



Full wwPDB EM Validation Report ⓘ

Mar 26, 2026 – 05:56 PM UTC

PDB ID : 7OLD / pdb_00007old
EMDB ID : EMD-12977
Title : Thermophilic eukaryotic 80S ribosome at pe/E (TI)-POST state
Authors : Kisonaite, M.; Wild, K.; Sinning, I.
Deposited on : 2021-05-19
Resolution : 3.00 Å(reported)
Based on initial model : 4V88

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:

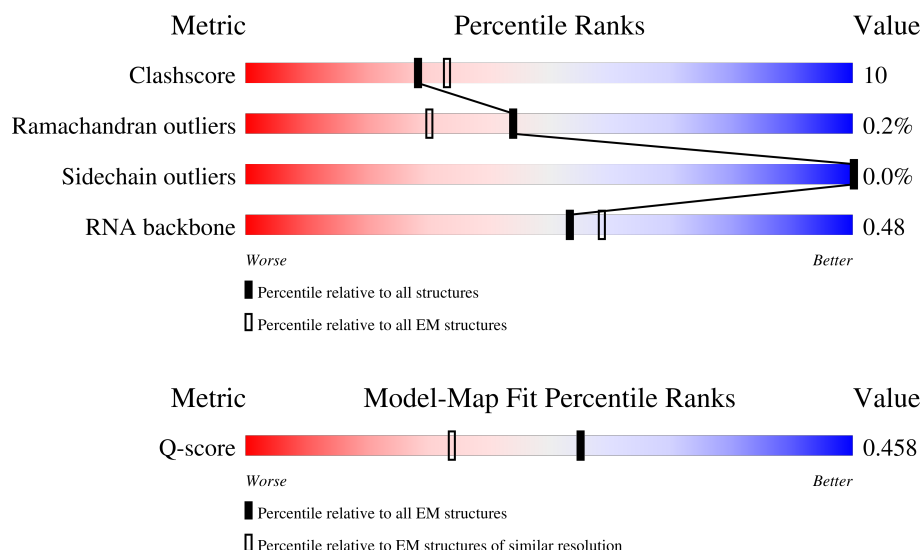
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 3.00 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.



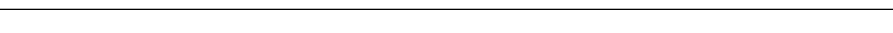
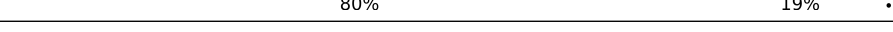
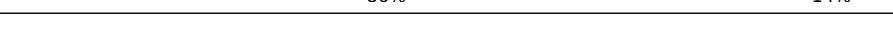
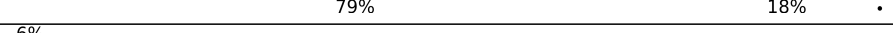
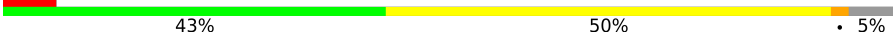
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14081 (2.50 - 3.50)

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	5	75	
6	A	316	
7	B	302	
8	C	845	
9	LA	254	
10	LB	392	
11	LC	365	
12	LD	304	
13	LE	200	
14	LF	249	
15	LG	262	
16	LH	229	
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	

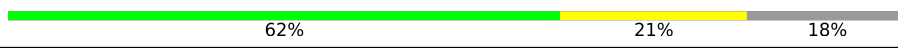
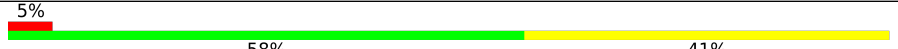
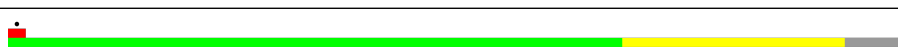
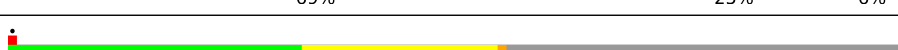
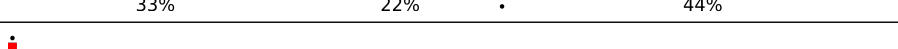
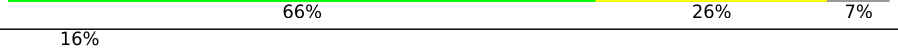
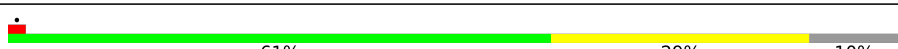
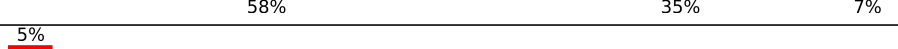
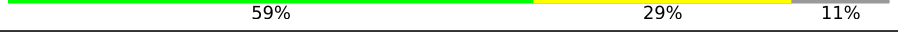
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Mol	Chain	Length	Quality of chain
29	LU	127	
30	LV	139	
31	LW	205	
32	LX	156	
33	LY	138	
34	LZ	135	
35	La	149	
36	Lb	65	
37	Lc	108	
38	Ld	120	
39	Le	131	
40	Lf	109	
41	Lg	119	
42	Lh	126	
43	Li	110	
44	Lj	95	
45	Lk	94	
46	Ll	51	
47	Lm	127	
48	Ln	25	
48	Lr	25	
49	Lo	106	
50	Lp	92	
51	Lq	147	
52	Ls	312	

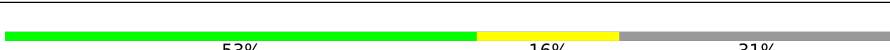
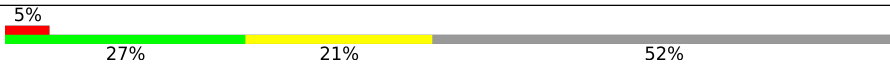
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Mol	Chain	Length	Quality of chain
53	SA	285	
54	SB	255	
55	SC	263	
56	SD	254	
57	SE	264	
58	SF	212	
59	SG	239	
60	SH	203	
61	SI	202	
62	SJ	190	
63	SK	159	
64	SL	161	
65	SM	144	
66	SN	151	
67	SO	150	
68	SP	153	
69	SQ	143	
70	SR	143	
71	SS	156	
72	ST	153	
73	SU	116	
74	SV	98	
75	SW	130	
76	SX	145	
77	SY	136	

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

2 Entry composition [i](#)

There are 87 unique types of molecules in this entry. The entry contains 214209 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	3192	Total	C	N	O	P	0	0
			68264	30474	12339	22259	3192		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	1765	Total	C	N	O	P	0	0
			37645	16822	6706	12352	1765		

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

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

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

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

- Molecule 5 is a RNA chain called pe/E tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	5	75	Total	C	N	O	P	0	0
			1589	710	279	525	75		

- Molecule 6 is a protein called Putative guanine nucleotide-binding protein.

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

- Molecule 7 is a protein called HABP4_PA1-RBP1 domain-containing protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	B	129	Total	C	N	O	0	0
			982	584	198	200		

- Molecule 8 is a protein called Elongation factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	C	813	Total	C	N	O	S	0	0
			6335	4024	1092	1192	27		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LA	248	Total	C	N	O	S	0	0
			1891	1182	378	328	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	234	Total	C	N	O	S	0	0
			1891	1212	349	325	5		

- Molecule 16 is a protein called 60S ribosomal protein l9-like protein.

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	156	Total	C	N	O	S	0	0
			1174	737	214	221	2		

- 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
			1610	1034	305	266	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LP	174	Total	C	N	O	S	0	0
			1378	856	278	241	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	100	Total	C	N	O	S	0	0
			810	526	140	143	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
30	LV	137	Total	C	N	O	S	0	0
			1012	644	189	172	7		

- Molecule 31 is a protein called 60S ribosomal protein L24-like protein.

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
			967	621	176	170		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
33	LY	133	Total	C	N	O	S	0	0
			1056	658	213	183	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	63	Total	C	N	O		0	0
			515	314	113	88			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Lc	95	Total	C	N	O	S	0	0
			708	450	122	131	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Ld	112	Total	C	N	O	S	0	0
			907	573	178	155	1		

- 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		
			1003	637	198	168	0	0

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

Mol	Chain	Residues	Atoms				AltConf	Trace
43	Li	101	Total	C	N	O	S	
			826	509	181	135	1	0

- Molecule 44 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	Lj	88	Total	C	N	O	S	
			698	427	154	112	5	0

- Molecule 45 is a protein called 60S ribosomal protein L38-like protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	Lk	76	Total	C	N	O	S	
			632	400	121	109	2	0

- Molecule 46 is a protein called Ribosomal protein eL39.

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

- Molecule 47 is a protein called Ubiquitin.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Lm	2	MET	-	initiating methionine	UNP G0S8G4

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

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Ln	25	Total	C	N	O	S	0	0
			233	142	63	27	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	S	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 40S ribosomal protein S0.

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

- Molecule 54 is a protein called 40S ribosomal protein S1.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SB	224	Total	C	N	O	S	0	0
			1810	1150	338	317	5		

- Molecule 55 is a protein called 40S ribosomal protein S2-like protein.

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

- Molecule 56 is a protein called 40S ribosomal protein S3-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SD	214	Total	C	N	O	S	0	0
			1683	1063	307	305	8		

- Molecule 57 is a protein called 40S ribosomal protein S4.

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

- Molecule 58 is a protein called 40S ribosomal protein s5-like protein.

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

- Molecule 59 is a protein called 40S ribosomal protein S6.

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

- Molecule 60 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SH	198	Total	C	N	O	S	0	0
			1584	997	303	284			

- Molecule 61 is a protein called 40S ribosomal protein S8.

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

- Molecule 62 is a protein called 40S ribosomal protein s9-like protein.

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

- Molecule 63 is a protein called 40S ribosomal protein s10-like protein.

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

- Molecule 64 is a protein called 40S ribosomal protein S11-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	SL	149	Total	C	N	O	S	0	0
			1214	775	235	199	5		

- Molecule 65 is a protein called 40S ribosomal protein S12.

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

- Molecule 66 is a protein called 40S ribosomal protein S13-like protein.

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

- Molecule 67 is a protein called 40S ribosomal protein S14-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	SO	135	Total	C	N	O	S	0	0
			1005	615	199	186	5		

- Molecule 68 is a protein called 40S ribosomal protein s15-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	SP	128	Total	C	N	O	S	0	0
			1036	659	197	177	3		

- Molecule 69 is a protein called 40S ribosomal protein S16-like protein.

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

- Molecule 70 is a protein called 40S ribosomal protein S17-like protein.

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

- Molecule 71 is a protein called Putative ribosomal protein.

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

- Molecule 72 is a protein called 40S ribosomal protein S19-like protein.

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

- Molecule 73 is a protein called 40S ribosomal protein S20-like protein.

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

- Molecule 74 is a protein called 40S ribosomal protein S21-like protein.

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

- Molecule 75 is a protein called 40S ribosomal protein S22-like protein.

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

- Molecule 76 is a protein called 40S ribosomal protein s23-like protein.

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

- Molecule 77 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	SY	121	Total	C	N	O	S	0	0
			977	614	192	169	2		

- Molecule 78 is a protein called 40S ribosomal protein S25.

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

- Molecule 79 is a protein called 40S ribosomal protein S26.

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

- Molecule 80 is a protein called Ribosomal protein s27-like protein.

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

- Molecule 81 is a protein called 40S ribosomal protein S28-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	Sc	60	Total	C	N	O	S	0	0
			473	292	93	87	1		

- Molecule 82 is a protein called Ribosomal protein uS14.

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

- Molecule 83 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms				AltConf	Trace
83	Se	43	Total	C	N	O	0	0
			347	217	73	57		

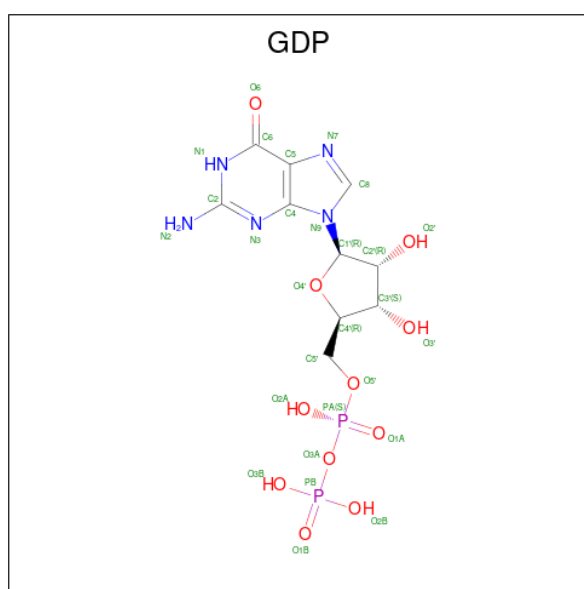
- Molecule 84 is a protein called 40S ribosomal protein S27a-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	Sf	74	Total	C	N	O	S	0	0
			613	388	117	102	6		

- Molecule 85 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
85	1	2	Total	Mg	0
			2	2	
85	C	1	Total	Mg	0
			1	1	

- Molecule 86 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
86	C	1	Total	C	N	O	P	0
			28	10	5	11	2	

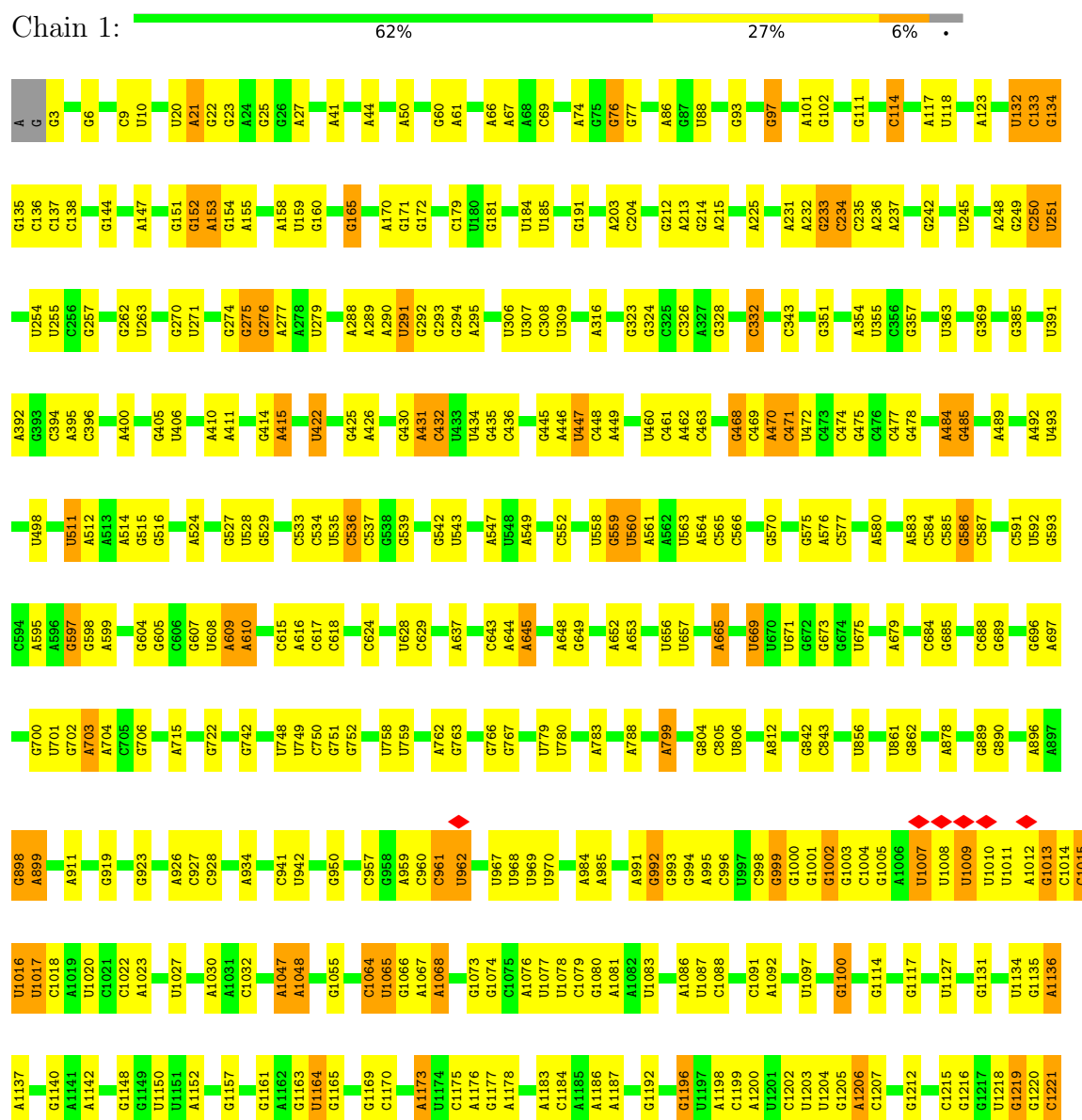
- Molecule 87 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
87	Lg	1	Total 1	Zn 1	0
87	Lj	1	Total 1	Zn 1	0
87	Lm	1	Total 1	Zn 1	0
87	Lo	1	Total 1	Zn 1	0
87	Lp	1	Total 1	Zn 1	0
87	Sa	1	Total 1	Zn 1	0
87	Sb	1	Total 1	Zn 1	0
87	Sd	1	Total 1	Zn 1	0

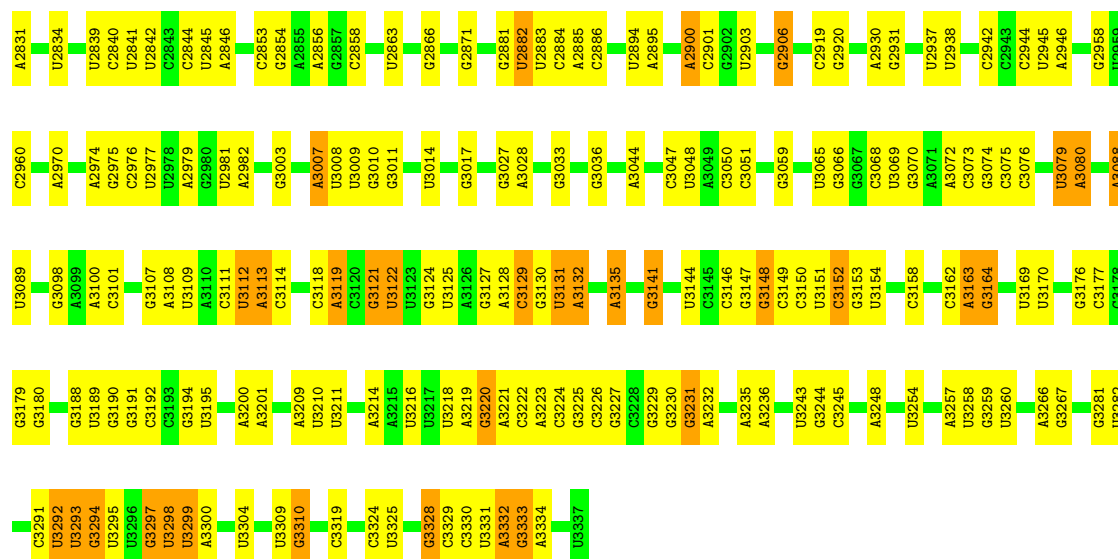
3 Residue-property plots

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.

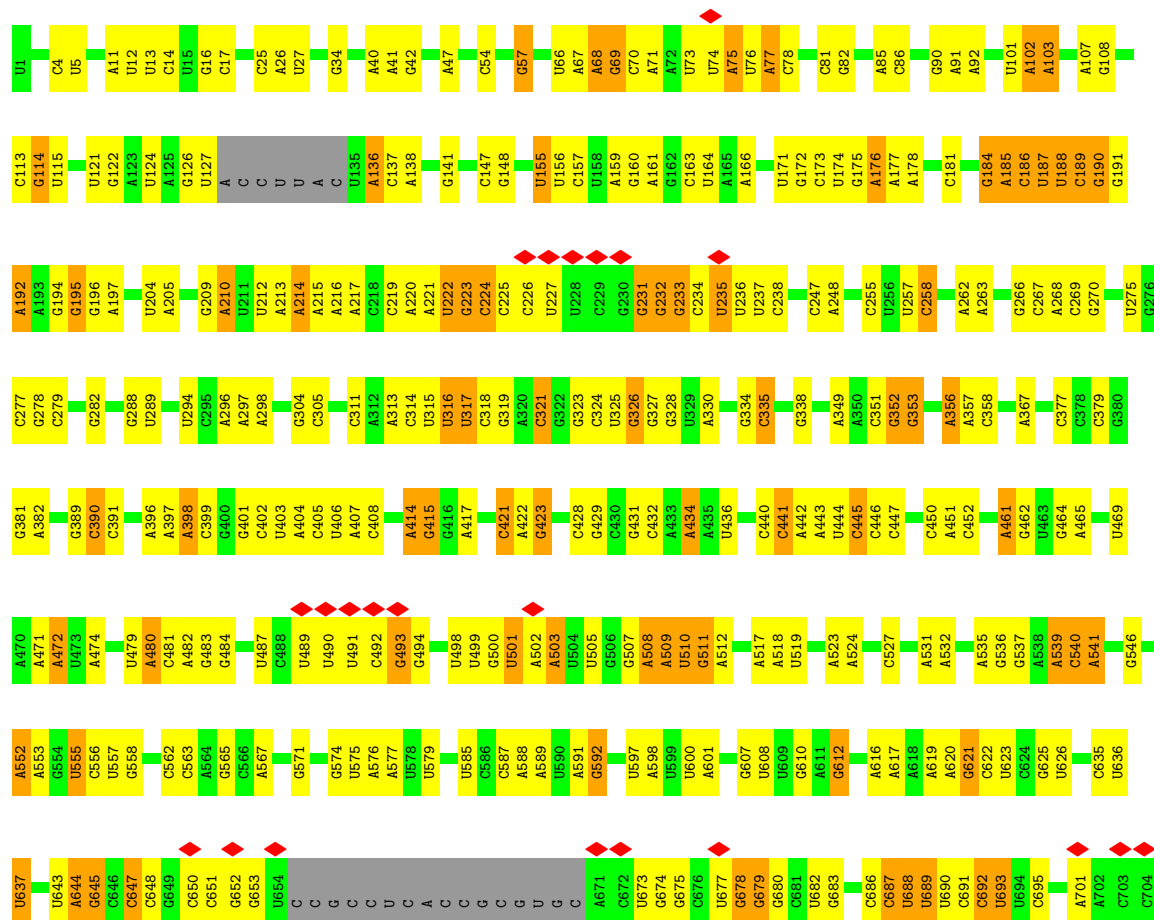
• Molecule 1: 26S rRNA

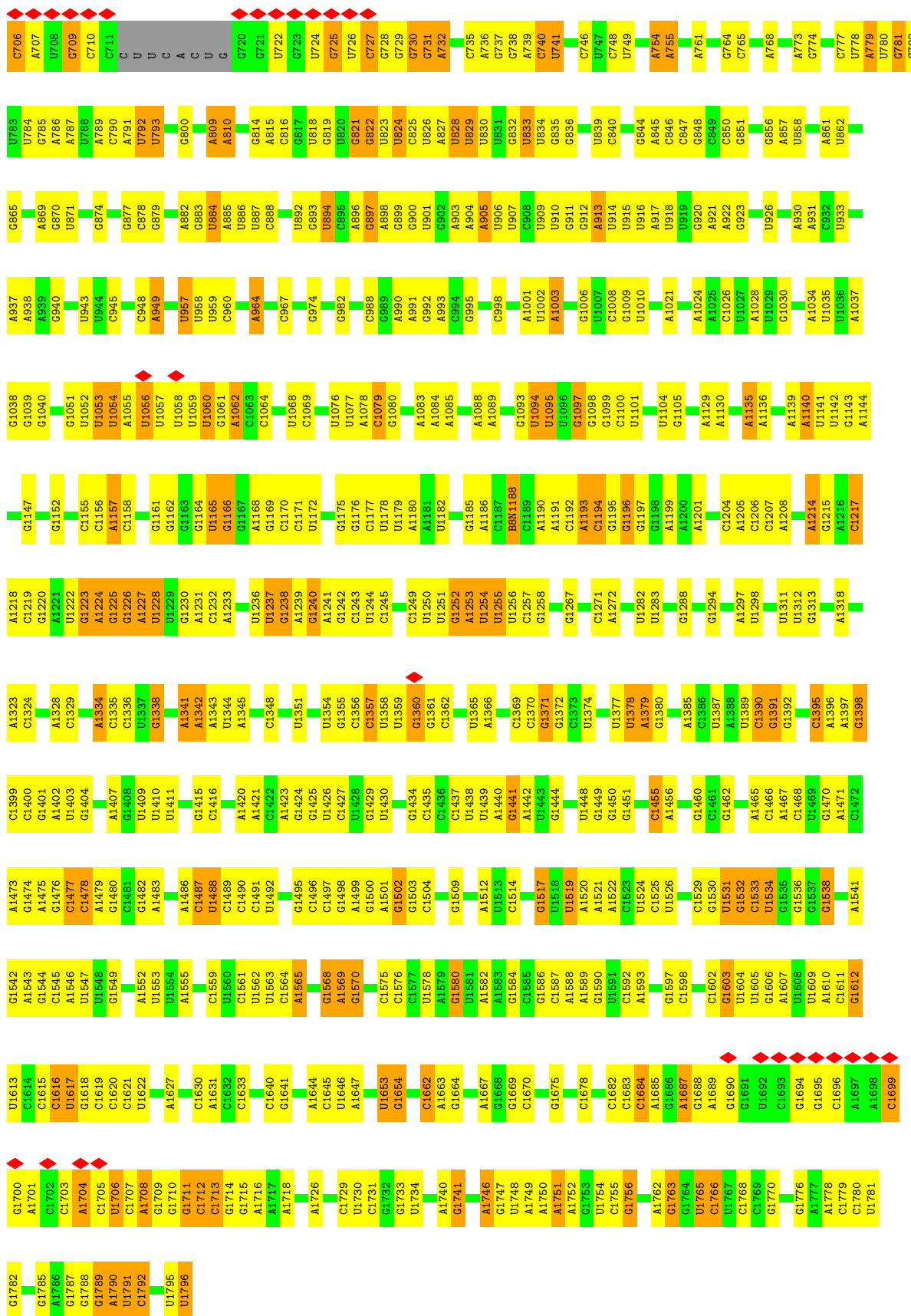






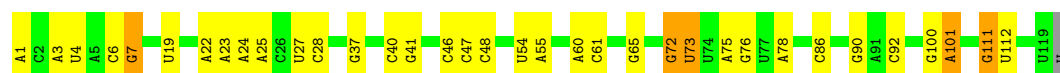
• Molecule 2: 18S rRNA





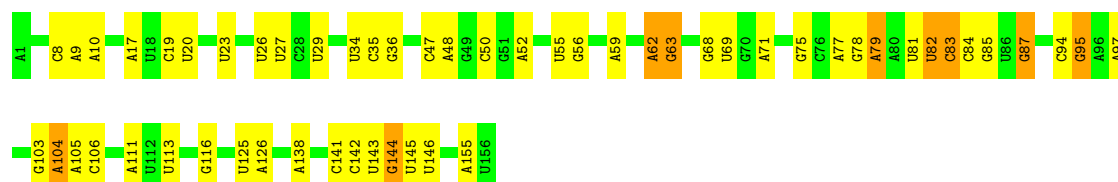
• Molecule 3: 5S rRNA

Chain 3:  70% 25%



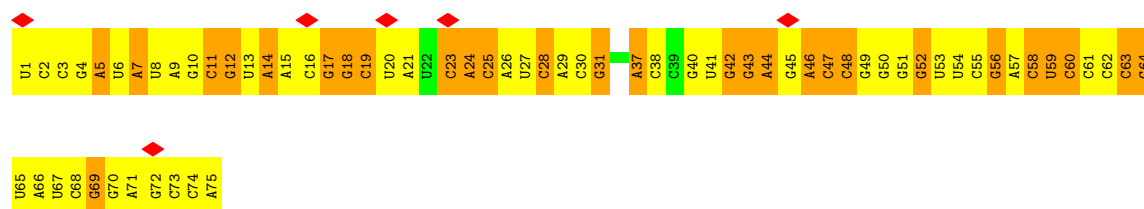
• Molecule 4: 5.8S rRNA

Chain 4:  65% 29% 6%



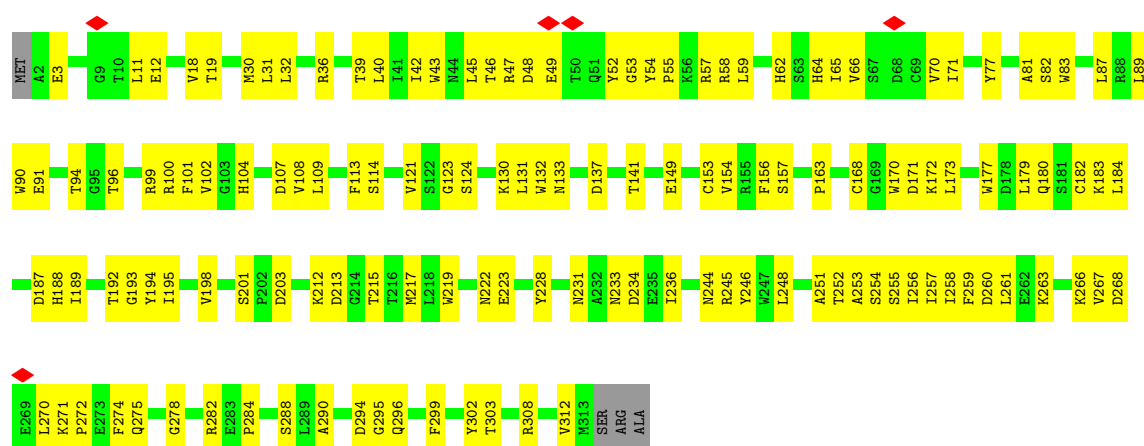
• Molecule 5: pe/E tRNA

Chain 5:  8% 9% 53% 37%



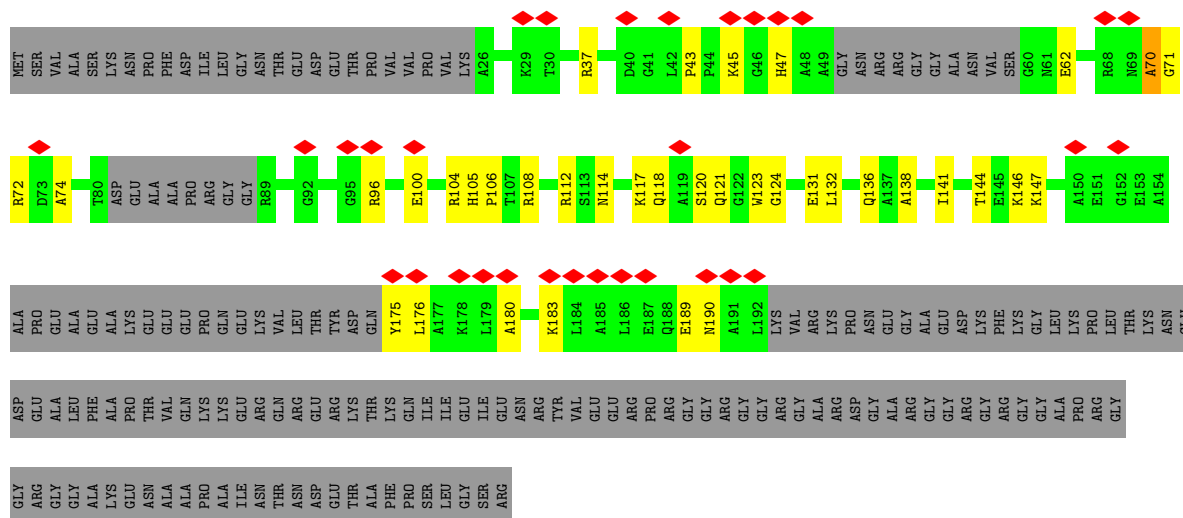
• Molecule 6: Putative guanine nucleotide-binding protein

Chain A:  56% 43%

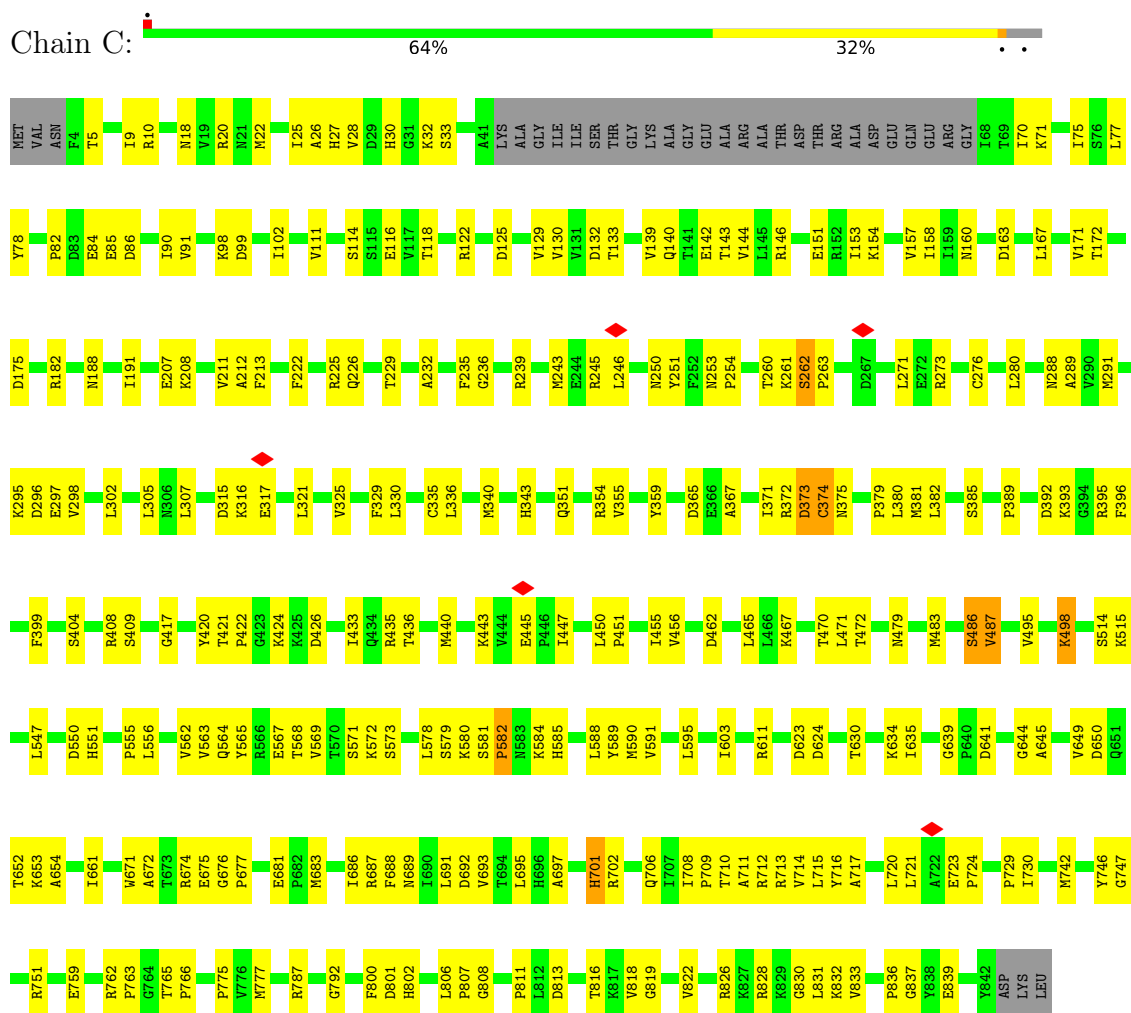


• Molecule 7: HABP4_PAIRBP1 domain-containing protein

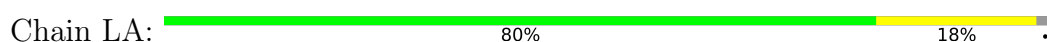
Chain B:  10% 30% 12% 57%

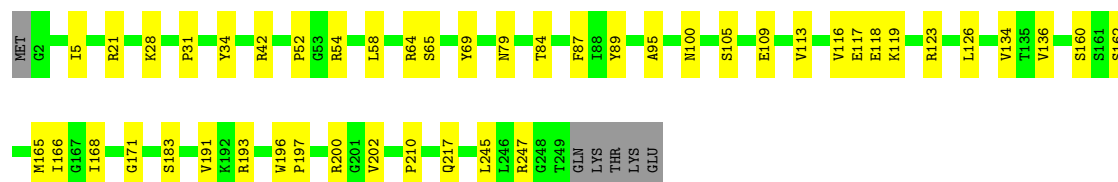


• Molecule 8: Elongation factor 2



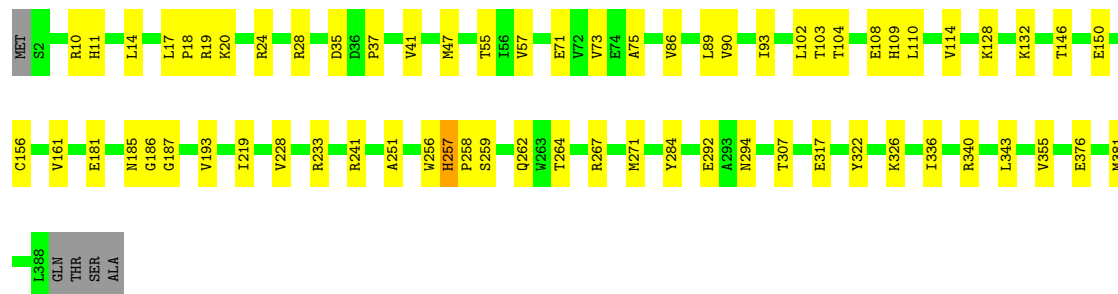
• Molecule 9: 60S ribosomal protein L2-like protein





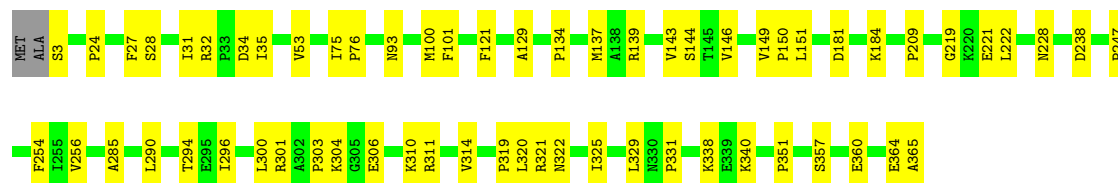
- Molecule 10: 60S ribosomal protein L3-like protein

Chain LB: 82% 17% .



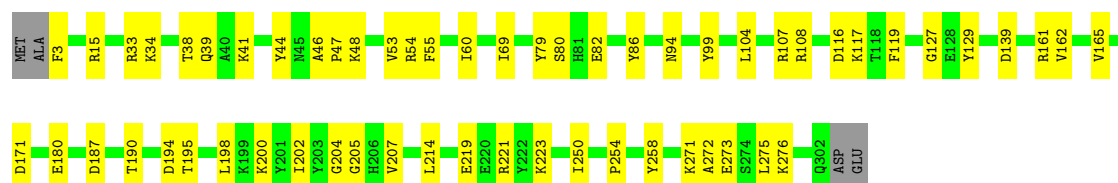
- Molecule 11: 60S ribosomal protein L4-like protein

Chain LC: 82% 17% .



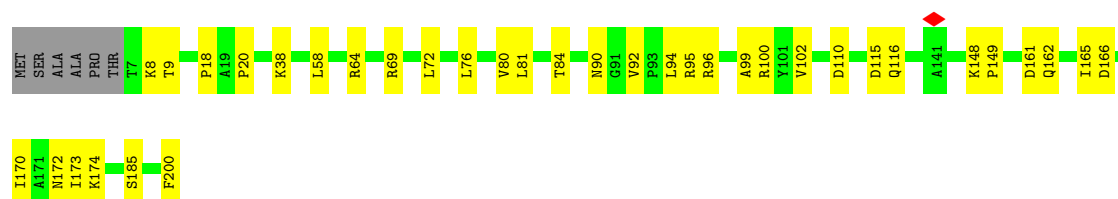
- Molecule 12: 60S ribosomal protein l5-like protein

Chain LD: 80% 19% .



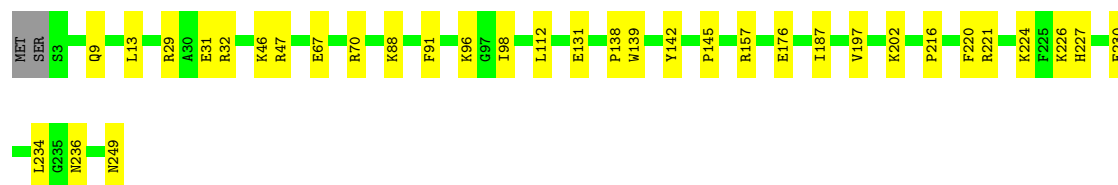
- Molecule 13: 60S ribosomal protein L6

Chain LE: 79% 18% .



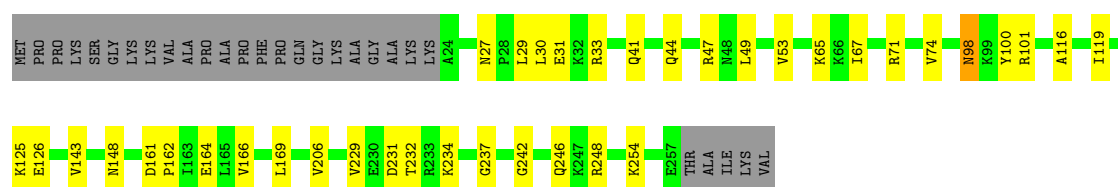
- Molecule 14: 60S ribosomal protein l7-like protein

Chain LF:  86% 14%



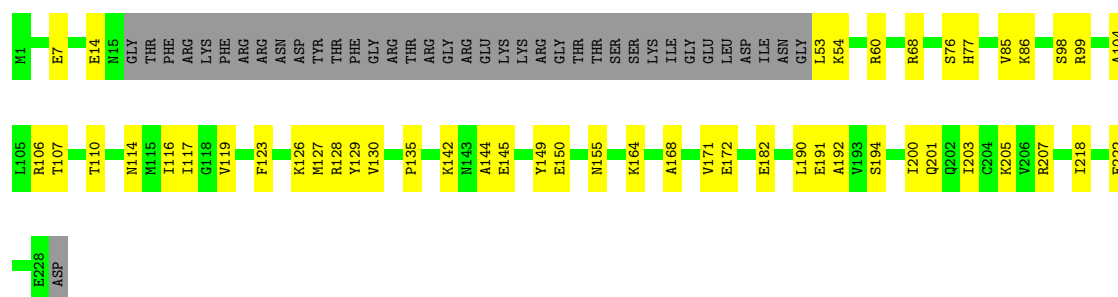
- Molecule 15: 60S ribosomal protein L8

Chain LG:  75% 14% 11%



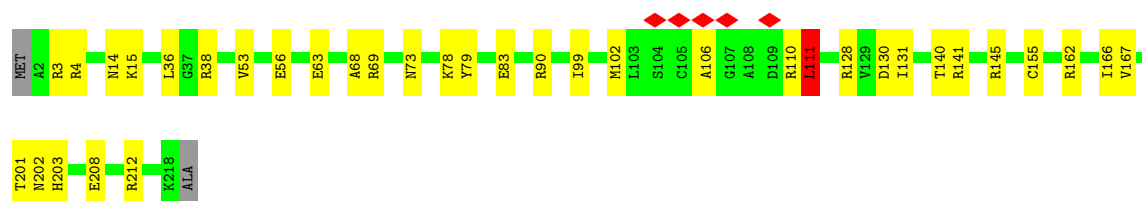
- Molecule 16: 60S ribosomal protein l9-like protein

Chain LH:  62% 21% 17%



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

Chain LI:  83% 16%

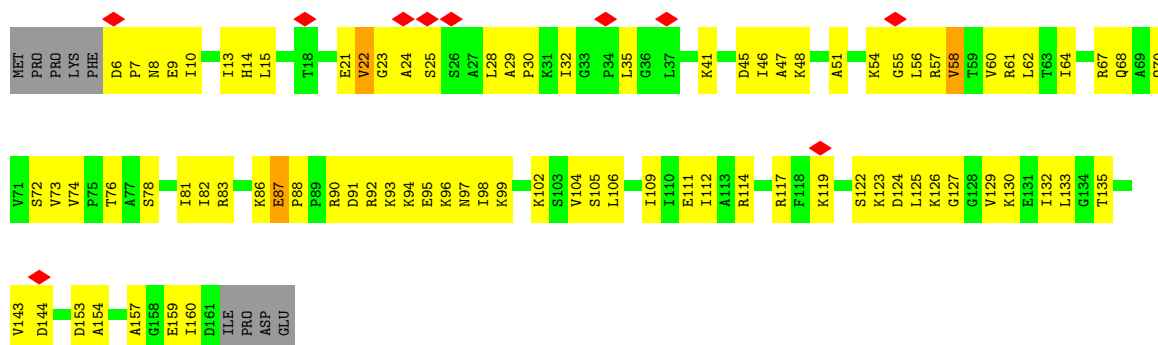
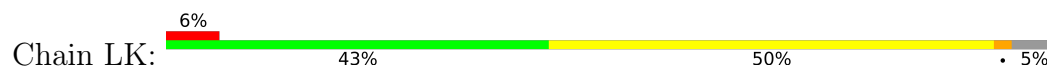


- Molecule 18: Putative ribosomal protein

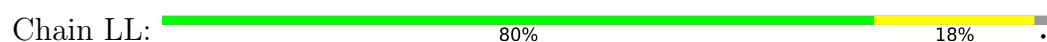
Chain LJ:  79% 18%



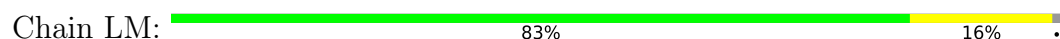
- Molecule 19: 60S ribosomal protein L12-like protein



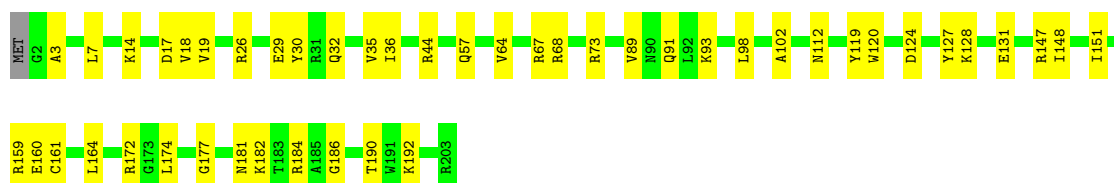
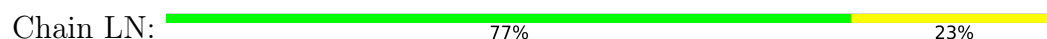
- Molecule 20: 60S ribosomal protein L13



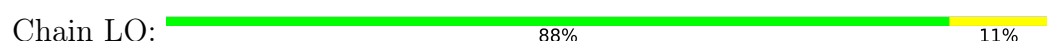
- Molecule 21: 60S ribosomal protein L14-like protein

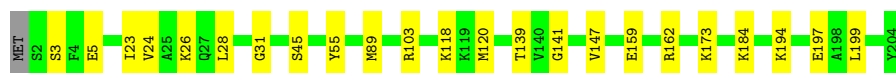


- Molecule 22: Ribosomal protein L15

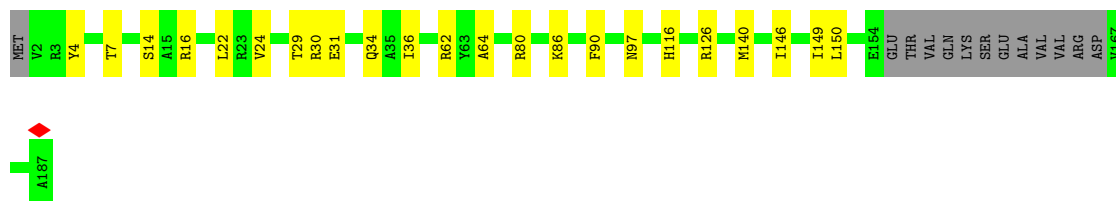
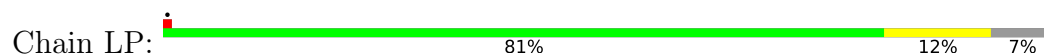


- Molecule 23: 60S ribosomal protein L16-like protein

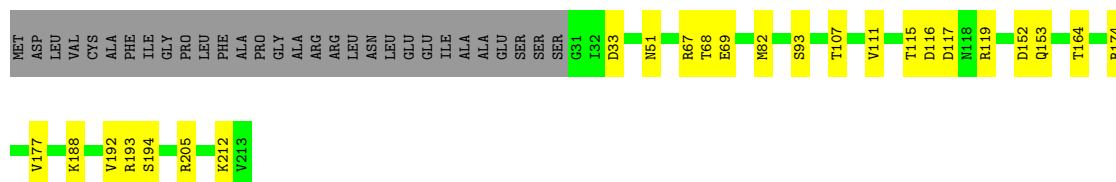
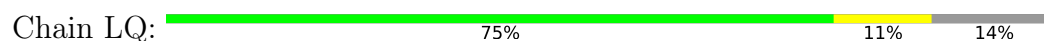




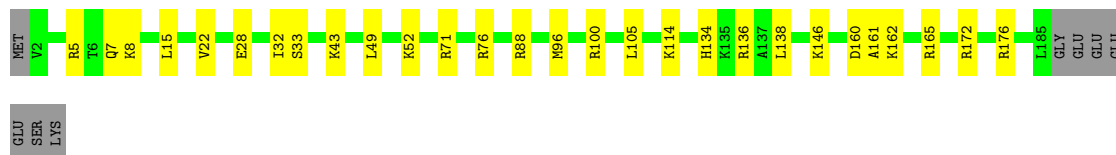
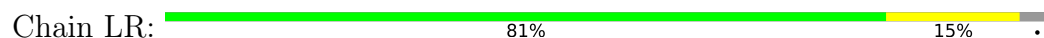
- Molecule 24: 60S ribosomal protein l17-like protein



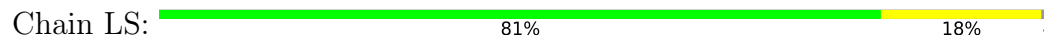
- Molecule 25: Ribosomal protein L18-like protein



- Molecule 26: Ribosomal protein L19



- Molecule 27: 60S ribosomal protein L20

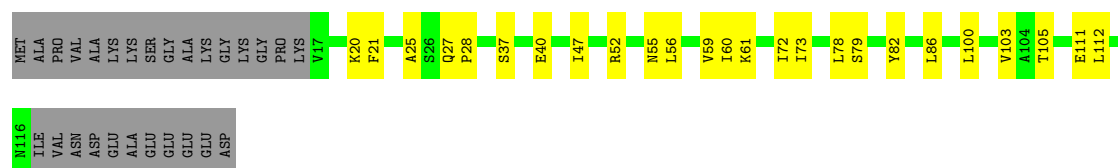


- Molecule 28: 60S ribosomal protein l21-like protein



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

Chain LU:  59% 20% 21%



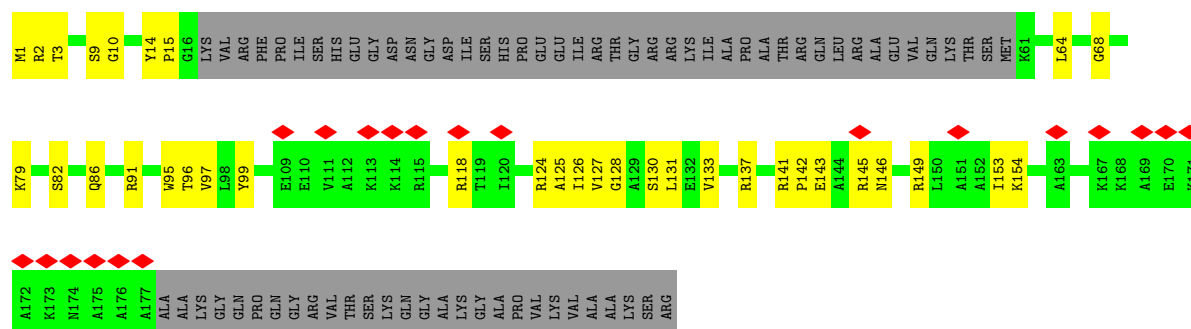
- Molecule 30: 60S ribosomal protein l23-like protein

Chain LV:  84% 14% .



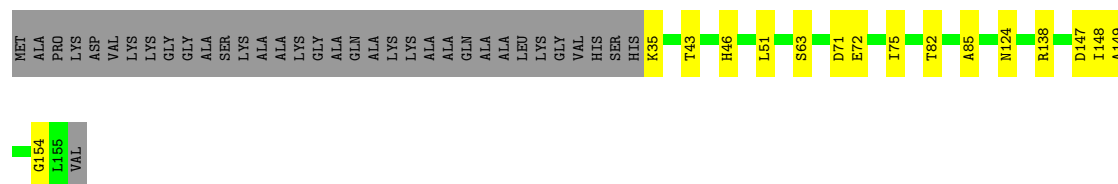
- Molecule 31: 60S ribosomal protein L24-like protein

Chain LW:  10% 48% 17% 35%



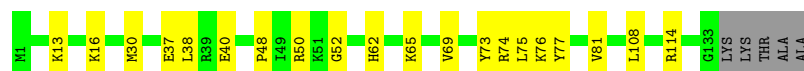
- Molecule 32: 60S ribosomal protein L25-like protein

Chain LX:  67% 10% 22%



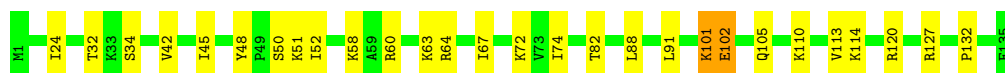
- Molecule 33: 60S ribosomal protein L26-like protein

Chain LY:  82% 14% .



- Molecule 34: 60S ribosomal protein L27

Chain LZ:  79% 19% .



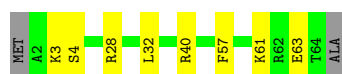
- Molecule 35: 60S ribosomal protein L28-like protein

Chain La: 81% 19% .



- Molecule 36: 60S ribosomal protein L29

Chain Lb: 85% 12% .



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

Chain Lc: 76% 12% 12%



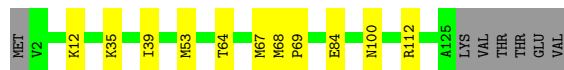
- Molecule 38: Putative 60S ribosomal protein

Chain Ld: 72% 21% 7%



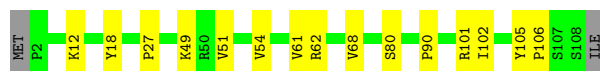
- Molecule 39: 60S ribosomal protein L32-like protein

Chain Le: 86% 8% 5%



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

Chain Lf: 84% 14% .

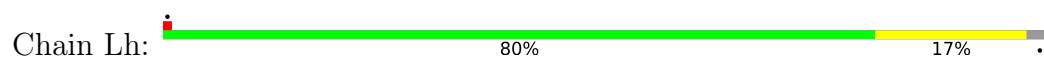


- Molecule 41: Ribosomal protein l34-like protein

Chain Lg: 76% 18% 6%



- Molecule 42: Dolichyl-diphosphooligosaccharide--protein glycotransferase



- Molecule 43: 60S ribosomal protein L36



- Molecule 44: Ribosomal protein L37



- Molecule 45: 60S ribosomal protein L38-like protein



- Molecule 46: Ribosomal protein eL39



- Molecule 47: Ubiquitin



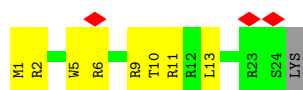
- Molecule 48: 60S ribosomal protein L41-A

Chain Ln:  76% 24%



- Molecule 48: 60S ribosomal protein L41-A

Chain Lr:  12% 64% 32% .



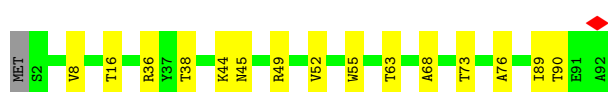
- Molecule 49: 60S ribosomal protein L44-like protein

Chain Lo:  92% 7% .



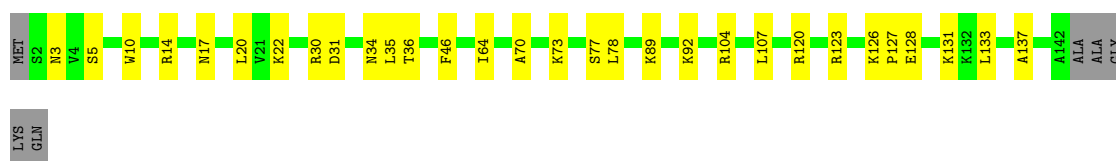
- Molecule 50: 60S ribosomal protein L43-like protein

Chain Lp:  83% 16% .



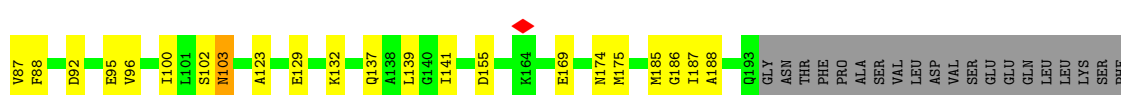
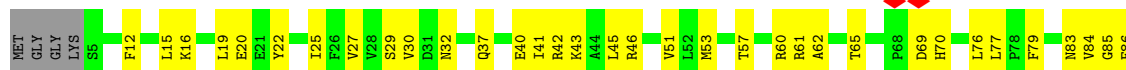
- Molecule 51: Putative 60S ribosomal protein

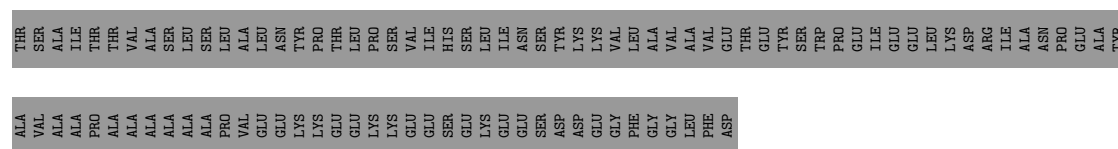
Chain Lq:  76% 20% .



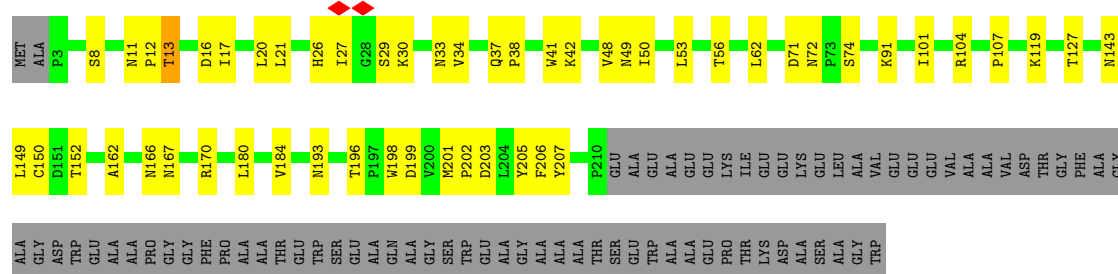
- Molecule 52: 60S acidic ribosomal protein P0

Chain Ls:  43% 18% 39%

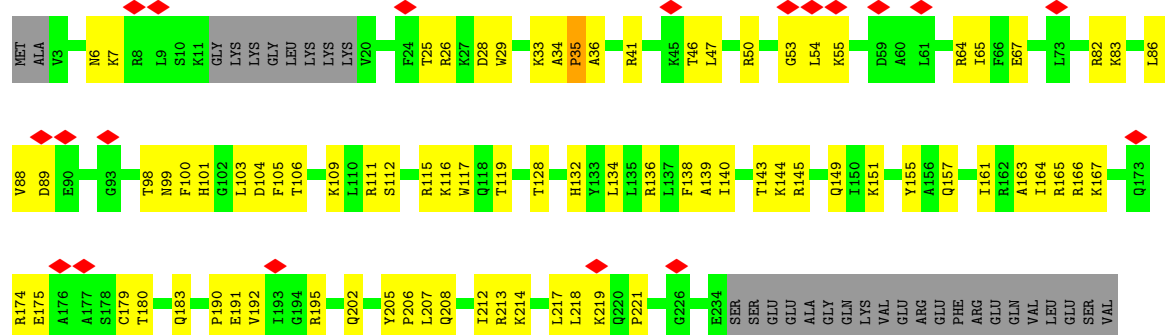




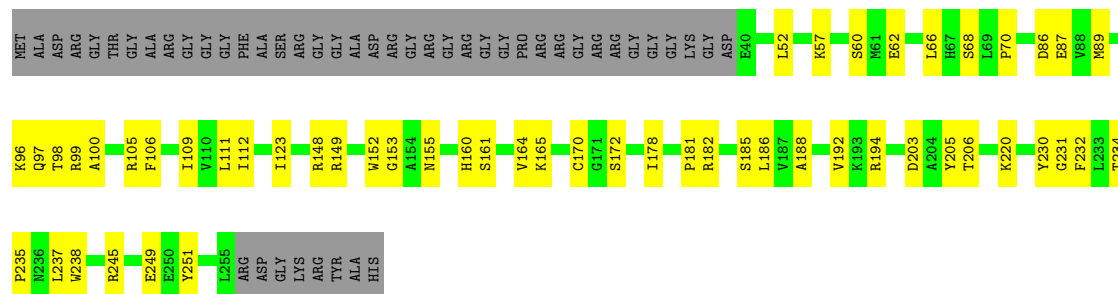
• Molecule 53: 40S ribosomal protein S0



• Molecule 54: 40S ribosomal protein S1

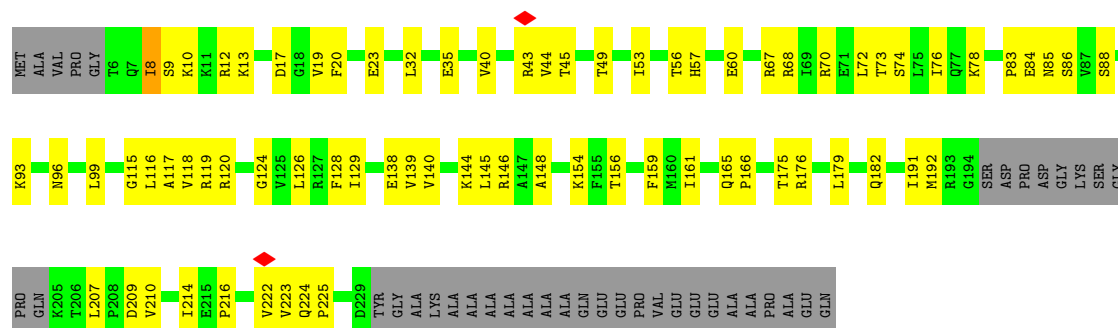


• Molecule 55: 40S ribosomal protein S2-like protein



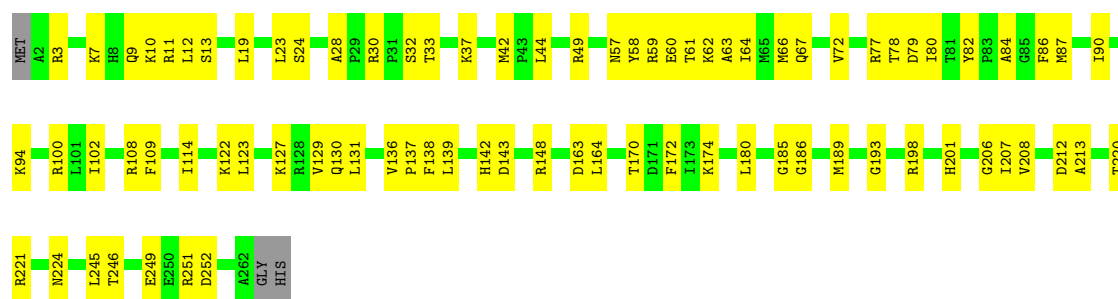
• Molecule 56: 40S ribosomal protein S3-like protein





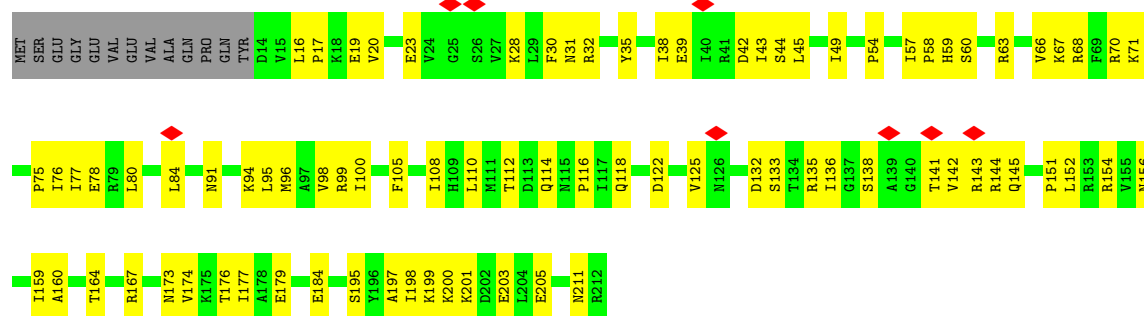
- Molecule 57: 40S ribosomal protein S4

Chain SE: 68% 31%



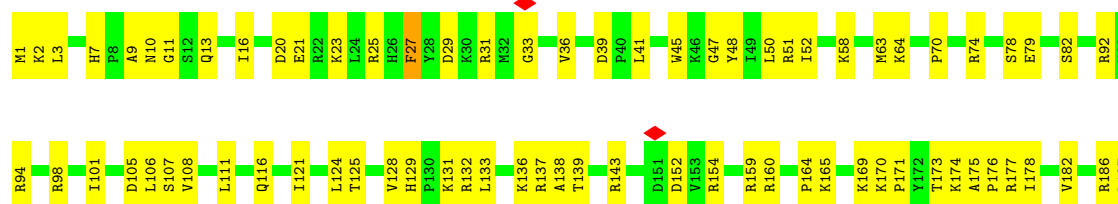
- Molecule 58: 40S ribosomal protein s5-like protein

Chain SF: 55% 39% 6%



- Molecule 59: 40S ribosomal protein S6

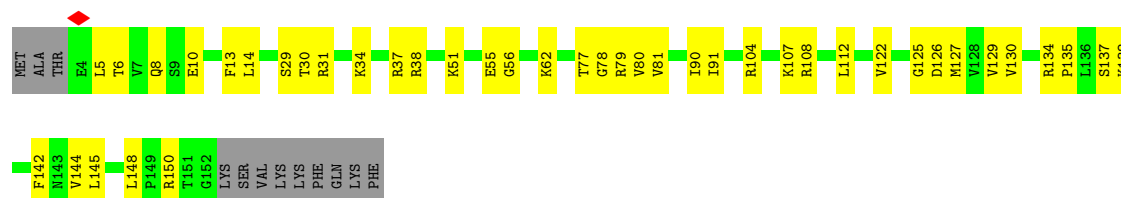
Chain SG: 62% 35%



GLY
ASP
ALA
PRO
SER
SER

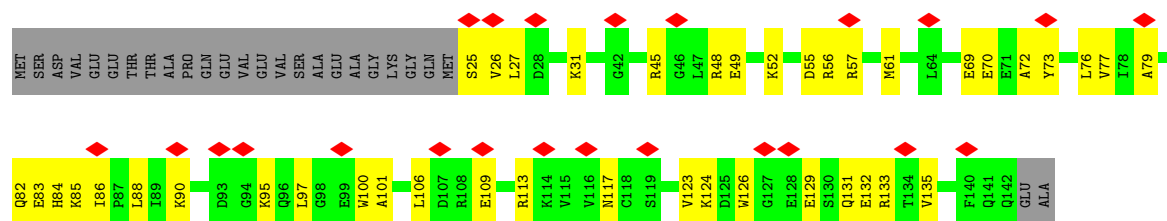
- Molecule 64: 40S ribosomal protein S11-like protein

Chain SL:  66% 26% 7%



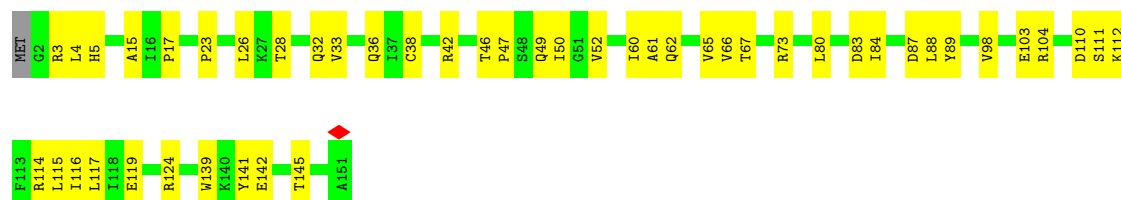
- Molecule 65: 40S ribosomal protein S12

Chain SM:  16% 53% 29% 18%



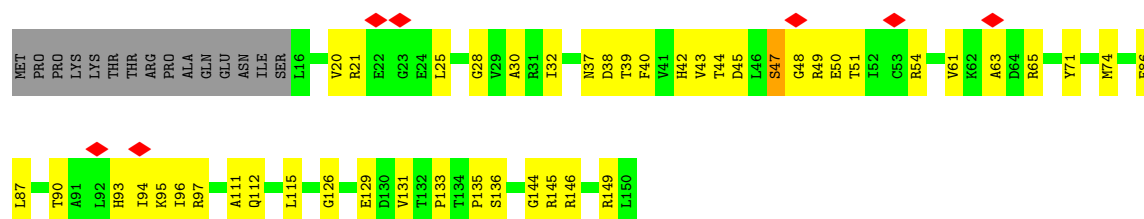
- Molecule 66: 40S ribosomal protein S13-like protein

Chain SN:  68% 31% 1%



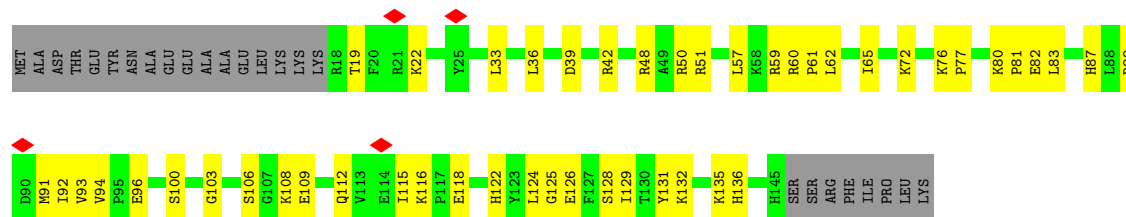
- Molecule 67: 40S ribosomal protein S14-like protein

Chain SO:  5% 59% 30% 10%

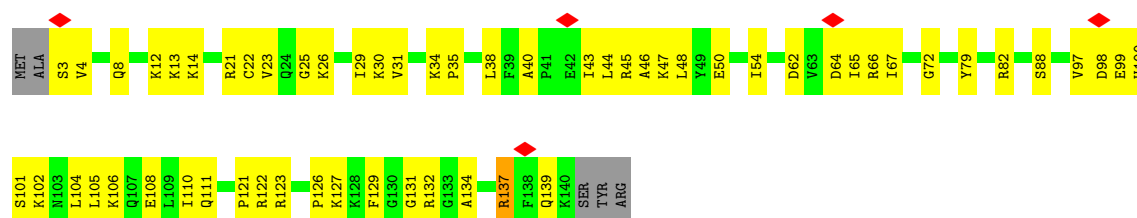


- Molecule 68: 40S ribosomal protein s15-like protein

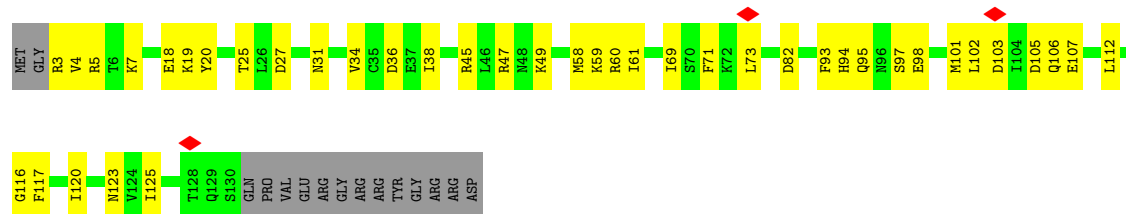
Chain SP:  52% 31% 16%



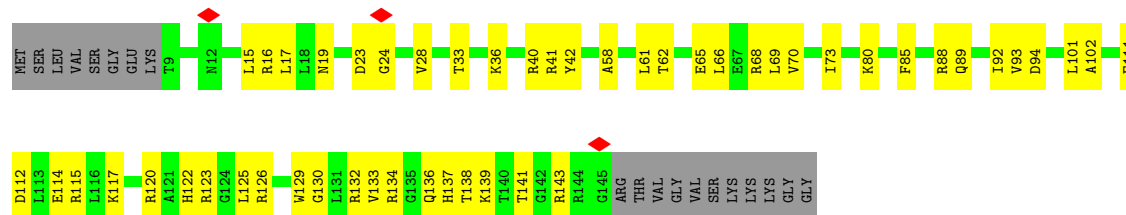
- Molecule 69: 40S ribosomal protein S16-like protein



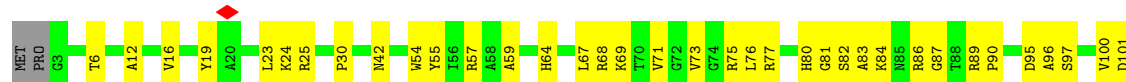
- Molecule 70: 40S ribosomal protein S17-like protein

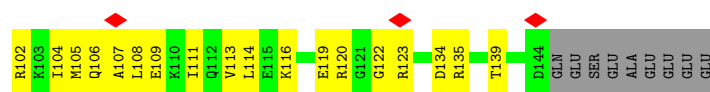


- Molecule 71: Putative ribosomal protein

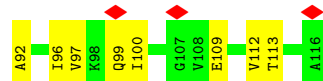
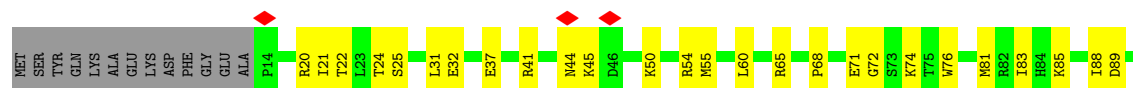


- Molecule 72: 40S ribosomal protein S19-like protein

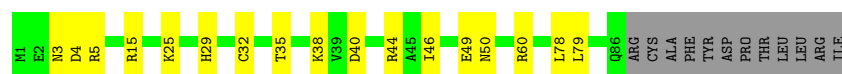




- Molecule 73: 40S ribosomal protein S20-like protein



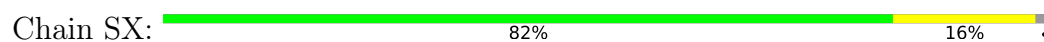
- Molecule 74: 40S ribosomal protein S21-like protein



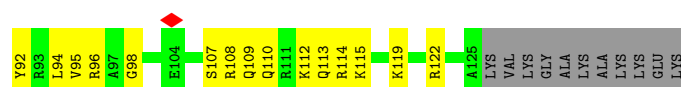
- Molecule 75: 40S ribosomal protein S22-like protein



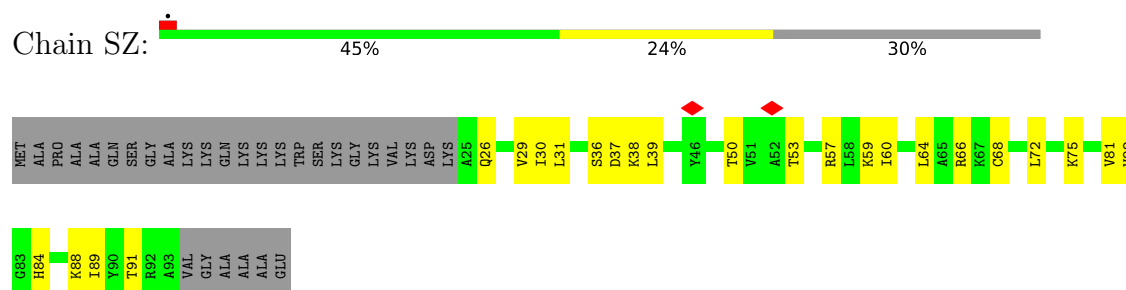
- Molecule 76: 40S ribosomal protein s23-like protein



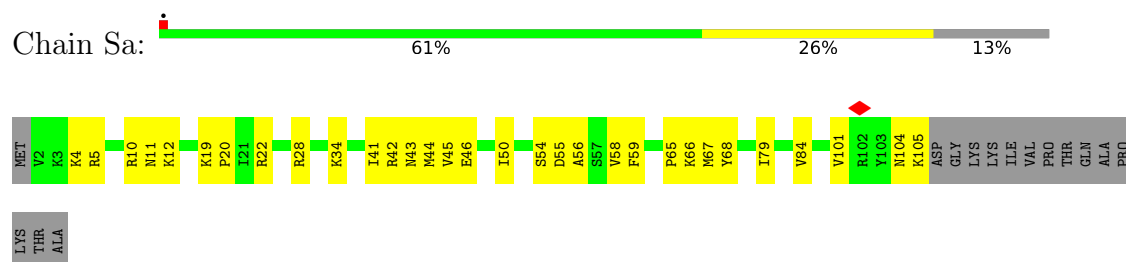
- Molecule 77: 40S ribosomal protein S24



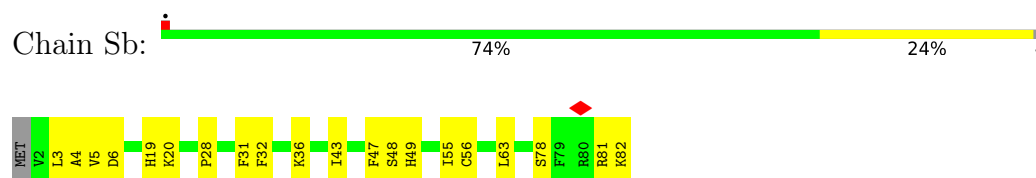
- Molecule 78: 40S ribosomal protein S25



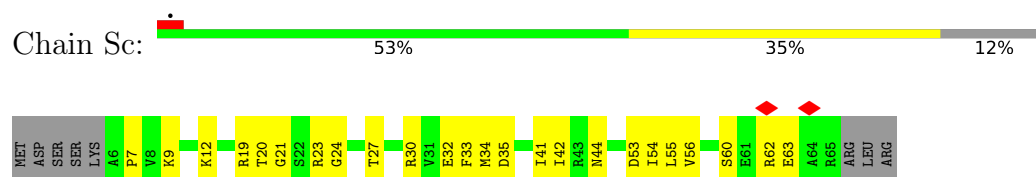
- Molecule 79: 40S ribosomal protein S26



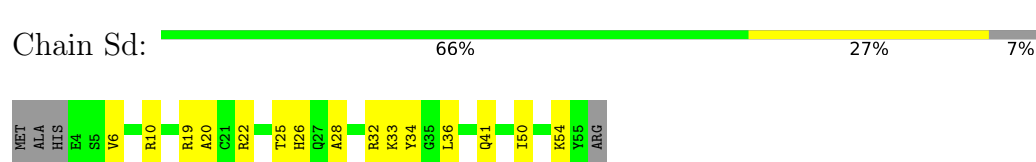
- Molecule 80: Ribosomal protein s27-like protein



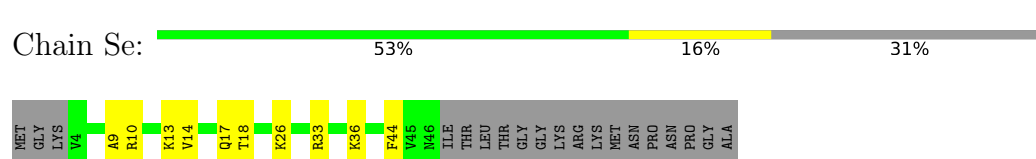
- Molecule 81: 40S ribosomal protein S28-like protein

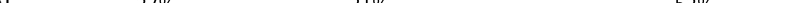


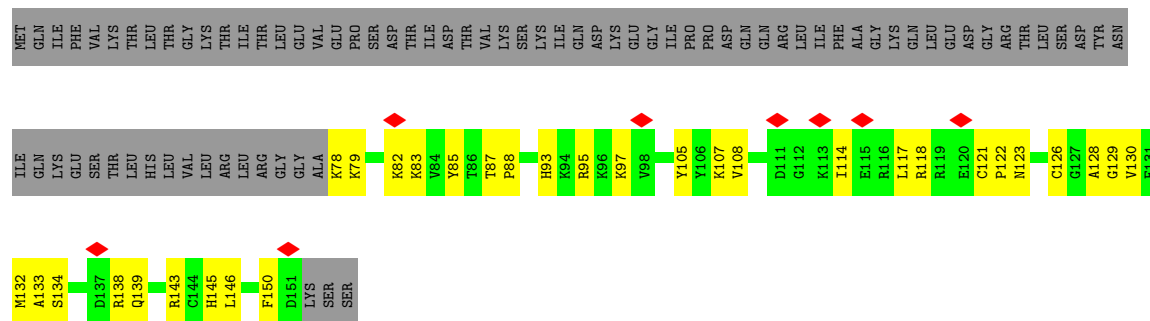
- Molecule 82: Ribosomal protein uS14



- Molecule 83: 40S ribosomal protein S30



- Chain Sf: 



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	35338	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 ($e^-/\text{\AA}^2$)	32.51	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	15.757	Depositor
Minimum map value	-8.328	Depositor
Average map value	0.026	Depositor
Map value standard deviation	0.575	Depositor
Recommended contour level	1.3	Depositor
Map size (Å)	534.60004, 534.60004, 534.60004	wwPDB
Map dimensions	486, 486, 486	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	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: ZN, DDE, GDP, MG, B8N

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	0.19	0/76390	0.34	0/119106
2	2	0.16	0/42072	0.38	0/65562
3	3	0.16	0/2833	0.29	0/4413
4	4	0.17	0/3710	0.30	0/5778
5	5	0.29	0/1773	0.88	0/2759
6	A	0.14	0/2495	0.44	0/3390
7	B	0.15	0/991	0.43	0/1319
8	C	0.16	0/6434	0.50	6/8716 (0.1%)
9	LA	0.21	0/1930	0.42	0/2597
10	LB	0.19	0/3156	0.37	0/4238
11	LC	0.17	0/2815	0.34	0/3795
12	LD	0.16	0/2487	0.35	0/3341
13	LE	0.15	0/1547	0.38	0/2081
14	LF	0.18	0/2055	0.34	0/2758
15	LG	0.15	0/1920	0.38	0/2568
16	LH	0.18	0/1525	0.37	0/2050
17	LI	0.17	0/1797	0.37	1/2413 (0.0%)
18	LJ	0.18	0/1389	0.48	0/1856
19	LK	0.20	0/1188	0.65	0/1597
20	LL	0.17	0/1695	0.40	0/2276
21	LM	0.14	0/1144	0.29	0/1539
22	LN	0.19	0/1740	0.32	0/2332
23	LO	0.18	0/1644	0.32	0/2205
24	LP	0.17	0/1400	0.33	0/1884
25	LQ	0.18	0/1507	0.35	0/2017
26	LR	0.17	0/1525	0.37	0/2028
27	LS	0.19	0/1460	0.34	0/1965
28	LT	0.17	0/1292	0.30	0/1738
29	LU	0.15	0/823	0.40	0/1101
30	LV	0.21	0/1030	0.42	0/1384
31	LW	0.16	0/1088	0.40	0/1443
32	LX	0.15	0/983	0.34	0/1325

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	LY	0.15	0/1070	0.34	0/1432
34	LZ	0.16	0/1134	0.41	2/1519 (0.1%)
35	La	0.18	0/1212	0.36	0/1627
36	Lb	0.15	0/525	0.29	0/694
37	Lc	0.15	0/717	0.31	0/964
38	Ld	0.20	0/921	0.39	0/1233
39	Le	0.18	0/1019	0.30	0/1358
40	Lf	0.20	0/874	0.36	0/1176
41	Lg	0.18	0/904	0.34	0/1210
42	Lh	0.14	0/1014	0.33	0/1349
43	Li	0.19	0/833	0.42	0/1100
44	Lj	0.20	0/712	0.40	0/944
45	Lk	0.18	0/640	0.45	1/850 (0.1%)
46	Ll	0.19	0/445	0.47	0/593
47	Lm	0.18	0/424	0.37	0/561
48	Ln	0.22	0/234	0.41	0/300
48	Lr	0.12	0/225	0.34	0/289
49	Lo	0.16	0/835	0.33	0/1105
50	Lp	0.19	0/705	0.41	0/940
51	Lq	0.15	0/1101	0.33	0/1482
52	Ls	0.15	0/1477	0.48	2/1995 (0.1%)
53	SA	0.16	0/1683	0.41	0/2299
54	SB	0.17	0/1838	0.51	1/2472 (0.0%)
55	SC	0.16	0/1703	0.40	0/2303
56	SD	0.16	0/1706	0.47	0/2291
57	SE	0.15	0/2112	0.41	0/2842
58	SF	0.15	0/1578	0.42	0/2130
59	SG	0.16	0/1906	0.46	0/2547
60	SH	0.15	0/1609	0.43	0/2171
61	SI	0.16	0/1654	0.45	0/2213
62	SJ	0.15	0/1489	0.41	0/1993
63	SK	0.18	0/764	0.50	0/1038
64	SL	0.15	0/1241	0.45	0/1666
65	SM	0.15	0/934	0.49	0/1255
66	SN	0.16	0/1205	0.41	0/1627
67	SO	0.15	0/1017	0.48	0/1365
68	SP	0.14	0/1055	0.42	0/1411
69	SQ	0.16	0/1098	0.51	1/1472 (0.1%)
70	SR	0.15	0/1060	0.44	0/1424
71	SS	0.14	0/1133	0.42	0/1520
72	ST	0.14	0/1137	0.41	0/1533
73	SU	0.18	0/828	0.47	0/1112
74	SV	0.16	0/671	0.38	0/900

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
75	SW	0.20	0/1055	0.54	0/1416
76	SX	0.18	0/1116	0.39	0/1489
77	SY	0.21	0/991	0.60	0/1324
78	SZ	0.12	0/550	0.40	0/736
79	Sa	0.16	0/852	0.43	0/1136
80	Sb	0.14	0/623	0.55	0/843
81	Sc	0.15	0/476	0.48	0/639
82	Sd	0.20	0/427	0.54	0/570
83	Se	0.19	0/351	0.47	0/463
84	Sf	0.14	0/623	0.46	0/824
All	All	0.18	0/229344	0.39	14/335319 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
10	LB	0	1

There are no bond length outliers.

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	SB	35	PRO	CA-N-CD	-8.11	100.64	112.00
69	SQ	137	ARG	CB-CG-CD	-6.95	95.32	111.30
8	C	373	ASP	CA-C-N	6.11	133.21	121.54
8	C	373	ASP	C-N-CA	6.11	133.21	121.54
52	Ls	102	SER	CA-C-N	5.71	132.45	121.54
52	Ls	102	SER	C-N-CA	5.71	132.45	121.54
8	C	498	LYS	CA-C-N	5.47	135.46	126.86
8	C	498	LYS	C-N-CA	5.47	135.46	126.86
8	C	486	SER	CA-C-N	5.18	131.29	121.97
8	C	486	SER	C-N-CA	5.18	131.29	121.97
34	LZ	101	LYS	CA-C-N	5.18	134.43	121.80
34	LZ	101	LYS	C-N-CA	5.18	134.43	121.80
17	LI	111	LEU	CA-CB-CG	5.05	133.99	116.30
45	Lk	74	ARG	CA-CB-CG	5.03	124.16	114.10

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
10	LB	257	HIS	Peptide

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	68264	0	34387	627	0
2	2	37645	0	18955	733	0
3	3	2535	0	1284	23	0
4	4	3319	0	1678	40	0
5	5	1589	0	810	63	0
6	A	2438	0	2385	109	0
7	B	982	0	948	37	0
8	C	6335	0	6419	190	0
9	LA	1891	0	1958	36	0
10	LB	3088	0	3206	49	0
11	LC	2758	0	2883	49	0
12	LD	2440	0	2431	40	0
13	LE	1518	0	1619	24	0
14	LF	2017	0	2130	26	0
15	LG	1891	0	2053	30	0
16	LH	1505	0	1581	37	0
17	LI	1760	0	1798	24	0
18	LJ	1367	0	1405	21	0
19	LK	1174	0	1247	83	0
20	LL	1666	0	1756	29	0
21	LM	1125	0	1198	16	0
22	LN	1703	0	1767	33	0
23	LO	1610	0	1702	16	0
24	LP	1378	0	1423	17	0
25	LQ	1481	0	1596	23	0
26	LR	1506	0	1603	26	0
27	LS	1425	0	1484	23	0
28	LT	1266	0	1328	13	0
29	LU	810	0	851	21	0
30	LV	1012	0	1076	16	0
31	LW	1075	0	1146	26	0
32	LX	967	0	1054	13	0
33	LY	1056	0	1143	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
34	LZ	1111	0	1181	20	0
35	La	1180	0	1203	23	0
36	Lb	515	0	533	6	0
37	Lc	708	0	753	9	0
38	Ld	907	0	961	17	0
39	Le	1001	0	1070	7	0
40	Lf	853	0	880	11	0
41	Lg	891	0	958	14	0
42	Lh	1003	0	1116	16	0
43	Li	826	0	908	27	0
44	Lj	698	0	726	15	0
45	Lk	632	0	693	8	0
46	Ll	435	0	473	23	0
47	Lm	418	0	459	8	0
48	Ln	233	0	284	8	0
48	Lr	224	0	271	7	0
49	Lo	822	0	891	5	0
50	Lp	697	0	737	11	0
51	Lq	1083	0	1140	24	0
52	Ls	1449	0	1488	41	0
53	SA	1641	0	1650	37	0
54	SB	1810	0	1906	71	0
55	SC	1672	0	1777	51	0
56	SD	1683	0	1748	64	0
57	SE	2072	0	2155	69	0
58	SF	1557	0	1608	79	0
59	SG	1875	0	1983	76	0
60	SH	1584	0	1666	50	0
61	SI	1621	0	1645	66	0
62	SJ	1466	0	1582	37	0
63	SK	742	0	738	35	0
64	SL	1214	0	1280	32	0
65	SM	923	0	946	36	0
66	SN	1182	0	1264	39	0
67	SO	1005	0	1036	40	0
68	SP	1036	0	1094	42	0
69	SQ	1081	0	1151	59	0
70	SR	1045	0	1083	35	0
71	SS	1118	0	1172	44	0
72	ST	1117	0	1133	43	0
73	SU	819	0	895	38	0
74	SV	664	0	662	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
75	SW	1037	0	1076	42	0
76	SX	1099	0	1169	19	0
77	SY	977	0	1044	54	0
78	SZ	546	0	591	18	0
79	Sa	839	0	891	35	0
80	Sb	611	0	634	17	0
81	Sc	473	0	500	25	0
82	Sd	419	0	419	18	0
83	Se	347	0	387	9	0
84	Sf	613	0	653	36	0
85	1	2	0	0	0	0
85	C	1	0	0	0	0
86	C	28	0	12	1	0
87	Lg	1	0	0	0	0
87	Lj	1	0	0	0	0
87	Lm	1	0	0	0	0
87	Lo	1	0	0	0	0
87	Lp	1	0	0	0	0
87	Sa	1	0	0	0	0
87	Sb	1	0	0	0	0
87	Sd	1	0	0	0	0
All	All	214209	0	162579	3550	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 10.

All (3550) 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)
46:Ll:48:ARG:HH21	46:Ll:49:LEU:HG	1.21	1.05
5:5:52:G:N2	5:5:61:C:C2	2.27	1.01
2:2:709:G:H1	2:2:722:U:H3	1.05	1.00
2:2:974:G:H1	2:2:1021:A:HO2'	1.13	0.95
19:LK:64:ILE:H	19:LK:70:GLN:HE21	1.14	0.95
1:1:1000:G:H1	1:1:1017:U:H3	1.00	0.94
2:2:487:U:H3	2:2:494:G:H1	0.93	0.92
10:LB:228:VAL:HG21	10:LB:271:MET:HE3	1.52	0.89
2:2:77:A:O2'	59:SG:177:ARG:NH2	2.05	0.89
2:2:695:C:O2	2:2:737:G:N2	2.07	0.88
2:2:1575:C:H4'	69:SQ:137:ARG:CZ	2.04	0.88
2:2:824:U:H3	2:2:844:G:H1	1.21	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:443:A:OP1	57:SE:57:ASN:ND2	2.09	0.86
1:1:3144:U:O2	1:1:3148:G:N2	2.09	0.86
22:LN:35:VAL:HG23	22:LN:36:ILE:HD12	1.58	0.86
2:2:1060:U:H2'	2:2:1061:G:H8	1.41	0.85
52:Ls:53:MET:HE3	52:Ls:85:GLY:HA3	1.59	0.84
8:C:182:ARG:HH21	52:Ls:137:GLN:HA	1.43	0.84
2:2:447:C:OP1	57:SE:7:LYS:NZ	2.11	0.84
63:SK:32:GLU:HG2	63:SK:33:ILE:H	1.43	0.83
2:2:164:U:O2'	59:SG:136:LYS:NZ	2.11	0.83
2:2:1297:A:O2'	55:SC:96:LYS:NZ	2.12	0.82
75:SW:42:GLN:NE2	75:SW:48:GLY:O	2.12	0.82
2:2:1675:G:H21	2:2:1718:A:H62	1.24	0.82
13:LE:58:LEU:HD12	13:LE:102:VAL:HG11	1.61	0.82
2:2:650:C:O2	2:2:675:G:N2	2.11	0.82
2:2:691:C:H4'	2:2:692:C:H5'	1.62	0.82
2:2:1415:G:O3'	82:Sd:54:LYS:NZ	2.12	0.81
8:C:276:CYS:HA	8:C:280:LEU:HB2	1.62	0.81
8:C:569:VAL:HG13	8:C:723:GLU:HG3	1.60	0.81
74:SV:35:THR:HB	74:SV:50:ASN:HD21	1.45	0.81
2:2:219:C:N3	2:2:835:G:N1	2.25	0.81
67:SO:96:ILE:HD11	67:SO:111:ALA:HB1	1.60	0.81
1:1:1782:C:H5''	48:Lr:2:ARG:HD3	1.61	0.81
65:SM:69:GLU:HG2	65:SM:70:GLU:HG3	1.63	0.81
2:2:1765:U:O2	67:SO:149:ARG:NH1	2.14	0.80
1:1:999:G:N2	1:1:1018:C:O2	2.12	0.80
1:1:675:U:OP2	20:LL:36:ARG:NH2	2.14	0.80
2:2:754:A:H2'	2:2:755:A:H8	1.46	0.80
8:C:371:ILE:HG12	8:C:379:PRO:HD2	1.62	0.80
54:SB:140:ILE:HG23	54:SB:213:ARG:HH11	1.47	0.79
56:SD:43:ARG:HH12	56:SD:45:THR:HG23	1.46	0.79
2:2:898:A:H3'	2:2:899:G:H21	1.47	0.79
19:LK:14:HIS:HE1	19:LK:32:ILE:HG12	1.47	0.79
8:C:635:ILE:HG22	8:C:649:VAL:HG22	1.64	0.79
13:LE:110:ASP:O	13:LE:172:ASN:ND2	2.16	0.79
82:Sd:20:ALA:HB1	82:Sd:25:THR:HA	1.65	0.79
17:LI:110:ARG:HG2	17:LI:111:LEU:H	1.48	0.79
67:SO:44:THR:HG22	67:SO:51:THR:HA	1.64	0.79
65:SM:126:TRP:HB2	65:SM:133:ARG:HH21	1.47	0.78
2:2:1559:C:OP1	72:ST:84:LYS:NZ	2.17	0.78
2:2:1578:U:N3	2:2:1610:A:C8	2.52	0.78
77:SY:23:ARG:HD2	77:SY:77:LEU:HD11	1.65	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:441:C:OP2	77:SY:108:ARG:NE	2.17	0.78
2:2:1252:G:O6	65:SM:48:ARG:NH1	2.16	0.78
46:LI:27:ILE:O	46:LI:33:ASN:ND2	2.17	0.78
56:SD:161:ILE:H	56:SD:192:MET:HE1	1.48	0.78
1:1:25:G:OP2	44:Lj:46:LYS:NZ	2.17	0.77
2:2:1531:U:H4'	2:2:1532:G:O5'	1.85	0.77
1:1:1940:U:H3	1:1:2045:G:H1	0.80	0.77
5:5:52:G:N2	5:5:61:C:O2	2.17	0.77
2:2:1245:C:OP2	84:Sf:93:HIS:ND1	2.18	0.76
2:2:1578:U:C2	2:2:1610:A:N7	2.52	0.76
8:C:226:GLN:NE2	8:C:335:CYS:SG	2.58	0.76
62:SJ:29:VAL:HG23	62:SJ:34:LEU:HB2	1.65	0.76
2:2:1438:U:H5'	8:C:654:ALA:HB2	1.66	0.76
5:5:52:G:N1	5:5:61:C:N3	2.32	0.76
2:2:754:A:H2'	2:2:755:A:C8	2.20	0.76
10:LB:258:PRO:HG2	10:LB:262:GLN:HE21	1.50	0.76
1:1:1202:C:H42	1:1:1270:A:N6	1.83	0.76
1:1:1635:G:N2	1:1:1781:U:O4	2.19	0.76
60:SH:64:ILE:HD11	60:SH:96:VAL:HG12	1.68	0.76
26:LR:114:LYS:O	26:LR:146:LYS:NZ	2.19	0.76
54:SB:36:ALA:O	54:SB:41:ARG:NH2	2.19	0.76
16:LH:144:ALA:O	16:LH:145:GLU:HG3	1.85	0.75
26:LR:96:MET:SD	26:LR:100:ARG:NH1	2.59	0.75
51:Lq:64:ILE:HD11	51:Lq:78:LEU:HD13	1.66	0.75
61:SI:110:ARG:HG3	61:SI:121:LEU:HD11	1.66	0.75
55:SC:98:THR:HG22	55:SC:99:ARG:H	1.51	0.75
52:Ls:30:VAL:HG11	52:Ls:53:MET:HE1	1.68	0.75
2:2:148:G:H22	2:2:160:G:H1	1.35	0.75
2:2:1249:C:OP1	84:Sf:118:ARG:NH1	2.20	0.75
27:LS:8:GLN:HE21	27:LS:62:ASN:HD22	1.34	0.75
55:SC:96:LYS:HG3	55:SC:97:GLN:HG3	1.68	0.75
61:SI:37:ARG:NH1	61:SI:93:THR:O	2.20	0.75
64:SL:79:ARG:NH2	64:SL:127:MET:SD	2.60	0.75
1:1:1599:A:OP1	48:Lr:11:ARG:NH1	2.20	0.74
16:LH:130:VAL:HG12	47:Lm:82:LEU:HD13	1.68	0.74
1:1:1337:G:N2	1:1:1339:U:O2'	2.20	0.74
2:2:77:A:N3	59:SG:177:ARG:NH1	2.35	0.74
7:B:123:TRP:HE3	56:SD:118:VAL:HG11	1.51	0.74
2:2:1420:A:H4'	55:SC:100:ALA:HB1	1.69	0.74
55:SC:231:GLY:HA3	74:SV:25:LYS:HZ3	1.51	0.74
1:1:1218:U:H4'	1:1:1219:G:H5'	1.68	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:1561:C:OP1	71:SS:41:ARG:NH1	2.20	0.74
2:2:11:A:H1'	55:SC:96:LYS:HZ3	1.53	0.74
27:LS:96:GLU:OE2	27:LS:102:ALA:N	2.21	0.74
1:1:3119:A:H61	1:1:3226:C:H42	1.35	0.73
7:B:131:GLU:OE2	56:SD:119:ARG:NH2	2.21	0.73
8:C:443:LYS:HZ1	8:C:445:GLU:HG2	1.53	0.73
73:SU:55:MET:HB2	73:SU:85:LYS:HB3	1.69	0.73
2:2:1561:C:H5''	71:SS:41:ARG:HH12	1.53	0.73
57:SE:87:MET:HE3	57:SE:100:ARG:HH21	1.52	0.73
64:SL:127:MET:HB2	64:SL:148:LEU:HB2	1.69	0.73
8:C:20:ARG:HB2	8:C:102:ILE:HG12	1.71	0.73
8:C:375:ASN:O	8:C:404:SER:OG	2.06	0.73
12:LD:41:LYS:NZ	28:LT:32:ARG:O	2.21	0.73
1:1:1469:G:H21	41:Lg:7:THR:HG22	1.54	0.73
22:LN:73:ARG:HB3	22:LN:89:VAL:HG23	1.71	0.73
1:1:1020:U:HO2'	12:LD:3:PHE:N	1.85	0.73
2:2:1201:A:H1'	82:Sd:10:ARG:HH22	1.53	0.73
4:4:8:C:H2'	4:4:9:A:H8	1.53	0.73
79:Sa:55:ASP:OD1	79:Sa:56:ALA:N	2.21	0.73
1:1:2222:A:H2'	1:1:2223:U:C6	2.24	0.72
2:2:1201:A:N3	82:Sd:10:ARG:NH2	2.37	0.72
1:1:2616:A:O4'	7:B:37:ARG:NH2	2.22	0.72
1:1:1202:C:N4	1:1:1270:A:H61	1.86	0.72
1:1:1238:C:H2'	1:1:1239:G:H8	1.52	0.72
2:2:103:A:OP2	2:2:305:C:N4	2.22	0.72
2:2:901:U:N3	2:2:904:A:OP2	2.21	0.72
19:LK:87:GLU:HB3	19:LK:88:PRO:HD2	1.69	0.72
1:1:406:U:OP1	24:LP:34:GLN:NE2	2.23	0.72
2:2:893:G:H22	2:2:915:U:H3	1.38	0.72
11:LC:329:LEU:HD12	14:LF:187:ILE:HG13	1.70	0.72
17:LI:14:ASN:O	17:LI:128:ARG:NH2	2.23	0.72
77:SY:45:GLU:HB3	77:SY:55:LYS:HE2	1.71	0.72
2:2:625:G:OP1	66:SN:124:ARG:NH2	2.22	0.72
60:SH:120:GLN:HG2	60:SH:121:LYS:H	1.54	0.72
64:SL:125:GLY:O	64:SL:150:ARG:NH1	2.22	0.72
2:2:136:A:N6	2:2:172:G:O2'	2.23	0.72
2:2:326:G:H5'	61:SI:98:LYS:HB2	1.69	0.72
19:LK:61:ARG:NH2	19:LK:73:VAL:O	2.19	0.72
2:2:869:A:H2'	2:2:870:G:C8	2.25	0.72
59:SG:23:LYS:NZ	59:SG:41:LEU:O	2.21	0.72
2:2:1336:C:O2'	2:2:1338:G:N7	2.22	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
72:ST:30:PRO:HD2	72:ST:107:ALA:HB1	1.72	0.71
2:2:1609:U:OP1	58:SF:156:ASN:ND2	2.23	0.71
15:LG:143:VAL:HG21	22:LN:3:ALA:HB2	1.71	0.71
2:2:428:C:OP1	8:C:395:ARG:NH2	2.20	0.71
2:2:1391:G:O6	2:2:1401:G:C6	2.42	0.71
2:2:1441:G:N2	84:Sf:88:PRO:O	2.23	0.71
1:1:2063:A:H5'	26:LR:71:ARG:HH12	1.54	0.71
5:5:25:C:H2'	5:5:26:A:H8	1.55	0.71
34:LZ:101:LYS:O	34:LZ:102:GLU:HG3	1.90	0.71
2:2:187:U:O2	2:2:190:G:N1	2.19	0.71
25:LQ:152:ASP:OD1	25:LQ:153:GLN:N	2.24	0.71
6:A:130:LYS:HB2	6:A:132:TRP:HE1	1.56	0.71
1:1:1560:U:H1'	1:1:1561:G:H4'	1.73	0.71
2:2:432:C:OP2	76:SX:50:LYS:NZ	2.24	0.71
2:2:1223:G:O2'	2:2:1253:A:N6	2.21	0.71
19:LK:123:LYS:HB2	19:LK:129:VAL:HB	1.72	0.71
53:SA:170:ARG:NH2	53:SA:207:TYR:O	2.24	0.71
2:2:850:C:H5''	26:LR:176:ARG:HH12	1.55	0.70
53:SA:71:ASP:OD1	53:SA:72:ASN:N	2.23	0.70
2:2:1592:C:OP1	82:Sd:19:ARG:NH2	2.24	0.70
55:SC:148:ARG:HH12	55:SC:237:LEU:HD11	1.56	0.70
1:1:1202:C:N4	1:1:1270:A:N6	2.39	0.70
8:C:26:ALA:HB3	8:C:32:LYS:HG2	1.72	0.70
2:2:834:U:H2'	2:2:835:G:H8	1.55	0.70
1:1:2621:G:H2'	1:1:2622:G:H8	1.56	0.70
2:2:219:C:O2	2:2:835:G:N2	2.20	0.70
11:LC:28:SER:O	51:Lq:3:ASN:ND2	2.25	0.70
19:LK:109:ILE:O	19:LK:112:ILE:HG12	1.91	0.70
52:Ls:69:ASP:OD1	52:Ls:70:HIS:N	2.25	0.70
82:Sd:22:ARG:NH2	82:Sd:36:LEU:O	2.25	0.70
2:2:282:G:OP1	59:SG:199:ARG:NH2	2.25	0.70
2:2:916:U:H1'	67:SO:48:GLY:HA3	1.72	0.70
58:SF:45:LEU:HD22	58:SF:125:VAL:HG23	1.74	0.70
58:SF:133:SER:OG	58:SF:144:ARG:NH2	2.20	0.70
70:SR:105:ASP:OD2	70:SR:106:GLN:N	2.24	0.70
8:C:229:THR:OG1	8:C:239:ARG:NH1	2.25	0.70
81:Sc:20:THR:HG22	81:Sc:21:GLY:H	1.55	0.70
1:1:309:U:O2'	43:Li:39:LYS:NZ	2.25	0.70
57:SE:185:GLY:O	57:SE:224:ASN:ND2	2.23	0.70
59:SG:175:ALA:HB3	59:SG:177:ARG:HH21	1.54	0.70
65:SM:55:ASP:OD1	65:SM:56:ARG:N	2.25	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
74:SV:40:ASP:HB3	74:SV:46:ILE:HD11	1.72	0.70
2:2:1168:A:H2'	2:2:1169:G:H8	1.56	0.69
2:2:1689:A:H2'	2:2:1690:G:H8	1.57	0.69
27:LS:31:ALA:HB1	27:LS:36:VAL:HG23	1.74	0.69
65:SM:31:LYS:HZ1	65:SM:100:TRP:HD1	1.39	0.69
8:C:336:LEU:O	8:C:340:MET:HG3	1.92	0.69
26:LR:28:GLU:HG2	26:LR:49:LEU:HD13	1.74	0.69
6:A:248:LEU:HD22	6:A:261:LEU:HD21	1.74	0.69
31:LW:124:ARG:NH2	59:SG:129:HIS:O	2.25	0.69
2:2:77:A:HO2'	59:SG:177:ARG:HH22	1.41	0.69
15:LG:166:VAL:HA	15:LG:169:LEU:HD23	1.75	0.69
16:LH:135:PRO:O	16:LH:155:ASN:ND2	2.24	0.69
33:LY:30:MET:HE1	33:LY:74:ARG:HA	1.73	0.69
62:SJ:167:PRO:O	62:SJ:172:ARG:NH1	2.24	0.69
1:1:780:U:O2'	20:LL:14:PHE:O	2.08	0.69
2:2:1785:G:OP2	67:SO:145:ARG:NH2	2.26	0.69
4:4:52:A:OP1	46:LI:21:ARG:NH2	2.20	0.69
11:LC:364:GLU:OE2	27:LS:26:ARG:NH1	2.25	0.69
33:LY:69:VAL:HG12	33:LY:81:VAL:HG12	1.74	0.69
69:SQ:34:LYS:HG2	69:SQ:35:PRO:HD2	1.75	0.69
53:SA:104:ARG:HH12	53:SA:107:PRO:HD2	1.57	0.69
28:LT:68:THR:HG22	28:LT:69:LYS:H	1.56	0.68
70:SR:95:GLN:HB2	70:SR:101:MET:HA	1.75	0.68
54:SB:138:PHE:HB3	54:SB:213:ARG:CZ	2.23	0.68
68:SP:100:SER:H	68:SP:115:ILE:HD11	1.59	0.68
1:1:3292:U:HO2'	1:1:3293:U:P	2.16	0.68
2:2:440:C:P	77:SY:108:ARG:HD2	2.34	0.68
6:A:253:ALA:HB1	6:A:282:ARG:HH22	1.59	0.68
1:1:114:C:OP1	22:LN:147:ARG:NE	2.21	0.68
1:1:275:G:O2'	1:1:276:G:OP2	2.12	0.68
2:2:815:A:H4'	60:SH:119:LYS:HE2	1.75	0.68
56:SD:224:GLN:HG2	56:SD:225:PRO:HD3	1.74	0.68
57:SE:201:HIS:HE1	57:SE:207:ILE:HG12	1.57	0.68
1:1:1476:G:P	46:LI:48:ARG:HH11	2.15	0.68
73:SU:92:ALA:HB1	73:SU:96:ILE:HD11	1.75	0.68
72:ST:108:LEU:HG	72:ST:113:VAL:HG11	1.75	0.68
1:1:446:A:HO2'	1:1:447:U:H6	1.42	0.68
2:2:1192:C:H41	69:SQ:139:GLN:HB2	1.56	0.68
2:2:1496:C:O5'	72:ST:102:ARG:NH2	2.27	0.68
53:SA:27:ILE:O	53:SA:166:ASN:ND2	2.27	0.68
79:Sa:10:ARG:HH12	79:Sa:12:LYS:HE2	1.57	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:SJ:170:VAL:HG13	62:SJ:171:ARG:HD3	1.75	0.67
2:2:41:A:HO2'	2:2:434:A:HO2'	1.40	0.67
55:SC:52:LEU:HD22	55:SC:251:TYR:HE2	1.58	0.67
55:SC:164:VAL:HG21	55:SC:232:PHE:HD1	1.59	0.67
59:SG:3:LEU:HD11	59:SG:111:LEU:HD23	1.76	0.67
1:1:968:U:O2'	14:LF:131:GLU:OE2	2.07	0.67
6:A:40:LEU:HB2	6:A:59:LEU:HB2	1.77	0.67
19:LK:13:ILE:O	19:LK:14:HIS:HD2	1.78	0.67
13:LE:162:GLN:NE2	13:LE:166:ASP:OD2	2.27	0.67
1:1:2528:U:C4	1:1:2529:U:H1'	2.30	0.67
1:1:2222:A:H2'	1:1:2223:U:H6	1.59	0.67
10:LB:340:ARG:HH22	10:LB:343:LEU:HD11	1.60	0.67
54:SB:82:ARG:NH2	54:SB:191:GLU:OE2	2.28	0.67
1:1:515:G:O6	1:1:559:G:N2	2.26	0.67
1:1:3124:G:N2	1:1:3222:C:O2	2.19	0.67
52:Ls:40:GLU:OE2	52:Ls:103:ASN:ND2	2.28	0.67
1:1:1527:G:OP1	22:LN:67:ARG:NH1	2.27	0.67
1:1:2719:C:N3	49:Lo:63:LYS:NZ	2.42	0.67
2:2:1206:C:N3	2:2:1451:G:N2	2.43	0.67
53:SA:8:SER:O	53:SA:11:ASN:ND2	2.27	0.67
58:SF:141:THR:HG22	58:SF:142:VAL:H	1.60	0.67
5:5:6:U:H2'	5:5:7:A:C8	2.30	0.66
66:SN:23:PRO:HB2	66:SN:26:LEU:HD23	1.76	0.66
1:1:1100:G:OP1	36:Lb:4:SER:OG	2.14	0.66
52:Ls:29:SER:HB3	52:Ls:188:ALA:HB2	1.76	0.66
69:SQ:137:ARG:HD3	69:SQ:137:ARG:H	1.60	0.66
71:SS:70:VAL:HA	71:SS:73:ILE:HD12	1.76	0.66
1:1:2637:A:O2'	1:1:2638:A:O5'	2.13	0.66
3:3:76:G:N2	3:3:101:A:OP2	2.27	0.66
8:C:154:LYS:NZ	8:C:343:HIS:O	2.28	0.66
11:LC:32:ARG:HH12	25:LQ:51:ASN:HD21	1.42	0.66
53:SA:53:LEU:O	53:SA:56:THR:OG1	2.12	0.66
1:1:1796:A:H2'	1:1:1797:A:H8	1.61	0.66
6:A:189:ILE:HD12	56:SD:222:VAL:HG11	1.78	0.66
66:SN:42:ARG:HE	66:SN:80:LEU:HD21	1.60	0.66
2:2:1177:C:H2'	2:2:1178:U:C6	2.31	0.66
2:2:1662:C:H2'	2:2:1663:A:C8	2.30	0.66
56:SD:35:GLU:HB2	56:SD:57:HIS:HB2	1.78	0.66
2:2:57:G:OP2	77:SY:119:LYS:NZ	2.28	0.66
2:2:66:U:O2	59:SG:160:ARG:NE	2.28	0.66
2:2:1172:U:OP2	71:SS:137:HIS:ND1	2.27	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:LR:105:LEU:HD23	26:LR:138:LEU:HD23	1.77	0.66
29:LU:27:GLN:NE2	29:LU:112:LEU:O	2.28	0.66
56:SD:223:VAL:HG22	56:SD:225:PRO:HD2	1.76	0.66
58:SF:99:ARG:HH22	78:SZ:84:HIS:CG	2.14	0.66
76:SX:37:ALA:O	76:SX:41:SER:OG	2.13	0.66
81:Sc:44:ASN:H	81:Sc:62:ARG:HH22	1.41	0.66
31:LW:126:ILE:HG22	31:LW:128:GLY:H	1.60	0.66
2:2:1101:U:OP1	76:SX:14:LYS:NZ	2.29	0.66
2:2:1400:C:H2'	2:2:1401:G:H8	1.61	0.66
5:5:23:C:H2'	5:5:24:A:H8	1.61	0.66
8:C:579:SER:HB3	8:C:714:VAL:HB	1.76	0.66
37:Lc:19:LEU:HD22	37:Lc:101:SER:HB2	1.76	0.66
56:SD:126:LEU:HD12	56:SD:139:VAL:HG12	1.76	0.66
81:Sc:41:ILE:HG13	81:Sc:42:ILE:H	1.61	0.66
28:LT:81:LYS:O	28:LT:82:HIS:ND1	2.29	0.66
59:SG:63:MET:HE1	59:SG:106:LEU:HD21	1.78	0.66
3:3:48:C:OP2	12:LD:94:ASN:ND2	2.28	0.65
8:C:288:ASN:OD1	8:C:289:ALA:N	2.29	0.65
59:SG:164:PRO:HD2	59:SG:171:PRO:HA	1.78	0.65
71:SS:101:LEU:HG	71:SS:102:ALA:H	1.62	0.65
78:SZ:26:GLN:O	78:SZ:59:LYS:NZ	2.30	0.65
1:1:1876:A:H61	1:1:2302:C:H42	1.44	0.65
2:2:1244:U:H3'	84:Sf:93:HIS:CE1	2.32	0.65
2:2:1590:G:OP2	2:2:1592:C:N4	2.30	0.65
19:LK:14:HIS:CE1	19:LK:32:ILE:HG12	2.29	0.65
69:SQ:43:ILE:HG23	69:SQ:44:LEU:HD22	1.78	0.65
2:2:916:U:H2'	2:2:917:A:H8	1.61	0.65
19:LK:70:GLN:HE22	19:LK:72:SER:HA	1.60	0.65
57:SE:9:GLN:HB2	57:SE:30:ARG:HD3	1.78	0.65
64:SL:77:THR:HG22	64:SL:129:VAL:HG22	1.79	0.65
2:2:1168:A:H2'	2:2:1169:G:C8	2.31	0.65
29:LU:105:THR:HG23	29:LU:111:GLU:OE2	1.95	0.65
2:2:1060:U:H2'	2:2:1061:G:C8	2.29	0.65
6:A:108:VAL:HG12	6:A:124:SER:HB2	1.78	0.65
8:C:420:TYR:O	8:C:479:ASN:ND2	2.30	0.65
19:LK:13:ILE:HD11	19:LK:62:LEU:HD11	1.79	0.65
50:Lp:49:ARG:HH21	50:Lp:52:VAL:HA	1.60	0.65
58:SF:195:SER:HB3	58:SF:198:ILE:HG12	1.77	0.65
72:ST:114:LEU:HD13	72:ST:123:ARG:HB3	1.79	0.65
2:2:1496:C:H3'	72:ST:102:ARG:HH22	1.62	0.65
6:A:246:TYR:HE2	6:A:261:LEU:HB2	1.62	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:Lk:29:PRO:O	45:Lk:32:GLN:NE2	2.29	0.65
63:SK:56:GLN:HE22	63:SK:58:SER:HB2	1.61	0.65
19:LK:104:VAL:HG12	19:LK:105:SER:H	1.61	0.65
70:SR:94:HIS:HD2	70:SR:97:SER:HB3	1.60	0.65
1:1:74:A:N7	20:LL:66:ASN:ND2	2.45	0.65
33:LY:73:TYR:HE2	33:LY:76:LYS:HD2	1.60	0.65
53:SA:201:MET:HE1	53:SA:203:ASP:HB2	1.79	0.65
68:SP:106:SER:OG	68:SP:129:ILE:O	2.14	0.65
80:Sb:81:ARG:O	80:Sb:82:LYS:HD2	1.97	0.65
2:2:294:U:O2	57:SE:33:THR:OG1	2.15	0.64
2:2:1675:G:N2	2:2:1718:A:H62	1.93	0.64
2:2:833:U:H2'	2:2:834:U:H6	1.61	0.64
2:2:913:A:H61	67:SO:54:ARG:HH22	1.45	0.64
1:1:2232:U:O2'	1:1:2234:A:OP2	2.14	0.64
7:B:100:GLU:OE1	8:C:701:DDE:NAD	2.29	0.64
1:1:2168:U:H2'	1:1:2169:G:C8	2.33	0.64
18:LJ:52:ARG:HG2	18:LJ:53:TYR:CD1	2.31	0.64
59:SG:182:VAL:HA	59:SG:186:ARG:HH21	1.63	0.64
61:SI:79:ILE:HB	61:SI:103:GLN:HB2	1.79	0.64
64:SL:107:LYS:O	76:SX:13:ARG:NH2	2.31	0.64
1:1:77:G:O2'	20:LL:100:ARG:NH1	2.30	0.64
1:1:1589:C:OP1	32:LX:138:ARG:NH1	2.30	0.64
2:2:210:A:H4'	64:SL:31:ARG:HE	1.63	0.64
6:A:101:PHE:HB3	6:A:132:TRP:CZ3	2.32	0.64
8:C:167:LEU:HD11	8:C:291:MET:HE3	1.80	0.64
65:SM:31:LYS:HZ1	65:SM:100:TRP:CD1	2.15	0.64
75:SW:24:GLN:NE2	80:Sb:5:VAL:O	2.22	0.64
2:2:964:A:OP2	66:SN:124:ARG:HD3	1.97	0.64
11:LC:149:VAL:HG13	11:LC:150:PRO:HD3	1.79	0.64
7:B:72:ARG:HH22	71:SS:130:GLY:HA3	1.63	0.64
8:C:465:LEU:O	8:C:515:LYS:NZ	2.26	0.64
43:Li:67:ILE:HD11	43:Li:99:LEU:HD11	1.80	0.64
63:SK:56:GLN:NE2	63:SK:57:PHE:O	2.30	0.64
75:SW:49:GLU:HB2	75:SW:64:GLN:HE22	1.62	0.64
75:SW:93:LEU:O	75:SW:94:LEU:HD22	1.97	0.64
1:1:1476:G:OP1	46:LI:48:ARG:HD2	1.97	0.64
1:1:2176:A:H2'	1:1:2177:A:H8	1.62	0.64
1:1:3135:A:OP2	23:LO:173:LYS:NZ	2.30	0.64
2:2:1584:G:H1	2:2:1604:U:H3	1.45	0.64
54:SB:138:PHE:HB3	54:SB:213:ARG:NH2	2.12	0.64
67:SO:144:GLY:O	79:Sa:22:ARG:NH2	2.31	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
74:SV:35:THR:HB	74:SV:50:ASN:ND2	2.12	0.64
42:Lh:15:LYS:HD2	42:Lh:19:GLU:HG3	1.80	0.63
1:1:1067:A:H2'	1:1:1068:A:C8	2.33	0.63
2:2:483:G:H2'	2:2:484:G:H8	1.63	0.63
2:2:833:U:H2'	2:2:834:U:C6	2.33	0.63
2:2:1254:U:O2'	2:2:1255:U:O4'	2.16	0.63
47:Lm:103:LEU:HD21	47:Lm:110:CYS:HA	1.80	0.63
52:Ls:62:ALA:O	52:Ls:65:THR:OG1	2.13	0.63
61:SI:79:ILE:HG21	61:SI:168:ARG:HH12	1.63	0.63
70:SR:36:ASP:HB2	70:SR:47:ARG:HH11	1.63	0.63
1:1:1371:U:O2'	39:Le:100:ASN:O	2.13	0.63
2:2:518:A:H1'	77:SY:37:ASN:HD21	1.64	0.63
2:2:1232:C:H5'	84:Sf:145:HIS:HD2	1.63	0.63
7:B:43:PRO:HB3	18:LJ:53:TYR:CD2	2.33	0.63
60:SH:47:LEU:HB3	60:SH:76:PHE:HE1	1.62	0.63
64:SL:91:ILE:HD11	64:SL:112:LEU:HD23	1.78	0.63
70:SR:71:PHE:HE2	70:SR:73:LEU:HB3	1.61	0.63
1:1:673:G:OP1	20:LL:39:ARG:NH2	2.32	0.63
5:5:11:C:H2'	5:5:12:G:C8	2.34	0.63
5:5:25:C:H2'	5:5:26:A:C8	2.32	0.63
1:1:1578:G:OP2	41:Lg:32:ARG:NH2	2.31	0.63
2:2:323:G:OP1	64:SL:62:LYS:NZ	2.32	0.63
2:2:1083:A:H5'	55:SC:172:SER:HB3	1.81	0.63
2:2:1584:G:O4'	58:SF:91:ASN:ND2	2.26	0.63
15:LG:161:ASP:HB2	15:LG:162:PRO:HD3	1.81	0.63
57:SE:57:ASN:OD1	57:SE:58:TYR:N	2.31	0.63
67:SO:97:ARG:HD2	67:SO:133:PRO:HD3	1.81	0.63
75:SW:90:VAL:HA	75:SW:94:LEU:HD23	1.80	0.63
77:SY:39:SER:N	77:SY:42:GLU:OE2	2.31	0.63
4:4:50:C:H2'	46:Ll:26:TRP:CH2	2.34	0.63
5:5:11:C:H2'	5:5:12:G:H8	1.62	0.63
72:ST:64:HIS:HE1	72:ST:71:VAL:HG11	1.62	0.63
1:1:957:C:H5''	25:LQ:82:MET:HE2	1.80	0.63
2:2:398:A:O3'	57:SE:3:ARG:NH1	2.32	0.63
2:2:1227:A:H2	2:2:1252:G:H21	1.45	0.63
6:A:234:ASP:OD2	6:A:254:SER:OG	2.17	0.63
58:SF:132:ASP:OD1	58:SF:133:SER:N	2.26	0.63
58:SF:184:GLU:OE2	58:SF:195:SER:OG	2.15	0.63
70:SR:93:PHE:CE2	70:SR:95:GLN:HB3	2.34	0.63
2:2:834:U:H2'	2:2:835:G:C8	2.33	0.62
16:LH:127:MET:HE2	16:LH:218:ILE:HG22	1.80	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:LK:123:LYS:HD3	19:LK:129:VAL:HG11	1.81	0.62
1:1:2518:G:OP1	9:LA:69:TYR:OH	2.15	0.62
2:2:379:C:OP2	57:SE:10:LYS:NZ	2.31	0.62
2:2:1563:U:O3'	71:SS:36:LYS:NZ	2.33	0.62
8:C:225:ARG:HG2	8:C:243:MET:HE1	1.79	0.62
19:LK:74:VAL:HG12	19:LK:76:THR:H	1.64	0.62
12:LD:60:ILE:HB	12:LD:80:SER:OG	1.99	0.62
69:SQ:99:GLU:HB2	69:SQ:102:LYS:HD2	1.81	0.62
1:1:3294:G:H1'	1:1:3297:G:H5'	1.81	0.62
2:2:231:G:H2'	2:2:232:G:C8	2.34	0.62
12:LD:187:ASP:HB3	12:LD:190:THR:HG22	1.81	0.62
26:LR:28:GLU:O	26:LR:32:ILE:HG12	1.99	0.62
75:SW:102:VAL:H	75:SW:113:HIS:CD2	2.18	0.62
2:2:148:G:N2	2:2:160:G:H22	1.97	0.62
2:2:315:U:O3'	61:SI:11:ARG:NH1	2.33	0.62
2:2:904:A:H2'	2:2:905:A:C8	2.35	0.62
2:2:1770:G:OP1	48:Ln:7:LYS:NZ	2.33	0.62
5:5:68:C:H2'	5:5:69:G:H8	1.64	0.62
6:A:109:LEU:N	6:A:123:GLY:O	2.33	0.62
8:C:675:GLU:OE2	8:C:712:ARG:NH2	2.32	0.62
12:LD:104:LEU:HB2	12:LD:250:ILE:HD11	1.82	0.62
2:2:222:U:O2'	2:2:223:G:OP1	2.15	0.62
3:3:7:G:OP1	12:LD:33:ARG:NH1	2.31	0.62
48:Lr:5:TRP:HB3	48:Lr:9:ARG:NH1	2.14	0.62
52:Ls:174:ASN:OD1	52:Ls:175:MET:N	2.32	0.62
1:1:575:G:H2'	1:1:576:A:H8	1.65	0.62
10:LB:90:VAL:HG22	10:LB:104:THR:HG22	1.80	0.62
24:LP:64:ALA:O	24:LP:80:ARG:NH1	2.33	0.62
45:Lk:74:ARG:HD2	45:Lk:74:ARG:O	1.99	0.62
58:SF:63:ARG:HH22	69:SQ:121:PRO:HD2	1.64	0.62
60:SH:36:ASN:OD1	60:SH:37:THR:N	2.32	0.62
2:2:1480:G:H21	2:2:1602:C:H1'	1.64	0.62
20:LL:55:ARG:NH1	20:LL:73:ARG:O	2.33	0.62
65:SM:95:LYS:HA	65:SM:117:ASN:HD21	1.63	0.62
1:1:2730:U:OP2	1:1:2731:C:N4	2.32	0.62
2:2:1378:U:O2	73:SU:54:ARG:NH2	2.33	0.62
4:4:87:G:OP1	42:Lh:8:LYS:NZ	2.29	0.62
1:1:1537:U:H3	1:1:1561:G:H1	1.45	0.62
51:Lq:104:ARG:HB3	51:Lq:107:LEU:HD13	1.81	0.62
52:Ls:30:VAL:HB	52:Ls:185:MET:HE1	1.81	0.62
53:SA:91:LYS:NZ	70:SR:82:ASP:O	2.32	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:SF:144:ARG:O	58:SF:211:ASN:ND2	2.26	0.62
2:2:523:A:P	77:SY:96:ARG:HH21	2.22	0.61
2:2:862:U:H5'	75:SW:28:ARG:HH21	1.63	0.61
5:5:62:C:H2'	5:5:63:C:C6	2.35	0.61
79:Sa:41:ILE:HG12	79:Sa:68:TYR:HD2	1.65	0.61
1:1:405:G:OP1	24:LP:62:ARG:NH1	2.31	0.61
1:1:1637:C:O2'	1:1:1777:A:OP2	2.17	0.61
2:2:1731:C:P	30:LV:34:ARG:HH22	2.23	0.61
56:SD:138:GLU:HG3	56:SD:156:THR:HG22	1.82	0.61
58:SF:135:ARG:NH1	58:SF:136:ILE:O	2.33	0.61
69:SQ:31:VAL:HG12	69:SQ:67:ILE:HD12	1.81	0.61
1:1:2408:A:H4'	43:Li:72:ASN:HB3	1.82	0.61
2:2:1297:A:O3'	55:SC:96:LYS:HE3	2.00	0.61
6:A:89:LEU:HB3	6:A:99:ARG:HB3	1.81	0.61
6:A:108:VAL:HA	6:A:124:SER:HA	1.81	0.61
7:B:121:GLN:OE1	56:SD:146:ARG:NH1	2.33	0.61
34:LZ:51:LYS:O	34:LZ:64:ARG:NH1	2.33	0.61
68:SP:72:LYS:NZ	68:SP:100:SER:OG	2.33	0.61
77:SY:17:ARG:HE	77:SY:24:LYS:HE2	1.65	0.61
1:1:1940:U:O2	1:1:2045:G:N2	2.31	0.61
1:1:2046:C:H2'	1:1:2047:G:H8	1.65	0.61
2:2:1078:A:O2'	2:2:1080:G:N7	2.31	0.61
57:SE:122:LYS:HE2	57:SE:164:LEU:HD21	1.81	0.61
1:1:1641:G:H2'	1:1:1642:G:C8	2.34	0.61
2:2:1240:G:H5'	68:SP:59:ARG:HH22	1.64	0.61
2:2:1519:U:H3	72:ST:75:ARG:HE	1.49	0.61
8:C:10:ARG:NH1	8:C:10:ARG:O	2.33	0.61
8:C:142:GLU:OE2	8:C:146:ARG:NH2	2.33	0.61
38:Ld:13:SER:HA	38:Ld:16:ALA:HB3	1.82	0.61
56:SD:144:LYS:NZ	56:SD:182:GLN:HE22	1.97	0.61
3:3:22:A:H2'	3:3:23:A:H8	1.66	0.61
8:C:495:VAL:HG13	8:C:556:LEU:HD13	1.82	0.61
24:LP:4:TYR:HE2	24:LP:16:ARG:HB2	1.64	0.61
59:SG:3:LEU:HD23	59:SG:16:ILE:HD11	1.81	0.61
61:SI:88:ASN:O	61:SI:91:VAL:HG22	2.01	0.61
1:1:1940:U:O4	1:1:2045:G:O6	2.18	0.61
51:Lq:128:GLU:OE2	51:Lq:131:LYS:NZ	2.33	0.61
66:SN:83:ASP:OD1	66:SN:84:ILE:N	2.34	0.61
84:Sf:139:GLN:HE21	84:Sf:150:PHE:HD2	1.47	0.61
2:2:1180:A:C6	68:SP:108:LYS:HB2	2.35	0.61
6:A:271:LYS:NZ	6:A:272:PRO:O	2.33	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:SB:140:ILE:HG23	54:SB:213:ARG:NH1	2.14	0.61
2:2:945:C:OP1	54:SB:165:ARG:NH2	2.34	0.61
2:2:1462:G:O2'	2:2:1598:C:OP1	2.18	0.61
10:LB:41:VAL:HA	10:LB:186:GLY:HA2	1.81	0.61
1:1:1704:U:H1'	1:1:1705:C:C6	2.36	0.61
2:2:682:U:OP1	75:SW:119:LYS:NZ	2.31	0.61
2:2:1061:G:H2'	2:2:1062:A:H8	1.66	0.61
78:SZ:72:LEU:HA	78:SZ:75:LYS:HE3	1.82	0.61
1:1:276:G:OP1	49:Lo:45:ARG:NH1	2.34	0.60
2:2:472:A:OP1	62:SJ:128:ARG:HG3	2.00	0.60
2:2:735:C:H2'	2:2:736:A:H8	1.66	0.60
2:2:900:G:N7	67:SO:37:ASN:ND2	2.49	0.60
16:LH:85:VAL:HG12	16:LH:86:LYS:HG3	1.83	0.60
55:SC:155:ASN:ND2	74:SV:3:ASN:O	2.34	0.60
57:SE:127:LYS:HZ1	57:SE:142:HIS:HB3	1.66	0.60
1:1:449:A:N6	1:1:468:G:O2'	2.33	0.60
1:1:1733:G:H2'	1:1:1734:C:H6	1.66	0.60
2:2:1176:G:H2'	2:2:1177:C:C6	2.37	0.60
2:2:1545:C:OP1	68:SP:50:ARG:NH2	2.33	0.60
2:2:1708:A:OP1	2:2:1708:A:H4'	2.01	0.60
14:LF:227:HIS:O	14:LF:230:GLU:HG3	2.01	0.60
19:LK:8:ASN:O	19:LK:9:GLU:HG2	2.01	0.60
60:SH:66:ILE:HD11	60:SH:98:ILE:HG22	1.83	0.60
73:SU:54:ARG:HD2	73:SU:54:ARG:O	2.01	0.60
9:LA:64:ARG:HG2	9:LA:65:SER:H	1.65	0.60
9:LA:79:ASN:HD22	9:LA:168:ILE:C	2.08	0.60
58:SF:142:VAL:HB	58:SF:144:ARG:HG3	1.83	0.60
68:SP:126:GLU:OE1	71:SS:122:HIS:N	2.35	0.60
1:1:2974:A:H2'	1:1:2975:G:H8	1.66	0.60
2:2:523:A:OP1	77:SY:96:ARG:NE	2.34	0.60
2:2:778:U:O2'	2:2:779:A:O4'	2.19	0.60
2:2:1161:G:H2'	2:2:1162:G:H8	1.67	0.60
2:2:1329:C:OP2	70:SR:45:ARG:NH2	2.33	0.60
2:2:1578:U:O2	2:2:1610:A:N7	2.34	0.60
8:C:125:ASP:OD1	8:C:354:ARG:NH1	2.33	0.60
54:SB:47:LEU:HD23	67:SO:50:GLU:HB3	1.82	0.60
1:1:1779:A:H2'	1:1:1780:A:H8	1.64	0.60
2:2:844:G:H2'	2:2:845:A:H8	1.67	0.60
2:2:1708:A:N1	31:LW:118:ARG:NH2	2.49	0.60
11:LC:303:PRO:O	11:LC:304:LYS:HG2	2.02	0.60
19:LK:61:ARG:HE	19:LK:62:LEU:H	1.48	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:LK:67:ARG:HG3	19:LK:68:GLN:H	1.65	0.60
66:SN:61:ALA:HB2	80:Sb:32:PHE:HZ	1.65	0.60
67:SO:94:ILE:HG21	67:SO:115:LEU:HD13	1.83	0.60
1:1:1795:U:H1'	1:1:1796:A:O4'	2.02	0.60
1:1:3292:U:O2'	61:SI:128:LYS:NZ	2.29	0.60
27:LS:130:GLU:OE1	27:LS:131:LYS:HG3	2.01	0.60
43:Li:74:LYS:HZ2	43:Li:76:LYS:HB3	1.66	0.60
51:Lq:120:ARG:HD2	51:Lq:123:ARG:HH12	1.65	0.60
53:SA:49:ASN:OD1	53:SA:50:ILE:N	2.33	0.60
70:SR:71:PHE:CE2	70:SR:73:LEU:HB3	2.36	0.60
78:SZ:31:LEU:HB2	78:SZ:64:LEU:HD11	1.83	0.60
2:2:1078:A:N3	2:2:1079:C:N4	2.50	0.60
2:2:1217:C:OP1	63:SK:46:SER:OG	2.19	0.60
2:2:1391:G:C6	2:2:1401:G:N1	2.69	0.60
19:LK:159:GLU:HG2	19:LK:160:ILE:HG12	1.84	0.60
58:SF:43:ILE:HG13	58:SF:44:SER:H	1.65	0.60
1:1:2495:U:H2'	1:1:2496:G:H8	1.67	0.60
2:2:922:A:H2'	2:2:923:G:C8	2.36	0.60
2:2:1371:G:H2'	2:2:1372:G:H8	1.66	0.60
42:Lh:43:GLY:H	42:Lh:46:LEU:HD23	1.67	0.60
54:SB:134:LEU:HD12	54:SB:219:LYS:HB2	1.83	0.60
78:SZ:31:LEU:HD21	78:SZ:36:SER:HB3	1.84	0.60
1:1:1632:G:H2'	1:1:1633:G:H8	1.67	0.60
2:2:1562:U:OP2	71:SS:41:ARG:NH2	2.34	0.60
6:A:77:TYR:HB3	6:A:89:LEU:HD11	1.83	0.60
39:Le:64:THR:HA	39:Le:67:MET:HE2	1.83	0.60
43:Li:74:LYS:HD2	43:Li:76:LYS:H	1.67	0.60
53:SA:26:HIS:HB3	53:SA:53:LEU:HD11	1.83	0.60
1:1:498:U:O4	11:LC:321:ARG:NH2	2.35	0.60
2:2:1294:G:N2	2:2:1297:A:OP2	2.32	0.60
2:2:321:C:OP1	64:SL:138:LYS:NZ	2.35	0.59
2:2:644:A:H2'	2:2:645:G:H8	1.67	0.59
6:A:253:ALA:HB1	6:A:282:ARG:NH2	2.17	0.59
13:LE:8:LYS:NZ	13:LE:9:THR:O	2.34	0.59
71:SS:65:GLU:HA	71:SS:68:ARG:HE	1.67	0.59
1:1:1619:C:OP2	41:Lg:75:ARG:NH2	2.35	0.59
2:2:701:A:H61	2:2:731:G:H22	1.50	0.59
6:A:121:VAL:HG12	6:A:131:LEU:HG	1.84	0.59
9:LA:89:TYR:HB2	9:LA:100:ASN:OD1	2.02	0.59
62:SJ:140:ASN:ND2	77:SY:67:TYR:OH	2.35	0.59
2:2:1425:G:H1'	73:SU:71:GLU:OE2	2.03	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:C:251:TYR:CD2	8:C:273:ARG:HA	2.37	0.59
9:LA:117:GLU:O	9:LA:162:SER:OG	2.19	0.59
2:2:177:A:H2'	2:2:178:A:H8	1.67	0.59
2:2:588:A:H2'	2:2:589:A:C8	2.37	0.59
4:4:9:A:H2'	4:4:10:A:H8	1.68	0.59
54:SB:174:ARG:NH2	54:SB:175:GLU:OE2	2.27	0.59
62:SJ:23:ASP:HB2	83:Se:44:PHE:HZ	1.67	0.59
77:SY:87:LYS:HG3	77:SY:88:PHE:CD1	2.37	0.59
2:2:1538:G:N2	2:2:1565:A:OP2	2.35	0.59
6:A:252:THR:OG1	6:A:255:SER:O	2.20	0.59
10:LB:35:ASP:HA	10:LB:185:ASN:HD22	1.67	0.59
56:SD:40:VAL:HG12	56:SD:53:ILE:HA	1.85	0.59
66:SN:28:THR:HG23	66:SN:32:GLN:HE21	1.67	0.59
6:A:130:LYS:HG2	6:A:141:THR:HG22	1.85	0.59
26:LR:162:LYS:HG3	26:LR:165:ARG:HH21	1.68	0.59
1:1:597:G:O6	11:LC:310:LYS:NZ	2.35	0.59
2:2:327:G:H2'	2:2:328:G:C8	2.37	0.59
2:2:1378:U:C2'	73:SU:54:ARG:HH12	2.15	0.59
2:2:1549:G:N7	68:SP:51:ARG:NH2	2.51	0.59
2:2:1662:C:H2'	2:2:1663:A:H8	1.67	0.59
2:2:1781:U:OP1	67:SO:149:ARG:NH2	2.35	0.59
3:3:22:A:H2'	3:3:23:A:C8	2.37	0.59
19:LK:87:GLU:HB3	19:LK:88:PRO:CD	2.33	0.59
19:LK:125:LEU:HD12	19:LK:127:GLY:H	1.68	0.59
35:La:112:LEU:HD13	35:La:125:VAL:HG11	1.82	0.59
79:Sa:58:VAL:O	79:Sa:59:PHE:HD1	1.85	0.59
1:1:742:G:N2	1:1:752:G:N3	2.50	0.59
1:1:1048:A:O4'	36:Lb:28:ARG:NH1	2.35	0.59
1:1:1222:C:OP2	19:LK:102:LYS:NZ	2.36	0.59
1:1:1561:G:C5	1:1:1562:U:H1'	2.38	0.59
2:2:585:U:OP2	83:Se:26:LYS:NZ	2.35	0.59
65:SM:57:ARG:HA	65:SM:85:LYS:HZ2	1.68	0.59
69:SQ:34:LYS:HZ3	69:SQ:38:LEU:HB2	1.68	0.59
79:Sa:44:MET:HE1	79:Sa:67:MET:HB3	1.85	0.59
1:1:3129:C:OP1	40:Lf:12:LYS:NZ	2.33	0.59
3:3:78:A:H62	3:3:100:G:H21	1.50	0.59
8:C:830:GLY:O	8:C:831:LEU:HD22	2.02	0.59
13:LE:8:LYS:HZ3	13:LE:20:PRO:HD3	1.67	0.59
52:Ls:123:ALA:N	52:Ls:155:ASP:OD1	2.34	0.59
58:SF:112:THR:HG22	58:SF:114:GLN:H	1.67	0.59
59:SG:7:HIS:CE1	59:SG:9:ALA:HB3	2.38	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
65:SM:61:MET:HB2	65:SM:123:VAL:HB	1.85	0.59
1:1:446:A:H1'	1:1:447:U:H5'	1.85	0.59
2:2:469:U:O2'	2:2:768:A:N3	2.36	0.59
2:2:898:A:H5''	67:SO:40:PHE:CZ	2.38	0.59
2:2:937:A:H2'	2:2:938:A:C8	2.37	0.59
6:A:70:VAL:HG13	6:A:113:PHE:CE2	2.38	0.59
6:A:244:ASN:OD1	6:A:245:ARG:N	2.35	0.59
8:C:182:ARG:NH2	52:Ls:137:GLN:OE1	2.35	0.59
36:Lb:32:LEU:O	36:Lb:40:ARG:NH1	2.36	0.59
43:Li:46:THR:O	43:Li:50:ARG:HG3	2.03	0.59
54:SB:35:PRO:HG3	54:SB:99:ASN:HA	1.85	0.59
56:SD:44:VAL:HG12	56:SD:49:THR:HB	1.85	0.59
61:SI:116:HIS:O	61:SI:117:TYR:HD2	1.86	0.59
1:1:1004:C:H2'	1:1:1005:G:H8	1.67	0.58
1:1:2111:U:H2'	1:1:2112:A:C8	2.37	0.58
2:2:1226:G:H22	2:2:1252:G:H2'	1.68	0.58
2:2:1227:A:H8	2:2:1255:U:C5	2.21	0.58
2:2:1398:G:OP2	70:SR:5:ARG:NH2	2.36	0.58
8:C:634:LYS:HB3	8:C:650:ASP:OD1	2.03	0.58
17:LI:110:ARG:HG2	17:LI:111:LEU:N	2.17	0.58
56:SD:145:LEU:HG	56:SD:146:ARG:HG3	1.83	0.58
1:1:462:A:OP1	51:Lq:92:LYS:NZ	2.33	0.58
1:1:1199:C:H2'	1:1:1200:A:H8	1.69	0.58
2:2:709:G:O6	2:2:722:U:O4	2.22	0.58
2:2:1755:C:H2'	2:2:1756:G:C8	2.38	0.58
19:LK:95:GLU:HB2	19:LK:99:LYS:HD3	1.84	0.58
61:SI:84:HIS:NE2	61:SI:97:THR:OG1	2.34	0.58
2:2:1479:A:H4'	69:SQ:72:GLY:H	1.68	0.58
8:C:578:LEU:HD12	8:C:589:TYR:HE1	1.68	0.58
10:LB:102:LEU:HG	10:LB:103:THR:HG23	1.86	0.58
58:SF:136:ILE:HD11	58:SF:145:GLN:HE22	1.67	0.58
1:1:2623:C:OP2	18:LJ:143:ARG:NH1	2.36	0.58
2:2:1396:A:H2'	2:2:1397:A:C8	2.39	0.58
2:2:1517:G:O2'	2:2:1519:U:OP2	2.16	0.58
9:LA:84:THR:HG22	50:Lp:63:THR:H	1.69	0.58
60:SH:81:GLN:NE2	60:SH:82:ARG:HG2	2.19	0.58
61:SI:37:ARG:HD2	61:SI:59:ARG:NH1	2.18	0.58
65:SM:45:ARG:NH2	65:SM:101:ALA:O	2.33	0.58
1:1:1506:U:O2'	32:LX:124:ASN:ND2	2.36	0.58
2:2:214:A:OP2	59:SG:230:ARG:NH2	2.36	0.58
2:2:865:G:O6	2:2:960:C:N4	2.35	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:1271:C:H5	7:B:108:ARG:H	1.50	0.58
2:2:1640:C:H2'	2:2:1641:G:H8	1.68	0.58
5:5:67:U:H2'	5:5:68:C:H6	1.68	0.58
10:LB:37:PRO:HA	10:LB:187:GLY:HA2	1.85	0.58
17:LI:208:GLU:OE2	17:LI:212:ARG:NH2	2.36	0.58
19:LK:32:ILE:HD12	19:LK:35:LEU:HB2	1.85	0.58
40:Lf:105:TYR:HB2	40:Lf:106:PRO:HD3	1.84	0.58
52:Ls:37:GLN:NE2	52:Ls:40:GLU:OE2	2.36	0.58
58:SF:58:PRO:HG3	58:SF:77:ILE:HG12	1.85	0.58
70:SR:123:ASN:HD21	70:SR:125:ILE:HD11	1.68	0.58
1:1:447:U:O2'	1:1:468:G:N1	2.36	0.58
2:2:92:A:H4'	57:SE:3:ARG:HH21	1.67	0.58
5:5:17:G:O2'	5:5:56:G:N2	2.36	0.58
6:A:66:VAL:HA	6:A:82:SER:HA	1.86	0.58
11:LC:300:LEU:HD13	25:LQ:67:ARG:HE	1.68	0.58
32:LX:71:ASP:OD1	32:LX:72:GLU:N	2.32	0.58
1:1:1464:A:O2'	1:1:1838:A:N3	2.32	0.58
2:2:510:U:H2'	2:2:511:G:C8	2.37	0.58
8:C:653:LYS:NZ	84:Sf:82:LYS:HA	2.18	0.58
30:LV:98:GLU:OE1	31:LW:68:GLY:N	2.37	0.58
1:1:97:G:H5'	20:LL:15:ARG:NH2	2.18	0.58
5:5:28:C:H2'	5:5:29:A:H8	1.68	0.58
6:A:256:ILE:HB	6:A:270:LEU:HB2	1.86	0.58
8:C:720:LEU:HD22	8:C:837:GLY:HA3	1.86	0.58
19:LK:25:SER:HB2	19:LK:28:LEU:HD11	1.86	0.58
35:La:82:VAL:O	35:La:87:ARG:NH1	2.36	0.58
65:SM:82:GLN:HA	65:SM:86:ILE:HD12	1.85	0.58
78:SZ:60:ILE:HD11	78:SZ:64:LEU:HD13	1.85	0.58
78:SZ:88:LYS:O	78:SZ:89:ILE:HD13	2.04	0.58
16:LH:201:GLN:HG3	16:LH:218:ILE:O	2.03	0.58
53:SA:29:SER:HB3	53:SA:152:THR:HG22	1.84	0.58
54:SB:33:LYS:O	54:SB:98:THR:OG1	2.22	0.58
77:SY:38:ILE:HB	77:SY:43:LEU:HD21	1.86	0.58
77:SY:41:ASP:OD1	77:SY:42:GLU:N	2.36	0.58
2:2:1500:G:N3	2:2:1559:C:O2'	2.37	0.58
30:LV:134:ASN:O	30:LV:134:ASN:ND2	2.36	0.58
75:SW:105:THR:HB	75:SW:126:ILE:HD11	1.86	0.58
1:1:2355:C:O2'	10:LB:267:ARG:NH2	2.35	0.57
2:2:451:A:N9	57:SE:66:MET:HE1	2.18	0.57
2:2:1470:G:H2'	2:2:1471:A:H8	1.69	0.57
8:C:382:LEU:HD23	8:C:471:LEU:HD12	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:LC:301:ARG:HD3	25:LQ:69:GLU:HG2	1.86	0.57
19:LK:114:ARG:NH2	19:LK:126:LYS:O	2.37	0.57
38:Ld:57:THR:HG23	38:Ld:59:ASP:H	1.67	0.57
56:SD:56:THR:O	56:SD:93:LYS:NZ	2.34	0.57
64:SL:79:ARG:O	64:SL:91:ILE:HA	2.05	0.57
64:SL:104:ARG:HB2	76:SX:9:LEU:O	2.04	0.57
1:1:665:A:OP2	25:LQ:115:THR:OG1	2.21	0.57
1:1:2140:G:O2'	9:LA:126:LEU:O	2.22	0.57
2:2:155:U:O2'	2:2:157:C:OP2	2.22	0.57
8:C:253:ASN:N	8:C:254:PRO:HD3	2.18	0.57
8:C:590:MET:CE	8:C:688:PHE:HB3	2.34	0.57
25:LQ:174:ARG:HB2	25:LQ:177:VAL:HG23	1.86	0.57
36:Lb:57:PHE:HB2	36:Lb:63:GLU:HB2	1.87	0.57
57:SE:44:LEU:HD23	57:SE:82:TYR:HB3	1.86	0.57
72:ST:16:VAL:HG23	72:ST:59:ALA:HB3	1.87	0.57
1:1:643:C:H2'	1:1:644:A:H8	1.69	0.57
1:1:701:U:P	43:Li:18:ARG:HH22	2.27	0.57
1:1:2112:A:C2	1:1:2151:A:H4'	2.39	0.57
2:2:644:A:H2'	2:2:645:G:C8	2.40	0.57
2:2:1400:C:H2'	2:2:1401:G:C8	2.39	0.57
6:A:253:ALA:O	6:A:282:ARG:NH2	2.35	0.57
53:SA:101:ILE:HD11	53:SA:119:LYS:HE3	1.86	0.57
1:1:2270:G:O2'	1:1:2273:U:OP2	2.22	0.57
2:2:904:A:P	67:SO:65:ARG:HH21	2.27	0.57
2:2:1749:A:H2'	2:2:1750:A:C8	2.40	0.57
3:3:1:A:C8	12:LD:271:LYS:HG3	2.39	0.57
6:A:157:SER:HB2	6:A:163:PRO:HA	1.86	0.57
6:A:272:PRO:HG2	6:A:274:PHE:HE1	1.68	0.57
30:LV:12:LYS:HZ1	30:LV:15:MET:HE2	1.69	0.57
84:Sf:123:ASN:HD22	84:Sf:126:CYS:HB2	1.69	0.57
1:1:3216:U:O2'	40:Lf:101:ARG:NH1	2.37	0.57
6:A:246:TYR:CE2	6:A:261:LEU:HB2	2.39	0.57
5:5:52:G:C2	5:5:61:C:C2	2.92	0.57
6:A:30:MET:HE2	6:A:42:ILE:HD11	1.86	0.57
43:Li:60:ALA:HB3	43:Li:63:GLU:HG3	1.87	0.57
62:SJ:83:VAL:HG23	62:SJ:84:LEU:HD12	1.85	0.57
68:SP:94:VAL:HG12	68:SP:96:GLU:H	1.70	0.57
1:1:203:A:N3	11:LC:228:ASN:ND2	2.53	0.57
1:1:1792:G:O6	34:LZ:63:LYS:NZ	2.33	0.57
1:1:3209:A:OP1	13:LE:64:ARG:NH2	2.31	0.57
2:2:191:G:O2'	2:2:192:A:H8	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:1343:A:OP2	2:2:1345:A:N6	2.31	0.57
2:2:1606:G:H5''	58:SF:94:LYS:NZ	2.20	0.57
6:A:233:ASN:OD1	6:A:234:ASP:N	2.38	0.57
40:Lf:54:VAL:HG12	40:Lf:68:VAL:HG22	1.86	0.57
57:SE:131:LEU:HA	57:SE:137:PRO:HA	1.87	0.57
61:SI:27:PHE:HD2	61:SI:28:GLU:HG3	1.69	0.57
67:SO:38:ASP:OD1	67:SO:39:THR:N	2.36	0.57
1:1:1938:G:H22	1:1:2047:G:H22	1.53	0.57
1:1:2853:C:OP2	16:LH:207:ARG:NH1	2.38	0.57
2:2:161:A:H1'	59:SG:13:GLN:HE21	1.69	0.57
2:2:471:A:O3'	62:SJ:128:ARG:NH1	2.38	0.57
2:2:1498:G:N2	2:2:1501:A:OP2	2.36	0.57
6:A:45:LEU:HD13	6:A:47:ARG:NE	2.20	0.57
21:LM:12:ARG:HB3	21:LM:18:ARG:HH21	1.70	0.57
57:SE:172:PHE:CE2	57:SE:174:LYS:HE3	2.40	0.57
61:SI:5:ARG:NH1	61:SI:29:LEU:O	2.37	0.57
65:SM:97:LEU:HA	65:SM:100:TRP:HE3	1.70	0.57
68:SP:100:SER:O	68:SP:115:ILE:HG12	2.04	0.57
1:1:154:G:H2'	1:1:155:A:H8	1.70	0.57
1:1:3141:G:OP1	16:LH:60:ARG:NH1	2.37	0.57
2:2:518:A:N3	77:SY:37:ASN:ND2	2.53	0.57
2:2:1190:A:H4'	73:SU:72:GLY:HA2	1.85	0.57
2:2:1552:A:H2'	68:SP:48:ARG:NH2	2.20	0.57
4:4:63:G:O3'	42:Lh:54:LYS:NZ	2.36	0.57
17:LI:78:LYS:HE3	17:LI:79:TYR:HE1	1.70	0.57
26:LR:134:HIS:CE1	26:LR:136:ARG:HB2	2.39	0.57
60:SH:54:GLU:OE2	60:SH:62:LYS:HB2	2.05	0.57
60:SH:70:VAL:HA	60:SH:73:LEU:HD23	1.86	0.57
69:SQ:45:ARG:HA	69:SQ:48:LEU:HD23	1.86	0.57
2:2:786:A:OP2	57:SE:108:ARG:NH2	2.37	0.57
1:1:2176:A:H2'	1:1:2177:A:C8	2.40	0.56
2:2:897:G:C8	54:SB:7:LYS:HE2	2.40	0.56
2:2:1653:U:O2'	2:2:1654:G:OP2	2.21	0.56
8:C:661:ILE:HD13	8:C:695:LEU:HD21	1.86	0.56
18:LJ:109:GLU:OE1	18:LJ:111:ILE:HG22	2.05	0.56
37:Lc:56:LYS:O	37:Lc:60:GLU:HG3	2.05	0.56
63:SK:4:PRO:HB2	63:SK:7:ASP:HB3	1.87	0.56
2:2:1619:C:H2'	2:2:1620:C:C6	2.40	0.56
8:C:372:ARG:HH22	8:C:381:MET:HG2	1.70	0.56
19:LK:88:PRO:HG2	19:LK:90:ARG:HH12	1.70	0.56
1:1:1016:U:H2'	1:1:1017:U:C6	2.40	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:1689:A:H2'	2:2:1690:G:C8	2.40	0.56
2:2:1694:G:H2'	2:2:1695:G:C8	2.40	0.56
7:B:71:GLY:H	7:B:74:ALA:HB3	1.69	0.56
19:LK:97:ASN:O	19:LK:99:LYS:N	2.37	0.56
25:LQ:107:THR:HB	25:LQ:164:THR:HG22	1.87	0.56
69:SQ:97:VAL:HG22	69:SQ:98:ASP:H	1.70	0.56
72:ST:23:LEU:HD11	72:ST:55:TYR:HB3	1.87	0.56
75:SW:30:SER:HA	75:SW:34:ILE:HD11	1.87	0.56
2:2:499:U:H2'	2:2:500:G:C8	2.40	0.56
5:5:6:U:H2'	5:5:7:A:H8	1.67	0.56
8:C:250:ASN:ND2	8:C:262:SER:O	2.39	0.56
8:C:351:GLN:O	8:C:355:VAL:HG23	2.04	0.56
19:LK:64:ILE:H	19:LK:70:GLN:NE2	1.94	0.56
22:LN:172:ARG:HB2	22:LN:174:LEU:HD13	1.87	0.56
71:SS:15:LEU:HD21	71:SS:17:LEU:HG	1.86	0.56
1:1:559:G:O2'	1:1:561:A:OP2	2.19	0.56
1:1:2533:G:H2'	1:1:2534:G:H8	1.68	0.56
2:2:163:C:O2'	59:SG:133:LEU:O	2.24	0.56
2:2:1441:G:N2	84:Sf:85:TYR:HD2	2.02	0.56
5:5:41:U:H2'	5:5:42:G:H8	1.71	0.56
15:LG:231:ASP:O	15:LG:234:LYS:NZ	2.38	0.56
17:LI:130:ASP:OD1	17:LI:131:ILE:N	2.39	0.56
49:Lo:38:GLN:OE1	49:Lo:41:ARG:NH2	2.38	0.56
1:1:101:A:H3'	1:1:102:G:H21	1.71	0.56
1:1:2625:C:H2'	1:1:2626:A:H8	1.70	0.56
2:2:607:G:O2'	2:2:610:G:O2'	2.13	0.56
2:2:1061:G:H2'	2:2:1062:A:C8	2.41	0.56
5:5:70:G:H2'	5:5:71:A:H8	1.69	0.56
6:A:30:MET:HB2	6:A:42:ILE:HD11	1.86	0.56
11:LC:311:ARG:HH21	11:LC:314:VAL:HG23	1.70	0.56
44:Lj:14:LYS:HZ2	46:Ll:51:LEU:HD21	1.70	0.56
51:Lq:133:LEU:HB3	51:Lq:137:ALA:HB3	1.88	0.56
66:SN:66:VAL:HG23	66:SN:67:THR:HG23	1.87	0.56
1:1:1799:U:H5'	48:Lr:13:LEU:HD12	1.88	0.56
1:1:2533:G:H2'	1:1:2534:G:C8	2.41	0.56
2:2:335:C:H1'	61:Sl:5:ARG:HG3	1.87	0.56
2:2:1161:G:H2'	2:2:1162:G:C8	2.41	0.56
2:2:1479:A:H2'	2:2:1480:G:C8	2.41	0.56
2:2:1542:G:OP1	71:SS:123:ARG:NH2	2.38	0.56
2:2:1663:A:H2'	2:2:1664:G:H8	1.71	0.56
6:A:54:TYR:OH	69:SQ:99:GLU:HG2	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:C:130:VAL:HG12	8:C:158:ILE:CG2	2.35	0.56
8:C:226:GLN:N	8:C:226:GLN:OE1	2.39	0.56
8:C:393:LYS:NZ	8:C:550:ASP:O	2.25	0.56
8:C:467:LYS:NZ	8:C:514:SER:O	2.38	0.56
13:LE:170:ILE:HA	13:LE:173:ILE:HG22	1.87	0.56
19:LK:86:LYS:HZ2	19:LK:104:VAL:HG21	1.71	0.56
52:Ls:29:SER:HA	52:Ls:84:VAL:HG12	1.88	0.56
58:SF:66:VAL:HG23	58:SF:67:LYS:HG2	1.87	0.56
59:SG:10:ASN:HB2	59:SG:128:VAL:HA	1.87	0.56
66:SN:5:HIS:ND1	66:SN:117:LEU:HD12	2.20	0.56
80:Sb:36:LYS:HB2	80:Sb:43:ILE:HD13	1.88	0.56
2:2:1587:C:H2'	2:2:1588:A:H8	1.71	0.56
5:5:63:C:H2'	5:5:64:G:C8	2.41	0.56
24:LP:4:TYR:HD2	24:LP:149:ILE:HD11	1.71	0.56
55:SC:235:PRO:HA	55:SC:238:TRP:CE2	2.40	0.56
82:Sd:33:LYS:HE2	82:Sd:34:TYR:CE2	2.41	0.56
1:1:351:G:N2	1:1:354:A:OP2	2.36	0.56
1:1:1242:A:O2'	1:1:1263:C:O2'	2.20	0.56
1:1:3328:G:O3'	38:Ld:12:ARG:NH2	2.39	0.56
2:2:738:G:H2'	2:2:739:A:H8	1.71	0.56
2:2:740:C:O2'	2:2:741:U:OP1	2.23	0.56
2:2:1390:C:H2'	2:2:1391:G:C8	2.41	0.56
2:2:1669:G:OP1	59:SG:94:ARG:NH2	2.39	0.56
8:C:808:GLY:HA3	8:C:818:VAL:HG23	1.88	0.56
30:LV:82:ARG:NH1	30:LV:99:ASP:OD1	2.38	0.56
43:Li:74:LYS:NZ	43:Li:76:LYS:HB3	2.20	0.56
54:SB:86:LEU:HD13	54:SB:98:THR:HG21	1.87	0.56
54:SB:128:THR:HB	54:SB:134:LEU:HD23	1.88	0.56
60:SH:149:ARG:HB3	75:SW:51:GLU:OE2	2.06	0.56
60:SH:183:TYR:HE2	60:SH:189:ARG:HB2	1.71	0.56
71:SS:62:THR:N	71:SS:65:GLU:OE2	2.31	0.56
1:1:1733:G:H2'	1:1:1734:C:C6	2.41	0.56
1:1:3291:C:O2'	1:1:3292:U:O2	2.23	0.56
2:2:67:A:O2'	2:2:69:G:OP1	2.22	0.56
2:2:209:G:N7	64:SL:34:LYS:NZ	2.41	0.56
2:2:865:G:OP2	66:SN:3:ARG:NH1	2.36	0.56
2:2:1097:G:H1'	76:SX:7:ARG:HH21	1.71	0.56
2:2:1323:A:H4'	56:SD:159:PHE:HE1	1.71	0.56
8:C:22:MET:HA	8:C:125:ASP:O	2.06	0.56
12:LD:41:LYS:HB2	28:LT:68:THR:O	2.06	0.56
39:Le:84:GLU:OE2	39:Le:112:ARG:NE	2.35	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:Ls:41:ILE:HB	52:Ls:103:ASN:HD21	1.71	0.56
58:SF:35:TYR:CD2	58:SF:54:PRO:HB3	2.41	0.56
69:SQ:127:LYS:NZ	69:SQ:132:ARG:HB2	2.21	0.56
75:SW:30:SER:OG	75:SW:58:SER:O	2.24	0.56
1:1:151:G:H5''	1:1:152:G:C8	2.41	0.55
2:2:195:G:H2'	2:2:196:G:H8	1.70	0.55
2:2:1712:C:O2'	2:2:1713:C:H5''	2.05	0.55
8:C:232:ALA:HA	8:C:236:GLY:HA3	1.86	0.55
14:LF:157:ARG:NE	14:LF:249:ASN:OD1	2.32	0.55
25:LQ:205:ARG:HH11	25:LQ:205:ARG:HG3	1.71	0.55
27:LS:12:ARG:NH2	27:LS:57:GLU:OE2	2.36	0.55
54:SB:190:PRO:O	54:SB:195:ARG:NH2	2.39	0.55
55:SC:87:GLU:OE2	55:SC:194:ARG:NH2	2.38	0.55
2:2:637:U:O2	60:SH:189:ARG:NH2	2.39	0.55
2:2:1208:A:N6	2:2:1449:G:O6	2.39	0.55
2:2:1253:A:H4'	63:SK:5:LYS:HZ1	1.71	0.55
5:5:67:U:H2'	5:5:68:C:C6	2.41	0.55
9:LA:52:PRO:HB2	9:LA:191:VAL:HG11	1.87	0.55
19:LK:132:ILE:HG13	19:LK:133:LEU:HD22	1.88	0.55
55:SC:160:HIS:CD2	55:SC:182:ARG:HE	2.23	0.55
65:SM:106:LEU:N	65:SM:113:ARG:HH22	2.03	0.55
81:Sc:20:THR:HG22	81:Sc:21:GLY:N	2.21	0.55
1:1:1695:A:H4'	1:1:1696:A:H5'	1.88	0.55
1:1:2221:U:H2'	1:1:2222:A:H8	1.70	0.55
2:2:122:G:P	57:SE:77:ARG:HH12	2.29	0.55
2:2:124:U:OP1	57:SE:148:ARG:NH2	2.39	0.55
2:2:487:U:O2	2:2:494:G:N2	2.25	0.55
5:5:48:C:H2'	5:5:49:G:C8	2.41	0.55
19:LK:114:ARG:NH1	19:LK:129:VAL:HG13	2.21	0.55
55:SC:57:LYS:HD2	55:SC:251:TYR:CZ	2.41	0.55
58:SF:197:ALA:HA	58:SF:200:LYS:HE3	1.89	0.55
63:SK:44:LEU:HD13	63:SK:64:TYR:CE2	2.41	0.55
65:SM:84:HIS:CD2	65:SM:85:LYS:HE2	2.41	0.55
72:ST:105:MET:HE1	72:ST:123:ARG:HH11	1.71	0.55
8:C:27:HIS:CD2	8:C:140:GLN:HB2	2.41	0.55
8:C:182:ARG:NH1	52:Ls:141:ILE:O	2.39	0.55
10:LB:110:LEU:HD12	10:LB:114:VAL:HG21	1.88	0.55
12:LD:53:VAL:HG11	12:LD:165:VAL:HG11	1.87	0.55
72:ST:77:ARG:NH1	72:ST:96:ALA:O	2.40	0.55
1:1:2266:A:OP1	48:Ln:23:ARG:NH2	2.39	0.55
1:1:2314:U:H2'	1:1:2315:A:H8	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:687:C:O2'	2:2:688:U:OP1	2.22	0.55
6:A:257:ILE:HD12	6:A:259:PHE:CZ	2.41	0.55
9:LA:171:GLY:O	50:Lp:68:ALA:HB2	2.07	0.55
2:2:746:C:O3'	75:SW:80:ASN:ND2	2.39	0.55
2:2:914:U:H2'	2:2:915:U:H6	1.72	0.55
2:2:920:G:H2'	2:2:921:A:H8	1.72	0.55
2:2:1475:A:H2'	2:2:1476:G:H8	1.72	0.55
2:2:1496:C:H3'	72:ST:102:ARG:NH2	2.21	0.55
2:2:1633:C:C4	7:B:96:ARG:HG2	2.42	0.55
6:A:45:LEU:HA	6:A:53:GLY:HA3	1.88	0.55
6:A:182:CYS:O	6:A:183:LYS:HD3	2.07	0.55
7:B:132:LEU:O	7:B:136:GLN:HG2	2.06	0.55
8:C:578:LEU:HD12	8:C:589:TYR:CE1	2.42	0.55
19:LK:83:ARG:HD3	19:LK:86:LYS:HE3	1.89	0.55
21:LM:35:ASP:OD1	21:LM:36:HIS:N	2.31	0.55
52:Ls:27:VAL:HG12	52:Ls:86:PHE:HB3	1.87	0.55
57:SE:163:ASP:OD1	57:SE:170:THR:OG1	2.23	0.55
70:SR:94:HIS:CE1	70:SR:98:GLU:HG2	2.41	0.55
1:1:3332:A:O2'	1:1:3333:G:OP1	2.23	0.55
2:2:204:U:H2'	2:2:205:A:H8	1.72	0.55
2:2:327:G:H2'	2:2:328:G:H8	1.70	0.55
2:2:906:U:H2'	2:2:907:U:H6	1.71	0.55
2:2:1437:C:H2'	2:2:1438:U:C6	2.41	0.55
2:2:1675:G:H21	2:2:1718:A:N6	2.01	0.55
17:LI:3:ARG:NE	17:LI:63:GLU:OE1	2.39	0.55
19:LK:153:ASP:OD1	19:LK:154:ALA:N	2.40	0.55
53:SA:33:ASN:OD1	53:SA:34:VAL:N	2.40	0.55
58:SF:59:HIS:O	69:SQ:79:TYR:OH	2.24	0.55
58:SF:110:LEU:HD11	78:SZ:91:THR:HB	1.89	0.55
66:SN:87:ASP:OD1	66:SN:88:LEU:N	2.38	0.55
76:SX:103:LEU:HB3	76:SX:126:LYS:HB2	1.89	0.55
77:SY:39:SER:O	77:SY:41:ASP:N	2.39	0.55
2:2:552:A:N3	2:2:587:C:O2'	2.35	0.55
2:2:822:G:H2'	2:2:823:U:C6	2.42	0.55
32:LX:147:ASP:OD1	32:LX:148:ILE:N	2.40	0.55
66:SN:84:ILE:HD11	66:SN:89:TYR:HD2	1.70	0.55
1:1:237:A:OP1	42:Lh:120:LYS:NZ	2.40	0.55
1:1:422:U:O2'	40:Lf:90:PRO:O	2.24	0.55
2:2:845:A:H2'	2:2:846:C:H6	1.72	0.55
2:2:1039:G:H2'	2:2:1040:G:C8	2.42	0.55
2:2:1251:U:OP2	65:SM:48:ARG:NH2	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:1465:A:H2'	2:2:1466:C:C6	2.42	0.55
2:2:1580:G:H5''	69:SQ:122:ARG:HG2	1.89	0.55
8:C:33:SER:OG	86:C:901:GDP:O2A	2.25	0.55
40:Lf:18:TYR:CD1	40:Lf:27:PRO:HA	2.42	0.55
53:SA:12:PRO:O	53:SA:13:THR:OG1	2.23	0.55
54:SB:88:VAL:HA	54:SB:98:THR:HG22	1.88	0.55
61:SI:67:TRP:NE1	61:SI:189:GLU:OE2	2.37	0.55
61:SI:176:ARG:HE	61:SI:179:GLN:HG3	1.72	0.55
1:1:1206:A:H2'	1:1:1207:C:C6	2.42	0.55
1:1:1464:A:O2'	1:1:1838:A:H1'	2.07	0.55
2:2:1232:C:H5'	84:Sf:145:HIS:CD2	2.41	0.55
2:2:1497:C:H5	72:ST:102:ARG:NH1	2.04	0.55
2:2:1569:A:H4'	2:2:1570:G:OP2	2.06	0.55
7:B:112:ARG:HG3	7:B:112:ARG:O	2.06	0.55
29:LU:27:GLN:HG2	29:LU:28:PRO:HD3	1.89	0.55
60:SH:165:ASP:OD1	60:SH:166:GLU:N	2.40	0.55
66:SN:110:ASP:OD1	66:SN:111:SER:N	2.39	0.55
66:SN:142:GLU:HB2	66:SN:145:THR:HG22	1.87	0.55
1:1:842:G:H8	9:LA:183:SER:HG	1.55	0.54
1:1:3068:C:H2'	1:1:3069:U:C6	2.42	0.54
1:1:3073:C:OP1	16:LH:99:ARG:NH2	2.39	0.54
2:2:176:A:H2'	2:2:177:A:C8	2.42	0.54
2:2:1178:U:H2'	2:2:1179:U:C6	2.42	0.54
2:2:1313:G:OP1	70:SR:7:LYS:N	2.41	0.54
6:A:45:LEU:HD13	6:A:47:ARG:HE	1.71	0.54
11:LC:32:ARG:HH12	25:LQ:51:ASN:ND2	2.04	0.54
15:LG:27:ASN:HB3	15:LG:30:LEU:HD23	1.88	0.54
19:LK:10:ILE:HD11	19:LK:67:ARG:HA	1.88	0.54
19:LK:22:VAL:HG12	19:LK:24:ALA:H	1.72	0.54
20:LL:47:ALA:HB3	20:LL:48:PRO:HD3	1.88	0.54
22:LN:64:VAL:HG11	22:LN:102:ALA:HB1	1.88	0.54
51:Lq:20:LEU:HD21	51:Lq:22:LYS:HB2	1.89	0.54
57:SE:9:GLN:OE1	57:SE:28:ALA:HB3	2.07	0.54
66:SN:116:ILE:HA	66:SN:119:GLU:OE1	2.07	0.54
77:SY:13:ARG:NH1	77:SY:29:ASP:OD2	2.40	0.54
1:1:1818:C:H5''	1:1:1819:A:H5'	1.89	0.54
2:2:318:C:N4	2:2:1663:A:OP1	2.40	0.54
2:2:828:U:O2'	2:2:829:U:H5'	2.07	0.54
2:2:850:C:P	26:LR:172:ARG:HH21	2.29	0.54
2:2:1611:C:OP1	58:SF:68:ARG:NH2	2.40	0.54
2:2:1751:A:H5'	76:SX:63:GLN:NE2	2.22	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:C:263:PRO:HA	8:C:271:LEU:HD12	1.89	0.54
22:LN:68:ARG:NH1	22:LN:124:ASP:O	2.40	0.54
23:LO:3:SER:OG	23:LO:5:GLU:OE2	2.26	0.54
29:LU:21:PHE:HE2	29:LU:78:LEU:HD23	1.72	0.54
73:SU:37:GLU:OE1	73:SU:41:ARG:NH1	2.40	0.54
82:Sd:19:ARG:CZ	82:Sd:32:ARG:HH21	2.20	0.54
1:1:2496:G:O2'	1:1:2497:G:H5'	2.07	0.54
1:1:2632:A:O2'	18:LJ:127:ASP:OD1	2.19	0.54
2:2:187:U:O2'	2:2:188:U:O5'	2.26	0.54
2:2:1789:G:O6	79:Sa:34:LYS:NZ	2.30	0.54
19:LK:124:ASP:O	19:LK:125:LEU:HG	2.07	0.54
31:LW:141:ARG:HG3	31:LW:143:GLU:OE2	2.07	0.54
57:SE:57:ASN:HB3	57:SE:60:GLU:OE1	2.08	0.54
1:1:2247:C:N4	1:1:2271:C:O4'	2.40	0.54
2:2:115:U:O2'	2:2:330:A:N3	2.39	0.54
2:2:917:A:H2'	2:2:918:U:C6	2.42	0.54
6:A:101:PHE:HB3	6:A:132:TRP:CE3	2.42	0.54
10:LB:219:ILE:HD11	10:LB:340:ARG:HE	1.72	0.54
16:LH:142:LYS:HB2	16:LH:149:TYR:HE1	1.72	0.54
53:SA:193:ASN:HB3	53:SA:196:THR:HG22	1.90	0.54
54:SB:132:HIS:HB2	54:SB:221:PRO:HB3	1.89	0.54
70:SR:117:PHE:HB3	70:SR:120:ILE:HD13	1.89	0.54
84:Sf:132:MET:SD	84:Sf:139:GLN:HB3	2.48	0.54
1:1:306:U:H2'	1:1:307:U:C6	2.43	0.54
1:1:3068:C:O2'	16:LH:194:SER:OG	2.26	0.54
2:2:510:U:OP1	62:SJ:131:HIS:NE2	2.40	0.54
8:C:77:LEU:HD23	8:C:78:TYR:O	2.08	0.54
8:C:367:ALA:HA	8:C:371:ILE:HD13	1.90	0.54
8:C:671:TRP:CZ3	8:C:712:ARG:HD2	2.42	0.54
61:SI:32:GLN:OE1	61:SI:33:PRO:HD2	2.08	0.54
69:SQ:64:ASP:OD1	69:SQ:66:ARG:NH1	2.40	0.54
73:SU:60:LEU:HD21	73:SU:81:MET:HE3	1.88	0.54
77:SY:108:ARG:HH11	77:SY:108:ARG:HG3	1.73	0.54
1:1:1537:U:O2	1:1:1561:G:N2	2.38	0.54
2:2:14:C:OP1	55:SC:172:SER:OG	2.26	0.54
2:2:1228:U:H5''	84:Sf:95:ARG:NH2	2.22	0.54
8:C:359:TYR:OH	8:C:365:ASP:OD2	2.22	0.54
17:LI:102:MET:O	17:LI:106:ALA:N	2.40	0.54
18:LJ:138:ARG:O	18:LJ:142:ARG:HG2	2.07	0.54
42:Lh:93:LEU:HD12	42:Lh:96:ARG:HE	1.71	0.54
60:SH:53:ARG:HD3	60:SH:54:GLU:H	1.73	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:SH:161:LYS:HE2	60:SH:163:ILE:HD11	1.90	0.54
62:SJ:134:VAL:HG22	62:SJ:154:ILE:HG22	1.88	0.54
72:ST:76:LEU:HD12	72:ST:80:HIS:CE1	2.42	0.54
84:Sf:121:CYS:SG	84:Sf:123:ASN:ND2	2.81	0.54
1:1:88:U:OP2	25:LQ:193:ARG:NH1	2.41	0.54
1:1:3121:G:O2'	1:1:3122:U:OP1	2.25	0.54
5:5:3:C:H2'	5:5:4:G:C8	2.43	0.54
8:C:486:SER:O	8:C:487:VAL:HG22	2.08	0.54
10:LB:258:PRO:HG2	10:LB:262:GLN:NE2	2.20	0.54
29:LU:78:LEU:HG	29:LU:79:SER:H	1.71	0.54
34:LZ:45:ILE:HD12	34:LZ:67:ILE:HG21	1.90	0.54
59:SG:132:ARG:HG3	59:SG:133:LEU:HD22	1.89	0.54
62:SJ:98:LYS:HE2	62:SJ:100:GLU:OE2	2.08	0.54
63:SK:36:ARG:HD3	63:SK:39:TYR:CE2	2.42	0.54
69:SQ:40:ALA:HB3	69:SQ:45:ARG:HG2	1.89	0.54
1:1:1064:C:O2'	1:1:1065:U:O5'	2.23	0.54
1:1:1229:G:N2	1:1:1247:C:O2'	2.41	0.54
2:2:740:C:HO2'	2:2:741:U:P	2.30	0.54
4:4:23:U:O3'	33:LY:16:LYS:NZ	2.39	0.54
65:SM:106:LEU:HA	65:SM:113:ARG:HH12	1.71	0.54
67:SO:25:LEU:HB2	67:SO:90:THR:HG21	1.89	0.54
1:1:1485:G:H2'	1:1:1486:A:H8	1.72	0.54
1:1:3109:U:OP2	10:LB:132:LYS:NZ	2.41	0.54
2:2:777:C:H2'	2:2:778:U:H2'	1.90	0.54
2:2:1398:G:H2'	2:2:1399:C:C6	2.42	0.54
4:4:75:G:OP2	33:LY:73:TYR:OH	2.26	0.54
5:5:68:C:H2'	5:5:69:G:C8	2.41	0.54
57:SE:32:SER:OG	57:SE:33:THR:N	2.41	0.54
57:SE:58:TYR:O	57:SE:61:THR:OG1	2.23	0.54
72:ST:81:GLY:HA3	72:ST:95:ASP:HA	1.88	0.54
1:1:563:U:H2'	1:1:564:A:H8	1.72	0.54
1:1:1766:G:H2'	1:1:1767:A:C8	2.43	0.54
1:1:1938:G:N2	1:1:2047:G:H22	2.06	0.54
1:1:2046:C:O2'	1:1:2047:G:OP1	2.25	0.54
1:1:3124:G:N1	1:1:3222:C:N3	2.33	0.54
1:1:3163:A:H4'	1:1:3164:G:O5'	2.08	0.54
2:2:1371:G:H2'	2:2:1372:G:C8	2.43	0.54
31:LW:9:SER:HA	31:LW:96:THR:HG23	1.90	0.54
59:SG:169:LYS:NZ	59:SG:170:LYS:HG2	2.23	0.54
60:SH:96:VAL:O	60:SH:97:LEU:HD23	2.08	0.54
60:SH:149:ARG:HG3	75:SW:53:VAL:HA	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1083:U:OP2	14:LF:202:LYS:NZ	2.42	0.53
1:1:1237:C:H1'	19:LK:135:THR:HB	1.90	0.53
1:1:2637:A:O2'	1:1:2638:A:O4'	2.23	0.53
2:2:54:C:H4'	77:SY:112:LYS:NZ	2.23	0.53
2:2:921:A:H2'	2:2:922:A:C8	2.43	0.53
2:2:1705:C:H2'	2:2:1706:U:C6	2.43	0.53
20:LL:76:THR:HG22	20:LL:101:ARG:HB3	1.89	0.53
55:SC:105:ARG:O	55:SC:106:PHE:HD1	1.90	0.53
61:SI:77:ARG:O	61:SI:104:ILE:HD12	2.08	0.53
69:SQ:137:ARG:HD3	69:SQ:137:ARG:N	2.23	0.53
76:SX:142:LYS:HG2	76:SX:143:PRO:HD2	1.90	0.53
1:1:425:G:H2'	1:1:426:A:H8	1.73	0.53
6:A:193:GLY:HA3	6:A:212:LYS:HB3	1.91	0.53
14:LF:96:LYS:HB3	14:LF:139:TRP:HD1	1.73	0.53
15:LG:44:GLN:OE1	15:LG:47:ARG:NH2	2.40	0.53
69:SQ:22:CYS:HB2	69:SQ:88:SER:HB3	1.90	0.53
1:1:2574:G:H2'	1:1:2575:C:H6	1.74	0.53
1:1:2960:C:O2'	10:LB:181:GLU:OE2	2.18	0.53
2:2:869:A:H2'	2:2:870:G:H8	1.73	0.53
5:5:43:G:H2'	5:5:44:A:C8	2.44	0.53
11:LC:34:ASP:OD1	11:LC:35:ILE:N	2.42	0.53
57:SE:201:HIS:ND1	57:SE:206:GLY:HA2	2.23	0.53
1:1:1067:A:H4'	12:LD:44:TYR:CE2	2.44	0.53
1:1:2137:G:OP2	9:LA:193:ARG:NH1	2.42	0.53
2:2:789:A:H2'	2:2:790:C:C6	2.43	0.53
5:5:27:U:O2'	5:5:28:C:H5'	2.08	0.53
6:A:43:TRP:HA	6:A:55:PRO:HA	1.91	0.53
9:LA:31:PRO:HD3	9:LA:123:ARG:HH12	1.73	0.53
10:LB:10:ARG:NH1	10:LB:11:HIS:O	2.42	0.53
29:LU:59:VAL:HG23	29:LU:60:ILE:HG23	1.90	0.53
48:Ln:12:ARG:HG2	48:Ln:15:ARG:NH2	2.23	0.53
54:SB:166:ARG:HG3	54:SB:167:LYS:HD3	1.90	0.53
62:SJ:155:ASP:OD1	62:SJ:156:PHE:N	2.34	0.53
1:1:1169:G:H2'	1:1:1170:C:C6	2.43	0.53
5:5:12:G:O6	5:5:24:A:N6	2.42	0.53
15:LG:100:TYR:HE2	15:LG:206:VAL:HG23	1.73	0.53
38:Ld:12:ARG:NH2	38:Ld:21:ARG:HH22	2.05	0.53
52:Ls:76:LEU:HA	52:Ls:79:PHE:HD2	1.73	0.53
58:SF:49:ILE:HB	58:SF:76:ILE:HD11	1.90	0.53
79:Sa:43:ASN:ND2	79:Sa:66:LYS:HB3	2.24	0.53
84:Sf:83:LYS:HE2	84:Sf:85:TYR:HB2	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:3:G:OP2	32:LX:35:LYS:N	2.42	0.53
1:1:1745:U:H5	26:LR:43:LYS:HE2	1.73	0.53
1:1:2637:A:H2'	1:1:2638:A:C8	2.44	0.53
1:1:2856:A:H5''	47:Lm:125:LYS:HG3	1.90	0.53
2:2:402:C:O2'	59:SG:92:ARG:O	2.27	0.53
2:2:493:G:H2'	2:2:494:G:H8	1.73	0.53
8:C:18:ASN:ND2	8:C:99:ASP:O	2.41	0.53
11:LC:319:PRO:O	11:LC:320:LEU:HG	2.08	0.53
21:LM:91:ASP:OD1	21:LM:92:ALA:N	2.40	0.53
56:SD:117:ALA:HB3	56:SD:120:ARG:HD3	1.89	0.53
57:SE:212:ASP:OD1	57:SE:213:ALA:N	2.38	0.53
72:ST:57:ARG:CZ	72:ST:104:ILE:HD12	2.38	0.53
1:1:1333:A:H2'	1:1:1335:A:H5''	1.91	0.53
2:2:390:C:OP2	61:SI:2:GLY:N	2.42	0.53
2:2:1391:G:C6	2:2:1401:G:C2	2.96	0.53
2:2:1497:C:H5	72:ST:102:ARG:HH12	1.56	0.53
2:2:1580:G:N2	2:2:1607:A:OP2	2.29	0.53
18:LJ:17:LYS:NZ	18:LJ:131:CYS:SG	2.74	0.53
18:LJ:134:ARG:HG3	18:LJ:155:ILE:HD11	1.90	0.53
25:LQ:68:THR:HG22	25:LQ:69:GLU:H	1.73	0.53
29:LU:61:LYS:HB2	29:LU:73:ILE:HB	1.90	0.53
54:SB:144:LYS:HB2	54:SB:208:GLN:HB3	1.89	0.53
61:SI:77:ARG:HH21	61:SI:79:ILE:HA	1.73	0.53
66:SN:62:GLN:HG2	66:SN:65:VAL:HG12	1.91	0.53
75:SW:28:ARG:HB3	75:SW:29:PRO:HD3	1.90	0.53
1:1:1202:C:N3	1:1:1270:A:C6	2.76	0.53
1:1:2552:A:H4'	1:1:2553:C:O5'	2.08	0.53
2:2:916:U:H2'	2:2:917:A:C8	2.41	0.53
2:2:1201:A:O2'	82:Sd:10:ARG:NH1	2.25	0.53
4:4:103:G:OP2	4:4:105:A:O2'	2.27	0.53
5:5:5:A:H2'	5:5:6:U:C6	2.44	0.53
8:C:296:ASP:OD1	8:C:297:GLU:N	2.42	0.53
16:LH:128:ARG:HD2	16:LH:182:GLU:HG3	1.91	0.53
18:LJ:110:HIS:N	18:LJ:124:TYR:O	2.41	0.53
33:LY:30:MET:HE2	33:LY:77:TYR:HA	1.90	0.53
56:SD:144:LYS:HZ3	56:SD:182:GLN:HE22	1.55	0.53
58:SF:30:PHE:O	58:SF:32:ARG:N	2.42	0.53
63:SK:44:LEU:HD12	63:SK:45:GLN:N	2.24	0.53
1:1:1368:C:O3'	51:Lq:30:ARG:NH1	2.41	0.53
1:1:2221:U:C2	1:1:2222:A:C8	2.97	0.53
2:2:746:C:H4'	75:SW:80:ASN:HD21	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:1348:C:H4'	69:SQ:21:ARG:NH1	2.24	0.53
2:2:1546:A:H2'	2:2:1547:U:C6	2.43	0.53
2:2:1588:A:H2'	2:2:1589:A:H8	1.73	0.53
3:3:48:C:P	12:LD:94:ASN:HD21	2.31	0.53
5:5:13:U:O2'	5:5:14:A:H5'	2.09	0.53
5:5:23:C:H2'	5:5:24:A:C8	2.44	0.53
7:B:105:HIS:CG	7:B:106:PRO:HD3	2.43	0.53
8:C:260:THR:HG22	8:C:261:LYS:H	1.74	0.53
14:LF:29:ARG:HE	14:LF:32:ARG:NH2	2.07	0.53
16:LH:14:GLU:HA	21:LM:2:ALA:HB2	1.91	0.53
17:LI:53:VAL:HG21	17:LI:166:ILE:HD12	1.91	0.53
75:SW:113:HIS:ND1	75:SW:114:GLU:HG2	2.24	0.53
1:1:410:A:H2'	1:1:411:A:C8	2.44	0.53
1:1:1152:A:H4'	14:LF:224:LYS:HE2	1.92	0.53
1:1:1164:U:H5	23:LO:23:ILE:HD11	1.73	0.53
1:1:1212:G:H4'	52:Ls:32:ASN:OD1	2.09	0.53
19:LK:124:ASP:OD2	52:Ls:46:ARG:NH2	2.42	0.53
27:LS:162:LYS:HE2	40:Lf:80:SER:HA	1.91	0.53
50:Lp:38:THR:HA	50:Lp:45:ASN:HA	1.91	0.53
58:SF:38:ILE:HG13	58:SF:39:GLU:H	1.74	0.53
62:SJ:125:VAL:O	62:SJ:129:GLN:HG3	2.08	0.53
66:SN:139:TRP:CH2	66:SN:141:TYR:HB2	2.44	0.53
1:1:289:A:N3	1:1:292:G:O2'	2.42	0.52
1:1:703:A:H3'	35:La:115:LYS:HG3	1.89	0.52
1:1:1596:U:H2'	1:1:1597:G:H8	1.73	0.52
1:1:1676:A:H2'	1:1:1677:A:C8	2.44	0.52
2:2:1703:C:H2'	2:2:1704:A:C8	2.45	0.52
5:5:65:U:H2'	5:5:66:A:H8	1.73	0.52
8:C:649:VAL:HG21	8:C:687:ARG:HE	1.74	0.52
35:La:149:ALA:HB2	43:Li:16:LEU:HA	1.90	0.52
57:SE:72:VAL:HG23	57:SE:90:ILE:HG22	1.91	0.52
84:Sf:108:VAL:HG23	84:Sf:114:ILE:HG13	1.90	0.52
1:1:400:A:C2	4:4:17:A:H1'	2.44	0.52
1:1:2117:U:H2'	1:1:2118:G:H8	1.74	0.52
2:2:643:U:H3	2:2:683:G:H1	1.57	0.52
8:C:676:GLY:H	8:C:681:GLU:N	2.08	0.52
8:C:832:LYS:HG3	8:C:833:VAL:H	1.74	0.52
73:SU:96:ILE:O	73:SU:99:GLN:HG3	2.09	0.52
1:1:2058:A:H2'	1:1:2059:A:H8	1.74	0.52
1:1:2740:U:H2'	1:1:2741:U:C6	2.44	0.52
1:1:3299:U:H2'	1:1:3300:A:H8	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:1157:A:H2'	2:2:1158:C:C6	2.45	0.52
15:LG:74:VAL:HB	15:LG:237:GLY:HA3	1.90	0.52
69:SQ:122:ARG:C	69:SQ:123:ARG:HD2	2.34	0.52
69:SQ:127:LYS:HZ3	69:SQ:132:ARG:HB2	1.74	0.52
72:ST:24:LYS:HD2	72:ST:25:ARG:HH21	1.74	0.52
73:SU:25:SER:HB2	73:SU:31:LEU:HD12	1.91	0.52
1:1:1744:C:H3'	1:1:1745:U:H5''	1.91	0.52
1:1:2407:C:H2'	1:1:2408:A:H8	1.74	0.52
2:2:597:U:H2'	2:2:598:A:H8	1.74	0.52
2:2:1064:C:OP1	54:SB:149:GLN:NE2	2.43	0.52
2:2:1746:A:H2'	2:2:1747:G:C8	2.44	0.52
5:5:50:G:H2'	5:5:51:G:C8	2.45	0.52
8:C:28:VAL:O	8:C:32:LYS:NZ	2.43	0.52
12:LD:34:LYS:O	12:LD:38:THR:HG23	2.08	0.52
59:SG:64:LYS:HZ1	59:SG:82:SER:H	1.58	0.52
60:SH:104:ILE:HD11	60:SH:131:VAL:HG21	1.90	0.52
60:SH:183:TYR:CE2	60:SH:189:ARG:HB2	2.45	0.52
65:SM:83:GLU:HG3	65:SM:84:HIS:ND1	2.25	0.52
74:SV:32:CYS:SG	74:SV:60:ARG:NH1	2.82	0.52
1:1:652:A:H2'	1:1:653:A:C8	2.44	0.52
1:1:1338:A:OP1	51:Lq:14:ARG:NH2	2.43	0.52
2:2:1709:G:H2'	2:2:1710:G:C8	2.45	0.52
4:4:9:A:H2'	4:4:10:A:C8	2.45	0.52
6:A:81:ALA:HB1	6:A:108:VAL:HG23	1.91	0.52
6:A:275:GLN:NE2	6:A:278:GLY:O	2.42	0.52
16:LH:60:ARG:HE	16:LH:76:SER:HA	1.73	0.52
17:LI:36:LEU:HD13	17:LI:73:ASN:ND2	2.25	0.52
18:LJ:151:ALA:O	18:LJ:154:ARG:HG2	2.09	0.52
24:LP:126:ARG:HG3	24:LP:126:ARG:HH11	1.75	0.52
56:SD:70:ARG:O	56:SD:73:THR:OG1	2.15	0.52
59:SG:138:ALA:HA	59:SG:178:ILE:HD11	1.92	0.52
2:2:508:A:H3'	62:SJ:171:ARG:NH2	2.25	0.52
2:2:1342:A:OP2	73:SU:50:LYS:NZ	2.43	0.52
6:A:290:ALA:HB3	6:A:299:PHE:HB2	1.92	0.52
58:SF:16:LEU:HG	58:SF:17:PRO:HD2	1.92	0.52
59:SG:132:ARG:HG3	59:SG:133:LEU:CD2	2.40	0.52
2:2:809:A:C4	2:2:856:G:H1'	2.45	0.52
2:2:815:A:H2'	2:2:816:C:C6	2.45	0.52
2:2:1205:A:O2'	2:2:1267:G:OP2	2.21	0.52
2:2:1582:A:OP1	69:SQ:132:ARG:N	2.40	0.52
2:2:1790:A:H1'	79:Sa:79:ILE:HD11	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:LJ:132:MET:O	18:LJ:133:THR:HG23	2.10	0.52
62:SJ:94:VAL:HA	62:SJ:97:LEU:HD13	1.92	0.52
67:SO:28:GLY:O	67:SO:93:HIS:N	2.32	0.52
76:SX:89:ASN:HB3	76:SX:92:CYS:SG	2.49	0.52
1:1:308:C:OP1	20:LL:102:LYS:NZ	2.37	0.52
1:1:669:U:O2	1:1:684:C:N4	2.35	0.52
2:2:1429:G:H2'	2:2:1430:U:C6	2.45	0.52
2:2:1533:C:O2'	2:2:1536:G:O6	2.25	0.52
10:LB:17:LEU:HB3	10:LB:18:PRO:HD3	1.91	0.52
17:LI:36:LEU:HD11	17:LI:69:ARG:HD3	1.91	0.52
23:LO:55:TYR:CE1	23:LO:147:VAL:HG21	2.45	0.52
70:SR:112:LEU:O	70:SR:116:GLY:N	2.38	0.52
1:1:76:G:H5'	20:LL:58:VAL:HG13	1.92	0.52
1:1:323:G:C2	1:1:324:G:C8	2.98	0.52
1:1:328:G:OP2	33:LY:13:LYS:NZ	2.29	0.52
1:1:1887:C:O2	10:LB:241:ARG:NH2	2.43	0.52
1:1:3298:U:O2'	1:1:3299:U:OP1	2.25	0.52
2:2:709:G:N2	2:2:722:U:O2	2.37	0.52
2:2:731:G:H8	2:2:731:G:OP2	1.92	0.52
2:2:1763:G:OP1	2:2:1766:C:H4'	2.10	0.52
2:2:1790:A:N3	79:Sa:79:ILE:HD11	2.25	0.52
8:C:417:GLY:HA3	8:C:420:TYR:HD2	1.75	0.52
19:LK:67:ARG:HG3	19:LK:68:GLN:OE1	2.10	0.52
22:LN:91:GLN:O	22:LN:93:LYS:NZ	2.38	0.52
24:LP:24:VAL:HG12	24:LP:86:LYS:HE2	1.91	0.52
54:SB:103:LEU:HD23	54:SB:104:ASP:N	2.25	0.52
60:SH:86:GLU:HA	60:SH:89:LYS:HE3	1.90	0.52
69:SQ:47:LYS:HA	69:SQ:50:GLU:HG2	1.92	0.52
71:SS:88:ARG:NH1	71:SS:89:GLN:O	2.43	0.52
71:SS:92:ILE:HG12	71:SS:93:VAL:H	1.75	0.52
72:ST:119:GLU:HG3	72:ST:120:ARG:H	1.75	0.52
80:Sb:5:VAL:HG12	80:Sb:6:ASP:N	2.24	0.52
1:1:1222:C:H2'	1:1:1223:A:O4'	2.10	0.52
1:1:2885:A:H2'	1:1:2886:C:C6	2.45	0.52
2:2:761:A:OP1	62:SJ:77:ARG:NH2	2.40	0.52
2:2:845:A:H2'	2:2:846:C:C6	2.45	0.52
2:2:913:A:N6	67:SO:54:ARG:HH22	2.06	0.52
14:LF:98:ILE:HD12	25:LQ:33:ASP:HB2	1.92	0.52
19:LK:57:ARG:HD3	19:LK:58:VAL:HG23	1.91	0.52
66:SN:46:THR:O	66:SN:50:ILE:HG23	2.10	0.52
77:SY:21:LEU:HD22	77:SY:23:ARG:CZ	2.40	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:586:G:H2'	1:1:587:C:C6	2.46	0.51
1:1:604:G:H2'	1:1:605:G:H8	1.76	0.51
1:1:702:G:C4	35:La:113:LEU:HD21	2.44	0.51
2:2:650:C:N3	2:2:675:G:N1	2.53	0.51
2:2:1378:U:H2'	73:SU:54:ARG:HH12	1.75	0.51
2:2:1533:C:N4	2:2:1568:G:H22	2.08	0.51
2:2:1740:A:H2'	2:2:1741:G:C8	2.44	0.51
5:5:46:A:O2'	5:5:47:C:O4'	2.28	0.51
34:LZ:91:LEU:O	34:LZ:91:LEU:HD12	2.10	0.51
57:SE:42:MET:HB2	57:SE:109:PHE:CE2	2.45	0.51
58:SF:108:ILE:HD11	58:SF:116:PRO:HB3	1.91	0.51
73:SU:71:GLU:OE1	73:SU:71:GLU:N	2.38	0.51
1:1:1241:U:H4'	52:Ls:42:ARG:HH22	1.76	0.51
1:1:1267:C:O2'	1:1:1268:G:OP1	2.27	0.51
1:1:2069:A:H2'	1:1:2070:A:H8	1.75	0.51
2:2:626:U:OP2	2:2:967:C:N4	2.43	0.51
2:2:1410:U:H5''	70:SR:3:ARG:HH21	1.74	0.51
19:LK:22:VAL:HG21	19:LK:47:ALA:HB1	1.92	0.51
19:LK:132:ILE:HG13	19:LK:133:LEU:N	2.24	0.51
41:Lg:46:GLY:N	41:Lg:80:SER:O	2.40	0.51
60:SH:51:SER:O	60:SH:67:PHE:N	2.40	0.51
71:SS:23:ASP:OD1	71:SS:24:GLY:N	2.44	0.51
1:1:1707:G:OP1	50:Lp:44:LYS:NZ	2.40	0.51
1:1:2336:A:N3	1:1:2783:G:O2'	2.40	0.51
1:1:2686:A:OP2	1:1:2687:G:N2	2.42	0.51
2:2:480:A:N1	2:2:503:A:N6	2.57	0.51
2:2:1663:A:H2'	2:2:1664:G:C8	2.45	0.51
6:A:83:TRP:HA	6:A:107:ASP:HB2	1.93	0.51
8:C:133:THR:OG1	8:C:160:ASN:O	2.27	0.51
9:LA:42:ARG:HD2	9:LA:87:PHE:CD1	2.46	0.51
31:LW:10:GLY:HA3	31:LW:97:VAL:HG11	1.92	0.51
35:La:75:ILE:HB	35:La:114:GLY:HA2	1.91	0.51
58:SF:84:LEU:O	58:SF:167:ARG:NH1	2.42	0.51
59:SG:175:ALA:HB3	59:SG:177:ARG:NH2	2.22	0.51
64:SL:8:GLN:NE2	64:SL:14:LEU:O	2.39	0.51
81:Sc:19:ARG:NH1	81:Sc:24:GLY:O	2.44	0.51
1:1:1000:G:N2	1:1:1017:U:O2	2.27	0.51
1:1:2794:C:H2'	1:1:2795:C:O2	2.10	0.51
2:2:822:G:O2'	2:2:823:U:H5'	2.10	0.51
2:2:1064:C:P	54:SB:149:GLN:HE22	2.34	0.51
2:2:1575:C:H2'	2:2:1576:C:C6	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:SC:66:LEU:O	74:SV:15:ARG:NH1	2.44	0.51
55:SC:105:ARG:C	55:SC:106:PHE:HD1	2.18	0.51
56:SD:129:ILE:HG21	56:SD:191:ILE:HD12	1.92	0.51
56:SD:216:PRO:HD3	70:SR:19:LYS:HD3	1.91	0.51
61:SI:134:GLU:HG3	61:SI:135:GLU:N	2.25	0.51
81:Sc:12:LYS:O	81:Sc:32:GLU:N	2.39	0.51
1:1:2064:C:O2'	1:1:2065:U:OP1	2.28	0.51
1:1:2065:U:O5'	26:LR:76:ARG:NH2	2.44	0.51
2:2:857:A:C6	66:SN:73:ARG:HD2	2.46	0.51
2:2:1348:C:H4'	69:SQ:21:ARG:HH12	1.76	0.51
4:4:8:C:H2'	4:4:9:A:C8	2.40	0.51
5:5:50:G:H2'	5:5:51:G:H8	1.74	0.51
6:A:168:CYS:SG	6:A:198:VAL:HB	2.50	0.51
19:LK:91:ASP:OD1	19:LK:92:ARG:N	2.42	0.51
22:LN:14:LYS:HA	22:LN:19:VAL:HG11	1.91	0.51
65:SM:55:ASP:O	65:SM:57:ARG:NH1	2.44	0.51
67:SO:112:GLN:HE22	79:Sa:45:VAL:HA	1.76	0.51
70:SR:103:ASP:OD1	70:SR:123:ASN:ND2	2.43	0.51
1:1:446:A:O2'	1:1:447:U:H6	1.94	0.51
1:1:1731:G:O6	45:Lk:37:LYS:NZ	2.32	0.51
1:1:1778:A:H2'	1:1:1779:A:C8	2.46	0.51
1:1:2058:A:H2'	1:1:2059:A:C8	2.46	0.51
1:1:2320:A:H2'	1:1:2321:A:H8	1.76	0.51
1:1:2496:G:H2'	1:1:2497:G:H8	1.75	0.51
1:1:3079:U:H1'	1:1:3080:A:H5''	1.93	0.51
2:2:612:G:H8	2:2:612:G:OP1	1.92	0.51
2:2:1052:U:H2'	2:2:1053:U:C6	2.45	0.51
2:2:1233:A:H1'	84:Sf:138:ARG:CZ	2.40	0.51
8:C:639:GLY:HA3	8:C:644:GLY:HA3	1.92	0.51
14:LF:67:GLU:OE2	14:LF:70:ARG:NH2	2.34	0.51
19:LK:58:VAL:HG12	19:LK:60:VAL:HG23	1.93	0.51
22:LN:67:ARG:NH1	22:LN:127:TYR:OH	2.44	0.51
31:LW:2:ARG:NH1	31:LW:3:THR:O	2.43	0.51
57:SE:129:VAL:HG22	57:SE:139:LEU:HB3	1.92	0.51
58:SF:164:THR:HA	58:SF:167:ARG:HD3	1.91	0.51
64:SL:134:ARG:HG2	64:SL:135:PRO:HD2	1.91	0.51
64:SL:137:SER:OG	64:SL:138:LYS:N	2.43	0.51
69:SQ:13:LYS:HG3	69:SQ:14:LYS:H	1.75	0.51
84:Sf:123:ASN:HD21	84:Sf:130:VAL:HG21	1.74	0.51
1:1:474:C:H2'	1:1:475:G:H8	1.76	0.51
1:1:985:A:H1'	12:LD:15:ARG:HH12	1.76	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1264:U:H2'	1:1:1265:G:H8	1.75	0.51
1:1:1779:A:H2'	1:1:1780:A:C8	2.44	0.51
1:1:2110:A:OP2	9:LA:200:ARG:NH1	2.44	0.51
1:1:2488:G:O6	15:LG:44:GLN:NE2	2.44	0.51
1:1:2497:G:H2'	1:1:2498:A:H8	1.76	0.51
1:1:3131:U:O2'	1:1:3132:A:OP1	2.23	0.51
2:2:893:G:O4'	67:SO:49:ARG:HG2	2.11	0.51
2:2:1425:G:H2'	2:2:1426:U:C6	2.45	0.51
2:2:1646:U:H2'	2:2:1647:A:C8	2.46	0.51
4:4:71:A:OP2	33:LY:50:ARG:NH1	2.44	0.51
5:5:63:C:H2'	5:5:64:G:H8	1.76	0.51
8:C:111:VAL:HG22	8:C:140:GLN:OE1	2.10	0.51
8:C:672:ALA:HB3	8:C:715:LEU:HD23	1.91	0.51
16:LH:104:ALA:O	16:LH:107:THR:OG1	2.29	0.51
38:Ld:12:ARG:CZ	38:Ld:21:ARG:HH22	2.22	0.51
44:Lj:14:LYS:NZ	46:Ll:51:LEU:HD21	2.25	0.51
55:SC:234:THR:HB	55:SC:235:PRO:HD2	1.91	0.51
69:SQ:50:GLU:HG3	69:SQ:82:ARG:HH21	1.76	0.51
79:Sa:101:VAL:HG22	79:Sa:104:ASN:H	1.75	0.51
1:1:171:G:H2'	1:1:172:G:H8	1.75	0.51
1:1:644:A:H2'	1:1:645:A:C8	2.45	0.51
1:1:1177:G:H2'	1:1:1178:A:C8	2.46	0.51
1:1:1198:A:H2'	1:1:1199:C:C6	2.46	0.51
1:1:2532:C:O2	34:LZ:60:ARG:NH2	2.44	0.51
1:1:3009:U:H2'	1:1:3010:G:H8	1.75	0.51
2:2:643:U:H2'	2:2:644:A:H8	1.76	0.51
2:2:1403:U:H2'	2:2:1404:G:H8	1.76	0.51
8:C:717:ALA:O	8:C:721:LEU:HG	2.11	0.51
13:LE:8:LYS:NZ	13:LE:18:PRO:O	2.44	0.51
16:LH:98:SER:OG	16:LH:99:ARG:N	2.44	0.51
20:LL:115:ARG:NH2	20:LL:155:PHE:O	2.33	0.51
48:Ln:2:ARG:HG3	48:Ln:5:TRP:HD1	1.76	0.51
60:SH:22:LEU:HD12	60:SH:23:GLU:N	2.26	0.51
1:1:470:A:O2'	1:1:471:C:OP2	2.26	0.51
1:1:542:G:H2'	1:1:543:U:C6	2.46	0.51
1:1:656:U:H2'	1:1:657:U:C6	2.46	0.51
1:1:2409:U:H2'	1:1:2410:A:H8	1.76	0.51
1:1:2496:G:H2'	1:1:2497:G:C8	2.46	0.51
1:1:2577:G:O2'	1:1:2824:U:OP1	2.22	0.51
2:2:914:U:H2'	2:2:915:U:C6	2.46	0.51
5:5:70:G:H2'	5:5:71:A:C8	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:171:ASP:C	6:A:172:LYS:HD2	2.35	0.51
8:C:450:LEU:HD22	8:C:456:VAL:HG12	1.92	0.51
10:LB:340:ARG:HH12	10:LB:343:LEU:HD11	1.76	0.51
14:LF:226:LYS:O	14:LF:234:LEU:HG	2.11	0.51
29:LU:100:LEU:HD23	29:LU:112:LEU:HD12	1.92	0.51
32:LX:149:ALA:O	32:LX:154:GLY:N	2.44	0.51
40:Lf:51:VAL:HG12	40:Lf:102:ILE:HG12	1.91	0.51
54:SB:87:ARG:NH1	54:SB:89:ASP:OD1	2.44	0.51
59:SG:64:LYS:NZ	59:SG:82:SER:H	2.08	0.51
63:SK:32:GLU:HG2	63:SK:33:ILE:N	2.20	0.51
73:SU:20:ARG:HA	73:SU:89:ASP:HA	1.93	0.51
84:Sf:122:PRO:HG2	84:Sf:146:LEU:HD13	1.92	0.51
1:1:2625:C:H2'	1:1:2626:A:C8	2.46	0.51
2:2:737:G:H2'	2:2:738:G:H8	1.75	0.51
16:LH:150:GLU:HG3	16:LH:164:LYS:HE3	1.93	0.51
29:LU:82:TYR:CE2	29:LU:86:LEU:HD11	2.46	0.51
40:Lf:61:VAL:HG23	40:Lf:62:ARG:H	1.76	0.51
52:Ls:95:GLU:HG2	52:Ls:96:VAL:HG23	1.93	0.51
63:SK:10:ALA:HA	63:SK:13:GLU:OE2	2.11	0.51
76:SX:117:ILE:H	76:SX:117:ILE:HD12	1.76	0.51
81:Sc:33:PHE:O	81:Sc:34:MET:HG3	2.11	0.51
1:1:137:C:H2'	1:1:138:C:C6	2.46	0.50
2:2:107:A:H2'	2:2:108:G:C8	2.46	0.50
2:2:921:A:H2'	2:2:922:A:H8	1.76	0.50
7:B:118:GLN:HE22	56:SD:146:ARG:CD	2.24	0.50
11:LC:53:VAL:HG11	11:LC:100:MET:HE1	1.92	0.50
19:LK:57:ARG:CD	19:LK:58:VAL:HG23	2.40	0.50
24:LP:14:SER:HB2	24:LP:150:LEU:O	2.12	0.50
30:LV:89:ARG:HH12	30:LV:95:LEU:HD11	1.75	0.50
46:Ll:28:ARG:HD2	46:Ll:36:ARG:NH2	2.26	0.50
56:SD:209:ASP:OD1	56:SD:210:VAL:N	2.44	0.50
58:SF:28:LYS:NZ	69:SQ:54:ILE:HA	2.26	0.50
58:SF:60:SER:OG	58:SF:78:GLU:OE2	2.22	0.50
78:SZ:29:VAL:HG23	78:SZ:30:ILE:HG13	1.93	0.50
1:1:435:G:OP1	51:Lq:126:LYS:NZ	2.44	0.50
1:1:1003:G:O6	1:1:1015:C:N4	2.44	0.50
1:1:2919:C:H2'	1:1:2920:G:H8	1.76	0.50
2:2:644:A:O2'	2:2:645:G:OP1	2.28	0.50
2:2:695:C:N3	2:2:737:G:N1	2.42	0.50
2:2:1645:C:H2'	2:2:1646:U:C6	2.47	0.50
4:4:63:G:O2'	42:Lh:54:LYS:NZ	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:B:62:GLU:HB2	71:SS:120:ARG:HH11	1.76	0.50
8:C:571:SER:O	8:C:572:LYS:HB3	2.10	0.50
9:LA:54:ARG:NH1	9:LA:58:LEU:HD21	2.25	0.50
15:LG:242:GLY:O	15:LG:246:GLN:HG2	2.11	0.50
19:LK:21:GLU:O	19:LK:23:GLY:N	2.42	0.50
28:LT:39:ILE:O	28:LT:99:SER:OG	2.25	0.50
30:LV:110:GLU:OE1	30:LV:110:GLU:N	2.44	0.50
54:SB:104:ASP:OD1	54:SB:105:PHE:N	2.45	0.50
55:SC:160:HIS:ND1	55:SC:203:ASP:OD2	2.44	0.50
55:SC:178:ILE:CG1	55:SC:205:TYR:HB2	2.41	0.50
61:SI:79:ILE:HD13	61:SI:168:ARG:NH1	2.26	0.50
63:SK:28:GLU:H	63:SK:38:LEU:HD21	1.76	0.50
68:SP:131:TYR:OH	71:SS:126:ARG:NH1	2.43	0.50
80:Sb:55:ILE:HA	80:Sb:63:LEU:HD13	1.91	0.50
1:1:1022:C:H2'	1:1:1023:A:C8	2.46	0.50
1:1:1907:G:C8	50:Lp:16:THR:HG22	2.46	0.50
1:1:2043:C:H2'	1:1:2044:G:C8	2.46	0.50
1:1:3231:G:H2'	1:1:3232:A:H8	1.76	0.50
2:2:248:A:N3	57:SE:131:LEU:HD21	2.25	0.50
2:2:1206:C:H42	2:2:1451:G:H22	1.58	0.50
2:2:1380:G:O2'	73:SU:32:GLU:OE2	2.18	0.50
2:2:1529:C:N4	2:2:1530:G:O6	2.43	0.50
2:2:1589:A:H2'	2:2:1590:G:H8	1.76	0.50
2:2:1700:G:H2'	2:2:1701:A:H8	1.76	0.50
2:2:1755:C:H2'	2:2:1756:G:H8	1.76	0.50
26:LR:8:LYS:HG3	26:LR:22:VAL:HG21	1.94	0.50
55:SC:160:HIS:CG	55:SC:182:ARG:HE	2.30	0.50
56:SD:10:LYS:HA	56:SD:13:LYS:HE2	1.92	0.50
75:SW:45:GLY:O	75:SW:68:ARG:NH2	2.45	0.50
1:1:2055:A:H2'	1:1:2055:A:N3	2.27	0.50
2:2:897:G:N7	54:SB:7:LYS:HE2	2.26	0.50
2:2:1687:A:H2'	2:2:1688:G:C8	2.46	0.50
10:LB:71:GLU:OE1	10:LB:71:GLU:N	2.45	0.50
15:LG:27:ASN:OD1	15:LG:29:LEU:HD23	2.11	0.50
15:LG:164:GLU:OE2	22:LN:26:ARG:NH1	2.28	0.50
17:LI:110:ARG:O	17:LI:111:LEU:HD23	2.11	0.50
19:LK:114:ARG:HH12	19:LK:129:VAL:HG13	1.75	0.50
53:SA:13:THR:OG1	53:SA:16:ASP:OD2	2.30	0.50
61:SI:37:ARG:HH12	61:SI:93:THR:HG23	1.76	0.50
64:SL:30:THR:HG23	64:SL:31:ARG:HG3	1.93	0.50
69:SQ:26:LYS:HA	69:SQ:62:ASP:HA	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:511:U:C4	11:LC:351:PRO:HB3	2.46	0.50
2:2:71:A:OP2	59:SG:165:LYS:NZ	2.45	0.50
2:2:1056:U:OP2	2:2:1056:U:H4'	2.12	0.50
2:2:1176:G:H2'	2:2:1177:C:H6	1.75	0.50
6:A:133:ASN:ND2	6:A:137:ASP:OD1	2.41	0.50
6:A:188:HIS:HB2	6:A:219:TRP:CZ3	2.46	0.50
7:B:124:GLY:HA3	56:SD:119:ARG:HD2	1.92	0.50
8:C:565:TYR:OH	8:C:777:MET:SD	2.70	0.50
11:LC:151:LEU:HD12	11:LC:256:VAL:HG12	1.92	0.50
31:LW:141:ARG:HB2	31:LW:142:PRO:CD	2.42	0.50
54:SB:163:ALA:O	54:SB:166:ARG:HG2	2.11	0.50
59:SG:98:ARG:NH2	59:SG:105:ASP:OD2	2.44	0.50
60:SH:200:ILE:H	60:SH:200:ILE:HD12	1.77	0.50
71:SS:114:GLU:HA	71:SS:117:LYS:HB3	1.93	0.50
1:1:357:G:OP2	44:Lj:52:LYS:NZ	2.42	0.50
1:1:1016:U:H2'	1:1:1017:U:H6	1.74	0.50
1:1:1439:A:N7	38:Ld:37:LYS:NZ	2.53	0.50
1:1:2148:G:O2'	1:1:2277:U:OP2	2.29	0.50
1:1:2731:C:H4'	1:1:2732:C:H5'	1.93	0.50
2:2:1008:C:H2'	2:2:1009:G:O4'	2.12	0.50
10:LB:284:TYR:CE1	10:LB:355:VAL:HG21	2.47	0.50
14:LF:220:PHE:O	14:LF:221:ARG:HG3	2.12	0.50
22:LN:98:LEU:HD12	22:LN:128:LYS:HD3	1.93	0.50
25:LQ:192:VAL:HG12	25:LQ:194:SER:H	1.76	0.50
58:SF:58:PRO:HB3	58:SF:78:GLU:HA	1.93	0.50
64:SL:38:ARG:HH21	64:SL:56:GLY:C	2.19	0.50
79:Sa:41:ILE:HG12	79:Sa:68:TYR:CD2	2.46	0.50
1:1:766:G:C8	25:LQ:93:SER:HB3	2.46	0.50
1:1:1117:G:O2'	1:1:2601:A:N3	2.39	0.50
1:1:2656:A:H2'	1:1:2657:G:H8	1.76	0.50
55:SC:86:ASP:HB3	55:SC:112:ILE:HG22	1.92	0.50
55:SC:238:TRP:CG	75:SW:68:ARG:HD2	2.47	0.50
57:SE:143:ASP:OD1	57:SE:143:ASP:N	2.44	0.50
59:SG:187:LEU:HA	59:SG:190:LYS:HE2	1.93	0.50
62:SJ:57:LEU:HD12	62:SJ:67:ARG:HA	1.94	0.50
69:SQ:30:LYS:HB2	69:SQ:35:PRO:HA	1.94	0.50
70:SR:45:ARG:O	70:SR:49:LYS:HG3	2.12	0.50
72:ST:122:GLY:C	72:ST:123:ARG:HD2	2.37	0.50
75:SW:23:ARG:HH22	80:Sb:4:ALA:HB1	1.76	0.50
80:Sb:36:LYS:N	80:Sb:78:SER:OG	2.45	0.50
1:1:307:U:H2'	1:1:308:C:C6	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2044:G:H4'	1:1:2045:G:OP1	2.11	0.50
1:1:2974:A:H2'	1:1:2975:G:C8	2.47	0.50
2:2:574:G:H2'	7:B:112:ARG:HA	1.94	0.50
2:2:1104:U:O2'	2:2:1105:G:H5'	2.12	0.50
2:2:1354:U:H2'	2:2:1355:G:C8	2.46	0.50
30:LV:106:ASN:OD1	30:LV:107:PRO:HD2	2.11	0.50
54:SB:179:CYS:HA	54:SB:183:GLN:NE2	2.27	0.50
59:SG:211:TYR:CE1	59:SG:215:LEU:HD12	2.47	0.50
70:SR:27:ASP:O	70:SR:31:ASN:ND2	2.45	0.50
77:SY:42:GLU:O	77:SY:45:GLU:HG3	2.12	0.50
1:1:1545:G:H2'	1:1:1546:G:H8	1.76	0.50
1:1:1778:A:H2'	1:1:1779:A:H8	1.77	0.50
1:1:2221:U:H2'	1:1:2222:A:C8	2.47	0.50
1:1:2882:U:H2'	1:1:2883:U:C6	2.47	0.50
2:2:294:U:H5''	57:SE:37:LYS:HD2	1.94	0.50
5:5:64:G:H2'	5:5:65:U:C6	2.47	0.50
5:5:69:G:HO2'	5:5:70:G:H8	1.60	0.50
8:C:380:LEU:O	8:C:472:THR:HA	2.12	0.50
8:C:765:THR:HG22	8:C:766:PRO:HD2	1.93	0.50
8:C:808:GLY:O	8:C:816:THR:OG1	2.24	0.50
27:LS:109:ASP:OD2	27:LS:113:ARG:NH1	2.45	0.50
29:LU:47:ILE:HD12	29:LU:82:TYR:HE2	1.77	0.50
38:Ld:75:ILE:H	38:Ld:75:ILE:HD12	1.77	0.50
54:SB:205:TYR:HD2	54:SB:207:LEU:HD22	1.77	0.50
57:SE:42:MET:N	57:SE:84:ALA:O	2.45	0.50
57:SE:180:LEU:HD12	57:SE:193:GLY:O	2.12	0.50
59:SG:41:LEU:HD22	59:SG:45:TRP:CD2	2.47	0.50
59:SG:78:SER:OG	59:SG:79:GLU:N	2.44	0.50
60:SH:64:ILE:N	60:SH:95:HIS:O	2.37	0.50
61:SI:157:ASP:O	61:SI:161:GLU:HG3	2.12	0.50
77:SY:51:TYR:O	77:SY:52:LYS:HD3	2.12	0.50
1:1:552:C:OP2	21:LM:77:ARG:NH1	2.45	0.49
1:1:604:G:H2'	1:1:605:G:C8	2.46	0.49
1:1:2616:A:C8	7:B:37:ARG:NH2	2.80	0.49
2:2:903:A:O3'	67:SO:65:ARG:NH2	2.37	0.49
2:2:1588:A:H2'	2:2:1589:A:C8	2.47	0.49
3:3:27:U:H2'	3:3:28:C:C6	2.47	0.49
11:LC:75:ILE:HG13	11:LC:76:PRO:HD2	1.94	0.49
53:SA:91:LYS:HB2	53:SA:205:TYR:CE1	2.47	0.49
60:SH:71:PRO:O	60:SH:74:GLN:NE2	2.38	0.49
60:SH:112:ALA:O	60:SH:113:ARG:HD3	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
69:SQ:34:LYS:HD3	69:SQ:35:PRO:O	2.12	0.49
80:Sb:19:HIS:CE1	80:Sb:20:LYS:HG2	2.47	0.49
1:1:669:U:O2'	1:1:685:G:O6	2.29	0.49
1:1:3124:G:O2'	1:1:3125:U:H5'	2.12	0.49
2:2:219:C:N4	2:2:835:G:O6	2.34	0.49
2:2:391:C:H42	2:2:398:A:H62	1.60	0.49
2:2:421:C:O2'	2:2:423:G:OP1	2.28	0.49
2:2:499:U:H2'	2:2:500:G:H8	1.76	0.49
2:2:1139:A:H2'	2:2:1140:A:C8	2.46	0.49
3:3:72:G:O2'	3:3:73:U:OP1	2.30	0.49
6:A:296:GLN:HB2	6:A:312:VAL:HG12	1.94	0.49
8:C:563:VAL:HG12	8:C:564:GLN:H	1.77	0.49
8:C:581:SER:OG	8:C:584:LYS:O	2.24	0.49
19:LK:6:ASP:N	19:LK:7:PRO:HD3	2.27	0.49
26:LR:7:GLN:NE2	26:LR:33:SER:O	2.46	0.49
33:LY:52:GLY:H	33:LY:69:VAL:HG23	1.77	0.49
58:SF:57:ILE:HG22	58:SF:59:HIS:H	1.77	0.49
59:SG:27:PHE:HE2	59:SG:36:VAL:HG11	1.76	0.49
62:SJ:117:ALA:O	62:SJ:122:HIS:ND1	2.45	0.49
63:SK:31:HIS:CE1	63:SK:36:ARG:HA	2.47	0.49
77:SY:23:ARG:HB3	77:SY:79:TYR:CD1	2.47	0.49
81:Sc:44:ASN:H	81:Sc:62:ARG:NH2	2.08	0.49
1:1:1480:C:H2'	1:1:1481:A:H8	1.77	0.49
1:1:1595:C:H2'	1:1:1596:U:C6	2.46	0.49
1:1:1732:A:H2'	1:1:1733:G:H8	1.77	0.49
1:1:2854:G:O2'	47:Lm:100:TYR:O	2.30	0.49
2:2:692:C:H4'	2:2:693:U:H5''	1.93	0.49
2:2:778:U:O2'	2:2:779:A:O5'	2.30	0.49
2:2:815:A:H2'	2:2:816:C:H6	1.77	0.49
6:A:94:THR:HG23	6:A:96:THR:HG22	1.94	0.49
56:SD:165:GLN:N	56:SD:166:PRO:HD2	2.27	0.49
59:SG:70:PRO:O	59:SG:98:ARG:NH2	2.45	0.49
75:SW:78:ARG:NH1	75:SW:126:ILE:HG13	2.27	0.49
1:1:3231:G:H2'	1:1:3232:A:C8	2.48	0.49
2:2:673:U:H2'	2:2:674:G:C8	2.47	0.49
2:2:1334:A:O5'	69:SQ:123:ARG:NH1	2.46	0.49
2:2:1441:G:H21	84:Sf:85:TYR:HD2	1.61	0.49
2:2:1685:A:H61	2:2:1708:A:N6	2.11	0.49
19:LK:45:ASP:OD1	19:LK:46:ILE:N	2.46	0.49
22:LN:30:TYR:C	22:LN:32:GLN:H	2.21	0.49
54:SB:87:ARG:HB2	54:SB:101:HIS:ND1	2.27	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:SI:59:ARG:O	61:SI:60:LEU:HD22	2.12	0.49
79:Sa:79:ILE:HG22	79:Sa:84:VAL:HG23	1.93	0.49
81:Sc:62:ARG:HD2	81:Sc:63:GLU:N	2.28	0.49
1:1:1198:A:H2'	1:1:1199:C:H6	1.77	0.49
2:2:1169:G:H2'	2:2:1170:C:H6	1.77	0.49
2:2:1455:C:OP2	2:2:1455:C:H6	1.96	0.49
5:5:41:U:H2'	5:5:42:G:C8	2.47	0.49
8:C:70:ILE:HG13	8:C:71:LYS:HG3	1.93	0.49
8:C:182:ARG:NH2	52:Ls:137:GLN:HA	2.20	0.49
8:C:567:GLU:OE1	8:C:677:PRO:HD2	2.12	0.49
8:C:729:PRO:HB2	8:C:800:PHE:HE1	1.76	0.49
12:LD:214:LEU:HD21	12:LD:221:ARG:HD2	1.94	0.49
56:SD:10:LYS:O	56:SD:13:LYS:HG2	2.13	0.49
59:SG:50:LEU:HD12	59:SG:111:LEU:HB3	1.93	0.49
60:SH:91:PHE:HB2	60:SH:94:ARG:NH2	2.26	0.49
74:SV:40:ASP:OD1	74:SV:44:ARG:N	2.45	0.49
1:1:425:G:H2'	1:1:426:A:C8	2.48	0.49
1:1:652:A:H2'	1:1:653:A:H8	1.78	0.49
1:1:1732:A:H2'	1:1:1733:G:C8	2.48	0.49
1:1:3152:C:N3	21:LM:102:LYS:NZ	2.58	0.49
2:2:441:C:P	77:SY:108:ARG:HE	2.35	0.49
2:2:724:U:H3'	2:2:725:G:H5''	1.94	0.49
16:LH:149:TYR:CE2	16:LH:172:GLU:HA	2.48	0.49
45:Lk:73:LYS:O	45:Lk:74:ARG:HG3	2.13	0.49
52:Ls:139:LEU:HD11	52:Ls:169:GLU:HG2	1.95	0.49
61:SI:175:SER:OG	61:SI:176:ARG:N	2.46	0.49
63:SK:12:HIS:HB3	63:SK:74:LEU:HD11	1.94	0.49
65:SM:129:GLU:OE1	65:SM:133:ARG:N	2.40	0.49
67:SO:45:ASP:O	67:SO:47:SER:N	2.45	0.49
75:SW:23:ARG:HG3	75:SW:65:LEU:O	2.13	0.49
1:1:1196:G:H5''	27:LS:137:ARG:HH12	1.77	0.49
1:1:2332:G:H2'	1:1:2333:G:C8	2.47	0.49
2:2:1185:G:H2'	2:2:1186:A:H8	1.78	0.49
2:2:1609:U:OP2	58:SF:71:LYS:NZ	2.25	0.49
4:4:141:C:O2	22:LN:112:ASN:ND2	2.45	0.49
9:LA:100:ASN:O	9:LA:165:MET:HG2	2.13	0.49
11:LC:322:ASN:O	11:LC:325:ILE:HG22	2.12	0.49
19:LK:7:PRO:O	19:LK:10:ILE:HG23	2.11	0.49
21:LM:44:PRO:HG3	21:LM:81:VAL:HG13	1.94	0.49
51:Lq:126:LYS:HG3	51:Lq:127:PRO:HD2	1.93	0.49
52:Ls:45:LEU:HD23	52:Ls:45:LEU:O	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:SB:144:LYS:HE3	54:SB:206:PRO:HB3	1.95	0.49
57:SE:198:ARG:HG3	57:SE:208:VAL:HG12	1.93	0.49
65:SM:49:GLU:HA	65:SM:52:LYS:HG2	1.95	0.49
81:Sc:19:ARG:HA	81:Sc:27:THR:HA	1.95	0.49
1:1:617:C:H2'	1:1:618:C:C6	2.48	0.49
1:1:1186:A:H2'	1:1:1187:A:H8	1.77	0.49
1:1:1199:C:H2'	1:1:1200:A:C8	2.48	0.49
2:2:1356:C:H2'	2:2:1357:C:C6	2.48	0.49
6:A:39:THR:HG21	6:A:58:ARG:HH21	1.78	0.49
8:C:372:ARG:HH12	8:C:381:MET:HG2	1.78	0.49
28:LT:77:TYR:CE1	28:LT:86:GLU:HB3	2.47	0.49
45:Lk:51:ASP:CG	45:Lk:52:SER:H	2.21	0.49
48:Ln:2:ARG:CG	48:Ln:5:TRP:HD1	2.26	0.49
52:Ls:129:GLU:OE2	52:Ls:132:LYS:NZ	2.37	0.49
69:SQ:34:LYS:NZ	69:SQ:38:LEU:HB2	2.27	0.49
71:SS:139:LYS:O	71:SS:143:ARG:NH1	2.45	0.49
74:SV:78:LEU:O	74:SV:79:LEU:HD22	2.12	0.49
77:SY:85:LEU:O	77:SY:89:GLU:HG3	2.12	0.49
79:Sa:10:ARG:HG2	79:Sa:34:LYS:HB2	1.93	0.49
1:1:132:U:H4'	1:1:134:G:H22	1.78	0.49
1:1:290:A:C8	1:1:292:G:H1'	2.48	0.49
5:5:28:C:H2'	5:5:29:A:C8	2.47	0.49
8:C:392:ASP:OD1	8:C:392:ASP:N	2.44	0.49
32:LX:51:LEU:HD23	32:LX:51:LEU:H	1.78	0.49
41:Lg:72:THR:HG22	41:Lg:73:VAL:N	2.28	0.49
48:Lr:5:TRP:HB3	48:Lr:9:ARG:HH12	1.74	0.49
63:SK:57:PHE:CZ	63:SK:60:GLN:HA	2.47	0.49
64:SL:80:VAL:CG1	64:SL:126:ASP:H	2.26	0.49
68:SP:80:LYS:HZ3	68:SP:81:PRO:HD2	1.77	0.49
72:ST:67:LEU:C	72:ST:68:ARG:HD2	2.36	0.49
1:1:701:U:OP1	43:Li:18:ARG:NH2	2.42	0.49
2:2:824:U:H2'	2:2:825:C:C6	2.47	0.49
2:2:1249:C:OP2	84:Sf:105:TYR:OH	2.18	0.49
8:C:329:PHE:CD2	8:C:330:LEU:HD22	2.48	0.49
16:LH:126:LYS:HD3	16:LH:182:GLU:OE2	2.13	0.49
19:LK:76:THR:HB	19:LK:81:ILE:HD11	1.95	0.49
19:LK:82:ILE:O	19:LK:86:LYS:HE2	2.13	0.49
27:LS:27:MET:HE1	27:LS:44:PHE:CB	2.42	0.49
30:LV:130:ARG:HH11	30:LV:130:ARG:HG3	1.77	0.49
42:Lh:90:THR:HB	42:Lh:93:LEU:HB2	1.94	0.49
56:SD:74:SER:O	56:SD:78:LYS:HG3	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
65:SM:123:VAL:C	65:SM:124:LYS:HD3	2.38	0.49
68:SP:61:PRO:HA	68:SP:91:MET:HE2	1.94	0.49
69:SQ:8:GLN:HE21	69:SQ:21:ARG:HD2	1.77	0.49
1:1:1047:A:H4'	1:1:1048:A:O5'	2.13	0.48
1:1:1439:A:N1	38:Ld:75:ILE:HD11	2.28	0.48
1:1:1758:G:O2'	1:1:1760:G:OP2	2.30	0.48
1:1:1759:C:N4	26:LR:88:ARG:O	2.46	0.48
1:1:2468:U:H2'	1:1:2469:U:C6	2.47	0.48
2:2:1385:A:N7	2:2:1407:A:N6	2.61	0.48
2:2:1483:A:OP1	82:Sd:34:TYR:OH	2.25	0.48
2:2:1787:G:OP2	79:Sa:10:ARG:NE	2.45	0.48
6:A:45:LEU:HD12	6:A:45:LEU:O	2.13	0.48
8:C:172:THR:HG23	8:C:175:ASP:H	1.78	0.48
8:C:724:PRO:HG2	8:C:811:PRO:HD2	1.95	0.48
12:LD:198:LEU:O	12:LD:202:ILE:HD12	2.13	0.48
19:LK:64:ILE:O	19:LK:64:ILE:HG13	2.12	0.48
22:LN:67:ARG:O	22:LN:68:ARG:HB3	2.12	0.48
24:LP:126:ARG:HG3	24:LP:140:MET:HE1	1.94	0.48
35:La:78:LEU:HD12	35:La:112:LEU:HD11	1.94	0.48
46:Ll:23:ILE:HD11	46:Ll:38:ASN:N	2.28	0.48
51:Lq:35:LEU:HD12	51:Lq:107:LEU:HD23	1.95	0.48
58:SF:173:ASN:OD1	58:SF:174:VAL:N	2.46	0.48
62:SJ:71:GLY:O	62:SJ:75:ILE:HG12	2.13	0.48
68:SP:76:LYS:HG2	68:SP:77:PRO:HD2	1.95	0.48
69:SQ:25:GLY:HA3	69:SQ:64:ASP:HB2	1.95	0.48
77:SY:94:LEU:O	77:SY:98:GLY:N	2.38	0.48
4:4:26:U:H2'	4:4:27:U:C6	2.48	0.48
4:4:94:C:OP1	44:Lj:75:LYS:NZ	2.43	0.48
5:5:1:U:H2'	5:5:2:C:C6	2.48	0.48
13:LE:69:ARG:NH1	13:LE:185:SER:OG	2.46	0.48
14:LF:138:PRO:HG2	14:LF:139:TRP:CE3	2.49	0.48
19:LK:29:ALA:N	19:LK:30:PRO:HD3	2.28	0.48
58:SF:42:ASP:OD1	58:SF:42:ASP:N	2.45	0.48
63:SK:84:ILE:O	63:SK:84:ILE:HG22	2.13	0.48
70:SR:58:MET:O	70:SR:61:ILE:HG22	2.13	0.48
75:SW:22:LYS:HA	80:Sb:3:LEU:HD12	1.95	0.48
1:1:1745:U:C5	26:LR:43:LYS:HE2	2.48	0.48
2:2:792:U:H1'	2:2:793:U:OP2	2.13	0.48
2:2:909:U:H3	54:SB:7:LYS:NZ	2.11	0.48
2:2:1228:U:H5''	84:Sf:95:ARG:HH22	1.77	0.48
3:3:46:C:OP1	12:LD:161:ARG:HG3	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:4:52:A:P	46:Ll:21:ARG:HH22	2.36	0.48
7:B:146:LYS:HB2	56:SD:128:PHE:HE1	1.77	0.48
8:C:565:TYR:N	8:C:681:GLU:OE2	2.39	0.48
30:LV:16:THR:HG21	30:LV:85:LYS:HE3	1.95	0.48
42:Lh:31:LEU:O	42:Lh:35:ARG:HG3	2.13	0.48
55:SC:89:MET:HE2	55:SC:111:LEU:HD21	1.96	0.48
58:SF:138:SER:HB3	58:SF:141:THR:O	2.14	0.48
61:SI:201:HIS:ND1	61:SI:202:LYS:HE3	2.28	0.48
66:SN:62:GLN:HG2	66:SN:62:GLN:O	2.14	0.48
72:ST:82:SER:OG	72:ST:83:ALA:N	2.46	0.48
78:SZ:81:VAL:HG23	78:SZ:82:VAL:H	1.78	0.48
1:1:1638:G:H2'	1:1:1639:A:C8	2.49	0.48
1:1:2307:U:H2'	1:1:2308:A:H8	1.77	0.48
1:1:2320:A:H2'	1:1:2321:A:C8	2.49	0.48
1:1:2627:U:H2'	1:1:2628:G:H8	1.78	0.48
1:1:3121:G:N3	1:1:3122:U:H5	2.11	0.48
2:2:1195:G:OP1	2:2:1196:G:O2'	2.21	0.48
2:2:1781:U:H2'	2:2:1782:G:H8	1.78	0.48
7:B:117:LYS:O	7:B:120:SER:OG	2.24	0.48
8:C:424:LYS:HE3	8:C:426:ASP:HB3	1.95	0.48
20:LL:158:GLU:HG2	20:LL:159:GLN:N	2.28	0.48
24:LP:30:ARG:NH1	24:LP:31:GLU:OE2	2.46	0.48
54:SB:116:LYS:HD3	54:SB:117:TRP:CZ3	2.48	0.48
55:SC:149:ARG:HH11	55:SC:149:ARG:HG3	1.77	0.48
73:SU:22:THR:OG1	73:SU:85:LYS:HE3	2.14	0.48
1:1:332:C:OP1	1:1:1363:G:O2'	2.32	0.48
1:1:1237:C:H2'	1:1:1238:C:C6	2.48	0.48
1:1:2882:U:H2'	1:1:2883:U:H6	1.78	0.48
2:2:66:U:C5	59:SG:176:PRO:HB3	2.49	0.48
2:2:85:A:H2'	2:2:86:C:H6	1.77	0.48
2:2:1391:G:C6	2:2:1401:G:C6	3.02	0.48
2:2:1561:C:C5'	71:SS:41:ARG:HH12	2.26	0.48
8:C:746:TYR:OH	8:C:759:GLU:OE1	2.30	0.48
29:LU:56:LEU:HD12	29:LU:56:LEU:O	2.13	0.48
54:SB:25:THR:O	54:SB:50:ARG:NH2	2.32	0.48
57:SE:86:PHE:HE1	57:SE:102:ILE:HD12	1.78	0.48
60:SH:112:ALA:C	60:SH:113:ARG:HD3	2.39	0.48
71:SS:111:GLU:OE1	71:SS:115:ARG:NH1	2.47	0.48
77:SY:110:GLN:O	77:SY:114:ARG:HG3	2.13	0.48
1:1:2538:G:OP2	1:1:2539:A:O2'	2.24	0.48
1:1:2840:C:H2'	1:1:2841:U:C6	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:1143:G:H2'	2:2:1144:A:C8	2.48	0.48
2:2:1685:A:H61	2:2:1708:A:H62	1.61	0.48
2:2:1731:C:OP1	30:LV:34:ARG:NH2	2.41	0.48
6:A:12:GLU:OE1	6:A:12:GLU:N	2.46	0.48
11:LC:32:ARG:HD3	11:LC:121:PHE:CE1	2.49	0.48
14:LF:138:PRO:HG2	14:LF:139:TRP:CZ3	2.48	0.48
19:LK:104:VAL:HG12	19:LK:105:SER:N	2.28	0.48
29:LU:52:ARG:NH2	29:LU:55:ASN:HD22	2.10	0.48
31:LW:14:TYR:HB3	31:LW:15:PRO:HD2	1.95	0.48
39:Le:68:MET:HB2	39:Le:69:PRO:HD2	1.95	0.48
54:SB:111:ARG:HE	79:Sa:68:TYR:HB2	1.78	0.48
56:SD:84:GLU:OE1	56:SD:85:ASN:ND2	2.46	0.48
60:SH:95:HIS:CG	60:SH:175:ARG:HH12	2.31	0.48
61:SI:104:ILE:HG23	61:SI:169:LEU:HB2	1.94	0.48
64:SL:5:LEU:HD12	64:SL:6:THR:N	2.28	0.48
1:1:1745:U:H4'	1:1:1745:U:OP1	2.13	0.48
1:1:2476:U:OP1	15:LG:248:ARG:NH1	2.46	0.48
1:1:3163:A:H5''	1:1:3164:G:C5	2.49	0.48
8:C:75:ILE:HD12	8:C:440:MET:HA	1.96	0.48
11:LC:31:ILE:HD12	11:LC:129:ALA:HB2	1.95	0.48
16:LH:149:TYR:HE2	16:LH:172:GLU:HA	1.77	0.48
29:LU:56:LEU:HD22	29:LU:60:ILE:HD11	1.96	0.48
54:SB:145:ARG:NH2	54:SB:151:LYS:O	2.46	0.48
68:SP:80:LYS:NZ	68:SP:81:PRO:HD2	2.28	0.48
69:SQ:3:SER:OG	69:SQ:4:VAL:N	2.47	0.48
1:1:911:A:O2'	44:Lj:49:TRP:O	2.29	0.48
1:1:1202:C:N3	1:1:1270:A:N1	2.61	0.48
1:1:2370:C:H2'	1:1:2371:U:H6	1.79	0.48
1:1:2512:U:C2	9:LA:89:TYR:HE2	2.31	0.48
1:1:3176:G:H2'	1:1:3177:C:C6	2.48	0.48
2:2:381:G:H2'	2:2:382:A:C8	2.49	0.48
2:2:781:G:H2'	2:2:782:C:H6	1.79	0.48
2:2:913:A:H61	67:SO:54:ARG:HH12	1.60	0.48
2:2:1272:A:H62	2:2:1427:C:H42	1.62	0.48
8:C:295:LYS:HA	8:C:298:VAL:HG22	1.95	0.48
9:LA:113:VAL:HG12	9:LA:166:ILE:HD13	1.96	0.48
13:LE:170:ILE:O	13:LE:174:LYS:HG2	2.13	0.48
21:LM:123:LEU:HB3	23:LO:199:LEU:HD21	1.96	0.48
28:LT:96:VAL:HG12	28:LT:97:LYS:N	2.29	0.48
41:Lg:79:GLY:O	41:Lg:80:SER:OG	2.29	0.48
57:SE:172:PHE:HE2	57:SE:174:LYS:HE3	1.77	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
75:SW:87:GLU:HA	75:SW:90:VAL:HG12	1.95	0.48
79:Sa:50:ILE:O	79:Sa:54:SER:N	2.41	0.48
1:1:779:U:H2'	1:1:780:U:C6	2.49	0.48
1:1:1796:A:O2'	1:1:1797:A:OP1	2.29	0.48
1:1:2621:G:O2'	1:1:2622:G:OP1	2.31	0.48
2:2:54:C:H4'	77:SY:112:LYS:HZ3	1.78	0.48
2:2:511:G:H22	2:2:540:C:H5	1.62	0.48
2:2:1441:G:N2	84:Sf:87:THR:O	2.47	0.48
2:2:1476:G:H4'	72:ST:12:ALA:HB1	1.96	0.48
6:A:260:ASP:OD2	6:A:263:LYS:HE2	2.13	0.48
8:C:125:ASP:HA	8:C:153:ILE:HD12	1.95	0.48
9:LA:95:ALA:O	9:LA:100:ASN:ND2	2.46	0.48
19:LK:13:ILE:O	19:LK:14:HIS:CD2	2.63	0.48
23:LO:139:THR:HG22	23:LO:141:GLY:H	1.77	0.48
32:LX:63:SER:HB2	42:Lh:71:LEU:HD11	1.96	0.48
55:SC:238:TRP:CD2	75:SW:68:ARG:HD2	2.49	0.48
56:SD:161:ILE:N	56:SD:192:MET:HE1	2.24	0.48
66:SN:28:THR:HG23	66:SN:32:GLN:NE2	2.29	0.48
69:SQ:29:ILE:HB	69:SQ:65:ILE:HD11	1.96	0.48
71:SS:132:ARG:HD2	71:SS:136:GLN:HE21	1.79	0.48
1:1:1223:A:N6	1:1:1224:U:O4	2.47	0.48
1:1:1547:C:H2'	1:1:1548:A:C8	2.47	0.48
1:1:2242:A:N7	1:1:2251:G:C8	2.82	0.48
1:1:2919:C:H2'	1:1:2920:G:C8	2.49	0.48
2:2:814:G:C2	2:2:815:A:C8	3.02	0.48
2:2:957:U:C2	66:SN:17:PRO:HG2	2.49	0.48
2:2:1354:U:H2'	2:2:1355:G:H8	1.79	0.48
2:2:1477:C:O2'	2:2:1478:C:O5'	2.31	0.48
2:2:1682:C:H2'	2:2:1683:C:C6	2.49	0.48
8:C:563:VAL:HG12	8:C:564:GLN:N	2.29	0.48
15:LG:65:LYS:HE2	22:LN:29:GLU:OE2	2.14	0.48
15:LG:100:TYR:CE2	15:LG:206:VAL:HG23	2.48	0.48
63:SK:60:GLN:NE2	82:Sd:25:THR:HG23	2.29	0.48
1:1:580:A:N6	1:1:598:G:H1'	2.29	0.47
1:1:2495:U:H2'	1:1:2496:G:C8	2.49	0.47
2:2:1177:C:H2'	2:2:1178:U:H6	1.79	0.47
8:C:421:THR:HB	8:C:422:PRO:HD2	1.95	0.47
12:LD:127:GLY:O	12:LD:195:THR:OG1	2.22	0.47
15:LG:33:ARG:O	15:LG:33:ARG:HG2	2.14	0.47
34:LZ:88:LEU:HD11	34:LZ:120:ARG:HD2	1.95	0.47
58:SF:76:ILE:H	58:SF:76:ILE:HD12	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:SF:176:THR:OG1	58:SF:179:GLU:OE1	2.32	0.47
67:SO:146:ARG:HA	79:Sa:28:ARG:HG3	1.95	0.47
70:SR:120:ILE:H	70:SR:120:ILE:HD12	1.78	0.47
77:SY:26:MET:HB2	77:SY:76:ALA:O	2.14	0.47
2:2:195:G:H2'	2:2:196:G:C8	2.49	0.47
2:2:1342:A:H5'	73:SU:50:LYS:HZ2	1.79	0.47
2:2:1580:G:H8	69:SQ:122:ARG:HB3	1.79	0.47
4:4:19:C:H2'	4:4:20:U:H6	1.78	0.47
15:LG:67:ILE:HB	15:LG:71:ARG:HH21	1.79	0.47
16:LH:168:ALA:O	16:LH:171:VAL:HG22	2.13	0.47
25:LQ:117:ASP:OD1	25:LQ:119:ARG:NE	2.38	0.47
41:Lg:86:VAL:O	41:Lg:90:ILE:HD12	2.14	0.47
47:Lm:88:LYS:HE3	47:Lm:89:PHE:HE1	1.78	0.47
53:SA:72:ASN:ND2	53:SA:74:SER:OG	2.47	0.47
53:SA:150:CYS:SG	53:SA:162:ALA:HB1	2.54	0.47
63:SK:75:ARG:NH2	63:SK:84:ILE:HA	2.30	0.47
66:SN:33:VAL:HA	66:SN:36:GLN:HE22	1.78	0.47
1:1:250:C:HO2'	1:1:251:U:P	2.38	0.47
1:1:1027:U:OP1	17:LI:90:ARG:NH2	2.35	0.47
1:1:1064:C:HO2'	1:1:1065:U:P	2.38	0.47
1:1:1242:A:H2'	1:1:1243:A:C5	2.48	0.47
2:2:91:A:H5''	2:2:92:A:H5''	1.96	0.47
2:2:519:U:H5''	77:SY:40:LYS:HG3	1.95	0.47
2:2:844:G:H2'	2:2:845:A:C8	2.48	0.47
2:2:1707:C:H3'	2:2:1708:A:H5''	1.95	0.47
11:LC:365:ALA:HB3	27:LS:28:ARG:HD2	1.96	0.47
16:LH:53:LEU:HD21	16:LH:116:ILE:HG23	1.95	0.47
37:Lc:19:LEU:HD21	37:Lc:100:ASP:OD1	2.14	0.47
43:Li:99:LEU:O	43:Li:102:ILE:HG22	2.14	0.47
58:SF:100:ILE:HG13	58:SF:177:ILE:HD11	1.96	0.47
59:SG:152:ASP:OD1	59:SG:154:ARG:HG2	2.15	0.47
73:SU:21:ILE:HG22	73:SU:112:VAL:HG23	1.96	0.47
77:SY:30:ILE:HG22	77:SY:32:HIS:HD2	1.79	0.47
1:1:1150:U:O2'	14:LF:216:PRO:O	2.33	0.47
2:2:222:U:HO2'	2:2:223:G:P	2.34	0.47
2:2:647:C:H2'	2:2:648:C:C6	2.50	0.47
2:2:1379:A:O2'	2:2:1380:G:H8	1.97	0.47
4:4:19:C:H2'	4:4:20:U:C6	2.50	0.47
8:C:611:ARG:HH22	83:Se:17:GLN:HA	1.79	0.47
8:C:652:THR:HG22	8:C:692:ASP:H	1.78	0.47
19:LK:21:GLU:OE2	19:LK:56:LEU:HD23	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:LK:111:GLU:HA	19:LK:114:ARG:HG3	1.96	0.47
22:LN:159:ARG:HB2	22:LN:164:LEU:HB2	1.96	0.47
57:SE:138:PHE:HA	57:SE:148:ARG:HA	1.95	0.47
61:SI:70:GLU:OE1	61:SI:70:GLU:N	2.46	0.47
61:SI:83:TYR:HB2	61:SI:200:LEU:HD13	1.96	0.47
64:SL:51:LYS:O	64:SL:55:GLU:HG3	2.15	0.47
65:SM:79:ALA:O	65:SM:82:GLN:HG3	2.15	0.47
70:SR:18:GLU:OE1	70:SR:69:ILE:HG23	2.15	0.47
75:SW:54:ASP:OD1	75:SW:55:ASN:N	2.46	0.47
1:1:1323:C:H2'	1:1:1324:U:C6	2.49	0.47
1:1:1454:U:OP1	26:LR:5:ARG:NH1	2.44	0.47
2:2:483:G:H1	2:2:498:U:H3	1.63	0.47
4:4:77:A:H2'	4:4:78:G:C8	2.49	0.47
5:5:27:U:HO2'	5:5:28:C:H6	1.61	0.47
5:5:48:C:H2'	5:5:49:G:H8	1.80	0.47
6:A:48:ASP:OD1	6:A:49:GLU:N	2.47	0.47
6:A:258:ILE:HD11	6:A:268:ASP:HB2	1.95	0.47
8:C:389:PRO:HG3	8:C:396:PHE:HE1	1.77	0.47
14:LF:31:GLU:H	14:LF:31:GLU:CD	2.22	0.47
20:LL:2:ALA:N	35:La:33:GLY:O	2.47	0.47
42:Lh:36:ILE:O	42:Lh:39:ILE:HG12	2.13	0.47
56:SD:214:ILE:O	70:SR:20:TYR:OH	2.26	0.47
58:SF:20:VAL:HG13	58:SF:20:VAL:O	2.14	0.47
62:SJ:168:GLY:O	62:SJ:172:ARG:HG3	2.13	0.47
69:SQ:129:PHE:HB3	69:SQ:134:ALA:HA	1.97	0.47
83:Se:33:ARG:O	83:Se:33:ARG:HG2	2.14	0.47
1:1:1460:A:OP1	1:1:3033:G:O2'	2.31	0.47
1:1:2616:A:C1'	7:B:37:ARG:HH22	2.25	0.47
1:1:3027:G:C2	1:1:3028:A:C8	3.03	0.47
2:2:652:G:H22	2:2:673:U:H3	1.61	0.47
2:2:858:U:P	60:SH:124:ARG:HH21	2.38	0.47
2:2:1473:A:H2'	2:2:1474:G:H8	1.80	0.47
2:2:1703:C:H2'	2:2:1704:A:H8	1.80	0.47
5:5:18:G:H4'	5:5:19:C:O5'	2.14	0.47
12:LD:39:GLN:HE22	12:LD:48:LYS:HD3	1.79	0.47
20:LL:60:CYS:HB2	20:LL:65:TYR:O	2.15	0.47
38:Ld:23:TYR:HE2	38:Ld:86:ILE:HD11	1.80	0.47
52:Ls:30:VAL:O	52:Ls:30:VAL:HG13	2.15	0.47
61:SI:107:ALA:HB3	61:SI:108:PRO:HD3	1.96	0.47
77:SY:71:LYS:HE3	77:SY:71:LYS:HB3	1.65	0.47
80:Sb:47:PHE:CE2	80:Sb:49:HIS:HB2	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:274:G:N7	22:LN:182:LYS:NZ	2.62	0.47
1:1:474:C:H2'	1:1:475:G:C8	2.49	0.47
1:1:492:A:H2'	1:1:493:U:C6	2.50	0.47
1:1:967:U:H2'	1:1:968:U:H6	1.80	0.47
2:2:204:U:H2'	2:2:205:A:C8	2.50	0.47
2:2:893:G:H2'	2:2:894:U:C6	2.49	0.47
5:5:2:C:H2'	5:5:3:C:C6	2.50	0.47
6:A:30:MET:HE1	6:A:71:ILE:HD13	1.97	0.47
8:C:213:PHE:HB2	8:C:222:PHE:CE1	2.49	0.47
12:LD:82:GLU:HA	12:LD:258:TYR:CE1	2.50	0.47
12:LD:107:ARG:NH2	12:LD:119:PHE:O	2.47	0.47
13:LE:115:ASP:OD1	13:LE:116:GLN:N	2.47	0.47
15:LG:98:ASN:HD22	15:LG:98:ASN:C	2.12	0.47
16:LH:106:ARG:HH12	16:LH:110:THR:HB	1.79	0.47
22:LN:36:ILE:HG13	22:LN:64:VAL:HG23	1.95	0.47
25:LQ:116:ASP:OD1	25:LQ:117:ASP:N	2.47	0.47
30:LV:88:LYS:HD2	30:LV:94:PHE:CZ	2.48	0.47
31:LW:141:ARG:HB2	31:LW:142:PRO:HD2	1.97	0.47
43:Li:102:ILE:O	43:Li:105:GLU:HG3	2.15	0.47
57:SE:11:ARG:NH1	57:SE:23:LEU:O	2.47	0.47
57:SE:23:LEU:HG	57:SE:24:SER:H	1.79	0.47
57:SE:94:LYS:NZ	77:SY:20:LEU:HA	2.30	0.47
60:SH:65:VAL:HG12	60:SH:97:LEU:HB2	1.95	0.47
78:SZ:84:HIS:O	78:SZ:88:LYS:NZ	2.35	0.47
1:1:152:G:C8	20:LL:99:HIS:NE2	2.83	0.47
1:1:3147:G:C8	1:1:3148:G:H1'	2.49	0.47
2:2:597:U:P	76:SX:108:GLY:HA2	2.55	0.47
2:2:1061:G:O2'	2:2:1062:A:H5'	2.14	0.47
2:2:1226:G:N2	2:2:1252:G:H2'	2.30	0.47
2:2:1768:C:OP2	48:Ln:2:ARG:NH1	2.48	0.47
8:C:822:VAL:O	8:C:826:ARG:HG3	2.15	0.47
23:LO:31:GLY:HA2	23:LO:103:ARG:NH1	2.29	0.47
61:SI:37:ARG:NH1	61:SI:95:THR:HB	2.29	0.47
1:1:1430:G:O2'	1:1:2318:G:O6	2.29	0.47
1:1:1932:G:O6	1:1:2058:A:N6	2.47	0.47
1:1:2206:A:C8	9:LA:245:LEU:HD11	2.50	0.47
1:1:3144:U:N3	1:1:3148:G:N1	2.38	0.47
2:2:78:C:O4'	59:SG:177:ARG:CZ	2.63	0.47
2:2:1479:A:H2	2:2:1603:G:H1'	1.80	0.47
4:4:95:G:OP2	44:Lj:72:ARG:NH1	2.48	0.47
8:C:250:ASN:HB2	8:C:262:SER:H	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:SF:17:PRO:HG2	58:SF:20:VAL:HG12	1.96	0.47
61:SI:96:LEU:H	61:SI:96:LEU:HD23	1.80	0.47
61:SI:103:GLN:HE22	61:SI:170:TYR:HE1	1.63	0.47
62:SJ:108:GLN:NE2	62:SJ:124:ARG:HB2	2.30	0.47
68:SP:19:THR:HA	68:SP:22:LYS:HE2	1.96	0.47
73:SU:44:ASN:OD1	73:SU:45:LYS:N	2.47	0.47
75:SW:111:MET:HE2	75:SW:115:GLU:HG3	1.96	0.47
81:Sc:53:ASP:OD1	81:Sc:54:ILE:N	2.47	0.47
1:1:468:G:OP2	1:1:468:G:H8	1.98	0.47
1:1:528:U:C2	1:1:529:G:C8	3.03	0.47
1:1:2466:G:H2'	1:1:2467:U:C6	2.50	0.47
1:1:2472:U:H2'	1:1:2473:U:C6	2.50	0.47
1:1:2487:A:H1'	1:1:2488:G:C8	2.50	0.47
2:2:316:U:O2'	2:2:317:U:OP1	2.23	0.47
2:2:906:U:H2'	2:2:907:U:C6	2.50	0.47
2:2:1222:U:H3'	2:2:1223:G:C8	2.50	0.47
2:2:1399:C:H2'	2:2:1400:C:C6	2.49	0.47
2:2:1495:G:OP2	72:ST:73:VAL:HG22	2.15	0.47
2:2:1602:C:H2'	2:2:1603:G:C8	2.50	0.47
6:A:234:ASP:HB3	6:A:253:ALA:HB3	1.97	0.47
8:C:806:LEU:HD12	8:C:807:PRO:HD2	1.97	0.47
9:LA:64:ARG:HG2	9:LA:65:SER:N	2.29	0.47
18:LJ:103:PHE:HE1	18:LJ:132:MET:HE3	1.80	0.47
21:LM:19:VAL:HG23	21:LM:65:THR:OG1	2.14	0.47
46:LI:48:ARG:NH2	46:LI:49:LEU:HG	2.06	0.47
53:SA:37:GLN:N	53:SA:38:PRO:HD2	2.30	0.47
56:SD:19:VAL:HG12	82:Sd:50:ILE:HD12	1.96	0.47
57:SE:185:GLY:C	57:SE:224:ASN:HD21	2.20	0.47
60:SH:107:LYS:O	60:SH:109:LYS:HD3	2.14	0.47
68:SP:61:PRO:O	68:SP:65:ILE:HG12	2.15	0.47
70:SR:25:THR:HG23	70:SR:27:ASP:H	1.79	0.47
83:Se:36:LYS:HA	83:Se:36:LYS:HD3	1.70	0.47
1:1:293:G:H2'	1:1:294:G:H8	1.80	0.46
1:1:1186:A:H2'	1:1:1187:A:C8	2.49	0.46
1:1:2355:C:H1'	10:LB:267:ARG:NH2	2.30	0.46
1:1:2881:G:N1	1:1:2882:U:O2	2.48	0.46
2:2:70:C:H5''	59:SG:165:LYS:HZ1	1.80	0.46
2:2:166:A:OP2	59:SG:137:ARG:NH2	2.48	0.46
2:2:231:G:H2'	2:2:232:G:H8	1.80	0.46
2:2:442:A:C2	2:2:443:A:C8	3.03	0.46
2:2:527:C:O2	77:SY:64:ARG:NH2	2.37	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:1219:C:H2'	2:2:1220:G:C8	2.50	0.46
2:2:1403:U:H2'	2:2:1404:G:C8	2.50	0.46
2:2:1617:U:N3	2:2:1618:G:N7	2.63	0.46
2:2:1708:A:N6	2:2:1709:G:O6	2.49	0.46
8:C:122:ARG:HA	8:C:151:GLU:OE2	2.15	0.46
8:C:710:THR:O	8:C:714:VAL:HG12	2.15	0.46
10:LB:93:ILE:HG22	10:LB:156:CYS:HA	1.97	0.46
26:LR:15:LEU:HD13	26:LR:52:LYS:HB3	1.97	0.46
31:LW:143:GLU:OE2	31:LW:143:GLU:N	2.46	0.46
54:SB:119:THR:HB	54:SB:143:THR:HG21	1.96	0.46
56:SD:118:VAL:HG13	56:SD:119:ARG:N	2.30	0.46
58:SF:19:GLU:HG2	58:SF:20:VAL:N	2.30	0.46
66:SN:98:VAL:HG21	66:SN:115:LEU:HD13	1.97	0.46
71:SS:33:THR:HG22	71:SS:40:ARG:HA	1.97	0.46
1:1:257:G:OP1	43:Li:44:LYS:HG2	2.15	0.46
1:1:1015:C:H2'	1:1:1016:U:O4'	2.15	0.46
1:1:1813:G:O2'	46:Ll:3:SER:O	2.32	0.46
1:1:1920:G:H2'	1:1:1921:C:C6	2.51	0.46
2:2:1298:U:OP1	55:SC:96:LYS:HG2	2.16	0.46
4:4:142:C:H2'	4:4:143:U:C6	2.50	0.46
8:C:27:HIS:HB3	8:C:30:HIS:ND1	2.30	0.46
8:C:435:ARG:HG3	8:C:436:THR:N	2.31	0.46
11:LC:285:ALA:O	51:Lq:5:SER:OG	2.20	0.46
18:LJ:111:ILE:HA	18:LJ:115:ILE:HD13	1.97	0.46
27:LS:8:GLN:NE2	27:LS:62:ASN:HD22	2.08	0.46
51:Lq:120:ARG:CD	51:Lq:123:ARG:HH12	2.26	0.46
57:SE:136:VAL:HG11	57:SE:148:ARG:HD2	1.98	0.46
60:SH:153:LYS:HA	75:SW:49:GLU:OE1	2.15	0.46
66:SN:60:ILE:HD13	66:SN:66:VAL:HG21	1.97	0.46
1:1:609:A:H1'	1:1:610:A:OP2	2.16	0.46
1:1:1762:U:H2'	1:1:1763:C:C6	2.50	0.46
1:1:1893:A:N3	1:1:2083:G:H2'	2.31	0.46
1:1:2148:G:OP1	9:LA:202:VAL:HG23	2.16	0.46
1:1:2488:G:C5	9:LA:34:TYR:HD2	2.32	0.46
1:1:2900:A:OP1	10:LB:256:TRP:HB3	2.15	0.46
2:2:66:U:O3'	59:SG:174:LYS:HD3	2.15	0.46
2:2:297:A:H2'	2:2:298:A:C8	2.50	0.46
2:2:784:U:H2'	2:2:785:G:C8	2.50	0.46
2:2:884:U:C2	2:2:885:A:C8	3.03	0.46
5:5:62:C:H2'	5:5:63:C:H6	1.80	0.46
5:5:66:A:H2'	5:5:67:U:H6	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:LD:194:ASP:O	12:LD:195:THR:HG22	2.16	0.46
17:LI:38:ARG:HD2	17:LI:83:GLU:HG3	1.96	0.46
19:LK:54:LYS:HG3	19:LK:55:GLY:H	1.81	0.46
39:Le:12:LYS:HD3	39:Le:12:LYS:HA	1.74	0.46
46:Ll:33:ASN:OD1	46:Ll:34:THR:N	2.48	0.46
46:Ll:42:ARG:HG2	46:Ll:42:ARG:HH11	1.79	0.46
58:SF:39:GLU:HB3	58:SF:118:GLN:OE1	2.16	0.46
66:SN:17:PRO:HG3	80:Sb:28:PRO:HG2	1.96	0.46
72:ST:106:GLN:O	72:ST:109:GLU:HG3	2.15	0.46
84:Sf:123:ASN:HB3	84:Sf:126:CYS:C	2.40	0.46
1:1:649:G:OP2	1:1:649:G:N2	2.35	0.46
1:1:1876:A:H61	1:1:2302:C:N4	2.13	0.46
1:1:2636:G:H2'	1:1:2636:G:N3	2.30	0.46
2:2:1172:U:P	71:SS:137:HIS:HD1	2.39	0.46
4:4:29:U:H5''	20:LL:27:ASP:HB3	1.96	0.46
5:5:19:C:H6	5:5:19:C:H2'	1.60	0.46
10:LB:47:MET:CE	10:LB:336:ILE:HD11	2.46	0.46
27:LS:32:PRO:HD2	27:LS:36:VAL:HG21	1.96	0.46
41:Lg:100:LYS:HE3	41:Lg:100:LYS:HB2	1.79	0.46
68:SP:33:LEU:HD11	71:SS:94:ASP:CG	2.40	0.46
68:SP:89:ARG:NH1	68:SP:128:SER:OG	2.48	0.46
73:SU:68:PRO:HB2	82:Sd:41:GLN:HE21	1.79	0.46
79:Sa:104:ASN:O	79:Sa:105:LYS:HG2	2.15	0.46
1:1:985:A:H1'	12:LD:15:ARG:NH1	2.30	0.46
1:1:2392:G:H2'	1:1:2393:A:H8	1.80	0.46
1:1:2467:U:H2'	1:1:2468:U:C6	2.51	0.46
1:1:2511:U:O4'	15:LG:41:GLN:NE2	2.49	0.46
1:1:2945:U:H2'	1:1:2946:A:H8	1.80	0.46
2:2:90:G:H2'	2:2:91:A:O4'	2.16	0.46
2:2:328:G:H21	61:SI:5:ARG:HD2	1.81	0.46
2:2:479:U:O4	2:2:480:A:N6	2.49	0.46
2:2:731:G:H2'	2:2:732:A:C8	2.51	0.46
2:2:1715:G:H2'	2:2:1716:A:O4'	2.14	0.46
2:2:1787:G:OP1	79:Sa:10:ARG:NH2	2.37	0.46
6:A:62:HIS:CE1	6:A:90:TRP:HH2	2.34	0.46
7:B:141:ILE:HD11	56:SD:124:GLY:HA3	1.97	0.46
8:C:470:THR:HG21	8:C:479:ASN:HA	1.98	0.46
8:C:801:ASP:CG	8:C:802:HIS:H	2.23	0.46
16:LH:191:GLU:HG2	16:LH:192:ALA:N	2.31	0.46
19:LK:119:LYS:HA	19:LK:123:LYS:HD2	1.98	0.46
28:LT:48:VAL:HG21	28:LT:94:GLU:OE1	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:LW:125:ALA:HA	31:LW:131:LEU:HD13	1.96	0.46
34:LZ:102:GLU:OE2	34:LZ:105:GLN:HB2	2.16	0.46
54:SB:83:LYS:N	54:SB:104:ASP:O	2.43	0.46
56:SD:23:GLU:HG3	63:SK:59:TRP:CD1	2.50	0.46
65:SM:52:LYS:HZ1	84:Sf:128:ALA:C	2.23	0.46
67:SO:20:VAL:HG12	67:SO:21:ARG:N	2.30	0.46
1:1:410:A:H2'	1:1:411:A:H8	1.80	0.46
1:1:1221:C:O3'	19:LK:57:ARG:NH2	2.48	0.46
1:1:1455:G:H2'	1:1:1456:A:H8	1.81	0.46
1:1:1751:G:H2'	1:1:1752:U:O4'	2.16	0.46
1:1:1782:C:H1'	41:Lg:60:PRO:O	2.16	0.46
2:2:482:A:H2'	2:2:483:G:C8	2.51	0.46
2:2:701:A:H61	2:2:731:G:N2	2.12	0.46
2:2:1257:C:H2'	2:2:1258:G:C8	2.51	0.46
9:LA:118:GLU:C	9:LA:119:LYS:HD2	2.40	0.46
34:LZ:48:TYR:HE2	34:LZ:132:PRO:HA	1.81	0.46
54:SB:144:LYS:HB3	54:SB:206:PRO:HB2	1.97	0.46
56:SD:57:HIS:HB3	56:SD:60:GLU:OE1	2.14	0.46
71:SS:122:HIS:NE2	71:SS:126:ARG:HD3	2.31	0.46
72:ST:116:LYS:HA	72:ST:123:ARG:HG3	1.97	0.46
1:1:1547:C:H2'	1:1:1548:A:H8	1.81	0.46
1:1:1843:G:N1	1:1:1846:C:OP2	2.42	0.46
1:1:2051:G:HO2'	1:1:2052:G:H8	1.62	0.46
1:1:2407:C:H2'	1:1:2408:A:C8	2.50	0.46
1:1:3007:A:N3	10:LB:55:THR:OG1	2.46	0.46
2:2:278:G:H2'	2:2:279:C:C6	2.51	0.46
2:2:913:A:H61	67:SO:54:ARG:NH2	2.13	0.46
2:2:1389:U:OP1	70:SR:59:LYS:NZ	2.42	0.46
5:5:69:G:H2'	5:5:70:G:H8	1.81	0.46
8:C:649:VAL:HG11	8:C:687:ARG:HH21	1.81	0.46
8:C:720:LEU:HD23	8:C:720:LEU:O	2.15	0.46
9:LA:196:TRP:HB3	9:LA:197:PRO:HD3	1.97	0.46
11:LC:3:SER:O	11:LC:3:SER:OG	2.31	0.46
16:LH:7:GLU:OE1	16:LH:7:GLU:N	2.49	0.46
17:LI:110:ARG:CG	17:LI:111:LEU:H	2.23	0.46
24:LP:116:HIS:HB3	24:LP:149:ILE:HB	1.97	0.46
38:Ld:30:ARG:HD3	38:Ld:46:GLU:HG2	1.97	0.46
55:SC:245:ARG:HH11	55:SC:249:GLU:HB3	1.81	0.46
57:SE:42:MET:HB2	57:SE:109:PHE:HE2	1.80	0.46
62:SJ:83:VAL:HG23	62:SJ:84:LEU:CD1	2.46	0.46
65:SM:52:LYS:NZ	84:Sf:128:ALA:O	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
77:SY:63:LEU:HD23	77:SY:63:LEU:H	1.80	0.46
1:1:159:U:H2'	1:1:160:G:C8	2.51	0.46
1:1:248:A:H2'	1:1:249:G:H8	1.80	0.46
1:1:898:G:H5'	1:1:899:A:OP1	2.16	0.46
1:1:1660:G:H2'	1:1:1661:U:C6	2.50	0.46
2:2:81:C:H2'	2:2:82:G:O4'	2.16	0.46
2:2:326:G:H2'	2:2:327:G:H8	1.81	0.46
2:2:1533:C:H5'	2:2:1534:U:OP1	2.14	0.46
2:2:1620:C:H2'	2:2:1621:C:C6	2.51	0.46
6:A:54:TYR:CD1	6:A:55:PRO:HD2	2.51	0.46
8:C:140:GLN:O	8:C:144:VAL:HG22	2.16	0.46
8:C:385:SER:HB2	8:C:483:MET:HE1	1.98	0.46
15:LG:29:LEU:HG	34:LZ:52:ILE:HD11	1.96	0.46
55:SC:52:LEU:HD22	55:SC:251:TYR:CE2	2.45	0.46
58:SF:141:THR:HG22	58:SF:142:VAL:N	2.30	0.46
1:1:3266:A:H2'	1:1:3267:G:H8	1.80	0.46
2:2:1379:A:O4'	73:SU:54:ARG:NH1	2.49	0.46
2:2:1416:C:H5'	82:Sd:54:LYS:HZ3	1.81	0.46
5:5:66:A:H2'	5:5:67:U:C6	2.50	0.46
6:A:3:GLU:HB3	6:A:312:VAL:HG22	1.96	0.46
8:C:595:LEU:HD23	8:C:595:LEU:H	1.81	0.46
19:LK:23:GLY:HA2	19:LK:48:LYS:NZ	2.31	0.46
22:LN:192:LYS:HB3	22:LN:192:LYS:HE2	1.71	0.46
30:LV:12:LYS:NZ	30:LV:15:MET:HE2	2.30	0.46
32:LX:71:ASP:O	32:LX:75:ILE:HG12	2.16	0.46
33:LY:73:TYR:CE2	33:LY:76:LYS:HD2	2.47	0.46
54:SB:139:ALA:O	54:SB:213:ARG:NH1	2.49	0.46
60:SH:120:GLN:HG2	60:SH:121:LYS:N	2.27	0.46
61:SI:160:LEU:HD23	61:SI:164:PHE:HE1	1.81	0.46
76:SX:63:GLN:HB2	76:SX:64:PRO:HD3	1.97	0.46
1:1:289:A:H2'	1:1:290:A:N3	2.31	0.46
1:1:445:G:H2'	1:1:446:A:C8	2.50	0.46
1:1:515:G:C2	1:1:516:G:N7	2.84	0.46
1:1:584:C:H5'	13:LE:38:LYS:NZ	2.31	0.46
1:1:615:C:H2'	1:1:616:A:H8	1.81	0.46
1:1:2227:U:H2'	1:1:2228:C:H6	1.80	0.46
1:1:2460:C:H2'	1:1:2461:C:C6	2.51	0.46
1:1:2642:U:H2'	1:1:2643:C:C6	2.51	0.46
1:1:2730:U:O2'	1:1:2731:C:O4'	2.30	0.46
1:1:2844:C:O2'	1:1:2845:U:H5'	2.16	0.46
2:2:54:C:O2'	77:SY:112:LYS:NZ	2.37	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:909:U:H3	54:SB:7:LYS:HZ3	1.63	0.46
6:A:193:GLY:N	6:A:213:ASP:OD1	2.49	0.46
7:B:180:ALA:HA	7:B:183:LYS:HB2	1.97	0.46
19:LK:73:VAL:HG12	19:LK:74:VAL:N	2.31	0.46
37:Lc:46:LEU:HB2	37:Lc:93:MET:HG2	1.98	0.46
66:SN:4:LEU:HD11	66:SN:124:ARG:NH1	2.31	0.46
77:SY:30:ILE:HG21	77:SY:38:ILE:HG21	1.97	0.46
78:SZ:50:THR:HG22	78:SZ:89:ILE:HD12	1.97	0.46
2:2:622:C:H2'	2:2:623:U:C6	2.51	0.45
2:2:886:U:H2'	2:2:887:U:C6	2.52	0.45
4:4:75:G:OP1	46:Ll:31:THR:HG22	2.16	0.45
5:5:28:C:N3	5:5:43:G:N1	2.64	0.45
6:A:87:LEU:HB3	6:A:101:PHE:HB2	1.98	0.45
8:C:787:ARG:HD3	8:C:792:GLY:HA2	1.97	0.45
10:LB:24:ARG:HH21	10:LB:28:ARG:HB2	1.81	0.45
14:LF:9:GLN:O	14:LF:13:LEU:HD23	2.16	0.45
19:LK:21:GLU:HA	19:LK:51:ALA:HB1	1.97	0.45
43:Li:31:LEU:HD23	43:Li:32:LYS:O	2.15	0.45
44:Lj:29:ASN:O	44:Lj:32:LYS:NZ	2.49	0.45
53:SA:143:ASN:ND2	55:SC:68:SER:O	2.49	0.45
53:SA:198:TRP:CD1	53:SA:199:ASP:H	2.34	0.45
54:SB:26:ARG:O	54:SB:50:ARG:N	2.47	0.45
54:SB:205:TYR:CG	54:SB:206:PRO:HD2	2.50	0.45
56:SD:115:GLY:O	56:SD:116:LEU:HG	2.16	0.45
1:1:147:A:P	22:LN:147:ARG:HH22	2.40	0.45
1:1:1549:C:H3'	1:1:1550:U:H3'	1.99	0.45
2:2:705:G:O6	2:2:728:G:N1	2.49	0.45
2:2:904:A:H2'	2:2:905:A:H8	1.81	0.45
2:2:1010:U:H4'	9:LA:247:ARG:HB3	1.97	0.45
2:2:1175:G:H2'	2:2:1176:G:C8	2.52	0.45
2:2:1377:U:OP1	69:SQ:12:LYS:NZ	2.31	0.45
2:2:1500:G:OP1	72:ST:97:SER:OG	2.32	0.45
2:2:1521:A:H2'	2:2:1522:A:O4'	2.15	0.45
6:A:114:SER:HA	6:A:156:PHE:CD2	2.51	0.45
6:A:296:GLN:N	6:A:296:GLN:OE1	2.49	0.45
8:C:652:THR:HG22	8:C:691:LEU:HA	1.98	0.45
19:LK:88:PRO:HB2	19:LK:90:ARG:HH22	1.81	0.45
34:LZ:110:LYS:HA	34:LZ:113:VAL:HG12	1.97	0.45
52:Ls:12:PHE:O	52:Ls:16:LYS:HG2	2.17	0.45
56:SD:32:LEU:HB3	56:SD:35:GLU:OE2	2.17	0.45
57:SE:66:MET:HA	57:SE:78:THR:OG1	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:SI:37:ARG:HD2	61:SI:59:ARG:HH12	1.80	0.45
66:SN:4:LEU:HG	66:SN:5:HIS:CD2	2.51	0.45
1:1:934:A:H4'	1:1:950:G:N2	2.32	0.45
1:1:1013:G:H2'	1:1:1014:C:C6	2.51	0.45
2:2:417:A:P	59:SG:74:ARG:HH22	2.39	0.45
2:2:1250:U:H4'	84:Sf:143:ARG:HE	1.81	0.45
8:C:630:THR:O	8:C:634:LYS:HG2	2.17	0.45
10:LB:284:TYR:OH	10:LB:326:LYS:HD2	2.17	0.45
14:LF:226:LYS:HE3	14:LF:230:GLU:OE2	2.16	0.45
47:Lm:78:ILE:HB	47:Lm:83:LYS:HD3	1.97	0.45
53:SA:170:ARG:HH22	53:SA:206:PHE:HB3	1.81	0.45
55:SC:165:LYS:HB2	55:SC:178:ILE:HG22	1.99	0.45
56:SD:23:GLU:HG3	63:SK:59:TRP:NE1	2.31	0.45
61:SI:110:ARG:HE	61:SI:121:LEU:HD21	1.81	0.45
61:SI:201:HIS:O	61:SI:202:LYS:HE2	2.15	0.45
68:SP:82:GLU:HG3	68:SP:83:LEU:H	1.81	0.45
1:1:22:G:OP2	4:4:36:G:N2	2.49	0.45
1:1:2621:G:H2'	1:1:2622:G:C8	2.43	0.45
2:2:68:A:OP2	59:SG:174:LYS:NZ	2.49	0.45
2:2:148:G:H21	2:2:160:G:H22	1.61	0.45
2:2:258:C:N4	61:SI:182:ARG:HH21	2.14	0.45
2:2:1402:A:OP1	58:SF:70:ARG:NH1	2.50	0.45
12:LD:104:LEU:CB	12:LD:250:ILE:HD11	2.46	0.45
16:LH:54:LYS:HE3	21:LM:3:GLU:OE2	2.17	0.45
18:LJ:47:VAL:HG22	18:LJ:69:HIS:O	2.16	0.45
26:LR:160:ASP:OD1	26:LR:161:ALA:N	2.49	0.45
47:Lm:79:GLU:HG2	47:Lm:80:PRO:HD2	1.98	0.45
55:SC:188:ALA:HB1	55:SC:192:VAL:HG13	1.98	0.45
59:SG:20:ASP:HB3	59:SG:23:LYS:HD3	1.98	0.45
62:SJ:75:ILE:HG21	62:SJ:89:MET:HG3	1.97	0.45
66:SN:49:GLN:O	66:SN:52:VAL:HG12	2.15	0.45
68:SP:59:ARG:O	68:SP:62:LEU:HG	2.17	0.45
75:SW:47:ILE:HD11	75:SW:63:VAL:HG21	1.98	0.45
1:1:3107:G:H2'	1:1:3108:A:C8	2.51	0.45
2:2:288:G:H2'	2:2:289:U:C5	2.51	0.45
2:2:403:U:H2'	2:2:404:A:C8	2.51	0.45
2:2:920:G:H2'	2:2:921:A:C8	2.50	0.45
2:2:1084:A:H2'	2:2:1085:A:C8	2.51	0.45
2:2:1587:C:H2'	2:2:1588:A:C8	2.51	0.45
6:A:272:PRO:HG3	6:A:302:TYR:OH	2.17	0.45
7:B:45:LYS:HG2	7:B:47:HIS:H	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:C:302:LEU:HG	8:C:307:LEU:HB2	1.97	0.45
8:C:568:THR:HA	8:C:686:ILE:HD11	1.98	0.45
11:LC:144:SER:O	11:LC:144:SER:OG	2.35	0.45
35:La:126:ARG:HB3	35:La:148:VAL:HG11	1.99	0.45
52:Ls:27:VAL:HA	52:Ls:86:PHE:HA	1.98	0.45
56:SD:179:LEU:HD23	56:SD:179:LEU:H	1.81	0.45
59:SG:169:LYS:HZ2	59:SG:170:LYS:HG2	1.81	0.45
63:SK:41:ILE:O	63:SK:44:LEU:HG	2.16	0.45
64:SL:144:VAL:O	64:SL:145:LEU:HD23	2.16	0.45
72:ST:111:ILE:HG22	72:ST:111:ILE:O	2.17	0.45
84:Sf:97:LYS:HA	84:Sf:97:LYS:HD2	1.76	0.45
84:Sf:134:SER:HA	84:Sf:139:GLN:OE1	2.17	0.45
1:1:644:A:H2'	1:1:645:A:H8	1.82	0.45
1:1:2059:A:H2'	1:1:2060:C:C6	2.51	0.45
1:1:2727:U:H2'	1:1:2728:A:H8	1.81	0.45
1:1:3220:G:O2'	1:1:3221:A:H5'	2.17	0.45
2:2:209:G:OP1	64:SL:31:ARG:NH2	2.49	0.45
2:2:687:C:HO2'	2:2:688:U:P	2.40	0.45
2:2:1254:U:N3	63:SK:3:ILE:HG12	2.31	0.45
2:2:1501:A:H5'	72:ST:42:ASN:ND2	2.31	0.45
5:5:3:C:O2'	5:5:4:G:O4'	2.30	0.45
8:C:373:ASP:O	8:C:374:CYS:SG	2.74	0.45
8:C:582:PRO:HG2	8:C:706:GLN:HG3	1.98	0.45
8:C:711:ALA:O	8:C:715:LEU:HB2	2.16	0.45
8:C:765:THR:CG2	8:C:766:PRO:HD2	2.46	0.45
12:LD:219:GLU:C	12:LD:223:LYS:HZ2	2.24	0.45
13:LE:84:THR:HB	13:LE:94:LEU:HD23	1.99	0.45
15:LG:31:GLU:HG2	34:LZ:127:ARG:HH12	1.82	0.45
44:Lj:39:TYR:CD1	44:Lj:40:PRO:HA	2.51	0.45
55:SC:245:ARG:NH1	55:SC:249:GLU:HB3	2.32	0.45
57:SE:59:ARG:O	57:SE:62:LYS:HG2	2.17	0.45
58:SF:200:LYS:O	58:SF:203:GLU:HG3	2.15	0.45
59:SG:193:ARG:NH1	59:SG:193:ARG:O	2.50	0.45
62:SJ:52:ARG:O	62:SJ:56:ILE:HD12	2.17	0.45
66:SN:111:SER:HA	66:SN:114:ARG:HB3	1.99	0.45
69:SQ:106:LYS:O	69:SQ:110:ILE:HG12	2.16	0.45
75:SW:77:PRO:HG2	75:SW:79:TYR:CZ	2.51	0.45
1:1:1879:G:O2'	1:1:2297:U:O4	2.28	0.45
1:1:2627:U:H2'	1:1:2628:G:C8	2.52	0.45
1:1:2673:G:H8	1:1:2710:G:H2'	1.82	0.45
1:1:3149:C:H2'	1:1:3150:C:O4'	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:121:U:O3'	57:SE:77:ARG:NH1	2.47	0.45
6:A:172:LYS:HE2	6:A:192:THR:O	2.17	0.45
8:C:816:THR:HG23	8:C:819:GLY:H	1.82	0.45
12:LD:200:LYS:HG3	12:LD:205:GLY:HA3	1.97	0.45
20:LL:64:LYS:HE2	20:LL:65:TYR:CE1	2.51	0.45
40:Lf:49:LYS:NZ	40:Lf:106:PRO:O	2.34	0.45
53:SA:143:ASN:OD1	74:SV:29:HIS:HA	2.17	0.45
54:SB:67:GLU:HG2	54:SB:67:GLU:O	2.15	0.45
61:SI:42:ARG:HG3	61:SI:58:LEU:HB2	1.99	0.45
64:SL:30:THR:HA	64:SL:37:ARG:HH22	1.80	0.45
80:Sb:31:PHE:O	80:Sb:48:SER:OG	2.17	0.45
1:1:565:C:H2'	1:1:566:C:C6	2.51	0.45
1:1:991:A:H2'	1:1:992:G:C8	2.52	0.45
1:1:1136:A:O2'	1:1:1137:A:H5'	2.16	0.45
1:1:1476:G:OP2	1:1:1476:G:N2	2.48	0.45
1:1:2065:U:H2'	1:1:2066:U:C6	2.51	0.45
1:1:2100:U:OP2	1:1:2105:A:N6	2.40	0.45
1:1:2497:G:H2'	1:1:2498:A:C8	2.52	0.45
2:2:184:G:H4'	2:2:185:A:OP1	2.17	0.45
2:2:196:G:H2'	2:2:197:A:C8	2.52	0.45
2:2:304:G:OP1	64:SL:108:ARG:NH1	2.43	0.45
12:LD:69:ILE:H	12:LD:69:ILE:HD12	1.82	0.45
31:LW:130:SER:HB3	31:LW:133:VAL:HG23	1.99	0.45
48:Lr:1:MET:O	48:Lr:6:ARG:NH1	2.49	0.45
52:Ls:25:ILE:HG12	52:Ls:88:PHE:CD1	2.52	0.45
57:SE:64:ILE:HD11	77:SY:21:LEU:HD11	1.97	0.45
60:SH:57:VAL:HG12	60:SH:62:LYS:HA	1.98	0.45
65:SM:129:GLU:OE2	65:SM:131:GLN:HG3	2.17	0.45
66:SN:103:GLU:OE2	66:SN:104:ARG:HG2	2.16	0.45
1:1:118:U:O4	15:LG:148:ASN:ND2	2.47	0.45
1:1:559:G:O2'	1:1:560:U:H3'	2.17	0.45
1:1:2181:G:H2'	1:1:2182:A:H8	1.82	0.45
2:2:187:U:P	2:2:187:U:O4'	2.74	0.45
2:2:483:G:H22	2:2:498:U:H3	1.65	0.45
2:2:930:A:OP2	54:SB:155:TYR:OH	2.31	0.45
2:2:1094:U:H4'	2:2:1095:U:O5'	2.17	0.45
2:2:1207:C:N3	2:2:1450:G:N1	2.65	0.45
7:B:189:GLU:HG3	7:B:190:ASN:H	1.82	0.45
9:LA:202:VAL:CG1	9:LA:217:GLN:HB3	2.46	0.45
12:LD:116:ASP:OD1	12:LD:117:LYS:N	2.49	0.45
22:LN:181:ASN:OD1	22:LN:184:ARG:NH2	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:La:75:ILE:HG22	35:La:115:LYS:H	1.81	0.45
43:Li:42:GLN:HG3	43:Li:47:GLN:OE1	2.16	0.45
50:Lp:73:THR:HG23	50:Lp:76:ALA:H	1.82	0.45
52:Ls:57:THR:HG22	52:Ls:60:ARG:HD2	1.99	0.45
53:SA:201:MET:HG2	53:SA:202:PRO:HD2	1.99	0.45
57:SE:10:LYS:O	57:SE:13:SER:OG	2.26	0.45
61:SI:125:ARG:NE	61:SI:131:GLN:OE1	2.50	0.45
63:SK:82:ALA:O	63:SK:84:ILE:HG12	2.17	0.45
77:SY:115:LYS:O	77:SY:119:LYS:HG3	2.16	0.45
1:1:2615:A:C8	1:1:2617:G:C8	3.05	0.45
1:1:2642:U:H1'	18:LJ:129:TYR:CE2	2.51	0.45
2:2:403:U:H2'	2:2:404:A:H8	1.80	0.45
2:2:835:G:H2'	2:2:836:G:C8	2.51	0.45
2:2:848:G:OP1	26:LR:165:ARG:NH2	2.50	0.45
2:2:1606:G:H5''	58:SF:94:LYS:HZ3	1.82	0.45
5:5:60:C:H2'	5:5:61:C:C6	2.52	0.45
6:A:222:ASN:OD1	6:A:223:GLU:N	2.50	0.45
7:B:70:ALA:HB3	68:SP:135:LYS:HG3	1.99	0.45
8:C:591:VAL:HG23	8:C:689:ASN:HB2	1.99	0.45
19:LK:114:ARG:HH12	19:LK:129:VAL:C	2.24	0.45
19:LK:130:LYS:NZ	19:LK:157:ALA:HB3	2.31	0.45
33:LY:75:LEU:HD22	46:LI:31:THR:HG21	1.99	0.45
52:Ls:51:VAL:HG13	52:Ls:87:VAL:HG22	1.97	0.45
54:SB:136:ARG:HE	54:SB:218:LEU:HD21	1.82	0.45
55:SC:231:GLY:HA3	74:SV:25:LYS:NZ	2.28	0.45
59:SG:2:LYS:HB2	59:SG:108:VAL:HG22	1.98	0.45
60:SH:80:GLN:OE1	60:SH:98:ILE:HD13	2.17	0.45
60:SH:92:SER:OG	60:SH:93:ASP:N	2.50	0.45
67:SO:30:ALA:HA	67:SO:43:VAL:HA	1.99	0.45
69:SQ:100:HIS:O	69:SQ:104:LEU:HD12	2.17	0.45
84:Sf:107:LYS:HG3	84:Sf:117:LEU:HD21	1.98	0.45
84:Sf:133:ALA:O	84:Sf:139:GLN:HG3	2.17	0.45
1:1:643:C:H2'	1:1:644:A:C8	2.49	0.44
1:1:1480:C:O2'	1:1:1582:A:N3	2.49	0.44
1:1:1643:C:H2'	1:1:1644:G:H8	1.81	0.44
2:2:557:U:H2'	2:2:558:G:H8	1.82	0.44
2:2:815:A:O2'	60:SH:119:LYS:HD3	2.17	0.44
2:2:883:G:H2'	2:2:884:U:C6	2.52	0.44
2:2:893:G:H1'	67:SO:49:ARG:HA	1.99	0.44
2:2:1076:U:H2'	2:2:1077:U:C6	2.52	0.44
2:2:1747:G:H2'	2:2:1748:U:C6	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:1780:C:N4	48:Ln:5:TRP:CH2	2.85	0.44
5:5:51:G:O2'	5:5:52:G:H5'	2.17	0.44
5:5:52:G:C2	5:5:61:C:O2	2.70	0.44
31:LW:82:SER:O	31:LW:86:GLN:HG3	2.17	0.44
33:LY:62:HIS:HB3	33:LY:65:LYS:HD2	1.98	0.44
54:SB:6:ASN:O	54:SB:7:LYS:HB2	2.17	0.44
55:SC:60:SER:OG	55:SC:62:GLU:OE1	2.26	0.44
56:SD:207:LEU:O	56:SD:210:VAL:HG12	2.18	0.44
59:SG:159:ARG:HB3	59:SG:173:THR:HG22	1.99	0.44
60:SH:98:ILE:O	60:SH:98:ILE:HG13	2.16	0.44
61:SI:26:ALA:O	61:SI:29:LEU:HD23	2.17	0.44
73:SU:65:ARG:HG3	73:SU:76:TRP:CZ3	2.52	0.44
1:1:9:C:H2'	1:1:10:U:C6	2.52	0.44
1:1:514:A:C5	1:1:515:G:C8	3.05	0.44
1:1:535:U:H2'	1:1:536:C:C6	2.52	0.44
1:1:799:A:N3	44:Lj:11:ARG:HB3	2.32	0.44
1:1:1273:U:H2'	1:1:1274:A:H8	1.82	0.44
1:1:1309:A:H2'	1:1:1310:C:O4'	2.18	0.44
1:1:1570:G:C2	1:1:1571:G:C8	3.05	0.44
1:1:2065:U:H2'	1:1:2066:U:H6	1.83	0.44
1:1:2753:G:O2'	1:1:2754:U:OP2	2.34	0.44
1:1:3098:G:OP1	10:LB:20:LYS:NZ	2.50	0.44
2:2:635:C:O2'	60:SH:107:LYS:NZ	2.34	0.44
2:2:688:U:H5''	2:2:689:U:C5'	2.47	0.44
2:2:784:U:H2'	2:2:785:G:H8	1.81	0.44
2:2:1233:A:H1'	84:Sf:138:ARG:NE	2.33	0.44
2:2:1434:G:H2'	2:2:1435:C:C6	2.53	0.44
2:2:1437:C:H2'	2:2:1438:U:H6	1.82	0.44
2:2:1699:C:H2'	2:2:1700:G:H8	1.82	0.44
7:B:62:GLU:HB2	71:SS:120:ARG:NH1	2.32	0.44
8:C:408:ARG:HD2	8:C:409:SER:O	2.17	0.44
10:LB:10:ARG:NH2	10:LB:264:THR:O	2.50	0.44
13:LE:100:ARG:HA	13:LE:100:ARG:HD3	1.82	0.44
16:LH:114:ASN:HA	16:LH:117:ILE:HG22	1.99	0.44
19:LK:111:GLU:O	19:LK:114:ARG:HB2	2.18	0.44
23:LO:159:GLU:OE1	23:LO:162:ARG:NH1	2.50	0.44
29:LU:52:ARG:CZ	29:LU:55:ASN:HD22	2.29	0.44
48:Ln:12:ARG:HG2	48:Ln:15:ARG:HH22	1.82	0.44
58:SF:136:ILE:CD1	58:SF:145:GLN:HE22	2.29	0.44
62:SJ:85:ASP:OD1	62:SJ:86:GLU:N	2.51	0.44
65:SM:26:VAL:HG12	65:SM:27:LEU:HD22	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
68:SP:124:LEU:HD23	68:SP:124:LEU:H	1.83	0.44
71:SS:61:LEU:HD12	71:SS:65:GLU:HG3	2.00	0.44
71:SS:125:LEU:HB3	71:SS:129:TRP:CZ3	2.52	0.44
73:SU:65:ARG:NH2	73:SU:74:LYS:HG3	2.32	0.44
1:1:706:G:OP2	1:1:706:G:N2	2.43	0.44
1:1:750:C:N4	1:1:751:G:O6	2.50	0.44
1:1:804:G:H2'	1:1:805:C:H6	1.82	0.44
1:1:2656:A:H2'	1:1:2657:G:C8	2.51	0.44
2:2:185:A:H2'	2:2:186:C:O4'	2.17	0.44
2:2:508:A:H3'	62:SJ:171:ARG:CZ	2.47	0.44
2:2:1468:C:O2	2:2:1530:G:N2	2.51	0.44
2:2:1541:A:H5''	71:SS:133:VAL:HG12	1.98	0.44
5:5:58:C:H2'	5:5:59:U:H6	1.82	0.44
8:C:158:ILE:HD12	8:C:212:ALA:O	2.18	0.44
14:LF:88:LYS:HE2	14:LF:197:VAL:HG21	1.97	0.44
19:LK:143:VAL:HG22	19:LK:144:ASP:H	1.82	0.44
24:LP:36:ILE:HG13	24:LP:36:ILE:O	2.18	0.44
37:Lc:101:SER:OG	37:Lc:102:ASP:N	2.50	0.44
56:SD:8:ILE:HG23	56:SD:9:SER:N	2.32	0.44
56:SD:17:ASP:O	56:SD:20:PHE:HB3	2.17	0.44
60:SH:23:GLU:HA	60:SH:26:ILE:HD13	1.97	0.44
65:SM:129:GLU:OE2	65:SM:132:GLU:N	2.41	0.44
77:SY:109:GLN:O	77:SY:113:GLN:HG2	2.17	0.44
1:1:133:C:H1'	1:1:134:G:OP2	2.17	0.44
1:1:575:G:H2'	1:1:576:A:C8	2.48	0.44
1:1:2064:C:H2'	1:1:2065:U:C6	2.53	0.44
1:1:2211:C:H5''	1:1:2212:G:OP1	2.16	0.44
1:1:2389:U:H2'	1:1:2390:U:C6	2.53	0.44
1:1:3329:C:O2'	1:1:3330:C:H5'	2.18	0.44
2:2:114:G:C8	64:SL:134:ARG:HG3	2.53	0.44
2:2:226:C:H2'	2:2:227:U:O4'	2.18	0.44
2:2:450:C:O2	2:2:450:C:H2'	2.17	0.44
2:2:729:G:H2'	2:2:730:G:C8	2.53	0.44
2:2:892:U:H2'	2:2:893:G:C8	2.52	0.44
2:2:1238:G:C4	68:SP:87:HIS:HD2	2.35	0.44
2:2:1416:C:P	82:Sd:54:LYS:HZ3	2.40	0.44
2:2:1538:G:H5''	72:ST:87:GLY:C	2.43	0.44
8:C:836:PRO:HD2	8:C:837:GLY:H	1.82	0.44
13:LE:76:LEU:HB2	13:LE:80:VAL:HG23	2.00	0.44
13:LE:200:PHE:HA	21:LM:114:ASP:HB2	1.98	0.44
20:LL:54:LEU:HD22	20:LL:119:TYR:CD2	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:LU:37:SER:O	29:LU:40:GLU:HG2	2.16	0.44
35:La:15:VAL:O	35:La:16:SER:OG	2.29	0.44
39:Le:35:LYS:HE3	39:Le:53:MET:HE1	1.99	0.44
59:SG:58:LYS:HA	59:SG:107:SER:HB2	1.99	0.44
71:SS:16:ARG:HH21	71:SS:19:ASN:HA	1.81	0.44
71:SS:112:ASP:HA	71:SS:115:ARG:NH1	2.31	0.44
79:Sa:43:ASN:ND2	79:Sa:66:LYS:HE2	2.33	0.44
1:1:615:C:H2'	1:1:616:A:C8	2.52	0.44
1:1:1266:C:H2'	1:1:1267:C:C6	2.53	0.44
1:1:1561:G:H3'	1:1:1562:U:O4'	2.17	0.44
1:1:2466:G:H2'	1:1:2467:U:H6	1.82	0.44
2:2:381:G:H2'	2:2:382:A:H8	1.83	0.44
2:2:428:C:H2'	2:2:429:G:C8	2.53	0.44
2:2:500:G:H2'	2:2:501:U:C6	2.53	0.44
2:2:781:G:H2'	2:2:782:C:C6	2.53	0.44
2:2:1170:C:H2'	2:2:1171:C:H6	1.82	0.44
2:2:1224:A:H4'	2:2:1225:G:H5'	1.98	0.44
2:2:1361:G:H2'	2:2:1362:C:C6	2.51	0.44
6:A:64:HIS:CG	6:A:65:ILE:H	2.36	0.44
6:A:70:VAL:HG13	6:A:113:PHE:HE2	1.80	0.44
7:B:144:THR:HA	7:B:147:LYS:HE2	1.99	0.44
8:C:371:ILE:H	8:C:371:ILE:HD12	1.82	0.44
8:C:832:LYS:HG3	8:C:833:VAL:N	2.32	0.44
24:LP:7:THR:O	24:LP:7:THR:HG22	2.18	0.44
26:LR:28:GLU:CG	26:LR:49:LEU:HD13	2.47	0.44
30:LV:19:LEU:O	30:LV:19:LEU:HD12	2.18	0.44
54:SB:64:ARG:O	54:SB:88:VAL:HG12	2.18	0.44
56:SD:175:THR:O	56:SD:176:ARG:HD2	2.17	0.44
59:SG:136:LYS:O	59:SG:178:ILE:HD12	2.18	0.44
61:SI:37:ARG:NH1	61:SI:93:THR:OG1	2.49	0.44
61:SI:116:HIS:C	61:SI:117:TYR:HD2	2.26	0.44
62:SJ:82:GLY:O	62:SJ:105:ARG:HG2	2.17	0.44
62:SJ:156:PHE:CE2	62:SJ:162:PHE:HB3	2.53	0.44
77:SY:60:VAL:HA	77:SY:76:ALA:HA	2.00	0.44
81:Sc:60:SER:O	81:Sc:60:SER:OG	2.36	0.44
1:1:961:C:H3'	1:1:962:U:H4'	1.98	0.44
1:1:2369:C:H2'	1:1:2370:C:C6	2.52	0.44
1:1:3070:G:O2'	16:LH:107:THR:HG22	2.18	0.44
2:2:159:A:H2'	2:2:160:G:C8	2.52	0.44
2:2:219:C:H2'	2:2:220:A:C8	2.53	0.44
2:2:231:G:O2'	2:2:232:G:OP1	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:509:A:OP2	62:SJ:171:ARG:NH2	2.51	0.44
2:2:884:U:O2	67:SO:136:SER:HB3	2.17	0.44
8:C:321:LEU:O	8:C:325:VAL:HG12	2.18	0.44
8:C:813:ASP:O	8:C:819:GLY:HA3	2.18	0.44
10:LB:233:ARG:HA	10:LB:271:MET:HE2	1.99	0.44
11:LC:137:MET:HE2	11:LC:143:VAL:HG23	2.00	0.44
25:LQ:205:ARG:O	25:LQ:212:LYS:HG3	2.18	0.44
34:LZ:72:LYS:HD3	34:LZ:74:ILE:HD11	1.99	0.44
58:SF:160:ALA:O	58:SF:164:THR:HG23	2.17	0.44
61:SI:140:LYS:HA	61:SI:143:GLU:OE1	2.17	0.44
67:SO:71:TYR:O	67:SO:74:MET:HG3	2.18	0.44
71:SS:111:GLU:HA	71:SS:114:GLU:OE2	2.18	0.44
72:ST:54:TRP:CZ2	72:ST:104:ILE:HG22	2.53	0.44
79:Sa:43:ASN:HD22	79:Sa:66:LYS:HB3	1.81	0.44
1:1:254:U:H2'	1:1:255:U:O4'	2.18	0.44
1:1:559:G:H3'	1:1:559:G:OP2	2.17	0.44
1:1:1676:A:H2'	1:1:1677:A:H8	1.82	0.44
1:1:2069:A:H2'	1:1:2070:A:C8	2.51	0.44
1:1:2460:C:H2'	1:1:2461:C:H6	1.83	0.44
1:1:2461:C:H2'	1:1:2462:U:C6	2.52	0.44
1:1:3009:U:C2	1:1:3010:G:C8	3.05	0.44
2:2:189:C:H5'	2:2:190:G:C5	2.53	0.44
2:2:404:A:H1'	2:2:1667:A:H2	1.81	0.44
2:2:417:A:OP2	59:SG:74:ARG:NH2	2.38	0.44
2:2:1169:G:H2'	2:2:1170:C:C6	2.53	0.44
2:2:1669:G:H2'	2:2:1670:C:C6	2.53	0.44
4:4:50:C:H2'	46:Ll:26:TRP:HH2	1.82	0.44
11:LC:32:ARG:NH1	25:LQ:51:ASN:OD1	2.51	0.44
16:LH:126:LYS:NZ	16:LH:222:GLU:OE2	2.35	0.44
17:LI:201:THR:O	17:LI:203:HIS:ND1	2.41	0.44
20:LL:201:ARG:O	20:LL:204:GLU:HG3	2.17	0.44
33:LY:37:GLU:O	33:LY:40:GLU:HG3	2.18	0.44
35:La:85:ASP:O	35:La:88:GLU:HG3	2.17	0.44
37:Lc:77:ASN:OD1	37:Lc:78:ILE:N	2.50	0.44
38:Ld:55:MET:HE3	38:Ld:88:ARG:HB2	2.00	0.44
59:SG:33:GLY:C	59:SG:51:ARG:HE	2.25	0.44
61:SI:87:ASN:OD1	61:SI:90:LEU:HD13	2.17	0.44
69:SQ:23:VAL:O	69:SQ:64:ASP:N	2.34	0.44
70:SR:102:LEU:O	70:SR:123:ASN:N	2.50	0.44
72:ST:86:ARG:NH2	72:ST:90:PRO:O	2.43	0.44
1:1:292:G:C6	43:Li:39:LYS:HB3	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1560:U:H1'	1:1:1561:G:C4'	2.46	0.44
1:1:2045:G:H2'	1:1:2046:C:C6	2.53	0.44
2:2:12:U:H2'	2:2:13:U:C6	2.53	0.44
2:2:481:C:H2'	2:2:482:A:C8	2.53	0.44
2:2:1328:A:H5''	70:SR:45:ARG:NH2	2.32	0.44
2:2:1730:U:H2'	2:2:1731:C:C6	2.52	0.44
3:3:23:A:H2'	3:3:24:A:C8	2.52	0.44
6:A:177:TRP:NE1	6:A:184:LEU:HB2	2.32	0.44
8:C:84:GLU:HG2	8:C:85:GLU:N	2.33	0.44
11:LC:134:PRO:HB3	51:Lq:46:PHE:O	2.17	0.44
15:LG:229:VAL:HA	15:LG:232:THR:HG22	1.99	0.44
16:LH:68:ARG:HB2	16:LH:119:VAL:O	2.17	0.44
35:La:104:LEU:HD12	35:La:127:ALA:HB2	2.00	0.44
55:SC:57:LYS:HD2	55:SC:251:TYR:CE2	2.53	0.44
58:SF:38:ILE:HG13	58:SF:39:GLU:N	2.32	0.44
59:SG:10:ASN:ND2	59:SG:124:LEU:O	2.51	0.44
59:SG:139:THR:OG1	59:SG:143:ARG:NH2	2.51	0.44
61:SI:35:ASN:O	61:SI:58:LEU:HA	2.18	0.44
61:SI:175:SER:HB3	61:SI:184:ASP:H	1.81	0.44
62:SJ:61:ASP:OD1	62:SJ:62:GLU:N	2.50	0.44
62:SJ:105:ARG:HD2	62:SJ:105:ARG:HA	1.76	0.44
68:SP:39:ASP:O	68:SP:42:ARG:HG2	2.18	0.44
75:SW:111:MET:CE	75:SW:115:GLU:HG3	2.48	0.44
80:Sb:56:CYS:SG	80:Sb:63:LEU:HD11	2.57	0.44
1:1:235:C:H2'	1:1:236:A:O4'	2.18	0.44
1:1:290:A:H4'	1:1:291:U:OP1	2.17	0.44
1:1:292:G:C8	43:Li:40:GLY:HA3	2.53	0.44
1:1:1638:G:H2'	1:1:1639:A:H8	1.83	0.44
1:1:2063:A:H2'	1:1:2064:C:C6	2.52	0.44
2:2:224:C:H2'	2:2:225:C:C6	2.53	0.44
2:2:257:U:H3'	2:2:258:C:H5'	1.99	0.44
2:2:643:U:H2'	2:2:644:A:C8	2.50	0.44
2:2:948:C:H2'	2:2:949:A:C8	2.53	0.44
2:2:1711:G:H2'	2:2:1712:C:H5'	1.99	0.44
6:A:99:ARG:HD3	6:A:100:ARG:H	1.82	0.44
7:B:118:GLN:HE22	56:SD:146:ARG:HD2	1.83	0.44
7:B:189:GLU:HG3	7:B:190:ASN:N	2.33	0.44
8:C:579:SER:OG	8:C:713:ARG:NH1	2.51	0.44
8:C:671:TRP:HD1	8:C:674:ARG:NH1	2.16	0.44
16:LH:200:ILE:O	16:LH:203:ILE:HG22	2.18	0.44
34:LZ:82:THR:HG22	41:Lg:94:PHE:CZ	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:SB:55:LYS:HA	54:SB:55:LYS:HD3	1.78	0.44
55:SC:57:LYS:HE2	55:SC:57:LYS:HB2	1.87	0.44
58:SF:57:ILE:CD1	69:SQ:46:ALA:HB3	2.48	0.44
58:SF:205:GLU:CD	58:SF:205:GLU:H	2.26	0.44
60:SH:134:ALA:HA	60:SH:137:THR:HG22	1.99	0.44
61:SI:78:ILE:HD11	61:SI:102:VAL:HG11	1.99	0.44
61:SI:98:LYS:HG2	61:SI:175:SER:O	2.18	0.44
77:SY:38:ILE:HD12	77:SY:43:LEU:HD21	2.00	0.44
80:Sb:36:LYS:HB3	80:Sb:78:SER:HB3	2.00	0.44
1:1:2051:G:O2'	1:1:2052:G:H5'	2.18	0.43
1:1:3298:U:HO2'	1:1:3299:U:P	2.41	0.43
2:2:235:U:H6	2:2:235:U:H2'	1.66	0.43
2:2:825:C:H2'	2:2:826:U:C6	2.52	0.43
2:2:1689:A:H2	2:2:1704:A:N1	2.15	0.43
2:2:1733:G:H2'	2:2:1734:U:C6	2.52	0.43
6:A:149:GLU:N	6:A:149:GLU:OE1	2.51	0.43
8:C:547:LEU:HA	8:C:551:HIS:HB3	2.00	0.43
8:C:580:LYS:HD2	8:C:585:HIS:ND1	2.33	0.43
9:LA:118:GLU:O	9:LA:119:LYS:HD2	2.18	0.43
11:LC:143:VAL:O	11:LC:146:VAL:HG12	2.18	0.43
11:LC:219:GLY:C	11:LC:221:GLU:H	2.26	0.43
12:LD:79:TYR:O	12:LD:82:GLU:HG2	2.18	0.43
19:LK:143:VAL:HG22	19:LK:144:ASP:N	2.33	0.43
21:LM:20:LEU:HB3	21:LM:62:ALA:HB1	2.00	0.43
29:LU:25:ALA:C	29:LU:28:PRO:HD2	2.43	0.43
55:SC:170:CYS:SG	55:SC:220:LYS:HE3	2.58	0.43
56:SD:83:PRO:O	56:SD:86:SER:OG	2.26	0.43
57:SE:131:LEU:HD23	57:SE:131:LEU:H	1.83	0.43
58:SF:96:MET:O	58:SF:100:ILE:HG12	2.18	0.43
59:SG:31:ARG:NH1	59:SG:101:ILE:HD11	2.33	0.43
68:SP:91:MET:HB2	68:SP:124:LEU:HD22	2.00	0.43
79:Sa:42:ARG:NH1	79:Sa:43:ASN:HB2	2.33	0.43
1:1:2223:U:H2'	1:1:2224:G:C8	2.52	0.43
1:1:2574:G:H2'	1:1:2575:C:C6	2.53	0.43
1:1:3194:G:H2'	1:1:3195:U:C6	2.54	0.43
2:2:407:A:H2'	2:2:408:C:H6	1.83	0.43
2:2:1129:A:H2'	2:2:1130:A:H8	1.82	0.43
2:2:1487:C:H4'	2:2:1488:U:O5'	2.18	0.43
2:2:1503:G:H2'	2:2:1504:C:H6	1.82	0.43
3:3:86:C:O2'	27:LS:119:ARG:NH1	2.50	0.43
8:C:409:SER:HA	8:C:433:ILE:HG13	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:LA:116:VAL:HG21	9:LA:134:VAL:HG21	1.99	0.43
12:LD:55:PHE:HE2	12:LD:162:VAL:HG12	1.83	0.43
12:LD:99:TYR:OH	12:LD:171:ASP:OD2	2.26	0.43
17:LI:68:ALA:HB1	17:LI:155:CYS:SG	2.58	0.43
19:LK:41:LYS:HD2	19:LK:41:LYS:O	2.17	0.43
43:Li:63:GLU:O	43:Li:67:ILE:HG12	2.17	0.43
53:SA:41:TRP:HD1	70:SR:107:GLU:OE2	2.00	0.43
54:SB:103:LEU:HD22	54:SB:214:LYS:HA	2.00	0.43
58:SF:195:SER:C	58:SF:199:LYS:HZ2	2.26	0.43
69:SQ:108:GLU:OE2	69:SQ:111:GLN:NE2	2.51	0.43
71:SS:138:THR:HA	71:SS:141:THR:OG1	2.17	0.43
74:SV:4:ASP:OD1	74:SV:5:ARG:N	2.50	0.43
1:1:431:A:H2'	1:1:432:C:C6	2.54	0.43
1:1:842:G:H8	9:LA:183:SER:OG	2.01	0.43
1:1:1595:C:H2'	1:1:1596:U:H6	1.81	0.43
1:1:2409:U:H2'	1:1:2410:A:C8	2.52	0.43
1:1:2493:G:C2	1:1:2494:C:C2	3.07	0.43
2:2:404:A:H2'	2:2:405:C:C6	2.52	0.43
2:2:651:C:H2'	2:2:652:G:C8	2.52	0.43
2:2:1434:G:H2'	2:2:1435:C:H6	1.82	0.43
4:4:47:C:O2'	4:4:62:A:OP2	2.36	0.43
4:4:97:A:OP1	42:Lh:72:ARG:NH2	2.52	0.43
8:C:71:LYS:HA	8:C:116:GLU:OE1	2.17	0.43
8:C:188:ASN:HA	8:C:191:ILE:HG22	2.01	0.43
10:LB:57:VAL:HG22	10:LB:73:VAL:HG22	2.00	0.43
10:LB:146:THR:O	10:LB:150:GLU:HG2	2.18	0.43
13:LE:81:LEU:HD13	13:LE:99:ALA:HB2	1.99	0.43
20:LL:57:ILE:HD12	20:LL:157:VAL:HG12	2.00	0.43
25:LQ:68:THR:HG22	25:LQ:69:GLU:N	2.32	0.43
27:LS:67:LYS:O	27:LS:68:HIS:ND1	2.52	0.43
37:Lc:59:LEU:HD23	37:Lc:59:LEU:HA	1.85	0.43
37:Lc:103:ILE:H	37:Lc:103:ILE:HD12	1.84	0.43
42:Lh:90:THR:HG22	42:Lh:92:ALA:H	1.84	0.43
53:SA:20:LEU:CD1	53:SA:53:LEU:HD23	2.48	0.43
53:SA:30:LYS:HG2	53:SA:48:VAL:HG12	1.99	0.43
56:SD:8:ILE:HG13	56:SD:9:SER:H	1.82	0.43
59:SG:39:ASP:OD1	59:SG:47:GLY:N	2.51	0.43
61:SI:113:TYR:CD2	61:SI:121:LEU:HD13	2.53	0.43
68:SP:92:ILE:HD12	68:SP:122:HIS:O	2.17	0.43
71:SS:42:TYR:CD2	71:SS:85:PHE:HE1	2.36	0.43
75:SW:76:SER:OG	75:SW:77:PRO:HD3	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
77:SY:12:THR:HA	77:SY:27:VAL:O	2.18	0.43
1:1:967:U:H2'	1:1:968:U:C6	2.53	0.43
1:1:1730:A:C4	1:1:1732:A:C8	3.07	0.43
1:1:2648:A:H2'	1:1:2648:A:N3	2.34	0.43
2:2:1378:U:C2	73:SU:54:ARG:NH2	2.86	0.43
2:2:1496:C:P	72:ST:102:ARG:HH21	2.41	0.43
4:4:82:U:H5'	4:4:83:C:H5'	2.01	0.43
7:B:105:HIS:ND1	7:B:106:PRO:HD3	2.34	0.43
8:C:697:ALA:HA	8:C:702:ARG:HH12	1.83	0.43
8:C:747:GLY:O	8:C:751:ARG:HG2	2.17	0.43
12:LD:129:TYR:CD1	12:LD:180:GLU:HB3	2.53	0.43
24:LP:22:LEU:HD22	24:LP:90:PHE:CE2	2.53	0.43
84:Sf:123:ASN:ND2	84:Sf:130:VAL:HG21	2.33	0.43
1:1:477:C:H2'	1:1:478:G:H8	1.84	0.43
1:1:1004:C:OP2	1:1:1007:U:O2'	2.36	0.43
1:1:1730:A:H4'	45:Lk:26:LYS:HE2	1.99	0.43
1:1:2063:A:H5'	26:LR:71:ARG:NH1	2.29	0.43
1:1:3007:A:C6	10:LB:75:ALA:HB2	2.54	0.43
2:2:621:G:H2'	2:2:622:C:C6	2.53	0.43
2:2:1226:G:O2'	2:2:1227:A:OP2	2.34	0.43
2:2:1335:C:O2'	2:2:1336:C:H5'	2.19	0.43
6:A:42:ILE:CG2	6:A:57:ARG:HB3	2.48	0.43
6:A:184:LEU:HD21	6:A:187:ASP:HB3	2.00	0.43
8:C:245:ARG:C	8:C:246:LEU:HD12	2.44	0.43
10:LB:294:ASN:O	10:LB:322:TYR:OH	2.37	0.43
11:LC:149:VAL:CG1	11:LC:150:PRO:HD3	2.46	0.43
14:LF:96:LYS:HB3	14:LF:139:TRP:CD1	2.53	0.43
15:LG:116:ALA:O	15:LG:119:ILE:HG22	2.18	0.43
19:LK:90:ARG:HD3	19:LK:94:LYS:HG3	2.00	0.43
27:LS:137:ARG:HA	27:LS:137:ARG:HD3	1.70	0.43
31:LW:127:VAL:HG23	59:SG:131:LYS:O	2.18	0.43
53:SA:149:LEU:O	53:SA:167:ASN:ND2	2.52	0.43
55:SC:178:ILE:HG13	55:SC:205:TYR:HB2	2.00	0.43
57:SE:220:THR:HG22	57:SE:221:ARG:N	2.33	0.43
59:SG:50:LEU:HB3	59:SG:111:LEU:HD12	2.00	0.43
60:SH:172:VAL:O	60:SH:172:VAL:HG13	2.18	0.43
61:SI:196:TYR:HE1	64:SL:13:PHE:HB2	1.83	0.43
68:SP:89:ARG:HG2	68:SP:125:GLY:HA2	2.01	0.43
70:SR:25:THR:O	70:SR:31:ASN:ND2	2.45	0.43
77:SY:87:LYS:HG3	77:SY:88:PHE:HD1	1.81	0.43
79:Sa:44:MET:HE3	79:Sa:65:PRO:O	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:586:G:H1	1:1:597:G:H5''	1.83	0.43
1:1:1273:U:H2'	1:1:1274:A:C8	2.54	0.43
1:1:1454:U:H2'	1:1:1455:G:H8	1.84	0.43
1:1:2230:C:H2'	1:1:2231:U:C6	2.54	0.43
1:1:2666:U:H2'	1:1:2667:C:C6	2.54	0.43
2:2:147:C:H2'	2:2:148:G:C8	2.53	0.43
2:2:188:U:H6	2:2:188:U:OP1	2.01	0.43
2:2:451:A:C8	57:SE:66:MET:HE1	2.53	0.43
2:2:846:C:H2'	2:2:847:C:C6	2.53	0.43
2:2:862:U:H6	2:2:862:U:H2'	1.62	0.43
2:2:1402:A:P	58:SF:70:ARG:HH12	2.42	0.43
2:2:1684:C:H3'	2:2:1685:A:C8	2.54	0.43
8:C:188:ASN:O	8:C:191:ILE:HG22	2.18	0.43
10:LB:47:MET:HE3	10:LB:336:ILE:HD11	1.99	0.43
20:LL:181:ALA:N	35:La:135:GLU:OE1	2.33	0.43
30:LV:24:ILE:HD11	30:LV:37:TYR:HD1	1.83	0.43
31:LW:1:MET:SD	31:LW:2:ARG:N	2.91	0.43
52:Ls:100:ILE:HD11	52:Ls:187:ILE:HD11	1.99	0.43
53:SA:143:ASN:ND2	55:SC:70:PRO:HD3	2.33	0.43
54:SB:106:THR:HB	54:SB:109:LYS:HG2	1.99	0.43
54:SB:138:PHE:O	54:SB:212:ILE:HG23	2.18	0.43
54:SB:192:VAL:HA	54:SB:195:ARG:HE	1.84	0.43
55:SC:185:SER:OG	55:SC:186:LEU:N	2.50	0.43
57:SE:62:LYS:HB3	57:SE:80:ILE:HD11	2.00	0.43
57:SE:251:ARG:HG3	57:SE:252:ASP:N	2.34	0.43
62:SJ:173:LYS:HA	62:SJ:173:LYS:HD3	1.79	0.43
65:SM:72:ALA:O	65:SM:76:LEU:HD23	2.18	0.43
67:SO:61:VAL:HG22	67:SO:63:ALA:H	1.84	0.43
69:SQ:79:TYR:O	69:SQ:82:ARG:HG2	2.19	0.43
69:SQ:127:LYS:HB2	69:SQ:131:GLY:O	2.19	0.43
73:SU:99:GLN:NE2	73:SU:100:ILE:HB	2.34	0.43
77:SY:23:ARG:HH11	77:SY:77:LEU:HD21	1.83	0.43
1:1:250:C:H2'	1:1:251:U:H6	1.83	0.43
1:1:415:A:C2	1:1:2326:A:H4'	2.53	0.43
1:1:1596:U:H2'	1:1:1597:G:C8	2.53	0.43
1:1:2330:A:H2'	1:1:2331:A:C8	2.54	0.43
1:1:2503:C:H1'	1:1:2504:G:OP2	2.18	0.43
1:1:3152:C:O2	1:1:3152:C:H2'	2.17	0.43
2:2:414:A:H4'	2:2:415:G:O5'	2.17	0.43
2:2:1751:A:H5'	76:SX:63:GLN:HE22	1.83	0.43
8:C:498:LYS:NZ	8:C:555:PRO:HB2	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:C:677:PRO:HD3	8:C:683:MET:HE3	2.01	0.43
9:LA:109:GLU:HA	9:LA:136:VAL:HG23	2.00	0.43
11:LC:181:ASP:O	11:LC:184:LYS:HG3	2.19	0.43
11:LC:357:SER:O	11:LC:360:GLU:HG2	2.19	0.43
17:LI:140:THR:OG1	17:LI:141:ARG:N	2.52	0.43
17:LI:145:ARG:HH22	17:LI:167:VAL:HG11	1.83	0.43
23:LO:194:LYS:O	23:LO:197:GLU:HG3	2.19	0.43
31:LW:124:ARG:HE	59:SG:131:LYS:HG3	1.82	0.43
43:Li:9:ALA:CB	43:Li:10:PRO:HD3	2.48	0.43
56:SD:140:VAL:HG22	56:SD:154:LYS:HG3	2.00	0.43
59:SG:21:GLU:O	59:SG:25:ARG:HG2	2.18	0.43
63:SK:7:ASP:OD2	63:SK:35:VAL:HG13	2.19	0.43
65:SM:73:TYR:O	65:SM:77:VAL:HG12	2.19	0.43
65:SM:109:GLU:CD	65:SM:109:GLU:H	2.26	0.43
66:SN:111:SER:O	66:SN:115:LEU:N	2.40	0.43
67:SO:93:HIS:HA	67:SO:126:GLY:O	2.18	0.43
72:ST:19:TYR:CD2	72:ST:23:LEU:HD23	2.54	0.43
78:SZ:53:THR:HB	78:SZ:57:ARG:HH21	1.84	0.43
1:1:171:G:H2'	1:1:172:G:C8	2.54	0.43
1:1:1242:A:H2'	1:1:1243:A:C4	2.54	0.43
1:1:2981:U:H2'	1:1:2982:A:H8	1.84	0.43
1:1:3147:G:C3'	1:1:3148:G:H4'	2.48	0.43
2:2:539:A:H1'	2:2:540:C:H5'	2.00	0.43
2:2:851:G:OP1	26:LR:176:ARG:NH2	2.51	0.43
2:2:905:A:HO2'	2:2:906:U:H6	1.67	0.43
2:2:918:U:H5'	54:SB:65:ILE:HD13	2.00	0.43
2:2:926:U:H2'	2:2:943:U:OP2	2.19	0.43
2:2:1644:A:H2'	2:2:1645:C:C6	2.54	0.43
6:A:100:ARG:HH12	6:A:102:VAL:HG11	1.84	0.43
6:A:274:PHE:HE2	6:A:284:PRO:HD2	1.83	0.43
8:C:5:THR:O	8:C:9:ILE:HG12	2.19	0.43
11:LC:303:PRO:HA	25:LQ:67:ARG:HH12	1.83	0.43
20:LL:79:GLU:OE2	20:LL:112:ASN:ND2	2.52	0.43
31:LW:91:ARG:O	31:LW:99:TYR:HD1	2.01	0.43
35:La:85:ASP:OD1	35:La:86:VAL:HG23	2.18	0.43
38:Ld:34:VAL:HG23	38:Ld:39:ARG:HG2	2.01	0.43
53:SA:62:LEU:HD22	74:SV:79:LEU:HD21	2.00	0.43
56:SD:9:SER:HB3	56:SD:12:ARG:HG2	2.01	0.43
61:SI:117:TYR:HE1	61:SI:150:PHE:HD1	1.65	0.43
61:SI:122:GLY:O	61:SI:123:ARG:HD3	2.19	0.43
78:SZ:60:ILE:HG12	78:SZ:64:LEU:HD22	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
81:Sc:33:PHE:C	81:Sc:35:ASP:H	2.26	0.43
1:1:1157:G:N2	23:LO:89:MET:HE2	2.34	0.43
1:1:1766:G:H2'	1:1:1767:A:H8	1.83	0.43
1:1:2170:A:H5''	1:1:2171:A:H2	1.83	0.43
2:2:1054:U:O2'	54:SB:202:GLN:OE1	2.32	0.43
2:2:1365:U:H5''	72:ST:69:LYS:HZ2	1.84	0.43
2:2:1420:A:OP2	56:SD:154:LYS:NZ	2.32	0.43
2:2:1605:U:H2'	2:2:1606:G:O4'	2.19	0.43
4:4:78:G:H2'	4:4:79:A:C8	2.54	0.43
8:C:305:LEU:HB3	8:C:307:LEU:HD12	2.01	0.43
11:LC:93:ASN:HD22	11:LC:101:PHE:HB2	1.84	0.43
14:LF:112:LEU:HD23	14:LF:112:LEU:HA	1.88	0.43
16:LH:205:LYS:HA	16:LH:205:LYS:HD2	1.88	0.43
17:LI:202:ASN:C	17:LI:203:HIS:HD1	2.27	0.43
19:LK:93:LYS:H	19:LK:96:LYS:NZ	2.17	0.43
36:Lb:61:LYS:HA	36:Lb:61:LYS:HD3	1.82	0.43
51:Lq:10:TRP:O	51:Lq:14:ARG:HB3	2.19	0.43
61:SI:76:THR:HG22	61:SI:77:ARG:N	2.34	0.43
62:SJ:39:GLU:N	62:SJ:39:GLU:OE1	2.51	0.43
69:SQ:121:PRO:O	69:SQ:122:ARG:HG3	2.18	0.43
70:SR:34:VAL:O	70:SR:38:ILE:HG12	2.19	0.43
79:Sa:19:LYS:HG3	79:Sa:20:PRO:HD2	2.01	0.43
1:1:6:G:C6	4:4:155:A:N6	2.87	0.43
1:1:20:U:H2'	1:1:21:A:C8	2.54	0.43
1:1:97:G:H5'	20:LL:15:ARG:HH22	1.84	0.43
1:1:270:G:H2'	1:1:271:U:C6	2.54	0.43
1:1:1300:A:O2'	1:1:1301:A:H3'	2.18	0.43
1:1:2544:G:H2'	1:1:2544:G:N3	2.34	0.43
2:2:800:G:P	60:SH:113:ARG:HH12	2.42	0.43
2:2:887:U:H2'	2:2:888:C:C6	2.53	0.43
2:2:897:G:H2'	2:2:898:A:H8	1.83	0.43
2:2:1342:A:N6	2:2:1374:U:O2	2.51	0.43
2:2:1498:G:C2	2:2:1502:G:C6	3.07	0.43
2:2:1602:C:OP1	69:SQ:126:PRO:HG3	2.19	0.43
6:A:188:HIS:HB2	6:A:219:TRP:HZ3	1.83	0.43
8:C:443:LYS:NZ	8:C:445:GLU:HG2	2.27	0.43
8:C:695:LEU:HD12	8:C:702:ARG:HB3	2.01	0.43
21:LM:131:GLU:OE1	23:LO:184:LYS:HA	2.18	0.43
27:LS:10:ILE:HG22	27:LS:59:VAL:HB	2.00	0.43
27:LS:110:MET:HE3	27:LS:110:MET:HB3	1.86	0.43
56:SD:35:GLU:CD	56:SD:35:GLU:H	2.27	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:SD:67:ARG:O	56:SD:68:ARG:HG2	2.19	0.43
58:SF:105:PHE:CD2	58:SF:116:PRO:HB2	2.53	0.43
61:SI:75:LYS:HG3	61:SI:75:LYS:O	2.19	0.43
63:SK:55:THR:HG22	63:SK:64:TYR:CD2	2.53	0.43
63:SK:84:ILE:O	63:SK:85:VAL:HB	2.19	0.43
65:SM:97:LEU:HA	65:SM:100:TRP:CE3	2.53	0.43
67:SO:42:HIS:CD2	67:SO:54:ARG:HB2	2.54	0.43
67:SO:97:ARG:HD3	67:SO:131:VAL:HG23	1.99	0.43
1:1:1001:G:H2'	1:1:1002:G:H8	1.83	0.42
1:1:1907:G:OP1	50:Lp:8:VAL:HG23	2.19	0.42
1:1:2307:U:H2'	1:1:2308:A:C8	2.54	0.42
1:1:2409:U:H5'	43:Li:72:ASN:OD1	2.18	0.42
2:2:189:C:H6	2:2:189:C:H2'	1.67	0.42
2:2:1490:C:H2'	2:2:1491:C:C6	2.54	0.42
6:A:46:THR:N	6:A:52:TYR:O	2.52	0.42
6:A:201:SER:OG	6:A:203:ASP:OD1	2.35	0.42
8:C:114:SER:O	8:C:118:THR:HG23	2.19	0.42
8:C:315:ASP:OD1	8:C:316:LYS:N	2.50	0.42
9:LA:5:ILE:HG21	9:LA:210:PRO:HD3	2.01	0.42
10:LB:292:GLU:OE1	10:LB:292:GLU:N	2.51	0.42
11:LC:53:VAL:HG11	11:LC:100:MET:CE	2.49	0.42
34:LZ:24:ILE:HA	34:LZ:42:VAL:HG12	2.00	0.42
54:SB:164:ILE:HD13	54:SB:207:LEU:HD21	2.01	0.42
58:SF:39:GLU:HB3	58:SF:118:GLN:HE22	1.82	0.42
58:SF:59:HIS:CE1	69:SQ:79:TYR:HE2	2.37	0.42
71:SS:65:GLU:HA	71:SS:68:ARG:HH21	1.83	0.42
74:SV:38:LYS:HD2	74:SV:49:GLU:HG2	2.01	0.42
1:1:132:U:O2	1:1:132:U:H2'	2.19	0.42
1:1:1091:C:H2'	1:1:1092:A:H8	1.83	0.42
1:1:1140:G:O2'	1:1:1152:A:N3	2.49	0.42
2:2:735:C:H2'	2:2:736:A:C8	2.50	0.42
2:2:835:G:H2'	2:2:836:G:H8	1.84	0.42
2:2:1355:G:H2'	2:2:1356:C:C6	2.54	0.42
2:2:1542:G:H2'	2:2:1543:A:H8	1.83	0.42
3:3:24:A:H2'	3:3:25:A:H8	1.83	0.42
6:A:182:CYS:C	6:A:183:LYS:HD3	2.43	0.42
6:A:294:ASP:OD1	6:A:295:GLY:N	2.52	0.42
11:LC:238:ASP:OD1	11:LC:238:ASP:N	2.52	0.42
33:LY:38:LEU:HD11	33:LY:108:LEU:HD22	2.00	0.42
34:LZ:48:TYR:CE2	34:LZ:132:PRO:HA	2.54	0.42
34:LZ:50:SER:OG	34:LZ:64:ARG:HB3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:Ls:61:ARG:HH22	52:Ls:77:LEU:HB2	1.85	0.42
58:SF:151:PRO:HD3	81:Sc:55:LEU:HD23	2.00	0.42
61:SI:6:ASP:OD2	61:SI:6:ASP:N	2.48	0.42
64:SL:78:GLY:O	64:SL:79:ARG:NH2	2.52	0.42
81:Sc:7:PRO:O	81:Sc:9:LYS:HD3	2.19	0.42
1:1:231:A:H2'	1:1:232:A:C8	2.55	0.42
1:1:1173:A:H2'	1:1:1173:A:N3	2.34	0.42
1:1:1265:G:H4'	52:Ls:83:ASN:HB2	2.01	0.42
1:1:1387:G:N2	1:1:1390:A:OP2	2.47	0.42
1:1:2186:A:H2'	1:1:2187:A:C8	2.54	0.42
1:1:3065:U:H2'	1:1:3066:G:H8	1.84	0.42
2:2:517:A:H2'	2:2:518:A:C8	2.54	0.42
2:2:957:U:H5''	66:SN:15:ALA:O	2.19	0.42
2:2:1217:C:H2'	2:2:1218:A:H8	1.85	0.42
2:2:1236:U:H2'	2:2:1237:U:C6	2.54	0.42
2:2:1361:G:H2'	2:2:1362:C:H6	1.84	0.42
6:A:18:VAL:HG13	6:A:18:VAL:O	2.20	0.42
6:A:36:ARG:HG2	6:A:65:ILE:CD1	2.50	0.42
6:A:170:TRP:HA	6:A:194:TYR:HB2	2.01	0.42
8:C:130:VAL:HG12	8:C:158:ILE:HG23	2.00	0.42
8:C:562:VAL:HG11	8:C:828:ARG:NH1	2.34	0.42
11:LC:209:PRO:HB3	11:LC:254:PHE:CE2	2.53	0.42
19:LK:13:ILE:C	19:LK:14:HIS:HD2	2.27	0.42
19:LK:54:LYS:HG3	19:LK:55:GLY:N	2.34	0.42
20:LL:125:LEU:HD21	42:Lh:119:ARG:NH2	2.34	0.42
35:La:24:LYS:HD2	35:La:26:ARG:NH2	2.34	0.42
38:Ld:64:PRO:O	38:Ld:68:LYS:HG2	2.19	0.42
53:SA:180:LEU:O	53:SA:184:VAL:HG23	2.19	0.42
66:SN:47:PRO:O	66:SN:50:ILE:HG12	2.18	0.42
72:ST:100:VAL:HG13	72:ST:101:ASP:N	2.34	0.42
73:SU:68:PRO:CB	82:Sd:41:GLN:HE21	2.33	0.42
75:SW:57:ARG:HH11	75:SW:57:ARG:HG3	1.84	0.42
79:Sa:42:ARG:O	79:Sa:67:MET:N	2.49	0.42
81:Sc:20:THR:CG2	81:Sc:21:GLY:H	2.28	0.42
1:1:1066:G:H2'	1:1:1067:A:C8	2.54	0.42
1:1:1777:A:H2'	1:1:1778:A:C8	2.54	0.42
1:1:3310:G:C6	10:LB:381:MET:HE3	2.53	0.42
2:2:85:A:H5''	77:SY:122:ARG:NH1	2.35	0.42
2:2:406:U:O4	2:2:407:A:N6	2.52	0.42
2:2:507:G:H2'	2:2:508:A:C8	2.55	0.42
2:2:1099:G:H2'	2:2:1100:C:C6	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:1214:A:H8	2:2:1214:A:OP1	2.03	0.42
6:A:32:LEU:HB2	6:A:71:ILE:HD11	2.01	0.42
6:A:228:TYR:OH	6:A:261:LEU:HD12	2.20	0.42
6:A:255:SER:HB3	6:A:270:LEU:O	2.19	0.42
8:C:762:ARG:HG3	8:C:763:PRO:HD2	2.00	0.42
9:LA:28:LYS:HB3	9:LA:123:ARG:HB3	2.00	0.42
13:LE:90:ASN:OD1	13:LE:92:VAL:HG22	2.20	0.42
15:LG:53:VAL:HG23	32:LX:43:THR:C	2.44	0.42
16:LH:123:PHE:CE2	16:LH:190:LEU:HB2	2.54	0.42
17:LI:4:ARG:NH1	17:LI:99:ILE:HG13	2.34	0.42
34:LZ:32:THR:HB	34:LZ:34:SER:O	2.19	0.42
41:Lg:48:CYS:SG	41:Lg:50:ILE:HG12	2.59	0.42
56:SD:96:ASN:OD1	56:SD:99:LEU:HD23	2.20	0.42
57:SE:87:MET:HE2	57:SE:123:LEU:HG	2.01	0.42
57:SE:100:ARG:HD2	57:SE:114:ILE:HG21	2.02	0.42
57:SE:127:LYS:HZ1	57:SE:142:HIS:CB	2.30	0.42
65:SM:86:ILE:HG22	65:SM:88:LEU:HD22	2.01	0.42
75:SW:2:VAL:O	75:SW:4:THR:HG23	2.19	0.42
80:Sb:5:VAL:HG12	80:Sb:6:ASP:H	1.85	0.42
84:Sf:117:LEU:HD23	84:Sf:117:LEU:HA	1.81	0.42
84:Sf:126:CYS:HB3	84:Sf:130:VAL:HG11	2.02	0.42
1:1:69:C:O3'	22:LN:177:GLY:HA2	2.19	0.42
1:1:1298:U:OP2	23:LO:45:SER:OG	2.31	0.42
1:1:2369:C:H2'	1:1:2370:C:H6	1.85	0.42
2:2:461:A:C2	2:2:462:G:C8	3.08	0.42
5:5:4:G:O2'	5:5:5:A:H5'	2.20	0.42
6:A:31:LEU:O	6:A:43:TRP:HD1	2.03	0.42
6:A:173:LEU:CD2	6:A:189:ILE:HG22	2.50	0.42
6:A:284:PRO:HB3	6:A:303:THR:OG1	2.19	0.42
7:B:176:LEU:HD23	7:B:176:LEU:H	1.85	0.42
10:LB:128:LYS:HE2	10:LB:128:LYS:HB3	1.89	0.42
11:LC:329:LEU:HD23	11:LC:329:LEU:H	1.84	0.42
15:LG:125:LYS:HD2	15:LG:126:GLU:N	2.34	0.42
19:LK:78:SER:OG	19:LK:117:ARG:NH1	2.49	0.42
22:LN:44:ARG:NH1	22:LN:120:TRP:O	2.52	0.42
31:LW:137:ARG:O	31:LW:145:ARG:NH2	2.53	0.42
45:Lk:58:LEU:O	45:Lk:61:SER:OG	2.34	0.42
58:SF:95:LEU:HA	58:SF:98:VAL:HG12	2.00	0.42
59:SG:121:ILE:H	59:SG:125:THR:HG22	1.85	0.42
71:SS:133:VAL:HG13	71:SS:134:ARG:N	2.35	0.42
72:ST:135:ARG:O	72:ST:139:THR:HG23	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
73:SU:60:LEU:HD21	73:SU:81:MET:CE	2.50	0.42
76:SX:62:LYS:NZ	76:SX:116:ASP:O	2.34	0.42
77:SY:31:LEU:HD12	77:SY:31:LEU:O	2.20	0.42
1:1:1337:G:H21	1:1:1339:U:HO2'	1.60	0.42
1:1:1601:G:H2'	1:1:1602:U:C6	2.54	0.42
1:1:2065:U:H3'	26:LR:76:ARG:HH21	1.85	0.42
2:2:678:G:O2'	2:2:679:G:OP1	2.35	0.42
2:2:821:G:H2'	2:2:822:G:O4'	2.20	0.42
2:2:882:A:H2'	2:2:883:G:H8	1.84	0.42
2:2:1034:A:H2'	2:2:1035:U:C6	2.55	0.42
2:2:1509:G:H1'	2:2:1514:C:O2	2.20	0.42
8:C:207:GLU:OE2	8:C:208:LYS:HG3	2.19	0.42
8:C:623:ASP:OD1	8:C:624:ASP:N	2.52	0.42
11:LC:222:LEU:HD23	11:LC:222:LEU:H	1.85	0.42
12:LD:204:GLY:O	12:LD:207:VAL:HG12	2.19	0.42
22:LN:148:ILE:O	22:LN:151:ILE:HG22	2.20	0.42
26:LR:28:GLU:HG3	26:LR:32:ILE:HG23	2.01	0.42
35:La:120:GLU:O	35:La:120:GLU:HG2	2.20	0.42
57:SE:19:LEU:HD21	57:SE:108:ARG:HH11	1.84	0.42
61:SI:12:SER:N	61:SI:18:ARG:HH21	2.18	0.42
1:1:1875:A:O2'	1:1:3011:G:H4'	2.19	0.42
1:1:2390:U:H2'	1:1:2391:U:C6	2.54	0.42
1:1:3179:G:H2'	1:1:3180:G:H8	1.85	0.42
2:2:70:C:P	59:SG:165:LYS:HZ2	2.43	0.42
2:2:171:U:H3	2:2:263:A:H62	1.67	0.42
2:2:352:G:O2'	2:2:353:G:OP1	2.36	0.42
2:2:444:U:H2'	2:2:445:C:O4'	2.20	0.42
2:2:445:C:H2'	2:2:446:C:H6	1.84	0.42
2:2:995:G:C6	2:2:1006:G:C6	3.08	0.42
2:2:1398:G:OP1	70:SR:4:VAL:HG13	2.20	0.42
2:2:1448:U:H2'	2:2:1449:G:H8	1.85	0.42
2:2:1529:C:OP2	78:SZ:66:ARG:NH2	2.46	0.42
5:5:69:G:H2'	5:5:70:G:C8	2.55	0.42
7:B:114:ASN:HB2	56:SD:148:ALA:HB2	2.02	0.42
8:C:641:ASP:HA	83:Se:9:ALA:HB1	2.02	0.42
9:LA:191:VAL:O	9:LA:191:VAL:HG12	2.20	0.42
13:LE:161:ASP:O	13:LE:165:ILE:HG12	2.20	0.42
41:Lg:26:THR:HG22	41:Lg:30:GLN:H	1.85	0.42
51:Lq:70:ALA:HB1	51:Lq:73:LYS:HG3	2.02	0.42
53:SA:20:LEU:HD12	53:SA:21:LEU:N	2.35	0.42
53:SA:127:THR:O	53:SA:167:ASN:ND2	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:SB:28:ASP:OD2	54:SB:50:ARG:HG3	2.19	0.42
54:SB:100:PHE:HE1	54:SB:217:LEU:HD11	1.85	0.42
54:SB:166:ARG:HE	54:SB:167:LYS:NZ	2.18	0.42
57:SE:57:ASN:O	57:SE:61:THR:HG23	2.19	0.42
57:SE:63:ALA:O	57:SE:67:GLN:HG2	2.20	0.42
57:SE:79:ASP:N	57:SE:79:ASP:OD1	2.52	0.42
57:SE:130:GLN:NE2	57:SE:138:PHE:HE1	2.18	0.42
58:SF:75:PRO:HG2	58:SF:78:GLU:OE1	2.19	0.42
58:SF:138:SER:HB2	58:SF:143:ARG:HG2	1.99	0.42
59:SG:159:ARG:CZ	59:SG:173:THR:HG21	2.49	0.42
63:SK:80:LEU:CD2	63:SK:83:GLU:H	2.32	0.42
67:SO:32:ILE:HA	67:SO:40:PHE:O	2.20	0.42
75:SW:34:ILE:HG13	75:SW:35:VAL:N	2.35	0.42
82:Sd:6:VAL:O	82:Sd:6:VAL:HG12	2.19	0.42
1:1:462:A:H2'	1:1:463:C:C6	2.55	0.42
1:1:1260:C:C2	1:1:1261:A:C8	3.08	0.42
2:2:191:G:HO2'	2:2:192:A:H8	1.68	0.42
2:2:266:G:H2'	2:2:267:C:C6	2.54	0.42
2:2:324:C:O2'	64:SL:10:GLU:OE1	2.28	0.42
2:2:389:G:OP1	61:SI:24:LYS:NZ	2.35	0.42
2:2:839:U:H2'	2:2:840:C:O4'	2.19	0.42
2:2:1359:U:H4'	2:2:1360:G:C6	2.55	0.42
4:4:145:U:H2'	4:4:146:U:C6	2.55	0.42
6:A:54:TYR:OH	69:SQ:100:HIS:N	2.52	0.42
6:A:132:TRP:N	6:A:132:TRP:CD1	2.88	0.42
8:C:675:GLU:OE2	8:C:716:TYR:OH	2.37	0.42
8:C:724:PRO:HB2	8:C:811:PRO:HG2	2.02	0.42
10:LB:108:GLU:HG2	10:LB:109:HIS:CE1	2.55	0.42
12:LD:272:ALA:O	12:LD:275:LEU:HG	2.19	0.42
13:LE:95:ARG:HG2	13:LE:96:ARG:N	2.35	0.42
18:LJ:82:GLU:OE2	18:LJ:90:TYR:OH	2.28	0.42
19:LK:83:ARG:HD3	19:LK:86:LYS:HG3	2.02	0.42
21:LM:23:GLU:OE1	21:LM:23:GLU:N	2.49	0.42
28:LT:96:VAL:CG1	28:LT:97:LYS:N	2.83	0.42
31:LW:154:LYS:HA	31:LW:154:LYS:HD3	1.79	0.42
49:Lo:82:GLN:C	49:Lo:83:LEU:HD12	2.45	0.42
58:SF:154:ARG:NH2	81:Sc:56:VAL:HG12	2.35	0.42
65:SM:25:SER:N	65:SM:135:VAL:HG11	2.34	0.42
67:SO:86:GLU:OE2	67:SO:87:LEU:HD22	2.19	0.42
68:SP:132:LYS:HE3	68:SP:132:LYS:HB3	1.82	0.42
71:SS:112:ASP:OD1	71:SS:115:ARG:NH1	2.44	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
75:SW:113:HIS:HD1	75:SW:114:GLU:HG2	1.84	0.42
1:1:609:A:H4'	1:1:610:A:O5'	2.20	0.42
1:1:1485:G:H2'	1:1:1486:A:C8	2.53	0.42
2:2:531:A:C5	2:2:532:A:C8	3.08	0.42
2:2:790:C:H2'	2:2:791:A:C8	2.55	0.42
2:2:877:G:H2'	2:2:878:C:C6	2.54	0.42
2:2:1206:C:N4	2:2:1451:G:H22	2.18	0.42
6:A:153:CYS:SG	6:A:154:VAL:N	2.93	0.42
6:A:179:LEU:HD12	6:A:180:GLN:N	2.35	0.42
8:C:171:VAL:HG12	8:C:172:THR:O	2.20	0.42
8:C:329:PHE:HD2	8:C:330:LEU:HD22	1.85	0.42
17:LI:130:ASP:CG	17:LI:131:ILE:H	2.28	0.42
18:LJ:15:ILE:CD1	18:LJ:132:MET:HE1	2.50	0.42
24:LP:22:LEU:HD22	24:LP:90:PHE:HE2	1.83	0.42
28:LT:77:TYR:HE1	28:LT:86:GLU:HB3	1.84	0.42
28:LT:126:VAL:HG23	28:LT:127:GLN:N	2.35	0.42
34:LZ:58:LYS:HE3	34:LZ:58:LYS:HB3	1.90	0.42
40:Lf:61:VAL:HG23	40:Lf:62:ARG:N	2.35	0.42
46:Ll:48:ARG:HE	46:Ll:49:LEU:N	2.17	0.42
50:Lp:49:ARG:HB2	50:Lp:55:TRP:CZ3	2.54	0.42
50:Lp:89:ILE:HG13	50:Lp:90:THR:N	2.35	0.42
66:SN:112:LYS:O	66:SN:116:ILE:HG12	2.19	0.42
67:SO:94:ILE:O	67:SO:95:LYS:HE2	2.19	0.42
71:SS:80:LYS:HB2	71:SS:80:LYS:HE2	1.86	0.42
78:SZ:81:VAL:HG23	78:SZ:82:VAL:N	2.35	0.42
1:1:1253:A:C8	8:C:742:MET:HE3	2.54	0.42
1:1:1620:G:O2'	1:1:1621:C:H5'	2.19	0.42
1:1:3118:C:O2'	1:1:3119:A:H8	2.03	0.42
2:2:324:C:H2'	2:2:325:U:C6	2.54	0.42
2:2:351:C:C2	2:2:352:G:C8	3.07	0.42
2:2:445:C:OP2	57:SE:49:ARG:NH1	2.53	0.42
2:2:565:G:N7	76:SX:69:ARG:NH2	2.67	0.42
2:2:652:G:H2'	2:2:653:G:H8	1.84	0.42
2:2:1199:A:H8	2:2:1204:C:H42	1.68	0.42
2:2:1401:G:H2'	2:2:1402:A:H8	1.85	0.42
2:2:1575:C:O2'	69:SQ:137:ARG:NH1	2.53	0.42
2:2:1584:G:C4'	58:SF:91:ASN:HD21	2.32	0.42
3:3:3:A:H2'	3:3:4:U:C6	2.55	0.42
3:3:37:G:N2	3:3:41:G:N3	2.68	0.42
6:A:62:HIS:ND1	6:A:82:SER:HB2	2.34	0.42
6:A:308:ARG:HG2	6:A:308:ARG:HH11	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:C:25:ILE:O	8:C:129:VAL:HA	2.20	0.42
8:C:317:GLU:HA	8:C:321:LEU:HG	2.02	0.42
11:LC:338:LYS:O	11:LC:340:LYS:NZ	2.52	0.42
13:LE:84:THR:O	13:LE:84:THR:HG23	2.20	0.42
13:LE:148:LYS:HD3	13:LE:149:PRO:HD2	2.02	0.42
19:LK:105:SER:C	19:LK:106:LEU:HD22	2.44	0.42
21:LM:71:LYS:HB2	21:LM:71:LYS:HE3	1.85	0.42
32:LX:71:ASP:CG	32:LX:72:GLU:H	2.25	0.42
32:LX:82:THR:H	32:LX:85:ALA:HB3	1.84	0.42
52:Ls:15:LEU:HG	52:Ls:19:LEU:HD23	2.02	0.42
55:SC:152:TRP:CE2	55:SC:181:PRO:HG3	2.55	0.42
57:SE:246:THR:N	57:SE:249:GLU:OE2	2.39	0.42
58:SF:80:LEU:HA	58:SF:159:ILE:HD11	2.01	0.42
58:SF:201:LYS:C	58:SF:201:LYS:HD3	2.45	0.42
61:SI:194:ALA:O	61:SI:198:ARG:HG3	2.18	0.42
1:1:934:A:C2	1:1:1097:U:H4'	2.55	0.41
1:1:993:G:H2'	1:1:994:G:H8	1.85	0.41
1:1:1332:G:H22	11:LC:294:THR:HB	1.85	0.41
1:1:1338:A:H4'	1:1:1339:U:O5'	2.20	0.41
1:1:1623:A:H5''	1:1:1624:C:C5	2.55	0.41
2:2:86:C:P	77:SY:122:ARG:HH22	2.43	0.41
2:2:443:A:C6	2:2:444:U:C4	3.08	0.41
2:2:563:C:O2'	83:Se:10:ARG:HD3	2.19	0.41
2:2:992:G:O2'	2:2:993:A:H5'	2.19	0.41
2:2:1222:U:H3'	2:2:1223:G:H8	1.85	0.41
2:2:1342:A:H5'	73:SU:50:LYS:NZ	2.34	0.41
2:2:1787:G:P	79:Sa:10:ARG:HE	2.43	0.41
6:A:11:LEU:HD11	6:A:52:TYR:CD2	2.55	0.41
6:A:19:THR:O	6:A:288:SER:OG	2.36	0.41
6:A:259:PHE:CD1	6:A:266:LYS:HA	2.55	0.41
8:C:90:ILE:HG22	8:C:91:VAL:O	2.20	0.41
8:C:132:ASP:OD1	8:C:133:THR:N	2.53	0.41
10:LB:89:LEU:HD11	10:LB:193:VAL:HG23	2.00	0.41
13:LE:8:LYS:HZ1	13:LE:18:PRO:C	2.28	0.41
14:LF:46:LYS:NZ	14:LF:176:GLU:OE1	2.43	0.41
19:LK:14:HIS:C	19:LK:15:LEU:HD12	2.44	0.41
24:LP:29:THR:HG21	24:LP:146:ILE:HD11	2.01	0.41
25:LQ:111:VAL:HG13	25:LQ:111:VAL:O	2.20	0.41
31:LW:79:LYS:HE3	31:LW:95:TRP:CZ2	2.55	0.41
31:LW:142:PRO:O	31:LW:146:ASN:ND2	2.52	0.41
33:LY:48:PRO:O	33:LY:114:ARG:NH2	2.52	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:Lg:92:ARG:O	41:Lg:96:ILE:HG12	2.20	0.41
49:Lo:29:LYS:HA	49:Lo:29:LYS:HE3	2.01	0.41
51:Lq:89:LYS:HB3	51:Lq:89:LYS:HE2	1.87	0.41
53:SA:104:ARG:HG2	53:SA:104:ARG:HH11	1.84	0.41
56:SD:43:ARG:HH22	56:SD:45:THR:HG21	1.85	0.41
57:SE:186:GLY:O	57:SE:189:MET:HG3	2.20	0.41
60:SH:65:VAL:HB	60:SH:99:LEU:HD22	2.01	0.41
71:SS:66:LEU:HD23	71:SS:69:LEU:HD12	2.02	0.41
80:Sb:81:ARG:C	80:Sb:82:LYS:HD2	2.45	0.41
84:Sf:78:LYS:O	84:Sf:79:LYS:HB3	2.20	0.41
1:1:154:G:N3	1:1:155:A:C8	2.89	0.41
1:1:565:C:H2'	1:1:566:C:H6	1.85	0.41
1:1:1196:G:OP1	27:LS:137:ARG:NH1	2.53	0.41
1:1:2043:C:HO2'	1:1:2044:G:P	2.41	0.41
2:2:754:A:O2'	2:2:755:A:P	2.79	0.41
8:C:157:VAL:CG2	8:C:211:VAL:HG12	2.50	0.41
10:LB:376:GLU:OE2	31:LW:14:TYR:OH	2.38	0.41
11:LC:24:PRO:HG2	11:LC:27:PHE:CD2	2.55	0.41
22:LN:17:ASP:OD1	22:LN:18:VAL:N	2.53	0.41
22:LN:67:ARG:HD2	22:LN:67:ARG:HA	1.81	0.41
26:LR:7:GLN:OE1	26:LR:7:GLN:N	2.52	0.41
29:LU:20:LYS:HA	29:LU:72:ILE:O	2.20	0.41
43:Li:9:ALA:HB1	43:Li:10:PRO:HD3	2.02	0.41
46:Ll:45:ARG:O	46:Ll:45:ARG:HG2	2.20	0.41
52:Ls:29:SER:N	52:Ls:186:GLY:O	2.53	0.41
54:SB:190:PRO:HB2	54:SB:195:ARG:HH22	1.84	0.41
61:SI:21:TYR:HD2	61:SI:22:ARG:HG2	1.85	0.41
61:SI:188:LEU:HD13	61:SI:192:GLU:OE1	2.20	0.41
63:SK:3:ILE:N	63:SK:4:PRO:HD2	2.35	0.41
63:SK:5:LYS:H	63:SK:5:LYS:HG3	1.64	0.41
73:SU:97:VAL:HA	73:SU:100:ILE:HG22	2.02	0.41
75:SW:103:ILE:HD11	75:SW:129:PHE:CD2	2.55	0.41
77:SY:107:SER:HB2	77:SY:110:GLN:HG3	2.02	0.41
79:Sa:4:LYS:C	79:Sa:5:ARG:HD2	2.45	0.41
81:Sc:30:ARG:HG3	81:Sc:30:ARG:NH1	2.35	0.41
81:Sc:41:ILE:HG13	81:Sc:42:ILE:N	2.33	0.41
1:1:405:G:H2'	1:1:406:U:C6	2.55	0.41
1:1:969:U:H2'	1:1:970:U:C6	2.55	0.41
1:1:1744:C:H3'	1:1:1745:U:C5'	2.50	0.41
1:1:2571:U:H2'	1:1:2572:U:C6	2.56	0.41
1:1:2944:C:H2'	1:1:2945:U:C6	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:3266:A:H2'	1:1:3267:G:C8	2.55	0.41
2:2:917:A:H2'	2:2:918:U:H6	1.84	0.41
2:2:1051:G:C6	2:2:1052:U:C4	3.09	0.41
2:2:1165:U:O2'	2:2:1166:G:OP1	2.36	0.41
2:2:1193:A:OP2	2:2:1460:G:N2	2.54	0.41
2:2:1224:A:OP1	2:2:1225:G:H3'	2.21	0.41
2:2:1604:U:H2'	2:2:1605:U:H6	1.86	0.41
3:3:6:C:H5''	12:LD:54:ARG:HH21	1.85	0.41
8:C:436:THR:OG1	8:C:447:ILE:O	2.35	0.41
8:C:713:ARG:NH2	8:C:839:GLU:O	2.54	0.41
14:LF:142:TYR:CZ	14:LF:236:ASN:HB2	2.56	0.41
20:LL:62:THR:HG22	20:LL:63:VAL:H	1.84	0.41
21:LM:97:THR:HG23	21:LM:100:ALA:H	1.85	0.41
27:LS:120:SER:O	27:LS:121:ILE:HG13	2.20	0.41
35:La:111:LYS:HG2	35:La:113:LEU:HD12	2.02	0.41
42:Lh:59:VAL:O	42:Lh:63:ILE:HG13	2.20	0.41
54:SB:109:LYS:HA	54:SB:109:LYS:HD3	1.93	0.41
59:SG:211:TYR:HE1	59:SG:215:LEU:HD12	1.84	0.41
63:SK:18:GLU:O	63:SK:87:ALA:HB2	2.20	0.41
69:SQ:13:LYS:HD2	69:SQ:13:LYS:HA	1.95	0.41
73:SU:20:ARG:O	73:SU:113:THR:OG1	2.30	0.41
77:SY:92:TYR:O	77:SY:95:VAL:HG22	2.20	0.41
81:Sc:30:ARG:HG3	81:Sc:30:ARG:HH11	1.85	0.41
83:Se:13:LYS:HG3	83:Se:17:GLN:HE22	1.85	0.41
1:1:136:C:H2'	1:1:137:C:C6	2.56	0.41
1:1:1560:U:O4	32:LX:46:HIS:ND1	2.53	0.41
1:1:2619:G:OP1	1:1:2709:U:O2'	2.38	0.41
2:2:1621:C:H2'	2:2:1622:U:H6	1.85	0.41
2:2:1791:U:H3'	79:Sa:5:ARG:HH22	1.86	0.41
2:2:1796:U:O2	54:SB:115:ARG:NH2	2.53	0.41
7:B:175:TYR:HE2	63:SK:84:ILE:HG13	1.86	0.41
8:C:82:PRO:HA	8:C:98:LYS:HD2	2.02	0.41
8:C:84:GLU:C	8:C:86:ASP:H	2.29	0.41
8:C:305:LEU:O	8:C:305:LEU:HD23	2.20	0.41
10:LB:284:TYR:HE1	10:LB:355:VAL:HG21	1.85	0.41
11:LC:306:GLU:HG2	14:LF:29:ARG:HH22	1.84	0.41
16:LH:201:GLN:HE22	47:Lm:89:PHE:HE2	1.63	0.41
18:LJ:126:MET:HE2	18:LJ:128:PHE:HE1	1.85	0.41
23:LO:24:VAL:O	23:LO:28:LEU:HD23	2.21	0.41
23:LO:26:LYS:HD2	23:LO:26:LYS:HA	1.80	0.41
24:LP:97:ASN:C	24:LP:97:ASN:HD22	2.27	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:LU:21:PHE:CE2	29:LU:78:LEU:HD23	2.55	0.41
35:La:82:VAL:HG13	35:La:87:ARG:HB2	2.03	0.41
38:Ld:52:GLN:HG3	38:Ld:58:SER:H	1.85	0.41
51:Lq:77:SER:O	51:Lq:78:LEU:HD23	2.19	0.41
59:SG:52:ILE:HA	59:SG:111:LEU:HD13	2.02	0.41
64:SL:122:VAL:O	64:SL:122:VAL:HG13	2.20	0.41
65:SM:88:LEU:HD12	65:SM:90:LYS:NZ	2.35	0.41
72:ST:100:VAL:O	72:ST:104:ILE:HG23	2.20	0.41
73:SU:21:ILE:N	73:SU:88:ILE:O	2.45	0.41
74:SV:46:ILE:H	74:SV:46:ILE:HD12	1.86	0.41
77:SY:89:GLU:OE2	77:SY:94:LEU:HD21	2.20	0.41
81:Sc:30:ARG:HA	81:Sc:42:ILE:HG22	2.03	0.41
1:1:165:G:OP2	1:1:165:G:H8	2.03	0.41
1:1:1322:C:H2'	1:1:1323:C:C6	2.56	0.41
1:1:1486:A:C4	1:1:1487:A:C8	3.08	0.41
1:1:2213:G:O6	1:1:2230:C:N4	2.54	0.41
1:1:2308:A:OP1	38:Ld:35:THR:HG22	2.21	0.41
1:1:3243:U:O2'	1:1:3244:G:H5'	2.20	0.41
2:2:1232:C:H2'	2:2:1233:A:O4'	2.20	0.41
4:4:144:G:OP1	22:LN:57:GLN:NE2	2.54	0.41
5:5:5:A:H2'	5:5:6:U:H6	1.83	0.41
5:5:58:C:H2'	5:5:59:U:C6	2.56	0.41
6:A:168:CYS:HB3	6:A:195:ILE:HG13	2.03	0.41
8:C:572:LYS:HD2	8:C:573:SER:H	1.86	0.41
8:C:588:LEU:HB2	8:C:693:VAL:HG22	2.03	0.41
10:LB:86:VAL:HG13	10:LB:161:VAL:HG13	2.02	0.41
10:LB:307:THR:HG21	10:LB:317:GLU:HG2	2.01	0.41
11:LC:228:ASN:OD1	11:LC:228:ASN:O	2.39	0.41
12:LD:46:ALA:HA	12:LD:47:PRO:HD3	1.95	0.41
12:LD:86:TYR:HE2	12:LD:250:ILE:HA	1.85	0.41
29:LU:20:LYS:HE2	29:LU:20:LYS:HB2	1.81	0.41
38:Ld:70:VAL:HG13	38:Ld:71:TRP:HD1	1.85	0.41
44:Lj:76:ASN:HD21	44:Lj:79:ARG:NH2	2.18	0.41
48:Lr:6:ARG:O	48:Lr:10:THR:HG23	2.20	0.41
54:SB:112:SER:HB3	79:Sa:68:TYR:CE1	2.56	0.41
55:SC:188:ALA:HB2	55:SC:206:THR:HG21	2.02	0.41
56:SD:8:ILE:HG23	56:SD:9:SER:H	1.84	0.41
57:SE:129:VAL:HG22	57:SE:139:LEU:CB	2.50	0.41
60:SH:87:LEU:HA	60:SH:90:LYS:HE2	2.01	0.41
68:SP:33:LEU:HB3	68:SP:36:LEU:HD11	2.02	0.41
72:ST:6:THR:HA	72:ST:134:ASP:OD1	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
75:SW:111:MET:HE1	75:SW:116:ALA:N	2.35	0.41
77:SY:40:LYS:NZ	77:SY:60:VAL:O	2.49	0.41
1:1:628:U:H2'	1:1:629:C:C6	2.55	0.41
1:1:1073:G:H2'	1:1:1074:G:H8	1.85	0.41
1:1:1226:G:N2	1:1:1253:A:O2'	2.39	0.41
1:1:1517:A:H2'	1:1:1518:A:C8	2.55	0.41
1:1:1643:C:H2'	1:1:1644:G:C8	2.55	0.41
1:1:2064:C:H2'	1:1:2065:U:H6	1.86	0.41
1:1:2487:A:C4	15:LG:49:LEU:HD21	2.56	0.41
1:1:3333:G:H2'	1:1:3334:A:H8	1.85	0.41
2:2:481:C:H2'	2:2:482:A:H8	1.86	0.41
2:2:555:U:O2	7:B:121:GLN:NE2	2.46	0.41
2:2:1238:G:N3	68:SP:87:HIS:HD2	2.18	0.41
2:2:1711:G:H2'	2:2:1711:G:N3	2.34	0.41
3:3:40:C:O2	18:LJ:73:ARG:NE	2.39	0.41
4:4:68:G:H2'	4:4:69:U:H6	1.85	0.41
6:A:65:ILE:HG23	6:A:83:TRP:HB2	2.02	0.41
6:A:91:GLU:OE1	6:A:94:THR:HG22	2.20	0.41
8:C:139:VAL:O	8:C:143:THR:HG23	2.21	0.41
8:C:417:GLY:O	8:C:479:ASN:ND2	2.53	0.41
8:C:708:ILE:HB	8:C:709:PRO:HD3	2.01	0.41
12:LD:104:LEU:HD21	12:LD:108:ARG:CZ	2.50	0.41
17:LI:56:GLU:OE2	17:LI:162:ARG:N	2.54	0.41
20:LL:106:GLU:OE2	43:Li:29:ARG:HD2	2.21	0.41
35:La:72:SER:HB2	35:La:113:LEU:HD13	2.02	0.41
51:Lq:35:LEU:O	51:Lq:36:THR:OG1	2.33	0.41
54:SB:53:GLY:O	54:SB:54:LEU:HB2	2.21	0.41
56:SD:49:THR:O	56:SD:88:SER:N	2.50	0.41
58:SF:20:VAL:HG22	58:SF:23:GLU:CD	2.44	0.41
64:SL:81:VAL:HG22	64:SL:90:ILE:O	2.20	0.41
66:SN:38:CYS:O	66:SN:42:ARG:HG2	2.21	0.41
66:SN:73:ARG:HG2	66:SN:73:ARG:HH11	1.86	0.41
69:SQ:99:GLU:HA	69:SQ:102:LYS:HB3	2.02	0.41
71:SS:15:LEU:HD23	71:SS:16:ARG:N	2.36	0.41
81:Sc:12:LYS:HG3	81:Sc:53:ASP:O	2.21	0.41
1:1:1323:C:H2'	1:1:1324:U:H6	1.86	0.41
1:1:1560:U:O2'	1:1:1561:G:P	2.79	0.41
1:1:1584:U:H2'	1:1:1585:A:O4'	2.20	0.41
1:1:1787:G:C6	1:1:1788:G:N1	2.88	0.41
2:2:255:C:C4'	61:SI:64:ASN:HD21	2.34	0.41
2:2:597:U:OP2	76:SX:108:GLY:HA2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:870:G:H2'	2:2:871:U:O4'	2.20	0.41
2:2:1205:A:H5''	2:2:1206:C:OP2	2.20	0.41
2:2:1612:G:O3'	81:Sc:19:ARG:HD2	2.20	0.41
3:3:75:A:N3	27:LS:50:LYS:NZ	2.68	0.41
8:C:235:PHE:O	8:C:235:PHE:CG	2.74	0.41
8:C:261:LYS:O	8:C:262:SER:OG	2.36	0.41
16:LH:142:LYS:HB2	16:LH:149:TYR:CE1	2.53	0.41
18:LJ:16:GLN:NE2	18:LJ:131:CYS:SG	2.77	0.41
22:LN:119:TYR:OH	22:LN:131:GLU:OE1	2.25	0.41
44:Lj:76:ASN:HD21	44:Lj:79:ARG:CZ	2.34	0.41
54:SB:111:ARG:HH21	79:Sa:67:MET:HA	1.85	0.41
59:SG:211:TYR:HA	59:SG:214:ILE:HG22	2.01	0.41
59:SG:222:ALA:O	59:SG:225:GLN:NE2	2.50	0.41
63:SK:44:LEU:HD13	63:SK:64:TYR:HE2	1.85	0.41
63:SK:84:ILE:HD12	63:SK:84:ILE:HG23	1.86	0.41
67:SO:112:GLN:NE2	79:Sa:46:GLU:OE1	2.47	0.41
68:SP:93:VAL:HG23	68:SP:122:HIS:O	2.20	0.41
75:SW:121:VAL:HG12	75:SW:122:ALA:N	2.35	0.41
78:SZ:39:LEU:HD11	78:SZ:68:CYS:SG	2.61	0.41
1:1:688:C:H2'	1:1:689:G:H8	1.85	0.41
1:1:1361:U:H2'	1:1:1362:G:H8	1.86	0.41
1:1:1934:G:H4'	1:1:1935:C:H6	1.86	0.41
1:1:2408:A:O2'	43:Li:72:ASN:OD1	2.27	0.41
1:1:3072:A:H62	1:1:3076:C:H42	1.67	0.41
1:1:3112:U:H6	1:1:3114:C:H41	1.69	0.41
2:2:524:A:OP2	77:SY:96:ARG:NH2	2.34	0.41
2:2:600:U:H2'	2:2:601:A:C8	2.56	0.41
2:2:885:A:H4'	67:SO:135:PRO:HA	2.02	0.41
2:2:1068:U:H2'	2:2:1069:C:C6	2.56	0.41
2:2:1341:A:H4'	2:2:1342:A:OP1	2.21	0.41
2:2:1366:A:OP2	72:ST:69:LYS:NZ	2.54	0.41
7:B:138:ALA:HA	7:B:141:ILE:HG12	2.01	0.41
8:C:435:ARG:HE	8:C:436:THR:H	1.69	0.41
11:LC:331:PRO:HB3	14:LF:47:ARG:NH2	2.36	0.41
15:LG:254:LYS:C	15:LG:254:LYS:HD3	2.46	0.41
54:SB:180:THR:N	54:SB:183:GLN:HE21	2.19	0.41
58:SF:59:HIS:HE1	69:SQ:79:TYR:HE2	1.67	0.41
58:SF:122:ASP:O	58:SF:125:VAL:HG12	2.21	0.41
59:SG:39:ASP:CG	59:SG:47:GLY:H	2.29	0.41
68:SP:103:GLY:HA2	68:SP:112:GLN:HA	2.03	0.41
81:Sc:19:ARG:HG3	81:Sc:19:ARG:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:294:G:H2'	1:1:295:A:H8	1.85	0.41
1:1:355:U:O4	44:Lj:24:ARG:NH2	2.53	0.41
1:1:435:G:H2'	1:1:436:C:C6	2.55	0.41
1:1:806:U:H5''	9:LA:21:ARG:HD3	2.03	0.41
1:1:1135:G:N2	1:1:1183:A:H61	2.18	0.41
1:1:1345:G:H2'	1:1:1346:A:C8	2.55	0.41
1:1:1587:U:O2'	1:1:1588:C:P	2.78	0.41
1:1:1796:A:H2'	1:1:1797:A:C8	2.47	0.41
1:1:2593:U:O3'	17:LI:15:LYS:NZ	2.54	0.41
1:1:2839:U:O2	10:LB:251:ALA:HB3	2.21	0.41
1:1:2871:G:N1	1:1:3088:A:C8	2.89	0.41
1:1:3003:G:OP1	10:LB:19:ARG:NH2	2.52	0.41
2:2:78:C:O4'	59:SG:177:ARG:NH1	2.54	0.41
2:2:187:U:HO2'	2:2:188:U:P	2.44	0.41
2:2:188:U:H3'	2:2:189:C:H5'	2.03	0.41
2:2:428:C:H2'	2:2:429:G:H8	1.85	0.41
2:2:508:A:H3'	62:SJ:171:ARG:NH1	2.36	0.41
2:2:592:G:H5'	62:SJ:38:ARG:HH22	1.85	0.41
2:2:846:C:H2'	2:2:847:C:H6	1.85	0.41
2:2:959:U:H2'	2:2:960:C:C6	2.56	0.41
2:2:998:C:H5''	5:5:37:A:O2'	2.21	0.41
2:2:1193:A:H4'	2:2:1194:C:O5'	2.20	0.41
2:2:1238:G:N3	68:SP:87:HIS:CD2	2.89	0.41
2:2:1380:G:H4'	73:SU:32:GLU:OE1	2.21	0.41
2:2:1500:G:H2'	2:2:1501:A:C8	2.56	0.41
2:2:1524:U:H2'	2:2:1525:C:C6	2.56	0.41
2:2:1700:G:H2'	2:2:1701:A:C8	2.54	0.41
2:2:1748:U:H2'	2:2:1749:A:C8	2.56	0.41
2:2:1792:C:OP2	79:Sa:5:ARG:NH2	2.54	0.41
3:3:111:G:H2'	3:3:112:U:C6	2.56	0.41
4:4:104:A:OP2	4:4:105:A:H2'	2.20	0.41
5:5:30:C:HO2'	5:5:31:G:P	2.43	0.41
6:A:54:TYR:CZ	69:SQ:100:HIS:HB2	2.56	0.41
6:A:104:HIS:CD2	6:A:132:TRP:HZ2	2.39	0.41
7:B:118:GLN:HE22	56:SD:146:ARG:HD3	1.85	0.41
8:C:163:ASP:OD1	8:C:163:ASP:N	2.47	0.41
8:C:723:GLU:N	8:C:724:PRO:CD	2.84	0.41
8:C:730:ILE:HA	8:C:775:PRO:HA	2.02	0.41
13:LE:72:LEU:H	13:LE:72:LEU:HD23	1.85	0.41
20:LL:106:GLU:OE2	43:Li:29:ARG:HB3	2.21	0.41
22:LN:160:GLU:HG2	22:LN:161:CYS:N	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:LU:103:VAL:HG13	29:LU:111:GLU:OE2	2.20	0.41
29:LU:111:GLU:N	29:LU:111:GLU:OE1	2.54	0.41
35:La:85:ASP:OD1	35:La:86:VAL:N	2.53	0.41
41:Lg:91:ILE:O	41:Lg:95:LEU:HD23	2.21	0.41
46:Ll:23:ILE:HD12	46:Ll:23:ILE:H	1.85	0.41
52:Ls:22:TYR:CG	52:Ls:88:PHE:HB3	2.55	0.41
52:Ls:92:ASP:HB2	52:Ls:95:GLU:OE1	2.21	0.41
54:SB:34:ALA:HA	54:SB:35:PRO:HD2	1.90	0.41
55:SC:153:GLY:O	75:SW:98:GLN:NE2	2.53	0.41
58:SF:135:ARG:O	81:Sc:23:ARG:NH2	2.53	0.41
59:SG:132:ARG:O	59:SG:133:LEU:HD22	2.21	0.41
60:SH:46:PRO:O	60:SH:48:GLN:HG3	2.21	0.41
60:SH:74:GLN:HG2	60:SH:75:GLY:N	2.36	0.41
60:SH:185:ARG:HD2	60:SH:185:ARG:HA	1.96	0.41
61:SI:160:LEU:CD2	61:SI:164:PHE:HE1	2.34	0.41
65:SM:95:LYS:HA	65:SM:117:ASN:ND2	2.32	0.41
66:SN:4:LEU:HD11	66:SN:124:ARG:HH12	1.85	0.41
68:SP:82:GLU:HG3	68:SP:83:LEU:N	2.36	0.41
68:SP:108:LYS:HB3	68:SP:109:GLU:OE1	2.21	0.41
68:SP:116:LYS:HB3	68:SP:118:GLU:OE1	2.21	0.41
68:SP:135:LYS:O	68:SP:136:HIS:HB2	2.21	0.41
69:SQ:101:SER:O	69:SQ:105:LEU:HG	2.21	0.41
72:ST:86:ARG:NH2	72:ST:89:ARG:HB3	2.36	0.41
73:SU:83:ILE:HD12	73:SU:83:ILE:HA	1.94	0.41
76:SX:53:VAL:HG13	76:SX:99:ASN:H	1.86	0.41
1:1:1476:G:O6	46:Ll:2:PRO:HD2	2.21	0.41
1:1:2110:A:H2'	1:1:2111:U:H6	1.86	0.41
1:1:3191:G:H2'	1:1:3192:C:C6	2.56	0.41
2:2:75:A:N3	2:2:75:A:H2'	2.35	0.41
2:2:356:A:N6	76:SX:39:LYS:HZ1	2.18	0.41
2:2:652:G:H2'	2:2:653:G:C8	2.56	0.41
2:2:706:C:H42	2:2:727:C:N4	2.19	0.41
2:2:729:G:H2'	2:2:730:G:H8	1.86	0.41
2:2:1238:G:H3'	2:2:1239:A:H8	1.85	0.41
2:2:1378:U:O2'	73:SU:54:ARG:NH1	2.50	0.41
2:2:1606:G:OP1	58:SF:59:HIS:NE2	2.52	0.41
4:4:36:G:C5	42:Lh:91:ARG:HD3	2.56	0.41
4:4:142:C:H2'	4:4:143:U:H6	1.86	0.41
5:5:4:G:H2'	5:5:5:A:H8	1.86	0.41
5:5:30:C:H42	5:5:40:G:H1	1.69	0.41
6:A:236:ILE:HA	6:A:251:ALA:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:258:ILE:HG13	6:A:267:VAL:HB	2.02	0.41
9:LA:105:SER:HB3	9:LA:160:SER:O	2.21	0.41
10:LB:10:ARG:NH2	10:LB:14:LEU:HD21	2.37	0.41
10:LB:340:ARG:NH2	10:LB:343:LEU:HD11	2.32	0.41
12:LD:139:ASP:OD1	12:LD:139:ASP:C	2.64	0.41
14:LF:91:PHE:HB2	14:LF:145:PRO:HG3	2.02	0.41
15:LG:31:GLU:N	15:LG:31:GLU:OE1	2.54	0.41
20:LL:150:SER:C	20:LL:152:ARG:H	2.29	0.41
22:LN:186:GLY:O	22:LN:190:THR:HG23	2.21	0.41
25:LQ:188:LYS:HA	25:LQ:188:LYS:HD2	1.81	0.41
43:Li:14:THR:HG23	43:Li:21:ASN:HB3	2.03	0.41
44:Lj:31:LYS:HB3	44:Lj:33:VAL:HG22	2.03	0.41
44:Lj:58:VAL:HG22	44:Lj:59:THR:N	2.36	0.41
50:Lp:36:ARG:HD2	50:Lp:45:ASN:OD1	2.21	0.41
51:Lq:17:ASN:OD1	51:Lq:20:LEU:HB2	2.21	0.41
51:Lq:120:ARG:HD2	51:Lq:123:ARG:NH1	2.35	0.41
52:Ls:19:LEU:HD12	52:Ls:20:GLU:N	2.36	0.41
56:SD:216:PRO:HG3	70:SR:20:TYR:CZ	2.56	0.41
59:SG:7:HIS:HB2	59:SG:124:LEU:HD21	2.03	0.41
62:SJ:47:LEU:HD13	62:SJ:102:PHE:CE1	2.56	0.41
65:SM:52:LYS:NZ	84:Sf:129:GLY:HA3	2.36	0.41
73:SU:60:LEU:H	73:SU:60:LEU:HD23	1.86	0.41
78:SZ:37:ASP:OD1	78:SZ:38:LYS:N	2.53	0.41
82:Sd:26:HIS:CE1	82:Sd:28:ALA:HB3	2.56	0.41
1:1:533:C:C2	1:1:534:C:C5	3.10	0.40
1:1:995:A:H2'	1:1:996:C:O4'	2.21	0.40
1:1:3121:G:N2	1:1:3122:U:O4	2.51	0.40
1:1:3148:G:C2	1:1:3149:C:C4	3.09	0.40
2:2:102:A:H4'	2:2:103:A:O5'	2.20	0.40
2:2:748:C:H2'	2:2:749:U:C6	2.56	0.40
2:2:1165:U:HO2'	2:2:1166:G:P	2.44	0.40
2:2:1503:G:H2'	2:2:1504:C:C6	2.56	0.40
2:2:1620:C:H2'	2:2:1621:C:H6	1.86	0.40
3:3:47:C:H2'	3:3:48:C:C6	2.56	0.40
8:C:245:ARG:O	8:C:245:ARG:HG3	2.20	0.40
8:C:305:LEU:HB3	8:C:307:LEU:CD1	2.50	0.40
8:C:399:PHE:HE1	8:C:455:ILE:HB	1.86	0.40
10:LB:257:HIS:HA	10:LB:259:SER:N	2.36	0.40
12:LD:273:GLU:HA	12:LD:276:LYS:HZ1	1.85	0.40
16:LH:129:TYR:CD2	16:LH:218:ILE:HD12	2.56	0.40
18:LJ:47:VAL:O	18:LJ:68:VAL:HG13	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:LK:122:SER:HA	52:Ls:43:LYS:NZ	2.36	0.40
27:LS:164:ILE:HG22	27:LS:165:PHE:N	2.36	0.40
28:LT:126:VAL:HG23	28:LT:127:GLN:H	1.86	0.40
46:Ll:7:PHE:CE2	46:Ll:11:GLN:NE2	2.89	0.40
53:SA:42:LYS:HB2	70:SR:107:GLU:OE2	2.20	0.40
54:SB:29:TRP:HA	54:SB:46:THR:O	2.21	0.40
55:SC:109:ILE:HG12	55:SC:123:ILE:HG22	2.03	0.40
56:SD:68:ARG:HE	56:SD:68:ARG:HB2	1.75	0.40
58:SF:49:ILE:O	58:SF:49:ILE:HG13	2.20	0.40
58:SF:200:LYS:HD2	58:SF:201:LYS:N	2.36	0.40
59:SG:11:GLY:O	59:SG:129:HIS:HB2	2.21	0.40
60:SH:54:GLU:OE1	60:SH:64:ILE:HG22	2.21	0.40
63:SK:10:ALA:HA	63:SK:13:GLU:CD	2.46	0.40
69:SQ:29:ILE:O	69:SQ:29:ILE:HG13	2.22	0.40
1:1:927:C:H2'	1:1:928:C:C6	2.56	0.40
1:1:1713:A:H2'	1:1:1714:G:H8	1.86	0.40
1:1:1796:A:N6	1:1:1797:A:H62	2.19	0.40
1:1:2082:A:H8	1:1:2082:A:O5'	2.04	0.40
1:1:2219:A:H61	2:2:1751:A:H8	1.70	0.40
1:1:2841:U:H2'	1:1:2842:U:C6	2.56	0.40
1:1:3147:G:O3'	1:1:3148:G:H4'	2.20	0.40
2:2:40:A:H62	2:2:464:G:H21	1.69	0.40
2:2:231:G:O2'	2:2:232:G:P	2.78	0.40
2:2:779:A:C6	2:2:781:G:H1'	2.56	0.40
2:2:810:A:H62	2:2:856:G:H2'	1.86	0.40
2:2:1001:A:C4	2:2:1003:A:N6	2.90	0.40
2:2:1396:A:OP1	70:SR:60:ARG:NH1	2.32	0.40
2:2:1654:G:C5	2:2:1740:A:N6	2.89	0.40
6:A:31:LEU:O	6:A:42:ILE:HD12	2.21	0.40
11:LC:290:LEU:O	11:LC:296:ILE:HD12	2.20	0.40
16:LH:77:HIS:CD2	16:LH:77:HIS:H	2.39	0.40
19:LK:114:ARG:NH2	19:LK:129:VAL:HG13	2.36	0.40
28:LT:51:GLY:HA3	28:LT:92:ARG:HG3	2.02	0.40
30:LV:95:LEU:HA	31:LW:64:LEU:O	2.22	0.40
43:Li:9:ALA:CB	43:Li:10:PRO:CD	3.00	0.40
51:Lq:31:ASP:HB2	51:Lq:34:ASN:CB	2.51	0.40
54:SB:157:GLN:O	54:SB:161:ILE:HG13	2.21	0.40
55:SC:161:SER:HB2	55:SC:203:ASP:HB2	2.03	0.40
56:SD:72:LEU:O	56:SD:76:ILE:HG12	2.22	0.40
57:SE:11:ARG:O	57:SE:12:LEU:HB2	2.22	0.40
58:SF:20:VAL:HG22	58:SF:23:GLU:OE2	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:SI:81:VAL:HG12	61:SI:94:ASN:HA	2.02	0.40
62:SJ:27:LYS:HE3	62:SJ:27:LYS:HB2	1.85	0.40
83:Se:14:VAL:O	83:Se:18:THR:HG23	2.21	0.40
1:1:152:G:O2'	1:1:153:A:H4'	2.21	0.40
1:1:484:A:H2'	1:1:485:G:O4'	2.22	0.40
1:1:2937:U:O2'	1:1:2938:U:H5'	2.22	0.40
1:1:2976:C:C4	1:1:2977:U:C4	3.09	0.40
1:1:3047:C:H2'	1:1:3048:U:O4'	2.21	0.40
2:2:225:C:N3	2:2:233:G:N2	2.69	0.40
2:2:352:G:H2'	2:2:353:G:H8	1.87	0.40
2:2:1230:G:H2'	2:2:1231:A:O4'	2.21	0.40
2:2:1395:C:H2'	2:2:1396:A:C8	2.56	0.40
2:2:1729:C:H2'	2:2:1730:U:H6	1.86	0.40
4:4:55:U:C2	4:4:56:G:C8	3.09	0.40
6:A:215:THR:HA	6:A:231:ASN:HA	2.02	0.40
19:LK:64:ILE:O	19:LK:70:GLN:HG2	2.22	0.40
19:LK:86:LYS:HD2	19:LK:104:VAL:HG21	2.03	0.40
33:LY:108:LEU:HD23	33:LY:108:LEU:H	1.86	0.40
34:LZ:67:ILE:O	34:LZ:114:LYS:HD2	2.21	0.40
35:La:21:ARG:CZ	39:Le:39:ILE:HD11	2.51	0.40
38:Ld:63:ASP:OD2	38:Ld:103:TYR:OH	2.36	0.40
45:Lk:66:LEU:HD23	45:Lk:66:LEU:H	1.86	0.40
52:Ls:46:ARG:HD2	52:Ls:46:ARG:HA	1.79	0.40
55:SC:148:ARG:HB2	55:SC:230:TYR:CE2	2.57	0.40
58:SF:58:PRO:O	58:SF:78:GLU:HG2	2.20	0.40
58:SF:152:LEU:HD23	58:SF:156:ASN:OD1	2.22	0.40
59:SG:48:TYR:CE1	59:SG:116:GLN:HA	2.56	0.40
67:SO:96:ILE:HG22	67:SO:129:GLU:O	2.21	0.40
73:SU:24:THR:OG1	73:SU:109:GLU:HB2	2.21	0.40
1:1:576:A:H2'	1:1:577:C:C6	2.57	0.40
1:1:1003:G:C6	1:1:1015:C:C4	3.10	0.40
1:1:1009:U:OP2	1:1:1009:U:H2'	2.22	0.40
1:1:1660:G:H2'	1:1:1661:U:H6	1.85	0.40
1:1:3144:U:O2	1:1:3148:G:C2	2.73	0.40
1:1:3176:G:H2'	1:1:3177:C:H6	1.85	0.40
1:1:3332:A:HO2'	1:1:3333:G:P	2.44	0.40
2:2:16:G:H21	2:2:1135:A:H62	1.69	0.40
2:2:194:G:O2'	2:2:195:G:H8	2.05	0.40
2:2:225:C:H2'	2:2:226:C:C6	2.56	0.40
2:2:540:C:O2'	2:2:541:A:OP1	2.36	0.40
2:2:1519:U:H3	72:ST:75:ARG:NE	2.15	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:1525:C:H2'	2:2:1526:U:C6	2.56	0.40
2:2:1616:C:O2'	2:2:1617:U:OP1	2.35	0.40
3:3:60:A:H2'	3:3:61:C:C6	2.56	0.40
6:A:89:LEU:HB2	6:A:101:PHE:HE1	1.87	0.40
6:A:217:MET:HB3	6:A:219:TRP:NE1	2.37	0.40
8:C:260:THR:HG22	8:C:261:LYS:N	2.34	0.40
8:C:603:ILE:HD12	8:C:645:ALA:HA	2.04	0.40
19:LK:94:LYS:H	19:LK:94:LYS:HG2	1.76	0.40
22:LN:7:LEU:HD12	22:LN:7:LEU:HA	1.83	0.40
23:LO:31:GLY:HA2	23:LO:103:ARG:HH11	1.85	0.40
35:La:7:LYS:HD3	35:La:7:LYS:HA	1.82	0.40
53:SA:12:PRO:HB2	53:SA:17:ILE:HD11	2.02	0.40
54:SB:34:ALA:HB3	54:SB:41:ARG:HA	2.03	0.40
54:SB:163:ALA:HB1	54:SB:167:LYS:HZ1	1.87	0.40
57:SE:245:LEU:H	57:SE:245:LEU:HD12	1.86	0.40
64:SL:130:VAL:HB	64:SL:142:PHE:HB3	2.03	0.40
71:SS:28:VAL:HG12	71:SS:58:ALA:HA	2.03	0.40
73:SU:44:ASN:OD1	73:SU:45:LYS:HG3	2.21	0.40
75:SW:47:ILE:HG12	75:SW:48:GLY:H	1.85	0.40
77:SY:87:LYS:HE2	77:SY:87:LYS:HB2	1.88	0.40
1:1:233:G:O2'	1:1:234:C:OP1	2.37	0.40
1:1:1216:G:C6	1:1:1239:G:C6	3.09	0.40
1:1:1463:G:O4'	1:1:1466:G:N2	2.53	0.40
1:1:2227:U:O2'	1:1:2228:C:OP1	2.38	0.40
1:1:2532:C:O2	1:1:2532:C:H2'	2.21	0.40
1:1:2682:U:H2'	1:1:2683:U:C6	2.57	0.40
1:1:2903:U:O2'	1:1:2906:G:N7	2.54	0.40
1:1:3111:C:N4	1:1:3113:A:H1'	2.37	0.40
2:2:1141:U:H2'	2:2:1142:U:C6	2.57	0.40
2:2:1240:G:H3'	68:SP:59:ARG:NH2	2.36	0.40
2:2:1298:U:P	55:SC:96:LYS:HE3	2.62	0.40
2:2:1477:C:H4'	2:2:1478:C:OP1	2.21	0.40
2:2:1612:G:H2'	2:2:1613:U:C6	2.56	0.40
3:3:60:A:H2'	3:3:61:C:H6	1.87	0.40
4:4:26:U:H2'	4:4:27:U:H6	1.87	0.40
8:C:396:PHE:HB2	8:C:462:ASP:OD1	2.22	0.40
11:LC:139:ARG:NH1	11:LC:247:PRO:HG2	2.36	0.40
15:LG:101:ARG:H	15:LG:101:ARG:HG2	1.72	0.40
23:LO:118:LYS:HG3	23:LO:120:MET:CE	2.51	0.40
27:LS:139:TYR:CD1	27:LS:140:ILE:HG13	2.57	0.40
31:LW:149:ARG:HH12	31:LW:153:ILE:HD13	1.85	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:Lb:3:LYS:HE3	36:Lb:3:LYS:HB3	1.84	0.40
37:Lc:46:LEU:HD13	37:Lc:71:HIS:HB3	2.04	0.40
56:SD:144:LYS:HE3	56:SD:144:LYS:HB3	1.81	0.40
59:SG:1:MET:C	59:SG:2:LYS:HD3	2.47	0.40
63:SK:27:TYR:C	63:SK:28:GLU:HG3	2.47	0.40
64:SL:29:SER:OG	64:SL:30:THR:N	2.55	0.40
66:SN:46:THR:HG22	66:SN:49:GLN:HG2	2.04	0.40
68:SP:57:LEU:HD12	68:SP:61:PRO:HG2	2.03	0.40
68:SP:60:ARG:HB2	68:SP:61:PRO:HD3	2.04	0.40
71:SS:33:THR:CG2	71:SS:40:ARG:HA	2.51	0.40
75:SW:81:VAL:HG22	75:SW:123:GLY:O	2.21	0.40
79:Sa:11:ASN:O	79:Sa:11:ASN:ND2	2.54	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	A	310/316 (98%)	298 (96%)	12 (4%)	0	100	100
7	B	121/302 (40%)	110 (91%)	9 (7%)	2 (2%)	7	32
8	C	808/845 (96%)	756 (94%)	47 (6%)	5 (1%)	21	56
9	LA	246/254 (97%)	222 (90%)	24 (10%)	0	100	100
10	LB	385/392 (98%)	363 (94%)	22 (6%)	0	100	100
11	LC	361/365 (99%)	331 (92%)	30 (8%)	0	100	100
12	LD	298/304 (98%)	289 (97%)	8 (3%)	1 (0%)	36	70
13	LE	192/200 (96%)	172 (90%)	20 (10%)	0	100	100
14	LF	245/249 (98%)	232 (95%)	13 (5%)	0	100	100
15	LG	232/262 (88%)	218 (94%)	14 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
16	LH	189/229 (82%)	183 (97%)	6 (3%)	0	100	100
17	LI	215/219 (98%)	201 (94%)	13 (6%)	1 (0%)	24	60
18	LJ	165/173 (95%)	154 (93%)	11 (7%)	0	100	100
19	LK	154/165 (93%)	129 (84%)	21 (14%)	4 (3%)	4	23
20	LL	207/213 (97%)	193 (93%)	14 (7%)	0	100	100
21	LM	139/142 (98%)	134 (96%)	5 (4%)	0	100	100
22	LN	200/203 (98%)	188 (94%)	12 (6%)	0	100	100
23	LO	201/204 (98%)	193 (96%)	8 (4%)	0	100	100
24	LP	170/187 (91%)	163 (96%)	7 (4%)	0	100	100
25	LQ	181/213 (85%)	174 (96%)	7 (4%)	0	100	100
26	LR	182/192 (95%)	180 (99%)	2 (1%)	0	100	100
27	LS	171/174 (98%)	160 (94%)	11 (6%)	0	100	100
28	LT	156/160 (98%)	152 (97%)	4 (3%)	0	100	100
29	LU	98/127 (77%)	90 (92%)	8 (8%)	0	100	100
30	LV	135/139 (97%)	129 (96%)	6 (4%)	0	100	100
31	LW	131/205 (64%)	123 (94%)	8 (6%)	0	100	100
32	LX	119/156 (76%)	116 (98%)	3 (2%)	0	100	100
33	LY	131/138 (95%)	128 (98%)	3 (2%)	0	100	100
34	LZ	133/135 (98%)	127 (96%)	5 (4%)	1 (1%)	16	50
35	La	146/149 (98%)	136 (93%)	10 (7%)	0	100	100
36	Lb	61/65 (94%)	60 (98%)	1 (2%)	0	100	100
37	Lc	93/108 (86%)	90 (97%)	3 (3%)	0	100	100
38	Ld	110/120 (92%)	105 (96%)	5 (4%)	0	100	100
39	Le	122/131 (93%)	118 (97%)	4 (3%)	0	100	100
40	Lf	105/109 (96%)	99 (94%)	6 (6%)	0	100	100
41	Lg	110/119 (92%)	104 (94%)	6 (6%)	0	100	100
42	Lh	120/126 (95%)	115 (96%)	5 (4%)	0	100	100
43	Li	99/110 (90%)	96 (97%)	3 (3%)	0	100	100
44	Lj	86/95 (90%)	79 (92%)	7 (8%)	0	100	100
45	Lk	74/94 (79%)	69 (93%)	5 (7%)	0	100	100
46	Ll	48/51 (94%)	42 (88%)	6 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
47	Lm	50/127 (39%)	48 (96%)	2 (4%)	0	100	100
48	Ln	23/25 (92%)	23 (100%)	0	0	100	100
48	Lr	22/25 (88%)	22 (100%)	0	0	100	100
49	Lo	102/106 (96%)	98 (96%)	4 (4%)	0	100	100
50	Lp	89/92 (97%)	83 (93%)	6 (7%)	0	100	100
51	Lq	139/147 (95%)	130 (94%)	9 (6%)	0	100	100
52	Ls	187/312 (60%)	180 (96%)	6 (3%)	1 (0%)	24	60
53	SA	206/285 (72%)	188 (91%)	17 (8%)	1 (0%)	24	60
54	SB	220/255 (86%)	196 (89%)	24 (11%)	0	100	100
55	SC	214/263 (81%)	201 (94%)	13 (6%)	0	100	100
56	SD	210/254 (83%)	196 (93%)	13 (6%)	1 (0%)	24	60
57	SE	259/264 (98%)	243 (94%)	16 (6%)	0	100	100
58	SF	197/212 (93%)	178 (90%)	18 (9%)	1 (0%)	24	60
59	SG	230/239 (96%)	221 (96%)	7 (3%)	2 (1%)	14	48
60	SH	196/203 (97%)	185 (94%)	11 (6%)	0	100	100
61	SI	199/202 (98%)	189 (95%)	10 (5%)	0	100	100
62	SJ	177/190 (93%)	169 (96%)	8 (4%)	0	100	100
63	SK	87/159 (55%)	81 (93%)	5 (6%)	1 (1%)	11	43
64	SL	147/161 (91%)	138 (94%)	9 (6%)	0	100	100
65	SM	116/144 (81%)	101 (87%)	15 (13%)	0	100	100
66	SN	148/151 (98%)	141 (95%)	7 (5%)	0	100	100
67	SO	133/150 (89%)	118 (89%)	14 (10%)	1 (1%)	16	50
68	SP	126/153 (82%)	114 (90%)	12 (10%)	0	100	100
69	SQ	136/143 (95%)	124 (91%)	12 (9%)	0	100	100
70	SR	126/143 (88%)	119 (94%)	7 (6%)	0	100	100
71	SS	135/156 (86%)	125 (93%)	10 (7%)	0	100	100
72	ST	140/153 (92%)	130 (93%)	10 (7%)	0	100	100
73	SU	101/116 (87%)	89 (88%)	12 (12%)	0	100	100
74	SV	84/98 (86%)	82 (98%)	2 (2%)	0	100	100
75	SW	127/130 (98%)	118 (93%)	9 (7%)	0	100	100
76	SX	140/145 (97%)	127 (91%)	13 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
77	SY	119/136 (88%)	112 (94%)	6 (5%)	1 (1%)	16	50
78	SZ	67/99 (68%)	64 (96%)	3 (4%)	0	100	100
79	Sa	102/119 (86%)	98 (96%)	4 (4%)	0	100	100
80	Sb	79/82 (96%)	72 (91%)	7 (9%)	0	100	100
81	Sc	58/68 (85%)	55 (95%)	3 (5%)	0	100	100
82	Sd	50/56 (89%)	45 (90%)	5 (10%)	0	100	100
83	Se	41/62 (66%)	38 (93%)	3 (7%)	0	100	100
84	Sf	72/154 (47%)	61 (85%)	11 (15%)	0	100	100
All	All	12503/14119 (89%)	11723 (94%)	757 (6%)	23 (0%)	44	76

All (23) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	C	487	VAL
7	B	104	ARG
8	C	374	CYS
52	Ls	103	ASN
58	SF	31	ASN
7	B	70	ALA
8	C	582	PRO
19	LK	87	GLU
34	LZ	102	GLU
56	SD	8	ILE
59	SG	29	ASP
63	SK	85	VAL
77	SY	40	LYS
8	C	451	PRO
19	LK	58	VAL
59	SG	27	PHE
67	SO	47	SER
17	LI	111	LEU
53	SA	13	THR
12	LD	254	PRO
19	LK	22	VAL
19	LK	98	ILE
8	C	262	SER

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	
6	A	271/274 (99%)	271 (100%)	0	100	100
7	B	93/224 (42%)	93 (100%)	0	100	100
8	C	693/719 (96%)	693 (100%)	0	100	100
9	LA	192/198 (97%)	192 (100%)	0	100	100
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	202/222 (91%)	201 (100%)	1 (0%)	81	89
16	LH	168/200 (84%)	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
19	LK	127/136 (93%)	127 (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	162/163 (99%)	162 (100%)	0	100	100
24	LP	140/152 (92%)	140 (100%)	0	100	100
25	LQ	155/178 (87%)	155 (100%)	0	100	100
26	LR	153/160 (96%)	153 (100%)	0	100	100
27	LS	153/154 (99%)	153 (100%)	0	100	100
28	LT	134/135 (99%)	134 (100%)	0	100	100
29	LU	88/108 (82%)	88 (100%)	0	100	100
30	LV	101/102 (99%)	101 (100%)	0	100	100
31	LW	107/163 (66%)	107 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
32	LX	108/129 (84%)	108 (100%)	0	100	100
33	LY	116/119 (98%)	116 (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	54/55 (98%)	54 (100%)	0	100	100
37	Lc	77/88 (88%)	77 (100%)	0	100	100
38	Ld	96/105 (91%)	96 (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	85/93 (91%)	85 (100%)	0	100	100
44	Lj	72/78 (92%)	72 (100%)	0	100	100
45	Lk	73/88 (83%)	73 (100%)	0	100	100
46	Ll	45/46 (98%)	45 (100%)	0	100	100
47	Lm	47/114 (41%)	47 (100%)	0	100	100
48	Ln	23/23 (100%)	23 (100%)	0	100	100
48	Lr	22/23 (96%)	22 (100%)	0	100	100
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
53	SA	178/225 (79%)	178 (100%)	0	100	100
54	SB	197/223 (88%)	197 (100%)	0	100	100
55	SC	181/206 (88%)	181 (100%)	0	100	100
56	SD	182/206 (88%)	182 (100%)	0	100	100
57	SE	219/221 (99%)	219 (100%)	0	100	100
58	SF	167/178 (94%)	167 (100%)	0	100	100
59	SG	198/204 (97%)	198 (100%)	0	100	100
60	SH	172/177 (97%)	172 (100%)	0	100	100
61	SI	163/164 (99%)	163 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
62	SJ	154/162 (95%)	154 (100%)	0	100	100
63	SK	77/126 (61%)	77 (100%)	0	100	100
64	SL	132/143 (92%)	132 (100%)	0	100	100
65	SM	101/121 (84%)	101 (100%)	0	100	100
66	SN	129/130 (99%)	129 (100%)	0	100	100
67	SO	103/117 (88%)	103 (100%)	0	100	100
68	SP	111/132 (84%)	111 (100%)	0	100	100
69	SQ	111/115 (96%)	111 (100%)	0	100	100
70	SR	119/131 (91%)	119 (100%)	0	100	100
71	SS	120/135 (89%)	120 (100%)	0	100	100
72	ST	114/124 (92%)	114 (100%)	0	100	100
73	SU	93/103 (90%)	93 (100%)	0	100	100
74	SV	69/80 (86%)	69 (100%)	0	100	100
75	SW	112/113 (99%)	112 (100%)	0	100	100
76	SX	113/116 (97%)	113 (100%)	0	100	100
77	SY	104/115 (90%)	104 (100%)	0	100	100
78	SZ	60/80 (75%)	60 (100%)	0	100	100
79	Sa	91/103 (88%)	91 (100%)	0	100	100
80	Sb	70/71 (99%)	70 (100%)	0	100	100
81	Sc	53/61 (87%)	53 (100%)	0	100	100
82	Sd	43/46 (94%)	43 (100%)	0	100	100
83	Se	37/51 (72%)	37 (100%)	0	100	100
84	Sf	67/139 (48%)	67 (100%)	0	100	100
All	All	10695/11815 (90%)	10694 (100%)	1 (0%)	100	100

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
15	LG	98	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (98) such sidechains are listed below:

Mol	Chain	Res	Type
7	B	136	GLN
8	C	27	HIS
8	C	93	GLN
8	C	103	ASN
8	C	147	GLN
8	C	170	GLN
8	C	343	HIS
8	C	454	ASN
9	LA	19	HIS
9	LA	79	ASN
9	LA	100	ASN
10	LB	185	ASN
10	LB	262	GLN
11	LC	115	ASN
11	LC	141	HIS
11	LC	203	HIS
11	LC	228	ASN
11	LC	292	ASN
11	LC	324	GLN
12	LD	39	GLN
12	LD	206	HIS
13	LE	162	GLN
14	LF	9	GLN
14	LF	242	ASN
15	LG	106	GLN
16	LH	95	HIS
16	LH	133	HIS
16	LH	137	ASN
16	LH	208	ASN
16	LH	225	ASN
17	LI	73	ASN
17	LI	170	ASN
19	LK	14	HIS
19	LK	70	GLN
20	LL	5	HIS
20	LL	103	ASN
22	LN	91	GLN
22	LN	153	ASN
23	LO	132	GLN
24	LP	49	GLN
26	LR	182	ASN
27	LS	8	GLN
27	LS	74	ASN

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Mol	Chain	Res	Type
28	LT	49	GLN
29	LU	55	ASN
33	LY	80	HIS
34	LZ	122	ASN
36	Lb	10	HIS
39	Le	90	ASN
39	Le	115	GLN
44	Lj	76	ASN
45	Lk	33	GLN
46	Ll	19	GLN
49	Lo	82	GLN
51	Lq	48	ASN
51	Lq	97	GLN
52	Ls	83	ASN
52	Ls	103	ASN
53	SA	72	ASN
53	SA	99	GLN
54	SB	31	ASN
54	SB	58	ASN
54	SB	124	ASN
54	SB	183	GLN
55	SC	228	ASN
56	SD	182	GLN
57	SE	197	HIS
58	SF	31	ASN
58	SF	118	GLN
58	SF	145	GLN
59	SG	200	GLN
61	SI	52	ASN
63	SK	56	GLN
64	SL	86	HIS
64	SL	97	HIS
64	SL	109	HIS
64	SL	111	ASN
66	SN	49	GLN
66	SN	123	HIS
67	SO	37	ASN
67	SO	112	GLN
68	SP	145	HIS
69	SQ	24	GLN
69	SQ	32	ASN
70	SR	94	HIS

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Mol	Chain	Res	Type
71	SS	136	GLN
72	ST	64	HIS
73	SU	103	ASN
75	SW	64	GLN
75	SW	80	ASN
76	SX	63	GLN
77	SY	37	ASN
78	SZ	80	GLN
79	Sa	43	ASN
79	Sa	94	ASN
80	Sb	65	GLN
82	Sd	41	GLN
84	Sf	123	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	3189/3337 (95%)	591 (18%)	75 (2%)
2	2	1761/1796 (98%)	391 (22%)	65 (3%)
3	3	118/120 (98%)	10 (8%)	1 (0%)
4	4	155/156 (99%)	23 (14%)	1 (0%)
5	5	74/75 (98%)	45 (60%)	9 (12%)
All	All	5297/5484 (96%)	1060 (20%)	151 (2%)

All (1060) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	21	A
1	1	23	G
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	76	G
1	1	86	A
1	1	93	G
1	1	97	G

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Mol	Chain	Res	Type
1	1	111	G
1	1	114	C
1	1	117	A
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	158	A
1	1	165	G
1	1	170	A
1	1	179	C
1	1	181	G
1	1	184	U
1	1	185	U
1	1	191	G
1	1	204	C
1	1	212	G
1	1	213	A
1	1	214	G
1	1	215	A
1	1	225	A
1	1	233	G
1	1	234	C
1	1	242	G
1	1	245	U
1	1	251	U
1	1	262	G
1	1	263	U
1	1	276	G
1	1	277	A
1	1	279	U
1	1	288	A
1	1	291	U
1	1	316	A
1	1	326	C
1	1	332	C
1	1	343	C
1	1	363	U

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Mol	Chain	Res	Type
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	430	G
1	1	432	C
1	1	434	U
1	1	447	U
1	1	448	C
1	1	460	U
1	1	461	C
1	1	468	G
1	1	469	C
1	1	470	A
1	1	471	C
1	1	472	U
1	1	485	G
1	1	489	A
1	1	511	U
1	1	512	A
1	1	524	A
1	1	527	G
1	1	536	C
1	1	537	C
1	1	539	G
1	1	547	A
1	1	549	A
1	1	558	U
1	1	559	G
1	1	560	U
1	1	570	G
1	1	583	A
1	1	585	C
1	1	586	G
1	1	591	C
1	1	592	U

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Mol	Chain	Res	Type
1	1	593	G
1	1	595	A
1	1	597	G
1	1	599	A
1	1	607	G
1	1	608	U
1	1	609	A
1	1	610	A
1	1	624	C
1	1	637	A
1	1	645	A
1	1	648	A
1	1	665	A
1	1	669	U
1	1	671	U
1	1	679	A
1	1	696	G
1	1	697	A
1	1	700	G
1	1	703	A
1	1	704	A
1	1	715	A
1	1	722	G
1	1	748	U
1	1	749	U
1	1	758	U
1	1	759	U
1	1	762	A
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

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Mol	Chain	Res	Type
1	1	898	G
1	1	899	A
1	1	919	G
1	1	923	G
1	1	926	A
1	1	941	C
1	1	942	U
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	1002	G
1	1	1007	U
1	1	1008	U
1	1	1009	U
1	1	1010	U
1	1	1011	U
1	1	1012	A
1	1	1013	G
1	1	1015	C
1	1	1017	U
1	1	1030	A
1	1	1032	C
1	1	1047	A
1	1	1048	A
1	1	1055	G
1	1	1064	C
1	1	1065	U
1	1	1068	A
1	1	1076	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

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Mol	Chain	Res	Type
1	1	1100	G
1	1	1114	G
1	1	1127	U
1	1	1131	G
1	1	1134	U
1	1	1136	A
1	1	1142	A
1	1	1148	G
1	1	1161	G
1	1	1163	G
1	1	1164	U
1	1	1165	G
1	1	1173	A
1	1	1175	C
1	1	1176	A
1	1	1184	C
1	1	1192	G
1	1	1196	G
1	1	1203	U
1	1	1204	U
1	1	1205	G
1	1	1206	A
1	1	1215	C
1	1	1219	G
1	1	1220	G
1	1	1222	C
1	1	1224	U
1	1	1225	G
1	1	1228	A
1	1	1229	G
1	1	1231	C
1	1	1237	C
1	1	1241	U
1	1	1242	A
1	1	1243	A
1	1	1244	G
1	1	1245	G
1	1	1246	A
1	1	1248	U
1	1	1255	C
1	1	1268	G
1	1	1269	A

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Mol	Chain	Res	Type
1	1	1270	A
1	1	1288	U
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	1368	C
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	1429	A
1	1	1433	G
1	1	1458	G
1	1	1464	A
1	1	1465	A
1	1	1466	G
1	1	1467	U
1	1	1474	A
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	1544	G

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Mol	Chain	Res	Type
1	1	1545	G
1	1	1549	C
1	1	1550	U
1	1	1551	C
1	1	1552	G
1	1	1554	G
1	1	1555	C
1	1	1559	G
1	1	1560	U
1	1	1561	G
1	1	1567	A
1	1	1569	A
1	1	1585	A
1	1	1587	U
1	1	1588	C
1	1	1602	U
1	1	1609	U
1	1	1611	C
1	1	1619	C
1	1	1623	A
1	1	1624	C
1	1	1625	U
1	1	1626	G
1	1	1637	C
1	1	1663	C
1	1	1685	U
1	1	1696	A
1	1	1697	C
1	1	1704	U
1	1	1730	A
1	1	1731	G
1	1	1732	A
1	1	1740	A
1	1	1742	U
1	1	1744	C
1	1	1745	U
1	1	1746	G
1	1	1750	G
1	1	1760	G
1	1	1777	A
1	1	1792	G
1	1	1793	A

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Mol	Chain	Res	Type
1	1	1794	A
1	1	1795	U
1	1	1796	A
1	1	1797	A
1	1	1798	U
1	1	1799	U
1	1	1800	C
1	1	1801	U
1	1	1819	A
1	1	1820	U
1	1	1821	A
1	1	1822	A
1	1	1826	C
1	1	1829	C
1	1	1830	A
1	1	1858	G
1	1	1859	A
1	1	1860	U
1	1	1866	A
1	1	1886	G
1	1	1887	C
1	1	1888	A
1	1	1906	C
1	1	1914	G
1	1	1934	G
1	1	1935	C
1	1	1936	A
1	1	1937	C
1	1	1942	G
1	1	2044	G
1	1	2045	G
1	1	2047	G
1	1	2048	U
1	1	2052	G
1	1	2053	U
1	1	2054	U
1	1	2055	A
1	1	2056	A
1	1	2063	A
1	1	2065	U
1	1	2074	G
1	1	2076	A

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Mol	Chain	Res	Type
1	1	2084	G
1	1	2085	G
1	1	2094	A
1	1	2096	U
1	1	2102	A
1	1	2107	A
1	1	2121	A
1	1	2123	G
1	1	2127	A
1	1	2132	G
1	1	2133	U
1	1	2134	G
1	1	2139	U
1	1	2149	U
1	1	2151	A
1	1	2155	C
1	1	2168	U
1	1	2169	G
1	1	2171	A
1	1	2172	U
1	1	2173	G
1	1	2186	A
1	1	2188	U
1	1	2192	A
1	1	2211	C
1	1	2216	G
1	1	2217	U
1	1	2218	A
1	1	2219	A
1	1	2220	C
1	1	2221	U
1	1	2228	C
1	1	2232	U
1	1	2233	A
1	1	2235	G
1	1	2236	G
1	1	2242	A
1	1	2244	A
1	1	2248	C
1	1	2251	G
1	1	2270	G
1	1	2273	U

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Mol	Chain	Res	Type
1	1	2276	A
1	1	2278	G
1	1	2281	U
1	1	2297	U
1	1	2299	U
1	1	2335	A
1	1	2336	A
1	1	2337	C
1	1	2338	G
1	1	2339	G
1	1	2356	G
1	1	2360	A
1	1	2364	A
1	1	2365	A
1	1	2366	G
1	1	2367	A
1	1	2368	C
1	1	2374	U
1	1	2382	A
1	1	2398	G
1	1	2464	U
1	1	2465	U
1	1	2474	A
1	1	2475	C
1	1	2477	U
1	1	2478	A
1	1	2485	G
1	1	2487	A
1	1	2488	G
1	1	2489	C
1	1	2492	G
1	1	2497	G
1	1	2501	U
1	1	2502	G
1	1	2503	C
1	1	2504	G
1	1	2506	C
1	1	2510	C
1	1	2511	U
1	1	2513	C
1	1	2521	A
1	1	2522	A

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Mol	Chain	Res	Type
1	1	2527	C
1	1	2529	U
1	1	2530	C
1	1	2531	G
1	1	2532	C
1	1	2533	G
1	1	2543	G
1	1	2544	G
1	1	2552	A
1	1	2553	C
1	1	2565	G
1	1	2566	G
1	1	2573	G
1	1	2585	A
1	1	2611	U
1	1	2615	A
1	1	2622	G
1	1	2625	C
1	1	2633	A
1	1	2636	G
1	1	2638	A
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	2678	U
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	2740	U
1	1	2741	U
1	1	2755	G
1	1	2758	A

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Mol	Chain	Res	Type
1	1	2759	G
1	1	2760	A
1	1	2762	A
1	1	2769	C
1	1	2776	A
1	1	2777	U
1	1	2788	U
1	1	2798	G
1	1	2802	U
1	1	2803	C
1	1	2804	A
1	1	2828	U
1	1	2830	G
1	1	2831	A
1	1	2834	U
1	1	2846	A
1	1	2858	C
1	1	2863	U
1	1	2866	G
1	1	2882	U
1	1	2884	C
1	1	2894	U
1	1	2895	A
1	1	2900	A
1	1	2901	C
1	1	2906	G
1	1	2930	A
1	1	2931	G
1	1	2942	C
1	1	2958	G
1	1	2970	A
1	1	2979	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

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Mol	Chain	Res	Type
1	1	3075	C
1	1	3079	U
1	1	3080	A
1	1	3088	A
1	1	3089	U
1	1	3100	A
1	1	3101	C
1	1	3112	U
1	1	3113	A
1	1	3119	A
1	1	3121	G
1	1	3122	U
1	1	3127	G
1	1	3128	A
1	1	3129	C
1	1	3130	G
1	1	3131	U
1	1	3132	A
1	1	3135	A
1	1	3141	G
1	1	3146	C
1	1	3148	G
1	1	3151	U
1	1	3152	C
1	1	3153	G
1	1	3154	U
1	1	3158	C
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	3190	G
1	1	3200	A
1	1	3201	A
1	1	3211	U
1	1	3214	A
1	1	3218	U
1	1	3219	A
1	1	3220	G
1	1	3223	A

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Mol	Chain	Res	Type
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	3236	A
1	1	3245	C
1	1	3248	A
1	1	3254	U
1	1	3257	A
1	1	3258	U
1	1	3259	G
1	1	3260	U
1	1	3282	U
1	1	3292	U
1	1	3293	U
1	1	3294	G
1	1	3295	U
1	1	3297	G
1	1	3299	U
1	1	3304	U
1	1	3309	U
1	1	3310	G
1	1	3319	C
1	1	3324	C
1	1	3325	U
1	1	3328	G
1	1	3331	U
1	1	3332	A
1	1	3333	G
2	2	4	C
2	2	5	U
2	2	17	C
2	2	25	C
2	2	26	A
2	2	27	U
2	2	34	G
2	2	42	G
2	2	47	A
2	2	57	G
2	2	68	A

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Mol	Chain	Res	Type
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	101	U
2	2	103	A
2	2	113	C
2	2	114	G
2	2	126	G
2	2	127	U
2	2	137	C
2	2	138	A
2	2	141	G
2	2	155	U
2	2	156	U
2	2	173	C
2	2	174	U
2	2	175	G
2	2	176	A
2	2	181	C
2	2	184	G
2	2	185	A
2	2	186	C
2	2	187	U
2	2	188	U
2	2	189	C
2	2	190	G
2	2	192	A
2	2	195	G
2	2	210	A
2	2	213	A
2	2	214	A
2	2	215	A
2	2	216	A
2	2	217	A
2	2	221	A
2	2	222	U
2	2	223	G
2	2	224	C
2	2	231	G

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Mol	Chain	Res	Type
2	2	232	G
2	2	234	C
2	2	235	U
2	2	236	U
2	2	237	U
2	2	238	C
2	2	247	C
2	2	258	C
2	2	262	A
2	2	268	A
2	2	269	C
2	2	270	G
2	2	275	U
2	2	277	C
2	2	296	A
2	2	311	C
2	2	313	A
2	2	314	C
2	2	317	U
2	2	319	G
2	2	321	C
2	2	326	G
2	2	334	G
2	2	335	C
2	2	338	G
2	2	349	A
2	2	353	G
2	2	356	A
2	2	357	A
2	2	358	C
2	2	367	A
2	2	377	C
2	2	390	C
2	2	396	A
2	2	397	A
2	2	398	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

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Mol	Chain	Res	Type
2	2	423	G
2	2	431	G
2	2	434	A
2	2	436	U
2	2	441	C
2	2	445	C
2	2	452	C
2	2	461	A
2	2	465	A
2	2	472	A
2	2	474	A
2	2	480	A
2	2	489	U
2	2	490	U
2	2	491	U
2	2	492	C
2	2	493	G
2	2	502	A
2	2	503	A
2	2	505	U
2	2	508	A
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	539	A
2	2	540	C
2	2	541	A
2	2	546	G
2	2	552	A
2	2	553	A
2	2	555	U
2	2	556	C
2	2	562	C
2	2	567	A
2	2	571	G
2	2	575	U
2	2	576	A
2	2	577	A
2	2	579	U

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Mol	Chain	Res	Type
2	2	591	A
2	2	592	G
2	2	608	U
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	637	U
2	2	645	G
2	2	647	C
2	2	677	U
2	2	678	G
2	2	679	G
2	2	680	G
2	2	686	C
2	2	688	U
2	2	689	U
2	2	690	U
2	2	692	C
2	2	693	U
2	2	705	G
2	2	706	C
2	2	707	A
2	2	709	G
2	2	710	C
2	2	725	G
2	2	726	U
2	2	727	C
2	2	730	G
2	2	731	G
2	2	732	A
2	2	741	U
2	2	754	A
2	2	755	A
2	2	764	G
2	2	765	C
2	2	773	A
2	2	774	G
2	2	779	A

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Mol	Chain	Res	Type
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	822	G
2	2	824	U
2	2	827	A
2	2	828	U
2	2	829	U
2	2	830	U
2	2	832	G
2	2	833	U
2	2	861	A
2	2	874	G
2	2	879	G
2	2	884	U
2	2	894	U
2	2	896	A
2	2	897	G
2	2	905	A
2	2	910	U
2	2	911	G
2	2	912	G
2	2	913	A
2	2	931	A
2	2	933	U
2	2	940	G
2	2	949	A
2	2	957	U
2	2	958	U
2	2	964	A
2	2	982	G
2	2	988	C
2	2	990	A
2	2	991	A
2	2	1002	U

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Mol	Chain	Res	Type
2	2	1003	A
2	2	1024	A
2	2	1026	C
2	2	1028	A
2	2	1030	G
2	2	1037	A
2	2	1038	G
2	2	1053	U
2	2	1054	U
2	2	1055	A
2	2	1056	U
2	2	1057	U
2	2	1058	U
2	2	1059	U
2	2	1060	U
2	2	1062	A
2	2	1079	C
2	2	1088	A
2	2	1089	A
2	2	1093	G
2	2	1094	U
2	2	1095	U
2	2	1097	G
2	2	1098	G
2	2	1135	A
2	2	1136	A
2	2	1140	A
2	2	1147	G
2	2	1152	G
2	2	1155	C
2	2	1156	C
2	2	1157	A
2	2	1164	G
2	2	1166	G
2	2	1182	U
2	2	1188	B8N
2	2	1191	A
2	2	1193	A
2	2	1194	C
2	2	1196	G
2	2	1197	G
2	2	1214	A

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Mol	Chain	Res	Type
2	2	1215	G
2	2	1217	C
2	2	1223	G
2	2	1225	G
2	2	1226	G
2	2	1227	A
2	2	1228	U
2	2	1237	U
2	2	1238	G
2	2	1240	G
2	2	1241	A
2	2	1242	G
2	2	1243	C
2	2	1252	G
2	2	1253	A
2	2	1254	U
2	2	1255	U
2	2	1256	U
2	2	1282	U
2	2	1283	U
2	2	1288	G
2	2	1311	U
2	2	1312	U
2	2	1318	A
2	2	1324	C
2	2	1334	A
2	2	1338	G
2	2	1341	A
2	2	1342	A
2	2	1344	U
2	2	1351	U
2	2	1357	C
2	2	1358	U
2	2	1360	G
2	2	1369	C
2	2	1370	C
2	2	1371	G
2	2	1379	A
2	2	1387	U
2	2	1390	C
2	2	1391	G
2	2	1392	G

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Mol	Chain	Res	Type
2	2	1395	C
2	2	1398	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	1440	A
2	2	1441	G
2	2	1442	A
2	2	1444	G
2	2	1455	C
2	2	1456	A
2	2	1467	A
2	2	1478	C
2	2	1482	G
2	2	1486	A
2	2	1487	C
2	2	1488	U
2	2	1489	C
2	2	1492	U
2	2	1499	A
2	2	1502	G
2	2	1512	A
2	2	1517	G
2	2	1519	U
2	2	1520	A
2	2	1531	U
2	2	1532	G
2	2	1533	C
2	2	1534	U
2	2	1538	G
2	2	1544	G
2	2	1553	U
2	2	1555	A
2	2	1565	A
2	2	1568	G
2	2	1570	G
2	2	1580	G
2	2	1586	G
2	2	1593	A

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Mol	Chain	Res	Type
2	2	1597	G
2	2	1603	G
2	2	1612	G
2	2	1615	C
2	2	1617	U
2	2	1627	A
2	2	1630	C
2	2	1631	A
2	2	1653	U
2	2	1654	G
2	2	1662	C
2	2	1678	C
2	2	1684	C
2	2	1687	A
2	2	1696	C
2	2	1699	C
2	2	1704	A
2	2	1706	U
2	2	1708	A
2	2	1711	G
2	2	1712	C
2	2	1713	C
2	2	1714	G
2	2	1726	A
2	2	1741	G
2	2	1746	A
2	2	1751	A
2	2	1752	A
2	2	1754	U
2	2	1756	G
2	2	1762	A
2	2	1763	G
2	2	1765	U
2	2	1766	C
2	2	1776	G
2	2	1778	A
2	2	1779	C
2	2	1788	G
2	2	1789	G
2	2	1790	A
2	2	1791	U
2	2	1792	C

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Mol	Chain	Res	Type
2	2	1795	U
2	2	1796	U
3	3	7	G
3	3	19	U
3	3	54	U
3	3	55	A
3	3	65	G
3	3	73	U
3	3	90	G
3	3	92	C
3	3	101	A
3	3	111	G
4	4	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	81	U
4	4	82	U
4	4	83	C
4	4	84	C
4	4	85	G
4	4	87	G
4	4	95	G
4	4	104	A
4	4	106	C
4	4	111	A
4	4	113	U
4	4	116	G
4	4	125	U
4	4	126	A
4	4	138	A
4	4	144	G
5	5	5	A
5	5	7	A
5	5	8	U
5	5	9	A
5	5	10	G
5	5	11	C
5	5	12	G

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Mol	Chain	Res	Type
5	5	14	A
5	5	15	A
5	5	16	C
5	5	17	G
5	5	18	G
5	5	19	C
5	5	20	U
5	5	21	A
5	5	23	C
5	5	24	A
5	5	25	C
5	5	28	C
5	5	31	G
5	5	37	A
5	5	38	C
5	5	42	G
5	5	43	G
5	5	44	A
5	5	45	G
5	5	46	A
5	5	47	C
5	5	48	C
5	5	52	G
5	5	53	U
5	5	54	U
5	5	55	C
5	5	56	G
5	5	57	A
5	5	58	C
5	5	59	U
5	5	60	C
5	5	63	C
5	5	64	G
5	5	69	G
5	5	72	G
5	5	73	C
5	5	74	C
5	5	75	A

All (151) RNA pucker outliers are listed below:

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Mol	Chain	Res	Type
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Mol	Chain	Res	Type
1	1	133	C
1	1	233	G
1	1	250	C
1	1	275	G
1	1	431	A
1	1	484	A
1	1	536	C
1	1	585	C
1	1	609	A
1	1	703	A
1	1	898	G
1	1	960	C
1	1	1016	U
1	1	1047	A
1	1	1064	C
1	1	1077	U
1	1	1203	U
1	1	1204	U
1	1	1205	G
1	1	1221	C
1	1	1224	U
1	1	1228	A
1	1	1236	U
1	1	1267	C
1	1	1269	A
1	1	1288	U
1	1	1290	G
1	1	1338	A
1	1	1543	G
1	1	1549	C
1	1	1550	U
1	1	1551	C
1	1	1587	U
1	1	1730	A
1	1	1731	G
1	1	1796	A
1	1	2043	C
1	1	2044	G
1	1	2046	C
1	1	2054	U
1	1	2064	C

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Mol	Chain	Res	Type
1	1	2075	U
1	1	2132	G
1	1	2167	C
1	1	2172	U
1	1	2217	U
1	1	2219	A
1	1	2227	U
1	1	2232	U
1	1	2337	C
1	1	2367	A
1	1	2503	C
1	1	2510	C
1	1	2531	G
1	1	2532	C
1	1	2552	A
1	1	2621	G
1	1	2637	A
1	1	2731	C
1	1	2900	A
1	1	2979	A
1	1	3074	G
1	1	3079	U
1	1	3121	G
1	1	3163	A
1	1	3169	U
1	1	3210	U
1	1	3224	C
1	1	3230	G
1	1	3258	U
1	1	3281	G
1	1	3292	U
1	1	3293	U
1	1	3298	U
1	1	3332	A
2	2	73	U
2	2	75	A
2	2	102	A
2	2	126	G
2	2	136	A
2	2	155	U
2	2	184	G
2	2	187	U

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Mol	Chain	Res	Type
2	2	188	U
2	2	212	U
2	2	221	A
2	2	222	U
2	2	231	G
2	2	233	G
2	2	236	U
2	2	269	C
2	2	316	U
2	2	352	G
2	2	414	A
2	2	501	U
2	2	509	A
2	2	539	A
2	2	552	A
2	2	576	A
2	2	644	A
2	2	678	G
2	2	687	C
2	2	725	G
2	2	726	U
2	2	740	C
2	2	754	A
2	2	792	U
2	2	827	A
2	2	829	U
2	2	832	G
2	2	896	A
2	2	910	U
2	2	911	G
2	2	912	G
2	2	1053	U
2	2	1055	A
2	2	1056	U
2	2	1057	U
2	2	1058	U
2	2	1094	U
2	2	1097	G
2	2	1165	U
2	2	1193	A
2	2	1214	A
2	2	1224	A

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Mol	Chain	Res	Type
2	2	1241	A
2	2	1252	G
2	2	1282	U
2	2	1341	A
2	2	1369	C
2	2	1378	U
2	2	1455	C
2	2	1477	C
2	2	1487	C
2	2	1531	U
2	2	1564	C
2	2	1569	A
2	2	1616	C
2	2	1653	U
2	2	1751	A
3	3	72	G
4	4	83	C
5	5	7	A
5	5	9	A
5	5	16	C
5	5	18	G
5	5	44	A
5	5	47	C
5	5	55	C
5	5	59	U
5	5	73	C

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	$\# Z > 2$
8	DDE	C	701	8	18,20,21	1.01	1 (5%)	17,28,30	0.92	1 (5%)
2	B8N	2	1188	2	25,29,30	2.57	5 (20%)	28,42,45	1.33	3 (10%)

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
8	DDE	C	701	8	-	6/20/21/23	0/1/1/1
2	B8N	2	1188	2	-	3/16/34/35	0/2/2/2

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	1188	B8N	O4-C4	9.49	1.42	1.23
2	2	1188	B8N	C2-N3	-3.89	1.32	1.38
2	2	1188	B8N	C4-N3	-3.86	1.33	1.40
2	2	1188	B8N	C4-C5	-3.57	1.39	1.47
2	2	1188	B8N	C6-C5	3.05	1.39	1.35
8	C	701	DDE	CD2-CG	2.60	1.41	1.36

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	1188	B8N	N3-C2-N1	3.41	120.88	116.72
2	2	1188	B8N	C4-N3-C2	-3.15	121.74	125.62
8	C	701	DDE	CA-CB-CG	-2.79	106.87	113.77
2	2	1188	B8N	O4'-C1'-C2'	2.12	108.09	105.15

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	C	701	DDE	NAD-CBI-CBW-NCB
8	C	701	DDE	CBI-CBW-NCB-CAC
8	C	701	DDE	CBI-CBW-NCB-CAA
8	C	701	DDE	CAU-CBW-NCB-CAC
8	C	701	DDE	CAU-CBW-NCB-CAA
2	2	1188	B8N	N3-C31-C32-C33
2	2	1188	B8N	O4'-C1'-C5-C4
2	2	1188	B8N	N34-C33-C34-O35
8	C	701	DDE	CA-CB-CG-ND1

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	C	701	DDE	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 11 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	$\# Z > 2$
86	GDP	C	901	85	29,30,30	1.16	3 (10%)	45,47,47	1.78	7 (15%)

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
86	GDP	C	901	85	-	5/16/32/32	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
86	C	901	GDP	C5-C4	3.08	1.47	1.38
86	C	901	GDP	C6-N1	-2.50	1.34	1.38
86	C	901	GDP	C5-N7	-2.08	1.34	1.39

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
86	C	901	GDP	C5-C4-N3	-6.21	118.51	128.39
86	C	901	GDP	C2-N3-C4	5.11	121.10	112.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
86	C	901	GDP	N9-C4-N3	4.58	135.11	125.95
86	C	901	GDP	C6-C5-N7	3.28	136.26	130.29
86	C	901	GDP	C4-C5-N7	-2.62	106.53	110.67
86	C	901	GDP	C3'-C2'-C1'	2.26	105.75	101.46
86	C	901	GDP	O6-C6-C5	-2.04	121.14	126.53

There are no chirality outliers.

All (5) torsion outliers are listed below:

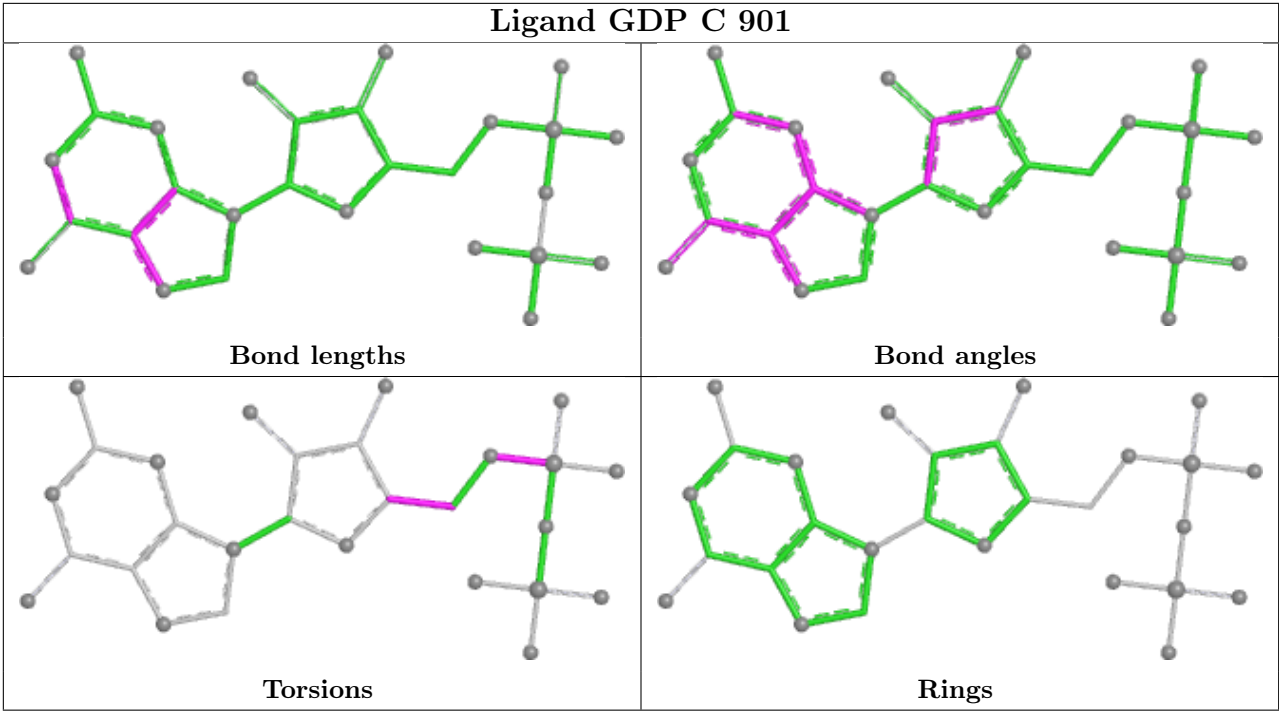
Mol	Chain	Res	Type	Atoms
86	C	901	GDP	C5'-O5'-PA-O3A
86	C	901	GDP	C5'-O5'-PA-O1A
86	C	901	GDP	C5'-O5'-PA-O2A
86	C	901	GDP	O4'-C4'-C5'-O5'
86	C	901	GDP	C3'-C4'-C5'-O5'

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
86	C	901	GDP	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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	1	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	1	1937:C	O3'	1938:G	P	5.81

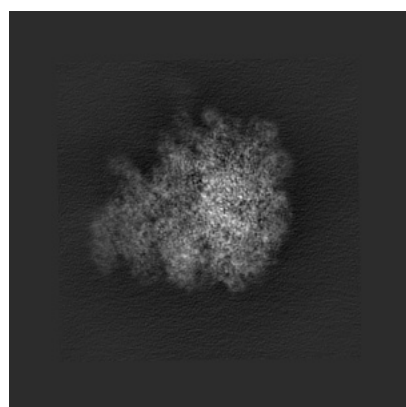
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12977. These allow visual inspection of the internal detail of the map and identification of artifacts.

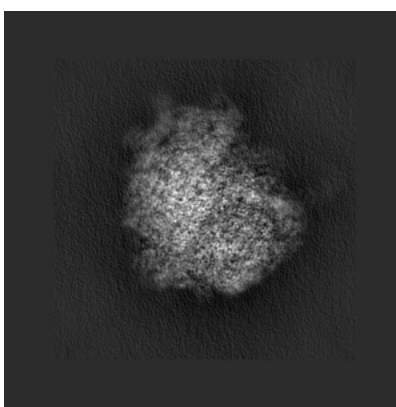
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

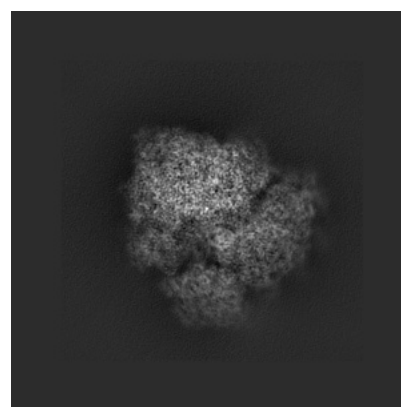
6.1.1 Primary map



X



Y

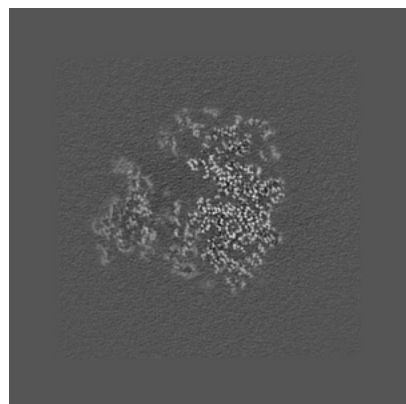


Z

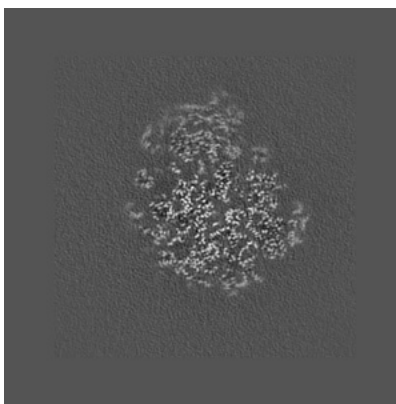
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

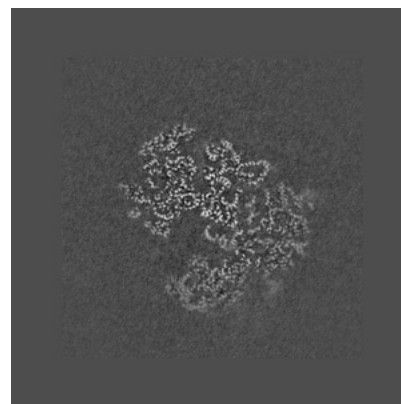
6.2.1 Primary map



X Index: 243



Y Index: 243

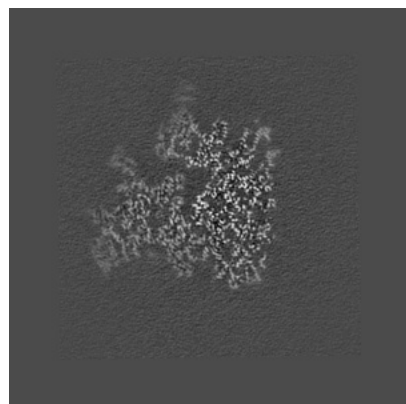


Z Index: 243

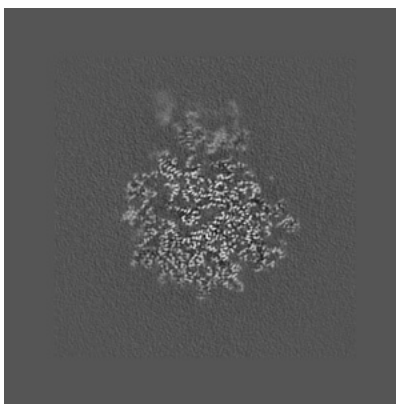
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

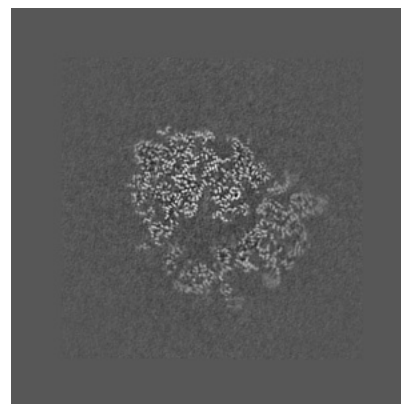
6.3.1 Primary map



X Index: 254



Y Index: 267

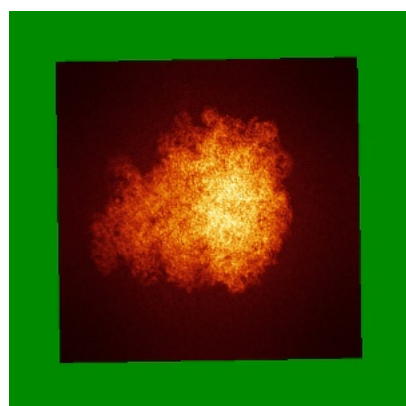


Z Index: 258

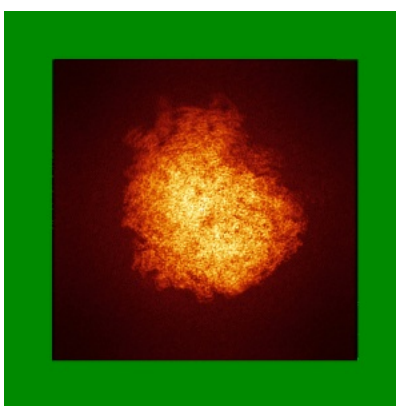
The images above show the largest variance slices of the map in three orthogonal directions.

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

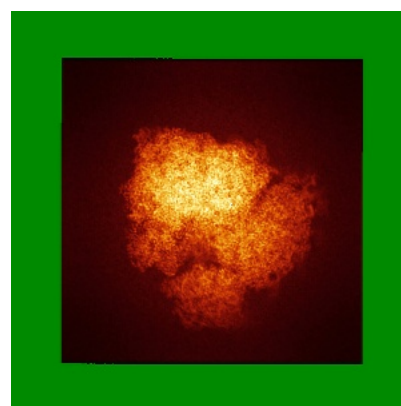
6.4.1 Primary map



X



Y

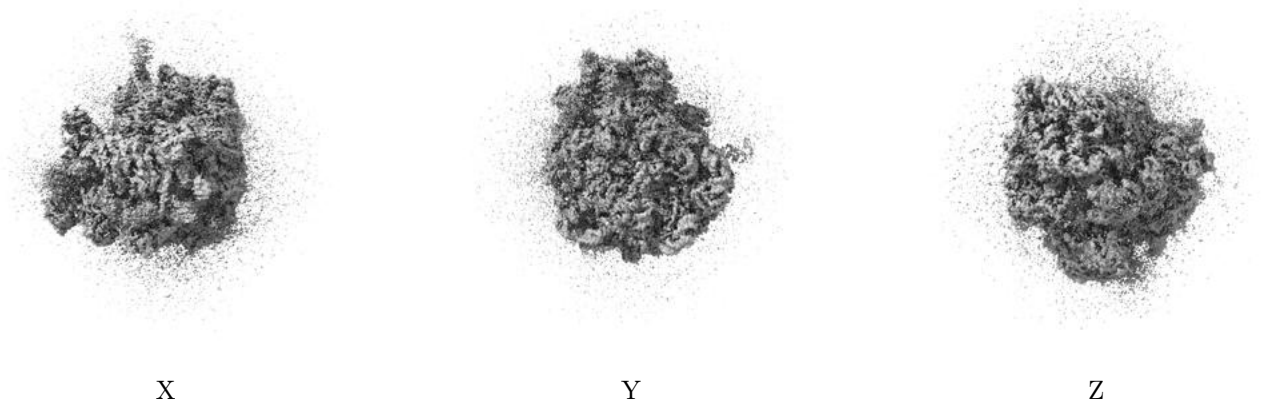


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 1.3. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

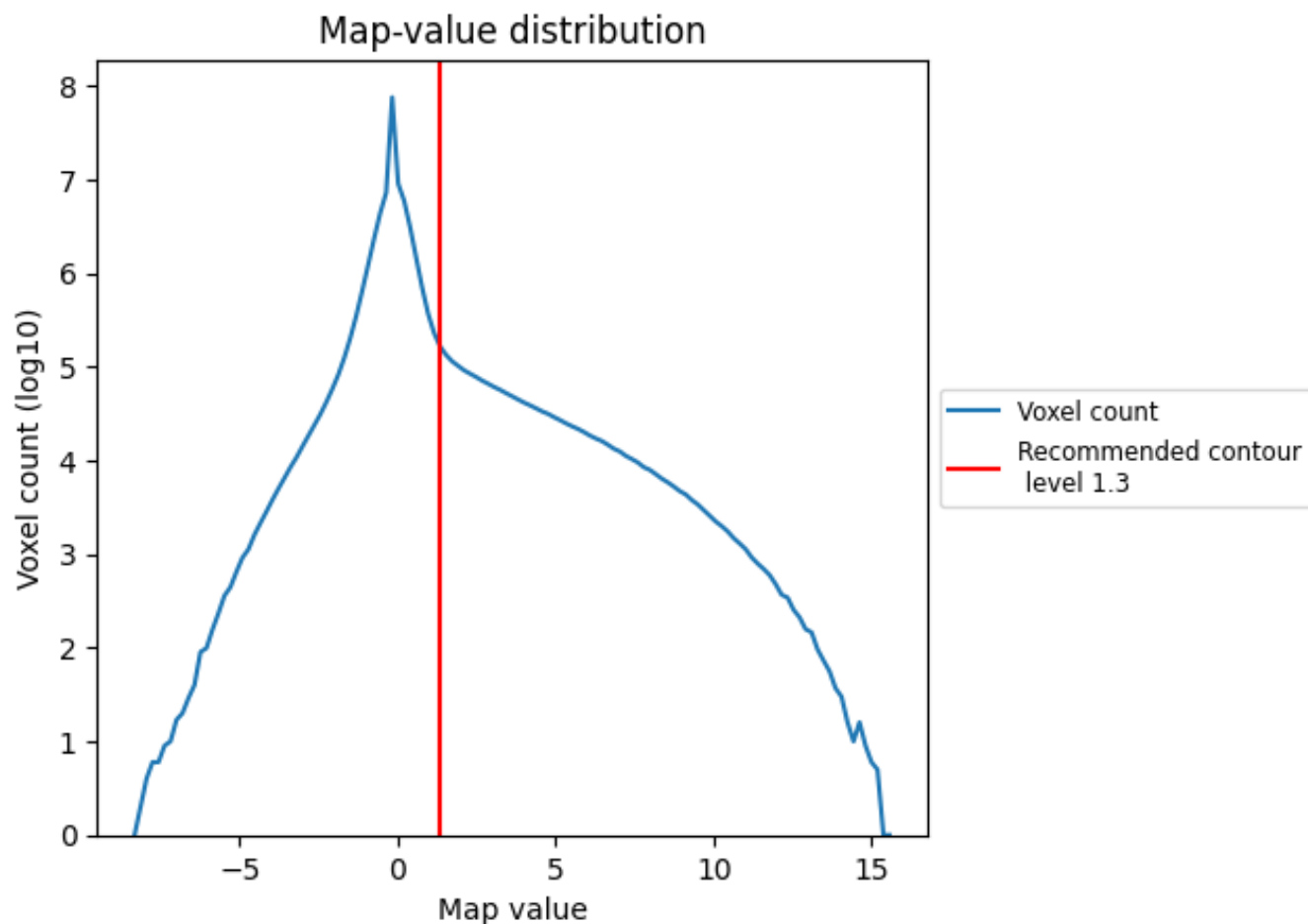
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

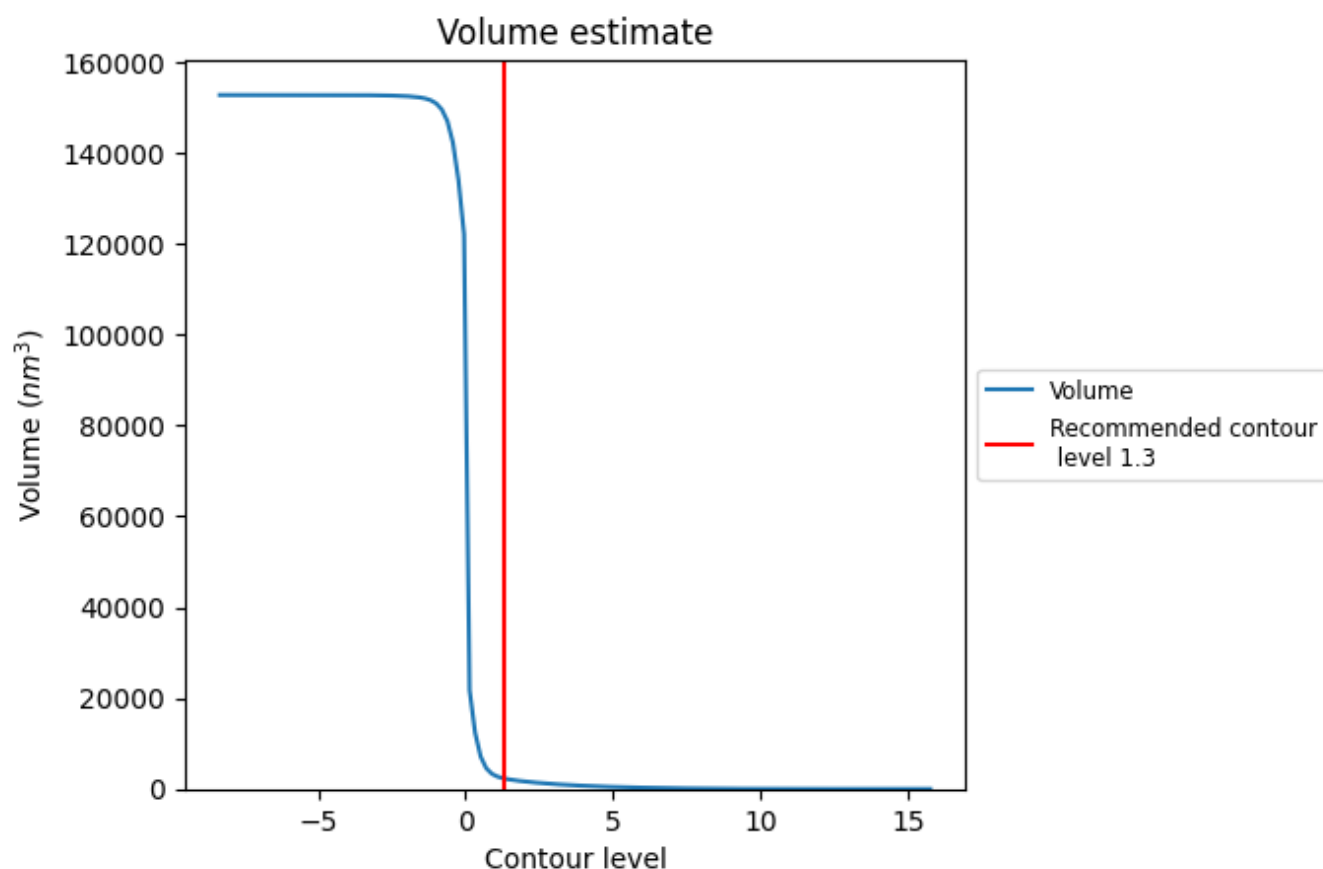
This section contains the results of statistical analysis of the map.

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.

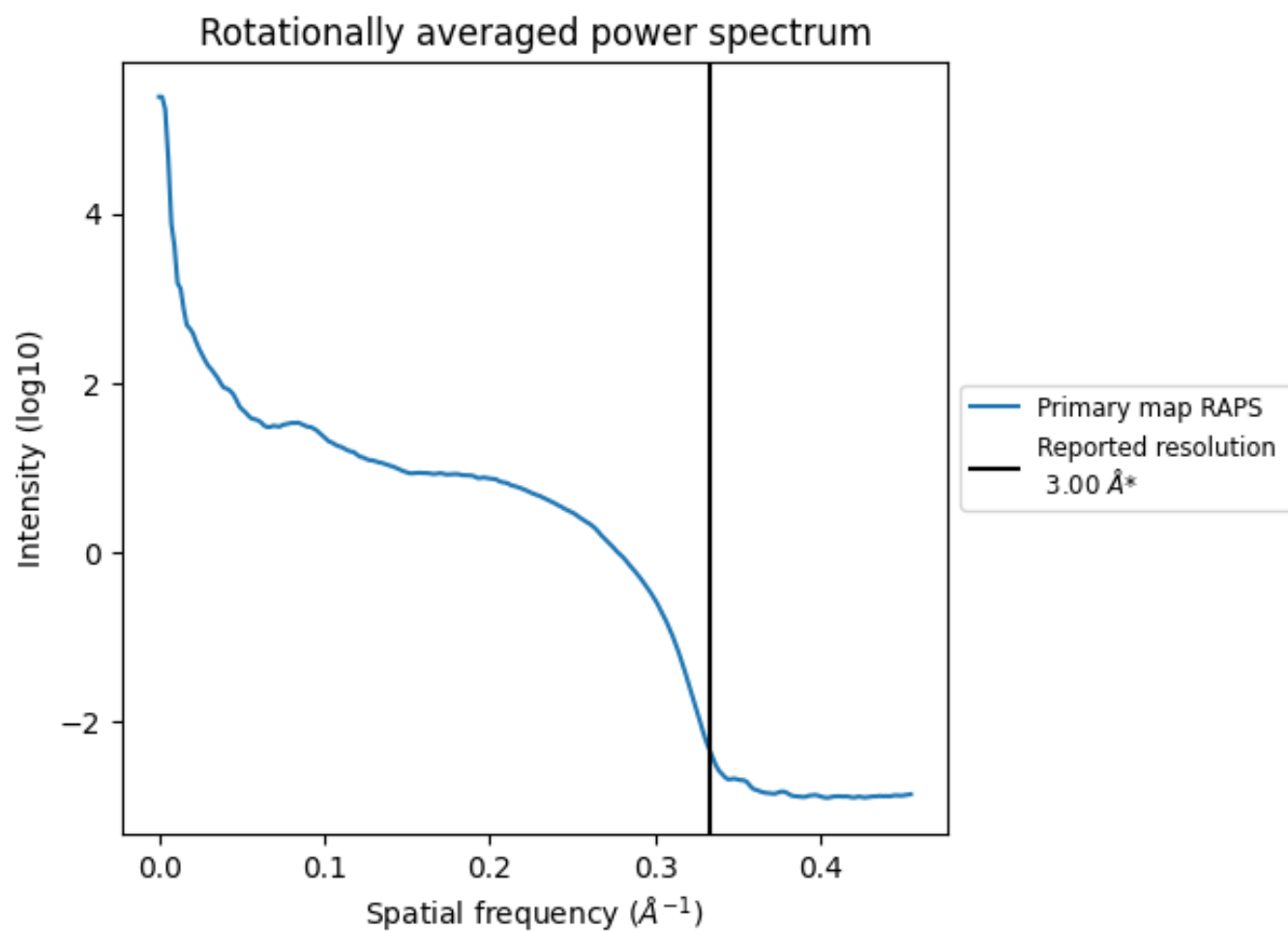
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2327 nm³; this corresponds to an approximate mass of 2102 kDa.

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

7.3 Rotationally averaged power spectrum [i](#)

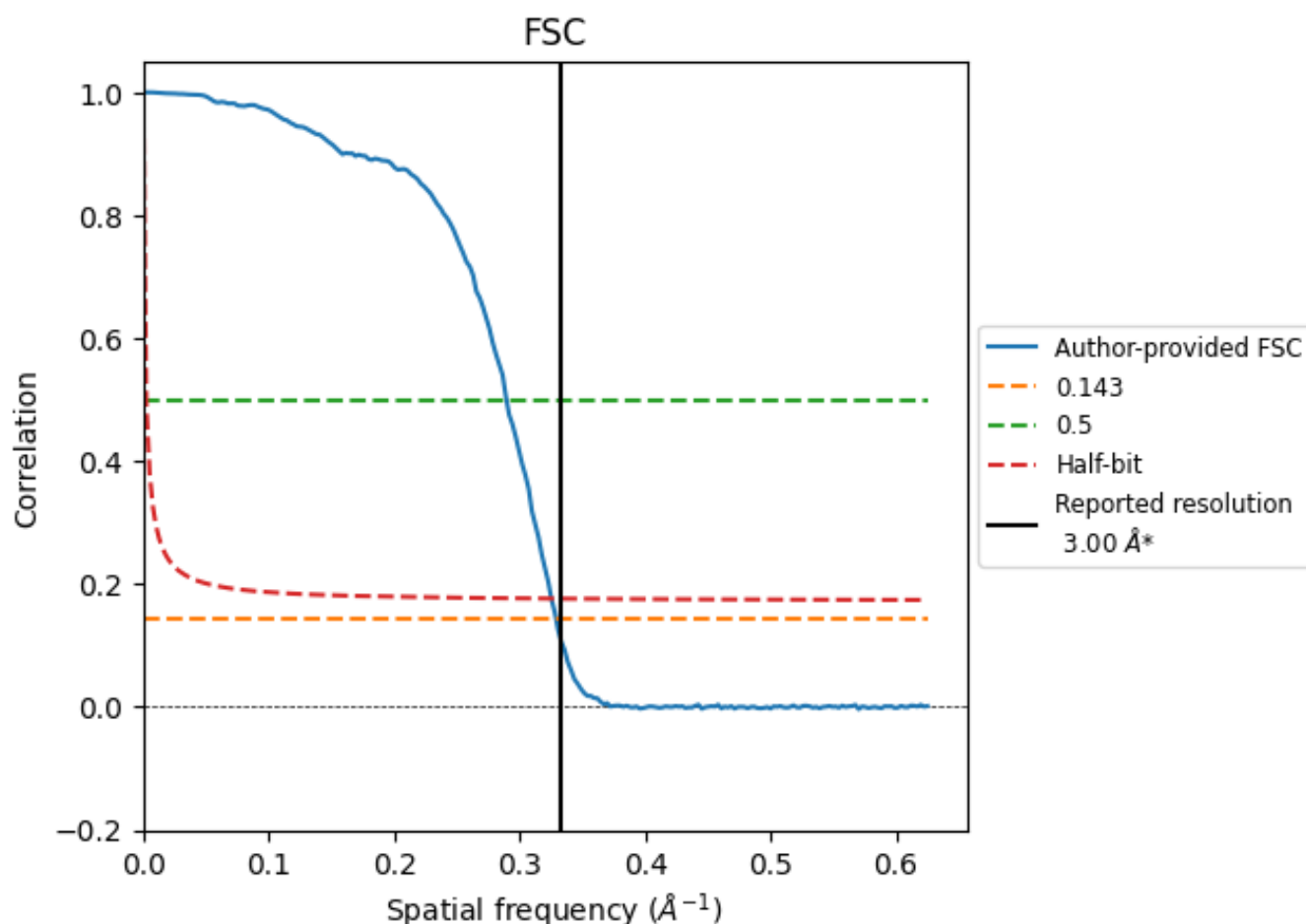


*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

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 0.333 Å⁻¹

8.2 Resolution estimates [i](#)

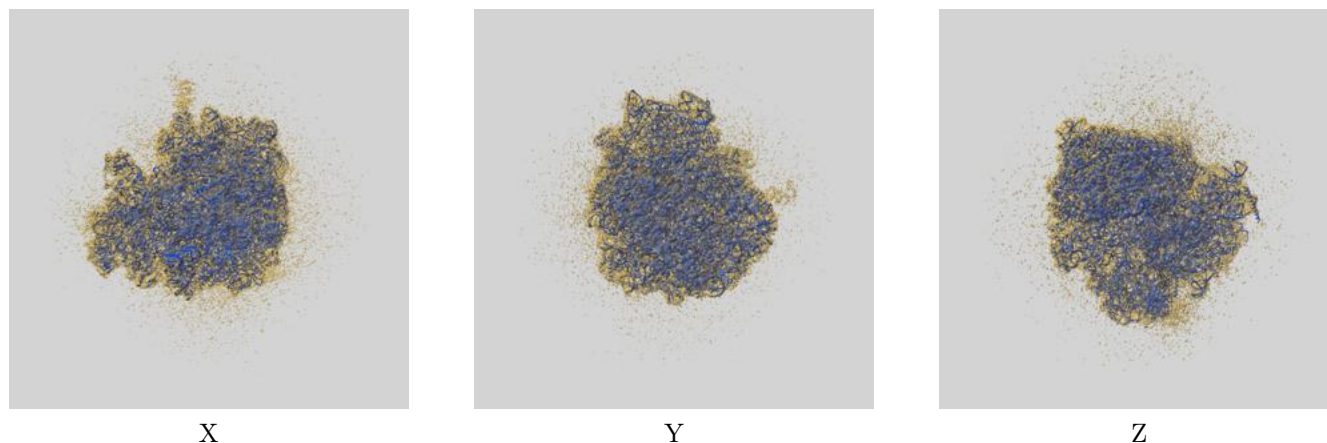
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	3.04	3.45	3.07
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

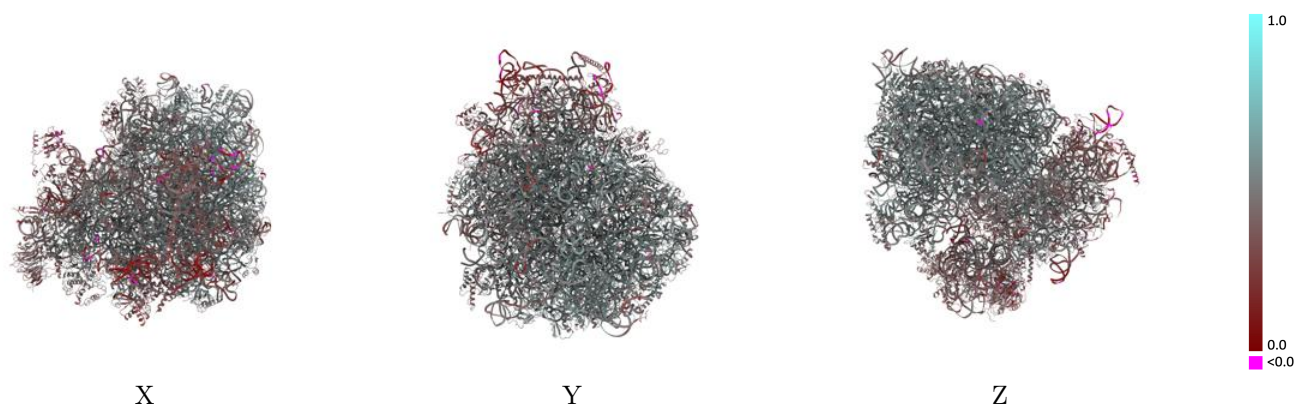
This section contains information regarding the fit between EMDB map EMD-12977 and PDB model 7OLD. Per-residue inclusion information can be found in section 3 on page 21.

9.1 Map-model overlay [i](#)



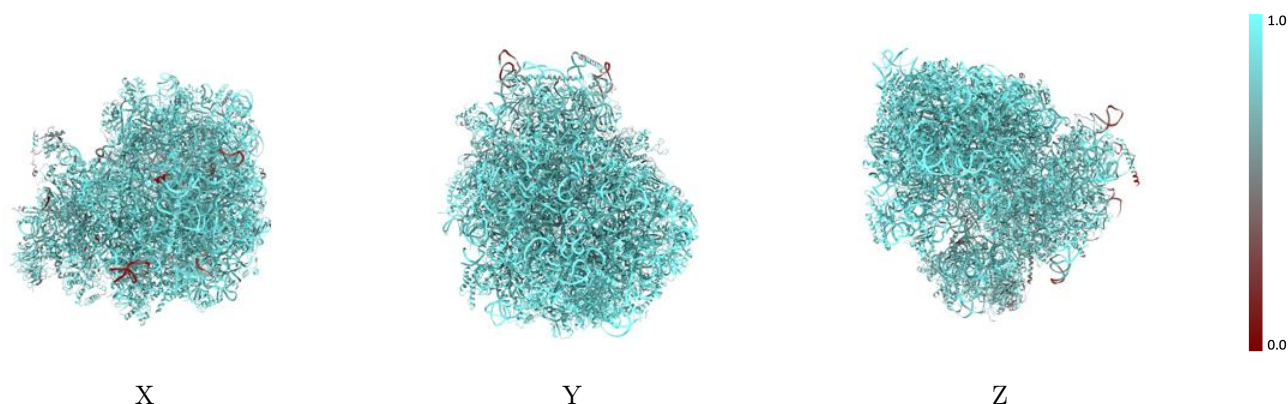
The images above show the 3D surface view of the map at the recommended contour level 1.3 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



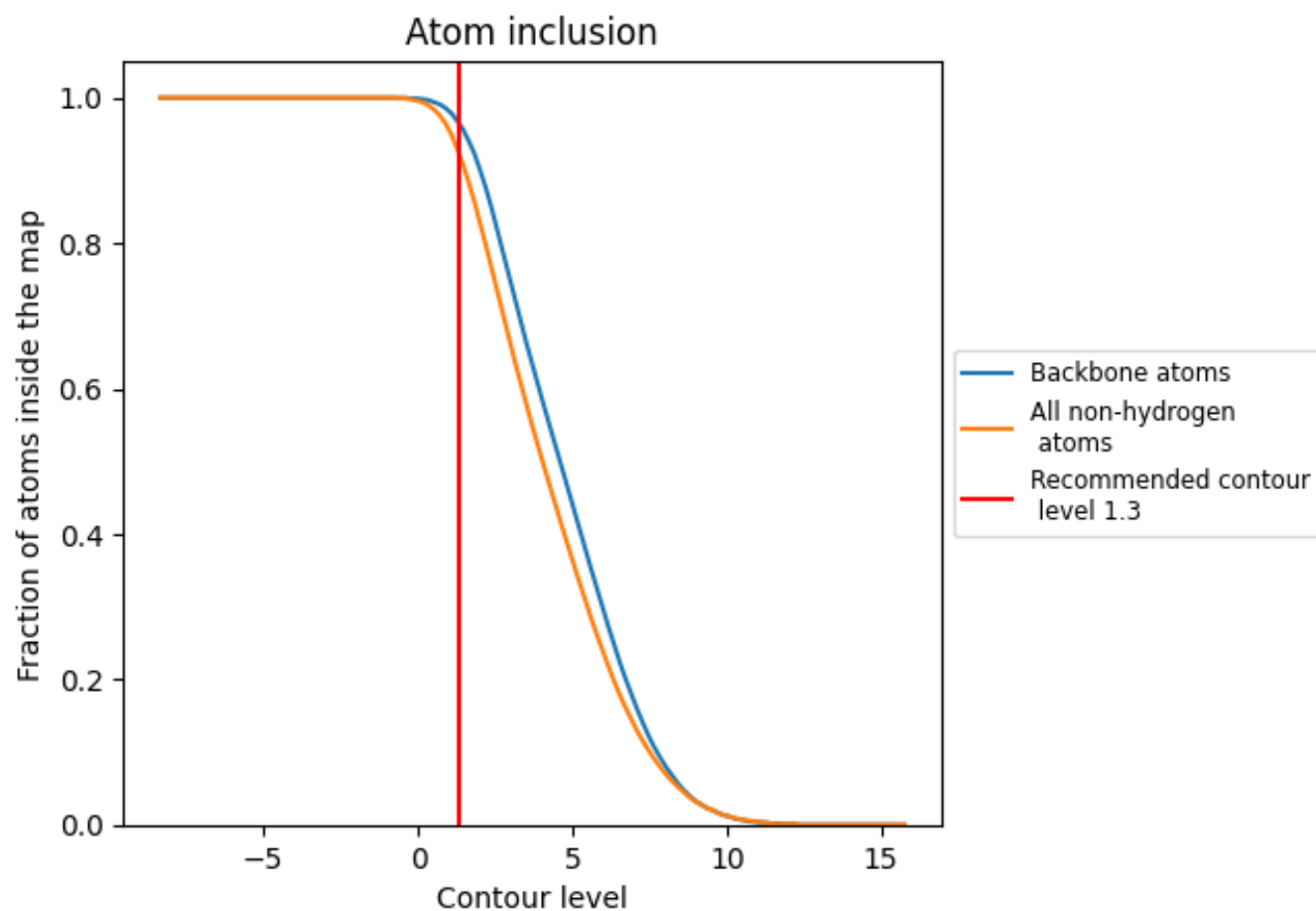
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (1.3).

9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 93% 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 (1.3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9270	 0.4580
1	 0.9780	 0.4930
2	 0.9300	 0.4030
3	 0.9910	 0.5110
4	 0.9830	 0.4840
5	 0.6780	 0.3570
A	 0.8020	 0.3700
B	 0.6150	 0.3830
C	 0.8720	 0.4370
LA	 0.9650	 0.5360
LB	 0.9590	 0.5330
LC	 0.9570	 0.5250
LD	 0.9260	 0.4780
LE	 0.9150	 0.4860
LF	 0.9470	 0.5210
LG	 0.9210	 0.4720
LH	 0.9300	 0.5120
LI	 0.9530	 0.5240
LJ	 0.9290	 0.4680
LK	 0.7890	 0.3150
LL	 0.9550	 0.5100
LM	 0.9360	 0.5080
LN	 0.9610	 0.5380
LO	 0.9610	 0.5320
LP	 0.9590	 0.5320
LQ	 0.9560	 0.5340
LR	 0.9410	 0.4900
LS	 0.9620	 0.5310
LT	 0.9570	 0.5280
LU	 0.9080	 0.4290
LV	 0.9580	 0.5320
LW	 0.7670	 0.4030
LX	 0.9440	 0.5030
LY	 0.9320	 0.5070
LZ	 0.9310	 0.4930



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Chain	Atom inclusion	Q-score
La	 0.9600	 0.5370
Lb	 0.9520	 0.4880
Lc	 0.9430	 0.4950
Ld	 0.9080	 0.4940
Le	 0.9740	 0.5480
Lf	 0.9590	 0.5440
Lg	 0.9550	 0.5140
Lh	 0.9070	 0.4760
Li	 0.9360	 0.4850
Lj	 0.9790	 0.5450
Lk	 0.9320	 0.4590
Ll	 0.9420	 0.4950
Lm	 0.9480	 0.5260
Ln	 0.9150	 0.5020
Lo	 0.9540	 0.5290
Lp	 0.9510	 0.5150
Lq	 0.9570	 0.5190
Lr	 0.7830	 0.4190
Ls	 0.8330	 0.4150
SA	 0.8880	 0.4490
SB	 0.7660	 0.2910
SC	 0.9100	 0.4910
SD	 0.8480	 0.4250
SE	 0.8910	 0.4490
SF	 0.7960	 0.3450
SG	 0.8230	 0.3420
SH	 0.8380	 0.3630
SI	 0.8570	 0.4040
SJ	 0.8970	 0.4560
SK	 0.8590	 0.3730
SL	 0.9080	 0.4630
SM	 0.6290	 0.2470
SN	 0.8850	 0.4120
SO	 0.8060	 0.3310
SP	 0.8330	 0.3510
SQ	 0.8040	 0.3680
SR	 0.8260	 0.4010
SS	 0.8160	 0.3510
ST	 0.8020	 0.3520
SU	 0.7740	 0.3670
SV	 0.9060	 0.4560
SW	 0.8950	 0.4760

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Chain	Atom inclusion	Q-score
SX	 0.9180	 0.5100
SY	 0.8600	 0.3990
SZ	 0.7860	 0.3200
Sa	 0.8810	 0.4260
Sb	 0.8320	 0.3420
Sc	 0.8510	 0.3760
Sd	 0.9050	 0.4180
Se	 0.8660	 0.4530
Sf	 0.6850	 0.2450