



Full wwPDB EM Validation Report ⓘ

Mar 30, 2026 – 03:50 AM UTC

PDB ID : 9Y44 / pdb_00009y44
EMDB ID : EMD-72470
Title : Structure of naked mole-rat ribosome (rotated, tRNAs, and mRNA)
Authors : Gutierrez-Vargas, C.; De, S.; Maji, S.; Liu, Z.; Nieb, M.; Seluanov, A.; Gorbunova, V.; Frank, J.
Deposited on : 2025-09-02
Resolution : 4.90 Å (reported)
Based on initial models : 4v6x, 707y

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

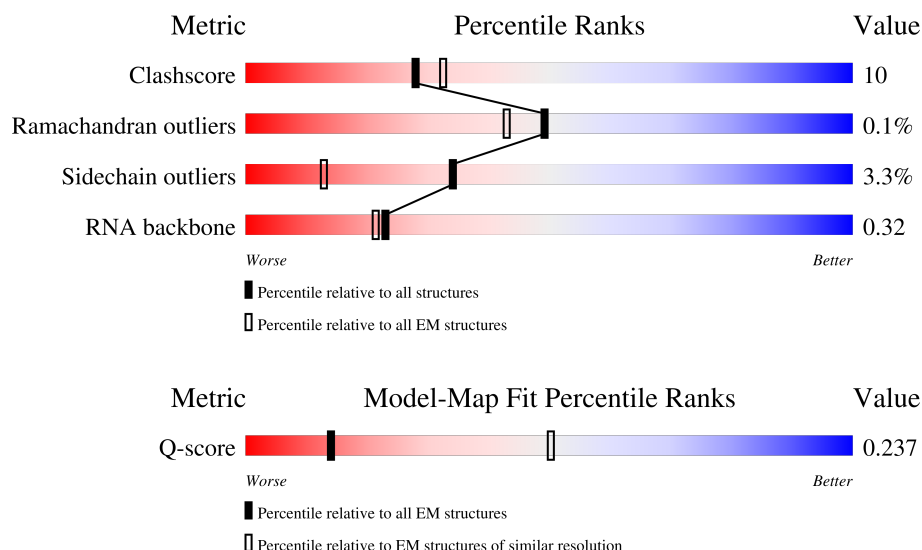
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.90 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.




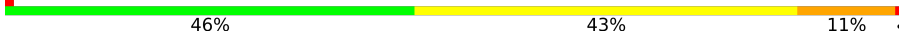























Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	1274 (4.40 - 5.40)

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	A5	1717	
2	A7	120	
3	A8	156	







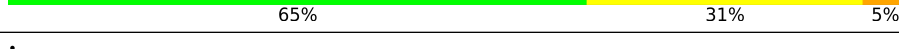
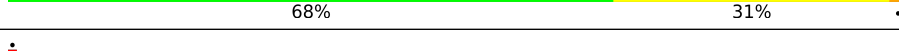
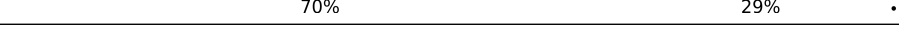
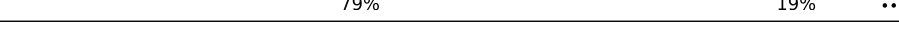
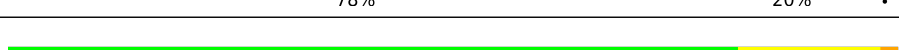

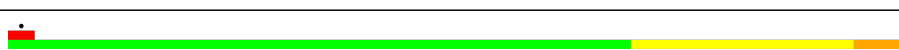

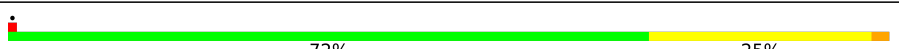





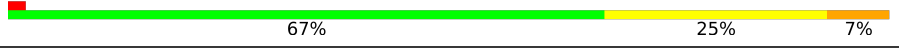
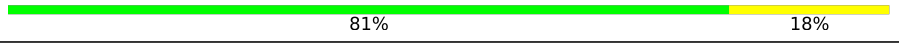



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Mol	Chain	Length	Quality of chain
4	B2	1804	
5	A6	2092	
6	A	248	
7	n	25	
8	B	398	
9	C	363	
10	D	293	
11	E	224	
12	F	225	
13	G	215	
14	H	190	
15	I	213	
16	J	170	
17	L	205	
18	M	136	
19	N	203	
20	O	199	
21	P	153	
22	Q	187	
23	S	176	
24	T	159	
25	U	99	
26	V	131	
27	X	118	
28	Y	134	


























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Mol	Chain	Length	Quality of chain
29	Z	135	
30	a	147	
31	b	100	
32	d	107	
33	e	128	
34	f	110	
35	g	110	
36	h	121	
37	i	102	
38	j	86	
39	k	69	
40	l	50	
41	m	51	
42	o	105	
43	p	91	
44	r	127	
45	s	103	
46	t	156	
47	cc	61	
48	ff	67	
49	gg	313	
50	dd	55	
51	AA	214	
52	BB	218	
53	DD	225	






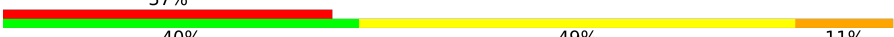

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Mol	Chain	Length	Quality of chain
54	FF	189	 79%16%...
55	KK	96	 73%24%.
56	MM	124	 13%78%21%.
57	OO	134	 69%28%.
58	PP	118	 70%28%..
59	QQ	141	 74%23%.
60	RR	132	 80%19%.
61	SS	145	 73%26%.
62	TT	141	 80%18%.
63	UU	99	 85%14%.
64	ZZ	75	 80%19%.
65	bb	82	 77%21%.
66	ee	49	 65%35%
67	aa	98	 78%22%
68	CC	218	 74%24%.
69	EE	262	 81%19%
70	GG	228	 78%21%.
71	HH	190	 77%19%..
72	II	206	 79%20%.
73	JJ	180	 68%30%..
74	LL	149	 73%21%5%
75	NN	149	 80%20%
76	VV	83	 83%17%
77	WW	129	 83%16%.
78	XX	122	 93%7%

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Mol	Chain	Length	Quality of chain
79	YY	125	
80	W	180	
81	c	121	
82	u	100	
83	Cc	76	
84	Bb	65	
85	Dd	13	

2 Entry composition [i](#)

There are 88 unique types of molecules in this entry. The entry contains 219186 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called LSU alpha rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A5	1717	Total	C	N	O	P	0	0
			36275	16121	6621	11816	1717		

- Molecule 2 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A7	120	Total	C	N	O	P	0	0
			2558	1140	453	845	120		

- Molecule 3 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A8	156	Total	C	N	O	P	0	0
			3317	1480	584	1097	156		

- Molecule 4 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	B2	1804	Total	C	N	O	P	0	0
			37897	16889	6738	12466	1804		

- Molecule 5 is a RNA chain called LSU beta rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	A6	2092	Total	C	N	O	P	0	0
			43564	19354	7784	14334	2092		

- Molecule 6 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	A	248	Total	C	N	O	S	0	0
			1648	1036	305	301	6		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	72	LYS	ARG	conflict	UNP A0A0P6J3A4
A	123	LYS	ARG	conflict	UNP A0A0P6J3A4
A	128	LYS	ARG	conflict	UNP A0A0P6J3A4
A	147	LYS	ARG	conflict	UNP A0A0P6J3A4

- Molecule 7 is a protein called 60S ribosomal protein L41.

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

- Molecule 8 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	B	398	Total	C	N	O	S	0	0
			3206	2042	605	546	13		

- Molecule 9 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	C	363	Total	C	N	O	S	0	0
			2884	1815	576	479	14		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	1	ACE	-	acetylation	UNP G5AN81
C	262	ASP	GLU	conflict	UNP G5AN81
C	362	GLY	-	expression tag	UNP G5AN81
C	363	GLY	-	expression tag	UNP G5AN81

- Molecule 10 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	D	293	Total	C	N	O	S	0	0
			2389	1511	437	427	14		

- Molecule 11 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	E	224	Total	C	N	O	S	0	0
			1789	1149	340	297	3		

- Molecule 12 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	F	225	Total	C	N	O	S	0	0
			1875	1205	358	303	9		

- Molecule 13 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	G	215	Total	C	N	O	S	0	0
			1741	1111	333	293	4		

- Molecule 14 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	H	190	Total	C	N	O	S	0	0
			1516	954	284	272	6		

- Molecule 15 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	I	199	Total	C	N	O	S	0	0
			1620	1029	313	266	12		

- Molecule 16 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	J	170	Total	C	N	O	S	0	0
			1362	861	254	241	6		

- Molecule 17 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	L	205	Total	C	N	O	S	0	0
			1658	1037	346	271	4		

- Molecule 18 is a protein called Large ribosomal subunit protein eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	M	136	Total	C	N	O	S	0	0
			1125	720	220	178	7		

- Molecule 19 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	N	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 20 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	O	199	Total	C	N	O	S	0	0
			1630	1051	319	255	5		

- Molecule 21 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	P	153	Total	C	N	O	S	0	0
			1242	777	241	215	9		

- Molecule 22 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Q	187	Total	C	N	O	S	0	0
			1512	946	313	249	4		

- Molecule 23 is a protein called Large ribosomal subunit protein eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	S	176	Total	C	N	O	S	0	0
			1461	930	284	236	11		

- Molecule 24 is a protein called Large ribosomal subunit protein eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	T	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 25 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	U	99	Total	C	N	O	S	0	0
			808	518	141	147	2		

- Molecule 26 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	V	131	Total	C	N	O	S	0	0
			979	618	184	172	5		

- Molecule 27 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	X	118	Total	C	N	O	S	0	0
			967	618	181	167	1		

- Molecule 28 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Y	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 29 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Z	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 30 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	a	147	Total	C	N	O	S	0	0
			1163	734	239	186	4		

- Molecule 31 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	b	65	Total	C	N	O	S	0	0
			545	338	122	84	1		

- Molecule 32 is a protein called Large ribosomal subunit protein eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	d	107	Total	C	N	O	S	0	0
			888	560	171	155	2		

- Molecule 33 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	e	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 34 is a protein called Large ribosomal subunit protein eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	f	110	Total	C	N	O	S	0	0
			884	560	175	144	5		

- Molecule 35 is a protein called Large ribosomal subunit protein eL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	g	110	Total	C	N	O	S	0	0
			873	547	180	140	6		

- Molecule 36 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	h	121	Total	C	N	O	S	0	0
			1011	640	204	166	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
h	119	TYR	PHE	conflict	UNP G5B6W3

- Molecule 37 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	i	102	Total	C	N	O	S	0	0
			830	520	176	129	5		

- Molecule 38 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	j	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 39 is a protein called Large ribosomal subunit protein eL38.

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

- Molecule 40 is a protein called Large ribosomal subunit protein eL39.

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

- Molecule 41 is a protein called Ubiquitin-ribosomal protein eL40 fusion protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	m	51	Total	C	N	O	S	0	0
			422	263	88	65	6		

- Molecule 42 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	o	105	Total	C	N	O	S	0	0
			863	543	175	139	6		

- Molecule 43 is a protein called Large ribosomal subunit protein eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	p	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 44 is a protein called Large ribosomal subunit protein eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	r	127	Total	C	N	O	S	0	0
			1015	630	209	170	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
r	1	ACE	-	acetylation	UNP G5BVZ2

- Molecule 45 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	s	103	Total	C	N	O	S	0	0
			825	525	150	143	7		

- Molecule 46 is a protein called 60S ribosomal protein L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	t	156	Total	C	N	O	S	0	0
			1178	733	221	220	4		

- Molecule 47 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	cc	61	Total	C	N	O	S	0	0
			479	292	95	90	2		

- Molecule 48 is a protein called Ubiquitin-ribosomal protein eS31 fusion protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	ff	67	Total	C	N	O	S	0	0
			548	346	102	93	7		

- Molecule 49 is a protein called Small ribosomal subunit protein RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	gg	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 50 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	dd	55	Total	C	N	O	S	0	0
			459	286	94	74	5		

- Molecule 51 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	AA	214	Total	C	N	O	S	0	0
			1689	1074	295	312	8		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AA	1	ACE	-	acetylation	UNP A0A0P6K1L6

- Molecule 52 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	BB	218	Total	C	N	O	S	0	0
			1768	1120	320	314	14		

- Molecule 53 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	DD	225	Total	C	N	O	S	0	0
			1751	1116	315	313	7		

- Molecule 54 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	FF	184	Total	C	N	O	S	0	0
			1461	914	276	264	7		

- Molecule 55 is a protein called Small ribosomal subunit protein eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	KK	96	Total	C	N	O	S	0	0
			810	530	143	131	6		

- Molecule 56 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	MM	124	Total	C	N	O	S	0	0
			958	600	170	179	9		

- Molecule 57 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	OO	134	Total	C	N	O	S	0	0
			1002	612	197	187	6		

- Molecule 58 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	PP	118	Total	C	N	O	S	0	0
			979	621	185	166	7		

- Molecule 59 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	QQ	141	Total	C	N	O	S	0	0
			1124	715	212	194	3		

- Molecule 60 is a protein called Small ribosomal subunit protein eS17.

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

- Molecule 61 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SS	145	Total	C	N	O	S	0	0
			1193	748	241	203	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SS	1	ACE	-	acetylation	UNP G5BAZ4

- Molecule 62 is a protein called Small ribosomal subunit protein eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	TT	141	Total	C	N	O	S	0	0
			1097	687	211	196	3		

- Molecule 63 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	UU	99	Total	C	N	O	S	0	0
			790	495	151	140	4		

- Molecule 64 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	ZZ	75	Total	C	N	O	S	0	0
			598	382	111	104	1		

- Molecule 65 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	bb	82	Total	C	N	O	S	0	0
			640	402	118	113	7		

- Molecule 66 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	ee	49	Total	C	N	O	S	0	0
			398	243	90	64	1		

- Molecule 67 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	aa	98	Total	C	N	O	S	0	0
			781	486	161	129	5		

- Molecule 68 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	CC	218	Total	C	N	O	S	0	0
			1689	1095	289	296	9		

- Molecule 69 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	EE	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		

- Molecule 70 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	GG	228	Total	C	N	O	S	0	0
			1848	1155	368	318	7		

- Molecule 71 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	HH	184	Total	C	N	O	S	0	0
			1490	953	271	265	1		

- Molecule 72 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	II	206	Total	C	N	O	S	0	0
			1686	1058	332	291	5		

- Molecule 73 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	JJ	180	Total	C	N	O	S	0	0
			1499	955	300	242	2		

- Molecule 74 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	LL	141	Total	C	N	O	S	0	0
			1157	737	218	196	6		

- Molecule 75 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	NN	149	Total	C	N	O	S	0	0
			1202	770	228	203	1		

- Molecule 76 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	VV	83	Total	C	N	O	S	0	0
			637	392	117	123	5		

- Molecule 77 is a protein called Small ribosomal subunit protein uS8.

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

- Molecule 78 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	XX	122	Total	C	N	O	S	0	0
			810	510	150	147	3		

- Molecule 79 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	YY	125	Total	C	N	O	S	0	0
			1015	642	199	169	5		

- Molecule 80 is a protein called Ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	W	180	Total	C	N	O	S	0	0
			1508	933	328	238	9		

- Molecule 81 is a protein called Large ribosomal subunit protein eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	c	113	Total	C	N	O	S	0	0
			921	575	190	153	3		

- Molecule 82 is a protein called Large ribosomal subunit protein eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	u	100	Total	C	N	O	S	0	0
			775	491	136	141	7		

- Molecule 83 is a RNA chain called P/E tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	Cc	76	Total	C	N	O	P	0	0
			1623	723	295	529	76		

- Molecule 84 is a RNA chain called tRNA (65-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
84	Bb	65	Total	C	N	O	P	0	0
			1409	633	258	453	65		

- Molecule 85 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	Dd	13	Total	C	N	O	P	0	0
			260	117	26	104	13		

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

Mol	Chain	Residues	Atoms		AltConf
86	A5	9	Total	Mg	0
			9	9	
86	A7	4	Total	Mg	0
			4	4	
86	A8	4	Total	Mg	0
			4	4	
86	B2	7	Total	Mg	0
			7	7	
86	A6	7	Total	Mg	0
			7	7	
86	P	1	Total	Mg	0
			1	1	
86	l	1	Total	Mg	0
			1	1	
86	BB	1	Total	Mg	0
			1	1	
86	Cc	1	Total	Mg	0
			1	1	
86	Bb	1	Total	Mg	0
			1	1	

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

Mol	Chain	Residues	Atoms		AltConf
87	B2	1	Total	Zn	0
			1	1	
87	g	1	Total	Zn	0
			1	1	
87	j	1	Total	Zn	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
87	m	1	Total 1	Zn 1	0
87	o	1	Total 1	Zn 1	0
87	p	1	Total 1	Zn 1	0
87	ff	1	Total 1	Zn 1	0
87	aa	1	Total 1	Zn 1	0

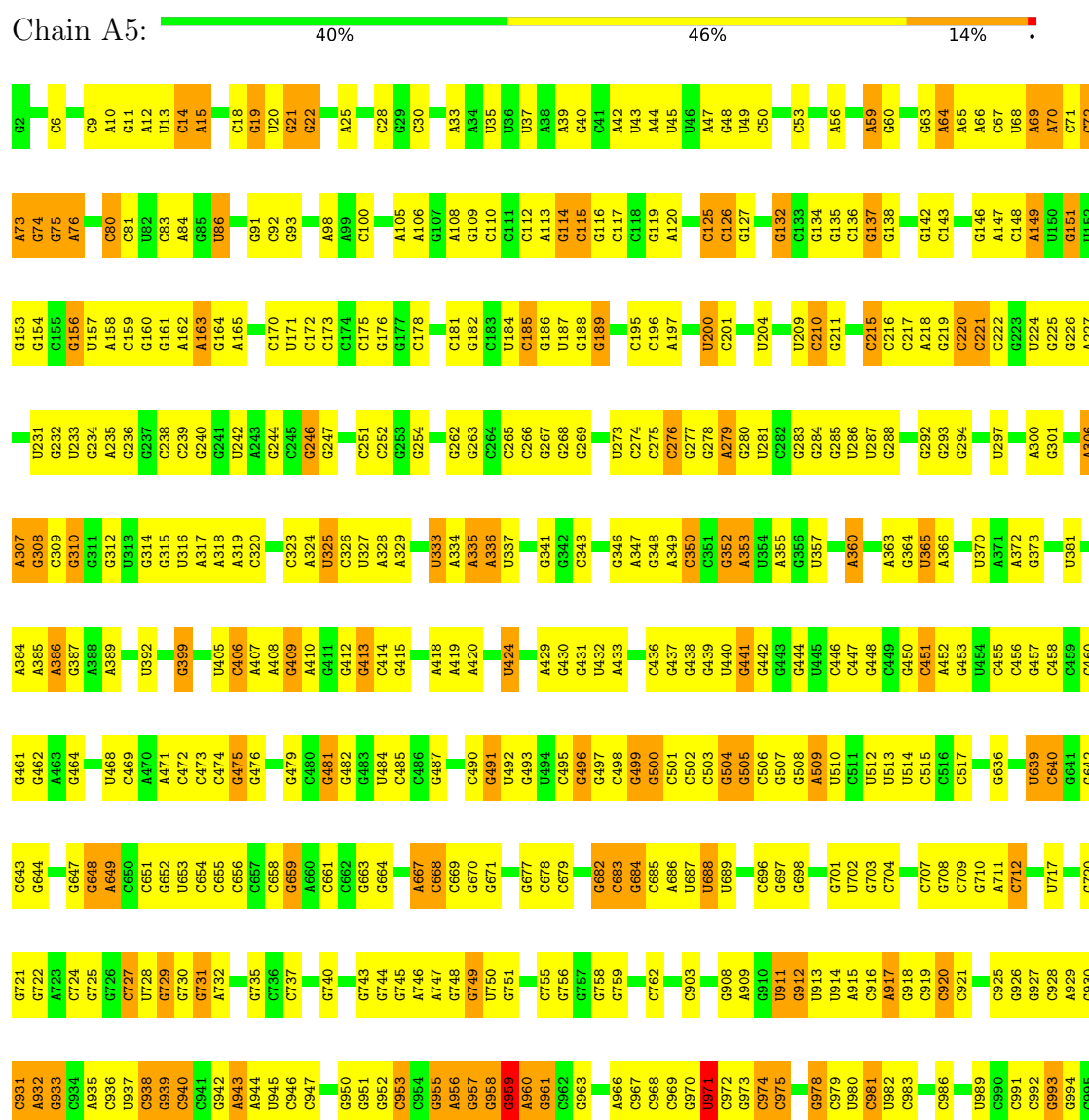
- Molecule 88 is water.

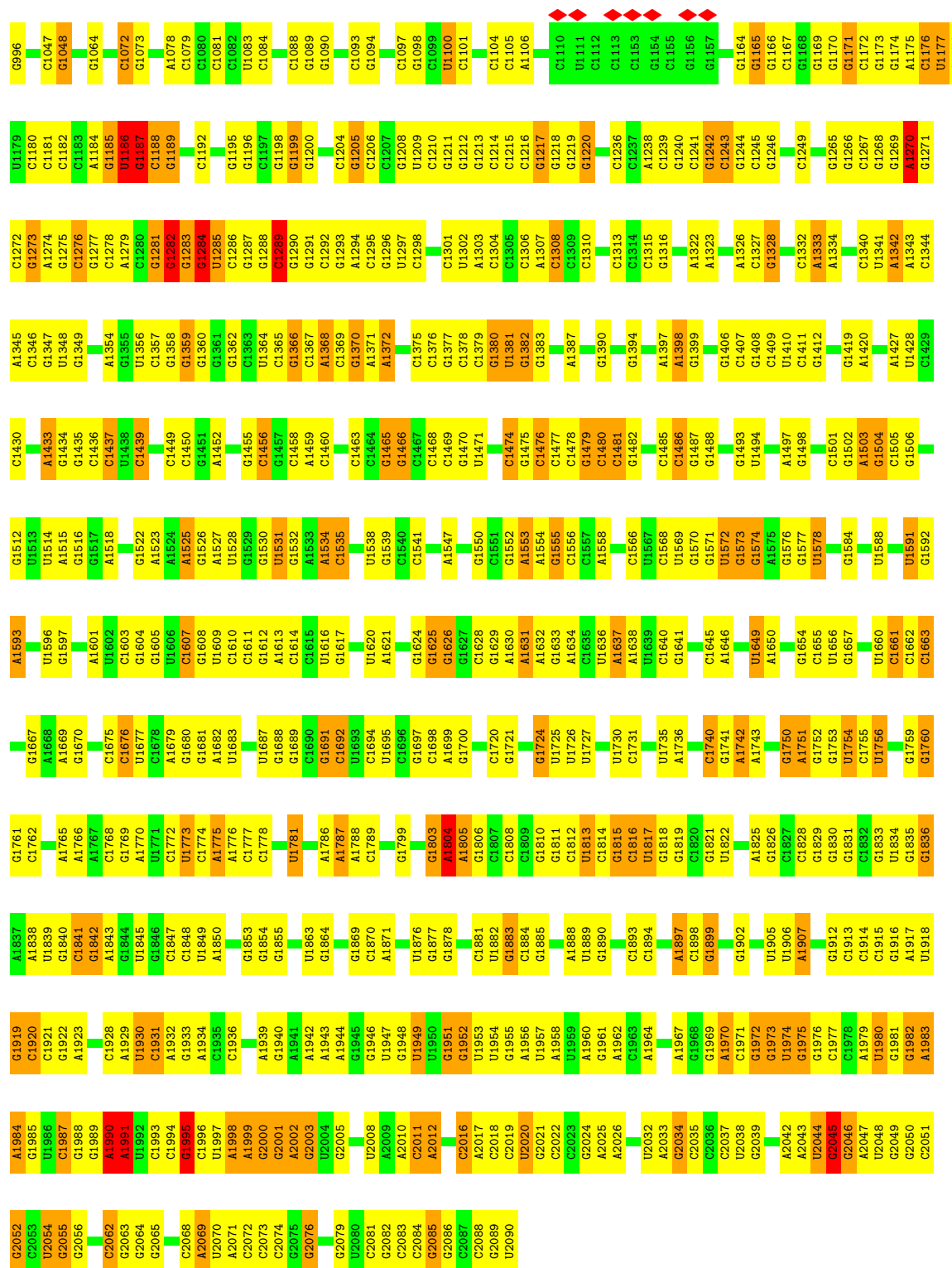
Mol	Chain	Residues	Atoms		AltConf
88	B2	4	Total 4	O 4	0
88	A6	1	Total 1	O 1	0
88	Cc	5	Total 5	O 5	0
88	Bb	5	Total 5	O 5	0

3 Residue-property plots

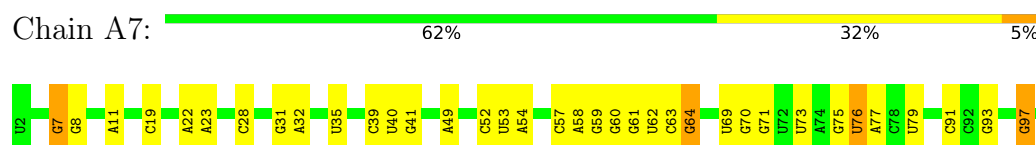
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: LSU alpha rRNA





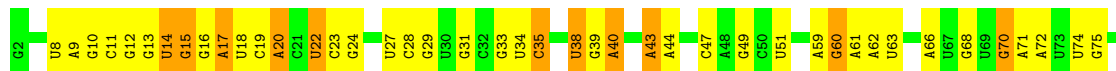
• Molecule 2: 5S ribosomal RNA





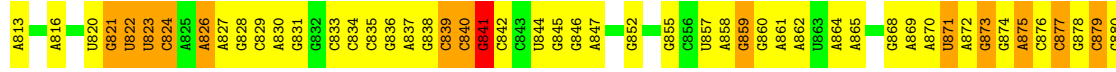
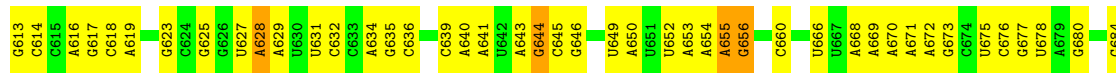
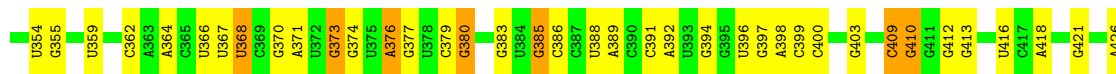
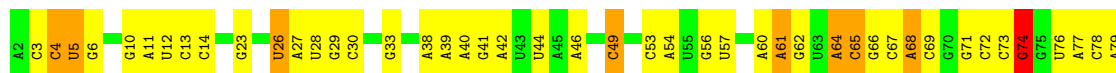
• Molecule 3: 5.8S ribosomal RNA

Chain A8: 44% 43% 13%



• Molecule 4: 18S ribosomal RNA

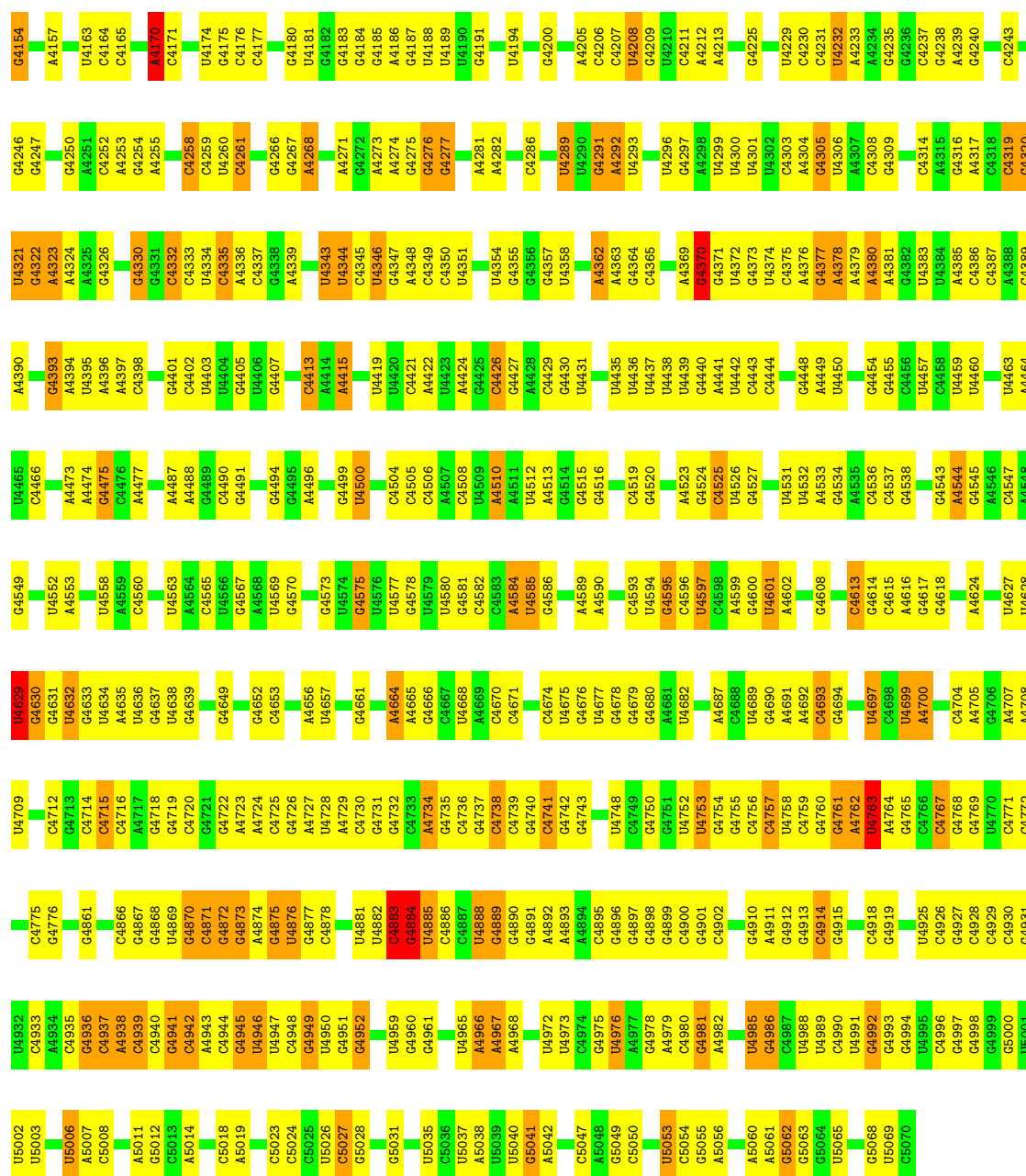
Chain B2: 42% 45% 12%



- Molecule 5: LSU beta rRNA

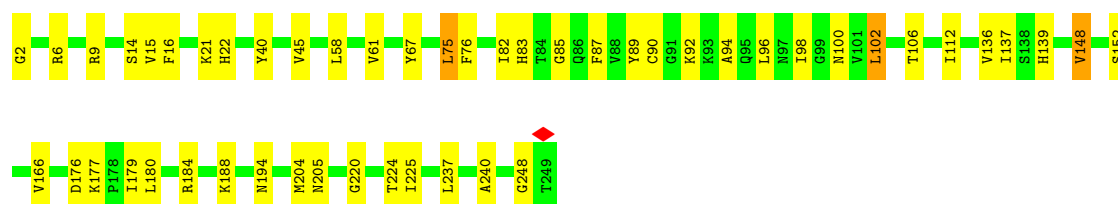


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U4071	A3942	U3790	A3702	U3806	G2898	A2806	G2785	G2662	G2590	G2514	G2415	C2334	A2263
A4072	A3943	C3791	G3705	A3611	G2899	G2811	G2736	G2663	G2596	G2515	U2416	C2335	G2264
A4073	G3944	C3794	C3706	C3612	G2900	C2814	U2740	G2665	A2598	G2517	A2417	G2336	G2265
U4074	G3945	C3795	U3707	U3613	G2902	A2815	U2741	G2668	A2599	C2520	C2422	G2341	U2267
A4075	G3946	C3796	C3708	U3616	G2903	G2816	G2742	G2669	A2601	G2521	A2423	G2342	U2268
U4076	A3947	U3798	U3709	G3617	G2904	C2820	A2744	G2670	A2602	G2522	G2424	G2343	C2269
A4077	G3948	A3799	G3710	C3618	G2905	G2827	G2745	G2671	A2603	G2523	U2425	U2344	G2270
	A3949	U3800	U3711	G3619	U2908	G2752	C2748	G2672	C2604	U2524	A2428	A2347	C2274
G4080	U3950	A3801	A3712	G3620	U2909	G2753	G2749	G2673	G2605	G2525	A2429	G2348	G2275
G4081	G3955	U3802	G3713	G3621	G2910	G2754	C2750	A2674	G2606	U2526	A2431	A2349	A2276
A4082	G3956	A3803	G3714	G3622	G2913	G2755	G2751	G2675	G2607	G2527	G2432	G2351	C2277
G4083	U3957	G3804		G3623	U2914	G2756	G2752	G2676	G2608	G2528	C2433	G2355	A2278
A4084	G3958	C3805	G3720	G3624	U2915	A2832	C2756	G2677	G2609	U2529	C2437	G2356	A2279
A4085	U3959	U3810	U3721	G3625	U2916	A2833	A2757	G2678	A2611	U2530	U2440	G2358	G2283
G4086	A3960	G3811	G3722	G3626	A2923	C2834	G2758	G2679	G2612	G2531	C2441	U2359	G2284
G4087	A3961	C3812	A3723	A3629	A2924	A2835	G2759	G2680	G2613	G2532	G2442	A2360	
A4088	A3962	A3813	A3724	A3630	A2925	A2836	G2760	G2681	G2614	G2533	G2443	A2361	G2288
G4089	G3896	U3814		A3631	G2926	G2837	G2761	G2682	G2615	U2536	G2444	A2362	G2289
G4090	G3897	U3817	A3727	A3632	G2927	U2838	U2762	G2683	G2616	G2541	A2449	A2363	
U4091	U3964	A3818	C3731	C3633	G2928	G2839	G2763	G2684	G2617	G2542	G2450		
A3965	A3966	G3819	A3732	G3634	G2929	G2840	U2764	G2685	G2618	G2543	G2455		
G4095	G3967	G3820	A3733	A3635	G2930	G2841	U2765	G2686	G2619	G2544	G2456		
G4096	G3970	C3833	G3743	C3636	G2931	A2842	A2766	G2687	G2620	G2545	G2457		
G4097	G3971	C3834	A3746	U3639	G2932	G2843	G2767	G2688	G2621	U2546	G2458		
A4098	A3905	C3835	A3747	A3646	U2933	A2844	U2768	G2689	G2622	G2547	G2459		
G4104	A3906	U3838	G3748	A3647	G2934	G2845	C2769	G2690	G2623				
A4105	G3907	G3839	C3749	A3652	G2935	G2846	U2769	G2691	G2624				
A4106	A3908	U3840	G3750	A3652	G2936	G2847	U2770	G2692	G2625				
G4107	C3911	G3841	G3751	C3658	G2937	G2848	C2771	U2693	G2626				
G4108	U3912	C3842	G3752	G3659	G2938	A2849	C2772	U2694	G2627				
		C3843	G3753	C3660	G2939	A2850	C2773	U2695	G2628				
		A3844	A3754	G3661	G2940	G2855	C2774	U2696	G2629				
		A3845	A3755	A3662	G2941	G2863	G2775	U2697	G2630				
		U3846	A3756	A3663	G2942	A2864	G2776	U2698	G2631				
		A3847	A3757	A3664	G2943	U2865	G2777	U2699	G2632				
		A3848	A3758	G3672	G2944	G2866	G2778	U2700	G2633				
		A3849	A3759	G3673	G2945	U2867	C2779	U2701	U2634				
		A3850	A3760	A3674	G2946	A2868	C2780	G2702	U2635				
		A3851	C3761	G3675	G2947	U2869	C2781	G2703	U2636				
		A3852	U3770	G3676	G2948	G2870	G2782	G2704	U2637				
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		C3855	U3773	U3679	G3292	G2873	G2785	G2707	G2640				
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		C3857	A3775	U3681	G3294	U2875	A2787	U2709	G2642				
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		A3865	A3783	A3689	G3302	G2886	C2795	G2717	G2650				
		A3866	A3784	U3690	G3303	U2887	G2796	G2718	G2651				
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		C3870	U3788	U3694	G3307	U2891	G2800	G2722	G2583				
		A3871	C3788	G3695	G3308	U2892	A2788	G2723	G2584				
		A3872		G3696	G3309	U2893	G2789	G2724	G2585				
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				G3698	G3311	U2895	G2791	G2726	G2587				
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				G3700	G3313	U2897	G2793	G2728					
				G3701	G3314	U2898	G2794	G2729					
				G3702	G3315	U2899	G2795	G2730					
				G3703	G3316	U2900	G2796						
				G3704	G3317	U2901	G2797						
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				G3708	G3321	U2905	G2801						
				G3709	G3322	U2906	G2802						
				G3710	G3323	U2907	G2803						
				G3711	G3324	U2908	G2804						
				G3712	G3325	U2909	G2805						
				G3713	G3326	U2910	G2806						
				G3714	G3327	U2911	G2807						
				G3715	G3328	U2912	G2808						
				G3716	G3329	U2913	G2809						
				G3717	G3330	U2914	G2810						
				G3718	G3331	U2915	G2811						
				G3719	G3332	U2916	G2812						
				G3720	G3333	U2917	G2813						
				G3721	G3334	U2918	G2814						
				G3722	G3335	U2919	G2815						
				G3723	G3336	U2920	G2816						
				G3724	G3337	U2921	G2817						
				G3725	G3338	U2922	G2818						
				G3726	G3339	U2923	G2819						
				G3727	G3340	U2924	G2820						
				G3728	G3341	U2925	G2821						
				G3729	G3342	U2926	G2822						
				G3730	G3343	U2927	G2823						
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				G3732	G3345	U2929	G2825						
				G3733	G3346	U2930	G2826						
				G3734	G3347	U2931	G2827						
				G3735	G3348	U2932	G2828						
				G3736	G3349	U2933	G2829						
				G3737	G3350	U2934	G2830						
				G3738	G3351	U2935	G2831						
				G3739	G3352	U2936	G2832						
				G3740	G3353	U2937	G2833						
				G3741	G3354	U2938	G2834						
				G3742	G3355	U2939	G2835						
				G3743	G3356	U2940	G2836						
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				G3745	G3358	U2942	G2838						
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				G3747	G3360	U2944	G2840						
				G3748	G3361	U2945	G2841						
				G3749	G3362	U2946	G2842						
				G3750	G3363	U2947	G2843						
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				G3757	G3370	U2954	G2850						
				G3758	G3371	U2955	G2851						
				G3759	G3372	U2956	G2852						
				G3760	G3373	U2957	G2853						
				G3761	G3374	U2958	G2854						




• Molecule 6: Large ribosomal subunit protein uL2

Chain A: 80% 19%




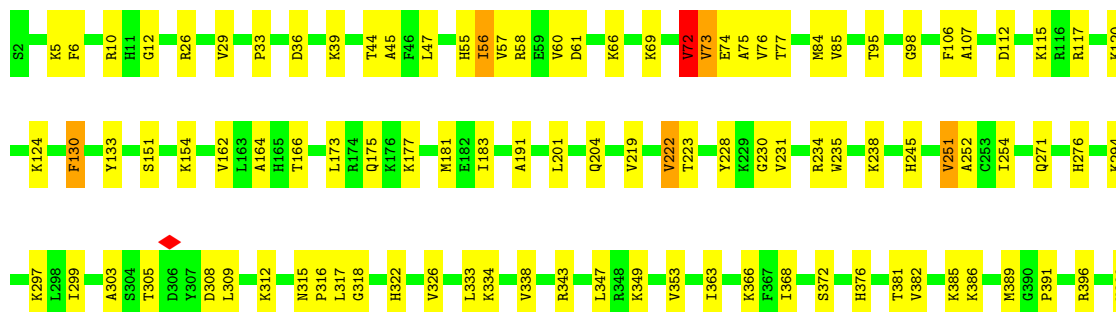
• Molecule 7: 60S ribosomal protein L41

Chain n:  52% 48%



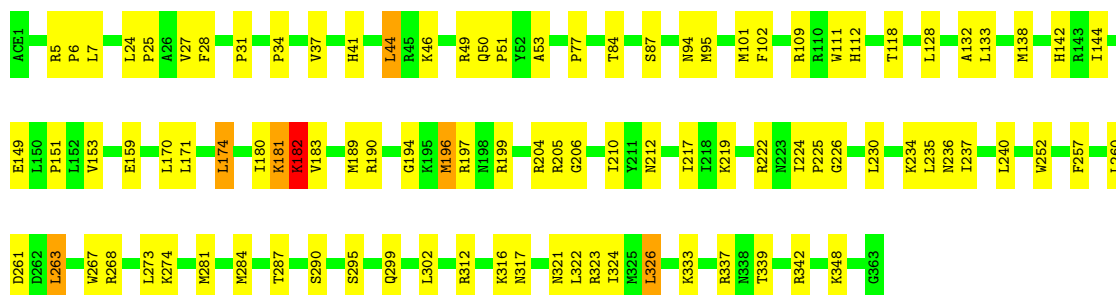
• Molecule 8: 60S ribosomal protein L3

Chain B:  75% 24%



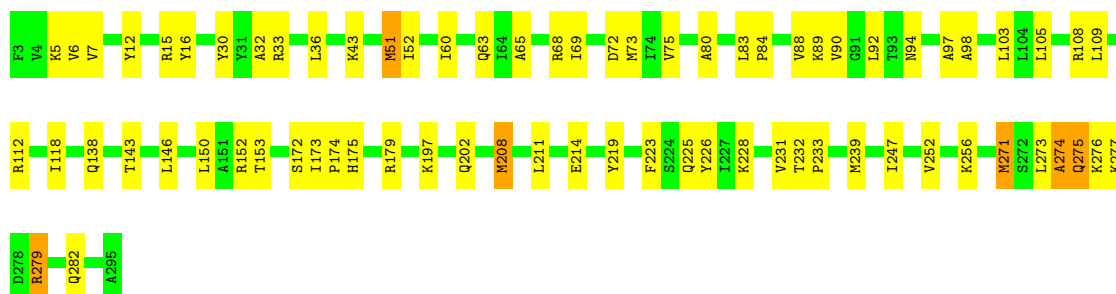
• Molecule 9: Large ribosomal subunit protein uL4

Chain C:  73% 25%



• Molecule 10: Large ribosomal subunit protein uL18

Chain D:  75% 23%



• Molecule 11: 60S ribosomal protein L6

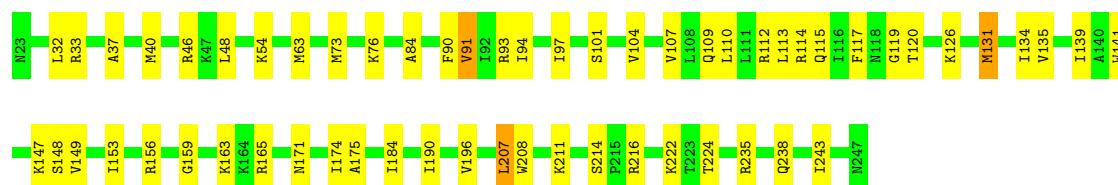
Chain E:  69% 28%





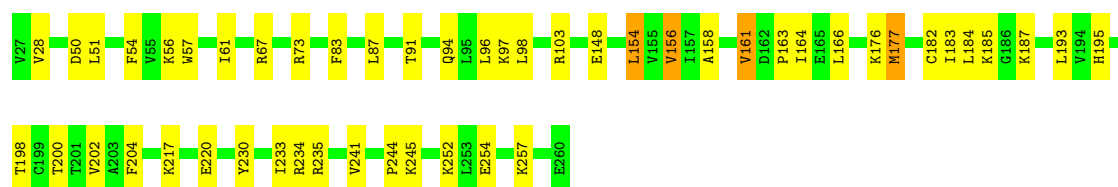
- Molecule 12: 60S ribosomal protein L7

Chain F: 74% 24% .



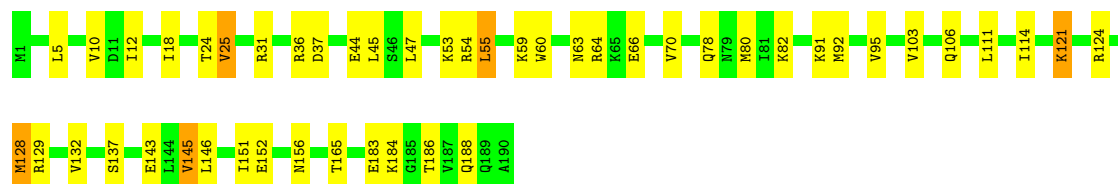
- Molecule 13: 60S ribosomal protein L7a

Chain G: 77% 21% .



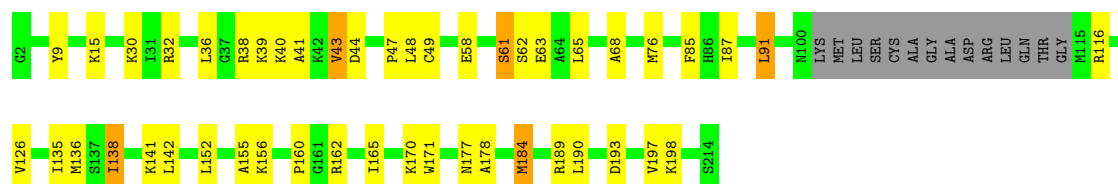
- Molecule 14: 60S ribosomal protein L9

Chain H: 75% 23% .

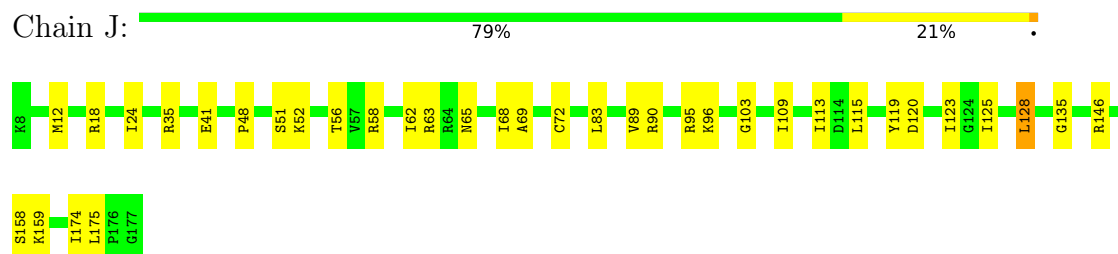


- Molecule 15: 60S ribosomal protein L10

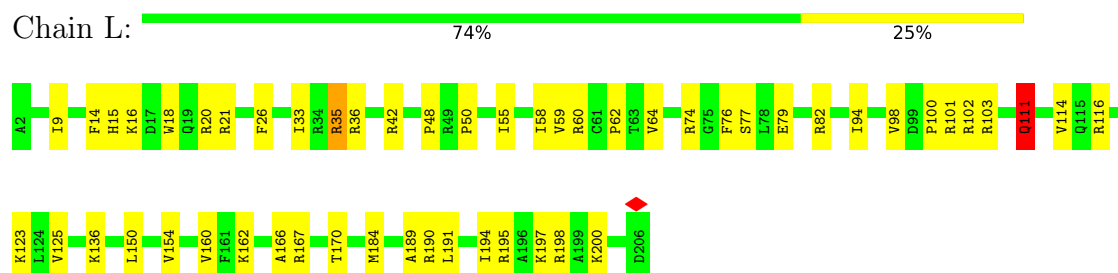
Chain I: 71% 20% 7% .



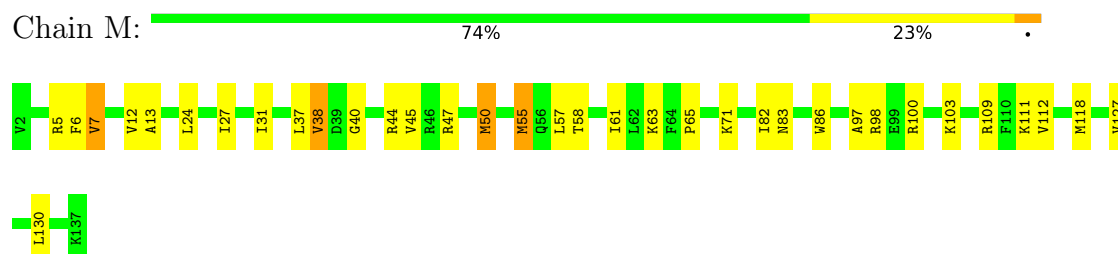
- Molecule 16: Large ribosomal subunit protein uL5



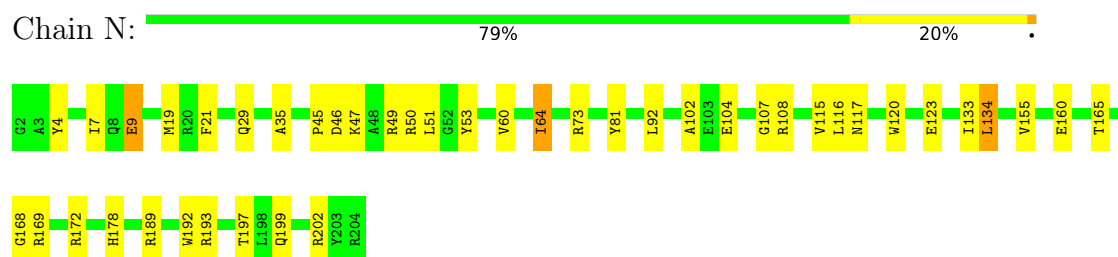
- Molecule 17: 60S ribosomal protein L13



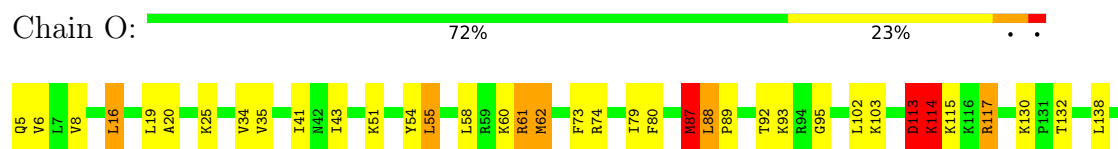
- Molecule 18: Large ribosomal subunit protein eL14



- Molecule 19: Ribosomal protein L15



- Molecule 20: 60S ribosomal protein L13a

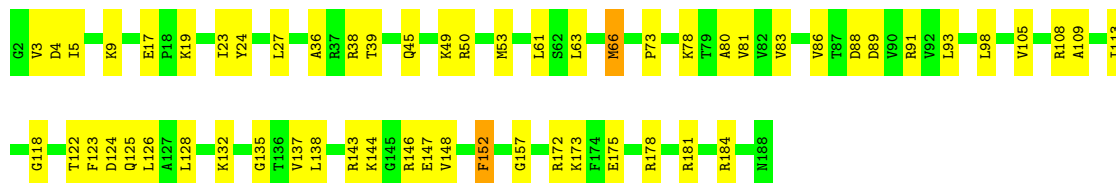




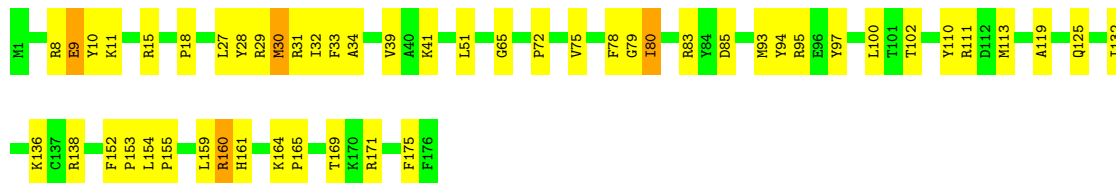
- Molecule 21: 60S ribosomal protein L17



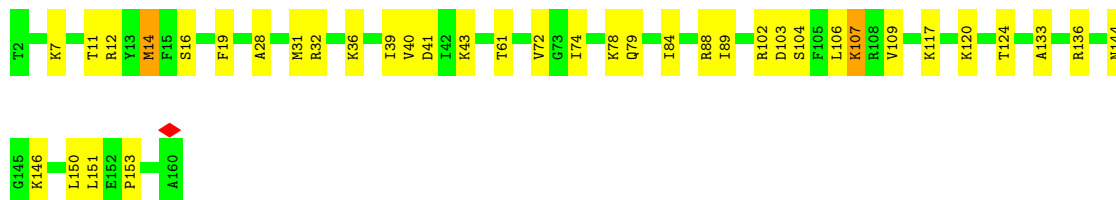
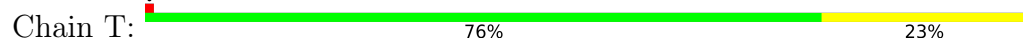
- Molecule 22: 60S ribosomal protein L18



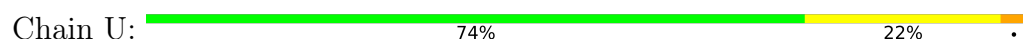
- Molecule 23: Large ribosomal subunit protein eL20



- Molecule 24: Large ribosomal subunit protein eL21

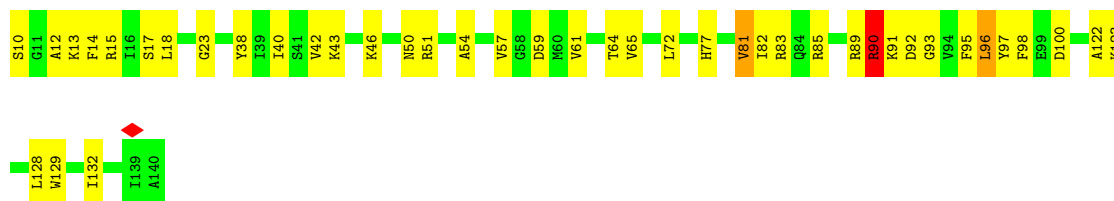


- Molecule 25: 60S ribosomal protein L22

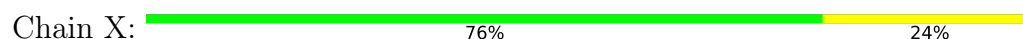




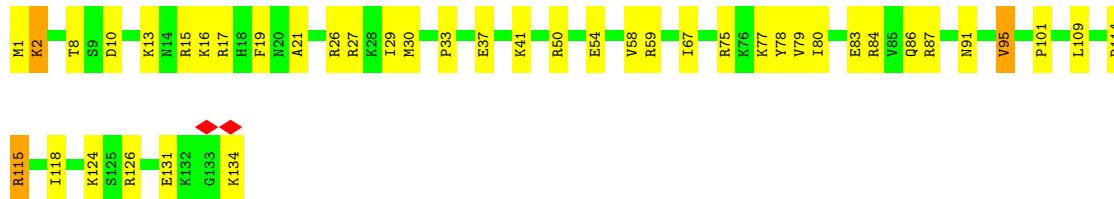
- Molecule 26: Large ribosomal subunit protein uL14



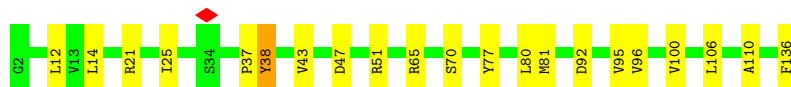
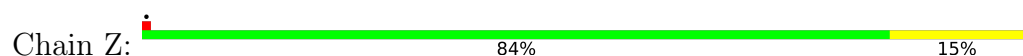
- Molecule 27: Large ribosomal subunit protein uL23



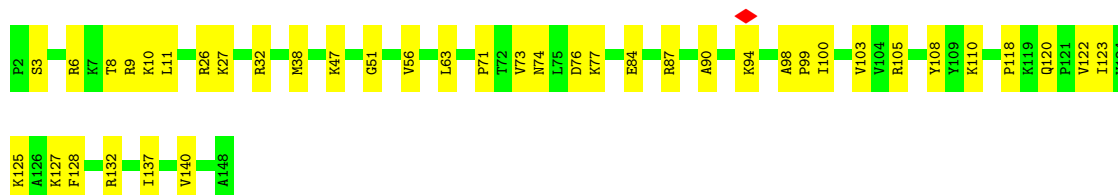
- Molecule 28: 60S ribosomal protein L26



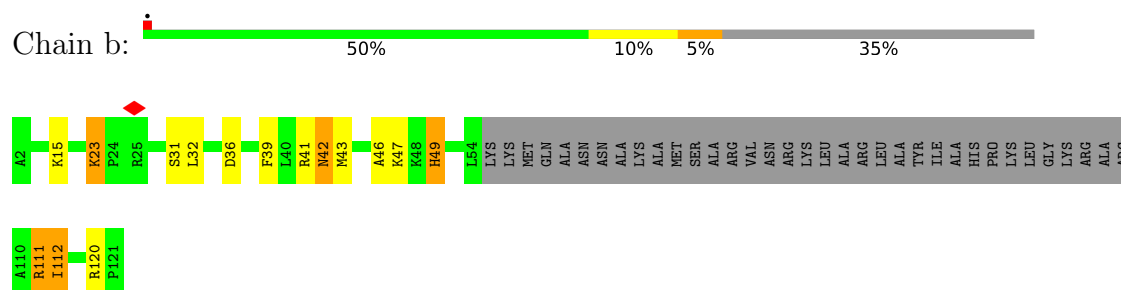
- Molecule 29: 60S ribosomal protein L27



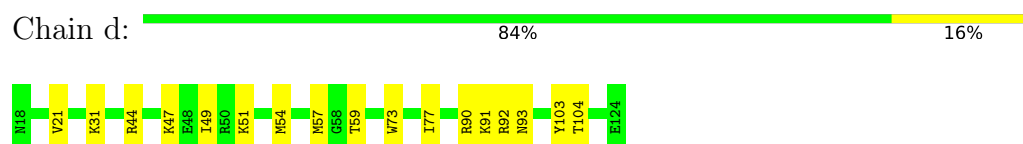
- Molecule 30: 60S ribosomal protein L27a



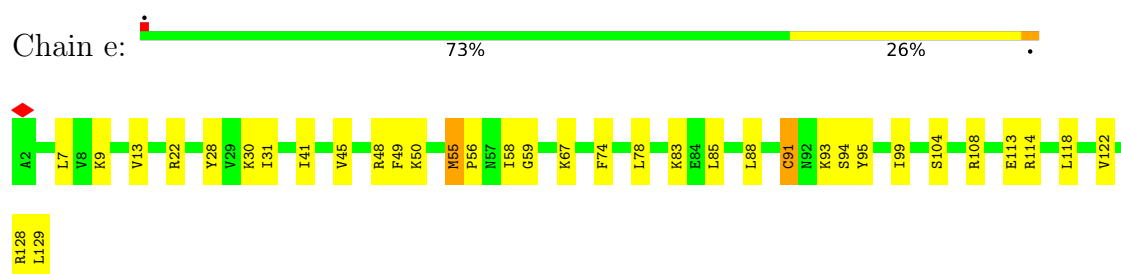
- Molecule 31: 60S ribosomal protein L29



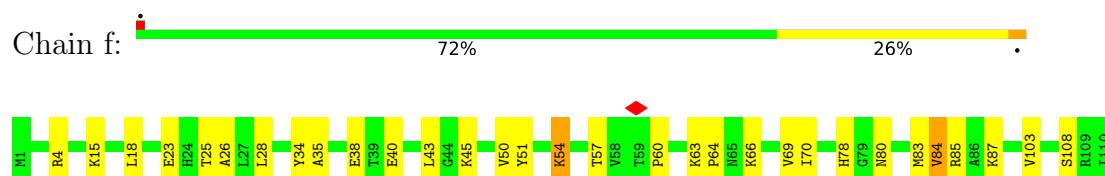
- Molecule 32: Large ribosomal subunit protein eL31



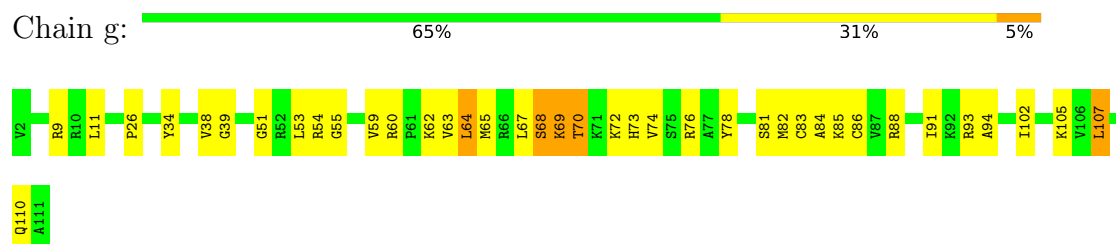
- Molecule 33: 60S ribosomal protein L32



- Molecule 34: Large ribosomal subunit protein eL33

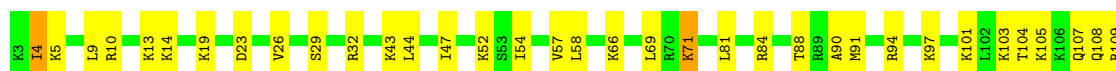


- Molecule 35: Large ribosomal subunit protein eL34



- Molecule 36: Large ribosomal subunit protein uL29

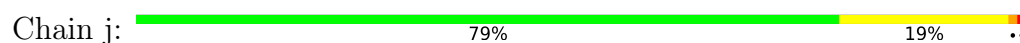




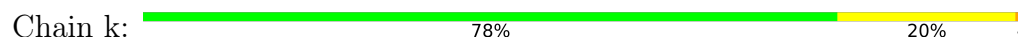
- Molecule 37: 60S ribosomal protein L36



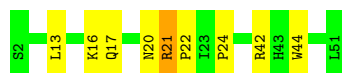
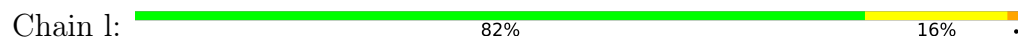
- Molecule 38: Ribosomal protein L37



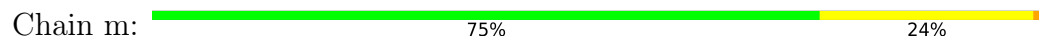
- Molecule 39: Large ribosomal subunit protein eL38



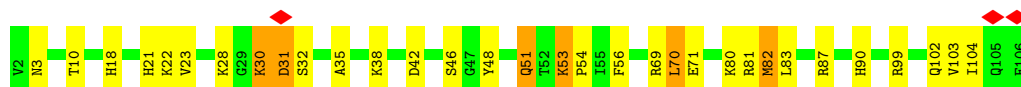
- Molecule 40: Large ribosomal subunit protein eL39




- Molecule 41: Ubiquitin-ribosomal protein eL40 fusion protein



- Molecule 42: 60S ribosomal protein L36a



- Molecule 43: Large ribosomal subunit protein eL43

Chain p:  76% 23%



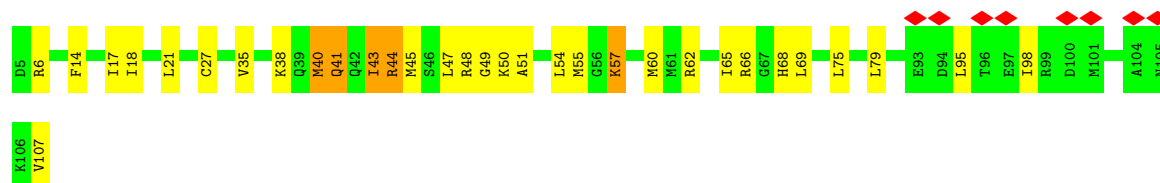
- Molecule 44: Large ribosomal subunit protein eL28

Chain r:  72% 25%




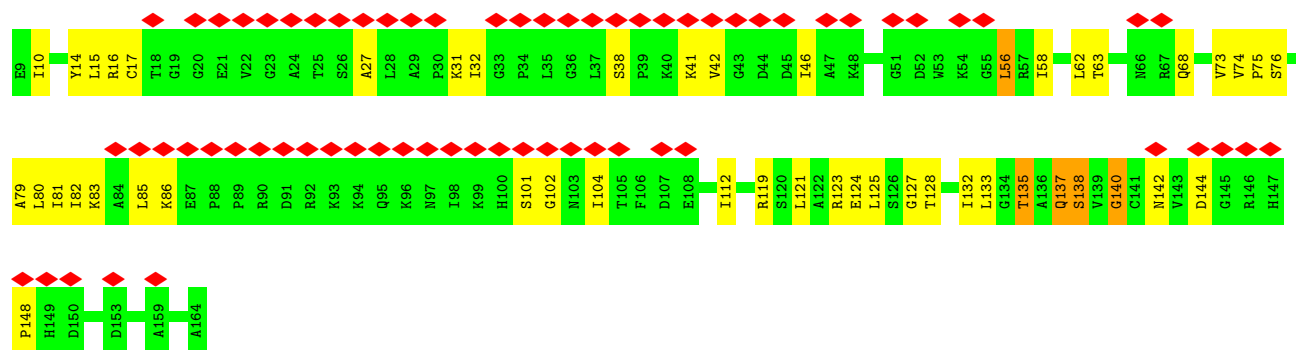
- Molecule 45: 60S acidic ribosomal protein P0

Chain s:  8% 69% 26% 5%



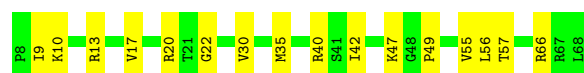
- Molecule 46: 60S ribosomal protein L12

Chain t:  43% 69% 28%

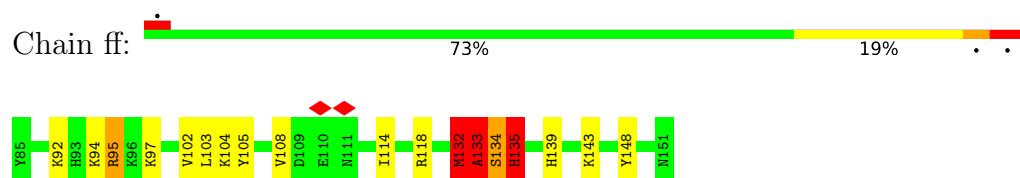


- Molecule 47: 40S ribosomal protein S28

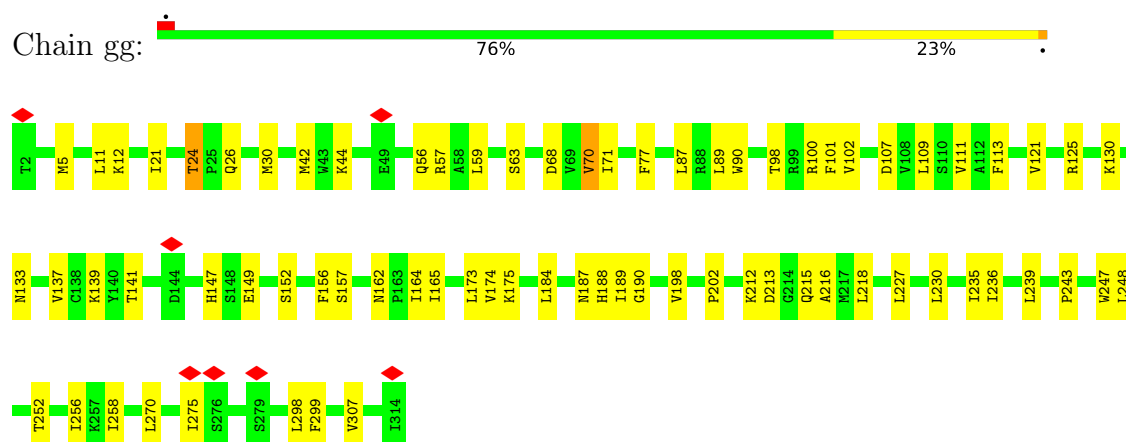
Chain cc:  74% 26%



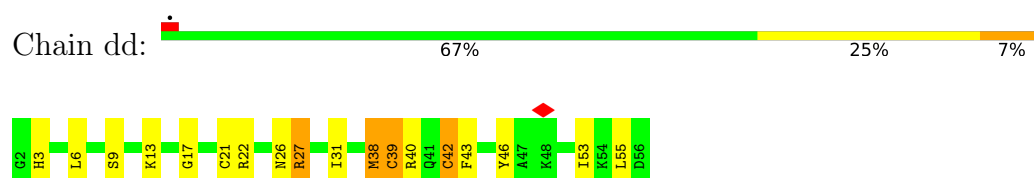
- Molecule 48: Ubiquitin-ribosomal protein eS31 fusion protein



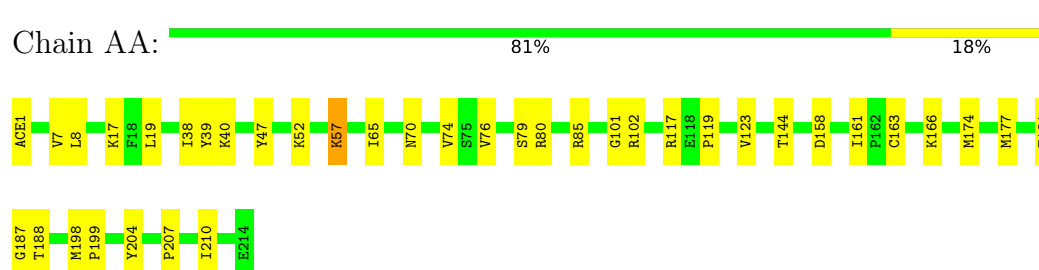
- Molecule 49: Small ribosomal subunit protein RACK1



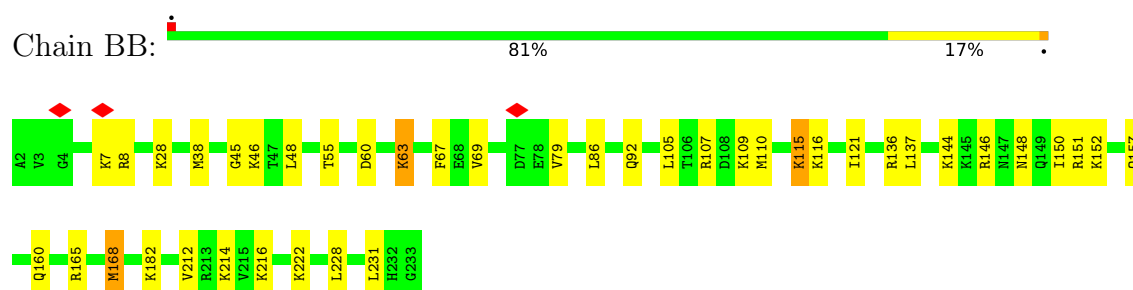
- Molecule 50: Small ribosomal subunit protein uS14



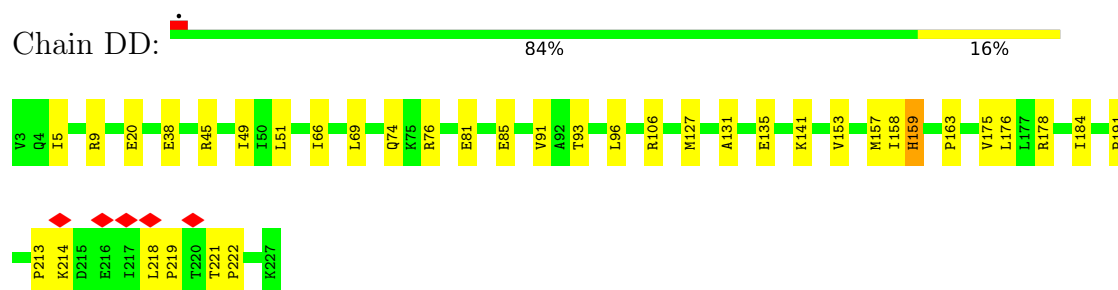
- Molecule 51: Small ribosomal subunit protein uS2



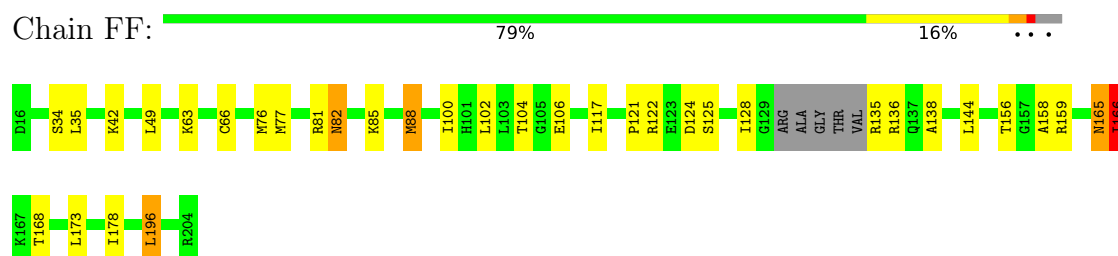
- Molecule 52: 40S ribosomal protein S3a



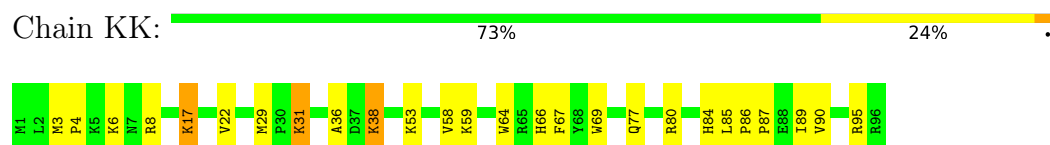
- Molecule 53: Small ribosomal subunit protein uS3



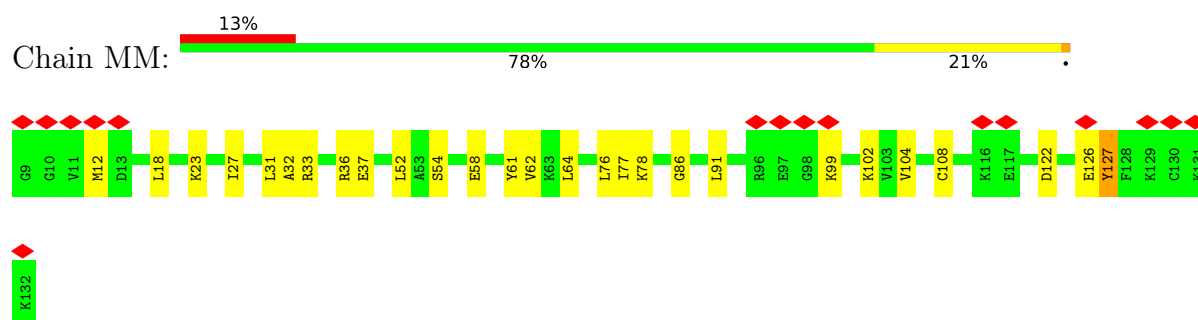
- Molecule 54: Small ribosomal subunit protein uS7



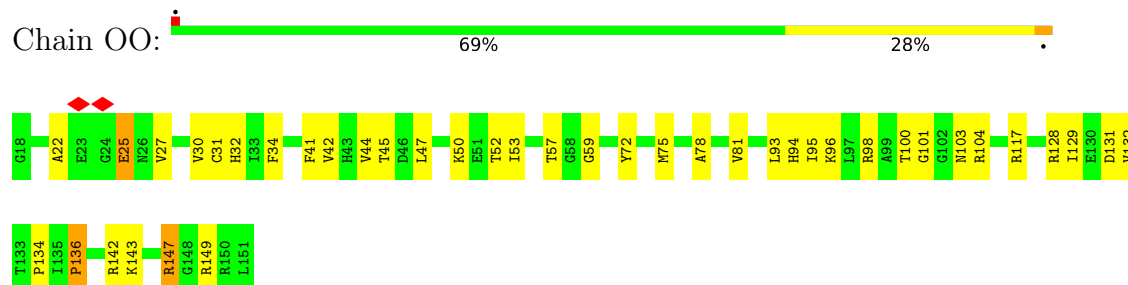
- Molecule 55: Small ribosomal subunit protein eS10



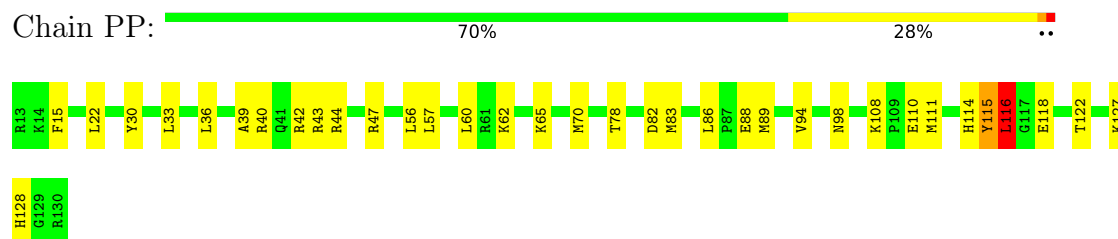
- Molecule 56: 40S ribosomal protein S12



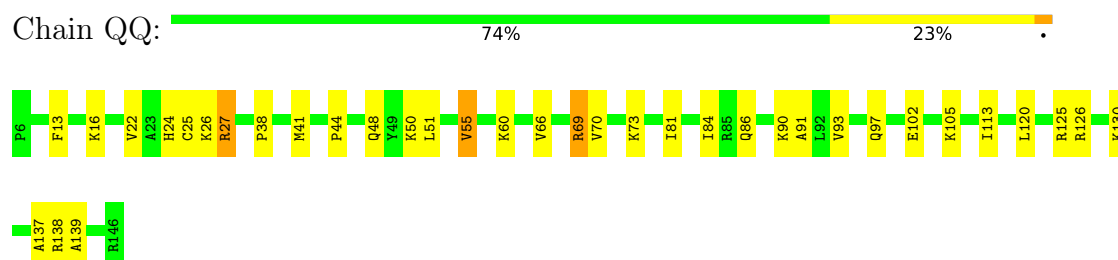
- Molecule 57: 40S ribosomal protein S14



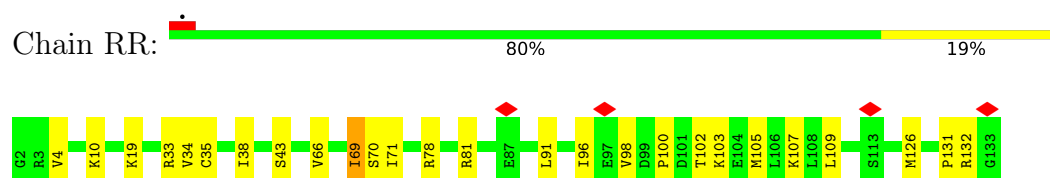
- Molecule 58: 40S ribosomal protein S15



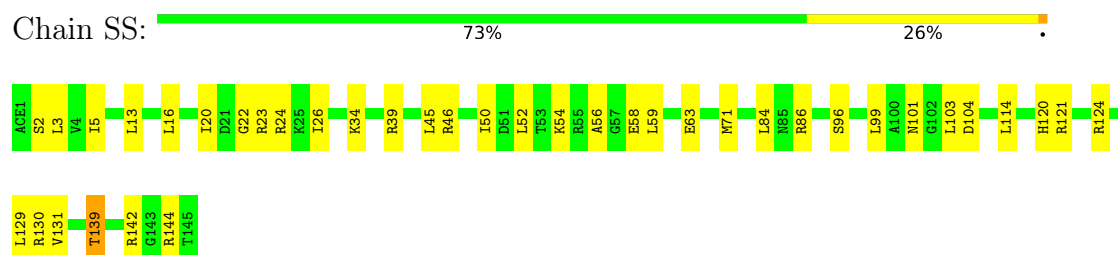
- Molecule 59: Small ribosomal subunit protein uS9



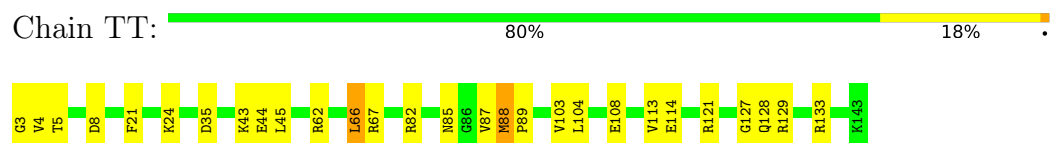
- Molecule 60: Small ribosomal subunit protein eS17



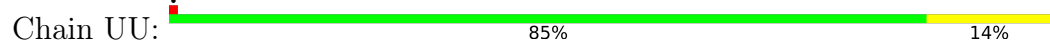
- Molecule 61: Small ribosomal subunit protein uS13



- Molecule 62: Small ribosomal subunit protein eS19

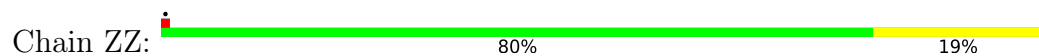


- Molecule 63: 40S ribosomal protein S20

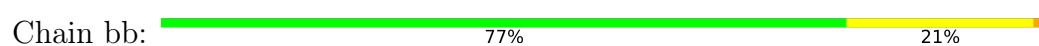




- Molecule 64: 40S ribosomal protein S25



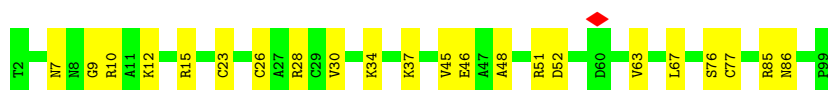
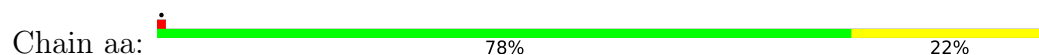
- Molecule 65: 40S ribosomal protein S27



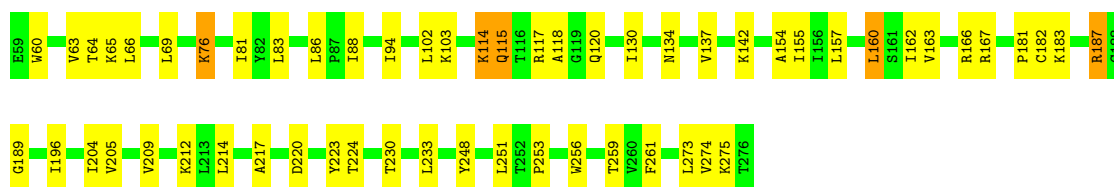
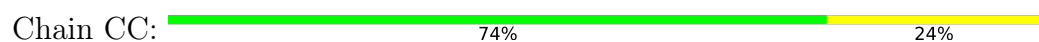
- Molecule 66: 40S ribosomal protein S30



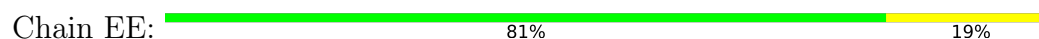
- Molecule 67: 40S ribosomal protein S26

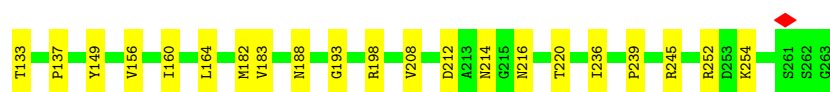


- Molecule 68: 40S ribosomal protein S2



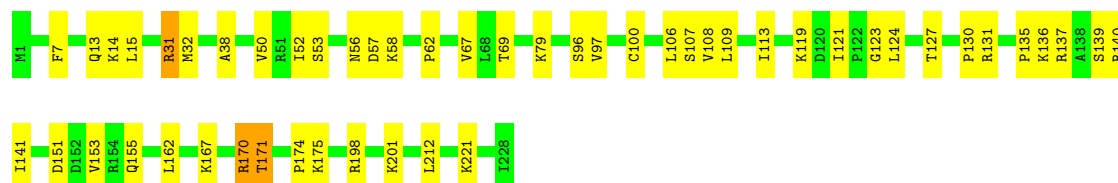
- Molecule 69: 40S ribosomal protein S4, X isoform





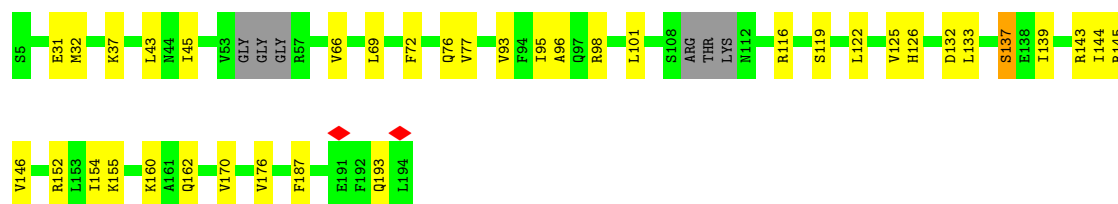
- Molecule 70: 40S ribosomal protein S6

Chain GG: 78% 21%



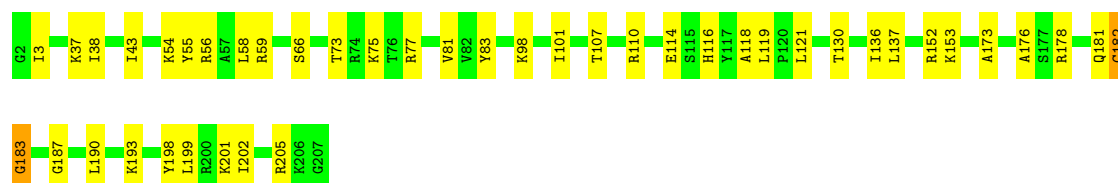
- Molecule 71: 40S ribosomal protein S7

Chain HH: 77% 19%



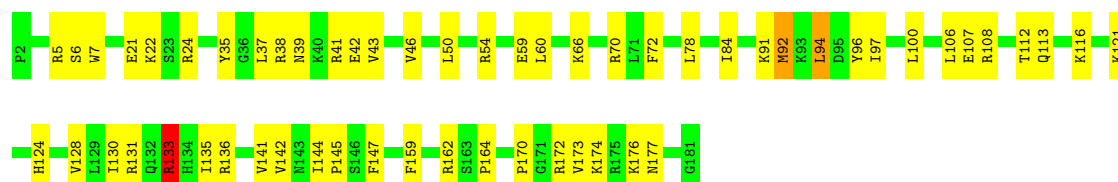
- Molecule 72: 40S ribosomal protein S8

Chain II: 79% 20%



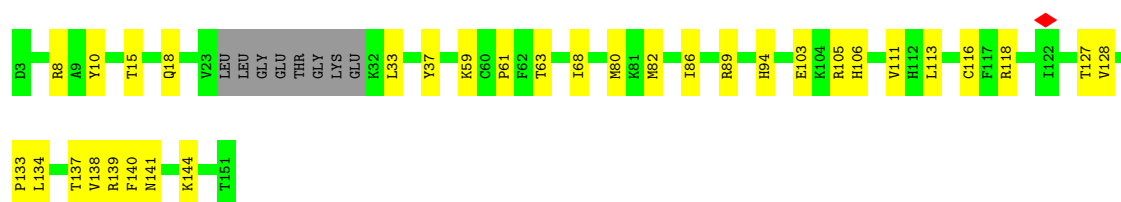
- Molecule 73: Small ribosomal subunit protein uS4

Chain JJ: 68% 30%



- Molecule 74: Small ribosomal subunit protein uS17

Chain LL: 73% 21% 5%



- Molecule 75: Small ribosomal subunit protein uS15

Chain NN: 80% 20%



- Molecule 76: 40S ribosomal protein S21

Chain VV: 83% 17%



- Molecule 77: Small ribosomal subunit protein uS8

Chain WW: 83% 16%



- Molecule 78: 40S ribosomal protein S23

Chain XX: 93% 7%



- Molecule 79: 40S ribosomal protein S24

Chain YY: 72% 26%



- Molecule 80: Ribosomal protein L19

Chain W: 72% 24%

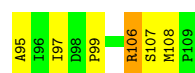




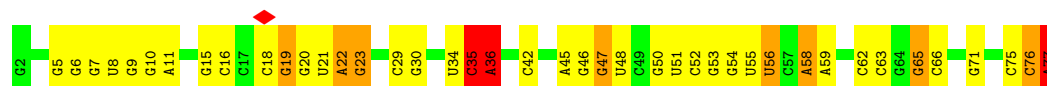
- Molecule 81: Large ribosomal subunit protein eL24



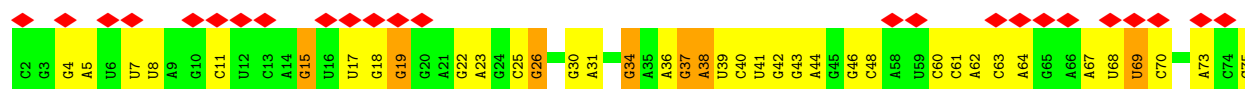
- Molecule 82: Large ribosomal subunit protein eL30



- Molecule 83: P/E tRNA



- Molecule 84: tRNA (65-MER)



- Molecule 85: mRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	48893	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.060	Depositor
Minimum map value	-0.019	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.009	Depositor
Map size (Å)	459.8, 459.8, 459.8	wwPDB
Map dimensions	440, 440, 440	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.045, 1.045, 1.045	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: NMM, V5N, ACE, M3L, ZN, MG, HIC, YYG, MLZ

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	A5	1.44	46/40529 (0.1%)	0.59	60/63155 (0.1%)
2	A7	0.23	0/2857	0.41	0/4452
3	A8	0.26	0/3704	0.51	1/5770 (0.0%)
4	B2	1.59	56/42333 (0.1%)	0.53	32/65918 (0.0%)
5	A6	1.39	49/48645 (0.1%)	0.53	39/75740 (0.1%)
6	A	0.28	0/1684	0.72	2/2307 (0.1%)
7	n	0.42	0/240	1.21	2/305 (0.7%)
8	B	0.26	0/3261	0.65	1/4364 (0.0%)
9	C	0.46	2/2936 (0.1%)	0.82	10/3941 (0.3%)
10	D	0.34	1/2435 (0.0%)	0.80	10/3261 (0.3%)
11	E	4.78	12/1823 (0.7%)	1.15	16/2445 (0.7%)
12	F	0.31	0/1911	0.85	5/2549 (0.2%)
13	G	0.25	0/1772	0.63	2/2387 (0.1%)
14	H	2.77	1/1535 (0.1%)	0.73	2/2063 (0.1%)
15	I	0.25	0/1658	0.68	2/2214 (0.1%)
16	J	0.27	0/1385	0.69	0/1852
17	L	0.31	0/1689	0.75	1/2261 (0.0%)
18	M	0.34	0/1146	0.90	8/1531 (0.5%)
19	N	0.32	0/1746	0.68	2/2338 (0.1%)
20	O	1.21	5/1661 (0.3%)	1.39	12/2219 (0.5%)
21	P	3.01	6/1268 (0.5%)	0.93	9/1700 (0.5%)
22	Q	0.31	0/1537	0.86	6/2052 (0.3%)
23	S	0.29	0/1501	0.73	2/2013 (0.1%)
24	T	0.29	0/1326	0.79	1/1770 (0.1%)
25	U	0.33	0/822	0.92	9/1103 (0.8%)
26	V	0.36	0/993	0.96	2/1332 (0.2%)
27	X	0.25	0/984	0.67	0/1323
28	Y	0.30	0/1132	0.78	1/1504 (0.1%)
29	Z	0.29	0/1130	0.78	4/1507 (0.3%)
30	a	0.30	0/1179	0.77	3/1572 (0.2%)
31	b	3.07	4/544 (0.7%)	1.73	11/717 (1.5%)
32	d	0.30	0/903	0.79	1/1216 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	e	0.30	0/1071	0.83	2/1429 (0.1%)
34	f	0.42	0/903	0.92	4/1208 (0.3%)
35	g	1.64	3/883 (0.3%)	1.46	6/1177 (0.5%)
36	h	0.23	0/1019	0.70	0/1344
37	i	0.39	0/841	1.05	7/1112 (0.6%)
38	j	0.36	0/720	0.82	2/952 (0.2%)
39	k	0.32	0/575	0.81	3/761 (0.4%)
40	l	0.29	0/454	0.82	0/599
41	m	0.40	0/416	1.06	1/553 (0.2%)
42	o	0.39	0/866	0.90	3/1141 (0.3%)
43	p	0.34	0/718	0.96	3/953 (0.3%)
44	r	0.30	0/1028	0.88	4/1377 (0.3%)
45	s	4.01	4/837 (0.5%)	1.46	9/1121 (0.8%)
46	t	0.42	1/1193 (0.1%)	0.83	5/1609 (0.3%)
47	cc	0.29	0/481	0.67	1/643 (0.2%)
48	ff	0.62	2/560 (0.4%)	1.16	10/745 (1.3%)
49	gg	0.24	0/2493	0.66	3/3394 (0.1%)
50	dd	0.71	2/470 (0.4%)	1.38	10/623 (1.6%)
51	AA	0.27	0/1724	0.69	3/2343 (0.1%)
52	BB	2.57	1/1794 (0.1%)	0.77	5/2396 (0.2%)
53	DD	0.25	0/1779	0.64	2/2395 (0.1%)
54	FF	3.00	3/1481 (0.2%)	1.16	10/1988 (0.5%)
55	KK	0.37	0/834	0.91	4/1125 (0.4%)
56	MM	0.34	0/968	0.80	3/1296 (0.2%)
57	OO	0.30	0/1015	0.79	2/1361 (0.1%)
58	PP	1.45	2/997 (0.2%)	1.30	6/1330 (0.5%)
59	QQ	0.21	0/1142	0.59	0/1528
60	RR	0.29	0/1082	0.80	1/1452 (0.1%)
61	SS	0.30	0/1209	0.71	2/1620 (0.1%)
62	TT	0.29	0/1102	0.73	4/1476 (0.3%)
63	UU	0.23	0/800	0.63	1/1074 (0.1%)
64	ZZ	0.41	0/604	0.71	1/810 (0.1%)
65	bb	0.25	0/653	0.68	4/876 (0.5%)
66	ee	0.29	0/399	0.82	0/520
67	aa	0.23	0/794	0.59	0/1065
68	CC	1.18	2/1725 (0.1%)	1.02	6/2332 (0.3%)
69	EE	0.24	0/2118	0.59	1/2849 (0.0%)
70	GG	0.33	1/1870 (0.1%)	0.62	1/2489 (0.0%)
71	HH	0.23	0/1509	0.59	3/2016 (0.1%)
72	II	1.01	2/1715 (0.1%)	1.01	5/2287 (0.2%)
73	JJ	0.30	0/1524	0.75	5/2035 (0.2%)
74	LL	0.29	0/1177	0.76	1/1575 (0.1%)
75	NN	0.20	0/1226	0.53	0/1649

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	VV	0.27	0/644	0.73	2/862 (0.2%)
77	WW	0.31	0/1051	0.76	2/1406 (0.1%)
78	XX	0.24	0/819	0.69	2/1115 (0.2%)
79	YY	1.50	3/1032 (0.3%)	1.00	8/1371 (0.6%)
80	W	1.14	3/1524 (0.2%)	1.38	9/2013 (0.4%)
81	c	0.36	0/935	0.99	4/1241 (0.3%)
82	u	3.42	1/786 (0.1%)	1.33	8/1055 (0.8%)
83	Cc	1.75	6/1812 (0.3%)	1.13	12/2821 (0.4%)
84	Bb	2.65	1/1531 (0.1%)	0.50	2/2380 (0.1%)
85	Dd	0.19	0/285	0.35	0/438
All	All	1.37	219/235457 (0.1%)	0.68	448/346211 (0.1%)

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
6	A	0	2
7	n	0	1
8	B	0	2
9	C	0	2
10	D	0	1
11	E	0	1
17	L	0	1
20	O	0	1
22	Q	0	1
23	S	0	1
26	V	0	1
28	Y	0	1
29	Z	0	1
32	d	0	1
36	h	0	1
41	m	0	1
42	o	0	2
44	r	0	1
45	s	0	2
46	t	0	1
48	ff	0	4
53	DD	0	1
54	FF	0	1
56	MM	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
57	OO	0	2
62	TT	0	1
68	CC	0	1
73	JJ	0	1
76	VV	0	1
80	W	0	1
81	c	0	1
82	u	0	2
All	All	0	42

All (219) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	E	104	ASN	CA-CB	113.02	3.18	1.53
52	BB	115	LYS	CB-CG	108.20	4.77	1.52
14	H	121	LYS	CG-CD	107.94	4.76	1.52
54	FF	82	ASN	CB-CG	107.34	4.20	1.52
11	E	127	LYS	CG-CD	106.23	4.71	1.52
45	s	41	GLN	CG-CD	104.77	4.13	1.52
84	Bb	38	A	C5'-C4'	103.15	3.57	1.51
82	u	32	LYS	CE-NZ	94.67	4.33	1.49
31	b	112	ILE	CA-CB	69.71	2.53	1.54
11	E	131	HIS	CB-CG	69.24	2.47	1.50
5	A6	2300	A	N7-C5	66.88	2.73	1.39
83	Cc	77	A	C5-C6	59.37	2.59	1.41
1	A5	1270	A	N1-C2	59.26	2.52	1.34
1	A5	1270	A	C6-N1	59.19	2.54	1.35
1	A5	684	G	N9-C8	59.06	2.56	1.37
4	B2	841	G	N1-C2	57.30	2.52	1.37
21	P	139	TYR	CD2-CE2	57.08	3.09	1.38
5	A6	2300	A	C8-N7	56.56	2.44	1.31
4	B2	841	G	C6-N1	56.52	2.52	1.39
5	A6	4370	G	N1-C2	56.26	2.50	1.37
1	A5	684	G	N7-C5	56.07	2.51	1.39
4	B2	841	G	C5-C6	56.03	2.54	1.42
5	A6	2300	A	N9-C4	55.85	2.49	1.37
4	B2	841	G	C2-N3	55.73	2.44	1.32
4	B2	841	G	N3-C4	55.71	2.46	1.35
4	B2	1599	U	N1-C2	55.53	2.49	1.38
1	A5	1995	G	C2-N3	55.51	2.43	1.32
5	A6	4370	G	C6-N1	55.43	2.50	1.39
5	A6	2300	A	N9-C8	55.13	2.48	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A6	2768	C	N1-C2	55.03	2.50	1.40
1	A5	684	G	C8-N7	54.98	2.40	1.30
1	A5	1270	A	C5-C6	54.86	2.50	1.41
5	A6	4370	G	C2-N3	54.74	2.42	1.32
5	A6	4370	G	N3-C4	54.64	2.44	1.35
1	A5	684	G	N9-C4	54.49	2.46	1.38
5	A6	4370	G	C5-C6	54.30	2.50	1.42
5	A6	2768	C	C2-N3	54.29	2.44	1.35
1	A5	1270	A	N3-C4	54.09	2.43	1.34
4	B2	1621	U	C2-N3	53.72	2.45	1.37
1	A5	1270	A	C2-N3	53.48	2.40	1.33
4	B2	1599	U	N3-C4	52.80	2.44	1.38
5	A6	2768	C	N3-C4	52.66	2.39	1.33
1	A5	1282	G	C2-N3	52.36	2.37	1.32
4	B2	1599	U	C2-N3	52.22	2.42	1.37
21	P	139	TYR	CD1-CE1	52.20	2.95	1.38
4	B2	1621	U	N1-C2	52.06	2.42	1.38
1	A5	1282	G	C6-N1	51.74	2.43	1.39
11	E	136	PHE	CE2-CZ	51.64	2.93	1.38
11	E	136	PHE	CE1-CZ	51.52	2.93	1.38
4	B2	305	U	N1-C2	51.51	2.41	1.38
1	A5	1995	G	N3-C4	51.38	2.38	1.35
1	A5	1282	G	N1-C2	51.37	2.40	1.37
5	A6	4757	C	N1-C2	51.09	2.42	1.40
1	A5	1282	G	N3-C4	50.98	2.37	1.35
4	B2	1621	U	N3-C4	50.96	2.40	1.38
4	B2	305	U	N3-C4	50.92	2.40	1.38
5	A6	2300	A	C5-C4	50.77	2.40	1.38
5	A6	4757	C	N3-C4	50.70	2.35	1.33
4	B2	1203	G	N3-C4	50.67	2.36	1.35
4	B2	1203	G	C2-N3	50.65	2.34	1.32
11	E	136	PHE	CD2-CE2	50.55	2.90	1.38
4	B2	305	U	C2-N3	50.34	2.38	1.37
5	A6	4757	C	C2-N3	50.33	2.36	1.35
4	B2	1599	U	N1-C6	50.32	2.38	1.38
5	A6	4370	G	C5-C4	49.75	2.37	1.38
1	A5	1282	G	C5-C6	49.69	2.41	1.42
1	A5	1270	A	C5-C4	49.43	2.37	1.38
5	A6	2889	G	C6-N1	49.40	2.38	1.39
5	A6	2768	C	N1-C6	49.35	2.35	1.37
4	B2	1621	U	N1-C6	49.32	2.36	1.38
4	B2	305	U	N1-C6	48.94	2.35	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B2	1203	G	C6-N1	48.90	2.37	1.39
4	B2	841	G	C5-C4	48.77	2.35	1.38
5	A6	2889	G	N3-C4	48.66	2.32	1.35
5	A6	2889	G	N1-C2	48.52	2.34	1.37
4	B2	1203	G	N1-C2	48.45	2.34	1.37
4	B2	305	U	C4-C5	48.45	2.40	1.43
4	B2	1599	U	C4-C5	48.23	2.40	1.43
5	A6	4757	C	C4-C5	47.85	2.38	1.43
5	A6	2889	G	C2-N3	47.70	2.28	1.32
11	E	136	PHE	CD1-CE1	47.60	2.81	1.38
5	A6	4757	C	N1-C6	47.37	2.31	1.37
5	A6	2889	G	C5-C6	47.29	2.37	1.42
4	B2	1621	U	C4-C5	47.22	2.38	1.43
4	B2	74	G	C6-N1	47.03	2.33	1.39
1	A5	684	G	C5-C4	46.97	2.32	1.38
4	B2	1248	U	C2-N3	46.64	2.31	1.37
79	YY	11	LYS	CA-CB	46.56	2.32	1.53
1	A5	1995	G	C6-N1	46.52	2.32	1.39
1	A5	2045	G	N1-C2	46.28	2.30	1.37
1	A5	1995	G	N1-C2	45.80	2.29	1.37
1	A5	2045	G	C6-N1	45.75	2.31	1.39
4	B2	1203	G	C5-C6	45.59	2.33	1.42
1	A5	1995	G	C5-C6	45.55	2.33	1.42
4	B2	1621	U	C5-C6	45.48	2.25	1.34
4	B2	1599	U	C5-C6	45.48	2.25	1.34
4	B2	1248	U	N1-C2	45.38	2.29	1.38
4	B2	1248	U	N3-C4	45.27	2.29	1.38
4	B2	74	G	N3-C4	44.85	2.25	1.35
4	B2	305	U	C5-C6	44.68	2.23	1.34
5	A6	2768	C	C4-C5	44.47	2.31	1.43
4	B2	74	G	N1-C2	44.38	2.26	1.37
5	A6	4757	C	C5-C6	44.06	2.22	1.34
4	B2	74	G	C2-N3	43.89	2.20	1.32
5	A6	2889	G	C5-C4	43.81	2.25	1.38
45	s	40	MET	C-N	43.64	1.94	1.33
68	CC	114	LYS	C-N	43.62	1.94	1.33
1	A5	2045	G	C2-N3	43.38	2.19	1.32
4	B2	1248	U	N1-C6	43.37	2.24	1.38
1	A5	1282	G	C5-C4	43.30	2.25	1.38
5	A6	2768	C	C5-C6	43.02	2.20	1.34
4	B2	1203	G	C5-C4	42.61	2.23	1.38
1	A5	2045	G	C5-C6	42.43	2.27	1.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
20	O	113	ASP	C-N	42.35	1.99	1.33
1	A5	2045	G	N3-C4	42.21	2.19	1.35
1	A5	1995	G	C5-C4	41.87	2.22	1.38
4	B2	1248	U	C4-C5	41.48	2.26	1.43
5	A6	3760	A	C6-N1	41.34	2.18	1.35
4	B2	74	G	C5-C6	41.00	2.24	1.42
5	A6	3760	A	C5-C6	40.24	2.21	1.41
5	A6	3760	A	N3-C4	39.83	2.14	1.34
1	A5	1289	C	C1'-N1	39.79	2.08	1.48
21	P	139	TYR	CE1-CZ	39.60	2.33	1.38
80	W	74	ARG	C-N	39.42	1.99	1.33
5	A6	3760	A	N1-C2	39.29	2.12	1.34
5	A6	3760	A	C2-N3	38.93	2.11	1.33
35	g	69	LYS	C-N	38.85	1.80	1.33
1	A5	2045	G	C5-C4	38.74	2.15	1.38
21	P	139	TYR	CE2-CZ	38.72	2.31	1.38
4	B2	1248	U	C5-C6	38.41	2.10	1.34
54	FF	166	ILE	N-CA	37.45	1.93	1.46
4	B2	74	G	C5-C4	37.15	2.12	1.38
58	PP	115	TYR	C-N	37.03	1.80	1.33
5	A6	3859	G	O3'-P	36.30	2.15	1.61
5	A6	3760	A	C5-C4	35.01	2.08	1.38
11	E	136	PHE	CG-CD2	34.26	2.10	1.38
21	P	139	TYR	CG-CD2	33.94	2.10	1.39
83	Cc	77	A	C2-N3	33.85	2.01	1.33
21	P	139	TYR	CG-CD1	33.66	2.10	1.39
11	E	136	PHE	CG-CD1	32.94	2.08	1.38
72	II	183	GLY	N-CA	29.14	1.87	1.45
72	II	182	CYS	C-N	27.76	1.74	1.33
35	g	70	THR	N-CA	26.34	1.77	1.46
4	B2	1535	U	C2-N3	25.49	1.88	1.37
4	B2	1535	U	N1-C2	25.45	1.89	1.38
1	A5	1972	G	N3-C4	25.22	1.85	1.35
1	A5	1972	G	C2-N3	25.11	1.82	1.32
58	PP	116	LEU	N-CA	25.01	1.76	1.46
4	B2	1535	U	N3-C4	24.83	1.88	1.38
1	A5	1289	C	N1-C2	24.29	1.88	1.40
1	A5	1972	G	C6-N1	23.90	1.87	1.39
4	B2	1535	U	N1-C6	23.84	1.85	1.38
1	A5	1972	G	N1-C2	23.61	1.84	1.37
1	A5	1972	G	C5-C6	22.07	1.86	1.42
1	A5	1972	G	C5-C4	20.62	1.79	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B2	1535	U	C4-C5	20.57	1.84	1.43
45	s	41	GLN	N-CA	20.57	1.72	1.46
5	A6	3859	G	C3'-O3'	20.14	1.72	1.42
5	A6	4613	C	C2-N3	19.20	1.74	1.35
68	CC	115	GLN	N-CA	18.75	1.70	1.46
4	B2	1535	U	C5-C6	18.64	1.71	1.34
5	A6	2677	G	N1-C2	18.49	1.74	1.37
5	A6	4613	C	N3-C4	18.40	1.70	1.33
5	A6	2677	G	C6-N1	18.39	1.76	1.39
1	A5	959	G	C6-N1	18.32	1.76	1.39
4	B2	1869	A	C6-N1	18.11	1.71	1.35
1	A5	959	G	N1-C2	17.98	1.73	1.37
20	O	114	LYS	N-CA	17.95	1.69	1.47
5	A6	4613	C	N1-C2	17.75	1.75	1.40
5	A6	2677	G	C2-N3	17.22	1.67	1.32
4	B2	1869	A	N1-C2	17.11	1.68	1.34
83	Cc	35	C	C3'-O3'	17.08	1.67	1.42
54	FF	165	ASN	C-N	17.01	1.56	1.33
1	A5	959	G	C2-N3	16.79	1.66	1.32
4	B2	1869	A	N3-C4	16.72	1.68	1.34
5	A6	2677	G	N3-C4	16.66	1.68	1.35
83	Cc	77	A	C6-N6	16.62	1.67	1.33
4	B2	1869	A	C5-C6	16.38	1.73	1.41
1	A5	959	G	N3-C4	16.32	1.68	1.35
4	B2	1869	A	C2-N3	16.01	1.65	1.33
5	A6	4613	C	N1-C6	15.87	1.68	1.37
1	A5	959	G	C5-C6	15.85	1.74	1.42
5	A6	2677	G	C5-C6	14.75	1.71	1.42
80	W	75	HIS	N-CA	14.56	1.66	1.46
9	C	181	LYS	CA-C	14.39	1.72	1.52
5	A6	4613	C	C4-C5	14.18	1.71	1.43
4	B2	1869	A	C5-C4	14.17	1.67	1.38
1	A5	959	G	C5-C4	13.61	1.65	1.38
5	A6	2677	G	C5-C4	13.26	1.64	1.38
5	A6	4613	C	C5-C6	13.05	1.60	1.34
9	C	182	LYS	N-CA	12.41	1.61	1.46
31	b	112	ILE	CB-CG2	11.35	1.90	1.52
70	GG	171	THR	N-CA	10.05	1.60	1.46
1	A5	1289	C	C2-N3	9.56	1.54	1.35
83	Cc	77	A	N7-C5	9.32	1.57	1.39
1	A5	1289	C	N1-C6	9.15	1.55	1.37
20	O	62	MET	N-CA	8.99	1.57	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
83	Cc	77	A	N3-C4	8.77	1.52	1.34
11	E	131	HIS	CA-CB	8.33	1.65	1.53
11	E	131	HIS	CG-CD2	8.22	1.44	1.35
50	dd	42	CYS	CB-SG	7.99	2.07	1.81
31	b	112	ILE	CB-CG1	7.62	1.68	1.53
79	YY	11	LYS	CB-CG	7.00	1.73	1.52
35	g	69	LYS	CA-C	6.92	1.61	1.52
11	E	104	ASN	CB-CG	6.52	1.68	1.52
48	ff	133	ALA	C-N	6.47	1.42	1.33
20	O	113	ASP	CA-C	6.29	1.61	1.53
46	t	137	GLN	C-N	6.26	1.45	1.34
50	dd	39	CYS	CB-SG	6.02	2.01	1.81
45	s	40	MET	CA-C	5.94	1.60	1.52
4	B2	1308	U	O3'-P	5.92	1.70	1.61
48	ff	134	SER	N-CA	5.87	1.53	1.45
80	W	74	ARG	CA-C	5.84	1.60	1.53
20	O	61	ARG	CA-C	5.76	1.60	1.52
1	A5	1187	G	C5'-C4'	5.74	1.59	1.51
31	b	112	ILE	CA-C	5.51	1.60	1.53
79	YY	11	LYS	N-CA	5.14	1.52	1.46
4	B2	1308	U	C3'-O3'	5.09	1.50	1.43
10	D	274	ALA	CA-C	5.04	1.58	1.52

All (448) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
83	Cc	77	A	N3-C4-C5	-36.20	18.21	126.80
83	Cc	77	A	C6-N1-C2	-34.66	14.62	118.60
20	O	113	ASP	CA-C-N	33.00	167.57	121.71
20	O	113	ASP	C-N-CA	33.00	167.57	121.71
80	W	74	ARG	CA-C-N	29.73	164.17	122.85
80	W	74	ARG	C-N-CA	29.73	164.17	122.85
5	A6	3859	G	P-O3'-C3'	29.67	164.70	120.20
35	g	69	LYS	CA-C-N	27.74	165.30	121.19
35	g	69	LYS	C-N-CA	27.74	165.30	121.19
1	A5	1289	C	C6-N1-C2	-26.09	41.93	120.20
11	E	131	HIS	CA-CB-CG	25.88	139.68	113.80
72	II	182	CYS	CA-C-N	25.01	170.44	121.41
72	II	182	CYS	C-N-CA	25.01	170.44	121.41
58	PP	115	TYR	CA-C-N	24.51	166.67	121.81
58	PP	115	TYR	C-N-CA	24.51	166.67	121.81
45	s	40	MET	CA-C-N	23.22	165.89	121.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
45	s	40	MET	C-N-CA	23.22	165.89	121.54
68	CC	114	LYS	CA-C-N	22.73	164.96	121.54
68	CC	114	LYS	C-N-CA	22.73	164.96	121.54
54	FF	165	ASN	CA-C-N	21.91	161.40	121.97
54	FF	165	ASN	C-N-CA	21.91	161.40	121.97
31	b	112	ILE	CA-CB-CG1	21.64	147.19	110.40
79	YY	11	LYS	CA-CB-CG	19.43	152.95	114.10
31	b	112	ILE	CA-CB-CG2	18.66	142.22	110.50
20	O	61	ARG	CA-C-O	-16.44	103.64	121.56
11	E	104	ASN	CA-CB-CG	16.41	129.01	112.60
80	W	74	ARG	CA-C-O	-16.10	100.19	120.31
20	O	113	ASP	CA-C-O	-15.68	100.71	120.31
9	C	181	LYS	CA-C-O	-15.44	101.37	119.59
11	E	131	HIS	ND1-CG-CD2	-15.00	91.10	106.10
35	g	69	LYS	CA-C-O	-14.81	104.70	120.55
68	CC	114	LYS	CA-C-O	-14.52	103.00	119.98
70	GG	170	ARG	CA-C-O	-14.27	104.82	120.38
31	b	112	ILE	CG1-CB-CG2	-14.07	68.50	110.70
45	s	40	MET	CA-C-O	-13.93	106.55	120.90
50	dd	39	CYS	CA-CB-SG	13.90	146.38	114.40
58	PP	115	TYR	CA-C-O	-13.75	106.57	121.56
1	A5	1289	C	C6-N1-C1'	13.67	161.81	120.80
1	A5	1289	C	N3-C2-O2	-13.65	80.95	121.90
54	FF	165	ASN	CA-C-O	-13.40	106.21	121.89
83	Cc	77	A	C2-N3-C4	13.19	150.18	110.60
31	b	112	ILE	CB-CA-C	13.15	130.19	111.65
31	b	112	ILE	N-CA-C	-13.12	93.85	112.35
1	A5	1289	C	C2-N1-C1'	12.48	156.26	118.80
50	dd	42	CYS	CA-CB-SG	12.43	142.99	114.40
1	A5	1289	C	N1-C1'-C2'	12.12	130.18	112.00
72	II	182	CYS	CA-C-O	-11.08	107.12	118.97
81	c	15	PRO	N-CA-C	10.69	127.61	110.40
84	Bb	38	A	C5'-C4'-C3'	10.63	137.26	116.00
10	D	271	MET	CA-C-N	10.53	134.41	123.04
10	D	271	MET	C-N-CA	10.53	134.41	123.04
5	A6	3859	G	C4'-C3'-O3'	10.36	128.53	113.00
11	E	104	ASN	CB-CA-C	10.27	130.24	111.03
1	A5	1289	C	N1-C2-N3	10.23	149.90	119.20
79	YY	11	LYS	CB-CA-C	10.20	130.71	110.42
1	A5	1289	C	C5-C6-N1	9.94	150.81	121.00
48	ff	134	SER	N-CA-C	9.83	125.96	110.32
5	A6	4763	U	OP2-P-O3'	-9.67	78.98	108.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	E	104	ASN	N-CA-C	-9.60	96.87	111.56
5	A6	4473	A	OP1-P-O3'	-9.51	79.48	108.00
4	B2	570	C	OP1-P-O3'	-9.39	79.83	108.00
54	FF	82	ASN	CA-CB-CG	9.10	121.70	112.60
31	b	112	ILE	CB-CG1-CD1	9.01	132.72	113.80
54	FF	166	ILE	N-CA-CB	8.76	125.68	111.23
21	P	95	LEU	CA-CB-CG	8.57	146.30	116.30
79	YY	11	LYS	N-CA-CB	8.53	124.91	110.49
4	B2	570	C	OP2-P-O3'	-8.51	82.46	108.00
45	s	41	GLN	CB-CG-CD	8.40	126.88	112.60
11	E	136	PHE	CD1-CG-CD2	8.35	131.12	118.60
83	Cc	77	A	N1-C6-N6	-8.23	93.89	118.60
20	O	55	LEU	CA-CB-CG	8.14	144.79	116.30
83	Cc	77	A	C4-C5-N7	-8.12	86.33	110.70
4	B2	1308	U	C3'-C2'-O2'	8.03	126.64	114.60
12	F	109	GLN	CA-CB-CG	7.86	129.81	114.10
54	FF	166	ILE	CA-CB-CG1	7.85	123.75	110.40
21	P	86	LYS	CA-CB-CG	7.83	129.76	114.10
37	i	7	MET	CB-CG-SD	7.78	136.03	112.70
37	i	7	MET	CA-CB-CG	7.75	129.59	114.10
1	A5	1995	G	N3-C4-N9	7.73	149.19	126.00
10	D	274	ALA	N-CA-C	7.71	125.57	114.16
80	W	152	LYS	CA-CB-CG	7.69	129.48	114.10
58	PP	116	LEU	N-CA-C	7.62	123.22	111.56
48	ff	133	ALA	CA-C-N	7.59	135.05	122.07
48	ff	133	ALA	C-N-CA	7.59	135.05	122.07
44	r	118	LEU	CA-CB-CG	7.56	142.77	116.30
1	A5	1289	C	O4'-C1'-N1	7.52	119.79	108.50
69	EE	87	MET	CA-CB-CG	7.50	129.10	114.10
11	E	131	HIS	CG-CD2-NE2	7.47	114.67	107.20
48	ff	133	ALA	CA-C-O	-7.47	109.83	120.51
4	B2	1308	U	P-O3'-C3'	7.37	131.26	120.20
72	II	183	GLY	N-CA-C	7.34	130.58	113.18
52	BB	168	MET	CA-CB-CG	7.34	128.78	114.10
4	B2	1308	U	O3'-P-O5'	7.27	114.91	104.00
82	u	18	LEU	CA-CB-CG	7.18	141.41	116.30
37	i	97	MET	CA-CB-CG	7.12	128.33	114.10
37	i	97	MET	CB-CG-SD	7.11	134.02	112.70
50	dd	38	MET	CA-C-N	7.09	136.34	122.73
50	dd	38	MET	C-N-CA	7.09	136.34	122.73
38	j	57	ASN	CA-CB-CG	7.08	119.68	112.60
48	ff	103	LEU	CA-CB-CG	7.06	141.01	116.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	t	137	GLN	N-CA-C	7.03	125.78	110.80
52	BB	168	MET	CB-CG-SD	7.00	133.69	112.70
7	n	19	LYS	CA-CB-CG	6.98	128.07	114.10
1	A5	1187	G	O5'-C5'-C4'	6.98	121.97	111.50
4	B2	1203	G	N3-C4-N9	6.96	146.89	126.00
26	V	90	ARG	CB-CG-CD	6.96	127.31	111.30
45	s	41	GLN	CA-CB-CG	-6.96	100.18	114.10
46	t	138	SER	N-CA-C	6.91	124.12	112.99
11	E	103	LYS	CA-CB-CG	6.89	127.89	114.10
31	b	112	ILE	N-CA-CB	6.89	125.30	111.24
4	B2	1203	G	N7-C8-N9	6.87	133.71	113.10
9	C	263	LEU	CA-CB-CG	6.81	140.14	116.30
1	A5	1398	A	P-O3'-C3'	6.79	130.39	120.20
5	A6	4473	A	OP2-P-O3'	-6.79	87.62	108.00
82	u	65	MET	CB-CG-SD	6.78	133.03	112.70
79	YY	11	LYS	N-CA-C	-6.76	96.41	110.80
62	TT	127	GLY	N-CA-C	6.73	129.13	113.18
55	KK	38	LYS	CA-CB-CG	6.71	127.51	114.10
1	A5	1289	C	C4-C5-C6	-6.67	97.39	117.40
4	B2	1309	C	O4'-C1'-N1	6.63	118.14	108.20
55	KK	17	LYS	CA-CB-CG	6.63	127.35	114.10
14	H	121	LYS	CG-CD-CE	6.62	126.54	111.30
39	k	58	GLN	CA-CB-CG	6.62	127.35	114.10
58	PP	116	LEU	N-CA-CB	6.62	120.46	110.14
4	B2	1309	C	C5'-C4'-C3'	6.61	125.12	115.20
5	A6	4883	C	O3'-P-O5'	6.61	113.92	104.00
5	A6	4370	G	N3-C4-N9	6.60	145.81	126.00
9	C	181	LYS	N-CA-CB	-6.59	100.51	110.73
5	A6	2670	C	P-O3'-C3'	6.59	130.08	120.20
84	Bb	38	A	O5'-C5'-C4'	6.59	123.67	110.50
49	gg	42	MET	CB-CG-SD	6.58	132.44	112.70
48	ff	135	HIS	N-CA-C	6.57	120.12	110.59
1	A5	1995	G	N3-C2-N2	6.57	139.59	119.90
49	gg	162	ASN	CB-CA-C	6.56	119.32	110.13
1	A5	1270	A	C4-C5-N7	-6.55	91.04	110.70
42	o	30	LYS	N-CA-C	6.55	119.17	110.53
29	Z	37	PRO	CA-C-N	6.52	133.99	121.54
29	Z	37	PRO	C-N-CA	6.52	133.99	121.54
9	C	181	LYS	CA-CB-CG	6.51	127.11	114.10
50	dd	39	CYS	N-CA-CB	-6.51	98.29	110.07
54	FF	166	ILE	CG1-CB-CG2	-6.50	91.20	110.70
4	B2	1308	U	C4'-C3'-C2'	-6.50	96.10	102.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A6	4343	U	N1-C1'-C2'	6.49	121.74	112.00
58	PP	116	LEU	CB-CA-C	-6.49	98.89	111.03
79	YY	39	GLU	CB-CG-CD	6.48	123.61	112.60
1	A5	1270	A	N7-C8-N9	6.47	133.20	113.80
35	g	69	LYS	N-CA-C	6.45	119.27	111.40
38	j	57	ASN	CB-CA-C	6.43	121.49	111.13
48	ff	102	VAL	CB-CA-C	6.43	120.68	111.88
1	A5	1187	G	C5'-C4'-C3'	6.42	125.62	116.00
50	dd	40	ARG	N-CA-C	6.41	121.36	111.56
1	A5	1995	G	N7-C8-N9	6.40	132.31	113.10
82	u	106	ARG	CB-CG-CD	6.40	126.02	111.30
60	RR	107	LYS	CA-CB-CG	6.40	126.90	114.10
83	Cc	36	A	OP1-P-OP2	-6.37	100.48	119.60
81	c	57	ARG	CA-CB-CG	6.36	126.81	114.10
5	A6	2670	C	C2'-C3'-O3'	6.34	119.02	109.50
14	H	121	LYS	CB-CG-CD	6.34	125.89	111.30
18	M	63	LYS	CB-CG-CD	6.34	125.88	111.30
64	ZZ	52	LYS	CB-CG-CD	6.33	125.86	111.30
1	A5	1990	A	P-O3'-C3'	6.32	129.68	120.20
7	n	20	MET	CA-CB-CG	6.32	126.73	114.10
21	P	139	TYR	CD1-CG-CD2	6.32	127.57	118.10
5	A6	4370	G	N7-C8-N9	6.30	132.01	113.10
83	Cc	77	A	N9-C4-C5	6.30	124.70	105.80
11	E	131	HIS	CG-ND1-CE1	6.29	119.99	109.30
18	M	27	ILE	CA-CB-CG1	6.29	121.08	110.40
50	dd	42	CYS	N-CA-CB	6.28	120.06	110.14
72	II	182	CYS	N-CA-C	6.26	121.98	113.97
56	MM	58	GLU	CA-CB-CG	6.25	126.61	114.10
9	C	174	LEU	CA-CB-CG	6.24	138.14	116.30
17	L	111	GLN	CA-CB-CG	6.24	126.58	114.10
26	V	90	ARG	CG-CD-NE	6.24	125.72	112.00
34	f	60	PRO	N-CA-C	6.22	120.19	110.80
1	A5	1995	G	C8-N9-C1'	-6.21	108.36	127.00
4	B2	1308	U	O4'-C1'-N1	6.21	117.52	108.20
5	A6	3859	G	OP2-P-O3'	6.18	126.54	108.00
1	A5	1186	U	P-O3'-C3'	6.16	129.45	120.20
48	ff	102	VAL	N-CA-CB	-6.15	103.11	112.15
29	Z	81	MET	CB-CG-SD	6.15	131.14	112.70
43	p	88	GLU	CA-CB-CG	6.14	126.37	114.10
83	Cc	77	A	N1-C2-N3	6.13	147.69	129.30
21	P	91	LEU	CA-CB-CG	6.13	137.75	116.30
63	UU	30	LYS	CB-CG-CD	6.11	125.35	111.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
78	XX	8	ARG	CA-CB-CG	6.10	126.31	114.10
5	A6	2300	A	C6-C5-N7	6.10	150.59	132.30
13	G	185	LYS	CA-CB-CG	6.09	126.28	114.10
33	e	55	MET	CB-CG-SD	6.07	130.91	112.70
4	B2	841	G	N7-C8-N9	6.07	131.30	113.10
35	g	107	LEU	CA-CB-CG	6.06	137.51	116.30
9	C	181	LYS	CB-CA-C	6.06	120.96	110.72
52	BB	115	LYS	CA-CB-CG	6.05	126.21	114.10
1	A5	1186	U	OP2-P-O3'	-6.03	89.92	108.00
21	P	94	MET	CA-CB-CG	6.01	126.12	114.10
11	E	203	LYS	CB-CG-CD	6.01	125.12	111.30
76	VV	41	LYS	CB-CG-CD	6.01	125.12	111.30
82	u	107	SER	CA-C-N	-6.00	112.80	121.20
82	u	107	SER	C-N-CA	-6.00	112.80	121.20
56	MM	12	MET	CB-CG-SD	5.99	130.68	112.70
6	A	180	LEU	CA-CB-CG	5.98	137.24	116.30
11	E	104	ASN	N-CA-CB	5.98	119.47	110.14
12	F	207	LEU	CA-CB-CG	5.97	137.20	116.30
20	O	115	LYS	CA-C-N	5.96	130.18	121.31
20	O	115	LYS	C-N-CA	5.96	130.18	121.31
5	A6	4763	U	OP1-P-O3'	-5.95	90.14	108.00
56	MM	12	MET	CA-CB-CG	5.95	126.00	114.10
44	r	96	MET	CB-CG-SD	5.95	130.54	112.70
4	B2	841	G	N3-C4-N9	5.94	143.82	126.00
5	A6	4370	G	C4-C5-N7	-5.94	92.99	110.80
4	B2	1309	C	O5'-P-OP2	-5.93	90.20	108.00
31	b	42	ASN	CA-CB-CG	5.93	118.53	112.60
45	s	43	ILE	CA-C-N	-5.91	111.68	122.38
45	s	43	ILE	C-N-CA	-5.91	111.68	122.38
18	M	44	ARG	CA-CB-CG	5.90	125.90	114.10
20	O	114	LYS	CB-CA-C	-5.90	101.44	112.00
5	A6	2889	G	N3-C4-N9	5.89	143.68	126.00
37	i	97	MET	N-CA-CB	5.89	120.31	110.41
80	W	139	MET	CA-CB-CG	5.87	125.85	114.10
4	B2	1869	A	N1-C2-N3	-5.87	111.69	129.30
12	F	109	GLN	N-CA-CB	5.86	120.25	110.41
11	E	131	HIS	CB-CG-CD2	5.85	138.81	131.20
22	Q	17	GLU	CA-CB-CG	5.85	125.80	114.10
82	u	33	GLN	CA-CB-CG	5.85	125.80	114.10
35	g	70	THR	N-CA-C	5.85	120.96	111.37
6	A	180	LEU	N-CA-CB	-5.84	107.51	114.17
25	U	55	ASN	CA-CB-CG	5.83	118.43	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	t	138	SER	CA-C-N	5.83	132.46	121.97
46	t	138	SER	C-N-CA	5.83	132.46	121.97
10	D	273	LEU	N-CA-C	5.82	117.52	109.54
1	A5	957	G	P-O3'-C3'	5.81	128.92	120.20
1	A5	2046	G	P-O3'-C3'	5.80	128.90	120.20
4	B2	841	G	C4-C5-N7	-5.80	93.41	110.80
11	E	127	LYS	CB-CG-CD	5.80	124.63	111.30
54	FF	166	ILE	CB-CA-C	-5.79	101.79	111.29
25	U	47	ILE	CA-CB-CG1	5.78	120.23	110.40
1	A5	1187	G	P-O5'-C5'	5.78	129.57	120.90
22	Q	66	MET	CA-CB-CG	5.78	125.66	114.10
1	A5	1187	G	C4'-C3'-O3'	5.78	121.66	113.00
5	A6	2889	G	N7-C8-N9	5.78	130.43	113.10
5	A6	4884	G	P-O5'-C5'	5.77	129.56	120.90
83	Cc	77	A	C4-C5-C6	5.77	134.32	117.00
77	WW	115	GLU	CA-CB-CG	5.76	125.61	114.10
1	A5	1284	G	P-O3'-C3'	5.75	128.83	120.20
33	e	113	GLU	CA-CB-CG	5.75	125.60	114.10
4	B2	1308	U	OP2-P-O3'	5.75	125.25	108.00
71	HH	32	MET	CB-CG-SD	5.74	129.92	112.70
46	t	140	GLY	N-CA-C	5.74	126.78	113.18
9	C	234	LYS	CB-CG-CD	5.73	124.48	111.30
10	D	239	MET	CA-CB-CG	5.73	125.56	114.10
5	A6	3760	A	N1-C2-N3	-5.72	112.14	129.30
44	r	96	MET	CA-CB-CG	5.71	125.52	114.10
20	O	88	LEU	CA-CB-CG	5.71	136.28	116.30
1	A5	1990	A	O3'-P-O5'	5.70	112.55	104.00
4	B2	1309	C	C6-N1-C1'	5.70	137.89	120.80
4	B2	1309	C	N1-C1'-C2'	5.69	122.53	114.00
44	r	52	GLU	CA-CB-CG	5.68	125.47	114.10
21	P	92	LEU	CA-CB-CG	5.67	136.14	116.30
42	o	82	MET	CB-CG-SD	5.67	129.70	112.70
5	A6	3859	G	O3'-P-O5'	5.66	112.49	104.00
10	D	51	MET	CB-CG-SD	5.66	129.67	112.70
1	A5	1270	A	C6-C5-N7	5.66	149.27	132.30
18	M	118	MET	CB-CG-SD	5.64	129.62	112.70
1	A5	1398	A	C2'-C3'-O3'	5.63	117.94	109.50
30	a	94	LYS	CB-CG-CD	5.63	124.24	111.30
78	XX	5	ARG	CA-CB-CG	5.61	125.32	114.10
11	E	213	LYS	CB-CG-CD	5.61	124.19	111.30
4	B2	1495	G	C2-N3-C4	5.60	128.71	111.90
73	JJ	66	LYS	CB-CG-CD	5.59	124.17	111.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
48	ff	132	MET	CA-C-N	5.59	132.22	121.54
48	ff	132	MET	C-N-CA	5.59	132.22	121.54
82	u	19	GLN	CA-CB-CG	5.58	125.27	114.10
4	B2	1418	C	P-O3'-C3'	5.58	128.57	120.20
11	E	64	MET	CA-CB-CG	5.58	125.27	114.10
24	T	107	LYS	CA-CB-CG	5.57	125.25	114.10
22	Q	5	ILE	CA-CB-CG1	5.57	119.87	110.40
31	b	111	ARG	CA-C-N	5.57	129.45	120.82
31	b	111	ARG	C-N-CA	5.57	129.45	120.82
30	a	127	LYS	CB-CG-CD	5.56	124.10	111.30
1	A5	1282	G	N7-C8-N9	5.56	129.78	113.10
4	B2	1830	U	P-O3'-C3'	5.55	128.53	120.20
12	F	211	LYS	CB-CA-C	5.55	119.72	111.17
81	c	91	MET	CB-CG-SD	5.55	129.36	112.70
25	U	93	LYS	CA-C-N	-5.54	113.78	122.65
25	U	93	LYS	C-N-CA	-5.54	113.78	122.65
1	A5	1186	U	C4'-C3'-O3'	5.53	121.30	113.00
4	B2	141	A	P-O3'-C3'	5.53	128.50	120.20
5	A6	3860	A	O5'-P-OP2	-5.53	91.41	108.00
18	M	7	VAL	CG1-CB-CG2	-5.52	98.65	110.80
19	N	199	GLN	CA-CB-CG	5.51	125.13	114.10
61	SS	16	LEU	CA-C-N	5.51	132.07	121.54
61	SS	16	LEU	C-N-CA	5.51	132.07	121.54
4	B2	797	C	P-O3'-C3'	5.51	128.46	120.20
5	A6	3618	C	C4'-C3'-O3'	5.50	117.66	109.40
45	s	45	MET	CB-CG-SD	5.50	129.19	112.70
79	YY	10	ARG	CA-C-N	5.48	132.00	121.54
79	YY	10	ARG	C-N-CA	5.48	132.00	121.54
79	YY	98	GLU	CA-CB-CG	5.47	125.05	114.10
1	A5	1270	A	N1-C2-N3	-5.46	112.92	129.30
4	B2	74	G	N3-C4-N9	5.46	142.38	126.00
10	D	275	GLN	N-CA-C	5.46	122.42	110.80
25	U	83	LEU	CA-CB-CG	5.46	135.40	116.30
76	VV	1	MET	CB-CG-SD	5.46	129.07	112.70
51	AA	177	MET	CB-CG-SD	5.46	129.07	112.70
4	B2	1495	G	C4-N9-C1'	5.45	142.86	126.50
5	A6	4966	A	P-O3'-C3'	5.45	128.38	120.20
4	B2	841	G	N3-C2-N2	5.43	136.20	119.90
1	A5	1270	A	C2-N3-C4	5.43	126.90	110.60
5	A6	4889	G	P-O3'-C3'	5.43	128.35	120.20
68	CC	76	LYS	CB-CG-CD	5.43	123.79	111.30
1	A5	931	C	P-O3'-C3'	5.43	128.34	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A5	1991	A	O5'-P-OP2	5.43	124.28	108.00
5	A6	5027	C	P-O3'-C3'	5.42	128.34	120.20
1	A5	971	U	P-O3'-C3'	5.42	128.33	120.20
22	Q	147	GLU	CA-CB-CG	5.42	124.94	114.10
1	A5	1804	A	P-O3'-C3'	5.42	128.33	120.20
34	f	43	LEU	CA-CB-CG	5.42	135.25	116.30
39	k	9	LYS	CB-CG-CD	5.41	123.74	111.30
73	JJ	59	GLU	CA-CB-CG	5.41	124.91	114.10
5	A6	2887	U	P-O3'-C3'	5.40	128.29	120.20
1	A5	1995	G	N9-C1'-C2'	5.40	120.09	112.00
20	O	117	ARG	CA-CB-CG	5.39	124.88	114.10
22	Q	175	GLU	CA-CB-CG	5.38	124.87	114.10
20	O	113	ASP	N-CA-C	5.38	119.79	112.04
50	dd	40	ARG	CA-C-N	5.38	132.37	122.79
50	dd	40	ARG	C-N-CA	5.38	132.37	122.79
42	o	51	GLN	CA-CB-CG	5.38	124.86	114.10
1	A5	2045	G	N3-C4-N9	5.38	142.13	126.00
11	E	103	LYS	CB-CG-CD	5.37	123.66	111.30
1	A5	1995	G	C4-N9-C1'	5.37	142.61	126.50
5	A6	2889	G	C4-C5-N7	-5.37	94.69	110.80
54	FF	196	LEU	CA-CB-CG	5.37	135.09	116.30
68	CC	205	VAL	CB-CA-C	5.36	117.96	110.99
5	A6	4885	U	P-O3'-C3'	5.36	128.24	120.20
77	WW	52	ILE	CA-CB-CG1	5.35	119.49	110.40
82	u	37	MET	N-CA-C	5.35	117.55	111.02
5	A6	3860	A	O5'-P-OP1	-5.34	91.97	108.00
1	A5	406	C	P-O3'-C3'	5.32	128.18	120.20
4	B2	841	G	C6-C5-N7	5.32	146.34	130.40
62	TT	88	MET	CB-CG-SD	5.31	128.63	112.70
8	B	72	VAL	CB-CA-C	5.31	120.00	111.29
5	A6	4629	U	C2'-C3'-O3'	5.31	121.66	113.70
15	I	58	GLU	CA-CB-CG	5.31	124.72	114.10
19	N	9	GLU	CA-CB-CG	5.30	124.71	114.10
10	D	208	MET	CA-CB-CG	5.30	124.70	114.10
57	OO	147	ARG	CG-CD-NE	-5.30	100.34	112.00
1	A5	1282	G	C4-C5-N7	-5.30	94.91	110.80
80	W	74	ARG	N-CA-C	5.29	119.66	112.04
5	A6	3760	A	C2-N3-C4	5.28	126.45	110.60
1	A5	451	C	P-O3'-C3'	5.28	128.12	120.20
4	B2	1495	G	N1-C6-O6	-5.27	104.08	119.90
12	F	63	MET	CA-CB-CG	5.27	124.64	114.10
51	AA	185	MET	CB-CG-SD	5.27	128.51	112.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A5	1991	A	P-O5'-C5'	5.26	128.79	120.90
83	Cc	77	A	C5-N7-C8	5.26	119.69	103.90
21	P	86	LYS	CB-CG-CD	-5.26	99.21	111.30
47	cc	47	LYS	CA-CB-CG	5.26	124.62	114.10
25	U	17	GLN	CB-CG-CD	5.26	121.54	112.60
41	m	113	LYS	CA-CB-CG	5.26	124.61	114.10
51	AA	40	LYS	CA-CB-CG	5.25	124.61	114.10
81	c	57	ARG	CB-CG-CD	5.25	123.39	111.30
52	BB	168	MET	N-CA-CB	5.25	118.21	110.33
4	B2	552	G	C2'-C3'-O3'	5.25	121.58	113.70
52	BB	63	LYS	CB-CG-CD	5.25	123.38	111.30
5	A6	4370	G	C6-C5-N7	5.25	146.15	130.40
18	M	118	MET	CA-CB-CG	5.25	124.60	114.10
43	p	80	LYS	CB-CG-CD	5.25	123.37	111.30
68	CC	115	GLN	N-CA-C	5.25	121.97	110.80
34	f	40	GLU	CB-CG-CD	5.22	121.47	112.60
45	s	41	GLN	N-CA-C	5.21	121.91	110.80
74	LL	113	LEU	CA-CB-CG	5.21	134.55	116.30
80	W	96	MET	CA-CB-CG	5.21	124.53	114.10
21	P	53	LEU	CA-CB-CG	5.21	134.54	116.30
1	A5	413	G	P-O3'-C3'	5.21	128.01	120.20
1	A5	917	A	P-O3'-C3'	5.21	128.01	120.20
32	d	49	ILE	CA-CB-CG1	5.21	119.25	110.40
54	FF	76	MET	CA-CB-CG	5.20	124.51	114.10
83	Cc	35	C	C4'-C3'-O3'	5.20	120.81	113.00
1	A5	1481	C	P-O3'-C3'	5.20	128.00	120.20
65	bb	16	LYS	CA-CB-CG	5.19	124.48	114.10
5	A6	3959	U	P-O3'-C3'	5.18	127.98	120.20
37	i	6	PRO	CA-C-N	5.18	128.23	120.87
37	i	6	PRO	C-N-CA	5.18	128.23	120.87
53	DD	157	MET	CA-CB-CG	5.18	124.47	114.10
1	A5	958	G	P-O3'-C3'	5.18	127.97	120.20
5	A6	4738	C	P-O3'-C3'	5.18	127.97	120.20
1	A5	1187	G	O5'-P-OP2	5.18	123.53	108.00
71	HH	32	MET	CA-C-N	-5.18	114.37	122.65
71	HH	32	MET	C-N-CA	-5.18	114.37	122.65
30	a	63	LEU	CA-CB-CG	5.17	134.41	116.30
83	Cc	77	A	N3-C4-N9	5.17	142.91	127.40
25	U	46	ARG	CA-C-N	-5.17	115.92	122.43
25	U	46	ARG	C-N-CA	-5.17	115.92	122.43
43	p	89	LEU	CA-CB-CG	5.17	134.38	116.30
5	A6	4738	C	C2'-C3'-O3'	5.16	121.44	113.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
65	bb	22	LYS	CB-CG-CD	5.16	123.17	111.30
1	A5	1186	U	O3'-P-O5'	5.16	111.73	104.00
1	A5	1282	G	N3-C4-N9	5.15	141.46	126.00
50	dd	39	CYS	CB-CA-C	5.15	123.76	112.63
3	A8	126	C	P-O3'-C3'	5.15	127.92	120.20
55	KK	29	MET	N-CA-C	-5.14	101.81	109.42
80	W	76	MET	CB-CG-SD	5.14	128.13	112.70
5	A6	4119	C	P-O3'-C3'	5.14	127.91	120.20
39	k	13	LEU	CA-CB-CG	5.14	134.29	116.30
73	JJ	59	GLU	CB-CG-CD	5.14	121.33	112.60
9	C	196	MET	CB-CG-SD	5.14	128.11	112.70
18	M	55	MET	CB-CG-SD	5.13	128.10	112.70
4	B2	228	C	P-O3'-C3'	5.13	127.89	120.20
1	A5	1474	C	C2'-C3'-O3'	5.12	121.38	113.70
28	Y	83	GLU	CB-CG-CD	5.12	121.30	112.60
1	A5	1186	U	C5'-C4'-O4'	-5.11	102.13	109.80
34	f	54	LYS	CA-CB-CG	5.10	124.31	114.10
53	DD	127	MET	CA-CB-CG	5.10	124.30	114.10
65	bb	13	GLU	CB-CG-CD	5.09	121.26	112.60
25	U	55	ASN	CB-CA-C	5.09	119.17	110.01
65	bb	13	GLU	CA-CB-CG	5.09	124.27	114.10
55	KK	31	LYS	CA-CB-CG	5.08	124.26	114.10
49	gg	162	ASN	CA-CB-CG	5.07	117.67	112.60
73	JJ	92	MET	CA-CB-CG	5.07	124.24	114.10
80	W	152	LYS	N-CA-CB	5.07	118.14	110.28
1	A5	2045	G	N7-C8-N9	5.06	128.29	113.10
4	B2	604	A	P-O3'-C3'	5.06	127.79	120.20
22	Q	9	LYS	CA-CB-CG	5.06	124.21	114.10
5	A6	3860	A	OP1-P-OP2	-5.06	104.43	119.60
10	D	274	ALA	CA-C-N	5.05	131.19	121.54
10	D	274	ALA	C-N-CA	5.05	131.19	121.54
15	I	184	MET	CA-CB-CG	5.05	124.21	114.10
18	M	50	MET	CB-CG-SD	5.05	127.84	112.70
23	S	9	GLU	CB-CG-CD	5.05	121.18	112.60
23	S	100	LEU	CA-CB-CG	5.04	133.96	116.30
5	A6	4170	A	P-O3'-C3'	5.04	127.77	120.20
62	TT	87	VAL	CA-C-N	5.04	128.32	120.60
62	TT	87	VAL	C-N-CA	5.04	128.32	120.60
21	P	86	LYS	CB-CA-C	-5.04	102.97	110.88
1	A5	1474	C	P-O3'-C3'	5.04	127.75	120.20
29	Z	38	TYR	CA-CB-CG	5.04	122.97	113.90
20	O	87	MET	CA-CB-CG	5.03	124.17	114.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A5	125	C	P-O3'-C3'	5.03	127.74	120.20
1	A5	69	A	P-O3'-C3'	5.03	127.74	120.20
1	A5	955	G	P-O3'-C3'	5.02	127.73	120.20
57	OO	25	GLU	CA-CB-CG	5.02	124.15	114.10
1	A5	682	G	O3'-P-O5'	5.02	111.53	104.00
1	A5	668	C	P-O3'-C3'	5.01	127.71	120.20
31	b	23	LYS	CA-CB-CG	5.01	124.11	114.10
73	JJ	121	LYS	CA-CB-CG	5.01	124.11	114.10
5	A6	4036	G	C2'-C3'-O3'	5.00	121.21	113.70
13	G	220	GLU	CA-CB-CG	5.00	124.11	114.10
9	C	281	MET	CA-CB-CG	5.00	124.11	114.10
9	C	281	MET	CB-CG-SD	5.00	127.70	112.70

There are no chirality outliers.

All (42) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	A	176	ASP	Peptide
6	A	96	LEU	Peptide
8	B	130	PHE	Peptide
8	B	73	VAL	Peptide
9	C	182	LYS	Peptide
9	C	196	MET	Peptide
68	CC	187	ARG	Peptide
10	D	279	ARG	Sidechain
53	DD	159	HIS	Peptide
11	E	136	PHE	Peptide
54	FF	168	THR	Peptide
73	JJ	133	ARG	Peptide
17	L	35	ARG	Sidechain
56	MM	36	ARG	Sidechain
20	O	60	LYS	Peptide
57	OO	136	PRO	Peptide
57	OO	147	ARG	Sidechain
22	Q	122	THR	Peptide
23	S	160	ARG	Peptide
62	TT	129	ARG	Sidechain
26	V	89	ARG	Peptide
76	VV	40	ASP	Peptide
80	W	71	ARG	Peptide
28	Y	115	ARG	Sidechain
29	Z	92	ASP	Peptide

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Mol	Chain	Res	Type	Group
81	c	115	ALA	Peptide
32	d	104	THR	Peptide
48	ff	132	MET	Peptide
48	ff	133	ALA	Peptide
48	ff	134	SER	Peptide
48	ff	135	HIS	Peptide
36	h	5	LYS	Peptide
41	m	99	CYS	Peptide
7	n	1	MET	Peptide
42	o	31	ASP	Peptide
42	o	53	MLZ	Peptide
44	r	21	ASN	Peptide
45	s	44	ARG	Peptide
45	s	57	LYS	Peptide
46	t	140	GLY	Peptide
82	u	35	LEU	Peptide
82	u	66	LEU	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A5	36275	0	18295	660	0
2	A7	2558	0	1294	20	0
3	A8	3317	0	1681	37	0
4	B2	37897	0	19056	706	0
5	A6	43564	0	21782	714	0
6	A	1648	0	1474	31	0
7	n	239	0	289	6	0
8	B	3206	0	3353	68	0
9	C	2884	0	3055	80	0
10	D	2389	0	2423	46	0
11	E	1789	0	1942	123	0
12	F	1875	0	1995	37	0
13	G	1741	0	1861	31	0
14	H	1516	0	1597	35	0
15	I	1620	0	1663	32	0
16	J	1362	0	1399	24	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
17	L	1658	0	1766	44	0
18	M	1125	0	1198	22	0
19	N	1701	0	1749	32	0
20	O	1630	0	1776	71	0
21	P	1242	0	1274	47	0
22	Q	1512	0	1629	40	0
23	S	1461	0	1502	35	0
24	T	1298	0	1366	24	0
25	U	808	0	831	13	0
26	V	979	0	1039	36	0
27	X	967	0	1040	20	0
28	Y	1115	0	1205	34	0
29	Z	1107	0	1182	12	0
30	a	1163	0	1202	31	0
31	b	545	0	578	39	0
32	d	888	0	930	11	0
33	e	1053	0	1147	17	0
34	f	884	0	924	17	0
35	g	873	0	963	47	0
36	h	1011	0	1150	31	0
37	i	830	0	916	18	0
38	j	705	0	737	13	0
39	k	569	0	637	8	0
40	l	444	0	483	7	0
41	m	422	0	457	7	0
42	o	863	0	927	27	0
43	p	708	0	756	15	0
44	r	1015	0	1085	22	0
45	s	825	0	865	52	0
46	t	1178	0	1235	31	0
47	cc	479	0	507	13	0
48	ff	548	0	552	15	0
49	gg	2436	0	2393	40	0
50	dd	459	0	449	18	0
51	AA	1689	0	1691	25	0
52	BB	1768	0	1846	37	0
53	DD	1751	0	1846	24	0
54	FF	1461	0	1511	52	0
55	KK	810	0	836	18	0
56	MM	958	0	993	15	0
57	OO	1002	0	1023	25	0
58	PP	979	0	1028	42	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
59	QQ	1124	0	1193	26	0
60	RR	1068	0	1121	22	0
61	SS	1193	0	1253	27	0
62	TT	1097	0	1123	14	0
63	UU	790	0	857	8	0
64	ZZ	598	0	656	13	0
65	bb	640	0	665	13	0
66	ee	398	0	443	14	0
67	aa	781	0	828	14	0
68	CC	1689	0	1778	58	0
69	EE	2076	0	2177	28	0
70	GG	1848	0	1999	52	0
71	HH	1490	0	1582	20	0
72	II	1686	0	1771	39	0
73	JJ	1499	0	1618	42	0
74	LL	1157	0	1223	21	0
75	NN	1202	0	1289	20	0
76	VV	637	0	631	7	0
77	WW	1034	0	1080	14	0
78	XX	810	0	711	3	0
79	YY	1015	0	1086	44	0
80	W	1508	0	1663	50	0
81	c	921	0	965	39	0
82	u	775	0	810	41	0
83	Cc	1623	0	827	69	0
84	Bb	1409	0	721	31	0
85	Dd	260	0	131	3	0
86	A5	9	0	0	0	0
86	A6	7	0	0	0	0
86	A7	4	0	0	0	0
86	A8	4	0	0	0	0
86	B2	7	0	0	0	0
86	BB	1	0	0	0	0
86	Bb	1	0	0	0	0
86	Cc	1	0	0	0	0
86	P	1	0	0	0	0
86	l	1	0	0	0	0
87	B2	1	0	0	0	0
87	aa	1	0	0	0	0
87	ff	1	0	0	0	0
87	g	1	0	0	0	0
87	j	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
87	m	1	0	0	0	0
87	o	1	0	0	0	0
87	p	1	0	0	0	0
88	A6	1	0	0	0	0
88	B2	4	0	0	0	0
88	Bb	5	0	0	0	0
88	Cc	5	0	0	0	0
All	All	219186	0	160584	3551	0

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

All (3551) 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)
1:A5:1972:G:C5	1:A5:1972:G:C6	1.86	1.62
5:A6:4613:C:N1	5:A6:4613:C:C6	1.68	1.60
4:B2:1869:A:C2	4:B2:1869:A:N1	1.68	1.60
5:A6:4613:C:C4	5:A6:4613:C:N3	1.70	1.59
4:B2:1869:A:C4	4:B2:1869:A:N3	1.68	1.58
1:A5:959:G:C4	1:A5:959:G:N3	1.68	1.57
1:A5:959:G:C2	1:A5:959:G:N1	1.73	1.56
4:B2:1535:U:C5	4:B2:1535:U:C4	1.84	1.56
5:A6:2677:G:C4	5:A6:2677:G:N3	1.68	1.55
5:A6:4613:C:N1	5:A6:4613:C:C2	1.75	1.53
68:CC:115:GLN:N	68:CC:115:GLN:CA	1.70	1.53
4:B2:1869:A:N1	4:B2:1869:A:C6	1.71	1.52
5:A6:2677:G:C2	5:A6:2677:G:N1	1.74	1.52
5:A6:2677:G:N1	5:A6:2677:G:C6	1.76	1.52
1:A5:1972:G:C5	1:A5:1972:G:C4	1.79	1.51
5:A6:4613:C:N3	5:A6:4613:C:C2	1.74	1.51
20:O:114:LYS:N	20:O:114:LYS:CA	1.69	1.51
1:A5:959:G:N1	1:A5:959:G:C6	1.76	1.51
45:s:41:GLN:N	45:s:41:GLN:CA	1.72	1.50
35:g:70:THR:N	35:g:70:THR:CA	1.77	1.47
1:A5:1972:G:N3	1:A5:1972:G:C2	1.83	1.46
31:b:112:ILE:CB	31:b:112:ILE:CG2	1.90	1.45
58:PP:116:LEU:N	58:PP:116:LEU:CA	1.76	1.45
4:B2:1535:U:N1	4:B2:1535:U:C6	1.85	1.45
72:II:182:CYS:C	72:II:183:GLY:N	1.74	1.44
1:A5:1972:G:C4	1:A5:1972:G:N3	1.85	1.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A5:1972:G:C2	1:A5:1972:G:N1	1.85	1.44
4:B2:1535:U:C4	4:B2:1535:U:N3	1.88	1.42
1:A5:1972:G:C6	1:A5:1972:G:N1	1.87	1.42
11:E:136:PHE:CD1	11:E:136:PHE:CG	2.08	1.42
50:dd:42:CYS:CB	50:dd:42:CYS:SG	2.07	1.42
31:b:112:ILE:CG2	31:b:112:ILE:HG13	1.47	1.41
83:Cc:35:C:C3'	83:Cc:35:C:O3'	1.67	1.41
4:B2:1535:U:N3	4:B2:1535:U:C2	1.88	1.41
21:P:139:TYR:CG	21:P:139:TYR:CD1	2.10	1.40
58:PP:115:TYR:C	58:PP:116:LEU:N	1.80	1.39
4:B2:1535:U:N1	4:B2:1535:U:C2	1.89	1.39
11:E:136:PHE:CG	11:E:136:PHE:CD2	2.10	1.39
35:g:69:LYS:C	35:g:70:THR:N	1.80	1.38
5:A6:3859:G:O3'	5:A6:3859:G:C3'	1.72	1.38
4:B2:1248:U:C5	4:B2:1248:U:C6	2.11	1.37
5:A6:3760:A:C4	5:A6:3760:A:C5	2.08	1.37
21:P:139:TYR:CG	21:P:139:TYR:CD2	2.10	1.37
31:b:112:ILE:CG2	31:b:112:ILE:CG1	2.02	1.35
72:II:183:GLY:N	72:II:183:GLY:CA	1.87	1.35
4:B2:74:G:C5	4:B2:74:G:C4	2.12	1.34
1:A5:2045:G:C5	1:A5:2045:G:C4	2.15	1.32
54:FF:166:ILE:N	54:FF:166:ILE:CA	1.93	1.31
5:A6:2768:C:C6	5:A6:2768:C:C5	2.20	1.29
5:A6:4757:C:C5	5:A6:4757:C:C6	2.22	1.28
1:A5:1995:G:C5	1:A5:1995:G:C4	2.22	1.28
83:Cc:77:A:N3	83:Cc:77:A:C2	2.01	1.28
5:A6:3760:A:C5	5:A6:3760:A:C6	2.21	1.27
4:B2:74:G:C5	4:B2:74:G:C6	2.24	1.26
4:B2:305:U:C6	4:B2:305:U:C5	2.23	1.26
45:s:40:MET:C	45:s:41:GLN:N	1.94	1.25
68:CC:114:LYS:C	68:CC:115:GLN:N	1.94	1.25
4:B2:1599:U:C6	4:B2:1599:U:C5	2.25	1.24
5:A6:2889:G:C5	5:A6:2889:G:C4	2.26	1.24
4:B2:1248:U:C5	4:B2:1248:U:C4	2.26	1.24
1:A5:2045:G:C5	1:A5:2045:G:C6	2.27	1.23
4:B2:1621:U:C5	4:B2:1621:U:C6	2.25	1.22
31:b:112:ILE:CA	31:b:112:ILE:HB	1.68	1.22
1:A5:1282:G:C5	1:A5:1282:G:C4	2.25	1.22
20:O:113:ASP:C	20:O:114:LYS:N	1.98	1.21
80:W:74:ARG:C	80:W:75:HIS:N	1.99	1.21
21:P:139:TYR:CZ	21:P:139:TYR:CE2	2.31	1.19

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A6:3760:A:N3	5:A6:3760:A:C2	2.11	1.19
4:B2:1203:G:C4	4:B2:1203:G:C5	2.23	1.18
5:A6:2768:C:C5	5:A6:2768:C:C4	2.31	1.17
1:A5:1289:C:C1'	1:A5:1289:C:N1	2.08	1.17
1:A5:684:G:C4	1:A5:684:G:C5	2.32	1.17
21:P:139:TYR:CZ	21:P:139:TYR:CE1	2.33	1.17
5:A6:3760:A:C2	5:A6:3760:A:N1	2.12	1.16
4:B2:1203:G:C5	4:B2:1203:G:C6	2.33	1.16
5:A6:3760:A:C4	5:A6:3760:A:N3	2.14	1.15
1:A5:1995:G:C5	1:A5:1995:G:C6	2.33	1.15
4:B2:841:G:C4	4:B2:841:G:C5	2.35	1.14
4:B2:841:G:C6	79:YY:11:LYS:HB2	1.83	1.14
5:A6:2889:G:C5	5:A6:2889:G:C6	2.36	1.14
4:B2:1621:U:C5	4:B2:1621:U:C4	2.38	1.12
1:A5:1270:A:C5	1:A5:1270:A:C4	2.37	1.12
5:A6:3760:A:C6	5:A6:3760:A:N1	2.18	1.11
5:A6:4757:C:C5	5:A6:4757:C:C4	2.38	1.11
1:A5:2045:G:C4	1:A5:2045:G:N3	2.19	1.10
5:A6:4370:G:C5	5:A6:4370:G:C4	2.37	1.10
1:A5:2045:G:N3	1:A5:2045:G:C2	2.19	1.10
5:A6:2300:A:C4	5:A6:2300:A:C5	2.40	1.09
4:B2:74:G:N3	4:B2:74:G:C2	2.20	1.09
4:B2:305:U:C5	4:B2:305:U:C4	2.40	1.09
1:A5:1282:G:C5	1:A5:1282:G:C6	2.41	1.08
4:B2:1599:U:C5	4:B2:1599:U:C4	2.40	1.08
79:YY:11:LYS:CA	79:YY:11:LYS:CB	2.32	1.07
4:B2:841:G:C4	79:YY:11:LYS:HB3	1.89	1.06
4:B2:74:G:C4	4:B2:74:G:N3	2.25	1.05
5:A6:2300:A:C5	9:C:182:LYS:N	2.24	1.05
5:A6:3859:G:O3'	5:A6:3860:A:P	2.15	1.05
4:B2:1248:U:C6	4:B2:1248:U:N1	2.24	1.04
31:b:112:ILE:CG1	31:b:112:ILE:HG21	1.76	1.04
4:B2:878:G:N1	4:B2:908:A:C2	2.25	1.04
4:B2:74:G:C2	4:B2:74:G:N1	2.26	1.03
1:A5:1270:A:N3	31:b:112:ILE:HA	1.75	1.02
4:B2:878:G:N1	4:B2:908:A:H2	1.55	1.02
5:A6:2889:G:N3	5:A6:2889:G:C2	2.28	1.02
83:Cc:77:A:N3	83:Cc:77:A:C6	2.17	1.02
1:A5:717:U:H3	1:A5:951:G:H1	1.06	1.02
1:A5:352:G:H21	1:A5:360:A:N6	1.59	1.01
1:A5:1995:G:C2	1:A5:1995:G:N1	2.29	1.01

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B2:568:C:N4	4:B2:582:U:H3	1.57	1.01
1:A5:684:G:N7	11:E:104:ASN:HA	1.76	1.01
9:C:181:LYS:C	9:C:182:LYS:N	2.19	1.01
5:A6:2300:A:N7	9:C:182:LYS:N	2.09	1.00
4:B2:934:G:H1	4:B2:1008:A:H2	1.04	1.00
5:A6:2768:C:C2	35:g:70:THR:N	2.30	1.00
4:B2:1248:U:N1	4:B2:1248:U:C2	2.29	1.00
4:B2:1248:U:C4	4:B2:1248:U:N3	2.29	1.00
1:A5:1550:G:H1	1:A5:1578:U:H3	1.10	1.00
5:A6:4370:G:C5	5:A6:4370:G:C6	2.50	0.99
5:A6:4748:U:H3	5:A6:4952:G:H1	1.09	0.99
1:A5:2045:G:C2	1:A5:2045:G:N1	2.30	0.99
5:A6:2300:A:C8	9:C:182:LYS:N	2.31	0.99
1:A5:1270:A:C5	1:A5:1270:A:C6	2.50	0.98
1:A5:2045:G:C6	1:A5:2045:G:N1	2.31	0.98
5:A6:4757:C:C6	5:A6:4757:C:N1	2.31	0.98
1:A5:352:G:H21	1:A5:360:A:H61	1.10	0.98
4:B2:1248:U:C2	4:B2:1248:U:N3	2.31	0.98
5:A6:4460:U:H3	5:A6:4516:G:H1	1.10	0.98
11:E:131:HIS:CB	11:E:131:HIS:CG	2.47	0.98
50:dd:21:CYS:HB2	50:dd:39:CYS:SG	2.03	0.98
4:B2:1244:U:H3	4:B2:1255:G:H1	1.05	0.98
35:g:83:CYS:HB2	35:g:86:CYS:SG	2.04	0.98
1:A5:1995:G:C6	1:A5:1995:G:N1	2.32	0.97
38:j:54:LYS:O	38:j:58:THR:HB	1.64	0.97
1:A5:1470:G:H1	1:A5:1494:U:H3	1.10	0.97
5:A6:2889:G:C4	5:A6:2889:G:N3	2.32	0.97
1:A5:1724:G:N1	1:A5:1838:A:H2	1.63	0.96
5:A6:2624:G:H1	5:A6:2632:U:H3	1.01	0.96
4:B2:74:G:C6	4:B2:74:G:N1	2.33	0.96
1:A5:1106:A:H62	1:A5:1164:G:N2	1.64	0.96
4:B2:1352:G:H1	4:B2:1359:U:H3	1.04	0.96
1:A5:684:G:C5	11:E:104:ASN:ND2	2.32	0.96
4:B2:1203:G:N3	4:B2:1203:G:C2	2.34	0.96
4:B2:841:G:C5	4:B2:841:G:C6	2.54	0.96
5:A6:3720:G:H1	5:A6:3733:A:H61	1.05	0.96
4:B2:1203:G:C2	4:B2:1203:G:N1	2.34	0.96
4:B2:1599:U:C4	54:FF:166:ILE:N	2.34	0.96
5:A6:3695:U:H3	5:A6:3820:G:H1	1.14	0.96
83:Cc:51:U:H3	83:Cc:65:G:H1	1.12	0.95
4:B2:305:U:C4	72:II:183:GLY:N	2.34	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A6:2889:G:C4	80:W:75:HIS:N	2.34	0.95
4:B2:1652:G:H1	4:B2:1672:U:H3	0.95	0.95
5:A6:3754:G:H1	5:A6:3770:U:H3	1.05	0.95
5:A6:4757:C:C4	5:A6:4757:C:N3	2.35	0.95
4:B2:822:U:H3	4:B2:826:A:N6	1.64	0.94
4:B2:1288:U:H3	4:B2:1311:C:N4	1.65	0.94
5:A6:2768:C:C6	5:A6:2768:C:N1	2.35	0.94
5:A6:2889:G:C2	5:A6:2889:G:N1	2.34	0.94
5:A6:4403:U:H3	5:A6:4440:G:H1	1.07	0.94
5:A6:4757:C:C4	20:O:114:LYS:N	2.35	0.94
3:A8:70:G:N2	3:A8:88:A:H62	1.65	0.94
4:B2:155:G:H1	4:B2:163:U:H3	1.15	0.94
5:A6:2300:A:C4	9:C:182:LYS:N	2.34	0.94
4:B2:305:U:C6	4:B2:305:U:N1	2.35	0.94
1:A5:1282:G:C2	11:E:131:HIS:HB3	2.02	0.94
4:B2:1621:U:C6	4:B2:1621:U:N1	2.36	0.94
1:A5:1995:G:C2	45:s:41:GLN:N	2.36	0.93
1:A5:1995:G:C6	45:s:41:GLN:N	2.37	0.93
4:B2:841:G:N3	79:YY:11:LYS:HA	1.83	0.93
1:A5:749:G:H1	1:A5:913:U:H3	1.06	0.93
5:A6:3944:G:H1	5:A6:4069:U:H3	1.00	0.93
84:Bb:34:G:H1	85:Dd:24:U:H3	0.95	0.93
1:A5:33:A:C8	1:A5:49:U:N3	2.36	0.93
5:A6:3946:G:H1	5:A6:4067:U:H3	1.16	0.93
5:A6:4757:C:N3	5:A6:4757:C:C2	2.36	0.93
1:A5:1282:G:C4	1:A5:1282:G:N3	2.37	0.93
4:B2:1203:G:C6	4:B2:1203:G:N1	2.37	0.93
4:B2:1203:G:C6	68:CC:115:GLN:N	2.37	0.93
2:A7:7:G:H1	2:A7:112:U:H3	1.15	0.92
5:A6:2849:A:N6	5:A6:3838:U:H3	1.66	0.92
1:A5:2045:G:C2	20:O:62:MET:N	2.37	0.92
1:A5:1282:G:C4	11:E:131:HIS:CG	2.58	0.92
5:A6:3865:A:H61	5:A6:3881:G:H1	1.06	0.92
5:A6:2889:G:C6	5:A6:2889:G:N1	2.38	0.92
1:A5:1282:G:C2	1:A5:1282:G:N3	2.37	0.92
4:B2:1203:G:C4	4:B2:1203:G:N3	2.36	0.92
5:A6:3930:U:H3	5:A6:4180:G:H1	1.08	0.92
4:B2:1726:G:H1	4:B2:1808:U:H3	0.94	0.92
5:A6:2889:G:C5	80:W:75:HIS:N	2.38	0.92
3:A8:70:G:H21	3:A8:88:A:H62	1.04	0.92
4:B2:1203:G:C5	68:CC:115:GLN:N	2.39	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B2:305:U:N3	4:B2:305:U:C2	2.38	0.91
1:A5:1726:U:H3	1:A5:1836:G:H1	1.11	0.91
1:A5:1995:G:C4	1:A5:1995:G:N3	2.38	0.91
5:A6:2768:C:C4	5:A6:2768:C:N3	2.39	0.91
1:A5:1724:G:N1	1:A5:1838:A:C2	2.35	0.91
4:B2:1656:G:H1	4:B2:1668:U:H3	0.94	0.91
4:B2:1089:G:H1	4:B2:1160:U:H3	1.18	0.90
4:B2:1599:U:C6	4:B2:1599:U:N1	2.38	0.90
1:A5:1106:A:H62	1:A5:1164:G:H21	1.20	0.90
4:B2:305:U:C2	72:II:183:GLY:N	2.38	0.90
4:B2:1621:U:C4	4:B2:1621:U:N3	2.40	0.90
5:A6:2768:C:N1	35:g:70:THR:N	2.20	0.90
4:B2:74:G:C4	70:GG:171:THR:N	2.40	0.90
4:B2:1748:G:H1	4:B2:1786:U:H3	1.02	0.90
1:A5:1282:G:C2	1:A5:1282:G:N1	2.40	0.90
1:A5:1949:U:H3	1:A5:2034:G:H1	1.20	0.89
1:A5:684:G:N7	1:A5:684:G:C8	2.40	0.89
4:B2:1227:G:H1	4:B2:1531:A:H61	1.18	0.89
5:A6:4757:C:C2	20:O:114:LYS:N	2.40	0.89
4:B2:1288:U:H3	4:B2:1311:C:H42	1.16	0.89
5:A6:2550:G:H1	5:A6:2767:U:H3	1.08	0.89
5:A6:4638:U:H3	5:A6:4661:G:H1	1.20	0.89
1:A5:1270:A:N3	1:A5:1270:A:C2	2.40	0.89
1:A5:1995:G:C5	45:s:41:GLN:N	2.41	0.89
4:B2:305:U:C4	4:B2:305:U:N3	2.40	0.89
4:B2:305:U:N3	72:II:183:GLY:N	2.21	0.89
4:B2:305:U:N1	4:B2:305:U:C2	2.41	0.89
4:B2:1621:U:C4	58:PP:116:LEU:N	2.40	0.88
1:A5:1929:A:N6	1:A5:2054:U:C2	2.41	0.88
1:A5:2045:G:C6	20:O:62:MET:N	2.41	0.88
4:B2:74:G:C2	70:GG:171:THR:N	2.41	0.88
4:B2:928:G:H1	4:B2:1013:U:H3	1.21	0.88
1:A5:684:G:C8	11:E:104:ASN:CB	2.57	0.88
4:B2:1203:G:C4	68:CC:115:GLN:N	2.42	0.88
4:B2:1621:U:C2	58:PP:116:LEU:N	2.41	0.88
5:A6:4757:C:N1	5:A6:4757:C:C2	2.42	0.87
4:B2:1621:U:N1	4:B2:1621:U:C2	2.42	0.87
5:A6:3720:G:H1	5:A6:3733:A:N6	1.71	0.87
4:B2:1203:G:C2	68:CC:115:GLN:N	2.42	0.87
4:B2:1599:U:N3	4:B2:1599:U:C2	2.42	0.87
4:B2:925:G:H1	4:B2:1017:U:H3	0.92	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A5:1282:G:C6	1:A5:1282:G:N1	2.43	0.87
5:A6:4370:G:N3	5:A6:4370:G:C2	2.42	0.87
31:b:112:ILE:CB	31:b:112:ILE:CA	2.53	0.87
4:B2:804:U:H3	4:B2:859:G:H1	1.21	0.87
1:A5:1995:G:C2	1:A5:1995:G:N3	2.43	0.87
1:A5:1995:G:N1	45:s:41:GLN:N	2.23	0.86
5:A6:2889:G:C2	80:W:75:HIS:N	2.43	0.86
5:A6:2605:G:H1	5:A6:2734:U:H3	1.23	0.86
5:A6:2889:G:C6	80:W:75:HIS:N	2.43	0.86
1:A5:1270:A:C4	1:A5:1270:A:N3	2.43	0.86
5:A6:3760:A:N3	84:Bb:38:A:H4'	1.91	0.86
3:A8:70:G:H21	3:A8:88:A:N6	1.73	0.86
4:B2:1640:A:N6	83:Cc:30:G:C6	2.42	0.86
5:A6:2768:C:C2	5:A6:2768:C:N3	2.44	0.86
5:A6:3865:A:N6	5:A6:3881:G:H1	1.73	0.86
5:A6:2643:G:H1	5:A6:2691:U:H3	1.21	0.86
1:A5:424:U:H3	3:A8:10:G:H1	1.19	0.86
5:A6:2300:A:N7	5:A6:2300:A:C8	2.44	0.86
1:A5:1995:G:C4	45:s:41:GLN:N	2.44	0.85
4:B2:1599:U:C4	4:B2:1599:U:N3	2.44	0.85
4:B2:1599:U:N3	54:FF:166:ILE:N	2.24	0.85
5:A6:4757:C:N3	20:O:114:LYS:N	2.24	0.85
1:A5:1289:C:H1'	11:E:136:PHE:CE1	2.11	0.85
4:B2:677:G:H21	4:B2:1028:A:H62	1.20	0.85
4:B2:841:G:N3	4:B2:841:G:C2	2.44	0.85
5:A6:4370:G:C4	5:A6:4370:G:N3	2.44	0.85
4:B2:1621:U:C6	58:PP:116:LEU:N	2.44	0.85
4:B2:1621:U:N3	4:B2:1621:U:C2	2.45	0.85
5:A6:3935:C:N4	5:A6:3936:A:N6	2.23	0.85
1:A5:1106:A:N6	1:A5:1164:G:H21	1.75	0.85
1:A5:392:U:H3	1:A5:399:G:H1	1.21	0.85
1:A5:2045:G:N1	20:O:62:MET:N	2.24	0.85
1:A5:1270:A:C6	31:b:112:ILE:HB	2.12	0.84
5:A6:2768:C:C6	35:g:70:THR:N	2.46	0.84
4:B2:1640:A:C6	83:Cc:30:G:C6	2.66	0.84
5:A6:2863:G:H1	5:A6:2887:U:H3	0.88	0.84
4:B2:1621:U:N1	58:PP:116:LEU:N	2.25	0.84
83:Cc:77:A:C2	83:Cc:77:A:C5	2.46	0.84
4:B2:74:G:C5	70:GG:171:THR:N	2.46	0.84
4:B2:1203:G:N1	68:CC:115:GLN:N	2.25	0.84
4:B2:841:G:C4	4:B2:841:G:N3	2.46	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B2:305:U:C5	72:II:183:GLY:N	2.46	0.83
4:B2:1599:U:C5	54:FF:166:ILE:N	2.46	0.83
4:B2:1599:U:C2	54:FF:166:ILE:N	2.46	0.83
5:A6:4370:G:C4	83:Cc:77:A:C5	2.66	0.83
5:A6:4997:G:H1	5:A6:5053:U:H3	1.24	0.83
31:b:112:ILE:HG13	31:b:112:ILE:HG21	0.86	0.83
1:A5:471:A:N6	1:A5:684:G:N2	2.26	0.83
5:A6:2300:A:N9	9:C:182:LYS:N	2.26	0.83
1:A5:684:G:C4	1:A5:684:G:N9	2.46	0.83
1:A5:1282:G:C6	11:E:131:HIS:HB2	2.14	0.82
1:A5:684:G:C8	11:E:104:ASN:HB2	2.14	0.82
22:Q:148:VAL:O	22:Q:152:PHE:HB2	1.77	0.82
5:A6:4757:C:C5	20:O:114:LYS:N	2.47	0.82
5:A6:2849:A:H62	5:A6:3838:U:H3	0.86	0.82
1:A5:1282:G:C6	11:E:131:HIS:CG	2.67	0.82
5:A6:2300:A:C8	5:A6:2300:A:N9	2.48	0.81
5:A6:2889:G:N3	80:W:75:HIS:N	2.28	0.81
4:B2:305:U:C6	72:II:183:GLY:N	2.48	0.81
5:A6:2590:G:H21	5:A6:2755:A:H62	1.28	0.81
4:B2:1621:U:C5	58:PP:116:LEU:N	2.49	0.81
5:A6:2300:A:C4	5:A6:2300:A:N9	2.49	0.81
5:A6:3898:G:H1	5:A6:4563:U:H3	1.28	0.81
4:B2:841:G:C6	79:YY:11:LYS:CB	2.64	0.80
4:B2:1599:U:N1	4:B2:1599:U:C2	2.49	0.80
5:A6:4370:G:C2	83:Cc:77:A:C2	2.69	0.80
80:W:70:ARG:HH21	80:W:80:LYS:HD2	1.46	0.80
4:B2:1050:A:H62	4:B2:1068:G:H21	1.29	0.80
1:A5:33:A:H8	1:A5:49:U:H3	1.28	0.80
5:A6:2768:C:N3	35:g:70:THR:N	2.30	0.80
5:A6:4500:U:H3	84:Bb:75:C:N4	1.80	0.80
38:j:22:CYS:SG	38:j:37:CYS:HB3	2.21	0.80
82:u:41:GLY:HA2	82:u:65:MET:H	1.46	0.80
5:A6:2768:C:C2	5:A6:2768:C:N1	2.50	0.80
1:A5:684:G:C4	11:E:104:ASN:CB	2.65	0.80
5:A6:4370:G:C5	83:Cc:77:A:C5	2.70	0.80
5:A6:4936:G:N2	5:A6:4938:A:N6	2.29	0.80
4:B2:944:A:H61	4:B2:982:G:H1	1.27	0.80
5:A6:4370:G:C2	5:A6:4370:G:N1	2.50	0.80
1:A5:1471:U:H3	1:A5:1493:G:H1	1.30	0.79
4:B2:656:G:H1	4:B2:1156:U:H3	1.25	0.79
4:B2:1599:U:C6	54:FF:166:ILE:N	2.50	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A6:2768:C:C4	35:g:70:THR:N	2.50	0.79
4:B2:74:G:N3	70:GG:171:THR:N	2.29	0.79
4:B2:74:G:C6	70:GG:171:THR:N	2.50	0.79
1:A5:1282:G:C5	11:E:131:HIS:CD2	2.70	0.79
8:B:72:VAL:HG13	81:c:15:PRO:HB3	1.64	0.79
5:A6:2300:A:C8	9:C:181:LYS:C	2.61	0.79
5:A6:4405:G:H1	5:A6:4439:U:H3	1.31	0.79
5:A6:4613:C:C6	5:A6:4613:C:C1'	2.65	0.79
83:Cc:55:U:N3	83:Cc:59:A:C8	2.50	0.79
1:A5:1282:G:N3	11:E:131:HIS:CG	2.50	0.79
4:B2:1653:U:H3	4:B2:1671:G:H1	1.26	0.79
4:B2:1248:U:C2	83:Cc:35:C:O3'	2.35	0.79
4:B2:1461:G:H21	4:B2:1465:A:H62	1.29	0.78
5:A6:4370:G:C4	83:Cc:77:A:C6	2.71	0.78
5:A6:4370:G:C6	5:A6:4370:G:N1	2.50	0.78
4:B2:305:U:N1	72:II:183:GLY:N	2.31	0.78
4:B2:359:U:H3	4:B2:403:G:H1	1.30	0.78
4:B2:1621:U:N3	58:PP:116:LEU:N	2.31	0.78
5:A6:4757:C:C6	20:O:114:LYS:N	2.51	0.78
1:A5:684:G:C5	1:A5:684:G:N7	2.51	0.78
1:A5:1995:G:N3	45:s:41:GLN:N	2.32	0.78
1:A5:420:A:H61	3:A8:14:U:H3	1.32	0.78
4:B2:841:G:C2	4:B2:841:G:N1	2.52	0.78
79:YY:11:LYS:CB	79:YY:11:LYS:HA	2.13	0.78
1:A5:1282:G:C2	11:E:131:HIS:CG	2.71	0.78
1:A5:1724:G:H1	1:A5:1838:A:H2	0.85	0.78
4:B2:841:G:C6	4:B2:841:G:N1	2.52	0.78
1:A5:2045:G:C4	20:O:62:MET:N	2.52	0.78
5:A6:4597:U:H3	5:A6:4614:G:H1	1.29	0.78
4:B2:526:A:N6	4:B2:559:G:H1	1.82	0.77
4:B2:1737:G:H1	4:B2:1797:U:H3	1.31	0.77
1:A5:1282:G:N1	11:E:131:HIS:CG	2.52	0.77
4:B2:841:G:C5	79:YY:11:LYS:CB	2.67	0.77
4:B2:934:G:N1	4:B2:1008:A:C2	2.48	0.77
1:A5:684:G:C4	11:E:104:ASN:HB3	2.19	0.77
1:A5:1282:G:C5	11:E:131:HIS:CG	2.72	0.77
1:A5:2045:G:C5	20:O:62:MET:N	2.52	0.77
1:A5:352:G:N2	1:A5:360:A:H61	1.81	0.77
4:B2:1232:U:H3	4:B2:1526:G:H1	0.82	0.77
1:A5:684:G:C8	11:E:104:ASN:CA	2.68	0.77
4:B2:822:U:H3	4:B2:826:A:H62	0.83	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B2:841:G:C5	79:YY:11:LYS:HB3	2.20	0.77
1:A5:960:A:N6	1:A5:1283:G:C6	2.52	0.77
1:A5:1282:G:C2	11:E:131:HIS:ND1	2.53	0.77
48:ff:132:MET:HE3	48:ff:143:LYS:HB2	1.67	0.77
1:A5:684:G:N9	11:E:104:ASN:CB	2.48	0.76
1:A5:1282:G:C2	11:E:131:HIS:CB	2.69	0.76
4:B2:841:G:C4	79:YY:11:LYS:HA	2.20	0.76
5:A6:3760:A:C4	84:Bb:38:A:H4'	2.18	0.76
1:A5:684:G:C5	11:E:104:ASN:CB	2.69	0.76
1:A5:1270:A:C6	1:A5:1270:A:N1	2.53	0.76
1:A5:1270:A:C2	1:A5:1270:A:N1	2.52	0.76
1:A5:310:G:H1	1:A5:327:U:H3	1.34	0.76
4:B2:1248:U:C2	83:Cc:36:A:P	2.78	0.76
4:B2:841:G:C4	79:YY:11:LYS:CB	2.67	0.76
5:A6:2300:A:C4	9:C:181:LYS:C	2.64	0.76
20:O:153:THR:O	20:O:157:GLU:HB2	1.85	0.76
58:PP:116:LEU:N	58:PP:116:LEU:HA	1.95	0.76
20:O:61:ARG:C	20:O:62:MET:N	2.44	0.75
5:A6:4370:G:C2	83:Cc:77:A:N3	2.54	0.75
4:B2:1640:A:N6	83:Cc:30:G:C5	2.54	0.75
1:A5:1185:G:H22	10:D:279:ARG:HH21	1.32	0.75
36:h:88:THR:HG22	36:h:91:MET:HG2	1.68	0.75
4:B2:1535:U:C2	54:FF:82:ASN:CG	2.64	0.75
5:A6:3780:G:H1	5:A6:3814:U:H3	1.34	0.75
5:A6:4757:C:N1	20:O:114:LYS:N	2.34	0.75
4:B2:841:G:C2	79:YY:11:LYS:CB	2.69	0.75
5:A6:3935:C:N4	5:A6:3936:A:H62	1.81	0.75
70:GG:170:ARG:C	70:GG:171:THR:N	2.45	0.75
8:B:130:PHE:HB3	8:B:133:TYR:H	1.52	0.74
4:B2:1248:U:C4	83:Cc:35:C:O3'	2.41	0.74
5:A6:2677:G:C2	82:u:32:LYS:NZ	2.55	0.74
13:G:176:LYS:HD3	37:i:43:MET:HE1	1.70	0.74
1:A5:684:G:C8	1:A5:684:G:N9	2.56	0.74
1:A5:1187:G:H4'	10:D:271:MET:HB3	1.68	0.74
4:B2:526:A:H61	4:B2:559:G:H1	1.34	0.74
5:A6:2300:A:C5	9:C:181:LYS:C	2.65	0.74
83:Cc:35:C:O3'	83:Cc:36:A:P	2.45	0.74
4:B2:1248:U:N1	83:Cc:35:C:O3'	2.21	0.74
5:A6:2768:C:C5	35:g:70:THR:N	2.55	0.74
1:A5:684:G:C5	11:E:104:ASN:CA	2.71	0.73
65:bb:19:HIS:HB3	65:bb:22:LYS:HG2	1.70	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B2:616:A:H62	4:B2:625:G:N2	1.86	0.73
5:A6:2889:G:N1	80:W:75:HIS:N	2.36	0.73
4:B2:920:A:H4'	77:WW:57:ARG:HH12	1.53	0.73
1:A5:1270:A:C6	31:b:112:ILE:CB	2.70	0.73
4:B2:1095:C:N3	4:B2:1149:A:N1	2.36	0.73
9:C:317:ASN:O	9:C:321:ASN:HB2	1.87	0.73
5:A6:4370:G:C6	83:Cc:77:A:C2	2.75	0.73
5:A6:4936:G:C2	5:A6:4938:A:N6	2.57	0.73
8:B:175:GLN:HE22	8:B:177:LYS:HB3	1.52	0.73
4:B2:1203:G:N3	68:CC:115:GLN:N	2.36	0.73
4:B2:1743:G:H21	4:B2:1791:A:H62	1.36	0.73
5:A6:4370:G:C6	83:Cc:77:A:N3	2.57	0.73
5:A6:4370:G:N1	83:Cc:77:A:C2	2.57	0.73
4:B2:1248:U:C6	83:Cc:35:C:O3'	2.41	0.73
1:A5:960:A:N6	1:A5:1283:G:N1	2.36	0.73
5:A6:4370:G:C5	83:Cc:77:A:C6	2.76	0.73
1:A5:33:A:N7	1:A5:49:U:C2	2.57	0.72
1:A5:1972:G:C2	45:s:41:GLN:CD	2.67	0.72
5:A6:3859:G:O3'	21:P:139:TYR:CD2	2.42	0.72
1:A5:2045:G:N3	20:O:62:MET:N	2.36	0.72
4:B2:1364:U:H3	4:B2:1375:G:H21	1.35	0.72
4:B2:1599:U:N1	54:FF:166:ILE:N	2.37	0.72
4:B2:1203:G:H21	68:CC:120:GLN:HA	1.54	0.72
5:A6:4407:G:H1	5:A6:4435:U:H3	1.37	0.72
62:TT:85:ASN:HB3	62:TT:88:MET:HB3	1.71	0.72
4:B2:841:G:N1	79:YY:11:LYS:CB	2.53	0.72
5:A6:4370:G:C6	83:Cc:77:A:C5	2.78	0.72
8:B:66:LYS:H	26:V:14:PHE:HZ	1.38	0.72
4:B2:1342:U:H3	4:B2:1483:A:N6	1.88	0.71
1:A5:512:U:H3	1:A5:647:G:H1	1.36	0.71
75:NN:70:LYS:HB3	75:NN:73:ARG:HD2	1.72	0.71
1:A5:105:A:H4'	17:L:35:ARG:HH12	1.53	0.71
4:B2:74:G:C2	70:GG:170:ARG:C	2.69	0.71
4:B2:74:G:N1	70:GG:171:THR:N	2.37	0.71
58:PP:118:GLU:HB3	61:SS:120:HIS:HB3	1.73	0.71
5:A6:2888:G:H5'	80:W:80:LYS:HD3	1.73	0.71
49:gg:157:SER:HB3	49:gg:164:ILE:HG22	1.72	0.71
4:B2:1083:A:H62	4:B2:1841:C:H1'	1.55	0.71
5:A6:3707:U:H3	5:A6:3743:G:H1	1.38	0.71
1:A5:1282:G:C6	11:E:131:HIS:CB	2.74	0.71
20:O:114:LYS:N	20:O:114:LYS:HA	1.99	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B2:842:C:H1'	79:YY:11:LYS:HD3	1.73	0.71
1:A5:1270:A:C5	31:b:112:ILE:HB	2.25	0.71
5:A6:4301:U:H3	5:A6:4309:G:H1	1.37	0.71
52:BB:107:ARG:HD2	57:OO:131:ASP:HB3	1.72	0.70
68:CC:182:CYS:HB2	77:WW:95:PRO:HB2	1.74	0.70
11:E:117:ARG:HH12	44:r:86:ALA:HB3	1.56	0.70
5:A6:3859:G:H3'	21:P:139:TYR:CE1	2.27	0.70
38:j:57:ASN:O	38:j:57:ASN:ND2	2.24	0.70
1:A5:684:G:N7	11:E:104:ASN:CB	2.55	0.70
1:A5:1460:C:H5''	22:Q:144:LYS:HG3	1.73	0.70
5:A6:3918:G:H1	5:A6:4383:U:H3	1.39	0.70
5:A6:2298:U:H3'	9:C:204:ARG:HH12	1.57	0.70
5:A6:3859:G:O3'	5:A6:3859:G:H3'	1.85	0.70
5:A6:4577:U:O2	5:A6:4726:G:N2	2.25	0.70
55:KK:53:LYS:HB2	55:KK:69:TRP:HE1	1.55	0.70
57:OO:34:PHE:HB3	57:OO:41:PHE:HB2	1.73	0.70
1:A5:751:G:H1	1:A5:911:U:H3	1.39	0.70
4:B2:1657:G:H1	4:B2:1667:U:H3	1.38	0.70
5:A6:2701:U:H3	5:A6:2715:G:H1	1.37	0.70
4:B2:677:G:N2	4:B2:1028:A:H62	1.90	0.69
66:ee:108:ARG:HE	73:JJ:39:ASN:HA	1.57	0.69
4:B2:934:G:N1	4:B2:1008:A:H2	1.84	0.69
26:V:85:ARG:HB3	26:V:98:PHE:HB2	1.72	0.69
4:B2:924:G:N2	4:B2:1018:U:O2	2.25	0.69
5:A6:2590:G:N2	5:A6:2755:A:H62	1.89	0.69
11:E:60:SER:O	11:E:64:MET:HB3	1.91	0.69
68:CC:204:ILE:HG21	68:CC:214:LEU:HD21	1.74	0.69
1:A5:1555:G:H1	1:A5:1572:U:H3	0.78	0.69
8:B:55:HIS:HB3	81:c:14:TYR:HB2	1.75	0.69
5:A6:4936:G:N3	5:A6:4938:A:N1	2.40	0.69
1:A5:312:G:H1	1:A5:325:U:H3	1.38	0.69
1:A5:974:C:H5''	12:F:46:ARG:HD2	1.74	0.69
1:A5:1289:C:N1	1:A5:1289:C:H1'	2.04	0.69
4:B2:1203:G:C2	68:CC:114:LYS:C	2.71	0.69
3:A8:70:G:H5''	28:Y:114:ASP:HB3	1.74	0.69
5:A6:2609:G:H1	5:A6:2730:U:H3	1.41	0.69
36:h:103:LYS:HB2	36:h:107:GLN:HE22	1.57	0.69
1:A5:86:U:O2	1:A5:98:A:N7	2.26	0.68
1:A5:1626:G:H1	1:A5:1636:U:H3	1.40	0.68
1:A5:684:G:C4	11:E:104:ASN:CA	2.76	0.68
11:E:136:PHE:CD1	11:E:136:PHE:CE1	2.81	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A5:286:U:H3	1:A5:301:G:H1	1.39	0.68
4:B2:693:A:H61	4:B2:736:C:H42	1.41	0.68
12:F:235:ARG:HB2	12:F:238:GLN:HB3	1.76	0.68
26:V:90:ARG:HE	81:c:20:ARG:HA	1.58	0.68
4:B2:1231:C:H42	4:B2:1527:C:H42	1.41	0.68
5:A6:3760:A:C6	84:Bb:38:A:C5'	2.77	0.68
6:A:45:VAL:HB	6:A:85:GLY:H	1.58	0.68
1:A5:1270:A:C5	31:b:112:ILE:CB	2.76	0.68
1:A5:1584:G:H1	1:A5:1609:U:H3	1.41	0.68
4:B2:878:G:H1	4:B2:908:A:H2	0.81	0.68
4:B2:1248:U:C4	83:Cc:36:A:P	2.87	0.68
4:B2:1342:U:O4	4:B2:1483:A:N7	2.27	0.68
4:B2:1599:U:N1	54:FF:166:ILE:HA	2.07	0.68
8:B:74:GLU:HB2	81:c:17:HIS:H	1.59	0.68
1:A5:1270:A:C2	31:b:112:ILE:HA	2.29	0.68
1:A5:1289:C:N1	11:E:136:PHE:CE2	2.62	0.68
4:B2:28:U:H3	4:B2:646:G:H1	1.41	0.68
1:A5:86:U:C2	1:A5:98:A:N7	2.62	0.68
83:Cc:23:G:N7	83:Cc:47:G:N2	2.35	0.68
1:A5:1972:G:C4	45:s:41:GLN:CD	2.72	0.68
4:B2:878:G:O6	4:B2:908:A:N1	2.26	0.68
1:A5:1289:C:N1	11:E:136:PHE:CZ	2.62	0.68
4:B2:1227:G:H1	4:B2:1531:A:N6	1.91	0.68
4:B2:1248:U:N3	83:Cc:35:C:O3'	2.28	0.68
4:B2:1674:G:H4'	54:FF:77:MET:HE1	1.75	0.68
5:A6:2677:G:C4	82:u:32:LYS:NZ	2.62	0.68
5:A6:4370:G:N3	83:Cc:77:A:C5	2.62	0.68
4:B2:944:A:N6	4:B2:982:G:H1	1.91	0.67
4:B2:1248:U:C5	83:Cc:35:C:O3'	2.47	0.67
19:N:115:VAL:HG11	19:N:160:GLU:HB3	1.76	0.67
5:A6:2677:G:C6	82:u:32:LYS:NZ	2.62	0.67
5:A6:3760:A:C4	84:Bb:38:A:C5'	2.77	0.67
28:Y:13:LYS:HA	28:Y:16:LYS:HG2	1.76	0.67
4:B2:74:G:C6	70:GG:170:ARG:C	2.72	0.67
4:B2:1621:U:N3	58:PP:116:LEU:HA	2.09	0.67
24:T:79:GLN:HA	24:T:84:ILE:HG22	1.77	0.67
3:A8:114:G:H1	3:A8:136:U:H3	1.41	0.67
4:B2:1385:G:H5''	53:DD:159:HIS:HB2	1.75	0.67
17:L:79:GLU:HA	17:L:82:ARG:HE	1.58	0.67
72:II:75:LYS:HB3	72:II:77:ARG:HH22	1.59	0.67
1:A5:1187:G:H3'	10:D:274:ALA:H	1.59	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
75:NN:4:MET:H	75:NN:4:MET:HE3	1.59	0.67
1:A5:471:A:C6	1:A5:684:G:N2	2.62	0.67
5:A6:3652:A:H5''	5:A6:3691:G:H22	1.59	0.67
35:g:64:LEU:O	35:g:67:LEU:O	2.12	0.67
45:s:41:GLN:N	45:s:41:GLN:HA	2.02	0.67
4:B2:1599:U:C2	54:FF:165:ASN:C	2.73	0.67
5:A6:2395:A:N6	5:A6:2820:C:O2	2.27	0.67
40:l:21:ARG:HH12	40:l:24:PRO:HD3	1.60	0.67
4:B2:1203:G:C6	68:CC:114:LYS:HA	2.30	0.67
5:A6:2657:G:H5''	82:u:35:LEU:H	1.60	0.67
5:A6:4757:C:C2	20:O:113:ASP:C	2.73	0.67
5:A6:2889:G:C2	80:W:74:ARG:C	2.73	0.66
45:s:40:MET:HB3	45:s:44:ARG:HH21	1.57	0.66
53:DD:106:ARG:HG3	53:DD:175:VAL:HG22	1.78	0.66
1:A5:651:C:H2'	1:A5:652:G:H8	1.61	0.66
15:I:87:ILE:HG13	15:I:138:ILE:HD13	1.77	0.66
46:t:80:LEU:HB3	46:t:112:ILE:HG12	1.77	0.66
51:AA:117:ARG:HG3	51:AA:119:PRO:HD3	1.77	0.66
1:A5:1593:A:H5''	5:A6:2839:U:H5''	1.77	0.66
5:A6:2863:G:N2	5:A6:2887:U:O2	2.24	0.66
5:A6:2889:G:C6	80:W:74:ARG:C	2.74	0.66
5:A6:4346:U:H5	42:o:30:LYS:HE2	1.59	0.66
6:A:204:MET:HE3	6:A:205:ASN:H	1.60	0.66
45:s:60:MET:H	45:s:60:MET:HE3	1.60	0.66
1:A5:1760:G:N1	1:A5:1773:U:N3	2.44	0.66
4:B2:1260:A:C2	4:B2:1617:G:N2	2.60	0.66
4:B2:1550:G:H21	4:B2:1559:C:H1'	1.58	0.66
1:A5:1282:G:N1	11:E:131:HIS:CB	2.58	0.66
4:B2:1324:G:N1	4:B2:1504:U:N3	2.44	0.66
5:A6:4682:U:O2	5:A6:4707:A:N7	2.28	0.66
4:B2:841:G:N3	79:YY:11:LYS:CB	2.59	0.66
5:A6:2300:A:N7	9:C:181:LYS:C	2.54	0.66
5:A6:4235:G:H5'	5:A6:4330:G:H21	1.59	0.66
1:A5:2045:G:C6	20:O:61:ARG:C	2.74	0.66
3:A8:8:U:H2'	3:A8:9:A:H8	1.61	0.66
4:B2:1248:U:N3	83:Cc:36:A:P	2.68	0.66
60:RR:35:CYS:HA	60:RR:38:ILE:HG12	1.78	0.66
80:W:126:LYS:HE2	80:W:131:VAL:HG21	1.77	0.66
1:A5:471:A:N6	1:A5:684:G:C2	2.64	0.66
1:A5:1774:C:H2'	1:A5:1775:A:H8	1.61	0.66
3:A8:70:G:H4'	28:Y:27:ARG:HH22	1.60	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B2:872:A:N6	4:B2:914:U:C2	2.64	0.66
4:B2:1050:A:H62	4:B2:1068:G:N2	1.93	0.66
5:A6:2521:G:H4'	35:g:26:PRO:HD2	1.78	0.66
50:dd:43:PHE:HA	50:dd:46:TYR:HB2	1.77	0.66
52:BB:214:LYS:HE3	52:BB:216:LYS:HD2	1.78	0.66
1:A5:1905:U:H4'	12:F:216:ARG:HH12	1.60	0.65
5:A6:2772:C:H5'	39:k:40:ARG:HG3	1.78	0.65
42:o:70:LEU:HD21	42:o:83:LEU:HD23	1.78	0.65
1:A5:1270:A:C4	31:b:112:ILE:CA	2.80	0.65
1:A5:1995:G:C2	45:s:40:MET:C	2.74	0.65
2:A7:69:U:H3	2:A7:106:G:H1	1.42	0.65
4:B2:95:G:N1	4:B2:435:A:C2	2.63	0.65
4:B2:568:C:H42	4:B2:582:U:H3	0.78	0.65
4:B2:822:U:O4	4:B2:826:A:N7	2.29	0.65
71:HH:143:ARG:HB2	71:HH:155:LYS:HB3	1.78	0.65
72:II:43:ILE:HD11	72:II:55:TYR:HB3	1.78	0.65
5:A6:2571:C:H41	5:A6:2761:U:H3	1.42	0.65
1:A5:1972:G:C6	45:s:41:GLN:CD	2.75	0.65
5:A6:4370:G:N1	83:Cc:77:A:N3	2.43	0.65
1:A5:1270:A:C5	31:b:112:ILE:N	2.65	0.65
4:B2:1101:U:O2	4:B2:1131:G:N2	2.28	0.65
1:A5:86:U:N3	1:A5:98:A:C8	2.65	0.65
4:B2:1608:U:H5''	61:SS:130:ARG:HD2	1.79	0.65
7:n:3:ALA:HA	7:n:6:ARG:HG2	1.79	0.65
4:B2:1308:U:H3'	48:ff:135:HIS:HA	1.78	0.65
1:A5:384:A:H2	28:Y:87:ARG:HH12	1.44	0.65
1:A5:1270:A:C4	31:b:112:ILE:CB	2.80	0.65
4:B2:1461:G:H21	4:B2:1465:A:N6	1.94	0.65
5:A6:2740:U:H3	6:A:184:ARG:HA	1.62	0.65
5:A6:3760:A:C5	84:Bb:38:A:C5'	2.79	0.65
5:A6:4728:U:H5''	5:A6:4729:A:H5'	1.79	0.65
4:B2:149:A:N7	4:B2:169:U:O2	2.30	0.65
4:B2:875:A:N1	4:B2:910:G:O6	2.30	0.65
5:A6:2411:C:H2'	5:A6:2412:A:H8	1.62	0.65
12:F:107:VAL:HA	12:F:110:LEU:HB2	1.79	0.65
49:gg:236:ILE:HG12	49:gg:252:THR:HG22	1.77	0.65
4:B2:110:U:O2	4:B2:351:G:N2	2.29	0.65
32:d:73:TRP:HZ3	32:d:77:ILE:HG13	1.62	0.65
43:p:39:CYS:HB3	43:p:42:CYS:SG	2.37	0.65
50:dd:3:HIS:HB3	50:dd:6:LEU:HB2	1.78	0.65
70:GG:137:ARG:HD2	70:GG:140:ARG:HG3	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A5:2045:G:C5	20:O:61:ARG:C	2.75	0.64
44:r:2:SER:H	44:r:5:LEU:HD23	1.60	0.64
1:A5:1468:C:H5''	30:a:132:ARG:HE	1.62	0.64
1:A5:1841:C:H2'	12:F:163:LYS:HD3	1.79	0.64
1:A5:33:A:N7	1:A5:49:U:O2	2.30	0.64
1:A5:1740:C:O2	1:A5:1786:A:N6	2.31	0.64
4:B2:1215:C:N3	4:B2:1220:A:N1	2.45	0.64
4:B2:1535:U:C4	54:FF:82:ASN:CG	2.75	0.64
4:B2:1854:U:H2'	4:B2:1855:G:H8	1.60	0.64
5:A6:4344:U:H5''	42:o:31:ASP:HA	1.79	0.64
15:I:47:PRO:HD2	15:I:141:LYS:HA	1.80	0.64
43:p:31:ILE:O	43:p:35:ALA:HB2	1.97	0.64
1:A5:2045:G:C2	20:O:61:ARG:C	2.76	0.64
4:B2:875:A:H2	4:B2:910:G:H1	1.41	0.64
5:A6:3936:A:N1	5:A6:4175:G:C6	2.65	0.64
21:P:126:ARG:HB3	21:P:128:ARG:HH12	1.63	0.64
43:p:42:CYS:HB3	43:p:60:CYS:SG	2.36	0.64
1:A5:1972:G:C5	45:s:41:GLN:CD	2.75	0.64
1:A5:2045:G:C4	20:O:61:ARG:C	2.76	0.64
4:B2:1172:U:O2	4:B2:1188:A:N7	2.31	0.64
4:B2:1203:G:C4	68:CC:114:LYS:C	2.75	0.64
1:A5:353:A:N7	3:A8:22:U:O2	2.31	0.64
4:B2:1621:U:C2	58:PP:115:TYR:C	2.76	0.64
1:A5:21:G:H21	3:A8:40:A:H1'	1.62	0.64
5:A6:3859:G:O3'	21:P:139:TYR:CE2	2.51	0.64
1:A5:684:G:N9	11:E:104:ASN:CA	2.61	0.64
4:B2:1461:G:N2	4:B2:1465:A:H62	1.94	0.64
50:dd:21:CYS:HB3	50:dd:26:ASN:H	1.62	0.64
73:JJ:173:VAL:HA	73:JJ:176:LYS:HB3	1.79	0.64
4:B2:327:G:H1'	81:c:116:LYS:HB3	1.80	0.64
4:B2:941:C:H4'	52:BB:136:ARG:HH22	1.63	0.64
5:A6:2849:A:N7	5:A6:3838:U:O4	2.31	0.64
5:A6:3859:G:O3'	21:P:139:TYR:CG	2.51	0.64
59:QQ:97:GLN:HA	59:QQ:102:GLU:HG3	1.80	0.64
1:A5:325:U:H5''	17:L:103:ARG:HH21	1.63	0.63
1:A5:1270:A:C6	31:b:112:ILE:CA	2.81	0.63
1:A5:1951:G:H1	1:A5:2032:U:H3	1.45	0.63
54:FF:158:ALA:HB2	54:FF:173:LEU:HB3	1.80	0.63
1:A5:231:U:O2	1:A5:235:A:N7	2.31	0.63
4:B2:680:G:H1	4:B2:1025:U:H3	1.45	0.63
5:A6:2704:C:H2'	5:A6:2705:G:H8	1.63	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:B:305:THR:H	8:B:308:ASP:HB3	1.62	0.63
1:A5:1270:A:N1	31:b:112:ILE:CB	2.61	0.63
1:A5:1289:C:N1	11:E:136:PHE:CE1	2.66	0.63
14:H:106:GLN:HB2	14:H:111:LEU:HB3	1.81	0.63
4:B2:1377:U:H3'	51:AA:102:ARG:HH12	1.61	0.63
53:DD:76:ARG:HA	55:KK:22:VAL:HG11	1.79	0.63
9:C:323:ARG:HA	9:C:326:LEU:HB3	1.80	0.63
16:J:56:THR:HG22	16:J:58:ARG:HH12	1.63	0.63
1:A5:59:A:N7	1:A5:337:U:C2	2.67	0.63
4:B2:1206:G:H21	4:B2:1700:C:H41	1.45	0.63
14:H:91:LYS:HB2	14:H:183:GLU:HG3	1.81	0.63
26:V:85:ARG:HD2	26:V:100:ASP:HA	1.79	0.63
50:dd:21:CYS:CB	50:dd:39:CYS:SG	2.85	0.63
1:A5:684:G:N7	11:E:104:ASN:CA	2.56	0.63
4:B2:934:G:O6	4:B2:1008:A:N1	2.31	0.63
28:Y:8:THR:HG22	28:Y:10:ASP:H	1.64	0.63
1:A5:59:A:N7	1:A5:337:U:O2	2.31	0.63
1:A5:1289:C:N1	11:E:136:PHE:CD1	2.67	0.63
4:B2:1402:A:N7	4:B2:1441:U:C4	2.67	0.63
5:A6:2300:A:N9	9:C:181:LYS:C	2.57	0.63
5:A6:3760:A:C6	84:Bb:38:A:C4'	2.82	0.63
5:A6:4370:G:N1	83:Cc:77:A:C4	2.67	0.63
8:B:376:HIS:HD2	81:c:35:LYS:HG2	1.63	0.63
42:o:28:LYS:HZ1	83:Cc:77:A:H61	1.46	0.63
81:c:98:PRO:HA	81:c:101:ARG:HB3	1.80	0.63
1:A5:53:C:H4'	5:A6:2462:C:H1'	1.81	0.62
4:B2:1535:U:C2	54:FF:82:ASN:CB	2.82	0.62
1:A5:1270:A:C2	31:b:112:ILE:CB	2.82	0.62
3:A8:60:G:H5''	36:h:58:LEU:HD21	1.80	0.62
4:B2:165:G:H2'	4:B2:166:A:H8	1.64	0.62
4:B2:1522:A:H5''	61:SS:144:ARG:HD2	1.81	0.62
4:B2:1743:G:N2	4:B2:1791:A:H62	1.96	0.62
5:A6:3760:A:C2	84:Bb:38:A:C5'	2.81	0.62
20:O:16:LEU:HA	20:O:19:LEU:HD12	1.81	0.62
4:B2:153:G:H21	70:GG:13:GLN:HG2	1.63	0.62
4:B2:616:A:H62	4:B2:625:G:H21	1.45	0.62
4:B2:1248:U:H3	83:Cc:34:U:H2'	1.64	0.62
5:A6:3705:G:H21	6:A:224:THR:HG21	1.62	0.62
5:A6:4888:U:O2	5:A6:4931:G:N2	2.32	0.62
4:B2:74:G:C5	70:GG:170:ARG:C	2.77	0.62
5:A6:2405:G:H21	5:A6:2791:C:H5'	1.62	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A6:4936:G:N2	5:A6:4938:A:C6	2.64	0.62
9:C:138:MET:HE1	9:C:144:ILE:H	1.64	0.62
54:FF:85:LYS:HB3	54:FF:88:MET:HG2	1.81	0.62
1:A5:1815:G:H1	1:A5:1825:A:H1'	1.64	0.62
1:A5:1972:G:C2	45:s:41:GLN:CG	2.83	0.62
4:B2:1288:U:O2	4:B2:1311:C:N3	2.32	0.62
5:A6:2677:G:C5	82:u:32:LYS:NZ	2.66	0.62
72:II:198:TYR:HA	72:II:201:LYS:HE3	1.81	0.62
80:W:151:ARG:HH21	80:W:155:LEU:HB3	1.65	0.62
1:A5:242:U:H4'	28:Y:2:LYS:HZ1	1.65	0.62
5:A6:2677:G:N1	82:u:32:LYS:NZ	2.48	0.62
5:A6:2663:G:H21	5:A6:2676:A:H1'	1.65	0.62
5:A6:3760:A:C4	84:Bb:38:A:C4'	2.82	0.62
4:B2:526:A:N6	4:B2:559:G:N1	2.37	0.62
4:B2:74:G:N1	70:GG:170:ARG:C	2.58	0.62
4:B2:526:A:N1	4:B2:559:G:N2	2.46	0.62
4:B2:1420:G:H1'	62:TT:3:GLY:HA3	1.81	0.62
69:EE:100:ARG:HB2	69:EE:114:ILE:HD13	1.81	0.62
5:A6:3859:G:O3'	21:P:139:TYR:CD1	2.53	0.62
5:A6:4369:A:H1'	42:o:28:LYS:HE2	1.81	0.62
5:A6:4613:C:C2	5:A6:4613:C:C1'	2.80	0.62
22:Q:50:ARG:HB3	22:Q:83:VAL:HG11	1.82	0.62
57:OO:22:ALA:HB3	57:OO:25:GLU:HB3	1.81	0.62
5:A6:2904:U:H5''	5:A6:2905:C:H5	1.65	0.61
5:A6:4632:U:H3	5:A6:4666:G:H1	1.46	0.61
4:B2:841:G:C2	79:YY:11:LYS:CA	2.83	0.61
4:B2:878:G:C6	4:B2:908:A:N1	2.68	0.61
5:A6:2324:C:H4'	33:e:78:LEU:HD21	1.81	0.61
4:B2:873:G:H2'	4:B2:874:G:H8	1.65	0.61
4:B2:925:G:N2	4:B2:1017:U:O2	2.31	0.61
5:A6:2335:C:H2'	5:A6:2336:G:H8	1.64	0.61
16:J:62:ILE:HG21	16:J:68:ILE:HD13	1.82	0.61
4:B2:379:C:H5''	72:II:56:ARG:HH22	1.66	0.61
4:B2:1069:U:H5''	6:A:248:GLY:HA3	1.82	0.61
4:B2:1288:U:H3'	48:ff:95:ARG:HH12	1.64	0.61
19:N:7:ILE:HG23	19:N:46:ASP:HB3	1.83	0.61
27:X:125:ASN:HB2	27:X:137:TYR:HB2	1.82	0.61
39:k:34:PHE:O	39:k:44:THR:HA	2.00	0.61
57:OO:57:THR:HG23	57:OO:59:GLY:H	1.65	0.61
1:A5:1273:G:H21	11:E:76:SER:HB2	1.65	0.61
5:A6:2659:A:H5'	82:u:31:TYR:H	1.66	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:Y:58:VAL:HG13	28:Y:59:ARG:HG2	1.83	0.61
53:DD:135:GLU:HB2	53:DD:153:VAL:HG13	1.82	0.61
73:JJ:131:ARG:HE	73:JJ:145:PRO:HD3	1.65	0.61
1:A5:471:A:H62	1:A5:684:G:N2	1.99	0.61
1:A5:1934:A:N1	1:A5:2052:G:O6	2.34	0.61
4:B2:876:C:H2'	4:B2:878:G:H5'	1.83	0.61
4:B2:900:C:H2'	4:B2:901:G:H8	1.64	0.61
5:A6:2768:C:C2	35:g:69:LYS:C	2.79	0.61
22:Q:50:ARG:HG2	22:Q:53:MET:HE1	1.82	0.61
1:A5:978:G:H5''	11:E:68:LYS:HE3	1.81	0.61
4:B2:1535:U:C6	4:B2:1535:U:C1'	2.83	0.61
9:C:183:VAL:HG12	9:C:204:ARG:HB3	1.82	0.61
5:A6:5000:G:H21	8:B:318:GLY:HA2	1.64	0.61
5:A6:2683:C:H4'	35:g:55:GLY:HA2	1.83	0.61
5:A6:4736:C:H2'	5:A6:4737:G:H8	1.65	0.61
5:A6:4763:U:H1'	14:H:44:GLU:HG2	1.83	0.61
47:cc:55:VAL:HB	54:FF:34:SER:HA	1.82	0.61
1:A5:1282:G:C5	11:E:131:HIS:CB	2.84	0.61
3:A8:112:G:H5''	5:A6:2778:G:H22	1.65	0.61
5:A6:3859:G:HO3'	5:A6:3860:A:P	2.22	0.61
5:A6:4064:C:H2'	5:A6:4065:G:H8	1.65	0.61
47:cc:40:ARG:HD2	67:aa:51:ARG:HH12	1.66	0.61
1:A5:684:G:C8	11:E:103:LYS:HG3	2.35	0.60
4:B2:1535:U:N3	54:FF:82:ASN:CG	2.59	0.60
5:A6:3842:C:H4'	26:V:51:ARG:HA	1.83	0.60
9:C:153:VAL:HG23	9:C:252:TRP:HB2	1.83	0.60
83:Cc:35:C:C3'	83:Cc:35:C:HO3'	2.11	0.60
1:A5:2020:U:H1'	45:s:57:LYS:HD3	1.83	0.60
4:B2:86:C:H1'	4:B2:170:A:H61	1.67	0.60
12:F:94:ILE:HG22	12:F:222:LYS:HE2	1.82	0.60
25:U:19:LEU:HB2	25:U:74:SER:O	2.02	0.60
44:r:61:VAL:HG13	44:r:79:ARG:HH22	1.66	0.60
5:A6:4613:C:C2	14:H:121:LYS:CD	2.84	0.60
12:F:37:ALA:HA	12:F:40:MET:HE2	1.82	0.60
36:h:4:ILE:HD13	36:h:9:LEU:HD11	1.82	0.60
46:t:133:LEU:HD22	46:t:148:PRO:HB3	1.82	0.60
2:A7:76:U:O2	2:A7:100:A:N7	2.35	0.60
5:A6:2550:G:H21	5:A6:2587:A:H1'	1.65	0.60
5:A6:2792:C:H1'	38:j:9:GLY:HA2	1.82	0.60
5:A6:4370:G:C2	83:Cc:77:A:C5	2.85	0.60
18:M:7:VAL:HG13	23:S:154:LEU:HD21	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:Z:25:ILE:HA	29:Z:43:VAL:HG12	1.84	0.60
40:l:16:LYS:O	40:l:20:ASN:HB2	2.01	0.60
74:LL:116:CYS:HA	74:LL:118:ARG:HH21	1.66	0.60
1:A5:70:A:H62	1:A5:314:G:H1'	1.64	0.60
1:A5:1282:G:C6	11:E:131:HIS:CD2	2.89	0.60
4:B2:616:A:N6	4:B2:625:G:H21	2.00	0.60
5:A6:2341:G:H5'	9:C:46:LYS:HE2	1.84	0.60
5:A6:4092:G:H3'	5:A6:4093:G:H21	1.67	0.60
5:A6:4692:A:H3'	5:A6:4693:C:H2'	1.83	0.60
74:LL:59:LYS:HB3	74:LL:134:LEU:HD23	1.83	0.60
1:A5:1463:C:H5''	31:b:31:SER:HB2	1.84	0.60
1:A5:1995:G:C4	45:s:40:MET:C	2.80	0.60
4:B2:1659:U:H5'	50:dd:31:ILE:HA	1.83	0.60
20:O:177:LEU:HA	20:O:180:GLN:HE21	1.67	0.60
28:Y:54:GLU:HB2	28:Y:67:ILE:HD11	1.83	0.60
81:c:34:ALA:HA	81:c:37:GLU:HB3	1.82	0.60
10:D:51:MET:HB3	10:D:146:LEU:HA	1.83	0.60
4:B2:924:G:H1	4:B2:1018:U:H3	1.50	0.60
20:O:88:LEU:HD22	20:O:89:PRO:HD2	1.83	0.60
66:ee:110:MET:HA	66:ee:113:ASN:HB2	1.84	0.60
69:EE:122:LYS:HG2	69:EE:164:LEU:HD11	1.84	0.60
4:B2:1656:G:N2	4:B2:1668:U:O2	2.32	0.60
5:A6:4613:C:C2	14:H:121:LYS:CG	2.85	0.60
17:L:123:LYS:HD2	36:h:122:LYS:HB2	1.83	0.60
4:B2:1374:C:H5'	60:RR:10:LYS:HZ3	1.67	0.59
4:B2:1757:G:O6	4:B2:1776:G:C2	2.55	0.59
7:n:13:LEU:HA	7:n:16:LYS:HE3	1.84	0.59
52:BB:7:LYS:HG2	52:BB:8:ARG:HG3	1.83	0.59
4:B2:1535:U:N1	54:FF:82:ASN:CG	2.60	0.59
4:B2:1215:C:O2	4:B2:1220:A:N6	2.34	0.59
4:B2:1407:U:H1'	4:B2:1443:C:H42	1.67	0.59
11:E:136:PHE:CD2	11:E:136:PHE:CE2	2.90	0.59
1:A5:72:C:H5'	37:i:15:HIS:HB2	1.84	0.59
1:A5:310:G:O6	1:A5:327:U:O4	2.20	0.59
1:A5:684:G:H8	11:E:103:LYS:HG3	1.67	0.59
1:A5:2000:G:H5'	1:A5:2001:G:H5'	1.83	0.59
5:A6:2431:A:H5''	40:l:22:PRO:HG3	1.84	0.59
5:A6:4258:C:H5'	16:J:68:ILE:HD11	1.84	0.59
5:A6:4946:U:C4	34:f:50:VAL:HA	2.37	0.59
23:S:30:MET:HB3	23:S:32:ILE:HG13	1.85	0.59
38:j:57:ASN:HD22	38:j:57:ASN:C	2.08	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A5:35:U:H4'	1:A5:1525:A:H2	1.66	0.59
1:A5:275:C:H5''	1:A5:276:C:H5'	1.84	0.59
5:A6:2266:C:H5''	5:A6:2270:G:H21	1.68	0.59
5:A6:2363:A:H62	5:A6:3859:G:H21	1.49	0.59
5:A6:3616:U:H5''	81:c:44:ARG:HD2	1.84	0.59
5:A6:3619:G:H5'	80:W:78:ILE:HB	1.84	0.59
5:A6:4870:G:H21	23:S:175:PHE:HE1	1.51	0.59
8:B:57:VAL:HA	81:c:15:PRO:HD2	1.85	0.59
4:B2:885:U:O2	4:B2:901:G:O6	2.20	0.59
14:H:114:ILE:HB	14:H:124:ARG:HB2	1.84	0.59
49:gg:77:PHE:HB3	49:gg:89:LEU:HD11	1.84	0.59
73:JJ:46:VAL:HG11	73:JJ:106:LEU:HG	1.82	0.59
1:A5:658:C:H2'	1:A5:659:G:H8	1.66	0.59
1:A5:1282:G:C4	11:E:131:HIS:CB	2.86	0.59
4:B2:368:U:H5	4:B2:371:A:H62	1.49	0.59
61:SS:13:LEU:HB2	61:SS:20:ILE:HB	1.85	0.59
1:A5:1943:A:H5''	15:I:162:ARG:HE	1.66	0.59
5:A6:4232:U:H5'	42:o:3:ASN:HB3	1.85	0.59
5:A6:4370:G:N3	83:Cc:77:A:C6	2.71	0.59
48:ff:108:VAL:HG22	56:MM:64:LEU:HD13	1.84	0.59
1:A5:484:U:O2	1:A5:671:G:N2	2.36	0.59
4:B2:1130:G:H4'	75:NN:9:LYS:HB2	1.85	0.59
35:g:64:LEU:O	35:g:67:LEU:C	2.45	0.59
46:t:17:CYS:HB3	46:t:46:ILE:HG21	1.84	0.59
52:BB:60:ASP:HA	52:BB:63:LYS:HG2	1.85	0.59
68:CC:115:GLN:N	68:CC:115:GLN:HA	2.03	0.59
5:A6:2768:C:N3	35:g:69:LYS:C	2.61	0.59
46:t:124:GLU:HG2	46:t:127:GLY:H	1.68	0.59
1:A5:1270:A:C2	31:b:112:ILE:CA	2.85	0.58
25:U:55:ASN:O	25:U:55:ASN:ND2	2.36	0.58
39:k:54:GLU:HA	39:k:57:LYS:HB2	1.84	0.58
1:A5:1972:G:N1	45:s:41:GLN:CD	2.62	0.58
5:A6:4370:G:N3	83:Cc:77:A:C2	2.71	0.58
5:A6:4752:U:H1'	5:A6:4949:G:H2'	1.85	0.58
12:F:107:VAL:HG11	12:F:134:ILE:HD11	1.86	0.58
41:m:110:CYS:HB3	41:m:115:CYS:SG	2.43	0.58
52:BB:45:GLY:HA3	57:OO:47:LEU:HD21	1.84	0.58
1:A5:639:U:H4'	1:A5:640:C:H5'	1.84	0.58
1:A5:1995:G:N2	45:s:43:ILE:H	2.00	0.58
4:B2:677:G:H21	4:B2:1028:A:N6	1.97	0.58
4:B2:1556:A:H2'	50:dd:13:LYS:HD2	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A6:2928:G:H5'	29:Z:96:VAL:H	1.68	0.58
14:H:152:GLU:O	14:H:156:ASN:HB2	2.03	0.58
57:OO:149:ARG:HB2	67:aa:26:CYS:HB2	1.83	0.58
61:SS:39:ARG:HG2	62:TT:45:LEU:HD23	1.85	0.58
4:B2:841:G:C4	79:YY:11:LYS:CA	2.87	0.58
5:A6:2768:C:C4	35:g:69:LYS:C	2.81	0.58
1:A5:1333:A:H2'	1:A5:1334:A:H8	1.68	0.58
1:A5:1759:G:N2	1:A5:1773:U:O2	2.36	0.58
5:A6:3860:A:P	21:P:139:TYR:CE1	2.97	0.58
30:a:73:VAL:HG11	30:a:103:VAL:HG21	1.85	0.58
34:f:25:THR:HG22	34:f:87:LYS:HE2	1.86	0.58
43:p:87:LYS:HA	43:p:90:LYS:HE2	1.83	0.58
83:Cc:55:U:C2	83:Cc:59:A:N7	2.72	0.58
1:A5:1282:G:N3	11:E:131:HIS:CB	2.67	0.58
3:A8:15:G:H4'	5:A6:2355:G:H4'	1.85	0.58
4:B2:1224:G:H1	4:B2:1642:U:H3	1.52	0.58
4:B2:1563:G:H5''	62:TT:121:ARG:HH21	1.68	0.58
46:t:74:VAL:HG12	46:t:119:ARG:HH22	1.68	0.58
68:CC:94:ILE:HG21	68:CC:162:ILE:HG13	1.85	0.58
81:c:109:ILE:HD12	81:c:112:ALA:HB3	1.85	0.58
5:A6:2910:G:H1'	5:A6:2914:U:H5'	1.85	0.58
45:s:65:ILE:HG21	45:s:79:LEU:HD13	1.84	0.58
54:FF:100:ILE:HA	54:FF:178:ILE:HD11	1.85	0.58
77:WW:25:VAL:HG13	77:WW:27:ILE:HD11	1.84	0.58
1:A5:709:C:H2'	1:A5:710:G:H8	1.69	0.58
5:A6:2550:G:N2	5:A6:2767:U:O2	2.29	0.58
54:FF:124:ASP:HB3	54:FF:196:LEU:HD12	1.86	0.58
4:B2:928:G:N2	4:B2:1013:U:O2	2.36	0.58
5:A6:4575:G:O6	5:A6:4728:U:O2	2.22	0.58
13:G:154:LEU:HB3	13:G:204:PHE:HB2	1.84	0.58
49:gg:107:ASP:HB2	49:gg:125:ARG:HD2	1.86	0.58
69:EE:137:PRO:HG2	69:EE:149:TYR:HA	1.86	0.58
70:GG:56:ASN:H	70:GG:108:VAL:HG13	1.69	0.58
82:u:37:MET:HB3	82:u:64:ALA:HB2	1.85	0.58
4:B2:185:G:O6	4:B2:214:U:O2	2.21	0.57
4:B2:377:G:H5''	72:II:98:LYS:HD3	1.86	0.57
5:A6:3760:A:C5	84:Bb:38:A:C4'	2.86	0.57
6:A:6:ARG:HA	6:A:9:ARG:HD3	1.86	0.57
9:C:182:LYS:HG2	9:C:204:ARG:HG2	1.86	0.57
14:H:82:LYS:HE2	14:H:186:THR:HG22	1.85	0.57
1:A5:176:G:H5''	36:h:101:LYS:HE3	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A6:3859:G:O3'	21:P:139:TYR:CZ	2.58	0.57
28:Y:26:ARG:HG3	28:Y:75:ARG:HB3	1.85	0.57
68:CC:76:LYS:HE2	68:CC:76:LYS:H	1.69	0.57
71:HH:66:VAL:HG22	71:HH:96:ALA:HB1	1.86	0.57
1:A5:350:C:H3'	9:C:197:ARG:HH12	1.69	0.57
22:Q:63:LEU:HG	22:Q:89:ASP:H	1.69	0.57
1:A5:1270:A:H5''	31:b:111:ARG:HH21	1.69	0.57
1:A5:1906:U:O2	1:A5:2069:A:N7	2.37	0.57
5:A6:3720:G:N2	5:A6:3733:A:N1	2.46	0.57
13:G:56:LYS:HB3	27:X:45:THR:HG23	1.86	0.57
23:S:51:LEU:HD21	24:T:153:PRO:HA	1.87	0.57
4:B2:1487:A:H1'	68:CC:118:ALA:HB1	1.85	0.57
5:A6:4370:G:C2	83:Cc:77:A:C4	2.91	0.57
22:Q:86:VAL:HB	22:Q:105:VAL:HG22	1.87	0.57
33:e:22:ARG:HD3	33:e:31:ILE:HG23	1.86	0.57
4:B2:1621:U:H1'	58:PP:118:GLU:H	1.69	0.57
5:A6:2524:U:O2	5:A6:2529:A:N7	2.37	0.57
5:A6:3929:G:H1	5:A6:4181:U:H3	1.49	0.57
8:B:173:LEU:HG	8:B:175:GLN:H	1.69	0.57
9:C:84:THR:HG23	9:C:87:SER:H	1.70	0.57
21:P:67:VAL:HG13	21:P:82:ARG:HH11	1.70	0.57
36:h:104:THR:O	36:h:108:GLN:HB2	2.04	0.57
65:bb:52:THR:HG21	75:NN:53:ILE:HG22	1.87	0.57
75:NN:71:ILE:HA	75:NN:74:ILE:HD12	1.87	0.57
4:B2:181:A:H4'	4:B2:182:C:H5'	1.87	0.57
4:B2:955:A:C5	4:B2:971:G:N2	2.72	0.57
5:A6:4981:G:H3'	5:A6:4982:A:H8	1.68	0.57
22:Q:39:THR:HB	22:Q:132:LYS:HE2	1.87	0.57
35:g:69:LYS:O	35:g:73:HIS:HB3	2.05	0.57
51:AA:187:GLY:HA2	76:VV:45:ARG:HH11	1.70	0.57
71:HH:31:GLU:HG3	71:HH:37:LYS:HA	1.86	0.57
1:A5:959:G:C2	11:E:127:LYS:CG	2.87	0.57
1:A5:2062:C:H1'	23:S:111:ARG:HH22	1.70	0.57
4:B2:1574:C:H2'	4:B2:1575:G:H8	1.69	0.57
9:C:34:PRO:HG2	44:r:9:ILE:HG21	1.87	0.57
20:O:92:THR:HG23	20:O:95:GLY:H	1.68	0.57
26:V:129:TRP:HB2	26:V:132:ILE:HB	1.87	0.57
46:t:73:VAL:HG13	46:t:75:PRO:HD3	1.87	0.57
77:WW:103:VAL:HB	77:WW:129:PHE:HE2	1.70	0.57
4:B2:1701:C:H2'	83:Cc:35:C:H42	1.69	0.57
11:E:136:PHE:CE1	11:E:136:PHE:CZ	2.93	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:E:136:PHE:CE2	11:E:136:PHE:CZ	2.93	0.57
18:M:12:VAL:HG11	18:M:82:ILE:HG21	1.86	0.57
28:Y:37:GLU:O	28:Y:41:LYS:HB2	2.04	0.57
49:gg:218:LEU:HB3	49:gg:227:LEU:HD12	1.87	0.57
57:OO:72:TYR:HA	57:OO:75:MET:HG3	1.85	0.57
68:CC:261:PHE:HB3	76:VV:52:THR:HB	1.86	0.57
4:B2:1142:G:H21	4:B2:1145:A:H62	1.52	0.57
5:A6:4597:U:O4	5:A6:4614:G:O6	2.23	0.57
5:A6:4618:G:H5''	26:V:15:ARG:HG3	1.86	0.57
55:KK:84:HIS:HB2	56:MM:27:ILE:HD13	1.87	0.57
80:W:149:LYS:HA	80:W:152:LYS:HD2	1.87	0.57
4:B2:5:U:H2'	4:B2:6:G:H8	1.70	0.56
4:B2:823:U:H1'	73:JJ:142:VAL:HG22	1.85	0.56
10:D:65:ALA:HB1	10:D:72:ASP:HB2	1.87	0.56
11:E:261:LEU:HD23	11:E:264:ILE:HD12	1.87	0.56
15:I:190:LEU:HA	15:I:198:LYS:O	2.04	0.56
17:L:20:ARG:H	17:L:20:ARG:HD3	1.69	0.56
21:P:92:LEU:HA	21:P:95:LEU:HD23	1.87	0.56
1:A5:1290:G:H21	5:A6:4942:C:H42	1.53	0.56
1:A5:1554:A:H3'	1:A5:1555:G:H8	1.70	0.56
1:A5:1724:G:O6	1:A5:1838:A:N1	2.38	0.56
4:B2:1203:G:C2	68:CC:115:GLN:HA	2.40	0.56
1:A5:959:G:C2	11:E:127:LYS:CD	2.88	0.56
1:A5:1456:C:H4'	22:Q:73:PRO:HG2	1.86	0.56
1:A5:1919:G:H21	34:f:34:TYR:HA	1.70	0.56
4:B2:1248:U:N1	83:Cc:36:A:P	2.78	0.56
4:B2:1324:G:N2	4:B2:1504:U:O2	2.37	0.56
5:A6:2300:A:C5	5:A6:2300:A:N7	2.73	0.56
5:A6:4871:C:H3'	5:A6:4872:G:H21	1.71	0.56
5:A6:5018:C:H2'	5:A6:5019:A:H8	1.70	0.56
13:G:244:PRO:HG2	13:G:245:LYS:HZ2	1.71	0.56
15:I:85:PHE:HB2	15:I:138:ILE:HD11	1.86	0.56
52:BB:38:MET:H	52:BB:38:MET:HE3	1.70	0.56
55:KK:3:MET:HE1	55:KK:8:ARG:HB2	1.86	0.56
77:WW:26:LEU:HD21	77:WW:60:LYS:HD2	1.87	0.56
1:A5:1270:A:N3	31:b:112:ILE:CB	2.69	0.56
1:A5:1975:G:H2'	46:t:14:TYR:HB2	1.88	0.56
4:B2:1130:G:H2'	4:B2:1131:G:H8	1.69	0.56
4:B2:1284:A:H2'	56:MM:91:LEU:HD11	1.87	0.56
10:D:90:VAL:HG11	10:D:231:VAL:HG21	1.88	0.56
51:AA:76:VAL:HA	51:AA:123:VAL:HB	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A5:1289:C:N1	11:E:136:PHE:CD2	2.73	0.56
4:B2:639:C:H2'	4:B2:640:A:H8	1.71	0.56
5:A6:3590:G:H5''	5:A6:3593:C:H42	1.71	0.56
5:A6:3860:A:P	21:P:139:TYR:CZ	2.99	0.56
21:P:119:VAL:HG22	21:P:146:ILE:HG22	1.87	0.56
30:a:38:MET:HE3	30:a:38:MET:H	1.71	0.56
1:A5:1972:G:C4	45:s:41:GLN:CG	2.89	0.56
4:B2:324:C:H5''	4:B2:325:C:H5'	1.86	0.56
4:B2:435:A:H2'	4:B2:450:C:H5'	1.87	0.56
4:B2:522:A:H3'	73:JJ:38:ARG:HD2	1.87	0.56
4:B2:1166:G:O6	4:B2:1193:U:O2	2.23	0.56
4:B2:1298:G:H4'	58:PP:78:THR:HA	1.88	0.56
4:B2:1372:U:H1'	60:RR:4:VAL:HG11	1.88	0.56
4:B2:1535:U:C6	54:FF:82:ASN:CG	2.84	0.56
5:A6:3845:A:H4'	5:A6:4668:U:H4'	1.88	0.56
12:F:93:ARG:HB2	12:F:113:LEU:HD12	1.88	0.56
29:Z:51:ARG:HB2	29:Z:65:ARG:HB3	1.87	0.56
30:a:123:ILE:HG22	30:a:125:LYS:HZ1	1.70	0.56
36:h:91:MET:HE3	36:h:94:ARG:HD2	1.87	0.56
59:QQ:48:GLN:HA	59:QQ:51:LEU:HD13	1.88	0.56
60:RR:34:VAL:HG12	60:RR:38:ILE:HD13	1.87	0.56
1:A5:643:C:H5''	17:L:162:LYS:HE3	1.88	0.56
1:A5:1282:G:C5	11:E:131:HIS:HD2	2.21	0.56
4:B2:74:G:C4	70:GG:170:ARG:C	2.83	0.56
4:B2:976:G:H21	57:OO:50:LYS:HE3	1.71	0.56
6:A:92:LYS:HG2	6:A:106:THR:HG21	1.87	0.56
56:MM:52:LEU:HB3	56:MM:76:LEU:HD11	1.87	0.56
73:JJ:144:ILE:HB	73:JJ:147:PHE:HB2	1.86	0.56
1:A5:1550:G:O6	1:A5:1578:U:O4	2.23	0.56
5:A6:4200:G:H1	15:I:116:ARG:CZ	2.19	0.56
5:A6:4370:G:N3	83:Cc:77:A:N3	2.51	0.56
35:g:60:ARG:HB2	35:g:63:VAL:HG22	1.87	0.56
49:gg:147:HIS:HA	49:gg:175:LYS:HZ3	1.69	0.56
51:AA:163:CYS:HB2	51:AA:174:MET:HE2	1.87	0.56
1:A5:751:G:O6	1:A5:911:U:O4	2.24	0.56
1:A5:1990:A:H5''	46:t:138:SER:HA	1.88	0.56
4:B2:520:A:H2'	4:B2:521:A:H8	1.71	0.56
4:B2:1406:G:H21	4:B2:1443:C:H41	1.53	0.56
5:A6:2652:G:H1'	35:g:51:GLY:HA3	1.87	0.56
5:A6:3870:C:H2'	5:A6:3871:A:H8	1.70	0.56
5:A6:4664:A:H3'	5:A6:4665:A:H8	1.71	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:o:22:LYS:O	42:o:70:LEU:HA	2.05	0.56
69:EE:183:VAL:HG11	69:EE:188:ASN:HB2	1.87	0.56
82:u:41:GLY:H	82:u:64:ALA:H	1.53	0.56
1:A5:1972:G:C6	45:s:41:GLN:CG	2.89	0.56
1:A5:2045:G:N3	20:O:61:ARG:C	2.63	0.56
5:A6:2597:G:H2'	5:A6:2598:A:H8	1.71	0.56
5:A6:4543:G:H5'	6:A:220:GLY:HA3	1.87	0.56
61:SS:54:LYS:HD2	61:SS:58:GLU:HB3	1.87	0.56
1:A5:490:C:H2'	9:C:5:ARG:HD2	1.88	0.55
4:B2:53:C:H2'	4:B2:54:A:H8	1.70	0.55
4:B2:1007:C:H4'	75:NN:104:ARG:HH12	1.71	0.55
4:B2:1095:C:O2	4:B2:1149:A:N6	2.32	0.55
5:A6:4510:A:H62	26:V:46:LYS:HD3	1.71	0.55
17:L:48:PRO:HG2	36:h:120:ALA:HB2	1.88	0.55
31:b:46:ALA:HA	31:b:49:HIS:CD2	2.41	0.55
35:g:70:THR:N	35:g:70:THR:HA	2.06	0.55
54:FF:49:LEU:HD12	59:QQ:50:LYS:HG2	1.88	0.55
81:c:104:GLN:HG3	81:c:107:GLN:HE21	1.71	0.55
83:Cc:77:A:C6	83:Cc:77:A:C5	2.59	0.55
1:A5:1616:U:H2'	1:A5:1617:G:H8	1.71	0.55
4:B2:1576:G:H21	4:B2:1582:C:H1'	1.72	0.55
5:A6:4134:C:H2'	5:A6:4135:G:H8	1.70	0.55
5:A6:4421:C:H42	5:A6:4475:G:N2	2.04	0.55
9:C:326:LEU:HD23	9:C:333:LYS:HB2	1.88	0.55
24:T:117:LYS:HD2	24:T:120:LYS:HZ1	1.70	0.55
26:V:57:VAL:HA	26:V:81:VAL:HG13	1.88	0.55
37:i:44:ILE:HA	37:i:47:VAL:HG22	1.88	0.55
71:HH:95:ILE:HG22	71:HH:132:ASP:HB2	1.87	0.55
1:A5:1913:C:H5''	20:O:25:LYS:HE2	1.87	0.55
1:A5:1995:G:N3	45:s:40:MET:O	2.40	0.55
5:A6:3760:A:N1	84:Bb:38:A:C5'	2.69	0.55
13:G:148:GLU:HA	13:G:177:MET:HE1	1.87	0.55
17:L:21:ARG:HH21	19:N:193:ARG:HA	1.70	0.55
82:u:90:ARG:H	82:u:90:ARG:HD3	1.71	0.55
1:A5:113:A:H1'	19:N:50:ARG:HA	1.88	0.55
1:A5:1662:C:H41	30:a:10:LYS:HA	1.70	0.55
4:B2:636:C:H5''	66:ee:96:GLN:HE22	1.71	0.55
4:B2:982:G:H2'	4:B2:983:A:H8	1.70	0.55
5:A6:3760:A:N3	84:Bb:38:A:C5'	2.70	0.55
5:A6:4973:U:H3	5:A6:4985:U:H3	1.55	0.55
8:B:316:PRO:HB2	8:B:372:SER:HA	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:E:108:ARG:HD3	11:E:110:VAL:HG22	1.89	0.55
22:Q:24:TYR:HA	22:Q:27:LEU:HD12	1.88	0.55
79:YY:15:ASN:HB2	79:YY:22:GLN:HG2	1.89	0.55
5:A6:2619:G:H3'	25:U:81:ARG:HH21	1.71	0.55
5:A6:4630:G:N2	5:A6:4668:U:O2	2.36	0.55
8:B:317:LEU:HD22	8:B:382:VAL:HG13	1.89	0.55
52:BB:228:LEU:HA	52:BB:231:LEU:HD12	1.88	0.55
71:HH:146:VAL:HG22	71:HH:152:ARG:HG3	1.89	0.55
1:A5:1972:G:N3	45:s:41:GLN:CD	2.64	0.55
4:B2:1699:A:H5''	4:B2:1700:C:H5'	1.88	0.55
5:A6:2403:A:H3'	5:A6:2404:A:H8	1.72	0.55
30:a:3:SER:HA	30:a:6:ARG:HD3	1.89	0.55
52:BB:28:LYS:HD2	52:BB:48:LEU:HG	1.88	0.55
5:A6:4757:C:C6	20:O:113:ASP:C	2.85	0.55
10:D:68:ARG:HB2	10:D:73:MET:HE1	1.88	0.55
11:E:65:TYR:O	11:E:69:ALA:HB2	2.06	0.55
16:J:24:ILE:HG12	16:J:128:LEU:HB3	1.87	0.55
21:P:139:TYR:CD1	21:P:139:TYR:CE1	2.95	0.55
22:Q:181:ARG:HD2	30:a:56:VAL:HG21	1.88	0.55
23:S:93:MET:HE3	23:S:94:TYR:H	1.72	0.55
29:Z:77:TYR:HA	29:Z:80:LEU:HG	1.89	0.55
69:EE:35:PRO:HD2	69:EE:83:PRO:HG2	1.88	0.55
4:B2:1329:U:O2	4:B2:1500:G:O6	2.25	0.55
4:B2:1394:G:H4'	59:QQ:126:ARG:HH21	1.72	0.55
4:B2:1505:U:H5''	4:B2:1506:A:H5'	1.87	0.55
4:B2:1598:G:H2'	64:ZZ:80:ARG:HH22	1.70	0.55
12:F:171:ASN:HA	12:F:174:ILE:HD12	1.89	0.55
20:O:8:VAL:HG12	20:O:117:ARG:HA	1.88	0.55
22:Q:108:ARG:HE	22:Q:108:ARG:H	1.54	0.55
26:V:90:ARG:HB3	81:c:20:ARG:HE	1.72	0.55
33:e:85:LEU:HD21	33:e:114:ARG:HG2	1.89	0.55
61:SS:26:ILE:HD11	61:SS:52:LEU:HA	1.89	0.55
65:bb:62:VAL:HG13	65:bb:74:THR:HG21	1.88	0.55
1:A5:960:A:N6	1:A5:1283:G:H1	2.04	0.55
3:A8:8:U:H2'	3:A8:9:A:C8	2.41	0.55
4:B2:1621:U:C5	58:PP:116:LEU:HB2	2.42	0.55
5:A6:3773:U:H3	5:A6:3776:G:H22	1.55	0.55
5:A6:3860:A:P	21:P:139:TYR:CD1	3.00	0.55
5:A6:4580:U:H5''	8:B:26:ARG:HH22	1.70	0.55
5:A6:4601:U:H2'	5:A6:4602:A:H8	1.70	0.55
17:L:111:GLN:HA	17:L:114:VAL:HB	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:s:44:ARG:HA	45:s:47:LEU:HB2	1.88	0.55
59:QQ:51:LEU:HG	59:QQ:84:ILE:HD11	1.89	0.55
68:CC:209:VAL:HG11	68:CC:233:LEU:HD21	1.89	0.55
82:u:55:LEU:HD12	82:u:56:ARG:HG3	1.89	0.55
82:u:99:PRO:HG2	82:u:106:ARG:HH12	1.72	0.55
1:A5:1204:C:H2'	1:A5:1205:G:H8	1.72	0.55
1:A5:1469:C:H2'	1:A5:1470:G:H8	1.72	0.55
3:A8:27:U:H4'	9:C:53:ALA:HB3	1.89	0.55
4:B2:1009:A:H5''	75:NN:94:LYS:HE3	1.89	0.55
4:B2:1535:U:C4	54:FF:82:ASN:CB	2.90	0.55
4:B2:1621:U:C4	58:PP:115:TYR:C	2.84	0.55
5:A6:3658:C:H2'	5:A6:3659:G:H8	1.72	0.55
5:A6:3690:U:H5'	5:A6:3818:U:H5''	1.88	0.55
15:I:152:LEU:HD12	15:I:165:ILE:HG23	1.89	0.55
56:MM:32:ALA:HB1	56:MM:37:GLU:HB3	1.89	0.55
61:SS:22:GLY:HA2	61:SS:56:ALA:HB3	1.89	0.55
66:ee:113:ASN:HA	66:ee:117:VAL:HB	1.88	0.55
70:GG:141:ILE:HG21	70:GG:153:VAL:HG13	1.88	0.55
1:A5:1270:A:C8	31:b:111:ARG:HB2	2.42	0.54
4:B2:305:U:C2	72:II:182:CYS:C	2.85	0.54
5:A6:2575:U:H5''	5:A6:2576:G:H5'	1.88	0.54
30:a:99:PRO:HG2	30:a:122:VAL:HG13	1.88	0.54
72:II:176:ALA:H	72:II:187:GLY:HA2	1.73	0.54
1:A5:683:C:H3'	11:E:103:LYS:HB2	1.88	0.54
1:A5:1289:C:N1	11:E:136:PHE:CG	2.76	0.54
5:A6:2701:U:O2	5:A6:2715:G:N2	2.36	0.54
5:A6:3760:A:C5	84:Bb:38:A:H5'	2.41	0.54
5:A6:4939:C:H5'	11:E:222:LYS:HE2	1.88	0.54
21:P:40:HIS:HA	21:P:113:VAL:HG22	1.89	0.54
49:gg:216:ALA:HB3	49:gg:230:LEU:HB3	1.87	0.54
1:A5:153:G:H2'	1:A5:154:G:H8	1.71	0.54
1:A5:439:G:H1'	34:f:23:GLU:HG2	1.88	0.54
1:A5:1270:A:C5	31:b:112:ILE:CA	2.91	0.54
1:A5:1576:G:H5'	43:p:13:LYS:HD2	1.89	0.54
1:A5:1726:U:O4	1:A5:1836:G:O6	2.25	0.54
4:B2:494:C:H42	4:B2:509:G:H21	1.54	0.54
4:B2:1174:U:H2'	4:B2:1175:G:H8	1.72	0.54
4:B2:1248:U:C6	83:Cc:36:A:P	3.00	0.54
5:A6:4370:G:C5	83:Cc:77:A:N3	2.69	0.54
5:A6:4690:G:H21	5:A6:4700:A:H62	1.54	0.54
8:B:222:VAL:HA	8:B:276:HIS:HA	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A5:727:C:H5''	1:A5:729:G:H5'	1.89	0.54
4:B2:28:U:H2'	4:B2:29:G:H8	1.73	0.54
4:B2:1352:G:O6	4:B2:1359:U:O4	2.25	0.54
4:B2:1679:A:H5'	47:cc:20:ARG:HH12	1.71	0.54
5:A6:2306:G:H3'	33:e:128:ARG:HH22	1.71	0.54
25:U:44:GLN:HG3	25:U:63:ILE:HD12	1.87	0.54
42:o:56:PHE:HB3	83:Cc:77:A:H5''	1.89	0.54
1:A5:755:C:H5'	14:H:54:ARG:HH22	1.73	0.54
1:A5:2045:G:C4	20:O:61:ARG:O	2.60	0.54
4:B2:1386:A:H3'	4:B2:1387:G:H8	1.72	0.54
4:B2:1740:C:H42	4:B2:1794:C:H42	1.54	0.54
5:A6:2677:G:C2	82:u:32:LYS:CE	2.91	0.54
5:A6:3935:C:H42	5:A6:3936:A:N6	2.04	0.54
6:A:58:LEU:HD12	6:A:75:LEU:HD11	1.88	0.54
19:N:64:ILE:HD13	19:N:102:ALA:HB1	1.89	0.54
22:Q:23:ILE:HB	44:r:8:MET:HE1	1.88	0.54
22:Q:36:ALA:HB1	22:Q:45:GLN:HG3	1.89	0.54
1:A5:1591:U:H5'	1:A5:1592:G:H5'	1.89	0.54
4:B2:655:A:H4'	4:B2:656:G:H3'	1.88	0.54
4:B2:1603:G:H8	61:SS:24:ARG:HH21	1.54	0.54
4:B2:1616:U:H5	58:PP:43:ARG:HH12	1.55	0.54
5:A6:2624:G:O6	5:A6:2632:U:O4	2.26	0.54
5:A6:2677:G:N3	82:u:32:LYS:NZ	2.55	0.54
5:A6:2889:G:C5	80:W:74:ARG:C	2.86	0.54
5:A6:4500:U:O2	84:Bb:75:C:N3	2.40	0.54
28:Y:67:ILE:H	28:Y:84:ARG:HH12	1.55	0.54
46:t:104:ILE:H	46:t:144:ASP:H	1.54	0.54
80:W:38:ARG:HA	80:W:41:ILE:HB	1.88	0.54
2:A7:79:U:O2	2:A7:97:G:N2	2.36	0.54
4:B2:639:C:H2'	4:B2:640:A:C8	2.43	0.54
4:B2:1532:C:H3'	4:B2:1637:A:H62	1.73	0.54
5:A6:2312:U:O2	5:A6:2326:G:O6	2.26	0.54
5:A6:3760:A:C2	84:Bb:38:A:C4'	2.91	0.54
15:I:91:LEU:HD23	15:I:135:ILE:HA	1.88	0.54
68:CC:142:LYS:HE2	68:CC:157:LEU:HD11	1.90	0.54
1:A5:436:C:H2'	1:A5:437:G:H8	1.70	0.54
1:A5:2074:C:H5'	12:F:156:ARG:HH12	1.71	0.54
4:B2:39:A:H5'	73:JJ:7:TRP:HE1	1.72	0.54
5:A6:4421:C:N4	5:A6:4475:G:H22	2.06	0.54
5:A6:4500:U:H3	84:Bb:75:C:H42	1.37	0.54
18:M:40:GLY:HA3	18:M:45:VAL:HB	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:N:35:ALA:O	19:N:64:ILE:HA	2.07	0.54
28:Y:30:MET:HE1	28:Y:78:TYR:HA	1.88	0.54
33:e:99:ILE:HG21	33:e:108:ARG:HG2	1.89	0.54
78:XX:74:LEU:HG	78:XX:76:LYS:H	1.73	0.54
1:A5:1751:A:H1'	15:I:193:ASP:HB2	1.90	0.54
1:A5:1788:A:H4'	24:T:12:ARG:HH22	1.73	0.54
3:A8:66:A:H5'	36:h:10:ARG:HH22	1.73	0.54
4:B2:580:U:H2'	79:YY:62:THR:HG23	1.90	0.54
4:B2:1203:G:C5	68:CC:114:LYS:C	2.86	0.54
4:B2:1599:U:C2	54:FF:166:ILE:CA	2.91	0.54
5:A6:3819:G:H2'	5:A6:3820:G:H8	1.73	0.54
62:TT:108:GLU:HG3	62:TT:113:VAL:HG12	1.90	0.54
82:u:11:LEU:HA	82:u:14:ILE:HG22	1.89	0.54
1:A5:310:G:H4'	37:i:85:ARG:HH12	1.73	0.54
4:B2:841:G:C6	79:YY:11:LYS:CA	2.90	0.54
4:B2:1172:U:C2	4:B2:1188:A:N7	2.76	0.54
4:B2:1652:G:O6	4:B2:1672:U:O4	2.26	0.54
5:A6:4235:G:O6	5:A6:4289:U:O2	2.25	0.54
12:F:73:MET:HA	12:F:76:LYS:HG2	1.90	0.54
24:T:103:ASP:HA	24:T:106:LEU:HB2	1.90	0.54
43:p:84:ARG:HH12	43:p:87:LYS:HD3	1.72	0.54
47:cc:13:ARG:H	47:cc:35:MET:HE1	1.72	0.54
81:c:6:CYS:HB3	81:c:10:GLY:H	1.72	0.54
3:A8:28:C:H2'	3:A8:29:G:C8	2.42	0.53
5:A6:2706:G:H1	80:W:46:LYS:HE2	1.73	0.53
5:A6:4891:G:H2'	5:A6:4892:A:H8	1.73	0.53
8:B:61:ASP:HA	8:B:69:LYS:HE3	1.90	0.53
46:t:85:LEU:HD21	46:t:102:GLY:HA3	1.90	0.53
49:gg:173:LEU:HD22	49:gg:189:ILE:HG22	1.90	0.53
51:AA:166:LYS:H	51:AA:166:LYS:HD3	1.73	0.53
58:PP:88:GLU:HG3	58:PP:89:MET:HE3	1.88	0.53
60:RR:102:THR:HA	60:RR:105:MET:HG2	1.90	0.53
69:EE:198:ARG:HG2	69:EE:208:VAL:HG22	1.90	0.53
80:W:104:ARG:HA	80:W:107:ARG:HG2	1.90	0.53
82:u:20:LEU:HA	82:u:23:LYS:HG2	1.90	0.53
1:A5:37:U:H5''	30:a:32:ARG:HD3	1.89	0.53
1:A5:654:C:H5'	9:C:268:ARG:HH11	1.73	0.53
1:A5:1676:C:H5	5:A6:4378:A:H5''	1.74	0.53
4:B2:74:G:C4	70:GG:171:THR:HG22	2.43	0.53
4:B2:608:C:H5''	66:ee:133:SER:H	1.73	0.53
5:A6:2378:G:H21	5:A6:2425:U:H3	1.56	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A6:4575:G:C6	5:A6:4728:U:O2	2.62	0.53
9:C:339:THR:HA	9:C:342:ARG:HH11	1.74	0.53
14:H:47:LEU:HD11	14:H:53:LYS:HB3	1.89	0.53
15:I:30:LYS:HE2	15:I:63:GLU:HB2	1.90	0.53
42:o:23:VAL:HA	42:o:69:ARG:O	2.09	0.53
45:s:62:ARG:HG2	45:s:66:ARG:HH21	1.73	0.53
1:A5:1289:C:C6	11:E:136:PHE:CD2	2.96	0.53
4:B2:1535:U:N3	54:FF:82:ASN:CB	2.72	0.53
5:A6:2889:G:N1	80:W:74:ARG:C	2.66	0.53
5:A6:2892:C:H4'	5:A6:5018:C:H4'	1.89	0.53
5:A6:4402:C:H42	5:A6:4441:A:H61	1.55	0.53
16:J:89:VAL:HG21	16:J:115:LEU:HA	1.91	0.53
22:Q:88:ASP:HB2	22:Q:109:ALA:HB2	1.91	0.53
33:e:55:MET:HE3	33:e:56:PRO:HD2	1.90	0.53
34:f:35:ALA:HB3	34:f:38:GLU:HB3	1.88	0.53
77:WW:27:ILE:HB	77:WW:61:ILE:HB	1.91	0.53
1:A5:1974:U:H3	1:A5:2002:A:H62	1.55	0.53
4:B2:1599:U:N1	54:FF:165:ASN:C	2.66	0.53
5:A6:4613:C:C6	5:A6:4613:C:O4'	2.62	0.53
5:A6:4689:U:H4'	14:H:151:ILE:HG12	1.90	0.53
22:Q:172:ARG:HG3	22:Q:173:LYS:HG3	1.91	0.53
35:g:102:ILE:HA	35:g:105:LYS:HD2	1.89	0.53
57:OO:31:CYS:HB3	57:OO:93:LEU:HD11	1.89	0.53
75:NN:40:LEU:HA	75:NN:43:LYS:HD3	1.91	0.53
77:WW:11:LEU:HD22	77:WW:74:VAL:HG13	1.89	0.53
1:A5:40:G:H21	5:A6:4380:A:H62	1.57	0.53
1:A5:1188:C:H2'	1:A5:1189:G:C8	2.44	0.53
4:B2:1203:G:N3	68:CC:114:LYS:C	2.67	0.53
4:B2:1214:A:N6	4:B2:1682:C:O2	2.42	0.53
27:X:110:LYS:HG3	27:X:121:VAL:HB	1.90	0.53
30:a:71:PRO:HG2	30:a:108:TYR:HA	1.90	0.53
59:QQ:102:GLU:HA	59:QQ:105:LYS:HB3	1.89	0.53
68:CC:65:LYS:HD2	68:CC:273:LEU:HD22	1.90	0.53
4:B2:525:A:H4'	66:ee:105:ARG:HH22	1.72	0.53
4:B2:1408:U:H5''	59:QQ:69:ARG:HH12	1.72	0.53
4:B2:1621:U:N3	58:PP:115:TYR:C	2.67	0.53
8:B:36:ASP:HB3	8:B:39:LYS:HE2	1.90	0.53
73:JJ:21:GLU:HB3	73:JJ:24:ARG:HB3	1.89	0.53
76:VV:59:ILE:HG23	76:VV:65:SER:HB3	1.91	0.53
4:B2:1397:U:H4'	4:B2:1398:G:H5''	1.91	0.53
4:B2:1535:U:C5	54:FF:82:ASN:CG	2.87	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:Q:80:ALA:HA	22:Q:137:VAL:O	2.08	0.53
30:a:99:PRO:HD2	30:a:122:VAL:HA	1.89	0.53
52:BB:110:MET:H	52:BB:110:MET:HE3	1.73	0.53
56:MM:31:LEU:HG	56:MM:33:ARG:HE	1.73	0.53
81:c:37:GLU:HA	81:c:40:PHE:HB2	1.90	0.53
1:A5:47:A:H5''	17:L:16:LYS:HD3	1.91	0.53
1:A5:989:U:O2	1:A5:1064:G:O6	2.27	0.53
1:A5:1218:G:O6	1:A5:1219:G:O6	2.27	0.53
1:A5:1628:C:H5''	6:A:15:VAL:HG21	1.91	0.53
4:B2:77:A:H1'	70:GG:175:LYS:HA	1.90	0.53
4:B2:443:U:O2	4:B2:447:A:N7	2.42	0.53
5:A6:3634:G:H21	5:A6:3636:C:H5'	1.73	0.53
5:A6:4126:C:H5'	5:A6:4127:A:H4'	1.91	0.53
5:A6:4617:G:H4'	26:V:14:PHE:HA	1.91	0.53
34:f:63:LYS:HE3	34:f:64:PRO:HD2	1.90	0.53
38:j:24:SER:HB2	38:j:36:LYS:HE2	1.90	0.53
55:KK:6:LYS:HG2	55:KK:38:LYS:NZ	2.24	0.53
4:B2:54:A:H3'	4:B2:451:G:H22	1.74	0.53
4:B2:1209:A:N1	4:B2:1691:U:C4	2.76	0.53
4:B2:1248:U:C5	83:Cc:36:A:P	3.02	0.53
4:B2:1535:U:C2	4:B2:1535:U:C1'	2.85	0.53
5:A6:4437:U:H1'	5:A6:4515:G:H4'	1.91	0.53
11:E:256:VAL:HG13	11:E:260:ILE:HD12	1.91	0.53
49:gg:130:LYS:HG2	49:gg:141:THR:HG23	1.90	0.53
58:PP:108:LYS:HB2	58:PP:111:MET:HE1	1.91	0.53
64:ZZ:46:ASN:HB3	64:ZZ:80:ARG:HA	1.90	0.53
4:B2:155:G:O6	4:B2:163:U:O4	2.27	0.53
5:A6:4072:C:H2'	5:A6:4073:A:H8	1.73	0.53
7:n:9:ARG:O	7:n:13:LEU:HB2	2.09	0.53
8:B:317:LEU:HB2	8:B:372:SER:HB2	1.91	0.53
11:E:154:ILE:HG12	11:E:164:ARG:HG2	1.92	0.53
11:E:169:LYS:HE3	11:E:171:LEU:HD23	1.90	0.53
34:f:78:HIS:HB2	34:f:85:ARG:HE	1.74	0.53
45:s:21:LEU:HD13	45:s:75:LEU:HD21	1.90	0.53
53:DD:38:GLU:HB2	53:DD:49:ILE:HB	1.91	0.53
1:A5:1995:G:C5	45:s:40:MET:HB2	2.44	0.52
4:B2:821:G:H21	4:B2:824:C:H4'	1.74	0.52
5:A6:2527:A:H5'	80:W:9:ARG:HH12	1.74	0.52
5:A6:4725:C:H2'	5:A6:4726:G:H8	1.73	0.52
10:D:80:ALA:HB1	10:D:92:LEU:HB3	1.90	0.52
26:V:82:ILE:HD11	26:V:122:ALA:H	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:t:76:SER:HA	46:t:119:ARG:HH21	1.74	0.52
67:aa:26:CYS:SG	67:aa:77:CYS:HB3	2.49	0.52
72:II:202:ILE:HG12	72:II:205:ARG:HH21	1.74	0.52
81:c:33:ASN:HB3	81:c:35:LYS:HE3	1.91	0.52
84:Bb:19:G:H5''	84:Bb:60:C:H42	1.73	0.52
1:A5:1089:G:H2'	1:A5:1090:G:H8	1.75	0.52
1:A5:1289:C:C2	11:E:136:PHE:CE1	2.98	0.52
1:A5:1333:A:H2'	1:A5:1334:A:C8	2.44	0.52
1:A5:1366:G:H5'	17:L:33:ILE:HG23	1.90	0.52
4:B2:436:G:H2'	4:B2:437:G:H8	1.74	0.52
4:B2:1010:G:H2'	4:B2:1011:A:H8	1.75	0.52
4:B2:1244:U:H2'	4:B2:1245:G:H8	1.74	0.52
4:B2:1825:A:H8	84:Bb:37:YYG:H1'	1.75	0.52
4:B2:1869:A:C4	52:BB:115:LYS:CB	2.92	0.52
5:A6:2753:G:H2'	5:A6:2754:G:C4	2.44	0.52
5:A6:3859:G:O3'	21:P:139:TYR:CE1	2.61	0.52
55:KK:85:LEU:HB3	55:KK:89:ILE:HD11	1.90	0.52
68:CC:142:LYS:HB3	68:CC:154:ALA:HB2	1.90	0.52
73:JJ:50:LEU:HG	73:JJ:54:ARG:HD3	1.92	0.52
1:A5:1787:A:H2'	1:A5:1788:A:H8	1.74	0.52
4:B2:283:G:H21	4:B2:284:C:H41	1.55	0.52
4:B2:1205:C:H2'	4:B2:1206:G:C4	2.43	0.52
4:B2:1869:A:C6	52:BB:115:LYS:CB	2.92	0.52
5:A6:3658:C:H2'	5:A6:3659:G:C8	2.44	0.52
5:A6:3927:U:H2'	5:A6:3928:A:H8	1.74	0.52
10:D:197:LYS:HG3	10:D:202:GLN:HB2	1.90	0.52
25:U:64:GLU:HB2	25:U:71:THR:HB	1.90	0.52
54:FF:135:ARG:HH21	54:FF:136:ARG:HG2	1.74	0.52
1:A5:28:C:H3'	19:N:189:ARG:HH21	1.74	0.52
1:A5:1995:G:C4	45:s:41:GLN:HA	2.44	0.52
3:A8:28:C:H2'	3:A8:29:G:H8	1.74	0.52
4:B2:93:U:H4'	69:EE:6:LYS:HA	1.90	0.52
4:B2:649:U:H2'	4:B2:650:A:H8	1.74	0.52
4:B2:840:C:H4'	4:B2:841:G:H4'	1.90	0.52
21:P:126:ARG:HH22	21:P:140:MET:HB3	1.73	0.52
42:o:10:THR:O	42:o:18:HIS:HA	2.09	0.52
58:PP:70:MET:HE3	58:PP:70:MET:H	1.73	0.52
70:GG:14:LYS:HD3	70:GG:123:GLY:HA3	1.91	0.52
79:YY:97:TYR:HE2	79:YY:99:LYS:HE3	1.73	0.52
83:Cc:55:U:O2	83:Cc:59:A:N7	2.43	0.52
1:A5:185:C:H5'	1:A5:189:G:H5''	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B2:1869:A:C6	52:BB:115:LYS:CG	2.92	0.52
5:A6:4757:C:C2	20:O:114:LYS:HA	2.44	0.52
8:B:73:VAL:HG22	81:c:13:ILE:HG12	1.92	0.52
26:V:42:VAL:HG13	26:V:61:VAL:HG12	1.92	0.52
80:W:8:LYS:HG2	80:W:24:LEU:HD11	1.91	0.52
1:A5:440:U:H2'	1:A5:441:G:H8	1.75	0.52
1:A5:750:U:H3	1:A5:912:G:H1	1.57	0.52
1:A5:1655:C:H3'	30:a:26:ARG:HH12	1.74	0.52
1:A5:1930:U:H5''	1:A5:1931:C:H3'	1.92	0.52
4:B2:197:U:O2	4:B2:202:G:O6	2.28	0.52
4:B2:1650:A:H5''	59:QQ:139:ALA:HB2	1.92	0.52
5:A6:3928:A:H3'	5:A6:3929:G:H8	1.75	0.52
5:A6:4941:G:H1	11:E:193:HIS:HB2	1.75	0.52
5:A6:4978:G:H1'	5:A6:4981:G:H1	1.74	0.52
20:O:5:GLN:HG3	20:O:6:VAL:HG23	1.90	0.52
24:T:39:ILE:HG13	24:T:102:ARG:HE	1.75	0.52
29:Z:12:LEU:HA	29:Z:21:ARG:O	2.10	0.52
53:DD:51:LEU:HB3	53:DD:91:VAL:HG23	1.92	0.52
1:A5:1952:G:H4'	23:S:93:MET:HE1	1.91	0.52
4:B2:1726:G:O6	4:B2:1808:U:O4	2.27	0.52
5:A6:2673:G:H21	82:u:91:VAL:HA	1.75	0.52
5:A6:2768:C:C4	35:g:69:LYS:O	2.62	0.52
5:A6:3760:A:N1	84:Bb:38:A:C4'	2.73	0.52
5:A6:4500:U:N3	84:Bb:75:C:N4	2.42	0.52
5:A6:4972:U:O2	5:A6:4986:G:O6	2.27	0.52
9:C:51:PRO:HB3	9:C:111:TRP:CD1	2.44	0.52
10:D:84:PRO:HG3	10:D:89:LYS:HA	1.92	0.52
15:I:43:VAL:HG11	15:I:197:VAL:HG22	1.91	0.52
27:X:81:LEU:HD13	27:X:97:VAL:HG13	1.90	0.52
31:b:112:ILE:CB	31:b:112:ILE:HA	2.38	0.52
47:cc:9:ILE:HD11	47:cc:57:THR:HB	1.90	0.52
65:bb:56:CYS:HB2	65:bb:63:LEU:HD21	1.91	0.52
73:JJ:94:LEU:HD23	73:JJ:97:ILE:HD11	1.92	0.52
1:A5:386:A:H5''	28:Y:95:VAL:HG11	1.90	0.52
1:A5:1088:C:H2'	1:A5:1089:G:C8	2.45	0.52
1:A5:1289:C:C2	11:E:136:PHE:CZ	2.98	0.52
1:A5:1995:G:N3	45:s:40:MET:C	2.68	0.52
3:A8:141:C:H5''	19:N:60:VAL:HG11	1.91	0.52
4:B2:148:U:H2'	4:B2:149:A:H8	1.75	0.52
4:B2:1358:U:H5'	68:CC:114:LYS:HG2	1.91	0.52
5:A6:2647:A:H62	5:A6:2686:G:H8	1.58	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:n:4:LYS:HA	7:n:7:LYS:HE2	1.92	0.52
46:t:81:ILE:HD11	46:t:132:ILE:HD12	1.91	0.52
47:cc:13:ARG:HE	47:cc:55:VAL:HG22	1.75	0.52
51:AA:85:ARG:HE	60:RR:81:ARG:HH22	1.57	0.52
1:A5:1186:U:H2'	10:D:275:GLN:O	2.09	0.52
1:A5:1382:G:H2'	1:A5:1383:G:C8	2.45	0.52
8:B:45:ALA:HB3	8:B:183:ILE:HD12	1.92	0.52
10:D:103:LEU:HG	10:D:247:ILE:HG21	1.92	0.52
12:F:91:VAL:O	12:F:119:GLY:HA2	2.10	0.52
34:f:45:LYS:HE3	34:f:108:SER:HA	1.92	0.52
34:f:54:LYS:HA	34:f:66:LYS:HB3	1.91	0.52
1:A5:72:C:H1'	17:L:60:ARG:HD2	1.92	0.52
1:A5:1332:C:H2'	1:A5:1333:A:C8	2.45	0.52
2:A7:117:G:H5''	10:D:256:LYS:HD2	1.92	0.52
4:B2:1166:G:C6	4:B2:1193:U:O2	2.63	0.52
4:B2:1869:A:C4	52:BB:115:LYS:CG	2.93	0.52
5:A6:2303:C:H5'	33:e:104:SER:HB3	1.91	0.52
23:S:132:ILE:HG23	23:S:136:LYS:HG3	1.91	0.52
57:OO:117:ARG:HH22	67:aa:52:ASP:HB2	1.74	0.52
79:YY:87:PRO:HD2	79:YY:90:ARG:HE	1.75	0.52
1:A5:151:G:H3'	19:N:49:ARG:HH22	1.74	0.51
1:A5:310:G:O6	1:A5:327:U:C4	2.63	0.51
1:A5:418:A:H4'	5:A6:2311:C:H5'	1.92	0.51
1:A5:1995:G:H21	45:s:43:ILE:H	1.55	0.51
4:B2:106:C:H2'	4:B2:107:A:C8	2.46	0.51
4:B2:180:G:H5''	4:B2:181:A:H3'	1.92	0.51
5:A6:2520:C:H2'	5:A6:2521:G:H8	1.75	0.51
5:A6:3932:U:H2'	5:A6:3933:G:H8	1.75	0.51
9:C:44:LEU:HB3	9:C:237:ILE:HD11	1.92	0.51
1:A5:1470:G:O6	1:A5:1494:U:O4	2.27	0.51
4:B2:23:G:O6	4:B2:652:U:O4	2.28	0.51
4:B2:167:G:H21	70:GG:131:ARG:HH12	1.58	0.51
4:B2:1049:A:H2	4:B2:1069:U:H3	1.59	0.51
4:B2:1748:G:O6	4:B2:1786:U:O4	2.27	0.51
5:A6:2300:A:N9	9:C:181:LYS:O	2.43	0.51
5:A6:2363:A:H62	5:A6:3859:G:N2	2.07	0.51
5:A6:4755:G:H2'	5:A6:4875:G:H21	1.74	0.51
10:D:52:ILE:HB	10:D:63:GLN:HG3	1.92	0.51
19:N:169:ARG:HG2	19:N:172:ARG:HH21	1.75	0.51
29:Z:100:VAL:HG12	29:Z:106:LEU:HG	1.92	0.51
36:h:44:LEU:HA	36:h:47:ILE:HD12	1.90	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:r:66:ARG:HH22	44:r:75:THR:HG23	1.75	0.51
47:cc:17:VAL:HA	47:cc:30:VAL:HG12	1.92	0.51
1:A5:114:G:H5''	19:N:4:TYR:HB2	1.93	0.51
1:A5:1270:A:N1	31:b:112:ILE:C	2.68	0.51
1:A5:1505:C:H2'	1:A5:1506:G:C8	2.46	0.51
1:A5:1555:G:O6	1:A5:1572:U:O4	2.27	0.51
1:A5:2016:C:H2'	1:A5:2017:A:H8	1.76	0.51
4:B2:864:A:H2'	4:B2:865:A:H8	1.74	0.51
4:B2:1455:A:H2'	4:B2:1456:G:H8	1.74	0.51
4:B2:1782:G:H2'	4:B2:1784:G:H8	1.74	0.51
5:A6:3860:A:P	21:P:139:TYR:CE2	3.04	0.51
5:A6:4757:C:N1	20:O:113:ASP:C	2.69	0.51
10:D:118:ILE:HG12	10:D:138:GLN:HG3	1.91	0.51
19:N:116:LEU:HD13	19:N:117:ASN:HB2	1.93	0.51
20:O:54:TYR:HE2	20:O:145:VAL:HG21	1.75	0.51
30:a:8:THR:HA	30:a:11:LEU:HG	1.91	0.51
34:f:28:LEU:HB3	34:f:84:VAL:HG13	1.93	0.51
51:AA:207:PRO:HA	51:AA:210:ILE:HD12	1.91	0.51
53:DD:45:ARG:HH22	53:DD:85:GLU:HG2	1.74	0.51
5:A6:2889:G:H1	5:A6:3612:C:H42	1.59	0.51
5:A6:4638:U:H2'	5:A6:4639:G:C8	2.46	0.51
5:A6:4896:G:H2'	5:A6:4897:G:H8	1.76	0.51
10:D:271:MET:HE3	10:D:276:LYS:HG2	1.92	0.51
11:E:121:THR:HA	44:r:112:ARG:HB3	1.92	0.51
16:J:41:GLU:HG3	16:J:48:PRO:HD2	1.92	0.51
70:GG:135:PRO:HB2	70:GG:141:ILE:HG12	1.91	0.51
1:A5:1692:C:H4'	22:Q:143:ARG:HH12	1.76	0.51
5:A6:2458:C:H1'	5:A6:3672:G:H21	1.76	0.51
5:A6:4757:C:N3	20:O:113:ASP:C	2.69	0.51
8:B:107:ALA:HB2	8:B:201:LEU:HD22	1.93	0.51
13:G:51:LEU:HB2	13:G:54:PHE:HD2	1.75	0.51
17:L:195:ARG:HA	17:L:198:ARG:HD2	1.93	0.51
1:A5:370:U:N3	1:A5:1637:A:C6	2.79	0.51
1:A5:1106:A:N6	1:A5:1164:G:N2	2.40	0.51
1:A5:1541:C:H5''	6:A:21:LYS:HG2	1.92	0.51
1:A5:1933:G:H2'	1:A5:1934:A:C8	2.46	0.51
4:B2:366:U:O2	4:B2:394:G:O6	2.29	0.51
4:B2:491:C:H2'	79:YY:104:ARG:HH21	1.76	0.51
19:N:53:TYR:HB2	19:N:133:ILE:HG12	1.93	0.51
27:X:129:ARG:HD3	27:X:130:PRO:HD2	1.92	0.51
74:LL:80:MET:HA	74:LL:86:ILE:HG22	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
79:YY:87:PRO:HG2	79:YY:90:ARG:HH21	1.74	0.51
1:A5:456:C:H2'	1:A5:457:G:H8	1.75	0.51
1:A5:1270:A:N1	31:b:112:ILE:CA	2.74	0.51
1:A5:1995:G:H2'	45:s:44:ARG:HG3	1.92	0.51
4:B2:1099:G:H22	4:B2:1133:A:H2	1.58	0.51
4:B2:1408:U:H2'	4:B2:1409:A:C4	2.46	0.51
5:A6:4613:C:C4	14:H:121:LYS:CD	2.93	0.51
6:A:82:ILE:HG23	6:A:98:ILE:HG22	1.93	0.51
15:I:38:ARG:HH22	15:I:40:LYS:HB2	1.75	0.51
23:S:113:MET:HG3	23:S:119:ALA:HB3	1.92	0.51
30:a:103:VAL:HG22	30:a:108:TYR:HB2	1.93	0.51
49:gg:44:LYS:HD2	49:gg:56:GLN:HB2	1.92	0.51
70:GG:131:ARG:HB3	81:c:82:ILE:HD13	1.92	0.51
4:B2:137:U:H5'	4:B2:1759:G:H21	1.75	0.51
4:B2:346:C:H5''	69:EE:38:LEU:HB2	1.92	0.51
4:B2:878:G:C2	4:B2:908:A:H2	2.25	0.51
4:B2:1550:G:H2'	4:B2:1579:A:H61	1.76	0.51
5:A6:2520:C:H2'	5:A6:2521:G:C8	2.46	0.51
5:A6:4946:U:H5''	34:f:69:VAL:HG22	1.93	0.51
8:B:47:LEU:HD11	8:B:181:MET:HB2	1.93	0.51
9:C:257:PHE:HA	9:C:260:LEU:HD12	1.93	0.51
9:C:284:MET:HG3	9:C:287:THR:HG22	1.91	0.51
48:ff:95:ARG:H	48:ff:95:ARG:HE	1.59	0.51
80:W:5:ARG:H	80:W:5:ARG:HD2	1.75	0.51
80:W:66:ASN:HA	80:W:69:ALA:HB3	1.92	0.51
1:A5:74:G:H5'	17:L:59:VAL:HG13	1.93	0.51
4:B2:957:A:H3'	4:B2:958:G:H21	1.76	0.51
5:A6:2330:G:H2'	5:A6:2331:G:C4	2.46	0.51
5:A6:4040:C:H1'	5:A6:4050:A:H62	1.75	0.51
5:A6:4274:A:H2'	5:A6:4275:G:H8	1.75	0.51
8:B:231:VAL:HG11	8:B:251:VAL:HG12	1.93	0.51
13:G:83:PHE:HA	13:G:183:ILE:HD13	1.92	0.51
1:A5:75:G:H2'	17:L:74:ARG:HB2	1.93	0.51
1:A5:959:G:C6	11:E:127:LYS:CD	2.94	0.51
1:A5:1825:A:H2'	1:A5:1826:G:C8	2.46	0.51
4:B2:96:C:H1'	4:B2:474:G:H5'	1.93	0.51
4:B2:841:G:C2	79:YY:11:LYS:N	2.79	0.51
5:A6:2623:A:H2'	5:A6:2624:G:H8	1.76	0.51
5:A6:3936:A:C6	5:A6:4175:G:C6	2.99	0.51
5:A6:3938:G:H5'	5:A6:4170:A:H2	1.75	0.51
5:A6:4595:G:H1'	26:V:12:ALA:HB2	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:V:40:ILE:HG21	26:V:64:THR:HG23	1.92	0.51
36:h:81:LEU:HD23	36:h:84:ARG:HD2	1.93	0.51
46:t:10:ILE:HD11	46:t:63:THR:HB	1.93	0.51
55:KK:6:LYS:HG2	55:KK:38:LYS:HZ3	1.75	0.51
56:MM:102:LYS:HE2	56:MM:104:VAL:HB	1.92	0.51
59:QQ:86:GLN:HG2	59:QQ:90:LYS:HE2	1.92	0.51
61:SS:23:ARG:HH11	64:ZZ:48:VAL:HG23	1.76	0.51
3:A8:120:G:H2'	3:A8:121:G:H8	1.76	0.50
4:B2:165:G:H4'	70:GG:53:SER:HB2	1.94	0.50
4:B2:934:G:C6	4:B2:1008:A:N1	2.79	0.50
5:A6:3868:G:H22	5:A6:3900:G:H1'	1.76	0.50
16:J:48:PRO:HB3	16:J:72:CYS:HB2	1.92	0.50
16:J:52:LYS:HD3	16:J:65:ASN:HA	1.92	0.50
18:M:31:ILE:HD11	18:M:37:LEU:HB2	1.92	0.50
42:o:21:HIS:HB3	42:o:70:LEU:HB2	1.93	0.50
69:EE:61:VAL:HA	69:EE:64:ILE:HD12	1.92	0.50
70:GG:38:ALA:HB2	70:GG:50:VAL:HG22	1.93	0.50
4:B2:1535:U:C6	4:B2:1535:U:C2'	2.94	0.50
4:B2:1869:A:C2	52:BB:115:LYS:CG	2.94	0.50
5:A6:2889:G:N1	80:W:74:ARG:O	2.44	0.50
5:A6:3859:G:C3'	5:A6:3859:G:HO3'	2.15	0.50
15:I:184:MET:HE1	15:I:189:ARG:HE	1.77	0.50
30:a:74:ASN:H	30:a:77:LYS:HB2	1.76	0.50
49:gg:256:ILE:HB	49:gg:270:LEU:HB2	1.94	0.50
1:A5:1999:A:H4'	1:A5:2018:C:H1'	1.94	0.50
4:B2:1342:U:N3	4:B2:1483:A:N6	2.55	0.50
4:B2:1523:C:H2'	4:B2:1524:G:H8	1.75	0.50
5:A6:2616:C:H2'	5:A6:2617:G:H8	1.76	0.50
8:B:151:SER:HA	8:B:154:LYS:HD2	1.92	0.50
10:D:12:TYR:O	10:D:16:TYR:HB2	2.11	0.50
10:D:225:GLN:HA	10:D:228:LYS:HE2	1.94	0.50
36:h:94:ARG:HH22	36:h:97:LYS:HZ3	1.58	0.50
49:gg:212:LYS:HA	49:gg:235:ILE:HD12	1.93	0.50
1:A5:284:G:H1'	37:i:78:GLY:HA3	1.94	0.50
1:A5:1669:A:H5''	31:b:15:LYS:HD3	1.93	0.50
4:B2:38:A:H5''	73:JJ:5:ARG:HD3	1.94	0.50
4:B2:1144:A:H2'	4:B2:1145:A:C8	2.47	0.50
5:A6:4474:A:H5''	41:m:125:LYS:HB2	1.94	0.50
5:A6:4490:C:H2'	5:A6:4491:G:H8	1.76	0.50
17:L:21:ARG:HG2	19:N:197:THR:HG23	1.93	0.50
45:s:38:LYS:HB2	45:s:107:VAL:HG22	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:gg:239:LEU:HD22	49:gg:248:LEU:HD11	1.94	0.50
57:OO:45:THR:HA	57:OO:52:THR:HA	1.93	0.50
57:OO:95:ILE:HD13	57:OO:129:ILE:HG22	1.93	0.50
4:B2:183:G:H1	4:B2:214:U:H2'	1.76	0.50
4:B2:841:G:C5	79:YY:11:LYS:C	2.89	0.50
4:B2:1018:U:H5''	75:NN:71:ILE:HD11	1.93	0.50
4:B2:1529:C:H4'	62:TT:89:PRO:HG3	1.94	0.50
4:B2:1562:C:H2'	4:B2:1563:G:H8	1.76	0.50
4:B2:1599:U:C4	54:FF:165:ASN:HB3	2.47	0.50
4:B2:1869:A:H2'	52:BB:115:LYS:HD2	1.93	0.50
8:B:58:ARG:HB2	8:B:363:ILE:HG23	1.93	0.50
9:C:333:LYS:HE2	9:C:337:ARG:HH12	1.77	0.50
20:O:20:ALA:HB1	20:O:87:MET:HG2	1.94	0.50
21:P:94:MET:HE3	21:P:148:MET:HE2	1.93	0.50
29:Z:95:VAL:HG13	29:Z:96:VAL:HG13	1.93	0.50
35:g:76:ARG:HH21	35:g:84:ALA:HB1	1.75	0.50
51:AA:52:LYS:HE2	60:RR:109:LEU:HA	1.93	0.50
61:SS:26:ILE:HG21	61:SS:59:LEU:HD21	1.93	0.50
72:II:98:LYS:HB3	72:II:178:ARG:HA	1.94	0.50
5:A6:4274:A:H2'	5:A6:4275:G:C8	2.46	0.50
5:A6:4403:U:O2	5:A6:4440:G:N2	2.42	0.50
21:P:24:VAL:HG23	21:P:86:LYS:HB3	1.94	0.50
25:U:88:LYS:HD2	25:U:97:ARG:HH22	1.75	0.50
39:k:9:LYS:H	39:k:9:LYS:HE2	1.75	0.50
71:HH:137:SER:HB3	71:HH:162:GLN:HB2	1.92	0.50
82:u:17:ARG:HH12	82:u:108:MET:HB2	1.77	0.50
1:A5:1522:G:H5'	9:C:77:PRO:HD3	1.94	0.50
1:A5:1972:G:C5	45:s:41:GLN:CG	2.94	0.50
4:B2:1562:C:H2'	4:B2:1563:G:C8	2.47	0.50
4:B2:1624:U:H3	58:PP:40:ARG:HH12	1.60	0.50
5:A6:3780:G:N2	5:A6:3814:U:O2	2.37	0.50
5:A6:4268:A:H61	5:A6:4281:A:H62	1.60	0.50
5:A6:4946:U:N3	34:f:69:VAL:HA	2.27	0.50
13:G:91:THR:HA	13:G:94:GLN:HE21	1.77	0.50
25:U:21:PHE:HA	25:U:108:GLU:HB2	1.94	0.50
43:p:87:LYS:HG3	43:p:90:LYS:HE2	1.94	0.50
62:TT:104:LEU:HD22	62:TT:121:ARG:HD3	1.93	0.50
4:B2:960:U:H1'	4:B2:963:A:H62	1.76	0.50
4:B2:1121:G:H2'	4:B2:1122:A:H8	1.77	0.50
4:B2:1580:A:H2'	63:UU:56:MET:HE1	1.93	0.50
5:A6:2677:G:C4	5:A6:2677:G:C2	2.96	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A6:4080:C:H2'	5:A6:4081:G:H8	1.77	0.50
10:D:94:ASN:HB2	10:D:97:ALA:H	1.77	0.50
16:J:95:ARG:HA	16:J:175:LEU:HB2	1.93	0.50
26:V:65:VAL:HG11	26:V:72:LEU:HG	1.93	0.50
26:V:96:LEU:HD21	81:c:28:VAL:HA	1.94	0.50
45:s:47:LEU:HD13	45:s:51:ALA:HB3	1.94	0.50
51:AA:1:ACE:H1	51:AA:8:LEU:HD12	1.93	0.50
58:PP:98:ASN:HB2	58:PP:122:THR:HA	1.94	0.50
1:A5:504:G:O6	1:A5:653:U:O2	2.30	0.50
4:B2:493:A:H1'	4:B2:574:A:H5'	1.92	0.50
4:B2:1495:G:C2	50:dd:39:CYS:HB3	2.47	0.50
4:B2:1621:U:C5	58:PP:115:TYR:HA	2.46	0.50
5:A6:3872:A:H2'	5:A6:3873:G:C8	2.47	0.50
5:A6:4455:G:H5''	8:B:5:LYS:HD2	1.93	0.50
5:A6:4613:C:C4	14:H:121:LYS:CG	2.95	0.50
9:C:263:LEU:HA	9:C:273:LEU:HB3	1.94	0.50
16:J:51:SER:HB3	16:J:69:ALA:HB3	1.94	0.50
53:DD:175:VAL:HG23	53:DD:184:ILE:HD11	1.93	0.50
58:PP:56:LEU:HD23	58:PP:83:MET:HE2	1.93	0.50
71:HH:144:ILE:HB	77:WW:52:ILE:HD12	1.94	0.50
74:LL:94:HIS:HB3	74:LL:103:GLU:HB3	1.94	0.50
1:A5:161:G:H2'	1:A5:162:A:H8	1.76	0.49
1:A5:471:A:N6	1:A5:684:G:H21	2.01	0.49
1:A5:959:G:C6	11:E:127:LYS:CG	2.95	0.49
4:B2:1096:G:H1	4:B2:1136:U:H3	1.59	0.49
5:A6:4386:C:H5''	5:A6:4533:A:H4'	1.94	0.49
5:A6:4584:A:H62	5:A6:4718:G:H21	1.59	0.49
5:A6:4757:C:C4	20:O:113:ASP:C	2.90	0.49
30:a:137:ILE:HA	30:a:140:VAL:HG22	1.93	0.49
49:gg:11:LEU:HB2	49:gg:307:VAL:HB	1.94	0.49
51:AA:85:ARG:HH21	60:RR:81:ARG:HH22	1.60	0.49
53:DD:93:THR:HB	53:DD:96:LEU:HB2	1.94	0.49
65:bb:54:VAL:HG12	65:bb:63:LEU:HD12	1.92	0.49
1:A5:181:C:H2'	1:A5:182:G:C8	2.47	0.49
4:B2:1501:C:H5'	53:DD:178:ARG:HH12	1.75	0.49
5:A6:2408:U:H2'	40:l:17:GLN:HE22	1.77	0.49
5:A6:2550:G:H2'	5:A6:2551:A:H8	1.77	0.49
5:A6:2583:C:H5''	35:g:74:VAL:HG21	1.94	0.49
5:A6:2752:G:H3'	5:A6:2753:G:C8	2.48	0.49
5:A6:3589:G:H2'	5:A6:3590:G:C8	2.46	0.49
5:A6:4291:G:H4'	5:A6:4292:A:H3'	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A6:4748:U:O4	5:A6:4952:G:O6	2.30	0.49
9:C:41:HIS:HA	9:C:237:ILE:HD13	1.94	0.49
34:f:51:TYR:HE1	34:f:70:ILE:HD13	1.76	0.49
41:m:78:ILE:HB	41:m:83:ARG:HD2	1.94	0.49
49:gg:30:MET:HE1	49:gg:71:ILE:HD13	1.93	0.49
68:CC:259:THR:HG21	76:VV:16:LYS:H	1.77	0.49
84:Bb:15:G:H22	84:Bb:48:C:H42	1.59	0.49
1:A5:209:U:H1'	1:A5:210:C:H2'	1.94	0.49
1:A5:959:G:C4	11:E:127:LYS:CD	2.95	0.49
1:A5:1995:G:C5	45:s:40:MET:C	2.91	0.49
4:B2:110:U:O2	4:B2:351:G:C2	2.66	0.49
4:B2:1484:A:H8	53:DD:159:HIS:HE1	1.59	0.49
4:B2:1549:U:O4	4:B2:1584:G:O6	2.30	0.49
4:B2:1640:A:N7	83:Cc:30:G:C2	2.81	0.49
5:A6:4097:G:H2'	5:A6:4098:A:H8	1.77	0.49
5:A6:5006:U:H3	5:A6:5041:G:H4'	1.77	0.49
9:C:194:GLY:HA2	9:C:197:ARG:HB2	1.94	0.49
9:C:322:LEU:HG	9:C:323:ARG:HG3	1.94	0.49
17:L:74:ARG:HE	17:L:102:ARG:HD3	1.76	0.49
30:a:90:ALA:HB3	30:a:120:GLN:HE21	1.77	0.49
1:A5:1177:U:H2'	1:A5:1178:G:C8	2.48	0.49
1:A5:1281:G:C8	9:C:323:ARG:HB2	2.47	0.49
1:A5:1972:G:N1	45:s:41:GLN:CG	2.75	0.49
3:A8:151:G:H4'	13:G:67:ARG:HH22	1.78	0.49
4:B2:74:G:C4	70:GG:170:ARG:HA	2.48	0.49
4:B2:1244:U:O2	4:B2:1255:G:N2	2.32	0.49
4:B2:1708:C:H2'	4:B2:1709:G:H8	1.78	0.49
5:A6:3892:U:H2'	5:A6:3893:C:H6	1.76	0.49
17:L:166:ALA:HA	30:a:100:ILE:HG13	1.94	0.49
19:N:51:LEU:HD13	19:N:117:ASN:HB3	1.94	0.49
20:O:117:ARG:HH11	20:O:117:ARG:H	1.60	0.49
65:bb:16:LYS:HA	65:bb:23:ARG:HH21	1.78	0.49
68:CC:196:ILE:HB	68:CC:223:TYR:HB2	1.94	0.49
70:GG:119:LYS:H	70:GG:119:LYS:HZ3	1.60	0.49
73:JJ:162:ARG:HE	79:YY:31:GLY:HA2	1.77	0.49
1:A5:959:G:C4	11:E:127:LYS:CG	2.96	0.49
1:A5:1724:G:H21	12:F:110:LEU:HD21	1.76	0.49
3:A8:11:C:H2'	3:A8:12:G:H8	1.78	0.49
4:B2:374:G:O6	4:B2:385:G:O6	2.29	0.49
4:B2:1050:A:N6	4:B2:1068:G:H21	2.04	0.49
5:A6:2411:C:H2'	5:A6:2412:A:C8	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A6:2643:G:N2	5:A6:2691:U:O2	2.35	0.49
5:A6:4997:G:N2	5:A6:5053:U:O2	2.38	0.49
37:i:2:ALA:HA	37:i:4:ARG:HH21	1.76	0.49
41:m:82:LEU:HA	41:m:85:LEU:HB3	1.95	0.49
48:ff:94:LYS:HD2	48:ff:95:ARG:HH21	1.78	0.49
49:gg:247:TRP:HB3	49:gg:258:ILE:HD11	1.95	0.49
59:QQ:13:PHE:HB3	59:QQ:22:VAL:HG13	1.94	0.49
81:c:96:GLN:HG3	81:c:100:VAL:HG13	1.93	0.49
1:A5:300:A:H2'	1:A5:301:G:H8	1.77	0.49
1:A5:956:A:H4'	1:A5:1284:G:H21	1.77	0.49
1:A5:1368:A:C8	28:Y:1:MET:HA	2.47	0.49
4:B2:1228:A:H2'	4:B2:1229:G:H8	1.77	0.49
10:D:150:LEU:HD11	16:J:146:ARG:HA	1.95	0.49
18:M:5:ARG:HB3	18:M:57:LEU:HD22	1.93	0.49
23:S:29:ARG:HB3	23:S:31:ARG:HH22	1.77	0.49
24:T:11:THR:HA	24:T:14:MET:HB2	1.95	0.49
38:j:26:ALA:HB2	38:j:36:LYS:HD3	1.94	0.49
45:s:14:PHE:HA	45:s:17:ILE:HD12	1.94	0.49
52:BB:146:ARG:HG2	52:BB:148:ASN:H	1.77	0.49
66:ee:104:GLY:O	66:ee:107:LYS:HG2	2.12	0.49
70:GG:32:MET:HB2	70:GG:100:CYS:HB2	1.94	0.49
73:JJ:136:ARG:HA	73:JJ:141:VAL:HA	1.94	0.49
82:u:46:VAL:HG23	82:u:65:MET:HG3	1.95	0.49
1:A5:1558:A:H4'	80:W:126:LYS:HD2	1.95	0.49
4:B2:1096:G:C2	4:B2:1137:U:O2	2.66	0.49
5:A6:2768:C:H1'	35:g:68:SER:HB3	1.94	0.49
5:A6:3932:U:H2'	5:A6:3933:G:C8	2.48	0.49
5:A6:4618:G:H5'	26:V:15:ARG:HA	1.95	0.49
27:X:102:VAL:HA	27:X:134:LYS:HD2	1.94	0.49
51:AA:39:TYR:HB3	60:RR:105:MET:HE1	1.94	0.49
54:FF:35:LEU:HD12	54:FF:117:ILE:HG22	1.94	0.49
58:PP:30:TYR:HA	58:PP:33:LEU:HD12	1.93	0.49
61:SS:3:LEU:HB2	64:ZZ:55:TYR:HE2	1.77	0.49
71:HH:122:LEU:HA	71:HH:125:VAL:HB	1.93	0.49
73:JJ:108:ARG:HA	73:JJ:113:GLN:HE21	1.77	0.49
1:A5:215:C:H2'	1:A5:220:C:H5''	1.94	0.49
1:A5:440:U:H2'	1:A5:441:G:C8	2.47	0.49
1:A5:1825:A:H2'	1:A5:1826:G:H8	1.76	0.49
2:A7:57:C:H2'	2:A7:58:A:H8	1.77	0.49
3:A8:70:G:H5'	28:Y:118:ILE:HD11	1.94	0.49
4:B2:925:G:O6	4:B2:1017:U:O4	2.30	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B2:1652:G:N2	4:B2:1672:U:O2	2.37	0.49
5:A6:2654:C:H2'	5:A6:2655:C:H6	1.78	0.49
5:A6:4736:C:H2'	5:A6:4737:G:C8	2.47	0.49
11:E:217:ASP:HA	11:E:220:PHE:HB2	1.95	0.49
20:O:196:LEU:HB3	20:O:202:LEU:HG	1.94	0.49
21:P:33:ALA:HA	21:P:36:ILE:HG22	1.95	0.49
54:FF:166:ILE:N	54:FF:166:ILE:HA	2.14	0.49
71:HH:93:VAL:HG21	71:HH:133:LEU:HD12	1.94	0.49
72:II:114:GLU:HB3	72:II:136:ILE:HG21	1.94	0.49
72:II:198:TYR:HE2	74:LL:10:TYR:HB2	1.78	0.49
1:A5:749:G:N2	1:A5:913:U:O2	2.35	0.49
1:A5:1306:C:H2'	1:A5:1307:A:H8	1.78	0.49
1:A5:1825:A:H5''	24:T:36:LYS:HE3	1.95	0.49
1:A5:1882:U:H5'	33:e:48:ARG:HH22	1.78	0.49
4:B2:305:U:C2	72:II:183:GLY:CA	2.96	0.49
4:B2:416:U:O2	4:B2:421:G:O6	2.30	0.49
4:B2:841:G:C5	79:YY:11:LYS:HB2	2.48	0.49
4:B2:1248:U:N3	83:Cc:35:C:H3'	2.28	0.49
4:B2:1845:A:H2'	4:B2:1846:G:C8	2.48	0.49
4:B2:1869:A:C5	52:BB:115:LYS:CB	2.96	0.49
5:A6:2300:A:H62	9:C:180:ILE:HA	1.76	0.49
5:A6:3731:C:H2'	5:A6:3732:A:H8	1.77	0.49
8:B:56:ILE:HG22	8:B:368:ILE:HG12	1.94	0.49
8:B:230:GLY:O	8:B:234:ARG:HB2	2.12	0.49
9:C:28:PHE:HD2	9:C:132:ALA:HB2	1.78	0.49
24:T:104:SER:HA	24:T:107:LYS:HE3	1.94	0.49
35:g:39:GLY:HA2	35:g:60:ARG:HH21	1.78	0.49
49:gg:184:LEU:HD21	49:gg:187:ASN:HB2	1.94	0.49
53:DD:131:ALA:HA	53:DD:191:PRO:HD3	1.94	0.49
59:QQ:113:ILE:HG23	59:QQ:120:LEU:HD12	1.94	0.49
61:SS:46:ARG:HH12	61:SS:52:LEU:HD21	1.77	0.49
69:EE:87:MET:HE1	69:EE:236:ILE:HG12	1.95	0.49
1:A5:1100:U:H3	1:A5:1195:G:H22	1.60	0.49
4:B2:216:C:H2'	4:B2:217:A:H8	1.77	0.49
4:B2:1406:G:H21	4:B2:1443:C:N4	2.10	0.49
4:B2:1476:A:H5'	4:B2:1477:U:H5''	1.94	0.49
5:A6:2597:G:H2'	5:A6:2598:A:C8	2.47	0.49
5:A6:2663:G:H2'	5:A6:2664:G:C8	2.48	0.49
10:D:32:ALA:O	10:D:36:LEU:HB2	2.13	0.49
14:H:60:TRP:HE1	23:S:152:PHE:HD2	1.61	0.49
18:M:13:ALA:HA	18:M:58:THR:HG23	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:GG:151:ASP:HB3	81:c:105:ARG:HH21	1.78	0.49
73:JJ:78:LEU:HD13	73:JJ:92:MET:HB3	1.95	0.49
1:A5:1804:A:H4'	1:A5:1805:A:H5'	1.94	0.48
1:A5:1982:G:H3'	46:t:31:LYS:HE2	1.95	0.48
4:B2:1741:U:H5''	72:II:59:ARG:HH21	1.78	0.48
5:A6:3598:C:H2'	5:A6:3599:A:H8	1.77	0.48
5:A6:4454:G:O6	5:A6:4526:U:O2	2.31	0.48
4:B2:1269:G:H21	4:B2:1298:G:H1	1.60	0.48
4:B2:1599:U:C6	54:FF:165:ASN:C	2.91	0.48
5:A6:2605:G:O6	5:A6:2734:U:O4	2.31	0.48
5:A6:2665:U:H3	5:A6:2670:C:H42	1.60	0.48
5:A6:2671:C:H1'	5:A6:2672:C:H5'	1.95	0.48
5:A6:2889:G:C4	80:W:74:ARG:C	2.91	0.48
5:A6:4765:G:C6	5:A6:4869:U:O2	2.66	0.48
28:Y:10:ASP:HB3	28:Y:13:LYS:HB2	1.95	0.48
82:u:44:LYS:H	82:u:65:MET:HA	1.78	0.48
83:Cc:51:U:O4	83:Cc:65:G:O6	2.30	0.48
1:A5:1278:C:H3'	1:A5:1279:A:H8	1.78	0.48
5:A6:2624:G:N2	5:A6:2632:U:O2	2.42	0.48
6:A:224:THR:HA	6:A:237:LEU:HD12	1.95	0.48
11:E:289:LEU:HD12	18:M:109:ARG:CZ	2.43	0.48
14:H:59:LYS:HB2	14:H:70:VAL:HG21	1.93	0.48
16:J:56:THR:HG23	16:J:63:ARG:HA	1.95	0.48
22:Q:98:LEU:HD23	22:Q:118:GLY:HA3	1.95	0.48
50:dd:22:ARG:HB3	50:dd:38:MET:HE1	1.95	0.48
54:FF:102:LEU:HD21	64:ZZ:110:THR:HB	1.95	0.48
1:A5:83:C:H1'	1:A5:100:C:H42	1.77	0.48
1:A5:456:C:H2'	1:A5:457:G:C8	2.48	0.48
1:A5:1088:C:H2'	1:A5:1089:G:H8	1.78	0.48
1:A5:1286:C:H1'	11:E:133:LYS:HB3	1.95	0.48
1:A5:1468:C:H2'	1:A5:1469:C:C6	2.48	0.48
3:A8:38:U:H5''	36:h:81:LEU:HD13	1.94	0.48
4:B2:1203:G:N1	68:CC:114:LYS:C	2.72	0.48
5:A6:2694:G:H5'	5:A6:2696:A:H62	1.79	0.48
5:A6:4276:G:H3'	5:A6:4277:G:H8	1.78	0.48
5:A6:4370:G:C4	83:Cc:77:A:N7	2.82	0.48
5:A6:4704:C:H2'	5:A6:4705:A:H8	1.77	0.48
50:dd:22:ARG:HH22	55:KK:66:HIS:HD2	1.60	0.48
62:TT:43:LYS:HE2	62:TT:44:GLU:H	1.78	0.48
1:A5:18:C:H2'	1:A5:19:G:C8	2.49	0.48
1:A5:960:A:N7	1:A5:1283:G:N2	2.50	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A5:2045:G:N1	20:O:61:ARG:C	2.71	0.48
2:A7:76:U:C2	2:A7:100:A:N7	2.82	0.48
4:B2:23:G:N1	4:B2:652:U:C4	2.81	0.48
4:B2:185:G:C6	4:B2:214:U:O2	2.65	0.48
4:B2:1101:U:H3	4:B2:1131:G:H1	1.61	0.48
4:B2:1232:U:O2	4:B2:1526:G:N2	2.31	0.48
5:A6:2768:C:C4	35:g:70:THR:CA	2.97	0.48
5:A6:3855:C:H2'	5:A6:3856:A:H8	1.78	0.48
5:A6:4123:C:H42	35:g:94:ALA:HA	1.78	0.48
15:I:61:SER:HA	15:I:126:VAL:HG12	1.96	0.48
73:JJ:97:ILE:HA	73:JJ:100:LEU:HG	1.94	0.48
75:NN:127:ARG:HA	75:NN:130:LYS:HD2	1.96	0.48
77:WW:28:ARG:HB2	77:WW:60:LYS:HG2	1.96	0.48
1:A5:1730:U:O2	1:A5:1799:G:N2	2.43	0.48
2:A7:7:G:O6	2:A7:112:U:O4	2.31	0.48
4:B2:1203:G:N3	68:CC:114:LYS:O	2.47	0.48
4:B2:1392:U:H3	4:B2:1478:U:H3	1.61	0.48
5:A6:4728:U:H4'	5:A6:4729:A:H8	1.78	0.48
5:A6:4736:C:H4'	5:A6:5068:G:H2'	1.95	0.48
9:C:190:ARG:HH21	9:C:199:ARG:HB3	1.78	0.48
9:C:219:LYS:HA	9:C:222:ARG:HE	1.79	0.48
13:G:50:ASP:HB2	27:X:40:ILE:HD12	1.95	0.48
21:P:50:ASP:HB2	21:P:55:LYS:HB3	1.94	0.48
36:h:23:ASP:HA	36:h:26:VAL:HG22	1.96	0.48
49:gg:147:HIS:CE1	49:gg:175:LYS:H	2.31	0.48
1:A5:33:A:H8	1:A5:49:U:N3	1.96	0.48
1:A5:1487:G:H1'	17:L:184:MET:HE1	1.94	0.48
1:A5:1920:C:H5'	23:S:160:ARG:HH12	1.77	0.48
4:B2:5:U:H2'	4:B2:6:G:C8	2.48	0.48
4:B2:820:U:O2	4:B2:828:G:O6	2.31	0.48
5:A6:2620:G:C2	5:A6:2636:U:O2	2.67	0.48
5:A6:3598:C:H2'	5:A6:3599:A:C8	2.48	0.48
16:J:119:TYR:HE2	61:SS:101:ASN:HB3	1.79	0.48
23:S:15:ARG:HB3	23:S:27:LEU:HD13	1.95	0.48
38:j:72:ARG:HA	38:j:75:ARG:HD2	1.95	0.48
1:A5:175:C:H2'	1:A5:176:G:H8	1.79	0.48
1:A5:266:C:H2'	1:A5:267:G:C8	2.47	0.48
1:A5:1375:C:H5''	9:C:274:LYS:HG2	1.95	0.48
1:A5:1569:U:H2'	1:A5:1570:G:H8	1.77	0.48
4:B2:89:C:H2'	4:B2:90:G:H8	1.79	0.48
4:B2:1234:C:H2'	4:B2:1235:G:H8	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B2:1244:U:H2'	4:B2:1245:G:C8	2.49	0.48
4:B2:1398:G:H1'	49:gg:63:SER:HB3	1.95	0.48
4:B2:1419:C:H4'	62:TT:133:ARG:HG2	1.96	0.48
4:B2:1640:A:C5	83:Cc:30:G:N1	2.82	0.48
5:A6:2908:U:O2	5:A6:3586:G:O6	2.32	0.48
5:A6:3935:C:C4	5:A6:3936:A:N6	2.82	0.48
5:A6:4258:C:H2'	5:A6:4259:C:C6	2.49	0.48
10:D:30:TYR:HA	10:D:33:ARG:HB3	1.95	0.48
17:L:14:PHE:HB3	17:L:18:TRP:HE1	1.79	0.48
24:T:84:ILE:HD11	31:b:23:LYS:HA	1.96	0.48
28:Y:131:GLU:HA	28:Y:134:LYS:HB3	1.95	0.48
33:e:74:PHE:HA	33:e:94:SER:O	2.13	0.48
72:II:54:LYS:HE2	72:II:181:GLN:HB3	1.94	0.48
74:LL:111:VAL:HG22	74:LL:140:PHE:HB2	1.96	0.48
82:u:29:LEU:HB2	82:u:94:LEU:HD23	1.94	0.48
1:A5:981:C:H5	11:E:73:ARG:HD3	1.79	0.48
4:B2:1203:G:N2	68:CC:120:GLN:HA	2.24	0.48
4:B2:1622:U:H5	58:PP:118:GLU:HA	1.78	0.48
5:A6:2343:G:C4	9:C:101:MET:HE1	2.49	0.48
5:A6:2604:C:H2'	5:A6:2605:G:H8	1.78	0.48
5:A6:4421:C:H42	5:A6:4475:G:H22	1.59	0.48
5:A6:4426:C:H3'	5:A6:4427:G:H8	1.79	0.48
8:B:33:PRO:HG2	8:B:349:LYS:HB2	1.96	0.48
12:F:117:PHE:HE2	12:F:214:SER:HA	1.79	0.48
19:N:49:ARG:HE	19:N:49:ARG:HB2	1.44	0.48
27:X:87:MET:HE2	27:X:156:ILE:HD11	1.96	0.48
57:OO:34:PHE:HE2	57:OO:100:THR:HA	1.77	0.48
61:SS:46:ARG:HD3	62:TT:35:ASP:HB2	1.96	0.48
72:II:173:ALA:HA	72:II:190:LEU:H	1.79	0.48
74:LL:133:PRO:HB3	74:LL:139:ARG:HG3	1.94	0.48
1:A5:53:C:H1'	5:A6:2461:G:H21	1.78	0.48
1:A5:943:A:H5''	12:F:147:LYS:HB2	1.96	0.48
1:A5:959:G:C5	11:E:127:LYS:CD	2.97	0.48
1:A5:1687:U:H2'	1:A5:1688:G:C8	2.49	0.48
4:B2:155:G:H2'	4:B2:156:G:H8	1.79	0.48
4:B2:376:A:H1'	74:LL:8:ARG:HH22	1.79	0.48
4:B2:839:C:H42	79:YY:9:THR:HG23	1.78	0.48
4:B2:875:A:C2	4:B2:910:G:N1	2.76	0.48
4:B2:1047:C:H5''	57:OO:143:LYS:HD3	1.95	0.48
4:B2:1177:U:O2	4:B2:1184:G:N2	2.44	0.48
4:B2:1283:C:H4'	4:B2:1286:G:H4'	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A6:2659:A:H8	82:u:30:GLY:HA2	1.78	0.48
9:C:224:ILE:HD12	9:C:225:PRO:HD2	1.96	0.48
12:F:93:ARG:HH12	12:F:97:ILE:HG23	1.79	0.48
14:H:95:VAL:HG22	41:m:82:LEU:HG	1.96	0.48
17:L:98:VAL:HG12	17:L:100:PRO:HD3	1.96	0.48
19:N:120:TRP:HE1	19:N:123:GLU:HB2	1.77	0.48
21:P:39:MET:HG3	21:P:43:LYS:HG2	1.96	0.48
22:Q:157:GLY:HA3	30:a:47:LYS:HA	1.96	0.48
32:d:91:LYS:HD3	32:d:103:TYR:CZ	2.49	0.48
37:i:79:THR:O	37:i:83:ALA:HB2	2.13	0.48
39:k:23:VAL:HA	39:k:35:LYS:O	2.14	0.48
49:gg:87:LEU:HB2	49:gg:101:PHE:HB2	1.96	0.48
1:A5:1815:G:H8	1:A5:1816:C:C6	2.32	0.47
1:A5:1899:G:H5'	5:A6:2279:A:H5'	1.95	0.47
1:A5:1914:C:H4'	20:O:89:PRO:HD3	1.96	0.47
1:A5:2019:C:H2'	45:s:57:LYS:HD2	1.95	0.47
3:A8:43:A:H2'	3:A8:44:A:H8	1.79	0.47
4:B2:1869:A:C2	52:BB:115:LYS:CB	2.97	0.47
4:B2:1869:A:C5	52:BB:115:LYS:CG	2.97	0.47
5:A6:3927:U:H2'	5:A6:3928:A:C8	2.49	0.47
5:A6:4080:C:H2'	5:A6:4081:G:C8	2.48	0.47
5:A6:4454:G:C6	5:A6:4526:U:O2	2.67	0.47
13:G:163:PRO:HG2	13:G:166:LEU:HG	1.96	0.47
17:L:58:ILE:HG12	17:L:116:ARG:HD2	1.96	0.47
20:O:138:LEU:HA	20:O:141:LEU:HD12	1.96	0.47
46:t:38:SER:HB3	46:t:41:LYS:HB2	1.96	0.47
46:t:56:LEU:HD22	46:t:82:ILE:HB	1.96	0.47
61:SS:124:ARG:HD3	61:SS:131:VAL:HA	1.94	0.47
71:HH:170:VAL:HG13	71:HH:187:PHE:HB2	1.95	0.47
1:A5:1282:G:N1	11:E:131:HIS:HB2	2.28	0.47
1:A5:1346:C:H2'	1:A5:1347:G:H8	1.78	0.47
1:A5:1538:U:H2'	1:A5:1539:G:H8	1.79	0.47
3:A8:43:A:H2'	3:A8:44:A:C8	2.49	0.47
4:B2:169:U:H5''	70:GG:135:PRO:HA	1.96	0.47
4:B2:185:G:O6	4:B2:214:U:C2	2.67	0.47
4:B2:841:G:N1	79:YY:11:LYS:HB2	2.28	0.47
5:A6:2677:G:C4	82:u:32:LYS:CE	2.98	0.47
9:C:284:MET:HE1	22:Q:124:ASP:HB3	1.95	0.47
13:G:254:GLU:HA	13:G:257:LYS:HD2	1.96	0.47
17:L:76:PHE:HA	17:L:102:ARG:HH21	1.79	0.47
24:T:12:ARG:O	24:T:16:SER:HB3	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:g:9:ARG:HB2	35:g:34:TYR:CZ	2.50	0.47
61:SS:5:ILE:HA	64:ZZ:49:LEU:HD13	1.94	0.47
1:A5:200:U:H2'	28:Y:59:ARG:HH22	1.79	0.47
2:A7:70:G:H2'	2:A7:71:G:H8	1.79	0.47
5:A6:2768:C:C5	35:g:70:THR:HA	2.50	0.47
5:A6:4460:U:O4	5:A6:4516:G:O6	2.31	0.47
13:G:234:ARG:HG3	13:G:235:ARG:HE	1.78	0.47
20:O:73:PHE:HB2	20:O:79:ILE:HG23	1.95	0.47
39:k:3:ARG:HB2	39:k:43:TYR:HD1	1.79	0.47
49:gg:100:ARG:HG2	49:gg:102:VAL:HG13	1.96	0.47
1:A5:231:U:C2	1:A5:235:A:N7	2.83	0.47
1:A5:648:G:H2'	1:A5:649:A:H8	1.80	0.47
1:A5:1348:U:H2'	1:A5:1349:G:H8	1.80	0.47
1:A5:1620:U:H2'	1:A5:1621:A:C8	2.49	0.47
1:A5:1882:U:O4	1:A5:1897:A:C6	2.68	0.47
4:B2:812:A:H3'	4:B2:813:A:H8	1.79	0.47
4:B2:1495:G:N1	50:dd:43:PHE:HB3	2.29	0.47
4:B2:1657:G:H2'	4:B2:1658:G:H8	1.79	0.47
8:B:223:THR:HG22	8:B:338:VAL:HB	1.96	0.47
33:e:91:CYS:HB2	33:e:95:TYR:HB2	1.96	0.47
37:i:58:MET:HB2	37:i:94:LEU:HD21	1.95	0.47
46:t:85:LEU:HG	46:t:104:ILE:HD11	1.96	0.47
52:BB:121:ILE:HD11	52:BB:165:ARG:HB2	1.96	0.47
61:SS:114:LEU:HD13	61:SS:121:ARG:HB3	1.96	0.47
74:LL:127:THR:HB	74:LL:144:LYS:HB2	1.96	0.47
1:A5:283:G:H1'	37:i:82:ARG:HH12	1.79	0.47
1:A5:1204:C:H2'	1:A5:1205:G:C8	2.48	0.47
1:A5:1270:A:C4	31:b:112:ILE:HA	2.49	0.47
1:A5:1951:G:N2	1:A5:2032:U:O2	2.39	0.47
2:A7:7:G:N2	2:A7:112:U:O2	2.42	0.47
4:B2:396:U:H2'	4:B2:397:G:H8	1.79	0.47
4:B2:841:G:N1	79:YY:11:LYS:CA	2.78	0.47
4:B2:1324:G:O6	4:B2:1504:U:O4	2.32	0.47
5:A6:2750:G:H4'	35:g:73:HIS:HB2	1.96	0.47
17:L:189:ALA:HB2	37:i:10:GLY:HA2	1.95	0.47
51:AA:38:ILE:HG21	51:AA:47:TYR:HB3	1.95	0.47
58:PP:44:ARG:HH12	58:PP:82:ASP:HB2	1.80	0.47
69:EE:252:ARG:HH11	73:JJ:72:PHE:HD2	1.62	0.47
73:JJ:131:ARG:NE	73:JJ:145:PRO:HD3	2.29	0.47
1:A5:1486:C:H5'	17:L:195:ARG:HH21	1.78	0.47
5:A6:4760:G:H2'	5:A6:4761:G:C8	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:C:260:LEU:HA	9:C:263:LEU:HD23	1.96	0.47
15:I:38:ARG:HB3	15:I:41:ALA:HB3	1.95	0.47
22:Q:178:ARG:HH11	22:Q:184:ARG:HB3	1.78	0.47
23:S:83:ARG:HB3	23:S:125:GLN:HE22	1.80	0.47
35:g:64:LEU:HA	35:g:67:LEU:HB3	1.97	0.47
42:o:32:SER:HB3	42:o:35:ALA:HB2	1.96	0.47
61:SS:139:THR:HG22	61:SS:142:ARG:HH22	1.80	0.47
73:JJ:130:ILE:HA	73:JJ:135:ILE:HB	1.96	0.47
1:A5:126:C:H2'	1:A5:127:G:C8	2.50	0.47
1:A5:323:C:H2'	1:A5:324:A:H8	1.78	0.47
1:A5:1527:A:H5''	19:N:81:TYR:HB3	1.96	0.47
3:A8:96:C:H4'	36:h:66:LYS:HG2	1.96	0.47
4:B2:53:C:H4'	79:YY:108:LYS:HB3	1.96	0.47
4:B2:373:G:H2'	4:B2:374:G:H8	1.78	0.47
4:B2:437:G:H3'	4:B2:438:G:H21	1.79	0.47
4:B2:804:U:O2	4:B2:859:G:N2	2.34	0.47
4:B2:885:U:O2	4:B2:901:G:C6	2.68	0.47
4:B2:1096:G:N1	4:B2:1137:U:N3	2.62	0.47
4:B2:1816:G:H2'	4:B2:1817:G:H8	1.80	0.47
5:A6:2373:C:H2'	5:A6:2374:A:C8	2.49	0.47
5:A6:2512:A:H61	5:A6:2781:G:H1'	1.78	0.47
5:A6:2864:A:H5''	80:W:84:THR:HG22	1.96	0.47
5:A6:3937:C:H2'	5:A6:3938:G:C2	2.49	0.47
5:A6:4976:U:H1'	8:B:343:ARG:HH21	1.80	0.47
8:B:58:ARG:HD3	81:c:15:PRO:HB2	1.95	0.47
9:C:25:PRO:HB3	9:C:261:ASP:HB3	1.96	0.47
10:D:150:LEU:HD21	16:J:146:ARG:HG3	1.96	0.47
11:E:65:TYR:O	11:E:69:ALA:CB	2.63	0.47
17:L:20:ARG:HH12	17:L:21:ARG:HB2	1.80	0.47
19:N:73:ARG:HB2	19:N:92:LEU:HD12	1.97	0.47
24:T:144:ASN:HB2	24:T:146:LYS:HE3	1.96	0.47
26:V:18:LEU:HB2	26:V:54:ALA:HB3	1.97	0.47
54:FF:121:PRO:HB3	54:FF:196:LEU:HD21	1.97	0.47
58:PP:57:LEU:HA	58:PP:60:LEU:HD12	1.95	0.47
59:QQ:130:LYS:HA	59:QQ:137:ALA:HA	1.96	0.47
60:RR:66:VAL:HB	60:RR:69:ILE:HD11	1.97	0.47
67:aa:23:CYS:HB3	67:aa:28:ARG:H	1.79	0.47
69:EE:43:PRO:HB2	69:EE:46:ILE:HG13	1.97	0.47
70:GG:52:ILE:HG23	70:GG:109:LEU:HD21	1.96	0.47
73:JJ:91:LYS:H	73:JJ:92:MET:HE2	1.79	0.47
73:JJ:113:GLN:HA	73:JJ:116:LYS:HE2	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
77:WW:11:LEU:HD21	77:WW:73:GLY:HA2	1.97	0.47
4:B2:23:G:C6	4:B2:652:U:C4	3.03	0.47
4:B2:297:A:H5''	69:EE:133:THR:HA	1.97	0.47
4:B2:1229:G:H4'	4:B2:1633:A:H2	1.80	0.47
4:B2:1430:C:H2'	4:B2:1431:G:C8	2.50	0.47
4:B2:1528:G:H2'	4:B2:1529:C:C6	2.50	0.47
5:A6:2677:G:C6	82:u:32:LYS:CE	2.98	0.47
5:A6:2770:C:H2'	5:A6:2771:G:H8	1.79	0.47
5:A6:3853:U:H2'	5:A6:3854:C:H6	1.79	0.47
15:I:198:LYS:HA	15:I:198:LYS:HD3	1.40	0.47
22:Q:61:LEU:HD21	22:Q:66:MET:HB3	1.97	0.47
23:S:10:TYR:HA	23:S:65:GLY:O	2.15	0.47
32:d:92:ARG:HH11	32:d:93:ASN:H	1.63	0.47
36:h:107:GLN:HA	36:h:110:LYS:HB3	1.97	0.47
54:FF:63:LYS:H	54:FF:63:LYS:HG2	1.50	0.47
56:MM:52:LEU:HD11	56:MM:62:VAL:HG13	1.97	0.47
58:PP:111:MET:HB3	58:PP:114:HIS:HB2	1.95	0.47
1:A5:287:U:H2'	1:A5:288:G:C8	2.50	0.47
1:A5:490:C:H1'	9:C:7:LEU:HD11	1.96	0.47
3:A8:84:A:H5'	3:A8:85:U:C2	2.49	0.47
4:B2:841:G:C5	79:YY:11:LYS:CA	2.97	0.47
4:B2:864:A:H2'	4:B2:865:A:C8	2.49	0.47
4:B2:1599:U:C2	54:FF:165:ASN:O	2.68	0.47
4:B2:1656:G:O6	4:B2:1668:U:O4	2.33	0.47
4:B2:1819:A:H4'	7:n:13:LEU:HD21	1.97	0.47
5:A6:2274:C:H2'	5:A6:2275:G:C8	2.50	0.47
5:A6:2319:C:H41	33:e:59:GLY:H	1.63	0.47
5:A6:2752:G:H4'	29:Z:136:PHE:HD1	1.79	0.47
5:A6:4537:C:H2'	5:A6:4538:G:C8	2.49	0.47
5:A6:4629:U:H2'	5:A6:4630:G:H8	1.80	0.47
8:B:55:HIS:HA	8:B:75:ALA:HA	1.97	0.47
11:E:157:THR:HA	11:E:161:ARG:HB3	1.97	0.47
28:Y:50:ARG:HE	28:Y:115:ARG:HD3	1.79	0.47
59:QQ:70:VAL:HG11	59:QQ:84:ILE:HG22	1.97	0.47
70:GG:58:LYS:HA	70:GG:107:SER:HB3	1.96	0.47
75:NN:100:LYS:HE3	75:NN:100:LYS:HB3	1.70	0.47
1:A5:262:G:H2'	1:A5:263:G:H8	1.80	0.47
4:B2:652:U:H2'	4:B2:653:A:C8	2.50	0.47
4:B2:935:G:H2'	4:B2:936:G:C8	2.50	0.47
4:B2:1358:U:H2'	4:B2:1359:U:H6	1.80	0.47
4:B2:1618:C:H5''	58:PP:47:ARG:HH21	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:45:VAL:HG13	6:A:61:VAL:HG22	1.97	0.47
8:B:154:LYS:HG2	8:B:191:ALA:HA	1.97	0.47
23:S:9:GLU:HG2	23:S:33:PHE:CE1	2.49	0.47
28:Y:2:LYS:HD3	28:Y:2:LYS:HA	1.58	0.47
45:s:18:ILE:HD12	45:s:68:HIS:CD2	2.50	0.47
54:FF:122:ARG:HA	54:FF:122:ARG:HD2	1.82	0.47
73:JJ:174:LYS:HA	73:JJ:177:ASN:HB3	1.97	0.47
1:A5:175:C:H2'	1:A5:176:G:C8	2.50	0.46
1:A5:709:C:H5''	11:E:195:LYS:HZ1	1.79	0.46
1:A5:1290:G:H2'	1:A5:1291:G:H8	1.79	0.46
1:A5:1998:A:H8	45:s:54:LEU:HD22	1.79	0.46
1:A5:2002:A:H4'	1:A5:2003:G:C8	2.50	0.46
4:B2:412:G:H21	4:B2:812:A:H61	1.62	0.46
4:B2:812:A:H5'	69:EE:16:LYS:HD2	1.97	0.46
4:B2:1621:U:C2	58:PP:116:LEU:CA	2.98	0.46
5:A6:2375:A:H2'	5:A6:2376:A:H8	1.79	0.46
5:A6:3794:C:H2'	5:A6:3795:A:C8	2.50	0.46
5:A6:4757:C:C2	20:O:114:LYS:HD2	2.50	0.46
5:A6:4876:U:H3	23:S:165:PRO:HG3	1.80	0.46
12:F:104:VAL:HA	12:F:107:VAL:HG22	1.96	0.46
50:dd:21:CYS:SG	50:dd:39:CYS:SG	3.13	0.46
51:AA:181:GLU:HA	51:AA:184:ARG:HB2	1.97	0.46
68:CC:117:ARG:HD2	68:CC:117:ARG:HA	1.73	0.46
69:EE:11:ARG:HA	69:EE:28:ALA:HB2	1.97	0.46
70:GG:137:ARG:HG2	70:GG:139:SER:H	1.80	0.46
1:A5:1436:C:H2'	1:A5:1437:C:H4'	1.96	0.46
4:B2:920:A:H2'	4:B2:922:A:H8	1.80	0.46
9:C:94:ASN:HB3	9:C:102:PHE:H	1.80	0.46
28:Y:109:LEU:HD22	28:Y:115:ARG:HH12	1.79	0.46
33:e:67:LYS:HE3	33:e:67:LYS:HB3	1.75	0.46
34:f:15:LYS:HD2	34:f:15:LYS:HA	1.61	0.46
65:bb:45:THR:HG23	65:bb:82:LYS:HD3	1.96	0.46
1:A5:306:A:H2'	1:A5:307:A:C8	2.50	0.46
1:A5:750:U:H3	1:A5:912:G:H22	1.62	0.46
1:A5:1072:C:H1'	1:A5:1073:G:C8	2.50	0.46
1:A5:1471:U:O4	1:A5:1493:G:O6	2.34	0.46
1:A5:1998:A:C8	45:s:54:LEU:HD22	2.51	0.46
4:B2:1228:A:H2'	4:B2:1229:G:C8	2.50	0.46
4:B2:1409:A:H2'	4:B2:1410:C:H4'	1.96	0.46
5:A6:3783:A:H2	5:A6:3790:U:H3	1.62	0.46
5:A6:4679:G:H2'	5:A6:4680:G:H8	1.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:D:223:PHE:HB3	10:D:226:TYR:HB2	1.97	0.46
15:I:44:ASP:HA	15:I:171:TRP:HE1	1.79	0.46
35:g:74:VAL:HG13	35:g:76:ARG:HB2	1.98	0.46
68:CC:63:VAL:HG13	68:CC:64:THR:HG23	1.98	0.46
73:JJ:78:LEU:HD22	73:JJ:92:MET:HA	1.97	0.46
1:A5:115:C:H41	1:A5:156:G:H1'	1.80	0.46
1:A5:938:C:H1'	1:A5:939:G:H5'	1.96	0.46
1:A5:1449:C:H2'	1:A5:1450:C:H6	1.81	0.46
4:B2:1342:U:H3	4:B2:1483:A:H62	1.58	0.46
4:B2:1621:U:C2	58:PP:115:TYR:O	2.68	0.46
4:B2:1647:A:H62	4:B2:1676:U:H5	1.63	0.46
5:A6:4086:G:H5'	6:A:67:TYR:HE2	1.78	0.46
5:A6:4089:G:H2'	5:A6:4090:G:H8	1.80	0.46
5:A6:4300:U:H4'	24:T:89:ILE:HD12	1.97	0.46
5:A6:4757:C:N3	20:O:113:ASP:HB2	2.30	0.46
13:G:166:LEU:HD21	19:N:45:PRO:HD2	1.97	0.46
13:G:230:TYR:HA	13:G:233:ILE:HB	1.97	0.46
14:H:137:SER:HB3	14:H:143:GLU:HB3	1.97	0.46
44:r:32:LEU:HD21	44:r:110:ALA:HA	1.96	0.46
47:cc:22:GLY:HA2	54:FF:128:ILE:HG13	1.97	0.46
54:FF:104:THR:HG23	54:FF:106:GLU:H	1.80	0.46
58:PP:15:PHE:HB3	58:PP:22:LEU:HD21	1.96	0.46
68:CC:253:PRO:HA	68:CC:256:TRP:CD2	2.50	0.46
80:W:4:LEU:H	80:W:5:ARG:HH11	1.64	0.46
1:A5:1186:U:N3	10:D:275:GLN:HG2	2.31	0.46
1:A5:1607:C:H2'	1:A5:1608:G:H8	1.79	0.46
1:A5:1884:C:H2'	1:A5:1885:G:H8	1.80	0.46
4:B2:28:U:H2'	4:B2:29:G:C8	2.51	0.46
4:B2:894:G:H2'	4:B2:895:G:H8	1.79	0.46
4:B2:1862:G:H22	67:aa:76:SER:HB3	1.80	0.46
4:B2:1865:C:H42	67:aa:9:GLY:H	1.63	0.46
5:A6:2663:G:H5''	80:W:118:HIS:HA	1.97	0.46
5:A6:3946:G:N2	5:A6:4067:U:O2	2.36	0.46
5:A6:4343:U:H2'	5:A6:4344:U:C5	2.51	0.46
5:A6:4753:U:H5	11:E:282:ASN:H	1.62	0.46
10:D:279:ARG:HA	10:D:282:GLN:HB2	1.97	0.46
11:E:176:LEU:O	11:E:191:ARG:HA	2.16	0.46
15:I:76:MET:HE2	15:I:85:PHE:HB3	1.97	0.46
47:cc:66:ARG:HH21	85:Dd:13:U:H5''	1.79	0.46
70:GG:121:ILE:HG21	70:GG:124:LEU:HD12	1.95	0.46
72:II:38:ILE:HD11	72:II:81:VAL:HG23	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A5:114:G:H21	1:A5:276:C:H6	1.63	0.46
1:A5:335:A:H2'	1:A5:336:A:C4	2.51	0.46
1:A5:1219:G:H2'	1:A5:1220:G:C4	2.51	0.46
1:A5:1610:C:H5''	1:A5:1611:C:H5'	1.98	0.46
1:A5:1628:C:H2'	1:A5:1629:G:H8	1.80	0.46
1:A5:1972:G:N3	45:s:41:GLN:CG	2.79	0.46
4:B2:560:A:H2	73:JJ:128:VAL:HG11	1.81	0.46
4:B2:1056:U:H1'	4:B2:1063:C:H41	1.80	0.46
4:B2:1478:U:H2'	4:B2:1479:G:C8	2.50	0.46
4:B2:1488:C:H3'	4:B2:1489:A:H4'	1.97	0.46
4:B2:1535:U:C6	4:B2:1535:U:H2'	2.50	0.46
5:A6:2334:C:H5	9:C:189:MET:HE1	1.79	0.46
5:A6:2832:A:H3'	32:d:44:ARG:HH22	1.81	0.46
5:A6:2835:A:H61	5:A6:3852:A:H2'	1.81	0.46
5:A6:2902:G:H8	5:A6:2903:G:H22	1.64	0.46
5:A6:3701:C:H4'	5:A6:3702:A:H5'	1.98	0.46
5:A6:3760:A:C6	84:Bb:37:YYG:H2'	2.51	0.46
5:A6:4134:C:H2'	5:A6:4135:G:C8	2.50	0.46
11:E:60:SER:O	11:E:64:MET:CB	2.59	0.46
16:J:63:ARG:HH12	42:o:103:VAL:HA	1.80	0.46
18:M:130:LEU:HD13	20:O:180:GLN:HE22	1.81	0.46
45:s:35:VAL:HG22	45:s:55:MET:HG2	1.98	0.46
51:AA:70:ASN:HD22	68:CC:274:VAL:HG13	1.81	0.46
57:OO:32:HIS:HA	57:OO:96:LYS:HB3	1.96	0.46
67:aa:10:ARG:HB3	67:aa:34:LYS:HG3	1.97	0.46
83:Cc:19:G:H1	83:Cc:56:U:H1'	1.80	0.46
1:A5:1169:G:H2'	1:A5:1170:G:H8	1.81	0.46
1:A5:1661:C:H41	30:a:9:ARG:HB3	1.80	0.46
3:A8:20:A:H4'	5:A6:2333:G:H4'	1.98	0.46
4:B2:74:G:C6	70:GG:170:ARG:O	2.68	0.46
4:B2:532:C:H2'	4:B2:533:A:C8	2.51	0.46
5:A6:3798:U:H2'	5:A6:3799:A:H3'	1.98	0.46
5:A6:4305:G:H22	24:T:78:LYS:HD3	1.80	0.46
12:F:114:ARG:NH2	22:Q:4:ASP:H	2.14	0.46
20:O:185:VAL:O	20:O:189:ILE:HG12	2.16	0.46
23:S:94:TYR:HE2	23:S:138:ARG:HD3	1.80	0.46
26:V:90:ARG:HH22	81:c:22:ALA:HB2	1.81	0.46
44:r:30:ASN:HD22	44:r:63:VAL:HG13	1.80	0.46
45:s:49:GLY:H	45:s:50:LYS:HD2	1.80	0.46
49:gg:133:ASN:HB3	49:gg:139:LYS:HE3	1.98	0.46
49:gg:213:ASP:HB3	49:gg:215:GLN:HB2	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
68:CC:66:LEU:HA	68:CC:69:LEU:HD12	1.98	0.46
71:HH:98:ARG:HB3	71:HH:125:VAL:HG22	1.96	0.46
71:HH:139:ILE:HG22	75:NN:18:TYR:HE2	1.81	0.46
80:W:60:ARG:HE	80:W:60:ARG:HB3	1.58	0.46
1:A5:1341:U:H2'	1:A5:1342:A:C8	2.50	0.46
1:A5:1942:A:H61	1:A5:2039:G:H2'	1.81	0.46
4:B2:412:G:N2	4:B2:812:A:H61	2.14	0.46
4:B2:752:G:H21	4:B2:753:C:H5	1.64	0.46
4:B2:924:G:C2	4:B2:1018:U:O2	2.69	0.46
5:A6:2889:G:N3	80:W:74:ARG:C	2.74	0.46
5:A6:3880:G:H2'	5:A6:3881:G:C8	2.51	0.46
5:A6:4613:C:N3	14:H:121:LYS:CD	2.79	0.46
5:A6:4682:U:O2	5:A6:4707:A:C5	2.69	0.46
5:A6:4699:U:H1'	5:A6:4700:A:H5''	1.98	0.46
5:A6:4759:C:H3'	5:A6:4760:G:C8	2.51	0.46
6:A:136:VAL:HA	6:A:148:VAL:HA	1.98	0.46
6:A:177:LYS:HG3	43:p:29:ILE:HD13	1.97	0.46
8:B:294:LYS:HB2	8:B:299:ILE:HD13	1.97	0.46
12:F:148:SER:HB3	12:F:243:ILE:HD13	1.97	0.46
18:M:103:LYS:HE3	18:M:103:LYS:HB3	1.62	0.46
22:Q:178:ARG:N	30:a:51:GLY:HA2	2.31	0.46
52:BB:67:PHE:HB2	52:BB:86:LEU:HB2	1.98	0.46
83:Cc:19:G:H2'	83:Cc:58:A:C4	2.51	0.46
1:A5:105:A:H4'	17:L:35:ARG:NH1	2.25	0.46
1:A5:961:G:H21	11:E:125:PRO:HG3	1.81	0.46
1:A5:1876:U:H2'	1:A5:1877:G:C8	2.51	0.46
2:A7:69:U:H2'	2:A7:70:G:C8	2.51	0.46
4:B2:992:A:H3'	67:aa:15:ARG:HH22	1.81	0.46
4:B2:1203:G:C6	68:CC:114:LYS:C	2.94	0.46
4:B2:1419:C:H2'	4:B2:1420:G:H8	1.81	0.46
9:C:49:ARG:HH21	9:C:111:TRP:HA	1.81	0.46
11:E:168:LEU:HD21	11:E:179:THR:HG22	1.98	0.46
20:O:142:ALA:HA	20:O:145:VAL:HG22	1.98	0.46
27:X:68:ARG:HH12	27:X:70:LYS:HG3	1.80	0.46
28:Y:80:ILE:HD11	28:Y:101:PRO:HG3	1.98	0.46
32:d:21:VAL:HB	32:d:90:ARG:HE	1.81	0.46
33:e:28:TYR:HD1	33:e:30:LYS:HB2	1.80	0.46
49:gg:156:PHE:HA	49:gg:165:ILE:HG22	1.98	0.46
59:QQ:27:ARG:H	59:QQ:27:ARG:HD3	1.81	0.46
68:CC:261:PHE:HZ	76:VV:18:SER:HB3	1.80	0.46
69:EE:43:PRO:HB3	69:EE:81:THR:HA	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
69:EE:103:TYR:HD2	69:EE:182:MET:HE2	1.81	0.46
72:II:110:ARG:HA	72:II:121:LEU:HD23	1.96	0.46
72:II:116:HIS:CE1	72:II:152:ARG:HE	2.33	0.46
82:u:52:CYS:HB3	82:u:56:ARG:HD3	1.97	0.46
1:A5:323:C:H2'	1:A5:324:A:C8	2.51	0.46
1:A5:437:G:H2'	1:A5:438:G:H8	1.81	0.46
1:A5:1370:G:H1'	1:A5:1372:A:C5	2.51	0.46
1:A5:1987:C:H2'	1:A5:1988:G:C4	2.51	0.46
3:A8:102:G:H3'	3:A8:104:A:H2'	1.98	0.46
4:B2:74:G:N3	70:GG:170:ARG:C	2.74	0.46
4:B2:409:C:H2'	4:B2:410:G:C8	2.51	0.46
4:B2:982:G:H2'	4:B2:983:A:C8	2.50	0.46
4:B2:1165:G:H2'	78:XX:23:HIS:CD2	2.51	0.46
4:B2:1217:A:H2'	4:B2:1218:C:C6	2.51	0.46
4:B2:1351:G:H1	4:B2:1360:U:H3	1.64	0.46
5:A6:3973:G:H2'	5:A6:3974:G:H8	1.81	0.46
5:A6:4370:G:C4	83:Cc:77:A:N6	2.84	0.46
5:A6:4675:U:H2'	5:A6:4676:G:C8	2.50	0.46
10:D:108:ARG:HG3	10:D:252:VAL:HA	1.97	0.46
10:D:208:MET:HE1	10:D:233:PRO:HG3	1.98	0.46
62:TT:5:THR:H	62:TT:8:ASP:HB2	1.81	0.46
68:CC:114:LYS:HA	68:CC:114:LYS:HD2	1.74	0.46
71:HH:69:LEU:HD22	71:HH:96:ALA:HB2	1.98	0.46
1:A5:300:A:H2'	1:A5:301:G:C8	2.51	0.45
1:A5:458:C:H5''	11:E:118:TYR:H	1.81	0.45
1:A5:1093:C:H2'	1:A5:1094:G:C8	2.51	0.45
1:A5:1282:G:C4	11:E:131:HIS:CD2	3.04	0.45
1:A5:1720:C:H2'	1:A5:1721:G:H8	1.81	0.45
1:A5:1803:G:C6	24:T:109:VAL:HG22	2.52	0.45
4:B2:808:A:H2	4:B2:855:G:H22	1.63	0.45
5:A6:4345:C:H5	42:o:30:LYS:HG2	1.81	0.45
5:A6:4757:C:N1	20:O:113:ASP:O	2.49	0.45
11:E:155:ILE:HG22	11:E:161:ARG:HA	1.97	0.45
28:Y:84:ARG:HA	28:Y:86:GLN:HE22	1.80	0.45
32:d:57:MET:HG2	32:d:59:THR:H	1.80	0.45
53:DD:66:ILE:HD12	53:DD:69:LEU:HD12	1.98	0.45
53:DD:213:PRO:HB3	60:RR:19:LYS:HB3	1.97	0.45
68:CC:166:ARG:HD3	68:CC:181:PRO:HG3	1.98	0.45
1:A5:709:C:H2'	1:A5:710:G:C8	2.50	0.45
1:A5:1813:U:H2'	31:b:49:HIS:HE1	1.81	0.45
1:A5:1870:C:H2'	1:A5:1871:A:C8	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B2:820:U:O2	4:B2:828:G:C6	2.69	0.45
4:B2:1010:G:H2'	4:B2:1011:A:C8	2.51	0.45
5:A6:2775:C:H2'	5:A6:2776:G:C8	2.50	0.45
5:A6:4519:C:H5''	5:A6:4520:G:H5''	1.97	0.45
22:Q:123:PHE:HA	22:Q:126:LEU:HB3	1.98	0.45
45:s:48:ARG:HB3	46:t:123:ARG:HG2	1.98	0.45
75:NN:43:LYS:HE3	75:NN:45:LEU:HD11	1.98	0.45
82:u:15:ASN:HA	82:u:18:LEU:HD23	1.98	0.45
82:u:32:LYS:HA	82:u:32:LYS:HD3	1.65	0.45
1:A5:1306:C:H2'	1:A5:1307:A:C8	2.51	0.45
4:B2:388:U:H2'	4:B2:389:A:C8	2.51	0.45
4:B2:879:C:H3'	4:B2:880:G:H21	1.81	0.45
4:B2:1030:A:H2'	4:B2:1031:A:H8	1.81	0.45
4:B2:1218:C:H2'	4:B2:1219:C:H6	1.81	0.45
4:B2:1829:G:H1'	4:B2:1850:A:H2	1.81	0.45
5:A6:3842:C:H3'	5:A6:3843:C:H2'	1.97	0.45
5:A6:4301:U:O2	5:A6:4309:G:N2	2.40	0.45
8:B:112:ASP:HA	8:B:115:LYS:HD3	1.98	0.45
11:E:74:LYS:HD2	11:E:74:LYS:HA	1.65	0.45
18:M:127:VAL:HA	18:M:130:LEU:HG	1.99	0.45
25:U:34:MET:HE3	25:U:39:PHE:HD1	1.82	0.45
28:Y:50:ARG:HD2	28:Y:115:ARG:NH1	2.32	0.45
69:EE:183:VAL:HG13	69:EE:220:THR:HG21	1.97	0.45
75:NN:62:GLN:HG3	75:NN:65:PHE:H	1.80	0.45
79:YY:38:THR:HA	79:YY:41:ARG:HD3	1.98	0.45
1:A5:75:G:C6	17:L:101:ARG:HB3	2.51	0.45
1:A5:471:A:C5	1:A5:684:G:N2	2.85	0.45
1:A5:1458:C:H3'	1:A5:1459:A:H8	1.80	0.45
4:B2:61:A:H1'	4:B2:335:G:H21	1.81	0.45
4:B2:379:C:H2'	4:B2:380:G:C8	2.51	0.45
4:B2:644:G:H5'	73:JJ:41:ARG:HH21	1.80	0.45
4:B2:1101:U:H2'	4:B2:1102:G:C8	2.51	0.45
4:B2:1174:U:H2'	4:B2:1175:G:C8	2.51	0.45
4:B2:1640:A:C6	83:Cc:30:G:O6	2.68	0.45
5:A6:2638:G:H2'	5:A6:2639:U:C6	2.50	0.45
5:A6:3860:A:P	21:P:139:TYR:CD2	3.09	0.45
8:B:85:VAL:HG22	8:B:204:GLN:HE22	1.82	0.45
13:G:57:TRP:HB3	13:G:61:ILE:HB	1.97	0.45
16:J:18:ARG:HG3	16:J:135:GLY:HA3	1.98	0.45
23:S:28:TYR:HB3	24:T:151:LEU:HD21	1.99	0.45
26:V:82:ILE:HG13	26:V:83:ARG:HG3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:d:51:LYS:HA	32:d:54:MET:HB2	1.97	0.45
33:e:7:LEU:HD22	33:e:93:LYS:HG2	1.98	0.45
51:AA:80:ARG:HH12	51:AA:166:LYS:HA	1.81	0.45
63:UU:30:LYS:HA	63:UU:30:LYS:HE3	1.97	0.45
69:EE:193:GLY:HA2	69:EE:212:ASP:HA	1.98	0.45
71:HH:145:ARG:HH11	71:HH:145:ARG:HA	1.80	0.45
73:JJ:107:GLU:HG2	73:JJ:116:LYS:NZ	2.31	0.45
82:u:41:GLY:N	82:u:63:TYR:H	2.15	0.45
1:A5:491:G:H5'	9:C:5:ARG:HB3	1.98	0.45
4:B2:1139:C:H4'	76:VV:62:MET:HE1	1.98	0.45
4:B2:1206:G:H1	4:B2:1694:U:H3	1.63	0.45
13:G:103:ARG:HE	13:G:195:HIS:CE1	2.34	0.45
13:G:158:ALA:HA	13:G:184:LEU:O	2.17	0.45
22:Q:78:LYS:HE3	22:Q:135:GLY:HA2	1.97	0.45
67:aa:46:GLU:HG2	67:aa:48:ALA:H	1.81	0.45
68:CC:183:LYS:HG2	68:CC:196:ILE:HA	1.99	0.45
77:WW:106:THR:HA	77:WW:123:GLY:HA3	1.97	0.45
1:A5:2034:G:H2'	1:A5:2035:C:C6	2.52	0.45
4:B2:877:C:H5'	4:B2:878:G:H5''	1.98	0.45
4:B2:1232:U:O4	4:B2:1526:G:O6	2.35	0.45
5:A6:4323:A:H2'	5:A6:4324:A:C4	2.51	0.45
5:A6:4370:G:C6	83:Cc:77:A:C6	2.89	0.45
5:A6:4413:C:H41	5:A6:4429:C:H41	1.63	0.45
15:I:156:LYS:HE3	15:I:156:LYS:HB3	1.69	0.45
16:J:103:GLY:HA2	16:J:159:LYS:HA	1.99	0.45
22:Q:125:GLN:HA	22:Q:128:LEU:HB2	1.99	0.45
40:l:42:ARG:HH12	40:l:44:TRP:HD1	1.65	0.45
52:BB:28:LYS:HB3	52:BB:48:LEU:HD11	1.97	0.45
56:MM:18:LEU:HD13	56:MM:77:ILE:HG21	1.99	0.45
72:II:66:SER:HA	72:II:73:THR:HA	1.99	0.45
73:JJ:60:LEU:HD22	73:JJ:70:ARG:HA	1.98	0.45
1:A5:268:G:H2'	1:A5:269:G:H8	1.81	0.45
1:A5:758:G:H21	1:A5:762:C:H5''	1.81	0.45
1:A5:1047:C:H2'	1:A5:1048:G:C8	2.52	0.45
1:A5:1089:G:H2'	1:A5:1090:G:C8	2.51	0.45
1:A5:1285:U:H1'	11:E:133:LYS:HD2	1.99	0.45
1:A5:1688:G:H2'	1:A5:1689:G:C8	2.52	0.45
4:B2:329:G:H2'	4:B2:330:G:C8	2.52	0.45
4:B2:502:C:C2	69:EE:66:MET:HE1	2.52	0.45
4:B2:1621:U:N1	58:PP:115:TYR:C	2.75	0.45
4:B2:1745:A:H4'	70:GG:31:ARG:HH22	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A6:2308:A:H61	5:A6:2330:G:H1'	1.81	0.45
5:A6:2407:G:H2'	40:l:13:LEU:HD13	1.98	0.45
5:A6:4321:U:H2'	5:A6:4322:G:C8	2.52	0.45
5:A6:4757:C:C5	20:O:113:ASP:C	2.95	0.45
5:A6:4918:C:H2'	5:A6:4919:G:C8	2.51	0.45
8:B:95:THR:HG23	8:B:98:GLY:H	1.81	0.45
9:C:31:PRO:HD3	9:C:267:TRP:HH2	1.82	0.45
12:F:90:PHE:O	12:F:141:TRP:HA	2.16	0.45
23:S:79:GLY:H	23:S:132:ILE:HD13	1.82	0.45
27:X:74:TYR:HE2	36:h:29:SER:HB3	1.80	0.45
36:h:71:LYS:HE3	36:h:71:LYS:HB3	1.73	0.45
40:l:21:ARG:NH1	40:l:24:PRO:HD3	2.31	0.45
54:FF:156:THR:HA	54:FF:159:ARG:HB2	1.98	0.45
61:SS:45:LEU:HD22	61:SS:50:ILE:HD11	1.98	0.45
63:UU:50:VAL:HG13	63:UU:89:ILE:HG23	1.98	0.45
1:A5:132:G:H4'	1:A5:178:C:H4'	1.99	0.45
1:A5:392:U:O2	1:A5:399:G:N2	2.40	0.45
1:A5:959:G:N1	11:E:127:LYS:CG	2.80	0.45
1:A5:1465:G:H3'	1:A5:1466:G:H8	1.81	0.45
1:A5:1469:C:H2'	1:A5:1470:G:C8	2.51	0.45
1:A5:1691:G:C6	1:A5:1845:U:O2	2.70	0.45
1:A5:1750:G:H2'	1:A5:1751:A:H8	1.82	0.45
4:B2:68:A:H61	4:B2:81:U:H3	1.65	0.45
5:A6:2503:G:H1'	5:A6:4084:G:C8	2.52	0.45
5:A6:2558:C:H2'	5:A6:2559:G:C8	2.51	0.45
5:A6:2572:C:H2'	5:A6:2573:A:H8	1.81	0.45
5:A6:2682:G:H21	35:g:54:ARG:HH22	1.64	0.45
5:A6:4089:G:H2'	5:A6:4090:G:C8	2.51	0.45
5:A6:4629:U:H2'	5:A6:4630:G:C8	2.52	0.45
9:C:210:ILE:HA	9:C:230:LEU:O	2.17	0.45
20:O:117:ARG:H	20:O:117:ARG:NH1	2.15	0.45
28:Y:26:ARG:HA	28:Y:29:ILE:HG22	1.98	0.45
42:o:42:ASP:O	42:o:46:SER:HB3	2.16	0.45
46:t:15:LEU:HD22	46:t:62:LEU:HD11	1.98	0.45
46:t:125:LEU:HA	46:t:128:THR:HG23	1.99	0.45
51:AA:17:LYS:HA	60:RR:91:LEU:HB3	1.98	0.45
66:ee:105:ARG:HH22	66:ee:106:ALA:HB2	1.81	0.45
70:GG:67:VAL:HG12	70:GG:69:THR:HG22	1.98	0.45
79:YY:7:ILE:HG22	79:YY:27:VAL:HG22	1.99	0.45
80:W:115:ILE:HD13	80:W:120:TYR:HB2	1.99	0.45
83:Cc:29:C:H2'	83:Cc:30:G:C8	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A5:59:A:C8	1:A5:337:U:N3	2.79	0.45
1:A5:137:G:H2'	1:A5:138:G:H8	1.82	0.45
1:A5:244:G:H2'	1:A5:246:G:H5''	1.99	0.45
1:A5:288:G:H5''	42:o:48:TYR:HB2	1.98	0.45
1:A5:326:C:H3'	37:i:28:ARG:HH21	1.82	0.45
1:A5:492:U:H2'	1:A5:493:G:C8	2.52	0.45
1:A5:1435:G:H22	1:A5:1449:C:H42	1.65	0.45
2:A7:63:C:H5'	2:A7:64:G:H5''	1.98	0.45
2:A7:79:U:H3	2:A7:97:G:H1	1.64	0.45
4:B2:12:U:H2'	4:B2:13:C:C6	2.51	0.45
4:B2:1599:U:N3	54:FF:165:ASN:C	2.73	0.45
5:A6:2749:C:H5'	35:g:65:MET:HE1	1.97	0.45
5:A6:3860:A:H2'	5:A6:3861:A:C8	2.52	0.45
11:E:264:ILE:HA	11:E:270:LEU:HD23	1.99	0.45
27:X:103:LYS:H	27:X:103:LYS:HE2	1.82	0.45
30:a:27:LYS:HE3	30:a:27:LYS:HB2	1.70	0.45
48:ff:139:HIS:HB3	48:ff:148:TYR:HB2	1.98	0.45
57:OO:98:ARG:HB3	57:OO:132:VAL:HG13	1.99	0.45
61:SS:86:ARG:HD2	61:SS:86:ARG:HA	1.61	0.45
72:II:199:LEU:HA	72:II:202:ILE:HB	1.99	0.45
4:B2:1096:G:N1	4:B2:1137:U:C2	2.85	0.45
4:B2:1598:G:H2'	64:ZZ:80:ARG:HH12	1.81	0.45
4:B2:1869:A:C2	4:B2:1869:A:C4	2.96	0.45
5:A6:4679:G:H2'	5:A6:4680:G:C8	2.51	0.45
5:A6:4993:G:H2'	5:A6:4994:G:H8	1.81	0.45
10:D:60:ILE:HD13	10:D:98:ALA:HB2	1.98	0.45
21:P:48:LEU:HD11	21:P:91:LEU:HB2	1.98	0.45
22:Q:98:LEU:HD21	22:Q:113:ILE:HB	1.99	0.45
25:U:47:ILE:HD11	25:U:56:LEU:HD23	1.99	0.45
26:V:123:LYS:HE3	81:c:20:ARG:HH22	1.81	0.45
30:a:110:LYS:HG3	30:a:128:PHE:HB2	1.99	0.45
49:gg:21:ILE:HG21	49:gg:299:PHE:HB2	1.98	0.45
50:dd:55:LEU:HD21	63:UU:83:ARG:HD2	1.97	0.45
51:AA:80:ARG:HH22	51:AA:166:LYS:HA	1.81	0.45
66:ee:103:THR:HA	66:ee:107:LYS:HB3	1.99	0.45
74:LL:134:LEU:HD21	74:LL:141:ASN:HD21	1.82	0.45
79:YY:15:ASN:HB3	79:YY:20:ARG:HG3	1.99	0.45
80:W:70:ARG:CZ	80:W:70:ARG:HA	2.47	0.45
82:u:42:LYS:HB2	82:u:62:TYR:O	2.17	0.45
1:A5:1284:G:N1	1:A5:2076:G:H5''	2.32	0.44
1:A5:1346:C:H2'	1:A5:1347:G:C8	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A5:1348:U:H2'	1:A5:1349:G:C8	2.52	0.44
1:A5:1515:A:H4'	17:L:15:HIS:HE1	1.81	0.44
4:B2:792:C:H2'	4:B2:793:G:C8	2.52	0.44
4:B2:1613:G:H2'	4:B2:1614:A:C8	2.52	0.44
5:A6:2283:G:H2'	5:A6:2284:G:H8	1.81	0.44
5:A6:3856:A:H4'	21:P:85:LYS:HD3	1.99	0.44
5:A6:4345:C:C5	42:o:30:LYS:HG2	2.52	0.44
5:A6:4393:G:H1	5:A6:4397:A:H62	1.63	0.44
12:F:84:ALA:HA	24:T:136:ARG:HH12	1.82	0.44
13:G:166:LEU:HD11	19:N:45:PRO:HG2	1.99	0.44
15:I:38:ARG:HD2	15:I:38:ARG:HA	1.76	0.44
15:I:135:ILE:HG22	15:I:136:MET:HB2	1.98	0.44
18:M:24:LEU:HD21	18:M:86:TRP:CE2	2.52	0.44
28:Y:17:ARG:O	28:Y:21:ALA:HB2	2.17	0.44
36:h:88:THR:HG23	36:h:90:ALA:H	1.82	0.44
46:t:56:LEU:HD21	46:t:79:ALA:HA	1.98	0.44
69:EE:23:LEU:HD11	73:JJ:6:SER:HB3	1.98	0.44
70:GG:130:PRO:HG2	81:c:83:THR:HG22	1.99	0.44
72:II:118:ALA:HB1	72:II:137:LEU:HA	1.99	0.44
1:A5:154:G:H4'	36:h:105:LYS:HD3	1.99	0.44
1:A5:307:A:H3'	1:A5:308:G:H21	1.82	0.44
4:B2:532:C:H2'	4:B2:533:A:N7	2.32	0.44
4:B2:1092:G:H2'	4:B2:1093:A:H8	1.82	0.44
4:B2:1264:C:H5'	4:B2:1265:A:C8	2.53	0.44
4:B2:1348:G:H1	4:B2:1381:G:H1	1.64	0.44
4:B2:1816:G:H2'	4:B2:1817:G:C8	2.52	0.44
4:B2:1859:A:H2'	4:B2:1860:A:C8	2.52	0.44
5:A6:2742:G:H4'	6:A:22:HIS:HD2	1.82	0.44
5:A6:3962:A:H5'	5:A6:4043:G:H21	1.82	0.44
5:A6:4121:G:H22	6:A:83:HIS:CE1	2.35	0.44
5:A6:4525:C:H5''	8:B:245:HIC:HB2	1.98	0.44
5:A6:4866:C:H2'	5:A6:4867:G:C8	2.52	0.44
5:A6:4896:G:H2'	5:A6:4897:G:C8	2.52	0.44
6:A:179:ILE:H	6:A:179:ILE:HG13	1.67	0.44
8:B:385:LYS:O	8:B:389:MET:HB3	2.18	0.44
10:D:75:VAL:HG12	10:D:112:ARG:HH12	1.80	0.44
13:G:96:LEU:HD22	13:G:193:LEU:HD21	1.99	0.44
13:G:103:ARG:HH21	13:G:195:HIS:CD2	2.36	0.44
13:G:217:LYS:HE3	13:G:217:LYS:HB3	1.89	0.44
14:H:12:ILE:HD11	14:H:55:LEU:HB2	1.99	0.44
18:M:97:ALA:HA	18:M:100:ARG:HG2	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:P:117:ILE:HD13	21:P:148:MET:HB3	1.98	0.44
30:a:98:ALA:HB3	30:a:123:ILE:HG13	1.99	0.44
54:FF:125:SER:HA	54:FF:138:ALA:HA	1.99	0.44
55:KK:67:PHE:HB3	55:KK:69:TRP:HZ3	1.82	0.44
56:MM:52:LEU:HD13	56:MM:108:CYS:HB2	1.98	0.44
57:OO:101:GLY:HA3	57:OO:134:PRO:HG2	1.99	0.44
1:A5:370:U:C4	1:A5:1637:A:C2	3.05	0.44
1:A5:1380:G:H21	1:A5:1381:U:H5	1.65	0.44
1:A5:1929:A:N6	1:A5:2054:U:N3	2.66	0.44
5:A6:2277:C:H5'	22:Q:3:VAL:HG21	1.99	0.44
5:A6:3731:C:H2'	5:A6:3732:A:C8	2.53	0.44
5:A6:4585:U:H2'	5:A6:4586:G:C8	2.52	0.44
5:A6:4992:G:H2'	5:A6:4993:G:C8	2.51	0.44
5:A6:5062:G:H1	8:B:124:LYS:HG2	1.81	0.44
10:D:15:ARG:HD3	24:T:19:PHE:HE1	1.81	0.44
11:E:212:PRO:HB2	11:E:215:LEU:HG	2.00	0.44
11:E:280:LEU:HB2	34:f:4:ARG:HB3	1.99	0.44
14:H:36:ARG:HG3	14:H:80:MET:HE2	1.99	0.44
22:Q:81:VAL:O	22:Q:138:LEU:HA	2.17	0.44
52:BB:182:LYS:HE3	52:BB:231:LEU:HD22	1.99	0.44
1:A5:1289:C:C6	11:E:136:PHE:CE2	3.06	0.44
1:A5:1724:G:C2	1:A5:1838:A:H2	2.31	0.44
1:A5:1742:A:H2'	1:A5:1743:A:H8	1.81	0.44
4:B2:1237:C:H1'	58:PP:128:HIS:CE1	2.53	0.44
4:B2:1787:G:H2'	4:B2:1788:A:C8	2.53	0.44
4:B2:1798:C:H3'	4:B2:1799:G:H8	1.83	0.44
5:A6:2683:C:H2'	5:A6:2684:C:C6	2.52	0.44
5:A6:2763:U:H2'	5:A6:2764:A:C4	2.52	0.44
5:A6:3892:U:H2'	5:A6:3893:C:C6	2.52	0.44
5:A6:4500:U:C2	84:Bb:75:C:N3	2.85	0.44
6:A:237:LEU:HD21	6:A:240:ALA:HB2	2.00	0.44
11:E:160:HIS:HB3	11:E:163:LYS:HD2	1.99	0.44
16:J:56:THR:HG22	16:J:58:ARG:NH1	2.32	0.44
21:P:6:LEU:HB2	21:P:116:HIS:CD2	2.52	0.44
39:k:55:LYS:HE3	39:k:55:LYS:HB3	1.82	0.44
47:cc:40:ARG:HH12	47:cc:42:ILE:HG23	1.82	0.44
49:gg:70:VAL:HG21	49:gg:113:PHE:H	1.81	0.44
49:gg:190:GLY:HA2	53:DD:219:PRO:HB2	1.99	0.44
55:KK:90:VAL:HG23	55:KK:95:ARG:HG3	1.99	0.44
60:RR:33:ARG:HA	60:RR:33:ARG:HD3	1.85	0.44
63:UU:38:ASP:HA	63:UU:41:ARG:HG2	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
71:HH:45:ILE:HD12	71:HH:45:ILE:HA	1.85	0.44
1:A5:181:C:H2'	1:A5:182:G:H8	1.82	0.44
1:A5:684:G:N9	11:E:104:ASN:N	2.65	0.44
1:A5:1348:U:H4'	22:Q:19:LYS:HZ1	1.83	0.44
1:A5:1778:C:H5''	10:D:5:LYS:HG3	2.00	0.44
4:B2:806:U:H3	4:B2:857:U:H3	1.66	0.44
4:B2:1234:C:H5''	4:B2:1246:A:H61	1.83	0.44
4:B2:1786:U:H2'	4:B2:1787:G:H8	1.82	0.44
5:A6:3860:A:H2'	5:A6:3861:A:H8	1.81	0.44
5:A6:3960:A:H61	5:A6:4047:A:H61	1.65	0.44
5:A6:3970:G:H21	5:A6:4052:C:H42	1.64	0.44
5:A6:4337:C:H3'	42:o:87:ARG:HH22	1.83	0.44
5:A6:4508:C:H4'	26:V:43:LYS:HA	2.00	0.44
5:A6:4552:U:H2'	5:A6:4553:A:H8	1.82	0.44
5:A6:4613:C:N3	14:H:121:LYS:CG	2.80	0.44
5:A6:4617:G:H2'	5:A6:4618:G:H8	1.82	0.44
5:A6:4935:C:H2'	11:E:186:ARG:HH21	1.82	0.44
5:A6:4945:G:N3	34:f:57:THR:HG23	2.32	0.44
5:A6:5037:U:H2'	5:A6:5038:A:C8	2.52	0.44
11:E:97:LYS:HB3	11:E:108:ARG:HB3	1.98	0.44
12:F:115:GLN:HG3	22:Q:3:VAL:HG13	1.99	0.44
14:H:31:ARG:HD2	14:H:188:GLN:HE22	1.81	0.44
16:J:174:ILE:HD12	16:J:174:ILE:HA	1.93	0.44
24:T:43:LYS:HE3	24:T:43:LYS:HB3	1.90	0.44
27:X:64:SER:HB2	36:h:69:LEU:HD13	2.00	0.44
36:h:19:LYS:HE3	36:h:19:LYS:HB3	1.68	0.44
38:j:26:ALA:HB1	38:j:35:GLY:H	1.82	0.44
43:p:26:VAL:O	43:p:30:GLU:HB2	2.17	0.44
49:gg:202:PRO:HG2	49:gg:243:PRO:HA	1.98	0.44
52:BB:151:ARG:HA	60:RR:132:ARG:HH12	1.82	0.44
56:MM:77:ILE:HD12	56:MM:127:TYR:HE2	1.83	0.44
61:SS:34:LYS:HG3	61:SS:103:LEU:HD22	2.00	0.44
62:TT:21:PHE:HA	62:TT:24:LYS:HG2	2.00	0.44
75:NN:133:ARG:HH12	75:NN:136:PRO:HA	1.82	0.44
1:A5:409:G:H8	5:A6:2329:U:H5''	1.81	0.44
1:A5:1173:G:H2'	1:A5:1174:G:C8	2.53	0.44
1:A5:2011:C:H3'	1:A5:2012:A:H8	1.83	0.44
4:B2:167:G:H21	70:GG:131:ARG:HH22	1.65	0.44
4:B2:355:G:H5''	74:LL:94:HIS:CE1	2.53	0.44
4:B2:359:U:O2	4:B2:403:G:N2	2.41	0.44
4:B2:944:A:H1'	57:OO:136:PRO:HB3	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A6:2327:G:H2'	5:A6:2328:G:H8	1.81	0.44
5:A6:3618:C:H2'	80:W:78:ILE:HG13	2.00	0.44
5:A6:4690:G:N2	5:A6:4700:A:H62	2.14	0.44
5:A6:4704:C:H2'	5:A6:4705:A:C8	2.51	0.44
5:A6:4939:C:H4'	11:E:190:ARG:HH12	1.83	0.44
11:E:184:LEU:HB3	11:E:275:ARG:HG3	2.00	0.44
13:G:97:LYS:HE3	13:G:97:LYS:HB3	1.66	0.44
17:L:94:ILE:HD12	17:L:94:ILE:HA	1.87	0.44
19:N:189:ARG:HA	19:N:192:TRP:HB3	2.00	0.44
20:O:58:LEU:HD11	20:O:74:ARG:HH21	1.83	0.44
22:Q:27:LEU:HD11	44:r:8:MET:HE2	1.99	0.44
23:S:80:ILE:HD11	23:S:97:TYR:HE2	1.83	0.44
33:e:83:LYS:HB3	33:e:83:LYS:HE2	1.63	0.44
60:RR:132:ARG:H	60:RR:132:ARG:HD3	1.81	0.44
70:GG:79:LYS:HB2	70:GG:79:LYS:HE2	1.72	0.44
72:II:116:HIS:CD2	72:II:152:ARG:HH21	2.34	0.44
81:c:81:ALA:HB2	81:c:87:LEU:HD23	1.99	0.44
84:Bb:34:G:O6	85:Dd:24:U:O4	2.35	0.44
1:A5:64:A:H1'	1:A5:76:A:H1'	2.00	0.44
1:A5:146:G:H2'	1:A5:147:A:H8	1.83	0.44
1:A5:684:G:C8	11:E:104:ASN:N	2.86	0.44
1:A5:1527:A:H2'	1:A5:1528:U:C6	2.53	0.44
1:A5:1662:C:H2'	1:A5:1663:C:C6	2.53	0.44
3:A8:13:G:H4'	21:P:145:HIS:HD2	1.82	0.44
4:B2:656:G:N2	4:B2:1156:U:O2	2.39	0.44
5:A6:2620:G:N1	5:A6:2636:U:C2	2.78	0.44
5:A6:4063:U:H2'	5:A6:4064:C:C2	2.52	0.44
5:A6:4584:A:H2'	5:A6:4585:U:O4'	2.17	0.44
11:E:155:ILE:HA	11:E:197:VAL:HG12	2.00	0.44
19:N:47:LYS:HD2	19:N:50:ARG:HD2	2.00	0.44
20:O:16:LEU:HD22	20:O:43:ILE:HD11	1.99	0.44
27:X:78:LYS:HD3	27:X:99:ILE:HG22	2.00	0.44
46:t:133:LEU:H	46:t:133:LEU:HG	1.66	0.44
71:HH:144:ILE:HG12	71:HH:154:ILE:HG23	2.00	0.44
74:LL:134:LEU:HD13	74:LL:138:VAL:HG12	2.00	0.44
1:A5:688:U:H5''	11:E:108:ARG:HG3	2.00	0.44
1:A5:1479:G:H2'	1:A5:1480:C:C2	2.53	0.44
4:B2:327:G:C4	81:c:117:LYS:HG2	2.53	0.44
4:B2:872:A:H3'	80:W:166:THR:HG21	1.99	0.44
4:B2:873:G:H2'	4:B2:874:G:C8	2.50	0.44
4:B2:936:G:H2'	4:B2:937:C:C6	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B2:1443:C:H1'	59:QQ:22:VAL:HG21	1.99	0.44
4:B2:1711:U:H2'	4:B2:1712:A:C8	2.52	0.44
5:A6:2768:C:C5	35:g:69:LYS:C	2.96	0.44
5:A6:3833:C:H2'	5:A6:3834:C:H6	1.82	0.44
5:A6:5062:G:H22	8:B:124:LYS:HD2	1.83	0.44
28:Y:124:LYS:HE3	28:Y:124:LYS:HB3	1.69	0.44
29:Z:47:ASP:H	29:Z:70:SER:HA	1.83	0.44
53:DD:51:LEU:HD22	53:DD:91:VAL:HA	2.00	0.44
57:OO:100:THR:HG22	57:OO:104:ARG:HE	1.83	0.44
60:RR:100:PRO:HA	60:RR:103:LYS:HD3	1.99	0.44
61:SS:71:MET:HB2	61:SS:99:LEU:HD21	1.99	0.44
65:bb:33:MET:SD	65:bb:79:PHE:HB2	2.58	0.44
80:W:52:ARG:HE	80:W:52:ARG:HB3	1.62	0.44
1:A5:126:C:H2'	1:A5:127:G:H8	1.83	0.44
1:A5:971:U:H3	1:A5:1282:G:H5'	1.83	0.44
2:A7:59:G:H2'	2:A7:60:G:C8	2.53	0.44
4:B2:57:U:H4'	4:B2:499:G:H21	1.82	0.44
4:B2:841:G:N1	79:YY:11:LYS:N	2.66	0.44
4:B2:858:A:H2'	4:B2:859:G:H8	1.83	0.44
4:B2:943:U:H2'	4:B2:944:A:H8	1.83	0.44
4:B2:1534:C:H42	4:B2:1598:G:H1'	1.83	0.44
4:B2:1722:G:O6	4:B2:1812:U:O2	2.35	0.44
5:A6:2449:A:H62	5:A6:2510:G:H21	1.65	0.44
5:A6:2910:G:H4'	5:A6:2913:C:H5''	2.00	0.44
5:A6:3936:A:N6	5:A6:4175:G:O6	2.50	0.44
5:A6:4343:U:H2'	5:A6:4344:U:C4	2.52	0.44
9:C:133:LEU:HD21	44:r:6:GLN:HE21	1.83	0.44
14:H:60:TRP:CD2	23:S:155:PRO:HD2	2.53	0.44
15:I:49:CYS:HA	15:I:138:ILE:O	2.17	0.44
17:L:50:PRO:HG3	17:L:150:LEU:HD13	2.00	0.44
27:X:127:LEU:HD21	27:X:135:LYS:HD2	2.00	0.44
30:a:84:GLU:HA	30:a:87:ARG:HB3	1.99	0.44
38:j:64:MET:HA	38:j:67:LEU:HD23	2.00	0.44
57:OO:94:HIS:CE1	57:OO:128:ARG:H	2.36	0.44
1:A5:460:C:H2'	1:A5:461:G:H8	1.83	0.43
1:A5:950:G:H2'	1:A5:951:G:H8	1.82	0.43
1:A5:1176:C:H3'	10:D:279:ARG:NH1	2.33	0.43
1:A5:1535:C:H42	1:A5:1636:U:H4'	1.83	0.43
4:B2:571:U:H3'	4:B2:572:U:H6	1.81	0.43
4:B2:640:A:H2'	4:B2:641:A:C8	2.53	0.43
4:B2:906:U:H2'	4:B2:907:G:C8	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B2:1544:C:O2	4:B2:1589:A:N6	2.51	0.43
4:B2:1648:G:H5''	59:QQ:125:ARG:HE	1.83	0.43
4:B2:1740:C:H5''	72:II:58:LEU:HD22	2.00	0.43
5:A6:2583:C:H2'	5:A6:2584:G:H8	1.83	0.43
5:A6:4334:U:H4'	24:T:7:LYS:HB2	2.00	0.43
5:A6:4351:U:H5''	17:L:190:ARG:HH12	1.82	0.43
5:A6:4937:C:H5'	11:E:159:ARG:NH2	2.32	0.43
9:C:50:GLN:HB2	17:L:26:PHE:CZ	2.53	0.43
9:C:109:ARG:H	9:C:111:TRP:HE1	1.66	0.43
10:D:173:ILE:HG23	10:D:175:HIS:HD1	1.82	0.43
12:F:117:PHE:CE2	12:F:214:SER:HA	2.53	0.43
12:F:131:MET:O	12:F:135:VAL:HG12	2.18	0.43
13:G:156:VAL:HG13	13:G:202:VAL:HB	1.99	0.43
42:o:30:LYS:HA	42:o:30:LYS:HD3	1.86	0.43
59:QQ:44:PRO:HD2	59:QQ:81:ILE:HD11	1.99	0.43
73:JJ:172:ARG:HD2	73:JJ:173:VAL:HG13	2.00	0.43
79:YY:12:PHE:HD1	79:YY:23:MET:HB3	1.82	0.43
1:A5:932:A:H5'	1:A5:933:G:H5''	2.00	0.43
1:A5:1175:A:H1'	1:A5:1187:G:N2	2.33	0.43
1:A5:1525:A:H61	1:A5:1649:U:H3	1.66	0.43
1:A5:1603:C:H2'	1:A5:1604:G:C8	2.52	0.43
1:A5:1724:G:C6	1:A5:1838:A:N1	2.86	0.43
4:B2:1208:A:H2'	4:B2:1209:A:H8	1.83	0.43
4:B2:1419:C:H2'	4:B2:1420:G:C8	2.53	0.43
5:A6:2372:U:H2'	5:A6:2373:C:C6	2.53	0.43
5:A6:2832:A:H2'	5:A6:2833:A:H8	1.83	0.43
5:A6:3941:G:H2'	5:A6:3942:A:C8	2.53	0.43
5:A6:4494:G:H5''	26:V:50:ASN:HA	2.00	0.43
5:A6:4993:G:H2'	5:A6:4994:G:C8	2.53	0.43
6:A:177:LYS:HD2	43:p:69:TRP:CE2	2.53	0.43
8:B:294:LYS:HB2	8:B:294:LYS:HE2	1.93	0.43
12:F:149:VAL:O	12:F:153:ILE:HG13	2.18	0.43
12:F:159:GLY:HA2	12:F:207:LEU:HA	2.00	0.43
13:G:98:LEU:HD12	13:G:98:LEU:HA	1.91	0.43
18:M:50:MET:HE1	18:M:55:MET:HG2	2.00	0.43
20:O:34:VAL:HG22	20:O:103:LYS:HB2	1.99	0.43
29:Z:14:LEU:HA	35:g:91:ILE:HD11	2.00	0.43
37:i:68:ARG:HA	37:i:68:ARG:HD2	1.80	0.43
51:AA:79:SER:HA	51:AA:101:GLY:HA2	2.00	0.43
73:JJ:91:LYS:NZ	73:JJ:96:TYR:HB3	2.33	0.43
73:JJ:107:GLU:HG2	73:JJ:116:LYS:HZ2	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
74:LL:61:PRO:HB3	74:LL:68:ILE:HD11	2.00	0.43
1:A5:161:G:H2'	1:A5:162:A:C8	2.53	0.43
1:A5:1276:C:H2'	1:A5:1277:G:C8	2.54	0.43
1:A5:1327:C:H2'	1:A5:1328:G:C8	2.54	0.43
4:B2:1577:G:H1'	4:B2:1582:C:C2	2.53	0.43
4:B2:1593:C:H2'	4:B2:1594:A:C8	2.54	0.43
5:A6:2555:G:H2'	5:A6:2556:G:C8	2.53	0.43
5:A6:2658:G:H2'	82:u:38:ILE:HD13	2.00	0.43
5:A6:2770:C:H2'	5:A6:2771:G:C8	2.53	0.43
5:A6:4389:C:H2'	5:A6:4390:A:C8	2.52	0.43
6:A:16:PHE:HA	6:A:194:ASN:HB3	1.99	0.43
9:C:205:ARG:HA	9:C:226:GLY:HA2	2.01	0.43
13:G:158:ALA:HB3	13:G:161:VAL:HG13	2.00	0.43
20:O:185:VAL:HB	20:O:188:LYS:HB3	1.99	0.43
37:i:13:LYS:HE3	37:i:13:LYS:HB2	1.88	0.43
42:o:81:ARG:C	42:o:82:MET:HE3	2.43	0.43
48:ff:97:LYS:HB2	48:ff:97:LYS:HE3	1.83	0.43
49:gg:57:ARG:HG2	49:gg:59:LEU:HG	2.01	0.43
49:gg:121:VAL:HG11	49:gg:165:ILE:HG21	2.00	0.43
50:dd:22:ARG:HH22	55:KK:66:HIS:CD2	2.36	0.43
65:bb:3:LEU:HD12	77:WW:22:LYS:HD2	2.00	0.43
80:W:60:ARG:HB2	80:W:64:ARG:HH21	1.82	0.43
80:W:100:ARG:HH11	80:W:104:ARG:HD3	1.82	0.43
1:A5:386:A:H1'	28:Y:87:ARG:NH2	2.33	0.43
1:A5:1278:C:H3'	1:A5:1279:A:C8	2.53	0.43
4:B2:443:U:C2	4:B2:447:A:N7	2.86	0.43
4:B2:635:G:H5''	66:ee:95:LYS:HE2	2.00	0.43
9:C:316:LYS:HD3	9:C:324:ILE:HD11	2.01	0.43
12:F:54:LYS:HE3	12:F:54:LYS:HB3	1.88	0.43
26:V:85:ARG:H	26:V:85:ARG:HD3	1.84	0.43
38:j:31:LYS:HE2	38:j:31:LYS:HB2	1.81	0.43
49:gg:5:MET:HE3	49:gg:298:LEU:HB2	1.99	0.43
53:DD:5:ILE:HD11	53:DD:9:ARG:HD2	1.99	0.43
61:SS:84:LEU:HD13	61:SS:96:SER:HA	1.99	0.43
74:LL:118:ARG:HE	74:LL:118:ARG:H	1.64	0.43
83:Cc:5:G:H2'	83:Cc:6:G:H8	1.83	0.43
1:A5:712:C:H42	1:A5:956:A:H61	1.66	0.43
1:A5:1741:G:H1'	1:A5:1781:U:H5'	2.00	0.43
1:A5:1883:G:H5'	33:e:49:PHE:HE1	1.83	0.43
4:B2:376:A:H2'	4:B2:377:G:C8	2.54	0.43
4:B2:1342:U:H1'	4:B2:1343:U:H5	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B2:1355:C:H2'	4:B2:1356:G:C2	2.54	0.43
4:B2:1655:C:H2'	4:B2:1656:G:H8	1.84	0.43
5:A6:4362:A:H2'	5:A6:4363:A:H8	1.82	0.43
5:A6:4577:U:O2	5:A6:4726:G:C2	2.71	0.43
5:A6:4883:C:H3'	5:A6:4884:G:H5''	2.00	0.43
15:I:190:LEU:HD22	15:I:197:VAL:HG12	2.01	0.43
22:Q:146:ARG:HB3	22:Q:148:VAL:HG22	2.00	0.43
64:ZZ:102:LYS:HA	64:ZZ:107:VAL:HG23	2.00	0.43
65:bb:46:VAL:HG22	65:bb:54:VAL:HG11	2.00	0.43
76:VV:15:ARG:HB3	76:VV:24:ILE:HD12	2.01	0.43
80:W:105:LEU:HD23	80:W:138:LEU:HD12	1.99	0.43
82:u:37:MET:HB2	82:u:38:ILE:HD12	2.00	0.43
83:Cc:22:A:H61	83:Cc:47:G:H2'	1.83	0.43
1:A5:1341:U:H2'	1:A5:1342:A:H8	1.84	0.43
1:A5:1476:C:H2'	1:A5:1477:C:H6	1.83	0.43
1:A5:1625:G:H21	6:A:2:GLY:HA3	1.84	0.43
4:B2:436:G:H2'	4:B2:437:G:C8	2.52	0.43
4:B2:640:A:H2'	4:B2:641:A:H8	1.84	0.43
5:A6:2572:C:H2'	5:A6:2573:A:C8	2.53	0.43
5:A6:2668:G:H22	5:A6:2735:G:H1'	1.82	0.43
5:A6:2772:C:H2'	5:A6:2773:G:H8	1.83	0.43
5:A6:4185:G:H2'	5:A6:4186:A:H8	1.84	0.43
5:A6:4593:C:H2'	5:A6:4594:U:H6	1.83	0.43
5:A6:4741:C:H2'	5:A6:4742:G:C8	2.53	0.43
8:B:317:LEU:HD21	8:B:381:THR:HA	2.00	0.43
20:O:196:LEU:HG	20:O:201:LEU:HD23	2.00	0.43
26:V:95:PHE:HA	81:c:21:TYR:HB3	2.01	0.43
36:h:103:LYS:HE2	36:h:103:LYS:HB3	1.88	0.43
44:r:86:ALA:HA	44:r:118:LEU:HD11	2.01	0.43
59:QQ:90:LYS:HA	59:QQ:93:VAL:HG12	1.99	0.43
66:ee:102:ARG:HB3	66:ee:106:ALA:HB1	2.00	0.43
68:CC:102:LEU:HD22	68:CC:130:ILE:HG13	2.01	0.43
70:GG:198:ARG:HA	70:GG:201:LYS:HE3	2.00	0.43
81:c:105:ARG:HD3	81:c:105:ARG:HA	1.83	0.43
1:A5:436:C:H2'	1:A5:437:G:C8	2.52	0.43
1:A5:959:G:C5	11:E:127:LYS:CG	3.01	0.43
1:A5:1186:U:H3'	10:D:274:ALA:C	2.44	0.43
1:A5:1315:C:H2'	1:A5:1316:G:H8	1.83	0.43
4:B2:65:C:H41	70:GG:136:LYS:HB2	1.83	0.43
4:B2:391:C:H2'	4:B2:392:A:H8	1.84	0.43
4:B2:1004:U:H2'	4:B2:1005:G:C8	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B2:1089:G:N2	4:B2:1160:U:O2	2.39	0.43
4:B2:1455:A:H2'	4:B2:1456:G:C8	2.52	0.43
5:A6:3942:A:H2'	5:A6:3943:A:C8	2.53	0.43
5:A6:4547:C:H2'	5:A6:4549:G:C8	2.54	0.43
5:A6:5000:G:N2	8:B:318:GLY:HA2	2.32	0.43
9:C:34:PRO:HA	9:C:37:VAL:HG22	2.00	0.43
16:J:90:ARG:HH11	16:J:109:ILE:HG22	1.83	0.43
16:J:113:ILE:HG12	16:J:125:ILE:HD11	2.00	0.43
23:S:15:ARG:HH12	23:S:18:PRO:HD3	1.83	0.43
24:T:74:ILE:O	24:T:88:ARG:HA	2.19	0.43
27:X:62:ARG:HG3	36:h:81:LEU:HD12	2.01	0.43
27:X:127:LEU:HG	27:X:135:LYS:HB3	2.01	0.43
53:DD:218:LEU:HA	53:DD:219:PRO:HD3	1.89	0.43
82:u:31:TYR:HB3	82:u:32:LYS:HE2	2.01	0.43
1:A5:318:A:H2'	1:A5:319:A:C8	2.53	0.43
1:A5:667:A:H5''	44:r:71:ARG:HH12	1.83	0.43
1:A5:1093:C:H2'	1:A5:1094:G:H8	1.82	0.43
1:A5:1980:U:H3'	46:t:27:ALA:HB3	2.01	0.43
2:A7:70:G:H2'	2:A7:71:G:C8	2.53	0.43
4:B2:871:U:H5''	75:NN:76:LYS:HG3	2.00	0.43
5:A6:2573:A:H62	5:A6:2760:G:N2	2.17	0.43
5:A6:3661:G:H4'	5:A6:3662:A:C8	2.53	0.43
5:A6:3760:A:N3	84:Bb:38:A:H5''	2.33	0.43
5:A6:3860:A:P	21:P:139:TYR:CG	3.12	0.43
5:A6:4260:U:H2'	5:A6:4261:C:C6	2.53	0.43
5:A6:4389:C:H2'	5:A6:4390:A:H8	1.83	0.43
5:A6:4704:C:H4'	14:H:129:ARG:HH22	1.83	0.43
9:C:142:HIS:CD2	9:C:206:GLY:HA2	2.53	0.43
16:J:96:LYS:HE3	16:J:96:LYS:HB3	1.72	0.43
23:S:34:ALA:HB1	23:S:39:VAL:HB	1.99	0.43
26:V:90:ARG:NH2	81:c:20:ARG:HG3	2.33	0.43
60:RR:70:SER:HA	60:RR:78:ARG:HH22	1.82	0.43
70:GG:56:ASN:HA	70:GG:62:PRO:HA	2.00	0.43
82:u:61:GLU:HG2	82:u:62:TYR:HB2	2.00	0.43
1:A5:49:U:H2'	1:A5:50:C:H6	1.83	0.43
1:A5:318:A:H2'	1:A5:319:A:H8	1.82	0.43
1:A5:743:G:H2'	1:A5:744:G:C8	2.54	0.43
1:A5:959:G:N1	11:E:127:LYS:CD	2.82	0.43
1:A5:993:G:H2'	1:A5:994:G:C8	2.53	0.43
1:A5:1164:G:H2'	1:A5:1165:G:C8	2.53	0.43
1:A5:1242:G:H2'	1:A5:1243:C:H4'	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A5:1675:C:H5''	5:A6:4377:G:P	2.59	0.43
1:A5:1863:U:H2'	1:A5:1864:G:H8	1.83	0.43
2:A7:31:G:H2'	2:A7:32:A:C8	2.54	0.43
4:B2:604:A:H5'	73:JJ:22:LYS:HE2	2.01	0.43
4:B2:875:A:N1	4:B2:910:G:C6	2.86	0.43
4:B2:1309:C:C2	48:ff:133:ALA:HA	2.53	0.43
4:B2:1337:C:H2'	4:B2:1338:G:C8	2.53	0.43
5:A6:2504:C:H2'	5:A6:2505:C:H2'	2.01	0.43
5:A6:3917:A:H2'	5:A6:3918:G:H8	1.84	0.43
5:A6:4044:U:H2'	5:A6:4045:G:C8	2.54	0.43
5:A6:4543:G:H2'	5:A6:4544:A:C4	2.53	0.43
5:A6:4675:U:H2'	5:A6:4676:G:H8	1.84	0.43
6:A:225:ILE:HD12	6:A:225:ILE:HA	1.92	0.43
9:C:149:GLU:HA	44:r:72:LYS:HA	2.00	0.43
11:E:52:LEU:HG	11:E:53:VAL:HG23	2.00	0.43
11:E:52:LEU:HD23	11:E:53:VAL:H	1.83	0.43
14:H:5:LEU:HD12	14:H:5:LEU:HA	1.78	0.43
18:M:38:VAL:O	18:M:47:ARG:HA	2.19	0.43
20:O:51:LYS:O	20:O:55:LEU:HD12	2.19	0.43
25:U:100:LEU:HD22	25:U:112:LEU:HB3	2.01	0.43
26:V:13:LYS:HD3	26:V:128:LEU:HD11	2.00	0.43
32:d:93:ASN:HA	32:d:103:TYR:CE1	2.52	0.43
35:g:107:LEU:HA	35:g:110:GLN:HG3	2.00	0.43
50:dd:6:LEU:HA	50:dd:9:SER:HB3	2.01	0.43
51:AA:65:ILE:HD11	51:AA:74:VAL:HG22	2.01	0.43
70:GG:50:VAL:HG12	70:GG:113:ILE:HA	2.01	0.43
70:GG:201:LYS:HE3	70:GG:201:LYS:HB3	1.81	0.43
80:W:144:LYS:HB3	80:W:144:LYS:HE3	1.69	0.43
1:A5:1270:A:C4	31:b:112:ILE:N	2.87	0.43
1:A5:1283:G:C6	11:E:128:LEU:HD12	2.54	0.43
1:A5:1364:U:H5	17:L:36:ARG:HH22	1.67	0.43
1:A5:1433:A:H3'	1:A5:1434:G:H8	1.84	0.43
1:A5:1957:U:H5''	45:s:6:ARG:HH12	1.84	0.43
1:A5:1983:A:H5'	46:t:16:ARG:HH22	1.83	0.43
4:B2:1464:C:H2'	4:B2:1465:A:C4	2.54	0.43
4:B2:1599:U:N1	54:FF:165:ASN:O	2.52	0.43
4:B2:1781:A:H2'	4:B2:1782:G:H8	1.84	0.43
5:A6:2521:G:H2'	5:A6:2522:G:C8	2.54	0.43
5:A6:3858:C:O5'	21:P:86:LYS:HE2	2.19	0.43
5:A6:4775:C:H2'	5:A6:4776:G:C8	2.54	0.43
10:D:83:LEU:HB3	10:D:88:VAL:HB	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:H:24:THR:HA	14:H:37:ASP:HA	2.01	0.43
17:L:20:ARG:NH1	17:L:21:ARG:HB2	2.34	0.43
17:L:167:ARG:HG2	30:a:100:ILE:HD11	2.01	0.43
19:N:60:VAL:HG23	19:N:134:LEU:HB2	2.01	0.43
21:P:58:VAL:O	21:P:81:GLY:HA2	2.18	0.43
26:V:96:LEU:HG	81:c:22:ALA:HA	2.01	0.43
31:b:36:ASP:HB3	31:b:39:PHE:HB2	2.00	0.43
43:p:22:LEU:O	43:p:26:VAL:HG13	2.19	0.43
46:t:101:SER:HA	46:t:142:ASN:HB2	2.00	0.43
57:OO:103:ASN:HD22	57:OO:142:ARG:HA	1.82	0.43
72:II:37:LYS:HA	72:II:37:LYS:HD3	1.83	0.43
72:II:119:LEU:HD11	72:II:153:LYS:HG3	2.01	0.43
82:u:16:SER:HA	82:u:19:GLN:HG2	2.00	0.43
1:A5:648:G:H2'	1:A5:649:A:C8	2.54	0.42
1:A5:708:G:H1'	5:A6:4942:C:C4	2.54	0.42
1:A5:1620:U:H2'	1:A5:1621:A:H8	1.83	0.42
1:A5:1645:C:H2'	1:A5:1646:A:C8	2.54	0.42
1:A5:1759:G:N1	1:A5:1773:U:N3	2.67	0.42
1:A5:1884:C:H2'	1:A5:1885:G:C8	2.54	0.42
4:B2:39:A:H3'	4:B2:40:A:H8	1.83	0.42
4:B2:535:G:H2'	4:B2:536:A:H8	1.83	0.42
5:A6:2654:C:H2'	5:A6:2655:C:C6	2.54	0.42
5:A6:2714:G:H2'	5:A6:2715:G:H8	1.84	0.42
5:A6:2768:C:N3	35:g:70:THR:C	2.77	0.42
5:A6:4208:U:H2'	5:A6:4209:G:C8	2.53	0.42
5:A6:4211:C:H4'	15:I:15:LYS:HE3	2.01	0.42
5:A6:4873:G:C2	20:O:175:MET:HG2	2.54	0.42
9:C:299:GLN:HA	9:C:302:LEU:HG	2.01	0.42
10:D:179:ARG:HD3	10:D:179:ARG:HA	1.82	0.42
12:F:175:ALA:HA	12:F:184:ILE:HG22	2.00	0.42
15:I:184:MET:SD	15:I:189:ARG:HB3	2.59	0.42
44:r:16:PHE:HB3	44:r:27:THR:H	1.84	0.42
61:SS:23:ARG:HD3	64:ZZ:48:VAL:HG23	2.01	0.42
1:A5:163:A:H2'	1:A5:164:G:C8	2.54	0.42
1:A5:163:A:H2'	1:A5:164:G:H8	1.83	0.42
1:A5:684:G:C5	11:E:104:ASN:C	2.97	0.42
1:A5:1954:U:H2'	1:A5:1955:G:H8	1.84	0.42
1:A5:1995:G:C6	45:s:40:MET:HB2	2.54	0.42
1:A5:2045:G:C6	20:O:61:ARG:HB2	2.54	0.42
4:B2:988:C:H5''	52:BB:116:LYS:HD3	2.00	0.42
4:B2:1203:G:C2	68:CC:115:GLN:CA	3.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B2:1832:A:H5''	4:B2:1840:U:H5''	2.01	0.42
5:A6:3723:A:H2'	5:A6:3724:A:H8	1.84	0.42
13:G:87:LEU:HD11	13:G:182:CYS:HB2	2.01	0.42
20:O:8:VAL:HA	20:O:34:VAL:O	2.19	0.42
41:m:93:LYS:HE3	41:m:102:ARG:HD3	2.01	0.42
61:SS:129:LEU:HD21	61:SS:144:ARG:HH12	1.84	0.42
67:aa:12:LYS:HE3	67:aa:12:LYS:HB3	1.94	0.42
68:CC:187:ARG:HE	68:CC:189:GLY:H	1.67	0.42
69:EE:105:THR:HG23	69:EE:245:ARG:HA	2.00	0.42
72:II:193:LYS:HE3	74:LL:33:LEU:HD22	2.01	0.42
73:JJ:35:TYR:CZ	73:JJ:106:LEU:HB3	2.54	0.42
84:Bb:63:C:H2'	84:Bb:64:A:C8	2.54	0.42
1:A5:74:G:H1'	17:L:62:PRO:HG3	2.00	0.42
1:A5:389:A:H1'	28:Y:91:ASN:HA	2.01	0.42
1:A5:731:G:H21	23:S:72:PRO:HD2	1.83	0.42
1:A5:1487:G:H2'	1:A5:1488:G:C8	2.53	0.42
1:A5:1607:C:H2'	1:A5:1608:G:C8	2.54	0.42
1:A5:1991:A:H8	46:t:137:GLN:HB3	1.84	0.42
3:A8:19:C:H2'	3:A8:20:A:C8	2.54	0.42
4:B2:448:A:H4'	4:B2:449:A:H5'	2.01	0.42
4:B2:859:G:H2'	4:B2:860:G:C8	2.54	0.42
4:B2:991:G:C6	4:B2:1134:G:H4'	2.54	0.42
4:B2:1309:C:H2'	48:ff:105:TYR:CE1	2.54	0.42
4:B2:1432:U:H2'	4:B2:1433:C:C6	2.54	0.42
4:B2:1653:U:H4'	62:TT:82:ARG:HH22	1.84	0.42
5:A6:2536:A:P	39:k:37:ARG:HE	2.43	0.42
5:A6:4069:U:H2'	5:A6:4070:U:C6	2.54	0.42
5:A6:4107:G:H2'	5:A6:4108:G:C8	2.54	0.42
5:A6:4614:G:N7	14:H:121:LYS:HD2	2.34	0.42
5:A6:4765:G:O6	5:A6:4869:U:O2	2.38	0.42
5:A6:5006:U:H4'	5:A6:5007:A:H5'	2.00	0.42
8:B:294:LYS:HE2	8:B:299:ILE:HD13	2.01	0.42
17:L:197:LYS:HA	17:L:200:LYS:HE3	2.00	0.42
52:BB:144:LYS:HE2	52:BB:144:LYS:HB3	1.73	0.42
52:BB:165:ARG:HA	52:BB:168:MET:SD	2.59	0.42
71:HH:160:LYS:HB2	71:HH:193:GLN:HE21	1.85	0.42
73:JJ:37:LEU:HD12	73:JJ:43:VAL:HG22	2.01	0.42
81:c:102:LYS:HD3	81:c:102:LYS:HA	1.83	0.42
1:A5:68:U:H5''	19:N:178:HIS:CD2	2.54	0.42
2:A7:76:U:H2'	2:A7:77:A:H8	1.85	0.42
4:B2:1367:U:H3	4:B2:1372:U:H3	1.67	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B2:1818:A:H2'	4:B2:1819:A:H8	1.84	0.42
5:A6:2412:A:H5''	80:W:6:LEU:HD22	2.01	0.42
5:A6:3859:G:H3'	21:P:139:TYR:CZ	2.54	0.42
5:A6:4073:A:H2'	5:A6:4074:C:C6	2.54	0.42
5:A6:4597:U:H5	26:V:10:SER:HA	1.84	0.42
5:A6:4967:A:H2'	5:A6:4968:A:C8	2.54	0.42
13:G:252:LYS:HE3	13:G:252:LYS:HB3	1.89	0.42
22:Q:178:ARG:H	30:a:51:GLY:HA2	1.85	0.42
25:U:55:ASN:C	25:U:55:ASN:HD22	2.21	0.42
30:a:125:LYS:HE3	30:a:125:LYS:HB3	1.90	0.42
56:MM:99:LYS:HB3	56:MM:99:LYS:HE3	1.81	0.42
58:PP:108:LYS:HB2	58:PP:108:LYS:HE2	1.89	0.42
64:ZZ:52:LYS:HA	64:ZZ:52:LYS:HE3	2.01	0.42
68:CC:212:LYS:HA	68:CC:212:LYS:HD3	1.89	0.42
75:NN:40:LEU:HB3	75:NN:45:LEU:HD12	2.01	0.42
80:W:4:LEU:H	80:W:5:ARG:NH1	2.16	0.42
1:A5:22:G:N1	3:A8:35:C:N3	2.68	0.42
1:A5:148:C:H2'	1:A5:149:A:C8	2.54	0.42
1:A5:481:G:H2'	1:A5:482:G:H8	1.84	0.42
1:A5:495:C:H2'	1:A5:496:G:H8	1.83	0.42
1:A5:743:G:H2'	1:A5:744:G:H8	1.84	0.42
1:A5:1342:A:H2'	1:A5:1343:A:C8	2.55	0.42
1:A5:1428:U:H1'	22:Q:138:LEU:HD21	2.01	0.42
1:A5:1630:A:H5''	1:A5:1631:A:C8	2.54	0.42
4:B2:197:U:C2	4:B2:202:G:O6	2.71	0.42
4:B2:1025:U:H2'	4:B2:1026:C:O4'	2.20	0.42
4:B2:1396:A:N7	4:B2:1449:G:O6	2.52	0.42
4:B2:1518:C:H5''	4:B2:1519:U:H5''	2.00	0.42
5:A6:2658:G:H4'	82:u:32:LYS:H	1.84	0.42
5:A6:2798:A:H3'	5:A6:2799:G:H8	1.85	0.42
5:A6:3754:G:O6	5:A6:3770:U:O4	2.36	0.42
5:A6:3760:A:C4	84:Bb:38:A:H5'	2.53	0.42
5:A6:4577:U:H3	5:A6:4726:G:H1	1.55	0.42
6:A:89:TYR:HB2	6:A:100:ASN:ND2	2.35	0.42
6:A:89:TYR:HB3	6:A:94:ALA:HB1	2.01	0.42
9:C:6:PRO:HD2	9:C:24:LEU:HB3	2.02	0.42
11:E:248:GLN:HA	11:E:251:VAL:HG12	2.02	0.42
15:I:48:LEU:HD13	15:I:142:LEU:HA	2.02	0.42
19:N:107:GLY:HA3	19:N:160:GLU:HG3	2.02	0.42
21:P:116:HIS:O	21:P:148:MET:HA	2.19	0.42
27:X:78:LYS:HE2	36:h:32:ARG:HH22	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:ff:92:LYS:HA	48:ff:92:LYS:HD3	1.84	0.42
52:BB:152:LYS:HA	52:BB:152:LYS:HD2	1.85	0.42
66:ee:101:LYS:HE2	66:ee:101:LYS:H	1.85	0.42
79:YY:68:LYS:HD2	79:YY:68:LYS:HA	1.61	0.42
79:YY:91:LEU:HB2	79:YY:97:TYR:HB3	2.01	0.42
83:Cc:53:G:H2'	83:Cc:54:G:C8	2.55	0.42
1:A5:196:C:H4'	28:Y:126:ARG:HG2	2.01	0.42
1:A5:446:C:H2'	1:A5:447:C:H6	1.85	0.42
1:A5:682:G:H3'	11:E:103:LYS:HD3	2.01	0.42
1:A5:940:C:H4'	23:S:8:ARG:HH22	1.84	0.42
1:A5:2055:G:C5	20:O:130:LYS:HB2	2.54	0.42
2:A7:116:G:H2'	2:A7:117:G:C8	2.55	0.42
4:B2:604:A:H2'	4:B2:605:A:C4	2.55	0.42
4:B2:1118:C:H5'	4:B2:1119:A:C6	2.54	0.42
4:B2:1535:U:N1	54:FF:82:ASN:CB	2.83	0.42
4:B2:1657:G:H2'	4:B2:1658:G:C8	2.55	0.42
4:B2:1737:G:N2	4:B2:1797:U:O2	2.47	0.42
5:A6:2299:G:C4	5:A6:2301:G:H1'	2.54	0.42
5:A6:2677:G:C5	82:u:32:LYS:CE	3.02	0.42
5:A6:3631:U:H2'	5:A6:3632:C:C6	2.54	0.42
5:A6:4370:G:C4	83:Cc:77:A:N3	2.70	0.42
5:A6:4459:U:H5''	8:B:10:ARG:HH21	1.84	0.42
5:A6:4691:A:C8	5:A6:4697:U:N3	2.74	0.42
5:A6:4740:G:H1	5:A6:4959:U:H3	1.67	0.42
8:B:297:LYS:HA	8:B:297:LYS:HD2	1.91	0.42
9:C:171:LEU:HA	9:C:174:LEU:HD23	2.01	0.42
15:I:68:ALA:HB1	15:I:155:ALA:HB1	2.01	0.42
29:Z:100:VAL:HG11	29:Z:110:ALA:HB2	2.01	0.42
33:e:50:LYS:H	33:e:50:LYS:HG2	1.59	0.42
36:h:13:LYS:HD2	36:h:14:LYS:H	1.84	0.42
44:r:66:ARG:HH21	44:r:69:GLY:H	1.67	0.42
46:t:80:LEU:HD23	46:t:83:LYS:HE3	2.01	0.42
50:dd:6:LEU:HA	50:dd:6:LEU:HD23	1.91	0.42
50:dd:17:GLY:HA2	50:dd:27:ARG:HD3	2.01	0.42
51:AA:85:ARG:HD3	51:AA:204:TYR:HA	2.01	0.42
68:CC:88:ILE:HG13	68:CC:160:LEU:HD13	1.99	0.42
68:CC:251:LEU:HB3	77:WW:70:ASN:HD21	1.84	0.42
79:YY:21:LYS:HB2	79:YY:75:ILE:HB	2.01	0.42
1:A5:43:U:H3'	1:A5:44:A:H8	1.84	0.42
1:A5:475:G:H2'	1:A5:476:G:C8	2.54	0.42
1:A5:499:G:H3'	1:A5:500:G:H5''	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A5:1754:U:H5	1:A5:1756:U:H3'	1.85	0.42
1:A5:1817:U:H4'	10:D:43:LYS:HE2	2.01	0.42
1:A5:2062:C:H2'	1:A5:2063:G:H8	1.84	0.42
4:B2:675:U:H2'	4:B2:676:C:H6	1.85	0.42
4:B2:900:C:H2'	4:B2:901:G:C8	2.50	0.42
4:B2:1756:C:O2	4:B2:1757:G:N7	2.52	0.42
5:A6:2608:G:H2'	5:A6:2609:G:H8	1.85	0.42
5:A6:2846:G:H3'	5:A6:2847:G:H8	1.83	0.42
5:A6:3794:C:H2'	5:A6:3795:A:H8	1.83	0.42
5:A6:4207:C:H1'	5:A6:4335:C:C4	2.55	0.42
5:A6:4319:C:H2'	5:A6:4320:G:C8	2.55	0.42
5:A6:4742:G:H2'	5:A6:4743:G:C8	2.54	0.42
5:A6:4861:G:H5''	20:O:169:ARG:NE	2.35	0.42
5:A6:4883:C:H4'	11:E:275:ARG:HB3	2.02	0.42
15:I:170:LYS:HA	15:I:177:ASN:HA	2.02	0.42
18:M:13:ALA:HB1	18:M:57:LEU:HA	2.02	0.42
26:V:23:GLY:HA2	26:V:38:TYR:HE1	1.85	0.42
28:Y:15:ARG:HH21	28:Y:19:PHE:HE2	1.68	0.42
31:b:120:ARG:HA	31:b:120:ARG:HD3	1.93	0.42
34:f:26:ALA:O	34:f:85:ARG:HA	2.19	0.42
46:t:32:ILE:HG13	46:t:42:VAL:HG21	2.01	0.42
49:gg:77:PHE:HE1	49:gg:98:THR:HG21	1.84	0.42
56:MM:23:LYS:HA	56:MM:23:LYS:HD3	1.85	0.42
66:ee:86:VAL:HA	66:ee:89:GLN:HG2	2.02	0.42
1:A5:60:G:H5''	19:N:155:VAL:HG21	2.02	0.42
1:A5:204:U:O2	1:A5:211:G:O6	2.38	0.42
1:A5:959:G:C4	1:A5:959:G:C2	2.95	0.42
1:A5:1289:C:C6	11:E:136:PHE:CG	3.08	0.42
4:B2:120:U:H3	4:B2:344:U:H3	1.68	0.42
4:B2:520:A:H1'	4:B2:826:A:N3	2.35	0.42
4:B2:1205:C:H2'	4:B2:1206:G:C5	2.55	0.42
4:B2:1358:U:H4'	68:CC:114:LYS:HE2	2.02	0.42
4:B2:1523:C:H2'	4:B2:1524:G:C8	2.54	0.42
4:B2:1649:U:H3	4:B2:1675:A:H2	1.67	0.42
5:A6:3936:A:C6	5:A6:4175:G:N1	2.87	0.42
5:A6:4457:U:H5''	8:B:238:LYS:HG2	2.02	0.42
5:A6:4762:A:H61	23:S:171:ARG:HD3	1.85	0.42
5:A6:4891:G:H2'	5:A6:4892:A:C8	2.54	0.42
6:A:98:ILE:HD11	43:p:83:ILE:HG12	2.00	0.42
6:A:102:LEU:HD13	6:A:102:LEU:HA	1.93	0.42
9:C:112:HIS:CG	19:N:202:ARG:HB3	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:E:114:LYS:HE2	44:r:87:ARG:HH21	1.85	0.42
14:H:128:MET:HE2	14:H:132:VAL:HG13	2.02	0.42
15:I:62:SER:HA	15:I:65:LEU:HG	2.01	0.42
18:M:71:LYS:HE3	18:M:71:LYS:HB2	1.81	0.42
27:X:104:ALA:HB1	27:X:108:GLN:HB2	2.02	0.42
37:i:44:ILE:O	37:i:48:CYS:HB2	2.19	0.42
48:ff:104:LYS:HB2	48:ff:118:ARG:HH21	1.85	0.42
51:AA:85:ARG:HE	60:RR:81:ARG:HH12	1.67	0.42
58:PP:39:ALA:HA	58:PP:42:ARG:HH21	1.84	0.42
62:TT:62:ARG:HH22	62:TT:66:LEU:HD13	1.83	0.42
74:LL:133:PRO:HA	74:LL:139:ARG:HA	2.01	0.42
75:NN:72:LEU:HD12	75:NN:72:LEU:HA	1.89	0.42
79:YY:21:LYS:HD2	79:YY:75:ILE:HG21	2.02	0.42
81:c:109:ILE:HD12	81:c:109:ILE:HA	1.89	0.42
84:Bb:67:A:H2'	84:Bb:68:U:C6	2.55	0.42
1:A5:20:U:H3'	1:A5:21:G:H8	1.84	0.42
1:A5:279:A:H62	1:A5:307:A:H62	1.68	0.42
1:A5:319:A:H5''	37:i:80:HIS:ND1	2.34	0.42
1:A5:1487:G:H2'	1:A5:1488:G:H8	1.84	0.42
1:A5:1974:U:H4'	1:A5:1975:G:H5'	2.01	0.42
1:A5:2081:C:H2'	1:A5:2082:G:C8	2.54	0.42
3:A8:17:A:H2'	3:A8:18:U:C6	2.55	0.42
4:B2:1270:G:H1'	4:B2:1299:A:H61	1.84	0.42
5:A6:2780:C:H2'	5:A6:2781:G:C8	2.55	0.42
5:A6:2792:C:H2'	5:A6:2793:G:C8	2.55	0.42
5:A6:4240:G:H5'	10:D:152:ARG:HD3	2.02	0.42
9:C:49:ARG:HE	9:C:49:ARG:HB2	1.59	0.42
10:D:143:THR:HA	10:D:172:SER:HB3	2.01	0.42
19:N:165:THR:HG23	19:N:168:GLY:H	1.84	0.42
21:P:122:ALA:HB3	21:P:143:PRO:HG2	2.02	0.42
22:Q:93:LEU:HD22	30:a:118:PRO:HD3	2.01	0.42
31:b:43:MET:C	31:b:47:LYS:HZ2	2.28	0.42
46:t:121:LEU:HB3	46:t:128:THR:HG22	2.01	0.42
47:cc:49:PRO:HG2	54:FF:144:LEU:HB3	2.02	0.42
52:BB:222:LYS:HA	52:BB:222:LYS:HD2	1.93	0.42
54:FF:63:LYS:HA	54:FF:66:CYS:HB3	2.01	0.42
70:GG:57:ASP:HA	70:GG:106:LEU:HA	2.02	0.42
72:II:3:ILE:H	72:II:3:ILE:HG13	1.68	0.42
73:JJ:84:ILE:HD12	73:JJ:84:ILE:HA	1.91	0.42
80:W:96:MET:O	80:W:100:ARG:HB2	2.19	0.42
1:A5:106:A:H5''	17:L:42:ARG:HH22	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A5:1531:U:H2'	1:A5:1532:G:H8	1.84	0.42
1:A5:1691:G:O6	1:A5:1845:U:O2	2.37	0.42
1:A5:1841:C:H1'	1:A5:1842:G:H8	1.84	0.42
4:B2:580:U:H5'	73:JJ:133:ARG:HH21	1.85	0.42
4:B2:1197:G:H2'	4:B2:1198:G:H8	1.85	0.42
4:B2:1224:G:O6	4:B2:1642:U:O4	2.38	0.42
4:B2:1423:C:H3'	4:B2:1424:G:H8	1.84	0.42
4:B2:1649:U:H4'	59:QQ:138:ARG:HG3	2.02	0.42
5:A6:2289:C:C5	44:r:22:LYS:HA	2.55	0.42
5:A6:3853:U:H2'	5:A6:3854:C:C6	2.55	0.42
5:A6:4415:A:H62	5:A6:4427:G:H21	1.68	0.42
5:A6:5018:C:H2'	5:A6:5019:A:C8	2.51	0.42
6:A:40:TYR:HA	6:A:90:CYS:O	2.20	0.42
8:B:386:LYS:HE2	8:B:391:PRO:HA	2.01	0.42
8:B:396:ARG:HA	8:B:399:LYS:HD2	2.02	0.42
9:C:302:LEU:HB3	22:Q:38:ARG:HG3	2.01	0.42
13:G:161:VAL:HG11	13:G:200:THR:HA	2.02	0.42
16:J:35:ARG:HD2	16:J:123:ILE:HA	2.02	0.42
42:o:38:LYS:HD2	83:Cc:76:C:H41	1.85	0.42
43:p:84:ARG:HH21	43:p:88:GLU:HB3	1.85	0.42
49:gg:68:ASP:HB3	49:gg:111:VAL:HG12	2.01	0.42
60:RR:96:ILE:HG22	60:RR:98:VAL:HG13	2.01	0.42
65:bb:43:ILE:HD12	65:bb:43:ILE:HA	1.89	0.42
67:aa:37:LYS:HB2	67:aa:37:LYS:HE2	1.91	0.42
1:A5:1308:C:H4'	20:O:93:LYS:HE2	2.02	0.41
1:A5:1870:C:H2'	1:A5:1871:A:H8	1.84	0.41
3:A8:148:A:H2'	3:A8:149:G:C8	2.55	0.41
4:B2:74:G:H1	70:GG:162:LEU:HB2	1.85	0.41
4:B2:1124:C:H2'	4:B2:1125:C:C6	2.55	0.41
4:B2:1163:C:H2'	4:B2:1164:G:C8	2.54	0.41
4:B2:1203:G:C6	68:CC:114:LYS:CA	3.01	0.41
4:B2:1250:A:C8	4:B2:1339:U:H4'	2.54	0.41
5:A6:2362:U:H2'	5:A6:2363:A:H8	1.85	0.41
5:A6:2633:U:H2'	5:A6:2634:C:C6	2.55	0.41
5:A6:3635:A:N1	43:p:17:ARG:HB2	2.35	0.41
5:A6:3949:A:H2'	5:A6:3950:U:H6	1.85	0.41
5:A6:4867:G:H2'	5:A6:4868:G:C8	2.55	0.41
8:B:57:VAL:HB	8:B:366:LYS:H	1.85	0.41
8:B:117:ARG:HA	8:B:177:LYS:HD3	2.02	0.41
8:B:228:TYR:HA	8:B:271:GLN:HA	2.02	0.41
8:B:238:LYS:HD3	8:B:238:LYS:HA	1.90	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:G:73:ARG:HH21	13:G:241:VAL:HG13	1.84	0.41
23:S:93:MET:HE3	23:S:94:TYR:N	2.35	0.41
25:U:47:ILE:HG22	25:U:86:LEU:HD13	2.02	0.41
51:AA:57:LYS:HB3	51:AA:161:ILE:HG12	2.01	0.41
52:BB:105:LEU:HD22	52:BB:109:LYS:HG2	2.02	0.41
55:KK:58:VAL:HG22	55:KK:69:TRP:HD1	1.85	0.41
58:PP:86:LEU:HB3	58:PP:89:MET:HE1	2.02	0.41
59:QQ:24:HIS:CE1	59:QQ:26:LYS:HD3	2.55	0.41
60:RR:69:ILE:HD13	60:RR:71:ILE:HG12	2.02	0.41
64:ZZ:79:ILE:HB	64:ZZ:83:LEU:HD23	2.01	0.41
68:CC:81:ILE:HG23	68:CC:86:LEU:HD12	2.02	0.41
71:HH:43:LEU:HD13	71:HH:72:PHE:HE1	1.85	0.41
72:II:83:TYR:HB3	72:II:101:ILE:HB	2.02	0.41
1:A5:1359:G:C6	1:A5:1360:G:O6	2.73	0.41
1:A5:1503:A:H4'	1:A5:1504:G:H5'	2.02	0.41
1:A5:1526:G:H2'	1:A5:1527:A:H8	1.85	0.41
1:A5:1636:U:H5''	1:A5:1637:A:H5'	2.02	0.41
1:A5:1839:U:H5''	12:F:112:ARG:HD3	2.02	0.41
1:A5:1954:U:H2'	1:A5:1955:G:C8	2.55	0.41
1:A5:1984:A:C8	1:A5:2011:C:H4'	2.54	0.41
1:A5:2044:U:H3	5:A6:3871:A:H5''	1.84	0.41
4:B2:955:A:N6	4:B2:971:G:N3	2.68	0.41
4:B2:1214:A:N6	4:B2:1682:C:C2	2.86	0.41
4:B2:1290:G:N2	48:ff:133:ALA:H	2.19	0.41
4:B2:1757:G:N7	4:B2:1776:G:N2	2.68	0.41
4:B2:1841:C:H5''	7:n:2:ARG:HG3	2.01	0.41
5:A6:2768:C:N3	35:g:69:LYS:O	2.52	0.41
5:A6:4237:C:H2'	5:A6:4238:G:C8	2.55	0.41
5:A6:4332:C:H2'	5:A6:4333:C:C6	2.55	0.41
12:F:112:ARG:HH21	12:F:120:THR:HG23	1.85	0.41
14:H:63:ASN:HB2	14:H:64:ARG:NH1	2.36	0.41
20:O:35:VAL:HG11	20:O:80:PHE:HE2	1.86	0.41
21:P:78:TRP:CD1	21:P:80:GLN:H	2.38	0.41
28:Y:77:LYS:HB2	28:Y:79:VAL:HG22	2.01	0.41
49:gg:70:VAL:HG12	49:gg:111:VAL:HG13	2.02	0.41
52:BB:150:ILE:HG23	60:RR:131:PRO:HA	2.02	0.41
55:KK:3:MET:HA	55:KK:4:PRO:HD3	1.91	0.41
56:MM:86:GLY:HA2	56:MM:91:LEU:HD12	2.02	0.41
57:OO:78:ALA:HA	57:OO:81:VAL:HG22	2.01	0.41
61:SS:120:HIS:CE1	61:SS:124:ARG:HD2	2.56	0.41
63:UU:46:LYS:HD3	63:UU:100:GLN:HE22	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
68:CC:166:ARG:HB2	68:CC:248:TYR:CG	2.55	0.41
84:Bb:26:G:H22	84:Bb:44:A:H2	1.68	0.41
1:A5:80:C:H2'	1:A5:81:C:C6	2.55	0.41
1:A5:239:C:H5'	28:Y:33:PRO:HD3	2.02	0.41
1:A5:1199:G:H2'	1:A5:1200:G:H8	1.84	0.41
1:A5:1273:G:H2'	11:E:75:TYR:CZ	2.56	0.41
1:A5:1439:C:H41	12:F:33:ARG:HB3	1.84	0.41
1:A5:1839:U:H2'	1:A5:1840:G:C8	2.55	0.41
1:A5:2085:G:H2'	1:A5:2086:G:C8	2.55	0.41
4:B2:11:A:H2	4:B2:1357:A:H1'	1.85	0.41
4:B2:65:C:C2	70:GG:174:PRO:HB3	2.55	0.41
4:B2:167:G:H2'	4:B2:168:C:C6	2.55	0.41
4:B2:475:C:H1'	4:B2:507:G:H1'	2.01	0.41
4:B2:502:C:H41	79:YY:84:LYS:HE3	1.85	0.41
4:B2:1355:C:H42	68:CC:187:ARG:HH21	1.68	0.41
5:A6:2277:C:H2'	5:A6:2278:G:C8	2.55	0.41
5:A6:2406:G:O6	5:A6:2785:C:N4	2.53	0.41
5:A6:2522:G:H2'	5:A6:2523:G:H8	1.85	0.41
5:A6:3920:U:H2'	5:A6:3921:U:C6	2.54	0.41
5:A6:4207:C:H2'	5:A6:4208:U:H6	1.85	0.41
5:A6:4239:A:H2'	5:A6:4240:G:C8	2.55	0.41
5:A6:4630:G:H2'	5:A6:4631:G:C8	2.56	0.41
12:F:153:ILE:HD11	12:F:190:ILE:HD11	2.02	0.41
49:gg:174:VAL:HB	49:gg:188:HIS:HB2	2.02	0.41
54:FF:42:LYS:HD3	54:FF:42:LYS:HA	1.78	0.41
55:KK:31:LYS:NZ	55:KK:36:ALA:HA	2.36	0.41
55:KK:86:PRO:HA	55:KK:87:PRO:HD3	1.92	0.41
59:QQ:16:LYS:HA	59:QQ:16:LYS:HD2	1.70	0.41
79:YY:61:ARG:HA	79:YY:61:ARG:HD2	1.85	0.41
81:c:46:PRO:HA	81:c:49:ILE:HG22	2.03	0.41
81:c:60:LYS:HG3	81:c:63:GLN:HB2	2.00	0.41
1:A5:33:A:H8	1:A5:49:U:C4	2.37	0.41
1:A5:509:A:H4'	30:a:105:ARG:HH22	1.83	0.41
1:A5:651:C:H2'	1:A5:652:G:C8	2.48	0.41
1:A5:1553:A:H2'	1:A5:1554:A:H8	1.86	0.41
1:A5:1817:U:H2'	1:A5:1818:G:C8	2.54	0.41
4:B2:102:A:H5'	4:B2:104:A:C4	2.55	0.41
4:B2:496:C:H2'	4:B2:497:C:C6	2.55	0.41
4:B2:744:G:H2'	4:B2:745:C:H6	1.85	0.41
4:B2:886:A:H2'	4:B2:887:U:C2	2.56	0.41
4:B2:894:G:H2'	4:B2:895:G:C8	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B2:1643:U:H2'	4:B2:1644:C:C6	2.55	0.41
5:A6:2777:G:H5''	5:A6:2778:G:H5'	2.03	0.41
5:A6:2835:A:H2'	5:A6:2836:A:C8	2.55	0.41
5:A6:3631:U:H2'	5:A6:3632:C:H6	1.85	0.41
5:A6:4107:G:H2'	5:A6:4108:G:H8	1.85	0.41
5:A6:4524:G:C2	8:B:252:ALA:HB1	2.56	0.41
5:A6:4537:C:H2'	5:A6:4538:G:H8	1.84	0.41
8:B:84:MET:HB3	8:B:164:ALA:HB1	2.02	0.41
8:B:303:ALA:HB3	8:B:312:LYS:HG3	2.02	0.41
9:C:290:SER:H	44:r:4:HIS:CE1	2.38	0.41
14:H:92:MET:HE3	14:H:146:LEU:HD13	2.02	0.41
15:I:36:LEU:HA	15:I:39:LYS:HD3	2.02	0.41
26:V:13:LYS:HG2	26:V:14:PHE:H	1.86	0.41
37:i:70:LEU:HA	37:i:87:ARG:HD2	2.00	0.41
45:s:95:LEU:HA	45:s:98:ILE:HG22	2.01	0.41
1:A5:10:A:H2'	1:A5:11:G:C8	2.55	0.41
1:A5:419:A:H1'	1:A5:1333:A:H5'	2.03	0.41
1:A5:461:G:H2'	1:A5:462:G:C8	2.55	0.41
1:A5:684:G:C4	11:E:104:ASN:C	2.98	0.41
1:A5:1573:G:H2'	1:A5:1574:G:C4	2.55	0.41
4:B2:551:U:H4'	66:ee:113:ASN:HB3	2.02	0.41
4:B2:586:G:H3'	73:JJ:172:ARG:HH12	1.85	0.41
4:B2:1451:G:H2'	4:B2:1452:A:H2'	2.03	0.41
5:A6:3890:A:H3'	5:A6:3891:A:H8	1.85	0.41
5:A6:4664:A:H3'	5:A6:4665:A:C8	2.54	0.41
5:A6:4767:C:H2'	5:A6:4768:G:C8	2.55	0.41
5:A6:4936:G:H1	11:E:245:ILE:HG12	1.85	0.41
5:A6:4960:G:H2'	5:A6:4961:G:C8	2.55	0.41
8:B:315:ASN:ND2	8:B:326:VAL:H	2.19	0.41
17:L:197:LYS:HE3	17:L:197:LYS:HB3	1.92	0.41
18:M:6:PHE:HD1	23:S:153:PRO:HA	1.85	0.41
23:S:159:LEU:HD21	23:S:161:HIS:HB2	2.02	0.41
26:V:90:ARG:CZ	81:c:20:ARG:HG3	2.51	0.41
32:d:31:LYS:HA	32:d:31:LYS:HD2	1.67	0.41
42:o:22:LYS:HE3	42:o:71:GLU:HB3	2.01	0.41
42:o:28:LYS:HA	42:o:28:LYS:HD2	1.79	0.41
43:p:6:LYS:HD2	43:p:7:LYS:HD2	2.02	0.41
49:gg:190:GLY:HA3	53:DD:222:PRO:HA	2.02	0.41
54:FF:85:LYS:HA	54:FF:85:LYS:HD3	1.82	0.41
57:OO:117:ARG:HH12	67:aa:52:ASP:HB2	1.84	0.41
63:UU:20:ILE:HG21	63:UU:98:VAL:HG21	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
69:EE:92:ILE:HG22	69:EE:94:LYS:H	1.86	0.41
69:EE:149:TYR:HE2	70:GG:212:LEU:HD23	1.85	0.41
81:c:96:GLN:HG2	81:c:101:ARG:HB2	2.02	0.41
83:Cc:5:G:H2'	83:Cc:6:G:C8	2.55	0.41
1:A5:148:C:H2'	1:A5:149:A:H8	1.85	0.41
1:A5:242:U:H4'	28:Y:2:LYS:NZ	2.34	0.41
1:A5:920:C:H1'	18:M:65:PRO:HG2	2.02	0.41
1:A5:1340:C:H4'	9:C:109:ARG:HH11	1.86	0.41
1:A5:1538:U:H2'	1:A5:1539:G:C8	2.54	0.41
1:A5:1995:G:C6	45:s:40:MET:C	2.99	0.41
4:B2:155:G:H2'	4:B2:156:G:C8	2.54	0.41
4:B2:1232:U:H2'	4:B2:1233:G:C8	2.56	0.41
4:B2:1869:A:N1	52:BB:115:LYS:CG	2.84	0.41
5:A6:2505:C:H1'	5:A6:2506:G:C2	2.56	0.41
5:A6:2677:G:N1	82:u:32:LYS:CE	2.83	0.41
5:A6:2685:C:H1'	5:A6:2686:G:H5'	2.02	0.41
5:A6:3785:A:C6	5:A6:4536:C:H1'	2.56	0.41
5:A6:4319:C:H2'	5:A6:4320:G:H8	1.84	0.41
5:A6:4375:C:H5'	5:A6:4377:G:H5'	2.03	0.41
5:A6:4552:U:H2'	5:A6:4553:A:C8	2.54	0.41
5:A6:4584:A:H62	5:A6:4718:G:N2	2.18	0.41
5:A6:4734:A:H3'	5:A6:4735:G:H8	1.86	0.41
17:L:136:LYS:HD3	17:L:136:LYS:H	1.85	0.41
17:L:191:LEU:HD22	17:L:194:ILE:HD11	2.02	0.41
18:M:109:ARG:HA	18:M:112:VAL:HG22	2.03	0.41
19:N:104:GLU:O	19:N:108:ARG:HB2	2.21	0.41
25:U:43:LEU:O	25:U:47:ILE:HG13	2.21	0.41
26:V:91:LYS:H	26:V:91:LYS:HD2	1.86	0.41
27:X:100:VAL:HG23	27:X:134:LYS:HB3	2.02	0.41
32:d:93:ASN:HA	32:d:103:TYR:HE1	1.84	0.41
44:r:82:ILE:HG21	44:r:89:THR:HG23	2.02	0.41
49:gg:133:ASN:HD21	49:gg:137:VAL:HB	1.85	0.41
74:LL:18:GLN:HG2	74:LL:33:LEU:HD11	2.01	0.41
1:A5:908:G:H2'	1:A5:909:A:C8	2.56	0.41
1:A5:975:C:H1'	9:C:326:LEU:HD11	2.01	0.41
1:A5:1569:U:H2'	1:A5:1570:G:C8	2.56	0.41
4:B2:26:U:H2'	4:B2:27:A:C8	2.56	0.41
4:B2:49:C:N4	4:B2:472:C:H2'	2.36	0.41
4:B2:523:A:H62	4:B2:594:A:H62	1.68	0.41
4:B2:526:A:H4'	73:JJ:124:HIS:CD2	2.56	0.41
4:B2:1655:C:H2'	4:B2:1656:G:C8	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B2:1787:G:H2'	4:B2:1788:A:H8	1.84	0.41
5:A6:2300:A:N7	9:C:181:LYS:N	2.68	0.41
5:A6:2620:G:N2	5:A6:2636:U:O2	2.53	0.41
5:A6:3628:G:H2'	5:A6:3629:A:H8	1.84	0.41
5:A6:4122:G:H8	35:g:93:ARG:HH11	1.69	0.41
5:A6:4597:U:N3	5:A6:4614:G:N1	2.43	0.41
5:A6:4613:C:H3'	14:H:121:LYS:NZ	2.36	0.41
5:A6:4759:C:H4'	20:O:161:LYS:HD3	2.03	0.41
5:A6:4968:A:H5''	8:B:120:LYS:NZ	2.35	0.41
8:B:33:PRO:HD2	8:B:44:THR:HB	2.03	0.41
8:B:84:MET:HE1	8:B:166:THR:HG22	2.03	0.41
9:C:25:PRO:HB2	9:C:27:VAL:HG12	2.03	0.41
10:D:211:LEU:HB3	10:D:219:TYR:HB2	2.03	0.41
11:E:161:ARG:H	11:E:161:ARG:HG2	1.60	0.41
21:P:153:LYS:HA	21:P:153:LYS:HD3	1.81	0.41
23:S:93:MET:HE2	23:S:95:ARG:HG2	2.02	0.41
42:o:102:GLN:HE21	42:o:104:ILE:HD11	1.84	0.41
53:DD:158:ILE:HG12	53:DD:163:PRO:HB2	2.01	0.41
55:KK:77:GLN:HA	55:KK:80:ARG:HG2	2.03	0.41
68:CC:134:ASN:HA	68:CC:167:ARG:HH12	1.85	0.41
80:W:28:GLU:HG3	80:W:49:LEU:HD13	2.02	0.41
1:A5:14:C:H2'	1:A5:15:A:C8	2.55	0.41
1:A5:73:A:H62	17:L:103:ARG:HH22	1.69	0.41
1:A5:1720:C:H2'	1:A5:1721:G:C8	2.56	0.41
1:A5:1969:G:H2'	1:A5:1970:A:C5	2.56	0.41
4:B2:4:C:H5'	68:CC:230:THR:HG21	2.02	0.41
4:B2:30:C:H4'	78:XX:131:LEU:HD22	2.02	0.41
4:B2:305:U:N1	72:II:182:CYS:C	2.78	0.41
4:B2:1452:A:H61	4:B2:1473:G:H4'	1.86	0.41
4:B2:1534:C:H5'	54:FF:81:ARG:HH22	1.86	0.41
4:B2:1588:A:H2'	4:B2:1589:A:C8	2.55	0.41
5:A6:3911:C:H2'	5:A6:3912:U:C6	2.56	0.41
5:A6:3973:G:H2'	5:A6:3974:G:C8	2.55	0.41
5:A6:4613:C:C6	14:H:121:LYS:CG	3.04	0.41
5:A6:4674:C:H5''	8:B:334:LYS:HZ3	1.85	0.41
5:A6:4741:C:H2'	5:A6:4742:G:H8	1.86	0.41
5:A6:4968:A:H5''	8:B:120:LYS:HZ3	1.85	0.41
8:B:315:ASN:HD21	8:B:326:VAL:H	1.68	0.41
9:C:348:LYS:HE3	9:C:348:LYS:HB3	1.90	0.41
14:H:91:LYS:HD3	14:H:145:VAL:HG13	2.01	0.41
20:O:16:LEU:HB3	20:O:41:ILE:HG21	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:O:41:ILE:H	20:O:41:ILE:HG12	1.73	0.41
21:P:47:TYR:HA	21:P:50:ASP:OD1	2.21	0.41
23:S:11:LYS:HA	23:S:31:ARG:HE	1.85	0.41
26:V:90:ARG:HD2	26:V:93:GLY:H	1.86	0.41
35:g:69:LYS:HE2	35:g:69:LYS:HB2	1.83	0.41
35:g:85:LYS:HA	35:g:88:ARG:HD3	2.03	0.41
42:o:21:HIS:HA	42:o:71:GLU:O	2.21	0.41
44:r:111:ILE:O	44:r:115:SER:HB2	2.20	0.41
51:AA:198:MET:HE2	51:AA:199:PRO:HD2	2.03	0.41
52:BB:157:GLN:HB2	52:BB:160:GLN:HG3	2.03	0.41
68:CC:137:VAL:HB	68:CC:217:ALA:HA	2.01	0.41
69:EE:68:ARG:HA	69:EE:76:VAL:HG11	2.02	0.41
69:EE:94:LYS:HA	69:EE:94:LYS:HD3	1.84	0.41
71:HH:66:VAL:HG21	71:HH:98:ARG:HD3	2.03	0.41
74:LL:37:TYR:HA	74:LL:63:THR:HA	2.02	0.41
79:YY:26:ASP:HB2	79:YY:68:LYS:HZ1	1.86	0.41
1:A5:284:G:H2'	1:A5:285:G:H8	1.86	0.41
1:A5:481:G:H2'	1:A5:482:G:C8	2.56	0.41
1:A5:684:G:C5	11:E:104:ASN:HA	2.51	0.41
1:A5:943:A:H3'	12:F:147:LYS:HG3	2.02	0.41
1:A5:1217:G:H2'	1:A5:1218:G:C4	2.55	0.41
1:A5:1526:G:H2'	1:A5:1527:A:C8	2.56	0.41
1:A5:1604:G:H2'	1:A5:1605:G:C8	2.56	0.41
1:A5:1656:U:H2'	1:A5:1657:G:H8	1.86	0.41
1:A5:1721:G:H5'	1:A5:1834:U:H5	1.85	0.41
1:A5:1849:U:H2'	1:A5:1850:A:H8	1.86	0.41
1:A5:1934:A:N1	1:A5:2052:G:C6	2.88	0.41
1:A5:1991:A:H5'	46:t:135:THR:O	2.21	0.41
4:B2:1101:U:H2'	4:B2:1102:G:H8	1.86	0.41
4:B2:1389:C:H5''	60:RR:43:SER:HB2	2.02	0.41
4:B2:1442:U:H4'	59:QQ:13:PHE:HE1	1.86	0.41
4:B2:1535:U:C6	54:FF:82:ASN:CB	3.03	0.41
4:B2:1599:U:N3	54:FF:166:ILE:C	2.79	0.41
4:B2:1621:U:N3	58:PP:115:TYR:O	2.54	0.41
4:B2:1725:U:H2'	4:B2:1726:G:H8	1.86	0.41
4:B2:1774:C:H2'	4:B2:1775:U:C6	2.55	0.41
5:A6:2695:A:H1'	5:A6:2697:A:N7	2.35	0.41
5:A6:2740:U:H5''	6:A:188:LYS:HA	2.01	0.41
5:A6:2889:G:C2	80:W:75:HIS:CA	3.04	0.41
5:A6:3770:U:H2'	5:A6:3771:C:C6	2.55	0.41
5:A6:3848:U:H2'	5:A6:3849:A:C8	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A6:3970:G:H21	5:A6:4052:C:N4	2.18	0.41
5:A6:4094:G:H2'	5:A6:4095:G:H8	1.86	0.41
5:A6:4174:U:H2'	5:A6:4175:G:C8	2.56	0.41
5:A6:4617:G:H2'	5:A6:4618:G:C8	2.56	0.41
9:C:132:ALA:HA	9:C:151:PRO:HG3	2.03	0.41
9:C:236:ASN:O	9:C:240:LEU:HD23	2.20	0.41
10:D:173:ILE:HD12	10:D:174:PRO:HD2	2.02	0.41
10:D:277:LYS:HE3	10:D:277:LYS:HB3	1.79	0.41
11:E:269:GLN:HB2	18:M:111:LYS:NZ	2.36	0.41
12:F:126:LYS:HD2	24:T:133:ALA:HB3	2.02	0.41
14:H:10:VAL:HG11	14:H:78:GLN:HB3	2.03	0.41
20:O:187:LYS:HB2	20:O:187:LYS:HE2	1.78	0.41
32:d:44:ARG:HA	32:d:47:LYS:HE2	2.03	0.41
35:g:78:TYR:HB3	35:g:82:MET:HB3	2.03	0.41
36:h:52:LYS:HA	36:h:52:LYS:HD3	1.77	0.41
36:h:104:THR:O	36:h:108:GLN:CB	2.69	0.41
37:i:35:LYS:HD3	37:i:36:HIS:H	1.86	0.41
47:cc:10:LYS:HE2	47:cc:10:LYS:HB2	1.96	0.41
47:cc:56:LEU:HD12	54:FF:122:ARG:HH22	1.86	0.41
57:OO:30:VAL:HG22	57:OO:96:LYS:HB2	2.02	0.41
59:QQ:38:PRO:HB2	59:QQ:41:MET:HE1	2.02	0.41
63:UU:87:ARG:HA	63:UU:87:ARG:HD3	1.84	0.41
70:GG:7:PHE:HD1	70:GG:113:ILE:HB	1.85	0.41
70:GG:221:LYS:HE3	70:GG:221:LYS:HB3	1.83	0.41
75:NN:132:LYS:HD3	75:NN:132:LYS:HA	1.83	0.41
80:W:39:GLN:O	80:W:43:LYS:HG2	2.21	0.41
80:W:171:LYS:HD2	80:W:171:LYS:HA	1.85	0.41
84:Bb:4:G:N1	84:Bb:69:U:N3	2.69	0.41
1:A5:113:A:H4'	19:N:49:ARG:HG3	2.03	0.41
1:A5:505:G:N1	1:A5:653:U:C2	2.89	0.41
1:A5:952:G:H2'	1:A5:953:C:C6	2.56	0.41
1:A5:1534:A:N7	38:j:11:ARG:HG3	2.36	0.41
1:A5:2037:C:H2'	1:A5:2038:U:H6	1.86	0.41
4:B2:676:C:H5''	75:NN:5:HIS:CD2	2.56	0.41
4:B2:936:G:H2'	4:B2:937:C:H6	1.86	0.41
4:B2:1128:C:H2'	4:B2:1129:G:C8	2.55	0.41
4:B2:1491:G:H2'	4:B2:1492:U:C6	2.55	0.41
4:B2:1613:G:H2'	4:B2:1614:A:H8	1.85	0.41
4:B2:1773:C:C4	4:B2:1774:C:N4	2.89	0.41
5:A6:2275:G:H2'	5:A6:2276:A:C8	2.56	0.41
5:A6:2373:C:H2'	5:A6:2374:A:H8	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A6:2928:G:H5''	29:Z:96:VAL:HG22	2.03	0.41
5:A6:4726:G:H5'	8:B:106:PHE:HE2	1.86	0.41
5:A6:4914:C:H2'	5:A6:4915:G:C8	2.55	0.41
8:B:12:GLY:HA3	8:B:235:TRP:HE3	1.85	0.41
10:D:152:ARG:HH11	10:D:153:THR:H	1.68	0.41
18:M:31:ILE:HG23	23:S:75:VAL:HG23	2.03	0.41
23:S:41:LYS:HB3	23:S:41:LYS:HE3	1.85	0.41
48:ff:108:VAL:HG12	48:ff:114:ILE:HG22	2.03	0.41
48:ff:143:LYS:HB2	48:ff:143:LYS:HE2	1.93	0.41
49:gg:24:THR:HG23	49:gg:26:GLN:H	1.85	0.41
58:PP:62:LYS:HA	58:PP:65:LYS:HG2	2.03	0.41
64:ZZ:66:LYS:HA	64:ZZ:111:ARG:HD2	2.03	0.41
65:bb:24:LEU:HA	77:WW:60:LYS:HZ1	1.85	0.41
68:CC:103:LYS:HA	68:CC:103:LYS:HD3	1.84	0.41
71:HH:101:LEU:HB2	71:HH:116:ARG:HD3	2.03	0.41
81:c:44:ARG:HD3	81:c:44:ARG:HA	1.93	0.41
82:u:95:ALA:HB1	82:u:97:ILE:HD11	2.02	0.41
1:A5:63:G:H22	1:A5:333:U:H2'	1.84	0.40
1:A5:71:C:H5''	17:L:64:VAL:HG13	2.03	0.40
1:A5:251:C:H2'	1:A5:252:C:C6	2.56	0.40
1:A5:365:U:H2'	1:A5:366:A:H8	1.86	0.40
1:A5:429:A:H2'	1:A5:430:G:C8	2.56	0.40
1:A5:724:C:H2'	1:A5:725:G:C8	2.55	0.40
1:A5:1171:G:H2'	1:A5:1172:C:C6	2.55	0.40
1:A5:1277:G:H2'	1:A5:1278:C:H6	1.85	0.40
1:A5:1493:G:H4'	31:b:41:ARG:NH1	2.36	0.40
1:A5:1760:G:N1	1:A5:1773:U:C2	2.89	0.40
1:A5:1813:U:H2'	31:b:49:HIS:CE1	2.56	0.40
1:A5:2045:G:C4	20:O:62:MET:CA	3.03	0.40
2:A7:31:G:H2'	2:A7:32:A:H8	1.86	0.40
4:B2:28:U:O2	4:B2:646:G:N2	2.41	0.40
4:B2:1121:G:H2'	4:B2:1122:A:C8	2.56	0.40
4:B2:1142:G:P	68:CC:187:ARG:HH12	2.44	0.40
4:B2:1703:C:H2'	4:B2:1704:C:O4'	2.21	0.40
5:A6:2283:G:H2'	5:A6:2284:G:C8	2.54	0.40
5:A6:2295:C:H2'	5:A6:2296:G:C8	2.55	0.40
5:A6:2468:U:H4'	5:A6:2469:C:H5'	2.03	0.40
5:A6:2541:G:H2'	5:A6:2542:G:C8	2.56	0.40
5:A6:2596:G:H2'	5:A6:2597:G:H8	1.86	0.40
5:A6:3727:A:H4'	37:i:74:LYS:HE2	2.02	0.40
5:A6:3856:A:H5''	21:P:83:TRP:O	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A6:4898:G:H2'	5:A6:4899:G:H8	1.86	0.40
5:A6:5003:U:H5'	8:B:376:HIS:CE1	2.56	0.40
10:D:68:ARG:HB3	10:D:69:ILE:H	1.77	0.40
15:I:171:TRP:HB2	15:I:178:ALA:HA	2.03	0.40
22:Q:50:ARG:HA	22:Q:53:MET:SD	2.61	0.40
22:Q:91:ARG:HA	30:a:76:ASP:HB2	2.02	0.40
35:g:67:LEU:HG	35:g:72:LYS:HB2	2.02	0.40
36:h:109:ARG:HA	36:h:112:ARG:HB3	2.02	0.40
38:j:28:HIS:HD2	38:j:31:LYS:H	1.68	0.40
49:gg:109:LEU:HD13	49:gg:152:SER:HA	2.03	0.40
52:BB:46:LYS:HD2	57:OO:27:VAL:HG22	2.02	0.40
59:QQ:25:CYS:HB2	59:QQ:91:ALA:HB1	2.02	0.40
69:EE:254:LYS:HE3	69:EE:254:LYS:HB3	1.84	0.40
74:LL:89:ARG:HG3	74:LL:106:HIS:CD2	2.56	0.40
82:u:77:ASN:HD21	82:u:79:ILE:HG12	1.87	0.40
1:A5:137:G:H2'	1:A5:138:G:C8	2.56	0.40
1:A5:1097:C:H2'	1:A5:1098:G:C8	2.56	0.40
1:A5:1198:G:H2'	1:A5:1199:G:C8	2.57	0.40
4:B2:305:U:N1	72:II:183:GLY:CA	2.84	0.40
4:B2:1114:U:H3'	4:B2:1115:U:H3'	2.03	0.40
4:B2:1219:C:H42	4:B2:1646:C:H42	1.67	0.40
4:B2:1353:A:H2'	4:B2:1354:G:O4'	2.21	0.40
4:B2:1402:A:N7	4:B2:1441:U:C5	2.89	0.40
4:B2:1468:C:H2'	4:B2:1469:A:C8	2.56	0.40
4:B2:1736:G:H2'	4:B2:1737:G:C8	2.56	0.40
4:B2:1818:A:H2'	4:B2:1819:A:C8	2.57	0.40
5:A6:2300:A:C8	9:C:182:LYS:HD2	2.56	0.40
5:A6:2583:C:H2'	5:A6:2584:G:C8	2.56	0.40
5:A6:2864:A:H2'	5:A6:2865:U:C6	2.56	0.40
5:A6:4188:U:H2'	5:A6:4189:U:C6	2.55	0.40
5:A6:4346:U:H4'	42:o:80:LYS:HE2	2.03	0.40
5:A6:4370:G:C5	83:Cc:77:A:C2	2.89	0.40
5:A6:4757:C:C2	20:O:114:LYS:CA	3.04	0.40
9:C:159:GLU:HA	9:C:217:ILE:HB	2.03	0.40
19:N:19:MET:HE3	19:N:19:MET:HB3	1.87	0.40
24:T:28:ALA:O	24:T:32:ARG:HB2	2.21	0.40
35:g:59:VAL:HB	35:g:63:VAL:HG23	2.03	0.40
41:m:106:ARG:HE	41:m:106:ARG:HB3	1.52	0.40
52:BB:7:LYS:HD3	52:BB:7:LYS:H	1.87	0.40
58:PP:127:LYS:HA	58:PP:127:LYS:HD3	1.92	0.40
59:QQ:55:VAL:HG12	59:QQ:60:LYS:HD3	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:QQ:73:LYS:HE2	59:QQ:73:LYS:HB2	1.92	0.40
64:ZZ:80:ARG:CZ	64:ZZ:81:GLY:H	2.35	0.40
73:JJ:42:GLU:O	73:JJ:46:VAL:HG23	2.21	0.40
73:JJ:164:PRO:HB3	73:JJ:170:PRO:HA	2.02	0.40
83:Cc:52:C:H2'	83:Cc:53:G:C8	2.56	0.40
1:A5:262:G:H2'	1:A5:263:G:C8	2.56	0.40
1:A5:1100:U:O2	1:A5:1196:G:C2	2.74	0.40
1:A5:1907:A:H4'	12:F:222:LYS:HE3	2.03	0.40
1:A5:1929:A:N1	1:A5:2054:U:C4	2.89	0.40
1:A5:1973:G:H2'	1:A5:1974:U:C6	2.56	0.40
2:A7:57:C:H2'	2:A7:58:A:C8	2.54	0.40
3:A8:114:G:N2	3:A8:136:U:O2	2.44	0.40
4:B2:64:A:H2	4:B2:83:A:H62	1.70	0.40
4:B2:861:A:O2'	4:B2:862:A:H8	2.04	0.40
4:B2:1030:A:H2'	4:B2:1031:A:C8	2.56	0.40
4:B2:1207:G:H4'	4:B2:1834:A:C5	2.57	0.40
5:A6:2606:G:H2'	5:A6:2607:C:C6	2.56	0.40
5:A6:4153:C:H2'	5:A6:4154:G:C8	2.56	0.40
5:A6:4775:C:H2'	5:A6:4776:G:H8	1.86	0.40
5:A6:4972:U:O2	5:A6:4986:G:C6	2.74	0.40
5:A6:5037:U:H2'	5:A6:5038:A:H8	1.86	0.40
12:F:165:ARG:HE	12:F:208:TRP:CD1	2.39	0.40
14:H:18:ILE:HG23	14:H:25:VAL:HG23	2.04	0.40
18:M:61:ILE:HA	18:M:61:ILE:HD13	1.87	0.40
36:h:54:ILE:HA	36:h:57:VAL:HG22	2.04	0.40
44:r:122:LYS:HE3	44:r:122:LYS:HB2	1.98	0.40
46:t:86:LYS:HE2	46:t:86:LYS:HB2	1.86	0.40
53:DD:74:GLN:HG3	53:DD:81:GLU:HA	2.03	0.40
65:bb:82:LYS:HE2	65:bb:82:LYS:HB3	1.95	0.40
69:EE:102:ILE:HD13	69:EE:239:PRO:HD3	2.03	0.40
74:LL:111:VAL:HG21	74:LL:128:VAL:HG11	2.04	0.40
82:u:87:LYS:HG3	82:u:89:TYR:HB2	2.02	0.40
1:A5:221:C:H2'	1:A5:222:C:C6	2.56	0.40
1:A5:1175:A:H1'	1:A5:1187:G:H22	1.86	0.40
1:A5:1830:G:H2'	1:A5:1831:G:C8	2.56	0.40
4:B2:74:G:N1	70:GG:170:ARG:O	2.55	0.40
4:B2:305:U:C4	72:II:182:CYS:N	2.89	0.40
4:B2:823:U:H6	73:JJ:142:VAL:HG13	1.86	0.40
4:B2:1209:A:N6	4:B2:1691:U:O4	2.54	0.40
5:A6:2399:G:H2'	5:A6:2400:G:C8	2.56	0.40
5:A6:4237:C:H2'	5:A6:4238:G:H8	1.87	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A6:4431:U:H4'	15:I:160:PRO:HD3	2.04	0.40
5:A6:4715:C:H2'	5:A6:4716:C:C6	2.57	0.40
10:D:69:ILE:HD13	24:T:31:MET:HE1	2.04	0.40
21:P:39:MET:HE3	21:P:39:MET:HB3	1.83	0.40
51:AA:144:THR:HB	51:AA:158:ASP:H	1.86	0.40
53:DD:20:GLU:HG3	55:KK:64:TRP:CE2	2.56	0.40
55:KK:59:LYS:HE3	55:KK:59:LYS:HB3	1.93	0.40
56:MM:54:SER:HB3	56:MM:78:LYS:HD2	2.03	0.40
67:aa:85:ARG:NH1	67:aa:86:ASN:HB3	2.36	0.40
80:W:44:LEU:HD13	80:W:44:LEU:HA	1.97	0.40
80:W:67:THR:HG22	80:W:71:ARG:HH21	1.86	0.40
1:A5:63:G:H1	1:A5:333:U:H3'	1.87	0.40
1:A5:239:C:H2'	1:A5:240:G:C8	2.56	0.40
1:A5:458:C:H5''	11:E:117:ARG:HB2	2.04	0.40
1:A5:1527:A:H2'	1:A5:1528:U:H6	1.86	0.40
1:A5:2049:G:H2'	1:A5:2050:G:C8	2.56	0.40
4:B2:376:A:H2'	4:B2:377:G:H8	1.87	0.40
4:B2:628:A:H61	53:DD:141:LYS:NZ	2.20	0.40
4:B2:980:A:H2'	4:B2:981:A:C8	2.56	0.40
4:B2:1267:C:H2'	4:B2:1268:C:C6	2.56	0.40
4:B2:1831:A:H2'	4:B2:1832:A:H8	1.85	0.40
4:B2:1869:A:N1	52:BB:115:LYS:CB	2.85	0.40
5:A6:2375:A:H2'	5:A6:2376:A:C8	2.57	0.40
5:A6:2457:G:H5'	5:A6:2470:C:N4	2.35	0.40
5:A6:2522:G:H2'	5:A6:2523:G:C8	2.56	0.40
5:A6:2583:C:H5'	35:g:55:GLY:HA3	2.02	0.40
5:A6:3857:G:O5'	21:P:86:LYS:HE3	2.22	0.40
5:A6:4291:G:H5'	5:A6:4293:U:H5'	2.04	0.40
5:A6:4454:G:H2'	5:A6:4455:G:C8	2.56	0.40
13:G:187:LYS:HB2	13:G:198:THR:HG23	2.03	0.40
16:J:35:ARG:HH11	16:J:123:ILE:HA	1.86	0.40
21:P:23:ARG:HA	21:P:143:PRO:HB3	2.03	0.40
21:P:30:ARG:HH22	21:P:62:ARG:HH21	1.70	0.40
23:S:78:PHE:HE2	23:S:102:THR:HG22	1.87	0.40
26:V:97:TYR:HA	81:c:21:TYR:CE1	2.57	0.40
27:X:87:MET:HA	27:X:90:ILE:HG22	2.03	0.40
42:o:99:ARG:NH1	42:o:99:ARG:H	2.19	0.40
49:gg:218:LEU:HD13	49:gg:218:LEU:HA	1.93	0.40
53:DD:214:LYS:HB2	53:DD:214:LYS:HE2	1.87	0.40
74:LL:103:GLU:HG3	74:LL:105:ARG:NE	2.36	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	
6	A	246/248 (99%)	229 (93%)	16 (6%)	1 (0%)	30	67
7	n	23/25 (92%)	23 (100%)	0	0	100	100
8	B	395/398 (99%)	369 (93%)	26 (7%)	0	100	100
9	C	359/363 (99%)	341 (95%)	18 (5%)	0	100	100
10	D	291/293 (99%)	271 (93%)	20 (7%)	0	100	100
11	E	218/224 (97%)	199 (91%)	19 (9%)	0	100	100
12	F	223/225 (99%)	210 (94%)	13 (6%)	0	100	100
13	G	211/215 (98%)	204 (97%)	7 (3%)	0	100	100
14	H	188/190 (99%)	182 (97%)	6 (3%)	0	100	100
15	I	195/213 (92%)	182 (93%)	13 (7%)	0	100	100
16	J	168/170 (99%)	161 (96%)	7 (4%)	0	100	100
17	L	203/205 (99%)	194 (96%)	9 (4%)	0	100	100
18	M	134/136 (98%)	128 (96%)	6 (4%)	0	100	100
19	N	201/203 (99%)	193 (96%)	8 (4%)	0	100	100
20	O	195/199 (98%)	188 (96%)	7 (4%)	0	100	100
21	P	151/153 (99%)	148 (98%)	3 (2%)	0	100	100
22	Q	185/187 (99%)	179 (97%)	6 (3%)	0	100	100
23	S	174/176 (99%)	161 (92%)	12 (7%)	1 (1%)	21	58
24	T	157/159 (99%)	148 (94%)	9 (6%)	0	100	100
25	U	97/99 (98%)	94 (97%)	3 (3%)	0	100	100
26	V	129/131 (98%)	114 (88%)	15 (12%)	0	100	100
27	X	116/118 (98%)	108 (93%)	8 (7%)	0	100	100
28	Y	132/134 (98%)	127 (96%)	5 (4%)	0	100	100
29	Z	133/135 (98%)	124 (93%)	9 (7%)	0	100	100
30	a	144/147 (98%)	136 (94%)	8 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
31	b	60/100 (60%)	56 (93%)	4 (7%)	0	100	100
32	d	105/107 (98%)	100 (95%)	5 (5%)	0	100	100
33	e	126/128 (98%)	120 (95%)	6 (5%)	0	100	100
34	f	108/110 (98%)	95 (88%)	13 (12%)	0	100	100
35	g	108/110 (98%)	103 (95%)	4 (4%)	1 (1%)	14	49
36	h	119/121 (98%)	116 (98%)	3 (2%)	0	100	100
37	i	100/102 (98%)	99 (99%)	1 (1%)	0	100	100
38	j	84/86 (98%)	73 (87%)	11 (13%)	0	100	100
39	k	67/69 (97%)	67 (100%)	0	0	100	100
40	l	48/50 (96%)	47 (98%)	1 (2%)	0	100	100
41	m	48/51 (94%)	44 (92%)	4 (8%)	0	100	100
42	o	102/105 (97%)	90 (88%)	11 (11%)	1 (1%)	12	47
43	p	89/91 (98%)	85 (96%)	4 (4%)	0	100	100
44	r	125/127 (98%)	112 (90%)	13 (10%)	0	100	100
45	s	101/103 (98%)	89 (88%)	12 (12%)	0	100	100
46	t	154/156 (99%)	135 (88%)	19 (12%)	0	100	100
47	cc	59/61 (97%)	54 (92%)	5 (8%)	0	100	100
48	ff	65/67 (97%)	56 (86%)	8 (12%)	1 (2%)	8	38
49	gg	311/313 (99%)	292 (94%)	19 (6%)	0	100	100
50	dd	53/55 (96%)	46 (87%)	7 (13%)	0	100	100
51	AA	212/214 (99%)	201 (95%)	11 (5%)	0	100	100
52	BB	214/218 (98%)	202 (94%)	12 (6%)	0	100	100
53	DD	223/225 (99%)	213 (96%)	10 (4%)	0	100	100
54	FF	180/189 (95%)	174 (97%)	6 (3%)	0	100	100
55	KK	94/96 (98%)	88 (94%)	6 (6%)	0	100	100
56	MM	122/124 (98%)	110 (90%)	12 (10%)	0	100	100
57	OO	132/134 (98%)	123 (93%)	9 (7%)	0	100	100
58	PP	116/118 (98%)	111 (96%)	5 (4%)	0	100	100
59	QQ	139/141 (99%)	131 (94%)	8 (6%)	0	100	100
60	RR	130/132 (98%)	125 (96%)	5 (4%)	0	100	100
61	SS	143/145 (99%)	134 (94%)	8 (6%)	1 (1%)	18	55

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
62	TT	138/141 (98%)	134 (97%)	4 (3%)	0	100	100
63	UU	97/99 (98%)	93 (96%)	4 (4%)	0	100	100
64	ZZ	73/75 (97%)	71 (97%)	2 (3%)	0	100	100
65	bb	80/82 (98%)	77 (96%)	3 (4%)	0	100	100
66	ee	45/49 (92%)	45 (100%)	0	0	100	100
67	aa	96/98 (98%)	90 (94%)	6 (6%)	0	100	100
68	CC	216/218 (99%)	203 (94%)	13 (6%)	0	100	100
69	EE	260/262 (99%)	248 (95%)	12 (5%)	0	100	100
70	GG	224/228 (98%)	215 (96%)	9 (4%)	0	100	100
71	HH	174/190 (92%)	168 (97%)	6 (3%)	0	100	100
72	II	204/206 (99%)	194 (95%)	10 (5%)	0	100	100
73	JJ	178/180 (99%)	166 (93%)	11 (6%)	1 (1%)	21	58
74	LL	137/149 (92%)	126 (92%)	11 (8%)	0	100	100
75	NN	147/149 (99%)	144 (98%)	3 (2%)	0	100	100
76	VV	81/83 (98%)	79 (98%)	2 (2%)	0	100	100
77	WW	127/129 (98%)	118 (93%)	9 (7%)	0	100	100
78	XX	114/122 (93%)	108 (95%)	6 (5%)	0	100	100
79	YY	123/125 (98%)	118 (96%)	5 (4%)	0	100	100
80	W	178/180 (99%)	165 (93%)	11 (6%)	2 (1%)	11	45
81	c	109/121 (90%)	93 (85%)	16 (15%)	0	100	100
82	u	98/100 (98%)	77 (79%)	21 (21%)	0	100	100
All	All	11304/11580 (98%)	10636 (94%)	659 (6%)	9 (0%)	49	83

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
23	S	169	THR
42	o	54	PRO
48	ff	133	ALA
35	g	68	SER
61	SS	2	SER
73	JJ	133	ARG
80	W	78	ILE
6	A	14	SER
80	W	133	LYS

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	A	136/190 (72%)	126 (93%)	10 (7%)	13	34
7	n	24/24 (100%)	23 (96%)	1 (4%)	26	48
8	B	344/344 (100%)	327 (95%)	17 (5%)	22	44
9	C	301/301 (100%)	290 (96%)	11 (4%)	30	51
10	D	247/247 (100%)	241 (98%)	6 (2%)	43	63
11	E	197/197 (100%)	191 (97%)	6 (3%)	36	57
12	F	196/196 (100%)	188 (96%)	8 (4%)	27	49
13	G	187/187 (100%)	181 (97%)	6 (3%)	34	55
14	H	169/169 (100%)	160 (95%)	9 (5%)	20	42
15	I	170/180 (94%)	164 (96%)	6 (4%)	32	53
16	J	143/143 (100%)	138 (96%)	5 (4%)	32	53
17	L	170/170 (100%)	162 (95%)	8 (5%)	23	45
18	M	116/116 (100%)	113 (97%)	3 (3%)	40	61
19	N	171/171 (100%)	166 (97%)	5 (3%)	37	58
20	O	171/171 (100%)	162 (95%)	9 (5%)	20	42
21	P	134/134 (100%)	133 (99%)	1 (1%)	76	79
22	Q	164/164 (100%)	162 (99%)	2 (1%)	63	74
23	S	157/157 (100%)	152 (97%)	5 (3%)	34	55
24	T	139/139 (100%)	132 (95%)	7 (5%)	22	43
25	U	89/89 (100%)	84 (94%)	5 (6%)	19	41
26	V	101/101 (100%)	94 (93%)	7 (7%)	14	36
27	X	106/106 (100%)	106 (100%)	0	100	100
28	Y	124/124 (100%)	122 (98%)	2 (2%)	55	69
29	Z	117/117 (100%)	116 (99%)	1 (1%)	70	77
30	a	118/118 (100%)	118 (100%)	0	100	100
31	b	56/82 (68%)	53 (95%)	3 (5%)	20	42

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
32	d	98/98 (100%)	98 (100%)	0	100	100
33	e	114/114 (100%)	104 (91%)	10 (9%)	9	29
34	f	89/89 (100%)	84 (94%)	5 (6%)	19	41
35	g	94/94 (100%)	88 (94%)	6 (6%)	16	38
36	h	109/109 (100%)	106 (97%)	3 (3%)	38	59
37	i	86/86 (100%)	81 (94%)	5 (6%)	18	40
38	j	73/73 (100%)	70 (96%)	3 (4%)	27	49
39	k	64/64 (100%)	63 (98%)	1 (2%)	55	69
40	l	47/47 (100%)	46 (98%)	1 (2%)	47	65
41	m	46/46 (100%)	44 (96%)	2 (4%)	26	48
42	o	92/92 (100%)	89 (97%)	3 (3%)	33	55
43	p	74/74 (100%)	73 (99%)	1 (1%)	59	72
44	r	110/110 (100%)	105 (96%)	5 (4%)	24	46
45	s	90/90 (100%)	88 (98%)	2 (2%)	45	64
46	t	128/128 (100%)	124 (97%)	4 (3%)	35	56
47	cc	54/54 (100%)	54 (100%)	0	100	100
48	ff	60/60 (100%)	59 (98%)	1 (2%)	53	68
49	gg	272/272 (100%)	265 (97%)	7 (3%)	40	61
50	dd	48/48 (100%)	46 (96%)	2 (4%)	26	48
51	AA	179/179 (100%)	175 (98%)	4 (2%)	45	64
52	BB	197/197 (100%)	191 (97%)	6 (3%)	36	57
53	DD	189/189 (100%)	187 (99%)	2 (1%)	65	74
54	FF	156/159 (98%)	154 (99%)	2 (1%)	61	72
55	KK	87/87 (100%)	86 (99%)	1 (1%)	65	74
56	MM	104/104 (100%)	100 (96%)	4 (4%)	29	51
57	OO	104/104 (100%)	101 (97%)	3 (3%)	37	58
58	PP	107/107 (100%)	103 (96%)	4 (4%)	30	51
59	QQ	117/117 (100%)	113 (97%)	4 (3%)	32	54
60	RR	119/119 (100%)	117 (98%)	2 (2%)	53	68
61	SS	125/125 (100%)	122 (98%)	3 (2%)	43	63
62	TT	110/110 (100%)	105 (96%)	5 (4%)	24	46

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
63	UU	92/92 (100%)	89 (97%)	3 (3%)	33	55
64	ZZ	66/66 (100%)	65 (98%)	1 (2%)	57	71
65	bb	74/74 (100%)	74 (100%)	0	100	100
66	ee	41/41 (100%)	40 (98%)	1 (2%)	43	63
67	aa	85/85 (100%)	80 (94%)	5 (6%)	18	40
68	CC	183/183 (100%)	175 (96%)	8 (4%)	25	47
69	EE	224/224 (100%)	215 (96%)	9 (4%)	28	49
70	GG	199/199 (100%)	192 (96%)	7 (4%)	32	53
71	HH	167/170 (98%)	161 (96%)	6 (4%)	31	52
72	II	178/178 (100%)	176 (99%)	2 (1%)	65	74
73	JJ	160/160 (100%)	157 (98%)	3 (2%)	50	66
74	LL	128/134 (96%)	125 (98%)	3 (2%)	44	63
75	NN	130/130 (100%)	124 (95%)	6 (5%)	24	46
76	VV	68/68 (100%)	66 (97%)	2 (3%)	37	58
77	WW	112/112 (100%)	109 (97%)	3 (3%)	39	60
78	XX	65/98 (66%)	63 (97%)	2 (3%)	35	56
79	YY	107/107 (100%)	100 (94%)	7 (6%)	15	37
80	W	159/159 (100%)	153 (96%)	6 (4%)	29	51
81	c	92/100 (92%)	88 (96%)	4 (4%)	26	48
82	u	85/85 (100%)	81 (95%)	4 (5%)	23	45
All	All	9804/9947 (99%)	9478 (97%)	326 (3%)	34	55

All (326) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	A	75	LEU
6	A	76	PHE
6	A	87	PHE
6	A	102	LEU
6	A	112	ILE
6	A	137	ILE
6	A	139	HIS
6	A	148	VAL
6	A	152	SER
6	A	166	VAL

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Mol	Chain	Res	Type
7	n	22	GLN
8	B	6	PHE
8	B	29	VAL
8	B	56	ILE
8	B	60	VAL
8	B	72	VAL
8	B	76	VAL
8	B	77	THR
8	B	162	VAL
8	B	219	VAL
8	B	222	VAL
8	B	251	VAL
8	B	254	ILE
8	B	309	LEU
8	B	322	HIS
8	B	333	LEU
8	B	347	LEU
8	B	353	VAL
9	C	44	LEU
9	C	95	MET
9	C	118	THR
9	C	128	LEU
9	C	170	LEU
9	C	182	LYS
9	C	212	ASN
9	C	235	LEU
9	C	295	SER
9	C	312	ARG
9	C	326	LEU
10	D	6	VAL
10	D	7	VAL
10	D	105	LEU
10	D	109	LEU
10	D	214	GLU
10	D	232	THR
11	E	64	MET
11	E	73	ARG
11	E	143	LEU
11	E	166	VAL
11	E	219	TYR
11	E	274	LEU
12	F	32	LEU

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Mol	Chain	Res	Type
12	F	48	LEU
12	F	91	VAL
12	F	101	SER
12	F	131	MET
12	F	139	ILE
12	F	196	VAL
12	F	224	THR
13	G	28	VAL
13	G	154	LEU
13	G	156	VAL
13	G	161	VAL
13	G	164	ILE
13	G	177	MET
14	H	25	VAL
14	H	45	LEU
14	H	55	LEU
14	H	66	GLU
14	H	103	VAL
14	H	128	MET
14	H	145	VAL
14	H	165	THR
14	H	184	LYS
15	I	9	TYR
15	I	32	ARG
15	I	43	VAL
15	I	61	SER
15	I	91	LEU
15	I	138	ILE
16	J	12	MET
16	J	83	LEU
16	J	120	ASP
16	J	128	LEU
16	J	158	SER
17	L	9	ILE
17	L	55	ILE
17	L	77	SER
17	L	111	GLN
17	L	125	VAL
17	L	154	VAL
17	L	160	VAL
17	L	170	THR
18	M	38	VAL

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Mol	Chain	Res	Type
18	M	83	ASN
18	M	98	ARG
19	N	9	GLU
19	N	21	PHE
19	N	29	GLN
19	N	64	ILE
19	N	134	LEU
20	O	16	LEU
20	O	87	MET
20	O	102	LEU
20	O	113	ASP
20	O	114	LYS
20	O	132	THR
20	O	143	HIS
20	O	175	MET
20	O	194	ASP
21	P	141	SER
22	Q	49	LYS
22	Q	152	PHE
23	S	30	MET
23	S	80	ILE
23	S	85	ASP
23	S	110	TYR
23	S	164	LYS
24	T	14	MET
24	T	40	VAL
24	T	41	ASP
24	T	61	THR
24	T	72	VAL
24	T	124	THR
24	T	150	LEU
25	U	55	ASN
25	U	81	ARG
25	U	97	ARG
25	U	98	ASP
25	U	102	VAL
26	V	17	SER
26	V	59	ASP
26	V	77	HIS
26	V	81	VAL
26	V	90	ARG
26	V	92	ASP

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Mol	Chain	Res	Type
26	V	96	LEU
28	Y	2	LYS
28	Y	95	VAL
29	Z	38	TYR
31	b	32	LEU
31	b	42	ASN
31	b	49	HIS
33	e	9	LYS
33	e	13	VAL
33	e	41	ILE
33	e	45	VAL
33	e	58	ILE
33	e	88	LEU
33	e	91	CYS
33	e	118	LEU
33	e	122	VAL
33	e	129	LEU
34	f	18	LEU
34	f	80	ASN
34	f	83	MET
34	f	84	VAL
34	f	103	VAL
35	g	11	LEU
35	g	38	VAL
35	g	53	LEU
35	g	62	LYS
35	g	64	LEU
35	g	81	SER
36	h	4	ILE
36	h	43	LYS
36	h	71	LYS
37	i	21	VAL
37	i	33	LEU
37	i	34	THR
37	i	61	LEU
37	i	79	THR
38	j	11	ARG
38	j	57	ASN
38	j	76	HIS
39	k	36	VAL
40	l	21	ARG
41	m	82	LEU

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Mol	Chain	Res	Type
41	m	121	LEU
42	o	51	GLN
42	o	70	LEU
42	o	90	HIS
43	p	59	SER
44	r	2	SER
44	r	18	ILE
44	r	24	THR
44	r	80	THR
44	r	87	ARG
45	s	27	CYS
45	s	69	LEU
46	t	56	LEU
46	t	58	ILE
46	t	68	GLN
46	t	135	THR
48	ff	95	ARG
49	gg	12	LYS
49	gg	24	THR
49	gg	70	VAL
49	gg	90	TRP
49	gg	149	GLU
49	gg	198	VAL
49	gg	275	ILE
50	dd	27	ARG
50	dd	53	ILE
51	AA	7	VAL
51	AA	19	LEU
51	AA	57	LYS
51	AA	188	THR
52	BB	55	THR
52	BB	69	VAL
52	BB	79	VAL
52	BB	92	GLN
52	BB	137	LEU
52	BB	212	VAL
53	DD	176	LEU
53	DD	221	THR
54	FF	88	MET
54	FF	166	ILE
55	KK	17	LYS
56	MM	61	TYR

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Mol	Chain	Res	Type
56	MM	122	ASP
56	MM	126	GLU
56	MM	127	TYR
57	OO	42	VAL
57	OO	44	VAL
57	OO	53	ILE
58	PP	36	LEU
58	PP	94	VAL
58	PP	110	GLU
58	PP	116	LEU
59	QQ	27	ARG
59	QQ	55	VAL
59	QQ	66	VAL
59	QQ	69	ARG
60	RR	69	ILE
60	RR	126	MET
61	SS	63	GLU
61	SS	104	ASP
61	SS	139	THR
62	TT	4	VAL
62	TT	66	LEU
62	TT	103	VAL
62	TT	114	GLU
62	TT	128	GLN
63	UU	63	ILE
63	UU	72	GLU
63	UU	79	ARG
64	ZZ	42	ASP
66	ee	90	THR
67	aa	7	ASN
67	aa	30	VAL
67	aa	45	VAL
67	aa	63	VAL
67	aa	67	LEU
68	CC	60	TRP
68	CC	83	LEU
68	CC	155	ILE
68	CC	160	LEU
68	CC	163	VAL
68	CC	220	ASP
68	CC	224	THR
68	CC	275	LYS

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Mol	Chain	Res	Type
69	EE	8	HIS
69	EE	12	VAL
69	EE	98	ASN
69	EE	108	ARG
69	EE	131	VAL
69	EE	156	VAL
69	EE	160	ILE
69	EE	214	ASN
69	EE	216	ASN
70	GG	15	LEU
70	GG	31	ARG
70	GG	96	SER
70	GG	97	VAL
70	GG	127	THR
70	GG	155	GLN
70	GG	167	LYS
71	HH	76	GLN
71	HH	77	VAL
71	HH	119	SER
71	HH	126	HIS
71	HH	137	SER
71	HH	176	VAL
72	II	107	THR
72	II	130	THR
73	JJ	94	LEU
73	JJ	112	THR
73	JJ	159	PHE
74	LL	15	THR
74	LL	82	MET
74	LL	137	THR
75	NN	27	LYS
75	NN	32	ASP
75	NN	37	ILE
75	NN	46	THR
75	NN	106	ARG
75	NN	117	LEU
76	VV	13	VAL
76	VV	79	VAL
77	WW	81	VAL
77	WW	121	THR
77	WW	126	LEU
78	XX	58	GLU

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Mol	Chain	Res	Type
78	XX	85	VAL
79	YY	48	TYR
79	YY	51	THR
79	YY	57	VAL
79	YY	68	LYS
79	YY	69	THR
79	YY	76	TYR
79	YY	103	SER
80	W	75	HIS
80	W	78	ILE
80	W	84	THR
80	W	91	GLU
80	W	110	ARG
80	W	178	GLN
81	c	29	PHE
81	c	31	PHE
81	c	43	LYS
81	c	54	LEU
82	u	21	VAL
82	u	62	TYR
82	u	71	VAL
82	u	90	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (106) such sidechains are listed below:

Mol	Chain	Res	Type
7	n	22	GLN
8	B	138	GLN
8	B	175	GLN
8	B	179	HIS
8	B	184	GLN
9	C	142	HIS
9	C	215	ASN
9	C	282	HIS
10	D	111	ASN
10	D	131	ASN
11	E	131	HIS
12	F	55	HIS
12	F	98	ASN
12	F	130	ASN
12	F	162	ASN
13	G	81	ASN

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Mol	Chain	Res	Type
13	G	225	ASN
14	H	189	GLN
15	I	144	ASN
17	L	175	ASN
17	L	205	GLN
18	M	48	GLN
18	M	120	ASN
19	N	99	GLN
19	N	149	GLN
19	N	178	HIS
20	O	26	GLN
20	O	180	GLN
20	O	184	ASN
21	P	28	ASN
21	P	116	HIS
21	P	133	HIS
23	S	37	HIS
23	S	161	HIS
23	S	163	HIS
27	X	57	GLN
27	X	69	ASN
29	Z	127	ASN
30	a	49	HIS
30	a	66	ASN
32	d	18	ASN
33	e	81	ASN
34	f	78	HIS
36	h	107	GLN
40	l	19	GLN
40	l	38	ASN
42	o	51	GLN
42	o	102	GLN
44	r	21	ASN
44	r	30	ASN
44	r	45	HIS
45	s	68	HIS
46	t	103	ASN
46	t	156	ASN
48	ff	91	ASN
49	gg	26	GLN
49	gg	222	ASN
49	gg	296	GLN

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Mol	Chain	Res	Type
50	dd	37	ASN
51	AA	141	ASN
52	BB	43	ASN
52	BB	101	HIS
52	BB	157	GLN
52	BB	159	GLN
53	DD	4	GLN
54	FF	65	GLN
54	FF	203	ASN
55	KK	7	ASN
55	KK	50	GLN
55	KK	77	GLN
56	MM	15	ASN
57	OO	79	GLN
57	OO	94	HIS
58	PP	32	GLN
58	PP	41	GLN
59	QQ	24	HIS
60	RR	93	GLN
62	TT	51	ASN
62	TT	85	ASN
64	ZZ	89	GLN
68	CC	115	GLN
68	CC	172	ASN
69	EE	67	GLN
71	HH	25	GLN
71	HH	97	GLN
71	HH	112	ASN
71	HH	168	HIS
72	II	116	HIS
72	II	138	ASN
72	II	146	GLN
73	JJ	113	GLN
74	LL	11	GLN
74	LL	94	HIS
74	LL	100	ASN
75	NN	13	GLN
75	NN	36	GLN
75	NN	105	ASN
76	VV	47	ASN
77	WW	120	HIS
78	XX	16	HIS

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Mol	Chain	Res	Type
78	XX	63	ASN
78	XX	127	ASN
81	c	107	GLN
82	u	51	ASN
82	u	77	ASN
82	u	78	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A5	1665/1717 (96%)	698 (41%)	66 (3%)
2	A7	119/120 (99%)	30 (25%)	0
3	A8	155/156 (99%)	66 (42%)	4 (2%)
4	B2	1754/1804 (97%)	686 (39%)	43 (2%)
5	A6	1994/2092 (95%)	737 (36%)	44 (2%)
83	Cc	75/76 (98%)	31 (41%)	0
84	Bb	62/65 (95%)	28 (45%)	0
85	Dd	12/13 (92%)	3 (25%)	0
All	All	5836/6043 (96%)	2279 (39%)	157 (2%)

All (2279) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A5	6	C
1	A5	9	C
1	A5	12	A
1	A5	13	U
1	A5	14	C
1	A5	15	A
1	A5	19	G
1	A5	21	G
1	A5	22	G
1	A5	25	A
1	A5	30	C
1	A5	39	A
1	A5	42	A
1	A5	45	U
1	A5	48	G
1	A5	56	A
1	A5	59	A
1	A5	64	A

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Mol	Chain	Res	Type
1	A5	65	A
1	A5	66	A
1	A5	67	C
1	A5	70	A
1	A5	72	C
1	A5	73	A
1	A5	74	G
1	A5	75	G
1	A5	76	A
1	A5	80	C
1	A5	84	A
1	A5	86	U
1	A5	91	G
1	A5	92	C
1	A5	93	G
1	A5	108	A
1	A5	109	G
1	A5	110	C
1	A5	112	C
1	A5	114	G
1	A5	115	C
1	A5	116	G
1	A5	117	C
1	A5	119	G
1	A5	120	A
1	A5	126	C
1	A5	132	G
1	A5	134	G
1	A5	135	G
1	A5	136	C
1	A5	137	G
1	A5	142	G
1	A5	143	C
1	A5	149	A
1	A5	151	G
1	A5	156	G
1	A5	157	U
1	A5	158	A
1	A5	159	C
1	A5	160	G
1	A5	163	A
1	A5	165	A

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Mol	Chain	Res	Type
1	A5	170	C
1	A5	171	U
1	A5	172	C
1	A5	173	C
1	A5	184	U
1	A5	185	C
1	A5	186	G
1	A5	188	G
1	A5	189	G
1	A5	195	C
1	A5	197	A
1	A5	200	U
1	A5	201	C
1	A5	210	C
1	A5	215	C
1	A5	216	C
1	A5	217	C
1	A5	218	A
1	A5	219	G
1	A5	220	C
1	A5	221	C
1	A5	224	U
1	A5	225	G
1	A5	226	G
1	A5	227	A
1	A5	232	G
1	A5	233	U
1	A5	234	G
1	A5	236	G
1	A5	238	C
1	A5	246	G
1	A5	247	G
1	A5	254	G
1	A5	265	C
1	A5	273	U
1	A5	274	C
1	A5	276	C
1	A5	277	G
1	A5	278	G
1	A5	279	A
1	A5	280	G
1	A5	281	U

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Mol	Chain	Res	Type
1	A5	292	G
1	A5	293	G
1	A5	294	G
1	A5	297	U
1	A5	306	A
1	A5	307	A
1	A5	308	G
1	A5	309	C
1	A5	310	G
1	A5	315	G
1	A5	316	U
1	A5	317	A
1	A5	320	C
1	A5	325	U
1	A5	328	A
1	A5	329	A
1	A5	334	A
1	A5	335	A
1	A5	336	A
1	A5	341	G
1	A5	343	C
1	A5	346	G
1	A5	347	A
1	A5	348	G
1	A5	349	A
1	A5	350	C
1	A5	352	G
1	A5	353	A
1	A5	355	A
1	A5	357	U
1	A5	360	A
1	A5	363	A
1	A5	364	G
1	A5	365	U
1	A5	372	A
1	A5	373	G
1	A5	381	U
1	A5	385	A
1	A5	386	A
1	A5	387	G
1	A5	399	G
1	A5	405	U

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Mol	Chain	Res	Type
1	A5	406	C
1	A5	407	A
1	A5	408	A
1	A5	409	G
1	A5	410	A
1	A5	412	G
1	A5	413	G
1	A5	414	C
1	A5	415	G
1	A5	424	U
1	A5	432	U
1	A5	433	A
1	A5	441	G
1	A5	442	G
1	A5	444	G
1	A5	448	G
1	A5	450	G
1	A5	451	C
1	A5	452	A
1	A5	453	G
1	A5	455	C
1	A5	464	G
1	A5	468	U
1	A5	469	C
1	A5	472	C
1	A5	473	C
1	A5	474	C
1	A5	475	G
1	A5	479	G
1	A5	481	G
1	A5	485	C
1	A5	487	G
1	A5	491	G
1	A5	496	G
1	A5	497	G
1	A5	498	C
1	A5	499	G
1	A5	500	G
1	A5	501	C
1	A5	502	C
1	A5	503	C
1	A5	504	G

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Mol	Chain	Res	Type
1	A5	505	G
1	A5	506	C
1	A5	507	G
1	A5	508	G
1	A5	509	A
1	A5	510	U
1	A5	513	U
1	A5	514	U
1	A5	515	C
1	A5	517	C
1	A5	636	G
1	A5	639	U
1	A5	640	C
1	A5	642	G
1	A5	644	G
1	A5	649	A
1	A5	656	C
1	A5	659	G
1	A5	661	C
1	A5	663	G
1	A5	664	G
1	A5	667	A
1	A5	668	C
1	A5	669	C
1	A5	670	G
1	A5	677	G
1	A5	678	C
1	A5	679	C
1	A5	683	C
1	A5	685	C
1	A5	686	A
1	A5	687	U
1	A5	688	U
1	A5	689	U
1	A5	696	C
1	A5	697	G
1	A5	698	G
1	A5	701	G
1	A5	702	U
1	A5	703	G
1	A5	704	C
1	A5	707	C

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Mol	Chain	Res	Type
1	A5	711	A
1	A5	712	C
1	A5	720	G
1	A5	721	G
1	A5	722	G
1	A5	727	C
1	A5	728	U
1	A5	729	G
1	A5	730	G
1	A5	731	G
1	A5	732	A
1	A5	735	G
1	A5	737	C
1	A5	740	G
1	A5	745	G
1	A5	746	A
1	A5	747	A
1	A5	748	G
1	A5	749	G
1	A5	756	G
1	A5	759	G
1	A5	903	C
1	A5	912	G
1	A5	914	U
1	A5	915	A
1	A5	916	C
1	A5	918	G
1	A5	919	C
1	A5	920	C
1	A5	921	C
1	A5	925	C
1	A5	926	G
1	A5	927	G
1	A5	928	C
1	A5	929	A
1	A5	930	G
1	A5	931	C
1	A5	932	A
1	A5	933	G
1	A5	935	A
1	A5	936	C
1	A5	937	U

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Mol	Chain	Res	Type
1	A5	938	C
1	A5	939	G
1	A5	940	C
1	A5	942	G
1	A5	943	A
1	A5	944	A
1	A5	945	U
1	A5	946	C
1	A5	947	C
1	A5	953	C
1	A5	956	A
1	A5	957	G
1	A5	958	G
1	A5	959	G
1	A5	960	A
1	A5	961	G
1	A5	963	G
1	A5	966	A
1	A5	967	C
1	A5	968	C
1	A5	969	C
1	A5	970	G
1	A5	971	U
1	A5	972	C
1	A5	973	G
1	A5	975	C
1	A5	978	G
1	A5	979	C
1	A5	980	U
1	A5	981	C
1	A5	982	U
1	A5	983	C
1	A5	986	C
1	A5	991	C
1	A5	992	C
1	A5	993	G
1	A5	996	G
1	A5	1048	G
1	A5	1072	C
1	A5	1078	A
1	A5	1079	C
1	A5	1081	C

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Mol	Chain	Res	Type
1	A5	1083	U
1	A5	1084	C
1	A5	1100	U
1	A5	1101	C
1	A5	1104	C
1	A5	1105	C
1	A5	1165	G
1	A5	1166	G
1	A5	1167	C
1	A5	1171	G
1	A5	1176	C
1	A5	1177	U
1	A5	1180	C
1	A5	1181	C
1	A5	1182	C
1	A5	1184	A
1	A5	1185	G
1	A5	1186	U
1	A5	1187	G
1	A5	1188	C
1	A5	1189	G
1	A5	1192	C
1	A5	1199	G
1	A5	1205	G
1	A5	1206	C
1	A5	1208	G
1	A5	1209	U
1	A5	1210	C
1	A5	1211	G
1	A5	1212	G
1	A5	1213	G
1	A5	1214	C
1	A5	1215	C
1	A5	1216	C
1	A5	1217	G
1	A5	1220	G
1	A5	1236	C
1	A5	1238	A
1	A5	1239	C
1	A5	1240	G
1	A5	1241	C
1	A5	1242	G

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Mol	Chain	Res	Type
1	A5	1243	C
1	A5	1244	G
1	A5	1245	C
1	A5	1246	G
1	A5	1249	C
1	A5	1265	G
1	A5	1266	G
1	A5	1267	C
1	A5	1268	G
1	A5	1269	G
1	A5	1270	A
1	A5	1271	G
1	A5	1272	C
1	A5	1273	G
1	A5	1274	A
1	A5	1275	G
1	A5	1276	C
1	A5	1282	G
1	A5	1283	G
1	A5	1284	G
1	A5	1285	U
1	A5	1287	G
1	A5	1288	G
1	A5	1289	C
1	A5	1292	C
1	A5	1293	G
1	A5	1294	A
1	A5	1295	C
1	A5	1296	G
1	A5	1297	U
1	A5	1298	C
1	A5	1301	C
1	A5	1302	U
1	A5	1303	A
1	A5	1304	C
1	A5	1308	C
1	A5	1310	C
1	A5	1313	C
1	A5	1322	A
1	A5	1323	A
1	A5	1326	A
1	A5	1328	G

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Mol	Chain	Res	Type
1	A5	1333	A
1	A5	1342	A
1	A5	1344	C
1	A5	1345	A
1	A5	1354	A
1	A5	1357	C
1	A5	1358	G
1	A5	1359	G
1	A5	1362	G
1	A5	1365	C
1	A5	1366	G
1	A5	1367	C
1	A5	1368	A
1	A5	1369	C
1	A5	1370	G
1	A5	1372	A
1	A5	1376	C
1	A5	1377	G
1	A5	1378	C
1	A5	1379	C
1	A5	1380	G
1	A5	1381	U
1	A5	1382	G
1	A5	1387	A
1	A5	1390	G
1	A5	1394	G
1	A5	1397	A
1	A5	1399	G
1	A5	1406	G
1	A5	1407	C
1	A5	1408	G
1	A5	1409	C
1	A5	1410	U
1	A5	1411	C
1	A5	1412	G
1	A5	1420	A
1	A5	1427	A
1	A5	1430	C
1	A5	1433	A
1	A5	1437	C
1	A5	1439	C
1	A5	1452	A

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Mol	Chain	Res	Type
1	A5	1456	C
1	A5	1465	G
1	A5	1466	G
1	A5	1475	G
1	A5	1476	C
1	A5	1478	C
1	A5	1479	G
1	A5	1480	C
1	A5	1481	C
1	A5	1482	G
1	A5	1485	C
1	A5	1486	C
1	A5	1497	A
1	A5	1498	G
1	A5	1501	C
1	A5	1502	G
1	A5	1503	A
1	A5	1504	G
1	A5	1512	G
1	A5	1514	U
1	A5	1516	G
1	A5	1518	A
1	A5	1523	A
1	A5	1525	A
1	A5	1530	G
1	A5	1531	U
1	A5	1534	A
1	A5	1535	C
1	A5	1547	A
1	A5	1552	G
1	A5	1553	A
1	A5	1555	G
1	A5	1556	C
1	A5	1566	C
1	A5	1568	C
1	A5	1571	G
1	A5	1572	U
1	A5	1573	G
1	A5	1574	G
1	A5	1577	G
1	A5	1578	U
1	A5	1588	U

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Mol	Chain	Res	Type
1	A5	1591	U
1	A5	1593	A
1	A5	1596	U
1	A5	1597	G
1	A5	1601	A
1	A5	1607	C
1	A5	1612	G
1	A5	1613	A
1	A5	1614	C
1	A5	1624	G
1	A5	1625	G
1	A5	1626	G
1	A5	1631	A
1	A5	1632	A
1	A5	1633	G
1	A5	1634	A
1	A5	1637	A
1	A5	1638	A
1	A5	1640	C
1	A5	1641	G
1	A5	1649	U
1	A5	1650	A
1	A5	1654	G
1	A5	1660	U
1	A5	1661	C
1	A5	1663	C
1	A5	1667	G
1	A5	1670	G
1	A5	1676	C
1	A5	1677	U
1	A5	1679	A
1	A5	1680	G
1	A5	1681	G
1	A5	1682	A
1	A5	1683	U
1	A5	1691	G
1	A5	1692	C
1	A5	1694	C
1	A5	1695	U
1	A5	1697	G
1	A5	1698	C
1	A5	1699	A

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Mol	Chain	Res	Type
1	A5	1700	G
1	A5	1724	G
1	A5	1725	U
1	A5	1727	U
1	A5	1731	C
1	A5	1735	U
1	A5	1736	A
1	A5	1740	C
1	A5	1742	A
1	A5	1750	G
1	A5	1751	A
1	A5	1752	G
1	A5	1753	G
1	A5	1754	U
1	A5	1755	C
1	A5	1756	U
1	A5	1760	G
1	A5	1761	G
1	A5	1762	C
1	A5	1765	A
1	A5	1766	A
1	A5	1768	C
1	A5	1769	G
1	A5	1770	A
1	A5	1772	C
1	A5	1773	U
1	A5	1775	A
1	A5	1776	A
1	A5	1777	C
1	A5	1781	U
1	A5	1787	A
1	A5	1789	C
1	A5	1803	G
1	A5	1804	A
1	A5	1805	A
1	A5	1806	G
1	A5	1808	C
1	A5	1810	G
1	A5	1811	G
1	A5	1812	C
1	A5	1813	U
1	A5	1814	C

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Mol	Chain	Res	Type
1	A5	1815	G
1	A5	1816	C
1	A5	1817	U
1	A5	1819	G
1	A5	1821	G
1	A5	1822	U
1	A5	1828	C
1	A5	1829	G
1	A5	1833	G
1	A5	1835	G
1	A5	1836	G
1	A5	1841	C
1	A5	1842	G
1	A5	1843	A
1	A5	1847	C
1	A5	1848	C
1	A5	1853	G
1	A5	1854	G
1	A5	1855	G
1	A5	1869	G
1	A5	1878	G
1	A5	1881	C
1	A5	1883	G
1	A5	1888	A
1	A5	1889	U
1	A5	1890	G
1	A5	1893	C
1	A5	1894	C
1	A5	1897	A
1	A5	1898	C
1	A5	1899	G
1	A5	1902	G
1	A5	1907	A
1	A5	1912	G
1	A5	1915	C
1	A5	1916	G
1	A5	1917	A
1	A5	1918	U
1	A5	1919	G
1	A5	1920	C
1	A5	1921	C
1	A5	1922	G

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Mol	Chain	Res	Type
1	A5	1923	A
1	A5	1928	C
1	A5	1930	U
1	A5	1931	C
1	A5	1932	A
1	A5	1936	C
1	A5	1939	A
1	A5	1940	G
1	A5	1944	A
1	A5	1946	G
1	A5	1947	U
1	A5	1948	G
1	A5	1949	U
1	A5	1951	G
1	A5	1952	G
1	A5	1953	U
1	A5	1956	A
1	A5	1958	A
1	A5	1960	A
1	A5	1961	G
1	A5	1962	A
1	A5	1964	A
1	A5	1967	A
1	A5	1970	A
1	A5	1971	C
1	A5	1973	G
1	A5	1974	U
1	A5	1975	G
1	A5	1976	G
1	A5	1977	C
1	A5	1979	A
1	A5	1980	U
1	A5	1981	G
1	A5	1982	G
1	A5	1983	A
1	A5	1984	A
1	A5	1985	G
1	A5	1987	C
1	A5	1989	G
1	A5	1990	A
1	A5	1991	A
1	A5	1993	C

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Mol	Chain	Res	Type
1	A5	1994	C
1	A5	1995	G
1	A5	1996	C
1	A5	1997	U
1	A5	1998	A
1	A5	1999	A
1	A5	2000	G
1	A5	2001	G
1	A5	2002	A
1	A5	2003	G
1	A5	2005	G
1	A5	2008	U
1	A5	2010	A
1	A5	2011	C
1	A5	2012	A
1	A5	2016	C
1	A5	2020	U
1	A5	2021	G
1	A5	2022	C
1	A5	2024	G
1	A5	2025	A
1	A5	2026	A
1	A5	2033	A
1	A5	2034	G
1	A5	2042	A
1	A5	2043	A
1	A5	2044	U
1	A5	2045	G
1	A5	2046	G
1	A5	2047	A
1	A5	2048	U
1	A5	2051	C
1	A5	2052	G
1	A5	2054	U
1	A5	2056	G
1	A5	2062	C
1	A5	2064	G
1	A5	2065	G
1	A5	2069	A
1	A5	2070	U
1	A5	2071	A
1	A5	2072	C

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Mol	Chain	Res	Type
1	A5	2073	C
1	A5	2076	G
1	A5	2079	G
1	A5	2084	C
1	A5	2085	G
1	A5	2088	C
1	A5	2089	G
1	A5	2090	U
2	A7	7	G
2	A7	8	G
2	A7	11	A
2	A7	19	C
2	A7	22	A
2	A7	23	A
2	A7	28	C
2	A7	35	U
2	A7	39	C
2	A7	40	U
2	A7	41	G
2	A7	49	A
2	A7	52	C
2	A7	53	U
2	A7	54	A
2	A7	61	G
2	A7	62	U
2	A7	64	G
2	A7	73	U
2	A7	75	G
2	A7	76	U
2	A7	91	C
2	A7	93	G
2	A7	97	G
2	A7	100	A
2	A7	109	U
2	A7	110	G
2	A7	117	G
2	A7	118	C
2	A7	121	U
3	A8	14	U
3	A8	15	G
3	A8	16	G
3	A8	17	A

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Mol	Chain	Res	Type
3	A8	20	A
3	A8	22	U
3	A8	23	C
3	A8	24	G
3	A8	31	G
3	A8	34	U
3	A8	35	C
3	A8	38	U
3	A8	39	G
3	A8	40	A
3	A8	43	A
3	A8	47	C
3	A8	49	G
3	A8	51	U
3	A8	59	A
3	A8	60	G
3	A8	61	A
3	A8	62	A
3	A8	63	U
3	A8	68	G
3	A8	70	G
3	A8	71	A
3	A8	72	A
3	A8	74	U
3	A8	75	G
3	A8	79	G
3	A8	80	A
3	A8	81	C
3	A8	82	A
3	A8	83	C
3	A8	84	A
3	A8	85	U
3	A8	86	U
3	A8	87	G
3	A8	88	A
3	A8	93	C
3	A8	94	G
3	A8	96	C
3	A8	97	A
3	A8	98	C
3	A8	103	A
3	A8	104	A

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Mol	Chain	Res	Type
3	A8	105	C
3	A8	106	G
3	A8	109	C
3	A8	110	U
3	A8	111	U
3	A8	112	G
3	A8	114	G
3	A8	122	G
3	A8	124	U
3	A8	125	C
3	A8	126	C
3	A8	127	U
3	A8	130	C
3	A8	137	A
3	A8	147	G
3	A8	148	A
3	A8	150	C
3	A8	154	G
3	A8	156	U
3	A8	157	U
4	B2	3	C
4	B2	4	C
4	B2	5	U
4	B2	10	G
4	B2	14	C
4	B2	26	U
4	B2	33	G
4	B2	41	G
4	B2	42	A
4	B2	44	U
4	B2	46	A
4	B2	49	C
4	B2	56	G
4	B2	60	A
4	B2	61	A
4	B2	62	G
4	B2	64	A
4	B2	65	C
4	B2	66	G
4	B2	67	C
4	B2	68	A
4	B2	69	C

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Mol	Chain	Res	Type
4	B2	71	G
4	B2	72	C
4	B2	73	C
4	B2	74	G
4	B2	76	U
4	B2	78	C
4	B2	79	A
4	B2	80	G
4	B2	83	A
4	B2	85	A
4	B2	86	C
4	B2	93	U
4	B2	95	G
4	B2	98	C
4	B2	99	A
4	B2	103	A
4	B2	113	G
4	B2	114	G
4	B2	115	U
4	B2	117	C
4	B2	118	C
4	B2	122	G
4	B2	125	C
4	B2	126	G
4	B2	127	C
4	B2	141	A
4	B2	142	C
4	B2	143	U
4	B2	144	U
4	B2	145	G
4	B2	146	G
4	B2	147	A
4	B2	149	A
4	B2	155	G
4	B2	158	A
4	B2	160	U
4	B2	163	U
4	B2	167	G
4	B2	170	A
4	B2	171	A
4	B2	176	U
4	B2	180	G

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Mol	Chain	Res	Type
4	B2	181	A
4	B2	182	C
4	B2	183	G
4	B2	184	G
4	B2	189	U
4	B2	190	G
4	B2	192	C
4	B2	199	C
4	B2	212	C
4	B2	213	G
4	B2	216	C
4	B2	226	A
4	B2	227	U
4	B2	228	C
4	B2	229	A
4	B2	230	A
4	B2	231	A
4	B2	232	A
4	B2	235	A
4	B2	237	C
4	B2	238	C
4	B2	239	C
4	B2	241	G
4	B2	242	U
4	B2	243	C
4	B2	244	A
4	B2	282	G
4	B2	284	C
4	B2	285	U
4	B2	286	U
4	B2	287	U
4	B2	288	G
4	B2	290	U
4	B2	291	G
4	B2	292	A
4	B2	294	U
4	B2	295	C
4	B2	302	A
4	B2	304	C
4	B2	305	U
4	B2	306	C
4	B2	307	G

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Mol	Chain	Res	Type
4	B2	308	G
4	B2	309	G
4	B2	312	G
4	B2	313	A
4	B2	318	A
4	B2	319	C
4	B2	322	C
4	B2	323	C
4	B2	324	C
4	B2	325	C
4	B2	326	C
4	B2	328	U
4	B2	330	G
4	B2	332	G
4	B2	338	G
4	B2	340	C
4	B2	343	A
4	B2	347	G
4	B2	348	A
4	B2	349	A
4	B2	350	C
4	B2	354	U
4	B2	362	C
4	B2	364	A
4	B2	367	U
4	B2	368	U
4	B2	370	G
4	B2	373	G
4	B2	376	A
4	B2	380	G
4	B2	383	G
4	B2	385	G
4	B2	386	C
4	B2	398	A
4	B2	399	C
4	B2	400	C
4	B2	409	C
4	B2	410	G
4	B2	413	G
4	B2	418	A
4	B2	426	A
4	B2	428	U

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Mol	Chain	Res	Type
4	B2	436	G
4	B2	448	A
4	B2	450	C
4	B2	452	G
4	B2	465	A
4	B2	466	G
4	B2	467	G
4	B2	471	G
4	B2	472	C
4	B2	473	A
4	B2	474	G
4	B2	475	C
4	B2	484	A
4	B2	487	U
4	B2	489	A
4	B2	495	U
4	B2	500	A
4	B2	501	C
4	B2	507	G
4	B2	508	A
4	B2	510	G
4	B2	516	A
4	B2	522	A
4	B2	523	A
4	B2	525	A
4	B2	526	A
4	B2	527	C
4	B2	528	A
4	B2	530	U
4	B2	532	C
4	B2	533	A
4	B2	534	G
4	B2	535	G
4	B2	550	C
4	B2	552	G
4	B2	553	U
4	B2	558	G
4	B2	559	G
4	B2	561	A
4	B2	562	U
4	B2	563	G
4	B2	564	A

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Mol	Chain	Res	Type
4	B2	568	C
4	B2	571	U
4	B2	572	U
4	B2	574	A
4	B2	576	A
4	B2	580	U
4	B2	581	U
4	B2	582	U
4	B2	583	A
4	B2	584	A
4	B2	588	G
4	B2	589	G
4	B2	590	A
4	B2	591	U
4	B2	592	C
4	B2	593	C
4	B2	594	A
4	B2	600	G
4	B2	603	C
4	B2	604	A
4	B2	605	A
4	B2	606	G
4	B2	607	U
4	B2	608	C
4	B2	609	U
4	B2	613	G
4	B2	614	C
4	B2	617	G
4	B2	618	C
4	B2	619	A
4	B2	623	G
4	B2	627	U
4	B2	628	A
4	B2	629	A
4	B2	631	U
4	B2	632	C
4	B2	634	A
4	B2	643	A
4	B2	644	G
4	B2	645	C
4	B2	654	A
4	B2	655	A

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Mol	Chain	Res	Type
4	B2	656	G
4	B2	660	C
4	B2	666	U
4	B2	668	A
4	B2	669	A
4	B2	670	A
4	B2	671	A
4	B2	672	A
4	B2	673	G
4	B2	678	U
4	B2	684	G
4	B2	687	C
4	B2	688	U
4	B2	689	U
4	B2	691	G
4	B2	692	G
4	B2	693	A
4	B2	697	G
4	B2	698	G
4	B2	699	C
4	B2	730	C
4	B2	731	G
4	B2	734	C
4	B2	739	C
4	B2	740	C
4	B2	741	C
4	B2	742	U
4	B2	743	U
4	B2	744	G
4	B2	747	U
4	B2	748	C
4	B2	749	U
4	B2	752	G
4	B2	753	C
4	B2	788	G
4	B2	791	C
4	B2	793	G
4	B2	796	G
4	B2	797	C
4	B2	798	G
4	B2	799	U
4	B2	800	U

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Mol	Chain	Res	Type
4	B2	804	U
4	B2	807	G
4	B2	810	A
4	B2	811	A
4	B2	812	A
4	B2	816	A
4	B2	821	G
4	B2	822	U
4	B2	823	U
4	B2	824	C
4	B2	826	A
4	B2	827	A
4	B2	829	C
4	B2	830	A
4	B2	831	G
4	B2	833	C
4	B2	834	C
4	B2	835	C
4	B2	836	G
4	B2	837	A
4	B2	838	G
4	B2	839	C
4	B2	840	C
4	B2	841	G
4	B2	844	U
4	B2	845	G
4	B2	846	G
4	B2	847	A
4	B2	852	G
4	B2	859	G
4	B2	868	G
4	B2	869	A
4	B2	870	A
4	B2	871	U
4	B2	873	G
4	B2	875	A
4	B2	877	C
4	B2	879	C
4	B2	881	G
4	B2	888	U
4	B2	890	U
4	B2	892	U

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Mol	Chain	Res	Type
4	B2	898	U
4	B2	903	A
4	B2	909	G
4	B2	910	G
4	B2	911	C
4	B2	913	A
4	B2	914	U
4	B2	917	U
4	B2	919	A
4	B2	920	A
4	B2	921	G
4	B2	927	C
4	B2	932	G
4	B2	933	G
4	B2	934	G
4	B2	942	G
4	B2	943	U
4	B2	944	A
4	B2	949	G
4	B2	954	U
4	B2	955	A
4	B2	956	G
4	B2	961	G
4	B2	962	A
4	B2	969	U
4	B2	970	G
4	B2	971	G
4	B2	976	G
4	B2	978	G
4	B2	979	C
4	B2	987	A
4	B2	989	C
4	B2	990	A
4	B2	991	G
4	B2	992	A
4	B2	999	G
4	B2	1001	A
4	B2	1014	G
4	B2	1019	C
4	B2	1021	U
4	B2	1022	U
4	B2	1023	A

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Mol	Chain	Res	Type
4	B2	1024	A
4	B2	1036	A
4	B2	1039	C
4	B2	1040	G
4	B2	1045	U
4	B2	1049	A
4	B2	1050	A
4	B2	1053	C
4	B2	1059	G
4	B2	1060	A
4	B2	1061	U
4	B2	1062	A
4	B2	1063	C
4	B2	1073	U
4	B2	1077	A
4	B2	1078	C
4	B2	1082	A
4	B2	1083	A
4	B2	1084	A
4	B2	1085	C
4	B2	1086	G
4	B2	1087	A
4	B2	1088	U
4	B2	1089	G
4	B2	1090	C
4	B2	1096	G
4	B2	1097	G
4	B2	1100	A
4	B2	1104	G
4	B2	1109	C
4	B2	1110	G
4	B2	1111	U
4	B2	1115	U
4	B2	1116	C
4	B2	1117	C
4	B2	1118	C
4	B2	1123	C
4	B2	1124	C
4	B2	1125	C
4	B2	1126	G
4	B2	1127	C
4	B2	1129	G

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Mol	Chain	Res	Type
4	B2	1133	A
4	B2	1138	C
4	B2	1139	C
4	B2	1143	A
4	B2	1146	C
4	B2	1148	A
4	B2	1150	A
4	B2	1153	C
4	B2	1154	U
4	B2	1155	U
4	B2	1157	G
4	B2	1158	G
4	B2	1165	G
4	B2	1166	G
4	B2	1168	G
4	B2	1170	A
4	B2	1172	U
4	B2	1181	A
4	B2	1182	A
4	B2	1183	A
4	B2	1184	G
4	B2	1194	A
4	B2	1195	A
4	B2	1199	A
4	B2	1202	U
4	B2	1204	A
4	B2	1206	G
4	B2	1207	G
4	B2	1214	A
4	B2	1215	C
4	B2	1216	C
4	B2	1217	A
4	B2	1221	G
4	B2	1222	G
4	B2	1224	G
4	B2	1227	G
4	B2	1228	A
4	B2	1240	A
4	B2	1242	U
4	B2	1243	U
4	B2	1244	U
4	B2	1247	C

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Mol	Chain	Res	Type
4	B2	1248	U
4	B2	1250	A
4	B2	1251	A
4	B2	1253	A
4	B2	1254	C
4	B2	1256	G
4	B2	1257	G
4	B2	1259	A
4	B2	1260	A
4	B2	1261	C
4	B2	1262	C
4	B2	1263	U
4	B2	1264	C
4	B2	1265	A
4	B2	1269	G
4	B2	1270	G
4	B2	1272	C
4	B2	1274	G
4	B2	1275	G
4	B2	1277	C
4	B2	1283	C
4	B2	1284	A
4	B2	1285	G
4	B2	1286	G
4	B2	1287	A
4	B2	1298	G
4	B2	1299	A
4	B2	1301	A
4	B2	1302	G
4	B2	1303	C
4	B2	1308	U
4	B2	1309	C
4	B2	1310	U
4	B2	1312	G
4	B2	1315	U
4	B2	1322	G
4	B2	1331	C
4	B2	1332	A
4	B2	1333	U
4	B2	1342	U
4	B2	1343	U
4	B2	1345	G

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Mol	Chain	Res	Type
4	B2	1348	G
4	B2	1352	G
4	B2	1354	G
4	B2	1355	C
4	B2	1356	G
4	B2	1357	A
4	B2	1358	U
4	B2	1360	U
4	B2	1364	U
4	B2	1371	U
4	B2	1372	U
4	B2	1378	A
4	B2	1382	A
4	B2	1394	G
4	B2	1395	C
4	B2	1396	A
4	B2	1397	U
4	B2	1398	G
4	B2	1401	A
4	B2	1402	A
4	B2	1404	U
4	B2	1405	A
4	B2	1408	U
4	B2	1410	C
4	B2	1411	G
4	B2	1412	C
4	B2	1416	C
4	B2	1417	C
4	B2	1418	C
4	B2	1419	C
4	B2	1424	G
4	B2	1425	G
4	B2	1426	U
4	B2	1430	C
4	B2	1431	G
4	B2	1435	C
4	B2	1437	C
4	B2	1438	A
4	B2	1441	U
4	B2	1442	U
4	B2	1444	U
4	B2	1445	U

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Mol	Chain	Res	Type
4	B2	1446	A
4	B2	1447	G
4	B2	1449	G
4	B2	1453	C
4	B2	1454	A
4	B2	1455	A
4	B2	1457	U
4	B2	1463	U
4	B2	1464	C
4	B2	1466	G
4	B2	1473	G
4	B2	1474	A
4	B2	1475	G
4	B2	1476	A
4	B2	1477	U
4	B2	1478	U
4	B2	1485	U
4	B2	1487	A
4	B2	1489	A
4	B2	1490	G
4	B2	1491	G
4	B2	1494	U
4	B2	1495	G
4	B2	1496	U
4	B2	1497	G
4	B2	1498	A
4	B2	1500	G
4	B2	1507	G
4	B2	1509	U
4	B2	1511	U
4	B2	1519	U
4	B2	1520	G
4	B2	1521	C
4	B2	1523	C
4	B2	1531	A
4	B2	1533	A
4	B2	1535	U
4	B2	1536	G
4	B2	1538	C
4	B2	1539	U
4	B2	1540	G
4	B2	1541	G

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Mol	Chain	Res	Type
4	B2	1544	C
4	B2	1545	A
4	B2	1548	G
4	B2	1550	G
4	B2	1552	G
4	B2	1553	C
4	B2	1555	U
4	B2	1556	A
4	B2	1557	C
4	B2	1558	C
4	B2	1560	U
4	B2	1565	C
4	B2	1567	G
4	B2	1569	A
4	B2	1570	G
4	B2	1574	C
4	B2	1575	G
4	B2	1577	G
4	B2	1578	U
4	B2	1579	A
4	B2	1580	A
4	B2	1582	C
4	B2	1585	U
4	B2	1586	U
4	B2	1587	G
4	B2	1588	A
4	B2	1592	C
4	B2	1597	C
4	B2	1598	G
4	B2	1599	U
4	B2	1600	G
4	B2	1601	A
4	B2	1602	U
4	B2	1604	G
4	B2	1606	G
4	B2	1607	A
4	B2	1621	U
4	B2	1622	U
4	B2	1623	A
4	B2	1624	U
4	B2	1629	C
4	B2	1630	A

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Mol	Chain	Res	Type
4	B2	1632	G
4	B2	1637	A
4	B2	1638	G
4	B2	1639	G
4	B2	1640	A
4	B2	1641	A
4	B2	1642	U
4	B2	1643	U
4	B2	1647	A
4	B2	1648	G
4	B2	1649	U
4	B2	1660	C
4	B2	1663	A
4	B2	1664	A
4	B2	1665	G
4	B2	1666	C
4	B2	1669	G
4	B2	1671	G
4	B2	1673	U
4	B2	1679	A
4	B2	1682	C
4	B2	1683	C
4	B2	1690	U
4	B2	1691	U
4	B2	1693	G
4	B2	1694	U
4	B2	1695	A
4	B2	1698	C
4	B2	1699	A
4	B2	1700	C
4	B2	1701	C
4	B2	1702	G
4	B2	1706	G
4	B2	1722	G
4	B2	1725	U
4	B2	1735	A
4	B2	1744	G
4	B2	1748	G
4	B2	1751	C
4	B2	1753	C
4	B2	1754	G
4	B2	1755	C

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Mol	Chain	Res	Type
4	B2	1756	C
4	B2	1757	G
4	B2	1783	C
4	B2	1785	C
4	B2	1786	U
4	B2	1790	A
4	B2	1798	C
4	B2	1805	G
4	B2	1806	A
4	B2	1808	U
4	B2	1823	A
4	B2	1824	A
4	B2	1825	A
4	B2	1826	G
4	B2	1829	G
4	B2	1831	A
4	B2	1833	C
4	B2	1834	A
4	B2	1835	A
4	B2	1836	G
4	B2	1837	G
4	B2	1838	U
4	B2	1839	U
4	B2	1851	A
4	B2	1852	C
4	B2	1854	U
4	B2	1861	G
4	B2	1862	G
4	B2	1863	A
4	B2	1864	U
4	B2	1865	C
4	B2	1866	A
4	B2	1867	U
4	B2	1869	A
5	A6	2263	A
5	A6	2264	C
5	A6	2265	G
5	A6	2266	C
5	A6	2267	U
5	A6	2268	A
5	A6	2269	C
5	A6	2270	G

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Mol	Chain	Res	Type
5	A6	2279	A
5	A6	2288	G
5	A6	2289	C
5	A6	2290	C
5	A6	2297	G
5	A6	2299	G
5	A6	2300	A
5	A6	2301	G
5	A6	2303	C
5	A6	2304	U
5	A6	2306	G
5	A6	2307	A
5	A6	2313	A
5	A6	2314	G
5	A6	2317	C
5	A6	2318	G
5	A6	2319	C
5	A6	2320	G
5	A6	2322	G
5	A6	2327	G
5	A6	2331	G
5	A6	2332	A
5	A6	2333	G
5	A6	2342	G
5	A6	2343	G
5	A6	2344	U
5	A6	2347	A
5	A6	2348	G
5	A6	2351	C
5	A6	2358	G
5	A6	2360	A
5	A6	2369	U
5	A6	2370	A
5	A6	2371	U
5	A6	2377	C
5	A6	2382	A
5	A6	2383	C
5	A6	2384	U
5	A6	2391	G
5	A6	2392	C
5	A6	2394	G
5	A6	2395	A

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Mol	Chain	Res	Type
5	A6	2396	A
5	A6	2397	G
5	A6	2399	G
5	A6	2401	A
5	A6	2402	G
5	A6	2403	A
5	A6	2404	A
5	A6	2407	G
5	A6	2408	U
5	A6	2409	U
5	A6	2411	C
5	A6	2415	U
5	A6	2416	G
5	A6	2417	A
5	A6	2422	C
5	A6	2423	A
5	A6	2424	G
5	A6	2425	U
5	A6	2428	A
5	A6	2437	C
5	A6	2440	U
5	A6	2441	C
5	A6	2443	G
5	A6	2450	G
5	A6	2455	G
5	A6	2460	A
5	A6	2462	C
5	A6	2463	G
5	A6	2469	C
5	A6	2470	C
5	A6	2471	G
5	A6	2474	G
5	A6	2475	G
5	A6	2476	G
5	A6	2477	G
5	A6	2479	G
5	A6	2488	C
5	A6	2489	C
5	A6	2490	U
5	A6	2503	G
5	A6	2504	C
5	A6	2505	C

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Mol	Chain	Res	Type
5	A6	2506	G
5	A6	2507	A
5	A6	2511	A
5	A6	2512	A
5	A6	2513	A
5	A6	2514	G
5	A6	2515	G
5	A6	2517	A
5	A6	2523	G
5	A6	2529	A
5	A6	2531	C
5	A6	2532	C
5	A6	2533	C
5	A6	2544	G
5	A6	2546	G
5	A6	2547	G
5	A6	2551	A
5	A6	2552	G
5	A6	2553	A
5	A6	2554	U
5	A6	2556	G
5	A6	2557	U
5	A6	2560	C
5	A6	2561	C
5	A6	2575	U
5	A6	2577	C
5	A6	2580	U
5	A6	2581	A
5	A6	2583	C
5	A6	2586	G
5	A6	2587	A
5	A6	2588	C
5	A6	2589	C
5	A6	2601	A
5	A6	2611	A
5	A6	2612	G
5	A6	2614	C
5	A6	2616	C
5	A6	2618	G
5	A6	2619	G
5	A6	2621	A
5	A6	2622	G

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Mol	Chain	Res	Type
5	A6	2627	C
5	A6	2631	U
5	A6	2632	U
5	A6	2633	U
5	A6	2635	U
5	A6	2637	U
5	A6	2638	G
5	A6	2639	U
5	A6	2641	A
5	A6	2647	A
5	A6	2648	G
5	A6	2649	G
5	A6	2652	G
5	A6	2653	C
5	A6	2657	G
5	A6	2658	G
5	A6	2659	A
5	A6	2660	A
5	A6	2661	U
5	A6	2662	G
5	A6	2664	G
5	A6	2669	C
5	A6	2670	C
5	A6	2671	C
5	A6	2672	C
5	A6	2673	G
5	A6	2674	A
5	A6	2675	G
5	A6	2677	G
5	A6	2684	C
5	A6	2686	G
5	A6	2687	C
5	A6	2689	C
5	A6	2692	U
5	A6	2694	G
5	A6	2695	A
5	A6	2696	A
5	A6	2697	A
5	A6	2708	U
5	A6	2710	C
5	A6	2711	G
5	A6	2712	G

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Mol	Chain	Res	Type
5	A6	2713	C
5	A6	2716	C
5	A6	2719	C
5	A6	2721	G
5	A6	2724	G
5	A6	2725	A
5	A6	2726	G
5	A6	2734	U
5	A6	2735	G
5	A6	2736	G
5	A6	2740	U
5	A6	2741	U
5	A6	2742	G
5	A6	2743	A
5	A6	2744	A
5	A6	2748	C
5	A6	2752	G
5	A6	2753	G
5	A6	2754	G
5	A6	2755	A
5	A6	2757	A
5	A6	2758	G
5	A6	2759	G
5	A6	2760	G
5	A6	2762	G
5	A6	2763	U
5	A6	2766	A
5	A6	2767	U
5	A6	2769	U
5	A6	2770	C
5	A6	2772	C
5	A6	2773	G
5	A6	2777	G
5	A6	2787	A
5	A6	2788	U
5	A6	2789	A
5	A6	2790	U
5	A6	2794	C
5	A6	2798	A
5	A6	2799	G
5	A6	2800	G
5	A6	2805	C

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Mol	Chain	Res	Type
5	A6	2806	A
5	A6	2811	G
5	A6	2814	C
5	A6	2816	G
5	A6	2824	C
5	A6	2826	U
5	A6	2828	U
5	A6	2829	U
5	A6	2833	A
5	A6	2835	A
5	A6	2838	G
5	A6	2842	G
5	A6	2845	A
5	A6	2846	G
5	A6	2847	G
5	A6	2849	A
5	A6	2850	A
5	A6	2855	G
5	A6	2863	G
5	A6	2869	U
5	A6	2870	A
5	A6	2876	G
5	A6	2879	A
5	A6	2880	U
5	A6	2881	A
5	A6	2882	A
5	A6	2887	U
5	A6	2888	G
5	A6	2889	G
5	A6	2890	C
5	A6	2891	U
5	A6	2892	C
5	A6	2894	A
5	A6	2897	G
5	A6	2899	C
5	A6	2902	G
5	A6	2903	G
5	A6	2904	U
5	A6	2905	C
5	A6	3590	G
5	A6	3591	C
5	A6	3592	G

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Mol	Chain	Res	Type
5	A6	3593	C
5	A6	3594	C
5	A6	3595	U
5	A6	3596	A
5	A6	3597	G
5	A6	3605	C
5	A6	3606	U
5	A6	3611	A
5	A6	3613	U
5	A6	3616	U
5	A6	3618	C
5	A6	3619	G
5	A6	3620	G
5	A6	3625	G
5	A6	3626	G
5	A6	3630	A
5	A6	3635	A
5	A6	3636	C
5	A6	3639	U
5	A6	3646	A
5	A6	3662	A
5	A6	3664	G
5	A6	3672	G
5	A6	3673	C
5	A6	3674	G
5	A6	3678	G
5	A6	3680	U
5	A6	3683	C
5	A6	3691	G
5	A6	3692	A
5	A6	3697	U
5	A6	3698	G
5	A6	3709	U
5	A6	3710	G
5	A6	3712	A
5	A6	3713	U
5	A6	3714	G
5	A6	3722	G
5	A6	3733	A
5	A6	3746	A
5	A6	3747	A
5	A6	3748	A

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Mol	Chain	Res	Type
5	A6	3750	G
5	A6	3756	A
5	A6	3759	A
5	A6	3760	A
5	A6	3761	C
5	A6	3772	U
5	A6	3773	U
5	A6	3774	A
5	A6	3776	G
5	A6	3777	G
5	A6	3778	U
5	A6	3780	G
5	A6	3783	A
5	A6	3784	A
5	A6	3785	A
5	A6	3786	U
5	A6	3788	C
5	A6	3789	C
5	A6	3790	U
5	A6	3791	C
5	A6	3799	A
5	A6	3800	A
5	A6	3802	U
5	A6	3804	G
5	A6	3810	C
5	A6	3811	G
5	A6	3812	C
5	A6	3817	A
5	A6	3818	U
5	A6	3819	G
5	A6	3838	U
5	A6	3839	G
5	A6	3840	U
5	A6	3843	C
5	A6	3858	C
5	A6	3860	A
5	A6	3867	A
5	A6	3868	G
5	A6	3877	A
5	A6	3878	C
5	A6	3879	G
5	A6	3880	G

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Mol	Chain	Res	Type
5	A6	3884	U
5	A6	3889	G
5	A6	3890	A
5	A6	3895	G
5	A6	3897	G
5	A6	3898	G
5	A6	3901	A
5	A6	3902	A
5	A6	3905	A
5	A6	3906	A
5	A6	3907	G
5	A6	3908	A
5	A6	3915	U
5	A6	3922	G
5	A6	3923	A
5	A6	3925	U
5	A6	3926	C
5	A6	3938	G
5	A6	3946	G
5	A6	3947	A
5	A6	3955	G
5	A6	3956	G
5	A6	3957	U
5	A6	3958	G
5	A6	3959	U
5	A6	3960	A
5	A6	3961	G
5	A6	3962	A
5	A6	3963	A
5	A6	3964	U
5	A6	3965	A
5	A6	3966	A
5	A6	3967	G
5	A6	3972	A
5	A6	4037	C
5	A6	4046	A
5	A6	4047	A
5	A6	4048	A
5	A6	4049	U
5	A6	4052	C
5	A6	4053	A
5	A6	4056	A

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Mol	Chain	Res	Type
5	A6	4057	C
5	A6	4059	C
5	A6	4072	C
5	A6	4073	A
5	A6	4076	G
5	A6	4077	A
5	A6	4083	U
5	A6	4085	A
5	A6	4086	G
5	A6	4087	G
5	A6	4088	C
5	A6	4089	G
5	A6	4092	G
5	A6	4104	G
5	A6	4105	A
5	A6	4106	G
5	A6	4107	G
5	A6	4114	C
5	A6	4115	G
5	A6	4116	C
5	A6	4117	U
5	A6	4118	U
5	A6	4119	C
5	A6	4120	U
5	A6	4121	G
5	A6	4122	G
5	A6	4123	C
5	A6	4125	C
5	A6	4127	A
5	A6	4128	A
5	A6	4142	C
5	A6	4144	C
5	A6	4145	C
5	A6	4154	G
5	A6	4157	A
5	A6	4163	U
5	A6	4164	C
5	A6	4165	C
5	A6	4170	A
5	A6	4171	C
5	A6	4176	C
5	A6	4177	C

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Mol	Chain	Res	Type
5	A6	4183	G
5	A6	4184	G
5	A6	4187	G
5	A6	4191	G
5	A6	4194	U
5	A6	4205	A
5	A6	4206	C
5	A6	4208	U
5	A6	4212	A
5	A6	4213	A
5	A6	4225	G
5	A6	4229	U
5	A6	4230	C
5	A6	4231	C
5	A6	4232	U
5	A6	4233	A
5	A6	4243	C
5	A6	4246	G
5	A6	4247	G
5	A6	4250	G
5	A6	4252	C
5	A6	4253	A
5	A6	4254	G
5	A6	4255	A
5	A6	4258	C
5	A6	4261	C
5	A6	4266	G
5	A6	4267	G
5	A6	4268	A
5	A6	4271	A
5	A6	4273	A
5	A6	4276	G
5	A6	4277	G
5	A6	4282	A
5	A6	4286	C
5	A6	4289	U
5	A6	4291	G
5	A6	4292	A
5	A6	4296	U
5	A6	4297	G
5	A6	4299	U
5	A6	4303	C

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Mol	Chain	Res	Type
5	A6	4304	A
5	A6	4305	G
5	A6	4306	U
5	A6	4308	C
5	A6	4314	C
5	A6	4316	G
5	A6	4317	A
5	A6	4319	C
5	A6	4320	G
5	A6	4321	U
5	A6	4322	G
5	A6	4323	A
5	A6	4326	G
5	A6	4330	G
5	A6	4332	C
5	A6	4335	C
5	A6	4336	A
5	A6	4339	A
5	A6	4344	U
5	A6	4346	U
5	A6	4347	G
5	A6	4348	A
5	A6	4349	C
5	A6	4350	C
5	A6	4354	U
5	A6	4355	G
5	A6	4357	G
5	A6	4358	U
5	A6	4362	A
5	A6	4364	G
5	A6	4365	C
5	A6	4370	G
5	A6	4371	G
5	A6	4372	U
5	A6	4373	G
5	A6	4374	U
5	A6	4376	A
5	A6	4377	G
5	A6	4378	A
5	A6	4379	A
5	A6	4380	A
5	A6	4381	A

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Mol	Chain	Res	Type
5	A6	4385	A
5	A6	4387	C
5	A6	4393	G
5	A6	4394	A
5	A6	4395	U
5	A6	4396	A
5	A6	4398	C
5	A6	4401	G
5	A6	4413	C
5	A6	4415	A
5	A6	4419	U
5	A6	4422	A
5	A6	4424	A
5	A6	4426	C
5	A6	4430	G
5	A6	4436	U
5	A6	4438	U
5	A6	4442	U
5	A6	4443	C
5	A6	4444	C
5	A6	4448	G
5	A6	4449	A
5	A6	4450	U
5	A6	4463	U
5	A6	4464	A
5	A6	4466	C
5	A6	4475	G
5	A6	4477	A
5	A6	4487	A
5	A6	4488	A
5	A6	4496	A
5	A6	4499	G
5	A6	4500	U
5	A6	4504	C
5	A6	4505	C
5	A6	4506	C
5	A6	4510	A
5	A6	4512	U
5	A6	4513	A
5	A6	4523	A
5	A6	4525	C
5	A6	4527	G

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Mol	Chain	Res	Type
5	A6	4531	U
5	A6	4532	U
5	A6	4534	G
5	A6	4544	A
5	A6	4545	G
5	A6	4558	U
5	A6	4560	C
5	A6	4565	C
5	A6	4567	G
5	A6	4569	U
5	A6	4570	G
5	A6	4573	G
5	A6	4575	G
5	A6	4578	G
5	A6	4581	G
5	A6	4582	C
5	A6	4584	A
5	A6	4585	U
5	A6	4589	A
5	A6	4590	A
5	A6	4595	G
5	A6	4596	C
5	A6	4597	U
5	A6	4599	A
5	A6	4600	G
5	A6	4601	U
5	A6	4608	G
5	A6	4615	C
5	A6	4616	A
5	A6	4624	A
5	A6	4627	U
5	A6	4628	U
5	A6	4629	U
5	A6	4630	G
5	A6	4632	U
5	A6	4633	G
5	A6	4634	U
5	A6	4635	A
5	A6	4636	U
5	A6	4637	G
5	A6	4649	G
5	A6	4652	G

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Mol	Chain	Res	Type
5	A6	4653	C
5	A6	4656	A
5	A6	4657	U
5	A6	4664	A
5	A6	4670	C
5	A6	4671	C
5	A6	4677	U
5	A6	4678	G
5	A6	4687	A
5	A6	4693	C
5	A6	4694	G
5	A6	4697	U
5	A6	4700	A
5	A6	4708	A
5	A6	4709	U
5	A6	4712	C
5	A6	4714	C
5	A6	4715	C
5	A6	4719	G
5	A6	4720	C
5	A6	4722	G
5	A6	4723	A
5	A6	4724	A
5	A6	4727	A
5	A6	4730	C
5	A6	4731	G
5	A6	4732	G
5	A6	4734	A
5	A6	4738	C
5	A6	4739	C
5	A6	4741	C
5	A6	4750	G
5	A6	4753	U
5	A6	4754	G
5	A6	4756	C
5	A6	4758	U
5	A6	4761	G
5	A6	4762	A
5	A6	4763	U
5	A6	4764	A
5	A6	4767	C
5	A6	4769	G

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Mol	Chain	Res	Type
5	A6	4771	C
5	A6	4772	C
5	A6	4870	G
5	A6	4871	C
5	A6	4872	G
5	A6	4873	G
5	A6	4874	A
5	A6	4875	G
5	A6	4876	U
5	A6	4877	G
5	A6	4878	C
5	A6	4881	U
5	A6	4882	U
5	A6	4883	C
5	A6	4884	G
5	A6	4885	U
5	A6	4886	C
5	A6	4888	U
5	A6	4889	G
5	A6	4890	G
5	A6	4893	A
5	A6	4895	C
5	A6	4900	C
5	A6	4901	G
5	A6	4902	C
5	A6	4910	G
5	A6	4911	A
5	A6	4912	G
5	A6	4913	G
5	A6	4914	C
5	A6	4925	U
5	A6	4926	C
5	A6	4927	G
5	A6	4928	C
5	A6	4929	C
5	A6	4930	C
5	A6	4933	C
5	A6	4936	G
5	A6	4937	C
5	A6	4938	A
5	A6	4939	C
5	A6	4940	C

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Mol	Chain	Res	Type
5	A6	4941	G
5	A6	4942	C
5	A6	4943	A
5	A6	4944	C
5	A6	4945	G
5	A6	4946	U
5	A6	4947	U
5	A6	4948	C
5	A6	4949	G
5	A6	4950	U
5	A6	4951	G
5	A6	4952	G
5	A6	4965	U
5	A6	4966	A
5	A6	4967	A
5	A6	4975	G
5	A6	4976	U
5	A6	4979	A
5	A6	4980	C
5	A6	4981	G
5	A6	4985	U
5	A6	4986	G
5	A6	4988	U
5	A6	4989	U
5	A6	4990	C
5	A6	4991	U
5	A6	4992	G
5	A6	4996	C
5	A6	4998	G
5	A6	5002	U
5	A6	5006	U
5	A6	5008	C
5	A6	5011	A
5	A6	5012	G
5	A6	5014	A
5	A6	5023	C
5	A6	5024	C
5	A6	5026	U
5	A6	5027	C
5	A6	5028	G
5	A6	5031	G
5	A6	5035	U

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Mol	Chain	Res	Type
5	A6	5040	U
5	A6	5041	G
5	A6	5042	A
5	A6	5047	C
5	A6	5050	C
5	A6	5053	U
5	A6	5054	C
5	A6	5055	G
5	A6	5056	A
5	A6	5060	A
5	A6	5061	A
5	A6	5062	G
5	A6	5063	G
5	A6	5065	U
5	A6	5069	U
83	Cc	7	G
83	Cc	8	U
83	Cc	9	G
83	Cc	10	G
83	Cc	11	A
83	Cc	15	G
83	Cc	16	C
83	Cc	18	C
83	Cc	19	G
83	Cc	20	G
83	Cc	21	U
83	Cc	22	A
83	Cc	23	G
83	Cc	35	C
83	Cc	36	A
83	Cc	42	C
83	Cc	45	A
83	Cc	46	G
83	Cc	47	G
83	Cc	48	U
83	Cc	50	G
83	Cc	56	U
83	Cc	58	A
83	Cc	62	C
83	Cc	63	C
83	Cc	65	G
83	Cc	66	C

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Mol	Chain	Res	Type
83	Cc	71	G
83	Cc	75	C
83	Cc	76	C
83	Cc	77	A
84	Bb	5	A
84	Bb	7	U
84	Bb	8	U
84	Bb	11	C
84	Bb	15	G
84	Bb	17	U
84	Bb	18	G
84	Bb	19	G
84	Bb	22	G
84	Bb	23	A
84	Bb	25	C
84	Bb	26	G
84	Bb	30	G
84	Bb	31	A
84	Bb	34	G
84	Bb	36	A
84	Bb	39	U
84	Bb	40	C
84	Bb	41	U
84	Bb	42	G
84	Bb	43	G
84	Bb	46	G
84	Bb	61	C
84	Bb	62	A
84	Bb	69	U
84	Bb	70	C
84	Bb	73	A
84	Bb	76	A
85	Dd	16	U
85	Dd	22	U
85	Dd	23	U

All (157) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A5	69	A
1	A5	75	G
1	A5	125	C

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Mol	Chain	Res	Type
1	A5	142	G
1	A5	187	U
1	A5	219	G
1	A5	220	C
1	A5	226	G
1	A5	333	U
1	A5	334	A
1	A5	406	C
1	A5	413	G
1	A5	431	G
1	A5	451	C
1	A5	497	G
1	A5	498	C
1	A5	648	G
1	A5	655	C
1	A5	668	C
1	A5	685	C
1	A5	703	G
1	A5	728	U
1	A5	911	U
1	A5	915	A
1	A5	917	A
1	A5	918	G
1	A5	926	G
1	A5	931	C
1	A5	939	G
1	A5	955	G
1	A5	957	G
1	A5	958	G
1	A5	971	U
1	A5	974	C
1	A5	1187	G
1	A5	1210	C
1	A5	1211	G
1	A5	1238	A
1	A5	1239	C
1	A5	1272	C
1	A5	1281	G
1	A5	1284	G
1	A5	1293	G
1	A5	1294	A
1	A5	1296	G

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Mol	Chain	Res	Type
1	A5	1356	U
1	A5	1366	G
1	A5	1371	A
1	A5	1398	A
1	A5	1407	C
1	A5	1419	G
1	A5	1455	G
1	A5	1474	C
1	A5	1481	C
1	A5	1633	G
1	A5	1804	A
1	A5	1813	U
1	A5	1816	C
1	A5	1835	G
1	A5	1841	C
1	A5	1997	U
1	A5	2045	G
1	A5	2046	G
1	A5	2055	G
1	A5	2068	C
1	A5	2083	C
3	A8	33	G
3	A8	60	G
3	A8	124	U
3	A8	126	C
4	B2	60	A
4	B2	102	A
4	B2	126	G
4	B2	127	C
4	B2	140	C
4	B2	141	A
4	B2	142	C
4	B2	228	C
4	B2	304	C
4	B2	399	C
4	B2	465	A
4	B2	532	C
4	B2	534	G
4	B2	552	G
4	B2	591	U
4	B2	604	A
4	B2	729	C

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Mol	Chain	Res	Type
4	B2	746	C
4	B2	797	C
4	B2	821	G
4	B2	840	C
4	B2	970	G
4	B2	989	C
4	B2	1115	U
4	B2	1137	U
4	B2	1253	A
4	B2	1309	C
4	B2	1395	C
4	B2	1396	A
4	B2	1401	A
4	B2	1417	C
4	B2	1418	C
4	B2	1474	A
4	B2	1543	U
4	B2	1585	U
4	B2	1598	G
4	B2	1637	A
4	B2	1692	U
4	B2	1756	C
4	B2	1823	A
4	B2	1830	U
4	B2	1834	A
4	B2	1865	C
5	A6	2263	A
5	A6	2264	C
5	A6	2266	C
5	A6	2268	A
5	A6	2312	U
5	A6	2319	C
5	A6	2395	A
5	A6	2531	C
5	A6	2670	C
5	A6	2695	A
5	A6	2743	A
5	A6	2766	A
5	A6	2825	A
5	A6	2887	U
5	A6	3590	G
5	A6	3618	C

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Mol	Chain	Res	Type
5	A6	3697	U
5	A6	3799	A
5	A6	3876	A
5	A6	3888	G
5	A6	3959	U
5	A6	3963	A
5	A6	4036	G
5	A6	4072	C
5	A6	4082	G
5	A6	4085	A
5	A6	4119	C
5	A6	4144	C
5	A6	4164	C
5	A6	4170	A
5	A6	4629	U
5	A6	4656	A
5	A6	4699	U
5	A6	4738	C
5	A6	4871	C
5	A6	4885	U
5	A6	4889	G
5	A6	4946	U
5	A6	4966	A
5	A6	4990	C
5	A6	4991	U
5	A6	5027	C
5	A6	5049	G
5	A6	5061	A

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

7 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
42	MLZ	o	53	42	8,9,10	1.35	1 (12%)	4,9,11	0.88	0
31	MLZ	b	5	31	8,9,10	0.80	0	4,9,11	0.67	0
84	YYG	Bb	37	85,86,84	38,42,43	0.63	0	45,62,65	1.40	9 (20%)
8	HIC	B	245	8	10,11,12	0.55	0	9,14,16	0.71	0
62	NMM	TT	67	62	8,11,12	0.67	0	7,12,14	2.15	2 (28%)
30	V5N	a	39	30	8,11,12	0.57	0	8,14,16	0.90	0
41	M3L	m	98	41	10,11,12	0.41	0	9,14,16	0.28	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
42	MLZ	o	53	42	-	3/7/8/10	-
31	MLZ	b	5	31	-	1/7/8/10	-
84	YYG	Bb	37	85,86,84	-	8/24/42/43	0/4/4/4
8	HIC	B	245	8	-	2/5/6/8	0/1/1/1
62	NMM	TT	67	62	-	2/9/11/13	-
30	V5N	a	39	30	-	5/9/10/12	0/1/1/1
41	M3L	m	98	41	-	1/9/10/12	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
42	o	53	MLZ	O-C	3.70	1.34	1.20

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
62	TT	67	NMM	NE-CZ-NH2	-4.84	115.05	119.48
84	Bb	37	YYG	O6-C6-N1	3.86	125.39	119.87
84	Bb	37	YYG	C5-C4-N3	-3.39	121.24	123.99
84	Bb	37	YYG	N9-C4-N3	2.87	134.10	129.45
84	Bb	37	YYG	C1'-N9-C8	-2.69	119.09	126.73
84	Bb	37	YYG	C2-N1-C12	-2.64	105.19	109.94
84	Bb	37	YYG	C6-C5-N7	-2.45	123.92	129.36
84	Bb	37	YYG	C3-N3-C4	2.44	127.84	123.11
62	TT	67	NMM	NE-CZ-NH1	2.39	124.67	120.26
84	Bb	37	YYG	C3-N3-C2	-2.13	116.02	120.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
84	Bb	37	YYG	N3-C2-N2	-2.01	123.86	126.62

There are no chirality outliers.

All (22) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
42	o	53	MLZ	N-CA-CB-CG
42	o	53	MLZ	C-CA-CB-CG
42	o	53	MLZ	CD-CE-NZ-CM
62	TT	67	NMM	C-CA-CB-CG
62	TT	67	NMM	N-CA-CB-CG
30	a	39	V5N	CA-CB-CG-CD2
84	Bb	37	YYG	C14-C15-N20-C21
84	Bb	37	YYG	O23-C21-N20-C15
84	Bb	37	YYG	N20-C21-O23-C24
84	Bb	37	YYG	O22-C21-O23-C24
84	Bb	37	YYG	O22-C21-N20-C15
84	Bb	37	YYG	C12-C13-C14-C15
31	b	5	MLZ	CA-CB-CG-CD
8	B	245	HIC	CA-CB-CG-ND1
8	B	245	HIC	CA-CB-CG-CD2
30	a	39	V5N	C-CA-CB-O2
84	Bb	37	YYG	O17-C16-O18-C19
30	a	39	V5N	CA-CB-CG-ND1
84	Bb	37	YYG	C15-C16-O18-C19
30	a	39	V5N	C-CA-CB-CG
41	m	98	M3L	CA-CB-CG-CD
30	a	39	V5N	O-C-CA-CB

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
84	Bb	37	YYG	2	0
8	B	245	HIC	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 44 ligands modelled in this entry, 44 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A5	11
5	A6	5
4	B2	4
78	XX	3
11	E	2
84	Bb	2
71	HH	2
20	O	2
52	BB	1
66	ee	1
13	G	1
70	GG	1
83	Cc	1
9	C	1
80	W	1
45	s	1
68	CC	1
35	g	1
58	PP	1
72	II	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	BB	8:ARG	C	23:ASP	N	19.98
1	E	78:ALA	C	90:LYS	N	19.53
1	A5	1249:C	O3'	1261:G	P	17.69
1	A6	3295:G	O3'	3571:C	P	16.69
1	A5	1703:C	O3'	1720:C	P	16.31
1	A5	1113:C	O3'	1153:C	P	15.98
1	Bb	48:C	O3'	58:A	P	15.44
1	B2	758:C	O3'	782:C	P	14.92
1	ee	119:VAL	C	126:LYS	N	13.82
1	A5	1439:C	O3'	1447:C	P	13.62
1	A5	763:C	O3'	886:C	P	13.61
1	B2	700:G	O3'	728:C	P	12.23
1	G	113:ARG	C	133:PRO	N	11.75
1	A5	1051:G	O3'	1061:C	P	11.71
1	A5	757:G	O3'	758:G	P	11.52
1	B2	250:U	O3'	265:G	P	11.04
1	XX	43:GLY	C	48:LYS	N	9.77
1	A5	888:G	O3'	894:C	P	8.44
1	XX	93:PHE	C	98:ASP	N	8.38
1	E	224:LYS	C	241:GLU	N	8.26
1	A5	525:G	O3'	632:G	P	7.62
1	A5	998:C	O3'	1044:G	P	7.44
1	XX	114:ASP	C	119:ARG	N	7.21
1	HH	103:LYS	C	104:PRO	N	7.06
1	B2	276:G	O3'	277:C	P	6.91
1	HH	119:SER	C	120:ARG	N	6.63
1	A5	1221:G	O3'	1234:G	P	5.74
1	A6	2939:G	O3'	3255:C	P	5.44
1	A6	3977:C	O3'	4028:C	P	5.37
1	A6	4779:U	O3'	4857:A	P	5.18
1	Bb	46:G	O3'	48:C	P	4.86
1	GG	170:ARG	C	171:THR	N	2.45
1	Cc	35:C	O3'	36:A	P	2.45
1	O	61:ARG	C	62:MET	N	2.44
1	C	181:LYS	C	182:LYS	N	2.19
1	A6	3859:G	O3'	3860:A	P	2.15
1	O	113:ASP	C	114:LYS	N	1.98
1	W	74:ARG	C	75:HIS	N	1.98
1	s	40:MET	C	41:GLN	N	1.94
1	CC	114:LYS	C	115:GLN	N	1.94
1	g	69:LYS	C	70:THR	N	1.80
1	PP	115:TYR	C	116:LEU	N	1.80
1	II	182:CYS	C	183:GLY	N	1.74

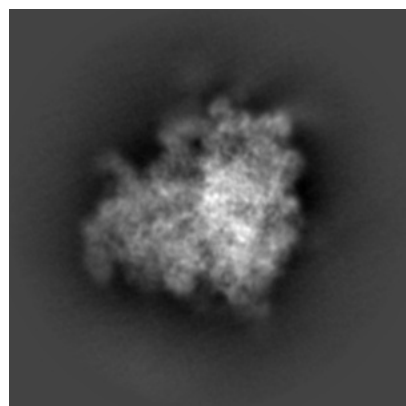
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-72470. These allow visual inspection of the internal detail of the map and identification of artifacts.

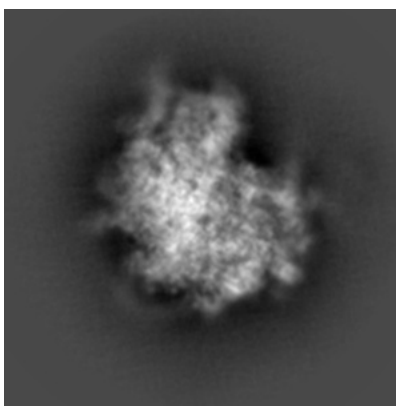
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

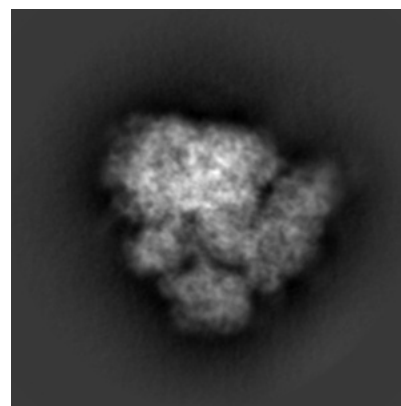
6.1.1 Primary map



X

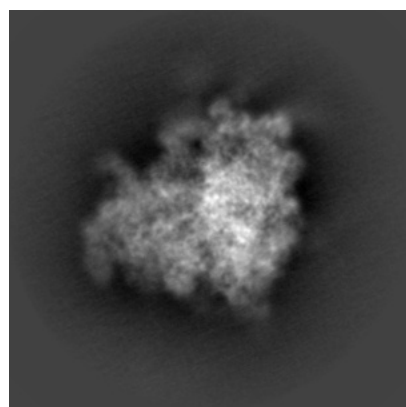


Y

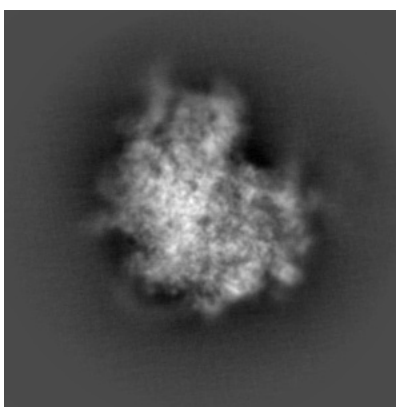


Z

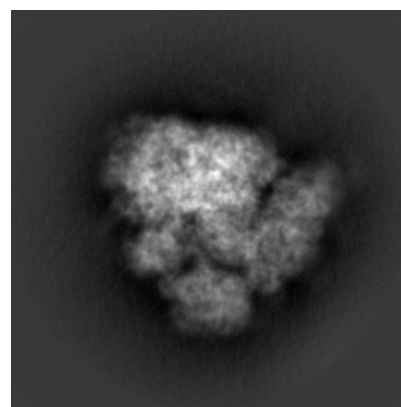
6.1.2 Raw map



X



Y

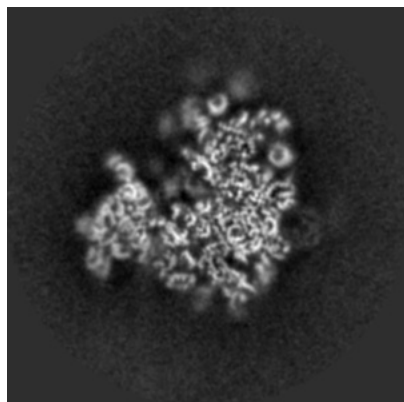


Z

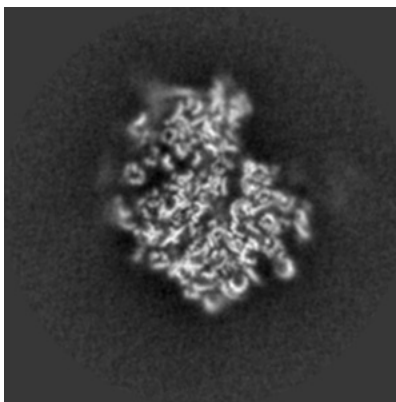
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

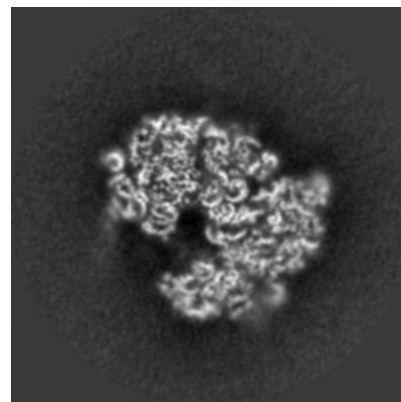
6.2.1 Primary map



X Index: 220

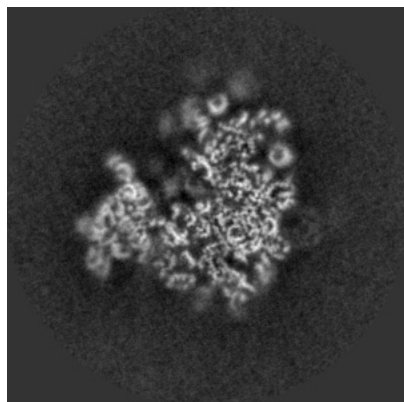


Y Index: 220

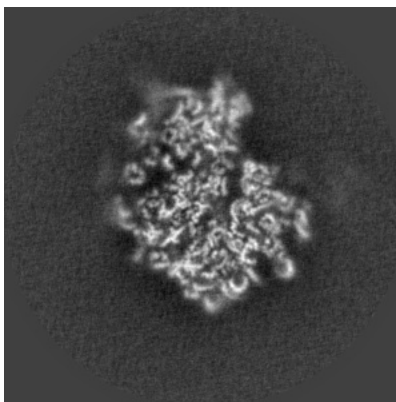


Z Index: 220

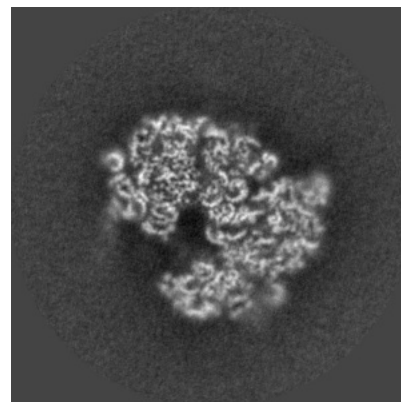
6.2.2 Raw map



X Index: 220



Y Index: 220

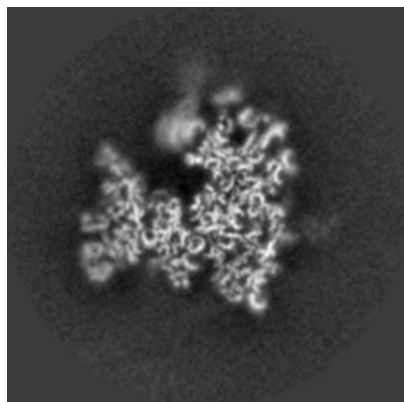


Z Index: 220

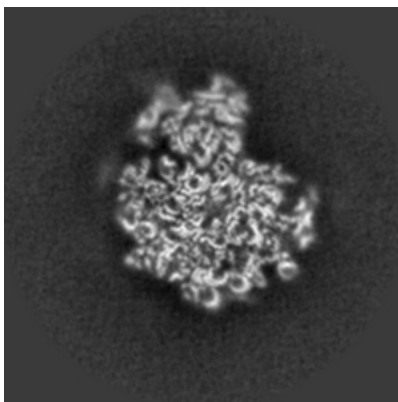
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

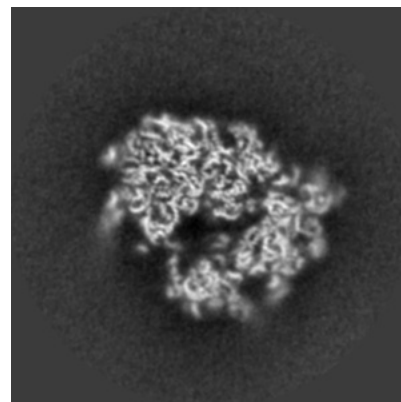
6.3.1 Primary map



X Index: 237

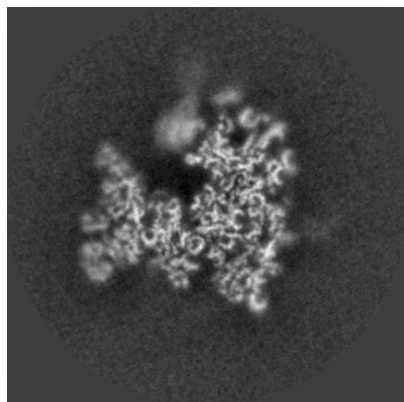


Y Index: 228

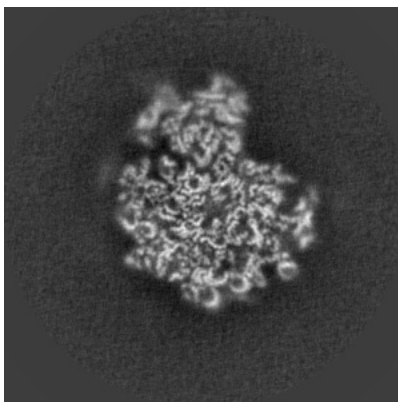


Z Index: 229

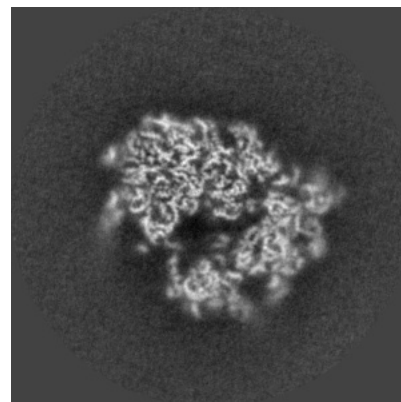
6.3.2 Raw map



X Index: 238



Y Index: 228

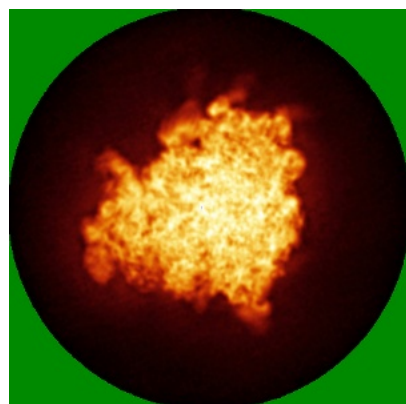


Z Index: 229

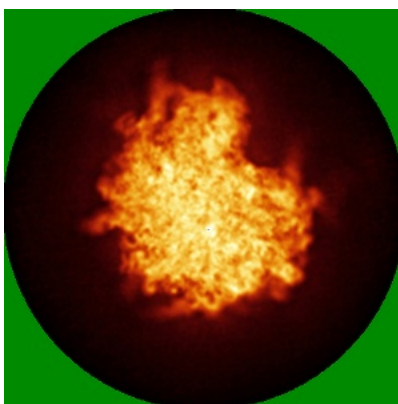
The images above show the largest variance slices of the map in three orthogonal directions.

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

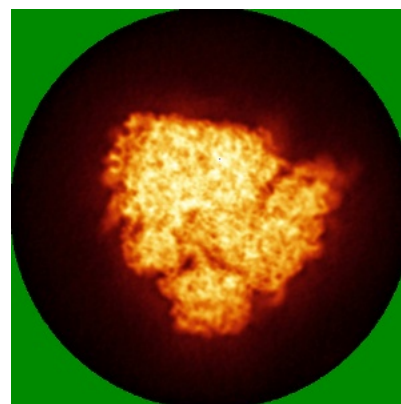
6.4.1 Primary map



X

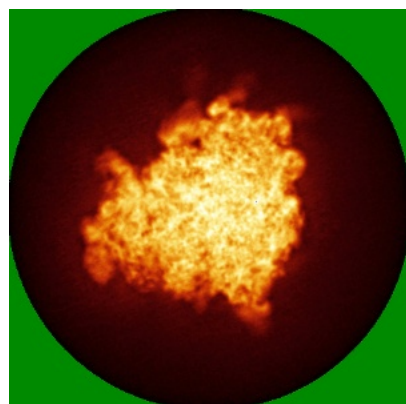


Y

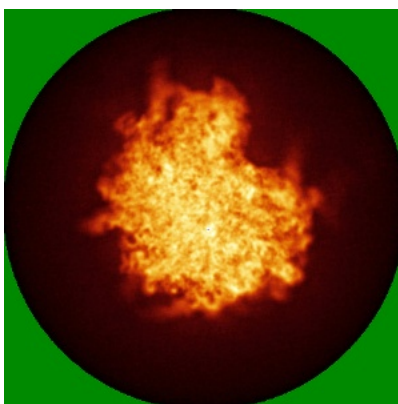


Z

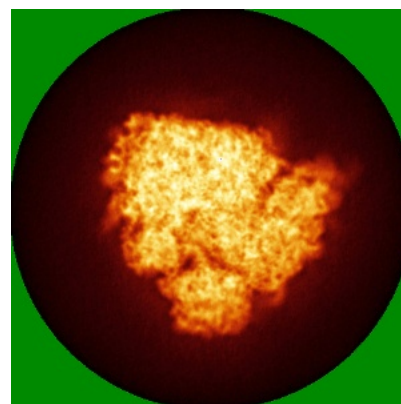
6.4.2 Raw map



X



Y

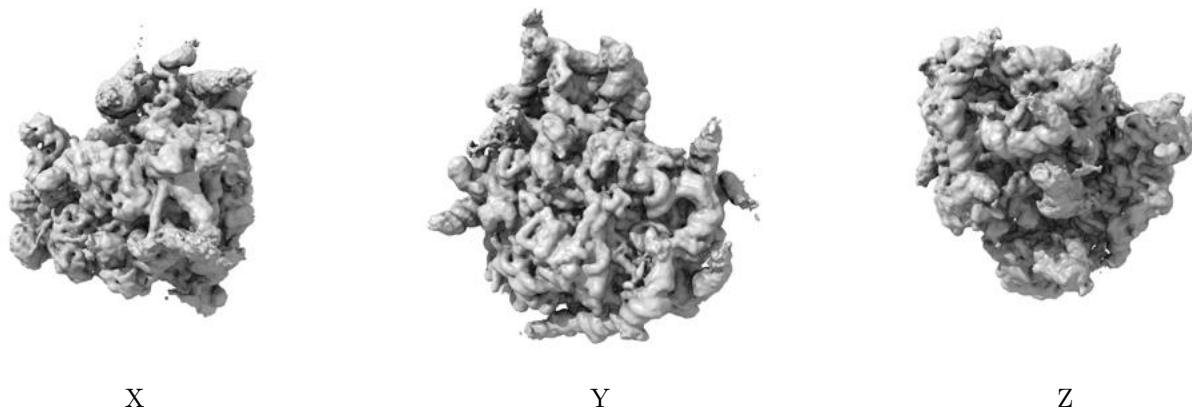


Z

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.

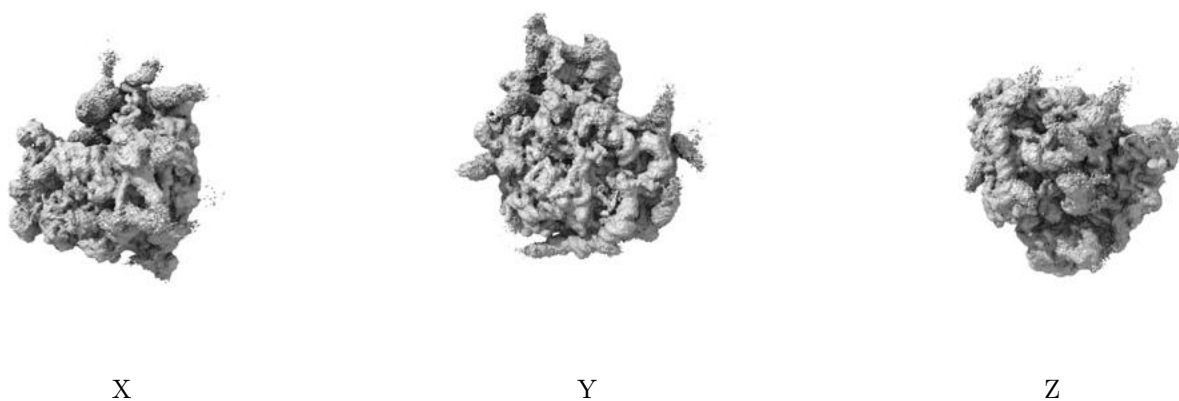
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.009. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

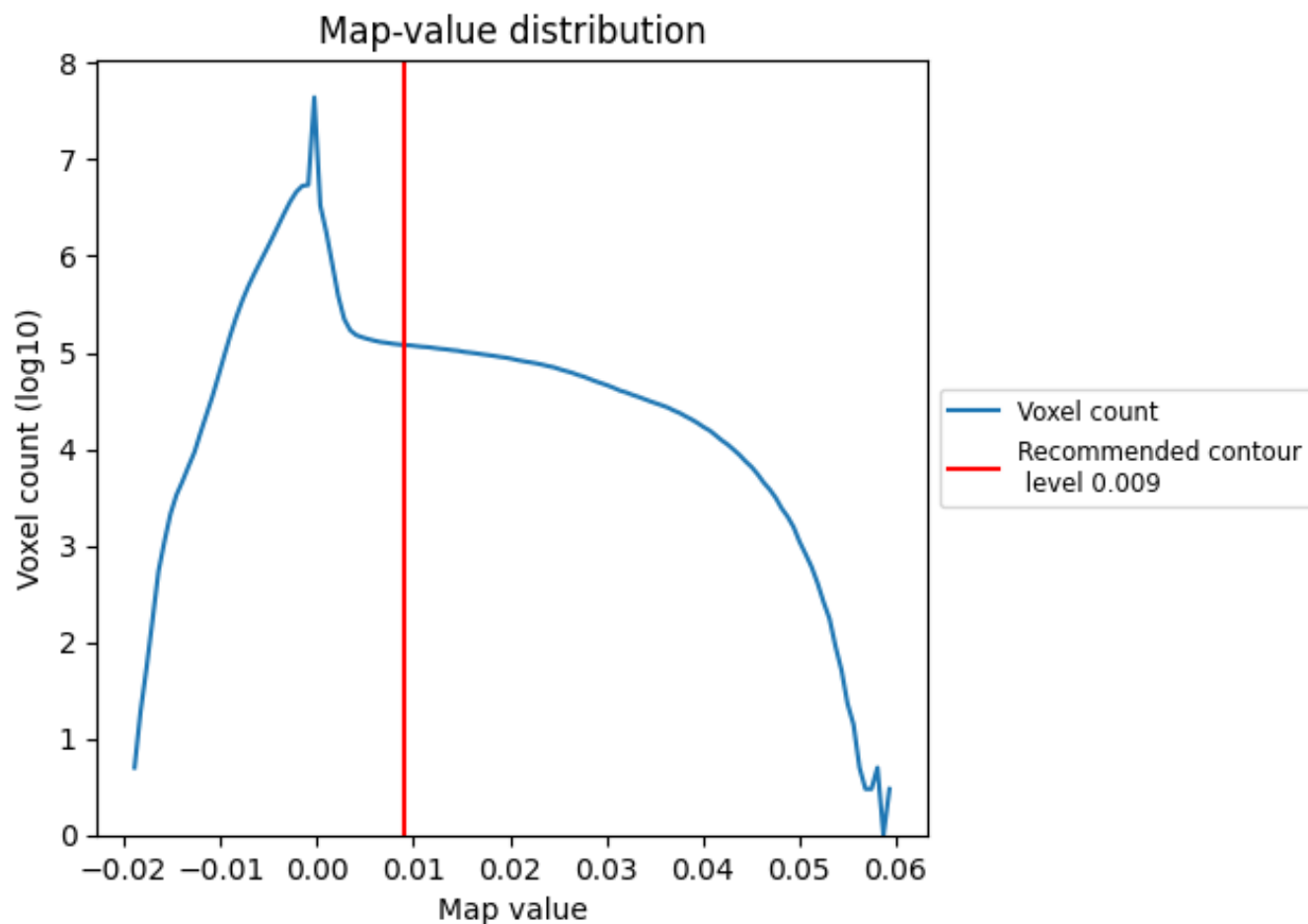
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

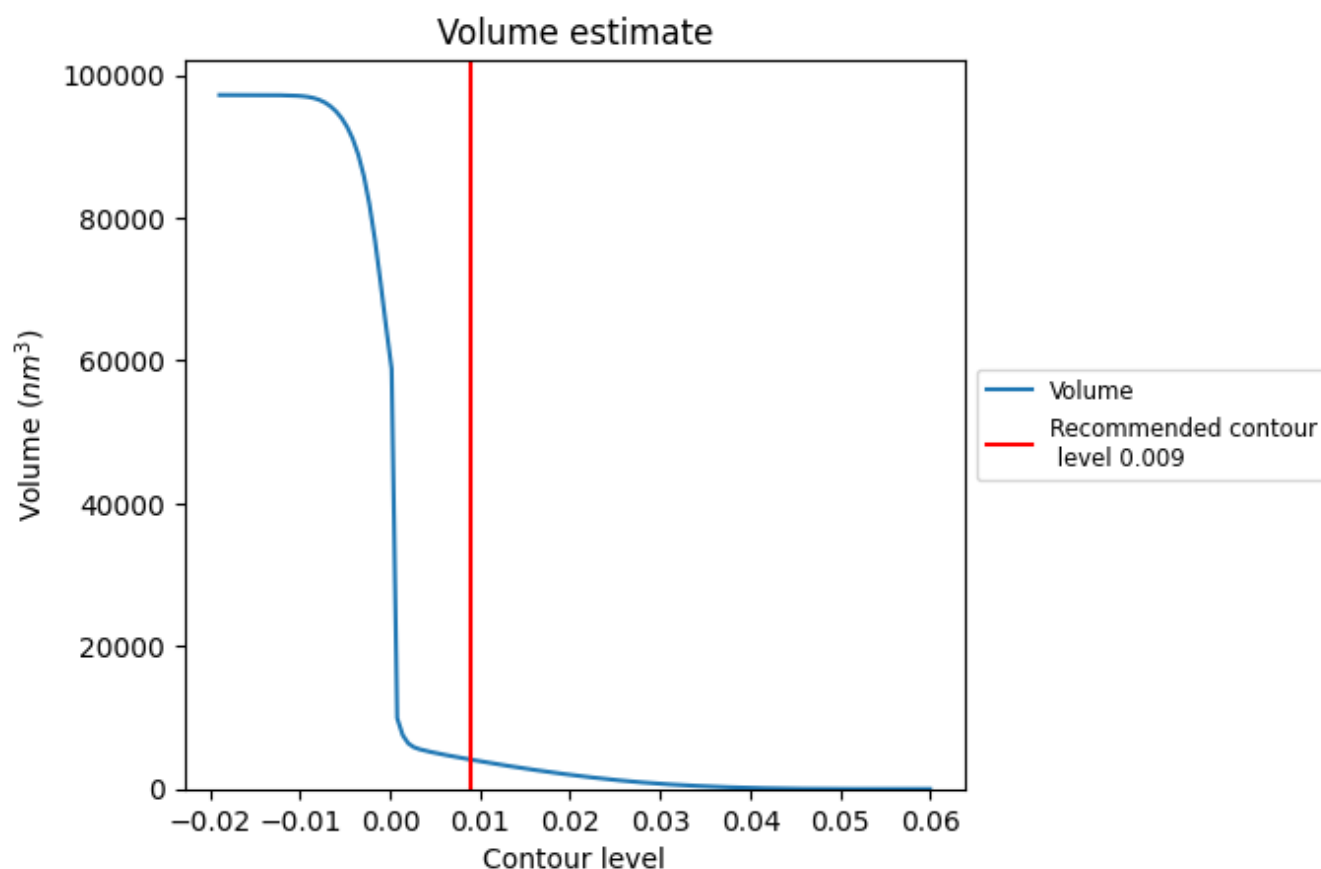
This section contains the results of statistical analysis of the map.

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.

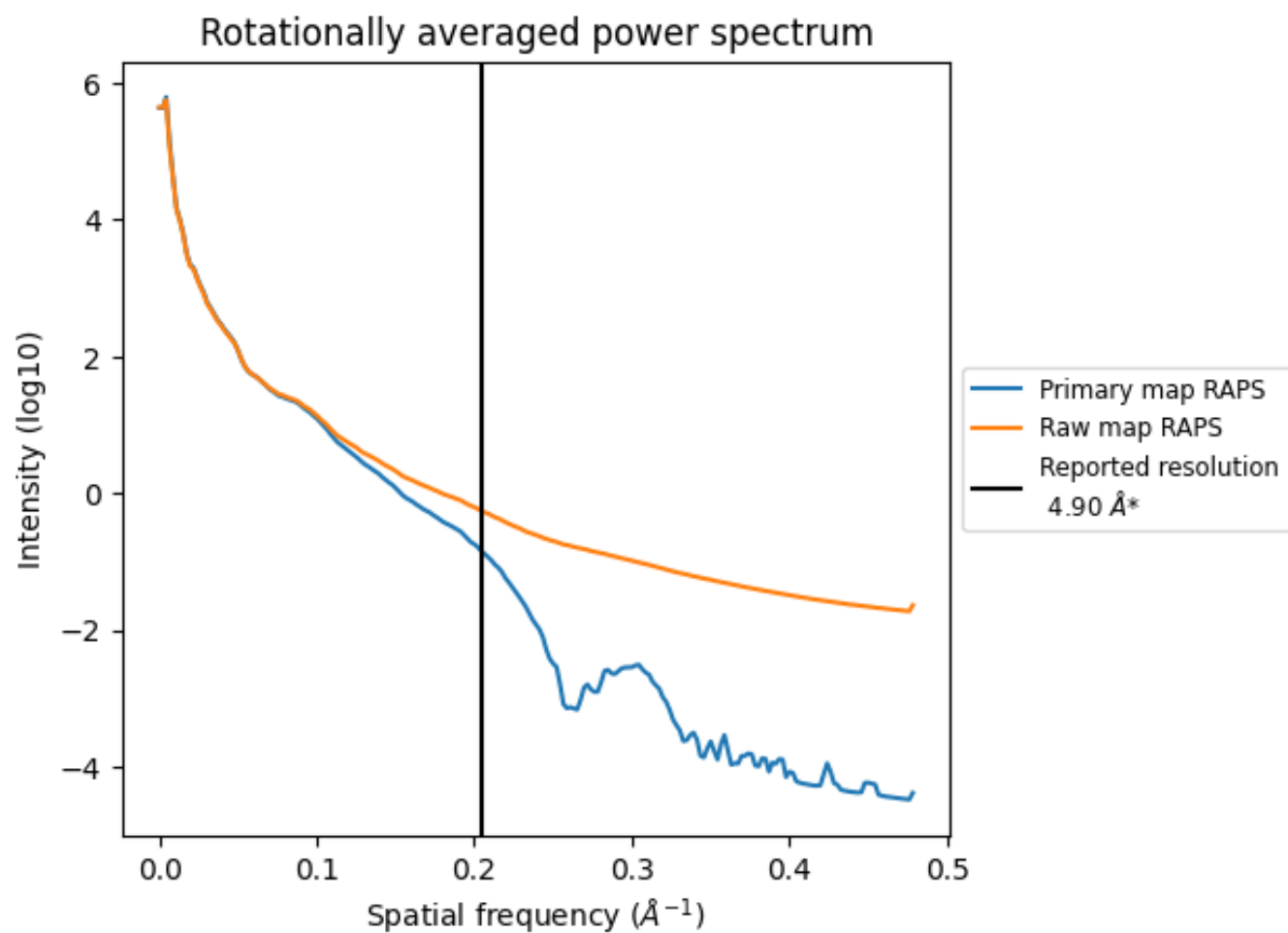
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4107 nm^3 ; this corresponds to an approximate mass of 3710 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 ⓘ

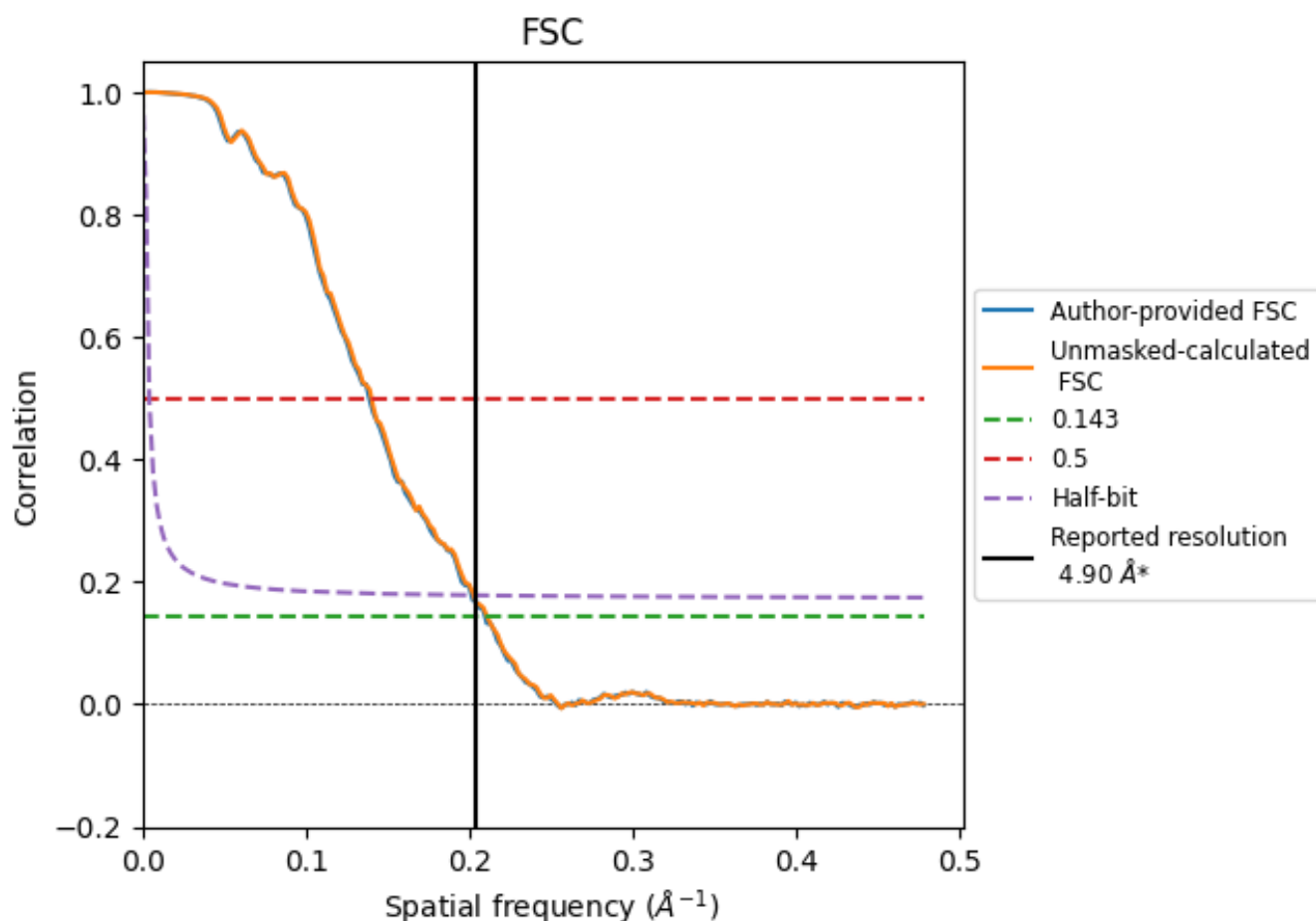


*Reported resolution corresponds to spatial frequency of 0.204 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.204 Å⁻¹

8.2 Resolution estimates [i](#)

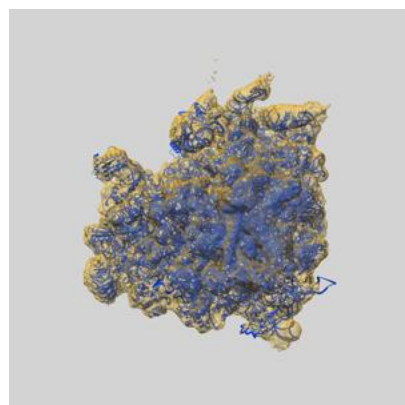
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.90	-	-
Author-provided FSC curve	4.76	7.20	4.96
Unmasked-calculated*	4.74	7.13	4.93

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

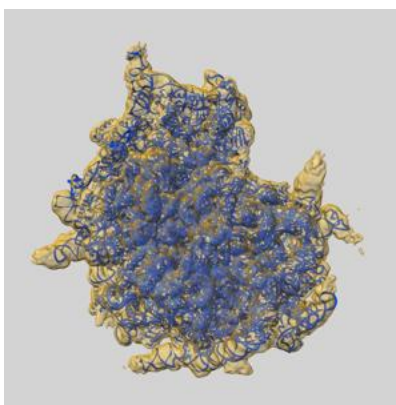
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-72470 and PDB model 9Y44. Per-residue inclusion information can be found in [section 3](#) on [page 22](#).

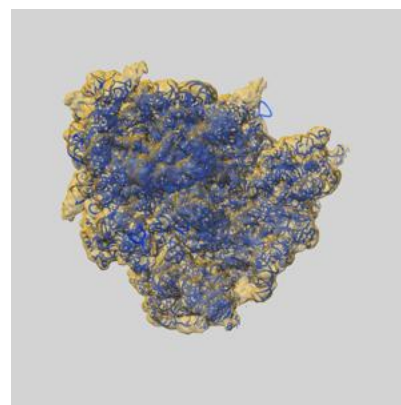
9.1 Map-model overlay [i](#)



X



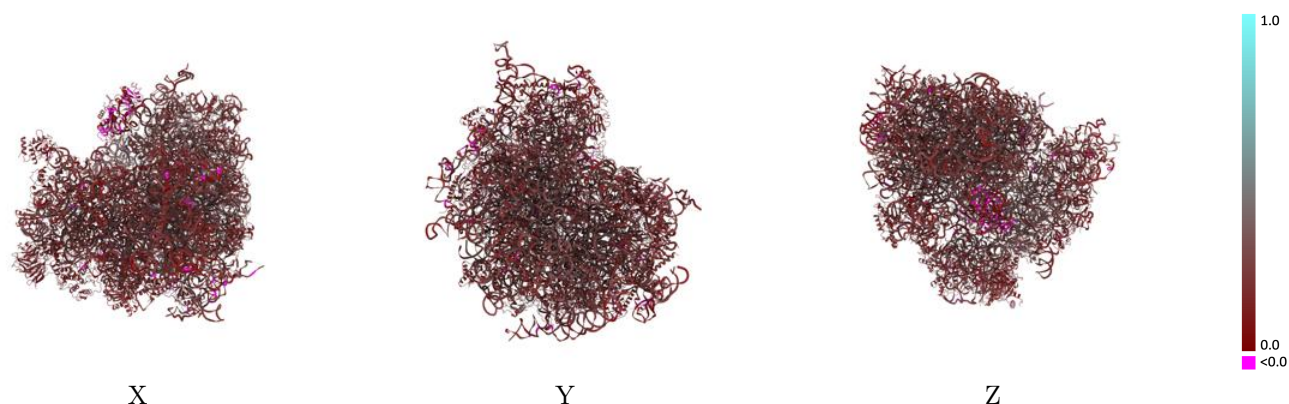
Y



Z

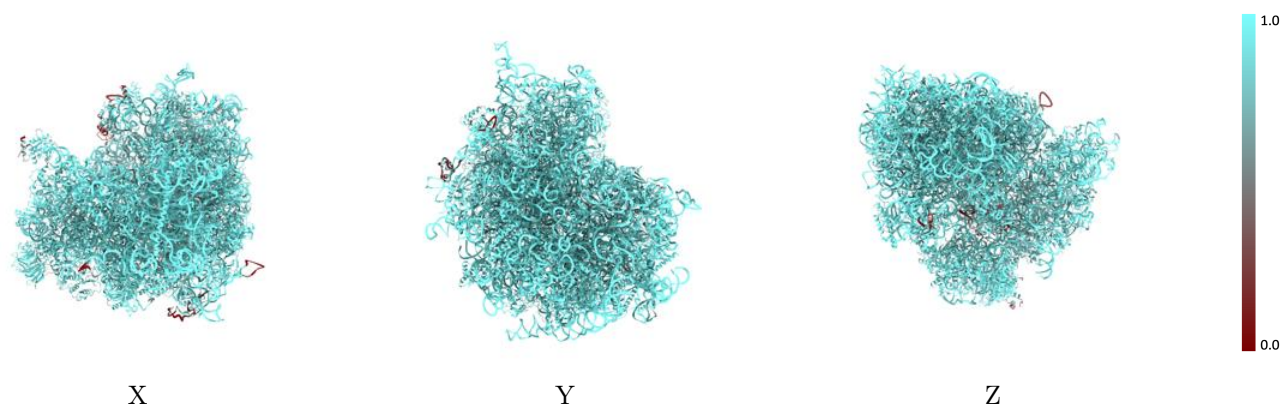
The images above show the 3D surface view of the map at the recommended contour level 0.009 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



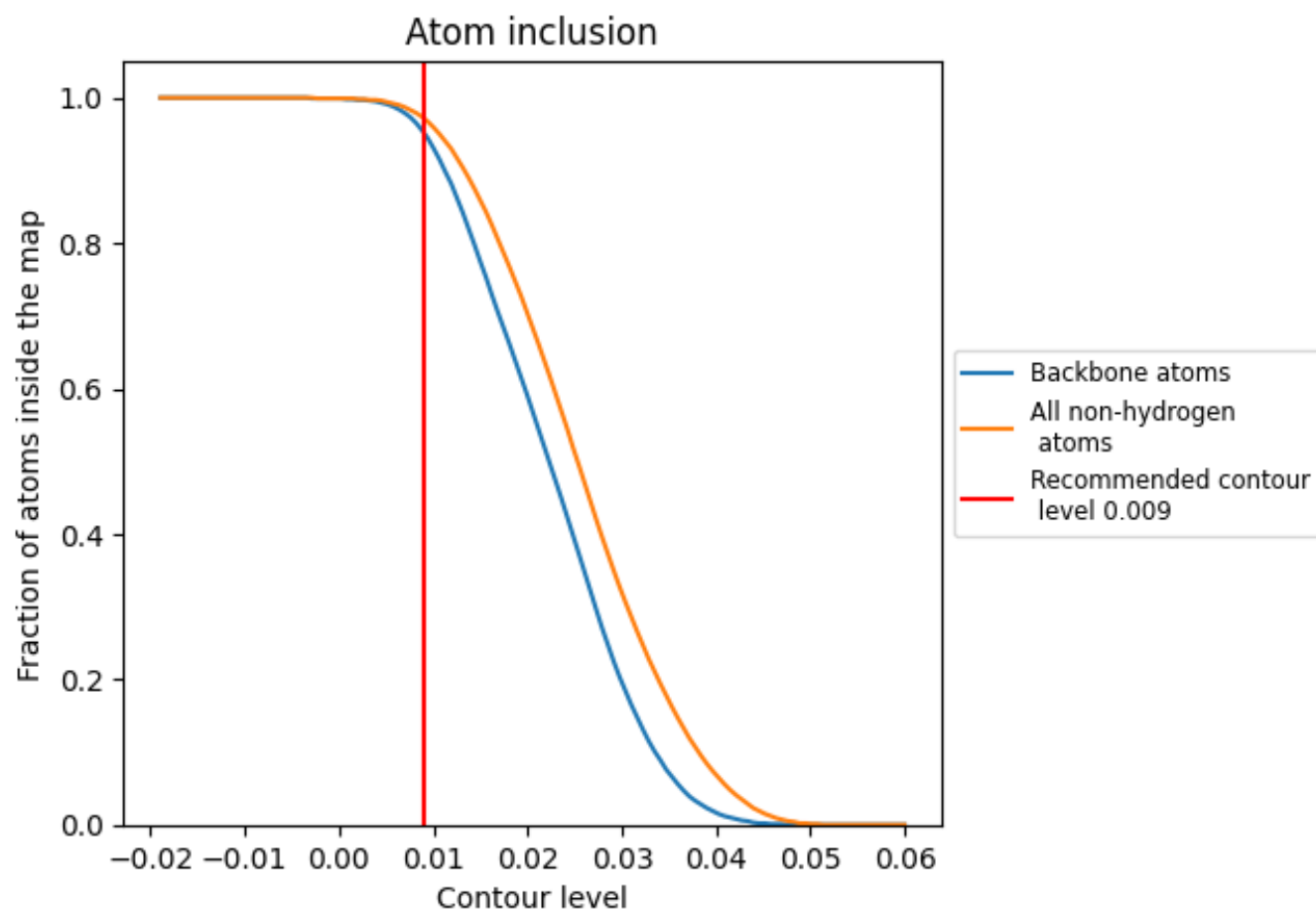
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.009).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 97% 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 (0.009) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9720	 0.2370
A	 0.9490	 0.2730
A5	 0.9930	 0.2540
A6	 0.9920	 0.2700
A7	 1.0000	 0.2790
A8	 0.9990	 0.2670
AA	 0.9320	 0.2090
B	 0.9660	 0.2300
B2	 0.9940	 0.2480
BB	 0.9510	 0.2150
Bb	 0.5620	 0.1610
C	 0.9600	 0.2360
CC	 0.9350	 0.2280
Cc	 0.9770	 0.2290
D	 0.9860	 0.2060
DD	 0.9020	 0.1990
Dd	 0.9580	 0.2620
E	 0.9770	 0.2270
EE	 0.9750	 0.1960
F	 0.9470	 0.2270
FF	 0.9590	 0.1900
G	 0.9660	 0.2180
GG	 0.9810	 0.1850
H	 0.9580	 0.2280
HH	 0.9100	 0.2060
I	 0.9540	 0.2460
II	 0.9690	 0.1920
J	 0.9750	 0.2090
JJ	 0.9700	 0.1750
KK	 0.9700	 0.1860
L	 0.9690	 0.2390
LL	 0.9490	 0.2350
M	 0.9860	 0.2330
MM	 0.7970	 0.1590
N	 0.9640	 0.2210





















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Chain	Atom inclusion	Q-score
NN	 0.9300	 0.2110
O	 0.9460	 0.2180
OO	 0.9530	 0.2140
P	 0.9710	 0.2310
PP	 0.9890	 0.1950
Q	 0.9400	 0.2400
QQ	 0.9840	 0.1700
RR	 0.8800	 0.1880
S	 0.9830	 0.2330
SS	 0.9740	 0.1880
T	 0.9570	 0.2500
TT	 0.9910	 0.1800
U	 0.9870	 0.2190
UU	 0.9550	 0.1890
V	 0.9230	 0.2160
VV	 0.9450	 0.2120
W	 0.9630	 0.1970
WW	 0.9220	 0.2210
X	 0.9770	 0.2330
XX	 0.9840	 0.2630
Y	 0.9810	 0.2200
YY	 0.9860	 0.1750
Z	 0.9740	 0.2160
ZZ	 0.9610	 0.1800
a	 0.9550	 0.2400
aa	 0.9720	 0.2340
b	 0.9730	 0.1950
bb	 0.9600	 0.2280
c	 0.9440	 0.1620
cc	 0.9390	 0.2200
d	 0.9770	 0.2350
dd	 0.9680	 0.1510
e	 0.9450	 0.2420
ee	 0.9970	 0.1770
f	 0.9570	 0.2220
ff	 0.9380	 0.1540
g	 0.9760	 0.2230
gg	 0.9610	 0.1820
h	 0.9790	 0.2110
i	 0.9560	 0.2200
j	 0.9690	 0.1990
k	 0.9430	 0.2130

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Chain	Atom inclusion	Q-score
l	 0.9740	 0.2180
m	 0.9760	 0.2310
n	 0.8900	 0.1680
o	 0.9180	 0.2120
p	 0.9060	 0.2200
r	 0.9620	 0.2560
s	 0.9010	 0.0860
t	 0.5540	 0.0650
u	 0.8550	 0.1450