



Full wwPDB EM Validation Report ⓘ

Sep 29, 2026 – 06:59 PM JST

PDB ID : 9X4D / pdb_00009x4d
EMDB ID : EMD-66542
Title : Structure of the old Killifish Ribosome
Authors : Kim, J.; Song, J.J.; Kim, Y.
Deposited on : 2025-10-10
Resolution : 2.93 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.dev133
MolProbity : 4-5-2 with Phenix2.2
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) : 2.51

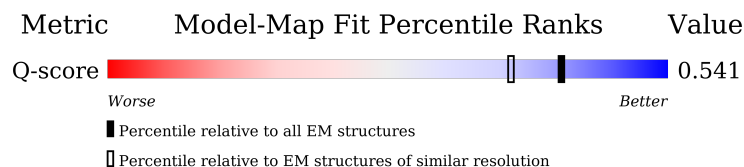
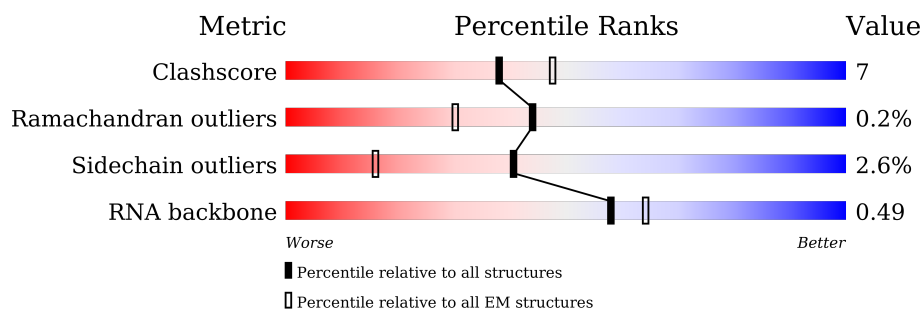
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.93 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.



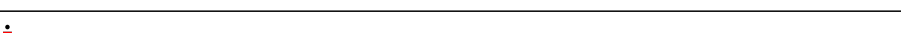
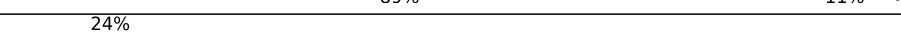
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13037 (2.43 - 3.43)

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	11	51	
2	21	128	
3	Z1	136	

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Mol	Chain	Length	Quality of chain
4	a1	257	
5	b1	64	
6	d2	69	
7	e1	117	
8	f1	110	
9	g1	92	
10	g2	313	
11	h1	297	
12	i1	120	
13	j1	161	
14	k1	192	
15	l1	259	
16	m1	266	
17	m2	132	
18	n1	148	
19	q2	119	
20	r2	130	
21	u2	203	
22	x2	133	
23	y2	143	
24	z2	166	
25	32	84	
26	41	137	
27	42	266	
28	K1	70	

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Mol	Chain	Length	Quality of chain
29	51	25	
30	61	215	
31	71	178	
32	72	151	
33	81	205	
34	82	142	
35	91	116	
36	B1	403	
37	B2	151	
38	C1	375	
39	D1	124	
40	E1	135	
41	F1	245	
42	H1	123	
43	H2	83	
44	I1	105	
45	J1	97	
46	J2	279	
47	K2	208	
48	L1	211	
49	L2	194	
50	M1	137	
51	A2	145	
52	P2	152	
53	i2	134	

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Mol	Chain	Length	Quality of chain
54	w2	247	
55	A1	4024	
56	C2	1838	
57	M2	146	
58	N1	204	
59	N2	73	
60	O1	106	
61	O2	263	
62	P1	184	
63	Q1	188	
64	R1	196	
65	S1	176	
66	S2	146	
67	T1	160	
68	T2	123	
69	U1	129	
70	U2	194	
71	V1	140	
72	W1	157	
73	W2	249	
74	X1	155	
75	Y1	145	
76	Y2	161	
77	k2	317	

2 Entry composition

There are 79 unique types of molecules in this entry. The entry contains 190927 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Large ribosomal subunit protein eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	11	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 2 is a protein called Ubiquitin-ribosomal protein eL40 fusion protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	21	47	Total	C	N	O	S	0	0
			387	238	84	59	6		

- Molecule 3 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	Z1	135	Total	C	N	O	S	0	0
			1107	715	208	180	4		

- Molecule 4 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	a1	246	Total	C	N	O	S	0	0
			1890	1186	387	311	6		

- Molecule 5 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	b1	50	Total	C	N	O	S	0	0
			428	265	94	68	1		

- Molecule 6 is a protein called Small ribosomal subunit protein eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	d2	56	Total	C	N	O	S	0	0
			443	270	91	80	2		

- Molecule 7 is a protein called Large ribosomal subunit protein eL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	e1	108	Total	C	N	O	S	0	0
			861	540	177	138	6		

- Molecule 8 is a protein called Large ribosomal subunit protein eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	f1	109	Total	C	N	O	S	0	0
			872	554	170	144	4		

- Molecule 9 is a protein called Large ribosomal subunit protein eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	g1	88	Total	C	N	O	S	0	0
			686	434	133	113	6		

- Molecule 10 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	g2	209	Total	C	N	O	S	0	0
			1660	1057	292	302	9		

- Molecule 11 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	h1	286	Total	C	N	O	S	0	0
			2311	1465	420	415	11		

- Molecule 12 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	i1	119	Total	C	N	O	P	0	0
			2541	1135	460	828	118		

- Molecule 13 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	j1	147	Total	C	N	O	P	0	0
			3135	1398	561	1029	147		

- Molecule 14 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	k1	189	Total	C	N	O	S	0	0
			1503	947	278	272	6		

- Molecule 15 is a protein called Large ribosomal subunit protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	l1	210	Total	C	N	O	S	0	0
			1677	1074	324	275	4		

- Molecule 16 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	m1	213	Total	C	N	O	S	0	0
			1730	1108	328	290	4		

- Molecule 17 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	m2	122	Total	C	N	O	S	0	0
			1001	635	195	166	5		

- Molecule 18 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	n1	147	Total	C	N	O	S	0	0
			1159	736	231	187	5		

- Molecule 19 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	q2	93	Total	C	N	O	S	0	0
			744	465	143	132	4		

- Molecule 20 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	r2	129	Total	C	N	O	S	0	0
			1036	660	193	177	6		

- Molecule 21 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	u2	177	Total	C	N	O	S	0	0
			1401	881	257	256	7		

- Molecule 22 is a protein called FAU ubiquitin like and ribosomal protein S30 fusion a.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	x2	47	Total	C	N	O		0	0
			380	233	85	62			

- Molecule 23 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	y2	139	Total	C	N	O	S	0	0
			1083	684	215	181	3		

- Molecule 24 is a protein called Ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	z2	37	Total	C	N	O	S	0	0
			317	212	54	47	4		

- Molecule 25 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	32	68	Total	C	N	O	S	0	0
			549	343	106	97	3		

- Molecule 26 is a protein called Large ribosomal subunit protein eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	41	123	Total	C	N	O	S	0	0
			979	610	200	166	3		

- Molecule 27 is a protein called Small ribosomal subunit protein eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	42	210	Total	C	N	O	S	0	0
			1708	1083	307	304	14		

- Molecule 28 is a protein called Large ribosomal subunit protein eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	K1	68	Total	C	N	O	S	0	0
			559	360	101	97	1		

- Molecule 29 is a protein called Small ribosomal subunit protein eS32.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	51	25	Total	C	N	O	S	0	0
			239	145	64	27	3		

- Molecule 30 is a protein called Ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	61	104	Total	C	N	O	S	0	0
			836	529	164	136	7		

- Molecule 31 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	71	149	Total	C	N	O	S	0	0
			1212	763	235	209	5		

- Molecule 32 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	72	131	Total	C	N	O	S	0	0
			981	600	193	182	6		

- Molecule 33 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	81	204	Total	C	N	O	S	0	0
			1660	1074	320	263	3		

- Molecule 34 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	82	95	Total	C	N	O	S	0	0
			756	468	155	127	6		

- Molecule 35 is a protein called Large ribosomal subunit protein eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	91	96	Total	C	N	O	S	0	0
			746	471	133	135	7		

- Molecule 36 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	B1	394	Total	C	N	O	S	0	0
			3173	2018	597	545	13		

- Molecule 37 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	B2	150	Total	C	N	O	S	0	0
			1205	771	229	204	1		

- Molecule 38 is a protein called Ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	C1	349	Total	C	N	O	S	0	0
			2788	1762	547	464	15		

- Molecule 39 is a protein called Large ribosomal subunit protein eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	D1	102	Total	C	N	O	S	0	0
			837	529	165	139	4		

- Molecule 40 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	E1	127	Total	C	N	O	S	0	0
			1042	663	208	165	6		

- Molecule 41 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	F1	226	Total	C	N	O	S	0	0
			1865	1200	360	296	9		

- Molecule 42 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	H1	121	Total	C	N	O	S	0	0
			1003	632	203	167	1		

- Molecule 43 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	H2	83	Total	C	N	O	S	0	0
			645	400	118	123	4		

- Molecule 44 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	I1	100	Total	C	N	O	S	0	0
			811	509	170	127	5		

- Molecule 45 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	J1	86	Total	C	N	O	S	0	0
			706	433	156	113	4		

- Molecule 46 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	J2	216	Total	C	N	O	S	0	0
			1671	1081	286	295	9		

- Molecule 47 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	K2	203	Total	C	N	O	S	0	0
			1652	1040	321	287	4		

- Molecule 48 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	L1	202	Total	C	N	O	S	0	0
			1632	1015	341	271	5		

- Molecule 49 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	L2	177	Total	C	N	O	S	0	0
			1473	939	293	239	2		

- Molecule 50 is a protein called Large ribosomal subunit protein eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	M1	133	Total	C	N	O	S	0	0
			1088	694	205	182	7		

- Molecule 51 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	A2	100	Total	C	N	O	S	0	0
			832	526	157	142	7		

- Molecule 52 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	P2	139	Total	C	N	O	S	0	0
			1155	725	234	195	1		

- Molecule 53 is a protein called Small ribosomal subunit protein eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	i2	119	Total	C	N	O	S	0	0
			969	608	180	178	3		

- Molecule 54 is a protein called DNA-(apurinic or apyrimidinic site) lyase.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	w2	206	Total	C	N	O	S	0	0
			1602	1023	290	282	7		

- Molecule 55 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	A1	3205	Total	C	N	O	P	0	0
			68707	30615	12552	22335	3205		

- Molecule 56 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	C2	1485	Total	C	N	O	P	0	0
			31719	14168	5722	10344	1485		

- Molecule 57 is a protein called Small ribosomal subunit protein eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	M2	141	Total	C	N	O	S	0	0
			1088	685	208	192	3		

- Molecule 58 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	N1	203	Total	C	N	O	S	0	0
			1697	1066	357	268	6		

- Molecule 59 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	N2	39	Total	C	N	O	S	0	0
			317	196	66	50	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
60	O1	93	Total	C	N	O	S	0	0
			770	484	156	124	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
61	O2	257	Total	C	N	O	S	0	0
			2040	1304	379	348	9		

- Molecule 62 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	P1	152	Total	C	N	O	S	0	0
			1232	770	243	210	9		

- Molecule 63 is a protein called Ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	Q1	187	Total	C	N	O	S	0	0
			1510	946	315	244	5		

- Molecule 64 is a protein called Ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	R1	171	Total	C	N	O	S	0	0
			1423	880	310	223	10		

- Molecule 65 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	S1	176	Total	C	N	O	S	0	0
			1458	932	286	231	9		

- Molecule 66 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	S2	138	Total	C	N	O	S	0	0
			1090	694	203	190	3		

- Molecule 67 is a protein called Large ribosomal subunit protein eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	T1	157	Total	C	N	O	S	0	0
			1290	818	252	216	4		

- Molecule 68 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	T2	70	Total	C	N	O	S	0	0
			568	367	102	98	1		

- Molecule 69 is a protein called Large ribosomal subunit protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	U1	91	Total	C	N	O	S	0	0
			757	488	132	135	2		

- Molecule 70 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	U2	177	Total	C	N	O	S	0	0
			1429	914	260	254	1		

- Molecule 71 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	V1	130	Total	C	N	O	S	0	0
			973	615	183	170	5		

- Molecule 72 is a protein called Large ribosomal subunit protein eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	W1	61	Total	C	N	O	S	0	0
			512	329	100	81	2		

- Molecule 73 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	W2	221	Total	C	N	O	S	0	0
			1791	1120	355	309	7		

- Molecule 74 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	X1	118	Total	C	N	O	S	0	0
			968	619	182	166	1		

- Molecule 75 is a protein called Ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	Y1	128	Total	C	N	O	S	0	0
			1067	670	219	175	3		

- Molecule 76 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Y2	138	Total	C	N	O	S	0	0
			1121	711	214	191	5		

- Molecule 77 is a protein called Small ribosomal subunit protein RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	k2	270	Total	C	N	O	S	0	0
			2138	1361	371	395	11		

- Molecule 78 is ZINC ION (CCD ID: ZN) (formula: Zn).

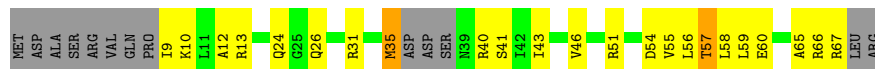
Mol	Chain	Residues	Atoms		AltConf
78	21	1	Total	Zn	0
			1	1	
78	e1	1	Total	Zn	0
			1	1	
78	g1	1	Total	Zn	0
			1	1	
78	82	1	Total	Zn	0
			1	1	
78	J1	1	Total	Zn	0
			1	1	
78	N2	1	Total	Zn	0
			1	1	
78	O1	1	Total	Zn	0
			1	1	

- Molecule 79 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

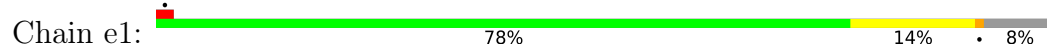
Mol	Chain	Residues	Atoms		AltConf
79	i1	1	Total	Mg	0
			1	1	
79	J1	1	Total	Mg	0
			1	1	
79	A1	62	Total	Mg	0
			62	62	
79	C2	21	Total	Mg	0
			21	21	



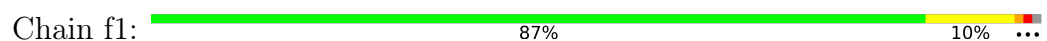
- Molecule 6: Small ribosomal subunit protein eS28



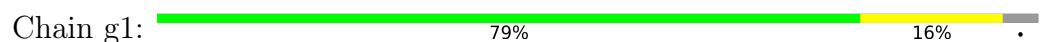
- Molecule 7: Large ribosomal subunit protein eL34



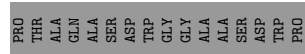
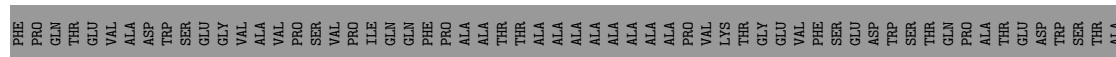
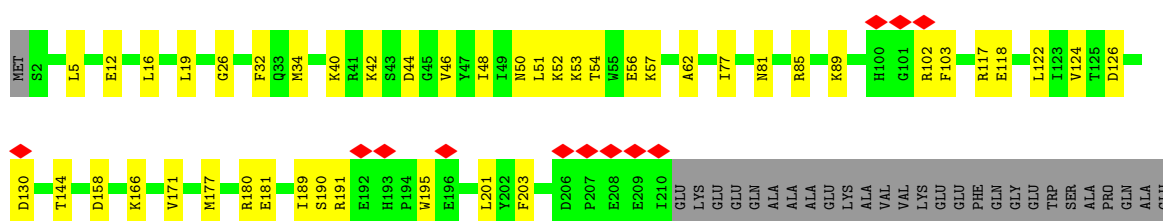
- Molecule 8: Large ribosomal subunit protein eL33



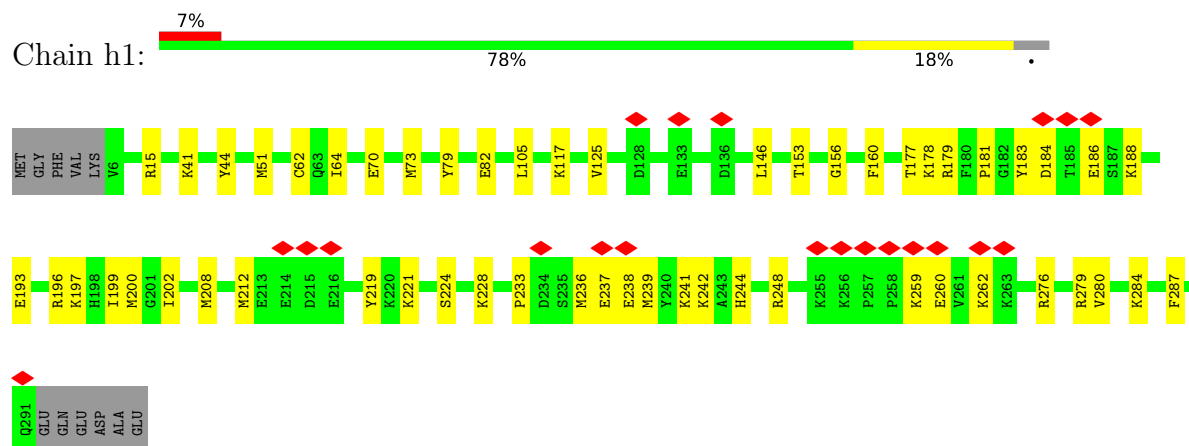
- Molecule 9: Large ribosomal subunit protein eL43



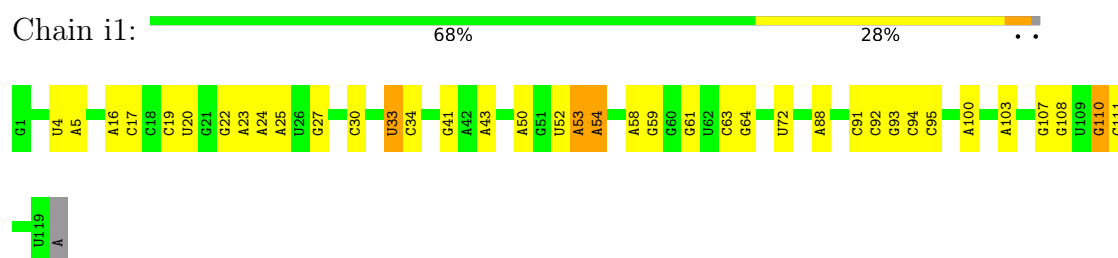
- Molecule 10: Small ribosomal subunit protein uS2



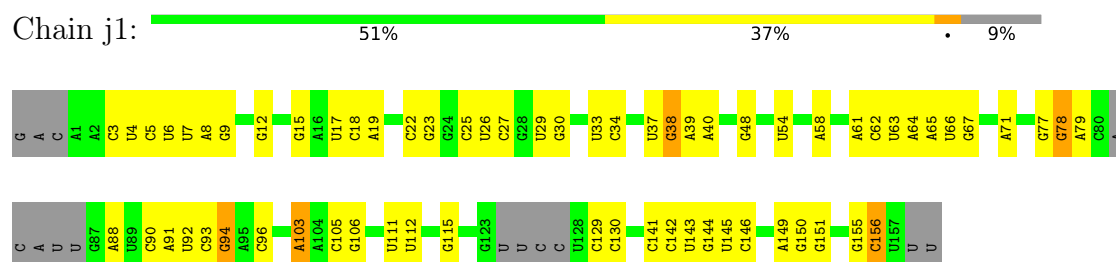
- Molecule 11: Large ribosomal subunit protein uL18



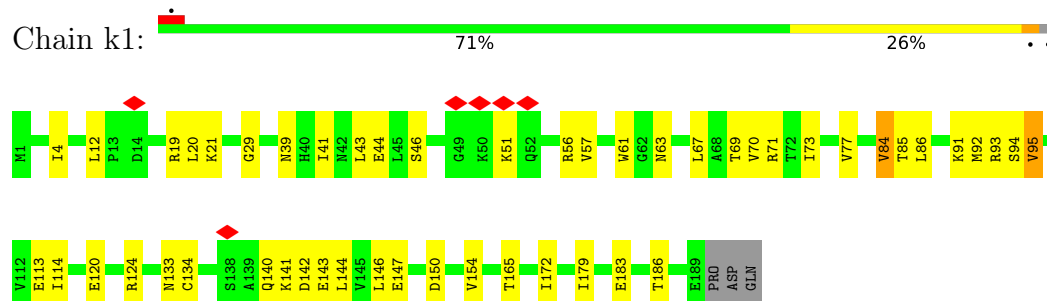
- Molecule 12: 5S rRNA



- Molecule 13: 5.8S rRNA

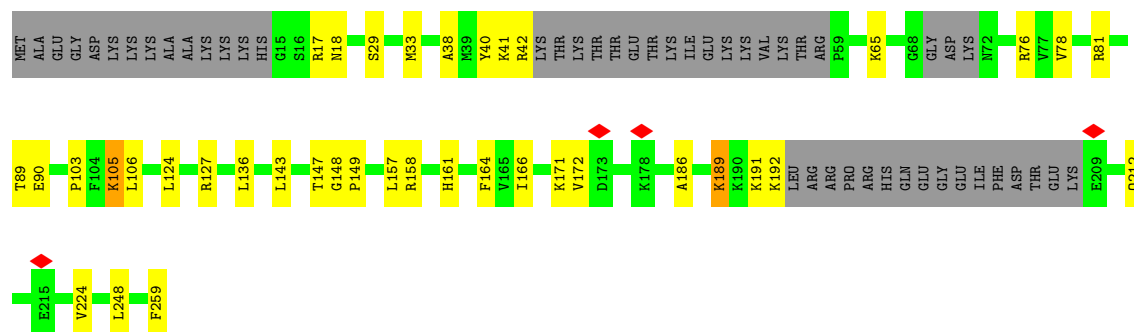


- Molecule 14: Large ribosomal subunit protein uL6

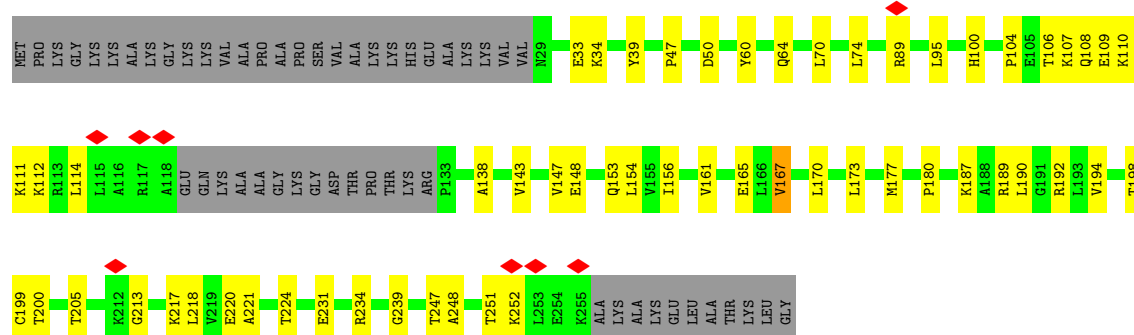


- Molecule 15: Large ribosomal subunit protein eL6

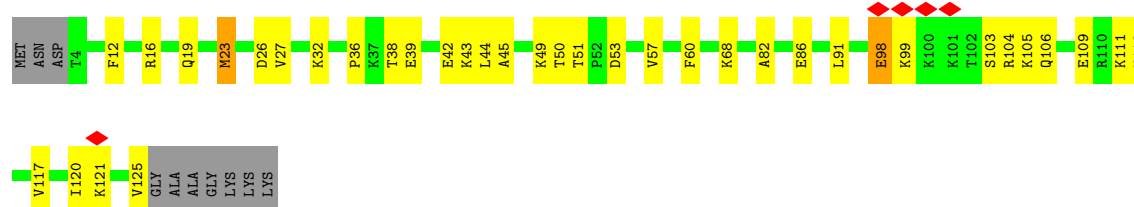




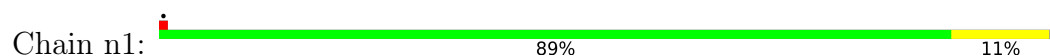
- Molecule 16: 60S ribosomal protein L7a



- Molecule 17: 40S ribosomal protein S24

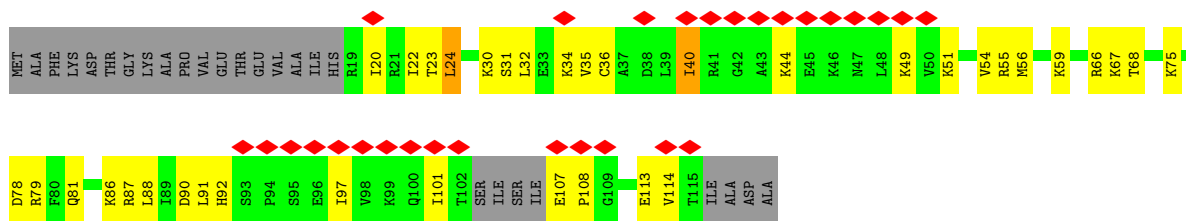


- Molecule 18: Large ribosomal subunit protein uL15



- Molecule 19: Small ribosomal subunit protein uS10





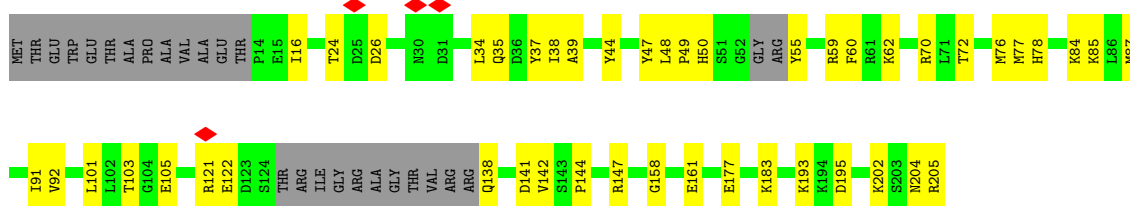
- Molecule 20: Small ribosomal subunit protein uS8

Chain r2: 73% 25% ..



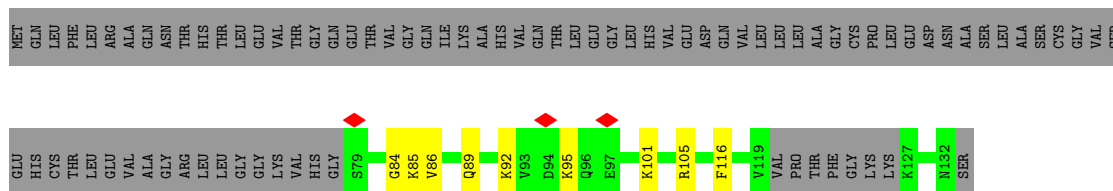
- Molecule 21: Small ribosomal subunit protein uS7

Chain u2: 65% 23% 13%



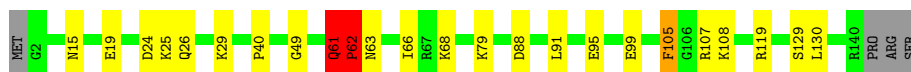
- Molecule 22: FAU ubiquitin like and ribosomal protein S30 fusion a

Chain x2: 29% 7% 65%



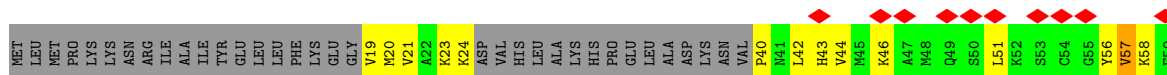
- Molecule 23: Small ribosomal subunit protein uS12

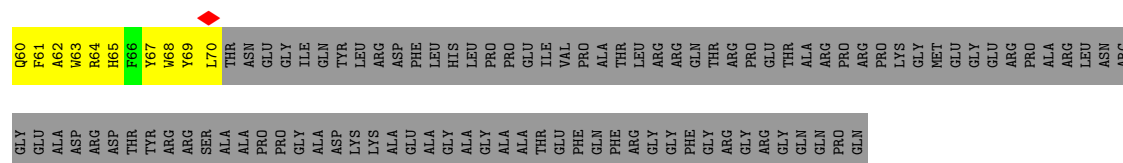
Chain y2: 80% 15% ..



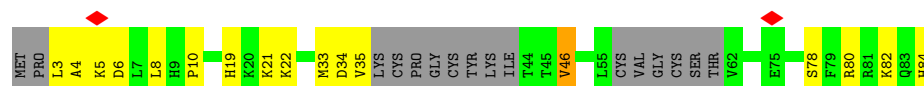
- Molecule 24: Ribosomal protein S10

Chain z2: 7% 8% 14% 78%

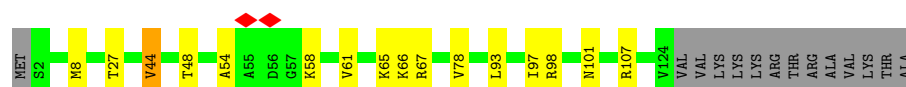
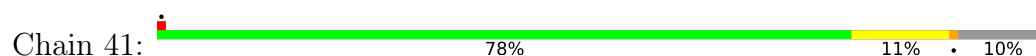




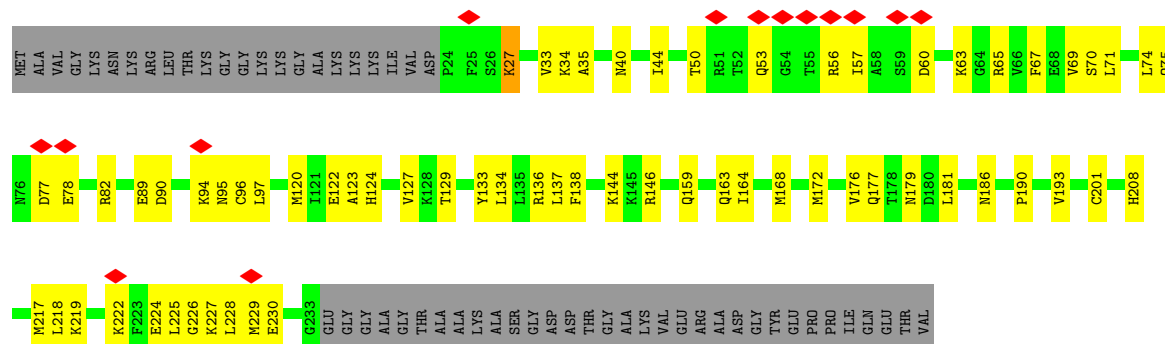
- Molecule 25: 40S ribosomal protein S27



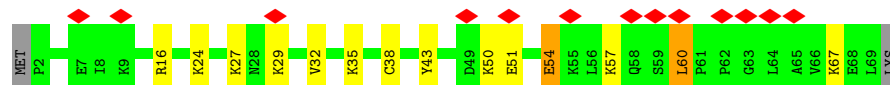
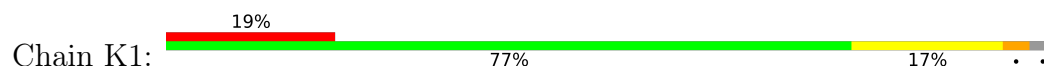
- Molecule 26: Large ribosomal subunit protein eL28



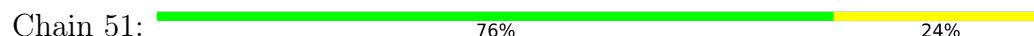
- Molecule 27: Small ribosomal subunit protein eS1



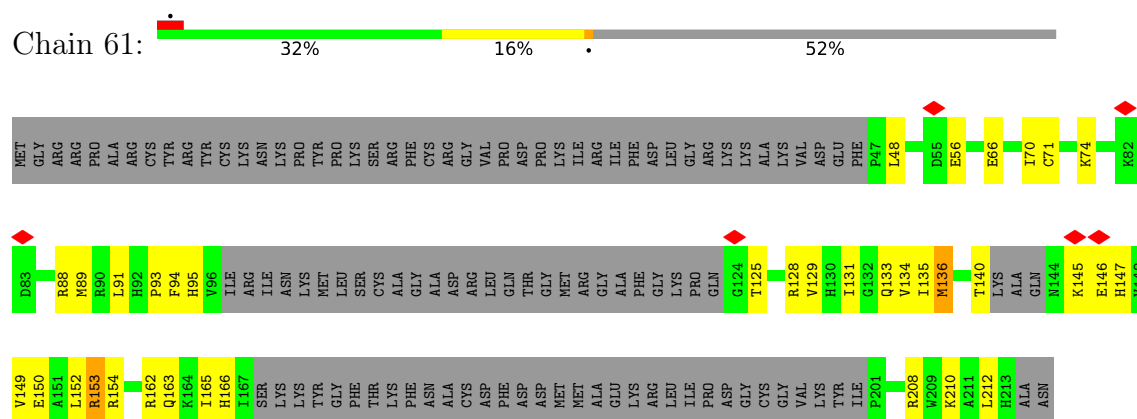
- Molecule 28: Large ribosomal subunit protein eL38



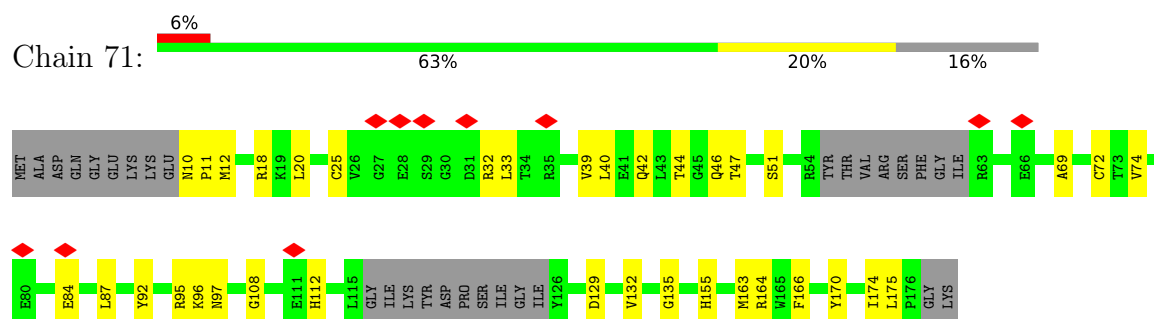
- Molecule 29: Small ribosomal subunit protein eS32



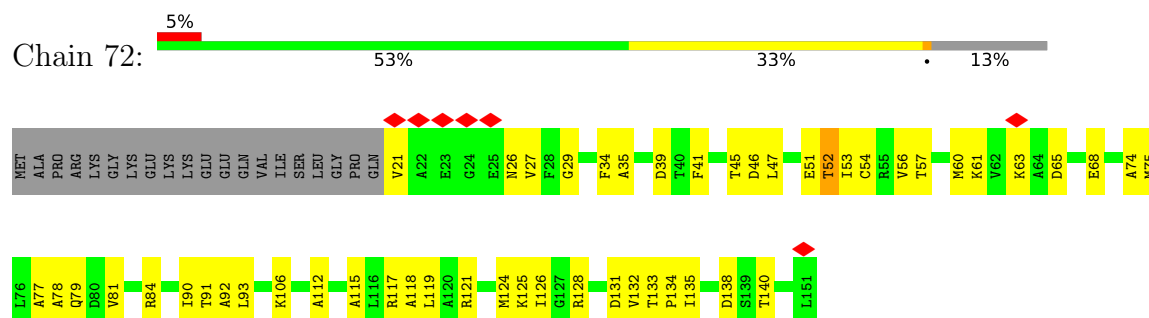
- Molecule 30: Ribosomal protein L10



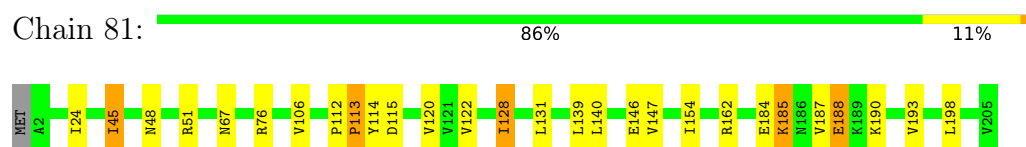
- Molecule 31: Large ribosomal subunit protein uL5



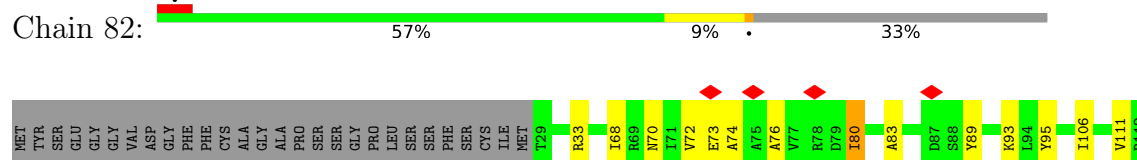
- Molecule 32: Small ribosomal subunit protein uS11

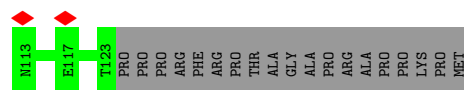


- Molecule 33: Large ribosomal subunit protein uL13



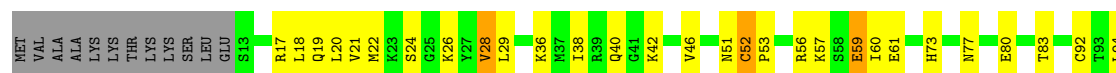
- Molecule 34: 40S ribosomal protein S26





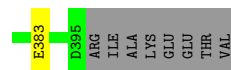
- Molecule 35: Large ribosomal subunit protein eL30

Chain 91: 52% 28% 17%



- Molecule 36: Large ribosomal subunit protein uL3

Chain B1: 81% 16%



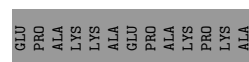
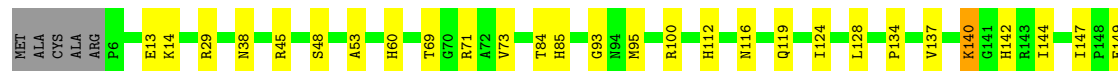
- Molecule 37: Small ribosomal subunit protein uS15

Chain B2: 77% 22%



- Molecule 38: Ribosomal protein L4

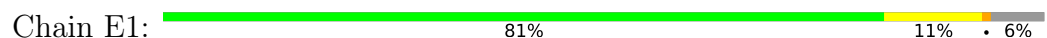
Chain C1: 77% 15% 7%



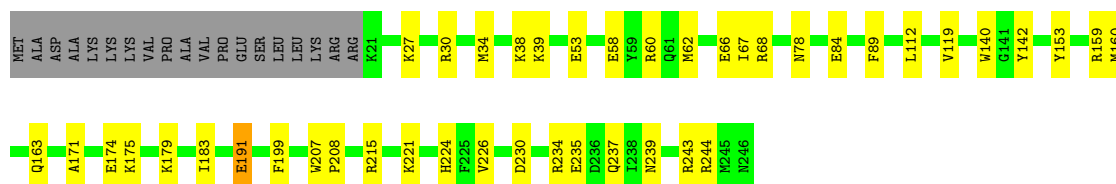
- Molecule 39: Large ribosomal subunit protein eL31



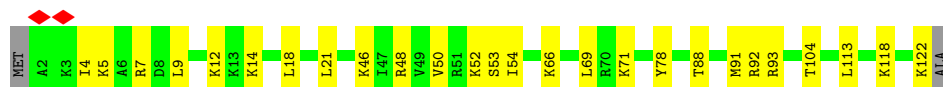
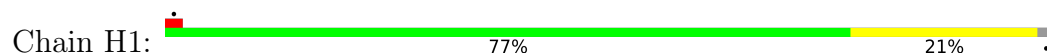
- Molecule 40: 60S ribosomal protein L32



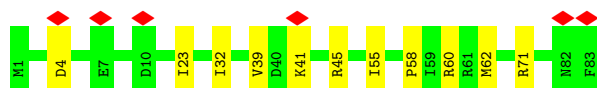
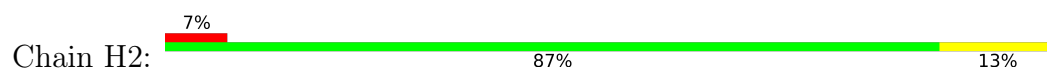
- Molecule 41: Large ribosomal subunit protein uL30



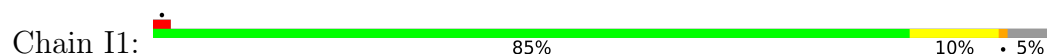
- Molecule 42: Large ribosomal subunit protein uL29



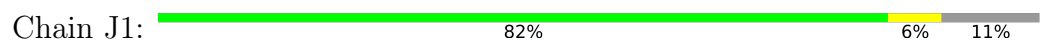
- Molecule 43: 40S ribosomal protein S21



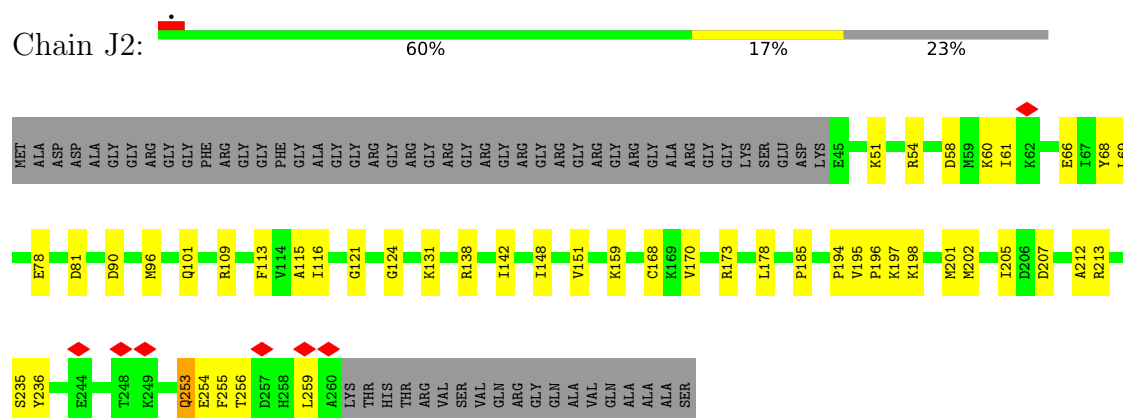
- Molecule 44: 60S ribosomal protein L36



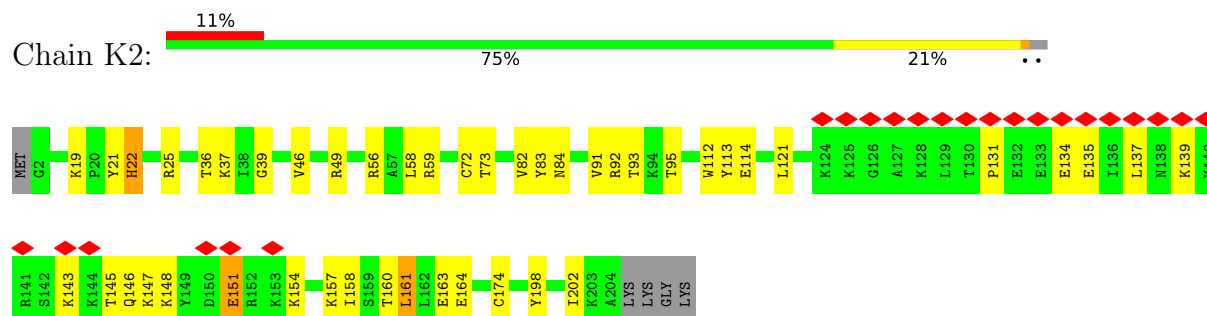
- Molecule 45: Ribosomal protein L37



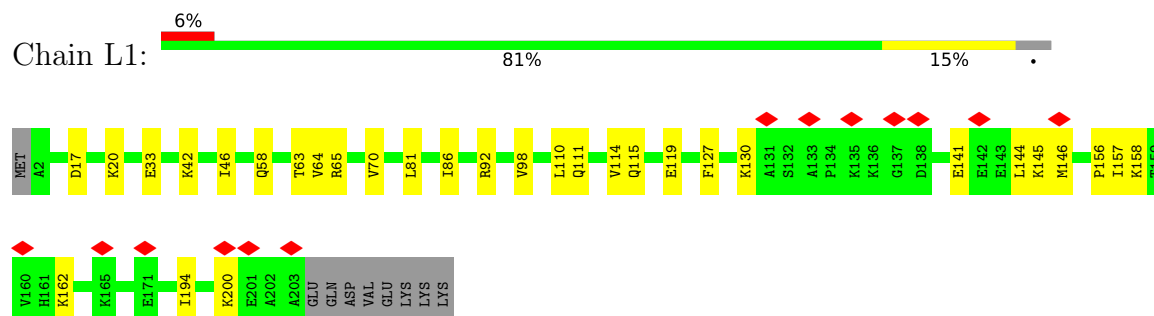
- Molecule 46: Small ribosomal subunit protein uS5



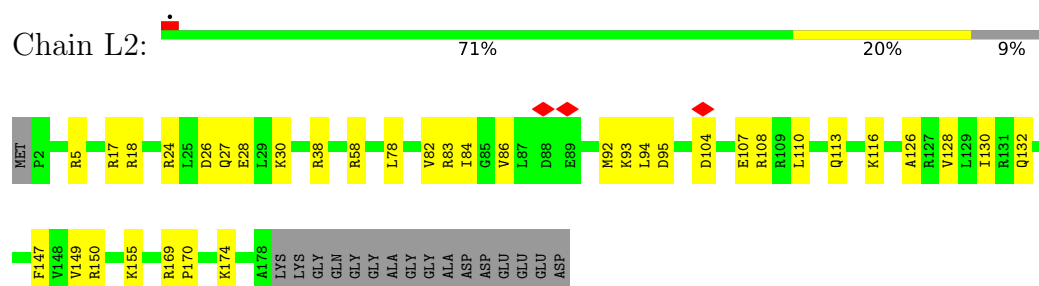
- Molecule 47: 40S ribosomal protein S8



- Molecule 48: 60S ribosomal protein L13



- Molecule 49: Small ribosomal subunit protein uS4

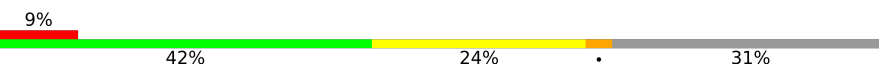


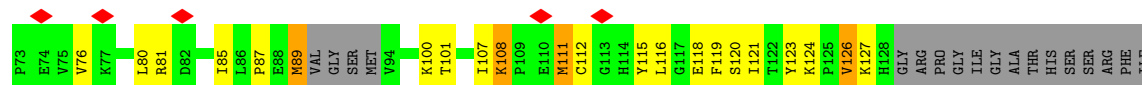
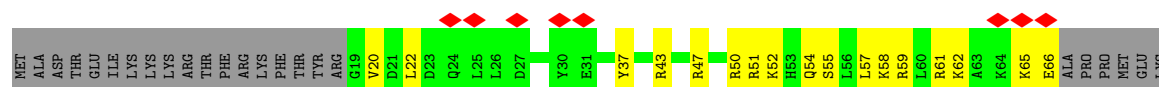
- Molecule 50: Large ribosomal subunit protein eL14

Chain M1: 



- Molecule 51: 40S ribosomal protein S15

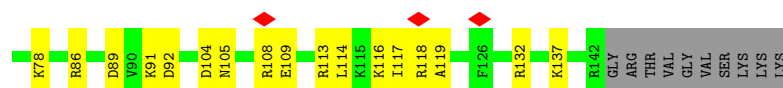
Chain A2: 



PRO, LEU, LYS

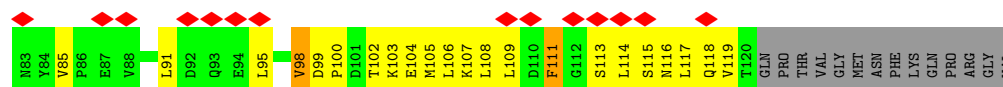
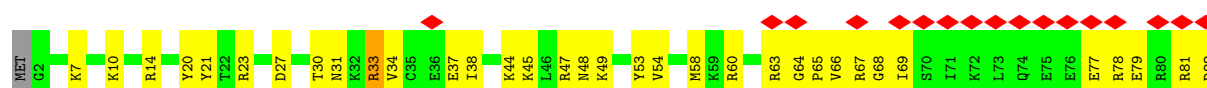
- Molecule 52: Small ribosomal subunit protein uS13

Chain P2: 



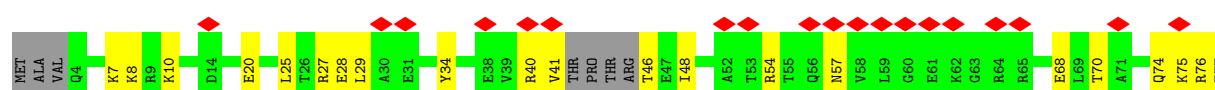
- Molecule 53: Small ribosomal subunit protein eS17

Chain i2: 

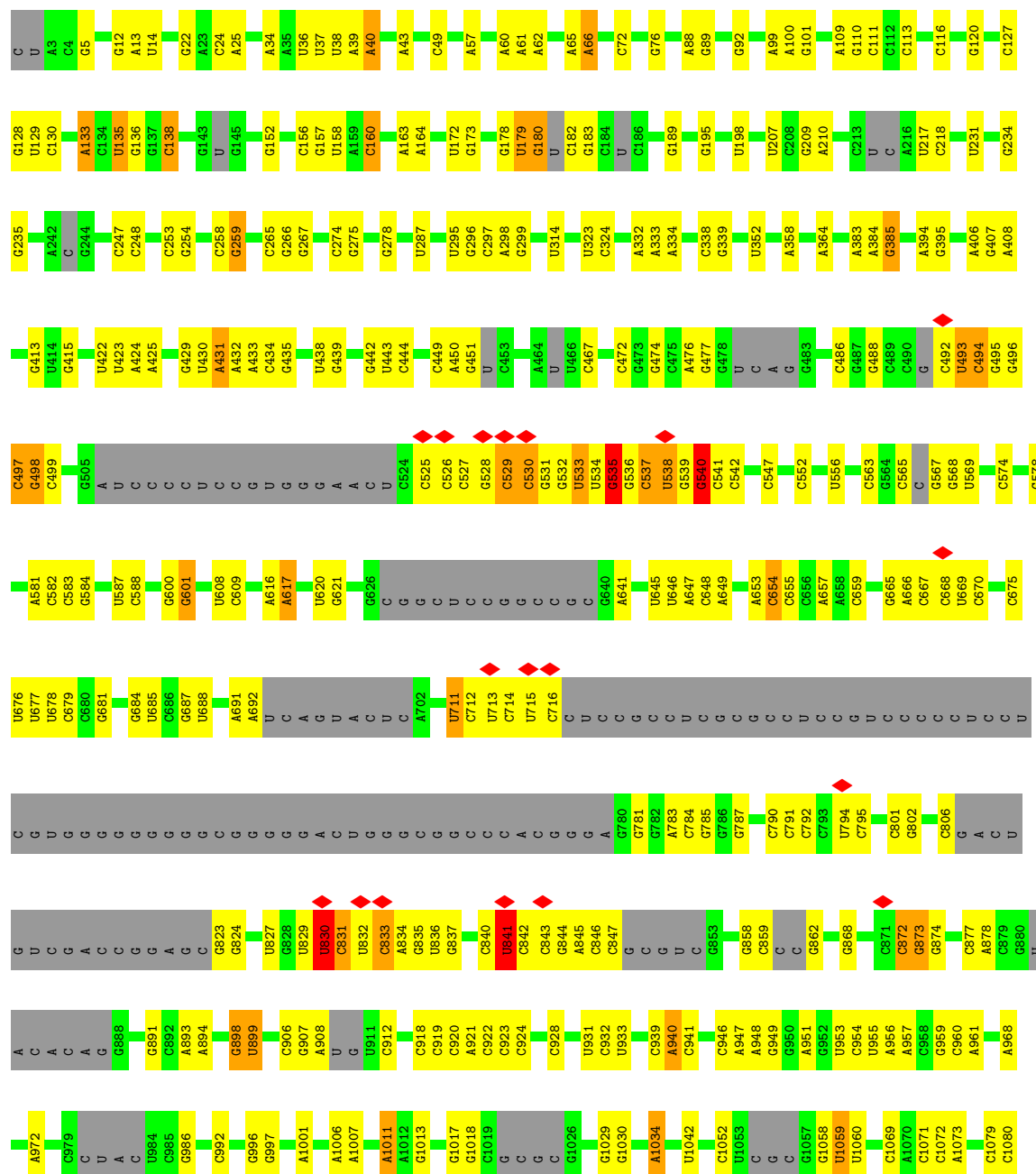


- Molecule 54: DNA-(apurinic or apyrimidinic site) lyase

Chain w2: 

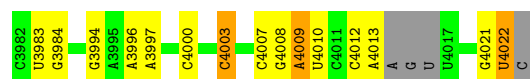


- Molecule 55: 28S rRNA



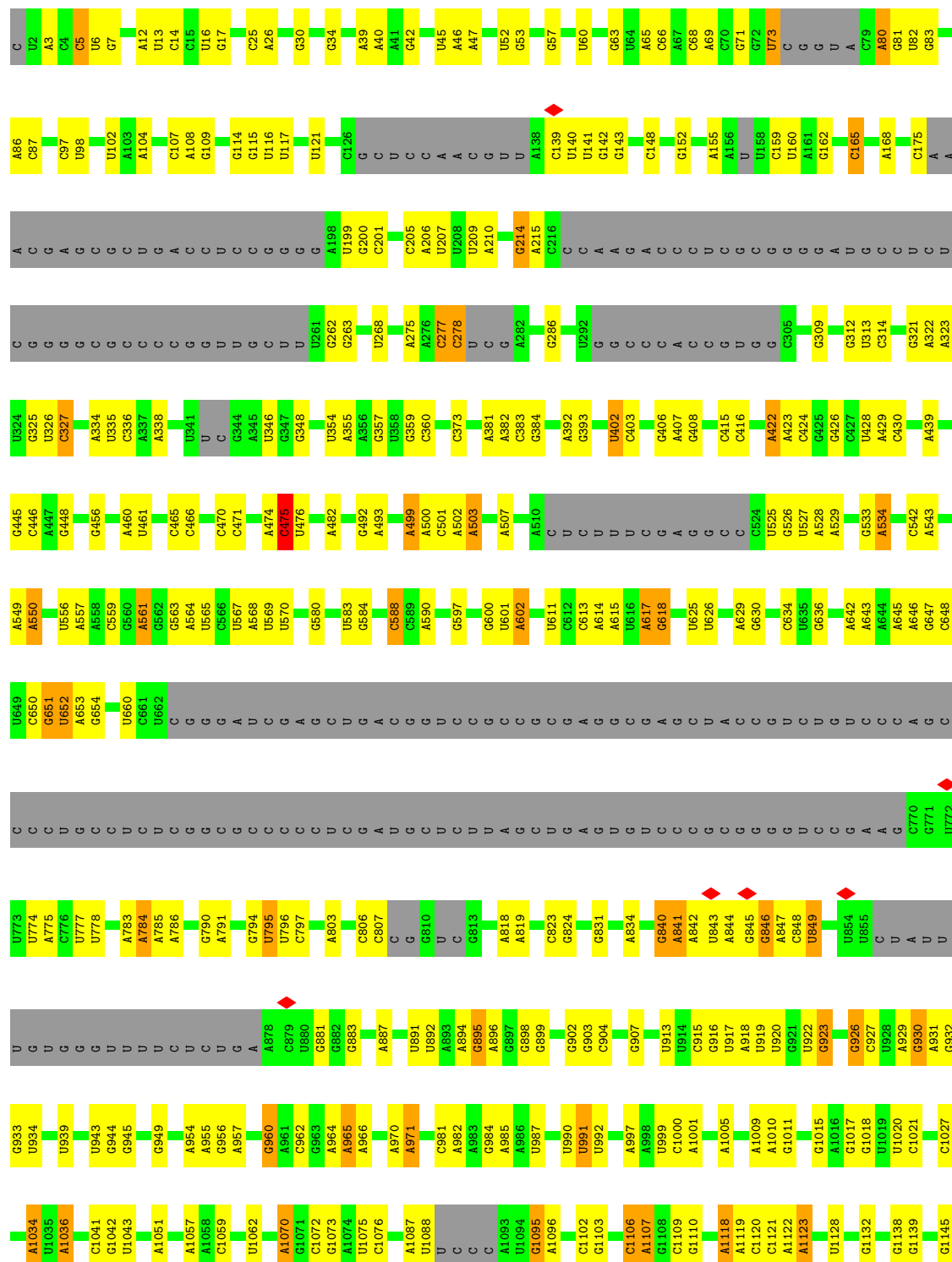
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U1320	U1321	A1322	C1324	G1327	C1333	G1335	A1336	A1337	G1338	U1340	U1341	A1342	G1343	A1344	G1439	G1440	C1441	C1442	G1448	A1449	C1450	C1451	A1452	C1453	A1461	A1462	G1463	C1464	C1469	U1470	G1471	U1476	G1477	A1482	A1486	C1487	C1488	G1489	A1490	A1491	A1502	G1503	U1512	G1513	C1514	G1515																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																							
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C3917	A3641	A3642	A3538	A3427	A3326	G3221	C2971	A	A2754	C	C
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A3969	A3739	A3740	A3587	A3476	A3375	G3270	A3022	U2958	U2703	C	C
U3970	A3741	A3742	A3588	A3477	A3376	G3271	A3023	A2959	U2703	C	C
C3971	A3743	A3744	A3589	A3478	A3377	G3272	A3024	G2960	U2703	C	C
A3972	A3745	A3746	A3590	A3479	A3378	G3273	A3025	A2961	U2703	C	C
G3973	A3747	A3748	A3591	A3480	A3379	G3274	A3026	U2962	U2703	C	C
U3974	A3749	A3750	A3592	A3481	A3380	G3275	A3027	A2963	U2703	C	C
C3975	A3751	A3752	A3593	A3482	A3381	G3276	A3028	U2964	U2703	C	C
A3976	A3753	A3754	A3594	A3483	A3382	G3277	A3029	U2965	U2703	C	C
U3977	A3755	A3756	A3595	A3484	A3383	G3278	A3030	U2966	U2703	C	C
C3978	A3757	A3758	A3596	A3485	A3384	G3279	A3031	U2967	U2703	C	C
A3979	A3759	A3760	A3597	A3486	A3385	G3280	A3032	U2968	U2703	C	C
U3980	A3761	A3762	A3598	A3487	A3386	G3281	A3033	U2969	U2703	C	C
C3981	A3763	A3764	A3599	A3488	A3387	G3282	A3034	U2970	U2703	C	C
A3982	A3765	A3766	A3600	A3489	A3388	G3283	A3035	U2971	U2703	C	C
G3983	A3767	A3768	A3601	A3490	A3389	G3284	A3036	U2972	U2703	C	C
U3984	A3769	A3770	A3602	A3491	A3390	G3285	A3037	U2973	U2703	C	C
C3985	A3771	A3772	A3603	A3492	A3391	G3286	A3038	U2974	U2703	C	C
A3986	A3773	A3774	A3604	A3493	A3392	G3287	A3039	U2975	U2703	C	C
U3987	A3775	A3776	A3605	A3494	A3393	G3288	A3040	U2976	U2703	C	C
C3988	A3777	A3778	A3606	A3495	A3394	G3289	A3041	U2977	U2703	C	C
A3989	A3779	A3780	A3607	A3496	A3395	G3290	A3042	U2978	U2703	C	C
U3990	A3781	A3782	A3608	A3497	A3396	G3291	A3043	U2979	U2703	C	C
C3991	A3783	A3784	A3609	A3498	A3397	G3292	A3044	U2980	U2703	C	C
A3992	A3785	A3786	A3610	A3499	A3398	G3293	A3045	U2981	U2703	C	C
G3993	A3787	A3788	A3611	A3500	A3399	G3294	A3046	U2982	U2703	C	C
U3994	A3789	A3790	A3612	A3501	A3400	G3295	A3047	U2983	U2703	C	C
C3995	A3791	A3792	A3613	A3502	A3401	G3296	A3048	U2984	U2703	C	C
A3996	A3793	A3794	A3614	A3503	A3402	G3297	A3049	U2985	U2703	C	C
U3997	A3795	A3796	A3615	A3504	A3403	G3298	A3050	U2986	U2703	C	C
C3998	A3797	A3798	A3616	A3505	A3404	G3299	A3051	U2987	U2703	C	C
A3999	A3799	A3800	A3617	A3506	A3405	G3300	A3052	U2988	U2703	C	C
U4000	A3801	A3802	A3618	A3507	A3406	G3301	A3053	U2989	U2703	C	C
C4001	A3803	A3804	A3619	A3508	A3407	G3302	A3054	U2990	U2703	C	C
A4002	A3805	A3806	A3620	A3509	A3408	G3303	A3055	U2991	U2703	C	C
U4003	A3807	A3808	A3621	A3510	A3409	G3304	A3056	U2992	U2703	C	C
C4004	A3809	A3810	A3622	A3511	A3410	G3305	A3057	U2993	U2703	C	C
A4005	A3811	A3812	A3623	A3512	A3411	G3306	A3058	U2994	U2703	C	C
U4006	A3813	A3814	A3624	A3513	A3412	G3307	A3059	U2995	U2703	C	C
C4007	A3815	A3816	A3625	A3514	A3413	G3308	A3060	U2996	U2703	C	C
A4008	A3817	A3818	A3626	A3515	A3414	G3309	A3061	U2997	U2703	C	C
U4009	A3819	A3820	A3627	A3516	A3415	G3310	A3062	U2998	U2703	C	C
C4010	A3821	A3822	A3628	A3517	A3416	G3311	A3063	U2999	U2703	C	C
A4011	A3823	A3824	A3629	A3518	A3417	G3312	A3064	U3000	U2703	C	C
U4012	A3825	A3826	A3630	A3519	A3418	G3313	A3065	U3001	U2703	C	C
C4013	A3827	A3828	A3631	A3520	A3419	G3314	A3066	U3002	U2703	C	C
A4014	A3829	A3830	A3632	A3521	A3420	G3315	A3067	U3003	U2703	C	C
U4015	A3831	A3832	A3633	A3522	A3421	G3316	A3068	U3004	U2703	C	C
C4016	A3833	A3834	A3634	A3523	A3422	G3317	A3069	U3005	U2703	C	C
A4017	A3835	A3836	A3635	A3524	A3423	G3318	A3070	U3006	U2703	C	C
U4018	A3837	A3838	A3636	A3525	A3424	G3319	A3071	U3007	U2703	C	C
C4019	A3839	A3840	A3637	A3526	A3425	G3320	A3072	U3008	U2703	C	C
A4020	A3841	A3842	A3638	A3527	A3426	G3321	A3073	U3009	U2703	C	C
U4021	A3843	A3844	A3639	A3528	A3427	G3322	A3074	U3010	U2703	C	C
C4022	A3845	A3846	A3640	A3529	A3428	G3323	A3075	U3011	U2703	C	C
A4023	A3847	A3848	A3641	A3530	A3429	G3324	A3076	U3012	U2703	C	C
U4024	A3849	A3850	A3642	A3531	A3430	G3325	A3077	U3013	U2703	C	C
C4025	A										



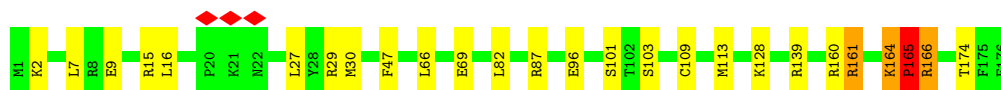
• Molecule 56: 18S rRNA

Chain C2: 50% 26% 19%



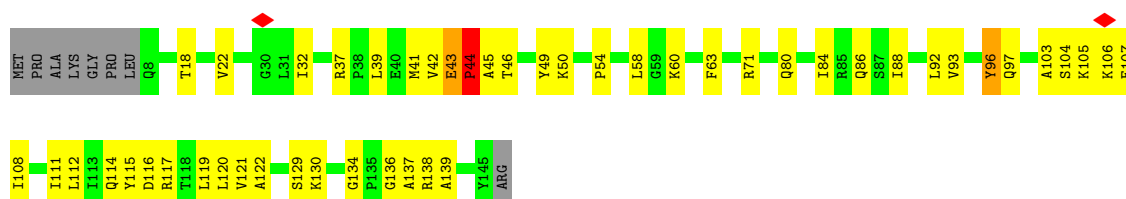
- Molecule 65: 60S ribosomal protein L18a

Chain S1: 



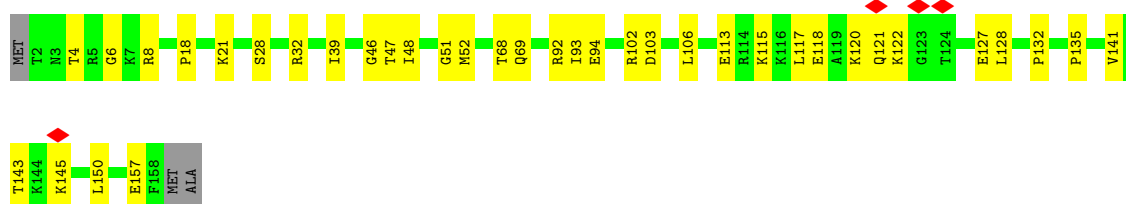
- Molecule 66: Small ribosomal subunit protein uS9

Chain S2: 



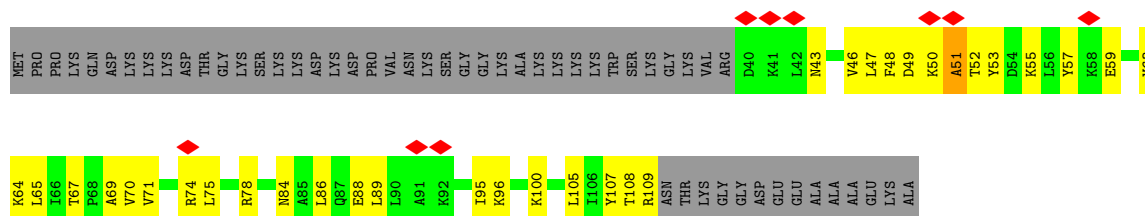
- Molecule 67: Large ribosomal subunit protein eL21

Chain T1: 



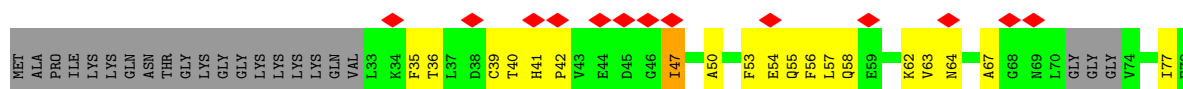
- Molecule 68: 40S ribosomal protein S25

Chain T2: 



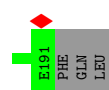
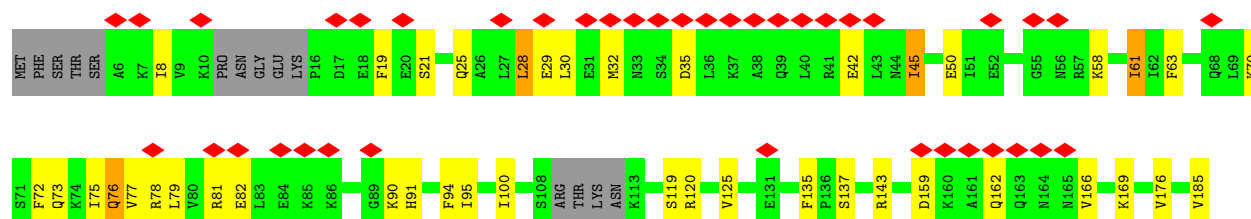
- Molecule 69: Large ribosomal subunit protein eL22

Chain U1: 

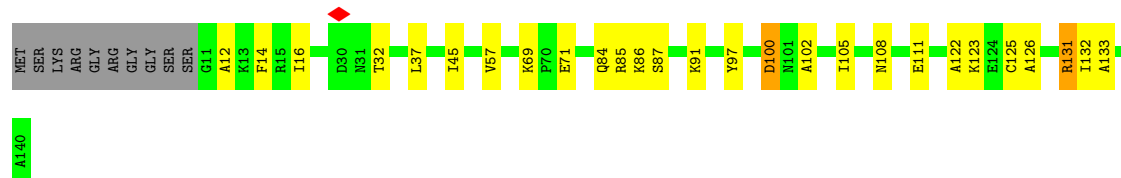
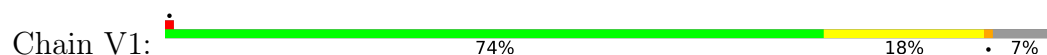




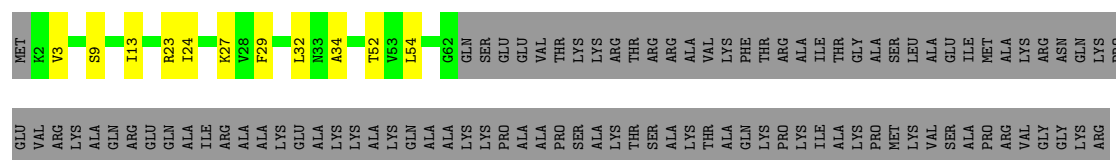
- Molecule 70: 40S ribosomal protein S7



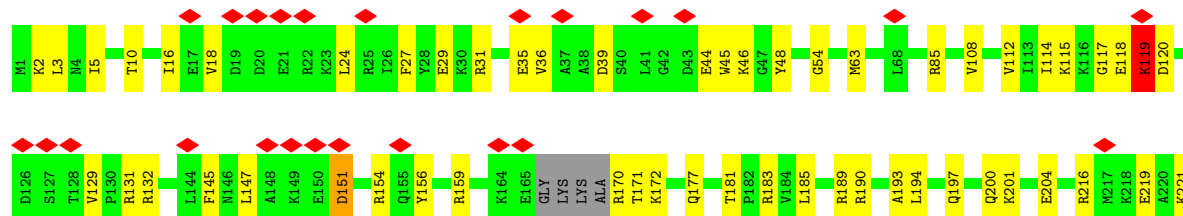
- Molecule 71: Large ribosomal subunit protein uL14

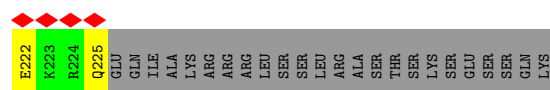


- Molecule 72: Large ribosomal subunit protein eL24

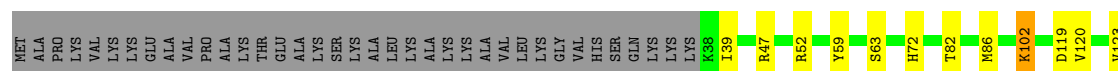


- Molecule 73: 40S ribosomal protein S6

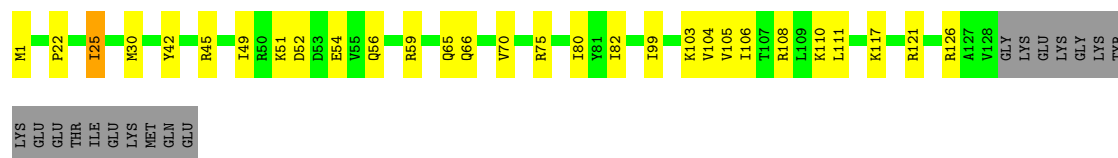




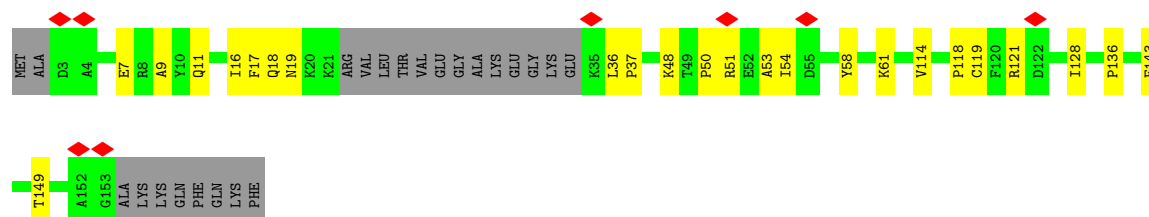
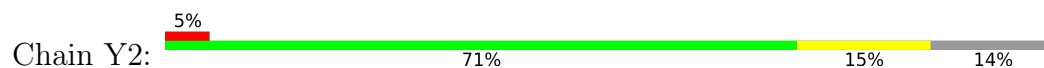
- Molecule 74: Large ribosomal subunit protein uL23



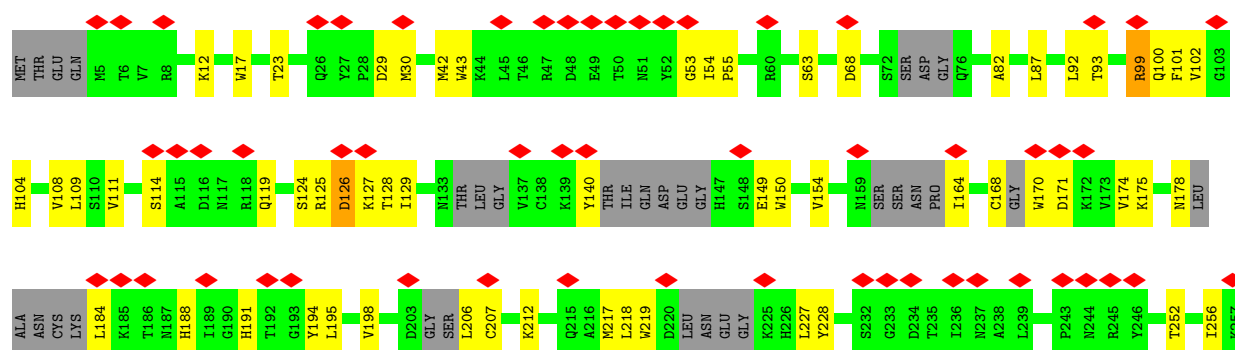
- Molecule 75: Ribosomal protein L26

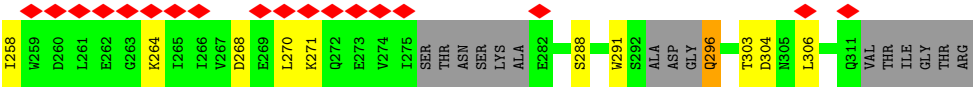


- Molecule 76: Small ribosomal subunit protein uS17



- Molecule 77: Small ribosomal subunit protein RACK1





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	115566	Depositor
Resolution determination method	OTHER	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60.23	Depositor
Minimum defocus (nm)	300	Depositor
Maximum defocus (nm)	1000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.577	Depositor
Minimum map value	-0.032	Depositor
Average map value	0.005	Depositor
Map value standard deviation	0.012	Depositor
Recommended contour level	0.05	Depositor
Map size (Å)	529.92, 529.92, 529.92	wwPDB
Map dimensions	640, 640, 640	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.82799995, 0.82799995, 0.82799995	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	11	0.19	0/454	0.39	0/599
2	21	0.15	0/393	0.35	0/519
3	Z1	0.18	0/1130	0.41	0/1507
4	a1	0.18	0/1929	0.40	0/2584
5	b1	0.26	0/438	0.48	0/579
6	d2	0.24	0/443	0.62	0/589
7	e1	0.29	0/871	0.46	0/1161
8	f1	0.23	0/892	0.48	0/1193
9	g1	0.16	0/696	0.38	0/924
10	g2	0.19	0/1699	0.48	0/2308
11	h1	0.17	0/2357	0.40	0/3158
12	i1	0.35	0/2842	0.76	0/4430
13	j1	0.32	0/3501	0.78	0/5451
14	k1	0.19	0/1521	0.43	0/2043
15	l1	0.18	0/1706	0.41	0/2282
16	m1	0.19	0/1764	0.44	0/2374
17	m2	0.20	0/1017	0.44	0/1351
18	n1	0.16	0/1191	0.33	0/1593
19	q2	0.20	0/752	0.54	0/1007
20	r2	0.16	0/1053	0.37	0/1409
21	u2	0.18	0/1421	0.49	0/1908
22	x2	0.17	0/382	0.45	0/501
23	y2	0.26	0/1100	0.52	1/1468 (0.1%)
24	z2	0.24	0/327	0.75	0/436
25	32	0.19	0/558	0.51	0/744
26	41	0.21	0/994	0.37	0/1332
27	42	0.19	0/1735	0.50	1/2321 (0.0%)
28	K1	0.21	0/565	0.57	0/750
29	51	0.20	0/240	0.49	0/305
30	61	0.21	0/853	0.58	0/1139
31	71	0.21	0/1229	0.50	0/1636
32	72	0.22	0/993	0.52	0/1332

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	81	0.23	0/1692	0.46	1/2268 (0.0%)
34	82	0.16	0/766	0.42	0/1024
35	91	0.32	0/756	0.61	1/1013 (0.1%)
36	B1	0.17	0/3243	0.38	0/4345
37	B2	0.16	0/1228	0.40	0/1649
38	C1	0.17	0/2845	0.38	0/3822
39	D1	0.17	0/850	0.39	0/1141
40	E1	0.16	0/1060	0.34	0/1413
41	F1	0.19	0/1901	0.39	0/2539
42	H1	0.17	0/1010	0.40	0/1334
43	H2	0.30	0/653	0.60	0/875
44	I1	0.18	0/823	0.46	0/1092
45	J1	0.16	0/720	0.38	0/953
46	J2	0.17	0/1707	0.42	0/2308
47	K2	0.20	0/1681	0.45	0/2243
48	L1	0.17	0/1661	0.40	0/2218
49	L2	0.17	0/1498	0.40	0/2003
50	M1	0.21	0/1108	0.44	0/1479
51	A2	0.23	0/844	0.60	1/1123 (0.1%)
52	P2	0.22	0/1173	0.63	0/1571
53	i2	0.23	0/980	0.64	0/1314
54	w2	0.21	0/1626	0.55	0/2184
55	A1	0.34	0/76831	0.80	14/119730 (0.0%)
56	C2	0.30	0/35470	0.76	4/55243 (0.0%)
57	M2	0.19	0/1105	0.44	0/1483
58	N1	0.17	0/1740	0.33	0/2327
59	N2	0.14	0/321	0.30	0/423
60	O1	0.17	0/783	0.41	0/1035
61	O2	0.15	0/2081	0.38	0/2800
62	P1	0.27	0/1258	0.46	0/1687
63	Q1	0.18	0/1536	0.36	0/2051
64	R1	0.20	0/1439	0.48	1/1902 (0.1%)
65	S1	0.22	0/1498	0.51	1/2011 (0.0%)
66	S2	0.25	0/1107	0.58	2/1484 (0.1%)
67	T1	0.17	0/1319	0.41	0/1765
68	T2	0.27	0/575	0.58	0/772
69	U1	0.25	0/769	0.61	0/1027
70	U2	0.19	0/1448	0.46	0/1937
71	V1	0.16	0/987	0.38	0/1324
72	W1	0.15	0/525	0.32	0/699
73	W2	0.21	0/1812	0.47	0/2412
74	X1	0.18	0/986	0.41	0/1326
75	Y1	0.18	0/1083	0.41	0/1442

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	Y2	0.22	0/1141	0.40	0/1528
77	k2	0.20	0/2184	0.52	1/2960 (0.0%)
All	All	0.28	0/204869	0.68	28/300212 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
23	y2	0	1
62	P1	0	1
77	k2	0	1
All	All	0	3

There are no bond length outliers.

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
77	k2	126	ASP	N-CA-C	-8.97	102.44	112.57
23	y2	62	PRO	O-C-N	-8.48	111.19	122.64
56	C2	73	U	C3'-C2'-C1'	-6.71	96.13	101.50
55	A1	830	U	P-O3'-C3'	6.59	127.61	119.70
56	C2	1247	C	N3-C2-O2	-6.54	117.32	121.90
55	A1	535	G	P-O3'-C3'	6.38	127.36	119.70
55	A1	535	G	C1'-O4'-C4'	-6.11	105.42	109.70
55	A1	2060	C	C2-N1-C1'	5.84	125.22	118.80
27	42	27	LYS	CA-CB-CG	5.75	125.61	114.10
35	91	103	ASP	N-CA-C	-5.63	106.63	112.93
55	A1	156	C	N3-C2-O2	-5.60	117.98	121.90
64	R1	138	LEU	N-CA-C	-5.58	98.91	110.80
65	S1	165	PRO	CB-CA-C	5.58	120.77	111.56
55	A1	841	U	N1-C1'-C2'	5.54	118.09	112.00
55	A1	830	U	C2'-C3'-O3'	-5.52	104.87	113.70
55	A1	540	G	C3'-C2'-C1'	-5.52	97.09	101.50
55	A1	2060	C	N1-C2-O2	5.50	122.20	118.90
55	A1	1312	U	C2-N1-C1'	5.48	124.27	117.70
66	S2	44	PRO	CA-N-CD	-5.38	104.47	112.00
55	A1	1843	C	C2-N1-C1'	5.33	124.66	118.80
33	81	188	GLU	CA-CB-CG	5.23	124.55	114.10
51	A2	108	LYS	CA-CB-CG	5.19	124.47	114.10
56	C2	475	C	C2-N1-C1'	5.18	124.50	118.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
55	A1	116	C	O4'-C1'-N1	5.17	112.12	108.50
55	A1	2840	C	N3-C2-O2	-5.13	118.31	121.90
56	C2	588	C	N1-C2-O2	5.06	121.94	118.90
55	A1	384	A	O5'-C5'-C4'	5.04	113.43	109.40
66	S2	44	PRO	CB-CA-C	5.02	119.84	111.56

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
62	P1	69	ARG	Sidechain
77	k2	99	ARG	Sidechain
23	y2	62	PRO	Mainchain

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	11	444	0	483	10	0
2	21	387	0	416	8	0
3	Z1	1107	0	1184	19	0
4	a1	1890	0	1985	35	0
5	b1	428	0	443	4	0
6	d2	443	0	473	21	0
7	e1	861	0	951	10	0
8	f1	872	0	911	9	0
9	g1	686	0	743	14	0
10	g2	1660	0	1655	43	0
11	h1	2311	0	2342	43	0
12	i1	2541	0	1286	19	0
13	j1	3135	0	1590	51	0
14	k1	1503	0	1586	42	0
15	l1	1677	0	1827	25	0
16	m1	1730	0	1845	39	0
17	m2	1001	0	1081	22	0
18	n1	1159	0	1197	10	0
19	q2	744	0	806	33	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
20	r2	1036	0	1082	24	0
21	u2	1401	0	1442	34	0
22	x2	380	0	418	9	0
23	y2	1083	0	1150	21	0
24	z2	317	0	320	26	0
25	32	549	0	562	13	0
26	41	979	0	1040	7	0
27	42	1708	0	1781	46	0
28	K1	559	0	624	10	0
29	51	239	0	289	5	0
30	61	836	0	858	36	0
31	71	1212	0	1254	23	0
32	72	981	0	1005	41	0
33	81	1660	0	1812	18	0
34	82	756	0	799	16	0
35	91	746	0	778	25	0
36	B1	3173	0	3294	50	0
37	B2	1205	0	1292	26	0
38	C1	2788	0	2954	38	0
39	D1	837	0	897	9	0
40	E1	1042	0	1138	10	0
41	F1	1865	0	2002	30	0
42	H1	1003	0	1131	22	0
43	H2	645	0	648	10	0
44	I1	811	0	887	8	0
45	J1	706	0	735	5	0
46	J2	1671	0	1751	35	0
47	K2	1652	0	1737	31	0
48	L1	1632	0	1733	22	0
49	L2	1473	0	1585	34	0
50	M1	1088	0	1144	13	0
51	A2	832	0	868	40	0
52	P2	1155	0	1209	50	0
53	i2	969	0	1020	53	0
54	w2	1602	0	1688	66	0
55	A1	68707	0	34705	550	0
56	C2	31719	0	16018	314	0
57	M2	1088	0	1135	22	0
58	N1	1697	0	1743	20	0
59	N2	317	0	323	6	0
60	O1	770	0	832	8	0
61	O2	2040	0	2152	30	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
62	P1	1232	0	1260	19	0
63	Q1	1510	0	1622	19	0
64	R1	1423	0	1566	31	0
65	S1	1458	0	1516	20	0
66	S2	1090	0	1151	42	0
67	T1	1290	0	1356	27	0
68	T2	568	0	619	29	0
69	U1	757	0	782	28	0
70	U2	1429	0	1527	31	0
71	V1	973	0	1034	19	0
72	W1	512	0	525	8	0
73	W2	1791	0	1936	39	0
74	X1	968	0	1039	14	0
75	Y1	1067	0	1162	19	0
76	Y2	1121	0	1178	16	0
77	k2	2138	0	2097	57	0
78	21	1	0	0	0	0
78	82	1	0	0	0	0
78	J1	1	0	0	0	0
78	N2	1	0	0	0	0
78	O1	1	0	0	0	0
78	e1	1	0	0	0	0
78	g1	1	0	0	0	0
79	A1	62	0	0	0	0
79	C2	21	0	0	0	0
79	J1	1	0	0	0	0
79	i1	1	0	0	0	0
All	All	190927	0	143009	2466	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 7.

All (2466) 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)
33:81:48:ASN:HB3	33:81:51:ARG:HG2	1.40	1.02
30:61:145:LYS:HE2	30:61:145:LYS:H	1.25	1.00
52:P2:113:ARG:HA	52:P2:116:LYS:HE3	1.43	0.99
8:f1:106:TYR:HB3	8:f1:107:PRO:HD2	1.47	0.95
54:w2:54:ARG:HH12	54:w2:57:ASN:HB3	1.30	0.94
54:w2:46:THR:O	54:w2:84:VAL:HA	1.69	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:72:117:ARG:HB3	32:72:121:ARG:HH12	1.34	0.90
37:B2:32:ASP:HA	37:B2:35:GLU:HG3	1.55	0.89
66:S2:43:GLU:HB3	66:S2:44:PRO:HD2	1.55	0.88
63:Q1:35:LEU:O	63:Q1:39:SER:HB3	1.74	0.88
76:Y2:7:GLU:HG3	76:Y2:11:GLN:HE21	1.36	0.87
14:k1:19:ARG:HH22	55:A1:3819:G:H5'	1.42	0.85
76:Y2:50:PRO:HG2	76:Y2:119:CYS:SG	2.17	0.85
77:k2:296:GLN:HE21	77:k2:296:GLN:N	1.75	0.84
48:L1:63:THR:HG22	48:L1:65:ARG:H	1.42	0.83
55:A1:3786:A:N6	55:A1:3911:G:C6	2.47	0.83
54:w2:94:ARG:HH22	54:w2:97:CYS:HB3	1.44	0.82
38:C1:150:VAL:HG13	38:C1:151:PRO:HD3	1.62	0.81
54:w2:141:LYS:HB2	54:w2:179:GLN:HE22	1.44	0.81
51:A2:85:ILE:HD13	51:A2:116:LEU:HD21	1.62	0.81
18:n1:66:ASN:HB3	48:L1:63:THR:HG21	1.64	0.79
55:A1:1123:G:H2'	55:A1:1124:A:H8	1.48	0.79
47:K2:83:TYR:HB2	47:K2:202:ILE:HD11	1.65	0.79
77:k2:217:MET:HE3	77:k2:219:TRP:HE1	1.48	0.79
4:a1:247:ARG:HG2	56:C2:1043:U:H5''	1.63	0.78
52:P2:78:LYS:HE3	52:P2:78:LYS:HA	1.63	0.78
39:D1:99:LYS:HA	39:D1:99:LYS:HE3	1.64	0.78
46:J2:116:ILE:HD11	46:J2:148:ILE:HD11	1.66	0.78
30:61:89:MET:HE3	30:61:89:MET:HA	1.67	0.77
10:g2:50:ASN:HA	53:i2:105:MET:HE1	1.66	0.77
26:41:58:LYS:HE3	26:41:58:LYS:HA	1.68	0.76
42:H1:69:LEU:HD13	74:X1:63:SER:HB3	1.67	0.76
69:U1:39:CYS:HB3	69:U1:126:LEU:HD22	1.66	0.76
38:C1:205:LYS:HB3	38:C1:248:ARG:HH12	1.51	0.76
38:C1:307:LYS:HA	38:C1:307:LYS:HE3	1.69	0.75
60:O1:24:THR:HG23	60:O1:69:ARG:HB3	1.66	0.75
38:C1:140:LYS:HE3	38:C1:245:HIS:HB3	1.69	0.74
30:61:131:ILE:H	30:61:131:ILE:HD12	1.51	0.74
42:H1:9:LEU:HA	42:H1:12:LYS:HZ3	1.53	0.74
53:i2:78:ARG:NH1	53:i2:78:ARG:HA	2.01	0.74
32:72:34:PHE:HB3	32:72:41:PHE:HB2	1.70	0.74
23:y2:68:LYS:HB3	23:y2:91:LEU:HD22	1.70	0.74
55:A1:920:C:H2'	55:A1:921:A:H8	1.52	0.73
27:42:229:MET:HA	27:42:229:MET:HE3	1.70	0.73
2:21:82:LEU:HD12	14:k1:95:VAL:HB	1.69	0.73
16:m1:167:VAL:HG12	16:m1:170:LEU:HD12	1.70	0.73
32:72:93:LEU:HG	32:72:124:MET:HE2	1.69	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
66:S2:106:LYS:HZ3	77:k2:55:PRO:HG2	1.52	0.73
76:Y2:36:LEU:HD12	76:Y2:37:PRO:HD2	1.71	0.73
8:f1:63:LYS:HD2	8:f1:64:PRO:HD2	1.70	0.73
49:L2:155:LYS:H	49:L2:155:LYS:HE2	1.54	0.73
51:A2:100:LYS:HG3	51:A2:101:THR:HG23	1.69	0.73
75:Y1:30:MET:HE1	75:Y1:75:ARG:HG2	1.71	0.73
66:S2:106:LYS:NZ	77:k2:55:PRO:HG2	2.03	0.72
48:L1:156:PRO:HB2	48:L1:158:LYS:HZ1	1.54	0.72
52:P2:23:ARG:HH22	68:T2:43:ASN:HB2	1.54	0.72
19:q2:30:LYS:HA	19:q2:30:LYS:HE3	1.72	0.72
21:u2:103:THR:HG23	21:u2:105:GLU:H	1.54	0.72
55:A1:3574:U:H4'	55:A1:3575:U:H5'	1.72	0.71
1:11:25:GLN:HA	1:11:28:ARG:HH12	1.54	0.71
10:g2:85:ARG:HE	10:g2:89:LYS:HE2	1.53	0.71
55:A1:525:C:H2'	55:A1:526:C:C6	2.25	0.71
62:P1:70:CYS:SG	62:P1:83:TRP:CH2	2.81	0.71
61:O2:127:LYS:HD2	61:O2:142:HIS:HA	1.70	0.71
71:V1:57:VAL:HG11	71:V1:122:ALA:HB3	1.71	0.71
70:U2:32:MET:HA	70:U2:32:MET:HE3	1.72	0.71
14:k1:41:ILE:HG21	14:k1:69:THR:HG21	1.73	0.70
48:L1:162:LYS:HD3	48:L1:162:LYS:H	1.56	0.70
55:A1:1891:C:H5'	58:N1:67:ARG:HD2	1.73	0.70
40:E1:107:ASN:HA	40:E1:110:LEU:HD12	1.74	0.70
55:A1:1683:G:H22	55:A1:1698:G:H1	1.39	0.70
73:W2:170:ARG:HH22	73:W2:172:LYS:HB2	1.56	0.70
49:L2:136:ARG:HD2	49:L2:139:LYS:HA	1.72	0.70
1:11:43:HIS:HB3	1:11:46:ARG:HG2	1.73	0.70
55:A1:2854:G:N2	55:A1:2874:U:O2	2.23	0.70
46:J2:51:LYS:HG2	46:J2:54:ARG:HH22	1.57	0.70
52:P2:50:ILE:H	52:P2:50:ILE:HD12	1.56	0.70
14:k1:71:ARG:HG2	55:A1:3734:A:H4'	1.73	0.69
55:A1:2177:A:H2'	55:A1:2178:A:C8	2.27	0.69
40:E1:78:LEU:HD12	40:E1:98:GLU:HB3	1.74	0.69
43:H2:41:LYS:HA	43:H2:41:LYS:HE3	1.75	0.69
75:Y1:54:GLU:HB2	75:Y1:108:ARG:HB3	1.74	0.69
32:72:54:CYS:HB3	32:72:84:ARG:HH21	1.58	0.69
52:P2:22:GLY:HA2	52:P2:56:ALA:HB3	1.75	0.69
55:A1:824:G:H1	55:A1:837:G:H22	1.38	0.68
56:C2:955:A:H2'	56:C2:956:G:C8	2.28	0.68
55:A1:1095:G:H2'	55:A1:1096:U:H4'	1.75	0.68
20:r2:88:LYS:HE2	56:C2:393:G:H4'	1.74	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:B2:67:THR:HG21	37:B2:74:ILE:HD11	1.75	0.68
55:A1:2818:A:H2'	55:A1:2819:A:H8	1.59	0.68
67:T1:103:ASP:HA	67:T1:106:LEU:HD12	1.74	0.68
12:i1:27:G:H1	12:i1:52:U:H3	1.39	0.68
32:72:106:LYS:HD2	32:72:135:ILE:HG22	1.74	0.68
53:i2:33:ARG:CG	77:k2:125:ARG:HH12	2.07	0.68
55:A1:2818:A:H2'	55:A1:2819:A:C8	2.28	0.68
61:O2:206:ASP:HB3	61:O2:222:LEU:HB2	1.76	0.68
10:g2:12:GLU:HA	53:i2:111:PHE:HE2	1.59	0.68
55:A1:3637:U:H2'	55:A1:3638:G:H8	1.55	0.68
27:42:27:LYS:O	27:42:27:LYS:HD2	1.94	0.68
52:P2:8:LYS:HE2	52:P2:8:LYS:H	1.57	0.68
56:C2:214:G:H2'	56:C2:215:A:H8	1.59	0.68
36:B1:181:MET:HE3	36:B1:183:VAL:HG22	1.76	0.67
54:w2:179:GLN:HG2	56:C2:602:A:N6	2.09	0.67
55:A1:2178:A:H2'	55:A1:2179:A:H8	1.60	0.67
62:P1:39:MET:HG2	62:P1:43:LYS:HE2	1.76	0.67
16:m1:187:LYS:HB2	16:m1:198:THR:HG23	1.76	0.67
22:x2:101:LYS:HE2	22:x2:101:LYS:N	2.09	0.67
63:Q1:63:ILE:O	63:Q1:67:ILE:HG13	1.94	0.67
32:72:134:PRO:HB2	56:C2:918:A:H5''	1.75	0.67
70:U2:30:LEU:HD21	70:U2:82:GLU:HB3	1.76	0.67
23:y2:61:GLN:C	23:y2:63:ASN:H	2.02	0.67
11:h1:260:GLU:HG2	11:h1:262:LYS:H	1.60	0.67
55:A1:946:C:H2'	55:A1:947:A:H8	1.58	0.67
61:O2:137:PRO:HG2	61:O2:150:PRO:HD2	1.76	0.67
15:l1:17:ARG:HB3	15:l1:33:MET:HE1	1.75	0.67
30:61:162:ARG:HA	30:61:162:ARG:CZ	2.24	0.67
47:K2:158:ILE:HG13	47:K2:163:GLU:OE2	1.94	0.67
51:A2:124:LYS:H	51:A2:124:LYS:HE2	1.59	0.67
55:A1:955:U:H2'	55:A1:956:A:C8	2.30	0.67
9:g1:3:LYS:HE3	9:g1:4:ARG:H	1.60	0.66
10:g2:50:ASN:HB3	10:g2:53:LYS:HG3	1.76	0.66
69:U1:62:LYS:HG2	69:U1:67:ALA:HB2	1.77	0.66
55:A1:2856:G:H5'	55:A1:2857:A:N3	2.11	0.66
35:91:52:CYS:HB2	35:91:92:CYS:SG	2.36	0.66
60:O1:10:THR:HG22	60:O1:11:TYR:H	1.60	0.66
61:O2:129:ILE:HG22	61:O2:139:LEU:HD12	1.77	0.66
77:k2:258:ILE:HB	77:k2:268:ASP:HB2	1.77	0.66
18:n1:72:THR:HG22	18:n1:110:LYS:HB3	1.77	0.66
32:72:45:THR:HG22	32:72:52:THR:HA	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:f1:57:THR:HG21	8:f1:68:ARG:HG2	1.78	0.66
51:A2:108:LYS:HD2	51:A2:108:LYS:O	1.94	0.66
55:A1:2178:A:H2'	55:A1:2179:A:C8	2.31	0.66
56:C2:1420:G:H3'	56:C2:1421:G:H21	1.59	0.66
67:T1:51:GLY:HA3	67:T1:92:ARG:HG3	1.78	0.66
72:W1:23:ARG:HG3	72:W1:29:PHE:HE1	1.60	0.66
26:41:48:THR:HG22	26:41:65:LYS:HB2	1.77	0.66
36:B1:63:PRO:HA	36:B1:68:ASN:HD21	1.61	0.66
17:m2:32:LYS:HA	17:m2:32:LYS:HE3	1.76	0.66
42:H1:4:ILE:HD12	42:H1:53:SER:HB3	1.78	0.66
55:A1:1123:G:H2'	55:A1:1124:A:C8	2.30	0.65
56:C2:1109:C:H2'	56:C2:1110:G:C8	2.31	0.65
46:J2:256:THR:HA	46:J2:259:LEU:HD12	1.77	0.65
53:i2:33:ARG:HG3	77:k2:125:ARG:HH12	1.61	0.65
41:F1:58:GLU:O	41:F1:62:MET:HG3	1.97	0.65
48:L1:111:GLN:O	48:L1:115:GLN:HG3	1.95	0.65
64:R1:151:ARG:HH11	64:R1:151:ARG:HA	1.62	0.65
4:a1:245:ARG:HH11	4:a1:245:ARG:HA	1.60	0.65
14:k1:94:SER:HB2	14:k1:142:ASP:HB3	1.79	0.65
10:g2:102:ARG:HH22	56:C2:1351:U:H3'	1.62	0.65
13:j1:66:U:H2'	13:j1:67:G:H8	1.61	0.65
30:61:93:PRO:HB2	30:61:125:THR:HG22	1.79	0.65
46:J2:197:LYS:HG2	46:J2:201:MET:HE3	1.79	0.65
55:A1:298:A:H2'	55:A1:299:G:H8	1.62	0.65
55:A1:2875:A:H2'	55:A1:2876:A:C8	2.31	0.65
55:A1:955:U:H2'	55:A1:956:A:H8	1.60	0.64
55:A1:3317:A:H2'	55:A1:3318:G:H8	1.63	0.64
57:M2:57:ALA:O	57:M2:61:VAL:HG23	1.97	0.64
37:B2:140:LYS:HD3	37:B2:141:TYR:H	1.62	0.64
23:y2:61:GLN:O	23:y2:63:ASN:N	2.29	0.64
24:z2:62:ALA:HB3	24:z2:67:TYR:HE2	1.62	0.64
4:a1:118:GLU:OE2	4:a1:126:LEU:HD11	1.97	0.64
27:42:186:ASN:O	27:42:190:PRO:HD2	1.98	0.64
56:C2:899:G:H1	56:C2:991:U:H3	1.44	0.64
65:S1:30:MET:HE1	65:S1:47:PHE:HB3	1.80	0.64
11:h1:221:LYS:HE2	11:h1:221:LYS:HA	1.80	0.64
15:l1:157:LEU:HD11	15:l1:224:VAL:HG21	1.78	0.64
30:61:146:GLU:O	30:61:150:GLU:HG3	1.98	0.64
20:r2:28:ARG:HB2	20:r2:29:PRO:HD3	1.80	0.64
31:71:108:GLY:HA3	55:A1:3294:A:H5''	1.79	0.64
56:C2:117:U:H3	56:C2:321:G:H1	1.46	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
77:k2:149:GLU:HG3	77:k2:170:TRP:HB3	1.80	0.64
19:q2:108:PRO:HA	54:w2:40:ARG:NE	2.13	0.64
54:w2:40:ARG:HA	54:w2:40:ARG:HH11	1.62	0.64
56:C2:1073:G:H22	56:C2:1107:A:H2	1.46	0.64
56:C2:1794:A:H1'	56:C2:1795:G:H5'	1.79	0.64
56:C2:402:U:H5'	56:C2:403:C:H5	1.64	0.63
54:w2:41:VAL:HG13	54:w2:46:THR:HG22	1.78	0.63
55:A1:3317:A:H2'	55:A1:3318:G:C8	2.33	0.63
30:61:70:ILE:O	30:61:74:LYS:HG3	1.97	0.63
55:A1:1163:G:H1'	55:A1:1186:A:N6	2.13	0.63
7:e1:5:LEU:HD21	7:e1:30:ILE:HG22	1.81	0.63
7:e1:46:CYS:HB2	7:e1:48:ILE:O	1.98	0.63
10:g2:126:ASP:O	10:g2:130:ASP:HB3	1.98	0.63
47:K2:82:VAL:HG12	47:K2:202:ILE:HD12	1.81	0.63
73:W2:147:LEU:HD13	73:W2:151:ASP:HB2	1.80	0.63
3:Z1:135:ARG:CZ	3:Z1:135:ARG:HA	2.28	0.63
62:P1:33:ALA:HB1	62:P1:117:ILE:HG12	1.80	0.63
56:C2:1558:A:H2'	56:C2:1559:A:C8	2.34	0.63
14:k1:19:ARG:NH2	55:A1:3819:G:H5'	2.14	0.62
52:P2:104:ASP:O	52:P2:108:ARG:HG2	1.99	0.62
76:Y2:118:PRO:HB3	76:Y2:121:ARG:HH12	1.63	0.62
48:L1:145:LYS:HE2	48:L1:145:LYS:HA	1.80	0.62
54:w2:178:ARG:HE	54:w2:178:ARG:C	2.07	0.62
55:A1:823:G:H2'	55:A1:824:G:C8	2.34	0.62
56:C2:1596:U:H2'	56:C2:1597:C:H6	1.64	0.62
27:42:222:LYS:HE2	27:42:222:LYS:N	2.14	0.62
52:P2:15:VAL:HG23	52:P2:16:LEU:H	1.64	0.62
56:C2:1506:G:H2'	56:C2:1507:A:C8	2.33	0.62
53:i2:98:VAL:HG21	53:i2:117:LEU:HD12	1.80	0.62
57:M2:6:VAL:HB	57:M2:65:TYR:HE2	1.64	0.62
55:A1:3034:G:H3'	55:A1:3035:G:H21	1.64	0.62
47:K2:19:LYS:HZ3	56:C2:102:U:H5''	1.64	0.62
52:P2:37:GLY:H	56:C2:1600:A:H5''	1.64	0.62
75:Y1:108:ARG:HB2	75:Y1:108:ARG:NH1	2.15	0.62
21:u2:34:LEU:HD11	21:u2:147:ARG:HE	1.65	0.62
77:k2:42:MET:HE1	77:k2:92:LEU:HB3	1.82	0.62
22:x2:101:LYS:HE2	22:x2:101:LYS:H	1.63	0.62
32:72:61:LYS:HB2	32:72:61:LYS:NZ	2.14	0.62
55:A1:2279:A:H61	55:A1:2944:C:H42	1.48	0.62
56:C2:1506:G:H2'	56:C2:1507:A:H8	1.63	0.62
61:O2:185:GLY:HA3	61:O2:224:ASN:HD22	1.64	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:a1:138:SER:HB3	4:a1:147:ARG:HB2	1.81	0.62
14:k1:91:LYS:HB2	14:k1:183:GLU:OE1	2.00	0.62
21:u2:50:HIS:CD2	21:u2:85:LYS:HD3	2.35	0.62
55:A1:266:G:H2'	55:A1:267:G:H8	1.65	0.62
57:M2:116:ASP:O	57:M2:119:GLY:HA2	1.99	0.62
61:O2:55:ALA:HB1	61:O2:60:GLU:HB2	1.82	0.62
77:k2:17:TRP:CD1	77:k2:303:THR:HG1	2.18	0.61
53:i2:31:ASN:HA	53:i2:34:VAL:HG22	1.81	0.61
69:U1:50:ALA:HB1	69:U1:79:ARG:HD2	1.80	0.61
64:R1:16:ARG:HA	64:R1:16:ARG:CZ	2.30	0.61
3:Z1:108:ARG:NH2	55:A1:1988:A:H4'	2.15	0.61
53:i2:99:ASP:OD1	53:i2:100:PRO:HD2	2.00	0.61
55:A1:617:A:H62	55:A1:645:U:H3	1.47	0.61
55:A1:920:C:H2'	55:A1:921:A:C8	2.34	0.61
56:C2:902:G:H2'	56:C2:903:G:C8	2.36	0.61
30:61:91:LEU:HD22	30:61:135:ILE:HD12	1.82	0.61
30:61:162:ARG:HH11	30:61:163:GLN:H	1.48	0.61
46:J2:194:PRO:O	46:J2:198:LYS:HD3	1.99	0.61
55:A1:3456:C:H5	55:A1:3472:C:H42	1.47	0.61
68:T2:96:LYS:HB3	68:T2:108:THR:HG22	1.82	0.61
75:Y1:56:GLN:HE21	75:Y1:65:GLN:HA	1.64	0.61
25:32:34:ASP:HB2	25:32:82:LYS:HD2	1.83	0.61
36:B1:56:ILE:HD13	36:B1:365:LEU:HD22	1.81	0.61
57:M2:130:ASP:O	57:M2:134:ILE:HG12	2.01	0.61
66:S2:37:ARG:HB3	66:S2:41:MET:HE1	1.82	0.61
16:m1:248:ALA:O	16:m1:252:LYS:HG2	1.99	0.61
56:C2:207:U:O4	56:C2:277:C:N3	2.34	0.61
56:C2:1648:A:H2'	56:C2:1649:A:C8	2.35	0.61
62:P1:22:LEU:HD12	62:P1:146:ILE:HD13	1.82	0.61
19:q2:22:ILE:HD13	19:q2:114:VAL:HG22	1.82	0.61
52:P2:75:ARG:HG2	52:P2:75:ARG:HH11	1.65	0.61
77:k2:206:LEU:HA	77:k2:219:TRP:O	2.00	0.61
13:j1:66:U:H2'	13:j1:67:G:C8	2.35	0.61
27:42:127:VAL:HB	27:42:177:GLN:HE22	1.66	0.61
30:61:89:MET:HE1	30:61:136:MET:HG2	1.83	0.61
46:J2:58:ASP:OD1	46:J2:60:LYS:HG2	2.01	0.61
58:N1:166:SER:O	58:N1:170:LYS:HG3	2.01	0.61
14:k1:41:ILE:HD13	14:k1:43:LEU:HD12	1.83	0.61
15:l1:161:HIS:HB3	15:l1:164:PHE:HD2	1.66	0.61
20:r2:51:GLU:HG2	25:32:8:LEU:HD21	1.81	0.61
36:B1:308:ASP:HB3	36:B1:310:THR:HG22	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:61:71:CYS:HA	30:61:74:LYS:HE3	1.82	0.60
56:C2:613:C:H2'	56:C2:614:A:H8	1.66	0.60
64:R1:3:MET:SD	64:R1:5:ARG:HG2	2.41	0.60
52:P2:9:PHE:CE1	52:P2:57:GLY:HA3	2.35	0.60
4:a1:158:ILE:HB	4:a1:162:ASN:HD22	1.66	0.60
24:z2:57:VAL:HA	24:z2:69:TYR:O	2.01	0.60
55:A1:163:A:H2'	55:A1:164:A:C8	2.37	0.60
55:A1:3637:U:H2'	55:A1:3638:G:C8	2.36	0.60
56:C2:1823:U:H2'	56:C2:1824:G:H8	1.66	0.60
55:A1:163:A:H2'	55:A1:164:A:H8	1.65	0.60
56:C2:107:C:H2'	56:C2:108:A:H8	1.66	0.60
6:d2:56:LEU:HD21	21:u2:141:ASP:OD1	2.02	0.60
20:r2:53:ILE:HG13	70:U2:143:ARG:HD3	1.83	0.60
36:B1:32:PHE:HD1	36:B1:44:THR:HG21	1.67	0.60
55:A1:1536:A:H2'	55:A1:1537:A:C8	2.36	0.60
20:r2:81:LEU:HD21	20:r2:89:TRP:CD1	2.36	0.60
67:T1:117:LEU:O	67:T1:121:GLN:HG2	2.02	0.60
6:d2:10:LYS:HE2	6:d2:10:LYS:H	1.67	0.60
20:r2:15:ASN:HD21	20:r2:71:LYS:HD2	1.67	0.60
27:42:144:LYS:HD3	27:42:208:HIS:HB3	1.84	0.60
55:A1:2278:A:O2'	55:A1:3674:G:H4'	2.02	0.60
25:32:3:LEU:HD12	25:32:4:ALA:H	1.65	0.60
36:B1:283:LYS:HD3	36:B1:363:ILE:HD11	1.82	0.60
69:U1:77:ILE:HD13	69:U1:86:VAL:HG22	1.82	0.60
71:V1:100:ASP:HB3	72:W1:24:ILE:HD11	1.83	0.60
38:C1:268:ARG:NH1	38:C1:268:ARG:HB2	2.16	0.60
56:C2:1191:A:H2'	56:C2:1192:C:H6	1.66	0.60
17:m2:82:ALA:O	17:m2:86:GLU:HB2	2.02	0.59
41:F1:191:GLU:OE2	41:F1:199:PHE:HA	2.02	0.59
55:A1:2765:G:H2'	55:A1:2766:G:H8	1.66	0.59
55:A1:3911:G:H2'	55:A1:3912:U:C6	2.37	0.59
55:A1:3944:U:H2'	55:A1:3945:G:C8	2.37	0.59
68:T2:71:VAL:HG21	68:T2:86:LEU:HD21	1.83	0.59
8:f1:106:TYR:O	8:f1:107:PRO:C	2.46	0.59
32:72:75:MET:HG3	32:72:118:ALA:HB2	1.84	0.59
9:g1:47:MET:HE2	9:g1:57:CYS:HB2	1.83	0.59
26:41:98:ARG:HD3	26:41:107:ARG:HD3	1.83	0.59
27:42:133:TYR:CE2	27:42:181:LEU:HD22	2.37	0.59
65:S1:109:CYS:O	65:S1:113:MET:HG2	2.02	0.59
54:w2:141:LYS:HB2	54:w2:179:GLN:NE2	2.15	0.59
13:j1:15:G:N2	55:A1:415:G:H1'	2.17	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:m2:51:THR:HG22	17:m2:53:ASP:H	1.67	0.59
19:q2:59:LYS:HZ1	54:w2:8:LYS:HE2	1.68	0.59
55:A1:1881:A:H2'	55:A1:1882:A:C8	2.37	0.59
56:C2:142:G:H2'	56:C2:143:G:C8	2.37	0.59
15:l1:158:ARG:HH21	55:A1:3893:U:H5'	1.68	0.59
28:K1:50:LYS:HE2	28:K1:50:LYS:N	2.18	0.59
35:91:17:ARG:O	35:91:21:VAL:HG23	2.03	0.59
55:A1:258:C:H2'	55:A1:259:G:H8	1.67	0.59
55:A1:534:U:H2'	55:A1:535:G:H5'	1.84	0.59
14:k1:85:THR:HG22	14:k1:86:LEU:HD12	1.84	0.59
37:B2:23:PRO:HG2	37:B2:26:LEU:HB2	1.83	0.59
26:41:97:ILE:HG21	26:41:107:ARG:HB2	1.84	0.59
27:42:164:ILE:O	27:42:168:MET:HG3	2.03	0.59
50:M1:38:VAL:HG11	50:M1:55:MET:HE1	1.83	0.59
54:w2:54:ARG:HG3	54:w2:54:ARG:HH11	1.68	0.59
65:S1:164:LYS:O	65:S1:165:PRO:C	2.46	0.59
68:T2:100:LYS:HZ3	68:T2:105:LEU:HD22	1.67	0.59
77:k2:12:LYS:HA	77:k2:12:LYS:HE2	1.85	0.59
10:g2:16:LEU:HD11	53:i2:116:ASN:HD21	1.68	0.59
17:m2:49:LYS:HE2	17:m2:49:LYS:HA	1.84	0.59
55:A1:1451:C:H2'	55:A1:1452:A:H8	1.68	0.59
55:A1:1972:C:H2'	55:A1:1973:U:C6	2.37	0.59
36:B1:224:LYS:HG2	36:B1:340:THR:HG22	1.83	0.59
53:i2:7:LYS:HE2	56:C2:1347:C:H5'	1.84	0.59
72:W1:9:SER:HA	72:W1:52:THR:HG23	1.85	0.58
32:72:74:ALA:HB1	32:72:115:ALA:HB2	1.84	0.58
35:91:26:LYS:HA	35:91:26:LYS:HE3	1.84	0.58
35:91:28:VAL:HG23	35:91:95:ALA:HB3	1.85	0.58
35:91:29:LEU:HD23	35:91:94:LEU:HD13	1.85	0.58
47:K2:73:THR:HG21	56:C2:275:A:N3	2.18	0.58
5:b1:51:LYS:HD2	5:b1:51:LYS:C	2.28	0.58
55:A1:1188:G:O2'	55:A1:1223:G:H4'	2.04	0.58
75:Y1:52:ASP:HB2	75:Y1:110:LYS:HD2	1.84	0.58
16:m1:112:LYS:HA	16:m1:112:LYS:HE2	1.85	0.58
54:w2:163:PRO:O	54:w2:167:TYR:HB2	2.03	0.58
47:K2:160:THR:O	47:K2:164:GLU:HG2	2.04	0.58
55:A1:947:A:H2'	55:A1:948:A:C8	2.39	0.58
55:A1:1162:C:H2'	55:A1:1163:G:O4'	2.03	0.58
55:A1:2191:A:H2'	55:A1:2192:G:C8	2.38	0.58
70:U2:75:ILE:HA	70:U2:78:ARG:HE	1.69	0.58
11:h1:153:THR:HG21	55:A1:3366:A:C8	2.38	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:A1:1708:G:H2'	55:A1:1709:A:C8	2.38	0.58
55:A1:3580:C:H2'	55:A1:3581:G:C8	2.39	0.58
56:C2:902:G:H1	56:C2:987:U:H3	1.52	0.58
65:S1:15:ARG:HB3	65:S1:27:LEU:HD23	1.85	0.58
21:u2:193:LYS:HE2	21:u2:193:LYS:HA	1.84	0.58
38:C1:71:ARG:HB2	38:C1:73:VAL:HG22	1.84	0.58
42:H1:46:LYS:O	42:H1:50:VAL:HG23	2.04	0.58
54:w2:100:ALA:HA	54:w2:103:GLU:HG3	1.84	0.58
55:A1:1656:C:H5'	65:S1:2:LYS:HE3	1.85	0.58
54:w2:120:TYR:HB3	54:w2:124:ARG:HH12	1.67	0.58
55:A1:931:U:H2'	55:A1:932:C:C6	2.39	0.58
55:A1:2854:G:H1	55:A1:2874:U:H3	1.52	0.58
55:A1:3580:C:H2'	55:A1:3581:G:H8	1.68	0.58
5:b1:22:LYS:HA	5:b1:22:LYS:HE3	1.85	0.57
24:z2:60:GLN:HE22	54:w2:28:GLU:HA	1.69	0.57
54:w2:25:LEU:O	54:w2:29:LEU:HB2	2.04	0.57
56:C2:1372:G:H1'	77:k2:63:SER:OG	2.05	0.57
72:W1:13:ILE:HG12	72:W1:32:LEU:HD12	1.85	0.57
74:X1:120:VAL:HG13	74:X1:137:VAL:HG13	1.86	0.57
55:A1:953:U:H2'	55:A1:954:C:C6	2.39	0.57
64:R1:90:PRO:HG2	64:R1:93:LEU:HD22	1.86	0.57
77:k2:68:ASP:HB3	77:k2:111:VAL:HG22	1.86	0.57
3:Z1:100:VAL:HG22	3:Z1:106:LEU:HB3	1.86	0.57
31:71:51:SER:HB2	31:71:69:ALA:HB3	1.85	0.57
42:H1:88:THR:HB	42:H1:91:MET:HG3	1.86	0.57
55:A1:1953:C:H2'	55:A1:1954:G:H8	1.70	0.57
38:C1:321:ASN:HB3	38:C1:324:ILE:HB	1.86	0.57
55:A1:801:C:H2'	55:A1:802:G:H8	1.69	0.57
55:A1:921:A:H2'	55:A1:922:C:H6	1.69	0.57
55:A1:1163:G:H1'	55:A1:1186:A:H61	1.67	0.57
11:h1:259:LYS:HD3	11:h1:259:LYS:H	1.69	0.57
55:A1:1228:G:H1'	55:A1:1946:A:N6	2.19	0.57
55:A1:1244:G:H5'	55:A1:1245:A:OP1	2.04	0.57
56:C2:262:G:O2'	61:O2:129:ILE:HD11	2.04	0.57
61:O2:147:ILE:HD11	61:O2:162:ILE:HD11	1.85	0.57
4:a1:245:ARG:HA	4:a1:245:ARG:NH1	2.19	0.57
33:81:128:ILE:HD11	65:S1:174:THR:HG21	1.87	0.57
52:P2:24:ARG:HH21	56:C2:1573:A:H2	1.52	0.57
54:w2:74:GLN:HA	54:w2:74:GLN:HE21	1.70	0.57
19:q2:20:ILE:HD11	19:q2:91:LEU:HB2	1.87	0.57
35:91:57:LYS:HD3	35:91:73:HIS:HE1	1.69	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:A1:824:G:H1	55:A1:837:G:N2	2.02	0.57
76:Y2:53:ALA:HB2	76:Y2:119:CYS:SG	2.45	0.57
32:72:91:THR:O	32:72:125:LYS:HB2	2.05	0.57
41:F1:224:HIS:ND1	41:F1:226:VAL:HG22	2.20	0.57
52:P2:132:ARG:HD3	56:C2:1593:A:C6	2.40	0.57
56:C2:614:A:H2'	56:C2:615:A:C8	2.40	0.57
56:C2:984:G:H2'	56:C2:985:A:H8	1.69	0.57
69:U1:39:CYS:HB2	69:U1:42:PRO:HG2	1.87	0.57
51:A2:57:LEU:O	51:A2:61:ARG:HG2	2.05	0.56
56:C2:648:C:H42	56:C2:1005:A:H61	1.53	0.56
70:U2:70:LYS:HE2	70:U2:70:LYS:H	1.70	0.56
14:k1:29:GLY:HA3	14:k1:84:VAL:HG13	1.87	0.56
19:q2:40:ILE:O	19:q2:44:LYS:HG2	2.04	0.56
37:B2:29:THR:O	37:B2:33:VAL:HG23	2.05	0.56
42:H1:122:LYS:HG3	48:L1:146:MET:HE1	1.87	0.56
55:A1:601:G:H1	55:A1:670:C:H5	1.51	0.56
55:A1:3561:A:H5''	55:A1:3563:G:H4'	1.87	0.56
62:P1:41:ILE:HG12	62:P1:99:GLU:OE1	2.05	0.56
68:T2:52:THR:HA	68:T2:55:LYS:HZ1	1.69	0.56
7:e1:11:LEU:HD23	7:e1:13:TYR:H	1.70	0.56
10:g2:52:LYS:HB3	53:i2:109:LEU:HD11	1.88	0.56
27:42:65:ARG:HH22	32:72:51:GLU:HG2	1.68	0.56
33:81:198:LEU:HD23	50:M1:112:VAL:HG13	1.86	0.56
49:L2:128:VAL:HG13	49:L2:132:GLN:HE22	1.70	0.56
50:M1:132:LYS:HE2	50:M1:132:LYS:HA	1.87	0.56
55:A1:946:C:H2'	55:A1:947:A:C8	2.39	0.56
10:g2:52:LYS:O	10:g2:56:GLU:HG2	2.06	0.56
18:n1:49:HIS:HB3	63:Q1:175:GLU:OE2	2.04	0.56
27:42:57:ILE:HG22	27:42:60:ASP:H	1.70	0.56
32:72:63:LYS:HE2	32:72:63:LYS:HA	1.87	0.56
51:A2:50:ARG:NH1	51:A2:50:ARG:HA	2.20	0.56
62:P1:70:CYS:SG	62:P1:83:TRP:CZ3	2.97	0.56
1:11:29:MET:HE2	1:11:29:MET:HA	1.86	0.56
13:j1:112:U:C4	74:X1:102:LYS:HE3	2.41	0.56
47:K2:72:CYS:HG	47:K2:112:TRP:CG	2.23	0.56
51:A2:57:LEU:HD22	51:A2:61:ARG:HH12	1.70	0.56
54:w2:115:VAL:HG21	54:w2:142:LEU:HD22	1.88	0.56
55:A1:535:G:H3'	55:A1:535:G:OP2	2.06	0.56
55:A1:2974:G:H2'	55:A1:2975:G:C8	2.41	0.56
56:C2:1713:G:H21	56:C2:1760:A:H62	1.52	0.56
69:U1:41:HIS:HB3	69:U1:128:TYR:CE1	2.40	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:B2:49:GLN:O	37:B2:53:ILE:HG12	2.04	0.56
47:K2:114:GLU:HG2	47:K2:137:LEU:HD21	1.87	0.56
52:P2:67:VAL:O	52:P2:71:MET:HG3	2.05	0.56
55:A1:253:C:H2'	55:A1:254:G:H8	1.71	0.56
55:A1:921:A:H2'	55:A1:922:C:C6	2.41	0.56
69:U1:40:THR:HG22	69:U1:83:LYS:NZ	2.19	0.56
14:k1:19:ARG:HH12	55:A1:3819:G:H5'	1.71	0.56
51:A2:100:LYS:HD2	56:C2:1214:A:C5	2.41	0.56
53:i2:95:LEU:HD11	53:i2:118:GLN:HE22	1.70	0.56
54:w2:161:GLY:HA3	56:C2:1362:A:H61	1.69	0.56
63:Q1:67:ILE:HD13	63:Q1:96:PRO:HD2	1.87	0.56
19:q2:55:ARG:NH1	19:q2:87:ARG:HE	2.03	0.56
56:C2:1520:G:H3'	56:C2:1549:A:H61	1.70	0.56
70:U2:100:ILE:HD11	70:U2:125:VAL:HG11	1.88	0.56
9:g1:85:ARG:HH11	56:C2:913:U:H5''	1.70	0.56
27:42:133:TYR:HE2	27:42:181:LEU:HD22	1.70	0.56
31:71:25:CYS:H	55:A1:3294:A:N6	2.04	0.56
55:A1:406:A:H4'	55:A1:407:G:H3'	1.88	0.56
55:A1:1280:A:H4'	55:A1:1296:G:N2	2.20	0.56
56:C2:984:G:H2'	56:C2:985:A:C8	2.39	0.56
56:C2:1567:C:H4'	56:C2:1573:A:N6	2.21	0.56
65:S1:69:GLU:OE1	65:S1:101:SER:HA	2.06	0.56
11:h1:280:VAL:HG12	11:h1:284:LYS:HE3	1.87	0.55
19:q2:107:GLU:HG2	19:q2:108:PRO:HD2	1.88	0.55
28:K1:57:LYS:HA	28:K1:60:LEU:HD23	1.88	0.55
36:B1:163:ILE:HG22	36:B1:180:LEU:HD22	1.88	0.55
54:w2:54:ARG:H	54:w2:90:LYS:HE2	1.70	0.55
56:C2:1202:A:H2'	56:C2:1203:G:H8	1.71	0.55
4:a1:129:ALA:HB3	4:a1:132:ASN:HD22	1.70	0.55
34:82:106:ILE:HD11	56:C2:1833:U:H5'	1.88	0.55
55:A1:3606:U:H2'	55:A1:3607:A:H8	1.70	0.55
56:C2:613:C:H2'	56:C2:614:A:C8	2.41	0.55
55:A1:1536:A:H2'	55:A1:1537:A:H8	1.70	0.55
55:A1:3018:A:H2'	55:A1:3019:G:H8	1.70	0.55
66:S2:104:SER:O	66:S2:108:ILE:HG23	2.06	0.55
17:m2:16:ARG:HA	17:m2:19:GLN:HA	1.89	0.55
53:i2:33:ARG:CB	77:k2:125:ARG:HH12	2.19	0.55
77:k2:227:LEU:HB3	77:k2:228:TYR:CE1	2.41	0.55
10:g2:77:ILE:HD12	10:g2:122:LEU:HD21	1.88	0.55
23:y2:49:GLY:O	23:y2:99:GLU:HA	2.06	0.55
24:z2:40:PRO:O	24:z2:44:VAL:HG22	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:F1:60:ARG:HG3	41:F1:60:ARG:HH11	1.71	0.55
55:A1:1683:G:H2'	55:A1:1684:C:O4'	2.06	0.55
21:u2:72:THR:HG22	21:u2:92:VAL:HG21	1.89	0.55
28:K1:27:LYS:HD2	28:K1:32:VAL:HG22	1.87	0.55
56:C2:650:C:H3'	56:C2:651:G:H8	1.71	0.55
66:S2:43:GLU:CB	66:S2:44:PRO:HD2	2.33	0.55
16:m1:138:ALA:HB1	16:m1:199:CYS:SG	2.46	0.55
55:A1:2857:A:H62	55:A1:2871:U:H3	1.54	0.55
70:U2:137:SER:HA	70:U2:162:GLN:NE2	2.22	0.55
4:a1:196:TRP:HB3	4:a1:197:PRO:HD3	1.89	0.55
47:K2:157:LYS:HA	47:K2:157:LYS:HE3	1.88	0.55
52:P2:9:PHE:HE1	52:P2:57:GLY:HA3	1.70	0.55
55:A1:1844:C:H2'	55:A1:1845:A:H8	1.72	0.55
55:A1:3685:U:H2'	55:A1:3686:G:H8	1.72	0.55
70:U2:100:ILE:HG13	70:U2:125:VAL:HG21	1.89	0.55
4:a1:101:VAL:HG22	4:a1:165:VAL:HG22	1.88	0.55
27:42:129:THR:HG22	27:42:133:TYR:H	1.71	0.55
37:B2:140:LYS:HE2	37:B2:140:LYS:HA	1.89	0.55
55:A1:2869:U:H2'	55:A1:2870:C:C6	2.42	0.55
56:C2:1201:G:C2	56:C2:1202:A:C8	2.95	0.55
11:h1:177:THR:HG22	11:h1:183:TYR:CD1	2.42	0.55
17:m2:57:VAL:HB	17:m2:60:PHE:HE2	1.70	0.55
19:q2:31:SER:O	19:q2:35:VAL:HG23	2.07	0.55
32:72:65:ASP:HA	32:72:68:GLU:HG3	1.88	0.55
41:F1:27:LYS:HB3	41:F1:27:LYS:NZ	2.22	0.55
55:A1:496:G:H21	55:A1:497:C:N4	2.05	0.55
55:A1:2064:U:H5''	55:A1:2065:U:H5'	1.89	0.55
56:C2:277:C:H5'	56:C2:278:C:H2'	1.89	0.55
61:O2:222:LEU:O	61:O2:225:ILE:HG13	2.07	0.55
67:T1:145:LYS:NZ	67:T1:145:LYS:HB3	2.22	0.55
2:21:93:LYS:HD2	2:21:102:ARG:HD2	1.88	0.54
13:j1:149:A:H2'	13:j1:150:G:C8	2.42	0.54
55:A1:1058:G:HO2'	55:A1:1059:U:H6	1.53	0.54
56:C2:916:G:H2'	56:C2:917:U:C6	2.42	0.54
59:N2:36:ARG:HH11	59:N2:49:ARG:NH1	2.03	0.54
10:g2:144:THR:O	10:g2:158:ASP:HB2	2.07	0.54
11:h1:200:MET:HB2	11:h1:202:ILE:HD13	1.88	0.54
54:w2:27:ARG:HH22	56:C2:1468:A:P	2.31	0.54
56:C2:16:U:H2'	56:C2:17:G:O4'	2.07	0.54
62:P1:27:LYS:O	62:P1:31:GLU:HG2	2.07	0.54
17:m2:105:LYS:O	17:m2:109:GLU:HG3	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:51:20:MET:O	29:51:23:ARG:HG3	2.06	0.54
33:81:76:ARG:HD2	33:81:147:VAL:HG12	1.89	0.54
56:C2:108:A:H2'	56:C2:109:G:C8	2.41	0.54
56:C2:1381:U:H2'	56:C2:1382:U:C6	2.43	0.54
60:O1:35:ALA:O	60:O1:39:ARG:HG3	2.08	0.54
64:R1:151:ARG:HA	64:R1:151:ARG:NH1	2.21	0.54
73:W2:85:ARG:HB3	73:W2:85:ARG:HH11	1.72	0.54
75:Y1:117:LYS:O	75:Y1:121:ARG:HG3	2.07	0.54
4:a1:9:ARG:HD2	55:A1:1239:C:OP2	2.07	0.54
10:g2:51:LEU:O	10:g2:54:THR:HG22	2.07	0.54
11:h1:208:MET:HE2	11:h1:233:PRO:HG3	1.88	0.54
13:j1:15:G:H22	55:A1:415:G:H1'	1.71	0.54
14:k1:86:LEU:HB3	14:k1:186:THR:HG21	1.89	0.54
16:m1:161:VAL:HG21	16:m1:200:THR:HG23	1.89	0.54
21:u2:158:GLY:HA3	21:u2:177:GLU:OE2	2.06	0.54
30:61:71:CYS:SG	30:61:154:ARG:HG2	2.47	0.54
50:M1:123:ILE:O	50:M1:127:VAL:HG23	2.08	0.54
55:A1:3912:U:H2'	55:A1:3913:G:C8	2.41	0.54
56:C2:1817:U:H2'	56:C2:1819:A:OP2	2.08	0.54
10:g2:40:LYS:HB2	10:g2:40:LYS:NZ	2.23	0.54
14:k1:86:LEU:HB3	14:k1:186:THR:CG2	2.37	0.54
36:B1:66:LYS:H	36:B1:66:LYS:HD3	1.72	0.54
53:i2:21:TYR:CE1	53:i2:58:MET:HE1	2.43	0.54
56:C2:25:C:H2'	56:C2:26:A:C8	2.42	0.54
57:M2:116:ASP:HB2	57:M2:122:ARG:HG3	1.89	0.54
66:S2:32:ILE:HD12	66:S2:32:ILE:O	2.08	0.54
69:U1:54:GLU:O	69:U1:58:GLN:HG2	2.08	0.54
74:X1:144:ASP:O	74:X1:148:VAL:HG23	2.07	0.54
15:l1:90:GLU:OE1	40:E1:7:LEU:HD22	2.07	0.54
41:F1:221:LYS:HA	41:F1:230:ASP:OD1	2.08	0.54
49:L2:126:ALA:O	49:L2:130:ILE:HG13	2.08	0.54
54:w2:54:ARG:NH1	54:w2:57:ASN:HB3	2.12	0.54
55:A1:493:U:H2'	55:A1:494:C:C5	2.42	0.54
55:A1:3628:U:H2'	55:A1:3629:A:C8	2.43	0.54
64:R1:50:ILE:C	64:R1:51:ILE:HD12	2.33	0.54
69:U1:115:ARG:HH12	69:U1:129:PHE:HA	1.73	0.54
13:j1:141:C:H2'	13:j1:142:C:C6	2.43	0.54
52:P2:5:ILE:HG12	68:T2:48:PHE:O	2.08	0.54
53:i2:95:LEU:HD11	53:i2:118:GLN:NE2	2.23	0.54
55:A1:2962:A:H2'	55:A1:2963:A:C8	2.42	0.54
56:C2:1620:A:H5''	66:S2:139:ALA:HB2	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
66:S2:107:GLU:O	66:S2:111:ILE:HG22	2.07	0.54
76:Y2:7:GLU:HG2	76:Y2:9:ALA:H	1.72	0.54
13:j1:54:U:H3	13:j1:61:A:H2	1.54	0.54
13:j1:145:U:H2'	13:j1:146:C:C6	2.43	0.54
15:l1:136:LEU:HD11	15:l1:147:THR:HG22	1.89	0.54
35:91:24:SER:HB2	35:91:100:GLY:HA3	1.90	0.54
55:A1:3780:G:H5''	55:A1:4022:U:H2'	1.90	0.54
56:C2:970:A:H2'	56:C2:971:A:C8	2.43	0.54
77:k2:191:HIS:NE2	77:k2:217:MET:HE2	2.22	0.54
25:32:5:LYS:HE3	25:32:5:LYS:HA	1.90	0.54
25:32:5:LYS:HD3	25:32:6:ASP:H	1.73	0.54
38:C1:331:TYR:CE1	41:F1:53:GLU:HG2	2.43	0.54
40:E1:84:GLU:O	40:E1:87:VAL:HG22	2.08	0.54
55:A1:1844:C:H2'	55:A1:1845:A:C8	2.42	0.54
56:C2:1199:U:H3	56:C2:1611:A:H62	1.54	0.54
7:e1:96:LEU:HD11	35:91:59:GLU:HB3	1.90	0.54
29:51:7:LYS:O	29:51:11:ARG:HG2	2.08	0.54
55:A1:1683:G:N2	55:A1:1698:G:H1	2.06	0.54
55:A1:3387:U:H2'	55:A1:3388:C:C6	2.42	0.54
67:T1:68:THR:HG22	67:T1:69:GLN:H	1.72	0.54
11:h1:202:ILE:HD11	11:h1:237:GLU:CD	2.33	0.53
27:42:137:LEU:HD11	27:42:176:VAL:HG21	1.90	0.53
34:82:68:ILE:HD13	34:82:95:TYR:CE2	2.43	0.53
39:D1:24:THR:HG23	55:A1:3949:C:H4'	1.90	0.53
52:P2:75:ARG:HG2	52:P2:75:ARG:NH1	2.23	0.53
54:w2:104:SER:O	54:w2:108:LYS:HG2	2.08	0.53
55:A1:266:G:H2'	55:A1:267:G:C8	2.41	0.53
55:A1:275:G:H5''	58:N1:5:ARG:NH2	2.23	0.53
55:A1:298:A:H2'	55:A1:299:G:C8	2.43	0.53
56:C2:429:A:H2'	56:C2:430:C:H6	1.73	0.53
56:C2:1794:A:O2'	56:C2:1795:G:H8	1.91	0.53
64:R1:23:TRP:CZ3	64:R1:25:ASP:HB2	2.42	0.53
51:A2:50:ARG:O	51:A2:54:GLN:HG2	2.07	0.53
53:i2:33:ARG:HB3	77:k2:125:ARG:NH1	2.22	0.53
53:i2:58:MET:HA	53:i2:58:MET:HE3	1.88	0.53
54:w2:120:TYR:HB3	54:w2:124:ARG:NH1	2.23	0.53
55:A1:133:A:N1	55:A1:259:G:H1'	2.23	0.53
66:S2:43:GLU:HB3	66:S2:44:PRO:CD	2.35	0.53
6:d2:51:ARG:HG3	21:u2:60:PHE:CE2	2.44	0.53
14:k1:56:ARG:NH1	14:k1:56:ARG:HB3	2.24	0.53
36:B1:141:GLU:HA	36:B1:144:LYS:NZ	2.23	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:w2:123:LEU:HD11	54:w2:152:PHE:HB3	1.88	0.53
55:A1:678:U:H2'	55:A1:679:C:C6	2.43	0.53
55:A1:1373:A:H2'	55:A1:1374:U:O4'	2.08	0.53
56:C2:1447:U:H2'	56:C2:1448:U:H5''	1.89	0.53
77:k2:174:VAL:HB	77:k2:188:HIS:HB2	1.91	0.53
29:51:16:LYS:HG2	29:51:20:MET:HE1	1.90	0.53
36:B1:103:LYS:HB3	36:B1:153:MET:HE2	1.88	0.53
6:d2:35:MET:HE1	6:d2:55:VAL:HG13	1.89	0.53
6:d2:67:ARG:NE	6:d2:67:ARG:HA	2.24	0.53
43:H2:45:ARG:NH1	43:H2:45:ARG:HB2	2.24	0.53
55:A1:1313:C:N4	55:A1:1397:A:H2'	2.24	0.53
55:A1:2840:C:H2'	55:A1:2841:G:H8	1.73	0.53
4:a1:206:PRO:HG3	4:a1:213:GLY:HA3	1.91	0.53
8:f1:106:TYR:HB3	8:f1:107:PRO:CD	2.32	0.53
11:h1:41:LYS:HB2	67:T1:68:THR:O	2.09	0.53
55:A1:3334:G:H5'	55:A1:3336:U:C6	2.43	0.53
77:k2:104:HIS:CE1	77:k2:124:SER:HB2	2.44	0.53
3:Z1:89:ILE:HG22	3:Z1:91:LEU:HD22	1.90	0.53
13:j1:142:C:H2'	13:j1:143:U:C6	2.44	0.53
21:u2:122:GLU:HA	21:u2:142:VAL:HG13	1.89	0.53
32:72:119:LEU:O	32:72:124:MET:HB2	2.08	0.53
55:A1:2190:A:H2'	55:A1:2191:A:C8	2.44	0.53
73:W2:181:THR:HG22	73:W2:183:ARG:H	1.73	0.53
77:k2:30:MET:HA	77:k2:43:TRP:O	2.09	0.53
38:C1:14:LYS:HD3	38:C1:14:LYS:N	2.24	0.53
39:D1:88:ARG:HD3	39:D1:100:LEU:HD13	1.90	0.53
48:L1:42:LYS:O	48:L1:46:ILE:HG12	2.08	0.53
57:M2:74:SER:O	57:M2:78:ILE:HG13	2.09	0.53
1:11:21:ARG:HE	1:11:22:PRO:HD2	1.73	0.53
11:h1:197:LYS:HD2	11:h1:202:ILE:HG21	1.91	0.53
16:m1:95:LEU:HD21	16:m1:156:ILE:HG12	1.90	0.53
46:J2:253:GLN:HA	46:J2:253:GLN:NE2	2.24	0.53
55:A1:3628:U:H2'	55:A1:3629:A:H8	1.74	0.53
73:W2:18:VAL:HG11	73:W2:24:LEU:HG	1.91	0.53
73:W2:45:TRP:C	73:W2:46:LYS:HD3	2.34	0.53
22:x2:85:LYS:O	22:x2:89:GLN:HG3	2.10	0.53
55:A1:1294:C:H2'	55:A1:1295:A:H8	1.73	0.53
15:l1:76:ARG:HH21	55:A1:467:C:H5	1.57	0.52
19:q2:59:LYS:HZ1	54:w2:8:LYS:CE	2.22	0.52
24:z2:23:LYS:HZ2	24:z2:24:LYS:H	1.57	0.52
52:P2:137:LYS:HA	52:P2:137:LYS:HE3	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:w2:212:GLU:OE1	54:w2:212:GLU:N	2.42	0.52
56:C2:25:C:H2'	56:C2:26:A:H8	1.73	0.52
66:S2:112:LEU:HD22	66:S2:119:LEU:HD13	1.91	0.52
71:V1:111:GLU:HA	71:V1:131:ARG:NH1	2.23	0.52
77:k2:53:GLY:C	77:k2:54:ILE:HD13	2.34	0.52
14:k1:165:THR:HG21	14:k1:179:ILE:HG13	1.91	0.52
30:61:71:CYS:O	30:61:74:LYS:HD2	2.09	0.52
30:61:146:GLU:O	30:61:149:VAL:HG12	2.10	0.52
32:72:29:GLY:O	32:72:93:LEU:HA	2.09	0.52
32:72:131:ASP:OD1	32:72:133:THR:HG22	2.08	0.52
36:B1:175:GLN:HG3	55:A1:3938:U:H4'	1.91	0.52
53:i2:48:ASN:HD22	56:C2:1422:A:H5''	1.74	0.52
55:A1:906:C:H2'	55:A1:907:G:C8	2.44	0.52
55:A1:1091:C:H3'	55:A1:1092:U:H5''	1.91	0.52
55:A1:3282:A:H2'	55:A1:3283:G:C8	2.43	0.52
56:C2:428:U:H2'	56:C2:429:A:H8	1.74	0.52
56:C2:475:C:H2'	56:C2:476:U:H5''	1.90	0.52
58:N1:120:TRP:HE1	58:N1:123:GLU:HG3	1.74	0.52
65:S1:160:ARG:HG2	65:S1:160:ARG:HH11	1.74	0.52
18:n1:89:ASN:HA	18:n1:92:LYS:HE3	1.89	0.52
35:91:36:LYS:NZ	35:91:36:LYS:HB3	2.25	0.52
49:L2:110:LEU:HD23	49:L2:130:ILE:HD13	1.91	0.52
51:A2:119:PHE:HB3	52:P2:118:ARG:HH22	1.74	0.52
55:A1:3221:A:H2'	55:A1:3222:G:C8	2.45	0.52
56:C2:898:G:H1	56:C2:992:U:H3	1.57	0.52
56:C2:1770:A:H2'	56:C2:1771:C:C6	2.44	0.52
66:S2:103:ALA:HA	66:S2:106:LYS:HD2	1.92	0.52
19:q2:32:LEU:HD23	19:q2:87:ARG:NH1	2.25	0.52
32:72:126:ILE:HG13	34:82:83:ALA:O	2.09	0.52
55:A1:581:A:H2'	55:A1:582:C:C6	2.44	0.52
56:C2:165:C:H4'	73:W2:131:ARG:HD2	1.90	0.52
56:C2:499:A:H2'	56:C2:500:A:H8	1.74	0.52
76:Y2:48:LYS:NZ	76:Y2:48:LYS:HB3	2.25	0.52
2:21:83:ARG:O	2:21:87:GLN:HG3	2.08	0.52
14:k1:41:ILE:HD12	14:k1:41:ILE:O	2.09	0.52
54:w2:107:TYR:HB2	54:w2:108:LYS:HZ2	1.73	0.52
55:A1:1059:U:H2'	55:A1:1060:U:H6	1.74	0.52
56:C2:415:C:H2'	56:C2:416:C:C6	2.45	0.52
56:C2:954:A:H2'	56:C2:955:A:C8	2.45	0.52
62:P1:117:ILE:HD12	62:P1:148:MET:HG3	1.92	0.52
16:m1:95:LEU:HD12	16:m1:218:LEU:HD13	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:L2:104:ASP:HA	49:L2:107:GLU:HG3	1.92	0.52
61:O2:104:ASP:HB3	61:O2:110:THR:HG21	1.92	0.52
68:T2:100:LYS:HE2	68:T2:100:LYS:HA	1.91	0.52
70:U2:58:LYS:O	70:U2:90:LYS:HA	2.10	0.52
47:K2:131:PRO:HA	47:K2:134:GLU:HB3	1.91	0.52
55:A1:3011:C:H2'	55:A1:3012:C:C6	2.45	0.52
58:N1:114:ARG:HG2	58:N1:137:PRO:HG3	1.91	0.52
66:S2:86:GLN:HE22	66:S2:122:ALA:HA	1.75	0.52
31:71:18:ARG:HD2	31:71:135:GLY:HA3	1.90	0.52
32:72:79:GLN:OE1	32:72:118:ALA:HB1	2.09	0.52
55:A1:829:U:H5''	55:A1:831:C:H42	1.73	0.52
55:A1:3387:U:H2'	55:A1:3388:C:H6	1.75	0.52
56:C2:71:G:H8	56:C2:80:A:H61	1.58	0.52
62:P1:87:SER:O	62:P1:91:LEU:HD12	2.09	0.52
11:h1:200:MET:HE3	11:h1:200:MET:HA	1.90	0.52
32:72:26:ASN:HB3	32:72:91:THR:HG23	1.92	0.52
36:B1:283:LYS:HE2	36:B1:358:ARG:O	2.10	0.52
49:L2:170:PRO:HB2	49:L2:174:LYS:HB2	1.92	0.52
52:P2:4:VAL:HG22	68:T2:53:TYR:CE2	2.45	0.52
54:w2:120:TYR:O	54:w2:124:ARG:HG2	2.09	0.52
1:11:6:THR:HG22	1:11:8:ARG:H	1.74	0.52
17:m2:12:PHE:CD2	17:m2:23:MET:HG2	2.45	0.52
27:42:124:HIS:HA	27:42:137:LEU:O	2.10	0.52
31:71:12:MET:HE2	31:71:12:MET:HA	1.92	0.52
42:H1:21:LEU:HD11	42:H1:54:ILE:HG23	1.91	0.52
42:H1:93:ARG:HG3	58:N1:138:PHE:HZ	1.75	0.52
51:A2:61:ARG:HH22	51:A2:89:MET:HG2	1.74	0.52
55:A1:801:C:H2'	55:A1:802:G:C8	2.44	0.52
55:A1:1294:C:H2'	55:A1:1295:A:C8	2.45	0.52
68:T2:89:LEU:HB3	68:T2:95:ILE:HD12	1.91	0.52
73:W2:44:GLU:N	73:W2:44:GLU:OE2	2.44	0.52
13:j1:18:C:H2'	13:j1:19:A:C8	2.45	0.51
27:42:33:VAL:HG12	27:42:96:CYS:HB2	1.91	0.51
27:42:159:GLN:O	27:42:163:GLN:HG3	2.09	0.51
46:J2:60:LYS:HB3	46:J2:255:PHE:CE1	2.46	0.51
55:A1:100:A:H3'	55:A1:101:G:H21	1.74	0.51
55:A1:824:G:H22	55:A1:837:G:N2	2.08	0.51
55:A1:960:C:H2'	55:A1:961:A:H8	1.75	0.51
63:Q1:79:ILE:H	63:Q1:79:ILE:HD12	1.74	0.51
66:S2:111:ILE:HG13	66:S2:114:GLN:HE21	1.74	0.51
15:l1:81:ARG:NH1	15:l1:81:ARG:HB2	2.25	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:42:53:GLN:HE22	27:42:56:ARG:HB3	1.75	0.51
55:A1:1527:G:H2'	55:A1:1528:A:C8	2.44	0.51
55:A1:3303:U:H2'	55:A1:3304:C:C6	2.45	0.51
56:C2:97:C:H2'	56:C2:98:U:C6	2.46	0.51
56:C2:846:G:H2'	56:C2:847:A:H8	1.76	0.51
56:C2:1191:A:H2'	56:C2:1192:C:C6	2.45	0.51
56:C2:1339:G:H2'	56:C2:1340:G:H8	1.75	0.51
66:S2:115:TYR:CD1	66:S2:116:ASP:HB2	2.45	0.51
75:Y1:49:ILE:HD12	75:Y1:106:ILE:HD11	1.93	0.51
4:a1:108:PRO:HG3	9:g1:90:LYS:NZ	2.25	0.51
19:q2:97:ILE:O	19:q2:101:ILE:HG13	2.10	0.51
47:K2:198:TYR:O	47:K2:202:ILE:HG12	2.11	0.51
54:w2:142:LEU:HB3	54:w2:143:ARG:CZ	2.40	0.51
55:A1:529:C:H2'	55:A1:530:C:C2	2.45	0.51
55:A1:1672:C:H2'	55:A1:1673:G:C8	2.45	0.51
56:C2:823:C:H5''	56:C2:824:G:H5'	1.91	0.51
56:C2:1490:G:H2'	56:C2:1490:G:N3	2.26	0.51
58:N1:59:TYR:CE2	58:N1:135:ILE:HD11	2.45	0.51
66:S2:111:ILE:HG13	66:S2:114:GLN:NE2	2.24	0.51
73:W2:27:PHE:HE1	73:W2:36:VAL:HG21	1.75	0.51
31:71:39:VAL:O	31:71:42:GLN:HG3	2.10	0.51
55:A1:1914:G:H2'	55:A1:1915:C:C6	2.46	0.51
55:A1:3543:U:H2'	55:A1:3544:U:H6	1.76	0.51
73:W2:35:GLU:OE1	73:W2:35:GLU:HA	2.11	0.51
74:X1:123:VAL:HG22	74:X1:137:VAL:HG22	1.91	0.51
11:h1:242:LYS:NZ	11:h1:242:LYS:HB3	2.24	0.51
27:42:33:VAL:HG23	27:42:44:ILE:HB	1.92	0.51
55:A1:1854:G:H4'	62:P1:127:ARG:HH12	1.75	0.51
56:C2:107:C:H2'	56:C2:108:A:C8	2.45	0.51
65:S1:96:GLU:HG3	65:S1:139:ARG:HG2	1.92	0.51
3:Z1:112:ARG:HH12	3:Z1:115:LYS:HD3	1.74	0.51
55:A1:1017:G:H2'	55:A1:1018:G:C8	2.46	0.51
55:A1:1017:G:H2'	55:A1:1018:G:H8	1.75	0.51
55:A1:1708:G:H2'	55:A1:1709:A:H8	1.76	0.51
55:A1:3221:A:H2'	55:A1:3222:G:H8	1.76	0.51
74:X1:102:LYS:HA	74:X1:102:LYS:HE2	1.92	0.51
77:k2:207:CYS:O	77:k2:218:LEU:HA	2.09	0.51
4:a1:147:ARG:HH11	4:a1:147:ARG:HG3	1.76	0.51
12:i1:23:A:H2'	12:i1:24:A:N3	2.25	0.51
13:j1:37:U:H3'	13:j1:38:G:H5'	1.92	0.51
15:l1:65:LYS:HD3	15:l1:78:VAL:HG21	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:z2:19:VAL:HG11	54:w2:68:GLU:HG2	1.92	0.51
52:P2:86:ARG:NH1	52:P2:86:ARG:HB3	2.25	0.51
53:i2:27:ASP:HB3	53:i2:30:THR:OG1	2.10	0.51
54:w2:54:ARG:HG3	54:w2:54:ARG:O	2.10	0.51
55:A1:3842:G:H1	55:A1:3886:U:H3	1.59	0.51
68:T2:67:THR:HG22	68:T2:69:ALA:H	1.74	0.51
16:m1:231:GLU:H	16:m1:231:GLU:CD	2.18	0.51
20:r2:37:PHE:O	20:r2:41:MET:HG3	2.11	0.51
22:x2:92:LYS:HA	22:x2:92:LYS:HE3	1.92	0.51
41:F1:142:TYR:HE2	41:F1:235:GLU:HG3	1.76	0.51
55:A1:918:C:H2'	55:A1:919:C:C6	2.46	0.51
55:A1:1163:G:H2'	55:A1:1185:G:N2	2.26	0.51
55:A1:3018:A:H2'	55:A1:3019:G:C8	2.46	0.51
56:C2:849:U:O4	56:C2:883:G:O6	2.28	0.51
70:U2:82:GLU:OE2	70:U2:82:GLU:HA	2.11	0.51
26:41:67:ARG:NH1	26:41:67:ARG:HB2	2.26	0.51
35:91:77:ASN:HB2	35:91:80:GLU:OE1	2.11	0.51
41:F1:215:ARG:O	41:F1:244:ARG:HD2	2.11	0.51
42:H1:71:LYS:NZ	42:H1:71:LYS:HB2	2.26	0.51
55:A1:1469:C:H2'	55:A1:1470:U:C6	2.46	0.51
55:A1:2006:A:H2'	55:A1:2007:G:O4'	2.11	0.51
64:R1:96:MET:O	64:R1:100:ARG:HG3	2.10	0.51
76:Y2:18:GLN:HB3	76:Y2:36:LEU:HD11	1.93	0.51
12:i1:58:A:H2'	12:i1:59:G:H8	1.76	0.51
14:k1:105:ILE:HD11	14:k1:144:LEU:HD11	1.93	0.51
14:k1:134:CYS:HB3	14:k1:146:LEU:HD23	1.93	0.51
16:m1:190:LEU:O	16:m1:194:VAL:HG22	2.11	0.51
33:81:67:ASN:HD22	55:A1:3608:C:H5''	1.75	0.51
38:C1:134:PRO:HG3	38:C1:150:VAL:HG11	1.92	0.51
42:H1:118:LYS:HB3	48:L1:127:PHE:HB2	1.91	0.51
53:i2:54:VAL:O	53:i2:58:MET:HG2	2.10	0.51
55:A1:394:A:H2'	55:A1:395:G:C8	2.46	0.51
55:A1:1215:G:H2'	55:A1:1216:G:C8	2.45	0.51
55:A1:2808:U:H2'	55:A1:2809:C:C6	2.46	0.51
21:u2:77:MET:HG3	21:u2:78:HIS:H	1.76	0.50
24:z2:43:HIS:HA	24:z2:46:LYS:HE2	1.92	0.50
33:81:185:LYS:HA	33:81:188:GLU:OE1	2.10	0.50
47:K2:143:LYS:HA	47:K2:146:GLN:HE22	1.76	0.50
54:w2:103:GLU:HA	54:w2:106:ARG:HB2	1.92	0.50
54:w2:108:LYS:HB3	54:w2:113:LEU:HD12	1.93	0.50
55:A1:922:C:H2'	55:A1:923:C:C6	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:C2:1683:C:H2'	56:C2:1684:U:C6	2.45	0.50
70:U2:8:ILE:HG22	70:U2:45:ILE:HG12	1.92	0.50
73:W2:29:GLU:HA	73:W2:29:GLU:OE2	2.11	0.50
11:h1:70:GLU:CD	11:h1:70:GLU:H	2.20	0.50
62:P1:116:HIS:HB3	62:P1:149:ILE:HB	1.93	0.50
63:Q1:35:LEU:O	63:Q1:39:SER:CB	2.54	0.50
74:X1:119:ASP:HB2	74:X1:143:TYR:CE1	2.47	0.50
47:K2:25:ARG:HA	56:C2:422:A:H5''	1.93	0.50
48:L1:110:LEU:O	48:L1:114:VAL:HG23	2.10	0.50
52:P2:27:ALA:O	52:P2:31:THR:HG23	2.12	0.50
55:A1:3011:C:H2'	55:A1:3012:C:H6	1.76	0.50
56:C2:1684:U:H2'	56:C2:1685:A:C8	2.46	0.50
64:R1:70:ARG:HH11	64:R1:70:ARG:HG3	1.77	0.50
52:P2:114:LEU:HA	52:P2:117:ILE:HD12	1.91	0.50
53:i2:104:GLU:O	53:i2:108:LEU:HD22	2.12	0.50
55:A1:711:U:H2'	55:A1:712:C:C6	2.47	0.50
55:A1:2176:A:H2'	55:A1:2177:A:C8	2.46	0.50
56:C2:917:U:H2'	56:C2:918:A:H8	1.77	0.50
66:S2:129:SER:O	66:S2:137:ALA:HB2	2.10	0.50
69:U1:115:ARG:HG2	69:U1:117:VAL:HG23	1.91	0.50
71:V1:131:ARG:CZ	71:V1:131:ARG:HB3	2.41	0.50
3:Z1:3:LYS:HD3	35:91:40:GLN:O	2.11	0.50
17:m2:104:ARG:HD2	56:C2:465:C:H3'	1.94	0.50
20:r2:81:LEU:HD23	20:r2:85:ASP:HB2	1.94	0.50
46:J2:178:LEU:HB3	46:J2:213:ARG:HG2	1.93	0.50
66:S2:41:MET:HE2	66:S2:41:MET:O	2.11	0.50
68:T2:48:PHE:HB3	68:T2:53:TYR:CD2	2.46	0.50
10:g2:16:LEU:HD11	53:i2:116:ASN:ND2	2.27	0.50
10:g2:50:ASN:HA	53:i2:105:MET:CE	2.41	0.50
11:h1:184:ASP:OD1	11:h1:186:GLU:HG3	2.11	0.50
16:m1:50:ASP:HB3	74:X1:39:ILE:HG13	1.92	0.50
23:y2:61:GLN:HB3	23:y2:62:PRO:CD	2.41	0.50
33:81:112:PRO:O	33:81:114:TYR:N	2.44	0.50
36:B1:46:PHE:CZ	36:B1:84:MET:HG3	2.46	0.50
53:i2:34:VAL:HG12	77:k2:150:TRP:CH2	2.47	0.50
55:A1:3606:U:C2	55:A1:3607:A:C8	3.00	0.50
55:A1:3685:U:H2'	55:A1:3686:G:C8	2.46	0.50
56:C2:1622:G:H1	56:C2:1642:U:H3	1.59	0.50
77:k2:228:TYR:CD2	77:k2:264:LYS:HE2	2.46	0.50
9:g1:85:ARG:NH1	56:C2:913:U:H5''	2.27	0.50
25:32:84:HIS:C	37:B2:19:ARG:HH21	2.20	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:C1:219:LYS:NZ	38:C1:219:LYS:HB3	2.27	0.50
42:H1:4:ILE:HG23	42:H1:9:LEU:HD11	1.94	0.50
55:A1:1441:C:H2'	55:A1:1442:C:C6	2.47	0.50
55:A1:2814:U:H3'	55:A1:2815:G:C8	2.47	0.50
55:A1:3282:A:H2'	55:A1:3283:G:H8	1.77	0.50
56:C2:277:C:H2'	56:C2:278:C:C5	2.47	0.50
56:C2:322:A:H2'	56:C2:323:A:C8	2.47	0.50
56:C2:1793:A:H2'	56:C2:1794:A:C8	2.47	0.50
30:61:66:GLU:O	30:61:70:ILE:HG13	2.11	0.50
32:72:126:ILE:HG12	34:82:80:ILE:HD12	1.94	0.50
44:I1:55:ARG:HA	44:I1:58:MET:HE3	1.94	0.50
55:A1:947:A:H2'	55:A1:948:A:H8	1.77	0.50
55:A1:960:C:H2'	55:A1:961:A:C8	2.46	0.50
56:C2:1770:A:H2'	56:C2:1771:C:H6	1.76	0.50
61:O2:233:LYS:HE2	61:O2:233:LYS:N	2.27	0.50
69:U1:41:HIS:HB3	69:U1:128:TYR:HE1	1.77	0.50
73:W2:85:ARG:HB3	73:W2:85:ARG:NH1	2.26	0.50
77:k2:194:TYR:CE2	77:k2:212:LYS:HB2	2.47	0.50
24:z2:58:LYS:HA	24:z2:58:LYS:HE3	1.94	0.50
27:42:94:LYS:HA	27:42:94:LYS:HE3	1.94	0.50
41:F1:175:LYS:NZ	41:F1:175:LYS:HB3	2.27	0.50
53:i2:63:ARG:HH22	53:i2:65:PRO:HD2	1.77	0.50
54:w2:142:LEU:HD22	54:w2:143:ARG:HH22	1.77	0.50
55:A1:498:G:H2'	55:A1:498:G:N3	2.27	0.50
55:A1:1684:C:H42	55:A1:1697:G:N2	2.10	0.50
56:C2:406:G:H2'	56:C2:407:A:C8	2.47	0.50
68:T2:52:THR:HA	68:T2:55:LYS:NZ	2.26	0.50
73:W2:201:LYS:HE3	73:W2:201:LYS:HA	1.92	0.50
9:g1:3:LYS:HE3	9:g1:4:ARG:N	2.27	0.49
36:B1:43:LEU:HD23	36:B1:183:VAL:HG11	1.92	0.49
42:H1:91:MET:HE1	45:J1:78:PHE:CD2	2.47	0.49
49:L2:78:LEU:HB3	49:L2:92:MET:HE2	1.92	0.49
55:A1:486:C:H42	55:A1:539:G:H1	1.60	0.49
55:A1:1149:U:H2'	55:A1:1150:G:H8	1.77	0.49
55:A1:1256:C:H2'	55:A1:1257:A:C8	2.46	0.49
55:A1:1451:C:H2'	55:A1:1452:A:C8	2.47	0.49
56:C2:214:G:H2'	56:C2:215:A:C8	2.45	0.49
64:R1:165:LYS:HD2	64:R1:165:LYS:C	2.37	0.49
75:Y1:117:LYS:NZ	75:Y1:117:LYS:HB3	2.27	0.49
4:a1:70:LYS:HG3	4:a1:71:LYS:N	2.27	0.49
19:q2:24:LEU:HD11	19:q2:87:ARG:HB2	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:u2:101:LEU:HD22	68:T2:65:LEU:HD23	1.93	0.49
27:42:67:PHE:HD2	32:72:47:LEU:HB3	1.77	0.49
36:B1:37:PRO:HA	36:B1:187:GLY:O	2.11	0.49
38:C1:284:MET:HE3	38:C1:287:THR:HG22	1.92	0.49
46:J2:168:CYS:SG	46:J2:236:TYR:HD2	2.35	0.49
48:L1:156:PRO:HB2	48:L1:158:LYS:NZ	2.25	0.49
54:w2:142:LEU:HB3	54:w2:143:ARG:NH2	2.27	0.49
55:A1:1706:G:H2'	55:A1:1707:C:C6	2.47	0.49
56:C2:527:U:H2'	56:C2:528:A:N9	2.27	0.49
56:C2:1106:C:H2'	56:C2:1107:A:O4'	2.13	0.49
69:U1:80:SER:O	69:U1:81:LYS:HG2	2.12	0.49
71:V1:14:PHE:CE2	71:V1:91:LYS:HG3	2.47	0.49
76:Y2:128:ILE:HG13	76:Y2:149:THR:HB	1.93	0.49
6:d2:43:ILE:HD12	6:d2:43:ILE:O	2.11	0.49
12:i1:4:U:H2'	12:i1:5:A:C8	2.48	0.49
13:j1:39:A:H2'	13:j1:40:A:C8	2.46	0.49
19:q2:67:LYS:HE3	19:q2:78:ASP:HB3	1.93	0.49
27:42:34:LYS:HG3	27:42:95:ASN:OD1	2.13	0.49
55:A1:1639:G:O2'	55:A1:1640:G:H5''	2.13	0.49
55:A1:2259:U:H4'	55:A1:2260:C:O4'	2.12	0.49
55:A1:2856:G:C6	55:A1:2872:C:C4	3.00	0.49
55:A1:3742:U:H1'	55:A1:3743:A:H5''	1.93	0.49
55:A1:3923:G:H2'	55:A1:3924:A:H8	1.76	0.49
55:A1:3959:U:H4'	55:A1:3960:G:H5'	1.93	0.49
77:k2:175:LYS:HD3	77:k2:184:LEU:HD11	1.93	0.49
4:a1:80:GLU:HG3	4:a1:168:VAL:HG23	1.94	0.49
9:g1:4:ARG:HG2	55:A1:1164:A:OP1	2.13	0.49
20:r2:111:MET:HE1	20:r2:119:LYS:HD2	1.95	0.49
27:42:35:ALA:HB2	27:42:44:ILE:HD11	1.92	0.49
36:B1:66:LYS:H	36:B1:66:LYS:CD	2.24	0.49
49:L2:82:VAL:HG21	49:L2:92:MET:HE3	1.95	0.49
52:P2:105:ASN:HA	52:P2:108:ARG:CG	2.41	0.49
52:P2:137:LYS:HD3	56:C2:1490:G:OP2	2.12	0.49
56:C2:1072:C:H2'	56:C2:1073:G:C8	2.48	0.49
67:T1:92:ARG:HB3	67:T1:94:GLU:OE1	2.13	0.49
71:V1:111:GLU:HA	71:V1:131:ARG:HH11	1.77	0.49
6:d2:65:ALA:HA	6:d2:66:ARG:NH1	2.28	0.49
11:h1:287:PHE:HB2	30:61:210:LYS:HZ2	1.78	0.49
13:j1:63:U:C2	13:j1:64:A:C8	3.00	0.49
41:F1:239:ASN:O	41:F1:243:ARG:HG2	2.13	0.49
55:A1:258:C:H2'	55:A1:259:G:C8	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:A1:476:A:H2'	55:A1:477:G:H8	1.78	0.49
55:A1:1042:U:H5''	63:Q1:42:PRO:HB2	1.93	0.49
55:A1:2159:G:H2'	55:A1:2160:C:C6	2.48	0.49
55:A1:2711:A:H2'	55:A1:2712:A:H8	1.77	0.49
55:A1:2946:A:H2'	55:A1:2947:C:C6	2.47	0.49
56:C2:1696:G:H1	56:C2:1777:U:H5	1.61	0.49
61:O2:152:PRO:HG2	73:W2:216:ARG:HG2	1.94	0.49
68:T2:50:LYS:HA	68:T2:50:LYS:HE2	1.95	0.49
31:71:25:CYS:H	55:A1:3294:A:H62	1.59	0.49
32:72:56:VAL:HG13	32:72:77:ALA:HB1	1.94	0.49
38:C1:144:ILE:O	38:C1:147:ILE:HG12	2.13	0.49
54:w2:107:TYR:HB2	54:w2:108:LYS:NZ	2.27	0.49
55:A1:2292:A:H2'	55:A1:2293:G:H8	1.77	0.49
55:A1:3858:G:H1	55:A1:3872:U:H3	1.59	0.49
56:C2:407:A:H2'	56:C2:408:G:C8	2.48	0.49
56:C2:1357:A:H2'	56:C2:1358:C:H6	1.78	0.49
56:C2:1380:G:H2'	56:C2:1381:U:C6	2.47	0.49
65:S1:7:LEU:O	65:S1:103:SER:HB3	2.12	0.49
73:W2:193:ALA:O	73:W2:197:GLN:HG2	2.13	0.49
12:i1:58:A:H2'	12:i1:59:G:C8	2.48	0.49
14:k1:150:ASP:O	14:k1:154:VAL:HG23	2.12	0.49
19:q2:49:LYS:HE3	19:q2:92:HIS:HB2	1.95	0.49
20:r2:107:SER:HA	56:C2:834:A:C8	2.48	0.49
21:u2:144:PRO:HA	21:u2:147:ARG:HB2	1.94	0.49
30:61:146:GLU:HG2	30:61:147:HIS:HD2	1.76	0.49
36:B1:49:TYR:HE1	36:B1:166:THR:HG21	1.78	0.49
49:L2:174:LYS:HE2	49:L2:174:LYS:HA	1.93	0.49
51:A2:58:LYS:C	51:A2:62:LYS:HZ1	2.20	0.49
55:A1:3012:C:H2'	55:A1:3013:U:H6	1.76	0.49
66:S2:93:VAL:HG21	66:S2:120:LEU:HD21	1.94	0.49
73:W2:190:ARG:O	73:W2:194:LEU:HD23	2.12	0.49
4:a1:58:LEU:HD13	4:a1:75:LEU:HD13	1.95	0.49
13:j1:8:A:H2'	13:j1:9:G:H8	1.78	0.49
16:m1:247:THR:O	16:m1:251:THR:HG23	2.12	0.49
19:q2:56:MET:HG3	19:q2:86:LYS:HG2	1.95	0.49
35:91:53:PRO:HB2	35:91:56:ARG:HG3	1.93	0.49
36:B1:145:GLN:HA	36:B1:148:LYS:NZ	2.27	0.49
39:D1:27:ILE:O	39:D1:31:ILE:HG12	2.12	0.49
42:H1:104:THR:HG23	58:N1:146:PRO:HB2	1.95	0.49
50:M1:53:LYS:HD3	65:S1:160:ARG:HD2	1.93	0.49
55:A1:2757:A:H2'	55:A1:2758:U:H6	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:A1:2814:U:H3'	55:A1:2815:G:H8	1.77	0.49
55:A1:3281:G:H2'	55:A1:3282:A:H8	1.78	0.49
55:A1:3731:C:H2'	55:A1:3732:U:C6	2.48	0.49
68:T2:67:THR:HB	68:T2:70:VAL:HG12	1.94	0.49
10:g2:42:LYS:HZ2	10:g2:46:VAL:HG23	1.78	0.49
12:i1:53:A:H4'	12:i1:54:A:H5'	1.94	0.49
13:j1:142:C:H2'	13:j1:143:U:H6	1.77	0.49
21:u2:48:LEU:HD12	21:u2:49:PRO:HD2	1.94	0.49
27:42:133:TYR:CD2	27:42:217:MET:HE1	2.48	0.49
32:72:54:CYS:HB3	32:72:84:ARG:HE	1.78	0.49
48:L1:58:GLN:HB3	48:L1:157:ILE:HG12	1.95	0.49
55:A1:1674:U:H2'	55:A1:1675:C:C6	2.48	0.49
56:C2:373:C:H5	56:C2:654:G:H5''	1.78	0.49
61:O2:36:HIS:CD2	61:O2:85:GLY:HA3	2.48	0.49
4:a1:158:ILE:HB	4:a1:162:ASN:ND2	2.27	0.49
31:71:87:LEU:HD12	31:71:170:TYR:CD2	2.48	0.49
38:C1:84:THR:HG22	55:A1:364:A:N1	2.28	0.49
41:F1:66:GLU:HA	41:F1:66:GLU:OE2	2.12	0.49
49:L2:169:ARG:HH12	56:C2:557:A:H5'	1.76	0.49
55:A1:1461:A:H2'	55:A1:1462:A:C8	2.48	0.49
55:A1:3501:C:H2'	55:A1:3502:U:C6	2.47	0.49
56:C2:1381:U:H2'	56:C2:1382:U:H6	1.78	0.49
56:C2:1470:G:H2'	56:C2:1471:C:C6	2.48	0.49
56:C2:1682:A:H2'	56:C2:1683:C:C6	2.47	0.49
64:R1:109:TYR:CD1	64:R1:114:LYS:HD3	2.48	0.49
68:T2:100:LYS:NZ	68:T2:105:LEU:HD22	2.28	0.49
72:W1:13:ILE:HG12	72:W1:32:LEU:CD1	2.43	0.49
72:W1:52:THR:HG22	72:W1:54:LEU:H	1.78	0.49
75:Y1:22:PRO:HG2	75:Y1:25:ILE:HD13	1.93	0.49
76:Y2:114:VAL:HG12	76:Y2:143:PHE:HB2	1.95	0.49
13:j1:141:C:H2'	13:j1:142:C:H6	1.78	0.48
25:32:8:LEU:C	25:32:10:PRO:HD3	2.38	0.48
27:42:27:LYS:NZ	27:42:50:THR:HB	2.27	0.48
27:42:70:SER:O	27:42:74:LEU:HD23	2.13	0.48
55:A1:678:U:H2'	55:A1:679:C:H6	1.78	0.48
55:A1:2711:A:H2'	55:A1:2712:A:C8	2.47	0.48
56:C2:13:U:H2'	56:C2:14:C:C6	2.48	0.48
56:C2:39:A:H2'	56:C2:40:A:H8	1.78	0.48
56:C2:168:A:H5''	73:W2:177:GLN:HG2	1.95	0.48
70:U2:79:LEU:HD22	70:U2:94:PHE:CZ	2.48	0.48
10:g2:102:ARG:NH2	56:C2:1351:U:H5''	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:j1:25:C:H2'	13:j1:26:U:C6	2.48	0.48
15:l1:127:ARG:HH22	55:A1:3892:C:H3'	1.78	0.48
34:82:68:ILE:HD11	34:82:93:LYS:CB	2.43	0.48
36:B1:143:LYS:O	36:B1:147:GLU:HG2	2.13	0.48
46:J2:60:LYS:HB3	46:J2:255:PHE:CZ	2.48	0.48
47:K2:147:LYS:NZ	47:K2:151:GLU:HB3	2.28	0.48
47:K2:161:LEU:H	47:K2:161:LEU:HD12	1.77	0.48
51:A2:50:ARG:HA	51:A2:50:ARG:HH11	1.79	0.48
55:A1:1953:C:H2'	55:A1:1954:G:C8	2.49	0.48
55:A1:3275:U:H4'	55:A1:3276:A:O4'	2.13	0.48
55:A1:3455:C:H2'	55:A1:3456:C:O2	2.12	0.48
55:A1:3606:U:H2'	55:A1:3607:A:C8	2.48	0.48
56:C2:1118:A:H2'	56:C2:1119:A:C8	2.48	0.48
56:C2:1306:A:H2	56:C2:1463:C:H42	1.61	0.48
56:C2:1596:U:H2'	56:C2:1597:C:C6	2.46	0.48
64:R1:91:GLU:H	64:R1:91:GLU:CD	2.22	0.48
66:S2:117:ARG:O	66:S2:121:VAL:HG22	2.13	0.48
11:h1:117:LYS:HB2	11:h1:117:LYS:NZ	2.28	0.48
14:k1:92:MET:HB3	14:k1:179:ILE:HG22	1.94	0.48
19:q2:55:ARG:HH22	19:q2:87:ARG:NH2	2.11	0.48
24:z2:56:TYR:O	24:z2:57:VAL:HG12	2.13	0.48
53:i2:60:ARG:NH2	53:i2:66:VAL:HG12	2.29	0.48
73:W2:159:ARG:HB3	73:W2:171:THR:OG1	2.13	0.48
15:l1:18:ASN:HB2	15:l1:33:MET:HE2	1.95	0.48
19:q2:55:ARG:HH12	19:q2:87:ARG:HH21	1.61	0.48
37:B2:115:LEU:O	37:B2:119:GLU:HG2	2.13	0.48
56:C2:159:C:H2'	56:C2:160:U:O4'	2.13	0.48
56:C2:1175:U:H2'	56:C2:1176:U:C6	2.48	0.48
56:C2:1706:G:H2'	56:C2:1707:G:H8	1.79	0.48
61:O2:157:ASN:O	61:O2:175:PHE:HB2	2.13	0.48
3:Z1:6:LYS:HB2	3:Z1:6:LYS:NZ	2.29	0.48
11:h1:212:MET:HG3	11:h1:219:TYR:CD1	2.47	0.48
14:k1:92:MET:O	14:k1:143:GLU:HA	2.14	0.48
20:r2:32:LYS:HG3	56:C2:660:U:OP1	2.14	0.48
24:z2:23:LYS:HZ2	24:z2:24:LYS:N	2.11	0.48
36:B1:66:LYS:NZ	71:V1:12:ALA:HB3	2.27	0.48
37:B2:3:ARG:NH1	37:B2:3:ARG:HG2	2.28	0.48
53:i2:98:VAL:HG13	53:i2:102:THR:HB	1.95	0.48
10:g2:189:ILE:HG13	10:g2:190:SER:N	2.27	0.48
14:k1:46:SER:HB2	14:k1:56:ARG:HH12	1.77	0.48
16:m1:107:LYS:O	16:m1:111:LYS:HD3	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:r2:76:SER:OG	20:r2:77:PRO:HD3	2.13	0.48
35:91:42:LYS:HB3	35:91:97:ILE:HG23	1.95	0.48
36:B1:383:GLU:CD	36:B1:383:GLU:H	2.21	0.48
38:C1:351:MET:HE1	55:A1:874:G:H21	1.78	0.48
49:L2:155:LYS:H	49:L2:155:LYS:CE	2.23	0.48
55:A1:1387:A:H5''	55:A1:3257:A:H61	1.79	0.48
55:A1:2319:A:H5''	56:C2:1702:G:H5'	1.95	0.48
55:A1:3231:U:H2'	55:A1:3232:U:C6	2.48	0.48
55:A1:3382:A:H2'	55:A1:3383:U:H6	1.79	0.48
55:A1:3944:U:H2'	55:A1:3945:G:H8	1.76	0.48
63:Q1:166:TYR:C	63:Q1:167:ILE:HD12	2.38	0.48
9:g1:84:ARG:HG2	9:g1:84:ARG:HH11	1.78	0.48
12:i1:4:U:H2'	12:i1:5:A:H8	1.77	0.48
24:z2:61:PHE:HE1	24:z2:65:HIS:N	2.12	0.48
29:51:3:ALA:HB3	56:C2:1811:C:OP1	2.13	0.48
47:K2:49:ARG:HD3	56:C2:355:A:N7	2.28	0.48
52:P2:137:LYS:HA	52:P2:137:LYS:CE	2.44	0.48
53:i2:79:GLU:HA	53:i2:82:ASP:OD1	2.14	0.48
55:A1:2040:C:H2'	55:A1:2041:G:H8	1.79	0.48
55:A1:3034:G:H2'	55:A1:3035:G:N3	2.28	0.48
55:A1:3844:C:H2'	55:A1:3845:U:C6	2.49	0.48
69:U1:40:THR:HG22	69:U1:83:LYS:HZ1	1.79	0.48
6:d2:24:GLN:HG2	56:C2:1653:C:C2	2.48	0.48
7:e1:6:THR:HG22	55:A1:1833:G:H21	1.79	0.48
7:e1:21:ARG:HD3	7:e1:35:THR:HG22	1.95	0.48
14:k1:120:GLU:HG3	14:k1:124:ARG:HH12	1.78	0.48
24:z2:20:MET:SD	24:z2:68:TRP:HB2	2.54	0.48
54:w2:127:MET:HE2	54:w2:154:ASP:OD2	2.13	0.48
55:A1:1174:A:H8	55:A1:1174:A:OP1	1.97	0.48
55:A1:2116:C:H2'	55:A1:2117:C:C6	2.49	0.48
55:A1:2279:A:H61	55:A1:2944:C:N4	2.11	0.48
56:C2:52:U:H2'	56:C2:53:G:C8	2.49	0.48
56:C2:774:U:H2'	56:C2:775:A:H8	1.78	0.48
56:C2:1369:C:O2'	56:C2:1370:A:H5'	2.13	0.48
70:U2:19:PHE:CE2	70:U2:50:GLU:HB2	2.49	0.48
73:W2:39:ASP:HA	73:W2:45:TRP:O	2.13	0.48
75:Y1:51:LYS:O	75:Y1:70:VAL:HB	2.13	0.48
2:21:90:ASN:HD22	14:k1:172:ILE:HG23	1.78	0.48
4:a1:147:ARG:HH21	4:a1:155:LYS:HD3	1.79	0.48
6:d2:59:LEU:HD12	6:d2:60:GLU:HG2	1.95	0.48
21:u2:72:THR:O	21:u2:76:MET:HG3	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:z2:21:VAL:HG13	54:w2:75:LYS:NZ	2.28	0.48
32:72:46:ASP:OD2	32:72:51:GLU:HB2	2.14	0.48
37:B2:3:ARG:HG2	37:B2:3:ARG:HH11	1.78	0.48
38:C1:124:ILE:HG21	38:C1:264:TYR:OH	2.13	0.48
44:I1:34:THR:HG21	55:A1:274:C:P	2.54	0.48
45:J1:8:PHE:O	45:J1:11:ARG:HG3	2.13	0.48
49:L2:5:ARG:HD3	56:C2:39:A:OP1	2.14	0.48
55:A1:3280:C:H2'	55:A1:3281:G:H8	1.79	0.48
55:A1:3518:G:H5''	55:A1:3519:C:C5'	2.44	0.48
56:C2:1202:A:H2'	56:C2:1203:G:C8	2.49	0.48
67:T1:68:THR:HG22	67:T1:69:GLN:N	2.29	0.48
11:h1:15:ARG:HH11	11:h1:15:ARG:HG3	1.78	0.48
21:u2:59:ARG:HG3	56:C2:1649:A:C8	2.49	0.48
24:z2:60:GLN:NE2	54:w2:28:GLU:HA	2.29	0.48
27:42:226:GLY:O	27:42:230:GLU:HG2	2.13	0.48
36:B1:53:MET:HG3	36:B1:76:VAL:O	2.14	0.48
41:F1:142:TYR:CE2	41:F1:235:GLU:HG3	2.49	0.48
43:H2:58:PRO:O	43:H2:62:MET:HG3	2.13	0.48
50:M1:7:VAL:HG23	50:M1:57:LEU:HD21	1.95	0.48
56:C2:630:G:H5'	56:C2:636:G:N2	2.29	0.48
56:C2:1501:A:H2'	56:C2:1502:C:C6	2.48	0.48
56:C2:1683:C:H2'	56:C2:1684:U:H6	1.78	0.48
57:M2:111:LYS:HA	57:M2:111:LYS:HE3	1.96	0.48
77:k2:271:LYS:HD2	77:k2:271:LYS:C	2.39	0.48
1:11:9:ILE:HD12	1:11:51:LEU:HD13	1.94	0.47
8:f1:4:ARG:O	15:l1:248:LEU:HB2	2.14	0.47
10:g2:180:ARG:HG3	10:g2:195:TRP:CD2	2.49	0.47
12:i1:16:A:H2'	12:i1:17:C:C6	2.48	0.47
12:i1:72:U:H3	12:i1:103:A:N6	2.12	0.47
16:m1:60:TYR:O	16:m1:64:GLN:HG2	2.14	0.47
16:m1:221:ALA:O	16:m1:224:THR:HG22	2.13	0.47
42:H1:14:LYS:HD3	42:H1:18:LEU:HG	1.96	0.47
55:A1:587:U:H2'	55:A1:588:C:C6	2.49	0.47
70:U2:166:VAL:HA	70:U2:169:LYS:HD3	1.96	0.47
35:91:18:LEU:O	35:91:22:MET:HG2	2.14	0.47
52:P2:10:GLN:NE2	52:P2:57:GLY:HA2	2.28	0.47
55:A1:495:G:O2'	55:A1:496:G:H2'	2.14	0.47
56:C2:1182:A:H2'	56:C2:1183:A:H8	1.77	0.47
66:S2:115:TYR:HD1	66:S2:116:ASP:HB2	1.79	0.47
12:i1:107:G:H2'	12:i1:108:G:H8	1.79	0.47
18:n1:92:LYS:HZ1	18:n1:93:LYS:HE3	1.78	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:n1:114:LYS:HD2	55:A1:1011:A:C8	2.49	0.47
21:u2:39:ALA:HB1	21:u2:44:TYR:CG	2.49	0.47
27:42:69:VAL:HG13	27:42:74:LEU:HD21	1.95	0.47
30:61:152:LEU:HD13	30:61:165:ILE:HG13	1.95	0.47
32:72:60:MET:HA	56:C2:930:G:H5'	1.95	0.47
42:H1:14:LYS:HA	42:H1:14:LYS:HE3	1.96	0.47
43:H2:4:ASP:OD1	46:J2:159:LYS:HB2	2.15	0.47
54:w2:94:ARG:CZ	54:w2:100:ALA:HB3	2.44	0.47
55:A1:1282:U:H2'	55:A1:1283:A:H8	1.78	0.47
56:C2:1011:G:H4'	56:C2:1814:A:H4'	1.97	0.47
56:C2:1715:A:H4'	73:W2:31:ARG:NH2	2.29	0.47
66:S2:58:LEU:HD21	66:S2:108:ILE:HB	1.94	0.47
66:S2:106:LYS:HZ3	77:k2:55:PRO:CG	2.24	0.47
77:k2:149:GLU:HB3	77:k2:171:ASP:HB2	1.95	0.47
14:k1:43:LEU:HD21	14:k1:70:VAL:HG22	1.96	0.47
24:z2:63:TRP:CD2	59:N2:40:VAL:HG12	2.49	0.47
27:42:146:ARG:HD3	27:42:146:ARG:HA	1.72	0.47
35:91:36:LYS:O	35:91:40:GLN:HG2	2.15	0.47
54:w2:7:LYS:HZ1	56:C2:1549:A:H5''	1.80	0.47
55:A1:2828:A:H2'	55:A1:2829:A:C8	2.49	0.47
73:W2:118:GLU:O	73:W2:119:LYS:HG2	2.14	0.47
75:Y1:45:ARG:HB2	75:Y1:126:ARG:HH22	1.80	0.47
10:g2:53:LYS:O	10:g2:57:LYS:HG2	2.15	0.47
23:y2:25:LYS:O	23:y2:29:LYS:HE3	2.14	0.47
37:B2:28:LEU:HD22	37:B2:33:VAL:CG2	2.44	0.47
38:C1:353:LYS:H	38:C1:353:LYS:HD2	1.78	0.47
55:A1:323:U:H2'	55:A1:324:C:C6	2.50	0.47
55:A1:858:G:H2'	55:A1:859:C:C6	2.49	0.47
55:A1:3810:U:H2'	55:A1:3811:G:H8	1.79	0.47
56:C2:1339:G:H2'	56:C2:1340:G:C8	2.49	0.47
56:C2:1682:A:H2'	56:C2:1683:C:H6	1.80	0.47
56:C2:1691:U:H5'	56:C2:1692:G:H5''	1.97	0.47
64:R1:151:ARG:HH22	64:R1:155:LEU:HG	1.78	0.47
69:U1:117:VAL:HB	69:U1:125:GLU:OE2	2.15	0.47
73:W2:221:LYS:NZ	73:W2:222:GLU:HB3	2.30	0.47
11:h1:125:VAL:HG11	11:h1:199:ILE:HG21	1.96	0.47
11:h1:193:GLU:O	11:h1:197:LYS:HG2	2.15	0.47
16:m1:104:PRO:HG2	16:m1:194:VAL:HG12	1.96	0.47
20:r2:106:THR:HG23	20:r2:122:GLY:O	2.14	0.47
36:B1:253:CYS:SG	55:A1:3564:U:H1'	2.54	0.47
38:C1:298:ILE:O	38:C1:302:LEU:HG	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:A2:59:ARG:HH21	51:A2:76:VAL:HB	1.80	0.47
55:A1:872:C:H4'	55:A1:873:G:OP2	2.14	0.47
56:C2:470:C:H2'	56:C2:471:C:H6	1.79	0.47
56:C2:1650:G:H2'	56:C2:1651:U:C6	2.49	0.47
4:a1:133:TYR:HB3	4:a1:168:VAL:HG12	1.97	0.47
10:g2:118:GLU:OE1	46:J2:51:LYS:HD2	2.15	0.47
10:g2:177:MET:O	10:g2:181:GLU:HG3	2.14	0.47
11:h1:236:MET:HA	11:h1:239:MET:HE2	1.97	0.47
13:j1:5:C:H2'	13:j1:6:U:H6	1.79	0.47
13:j1:26:U:H4'	38:C1:53:ALA:HB3	1.96	0.47
16:m1:143:VAL:O	16:m1:147:VAL:HG23	2.14	0.47
17:m2:36:PRO:HB2	17:m2:39:GLU:HG2	1.96	0.47
20:r2:28:ARG:HD2	56:C2:895:G:C6	2.50	0.47
51:A2:85:ILE:HD12	51:A2:89:MET:HE1	1.97	0.47
51:A2:111:MET:HG3	51:A2:119:PHE:CZ	2.48	0.47
55:A1:182:C:H2'	55:A1:183:G:H8	1.79	0.47
55:A1:297:C:H2'	55:A1:298:A:C8	2.49	0.47
55:A1:1645:C:H2'	55:A1:1646:G:O4'	2.14	0.47
55:A1:2736:A:C8	55:A1:2793:A:C8	3.02	0.47
55:A1:3357:C:C2	55:A1:3358:A:C8	3.02	0.47
55:A1:3432:C:H2'	55:A1:3433:A:C8	2.50	0.47
55:A1:3922:U:H2'	55:A1:3923:G:H8	1.78	0.47
56:C2:52:U:H2'	56:C2:53:G:H8	1.79	0.47
56:C2:1177:G:H2'	56:C2:1178:A:C8	2.49	0.47
56:C2:1380:G:H2'	56:C2:1381:U:H6	1.78	0.47
56:C2:1806:G:H2'	56:C2:1806:G:N3	2.29	0.47
64:R1:16:ARG:HA	64:R1:16:ARG:NE	2.30	0.47
68:T2:55:LYS:O	68:T2:59:GLU:HG3	2.15	0.47
3:Z1:135:ARG:HA	3:Z1:135:ARG:NH1	2.30	0.47
6:d2:13:ARG:NH1	6:d2:13:ARG:HB2	2.30	0.47
16:m1:234:ARG:HB3	16:m1:234:ARG:HH11	1.79	0.47
17:m2:86:GLU:HA	17:m2:86:GLU:OE2	2.14	0.47
32:72:92:ALA:HA	32:72:125:LYS:O	2.14	0.47
55:A1:179:U:H2'	55:A1:180:G:C8	2.49	0.47
55:A1:2100:C:O4'	64:R1:96:MET:HG2	2.15	0.47
55:A1:3309:G:H2'	55:A1:3309:G:N3	2.30	0.47
56:C2:919:U:H2'	56:C2:920:U:C6	2.50	0.47
67:T1:28:SER:O	67:T1:32:ARG:HG2	2.15	0.47
13:j1:7:U:H2'	13:j1:8:A:C8	2.50	0.47
19:q2:22:ILE:HD12	19:q2:113:GLU:O	2.15	0.47
24:z2:20:MET:HE2	24:z2:21:VAL:N	2.30	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:42:97:LEU:HB3	27:42:228:LEU:HD11	1.97	0.47
35:91:38:ILE:HD11	35:91:46:VAL:HG21	1.96	0.47
41:F1:234:ARG:HB2	41:F1:237:GLN:HB2	1.96	0.47
51:A2:37:TYR:OH	51:A2:87:PRO:HD3	2.15	0.47
55:A1:297:C:H2'	55:A1:298:A:H8	1.80	0.47
55:A1:1006:A:H2'	55:A1:1007:A:C8	2.50	0.47
55:A1:1188:G:H5'	55:A1:1189:C:H5''	1.97	0.47
55:A1:1320:U:H2'	55:A1:1321:U:C6	2.50	0.47
55:A1:2121:G:H2'	55:A1:2122:C:C6	2.50	0.47
55:A1:3955:U:H2'	55:A1:3956:U:C6	2.49	0.47
11:h1:153:THR:HG23	11:h1:160:PHE:CZ	2.50	0.47
13:j1:92:U:H2'	13:j1:93:C:O4'	2.14	0.47
25:32:80:ARG:NH1	25:32:80:ARG:HB2	2.30	0.47
38:C1:93:GLY:HA3	38:C1:95:MET:HE3	1.96	0.47
48:L1:194:ILE:HD12	48:L1:194:ILE:HA	1.81	0.47
54:w2:103:GLU:O	54:w2:107:TYR:HD1	1.98	0.47
55:A1:954:C:H2'	55:A1:955:U:H6	1.80	0.47
55:A1:1059:U:H2'	55:A1:1060:U:C6	2.49	0.47
55:A1:1502:A:H2'	55:A1:1503:G:O4'	2.15	0.47
55:A1:1740:A:H2'	55:A1:1741:A:H8	1.80	0.47
55:A1:1849:G:C2	55:A1:1858:U:H5''	2.50	0.47
66:S2:97:GLN:HB2	66:S2:105:LYS:HD2	1.97	0.47
9:g1:74:THR:O	9:g1:78:THR:HG23	2.16	0.46
16:m1:165:GLU:OE2	58:N1:22:LEU:HD13	2.16	0.46
35:91:38:ILE:HD11	35:91:46:VAL:CG2	2.44	0.46
38:C1:351:MET:SD	55:A1:790:C:H1'	2.55	0.46
49:L2:18:ARG:NH2	56:C2:5:C:H1'	2.31	0.46
55:A1:2163:U:H2'	55:A1:2164:C:C6	2.50	0.46
56:C2:960:G:H5''	56:C2:962:C:H41	1.79	0.46
56:C2:1070:A:H2	56:C2:1110:G:H22	1.61	0.46
58:N1:11:TRP:O	58:N1:14:LYS:HG3	2.15	0.46
64:R1:64:ARG:O	64:R1:68:LEU:HD23	2.14	0.46
2:21:95:ILE:HA	2:21:101:ALA:O	2.15	0.46
15:l1:105:LYS:H	15:l1:105:LYS:HD2	1.79	0.46
23:y2:15:ASN:O	23:y2:19:GLU:HG3	2.14	0.46
24:z2:42:LEU:H	24:z2:42:LEU:HD12	1.79	0.46
25:32:33:MET:HE3	25:32:46:VAL:HG23	1.96	0.46
34:82:68:ILE:HD11	34:82:93:LYS:HB2	1.96	0.46
36:B1:212:THR:HG22	36:B1:215:GLU:HG3	1.97	0.46
51:A2:127:LYS:H	51:A2:127:LYS:HD2	1.79	0.46
55:A1:13:A:H4'	74:X1:52:ARG:HD3	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:A1:940:A:H2'	55:A1:941:C:C6	2.50	0.46
55:A1:1898:C:H2'	55:A1:1899:G:O4'	2.15	0.46
56:C2:403:C:OP1	61:O2:10:LYS:HE2	2.14	0.46
56:C2:470:C:H2'	56:C2:471:C:C6	2.51	0.46
56:C2:1041:C:H2'	56:C2:1042:G:O4'	2.15	0.46
67:T1:115:LYS:HA	67:T1:118:GLU:OE1	2.15	0.46
69:U1:53:PHE:HE1	69:U1:57:LEU:HD21	1.80	0.46
69:U1:55:GLN:HA	69:U1:58:GLN:HG3	1.96	0.46
73:W2:201:LYS:O	73:W2:204:GLU:HG3	2.15	0.46
36:B1:287:ILE:HD13	36:B1:331:VAL:HG22	1.97	0.46
39:D1:82:MET:HE2	39:D1:82:MET:HB3	1.55	0.46
41:F1:34:MET:O	41:F1:38:LYS:HG2	2.15	0.46
52:P2:25:LYS:HG3	56:C2:1573:A:H61	1.79	0.46
55:A1:898:G:O2'	55:A1:899:U:H5''	2.16	0.46
55:A1:3518:G:H4'	55:A1:3519:C:OP2	2.15	0.46
56:C2:262:G:H1'	61:O2:131:ILE:HD13	1.97	0.46
56:C2:1138:G:O2'	56:C2:1139:G:H5'	2.16	0.46
64:R1:164:SER:HA	64:R1:167:LYS:HE3	1.96	0.46
65:S1:128:LYS:HB2	65:S1:128:LYS:HE2	1.76	0.46
66:S2:42:VAL:HG12	66:S2:43:GLU:N	2.30	0.46
66:S2:63:PHE:CZ	66:S2:92:LEU:HD22	2.50	0.46
77:k2:191:HIS:CD2	77:k2:195:LEU:HD11	2.50	0.46
10:g2:181:GLU:C	10:g2:181:GLU:OE1	2.58	0.46
11:h1:241:LYS:HD2	11:h1:241:LYS:N	2.30	0.46
14:k1:43:LEU:HD22	14:k1:57:VAL:HG12	1.97	0.46
28:K1:51:GLU:HA	28:K1:54:GLU:OE2	2.15	0.46
37:B2:26:LEU:HD21	37:B2:60:VAL:HG22	1.97	0.46
37:B2:46:THR:OG1	37:B2:49:GLN:HG3	2.15	0.46
48:L1:162:LYS:HD3	48:L1:162:LYS:N	2.27	0.46
52:P2:15:VAL:HG23	52:P2:16:LEU:N	2.31	0.46
52:P2:105:ASN:O	52:P2:109:GLU:HG3	2.15	0.46
55:A1:129:U:H2'	55:A1:130:C:C6	2.50	0.46
55:A1:443:U:H2'	55:A1:444:C:O4'	2.16	0.46
55:A1:3355:U:H2'	55:A1:3356:A:C8	2.51	0.46
56:C2:917:U:H2'	56:C2:918:A:C8	2.50	0.46
66:S2:32:ILE:HD13	66:S2:39:LEU:HB2	1.97	0.46
75:Y1:42:TYR:OH	75:Y1:111:LEU:HD11	2.15	0.46
13:j1:3:C:H2'	13:j1:4:U:C6	2.50	0.46
16:m1:153:GLN:O	16:m1:180:PRO:HD2	2.14	0.46
20:r2:6:VAL:HG12	20:r2:34:ILE:HD11	1.98	0.46
29:51:16:LYS:HB2	29:51:16:LYS:NZ	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:81:185:LYS:N	33:81:185:LYS:HD2	2.29	0.46
49:L2:17:ARG:HB2	49:L2:17:ARG:HH11	1.81	0.46
52:P2:89:ASP:HB2	52:P2:92:ASP:O	2.15	0.46
55:A1:247:C:H2'	55:A1:248:C:C6	2.51	0.46
55:A1:383:A:N3	55:A1:385:G:H5''	2.30	0.46
55:A1:1850:A:C4	55:A1:1851:A:C8	3.04	0.46
55:A1:2956:U:H2'	55:A1:2957:A:H8	1.79	0.46
55:A1:3790:U:H2'	55:A1:3791:U:C6	2.50	0.46
56:C2:475:C:H2'	56:C2:475:C:O2	2.16	0.46
56:C2:492:G:H2'	56:C2:493:A:C8	2.51	0.46
56:C2:556:U:H2'	56:C2:557:A:H8	1.81	0.46
56:C2:1381:U:H4'	66:S2:71:ARG:CZ	2.45	0.46
73:W2:170:ARG:HH22	73:W2:172:LYS:CB	2.27	0.46
1:11:46:ARG:HB3	1:11:46:ARG:NH1	2.30	0.46
10:g2:19:LEU:HD11	53:i2:106:LEU:HD11	1.98	0.46
13:j1:23:G:H1'	55:A1:358:A:C4	2.51	0.46
16:m1:107:LYS:HA	16:m1:110:LYS:HB3	1.97	0.46
27:42:224:GLU:OE2	27:42:227:LYS:HG3	2.16	0.46
28:K1:24:LYS:HD2	28:K1:67:LYS:NZ	2.30	0.46
30:61:150:GLU:HA	30:61:153:ARG:HG3	1.97	0.46
34:82:70:ASN:HB3	34:82:72:VAL:O	2.16	0.46
36:B1:141:GLU:HA	36:B1:144:LYS:HZ2	1.80	0.46
36:B1:222:VAL:HA	36:B1:275:HIS:O	2.16	0.46
38:C1:275:VAL:HG23	55:A1:992:C:OP1	2.16	0.46
53:i2:100:PRO:HA	53:i2:103:LYS:HB3	1.97	0.46
55:A1:1452:A:H2'	55:A1:1453:C:H6	1.79	0.46
56:C2:1774:G:H2'	56:C2:1775:A:H8	1.79	0.46
62:P1:145:HIS:C	62:P1:146:ILE:HD12	2.41	0.46
70:U2:77:VAL:HG23	70:U2:78:ARG:HH22	1.79	0.46
3:Z1:84:ARG:HG2	3:Z1:84:ARG:HH11	1.80	0.46
14:k1:39:ASN:C	14:k1:39:ASN:HD22	2.23	0.46
17:m2:57:VAL:HB	17:m2:60:PHE:CE2	2.48	0.46
23:y2:26:GLN:HG3	23:y2:29:LYS:NZ	2.31	0.46
30:61:95:HIS:HD2	30:61:128:ARG:NH2	2.13	0.46
30:61:145:LYS:HE2	30:61:145:LYS:N	2.09	0.46
30:61:162:ARG:HA	30:61:162:ARG:NH1	2.30	0.46
36:B1:371:THR:HG22	36:B1:377:GLY:HA3	1.97	0.46
43:H2:23:ILE:HG21	46:J2:235:SER:HA	1.97	0.46
44:I1:25:LYS:HB3	55:A1:160:C:OP2	2.16	0.46
46:J2:90:ASP:HB3	46:J2:116:ILE:HG22	1.97	0.46
46:J2:115:ALA:O	46:J2:202:MET:HE1	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:J2:124:GLY:HA3	46:J2:148:ILE:HD13	1.97	0.46
48:L1:115:GLN:O	48:L1:119:GLU:HG3	2.15	0.46
51:A2:43:ARG:NH1	51:A2:47:ARG:HD2	2.31	0.46
54:w2:207:HIS:HE1	54:w2:209:SER:HB3	1.81	0.46
55:A1:784:C:H2'	55:A1:785:G:H8	1.80	0.46
55:A1:2073:G:H2'	55:A1:2074:A:C8	2.50	0.46
55:A1:2972:A:H2'	55:A1:2973:A:C8	2.51	0.46
55:A1:3215:A:H3'	55:A1:3216:G:H8	1.80	0.46
56:C2:406:G:H2'	56:C2:407:A:H8	1.79	0.46
13:j1:64:A:C4	13:j1:65:A:C8	3.03	0.46
16:m1:74:LEU:O	16:m1:239:GLY:HA3	2.16	0.46
19:q2:31:SER:O	19:q2:34:LYS:HG3	2.16	0.46
24:z2:21:VAL:HG22	54:w2:75:LYS:HD3	1.98	0.46
36:B1:66:LYS:HE2	71:V1:14:PHE:CZ	2.51	0.46
36:B1:66:LYS:HE2	71:V1:14:PHE:CE2	2.50	0.46
40:E1:64:LYS:HE2	55:A1:1673:G:P	2.56	0.46
54:w2:94:ARG:CZ	54:w2:95:GLY:H	2.29	0.46
55:A1:3803:G:H2'	55:A1:3804:G:O4'	2.15	0.46
56:C2:277:C:H2'	56:C2:278:C:C6	2.51	0.46
56:C2:1684:U:H2'	56:C2:1685:A:H8	1.80	0.46
58:N1:104:GLU:HA	58:N1:104:GLU:OE2	2.16	0.46
66:S2:84:ILE:O	66:S2:88:ILE:HG12	2.15	0.46
72:W1:27:LYS:HE3	72:W1:27:LYS:HB2	1.74	0.46
73:W2:170:ARG:NH2	73:W2:172:LYS:HB2	2.26	0.46
10:g2:102:ARG:HH21	56:C2:1351:U:H5''	1.80	0.46
15:l1:186:ALA:HA	15:l1:189:LYS:HD2	1.98	0.46
19:q2:31:SER:HB3	19:q2:107:GLU:CD	2.41	0.46
21:u2:202:LYS:HD2	21:u2:205:ARG:CZ	2.46	0.46
39:D1:66:LEU:HD13	39:D1:82:MET:HE1	1.98	0.46
44:I1:26:HIS:O	44:I1:29:ARG:HG3	2.16	0.46
47:K2:84:ASN:HB2	47:K2:91:VAL:HG23	1.97	0.46
55:A1:1315:C:H2'	55:A1:1316:A:C8	2.50	0.46
55:A1:3021:U:H2'	55:A1:3022:U:C6	2.51	0.46
55:A1:3279:G:H2'	55:A1:3280:C:C6	2.51	0.46
55:A1:3902:G:H1'	55:A1:3903:U:H5''	1.98	0.46
56:C2:1442:C:O2	56:C2:1446:A:N6	2.48	0.46
68:T2:59:GLU:OE2	68:T2:75:LEU:HD11	2.16	0.46
10:g2:34:MET:HE3	10:g2:34:MET:HB3	1.70	0.46
11:h1:179:ARG:HD2	11:h1:179:ARG:HA	1.76	0.46
13:j1:155:G:H2'	13:j1:156:C:C6	2.50	0.46
34:82:68:ILE:HD13	34:82:95:TYR:CD2	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:L2:113:GLN:HG3	49:L2:149:VAL:HG21	1.98	0.46
52:P2:59:LEU:HD11	52:P2:63:GLU:HG3	1.97	0.46
54:w2:25:LEU:HB3	54:w2:34:TYR:CE1	2.51	0.46
54:w2:70:THR:O	54:w2:74:GLN:HG2	2.14	0.46
55:A1:209:G:H2'	55:A1:210:A:H8	1.81	0.46
55:A1:496:G:H21	55:A1:497:C:H42	1.63	0.46
55:A1:1161:G:OP1	64:R1:86:ASN:HB3	2.16	0.46
55:A1:1973:U:H2'	55:A1:1974:G:C8	2.50	0.46
55:A1:2160:C:H2'	55:A1:2161:U:C6	2.51	0.46
55:A1:2209:A:H2'	55:A1:2210:G:C8	2.50	0.46
55:A1:2292:A:H2'	55:A1:2293:G:C8	2.51	0.46
55:A1:2801:C:H2'	55:A1:2847:A:H61	1.80	0.46
55:A1:3464:C:H42	55:A1:3518:G:H22	1.64	0.46
56:C2:922:U:H2'	56:C2:923:G:C8	2.51	0.46
56:C2:1182:A:H2'	56:C2:1183:A:C8	2.51	0.46
56:C2:1615:C:H4'	66:S2:138:ARG:O	2.16	0.46
60:O1:74:GLU:N	60:O1:74:GLU:OE2	2.49	0.46
69:U1:41:HIS:N	69:U1:42:PRO:HD2	2.31	0.46
77:k2:150:TRP:HB2	77:k2:170:TRP:HB2	1.97	0.46
6:d2:26:GLN:CD	6:d2:26:GLN:H	2.24	0.45
16:m1:95:LEU:HD11	16:m1:154:LEU:HD21	1.98	0.45
50:M1:58:THR:HG22	50:M1:59:ASP:H	1.81	0.45
53:i2:77:GLU:O	53:i2:81:ARG:HG2	2.15	0.45
54:w2:133:GLY:HA2	54:w2:155:GLY:HA3	1.98	0.45
55:A1:526:C:H2'	55:A1:527:C:C6	2.51	0.45
55:A1:996:G:H2'	55:A1:997:G:H8	1.81	0.45
60:O1:26:TYR:HB3	60:O1:67:VAL:HB	1.98	0.45
64:R1:13:SER:HA	64:R1:16:ARG:HH12	1.80	0.45
68:T2:84:ASN:O	68:T2:88:GLU:HG3	2.16	0.45
77:k2:125:ARG:HD2	77:k2:150:TRP:CD2	2.51	0.45
4:a1:142:GLU:OE1	4:a1:142:GLU:HA	2.15	0.45
6:d2:12:ALA:CB	6:d2:58:LEU:HD11	2.46	0.45
11:h1:224:SER:O	11:h1:228:LYS:HG3	2.16	0.45
15:l1:42:ARG:N	15:l1:42:ARG:HD2	2.31	0.45
19:q2:51:LYS:HD3	19:q2:90:ASP:HB2	1.98	0.45
19:q2:79:ARG:CZ	19:q2:79:ARG:HB2	2.46	0.45
23:y2:61:GLN:HB3	23:y2:62:PRO:HD3	1.98	0.45
25:32:21:LYS:HE3	37:B2:13:GLN:HG3	1.98	0.45
27:42:69:VAL:CG1	27:42:74:LEU:HD21	2.46	0.45
31:71:96:LYS:HG2	31:71:174:ILE:HG22	1.98	0.45
52:P2:4:VAL:O	52:P2:6:PRO:HD3	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:A1:434:C:H2'	55:A1:435:G:H8	1.82	0.45
55:A1:830:U:H2'	55:A1:833:C:O2	2.16	0.45
55:A1:2930:G:C2	55:A1:2931:A:C8	3.05	0.45
55:A1:3502:U:H2'	55:A1:3503:U:C6	2.51	0.45
55:A1:3983:U:H2'	55:A1:3984:G:H8	1.81	0.45
56:C2:429:A:H2'	56:C2:430:C:C6	2.51	0.45
56:C2:777:U:H2'	56:C2:778:U:C6	2.51	0.45
61:O2:250:GLU:HA	61:O2:253:ASP:HB3	1.97	0.45
13:j1:4:U:H2'	13:j1:5:C:H6	1.81	0.45
13:j1:5:C:H2'	13:j1:6:U:C6	2.51	0.45
13:j1:96:C:H5''	42:H1:66:LYS:HD3	1.98	0.45
15:l1:191:LYS:HE3	15:l1:192:LYS:H	1.82	0.45
26:41:54:ALA:HA	26:41:61:VAL:HG23	1.97	0.45
36:B1:303:ALA:HB3	36:B1:312:LYS:HG3	1.99	0.45
38:C1:190:ARG:HG2	38:C1:191:ALA:H	1.80	0.45
40:E1:107:ASN:O	40:E1:111:ILE:HG13	2.16	0.45
55:A1:1072:C:H2'	55:A1:1073:A:H8	1.81	0.45
55:A1:1079:C:H2'	55:A1:1080:C:H6	1.81	0.45
55:A1:1082:U:H2'	55:A1:1083:C:H6	1.82	0.45
55:A1:1280:A:H4'	55:A1:1296:G:H22	1.80	0.45
55:A1:1807:A:H2'	55:A1:1808:A:H8	1.82	0.45
55:A1:3706:G:OP1	72:W1:34:ALA:HB3	2.17	0.45
55:A1:3956:U:H2'	55:A1:3957:C:C6	2.52	0.45
56:C2:86:A:H2'	56:C2:87:C:H6	1.80	0.45
56:C2:528:A:H2'	56:C2:529:A:C8	2.52	0.45
56:C2:1173:A:H2'	56:C2:1174:A:C8	2.51	0.45
67:T1:18:PRO:HB2	67:T1:21:LYS:HB2	1.98	0.45
77:k2:129:ILE:HD12	77:k2:154:VAL:HG11	1.97	0.45
11:h1:64:ILE:HG13	11:h1:105:LEU:HD21	1.98	0.45
12:i1:22:G:H2'	12:i1:23:A:C8	2.51	0.45
25:32:35:VAL:HG12	25:32:78:SER:O	2.16	0.45
30:61:134:VAL:C	30:61:135:ILE:HD13	2.41	0.45
46:J2:178:LEU:O	46:J2:212:ALA:HA	2.16	0.45
48:L1:130:LYS:HD3	48:L1:130:LYS:N	2.31	0.45
51:A2:52:LYS:NZ	51:A2:80:LEU:HD11	2.31	0.45
55:A1:1090:G:H2'	55:A1:1091:C:C6	2.51	0.45
55:A1:1817:U:H2'	55:A1:1818:U:C6	2.51	0.45
55:A1:3017:G:H2'	55:A1:3018:A:C8	2.51	0.45
55:A1:3456:C:H2'	55:A1:3457:A:O4'	2.17	0.45
56:C2:1017:G:H2'	56:C2:1018:G:O4'	2.17	0.45
58:N1:120:TRP:HE1	58:N1:123:GLU:CG	2.30	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:R1:172:ARG:HE	64:R1:172:ARG:C	2.24	0.45
70:U2:78:ARG:HA	70:U2:81:ARG:CZ	2.46	0.45
73:W2:3:LEU:HB2	73:W2:16:ILE:HG13	1.97	0.45
1:11:43:HIS:CE1	1:11:45:ARG:HB2	2.52	0.45
13:j1:18:C:H2'	13:j1:19:A:H8	1.79	0.45
17:m2:38:THR:O	17:m2:42:GLU:HG3	2.16	0.45
30:61:88:ARG:HG3	30:61:88:ARG:NH1	2.32	0.45
42:H1:48:ARG:O	42:H1:52:LYS:HG2	2.16	0.45
47:K2:37:LYS:HE2	47:K2:93:THR:HG22	1.99	0.45
54:w2:76:ARG:HD3	54:w2:77:PHE:CE1	2.52	0.45
55:A1:275:G:H5''	58:N1:5:ARG:HH22	1.81	0.45
55:A1:956:A:H2'	55:A1:957:A:C8	2.51	0.45
55:A1:1768:C:H2'	55:A1:1769:G:H8	1.81	0.45
55:A1:3442:U:H2'	55:A1:3443:G:O4'	2.16	0.45
55:A1:3918:U:H4'	55:A1:3919:A:O5'	2.17	0.45
55:A1:3930:A:H2'	55:A1:3931:G:O4'	2.16	0.45
56:C2:650:C:H3'	56:C2:651:G:C8	2.52	0.45
56:C2:1330:G:H2'	56:C2:1331:A:C8	2.52	0.45
13:j1:112:U:N3	74:X1:102:LYS:HE3	2.31	0.45
17:m2:23:MET:HE2	17:m2:23:MET:HB2	1.69	0.45
24:z2:24:LYS:N	24:z2:24:LYS:HE2	2.31	0.45
41:F1:159:ARG:HA	41:F1:163:GLN:O	2.16	0.45
43:H2:71:ARG:CZ	43:H2:71:ARG:HB2	2.47	0.45
46:J2:61:ILE:HG23	46:J2:66:GLU:OE2	2.16	0.45
52:P2:105:ASN:HA	52:P2:108:ARG:HG2	1.98	0.45
53:i2:10:LYS:O	53:i2:14:ARG:HG3	2.16	0.45
54:w2:40:ARG:HG3	54:w2:41:VAL:N	2.31	0.45
54:w2:75:LYS:HE3	54:w2:75:LYS:HB3	1.72	0.45
55:A1:295:U:H2'	55:A1:296:G:C8	2.52	0.45
55:A1:431:A:H2'	55:A1:432:A:C8	2.51	0.45
55:A1:1430:A:O2'	67:T1:132:PRO:HD3	2.17	0.45
55:A1:3458:A:H2'	55:A1:3459:G:O4'	2.17	0.45
70:U2:42:GLU:N	70:U2:42:GLU:OE2	2.49	0.45
9:g1:29:ILE:HG23	9:g1:69:TRP:HB3	1.97	0.45
14:k1:73:ILE:O	14:k1:77:VAL:HG23	2.16	0.45
14:k1:140:GLN:HB3	14:k1:143:GLU:HG3	1.99	0.45
23:y2:95:GLU:OE1	23:y2:95:GLU:N	2.49	0.45
28:K1:35:LYS:NZ	55:A1:2129:A:H62	2.14	0.45
47:K2:39:GLY:HA3	47:K2:59:ARG:HD2	1.99	0.45
53:i2:68:GLY:C	53:i2:69:ILE:HD13	2.41	0.45
55:A1:1115:G:H2'	55:A1:1116:C:C6	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:A1:2822:U:H2'	55:A1:2823:G:H8	1.82	0.45
55:A1:2827:A:H2'	55:A1:2828:A:C8	2.52	0.45
56:C2:86:A:H2'	56:C2:87:C:C6	2.52	0.45
56:C2:847:A:H2'	56:C2:848:C:C6	2.52	0.45
64:R1:23:TRP:CE3	64:R1:51:ILE:HD13	2.52	0.45
65:S1:29:ARG:NH2	67:T1:150:LEU:HD21	2.32	0.45
70:U2:61:ILE:HD13	70:U2:176:VAL:HG13	1.99	0.45
70:U2:119:SER:HB2	70:U2:120:ARG:HH11	1.81	0.45
73:W2:2:LYS:HB2	73:W2:108:VAL:HG22	1.98	0.45
76:Y2:51:ARG:HA	76:Y2:54:ILE:HB	1.98	0.45
77:k2:126:ASP:O	77:k2:126:ASP:OD2	2.34	0.45
7:e1:48:ILE:HG13	7:e1:49:CYS:SG	2.57	0.45
11:h1:153:THR:HG23	11:h1:160:PHE:HZ	1.82	0.45
15:l1:143:LEU:HD21	55:A1:3894:G:C8	2.52	0.45
16:m1:173:LEU:HA	44:I1:43:MET:HE2	1.99	0.45
33:81:112:PRO:N	33:81:113:PRO:HD2	2.32	0.45
38:C1:222:ARG:HG2	75:Y1:1:MET:CE	2.46	0.45
46:J2:121:GLY:HA2	46:J2:151:VAL:HG22	1.98	0.45
50:M1:71:LYS:HA	50:M1:74:LYS:NZ	2.31	0.45
52:P2:113:ARG:HG3	52:P2:116:LYS:NZ	2.32	0.45
55:A1:88:A:H2'	55:A1:89:G:O4'	2.17	0.45
55:A1:476:A:H2'	55:A1:477:G:C8	2.52	0.45
55:A1:3281:G:H2'	55:A1:3282:A:C8	2.52	0.45
56:C2:6:U:H2'	56:C2:7:G:H8	1.82	0.45
58:N1:96:ARG:HH12	58:N1:104:GLU:HG3	1.81	0.45
67:T1:39:ILE:HD12	67:T1:102:ARG:HD3	1.98	0.45
69:U1:122:GLU:N	69:U1:122:GLU:OE2	2.50	0.45
70:U2:21:SER:O	70:U2:25:GLN:HG2	2.16	0.45
77:k2:129:ILE:HG23	77:k2:140:TYR:CD1	2.52	0.45
4:a1:122:ASP:OD1	4:a1:125:LYS:HG2	2.16	0.45
10:g2:201:LEU:HD23	53:i2:85:VAL:HG22	1.98	0.45
18:n1:35:ALA:HB1	55:A1:40:A:H5''	1.98	0.45
19:q2:90:ASP:O	19:q2:91:LEU:HD13	2.17	0.45
30:61:56:GLU:N	30:61:56:GLU:OE2	2.50	0.45
41:F1:174:GLU:HA	41:F1:174:GLU:OE2	2.17	0.45
51:A2:81:ARG:HH12	51:A2:120:SER:HB3	1.82	0.45
53:i2:60:ARG:HH21	53:i2:66:VAL:HG12	1.81	0.45
55:A1:1807:A:H2'	55:A1:1808:A:C8	2.52	0.45
55:A1:1988:A:H2'	55:A1:1989:G:O4'	2.17	0.45
55:A1:2785:G:H2'	55:A1:2786:C:C6	2.52	0.45
56:C2:499:A:H2'	56:C2:500:A:C8	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:C2:502:A:H2'	56:C2:503:A:C8	2.51	0.45
56:C2:1710:C:H2'	56:C2:1711:U:C6	2.51	0.45
66:S2:130:LYS:HG3	66:S2:136:GLY:HA2	1.98	0.45
68:T2:96:LYS:HB2	68:T2:96:LYS:NZ	2.31	0.45
3:Z1:93:LYS:O	3:Z1:97:ASN:HB3	2.16	0.45
7:e1:97:ILE:HG21	55:A1:3170:G:O6	2.17	0.45
10:g2:48:ILE:CG2	53:i2:105:MET:HE2	2.47	0.45
13:j1:129:C:H2'	13:j1:130:C:H6	1.82	0.45
16:m1:234:ARG:HB3	16:m1:234:ARG:NH1	2.32	0.45
32:72:27:VAL:HG12	32:72:90:ILE:HG13	1.99	0.45
51:A2:85:ILE:HG23	51:A2:112:CYS:HA	1.99	0.45
51:A2:115:TYR:O	51:A2:118:GLU:HB3	2.16	0.45
55:A1:1703:G:H2'	55:A1:1704:C:C6	2.52	0.45
55:A1:3280:C:H2'	55:A1:3281:G:C8	2.52	0.45
56:C2:1087:A:H2'	56:C2:1088:U:C6	2.51	0.45
56:C2:1442:C:H2'	56:C2:1443:G:O4'	2.17	0.45
62:P1:41:ILE:HD13	62:P1:150:LEU:HD21	1.98	0.45
64:R1:3:MET:O	64:R1:3:MET:HE3	2.17	0.45
64:R1:168:GLU:O	64:R1:171:LYS:HB3	2.17	0.45
66:S2:32:ILE:HD13	66:S2:39:LEU:CB	2.48	0.45
67:T1:68:THR:CG2	67:T1:69:GLN:H	2.30	0.45
4:a1:183:GLY:HA3	55:A1:1224:A:H5''	1.99	0.44
10:g2:191:ARG:HG3	10:g2:191:ARG:O	2.16	0.44
23:y2:107:ARG:C	23:y2:108:LYS:HG2	2.42	0.44
28:K1:35:LYS:HZ1	55:A1:2129:A:H62	1.66	0.44
55:A1:422:U:H2'	55:A1:423:U:C6	2.52	0.44
55:A1:539:G:N2	55:A1:540:G:O6	2.50	0.44
55:A1:1115:G:H2'	55:A1:1116:C:H6	1.81	0.44
55:A1:1728:C:H2'	55:A1:1729:G:H8	1.83	0.44
55:A1:1845:A:H2'	55:A1:1846:U:C6	2.52	0.44
55:A1:2791:U:H2'	55:A1:2792:G:O4'	2.17	0.44
55:A1:3529:C:H2'	55:A1:3530:A:O4'	2.17	0.44
55:A1:3538:G:C2	55:A1:3539:A:N7	2.85	0.44
55:A1:3885:U:H2'	55:A1:3886:U:O4'	2.16	0.44
56:C2:561:A:O2'	56:C2:564:A:H1'	2.17	0.44
58:N1:178:HIS:HA	58:N1:181:HIS:CE1	2.53	0.44
61:O2:129:ILE:C	61:O2:129:ILE:HD12	2.41	0.44
64:R1:157:ASP:HA	64:R1:160:GLU:OE1	2.17	0.44
65:S1:165:PRO:O	65:S1:166:ARG:C	2.60	0.44
4:a1:122:ASP:C	4:a1:123:ARG:HG2	2.42	0.44
13:j1:29:U:H2'	13:j1:30:G:C8	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:j1:93:C:O2'	13:j1:94:G:H8	2.00	0.44
21:u2:16:ILE:HG23	21:u2:47:TYR:CE1	2.52	0.44
23:y2:62:PRO:O	23:y2:63:ASN:ND2	2.50	0.44
30:61:88:ARG:HG3	30:61:88:ARG:HH11	1.82	0.44
52:P2:27:ALA:O	52:P2:30:ILE:HG22	2.17	0.44
56:C2:956:G:H2'	56:C2:957:A:H8	1.82	0.44
56:C2:1627:G:H1	56:C2:1637:U:H3	1.64	0.44
57:M2:50:GLU:N	57:M2:50:GLU:OE2	2.48	0.44
69:U1:54:GLU:OE1	69:U1:77:ILE:HG13	2.17	0.44
73:W2:5:ILE:HD12	73:W2:5:ILE:HA	1.87	0.44
16:m1:108:GLN:OE1	16:m1:108:GLN:N	2.49	0.44
21:u2:37:TYR:CD2	21:u2:144:PRO:HB2	2.52	0.44
30:61:91:LEU:HD11	30:61:133:GLN:NE2	2.32	0.44
31:71:20:LEU:HD12	31:71:132:VAL:HG22	1.98	0.44
33:81:115:ASP:OD1	33:81:162:ARG:HD2	2.17	0.44
35:91:51:ASN:CG	35:91:51:ASN:O	2.60	0.44
55:A1:287:U:H3	55:A1:296:G:H1	1.65	0.44
55:A1:2191:A:H2'	55:A1:2192:G:N7	2.33	0.44
57:M2:11:GLN:HB3	57:M2:62:ARG:HH11	1.83	0.44
61:O2:131:ILE:H	61:O2:131:ILE:HG12	1.56	0.44
62:P1:54:LYS:HA	62:P1:83:TRP:CD1	2.53	0.44
65:S1:160:ARG:O	65:S1:161:ARG:HB3	2.17	0.44
69:U1:79:ARG:NH1	69:U1:79:ARG:HB3	2.31	0.44
77:k2:188:HIS:HB3	77:k2:219:TRP:CZ2	2.53	0.44
77:k2:191:HIS:CE1	77:k2:195:LEU:HD21	2.52	0.44
13:j1:38:G:H1'	13:j1:103:A:N6	2.32	0.44
15:l1:212:GLN:HA	15:l1:212:GLN:NE2	2.33	0.44
17:m2:111:LYS:HG3	17:m2:112:ASN:N	2.32	0.44
25:32:84:HIS:CE1	56:C2:990:U:H3	2.35	0.44
33:81:112:PRO:C	33:81:114:TYR:N	2.76	0.44
38:C1:352:LEU:HD23	38:C1:352:LEU:HA	1.82	0.44
39:D1:39:ARG:HD3	39:D1:76:ARG:O	2.18	0.44
51:A2:65:LYS:HD2	51:A2:65:LYS:C	2.43	0.44
54:w2:156:LEU:O	54:w2:157:MET:HE2	2.17	0.44
55:A1:2156:U:H2'	55:A1:2157:G:C8	2.52	0.44
55:A1:2808:U:H2'	55:A1:2809:C:H6	1.83	0.44
55:A1:3141:G:H3'	55:A1:3142:G:C8	2.52	0.44
55:A1:3386:U:H2'	55:A1:3387:U:C6	2.52	0.44
55:A1:3449:U:C2	55:A1:3450:G:C8	3.05	0.44
70:U2:79:LEU:HD22	70:U2:94:PHE:HZ	1.80	0.44
73:W2:35:GLU:OE2	73:W2:114:ILE:HD13	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:i1:92:C:H2'	12:i1:93:G:H8	1.82	0.44
16:m1:39:TYR:CD1	16:m1:47:PRO:HD3	2.52	0.44
18:n1:26:ARG:HB2	18:n1:29:PRO:HG3	2.00	0.44
21:u2:48:LEU:HD23	66:S2:50:LYS:HG3	1.99	0.44
30:61:48:LEU:HB3	30:61:140:THR:O	2.18	0.44
32:72:54:CYS:HB3	32:72:84:ARG:NH2	2.31	0.44
33:81:187:VAL:HG22	33:81:190:LYS:HB2	1.98	0.44
37:B2:4:MET:HE3	37:B2:121:ARG:HG2	1.99	0.44
37:B2:22:VAL:HG22	37:B2:23:PRO:HD2	1.98	0.44
40:E1:108:ARG:NH2	40:E1:127:ALA:HB3	2.33	0.44
41:F1:171:ALA:O	41:F1:174:GLU:HB2	2.17	0.44
53:i2:21:TYR:HE1	53:i2:58:MET:HE1	1.82	0.44
53:i2:33:ARG:HB3	77:k2:125:ARG:HH12	1.81	0.44
54:w2:124:ARG:HG2	54:w2:124:ARG:HH11	1.82	0.44
55:A1:1818:U:H2'	55:A1:1819:U:C6	2.53	0.44
55:A1:3581:G:H2'	55:A1:3582:U:C6	2.53	0.44
55:A1:3804:G:H2'	55:A1:3805:A:C8	2.53	0.44
55:A1:4009:A:H2'	55:A1:4010:U:C6	2.53	0.44
57:M2:16:ARG:HG3	57:M2:16:ARG:NH1	2.32	0.44
59:N2:38:CYS:HB3	59:N2:41:CYS:O	2.18	0.44
68:T2:95:ILE:HG23	68:T2:107:TYR:HB3	2.00	0.44
71:V1:87:SER:HA	71:V1:97:TYR:HB3	1.98	0.44
14:k1:4:ILE:HG12	14:k1:61:TRP:CH2	2.52	0.44
32:72:35:ALA:HB2	32:72:112:ALA:HB2	2.00	0.44
34:82:33:ARG:HD2	56:C2:1121:C:OP1	2.17	0.44
35:91:57:LYS:HD3	35:91:73:HIS:CE1	2.50	0.44
47:K2:92:ARG:HB3	47:K2:92:ARG:NH1	2.33	0.44
55:A1:1114:A:H5'	63:Q1:145:GLY:O	2.17	0.44
56:C2:501:C:H2'	56:C2:502:A:H8	1.83	0.44
56:C2:652:U:H2'	56:C2:653:A:H8	1.82	0.44
56:C2:932:G:H2'	56:C2:933:G:C8	2.52	0.44
56:C2:1512:A:H5''	57:M2:62:ARG:NH1	2.32	0.44
57:M2:126:GLN:OE1	57:M2:126:GLN:N	2.49	0.44
65:S1:9:GLU:O	65:S1:66:LEU:HD23	2.18	0.44
68:T2:63:TYR:OH	68:T2:74:ARG:HG2	2.17	0.44
73:W2:145:PHE:O	73:W2:147:LEU:HG	2.18	0.44
77:k2:114:SER:HB3	77:k2:119:GLN:HB2	1.99	0.44
3:Z1:55:THR:HG23	55:A1:3177:G:OP1	2.17	0.44
3:Z1:60:LYS:HD3	3:Z1:61:LYS:H	1.82	0.44
10:g2:122:LEU:HD22	10:g2:124:VAL:HG13	1.99	0.44
10:g2:180:ARG:HG3	10:g2:195:TRP:CE3	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:h1:279:ARG:HG2	55:A1:827:U:O2'	2.18	0.44
13:j1:39:A:H2'	13:j1:40:A:H8	1.82	0.44
17:m2:26:ASP:HB3	17:m2:68:LYS:NZ	2.33	0.44
18:n1:56:VAL:HG21	63:Q1:181:ARG:HD2	1.99	0.44
24:z2:61:PHE:HD2	56:C2:1467:G:C4	2.36	0.44
27:42:67:PHE:CD2	32:72:47:LEU:HB3	2.53	0.44
27:42:134:LEU:HB2	27:42:219:LYS:HB3	1.99	0.44
51:A2:124:LYS:H	51:A2:124:LYS:CE	2.30	0.44
55:A1:3116:U:H2'	55:A1:3117:U:C6	2.52	0.44
55:A1:3320:G:H2'	55:A1:3321:C:C6	2.52	0.44
56:C2:357:G:H21	76:Y2:136:PRO:HG2	1.83	0.44
56:C2:846:G:H2'	56:C2:847:A:C8	2.52	0.44
56:C2:891:U:H2'	56:C2:892:U:C6	2.53	0.44
56:C2:1369:C:H1'	56:C2:1444:A:C4	2.53	0.44
56:C2:1697:G:H2'	56:C2:1698:U:H5'	2.00	0.44
66:S2:117:ARG:NH2	66:S2:121:VAL:HG21	2.32	0.44
76:Y2:61:LYS:O	76:Y2:61:LYS:HG2	2.17	0.44
4:a1:104:VAL:HG23	4:a1:162:ASN:O	2.18	0.44
6:d2:31:ARG:HG3	6:d2:31:ARG:HH11	1.81	0.44
6:d2:56:LEU:HD23	6:d2:57:THR:N	2.32	0.44
10:g2:102:ARG:HG2	10:g2:103:PHE:N	2.33	0.44
12:i1:41:G:H4'	12:i1:43:A:N1	2.32	0.44
38:C1:325:MET:HE1	41:F1:153:TYR:CE2	2.53	0.44
46:J2:54:ARG:HB2	46:J2:54:ARG:NH1	2.33	0.44
51:A2:58:LYS:HA	51:A2:61:ARG:HG2	1.98	0.44
55:A1:1487:C:H1'	55:A1:1531:C:O2	2.18	0.44
55:A1:1684:C:H42	55:A1:1697:G:H22	1.65	0.44
56:C2:492:G:H2'	56:C2:493:A:H8	1.83	0.44
58:N1:194:ARG:O	58:N1:197:THR:HG22	2.18	0.44
4:a1:229:ALA:HB3	4:a1:234:LYS:HG3	1.99	0.44
23:y2:66:ILE:HD13	23:y2:66:ILE:HA	1.87	0.44
24:z2:69:TYR:CE1	54:w2:68:GLU:HB3	2.53	0.44
38:C1:218:THR:HA	38:C1:229:LEU:HD13	2.00	0.44
41:F1:84:GLU:HB2	67:T1:135:PRO:HB3	2.00	0.44
49:L2:18:ARG:HH21	56:C2:5:C:H1'	1.82	0.44
51:A2:107:ILE:H	51:A2:107:ILE:HD12	1.82	0.44
55:A1:36:U:H5'	55:A1:37:U:OP2	2.18	0.44
55:A1:831:C:H1'	55:A1:833:C:N4	2.33	0.44
55:A1:1337:U:H2'	55:A1:1338:G:O4'	2.17	0.44
55:A1:2040:C:H2'	55:A1:2041:G:C8	2.53	0.44
55:A1:2274:G:H3'	55:A1:2275:U:H4'	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:A1:2752:A:H2'	55:A1:2753:A:C8	2.53	0.44
55:A1:2757:A:H2'	55:A1:2758:U:C6	2.52	0.44
55:A1:2962:A:H2'	55:A1:2963:A:H8	1.82	0.44
55:A1:3012:C:H2'	55:A1:3013:U:C6	2.52	0.44
55:A1:3996:A:H2'	55:A1:3997:A:C8	2.52	0.44
56:C2:373:C:C5	56:C2:654:G:H5''	2.53	0.44
56:C2:629:A:H4'	56:C2:630:G:H3'	2.00	0.44
56:C2:790:G:H2'	56:C2:791:A:H8	1.83	0.44
57:M2:16:ARG:HG3	57:M2:16:ARG:HH11	1.82	0.44
57:M2:117:PRO:O	57:M2:118:ASN:OD1	2.35	0.44
66:S2:60:LYS:HA	66:S2:60:LYS:HE3	2.00	0.44
6:d2:46:VAL:HA	21:u2:141:ASP:O	2.18	0.43
13:j1:26:U:H2'	13:j1:27:C:C6	2.53	0.43
13:j1:93:C:HO2'	13:j1:94:G:H8	1.64	0.43
17:m2:103:SER:HB3	17:m2:106:GLN:OE1	2.18	0.43
19:q2:55:ARG:HG2	19:q2:55:ARG:HH11	1.82	0.43
28:K1:38:CYS:HB2	28:K1:43:TYR:HE2	1.83	0.43
33:81:184:GLU:OE1	33:81:184:GLU:HA	2.18	0.43
46:J2:195:VAL:HB	46:J2:196:PRO:HD3	1.99	0.43
47:K2:58:LEU:HD11	56:C2:1710:C:H5''	1.99	0.43
51:A2:55:SER:HA	51:A2:58:LYS:HG2	2.00	0.43
55:A1:424:A:H2'	55:A1:425:A:H8	1.82	0.43
55:A1:2066:U:H2'	55:A1:2067:C:H6	1.82	0.43
55:A1:2126:G:H2'	55:A1:2127:G:N2	2.33	0.43
55:A1:2183:G:H2'	55:A1:2184:A:H8	1.83	0.43
55:A1:3955:U:H2'	55:A1:3956:U:H6	1.83	0.43
56:C2:200:G:H2'	56:C2:201:C:C6	2.53	0.43
56:C2:569:U:H2'	56:C2:570:U:C6	2.53	0.43
56:C2:785:A:C4	56:C2:786:A:C8	3.06	0.43
68:T2:46:VAL:HB	68:T2:78:ARG:HD2	2.00	0.43
13:j1:26:U:H2'	13:j1:27:C:H6	1.83	0.43
21:u2:121:ARG:O	21:u2:142:VAL:HG22	2.18	0.43
30:61:145:LYS:H	30:61:145:LYS:CE	2.13	0.43
35:91:21:VAL:HG11	35:91:96:ILE:HG12	2.00	0.43
37:B2:150:VAL:HG22	37:B2:151:ALA:H	1.83	0.43
41:F1:68:ARG:HD2	55:A1:862:G:O4'	2.17	0.43
55:A1:3456:C:H5	55:A1:3472:C:N4	2.15	0.43
56:C2:313:U:H2'	56:C2:314:C:C6	2.53	0.43
56:C2:806:C:H2'	56:C2:807:C:C6	2.52	0.43
56:C2:965:A:N3	56:C2:965:A:H2'	2.33	0.43
56:C2:1341:U:O2	56:C2:1346:U:H5	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
67:T1:47:THR:HB	67:T1:48:ILE:HD12	2.00	0.43
19:q2:49:LYS:O	19:q2:49:LYS:HD2	2.18	0.43
30:61:91:LEU:HD21	30:61:129:VAL:HG22	1.99	0.43
35:91:19:GLN:HE21	35:91:19:GLN:HB3	1.47	0.43
35:91:57:LYS:O	35:91:61:GLU:HG2	2.18	0.43
36:B1:53:MET:HE3	36:B1:53:MET:HB2	1.85	0.43
36:B1:317:LEU:HB3	55:A1:3954:U:H4'	1.99	0.43
46:J2:138:ARG:O	46:J2:142:ILE:HG12	2.18	0.43
47:K2:56:ARG:HH22	56:C2:354:U:P	2.41	0.43
48:L1:81:LEU:HD11	48:L1:98:VAL:HG22	2.00	0.43
50:M1:12:VAL:HG12	50:M1:24:LEU:HD22	2.00	0.43
50:M1:118:MET:HE2	50:M1:118:MET:HB2	1.65	0.43
53:i2:67:ARG:HH21	56:C2:1349:G:P	2.41	0.43
55:A1:1385:U:H3'	55:A1:1386:A:H8	1.82	0.43
55:A1:2971:C:H2'	55:A1:2972:A:H8	1.83	0.43
55:A1:3363:G:H2'	55:A1:3364:U:C6	2.53	0.43
55:A1:3543:U:H2'	55:A1:3544:U:C6	2.52	0.43
56:C2:39:A:H2'	56:C2:40:A:C8	2.53	0.43
56:C2:402:U:H5'	56:C2:403:C:C5	2.48	0.43
56:C2:917:U:C2	56:C2:918:A:C8	3.07	0.43
56:C2:1118:A:OP2	56:C2:1118:A:H8	2.00	0.43
57:M2:6:VAL:HB	57:M2:65:TYR:CE2	2.48	0.43
58:N1:123:GLU:HG2	58:N1:128:LYS:HG2	1.99	0.43
68:T2:53:TYR:CD1	68:T2:57:TYR:HE1	2.37	0.43
69:U1:121:LYS:HB2	69:U1:121:LYS:HE2	1.76	0.43
70:U2:76:GLN:HE21	70:U2:94:PHE:HB2	1.82	0.43
77:k2:17:TRP:CG	77:k2:303:THR:HG1	2.36	0.43
77:k2:87:LEU:HB2	77:k2:101:PHE:HB2	2.00	0.43
10:g2:16:LEU:CD2	53:i2:114:LEU:HD23	2.48	0.43
10:g2:85:ARG:HG2	10:g2:203:PHE:O	2.19	0.43
15:l1:124:LEU:HD11	15:l1:166:ILE:HG13	2.00	0.43
27:42:65:ARG:NH2	32:72:51:GLU:HG2	2.33	0.43
47:K2:154:LYS:HE3	47:K2:154:LYS:HB3	1.87	0.43
49:L2:24:ARG:HG2	49:L2:28:GLU:OE2	2.18	0.43
51:A2:87:PRO:HG3	51:A2:112:CYS:SG	2.58	0.43
54:w2:157:MET:HE2	54:w2:157:MET:HA	2.00	0.43
55:A1:61:A:H2'	55:A1:62:A:H8	1.84	0.43
55:A1:100:A:H2'	55:A1:101:G:N3	2.33	0.43
55:A1:1273:C:H2'	55:A1:1274:U:C6	2.52	0.43
55:A1:1301:C:H2'	55:A1:1302:G:O4'	2.19	0.43
55:A1:3367:A:H2'	55:A1:3368:A:C8	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:A1:3589:A:O2'	55:A1:3590:C:H5'	2.18	0.43
56:C2:933:G:H2'	56:C2:934:U:C6	2.53	0.43
56:C2:1034:A:H1'	56:C2:1036:A:N7	2.34	0.43
3:Z1:36:ARG:HH21	55:A1:2013:U:H5'	1.83	0.43
4:a1:129:ALA:HB3	4:a1:132:ASN:ND2	2.32	0.43
11:h1:79:TYR:HB2	11:h1:82:GLU:CD	2.42	0.43
13:j1:8:A:H2'	13:j1:9:G:C8	2.53	0.43
14:k1:46:SER:HB2	14:k1:56:ARG:NH1	2.33	0.43
14:k1:140:GLN:HE21	14:k1:143:GLU:HG3	1.83	0.43
23:y2:40:PRO:HA	23:y2:79:LYS:NZ	2.34	0.43
27:42:123:ALA:HB3	27:42:168:MET:HE2	2.00	0.43
36:B1:148:LYS:NZ	36:B1:148:LYS:HB2	2.34	0.43
37:B2:142:GLU:OE1	37:B2:142:GLU:N	2.50	0.43
46:J2:173:ARG:HB3	46:J2:173:ARG:NH1	2.34	0.43
48:L1:17:ASP:OD1	48:L1:20:LYS:HG2	2.17	0.43
48:L1:92:ARG:HG2	48:L1:92:ARG:HH11	1.83	0.43
52:P2:49:ASP:C	52:P2:49:ASP:OD1	2.61	0.43
53:i2:63:ARG:NH2	53:i2:64:GLY:HA3	2.32	0.43
55:A1:24:C:H2'	55:A1:25:A:O4'	2.19	0.43
55:A1:923:C:H2'	55:A1:924:C:C6	2.53	0.43
55:A1:954:C:H2'	55:A1:955:U:C6	2.53	0.43
56:C2:915:C:H2'	56:C2:916:G:C8	2.54	0.43
56:C2:1458:C:O2'	56:C2:1460:G:H5'	2.19	0.43
73:W2:45:TRP:O	73:W2:46:LYS:HD3	2.19	0.43
73:W2:54:GLY:HA2	73:W2:63:MET:HE2	2.00	0.43
4:a1:179:ILE:O	55:A1:2754:A:H4'	2.18	0.43
11:h1:51:MET:HE3	11:h1:146:LEU:HD13	2.00	0.43
12:i1:94:C:H2'	12:i1:95:C:H6	1.82	0.43
13:j1:129:C:H2'	13:j1:130:C:C6	2.53	0.43
13:j1:155:G:C5'	16:m1:89:ARG:HH12	2.31	0.43
28:K1:29:LYS:HE2	28:K1:29:LYS:HA	2.01	0.43
34:82:74:ALA:C	34:82:76:ALA:H	2.26	0.43
37:B2:50:ILE:O	37:B2:54:LEU:HG	2.18	0.43
52:P2:12:ILE:HD11	52:P2:19:ASN:HB3	2.01	0.43
55:A1:948:A:H2'	55:A1:949:G:H8	1.84	0.43
55:A1:1079:C:H2'	55:A1:1080:C:C6	2.54	0.43
56:C2:148:C:H1'	73:W2:132:ARG:HH22	1.84	0.43
56:C2:501:C:H2'	56:C2:502:A:C8	2.53	0.43
61:O2:87:MET:HE1	61:O2:236:VAL:HG21	2.00	0.43
66:S2:42:VAL:HG12	66:S2:43:GLU:H	1.84	0.43
66:S2:80:GLN:O	66:S2:84:ILE:HD13	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
67:T1:157:GLU:OE2	67:T1:157:GLU:N	2.51	0.43
68:T2:109:ARG:HH11	68:T2:109:ARG:HG3	1.83	0.43
69:U1:35:PHE:CE1	69:U1:94:LYS:HG2	2.53	0.43
8:f1:10:ILE:HD13	8:f1:10:ILE:HA	1.84	0.43
8:f1:47:CYS:HA	8:f1:102:ARG:O	2.19	0.43
12:i1:110:G:H2'	12:i1:111:C:C6	2.54	0.43
13:j1:4:U:H2'	13:j1:5:C:C6	2.53	0.43
14:k1:51:LYS:HB3	14:k1:51:LYS:HE3	1.76	0.43
15:l1:148:GLY:O	15:l1:149:PRO:C	2.62	0.43
37:B2:104:ARG:HB3	37:B2:104:ARG:CZ	2.49	0.43
53:i2:105:MET:O	53:i2:109:LEU:HD23	2.18	0.43
55:A1:423:U:H2'	55:A1:424:A:H8	1.84	0.43
55:A1:583:C:H2'	55:A1:584:G:H8	1.83	0.43
55:A1:1273:C:H2'	55:A1:1274:U:H6	1.83	0.43
55:A1:2166:C:H2'	55:A1:2167:U:C6	2.53	0.43
55:A1:3340:G:H22	55:A1:3356:A:H2	1.66	0.43
55:A1:3432:C:H2'	55:A1:3433:A:H8	1.83	0.43
56:C2:549:A:H2'	56:C2:550:A:O4'	2.18	0.43
60:O1:81:ARG:HG3	60:O1:82:MET:N	2.34	0.43
61:O2:9:LEU:HB2	61:O2:30:ARG:HG3	2.01	0.43
62:P1:122:ALA:HB3	62:P1:143:PRO:HG2	1.99	0.43
67:T1:8:ARG:HH21	67:T1:52:MET:HE1	1.84	0.43
67:T1:113:GLU:O	67:T1:117:LEU:HD13	2.19	0.43
69:U1:36:THR:HG23	69:U1:123:SER:HA	1.99	0.43
70:U2:137:SER:HA	70:U2:162:GLN:HE22	1.84	0.43
3:Z1:89:ILE:HD11	3:Z1:121:ARG:HB2	2.00	0.43
16:m1:109:GLU:OE2	16:m1:109:GLU:N	2.48	0.43
16:m1:220:GLU:OE2	16:m1:220:GLU:HA	2.18	0.43
20:r2:76:SER:HB3	56:C2:1132:G:H5''	1.99	0.43
31:71:44:THR:HG22	31:71:46:GLN:HG2	2.00	0.43
36:B1:309:LEU:HA	36:B1:309:LEU:HD12	1.75	0.43
43:H2:32:ILE:HG12	43:H2:55:ILE:HB	2.01	0.43
43:H2:32:ILE:HG23	43:H2:60:ARG:HD2	2.01	0.43
48:L1:141:GLU:HA	48:L1:144:LEU:HB2	2.00	0.43
51:A2:85:ILE:HD12	51:A2:85:ILE:HA	1.83	0.43
52:P2:5:ILE:HD12	52:P2:9:PHE:HD2	1.83	0.43
52:P2:39:ARG:HD3	56:C2:1599:C:OP1	2.18	0.43
53:i2:48:ASN:ND2	56:C2:1422:A:H5''	2.33	0.43
55:A1:12:G:H2'	55:A1:13:A:C8	2.54	0.43
55:A1:432:A:H2'	55:A1:433:A:O4'	2.19	0.43
55:A1:616:A:HO2'	55:A1:617:A:H8	1.65	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:A1:1034:A:H2'	55:A1:1034:A:N3	2.34	0.43
55:A1:1303:C:H5''	63:Q1:53:MET:HE2	2.01	0.43
55:A1:2946:A:H2'	55:A1:2947:C:H6	1.82	0.43
55:A1:3024:A:H2'	55:A1:3025:C:C6	2.54	0.43
55:A1:3622:U:H2'	55:A1:3623:U:C6	2.53	0.43
61:O2:100:ARG:HG2	61:O2:102:ILE:HD11	2.00	0.43
74:X1:82:THR:O	74:X1:86:MET:HG2	2.19	0.43
75:Y1:66:GLN:H	75:Y1:66:GLN:CD	2.26	0.43
77:k2:217:MET:HE3	77:k2:219:TRP:NE1	2.26	0.43
5:b1:38:LYS:HB3	5:b1:38:LYS:HE3	1.76	0.43
7:e1:86:CYS:O	7:e1:87:VAL:C	2.62	0.43
9:g1:50:ARG:HH21	9:g1:56:HIS:CG	2.37	0.43
20:r2:90:GLN:HG2	20:r2:94:LEU:HD12	2.01	0.43
27:42:89:GLU:OE1	27:42:89:GLU:N	2.52	0.43
31:71:87:LEU:HB3	31:71:92:TYR:CD1	2.54	0.43
37:B2:28:LEU:HD22	37:B2:33:VAL:HG22	2.01	0.43
47:K2:22:HIS:HB2	56:C2:407:A:H5''	2.01	0.43
54:w2:7:LYS:HG3	54:w2:10:LYS:NZ	2.34	0.43
55:A1:1071:C:H2'	55:A1:1072:C:C6	2.53	0.43
55:A1:1628:G:OP1	65:S1:87:ARG:HG3	2.19	0.43
55:A1:1714:U:C2	55:A1:1715:A:C8	3.06	0.43
55:A1:1892:G:H2'	55:A1:1894:A:OP2	2.19	0.43
55:A1:2820:A:H2'	55:A1:2821:G:H8	1.83	0.43
55:A1:3350:A:H5''	63:Q1:188:ASN:OD1	2.19	0.43
56:C2:981:C:H2'	56:C2:982:A:C8	2.54	0.43
56:C2:1774:G:H2'	56:C2:1775:A:C8	2.54	0.43
69:U1:63:VAL:O	69:U1:64:ASN:HB3	2.19	0.43
6:d2:24:GLN:H	6:d2:26:GLN:NE2	2.17	0.43
10:g2:44:ASP:OD1	10:g2:44:ASP:C	2.62	0.43
12:i1:92:C:H2'	12:i1:93:G:C8	2.54	0.43
17:m2:45:ALA:HB1	17:m2:50:THR:O	2.19	0.43
20:r2:81:LEU:HB2	20:r2:123:GLY:O	2.18	0.43
21:u2:62:LYS:HD3	21:u2:70:ARG:NH2	2.33	0.43
33:81:154:ILE:HD13	36:B1:94:ASN:HB3	2.01	0.43
49:L2:93:LYS:HB3	49:L2:95:ASP:OD1	2.19	0.43
55:A1:620:U:C2	55:A1:621:G:C8	3.07	0.43
55:A1:1072:C:H2'	55:A1:1073:A:C8	2.54	0.43
55:A1:1489:G:H2'	55:A1:1490:A:O4'	2.19	0.43
55:A1:2076:G:H2'	55:A1:2077:G:H8	1.84	0.43
56:C2:915:C:H2'	56:C2:916:G:H8	1.84	0.43
57:M2:24:LYS:NZ	57:M2:24:LYS:HB3	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
73:W2:27:PHE:CE1	73:W2:36:VAL:HG21	2.53	0.43
4:a1:241:ARG:HG3	55:A1:2760:G:OP1	2.18	0.42
10:g2:42:LYS:NZ	10:g2:46:VAL:HG23	2.34	0.42
14:k1:133:ASN:HB3	14:k1:147:GLU:HG3	2.00	0.42
33:81:24:ILE:HD12	33:81:122:VAL:HG11	2.01	0.42
37:B2:104:ARG:HB3	37:B2:104:ARG:NH1	2.34	0.42
38:C1:128:LEU:HD23	38:C1:128:LEU:HA	1.88	0.42
46:J2:109:ARG:CZ	46:J2:131:LYS:HG2	2.49	0.42
49:L2:108:ARG:O	49:L2:149:VAL:HG22	2.18	0.42
49:L2:110:LEU:HD13	49:L2:147:PHE:HD2	1.83	0.42
55:A1:1973:U:H2'	55:A1:1974:G:H8	1.83	0.42
55:A1:2753:A:H2'	55:A1:2754:A:C8	2.54	0.42
55:A1:2840:C:H2'	55:A1:2841:G:C8	2.53	0.42
55:A1:3342:U:H2'	55:A1:3343:U:H6	1.84	0.42
55:A1:3625:C:H2'	55:A1:3626:A:O4'	2.19	0.42
55:A1:3996:A:H2'	55:A1:3997:A:H8	1.84	0.42
56:C2:13:U:H2'	56:C2:14:C:H6	1.82	0.42
56:C2:1163:A:H2'	56:C2:1164:A:C8	2.54	0.42
3:Z1:29:ILE:HD13	3:Z1:40:HIS:NE2	2.34	0.42
11:h1:156:GLY:HA2	11:h1:181:PRO:HG3	2.01	0.42
13:j1:3:C:H2'	13:j1:4:U:H6	1.83	0.42
20:r2:88:LYS:HA	20:r2:88:LYS:HE3	2.01	0.42
35:91:80:GLU:HA	35:91:83:THR:HG22	2.01	0.42
38:C1:137:VAL:HG12	38:C1:142:HIS:HB2	2.00	0.42
41:F1:174:GLU:OE2	41:F1:183:ILE:HA	2.19	0.42
43:H2:39:VAL:HB	43:H2:45:ARG:H	1.84	0.42
44:I1:58:MET:HG3	44:I1:90:LEU:HD22	1.99	0.42
47:K2:148:LYS:O	47:K2:151:GLU:HG3	2.18	0.42
49:L2:27:GLN:HA	49:L2:27:GLN:OE1	2.19	0.42
50:M1:55:MET:HE2	50:M1:55:MET:HB3	1.78	0.42
55:A1:537:C:H2'	55:A1:538:U:O4'	2.19	0.42
55:A1:2116:C:H2'	55:A1:2117:C:H6	1.83	0.42
55:A1:3713:C:O3'	55:A1:3714:C:H3'	2.19	0.42
56:C2:326:U:H2'	56:C2:327:C:C6	2.54	0.42
56:C2:1122:A:H4'	56:C2:1123:A:O4'	2.18	0.42
56:C2:1418:A:H2'	56:C2:1419:G:O4'	2.19	0.42
77:k2:23:THR:HG21	77:k2:291:TRP:O	2.20	0.42
15:l1:171:LYS:HE3	15:l1:171:LYS:HB3	1.87	0.42
16:m1:114:LEU:HD13	16:m1:114:LEU:HA	1.90	0.42
23:y2:62:PRO:O	23:y2:63:ASN:CG	2.63	0.42
23:y2:129:SER:HB2	56:C2:30:G:H4'	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:42:136:ARG:CZ	27:42:218:LEU:HD21	2.49	0.42
28:K1:16:ARG:HH11	28:K1:16:ARG:HG2	1.83	0.42
36:B1:140:ASP:O	36:B1:143:LYS:HB2	2.19	0.42
36:B1:370:THR:O	36:B1:370:THR:HG22	2.19	0.42
42:H1:5:LYS:HD2	42:H1:7:ARG:NH1	2.34	0.42
48:L1:200:LYS:NZ	48:L1:200:LYS:HB3	2.34	0.42
52:P2:27:ALA:HA	52:P2:30:ILE:HG22	2.01	0.42
52:P2:43:VAL:HG23	57:M2:36:LEU:HB3	2.00	0.42
53:i2:7:LYS:HD3	53:i2:7:LYS:HA	1.82	0.42
54:w2:141:LYS:HZ3	54:w2:146:ARG:CA	2.33	0.42
55:A1:38:U:H2'	55:A1:39:A:O4'	2.18	0.42
55:A1:127:C:H2'	55:A1:128:G:H8	1.82	0.42
55:A1:1673:G:H2'	55:A1:1674:U:C6	2.54	0.42
56:C2:527:U:H2'	56:C2:528:A:C4	2.54	0.42
64:R1:153:LYS:HD3	64:R1:153:LYS:HA	1.69	0.42
71:V1:84:GLN:HE21	71:V1:86:LYS:HB3	1.84	0.42
75:Y1:108:ARG:CB	75:Y1:108:ARG:HH11	2.33	0.42
2:21:120:ASN:O	2:21:121:LEU:HD23	2.20	0.42
10:g2:5:LEU:HD11	43:H2:41:LYS:NZ	2.34	0.42
11:h1:177:THR:HG22	11:h1:183:TYR:HD1	1.82	0.42
13:j1:29:U:H2'	13:j1:30:G:H8	1.85	0.42
13:j1:77:G:H2'	13:j1:78:G:O4'	2.19	0.42
24:z2:20:MET:SD	24:z2:68:TRP:HE3	2.43	0.42
31:71:164:ARG:NH1	31:71:164:ARG:HB2	2.34	0.42
36:B1:174:ARG:HH22	55:A1:3939:G:H5'	1.85	0.42
39:D1:25:ILE:HD11	39:D1:84:VAL:HG21	2.02	0.42
49:L2:95:ASP:OD1	49:L2:95:ASP:N	2.52	0.42
51:A2:65:LYS:HD2	51:A2:66:GLU:N	2.35	0.42
51:A2:118:GLU:OE2	52:P2:119:ALA:HB1	2.19	0.42
53:i2:37:GLU:CD	53:i2:38:ILE:HG23	2.45	0.42
55:A1:66:A:N6	55:A1:76:G:H1'	2.35	0.42
55:A1:2159:G:H2'	55:A1:2160:C:H6	1.84	0.42
55:A1:3217:U:H2'	55:A1:3218:G:H8	1.84	0.42
56:C2:1020:U:H2'	56:C2:1021:C:O4'	2.19	0.42
56:C2:1651:U:H2'	56:C2:1652:C:C6	2.55	0.42
56:C2:1695:U:H2'	56:C2:1696:G:O4'	2.19	0.42
4:a1:183:GLY:CA	55:A1:1224:A:H5''	2.50	0.42
19:q2:20:ILE:O	19:q2:20:ILE:HD12	2.19	0.42
30:61:150:GLU:O	30:61:153:ARG:HG3	2.19	0.42
36:B1:136:LYS:O	36:B1:142:GLY:HA3	2.20	0.42
40:E1:83:LYS:O	40:E1:86:GLU:HB2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:K2:135:GLU:O	47:K2:139:LYS:HE3	2.19	0.42
54:w2:48:ILE:O	54:w2:86:LEU:HA	2.19	0.42
55:A1:496:G:H22	55:A1:530:C:N4	2.17	0.42
55:A1:1029:G:H2'	55:A1:1030:G:C8	2.55	0.42
55:A1:1672:C:H2'	55:A1:1673:G:H8	1.83	0.42
55:A1:1972:C:H2'	55:A1:1973:U:H6	1.83	0.42
55:A1:2765:G:H2'	55:A1:2766:G:C8	2.49	0.42
55:A1:2885:A:O2'	55:A1:2886:A:H3'	2.19	0.42
56:C2:1572:U:C4	56:C2:1574:G:C8	3.08	0.42
63:Q1:79:ILE:HD12	63:Q1:79:ILE:N	2.34	0.42
63:Q1:177:ALA:O	63:Q1:181:ARG:HG3	2.19	0.42
65:S1:29:ARG:CZ	67:T1:150:LEU:HD21	2.50	0.42
70:U2:63:PHE:HA	70:U2:95:ILE:O	2.19	0.42
70:U2:73:GLN:HG2	70:U2:135:PHE:CD1	2.54	0.42
6:d2:9:ILE:HD12	6:d2:59:LEU:HA	2.01	0.42
11:h1:41:LYS:HE3	67:T1:93:ILE:HD13	2.01	0.42
13:j1:94:G:N3	45:J1:82:THR:HG23	2.35	0.42
16:m1:70:LEU:HD23	16:m1:70:LEU:HA	1.88	0.42
16:m1:148:GLU:OE1	16:m1:177:MET:HE3	2.20	0.42
23:y2:105:PHE:HB2	23:y2:119:ARG:O	2.19	0.42
31:71:18:ARG:HD2	31:71:135:GLY:CA	2.49	0.42
31:71:87:LEU:HD11	31:71:166:PHE:HE1	1.85	0.42
33:81:112:PRO:C	33:81:114:TYR:H	2.27	0.42
36:B1:213:GLN:NE2	36:B1:286:LYS:HA	2.35	0.42
39:D1:52:MET:HE1	39:D1:58:PRO:HA	2.02	0.42
41:F1:112:LEU:HD21	41:F1:119:VAL:HG22	2.02	0.42
45:J1:67:LEU:HD12	45:J1:67:LEU:HA	1.78	0.42
47:K2:36:THR:O	47:K2:95:THR:HA	2.19	0.42
50:M1:93:LYS:HA	50:M1:96:GLU:HG2	2.01	0.42
55:A1:1449:G:H2'	55:A1:1450:C:C6	2.55	0.42
55:A1:3217:U:H2'	55:A1:3218:G:C8	2.54	0.42
55:A1:3694:A:H2'	55:A1:3695:G:O4'	2.19	0.42
56:C2:312:G:C2	56:C2:313:U:C5	3.07	0.42
56:C2:1558:A:H2'	56:C2:1559:A:H8	1.81	0.42
77:k2:168:CYS:SG	77:k2:198:VAL:HG13	2.58	0.42
4:a1:116:LEU:HD21	4:a1:158:ILE:HD13	2.01	0.42
11:h1:62:CYS:HB3	11:h1:105:LEU:HD22	2.02	0.42
16:m1:217:LYS:HB2	16:m1:217:LYS:HE2	1.77	0.42
24:z2:61:PHE:CD2	56:C2:1467:G:C4	3.08	0.42
30:61:150:GLU:HA	30:61:153:ARG:CG	2.49	0.42
33:81:112:PRO:HA	33:81:115:ASP:HB2	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:B1:258:HIS:HA	36:B1:259:PRO:C	2.45	0.42
46:J2:90:ASP:CB	46:J2:116:ILE:HG22	2.49	0.42
54:w2:20:GLU:HG3	54:w2:77:PHE:HZ	1.85	0.42
55:A1:442:G:H2'	55:A1:443:U:C6	2.55	0.42
55:A1:922:C:H2'	55:A1:923:C:H6	1.84	0.42
55:A1:3839:C:H2'	55:A1:3840:G:H8	1.84	0.42
56:C2:617:A:H4'	56:C2:618:G:H5'	2.01	0.42
56:C2:1218:U:H2'	56:C2:1219:G:H8	1.84	0.42
62:P1:19:GLY:HA3	62:P1:94:MET:HE1	2.01	0.42
69:U1:56:PHE:CE2	69:U1:104:TYR:HB2	2.55	0.42
1:11:51:LEU:HD23	1:11:51:LEU:HA	1.89	0.42
4:a1:27:ALA:HB1	4:a1:77:ILE:HG12	2.02	0.42
21:u2:138:GLN:HA	21:u2:204:ASN:OD1	2.19	0.42
31:71:33:LEU:HD23	31:71:33:LEU:HA	1.85	0.42
32:72:128:ARG:HA	34:82:89:TYR:CE2	2.54	0.42
49:L2:86:VAL:HG13	49:L2:104:ASP:HB2	2.02	0.42
55:A1:488:G:H1	55:A1:537:C:H5	1.68	0.42
55:A1:2067:C:H2'	55:A1:2068:U:H6	1.84	0.42
55:A1:2857:A:N6	55:A1:2871:U:H3	2.16	0.42
55:A1:3483:G:C4	55:A1:3484:A:C8	3.08	0.42
56:C2:818:A:C6	61:O2:19:MET:HE3	2.54	0.42
56:C2:849:U:H3	56:C2:883:G:H1	1.67	0.42
56:C2:1415:U:O2'	56:C2:1416:A:H8	2.03	0.42
56:C2:1706:G:H2'	56:C2:1707:G:C8	2.54	0.42
12:i1:54:A:N3	31:71:155:HIS:CE1	2.87	0.42
15:l1:103:PRO:HD2	15:l1:106:LEU:HD23	2.01	0.42
23:y2:130:LEU:HA	23:y2:130:LEU:HD23	1.82	0.42
31:71:84:GLU:OE2	31:71:84:GLU:HA	2.20	0.42
42:H1:113:LEU:HD21	55:A1:265:C:H5'	2.02	0.42
55:A1:1477:G:O6	55:A1:1490:A:H2	2.03	0.42
55:A1:2720:G:H4'	64:R1:79:GLY:O	2.19	0.42
55:A1:3135:C:H2'	55:A1:3136:G:H8	1.85	0.42
55:A1:3673:G:H2'	55:A1:3674:G:H8	1.85	0.42
55:A1:3696:C:H2'	55:A1:3697:C:C6	2.55	0.42
56:C2:1357:A:H2'	56:C2:1358:C:C6	2.55	0.42
61:O2:32:SER:O	61:O2:83:PRO:HG3	2.19	0.42
64:R1:113:LYS:HE3	64:R1:113:LYS:HB3	1.72	0.42
67:T1:46:GLY:HA2	67:T1:52:MET:HE1	2.02	0.42
69:U1:47:ILE:N	69:U1:47:ILE:HD12	2.35	0.42
8:f1:33:CYS:SG	8:f1:38:GLU:HG3	2.60	0.42
13:j1:78:G:H2'	13:j1:79:A:O4'	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:m1:34:LYS:NZ	16:m1:34:LYS:HB2	2.35	0.42
31:71:40:LEU:HD13	31:71:72:CYS:HB2	2.01	0.42
33:81:45:ILE:HD11	33:81:140:LEU:HD13	2.01	0.42
46:J2:66:GLU:HA	46:J2:69:LEU:HB2	2.01	0.42
52:P2:23:ARG:HD2	68:T2:46:VAL:HG12	2.02	0.42
55:A1:135:U:H1'	55:A1:138:C:C4	2.55	0.42
55:A1:1482:A:N7	55:A1:1643:G:H5'	2.35	0.42
55:A1:1632:U:H2'	55:A1:1633:G:O4'	2.20	0.42
55:A1:2971:C:H2'	55:A1:2972:A:C8	2.55	0.42
55:A1:3415:U:OP2	60:O1:61:LYS:HG3	2.20	0.42
55:A1:3497:G:H2'	55:A1:3498:G:H8	1.85	0.42
56:C2:795:U:H5'	56:C2:796:U:H5''	2.01	0.42
57:M2:14:PHE:CE2	57:M2:62:ARG:HG3	2.55	0.42
71:V1:85:ARG:HH11	71:V1:85:ARG:HG3	1.85	0.42
77:k2:125:ARG:C	77:k2:127:LYS:H	2.27	0.42
12:i1:19:C:H2'	12:i1:20:U:C6	2.55	0.41
17:m2:43:LYS:HB3	17:m2:43:LYS:HE2	1.84	0.41
18:n1:75:LEU:HG	18:n1:113:GLY:HA2	2.01	0.41
20:r2:86:LEU:HD23	20:r2:86:LEU:HA	1.85	0.41
26:41:66:LYS:HE2	26:41:78:VAL:HG23	2.02	0.41
27:42:164:ILE:HG23	27:42:201:CYS:SG	2.60	0.41
30:61:95:HIS:O	30:61:125:THR:HA	2.20	0.41
31:71:10:ASN:N	31:71:11:PRO:HD2	2.35	0.41
32:72:53:ILE:HG22	32:72:54:CYS:SG	2.59	0.41
40:E1:26:ASP:OD1	40:E1:26:ASP:N	2.53	0.41
47:K2:113:TYR:CG	47:K2:121:LEU:HD22	2.55	0.41
47:K2:145:THR:O	47:K2:148:LYS:HG2	2.19	0.41
49:L2:144:ILE:HG21	56:C2:797:C:H1'	2.01	0.41
54:w2:74:GLN:OE1	54:w2:84:VAL:HG13	2.19	0.41
55:A1:1432:U:H2'	55:A1:1433:G:C8	2.55	0.41
55:A1:2853:C:O2'	55:A1:2877:G:H1'	2.20	0.41
55:A1:3334:G:H4'	55:A1:3335:A:H5''	2.02	0.41
56:C2:526:G:H2'	56:C2:527:U:C6	2.55	0.41
56:C2:1217:U:H2'	56:C2:1218:U:O4'	2.20	0.41
56:C2:1372:G:C2	56:C2:1373:C:C6	3.08	0.41
61:O2:221:ARG:HB2	61:O2:224:ASN:OD1	2.20	0.41
63:Q1:22:ASP:O	63:Q1:26:ARG:HG3	2.20	0.41
70:U2:76:GLN:NE2	70:U2:94:PHE:HB2	2.35	0.41
71:V1:69:LYS:HB3	71:V1:71:GLU:OE1	2.20	0.41
75:Y1:108:ARG:NH1	75:Y1:108:ARG:CB	2.83	0.41
77:k2:304:ASP:OD1	77:k2:306:LEU:HB2	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:z2:63:TRP:CE3	59:N2:40:VAL:HG12	2.55	0.41
27:42:136:ARG:HG2	27:42:138:PHE:CE1	2.56	0.41
38:C1:152:LEU:HD12	38:C1:152:LEU:HA	1.94	0.41
46:J2:68:TYR:OH	46:J2:148:ILE:HG22	2.20	0.41
50:M1:24:LEU:O	50:M1:43:THR:HG21	2.21	0.41
55:A1:1341:U:H3	55:A1:1375:U:H3	1.68	0.41
55:A1:2183:G:H2'	55:A1:2184:A:C8	2.55	0.41
55:A1:2872:C:C4	55:A1:2873:U:C4	3.08	0.41
55:A1:3913:G:H2'	55:A1:3914:G:C8	2.56	0.41
55:A1:3916:G:C6	55:A1:3917:C:N4	2.88	0.41
56:C2:542:C:H2'	56:C2:543:A:C8	2.55	0.41
56:C2:840:G:H3'	56:C2:841:A:H5''	2.02	0.41
58:N1:60:VAL:HG22	58:N1:134:LEU:HB2	2.01	0.41
67:T1:120:LYS:HB2	67:T1:120:LYS:HE2	1.91	0.41
69:U1:83:LYS:HA	69:U1:83:LYS:HD3	1.91	0.41
71:V1:126:ALA:HA	71:V1:133:ALA:HB2	2.02	0.41
73:W2:185:LEU:O	73:W2:189:ARG:HG3	2.20	0.41
73:W2:197:GLN:HA	73:W2:200:GLN:HE21	1.84	0.41
3:Z1:39:SER:HB2	3:Z1:77:TYR:CD2	2.54	0.41
10:g2:81:ASN:OD1	10:g2:81:ASN:C	2.63	0.41
14:k1:103:VAL:HG11	14:k1:144:LEU:HD13	2.02	0.41
15:l1:161:HIS:HD2	55:A1:3894:G:C2	2.39	0.41
19:q2:67:LYS:HB3	56:C2:1311:C:H4'	2.02	0.41
21:u2:84:LYS:HB3	21:u2:87:MET:HB3	2.02	0.41
21:u2:101:LEU:HD21	68:T2:64:LYS:O	2.20	0.41
24:z2:62:ALA:HB3	24:z2:67:TYR:CE2	2.49	0.41
24:z2:64:ARG:HD3	59:N2:39:ARG:O	2.20	0.41
32:72:125:LYS:HZ1	34:82:83:ALA:C	2.28	0.41
41:F1:179:LYS:H	41:F1:179:LYS:HG3	1.60	0.41
42:H1:5:LYS:HD2	42:H1:7:ARG:HH12	1.85	0.41
51:A2:62:LYS:O	51:A2:65:LYS:HE3	2.21	0.41
52:P2:116:LYS:HD2	52:P2:117:ILE:N	2.35	0.41
55:A1:253:C:H2'	55:A1:254:G:C8	2.54	0.41
55:A1:431:A:C2	55:A1:2968:A:H4'	2.56	0.41
55:A1:654:C:H2'	55:A1:655:C:C6	2.56	0.41
55:A1:3229:A:H2'	55:A1:3230:G:C8	2.56	0.41
55:A1:3844:C:H2'	55:A1:3845:U:H6	1.84	0.41
67:T1:121:GLN:C	67:T1:122:LYS:HD3	2.45	0.41
71:V1:57:VAL:HG12	71:V1:125:CYS:HB2	2.01	0.41
71:V1:69:LYS:HD3	71:V1:69:LYS:HA	1.82	0.41
73:W2:114:ILE:HG13	73:W2:115:LYS:N	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:21:82:LEU:HD21	14:k1:93:ARG:CZ	2.49	0.41
3:Z1:12:MET:HE1	3:Z1:134:LEU:HD13	2.01	0.41
4:a1:44:ILE:HD11	4:a1:85:GLY:HA2	2.02	0.41
12:i1:33:U:H2'	12:i1:34:C:C6	2.55	0.41
35:91:98:ASP:OD1	35:91:98:ASP:N	2.53	0.41
38:C1:112:HIS:HB3	58:N1:203:TYR:CE1	2.56	0.41
53:i2:20:TYR:HD2	53:i2:23:ARG:HD3	1.85	0.41
55:A1:535:G:H3'	55:A1:535:G:P	2.59	0.41
55:A1:1082:U:H2'	55:A1:1083:C:C6	2.55	0.41
55:A1:1168:C:H2'	55:A1:1169:A:C8	2.56	0.41
55:A1:2295:C:H2'	55:A1:2296:A:O4'	2.20	0.41
55:A1:3596:A:H2'	55:A1:3597:G:O4'	2.20	0.41
55:A1:3794:G:H1	55:A1:3901:U:H3	1.68	0.41
56:C2:777:U:H3	56:C2:831:G:H1	1.67	0.41
56:C2:1369:C:H1'	56:C2:1444:A:C5	2.55	0.41
56:C2:1396:U:H2'	56:C2:1397:G:O4'	2.20	0.41
56:C2:1613:U:H2'	56:C2:1614:C:C6	2.56	0.41
61:O2:31:PRO:HG2	61:O2:38:LEU:HG	2.02	0.41
66:S2:44:PRO:C	66:S2:46:THR:H	2.28	0.41
68:T2:50:LYS:O	68:T2:51:ALA:HB2	2.20	0.41
77:k2:99:ARG:O	77:k2:101:PHE:N	2.54	0.41
77:k2:109:LEU:HD11	77:k2:125:ARG:HE	1.84	0.41
77:k2:124:SER:HB3	77:k2:128:THR:HG22	2.01	0.41
77:k2:256:ILE:HB	77:k2:270:LEU:HD23	2.03	0.41
7:e1:19:LYS:HD3	7:e1:19:LYS:HA	1.84	0.41
11:h1:73:MET:HE3	11:h1:73:MET:HB3	1.77	0.41
23:y2:88:ASP:OD1	23:y2:88:ASP:C	2.63	0.41
27:42:172:MET:HG2	27:42:193:VAL:HG21	2.03	0.41
46:J2:115:ALA:C	46:J2:202:MET:HE1	2.46	0.41
49:L2:128:VAL:HG13	49:L2:132:GLN:NE2	2.34	0.41
51:A2:121:ILE:HG12	51:A2:123:TYR:O	2.20	0.41
53:i2:45:LYS:NZ	53:i2:49:LYS:HE2	2.35	0.41
55:A1:424:A:H2'	55:A1:425:A:C8	2.56	0.41
55:A1:823:G:H2'	55:A1:824:G:H8	1.84	0.41
55:A1:1808:A:H2'	55:A1:1809:A:H8	1.86	0.41
55:A1:2820:A:H2'	55:A1:2821:G:C8	2.55	0.41
55:A1:3786:A:C5	55:A1:3911:G:C2	3.08	0.41
56:C2:82:U:H2'	56:C2:83:G:O4'	2.20	0.41
56:C2:533:G:O2'	56:C2:534:A:H5''	2.20	0.41
56:C2:777:U:H2'	56:C2:778:U:H6	1.85	0.41
56:C2:1631:A:P	59:N2:36:ARG:HH12	2.43	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:P1:32:THR:O	62:P1:36:ILE:HG23	2.20	0.41
69:U1:53:PHE:CE1	69:U1:57:LEU:HD21	2.56	0.41
70:U2:119:SER:HB2	70:U2:120:ARG:NH1	2.36	0.41
73:W2:48:TYR:HE1	73:W2:117:GLY:H	1.68	0.41
76:Y2:16:ILE:HD12	76:Y2:16:ILE:O	2.21	0.41
4:a1:42:LYS:HE2	4:a1:42:LYS:HB3	1.91	0.41
15:l1:38:ALA:HA	15:l1:40:TYR:CE2	2.55	0.41
16:m1:189:ARG:HG3	16:m1:192:ARG:NH2	2.36	0.41
27:42:71:LEU:HD22	27:42:82:ARG:HD2	2.02	0.41
32:72:39:ASP:OD1	32:72:68:GLU:HB3	2.21	0.41
37:B2:87:ASP:HB2	37:B2:125:LEU:HD21	2.01	0.41
40:E1:64:LYS:HE3	40:E1:64:LYS:HB2	1.79	0.41
41:F1:89:PHE:O	41:F1:140:TRP:HA	2.21	0.41
51:A2:126:VAL:HG11	56:C2:1491:C:O4'	2.20	0.41
55:A1:616:A:O2'	55:A1:617:A:H8	2.04	0.41
55:A1:791:C:H2'	55:A1:792:C:H6	1.85	0.41
55:A1:1476:U:C4	55:A1:1712:A:C2	3.09	0.41
55:A1:3668:C:O2'	55:A1:3669:A:H5'	2.19	0.41
57:M2:112:MET:O	57:M2:123:LEU:HD23	2.20	0.41
70:U2:28:LEU:HD13	70:U2:28:LEU:HA	1.90	0.41
3:Z1:12:MET:HE1	3:Z1:134:LEU:HD22	2.02	0.41
13:j1:90:C:H2'	13:j1:91:A:C8	2.56	0.41
16:m1:33:GLU:OE2	16:m1:33:GLU:C	2.63	0.41
16:m1:213:GLY:O	16:m1:217:LYS:HD3	2.21	0.41
27:42:63:LYS:HZ2	27:42:90:ASP:HA	1.86	0.41
37:B2:91:LEU:HB3	37:B2:122:ILE:HG12	2.03	0.41
38:C1:189:MET:HE3	55:A1:1766:G:N7	2.35	0.41
46:J2:96:MET:HE2	46:J2:113:PHE:HE1	1.86	0.41
49:L2:116:LYS:HE3	49:L2:116:LYS:HB3	1.63	0.41
55:A1:61:A:H2'	55:A1:62:A:C8	2.56	0.41
55:A1:438:U:H2'	55:A1:439:G:H8	1.86	0.41
55:A1:533:U:H2'	55:A1:534:U:H6	1.86	0.41
55:A1:1176:A:C5	55:A1:1177:C:H1'	2.56	0.41
55:A1:1199:U:H2'	55:A1:1200:C:C6	2.56	0.41
55:A1:1851:A:C5	55:A1:1852:C:C5	3.09	0.41
55:A1:2957:A:H5''	62:P1:83:TRP:O	2.20	0.41
56:C2:97:C:H2'	56:C2:98:U:H6	1.83	0.41
56:C2:1095:G:C2	56:C2:1096:A:C8	3.09	0.41
56:C2:1178:A:H2'	56:C2:1179:C:C6	2.55	0.41
56:C2:1506:G:C2	56:C2:1507:A:C5	3.08	0.41
56:C2:1553:C:H3'	56:C2:1554:G:H8	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:M2:32:ASP:C	57:M2:32:ASP:OD1	2.63	0.41
60:O1:23:VAL:HG22	60:O1:70:LEU:HD22	2.03	0.41
62:P1:136:ILE:HD12	62:P1:136:ILE:N	2.36	0.41
63:Q1:105:VAL:HG21	63:Q1:120:VAL:HG11	2.01	0.41
64:R1:155:LEU:HD23	64:R1:155:LEU:HA	1.96	0.41
65:S1:160:ARG:HG2	65:S1:160:ARG:NH1	2.36	0.41
10:g2:26:GLY:O	10:g2:46:VAL:HB	2.20	0.41
10:g2:48:ILE:HD13	10:g2:48:ILE:HA	1.84	0.41
14:k1:69:THR:O	14:k1:73:ILE:HG12	2.21	0.41
15:l1:41:LYS:NZ	15:l1:41:LYS:HB3	2.35	0.41
21:u2:87:MET:O	21:u2:91:ILE:HG13	2.20	0.41
30:61:146:GLU:HG2	30:61:147:HIS:CD2	2.54	0.41
32:72:78:ALA:HA	32:72:81:VAL:HG12	2.01	0.41
32:72:117:ARG:HD2	34:82:76:ALA:HB2	2.02	0.41
44:l1:70:LEU:HD22	44:l1:70:LEU:HA	1.92	0.41
51:A2:119:PHE:HE1	52:P2:119:ALA:HB2	1.86	0.41
52:P2:91:LYS:HA	52:P2:91:LYS:HE3	2.03	0.41
55:A1:684:G:H2'	55:A1:685:U:C6	2.56	0.41
55:A1:1069:C:H5''	63:Q1:69:LYS:HD2	2.02	0.41
55:A1:1295:A:C4	55:A1:1296:G:C8	3.09	0.41
55:A1:2023:G:H2'	55:A1:2187:G:N2	2.36	0.41
55:A1:3039:C:H4'	55:A1:3040:G:O5'	2.21	0.41
55:A1:3279:G:H2'	55:A1:3280:C:H6	1.86	0.41
55:A1:3839:C:H2'	55:A1:3840:G:C8	2.55	0.41
55:A1:3920:A:H2'	55:A1:3921:A:C8	2.56	0.41
56:C2:108:A:H2'	56:C2:109:G:H8	1.84	0.41
56:C2:121:U:H1'	61:O2:33:THR:O	2.21	0.41
56:C2:525:U:H2'	56:C2:526:G:C8	2.56	0.41
56:C2:1102:C:H2'	56:C2:1103:G:H8	1.86	0.41
77:k2:29:ASP:OD2	77:k2:29:ASP:N	2.52	0.41
4:a1:108:PRO:HD2	4:a1:111:THR:OG1	2.21	0.41
10:g2:62:ALA:HB2	10:g2:181:GLU:OE2	2.21	0.41
11:h1:153:THR:HG21	55:A1:3366:A:N7	2.35	0.41
11:h1:238:GLU:OE2	11:h1:238:GLU:HA	2.21	0.41
11:h1:276:ARG:O	11:h1:280:VAL:HG23	2.20	0.41
14:k1:111:LEU:HD23	14:k1:113:GLU:OE2	2.21	0.41
14:k1:114:ILE:HB	14:k1:124:ARG:HB2	2.02	0.41
19:q2:66:ARG:HE	19:q2:68:THR:HG22	1.86	0.41
21:u2:105:GLU:OE2	21:u2:105:GLU:N	2.54	0.41
22:x2:105:ARG:HB3	49:L2:38:ARG:HA	2.02	0.41
27:42:40:ASN:OD1	27:42:75:GLN:HG3	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:61:162:ARG:HA	30:61:162:ARG:NE	2.36	0.41
31:71:87:LEU:HD23	31:71:87:LEU:HA	1.81	0.41
36:B1:2:SER:HB3	55:A1:3560:A:N7	2.36	0.41
36:B1:47:LEU:HD23	36:B1:47:LEU:HA	1.91	0.41
37:B2:125:LEU:HD12	37:B2:125:LEU:HA	1.87	0.41
41:F1:78:ASN:HB3	67:T1:141:VAL:O	2.21	0.41
41:F1:207:TRP:CD1	41:F1:208:PRO:HD2	2.56	0.41
46:J2:205:ILE:HG22	46:J2:207:ASP:H	1.85	0.41
49:L2:107:GLU:CD	49:L2:108:ARG:HG2	2.45	0.41
52:P2:34:LYS:HB2	52:P2:34:LYS:HE3	1.87	0.41
54:w2:142:LEU:CD2	54:w2:143:ARG:HH22	2.33	0.41
55:A1:1163:G:H2'	55:A1:1185:G:H22	1.85	0.41
55:A1:2109:A:C4	55:A1:2110:G:C8	3.08	0.41
55:A1:2952:U:H2'	55:A1:2953:A:O4'	2.21	0.41
55:A1:3303:U:H2'	55:A1:3304:C:H6	1.85	0.41
55:A1:3464:C:H42	55:A1:3518:G:N2	2.19	0.41
55:A1:3788:U:H2'	55:A1:3789:C:C6	2.55	0.41
56:C2:205:C:C2	56:C2:206:A:C8	3.09	0.41
56:C2:625:U:H2'	56:C2:626:U:C6	2.55	0.41
56:C2:847:A:H2'	56:C2:848:C:H6	1.85	0.41
56:C2:1075:U:H2'	56:C2:1076:C:C6	2.55	0.41
56:C2:1553:C:H5''	56:C2:1554:G:H2'	2.02	0.41
57:M2:33:TRP:HZ2	57:M2:102:LYS:HG3	1.86	0.41
58:N1:136:ASP:OD1	58:N1:136:ASP:C	2.64	0.41
61:O2:36:HIS:CG	61:O2:85:GLY:HA3	2.55	0.41
63:Q1:76:GLU:H	63:Q1:76:GLU:CD	2.28	0.41
66:S2:54:PRO:HG2	66:S2:88:ILE:HD11	2.02	0.41
66:S2:111:ILE:HA	66:S2:114:GLN:HG3	2.03	0.41
71:V1:37:LEU:HD21	71:V1:105:ILE:HD11	2.03	0.41
4:a1:108:PRO:HG3	9:g1:90:LYS:HZ2	1.85	0.41
5:b1:30:GLU:OE1	5:b1:30:GLU:HA	2.20	0.41
10:g2:117:ARG:NH1	10:g2:117:ARG:HB2	2.36	0.41
11:h1:202:ILE:HD11	11:h1:237:GLU:OE2	2.21	0.41
17:m2:44:LEU:HD23	17:m2:44:LEU:HA	1.86	0.41
19:q2:34:LYS:HE3	19:q2:107:GLU:HG3	2.03	0.41
20:r2:41:MET:HE2	20:r2:47:ILE:HG23	2.03	0.41
22:x2:86:VAL:HG21	56:C2:590:A:N3	2.36	0.41
22:x2:95:LYS:HD3	22:x2:95:LYS:HA	1.95	0.41
23:y2:25:LYS:HB2	23:y2:25:LYS:NZ	2.36	0.41
27:42:78:GLU:OE1	27:42:78:GLU:N	2.54	0.41
34:82:73:GLU:OE2	34:82:73:GLU:N	2.47	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:B1:23:ARG:HG3	55:A1:3761:G:OP1	2.21	0.41
36:B1:288:GLY:HA3	36:B1:330:PHE:CZ	2.56	0.41
42:H1:78:TYR:HB3	74:X1:59:TYR:HB3	2.02	0.41
44:I1:67:LYS:O	44:I1:71:LYS:HG3	2.21	0.41
47:K2:19:LYS:NZ	56:C2:102:U:H5'	2.34	0.41
51:A2:119:PHE:HB3	52:P2:118:ARG:HH12	1.85	0.41
55:A1:1323:U:H2'	55:A1:1324:C:H6	1.85	0.41
55:A1:2807:C:H2'	55:A1:2808:U:H6	1.86	0.41
55:A1:3605:C:H2'	55:A1:3606:U:H6	1.85	0.41
56:C2:117:U:H3	56:C2:321:G:H22	1.68	0.41
56:C2:325:G:C2	56:C2:326:U:C6	3.09	0.41
56:C2:783:A:H5'	56:C2:784:A:P	2.61	0.41
56:C2:903:G:H2'	56:C2:904:C:O4'	2.21	0.41
56:C2:999:U:H2'	56:C2:1000:C:O4'	2.21	0.41
56:C2:1352:A:H4'	56:C2:1353:A:O5'	2.21	0.41
64:R1:48:GLY:O	64:R1:51:ILE:HD11	2.21	0.41
67:T1:4:THR:HG22	67:T1:6:GLY:H	1.86	0.41
71:V1:100:ASP:OD2	71:V1:102:ALA:HB2	2.21	0.41
75:Y1:80:ILE:HG12	75:Y1:99:ILE:O	2.20	0.41
77:k2:82:ALA:O	77:k2:108:VAL:HG22	2.21	0.41
3:Z1:121:ARG:HA	3:Z1:124:THR:HG22	2.03	0.40
6:d2:13:ARG:HB2	6:d2:13:ARG:CZ	2.51	0.40
13:j1:65:A:H2'	13:j1:66:U:C6	2.55	0.40
21:u2:34:LEU:O	21:u2:38:ILE:HG12	2.21	0.40
22:x2:84:GLY:HA2	23:y2:88:ASP:OD1	2.21	0.40
22:x2:116:PHE:HZ	49:L2:26:ASP:HB2	1.86	0.40
27:42:77:ASP:OD1	27:42:77:ASP:C	2.64	0.40
30:61:208:ARG:O	30:61:212:LEU:HD22	2.21	0.40
31:71:95:ARG:HD2	31:71:175:LEU:O	2.20	0.40
36:B1:66:LYS:HZ1	71:V1:12:ALA:HB3	1.85	0.40
36:B1:180:LEU:HD23	36:B1:180:LEU:HA	1.90	0.40
38:C1:13:GLU:CD	38:C1:13:GLU:H	2.29	0.40
38:C1:116:ASN:HB2	38:C1:119:GLN:HG3	2.03	0.40
38:C1:283:LYS:HD3	63:Q1:103:LEU:HD22	2.02	0.40
41:F1:30:ARG:O	41:F1:34:MET:HG2	2.21	0.40
41:F1:234:ARG:H	41:F1:234:ARG:HG2	1.76	0.40
42:H1:88:THR:O	42:H1:92:ARG:HG3	2.21	0.40
45:J1:80:GLU:C	45:J1:80:GLU:OE1	2.65	0.40
51:A2:51:ARG:HH22	51:A2:52:LYS:HB3	1.86	0.40
53:i2:78:ARG:HA	53:i2:78:ARG:HH11	1.79	0.40
55:A1:567:G:H2'	55:A1:568:G:C8	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:A1:1470:U:H2'	55:A1:1471:G:C8	2.56	0.40
55:A1:1968:G:H2'	55:A1:1969:A:C8	2.57	0.40
55:A1:3634:U:H2'	55:A1:3635:C:C6	2.56	0.40
55:A1:3753:C:H2'	55:A1:3754:C:C6	2.56	0.40
55:A1:3786:A:N6	55:A1:3911:G:N1	2.69	0.40
56:C2:209:U:H2'	56:C2:210:A:H8	1.85	0.40
56:C2:931:A:C4	56:C2:932:G:C8	3.08	0.40
56:C2:1181:G:H2'	56:C2:1806:G:C8	2.56	0.40
56:C2:1427:U:H2'	56:C2:1428:G:H8	1.85	0.40
56:C2:1708:U:H2'	56:C2:1709:C:C6	2.56	0.40
56:C2:1823:U:C2	56:C2:1824:G:C8	3.09	0.40
61:O2:80:ILE:HG13	61:O2:81:THR:HG23	2.03	0.40
65:S1:113:MET:HE3	65:S1:113:MET:HB3	1.98	0.40
76:Y2:17:PHE:CE1	76:Y2:19:ASN:HB2	2.56	0.40
77:k2:104:HIS:ND1	77:k2:124:SER:HB2	2.36	0.40
77:k2:227:LEU:HB3	77:k2:228:TYR:CD1	2.57	0.40
2:21:124:LYS:HE2	55:A1:3516:A:OP1	2.22	0.40
6:d2:60:GLU:OE2	21:u2:205:ARG:HD3	2.22	0.40
10:g2:203:PHE:HZ	53:i2:91:LEU:HD11	1.87	0.40
14:k1:21:LYS:H	14:k1:21:LYS:HE2	1.86	0.40
16:m1:34:LYS:HB2	16:m1:34:LYS:HZ3	1.84	0.40
19:q2:24:LEU:CD1	19:q2:87:ARG:HB2	2.50	0.40
21:u2:26:ASP:OD1	21:u2:26:ASP:N	2.54	0.40
21:u2:35:GLN:OE1	21:u2:35:GLN:C	2.64	0.40
36:B1:224:LYS:O	36:B1:273:GLY:HA2	2.21	0.40
48:L1:158:LYS:HA	48:L1:158:LYS:HD3	1.79	0.40
51:A2:51:ARG:HH12	51:A2:52:LYS:HA	1.86	0.40
53:i2:113:SER:C	53:i2:115:SER:H	2.28	0.40
54:w2:94:ARG:NH2	54:w2:100:ALA:HB3	2.37	0.40
55:A1:712:C:H2'	55:A1:713:U:H6	1.87	0.40
55:A1:1847:G:O2'	55:A1:1848:U:H5'	2.22	0.40
55:A1:2265:A:H2'	55:A1:2266:A:H8	1.86	0.40
55:A1:2869:U:H2'	55:A1:2870:C:C5	2.57	0.40
55:A1:3542:G:C2	55:A1:3572:G:H1'	2.57	0.40
55:A1:3908:A:H2'	55:A1:3909:A:C8	2.56	0.40
56:C2:507:A:C2	56:C2:526:G:N1	2.89	0.40
56:C2:583:U:H2'	56:C2:584:G:H8	1.86	0.40
56:C2:926:G:H2'	56:C2:927:C:C6	2.56	0.40
56:C2:1146:U:O2	56:C2:1146:U:H2'	2.21	0.40
64:R1:13:SER:HA	64:R1:16:ARG:NH1	2.37	0.40
64:R1:162:ARG:O	64:R1:165:LYS:HG3	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:h1:178:LYS:NZ	11:h1:178:LYS:HB3	2.36	0.40
11:h1:244:HIS:O	11:h1:248:ARG:HG3	2.22	0.40
19:q2:59:LYS:NZ	54:w2:8:LYS:HE2	2.33	0.40
20:r2:115:GLU:HA	20:r2:118:ARG:HB2	2.03	0.40
21:u2:183:LYS:HA	21:u2:183:LYS:HD3	1.84	0.40
27:42:120:MET:HE2	27:42:122:GLU:OE2	2.21	0.40
31:71:97:ASN:OD1	31:71:97:ASN:N	2.55	0.40
32:72:140:THR:HB	56:C2:1020:U:H1'	2.03	0.40
35:91:18:LEU:HD23	35:91:18:LEU:HA	1.87	0.40
38:C1:60:HIS:CE1	38:C1:100:ARG:HH11	2.40	0.40
38:C1:149:GLU:HB3	38:C1:151:PRO:HD2	2.04	0.40
55:A1:824:G:H22	55:A1:837:G:H21	1.70	0.40
55:A1:2065:U:H2'	55:A1:2066:U:C6	2.56	0.40
55:A1:2298:A:H2'	55:A1:2299:U:C6	2.56	0.40
55:A1:3294:A:H2'	55:A1:3295:C:O4'	2.20	0.40
55:A1:3860:C:H2'	55:A1:3861:C:C6	2.56	0.40
55:A1:4012:C:H2'	55:A1:4013:A:C8	2.56	0.40
56:C2:1009:A:H2'	56:C2:1010:A:O4'	2.22	0.40
56:C2:1700:U:H2'	56:C2:1701:A:C8	2.57	0.40
57:M2:39:LEU:HD23	57:M2:39:LEU:HA	1.95	0.40
66:S2:22:VAL:HB	66:S2:71:ARG:HG3	2.02	0.40
73:W2:10:THR:O	73:W2:129:VAL:HG12	2.21	0.40
74:X1:47:ARG:HB3	74:X1:47:ARG:CZ	2.51	0.40
74:X1:126:LEU:HD11	74:X1:134:LYS:HE3	2.04	0.40
75:Y1:59:ARG:HB2	75:Y1:103:LYS:HD2	2.03	0.40
75:Y1:80:ILE:HD11	75:Y1:104:VAL:HG11	2.03	0.40
1:11:23:ILE:HD12	1:11:23:ILE:HA	1.89	0.40
6:d2:54:ASP:OD1	6:d2:54:ASP:C	2.65	0.40
9:g1:39:CYS:SG	9:g1:41:PHE:HD1	2.44	0.40
11:h1:188:LYS:HD3	11:h1:188:LYS:N	2.36	0.40
14:k1:63:ASN:O	14:k1:67:LEU:HG	2.21	0.40
14:k1:141:LYS:HA	14:k1:141:LYS:HE3	2.03	0.40
17:m2:120:ILE:HD12	17:m2:121:LYS:N	2.37	0.40
20:r2:15:ASN:HA	20:r2:18:GLU:HG3	2.04	0.40
20:r2:41:MET:HE2	20:r2:41:MET:HB3	1.84	0.40
21:u2:48:LEU:HA	21:u2:49:PRO:HD3	1.99	0.40
25:32:19:HIS:HB3	25:32:22:LYS:HG3	2.02	0.40
32:72:57:THR:OG1	32:72:60:MET:HG3	2.20	0.40
34:82:68:ILE:CG1	34:82:93:LYS:HE3	2.52	0.40
46:J2:148:ILE:HD13	46:J2:148:ILE:HA	1.73	0.40
46:J2:253:GLN:NE2	46:J2:253:GLN:CA	2.84	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:L2:84:ILE:HD12	49:L2:84:ILE:HA	1.80	0.40
49:L2:174:LYS:HD2	56:C2:534:A:H5'	2.03	0.40
52:P2:5:ILE:HD12	52:P2:9:PHE:CD2	2.55	0.40
53:i2:44:LYS:HG3	53:i2:47:ARG:NH2	2.37	0.40
54:w2:54:ARG:HG3	54:w2:54:ARG:NH1	2.33	0.40
55:A1:438:U:H2'	55:A1:439:G:C8	2.56	0.40
55:A1:840:C:H2'	55:A1:841:U:C5	2.57	0.40
55:A1:1122:C:H2'	55:A1:1123:G:H8	1.85	0.40
55:A1:3670:U:C2	55:A1:3671:U:C6	3.09	0.40
55:A1:4000:C:O2	55:A1:4003:C:H5''	2.22	0.40
56:C2:1212:U:O2	56:C2:1216:U:H5	2.04	0.40
56:C2:1214:A:H1'	56:C2:1241:C:O2'	2.21	0.40
56:C2:1697:G:OP1	56:C2:1697:G:O4'	2.39	0.40
66:S2:134:GLY:HA3	66:S2:139:ALA:O	2.22	0.40
70:U2:35:ASP:OD1	70:U2:35:ASP:C	2.64	0.40
70:U2:77:VAL:H	70:U2:78:ARG:NH2	2.20	0.40
76:Y2:53:ALA:HA	76:Y2:58:TYR:OH	2.21	0.40
77:k2:150:TRP:HB2	77:k2:170:TRP:CB	2.51	0.40
77:k2:164:ILE:HG22	77:k2:178:ASN:HB2	2.03	0.40
6:d2:31:ARG:HE	6:d2:41:SER:HB3	1.87	0.40
9:g1:29:ILE:HG23	9:g1:69:TRP:CG	2.57	0.40
13:j1:17:U:H2'	13:j1:18:C:C6	2.57	0.40
17:m2:117:VAL:HG21	17:m2:125:VAL:HG21	2.03	0.40
19:q2:54:VAL:HB	19:q2:88:LEU:HB2	2.04	0.40
32:72:47:LEU:HD23	32:72:47:LEU:HA	1.83	0.40
34:82:80:ILE:HA	34:82:80:ILE:HD13	1.77	0.40
38:C1:29:ARG:HD3	38:C1:29:ARG:HA	1.79	0.40
41:F1:160:MET:HE3	41:F1:160:MET:HB3	1.71	0.40
46:J2:78:GLU:HA	46:J2:81:ASP:OD2	2.21	0.40
46:J2:185:PRO:HG2	49:L2:58:ARG:HD3	2.04	0.40
47:K2:146:GLN:H	47:K2:146:GLN:CD	2.29	0.40
49:L2:83:ARG:HH21	49:L2:150:ARG:CZ	2.35	0.40
51:A2:20:VAL:O	51:A2:20:VAL:HG23	2.21	0.40
53:i2:10:LYS:HD3	53:i2:53:TYR:CZ	2.57	0.40
53:i2:103:LYS:O	53:i2:107:LYS:HG2	2.21	0.40
55:A1:711:U:H2'	55:A1:712:C:H6	1.87	0.40
55:A1:932:C:H2'	55:A1:933:U:O4'	2.22	0.40
55:A1:3627:A:H2'	55:A1:3628:U:O4'	2.22	0.40
61:O2:72:ILE:HG13	61:O2:90:ILE:HG12	2.03	0.40
68:T2:74:ARG:O	68:T2:74:ARG:HG3	2.20	0.40
70:U2:25:GLN:O	70:U2:29:GLU:HG3	2.21	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	
1	11	48/51 (94%)	48 (100%)	0	0	100	100
2	21	45/128 (35%)	42 (93%)	3 (7%)	0	100	100
3	Z1	133/136 (98%)	127 (96%)	6 (4%)	0	100	100
4	a1	244/257 (95%)	234 (96%)	10 (4%)	0	100	100
5	b1	48/64 (75%)	42 (88%)	5 (10%)	1 (2%)	5	15
6	d2	52/69 (75%)	51 (98%)	1 (2%)	0	100	100
7	e1	106/117 (91%)	100 (94%)	6 (6%)	0	100	100
8	f1	107/110 (97%)	100 (94%)	5 (5%)	2 (2%)	6	17
9	g1	86/92 (94%)	86 (100%)	0	0	100	100
10	g2	207/313 (66%)	197 (95%)	10 (5%)	0	100	100
11	h1	284/297 (96%)	271 (95%)	13 (5%)	0	100	100
14	k1	187/192 (97%)	180 (96%)	7 (4%)	0	100	100
15	l1	202/259 (78%)	194 (96%)	8 (4%)	0	100	100
16	m1	209/266 (79%)	206 (99%)	3 (1%)	0	100	100
17	m2	120/132 (91%)	116 (97%)	3 (2%)	1 (1%)	16	36
18	n1	145/148 (98%)	142 (98%)	3 (2%)	0	100	100
19	q2	89/119 (75%)	83 (93%)	6 (7%)	0	100	100
20	r2	127/130 (98%)	122 (96%)	5 (4%)	0	100	100
21	u2	171/203 (84%)	164 (96%)	7 (4%)	0	100	100
22	x2	43/133 (32%)	42 (98%)	1 (2%)	0	100	100
23	y2	137/143 (96%)	130 (95%)	5 (4%)	2 (2%)	8	23
24	z2	33/166 (20%)	28 (85%)	4 (12%)	1 (3%)	3	9

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
25	32	62/84 (74%)	57 (92%)	5 (8%)	0	100	100
26	41	121/137 (88%)	115 (95%)	5 (4%)	1 (1%)	16	36
27	42	208/266 (78%)	198 (95%)	10 (5%)	0	100	100
28	K1	66/70 (94%)	63 (96%)	3 (4%)	0	100	100
29	51	23/25 (92%)	23 (100%)	0	0	100	100
30	61	96/215 (45%)	93 (97%)	3 (3%)	0	100	100
31	71	143/178 (80%)	138 (96%)	5 (4%)	0	100	100
32	72	129/151 (85%)	124 (96%)	4 (3%)	1 (1%)	16	36
33	81	202/205 (98%)	193 (96%)	8 (4%)	1 (0%)	24	49
34	82	93/142 (66%)	89 (96%)	4 (4%)	0	100	100
35	91	94/116 (81%)	90 (96%)	4 (4%)	0	100	100
36	B1	392/403 (97%)	382 (97%)	10 (3%)	0	100	100
37	B2	148/151 (98%)	144 (97%)	4 (3%)	0	100	100
38	C1	347/375 (92%)	340 (98%)	7 (2%)	0	100	100
39	D1	98/124 (79%)	96 (98%)	2 (2%)	0	100	100
40	E1	125/135 (93%)	124 (99%)	1 (1%)	0	100	100
41	F1	224/245 (91%)	217 (97%)	7 (3%)	0	100	100
42	H1	119/123 (97%)	116 (98%)	3 (2%)	0	100	100
43	H2	81/83 (98%)	77 (95%)	4 (5%)	0	100	100
44	I1	98/105 (93%)	96 (98%)	2 (2%)	0	100	100
45	J1	84/97 (87%)	84 (100%)	0	0	100	100
46	J2	214/279 (77%)	208 (97%)	6 (3%)	0	100	100
47	K2	201/208 (97%)	190 (94%)	11 (6%)	0	100	100
48	L1	200/211 (95%)	190 (95%)	10 (5%)	0	100	100
49	L2	175/194 (90%)	169 (97%)	6 (3%)	0	100	100
50	M1	131/137 (96%)	127 (97%)	4 (3%)	0	100	100
51	A2	94/145 (65%)	85 (90%)	9 (10%)	0	100	100
52	P2	137/152 (90%)	127 (93%)	10 (7%)	0	100	100
53	i2	117/134 (87%)	109 (93%)	8 (7%)	0	100	100
54	w2	202/247 (82%)	193 (96%)	9 (4%)	0	100	100
57	M2	139/146 (95%)	132 (95%)	7 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
58	N1	201/204 (98%)	196 (98%)	5 (2%)	0	100	100
59	N2	37/73 (51%)	37 (100%)	0	0	100	100
60	O1	91/106 (86%)	85 (93%)	6 (7%)	0	100	100
61	O2	255/263 (97%)	246 (96%)	9 (4%)	0	100	100
62	P1	150/184 (82%)	146 (97%)	4 (3%)	0	100	100
63	Q1	185/188 (98%)	177 (96%)	6 (3%)	2 (1%)	11	29
64	R1	169/196 (86%)	165 (98%)	3 (2%)	1 (1%)	21	45
65	S1	174/176 (99%)	161 (92%)	10 (6%)	3 (2%)	7	20
66	S2	136/146 (93%)	124 (91%)	8 (6%)	4 (3%)	3	9
67	T1	155/160 (97%)	151 (97%)	4 (3%)	0	100	100
68	T2	68/123 (55%)	65 (96%)	1 (2%)	2 (3%)	3	9
69	U1	85/129 (66%)	78 (92%)	7 (8%)	0	100	100
70	U2	171/194 (88%)	158 (92%)	13 (8%)	0	100	100
71	V1	128/140 (91%)	124 (97%)	4 (3%)	0	100	100
72	W1	59/157 (38%)	59 (100%)	0	0	100	100
73	W2	217/249 (87%)	203 (94%)	13 (6%)	1 (0%)	24	49
74	X1	116/155 (75%)	112 (97%)	4 (3%)	0	100	100
75	Y1	126/145 (87%)	120 (95%)	6 (5%)	0	100	100
76	Y2	134/161 (83%)	130 (97%)	4 (3%)	0	100	100
77	k2	248/317 (78%)	231 (93%)	15 (6%)	2 (1%)	16	36
All	All	10291/12274 (84%)	9862 (96%)	404 (4%)	25 (0%)	44	65

All (25) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	f1	107	PRO
65	S1	161	ARG
65	S1	165	PRO
66	S2	44	PRO
66	S2	45	ALA
66	S2	96	TYR
68	T2	51	ALA
23	y2	61	GLN
26	41	44	VAL
64	R1	138	LEU

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Mol	Chain	Res	Type
77	k2	100	GLN
17	m2	98	GLU
24	z2	57	VAL
66	S2	43	GLU
5	b1	26	SER
8	f1	106	TYR
65	S1	166	ARG
68	T2	47	LEU
73	W2	119	LYS
23	y2	62	PRO
63	Q1	155	ALA
63	Q1	185	ALA
77	k2	288	SER
32	72	138	ASP
33	81	113	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	11	47/48 (98%)	47 (100%)	0	100	100
2	21	43/116 (37%)	41 (95%)	2 (5%)	23	48
3	Z1	116/117 (99%)	114 (98%)	2 (2%)	53	73
4	a1	189/199 (95%)	186 (98%)	3 (2%)	55	74
5	b1	46/54 (85%)	44 (96%)	2 (4%)	26	51
6	d2	49/61 (80%)	46 (94%)	3 (6%)	17	38
7	e1	93/101 (92%)	90 (97%)	3 (3%)	34	59
8	f1	90/91 (99%)	88 (98%)	2 (2%)	45	69
9	g1	72/75 (96%)	72 (100%)	0	100	100
10	g2	178/253 (70%)	175 (98%)	3 (2%)	53	73
11	h1	243/252 (96%)	241 (99%)	2 (1%)	73	84
14	k1	168/171 (98%)	162 (96%)	6 (4%)	31	56

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	l1	183/226 (81%)	177 (97%)	6 (3%)	33	58
16	m1	186/224 (83%)	182 (98%)	4 (2%)	45	69
17	m2	108/114 (95%)	103 (95%)	5 (5%)	24	49
18	n1	118/119 (99%)	116 (98%)	2 (2%)	53	73
19	q2	86/106 (81%)	80 (93%)	6 (7%)	14	32
20	r2	112/113 (99%)	107 (96%)	5 (4%)	24	49
21	u2	151/170 (89%)	147 (97%)	4 (3%)	40	65
22	x2	39/109 (36%)	39 (100%)	0	100	100
23	y2	111/115 (96%)	108 (97%)	3 (3%)	39	64
24	z2	33/134 (25%)	31 (94%)	2 (6%)	17	38
25	32	62/76 (82%)	61 (98%)	1 (2%)	55	74
26	41	108/120 (90%)	103 (95%)	5 (5%)	24	49
27	42	191/229 (83%)	189 (99%)	2 (1%)	68	81
28	K1	63/65 (97%)	61 (97%)	2 (3%)	34	59
29	51	24/24 (100%)	24 (100%)	0	100	100
30	61	89/181 (49%)	85 (96%)	4 (4%)	24	49
31	71	126/149 (85%)	120 (95%)	6 (5%)	23	47
32	72	102/119 (86%)	99 (97%)	3 (3%)	37	62
33	81	174/175 (99%)	165 (95%)	9 (5%)	21	44
34	82	83/119 (70%)	81 (98%)	2 (2%)	43	67
35	91	81/98 (83%)	75 (93%)	6 (7%)	13	30
36	B1	343/351 (98%)	337 (98%)	6 (2%)	53	73
37	B2	129/130 (99%)	129 (100%)	0	100	100
38	C1	296/314 (94%)	287 (97%)	9 (3%)	36	61
39	D1	92/110 (84%)	89 (97%)	3 (3%)	33	58
40	E1	114/121 (94%)	109 (96%)	5 (4%)	25	50
41	F1	194/210 (92%)	191 (98%)	3 (2%)	57	75
42	H1	109/110 (99%)	109 (100%)	0	100	100
43	H2	69/69 (100%)	69 (100%)	0	100	100
44	I1	84/88 (96%)	83 (99%)	1 (1%)	63	78
45	J1	73/80 (91%)	73 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
46	J2	181/216 (84%)	177 (98%)	4 (2%)	45	69
47	K2	174/178 (98%)	168 (97%)	6 (3%)	32	58
48	L1	168/177 (95%)	164 (98%)	4 (2%)	43	67
49	L2	158/168 (94%)	156 (99%)	2 (1%)	61	77
50	M1	115/118 (98%)	114 (99%)	1 (1%)	70	82
51	A2	92/130 (71%)	88 (96%)	4 (4%)	26	51
52	P2	121/132 (92%)	119 (98%)	2 (2%)	53	73
53	i2	108/121 (89%)	104 (96%)	4 (4%)	30	55
54	w2	170/205 (83%)	167 (98%)	3 (2%)	51	72
57	M2	112/117 (96%)	108 (96%)	4 (4%)	31	56
58	N1	171/172 (99%)	168 (98%)	3 (2%)	51	72
59	N2	34/64 (53%)	33 (97%)	1 (3%)	37	62
60	O1	84/95 (88%)	78 (93%)	6 (7%)	13	31
61	O2	221/226 (98%)	214 (97%)	7 (3%)	34	59
62	P1	132/162 (82%)	129 (98%)	3 (2%)	44	68
63	Q1	159/160 (99%)	157 (99%)	2 (1%)	61	77
64	R1	149/173 (86%)	146 (98%)	3 (2%)	48	70
65	S1	155/155 (100%)	151 (97%)	4 (3%)	40	65
66	S2	113/119 (95%)	109 (96%)	4 (4%)	32	56
67	T1	140/142 (99%)	137 (98%)	3 (2%)	47	70
68	T2	62/104 (60%)	61 (98%)	1 (2%)	55	74
69	U1	84/115 (73%)	83 (99%)	1 (1%)	63	78
70	U2	161/177 (91%)	153 (95%)	8 (5%)	22	46
71	V1	100/107 (94%)	92 (92%)	8 (8%)	11	27
72	W1	53/126 (42%)	52 (98%)	1 (2%)	50	71
73	W2	194/218 (89%)	186 (96%)	8 (4%)	27	52
74	X1	106/135 (78%)	103 (97%)	3 (3%)	38	63
75	Y1	119/134 (89%)	116 (98%)	3 (2%)	42	66
76	Y2	124/142 (87%)	124 (100%)	0	100	100
77	k2	238/274 (87%)	234 (98%)	4 (2%)	53	73
All	All	9065/10468 (87%)	8826 (97%)	239 (3%)	41	65

All (239) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	21	108	VAL
2	21	119	ASN
3	Z1	100	VAL
3	Z1	103	ASP
4	a1	49	ILE
4	a1	143	THR
4	a1	218	HIS
5	b1	18	ARG
5	b1	26	SER
6	d2	35	MET
6	d2	40	ARG
6	d2	57	THR
7	e1	5	LEU
7	e1	83	CYS
7	e1	85	LYS
8	f1	37	ASP
8	f1	107	PRO
10	g2	32	PHE
10	g2	166	LYS
10	g2	171	VAL
11	h1	44	TYR
11	h1	196	ARG
14	k1	12	LEU
14	k1	20	LEU
14	k1	44	GLU
14	k1	84	VAL
14	k1	95	VAL
14	k1	103	VAL
15	l1	29	SER
15	l1	89	THR
15	l1	105	LYS
15	l1	172	VAL
15	l1	189	LYS
15	l1	259	PHE
16	m1	100	HIS
16	m1	106	THR
16	m1	167	VAL
16	m1	205	THR
17	m2	23	MET
17	m2	27	VAL
17	m2	91	LEU
17	m2	98	GLU

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Mol	Chain	Res	Type
17	m2	99	LYS
18	n1	9	ARG
18	n1	70	CYS
19	q2	23	THR
19	q2	24	LEU
19	q2	36	CYS
19	q2	40	ILE
19	q2	75	LYS
19	q2	81	GLN
20	r2	5	ASN
20	r2	70	ASN
20	r2	87	GLU
20	r2	112	ASP
20	r2	115	GLU
21	u2	24	THR
21	u2	55	TYR
21	u2	161	GLU
21	u2	195	ASP
23	y2	24	ASP
23	y2	61	GLN
23	y2	105	PHE
24	z2	51	LEU
24	z2	70	LEU
25	32	46	VAL
26	41	8	MET
26	41	27	THR
26	41	44	VAL
26	41	93	LEU
26	41	101	ASN
27	42	179	ASN
27	42	225	LEU
28	K1	54	GLU
28	K1	60	LEU
30	61	94	PHE
30	61	136	MET
30	61	153	ARG
30	61	166	HIS
31	71	32	ARG
31	71	47	THR
31	71	74	VAL
31	71	112	HIS
31	71	129	ASP

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Mol	Chain	Res	Type
31	71	163	MET
32	72	21	VAL
32	72	52	THR
32	72	132	VAL
33	81	45	ILE
33	81	106	VAL
33	81	120	VAL
33	81	128	ILE
33	81	131	LEU
33	81	139	LEU
33	81	146	GLU
33	81	185	LYS
33	81	193	VAL
34	82	80	ILE
34	82	111	VAL
35	91	20	LEU
35	91	28	VAL
35	91	52	CYS
35	91	59	GLU
35	91	60	ILE
35	91	105	ILE
36	B1	43	LEU
36	B1	44	THR
36	B1	103	LYS
36	B1	168	MET
36	B1	183	VAL
36	B1	203	GLN
38	C1	38	ASN
38	C1	45	ARG
38	C1	48	SER
38	C1	69	THR
38	C1	85	HIS
38	C1	140	LYS
38	C1	150	VAL
38	C1	217	LEU
38	C1	240	LEU
39	D1	20	THR
39	D1	24	THR
39	D1	82	MET
40	E1	7	LEU
40	E1	33	LYS
40	E1	64	LYS

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Mol	Chain	Res	Type
40	E1	101	HIS
40	E1	123	THR
41	F1	39	LYS
41	F1	67	ILE
41	F1	191	GLU
44	I1	70	LEU
46	J2	101	GLN
46	J2	170	VAL
46	J2	253	GLN
46	J2	254	GLU
47	K2	21	TYR
47	K2	22	HIS
47	K2	46	VAL
47	K2	151	GLU
47	K2	161	LEU
47	K2	174	CYS
48	L1	33	GLU
48	L1	64	VAL
48	L1	70	VAL
48	L1	86	ILE
49	L2	30	LYS
49	L2	94	LEU
50	M1	113	MET
51	A2	22	LEU
51	A2	89	MET
51	A2	111	MET
51	A2	126	VAL
52	P2	45	LEU
52	P2	61	GLU
53	i2	33	ARG
53	i2	98	VAL
53	i2	111	PHE
53	i2	119	VAL
54	w2	106	ARG
54	w2	139	SER
54	w2	154	ASP
57	M2	22	LEU
57	M2	25	SER
57	M2	56	ARG
57	M2	62	ARG
58	N1	126	THR
58	N1	131	GLU

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Mol	Chain	Res	Type
58	N1	161	MET
59	N2	66	ASP
60	O1	9	ARG
60	O1	24	THR
60	O1	30	LYS
60	O1	43	ARG
60	O1	83	LEU
60	O1	91	PHE
61	O2	91	SER
61	O2	131	ILE
61	O2	133	THR
61	O2	221	ARG
61	O2	232	ASN
61	O2	248	ILE
61	O2	250	GLU
62	P1	57	CYS
62	P1	69	ARG
62	P1	137	ASN
63	Q1	61	MET
63	Q1	88	ASP
64	R1	36	ASN
64	R1	134	ASN
64	R1	163	ARG
65	S1	16	LEU
65	S1	82	LEU
65	S1	164	LYS
65	S1	165	PRO
66	S2	18	THR
66	S2	44	PRO
66	S2	49	TYR
66	S2	96	TYR
67	T1	127	GLU
67	T1	128	LEU
67	T1	143	THR
68	T2	49	ASP
69	U1	47	ILE
70	U2	28	LEU
70	U2	45	ILE
70	U2	61	ILE
70	U2	72	PHE
70	U2	76	GLN
70	U2	91	HIS

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Mol	Chain	Res	Type
70	U2	159	ASP
70	U2	185	VAL
71	V1	16	ILE
71	V1	32	THR
71	V1	45	ILE
71	V1	100	ASP
71	V1	108	ASN
71	V1	123	LYS
71	V1	131	ARG
71	V1	132	ILE
72	W1	3	VAL
73	W2	112	VAL
73	W2	119	LYS
73	W2	120	ASP
73	W2	151	ASP
73	W2	154	ARG
73	W2	156	TYR
73	W2	219	GLU
73	W2	225	GLN
74	X1	72	HIS
74	X1	102	LYS
74	X1	142	ASP
75	Y1	25	ILE
75	Y1	82	ILE
75	Y1	105	VAL
77	k2	93	THR
77	k2	102	VAL
77	k2	252	THR
77	k2	296	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (89) such sidechains are listed below:

Mol	Chain	Res	Type
2	21	90	ASN
3	Z1	28	ASN
4	a1	8	GLN
4	a1	132	ASN
4	a1	162	ASN
5	b1	12	GLN
5	b1	17	HIS
8	f1	21	GLN
10	g2	110	ASN

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Mol	Chain	Res	Type
10	g2	113	GLN
10	g2	164	ASN
11	h1	229	ASN
14	k1	133	ASN
16	m1	141	ASN
16	m1	225	ASN
18	n1	17	HIS
20	r2	24	GLN
21	u2	100	HIS
22	x2	132	ASN
25	32	9	HIS
25	32	19	HIS
25	32	26	GLN
26	41	21	ASN
26	41	30	ASN
26	41	95	HIS
27	42	149	GLN
27	42	179	ASN
27	42	186	ASN
30	61	95	HIS
30	61	130	HIS
30	61	166	HIS
31	71	155	HIS
33	81	67	ASN
34	82	44	HIS
35	91	15	ASN
35	91	19	GLN
35	91	77	ASN
36	B1	68	ASN
36	B1	109	HIS
36	B1	175	GLN
37	B2	36	GLN
37	B2	90	HIS
38	C1	230	GLN
38	C1	233	ASN
39	D1	67	ASN
40	E1	23	HIS
40	E1	95	HIS
41	F1	61	GLN
41	F1	190	HIS
41	F1	239	ASN
42	H1	20	GLN

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Mol	Chain	Res	Type
45	J1	13	ASN
45	J1	66	HIS
46	J2	164	HIS
46	J2	258	HIS
52	P2	42	HIS
52	P2	76	GLN
53	i2	48	ASN
53	i2	116	ASN
54	w2	179	GLN
57	M2	51	ASN
58	N1	91	GLN
58	N1	201	HIS
60	O1	3	ASN
60	O1	36	GLN
61	O2	224	ASN
62	P1	21	ASN
62	P1	55	HIS
63	Q1	7	HIS
63	Q1	14	HIS
63	Q1	44	ASN
63	Q1	125	GLN
64	R1	58	HIS
65	S1	77	ASN
65	S1	135	ASN
65	S1	173	ASN
66	S2	86	GLN
66	S2	114	GLN
67	T1	70	HIS
67	T1	149	GLN
70	U2	162	GLN
72	W1	17	HIS
73	W2	4	ASN
73	W2	81	HIS
73	W2	110	ASN
75	Y1	14	ASN
75	Y1	56	GLN
75	Y1	100	HIS
76	Y2	11	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
12	i1	118/120 (98%)	13 (11%)	0
13	j1	144/161 (89%)	20 (13%)	0
55	A1	3151/4024 (78%)	526 (16%)	19 (0%)
56	C2	1463/1838 (79%)	256 (17%)	4 (0%)
All	All	4876/6143 (79%)	815 (16%)	23 (0%)

All (815) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
12	i1	25	A
12	i1	30	C
12	i1	33	U
12	i1	50	A
12	i1	53	A
12	i1	54	A
12	i1	61	G
12	i1	63	C
12	i1	64	G
12	i1	88	A
12	i1	91	C
12	i1	100	A
12	i1	110	G
13	j1	12	G
13	j1	22	C
13	j1	33	U
13	j1	34	C
13	j1	38	G
13	j1	48	G
13	j1	58	A
13	j1	62	C
13	j1	71	A
13	j1	78	G
13	j1	88	A
13	j1	94	G
13	j1	103	A
13	j1	105	C
13	j1	106	G
13	j1	111	U
13	j1	115	G
13	j1	144	G
13	j1	151	G
13	j1	156	C
55	A1	5	G

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Mol	Chain	Res	Type
55	A1	14	U
55	A1	22	G
55	A1	34	A
55	A1	40	A
55	A1	43	A
55	A1	49	C
55	A1	57	A
55	A1	60	A
55	A1	65	A
55	A1	66	A
55	A1	72	C
55	A1	92	G
55	A1	99	A
55	A1	109	A
55	A1	110	G
55	A1	111	C
55	A1	113	C
55	A1	120	G
55	A1	133	A
55	A1	135	U
55	A1	136	G
55	A1	138	C
55	A1	152	G
55	A1	157	G
55	A1	158	U
55	A1	160	C
55	A1	172	U
55	A1	173	G
55	A1	178	G
55	A1	180	G
55	A1	189	G
55	A1	195	G
55	A1	198	U
55	A1	207	U
55	A1	217	U
55	A1	218	C
55	A1	231	U
55	A1	234	G
55	A1	235	G
55	A1	259	G
55	A1	278	G
55	A1	314	U

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Mol	Chain	Res	Type
55	A1	332	A
55	A1	333	A
55	A1	334	A
55	A1	338	C
55	A1	339	G
55	A1	352	U
55	A1	385	G
55	A1	408	A
55	A1	413	G
55	A1	429	G
55	A1	430	U
55	A1	431	A
55	A1	449	C
55	A1	450	A
55	A1	451	G
55	A1	472	C
55	A1	474	G
55	A1	493	U
55	A1	494	C
55	A1	497	C
55	A1	498	G
55	A1	499	C
55	A1	528	G
55	A1	529	C
55	A1	530	C
55	A1	531	G
55	A1	532	G
55	A1	533	U
55	A1	535	G
55	A1	536	G
55	A1	537	C
55	A1	538	U
55	A1	540	G
55	A1	541	C
55	A1	542	C
55	A1	547	C
55	A1	552	C
55	A1	556	U
55	A1	563	C
55	A1	565	C
55	A1	569	U
55	A1	574	C

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Mol	Chain	Res	Type
55	A1	578	G
55	A1	600	G
55	A1	601	G
55	A1	608	U
55	A1	609	C
55	A1	617	A
55	A1	641	A
55	A1	646	U
55	A1	647	A
55	A1	648	C
55	A1	649	A
55	A1	653	A
55	A1	654	C
55	A1	657	A
55	A1	659	C
55	A1	665	G
55	A1	666	A
55	A1	667	C
55	A1	668	C
55	A1	669	U
55	A1	675	C
55	A1	676	U
55	A1	677	U
55	A1	681	G
55	A1	687	G
55	A1	688	U
55	A1	691	A
55	A1	692	A
55	A1	711	U
55	A1	715	U
55	A1	716	C
55	A1	781	G
55	A1	783	A
55	A1	787	G
55	A1	794	U
55	A1	795	C
55	A1	806	C
55	A1	830	U
55	A1	831	C
55	A1	832	U
55	A1	833	C
55	A1	834	A

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Mol	Chain	Res	Type
55	A1	835	G
55	A1	836	U
55	A1	841	U
55	A1	842	C
55	A1	843	C
55	A1	844	G
55	A1	845	A
55	A1	846	C
55	A1	847	C
55	A1	868	G
55	A1	873	G
55	A1	877	C
55	A1	878	A
55	A1	891	G
55	A1	893	A
55	A1	894	A
55	A1	898	G
55	A1	899	U
55	A1	908	A
55	A1	912	C
55	A1	928	C
55	A1	939	C
55	A1	940	A
55	A1	951	A
55	A1	959	G
55	A1	968	A
55	A1	972	A
55	A1	986	G
55	A1	1001	A
55	A1	1011	A
55	A1	1013	G
55	A1	1034	A
55	A1	1052	C
55	A1	1059	U
55	A1	1092	U
55	A1	1096	U
55	A1	1109	G
55	A1	1113	G
55	A1	1114	A
55	A1	1134	A
55	A1	1145	A
55	A1	1158	A

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Mol	Chain	Res	Type
55	A1	1165	A
55	A1	1172	G
55	A1	1175	A
55	A1	1176	A
55	A1	1177	C
55	A1	1186	A
55	A1	1189	C
55	A1	1202	U
55	A1	1207	U
55	A1	1208	G
55	A1	1222	C
55	A1	1224	A
55	A1	1225	C
55	A1	1235	G
55	A1	1242	A
55	A1	1244	G
55	A1	1252	G
55	A1	1265	G
55	A1	1272	C
55	A1	1287	C
55	A1	1288	U
55	A1	1290	A
55	A1	1291	G
55	A1	1309	G
55	A1	1311	C
55	A1	1313	C
55	A1	1314	G
55	A1	1317	G
55	A1	1327	G
55	A1	1339	A
55	A1	1342	A
55	A1	1373	A
55	A1	1375	U
55	A1	1376	C
55	A1	1378	C
55	A1	1380	A
55	A1	1381	A
55	A1	1389	U
55	A1	1397	A
55	A1	1408	G
55	A1	1414	A
55	A1	1423	G

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Mol	Chain	Res	Type
55	A1	1428	G
55	A1	1429	G
55	A1	1430	A
55	A1	1435	G
55	A1	1439	C
55	A1	1440	G
55	A1	1448	G
55	A1	1449	G
55	A1	1463	G
55	A1	1464	C
55	A1	1486	A
55	A1	1491	A
55	A1	1512	U
55	A1	1513	G
55	A1	1515	C
55	A1	1516	G
55	A1	1525	C
55	A1	1526	A
55	A1	1533	A
55	A1	1540	G
55	A1	1541	U
55	A1	1542	G
55	A1	1546	G
55	A1	1638	U
55	A1	1640	G
55	A1	1642	U
55	A1	1646	G
55	A1	1649	G
55	A1	1650	G
55	A1	1663	A
55	A1	1678	C
55	A1	1679	G
55	A1	1683	G
55	A1	1691	C
55	A1	1694	G
55	A1	1697	G
55	A1	1700	U
55	A1	1701	A
55	A1	1722	C
55	A1	1733	A
55	A1	1734	G
55	A1	1739	G

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Mol	Chain	Res	Type
55	A1	1746	A
55	A1	1747	G
55	A1	1749	G
55	A1	1765	A
55	A1	1766	G
55	A1	1778	G
55	A1	1781	G
55	A1	1784	C
55	A1	1793	A
55	A1	1794	G
55	A1	1797	G
55	A1	1812	A
55	A1	1828	A
55	A1	1829	A
55	A1	1830	G
55	A1	1837	A
55	A1	1849	G
55	A1	1850	A
55	A1	1859	U
55	A1	1880	U
55	A1	1886	A
55	A1	1902	C
55	A1	1904	G
55	A1	1906	A
55	A1	1910	C
55	A1	1911	G
55	A1	1912	G
55	A1	1944	A
55	A1	1945	A
55	A1	1946	A
55	A1	1976	A
55	A1	1986	A
55	A1	1987	C
55	A1	1990	G
55	A1	1992	G
55	A1	2000	G
55	A1	2001	C
55	A1	2002	G
55	A1	2008	U
55	A1	2019	A
55	A1	2020	A
55	A1	2022	C

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Mol	Chain	Res	Type
55	A1	2034	A
55	A1	2035	G
55	A1	2050	G
55	A1	2051	G
55	A1	2064	U
55	A1	2071	G
55	A1	2085	G
55	A1	2086	C
55	A1	2102	C
55	A1	2120	U
55	A1	2128	A
55	A1	2129	A
55	A1	2133	G
55	A1	2135	C
55	A1	2136	G
55	A1	2175	G
55	A1	2176	A
55	A1	2195	G
55	A1	2202	U
55	A1	2221	U
55	A1	2223	U
55	A1	2231	A
55	A1	2248	A
55	A1	2258	G
55	A1	2259	U
55	A1	2260	C
55	A1	2261	U
55	A1	2268	A
55	A1	2272	G
55	A1	2275	U
55	A1	2276	G
55	A1	2289	G
55	A1	2290	C
55	A1	2291	A
55	A1	2308	U
55	A1	2309	C
55	A1	2333	C
55	A1	2334	U
55	A1	2700	A
55	A1	2701	G
55	A1	2702	C
55	A1	2703	U

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Mol	Chain	Res	Type
55	A1	2716	G
55	A1	2719	C
55	A1	2727	G
55	A1	2736	A
55	A1	2763	A
55	A1	2815	G
55	A1	2833	A
55	A1	2837	A
55	A1	2854	G
55	A1	2855	G
55	A1	2856	G
55	A1	2857	A
55	A1	2858	G
55	A1	2859	U
55	A1	2866	G
55	A1	2869	U
55	A1	2871	U
55	A1	2872	C
55	A1	2874	U
55	A1	2877	G
55	A1	2878	G
55	A1	2885	A
55	A1	2887	U
55	A1	2889	C
55	A1	2903	U
55	A1	2910	G
55	A1	2912	G
55	A1	2915	U
55	A1	2918	A
55	A1	2919	U
55	A1	2920	G
55	A1	2937	A
55	A1	2939	U
55	A1	2941	U
55	A1	2978	A
55	A1	2979	C
55	A1	2980	G
55	A1	2998	G
55	A1	3002	A
55	A1	3006	A
55	A1	3007	A
55	A1	3008	G

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Mol	Chain	Res	Type
55	A1	3009	A
55	A1	3016	U
55	A1	3033	U
55	A1	3039	C
55	A1	3123	U
55	A1	3129	G
55	A1	3131	G
55	A1	3142	G
55	A1	3169	G
55	A1	3170	G
55	A1	3205	C
55	A1	3206	U
55	A1	3213	A
55	A1	3226	G
55	A1	3227	G
55	A1	3234	G
55	A1	3246	A
55	A1	3247	C
55	A1	3255	A
55	A1	3268	G
55	A1	3271	G
55	A1	3272	U
55	A1	3276	A
55	A1	3277	A
55	A1	3294	A
55	A1	3309	G
55	A1	3311	A
55	A1	3316	A
55	A1	3323	A
55	A1	3324	A
55	A1	3325	A
55	A1	3328	U
55	A1	3346	C
55	A1	3347	A
55	A1	3348	G
55	A1	3349	U
55	A1	3357	C
55	A1	3372	G
55	A1	3373	G
55	A1	3375	C
55	A1	3380	C
55	A1	3381	G

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Mol	Chain	Res	Type
55	A1	3382	A
55	A1	3398	G
55	A1	3416	G
55	A1	3419	A
55	A1	3420	G
55	A1	3421	A
55	A1	3423	A
55	A1	3424	A
55	A1	3430	C
55	A1	3436	G
55	A1	3437	A
55	A1	3454	G
55	A1	3458	A
55	A1	3464	C
55	A1	3465	A
55	A1	3473	G
55	A1	3479	U
55	A1	3480	U
55	A1	3481	U
55	A1	3491	G
55	A1	3492	A
55	A1	3496	C
55	A1	3507	A
55	A1	3508	U
55	A1	3509	C
55	A1	3518	G
55	A1	3519	C
55	A1	3543	U
55	A1	3555	U
55	A1	3556	A
55	A1	3561	A
55	A1	3562	C
55	A1	3568	C
55	A1	3570	G
55	A1	3571	G
55	A1	3572	G
55	A1	3591	A
55	A1	3598	U
55	A1	3600	U
55	A1	3603	C
55	A1	3610	G
55	A1	3633	A

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Mol	Chain	Res	Type
55	A1	3635	C
55	A1	3678	A
55	A1	3679	U
55	A1	3680	G
55	A1	3690	G
55	A1	3691	A
55	A1	3699	A
55	A1	3713	C
55	A1	3715	A
55	A1	3720	U
55	A1	3734	A
55	A1	3736	C
55	A1	3742	U
55	A1	3743	A
55	A1	3751	A
55	A1	3752	U
55	A1	3763	C
55	A1	3769	G
55	A1	3778	G
55	A1	3779	C
55	A1	3788	U
55	A1	3792	C
55	A1	3797	G
55	A1	3799	U
55	A1	3800	C
55	A1	3801	C
55	A1	3802	C
55	A1	3808	G
55	A1	3819	G
55	A1	3826	G
55	A1	3827	C
55	A1	3830	A
55	A1	3833	G
55	A1	3838	U
55	A1	3839	C
55	A1	3843	A
55	A1	3857	C
55	A1	3864	A
55	A1	3876	C
55	A1	3883	A
55	A1	3886	U
55	A1	3889	G

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Mol	Chain	Res	Type
55	A1	3890	C
55	A1	3893	U
55	A1	3894	G
55	A1	3897	C
55	A1	3902	G
55	A1	3903	U
55	A1	3916	G
55	A1	3919	A
55	A1	3928	G
55	A1	3929	C
55	A1	3941	U
55	A1	3942	U
55	A1	3948	U
55	A1	3970	G
55	A1	3994	G
55	A1	4003	C
55	A1	4007	C
55	A1	4008	G
55	A1	4009	A
55	A1	4021	G
55	A1	4022	U
56	C2	3	A
56	C2	5	C
56	C2	12	A
56	C2	34	G
56	C2	42	G
56	C2	45	U
56	C2	46	A
56	C2	47	A
56	C2	57	G
56	C2	60	U
56	C2	63	G
56	C2	65	A
56	C2	66	C
56	C2	68	C
56	C2	69	A
56	C2	73	U
56	C2	80	A
56	C2	81	G
56	C2	104	A
56	C2	114	G
56	C2	115	G

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Mol	Chain	Res	Type
56	C2	116	U
56	C2	139	C
56	C2	141	U
56	C2	152	G
56	C2	155	A
56	C2	162	G
56	C2	165	C
56	C2	175	C
56	C2	199	U
56	C2	214	G
56	C2	263	G
56	C2	268	U
56	C2	277	C
56	C2	278	C
56	C2	286	G
56	C2	309	G
56	C2	327	C
56	C2	334	A
56	C2	335	U
56	C2	336	C
56	C2	338	A
56	C2	346	U
56	C2	348	G
56	C2	359	G
56	C2	360	C
56	C2	381	A
56	C2	382	A
56	C2	383	C
56	C2	384	G
56	C2	392	A
56	C2	402	U
56	C2	422	A
56	C2	423	A
56	C2	424	C
56	C2	426	G
56	C2	439	A
56	C2	445	G
56	C2	446	C
56	C2	448	G
56	C2	456	G
56	C2	460	A
56	C2	461	U

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Mol	Chain	Res	Type
56	C2	466	C
56	C2	474	A
56	C2	475	C
56	C2	482	A
56	C2	499	A
56	C2	503	A
56	C2	534	A
56	C2	550	A
56	C2	559	C
56	C2	561	A
56	C2	563	G
56	C2	565	U
56	C2	567	U
56	C2	568	A
56	C2	580	G
56	C2	588	C
56	C2	597	G
56	C2	600	G
56	C2	601	U
56	C2	602	A
56	C2	611	U
56	C2	617	A
56	C2	618	G
56	C2	634	C
56	C2	642	A
56	C2	643	A
56	C2	645	A
56	C2	646	A
56	C2	647	G
56	C2	651	G
56	C2	652	U
56	C2	784	A
56	C2	794	G
56	C2	795	U
56	C2	803	A
56	C2	819	A
56	C2	840	G
56	C2	841	A
56	C2	842	A
56	C2	843	U
56	C2	844	A
56	C2	845	G

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Mol	Chain	Res	Type
56	C2	846	G
56	C2	849	U
56	C2	881	G
56	C2	887	A
56	C2	894	A
56	C2	895	G
56	C2	896	A
56	C2	907	G
56	C2	923	G
56	C2	926	G
56	C2	929	A
56	C2	930	G
56	C2	939	U
56	C2	944	G
56	C2	945	G
56	C2	949	G
56	C2	960	G
56	C2	964	A
56	C2	965	A
56	C2	966	A
56	C2	971	A
56	C2	991	U
56	C2	997	A
56	C2	1001	A
56	C2	1015	G
56	C2	1027	C
56	C2	1034	A
56	C2	1036	A
56	C2	1051	A
56	C2	1057	A
56	C2	1059	C
56	C2	1062	U
56	C2	1070	A
56	C2	1095	G
56	C2	1106	C
56	C2	1107	A
56	C2	1118	A
56	C2	1120	C
56	C2	1123	A
56	C2	1128	U
56	C2	1145	G
56	C2	1146	U

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Mol	Chain	Res	Type
56	C2	1169	A
56	C2	1181	G
56	C2	1189	C
56	C2	1190	C
56	C2	1202	A
56	C2	1205	C
56	C2	1211	C
56	C2	1216	U
56	C2	1222	U
56	C2	1225	A
56	C2	1227	A
56	C2	1231	G
56	C2	1232	A
56	C2	1233	A
56	C2	1237	U
56	C2	1238	C
56	C2	1247	C
56	C2	1248	G
56	C2	1298	G
56	C2	1301	G
56	C2	1302	G
56	C2	1303	U
56	C2	1304	G
56	C2	1305	C
56	C2	1306	A
56	C2	1307	U
56	C2	1315	C
56	C2	1322	G
56	C2	1323	G
56	C2	1324	U
56	C2	1328	G
56	C2	1345	U
56	C2	1346	U
56	C2	1352	A
56	C2	1371	U
56	C2	1375	A
56	C2	1377	C
56	C2	1378	U
56	C2	1388	G
56	C2	1404	G
56	C2	1409	A
56	C2	1411	U

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Mol	Chain	Res	Type
56	C2	1412	U
56	C2	1421	G
56	C2	1423	C
56	C2	1424	A
56	C2	1441	A
56	C2	1446	A
56	C2	1447	U
56	C2	1448	U
56	C2	1459	A
56	C2	1460	G
56	C2	1462	U
56	C2	1468	A
56	C2	1470	G
56	C2	1471	C
56	C2	1491	C
56	C2	1492	A
56	C2	1496	G
56	C2	1502	C
56	C2	1503	A
56	C2	1506	G
56	C2	1548	U
56	C2	1549	A
56	C2	1550	A
56	C2	1555	C
56	C2	1556	U
56	C2	1558	A
56	C2	1571	A
56	C2	1576	G
56	C2	1577	A
56	C2	1589	A
56	C2	1591	U
56	C2	1593	A
56	C2	1606	G
56	C2	1611	A
56	C2	1612	U
56	C2	1617	A
56	C2	1624	G
56	C2	1635	G
56	C2	1641	G
56	C2	1645	A
56	C2	1649	A
56	C2	1650	G

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Mol	Chain	Res	Type
56	C2	1653	C
56	C2	1662	U
56	C2	1668	C
56	C2	1669	A
56	C2	1675	C
56	C2	1691	U
56	C2	1692	G
56	C2	1696	G
56	C2	1697	G
56	C2	1698	U
56	C2	1714	G
56	C2	1756	G
56	C2	1777	U
56	C2	1778	A
56	C2	1788	A
56	C2	1793	A
56	C2	1794	A
56	C2	1795	G
56	C2	1804	A
56	C2	1818	G
56	C2	1828	A
56	C2	1830	G
56	C2	1831	G
56	C2	1832	A
56	C2	1833	U

All (23) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
55	A1	179	U
55	A1	492	C
55	A1	532	G
55	A1	535	G
55	A1	536	G
55	A1	541	C
55	A1	714	C
55	A1	715	U
55	A1	830	U
55	A1	831	C
55	A1	841	U
55	A1	872	C
55	A1	877	C

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Mol	Chain	Res	Type
55	A1	1909	G
55	A1	2085	G
55	A1	3518	G
55	A1	3742	U
55	A1	3918	U
55	A1	4021	G
56	C2	140	U
56	C2	943	U
56	C2	965	A
56	C2	1648	A

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 [i](#)

Of 92 ligands modelled in this entry, 92 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 [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

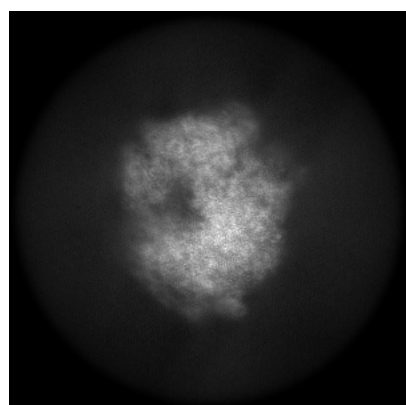
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-66542. These allow visual inspection of the internal detail of the map and identification of artifacts.

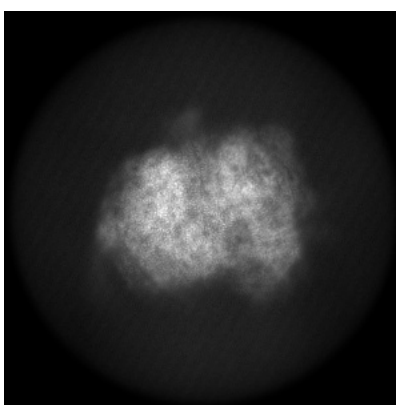
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

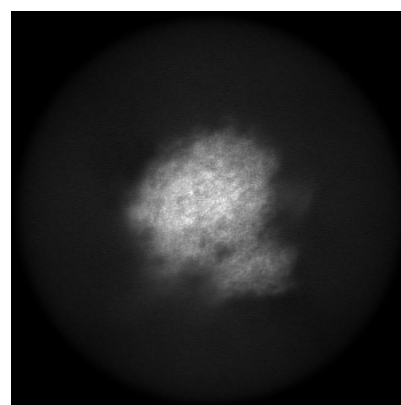
6.1.1 Primary map



X



Y

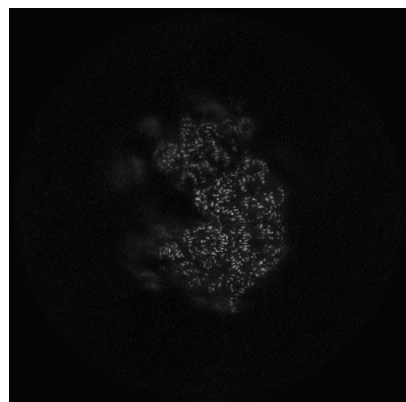


Z

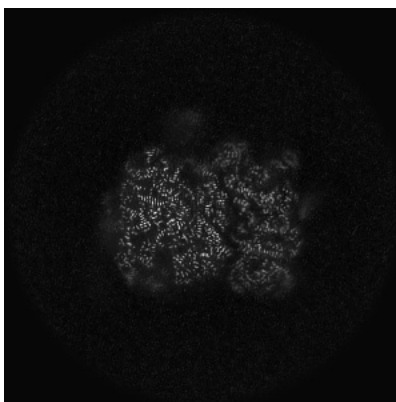
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

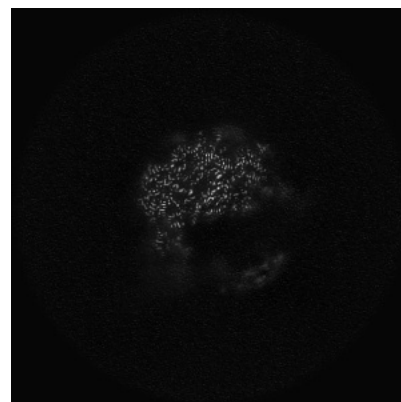
6.2.1 Primary map



X Index: 320



Y Index: 320

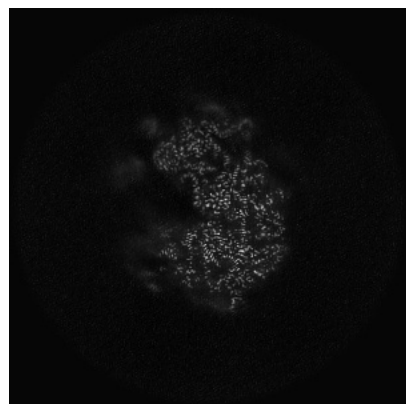


Z Index: 320

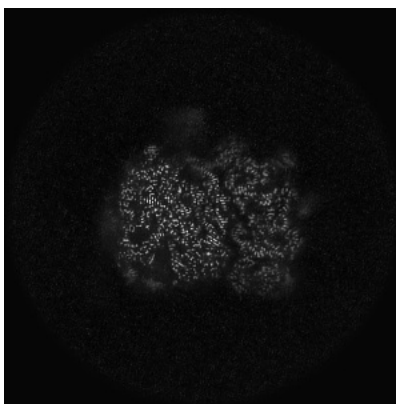
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

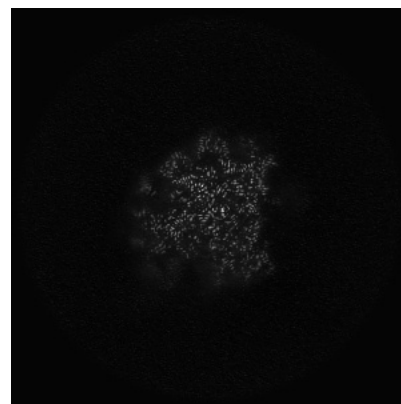
6.3.1 Primary map



X Index: 317



Y Index: 323

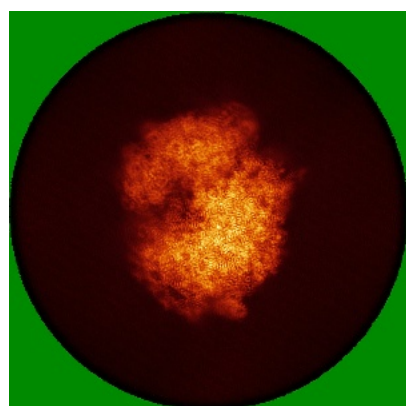


Z Index: 260

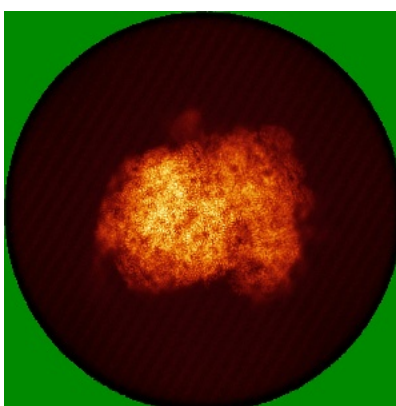
The images above show the largest variance slices of the map in three orthogonal directions.

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

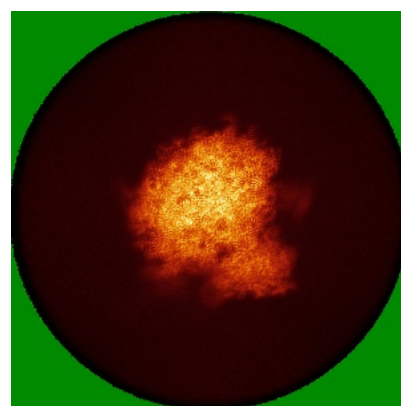
6.4.1 Primary map



X



Y

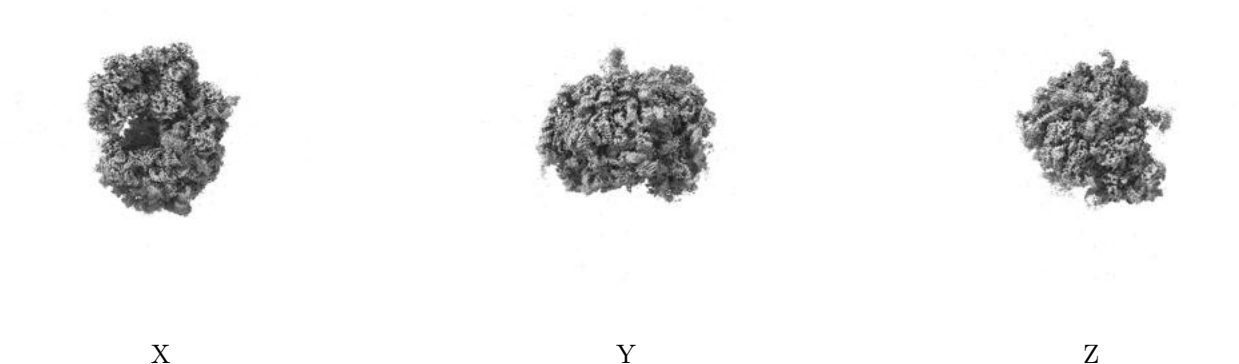


Z

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

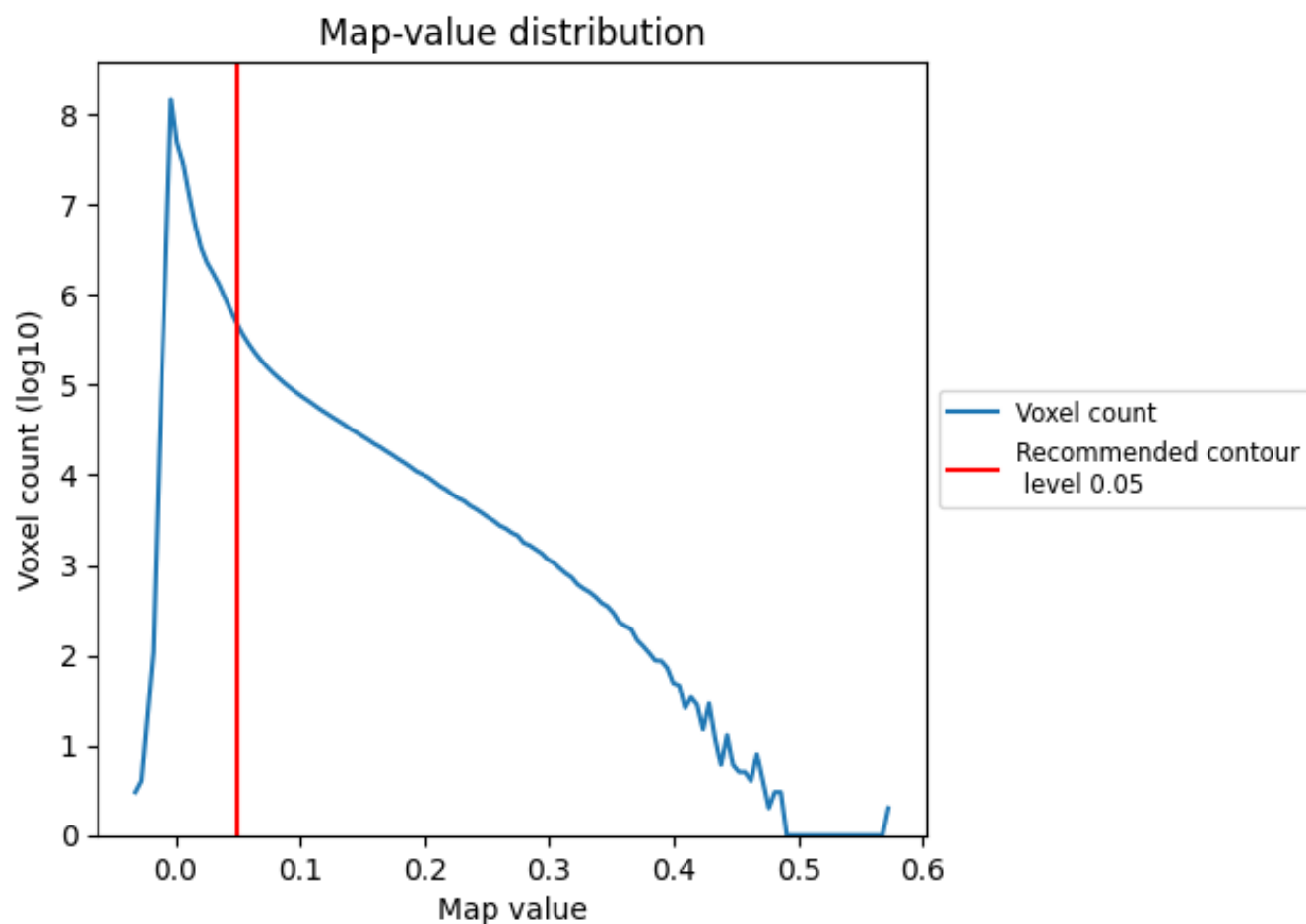
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

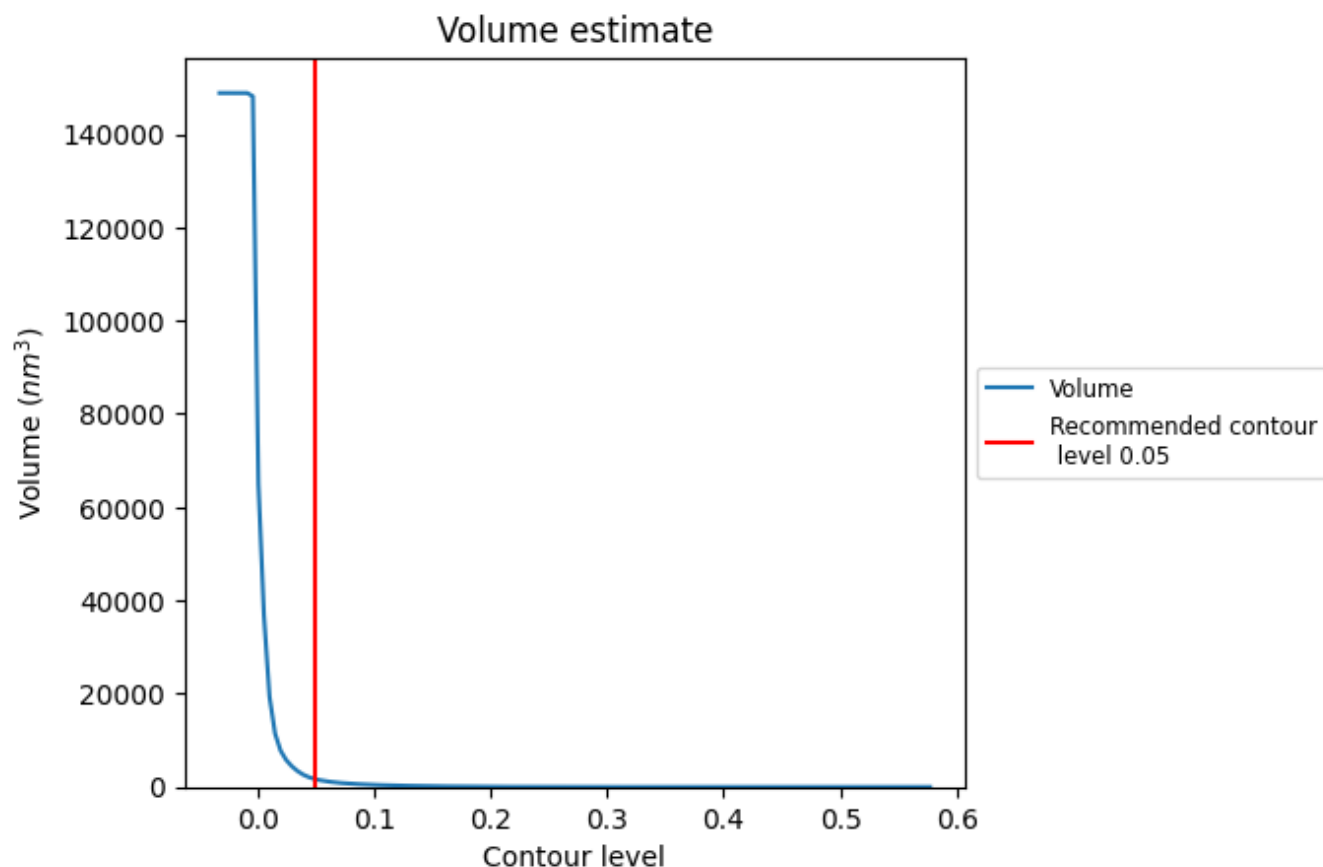
This section contains the results of statistical analysis of the map.

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.

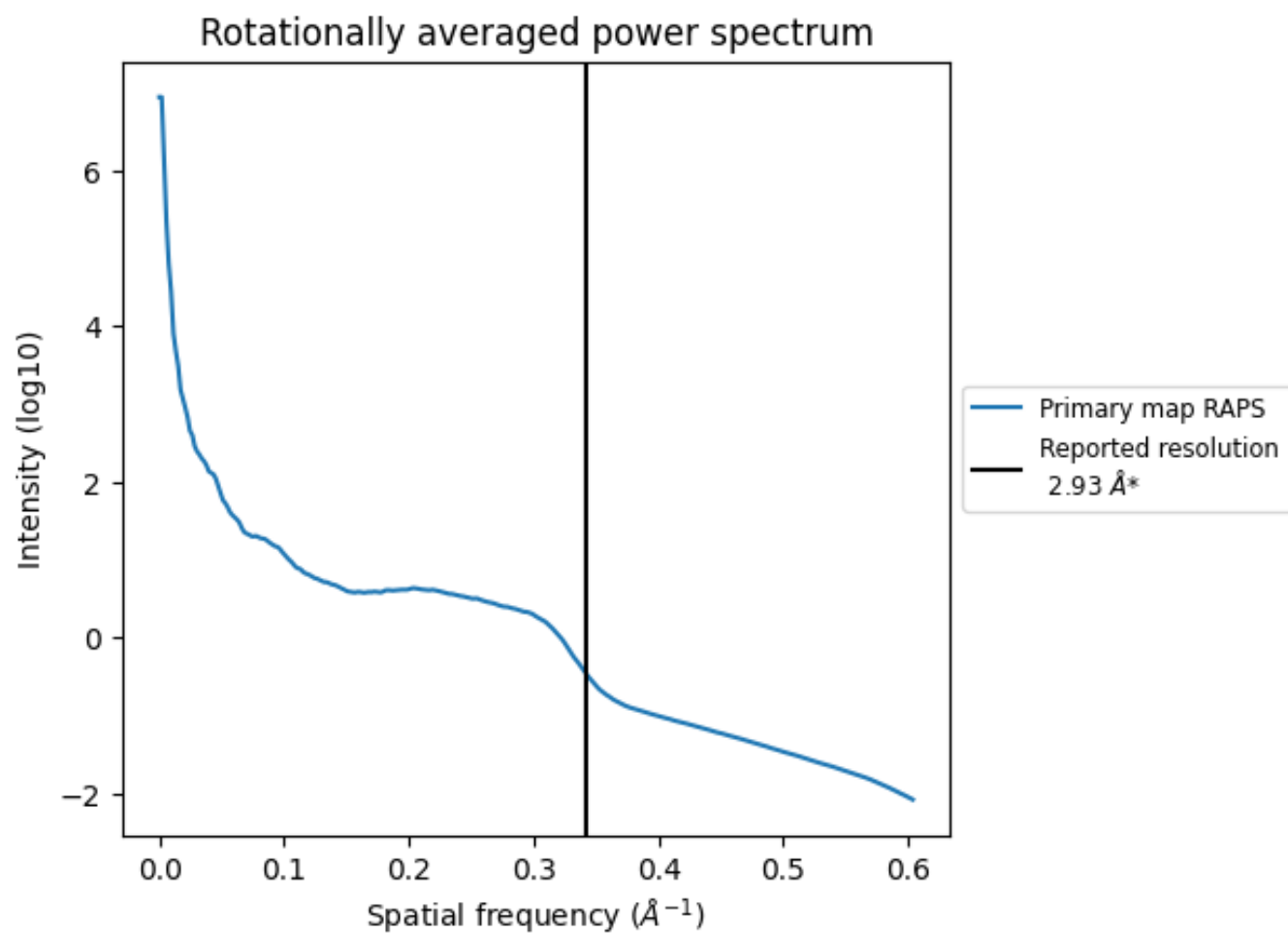
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1665 nm^3 ; this corresponds to an approximate mass of 1504 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 0.341 Å⁻¹

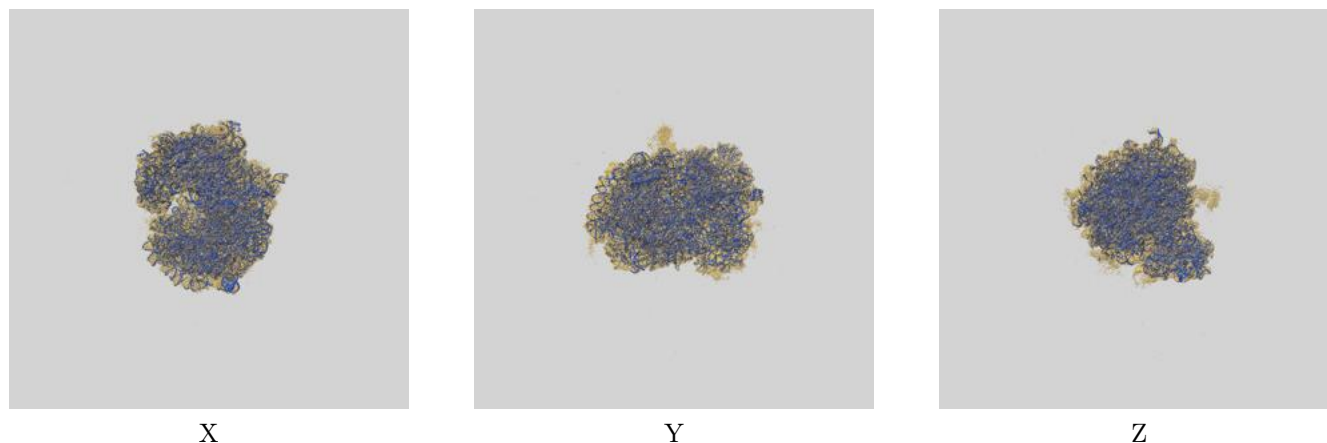
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

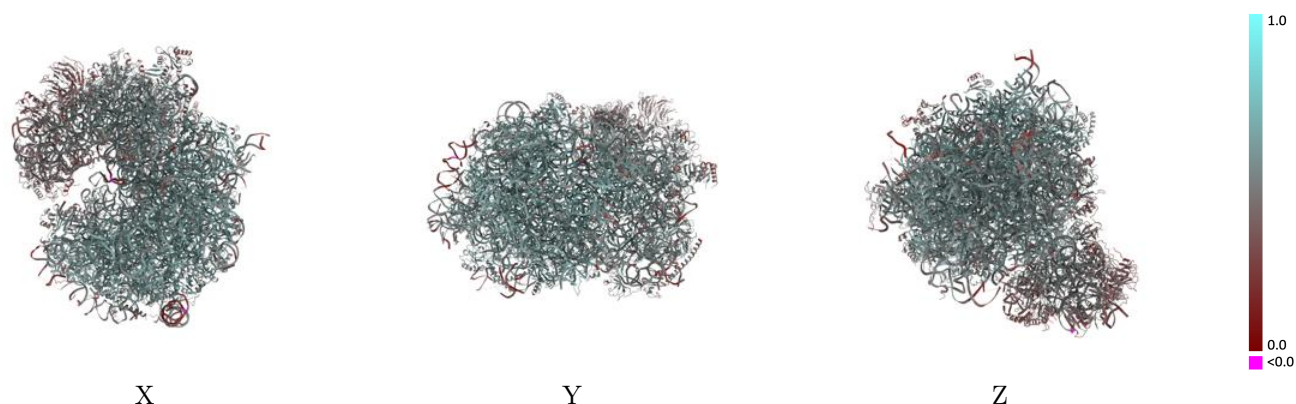
This section contains information regarding the fit between EMDB map EMD-66542 and PDB model 9X4D. Per-residue inclusion information can be found in section [3](#) on page [18](#).

9.1 Map-model overlay [i](#)



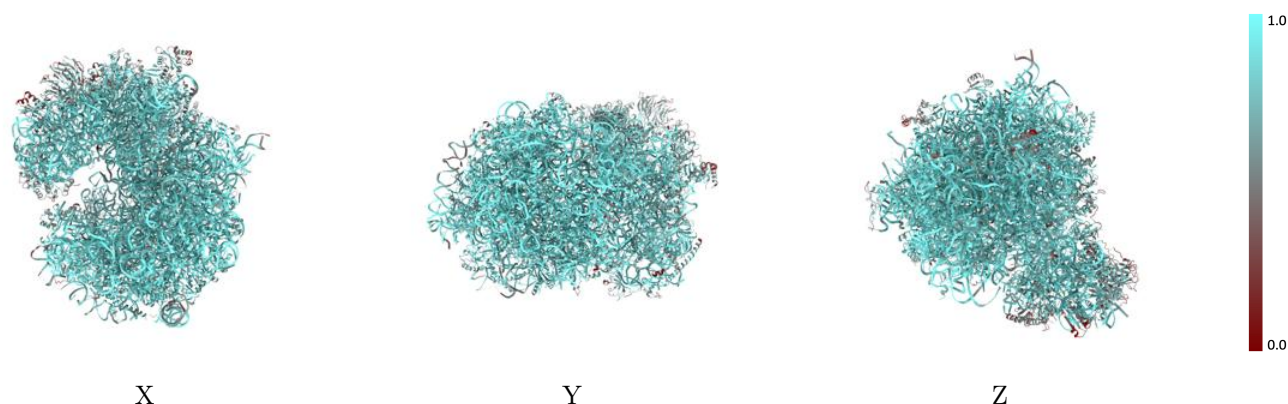
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



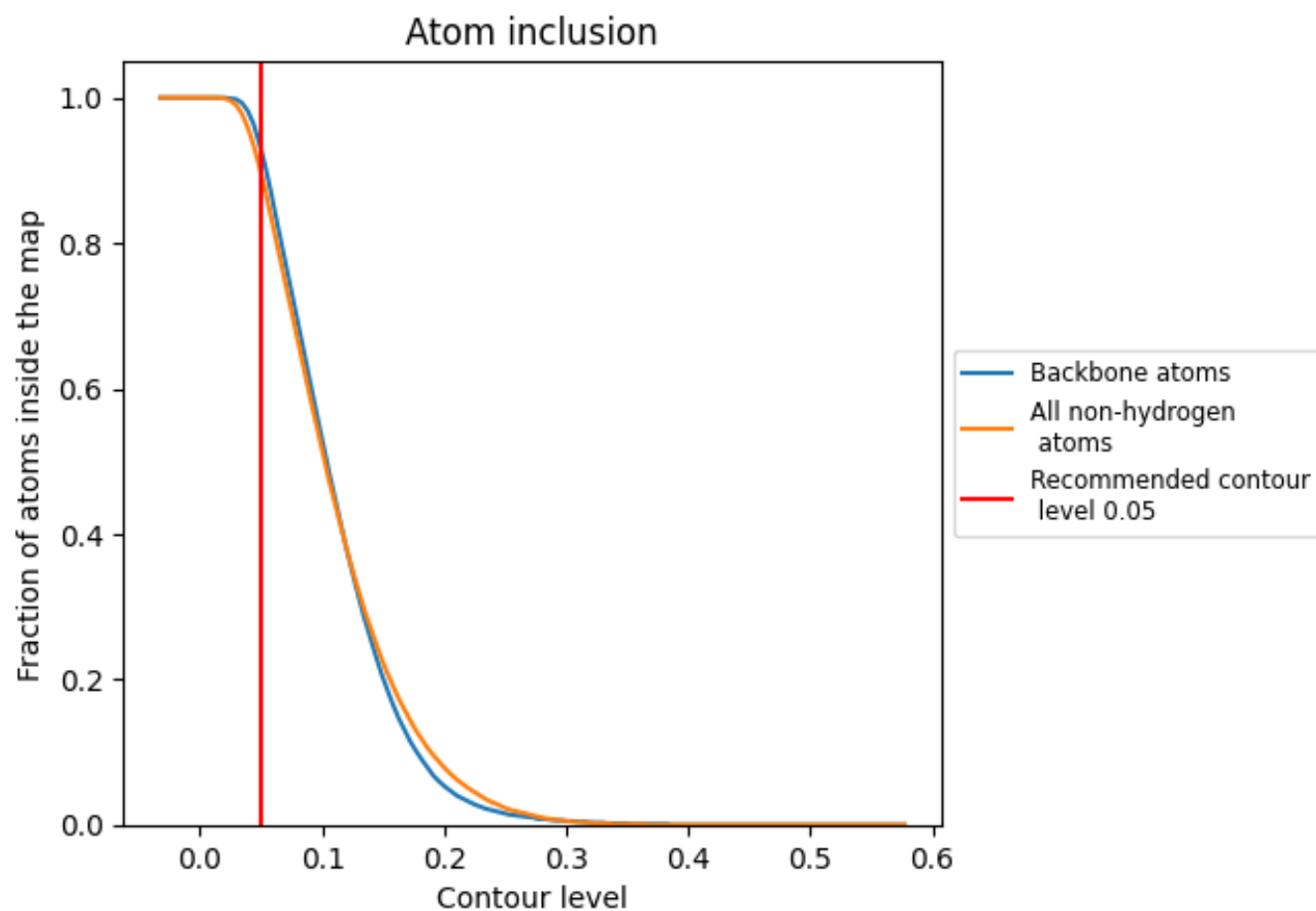
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.05).

9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 90% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8960	 0.5410
11	 0.9220	 0.5800
21	 0.7110	 0.5230
32	 0.7780	 0.4990
41	 0.9010	 0.5850
42	 0.7480	 0.4810
51	 0.8670	 0.5560
61	 0.7360	 0.4520
71	 0.7420	 0.4820
72	 0.8010	 0.4800
81	 0.9290	 0.5850
82	 0.7930	 0.5010
91	 0.8750	 0.5330
A1	 0.9500	 0.5680
A2	 0.6750	 0.3970
B1	 0.9010	 0.5880
B2	 0.8110	 0.5170
C1	 0.9100	 0.5910
C2	 0.9530	 0.5120
D1	 0.8940	 0.5700
E1	 0.9240	 0.5910
F1	 0.9140	 0.5820
H1	 0.8710	 0.5650
H2	 0.7100	 0.4990
I1	 0.8540	 0.5490
J1	 0.9660	 0.6100
J2	 0.8160	 0.5170
K1	 0.6950	 0.4890
K2	 0.7500	 0.4980
L1	 0.8480	 0.5620
L2	 0.8500	 0.5130
M1	 0.9020	 0.5700
M2	 0.7610	 0.4570
N1	 0.9670	 0.6140
N2	 0.9080	 0.5200



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Chain	Atom inclusion	Q-score
O1	 0.8750	 0.5760
O2	 0.8660	 0.5320
P1	 0.9380	 0.5930
P2	 0.6610	 0.3890
Q1	 0.9260	 0.6020
R1	 0.8660	 0.5490
S1	 0.9150	 0.5790
S2	 0.7690	 0.4400
T1	 0.8860	 0.5710
T2	 0.6790	 0.3790
U1	 0.6510	 0.4430
U2	 0.6270	 0.4500
V1	 0.8720	 0.5790
W1	 0.9130	 0.6000
W2	 0.6880	 0.4570
X1	 0.8610	 0.5580
Y1	 0.9090	 0.5820
Y2	 0.8340	 0.5460
Z1	 0.8270	 0.5450
a1	 0.9410	 0.6060
b1	 0.8990	 0.5640
d2	 0.7810	 0.4270
e1	 0.9210	 0.5800
f1	 0.9570	 0.6040
g1	 0.8950	 0.5810
g2	 0.7460	 0.4900
h1	 0.8240	 0.5310
i1	 0.9850	 0.5880
i2	 0.5880	 0.4020
j1	 0.9760	 0.5890
k1	 0.8110	 0.5320
k2	 0.5250	 0.3700
l1	 0.8590	 0.5580
m1	 0.8370	 0.5440
m2	 0.8190	 0.4960
n1	 0.9320	 0.6070
q2	 0.5780	 0.4130
r2	 0.8930	 0.5390
u2	 0.7940	 0.4270
w2	 0.6280	 0.3940
x2	 0.7560	 0.4890
y2	 0.8470	 0.5410

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Chain	Atom inclusion	Q-score
z2	 0.5900	 0.3550