



Full wwPDB EM Validation Report ⓘ

Mar 6, 2026 – 05:13 PM UTC

PDB ID : 7OYB / pdb_00007oyb
EMDB ID : EMD-13112
Title : Cryo-EM structure of the 6 hpf zebrafish embryo 80S ribosome
Authors : Leesch, F.; Lorenzo-Orts, L.; Grishkovskaya, I.; Kandolf, S.; Belacic, K.; Meinhart, A.; Haselbach, D.; Pauli, A.
Deposited on : 2021-06-24
Resolution : 2.40 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

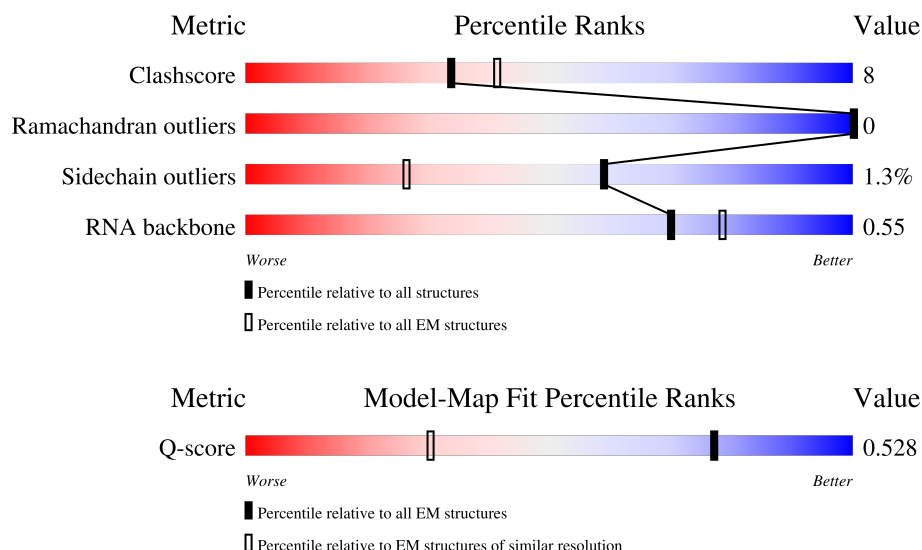
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.40 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.



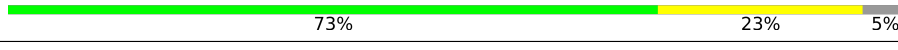
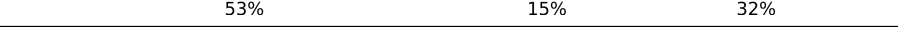
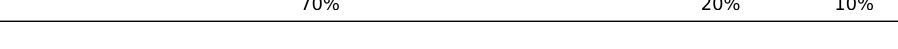
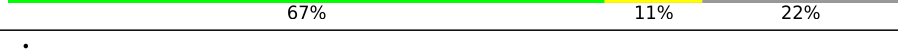
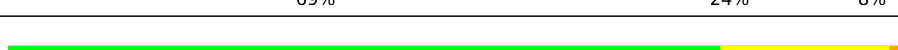
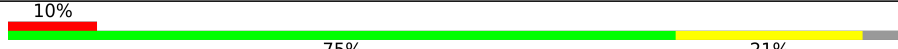
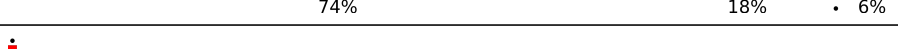
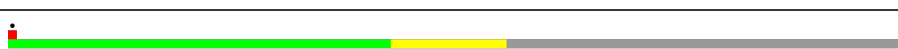
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	5628 (1.90 - 2.90)

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	22	1939	42% 31% 5% 23%
2	51	4269	46% 25% 6% 24%
3	71	120	73% 25% .

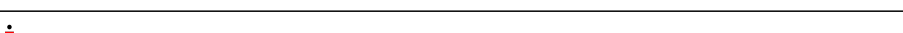
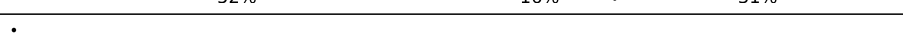
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Mol	Chain	Length	Quality of chain
4	81	158	
5	A1	257	
6	A2	308	
7	B1	403	
8	B2	267	
9	C1	375	
10	C2	280	
11	D1	296	
12	D2	245	
13	E1	265	
14	E2	263	
15	F1	246	
16	F2	204	
17	G1	266	
18	G2	249	
19	H1	192	
20	H2	194	
21	I1	215	
22	I2	208	
23	J1	178	
24	J2	194	
25	K2	166	
26	L1	211	
27	L2	159	
28	M1	139	

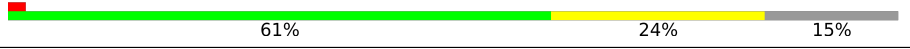
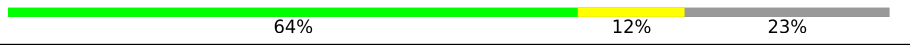
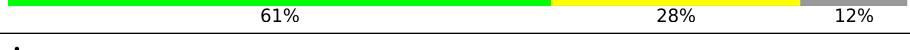
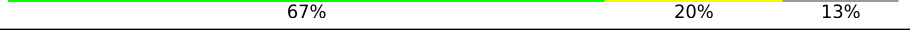
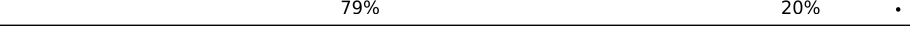
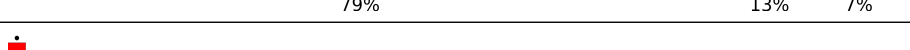
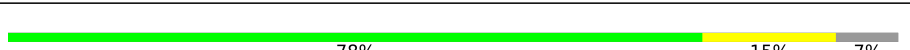
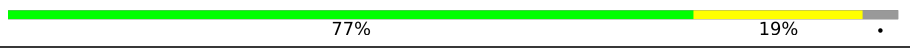
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Mol	Chain	Length	Quality of chain
29	N1	204	
30	N2	151	
31	O1	205	
32	O2	151	
33	P1	184	
34	P2	145	
35	Q1	182	
36	Q2	146	
37	R1	196	
38	R2	134	
39	S1	176	
40	S2	152	
41	T1	160	
42	T2	146	
43	U1	141	
44	U2	119	
45	V1	140	
46	V2	81	
47	W1	157	
48	W2	130	
49	X1	155	
50	X2	143	
51	Y1	145	
52	Y2	132	
53	Z1	136	

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Mol	Chain	Length	Quality of chain
54	Z2	124	
55	a1	148	
56	a2	115	
57	b1	64	
58	b2	84	
59	c1	117	
60	c2	69	
61	d1	123	
62	d2	56	
63	e1	135	
64	e2	133	
65	f1	110	
66	g1	117	
67	g2	317	
68	h1	123	
69	i1	105	
70	j1	97	
71	k1	70	
72	l1	50	
73	m1	128	
74	n1	25	
75	o1	106	
76	p1	92	
77	r1	138	

2 Entry composition

There are 79 unique types of molecules in this entry. The entry contains 194863 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 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	22	1502	Total	C	N	O	P	0	0
			32102	14330	5809	10462	1501		

- Molecule 2 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	51	3263	Total	C	N	O	P	0	0
			69917	31143	12776	22736	3262		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	71	120	Total	C	N	O	P	0	0
			2563	1145	465	834	119		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	81	150	Total	C	N	O	P	0	0
			3199	1427	574	1048	150		

- Molecule 5 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	A1	245	Total	C	N	O	S	0	0
			1879	1181	381	310	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	A2	210	Total	C	N	O	S	0	0
			1665	1061	290	305	9		

- Molecule 7 is a protein called Ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	B1	394	Total	C	N	O	S	0	0
			3181	2021	600	544	16		

- Molecule 8 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	B2	213	Total	C	N	O	S	0	0
			1730	1097	310	309	14		

- Molecule 9 is a protein called Ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	C1	348	Total	C	N	O	S	0	0
			2774	1741	551	464	18		

- Molecule 10 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	C2	213	Total	C	N	O	S	0	0
			1651	1069	283	290	9		

- Molecule 11 is a protein called Ribosomal protein L5b.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	D1	288	Total	C	N	O	S	0	0
			2337	1482	429	415	11		

- Molecule 12 is a protein called DNA-(apurinic or apyrimidinic site) lyase.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	D2	221	Total	C	N	O	S	0	0
			1713	1091	309	306	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
13	E1	206	Total	C	N	O	S	0	0
			1671	1065	327	272	7		

- Molecule 14 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	E2	261	Total	C	N	O	S	0	0
			2070	1320	385	357	8		

- Molecule 15 is a protein called Ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	F1	222	Total	C	N	O	S	0	0
			1811	1160	346	298	7		

- Molecule 16 is a protein called Ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	F2	183	Total	C	N	O	S	0	0
			1442	904	268	264	6		

- Molecule 17 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	G1	207	Total	C	N	O	S	0	0
			1683	1076	322	281	4		

- Molecule 18 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	G2	230	Total	C	N	O	S	0	0
			1864	1163	375	319	7		

- Molecule 19 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	H1	190	Total	C	N	O	S	0	0
			1505	949	279	271	6		

- Molecule 20 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	H2	186	Total	C	N	O	S	0	0
			1492	952	276	264			

- Molecule 21 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	I1	211	Total	C	N	O	S	0	0
			1699	1076	329	279	15		

- Molecule 22 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	I2	206	Total	C	N	O	S	0	0
			1666	1047	329	285	5		

- Molecule 23 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	J1	167	Total	C	N	O	S	0	0
			1348	854	254	235	5		

- Molecule 24 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	J2	180	Total	C	N	O	S	0	0
			1492	952	295	243	2		

- Molecule 25 is a protein called Ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	K2	93	Total	C	N	O	S	0	0
			769	507	131	127	4		

- Molecule 26 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	L1	197	Total	C	N	O	S	0	0
			1603	1003	335	260	5		

- Molecule 27 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	L2	133	Total	C	N	O	S	0	0
			1086	686	211	183	6		

- Molecule 28 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	M1	134	Total	C	N	O	S	0	0
			1094	702	207	180	5		

- Molecule 29 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	N1	202	Total	C	N	O	S	0	0
			1689	1065	352	267	5		

- Molecule 30 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	N2	149	Total	C	N	O	S	0	0
			1200	767	230	202	1		

- Molecule 31 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	O1	204	Total	C	N	O	S	0	0
			1662	1073	318	266	5		

- Molecule 32 is a protein called Ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	O2	126	Total	C	N	O	S	0	0
			943	579	186	172	6		

- Molecule 33 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	P1	152	Total	C	N	O	S	0	0
			1235	770	243	213	9		

- Molecule 34 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	P2	116	Total	C	N	O	S	0	0
			957	608	177	165	7		

- Molecule 35 is a protein called Ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Q1	180	Total	C	N	O	S	0	0
			1459	917	302	236	4		

- Molecule 36 is a protein called Ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Q2	134	Total	C	N	O	S	0	0
			1052	671	196	182	3		

- Molecule 37 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	R1	166	Total	C	N	O	S	0	0
			1381	856	300	215	10		

- Molecule 38 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	R2	132	Total	C	N	O	S	0	0
			1068	670	199	195	4		

- Molecule 39 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	S1	176	Total	C	N	O	S	0	0
			1457	934	284	230	9		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
40	S2	136	Total	C	N	O	S	0	0
			1129	708	228	192	1		

- Molecule 41 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	T1	157	Total	C	N	O	S	0	0
			1283	816	250	213	4		

- Molecule 42 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	T2	137	Total	C	N	O	S	0	0
			1058	667	202	185	4		

- Molecule 43 is a protein called Ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	U1	97	Total	C	N	O	S	0	0
			792	508	138	144	2		

- Molecule 44 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	U2	97	Total	C	N	O	S	0	0
			754	473	139	138	4		

- Molecule 45 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	V1	129	Total	C	N	O	S	0	0
			970	613	182	170	5		

- Molecule 46 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	V2	81	Total	C	N	O	S	0	0
			623	384	116	119	4		

- Molecule 47 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	W1	60	Total	C	N	O	S	0	0
			503	323	98	80	2		

- Molecule 48 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	W2	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 49 is a protein called Ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	X1	117	Total	C	N	O	S	0	0
			959	614	179	165	1		

- Molecule 50 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	X2	139	Total	C	N	O	S	0	0
			1083	684	215	181	3		

- Molecule 51 is a protein called ATPase H⁺ transporting V0 subunit e1.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	Y1	122	Total	C	N	O	S	0	0
			1024	643	209	169	3		

- Molecule 52 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	Y2	124	Total	C	N	O	S	0	0
			1011	643	193	170	5		

- Molecule 53 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	Z1	135	Total	C	N	O	S	0	0
			1105	714	208	179	4		

- Molecule 54 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms				AltConf	Trace
54	Z2	66	Total	C	N	O	0	0
			529	343	95	91		

- Molecule 55 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	a1	147	Total	C	N	O	S	0	0
			1164	740	233	188	3		

- Molecule 56 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	a2	98	Total	C	N	O	S	0	0
			782	486	161	130	5		

- Molecule 57 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	b1	49	Total	C	N	O	S	0	0
			419	259	92	67	1		

- Molecule 58 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	b2	81	Total	C	N	O	S	0	0
			636	398	120	111	7		

- Molecule 59 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	c1	93	Total	C	N	O	S	0	0
			721	457	127	131	6		

- Molecule 60 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	c2	61	Total	C	N	O	S	0	0
			475	288	94	91	2		

- Molecule 61 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	d1	107	Total	C	N	O	S	0	0
			888	558	172	156	2		

- Molecule 62 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	d2	55	Total	C	N	O	S	0	0
			459	285	94	75	5		

- Molecule 63 is a protein called Ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	e1	125	Total	C	N	O	S	0	0
			1030	649	212	163	6		

- Molecule 64 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms				AltConf	Trace
64	e2	50	Total	C	N	O	0	0
			399	244	88	67		

- Molecule 65 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	f1	107	Total	C	N	O	S	0	0
			861	550	171	137	3		

- Molecule 66 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	g1	104	Total	C	N	O	S	0	0
			833	519	172	136	6		

- Molecule 67 is a protein called Guanine nucleotide-binding protein subunit beta-2-like 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	g2	310	Total	C	N	O	S	0	0
			2394	1507	418	457	12		

- Molecule 68 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	h1	120	Total	C	N	O	S	0	0
			991	627	197	165	2		

- Molecule 69 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	i1	98	Total	C	N	O	S	0	0
			801	502	170	125	4		

- Molecule 70 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	j1	86	Total	C	N	O	S	0	0
			701	430	155	110	6		

- Molecule 71 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	k1	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

- Molecule 72 is a protein called Ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	l1	49	Total	C	N	O	S	0	0
			434	275	97	61	1		

- Molecule 73 is a protein called 60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	m1	50	Total	C	N	O	S	0	0
			413	256	87	64	6		

- Molecule 74 is a protein called Rpl41.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	n1	24	Total	C	N	O	S	0	0
			231	140	63	26	2		

- Molecule 75 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	o1	102	Total	C	N	O	S	0	0
			840	526	172	136	6		

- Molecule 76 is a protein called Zgc:171772.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	p1	91	Total	C	N	O	S	0	0
			703	444	132	120	7		

- Molecule 77 is a protein called 60S ribosomal protein L28.

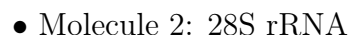
Mol	Chain	Residues	Atoms					AltConf	Trace
77	r1	118	Total	C	N	O	S	0	0
			943	589	193	159	2		

- Molecule 78 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
78	51	189	Total	Mg	0
			189	189	
78	71	3	Total	Mg	0
			3	3	
78	81	4	Total	Mg	0
			4	4	
78	A1	2	Total	Mg	0
			2	2	
78	B1	1	Total	Mg	0
			1	1	
78	V1	1	Total	Mg	0
			1	1	
78	b1	1	Total	Mg	0
			1	1	
78	e1	1	Total	Mg	0
			1	1	
78	m1	1	Total	Mg	0
			1	1	

- Molecule 79 is ZINC ION (CCD ID: ZN) (formula: Zn).

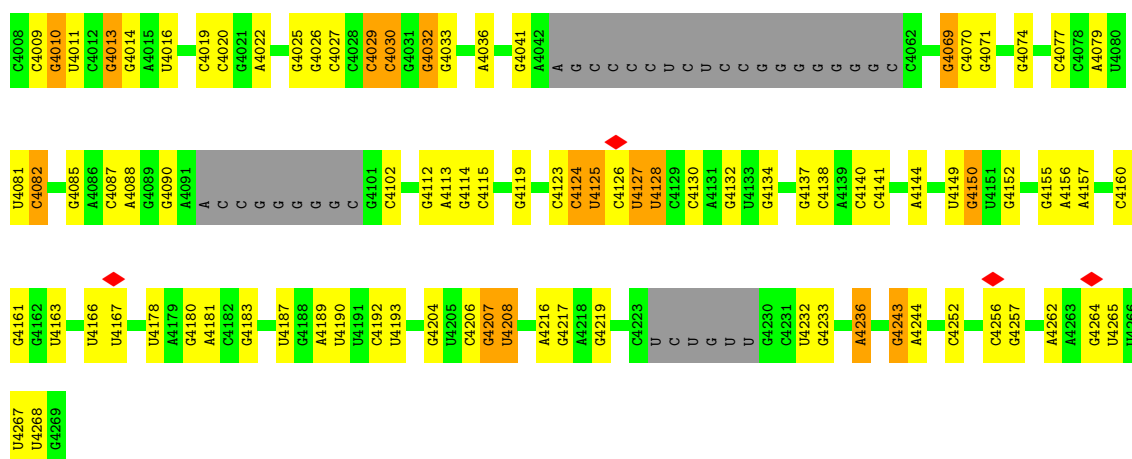
Mol	Chain	Residues	Atoms		AltConf
79	a2	1	Total	Zn	0
			1	1	
79	d2	1	Total	Zn	0
			1	1	
79	g1	1	Total	Zn	0
			1	1	
79	j1	1	Total	Zn	0
			1	1	
79	m1	1	Total	Zn	0
			1	1	
79	o1	1	Total	Zn	0
			1	1	
79	p1	1	Total	Zn	0
			1	1	











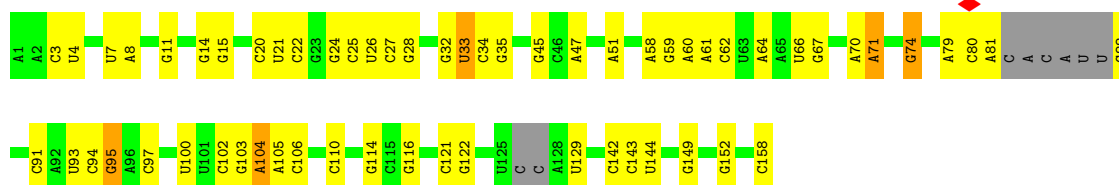
- Molecule 3: 5S rRNA

Chain 71: 73% 25%



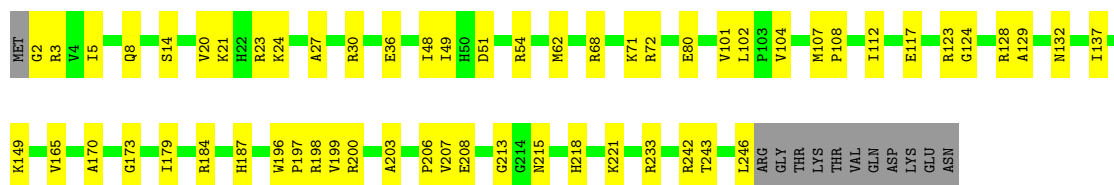
- Molecule 4: 5.8S rRNA

Chain 81: 57% 35% 5%



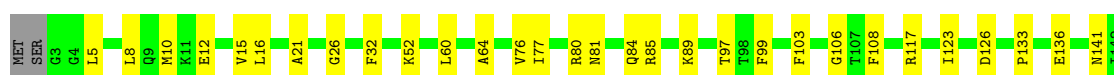
- Molecule 5: 60S ribosomal protein L8

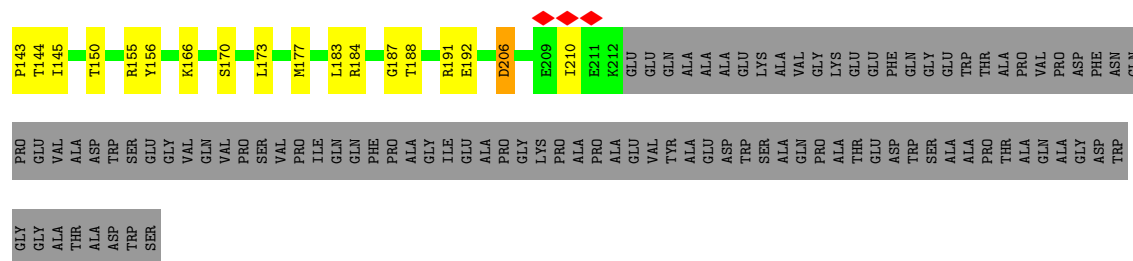
Chain A1: 73% 23% 5%



- Molecule 6: 40S ribosomal protein SA

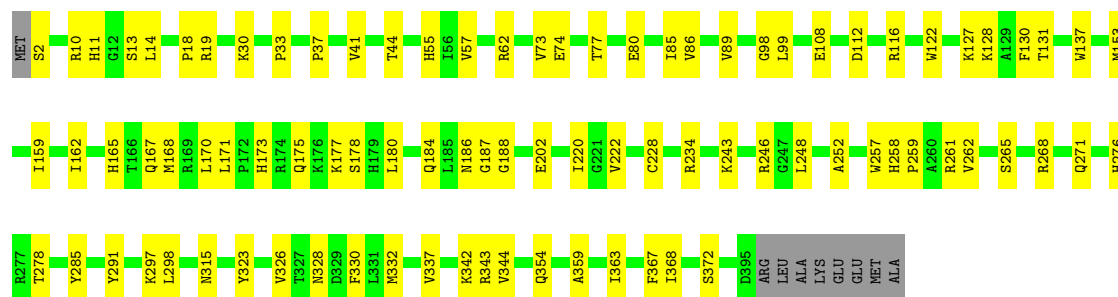
Chain A2: 53% 15% 32%





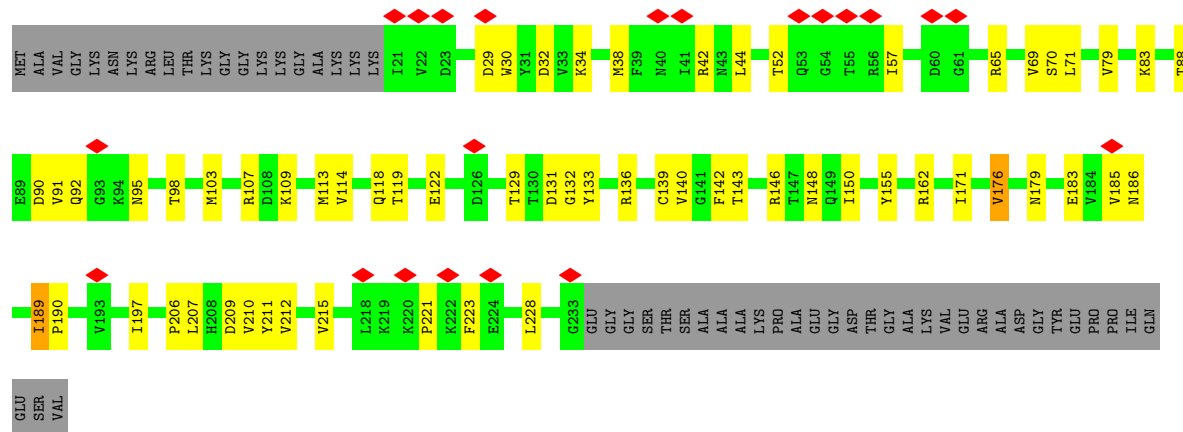
• Molecule 7: Ribosomal protein L3

Chain B1: 76% 22%



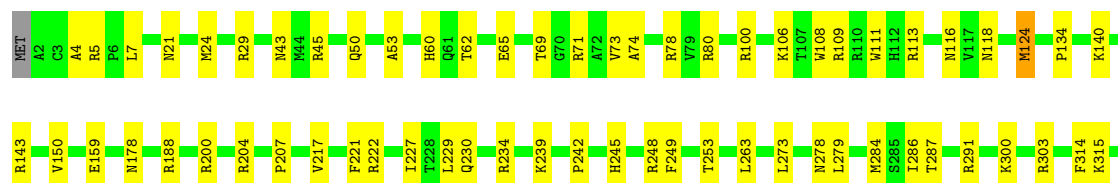
• Molecule 8: 40S ribosomal protein S3a

Chain B2: 8% 57% 22% 20%

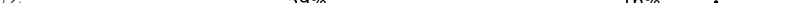


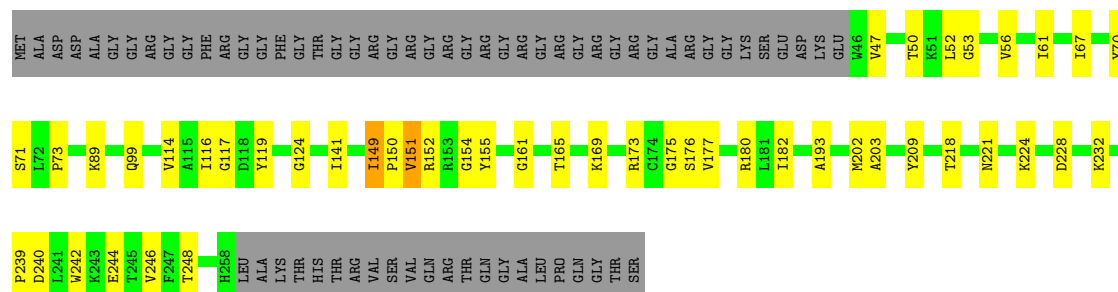
• Molecule 9: Ribosomal protein L4

Chain C1: 74% 18% 7%



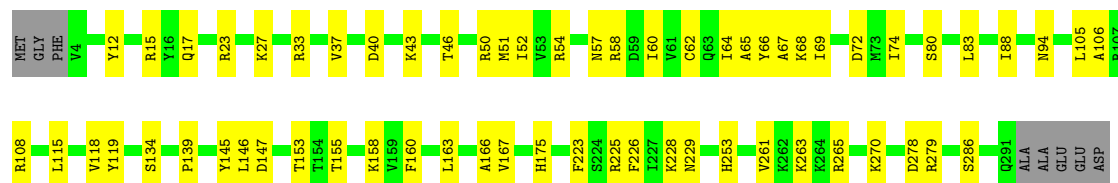
- Molecule 10: 40S ribosomal protein S2

Chain C2:  59% 16% 24%

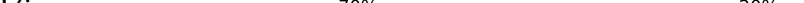


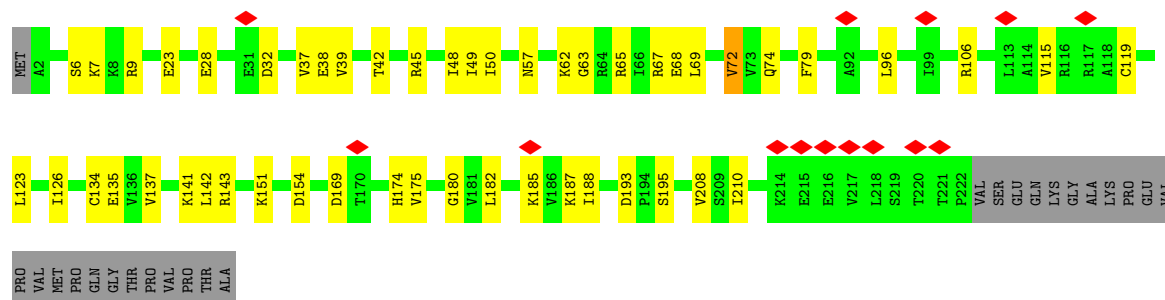
- Molecule 11: Ribosomal protein L5b

Chain D1:  76% 21%



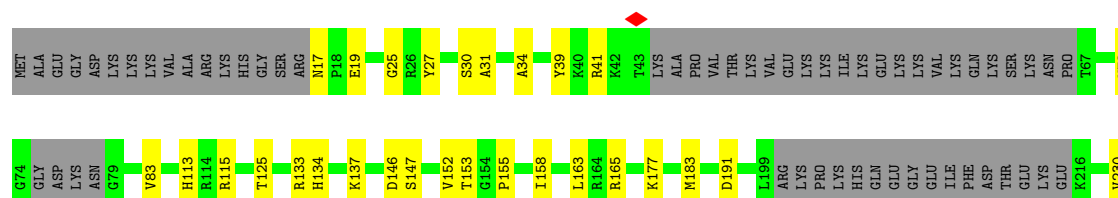
- Molecule 12: DNA-(apurinic or apyrimidinic site) lyase

Chain D2: 



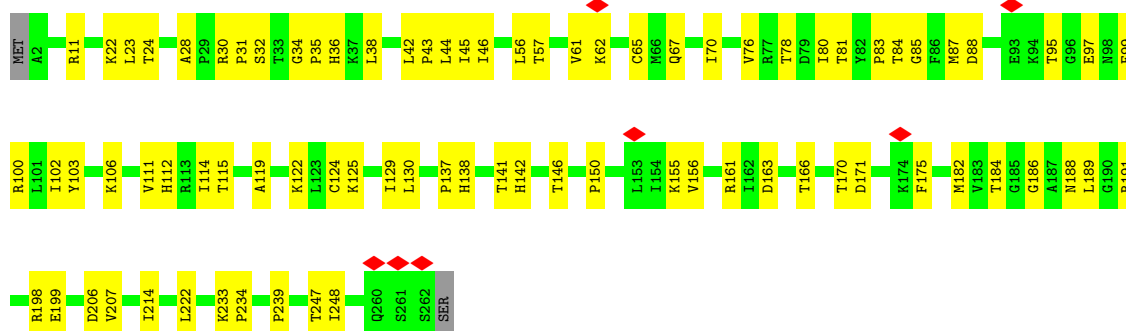
- Molecule 13: 60S ribosomal protein L6

Chain E1: 64% 14% 22%

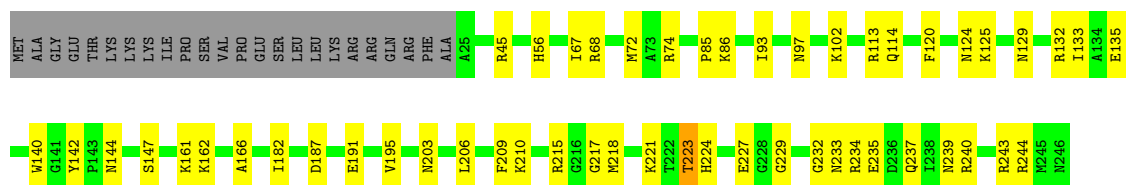




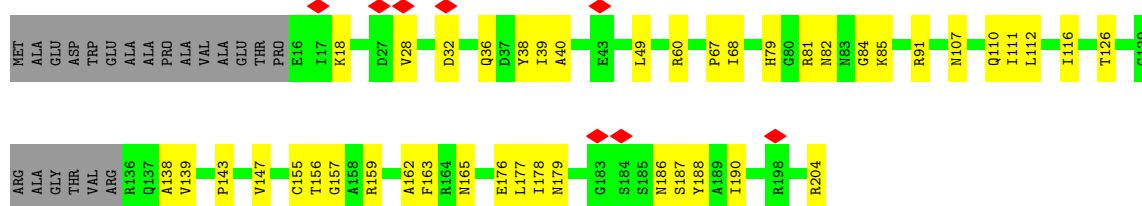
- Molecule 14: 40S ribosomal protein S4, X isoform



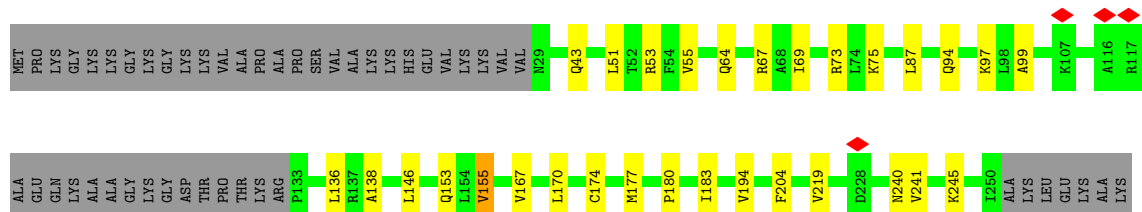
- Molecule 15: Ribosomal protein L7



- Molecule 16: Ribosomal protein S5



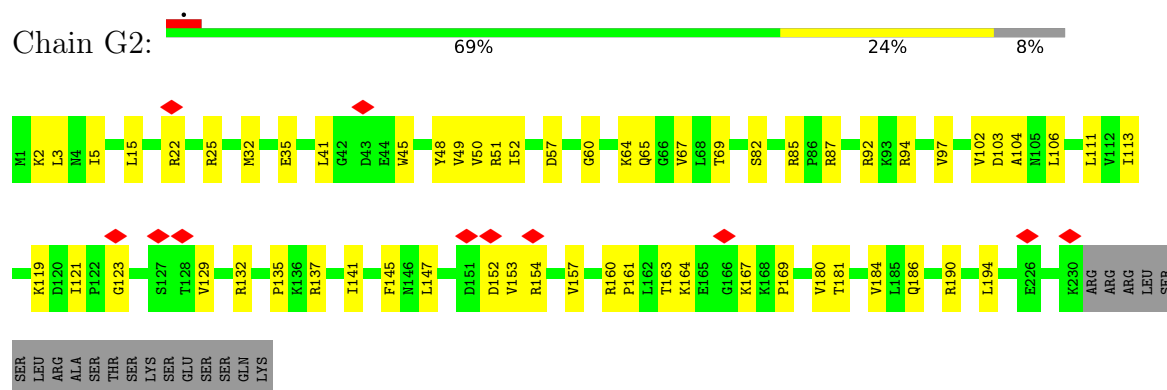
- Molecule 17: 60S ribosomal protein L7a



ALA
LYS
GLU
LEU
ALA
THR
LYS
LEU
GLY

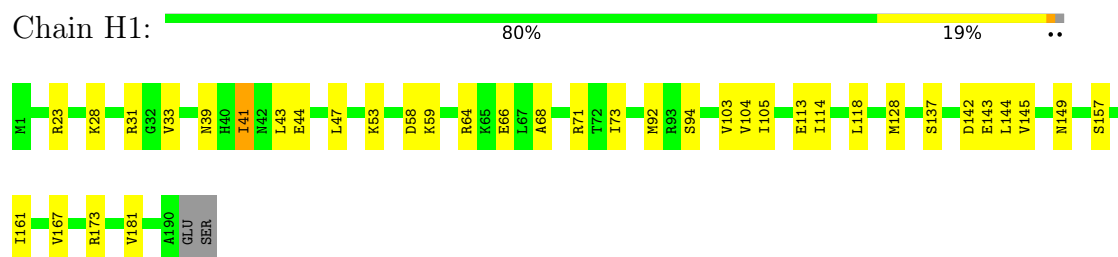
• Molecule 18: 40S ribosomal protein S6

Chain G2:



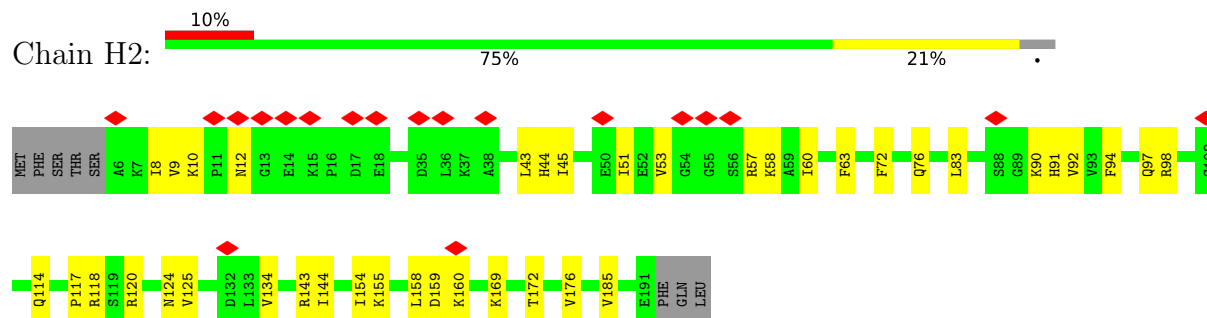
• Molecule 19: 60S ribosomal protein L9

Chain H1:



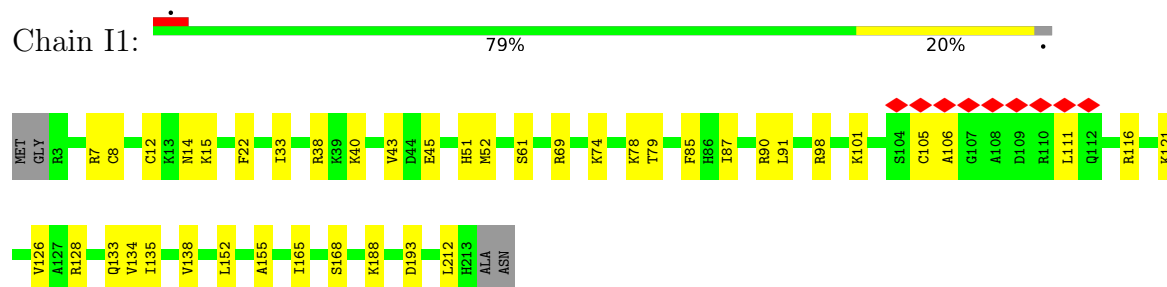
• Molecule 20: 40S ribosomal protein S7

Chain H2:

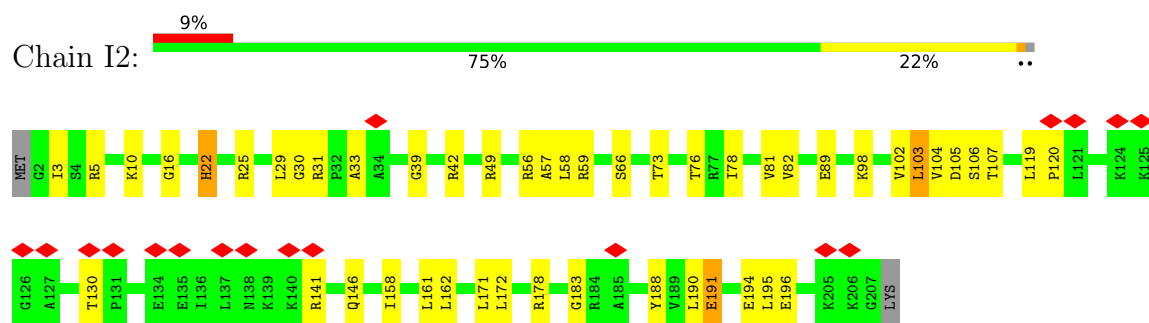


• Molecule 21: 60S ribosomal protein L10

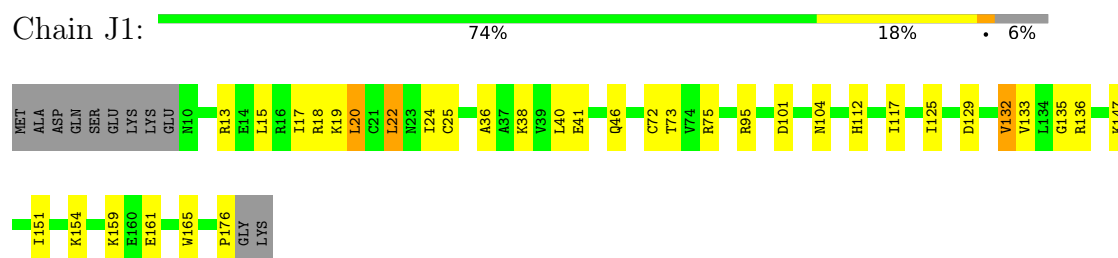
Chain I1:



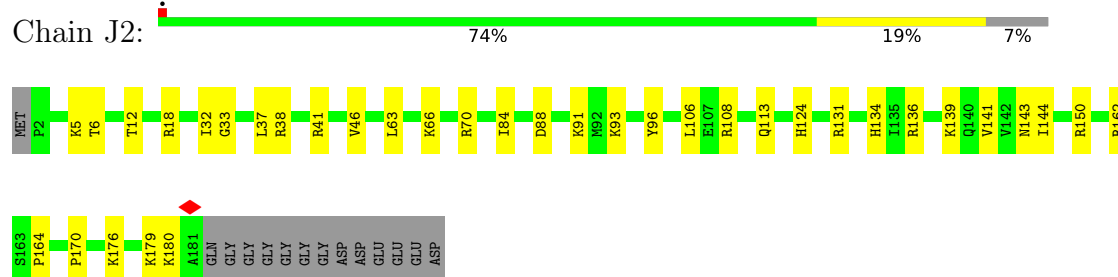
• Molecule 22: 40S ribosomal protein S8



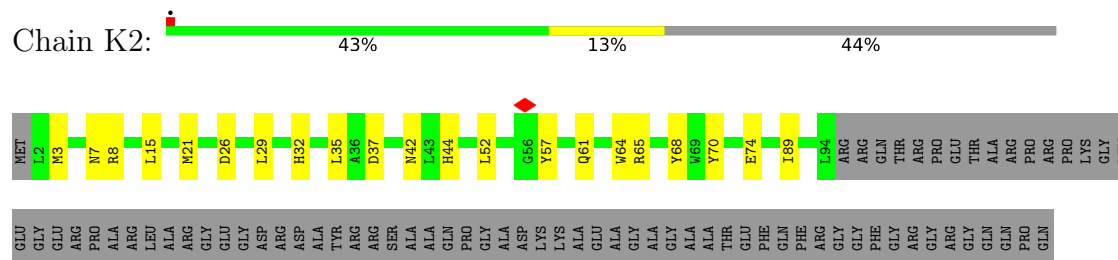
- Molecule 23: 60S ribosomal protein L11



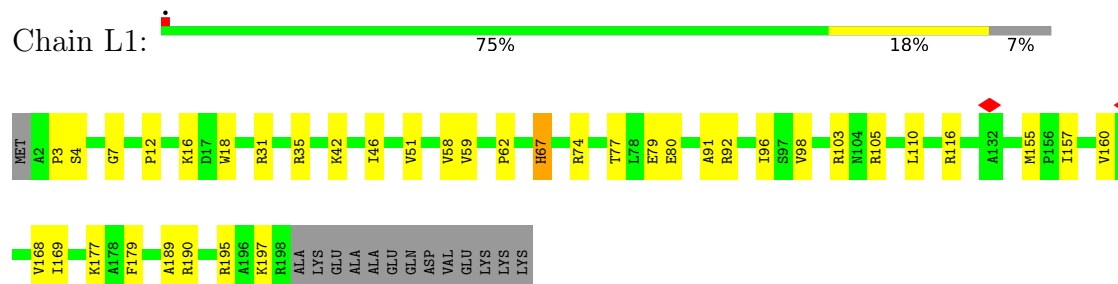
- Molecule 24: 40S ribosomal protein S9



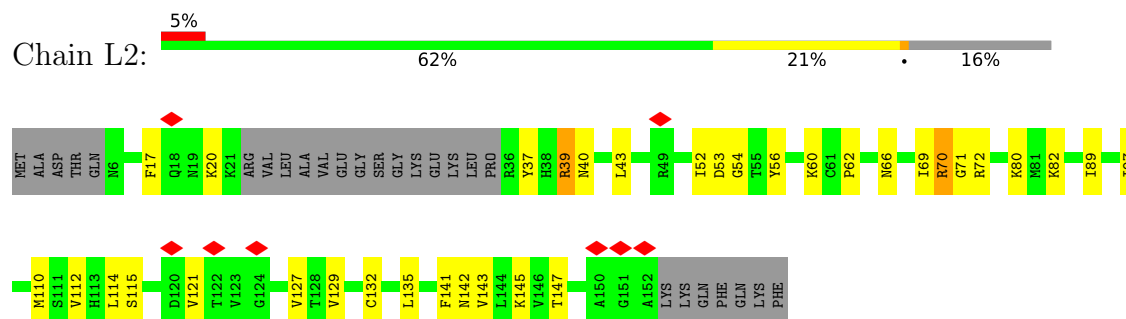
- Molecule 25: Ribosomal protein S10



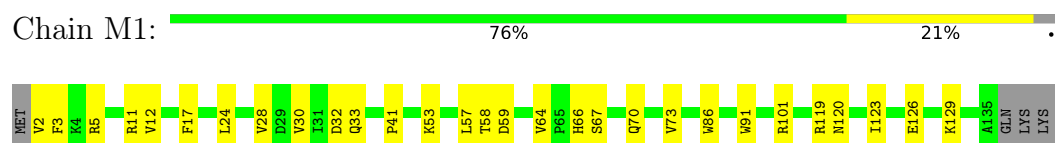
- Molecule 26: 60S ribosomal protein L13



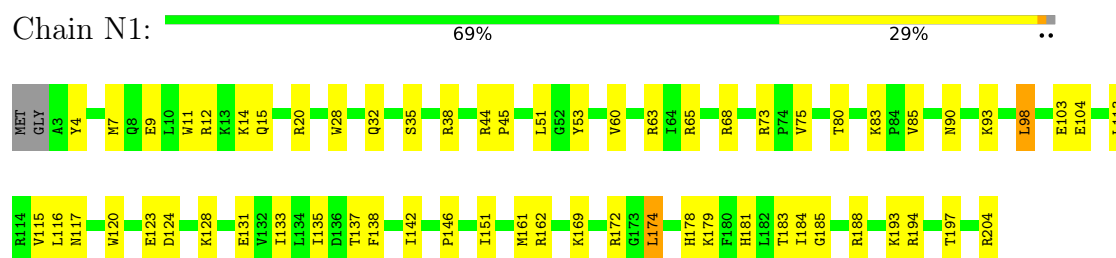
- Molecule 27: 40S ribosomal protein S11



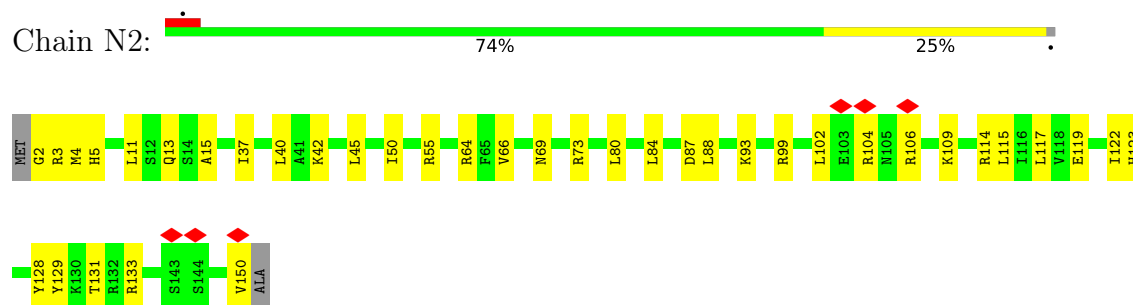
- Molecule 28: 60S ribosomal protein L14



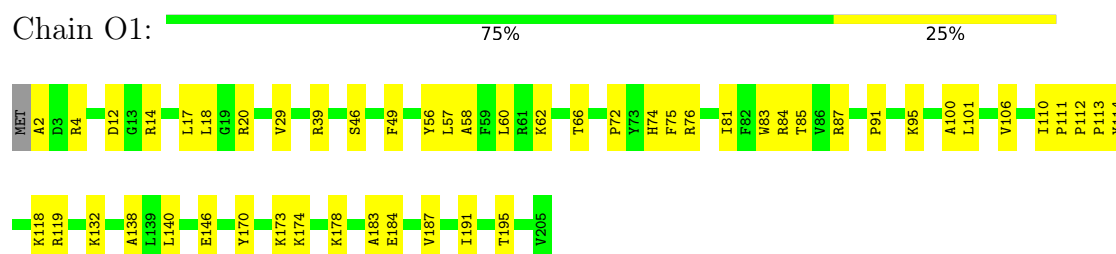
- Molecule 29: Ribosomal protein L15



- Molecule 30: 40S ribosomal protein S13

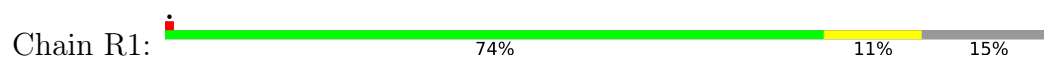


- Molecule 31: 60S ribosomal protein L13a

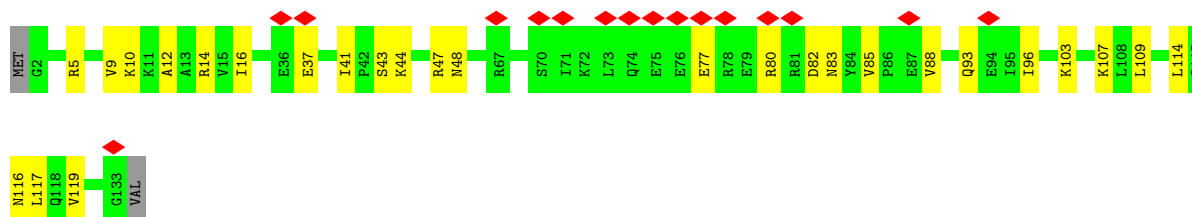
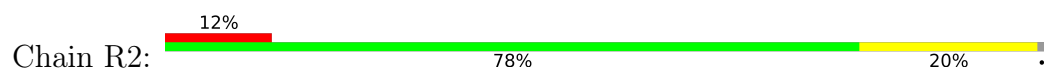




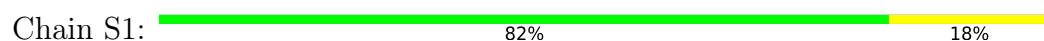
- Molecule 37: 60S ribosomal protein L19



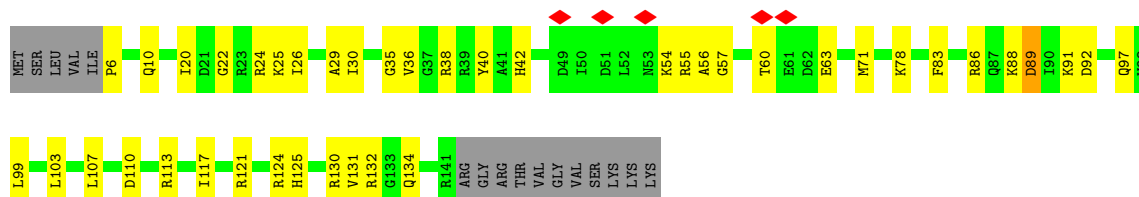
- Molecule 38: 40S ribosomal protein S17



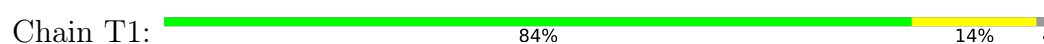
- Molecule 39: 60S ribosomal protein L18a



- Molecule 40: 40S ribosomal protein S18



- Molecule 41: 60S ribosomal protein L21



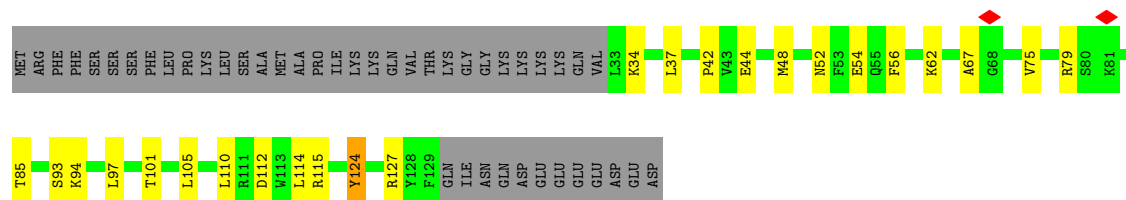
- Molecule 42: 40S ribosomal protein S19

Chain T2: 



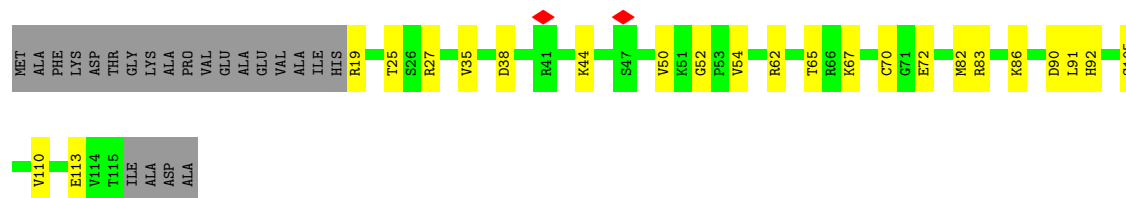
- Molecule 43: Ribosomal protein L22

Chain U1: 



- Molecule 44: 40S ribosomal protein S20

Chain U2: 



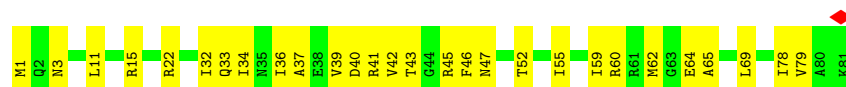
- Molecule 45: 60S ribosomal protein L23

Chain V1: 



- Molecule 46: 40S ribosomal protein S21

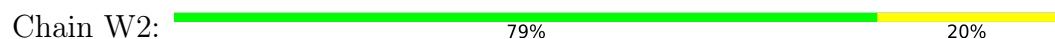
Chain V2: 



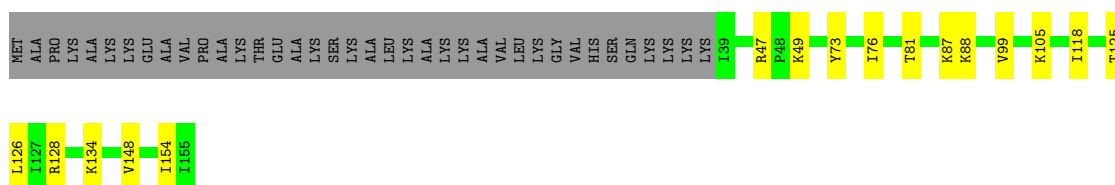
- Molecule 47: 60S ribosomal protein L24

Chain W1: 

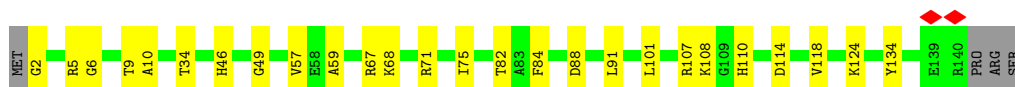
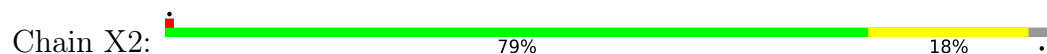
- Molecule 48: 40S ribosomal protein S15a



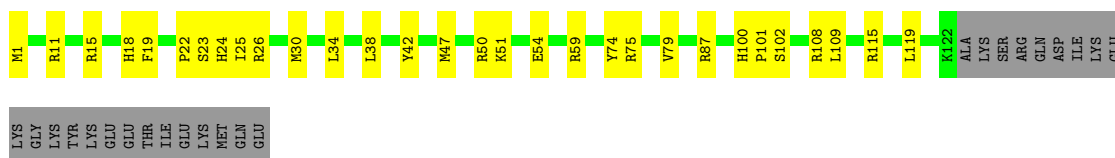
- Molecule 49: Ribosomal protein L23a



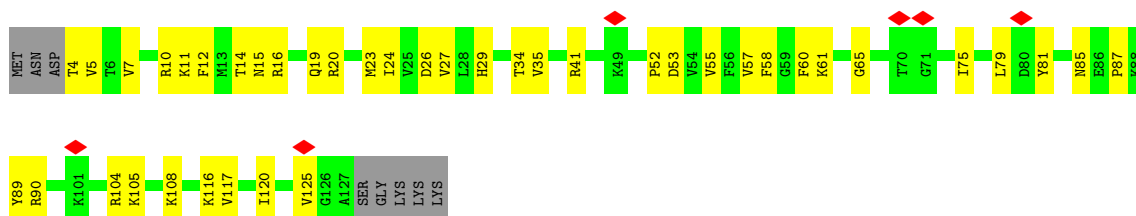
- Molecule 50: 40S ribosomal protein S23



- Molecule 51: ATPase H⁺ transporting V0 subunit e1



- Molecule 52: 40S ribosomal protein S24



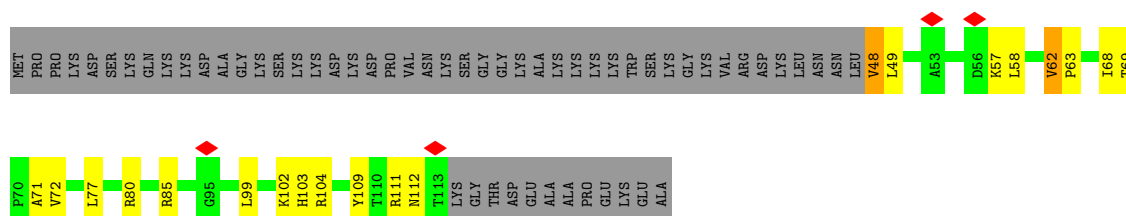
- Molecule 53: 60S ribosomal protein L27

Chain Z1:  83% 16%



- Molecule 54: 40S ribosomal protein S25

Chain Z2:  37% 15% 47%



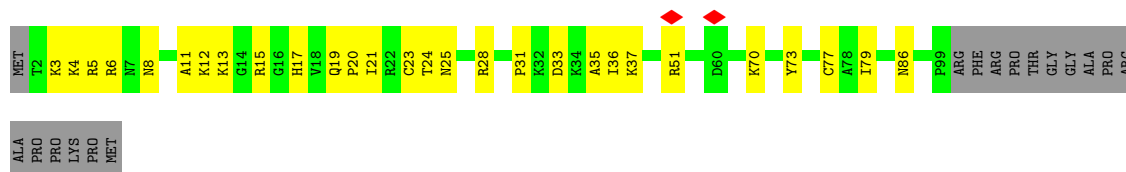
- Molecule 55: 60S ribosomal protein L27a

Chain a1:  71% 27%



- Molecule 56: 40S ribosomal protein S26

Chain a2:  61% 24% 15%



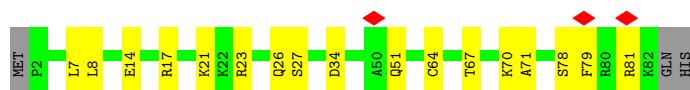
- Molecule 57: 60S ribosomal protein L29

Chain b1:  64% 12% 23%



- Molecule 58: 40S ribosomal protein S27

Chain b2:  76% 20%



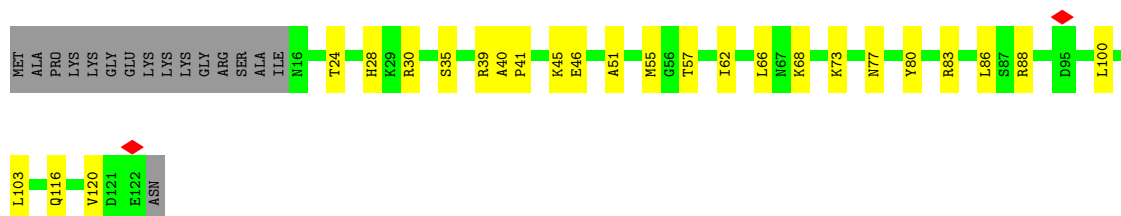
- Molecule 59: 60S ribosomal protein L30



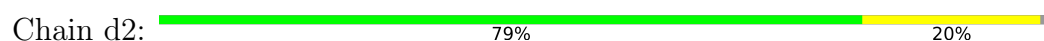
- Molecule 60: 40S ribosomal protein S28



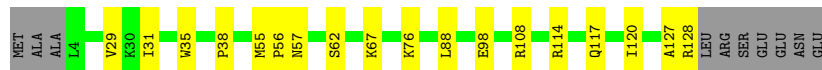
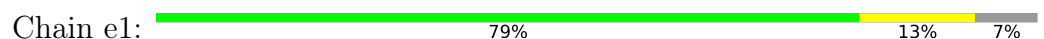
- Molecule 61: 60S ribosomal protein L31



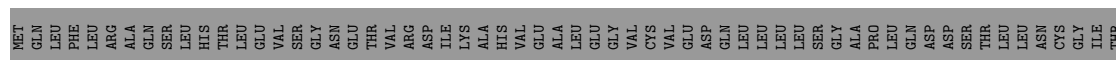
- Molecule 62: 40S ribosomal protein S29

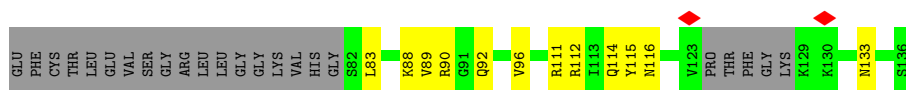


- Molecule 63: Ribosomal protein L32



- Molecule 64: 40S ribosomal protein S30





- Molecule 65: 60S ribosomal protein L35a

Chain f1: 80% 17%



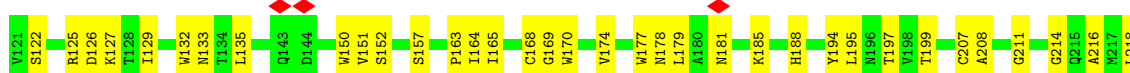
- Molecule 66: 60S ribosomal protein L34

Chain g1: 71% 18% 11%



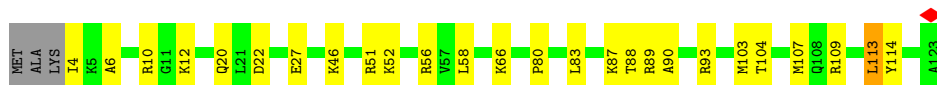
- Molecule 67: Guanine nucleotide-binding protein subunit beta-2-like 1

Chain g2: 5% 66% 31%



- Molecule 68: 60S ribosomal protein L35

Chain h1: 76% 20%



- Molecule 69: 60S ribosomal protein L36

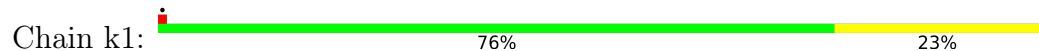
Chain i1: 78% 15% 7%



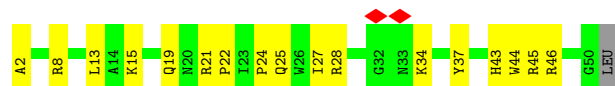
- Molecule 70: Ribosomal protein L37



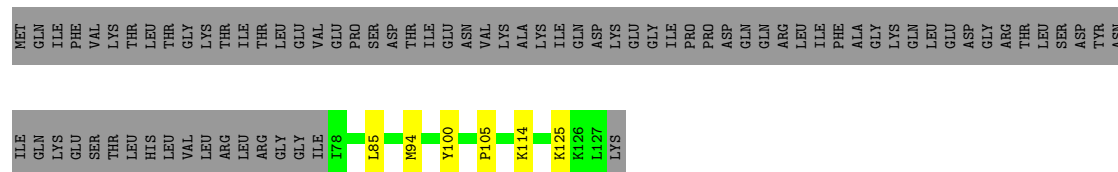
- Molecule 71: 60S ribosomal protein L38



- Molecule 72: Ribosomal protein L39



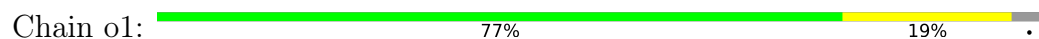
- Molecule 73: 60S ribosomal protein L40



- Molecule 74: Rpl41



- Molecule 75: 60S ribosomal protein L36a



- Molecule 76: Zgc:171772





• Molecule 77: 60S ribosomal protein L28



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	775288	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 ($e^-/\text{\AA}^2$)	48.3	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	10.815	Depositor
Minimum map value	-0.721	Depositor
Average map value	0.068	Depositor
Map value standard deviation	0.247	Depositor
Recommended contour level	0.7	Depositor
Map size (Å)	508.8, 508.8, 508.8	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	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, MG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	22	0.07	0/35898	0.15	0/55926
2	51	0.11	0/78190	0.19	0/121918
3	71	0.10	0/2867	0.15	0/4469
4	81	0.11	0/3573	0.16	0/5563
5	A1	0.12	0/1918	0.30	0/2569
6	A2	0.08	0/1703	0.24	0/2313
7	B1	0.12	0/3251	0.29	0/4351
8	B2	0.09	0/1757	0.26	0/2353
9	C1	0.13	0/2828	0.29	0/3797
10	C2	0.09	0/1687	0.24	0/2281
11	D1	0.10	0/2380	0.27	0/3185
12	D2	0.10	0/1740	0.29	0/2342
13	E1	0.11	0/1697	0.28	0/2264
14	E2	0.09	0/2110	0.30	0/2839
15	F1	0.13	0/1842	0.29	0/2460
16	F2	0.08	0/1462	0.28	0/1966
17	G1	0.11	0/1717	0.28	0/2316
18	G2	0.09	0/1887	0.28	0/2515
19	H1	0.11	0/1523	0.26	0/2048
20	H2	0.10	0/1515	0.28	0/2033
21	I1	0.11	0/1738	0.29	0/2325
22	I2	0.09	0/1695	0.29	0/2267
23	J1	0.10	0/1371	0.30	0/1833
24	J2	0.09	0/1517	0.27	0/2028
25	K2	0.07	0/792	0.29	0/1072
26	L1	0.12	0/1631	0.31	0/2178
27	L2	0.09	0/1105	0.30	0/1479
28	M1	0.11	0/1115	0.25	0/1488
29	N1	0.13	0/1731	0.30	0/2314
30	N2	0.08	0/1223	0.25	0/1644
31	O1	0.12	0/1694	0.29	0/2267
32	O2	0.09	0/955	0.27	0/1279

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	P1	0.12	0/1261	0.30	0/1691
34	P2	0.09	0/974	0.26	0/1301
35	Q1	0.13	0/1484	0.32	0/1985
36	Q2	0.09	0/1068	0.29	0/1434
37	R1	0.10	0/1397	0.29	0/1849
38	R2	0.09	0/1082	0.24	0/1452
39	S1	0.13	0/1496	0.31	0/2009
40	S2	0.10	0/1147	0.29	0/1535
41	T1	0.12	0/1312	0.27	0/1756
42	T2	0.09	0/1076	0.26	0/1445
43	U1	0.10	0/806	0.29	0/1081
44	U2	0.08	0/763	0.26	0/1027
45	V1	0.11	0/984	0.27	0/1320
46	V2	0.09	0/629	0.26	0/842
47	W1	0.11	0/516	0.29	0/688
48	W2	0.10	0/1051	0.29	0/1406
49	X1	0.10	0/978	0.26	0/1318
50	X2	0.09	0/1100	0.27	0/1468
51	Y1	0.11	0/1039	0.28	0/1383
52	Y2	0.10	0/1027	0.29	0/1364
53	Z1	0.10	0/1128	0.27	0/1504
54	Z2	0.09	0/536	0.29	0/721
55	a1	0.11	0/1196	0.28	0/1601
56	a2	0.09	0/795	0.27	0/1066
57	b1	0.11	0/429	0.29	0/568
58	b2	0.08	0/649	0.26	0/872
59	c1	0.09	0/731	0.21	0/981
60	c2	0.09	0/477	0.29	0/639
61	d1	0.12	0/903	0.30	0/1217
62	d2	0.09	0/470	0.27	0/624
63	e1	0.12	0/1048	0.29	0/1396
64	e2	0.09	0/401	0.29	0/526
65	f1	0.13	0/880	0.29	0/1175
66	g1	0.12	0/843	0.31	0/1123
67	g2	0.08	0/2451	0.24	0/3343
68	h1	0.10	0/998	0.28	0/1318
69	i1	0.11	0/812	0.30	0/1074
70	j1	0.13	0/715	0.33	0/944
71	k1	0.10	0/575	0.25	0/761
72	l1	0.12	0/444	0.31	0/587
73	m1	0.11	0/419	0.30	0/555
74	n1	0.12	0/232	0.38	0/295
75	o1	0.10	0/853	0.28	0/1125

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	p1	0.11	0/713	0.26	0/945
77	r1	0.12	0/956	0.30	0/1279
All	All	0.10	0/208956	0.22	0/306275

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
39	S1	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
39	S1	164	LYS	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	22	32102	0	16222	459	0
2	51	69917	0	35356	829	0
3	71	2563	0	1297	24	0
4	81	3199	0	1623	55	0
5	A1	1879	0	1974	47	0
6	A2	1665	0	1667	34	0
7	B1	3181	0	3303	67	0
8	B2	1730	0	1802	37	0
9	C1	2774	0	2909	57	0
10	C2	1651	0	1733	29	0
11	D1	2337	0	2389	46	0
12	D2	1713	0	1804	34	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	E1	1671	0	1819	24	0
14	E2	2070	0	2180	53	0
15	F1	1811	0	1937	41	0
16	F2	1442	0	1480	33	0
17	G1	1683	0	1787	20	0
18	G2	1864	0	2018	40	0
19	H1	1505	0	1589	24	0
20	H2	1492	0	1583	22	0
21	I1	1699	0	1756	29	0
22	I2	1666	0	1749	33	0
23	J1	1348	0	1393	21	0
24	J2	1492	0	1610	30	0
25	K2	769	0	783	16	0
26	L1	1603	0	1726	35	0
27	L2	1086	0	1135	29	0
28	M1	1094	0	1161	21	0
29	N1	1689	0	1744	49	0
30	N2	1200	0	1285	29	0
31	O1	1662	0	1806	41	0
32	O2	943	0	974	26	0
33	P1	1235	0	1261	31	0
34	P2	957	0	1003	27	0
35	Q1	1459	0	1580	40	0
36	Q2	1052	0	1111	29	0
37	R1	1381	0	1520	22	0
38	R2	1068	0	1121	19	0
39	S1	1457	0	1518	23	0
40	S2	1129	0	1177	29	0
41	T1	1283	0	1355	16	0
42	T2	1058	0	1100	36	0
43	U1	792	0	814	14	0
44	U2	754	0	805	18	0
45	V1	970	0	1031	18	0
46	V2	623	0	630	21	0
47	W1	503	0	512	6	0
48	W2	1034	0	1080	22	0
49	X1	959	0	1022	11	0
50	X2	1083	0	1150	19	0
51	Y1	1024	0	1112	25	0
52	Y2	1011	0	1085	34	0
53	Z1	1105	0	1182	18	0
54	Z2	529	0	578	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
55	a1	1164	0	1205	35	0
56	a2	782	0	832	23	0
57	b1	419	0	430	5	0
58	b2	636	0	659	11	0
59	c1	721	0	751	6	0
60	c2	475	0	491	11	0
61	d1	888	0	927	13	0
62	d2	459	0	447	14	0
63	e1	1030	0	1116	14	0
64	e2	399	0	434	11	0
65	f1	861	0	912	11	0
66	g1	833	0	910	18	0
67	g2	2394	0	2325	58	0
68	h1	991	0	1122	20	0
69	i1	801	0	881	10	0
70	j1	701	0	733	21	0
71	k1	569	0	637	12	0
72	l1	434	0	472	12	0
73	m1	413	0	446	5	0
74	n1	231	0	277	8	0
75	o1	840	0	911	14	0
76	p1	703	0	754	20	0
77	r1	943	0	1013	16	0
78	51	189	0	0	0	0
78	71	3	0	0	0	0
78	81	4	0	0	0	0
78	A1	2	0	0	0	0
78	B1	1	0	0	0	0
78	V1	1	0	0	0	0
78	b1	1	0	0	0	0
78	e1	1	0	0	0	0
78	m1	1	0	0	0	0
79	a2	1	0	0	0	0
79	d2	1	0	0	0	0
79	g1	1	0	0	0	0
79	j1	1	0	0	0	0
79	m1	1	0	0	0	0
79	o1	1	0	0	0	0
79	p1	1	0	0	0	0
All	All	194863	0	146026	2496	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 8.

All (2496) 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)
70:j1:2:THR:N	70:j1:6:SER:HG	1.69	0.89
2:51:491:G:H1	2:51:566:U:H3	1.20	0.88
2:51:460:C:H42	2:51:596:G:H1	1.23	0.84
2:51:810:A:H61	2:51:843:U:H3	1.27	0.83
2:51:2952:A:H62	2:51:3083:G:H21	1.23	0.82
2:51:1983:G:H1	2:51:2204:U:H3	1.27	0.82
2:51:3557:U:HO2'	2:51:3588:G:HO2'	1.23	0.82
2:51:623:G:H1'	2:51:709:G:H1	1.44	0.81
2:51:1988:C:N4	2:51:2008:G:N3	2.29	0.81
1:22:40:A:HO2'	1:22:531:A:HO2'	1.24	0.80
32:O2:34:PHE:HB3	32:O2:41:PHE:HB2	1.62	0.80
7:B1:41:VAL:HA	7:B1:187:GLY:HA3	1.64	0.79
2:51:615:U:H3	2:51:717:G:H1	1.31	0.79
2:51:1290:C:H4'	35:Q1:143:ARG:HH22	1.46	0.79
67:g2:87:LEU:HB2	67:g2:101:PHE:HB2	1.63	0.78
2:51:619:G:H1	2:51:712:C:H42	1.28	0.78
2:51:751:C:H41	2:51:881:C:H41	1.32	0.77
1:22:907:A:O2'	1:22:908:A:OP2	2.03	0.77
51:Y1:50:ARG:HB2	51:Y1:115:ARG:HH22	1.50	0.76
2:51:1796:U:H5'	33:P1:66:GLY:HA3	1.65	0.76
2:51:1302:G:H1	2:51:1423:C:H5	1.34	0.75
2:51:647:G:H22	2:51:678:A:H8	1.32	0.75
25:K2:61:GLN:HB2	25:K2:68:TYR:HB2	1.69	0.75
2:51:2045:U:H5'	2:51:2123:G:H4'	1.67	0.74
2:51:4020:C:H5	2:51:4152:G:H1	1.33	0.74
2:51:211:G:N2	2:51:235:G:OP2	2.20	0.73
40:S2:22:GLY:HA2	40:S2:56:ALA:HB3	1.69	0.73
43:U1:54:GLU:HG3	43:U1:79:ARG:HB2	1.71	0.73
4:81:97:C:H5''	68:h1:66:LYS:HD3	1.71	0.72
2:51:989:G:H21	2:51:990:C:H41	1.37	0.72
2:51:2901:U:OP2	2:51:2906:A:N6	2.23	0.72
2:51:1980:G:N2	2:51:1981:G:N7	2.37	0.72
29:N1:120:TRP:HE1	29:N1:123:GLU:HG3	1.55	0.72
5:A1:62:MET:HE3	5:A1:71:LYS:HB3	1.71	0.71
2:51:3571:C:H2'	2:51:3573:G:H8	1.54	0.71
37:R1:133:LYS:H	37:R1:137:ILE:HD11	1.55	0.71
2:51:3117:G:H5''	33:P1:86:LYS:HB2	1.71	0.71
2:51:3793:C:OP1	7:B1:246:ARG:NH2	2.23	0.71
12:D2:23:GLU:HG2	25:K2:64:TRP:HE1	1.55	0.71
67:g2:78:ALA:HB3	67:g2:90:TRP:HB2	1.70	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:51:3429:G:H21	17:G1:245:LYS:HE3	1.56	0.71
1:22:1415:G:OP2	1:22:1415:G:N2	2.23	0.70
67:g2:39:THR:HG22	67:g2:60:ARG:HG2	1.72	0.70
1:22:538:C:OP2	52:Y2:104:ARG:NH1	2.24	0.70
1:22:1022:G:OP2	1:22:1022:G:N2	2.23	0.70
1:22:1597:C:OP1	1:22:1669:G:N2	2.18	0.70
2:51:1971:G:OP2	71:k1:37:ARG:NH2	2.23	0.70
2:51:3147:C:OP2	31:O1:87:ARG:NH1	2.24	0.70
2:51:3940:C:O2'	2:51:3942:A:OP2	2.09	0.70
1:22:1544:G:OP1	36:Q2:138:ARG:NH1	2.24	0.70
1:22:615:A:H61	1:22:627:U:H3	1.40	0.70
2:51:550:A:H61	35:Q1:114:LEU:HB3	1.55	0.70
2:51:1418:G:H4'	41:T1:129:LYS:HG2	1.74	0.70
2:51:4007:G:H1	2:51:4163:U:H3	1.40	0.69
2:51:625:C:OP1	15:F1:74:ARG:NH2	2.25	0.69
2:51:1623:A:H4'	2:51:1624:A:H5''	1.73	0.69
2:51:68:C:OP1	29:N1:178:HIS:ND1	2.26	0.69
2:51:496:G:OP1	9:C1:5:ARG:NH2	2.25	0.69
55:a1:103:VAL:HG12	55:a1:108:TYR:HB2	1.74	0.69
2:51:3915:C:H3'	37:R1:62:ARG:HH22	1.58	0.68
2:51:2012:G:N7	53:Z1:17:ARG:NH1	2.41	0.68
2:51:474:C:H42	2:51:580:G:H1	1.40	0.68
2:51:1639:G:O2'	31:O1:20:ARG:NH2	2.26	0.68
2:51:2082:A:H62	2:51:2121:G:H8	1.40	0.68
23:J1:18:ARG:HG3	23:J1:135:GLY:HA3	1.75	0.68
1:22:1325:G:N2	1:22:1728:C:O2'	2.26	0.68
1:22:1342:G:N2	1:22:1571:A:N7	2.39	0.68
2:51:3987:A:OP2	7:B1:30:LYS:NZ	2.23	0.68
1:22:27:A:HO2'	1:22:529:C:HO2'	1.39	0.68
2:51:2138:G:H1	2:51:2148:C:H42	1.42	0.68
9:C1:286:ILE:HG23	9:C1:291:ARG:HH11	1.58	0.68
2:51:2137:C:OP1	43:U1:115:ARG:NH2	2.27	0.67
8:B2:65:ARG:HG2	32:O2:50:LYS:HE3	1.76	0.67
1:22:1579:G:N2	34:P2:97:TYR:O	2.27	0.67
2:51:175:U:H3	2:51:264:G:H1	1.41	0.67
2:51:2093:G:N2	2:51:2111:A:OP2	2.26	0.67
19:H1:31:ARG:NH2	19:H1:149:ASN:OD1	2.27	0.67
36:Q2:42:ILE:HG22	36:Q2:44:PRO:HD2	1.76	0.67
2:51:1005:G:HO2'	2:51:1065:C:HO2'	1.36	0.67
8:B2:146:ARG:HE	8:B2:206:PRO:HG3	1.59	0.67
65:f1:10:ILE:HB	65:f1:29:LYS:HB3	1.75	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:51:1871:G:H5'	49:X1:126:LEU:HD13	1.74	0.67
2:51:3890:U:OP2	2:51:3940:C:N4	2.27	0.67
3:71:7:G:OP1	11:D1:33:ARG:NH2	2.28	0.67
51:Y1:54:GLU:HB2	51:Y1:108:ARG:HB3	1.76	0.67
52:Y2:15:ASN:HD21	52:Y2:20:ARG:HB2	1.59	0.67
9:C1:221:PHE:HB3	9:C1:227:ILE:HG21	1.77	0.67
51:Y1:23:SER:O	51:Y1:75:ARG:NH1	2.28	0.67
2:51:3156:C:O2'	7:B1:268:ARG:NH2	2.26	0.67
2:51:221:C:H42	2:51:238:G:H1	1.43	0.67
2:51:3011:G:H21	2:51:3035:A:H8	1.42	0.67
70:j1:2:THR:N	70:j1:6:SER:OG	2.27	0.67
2:51:3961:A:H5'	19:H1:71:ARG:HE	1.59	0.66
1:22:1631:G:H1	42:T2:102:ARG:HH22	1.44	0.66
2:51:980:C:H4'	2:51:981:G:H5'	1.76	0.66
2:51:2940:U:OP1	5:A1:54:ARG:NH2	2.26	0.66
2:51:1535:G:H4'	39:S1:93:MET:HG3	1.77	0.66
7:B1:73:VAL:O	45:V1:89:ARG:NH2	2.28	0.66
14:E2:11:ARG:HH12	14:E2:24:THR:HB	1.60	0.66
14:E2:11:ARG:HA	14:E2:28:ALA:HB2	1.77	0.66
1:22:424:G:OP2	22:I2:178:ARG:NH1	2.28	0.66
2:51:706:C:OP1	15:F1:240:ARG:NH2	2.27	0.66
30:N2:102:LEU:O	30:N2:106:ARG:NH1	2.28	0.66
2:51:3852:C:O2'	7:B1:99:LEU:O	2.14	0.66
14:E2:122:LYS:NZ	14:E2:124:CYS:SG	2.68	0.66
1:22:49:C:H2'	1:22:518:C:H41	1.61	0.66
1:22:1607:A:OP1	42:T2:63:ARG:NH2	2.29	0.66
2:51:877:C:H2'	2:51:878:G:H4'	1.78	0.66
1:22:1331:C:O2	1:22:1582:G:N2	2.29	0.66
2:51:1254:U:H5	55:a1:26:ARG:HH12	1.44	0.66
1:22:1003:U:OP1	76:p1:85:ARG:NH2	2.29	0.66
1:22:1482:C:OP1	42:T2:130:ARG:NH2	2.29	0.66
7:B1:10:ARG:NH1	7:B1:11:HIS:O	2.29	0.66
2:51:1222:G:H4'	2:51:1223:G:H5'	1.78	0.66
2:51:1829:A:N3	2:51:2241:A:O2'	2.29	0.66
10:C2:154:GLY:HA2	46:V2:1:MET:HE1	1.77	0.66
42:T2:41:ALA:HB3	42:T2:44:LYS:HG2	1.78	0.66
1:22:1079:U:O2'	30:N2:55:ARG:NH1	2.29	0.65
2:51:281:A:O2'	29:N1:14:LYS:NZ	2.29	0.65
55:a1:76:ASP:HB3	55:a1:115:GLY:HA3	1.77	0.65
2:51:2017:C:OP2	66:g1:76:ARG:NH2	2.29	0.65
2:51:4081:U:H1'	13:E1:250:SER:HB3	1.76	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:51:606:G:N2	2:51:898:C:O2	2.30	0.65
2:51:1226:C:OP1	5:A1:14:SER:OG	2.13	0.65
2:51:3626:U:H4'	26:L1:197:LYS:HD2	1.77	0.65
1:22:1612:C:H1'	1:22:1735:C:H4'	1.78	0.65
1:22:479:A:H5''	22:I2:22:HIS:HB3	1.77	0.65
15:F1:217:GLY:O	15:F1:244:ARG:NH2	2.30	0.65
17:G1:167:VAL:HG12	17:G1:170:LEU:HD12	1.77	0.65
2:51:3851:G:H1	2:51:3992:C:H5	1.44	0.65
30:N2:69:ASN:HB3	30:N2:73:ARG:HB2	1.79	0.65
2:51:1795:G:O2'	33:P1:82:ARG:NH2	2.30	0.65
2:51:2949:G:O2'	2:51:3078:U:OP2	2.15	0.65
2:51:3303:G:O6	5:A1:72:ARG:NH2	2.27	0.65
43:U1:42:PRO:HB2	43:U1:48:MET:HB3	1.78	0.65
2:51:1267:A:OP1	57:b1:18:ARG:NH1	2.29	0.64
2:51:3362:C:O2	2:51:3419:G:N2	2.26	0.64
1:22:1385:G:H5'	1:22:1386:U:H5'	1.79	0.64
18:G2:121:ILE:HG22	18:G2:123:GLY:H	1.62	0.64
2:51:1383:A:O2'	41:T1:108:ARG:NH1	2.29	0.64
2:51:2325:G:H21	2:51:4236:A:H8	1.44	0.64
1:22:528:G:N1	1:22:531:A:OP2	2.28	0.64
29:N1:68:ARG:NH1	29:N1:124:ASP:O	2.30	0.64
1:22:1662:C:OP2	54:Z2:85:ARG:NH1	2.31	0.64
1:22:1024:U:OP2	32:O2:38:ASN:ND2	2.27	0.64
1:22:1519:A:N1	1:22:1541:A:O2'	2.30	0.64
70:j1:27:TYR:HA	70:j1:34:CYS:HA	1.79	0.64
1:22:117:C:N4	1:22:391:U:O4	2.31	0.64
2:51:339:U:OP1	26:L1:31:ARG:NH1	2.30	0.64
7:B1:10:ARG:NH2	7:B1:265:SER:O	2.29	0.64
8:B2:92:GLN:O	8:B2:95:ASN:ND2	2.31	0.64
1:22:616:U:O2'	52:Y2:34:THR:O	2.15	0.64
1:22:1630:C:O2'	1:22:1631:G:N2	2.27	0.64
2:51:624:G:OP1	2:51:860:G:N2	2.31	0.64
2:51:1138:C:HO2'	2:51:1883:A:HO2'	1.46	0.64
2:51:4088:A:H61	2:51:4130:C:H42	1.46	0.64
9:C1:330:PRO:HG3	15:F1:45:ARG:HH11	1.63	0.64
1:22:1101:G:H4'	1:22:1915:A:H4'	1.80	0.64
1:22:1615:G:H3'	1:22:1644:A:H61	1.63	0.64
2:51:603:G:N2	2:51:901:C:O2	2.31	0.64
59:c1:37:MET:SD	59:c1:40:GLN:NE2	2.71	0.64
2:51:981:G:O6	4:81:27:C:O2'	2.13	0.63
2:51:3918:A:OP1	37:R1:62:ARG:NH1	2.31	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:22:1143:C:O2'	1:22:1249:A:N1	2.31	0.63
1:22:1284:A:N6	1:22:1745:G:O6	2.30	0.63
2:51:3740:G:O2'	73:m1:100:TYR:O	2.15	0.63
2:51:3295:U:H5'	17:G1:73:ARG:HG3	1.79	0.63
1:22:244:A:H61	1:22:350:C:H42	1.44	0.63
2:51:4079:A:OP2	28:M1:120:ASN:ND2	2.31	0.63
2:51:160:A:N1	2:51:278:C:O2'	2.32	0.63
48:W2:3:ARG:HH22	48:W2:29:PRO:HG3	1.64	0.63
67:g2:174:VAL:HB	67:g2:188:HIS:HB2	1.80	0.63
1:22:163:G:N2	1:22:163:G:OP2	2.31	0.63
1:22:1608:U:OP2	42:T2:63:ARG:NH1	2.32	0.63
72:l1:43:HIS:HB3	72:l1:46:ARG:HG2	1.79	0.63
1:22:159:U:H5'	52:Y2:116:LYS:HB3	1.80	0.63
1:22:1213:C:OP1	56:a2:6:ARG:NH1	2.32	0.63
2:51:2913:A:O2'	5:A1:179:ILE:O	2.15	0.63
42:T2:40:LEU:O	42:T2:97:SER:OG	2.15	0.63
48:W2:49:GLU:O	48:W2:64:ASN:ND2	2.31	0.63
1:22:1310:U:O4	1:22:1326:A:N6	2.32	0.63
14:E2:137:PRO:HG2	14:E2:150:PRO:HD2	1.80	0.63
75:o1:26:TYR:HB3	75:o1:67:VAL:HB	1.81	0.63
2:51:566:U:OP2	77:r1:68:ARG:NH1	2.32	0.63
11:D1:65:ALA:HB2	11:D1:74:ILE:HD13	1.81	0.63
2:51:974:G:H1	2:51:982:A:H61	1.45	0.62
13:E1:163:LEU:HD21	13:E1:230:VAL:HG21	1.81	0.62
10:C2:152:ARG:NH1	10:C2:240:ASP:OD1	2.28	0.62
1:22:1078:G:N2	58:b2:51:GLN:OE1	2.32	0.62
18:G2:145:PHE:HB3	18:G2:147:LEU:HG	1.79	0.62
2:51:1907:G:O2'	2:51:1940:G:N2	2.26	0.62
44:U2:50:VAL:HG22	44:U2:91:LEU:HD13	1.81	0.62
1:22:1396:U:O2'	1:22:1399:A:OP2	2.18	0.62
2:51:1006:A:N1	2:51:1096:G:O2'	2.33	0.62
2:51:1032:U:H5''	35:Q1:42:PRO:HB2	1.81	0.62
2:51:1758:C:O2'	63:e1:98:GLU:OE1	2.16	0.62
2:51:2138:G:H5''	43:U1:127:ARG:HH22	1.64	0.62
1:22:1934:U:OP2	56:a2:5:ARG:NH1	2.31	0.62
2:51:3809:G:N2	2:51:3812:A:OP2	2.30	0.62
30:N2:88:LEU:HD11	30:N2:122:ILE:HG23	1.82	0.62
2:51:310:G:O6	29:N1:12:ARG:NH1	2.33	0.62
15:F1:102:LYS:HD3	15:F1:133:ILE:HD11	1.80	0.62
1:22:933:A:OP1	37:R1:163:ARG:NH1	2.32	0.62
2:51:1840:G:N7	72:l1:2:ALA:N	2.47	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:S1:3:ALA:HA	39:S1:7:LEU:HD21	1.82	0.62
1:22:385:G:OP2	1:22:385:G:N2	2.33	0.62
1:22:1100:A:N3	1:22:1914:U:O2'	2.31	0.62
1:22:1628:G:H22	42:T2:102:ARG:HH11	1.48	0.62
2:51:406:U:O3'	51:Y1:87:ARG:NH1	2.32	0.62
34:P2:18:ARG:NH1	40:S2:88:LYS:O	2.32	0.62
1:22:423:G:H5''	22:I2:98:LYS:HB3	1.82	0.61
2:51:1534:G:HO2'	39:S1:95:ARG:HH12	1.46	0.61
21:I1:33:ILE:O	21:I1:69:ARG:NH1	2.33	0.61
67:g2:226:HIS:NE2	67:g2:229:THR:OG1	2.28	0.61
2:51:321:A:H1'	2:51:2986:A:H8	1.66	0.61
2:51:2195:G:O6	53:Z1:64:LYS:NZ	2.33	0.61
14:E2:95:THR:O	52:Y2:16:ARG:NH2	2.32	0.61
2:51:983:G:H22	9:C1:234:ARG:HH21	1.48	0.61
11:D1:50:ARG:NH2	11:D1:147:ASP:OD2	2.33	0.61
2:51:328:C:OP1	69:i1:25:LYS:NZ	2.33	0.61
2:51:782:C:H41	13:E1:34:ALA:HA	1.65	0.61
2:51:1984:G:H1	2:51:2202:U:H3	1.48	0.61
30:N2:13:GLN:HE21	58:b2:21:LYS:HE2	1.64	0.61
2:51:1081:C:O2'	26:L1:195:ARG:NH1	2.33	0.61
8:B2:107:ARG:NH2	32:O2:133:THR:O	2.25	0.61
16:F2:32:ASP:O	16:F2:36:GLN:NE2	2.34	0.61
65:f1:43:LEU:O	65:f1:109:ARG:NH2	2.33	0.61
1:22:1509:U:OP2	36:Q2:15:ARG:NH1	2.34	0.61
2:51:516:G:H1	2:51:543:G:H22	1.47	0.61
2:51:2023:C:HO2'	2:51:2201:A:HO2'	1.47	0.61
2:51:2914:G:O2'	2:51:2953:U:OP1	2.12	0.61
2:51:3903:U:O2'	2:51:3905:G:OP1	2.15	0.61
2:51:4029:C:H4'	31:O1:118:LYS:HD3	1.83	0.61
9:C1:7:LEU:HG	9:C1:21:ASN:HB3	1.82	0.61
19:H1:92:MET:HB3	19:H1:181:VAL:HA	1.82	0.61
2:51:1938:U:O4	5:A1:72:ARG:NH1	2.33	0.61
20:H2:143:ARG:HB2	20:H2:155:LYS:HB2	1.82	0.61
27:L2:145:LYS:NZ	27:L2:147:THR:OG1	2.34	0.61
39:S1:161:ARG:HD2	39:S1:164:LYS:HB2	1.82	0.61
4:81:70:A:OP2	51:Y1:50:ARG:NH1	2.34	0.61
2:51:75:G:H3'	26:L1:74:ARG:HG3	1.81	0.61
2:51:1740:G:OP1	63:e1:128:ARG:NH2	2.33	0.61
8:B2:122:GLU:HG2	8:B2:140:VAL:HG22	1.83	0.61
22:I2:81:VAL:HG12	22:I2:102:VAL:HG12	1.82	0.61
25:K2:15:LEU:HD13	25:K2:21:MET:HB2	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:R2:93:GLN:HE21	38:R2:96:ILE:HG12	1.66	0.61
1:22:998:G:OP2	1:22:1057:G:N2	2.27	0.61
1:22:1643:U:O2	12:D2:9:ARG:NH2	2.34	0.61
6:A2:85:ARG:NH2	38:R2:82:ASP:O	2.34	0.61
9:C1:74:ALA:H	9:C1:78:ARG:HH21	1.48	0.61
13:E1:165:ARG:NH2	13:E1:191:ASP:OD1	2.34	0.61
18:G2:85:ARG:O	18:G2:87:ARG:NH1	2.33	0.61
22:I2:33:ALA:O	22:I2:56:ARG:NH2	2.34	0.61
1:22:1421:G:N2	1:22:1424:A:OP2	2.31	0.60
2:51:1824:G:H22	2:51:2260:G:H22	1.48	0.60
16:F2:138:ALA:O	16:F2:204:ARG:NH1	2.34	0.60
19:H1:44:GLU:OE1	28:M1:2:VAL:N	2.33	0.60
28:M1:64:VAL:HG21	28:M1:73:VAL:HG22	1.83	0.60
29:N1:135:ILE:HG23	29:N1:142:ILE:HD13	1.83	0.60
2:51:2007:A:O2'	53:Z1:112:ARG:NH1	2.35	0.60
12:D2:28:GLU:OE1	12:D2:65:ARG:NH1	2.34	0.60
16:F2:126:THR:HG22	60:c2:47:LYS:HD2	1.83	0.60
20:H2:57:ARG:HH11	20:H2:91:HIS:HE1	1.47	0.60
30:N2:99:ARG:HE	30:N2:115:LEU:HD21	1.66	0.60
2:51:618:G:H1	2:51:713:U:H3	1.50	0.60
2:51:2910:C:OP1	5:A1:200:ARG:NH2	2.33	0.60
2:51:3681:C:H5	2:51:3697:C:H42	1.49	0.60
2:51:3963:C:OP1	19:H1:64:ARG:NH2	2.33	0.60
34:P2:121:ILE:HG22	34:P2:123:TYR:H	1.66	0.60
52:Y2:29:HIS:HE1	52:Y2:35:VAL:HG22	1.66	0.60
2:51:81:C:H1'	2:51:968:G:H21	1.66	0.60
2:51:231:G:OP1	51:Y1:15:ARG:NH1	2.30	0.60
2:51:2879:G:H22	2:51:2884:A:H1'	1.66	0.60
7:B1:261:ARG:HB2	31:O1:66:THR:HG21	1.84	0.60
66:g1:40:LYS:HD3	66:g1:52:ARG:HH22	1.67	0.60
67:g2:238:ALA:H	67:g2:251:ALA:HB3	1.67	0.60
1:22:539:A:H61	1:22:556:G:H1'	1.67	0.60
1:22:1693:C:OP1	42:T2:39:LYS:NZ	2.35	0.60
2:51:1403:C:O2	2:51:1405:G:N2	2.34	0.60
2:51:3128:G:H22	2:51:3160:G:H1'	1.66	0.60
2:51:3893:G:OP1	7:B1:19:ARG:NH2	2.33	0.60
22:I2:141:ARG:H	22:I2:146:GLN:HE21	1.48	0.60
45:V1:13:LYS:HD2	45:V1:128:LEU:HD11	1.83	0.60
1:22:1303:G:H21	1:22:1587:A:H61	1.49	0.60
2:51:2013:G:N2	2:51:2016:A:OP2	2.30	0.60
31:O1:2:ALA:HB3	39:S1:167:PHE:HB2	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
76:p1:38:THR:HA	76:p1:45:THR:HA	1.84	0.60
2:51:4026:G:O6	31:O1:4:ARG:NH1	2.34	0.60
13:E1:125:THR:HG22	13:E1:177:LYS:HG2	1.82	0.60
67:g2:11:LEU:HB2	67:g2:307:ILE:HB	1.83	0.60
2:51:1771:C:H4'	77:r1:20:LYS:HB2	1.84	0.60
31:O1:56:TYR:OH	31:O1:75:PHE:O	2.20	0.60
1:22:149:C:O2	18:G2:132:ARG:NH2	2.35	0.60
2:51:349:A:O2'	9:C1:50:GLN:NE2	2.35	0.60
2:51:1628:G:O6	2:51:3130:C:O2'	2.19	0.60
7:B1:99:LEU:HD21	7:B1:159:ILE:HD12	1.84	0.60
28:M1:119:ARG:HE	31:O1:195:THR:HG22	1.67	0.60
46:V2:15:ARG:NH1	46:V2:33:GLN:OE1	2.35	0.60
1:22:707:U:OP1	50:X2:5:ARG:NH1	2.32	0.60
6:A2:16:LEU:HD22	38:R2:116:ASN:HD21	1.66	0.60
16:F2:162:ALA:HA	16:F2:165:ASN:HD22	1.65	0.60
1:22:982:C:H2'	1:22:983:G:C4	2.37	0.59
6:A2:144:THR:OG1	6:A2:156:TYR:O	2.19	0.59
11:D1:66:TYR:HE2	11:D1:68:LYS:HE3	1.66	0.59
1:22:985:G:H4'	30:N2:11:LEU:HD11	1.84	0.59
1:22:1005:C:OP1	8:B2:136:ARG:NH1	2.35	0.59
1:22:1297:C:O2	1:22:1593:G:N2	2.35	0.59
2:51:99:A:H5''	29:N1:184:ILE:HD12	1.84	0.59
2:51:823:G:HO2'	11:D1:286:SER:HG	1.49	0.59
2:51:1267:A:N3	2:51:1435:U:O2'	2.32	0.59
8:B2:197:ILE:HB	8:B2:210:VAL:HG11	1.83	0.59
1:22:1081:U:H5''	30:N2:55:ARG:HD3	1.84	0.59
1:22:1663:G:O6	54:Z2:85:ARG:NH2	2.35	0.59
2:51:3043:A:H2	2:51:3050:U:H3	1.50	0.59
2:51:3826:U:OP2	7:B1:246:ARG:NH1	2.36	0.59
45:V1:65:VAL:HB	45:V1:73:ARG:HA	1.85	0.59
67:g2:40:ILE:HD11	67:g2:66:VAL:HG11	1.84	0.59
1:22:43:U:OP2	1:22:531:A:N6	2.33	0.59
2:51:3500:U:O4	75:o1:8:ARG:NH2	2.36	0.59
1:22:365:G:H22	18:G2:186:GLN:HE22	1.50	0.59
1:22:1404:C:H2'	1:22:1405:G:H8	1.67	0.59
1:22:1628:G:H4'	42:T2:116:LYS:HE3	1.83	0.59
1:22:1719:G:OP1	42:T2:91:SER:OG	2.20	0.59
2:51:21:G:H5'	70:j1:43:ARG:HG2	1.84	0.59
10:C2:151:VAL:HG11	10:C2:203:ALA:HB1	1.84	0.59
22:I2:39:GLY:HA3	22:I2:59:ARG:HD3	1.83	0.59
35:Q1:178:ARG:H	55:a1:51:GLY:HA2	1.67	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:d2:17:GLY:O	62:d2:27:ARG:NH1	2.36	0.59
1:22:1300:G:N3	1:22:1319:C:O2'	2.31	0.59
2:51:608:G:H1	2:51:894:U:H3	1.51	0.59
10:C2:149:ILE:HG12	10:C2:150:PRO:HD2	1.83	0.59
11:D1:67:ALA:HA	11:D1:72:ASP:HB3	1.84	0.59
19:H1:43:LEU:HD23	19:H1:59:LYS:HD3	1.83	0.59
36:Q2:53:GLU:OE2	36:Q2:85:ARG:NH1	2.36	0.59
51:Y1:50:ARG:HG2	51:Y1:51:LYS:H	1.66	0.59
1:22:1684:A:N6	62:d2:14:TYR:OH	2.35	0.59
1:22:1733:U:OP2	36:Q2:141:TYR:OH	2.21	0.59
2:51:3583:G:OP1	41:T1:69:GLN:NE2	2.35	0.59
5:A1:101:VAL:HG22	5:A1:165:VAL:HG22	1.83	0.59
7:B1:55:HIS:CE1	47:W1:16:GLY:HA3	2.37	0.59
58:b2:23:ARG:NH1	58:b2:27:SER:OG	2.34	0.59
68:h1:103:MET:HA	68:h1:107:MET:HE3	1.85	0.59
1:22:1290:A:OP1	16:F2:79:HIS:N	2.35	0.59
2:51:1281:U:OP1	55:a1:44:ASN:ND2	2.32	0.59
8:B2:70:SER:HA	8:B2:83:LYS:HA	1.84	0.59
18:G2:154:ARG:NH2	18:G2:180:VAL:O	2.36	0.59
48:W2:102:ILE:H	48:W2:113:HIS:HD2	1.50	0.59
64:e2:112:ARG:O	64:e2:116:ASN:ND2	2.35	0.59
1:22:1915:A:H2'	1:22:1916:G:C8	2.38	0.59
2:51:371:G:N2	2:51:374:A:OP2	2.29	0.59
2:51:742:C:H41	2:51:890:G:H21	1.49	0.59
2:51:1399:G:OP2	2:51:1399:G:N2	2.31	0.59
2:51:2091:U:H5''	53:Z1:38:TYR:HB3	1.85	0.59
2:51:4180:G:OP1	7:B1:271:GLN:NE2	2.36	0.59
15:F1:129:ASN:OD1	15:F1:132:ARG:NH1	2.36	0.59
42:T2:130:ARG:HG2	42:T2:134:ARG:HE	1.67	0.59
2:51:1215:G:H1'	2:51:1947:A:N6	2.18	0.59
2:51:2267:A:OP1	61:d1:45:LYS:NZ	2.30	0.59
6:A2:106:GLY:N	6:A2:136:GLU:OE2	2.36	0.59
7:B1:33:PRO:O	7:B1:186:ASN:ND2	2.36	0.59
11:D1:60:ILE:HB	11:D1:80:SER:HB2	1.85	0.59
2:51:1116:A:H5'	55:a1:27:LYS:HE3	1.85	0.58
2:51:1282:A:OP1	55:a1:47:LYS:NZ	2.36	0.58
5:A1:5:ILE:HG12	5:A1:8:GLN:HE21	1.68	0.58
6:A2:60:LEU:HD11	46:V2:36:ILE:HD13	1.85	0.58
63:e1:38:PRO:HD2	63:e1:55:MET:HE3	1.85	0.58
1:22:154:G:N2	18:G2:60:GLY:O	2.33	0.58
1:22:1492:U:OP1	36:Q2:69:ARG:NH2	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:51:819:G:H2'	2:51:820:A:C8	2.38	0.58
2:51:2270:A:O2'	7:B1:228:CYS:O	2.17	0.58
6:A2:8:LEU:HD11	46:V2:39:VAL:HG21	1.85	0.58
23:J1:136:ARG:NH2	23:J1:161:GLU:OE2	2.35	0.58
46:V2:42:VAL:HG23	46:V2:43:THR:HG23	1.85	0.58
1:22:983:G:OP2	30:N2:64:ARG:NH2	2.36	0.58
2:51:310:G:OP2	2:51:310:G:N2	2.30	0.58
2:51:1044:G:O2'	2:51:1045:G:O4'	2.17	0.58
2:51:1403:C:H42	2:51:1407:A:H61	1.50	0.58
5:A1:27:ALA:O	5:A1:128:ARG:NH1	2.36	0.58
12:D2:137:VAL:HG22	12:D2:151:LYS:HG3	1.85	0.58
47:W1:23:ARG:NH2	47:W1:25:ASP:OD2	2.36	0.58
33:P1:89:GLU:O	33:P1:93:HIS:ND1	2.36	0.58
40:S2:35:GLY:O	40:S2:97:GLN:NE2	2.36	0.58
56:a2:23:CYS:SG	56:a2:24:THR:N	2.76	0.58
77:r1:27:SER:OG	77:r1:29:GLU:OE1	2.21	0.58
1:22:904:U:N3	14:E2:111:VAL:O	2.35	0.58
2:51:227:G:OP2	51:Y1:1:MET:N	2.34	0.58
2:51:467:G:H1	2:51:588:C:H5	1.49	0.58
2:51:1951:A:O2'	66:g1:66:ARG:NH2	2.37	0.58
3:71:6:C:H4'	11:D1:52:ILE:HD13	1.85	0.58
19:H1:23:ARG:HE	19:H1:39:ASN:HA	1.69	0.58
2:51:2858:C:H2'	2:51:2859:A:C8	2.38	0.58
1:22:4:C:H4'	10:C2:193:ALA:HB2	1.85	0.58
16:F2:40:ALA:HB3	16:F2:67:PRO:HA	1.86	0.58
2:51:636:C:H2'	2:51:637:A:H8	1.69	0.58
2:51:3069:G:OP2	2:51:3069:G:N2	2.32	0.58
2:51:4264:G:N2	2:51:4264:G:OP2	2.33	0.58
1:22:643:G:O6	1:22:687:A:N6	2.37	0.58
2:51:697:A:O2'	2:51:698:C:OP2	2.21	0.58
9:C1:286:ILE:N	35:Q1:124:ASP:OD2	2.37	0.58
11:D1:225:ARG:HA	11:D1:228:LYS:HG2	1.85	0.58
1:22:169:A:OP2	18:G2:137:ARG:NH2	2.37	0.58
2:51:961:C:H5'	9:C1:118:ASN:HD21	1.68	0.58
2:51:3743:G:N7	73:m1:125:LYS:NZ	2.49	0.58
5:A1:117:GLU:HG2	5:A1:124:GLY:H	1.69	0.58
7:B1:168:MET:HA	7:B1:171:LEU:HD12	1.85	0.58
10:C2:50:THR:HG23	10:C2:53:GLY:H	1.68	0.58
12:D2:32:ASP:OD1	12:D2:57:ASN:ND2	2.36	0.58
33:P1:36:ILE:HD11	33:P1:91:LEU:HD13	1.85	0.58
1:22:979:G:N2	1:22:979:G:OP2	2.35	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:22:1033:U:O2'	2:51:2971:A:N6	2.28	0.57
2:51:1734:G:O6	9:C1:188:ARG:NH1	2.36	0.57
2:51:3612:U:O2'	75:o1:28:LYS:O	2.22	0.57
67:g2:40:ILE:HB	67:g2:59:LEU:HB2	1.85	0.57
1:22:114:G:OP1	27:L2:70:ARG:NH2	2.36	0.57
1:22:933:A:O2'	1:22:935:G:OP2	2.21	0.57
1:22:1382:U:O4	25:K2:8:ARG:NH1	2.36	0.57
2:51:917:C:OP1	31:O1:95:LYS:NZ	2.34	0.57
5:A1:129:ALA:HB3	5:A1:132:ASN:HD22	1.67	0.57
29:N1:63:ARG:NH1	29:N1:131:GLU:OE2	2.36	0.57
77:r1:52:ILE:HD13	77:r1:115:VAL:HG23	1.85	0.57
77:r1:70:GLY:HA3	77:r1:77:SER:HA	1.85	0.57
2:51:888:C:O2'	2:51:890:G:N7	2.35	0.57
19:H1:94:SER:HB2	19:H1:142:ASP:HB3	1.86	0.57
1:22:1320:A:N6	1:22:1730:G:O2'	2.37	0.57
2:51:230:G:H5''	51:Y1:11:ARG:HD2	1.86	0.57
6:A2:26:GLY:O	6:A2:150:THR:OG1	2.22	0.57
15:F1:125:LYS:HB2	41:T1:133:ALA:HB3	1.86	0.57
52:Y2:41:ARG:NH2	52:Y2:52:PRO:O	2.37	0.57
1:22:1228:U:O4	50:X2:2:GLY:N	2.38	0.57
2:51:108:A:N1	2:51:335:U:O2'	2.36	0.57
2:51:1122:A:H61	2:51:1249:G:H22	1.52	0.57
2:51:2244:G:O2'	2:51:3914:G:OP1	2.21	0.57
2:51:3140:G:HO2'	2:51:3141:G:H8	1.52	0.57
2:51:3964:G:N2	2:51:3964:G:OP1	2.38	0.57
30:N2:119:GLU:O	30:N2:123:HIS:ND1	2.37	0.57
61:d1:88:ARG:HD3	61:d1:100:LEU:HD13	1.85	0.57
1:22:114:G:N7	27:L2:70:ARG:NH1	2.53	0.57
2:51:109:G:OP2	26:L1:74:ARG:NH1	2.38	0.57
36:Q2:15:ARG:HG2	36:Q2:20:THR:HG22	1.86	0.57
42:T2:61:THR:HG23	42:T2:76:MET:HE2	1.86	0.57
1:22:628:G:OP1	24:J2:162:ARG:NH1	2.37	0.57
1:22:1734:G:H4'	44:U2:62:ARG:HH22	1.68	0.57
1:22:1188:C:O2'	8:B2:148:ASN:ND2	2.38	0.57
2:51:750:G:H3'	2:51:751:C:H3'	1.86	0.57
14:E2:56:LEU:HG	52:Y2:58:PHE:HZ	1.70	0.57
21:I1:14:ASN:O	21:I1:128:ARG:NH2	2.37	0.57
24:J2:93:LYS:HE3	24:J2:96:TYR:HE2	1.69	0.57
1:22:379:G:O6	18:G2:186:GLN:NE2	2.38	0.57
2:51:198:A:N3	2:51:223:C:O2'	2.38	0.57
4:81:95:G:OP2	70:j1:72:ARG:NH2	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:B1:85:ILE:HD11	7:B1:167:GLN:HE21	1.69	0.57
11:D1:223:PHE:HB3	11:D1:226:PHE:HB2	1.86	0.57
14:E2:233:LYS:HD2	14:E2:234:PRO:HD2	1.87	0.57
22:I2:5:ARG:NH1	22:I2:29:LEU:O	2.38	0.57
40:S2:132:ARG:HB2	40:S2:134:GLN:HE22	1.69	0.57
67:g2:207:CYS:SG	67:g2:208:ALA:N	2.78	0.57
1:22:1542:C:H2'	1:22:1543:U:H5''	1.86	0.57
2:51:1841:G:OP2	2:51:1841:G:N2	2.34	0.57
1:22:1056:A:N7	56:a2:15:ARG:NH2	2.53	0.56
2:51:1274:C:H41	2:51:3646:A:H5''	1.70	0.56
26:L1:7:GLY:O	55:a1:49:HIS:NE2	2.33	0.56
2:51:1315:G:N2	2:51:1316:U:O4	2.35	0.56
2:51:3046:U:OP1	2:51:3818:G:O2'	2.23	0.56
2:51:3683:A:O2'	21:I1:74:LYS:NZ	2.34	0.56
4:81:11:G:OP1	33:P1:3:ARG:NH2	2.38	0.56
11:D1:51:MET:HE1	11:D1:163:LEU:HA	1.86	0.56
26:L1:77:THR:HB	26:L1:80:GLU:HG3	1.86	0.56
1:22:1681:U:OP2	34:P2:43:ARG:NH2	2.37	0.56
2:51:269:G:OP1	68:h1:114:TYR:OH	2.23	0.56
2:51:282:G:H5''	29:N1:14:LYS:HE2	1.87	0.56
2:51:689:C:OP1	2:51:691:G:O2'	2.20	0.56
2:51:1114:G:O2'	26:L1:18:TRP:NE1	2.34	0.56
2:51:2074:U:H1'	66:g1:26:PRO:HA	1.87	0.56
2:51:2193:A:O2'	2:51:2199:A:N3	2.32	0.56
2:51:3008:A:H5''	5:A1:243:THR:HB	1.87	0.56
2:51:3113:U:O2'	2:51:4181:A:N3	2.38	0.56
2:51:3590:G:N2	2:51:3593:A:OP2	2.35	0.56
2:51:3891:C:OP1	45:V1:48:ARG:NE	2.33	0.56
4:81:70:A:N1	4:81:81:A:O2'	2.33	0.56
6:A2:89:LYS:NZ	38:R2:83:ASN:OD1	2.35	0.56
7:B1:222:VAL:O	7:B1:343:ARG:NH1	2.39	0.56
22:I2:119:LEU:HD12	22:I2:120:PRO:HD2	1.86	0.56
29:N1:75:VAL:HG11	29:N1:80:THR:HG22	1.88	0.56
52:Y2:117:VAL:HG21	52:Y2:125:VAL:HG21	1.87	0.56
58:b2:34:ASP:O	58:b2:78:SER:OG	2.21	0.56
1:22:499:C:O2'	18:G2:92:ARG:O	2.22	0.56
2:51:2130:A:OP1	71:k1:35:LYS:NZ	2.30	0.56
2:51:3786:A:OP1	2:51:3788:G:O2'	2.22	0.56
14:E2:188:ASN:HD22	14:E2:191:ARG:HD3	1.69	0.56
14:E2:206:ASP:O	14:E2:222:LEU:N	2.38	0.56
20:H2:117:PRO:HG2	20:H2:120:ARG:HD3	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:S1:83:ARG:NH1	39:S1:125:GLN:OE1	2.38	0.56
1:22:493:A:OP1	22:I2:49:ARG:NH1	2.38	0.56
1:22:899:C:O2'	52:Y2:12:PHE:O	2.20	0.56
1:22:1493:C:H4'	42:T2:8:LYS:HD2	1.88	0.56
2:51:1804:A:HO2'	2:51:2260:G:H21	1.49	0.56
2:51:2189:G:O2'	53:Z1:51:ARG:NH1	2.39	0.56
8:B2:90:ASP:OD2	8:B2:92:GLN:NE2	2.38	0.56
18:G2:190:ARG:HH22	18:G2:194:LEU:HD21	1.70	0.56
27:L2:114:LEU:HD12	27:L2:143:VAL:HG11	1.88	0.56
39:S1:115:ALA:O	39:S1:118:ARG:NH1	2.38	0.56
65:f1:40:ASP:O	65:f1:109:ARG:NH1	2.38	0.56
1:22:982:C:N4	1:22:1085:U:OP2	2.34	0.56
2:51:2160:A:N6	37:R1:88:ARG:O	2.39	0.56
2:51:3153:C:O2'	2:51:4181:A:N1	2.37	0.56
12:D2:135:GLU:HB2	12:D2:187:LYS:HB2	1.87	0.56
14:E2:45:ILE:HA	14:E2:61:VAL:HG21	1.88	0.56
1:22:1320:A:HO2'	1:22:1731:C:HO2'	1.52	0.56
2:51:3905:G:N2	2:51:3933:G:H21	2.02	0.56
9:C1:71:ARG:HB2	9:C1:73:VAL:HG22	1.87	0.56
11:D1:261:VAL:HG23	11:D1:263:LYS:H	1.70	0.56
19:H1:173:ARG:NH1	73:m1:125:LYS:O	2.36	0.56
35:Q1:155:ALA:O	35:Q1:161:SER:OG	2.22	0.56
36:Q2:139:ALA:O	36:Q2:140:ARG:NH2	2.37	0.56
2:51:46:U:OP1	26:L1:16:LYS:NZ	2.33	0.56
2:51:3753:C:O2'	73:m1:114:LYS:NZ	2.37	0.56
2:51:1232:A:H62	5:A1:3:ARG:HH12	1.54	0.56
2:51:3297:C:OP1	29:N1:32:GLN:NE2	2.39	0.56
1:22:392:C:O3'	14:E2:30:ARG:NH2	2.39	0.56
1:22:876:U:H3	1:22:880:A:H62	1.53	0.56
1:22:1468:A:H4'	44:U2:52:GLY:HA3	1.87	0.56
2:51:719:G:H5''	65:f1:73:LYS:HE2	1.87	0.56
2:51:1076:C:H42	2:51:1085:G:H1	1.54	0.56
27:L2:62:PRO:HG3	27:L2:142:ASN:HB3	1.88	0.56
54:Z2:58:LEU:HA	54:Z2:62:VAL:HG13	1.88	0.56
1:22:1156:G:OP1	30:N2:2:GLY:N	2.38	0.55
2:51:1253:C:OP1	2:51:1277:A:O2'	2.21	0.55
2:51:1752:G:N2	2:51:1755:G:OP2	2.34	0.55
2:51:3549:A:H2'	2:51:3550:A:H8	1.70	0.55
27:L2:39:ARG:HH21	27:L2:52:ILE:HG12	1.72	0.55
33:P1:6:LEU:HD12	33:P1:116:HIS:CD2	2.41	0.55
41:T1:45:THR:HG22	41:T1:47:THR:H	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:V2:78:ILE:HG22	46:V2:79:VAL:HG13	1.87	0.55
49:X1:73:TYR:OH	68:h1:22:ASP:OD1	2.23	0.55
2:51:1139:C:H5''	5:A1:21:LYS:HG2	1.88	0.55
2:51:2087:G:N2	76:p1:59:SER:O	2.40	0.55
18:G2:52:ILE:HD13	18:G2:102:VAL:HG21	1.87	0.55
66:g1:56:ILE:HD11	66:g1:80:GLY:HA2	1.88	0.55
67:g2:70:VAL:HG11	67:g2:112:ALA:HA	1.88	0.55
67:g2:218:LEU:HB2	67:g2:228:TYR:HB2	1.87	0.55
1:22:465:G:N2	1:22:707:U:O2	2.40	0.55
1:22:1297:C:OP1	40:S2:130:ARG:NH2	2.31	0.55
1:22:1933:A:OP2	56:a2:4:LYS:NZ	2.38	0.55
2:51:86:U:O2'	55:a1:65:ARG:NH1	2.39	0.55
2:51:1092:U:H2'	2:51:1093:G:H8	1.72	0.55
2:51:3887:G:OP1	7:B1:62:ARG:NH1	2.39	0.55
5:A1:173:GLY:O	76:p1:69:TRP:NE1	2.39	0.55
67:g2:298:LEU:HB2	67:g2:310:TRP:HB2	1.88	0.55
2:51:90:G:OP2	2:51:92:C:N4	2.37	0.55
2:51:1030:G:N1	2:51:1055:C:OP2	2.30	0.55
6:A2:206:ASP:OD1	6:A2:206:ASP:N	2.28	0.55
29:N1:169:LYS:HG2	29:N1:174:LEU:HD11	1.87	0.55
34:P2:85:ILE:HG22	34:P2:112:ILE:HD13	1.88	0.55
1:22:1311:U:H3	1:22:1322:G:H1	1.53	0.55
1:22:1682:G:O6	34:P2:43:ARG:NH1	2.39	0.55
2:51:501:G:H4'	2:51:502:U:H5'	1.88	0.55
2:51:4124:C:H4'	2:51:4125:U:O5'	2.05	0.55
27:L2:112:VAL:HG11	27:L2:129:VAL:HG11	1.88	0.55
34:P2:43:ARG:HH12	34:P2:47:ARG:HH11	1.54	0.55
75:o1:11:TYR:O	75:o1:81:ARG:NH1	2.39	0.55
1:22:1310:U:H1'	1:22:1332:A:H61	1.71	0.55
2:51:3188:A:OP1	29:N1:90:ASN:ND2	2.39	0.55
2:51:3888:G:H5''	45:V1:15:ARG:HB2	1.87	0.55
2:51:3969:U:H1'	2:51:3970:A:H5''	1.88	0.55
16:F2:157:GLY:HA2	16:F2:188:TYR:HB3	1.89	0.55
23:J1:22:LEU:HD13	23:J1:40:LEU:HD22	1.89	0.55
56:a2:13:LYS:H	56:a2:15:ARG:NH1	2.05	0.55
1:22:878:C:H1'	24:J2:144:ILE:HD11	1.88	0.55
2:51:40:G:N2	2:51:3648:A:N7	2.54	0.55
2:51:935:A:OP2	2:51:3713:U:O2'	2.20	0.55
2:51:1796:U:OP2	2:51:3119:G:N1	2.39	0.55
2:51:2054:A:H5''	43:U1:93:SER:HB2	1.88	0.55
12:D2:137:VAL:HB	12:D2:185:LYS:HB2	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:D2:141:LYS:HD2	12:D2:180:GLY:HA3	1.88	0.55
23:J1:46:GLN:NE2	23:J1:73:THR:O	2.39	0.55
38:R2:10:LYS:HB3	38:R2:14:ARG:HH12	1.72	0.55
54:Z2:69:THR:HG22	54:Z2:71:ALA:H	1.71	0.55
1:22:1463:A:O2'	1:22:1465:G:N7	2.32	0.55
2:51:1244:A:O2'	70:j1:49:TRP:O	2.23	0.55
9:C1:159:GLU:HA	9:C1:217:VAL:HB	1.89	0.55
18:G2:160:ARG:HD2	18:G2:161:PRO:HD2	1.88	0.55
65:f1:39:VAL:HG21	65:f1:77:ALA:HB2	1.89	0.55
70:j1:73:ARG:NH2	70:j1:80:GLU:OE2	2.40	0.55
73:m1:94:MET:HG2	73:m1:105:PRO:HA	1.88	0.55
1:22:1517:A:H5''	38:R2:48:ASN:HD22	1.72	0.55
2:51:1383:A:H5'	2:51:1384:G:H5'	1.89	0.55
4:81:103:G:OP2	4:81:105:A:O2'	2.25	0.55
67:g2:220:ASP:HB2	67:g2:227:LEU:HD11	1.89	0.55
1:22:1071:C:O2'	30:N2:104:ARG:NH1	2.40	0.55
1:22:1124:A:O2'	1:22:1126:A:N7	2.31	0.55
1:22:1594:C:N3	1:22:1595:C:N4	2.54	0.55
2:51:3905:G:H21	2:51:3933:G:H21	1.55	0.55
30:N2:40:LEU:HB3	30:N2:45:LEU:HD12	1.89	0.55
1:22:1744:A:OP1	60:c2:20:ARG:NH2	2.40	0.54
2:51:747:U:OP1	13:E1:17:ASN:ND2	2.40	0.54
2:51:4033:G:OP2	31:O1:14:ARG:NH1	2.37	0.54
4:81:64:A:O2'	68:h1:10:ARG:NH2	2.40	0.54
14:E2:23:LEU:HD11	24:J2:6:THR:HG22	1.88	0.54
61:d1:24:THR:OG1	61:d1:83:ARG:NH1	2.39	0.54
1:22:923:A:H4'	48:W2:36:ARG:HH12	1.71	0.54
2:51:358:G:O2'	4:81:24:G:N3	2.41	0.54
6:A2:77:ILE:HG12	6:A2:99:PHE:HB2	1.88	0.54
11:D1:43:LYS:HB3	11:D1:46:THR:HB	1.89	0.54
13:E1:113:HIS:HB2	13:E1:115:ARG:HH12	1.72	0.54
26:L1:116:ARG:NH2	26:L1:155:MET:O	2.39	0.54
40:S2:110:ASP:HB2	40:S2:113:ARG:HH21	1.73	0.54
1:22:566:A:H5''	24:J2:12:THR:HG23	1.89	0.54
1:22:907:A:HO2'	1:22:908:A:P	2.28	0.54
1:22:1630:C:HO2'	1:22:1631:G:H21	1.54	0.54
2:51:71:C:O3'	26:L1:67:HIS:NE2	2.34	0.54
2:51:196:C:H2'	2:51:197:A:H8	1.73	0.54
2:51:1188:C:H4'	2:51:2293:A:H5'	1.88	0.54
13:E1:155:PRO:HG3	13:E1:234:LEU:HD23	1.89	0.54
70:j1:2:THR:O	70:j1:7:SER:OG	2.17	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:51:1324:A:O2'	11:D1:15:ARG:NH1	2.41	0.54
2:51:3059:A:N3	2:51:3774:C:O2'	2.36	0.54
2:51:3498:C:O2'	2:51:3502:A:N1	2.31	0.54
2:51:3620:U:OP1	26:L1:190:ARG:NH1	2.39	0.54
2:51:3859:A:N1	2:51:3891:C:O2'	2.40	0.54
6:A2:123:ILE:HG13	6:A2:145:ILE:HB	1.90	0.54
11:D1:62:CYS:HB3	11:D1:105:LEU:HD22	1.89	0.54
16:F2:187:SER:HB3	16:F2:190:ILE:HG12	1.89	0.54
52:Y2:55:VAL:HG12	52:Y2:75:ILE:HG12	1.88	0.54
53:Z1:22:LYS:NZ	53:Z1:132:GLN:O	2.41	0.54
2:51:2913:A:N6	2:51:2951:G:O2'	2.39	0.54
10:C2:116:ILE:HD11	10:C2:141:ILE:HG23	1.90	0.54
1:22:552:A:OP1	52:Y2:108:LYS:NZ	2.35	0.54
1:22:1599:A:OP1	16:F2:81:ARG:NH1	2.39	0.54
2:51:1970:A:O2'	2:51:2076:A:N1	2.39	0.54
6:A2:76:VAL:HG12	6:A2:123:ILE:HB	1.90	0.54
20:H2:53:VAL:HG21	20:H2:172:THR:HG22	1.88	0.54
32:O2:100:THR:HG21	32:O2:104:ARG:HD2	1.90	0.54
43:U1:37:LEU:HD11	43:U1:97:LEU:HD13	1.90	0.54
67:g2:197:THR:OG1	67:g2:237:ASN:O	2.25	0.54
2:51:35:U:O2'	2:51:1123:A:N1	2.32	0.54
2:51:4032:G:OP2	31:O1:39:ARG:NH1	2.41	0.54
30:N2:87:ASP:OD1	30:N2:129:TYR:OH	2.24	0.54
40:S2:60:THR:OG1	40:S2:63:GLU:OE1	2.25	0.54
1:22:1147:A:N7	1:22:1911:C:O2'	2.40	0.54
1:22:1630:C:N4	1:22:1636:G:O6	2.40	0.54
2:51:3780:C:N4	45:V1:46:LYS:O	2.39	0.54
7:B1:74:GLU:OE1	7:B1:285:TYR:OH	2.25	0.54
75:o1:3:ASN:HB3	75:o1:92:GLU:HG3	1.90	0.54
1:22:1320:A:O2'	1:22:1731:C:O2'	2.26	0.54
2:51:623:G:H2'	2:51:624:G:C8	2.43	0.54
2:51:983:G:N2	9:C1:234:ARG:HH21	2.06	0.54
13:E1:237:LEU:HD23	13:E1:240:LYS:HZ1	1.73	0.54
14:E2:35:PRO:HG2	14:E2:36:HIS:CD2	2.43	0.54
22:I2:82:VAL:HB	22:I2:103:LEU:HD23	1.89	0.54
1:22:695:U:H2'	1:22:696:G:H8	1.73	0.54
1:22:935:G:H2'	1:22:936:A:C8	2.43	0.54
2:51:1503:C:H3'	2:51:1504:C:H5''	1.89	0.54
2:51:3814:A:N7	5:A1:215:ASN:ND2	2.55	0.54
7:B1:57:VAL:HG22	7:B1:73:VAL:HG22	1.89	0.54
9:C1:5:ARG:NE	9:C1:24:MET:O	2.34	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:Q2:34:VAL:HG12	36:Q2:35:ASN:HD22	1.73	0.54
1:22:989:G:H1	1:22:1081:U:H3	1.55	0.53
1:22:1682:G:O2'	62:d2:14:TYR:OH	2.26	0.53
2:51:384:G:N1	2:51:387:A:OP2	2.38	0.53
2:51:636:C:H2'	2:51:637:A:C8	2.42	0.53
2:51:1101:A:H4'	2:51:1102:G:H5'	1.89	0.53
2:51:2985:G:N2	2:51:2988:A:OP2	2.34	0.53
7:B1:37:PRO:HA	7:B1:188:GLY:HA2	1.90	0.53
10:C2:52:LEU:HD11	10:C2:67:ILE:HD12	1.89	0.53
18:G2:35:GLU:HA	18:G2:51:ARG:HA	1.91	0.53
22:I2:141:ARG:HB2	22:I2:146:GLN:HG2	1.90	0.53
29:N1:116:LEU:HD22	29:N1:135:ILE:HD11	1.90	0.53
53:Z1:36:ARG:NH1	53:Z1:38:TYR:OH	2.40	0.53
54:Z2:68:ILE:HB	54:Z2:109:TYR:HB2	1.89	0.53
69:i1:9:VAL:HA	69:i1:13:LYS:HE2	1.89	0.53
1:22:651:A:O2'	1:22:684:C:O2'	2.26	0.53
2:51:458:C:H2'	2:51:459:G:C8	2.43	0.53
2:51:603:G:H1	2:51:900:G:H1	1.57	0.53
2:51:4009:C:H2'	2:51:4010:G:H4'	1.90	0.53
2:51:4082:C:H5	13:E1:249:ARG:HG2	1.73	0.53
12:D2:106:ARG:NH1	12:D2:174:HIS:O	2.38	0.53
15:F1:93:ILE:O	15:F1:221:LYS:HD2	2.08	0.53
15:F1:124:ASN:HB2	41:T1:132:PRO:HB2	1.90	0.53
21:I1:38:ARG:NH1	21:I1:45:GLU:OE1	2.38	0.53
32:O2:39:ASP:OD1	32:O2:40:THR:N	2.42	0.53
36:Q2:34:VAL:HG13	36:Q2:70:VAL:HB	1.89	0.53
1:22:988:G:H21	30:N2:87:ASP:HB3	1.72	0.53
2:51:364:A:N6	72:l1:37:TYR:O	2.36	0.53
2:51:645:A:O2'	28:M1:66:HIS:NE2	2.39	0.53
21:I1:87:ILE:HG12	21:I1:138:VAL:HG22	1.90	0.53
60:c2:40:ARG:NH1	60:c2:61:SER:O	2.42	0.53
72:l1:25:GLN:HA	72:l1:28:ARG:HH11	1.73	0.53
1:22:1404:C:H2'	1:22:1405:G:C8	2.43	0.53
2:51:224:G:O2'	2:51:226:G:OP2	2.26	0.53
2:51:4085:G:H22	2:51:4134:G:H1	1.55	0.53
9:C1:65:GLU:OE1	9:C1:80:ARG:NH2	2.41	0.53
16:F2:111:ILE:HD11	16:F2:178:ILE:HA	1.90	0.53
21:I1:91:LEU:HD12	21:I1:135:ILE:HG23	1.89	0.53
30:N2:69:ASN:HA	30:N2:73:ARG:HH21	1.73	0.53
68:h1:88:THR:HG22	68:h1:90:ALA:H	1.73	0.53
2:51:459:G:H22	2:51:597:U:H3	1.56	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:51:1635:G:H5'	31:O1:85:THR:HG23	1.90	0.53
2:51:2214:C:O2'	4:81:114:G:OP1	2.26	0.53
6:A2:10:MET:HE2	6:A2:15:VAL:HG22	1.90	0.53
9:C1:134:PRO:HG3	9:C1:150:VAL:HG21	1.90	0.53
17:G1:138:ALA:HB2	17:G1:194:VAL:HG11	1.91	0.53
20:H2:154:ILE:HB	20:H2:185:VAL:HG22	1.89	0.53
25:K2:26:ASP:O	25:K2:42:ASN:ND2	2.37	0.53
2:51:3634:G:OP1	35:Q1:181:ARG:NH1	2.41	0.53
3:71:27:G:O6	11:D1:58:ARG:NH2	2.38	0.53
10:C2:182:ILE:HB	10:C2:209:TYR:HB2	1.91	0.53
14:E2:115:THR:O	14:E2:119:ALA:N	2.36	0.53
23:J1:95:ARG:NH2	23:J1:176:PRO:O	2.41	0.53
30:N2:5:HIS:HB3	30:N2:117:LEU:HD22	1.91	0.53
38:R2:41:ILE:HG22	38:R2:43:SER:H	1.74	0.53
40:S2:89:ASP:OD1	40:S2:89:ASP:N	2.38	0.53
1:22:924:U:O2'	48:W2:78:ARG:NH1	2.40	0.53
1:22:940:C:N3	1:22:971:G:N1	2.57	0.53
2:51:100:G:OP2	2:51:100:G:N2	2.34	0.53
2:51:1670:C:OP2	35:Q1:37:ARG:NH1	2.41	0.53
2:51:3353:G:N2	17:G1:43:GLN:O	2.41	0.53
14:E2:32:SER:N	14:E2:81:THR:O	2.38	0.53
67:g2:129:ILE:HD11	67:g2:151:VAL:HG11	1.90	0.53
2:51:743:C:O2'	9:C1:327:LYS:NZ	2.42	0.53
2:51:2074:U:H2'	2:51:2129:G:H1	1.74	0.53
2:51:3533:U:N3	11:D1:17:GLN:O	2.39	0.53
11:D1:64:ILE:HG13	11:D1:105:LEU:HD21	1.90	0.53
19:H1:41:ILE:HD13	19:H1:43:LEU:HD12	1.91	0.53
25:K2:29:LEU:HB3	25:K2:42:ASN:HB2	1.91	0.53
67:g2:37:ASP:OD1	67:g2:39:THR:OG1	2.25	0.53
68:h1:87:LYS:NZ	70:j1:78:PHE:O	2.33	0.53
1:22:888:C:N4	52:Y2:10:ARG:O	2.42	0.53
2:51:500:G:N2	2:51:555:C:O2	2.33	0.53
2:51:708:U:OP1	15:F1:144:ASN:ND2	2.42	0.53
2:51:1079:U:OP2	2:51:1084:G:N1	2.42	0.53
2:51:1087:G:H3'	2:51:1088:C:H4'	1.91	0.53
2:51:1111:A:H4'	26:L1:4:SER:HB2	1.89	0.53
2:51:1150:G:H2'	2:51:1172:G:N2	2.23	0.53
2:51:3646:A:O2'	2:51:3647:A:H2'	2.09	0.53
16:F2:176:GLU:OE1	16:F2:187:SER:OG	2.25	0.53
31:O1:58:ALA:O	31:O1:62:LYS:NZ	2.42	0.53
69:i1:70:LEU:HD13	69:i1:87:ARG:HE	1.74	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:22:538:C:N4	1:22:553:G:OP2	2.33	0.53
2:51:1834:G:H21	66:g1:6:THR:HG22	1.74	0.53
9:C1:321:ASN:HB3	9:C1:324:VAL:HG22	1.91	0.53
1:22:1023:G:OP1	32:O2:104:ARG:NH1	2.36	0.52
1:22:1208:G:N2	1:22:1211:A:OP2	2.39	0.52
1:22:1458:C:O2'	44:U2:83:ARG:NH2	2.42	0.52
1:22:1739:G:N7	36:Q2:17:LYS:NZ	2.58	0.52
2:51:299:U:O2'	29:N1:179:LYS:O	2.23	0.52
2:51:500:G:OP2	2:51:501:G:N2	2.41	0.52
2:51:877:C:H5	13:E1:30:SER:HB2	1.73	0.52
2:51:978:C:O2'	2:51:979:G:O5'	2.28	0.52
2:51:3520:C:H42	23:J1:25:CYS:HB3	1.74	0.52
9:C1:159:GLU:HG3	9:C1:253:THR:HG21	1.90	0.52
15:F1:113:ARG:NH1	35:Q1:4:ASP:O	2.37	0.52
27:L2:70:ARG:H	27:L2:70:ARG:HD3	1.74	0.52
1:22:1322:G:OP1	1:22:1323:G:O2'	2.23	0.52
2:51:3611:U:O2'	75:o1:31:ASP:OD2	2.26	0.52
29:N1:178:HIS:HA	29:N1:181:HIS:CE1	2.45	0.52
1:22:935:G:H2'	1:22:936:A:H8	1.74	0.52
1:22:1085:U:OP1	30:N2:128:TYR:OH	2.27	0.52
2:51:88:G:OP2	35:Q1:173:LYS:NZ	2.42	0.52
2:51:1824:G:H22	2:51:2260:G:N2	2.07	0.52
2:51:3864:C:H2'	2:51:3865:G:H8	1.74	0.52
4:81:81:A:H4'	4:81:88:G:H4'	1.90	0.52
32:O2:101:GLY:HA3	32:O2:134:PRO:HD2	1.92	0.52
51:Y1:22:PRO:HD2	51:Y1:25:ILE:HD12	1.91	0.52
54:Z2:57:LYS:HZ2	54:Z2:77:LEU:HD21	1.73	0.52
1:22:5:U:H2'	1:22:6:G:H8	1.74	0.52
1:22:28:U:H2'	1:22:29:G:H8	1.74	0.52
1:22:1928:G:OP1	56:a2:17:HIS:NE2	2.27	0.52
21:I1:61:SER:HA	21:I1:126:VAL:HG12	1.91	0.52
67:g2:214:GLY:HA2	67:g2:236:ILE:HG12	1.92	0.52
68:h1:27:GLU:OE2	68:h1:46:LYS:NZ	2.41	0.52
1:22:1210:A:H2'	1:22:1211:A:C8	2.45	0.52
2:51:941:C:H2'	2:51:942:A:C8	2.44	0.52
2:51:1957:G:OP1	37:R1:16:ARG:NH2	2.31	0.52
52:Y2:53:ASP:HB3	52:Y2:79:LEU:HD13	1.89	0.52
2:51:1956:G:OP1	66:g1:29:ARG:NH2	2.42	0.52
8:B2:189:ILE:HG13	8:B2:190:PRO:HD3	1.90	0.52
17:G1:73:ARG:NE	17:G1:241:VAL:O	2.38	0.52
31:O1:17:LEU:HB2	31:O1:20:ARG:HB2	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:Q1:122:THR:OG1	35:Q1:124:ASP:OD1	2.17	0.52
38:R2:37:GLU:OE1	67:g2:150:TRP:NE1	2.43	0.52
59:c1:20:LEU:HB3	59:c1:102:SER:HB2	1.90	0.52
1:22:423:G:H2'	1:22:424:G:H8	1.74	0.52
1:22:426:C:H5''	22:I2:31:ARG:HH11	1.75	0.52
2:51:1235:A:OP1	2:51:1238:C:N4	2.35	0.52
2:51:2246:G:N1	2:51:2249:C:OP2	2.40	0.52
2:51:3005:U:O2'	5:A1:243:THR:N	2.34	0.52
2:51:3431:C:H1'	17:G1:69:ILE:HD13	1.92	0.52
2:51:3505:C:OP1	2:51:3595:C:O2'	2.23	0.52
2:51:3542:A:H2'	2:51:3543:G:C8	2.45	0.52
2:51:3561:U:O2'	75:o1:81:ARG:NH2	2.43	0.52
2:51:3790:G:O2'	2:51:3793:C:OP2	2.21	0.52
4:81:143:C:H5''	29:N1:60:VAL:HG11	1.91	0.52
12:D2:169:ASP:OD1	12:D2:169:ASP:N	2.43	0.52
22:I2:106:SER:HB2	22:I2:171:LEU:HG	1.92	0.52
34:P2:92:SER:HB3	34:P2:107:ILE:HD12	1.91	0.52
77:r1:29:GLU:HG2	77:r1:32:ASN:HB2	1.91	0.52
2:51:514:U:O2	2:51:546:G:N2	2.43	0.52
2:51:1637:U:H4'	2:51:1639:G:C4	2.45	0.52
2:51:1854:A:OP2	33:P1:127:ARG:NH1	2.40	0.52
2:51:2971:A:H4'	2:51:2972:A:O5'	2.09	0.52
8:B2:143:THR:HA	8:B2:207:LEU:HA	1.91	0.52
10:C2:117:GLY:HA3	10:C2:202:MET:HB3	1.90	0.52
2:51:459:G:H1	2:51:597:U:H3	1.58	0.52
2:51:1653:U:OP1	65:f1:22:ARG:NH2	2.43	0.52
2:51:1812:G:N2	2:51:1815:A:OP2	2.43	0.52
32:O2:28:PHE:HA	32:O2:92:ALA:HB3	1.92	0.52
1:22:1483:C:O2	1:22:1491:G:N2	2.39	0.52
2:51:689:C:O2'	2:51:692:C:OP1	2.25	0.52
2:51:1044:G:H5''	9:C1:300:LYS:HE3	1.92	0.52
7:B1:128:LYS:O	7:B1:131:THR:OG1	2.28	0.52
15:F1:86:LYS:HD2	15:F1:195:VAL:HG22	1.91	0.52
21:I1:188:LYS:NZ	21:I1:212:LEU:O	2.42	0.52
33:P1:10:ASN:OD1	33:P1:12:THR:OG1	2.23	0.52
53:Z1:11:VAL:HG21	53:Z1:80:LEU:HB3	1.92	0.52
1:22:613:G:H22	1:22:629:G:H1	1.58	0.51
1:22:1593:G:H21	1:22:1730:G:N2	2.08	0.51
2:51:3533:U:OP1	11:D1:12:TYR:OH	2.28	0.51
2:51:3548:A:OP2	11:D1:23:ARG:NE	2.29	0.51
2:51:3657:C:H2'	2:51:3658:A:C8	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:H2:10:LYS:HE2	20:H2:12:ASN:HD21	1.74	0.51
39:S1:112:ASP:OD1	39:S1:116:ARG:NH1	2.40	0.51
60:c2:31:ARG:HA	60:c2:43:ILE:HA	1.91	0.51
1:22:348:A:O2'	22:I2:73:THR:N	2.40	0.51
2:51:422:A:H61	4:81:14:G:H1'	1.74	0.51
2:51:1041:C:O2'	2:51:1044:G:O6	2.22	0.51
2:51:3616:G:H22	2:51:3632:G:H22	1.59	0.51
3:71:22:G:N1	3:71:53:A:O2'	2.42	0.51
4:81:59:G:O6	4:81:97:C:O2'	2.23	0.51
18:G2:48:TYR:OH	18:G2:119:LYS:O	2.26	0.51
50:X2:134:TYR:O	64:e2:90:ARG:NH2	2.36	0.51
58:b2:14:GLU:OE1	58:b2:17:ARG:NH2	2.44	0.51
67:g2:72:SER:OG	67:g2:74:ASP:OD1	2.26	0.51
75:o1:8:ARG:O	75:o1:21:HIS:N	2.41	0.51
1:22:1541:A:H4'	1:22:1542:C:H4'	1.91	0.51
1:22:1934:U:H5'	56:a2:79:ILE:HD11	1.93	0.51
2:51:62:A:OP1	29:N1:172:ARG:NH1	2.43	0.51
2:51:968:G:O2'	2:51:969:A:H8	1.93	0.51
4:81:91:C:HO2'	51:Y1:24:HIS:HD1	1.57	0.51
6:A2:183:LEU:HB3	6:A2:188:THR:HB	1.92	0.51
10:C2:89:LYS:HB2	10:C2:119:TYR:HE1	1.76	0.51
17:G1:75:LYS:HG2	17:G1:240:ASN:HB2	1.92	0.51
42:T2:28:LYS:HB2	42:T2:111:LEU:HD21	1.91	0.51
53:Z1:12:MET:HG3	53:Z1:81:MET:HB3	1.92	0.51
55:a1:125:LYS:HG2	55:a1:145:VAL:HB	1.91	0.51
67:g2:251:ALA:HB2	67:g2:289:LEU:HD22	1.93	0.51
1:22:1293:G:N1	1:22:1704:G:OP2	2.30	0.51
1:22:1627:C:H4'	42:T2:120:GLY:HA3	1.92	0.51
2:51:1703:A:OP2	77:r1:12:ARG:NE	2.43	0.51
2:51:3071:G:O2'	2:51:3074:U:OP2	2.28	0.51
2:51:3844:C:N4	2:51:4007:G:O2'	2.44	0.51
10:C2:70:TYR:HH	10:C2:248:THR:HG1	1.57	0.51
32:O2:45:THR:HG22	32:O2:52:THR:HA	1.92	0.51
34:P2:123:TYR:OH	40:S2:124:ARG:NH1	2.43	0.51
36:Q2:85:ARG:HE	36:Q2:119:LEU:HD13	1.76	0.51
58:b2:67:THR:OG1	58:b2:70:LYS:O	2.29	0.51
60:c2:12:ALA:HB2	60:c2:34:PHE:HD1	1.75	0.51
1:22:109:U:O2'	27:L2:72:ARG:NH2	2.44	0.51
1:22:365:G:N1	18:G2:186:GLN:OE1	2.37	0.51
1:22:1028:A:N3	1:22:1118:G:O2'	2.40	0.51
2:51:462:C:H2'	2:51:463:G:H8	1.74	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:71:95:C:OP1	39:S1:43:ARG:NH2	2.42	0.51
42:T2:63:ARG:HH12	42:T2:64:HIS:CE1	2.29	0.51
63:e1:114:ARG:NH1	63:e1:117:GLN:OE1	2.39	0.51
2:51:420:A:H62	4:81:15:G:H1'	1.76	0.51
2:51:2128:G:OP2	71:k1:33:LYS:NZ	2.41	0.51
2:51:3303:G:O6	5:A1:68:ARG:NH1	2.43	0.51
4:81:21:U:OP1	51:Y1:11:ARG:NH2	2.43	0.51
10:C2:228:ASP:OD2	10:C2:232:LYS:NZ	2.43	0.51
14:E2:43:PRO:HD2	14:E2:46:ILE:HD12	1.93	0.51
20:H2:51:ILE:HD11	20:H2:176:VAL:HG12	1.91	0.51
39:S1:13:VAL:HG22	39:S1:63:TYR:HB3	1.92	0.51
40:S2:24:ARG:HG3	40:S2:29:ALA:HB2	1.92	0.51
46:V2:55:ILE:HD11	46:V2:69:LEU:HD21	1.92	0.51
2:51:420:A:N6	4:81:15:G:H1'	2.26	0.51
2:51:1006:A:H5''	55:a1:114:LYS:HA	1.93	0.51
10:C2:169:LYS:NZ	48:W2:91:ASN:O	2.43	0.51
12:D2:96:LEU:HA	12:D2:188:ILE:HG21	1.92	0.51
29:N1:137:THR:HG22	29:N1:151:ILE:HG23	1.92	0.51
67:g2:33:SER:HB2	67:g2:43:TRP:HE1	1.75	0.51
2:51:2883:C:O2	37:R1:82:LYS:NZ	2.44	0.51
9:C1:207:PRO:HB3	9:C1:249:PHE:CD2	2.46	0.51
14:E2:199:GLU:N	14:E2:207:VAL:O	2.41	0.51
23:J1:38:LYS:HA	23:J1:41:GLU:HG2	1.93	0.51
32:O2:103:ASN:HD22	32:O2:142:ARG:HA	1.76	0.51
2:51:466:G:H1	2:51:589:C:H42	1.58	0.51
2:51:963:A:N1	2:51:994:G:O2'	2.42	0.51
2:51:2305:U:O2'	2:51:2317:A:N7	2.39	0.51
16:F2:179:ASN:HD22	16:F2:186:ASN:HB3	1.76	0.51
22:I2:3:ILE:O	22:I2:30:GLY:N	2.43	0.51
35:Q1:178:ARG:N	55:a1:51:GLY:HA2	2.25	0.51
1:22:4:C:O2'	24:J2:18:ARG:NH1	2.44	0.51
1:22:539:A:N1	1:22:556:G:O2'	2.41	0.51
2:51:625:C:H3'	15:F1:74:ARG:HH12	1.76	0.51
2:51:634:G:H2'	2:51:636:C:H4'	1.93	0.51
2:51:750:G:H1	2:51:882:G:H1	1.56	0.51
2:51:941:C:H5''	63:e1:29:VAL:HB	1.91	0.51
2:51:2310:U:O2'	2:51:2312:G:N7	2.42	0.51
2:51:3673:G:OP2	21:I1:7:ARG:NH2	2.41	0.51
4:81:95:G:H8	70:j1:82:THR:HG23	1.75	0.51
1:22:1048:C:N4	1:22:1049:G:O6	2.45	0.50
1:22:1121:C:N4	1:22:1124:A:OP2	2.43	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:22:1632:A:H5''	42:T2:99:ASN:HD22	1.76	0.50
2:51:3199:G:OP1	29:N1:20:ARG:NH2	2.44	0.50
14:E2:129:ILE:HG13	14:E2:156:VAL:HG12	1.93	0.50
21:I1:101:LYS:HE3	21:I1:121:LYS:HE2	1.92	0.50
24:J2:84:ILE:HA	24:J2:150:ARG:HA	1.93	0.50
30:N2:131:THR:O	30:N2:133:ARG:NH1	2.44	0.50
33:P1:124:LYS:NZ	33:P1:142:SER:OG	2.44	0.50
45:V1:13:LYS:NZ	45:V1:57:VAL:O	2.44	0.50
1:22:1303:G:N2	1:22:1587:A:H61	2.09	0.50
1:22:1810:A:N6	1:22:1859:G:O2'	2.44	0.50
2:51:516:G:H22	2:51:543:G:H22	1.59	0.50
2:51:1829:A:O2'	2:51:2242:A:OP2	2.29	0.50
2:51:3505:C:H2'	2:51:3506:G:C8	2.46	0.50
10:C2:155:TYR:OH	10:C2:161:GLY:O	2.29	0.50
18:G2:67:VAL:HG12	18:G2:69:THR:HG22	1.93	0.50
1:22:1596:A:OP1	1:22:1669:G:O2'	2.29	0.50
1:22:1627:C:H5'	42:T2:72:GLY:HA3	1.93	0.50
1:22:1657:C:O2'	36:Q2:43:GLU:O	2.30	0.50
1:22:1743:A:H2'	1:22:1744:A:H5''	1.92	0.50
14:E2:65:CYS:HB3	14:E2:78:THR:HA	1.93	0.50
16:F2:81:ARG:HG3	16:F2:82:ASN:HD22	1.76	0.50
20:H2:83:LEU:HD23	20:H2:92:VAL:HG11	1.93	0.50
31:O1:87:ARG:HG3	31:O1:101:LEU:HD11	1.92	0.50
39:S1:13:VAL:HG23	39:S1:62:VAL:HB	1.93	0.50
53:Z1:17:ARG:NH2	53:Z1:18:TYR:OH	2.33	0.50
67:g2:245:ARG:NE	67:g2:296:GLN:OE1	2.39	0.50
1:22:522:A:N3	1:22:534:U:O2'	2.39	0.50
1:22:540:U:H5''	14:E2:57:THR:HB	1.93	0.50
1:22:607:A:O2'	24:J2:134:HIS:NE2	2.36	0.50
1:22:1473:G:H21	1:22:1508:C:H42	1.59	0.50
2:51:488:G:H4'	2:51:489:U:OP1	2.10	0.50
2:51:4069:G:OP2	28:M1:5:ARG:NH1	2.45	0.50
7:B1:165:HIS:HB3	7:B1:180:LEU:HD23	1.93	0.50
24:J2:32:ILE:HG21	64:e2:111:ARG:HB3	1.92	0.50
35:Q1:172:ARG:NH1	55:a1:56:VAL:O	2.41	0.50
1:22:987:G:OP1	30:N2:3:ARG:NH1	2.44	0.50
1:22:1308:A:H2'	1:22:1309:U:H4'	1.93	0.50
2:51:198:A:N1	2:51:226:G:O2'	2.39	0.50
2:51:309:A:OP1	69:i1:86:LYS:NZ	2.45	0.50
2:51:1078:C:N3	26:L1:177:LYS:NZ	2.54	0.50
2:51:2086:C:O2'	66:g1:54:ARG:NH2	2.37	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:D2:175:VAL:HB	12:D2:182:LEU:HB2	1.94	0.50
13:E1:155:PRO:HD2	13:E1:158:ILE:HD12	1.94	0.50
15:F1:142:TYR:HE2	15:F1:235:GLU:HG3	1.77	0.50
16:F2:111:ILE:HG23	16:F2:177:LEU:HD23	1.93	0.50
24:J2:46:VAL:HG11	24:J2:106:LEU:HD21	1.94	0.50
35:Q1:88:ASP:OD1	35:Q1:112:ARG:NH1	2.45	0.50
1:22:727:U:H4'	50:X2:9:THR:HG22	1.93	0.50
1:22:1097:G:N1	1:22:1144:G:O2'	2.34	0.50
1:22:1439:U:OP1	1:22:1452:G:N2	2.41	0.50
1:22:1934:U:P	56:a2:5:ARG:HH12	2.34	0.50
2:51:806:C:H42	2:51:848:C:H42	1.58	0.50
2:51:3784:G:OP2	7:B1:2:SER:N	2.44	0.50
9:C1:106:LYS:HG2	9:C1:108:TRP:CZ2	2.46	0.50
11:D1:83:LEU:HB3	11:D1:88:ILE:HB	1.93	0.50
11:D1:119:TYR:OH	11:D1:139:PRO:O	2.28	0.50
14:E2:100:ARG:HH22	14:E2:122:LYS:HA	1.76	0.50
37:R1:162:ARG:HA	37:R1:165:LYS:HD3	1.94	0.50
53:Z1:47:ASP:N	53:Z1:69:LYS:O	2.44	0.50
67:g2:165:ILE:HB	67:g2:177:TRP:HB2	1.94	0.50
1:22:620:A:H4'	52:Y2:89:TYR:CG	2.47	0.50
1:22:689:A:OP1	24:J2:38:ARG:NH1	2.44	0.50
1:22:1469:A:H1'	44:U2:54:VAL:HG13	1.94	0.50
1:22:1631:G:H1	42:T2:102:ARG:NH2	2.09	0.50
2:51:196:C:H2'	2:51:197:A:C8	2.47	0.50
2:51:507:G:H22	2:51:552:G:H1	1.59	0.50
2:51:843:U:H2'	2:51:844:G:H8	1.76	0.50
2:51:1497:C:H4'	31:O1:91:PRO:HD3	1.93	0.50
22:I2:105:ASP:OD1	22:I2:106:SER:N	2.44	0.50
52:Y2:15:ASN:OD1	52:Y2:16:ARG:N	2.45	0.50
62:d2:17:GLY:HA2	62:d2:27:ARG:HD3	1.93	0.50
64:e2:111:ARG:HH21	64:e2:114:GLN:HG3	1.77	0.50
1:22:1924:U:OP1	32:O2:150:ARG:NH1	2.44	0.50
4:81:35:G:O2'	4:81:104:A:N1	2.41	0.50
7:B1:262:VAL:HG11	7:B1:268:ARG:NH1	2.27	0.50
13:E1:237:LEU:HA	13:E1:240:LYS:HZ3	1.77	0.50
14:E2:125:LYS:H	14:E2:142:HIS:HB2	1.77	0.50
39:S1:25:PRO:O	41:T1:146:ASN:ND2	2.45	0.50
48:W2:3:ARG:HH12	48:W2:28:ARG:HD2	1.77	0.50
51:Y1:11:ARG:HE	51:Y1:15:ARG:HD2	1.77	0.50
67:g2:199:THR:HG21	67:g2:240:CYS:HA	1.93	0.50
76:p1:47:MET:SD	76:p1:57:CYS:HB2	2.52	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:51:85:G:O2'	2:51:97:G:O6	2.24	0.50
2:51:960:G:O2'	9:C1:118:ASN:ND2	2.45	0.50
2:51:1795:G:H4'	2:51:1796:U:O5'	2.12	0.50
3:71:49:A:N6	11:D1:57:ASN:O	2.44	0.50
27:L2:132:CYS:SG	27:L2:142:ASN:ND2	2.84	0.50
28:M1:123:ILE:HD13	31:O1:184:GLU:HG2	1.94	0.50
34:P2:98:ASN:ND2	34:P2:103:ASN:OD1	2.45	0.50
35:Q1:66:LEU:HD22	35:Q1:98:LEU:HD13	1.93	0.50
1:22:42:A:O2'	1:22:98:C:OP1	2.25	0.49
1:22:338:G:H21	27:L2:43:LEU:HB2	1.76	0.49
1:22:1329:C:H2'	1:22:1330:U:C6	2.47	0.49
2:51:611:C:H42	2:51:721:C:H42	1.60	0.49
2:51:1045:G:H5'	35:Q1:132:ARG:HH22	1.76	0.49
2:51:3116:A:H5''	33:P1:83:TRP:O	2.11	0.49
5:A1:30:ARG:HH11	5:A1:36:GLU:HG3	1.77	0.49
30:N2:4:MET:HG2	30:N2:5:HIS:CD2	2.47	0.49
31:O1:12:ASP:HB2	31:O1:119:ARG:HB3	1.93	0.49
51:Y1:30:MET:HB3	51:Y1:101:PRO:HG2	1.93	0.49
67:g2:157:SER:HB2	67:g2:164:ILE:HD11	1.94	0.49
1:22:1510:U:O4	1:22:1511:A:N6	2.45	0.49
2:51:823:G:O2'	11:D1:286:SER:OG	2.24	0.49
2:51:3566:A:H5''	35:Q1:160:HIS:HE1	1.76	0.49
5:A1:137:ILE:HD11	5:A1:149:LYS:HB2	1.94	0.49
13:E1:115:ARG:NE	13:E1:146:ASP:O	2.45	0.49
14:E2:124:CYS:HB3	14:E2:141:THR:HB	1.93	0.49
15:F1:147:SER:OG	15:F1:243:ARG:NH2	2.41	0.49
29:N1:9:GLU:HB2	69:i1:44:ILE:HD12	1.94	0.49
67:g2:163:PRO:HB2	67:g2:179:LEU:HB2	1.94	0.49
1:22:122:G:H21	14:E2:146:THR:HG21	1.76	0.49
13:E1:147:SER:OG	13:E1:191:ASP:OD2	2.22	0.49
18:G2:57:ASP:HA	18:G2:106:LEU:HA	1.94	0.49
23:J1:46:GLN:NE2	23:J1:72:CYS:SG	2.73	0.49
2:51:2243:G:O3'	37:R1:60:ARG:NH1	2.45	0.49
9:C1:140:LYS:HE2	9:C1:245:HIS:HB2	1.94	0.49
11:D1:225:ARG:O	11:D1:229:ASN:ND2	2.32	0.49
12:D2:106:ARG:HG2	12:D2:175:VAL:HG22	1.94	0.49
16:F2:139:VAL:HG11	60:c2:45:ASN:H	1.76	0.49
22:I2:78:ILE:HA	22:I2:104:VAL:HG23	1.94	0.49
24:J2:136:ARG:HD2	24:J2:139:LYS:HA	1.94	0.49
27:L2:89:ILE:HD11	27:L2:110:MET:HE3	1.94	0.49
31:O1:170:TYR:CE2	31:O1:174:LYS:HD2	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:P2:34:MET:HB3	34:P2:42:ARG:HG3	1.95	0.49
67:g2:62:HIS:CE1	67:g2:88:ARG:HB2	2.48	0.49
71:k1:37:ARG:HH21	71:k1:42:LEU:HB2	1.77	0.49
1:22:908:A:OP1	1:22:908:A:H4'	2.10	0.49
1:22:1323:G:C4	62:d2:40:ARG:HD3	2.47	0.49
1:22:1495:G:O3'	42:T2:123:ARG:NH2	2.45	0.49
2:51:756:C:H2'	2:51:757:C:C6	2.47	0.49
2:51:1804:A:O2'	2:51:2260:G:N2	2.32	0.49
2:51:2867:U:H2'	2:51:2868:A:C8	2.47	0.49
9:C1:239:LYS:O	9:C1:248:ARG:NH1	2.46	0.49
12:D2:208:VAL:HG11	38:R2:12:ALA:HB2	1.94	0.49
14:E2:42:LEU:O	14:E2:84:THR:OG1	2.30	0.49
19:H1:47:LEU:HG	19:H1:53:LYS:HG3	1.94	0.49
43:U1:34:LYS:HE2	43:U1:85:THR:HG23	1.94	0.49
65:f1:36:ARG:HB2	65:f1:80:ASN:HA	1.95	0.49
77:r1:29:GLU:OE2	77:r1:32:ASN:ND2	2.44	0.49
1:22:428:G:O6	22:I2:5:ARG:NH2	2.46	0.49
1:22:1597:C:H2'	16:F2:163:PHE:HE1	1.77	0.49
2:51:776:C:H2'	2:51:777:G:C8	2.47	0.49
2:51:3437:G:H4'	2:51:3439:C:C2	2.47	0.49
2:51:4217:G:H21	2:51:4236:A:H2	1.59	0.49
6:A2:97:THR:HB	6:A2:117:ARG:HH11	1.77	0.49
12:D2:74:GLN:HA	12:D2:79:PHE:HB2	1.94	0.49
16:F2:28:VAL:HB	16:F2:110:GLN:HB2	1.95	0.49
20:H2:118:ARG:O	20:H2:124:ASN:ND2	2.46	0.49
32:O2:136:PRO:HG2	32:O2:139:SER:HB2	1.93	0.49
33:P1:131:ARG:HG3	33:P1:137:ASN:ND2	2.28	0.49
50:X2:84:PHE:HB2	50:X2:118:VAL:HG11	1.95	0.49
54:Z2:111:ARG:HG2	54:Z2:112:ASN:H	1.78	0.49
56:a2:11:ALA:HB3	56:a2:33:ASP:HB2	1.95	0.49
67:g2:20:GLN:HG2	67:g2:69:VAL:H	1.77	0.49
1:22:416:G:O2'	22:I2:10:LYS:NZ	2.46	0.49
1:22:1024:U:O2'	1:22:1026:A:N7	2.42	0.49
1:22:1625:U:H2'	1:22:1626:G:H8	1.77	0.49
1:22:1628:G:N7	1:22:1638:G:N1	2.60	0.49
2:51:941:C:H2'	2:51:942:A:H8	1.78	0.49
2:51:3108:U:H2'	2:51:3109:G:C8	2.48	0.49
15:F1:218:MET:HE1	15:F1:221:LYS:HD3	1.95	0.49
16:F2:91:ARG:HH11	54:Z2:103:HIS:HE1	1.60	0.49
44:U2:19:ARG:HA	44:U2:92:HIS:HA	1.94	0.49
2:51:3856:A:OP2	31:O1:76:ARG:NH1	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A2:80:ARG:HH21	6:A2:126:ASP:HB2	1.78	0.49
7:B1:86:VAL:O	7:B1:202:GLU:N	2.46	0.49
27:L2:60:LYS:HB3	27:L2:135:LEU:HD13	1.95	0.49
34:P2:16:THR:HA	34:P2:21:ASP:HA	1.94	0.49
55:a1:117:LEU:HD23	55:a1:140:VAL:HG11	1.93	0.49
56:a2:25:ASN:HD21	56:a2:77:CYS:HB3	1.78	0.49
58:b2:8:LEU:HD23	58:b2:8:LEU:H	1.78	0.49
1:22:90:G:OP1	1:22:491:A:N6	2.42	0.49
1:22:115:U:O2'	1:22:427:C:O2	2.25	0.49
2:51:710:C:H5''	15:F1:56:HIS:CE1	2.48	0.49
2:51:1366:C:OP1	21:I1:133:GLN:NE2	2.43	0.49
2:51:3452:G:H5'	5:A1:233:ARG:HB2	1.95	0.49
5:A1:104:VAL:HA	5:A1:107:MET:HE3	1.95	0.49
9:C1:200:ARG:NH1	51:Y1:11:ARG:HH12	2.10	0.49
11:D1:69:ILE:HG12	41:T1:31:MET:HG3	1.95	0.49
14:E2:85:GLY:N	14:E2:88:ASP:OD2	2.46	0.49
15:F1:120:PHE:O	15:F1:203:ASN:ND2	2.43	0.49
19:H1:137:SER:HB3	19:H1:143:GLU:HB3	1.95	0.49
23:J1:101:ASP:HA	23:J1:159:LYS:HB2	1.95	0.49
25:K2:64:TRP:CD2	62:d2:23:VAL:HG13	2.48	0.49
26:L1:169:ILE:HD13	55:a1:142:GLY:HA2	1.95	0.49
44:U2:35:VAL:HG21	44:U2:110:VAL:HG11	1.95	0.49
45:V1:21:PRO:HA	45:V1:54:SER:HA	1.93	0.49
76:p1:36:LYS:HE3	76:p1:48:LYS:HB3	1.94	0.49
1:22:1556:G:H1'	44:U2:72:GLU:HG2	1.95	0.49
1:22:1637:C:H2'	1:22:1638:G:C8	2.47	0.49
2:51:1824:G:N2	2:51:2260:G:H22	2.09	0.49
2:51:3761:U:H2'	2:51:3762:G:H8	1.77	0.49
2:51:3792:G:N3	7:B1:252:ALA:HB1	2.28	0.49
6:A2:143:PRO:HG3	46:V2:32:ILE:HB	1.95	0.49
10:C2:173:ARG:NH1	10:C2:175:GLY:O	2.46	0.49
21:I1:33:ILE:HB	21:I1:69:ARG:HH12	1.78	0.49
23:J1:19:LYS:HB3	23:J1:75:ARG:HD3	1.95	0.49
25:K2:64:TRP:HB3	62:d2:23:VAL:HA	1.95	0.49
28:M1:126:GLU:HG3	28:M1:129:LYS:HE2	1.95	0.49
1:22:336:G:OP2	14:E2:155:LYS:NZ	2.46	0.48
2:51:633:G:O6	2:51:692:C:N4	2.46	0.48
2:51:1612:A:H2'	2:51:1613:A:C8	2.48	0.48
2:51:2101:U:OP2	37:R1:124:TYR:OH	2.24	0.48
2:51:3892:A:H4'	7:B1:13:SER:HB2	1.95	0.48
2:51:3950:G:H2'	2:51:3951:A:C8	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:81:102:C:O2'	70:j1:20:ARG:O	2.29	0.48
11:D1:119:TYR:HE1	11:D1:134:SER:HA	1.77	0.48
1:22:490:G:H22	1:22:493:A:H5'	1.77	0.48
1:22:1540:G:OP1	36:Q2:117:ARG:NH2	2.46	0.48
1:22:1543:U:O2'	1:22:1544:G:H8	1.96	0.48
2:51:2901:U:H5	2:51:2906:A:N7	2.11	0.48
7:B1:354:GLN:HB3	7:B1:359:ALA:HB1	1.95	0.48
15:F1:239:ASN:O	15:F1:243:ARG:HG2	2.13	0.48
16:F2:49:LEU:HB3	36:Q2:50:LYS:HE3	1.94	0.48
22:I2:161:LEU:HD22	22:I2:196:GLU:HG2	1.95	0.48
33:P1:94:MET:HE1	33:P1:146:ILE:HB	1.94	0.48
65:f1:75:THR:HG21	65:f1:87:LYS:HG3	1.94	0.48
2:51:158:G:OP1	68:h1:109:ARG:NH1	2.46	0.48
2:51:712:C:H5''	9:C1:339:ALA:HB1	1.95	0.48
2:51:962:G:O6	35:Q1:85:THR:HG21	2.13	0.48
2:51:1074:G:H1'	2:51:1075:A:C8	2.48	0.48
7:B1:19:ARG:HB2	7:B1:234:ARG:NH1	2.28	0.48
18:G2:147:LEU:HD13	18:G2:153:VAL:HG12	1.94	0.48
28:M1:30:VAL:O	39:S1:98:ARG:NH2	2.46	0.48
38:R2:103:LYS:HG3	38:R2:107:LYS:HE3	1.94	0.48
40:S2:124:ARG:HB2	40:S2:131:VAL:HG23	1.95	0.48
44:U2:27:ARG:HH22	44:U2:82:MET:HE3	1.79	0.48
44:U2:90:ASP:OD1	44:U2:91:LEU:N	2.46	0.48
48:W2:70:ASN:ND2	48:W2:130:PHE:O	2.44	0.48
1:22:444:A:H5''	1:22:445:C:H3'	1.95	0.48
1:22:494:A:H5''	22:I2:25:ARG:HA	1.95	0.48
1:22:928:G:N2	1:22:929:G:O6	2.46	0.48
1:22:1803:U:OP1	18:G2:92:ARG:NH1	2.46	0.48
2:51:74:G:H5'	26:L1:59:VAL:HB	1.94	0.48
2:51:76:A:N7	26:L1:74:ARG:NH2	2.61	0.48
2:51:723:C:N4	2:51:892:G:O2'	2.45	0.48
2:51:2308:C:H5''	74:n1:25:LYS:HD2	1.96	0.48
2:51:3571:C:H2'	2:51:3573:G:C8	2.42	0.48
4:81:74:G:OP2	51:Y1:74:TYR:OH	2.28	0.48
11:D1:160:PHE:HA	11:D1:163:LEU:HB3	1.94	0.48
12:D2:37:VAL:HG12	12:D2:50:ILE:HA	1.94	0.48
12:D2:193:ASP:OD2	12:D2:195:SER:OG	2.27	0.48
1:22:935:G:H1	1:22:976:C:H42	1.62	0.48
4:81:11:G:H21	33:P1:120:ASN:ND2	2.11	0.48
18:G2:22:ARG:HA	18:G2:25:ARG:HE	1.77	0.48
23:J1:72:CYS:SG	23:J1:73:THR:N	2.87	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:L2:112:VAL:HG12	27:L2:141:PHE:HB2	1.95	0.48
29:N1:98:LEU:HD23	29:N1:128:LYS:HD2	1.94	0.48
30:N2:15:ALA:HB1	58:b2:26:GLN:HB3	1.96	0.48
58:b2:79:PHE:HD2	58:b2:81:ARG:H	1.61	0.48
67:g2:234:ASP:OD1	67:g2:235:THR:N	2.39	0.48
1:22:108:G:O2'	1:22:915:A:N1	2.45	0.48
1:22:908:A:H2'	1:22:909:U:O4'	2.14	0.48
1:22:1556:G:N2	44:U2:70:CYS:SG	2.80	0.48
1:22:1745:G:O2'	60:c2:20:ARG:NH1	2.46	0.48
1:22:1784:A:N6	1:22:1884:G:O2'	2.46	0.48
2:51:1909:G:N7	49:X1:47:ARG:NH2	2.58	0.48
2:51:3864:C:H2'	2:51:3865:G:C8	2.48	0.48
7:B1:112:ASP:O	7:B1:116:ARG:HG3	2.14	0.48
7:B1:122:TRP:O	7:B1:127:LYS:NZ	2.46	0.48
1:22:1189:C:H5''	8:B2:150:ILE:HG12	1.95	0.48
1:22:1296:G:H1	1:22:1593:G:H1	1.62	0.48
1:22:1307:A:O2'	1:22:1308:A:OP1	2.32	0.48
2:51:1113:G:H1'	26:L1:12:PRO:HB2	1.95	0.48
2:51:1278:G:O2'	55:a1:29:PRO:O	2.25	0.48
2:51:4204:G:H5'	7:B1:372:SER:HB3	1.95	0.48
15:F1:223:THR:HG22	15:F1:227:GLU:HG3	1.96	0.48
23:J1:15:LEU:HD23	23:J1:165:TRP:HB2	1.95	0.48
38:R2:5:ARG:HB2	38:R2:10:LYS:HE2	1.95	0.48
40:S2:78:LYS:HG3	42:T2:34:TRP:HE1	1.78	0.48
50:X2:101:LEU:HB3	50:X2:124:LYS:HB2	1.96	0.48
51:Y1:34:LEU:HD11	51:Y1:47:MET:HB2	1.96	0.48
2:51:78:U:H5''	29:N1:185:GLY:HA2	1.96	0.48
2:51:758:U:H3	2:51:775:G:H1	1.61	0.48
2:51:1274:C:H4'	2:51:1275:U:H5''	1.96	0.48
2:51:2094:A:N6	2:51:2110:G:O2'	2.47	0.48
2:51:2870:A:O2'	22:I2:89:GLU:OE1	2.31	0.48
18:G2:135:PRO:HG2	18:G2:141:ILE:HG12	1.94	0.48
41:T1:17:ARG:HD2	41:T1:47:THR:OG1	2.14	0.48
46:V2:22:ARG:NH2	48:W2:19:LYS:O	2.46	0.48
49:X1:105:LYS:NZ	49:X1:125:THR:H	2.12	0.48
55:a1:72:THR:HG22	55:a1:110:LYS:HB3	1.95	0.48
1:22:448:C:H5''	22:I2:16:GLY:HA3	1.95	0.48
1:22:861:G:H2'	1:22:862:A:H8	1.78	0.48
1:22:1065:G:N7	56:a2:19:GLN:NE2	2.62	0.48
1:22:1643:U:H1'	12:D2:6:SER:HB3	1.96	0.48
2:51:904:C:O2	2:51:905:G:N2	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:51:1281:U:H2'	2:51:1282:A:C8	2.49	0.48
2:51:2881:A:O2'	2:51:3928:G:O2'	2.26	0.48
16:F2:28:VAL:HG11	16:F2:107:ASN:HD22	1.78	0.48
20:H2:91:HIS:HD2	20:H2:169:LYS:HG2	1.79	0.48
24:J2:176:LYS:HA	24:J2:179:LYS:HE2	1.95	0.48
26:L1:103:ARG:NH2	69:i1:23:LYS:O	2.43	0.48
35:Q1:70:MET:HE1	35:Q1:137:VAL:HB	1.96	0.48
1:22:1307:A:H3'	1:22:1308:A:H5''	1.96	0.48
1:22:1627:C:H5	1:22:1638:G:H1	1.62	0.48
2:51:642:G:H1	2:51:682:C:H5	1.60	0.48
2:51:806:C:N4	2:51:848:C:H42	2.12	0.48
2:51:1471:A:N6	2:51:3133:G:O2'	2.47	0.48
2:51:2087:G:N1	76:p1:58:GLY:O	2.47	0.48
2:51:2108:G:H5''	2:51:2110:G:H1'	1.95	0.48
23:J1:104:ASN:HD22	23:J1:133:VAL:HG13	1.78	0.48
27:L2:62:PRO:HD2	27:L2:115:SER:HB2	1.95	0.48
43:U1:115:ARG:N	43:U1:127:ARG:O	2.45	0.48
44:U2:25:THR:HG22	44:U2:86:LYS:HG3	1.96	0.48
1:22:982:C:O2'	1:22:983:G:O4'	2.20	0.47
1:22:1239:U:H5''	74:n1:14:LYS:HD2	1.96	0.47
2:51:320:A:H2'	2:51:321:A:C8	2.49	0.47
2:51:329:U:O2'	69:i1:30:ARG:NH1	2.47	0.47
2:51:1189:U:N3	2:51:3823:U:OP1	2.33	0.47
2:51:3430:C:N3	17:G1:73:ARG:NH2	2.49	0.47
2:51:3787:C:H5''	2:51:3788:G:H5''	1.96	0.47
9:C1:143:ARG:HH21	9:C1:178:ASN:HB3	1.79	0.47
14:E2:45:ILE:HG13	14:E2:61:VAL:HG11	1.96	0.47
19:H1:59:LYS:HE3	19:H1:66:GLU:HB3	1.95	0.47
23:J1:20:LEU:HD23	23:J1:132:VAL:HB	1.95	0.47
55:a1:35:ALA:O	55:a1:41:HIS:ND1	2.45	0.47
1:22:1112:G:H4'	1:22:1925:G:H4'	1.96	0.47
2:51:38:A:H5''	55:a1:35:ALA:HB2	1.95	0.47
2:51:511:C:O2'	2:51:513:U:OP1	2.24	0.47
2:51:1376:A:N3	3:71:79:U:O2'	2.45	0.47
2:51:1868:G:O2'	2:51:1961:A:N1	2.43	0.47
2:51:1979:C:H5''	2:51:1980:G:H4'	1.96	0.47
16:F2:116:ILE:HD11	16:F2:147:VAL:HG23	1.94	0.47
26:L1:91:ALA:HB1	26:L1:96:ILE:HB	1.95	0.47
32:O2:80:ASP:OD1	32:O2:84:LYS:NZ	2.42	0.47
67:g2:120:ILE:N	67:g2:132:TRP:O	2.42	0.47
67:g2:254:PRO:HA	67:g2:285:GLN:HA	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
71:k1:40:ARG:HD2	71:k1:41:TYR:CE2	2.49	0.47
2:51:3044:A:O2'	2:51:3045:A:H3'	2.14	0.47
16:F2:38:TYR:HE2	16:F2:143:PRO:HG2	1.80	0.47
27:L2:127:VAL:HG13	27:L2:143:VAL:HG23	1.96	0.47
38:R2:114:LEU:HB2	38:R2:117:LEU:HG	1.96	0.47
44:U2:65:THR:HG23	62:d2:40:ARG:HB2	1.95	0.47
49:X1:128:ARG:HD2	49:X1:134:LYS:HB2	1.96	0.47
61:d1:35:SER:O	61:d1:39:ARG:HG3	2.14	0.47
67:g2:226:HIS:NE2	67:g2:228:TYR:O	2.48	0.47
1:22:487:C:O2'	18:G2:92:ARG:NH2	2.47	0.47
2:51:792:C:H42	2:51:865:G:H1	1.62	0.47
29:N1:104:GLU:HG2	29:N1:161:MET:HG2	1.96	0.47
67:g2:216:ALA:N	67:g2:230:LEU:O	2.46	0.47
1:22:1204:G:O2'	1:22:1205:C:OP2	2.31	0.47
1:22:1209:A:H5'	10:C2:176:SER:HB3	1.97	0.47
1:22:1615:G:O2'	1:22:1623:C:O2	2.29	0.47
2:51:458:C:H2'	2:51:459:G:H8	1.78	0.47
2:51:798:C:H2'	2:51:799:G:H8	1.79	0.47
2:51:1415:G:O2'	2:51:1417:G:N2	2.47	0.47
2:51:2052:G:H3'	2:51:2053:G:H4'	1.96	0.47
2:51:3476:U:OP1	2:51:3602:U:O2'	2.27	0.47
2:51:3852:C:H2'	2:51:3853:A:O4'	2.14	0.47
6:A2:141:ASN:ND2	10:C2:71:SER:O	2.39	0.47
7:B1:80:GLU:OE1	7:B1:323:TYR:OH	2.24	0.47
28:M1:11:ARG:HG2	28:M1:57:LEU:HD22	1.97	0.47
29:N1:53:TYR:HB2	29:N1:133:ILE:HD13	1.97	0.47
33:P1:125:MET:HB2	33:P1:141:SER:HB3	1.97	0.47
63:e1:35:TRP:CZ2	63:e1:56:PRO:HD2	2.50	0.47
1:22:1052:C:O2'	8:B2:118:GLN:O	2.31	0.47
1:22:1465:G:H22	1:22:1513:A:H2	1.62	0.47
1:22:1584:U:H3	34:P2:123:TYR:HB3	1.80	0.47
2:51:677:U:H5	2:51:680:A:N7	2.12	0.47
2:51:889:C:O2'	9:C1:321:ASN:OD1	2.22	0.47
2:51:3167:G:H2'	2:51:3715:C:O2'	2.15	0.47
3:71:63:C:H5'	3:71:64:G:H5''	1.97	0.47
18:G2:32:MET:O	18:G2:65:GLN:NE2	2.48	0.47
20:H2:58:LYS:HB2	20:H2:90:LYS:HG2	1.95	0.47
33:P1:52:ILE:HG23	33:P1:85:LYS:HG3	1.97	0.47
48:W2:40:VAL:O	48:W2:44:HIS:ND1	2.35	0.47
54:Z2:69:THR:HB	54:Z2:72:VAL:HG12	1.96	0.47
55:a1:88:VAL:O	55:a1:91:SER:OG	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
67:g2:87:LEU:HD21	67:g2:122:SER:HB3	1.97	0.47
1:22:384:G:N2	1:22:385:G:N7	2.63	0.47
1:22:423:G:H2'	1:22:424:G:C8	2.49	0.47
1:22:1758:G:N2	1:22:1904:A:H8	2.13	0.47
1:22:1785:U:OP1	1:22:1786:U:O2'	2.24	0.47
2:51:92:C:C2	55:a1:55:LYS:HE2	2.49	0.47
2:51:1418:G:H5'	41:T1:129:LYS:HE2	1.96	0.47
2:51:1482:G:O2'	63:e1:57:ASN:OD1	2.24	0.47
2:51:2280:A:O2'	2:51:3901:G:H4'	2.14	0.47
2:51:2314:G:OP2	2:51:2315:A:O2'	2.29	0.47
3:71:60:G:H5'	11:D1:270:LYS:HG2	1.95	0.47
6:A2:141:ASN:ND2	10:C2:73:PRO:HD3	2.30	0.47
8:B2:142:PHE:HD1	8:B2:209:ASP:HB2	1.79	0.47
12:D2:115:VAL:HG21	12:D2:142:LEU:HD11	1.97	0.47
15:F1:114:GLN:HE21	15:F1:210:LYS:HD2	1.80	0.47
20:H2:8:ILE:HA	20:H2:45:ILE:H	1.80	0.47
20:H2:98:ARG:HB2	20:H2:125:VAL:HG23	1.96	0.47
29:N1:183:THR:HG22	29:N1:188:ARG:HB3	1.97	0.47
35:Q1:50:ARG:O	35:Q1:58:ARG:HD3	2.15	0.47
35:Q1:57:ASN:OD1	35:Q1:143:ARG:NH2	2.48	0.47
50:X2:71:ARG:HH11	50:X2:82:THR:HG23	1.80	0.47
56:a2:13:LYS:H	56:a2:15:ARG:HH12	1.62	0.47
63:e1:108:ARG:HD3	63:e1:127:ALA:HB3	1.96	0.47
75:o1:6:LYS:HG2	75:o1:93:LEU:HG	1.97	0.47
1:22:1094:A:H2'	1:22:1095:A:H8	1.78	0.47
1:22:1330:U:H1'	1:22:1331:C:H5'	1.97	0.47
2:51:307:A:P	29:N1:15:GLN:HE22	2.38	0.47
2:51:1953:U:H1'	2:51:1954:C:C6	2.50	0.47
2:51:2311:C:H5''	76:p1:8:VAL:HG13	1.97	0.47
2:51:3166:A:H5''	9:C1:69:THR:HB	1.96	0.47
17:G1:94:GLN:HA	17:G1:97:LYS:HD3	1.96	0.47
18:G2:103:ASP:OD1	18:G2:104:ALA:N	2.40	0.47
29:N1:184:ILE:O	29:N1:194:ARG:NH1	2.39	0.47
31:O1:112:PRO:N	31:O1:113:PRO:HD2	2.29	0.47
68:h1:80:PRO:HD2	68:h1:83:LEU:HD12	1.96	0.47
1:22:662:A:H1'	64:e2:89:VAL:HG13	1.96	0.47
1:22:689:A:OP1	24:J2:41:ARG:NH1	2.44	0.47
1:22:934:G:O4'	37:R1:162:ARG:NH1	2.48	0.47
1:22:1007:U:H3	1:22:1047:A:H61	1.63	0.47
1:22:1150:G:OP2	56:a2:12:LYS:NZ	2.34	0.47
1:22:1794:U:H3	1:22:1875:G:H1	1.63	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:51:158:G:N2	2:51:159:U:O4	2.48	0.47
2:51:626:U:OP1	39:S1:63:TYR:OH	2.27	0.47
2:51:983:G:N2	9:C1:234:ARG:HD3	2.29	0.47
2:51:1639:G:OP1	2:51:1639:G:H4'	2.15	0.47
2:51:1823:A:H4'	61:d1:68:LYS:HG2	1.97	0.47
2:51:4207:G:N2	2:51:4243:G:O2'	2.48	0.47
5:A1:48:ILE:HD13	76:p1:65:ALA:HB2	1.97	0.47
6:A2:103:PHE:CG	6:A2:133:PRO:HG3	2.50	0.47
7:B1:332:MET:HE1	7:B1:368:ILE:HD13	1.97	0.47
9:C1:230:GLN:HE21	9:C1:239:LYS:HD2	1.79	0.47
12:D2:154:ASP:OD1	12:D2:154:ASP:N	2.48	0.47
47:W1:21:TYR:HB3	47:W1:31:PHE:HE2	1.80	0.47
52:Y2:12:PHE:HD1	52:Y2:23:MET:HB3	1.80	0.47
75:o1:44:LYS:HE3	75:o1:52:THR:HB	1.96	0.47
1:22:106:C:OP1	1:22:477:G:O2'	2.31	0.47
1:22:557:U:H2'	1:22:558:A:C8	2.50	0.47
2:51:617:C:H2'	2:51:618:G:C8	2.50	0.47
2:51:904:C:O2'	2:51:907:C:N4	2.48	0.47
2:51:3955:U:H2'	2:51:3956:G:C8	2.50	0.47
2:51:4102:C:H42	2:51:4119:G:H1	1.63	0.47
8:B2:38:MET:SD	8:B2:186:ASN:HB2	2.55	0.47
29:N1:146:PRO:HB2	68:h1:104:THR:HG23	1.96	0.47
43:U1:52:ASN:O	43:U1:56:PHE:N	2.46	0.47
46:V2:15:ARG:HH12	46:V2:33:GLN:HB2	1.79	0.47
46:V2:60:ARG:HA	46:V2:65:ALA:HB2	1.97	0.47
51:Y1:109:LEU:HD13	51:Y1:119:LEU:HD11	1.96	0.47
1:22:153:G:H4'	18:G2:15:LEU:HD22	1.97	0.46
2:51:383:U:H4'	2:51:417:G:H5'	1.97	0.46
2:51:482:G:H22	2:51:572:G:H1	1.64	0.46
2:51:492:G:N1	2:51:566:U:O2	2.49	0.46
2:51:990:C:H2'	2:51:991:G:O4'	2.15	0.46
2:51:1892:C:O2'	2:51:2931:G:N3	2.48	0.46
2:51:2191:G:O6	53:Z1:51:ARG:NH2	2.48	0.46
4:81:26:U:H4'	9:C1:53:ALA:HB3	1.97	0.46
6:A2:108:PHE:HB2	6:A2:136:GLU:HG2	1.96	0.46
30:N2:114:ARG:HD3	30:N2:117:LEU:HD12	1.97	0.46
31:O1:18:LEU:HG	31:O1:85:THR:HG21	1.96	0.46
44:U2:44:LYS:HB2	44:U2:44:LYS:HZ2	1.80	0.46
45:V1:89:ARG:HB2	45:V1:95:PHE:CZ	2.49	0.46
67:g2:178:ASN:HB2	67:g2:185:LYS:HD2	1.97	0.46
1:22:432:C:H1'	22:I2:5:ARG:HB3	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:22:608:U:H3	1:22:633:A:H62	1.63	0.46
2:51:435:A:C2	2:51:3127:A:H4'	2.50	0.46
2:51:3352:C:N4	2:51:3353:G:O6	2.48	0.46
4:81:45:G:O2'	4:81:60:A:N1	2.38	0.46
11:D1:72:ASP:N	11:D1:72:ASP:OD1	2.46	0.46
12:D2:210:ILE:HD13	38:R2:16:ILE:HD13	1.98	0.46
14:E2:161:ARG:HD3	14:E2:171:ASP:HB2	1.97	0.46
18:G2:32:MET:HG3	18:G2:52:ILE:HG22	1.97	0.46
25:K2:65:ARG:NH2	62:d2:21:CYS:O	2.48	0.46
27:L2:129:VAL:HB	27:L2:141:PHE:HB3	1.97	0.46
48:W2:28:ARG:HB3	48:W2:29:PRO:HD3	1.97	0.46
67:g2:207:CYS:N	67:g2:219:TRP:O	2.46	0.46
76:p1:26:VAL:HG12	76:p1:30:GLU:HG3	1.96	0.46
1:22:1916:G:H2'	1:22:1917:G:C8	2.49	0.46
2:51:2021:A:H4'	2:51:2204:U:H5'	1.97	0.46
2:51:2175:U:O4'	5:A1:187:HIS:HB3	2.16	0.46
2:51:2927:C:H4'	5:A1:8:GLN:HA	1.96	0.46
2:51:2942:A:H5''	5:A1:132:ASN:ND2	2.30	0.46
2:51:3187:U:H2'	2:51:3188:A:C8	2.51	0.46
2:51:3728:U:H2'	2:51:3729:C:C6	2.50	0.46
7:B1:77:THR:HG21	7:B1:337:VAL:HG22	1.96	0.46
7:B1:326:VAL:HG11	7:B1:330:PHE:HB3	1.96	0.46
10:C2:154:GLY:N	10:C2:165:THR:O	2.43	0.46
14:E2:184:THR:HA	14:E2:189:LEU:HD12	1.98	0.46
39:S1:55:LYS:H	39:S1:58:SER:HB2	1.81	0.46
1:22:1511:A:O2'	1:22:1512:G:H5''	2.15	0.46
2:51:2209:C:OP2	71:k1:39:SER:OG	2.26	0.46
2:51:2280:A:N6	2:51:3099:G:O2'	2.48	0.46
2:51:2992:A:H2'	2:51:2993:A:C8	2.51	0.46
2:51:3622:G:O6	55:a1:60:HIS:HA	2.15	0.46
2:51:4090:G:H1	2:51:4128:U:H3	1.61	0.46
7:B1:170:LEU:O	7:B1:328:ASN:ND2	2.30	0.46
18:G2:164:LYS:HE3	18:G2:167:LYS:HB2	1.97	0.46
1:22:17:C:H2'	1:22:18:C:C6	2.50	0.46
1:22:912:C:H5''	1:22:913:C:H5'	1.97	0.46
2:51:6:C:H2'	2:51:7:C:C6	2.50	0.46
2:51:70:A:OP2	55:a1:64:LYS:NZ	2.35	0.46
2:51:222:C:H2'	2:51:223:C:C6	2.51	0.46
2:51:707:U:OP2	15:F1:240:ARG:NE	2.35	0.46
2:51:890:G:H5'	9:C1:323:ARG:HB2	1.97	0.46
2:51:999:G:N2	2:51:1002:G:OP2	2.40	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:51:1399:G:O2'	2:51:1401:C:OP2	2.31	0.46
2:51:1664:C:H5''	35:Q1:11:ARG:HG2	1.96	0.46
2:51:1667:C:H42	15:F1:162:LYS:HB2	1.80	0.46
2:51:3786:A:OP2	7:B1:257:TRP:HB3	2.16	0.46
4:81:27:C:H2'	4:81:28:G:H8	1.81	0.46
10:C2:116:ILE:O	10:C2:124:GLY:N	2.42	0.46
21:I1:85:PHE:HD2	21:I1:87:ILE:HG13	1.81	0.46
29:N1:7:MET:HE1	29:N1:45:PRO:HD2	1.97	0.46
31:O1:83:TRP:HB2	31:O1:106:VAL:HG21	1.98	0.46
37:R1:95:TRP:HE3	37:R1:98:ARG:HH21	1.63	0.46
45:V1:106:VAL:HG12	45:V1:112:MET:HG2	1.97	0.46
75:o1:6:LYS:HE3	75:o1:94:GLY:HA2	1.97	0.46
1:22:111:A:H5'	27:L2:71:GLY:HA2	1.96	0.46
1:22:1077:C:OP1	1:22:1194:G:O2'	2.33	0.46
1:22:1096:C:H4'	30:N2:109:LYS:HB3	1.97	0.46
1:22:1271:A:N6	1:22:1758:G:O6	2.49	0.46
1:22:1584:U:O2'	1:22:1585:G:OP2	2.33	0.46
1:22:1635:G:H1	42:T2:98:LYS:NZ	2.14	0.46
2:51:25:A:N3	2:51:341:C:O2'	2.42	0.46
2:51:619:G:H1	2:51:712:C:N4	2.05	0.46
2:51:3735:A:O2'	2:51:3778:A:N3	2.42	0.46
3:71:39:C:O2	23:J1:73:THR:N	2.48	0.46
5:A1:2:GLY:HA2	5:A1:207:VAL:HG23	1.97	0.46
10:C2:218:THR:HG22	10:C2:221:ASN:H	1.81	0.46
15:F1:223:THR:HB	15:F1:229:GLY:HA3	1.97	0.46
16:F2:155:CYS:SG	16:F2:159:ARG:NH1	2.88	0.46
27:L2:37:TYR:OH	27:L2:56:TYR:O	2.26	0.46
29:N1:35:SER:OG	29:N1:65:ARG:NH1	2.48	0.46
30:N2:37:ILE:HG23	30:N2:50:ILE:HG21	1.98	0.46
45:V1:13:LYS:NZ	45:V1:59:ASP:OD1	2.47	0.46
50:X2:49:GLY:HA2	50:X2:75:ILE:HG13	1.98	0.46
52:Y2:26:ASP:OD1	52:Y2:26:ASP:N	2.47	0.46
54:Z2:62:VAL:N	54:Z2:63:PRO:HD2	2.31	0.46
62:d2:19:ARG:HD2	62:d2:32:ARG:HD2	1.97	0.46
1:22:66:A:N7	1:22:68:A:N6	2.64	0.46
1:22:341:U:C4	27:L2:66:ASN:HB2	2.51	0.46
1:22:682:C:H2'	1:22:683:U:O4'	2.16	0.46
2:51:68:C:H2'	2:51:69:A:O4'	2.16	0.46
2:51:574:C:H2'	2:51:575:G:C8	2.50	0.46
2:51:751:C:O2	13:E1:41:ARG:NE	2.48	0.46
2:51:964:G:OP1	35:Q1:108:ARG:NH2	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:51:1229:A:N7	5:A1:199:VAL:HG21	2.30	0.46
2:51:2870:A:H2'	2:51:2871:A:C8	2.50	0.46
2:51:3853:A:H5'	7:B1:98:GLY:HA3	1.97	0.46
4:81:95:G:C8	70:j1:79:ARG:HD2	2.51	0.46
8:B2:139:CYS:HA	8:B2:212:VAL:HA	1.98	0.46
21:I1:52:MET:HE1	21:I1:155:ALA:HB3	1.98	0.46
23:J1:13:ARG:NH1	23:J1:154:LYS:O	2.44	0.46
26:L1:169:ILE:HG12	55:a1:123:ILE:HD11	1.96	0.46
67:g2:17:TRP:HB2	67:g2:36:ARG:HG3	1.96	0.46
1:22:547:C:H2'	1:22:548:A:H5''	1.97	0.46
1:22:566:A:O2'	1:22:879:A:N3	2.42	0.46
1:22:695:U:OP2	50:X2:108:LYS:NZ	2.49	0.46
1:22:1301:C:O3'	1:22:1313:A:N6	2.48	0.46
1:22:1696:A:OP1	40:S2:35:GLY:N	2.43	0.46
2:51:1794:A:N1	2:51:3120:A:H5''	2.31	0.46
2:51:3496:G:H5''	2:51:3497:U:O4'	2.15	0.46
2:51:4082:C:C5	13:E1:249:ARG:HG2	2.50	0.46
4:81:35:G:C5	68:h1:89:ARG:HD3	2.51	0.46
4:81:95:G:C6	70:j1:84:PRO:HG3	2.51	0.46
6:A2:184:ARG:HD3	6:A2:191:ARG:HG2	1.97	0.46
10:C2:161:GLY:O	46:V2:3:ASN:ND2	2.48	0.46
14:E2:67:GLN:NE2	52:Y2:85:ASN:OD1	2.49	0.46
19:H1:41:ILE:HG21	19:H1:73:ILE:HD11	1.98	0.46
22:I2:158:ILE:HG21	22:I2:162:LEU:HD22	1.97	0.46
36:Q2:27:ARG:HE	36:Q2:66:VAL:HA	1.81	0.46
37:R1:23:TRP:HB3	37:R1:51:ILE:HG13	1.98	0.46
66:g1:74:VAL:HG23	66:g1:76:ARG:H	1.80	0.46
67:g2:195:LEU:HA	67:g2:211:GLY:HA3	1.98	0.46
1:22:10:G:O2'	10:C2:99:GLN:OE1	2.31	0.46
1:22:1336:G:H2'	1:22:1337:G:C8	2.51	0.46
1:22:1456:C:OP1	38:R2:43:SER:OG	2.33	0.46
2:51:511:C:N4	2:51:547:U:H3	2.14	0.46
2:51:4140:C:H3'	13:E1:133:ARG:HH22	1.80	0.46
25:K2:32:HIS:HB3	25:K2:35:LEU:HB2	1.96	0.46
32:O2:140:THR:OG1	32:O2:141:ARG:N	2.49	0.46
38:R2:5:ARG:HB3	38:R2:9:VAL:HB	1.98	0.46
49:X1:76:ILE:HD13	49:X1:99:VAL:HG12	1.98	0.46
1:22:385:G:H2'	1:22:386:U:C6	2.51	0.46
1:22:1354:A:N6	1:22:1379:G:H22	2.13	0.46
1:22:1905:A:H5'	1:22:1933:A:C2	2.50	0.46
2:51:54:G:OP1	70:j1:43:ARG:NH1	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:51:219:A:H5'	2:51:221:C:H5'	1.96	0.46
2:51:1057:C:H5''	35:Q1:144:LYS:HG2	1.98	0.46
2:51:1276:C:O2'	2:51:3461:C:OP1	2.28	0.46
2:51:1448:G:OP2	21:I1:98:ARG:NH1	2.34	0.46
2:51:3582:C:O2'	57:b1:36:ASP:OD1	2.31	0.46
2:51:3951:A:O2'	31:O1:146:GLU:OE1	2.32	0.46
9:C1:4:ALA:O	9:C1:29:ARG:NE	2.49	0.46
14:E2:124:CYS:HB3	14:E2:142:HIS:H	1.81	0.46
25:K2:7:ASN:HB2	25:K2:44:HIS:CE1	2.51	0.46
26:L1:42:LYS:O	26:L1:46:ILE:HG12	2.16	0.46
26:L1:189:ALA:HB2	69:i1:10:GLY:HA2	1.98	0.46
32:O2:151:LEU:HD23	32:O2:151:LEU:H	1.81	0.46
54:Z2:48:VAL:HG11	54:Z2:80:ARG:HB2	1.98	0.46
1:22:434:U:H2'	1:22:435:A:C8	2.51	0.45
1:22:1251:G:OP1	74:n1:11:ARG:NH2	2.49	0.45
1:22:1597:C:H2'	16:F2:163:PHE:CE1	2.50	0.45
2:51:903:A:H4'	2:51:904:C:OP1	2.15	0.45
2:51:947:G:H22	55:a1:25:HIS:CD2	2.34	0.45
2:51:1073:C:O2	2:51:1074:G:N1	2.49	0.45
2:51:1211:A:OP2	5:A1:187:HIS:HE1	1.99	0.45
2:51:1953:U:O2'	2:51:1964:U:O2	2.33	0.45
2:51:2075:G:OP2	2:51:2128:G:N1	2.44	0.45
2:51:2088:C:O4'	66:g1:54:ARG:NE	2.49	0.45
2:51:3166:A:H2'	9:C1:69:THR:HG21	1.97	0.45
2:51:3974:C:H2'	2:51:3975:A:C8	2.51	0.45
2:51:4041:G:OP1	31:O1:178:LYS:NZ	2.43	0.45
7:B1:89:VAL:HG22	7:B1:153:MET:HE1	1.97	0.45
15:F1:85:PRO:HG2	15:F1:142:TYR:CD2	2.51	0.45
26:L1:92:ARG:HE	26:L1:98:VAL:HB	1.80	0.45
29:N1:11:TRP:O	29:N1:14:LYS:NZ	2.48	0.45
31:O1:81:ILE:HG21	31:O1:140:LEU:HD11	1.97	0.45
48:W2:102:ILE:H	48:W2:113:HIS:CD2	2.32	0.45
56:a2:86:ASN:OD1	56:a2:86:ASN:N	2.45	0.45
1:22:1018:U:H2'	1:22:1019:A:H8	1.81	0.45
1:22:1028:A:O2'	1:22:1118:G:O3'	2.33	0.45
1:22:1110:U:H2'	1:22:1111:C:O4'	2.16	0.45
1:22:1682:G:H22	1:22:1685:A:H5'	1.80	0.45
2:51:170:G:H1	2:51:268:C:H41	1.64	0.45
2:51:425:G:H5'	33:P1:26:PHE:HZ	1.81	0.45
2:51:1734:G:OP2	9:C1:204:ARG:HD3	2.16	0.45
2:51:1838:A:O2'	70:j1:12:ARG:O	2.24	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:51:2299:G:O2'	37:R1:82:LYS:O	2.29	0.45
2:51:3433:C:P	17:G1:53:ARG:HH12	2.40	0.45
7:B1:285:TYR:CE1	7:B1:363:ILE:HG12	2.51	0.45
9:C1:60:HIS:NE2	9:C1:100:ARG:HD3	2.32	0.45
24:J2:164:PRO:HB3	24:J2:170:PRO:HA	1.97	0.45
26:L1:58:VAL:HG13	26:L1:157:ILE:HD13	1.98	0.45
41:T1:28:SER:O	41:T1:32:ARG:HG3	2.17	0.45
60:c2:44:ARG:NH2	60:c2:60:GLU:OE2	2.46	0.45
67:g2:197:THR:HG21	67:g2:239:LEU:H	1.81	0.45
2:51:377:G:OP1	9:C1:62:THR:HG23	2.16	0.45
2:51:2948:U:OP2	5:A1:198:ARG:NH1	2.48	0.45
2:51:3792:G:C2	7:B1:252:ALA:HB1	2.51	0.45
3:71:55:A:O2'	23:J1:151:ILE:O	2.23	0.45
8:B2:44:LEU:HD12	8:B2:69:VAL:HG11	1.96	0.45
8:B2:119:THR:HG23	8:B2:155:TYR:HA	1.96	0.45
9:C1:278:ASN:OD1	9:C1:279:LEU:N	2.44	0.45
16:F2:112:LEU:HD23	16:F2:177:LEU:HD21	1.98	0.45
31:O1:17:LEU:HD12	31:O1:20:ARG:HG3	1.99	0.45
35:Q1:78:LEU:HD22	35:Q1:135:GLY:HA2	1.98	0.45
37:R1:105:LEU:HD23	37:R1:138:LEU:HD23	1.99	0.45
52:Y2:19:GLN:OE1	52:Y2:81:TYR:OH	2.26	0.45
67:g2:120:ILE:HB	67:g2:132:TRP:HB2	1.98	0.45
1:22:1010:U:H2'	1:22:1011:G:H8	1.81	0.45
1:22:1148:A:OP1	1:22:1928:G:O2'	2.23	0.45
2:51:830:G:O2'	11:D1:278:ASP:OD2	2.33	0.45
2:51:1739:C:H3'	2:51:1740:G:H5'	1.98	0.45
4:81:27:C:H2'	4:81:28:G:C8	2.52	0.45
8:B2:109:LYS:HD2	8:B2:113:MET:HE3	1.98	0.45
12:D2:126:ILE:HG21	12:D2:134:CYS:HB3	1.98	0.45
14:E2:163:ASP:HB3	14:E2:166:THR:HG22	1.98	0.45
18:G2:3:LEU:HB3	18:G2:5:ILE:HD11	1.97	0.45
19:H1:28:LYS:HD3	19:H1:33:VAL:HG22	1.97	0.45
27:L2:17:PHE:HE2	27:L2:20:LYS:HB3	1.80	0.45
33:P1:64:ASN:O	33:P1:80:GLN:NE2	2.47	0.45
34:P2:68:PRO:HB2	34:P2:71:GLU:HB2	1.98	0.45
35:Q1:23:ILE:HG23	77:r1:9:MET:HB2	1.97	0.45
41:T1:51:GLY:HA3	41:T1:92:ARG:HG3	1.97	0.45
50:X2:57:VAL:HG13	50:X2:67:ARG:HB2	1.97	0.45
55:a1:24:LYS:HD2	55:a1:24:LYS:H	1.82	0.45
70:j1:20:ARG:HD3	72:l1:8:ARG:HH22	1.82	0.45
1:22:31:U:O2'	1:22:689:A:N1	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:22:106:C:O3'	1:22:456:G:N2	2.45	0.45
1:22:415:C:H41	1:22:1796:A:P	2.40	0.45
1:22:1023:G:O2'	1:22:1129:G:H4'	2.16	0.45
1:22:1415:G:H2'	1:22:1416:G:C8	2.52	0.45
2:51:793:G:H1	2:51:864:G:H22	1.65	0.45
2:51:957:C:H2'	2:51:958:G:H8	1.82	0.45
2:51:1769:C:H2'	2:51:1770:G:H8	1.80	0.45
2:51:2103:G:N1	2:51:2169:C:O2'	2.46	0.45
2:51:2950:U:H2'	2:51:2951:G:O4'	2.16	0.45
5:A1:112:ILE:HG13	76:p1:79:VAL:HG22	1.98	0.45
6:A2:64:ALA:HB1	46:V2:34:ILE:HD11	1.97	0.45
11:D1:27:LYS:HE2	23:J1:147:LYS:HE2	1.98	0.45
13:E1:134:HIS:HB3	13:E1:137:LYS:HD2	1.99	0.45
20:H2:159:ASP:OD1	20:H2:160:LYS:N	2.50	0.45
21:I1:152:LEU:HB3	21:I1:165:ILE:HD12	1.98	0.45
24:J2:88:ASP:HB2	24:J2:91:LYS:HG2	1.98	0.45
36:Q2:33:LYS:HG2	36:Q2:38:PRO:HA	1.96	0.45
58:b2:64:CYS:HB3	58:b2:71:ALA:HB1	1.97	0.45
69:i1:45:ARG:NH1	69:i1:49:GLY:O	2.44	0.45
1:22:379:G:H2'	1:22:380:C:H5''	1.98	0.45
1:22:1738:U:O2'	16:F2:84:GLY:O	2.21	0.45
2:51:879:U:O2'	2:51:880:U:OP1	2.29	0.45
2:51:1455:G:O2'	2:51:3487:A:N3	2.38	0.45
2:51:1908:G:O4'	2:51:1939:C:N4	2.48	0.45
2:51:1947:A:N6	2:51:2237:C:O2'	2.49	0.45
2:51:4207:G:H1'	2:51:4244:A:N6	2.32	0.45
6:A2:173:LEU:HD11	6:A2:177:MET:HE2	1.99	0.45
7:B1:44:THR:HG21	7:B1:186:ASN:ND2	2.32	0.45
7:B1:184:GLN:NE2	7:B1:186:ASN:OD1	2.41	0.45
20:H2:43:LEU:HD22	20:H2:72:PHE:HD2	1.80	0.45
20:H2:63:PHE:HB3	20:H2:97:GLN:HB2	1.98	0.45
21:I1:105:CYS:SG	21:I1:106:ALA:N	2.90	0.45
24:J2:108:ARG:HA	24:J2:113:GLN:HE21	1.82	0.45
29:N1:73:ARG:HG2	29:N1:75:VAL:HG13	1.98	0.45
35:Q1:16:LYS:O	35:Q1:33:ARG:NH2	2.50	0.45
35:Q1:95:ILE:HD11	35:Q1:112:ARG:HH21	1.81	0.45
1:22:110:U:H4'	1:22:111:A:OP1	2.17	0.45
1:22:683:U:O2	64:e2:133:ASN:ND2	2.48	0.45
2:51:91:G:O5'	2:51:92:C:H5''	2.17	0.45
2:51:483:G:OP1	77:r1:48:LYS:NZ	2.45	0.45
2:51:1109:C:H2'	2:51:1110:G:C8	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:51:1223:G:N1	2:51:3178:G:OP1	2.47	0.45
2:51:1243:C:H2'	2:51:1244:A:C8	2.52	0.45
2:51:2312:G:C8	76:p1:16:THR:HG22	2.51	0.45
2:51:3834:U:O2'	7:B1:234:ARG:NH2	2.42	0.45
8:B2:179:ASN:HB3	8:B2:183:GLU:HB2	1.97	0.45
14:E2:44:LEU:HD21	14:E2:70:ILE:HD13	1.97	0.45
33:P1:120:ASN:HB2	33:P1:145:HIS:HB2	1.98	0.45
42:T2:62:VAL:HG22	42:T2:108:LEU:HD13	1.98	0.45
77:r1:95:ARG:HD3	77:r1:112:LEU:HD21	1.98	0.45
1:22:39:A:H62	1:22:561:G:H21	1.64	0.45
1:22:542:U:H3	1:22:552:A:H61	1.64	0.45
1:22:935:G:H21	20:H2:114:GLN:HE22	1.65	0.45
2:51:70:A:H61	2:51:316:G:H1'	1.81	0.45
2:51:722:G:H4'	2:51:723:C:C2	2.52	0.45
2:51:880:U:H2'	2:51:881:C:O4'	2.17	0.45
2:51:1841:G:H2'	72:l1:13:LEU:HD22	1.98	0.45
2:51:2168:U:H2'	2:51:2169:C:C6	2.52	0.45
2:51:3961:A:O2'	19:H1:68:ALA:O	2.28	0.45
3:71:6:C:O2'	11:D1:50:ARG:NH1	2.50	0.45
36:Q2:86:GLN:HG3	36:Q2:90:LYS:HE2	1.97	0.45
42:T2:123:ARG:H	42:T2:123:ARG:HD2	1.80	0.45
51:Y1:19:PHE:O	51:Y1:26:ARG:NH2	2.50	0.45
60:c2:10:LYS:HE3	60:c2:36:ASP:HB3	1.98	0.45
67:g2:18:VAL:O	67:g2:287:THR:OG1	2.24	0.45
75:o1:12:CYS:HB3	75:o1:15:CYS:HB2	1.99	0.45
2:51:224:G:H4'	2:51:226:G:N7	2.32	0.45
2:51:396:G:N2	2:51:399:G:OP2	2.40	0.45
2:51:3595:C:OP1	41:T1:70:HIS:NE2	2.50	0.45
8:B2:32:ASP:OD1	8:B2:32:ASP:N	2.42	0.45
9:C1:315:LYS:HD2	15:F1:166:ALA:HB1	1.99	0.45
14:E2:102:ILE:HD13	14:E2:239:PRO:HD3	1.99	0.45
20:H2:134:VAL:HG21	20:H2:158:LEU:HD22	1.99	0.45
39:S1:31:ARG:HH21	39:S1:102:THR:HG21	1.81	0.45
40:S2:38:ARG:O	40:S2:42:HIS:ND1	2.49	0.45
1:22:107:A:H2'	1:22:108:G:C8	2.52	0.45
1:22:634:G:N2	1:22:634:G:OP2	2.50	0.45
1:22:1718:C:H2'	1:22:1719:G:C8	2.52	0.45
1:22:1757:U:H2'	1:22:1758:G:C8	2.51	0.45
2:51:490:C:N4	2:51:567:C:H42	2.15	0.45
2:51:594:C:H2'	2:51:595:G:C8	2.52	0.45
2:51:594:C:H2'	2:51:595:G:H8	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:51:1331:G:N2	21:I1:193:ASP:OD1	2.49	0.45
2:51:2222:A:H2'	2:51:2222:A:N3	2.32	0.45
6:A2:5:LEU:HD13	46:V2:41:ARG:HA	1.97	0.45
13:E1:183:MET:HE1	13:E1:234:LEU:HD13	1.99	0.45
23:J1:112:HIS:CE1	23:J1:125:ILE:HA	2.52	0.45
31:O1:72:PRO:HB2	31:O1:74:HIS:CE1	2.52	0.45
40:S2:20:ILE:HD13	40:S2:30:ILE:HA	1.97	0.45
57:b1:32:LEU:HD13	57:b1:43:MET:HE1	1.98	0.45
77:r1:94:VAL:HG21	77:r1:115:VAL:HG21	1.99	0.45
2:51:1058:C:OP1	35:Q1:144:LYS:NZ	2.35	0.44
2:51:2932:G:OP2	2:51:2932:G:N2	2.40	0.44
5:A1:51:ASP:HB3	5:A1:54:ARG:HG2	1.98	0.44
5:A1:80:GLU:HB2	5:A1:170:ALA:HA	1.98	0.44
7:B1:175:GLN:HE21	7:B1:177:LYS:HB2	1.82	0.44
10:C2:114:VAL:HG11	10:C2:141:ILE:HG12	1.99	0.44
10:C2:239:PRO:HA	10:C2:242:TRP:CD2	2.52	0.44
11:D1:108:ARG:CZ	11:D1:253:HIS:HB2	2.47	0.44
12:D2:69:LEU:HA	12:D2:72:VAL:HB	1.99	0.44
15:F1:68:ARG:HG2	15:F1:72:MET:HE3	1.98	0.44
15:F1:224:HIS:CD2	15:F1:232:GLY:HA3	2.51	0.44
29:N1:28:TRP:O	29:N1:32:GLN:HG2	2.18	0.44
42:T2:84:LYS:HE3	42:T2:92:HIS:HB2	1.98	0.44
50:X2:68:LYS:HB3	50:X2:91:LEU:HD22	1.98	0.44
55:a1:132:ARG:HA	55:a1:135:GLU:HG2	1.99	0.44
61:d1:73:LYS:HB2	61:d1:77:ASN:O	2.17	0.44
2:51:268:C:H4'	68:h1:113:LEU:HD13	2.00	0.44
2:51:550:A:H5''	35:Q1:115:LYS:HE3	1.99	0.44
2:51:697:A:H5''	2:51:698:C:C6	2.52	0.44
2:51:798:C:H2'	2:51:799:G:C8	2.52	0.44
2:51:1525:A:N6	2:51:1622:G:H2'	2.32	0.44
2:51:3761:U:O2'	2:51:3762:G:H5'	2.17	0.44
2:51:3915:C:H3'	37:R1:62:ARG:NH2	2.29	0.44
3:71:22:G:H1	3:71:53:A:HO2'	1.63	0.44
5:A1:108:PRO:HD3	76:p1:90:LYS:HD2	2.00	0.44
31:O1:49:PHE:HA	31:O1:138:ALA:HB2	1.97	0.44
1:22:1205:C:N4	48:W2:20:ARG:O	2.48	0.44
1:22:1594:C:O2'	42:T2:87:GLY:O	2.30	0.44
2:51:989:G:H21	2:51:990:C:N4	2.12	0.44
2:51:1365:U:OP1	21:I1:90:ARG:NH2	2.45	0.44
2:51:1760:G:H5''	63:e1:127:ALA:HB1	1.98	0.44
2:51:1845:C:H2'	2:51:1846:A:C8	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:51:2967:U:H2'	2:51:2968:C:C6	2.52	0.44
4:81:59:G:H8	68:h1:58:LEU:HD23	1.83	0.44
6:A2:81:ASN:HA	6:A2:84:GLN:HG3	2.00	0.44
14:E2:35:PRO:HD2	14:E2:83:PRO:HG2	1.99	0.44
28:M1:17:PHE:HZ	28:M1:53:LYS:HE2	1.81	0.44
31:O1:111:PRO:HG2	31:O1:114:TYR:HD2	1.82	0.44
53:Z1:41:ALA:HB2	53:Z1:77:TYR:HE1	1.80	0.44
53:Z1:89:ILE:HG22	53:Z1:91:LEU:HB2	2.00	0.44
56:a2:36:ILE:HB	56:a2:73:TYR:HB2	1.97	0.44
1:22:511:A:H4'	1:22:512:G:O5'	2.17	0.44
1:22:521:C:O2'	1:22:553:G:N3	2.45	0.44
1:22:729:G:H4'	48:W2:4:MET:HA	1.98	0.44
1:22:980:A:C5	30:N2:73:ARG:HD2	2.52	0.44
1:22:1604:C:H2'	1:22:1605:G:C8	2.52	0.44
2:51:516:G:H1	2:51:543:G:H1	1.65	0.44
2:51:617:C:H2'	2:51:618:G:H8	1.83	0.44
2:51:871:G:O6	2:51:872:A:N6	2.50	0.44
2:51:3844:C:H41	2:51:4007:G:H4'	1.83	0.44
8:B2:129:THR:HG22	8:B2:176:VAL:HG22	1.98	0.44
9:C1:221:PHE:HB2	9:C1:229:LEU:HD21	1.98	0.44
21:I1:51:HIS:HB3	21:I1:134:VAL:HG13	2.00	0.44
52:Y2:87:PRO:HD2	52:Y2:90:ARG:HD2	1.98	0.44
62:d2:33:LYS:HE2	62:d2:34:TYR:CZ	2.52	0.44
65:f1:14:TYR:OH	65:f1:92:LEU:O	2.28	0.44
1:22:1433:G:H21	1:22:1530:A:H1'	1.82	0.44
2:51:177:U:H3	2:51:262:G:H1	1.65	0.44
2:51:815:G:H2'	2:51:816:G:H8	1.83	0.44
2:51:1369:A:H2'	21:I1:22:PHE:CZ	2.52	0.44
2:51:1449:U:H4'	21:I1:8:CYS:HB3	2.00	0.44
2:51:3421:C:H2'	2:51:3422:G:C8	2.52	0.44
2:51:3536:A:H2'	2:51:3537:G:O4'	2.18	0.44
2:51:3916:U:OP2	37:R1:62:ARG:NH2	2.49	0.44
2:51:4069:G:H3'	28:M1:91:TRP:CE3	2.53	0.44
14:E2:36:HIS:NE2	14:E2:88:ASP:OD2	2.50	0.44
25:K2:3:MET:HB3	25:K2:44:HIS:NE2	2.33	0.44
32:O2:27:VAL:N	32:O2:91:THR:OG1	2.50	0.44
44:U2:38:ASP:OD2	44:U2:105:SER:OG	2.29	0.44
1:22:1246:G:N2	1:22:1249:A:OP2	2.41	0.44
1:22:1924:U:H2'	1:22:1925:G:C8	2.53	0.44
2:51:1175:G:N2	76:p1:17:ARG:HD2	2.32	0.44
2:51:1205:C:O2'	2:51:3088:A:N3	2.40	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:51:1871:G:O6	49:X1:88:LYS:NZ	2.43	0.44
2:51:1876:G:O2'	2:51:1946:A:N3	2.42	0.44
2:51:2024:G:H2'	2:51:2189:G:N2	2.31	0.44
2:51:2036:G:O4'	2:51:2177:G:H2'	2.17	0.44
2:51:2193:A:N6	53:Z1:64:LYS:HE3	2.33	0.44
2:51:3463:G:OP1	2:51:3489:C:O2'	2.30	0.44
2:51:3890:U:OP1	45:V1:51:ARG:NH2	2.50	0.44
2:51:4127:U:H5''	2:51:4128:U:C6	2.52	0.44
35:Q1:67:ILE:HG12	35:Q1:98:LEU:HD11	1.99	0.44
42:T2:58:ALA:O	42:T2:62:VAL:HG23	2.18	0.44
46:V2:33:GLN:HE21	46:V2:52:THR:HG21	1.82	0.44
1:22:553:G:O6	52:Y2:105:LYS:NZ	2.36	0.44
1:22:883:C:OP1	14:E2:22:LYS:N	2.46	0.44
1:22:983:G:N2	1:22:1084:A:O2'	2.37	0.44
1:22:1115:G:H2'	1:22:1116:A:C8	2.53	0.44
1:22:1713:G:N7	36:Q2:17:LYS:HE2	2.32	0.44
1:22:1801:G:H2'	1:22:1802:G:C8	2.53	0.44
2:51:819:G:H2'	2:51:820:A:H8	1.81	0.44
2:51:2197:G:H1'	2:51:2198:U:O4'	2.18	0.44
3:71:11:A:N1	3:71:66:G:O2'	2.45	0.44
6:A2:155:ARG:HG2	6:A2:156:TYR:CD2	2.53	0.44
9:C1:263:LEU:HG	9:C1:273:LEU:HD12	2.00	0.44
9:C1:284:MET:HE2	9:C1:287:THR:HA	1.99	0.44
12:D2:7:LYS:NZ	44:U2:113:GLU:OE2	2.45	0.44
14:E2:103:TYR:HB2	14:E2:182:MET:HE2	1.99	0.44
40:S2:103:LEU:HD12	40:S2:107:LEU:HD23	1.99	0.44
77:r1:97:ILE:O	77:r1:101:ASN:HB2	2.18	0.44
1:22:1214:A:OP1	56:a2:6:ARG:NH2	2.44	0.44
2:51:1334:G:H1	2:51:1358:C:H42	1.65	0.44
2:51:2099:G:H4'	2:51:2112:G:H4'	2.00	0.44
2:51:2165:U:H2'	2:51:2166:C:C6	2.52	0.44
2:51:3616:G:H1	2:51:3632:G:H1	1.65	0.44
2:51:3871:U:H2'	2:51:3872:A:H8	1.82	0.44
8:B2:29:ASP:OD1	8:B2:29:ASP:N	2.50	0.44
27:L2:97:ILE:HD12	50:X2:10:ALA:HB1	1.99	0.44
33:P1:122:ALA:HB3	33:P1:143:PRO:HG2	2.00	0.44
34:P2:56:LEU:HD12	34:P2:80:LEU:HD12	1.99	0.44
38:R2:77:GLU:O	38:R2:80:ARG:NH1	2.51	0.44
45:V1:48:ARG:HB3	45:V1:51:ARG:HB3	1.99	0.44
53:Z1:81:MET:HE1	59:c1:59:GLU:HG3	1.99	0.44
66:g1:5:LEU:HD23	66:g1:5:LEU:H	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:22:858:U:H5''	48:W2:82:GLN:HG2	2.00	0.44
1:22:1094:A:H2'	1:22:1095:A:C8	2.53	0.44
1:22:1802:G:P	18:G2:94:ARG:HH22	2.41	0.44
2:51:71:C:H1'	26:L1:62:PRO:O	2.17	0.44
2:51:3518:G:O2'	23:J1:129:ASP:OD1	2.27	0.44
2:51:3858:U:H5'	7:B1:14:LEU:HB2	1.98	0.44
2:51:4149:U:H2'	2:51:4150:G:N2	2.33	0.44
2:51:4208:U:C5	47:W1:50:ASN:HB3	2.53	0.44
14:E2:87:MET:SD	14:E2:100:ARG:NH1	2.91	0.44
16:F2:91:ARG:HH12	54:Z2:104:ARG:HH22	1.65	0.44
40:S2:26:ILE:HD11	40:S2:54:LYS:HB2	1.98	0.44
41:T1:9:ARG:O	41:T1:55:LYS:NZ	2.39	0.44
52:Y2:20:ARG:HA	52:Y2:75:ILE:O	2.18	0.44
65:f1:48:ALA:HB3	65:f1:102:ARG:HB2	2.00	0.44
76:p1:29:ILE:HG23	76:p1:69:TRP:HB3	1.99	0.44
1:22:1127:C:H4'	32:O2:150:ARG:HH11	1.83	0.43
2:51:366:G:O6	70:j1:52:LYS:NZ	2.46	0.43
2:51:488:G:H1'	2:51:489:U:O5'	2.18	0.43
4:81:144:U:OP1	29:N1:38:ARG:NH2	2.46	0.43
11:D1:146:LEU:HD22	11:D1:163:LEU:HD22	1.99	0.43
22:I2:42:ARG:HG2	22:I2:58:LEU:HD13	2.00	0.43
31:O1:183:ALA:O	31:O1:187:VAL:HG22	2.18	0.43
33:P1:4:TYR:OH	33:P1:18:ARG:HB2	2.18	0.43
40:S2:92:ASP:OD1	40:S2:92:ASP:N	2.45	0.43
76:p1:13:LYS:HE3	76:p1:14:TYR:CZ	2.52	0.43
1:22:693:U:H2'	1:22:694:A:C8	2.53	0.43
1:22:1111:C:H2'	1:22:1112:G:O4'	2.18	0.43
1:22:1250:A:OP2	74:n1:18:ARG:NH2	2.47	0.43
1:22:1256:A:H4'	50:X2:34:THR:HG21	2.00	0.43
1:22:1608:U:OP1	36:Q2:37:ARG:NH2	2.51	0.43
2:51:45:U:O4	29:N1:83:LYS:NZ	2.45	0.43
2:51:1314:G:N3	2:51:3482:A:H2'	2.33	0.43
2:51:1838:A:H1'	70:j1:12:ARG:HH11	1.83	0.43
2:51:2042:G:H2'	2:51:2043:G:H8	1.83	0.43
2:51:3528:U:H2'	2:51:3529:C:C6	2.53	0.43
2:51:3534:A:N6	2:51:3547:A:O2'	2.51	0.43
2:51:3836:A:O2'	2:51:4183:G:N7	2.48	0.43
2:51:4232:U:H2'	2:51:4233:G:H8	1.83	0.43
3:71:61:G:O3'	11:D1:279:ARG:NH1	2.50	0.43
4:81:26:U:H2'	4:81:27:C:C6	2.54	0.43
8:B2:88:THR:HG22	8:B2:98:THR:HG22	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:B2:171:ILE:HD12	8:B2:197:ILE:HG12	2.00	0.43
11:D1:167:VAL:HG11	11:D1:175:HIS:CD2	2.53	0.43
21:I1:51:HIS:CD2	21:I1:168:SER:HB2	2.53	0.43
32:O2:79:GLN:O	32:O2:83:GLN:NE2	2.51	0.43
34:P2:37:TYR:HB3	34:P2:41:GLN:HB2	2.00	0.43
34:P2:79:HIS:HA	34:P2:97:TYR:HB3	2.00	0.43
35:Q1:180:ARG:HD3	55:a1:50:PRO:HG2	2.00	0.43
68:h1:12:LYS:NZ	68:h1:20:GLN:OE1	2.49	0.43
72:l1:34:LYS:HE3	72:l1:34:LYS:HB3	1.84	0.43
1:22:247:U:O4	1:22:248:A:N6	2.51	0.43
1:22:1275:A:OP1	1:22:1905:A:O2'	2.24	0.43
1:22:1330:U:H5'	62:d2:17:GLY:HA3	1.99	0.43
1:22:1404:C:H5''	44:U2:67:LYS:HB3	2.00	0.43
1:22:1614:U:H2'	1:22:1615:G:H8	1.83	0.43
2:51:73:G:H5''	26:L1:105:ARG:HD3	2.00	0.43
2:51:211:G:OP1	51:Y1:59:ARG:NH2	2.50	0.43
2:51:556:G:O2'	2:51:557:G:H8	2.01	0.43
2:51:1280:A:H5''	26:L1:3:PRO:O	2.18	0.43
2:51:2131:A:H62	71:k1:35:LYS:NZ	2.17	0.43
8:B2:71:LEU:HD23	8:B2:79:VAL:HG22	1.99	0.43
15:F1:182:ILE:HD11	15:F1:191:GLU:HG2	2.00	0.43
17:G1:155:VAL:HG11	17:G1:174:CYS:SG	2.58	0.43
21:I1:12:CYS:HB3	21:I1:128:ARG:NH2	2.33	0.43
36:Q2:100:VAL:HG12	36:Q2:101:ASP:H	1.82	0.43
40:S2:40:TYR:HA	40:S2:83:PHE:HE2	1.83	0.43
59:c1:37:MET:HA	59:c1:40:GLN:HE21	1.83	0.43
60:c2:27:CYS:HB3	60:c2:45:ASN:HD21	1.83	0.43
1:22:664:C:O4'	1:22:678:C:O2'	2.34	0.43
1:22:1508:C:H5''	36:Q2:15:ARG:HH11	1.83	0.43
2:51:1296:G:C6	35:Q1:42:PRO:HB3	2.53	0.43
2:51:1446:U:OP1	21:I1:15:LYS:HG3	2.18	0.43
2:51:2109:A:C6	76:p1:42:CYS:HA	2.54	0.43
2:51:2284:G:O2'	2:51:3098:U:O4	2.26	0.43
2:51:3726:C:H2'	2:51:3727:U:C6	2.54	0.43
4:81:91:C:O2'	51:Y1:24:HIS:ND1	2.47	0.43
8:B2:103:MET:HE3	8:B2:215:VAL:HG23	2.00	0.43
14:E2:175:PHE:HE2	14:E2:198:ARG:HD2	1.83	0.43
15:F1:142:TYR:CE2	15:F1:235:GLU:HG3	2.53	0.43
30:N2:42:LYS:HG2	30:N2:80:LEU:HD11	2.00	0.43
40:S2:91:LYS:HE3	40:S2:113:ARG:HD3	2.00	0.43
43:U1:101:THR:O	43:U1:105:LEU:HG	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:X1:87:LYS:HE3	49:X1:87:LYS:HB3	1.84	0.43
1:22:568:A:O2'	24:J2:131:ARG:NH1	2.51	0.43
1:22:1204:G:H21	1:22:1204:G:P	2.42	0.43
2:51:28:C:O2'	29:N1:162:ARG:O	2.33	0.43
2:51:231:G:H4'	51:Y1:18:HIS:CE1	2.53	0.43
2:51:1044:G:O2'	2:51:1045:G:OP2	2.36	0.43
2:51:2867:U:H2'	2:51:2868:A:H8	1.81	0.43
2:51:3489:C:N3	21:I1:116:ARG:NH2	2.65	0.43
3:71:74:A:H8	3:71:74:A:OP1	2.02	0.43
4:81:143:C:OP1	29:N1:38:ARG:HD2	2.18	0.43
13:E1:258:VAL:HG13	13:E1:263:LEU:HD21	1.99	0.43
16:F2:204:ARG:OXT	60:c2:63:ARG:NH2	2.36	0.43
24:J2:33:GLY:HA3	64:e2:115:TYR:CG	2.52	0.43
24:J2:63:LEU:O	24:J2:70:ARG:NH1	2.51	0.43
27:L2:40:ASN:OD1	27:L2:40:ASN:N	2.50	0.43
31:O1:14:ARG:HD3	31:O1:39:ARG:NH2	2.33	0.43
51:Y1:100:HIS:ND1	51:Y1:102:SER:OG	2.43	0.43
1:22:392:C:H5''	14:E2:38:LEU:HB2	2.00	0.43
1:22:923:A:O2'	48:W2:36:ARG:NH2	2.52	0.43
1:22:1241:U:H2'	1:22:1242:G:C8	2.54	0.43
1:22:1262:A:H2'	1:22:1263:A:H8	1.82	0.43
1:22:1793:C:H42	1:22:1876:G:H1	1.65	0.43
2:51:749:U:H2'	2:51:750:G:C8	2.53	0.43
2:51:1908:G:O2'	49:X1:49:LYS:NZ	2.50	0.43
2:51:3150:A:N6	2:51:3838:G:O2'	2.52	0.43
2:51:3421:C:H2'	2:51:3422:G:H8	1.84	0.43
2:51:3805:C:H2'	2:51:3806:G:C8	2.53	0.43
2:51:3986:U:H5''	7:B1:276:HIS:O	2.18	0.43
2:51:4010:G:C2	2:51:4013:G:H1'	2.53	0.43
3:71:73:U:H3'	3:71:74:A:H5''	2.01	0.43
7:B1:291:TYR:OH	7:B1:315:ASN:ND2	2.51	0.43
8:B2:30:TRP:HZ2	32:O2:88:LEU:HG	1.82	0.43
13:E1:27:TYR:HB3	13:E1:31:ALA:HB3	2.00	0.43
17:G1:180:PRO:HG3	17:G1:219:VAL:HG13	2.00	0.43
22:I2:57:ALA:HB2	22:I2:183:GLY:HA2	2.00	0.43
24:J2:136:ARG:HA	24:J2:141:VAL:HA	2.00	0.43
29:N1:51:LEU:O	29:N1:117:ASN:ND2	2.35	0.43
42:T2:115:GLU:HG2	42:T2:125:THR:HG22	2.01	0.43
45:V1:106:VAL:HA	45:V1:112:MET:HA	2.00	0.43
56:a2:21:ILE:HD11	56:a2:35:ALA:HB2	1.99	0.43
67:g2:152:SER:OG	67:g2:168:CYS:SG	2.71	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
67:g2:178:ASN:HB3	67:g2:181:ASN:HB2	2.01	0.43
72:l1:44:TRP:CE3	72:l1:45:ARG:HG2	2.53	0.43
1:22:1167:C:H2'	1:22:1168:G:C8	2.53	0.43
1:22:1401:G:H21	12:D2:174:HIS:CE1	2.36	0.43
2:51:2040:G:O2'	2:51:2102:C:N3	2.50	0.43
2:51:3468:G:H21	21:l1:111:LEU:HG	1.84	0.43
2:51:3531:C:H2'	2:51:3532:G:O4'	2.18	0.43
2:51:3987:A:H4'	7:B1:18:PRO:HD2	2.00	0.43
2:51:4206:C:H2'	2:51:4207:G:O4'	2.18	0.43
4:81:4:U:OP2	33:P1:62:ARG:NH2	2.51	0.43
7:B1:86:VAL:HG22	7:B1:162:ILE:HD13	2.01	0.43
7:B1:173:HIS:CE1	7:B1:342:LYS:HB2	2.54	0.43
12:D2:39:VAL:HG12	12:D2:48:ILE:HD12	2.00	0.43
34:P2:56:LEU:HD11	34:P2:78:THR:HG21	2.01	0.43
46:V2:62:MET:HE2	46:V2:62:MET:HA	2.00	0.43
55:a1:36:GLY:HA3	55:a1:40:HIS:CE1	2.53	0.43
1:22:103:A:N6	1:22:402:C:H5'	2.33	0.43
2:51:82:C:H2'	2:51:83:C:O4'	2.19	0.43
2:51:262:G:H2'	2:51:263:G:H8	1.83	0.43
2:51:832:C:H2'	2:51:833:C:C6	2.53	0.43
2:51:1189:U:OP2	7:B1:243:LYS:HE2	2.18	0.43
2:51:3610:C:O3'	75:o1:37:GLY:HA3	2.18	0.43
2:51:3714:U:O2'	2:51:3718:U:OP1	2.32	0.43
15:F1:182:ILE:HG23	15:F1:187:ASP:HB3	2.00	0.43
16:F2:155:CYS:SG	16:F2:156:THR:N	2.92	0.43
17:G1:99:ALA:HB1	17:G1:136:LEU:HD11	1.99	0.43
18:G2:64:LYS:HE3	18:G2:82:SER:H	1.84	0.43
55:a1:71:PRO:HG2	55:a1:108:TYR:HA	2.01	0.43
59:c1:47:ILE:HD12	59:c1:94:LEU:HD11	2.01	0.43
61:d1:28:HIS:CG	61:d1:80:TYR:HD1	2.37	0.43
1:22:112:U:O2'	1:22:114:G:O2'	2.21	0.43
1:22:860:U:H2'	1:22:861:G:C8	2.53	0.43
1:22:918:U:H2'	1:22:919:A:C8	2.54	0.43
1:22:1862:G:H2'	1:22:1863:A:H8	1.84	0.43
2:51:33:A:H3'	2:51:47:A:H61	1.84	0.43
2:51:507:G:H1	2:51:552:G:H1	1.67	0.43
2:51:612:G:H4'	9:C1:314:PHE:HE2	1.83	0.43
2:51:3870:G:O2'	2:51:3871:U:O5'	2.36	0.43
4:81:20:C:N4	4:81:21:U:O4	2.52	0.43
7:B1:220:ILE:HG13	7:B1:278:THR:HG23	2.01	0.43
11:D1:40:ASP:HB2	11:D1:43:LYS:HG2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:H1:47:LEU:HB3	19:H1:53:LYS:HE2	2.01	0.43
20:H2:60:ILE:HD11	20:H2:90:LYS:HD3	1.99	0.43
22:I2:66:SER:H	22:I2:188:TYR:HA	1.84	0.43
23:J1:24:ILE:HG21	23:J1:36:ALA:HB1	2.01	0.43
36:Q2:134:GLY:HA3	36:Q2:139:ALA:O	2.18	0.43
39:S1:74:LYS:O	39:S1:76:LYS:NZ	2.52	0.43
76:p1:22:LEU:O	76:p1:26:VAL:HG23	2.18	0.43
1:22:39:A:OP2	24:J2:5:LYS:NZ	2.51	0.43
1:22:993:G:H21	1:22:1168:G:H4'	1.84	0.43
1:22:1026:A:N1	1:22:1119:A:O2'	2.51	0.43
1:22:1166:C:H2'	1:22:1167:C:C6	2.54	0.43
1:22:1397:G:H5''	1:22:1558:C:H41	1.84	0.43
1:22:1813:G:H1	1:22:1856:C:H42	1.67	0.43
2:51:259:G:H2'	2:51:260:C:C6	2.54	0.43
2:51:1143:G:H2'	2:51:1144:C:C6	2.54	0.43
2:51:1478:G:H2'	2:51:1479:A:O4'	2.18	0.43
2:51:2098:G:H4'	37:R1:117:ARG:HH11	1.83	0.43
2:51:2273:G:OP1	7:B1:248:LEU:N	2.51	0.43
4:81:71:A:OP2	51:Y1:51:LYS:HB2	2.19	0.43
5:A1:20:VAL:HG12	5:A1:23:ARG:HD2	1.99	0.43
8:B2:52:THR:HG23	8:B2:57:ILE:HA	2.01	0.43
15:F1:206:LEU:HD13	15:F1:209:PHE:HZ	1.83	0.43
24:J2:32:ILE:HD13	24:J2:37:LEU:HB2	2.01	0.43
25:K2:37:ASP:N	25:K2:37:ASP:OD1	2.52	0.43
34:P2:81:ARG:NH2	34:P2:117:GLY:O	2.52	0.43
48:W2:36:ARG:HB2	48:W2:110:ILE:HD12	2.01	0.43
67:g2:83:TRP:HA	67:g2:107:ASP:HB3	2.01	0.43
1:22:400:U:H2'	1:22:401:G:C8	2.54	0.42
1:22:1012:C:H2'	1:22:1013:G:C8	2.54	0.42
2:51:582:G:O2'	2:51:583:C:H5'	2.19	0.42
2:51:750:G:H22	2:51:882:G:H1	1.67	0.42
2:51:1071:C:H2'	2:51:1072:G:C8	2.54	0.42
2:51:1542:U:O2	2:51:1544:G:N1	2.52	0.42
2:51:1730:C:O2'	9:C1:45:ARG:NH1	2.49	0.42
2:51:3476:U:OP2	41:T1:4:THR:OG1	2.25	0.42
2:51:3725:U:H1'	7:B1:252:ALA:HB3	2.01	0.42
2:51:4257:G:N2	61:d1:116:GLN:OE1	2.46	0.42
7:B1:108:GLU:HB2	7:B1:137:TRP:CG	2.54	0.42
7:B1:168:MET:HG3	7:B1:177:LYS:O	2.19	0.42
12:D2:23:GLU:HG2	25:K2:64:TRP:NE1	2.30	0.42
14:E2:34:GLY:HA3	14:E2:83:PRO:HG2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:G2:152:ASP:OD2	18:G2:154:ARG:HG3	2.20	0.42
27:L2:53:ASP:OD1	27:L2:54:GLY:N	2.51	0.42
34:P2:21:ASP:OD1	34:P2:21:ASP:N	2.52	0.42
40:S2:71:MET:HB3	40:S2:99:LEU:HD11	2.01	0.42
1:22:544:C:H2'	1:22:545:G:C8	2.54	0.42
1:22:1262:A:H2'	1:22:1263:A:C8	2.54	0.42
1:22:1278:G:H1	1:22:1753:C:H42	1.68	0.42
1:22:1506:U:O2	1:22:1508:C:N4	2.53	0.42
1:22:1681:U:O4	34:P2:40:ARG:NH2	2.53	0.42
2:51:623:G:C1'	2:51:709:G:H22	2.31	0.42
2:51:843:U:H2'	2:51:844:G:C8	2.52	0.42
2:51:930:G:H2'	2:51:3136:A:N7	2.34	0.42
2:51:1229:A:O2'	5:A1:203:ALA:O	2.36	0.42
2:51:2873:U:H2'	2:51:2874:G:C8	2.55	0.42
4:81:121:C:H2'	4:81:122:G:C8	2.54	0.42
4:81:143:C:H2'	4:81:144:U:C6	2.54	0.42
11:D1:37:VAL:HB	11:D1:67:ALA:HB2	2.01	0.42
19:H1:114:ILE:HD11	19:H1:161:ILE:HG23	1.99	0.42
19:H1:128:MET:SD	19:H1:157:SER:HB3	2.59	0.42
36:Q2:93:VAL:HG11	36:Q2:109:LYS:HE3	2.02	0.42
42:T2:63:ARG:NH2	42:T2:63:ARG:HB3	2.34	0.42
68:h1:4:ILE:O	68:h1:56:ARG:NE	2.53	0.42
1:22:557:U:H2'	1:22:558:A:H8	1.84	0.42
2:51:99:A:H4'	29:N1:181:HIS:CE1	2.54	0.42
2:51:1438:G:OP1	57:b1:4:SER:HB2	2.19	0.42
2:51:1638:G:N3	31:O1:132:LYS:NZ	2.67	0.42
2:51:1700:U:OP1	77:r1:36:ARG:NH1	2.52	0.42
2:51:1824:G:H1	2:51:2260:G:H1	1.68	0.42
2:51:3707:U:H2'	2:51:3708:G:O4'	2.19	0.42
5:A1:242:ARG:NH1	5:A1:246:LEU:HB2	2.34	0.42
11:D1:106:ALA:HB2	11:D1:166:ALA:HA	1.99	0.42
19:H1:105:ILE:HD11	19:H1:144:LEU:HD11	2.02	0.42
34:P2:111:MET:HG2	40:S2:117:ILE:HB	2.00	0.42
37:R1:81:ARG:HG2	37:R1:88:ARG:CZ	2.49	0.42
43:U1:62:LYS:HG2	43:U1:67:ALA:HB2	2.01	0.42
61:d1:62:ILE:HG23	61:d1:66:LEU:HD23	1.99	0.42
1:22:678:C:H5'	1:22:679:C:OP2	2.18	0.42
1:22:1019:A:N1	1:22:1032:U:O2'	2.49	0.42
1:22:1223:U:OP1	48:W2:71:LYS:NZ	2.49	0.42
1:22:1473:G:N1	1:22:1474:U:O4	2.53	0.42
1:22:1742:U:H2'	1:22:1743:A:C8	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:22:1808:G:H21	1:22:1861:A:H62	1.66	0.42
2:51:1358:C:O2'	2:51:1359:C:OP1	2.31	0.42
2:51:2022:A:OP1	2:51:2202:U:O2'	2.30	0.42
2:51:3997:A:H5'	7:B1:130:PHE:H	1.84	0.42
2:51:4069:G:H3'	28:M1:91:TRP:CD2	2.54	0.42
2:51:4232:U:H2'	2:51:4233:G:C8	2.55	0.42
9:C1:124:MET:HA	9:C1:124:MET:HE3	2.01	0.42
14:E2:186:GLY:C	14:E2:188:ASN:H	2.28	0.42
20:H2:9:VAL:HB	20:H2:44:HIS:CD2	2.55	0.42
32:O2:33:ILE:HD13	32:O2:95:ILE:HG23	2.00	0.42
33:P1:117:ILE:HD12	33:P1:148:MET:HE3	2.02	0.42
42:T2:130:ARG:HD3	42:T2:134:ARG:HH21	1.84	0.42
43:U1:94:LYS:HG2	43:U1:124:TYR:CE2	2.54	0.42
47:W1:8:PHE:CD1	47:W1:46:PRO:HG3	2.54	0.42
1:22:1734:G:H4'	44:U2:62:ARG:HH12	1.85	0.42
2:51:153:G:OP2	29:N1:4:TYR:OH	2.25	0.42
2:51:978:C:O2'	2:51:979:G:C8	2.71	0.42
2:51:1227:G:H2'	2:51:1229:A:N7	2.34	0.42
2:51:1301:A:H3'	2:51:1302:G:H8	1.85	0.42
2:51:1410:C:H2'	2:51:1411:G:C8	2.54	0.42
2:51:1643:G:N2	39:S1:115:ALA:HB2	2.33	0.42
2:51:3548:A:N3	2:51:3548:A:H2'	2.35	0.42
2:51:4113:A:N3	2:51:4113:A:H2'	2.35	0.42
16:F2:18:LYS:HE2	36:Q2:57:LEU:HB3	2.02	0.42
17:G1:51:LEU:O	17:G1:55:VAL:HG23	2.19	0.42
22:I2:190:LEU:HD23	22:I2:195:LEU:HA	2.02	0.42
28:M1:32:ASP:OD1	28:M1:33:GLN:N	2.44	0.42
39:S1:159:LEU:HD22	39:S1:172:PRO:HG3	2.01	0.42
42:T2:42:LYS:HE2	42:T2:42:LYS:HB3	1.89	0.42
63:e1:76:LYS:HD2	63:e1:98:GLU:OE1	2.19	0.42
67:g2:170:TRP:HA	67:g2:194:TYR:HB2	2.01	0.42
71:k1:13:LEU:HD23	71:k1:16:ARG:HH21	1.84	0.42
1:22:106:C:O2'	1:22:456:G:N3	2.44	0.42
1:22:568:A:HO2'	24:J2:131:ARG:HH11	1.67	0.42
1:22:1758:G:H21	1:22:1904:A:H8	1.68	0.42
1:22:1922:C:OP2	74:n1:5:TRP:HD1	2.02	0.42
2:51:210:U:O2'	2:51:211:G:H2'	2.19	0.42
2:51:1375:A:H5''	2:51:3482:A:N6	2.34	0.42
2:51:1781:A:C4	63:e1:31:ILE:HD11	2.55	0.42
2:51:3540:G:OP2	2:51:3540:G:N2	2.31	0.42
4:81:47:A:H5''	68:h1:51:ARG:HH12	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:L1:46:ILE:HD11	26:L1:51:VAL:HA	2.01	0.42
28:M1:28:VAL:HG12	28:M1:67:SER:H	1.84	0.42
31:O1:39:ARG:HD2	31:O1:110:ILE:HD11	2.00	0.42
35:Q1:159:PRO:HB2	35:Q1:160:HIS:HD2	1.84	0.42
42:T2:63:ARG:HH22	42:T2:64:HIS:CD2	2.38	0.42
46:V2:59:ILE:HG23	46:V2:64:GLU:HB2	2.01	0.42
64:e2:88:LYS:NZ	64:e2:92:GLN:HG3	2.34	0.42
1:22:1715:A:OP1	36:Q2:137:ALA:N	2.52	0.42
1:22:1726:A:OP2	62:d2:32:ARG:NH1	2.33	0.42
2:51:183:C:N4	2:51:256:C:H42	2.18	0.42
2:51:258:C:H2'	2:51:259:G:H8	1.85	0.42
2:51:1449:U:H2'	2:51:1450:A:O4'	2.19	0.42
2:51:1510:U:H3	2:51:1639:G:H22	1.66	0.42
2:51:3192:U:H2'	2:51:3193:G:C8	2.54	0.42
2:51:3507:A:H2'	2:51:3508:G:C8	2.55	0.42
4:81:142:C:H2'	4:81:143:C:C6	2.55	0.42
12:D2:62:LYS:O	12:D2:67:ARG:NH2	2.45	0.42
14:E2:31:PRO:HA	14:E2:81:THR:HB	2.00	0.42
20:H2:76:GLN:NE2	20:H2:94:PHE:HB2	2.34	0.42
28:M1:5:ARG:NE	28:M1:59:ASP:OD1	2.40	0.42
38:R2:44:LYS:HG3	38:R2:47:ARG:HH12	1.83	0.42
57:b1:36:ASP:HB3	57:b1:39:PHE:HB3	2.00	0.42
65:f1:46:ARG:HD3	65:f1:106:TYR:CE2	2.55	0.42
72:l1:24:PRO:HD2	72:l1:27:ILE:HG13	2.00	0.42
75:o1:22:LYS:HG3	75:o1:73:VAL:HG12	2.02	0.42
1:22:723:G:N2	1:22:1091:A:OP2	2.53	0.42
1:22:1404:C:OP1	62:d2:44:ARG:NH2	2.53	0.42
1:22:1868:C:H2'	1:22:1869:G:O4'	2.20	0.42
2:51:339:U:OP1	26:L1:35:ARG:NH2	2.51	0.42
2:51:377:G:OP2	70:j1:52:LYS:HE2	2.19	0.42
2:51:937:G:O2'	2:51:1783:A:OP1	2.35	0.42
2:51:1279:G:OP2	2:51:1436:G:N1	2.46	0.42
2:51:1954:C:H2'	2:51:1955:G:H8	1.85	0.42
2:51:2977:A:H2'	2:51:2978:A:C8	2.55	0.42
8:B2:185:VAL:O	8:B2:189:ILE:HG12	2.20	0.42
9:C1:109:ARG:HG2	9:C1:111:TRP:CE2	2.54	0.42
18:G2:50:VAL:HG21	18:G2:111:LEU:HD13	2.02	0.42
52:Y2:11:LYS:HE3	52:Y2:24:ILE:HG13	2.02	0.42
67:g2:133:ASN:HD21	67:g2:135:LEU:HG	1.84	0.42
74:n1:15:ARG:HA	74:n1:18:ARG:HE	1.85	0.42
1:22:1517:A:H5''	38:R2:48:ASN:ND2	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:22:1604:C:H4'	42:T2:48:PRO:HA	2.01	0.42
1:22:1808:G:N2	1:22:1861:A:H62	2.18	0.42
2:51:35:U:O4	2:51:46:U:O2'	2.27	0.42
2:51:419:G:H1'	4:81:15:G:H22	1.85	0.42
2:51:488:G:H2'	2:51:488:G:N3	2.34	0.42
2:51:624:G:H4'	15:F1:67:ILE:HD13	2.02	0.42
2:51:968:G:HO2'	2:51:969:A:H8	1.67	0.42
2:51:1072:G:H3'	2:51:1073:C:H5''	2.01	0.42
2:51:1732:G:H4'	9:C1:242:PRO:HB2	2.02	0.42
2:51:2021:A:H2'	2:51:2022:A:C4	2.55	0.42
2:51:2965:G:H2'	2:51:2966:C:C6	2.54	0.42
4:81:61:A:OP1	68:h1:52:LYS:NZ	2.44	0.42
4:81:100:U:O4	70:j1:65:ARG:NH1	2.51	0.42
8:B2:132:GLY:HA3	8:B2:221:PRO:HB3	2.01	0.42
9:C1:303:ARG:HH11	35:Q1:40:ASP:HB2	1.82	0.42
12:D2:38:GLU:HB3	12:D2:49:ILE:HD11	2.01	0.42
13:E1:19:GLU:HA	13:E1:25:GLY:HA2	2.00	0.42
14:E2:36:HIS:CG	14:E2:85:GLY:HA3	2.54	0.42
14:E2:62:LYS:HG2	14:E2:80:ILE:HD13	2.02	0.42
18:G2:50:VAL:HG12	18:G2:113:ILE:HA	2.02	0.42
26:L1:77:THR:HG22	26:L1:79:GLU:H	1.84	0.42
31:O1:57:LEU:HD23	31:O1:60:LEU:HD12	2.01	0.42
31:O1:111:PRO:HB2	31:O1:113:PRO:HD2	2.02	0.42
34:P2:121:ILE:HD12	34:P2:121:ILE:H	1.85	0.42
40:S2:10:GLN:HB2	40:S2:57:GLY:HA2	2.01	0.42
59:c1:78:ASN:HB2	59:c1:90:ARG:HB3	2.02	0.42
61:d1:40:ALA:HB3	61:d1:41:PRO:HD3	2.02	0.42
1:22:1089:U:OP1	1:22:1154:C:O2'	2.37	0.42
1:22:1128:C:H5''	32:O2:149:ARG:HG3	2.01	0.42
1:22:1297:C:H2'	1:22:1298:C:C6	2.55	0.42
1:22:1604:C:H5'	42:T2:46:LEU:HD12	2.02	0.42
1:22:1735:C:H2'	1:22:1736:G:C8	2.55	0.42
1:22:1878:C:H2'	1:22:1879:G:C8	2.55	0.42
2:51:19:G:P	68:h1:93:ARG:HE	2.43	0.42
2:51:130:C:H42	2:51:140:G:H1	1.68	0.42
2:51:721:C:O2'	2:51:722:G:H5'	2.19	0.42
2:51:1977:A:O2'	2:51:1978:G:OP1	2.35	0.42
2:51:3121:A:H2'	2:51:3122:A:C8	2.55	0.42
3:71:48:G:OP2	11:D1:94:ASN:HB3	2.20	0.42
46:V2:37:ALA:HB1	46:V2:46:PHE:CD1	2.55	0.42
53:Z1:51:ARG:HB2	53:Z1:65:ARG:HB3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:22:25:A:O2'	1:22:26:U:H5''	2.20	0.41
1:22:1242:G:OP1	74:n1:21:ARG:NH1	2.53	0.41
1:22:1540:G:O2'	1:22:1541:A:O5'	2.35	0.41
2:51:351:A:OP1	9:C1:50:GLN:N	2.48	0.41
2:51:3476:U:H2'	2:51:3477:G:C8	2.54	0.41
4:81:25:C:O2'	9:C1:53:ALA:O	2.28	0.41
4:81:32:G:H4'	4:81:33:U:C6	2.55	0.41
7:B1:291:TYR:HB3	7:B1:298:LEU:HD11	2.01	0.41
18:G2:64:LYS:HB2	18:G2:97:VAL:HG11	2.01	0.41
29:N1:103:GLU:HB2	29:N1:115:VAL:HG11	2.01	0.41
45:V1:40:ILE:HG12	45:V1:62:MET:O	2.20	0.41
52:Y2:57:VAL:HB	52:Y2:60:PHE:CE2	2.55	0.41
67:g2:256:ILE:HD13	67:g2:289:LEU:HD13	2.01	0.41
1:22:511:A:H5''	1:22:512:G:C4	2.55	0.41
1:22:608:U:H3	1:22:633:A:N6	2.19	0.41
1:22:1068:U:OP1	8:B2:162:ARG:NE	2.53	0.41
1:22:1320:A:H4'	1:22:1321:C:OP2	2.20	0.41
1:22:1653:A:H2'	1:22:1654:A:C8	2.55	0.41
1:22:1727:U:O4	1:22:1728:C:N4	2.53	0.41
2:51:36:U:H5''	2:51:1250:U:O4'	2.20	0.41
2:51:256:C:H2'	2:51:257:C:C6	2.54	0.41
2:51:1100:G:O6	35:Q1:90:VAL:HG22	2.20	0.41
2:51:1667:C:H2'	15:F1:161:LYS:HD2	2.01	0.41
2:51:1873:G:H5'	2:51:2213:G:OP2	2.20	0.41
2:51:2212:G:H5''	2:51:2213:G:H5'	2.02	0.41
2:51:3119:G:OP2	33:P1:25:HIS:NE2	2.42	0.41
2:51:3139:G:O2'	2:51:3141:G:OP2	2.31	0.41
2:51:3181:U:OP1	5:A1:221:LYS:NZ	2.49	0.41
2:51:3773:C:H2'	2:51:3774:C:H6	1.85	0.41
3:71:47:G:H2'	3:71:48:G:O4'	2.20	0.41
8:B2:34:LYS:HE2	8:B2:42:ARG:HH21	1.84	0.41
8:B2:131:ASP:HB3	8:B2:133:TYR:CD2	2.55	0.41
8:B2:131:ASP:OD1	8:B2:132:GLY:N	2.46	0.41
9:C1:43:ASN:HB3	9:C1:113:ARG:HB2	2.02	0.41
12:D2:42:THR:HB	12:D2:45:ARG:O	2.20	0.41
14:E2:130:LEU:O	14:E2:138:HIS:N	2.53	0.41
33:P1:54:LYS:HA	33:P1:83:TRP:CD1	2.54	0.41
55:a1:121:PRO:HA	55:a1:141:GLY:O	2.20	0.41
66:g1:69:LYS:HG2	66:g1:73:HIS:NE2	2.36	0.41
1:22:992:G:H2'	1:22:993:G:C8	2.55	0.41
1:22:1008:A:H2'	1:22:1009:U:C6	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:22:1880:U:H2'	1:22:1881:U:C6	2.54	0.41
2:51:109:G:H5'	26:L1:92:ARG:NH2	2.34	0.41
2:51:786:G:H1	2:51:873:C:H42	1.68	0.41
2:51:2868:A:H2'	2:51:2869:G:H8	1.85	0.41
6:A2:206:ASP:O	6:A2:210:ILE:HG13	2.20	0.41
10:C2:180:ARG:HE	10:C2:182:ILE:HD11	1.84	0.41
14:E2:99:PHE:HA	14:E2:112:HIS:O	2.20	0.41
19:H1:104:VAL:HG13	19:H1:113:GLU:HB2	2.02	0.41
20:H2:144:ILE:HB	48:W2:52:ILE:HB	2.01	0.41
24:J2:176:LYS:HG2	24:J2:180:LYS:HE2	2.02	0.41
30:N2:93:LYS:HE2	30:N2:150:VAL:HG13	2.03	0.41
33:P1:14:SER:O	33:P1:105:LYS:NZ	2.49	0.41
52:Y2:7:VAL:HG12	52:Y2:27:VAL:HB	2.02	0.41
72:I1:15:LYS:HE3	72:I1:19:GLN:NE2	2.36	0.41
1:22:676:U:O2	1:22:676:U:H2'	2.20	0.41
1:22:1216:G:O2'	1:22:1217:A:H3'	2.20	0.41
2:51:614:C:H2'	2:51:615:U:C6	2.56	0.41
2:51:938:G:OP1	2:51:1784:U:O2'	2.35	0.41
2:51:959:C:H2'	2:51:960:G:C8	2.55	0.41
2:51:1231:G:H5'	2:51:1232:A:OP1	2.20	0.41
2:51:2943:C:H2'	5:A1:132:ASN:HD21	1.85	0.41
2:51:3108:U:H2'	2:51:3109:G:H8	1.85	0.41
2:51:3786:A:H5''	2:51:3788:G:H4'	2.02	0.41
4:81:93:U:H2'	4:81:94:C:O4'	2.21	0.41
6:A2:52:LYS:HD2	38:R2:109:LEU:HD22	2.02	0.41
14:E2:106:LYS:HE3	14:E2:106:LYS:HB2	1.86	0.41
15:F1:224:HIS:HB3	15:F1:227:GLU:HG2	2.03	0.41
17:G1:87:LEU:N	17:G1:183:ILE:O	2.50	0.41
18:G2:181:THR:H	18:G2:184:VAL:HG12	1.85	0.41
24:J2:124:HIS:CD2	64:e2:112:ARG:HD2	2.56	0.41
24:J2:162:ARG:NH1	52:Y2:65:GLY:O	2.54	0.41
26:L1:80:GLU:HG2	26:L1:110:LEU:HD12	2.01	0.41
32:O2:40:THR:HG21	32:O2:111:GLY:HA3	2.03	0.41
34:P2:59:ARG:HH11	34:P2:76:VAL:HG12	1.84	0.41
52:Y2:4:THR:OG1	52:Y2:5:VAL:N	2.51	0.41
67:g2:249:CYS:HB2	67:g2:289:LEU:HD11	2.03	0.41
1:22:888:C:H41	52:Y2:10:ARG:HA	1.86	0.41
2:51:507:G:H22	2:51:552:G:H22	1.68	0.41
2:51:1121:A:N3	2:51:3657:C:O2'	2.52	0.41
2:51:1202:G:H2'	2:51:1203:G:C8	2.55	0.41
2:51:1226:C:H42	5:A1:3:ARG:HH11	1.68	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:51:1440:C:H2'	2:51:1441:A:C8	2.56	0.41
2:51:1510:U:OP1	2:51:1532:U:O2'	2.30	0.41
2:51:1955:G:H5'	2:51:2075:G:H1'	2.03	0.41
2:51:2859:A:H2'	2:51:2860:G:C8	2.56	0.41
2:51:3573:G:H22	41:T1:87:LYS:CD	2.34	0.41
4:81:143:C:H5'	29:N1:113:LEU:HD11	2.02	0.41
6:A2:187:GLY:HA2	46:V2:45:ARG:HE	1.85	0.41
13:E1:153:THR:HB	13:E1:163:LEU:HD23	2.01	0.41
14:E2:97:GLU:HA	14:E2:114:ILE:HG12	2.03	0.41
36:Q2:76:GLY:H	36:Q2:79:ALA:HB3	1.85	0.41
40:S2:25:LYS:HA	40:S2:55:ARG:HA	2.03	0.41
40:S2:121:ARG:O	40:S2:125:HIS:ND1	2.47	0.41
43:U1:105:LEU:HD13	43:U1:114:LEU:HB2	2.01	0.41
51:Y1:38:LEU:HD22	51:Y1:42:TYR:HE2	1.85	0.41
52:Y2:61:LYS:HE3	52:Y2:61:LYS:HB3	1.85	0.41
56:a2:23:CYS:HB3	56:a2:28:ARG:H	1.85	0.41
63:e1:88:LEU:HB2	63:e1:120:ILE:HD13	2.03	0.41
66:g1:56:ILE:HG23	66:g1:72:LYS:HA	2.01	0.41
1:22:426:C:H5''	22:I2:31:ARG:NH1	2.36	0.41
1:22:1033:U:O5'	1:22:1034:G:H5'	2.19	0.41
1:22:1611:A:H5'	36:Q2:18:THR:HG21	2.03	0.41
1:22:1715:A:H2'	1:22:1716:A:O4'	2.21	0.41
2:51:1092:U:H2'	2:51:1093:G:C8	2.52	0.41
2:51:1836:G:O2'	66:g1:10:ARG:O	2.38	0.41
2:51:3052:G:O6	2:51:3067:A:N6	2.53	0.41
2:51:3456:U:H2'	2:51:3457:U:C6	2.56	0.41
2:51:3542:A:H2'	2:51:3543:G:H8	1.86	0.41
3:71:5:A:O3'	11:D1:54:ARG:HG3	2.20	0.41
5:A1:206:PRO:HG3	5:A1:213:GLY:HA3	2.03	0.41
8:B2:223:PHE:HZ	8:B2:228:LEU:HD13	1.85	0.41
11:D1:153:THR:HB	11:D1:160:PHE:HZ	1.85	0.41
12:D2:63:GLY:O	12:D2:67:ARG:NH2	2.53	0.41
18:G2:163:THR:HA	18:G2:169:PRO:HB3	2.02	0.41
34:P2:77:LYS:HB2	34:P2:102:PHE:CD1	2.55	0.41
40:S2:86:ARG:HD2	40:S2:86:ARG:HA	1.80	0.41
1:22:663:G:H4'	50:X2:88:ASP:HB2	2.03	0.41
1:22:1077:C:H1'	1:22:1168:G:H1'	2.03	0.41
2:51:419:G:H1'	4:81:15:G:N2	2.36	0.41
2:51:1191:A:H5''	2:51:2274:C:H5''	2.02	0.41
2:51:2173:C:H5''	5:A1:184:ARG:HH12	1.86	0.41
2:51:2246:G:H4'	37:R1:82:LYS:HG3	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:51:2870:A:H2'	2:51:2871:A:H8	1.85	0.41
2:51:3613:C:H2'	2:51:3614:C:C6	2.56	0.41
2:51:4267:U:H2'	2:51:4268:U:C6	2.56	0.41
5:A1:117:GLU:HG2	5:A1:124:GLY:N	2.35	0.41
7:B1:165:HIS:HB2	7:B1:178:SER:HB3	2.03	0.41
7:B1:258:HIS:HA	7:B1:259:PRO:C	2.45	0.41
11:D1:51:MET:N	11:D1:145:TYR:O	2.35	0.41
14:E2:161:ARG:HG3	14:E2:170:THR:HB	2.03	0.41
28:M1:12:VAL:O	28:M1:58:THR:OG1	2.28	0.41
34:P2:108:LYS:HB3	34:P2:111:MET:HG3	2.03	0.41
37:R1:133:LYS:N	37:R1:137:ILE:HD11	2.29	0.41
46:V2:40:ASP:OD1	46:V2:47:ASN:ND2	2.49	0.41
48:W2:55:ASP:OD1	48:W2:56:HIS:N	2.53	0.41
49:X1:81:THR:HG22	49:X1:154:ILE:HG23	2.02	0.41
56:a2:3:LYS:HE3	56:a2:8:ASN:HD21	1.85	0.41
63:e1:35:TRP:CE2	63:e1:56:PRO:HD2	2.55	0.41
63:e1:62:SER:HB2	63:e1:67:LYS:HG2	2.03	0.41
67:g2:266:ILE:HD11	67:g2:269:GLU:HG3	2.02	0.41
1:22:84:A:H1'	52:Y2:120:ILE:HG22	2.02	0.41
1:22:490:G:N2	1:22:493:A:OP2	2.52	0.41
1:22:537:C:H3'	52:Y2:104:ARG:HD2	2.03	0.41
1:22:695:U:H2'	1:22:696:G:C8	2.55	0.41
1:22:877:U:H5	24:J2:143:ASN:HB3	1.84	0.41
1:22:909:U:H2'	1:22:910:A:H8	1.86	0.41
1:22:1021:A:H3'	1:22:1022:G:H21	1.85	0.41
1:22:1161:G:H4'	6:A2:32:PHE:CG	2.56	0.41
1:22:1914:U:H2'	1:22:1915:A:C8	2.56	0.41
2:51:409:A:O2'	2:51:412:A:OP1	2.25	0.41
2:51:482:G:OP1	77:r1:68:ARG:N	2.43	0.41
2:51:507:G:N2	2:51:552:G:H22	2.19	0.41
2:51:600:A:H3'	2:51:601:G:N2	2.35	0.41
2:51:821:C:H2'	2:51:822:U:C6	2.56	0.41
2:51:898:C:H2'	2:51:899:G:H8	1.86	0.41
2:51:951:A:OP1	29:N1:204:ARG:NE	2.45	0.41
2:51:1504:C:H1'	39:S1:160:ARG:HB3	2.03	0.41
2:51:1637:U:OP2	31:O1:46:SER:OG	2.35	0.41
2:51:1955:G:H4'	66:g1:26:PRO:HD2	2.03	0.41
2:51:3183:A:H2'	2:51:3184:C:C6	2.56	0.41
4:81:3:C:H5'	33:P1:61:ARG:HB3	2.03	0.41
4:81:64:A:H5''	68:h1:6:ALA:HB2	2.03	0.41
7:B1:57:VAL:HB	7:B1:367:PHE:HB3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:D2:115:VAL:HG22	12:D2:143:ARG:NH1	2.36	0.41
33:P1:128:ARG:HD2	33:P1:136:ILE:HG21	2.03	0.41
34:P2:124:LYS:HB2	34:P2:125:PRO:HD3	2.03	0.41
35:Q1:23:ILE:HD12	77:r1:9:MET:HB3	2.03	0.41
50:X2:46:HIS:HB3	50:X2:101:LEU:HD11	2.03	0.41
54:Z2:99:LEU:HD21	54:Z2:102:LYS:HB2	2.02	0.41
76:p1:6:LYS:HG2	76:p1:7:LYS:HG3	2.02	0.41
1:22:338:G:H22	27:L2:69:ILE:HB	1.86	0.41
1:22:385:G:H2'	1:22:386:U:H6	1.85	0.41
1:22:607:A:H5''	24:J2:164:PRO:HB2	2.02	0.41
1:22:705:G:O2'	1:22:708:G:O3'	2.38	0.41
1:22:989:G:H22	1:22:1081:U:H3	1.68	0.41
1:22:995:C:H2'	1:22:996:G:C8	2.56	0.41
1:22:1611:A:H2'	1:22:1612:C:C6	2.56	0.41
1:22:1654:A:N3	1:22:1718:C:O2'	2.41	0.41
2:51:18:C:H4'	29:N1:138:PHE:CD1	2.56	0.41
2:51:226:G:OP1	9:C1:222:ARG:HD2	2.21	0.41
2:51:446:G:H2'	2:51:447:A:C8	2.56	0.41
2:51:615:U:OP1	15:F1:215:ARG:NH1	2.50	0.41
2:51:647:G:H1'	2:51:680:A:C4	2.56	0.41
2:51:1136:U:H2'	2:51:1137:G:C8	2.56	0.41
2:51:1298:U:H4'	2:51:1299:C:H5'	2.03	0.41
2:51:1375:A:H5''	2:51:3482:A:H61	1.86	0.41
2:51:1645:C:H5'	39:S1:2:LYS:HE2	2.02	0.41
2:51:2072:U:H2'	2:51:2154:C:H5	1.85	0.41
2:51:3302:U:OP1	5:A1:123:ARG:NH2	2.49	0.41
2:51:3857:G:O2'	7:B1:14:LEU:O	2.25	0.41
2:51:3863:C:H2'	2:51:3864:C:C6	2.56	0.41
2:51:3915:C:P	37:R1:62:ARG:HH21	2.43	0.41
3:71:28:C:O2'	3:71:54:A:N1	2.53	0.41
4:81:7:U:H2'	4:81:8:A:C8	2.55	0.41
11:D1:119:TYR:CE1	11:D1:134:SER:HA	2.56	0.41
12:D2:119:CYS:O	12:D2:123:LEU:HG	2.20	0.41
15:F1:135:GLU:HG3	15:F1:232:GLY:HA2	2.03	0.41
15:F1:140:TRP:CE2	15:F1:233:ASN:HB2	2.56	0.41
16:F2:39:ILE:HG23	16:F2:68:ILE:HD13	2.03	0.41
16:F2:82:ASN:HA	16:F2:85:LYS:HD2	2.03	0.41
26:L1:179:PHE:N	55:a1:134:GLU:OE1	2.43	0.41
28:M1:24:LEU:HD11	28:M1:86:TRP:CD2	2.56	0.41
32:O2:85:CYS:O	32:O2:90:ILE:N	2.52	0.41
35:Q1:43:PHE:HZ	35:Q1:81:VAL:HG11	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:U1:112:ASP:OD1	43:U1:112:ASP:N	2.54	0.41
53:Z1:11:VAL:HG23	53:Z1:82:PRO:HA	2.02	0.41
56:a2:20:PRO:HA	56:a2:31:PRO:HA	2.03	0.41
61:d1:55:MET:O	61:d1:57:THR:N	2.48	0.41
66:g1:74:VAL:HG22	66:g1:79:GLY:HA3	2.02	0.41
67:g2:89:LEU:HD12	67:g2:101:PHE:HZ	1.86	0.41
67:g2:126:ASP:OD1	67:g2:127:LYS:N	2.54	0.41
67:g2:220:ASP:HB3	67:g2:223:GLU:O	2.21	0.41
71:k1:23:VAL:HB	71:k1:66:VAL:HG12	2.03	0.41
72:l1:21:ARG:HG2	72:l1:22:PRO:O	2.21	0.41
1:22:440:G:H5'	27:L2:82:LYS:HE3	2.03	0.41
1:22:1012:C:H2'	1:22:1013:G:H8	1.85	0.41
1:22:1335:C:HO2'	1:22:1336:G:H8	1.66	0.41
2:51:710:C:H41	9:C1:331:TYR:HD2	1.69	0.41
2:51:1057:C:H5''	35:Q1:144:LYS:CG	2.51	0.41
2:51:1254:U:OP2	55:a1:26:ARG:NH2	2.54	0.41
2:51:1331:G:H5'	21:I1:40:LYS:HE3	2.03	0.41
2:51:1464:C:H4'	2:51:1465:U:OP2	2.21	0.41
2:51:2176:U:H4'	2:51:2177:G:O4'	2.21	0.41
2:51:4077:C:OP2	28:M1:101:ARG:NH1	2.46	0.41
2:51:4207:G:O2'	2:51:4208:U:O5'	2.30	0.41
6:A2:21:ALA:HB1	6:A2:170:SER:HA	2.02	0.41
27:L2:80:LYS:HD2	27:L2:82:LYS:HE2	2.02	0.41
36:Q2:21:ALA:HB2	36:Q2:72:VAL:HG13	2.03	0.41
39:S1:99:ASP:OD1	39:S1:108:GLN:NE2	2.54	0.41
40:S2:6:PRO:HD3	54:Z2:49:LEU:HB3	2.03	0.41
52:Y2:15:ASN:ND2	52:Y2:20:ARG:HB2	2.33	0.41
61:d1:30:ARG:HD3	61:d1:46:GLU:HB3	2.02	0.41
67:g2:107:ASP:HB2	67:g2:125:ARG:HH11	1.86	0.41
71:k1:24:LYS:HB3	71:k1:69:LEU:HD11	2.03	0.41
72:l1:43:HIS:CE1	72:l1:45:ARG:HG3	2.56	0.41
1:22:338:G:N1	27:L2:69:ILE:O	2.38	0.40
1:22:642:U:N3	1:22:643:G:N7	2.69	0.40
1:22:974:G:H2'	1:22:975:C:O4'	2.22	0.40
1:22:1195:G:HO2'	1:22:1196:G:C5'	2.34	0.40
1:22:1415:G:H2'	1:22:1416:G:H8	1.86	0.40
1:22:1674:C:H5'	40:S2:131:VAL:HG12	2.02	0.40
2:51:305:C:OP2	29:N1:68:ARG:NH2	2.54	0.40
2:51:632:G:H1	2:51:693:C:H42	1.68	0.40
2:51:1053:C:H2'	35:Q1:75:ARG:HH21	1.86	0.40
2:51:1069:C:H2'	2:51:1070:U:C6	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:51:3177:A:H2'	2:51:3178:G:H8	1.87	0.40
2:51:3572:A:C2	55:a1:43:ILE:HG23	2.56	0.40
2:51:3580:U:H2'	2:51:3581:A:C8	2.55	0.40
2:51:3982:C:H2'	2:51:3983:G:H8	1.87	0.40
3:71:112:U:H2'	3:71:113:G:H8	1.86	0.40
10:C2:56:VAL:HG12	10:C2:61:ILE:HB	2.02	0.40
12:D2:68:GLU:HG3	25:K2:70:TYR:CG	2.55	0.40
19:H1:44:GLU:HB3	19:H1:58:ASP:HB2	2.04	0.40
19:H1:118:LEU:HD11	19:H1:167:VAL:HG22	2.03	0.40
26:L1:168:VAL:HA	55:a1:96:GLY:O	2.21	0.40
27:L2:60:LYS:HD3	27:L2:135:LEU:HB3	2.02	0.40
29:N1:193:LYS:O	29:N1:197:THR:OG1	2.29	0.40
33:P1:64:ASN:ND2	33:P1:80:GLN:OE1	2.45	0.40
48:W2:24:GLN:NE2	58:b2:7:LEU:H	2.19	0.40
50:X2:107:ARG:HB2	50:X2:110:HIS:HB3	2.03	0.40
52:Y2:57:VAL:HB	52:Y2:60:PHE:HE2	1.86	0.40
61:d1:51:ALA:HA	61:d1:86:LEU:HD21	2.04	0.40
67:g2:297:THR:HG22	67:g2:311:GLN:HG2	2.02	0.40
69:i1:26:HIS:O	69:i1:29:ARG:HG2	2.21	0.40
71:k1:25:ILE:HD13	71:k1:57:LYS:HE2	2.03	0.40
1:22:5:U:H2'	1:22:6:G:C8	2.53	0.40
1:22:605:G:O2'	1:22:606:A:O4'	2.39	0.40
1:22:658:U:O2'	64:e2:89:VAL:HG12	2.21	0.40
1:22:921:G:N3	48:W2:107:SER:OG	2.44	0.40
1:22:1378:C:H2'	1:22:1379:G:C8	2.56	0.40
1:22:1668:G:H4'	40:S2:38:ARG:HE	1.86	0.40
1:22:1785:U:O2'	2:51:3056:U:O2'	2.22	0.40
2:51:1843:U:H5	2:51:2218:A:N1	2.19	0.40
2:51:3870:G:HO2'	2:51:3871:U:P	2.45	0.40
2:51:3871:U:H2'	2:51:3872:A:C8	2.56	0.40
2:51:4207:G:H1'	2:51:4244:A:H61	1.86	0.40
4:81:66:U:H2'	4:81:67:G:C8	2.56	0.40
5:A1:196:TRP:HB3	5:A1:197:PRO:HD3	2.02	0.40
18:G2:41:LEU:HB2	18:G2:45:TRP:HB2	2.02	0.40
22:I2:191:GLU:O	22:I2:194:GLU:HG2	2.21	0.40
24:J2:66:LYS:HE2	24:J2:66:LYS:HB2	1.95	0.40
33:P1:50:ASP:HA	33:P1:53:VAL:HG22	2.02	0.40
45:V1:96:LEU:HD13	47:W1:20:ARG:HG3	2.03	0.40
50:X2:59:ALA:HB1	50:X2:114:ASP:HB2	2.04	0.40
50:X2:91:LEU:HD21	64:e2:83:LEU:HD23	2.03	0.40
1:22:16:G:H2'	1:22:17:C:C6	2.55	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:22:402:C:O2	1:22:402:C:H2'	2.22	0.40
1:22:724:U:H2'	1:22:725:A:C8	2.56	0.40
1:22:1422:C:O3'	10:C2:224:LYS:NZ	2.55	0.40
1:22:1482:C:H4'	42:T2:133:ASP:OD1	2.21	0.40
1:22:1916:G:H2'	1:22:1917:G:H8	1.85	0.40
2:51:258:C:H2'	2:51:259:G:C8	2.57	0.40
2:51:282:G:P	29:N1:44:ARG:HH12	2.45	0.40
2:51:1295:C:H3'	2:51:1296:G:C8	2.56	0.40
2:51:1740:G:H8	2:51:1740:G:OP2	2.03	0.40
2:51:1782:G:OP1	2:51:1785:C:N4	2.55	0.40
2:51:1795:G:N7	33:P1:27:LYS:HB2	2.36	0.40
2:51:2077:A:C2	71:k1:2:PRO:HD2	2.56	0.40
2:51:2194:G:O2'	2:51:2197:G:N1	2.52	0.40
2:51:3685:C:N4	2:51:3690:A:O2'	2.54	0.40
2:51:4160:C:O2	2:51:4161:G:N2	2.54	0.40
3:71:46:C:OP1	11:D1:158:LYS:N	2.42	0.40
6:A2:5:LEU:HD22	46:V2:41:ARG:HG3	2.03	0.40
17:G1:153:GLN:N	17:G1:204:PHE:O	2.43	0.40
17:G1:170:LEU:HD23	17:G1:170:LEU:HA	1.93	0.40
17:G1:177:MET:HE2	17:G1:177:MET:HA	2.04	0.40
21:I1:78:LYS:HG3	21:I1:79:THR:HG23	2.04	0.40
28:M1:3:PHE:CZ	39:S1:155:PRO:HB3	2.56	0.40
31:O1:187:VAL:O	31:O1:191:ILE:HG12	2.21	0.40
45:V1:42:VAL:HG13	45:V1:61:VAL:HG12	2.02	0.40
50:X2:6:GLY:O	50:X2:9:THR:OG1	2.36	0.40
67:g2:152:SER:H	67:g2:169:GLY:HA2	1.86	0.40
67:g2:257:LYS:HG2	67:g2:269:GLU:HG2	2.02	0.40
76:p1:89:LEU:HA	76:p1:92:GLN:HE21	1.86	0.40
1:22:1744:A:H2'	16:F2:60:ARG:HD3	2.02	0.40
2:51:376:G:OP2	70:j1:56:ARG:NH1	2.52	0.40
2:51:887:C:H2'	2:51:888:C:O4'	2.21	0.40
2:51:963:A:H62	2:51:1100:G:HO2'	1.63	0.40
2:51:3146:G:H5''	31:O1:84:ARG:HH21	1.86	0.40
2:51:3800:U:OP2	2:51:3822:G:N1	2.43	0.40
2:51:3893:G:H2'	2:51:3894:A:O4'	2.21	0.40
2:51:3978:A:N3	2:51:3979:U:H5'	2.36	0.40
3:71:9:C:OP2	3:71:10:C:N4	2.53	0.40
15:F1:206:LEU:HD23	15:F1:206:LEU:HA	1.95	0.40
17:G1:64:GLN:HA	17:G1:67:ARG:HG2	2.03	0.40
18:G2:2:LYS:HD3	18:G2:15:LEU:HD21	2.02	0.40
18:G2:5:ILE:HG23	18:G2:111:LEU:HB2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:H1:137:SER:HB2	19:H1:145:VAL:HG13	2.01	0.40
28:M1:41:PRO:HB3	28:M1:70:GLN:HG3	2.04	0.40
30:N2:84:LEU:H	30:N2:84:LEU:HD23	1.87	0.40
32:O2:130:GLU:OE1	32:O2:131:ASP:N	2.53	0.40
56:a2:19:GLN:CD	56:a2:19:GLN:H	2.29	0.40
67:g2:252:THR:HG21	67:g2:257:LYS:HG3	2.03	0.40
74:n1:7:LYS:HE2	74:n1:11:ARG:HE	1.87	0.40
1:22:421:U:H2'	1:22:422:A:C8	2.57	0.40
1:22:1049:G:H4'	1:22:1050:G:H5'	2.03	0.40
1:22:1089:U:H2'	1:22:1090:C:O4'	2.22	0.40
1:22:1204:G:N2	1:22:1204:G:OP1	2.54	0.40
1:22:1238:G:O2'	1:22:1254:G:O6	2.32	0.40
1:22:1628:G:H21	42:T2:102:ARG:HE	1.70	0.40
1:22:1692:C:H2'	1:22:1693:C:C6	2.57	0.40
2:51:28:C:H4'	2:51:61:A:H4'	2.03	0.40
2:51:289:U:O2'	29:N1:93:LYS:NZ	2.53	0.40
2:51:806:C:N4	2:51:807:G:O6	2.55	0.40
2:51:967:A:OP1	9:C1:116:ASN:HA	2.22	0.40
2:51:1192:C:O2'	2:51:1195:G:H1'	2.22	0.40
2:51:1979:C:H3'	2:51:1980:G:H4'	2.04	0.40
2:51:2021:A:H8	2:51:2022:A:C2	2.39	0.40
2:51:2241:A:H1'	66:g1:4:ARG:HD3	2.04	0.40
2:51:3115:U:H2'	2:51:3116:A:H8	1.86	0.40
2:51:4030:C:OP2	31:O1:173:LYS:NZ	2.43	0.40
4:81:66:U:H2'	4:81:67:G:H8	1.86	0.40
5:A1:24:LYS:HG3	5:A1:49:ILE:HD12	2.03	0.40
6:A2:166:LYS:HE3	6:A2:166:LYS:HB3	1.87	0.40
15:F1:114:GLN:NE2	15:F1:210:LYS:HD2	2.35	0.40
15:F1:234:ARG:HB2	15:F1:237:GLN:HB2	2.03	0.40
22:I2:172:LEU:HD23	22:I2:195:LEU:HD12	2.02	0.40
25:K2:52:LEU:HB3	25:K2:57:TYR:HB2	2.03	0.40
31:O1:29:VAL:HG23	31:O1:100:ALA:HB1	2.04	0.40
32:O2:30:VAL:HG23	32:O2:47:LEU:HA	2.04	0.40
45:V1:91:LYS:HD3	45:V1:91:LYS:HA	1.83	0.40
49:X1:118:ILE:HD13	49:X1:148:VAL:HG11	2.02	0.40
56:a2:37:LYS:HD2	56:a2:70:LYS:HE3	2.03	0.40
66:g1:60:ARG:HB2	66:g1:63:VAL:HG23	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	A1	243/257 (95%)	236 (97%)	7 (3%)	0	100	100
6	A2	208/308 (68%)	204 (98%)	4 (2%)	0	100	100
7	B1	392/403 (97%)	381 (97%)	11 (3%)	0	100	100
8	B2	211/267 (79%)	205 (97%)	6 (3%)	0	100	100
9	C1	346/375 (92%)	336 (97%)	10 (3%)	0	100	100
10	C2	211/280 (75%)	210 (100%)	1 (0%)	0	100	100
11	D1	286/296 (97%)	278 (97%)	8 (3%)	0	100	100
12	D2	219/245 (89%)	208 (95%)	11 (5%)	0	100	100
13	E1	198/265 (75%)	191 (96%)	7 (4%)	0	100	100
14	E2	259/263 (98%)	243 (94%)	16 (6%)	0	100	100
15	F1	220/246 (89%)	215 (98%)	5 (2%)	0	100	100
16	F2	179/204 (88%)	171 (96%)	8 (4%)	0	100	100
17	G1	203/266 (76%)	196 (97%)	7 (3%)	0	100	100
18	G2	228/249 (92%)	220 (96%)	8 (4%)	0	100	100
19	H1	188/192 (98%)	184 (98%)	4 (2%)	0	100	100
20	H2	184/194 (95%)	174 (95%)	10 (5%)	0	100	100
21	I1	209/215 (97%)	201 (96%)	8 (4%)	0	100	100
22	I2	204/208 (98%)	194 (95%)	10 (5%)	0	100	100
23	J1	165/178 (93%)	161 (98%)	4 (2%)	0	100	100
24	J2	178/194 (92%)	177 (99%)	1 (1%)	0	100	100
25	K2	91/166 (55%)	86 (94%)	5 (6%)	0	100	100
26	L1	195/211 (92%)	188 (96%)	7 (4%)	0	100	100
27	L2	129/159 (81%)	123 (95%)	6 (5%)	0	100	100
28	M1	132/139 (95%)	129 (98%)	3 (2%)	0	100	100
29	N1	200/204 (98%)	195 (98%)	5 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
30	N2	147/151 (97%)	145 (99%)	2 (1%)	0	100	100
31	O1	202/205 (98%)	199 (98%)	3 (2%)	0	100	100
32	O2	124/151 (82%)	120 (97%)	4 (3%)	0	100	100
33	P1	150/184 (82%)	143 (95%)	7 (5%)	0	100	100
34	P2	114/145 (79%)	111 (97%)	3 (3%)	0	100	100
35	Q1	178/182 (98%)	171 (96%)	7 (4%)	0	100	100
36	Q2	132/146 (90%)	127 (96%)	5 (4%)	0	100	100
37	R1	164/196 (84%)	163 (99%)	1 (1%)	0	100	100
38	R2	130/134 (97%)	127 (98%)	3 (2%)	0	100	100
39	S1	174/176 (99%)	170 (98%)	4 (2%)	0	100	100
40	S2	134/152 (88%)	127 (95%)	7 (5%)	0	100	100
41	T1	155/160 (97%)	151 (97%)	4 (3%)	0	100	100
42	T2	135/146 (92%)	127 (94%)	8 (6%)	0	100	100
43	U1	95/141 (67%)	90 (95%)	5 (5%)	0	100	100
44	U2	95/119 (80%)	93 (98%)	2 (2%)	0	100	100
45	V1	127/140 (91%)	125 (98%)	2 (2%)	0	100	100
46	V2	79/81 (98%)	78 (99%)	1 (1%)	0	100	100
47	W1	58/157 (37%)	57 (98%)	1 (2%)	0	100	100
48	W2	127/130 (98%)	121 (95%)	6 (5%)	0	100	100
49	X1	115/155 (74%)	112 (97%)	3 (3%)	0	100	100
50	X2	137/143 (96%)	132 (96%)	5 (4%)	0	100	100
51	Y1	120/145 (83%)	116 (97%)	4 (3%)	0	100	100
52	Y2	122/132 (92%)	115 (94%)	7 (6%)	0	100	100
53	Z1	133/136 (98%)	129 (97%)	4 (3%)	0	100	100
54	Z2	64/124 (52%)	61 (95%)	3 (5%)	0	100	100
55	a1	145/148 (98%)	135 (93%)	10 (7%)	0	100	100
56	a2	96/115 (84%)	95 (99%)	1 (1%)	0	100	100
57	b1	47/64 (73%)	44 (94%)	3 (6%)	0	100	100
58	b2	79/84 (94%)	75 (95%)	4 (5%)	0	100	100
59	c1	91/117 (78%)	90 (99%)	1 (1%)	0	100	100
60	c2	59/69 (86%)	58 (98%)	1 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
61	d1	105/123 (85%)	102 (97%)	3 (3%)	0	100	100
62	d2	53/56 (95%)	53 (100%)	0	0	100	100
63	e1	123/135 (91%)	121 (98%)	2 (2%)	0	100	100
64	e2	46/133 (35%)	45 (98%)	1 (2%)	0	100	100
65	f1	105/110 (96%)	104 (99%)	1 (1%)	0	100	100
66	g1	102/117 (87%)	99 (97%)	3 (3%)	0	100	100
67	g2	308/317 (97%)	291 (94%)	17 (6%)	0	100	100
68	h1	118/123 (96%)	114 (97%)	4 (3%)	0	100	100
69	i1	96/105 (91%)	94 (98%)	2 (2%)	0	100	100
70	j1	84/97 (87%)	84 (100%)	0	0	100	100
71	k1	67/70 (96%)	67 (100%)	0	0	100	100
72	l1	47/50 (94%)	46 (98%)	1 (2%)	0	100	100
73	m1	48/128 (38%)	48 (100%)	0	0	100	100
74	n1	22/25 (88%)	22 (100%)	0	0	100	100
75	o1	100/106 (94%)	96 (96%)	4 (4%)	0	100	100
76	p1	89/92 (97%)	88 (99%)	1 (1%)	0	100	100
77	r1	116/138 (84%)	114 (98%)	2 (2%)	0	100	100
All	All	10635/12237 (87%)	10301 (97%)	334 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	A1	189/200 (94%)	186 (98%)	3 (2%)	55	76
6	A2	179/250 (72%)	176 (98%)	3 (2%)	53	74
7	B1	346/353 (98%)	344 (99%)	2 (1%)	78	89
8	B2	194/231 (84%)	189 (97%)	5 (3%)	40	63

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	C1	291/313 (93%)	290 (100%)	1 (0%)	86	93
10	C2	179/220 (81%)	173 (97%)	6 (3%)	32	54
11	D1	244/249 (98%)	240 (98%)	4 (2%)	55	76
12	D2	184/204 (90%)	183 (100%)	1 (0%)	81	91
13	E1	182/234 (78%)	178 (98%)	4 (2%)	45	67
14	E2	226/229 (99%)	222 (98%)	4 (2%)	51	73
15	F1	189/210 (90%)	187 (99%)	2 (1%)	65	82
16	F2	154/170 (91%)	154 (100%)	0	100	100
17	G1	181/224 (81%)	179 (99%)	2 (1%)	65	82
18	G2	201/219 (92%)	198 (98%)	3 (2%)	57	77
19	H1	167/169 (99%)	165 (99%)	2 (1%)	63	81
20	H2	165/176 (94%)	165 (100%)	0	100	100
21	I1	180/182 (99%)	179 (99%)	1 (1%)	78	89
22	I2	176/181 (97%)	170 (97%)	6 (3%)	32	54
23	J1	141/150 (94%)	136 (96%)	5 (4%)	32	53
24	J2	160/168 (95%)	160 (100%)	0	100	100
25	K2	82/132 (62%)	80 (98%)	2 (2%)	43	65
26	L1	167/178 (94%)	165 (99%)	2 (1%)	63	81
27	L2	119/141 (84%)	116 (98%)	3 (2%)	42	64
28	M1	113/117 (97%)	113 (100%)	0	100	100
29	N1	171/172 (99%)	168 (98%)	3 (2%)	51	73
30	N2	129/130 (99%)	128 (99%)	1 (1%)	73	86
31	O1	175/176 (99%)	175 (100%)	0	100	100
32	O2	98/119 (82%)	96 (98%)	2 (2%)	48	70
33	P1	134/165 (81%)	133 (99%)	1 (1%)	76	88
34	P2	105/130 (81%)	104 (99%)	1 (1%)	68	84
35	Q1	158/160 (99%)	156 (99%)	2 (1%)	61	80
36	Q2	108/119 (91%)	105 (97%)	3 (3%)	38	60
37	R1	145/173 (84%)	143 (99%)	2 (1%)	59	79
38	R2	119/121 (98%)	116 (98%)	3 (2%)	42	64
39	S1	155/155 (100%)	155 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
40	S2	118/132 (89%)	116 (98%)	2 (2%)	53	74
41	T1	138/140 (99%)	135 (98%)	3 (2%)	45	67
42	T2	110/117 (94%)	108 (98%)	2 (2%)	51	73
43	U1	87/127 (68%)	83 (95%)	4 (5%)	24	41
44	U2	87/105 (83%)	87 (100%)	0	100	100
45	V1	101/108 (94%)	101 (100%)	0	100	100
46	V2	65/65 (100%)	64 (98%)	1 (2%)	57	77
47	W1	52/129 (40%)	52 (100%)	0	100	100
48	W2	112/113 (99%)	111 (99%)	1 (1%)	70	85
49	X1	105/134 (78%)	105 (100%)	0	100	100
50	X2	111/115 (96%)	111 (100%)	0	100	100
51	Y1	115/136 (85%)	114 (99%)	1 (1%)	70	85
52	Y2	108/116 (93%)	107 (99%)	1 (1%)	70	85
53	Z1	115/116 (99%)	114 (99%)	1 (1%)	70	85
54	Z2	57/105 (54%)	55 (96%)	2 (4%)	32	53
55	a1	121/122 (99%)	119 (98%)	2 (2%)	53	74
56	a2	86/99 (87%)	85 (99%)	1 (1%)	63	81
57	b1	45/56 (80%)	43 (96%)	2 (4%)	25	43
58	b2	73/76 (96%)	73 (100%)	0	100	100
59	c1	78/98 (80%)	77 (99%)	1 (1%)	61	80
60	c2	53/61 (87%)	49 (92%)	4 (8%)	12	21
61	d1	98/110 (89%)	96 (98%)	2 (2%)	48	70
62	d2	48/49 (98%)	48 (100%)	0	100	100
63	e1	113/121 (93%)	113 (100%)	0	100	100
64	e2	41/112 (37%)	40 (98%)	1 (2%)	43	65
65	f1	86/88 (98%)	86 (100%)	0	100	100
66	g1	91/102 (89%)	90 (99%)	1 (1%)	65	82
67	g2	263/274 (96%)	258 (98%)	5 (2%)	50	71
68	h1	108/110 (98%)	107 (99%)	1 (1%)	70	85
69	i1	83/88 (94%)	81 (98%)	2 (2%)	43	65
70	j1	73/80 (91%)	73 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
71	k1	64/65 (98%)	64 (100%)	0	100	100
72	l1	45/46 (98%)	45 (100%)	0	100	100
73	m1	46/116 (40%)	45 (98%)	1 (2%)	45	67
74	n1	23/24 (96%)	23 (100%)	0	100	100
75	o1	91/95 (96%)	91 (100%)	0	100	100
76	p1	74/75 (99%)	74 (100%)	0	100	100
77	r1	102/120 (85%)	99 (97%)	3 (3%)	37	60
All	All	9292/10465 (89%)	9169 (99%)	123 (1%)	59	80

All (123) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	A1	102	LEU
5	A1	208	GLU
5	A1	218	HIS
6	A2	12	GLU
6	A2	192	GLU
6	A2	206	ASP
7	B1	297	LYS
7	B1	344	VAL
8	B2	91	VAL
8	B2	114	VAL
8	B2	176	VAL
8	B2	189	ILE
8	B2	211	TYR
9	C1	124	MET
10	C2	47	VAL
10	C2	149	ILE
10	C2	151	VAL
10	C2	177	VAL
10	C2	244	GLU
10	C2	246	VAL
11	D1	115	LEU
11	D1	118	VAL
11	D1	155	THR
11	D1	265	ARG
12	D2	72	VAL
13	E1	39	TYR
13	E1	73	VAL
13	E1	83	VAL

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Mol	Chain	Res	Type
13	E1	152	VAL
14	E2	76	VAL
14	E2	214	ILE
14	E2	247	THR
14	E2	248	ILE
15	F1	97	ASN
15	F1	223	THR
17	G1	146	LEU
17	G1	155	VAL
18	G2	49	VAL
18	G2	129	VAL
18	G2	157	VAL
19	H1	41	ILE
19	H1	103	VAL
21	I1	43	VAL
22	I2	22	HIS
22	I2	76	THR
22	I2	103	LEU
22	I2	107	THR
22	I2	130	THR
22	I2	191	GLU
23	J1	17	ILE
23	J1	20	LEU
23	J1	22	LEU
23	J1	117	ILE
23	J1	132	VAL
25	K2	74	GLU
25	K2	89	ILE
26	L1	67	HIS
26	L1	160	VAL
27	L2	39	ARG
27	L2	70	ARG
27	L2	121	VAL
29	N1	85	VAL
29	N1	98	LEU
29	N1	174	LEU
30	N2	66	VAL
32	O2	42	VAL
32	O2	119	LEU
33	P1	24	VAL
34	P2	76	VAL
35	Q1	63	LEU

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Mol	Chain	Res	Type
35	Q1	82	VAL
36	Q2	100	VAL
36	Q2	107	GLU
36	Q2	141	TYR
37	R1	3	MET
37	R1	93	LEU
38	R2	85	VAL
38	R2	88	VAL
38	R2	119	VAL
40	S2	36	VAL
40	S2	89	ASP
41	T1	72	VAL
41	T1	114	LYS
41	T1	126	ILE
42	T2	46	LEU
42	T2	105	LEU
43	U1	44	GLU
43	U1	75	VAL
43	U1	110	LEU
43	U1	124	TYR
46	V2	11	LEU
48	W2	18	GLU
51	Y1	79	VAL
52	Y2	14	THR
53	Z1	33	THR
54	Z2	48	VAL
54	Z2	62	VAL
55	a1	24	LYS
55	a1	140	VAL
56	a2	51	ARG
57	b1	8	THR
57	b1	35	VAL
59	c1	28	VAL
60	c2	17	VAL
60	c2	32	VAL
60	c2	46	VAL
60	c2	64	GLU
61	d1	103	LEU
61	d1	120	VAL
64	e2	96	VAL
66	g1	2	VAL
67	g2	7	VAL

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Mol	Chain	Res	Type
67	g2	104	HIS
67	g2	252	THR
67	g2	260	ASP
67	g2	270	LEU
68	h1	113	LEU
69	i1	18	THR
69	i1	63	VAL
73	m1	85	LEU
77	r1	44	LEU
77	r1	45	ILE
77	r1	62	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (159) such sidechains are listed below:

Mol	Chain	Res	Type
5	A1	8	GLN
5	A1	132	ASN
5	A1	205	ASN
5	A1	216	HIS
6	A2	24	HIS
6	A2	132	GLN
6	A2	141	ASN
7	B1	55	HIS
7	B1	109	HIS
7	B1	138	GLN
7	B1	165	HIS
7	B1	167	GLN
7	B1	173	HIS
7	B1	179	HIS
8	B2	124	HIS
8	B2	148	ASN
8	B2	160	GLN
8	B2	163	GLN
9	C1	50	GLN
9	C1	112	HIS
9	C1	118	ASN
9	C1	187	GLN
9	C1	203	GLN
9	C1	230	GLN
9	C1	306	ASN
10	C2	164	HIS
11	D1	81	HIS

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Mol	Chain	Res	Type
11	D1	111	ASN
11	D1	291	GLN
12	D2	174	HIS
13	E1	105	HIS
14	E2	67	GLN
14	E2	142	HIS
14	E2	179	ASN
14	E2	188	ASN
15	F1	56	HIS
15	F1	114	GLN
16	F2	65	GLN
16	F2	82	ASN
16	F2	107	ASN
16	F2	118	ASN
16	F2	165	ASN
17	G1	81	ASN
17	G1	94	GLN
17	G1	225	ASN
18	G2	59	GLN
18	G2	81	HIS
18	G2	197	GLN
19	H1	52	GLN
19	H1	98	HIS
19	H1	156	ASN
20	H2	76	GLN
20	H2	91	HIS
20	H2	165	ASN
21	I1	183	ASN
22	I2	7	ASN
22	I2	35	ASN
22	I2	146	GLN
23	J1	42	GLN
23	J1	71	HIS
23	J1	97	ASN
23	J1	110	GLN
23	J1	168	GLN
24	J2	124	HIS
24	J2	125	HIS
24	J2	140	GLN
24	J2	177	ASN
25	K2	44	HIS
25	K2	61	GLN

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Mol	Chain	Res	Type
25	K2	66	HIS
25	K2	77	GLN
26	L1	13	HIS
26	L1	104	ASN
27	L2	18	GLN
27	L2	84	GLN
27	L2	142	ASN
28	M1	20	HIS
29	N1	145	ASN
29	N1	181	HIS
30	N2	13	GLN
30	N2	62	GLN
30	N2	69	ASN
31	O1	28	GLN
31	O1	52	ASN
31	O1	145	HIS
31	O1	182	GLN
32	O2	83	GLN
33	P1	45	ASN
33	P1	97	ASN
33	P1	118	GLN
33	P1	120	ASN
34	P2	54	GLN
35	Q1	14	HIS
35	Q1	160	HIS
36	Q2	24	HIS
36	Q2	35	ASN
36	Q2	97	GLN
37	R1	34	ASN
37	R1	141	HIS
37	R1	158	GLN
38	R2	93	GLN
38	R2	116	ASN
39	S1	108	GLN
39	S1	122	HIS
39	S1	163	HIS
42	T2	43	HIS
42	T2	106	GLN
42	T2	127	GLN
42	T2	138	GLN
44	U2	85	HIS
44	U2	92	HIS

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Mol	Chain	Res	Type
45	V1	36	ASN
45	V1	77	HIS
47	W1	17	HIS
47	W1	48	GLN
48	W2	24	GLN
48	W2	82	GLN
48	W2	113	HIS
49	X1	56	GLN
49	X1	92	ASN
49	X1	106	HIS
50	X2	15	ASN
50	X2	92	ASN
51	Y1	18	HIS
51	Y1	56	GLN
51	Y1	65	GLN
52	Y2	85	ASN
55	a1	40	HIS
56	a2	8	ASN
56	a2	72	HIS
58	b2	9	HIS
59	c1	33	GLN
59	c1	40	GLN
59	c1	72	HIS
59	c1	73	HIS
61	d1	77	ASN
61	d1	98	ASN
62	d2	4	GLN
62	d2	45	GLN
63	e1	52	GLN
64	e2	116	ASN
65	f1	21	GLN
67	g2	20	GLN
67	g2	143	GLN
67	g2	237	ASN
67	g2	244	ASN
68	h1	63	GLN
69	i1	36	HIS
69	i1	80	HIS
70	j1	76	ASN
72	l1	19	GLN
72	l1	33	ASN
73	m1	84	GLN

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Mol	Chain	Res	Type
73	m1	104	HIS
73	m1	109	ASN
75	o1	25	GLN
75	o1	45	GLN
77	r1	46	HIS
77	r1	71	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	22	1483/1939 (76%)	290 (19%)	10 (0%)
2	51	3237/4269 (75%)	571 (17%)	37 (1%)
3	71	119/120 (99%)	6 (5%)	0
4	81	147/158 (93%)	19 (12%)	0
All	All	4986/6486 (76%)	886 (17%)	47 (0%)

All (886) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	22	3	C
1	22	4	C
1	22	33	G
1	22	41	G
1	22	46	A
1	22	56	G
1	22	66	A
1	22	67	C
1	22	82	G
1	22	83	A
1	22	103	A
1	22	111	A
1	22	113	G
1	22	115	U
1	22	123	A
1	22	140	C
1	22	142	U
1	22	145	A
1	22	161	C
1	22	184	C
1	22	241	U
1	22	242	G

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Mol	Chain	Res	Type
1	22	243	C
1	22	336	G
1	22	349	A
1	22	350	C
1	22	359	G
1	22	360	A
1	22	361	U
1	22	365	G
1	22	377	C
1	22	380	C
1	22	387	U
1	22	389	A
1	22	393	G
1	22	402	C
1	22	410	A
1	22	414	U
1	22	416	G
1	22	431	G
1	22	432	C
1	22	444	A
1	22	446	C
1	22	453	G
1	22	455	C
1	22	484	G
1	22	494	A
1	22	496	C
1	22	510	A
1	22	511	A
1	22	512	G
1	22	516	G
1	22	517	G
1	22	518	C
1	22	519	A
1	22	520	G
1	22	528	G
1	22	532	A
1	22	533	U
1	22	539	A
1	22	542	U
1	22	548	A
1	22	571	A
1	22	574	A

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Mol	Chain	Res	Type
1	22	605	G
1	22	606	A
1	22	609	G
1	22	610	A
1	22	625	C
1	22	629	G
1	22	636	A
1	22	637	C
1	22	640	A
1	22	644	G
1	22	652	G
1	22	653	U
1	22	654	C
1	22	660	C
1	22	672	G
1	22	673	U
1	22	674	A
1	22	678	C
1	22	679	C
1	22	686	A
1	22	687	A
1	22	689	A
1	22	690	G
1	22	706	C
1	22	715	A
1	22	717	A
1	22	718	A
1	22	734	U
1	22	735	C
1	22	865	A
1	22	866	A
1	22	875	G
1	22	876	U
1	22	884	A
1	22	889	C
1	22	902	C
1	22	903	A
1	22	904	U
1	22	905	U
1	22	907	A
1	22	908	A
1	22	930	A

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Mol	Chain	Res	Type
1	22	931	A
1	22	932	U
1	22	933	A
1	22	934	G
1	22	936	A
1	22	972	G
1	22	977	A
1	22	982	C
1	22	983	G
1	22	984	A
1	22	986	A
1	22	994	C
1	22	997	G
1	22	998	G
1	22	1020	G
1	22	1034	G
1	22	1035	G
1	22	1042	G
1	22	1054	G
1	22	1056	A
1	22	1063	G
1	22	1065	G
1	22	1066	U
1	22	1081	U
1	22	1087	A
1	22	1091	A
1	22	1109	U
1	22	1113	A
1	22	1124	A
1	22	1125	U
1	22	1126	A
1	22	1137	U
1	22	1147	A
1	22	1149	C
1	22	1153	G
1	22	1172	G
1	22	1173	C
1	22	1174	G
1	22	1177	U
1	22	1191	G
1	22	1196	G
1	22	1198	A

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Mol	Chain	Res	Type
1	22	1203	U
1	22	1204	G
1	22	1205	C
1	22	1206	G
1	22	1216	G
1	22	1220	C
1	22	1221	U
1	22	1255	A
1	22	1262	A
1	22	1274	G
1	22	1275	A
1	22	1282	C
1	22	1283	C
1	22	1288	G
1	22	1299	U
1	22	1306	U
1	22	1308	A
1	22	1309	U
1	22	1314	C
1	22	1315	U
1	22	1318	A
1	22	1320	A
1	22	1321	C
1	22	1323	G
1	22	1324	G
1	22	1325	G
1	22	1326	A
1	22	1330	U
1	22	1331	C
1	22	1336	G
1	22	1339	C
1	22	1340	C
1	22	1341	G
1	22	1355	U
1	22	1357	G
1	22	1359	C
1	22	1362	A
1	22	1375	U
1	22	1381	U
1	22	1382	U
1	22	1383	C
1	22	1384	U

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Mol	Chain	Res	Type
1	22	1385	G
1	22	1387	G
1	22	1390	U
1	22	1393	U
1	22	1394	G
1	22	1398	C
1	22	1400	U
1	22	1408	C
1	22	1409	G
1	22	1438	U
1	22	1439	U
1	22	1445	A
1	22	1460	G
1	22	1461	G
1	22	1463	A
1	22	1464	U
1	22	1475	U
1	22	1478	G
1	22	1480	G
1	22	1498	U
1	22	1504	A
1	22	1506	U
1	22	1518	C
1	22	1519	A
1	22	1527	U
1	22	1528	U
1	22	1529	C
1	22	1531	G
1	22	1536	G
1	22	1541	A
1	22	1542	C
1	22	1544	G
1	22	1548	A
1	22	1550	U
1	22	1551	A
1	22	1554	A
1	22	1555	G
1	22	1559	U
1	22	1562	G
1	22	1563	A
1	22	1571	A
1	22	1572	G

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Mol	Chain	Res	Type
1	22	1573	A
1	22	1575	G
1	22	1576	U
1	22	1579	G
1	22	1580	G
1	22	1583	C
1	22	1584	U
1	22	1585	G
1	22	1586	C
1	22	1588	C
1	22	1596	A
1	22	1597	C
1	22	1598	A
1	22	1599	A
1	22	1600	U
1	22	1601	G
1	22	1602	G
1	22	1609	C
1	22	1612	C
1	22	1629	C
1	22	1631	G
1	22	1644	A
1	22	1645	A
1	22	1652	G
1	22	1653	A
1	22	1664	U
1	22	1665	G
1	22	1666	A
1	22	1686	C
1	22	1688	A
1	22	1697	G
1	22	1713	G
1	22	1729	A
1	22	1730	G
1	22	1745	G
1	22	1760	A
1	22	1761	C
1	22	1764	A
1	22	1786	U
1	22	1787	G
1	22	1790	C
1	22	1813	G

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Mol	Chain	Res	Type
1	22	1815	C
1	22	1857	G
1	22	1893	A
1	22	1895	A
1	22	1896	G
1	22	1901	A
1	22	1905	A
1	22	1906	G
1	22	1908	U
1	22	1919	G
1	22	1921	A
1	22	1922	C
1	22	1931	G
1	22	1932	G
1	22	1933	A
1	22	1935	C
2	51	13	U
2	51	21	G
2	51	25	A
2	51	33	A
2	51	39	A
2	51	42	A
2	51	48	C
2	51	49	U
2	51	59	A
2	51	64	A
2	51	65	A
2	51	66	A
2	51	69	A
2	51	71	C
2	51	76	A
2	51	91	G
2	51	109	G
2	51	119	G
2	51	120	A
2	51	128	C
2	51	145	A
2	51	146	G
2	51	148	G
2	51	161	C
2	51	171	C
2	51	173	U

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Mol	Chain	Res	Type
2	51	174	C
2	51	175	U
2	51	179	G
2	51	201	U
2	51	210	U
2	51	217	U
2	51	219	A
2	51	220	G
2	51	221	C
2	51	222	C
2	51	234	U
2	51	245	U
2	51	246	C
2	51	247	G
2	51	266	U
2	51	267	G
2	51	272	U
2	51	273	C
2	51	281	A
2	51	282	G
2	51	299	U
2	51	308	A
2	51	311	C
2	51	312	G
2	51	318	U
2	51	336	A
2	51	337	A
2	51	338	A
2	51	342	C
2	51	343	G
2	51	356	U
2	51	363	C
2	51	365	A
2	51	388	A
2	51	389	G
2	51	411	C
2	51	434	U
2	51	442	U
2	51	458	C
2	51	464	G
2	51	469	U
2	51	470	U

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Mol	Chain	Res	Type
2	51	471	C
2	51	484	C
2	51	485	G
2	51	486	G
2	51	487	G
2	51	488	G
2	51	489	U
2	51	492	G
2	51	496	G
2	51	501	G
2	51	502	U
2	51	503	G
2	51	508	C
2	51	510	C
2	51	511	C
2	51	514	U
2	51	515	C
2	51	549	G
2	51	550	A
2	51	551	C
2	51	552	G
2	51	553	C
2	51	556	G
2	51	558	G
2	51	561	A
2	51	562	A
2	51	564	G
2	51	565	C
2	51	581	U
2	51	582	G
2	51	583	C
2	51	584	A
2	51	585	U
2	51	590	G
2	51	593	G
2	51	594	C
2	51	601	G
2	51	622	C
2	51	627	U
2	51	628	G
2	51	633	G
2	51	634	G

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Mol	Chain	Res	Type
2	51	635	U
2	51	636	C
2	51	644	G
2	51	646	A
2	51	647	G
2	51	678	A
2	51	680	A
2	51	683	G
2	51	691	G
2	51	694	C
2	51	695	C
2	51	697	A
2	51	698	C
2	51	702	G
2	51	704	C
2	51	708	U
2	51	709	G
2	51	710	C
2	51	711	U
2	51	712	C
2	51	714	C
2	51	721	C
2	51	722	G
2	51	745	U
2	51	746	C
2	51	751	C
2	51	752	C
2	51	753	C
2	51	778	G
2	51	780	G
2	51	782	C
2	51	791	C
2	51	792	C
2	51	804	G
2	51	805	G
2	51	806	C
2	51	807	G
2	51	811	C
2	51	820	A
2	51	827	U
2	51	828	C
2	51	860	G

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Mol	Chain	Res	Type
2	51	873	C
2	51	874	C
2	51	875	C
2	51	876	A
2	51	878	G
2	51	879	U
2	51	880	U
2	51	886	G
2	51	893	G
2	51	894	U
2	51	896	C
2	51	902	G
2	51	903	A
2	51	904	C
2	51	905	G
2	51	935	A
2	51	963	A
2	51	968	G
2	51	969	A
2	51	974	G
2	51	975	G
2	51	976	C
2	51	978	C
2	51	979	G
2	51	980	C
2	51	981	G
2	51	987	C
2	51	988	U
2	51	989	G
2	51	996	A
2	51	1003	G
2	51	1007	G
2	51	1042	C
2	51	1043	C
2	51	1044	G
2	51	1045	G
2	51	1050	G
2	51	1053	C
2	51	1054	G
2	51	1062	G
2	51	1074	G
2	51	1075	A

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Mol	Chain	Res	Type
2	51	1077	C
2	51	1078	C
2	51	1079	U
2	51	1080	C
2	51	1081	C
2	51	1082	G
2	51	1087	G
2	51	1088	C
2	51	1095	A
2	51	1096	G
2	51	1100	G
2	51	1116	A
2	51	1121	A
2	51	1123	A
2	51	1128	G
2	51	1132	A
2	51	1145	A
2	51	1150	G
2	51	1164	C
2	51	1176	C
2	51	1189	U
2	51	1194	U
2	51	1210	G
2	51	1222	G
2	51	1229	A
2	51	1231	G
2	51	1232	A
2	51	1236	A
2	51	1238	C
2	51	1239	G
2	51	1240	A
2	51	1252	G
2	51	1259	C
2	51	1274	C
2	51	1275	U
2	51	1276	C
2	51	1277	A
2	51	1292	C
2	51	1296	G
2	51	1297	A
2	51	1298	U
2	51	1312	C

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Mol	Chain	Res	Type
2	51	1322	C
2	51	1323	A
2	51	1331	G
2	51	1358	C
2	51	1359	C
2	51	1368	A
2	51	1369	A
2	51	1384	G
2	51	1385	A
2	51	1387	G
2	51	1402	G
2	51	1403	C
2	51	1404	U
2	51	1405	G
2	51	1415	G
2	51	1417	G
2	51	1419	A
2	51	1424	G
2	51	1426	C
2	51	1427	G
2	51	1438	G
2	51	1452	G
2	51	1453	C
2	51	1464	C
2	51	1465	U
2	51	1473	G
2	51	1474	A
2	51	1475	A
2	51	1480	A
2	51	1481	C
2	51	1501	U
2	51	1502	G
2	51	1503	C
2	51	1504	C
2	51	1505	G
2	51	1513	U
2	51	1514	C
2	51	1515	A
2	51	1523	U
2	51	1531	G
2	51	1541	A
2	51	1543	A

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Mol	Chain	Res	Type
2	51	1544	G
2	51	1609	A
2	51	1624	A
2	51	1629	G
2	51	1631	U
2	51	1635	G
2	51	1638	G
2	51	1639	G
2	51	1645	C
2	51	1652	A
2	51	1653	U
2	51	1667	C
2	51	1668	G
2	51	1669	G
2	51	1701	G
2	51	1703	A
2	51	1724	C
2	51	1740	G
2	51	1747	A
2	51	1750	G
2	51	1767	G
2	51	1779	G
2	51	1782	G
2	51	1785	C
2	51	1795	G
2	51	1796	U
2	51	1801	A
2	51	1804	A
2	51	1829	A
2	51	1830	A
2	51	1831	G
2	51	1851	A
2	51	1855	G
2	51	1859	U
2	51	1860	U
2	51	1882	A
2	51	1887	A
2	51	1901	U
2	51	1902	U
2	51	1904	G
2	51	1908	G
2	51	1912	G

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Mol	Chain	Res	Type
2	51	1913	G
2	51	1933	C
2	51	1934	C
2	51	1935	C
2	51	1936	G
2	51	1937	C
2	51	1938	U
2	51	1939	C
2	51	1940	G
2	51	1941	A
2	51	1945	A
2	51	1954	C
2	51	1977	A
2	51	1978	G
2	51	1979	C
2	51	1980	G
2	51	1981	G
2	51	1988	C
2	51	1989	G
2	51	2007	A
2	51	2008	G
2	51	2017	C
2	51	2020	A
2	51	2021	A
2	51	2022	A
2	51	2023	C
2	51	2035	U
2	51	2053	G
2	51	2054	A
2	51	2062	C
2	51	2073	G
2	51	2088	C
2	51	2104	C
2	51	2110	G
2	51	2121	G
2	51	2122	C
2	51	2129	G
2	51	2130	A
2	51	2131	A
2	51	2158	U
2	51	2161	G
2	51	2178	A

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Mol	Chain	Res	Type
2	51	2179	A
2	51	2189	G
2	51	2197	G
2	51	2202	U
2	51	2203	C
2	51	2205	C
2	51	2206	G
2	51	2222	A
2	51	2229	C
2	51	2233	A
2	51	2248	A
2	51	2249	C
2	51	2261	U
2	51	2262	G
2	51	2270	A
2	51	2277	A
2	51	2291	G
2	51	2295	G
2	51	2306	A
2	51	2313	G
2	51	2858	C
2	51	2859	A
2	51	2876	C
2	51	2886	G
2	51	2895	A
2	51	2904	U
2	51	2908	A
2	51	2909	A
2	51	2913	A
2	51	2922	A
2	51	2952	A
2	51	2956	C
2	51	2969	U
2	51	2971	A
2	51	2972	A
2	51	3010	G
2	51	3013	G
2	51	3034	A
2	51	3035	A
2	51	3036	G
2	51	3037	G
2	51	3044	A

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Mol	Chain	Res	Type
2	51	3046	U
2	51	3049	C
2	51	3071	G
2	51	3072	C
2	51	3074	U
2	51	3077	A
2	51	3078	U
2	51	3079	G
2	51	3098	U
2	51	3100	U
2	51	3137	A
2	51	3138	C
2	51	3139	G
2	51	3141	G
2	51	3147	C
2	51	3157	G
2	51	3161	A
2	51	3165	A
2	51	3166	A
2	51	3167	G
2	51	3168	A
2	51	3175	U
2	51	3176	G
2	51	3182	G
2	51	3295	U
2	51	3296	A
2	51	3305	G
2	51	3348	C
2	51	3350	G
2	51	3351	G
2	51	3356	A
2	51	3417	G
2	51	3430	C
2	51	3431	C
2	51	3438	A
2	51	3439	C
2	51	3451	G
2	51	3452	G
2	51	3459	G
2	51	3471	A
2	51	3490	G
2	51	3493	G

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Mol	Chain	Res	Type
2	51	3497	U
2	51	3501	A
2	51	3517	G
2	51	3522	G
2	51	3536	A
2	51	3541	A
2	51	3548	A
2	51	3549	A
2	51	3556	C
2	51	3558	U
2	51	3559	G
2	51	3572	A
2	51	3573	G
2	51	3574	U
2	51	3582	C
2	51	3598	G
2	51	3600	C
2	51	3605	C
2	51	3616	G
2	51	3617	C
2	51	3644	A
2	51	3645	G
2	51	3646	A
2	51	3648	A
2	51	3650	G
2	51	3655	C
2	51	3659	G
2	51	3662	A
2	51	3666	C
2	51	3689	C
2	51	3690	A
2	51	3694	C
2	51	3701	G
2	51	3708	G
2	51	3716	G
2	51	3717	A
2	51	3721	C
2	51	3732	A
2	51	3733	U
2	51	3743	G
2	51	3744	C
2	51	3762	G

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Mol	Chain	Res	Type
2	51	3768	U
2	51	3775	A
2	51	3780	C
2	51	3781	A
2	51	3786	A
2	51	3787	C
2	51	3792	G
2	51	3793	C
2	51	3796	G
2	51	3816	A
2	51	3817	G
2	51	3828	C
2	51	3835	G
2	51	3841	A
2	51	3843	C
2	51	3844	C
2	51	3845	G
2	51	3851	G
2	51	3859	A
2	51	3860	A
2	51	3870	G
2	51	3871	U
2	51	3904	C
2	51	3905	G
2	51	3906	U
2	51	3940	C
2	51	3942	A
2	51	3970	A
2	51	3978	A
2	51	3979	U
2	51	4010	G
2	51	4011	U
2	51	4013	G
2	51	4014	G
2	51	4016	U
2	51	4019	C
2	51	4022	A
2	51	4025	G
2	51	4027	C
2	51	4029	C
2	51	4030	C
2	51	4032	G

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Mol	Chain	Res	Type
2	51	4036	A
2	51	4069	G
2	51	4070	C
2	51	4071	G
2	51	4074	G
2	51	4082	C
2	51	4087	C
2	51	4112	G
2	51	4114	G
2	51	4115	C
2	51	4124	C
2	51	4125	U
2	51	4126	C
2	51	4127	U
2	51	4128	U
2	51	4132	G
2	51	4137	G
2	51	4138	C
2	51	4141	C
2	51	4144	A
2	51	4150	G
2	51	4155	G
2	51	4156	A
2	51	4157	A
2	51	4166	U
2	51	4167	U
2	51	4178	U
2	51	4187	U
2	51	4189	A
2	51	4190	U
2	51	4192	C
2	51	4193	U
2	51	4208	U
2	51	4216	A
2	51	4219	G
2	51	4236	A
2	51	4243	G
2	51	4252	C
2	51	4256	C
2	51	4262	A
2	51	4265	U
3	71	38	U

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Mol	Chain	Res	Type
3	71	64	G
3	71	74	A
3	71	100	A
3	71	110	G
3	71	120	A
4	81	22	C
4	81	33	U
4	81	34	C
4	81	51	A
4	81	58	A
4	81	62	C
4	81	71	A
4	81	74	G
4	81	79	A
4	81	80	C
4	81	95	G
4	81	104	A
4	81	106	C
4	81	110	C
4	81	116	G
4	81	129	U
4	81	149	G
4	81	152	G
4	81	158	C

All (47) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	22	110	U
1	22	511	A
1	22	907	A
1	22	935	G
1	22	1203	U
1	22	1204	G
1	22	1330	U
1	22	1462	C
1	22	1503	A
1	22	1905	A
2	51	170	G
2	51	221	C
2	51	265	G
2	51	387	A

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Mol	Chain	Res	Type
2	51	457	C
2	51	469	U
2	51	488	G
2	51	495	C
2	51	507	G
2	51	552	G
2	51	560	G
2	51	600	A
2	51	697	A
2	51	804	G
2	51	819	G
2	51	875	C
2	51	879	U
2	51	903	A
2	51	1052	G
2	51	1079	U
2	51	1231	G
2	51	1358	C
2	51	1651	C
2	51	1795	G
2	51	1937	C
2	51	1977	A
2	51	2205	C
2	51	2858	C
2	51	2971	A
2	51	3048	C
2	51	3743	G
2	51	3870	G
2	51	3969	U
2	51	4123	C
2	51	4124	C
2	51	4156	A
2	51	4207	G

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 210 ligands modelled in this entry, 210 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

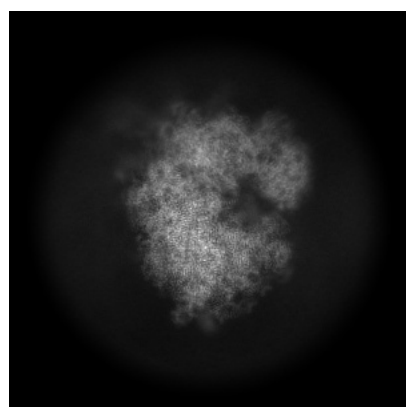
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13112. These allow visual inspection of the internal detail of the map and identification of artifacts.

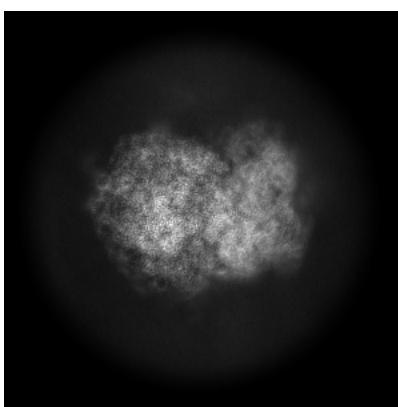
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

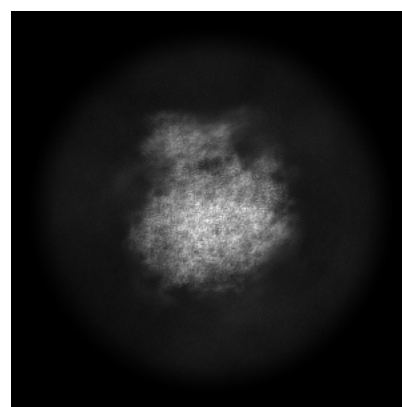
6.1.1 Primary map



X



Y

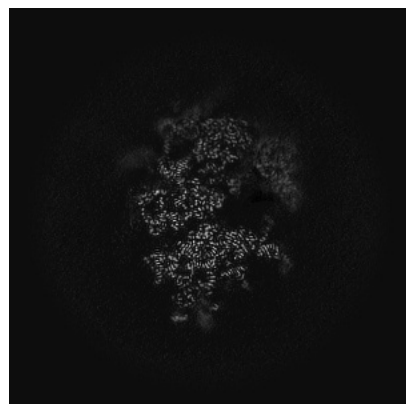


Z

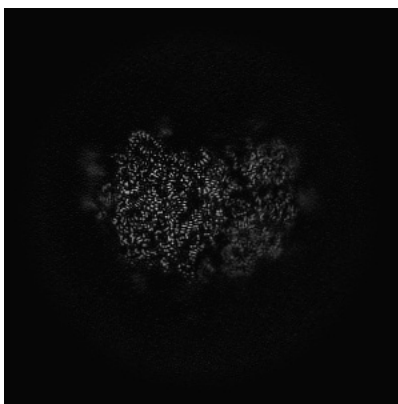
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

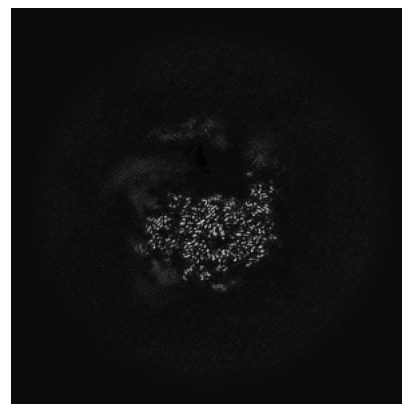
6.2.1 Primary map



X Index: 240



Y Index: 240

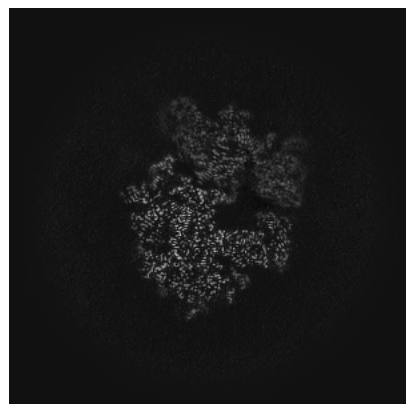


Z Index: 240

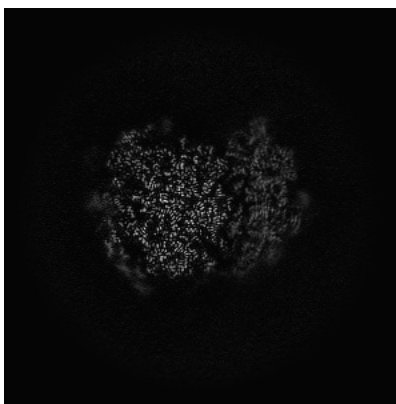
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

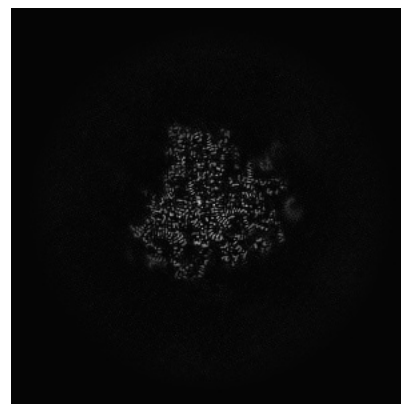
6.3.1 Primary map



X Index: 221



Y Index: 228

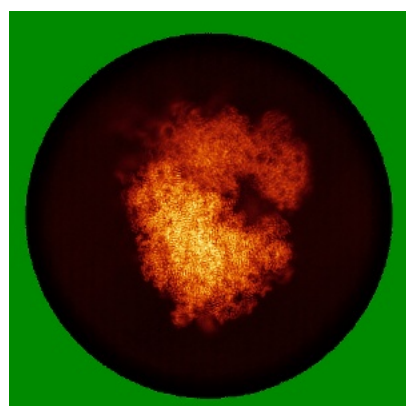


Z Index: 195

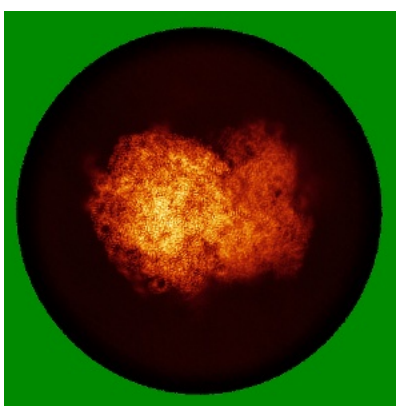
The images above show the largest variance slices of the map in three orthogonal directions.

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

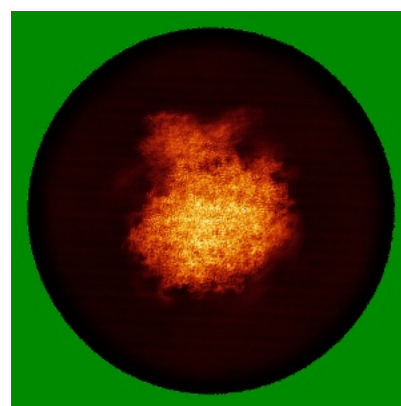
6.4.1 Primary map



X



Y

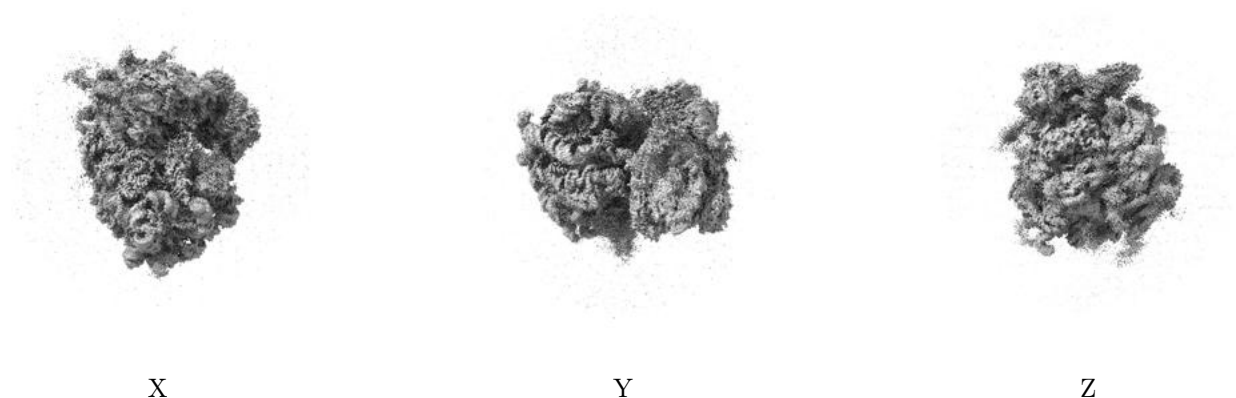


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.7. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

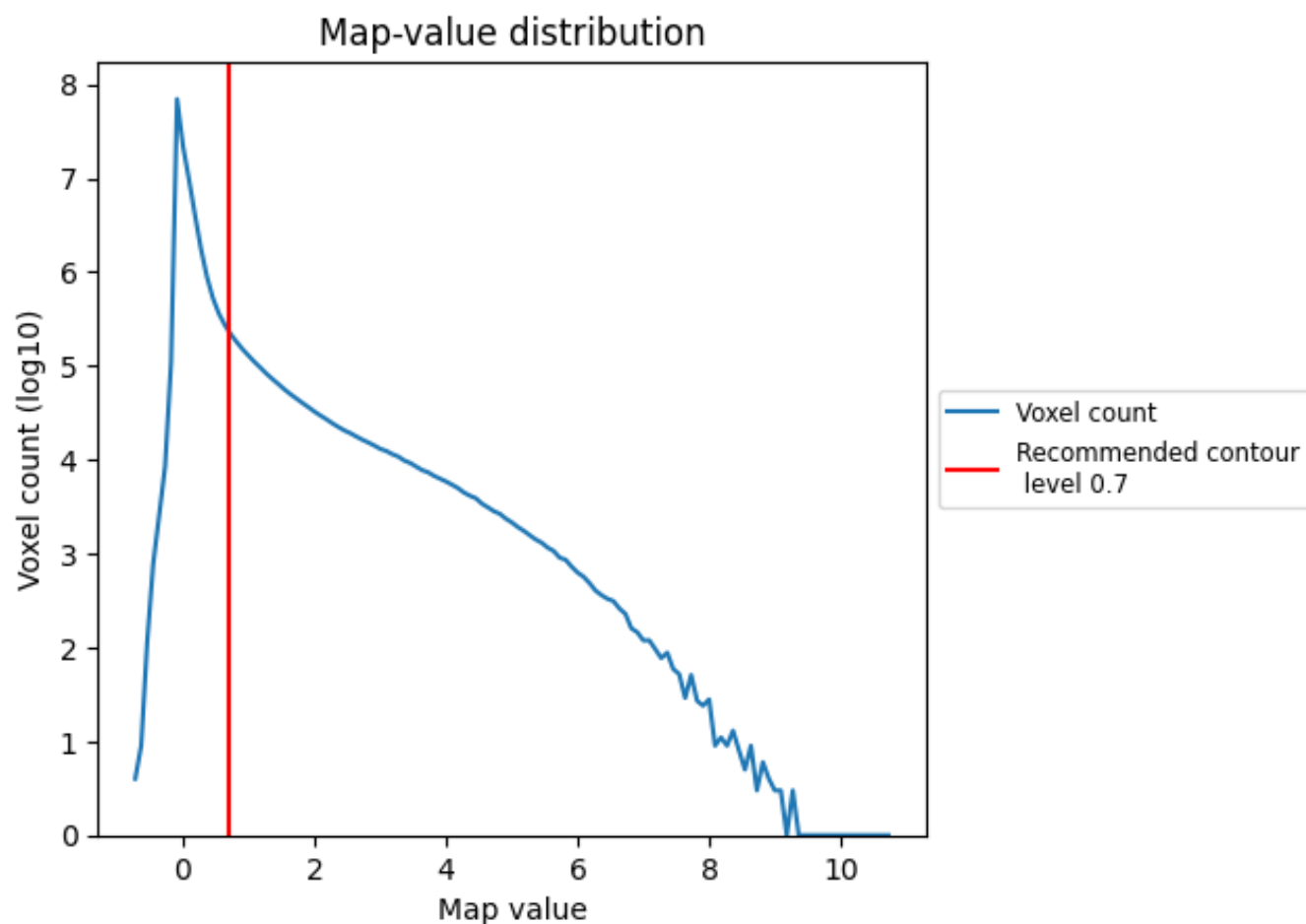
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

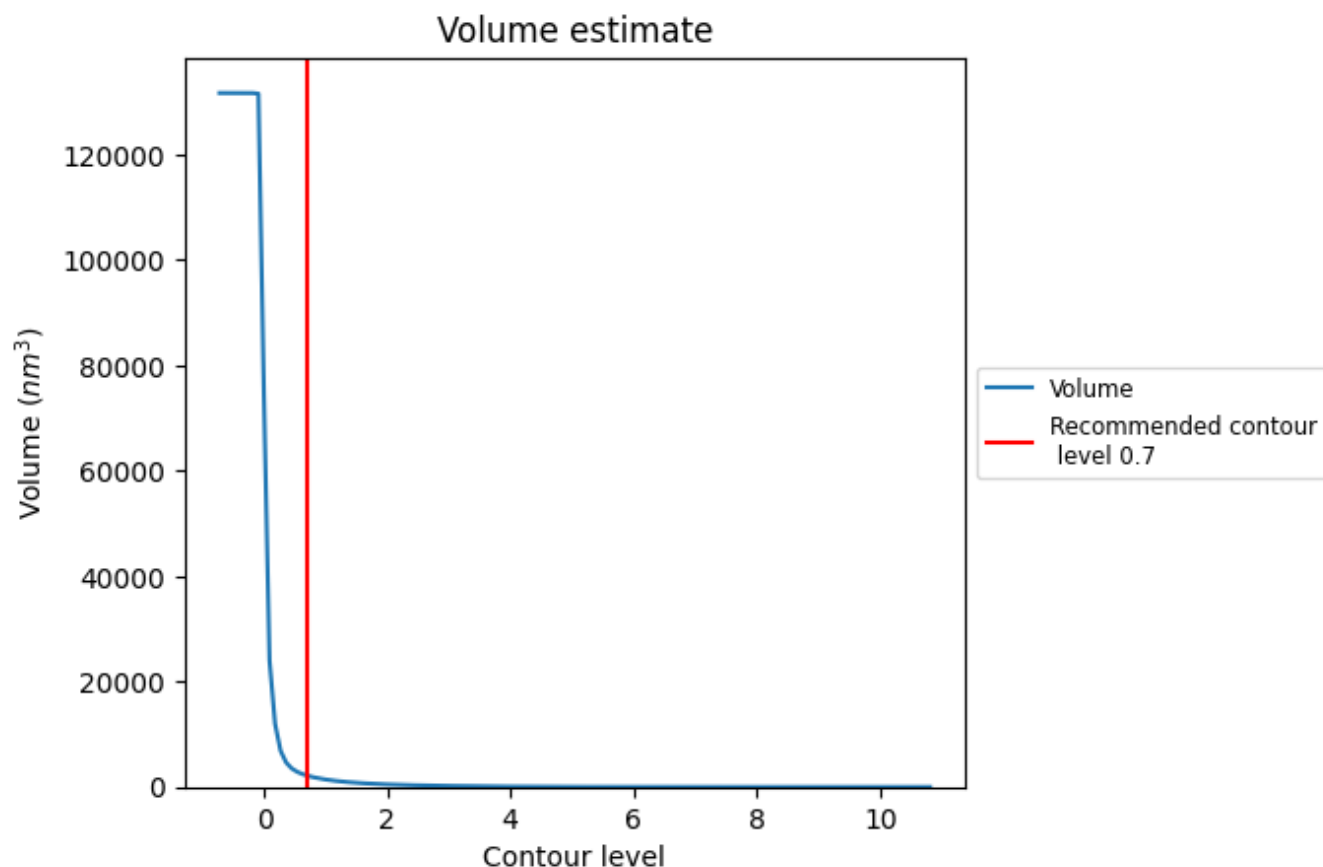
This section contains the results of statistical analysis of the map.

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.

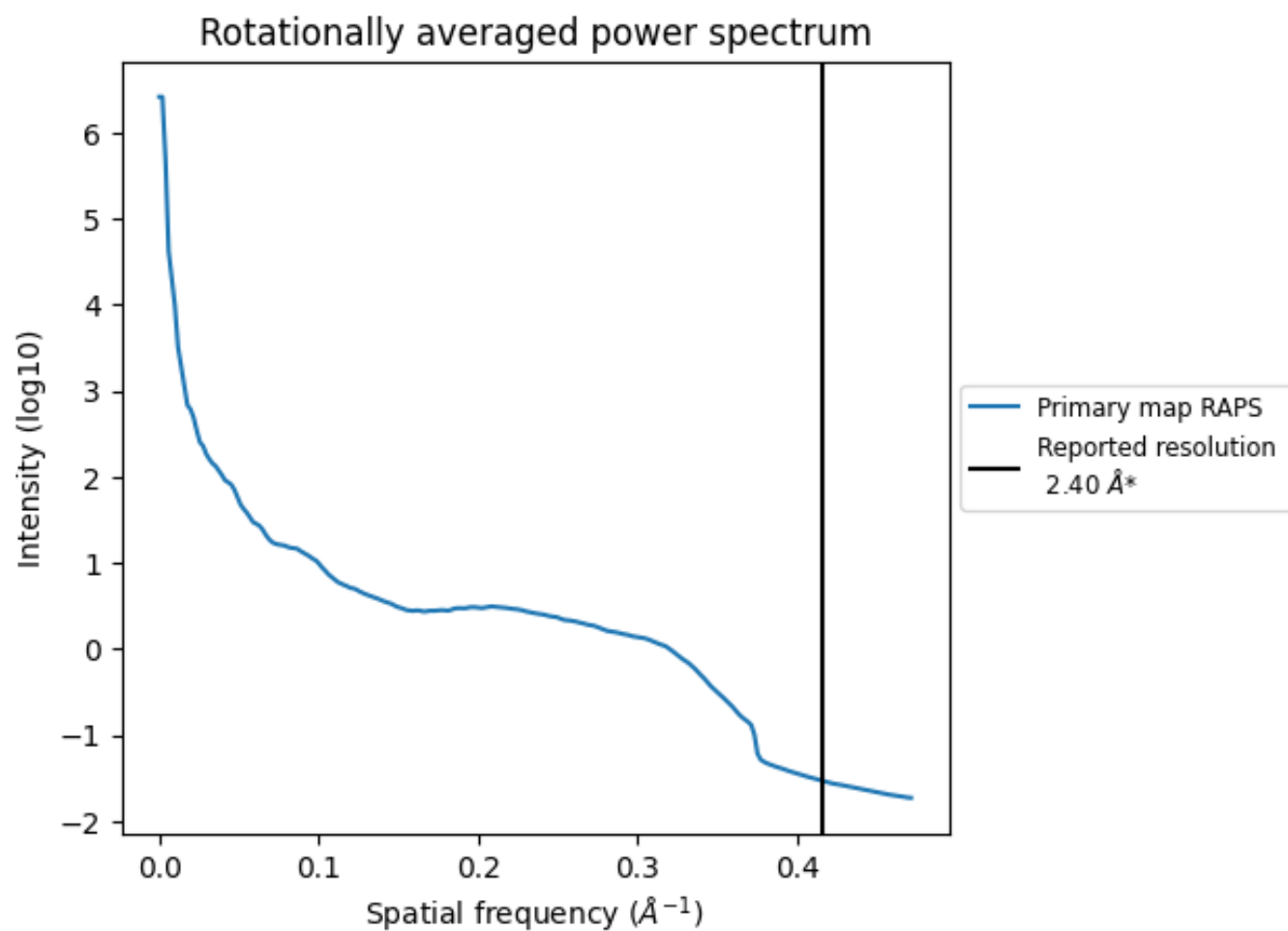
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2168 nm^3 ; this corresponds to an approximate mass of 1959 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.417 Å⁻¹

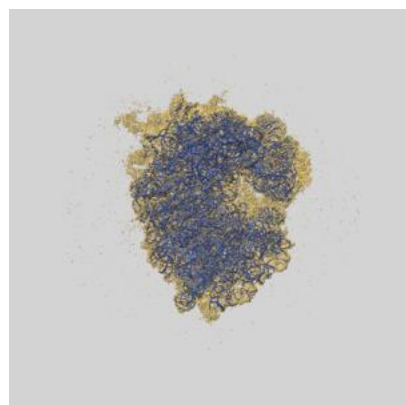
8 Fourier-Shell correlation

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

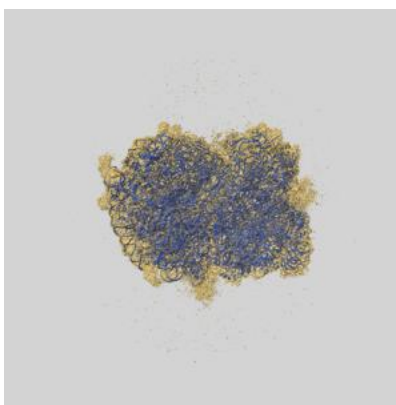
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-13112 and PDB model 7OYB. Per-residue inclusion information can be found in section [3](#) on page [18](#).

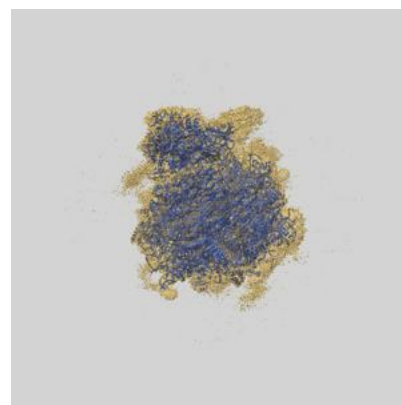
9.1 Map-model overlay [i](#)



X



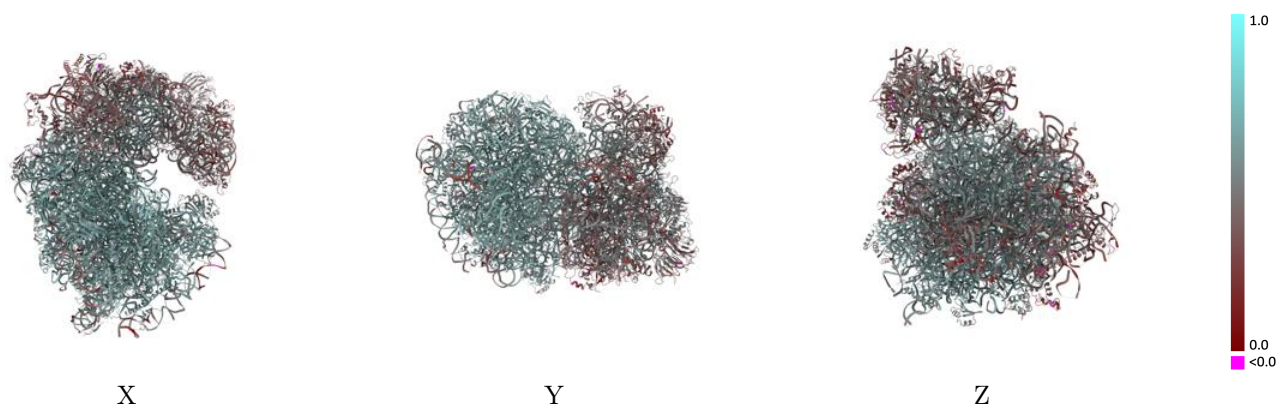
Y



Z

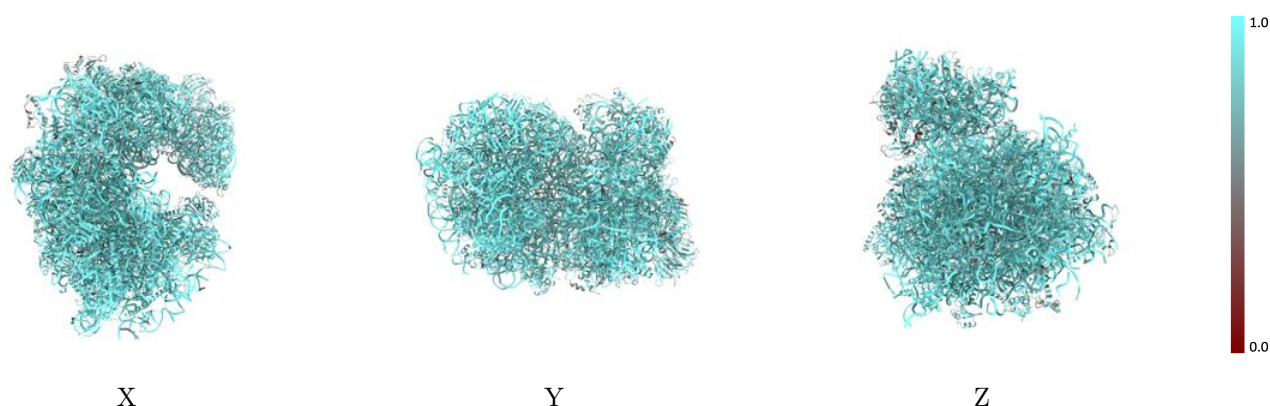
The images above show the 3D surface view of the map at the recommended contour level 0.7 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



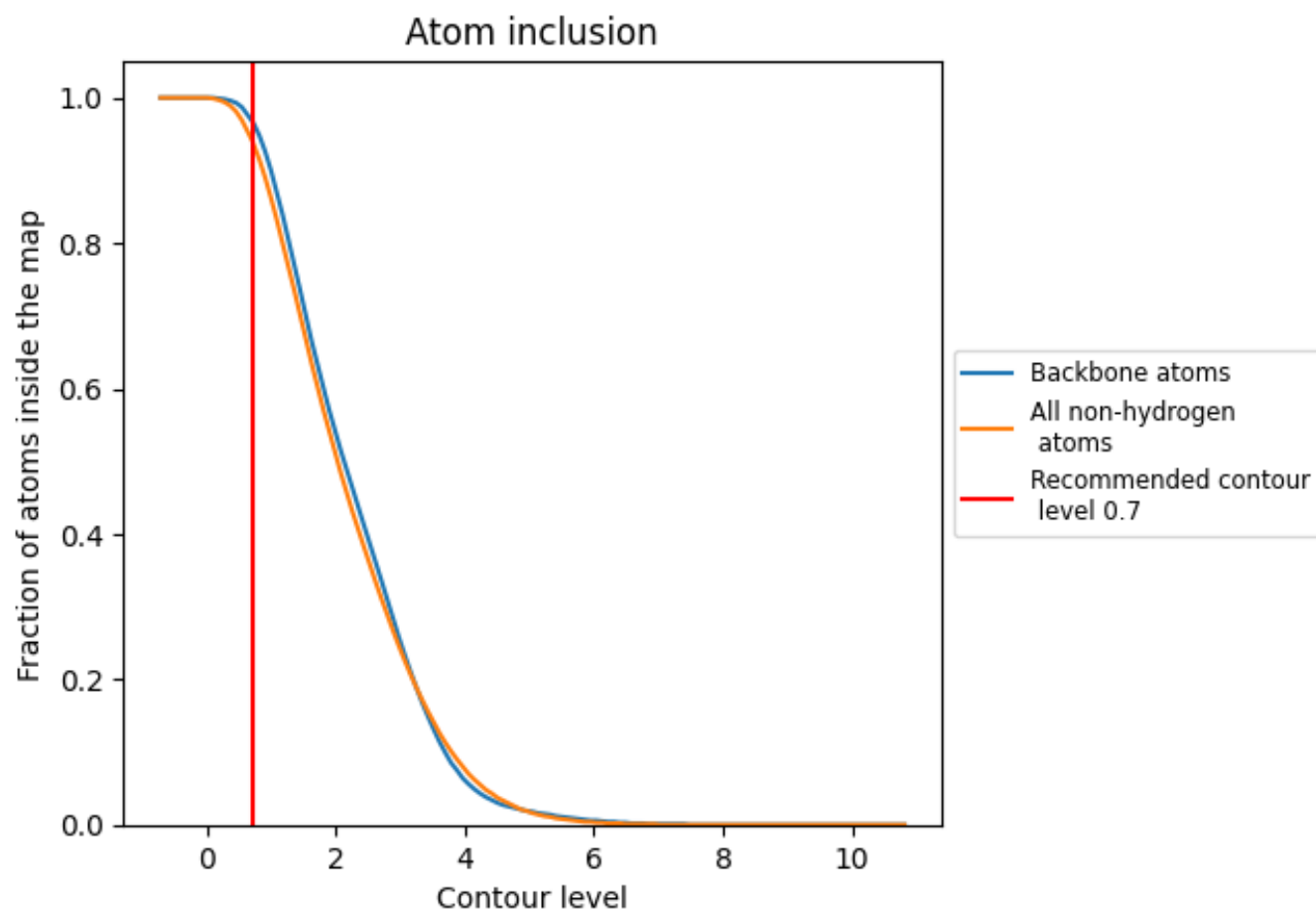
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.7).

9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 94% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.7) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9410	 0.5280
22	 0.9610	 0.4440
51	 0.9770	 0.5840
71	 0.9980	 0.6170
81	 0.9850	 0.5990
A1	 0.9720	 0.6120
A2	 0.9080	 0.4950
B1	 0.9640	 0.6140
B2	 0.7720	 0.3260
C1	 0.9640	 0.6040
C2	 0.9190	 0.5240
D1	 0.9390	 0.5730
D2	 0.8190	 0.3590
E1	 0.9380	 0.5720
E2	 0.8430	 0.3590
F1	 0.9620	 0.6130
F2	 0.7950	 0.3820
G1	 0.9030	 0.5450
G2	 0.7820	 0.3760
H1	 0.9420	 0.5930
H2	 0.7590	 0.3530
I1	 0.9110	 0.5850
I2	 0.7900	 0.3790
J1	 0.8790	 0.5300
J2	 0.8980	 0.4040
K2	 0.8680	 0.3160
L1	 0.9020	 0.5750
L2	 0.8110	 0.3640
M1	 0.9600	 0.6040
N1	 0.9800	 0.6220
N2	 0.8260	 0.3430
O1	 0.9680	 0.6150
O2	 0.8220	 0.3390
P1	 0.9670	 0.6160
P2	 0.8700	 0.3940



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Chain	Atom inclusion	Q-score
Q1	 0.9730	 0.6120
Q2	 0.8710	 0.4080
R1	 0.9390	 0.5540
R2	 0.7600	 0.3950
S1	 0.9730	 0.6220
S2	 0.8100	 0.3730
T1	 0.9420	 0.6060
T2	 0.8990	 0.4280
U1	 0.8660	 0.4930
U2	 0.8320	 0.3990
V1	 0.9540	 0.5990
V2	 0.8800	 0.5180
W1	 0.9630	 0.5890
W2	 0.9260	 0.5050
X1	 0.9320	 0.5930
X2	 0.8830	 0.4930
Y1	 0.9420	 0.5890
Y2	 0.7760	 0.3070
Z1	 0.9550	 0.5570
Z2	 0.7770	 0.3320
a1	 0.9690	 0.6070
a2	 0.8980	 0.4490
b1	 0.9430	 0.5940
b2	 0.8360	 0.3450
c1	 0.9700	 0.5630
c2	 0.7730	 0.3430
d1	 0.9320	 0.5840
d2	 0.9360	 0.4270
e1	 0.9730	 0.6190
e2	 0.7790	 0.3640
f1	 0.9760	 0.6320
g1	 0.9700	 0.5990
g2	 0.8050	 0.3800
h1	 0.9230	 0.5820
i1	 0.9260	 0.5740
j1	 0.9750	 0.6200
k1	 0.8440	 0.5270
l1	 0.9250	 0.5740
m1	 0.9650	 0.6110
n1	 0.8710	 0.5300
o1	 0.9370	 0.5960
p1	 0.9380	 0.5820

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Chain	Atom inclusion	Q-score
r1	 0.9640	 0.5940