lh:90:THR:HG22	42:Lh:92:ALA:H	1.81	0.46
43:Li:94:ARG:HA	43:Li:97:GLU:CD	2.40	0.46
56:SC:182:ARG:HA	56:SC:203:ASP:OD2	2.16	0.46
66:SM:36:LEU:HD22	66:SM:129:GLU:HB2	1.98	0.46
72:SS:42:TYR:HD1	72:SS:85:PHE:CE2	2.32	0.46
74:SU:33:LYS:HA	74:SU:36:GLN:HB2	1.97	0.46
75:SV:32:CYS:SG	75:SV:60:ARG:NH1	2.88	0.46
1:1:1638:G:H2'	1:1:1639:A:C8	2.51	0.46
1:1:1745:U:H4'	1:1:1745:U:OP1	2.14	0.46
1:1:2336:A:N3	1:1:2783:G:O2'	2.43	0.46
1:1:3224:C:H2'	1:1:3225:G:H8	1.79	0.46
5:A:251:ALA:HB2	5:A:289:LEU:HD11	1.97	0.46
7:C:164:LYS:O	7:C:167:GLN:HG3	2.16	0.46
8:D:420:MET:HE3	8:D:449:ALA:HB1	1.98	0.46
12:LD:90:HIS:CE1	12:LD:228:LYS:HB3	2.51	0.46
17:LI:30:LYS:HG3	17:LI:66:GLU:OE1	2.16	0.46
20:LL:76:THR:HG22	20:LL:101:ARG:HB3	1.97	0.46
24:LP:154:GLU:OE1	24:LP:154:GLU:N	2.49	0.46
54:SA:163:ILE:HG22	54:SA:165:THR:HG23	1.96	0.46
58:SE:65:MET:HE1	58:SE:70:VAL:O	2.15	0.46
70:SQ:101:SER:O	70:SQ:105:LEU:HD23	2.16	0.46
81:Sb:35:VAL:HG11	81:Sb:63:LEU:HD23	1.98	0.46
85:Sf:119:ARG:HH21	85:Sf:150:PHE:HZ	1.63	0.46
1:1:137:C:H2'	1:1:138:C:C6	2.51	0.46
1:1:775:A:H2'	1:1:776:G:H8	1.81	0.46
1:1:1759:C:N4	26:LR:88:ARG:O	2.48	0.46
2:2:195:G:H2'	2:2:196:G:C8	2.51	0.46
2:2:509:A:OP2	63:SJ:170:VAL:HG12	2.16	0.46
2:2:826:U:H2'	2:2:827:A:C8	2.51	0.46
2:2:1260:G:H2'	2:2:1261:G:O4'	2.16	0.46
2:2:1397:A:O3'	71:SR:5:ARG:NH1	2.48	0.46
3:3:44:C:OP2	18:LJ:138:ARG:NH1	2.35	0.46
3:3:46:C:OP1	12:LD:161:ARG:HG3	2.16	0.46
11:LC:284:GLN:NE2	11:LC:286:ASP:HB3	2.31	0.46
11:LC:300:LEU:HD21	25:LQ:67:ARG:HH21	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:LE:115:ASP:OD1	13:LE:116:GLN:N	2.48	0.46
39:Le:68:MET:HB2	39:Le:69:PRO:HD2	1.98	0.46
41:Lg:96:ILE:HG22	41:Lg:100:LYS:HE3	1.98	0.46
43:Li:71:ARG:HB3	43:Li:103:ILE:HD11	1.97	0.46
61:SH:169:ARG:NH1	61:SH:195:PHE:HB2	2.30	0.46
63:SJ:23:ASP:N	63:SJ:23:ASP:OD1	2.46	0.46
73:ST:99:SER:HA	73:ST:103:LYS:HZ3	1.81	0.46
1:1:1255:C:H3'	1:1:1256:A:H8	1.80	0.46
2:2:510:U:H5'	63:SJ:129:GLN:HE21	1.81	0.46
4:4:95:G:OP1	44:Lj:76:ASN:ND2	2.41	0.46
7:C:148:PHE:O	7:C:152:ILE:HG13	2.16	0.46
7:C:279:ARG:HD3	38:Ld:89:ASP:OD1	2.16	0.46
10:LB:47:MET:CE	10:LB:336:ILE:HD11	2.46	0.46
11:LC:223:VAL:O	11:LC:227:ARG:HB2	2.16	0.46
14:LF:7:PRO:HG2	51:Lq:88:ARG:HB3	1.99	0.46
14:LF:62:ARG:O	14:LF:66:ARG:HG2	2.16	0.46
14:LF:136:VAL:O	14:LF:136:VAL:HG13	2.16	0.46
26:LR:170:ARG:HH12	26:LR:173:LYS:HD2	1.81	0.46
34:LZ:69:PRO:HG3	34:LZ:114:LYS:HB2	1.97	0.46
42:Lh:96:ARG:HB3	42:Lh:96:ARG:HH11	1.81	0.46
46:Ll:24:PRO:HG2	46:Ll:27:ILE:HG12	1.97	0.46
55:SB:124:ASN:HB3	55:SB:138:PHE:CD1	2.51	0.46
61:SH:33:LEU:HA	61:SH:36:ASN:OD1	2.16	0.46
61:SH:47:LEU:HD21	61:SH:76:PHE:CD1	2.51	0.46
64:SK:13:GLU:HB2	64:SK:17:ARG:NH2	2.31	0.46
71:SR:5:ARG:HH21	71:SR:10:LYS:NZ	2.13	0.46
74:SU:32:GLU:OE1	74:SU:86:ARG:NH1	2.49	0.46
77:SX:114:LYS:O	77:SX:117:ILE:HG12	2.16	0.46
78:SY:43:LEU:HD22	78:SY:60:VAL:HG11	1.96	0.46
1:1:2517:A:H61	41:Lg:100:LYS:NZ	2.14	0.45
1:1:3194:G:H2'	1:1:3195:U:C6	2.50	0.45
2:2:22:A:H4'	63:SJ:14:ARG:HA	1.97	0.45
2:2:381:G:H2'	2:2:382:A:H8	1.79	0.45
2:2:588:A:H4'	63:SJ:17:TYR:HE1	1.80	0.45
2:2:1219:C:H2'	2:2:1220:G:H8	1.81	0.45
5:A:240:VAL:O	5:A:248:LEU:HD12	2.16	0.45
7:C:79:ASP:HB2	7:C:82:ILE:HG12	1.97	0.45
9:LA:79:ASN:OD1	9:LA:165:MET:HE2	2.16	0.45
15:LG:53:VAL:HG12	32:LX:43:THR:HA	1.98	0.45
22:LN:65:ARG:HA	22:LN:128:LYS:O	2.16	0.45
24:LP:6:ALA:O	24:LP:7:THR:OG1	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:Lc:48:ALA:HB2	37:Lc:80:LEU:HD22	1.98	0.45
38:Ld:4:THR:HA	38:Ld:7:LYS:HG2	1.98	0.45
50:Lp:77:ALA:O	50:Lp:80:ARG:HG2	2.16	0.45
52:Ls:22:TYR:CD2	52:Ls:88:PHE:HB3	2.45	0.45
56:SC:175:VAL:HG21	56:SC:222:THR:HA	1.99	0.45
59:SF:14:ASP:OD1	59:SF:15:VAL:N	2.47	0.45
61:SH:177:ASP:OD1	61:SH:178:THR:N	2.49	0.45
62:SI:182:ARG:HB3	62:SI:184:ASP:OD1	2.16	0.45
68:SO:74:MET:HE2	68:SO:75:LEU:HD12	1.98	0.45
70:SQ:120:ASP:OD2	70:SQ:122:ARG:NE	2.49	0.45
76:SW:26:MET:HE1	76:SW:62:VAL:HG22	1.98	0.45
1:1:341:C:O2	1:1:345:A:O2'	2.34	0.45
1:1:2307:U:H2'	1:1:2308:A:C8	2.52	0.45
1:1:2642:U:H2'	1:1:2643:C:C6	2.51	0.45
1:1:2945:U:H2'	1:1:2946:A:H8	1.81	0.45
1:1:3179:G:H2'	1:1:3180:G:H8	1.80	0.45
1:1:3186:A:H4'	10:LB:95:THR:HG22	1.98	0.45
2:2:442:A:C2	2:2:443:A:C8	3.05	0.45
4:4:4:C:H2'	4:4:5:U:C6	2.51	0.45
5:A:5:LEU:HB3	5:A:310:TRP:CE3	2.52	0.45
8:D:62:GLN:HA	8:D:65:LYS:CG	2.46	0.45
8:D:326:GLY:O	8:D:330:LEU:HD23	2.15	0.45
15:LG:67:ILE:HA	15:LG:70:MET:HG2	1.96	0.45
15:LG:241:MET:HE3	15:LG:241:MET:HB3	1.85	0.45
26:LR:172:ARG:O	26:LR:175:GLU:HG3	2.16	0.45
34:LZ:8:ARG:HD3	34:LZ:8:ARG:HA	1.70	0.45
42:Lh:76:LYS:NZ	42:Lh:77:ASN:HB2	2.32	0.45
54:SA:65:ARG:NH2	75:SV:37:ALA:O	2.49	0.45
57:SD:12:ARG:O	57:SD:15:VAL:HG12	2.16	0.45
59:SF:99:ARG:HH12	79:SZ:84:HIS:CE1	2.34	0.45
60:SG:57:ASP:HA	60:SG:106:LEU:HA	1.98	0.45
61:SH:34:GLU:HA	61:SH:41:LYS:HD2	1.97	0.45
66:SM:63:VAL:HA	66:SM:89:ILE:O	2.16	0.45
67:SN:99:ARG:O	67:SN:102:LEU:HG	2.16	0.45
77:SX:69:ARG:NH2	77:SX:116:ASP:OD2	2.50	0.45
85:Sf:98:VAL:HG11	85:Sf:101:ALA:HB2	1.97	0.45
85:Sf:119:ARG:NH1	85:Sf:121:CYS:SG	2.89	0.45
1:1:300:A:H2'	1:1:301:A:H8	1.80	0.45
1:1:372:C:H2'	1:1:373:U:H6	1.82	0.45
1:1:474:C:H2'	1:1:475:G:C8	2.51	0.45
1:1:533:C:H2'	1:1:534:C:C6	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:725:C:O2	25:LQ:168:ARG:NH1	2.49	0.45
2:2:948:C:HO2'	67:SN:101:HIS:HD1	1.57	0.45
2:2:948:C:H2'	2:2:949:A:C8	2.51	0.45
2:2:1245:C:H2'	2:2:1246:U:C6	2.51	0.45
2:2:1472:C:H5''	73:ST:45:GLU:OE2	2.16	0.45
2:2:1790:A:N3	80:Sa:79:ILE:HD11	2.31	0.45
3:3:16:U:H2'	3:3:17:A:H8	1.80	0.45
5:A:79:LEU:HB2	5:A:113:PHE:CZ	2.51	0.45
5:A:241:PHE:CD2	5:A:248:LEU:HD13	2.51	0.45
7:C:41:PRO:O	8:D:182:GLN:NE2	2.35	0.45
9:LA:206:PRO:HG3	9:LA:213:GLY:H	1.80	0.45
11:LC:32:ARG:HB3	11:LC:35:ILE:HD12	1.98	0.45
11:LC:149:VAL:HG13	11:LC:150:PRO:HD3	1.97	0.45
12:LD:265:LYS:HB2	12:LD:270:TRP:CE2	2.51	0.45
16:LH:23:ARG:HD2	16:LH:38:LEU:O	2.16	0.45
16:LH:36:LYS:CE	16:LH:78:MET:HG3	2.45	0.45
21:LM:13:ARG:HH12	27:LS:150:PHE:C	2.24	0.45
32:LX:87:LYS:HG2	32:LX:91:GLU:OE2	2.17	0.45
55:SB:146:ARG:HD3	55:SB:147:PRO:HD2	1.98	0.45
63:SJ:4:ARG:HA	63:SJ:4:ARG:HD2	1.85	0.45
63:SJ:74:LEU:O	63:SJ:78:LEU:HD23	2.17	0.45
63:SJ:98:LYS:HG2	63:SJ:99:ALA:H	1.81	0.45
67:SN:88:LEU:O	67:SN:92:ILE:HG12	2.16	0.45
72:SS:117:LYS:HE3	72:SS:128:TYR:HB2	1.99	0.45
1:1:372:C:H2'	1:1:373:U:C6	2.52	0.45
1:1:1059:C:H2'	1:1:1060:U:C6	2.51	0.45
1:1:1213:G:H3'	1:1:1214:A:C8	2.51	0.45
1:1:1409:C:H3'	35:La:4:ARG:NH2	2.31	0.45
1:1:1597:G:OP2	48:Lr:5:TRP:HH2	1.98	0.45
2:2:469:U:O2'	2:2:768:A:N3	2.44	0.45
2:2:1457:C:H2'	2:2:1458:G:C8	2.51	0.45
2:2:1535:G:C8	72:SS:30:TYR:HE2	2.34	0.45
5:A:242:SER:OG	5:A:245:ARG:HD2	2.17	0.45
8:D:50:ILE:HG13	8:D:77:ALA:HB2	1.98	0.45
22:LN:6:TYR:HA	22:LN:9:GLU:OE2	2.16	0.45
28:LT:134:MET:HE3	28:LT:134:MET:HA	1.98	0.45
33:LY:73:TYR:CE2	33:LY:76:LYS:HG3	2.52	0.45
35:La:15:VAL:O	35:La:16:SER:OG	2.26	0.45
56:SC:114:ASP:OD2	56:SC:118:HIS:HB2	2.16	0.45
57:SD:188:LYS:HB3	57:SD:190:LYS:HZ1	1.80	0.45
64:SK:86:PRO:HA	64:SK:89:HIS:HB3	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:SQ:74:HIS:CD2	70:SQ:75:THR:HG23	2.52	0.45
71:SR:72:LYS:O	71:SR:76:GLU:OE1	2.35	0.45
74:SU:28:VAL:O	74:SU:31:LEU:HG	2.17	0.45
79:SZ:91:THR:OG1	79:SZ:92:ARG:N	2.49	0.45
1:1:1092:A:H4'	25:LQ:180:PHE:CE1	2.52	0.45
1:1:1212:G:H2'	1:1:1213:G:C8	2.52	0.45
1:1:1779:A:H2'	1:1:1780:A:C8	2.52	0.45
2:2:481:C:H2'	2:2:482:A:H8	1.81	0.45
2:2:1355:G:H5'	73:ST:127:GLN:NE2	2.31	0.45
2:2:1387:U:OP1	71:SR:3:ARG:NH2	2.49	0.45
2:2:1392:G:OP2	5:A:279:LYS:HE3	2.17	0.45
7:C:353:ALA:O	7:C:357:VAL:HG22	2.16	0.45
8:D:240:TYR:HB3	8:D:323:VAL:HG23	1.98	0.45
18:LJ:30:ARG:HD3	18:LJ:33:ARG:NH2	2.32	0.45
18:LJ:88:LYS:HG3	18:LJ:88:LYS:O	2.16	0.45
22:LN:66:VAL:O	22:LN:127:TYR:HA	2.15	0.45
23:LO:60:ARG:HH11	23:LO:60:ARG:HG3	1.82	0.45
40:Lf:61:VAL:HG23	40:Lf:62:ARG:N	2.31	0.45
50:Lp:30:GLU:OE2	50:Lp:34:HIS:NE2	2.49	0.45
52:Ls:61:ARG:HA	52:Ls:64:LYS:CD	2.44	0.45
56:SC:245:ARG:NE	56:SC:250:GLU:HB3	2.32	0.45
60:SG:163:GLN:HB3	60:SG:171:PRO:HB3	1.97	0.45
62:SI:188:LEU:HB2	62:SI:192:GLU:OE1	2.16	0.45
62:SI:189:GLU:HA	62:SI:193:LEU:HB2	1.98	0.45
83:Sd:54:LYS:NZ	83:Sd:55:TYR:O	2.44	0.45
1:1:491:C:H2'	1:1:492:A:C8	2.52	0.45
1:1:766:G:N2	25:LQ:97:ARG:HE	2.15	0.45
1:1:1211:A:H2'	1:1:1212:G:C8	2.52	0.45
1:1:1319:C:H2'	1:1:1320:G:H8	1.82	0.45
1:1:1323:C:H2'	1:1:1324:U:C6	2.52	0.45
1:1:1330:U:OP2	25:LQ:66:ARG:NH1	2.48	0.45
1:1:2947:C:H2'	1:1:2948:U:C6	2.51	0.45
1:1:3179:G:H2'	1:1:3180:G:C8	2.52	0.45
2:2:164:U:HO2'	60:SG:136:LYS:HG3	1.82	0.45
2:2:278:G:H2'	2:2:279:C:C6	2.51	0.45
2:2:1229:U:H2'	2:2:1230:G:C8	2.52	0.45
5:A:99:ARG:HD2	5:A:99:ARG:HA	1.76	0.45
11:LC:344:VAL:HG11	14:LF:62:ARG:HH11	1.81	0.45
43:Li:88:THR:HG23	43:Li:91:ARG:H	1.81	0.45
47:Lm:111:ARG:HG3	47:Lm:112:LYS:HD3	1.97	0.45
54:SA:60:LEU:CD2	54:SA:179:MET:HE3	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
73:ST:114:LEU:HD13	73:ST:123:ARG:HB3	1.98	0.45
74:SU:55:MET:HG2	74:SU:85:LYS:HB3	1.97	0.45
75:SV:4:ASP:C	75:SV:5:ARG:HD2	2.42	0.45
82:Sc:23:ARG:NE	82:Sc:23:ARG:HA	2.30	0.45
1:1:921:U:OP2	35:La:26:ARG:NH2	2.40	0.45
1:1:1739:C:H2'	1:1:1740:A:H8	1.81	0.45
1:1:2058:A:H2'	1:1:2059:A:H8	1.80	0.45
1:1:2320:A:H2'	1:1:2321:A:C8	2.51	0.45
1:1:2704:G:N2	1:1:2707:A:OP2	2.43	0.45
1:1:2849:A:O2'	1:1:2892:A:N3	2.41	0.45
2:2:706:C:H2'	2:2:707:A:H8	1.80	0.45
2:2:870:G:N2	2:2:1045:G:H4'	2.32	0.45
5:A:108:VAL:HG12	5:A:124:SER:HB2	1.99	0.45
7:C:239:PHE:HB2	7:C:270:LYS:HE2	1.98	0.45
9:LA:44:ILE:HG12	9:LA:87:PHE:HE1	1.81	0.45
9:LA:90:ALA:HA	9:LA:101:ILE:O	2.17	0.45
11:LC:360:GLU:O	11:LC:364:GLU:HB3	2.17	0.45
22:LN:118:SER:HA	22:LN:131:GLU:O	2.17	0.45
37:Lc:37:LEU:HD11	37:Lc:66:SER:OG	2.17	0.45
58:SE:6:LYS:O	58:SE:7:LYS:HE2	2.16	0.45
62:SI:175:SER:OG	62:SI:176:ARG:N	2.50	0.45
69:SP:47:ALA:HB1	69:SP:51:ARG:HH21	1.81	0.45
72:SS:88:ARG:HD3	72:SS:108:LYS:NZ	2.32	0.45
78:SY:5:ASP:CG	78:SY:6:SER:H	2.25	0.45
1:1:171:G:H2'	1:1:172:G:H8	1.81	0.45
1:1:478:G:H2'	1:1:479:G:C8	2.52	0.45
1:1:2615:A:C8	1:1:2617:G:C8	3.05	0.45
1:1:3244:G:O2'	1:1:3246:A:N6	2.45	0.45
2:2:102:A:H4'	2:2:103:A:O5'	2.16	0.45
2:2:204:U:H2'	2:2:205:A:C8	2.51	0.45
2:2:563:C:O2'	84:Se:10:ARG:HD3	2.17	0.45
2:2:786:A:C4	58:SE:19:LEU:HD11	2.52	0.45
2:2:1094:U:H4'	2:2:1095:U:O5'	2.16	0.45
2:2:1492:U:H4'	2:2:1515:U:O2'	2.17	0.45
2:2:1602:C:H2'	2:2:1603:G:H8	1.80	0.45
7:C:98:TRP:HD1	7:C:99:LYS:NZ	2.14	0.45
7:C:270:LYS:HE3	7:C:270:LYS:HB3	1.62	0.45
7:C:303:LYS:HA	7:C:306:LYS:NZ	2.32	0.45
7:C:316:LYS:HA	7:C:319:GLU:OE1	2.16	0.45
9:LA:79:ASN:HD22	9:LA:168:ILE:C	2.24	0.45
10:LB:133:TYR:O	10:LB:136:LYS:HG2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:LD:194:ASP:O	12:LD:195:THR:OG1	2.28	0.45
12:LD:238:SER:HA	12:LD:241:GLU:OE2	2.16	0.45
13:LE:8:LYS:HG3	13:LE:20:PRO:HD3	1.98	0.45
28:LT:79:ARG:HG2	28:LT:79:ARG:NH1	2.31	0.45
38:Ld:31:VAL:HG23	38:Ld:36:ARG:HG2	1.99	0.45
56:SC:82:PRO:HG2	56:SC:83:LYS:NZ	2.32	0.45
59:SF:63:ARG:HH12	70:SQ:122:ARG:HD3	1.82	0.45
59:SF:173:ASN:HD22	59:SF:175:LYS:HZ2	1.65	0.45
61:SH:66:ILE:HB	61:SH:98:ILE:HD13	1.99	0.45
62:SI:65:PHE:HA	62:SI:185:GLY:O	2.16	0.45
63:SJ:10:TYR:CD1	63:SJ:38:ARG:HD2	2.51	0.45
67:SN:11:ILE:O	67:SN:11:ILE:HG22	2.17	0.45
68:SO:128:ILE:HG21	80:Sa:44:MET:HG3	1.97	0.45
77:SX:49:ALA:O	77:SX:103:LEU:HD12	2.17	0.45
1:1:1630:G:H2'	1:1:1631:C:C6	2.52	0.45
1:1:2514:U:O2'	41:Lg:92:ARG:NH1	2.49	0.45
1:1:3224:C:H2'	1:1:3225:G:C8	2.52	0.45
2:2:646:C:H2'	2:2:647:C:C6	2.51	0.45
2:2:903:A:O5'	68:SO:65:ARG:NH1	2.50	0.45
2:2:1211:U:H2'	2:2:1212:C:C6	2.52	0.45
2:2:1669:G:H2'	2:2:1670:C:C6	2.52	0.45
6:B:141:ILE:HD11	56:SC:89:MET:HE1	1.99	0.45
10:LB:10:ARG:NH2	10:LB:264:THR:O	2.49	0.45
13:LE:11:GLY:O	13:LE:12:LYS:HE2	2.17	0.45
17:LI:115:MET:O	17:LI:118:ALA:HB2	2.17	0.45
54:SA:150:CYS:SG	54:SA:162:ALA:HB1	2.57	0.45
55:SB:181:LEU:HA	55:SB:184:LEU:HG	1.99	0.45
61:SH:33:LEU:HA	61:SH:36:ASN:CG	2.42	0.45
68:SO:57:GLY:O	68:SO:61:VAL:HG12	2.17	0.45
69:SP:42:ARG:HH21	69:SP:45:LEU:HD12	1.82	0.45
69:SP:115:ILE:HD12	69:SP:119:MET:HE3	1.98	0.45
70:SQ:97:VAL:HG12	70:SQ:98:ASP:N	2.31	0.45
71:SR:98:GLU:HG2	71:SR:99:THR:N	2.31	0.45
73:ST:119:GLU:OE2	73:ST:120:ARG:NE	2.47	0.45
1:1:96:A:H5''	35:La:34:MET:CB	2.47	0.45
1:1:100:A:H1'	1:1:274:G:N7	2.31	0.45
1:1:1017:U:H2'	1:1:1018:C:H6	1.82	0.45
1:1:1643:C:H2'	1:1:1644:G:C8	2.52	0.45
2:2:122:G:O2'	58:SE:145:ARG:NH1	2.30	0.45
2:2:1248:U:HO2'	2:2:1249:C:H6	1.61	0.45
2:2:1377:U:H2'	2:2:1378:U:C6	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:B:139:GLU:OE1	6:B:139:GLU:N	2.50	0.45
8:D:250:ILE:HD11	8:D:278:ARG:HA	1.98	0.45
10:LB:92:TYR:CE1	10:LB:101:SER:HB3	2.52	0.45
14:LF:227:HIS:N	14:LF:230:GLU:OE2	2.41	0.45
41:Lg:109:GLN:HG2	41:Lg:110:SER:N	2.32	0.45
52:Ls:175:MET:SD	52:Ls:175:MET:N	2.87	0.45
58:SE:65:MET:HG3	58:SE:68:ARG:HH21	1.82	0.45
66:SM:71:GLU:O	66:SM:75:LYS:HG2	2.17	0.45
70:SQ:9:VAL:HG11	70:SQ:88:SER:HB3	1.99	0.45
82:Sc:32:GLU:CD	82:Sc:34:MET:H	2.25	0.45
1:1:1067:A:H2'	1:1:1068:A:C8	2.52	0.44
1:1:1345:G:H2'	1:1:1346:A:C8	2.52	0.44
1:1:1796:A:O2'	1:1:1797:A:OP1	2.33	0.44
2:2:5:U:O2'	2:2:550:G:H4'	2.17	0.44
2:2:301:U:OP1	65:SL:141:ARG:NH1	2.50	0.44
2:2:447:C:H2'	2:2:448:G:C8	2.51	0.44
2:2:650:C:H2'	2:2:651:C:C6	2.52	0.44
2:2:1244:U:C2	2:2:1245:C:C5	3.05	0.44
3:3:3:A:H2'	3:3:4:U:H6	1.83	0.44
5:A:59:LEU:HD23	5:A:90:TRP:CZ3	2.52	0.44
7:C:115:ARG:HA	7:C:115:ARG:NE	2.32	0.44
8:D:359:ARG:C	8:D:359:ARG:HD3	2.42	0.44
13:LE:141:ALA:HA	13:LE:144:LYS:HZ3	1.80	0.44
14:LF:48:GLN:HB3	14:LF:52:LYS:NZ	2.32	0.44
21:LM:98:ASN:HA	21:LM:101:LYS:HG2	1.99	0.44
31:LW:86:SER:O	31:LW:90:ILE:HD12	2.17	0.44
32:LX:97:PHE:HE2	32:LX:112:LEU:HD21	1.83	0.44
51:Lq:139:ARG:HB3	51:Lq:140:ARG:NH2	2.32	0.44
54:SA:61:VAL:O	54:SA:65:ARG:HG3	2.17	0.44
57:SD:121:ALA:O	57:SD:125:VAL:HG23	2.16	0.44
61:SH:175:ARG:O	61:SH:178:THR:OG1	2.27	0.44
62:SI:48:THR:OG1	62:SI:49:ARG:N	2.50	0.44
63:SJ:114:LEU:HD12	63:SJ:114:LEU:O	2.17	0.44
74:SU:20:ARG:HD2	74:SU:87:LEU:HD21	1.98	0.44
77:SX:38:TYR:HD2	77:SX:39:LYS:HE2	1.82	0.44
1:1:766:G:C8	25:LQ:93:SER:HB2	2.52	0.44
1:1:948:U:H2'	1:1:949:A:H8	1.82	0.44
1:1:1203:U:O5'	1:1:1205:G:H5'	2.18	0.44
1:1:1769:G:H2'	1:1:1770:U:H6	1.82	0.44
2:2:1560:U:H2'	2:2:1561:C:C6	2.52	0.44
5:A:156:PHE:CD1	5:A:165:ILE:HG22	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:LE:28:TYR:OH	51:Lq:116:SER:HB3	2.17	0.44
13:LE:33:GLU:OE2	13:LE:35:GLN:NE2	2.50	0.44
38:Ld:28:LEU:HD11	38:Ld:40:ALA:HB2	1.99	0.44
41:Lg:102:VAL:HA	41:Lg:105:VAL:HG12	1.99	0.44
56:SC:105:ARG:HG3	56:SC:105:ARG:NH1	2.31	0.44
58:SE:182:MET:O	58:SE:226:PHE:N	2.49	0.44
59:SF:86:MET:HE1	59:SF:164:THR:HA	1.99	0.44
62:SI:29:LEU:H	62:SI:29:LEU:HD23	1.83	0.44
67:SN:117:LEU:O	67:SN:121:ARG:HG3	2.17	0.44
72:SS:50:ALA:HA	72:SS:68:ARG:NH1	2.32	0.44
76:SW:33:VAL:O	76:SW:37:PHE:HB2	2.17	0.44
79:SZ:35:THR:O	79:SZ:38:LYS:HG2	2.17	0.44
81:Sb:20:LYS:HG2	81:Sb:21:LEU:HD12	1.98	0.44
84:Se:29:THR:OG1	84:Se:35:LYS:NZ	2.31	0.44
1:1:934:A:C2	1:1:1097:U:H4'	2.52	0.44
1:1:2471:U:H2'	1:1:2472:U:C6	2.52	0.44
1:1:3062:U:H2'	1:1:3063:A:H8	1.82	0.44
2:2:481:C:H2'	2:2:482:A:C8	2.52	0.44
2:2:537:G:N2	2:2:539:A:N7	2.65	0.44
2:2:904:A:OP2	68:SO:65:ARG:HD3	2.18	0.44
2:2:1329:C:O2'	57:SD:165:GLN:NE2	2.49	0.44
2:2:1375:U:H2'	2:2:1376:C:H6	1.82	0.44
2:2:1521:A:H2'	2:2:1522:A:O4'	2.18	0.44
2:2:1531:U:O2'	2:2:1532:G:OP2	2.28	0.44
2:2:1586:G:OP1	73:ST:91:SER:OG	2.35	0.44
4:4:29:U:H5''	20:LL:27:ASP:OD1	2.16	0.44
4:4:77:A:H2'	4:4:78:G:C8	2.52	0.44
9:LA:70:LYS:HG3	9:LA:71:GLN:N	2.32	0.44
17:LI:44:ASP:OD2	17:LI:185:LYS:HE3	2.17	0.44
22:LN:30:TYR:O	22:LN:31:ARG:HG2	2.17	0.44
29:LU:36:VAL:O	29:LU:40:GLU:OE1	2.35	0.44
33:LY:2:LYS:HE3	33:LY:7:VAL:O	2.17	0.44
52:Ls:172:LEU:HA	52:Ls:175:MET:SD	2.58	0.44
58:SE:37:LYS:HB3	58:SE:40:ASP:OD1	2.17	0.44
63:SJ:167:PRO:HB3	63:SJ:171:ARG:HD2	1.98	0.44
81:Sb:7:LEU:HD23	81:Sb:7:LEU:H	1.83	0.44
1:1:77:G:O2'	20:LL:100:ARG:NE	2.49	0.44
1:1:535:U:H2'	1:1:536:C:H5''	1.99	0.44
1:1:2153:U:H2'	1:1:2154:U:C6	2.53	0.44
1:1:3211:U:O4	24:LP:181:ARG:HD2	2.17	0.44
2:2:106:C:H2'	2:2:107:A:H8	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:1020:C:O2'	2:2:1122:A:N1	2.50	0.44
2:2:1039:G:H2'	2:2:1040:G:C8	2.52	0.44
2:2:1224:A:H3'	66:SM:45:ARG:NH2	2.31	0.44
2:2:1388:A:N6	2:2:1403:U:H3	2.04	0.44
4:4:6:U:H2'	4:4:7:U:H6	1.83	0.44
5:A:189:ILE:CD1	57:SD:226:MET:HE3	2.47	0.44
8:D:284:THR:HG22	8:D:295:SER:O	2.17	0.44
10:LB:216:ILE:HD13	10:LB:283:ILE:HD11	1.98	0.44
13:LE:58:LEU:HD13	13:LE:102:VAL:HG13	1.99	0.44
42:Lh:82:PRO:HG2	42:Lh:85:LEU:HD12	1.99	0.44
50:Lp:36:ARG:HH12	50:Lp:48:ARG:NH1	2.14	0.44
54:SA:201:MET:CE	71:SR:85:VAL:HG13	2.47	0.44
57:SD:207:LEU:HD23	57:SD:209:ASP:N	2.31	0.44
62:SI:40:PRO:O	62:SI:59:ARG:NH1	2.50	0.44
62:SI:104:ILE:O	62:SI:168:ARG:HA	2.17	0.44
62:SI:129:GLN:NE2	62:SI:132:VAL:HG11	2.33	0.44
67:SN:60:ILE:HG23	67:SN:66:VAL:HG21	1.98	0.44
73:ST:135:ARG:O	73:ST:139:THR:HG23	2.17	0.44
76:SW:32:LYS:O	76:SW:36:LYS:HG2	2.17	0.44
1:1:1227:A:O5'	1:1:1254:A:O2'	2.34	0.44
1:1:2619:G:OP1	1:1:2709:U:O2'	2.35	0.44
1:1:3292:U:OP1	62:SI:124:ARG:NH1	2.50	0.44
2:2:222:U:O2'	2:2:223:G:OP2	2.33	0.44
2:2:230:G:H2'	2:2:231:G:O4'	2.18	0.44
18:LJ:72:VAL:HG23	18:LJ:76:LYS:HE2	1.99	0.44
26:LR:154:GLN:HA	26:LR:157:GLU:HG2	1.99	0.44
38:Ld:20:TYR:CD1	38:Ld:83:ILE:HD12	2.53	0.44
54:SA:41:TRP:NE1	71:SR:111:LEU:HD11	2.32	0.44
58:SE:23:LEU:HG	58:SE:24:SER:H	1.81	0.44
59:SF:38:ILE:HA	59:SF:118:GLN:HE22	1.83	0.44
72:SS:70:VAL:HG22	72:SS:74:GLN:OE1	2.18	0.44
72:SS:117:LYS:HE2	72:SS:117:LYS:HB2	1.76	0.44
72:SS:132:ARG:NE	72:SS:133:VAL:H	2.16	0.44
1:1:859:C:O2'	1:1:862:G:O2'	2.26	0.44
1:1:2469:U:H2'	1:1:2470:U:H6	1.83	0.44
2:2:283:C:OP1	60:SG:199:ARG:NH1	2.51	0.44
2:2:539:A:O2'	2:2:540:C:H3'	2.17	0.44
2:2:606:U:H1'	77:SX:19:ARG:HH22	1.82	0.44
2:2:642:C:H2'	2:2:643:U:C6	2.52	0.44
2:2:1222:U:H3'	2:2:1223:G:H8	1.83	0.44
2:2:1243:C:H2'	2:2:1244:U:H6	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:1387:U:H5'	71:SR:3:ARG:NH2	2.33	0.44
2:2:1603:G:C2	2:2:1604:U:C5	3.05	0.44
4:4:47:C:O2'	4:4:62:A:OP2	2.35	0.44
10:LB:24:ARG:HH12	10:LB:26:ARG:HH22	1.65	0.44
10:LB:143:ALA:O	10:LB:147:ARG:HG3	2.18	0.44
12:LD:207:VAL:O	12:LD:211:MET:HG3	2.18	0.44
14:LF:104:LYS:HB3	14:LF:105:PRO:HD3	2.00	0.44
22:LN:108:ARG:HH11	22:LN:108:ARG:HG3	1.83	0.44
25:LQ:203:ARG:O	35:La:51:GLY:HA2	2.17	0.44
37:Lc:93:MET:HE3	37:Lc:93:MET:HB2	1.82	0.44
58:SE:10:LYS:O	58:SE:13:SER:OG	2.27	0.44
70:SQ:123:ARG:HG3	70:SQ:124:CYS:H	1.83	0.44
73:ST:39:LYS:HG2	73:ST:41:GLY:O	2.17	0.44
76:SW:34:ILE:O	76:SW:38:LEU:HD13	2.18	0.44
80:Sa:36:ILE:O	80:Sa:72:GLN:HA	2.17	0.44
83:Sd:53:VAL:HG22	83:Sd:54:LYS:N	2.32	0.44
1:1:175:C:H2'	1:1:176:C:C6	2.53	0.44
1:1:528:U:C2	1:1:529:G:C8	3.05	0.44
1:1:650:U:H2'	1:1:651:C:C6	2.53	0.44
1:1:1001:G:H2'	1:1:1002:G:H8	1.80	0.44
1:1:1632:G:H2'	1:1:1633:G:C8	2.52	0.44
1:1:2127:A:OP1	9:LA:8:GLN:NE2	2.46	0.44
1:1:2533:G:O5'	34:LZ:55:ARG:NH2	2.44	0.44
1:1:2854:G:O2'	47:Lm:100:TYR:O	2.36	0.44
1:1:3111:C:N4	1:1:3113:A:H1'	2.33	0.44
2:2:624:C:H5''	67:SN:5:HIS:CD2	2.52	0.44
2:2:835:G:H2'	2:2:836:G:C8	2.53	0.44
2:2:1587:C:H2'	2:2:1588:A:C8	2.50	0.44
2:2:1659:G:H2'	2:2:1660:C:C6	2.53	0.44
8:D:249:LEU:HD21	8:D:316:TYR:CE1	2.53	0.44
9:LA:53:GLY:O	9:LA:192:LYS:HE3	2.18	0.44
14:LF:96:LYS:HB3	14:LF:139:TRP:HD1	1.81	0.44
16:LH:116:ILE:HB	16:LH:126:ARG:HG3	2.00	0.44
22:LN:15:GLN:O	22:LN:15:GLN:HG3	2.17	0.44
22:LN:31:ARG:HB3	22:LN:129:TYR:OH	2.18	0.44
23:LO:123:PRO:HA	23:LO:126:LEU:HD23	2.00	0.44
26:LR:106:LEU:HB3	26:LR:120:TYR:HE1	1.83	0.44
27:LS:109:ASP:OD1	27:LS:113:ARG:NH1	2.48	0.44
28:LT:128:LEU:H	28:LT:128:LEU:HD23	1.83	0.44
51:Lq:139:ARG:HB3	51:Lq:140:ARG:HH22	1.81	0.44
67:SN:28:THR:HG23	67:SN:32:GLN:NE2	2.28	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:Sf:92:LYS:HA	85:Sf:92:LYS:HD2	1.88	0.44
1:1:282:U:H2'	1:1:283:G:H8	1.82	0.44
1:1:439:C:H2'	1:1:440:C:C6	2.53	0.44
1:1:505:G:O2'	11:LC:343:GLU:OE2	2.34	0.44
1:1:2227:U:HO2'	1:1:2228:C:P	2.40	0.44
1:1:3106:C:H2'	1:1:3107:G:H8	1.82	0.44
2:2:184:G:O2'	2:2:185:A:O5'	2.28	0.44
2:2:913:A:N6	68:SO:54:ARG:HH12	2.16	0.44
2:2:959:U:H5''	67:SN:71:ILE:HG21	1.99	0.44
2:2:1065:C:H2'	2:2:1066:G:H8	1.83	0.44
8:D:52:SER:HG	8:D:71:ASN:ND2	2.16	0.44
8:D:62:GLN:HA	8:D:65:LYS:HG2	1.98	0.44
16:LH:105:LYS:HD3	16:LH:105:LYS:HA	1.85	0.44
21:LM:119:LYS:O	21:LM:123:LEU:HD23	2.17	0.44
23:LO:180:LEU:O	23:LO:184:LYS:HG2	2.17	0.44
27:LS:34:GLU:HA	27:LS:37:ALA:HB3	1.99	0.44
35:La:135:GLU:O	35:La:139:LYS:HG2	2.18	0.44
56:SC:61:MET:N	56:SC:61:MET:SD	2.91	0.44
59:SF:76:ILE:HA	59:SF:79:ARG:HH12	1.82	0.44
61:SH:97:LEU:HD23	61:SH:97:LEU:HA	1.82	0.44
73:ST:132:ASP:O	73:ST:136:ILE:HG12	2.18	0.44
84:Se:36:LYS:HA	84:Se:39:THR:HG22	1.99	0.44
1:1:1414:G:OP2	35:La:9:ARG:NH1	2.42	0.44
1:1:2092:U:H2'	1:1:2093:G:C8	2.53	0.44
1:1:2096:U:O4	1:1:2110:A:H2	2.01	0.44
2:2:5:U:H3'	56:SC:213:LYS:NZ	2.33	0.44
2:2:403:U:H2'	2:2:404:A:C8	2.53	0.44
2:2:404:A:H2'	2:2:405:C:C6	2.53	0.44
2:2:761:A:O2'	58:SE:251:ARG:NH2	2.50	0.44
2:2:816:C:O2'	2:2:817:G:H5'	2.18	0.44
2:2:832:G:C4	2:2:833:U:C5	3.06	0.44
6:B:93:PHE:CG	6:B:94:ARG:N	2.86	0.44
7:C:325:LYS:HA	7:C:328:GLU:OE1	2.17	0.44
13:LE:57:VAL:HG12	13:LE:71:VAL:HG22	2.00	0.44
13:LE:118:LYS:HA	13:LE:121:GLU:OE2	2.18	0.44
17:LI:129:VAL:HG11	17:LI:135:LEU:HD21	1.99	0.44
26:LR:78:PHE:HA	26:LR:81:ARG:NH1	2.32	0.44
33:LY:47:ILE:HD12	33:LY:48:PRO:HD2	2.00	0.44
34:LZ:48:TYR:HD2	34:LZ:132:PRO:HB3	1.82	0.44
34:LZ:49:PRO:HD3	34:LZ:67:ILE:HG13	1.99	0.44
54:SA:105:PHE:O	54:SA:106:THR:OG1	2.31	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
66:SM:129:GLU:HB3	66:SM:133:ARG:HH11	1.83	0.44
76:SW:22:LYS:NZ	81:Sb:3:LEU:HD13	2.30	0.44
1:1:410:A:H2'	1:1:411:A:C8	2.53	0.43
1:1:465:G:H2'	1:1:466:G:C8	2.53	0.43
1:1:1158:C:H2'	1:1:1159:C:C6	2.53	0.43
2:2:404:A:H2'	2:2:405:C:H6	1.83	0.43
2:2:550:G:N2	2:2:568:G:N7	2.66	0.43
2:2:696:U:C2	2:2:697:G:C8	3.06	0.43
2:2:1123:G:C5'	48:Ln:11:ARG:HD3	2.46	0.43
2:2:1172:U:H2'	2:2:1173:G:H8	1.81	0.43
2:2:1193:A:H4'	2:2:1194:C:O5'	2.16	0.43
2:2:1226:G:H22	2:2:1252:G:H2'	1.83	0.43
8:D:288:LEU:HD23	8:D:316:TYR:CD2	2.52	0.43
13:LE:61:LEU:HD11	13:LE:103:ILE:HG13	2.00	0.43
14:LF:127:LYS:HB2	28:LT:133:ALA:HB3	2.00	0.43
15:LG:61:LEU:HD21	22:LN:29:GLU:OE1	2.18	0.43
22:LN:104:GLU:HG3	22:LN:108:ARG:NH1	2.33	0.43
24:LP:56:GLU:OE1	24:LP:56:GLU:N	2.51	0.43
32:LX:103:ALA:HA	32:LX:107:GLN:NE2	2.31	0.43
35:La:126:ARG:HG2	35:La:146:GLU:OE2	2.17	0.43
54:SA:59:LYS:NZ	54:SA:164:PRO:HD3	2.33	0.43
57:SD:138:GLU:CD	57:SD:190:LYS:HB2	2.42	0.43
59:SF:67:LYS:HG3	59:SF:68:ARG:N	2.32	0.43
59:SF:90:ASN:HA	59:SF:93:LYS:NZ	2.32	0.43
60:SG:30:LYS:O	60:SG:102:VAL:HG12	2.18	0.43
60:SG:226:LYS:O	60:SG:229:LEU:HG	2.17	0.43
61:SH:80:GLN:NE2	61:SH:98:ILE:HG13	2.33	0.43
64:SK:7:ASP:OD1	64:SK:8:ARG:HG3	2.18	0.43
66:SM:31:LYS:HD2	66:SM:100:TRP:HB3	2.00	0.43
71:SR:104:ILE:HG13	71:SR:124:VAL:HG22	2.01	0.43
71:SR:107:GLU:O	71:SR:111:LEU:HD23	2.17	0.43
73:ST:116:LYS:HD2	73:ST:117:ASP:N	2.27	0.43
79:SZ:33:LYS:HA	79:SZ:33:LYS:HD3	1.70	0.43
1:1:54:G:P	44:Lj:48:ASN:HB2	2.58	0.43
1:1:401:A:N3	1:1:643:C:O2'	2.50	0.43
1:1:644:A:H2'	1:1:645:A:C8	2.53	0.43
1:1:669:U:O2'	1:1:685:G:O6	2.35	0.43
1:1:2471:U:H2'	1:1:2472:U:H6	1.83	0.43
2:2:222:U:HO2'	2:2:223:G:P	2.41	0.43
2:2:1245:C:H2'	2:2:1246:U:H6	1.81	0.43
2:2:1246:U:H2'	2:2:1247:U:C6	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:1791:U:H3'	80:Sa:5:ARG:HH21	1.83	0.43
4:4:82:U:H5'	4:4:83:C:H5'	2.00	0.43
7:C:228:ASN:ND2	38:Ld:11:ALA:HB3	2.34	0.43
10:LB:45:ALA:HB3	10:LB:182:ILE:HG12	2.00	0.43
10:LB:181:GLU:OE1	10:LB:181:GLU:N	2.50	0.43
13:LE:159:ALA:O	13:LE:163:LYS:HG3	2.18	0.43
16:LH:24:LEU:HD12	16:LH:36:LYS:O	2.19	0.43
24:LP:14:SER:HB2	24:LP:150:LEU:O	2.19	0.43
27:LS:81:TYR:CE1	27:LS:90:MET:HE3	2.53	0.43
42:Lh:49:ILE:HG13	42:Lh:50:HIS:N	2.34	0.43
58:SE:73:ASP:HA	58:SE:164:LEU:HD11	1.98	0.43
81:Sb:20:LYS:CG	81:Sb:21:LEU:HD12	2.48	0.43
84:Se:20:LYS:NZ	84:Se:22:GLU:HG3	2.33	0.43
1:1:967:U:H2'	1:1:968:U:H6	1.83	0.43
1:1:1599:A:H5'	48:Lr:15:ARG:CZ	2.48	0.43
1:1:1919:G:H5''	26:LR:80:LYS:HE2	1.99	0.43
1:1:2633:A:N1	18:LJ:125:GLY:HA3	2.33	0.43
1:1:2636:G:H2'	1:1:2636:G:N3	2.33	0.43
1:1:2642:U:H2'	1:1:2643:C:H6	1.83	0.43
1:1:2727:U:H2'	1:1:2728:A:H8	1.83	0.43
1:1:3005:U:O2'	1:1:3006:A:H5'	2.19	0.43
2:2:138:A:H62	60:SG:187:LEU:HD12	1.83	0.43
2:2:282:G:H2'	2:2:283:C:C6	2.54	0.43
2:2:882:A:H2'	2:2:883:G:C8	2.53	0.43
2:2:1301:G:OP2	2:2:1302:U:O2'	2.24	0.43
2:2:1398:G:P	71:SR:5:ARG:HH11	2.41	0.43
5:A:161:GLN:HG2	5:A:162:ASN:N	2.33	0.43
7:C:239:PHE:HB2	7:C:270:LYS:CE	2.49	0.43
11:LC:233:GLU:CD	11:LC:253:ARG:HH22	2.26	0.43
18:LJ:33:ARG:O	18:LJ:37:VAL:HG23	2.18	0.43
20:LL:29:PRO:O	20:LL:33:VAL:HG23	2.17	0.43
25:LQ:90:VAL:HG21	25:LQ:110:VAL:HG21	2.00	0.43
37:Lc:30:TYR:CE2	37:Lc:55:ARG:HD2	2.54	0.43
52:Ls:5:SER:HB3	52:Ls:8:LYS:HE3	2.00	0.43
66:SM:45:ARG:HB2	66:SM:118:CYS:SG	2.59	0.43
70:SQ:55:LEU:HD22	70:SQ:105:LEU:HD13	1.99	0.43
72:SS:140:THR:O	72:SS:140:THR:HG22	2.18	0.43
84:Se:29:THR:OG1	84:Se:30:PRO:HD3	2.18	0.43
85:Sf:120:GLU:OE2	85:Sf:123:ASN:ND2	2.48	0.43
1:1:985:A:N1	1:1:1032:C:O2'	2.51	0.43
1:1:1243:A:H1'	1:1:1263:C:H1'	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1299:C:OP2	23:LO:132:GLN:HG2	2.19	0.43
1:1:2166:U:H2'	1:1:2167:C:C6	2.53	0.43
1:1:2570:U:H2'	1:1:2571:U:C6	2.54	0.43
2:2:487:U:H2'	2:2:488:C:C6	2.53	0.43
2:2:512:A:H2'	2:2:513:G:O4'	2.19	0.43
2:2:695:C:H2'	2:2:696:U:C6	2.53	0.43
2:2:962:U:H5'	67:SN:128:TYR:OH	2.18	0.43
2:2:1161:G:O2'	2:2:1608:U:O2	2.36	0.43
2:2:1473:A:H2'	2:2:1474:G:C8	2.53	0.43
3:3:108:C:H2'	3:3:109:G:C8	2.52	0.43
4:4:6:U:H2'	4:4:7:U:C6	2.54	0.43
4:4:26:U:H2'	4:4:27:U:C6	2.53	0.43
5:A:281:SER:OG	5:A:282:ARG:N	2.49	0.43
7:C:148:PHE:CE2	7:C:152:ILE:HD11	2.53	0.43
11:LC:332:TYR:CE2	14:LF:58:VAL:HG11	2.53	0.43
12:LD:34:LYS:HE2	28:LT:30:TYR:CE2	2.54	0.43
14:LF:7:PRO:HB3	51:Lq:92:LYS:HD2	2.00	0.43
15:LG:207:ARG:HD2	15:LG:209:GLU:HG2	2.01	0.43
18:LJ:85:LEU:HD12	18:LJ:168:PHE:HD2	1.83	0.43
28:LT:107:ARG:HD2	28:LT:107:ARG:C	2.42	0.43
29:LU:87:THR:O	29:LU:91:LEU:HD23	2.17	0.43
34:LZ:7:SER:OG	34:LZ:86:LEU:O	2.34	0.43
37:Lc:43:LYS:HZ1	37:Lc:97:ASP:HA	1.83	0.43
45:Lk:12:ILE:O	45:Lk:16:ARG:HG2	2.18	0.43
54:SA:155:PRO:HB2	54:SA:157:GLU:OE1	2.19	0.43
58:SE:141:THR:CG2	58:SE:145:ARG:HB2	2.48	0.43
58:SE:183:ILE:HG22	58:SE:189:MET:HE1	2.00	0.43
59:SF:141:THR:HG22	59:SF:142:VAL:H	1.84	0.43
63:SJ:42:ARG:O	63:SJ:46:THR:HG23	2.18	0.43
68:SO:95:LYS:HE2	68:SO:131:VAL:HG21	2.01	0.43
72:SS:15:LEU:HB2	72:SS:22:VAL:CG2	2.49	0.43
73:ST:32:PRO:HG2	73:ST:34:TRP:HD1	1.83	0.43
78:SY:21:LEU:HD12	78:SY:88:PHE:CE2	2.54	0.43
80:Sa:4:LYS:HE2	80:Sa:5:ARG:NH1	2.34	0.43
1:1:300:A:H2'	1:1:301:A:C8	2.53	0.43
1:1:702:G:C4	35:La:113:LEU:HD21	2.54	0.43
1:1:1599:A:C5'	48:Lr:15:ARG:NH2	2.81	0.43
1:1:2556:U:H2'	1:1:2557:G:H8	1.82	0.43
2:2:1217:C:H2'	2:2:1218:A:C8	2.53	0.43
2:2:1473:A:H2'	2:2:1474:G:H8	1.84	0.43
2:2:1534:U:O2'	2:2:1535:G:N2	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:1736:G:H2'	2:2:1737:U:C6	2.54	0.43
7:C:219:THR:O	7:C:223:VAL:HG13	2.18	0.43
13:LE:118:LYS:HD3	13:LE:121:GLU:OE2	2.19	0.43
20:LL:107:GLU:OE1	20:LL:107:GLU:N	2.50	0.43
52:Ls:15:LEU:HB3	52:Ls:60:ARG:NH2	2.24	0.43
54:SA:108:GLY:HA2	54:SA:111:THR:HG22	2.00	0.43
59:SF:115:ASN:OD1	59:SF:116:PRO:HD2	2.18	0.43
67:SN:46:THR:OG1	67:SN:47:PRO:HD2	2.19	0.43
81:Sb:19:HIS:CE1	81:Sb:21:LEU:HD13	2.51	0.43
83:Sd:22:ARG:HB2	83:Sd:38:ILE:HG12	1.99	0.43
1:1:145:U:P	22:LN:49:ARG:HH22	2.41	0.43
1:1:1244:G:OP2	1:1:1244:G:N2	2.41	0.43
1:1:2470:U:H2'	1:1:2471:U:H6	1.84	0.43
1:1:2544:G:C8	15:LG:51:ARG:HG3	2.52	0.43
2:2:194:G:H2'	2:2:195:G:H8	1.83	0.43
2:2:1040:G:H22	2:2:1073:A:H2	1.66	0.43
2:2:1199:A:H1'	2:2:1204:C:N4	2.33	0.43
2:2:1389:U:H5''	5:A:282:ARG:HH22	1.84	0.43
7:C:154:LYS:O	7:C:158:ILE:HG13	2.19	0.43
7:C:265:ASN:HD22	7:C:269:LYS:NZ	2.16	0.43
10:LB:180:MET:HE2	10:LB:182:ILE:HD11	2.00	0.43
12:LD:106:ALA:O	12:LD:110:LEU:HD23	2.19	0.43
16:LH:154:GLU:HG2	16:LH:155:ALA:N	2.33	0.43
17:LI:78:LYS:HE2	17:LI:79:TYR:CE1	2.53	0.43
18:LJ:165:LYS:NZ	18:LJ:171:ILE:HA	2.34	0.43
22:LN:172:ARG:HB2	22:LN:174:LEU:HD13	2.01	0.43
24:LP:91:LEU:HD23	24:LP:91:LEU:HA	1.86	0.43
24:LP:114:ILE:HD13	24:LP:150:LEU:CD2	2.48	0.43
32:LX:128:ARG:HD3	32:LX:134:LYS:HE2	2.01	0.43
35:La:82:VAL:HG13	35:La:87:ARG:HB3	2.00	0.43
67:SN:46:THR:OG1	67:SN:86:GLU:OE1	2.28	0.43
71:SR:23:ARG:HD2	71:SR:23:ARG:C	2.43	0.43
1:1:191:G:H21	1:1:212:G:H21	1.67	0.43
1:1:250:C:H2'	1:1:251:U:H6	1.84	0.43
1:1:301:A:H1'	1:1:2185:A:C2	2.54	0.43
1:1:539:G:H2'	1:1:540:G:H8	1.83	0.43
1:1:2633:A:C6	18:LJ:125:GLY:HA3	2.54	0.43
1:1:3163:A:H4'	1:1:3164:G:O5'	2.19	0.43
2:2:1375:U:H2'	2:2:1376:C:C6	2.53	0.43
5:A:94:THR:HG23	5:A:96:THR:HG23	2.01	0.43
5:A:239:LEU:HD13	5:A:250:ALA:HB2	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:LB:20:LYS:HZ3	10:LB:270:GLN:HB3	1.84	0.43
11:LC:345:LYS:HE2	11:LC:345:LYS:HB3	1.78	0.43
12:LD:245:GLU:OE2	12:LD:249:GLN:NE2	2.50	0.43
18:LJ:38:LEU:HD23	18:LJ:38:LEU:HA	1.83	0.43
18:LJ:119:PRO:HD3	72:SS:14:ILE:HG13	2.01	0.43
35:La:79:TRP:O	35:La:82:VAL:HG12	2.19	0.43
39:Le:6:LYS:HB3	39:Le:6:LYS:HE2	1.84	0.43
56:SC:89:MET:HE3	56:SC:111:LEU:CD2	2.49	0.43
57:SD:11:LYS:HG3	83:Sd:34:TYR:HE1	1.83	0.43
57:SD:43:ARG:NH2	74:SU:104:ILE:HG23	2.33	0.43
58:SE:11:ARG:O	58:SE:12:LEU:HB2	2.19	0.43
61:SH:9:ILE:HD11	61:SH:16:ARG:HA	2.00	0.43
67:SN:52:VAL:HG23	67:SN:55:ARG:NH2	2.34	0.43
68:SO:112:GLN:NE2	80:Sa:44:MET:O	2.51	0.43
70:SQ:13:LYS:HG3	70:SQ:14:LYS:H	1.84	0.43
70:SQ:32:ASN:OD1	70:SQ:69:VAL:HG12	2.19	0.43
72:SS:127:HIS:CG	72:SS:133:VAL:HG11	2.54	0.43
76:SW:36:LYS:HG3	76:SW:110:ILE:HD11	2.00	0.43
76:SW:77:PRO:HG2	76:SW:79:TYR:CE2	2.53	0.43
77:SX:17:ASN:HA	77:SX:20:ARG:HH21	1.83	0.43
1:1:1159:C:H4'	23:LO:91:PRO:HD3	2.00	0.43
2:2:792:U:H1'	2:2:793:U:OP2	2.18	0.43
2:2:1214:A:H4'	2:2:1215:G:OP2	2.19	0.43
5:A:68:ASP:OD1	5:A:69:CYS:N	2.52	0.43
8:D:14:VAL:O	8:D:152:SER:N	2.51	0.43
8:D:373:ARG:HE	8:D:374:ILE:N	2.16	0.43
10:LB:167:ILE:O	10:LB:170:THR:HG22	2.18	0.43
10:LB:167:ILE:HG13	10:LB:177:ALA:HA	2.00	0.43
17:LI:50:VAL:HG12	17:LI:167:VAL:HG22	1.99	0.43
24:LP:165:ARG:NH2	51:Lq:138:ALA:HA	2.33	0.43
27:LS:36:VAL:O	27:LS:40:ARG:HG2	2.19	0.43
38:Ld:37:ALA:HB2	38:Ld:72:ILE:HA	2.01	0.43
41:Lg:104:LYS:HE2	41:Lg:104:LYS:HB3	1.83	0.43
45:Lk:71:VAL:HG13	45:Lk:71:VAL:O	2.19	0.43
55:SB:129:THR:HB	55:SB:179:CYS:O	2.19	0.43
58:SE:98:ASN:O	58:SE:114:ILE:HG22	2.18	0.43
58:SE:257:ARG:NH1	58:SE:258:ALA:HB2	2.34	0.43
61:SH:176:LEU:HD13	61:SH:193:PHE:O	2.18	0.43
62:SI:45:ILE:HD11	62:SI:53:HIS:HB3	1.99	0.43
62:SI:66:ALA:H	62:SI:186:TYR:HA	1.83	0.43
70:SQ:97:VAL:HG12	70:SQ:98:ASP:OD1	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:SQ:127:LYS:HD3	70:SQ:129:PHE:H	1.84	0.43
72:SS:125:LEU:HB3	72:SS:129:TRP:CZ3	2.54	0.43
73:ST:29:LEU:HD22	73:ST:54:TRP:CZ2	2.52	0.43
77:SX:136:TRP:CZ2	84:Se:15:LYS:HD2	2.53	0.43
82:Sc:9:LYS:NZ	82:Sc:57:LEU:HD23	2.34	0.43
1:1:346:G:N7	44:Lj:55:ARG:HD2	2.34	0.43
1:1:961:C:OP1	1:1:962:U:H1'	2.19	0.43
1:1:2900:A:OP2	1:1:2900:A:H8	2.02	0.43
2:2:352:G:O2'	2:2:353:G:OP1	2.33	0.43
2:2:643:U:H3	2:2:683:G:H1	1.66	0.43
2:2:834:U:C2	2:2:835:G:C8	3.07	0.43
2:2:988:C:H2'	2:2:989:G:O4'	2.19	0.43
3:3:12:U:OP2	3:3:68:C:O2'	2.37	0.43
4:4:139:U:H2'	4:4:140:G:H8	1.83	0.43
5:A:40:LEU:HB2	5:A:59:LEU:HD22	1.99	0.43
7:C:425:GLU:HG3	7:C:429:ARG:NE	2.34	0.43
10:LB:19:ARG:O	10:LB:274:HIS:HE1	2.01	0.43
10:LB:47:MET:HG2	10:LB:84:MET:HE1	2.00	0.43
12:LD:99:TYR:OH	12:LD:171:ASP:OD2	2.30	0.43
17:LI:171:TRP:HE3	17:LI:178:ARG:HG3	1.84	0.43
26:LR:45:VAL:HG23	26:LR:50:ILE:O	2.19	0.43
30:LV:138:VAL:HG12	30:LV:139:MET:SD	2.59	0.43
51:Lq:35:LEU:O	51:Lq:36:THR:OG1	2.31	0.43
51:Lq:55:VAL:HG13	51:Lq:62:LYS:HB3	2.01	0.43
54:SA:123:LEU:O	54:SA:124:ILE:HD13	2.19	0.43
59:SF:94:LYS:O	59:SF:98:VAL:HG23	2.18	0.43
60:SG:32:MET:HE3	60:SG:65:GLN:HB2	2.01	0.43
62:SI:192:GLU:OE2	62:SI:196:TYR:HE2	2.02	0.43
66:SM:47:LEU:HD13	66:SM:73:TYR:CE1	2.54	0.43
67:SN:9:LYS:HE3	67:SN:9:LYS:HB3	1.77	0.43
77:SX:109:ARG:HG3	77:SX:112:LYS:CG	2.45	0.43
1:1:441:G:H2'	1:1:442:G:H8	1.84	0.43
1:1:1610:G:H1	1:1:1792:G:H2'	1.84	0.43
2:2:443:A:H5''	58:SE:57:ASN:HD22	1.84	0.43
2:2:1209:G:H2'	2:2:1210:G:H8	1.83	0.43
2:2:1560:U:H2'	2:2:1561:C:H6	1.84	0.43
2:2:1588:A:H2'	2:2:1589:A:C8	2.54	0.43
4:4:5:U:H2'	4:4:6:U:H6	1.84	0.43
5:A:200:ILE:HG22	5:A:207:CYS:SG	2.59	0.43
8:D:314:LEU:O	8:D:318:THR:HG23	2.19	0.43
9:LA:24:LYS:HD3	9:LA:24:LYS:HA	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:LC:343:GLU:O	11:LC:343:GLU:HG3	2.18	0.43
15:LG:99:LYS:C	15:LG:100:TYR:HD1	2.26	0.43
17:LI:140:THR:OG1	17:LI:141:ARG:N	2.52	0.43
29:LU:19:LYS:HD3	29:LU:21:PHE:CZ	2.54	0.43
37:Lc:79:GLU:OE1	37:Lc:79:GLU:N	2.41	0.43
49:Lo:23:HIS:HA	49:Lo:73:GLU:O	2.19	0.43
50:Lp:11:SER:HB3	50:Lp:27:LYS:HB2	2.00	0.43
54:SA:52:ASN:HD22	54:SA:55:LYS:HZ2	1.67	0.43
58:SE:97:GLU:N	58:SE:97:GLU:OE1	2.52	0.43
58:SE:251:ARG:HH11	58:SE:254:ARG:HH22	1.65	0.43
60:SG:192:HIS:HE1	60:SG:196:LEU:HD21	1.84	0.43
61:SH:131:VAL:O	61:SH:135:ILE:HG13	2.19	0.43
63:SJ:108:GLN:OE1	63:SJ:127:ILE:HD12	2.19	0.43
67:SN:99:ARG:O	67:SN:103:GLU:OE1	2.35	0.43
72:SS:88:ARG:HB3	72:SS:98:SER:HB2	2.01	0.43
73:ST:105:MET:HE1	73:ST:123:ARG:HD3	2.00	0.43
74:SU:85:LYS:HZ3	74:SU:87:LEU:HB2	1.83	0.43
75:SV:62:MET:HB2	75:SV:64:GLU:OE1	2.19	0.43
81:Sb:2:VAL:O	81:Sb:3:LEU:HB2	2.19	0.43
1:1:585:C:P	1:1:597:G:H1	2.42	0.42
1:1:911:A:H1'	44:Lj:49:TRP:CE3	2.54	0.42
1:1:2535:G:H2'	1:1:2536:C:C6	2.55	0.42
2:2:96:C:H2'	2:2:97:U:C6	2.54	0.42
2:2:209:G:H21	2:2:248:A:H62	1.67	0.42
2:2:508:A:O3'	63:SJ:171:ARG:NH2	2.52	0.42
2:2:1521:A:O2'	2:2:1585:C:O2'	2.33	0.42
2:2:1589:A:H2'	2:2:1590:G:H8	1.83	0.42
3:3:39:C:C6	18:LJ:47:VAL:HG21	2.54	0.42
5:A:308:ARG:HD3	5:A:308:ARG:HA	1.84	0.42
8:D:29:HIS:CG	8:D:30:THR:H	2.37	0.42
12:LD:93:THR:O	12:LD:93:THR:HG22	2.19	0.42
18:LJ:144:ARG:NH1	18:LJ:145:CYS:HB2	2.34	0.42
31:LW:108:ALA:HA	31:LW:111:GLU:OE2	2.19	0.42
33:LY:116:ASN:O	33:LY:120:ARG:HG3	2.19	0.42
37:Lc:57:SER:OG	41:Lg:95:LEU:HD23	2.19	0.42
38:Ld:62:GLN:OE1	38:Ld:62:GLN:HA	2.18	0.42
50:Lp:89:ILE:HG13	50:Lp:90:THR:N	2.34	0.42
54:SA:135:ALA:HA	54:SA:138:GLU:OE2	2.19	0.42
55:SB:11:LYS:NZ	55:SB:16:LEU:O	2.51	0.42
56:SC:87:GLU:O	56:SC:111:LEU:HD23	2.18	0.42
57:SD:15:VAL:HB	83:Sd:34:TYR:CE2	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:SG:64:LYS:HZ2	60:SG:82:SER:N	2.14	0.42
62:SI:201:HIS:ND1	62:SI:201:HIS:O	2.52	0.42
64:SK:46:SER:O	64:SK:49:SER:OG	2.33	0.42
66:SM:57:ARG:N	66:SM:57:ARG:HD2	2.34	0.42
68:SO:56:THR:HG22	68:SO:59:MET:HE1	2.01	0.42
75:SV:3:ASN:OD1	75:SV:6:GLY:N	2.52	0.42
79:SZ:86:LYS:HE3	79:SZ:87:MET:HE1	2.01	0.42
1:1:383:G:H3'	1:1:384:G:H8	1.84	0.42
1:1:1004:C:H2'	1:1:1005:G:H8	1.85	0.42
1:1:1092:A:H2'	1:1:1093:C:C6	2.54	0.42
1:1:1129:C:H2'	1:1:1130:G:H8	1.85	0.42
1:1:2392:G:H2'	1:1:2393:A:H8	1.83	0.42
2:2:529:U:OP1	63:SJ:130:ARG:NH2	2.52	0.42
2:2:1205:A:H5''	2:2:1206:C:OP2	2.18	0.42
5:A:5:LEU:HB2	5:A:270:LEU:HD11	2.01	0.42
7:C:220:ARG:HA	7:C:223:VAL:HG22	2.01	0.42
7:C:279:ARG:CZ	7:C:279:ARG:HB3	2.50	0.42
10:LB:307:THR:HG21	10:LB:317:GLU:HG2	2.01	0.42
14:LF:227:HIS:CE1	14:LF:229:ILE:HG12	2.53	0.42
17:LI:191:ARG:NH2	17:LI:212:ARG:HD2	2.34	0.42
22:LN:66:VAL:HG12	22:LN:67:ARG:H	1.85	0.42
52:Ls:35:SER:O	52:Ls:38:MET:HG3	2.19	0.42
52:Ls:65:THR:HG21	52:Ls:77:LEU:HD21	2.00	0.42
54:SA:41:TRP:HE1	54:SA:52:ASN:HD22	1.67	0.42
58:SE:115:THR:O	58:SE:119:ALA:CB	2.67	0.42
59:SF:57:ILE:HG13	59:SF:58:PRO:HD2	2.01	0.42
61:SH:99:LEU:HD11	61:SH:139:LEU:CD1	2.49	0.42
67:SN:110:ASP:OD1	67:SN:111:SER:N	2.52	0.42
70:SQ:86:ALA:HB2	70:SQ:116:LEU:HD12	2.00	0.42
1:1:250:C:H2'	1:1:251:U:C6	2.54	0.42
1:1:1600:U:H2'	1:1:1601:G:C8	2.55	0.42
1:1:1670:C:H2'	1:1:1671:U:C6	2.54	0.42
1:1:1740:A:H2'	1:1:1740:A:N3	2.34	0.42
1:1:2461:C:H2'	1:1:2462:U:C6	2.54	0.42
1:1:2478:A:O3'	22:LN:31:ARG:NH2	2.53	0.42
2:2:390:C:HO2'	60:SG:92:ARG:HH22	1.63	0.42
2:2:764:G:H2'	2:2:764:G:N3	2.33	0.42
2:2:1075:C:H2'	2:2:1076:U:H6	1.84	0.42
2:2:1480:G:H21	2:2:1602:C:H1'	1.83	0.42
2:2:1526:U:O5'	79:SZ:85:SER:OG	2.38	0.42
5:A:38:LYS:HB3	5:A:62:HIS:O	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:C:40:GLU:HB2	8:D:229:TYR:HE2	1.83	0.42
14:LF:228:PHE:HE2	27:LS:35:VAL:HG11	1.84	0.42
16:LH:114:VAL:HB	16:LH:128:VAL:CG2	2.50	0.42
22:LN:60:VAL:HG23	22:LN:134:LEU:HB2	2.02	0.42
31:LW:97:ARG:NH1	31:LW:99:GLU:HB2	2.35	0.42
43:Li:94:ARG:HA	43:Li:97:GLU:OE1	2.19	0.42
57:SD:71:GLU:O	57:SD:74:SER:OG	2.22	0.42
64:SK:8:ARG:HA	64:SK:11:ILE:HG22	2.02	0.42
67:SN:36:GLN:HA	67:SN:39:LYS:HG2	2.01	0.42
70:SQ:34:LYS:HZ2	73:ST:8:ARG:HG3	1.82	0.42
70:SQ:78:VAL:O	70:SQ:82:ARG:HG2	2.19	0.42
75:SV:68:ALA:O	75:SV:72:LEU:HD23	2.19	0.42
1:1:919:G:N2	1:1:943:C:OP1	2.51	0.42
1:1:1252:U:H1'	1:1:1255:C:H5	1.84	0.42
1:1:2389:U:H2'	1:1:2390:U:C6	2.54	0.42
1:1:2574:G:H2'	1:1:2575:C:C6	2.54	0.42
2:2:335:C:H1'	62:SI:5:ARG:HG3	2.00	0.42
2:2:920:G:H2'	2:2:921:A:C8	2.54	0.42
2:2:959:U:H2'	2:2:960:C:C6	2.54	0.42
2:2:1189:C:HO2'	70:SQ:137:ARG:NH2	2.16	0.42
2:2:1675:G:N2	2:2:1718:A:H62	2.16	0.42
2:2:1697:A:H5''	7:C:358:LYS:HD3	2.02	0.42
4:4:142:C:H2'	4:4:143:U:C6	2.54	0.42
5:A:81:ALA:HB1	5:A:108:VAL:HG23	2.00	0.42
7:C:103:HIS:HB2	7:C:168:PHE:CE2	2.49	0.42
8:D:78:TYR:OH	8:D:243:ILE:HD11	2.19	0.42
18:LJ:61:ARG:HH12	49:Lo:104:LEU:HA	1.84	0.42
18:LJ:115:ILE:O	18:LJ:115:ILE:HG22	2.19	0.42
22:LN:150:TRP:CD1	22:LN:150:TRP:H	2.37	0.42
23:LO:82:PHE:O	23:LO:86:VAL:HG23	2.18	0.42
24:LP:48:LEU:HD22	24:LP:92:ILE:CD1	2.49	0.42
52:Ls:45:LEU:HD11	52:Ls:51:VAL:HG22	2.00	0.42
55:SB:199:LYS:O	55:SB:202:GLN:OE1	2.38	0.42
61:SH:69:PRO:HG2	61:SH:72:ALA:HB3	2.02	0.42
63:SJ:12:VAL:HG22	63:SJ:41:TRP:CZ3	2.54	0.42
66:SM:63:VAL:HG12	66:SM:121:VAL:HB	2.01	0.42
1:1:405:G:H2'	1:1:406:U:C6	2.54	0.42
1:1:1322:C:H2'	1:1:1323:C:C6	2.55	0.42
1:1:1769:G:H2'	1:1:1770:U:C6	2.55	0.42
1:1:2258:A:N3	1:1:2888:C:O2'	2.49	0.42
2:2:639:G:H2'	2:2:640:G:C8	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:761:A:H2'	2:2:762:U:C6	2.55	0.42
2:2:960:C:OP1	67:SN:72:LEU:HD23	2.20	0.42
2:2:1477:C:H4'	2:2:1478:C:OP1	2.18	0.42
2:2:1694:G:H2'	2:2:1695:G:C8	2.54	0.42
7:C:264:ALA:HA	7:C:267:ARG:HG2	2.00	0.42
7:C:265:ASN:HA	7:C:268:LYS:HG2	2.01	0.42
8:D:225:ARG:HH21	8:D:449:ALA:H	1.68	0.42
8:D:276:LYS:NZ	8:D:298:VAL:HB	2.33	0.42
10:LB:278:SER:OG	10:LB:281:HIS:NE2	2.39	0.42
11:LC:301:ARG:HG2	11:LC:302:ALA:N	2.34	0.42
11:LC:365:ALA:HB2	27:LS:26:ARG:HH12	1.84	0.42
12:LD:51:LEU:HD12	12:LD:63:GLN:O	2.19	0.42
14:LF:244:LEU:O	14:LF:248:MET:HG3	2.20	0.42
15:LG:146:ILE:HG23	15:LG:178:ILE:HD12	2.02	0.42
18:LJ:76:LYS:HA	18:LJ:79:GLU:HG3	2.01	0.42
19:LK:11:LYS:HA	19:LK:65:GLN:O	2.20	0.42
20:LL:134:LYS:HB2	20:LL:137:ASP:OD2	2.19	0.42
45:Lk:33:GLN:HG3	45:Lk:50:LYS:NZ	2.35	0.42
56:SC:45:PRO:HD3	56:SC:54:LYS:NZ	2.33	0.42
57:SD:75:LEU:HD21	64:SK:63:TYR:CE1	2.55	0.42
58:SE:91:THR:HG23	58:SE:98:ASN:OD1	2.19	0.42
58:SE:251:ARG:HD2	58:SE:255:ARG:HH12	1.84	0.42
60:SG:7:HIS:HA	60:SG:113:ILE:HG22	2.02	0.42
62:SI:161:GLU:O	62:SI:165:GLU:HG3	2.19	0.42
66:SM:30:LEU:O	66:SM:33:VAL:HB	2.20	0.42
67:SN:46:THR:O	67:SN:50:ILE:HD12	2.20	0.42
67:SN:118:ILE:O	67:SN:122:ILE:HG13	2.19	0.42
74:SU:97:VAL:O	74:SU:100:ILE:HG22	2.20	0.42
1:1:948:U:H2'	1:1:949:A:C8	2.53	0.42
1:1:1246:A:H2'	1:1:1246:A:N3	2.34	0.42
1:1:1278:G:OP1	27:LS:84:ARG:HG3	2.18	0.42
1:1:1545:G:H2'	1:1:1546:G:C8	2.54	0.42
1:1:1595:C:H2'	1:1:1596:U:C6	2.54	0.42
1:1:2181:G:H2'	1:1:2182:A:C8	2.54	0.42
2:2:1457:C:OP1	72:SS:143:ARG:HG2	2.20	0.42
2:2:1728:A:H2'	2:2:1729:C:H6	1.84	0.42
2:2:1749:A:H2'	2:2:1750:A:C8	2.54	0.42
3:3:45:U:H2'	3:3:46:C:C6	2.55	0.42
3:3:111:G:H2'	3:3:112:U:C6	2.54	0.42
7:C:279:ARG:NH2	38:Ld:87:ARG:HD2	2.34	0.42
8:D:320:ALA:O	8:D:323:VAL:HG12	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:LB:17:LEU:O	10:LB:19:ARG:HG3	2.20	0.42
13:LE:95:ARG:HG3	13:LE:96:ARG:N	2.34	0.42
20:LL:110:ALA:HA	20:LL:113:VAL:HG12	2.01	0.42
22:LN:6:TYR:CE2	43:Li:49:VAL:HG23	2.53	0.42
43:Li:93:LYS:O	43:Li:97:GLU:OE1	2.38	0.42
49:Lo:10:THR:CG2	49:Lo:11:PHE:H	2.32	0.42
52:Ls:8:LYS:HD3	52:Ls:12:PHE:CZ	2.55	0.42
54:SA:91:LYS:O	54:SA:95:HIS:ND1	2.36	0.42
56:SC:47:THR:HG23	56:SC:50:GLY:H	1.84	0.42
56:SC:90:LYS:HD3	56:SC:91:ILE:N	2.34	0.42
58:SE:85:GLY:N	58:SE:88:ASP:OD2	2.48	0.42
58:SE:155:LYS:HD3	58:SE:155:LYS:HA	1.80	0.42
69:SP:97:MET:HG3	69:SP:97:MET:O	2.19	0.42
71:SR:5:ARG:HE	71:SR:10:LYS:HZ3	1.67	0.42
72:SS:32:LEU:O	72:SS:35:ILE:HG12	2.20	0.42
77:SX:16:ARG:HG2	77:SX:16:ARG:HH11	1.85	0.42
78:SY:26:MET:HE1	78:SY:51:TYR:OH	2.19	0.42
1:1:290:A:C8	1:1:292:G:H1'	2.54	0.42
1:1:804:G:H2'	1:1:805:C:H6	1.84	0.42
1:1:2648:A:H2'	1:1:2648:A:N3	2.34	0.42
1:1:2740:U:H2'	1:1:2741:U:C6	2.55	0.42
1:1:3093:U:C2	1:1:3094:G:C8	3.08	0.42
1:1:3141:G:H1'	27:LS:173:PHE:HE2	1.85	0.42
2:2:564:A:H5'	84:Se:10:ARG:HG3	2.02	0.42
2:2:1479:A:H2'	2:2:1480:G:C8	2.54	0.42
2:2:1554:U:OP1	72:SS:122:HIS:NE2	2.53	0.42
4:4:5:U:H2'	4:4:6:U:C6	2.54	0.42
13:LE:23:LYS:HD2	14:LF:6:VAL:HG21	2.00	0.42
13:LE:72:LEU:HD11	13:LE:81:LEU:HD22	2.02	0.42
16:LH:7:GLU:HG3	16:LH:56:GLU:HB3	2.00	0.42
16:LH:36:LYS:HE3	16:LH:78:MET:HG3	2.00	0.42
25:LQ:69:GLU:OE1	25:LQ:69:GLU:N	2.49	0.42
28:LT:82:HIS:CE1	36:Lb:16:ALA:HA	2.54	0.42
33:LY:97:GLY:O	33:LY:98:ILE:HD13	2.19	0.42
35:La:93:GLY:O	35:La:96:LYS:NZ	2.53	0.42
39:Le:84:GLU:CD	39:Le:112:ARG:HH21	2.26	0.42
50:Lp:84:ARG:HG2	50:Lp:84:ARG:HH11	1.83	0.42
54:SA:57:TRP:O	54:SA:61:VAL:HG23	2.19	0.42
61:SH:57:VAL:HG12	61:SH:62:LYS:HA	2.02	0.42
66:SM:73:TYR:O	66:SM:77:VAL:HG12	2.20	0.42
66:SM:96:GLN:HG2	66:SM:100:TRP:CD1	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
73:ST:114:LEU:HB2	73:ST:124:ARG:O	2.19	0.42
74:SU:66:LYS:HG3	74:SU:67:THR:N	2.35	0.42
80:Sa:70:LYS:HE2	80:Sa:72:GLN:NE2	2.28	0.42
81:Sb:57:GLN:OE1	81:Sb:57:GLN:N	2.53	0.42
1:1:438:C:H2'	1:1:439:C:C6	2.55	0.42
1:1:565:C:H2'	1:1:566:C:C6	2.54	0.42
1:1:580:A:N6	1:1:598:G:H1'	2.34	0.42
1:1:626:C:N4	1:1:627:G:O6	2.53	0.42
1:1:714:G:N1	1:1:725:C:OP2	2.46	0.42
1:1:1300:A:O2'	1:1:1301:A:H3'	2.20	0.42
1:1:1464:A:O2'	1:1:1838:A:N3	2.37	0.42
1:1:1633:G:H2'	1:1:1634:A:H8	1.84	0.42
1:1:1744:C:H3'	1:1:1745:U:C5'	2.49	0.42
1:1:2169:G:O2'	1:1:2171:A:N6	2.53	0.42
1:1:2782:G:C2	1:1:2783:G:C8	3.08	0.42
2:2:394:A:OP2	62:SI:47:ARG:NH2	2.52	0.42
2:2:1215:G:H1	2:2:1440:A:H2'	1.85	0.42
2:2:1446:U:H1'	83:Sd:7:TRP:NE1	2.35	0.42
4:4:4:C:H2'	4:4:5:U:H6	1.85	0.42
5:A:22:ALA:HB3	5:A:32:LEU:HB2	2.01	0.42
7:C:72:LYS:HB3	7:C:72:LYS:HE3	1.78	0.42
8:D:266:ASP:OD1	8:D:268:ARG:HD3	2.19	0.42
12:LD:301:GLU:HG2	12:LD:302:GLN:CD	2.45	0.42
17:LI:101:LYS:HG2	17:LI:104:SER:HB3	2.02	0.42
20:LL:167:GLU:OE2	20:LL:168:ILE:N	2.53	0.42
27:LS:137:ARG:HD3	27:LS:137:ARG:HA	1.72	0.42
29:LU:39:PHE:O	29:LU:43:LEU:HD12	2.20	0.42
33:LY:26:ARG:HG3	33:LY:77:TYR:HE1	1.84	0.42
34:LZ:59:ALA:O	34:LZ:62:GLU:HG3	2.20	0.42
38:Ld:108:ASN:HA	38:Ld:109:PRO:HD3	1.87	0.42
41:Lg:86:VAL:O	41:Lg:90:ILE:HG12	2.20	0.42
44:Lj:39:TYR:CB	44:Lj:40:PRO:HD3	2.38	0.42
54:SA:17:ILE:O	54:SA:21:LEU:HD23	2.20	0.42
55:SB:7:LYS:HE3	55:SB:10:SER:HA	2.02	0.42
55:SB:167:LYS:O	55:SB:170:GLU:HG3	2.19	0.42
58:SE:195:ILE:HA	58:SE:210:LEU:HD13	2.02	0.42
59:SF:68:ARG:HB2	59:SF:69:PHE:CD1	2.55	0.42
65:SL:140:VAL:C	65:SL:141:ARG:HD2	2.45	0.42
78:SY:45:GLU:HB3	78:SY:55:LYS:NZ	2.35	0.42
78:SY:45:GLU:HB3	78:SY:55:LYS:HZ1	1.85	0.42
1:1:438:C:H2'	1:1:439:C:H6	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:542:G:H2'	1:1:543:U:C6	2.55	0.42
1:1:558:U:H2'	1:1:559:G:N2	2.34	0.42
1:1:910:C:H2'	1:1:911:A:C8	2.55	0.42
1:1:2544:G:H2'	1:1:2544:G:N3	2.34	0.42
1:1:2734:U:H1'	35:La:58:MET:HE1	2.02	0.42
1:1:3332:A:HO2'	1:1:3333:G:P	2.41	0.42
2:2:781:G:H2'	2:2:782:C:H6	1.84	0.42
2:2:1479:A:N3	2:2:1603:G:O2'	2.46	0.42
3:3:88:G:H5''	27:LS:84:ARG:NH1	2.35	0.42
5:A:11:LEU:HD21	5:A:52:TYR:HD2	1.84	0.42
5:A:79:LEU:HD23	5:A:80:SER:N	2.35	0.42
5:A:178:ASP:HB3	5:A:181:SER:HB2	2.01	0.42
7:C:171:VAL:HA	7:C:239:PHE:CD1	2.55	0.42
8:D:72:PRO:HD3	8:D:272:ARG:HH22	1.84	0.42
9:LA:104:LEU:O	9:LA:107:VAL:HG22	2.19	0.42
9:LA:113:VAL:HG12	9:LA:166:ILE:HD13	2.01	0.42
10:LB:332:VAL:HG22	10:LB:333:LYS:N	2.35	0.42
18:LJ:26:GLU:OE2	18:LJ:30:ARG:NH2	2.53	0.42
24:LP:120:ASN:OD1	24:LP:121:GLN:N	2.53	0.42
27:LS:130:GLU:OE2	27:LS:131:LYS:HG2	2.20	0.42
34:LZ:2:LYS:HE2	34:LZ:2:LYS:HB2	1.69	0.42
52:Ls:41:ILE:O	52:Ls:45:LEU:HG	2.20	0.42
55:SB:11:LYS:HZ2	55:SB:17:LYS:HA	1.85	0.42
57:SD:20:PHE:HE2	57:SD:42:VAL:HG21	1.84	0.42
57:SD:169:GLU:HG2	57:SD:170:PHE:N	2.34	0.42
58:SE:181:ALA:HA	58:SE:227:VAL:HA	2.01	0.42
64:SK:13:GLU:HB2	64:SK:17:ARG:HH22	1.84	0.42
64:SK:42:LYS:HA	64:SK:45:GLN:HG3	2.01	0.42
67:SN:115:LEU:HD12	67:SN:115:LEU:HA	1.93	0.42
73:ST:112:GLN:HB3	73:ST:128:GLN:HE22	1.84	0.42
76:SW:101:TYR:HB2	76:SW:129:PHE:CZ	2.55	0.42
79:SZ:68:CYS:HA	79:SZ:71:ASP:OD1	2.18	0.42
1:1:40:A:H5''	35:La:35:ALA:HB2	2.02	0.42
1:1:441:G:H2'	1:1:442:G:C8	2.55	0.42
1:1:1052:C:H2'	1:1:1053:U:H6	1.85	0.42
1:1:3141:G:H1'	27:LS:173:PHE:CE2	2.54	0.42
2:2:115:U:H2'	2:2:116:U:C6	2.54	0.42
2:2:523:A:OP1	78:SY:96:ARG:NE	2.52	0.42
2:2:591:A:P	63:SJ:35:ARG:HH12	2.43	0.42
2:2:866:G:OP1	67:SN:121:ARG:NH1	2.50	0.42
2:2:1327:G:H2'	2:2:1328:A:O4'	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A:48:ASP:OD1	5:A:51:GLN:O	2.38	0.42
7:C:329:GLU:O	7:C:333:LYS:HD3	2.20	0.42
10:LB:216:ILE:HD12	10:LB:339:LEU:HD22	2.02	0.42
15:LG:113:LEU:O	15:LG:117:THR:HG23	2.20	0.42
17:LI:35:ASP:C	17:LI:36:LEU:HD12	2.44	0.42
24:LP:22:LEU:HD23	24:LP:90:PHE:HD2	1.85	0.42
41:Lg:20:ARG:HG3	41:Lg:20:ARG:NH1	2.33	0.42
42:Lh:91:ARG:O	42:Lh:95:ARG:HG3	2.20	0.42
42:Lh:105:VAL:HG22	42:Lh:109:THR:OG1	2.19	0.42
55:SB:145:ARG:HD2	55:SB:149:GLN:OE1	2.18	0.42
56:SC:57:LYS:HG3	56:SC:251:TYR:CE1	2.55	0.42
58:SE:101:LEU:HD12	58:SE:109:PHE:HD2	1.85	0.42
58:SE:125:LYS:CE	58:SE:227:VAL:H	2.33	0.42
60:SG:116:GLN:OE1	60:SG:117:GLY:N	2.52	0.42
60:SG:160:ARG:O	60:SG:174:LYS:HG2	2.20	0.42
62:SI:9:HIS:NE2	62:SI:10:LYS:HE2	2.34	0.42
62:SI:42:ARG:HD3	62:SI:58:LEU:HD12	2.02	0.42
66:SM:63:VAL:CG1	66:SM:121:VAL:HB	2.49	0.42
67:SN:31:GLU:O	67:SN:34:VAL:HG22	2.19	0.42
70:SQ:82:ARG:NH1	70:SQ:83:GLN:OE1	2.53	0.42
76:SW:33:VAL:HA	76:SW:36:LYS:NZ	2.35	0.42
1:1:64:A:H5'	22:LN:174:LEU:CD2	2.50	0.41
1:1:1517:A:H2'	1:1:1518:A:C8	2.55	0.41
1:1:1626:G:C2	1:1:1788:G:C4	3.08	0.41
1:1:1676:A:H2'	1:1:1677:A:C8	2.55	0.41
1:1:2112:A:C2	1:1:2151:A:H4'	2.54	0.41
1:1:3287:U:P	62:SI:92:ARG:HE	2.39	0.41
1:1:3334:A:H2'	1:1:3335:U:C6	2.55	0.41
2:2:179:A:H2'	2:2:180:U:C6	2.55	0.41
2:2:535:A:H5'	2:2:540:C:C5	2.55	0.41
2:2:909:U:H1'	2:2:913:A:H1'	2.02	0.41
2:2:910:U:H1'	2:2:912:G:C2	2.54	0.41
2:2:1341:A:O2'	74:SU:51:GLY:HA3	2.20	0.41
2:2:1484:G:H3'	2:2:1511:A:N6	2.33	0.41
2:2:1555:A:O4'	72:SS:134:ARG:NH1	2.46	0.41
4:4:76:C:H2'	4:4:77:A:C8	2.55	0.41
7:C:81:ASP:OD1	7:C:81:ASP:N	2.53	0.41
8:D:208:VAL:HB	8:D:348:VAL:HG23	2.02	0.41
9:LA:177:LYS:HD3	50:Lp:69:TYR:CZ	2.55	0.41
13:LE:136:LYS:O	13:LE:139:GLU:HG3	2.20	0.41
17:LI:36:LEU:HD11	17:LI:69:ARG:HD3	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:LJ:18:LEU:HD12	18:LJ:129:TYR:O	2.20	0.41
20:LL:158:GLU:OE2	20:LL:159:GLN:HG2	2.19	0.41
20:LL:204:GLU:HA	20:LL:207:GLU:OE2	2.20	0.41
31:LW:93:ARG:HH21	60:SG:147:LEU:HD21	1.85	0.41
35:La:4:ARG:HH11	35:La:5:PHE:HE2	1.67	0.41
42:Lh:26:GLU:O	42:Lh:30:GLU:OE1	2.38	0.41
49:Lo:70:LEU:HD11	49:Lo:83:LEU:HB2	2.02	0.41
52:Ls:42:ARG:HH22	52:Ls:52:LEU:HD23	1.85	0.41
52:Ls:173:LEU:HD22	52:Ls:178:ILE:HG13	2.02	0.41
55:SB:32:ILE:HD11	55:SB:46:THR:HB	2.02	0.41
56:SC:81:LEU:O	56:SC:84:LEU:HD23	2.19	0.41
57:SD:144:LYS:O	57:SD:144:LYS:HD2	2.19	0.41
58:SE:125:LYS:CE	58:SE:226:PHE:HA	2.48	0.41
59:SF:129:PRO:O	59:SF:154:ARG:HG3	2.20	0.41
60:SG:32:MET:CE	60:SG:65:GLN:HB2	2.50	0.41
60:SG:38:GLY:HA2	60:SG:41:LEU:HD13	2.01	0.41
68:SO:104:THR:O	68:SO:105:LYS:HG2	2.20	0.41
72:SS:106:ASP:O	72:SS:110:ARG:NH1	2.52	0.41
74:SU:80:GLU:O	74:SU:81:MET:SD	2.78	0.41
76:SW:32:LYS:HA	76:SW:35:VAL:HG12	2.02	0.41
77:SX:87:VAL:HG12	77:SX:124:VAL:HG11	2.02	0.41
1:1:193:A:O2'	1:1:195:G:N7	2.47	0.41
1:1:1549:C:N4	1:1:1552:G:OP2	2.53	0.41
1:1:2468:U:H2'	1:1:2469:U:H6	1.85	0.41
1:1:3212:G:H1	13:LE:135:GLU:CD	2.28	0.41
1:1:3329:C:O2'	1:1:3330:C:H5'	2.20	0.41
2:2:196:G:H2'	2:2:197:A:C8	2.56	0.41
2:2:863:A:OP1	76:SW:3:ARG:NH2	2.44	0.41
5:A:192:THR:OG1	5:A:213:ASP:OD1	2.24	0.41
8:D:38:ILE:HG23	8:D:145:TYR:CG	2.55	0.41
10:LB:293:ALA:HB2	10:LB:303:LYS:HG3	2.01	0.41
12:LD:298:LEU:HD23	17:LI:210:MET:HE2	2.02	0.41
14:LF:96:LYS:HB3	14:LF:139:TRP:CD1	2.55	0.41
24:LP:76:TRP:HB2	24:LP:78:VAL:HG22	2.02	0.41
25:LQ:95:ILE:O	25:LQ:99:LEU:HG	2.20	0.41
33:LY:117:ILE:O	33:LY:121:ILE:HG13	2.20	0.41
34:LZ:30:GLN:OE1	34:LZ:30:GLN:N	2.50	0.41
51:Lq:31:ASP:HB3	51:Lq:34:ASN:HB2	2.01	0.41
54:SA:178:TRP:CD1	54:SA:178:TRP:C	2.97	0.41
55:SB:91:VAL:O	55:SB:91:VAL:HG13	2.19	0.41
56:SC:119:VAL:O	56:SC:145:ILE:N	2.44	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:SC:238:TRP:CE3	76:SW:68:ARG:NH2	2.87	0.41
61:SH:148:LYS:C	61:SH:149:ARG:HD2	2.46	0.41
61:SH:153:LYS:HE2	61:SH:153:LYS:HB2	1.78	0.41
61:SH:155:ASP:OD1	61:SH:156:GLY:N	2.53	0.41
64:SK:31:HIS:CE1	64:SK:37:ASN:H	2.38	0.41
67:SN:129:TYR:HA	67:SN:132:VAL:HG22	2.02	0.41
70:SQ:15:ASN:HD21	70:SQ:123:ARG:NH2	2.18	0.41
72:SS:29:VAL:HG13	72:SS:30:TYR:CD1	2.55	0.41
73:ST:136:ILE:HA	73:ST:139:THR:OG1	2.20	0.41
77:SX:13:ARG:HE	77:SX:16:ARG:HH12	1.68	0.41
78:SY:125:ALA:HA	78:SY:128:LYS:HE2	2.02	0.41
79:SZ:78:ILE:HG23	79:SZ:91:THR:O	2.20	0.41
81:Sb:40:CYS:SG	81:Sb:42:THR:HG22	2.60	0.41
1:1:424:U:H2'	1:1:425:G:H8	1.85	0.41
1:1:1463:G:O4'	1:1:1466:G:N2	2.53	0.41
1:1:2615:A:OP2	49:Lo:97:LYS:HD2	2.20	0.41
1:1:2945:U:C2	1:1:2946:A:C8	3.09	0.41
2:2:54:C:O3'	78:SY:112:LYS:HD3	2.20	0.41
2:2:511:G:O2'	2:2:512:A:H5'	2.21	0.41
2:2:1385:A:H5'	71:SR:48:ASN:ND2	2.35	0.41
4:4:10:A:H2'	4:4:11:C:C6	2.55	0.41
5:A:172:LYS:O	5:A:189:ILE:HG22	2.20	0.41
7:C:355:ASN:O	7:C:358:LYS:HG2	2.21	0.41
14:LF:65:GLU:HA	14:LF:68:LYS:HG2	2.01	0.41
16:LH:115:GLU:OE2	16:LH:117:ARG:NH2	2.53	0.41
18:LJ:84:GLY:O	18:LJ:87:VAL:HG12	2.21	0.41
19:LK:87:GLU:O	19:LK:88:PRO:CB	2.68	0.41
22:LN:160:GLU:HG2	22:LN:161:CYS:N	2.35	0.41
46:Ll:28:ARG:NH1	46:Ll:36:ARG:O	2.51	0.41
57:SD:77:GLN:HA	57:SD:82:PHE:HB2	2.02	0.41
57:SD:138:GLU:HB3	57:SD:160:MET:HE1	2.01	0.41
57:SD:150:ALA:O	57:SD:151:LYS:HD3	2.21	0.41
57:SD:216:PRO:HB3	71:SR:20:TYR:CE1	2.54	0.41
60:SG:98:ARG:HD3	60:SG:99:GLY:O	2.21	0.41
60:SG:201:GLN:O	60:SG:205:LYS:HG2	2.20	0.41
61:SH:82:ARG:O	61:SH:85:ARG:HG2	2.20	0.41
62:SI:117:TYR:HB3	62:SI:119:GLN:NE2	2.34	0.41
63:SJ:88:ARG:HG3	63:SJ:88:ARG:O	2.20	0.41
65:SL:68:MET:O	65:SL:68:MET:HG3	2.20	0.41
68:SO:46:LEU:O	68:SO:46:LEU:HD23	2.19	0.41
72:SS:117:LYS:NZ	72:SS:125:LEU:HA	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
78:SY:9:THR:HG23	78:SY:31:LEU:HB2	2.02	0.41
78:SY:90:PRO:HD2	78:SY:93:ARG:CD	2.50	0.41
1:1:435:G:OP1	51:Lq:126:LYS:NZ	2.44	0.41
1:1:882:G:H1'	1:1:1569:A:N6	2.34	0.41
2:2:175:G:H1'	60:SG:198:ARG:NH2	2.29	0.41
2:2:223:G:H8	2:2:223:G:P	2.43	0.41
2:2:530:U:H4'	78:SY:36:PRO:HG3	2.01	0.41
2:2:1384:G:N2	2:2:1406:A:H61	2.18	0.41
2:2:1447:C:P	83:Sd:12:ARG:HH22	2.43	0.41
2:2:1564:C:H4'	2:2:1565:A:O5'	2.20	0.41
3:3:44:C:H2'	3:3:45:U:H6	1.85	0.41
10:LB:348:SER:C	10:LB:350:LYS:H	2.29	0.41
14:LF:159:TYR:CD1	14:LF:168:PRO:HA	2.55	0.41
16:LH:75:ILE:O	16:LH:79:ILE:HG12	2.20	0.41
22:LN:101:THR:O	22:LN:105:ARG:HG3	2.20	0.41
27:LS:110:MET:HE3	27:LS:110:MET:HB3	1.88	0.41
29:LU:62:ILE:O	29:LU:62:ILE:HG22	2.21	0.41
31:LW:3:THR:C	31:LW:4:TYR:HD1	2.28	0.41
33:LY:26:ARG:HD2	33:LY:74:ARG:HB3	2.03	0.41
38:Ld:49:GLN:HG2	38:Ld:55:SER:HA	2.02	0.41
42:Lh:19:GLU:HA	42:Lh:22:LYS:HG2	2.03	0.41
47:Lm:93:LYS:HG3	47:Lm:102:ARG:HD3	2.02	0.41
52:Ls:48:GLN:NE2	52:Ls:89:THR:OG1	2.38	0.41
55:SB:144:LYS:HE3	55:SB:206:PRO:CB	2.47	0.41
59:SF:76:ILE:CD1	59:SF:79:ARG:HH12	2.33	0.41
62:SI:38:ILE:HD11	62:SI:96:LEU:HB2	2.02	0.41
63:SJ:98:LYS:HB3	63:SJ:98:LYS:HE3	1.85	0.41
66:SM:29:ALA:O	66:SM:33:VAL:HG23	2.20	0.41
74:SU:31:LEU:HD13	74:SU:86:ARG:HG3	2.00	0.41
84:Se:39:THR:O	84:Se:43:ARG:HG2	2.20	0.41
1:1:1008:U:H2'	1:1:1009:U:H5'	2.03	0.41
1:1:1582:A:OP2	26:LR:38:ARG:HG2	2.21	0.41
1:1:1587:U:O2'	1:1:1588:C:P	2.78	0.41
1:1:2071:C:H1'	1:1:3285:A:H1'	2.02	0.41
1:1:3316:A:H5''	38:Ld:26:LYS:HG3	2.03	0.41
2:2:1396:A:H4'	71:SR:60:ARG:CZ	2.51	0.41
2:2:1555:A:C1'	72:SS:134:ARG:HH12	2.33	0.41
8:D:48:PRO:HB2	8:D:50:ILE:HG22	2.02	0.41
10:LB:324:MET:HE1	10:LB:357:LEU:HD11	2.02	0.41
12:LD:122:VAL:C	12:LD:124:GLU:H	2.27	0.41
13:LE:59:ILE:HG12	13:LE:69:ARG:HG2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:LF:105:PRO:O	14:LF:108:ILE:HG22	2.20	0.41
16:LH:18:VAL:HG23	16:LH:27:VAL:HG22	2.02	0.41
18:LJ:118:ASP:HB3	18:LJ:121:ILE:HD13	2.01	0.41
20:LL:191:ASP:N	20:LL:191:ASP:OD1	2.53	0.41
25:LQ:45:LYS:NZ	25:LQ:45:LYS:HB2	2.35	0.41
28:LT:82:HIS:ND1	36:Lb:16:ALA:HA	2.35	0.41
30:LV:123:GLU:O	30:LV:127:LEU:HD23	2.20	0.41
33:LY:73:TYR:CD2	33:LY:76:LYS:HG3	2.56	0.41
52:Ls:5:SER:HB3	52:Ls:8:LYS:HB3	2.01	0.41
62:SI:82:VAL:HG22	62:SI:200:LEU:HD11	2.03	0.41
62:SI:146:GLN:HE22	62:SI:149:ARG:HH11	1.68	0.41
63:SJ:52:ARG:HH21	63:SJ:55:ARG:NH1	2.19	0.41
63:SJ:54:ALA:O	63:SJ:58:LEU:HD23	2.20	0.41
67:SN:26:LEU:HD23	67:SN:28:THR:H	1.86	0.41
67:SN:134:VAL:HG13	67:SN:135:LEU:HD12	2.02	0.41
70:SQ:135:ARG:HG2	70:SQ:136:ALA:N	2.35	0.41
72:SS:16:ARG:HD3	72:SS:21:ASN:OD1	2.20	0.41
1:1:638:C:H2'	1:1:639:G:C8	2.56	0.41
1:1:991:A:H2'	1:1:992:G:C8	2.56	0.41
1:1:1260:C:C2	1:1:1261:A:C8	3.08	0.41
1:1:2771:C:H2'	1:1:2772:A:H8	1.85	0.41
1:1:3124:G:O2'	1:1:3125:U:H5'	2.20	0.41
2:2:12:U:H2'	2:2:13:U:H6	1.86	0.41
2:2:611:A:N3	2:2:611:A:H2'	2.35	0.41
2:2:650:C:H2'	2:2:651:C:H6	1.85	0.41
2:2:1199:A:H3'	2:2:1199:A:N3	2.36	0.41
4:4:63:G:H22	4:4:97:A:H2	1.69	0.41
5:A:185:GLN:HG2	5:A:186:THR:N	2.35	0.41
10:LB:102:LEU:HD23	10:LB:102:LEU:H	1.86	0.41
10:LB:284:TYR:OH	10:LB:326:LYS:HD2	2.21	0.41
11:LC:268:VAL:HG23	11:LC:269:TYR:HD1	1.85	0.41
12:LD:95:TRP:CD1	12:LD:161:ARG:HA	2.56	0.41
16:LH:12:VAL:HG12	16:LH:51:GLY:O	2.21	0.41
16:LH:16:LEU:HD11	16:LH:79:ILE:HD12	2.02	0.41
17:LI:176:LEU:HD23	17:LI:177:ARG:O	2.21	0.41
23:LO:115:ASP:OD1	23:LO:115:ASP:N	2.53	0.41
24:LP:122:ALA:HB3	24:LP:143:PRO:HG2	2.02	0.41
25:LQ:48:LYS:HE2	25:LQ:48:LYS:HB2	1.80	0.41
26:LR:173:LYS:O	26:LR:176:ARG:HG2	2.21	0.41
31:LW:112:SER:O	31:LW:115:LYS:HG2	2.20	0.41
34:LZ:111:LYS:HE2	34:LZ:111:LYS:HB2	1.88	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:La:85:ASP:O	35:La:89:GLN:HG3	2.21	0.41
42:Lh:90:THR:HB	42:Lh:93:LEU:HG	2.03	0.41
45:Lk:78:LYS:HE2	45:Lk:78:LYS:HB2	1.86	0.41
47:Lm:79:GLU:OE2	47:Lm:82:LEU:N	2.49	0.41
51:Lq:22:LYS:HG3	51:Lq:27:THR:HG22	2.02	0.41
52:Ls:74:GLU:HA	52:Ls:77:LEU:HG	2.02	0.41
54:SA:117:SER:HB2	54:SA:119:LYS:HZ3	1.86	0.41
56:SC:247:PRO:HA	56:SC:250:GLU:HG2	2.02	0.41
57:SD:122:CYS:O	57:SD:126:LEU:HD23	2.21	0.41
60:SG:175:ALA:HA	60:SG:176:PRO:HD3	1.77	0.41
61:SH:104:ILE:HG13	61:SH:131:VAL:HG11	2.02	0.41
67:SN:39:LYS:HG3	67:SN:40:LEU:HD22	2.02	0.41
77:SX:52:ILE:HD13	77:SX:101:GLU:HA	2.03	0.41
78:SY:105:LYS:HD3	78:SY:111:ARG:HD3	2.02	0.41
79:SZ:81:VAL:HG23	79:SZ:82:VAL:N	2.35	0.41
85:Sf:123:ASN:HB3	85:Sf:126:CYS:C	2.46	0.41
1:1:42:G:N2	1:1:2762:A:H62	2.19	0.41
1:1:455:U:H2'	1:1:456:G:C8	2.55	0.41
1:1:613:G:H2'	1:1:614:U:C6	2.56	0.41
1:1:628:U:H2'	1:1:629:C:C6	2.56	0.41
1:1:1134:U:H5''	1:1:1135:G:OP2	2.21	0.41
1:1:1171:U:OP1	1:1:1193:U:O2'	2.38	0.41
1:1:2668:C:H2'	1:1:2669:C:C6	2.55	0.41
1:1:3009:U:H2'	1:1:3010:G:C8	2.53	0.41
1:1:3160:A:O2'	1:1:3200:A:N6	2.52	0.41
1:1:3209:A:C5	13:LE:154:VAL:HG21	2.55	0.41
2:2:301:U:H2'	2:2:302:C:C6	2.56	0.41
2:2:781:G:H2'	2:2:782:C:C6	2.56	0.41
2:2:1243:C:H2'	2:2:1244:U:C6	2.55	0.41
2:2:1426:U:H1'	74:SU:69:CYS:SG	2.61	0.41
2:2:1498:G:N2	2:2:1501:A:OP2	2.53	0.41
2:2:1549:G:H4'	83:Sd:14:TYR:CE1	2.56	0.41
2:2:1616:C:HO2'	2:2:1617:U:P	2.42	0.41
5:A:192:THR:HG1	5:A:213:ASP:CG	2.22	0.41
7:C:96:LYS:NZ	7:C:147:ASN:OD1	2.23	0.41
7:C:206:LYS:HG2	7:C:236:TRP:CZ2	2.56	0.41
7:C:384:ILE:HG23	7:C:388:LEU:HD12	2.02	0.41
8:D:549:VAL:HA	8:D:562:THR:O	2.20	0.41
11:LC:212:VAL:O	11:LC:258:THR:HG23	2.21	0.41
22:LN:132:VAL:HG12	22:LN:134:LEU:HD22	2.01	0.41
27:LS:73:LYS:HD3	27:LS:128:GLU:OE2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:LS:101:ALA:HA	27:LS:104:GLU:OE1	2.20	0.41
33:LY:56:GLN:HG3	33:LY:66:GLU:OE2	2.21	0.41
38:Ld:118:GLU:OE1	38:Ld:118:GLU:HA	2.20	0.41
42:Lh:48:LYS:O	42:Lh:52:LEU:HD23	2.21	0.41
50:Lp:73:THR:HG22	50:Lp:75:ALA:H	1.86	0.41
52:Ls:106:LYS:O	52:Ls:106:LYS:HD3	2.20	0.41
52:Ls:128:MET:HG2	52:Ls:129:GLU:N	2.35	0.41
54:SA:4:ALA:HB3	75:SV:77:GLY:HA3	2.02	0.41
54:SA:59:LYS:HB2	54:SA:59:LYS:HE2	1.87	0.41
55:SB:141:ALA:HA	55:SB:209:ASN:O	2.20	0.41
58:SE:208:VAL:HG22	58:SE:220:THR:O	2.21	0.41
59:SF:76:ILE:HD13	59:SF:79:ARG:HH12	1.85	0.41
59:SF:95:LEU:HA	70:SQ:43:ILE:HD11	2.02	0.41
61:SH:139:LEU:O	61:SH:179:TYR:HE1	2.03	0.41
61:SH:164:LEU:HD21	61:SH:193:PHE:HD2	1.84	0.41
62:SI:93:THR:HG23	62:SI:95:THR:HG23	2.03	0.41
67:SN:134:VAL:HG13	67:SN:135:LEU:CD1	2.51	0.41
68:SO:124:LYS:HE3	80:Sa:58:VAL:HG12	2.03	0.41
77:SX:111:GLY:H	77:SX:121:ARG:CZ	2.34	0.41
77:SX:121:ARG:HE	77:SX:121:ARG:HB3	1.55	0.41
78:SY:23:ARG:HG3	78:SY:23:ARG:NH1	2.36	0.41
80:Sa:44:MET:HE1	80:Sa:67:MET:HB2	2.03	0.41
80:Sa:44:MET:CE	80:Sa:67:MET:HB2	2.50	0.41
85:Sf:140:TYR:HA	85:Sf:146:LEU:O	2.21	0.41
1:1:742:G:N2	1:1:752:G:N3	2.69	0.41
1:1:2470:U:H2'	1:1:2471:U:C6	2.56	0.41
2:2:233:G:H3'	2:2:234:C:C6	2.56	0.41
2:2:698:G:H3'	2:2:699:A:H8	1.86	0.41
7:C:263:ASN:HB3	7:C:267:ARG:NH2	2.36	0.41
8:D:299:GLU:HG3	8:D:306:ASP:OD2	2.20	0.41
8:D:326:GLY:HA2	8:D:329:ARG:CZ	2.51	0.41
8:D:555:THR:C	8:D:557:LEU:N	2.63	0.41
9:LA:171:GLY:O	50:Lp:68:ALA:HB2	2.20	0.41
11:LC:326:MET:HA	11:LC:326:MET:HE2	2.03	0.41
14:LF:63:GLU:OE1	14:LF:63:GLU:N	2.46	0.41
15:LG:231:ASP:OD1	15:LG:232:THR:N	2.53	0.41
17:LI:177:ARG:HG2	17:LI:179:GLU:OE1	2.20	0.41
24:LP:172:SER:O	24:LP:176:ARG:HG3	2.20	0.41
25:LQ:111:VAL:HG13	25:LQ:111:VAL:O	2.21	0.41
47:Lm:104:PRO:HD3	47:Lm:111:ARG:NH2	2.36	0.41
54:SA:41:TRP:HE1	54:SA:52:ASN:ND2	2.18	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:SC:245:ARG:HH21	56:SC:249:GLU:HB3	1.84	0.41
58:SE:90:ILE:CG1	58:SE:99:PHE:HB2	2.51	0.41
58:SE:196:THR:OG1	58:SE:197:HIS:N	2.54	0.41
59:SF:61:ALA:HB1	70:SQ:122:ARG:HH22	1.86	0.41
64:SK:7:ASP:OD1	64:SK:8:ARG:N	2.53	0.41
67:SN:69:ASN:HB2	67:SN:74:ILE:HD11	2.03	0.41
70:SQ:113:ASP:HB3	70:SQ:116:LEU:HD23	2.03	0.41
74:SU:28:VAL:HG13	74:SU:29:GLN:OE1	2.20	0.41
74:SU:58:LYS:HB2	74:SU:83:ILE:HB	2.03	0.41
74:SU:66:LYS:HE3	74:SU:75:THR:HG21	2.03	0.41
75:SV:4:ASP:HB2	75:SV:5:ARG:HH11	1.86	0.41
83:Sd:54:LYS:NZ	83:Sd:55:TYR:H	2.19	0.41
1:1:331:A:H2'	11:LC:48:ARG:NH2	2.36	0.41
1:1:424:U:H2'	1:1:425:G:C8	2.56	0.41
1:1:498:U:H2'	1:1:499:C:C6	2.56	0.41
1:1:1637:C:O2'	1:1:1777:A:OP2	2.30	0.41
1:1:2221:U:H2'	1:1:2222:A:H8	1.86	0.41
1:1:2314:U:H2'	1:1:2315:A:H8	1.85	0.41
1:1:2469:U:H2'	1:1:2470:U:C6	2.56	0.41
1:1:2642:U:H1'	18:LJ:129:TYR:CE2	2.56	0.41
1:1:2686:A:OP2	1:1:2687:G:N2	2.50	0.41
1:1:2705:A:O2'	12:LD:178:HIS:HA	2.21	0.41
2:2:496:U:H2'	2:2:497:C:C6	2.56	0.41
2:2:653:G:H2'	2:2:654:U:O4'	2.21	0.41
2:2:681:C:O3'	76:SW:118:ARG:NH1	2.51	0.41
2:2:748:C:H2'	2:2:749:U:C6	2.56	0.41
2:2:777:C:H41	78:SY:13:ARG:HH12	1.69	0.41
2:2:1224:A:C2	66:SM:45:ARG:HD3	2.56	0.41
2:2:1396:A:H4'	71:SR:60:ARG:NH2	2.36	0.41
2:2:1437:C:H2'	2:2:1438:U:C6	2.56	0.41
4:4:14:C:C4	4:4:15:G:C6	3.09	0.41
5:A:54:TYR:CG	5:A:55:PRO:HD2	2.55	0.41
7:C:73:LYS:HD2	7:C:73:LYS:HA	1.97	0.41
7:C:102:ASP:C	7:C:103:HIS:HD1	2.29	0.41
7:C:238:SER:HB2	7:C:240:GLU:OE2	2.21	0.41
7:C:322:ARG:O	7:C:326:GLU:HG2	2.20	0.41
7:C:359:LYS:O	7:C:363:VAL:HG22	2.21	0.41
8:D:241:HIS:HD1	8:D:243:ILE:HB	1.86	0.41
9:LA:135:THR:CG2	9:LA:149:LYS:HB3	2.51	0.41
10:LB:80:ASP:OD2	10:LB:318:VAL:HG12	2.21	0.41
10:LB:227:PHE:HE1	10:LB:269:GLY:HA2	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:LE:119:ILE:HA	13:LE:122:VAL:CG1	2.51	0.41
14:LF:154:ILE:HG22	14:LF:187:ILE:HD11	2.03	0.41
15:LG:136:LYS:HD2	15:LG:141:HIS:HE1	1.84	0.41
16:LH:90:MET:HE1	16:LH:163:ILE:HG21	2.02	0.41
17:LI:184:LYS:HG2	17:LI:190:VAL:HG23	2.03	0.41
18:LJ:76:LYS:O	18:LJ:79:GLU:HG3	2.21	0.41
20:LL:21:ARG:HB3	22:LN:196:THR:HG22	2.03	0.41
20:LL:60:CYS:HA	20:LL:61:PRO:HD3	1.93	0.41
21:LM:19:VAL:HG23	21:LM:65:THR:OG1	2.21	0.41
22:LN:85:THR:HA	49:Lo:51:GLY:HA2	2.03	0.41
23:LO:59:LEU:HA	23:LO:74:HIS:CD2	2.56	0.41
23:LO:61:LYS:O	23:LO:62:MET:HE2	2.21	0.41
25:LQ:72:PHE:CE1	25:LQ:166:LEU:HD21	2.55	0.41
26:LR:64:ARG:O	26:LR:68:LEU:HD23	2.21	0.41
29:LU:101:ARG:HB3	29:LU:115:TYR:CE1	2.56	0.41
35:La:82:VAL:HG22	35:La:86:VAL:HG23	2.03	0.41
37:Lc:46:LEU:HD12	37:Lc:93:MET:SD	2.61	0.41
39:Le:14:ARG:HG3	39:Le:15:THR:N	2.36	0.41
39:Le:62:LYS:H	39:Le:62:LYS:HG2	1.64	0.41
43:Li:82:SER:OG	43:Li:92:ALA:HB1	2.20	0.41
48:Ln:6:ARG:O	48:Ln:10:THR:HG23	2.20	0.41
51:Lq:59:LYS:HD2	51:Lq:84:LYS:HB2	2.03	0.41
48:Lr:6:ARG:O	48:Lr:10:THR:HG23	2.20	0.41
52:Ls:19:LEU:HD12	52:Ls:20:GLU:N	2.36	0.41
52:Ls:64:LYS:HB3	52:Ls:73:TYR:HD2	1.86	0.41
55:SB:109:LYS:O	55:SB:113:LEU:HD23	2.21	0.41
56:SC:81:LEU:HB3	56:SC:84:LEU:HD21	2.03	0.41
56:SC:85:LYS:O	56:SC:112:ILE:HD12	2.21	0.41
56:SC:151:TYR:OH	75:SV:9:VAL:HG21	2.20	0.41
57:SD:57:HIS:HB3	57:SD:60:GLU:OE1	2.21	0.41
57:SD:216:PRO:CG	71:SR:19:LYS:HD2	2.49	0.41
59:SF:76:ILE:HG22	59:SF:80:LEU:CD1	2.51	0.41
59:SF:201:LYS:HG2	59:SF:205:GLU:OE2	2.21	0.41
60:SG:213:GLN:NE2	60:SG:214:ILE:HG12	2.36	0.41
62:SI:40:PRO:HG2	62:SI:59:ARG:HH12	1.82	0.41
65:SL:104:ARG:HG3	77:SX:12:ALA:HB2	2.02	0.41
66:SM:52:LYS:HE3	66:SM:52:LYS:HB2	1.85	0.41
70:SQ:55:LEU:HD13	70:SQ:105:LEU:HD12	2.03	0.41
73:ST:116:LYS:HD3	73:ST:123:ARG:HE	1.85	0.41
73:ST:127:GLN:O	73:ST:130:GLN:HG2	2.20	0.41
76:SW:20:MET:HE2	76:SW:20:MET:HB2	1.96	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
77: SX:117: ILE: HD12	77: SX:120: VAL: HG13	2.03	0.41
79: SZ:69: LEU: HD12	79: SZ:90: TYR: CD2	2.53	0.41
83: Sd:39: CYS: O	83: Sd:43: PHE: HB2	2.21	0.41
1:1:1599: A: C2	1:1:1806: C: C2	3.09	0.41
1:1:1607: U: H2'	1:1:1794: A: N6	2.35	0.41
1:1:2937: U: O2'	1:1:2938: U: H5'	2.21	0.41
1:1:3281: G: O2'	1:1:3282: U: OP1	2.31	0.41
2:2:293: U: H2'	2:2:294: U: C6	2.56	0.41
2:2:303: U: P	65: SL:93: ARG: HH12	2.44	0.41
2:2:587: C: H2'	2:2:588: A: H8	1.86	0.41
2:2:900: G: H2'	2:2:901: U: C6	2.56	0.41
2:2:1129: A: H2'	2:2:1130: A: H8	1.85	0.41
2:2:1213: C: O2'	2:2:1440: A: N1	2.44	0.41
5: A:79: LEU: HD22	5: A:111: VAL: HG21	2.03	0.41
8: D:129: GLU: OE2	8: D:133: ARG: NE	2.47	0.41
8: D:296: PHE: CE1	8: D:298: VAL: HG13	2.56	0.41
9: LA:135: THR: HG22	9: LA:149: LYS: HB3	2.02	0.41
13: LE:118: LYS: HB2	13: LE:118: LYS: HE2	1.75	0.41
16: LH:88: TYR: CZ	16: LH:186: LYS: HG2	2.56	0.41
18: LJ:156: THR: HG23	18: LJ:159: GLU: H	1.86	0.41
21: LM:130: GLU: HG2	23: LO:191: VAL: HG11	2.03	0.41
24: LP:182: ARG: HH11	24: LP:182: ARG: HG3	1.85	0.41
25: LQ:72: PHE: O	25: LQ:76: VAL: HG12	2.21	0.41
29: LU:39: PHE: CE1	29: LU:43: LEU: HD11	2.56	0.41
32: LX:56: ALA: N	32: LX:57: PRO: HD3	2.36	0.41
41: Lg:26: THR: HG22	41: Lg:30: GLN: H	1.86	0.41
51: Lq:115: ALA: O	51: Lq:119: LEU: HD23	2.22	0.41
55: SB:165: ARG: O	55: SB:169: VAL: HG23	2.21	0.41
56: SC:45: PRO: HD3	56: SC:54: LYS: HZ2	1.86	0.41
56: SC:119: VAL: HG21	56: SC:199: ALA: HA	2.02	0.41
56: SC:215: LEU: HD12	56: SC:216: GLU: N	2.36	0.41
58: SE:159: THR: CG2	58: SE:173: ILE: HB	2.51	0.41
59: SF:18: LYS: HA	59: SF:21: LEU: HD12	2.03	0.41
62: SI:103: GLN: HA	62: SI:169: LEU: O	2.21	0.41
62: SI:125: ARG: O	62: SI:125: ARG: HD2	2.20	0.41
71: SR:104: ILE: HG23	71: SR:122: VAL: HG11	2.02	0.41
1:1:1304: G: H2'	1:1:1305: U: C6	2.56	0.40
1:1:2656: A: H2'	1:1:2657: G: C8	2.56	0.40
1:1:2771: C: H2'	1:1:2772: A: C8	2.56	0.40
2:2:132: U: H6	2:2:132: U: H2'	1.70	0.40
2:2:379: C: OP2	58: SE:10: LYS: NZ	2.53	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:1172:U:H2'	2:2:1173:G:C8	2.56	0.40
2:2:1469:U:HO2'	59:SF:89:ARG:HH21	1.62	0.40
5:A:40:LEU:CB	5:A:59:LEU:HD22	2.50	0.40
7:C:112:TYR:HB3	7:C:115:ARG:O	2.21	0.40
8:D:243:ILE:O	8:D:247:LYS:HD3	2.20	0.40
8:D:246:ASP:O	8:D:250:ILE:HG13	2.21	0.40
8:D:274:LEU:HD22	8:D:278:ARG:NH2	2.36	0.40
8:D:351:SER:O	8:D:355:SER:OG	2.35	0.40
11:LC:15:LYS:HA	11:LC:15:LYS:HD3	1.92	0.40
11:LC:240:LEU:HB3	11:LC:245:LEU:HD11	2.02	0.40
11:LC:287:LEU:HA	11:LC:290:LEU:HD12	2.03	0.40
13:LE:163:LYS:HE3	13:LE:163:LYS:HB3	1.85	0.40
17:LI:193:ASP:OD1	17:LI:194:GLY:N	2.46	0.40
22:LN:46:ASP:HB2	22:LN:50:ARG:HH21	1.86	0.40
27:LS:158:LYS:HE2	27:LS:158:LYS:HB2	1.88	0.40
28:LT:81:LYS:HB3	28:LT:81:LYS:HE3	1.92	0.40
35:La:84:SER:CA	35:La:87:ARG:HG2	2.44	0.40
37:Lc:96:LEU:HD23	37:Lc:96:LEU:HA	1.79	0.40
51:Lq:59:LYS:NZ	51:Lq:84:LYS:O	2.50	0.40
54:SA:37:GLN:N	54:SA:38:PRO:HD2	2.35	0.40
54:SA:201:MET:HG3	54:SA:202:PRO:HD2	2.03	0.40
58:SE:125:LYS:NZ	58:SE:227:VAL:N	2.69	0.40
59:SF:141:THR:HG22	59:SF:142:VAL:N	2.35	0.40
60:SG:183:THR:HG21	60:SG:185:GLN:HE21	1.85	0.40
61:SH:82:ARG:O	61:SH:82:ARG:NH1	2.50	0.40
69:SP:33:LEU:HA	69:SP:36:LEU:HD13	2.01	0.40
71:SR:23:ARG:NH1	71:SR:24:LEU:HB2	2.36	0.40
73:ST:16:VAL:HG12	73:ST:63:ARG:CZ	2.51	0.40
73:ST:66:TYR:HD2	73:ST:67:LEU:HD22	1.85	0.40
76:SW:24:GLN:NE2	81:Sb:5:VAL:O	2.53	0.40
78:SY:63:LEU:H	78:SY:63:LEU:HD23	1.85	0.40
1:1:784:C:H2'	1:1:785:C:H6	1.85	0.40
1:1:1577:C:H2'	1:1:1578:G:C8	2.55	0.40
1:1:1632:G:C2	1:1:1784:G:C2	3.10	0.40
1:1:2566:G:OP1	9:LA:233:GLN:NE2	2.42	0.40
2:2:269:C:H6	2:2:269:C:H2'	1.67	0.40
2:2:1095:U:P	56:SC:176:ARG:NH2	2.92	0.40
2:2:1250:U:H2'	2:2:1251:U:C6	2.56	0.40
2:2:1278:G:OP1	74:SU:66:LYS:HE2	2.21	0.40
2:2:1362:C:H2'	2:2:1363:A:C8	2.56	0.40
4:4:103:G:OP2	4:4:105:A:O2'	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A:59:LEU:HB3	5:A:90:TRP:CZ3	2.56	0.40
5:A:159:ASN:ND2	5:A:203:ASP:O	2.55	0.40
7:C:150:LYS:HB3	7:C:154:LYS:HE3	2.04	0.40
8:D:121:GLU:HG2	8:D:122:PRO:HD2	2.03	0.40
10:LB:282:LYS:O	10:LB:325:ILE:HD12	2.20	0.40
16:LH:40:HIS:CD2	16:LH:40:HIS:H	2.40	0.40
22:LN:66:VAL:HG12	22:LN:67:ARG:N	2.37	0.40
42:Lh:23:ILE:HA	42:Lh:26:GLU:CD	2.46	0.40
50:Lp:49:ARG:NH1	50:Lp:51:ALA:O	2.54	0.40
54:SA:39:TYR:CD1	54:SA:55:LYS:HD3	2.47	0.40
55:SB:159:SER:HA	55:SB:162:ARG:NH2	2.36	0.40
56:SC:148:ARG:HG3	56:SC:230:TYR:CE1	2.56	0.40
57:SD:107:SER:O	57:SD:111:LYS:HG2	2.21	0.40
61:SH:50:VAL:HG13	61:SH:51:SER:N	2.37	0.40
63:SJ:52:ARG:NH2	63:SJ:55:ARG:HH12	2.19	0.40
66:SM:129:GLU:CD	66:SM:132:GLU:H	2.29	0.40
68:SO:29:VAL:HG12	68:SO:46:LEU:H	1.86	0.40
71:SR:102:LEU:HD12	71:SR:103:ASP:H	1.85	0.40
76:SW:90:VAL:HG21	76:SW:113:HIS:CD2	2.56	0.40
80:Sa:36:ILE:HD11	80:Sa:73:TYR:HB2	2.04	0.40
1:1:171:G:H2'	1:1:172:G:C8	2.57	0.40
1:1:533:C:H2'	1:1:534:C:H6	1.86	0.40
1:1:1460:A:OP1	1:1:3033:G:O2'	2.38	0.40
2:2:294:U:O2	58:SE:33:THR:OG1	2.35	0.40
2:2:348:C:N4	2:2:628:G:OP1	2.54	0.40
2:2:491:U:O2'	2:2:492:C:H5'	2.21	0.40
2:2:1689:A:H2'	2:2:1690:G:C8	2.57	0.40
8:D:139:VAL:HG13	8:D:150:VAL:HB	2.03	0.40
8:D:167:ALA:HA	8:D:170:ILE:HG22	2.01	0.40
26:LR:95:TRP:NE1	26:LR:99:GLN:HE21	2.18	0.40
38:Ld:96:LYS:O	38:Ld:97:LEU:HD23	2.22	0.40
40:Lf:17:SER:HA	40:Lf:96:PHE:CE1	2.56	0.40
50:Lp:49:ARG:HB2	50:Lp:55:TRP:CZ3	2.56	0.40
50:Lp:85:ARG:HG2	50:Lp:85:ARG:NH1	2.32	0.40
52:Ls:144:LYS:HE3	52:Ls:144:LYS:HB2	1.90	0.40
58:SE:125:LYS:NZ	58:SE:227:VAL:H	2.19	0.40
62:SI:101:VAL:HA	62:SI:171:ALA:O	2.21	0.40
64:SK:13:GLU:HB2	64:SK:17:ARG:CZ	2.52	0.40
69:SP:64:LEU:HD21	69:SP:91:MET:SD	2.62	0.40
70:SQ:73:GLY:H	70:SQ:76:SER:HB2	1.87	0.40
77:SX:42:PRO:HB3	77:SX:81:LYS:HZ3	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:Sa:23:CYS:HB3	80:Sa:28:ARG:H	1.87	0.40
85:Sf:113:LYS:HD3	85:Sf:114:ILE:N	2.36	0.40
1:1:44:A:H4'	22:LN:84:PRO:HG2	2.01	0.40
1:1:575:G:H2'	1:1:576:A:C8	2.52	0.40
1:1:626:C:OP2	39:Le:42:ARG:NH1	2.53	0.40
1:1:769:G:H2'	1:1:770:C:C6	2.56	0.40
1:1:2667:C:H2'	1:1:2668:C:C6	2.54	0.40
1:1:2904:G:O2'	1:1:2907:C:OP2	2.36	0.40
1:1:2993:C:C2	1:1:2994:G:C8	3.10	0.40
2:2:467:A:H2	63:SJ:6:TYR:CE2	2.40	0.40
2:2:773:A:C6	2:2:774:G:H1'	2.56	0.40
2:2:820:U:H2'	2:2:821:G:H5''	2.02	0.40
2:2:903:A:H5''	68:SO:65:ARG:HG3	2.03	0.40
2:2:1291:G:O2'	2:2:1318:A:N1	2.48	0.40
2:2:1486:A:H2'	2:2:1487:C:H4'	2.03	0.40
2:2:1613:U:O2	82:Sc:23:ARG:NH1	2.50	0.40
2:2:1781:U:OP1	68:SO:149:ARG:NH2	2.52	0.40
4:4:97:A:OP1	42:Lh:68:ARG:NH1	2.55	0.40
4:4:127:U:O4	48:Lr:18:ARG:NH2	2.54	0.40
5:A:201:SER:OG	5:A:203:ASP:OD1	2.31	0.40
8:D:405:GLU:O	8:D:409:ILE:HG12	2.22	0.40
10:LB:54:THR:HG22	10:LB:55:THR:N	2.33	0.40
16:LH:164:GLN:HG3	16:LH:181:ILE:O	2.21	0.40
20:LL:170:LYS:HE3	20:LL:170:LYS:HB2	1.83	0.40
23:LO:77:ALA:HB3	23:LO:80:ARG:HG2	2.03	0.40
26:LR:98:ARG:HA	26:LR:101:VAL:HG12	2.04	0.40
27:LS:9:VAL:HG12	27:LS:61:VAL:HG23	2.04	0.40
33:LY:53:ASP:HB2	33:LY:108:LEU:HA	2.04	0.40
33:LY:115:GLU:H	33:LY:115:GLU:CD	2.28	0.40
40:Lf:87:PHE:HE2	40:Lf:91:LEU:HD11	1.85	0.40
49:Lo:93:LEU:HD23	49:Lo:93:LEU:H	1.87	0.40
51:Lq:118:ILE:O	51:Lq:122:GLN:HG3	2.22	0.40
55:SB:142:PHE:O	55:SB:207:LEU:HA	2.21	0.40
56:SC:237:LEU:O	75:SV:16:LYS:NZ	2.47	0.40
57:SD:19:VAL:O	57:SD:23:GLU:HG2	2.21	0.40
58:SE:126:VAL:CG1	58:SE:139:LEU:HD12	2.51	0.40
58:SE:254:ARG:HA	58:SE:257:ARG:CD	2.51	0.40
61:SH:9:ILE:HG22	61:SH:49:PHE:CZ	2.57	0.40
63:SJ:11:LYS:HB3	63:SJ:11:LYS:HE3	1.77	0.40
64:SK:48:GLN:HE22	64:SK:54:LYS:C	2.30	0.40
64:SK:80:LEU:HD12	64:SK:80:LEU:HA	1.88	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
66:SM:99:GLU:OE1	66:SM:99:GLU:N	2.53	0.40
76:SW:38:LEU:HD23	76:SW:50:PHE:CG	2.55	0.40
76:SW:39:GLN:O	76:SW:43:ARG:HG2	2.21	0.40
77:SX:13:ARG:HA	77:SX:16:ARG:HH11	1.83	0.40
78:SY:35:ARG:HH21	78:SY:38:ILE:HD11	1.87	0.40
1:1:14:A:O2'	32:LX:52:VAL:HG13	2.21	0.40
1:1:898:G:H5'	1:1:899:A:OP1	2.22	0.40
1:1:1198:A:H2'	1:1:1199:C:C6	2.56	0.40
1:1:2469:U:C2	1:1:2470:U:C5	3.10	0.40
1:1:2487:A:C4	15:LG:49:LEU:HD21	2.57	0.40
1:1:3176:G:H2'	1:1:3177:C:H6	1.87	0.40
2:2:777:C:H2'	2:2:778:U:H2'	2.03	0.40
2:2:951:G:H2'	2:2:952:G:H8	1.86	0.40
2:2:1188:U:O2'	2:2:1189:C:O4'	2.28	0.40
2:2:1624:U:H2'	2:2:1625:G:H8	1.87	0.40
2:2:1728:A:H2'	2:2:1729:C:C6	2.56	0.40
5:A:29:ASN:C	5:A:45:LEU:HD23	2.46	0.40
9:LA:44:ILE:HG12	9:LA:87:PHE:CE1	2.57	0.40
11:LC:105:LYS:HD2	11:LC:107:TRP:CH2	2.57	0.40
28:LT:97:LYS:HG3	28:LT:98:PRO:HD2	2.03	0.40
35:La:133:GLU:OE1	35:La:136:ARG:NH2	2.50	0.40
51:Lq:21:VAL:HG13	51:Lq:21:VAL:O	2.22	0.40
54:SA:126:VAL:O	54:SA:148:ALA:HA	2.22	0.40
54:SA:198:TRP:CD1	54:SA:199:ASP:H	2.40	0.40
55:SB:157:GLN:HB2	55:SB:160:GLN:NE2	2.37	0.40
56:SC:64:ILE:HD12	56:SC:64:ILE:H	1.86	0.40
58:SE:126:VAL:HG12	58:SE:139:LEU:HD12	2.02	0.40
58:SE:137:PRO:HB2	58:SE:150:PRO:HD2	2.03	0.40
69:SP:35:ASP:O	69:SP:36:LEU:HD12	2.21	0.40
69:SP:89:ARG:HE	69:SP:125:GLY:HA3	1.87	0.40
71:SR:40:VAL:O	71:SR:40:VAL:HG23	2.21	0.40
71:SR:58:MET:SD	71:SR:61:ILE:HD12	2.62	0.40
73:ST:43:ALA:HA	73:ST:84:LYS:HB2	2.03	0.40
80:Sa:67:MET:HE2	80:Sa:69:LEU:HD21	2.02	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	A	310/316 (98%)	287 (93%)	23 (7%)	0	100	100
6	B	27/302 (9%)	19 (70%)	8 (30%)	0	100	100
7	C	442/446 (99%)	423 (96%)	18 (4%)	1 (0%)	43	73
8	D	511/578 (88%)	496 (97%)	11 (2%)	4 (1%)	16	50
9	LA	250/254 (98%)	239 (96%)	11 (4%)	0	100	100
10	LB	385/392 (98%)	365 (95%)	20 (5%)	0	100	100
11	LC	361/365 (99%)	346 (96%)	15 (4%)	0	100	100
12	LD	298/304 (98%)	290 (97%)	8 (3%)	0	100	100
13	LE	192/200 (96%)	178 (93%)	14 (7%)	0	100	100
14	LF	245/249 (98%)	237 (97%)	8 (3%)	0	100	100
15	LG	233/262 (89%)	229 (98%)	4 (2%)	0	100	100
16	LH	189/192 (98%)	184 (97%)	5 (3%)	0	100	100
17	LI	215/219 (98%)	202 (94%)	13 (6%)	0	100	100
18	LJ	165/173 (95%)	160 (97%)	5 (3%)	0	100	100
19	LK	153/165 (93%)	135 (88%)	17 (11%)	1 (1%)	18	52
20	LL	207/213 (97%)	201 (97%)	6 (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%)	196 (98%)	5 (2%)	0	100	100
24	LP	184/187 (98%)	177 (96%)	7 (4%)	0	100	100
25	LQ	181/213 (85%)	174 (96%)	7 (4%)	0	100	100
26	LR	182/192 (95%)	176 (97%)	6 (3%)	0	100	100
27	LS	171/174 (98%)	166 (97%)	5 (3%)	0	100	100
28	LT	156/160 (98%)	154 (99%)	2 (1%)	0	100	100
29	LU	100/127 (79%)	99 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
30	LV	133/139 (96%)	130 (98%)	3 (2%)	0	100	100
31	LW	131/161 (81%)	129 (98%)	2 (2%)	0	100	100
32	LX	119/156 (76%)	112 (94%)	7 (6%)	0	100	100
33	LY	132/138 (96%)	130 (98%)	2 (2%)	0	100	100
34	LZ	133/135 (98%)	132 (99%)	1 (1%)	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%)	119 (98%)	3 (2%)	0	100	100
40	Lf	105/109 (96%)	100 (95%)	5 (5%)	0	100	100
41	Lg	110/119 (92%)	105 (96%)	5 (4%)	0	100	100
42	Lh	120/126 (95%)	116 (97%)	4 (3%)	0	100	100
43	Li	100/110 (91%)	95 (95%)	5 (5%)	0	100	100
44	Lj	84/95 (88%)	78 (93%)	5 (6%)	1 (1%)	10	42
45	Lk	78/81 (96%)	77 (99%)	1 (1%)	0	100	100
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%)	83 (93%)	6 (7%)	0	100	100
51	Lq	139/147 (95%)	135 (97%)	4 (3%)	0	100	100
52	Ls	187/312 (60%)	182 (97%)	5 (3%)	0	100	100
54	SA	206/285 (72%)	195 (95%)	11 (5%)	0	100	100
55	SB	230/255 (90%)	214 (93%)	16 (7%)	0	100	100
56	SC	214/263 (81%)	206 (96%)	8 (4%)	0	100	100
57	SD	210/254 (83%)	199 (95%)	11 (5%)	0	100	100
58	SE	259/264 (98%)	245 (95%)	14 (5%)	0	100	100
59	SF	197/212 (93%)	187 (95%)	10 (5%)	0	100	100
60	SG	230/239 (96%)	223 (97%)	7 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
61	SH	193/203 (95%)	187 (97%)	6 (3%)	0	100	100
62	SI	199/202 (98%)	196 (98%)	3 (2%)	0	100	100
63	SJ	177/190 (93%)	172 (97%)	5 (3%)	0	100	100
64	SK	87/159 (55%)	84 (97%)	3 (3%)	0	100	100
65	SL	148/161 (92%)	145 (98%)	3 (2%)	0	100	100
66	SM	116/144 (81%)	105 (90%)	11 (10%)	0	100	100
67	SN	148/151 (98%)	144 (97%)	4 (3%)	0	100	100
68	SO	133/150 (89%)	124 (93%)	9 (7%)	0	100	100
69	SP	113/153 (74%)	109 (96%)	4 (4%)	0	100	100
70	SQ	136/143 (95%)	128 (94%)	8 (6%)	0	100	100
71	SR	126/143 (88%)	121 (96%)	5 (4%)	0	100	100
72	SS	135/156 (86%)	125 (93%)	10 (7%)	0	100	100
73	ST	140/153 (92%)	135 (96%)	5 (4%)	0	100	100
74	SU	101/116 (87%)	95 (94%)	6 (6%)	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
77	SX	140/145 (97%)	130 (93%)	10 (7%)	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%)	57 (97%)	2 (3%)	0	100	100
83	Sd	50/56 (89%)	47 (94%)	3 (6%)	0	100	100
84	Se	38/62 (61%)	38 (100%)	0	0	100	100
85	Sf	71/154 (46%)	64 (90%)	7 (10%)	0	100	100
All	All	12586/14205 (89%)	12071 (96%)	508 (4%)	7 (0%)	49	79

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	C	251	GLU
8	D	450	VAL
8	D	556	ASP

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Mol	Chain	Res	Type
19	LK	88	PRO
44	Lj	39	TYR
8	D	421	PRO
8	D	555	THR

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	358/367 (98%)	357 (100%)	1 (0%)	86	88
8	D	427/474 (90%)	427 (100%)	0	100	100
9	LA	196/198 (99%)	194 (99%)	2 (1%)	68	80
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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	90/108 (83%)	90 (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
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%)	17 (77%)	5 (23%)	1	5
48	Lr	22/23 (96%)	17 (77%)	5 (23%)	1	5
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
57	SD	182/206 (88%)	182 (100%)	0	100	100
58	SE	219/221 (99%)	219 (100%)	0	100	100
59	SF	167/178 (94%)	166 (99%)	1 (1%)	78	84
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%)	101 (100%)	0	100	100
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
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	10610/11721 (90%)	10596 (100%)	14 (0%)	87	91

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

Mol	Chain	Res	Type
7	C	246	VAL
9	LA	139	HIS
9	LA	194	ASN
48	Ln	4	LYS
48	Ln	10	THR
48	Ln	11	ARG
48	Ln	15	ARG
48	Ln	20	VAL
48	Lr	4	LYS
48	Lr	10	THR
48	Lr	11	ARG
48	Lr	15	ARG
48	Lr	20	VAL
59	SF	211	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (113) such sidechains are listed below:

Mol	Chain	Res	Type
5	A	44	ASN
5	A	60	HIS
5	A	296	GLN
7	C	153	GLN
7	C	252	ASN
7	C	265	ASN
7	C	355	ASN
8	D	85	GLN
8	D	94	HIS
8	D	328	ASN
8	D	363	ASN
8	D	414	HIS
9	LA	93	ASN
9	LA	100	ASN
9	LA	140	ASN
10	LB	166	GLN
10	LB	174	GLN
10	LB	346	HIS
11	LC	141	HIS
11	LC	284	GLN
11	LC	330	ASN
12	LD	39	GLN
12	LD	57	ASN
14	LF	25	GLN
14	LF	82	HIS

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Mol	Chain	Res	Type
14	LF	99	ASN
14	LF	165	GLN
14	LF	206	ASN
14	LF	242	ASN
15	LG	194	HIS
16	LH	58	HIS
18	LJ	44	GLN
18	LJ	96	ASN
20	LL	5	HIS
20	LL	11	ASN
20	LL	25	HIS
20	LL	99	HIS
22	LN	91	GLN
22	LN	117	ASN
23	LO	56	HIS
25	LQ	86	ASN
25	LQ	98	ASN
26	LR	67	ASN
26	LR	91	GLN
26	LR	99	GLN
27	LS	5	GLN
27	LS	74	ASN
30	LV	106	ASN
31	LW	11	GLN
31	LW	33	ASN
31	LW	130	ASN
32	LX	73	HIS
32	LX	81	ASN
32	LX	92	GLN
32	LX	107	GLN
33	LY	109	HIS
34	LZ	105	GLN
35	La	25	HIS
35	La	28	HIS
37	Lc	71	HIS
39	Le	21	HIS
40	Lf	26	HIS
40	Lf	79	ASN
40	Lf	89	HIS
44	Lj	29	ASN
44	Lj	30	GLN
45	Lk	3	GLN

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Mol	Chain	Res	Type
45	Lk	60	GLN
50	Lp	45	ASN
51	Lq	38	GLN
54	SA	37	GLN
54	SA	52	ASN
54	SA	86	GLN
55	SB	21	GLN
55	SB	79	HIS
55	SB	173	GLN
55	SB	211	HIS
56	SC	44	GLN
57	SD	29	GLN
57	SD	104	GLN
58	SE	130	GLN
58	SE	197	HIS
59	SF	118	GLN
59	SF	173	ASN
60	SG	189	HIS
60	SG	225	GLN
61	SH	17	GLN
61	SH	18	ASN
61	SH	80	GLN
61	SH	81	GLN
62	SI	119	GLN
62	SI	146	GLN
63	SJ	108	GLN
63	SJ	121	HIS
64	SK	48	GLN
67	SN	32	GLN
67	SN	62	GLN
70	SQ	5	GLN
71	SR	31	ASN
71	SR	123	ASN
72	SS	19	ASN
72	SS	26	GLN
72	SS	103	ASN
72	SS	137	HIS
73	ST	127	GLN
75	SV	74	GLN
77	SX	22	GLN
77	SX	48	HIS
79	SZ	80	GLN

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Mol	Chain	Res	Type
80	Sa	80	HIS
81	Sb	61	ASN
85	Sf	123	ASN
85	Sf	136	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	3188/3337 (95%)	526 (16%)	51 (1%)
2	2	1770/1796 (98%)	377 (21%)	48 (2%)
3	3	118/120 (98%)	9 (7%)	1 (0%)
4	4	155/156 (99%)	26 (16%)	3 (1%)
All	All	5231/5409 (96%)	938 (17%)	103 (1%)

All (938) 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
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

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Mol	Chain	Res	Type
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
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	448	C
1	1	456	G

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Mol	Chain	Res	Type
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	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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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	1161	G
1	1	1163	G
1	1	1164	U
1	1	1165	G
1	1	1175	C
1	1	1184	C
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
1	1	1748	C
1	1	1750	G
1	1	1760	G
1	1	1774	U
1	1	1775	U
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	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
1	1	1941	G
1	1	2045	G
1	1	2046	C
1	1	2047	G
1	1	2048	U
1	1	2054	U
1	1	2055	A
1	1	2063	A

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Mol	Chain	Res	Type
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	2123	G
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	2186	A
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
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

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Mol	Chain	Res	Type
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
1	1	2513	C
1	1	2521	A
1	1	2529	U
1	1	2530	C
1	1	2531	G
1	1	2532	C
1	1	2533	G

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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	2900	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
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

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Mol	Chain	Res	Type
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	3248	A
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
1	1	3325	U
1	1	3331	U
1	1	3332	A
1	1	3333	G
2	2	17	C
2	2	25	C

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Mol	Chain	Res	Type
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	82	G
2	2	83	A
2	2	103	A
2	2	113	C
2	2	115	U
2	2	126	G
2	2	127	U
2	2	128	A
2	2	129	C
2	2	130	C
2	2	131	U
2	2	132	U
2	2	133	A
2	2	134	C
2	2	135	U
2	2	136	A
2	2	137	C
2	2	138	A
2	2	155	U
2	2	156	U
2	2	173	C
2	2	175	G
2	2	177	A
2	2	185	A
2	2	186	C
2	2	187	U
2	2	188	U
2	2	189	C
2	2	190	G

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Mol	Chain	Res	Type
2	2	192	A
2	2	210	A
2	2	211	U
2	2	212	U
2	2	213	A
2	2	214	A
2	2	215	A
2	2	216	A
2	2	218	C
2	2	219	C
2	2	222	U
2	2	223	G
2	2	224	C
2	2	228	U
2	2	229	C
2	2	230	G
2	2	231	G
2	2	232	G
2	2	233	G
2	2	234	C
2	2	235	U
2	2	236	U
2	2	237	U
2	2	247	C
2	2	258	C
2	2	262	A
2	2	269	C
2	2	270	G
2	2	272	C
2	2	273	C
2	2	274	U
2	2	275	U
2	2	276	G
2	2	277	C
2	2	278	G
2	2	284	G
2	2	287	G
2	2	296	A
2	2	311	C
2	2	313	A
2	2	317	U
2	2	319	G

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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	641	C
2	2	646	C
2	2	647	C
2	2	652	G
2	2	674	G
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

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Mol	Chain	Res	Type
2	2	693	U
2	2	703	C
2	2	705	G
2	2	710	C
2	2	723	G
2	2	725	G
2	2	726	U
2	2	727	C
2	2	728	G
2	2	730	G
2	2	731	G
2	2	732	A
2	2	734	C
2	2	737	G
2	2	740	C
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
2	2	787	A
2	2	792	U
2	2	793	U
2	2	809	A
2	2	810	A
2	2	818	U
2	2	819	G
2	2	821	G
2	2	823	U
2	2	827	A
2	2	829	U
2	2	830	U
2	2	832	G
2	2	861	A
2	2	884	U
2	2	896	A
2	2	910	U

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Mol	Chain	Res	Type
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	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
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

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Mol	Chain	Res	Type
2	2	1196	G
2	2	1197	G
2	2	1214	A
2	2	1215	G
2	2	1223	G
2	2	1224	A
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
2	2	1312	U
2	2	1313	G
2	2	1318	A
2	2	1335	C
2	2	1336	C
2	2	1337	U
2	2	1338	G
2	2	1341	A
2	2	1342	A
2	2	1344	U
2	2	1345	A
2	2	1348	C
2	2	1358	U
2	2	1359	U
2	2	1360	G
2	2	1364	G
2	2	1365	U

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Mol	Chain	Res	Type
2	2	1374	U
2	2	1375	U
2	2	1378	U
2	2	1379	A
2	2	1380	G
2	2	1382	G
2	2	1383	G
2	2	1384	G
2	2	1385	A
2	2	1387	U
2	2	1388	A
2	2	1406	A
2	2	1408	G
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

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Mol	Chain	Res	Type
2	2	1570	G
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	1684	C
2	2	1686	G
2	2	1691	G
2	2	1693	C
2	2	1696	C
2	2	1700	G
2	2	1701	A
2	2	1704	A
2	2	1708	A
2	2	1709	G
2	2	1711	G
2	2	1714	G
2	2	1726	A
2	2	1756	G
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
3	3	7	G
3	3	54	U
3	3	55	A

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Mol	Chain	Res	Type
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	103	G
4	4	104	A
4	4	105	A
4	4	106	C
4	4	111	A
4	4	113	U
4	4	125	U
4	4	138	A

All (103) 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
1	1	469	C

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Mol	Chain	Res	Type
1	1	484	A
1	1	609	A
1	1	703	A
1	1	898	G
1	1	960	C
1	1	1009	U
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	1774	U
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
1	1	3258	U
1	1	3281	G

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Mol	Chain	Res	Type
1	1	3298	U
1	1	3323	C
1	1	3332	A
2	2	75	A
2	2	102	A
2	2	125	A
2	2	131	U
2	2	184	G
2	2	187	U
2	2	211	U
2	2	222	U
2	2	228	U
2	2	231	G
2	2	233	G
2	2	269	C
2	2	273	C
2	2	274	U
2	2	275	U
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	678	G
2	2	720	G
2	2	725	G
2	2	740	C
2	2	754	A
2	2	792	U
2	2	827	A
2	2	1094	U
2	2	1165	U
2	2	1193	A
2	2	1197	G
2	2	1224	A
2	2	1241	A
2	2	1252	G
2	2	1282	U
2	2	1337	U
2	2	1341	A

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Mol	Chain	Res	Type
2	2	1374	U
2	2	1378	U
2	2	1387	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	103	G
4	4	104	A

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	1.03	0	7,9,11	0.99	0
1	OMG	1	2578	1	23,26,27	0.43	0	32,38,41	0.50	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 464 ligands modelled in this entry, 463 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	0.26	0	48,52,52	0.28	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	-	9/22/38/38	0/3/3/3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (9) torsion outliers are listed below:

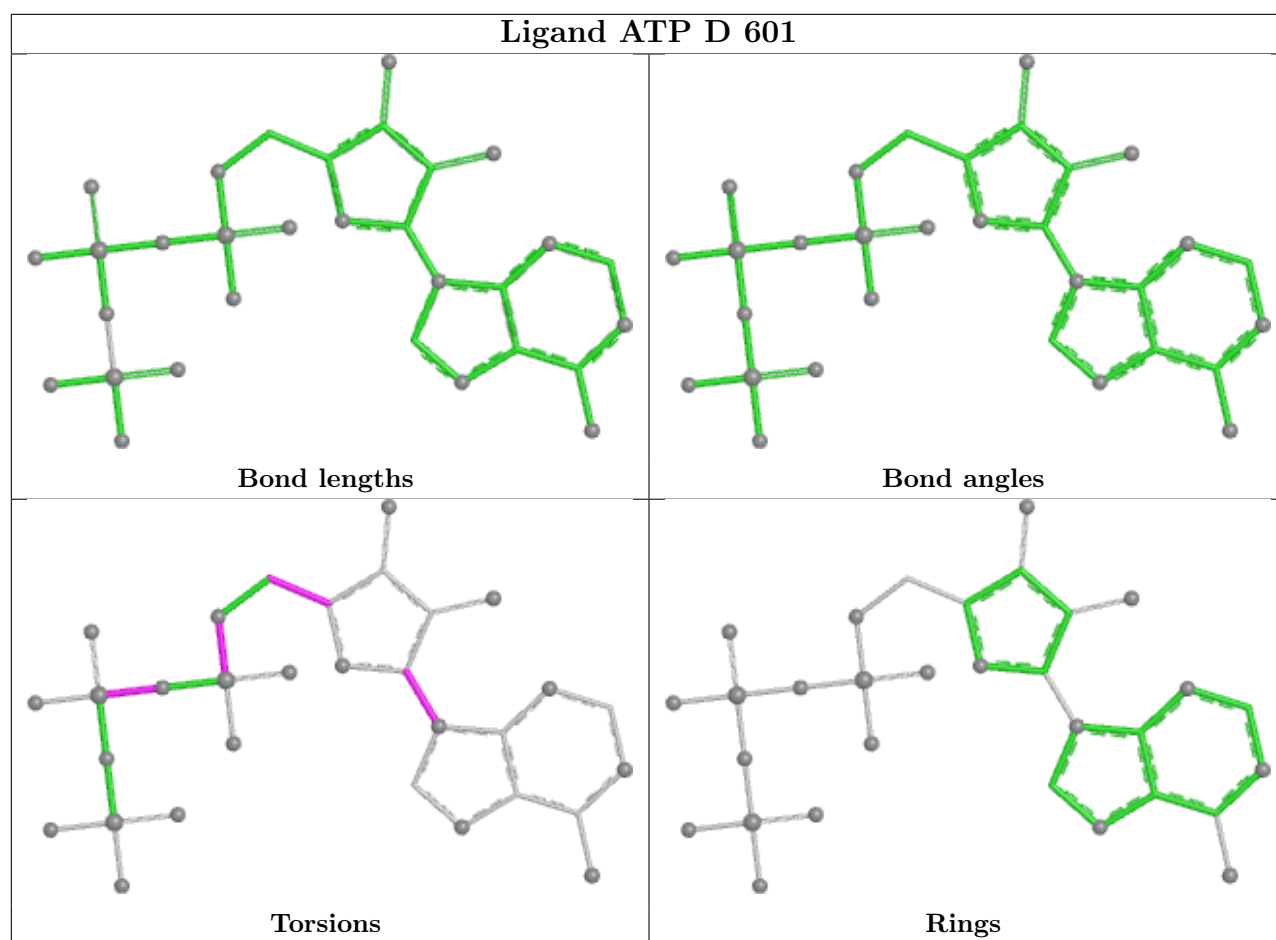
Mol	Chain	Res	Type	Atoms
87	D	601	ATP	C5'-O5'-PA-O3A
87	D	601	ATP	C3'-C4'-C5'-O5'
87	D	601	ATP	O4'-C4'-C5'-O5'
87	D	601	ATP	C2'-C1'-N9-C8
87	D	601	ATP	C2'-C1'-N9-C4
87	D	601	ATP	PA-O3A-PB-O2B
87	D	601	ATP	O4'-C1'-N9-C8
87	D	601	ATP	O4'-C1'-N9-C4
87	D	601	ATP	PA-O3A-PB-O1B

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
87	D	601	ATP	1	0

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

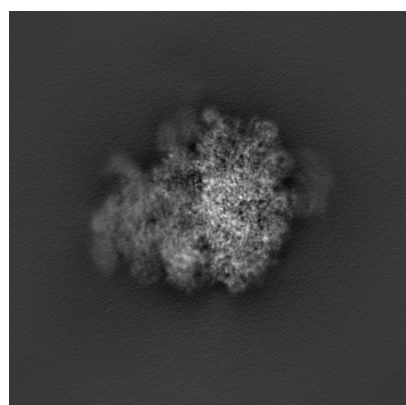
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14479. These allow visual inspection of the internal detail of the map and identification of artifacts.

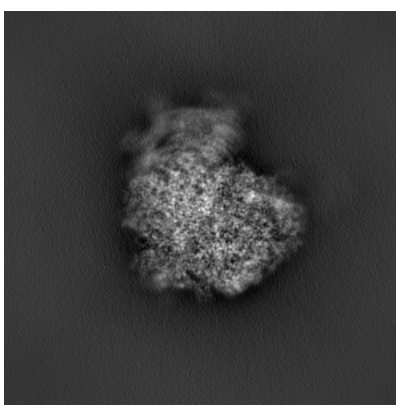
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

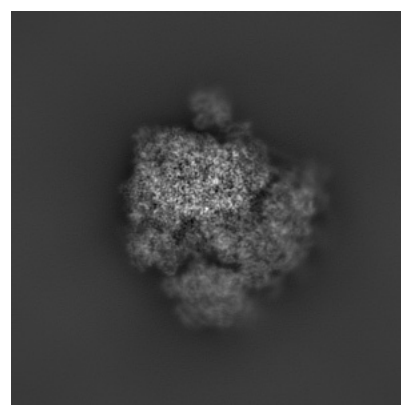
6.1.1 Primary map



X



Y

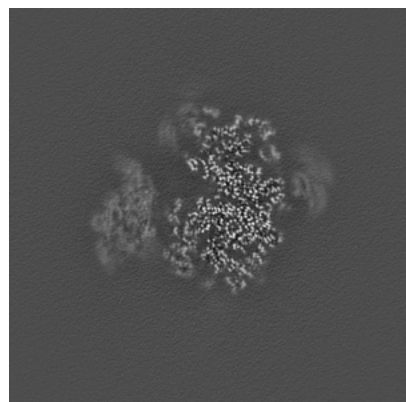


Z

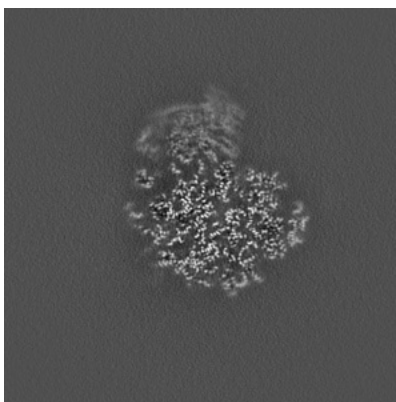
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

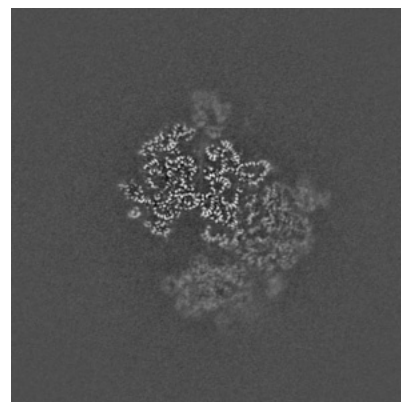
6.2.1 Primary map



X Index: 243



Y Index: 243

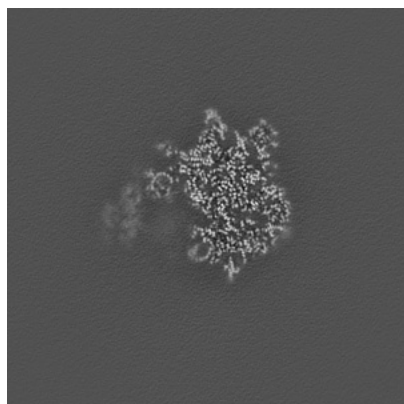


Z Index: 243

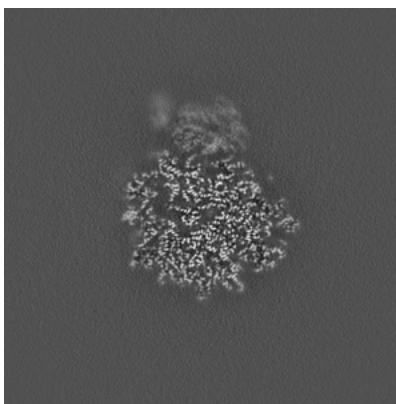
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

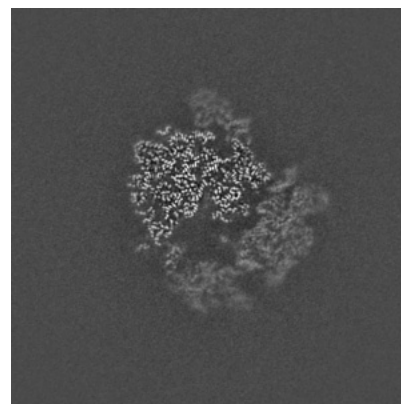
6.3.1 Primary map



X Index: 201



Y Index: 267

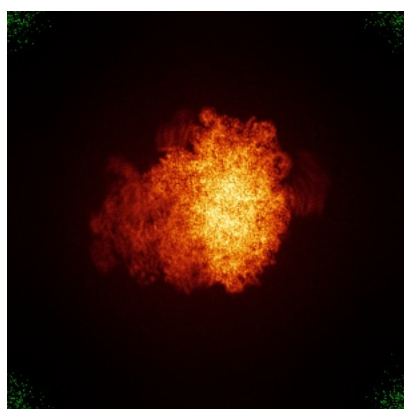


Z Index: 258

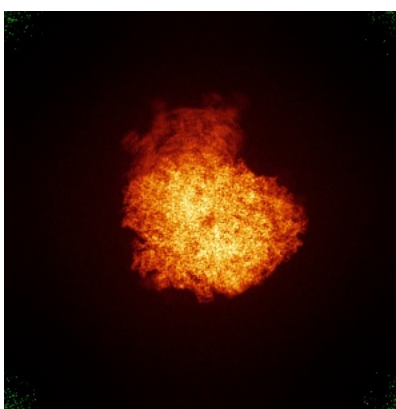
The images above show the largest variance slices of the map in three orthogonal directions.

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

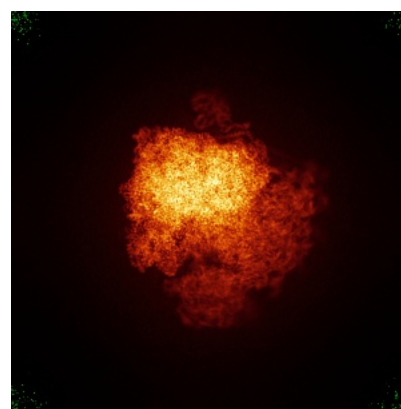
6.4.1 Primary map



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



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 1.8. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

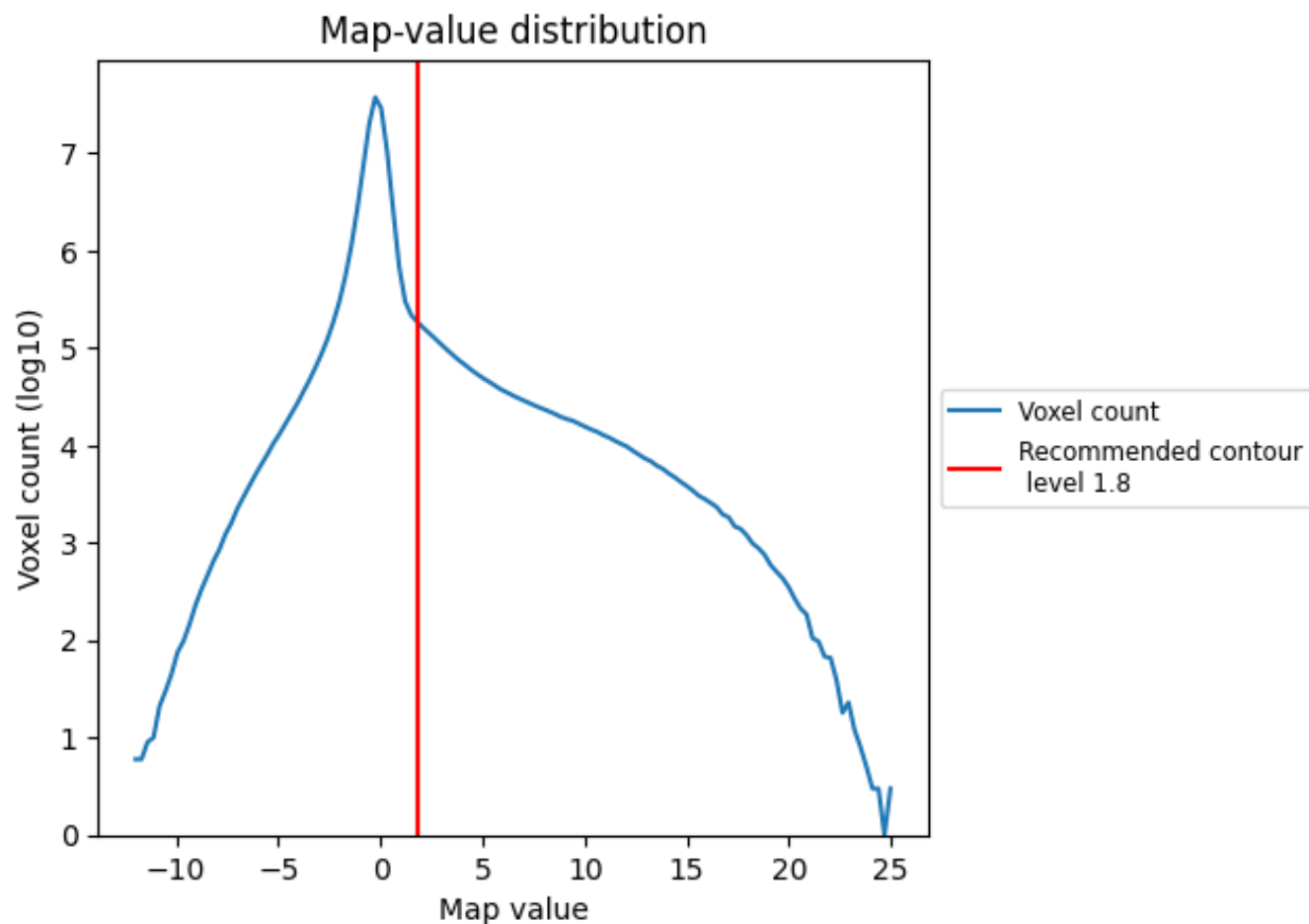
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

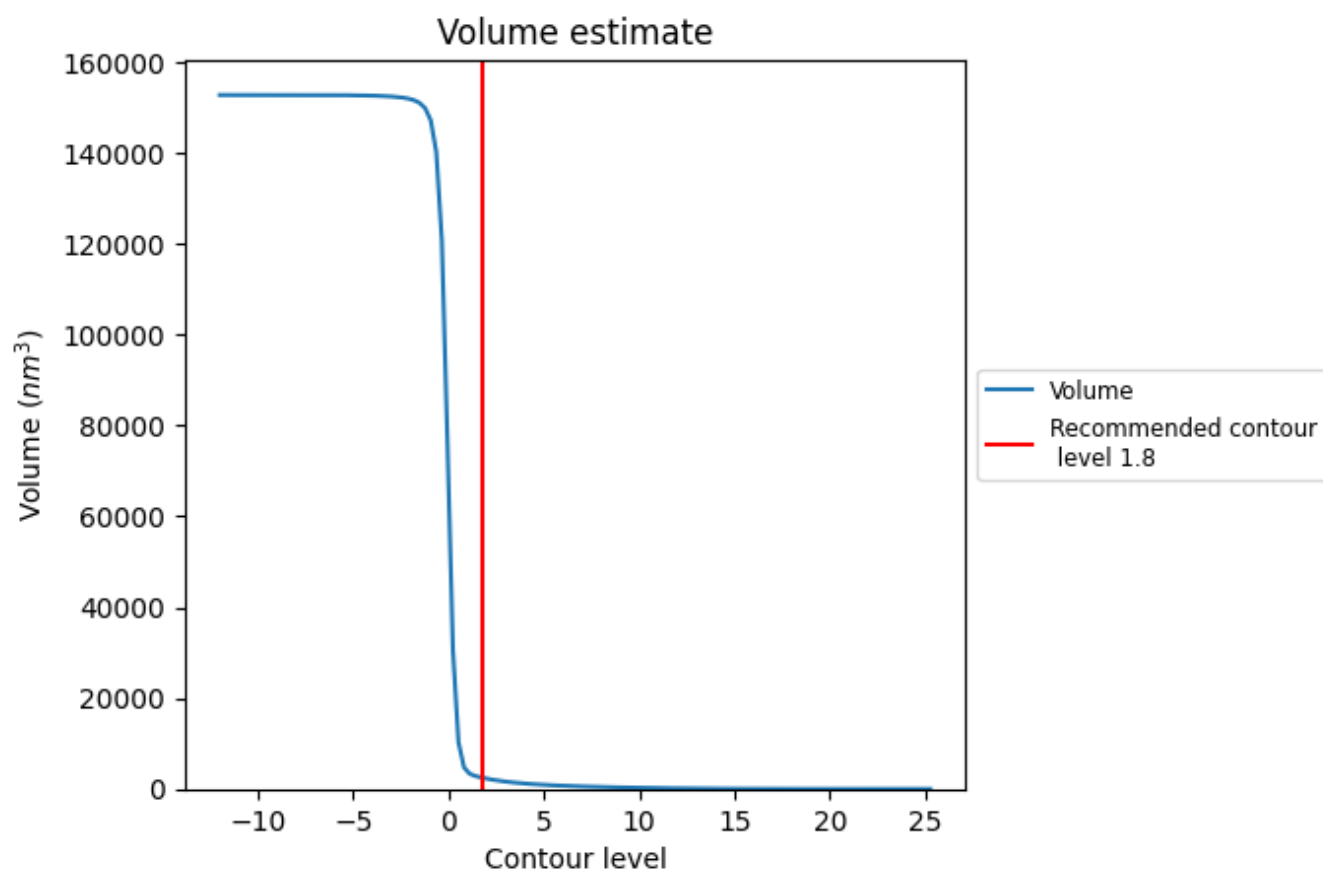
This section contains the results of statistical analysis of the map.

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.

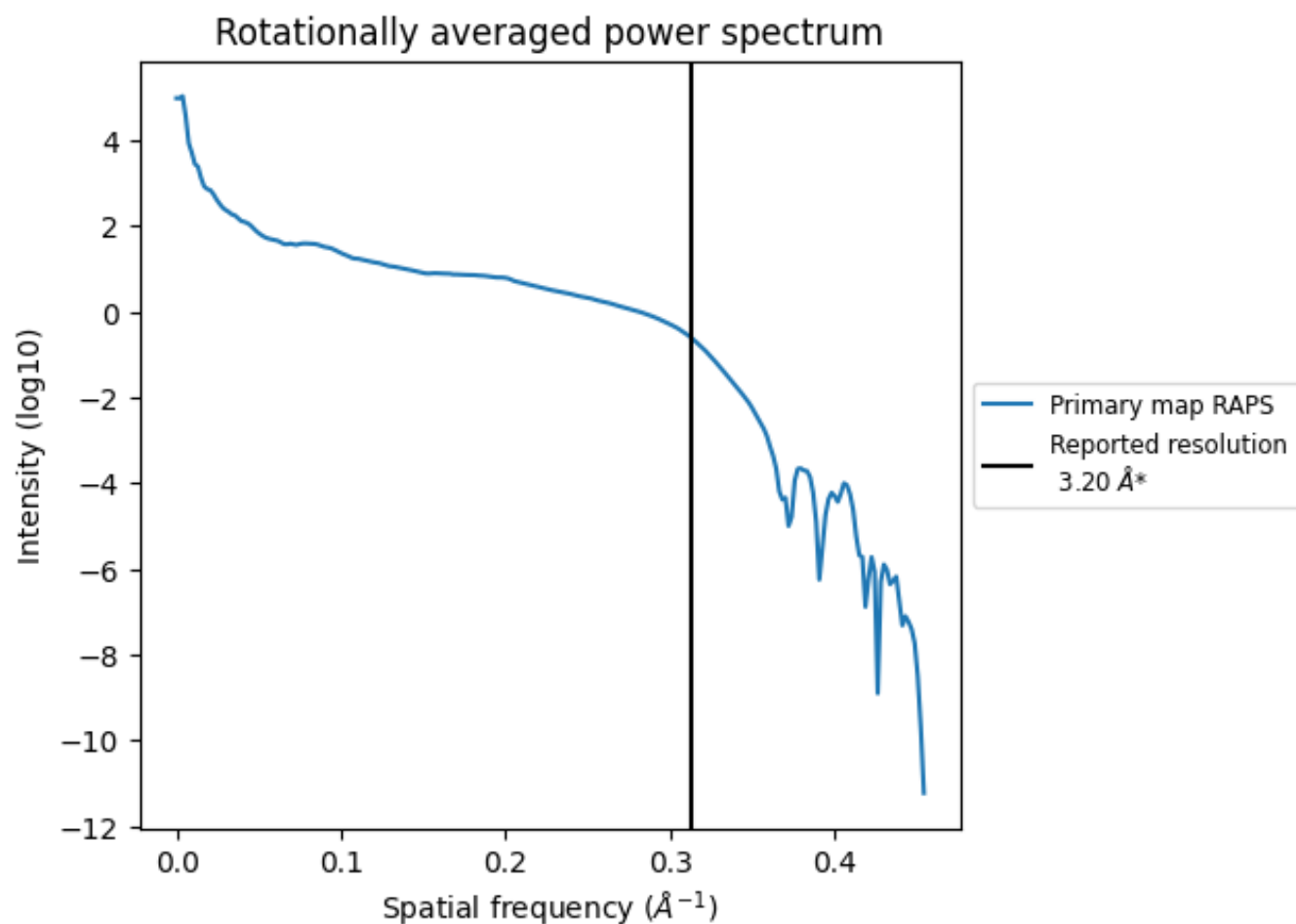
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2455 nm³; this corresponds to an approximate mass of 2218 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 ⓘ

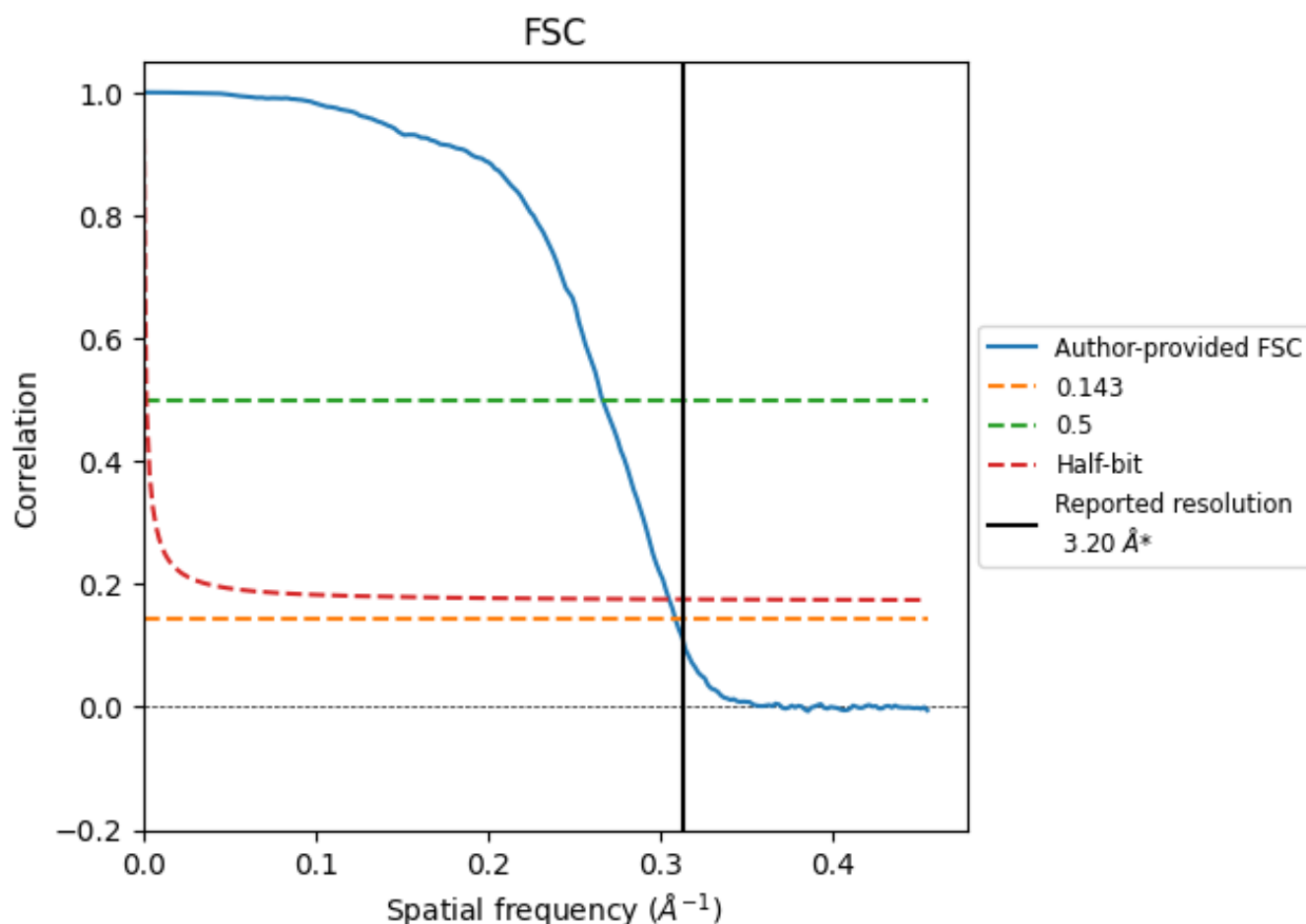


*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

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 0.312 Å⁻¹

8.2 Resolution estimates [i](#)

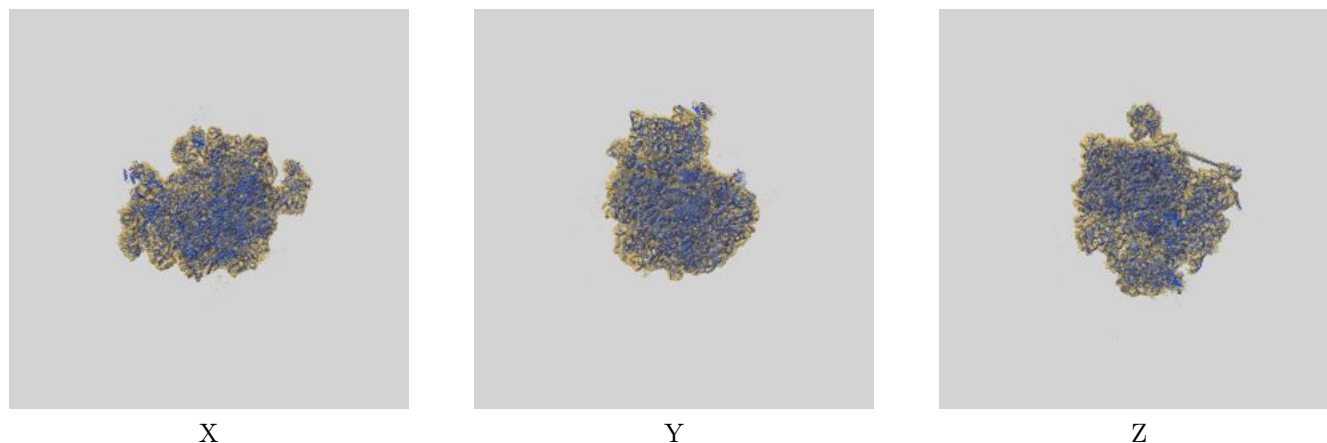
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	3.24	3.76	3.28
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

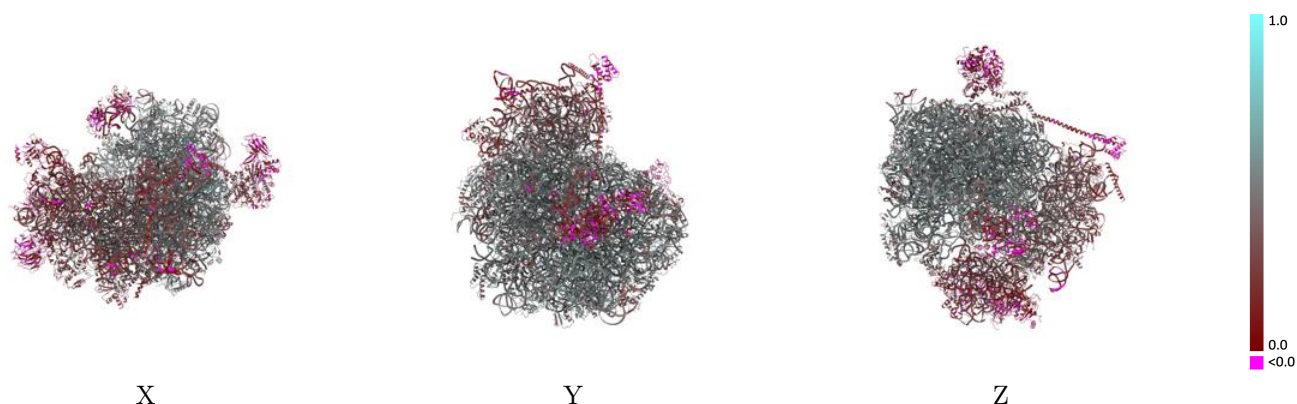
This section contains information regarding the fit between EMDB map EMD-14479 and PDB model 7Z3N. Per-residue inclusion information can be found in [section 3](#) on [page 22](#).

9.1 Map-model overlay [i](#)



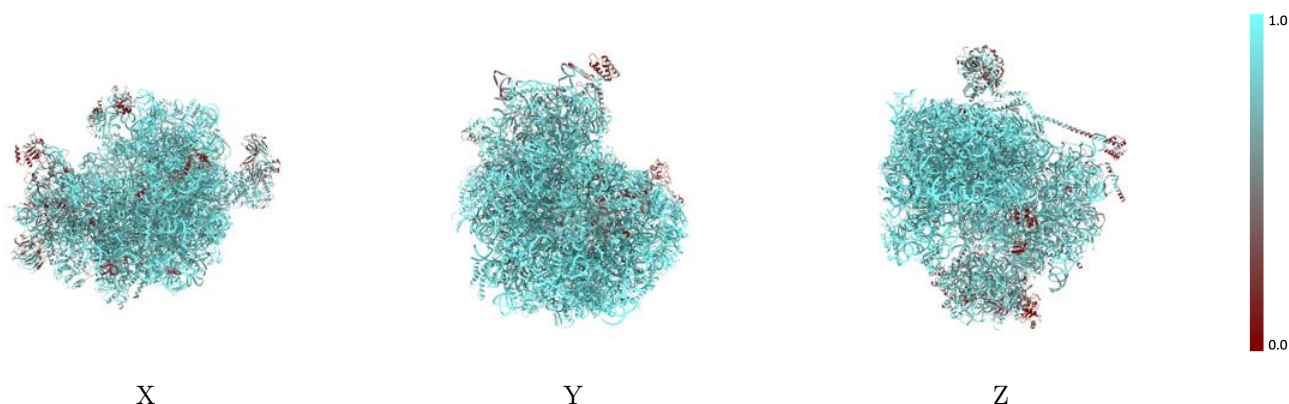
The images above show the 3D surface view of the map at the recommended contour level 1.8 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



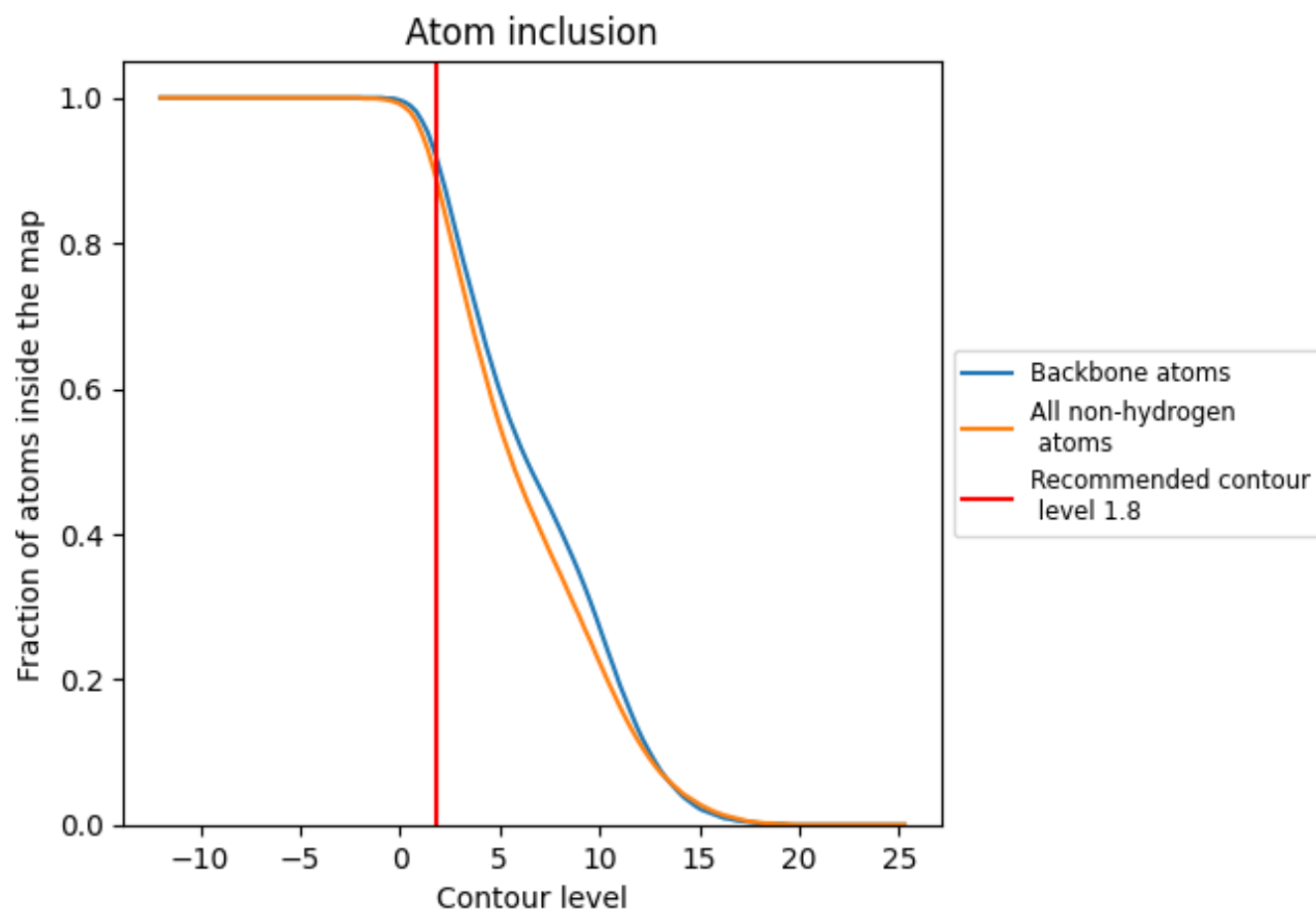
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (1.8).

9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 89% 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 (1.8) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8910	 0.4120
1	 0.9880	 0.4980
2	 0.8990	 0.3370
3	 0.9980	 0.5030
4	 0.9910	 0.5000
A	 0.4790	 0.0780
B	 0.2210	 0.2020
C	 0.6150	 0.1840
D	 0.6300	 0.1330
LA	 0.9210	 0.5190
LB	 0.9500	 0.5120
LC	 0.9510	 0.5120
LD	 0.9420	 0.4510
LE	 0.9410	 0.4580
LF	 0.9420	 0.5010
LG	 0.9370	 0.4780
LH	 0.9400	 0.4780
LI	 0.9170	 0.4930
LJ	 0.9280	 0.4250
LK	 0.5540	 0.0750
LL	 0.9560	 0.4950
LM	 0.9410	 0.4810
LN	 0.9520	 0.5280
LO	 0.9520	 0.5010
LP	 0.8870	 0.4810
LQ	 0.9520	 0.5230
LR	 0.8990	 0.4550
LS	 0.9580	 0.5150
LT	 0.9530	 0.5120
LU	 0.9300	 0.4270
LV	 0.9370	 0.5110
LW	 0.7230	 0.3370
LX	 0.9310	 0.4820
LY	 0.9590	 0.5010
LZ	 0.9470	 0.4850



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Chain	Atom inclusion	Q-score
La	 0.9600	 0.5320
Lb	 0.9250	 0.4680
Lc	 0.9270	 0.4700
Ld	 0.8700	 0.4710
Le	 0.9490	 0.5300
Lf	 0.9540	 0.5330
Lg	 0.9350	 0.5080
Lh	 0.9310	 0.4610
Li	 0.9160	 0.4590
Lj	 0.9540	 0.5340
Lk	 0.8970	 0.4310
Ll	 0.9300	 0.4980
Lm	 0.9560	 0.5050
Ln	 0.7980	 0.4250
Lo	 0.9390	 0.5050
Lp	 0.9030	 0.4970
Lq	 0.9500	 0.5070
Lr	 0.6110	 0.2540
Ls	 0.4020	 0.1260
NC	 0.1630	 0.3150
SA	 0.8330	 0.3400
SB	 0.8310	 0.3800
SC	 0.8080	 0.3360
SD	 0.6140	 0.2280
SE	 0.7390	 0.3350
SF	 0.6190	 0.2630
SG	 0.8100	 0.3030
SH	 0.7880	 0.3120
SI	 0.7820	 0.3660
SJ	 0.7260	 0.3100
SK	 0.6310	 0.1850
SL	 0.7050	 0.3840
SM	 0.1260	 0.1360
SN	 0.8100	 0.3910
SO	 0.8760	 0.4160
SP	 0.6340	 0.1810
SQ	 0.6910	 0.2270
SR	 0.7400	 0.2330
SS	 0.6790	 0.1810
ST	 0.6450	 0.2010
SU	 0.6450	 0.2100
SV	 0.8390	 0.3370

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Chain	Atom inclusion	Q-score
SW	 0.8200	 0.3750
SX	 0.7890	 0.3600
SY	 0.7750	 0.2890
SZ	 0.7070	 0.1960
Sa	 0.8710	 0.4350
Sb	 0.8140	 0.3790
Sc	 0.7630	 0.3220
Sd	 0.6670	 0.2440
Se	 0.8520	 0.3280
Sf	 0.6220	 0.1060