



Full wwPDB EM Validation Report ⓘ

Mar 20, 2026 – 10:43 AM UTC

PDB ID : 5MMM / pdb_00005mmm
EMDB ID : EMD-3533
Title : Structure of the 70S chloroplast ribosome
Authors : Bieri, P.; Leibundgut, M.; Saurer, M.; Boehringer, D.; Ban, N.
Deposited on : 2016-12-11
Resolution : 3.40 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

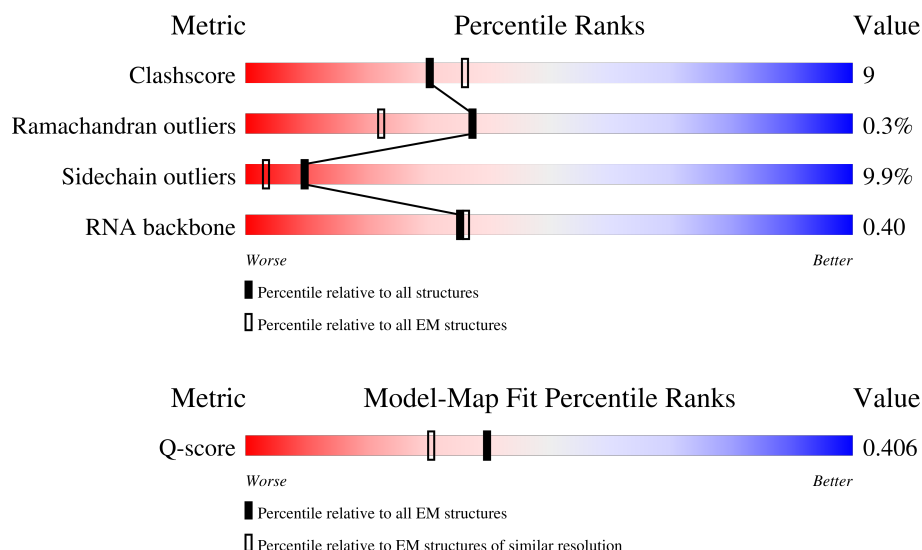
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



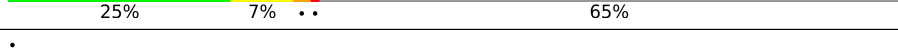
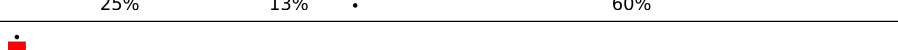
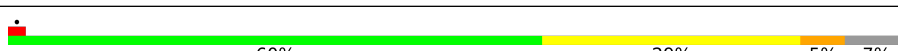
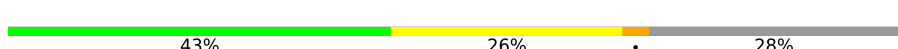
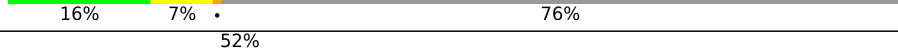
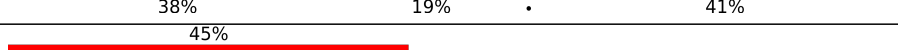
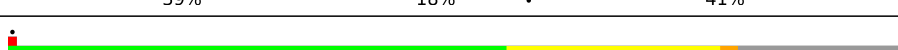
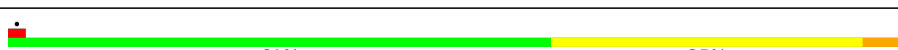
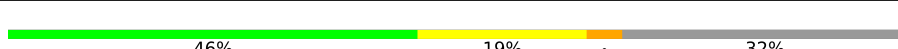
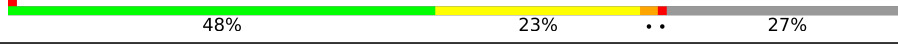
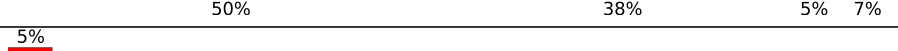
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14717 (2.90 - 3.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	0	130	
2	1	57	
3	2	66	

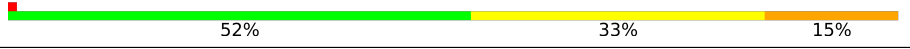
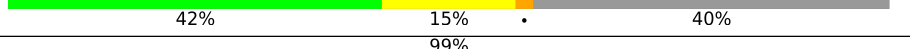
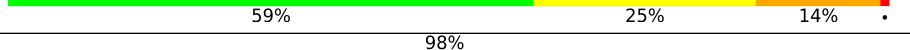
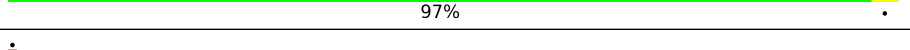
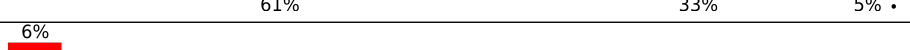
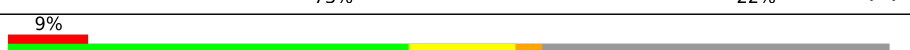
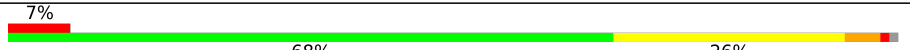
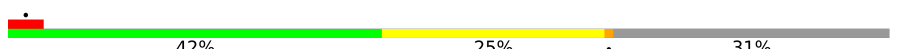
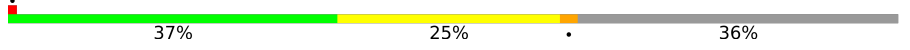
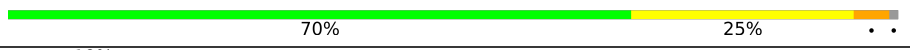
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Mol	Chain	Length	Quality of chain
4	3	152	
5	4	159	
6	5	37	
7	6	142	
8	7	116	
9	A	2810	
10	B	121	
11	C	272	
12	D	305	
13	E	293	
14	F	258	
15	G	220	
16	H	196	
17	I	232	
18	J	224	
19	K	250	
20	L	121	
21	M	271	
22	N	135	
23	O	126	
24	P	166	
25	Q	233	
26	R	128	
27	S	256	
28	T	199	

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Mol	Chain	Length	Quality of chain
29	U	198	
30	V	192	
31	W	106	
32	X	194	
33	Y	148	
34	Z	168	
35	z	76	
36	8	174	
37	a	1491	
38	b	236	
39	c	218	
40	d	201	
41	e	308	
42	f	211	
43	g	155	
44	h	134	
45	i	208	
46	j	195	
47	k	138	
48	l	123	
49	m	172	
50	n	100	
51	o	90	
52	p	88	
53	q	165	

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Mol	Chain	Length	Quality of chain
54	r	101	
55	s	92	
56	t	183	
57	u	180	
58	v	260	
59	w	179	
60	x	101	
61	y	302	

2 Entry composition

There are 63 unique types of molecules in this entry. The entry contains 152465 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	66	Total	C	N	O	S	0	0
			536	338	94	102	2		

- Molecule 2 is a protein called 50S ribosomal protein L32, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	48	Total	C	N	O		0	0
			396	261	75	60			

- Molecule 3 is a protein called 50S ribosomal protein L33, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	60	Total	C	N	O	S	0	0
			489	304	98	83	4		

- Molecule 4 is a protein called 50S ribosomal protein L34, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	60	Total	C	N	O	S	0	0
			467	282	107	75	3		

- Molecule 5 is a protein called 50S ribosomal protein L35, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	72	Total	C	N	O	S	0	0
			588	370	124	93	1		

- Molecule 6 is a protein called 50S ribosomal protein L36, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	5	37	Total	C	N	O	S	0	0
			305	186	70	45	4		

- Molecule 7 is a protein called plastid ribosomal protein cL37, PSRP5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	6	49	Total	C	N	O	S	0	0
			422	268	92	57	5		

- Molecule 8 is a protein called 50S ribosomal protein 6, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	7	46	Total	C	N	O	S	0	0
			368	237	71	59	1		

- Molecule 9 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	A	2798	Total	C	N	O	P	0	0
			60083	26804	11116	19365	2798		

- Molecule 10 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	B	121	Total	C	N	O	P	0	0
			2584	1154	466	843	121		

- Molecule 11 is a protein called 50S ribosomal protein L2, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	C	253	Total	C	N	O	S	0	0
			1952	1209	401	336	6		

- Molecule 12 is a protein called plastid ribosomal protein uL3c.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	D	221	Total	C	N	O	S	0	0
			1686	1066	308	301	11		

- Molecule 13 is a protein called plastid ribosomal protein uL4c.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	E	212	Total	C	N	O	S	0	0
			1676	1061	312	300	3		

- Molecule 14 is a protein called plastid ribosomal protein uL5c.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	F	193	Total	C	N	O	S	0	0
			1454	923	255	268	8		

- Molecule 15 is a protein called plastid ribosomal protein uL6c.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	G	178	Total	C	N	O	S	0	0
			1391	878	256	253	4		

- Molecule 16 is a protein called plastid ribosomal protein bL9c.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	H	48	Total	C	N	O	0	0
			382	251	69	62		

- Molecule 17 is a protein called plastid ribosomal protein uL10c.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	I	137	Total	C	N	O	S	0	0
			1106	711	186	203	6		

- Molecule 18 is a protein called 50S ribosomal protein L11, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	J	133	Total	C	N	O	S	0	0
			977	624	161	186	6		

- Molecule 19 is a protein called 50S ribosomal protein L13, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	K	203	Total	C	N	O	S	0	0
			1648	1047	307	289	5		

- Molecule 20 is a protein called 50S ribosomal protein L14, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	L	121	Total	C	N	O	S	0	0
			942	588	179	170	5		

- Molecule 21 is a protein called plastid ribosomal protein uL15c.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	M	185	Total	C	N	O	S	0	0
			1410	879	280	245	6		

- Molecule 22 is a protein called 50S ribosomal protein L16, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	N	135	Total	C	N	O	S	0	0
			1075	677	218	174	6		

- Molecule 23 is a protein called plastid ribosomal protein uL14c.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	O	116	Total	C	N	O	S	0	0
			944	592	193	155	4		

- Molecule 24 is a protein called plastid ribosomal protein uL18c.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	P	122	Total	C	N	O	S	0	0
			962	598	186	173	5		

- Molecule 25 is a protein called 50S ribosomal protein L19, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Q	118	Total	C	N	O	S	0	0
			953	611	186	155	1		

- Molecule 26 is a protein called 50S ribosomal protein L20, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	R	119	Total	C	N	O	S	0	0
			1029	652	213	162	2		

- Molecule 27 is a protein called 50S ribosomal protein L21, chloroplastic.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	S	170	Total	C	N	O	0	0
			1310	844	227	239		

- Molecule 28 is a protein called 50S ribosomal protein L22, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	T	172	Total	C	N	O	S	0	0
			1395	892	257	237	9		

- Molecule 29 is a protein called 50S ribosomal protein L23, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	U	96	Total	C	N	O	S	0	0
			776	503	135	136	2		

- Molecule 30 is a protein called plastid ribosomal protein uL24c.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	V	134	Total	C	N	O	S	0	0
			1078	677	203	195	3		

- Molecule 31 is a RNA chain called 4.5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	W	106	Total	C	N	O	P	0	0
			2277	1017	423	731	106		

- Molecule 32 is a protein called plastid ribosomal protein bL27c.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	X	109	Total	C	N	O	0	0
			888	560	175	153		

- Molecule 33 is a protein called plastid ribosomal protein bL28c.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Y	77	Total	C	N	O	S	0	0
			634	402	128	103	1		

- Molecule 34 is a protein called plastid ribosomal protein uL29c.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Z	101	Total	C	N	O	S	0	0
			846	529	167	147	3		

- Molecule 35 is a RNA chain called tRNA-Phe.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	z	76	Total	C	N	O	P	0	0
			1623	723	290	534	76		

- Molecule 36 is a protein called plastid ribosomal protein bS1c.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	8	174	Total	C	N	O		0	0
			870	522	174	174			

- Molecule 37 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	a	1484	Total	C	N	O	P	0	0
			31868	14208	5881	10295	1484		

- Molecule 38 is a protein called 30S ribosomal protein S2, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	b	233	Total	C	N	O	S	0	0
			1844	1163	339	329	13		

- Molecule 39 is a protein called 30S ribosomal protein S3, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	c	216	Total	C	N	O	S	0	0
			1736	1108	313	309	6		

- Molecule 40 is a protein called 30S ribosomal protein S4, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	d	199	Total	C	N	O	S	0	0
			1633	1032	319	278	4		

- Molecule 41 is a protein called 30S ribosomal protein S5, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	e	187	Total	C	N	O	S	0	0
			1331	826	259	240	6		

- Molecule 42 is a protein called plastid ribosomal protein bS6c.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	f	113	Total	C	N	O	S	0	0
			911	583	152	172	4		

- Molecule 43 is a protein called 30S ribosomal protein S7, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	g	154	Total	C	N	O	S	0	0
			1210	753	244	210	3		

- Molecule 44 is a protein called 30S ribosomal protein S8, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	h	133	Total	C	N	O	S	0	0
			1079	679	210	185	5		

- Molecule 45 is a protein called plastid ribosomal protein uS9c.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	i	144	Total	C	N	O	S	0	0
			1119	712	211	195	1		

- Molecule 46 is a protein called plastid ribosomal protein uS10c.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	j	99	Total	C	N	O	S	0	0
			805	517	144	139	5		

- Molecule 47 is a protein called 30S ribosomal protein S11, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	k	117	Total	C	N	O	S	0	0
			882	546	181	150	5		

- Molecule 48 is a protein called 30S ribosomal protein S12, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	l	122	Total	C	N	O	S	0	0
			959	599	197	161	2		

- Molecule 49 is a protein called plastid ribosomal protein uS13c.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	m	110	Total	C	N	O	S	0	0
			904	556	182	161	5		

- Molecule 50 is a protein called 30S ribosomal protein S14, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	n	99	Total	C	N	O	S	0	0
			820	507	174	136	3		

- Molecule 51 is a protein called 30S ribosomal protein S15, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	o	75	Total	C	N	O	S	0	0
			635	404	123	107	1		

- Molecule 52 is a protein called 30S ribosomal protein S16, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	p	80	Total	C	N	O	S	0	0
			664	425	123	114	2		

- Molecule 53 is a protein called plastid ribosomal protein uS17c.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	q	86	Total	C	N	O	S	0	0
			693	434	136	119	4		

- Molecule 54 is a protein called 30S ribosomal protein S18, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	r	60	Total	C	N	O	S	0	0
			490	308	96	85	1		

- Molecule 55 is a protein called 30S ribosomal protein S19 alpha, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	s	78	Total	C	N	O	S	0	0
			631	406	119	104	2		

- Molecule 56 is a protein called plastid ribosomal protein bS20c.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	t	107	Total	C	N	O	S	0	0
			853	528	173	151	1		

- Molecule 57 is a protein called plastid ribosomal protein bS21c.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	u	65	Total	C	N	O	S	0	0
			568	339	127	100	2		

- Molecule 58 is a protein called 30S ribosomal protein 2, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	v	80	Total	C	N	O	S	0	0
			613	388	104	121			

- Molecule 59 is a protein called 30S ribosomal protein 3, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	w	82	Total	C	N	O	S	0	0
			686	454	113	116	3		

- Molecule 60 is a protein called 30S ribosomal protein S31, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	x	40	Total	C	N	O	S	0	0
			309	192	69	48			

- Molecule 61 is a protein called Ribosome-binding factor PSRP1, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	y	116	Total	C	N	O	S	0	0
			919	567	181	169	2		

- Molecule 62 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
62	2	1	Total	Zn	0
			1	1	
62	5	1	Total	Zn	0
			1	1	

- Molecule 63 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	AltConf
63	4	1	Total Mg 1 1	0
63	6	1	Total Mg 1 1	0
63	7	1	Total Mg 1 1	0
63	A	511	Total Mg 511 511	0
63	B	15	Total Mg 15 15	0
63	C	1	Total Mg 1 1	0
63	D	1	Total Mg 1 1	0
63	E	1	Total Mg 1 1	0
63	F	1	Total Mg 1 1	0
63	H	1	Total Mg 1 1	0
63	M	2	Total Mg 2 2	0
63	P	1	Total Mg 1 1	0
63	R	1	Total Mg 1 1	0
63	S	1	Total Mg 1 1	0
63	T	1	Total Mg 1 1	0
63	U	1	Total Mg 1 1	0
63	V	1	Total Mg 1 1	0
63	W	14	Total Mg 14 14	0
63	a	219	Total Mg 219 219	0
63	k	1	Total Mg 1 1	0
63	l	1	Total Mg 1 1	0
63	n	1	Total Mg 1 1	0

Continued on next page...

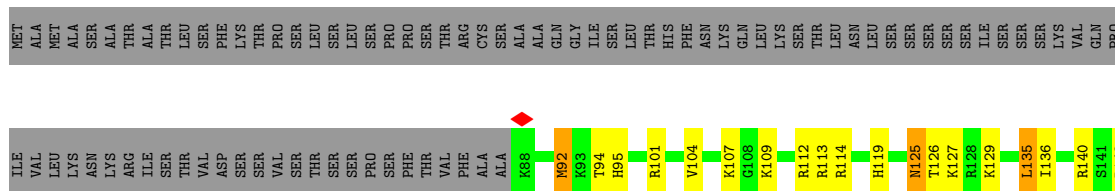
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Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
63	x	1	1	1	0



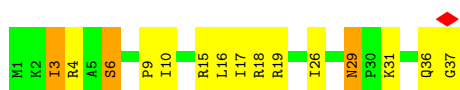
- Molecule 5: 50S ribosomal protein L35, chloroplastic

Chain 4: 31% 12% 55%



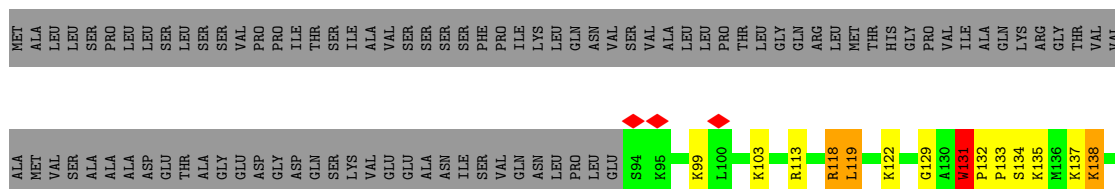
- Molecule 6: 50S ribosomal protein L36, chloroplastic

Chain 5: 59% 32% 8%



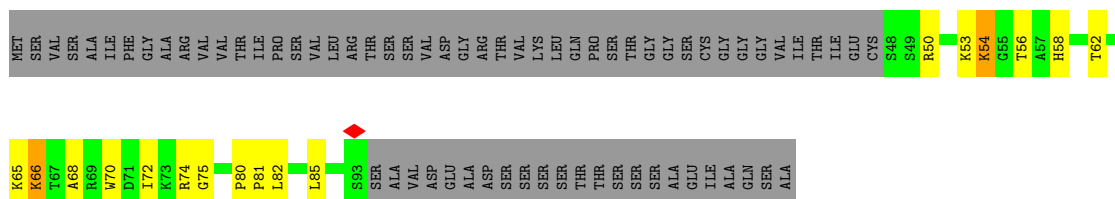
- Molecule 7: plastid ribosomal protein cL37, PSRP5

Chain 6: 25% 7% 65%



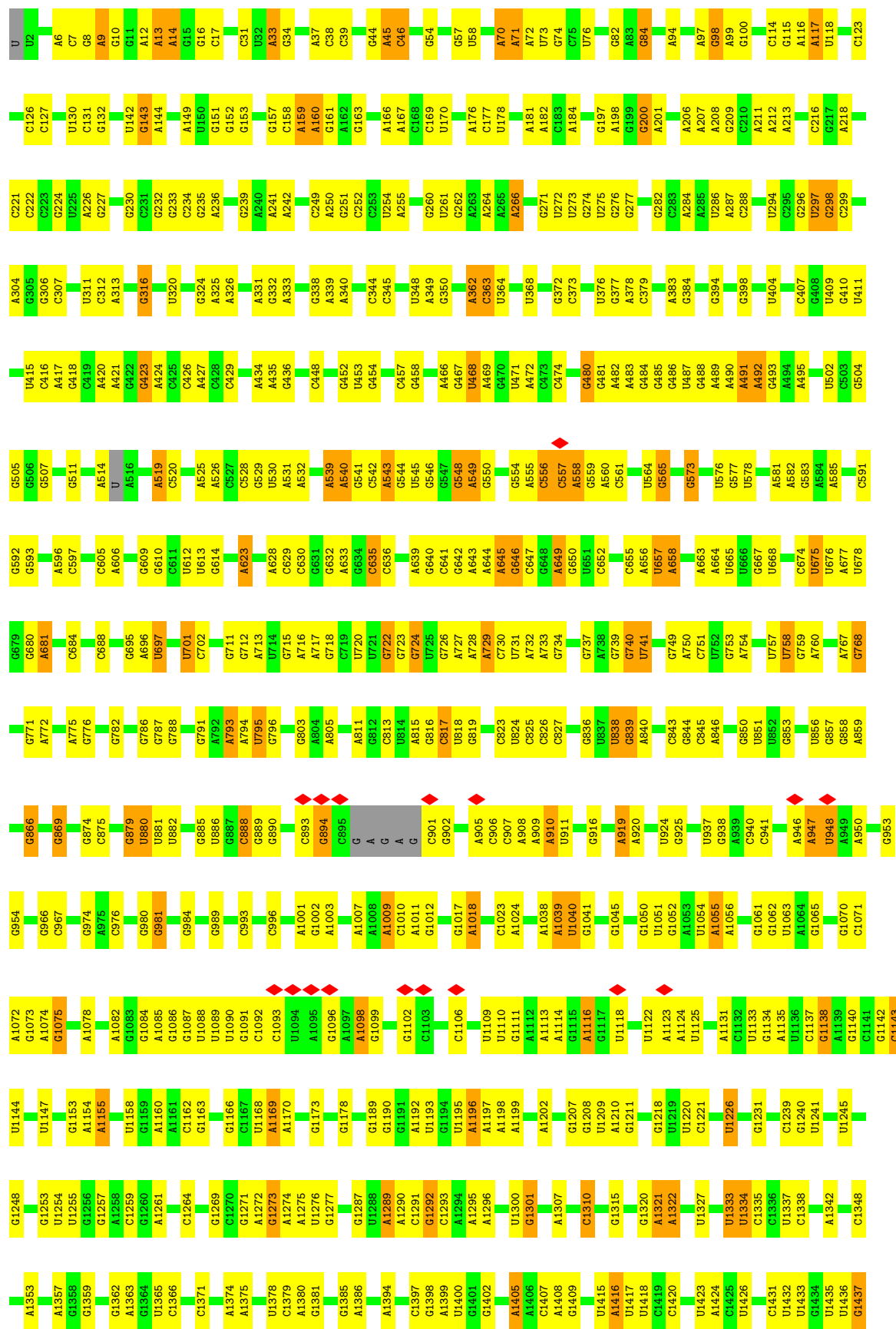
- Molecule 8: 50S ribosomal protein 6, chloroplastic

Chain 7: 25% 13% 60%

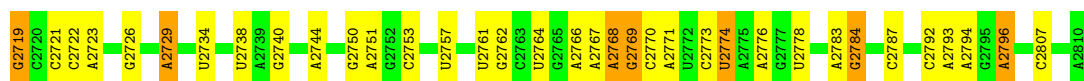


- Molecule 9: 23S ribosomal RNA

Chain A: 56% 36% 8%

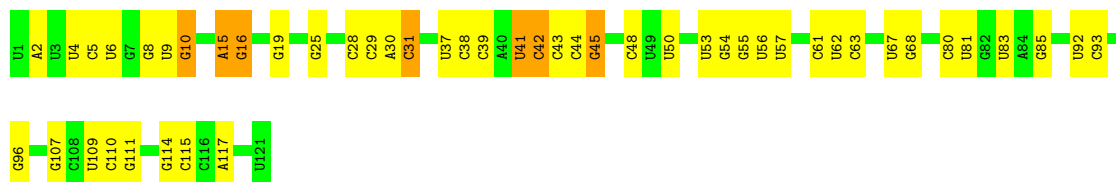


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G2620	C2515	G2427	U2264	U2194	A2133	G2051	C1854	C1750	A1616	A1522	A1444
U2621	G2518	A2428	U2266	G2195	G2194	G2052	A1857	A	U1620	G1524	G1445
G2624	G2519	A2429	G2267	A2198	G2135	G2053	A1858	C	C1621	G1526	G1446
G2625	A2520	G2430	G2268	G2199	G2136	G2054	U1861	A	G1629	U1527	G1447
G2626	U2521	G2431	G2269	A2200	G2137	A2056	C1862	A	U1630	G1528	A1448
G2627	G2522	G2432	C2271	G2201	G2138	C2057	U1863	G1756	G1631	U1529	C1449
G2628	U2523	C2439	C2272	C2202	A2139		A1864		G1632	G1530	G1450
A2629	G2524	A2442	C2278	U2203	A2140	A2062	A1865		U1633	G1531	G1454
U2630	G2525	A2443	C2281	A2204	G2141	C2063	A1866		U1634	A1532	A1531
G2636	G2526	G2444	G2286	G2205	G2142	C2064	G1865		C1635	G1533	A1455
U2637	G2527	G2445	C2287	A2206	G2143	U2065	A1867		U1636	A1534	G1456
C2640	U2528	A2446	A2285	A2207	G2144	G2066	U1870		G1642	C1535	G1457
U2646	U2529	A2447	A2288	U2208	A2145	C2069	U1874		A1643	A1536	C1458
A2649	U2530	U2448	A2289	U2209	A2146	A2070	U1875		A1644	A1537	A1465
A2652	C2535	A2452	A2290	A2212	A2147	A2073	U1876		A1645	G1543	G1468
A2656	G2542	A2456	A2291	A2213	G2148	A2074	A1877		G1649	A1544	C1469
A2657	G2543	A2457	C2292	U2217	A2149	G2075	C1877		G1655	C1546	
A2658	G2544	G2458	G2296	G2218	G2150	C2076	G1880		A1666	U1550	A1472
A2660	U2549	A2461	G2297	U2219	G2151	C2077	U1881		U1557	G1557	A1475
A2661	U2552	G2462	U2300	U2220	C2152	C2078	G1882		U1558	A1559	G1476
C2662	G2555	G2463	A2301	G2220	C2153	C2079	G1883		C1560	G1563	G1477
A2671	G2556	A2465	A2302	U2221	C2154	U2080	A1884				A1480
A2672	G2561	A2466	A2303	G2222	C2155	U2081	C1885				G1483
G2680	U2562	G2467	A2304	A2223	C2156	U2082	A1886				A1484
A2688	G2570	A2470	A2305	G2224	U2157	G2083	C1887				U1485
G2689	U2571	G2472	U2310	G2225	C2158	A2091	G1888				U1486
G2691	C2576	C2473	A2337	G2226	C2159	C2092	G1889				A1487
A2696	U2579	G2481	A2342	G2227	C2160	G2094	G1896				A1488
C2697	A2583	G2482	C2343	A2242	G2161	U2102	G1897				A1489
C2698	G2584	A2486	U2245	A2243	G2162	G2103	C1898				G1490
U2699	C2585	G2487	U2246	A2244	G2165	A2104	G1899				G1491
U2701	A2589	U2490	C2347	A2245	G2166	U2105	C1900				C1492
C2702	C2590	G2493	U2248	A2246	G2167	G2106	G1901				C1493
G2705	U2591	A2494	C2349	U2247	G2168	A2107	G1902				A1494
U2706	G2592	A2495	G2350	U2248	C2169	U2108	G1903				A1497
A2707	G2593	G2496	G2351	U2249	C2170	G2112	G1904				G1498
C2708	U2594	G2498	G2352	U2250	C2171	G2113	U1922				G1501
A2714	G2595		G2353	G2251	G2172	G2114	G1923				A1502
U2715	C2599	A2505	A2354	A2254	G2173	C2115	A1926				G1507
U2716	G2600	G2506	G2255	A2255	C2174	U2116	C1927				U1508
G2717	U2601	U2507	G2256	A2256	C2175	U2117	U1928				U1509
G2718	U2602	U2508	U2257	A2257	A2176	U2118	C1929				U1510
		U2509	U2261	A2258	C2177	U2119	U1930				U1511
			U2262	A2259	A2178	C2122	U1931				U1512
				A2260	C2179	G2125	U1932				C1513
				U2263	A2180	G2126	A1933				U1518
				G2264	U2181	C2127	C1938				A1519
				A2265	C2182	A2128	U1940				A1520
				G2256	A2183	G2129					
				A2257	C2184	C2130					
				G2258	A2185	U2131					
				A2259	U2186						
				G2260	A2187						
				U2261	C2188						
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				G2263	A2190						
				U2264	C2191						
				A2265	U2192						



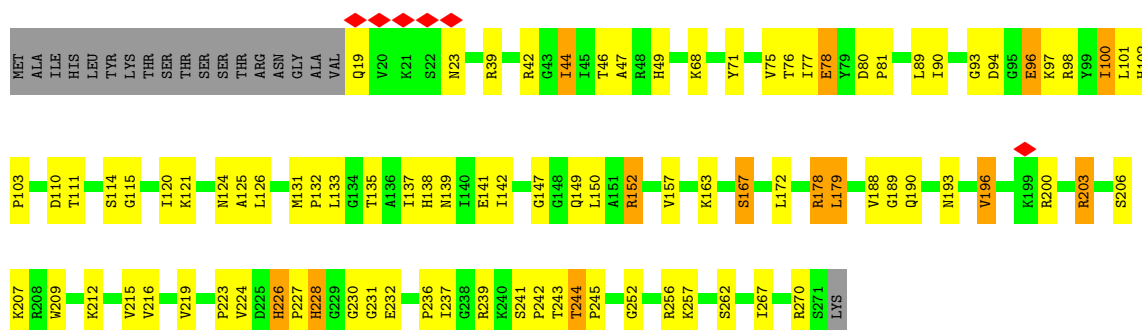
• Molecule 10: 5S ribosomal RNA

Chain B: 60% 35% 6%



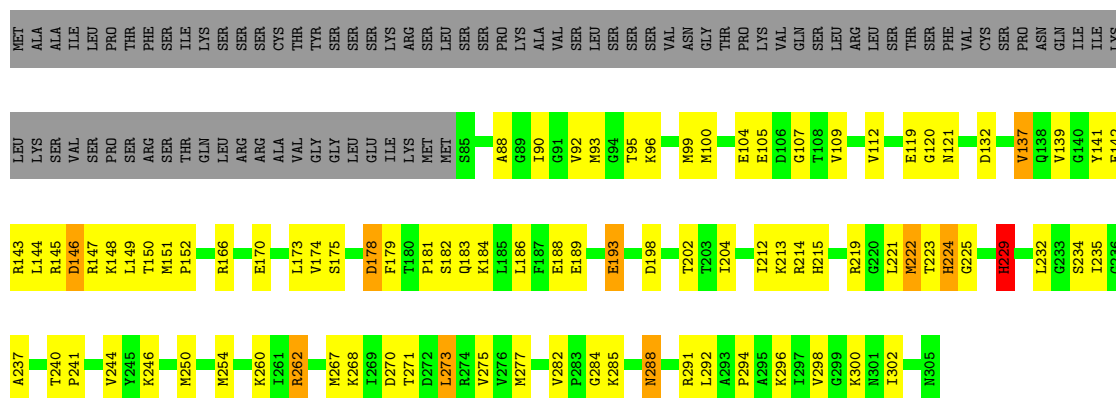
• Molecule 11: 50S ribosomal protein L2, chloroplastic

Chain C: 60% 29% 5% 7%



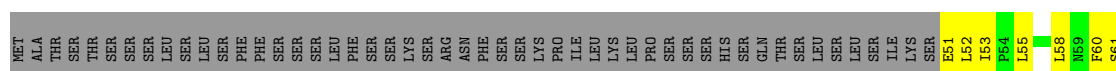
• Molecule 12: plastid ribosomal protein uL3c

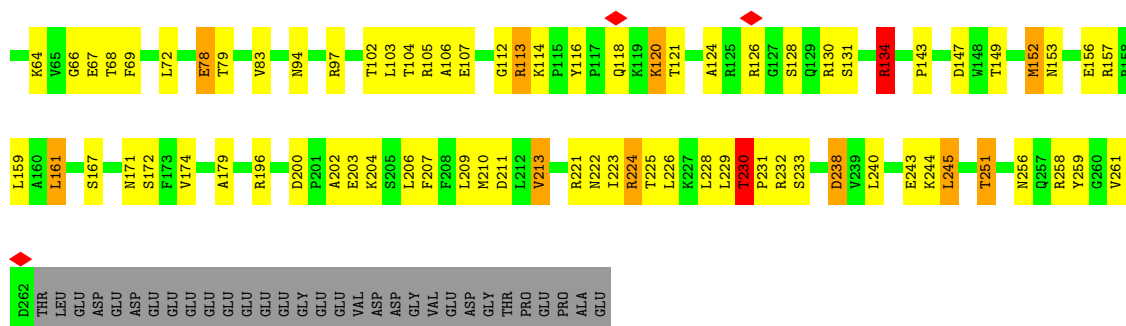
Chain D: 43% 26% 28%



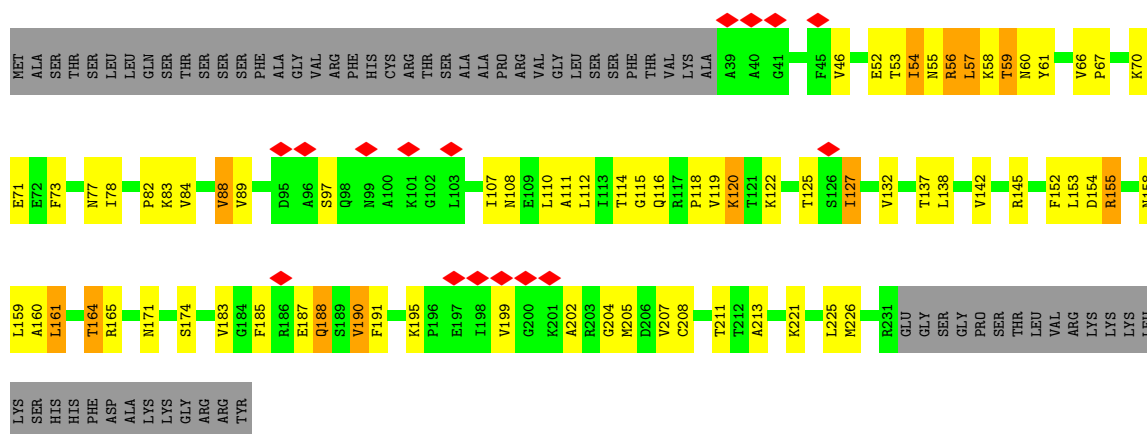
• Molecule 13: plastid ribosomal protein uL4c

Chain E: 44% 25% 28%

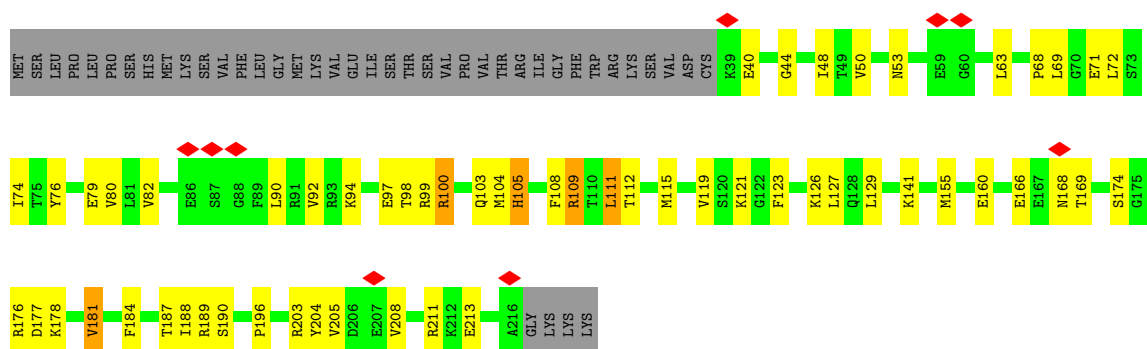




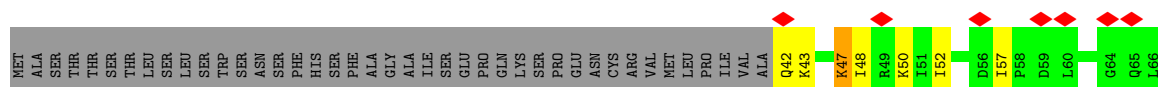
• Molecule 14: plastid ribosomal protein uL5c

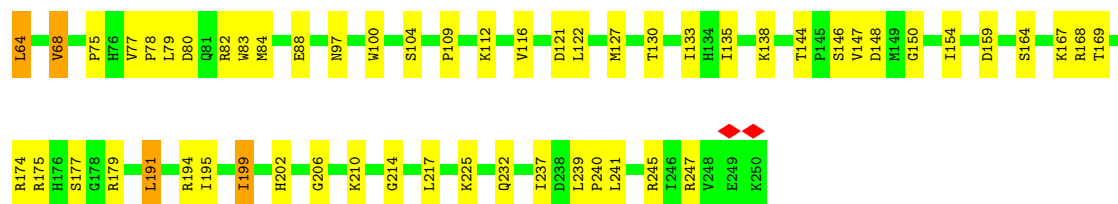


• Molecule 15: plastid ribosomal protein uL6c

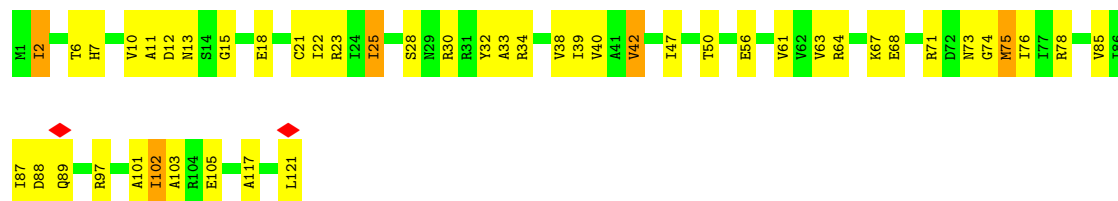


• Molecule 16: plastid ribosomal protein bL9c

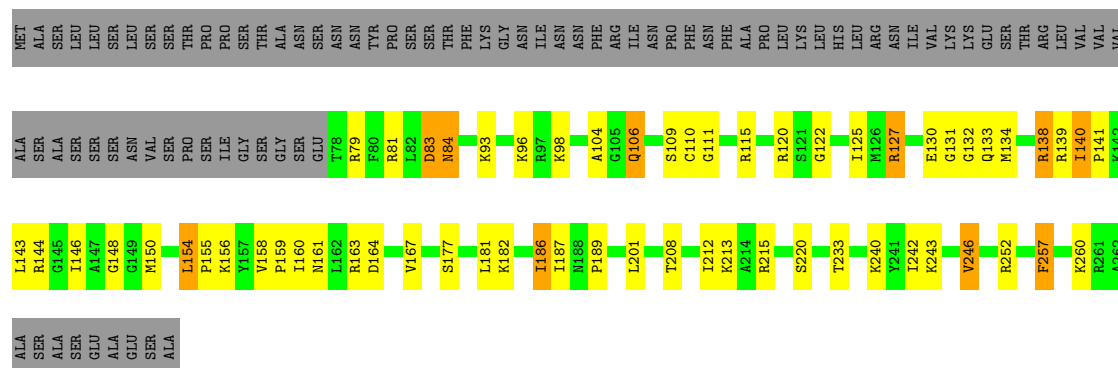




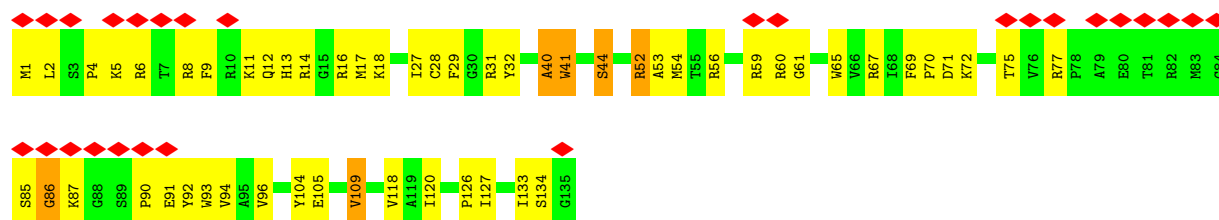
- Molecule 20: 50S ribosomal protein L14, chloroplastic



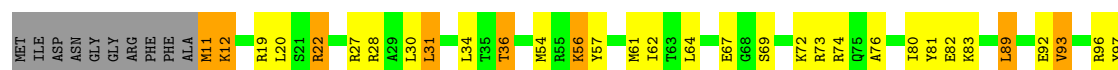
- Molecule 21: plastid ribosomal protein uL15c



- Molecule 22: 50S ribosomal protein L16, chloroplastic

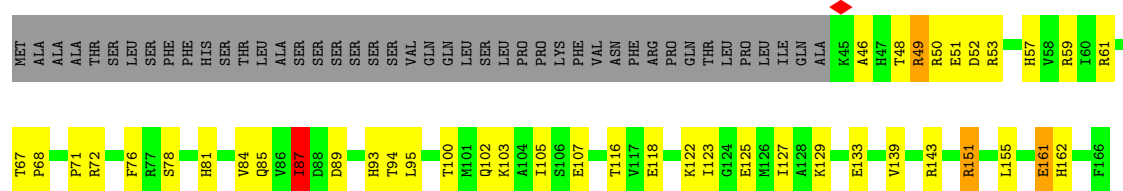


- Molecule 23: plastid ribosomal protein uL14c

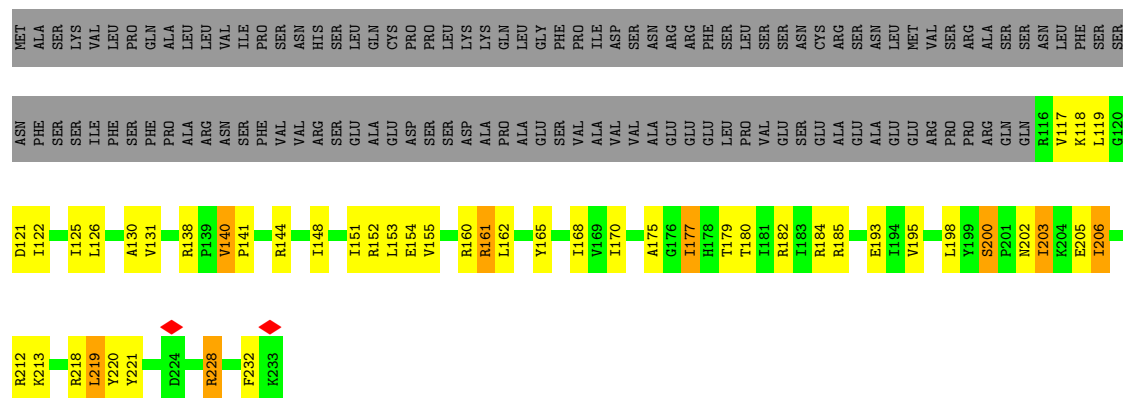
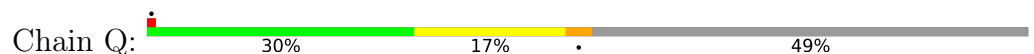




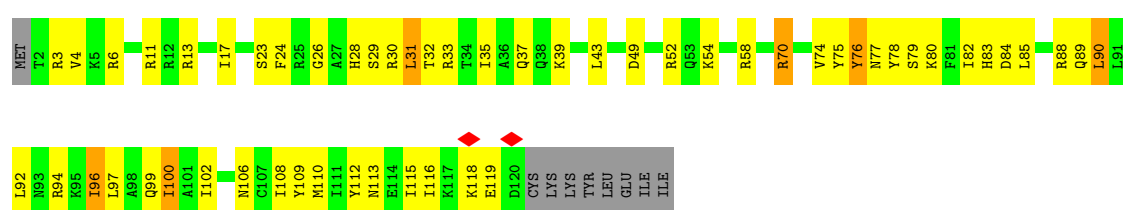
- Molecule 24: plastid ribosomal protein uL18c



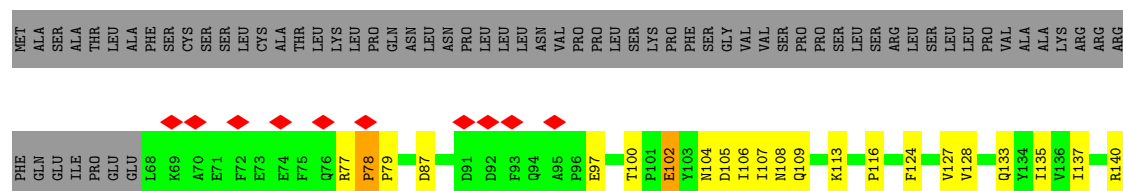
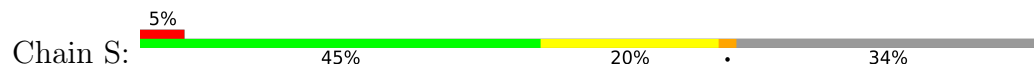
- Molecule 25: 50S ribosomal protein L19, chloroplastic



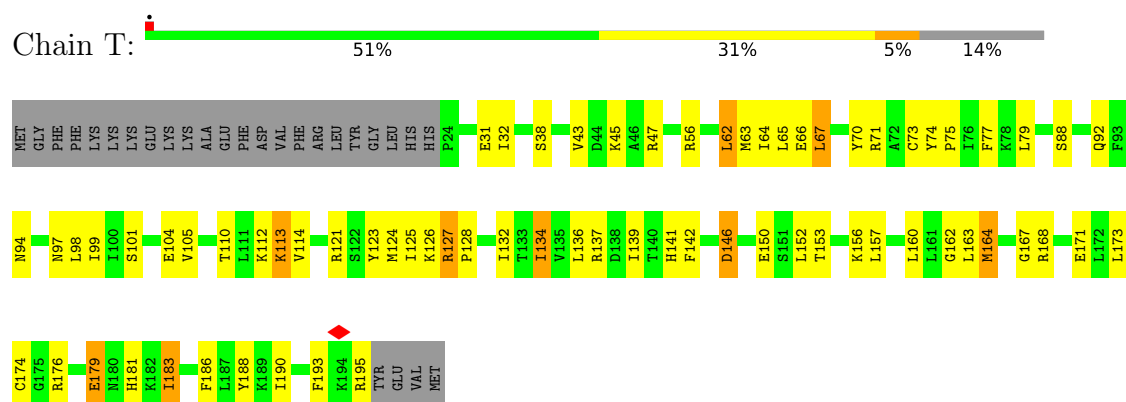
- Molecule 26: 50S ribosomal protein L20, chloroplastic



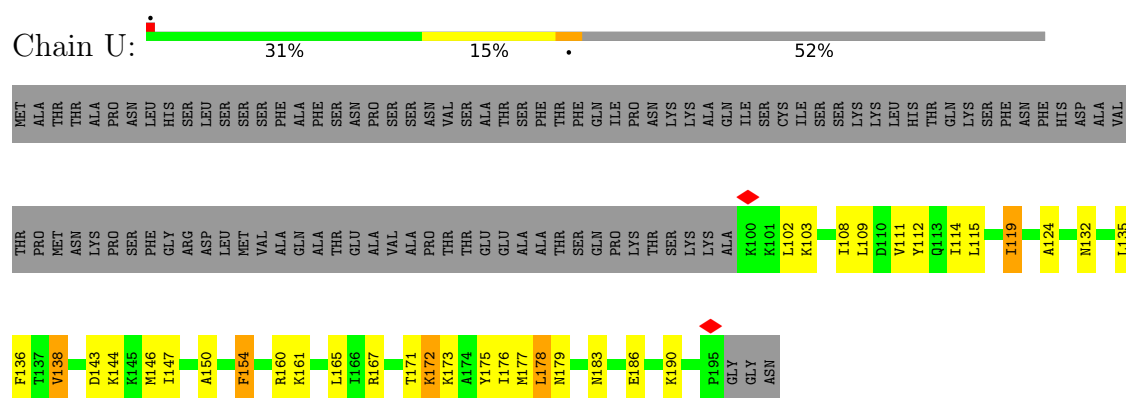
- Molecule 27: 50S ribosomal protein L21, chloroplastic



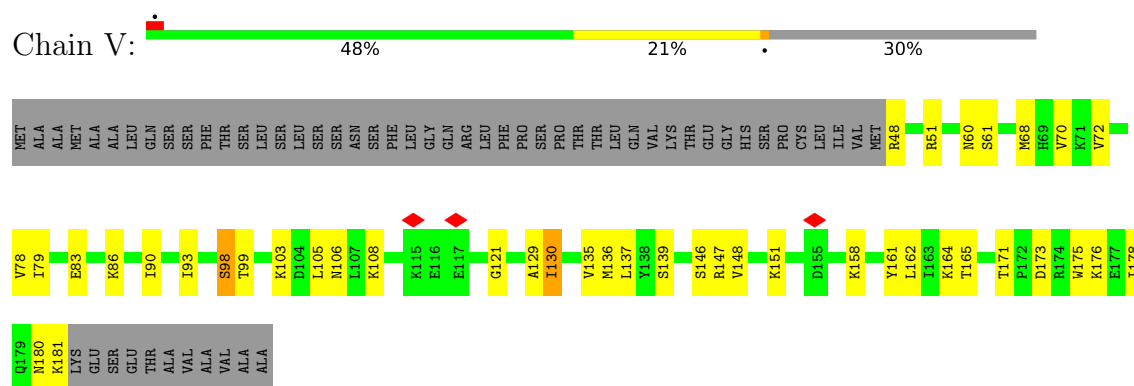
- Molecule 28: 50S ribosomal protein L22, chloroplastic



- Molecule 29: 50S ribosomal protein L23, chloroplastic

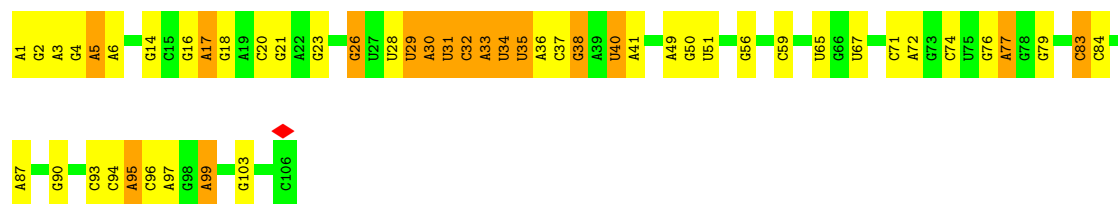


- Molecule 30: plastid ribosomal protein uL24c

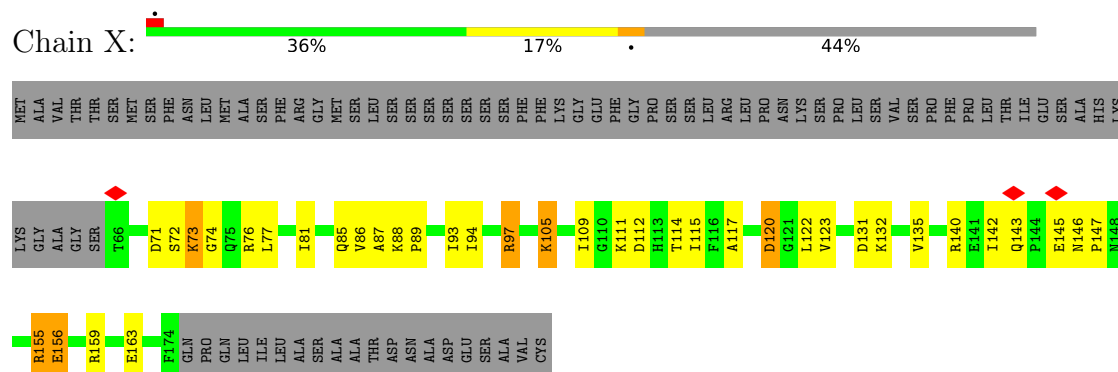


- Molecule 31: 4.5S ribosomal RNA

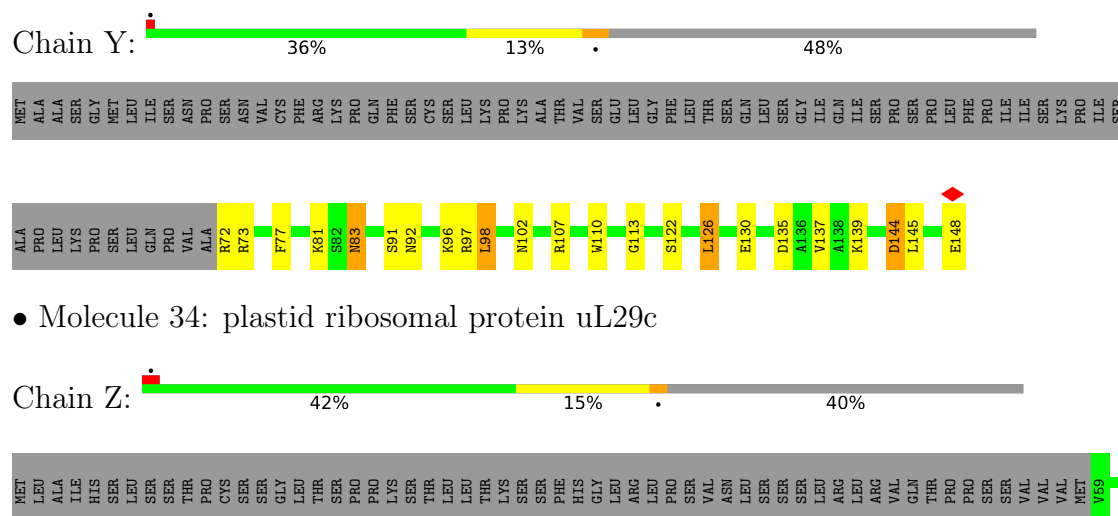




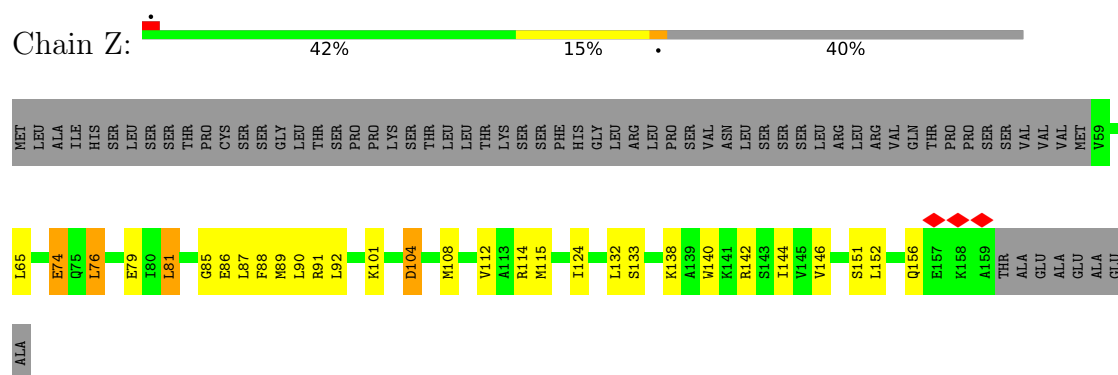
• Molecule 32: plastid ribosomal protein bL27c



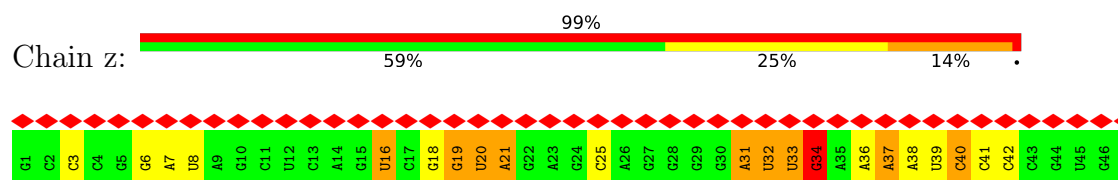
• Molecule 33: plastid ribosomal protein bL28c



• Molecule 34: plastid ribosomal protein uL29c

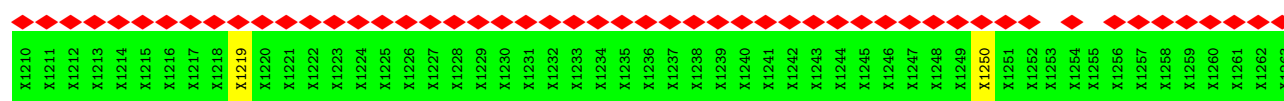
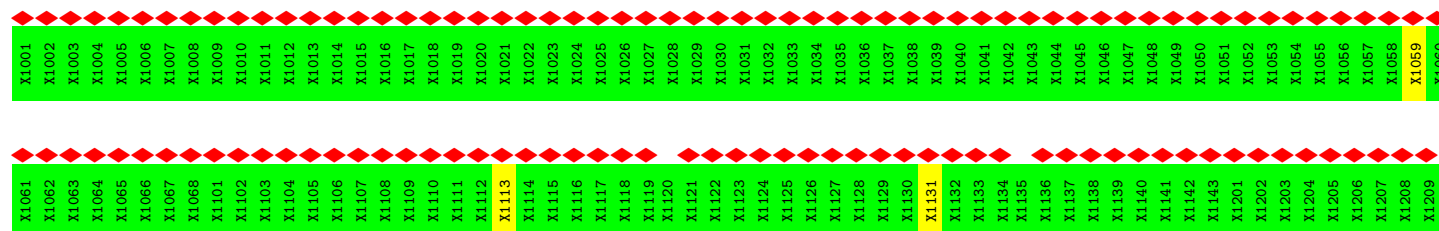


• Molecule 35: tRNA-Phe

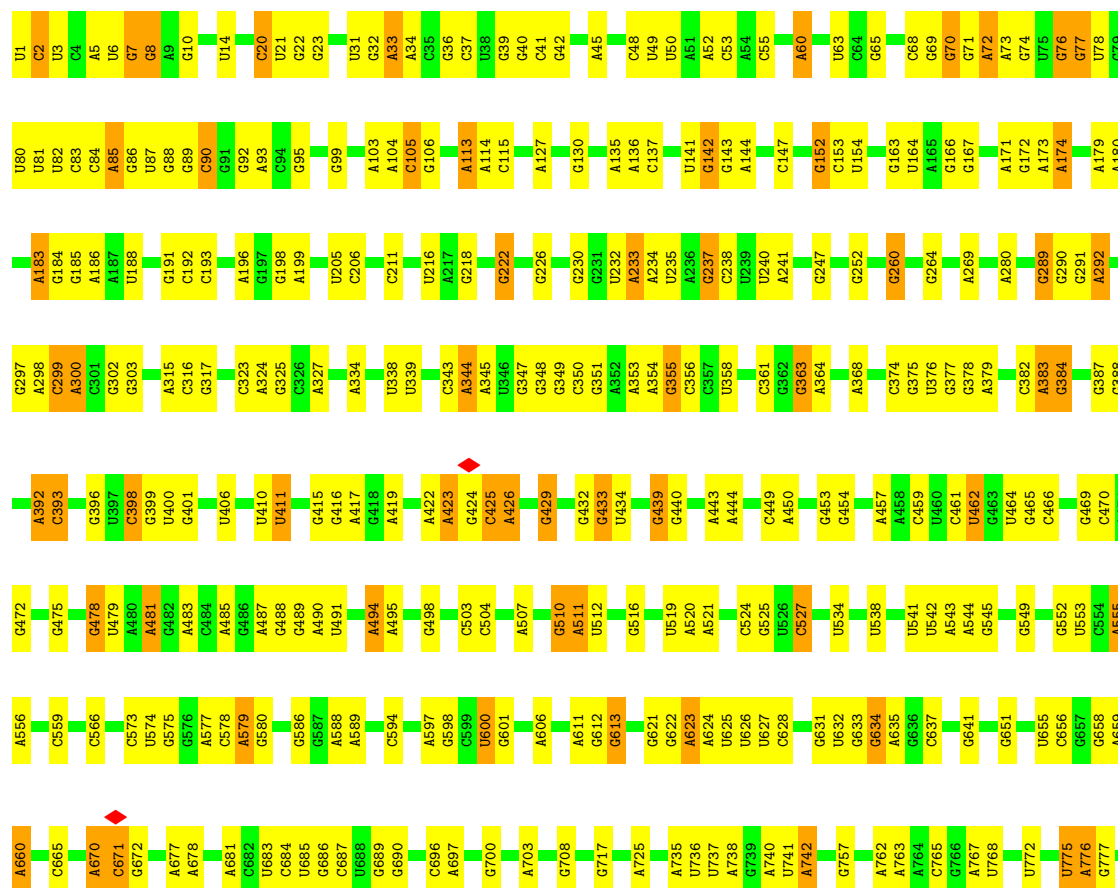


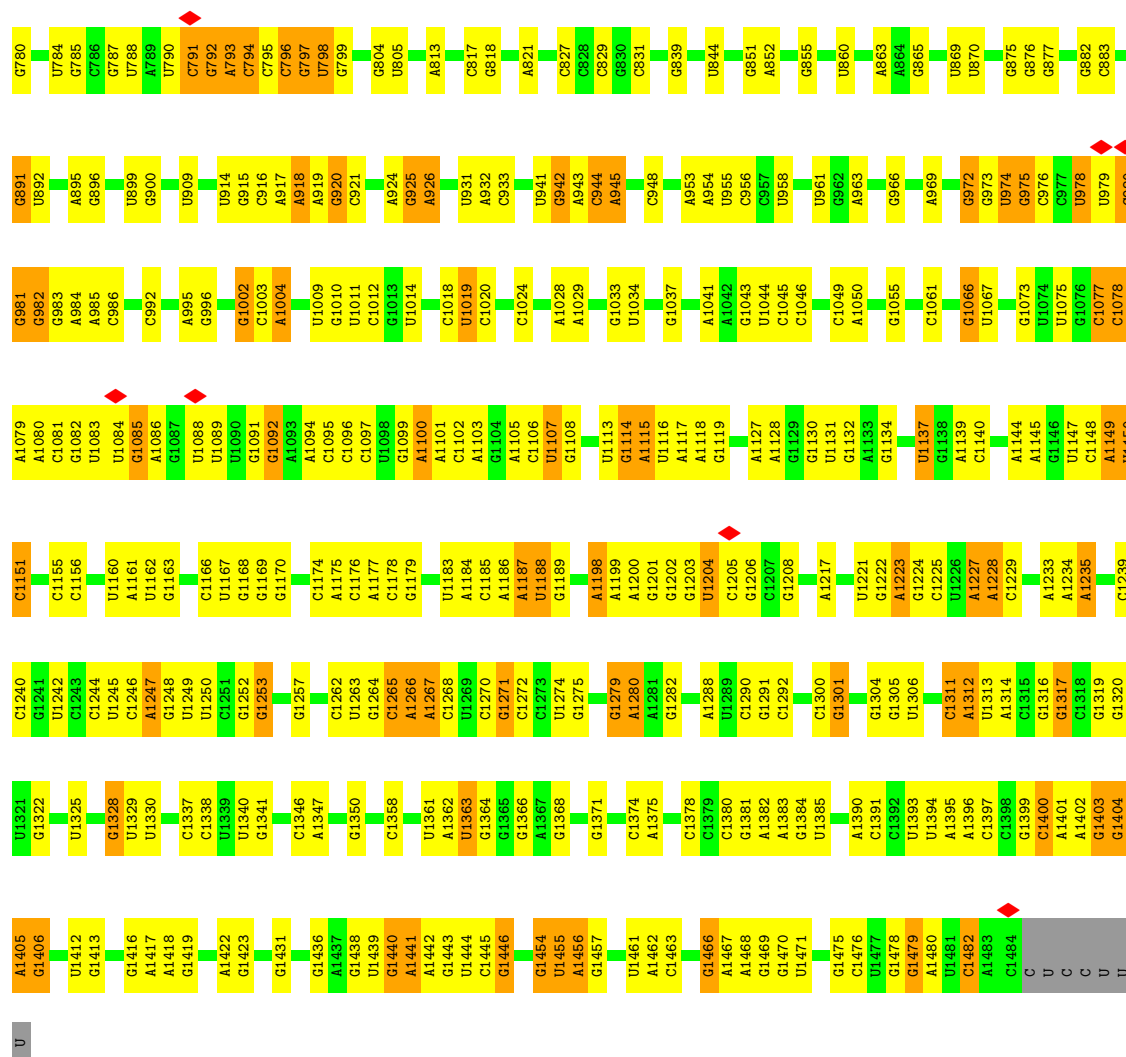


- Molecule 36: plastid ribosomal protein bS1c

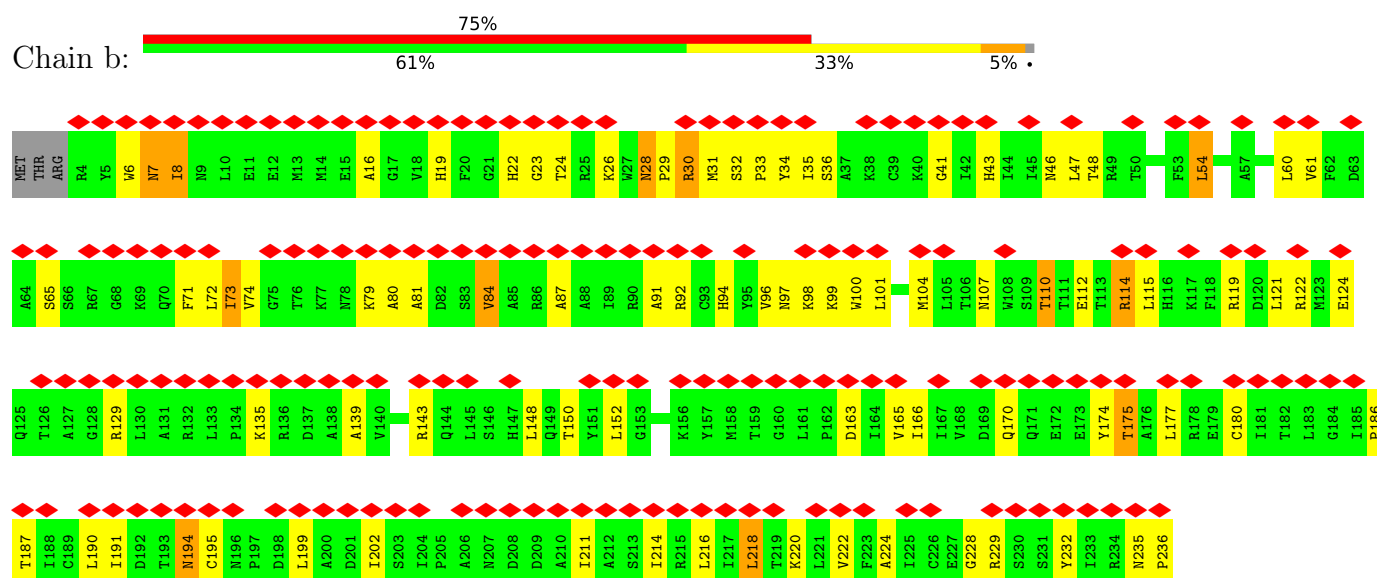


- Molecule 37: 16S ribosomal RNA





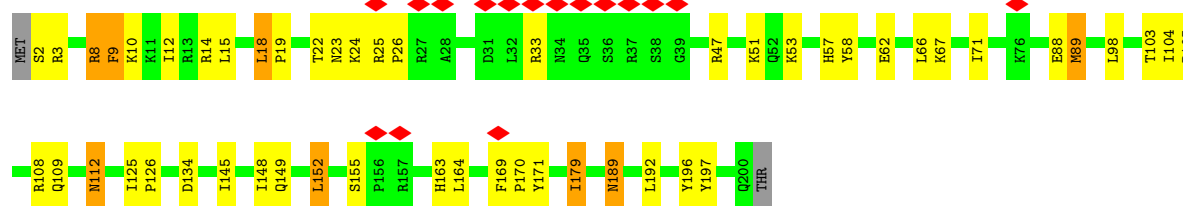
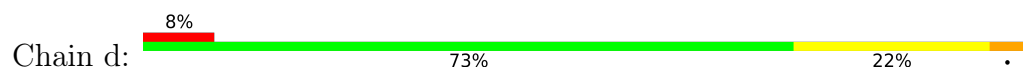
- Molecule 38: 30S ribosomal protein S2, chloroplastic



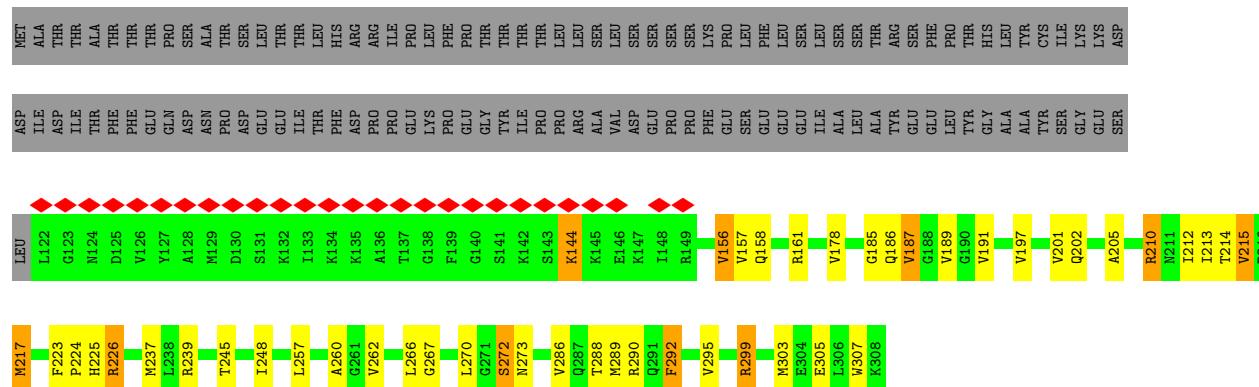
- Molecule 39: 30S ribosomal protein S3, chloroplastic



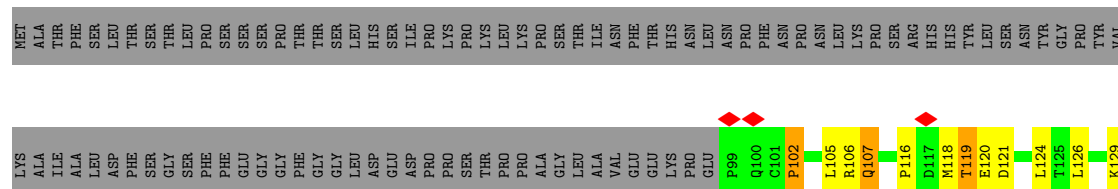
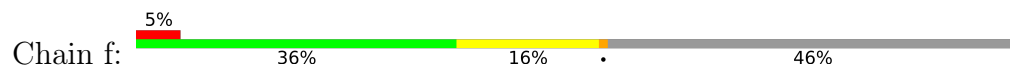
- Molecule 40: 30S ribosomal protein S4, chloroplastic



- Molecule 41: 30S ribosomal protein S5, chloroplastic

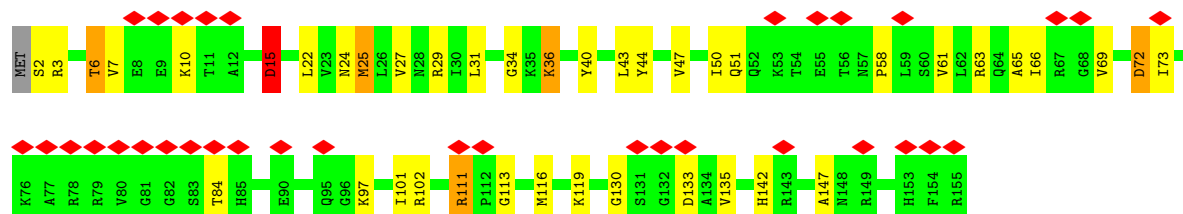
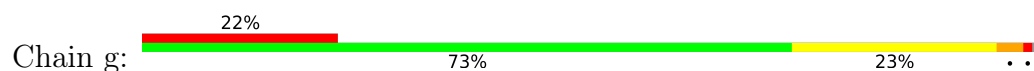


- Molecule 42: plastid ribosomal protein bS6c

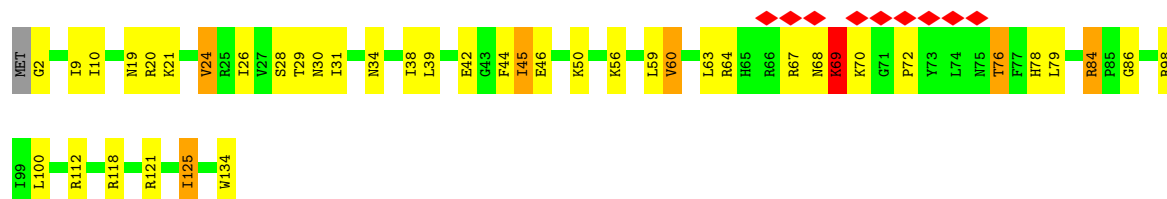




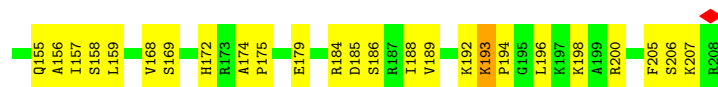
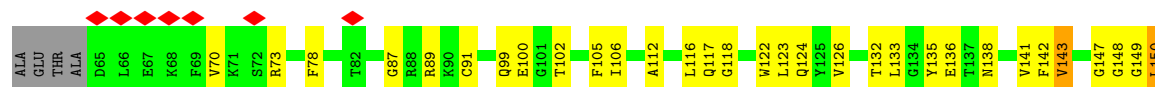
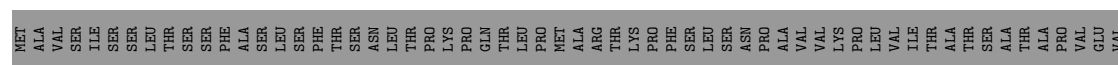
- Molecule 43: 30S ribosomal protein S7, chloroplastic



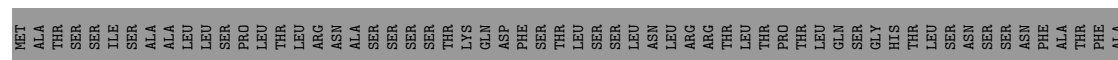
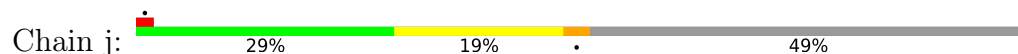
- Molecule 44: 30S ribosomal protein S8, chloroplastic

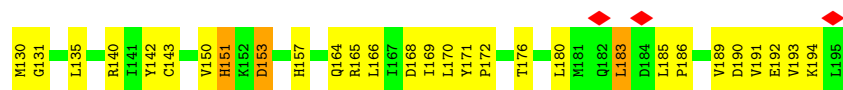


- Molecule 45: plastid ribosomal protein uS9c

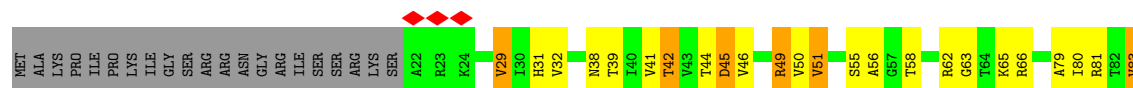


- Molecule 46: plastid ribosomal protein uS10c





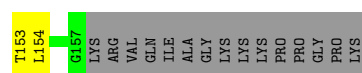
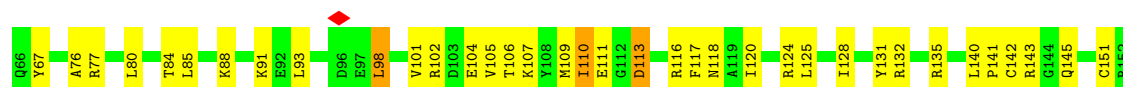
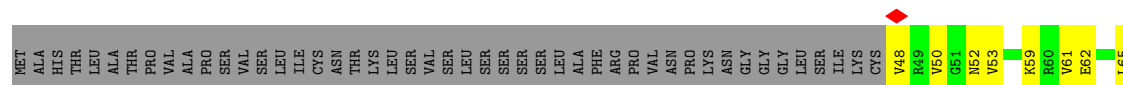
- Molecule 47: 30S ribosomal protein S11, chloroplastic



- Molecule 48: 30S ribosomal protein S12, chloroplastic



- Molecule 49: plastid ribosomal protein uS13c

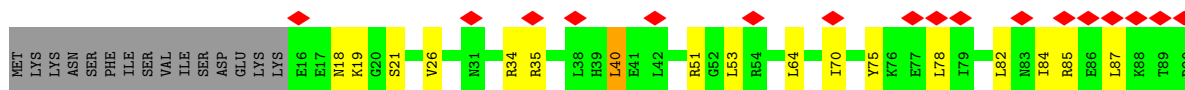


- Molecule 50: 30S ribosomal protein S14, chloroplastic

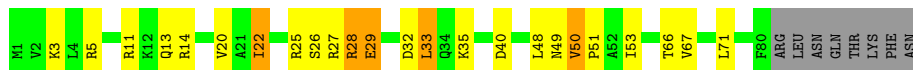


- Molecule 51: 30S ribosomal protein S15, chloroplastic

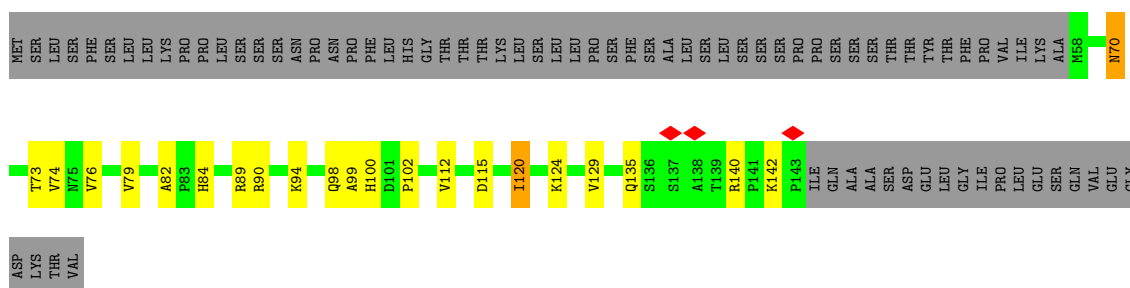
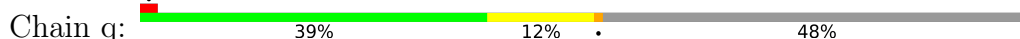




- Molecule 52: 30S ribosomal protein S16, chloroplastic



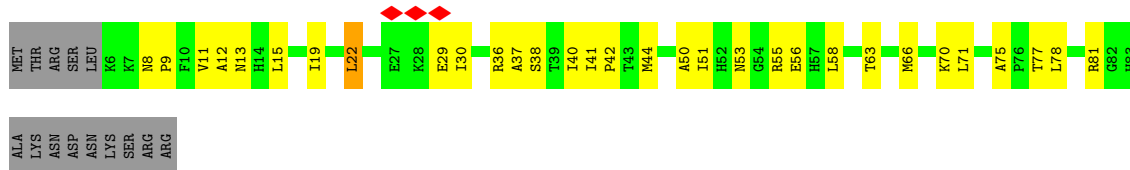
- Molecule 53: plastid ribosomal protein uS17c



- Molecule 54: 30S ribosomal protein S18, chloroplastic

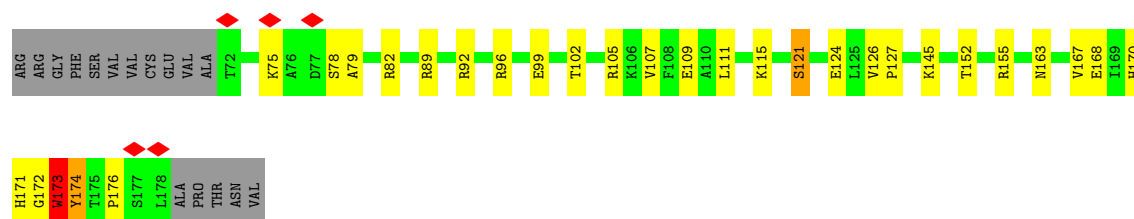


- Molecule 55: 30S ribosomal protein S19 alpha, chloroplastic

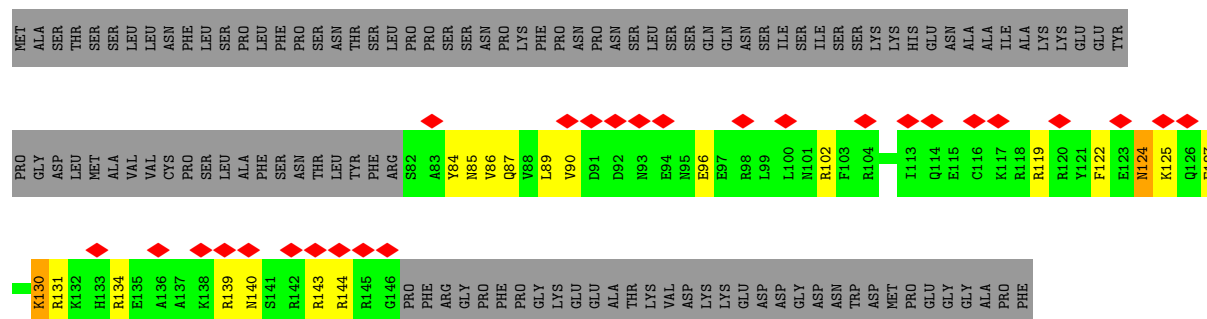


- Molecule 56: plastid ribosomal protein bS20c

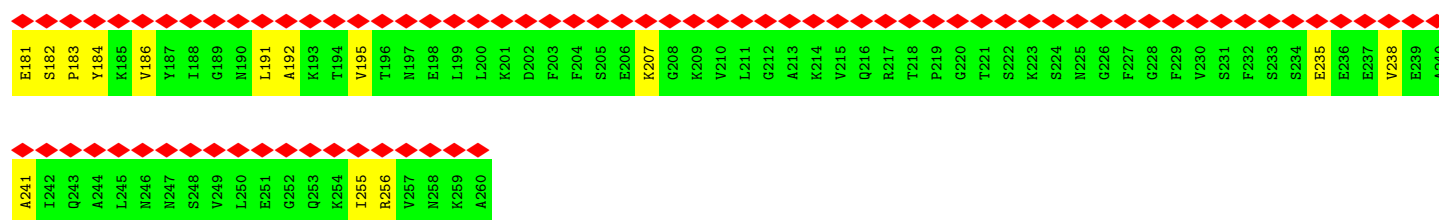
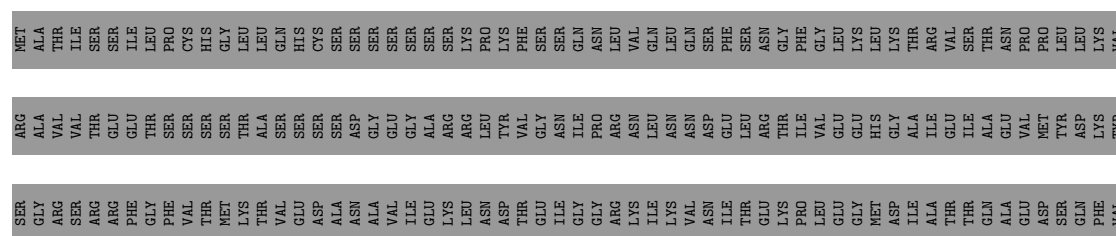




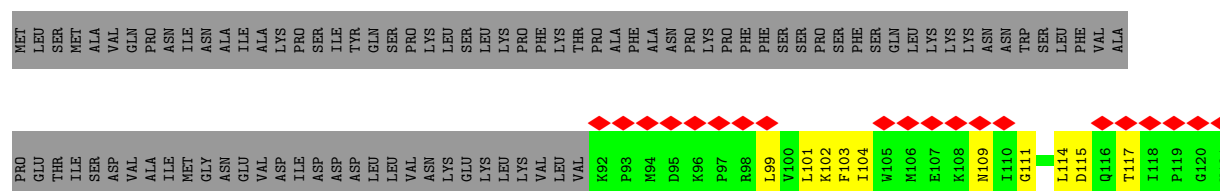
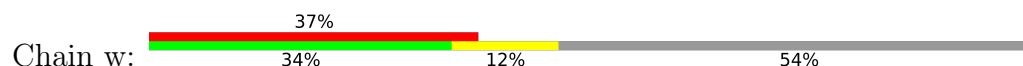
- Molecule 57: plastid ribosomal protein bS21c



- Molecule 58: 30S ribosomal protein 2, chloroplastic

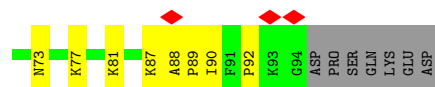
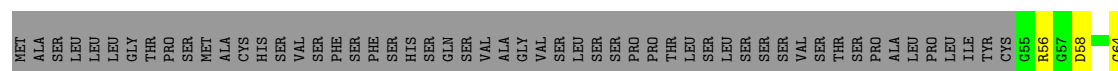


- Molecule 59: 30S ribosomal protein 3, chloroplastic

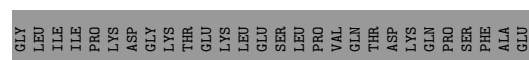
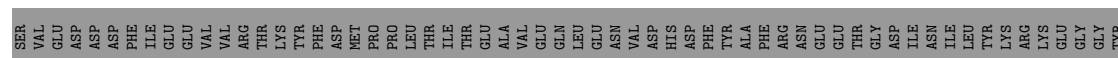




- Molecule 60: 30S ribosomal protein S31, chloroplastic



- Molecule 61: Ribosome-binding factor PSRP1, chloroplastic



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	140583	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	59000	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.481	Depositor
Minimum map value	-0.179	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.018	Depositor
Recommended contour level	0.06	Depositor
Map size (Å)	444.8, 444.8, 444.8	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.39, 1.39, 1.39	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	0	0.85	0/548	1.23	5/737 (0.7%)
2	1	0.69	0/405	1.03	2/537 (0.4%)
3	2	0.58	0/497	1.06	3/664 (0.5%)
4	3	0.69	0/470	1.02	2/619 (0.3%)
5	4	0.68	0/594	1.03	0/784
6	5	0.49	0/307	0.91	0/403
7	6	0.57	0/425	1.23	4/551 (0.7%)
8	7	0.56	0/382	0.92	2/520 (0.4%)
9	A	0.39	0/67297	0.49	0/104984
10	B	0.28	0/2890	0.40	0/4503
11	C	0.62	0/1986	1.06	4/2666 (0.2%)
12	D	0.68	0/1713	1.06	5/2291 (0.2%)
13	E	0.68	0/1707	1.12	10/2298 (0.4%)
14	F	0.52	0/1475	0.98	6/1990 (0.3%)
15	G	0.51	0/1412	0.97	0/1898
16	H	0.55	0/386	0.90	1/514 (0.2%)
17	I	0.85	0/1129	0.89	1/1521 (0.1%)
18	J	0.96	3/992 (0.3%)	1.01	3/1343 (0.2%)
19	K	0.64	0/1688	0.95	2/2279 (0.1%)
20	L	0.64	0/951	1.07	5/1282 (0.4%)
21	M	0.63	0/1430	1.06	1/1896 (0.1%)
22	N	0.58	0/1097	0.99	2/1471 (0.1%)
23	O	0.71	0/959	1.02	1/1280 (0.1%)
24	P	0.48	0/978	0.91	1/1311 (0.1%)
25	Q	0.71	0/967	1.14	8/1299 (0.6%)
26	R	0.75	0/1046	1.01	0/1395
27	S	0.62	0/1339	1.08	7/1826 (0.4%)
28	T	0.64	0/1420	0.98	3/1900 (0.2%)
29	U	0.63	0/787	0.99	0/1056
30	V	0.53	0/1093	1.00	1/1457 (0.1%)
31	W	0.36	0/2551	0.49	0/3977
32	X	0.55	0/905	0.93	2/1204 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Y	0.57	0/644	0.90	0/856
34	Z	0.48	0/854	0.84	0/1131
35	z	0.74	0/1813	0.93	1/2823 (0.0%)
37	a	0.28	0/35687	0.39	0/55680
38	b	0.57	0/1878	0.88	2/2538 (0.1%)
39	c	0.51	0/1763	0.98	1/2370 (0.0%)
40	d	0.46	0/1661	0.95	4/2230 (0.2%)
41	e	0.60	0/1345	1.00	4/1817 (0.2%)
42	f	0.44	0/929	0.90	2/1255 (0.2%)
43	g	0.52	0/1226	0.89	5/1641 (0.3%)
44	h	0.47	0/1094	0.91	0/1467
45	i	0.47	0/1138	0.99	5/1526 (0.3%)
46	j	0.55	0/822	0.88	0/1111
47	k	0.46	0/896	1.04	4/1206 (0.3%)
48	l	0.55	0/975	0.94	1/1312 (0.1%)
49	m	0.50	0/912	0.95	0/1219
50	n	0.55	0/836	0.91	0/1116
51	o	0.46	0/642	0.83	1/852 (0.1%)
52	p	0.48	0/674	0.96	2/902 (0.2%)
53	q	0.47	0/707	0.97	4/949 (0.4%)
54	r	0.48	0/494	0.84	0/660
55	s	0.53	0/646	0.92	0/870
56	t	0.52	0/862	0.95	3/1151 (0.3%)
57	u	0.43	0/572	0.79	0/754
58	v	0.87	0/621	0.87	0/833
59	w	0.91	0/707	0.91	0/962
60	x	0.63	0/317	1.13	3/418 (0.7%)
61	y	0.52	0/930	1.01	3/1243 (0.2%)
All	All	0.46	3/163471 (0.0%)	0.66	126/243348 (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
13	E	0	1
21	M	0	1
38	b	0	1
41	e	0	1
56	t	0	2
All	All	0	6

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
18	J	93	PRO	CA-C	6.57	1.58	1.52
18	J	125	ILE	CA-CB	5.94	1.59	1.54
18	J	90	THR	CA-CB	5.18	1.57	1.52

All (126) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	6	131	TRP	CA-C-N	-10.00	110.08	120.38
7	6	131	TRP	C-N-CA	-10.00	110.08	120.38
47	k	97	GLY	CA-C-N	9.71	129.97	119.87
47	k	97	GLY	C-N-CA	9.71	129.97	119.87
11	C	231	GLY	N-CA-C	-8.73	99.25	112.60
13	E	112	GLY	N-CA-C	-8.10	96.56	111.14
18	J	93	PRO	N-CA-C	8.00	120.46	110.70
27	S	78	PRO	N-CA-CB	7.79	110.64	103.08
12	D	300	LYS	N-CA-C	7.76	122.93	113.38
20	L	74	GLY	N-CA-C	-7.72	104.54	115.43
22	N	86	GLY	N-CA-C	7.59	119.16	111.95
13	E	131	SER	CA-C-N	7.23	126.86	119.56
13	E	131	SER	C-N-CA	7.23	126.86	119.56
1	0	75	GLY	N-CA-C	-7.12	102.95	112.14
22	N	40	ALA	N-CA-C	6.98	118.70	108.86
13	E	172	SER	N-CA-C	6.90	119.97	110.24
28	T	127	ARG	CA-C-N	6.88	126.87	119.78
28	T	127	ARG	C-N-CA	6.88	126.87	119.78
20	L	117	ALA	CA-C-N	6.80	126.42	119.56
20	L	117	ALA	C-N-CA	6.80	126.42	119.56
56	t	172	GLY	N-CA-C	6.79	125.74	115.63
13	E	230	THR	CA-C-N	-6.75	112.04	119.19
13	E	230	THR	C-N-CA	-6.75	112.04	119.19
47	k	63	GLY	N-CA-C	6.61	120.64	112.64
35	z	34	G	O3'-P-O5'	-6.54	94.18	104.00
27	S	79	PRO	N-CA-CB	6.41	109.98	103.25
40	d	155	SER	CA-C-N	6.40	126.02	119.56
40	d	155	SER	C-N-CA	6.40	126.02	119.56
3	2	52	CYS	CA-C-N	6.34	126.03	119.56
3	2	52	CYS	C-N-CA	6.34	126.03	119.56
25	Q	200	SER	CA-C-N	6.30	125.87	119.19
25	Q	200	SER	C-N-CA	6.30	125.87	119.19
47	k	129	GLY	N-CA-C	6.30	118.35	110.29
12	D	215	HIS	N-CA-C	6.26	121.69	113.30
30	V	103	LYS	N-CA-C	6.24	118.60	111.11

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
56	t	172	GLY	CA-C-N	-6.22	113.67	123.12
56	t	172	GLY	C-N-CA	-6.22	113.67	123.12
61	y	126	GLY	CA-C-N	6.16	127.01	120.11
61	y	126	GLY	C-N-CA	6.16	127.01	120.11
60	x	88	ALA	CA-C-N	-6.11	113.49	119.90
60	x	88	ALA	C-N-CA	-6.11	113.49	119.90
52	p	40	ASP	CA-C-N	6.10	125.50	118.85
52	p	40	ASP	C-N-CA	6.10	125.50	118.85
21	M	177	SER	CB-CA-C	-6.09	108.54	115.79
13	E	203	GLU	N-CA-C	6.06	120.41	113.19
7	6	129	GLY	CA-C-N	-6.03	113.85	122.77
7	6	129	GLY	C-N-CA	-6.03	113.85	122.77
25	Q	155	VAL	CA-C-N	6.03	125.71	119.56
25	Q	155	VAL	C-N-CA	6.03	125.71	119.56
13	E	126	ARG	N-CA-C	6.02	117.64	111.14
16	H	87	VAL	N-CA-C	5.98	116.47	107.80
53	q	84	HIS	CA-C-N	5.95	125.42	119.24
53	q	84	HIS	C-N-CA	5.95	125.42	119.24
3	2	65	LYS	CD-CE-NZ	-5.91	92.98	111.90
18	J	90	THR	CA-C-N	-5.90	114.53	120.31
18	J	90	THR	C-N-CA	-5.90	114.53	120.31
43	g	111	ARG	CA-C-N	5.90	126.00	119.87
43	g	111	ARG	C-N-CA	5.90	126.00	119.87
11	C	93	GLY	N-CA-C	-5.88	107.37	114.66
41	e	187	VAL	N-CA-C	5.82	117.47	108.44
20	L	22	ILE	N-CA-C	5.82	119.77	113.43
12	D	175	SER	CA-C-N	-5.78	115.94	122.93
12	D	175	SER	C-N-CA	-5.78	115.94	122.93
23	O	93	VAL	CB-CA-C	-5.71	108.28	113.70
14	F	191	PHE	CA-C-N	5.69	125.22	119.19
14	F	191	PHE	C-N-CA	5.69	125.22	119.19
43	g	15	ASP	CA-C-N	5.63	125.74	119.32
43	g	15	ASP	C-N-CA	5.63	125.74	119.32
53	q	82	ALA	CA-C-N	5.61	126.85	119.84
53	q	82	ALA	C-N-CA	5.61	126.85	119.84
17	I	96	LEU	N-CA-C	5.61	119.86	112.35
1	0	83	ASN	N-CA-C	5.61	118.32	111.82
27	S	97	GLU	CA-C-N	5.60	125.28	119.56
27	S	97	GLU	C-N-CA	5.60	125.28	119.56
24	P	87	ILE	N-CA-C	5.58	116.78	108.46
51	o	70	ILE	N-CA-C	5.57	115.65	110.42
2	1	3	VAL	CA-C-N	5.56	126.80	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	1	3	VAL	C-N-CA	5.56	126.80	119.84
41	e	212	ILE	N-CA-C	5.54	117.17	109.80
32	X	88	LYS	CA-C-N	-5.51	114.25	119.76
32	X	88	LYS	C-N-CA	-5.51	114.25	119.76
25	Q	140	VAL	N-CA-C	5.50	113.89	107.89
25	Q	220	TYR	N-CA-C	-5.50	106.61	113.38
41	e	144	LYS	N-CA-C	5.47	117.59	108.02
25	Q	218	ARG	CA-C-N	-5.47	115.25	122.85
25	Q	218	ARG	C-N-CA	-5.47	115.25	122.85
27	S	116	PRO	CA-C-N	5.47	126.01	120.38
27	S	116	PRO	C-N-CA	5.47	126.01	120.38
45	i	141	VAL	N-CA-C	5.43	115.67	107.80
20	L	12	ASP	N-CA-C	5.42	116.50	108.86
11	C	226	HIS	CA-C-N	5.42	126.61	119.84
11	C	226	HIS	C-N-CA	5.42	126.61	119.84
1	0	79	PHE	N-CA-C	5.41	117.61	111.11
45	i	193	LYS	CA-C-N	5.37	125.63	119.83
45	i	193	LYS	C-N-CA	5.37	125.63	119.83
60	x	89	PRO	N-CA-C	5.31	118.82	110.80
1	0	90	ASP	N-CA-C	5.30	119.37	113.01
27	S	188	GLU	N-CA-C	5.28	116.87	108.79
19	K	195	ILE	CA-C-N	5.27	124.94	119.56
19	K	195	ILE	C-N-CA	5.27	124.94	119.56
39	c	102	GLU	N-CA-C	5.26	116.82	111.14
28	T	67	LEU	N-CA-C	5.26	119.79	113.17
41	e	215	VAL	N-CA-C	5.23	113.04	107.76
38	b	28	ASN	CA-C-N	5.22	124.94	119.82
38	b	28	ASN	C-N-CA	5.22	124.94	119.82
8	7	75	GLY	CA-C-N	5.21	125.21	119.90
8	7	75	GLY	C-N-CA	5.21	125.21	119.90
12	D	229	HIS	CB-CA-C	-5.14	110.24	117.23
43	g	113	GLY	N-CA-C	5.14	120.36	111.98
45	i	174	ALA	CA-C-N	-5.14	113.62	118.97
45	i	174	ALA	C-N-CA	-5.14	113.62	118.97
4	3	143	ASN	CA-C-N	5.14	125.14	119.90
4	3	143	ASN	C-N-CA	5.14	125.14	119.90
42	f	102	PRO	CA-C-N	5.11	126.22	119.84
42	f	102	PRO	C-N-CA	5.11	126.22	119.84
13	E	134	ARG	CA-C-N	5.10	124.86	119.76
13	E	134	ARG	C-N-CA	5.10	124.86	119.76
61	y	140	ARG	NE-CZ-NH2	-5.09	114.62	119.20
1	0	94	VAL	CB-CA-C	-5.07	105.48	111.97

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
48	l	47	SER	N-CA-C	5.07	117.82	110.42
14	F	161	LEU	CA-C-N	-5.04	114.46	119.56
14	F	161	LEU	C-N-CA	-5.04	114.46	119.56
40	d	18	LEU	CA-C-N	5.01	124.45	119.24
40	d	18	LEU	C-N-CA	5.01	124.45	119.24
14	F	171	ASN	CA-C-N	5.00	125.07	119.87
14	F	171	ASN	C-N-CA	5.00	125.07	119.87

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
13	E	134	ARG	Peptide
21	M	104	ALA	Peptide
38	b	74	VAL	Peptide
41	e	144	LYS	Peptide
56	t	173	TRP	Peptide
56	t	75	LYS	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	536	0	515	30	0
2	1	396	0	437	11	0
3	2	489	0	507	9	0
4	3	467	0	526	12	0
5	4	588	0	658	15	0
6	5	305	0	344	14	0
7	6	422	0	508	9	0
8	7	368	0	386	7	0
9	A	60083	0	30259	642	0
10	B	2584	0	1305	36	0
11	C	1952	0	2038	61	0
12	D	1686	0	1772	59	0
13	E	1676	0	1737	49	0
14	F	1454	0	1488	46	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
15	G	1391	0	1458	39	0
16	H	382	0	437	10	0
17	I	1106	0	1122	40	0
18	J	977	0	1027	33	0
19	K	1648	0	1684	44	0
20	L	942	0	996	27	0
21	M	1410	0	1495	46	0
22	N	1075	0	1134	43	0
23	O	944	0	1004	30	0
24	P	962	0	984	31	0
25	Q	953	0	1050	35	0
26	R	1029	0	1092	42	0
27	S	1310	0	1315	33	0
28	T	1395	0	1482	47	0
29	U	776	0	837	24	0
30	V	1078	0	1144	21	0
31	W	2277	0	1146	27	0
32	X	888	0	923	21	0
33	Y	634	0	684	14	0
34	Z	846	0	918	19	0
35	z	1623	0	821	26	0
36	8	870	0	184	4	0
37	a	31868	0	16050	400	0
38	b	1844	0	1887	62	0
39	c	1736	0	1819	54	0
40	d	1633	0	1730	36	0
41	e	1331	0	1312	29	0
42	f	911	0	923	20	0
43	g	1210	0	1284	27	0
44	h	1079	0	1137	31	0
45	i	1119	0	1181	32	0
46	j	805	0	849	37	0
47	k	882	0	928	39	0
48	l	959	0	1035	22	0
49	m	904	0	943	31	0
50	n	820	0	858	26	0
51	o	635	0	686	10	0
52	p	664	0	703	18	0
53	q	693	0	729	13	0
54	r	490	0	532	11	0
55	s	631	0	661	21	0
56	t	853	0	915	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	u	568	0	576	15	0
58	v	613	0	621	9	0
59	w	686	0	706	15	0
60	x	309	0	323	11	0
61	y	919	0	958	45	0
62	2	1	0	0	0	0
62	5	1	0	0	0	0
63	4	1	0	0	0	0
63	6	1	0	0	0	0
63	7	1	0	0	0	0
63	A	511	0	0	0	0
63	B	15	0	0	0	0
63	C	1	0	0	0	0
63	D	1	0	0	0	0
63	E	1	0	0	0	0
63	F	1	0	0	0	0
63	H	1	0	0	0	0
63	M	2	0	0	0	0
63	P	1	0	0	0	0
63	R	1	0	0	0	0
63	S	1	0	0	0	0
63	T	1	0	0	0	0
63	U	1	0	0	0	0
63	V	1	0	0	0	0
63	W	14	0	0	0	0
63	a	219	0	0	0	0
63	k	1	0	0	0	0
63	l	1	0	0	0	0
63	n	1	0	0	0	0
63	x	1	0	0	0	0
All	All	152465	0	104763	2278	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 9.

All (2278) 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)
37:a:1288:A:OP1	61:y:140:ARG:NH2	1.93	1.02
17:I:122:ILE:HD12	17:I:165:CYS:HB2	1.50	0.94
9:A:652:C:N4	9:A:657:U:O4	2.01	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:B:54:G:HO2'	10:B:55:G:H8	1.00	0.93
9:A:817:C:OP2	21:M:120:ARG:NH1	2.03	0.92
14:F:55:ASN:HA	14:F:59:THR:HB	1.52	0.89
37:a:955:U:O4	37:a:972:G:N2	2.06	0.89
37:a:776:A:OP1	44:h:21:LYS:NZ	2.08	0.87
20:L:15:GLY:HA3	20:L:50:THR:HG21	1.57	0.87
35:z:34:G:H21	61:y:140:ARG:HB2	1.40	0.86
55:s:36:ARG:NH2	55:s:75:ALA:O	2.08	0.86
9:A:1828:U:OP2	11:C:152:ARG:NH1	2.08	0.86
35:z:8:U:HO2'	35:z:21:A:H61	1.24	0.86
37:a:1288:A:H5''	61:y:140:ARG:NH1	1.90	0.86
9:A:540:A:H62	9:A:2055:U:H3	1.24	0.85
9:A:1086:G:H21	18:J:198:ILE:HG12	1.43	0.83
25:Q:160:ARG:NH2	37:a:144:A:OP1	2.11	0.83
9:A:1485:U:H5'	9:A:1486:U:H5'	1.60	0.83
37:a:137:C:N4	37:a:152:G:O6	2.10	0.83
10:B:15:A:H4'	10:B:16:G:H5''	1.60	0.83
9:A:2767:A:H3'	9:A:2768:A:H5''	1.60	0.82
35:z:8:U:O2'	35:z:21:A:N6	2.13	0.82
37:a:877:G:O2'	37:a:1482:C:OP1	1.97	0.81
37:a:671:C:H41	57:u:144:ARG:HH12	1.28	0.81
2:1:6:LYS:NZ	9:A:2033:A:N7	2.29	0.81
9:A:2345:A:H2'	9:A:2346:A:C8	2.16	0.80
9:A:2456:A:H4'	9:A:2457:C:H5''	1.62	0.80
37:a:232:U:OP2	56:t:155:ARG:NH2	2.15	0.80
13:E:128:SER:HB2	13:E:134:ARG:HH22	1.47	0.80
17:I:139:GLU:HB3	17:I:141:PRO:HD2	1.65	0.79
41:e:156:VAL:HA	41:e:178:VAL:HG22	1.64	0.79
3:2:49:ARG:HG3	3:2:60:ILE:HD12	1.65	0.79
9:A:1810:C:OP2	11:C:178:ARG:NH2	2.16	0.78
9:A:2142:G:H1	9:A:2174:C:H42	1.28	0.78
2:1:13:LYS:NZ	9:A:528:C:OP1	2.16	0.78
9:A:2122:C:O2	9:A:2195:G:N1	2.15	0.78
37:a:612:G:H22	37:a:689:G:H1	1.32	0.78
35:z:8:U:HO2'	35:z:21:A:N6	1.81	0.78
45:i:118:GLY:HA2	45:i:123:LEU:HD11	1.65	0.78
9:A:1082:A:H4'	17:I:83:GLY:HA2	1.65	0.78
9:A:844:G:H1'	21:M:130:GLU:HB3	1.66	0.77
14:F:107:ILE:HG23	14:F:118:PRO:HD2	1.66	0.77
9:A:2267:G:O6	9:A:2271:C:N4	2.17	0.77
49:m:93:LEU:HD23	49:m:98:LEU:HD13	1.66	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:B:8:G:H21	24:P:85:GLN:HE22	1.30	0.77
9:A:311:U:OP2	30:V:147:ARG:NH2	2.16	0.77
9:A:2310:U:H5''	24:P:143:ARG:HH12	1.50	0.77
41:e:248:ILE:HD11	41:e:266:LEU:HD22	1.66	0.76
44:h:30:ASN:O	44:h:34:ASN:ND2	2.18	0.76
9:A:2464:G:N7	9:A:2518:C:H2'	2.00	0.76
61:y:114:VAL:HG13	61:y:134:VAL:HG12	1.68	0.76
9:A:596:A:H62	9:A:1272:A:H2	1.33	0.76
9:A:2077:C:H42	9:A:2464:G:H1	1.32	0.76
19:K:97:ASN:HD21	27:S:135:ILE:H	1.31	0.76
37:a:8:G:O6	41:e:226:ARG:NH2	2.19	0.76
45:i:73:ARG:NH2	45:i:100:GLU:O	2.18	0.76
35:z:32:U:H5'	35:z:33:U:H5''	1.67	0.76
25:Q:138:ARG:HH12	25:Q:203:ILE:HB	1.51	0.75
47:k:31:HIS:HB2	47:k:42:THR:HG22	1.66	0.75
9:A:13:A:H2'	9:A:14:A:C8	2.21	0.75
9:A:2105:U:OP1	16:H:47:LYS:NZ	2.16	0.75
9:A:2657:G:OP2	19:K:194:ARG:NH2	2.20	0.75
9:A:2151:G:N1	9:A:2169:C:O2	2.20	0.75
47:k:80:ILE:HD11	47:k:109:ILE:HD13	1.69	0.75
9:A:1098:A:N7	9:A:1124:A:O2'	2.20	0.75
20:L:30:ARG:HG2	20:L:32:TYR:H	1.52	0.75
40:d:22:THR:HG22	40:d:24:LYS:H	1.52	0.75
1:O:37:ARG:N	10:B:45:G:OP1	2.19	0.74
7:6:118:ARG:NH1	9:A:1491:G:OP2	2.15	0.74
9:A:1693:U:H2'	9:A:1694:C:H6	1.52	0.74
55:s:55:ARG:HG3	55:s:56:GLU:HG3	1.66	0.74
37:a:136:A:N6	37:a:153:C:O2	2.20	0.74
37:a:1316:G:OP2	45:i:192:LYS:NZ	2.21	0.74
9:A:2601:U:H5'	9:A:2602:U:H5'	1.69	0.74
19:K:75:PRO:HD2	19:K:88:GLU:HG2	1.68	0.74
37:a:374:C:H5''	40:d:126:PRO:HD2	1.69	0.74
6:5:6:SER:HB2	9:A:2483:C:H5''	1.70	0.73
20:L:2:ILE:HB	20:L:33:ALA:HB3	1.70	0.73
37:a:465:G:N1	37:a:481:A:OP2	2.21	0.73
37:a:1055:G:H5''	39:c:183:ARG:HG3	1.70	0.73
56:t:121:SER:HB2	56:t:173:TRP:CH2	2.24	0.73
9:A:316:G:H22	9:A:339:A:H61	1.35	0.73
35:z:58:A:O2'	35:z:60:U:OP2	2.04	0.73
9:A:2726:G:OP1	23:O:28:ARG:NH1	2.22	0.72
22:N:13:HIS:O	22:N:72:LYS:NZ	2.22	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:k:110:ARG:HG2	57:u:96:GLU:HB3	1.70	0.72
12:D:296:LYS:HB3	12:D:302:ILE:HD11	1.71	0.72
24:P:81:HIS:HD2	24:P:100:THR:HB	1.54	0.72
37:a:914:U:OP2	61:y:82:ARG:NH2	2.21	0.72
9:A:2256:A:OP1	11:C:239:ARG:NH2	2.23	0.72
15:G:189:ARG:HD2	15:G:204:TYR:HE1	1.55	0.72
9:A:885:G:H1	9:A:911:U:H3	1.38	0.72
9:A:888:C:H3'	9:A:889:G:H8	1.54	0.72
6:5:19:ARG:HG2	9:A:2774:U:H5''	1.72	0.71
9:A:894:G:N2	9:A:901:C:O2	2.23	0.71
11:C:42:ARG:CZ	11:C:44:ILE:HD11	2.21	0.71
12:D:93:MET:H	12:D:121:ASN:HD21	1.36	0.71
10:B:44:C:O2	14:F:145:ARG:NH1	2.23	0.71
1:0:61:THR:HG22	1:0:62:GLY:H	1.56	0.71
37:a:671:C:N4	57:u:144:ARG:HH12	1.88	0.71
37:a:1253:G:H21	37:a:1280:A:H2	1.39	0.71
38:b:100:TRP:HZ3	38:b:175:THR:HB	1.55	0.71
51:o:18:ASN:HB2	51:o:21:SER:HB3	1.73	0.70
38:b:98:LYS:HD2	38:b:150:THR:HA	1.73	0.70
21:M:134:MET:SD	21:M:138:ARG:NH1	2.65	0.70
38:b:22:HIS:HB2	38:b:194:ASN:HD21	1.54	0.70
14:F:211:THR:HG22	14:F:213:ALA:H	1.57	0.70
37:a:1167:U:OP1	50:n:58:ARG:NH2	2.25	0.70
28:T:164:MET:HB2	28:T:168:ARG:HB2	1.74	0.70
59:w:117:THR:HG22	59:w:123:THR:HG22	1.74	0.70
37:a:1078:C:O2	37:a:1094:A:N6	2.25	0.70
52:p:50:VAL:HG23	52:p:51:PRO:HD3	1.74	0.70
9:A:2075:G:N2	9:A:2076:A:N1	2.40	0.69
9:A:1090:U:H1'	18:J:205:ASN:HD21	1.58	0.69
21:M:240:LYS:HE3	21:M:242:ILE:HD11	1.75	0.69
9:A:2125:C:O2	9:A:2161:G:N2	2.23	0.69
12:D:146:ASP:N	12:D:146:ASP:OD1	2.24	0.69
21:M:182:LYS:HE2	21:M:189:PRO:HG2	1.75	0.69
37:a:1265:C:OP2	50:n:28:LYS:NZ	2.25	0.69
38:b:91:ALA:HB2	38:b:222:VAL:HG13	1.75	0.69
9:A:376:U:O2'	9:A:378:A:N1	2.25	0.69
37:a:660:A:OP1	42:f:159:LYS:NZ	2.24	0.69
1:0:60:THR:HB	14:F:52:GLU:HA	1.74	0.69
47:k:127:HIS:O	47:k:128:ASN:ND2	2.25	0.69
9:A:45:A:H2'	9:A:46:C:H5'	1.74	0.69
21:M:143:LEU:HB2	21:M:146:ILE:HD12	1.73	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:681:A:H5''	21:M:122:GLY:HA2	1.75	0.69
9:A:879:G:O3'	22:N:6:ARG:NH1	2.25	0.69
25:Q:161:ARG:NH2	37:a:316:C:OP1	2.26	0.69
9:A:9:A:C2	31:W:99:A:H1'	2.28	0.68
9:A:182:A:N6	9:A:2447:A:O2'	2.26	0.68
17:I:77:ALA:HB3	17:I:133:LEU:HB3	1.76	0.68
9:A:1928:C:N4	37:a:1358:C:O2'	2.26	0.68
27:S:192:ASP:OD1	27:S:193:ASP:N	2.25	0.68
37:a:1097:C:O2'	37:a:1228:A:N1	2.24	0.68
38:b:72:LEU:HD23	38:b:94:HIS:HB2	1.74	0.68
39:c:26:PRO:HG3	46:j:140:ARG:HH22	1.58	0.68
9:A:1693:U:H2'	9:A:1694:C:C6	2.28	0.68
37:a:376:U:O4	40:d:2:SER:N	2.26	0.68
38:b:174:TYR:HA	38:b:177:LEU:HD12	1.74	0.68
10:B:43:C:O2'	14:F:116:GLN:NE2	2.26	0.68
37:a:839:G:O2'	37:a:855:G:O6	2.11	0.68
9:A:757:U:O2'	9:A:2628:C:O2'	2.12	0.68
37:a:205:U:H2'	37:a:206:C:C6	2.28	0.68
26:R:76:TYR:OH	26:R:84:ASP:OD2	2.11	0.68
40:d:9:PHE:CE2	40:d:26:PRO:HA	2.28	0.68
55:s:40:ILE:HG23	55:s:44:MET:HE3	1.74	0.68
37:a:1325:U:H5'	43:g:102:ARG:HH22	1.59	0.68
9:A:1817:G:H5'	9:A:1818:U:OP2	1.94	0.67
9:A:1106:C:O2'	9:A:1116:A:OP1	2.13	0.67
9:A:1604:A:H2'	9:A:1605:A:C8	2.29	0.67
15:G:126:LYS:HE3	15:G:205:VAL:HG11	1.76	0.67
28:T:181:HIS:HB2	28:T:183:ILE:HD11	1.76	0.67
40:d:189:ASN:N	40:d:189:ASN:OD1	2.27	0.67
49:m:113:ASP:N	49:m:113:ASP:OD1	2.27	0.67
9:A:646:G:OP2	21:M:156:LYS:NZ	2.26	0.67
35:z:19:G:H4'	35:z:20:U:OP2	1.94	0.67
37:a:665:C:O3'	47:k:128:ASN:ND2	2.28	0.67
9:A:1220:U:H1'	26:R:4:VAL:HG22	1.77	0.67
13:E:128:SER:HB2	13:E:134:ARG:NH2	2.09	0.67
9:A:255:A:OP2	9:A:271:G:N1	2.20	0.67
9:A:545:U:H2'	9:A:546:G:C8	2.30	0.67
9:A:1978:G:O2'	9:A:1981:C:OP2	2.09	0.67
46:j:99:ILE:HG13	46:j:169:ILE:HB	1.76	0.67
19:K:100:TRP:H	26:R:99:GLN:HE22	1.42	0.66
37:a:634:G:H1	37:a:651:G:HO2'	1.42	0.66
9:A:723:G:H2'	9:A:724:G:H5''	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:l:68:PRO:O	48:l:99:ARG:NH1	2.28	0.66
61:y:130:ARG:HD3	61:y:153:LEU:HG	1.77	0.66
17:I:63:VAL:HG13	17:I:113:ALA:HB2	1.78	0.66
20:L:88:ASP:OD1	20:L:89:GLN:N	2.27	0.66
37:a:1288:A:H5'	61:y:140:ARG:HH12	1.57	0.66
9:A:1074:A:O2'	17:I:59:LYS:HD2	1.96	0.66
11:C:23:ASN:HD21	11:C:76:THR:HG21	1.60	0.66
37:a:84:C:H2'	37:a:85:A:C8	2.31	0.66
37:a:1462:A:H2'	37:a:1463:C:H6	1.60	0.66
41:e:286:VAL:HA	41:e:289:MET:HE2	1.76	0.66
9:A:312:C:OP1	30:V:164:LYS:NZ	2.29	0.66
17:I:56:ARG:HA	17:I:59:LYS:HE2	1.78	0.65
29:U:108:ILE:HD13	34:Z:138:LYS:HD2	1.78	0.65
37:a:631:G:O2'	47:k:49:ARG:NH1	2.29	0.65
37:a:1475:G:OP1	57:u:125:LYS:NZ	2.28	0.65
34:Z:90:LEU:HD21	34:Z:104:ASP:HB3	1.77	0.65
27:S:127:VAL:HG11	27:S:182:VAL:HG21	1.77	0.65
37:a:1077:C:O2'	37:a:1096:C:O2	2.14	0.65
37:a:1264:G:N2	37:a:1267:A:OP2	2.25	0.65
48:l:79:VAL:N	48:l:103:ASP:OD2	2.27	0.65
28:T:112:LYS:HB3	28:T:124:MET:HE1	1.77	0.65
37:a:1187:A:H62	37:a:1247:A:N6	1.94	0.65
9:A:1520:A:O2'	9:A:1543:G:O6	2.13	0.65
11:C:132:PRO:O	11:C:135:THR:OG1	2.14	0.65
52:p:5:ARG:HA	52:p:67:VAL:HG21	1.77	0.65
5:4:107:LYS:HB2	9:A:663:A:H5'	1.79	0.65
9:A:1075:G:N2	9:A:1138:G:O2'	2.30	0.65
9:A:1122:U:H1'	9:A:1125:U:H5	1.62	0.65
12:D:93:MET:H	12:D:121:ASN:ND2	1.94	0.65
13:E:104:THR:HG22	13:E:107:GLU:HG2	1.79	0.65
2:1:3:VAL:HG12	9:A:2029:A:C2	2.32	0.65
9:A:1494:G:H22	9:A:1550:U:H3	1.43	0.65
9:A:2486:A:N6	9:A:2498:G:O2'	2.30	0.64
13:E:103:LEU:HB3	13:E:107:GLU:HB2	1.78	0.64
20:L:13:ASN:HD21	20:L:97:ARG:HB3	1.62	0.64
37:a:41:C:H2'	37:a:42:G:C8	2.31	0.64
9:A:176:A:H2'	9:A:177:C:C6	2.32	0.64
48:l:50:ARG:HG3	48:l:90:LEU:HD21	1.79	0.64
56:t:115:LYS:HB2	56:t:167:VAL:HG12	1.79	0.64
8:7:50:ARG:NH1	9:A:1055:A:O2'	2.30	0.64
9:A:555:A:N6	9:A:558:A:O2'	2.27	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:1092:C:H4'	18:J:161:LYS:HG2	1.79	0.64
9:A:2073:A:N6	9:A:2520:A:O5'	2.30	0.64
56:t:92:ARG:HB3	56:t:96:ARG:NH2	2.12	0.64
37:a:68:C:H2'	37:a:69:G:C8	2.33	0.64
11:C:157:VAL:HB	11:C:190:GLN:HG3	1.80	0.64
45:i:133:LEU:HB3	45:i:135:TYR:CD1	2.33	0.64
9:A:1091:G:O2'	18:J:160:SER:O	2.16	0.64
12:D:90:ILE:HD11	12:D:137:VAL:HG11	1.78	0.64
38:b:22:HIS:ND1	38:b:194:ASN:OD1	2.31	0.64
9:A:2069:C:H5'	9:A:2070:A:H5''	1.79	0.64
9:A:2077:C:N4	9:A:2464:G:H1	1.95	0.64
19:K:206:GLY:O	19:K:210:LYS:NZ	2.31	0.64
39:c:51:THR:HG21	39:c:58:GLU:HB3	1.80	0.64
46:j:100:ARG:HD2	46:j:194:LYS:HD3	1.80	0.63
9:A:426:C:H2'	9:A:427:A:C8	2.33	0.63
9:A:1211:G:H5''	21:M:111:GLY:HA2	1.80	0.63
9:A:2719:G:OP1	23:O:83:LYS:NZ	2.32	0.63
20:L:76:ILE:HB	25:Q:195:VAL:HB	1.78	0.63
23:O:72:LYS:NZ	31:W:74:C:OP1	2.24	0.63
37:a:1328:G:O6	43:g:2:SER:OG	2.15	0.63
9:A:1531:A:N6	11:C:94:ASP:OD2	2.31	0.63
59:w:99:LEU:HB2	59:w:159:LEU:HD11	1.79	0.63
34:Z:81:LEU:HD11	34:Z:144:ILE:HD12	1.81	0.63
37:a:527:C:O2'	51:o:51:ARG:NH1	2.31	0.63
9:A:869:G:O2'	9:A:925:G:O6	2.12	0.63
26:R:26:GLY:O	26:R:30:ARG:NH1	2.32	0.63
55:s:63:THR:H	55:s:66:MET:HG3	1.63	0.63
61:y:134:VAL:HG22	61:y:146:ALA:HB3	1.81	0.63
9:A:555:A:H61	9:A:558:A:HO2'	1.45	0.63
9:A:2628:C:H5'	9:A:2629:A:OP2	1.99	0.63
37:a:1361:U:H2'	37:a:1362:A:C8	2.34	0.63
38:b:115:LEU:HD23	38:b:152:LEU:HD13	1.80	0.63
11:C:133:LEU:HD21	11:C:163:LYS:HE2	1.81	0.63
25:Q:184:ARG:HG3	25:Q:193:GLU:HG2	1.80	0.63
29:U:183:ASN:HB3	29:U:186:GLU:HG3	1.79	0.63
9:A:157:G:O2'	9:A:159:A:OP1	2.12	0.62
9:A:2290:A:H2'	9:A:2291:A:C8	2.34	0.62
45:i:192:LYS:HG2	45:i:198:LYS:O	1.99	0.62
9:A:394:G:H22	9:A:404:U:H3	1.46	0.62
14:F:56:ARG:O	14:F:60:ASN:HB3	1.98	0.62
9:A:757:U:HO2'	9:A:2628:C:HO2'	1.47	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:2142:G:H1	9:A:2174:C:N4	1.97	0.62
9:A:468:U:O2	9:A:471:U:O2'	2.16	0.62
9:A:2047:A:O2'	9:A:2049:G:OP2	2.17	0.62
23:O:89:LEU:HD22	23:O:93:VAL:HG23	1.81	0.62
37:a:92:G:H5'	37:a:93:A:H5''	1.82	0.62
37:a:280:A:OP1	52:p:27:ARG:NH2	2.30	0.62
37:a:594:C:O2	53:q:135:GLN:NE2	2.31	0.62
37:a:1304:G:H2'	37:a:1305:G:C8	2.35	0.62
39:c:22:TRP:CD1	39:c:22:TRP:H	2.18	0.62
14:F:160:ALA:HB1	14:F:190:VAL:HB	1.82	0.62
12:D:88:ALA:O	12:D:294:PRO:HG2	1.99	0.62
18:J:84:LEU:HD21	18:J:95:VAL:HB	1.81	0.62
61:y:72:LEU:HD21	61:y:103:ALA:HA	1.79	0.62
9:A:701:U:O2'	9:A:791:G:OP1	2.16	0.62
25:Q:153:LEU:HD12	25:Q:165:TYR:HE2	1.62	0.62
36:8:1250:UNK:HA	38:b:92:ARG:HH12	1.63	0.62
37:a:449:C:OP1	48:l:114:ARG:NH2	2.32	0.62
37:a:1325:U:H5'	43:g:102:ARG:NH2	2.15	0.62
23:O:11:MET:N	23:O:11:MET:SD	2.73	0.62
37:a:41:C:H2'	37:a:42:G:H8	1.65	0.62
41:e:305:GLU:HB3	44:h:118:ARG:HH12	1.63	0.62
9:A:577:G:O3'	21:M:115:ARG:NH2	2.32	0.62
9:A:2761:U:OP2	9:A:2773:C:N4	2.32	0.62
25:Q:160:ARG:HH22	37:a:144:A:P	2.22	0.62
21:M:98:LYS:HE2	21:M:106:GLN:HG3	1.80	0.62
37:a:1446:G:OP2	61:y:104:LYS:NZ	2.33	0.62
54:r:36:ILE:HG23	54:r:66:ILE:HG12	1.82	0.62
23:O:67:GLU:OE1	23:O:72:LYS:HE3	2.00	0.61
9:A:2807:C:HO2'	31:W:95:A:HO2'	1.43	0.61
11:C:75:VAL:HG13	11:C:76:THR:HG22	1.83	0.61
20:L:30:ARG:HD3	20:L:32:TYR:O	2.00	0.61
9:A:635:C:H2'	9:A:636:C:C6	2.35	0.61
37:a:375:G:OP1	40:d:112:ASN:ND2	2.33	0.61
37:a:1271:G:H4'	37:a:1311:C:C5	2.35	0.61
61:y:139:LYS:C	61:y:140:ARG:HD2	2.25	0.61
9:A:1362:G:H21	29:U:177:MET:HE1	1.66	0.61
9:A:2767:A:H3'	9:A:2768:A:C5'	2.30	0.61
13:E:104:THR:HG23	13:E:106:ALA:H	1.65	0.61
17:I:100:THR:HG21	17:I:143:ALA:HB2	1.83	0.61
37:a:622:G:H2'	37:a:623:A:C8	2.35	0.61
58:v:184:TYR:HA	58:v:238:VAL:HG21	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:E:230:THR:HG22	13:E:231:PRO:HD2	1.81	0.61
32:X:120:ASP:OD1	32:X:120:ASP:N	2.34	0.61
9:A:241:A:H2'	9:A:242:A:C8	2.34	0.61
29:U:119:ILE:HG13	29:U:135:LEU:HB3	1.82	0.61
37:a:63:U:O2'	37:a:350:C:O2	2.18	0.61
37:a:793:A:H1'	54:r:23:GLN:HG2	1.81	0.61
9:A:98:G:H2'	30:V:175:TRP:CZ2	2.36	0.61
9:A:2284:A:H5''	9:A:2285:A:H5'	1.82	0.61
37:a:914:U:H6	61:y:82:ARG:HH21	1.49	0.61
9:A:420:A:H2'	9:A:421:A:H8	1.65	0.61
9:A:1883:G:H2'	9:A:1884:A:O4'	2.01	0.61
9:A:2206:A:H2'	9:A:2207:A:C8	2.36	0.61
13:E:60:PHE:O	13:E:196:ARG:NH1	2.33	0.61
13:E:243:GLU:OE1	21:M:81:ARG:NH2	2.34	0.61
19:K:121:ASP:O	19:K:247:ARG:NH1	2.32	0.61
32:X:93:ILE:HG22	32:X:94:ILE:HG13	1.83	0.61
39:c:20:SER:OG	39:c:40:ARG:NH2	2.31	0.61
39:c:22:TRP:HB3	39:c:67:LYS:HB2	1.83	0.61
20:L:68:GLU:HG3	20:L:78:ARG:HB2	1.83	0.61
37:a:772:U:HO2'	44:h:2:GLY:N	1.99	0.61
4:3:99:THR:O	9:A:697:U:O2'	2.20	0.60
37:a:1018:C:O2'	37:a:1140:C:H1'	2.00	0.60
12:D:143:ARG:HG2	12:D:144:LEU:H	1.65	0.60
23:O:54:MET:HE1	23:O:123:ILE:HG21	1.83	0.60
37:a:1024:C:OP2	41:e:210:ARG:NH2	2.34	0.60
40:d:98:LEU:HD21	40:d:164:LEU:HB3	1.84	0.60
37:a:419:A:OP2	37:a:433:G:N2	2.30	0.60
26:R:112:TYR:CZ	26:R:116:ILE:HD11	2.37	0.60
37:a:1118:A:H5'	38:b:143:ARG:HH22	1.66	0.60
9:A:1837:U:H5'	9:A:1985:A:H5'	1.83	0.60
22:N:17:MET:HE3	22:N:96:VAL:HG13	1.83	0.60
27:S:208:ARG:HG3	27:S:208:ARG:HH11	1.65	0.60
37:a:1363:U:H2'	37:a:1364:G:H8	1.66	0.60
15:G:74:ILE:HG21	15:G:115:MET:HE1	1.84	0.60
15:G:166:GLU:HG3	15:G:168:ASN:HB2	1.84	0.60
26:R:92:LEU:HD22	26:R:96:ILE:HG21	1.84	0.60
38:b:170:GLN:HB2	38:b:177:LEU:HD11	1.84	0.60
17:I:100:THR:HG22	17:I:135:VAL:HG12	1.84	0.59
38:b:96:VAL:HG11	38:b:100:TRP:CD1	2.37	0.59
1:O:43:PRO:HG3	14:F:111:ALA:HB1	1.84	0.59
9:A:530:U:H2'	9:A:531:A:H8	1.67	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:R:49:ASP:HA	26:R:52:ARG:HB2	1.84	0.59
1:O:77:HIS:CG	1:O:78:PRO:HD2	2.38	0.59
9:A:490:A:H1'	30:V:108:LYS:HZ1	1.67	0.59
9:A:2345:A:H2'	9:A:2346:A:H8	1.62	0.59
37:a:1264:G:N2	37:a:1266:A:H3'	2.16	0.59
47:k:126:PRO:O	57:u:119:ARG:NH1	2.34	0.59
19:K:191:LEU:HD13	19:K:199:ILE:HG13	1.85	0.59
27:S:208:ARG:HH11	27:S:208:ARG:CG	2.16	0.59
35:z:34:G:N2	61:y:140:ARG:HB2	2.14	0.59
37:a:7:G:H1	41:e:245:THR:HG21	1.66	0.59
9:A:1090:U:H1'	18:J:205:ASN:ND2	2.17	0.59
24:P:129:LYS:O	24:P:133:GLU:HG2	2.01	0.59
37:a:944:C:H2'	37:a:945:A:H5''	1.83	0.59
43:g:24:ASN:HA	43:g:27:VAL:HG22	1.85	0.59
9:A:1291:C:H5''	9:A:1292:G:H5'	1.84	0.59
9:A:1570:C:H4'	9:A:1571:G:C2	2.37	0.59
23:O:106:ARG:HH11	23:O:126:VAL:HG21	1.68	0.59
37:a:392:A:H5'	37:a:393:C:C5	2.38	0.59
37:a:685:U:H2'	37:a:686:G:H8	1.67	0.59
38:b:229:ARG:HA	38:b:232:TYR:CD2	2.38	0.59
9:A:1055:A:C2	9:A:2505:A:H5'	2.38	0.59
39:c:97:ILE:HG12	39:c:101:LYS:HE3	1.84	0.59
49:m:102:ARG:O	49:m:106:THR:OG1	2.16	0.59
35:z:34:G:H1	61:y:175:VAL:HG11	1.67	0.59
38:b:214:ILE:O	38:b:218:LEU:HB2	2.03	0.59
11:C:223:PRO:HD3	11:C:230:GLY:H	1.66	0.59
30:V:176:LYS:O	30:V:180:ASN:ND2	2.36	0.59
37:a:76:G:H5''	59:w:102:LYS:HD2	1.84	0.59
37:a:1203:G:H2'	37:a:1227:A:N6	2.16	0.59
46:j:118:ILE:HD11	46:j:185:LEU:HD11	1.85	0.59
3:2:59:THR:HG22	3:2:60:ILE:H	1.68	0.58
9:A:76:U:OP1	34:Z:114:ARG:NH2	2.36	0.58
9:A:474:C:O2'	13:E:118:GLN:NE2	2.36	0.58
9:A:2269:G:H2'	9:A:2270:G:C8	2.38	0.58
37:a:490:A:OP1	40:d:10:LYS:NZ	2.32	0.58
37:a:895:A:H2'	37:a:896:G:C8	2.38	0.58
37:a:1253:G:H5''	60:x:58:ASP:OD1	2.03	0.58
41:e:225:HIS:CD2	44:h:100:LEU:HD13	2.38	0.58
5:4:101:ARG:NH2	9:A:235:G:OP2	2.35	0.58
9:A:1857:A:O2'	9:A:1858:A:H8	1.86	0.58
21:M:83:ASP:N	21:M:83:ASP:OD1	2.35	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:Y:97:ARG:HG2	33:Y:98:LEU:N	2.17	0.58
44:h:63:LEU:HD12	44:h:64:ARG:H	1.68	0.58
37:a:1454:G:H4'	37:a:1455:U:H5''	1.85	0.58
9:A:2203:U:H2'	9:A:2204:A:O4'	2.04	0.58
10:B:29:C:OP1	24:P:78:SER:OG	2.21	0.58
17:I:73:CYS:SG	17:I:134:PHE:HB3	2.44	0.58
40:d:145:ILE:O	40:d:149:GLN:HG2	2.04	0.58
11:C:244:THR:HG22	11:C:245:PRO:HD2	1.85	0.58
20:L:15:GLY:HA2	20:L:47:ILE:HD12	1.84	0.58
20:L:102:ILE:HG22	20:L:103:ALA:H	1.69	0.58
35:z:16:U:C5	35:z:18:G:H5'	2.37	0.58
61:y:134:VAL:HG21	61:y:164:ILE:HD11	1.86	0.58
27:S:128:VAL:HG22	27:S:133:GLN:HG2	1.85	0.58
28:T:79:LEU:HB3	28:T:134:ILE:HD11	1.85	0.58
1:O:42:HIS:CE1	14:F:116:GLN:HE22	2.22	0.58
9:A:2340:G:C2'	9:A:2341:U:H5'	2.33	0.58
21:M:84:ASN:OD1	21:M:84:ASN:N	2.37	0.58
23:O:113:ARG:HD3	23:O:120:MET:HE2	1.86	0.58
56:t:111:LEU:HD13	56:t:163:ASN:HB3	1.86	0.58
9:A:2198:A:H2'	9:A:2199:G:C8	2.38	0.58
9:A:296:G:H2'	9:A:297:U:C6	2.39	0.58
9:A:1689:C:O2'	23:O:19:ARG:NH2	2.37	0.58
17:I:103:ILE:HD12	17:I:134:PHE:HE2	1.69	0.58
38:b:6:TRP:CH2	38:b:224:ALA:HA	2.39	0.58
38:b:60:LEU:HD12	38:b:202:ILE:HD11	1.85	0.58
56:t:121:SER:HB2	56:t:173:TRP:CZ3	2.39	0.58
61:y:169:ARG:O	61:y:173:ASP:HB2	2.04	0.58
9:A:1074:A:N1	17:I:63:VAL:HG21	2.19	0.57
9:A:2329:U:H5'	14:F:138:LEU:HD12	1.85	0.57
22:N:44:SER:HB3	22:N:70:PRO:HG3	1.85	0.57
29:U:135:LEU:HD21	29:U:175:TYR:CD2	2.39	0.57
37:a:978:U:H3	37:a:981:G:H22	1.52	0.57
37:a:1066:G:H5'	37:a:1067:U:OP2	2.04	0.57
19:K:52:SER:HB3	31:W:1:A:O4'	2.04	0.57
15:G:44:GLY:HA3	15:G:105:HIS:CD2	2.40	0.57
15:G:189:ARG:HD2	15:G:204:TYR:CE1	2.39	0.57
60:x:58:ASP:O	60:x:64:GLY:HA3	2.03	0.57
8:7:68:ALA:HB1	8:7:70:TRP:CD1	2.39	0.57
9:A:548:G:O2'	9:A:549:A:O5'	2.23	0.57
9:A:1385:G:H5''	33:Y:73:ARG:HH21	1.70	0.57
9:A:1887:G:H2'	9:A:1888:G:H8	1.69	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:G:76:TYR:OH	15:G:112:THR:HG21	2.04	0.57
46:j:128:LYS:HD3	46:j:170:LEU:HD12	1.86	0.57
53:q:74:VAL:HG23	53:q:99:ALA:HB3	1.87	0.57
60:x:77:LYS:HD2	60:x:81:LYS:HZ3	1.68	0.57
6:5:17:ILE:HG22	6:5:18:ARG:H	1.68	0.57
9:A:1497:A:O2'	9:A:1498:G:H5'	2.04	0.57
9:A:1559:A:H3'	9:A:1560:C:H6	1.68	0.57
14:F:54:ILE:HG23	14:F:58:LYS:HZ2	1.69	0.57
28:T:63:MET:HA	28:T:66:GLU:CD	2.29	0.57
28:T:141:HIS:O	28:T:142:PHE:HB2	2.04	0.57
37:a:606:A:HO2'	51:o:19:LYS:HZ3	1.49	0.57
47:k:83:VAL:HB	47:k:88:MET:SD	2.43	0.57
12:D:273:LEU:HD13	25:Q:126:LEU:HD21	1.85	0.57
30:V:98:SER:O	30:V:98:SER:OG	2.18	0.57
37:a:291:G:H5'	37:a:292:A:OP2	2.05	0.57
46:j:135:LEU:HB2	46:j:164:GLN:HB2	1.87	0.57
49:m:125:LEU:HA	49:m:128:ILE:HD12	1.86	0.57
28:T:62:LEU:HD22	28:T:77:PHE:CE1	2.39	0.57
37:a:396:G:H4'	40:d:33:ARG:HG3	1.85	0.57
38:b:180:CYS:SG	38:b:187:THR:OG1	2.61	0.57
9:A:1812:A:H2'	9:A:1813:A:C8	2.40	0.57
27:S:208:ARG:HG3	27:S:208:ARG:NH1	2.19	0.57
37:a:226:G:OP1	53:q:124:LYS:NZ	2.37	0.57
37:a:622:G:H2'	37:a:623:A:H8	1.70	0.57
37:a:1462:A:H2'	37:a:1463:C:C6	2.40	0.57
9:A:531:A:H2'	9:A:532:A:C8	2.40	0.57
15:G:48:ILE:HB	15:G:90:LEU:HB2	1.87	0.57
37:a:827:C:OP1	44:h:84:ARG:NH1	2.38	0.57
37:a:1037:G:H21	37:a:1115:A:H61	1.51	0.57
37:a:1444:U:H5''	61:y:100:LYS:NZ	2.19	0.57
38:b:19:HIS:HB3	38:b:47:LEU:HD11	1.85	0.57
43:g:15:ASP:OD1	43:g:44:TYR:OH	2.21	0.57
46:j:130:MET:HB2	46:j:168:ASP:HB2	1.87	0.57
9:A:1133:U:H2'	9:A:1134:G:H8	1.70	0.57
11:C:121:LYS:HG2	11:C:124:ASN:ND2	2.20	0.57
13:E:240:LEU:O	21:M:81:ARG:HD3	2.05	0.57
14:F:155:ARG:HG2	14:F:159:LEU:HD23	1.87	0.57
49:m:104:GLU:O	49:m:107:LYS:HG2	2.05	0.57
9:A:1444:A:H2'	9:A:1445:G:C8	2.40	0.56
9:A:2250:A:H2'	9:A:2251:G:C8	2.39	0.56
17:I:161:PHE:HE2	17:I:176:VAL:HG11	1.69	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:T:31:GLU:OE2	28:T:176:ARG:NH2	2.37	0.56
17:I:120:ALA:HB1	17:I:123:LYS:HE3	1.87	0.56
9:A:1690:A:OP2	23:O:11:MET:HA	2.05	0.56
9:A:2352:A:N7	9:A:2354:G:C5	2.72	0.56
10:B:4:U:H2'	10:B:5:C:C6	2.41	0.56
18:J:79:VAL:HG22	18:J:130:THR:HG23	1.87	0.56
28:T:88:SER:O	28:T:92:GLN:HA	2.05	0.56
37:a:60:A:H3'	37:a:302:G:H22	1.70	0.56
37:a:684:C:H2'	37:a:685:U:C6	2.41	0.56
39:c:141:PHE:HE2	39:c:177:GLU:HG2	1.70	0.56
50:n:65:LEU:HD23	50:n:82:ILE:HG21	1.87	0.56
47:k:135:LYS:NZ	57:u:127:GLU:HG3	2.21	0.56
48:l:75:GLN:O	48:l:78:SER:HB2	2.05	0.56
5:4:125:ASN:ND2	5:4:127:LYS:H	2.04	0.56
9:A:2546:G:H5''	9:A:2547:U:H5''	1.87	0.56
37:a:1092:G:H21	37:a:1094:A:H62	1.52	0.56
37:a:1396:A:H5''	37:a:1397:C:OP2	2.06	0.56
61:y:136:LEU:HB2	61:y:144:ILE:HB	1.86	0.56
6:5:31:LYS:HE2	9:A:2495:A:H5'	1.88	0.56
9:A:232:G:OP2	9:A:234:C:N4	2.36	0.56
9:A:754:A:O2'	9:A:1695:U:OP1	2.23	0.56
9:A:1289:A:H2'	9:A:1290:A:O4'	2.06	0.56
13:E:72:LEU:HD22	13:E:259:TYR:HB2	1.88	0.56
34:Z:108:MET:O	34:Z:112:VAL:HG23	2.06	0.56
60:x:90:ILE:HG22	60:x:92:PRO:HD3	1.87	0.56
1:0:37:ARG:HB3	1:0:42:HIS:HD2	1.69	0.56
13:E:238:ASP:N	13:E:238:ASP:OD1	2.38	0.56
32:X:93:ILE:HD11	32:X:117:ALA:HB2	1.87	0.56
50:n:66:THR:HG23	50:n:82:ILE:HD11	1.87	0.56
54:r:76:PRO:HB2	54:r:78:LEU:O	2.05	0.56
6:5:3:ILE:HD13	9:A:2556:C:H4'	1.86	0.56
18:J:164:GLN:NE2	18:J:204:ALA:O	2.38	0.56
31:W:32:C:H2'	31:W:33:A:H2'	1.86	0.56
37:a:1019:U:H2'	37:a:1020:C:C6	2.40	0.56
39:c:20:SER:HB3	39:c:22:TRP:HE1	1.71	0.56
39:c:26:PRO:CG	46:j:140:ARG:HH22	2.19	0.56
41:e:305:GLU:O	44:h:118:ARG:NH1	2.39	0.56
56:t:92:ARG:HB3	56:t:96:ARG:HH21	1.68	0.56
58:v:192:ALA:HB3	58:v:195:VAL:HG23	1.86	0.56
9:A:1497:A:H2'	9:A:1497:A:N3	2.21	0.56
29:U:138:VAL:HG22	29:U:172:LYS:HB3	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:a:422:A:H4'	37:a:423:A:H5'	1.86	0.56
37:a:740:A:O2'	37:a:742:A:N7	2.39	0.56
9:A:1603:A:H2'	9:A:1604:A:C8	2.41	0.56
22:N:91:GLU:HB2	22:N:92:TYR:CD1	2.40	0.56
9:A:628:A:OP1	13:E:157:ARG:HD3	2.06	0.55
30:V:68:MET:HE1	30:V:98:SER:HA	1.88	0.55
33:Y:77:PHE:HD2	33:Y:137:VAL:HG12	1.71	0.55
39:c:25:GLN:HG3	39:c:26:PRO:HD2	1.88	0.55
41:e:186:GLN:OE1	41:e:214:THR:OG1	2.21	0.55
45:i:87:GLY:HA3	45:i:156:ALA:O	2.06	0.55
47:k:32:VAL:HG13	47:k:41:VAL:HG22	1.88	0.55
49:m:59:LYS:NZ	49:m:67:TYR:OH	2.39	0.55
56:t:124:GLU:O	56:t:127:PRO:HD2	2.06	0.55
9:A:411:U:H1'	16:H:42:GLN:HE21	1.70	0.55
12:D:186:LEU:HB2	12:D:189:GLU:HG3	1.89	0.55
29:U:138:VAL:HG21	29:U:147:ILE:HD11	1.88	0.55
9:A:495:A:O2'	30:V:121:GLY:HA3	2.06	0.55
9:A:953:G:H2'	9:A:954:G:H8	1.69	0.55
9:A:1593:U:O2'	9:A:1594:A:OP1	2.23	0.55
10:B:29:C:H2'	10:B:30:A:O4'	2.07	0.55
14:F:188:GLN:OE1	14:F:205:MET:HG3	2.07	0.55
25:Q:213:LYS:NZ	31:W:67:U:OP1	2.25	0.55
38:b:72:LEU:HD12	38:b:165:VAL:HG22	1.87	0.55
52:p:28:ARG:HG3	52:p:29:GLU:N	2.20	0.55
9:A:2439:C:O4'	35:z:76:A:N6	2.40	0.55
18:J:176:LEU:HB3	18:J:196:MET:HG3	1.88	0.55
20:L:101:ALA:C	20:L:102:ILE:HG12	2.32	0.55
26:R:96:ILE:HG23	26:R:100:ILE:HD12	1.88	0.55
37:a:466:C:H2'	37:a:478:G:C8	2.41	0.55
59:w:103:PHE:CZ	59:w:166:ILE:HG13	2.42	0.55
9:A:1854:C:H5'	11:C:252:GLY:O	2.07	0.55
19:K:57:CYS:HG	19:K:61:TRP:CD1	2.24	0.55
46:j:185:LEU:HD12	46:j:191:VAL:HG11	1.88	0.55
51:o:34:ARG:NH2	51:o:82:LEU:O	2.40	0.55
9:A:2292:C:H1'	22:N:85:SER:H	1.72	0.55
15:G:76:TYR:HE1	15:G:108:PHE:HB3	1.70	0.55
30:V:83:GLU:CD	30:V:106:ASN:H	2.14	0.55
30:V:178:ILE:HA	30:V:181:LYS:HD2	1.87	0.55
37:a:1045:C:H2'	37:a:1046:C:H6	1.72	0.55
39:c:39:ILE:HD11	39:c:65:ILE:HD13	1.87	0.55
9:A:543:A:H2'	9:A:543:A:N3	2.21	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:F:61:TYR:OH	14:F:82:PRO:O	2.17	0.55
37:a:1374:C:H2'	37:a:1375:A:C8	2.42	0.55
9:A:2519:G:O2'	9:A:2521:U:OP2	2.25	0.55
19:K:130:THR:HG21	19:K:241:LEU:HD23	1.87	0.55
38:b:101:LEU:HB3	38:b:104:MET:HE3	1.89	0.55
50:n:9:ARG:HB3	50:n:13:ARG:HH12	1.72	0.55
14:F:153:LEU:HD21	14:F:226:MET:HE1	1.88	0.55
21:M:159:PRO:O	21:M:160:ILE:HD13	2.07	0.55
3:2:36:GLN:HE21	9:A:2302:C:H41	1.53	0.55
9:A:1073:G:H4'	9:A:1074:A:H5''	1.89	0.55
9:A:2142:G:N3	9:A:2187:A:O2'	2.37	0.55
9:A:2715:U:H2'	9:A:2716:C:C6	2.42	0.55
14:F:187:GLU:HG2	14:F:202:ALA:HB1	1.89	0.55
23:O:34:LEU:HB3	23:O:54:MET:SD	2.47	0.55
37:a:670:A:O2'	37:a:671:C:H5'	2.07	0.55
14:F:97:SER:HB3	14:F:137:THR:O	2.06	0.54
37:a:573:C:H2'	37:a:574:U:H6	1.72	0.54
37:a:1137:U:O2'	39:c:187:GLN:OE1	2.21	0.54
37:a:1442:A:H5'	37:a:1443:G:OP2	2.07	0.54
40:d:89:MET:HE3	40:d:179:ILE:HD11	1.89	0.54
46:j:129:ILE:HG22	46:j:131:GLY:H	1.71	0.54
50:n:38:SER:HA	50:n:41:TRP:HD1	1.72	0.54
9:A:420:A:H2'	9:A:421:A:C8	2.41	0.54
9:A:548:G:O2'	9:A:549:A:H8	1.89	0.54
9:A:1111:G:N1	9:A:1114:A:OP2	2.39	0.54
9:A:1917:G:OP1	11:C:236:PRO:HB2	2.07	0.54
10:B:92:U:OP1	22:N:16:ARG:HG3	2.08	0.54
27:S:104:ASN:HA	27:S:107:ILE:HG22	1.89	0.54
37:a:1380:C:H2'	37:a:1381:G:O4'	2.07	0.54
49:m:124:ARG:NE	49:m:128:ILE:HD11	2.21	0.54
53:q:70:ASN:HB3	53:q:73:THR:OG1	2.07	0.54
9:A:1073:G:OP1	17:I:59:LYS:NZ	2.39	0.54
23:O:62:ILE:HG21	23:O:104:TYR:CD2	2.42	0.54
27:S:137:ILE:HG13	27:S:140:ARG:HG3	1.88	0.54
37:a:487:A:H2'	37:a:488:G:C8	2.43	0.54
46:j:100:ARG:HG3	46:j:194:LYS:HB3	1.89	0.54
8:7:54:LYS:HE2	9:A:2473:C:O3'	2.07	0.54
9:A:2116:C:N3	9:A:2201:G:N2	2.52	0.54
18:J:179:ILE:HG22	18:J:199:ILE:HD12	1.89	0.54
9:A:211:A:H2'	9:A:212:A:C8	2.43	0.54
17:I:154:ARG:HD2	17:I:159:ASN:HB2	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:S:166:THR:HG22	27:S:168:ALA:H	1.73	0.54
29:U:165:LEU:HD23	29:U:173:LYS:HD3	1.90	0.54
32:X:71:ASP:CG	32:X:72:SER:H	2.15	0.54
37:a:955:U:H2'	37:a:956:C:O4'	2.08	0.54
44:h:9:ILE:HG23	44:h:26:ILE:HG21	1.89	0.54
46:j:101:ILE:HG23	46:j:193:VAL:HG22	1.88	0.54
61:y:173:ASP:O	61:y:177:ASP:HB2	2.07	0.54
10:B:31:C:OP1	24:P:49:ARG:HD2	2.07	0.54
25:Q:118:LYS:HB2	25:Q:121:ASP:OD2	2.08	0.54
44:h:78:HIS:HB2	44:h:134:TRP:HB2	1.90	0.54
9:A:1189:G:H5'	27:S:148:LYS:HE2	1.89	0.54
11:C:256:ARG:HH22	11:C:262:SER:HB2	1.71	0.54
22:N:91:GLU:HB2	22:N:92:TYR:HD1	1.73	0.54
23:O:61:MET:HG3	23:O:80:ILE:HD11	1.90	0.54
38:b:7:ASN:OD1	38:b:7:ASN:N	2.39	0.54
9:A:1073:G:H5''	9:A:1075:G:H5''	1.88	0.54
9:A:1840:C:OP1	11:C:200:ARG:NH2	2.41	0.54
9:A:2254:A:H2'	9:A:2256:A:N7	2.23	0.54
44:h:34:ASN:O	44:h:38:ILE:HG13	2.08	0.54
59:w:101:LEU:HD21	59:w:163:ALA:HB2	1.90	0.54
9:A:70:A:H4'	9:A:71:A:H5''	1.90	0.54
9:A:126:C:H2'	9:A:127:C:H6	1.73	0.54
9:A:726:G:C2	51:o:53:LEU:HD21	2.43	0.54
9:A:2154:C:H42	9:A:2165:G:H22	1.55	0.54
9:A:2549:G:N2	9:A:2680:G:O2'	2.41	0.54
10:B:5:C:H2'	10:B:6:U:C6	2.42	0.54
14:F:161:LEU:O	14:F:164:THR:OG1	2.19	0.54
18:J:150:LEU:HD13	18:J:203:ALA:HB2	1.89	0.54
19:K:80:ASP:OD1	19:K:80:ASP:N	2.40	0.54
21:M:161:ASN:HA	21:M:201:LEU:O	2.08	0.54
49:m:62:GLU:HG3	49:m:76:ALA:HB1	1.90	0.54
37:a:192:C:H2'	37:a:193:C:H6	1.73	0.54
37:a:298:A:C4	37:a:300:A:C8	2.96	0.54
37:a:1019:U:H2'	37:a:1020:C:H6	1.73	0.54
37:a:1108:G:H4'	38:b:135:LYS:HD2	1.90	0.54
47:k:32:VAL:HG22	47:k:41:VAL:HG13	1.90	0.54
47:k:83:VAL:O	47:k:88:MET:HG2	2.08	0.54
55:s:40:ILE:HG23	55:s:44:MET:CE	2.37	0.54
9:A:13:A:H2'	9:A:14:A:H8	1.70	0.53
26:R:17:ILE:HG23	26:R:39:LYS:HD2	1.89	0.53
41:e:224:PRO:HD2	41:e:289:MET:HG2	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:6:99:LYS:O	7:6:103:LYS:HG2	2.07	0.53
9:A:1084:G:H5''	9:A:1085:A:H5'	1.89	0.53
10:B:50:U:P	24:P:151:ARG:HE	2.32	0.53
11:C:207:LYS:HD2	11:C:212:LYS:HD3	1.89	0.53
18:J:189:CYS:SG	18:J:195:ALA:HB2	2.49	0.53
37:a:1239:C:H2'	37:a:1240:C:C6	2.43	0.53
37:a:1306:U:OP1	50:n:74:ARG:HB2	2.07	0.53
38:b:232:TYR:O	38:b:236:PRO:HD2	2.07	0.53
9:A:656:A:H2'	9:A:658:A:C8	2.43	0.53
9:A:2464:G:H2'	9:A:2518:C:C5	2.43	0.53
19:K:97:ASN:HD21	27:S:135:ILE:N	2.04	0.53
37:a:632:U:O2	47:k:50:VAL:HB	2.09	0.53
37:a:851:G:H2'	37:a:852:A:H8	1.73	0.53
37:a:1438:G:H2'	37:a:1439:U:C6	2.44	0.53
38:b:121:LEU:HD23	38:b:148:LEU:HD12	1.90	0.53
9:A:2154:C:N4	9:A:2165:G:H22	2.07	0.53
32:X:143:GLN:O	32:X:145:GLU:N	2.40	0.53
43:g:25:MET:O	43:g:29:ARG:HG2	2.09	0.53
45:i:105:PHE:HB3	45:i:112:ALA:HB2	1.89	0.53
1:0:57:LEU:HD21	1:0:59:MET:HG2	1.90	0.53
9:A:423:G:OP2	9:A:2423:A:O2'	2.25	0.53
9:A:2447:A:H2'	9:A:2447:A:N3	2.24	0.53
15:G:112:THR:HA	15:G:115:MET:HE3	1.90	0.53
31:W:29:U:H2'	31:W:83:C:H42	1.73	0.53
37:a:632:U:O2'	47:k:50:VAL:O	2.23	0.53
37:a:1183:U:OP1	60:x:56:ARG:NH1	2.42	0.53
49:m:77:ARG:HH11	60:x:87:LYS:HE3	1.73	0.53
9:A:177:C:H2'	9:A:178:U:H5'	1.89	0.53
14:F:164:THR:HG22	14:F:165:ARG:H	1.73	0.53
24:P:46:ALA:HB1	24:P:51:GLU:OE1	2.09	0.53
30:V:60:ASN:O	30:V:61:SER:OG	2.21	0.53
37:a:1200:A:H2'	37:a:1201:G:O4'	2.08	0.53
9:A:1211:G:OP1	21:M:109:SER:OG	2.24	0.53
15:G:71:GLU:O	15:G:176:ARG:NH1	2.41	0.53
28:T:113:LYS:HG3	28:T:125:ILE:HB	1.91	0.53
9:A:306:G:H2'	9:A:307:C:H6	1.74	0.53
9:A:1844:U:H5''	9:A:1845:G:H5'	1.89	0.53
9:A:2729:A:H2'	9:A:2729:A:N3	2.24	0.53
18:J:129:ILE:HD11	18:J:137:PHE:HB2	1.90	0.53
20:L:13:ASN:ND2	20:L:97:ARG:HB3	2.23	0.53
22:N:126:PRO:HG2	22:N:127:ILE:HG23	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:O:20:LEU:HD13	23:O:30:LEU:HD23	1.91	0.53
37:a:401:G:OP1	40:d:9:PHE:HB2	2.09	0.53
37:a:738:A:N7	61:y:172:LYS:NZ	2.55	0.53
45:i:116:LEU:HD11	45:i:126:VAL:HG21	1.91	0.53
46:j:153:ASP:N	46:j:153:ASP:OD1	2.41	0.53
9:A:37:A:H2'	9:A:38:C:C6	2.44	0.53
9:A:2390:A:H2'	9:A:2391:C:C6	2.44	0.53
10:B:9:U:OP1	24:P:53:ARG:NH2	2.41	0.53
12:D:170:GLU:O	12:D:291:ARG:NH2	2.41	0.53
19:K:83:TRP:CG	19:K:84:MET:H	2.27	0.53
37:a:882:G:N7	43:g:3:ARG:NH1	2.57	0.53
1:0:53:CYS:HB3	1:0:57:LEU:HB3	1.91	0.53
9:A:58:U:H1'	9:A:72:A:H2'	1.91	0.53
17:I:76:LEU:HD22	17:I:134:PHE:HD1	1.74	0.53
25:Q:138:ARG:NH1	25:Q:203:ILE:HB	2.22	0.53
37:a:1482:C:O2	57:u:134:ARG:NH2	2.42	0.53
6:5:10:ILE:HG13	9:A:2494:C:N4	2.23	0.52
9:A:297:U:C5	9:A:298:G:C8	2.97	0.52
9:A:576:U:H2'	9:A:577:G:O4'	2.09	0.52
9:A:793:A:N7	11:C:216:VAL:HG21	2.24	0.52
9:A:2464:G:H2'	9:A:2518:C:H5	1.74	0.52
12:D:214:ARG:NH1	12:D:250:MET:O	2.42	0.52
20:L:63:VAL:HG23	20:L:64:ARG:HG3	1.91	0.52
35:z:57:G:H2'	35:z:58:A:H5'	1.91	0.52
37:a:1471:U:H5''	47:k:137:ARG:NH2	2.24	0.52
49:m:48:VAL:N	49:m:91:LYS:HZ3	2.05	0.52
9:A:640:G:H2'	9:A:641:C:C6	2.44	0.52
9:A:2133:A:H62	9:A:2181:U:H1'	1.73	0.52
9:A:2396:G:H2'	9:A:2397:U:C6	2.44	0.52
9:A:2470:A:H2'	9:A:2471:G:H8	1.74	0.52
24:P:76:PHE:CE2	24:P:78:SER:HB3	2.45	0.52
32:X:97:ARG:HA	32:X:97:ARG:HH11	1.74	0.52
35:z:32:U:H3'	35:z:33:U:H5''	1.91	0.52
37:a:1083:U:O2'	37:a:1085:G:N7	2.40	0.52
39:c:34:GLN:HG2	39:c:38:LYS:HE3	1.91	0.52
42:f:107:GLN:CG	42:f:206:ILE:HB	2.39	0.52
48:l:111:GLN:HE22	48:l:122:PRO:HG3	1.73	0.52
9:A:2464:G:H4'	9:A:2465:A:H5'	1.92	0.52
37:a:171:A:H2'	37:a:172:G:O4'	2.08	0.52
41:e:290:ARG:NH2	44:h:76:THR:O	2.43	0.52
46:j:103:LEU:CD2	46:j:191:VAL:HG12	2.39	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:m:143:ARG:HB2	49:m:145:GLN:HE21	1.74	0.52
45:i:135:TYR:HA	45:i:138:ASN:HD22	1.75	0.52
9:A:1887:G:H2'	9:A:1888:G:C8	2.43	0.52
14:F:88:VAL:HG13	14:F:208:CYS:HB2	1.91	0.52
19:K:177:SER:OG	19:K:179:ARG:HG3	2.10	0.52
37:a:172:G:H2'	37:a:173:A:C8	2.43	0.52
44:h:10:ILE:HG23	44:h:79:LEU:HB3	1.90	0.52
3:2:20:ARG:HG2	3:2:30:VAL:HG21	1.92	0.52
7:6:132:PRO:O	7:6:135:LYS:N	2.39	0.52
9:A:1408:A:H5'	9:A:1488:A:H1'	1.90	0.52
15:G:187:THR:O	15:G:190:SER:OG	2.22	0.52
23:O:64:LEU:HD23	23:O:76:ALA:HB2	1.92	0.52
24:P:84:VAL:HG21	24:P:155:LEU:HD11	1.91	0.52
26:R:31:LEU:O	26:R:35:ILE:HG13	2.09	0.52
26:R:79:SER:OG	26:R:80:LYS:N	2.41	0.52
37:a:387:G:H2'	37:a:388:G:C8	2.45	0.52
37:a:621:G:H5''	42:f:200:ARG:NH1	2.24	0.52
39:c:7:PRO:HG2	39:c:195:TYR:HB2	1.92	0.52
42:f:106:ARG:HH11	42:f:205:LYS:HZ2	1.57	0.52
42:f:119:THR:HG22	42:f:120:GLU:H	1.74	0.52
52:p:20:VAL:HG12	52:p:35:LYS:HA	1.90	0.52
61:y:98:VAL:HG11	61:y:112:VAL:HG11	1.91	0.52
9:A:1168:U:H4'	9:A:1169:A:O4'	2.10	0.52
9:A:1764:A:N1	9:A:2734:U:O2'	2.43	0.52
9:A:1813:A:OP1	11:C:257:LYS:HE3	2.10	0.52
10:B:114:G:H2'	10:B:115:C:C6	2.44	0.52
18:J:92:ALA:HB3	18:J:93:PRO:HD3	1.92	0.52
40:d:18:LEU:HD21	40:d:53:LYS:HG3	1.91	0.52
50:n:40:LYS:HA	50:n:43:ILE:HG12	1.90	0.52
1:0:74:SER:OG	1:0:75:GLY:N	2.43	0.52
6:5:9:PRO:HD3	6:5:16:LEU:HD21	1.91	0.52
9:A:815:A:H2'	9:A:817:C:C4	2.45	0.52
9:A:1487:C:H5'	9:A:1488:A:OP1	2.10	0.52
37:a:785:G:H1	37:a:798:U:H3	1.57	0.52
9:A:296:G:H2'	9:A:297:U:C5	2.44	0.52
9:A:984:G:OP2	22:N:14:ARG:NH1	2.43	0.52
9:A:1195:U:H5''	9:A:1196:A:H2'	1.90	0.52
20:L:21:CYS:HB2	20:L:39:ILE:HD12	1.92	0.52
37:a:89:G:OP2	56:t:89:ARG:NH2	2.43	0.52
37:a:334:A:OP2	48:l:31:ARG:NH1	2.42	0.52
37:a:398:C:O2'	37:a:489:G:OP1	2.28	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:a:916:C:O3'	45:i:205:PHE:HZ	1.93	0.52
37:a:1002:G:N7	37:a:1148:C:H5''	2.25	0.52
9:A:1321:A:H4'	9:A:1322:A:H5''	1.92	0.52
9:A:1437:G:H2'	9:A:1438:G:C8	2.45	0.52
9:A:2330:U:H2'	9:A:2331:G:H8	1.74	0.52
9:A:2524:C:C2	9:A:2599:G:N2	2.78	0.52
37:a:1444:U:OP1	61:y:97:LYS:NZ	2.42	0.52
39:c:164:ILE:HG12	39:c:209:ILE:HG23	1.92	0.52
9:A:488:G:N2	9:A:491:A:OP2	2.43	0.51
9:A:530:U:H2'	9:A:531:A:C8	2.45	0.51
9:A:2332:G:H2'	9:A:2333:C:C6	2.45	0.51
28:T:70:TYR:HB2	28:T:73:CYS:SG	2.50	0.51
43:g:72:ASP:OD1	43:g:142:HIS:NE2	2.43	0.51
44:h:9:ILE:HG23	44:h:26:ILE:HD13	1.92	0.51
55:s:63:THR:H	55:s:66:MET:CG	2.23	0.51
9:A:1689:C:OP1	31:W:18:G:N1	2.33	0.51
9:A:1953:U:OP1	9:A:2621:U:O2'	2.27	0.51
9:A:2249:C:P	33:Y:97:ARG:HH22	2.34	0.51
19:K:239:LEU:HD12	19:K:240:PRO:HD2	1.91	0.51
22:N:61:GLY:HA3	22:N:109:VAL:HG13	1.92	0.51
37:a:69:G:H1	37:a:85:A:H61	1.56	0.51
37:a:579:A:H3'	37:a:580:G:H8	1.75	0.51
37:a:1187:A:H62	37:a:1247:A:H62	1.59	0.51
45:i:87:GLY:HA2	45:i:159:LEU:HD23	1.92	0.51
50:n:9:ARG:HB3	50:n:13:ARG:NH1	2.26	0.51
9:A:261:U:H3	9:A:266:A:H61	1.58	0.51
11:C:237:ILE:HD11	11:C:242:PRO:HG3	1.92	0.51
32:X:159:ARG:HG2	32:X:163:GLU:OE2	2.10	0.51
37:a:983:G:H2'	37:a:984:A:H8	1.75	0.51
41:e:215:VAL:HG11	41:e:260:ALA:HB1	1.91	0.51
47:k:79:ALA:O	47:k:83:VAL:HG13	2.10	0.51
9:A:843:C:H2'	9:A:844:G:C8	2.45	0.51
9:A:1559:A:H5'	9:A:1560:C:OP2	2.11	0.51
19:K:164:SER:O	19:K:167:LYS:HB2	2.09	0.51
22:N:77:ARG:NH2	22:N:86:GLY:O	2.37	0.51
37:a:677:A:H2'	37:a:678:A:O4'	2.10	0.51
40:d:58:TYR:OH	40:d:88:GLU:OE1	2.21	0.51
45:i:106:ILE:HB	45:i:142:PHE:HD1	1.76	0.51
46:j:125:THR:HG21	46:j:176:THR:HA	1.93	0.51
5:4:113:ARG:HB2	21:M:141:PRO:HG2	1.92	0.51
9:A:758:U:H4'	28:T:121:ARG:HH21	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:R:110:MET:HE1	27:S:170:THR:HB	1.92	0.51
28:T:152:LEU:HD22	28:T:156:LYS:HB3	1.93	0.51
37:a:1045:C:H2'	37:a:1046:C:C6	2.45	0.51
54:r:44:GLY:O	54:r:70:ARG:NH2	2.43	0.51
13:E:206:LEU:HD11	13:E:229:LEU:HG	1.91	0.51
16:H:69:VAL:HG12	16:H:70:ARG:O	2.11	0.51
25:Q:130:ALA:HB1	25:Q:177:ILE:HD12	1.91	0.51
37:a:65:G:C6	37:a:84:C:N4	2.78	0.51
3:2:42:THR:O	3:2:42:THR:OG1	2.29	0.51
4:3:123:GLY:O	4:3:126:LEU:HB2	2.10	0.51
9:A:2103:G:C6	9:A:2104:A:N7	2.78	0.51
22:N:59:ARG:HG3	22:N:60:ARG:H	1.75	0.51
37:a:1009:U:OP1	50:n:84:ARG:NH2	2.44	0.51
37:a:1461:U:H2'	37:a:1462:A:C8	2.46	0.51
38:b:98:LYS:HB3	38:b:150:THR:HG23	1.93	0.51
44:h:38:ILE:HG22	44:h:42:GLU:OE2	2.09	0.51
48:l:111:GLN:HE22	48:l:122:PRO:CG	2.24	0.51
9:A:2528:U:H2'	9:A:2529:C:O4'	2.11	0.51
10:B:61:C:H2'	10:B:62:U:H6	1.76	0.51
24:P:71:PRO:HD2	24:P:139:VAL:HG12	1.93	0.51
27:S:106:ILE:HD13	28:T:162:GLY:HA3	1.92	0.51
28:T:167:GLY:O	28:T:171:GLU:HG2	2.10	0.51
30:V:99:THR:HB	30:V:129:ALA:HB1	1.93	0.51
37:a:1151:C:H4'	50:n:66:THR:HG22	1.91	0.51
40:d:149:GLN:HE22	40:d:171:TYR:HD2	1.59	0.51
43:g:6:THR:HG22	43:g:7:VAL:H	1.75	0.51
49:m:61:VAL:HB	49:m:80:LEU:HD11	1.93	0.51
9:A:2147:G:H21	9:A:2172:A:H61	1.57	0.51
9:A:2149:A:H1'	9:A:2173:G:O2'	2.11	0.51
23:O:106:ARG:NH1	23:O:126:VAL:HG21	2.26	0.51
37:a:2:C:C4	41:e:307:TRP:CD1	2.98	0.51
37:a:1114:G:N1	37:a:1117:A:OP2	2.43	0.51
44:h:86:GLY:HA2	53:q:89:ARG:HH21	1.75	0.51
9:A:880:U:P	22:N:6:ARG:HH11	2.34	0.50
9:A:2078:C:C2	9:A:2464:G:N2	2.79	0.50
9:A:2381:C:H2'	9:A:2382:G:O4'	2.11	0.50
22:N:1:MET:HG2	22:N:44:SER:HB2	1.91	0.50
37:a:299:C:H4'	37:a:300:A:H5''	1.92	0.50
37:a:1317:G:H5''	45:i:192:LYS:HB3	1.93	0.50
37:a:1361:U:H2'	37:a:1362:A:H8	1.76	0.50
38:b:73:ILE:HD13	38:b:84:VAL:HG22	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:d:62:GLU:OE1	40:d:197:TYR:OH	2.23	0.50
9:A:548:G:HO2'	9:A:549:A:P	2.33	0.50
9:A:2136:U:OP2	9:A:2183:A:O2'	2.27	0.50
11:C:138:HIS:ND1	11:C:189:GLY:O	2.26	0.50
12:D:166:ARG:NH1	31:W:26:G:OP1	2.44	0.50
12:D:193:GLU:OE2	12:D:268:LYS:HA	2.11	0.50
13:E:206:LEU:HB3	13:E:245:LEU:HD22	1.92	0.50
37:a:76:G:C5'	59:w:102:LYS:HD2	2.41	0.50
41:e:272:SER:OG	41:e:273:ASN:N	2.45	0.50
9:A:1087:G:H1'	18:J:198:ILE:HG23	1.93	0.50
9:A:1273:G:H1	26:R:37:GLN:HE21	1.59	0.50
9:A:2066:G:H4'	12:D:237:ALA:O	2.11	0.50
9:A:2150:G:N1	9:A:2170:C:H1'	2.26	0.50
9:A:2204:A:H3'	9:A:2205:G:H8	1.76	0.50
9:A:2722:C:O2'	31:W:56:G:OP1	2.23	0.50
13:E:167:SER:O	21:M:79:ARG:HG3	2.11	0.50
17:I:75:LEU:HD13	17:I:140:ILE:HB	1.93	0.50
28:T:94:ASN:HB3	28:T:97:ASN:ND2	2.26	0.50
37:a:831:C:N4	48:l:2:PRO:HG3	2.26	0.50
37:a:1203:G:H2'	37:a:1227:A:H61	1.76	0.50
43:g:147:ALA:O	47:k:65:LYS:NZ	2.44	0.50
4:3:111:THR:O	4:3:116:LEU:HD23	2.10	0.50
9:A:1040:U:OP1	26:R:70:ARG:NH2	2.45	0.50
9:A:1363:A:O2'	9:A:1365:U:OP2	2.27	0.50
9:A:2221:U:H2'	9:A:2222:C:C6	2.47	0.50
9:A:2331:G:H5'	14:F:88:VAL:HG11	1.92	0.50
14:F:67:PRO:O	14:F:71:GLU:HG2	2.11	0.50
14:F:73:PHE:CE2	14:F:221:LYS:HD2	2.46	0.50
15:G:82:VAL:HG22	15:G:92:VAL:HG22	1.93	0.50
19:K:75:PRO:CD	19:K:88:GLU:HG2	2.39	0.50
35:z:16:U:H5	35:z:18:G:H5'	1.76	0.50
45:i:122:TRP:CZ3	45:i:150:LEU:HB2	2.46	0.50
58:v:191:LEU:HD23	58:v:255:ILE:HG21	1.93	0.50
4:3:144:PRO:HG2	4:3:149:ARG:HB2	1.94	0.50
9:A:1133:U:H2'	9:A:1134:G:C8	2.45	0.50
11:C:121:LYS:HE2	11:C:124:ASN:HD21	1.77	0.50
15:G:94:LYS:HE2	15:G:105:HIS:CE1	2.46	0.50
37:a:7:G:H22	41:e:245:THR:HG22	1.77	0.50
37:a:555:A:H2'	37:a:556:A:C8	2.47	0.50
37:a:788:U:H3	37:a:795:C:H42	1.58	0.50
37:a:1188:U:C5	43:g:116:MET:HE3	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:k:55:SER:O	47:k:58:THR:HG22	2.11	0.50
50:n:48:GLN:HE22	55:s:12:ALA:HA	1.75	0.50
1:0:73:TRP:H	1:0:73:TRP:CD1	2.29	0.50
2:1:22:LYS:O	2:1:25:TYR:HB3	2.12	0.50
6:5:37:GLY:HA2	9:A:1153:G:H5'	1.92	0.50
12:D:237:ALA:HB3	12:D:241:PRO:HD2	1.94	0.50
17:I:154:ARG:HA	17:I:157:GLU:HB2	1.94	0.50
22:N:52:ARG:HB3	22:N:52:ARG:HH11	1.76	0.50
28:T:186:PHE:O	28:T:190:ILE:HG13	2.12	0.50
39:c:166:GLY:HA3	39:c:207:LEU:HD12	1.94	0.50
9:A:1635:C:OP1	29:U:144:LYS:HB2	2.12	0.50
9:A:2464:G:N2	9:A:2467:A:C6	2.80	0.50
25:Q:138:ARG:HH22	25:Q:203:ILE:CG2	2.25	0.50
35:z:16:U:H4'	35:z:16:U:OP1	2.12	0.50
9:A:591:C:H2'	9:A:592:G:C8	2.46	0.50
9:A:1209:U:O2'	9:A:1210:A:H5'	2.11	0.50
9:A:2460:U:H2'	9:A:2461:A:C8	2.47	0.50
19:K:159:ASP:OD1	19:K:159:ASP:N	2.37	0.50
34:Z:89:MET:HG2	34:Z:152:LEU:HB2	1.94	0.50
47:k:102:ARG:NH2	47:k:121:ASP:OD1	2.45	0.50
57:u:139:ARG:HD2	57:u:143:ARG:HH21	1.76	0.50
9:A:1420:C:OP1	29:U:160:ARG:NH2	2.45	0.50
37:a:375:G:P	40:d:112:ASN:HD21	2.34	0.50
37:a:422:A:H61	37:a:429:G:H5'	1.77	0.50
37:a:1202:G:OP1	46:j:140:ARG:HG2	2.12	0.50
43:g:31:LEU:HD21	43:g:34:GLY:HA2	1.93	0.50
9:A:312:C:H2'	9:A:313:A:C8	2.47	0.49
9:A:740:G:C8	11:C:203:ARG:NH1	2.80	0.49
10:B:83:U:H3	10:B:96:G:H1	1.59	0.49
37:a:378:G:H1	37:a:406:U:H3	1.60	0.49
37:a:632:U:H4'	47:k:49:ARG:HD2	1.94	0.49
37:a:775:U:O2'	44:h:19:ASN:ND2	2.45	0.49
38:b:107:ASN:HD21	38:b:110:THR:HB	1.77	0.49
53:q:79:VAL:HG22	53:q:94:LYS:HG2	1.94	0.49
9:A:640:G:H2'	9:A:641:C:H6	1.76	0.49
9:A:644:A:O4'	21:M:150:MET:HE3	2.12	0.49
9:A:1557:G:H2'	9:A:1557:G:N3	2.26	0.49
15:G:99:ARG:O	15:G:103:GLN:HG3	2.12	0.49
35:z:34:G:H21	61:y:140:ARG:CB	2.18	0.49
37:a:36:G:C2	37:a:498:G:C2	3.00	0.49
37:a:198:G:H2'	37:a:199:A:C8	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:a:1061:C:N3	39:c:189:ILE:HG13	2.27	0.49
53:q:100:HIS:CG	53:q:120:ILE:HD12	2.47	0.49
3:2:45:ARG:NH2	3:2:47:GLU:OE1	2.45	0.49
9:A:241:A:H2'	9:A:242:A:H8	1.77	0.49
22:N:67:ARG:NH1	22:N:105:GLU:OE1	2.43	0.49
35:z:33:U:O5'	43:g:84:THR:OG1	2.29	0.49
37:a:387:G:H2'	37:a:388:G:H8	1.77	0.49
38:b:87:ALA:HB1	38:b:222:VAL:HG21	1.93	0.49
44:h:98:ARG:HB3	44:h:121:ARG:NH2	2.26	0.49
1:0:62:GLY:O	14:F:155:ARG:HD3	2.13	0.49
3:2:56:TYR:O	9:A:2388:G:H4'	2.12	0.49
9:A:888:C:H5	9:A:908:A:H2	1.61	0.49
9:A:947:A:H2'	9:A:948:U:H5''	1.94	0.49
9:A:1933:A:O3'	37:a:1466:G:H1'	2.13	0.49
28:T:188:TYR:HE2	28:T:195:ARG:HB2	1.76	0.49
49:m:135:ARG:HB3	49:m:140:LEU:O	2.12	0.49
55:s:22:LEU:HD21	55:s:29:GLU:HB2	1.94	0.49
9:A:984:G:N7	22:N:14:ARG:NH2	2.60	0.49
9:A:1700:A:H61	9:A:2010:C:H42	1.60	0.49
9:A:1837:U:H2'	9:A:1838:G:O4'	2.12	0.49
25:Q:118:LYS:O	25:Q:121:ASP:HB2	2.13	0.49
33:Y:110:TRP:CE3	33:Y:113:GLY:HA3	2.47	0.49
37:a:831:C:H42	48:l:2:PRO:HG3	1.78	0.49
37:a:1010:G:H1'	46:j:151:HIS:CE1	2.47	0.49
37:a:1166:C:H2'	37:a:1167:U:C6	2.47	0.49
38:b:124:GLU:HG2	38:b:129:ARG:HE	1.77	0.49
47:k:44:THR:HA	47:k:51:VAL:HG23	1.94	0.49
47:k:90:ARG:HG2	47:k:115:LEU:HD23	1.93	0.49
1:0:38:LYS:HD2	1:0:41:ILE:HD13	1.95	0.49
9:A:2093:U:H2'	9:A:2094:G:O4'	2.12	0.49
16:H:69:VAL:HG13	16:H:73:PHE:HD2	1.78	0.49
17:I:54:ILE:HG23	17:I:58:LYS:HD3	1.95	0.49
21:M:140:ILE:HG23	21:M:141:PRO:HD2	1.94	0.49
38:b:32:SER:N	38:b:33:PRO:HD2	2.28	0.49
39:c:100:GLN:HG2	39:c:105:CYS:SG	2.52	0.49
42:f:130:TYR:HD1	42:f:133:LEU:HD12	1.77	0.49
43:g:22:LEU:HD11	43:g:66:ILE:HD12	1.93	0.49
45:i:105:PHE:CB	45:i:112:ALA:HB2	2.43	0.49
49:m:101:VAL:O	49:m:105:VAL:HG23	2.12	0.49
5:4:95:HIS:NE2	9:A:236:A:OP1	2.46	0.49
9:A:874:G:H2'	9:A:875:C:C6	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:C:167:SER:HB2	11:C:179:LEU:HG	1.94	0.49
20:L:61:VAL:HG13	20:L:87:ILE:HD13	1.95	0.49
22:N:8:ARG:H	22:N:8:ARG:HD2	1.76	0.49
22:N:41:TRP:CZ2	22:N:72:LYS:HE2	2.47	0.49
38:b:170:GLN:HE21	38:b:195:CYS:HB3	1.78	0.49
49:m:61:VAL:HG23	49:m:88:LYS:O	2.13	0.49
9:A:635:C:H2'	9:A:636:C:H6	1.76	0.49
9:A:2206:A:H2'	9:A:2207:A:H8	1.75	0.49
12:D:120:GLY:HA3	12:D:141:TYR:O	2.13	0.49
17:I:140:ILE:HG12	17:I:141:PRO:HD3	1.95	0.49
43:g:130:GLY:HA2	43:g:135:VAL:HG21	1.95	0.49
4:3:118:MET:HE1	4:3:127:LEU:HD12	1.94	0.49
9:A:2208:U:H2'	9:A:2209:U:O4'	2.13	0.49
9:A:2369:A:H2'	9:A:2370:G:O4'	2.12	0.49
14:F:46:VAL:O	14:F:56:ARG:NH2	2.46	0.49
19:K:135:ILE:HG22	19:K:217:LEU:HD22	1.95	0.49
37:a:491:U:H5''	40:d:14:ARG:NH1	2.27	0.49
38:b:35:ILE:HG22	38:b:36:SER:H	1.78	0.49
42:f:102:PRO:HB3	42:f:179:PHE:CD2	2.48	0.49
46:j:118:ILE:HG12	46:j:183:LEU:HD13	1.94	0.49
9:A:17:C:O2'	9:A:564:U:OP1	2.29	0.49
9:A:717:A:H2'	9:A:718:G:O4'	2.12	0.49
9:A:1003:A:H1'	9:A:1018:A:C2	2.47	0.49
9:A:2075:G:H5''	9:A:2520:A:OP1	2.13	0.49
9:A:2136:U:OP1	9:A:2182:G:N2	2.46	0.49
9:A:2258:A:H2'	9:A:2259:G:C8	2.48	0.49
12:D:232:LEU:HD21	12:D:250:MET:HG2	1.94	0.49
14:F:183:VAL:HG13	14:F:185:PHE:HE1	1.77	0.49
15:G:108:PHE:HA	15:G:111:LEU:HB2	1.95	0.49
24:P:81:HIS:CD2	24:P:100:THR:HB	2.42	0.49
29:U:109:LEU:HB2	29:U:146:MET:HE1	1.94	0.49
30:V:78:VAL:HG22	30:V:135:VAL:HG12	1.95	0.49
37:a:600:U:C5	37:a:700:G:C2	3.01	0.49
37:a:1253:G:H2'	37:a:1279:G:N2	2.27	0.49
37:a:1412:U:H2'	37:a:1413:G:H8	1.78	0.49
49:m:48:VAL:HG11	49:m:98:LEU:HD11	1.94	0.49
9:A:646:G:H2'	9:A:647:C:C6	2.48	0.48
9:A:881:U:H4'	22:N:69:PHE:CE2	2.48	0.48
9:A:1348:C:H5''	28:T:71:ARG:NH2	2.28	0.48
9:A:1394:A:H5'	9:A:2230:A:H1'	1.94	0.48
12:D:95:THR:HG23	12:D:288:ASN:O	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:W:5:A:H5'	31:W:6:A:OP2	2.13	0.48
37:a:860:U:OP2	48:l:94:ARG:NH2	2.46	0.48
37:a:1467:A:H2'	37:a:1468:A:C8	2.47	0.48
61:y:102:VAL:HG13	61:y:109:VAL:HG11	1.94	0.48
1:0:51:VAL:HB	1:0:59:MET:HG3	1.95	0.48
6:5:9:PRO:HD3	6:5:16:LEU:HD11	1.95	0.48
9:A:642:G:N2	9:A:645:A:OP2	2.29	0.48
9:A:1039:A:OP1	26:R:77:ASN:HB3	2.13	0.48
9:A:1485:U:H5'	9:A:1486:U:C5'	2.38	0.48
11:C:150:LEU:HD13	11:C:172:LEU:HD11	1.95	0.48
12:D:100:MET:HE1	25:Q:126:LEU:HB2	1.95	0.48
12:D:149:LEU:HD12	12:D:149:LEU:HA	1.61	0.48
28:T:146:ASP:O	28:T:150:GLU:HG2	2.13	0.48
32:X:89:PRO:HD3	32:X:120:ASP:OD1	2.14	0.48
37:a:626:U:H2'	37:a:627:U:C6	2.48	0.48
38:b:101:LEU:HD23	38:b:104:MET:HE3	1.95	0.48
9:A:236:A:H8	9:A:236:A:O5'	1.96	0.48
9:A:1444:A:H2'	9:A:1445:G:H8	1.76	0.48
9:A:1582:A:H2'	9:A:1583:A:C8	2.48	0.48
11:C:100:ILE:HD12	11:C:101:LEU:O	2.14	0.48
14:F:111:ALA:O	14:F:115:GLY:N	2.45	0.48
17:I:100:THR:CG2	17:I:135:VAL:HG12	2.43	0.48
37:a:21:U:H2'	37:a:22:G:O4'	2.12	0.48
37:a:1223:A:H5'	37:a:1224:G:OP2	2.13	0.48
39:c:71:LEU:HD12	39:c:109:LYS:HG3	1.95	0.48
44:h:24:VAL:O	44:h:60:VAL:HA	2.12	0.48
9:A:126:C:H2'	9:A:127:C:C6	2.48	0.48
9:A:824:U:H2'	9:A:825:C:C6	2.48	0.48
11:C:78:GLU:OE2	11:C:89:LEU:HB2	2.13	0.48
11:C:193:ASN:OD1	11:C:196:VAL:HG23	2.13	0.48
15:G:196:PRO:O	15:G:211:ARG:HA	2.13	0.48
17:I:119:TRP:HE1	17:I:165:CYS:HB3	1.78	0.48
25:Q:153:LEU:HD12	25:Q:165:TYR:CE2	2.47	0.48
25:Q:170:ILE:HD11	25:Q:182:ARG:HD3	1.94	0.48
37:a:573:C:H2'	37:a:574:U:C6	2.49	0.48
40:d:169:PHE:HB2	40:d:170:PRO:HD3	1.93	0.48
47:k:38:ASN:HB2	47:k:66:ARG:HE	1.78	0.48
1:0:50:LYS:HG3	1:0:58:VAL:HG13	1.95	0.48
4:3:135:ARG:NH2	9:A:480:G:N7	2.61	0.48
6:5:19:ARG:HG2	9:A:2774:U:C5'	2.42	0.48
8:7:85:LEU:HD13	27:S:160:LYS:HE3	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:227:G:O2'	9:A:239:G:O6	2.27	0.48
9:A:564:U:C2'	9:A:565:G:H5'	2.43	0.48
9:A:581:A:O2'	27:S:203:LYS:NZ	2.46	0.48
9:A:839:G:C2	9:A:840:A:N6	2.82	0.48
9:A:2290:A:H2'	9:A:2291:A:H8	1.76	0.48
14:F:89:VAL:HG23	14:F:207:VAL:HG22	1.96	0.48
20:L:25:ILE:HD11	20:L:40:VAL:HG23	1.95	0.48
28:T:105:VAL:HG22	28:T:132:ILE:HG23	1.95	0.48
37:a:980:C:H5'	37:a:981:G:O4'	2.14	0.48
37:a:1155:C:H2'	37:a:1156:C:C6	2.49	0.48
37:a:1300:C:P	60:x:56:ARG:HH22	2.37	0.48
38:b:100:TRP:CZ3	38:b:175:THR:HB	2.42	0.48
43:g:51:GLN:OE1	43:g:58:PRO:HD3	2.13	0.48
12:D:224:HIS:H	12:D:224:HIS:CD2	2.30	0.48
37:a:685:U:H2'	37:a:686:G:C8	2.48	0.48
45:i:70:VAL:HG21	45:i:106:ILE:HG21	1.96	0.48
9:A:490:A:H1'	30:V:108:LYS:NZ	2.28	0.48
9:A:629:C:O3'	13:E:258:ARG:NH2	2.47	0.48
27:S:105:ASP:O	27:S:109:GLN:HG2	2.14	0.48
28:T:123:TYR:HE2	28:T:125:ILE:HD11	1.78	0.48
39:c:20:SER:HB3	39:c:22:TRP:NE1	2.29	0.48
47:k:44:THR:HG1	47:k:49:ARG:C	2.18	0.48
49:m:116:ARG:O	49:m:120:ILE:HG23	2.14	0.48
50:n:40:LYS:HB3	55:s:8:ASN:HD21	1.78	0.48
9:A:1408:A:H2'	9:A:1409:G:C8	2.48	0.48
9:A:2403:U:H4'	32:X:112:ASP:HA	1.96	0.48
9:A:2662:C:HO2'	9:A:2750:G:HO2'	1.59	0.48
37:a:896:G:N2	37:a:1183:U:O2	2.46	0.48
37:a:1274:U:H2'	37:a:1275:G:C8	2.48	0.48
41:e:185:GLY:O	41:e:214:THR:HG23	2.13	0.48
48:l:67:ILE:HG12	48:l:97:ILE:HD12	1.96	0.48
5:4:112:ARG:O	5:4:135:LEU:HD22	2.14	0.48
9:A:866:G:H5''	9:A:866:G:H8	1.79	0.48
9:A:1832:G:H2'	9:A:1833:G:H5''	1.96	0.48
10:B:28:C:H2'	10:B:29:C:H6	1.79	0.48
10:B:56:U:O2'	14:F:77:ASN:ND2	2.35	0.48
37:a:378:G:H5''	40:d:105:PRO:HB2	1.96	0.48
37:a:1225:C:O2'	37:a:1227:A:C8	2.63	0.48
4:3:126:LEU:HD23	4:3:129:ARG:NH2	2.29	0.48
9:A:880:U:OP1	22:N:6:ARG:HD3	2.14	0.48
9:A:2307:G:H2'	9:A:2308:U:O4'	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:F:53:THR:O	14:F:56:ARG:HB2	2.14	0.48
37:a:1479:G:H2'	37:a:1480:A:C8	2.49	0.48
38:b:35:ILE:HG22	38:b:36:SER:N	2.29	0.48
1:0:53:CYS:HG	1:0:73:TRP:CD1	2.32	0.47
9:A:273:U:O2'	9:A:274:G:H5'	2.14	0.47
9:A:555:A:C6	9:A:558:A:H1'	2.49	0.47
9:A:2213:A:OP1	33:Y:107:ARG:NH2	2.46	0.47
37:a:1384:G:H2'	37:a:1385:U:C6	2.49	0.47
49:m:110:ILE:HD13	49:m:111:GLU:H	1.79	0.47
9:A:1817:G:H5''	9:A:1817:G:H8	1.79	0.47
9:A:2339:A:C6	9:A:2350:A:N6	2.82	0.47
10:B:117:A:H4'	24:P:102:GLN:HE21	1.78	0.47
22:N:4:PRO:HG2	22:N:93:TRP:CZ3	2.49	0.47
29:U:150:ALA:O	29:U:154:PHE:HB2	2.14	0.47
35:z:38:A:H2'	35:z:39:U:H5'	1.96	0.47
39:c:26:PRO:HB3	46:j:140:ARG:HH22	1.80	0.47
43:g:72:ASP:OD1	43:g:72:ASP:N	2.34	0.47
43:g:73:ILE:HG22	43:g:142:HIS:CD2	2.49	0.47
9:A:555:A:N6	9:A:558:A:HO2'	2.07	0.47
9:A:677:A:O2'	9:A:678:U:H5'	2.14	0.47
9:A:1269:G:P	13:E:143:PRO:HG3	2.54	0.47
9:A:1333:U:H4'	9:A:1334:U:O5'	2.15	0.47
9:A:1337:U:H2'	9:A:1338:C:C6	2.50	0.47
11:C:239:ARG:C	11:C:241:SER:H	2.22	0.47
18:J:150:LEU:HD23	18:J:171:ILE:HD13	1.96	0.47
24:P:116:THR:HG22	24:P:118:GLU:H	1.79	0.47
29:U:119:ILE:HG21	29:U:167:ARG:HH22	1.79	0.47
37:a:655:U:OP1	47:k:96:LYS:NZ	2.31	0.47
39:c:51:THR:HG23	39:c:83:LEU:HD22	1.95	0.47
5:4:126:THR:HA	5:4:129:LYS:HE3	1.96	0.47
9:A:1088:U:O4	18:J:205:ASN:ND2	2.37	0.47
9:A:1615:G:H2'	9:A:1616:A:C8	2.49	0.47
9:A:2691:G:H5''	20:L:30:ARG:HB2	1.97	0.47
9:A:2722:C:H2'	9:A:2723:A:O4'	2.14	0.47
27:S:171:TYR:CE2	27:S:232:ALA:HB2	2.48	0.47
37:a:641:G:OP1	61:y:180:ARG:NH1	2.41	0.47
37:a:683:U:H2'	37:a:684:C:C6	2.49	0.47
37:a:925:G:C8	37:a:1306:U:H2'	2.49	0.47
43:g:31:LEU:HD13	43:g:36:LYS:HD3	1.97	0.47
59:w:102:LYS:HE2	59:w:129:TYR:OH	2.14	0.47
5:4:142:ASP:O	5:4:146:VAL:HG23	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:E:116:TYR:CZ	13:E:130:ARG:HD3	2.49	0.47
15:G:69:LEU:HD11	15:G:121:LYS:O	2.15	0.47
20:L:121:LEU:HD22	25:Q:165:TYR:HE1	1.79	0.47
37:a:113:A:H8	37:a:113:A:OP2	1.98	0.47
37:a:1168:G:OP1	50:n:52:ARG:NH1	2.47	0.47
37:a:1199:A:H4'	45:i:91:CYS:SG	2.54	0.47
37:a:1445:C:H2'	37:a:1446:G:O4'	2.15	0.47
49:m:141:PRO:HD3	49:m:154:LEU:HD22	1.96	0.47
50:n:38:SER:HA	50:n:41:TRP:CD1	2.50	0.47
52:p:5:ARG:NH2	52:p:22:ILE:HD11	2.29	0.47
59:w:102:LYS:HD3	59:w:115:ASP:OD2	2.14	0.47
1:0:53:CYS:SG	1:0:73:TRP:NE1	2.85	0.47
9:A:176:A:H2'	9:A:177:C:H6	1.78	0.47
9:A:724:G:OP2	51:o:85:ARG:NH2	2.48	0.47
18:J:151:LEU:HG	18:J:206:MET:HE1	1.95	0.47
26:R:109:TYR:HB3	27:S:235:LEU:HD11	1.96	0.47
37:a:804:G:H2'	37:a:805:U:H6	1.80	0.47
38:b:54:LEU:HG	38:b:220:LYS:HD2	1.97	0.47
42:f:152:LEU:HG	42:f:169:LEU:O	2.14	0.47
47:k:107:ARG:HD3	47:k:111:ARG:NH2	2.30	0.47
58:v:207:LYS:HG3	58:v:241:ALA:HA	1.97	0.47
8:7:53:LYS:O	8:7:58:HIS:HB2	2.15	0.47
9:A:511:G:N1	9:A:514:A:OP2	2.46	0.47
9:A:1275:A:H5''	9:A:1276:U:H5''	1.96	0.47
9:A:1523:A:N3	9:A:1546:C:H4'	2.30	0.47
9:A:1632:U:C2'	9:A:1633:A:H5'	2.45	0.47
12:D:148:LYS:NZ	31:W:38:G:OP2	2.47	0.47
12:D:222:MET:HE1	12:D:229:HIS:HB3	1.96	0.47
13:E:207:PHE:HB2	13:E:228:LEU:HD22	1.96	0.47
19:K:116:VAL:HG12	19:K:154:ILE:HB	1.95	0.47
21:M:154:LEU:HD12	21:M:155:PRO:HD2	1.97	0.47
31:W:34:U:O3'	31:W:35:U:H4'	2.15	0.47
37:a:93:A:C6	37:a:297:G:C6	3.02	0.47
37:a:613:G:H1'	37:a:681:A:H5'	1.97	0.47
37:a:625:U:H2'	37:a:626:U:C6	2.49	0.47
37:a:670:A:H61	37:a:681:A:H61	1.63	0.47
37:a:932:A:H5''	37:a:933:C:OP2	2.15	0.47
37:a:1271:G:H2'	37:a:1272:C:C6	2.49	0.47
39:c:134:GLN:HE22	39:c:147:LYS:HD3	1.79	0.47
50:n:30:GLU:O	50:n:34:VAL:HB	2.14	0.47
61:y:155:SER:O	61:y:159:LEU:HG	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:4:140:ARG:O	5:4:143:TYR:HB2	2.15	0.47
9:A:142:U:H1'	9:A:153:G:N2	2.29	0.47
9:A:407:C:O2'	33:Y:83:ASN:HB2	2.15	0.47
9:A:1074:A:C8	17:I:59:LYS:HE3	2.50	0.47
9:A:1096:G:N2	9:A:1123:A:O2'	2.48	0.47
9:A:1692:C:H2'	9:A:1693:U:C6	2.49	0.47
9:A:2373:C:H2'	9:A:2374:C:O4'	2.15	0.47
9:A:2757:U:O2	9:A:2784:G:N2	2.48	0.47
11:C:243:THR:HG22	11:C:244:THR:O	2.14	0.47
18:J:123:PHE:HE1	18:J:152:LYS:HD2	1.80	0.47
32:X:131:ASP:OD1	32:X:132:LYS:N	2.47	0.47
37:a:611:A:H5''	54:r:57:LYS:HE3	1.96	0.47
39:c:42:CYS:HB2	39:c:102:GLU:OE2	2.15	0.47
40:d:103:THR:HB	40:d:105:PRO:HD2	1.97	0.47
2:1:11:TYR:CD1	2:1:11:TYR:C	2.93	0.47
9:A:306:G:O3'	30:V:158:LYS:NZ	2.47	0.47
9:A:628:A:H2'	9:A:629:C:O4'	2.14	0.47
9:A:2039:C:H2'	9:A:2040:U:O4'	2.15	0.47
9:A:2600:G:OP2	9:A:2600:G:N2	2.39	0.47
9:A:2706:U:O2	9:A:2706:U:H2'	2.14	0.47
12:D:214:ARG:HA	12:D:254:MET:SD	2.55	0.47
15:G:53:ASN:HB3	15:G:68:PRO:HG3	1.97	0.47
27:S:146:ARG:HA	27:S:217:THR:OG1	2.15	0.47
37:a:633:G:O2'	37:a:634:G:H5'	2.15	0.47
9:A:695:G:C2	9:A:805:A:C2	3.03	0.47
9:A:767:A:H2'	9:A:768:G:O4'	2.14	0.47
9:A:2260:U:H2'	9:A:2261:U:C6	2.49	0.47
13:E:58:LEU:HD23	13:E:64:LYS:HA	1.97	0.47
15:G:104:MET:HE2	15:G:104:MET:HA	1.97	0.47
16:H:52:ILE:HD12	16:H:87:VAL:HG11	1.97	0.47
22:N:31:ARG:O	22:N:134:SER:HB2	2.15	0.47
25:Q:144:ARG:HE	25:Q:144:ARG:HB3	1.52	0.47
26:R:88:ARG:HE	26:R:118:LYS:HG3	1.80	0.47
31:W:30:A:H2'	31:W:31:U:O4'	2.14	0.47
37:a:247:G:H5''	53:q:98:GLN:NE2	2.29	0.47
37:a:792:G:H1'	37:a:793:A:H5''	1.96	0.47
39:c:43:ILE:HG13	39:c:95:LEU:HD13	1.97	0.47
39:c:92:VAL:O	39:c:96:LYS:HB2	2.15	0.47
9:A:2025:U:OP2	28:T:45:LYS:NZ	2.46	0.46
9:A:2414:A:H2'	9:A:2415:C:C6	2.49	0.46
9:A:2636:G:OP1	12:D:246:LYS:NZ	2.47	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:2697:C:H2'	9:A:2698:C:C6	2.50	0.46
13:E:210:MET:HE3	13:E:251:THR:HA	1.96	0.46
15:G:72:LEU:HD13	15:G:115:MET:HB2	1.96	0.46
15:G:92:VAL:HG21	15:G:109:ARG:HB2	1.96	0.46
17:I:99:ASN:HB3	17:I:138:GLU:HB2	1.97	0.46
19:K:83:TRP:CG	19:K:84:MET:N	2.83	0.46
21:M:187:ILE:O	21:M:189:PRO:HD3	2.14	0.46
29:U:136:PHE:HD2	29:U:176:ILE:HD13	1.80	0.46
37:a:461:C:H2'	37:a:462:U:H6	1.80	0.46
37:a:632:U:C4'	47:k:49:ARG:HD2	2.45	0.46
37:a:1274:U:H2'	37:a:1275:G:H8	1.79	0.46
39:c:118:ALA:O	39:c:120:PRO:HD3	2.15	0.46
44:h:98:ARG:HD3	44:h:121:ARG:HH22	1.79	0.46
49:m:117:PHE:O	49:m:120:ILE:HG12	2.15	0.46
1:0:46:ARG:HG2	1:0:48:ASP:OD1	2.15	0.46
3:2:56:TYR:OH	9:A:655:C:O4'	2.31	0.46
9:A:349:A:H2'	9:A:350:G:O4'	2.14	0.46
9:A:2792:C:H2'	9:A:2793:A:O4'	2.15	0.46
24:P:93:HIS:HD2	24:P:95:LEU:HD23	1.80	0.46
29:U:111:VAL:O	29:U:114:ILE:HG12	2.15	0.46
32:X:122:LEU:HD21	32:X:140:ARG:HH11	1.80	0.46
33:Y:102:ASN:O	33:Y:122:SER:HA	2.15	0.46
34:Z:85:GLY:O	34:Z:88:PHE:HB3	2.16	0.46
41:e:237:MET:O	41:e:267:GLY:HA2	2.15	0.46
43:g:111:ARG:HB3	43:g:119:LYS:HG2	1.96	0.46
1:0:76:ASN:O	1:0:76:ASN:ND2	2.48	0.46
9:A:545:U:H2'	9:A:546:G:H8	1.80	0.46
9:A:1416:A:O2'	9:A:1418:U:OP2	2.33	0.46
10:B:30:A:P	24:P:78:SER:HB2	2.55	0.46
23:O:36:THR:HG21	23:O:81:TYR:H	1.80	0.46
23:O:69:SER:OG	23:O:72:LYS:HG2	2.15	0.46
23:O:111:LEU:HD12	23:O:111:LEU:HA	1.73	0.46
35:z:34:G:N1	61:y:175:VAL:HG11	2.31	0.46
37:a:900:G:C6	37:a:1179:G:C6	3.04	0.46
37:a:1127:A:H2'	37:a:1128:A:O4'	2.16	0.46
39:c:22:TRP:CZ3	39:c:24:SER:HB2	2.50	0.46
9:A:70:A:H5''	9:A:72:A:C8	2.49	0.46
9:A:702:C:O2'	11:C:39:ARG:NH2	2.48	0.46
9:A:1502:A:H8	9:A:1502:A:O5'	1.98	0.46
9:A:2155:C:N3	9:A:2165:G:N2	2.63	0.46
11:C:149:GLN:O	11:C:152:ARG:HG3	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:F:66:VAL:O	14:F:70:LYS:HB2	2.15	0.46
17:I:105:ALA:HB1	17:I:109:LEU:HD22	1.97	0.46
26:R:58:ARG:HH12	26:R:94:ARG:NH1	2.14	0.46
26:R:116:ILE:HA	26:R:119:GLU:OE2	2.16	0.46
28:T:79:LEU:HD13	28:T:134:ILE:HD11	1.98	0.46
33:Y:144:ASP:O	33:Y:148:GLU:HG3	2.16	0.46
37:a:503:C:H2'	37:a:504:C:C6	2.50	0.46
37:a:717:G:H4'	37:a:1462:A:H4'	1.96	0.46
37:a:925:G:H8	37:a:1306:U:H2'	1.79	0.46
15:G:184:PHE:O	15:G:188:ILE:HG12	2.15	0.46
32:X:73:LYS:H	32:X:73:LYS:HG2	1.49	0.46
37:a:736:U:C4	37:a:737:U:C4	3.04	0.46
37:a:995:A:H3'	37:a:996:G:H8	1.80	0.46
38:b:122:ARG:HD2	38:b:122:ARG:HA	1.78	0.46
46:j:130:MET:HB2	46:j:168:ASP:CB	2.46	0.46
57:u:140:ASN:HD21	57:u:144:ARG:NH2	2.13	0.46
9:A:143:G:OP2	9:A:143:G:H8	1.99	0.46
9:A:794:A:H2'	9:A:795:U:H4'	1.96	0.46
9:A:1110:U:O2'	17:I:90:GLN:NE2	2.48	0.46
9:A:1567:C:H5'	9:A:1568:U:OP2	2.15	0.46
9:A:2340:G:H2'	9:A:2341:U:H5'	1.97	0.46
9:A:2535:C:H5'	9:A:2535:C:O2	2.16	0.46
10:B:48:C:OP1	24:P:49:ARG:HG3	2.16	0.46
20:L:75:MET:HE2	20:L:75:MET:HB3	1.76	0.46
24:P:103:LYS:O	24:P:107:GLU:HG2	2.15	0.46
37:a:76:G:N3	37:a:77:G:H1'	2.30	0.46
40:d:19:PRO:HD2	40:d:57:HIS:HD2	1.80	0.46
48:l:114:ARG:HH12	48:l:121:LYS:HG3	1.81	0.46
54:r:70:ARG:HD3	54:r:77:PHE:CD1	2.51	0.46
9:A:17:C:O3'	26:R:23:SER:HA	2.15	0.46
9:A:573:G:H21	26:R:37:GLN:HE22	1.62	0.46
9:A:1511:U:O5'	9:A:1511:U:H6	1.98	0.46
9:A:2113:G:H2'	9:A:2114:G:C8	2.51	0.46
9:A:2263:C:H2'	9:A:2264:U:C6	2.51	0.46
22:N:53:ALA:HB1	22:N:120:ILE:HG22	1.98	0.46
22:N:54:MET:HE1	22:N:104:TYR:HB3	1.98	0.46
28:T:112:LYS:HB3	28:T:124:MET:CE	2.43	0.46
34:Z:140:TRP:O	34:Z:144:ILE:HG12	2.16	0.46
40:d:19:PRO:HD2	40:d:57:HIS:CD2	2.51	0.46
41:e:225:HIS:HE1	41:e:290:ARG:H	1.63	0.46
42:f:129:LYS:O	42:f:133:LEU:HG	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:n:12:LYS:HE2	50:n:53:ASN:HD22	1.81	0.46
9:A:316:G:N2	9:A:339:A:H61	2.11	0.46
9:A:1090:U:H2'	9:A:1091:G:H8	1.81	0.46
9:A:1207:G:H2'	9:A:1208:G:O4'	2.16	0.46
9:A:2463:G:H2'	9:A:2464:G:O4'	2.15	0.46
37:a:611:A:OP2	42:f:207:ARG:NH2	2.49	0.46
37:a:796:C:H3'	37:a:797:G:H8	1.81	0.46
37:a:982:G:H4'	37:a:982:G:OP1	2.16	0.46
46:j:122:ALA:HB2	46:j:180:LEU:HD21	1.97	0.46
56:t:126:VAL:HB	56:t:127:PRO:HD3	1.97	0.46
9:A:166:A:H2'	9:A:167:A:C8	2.51	0.46
9:A:623:A:N6	13:E:233:SER:HB3	2.31	0.46
9:A:1264:C:H1'	21:M:83:ASP:O	2.16	0.46
9:A:2660:G:H2'	9:A:2661:A:O4'	2.14	0.46
12:D:90:ILE:HA	12:D:90:ILE:HD13	1.69	0.46
25:Q:152:ARG:HD2	25:Q:205:GLU:OE1	2.16	0.46
9:A:197:G:H2'	9:A:198:A:C8	2.51	0.46
9:A:221:C:H2'	9:A:222:C:C6	2.51	0.46
9:A:306:G:H2'	9:A:307:C:C6	2.51	0.46
9:A:1849:A:H5'	9:A:1850:G:OP2	2.16	0.46
9:A:1976:C:H4'	9:A:1977:C:C5	2.51	0.46
26:R:88:ARG:HH22	27:S:174:THR:HG21	1.81	0.46
42:f:184:SER:O	42:f:187:PRO:HD2	2.15	0.46
45:i:122:TRP:N	45:i:122:TRP:CD1	2.80	0.46
56:t:115:LYS:NZ	56:t:170:HIS:HB2	2.31	0.46
58:v:184:TYR:CE1	58:v:235:GLU:HB2	2.50	0.46
9:A:739:G:O2'	9:A:741:U:H5''	2.16	0.45
9:A:2714:A:H2'	9:A:2715:U:O4'	2.17	0.45
18:J:113:TYR:HD1	18:J:141:LEU:HD21	1.80	0.45
25:Q:119:LEU:HD22	25:Q:122:ILE:HD12	1.97	0.45
26:R:78:TYR:CZ	26:R:82:ILE:HG13	2.51	0.45
28:T:56:ARG:NH1	28:T:64:ILE:HD11	2.31	0.45
37:a:351:G:N2	37:a:355:G:C5	2.84	0.45
37:a:574:U:H2'	37:a:575:G:H8	1.81	0.45
39:c:62:ARG:HG2	39:c:77:HIS:HB2	1.98	0.45
40:d:163:HIS:CD2	40:d:164:LEU:HG	2.51	0.45
54:r:41:SER:OG	54:r:42:GLU:N	2.49	0.45
61:y:102:VAL:CG1	61:y:109:VAL:HG11	2.46	0.45
6:5:15:ARG:HH12	9:A:2771:A:H1'	1.81	0.45
9:A:316:G:H22	9:A:339:A:N6	2.08	0.45
9:A:1573:C:H2'	9:A:1574:G:C8	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:B:30:A:H2'	10:B:31:C:C6	2.51	0.45
13:E:51:GLU:HB3	13:E:69:PHE:CD1	2.51	0.45
14:F:195:LYS:O	14:F:199:VAL:HG23	2.16	0.45
32:X:87:ALA:O	32:X:120:ASP:HA	2.16	0.45
37:a:1320:G:O3'	45:i:149:GLY:HA3	2.16	0.45
47:k:132:PRO:HG2	57:u:122:PHE:HB2	1.97	0.45
61:y:140:ARG:HD2	61:y:140:ARG:N	2.31	0.45
7:6:118:ARG:O	7:6:122:LYS:HG3	2.15	0.45
9:A:1689:C:H3'	23:O:12:LYS:HG2	1.98	0.45
14:F:120:LYS:HE3	14:F:137:THR:HG21	1.98	0.45
37:a:86:G:H2'	37:a:87:U:H6	1.81	0.45
37:a:899:U:H2'	37:a:900:G:H8	1.82	0.45
37:a:1113:U:H5'	37:a:1114:G:OP2	2.17	0.45
37:a:1139:A:H2'	37:a:1140:C:C6	2.51	0.45
38:b:8:ILE:HD11	38:b:54:LEU:HD23	1.98	0.45
39:c:39:ILE:HG23	39:c:103:LEU:HD21	1.99	0.45
39:c:72:ILE:HD12	39:c:103:LEU:HD12	1.97	0.45
56:t:171:HIS:HB2	56:t:173:TRP:CZ3	2.51	0.45
9:A:539:A:H62	9:A:2056:A:H3'	1.82	0.45
9:A:947:A:H61	9:A:950:A:H61	1.64	0.45
9:A:1569:A:H2'	9:A:1569:A:N3	2.31	0.45
9:A:1704:A:O2'	9:A:1710:G:N7	2.41	0.45
14:F:114:THR:HG22	14:F:152:PHE:CE1	2.51	0.45
14:F:226:MET:HE2	14:F:226:MET:HB3	1.75	0.45
18:J:180:ALA:O	18:J:184:LEU:HB2	2.16	0.45
32:X:105:LYS:HB2	32:X:105:LYS:HE2	1.68	0.45
37:a:95:G:H5''	52:p:27:ARG:HG2	1.98	0.45
37:a:1002:G:HO2'	37:a:1147:U:H5	1.62	0.45
52:p:49:ASN:OD1	52:p:51:PRO:HD2	2.16	0.45
9:A:1142:G:H2'	9:A:1143:C:C6	2.51	0.45
9:A:1880:G:N7	21:M:252:ARG:NH1	2.65	0.45
12:D:96:LYS:HD2	12:D:282:VAL:HG23	1.99	0.45
13:E:204:LYS:HA	13:E:225:THR:HB	1.99	0.45
26:R:116:ILE:O	26:R:119:GLU:HG2	2.17	0.45
29:U:119:ILE:HD12	29:U:135:LEU:HD13	1.98	0.45
37:a:89:G:H2'	37:a:90:C:C6	2.52	0.45
37:a:347:G:O3'	52:p:5:ARG:NH1	2.49	0.45
37:a:470:C:H41	48:l:50:ARG:HH22	1.64	0.45
37:a:538:U:OP1	44:h:29:THR:HG23	2.16	0.45
37:a:552:G:C6	37:a:553:U:N3	2.84	0.45
37:a:655:U:H2'	37:a:656:C:C6	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:a:790:U:H2'	37:a:791:C:H4'	1.99	0.45
37:a:1105:A:H4'	37:a:1106:C:O5'	2.16	0.45
37:a:1399:G:O2'	37:a:1400:C:H2'	2.17	0.45
44:h:50:LYS:HG2	44:h:59:LEU:HD22	1.98	0.45
52:p:33:LEU:H	52:p:33:LEU:HG	1.52	0.45
9:A:221:C:H2'	9:A:222:C:H6	1.82	0.45
9:A:2221:U:H2'	9:A:2222:C:H6	1.82	0.45
10:B:16:G:H2'	10:B:16:G:N3	2.30	0.45
10:B:61:C:H2'	10:B:62:U:C6	2.51	0.45
17:I:56:ARG:HA	17:I:59:LYS:CE	2.46	0.45
21:M:186:ILE:H	21:M:186:ILE:HG13	1.45	0.45
26:R:24:PHE:O	26:R:29:SER:HB3	2.16	0.45
27:S:100:THR:HG22	27:S:102:GLU:H	1.81	0.45
37:a:559:C:H42	37:a:577:A:H61	1.65	0.45
37:a:1178:C:OP1	61:y:76:LYS:NZ	2.44	0.45
38:b:177:LEU:HD13	38:b:199:LEU:HD13	1.99	0.45
39:c:88:ARG:HB2	39:c:89:PRO:HD3	1.97	0.45
39:c:134:GLN:HE22	39:c:147:LYS:CD	2.29	0.45
47:k:62:ARG:HA	47:k:62:ARG:HD3	1.62	0.45
54:r:43:GLN:NE2	57:u:85:ASN:O	2.49	0.45
61:y:141:HIS:NE2	61:y:175:VAL:HG21	2.31	0.45
9:A:84:G:OP2	30:V:72:VAL:N	2.50	0.45
9:A:1272:A:OP1	26:R:13:ARG:NH1	2.49	0.45
9:A:1448:A:H4'	9:A:1449:C:O4'	2.16	0.45
9:A:1592:A:H8	9:A:1592:A:OP1	1.99	0.45
9:A:1714:A:H2'	9:A:1715:A:O4'	2.17	0.45
22:N:65:TRP:HB2	22:N:105:GLU:HB2	1.99	0.45
25:Q:160:ARG:HH12	37:a:144:A:H5'	1.81	0.45
26:R:43:LEU:HA	26:R:43:LEU:HD23	1.73	0.45
26:R:88:ARG:NH1	26:R:88:ARG:O	2.50	0.45
28:T:62:LEU:HD22	28:T:77:PHE:HE1	1.79	0.45
34:Z:90:LEU:HD12	34:Z:90:LEU:HA	1.76	0.45
37:a:344:A:H2'	37:a:345:A:H8	1.82	0.45
37:a:449:C:H2'	37:a:450:A:H8	1.82	0.45
37:a:574:U:OP1	52:p:35:LYS:NZ	2.47	0.45
39:c:127:LEU:O	39:c:130:PHE:HB3	2.16	0.45
42:f:107:GLN:HG2	42:f:206:ILE:HB	1.98	0.45
48:l:54:ARG:HG3	48:l:64:THR:HG22	1.98	0.45
9:A:1801:A:OP1	11:C:207:LYS:HG3	2.17	0.45
10:B:67:U:C4	10:B:109:U:C4	3.05	0.45
18:J:176:LEU:HD11	18:J:210:ILE:HG21	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:M:257:PHE:N	21:M:257:PHE:CD1	2.84	0.45
22:N:75:THR:HA	22:N:90:PRO:HA	1.99	0.45
25:Q:138:ARG:HH22	25:Q:203:ILE:HB	1.81	0.45
27:S:230:TYR:CG	27:S:231:PRO:HD2	2.52	0.45
31:W:32:C:H5'	31:W:33:A:OP2	2.17	0.45
35:z:31:A:C2	35:z:32:U:H1'	2.52	0.45
37:a:222:G:C6	37:a:237:G:O6	2.69	0.45
37:a:1176:C:H2'	37:a:1177:A:H8	1.80	0.45
37:a:1257:G:P	49:m:132:ARG:HH21	2.39	0.45
37:a:1456:A:H2'	37:a:1457:G:C8	2.51	0.45
38:b:114:ARG:HA	38:b:114:ARG:HD2	1.80	0.45
38:b:139:ALA:O	38:b:143:ARG:HG2	2.17	0.45
1:0:70:VAL:HG11	1:0:73:TRP:HB3	1.98	0.45
2:1:5:LYS:NZ	9:A:2069:C:OP1	2.36	0.45
8:7:66:LYS:O	8:7:72:ILE:HD11	2.16	0.45
9:A:1056:A:N6	9:A:1153:G:H2'	2.32	0.45
9:A:1116:A:H2'	9:A:1116:A:N3	2.32	0.45
9:A:1116:A:N6	18:J:205:ASN:HB2	2.32	0.45
9:A:1473:G:H5'	9:A:1474:A:H5''	1.98	0.45
9:A:1870:U:H3	9:A:1896:G:H1	1.63	0.45
11:C:101:LEU:HA	11:C:101:LEU:HD23	1.79	0.45
14:F:108:ASN:O	14:F:112:LEU:HG	2.16	0.45
37:a:1340:U:H2'	37:a:1341:G:C8	2.52	0.45
39:c:71:LEU:HD11	39:c:111:ASN:HB2	1.99	0.45
41:e:157:VAL:HG12	41:e:158:GLN:HB2	1.98	0.45
52:p:50:VAL:HA	52:p:53:ILE:HD12	1.98	0.45
4:3:96:LEU:HD23	4:3:96:LEU:HA	1.71	0.45
9:A:213:A:N1	9:A:429:C:O2'	2.39	0.45
9:A:550:G:H5'	19:K:104:SER:HB2	1.99	0.45
9:A:1269:G:C5	26:R:3:ARG:HB2	2.52	0.45
9:A:1857:A:O2'	9:A:1858:A:C8	2.69	0.45
9:A:1886:A:H2'	9:A:1887:G:H8	1.81	0.45
17:I:96:LEU:HD13	17:I:102:LEU:HB2	1.97	0.45
26:R:28:HIS:O	26:R:35:ILE:HG12	2.17	0.45
37:a:918:A:H2'	37:a:919:A:O4'	2.17	0.45
43:g:43:LEU:O	43:g:47:VAL:HG23	2.17	0.45
45:i:133:LEU:HB3	45:i:135:TYR:HD1	1.81	0.45
54:r:62:ILE:O	54:r:66:ILE:HG13	2.17	0.45
55:s:51:ILE:HD13	55:s:71:LEU:HB3	1.99	0.45
9:A:556:C:H4'	9:A:557:C:OP1	2.16	0.44
15:G:177:ASP:O	15:G:181:VAL:HG12	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:G:184:PHE:CE2	15:G:188:ILE:HD11	2.52	0.44
22:N:29:PHE:CE2	22:N:67:ARG:HD3	2.53	0.44
32:X:146:ASN:HA	32:X:147:PRO:HD3	1.85	0.44
35:z:6:G:O2'	35:z:7:A:H5'	2.16	0.44
37:a:80:U:H2'	37:a:81:U:O4'	2.17	0.44
37:a:579:A:H5'	37:a:580:G:OP2	2.17	0.44
37:a:942:G:H2'	37:a:944:C:H41	1.82	0.44
37:a:1290:C:H2'	37:a:1291:G:H8	1.82	0.44
46:j:105:SER:HB2	46:j:189:VAL:HA	1.99	0.44
46:j:166:LEU:HD12	46:j:166:LEU:HA	1.80	0.44
49:m:52:ASN:HD21	49:m:105:VAL:HG12	1.82	0.44
50:n:41:TRP:CH2	55:s:9:PRO:HG2	2.52	0.44
57:u:84:TYR:CE1	57:u:87:GLN:HB2	2.53	0.44
58:v:181:GLU:HG3	58:v:183:PRO:HD2	1.98	0.44
5:4:140:ARG:HD2	5:4:140:ARG:HA	1.71	0.44
9:A:1809:G:OP1	11:C:256:ARG:NH1	2.44	0.44
9:A:1921:G:N2	9:A:1938:C:H1'	2.32	0.44
9:A:2062:A:H2'	9:A:2063:C:O4'	2.17	0.44
9:A:2393:A:H8	9:A:2393:A:OP1	2.00	0.44
19:K:214:GLY:O	19:K:217:LEU:HB2	2.18	0.44
21:M:163:ARG:O	21:M:167:VAL:HG23	2.17	0.44
23:O:92:GLU:OE2	23:O:96:ARG:HD2	2.18	0.44
23:O:96:ARG:HD3	23:O:97:TYR:CE2	2.53	0.44
29:U:135:LEU:HD23	29:U:135:LEU:HA	1.54	0.44
37:a:511:A:H2'	37:a:511:A:N3	2.33	0.44
37:a:1096:C:H2'	37:a:1097:C:O4'	2.17	0.44
39:c:10:PHE:CE2	39:c:189:ILE:HG12	2.52	0.44
41:e:299:ARG:HD3	44:h:44:PHE:CE1	2.53	0.44
49:m:125:LEU:HD23	49:m:128:ILE:HD12	1.98	0.44
50:n:66:THR:CG2	50:n:82:ILE:HD11	2.47	0.44
52:p:67:VAL:O	52:p:71:LEU:HG	2.17	0.44
53:q:89:ARG:HG2	53:q:90:ARG:N	2.32	0.44
9:A:636:C:O2'	9:A:668:U:H5''	2.17	0.44
9:A:711:G:H2'	9:A:712:G:O4'	2.18	0.44
9:A:1078:A:N1	9:A:2769:G:C6	2.86	0.44
10:B:8:G:N2	24:P:85:GLN:HE22	2.07	0.44
12:D:119:GLU:HB2	31:W:36:A:C5	2.52	0.44
14:F:83:LYS:O	14:F:211:THR:HG23	2.17	0.44
18:J:109:PHE:CD1	18:J:129:ILE:HD13	2.51	0.44
20:L:73:ASN:HB2	20:L:75:MET:HB2	2.00	0.44
28:T:74:TYR:HB3	28:T:75:PRO:HD3	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:a:1100:A:H5'	46:j:165:ARG:HH22	1.82	0.44
37:a:1444:U:H5''	61:y:100:LYS:HZ2	1.82	0.44
38:b:80:ALA:HB2	38:b:214:ILE:HD13	1.99	0.44
40:d:66:LEU:HD12	40:d:66:LEU:HA	1.85	0.44
45:i:175:PRO:O	45:i:179:GLU:HG2	2.17	0.44
56:t:96:ARG:NH1	56:t:145:LYS:HB3	2.33	0.44
9:A:266:A:OP2	33:Y:139:LYS:NZ	2.51	0.44
9:A:881:U:H2'	9:A:882:U:C6	2.53	0.44
9:A:1864:A:H2'	9:A:1865:G:O4'	2.16	0.44
9:A:2236:C:H2'	9:A:2237:A:O4'	2.18	0.44
9:A:2303:A:H4'	9:A:2304:A:O4'	2.18	0.44
10:B:53:U:C4	10:B:54:G:C2	3.05	0.44
13:E:79:THR:O	13:E:83:VAL:HG23	2.17	0.44
13:E:113:ARG:O	13:E:114:LYS:HG2	2.17	0.44
19:K:202:HIS:ND1	19:K:202:HIS:O	2.51	0.44
21:M:243:LYS:O	21:M:246:VAL:HG23	2.18	0.44
37:a:143:G:H5'	37:a:144:A:OP2	2.18	0.44
37:a:425:C:H2'	37:a:426:A:C8	2.53	0.44
37:a:542:U:H1'	53:q:135:GLN:NE2	2.33	0.44
43:g:22:LEU:HD12	43:g:25:MET:HE2	2.00	0.44
49:m:110:ILE:HG22	49:m:113:ASP:CG	2.43	0.44
51:o:40:LEU:HD13	51:o:40:LEU:HA	1.85	0.44
1:0:46:ARG:NH1	1:0:66:LYS:HB2	2.32	0.44
1:0:50:LYS:HB3	1:0:67:ASP:OD1	2.17	0.44
1:0:79:PHE:CG	1:0:80:TYR:N	2.85	0.44
9:A:1154:A:H4'	9:A:1155:A:H5''	1.99	0.44
9:A:2250:A:H2'	9:A:2251:G:H8	1.80	0.44
9:A:2430:G:H2'	9:A:2431:G:O4'	2.17	0.44
11:C:97:LYS:O	11:C:98:ARG:HD3	2.18	0.44
19:K:61:TRP:HZ2	28:T:157:LEU:HD23	1.82	0.44
28:T:124:MET:HE3	28:T:124:MET:HB3	1.82	0.44
30:V:86:LYS:HD2	30:V:105:LEU:HD22	2.00	0.44
31:W:76:G:H5''	31:W:77:A:OP1	2.18	0.44
37:a:1:U:H3	41:e:303:MET:CE	2.31	0.44
37:a:192:C:H2'	37:a:193:C:C6	2.53	0.44
37:a:205:U:H2'	37:a:206:C:H6	1.76	0.44
37:a:510:G:H2'	37:a:510:G:OP2	2.18	0.44
40:d:3:ARG:HD2	40:d:108:ARG:HE	1.83	0.44
40:d:148:ILE:O	40:d:152:LEU:HB2	2.18	0.44
41:e:239:ARG:HG3	41:e:266:LEU:HB2	1.98	0.44
44:h:112:ARG:HD2	44:h:125:ILE:HD11	1.97	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:114:C:H2'	9:A:115:G:O4'	2.17	0.44
9:A:684:C:OP1	13:E:105:ARG:NH1	2.51	0.44
9:A:966:G:C6	9:A:967:C:C4	3.06	0.44
9:A:1113:A:N6	9:A:1114:A:H62	2.14	0.44
9:A:2112:U:H2'	9:A:2113:G:O4'	2.17	0.44
9:A:2142:G:H21	9:A:2187:A:H4'	1.82	0.44
11:C:46:THR:OG1	11:C:47:ALA:N	2.51	0.44
11:C:68:LYS:HD2	11:C:115:GLY:HA2	1.98	0.44
12:D:202:THR:HG22	12:D:288:ASN:HD21	1.82	0.44
25:Q:200:SER:HB3	25:Q:203:ILE:HG13	1.99	0.44
28:T:98:LEU:HD13	28:T:136:LEU:HD13	1.99	0.44
37:a:33:A:H2'	37:a:34:A:C8	2.53	0.44
37:a:1198:A:OP1	45:i:147:GLY:N	2.51	0.44
37:a:1234:A:H2'	37:a:1235:A:H4'	1.99	0.44
43:g:65:ALA:O	43:g:69:VAL:HG22	2.17	0.44
49:m:61:VAL:O	49:m:65:LEU:HG	2.16	0.44
49:m:131:TYR:O	49:m:135:ARG:HG2	2.17	0.44
61:y:157:ILE:O	61:y:160:VAL:HG22	2.17	0.44
9:A:555:A:H2	9:A:558:A:OP1	1.99	0.44
9:A:1169:A:H5'	19:K:245:ARG:CZ	2.47	0.44
9:A:2278:C:C2	9:A:2297:G:N2	2.86	0.44
9:A:2320:G:O2'	14:F:174:SER:O	2.34	0.44
11:C:172:LEU:HD23	11:C:172:LEU:HA	1.74	0.44
22:N:32:TYR:HD1	22:N:133:ILE:HG22	1.81	0.44
22:N:71:ASP:OD1	22:N:71:ASP:N	2.41	0.44
27:S:191:LEU:HD23	27:S:215:PRO:HA	1.99	0.44
29:U:124:ALA:HB2	29:U:135:LEU:HD12	1.99	0.44
29:U:161:LYS:O	29:U:177:MET:HG2	2.18	0.44
37:a:375:G:N7	40:d:2:SER:OG	2.47	0.44
37:a:1037:G:N2	37:a:1115:A:H61	2.16	0.44
37:a:1155:C:H2'	37:a:1156:C:H6	1.82	0.44
38:b:79:LYS:H	38:b:79:LYS:HD3	1.82	0.44
40:d:125:ILE:HA	40:d:126:PRO:HD3	1.85	0.44
45:i:184:ARG:NH1	45:i:185:ASP:O	2.47	0.44
46:j:143:CYS:HB2	46:j:157:HIS:CE1	2.52	0.44
47:k:38:ASN:OD1	47:k:56:ALA:HB3	2.17	0.44
47:k:118:PHE:CE1	57:u:89:LEU:HD13	2.52	0.44
9:A:169:C:H2'	9:A:170:U:C6	2.53	0.44
9:A:331:A:OP2	13:E:222:ASN:HB2	2.18	0.44
9:A:525:A:H2'	9:A:526:A:O4'	2.18	0.44
9:A:716:A:H2'	9:A:717:A:O4'	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:750:A:H1'	9:A:751:C:H5	1.82	0.44
9:A:753:G:H2'	9:A:754:A:C8	2.53	0.44
9:A:838:U:H4'	9:A:839:G:C8	2.52	0.44
9:A:1468:C:H2'	9:A:1469:G:C8	2.53	0.44
9:A:1488:A:H2'	9:A:1489:A:C8	2.53	0.44
9:A:2624:G:H2'	9:A:2625:G:O4'	2.18	0.44
14:F:221:LYS:O	14:F:225:LEU:HG	2.18	0.44
19:K:127:MET:HB3	19:K:127:MET:HE2	1.80	0.44
37:a:1470:G:H2'	37:a:1471:U:C6	2.53	0.44
61:y:91:ARG:HD3	61:y:91:ARG:HA	1.80	0.44
9:A:362:A:H5'	9:A:363:C:OP2	2.18	0.44
9:A:540:A:C2	9:A:2037:G:C8	3.06	0.44
9:A:1088:U:C2	9:A:1090:U:H5'	2.52	0.44
9:A:1520:A:H4'	9:A:1521:G:OP1	2.17	0.44
11:C:138:HIS:HD2	11:C:139:ASN:HB2	1.83	0.44
28:T:123:TYR:CE2	28:T:125:ILE:HD11	2.53	0.44
28:T:173:LEU:HD12	28:T:193:PHE:CE2	2.53	0.44
37:a:1399:G:C2	37:a:1403:G:C6	3.05	0.44
38:b:235:ASN:HB2	38:b:236:PRO:HD3	2.00	0.44
39:c:26:PRO:CB	46:j:140:ARG:HH22	2.30	0.44
40:d:25:ARG:HA	40:d:26:PRO:HD3	1.86	0.44
41:e:217:MET:HE1	41:e:262:VAL:HG13	2.00	0.44
42:f:116:PRO:HA	42:f:172:ILE:HD11	2.00	0.44
44:h:31:ILE:H	44:h:31:ILE:HG13	1.53	0.44
48:l:114:ARG:HB3	48:l:119:VAL:HB	2.00	0.44
54:r:70:ARG:HB3	54:r:77:PHE:CE1	2.53	0.44
5:4:92:MET:HB3	5:4:92:MET:HE2	1.50	0.43
9:A:578:U:P	21:M:115:ARG:HH21	2.41	0.43
9:A:1088:U:H5	18:J:202:THR:HG23	1.83	0.43
9:A:1226:U:O4	13:E:224:ARG:NE	2.51	0.43
9:A:1530:G:H2'	9:A:1532:G:N7	2.33	0.43
9:A:2116:C:C2	9:A:2201:G:N2	2.86	0.43
9:A:2154:C:H42	9:A:2165:G:H1	1.66	0.43
9:A:2304:A:C8	9:A:2306:G:C8	3.06	0.43
13:E:152:MET:HE2	13:E:152:MET:HB3	1.61	0.43
15:G:115:MET:HE2	15:G:115:MET:HB3	1.66	0.43
17:I:69:HIS:ND1	17:I:103:ILE:HD11	2.32	0.43
37:a:76:G:O6	59:w:103:PHE:HB2	2.18	0.43
37:a:173:A:C4	37:a:174:A:H1'	2.53	0.43
37:a:1092:G:N2	37:a:1094:A:H62	2.14	0.43
40:d:67:LYS:O	40:d:71:ILE:HG13	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:h:67:ARG:C	44:h:69:LYS:H	2.26	0.43
55:s:11:VAL:HG23	55:s:38:SER:HB2	1.99	0.43
55:s:19:ILE:HG21	55:s:44:MET:HB2	1.99	0.43
55:s:41:ILE:HG23	55:s:42:PRO:HD2	2.00	0.43
59:w:111:GLY:HA2	59:w:130:TYR:O	2.17	0.43
5:4:156:ASN:OD1	5:4:158:LYS:HD3	2.19	0.43
6:5:29:ASN:HD21	6:5:31:LYS:HB2	1.84	0.43
9:A:824:U:H2'	9:A:825:C:H6	1.84	0.43
9:A:845:C:H2'	9:A:846:A:H8	1.82	0.43
9:A:1073:G:C5'	9:A:1075:G:H5''	2.48	0.43
9:A:1861:U:H4'	35:z:71:G:H4'	2.00	0.43
9:A:2150:G:H1	9:A:2170:C:H1'	1.83	0.43
10:B:80:C:H2'	10:B:81:U:O4'	2.18	0.43
12:D:188:GLU:OE2	12:D:271:THR:HG23	2.18	0.43
13:E:55:LEU:O	13:E:67:GLU:HA	2.19	0.43
13:E:102:THR:O	13:E:103:LEU:HD23	2.18	0.43
16:H:42:GLN:HB2	16:H:43:LYS:H	1.59	0.43
19:K:148:ASP:OD1	19:K:150:GLY:N	2.52	0.43
35:z:34:G:N2	61:y:140:ARG:CB	2.79	0.43
37:a:790:U:O2'	37:a:792:G:C6	2.70	0.43
44:h:39:LEU:HB3	44:h:45:ILE:HG21	2.00	0.43
50:n:12:LYS:HE2	50:n:53:ASN:ND2	2.33	0.43
50:n:40:LYS:HG2	50:n:43:ILE:HD11	2.00	0.43
61:y:168:LEU:HD23	61:y:168:LEU:HA	1.75	0.43
9:A:9:A:H1'	31:W:99:A:C2	2.53	0.43
9:A:818:U:H2'	9:A:819:G:H8	1.84	0.43
9:A:1415:U:C4	9:A:1416:A:C6	3.06	0.43
9:A:1493:C:H5'	9:A:1494:G:OP2	2.19	0.43
9:A:2075:G:N2	9:A:2076:A:C6	2.86	0.43
12:D:270:ASP:HB2	12:D:275:VAL:HG22	1.99	0.43
13:E:120:LYS:HG3	13:E:124:ALA:HB3	2.00	0.43
14:F:127:ILE:HD12	14:F:132:VAL:HB	2.01	0.43
15:G:74:ILE:HG12	15:G:115:MET:HE1	2.00	0.43
15:G:155:MET:SD	15:G:188:ILE:HD13	2.59	0.43
21:M:213:LYS:HD3	21:M:233:THR:HB	1.99	0.43
22:N:32:TYR:CD1	22:N:133:ILE:HG22	2.52	0.43
23:O:64:LEU:HD12	23:O:64:LEU:HA	1.67	0.43
24:P:67:THR:HB	24:P:68:PRO:HD2	2.00	0.43
28:T:114:VAL:HG22	28:T:124:MET:SD	2.58	0.43
37:a:105:C:H5	37:a:206:C:C5	2.36	0.43
38:b:79:LYS:HG2	38:b:80:ALA:N	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:b:81:ALA:HB1	38:b:97:ASN:HB2	2.01	0.43
45:i:186:SER:O	45:i:188:ILE:HG23	2.19	0.43
50:n:31:ILE:HG13	50:n:43:ILE:HD11	2.00	0.43
56:t:174:TYR:CZ	56:t:176:PRO:HD3	2.53	0.43
9:A:836:G:H1'	21:M:133:GLN:NE2	2.33	0.43
9:A:1195:U:H3'	9:A:1196:A:C8	2.53	0.43
9:A:2322:A:C2	14:F:204:GLY:HA3	2.53	0.43
11:C:206:SER:HA	11:C:209:TRP:CE3	2.53	0.43
14:F:57:LEU:HD21	14:F:154:ASP:HB2	2.01	0.43
17:I:110:VAL:HG12	17:I:126:MET:HE2	2.01	0.43
19:K:50:SER:HA	31:W:1:A:N7	2.34	0.43
20:L:11:ALA:HB3	20:L:85:VAL:HG22	1.99	0.43
21:M:134:MET:O	21:M:139:ARG:NH1	2.51	0.43
23:O:56:LYS:HG2	23:O:57:TYR:CD1	2.54	0.43
24:P:61:ARG:NH2	24:P:89:ASP:OD2	2.52	0.43
25:Q:154:GLU:HA	25:Q:162:LEU:HD22	2.01	0.43
25:Q:228:ARG:HH11	25:Q:228:ARG:HB2	1.84	0.43
26:R:32:THR:OG1	26:R:33:ARG:N	2.52	0.43
37:a:183:A:H5'	37:a:184:G:OP2	2.18	0.43
37:a:891:G:N2	37:a:892:U:C2	2.87	0.43
37:a:1301:G:P	60:x:56:ARG:HH21	2.41	0.43
38:b:31:MET:O	38:b:35:ILE:HG13	2.18	0.43
51:o:75:TYR:OH	51:o:87:LEU:HB2	2.18	0.43
9:A:1142:G:C6	9:A:1143:C:N4	2.87	0.43
9:A:1320:G:O5'	9:A:1320:G:H8	2.01	0.43
9:A:1702:G:O3'	20:L:6:THR:HG23	2.19	0.43
11:C:76:THR:OG1	11:C:77:ILE:N	2.51	0.43
12:D:284:GLY:HA3	12:D:288:ASN:OD1	2.18	0.43
22:N:17:MET:HE1	22:N:40:ALA:C	2.43	0.43
29:U:114:ILE:HG13	29:U:115:LEU:HG	2.00	0.43
34:Z:86:GLU:HB3	34:Z:108:MET:HE1	1.99	0.43
36:8:1113:UNK:CB	38:b:186:PRO:HG3	2.48	0.43
37:a:541:U:H4'	53:q:140:ARG:HH12	1.84	0.43
37:a:621:G:H2'	37:a:622:G:C8	2.53	0.43
37:a:627:U:H2'	37:a:628:C:H6	1.83	0.43
38:b:23:GLY:HA2	38:b:41:GLY:O	2.18	0.43
9:A:519:A:N6	28:T:38:SER:OG	2.52	0.43
11:C:23:ASN:ND2	11:C:76:THR:HG21	2.30	0.43
11:C:80:ASP:OD1	11:C:81:PRO:HD2	2.18	0.43
11:C:94:ASP:HB3	11:C:96:GLU:CD	2.44	0.43
12:D:150:THR:OG1	12:D:152:PRO:HD2	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:E:51:GLU:HG3	13:E:53:ILE:H	1.82	0.43
30:V:151:LYS:HB2	30:V:161:TYR:CE1	2.54	0.43
37:a:566:C:H1'	52:p:14:ARG:NH1	2.33	0.43
37:a:776:A:H2'	37:a:777:G:O4'	2.19	0.43
37:a:1137:U:H5'	39:c:5:ILE:HD12	2.01	0.43
55:s:15:LEU:O	55:s:19:ILE:HG12	2.19	0.43
6:5:17:ILE:HG22	6:5:18:ARG:N	2.32	0.43
9:A:649:A:H4'	9:A:650:G:O5'	2.19	0.43
9:A:675:U:H2'	9:A:676:U:C6	2.53	0.43
9:A:2028:A:H2'	9:A:2029:A:C8	2.53	0.43
9:A:2118:U:H2'	9:A:2119:U:H5''	2.00	0.43
9:A:2570:G:H2'	9:A:2571:U:O4'	2.19	0.43
9:A:2718:U:O2'	23:O:83:LYS:HE3	2.18	0.43
9:A:2764:U:H4'	15:G:178:LYS:HG2	2.00	0.43
20:L:7:HIS:HB3	20:L:18:GLU:OE2	2.18	0.43
24:P:105:ILE:HD13	24:P:123:ILE:HG12	2.01	0.43
28:T:179:GLU:H	28:T:179:GLU:HG3	1.63	0.43
29:U:132:ASN:O	29:U:178:LEU:HD12	2.19	0.43
31:W:1:A:H2'	31:W:2:G:H8	1.83	0.43
37:a:538:U:OP1	44:h:30:ASN:ND2	2.51	0.43
37:a:817:C:H2'	37:a:818:G:O4'	2.18	0.43
37:a:1049:C:OP2	38:b:99:LYS:NZ	2.45	0.43
46:j:165:ARG:HA	46:j:165:ARG:HD3	1.80	0.43
53:q:115:ASP:OD2	53:q:129:VAL:HG21	2.19	0.43
1:0:37:ARG:HB3	1:0:42:HIS:CD2	2.52	0.43
2:1:40:THR:HG23	2:1:42:ASN:H	1.84	0.43
4:3:146:SER:HA	4:3:150:ALA:HB2	2.00	0.43
7:6:138:LYS:HE2	7:6:138:LYS:HB3	1.78	0.43
9:A:1137:C:C5	9:A:1138:G:C6	3.07	0.43
9:A:1535:A:H2'	9:A:1536:A:C8	2.54	0.43
9:A:2045:A:C6	9:A:2515:C:H1'	2.54	0.43
12:D:104:GLU:OE2	12:D:267:MET:HE1	2.19	0.43
37:a:624:A:H5''	47:k:124:PRO:HB3	2.00	0.43
37:a:1288:A:C5'	61:y:140:ARG:NH1	2.73	0.43
37:a:1475:G:H2'	37:a:1476:C:C6	2.53	0.43
40:d:47:ARG:HG2	40:d:192:LEU:HD22	2.01	0.43
42:f:107:GLN:HB2	42:f:179:PHE:CE2	2.54	0.43
48:l:24:LEU:HD12	48:l:24:LEU:HA	1.80	0.43
7:6:122:LYS:NZ	9:A:1407:C:OP1	2.34	0.43
9:A:472:A:C2	9:A:482:A:C5	3.07	0.43
9:A:980:G:H2'	9:A:981:G:O4'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:D:184:LYS:HB2	12:D:184:LYS:HE2	1.77	0.43
18:J:146:ALA:HB2	18:J:183:LYS:HZ3	1.83	0.43
24:P:72:ARG:NH2	24:P:87:ILE:HD12	2.34	0.43
24:P:125:GLU:HG2	24:P:162:HIS:CD2	2.54	0.43
32:X:74:GLY:O	32:X:76:ARG:NH1	2.52	0.43
37:a:20:C:H2'	37:a:21:U:C6	2.54	0.43
37:a:1149:A:H4'	37:a:1150:U:H5'	2.00	0.43
37:a:1170:G:H5''	55:s:78:LEU:HD21	2.01	0.43
43:g:97:LYS:O	43:g:101:ILE:HG13	2.19	0.43
47:k:38:ASN:OD1	47:k:39:THR:N	2.51	0.43
55:s:50:ALA:HA	55:s:58:LEU:O	2.19	0.43
61:y:171:ILE:HD13	61:y:171:ILE:HA	1.89	0.43
9:A:348:U:O5'	9:A:348:U:H6	2.02	0.43
9:A:645:A:H5'	21:M:156:LYS:HZ1	1.84	0.43
9:A:2341:U:H3'	9:A:2342:G:H5'	2.01	0.43
12:D:235:ILE:HD12	12:D:244:VAL:HG11	2.01	0.43
14:F:155:ARG:O	14:F:159:LEU:HB3	2.18	0.43
15:G:160:GLU:OE2	15:G:176:ARG:HG3	2.19	0.43
19:K:64:LEU:O	19:K:68:VAL:HG13	2.19	0.43
20:L:42:VAL:HA	20:L:56:GLU:O	2.18	0.43
22:N:12:GLN:HG3	22:N:13:HIS:H	1.84	0.43
23:O:89:LEU:HD23	23:O:89:LEU:HA	1.79	0.43
27:S:190:LEU:HB2	27:S:216:ILE:HG22	2.01	0.43
37:a:234:A:H2'	37:a:235:U:C6	2.54	0.43
37:a:299:C:H2'	37:a:299:C:O2	2.18	0.43
37:a:542:U:C4	37:a:543:A:C6	3.06	0.43
38:b:65:SER:OG	38:b:228:GLY:HA3	2.19	0.43
1:O:46:ARG:CZ	1:O:66:LYS:HB2	2.48	0.42
9:A:976:C:H1'	9:A:1012:G:C8	2.53	0.42
9:A:2794:A:C2	9:A:2796:A:C4	3.07	0.42
11:C:49:HIS:CE1	11:C:215:VAL:HG22	2.54	0.42
12:D:112:VAL:HG21	12:D:277:MET:HE2	2.01	0.42
12:D:229:HIS:ND1	12:D:229:HIS:N	2.65	0.42
28:T:62:LEU:HD23	28:T:62:LEU:HA	1.74	0.42
28:T:63:MET:H	28:T:63:MET:HG2	1.67	0.42
47:k:44:THR:OG1	47:k:45:ASP:N	2.52	0.42
5:4:114:ARG:HD3	5:4:136:ILE:CG1	2.50	0.42
9:A:344:C:H2'	9:A:345:C:H6	1.84	0.42
9:A:426:C:H2'	9:A:427:A:H8	1.80	0.42
9:A:564:U:H2'	9:A:565:G:H5'	2.01	0.42
9:A:910:A:H8	9:A:910:A:OP2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:1063:U:OP1	15:G:99:ARG:NH2	2.52	0.42
9:A:1090:U:H2'	9:A:1091:G:C8	2.53	0.42
9:A:1109:U:H2'	9:A:1110:U:C6	2.54	0.42
9:A:1226:U:O5'	9:A:1226:U:H6	2.02	0.42
9:A:1518:U:C5	9:A:1519:A:H2	2.37	0.42
9:A:1583:A:H2'	9:A:1584:C:C6	2.54	0.42
9:A:1882:U:C4	21:M:260:LYS:HD3	2.55	0.42
9:A:2456:A:N6	9:A:2602:U:OP1	2.52	0.42
12:D:90:ILE:HD12	12:D:90:ILE:HG23	1.76	0.42
13:E:171:ASN:HD22	13:E:244:LYS:HD3	1.84	0.42
20:L:71:ARG:HD3	20:L:75:MET:HE2	2.01	0.42
27:S:204:LYS:HD3	27:S:204:LYS:HA	1.69	0.42
28:T:164:MET:HE2	28:T:164:MET:HB3	1.81	0.42
32:X:155:ARG:HG2	32:X:156:GLU:N	2.28	0.42
33:Y:110:TRP:CE2	33:Y:145:LEU:HD12	2.54	0.42
37:a:920:G:H1'	37:a:1314:A:O2'	2.20	0.42
37:a:1100:A:H2'	37:a:1101:A:C8	2.55	0.42
37:a:1262:C:H2'	37:a:1263:U:C6	2.54	0.42
51:o:26:VAL:HG11	51:o:78:LEU:HD21	2.01	0.42
9:A:548:G:O2'	9:A:549:A:P	2.75	0.42
9:A:1009:A:H5''	9:A:1010:C:OP2	2.18	0.42
9:A:1114:A:H4'	9:A:1131:A:C2	2.54	0.42
9:A:1348:C:H5''	28:T:71:ARG:HH22	1.85	0.42
9:A:1897:C:H2'	9:A:1898:G:O4'	2.20	0.42
10:B:41:U:H3'	10:B:42:C:C5'	2.49	0.42
13:E:179:ALA:HB1	13:E:213:VAL:HG11	2.01	0.42
19:K:56:LYS:O	19:K:60:GLU:HG3	2.20	0.42
27:S:184:ALA:HB2	27:S:221:ILE:HD13	2.01	0.42
27:S:191:LEU:HB2	27:S:213:ARG:NH1	2.35	0.42
31:W:17:A:H1'	31:W:23:G:C2	2.54	0.42
34:Z:79:GLU:HB3	34:Z:115:MET:HE1	2.01	0.42
37:a:185:G:H2'	37:a:186:A:C8	2.54	0.42
37:a:600:U:O4	37:a:700:G:O2'	2.34	0.42
37:a:683:U:H2'	37:a:684:C:H6	1.82	0.42
37:a:869:U:H2'	37:a:870:U:C6	2.54	0.42
37:a:1290:C:H4'	45:i:205:PHE:O	2.19	0.42
39:c:22:TRP:HZ3	39:c:24:SER:HB2	1.85	0.42
51:o:64:LEU:HD11	51:o:84:ILE:HG21	2.02	0.42
57:u:124:ASN:OD1	57:u:124:ASN:N	2.52	0.42
59:w:156:MET:O	59:w:160:LEU:HG	2.19	0.42
1:0:61:THR:HG22	1:0:62:GLY:N	2.29	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:3:105:ARG:NH1	4:3:149:ARG:O	2.52	0.42
9:A:483:A:H2'	9:A:484:G:C8	2.54	0.42
9:A:984:G:OP1	22:N:87:LYS:HG3	2.19	0.42
9:A:1089:U:O4	18:J:83:ALA:HB2	2.19	0.42
9:A:1287:G:O2'	9:A:2026:G:O6	2.33	0.42
9:A:1397:C:N4	9:A:1398:G:C6	2.88	0.42
9:A:1928:C:H2'	9:A:1929:U:C6	2.55	0.42
9:A:2008:C:P	12:D:222:MET:HB2	2.59	0.42
9:A:2432:G:H5'	21:M:148:GLY:HA3	2.01	0.42
12:D:90:ILE:HD11	12:D:173:LEU:HD11	2.01	0.42
13:E:256:ASN:O	13:E:256:ASN:ND2	2.53	0.42
23:O:31:LEU:HD23	23:O:31:LEU:HA	1.63	0.42
27:S:124:PHE:CE1	27:S:165:GLY:HA3	2.55	0.42
30:V:137:LEU:HA	30:V:137:LEU:HD23	1.77	0.42
35:z:32:U:H3'	35:z:33:U:C5'	2.49	0.42
35:z:39:U:H2'	35:z:40:C:O4'	2.20	0.42
37:a:7:G:H22	41:e:245:THR:CG2	2.32	0.42
37:a:33:A:C2	37:a:34:A:C5	3.07	0.42
37:a:153:C:H2'	37:a:154:U:C6	2.54	0.42
37:a:439:G:H2'	37:a:440:G:C8	2.54	0.42
37:a:485:A:H5''	48:l:110:ARG:NH1	2.35	0.42
37:a:687:C:O5'	37:a:687:C:H6	2.01	0.42
37:a:1198:A:O2'	45:i:148:GLY:N	2.51	0.42
37:a:1393:U:H2'	37:a:1394:U:C6	2.55	0.42
37:a:1404:G:H5'	37:a:1405:A:OP2	2.20	0.42
59:w:104:ILE:HG13	59:w:129:TYR:CE1	2.54	0.42
9:A:6:A:H2'	9:A:7:C:O4'	2.19	0.42
9:A:254:U:C5	9:A:272:U:C4	3.07	0.42
9:A:920:A:O5'	9:A:920:A:H8	2.01	0.42
9:A:2561:G:H2'	9:A:2562:G:O4'	2.19	0.42
9:A:2656:A:C2	9:A:2796:A:C8	3.07	0.42
12:D:223:THR:O	12:D:225:GLY:N	2.52	0.42
12:D:232:LEU:HD12	12:D:232:LEU:HA	1.65	0.42
15:G:98:THR:CG2	15:G:100:ARG:HB2	2.49	0.42
17:I:161:PHE:CE2	17:I:176:VAL:HG21	2.54	0.42
25:Q:119:LEU:O	25:Q:122:ILE:HB	2.19	0.42
29:U:112:TYR:O	34:Z:91:ARG:NH2	2.53	0.42
37:a:141:U:O2'	37:a:142:G:H5'	2.19	0.42
37:a:1139:A:H2'	37:a:1140:C:H6	1.84	0.42
42:f:105:LEU:HD22	42:f:181:LYS:HG2	2.01	0.42
48:l:2:PRO:HG2	48:l:3:THR:H	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:m:77:ARG:HH11	60:x:87:LYS:CE	2.32	0.42
9:A:115:G:C6	9:A:117:A:N6	2.87	0.42
9:A:605:C:H2'	9:A:606:A:C8	2.54	0.42
9:A:1632:U:O2'	9:A:1633:A:H5'	2.19	0.42
9:A:1875:G:H2'	9:A:1889:G:N2	2.34	0.42
9:A:2073:A:O2'	9:A:2074:A:P	2.78	0.42
9:A:2260:U:H2'	9:A:2261:U:H6	1.83	0.42
12:D:224:HIS:CD2	12:D:224:HIS:N	2.87	0.42
25:Q:138:ARG:O	25:Q:138:ARG:HD3	2.20	0.42
25:Q:140:VAL:HA	25:Q:141:PRO:HD3	1.85	0.42
37:a:974:U:H5'	37:a:975:G:OP1	2.20	0.42
39:c:97:ILE:O	39:c:101:LYS:HG3	2.19	0.42
42:f:156:ILE:HG21	42:f:199:ILE:HD12	2.01	0.42
42:f:211:TYR:CZ	54:r:61:LEU:HD13	2.54	0.42
50:n:35:THR:HG22	50:n:36:SER:H	1.85	0.42
9:A:262:G:C2	9:A:264:A:H5''	2.54	0.42
9:A:504:G:H2'	9:A:505:G:O4'	2.20	0.42
9:A:720:U:H3	9:A:733:A:H61	1.67	0.42
9:A:880:U:H5''	22:N:6:ARG:HG3	2.01	0.42
9:A:886:U:H3	9:A:910:A:H61	1.68	0.42
9:A:2595:G:N7	12:D:234:SER:HB2	2.33	0.42
11:C:178:ARG:HG2	11:C:179:LEU:N	2.34	0.42
17:I:133:LEU:HD21	17:I:143:ALA:HB1	2.02	0.42
24:P:122:LYS:HA	24:P:122:LYS:HD2	1.81	0.42
26:R:74:VAL:HB	26:R:75:TYR:CD2	2.54	0.42
26:R:84:ASP:HB3	26:R:115:ILE:CG2	2.49	0.42
34:Z:108:MET:HE2	34:Z:108:MET:HB3	1.49	0.42
37:a:348:G:OP1	52:p:3:LYS:HD3	2.20	0.42
37:a:351:G:C2	37:a:355:G:C6	3.08	0.42
37:a:549:G:C6	37:a:586:G:C6	3.07	0.42
37:a:865:G:H2'	37:a:865:G:N3	2.33	0.42
37:a:926:A:H1'	37:a:931:U:O4	2.20	0.42
37:a:983:G:H2'	37:a:984:A:C8	2.54	0.42
41:e:223:PHE:CD1	41:e:289:MET:HE3	2.55	0.42
49:m:80:LEU:HD23	49:m:80:LEU:HA	1.79	0.42
9:A:151:G:H2'	9:A:152:G:O4'	2.20	0.42
9:A:2212:A:C2	16:H:77:PHE:HB2	2.55	0.42
9:A:2461:A:H2'	9:A:2462:G:O4'	2.20	0.42
12:D:107:GLY:HA3	25:Q:202:ASN:ND2	2.35	0.42
12:D:178:ASP:OD1	12:D:178:ASP:N	2.51	0.42
17:I:130:ASN:ND2	17:I:132:TRP:HE1	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:K:64:LEU:HD23	19:K:64:LEU:HA	1.83	0.42
19:K:130:THR:HA	19:K:133:ILE:HD12	2.01	0.42
28:T:183:ILE:H	28:T:183:ILE:HG12	1.65	0.42
30:V:139:SER:HB2	30:V:162:LEU:HD12	2.01	0.42
32:X:146:ASN:HD22	32:X:149:SER:HB2	1.85	0.42
33:Y:126:LEU:O	33:Y:130:GLU:HG3	2.20	0.42
37:a:69:G:H2'	37:a:70:G:O4'	2.18	0.42
37:a:1300:C:OP1	60:x:56:ARG:NH2	2.52	0.42
38:b:16:ALA:HB3	38:b:216:LEU:HD22	2.02	0.42
38:b:24:THR:HG22	38:b:43:HIS:CD2	2.55	0.42
46:j:171:TYR:HA	46:j:172:PRO:HD3	1.56	0.42
9:A:674:C:H5''	21:M:96:LYS:HG3	2.02	0.42
9:A:1158:U:O4	12:D:241:PRO:HA	2.20	0.42
9:A:1883:G:C2	21:M:257:PHE:CE1	3.08	0.42
9:A:2014:G:C2'	9:A:2015:A:H5'	2.49	0.42
12:D:92:VAL:HB	12:D:121:ASN:ND2	2.35	0.42
18:J:180:ALA:HB1	18:J:195:ALA:HB1	2.01	0.42
21:M:181:LEU:HB3	21:M:187:ILE:HD12	2.02	0.42
24:P:161:GLU:OE2	24:P:162:HIS:HD2	2.03	0.42
37:a:289:G:N1	37:a:290:G:C5	2.87	0.42
37:a:519:U:O4	37:a:813:A:N6	2.53	0.42
37:a:793:A:H2'	37:a:794:C:O4'	2.20	0.42
41:e:257:LEU:HD23	41:e:257:LEU:HA	1.73	0.42
46:j:104:ARG:HG3	46:j:190:ASP:HB3	2.01	0.42
46:j:151:HIS:CD2	46:j:151:HIS:H	2.36	0.42
56:t:78:SER:O	56:t:82:ARG:HB2	2.20	0.42
2:1:18:ASN:ND2	9:A:14:A:O3'	2.53	0.42
7:6:131:TRP:CD2	7:6:131:TRP:C	2.92	0.42
9:A:489:A:H2'	9:A:490:A:C8	2.54	0.42
9:A:888:C:H3'	9:A:889:G:C8	2.44	0.42
9:A:1300:U:H2'	9:A:1301:G:O4'	2.20	0.42
9:A:1701:A:H2'	9:A:1702:G:O4'	2.20	0.42
13:E:161:LEU:HD23	13:E:161:LEU:HA	1.75	0.42
18:J:171:ILE:HG12	18:J:210:ILE:HG12	2.01	0.42
26:R:58:ARG:NH1	26:R:94:ARG:HD2	2.35	0.42
26:R:89:GLN:C	26:R:90:LEU:HD23	2.45	0.42
28:T:45:LYS:H	28:T:45:LYS:HG2	1.58	0.42
31:W:93:C:H2'	31:W:94:C:O4'	2.19	0.42
37:a:383:A:O2'	37:a:384:G:OP2	2.28	0.42
37:a:449:C:H2'	37:a:450:A:C8	2.55	0.42
37:a:516:G:O6	48:l:2:PRO:HB3	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:c:141:PHE:H	39:c:141:PHE:HD1	1.68	0.42
47:k:95:ILE:HG22	47:k:102:ARG:HH21	1.85	0.42
61:y:135:THR:O	61:y:136:LEU:HD23	2.19	0.42
2:1:13:LYS:HG2	2:1:14:ARG:N	2.31	0.41
6:5:17:ILE:HD11	6:5:26:ILE:HG12	2.02	0.41
9:A:984:G:P	22:N:87:LYS:HG3	2.60	0.41
9:A:1088:U:N1	9:A:1090:U:H5'	2.35	0.41
9:A:1135:A:H4'	17:I:129:MET:HG2	2.01	0.41
9:A:1307:A:C6	9:A:1310:C:C2	3.08	0.41
9:A:2313:U:H4'	9:A:2314:C:OP1	2.20	0.41
9:A:2391:C:H2'	9:A:2392:G:O4'	2.20	0.41
9:A:2625:G:H5''	9:A:2626:U:OP1	2.19	0.41
12:D:179:PHE:HA	12:D:183:GLN:OE1	2.19	0.41
16:H:50:LYS:HG2	16:H:67:LEU:O	2.20	0.41
28:T:79:LEU:HD23	28:T:79:LEU:HA	1.66	0.41
32:X:93:ILE:C	32:X:94:ILE:HG13	2.45	0.41
34:Z:74:GLU:H	34:Z:74:GLU:HG3	1.41	0.41
37:a:611:A:H2'	37:a:612:G:O4'	2.20	0.41
37:a:804:G:H2'	37:a:805:U:C6	2.54	0.41
37:a:1011:U:H2'	37:a:1012:C:C6	2.55	0.41
37:a:1067:U:H1'	37:a:1127:A:C5	2.55	0.41
39:c:58:GLU:H	39:c:58:GLU:HG3	1.63	0.41
40:d:51:LYS:HD3	40:d:196:TYR:CE1	2.55	0.41
47:k:81:ARG:HA	47:k:81:ARG:HD3	1.88	0.41
49:m:84:THR:O	49:m:85:LEU:HB2	2.18	0.41
49:m:109:MET:HE2	49:m:109:MET:HB3	1.93	0.41
1:0:93:GLN:HG3	49:m:124:ARG:NH2	2.35	0.41
2:1:26:TRP:O	2:1:30:LYS:HG2	2.21	0.41
5:4:136:ILE:HD13	5:4:136:ILE:HA	1.90	0.41
9:A:44:G:N7	9:A:200:G:O2'	2.48	0.41
9:A:434:A:H2'	9:A:435:A:C8	2.55	0.41
9:A:722:G:C2	9:A:732:A:C6	3.08	0.41
9:A:844:G:C6	9:A:845:C:N4	2.87	0.41
9:A:1557:G:C4	9:A:1559:A:C8	3.09	0.41
9:A:1853:C:H2'	9:A:1854:C:C6	2.54	0.41
9:A:2212:A:N3	16:H:77:PHE:HB2	2.35	0.41
9:A:2469:C:H2'	9:A:2470:A:C8	2.55	0.41
10:B:48:C:OP2	24:P:49:ARG:NH2	2.53	0.41
10:B:54:G:H8	10:B:54:G:O5'	2.03	0.41
11:C:226:HIS:HA	11:C:227:PRO:HD3	1.92	0.41
12:D:151:MET:HE2	12:D:151:MET:HB3	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:G:123:PHE:O	15:G:174:SER:HA	2.20	0.41
19:K:109:PRO:O	19:K:112:LYS:HG3	2.20	0.41
26:R:106:ASN:O	26:R:110:MET:HG3	2.19	0.41
27:S:105:ASP:OD1	27:S:106:ILE:N	2.53	0.41
32:X:131:ASP:OD1	32:X:132:LYS:HG3	2.20	0.41
34:Z:76:LEU:HD22	34:Z:115:MET:CE	2.50	0.41
35:z:37:A:H2'	35:z:38:A:O4'	2.21	0.41
37:a:99:G:C2	37:a:260:G:N7	2.88	0.41
37:a:736:U:O3'	61:y:178:HIS:NE2	2.49	0.41
37:a:829:C:OP2	48:l:3:THR:HG21	2.20	0.41
38:b:46:ASN:ND2	38:b:48:THR:HG22	2.35	0.41
56:t:105:ARG:O	56:t:109:GLU:HG2	2.20	0.41
7:6:119:LEU:HD13	9:A:1405:A:H5'	2.03	0.41
9:A:592:G:OP1	26:R:32:THR:HG21	2.20	0.41
9:A:1269:G:OP1	13:E:143:PRO:HG3	2.20	0.41
9:A:1604:A:H2'	9:A:1605:A:H8	1.83	0.41
9:A:2705:G:N1	9:A:2738:U:OP2	2.32	0.41
13:E:64:LYS:HE3	13:E:66:GLY:O	2.21	0.41
17:I:76:LEU:HD22	17:I:134:PHE:CD1	2.55	0.41
22:N:1:MET:HE3	22:N:44:SER:OG	2.20	0.41
25:Q:168:ILE:HB	25:Q:232:PHE:CE2	2.56	0.41
26:R:96:ILE:HD12	26:R:96:ILE:HA	1.81	0.41
32:X:71:ASP:OD1	32:X:72:SER:N	2.53	0.41
37:a:233:A:H2'	37:a:234:A:C8	2.55	0.41
37:a:401:G:OP2	40:d:8:ARG:HG3	2.20	0.41
37:a:481:A:O2'	37:a:483:A:OP2	2.33	0.41
37:a:634:G:N1	37:a:651:G:O2'	2.39	0.41
37:a:776:A:OP1	37:a:776:A:H4'	2.21	0.41
37:a:1028:A:H2'	37:a:1029:A:C8	2.55	0.41
37:a:1118:A:H5'	38:b:143:ARG:NH2	2.33	0.41
37:a:1275:G:H5''	60:x:73:ASN:HB2	2.02	0.41
37:a:1329:U:C4	43:g:3:ARG:HG3	2.55	0.41
37:a:1382:A:N1	37:a:1383:A:C2	2.89	0.41
38:b:229:ARG:HG3	38:b:232:TYR:CE2	2.55	0.41
42:f:166:ASN:HB3	42:f:168:TYR:CZ	2.55	0.41
46:j:185:LEU:HA	46:j:186:PRO:HD3	1.91	0.41
52:p:32:ASP:OD1	52:p:32:ASP:N	2.52	0.41
9:A:160:A:C2	9:A:161:G:C4	3.08	0.41
9:A:1863:A:H2'	9:A:1864:A:C8	2.56	0.41
9:A:2082:U:H5'	9:A:2082:U:H6	1.85	0.41
9:A:2139:A:O2'	9:A:2187:A:N6	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:2410:U:H2'	9:A:2411:C:H6	1.86	0.41
13:E:78:GLU:H	13:E:78:GLU:HG3	1.63	0.41
13:E:159:LEU:HD12	13:E:159:LEU:HA	1.90	0.41
22:N:11:LYS:HB3	22:N:87:LYS:HE3	2.03	0.41
24:P:48:THR:HG22	24:P:50:ARG:HB3	2.01	0.41
27:S:127:VAL:HG12	27:S:161:VAL:HG22	2.01	0.41
37:a:577:A:H2'	37:a:578:C:C6	2.56	0.41
37:a:920:G:H1'	37:a:1314:A:HO2'	1.85	0.41
37:a:1185:C:O4'	37:a:1282:G:N2	2.54	0.41
38:b:71:PHE:HD2	38:b:166:ILE:HD11	1.86	0.41
47:k:29:VAL:HG13	47:k:92:GLU:HB2	2.02	0.41
58:v:186:VAL:HG23	58:v:238:VAL:HG13	2.02	0.41
7:6:134:SER:O	7:6:138:LYS:HG2	2.20	0.41
9:A:1454:G:H2'	9:A:1455:A:C8	2.56	0.41
9:A:2245:U:H2'	9:A:2246:U:C6	2.55	0.41
9:A:2490:U:OP1	9:A:2546:G:N2	2.50	0.41
9:A:2658:A:P	19:K:175:ARG:HH12	2.42	0.41
17:I:122:ILE:HG23	17:I:126:MET:HE3	2.02	0.41
19:K:144:THR:HG22	19:K:146:SER:H	1.85	0.41
37:a:163:G:H2'	37:a:164:U:C6	2.55	0.41
37:a:494:A:P	40:d:62:GLU:HB3	2.61	0.41
37:a:1363:U:H2'	37:a:1364:G:C8	2.52	0.41
45:i:207:LYS:HA	45:i:207:LYS:HD3	1.85	0.41
46:j:101:ILE:O	46:j:166:LEU:HD12	2.20	0.41
61:y:84:LEU:HD22	61:y:118:ALA:HB2	2.02	0.41
5:4:95:HIS:HE2	9:A:236:A:P	2.43	0.41
9:A:409:U:H1'	9:A:2248:U:O2'	2.20	0.41
9:A:724:G:H1'	9:A:729:A:H62	1.84	0.41
9:A:794:A:C5	9:A:796:G:H1'	2.56	0.41
9:A:919:A:N3	9:A:2281:C:O2'	2.43	0.41
9:A:1804:U:H2'	9:A:1805:C:C6	2.56	0.41
9:A:1874:U:OP1	9:A:2427:G:O2'	2.37	0.41
9:A:1875:G:H2'	9:A:1889:G:H22	1.86	0.41
9:A:2292:C:H6	9:A:2292:C:H2'	1.69	0.41
9:A:2584:G:H2'	9:A:2585:C:C6	2.56	0.41
13:E:153:ASN:HB2	13:E:156:GLU:HB2	2.03	0.41
17:I:66:VAL:HG22	17:I:103:ILE:HG21	2.01	0.41
18:J:86:ALA:HA	18:J:117:THR:HG21	2.02	0.41
19:K:100:TRP:CE3	26:R:102:ILE:HD13	2.56	0.41
20:L:13:ASN:O	20:L:15:GLY:N	2.54	0.41
22:N:16:ARG:NE	22:N:18:LYS:HE3	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:V:130:ILE:HD13	30:V:130:ILE:HG21	1.83	0.41
37:a:410:U:C5	37:a:411:U:C4	3.09	0.41
37:a:588:A:C6	37:a:589:A:C6	3.09	0.41
37:a:601:G:N2	44:h:56:LYS:HB3	2.35	0.41
37:a:1337:C:H2'	37:a:1338:C:C6	2.56	0.41
38:b:34:TYR:OH	38:b:191:ILE:HG21	2.20	0.41
41:e:202:GLN:O	41:e:205:ALA:HB3	2.20	0.41
46:j:101:ILE:HA	46:j:192:GLU:O	2.21	0.41
46:j:107:TRP:HE1	46:j:110:LEU:HD22	1.84	0.41
1:0:39:SER:O	1:0:40:ASP:HB3	2.20	0.41
9:A:1378:U:H2'	9:A:1379:C:O4'	2.20	0.41
9:A:2341:U:H3'	9:A:2342:G:C5'	2.51	0.41
10:B:62:U:H2'	10:B:63:C:C6	2.54	0.41
11:C:102:HIS:HA	11:C:103:PRO:HD3	1.91	0.41
11:C:114:SER:HB3	11:C:125:ALA:HB3	2.01	0.41
12:D:142:GLU:HB3	12:D:166:ARG:HB3	2.02	0.41
18:J:85:GLU:OE1	18:J:88:LYS:HD2	2.20	0.41
19:K:77:VAL:HA	19:K:78:PRO:HD3	1.90	0.41
25:Q:148:ILE:HD13	25:Q:168:ILE:HG13	2.03	0.41
25:Q:151:ILE:HG12	25:Q:206:ILE:HG13	2.01	0.41
28:T:65:LEU:HD23	28:T:65:LEU:HA	1.88	0.41
31:W:49:A:O2'	31:W:50:G:H5'	2.21	0.41
37:a:36:G:H2'	37:a:37:C:C6	2.55	0.41
37:a:71:G:O2'	37:a:72:A:H8	2.03	0.41
37:a:240:U:H2'	37:a:241:A:C8	2.55	0.41
37:a:574:U:H2'	37:a:575:G:C8	2.55	0.41
37:a:926:A:OP1	37:a:926:A:H4'	2.20	0.41
37:a:1264:G:H2'	37:a:1266:A:OP2	2.21	0.41
37:a:1366:G:C6	37:a:1431:G:C6	3.08	0.41
39:c:81:PRO:HD2	39:c:116:ARG:NE	2.35	0.41
39:c:91:GLY:O	39:c:95:LEU:HB2	2.20	0.41
59:w:109:ASN:OD1	59:w:133:PRO:HD2	2.21	0.41
61:y:106:SER:HA	61:y:109:VAL:HG12	2.02	0.41
1:0:74:SER:HB3	14:F:158:ASN:HA	2.03	0.41
4:3:96:LEU:HD21	9:A:1790:A:C4	2.55	0.41
9:A:372:G:H2'	9:A:373:C:C6	2.56	0.41
9:A:701:U:H5''	9:A:702:C:OP2	2.21	0.41
9:A:1023:C:OP2	26:R:54:LYS:NZ	2.54	0.41
9:A:1374:A:H2'	9:A:1375:A:C8	2.55	0.41
9:A:1690:A:N7	9:A:2019:G:N2	2.69	0.41
9:A:1818:U:H3'	9:A:1819:A:C8	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:2410:U:H2'	9:A:2411:C:C6	2.55	0.41
11:C:138:HIS:CD2	11:C:139:ASN:HB2	2.55	0.41
11:C:179:LEU:HD13	11:C:267:ILE:HD11	2.03	0.41
12:D:204:ILE:HD11	12:D:285:LYS:HD3	2.03	0.41
26:R:97:LEU:HD23	26:R:97:LEU:HA	1.73	0.41
27:S:108:ASN:ND2	27:S:113:LYS:HE3	2.35	0.41
34:Z:140:TRP:CE2	34:Z:144:ILE:HD11	2.56	0.41
37:a:184:G:H4'	58:v:256:ARG:HH12	1.86	0.41
37:a:439:G:H2'	37:a:440:G:H8	1.86	0.41
37:a:787:G:C2	37:a:797:G:C2	3.08	0.41
37:a:1004:A:O2'	39:c:172:GLU:O	2.37	0.41
37:a:1252:G:C6	37:a:1253:G:C2	3.09	0.41
37:a:1350:G:O6	61:y:166:ARG:NH2	2.35	0.41
39:c:189:ILE:HG13	39:c:189:ILE:H	1.67	0.41
41:e:292:PHE:HA	41:e:295:VAL:HG22	2.01	0.41
46:j:103:LEU:HD22	46:j:191:VAL:HG12	2.01	0.41
53:q:100:HIS:CD2	53:q:102:PRO:HD3	2.56	0.41
2:1:6:LYS:HD3	2:1:6:LYS:HA	1.72	0.41
9:A:410:G:H21	16:H:42:GLN:NE2	2.19	0.41
9:A:457:C:O2'	9:A:458:G:H5'	2.21	0.41
9:A:481:G:H4'	13:E:120:LYS:HD2	2.03	0.41
9:A:1195:U:H3'	9:A:1196:A:H8	1.86	0.41
9:A:1335:C:O5'	9:A:1335:C:H6	2.04	0.41
9:A:1454:G:N2	9:A:1595:C:O2	2.54	0.41
9:A:1636:U:OP1	29:U:172:LYS:HE3	2.21	0.41
9:A:2080:U:O2'	9:A:2081:A:H5'	2.21	0.41
9:A:2165:G:H2'	9:A:2166:G:C8	2.56	0.41
9:A:2204:A:H3'	9:A:2205:G:C8	2.55	0.41
9:A:2356:G:C2	9:A:2357:A:C4	3.09	0.41
9:A:2467:A:OP1	9:A:2514:A:O2'	2.28	0.41
9:A:2555:U:H2'	9:A:2556:C:H6	1.85	0.41
9:A:2699:U:H2'	9:A:2700:C:C6	2.56	0.41
17:I:154:ARG:CD	17:I:159:ASN:HB2	2.51	0.41
18:J:120:LYS:HD2	18:J:125:ILE:HD11	2.03	0.41
21:M:158:VAL:HA	21:M:159:PRO:HD3	1.81	0.41
28:T:127:ARG:HA	28:T:128:PRO:HD3	1.82	0.41
33:Y:98:LEU:HD12	33:Y:98:LEU:HA	1.66	0.41
36:8:1059:UNK:O	38:b:26:LYS:HD2	2.20	0.41
37:a:353:A:C2	37:a:354:A:C4	3.09	0.41
37:a:574:U:C2	37:a:575:G:C8	3.09	0.41
37:a:917:A:H8	37:a:917:A:OP1	2.04	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:a:1102:C:H2'	37:a:1103:A:H8	1.86	0.41
37:a:1204:U:H3'	39:c:27:LYS:NZ	2.35	0.41
37:a:1393:U:H2'	37:a:1394:U:H6	1.86	0.41
37:a:1455:U:O2'	37:a:1456:A:H5'	2.20	0.41
37:a:1471:U:H5''	47:k:137:ARG:HH22	1.86	0.41
38:b:73:ILE:HD11	38:b:218:LEU:HD11	2.03	0.41
43:g:27:VAL:HG21	43:g:40:TYR:CE1	2.55	0.41
45:i:193:LYS:HA	45:i:194:PRO:HD3	1.79	0.41
55:s:37:ALA:O	55:s:70:LYS:HD2	2.21	0.41
58:v:182:SER:HB2	58:v:183:PRO:HD3	2.02	0.41
8:7:80:PRO:HA	8:7:81:PRO:HD3	1.93	0.41
9:A:324:G:H2'	9:A:325:A:O4'	2.21	0.41
9:A:715:G:N2	9:A:737:G:C4	2.88	0.41
9:A:1178:G:H4'	26:R:83:HIS:CD2	2.56	0.41
9:A:2225:G:H2'	9:A:2226:A:C8	2.56	0.41
9:A:2256:A:P	11:C:239:ARG:NH2	2.93	0.41
9:A:2288:G:H8	9:A:2288:G:O5'	2.04	0.41
9:A:2342:G:C6	9:A:2343:C:N3	2.89	0.41
12:D:99:MET:HB3	12:D:99:MET:HE2	1.56	0.41
19:K:217:LEU:HD23	19:K:217:LEU:HA	1.90	0.41
25:Q:219:LEU:HB3	25:Q:221:TYR:CE1	2.56	0.41
37:a:7:G:O2'	37:a:8:G:H5'	2.21	0.41
37:a:280:A:P	52:p:27:ARG:HH22	2.44	0.41
37:a:379:A:OP1	40:d:103:THR:OG1	2.35	0.41
37:a:1456:A:H2'	37:a:1457:G:H8	1.85	0.41
39:c:76:ILE:HD12	39:c:114:ILE:HG12	2.03	0.41
50:n:28:LYS:HD3	50:n:28:LYS:HA	1.92	0.41
50:n:82:ILE:H	50:n:82:ILE:HG13	1.65	0.41
9:A:826:C:H2'	9:A:827:C:H6	1.85	0.40
9:A:1074:A:C2	17:I:63:VAL:HG21	2.56	0.40
9:A:1093:C:H1'	9:A:1102:G:N2	2.36	0.40
9:A:1407:C:H2'	9:A:1408:A:C8	2.56	0.40
12:D:145:ARG:NH1	12:D:147:ARG:HH11	2.19	0.40
13:E:200:ASP:O	13:E:202:ALA:N	2.45	0.40
13:E:200:ASP:C	13:E:202:ALA:H	2.27	0.40
13:E:232:ARG:O	13:E:232:ARG:NH1	2.51	0.40
15:G:141:LYS:HD3	15:G:141:LYS:HA	1.88	0.40
15:G:203:ARG:HG3	15:G:204:TYR:O	2.21	0.40
22:N:2:LEU:HD13	22:N:69:PHE:HD1	1.86	0.40
22:N:54:MET:HE1	22:N:104:TYR:CG	2.57	0.40
23:O:36:THR:HG22	23:O:80:ILE:HG23	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:Q:175:ALA:O	25:Q:179:THR:N	2.53	0.40
28:T:126:LYS:O	28:T:128:PRO:HD3	2.20	0.40
31:W:40:U:H2'	31:W:41:A:C8	2.56	0.40
31:W:50:G:H2'	31:W:51:U:O4'	2.21	0.40
34:Z:101:LYS:O	34:Z:104:ASP:HB2	2.20	0.40
37:a:363:G:H4'	52:p:13:GLN:HE22	1.87	0.40
37:a:954:A:H3'	37:a:955:U:C6	2.56	0.40
37:a:1440:G:H5'	37:a:1441:A:OP2	2.21	0.40
38:b:28:ASN:HA	38:b:29:PRO:HD2	1.90	0.40
59:w:130:TYR:OH	59:w:144:LEU:HD11	2.21	0.40
1:0:101:TYR:CD1	55:s:9:PRO:HD3	2.56	0.40
4:3:104:SER:O	4:3:107:SER:N	2.54	0.40
9:A:850:G:C6	9:A:851:U:N3	2.89	0.40
9:A:1087:G:H3'	9:A:1088:U:H2'	2.03	0.40
9:A:1168:U:C6	9:A:1168:U:H5'	2.56	0.40
9:A:1809:G:N2	11:C:150:LEU:HD22	2.35	0.40
9:A:1886:A:H2'	9:A:1887:G:C8	2.55	0.40
9:A:2113:G:N2	9:A:2204:A:H62	2.19	0.40
9:A:2652:A:O2'	12:D:170:GLU:OE1	2.27	0.40
10:B:29:C:C2	10:B:30:A:C8	3.08	0.40
11:C:141:GLU:HG2	11:C:147:GLY:C	2.46	0.40
11:C:228:HIS:CD2	11:C:228:HIS:N	2.88	0.40
14:F:54:ILE:H	14:F:54:ILE:HG13	1.41	0.40
19:K:97:ASN:ND2	27:S:135:ILE:H	2.09	0.40
19:K:135:ILE:O	19:K:150:GLY:HA3	2.21	0.40
19:K:164:SER:O	19:K:167:LYS:HE3	2.21	0.40
20:L:67:LYS:HG3	20:L:68:GLU:H	1.87	0.40
21:M:109:SER:O	21:M:110:CYS:HB2	2.22	0.40
21:M:130:GLU:O	21:M:132:GLY:N	2.54	0.40
22:N:77:ARG:HH21	22:N:86:GLY:C	2.27	0.40
28:T:67:LEU:HA	28:T:67:LEU:HD23	1.81	0.40
29:U:190:LYS:HE2	34:Z:156:GLN:HB3	2.02	0.40
34:Z:92:LEU:HD23	34:Z:92:LEU:HA	1.87	0.40
37:a:1292:C:H5'	45:i:200:ARG:O	2.21	0.40
39:c:26:PRO:HB3	46:j:140:ARG:HH12	1.86	0.40
39:c:106:VAL:C	39:c:108:ARG:H	2.29	0.40
42:f:106:ARG:HH11	42:f:205:LYS:NZ	2.18	0.40
44:h:69:LYS:HB3	44:h:72:PRO:HD2	2.03	0.40
45:i:143:VAL:HG21	45:i:157:ILE:HG12	2.03	0.40
45:i:169:SER:HB2	45:i:172:HIS:CD2	2.56	0.40
48:l:24:LEU:HD13	48:l:95:TYR:HE2	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:378:A:N3	9:A:378:A:H2'	2.35	0.40
9:A:675:U:H2'	9:A:676:U:H6	1.87	0.40
9:A:1649:G:C2	9:A:1655:G:C5	3.09	0.40
9:A:1673:A:H2'	9:A:1674:C:C6	2.56	0.40
12:D:145:ARG:CZ	12:D:147:ARG:HD3	2.51	0.40
12:D:198:ASP:OD1	12:D:262:ARG:HA	2.22	0.40
13:E:94:ASN:OD1	13:E:149:THR:HA	2.21	0.40
15:G:72:LEU:HD12	15:G:119:VAL:HG13	2.02	0.40
15:G:94:LYS:HB2	15:G:97:GLU:OE2	2.22	0.40
19:K:48:ARG:NH2	31:W:2:G:N7	2.70	0.40
37:a:775:U:H5''	37:a:776:A:OP2	2.21	0.40
37:a:1312:A:H4'	37:a:1313:U:O5'	2.21	0.40
42:f:189:GLU:O	42:f:193:VAL:HG23	2.21	0.40
43:g:50:ILE:HD11	43:g:61:VAL:HG11	2.02	0.40
45:i:155:GLN:O	45:i:158:SER:HB3	2.21	0.40
47:k:84:VAL:HG22	47:k:114:ILE:HD11	2.02	0.40
50:n:45:GLY:HA2	55:s:13:ASN:HD21	1.86	0.40
57:u:130:LYS:O	57:u:134:ARG:HB2	2.20	0.40
59:w:114:LEU:HG	59:w:141:LEU:HD11	2.02	0.40
61:y:182:MET:O	61:y:183:LYS:HB2	2.20	0.40
9:A:33:A:O2'	9:A:466:A:N3	2.52	0.40
9:A:771:G:H2'	9:A:772:A:O4'	2.22	0.40
9:A:888:C:C4	9:A:909:A:C5	3.09	0.40
9:A:2051:G:H2'	9:A:2052:G:C8	2.56	0.40
10:B:10:G:OP1	24:P:57:HIS:NE2	2.53	0.40
11:C:110:ASP:OD1	11:C:111:THR:N	2.53	0.40
11:C:131:MET:HE2	11:C:131:MET:HB3	1.88	0.40
11:C:256:ARG:NH2	11:C:262:SER:HB2	2.35	0.40
12:D:181:PRO:O	12:D:182:SER:HB3	2.21	0.40
15:G:79:GLU:H	15:G:79:GLU:CD	2.29	0.40
21:M:127:ARG:HD2	21:M:127:ARG:HA	1.85	0.40
21:M:154:LEU:HD12	21:M:154:LEU:HA	1.83	0.40
31:W:40:U:C4	31:W:87:A:N6	2.89	0.40
37:a:1406:G:H5'	56:t:102:THR:HG21	2.03	0.40
37:a:1422:A:H2'	37:a:1423:G:C8	2.56	0.40
39:c:10:PHE:HE2	39:c:189:ILE:HG12	1.86	0.40
3:2:30:VAL:HG23	9:A:2417:G:H4'	2.04	0.40
9:A:16:G:H2'	9:A:17:C:C6	2.57	0.40
9:A:491:A:C2	9:A:492:A:C5	3.10	0.40
9:A:826:C:H2'	9:A:827:C:C6	2.57	0.40
9:A:940:C:H2'	9:A:941:C:C6	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:1086:G:N2	18:J:198:ILE:HG12	2.22	0.40
9:A:1192:A:H2'	9:A:1193:U:C6	2.56	0.40
9:A:1866:G:H5''	9:A:1867:A:OP2	2.21	0.40
9:A:2432:G:C5'	21:M:148:GLY:HA3	2.51	0.40
10:B:10:G:O5'	24:P:61:ARG:NH1	2.54	0.40
11:C:237:ILE:HD13	11:C:237:ILE:HG21	1.82	0.40
15:G:44:GLY:HA3	15:G:105:HIS:NE2	2.35	0.40
19:K:225:LYS:HB2	19:K:225:LYS:HE3	1.63	0.40
23:O:20:LEU:O	23:O:22:ARG:HG2	2.21	0.40
33:Y:96:LYS:HA	33:Y:96:LYS:HD3	1.83	0.40
36:8:1131:UNK:CB	36:8:1219:UNK:HA	2.51	0.40
37:a:355:G:H2'	37:a:356:C:C6	2.57	0.40
37:a:392:A:C6	39:c:138:ARG:NH2	2.89	0.40
37:a:1107:U:C2	37:a:1130:G:C2	3.09	0.40
37:a:1221:U:H2'	37:a:1222:G:O4'	2.22	0.40
38:b:30:ARG:NH1	44:h:70:LYS:HD2	2.37	0.40
39:c:7:PRO:HG3	39:c:212:TRP:HE1	1.85	0.40
46:j:140:ARG:HD2	46:j:142:TYR:OH	2.21	0.40
55:s:51:ILE:HD11	55:s:71:LEU:HD22	2.03	0.40
61:y:108:LEU:O	61:y:139:LYS:HG3	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	64/130 (49%)	56 (88%)	5 (8%)	3 (5%)	2	12
2	1	46/57 (81%)	45 (98%)	1 (2%)	0	100	100
3	2	58/66 (88%)	53 (91%)	5 (9%)	0	100	100
4	3	58/152 (38%)	54 (93%)	4 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	4	70/159 (44%)	66 (94%)	4 (6%)	0	100	100
6	5	35/37 (95%)	34 (97%)	1 (3%)	0	100	100
7	6	47/142 (33%)	46 (98%)	0	1 (2%)	5	24
8	7	44/116 (38%)	41 (93%)	3 (7%)	0	100	100
11	C	251/272 (92%)	235 (94%)	15 (6%)	1 (0%)	30	59
12	D	219/305 (72%)	206 (94%)	12 (6%)	1 (0%)	24	54
13	E	210/293 (72%)	196 (93%)	14 (7%)	0	100	100
14	F	191/258 (74%)	178 (93%)	13 (7%)	0	100	100
15	G	176/220 (80%)	165 (94%)	11 (6%)	0	100	100
16	H	46/196 (24%)	43 (94%)	3 (6%)	0	100	100
17	I	135/232 (58%)	132 (98%)	3 (2%)	0	100	100
18	J	131/224 (58%)	126 (96%)	5 (4%)	0	100	100
19	K	201/250 (80%)	193 (96%)	8 (4%)	0	100	100
20	L	119/121 (98%)	113 (95%)	6 (5%)	0	100	100
21	M	183/271 (68%)	168 (92%)	13 (7%)	2 (1%)	11	38
22	N	133/135 (98%)	121 (91%)	12 (9%)	0	100	100
23	O	114/126 (90%)	108 (95%)	6 (5%)	0	100	100
24	P	120/166 (72%)	113 (94%)	7 (6%)	0	100	100
25	Q	116/233 (50%)	114 (98%)	2 (2%)	0	100	100
26	R	117/128 (91%)	110 (94%)	7 (6%)	0	100	100
27	S	168/256 (66%)	158 (94%)	8 (5%)	2 (1%)	10	35
28	T	170/199 (85%)	162 (95%)	7 (4%)	1 (1%)	21	50
29	U	94/198 (48%)	89 (95%)	5 (5%)	0	100	100
30	V	132/192 (69%)	123 (93%)	9 (7%)	0	100	100
32	X	107/194 (55%)	96 (90%)	11 (10%)	0	100	100
33	Y	75/148 (51%)	73 (97%)	2 (3%)	0	100	100
34	Z	99/168 (59%)	95 (96%)	3 (3%)	1 (1%)	12	40
38	b	231/236 (98%)	221 (96%)	10 (4%)	0	100	100
39	c	214/218 (98%)	201 (94%)	13 (6%)	0	100	100
40	d	197/201 (98%)	186 (94%)	11 (6%)	0	100	100
41	e	185/308 (60%)	182 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
42	f	111/211 (53%)	106 (96%)	4 (4%)	1 (1%)	14	42
43	g	152/155 (98%)	146 (96%)	6 (4%)	0	100	100
44	h	131/134 (98%)	127 (97%)	2 (2%)	2 (2%)	8	30
45	i	142/208 (68%)	136 (96%)	6 (4%)	0	100	100
46	j	97/195 (50%)	93 (96%)	3 (3%)	1 (1%)	12	40
47	k	115/138 (83%)	108 (94%)	7 (6%)	0	100	100
48	l	120/123 (98%)	114 (95%)	6 (5%)	0	100	100
49	m	108/172 (63%)	101 (94%)	6 (6%)	1 (1%)	14	42
50	n	97/100 (97%)	92 (95%)	5 (5%)	0	100	100
51	o	73/90 (81%)	72 (99%)	1 (1%)	0	100	100
52	p	78/88 (89%)	74 (95%)	4 (5%)	0	100	100
53	q	84/165 (51%)	78 (93%)	6 (7%)	0	100	100
54	r	58/101 (57%)	55 (95%)	3 (5%)	0	100	100
55	s	76/92 (83%)	75 (99%)	1 (1%)	0	100	100
56	t	105/183 (57%)	100 (95%)	3 (3%)	2 (2%)	6	26
57	u	63/180 (35%)	62 (98%)	1 (2%)	0	100	100
58	v	78/260 (30%)	76 (97%)	2 (3%)	0	100	100
59	w	80/179 (45%)	78 (98%)	2 (2%)	0	100	100
60	x	38/101 (38%)	37 (97%)	1 (3%)	0	100	100
61	y	114/302 (38%)	106 (93%)	8 (7%)	0	100	100
All	All	6476/9784 (66%)	6138 (95%)	319 (5%)	19 (0%)	37	65

All (19) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	0	92	ASP
27	S	78	PRO
49	m	53	VAL
56	t	174	TYR
11	C	232	GLU
34	Z	151	SER
46	j	150	VAL
21	M	144	ARG
44	h	68	ASN
44	h	69	LYS

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Mol	Chain	Res	Type
56	t	79	ALA
21	M	131	GLY
28	T	146	ASP
1	0	91	ALA
12	D	212	ILE
42	f	149	VAL
1	0	72	VAL
7	6	131	TRP
27	S	77	ARG

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	57/117 (49%)	54 (95%)	3 (5%)	20	47
2	1	41/50 (82%)	37 (90%)	4 (10%)	7	27
3	2	56/60 (93%)	50 (89%)	6 (11%)	6	23
4	3	50/125 (40%)	41 (82%)	9 (18%)	2	7
5	4	62/140 (44%)	54 (87%)	8 (13%)	4	16
6	5	34/34 (100%)	29 (85%)	5 (15%)	3	12
7	6	46/124 (37%)	40 (87%)	6 (13%)	4	16
8	7	40/96 (42%)	33 (82%)	7 (18%)	2	8
11	C	201/217 (93%)	178 (89%)	23 (11%)	5	21
12	D	182/259 (70%)	160 (88%)	22 (12%)	5	19
13	E	179/255 (70%)	155 (87%)	24 (13%)	4	15
14	F	152/214 (71%)	134 (88%)	18 (12%)	5	20
15	G	151/190 (80%)	137 (91%)	14 (9%)	8	29
16	H	42/170 (25%)	36 (86%)	6 (14%)	3	13
17	I	119/204 (58%)	109 (92%)	10 (8%)	10	34
18	J	106/189 (56%)	100 (94%)	6 (6%)	18	45
19	K	176/213 (83%)	160 (91%)	16 (9%)	9	30

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
20	L	101/101 (100%)	90 (89%)	11 (11%)	6	22
21	M	141/215 (66%)	124 (88%)	17 (12%)	5	19
22	N	108/108 (100%)	97 (90%)	11 (10%)	7	25
23	O	96/103 (93%)	81 (84%)	15 (16%)	2	10
24	P	100/139 (72%)	92 (92%)	8 (8%)	11	36
25	Q	104/207 (50%)	91 (88%)	13 (12%)	4	18
26	R	106/115 (92%)	95 (90%)	11 (10%)	7	24
27	S	137/223 (61%)	129 (94%)	8 (6%)	18	45
28	T	152/176 (86%)	133 (88%)	19 (12%)	4	18
29	U	85/171 (50%)	75 (88%)	10 (12%)	5	20
30	V	121/169 (72%)	107 (88%)	14 (12%)	5	20
32	X	92/163 (56%)	75 (82%)	17 (18%)	1	7
33	Y	67/130 (52%)	58 (87%)	9 (13%)	4	15
34	Z	93/153 (61%)	82 (88%)	11 (12%)	5	20
38	b	198/201 (98%)	181 (91%)	17 (9%)	10	33
39	c	186/188 (99%)	171 (92%)	15 (8%)	11	36
40	d	178/180 (99%)	165 (93%)	13 (7%)	13	39
41	e	121/255 (48%)	105 (87%)	16 (13%)	4	16
42	f	100/186 (54%)	92 (92%)	8 (8%)	11	36
43	g	125/126 (99%)	117 (94%)	8 (6%)	16	42
44	h	116/117 (99%)	106 (91%)	10 (9%)	10	33
45	i	114/169 (68%)	100 (88%)	14 (12%)	4	18
46	j	91/173 (53%)	84 (92%)	7 (8%)	12	37
47	k	91/109 (84%)	81 (89%)	10 (11%)	6	22
48	l	105/106 (99%)	95 (90%)	10 (10%)	8	29
49	m	99/151 (66%)	91 (92%)	8 (8%)	11	36
50	n	89/90 (99%)	79 (89%)	10 (11%)	6	21
51	o	70/85 (82%)	68 (97%)	2 (3%)	37	60
52	p	71/79 (90%)	61 (86%)	10 (14%)	3	13
53	q	77/149 (52%)	72 (94%)	5 (6%)	15	42
54	r	56/96 (58%)	49 (88%)	7 (12%)	4	18

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
55	s	68/81 (84%)	63 (93%)	5 (7%)	13	38
56	t	89/156 (57%)	83 (93%)	6 (7%)	15	41
57	u	59/160 (37%)	53 (90%)	6 (10%)	7	25
58	v	67/225 (30%)	67 (100%)	0	100	100
59	w	76/162 (47%)	75 (99%)	1 (1%)	61	71
60	x	30/85 (35%)	30 (100%)	0	100	100
61	y	104/275 (38%)	99 (95%)	5 (5%)	23	50
All	All	5577/8434 (66%)	5023 (90%)	554 (10%)	10	26

All (554) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	0	51	VAL
1	0	57	LEU
1	0	59	MET
2	1	6	LYS
2	1	7	ARG
2	1	11	TYR
2	1	13	LYS
3	2	6	ASP
3	2	19	VAL
3	2	28	ARG
3	2	34	ILE
3	2	42	THR
3	2	60	ILE
4	3	97	CYS
4	3	98	LEU
4	3	115	ARG
4	3	118	MET
4	3	126	LEU
4	3	127	LEU
4	3	129	ARG
4	3	142	THR
4	3	143	ASN
5	4	92	MET
5	4	94	THR
5	4	104	VAL
5	4	109	LYS
5	4	119	HIS
5	4	125	ASN

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Mol	Chain	Res	Type
5	4	135	LEU
5	4	143	TYR
6	5	3	ILE
6	5	4	ARG
6	5	6	SER
6	5	29	ASN
6	5	36	GLN
7	6	113	ARG
7	6	118	ARG
7	6	119	LEU
7	6	133	PRO
7	6	137	LYS
7	6	138	LYS
8	7	54	LYS
8	7	56	THR
8	7	62	THR
8	7	65	LYS
8	7	66	LYS
8	7	74	ARG
8	7	82	LEU
11	C	19	GLN
11	C	44	ILE
11	C	71	TYR
11	C	78	GLU
11	C	90	ILE
11	C	96	GLU
11	C	100	ILE
11	C	120	ILE
11	C	126	LEU
11	C	137	ILE
11	C	142	ILE
11	C	152	ARG
11	C	167	SER
11	C	178	ARG
11	C	179	LEU
11	C	188	VAL
11	C	196	VAL
11	C	203	ARG
11	C	219	VAL
11	C	224	VAL
11	C	228	HIS
11	C	244	THR

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Mol	Chain	Res	Type
11	C	270	ARG
12	D	105	GLU
12	D	109	VAL
12	D	132	ASP
12	D	137	VAL
12	D	139	VAL
12	D	146	ASP
12	D	174	VAL
12	D	178	ASP
12	D	193	GLU
12	D	213	LYS
12	D	219	ARG
12	D	221	LEU
12	D	222	MET
12	D	224	HIS
12	D	229	HIS
12	D	240	THR
12	D	260	LYS
12	D	262	ARG
12	D	273	LEU
12	D	288	ASN
12	D	292	LEU
12	D	298	VAL
13	E	52	LEU
13	E	61	SER
13	E	68	THR
13	E	78	GLU
13	E	97	ARG
13	E	113	ARG
13	E	120	LYS
13	E	121	THR
13	E	147	ASP
13	E	152	MET
13	E	161	LEU
13	E	174	VAL
13	E	209	LEU
13	E	211	ASP
13	E	213	VAL
13	E	221	ARG
13	E	223	ILE
13	E	224	ARG
13	E	226	LEU

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Mol	Chain	Res	Type
13	E	230	THR
13	E	238	ASP
13	E	245	LEU
13	E	251	THR
13	E	261	VAL
14	F	54	ILE
14	F	56	ARG
14	F	57	LEU
14	F	59	THR
14	F	78	ILE
14	F	84	VAL
14	F	88	VAL
14	F	110	LEU
14	F	119	VAL
14	F	120	LYS
14	F	122	LYS
14	F	125	THR
14	F	127	ILE
14	F	142	VAL
14	F	155	ARG
14	F	164	THR
14	F	188	GLN
14	F	190	VAL
15	G	40	GLU
15	G	50	VAL
15	G	63	LEU
15	G	80	VAL
15	G	100	ARG
15	G	105	HIS
15	G	109	ARG
15	G	111	LEU
15	G	127	LEU
15	G	129	LEU
15	G	169	THR
15	G	181	VAL
15	G	208	VAL
15	G	213	GLU
16	H	47	LYS
16	H	48	ILE
16	H	57	ILE
16	H	75	ARG
16	H	79	LEU

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Mol	Chain	Res	Type
16	H	85	GLU
17	I	75	LEU
17	I	79	ILE
17	I	89	PHE
17	I	101	THR
17	I	114	VAL
17	I	119	TRP
17	I	140	ILE
17	I	147	TYR
17	I	154	ARG
17	I	165	CYS
18	J	90	THR
18	J	95	VAL
18	J	99	LEU
18	J	129	ILE
18	J	131	VAL
18	J	171	ILE
19	K	48	ARG
19	K	62	ARG
19	K	64	LEU
19	K	68	VAL
19	K	79	LEU
19	K	82	ARG
19	K	122	LEU
19	K	138	LYS
19	K	147	VAL
19	K	168	ARG
19	K	169	THR
19	K	174	ARG
19	K	191	LEU
19	K	199	ILE
19	K	232	GLN
19	K	237	ILE
20	L	2	ILE
20	L	10	VAL
20	L	23	ARG
20	L	25	ILE
20	L	28	SER
20	L	34	ARG
20	L	38	VAL
20	L	42	VAL
20	L	75	MET

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Mol	Chain	Res	Type
20	L	102	ILE
20	L	105	GLU
21	M	83	ASP
21	M	84	ASN
21	M	93	LYS
21	M	106	GLN
21	M	125	ILE
21	M	127	ARG
21	M	138	ARG
21	M	140	ILE
21	M	154	LEU
21	M	164	ASP
21	M	186	ILE
21	M	208	THR
21	M	212	ILE
21	M	215	ARG
21	M	220	SER
21	M	246	VAL
21	M	257	PHE
22	N	5	LYS
22	N	9	PHE
22	N	27	ILE
22	N	28	CYS
22	N	41	TRP
22	N	44	SER
22	N	52	ARG
22	N	56	ARG
22	N	94	VAL
22	N	109	VAL
22	N	118	VAL
23	O	11	MET
23	O	12	LYS
23	O	22	ARG
23	O	27	ARG
23	O	31	LEU
23	O	36	THR
23	O	56	LYS
23	O	73	ARG
23	O	74	ARG
23	O	82	GLU
23	O	89	LEU
23	O	105	THR

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Mol	Chain	Res	Type
23	O	111	LEU
23	O	123	ILE
23	O	126	VAL
24	P	49	ARG
24	P	52	ASP
24	P	59	ARG
24	P	87	ILE
24	P	94	THR
24	P	127	ILE
24	P	151	ARG
24	P	161	GLU
25	Q	117	VAL
25	Q	125	ILE
25	Q	131	VAL
25	Q	161	ARG
25	Q	177	ILE
25	Q	180	THR
25	Q	185	ARG
25	Q	198	LEU
25	Q	203	ILE
25	Q	206	ILE
25	Q	212	ARG
25	Q	219	LEU
25	Q	228	ARG
26	R	6	ARG
26	R	11	ARG
26	R	31	LEU
26	R	70	ARG
26	R	76	TYR
26	R	85	LEU
26	R	90	LEU
26	R	96	ILE
26	R	100	ILE
26	R	108	ILE
26	R	113	ASN
27	S	87	ASP
27	S	102	GLU
27	S	151	THR
27	S	163	LEU
27	S	195	VAL
27	S	208	ARG
27	S	216	ILE

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Mol	Chain	Res	Type
27	S	228	GLU
28	T	32	ILE
28	T	43	VAL
28	T	47	ARG
28	T	62	LEU
28	T	99	ILE
28	T	101	SER
28	T	104	GLU
28	T	110	THR
28	T	113	LYS
28	T	134	ILE
28	T	137	ARG
28	T	139	ILE
28	T	153	THR
28	T	160	LEU
28	T	163	LEU
28	T	164	MET
28	T	174	CYS
28	T	179	GLU
28	T	183	ILE
29	U	102	LEU
29	U	103	LYS
29	U	119	ILE
29	U	138	VAL
29	U	143	ASP
29	U	154	PHE
29	U	171	THR
29	U	172	LYS
29	U	178	LEU
29	U	179	ASN
30	V	48	ARG
30	V	51	ARG
30	V	70	VAL
30	V	79	ILE
30	V	90	ILE
30	V	93	ILE
30	V	98	SER
30	V	130	ILE
30	V	136	MET
30	V	146	SER
30	V	148	VAL
30	V	165	THR

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Mol	Chain	Res	Type
30	V	171	THR
30	V	173	ASP
32	X	73	LYS
32	X	77	LEU
32	X	81	ILE
32	X	85	GLN
32	X	86	VAL
32	X	97	ARG
32	X	105	LYS
32	X	109	ILE
32	X	111	LYS
32	X	114	THR
32	X	115	ILE
32	X	120	ASP
32	X	123	VAL
32	X	135	VAL
32	X	142	ILE
32	X	155	ARG
32	X	156	GLU
33	Y	72	ARG
33	Y	81	LYS
33	Y	83	ASN
33	Y	91	SER
33	Y	92	ASN
33	Y	98	LEU
33	Y	126	LEU
33	Y	135	ASP
33	Y	144	ASP
34	Z	65	LEU
34	Z	74	GLU
34	Z	76	LEU
34	Z	81	LEU
34	Z	87	LEU
34	Z	104	ASP
34	Z	124	ILE
34	Z	132	LEU
34	Z	133	SER
34	Z	142	ARG
34	Z	146	VAL
38	b	7	ASN
38	b	8	ILE
38	b	30	ARG

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Mol	Chain	Res	Type
38	b	54	LEU
38	b	61	VAL
38	b	73	ILE
38	b	84	VAL
38	b	110	THR
38	b	112	GLU
38	b	114	ARG
38	b	119	ARG
38	b	163	ASP
38	b	175	THR
38	b	190	LEU
38	b	194	ASN
38	b	211	ILE
38	b	218	LEU
39	c	4	LYS
39	c	5	ILE
39	c	21	LEU
39	c	24	SER
39	c	42	CYS
39	c	58	GLU
39	c	78	MET
39	c	83	LEU
39	c	103	LEU
39	c	107	ASN
39	c	110	LEU
39	c	116	ARG
39	c	189	ILE
39	c	206	VAL
39	c	209	ILE
40	d	8	ARG
40	d	9	PHE
40	d	12	ILE
40	d	15	LEU
40	d	23	ASN
40	d	89	MET
40	d	104	ILE
40	d	109	GLN
40	d	112	ASN
40	d	134	ASP
40	d	152	LEU
40	d	179	ILE
40	d	189	ASN

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Mol	Chain	Res	Type
41	e	156	VAL
41	e	161	ARG
41	e	187	VAL
41	e	189	VAL
41	e	191	VAL
41	e	197	VAL
41	e	201	VAL
41	e	210	ARG
41	e	213	ILE
41	e	217	MET
41	e	226	ARG
41	e	270	LEU
41	e	272	SER
41	e	288	THR
41	e	292	PHE
41	e	299	ARG
42	f	107	GLN
42	f	118	MET
42	f	119	THR
42	f	121	ASP
42	f	124	LEU
42	f	126	LEU
42	f	198	VAL
42	f	208	LYS
43	g	6	THR
43	g	10	LYS
43	g	15	ASP
43	g	25	MET
43	g	36	LYS
43	g	63	ARG
43	g	72	ASP
43	g	133	ASP
44	h	20	ARG
44	h	24	VAL
44	h	28	SER
44	h	45	ILE
44	h	46	GLU
44	h	60	VAL
44	h	69	LYS
44	h	76	THR
44	h	84	ARG
44	h	125	ILE

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Mol	Chain	Res	Type
45	i	78	PHE
45	i	89	ARG
45	i	99	GLN
45	i	102	THR
45	i	117	GLN
45	i	124	GLN
45	i	132	THR
45	i	136	GLU
45	i	143	VAL
45	i	150	LEU
45	i	168	VAL
45	i	189	VAL
45	i	196	LEU
45	i	206	SER
46	j	101	ILE
46	j	104	ARG
46	j	107	TRP
46	j	115	CYS
46	j	151	HIS
46	j	153	ASP
46	j	183	LEU
47	k	29	VAL
47	k	42	THR
47	k	45	ASP
47	k	46	VAL
47	k	49	ARG
47	k	51	VAL
47	k	83	VAL
47	k	102	ARG
47	k	114	ILE
47	k	122	VAL
48	l	8	ILE
48	l	11	THR
48	l	24	LEU
48	l	31	ARG
48	l	34	CYS
48	l	35	THR
48	l	54	ARG
48	l	78	SER
48	l	82	VAL
48	l	101	THR
49	m	50	VAL

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Mol	Chain	Res	Type
49	m	98	LEU
49	m	110	ILE
49	m	113	ASP
49	m	118	ASN
49	m	142	CYS
49	m	151	CYS
49	m	153	THR
50	n	3	ARG
50	n	5	SER
50	n	12	LYS
50	n	35	THR
50	n	37	LEU
50	n	43	ILE
50	n	49	SER
50	n	59	LEU
50	n	65	LEU
50	n	92	LEU
51	o	35	ARG
51	o	40	LEU
52	p	11	ARG
52	p	22	ILE
52	p	25	ARG
52	p	26	SER
52	p	28	ARG
52	p	29	GLU
52	p	33	LEU
52	p	48	LEU
52	p	50	VAL
52	p	66	THR
53	q	70	ASN
53	q	76	VAL
53	q	112	VAL
53	q	120	ILE
53	q	142	LYS
54	r	22	ILE
54	r	28	ILE
54	r	31	ARG
54	r	32	ASN
54	r	55	THR
54	r	62	ILE
54	r	71	ILE
55	s	22	LEU

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Mol	Chain	Res	Type
55	s	30	ILE
55	s	53	ASN
55	s	77	THR
55	s	81	ARG
56	t	99	GLU
56	t	107	VAL
56	t	121	SER
56	t	152	THR
56	t	168	GLU
56	t	173	TRP
57	u	86	VAL
57	u	90	VAL
57	u	102	ARG
57	u	124	ASN
57	u	130	LYS
57	u	131	ARG
59	w	151	ILE
61	y	82	ARG
61	y	114	VAL
61	y	122	ASP
61	y	134	VAL
61	y	140	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (93) such sidechains are listed below:

Mol	Chain	Res	Type
1	0	42	HIS
3	2	36	GLN
4	3	143	ASN
5	4	130	ASN
7	6	141	ASN
11	C	23	ASN
11	C	26	ASN
11	C	149	GLN
12	D	121	ASN
12	D	138	GLN
12	D	215	HIS
12	D	224	HIS
12	D	229	HIS
12	D	243	HIS
12	D	288	ASN
13	E	91	HIS

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Mol	Chain	Res	Type
13	E	118	GLN
13	E	171	ASN
14	F	99	ASN
14	F	158	ASN
16	H	42	GLN
17	I	90	GLN
17	I	130	ASN
18	J	205	ASN
19	K	97	ASN
20	L	73	ASN
20	L	92	ASN
21	M	133	GLN
22	N	130	GLN
23	O	18	HIS
23	O	87	HIS
24	P	81	HIS
24	P	85	GLN
24	P	93	HIS
24	P	149	HIS
24	P	162	HIS
25	Q	202	ASN
26	R	37	GLN
26	R	38	GLN
26	R	53	GLN
26	R	83	HIS
26	R	99	GLN
26	R	113	ASN
27	S	108	ASN
27	S	153	ASN
28	T	97	ASN
29	U	153	ASN
30	V	179	GLN
30	V	180	ASN
38	b	107	ASN
38	b	170	GLN
38	b	194	ASN
39	c	98	ASN
39	c	125	ASN
40	d	57	HIS
40	d	112	ASN
40	d	115	HIS
40	d	149	GLN

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Mol	Chain	Res	Type
41	e	225	HIS
42	f	160	ASN
43	g	20	ASN
44	h	19	ASN
44	h	30	ASN
45	i	138	ASN
46	j	149	HIS
46	j	151	HIS
47	k	31	HIS
48	l	111	GLN
49	m	52	ASN
49	m	57	ASN
49	m	58	ASN
49	m	87	ASN
49	m	145	GLN
49	m	149	ASN
50	n	21	HIS
50	n	48	GLN
50	n	60	HIS
50	n	72	ASN
50	n	81	HIS
51	o	18	ASN
51	o	43	HIS
53	q	98	GLN
54	r	23	GLN
55	s	8	ASN
55	s	47	HIS
55	s	69	HIS
56	t	85	GLN
57	u	126	GLN
57	u	140	ASN
58	v	258	ASN
59	w	162	GLN
59	w	168	ASN
59	w	171	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	B	120/121 (99%)	20 (16%)	0
31	W	105/106 (99%)	34 (32%)	1 (0%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
35	z	75/76 (98%)	22 (29%)	0
37	a	1483/1491 (99%)	349 (23%)	0
9	A	2794/2810 (99%)	658 (23%)	8 (0%)
All	All	4577/4604 (99%)	1083 (23%)	9 (0%)

All (1083) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
9	A	8	G
9	A	9	A
9	A	10	G
9	A	12	A
9	A	13	A
9	A	14	A
9	A	31	C
9	A	33	A
9	A	34	G
9	A	39	C
9	A	45	A
9	A	46	C
9	A	54	G
9	A	57	G
9	A	70	A
9	A	71	A
9	A	73	U
9	A	74	G
9	A	82	G
9	A	84	G
9	A	94	A
9	A	97	A
9	A	98	G
9	A	99	A
9	A	100	G
9	A	116	A
9	A	117	A
9	A	118	U
9	A	123	C
9	A	130	U
9	A	131	C
9	A	132	G
9	A	143	G
9	A	144	A

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Mol	Chain	Res	Type
9	A	149	A
9	A	158	C
9	A	159	A
9	A	160	A
9	A	163	G
9	A	181	A
9	A	184	A
9	A	200	G
9	A	201	A
9	A	206	A
9	A	207	A
9	A	208	A
9	A	209	G
9	A	216	C
9	A	218	A
9	A	224	G
9	A	226	A
9	A	230	G
9	A	233	G
9	A	249	C
9	A	250	A
9	A	251	G
9	A	252	C
9	A	260	G
9	A	266	A
9	A	275	U
9	A	276	G
9	A	277	G
9	A	282	G
9	A	284	A
9	A	286	U
9	A	287	A
9	A	288	C
9	A	294	U
9	A	297	U
9	A	298	G
9	A	299	C
9	A	304	A
9	A	316	G
9	A	320	U
9	A	326	A
9	A	332	G

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Mol	Chain	Res	Type
9	A	333	A
9	A	338	G
9	A	340	A
9	A	362	A
9	A	363	C
9	A	364	U
9	A	368	U
9	A	377	G
9	A	379	C
9	A	383	A
9	A	384	G
9	A	398	G
9	A	415	U
9	A	416	C
9	A	417	A
9	A	418	G
9	A	423	G
9	A	424	A
9	A	436	G
9	A	448	C
9	A	452	G
9	A	453	U
9	A	454	G
9	A	467	G
9	A	468	U
9	A	469	A
9	A	480	G
9	A	485	G
9	A	487	U
9	A	491	A
9	A	492	A
9	A	493	G
9	A	502	U
9	A	507	G
9	A	519	A
9	A	520	C
9	A	529	G
9	A	539	A
9	A	540	A
9	A	541	G
9	A	542	C
9	A	543	A

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Mol	Chain	Res	Type
9	A	544	G
9	A	549	A
9	A	554	G
9	A	557	C
9	A	558	A
9	A	559	G
9	A	560	A
9	A	561	C
9	A	565	G
9	A	573	G
9	A	582	A
9	A	583	G
9	A	585	A
9	A	593	G
9	A	597	C
9	A	609	G
9	A	610	G
9	A	612	U
9	A	613	U
9	A	614	G
9	A	623	A
9	A	630	C
9	A	632	G
9	A	633	A
9	A	635	C
9	A	639	A
9	A	643	A
9	A	645	A
9	A	646	G
9	A	649	A
9	A	657	U
9	A	658	A
9	A	664	A
9	A	665	U
9	A	667	G
9	A	675	U
9	A	680	G
9	A	681	A
9	A	688	C
9	A	696	A
9	A	697	U
9	A	701	U

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Mol	Chain	Res	Type
9	A	713	A
9	A	722	G
9	A	724	G
9	A	727	A
9	A	728	A
9	A	729	A
9	A	730	C
9	A	731	U
9	A	734	G
9	A	740	G
9	A	741	U
9	A	749	G
9	A	758	U
9	A	759	G
9	A	760	A
9	A	768	G
9	A	775	A
9	A	776	G
9	A	782	G
9	A	786	G
9	A	787	G
9	A	788	G
9	A	793	A
9	A	795	U
9	A	803	G
9	A	811	A
9	A	813	C
9	A	816	G
9	A	817	C
9	A	823	C
9	A	838	U
9	A	839	G
9	A	853	G
9	A	856	U
9	A	857	G
9	A	858	G
9	A	859	A
9	A	866	G
9	A	869	G
9	A	879	G
9	A	880	U
9	A	888	C

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Mol	Chain	Res	Type
9	A	890	G
9	A	893	C
9	A	894	G
9	A	902	G
9	A	905	A
9	A	906	C
9	A	907	C
9	A	910	A
9	A	916	G
9	A	919	A
9	A	924	U
9	A	937	U
9	A	938	G
9	A	946	A
9	A	947	A
9	A	948	U
9	A	974	G
9	A	981	G
9	A	989	G
9	A	993	C
9	A	996	C
9	A	1001	A
9	A	1002	G
9	A	1007	A
9	A	1009	A
9	A	1011	A
9	A	1017	G
9	A	1018	A
9	A	1024	A
9	A	1038	A
9	A	1039	A
9	A	1040	U
9	A	1041	G
9	A	1045	G
9	A	1050	G
9	A	1051	U
9	A	1052	G
9	A	1054	U
9	A	1055	A
9	A	1061	G
9	A	1062	G
9	A	1065	G

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Mol	Chain	Res	Type
9	A	1070	G
9	A	1071	C
9	A	1072	A
9	A	1075	G
9	A	1098	A
9	A	1099	G
9	A	1116	A
9	A	1118	U
9	A	1138	G
9	A	1140	G
9	A	1143	C
9	A	1144	U
9	A	1147	U
9	A	1155	A
9	A	1160	A
9	A	1162	C
9	A	1163	G
9	A	1166	G
9	A	1169	A
9	A	1170	A
9	A	1173	G
9	A	1190	G
9	A	1196	A
9	A	1197	A
9	A	1198	A
9	A	1199	A
9	A	1202	A
9	A	1218	G
9	A	1221	C
9	A	1226	U
9	A	1231	G
9	A	1239	C
9	A	1240	G
9	A	1241	U
9	A	1245	U
9	A	1248	G
9	A	1253	G
9	A	1254	U
9	A	1255	U
9	A	1257	G
9	A	1259	C
9	A	1261	A

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Mol	Chain	Res	Type
9	A	1271	G
9	A	1273	G
9	A	1274	A
9	A	1277	G
9	A	1289	A
9	A	1292	G
9	A	1293	C
9	A	1295	A
9	A	1296	A
9	A	1301	G
9	A	1310	C
9	A	1315	G
9	A	1321	A
9	A	1322	A
9	A	1327	U
9	A	1333	U
9	A	1334	U
9	A	1342	A
9	A	1353	A
9	A	1357	A
9	A	1359	G
9	A	1366	C
9	A	1371	C
9	A	1380	A
9	A	1381	G
9	A	1386	A
9	A	1399	A
9	A	1400	U
9	A	1402	G
9	A	1405	A
9	A	1416	A
9	A	1417	U
9	A	1423	U
9	A	1424	A
9	A	1426	U
9	A	1431	C
9	A	1432	U
9	A	1433	U
9	A	1435	U
9	A	1436	U
9	A	1437	G
9	A	1444	A

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Mol	Chain	Res	Type
9	A	1446	G
9	A	1449	C
9	A	1450	G
9	A	1456	G
9	A	1458	C
9	A	1465	A
9	A	1472	A
9	A	1476	G
9	A	1477	G
9	A	1480	A
9	A	1483	G
9	A	1484	G
9	A	1485	U
9	A	1488	A
9	A	1493	C
9	A	1494	G
9	A	1497	A
9	A	1501	G
9	A	1507	G
9	A	1513	C
9	A	1519	A
9	A	1520	A
9	A	1521	G
9	A	1523	A
9	A	1524	G
9	A	1526	G
9	A	1527	G
9	A	1528	U
9	A	1533	A
9	A	1544	A
9	A	1557	G
9	A	1558	U
9	A	1559	A
9	A	1563	G
9	A	1566	G
9	A	1568	U
9	A	1570	C
9	A	1571	G
9	A	1588	U
9	A	1594	A
9	A	1600	A
9	A	1603	A

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Mol	Chain	Res	Type
9	A	1612	A
9	A	1620	U
9	A	1621	C
9	A	1629	G
9	A	1630	G
9	A	1632	U
9	A	1633	A
9	A	1634	C
9	A	1635	C
9	A	1642	C
9	A	1643	G
9	A	1644	A
9	A	1645	A
9	A	1649	G
9	A	1666	A
9	A	1670	A
9	A	1682	C
9	A	1683	G
9	A	1684	C
9	A	1685	G
9	A	1687	G
9	A	1710	G
9	A	1711	C
9	A	1734	A
9	A	1746	C
9	A	1750	C
9	A	1760	G
9	A	1762	C
9	A	1774	G
9	A	1778	G
9	A	1783	A
9	A	1791	C
9	A	1801	A
9	A	1810	C
9	A	1812	A
9	A	1818	U
9	A	1819	A
9	A	1821	G
9	A	1826	U
9	A	1833	G
9	A	1836	C
9	A	1839	A

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Mol	Chain	Res	Type
9	A	1849	A
9	A	1858	A
9	A	1866	G
9	A	1870	U
9	A	1877	C
9	A	1882	U
9	A	1883	G
9	A	1884	A
9	A	1885	C
9	A	1900	C
9	A	1914	A
9	A	1920	G
9	A	1923	C
9	A	1926	A
9	A	1927	A
9	A	1928	C
9	A	1930	A
9	A	1931	U
9	A	1933	A
9	A	1940	U
9	A	1943	G
9	A	1944	G
9	A	1950	A
9	A	1952	A
9	A	1969	U
9	A	1974	A
9	A	1975	C
9	A	1980	A
9	A	1981	C
9	A	1984	A
9	A	1985	A
9	A	1986	G
9	A	2005	U
9	A	2006	G
9	A	2007	U
9	A	2011	G
9	A	2015	A
9	A	2017	A
9	A	2034	C
9	A	2035	A
9	A	2037	G
9	A	2044	A

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Mol	Chain	Res	Type
9	A	2045	A
9	A	2046	G
9	A	2047	A
9	A	2053	A
9	A	2057	C
9	A	2064	C
9	A	2065	U
9	A	2069	C
9	A	2073	A
9	A	2074	A
9	A	2075	G
9	A	2076	A
9	A	2077	C
9	A	2082	U
9	A	2083	G
9	A	2091	A
9	A	2102	G
9	A	2103	G
9	A	2107	G
9	A	2115	G
9	A	2116	C
9	A	2119	U
9	A	2125	C
9	A	2126	G
9	A	2127	C
9	A	2129	G
9	A	2130	C
9	A	2131	U
9	A	2132	U
9	A	2133	A
9	A	2137	G
9	A	2139	A
9	A	2140	A
9	A	2145	A
9	A	2146	A
9	A	2147	G
9	A	2148	A
9	A	2151	G
9	A	2159	C
9	A	2160	C
9	A	2161	G
9	A	2162	G

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Mol	Chain	Res	Type
9	A	2173	G
9	A	2175	C
9	A	2176	A
9	A	2177	U
9	A	2178	C
9	A	2179	A
9	A	2181	U
9	A	2182	G
9	A	2183	A
9	A	2184	G
9	A	2185	A
9	A	2186	U
9	A	2187	A
9	A	2191	C
9	A	2192	U
9	A	2193	C
9	A	2195	G
9	A	2199	G
9	A	2201	G
9	A	2202	C
9	A	2204	A
9	A	2205	G
9	A	2206	A
9	A	2209	U
9	A	2212	A
9	A	2213	A
9	A	2217	U
9	A	2219	U
9	A	2220	G
9	A	2223	A
9	A	2227	C
9	A	2229	U
9	A	2230	A
9	A	2232	G
9	A	2242	A
9	A	2243	C
9	A	2254	A
9	A	2255	G
9	A	2256	A
9	A	2260	U
9	A	2266	U
9	A	2267	G

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Mol	Chain	Res	Type
9	A	2269	G
9	A	2296	G
9	A	2297	G
9	A	2300	U
9	A	2303	A
9	A	2304	A
9	A	2305	A
9	A	2315	G
9	A	2316	G
9	A	2322	A
9	A	2323	C
9	A	2324	G
9	A	2325	G
9	A	2338	G
9	A	2339	A
9	A	2341	U
9	A	2342	G
9	A	2343	C
9	A	2344	A
9	A	2349	C
9	A	2351	G
9	A	2352	A
9	A	2364	C
9	A	2367	C
9	A	2372	C
9	A	2375	A
9	A	2378	C
9	A	2400	G
9	A	2402	C
9	A	2408	G
9	A	2419	G
9	A	2423	A
9	A	2428	A
9	A	2442	A
9	A	2444	C
9	A	2446	G
9	A	2447	A
9	A	2448	U
9	A	2452	A
9	A	2457	C
9	A	2458	U
9	A	2462	G

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Mol	Chain	Res	Type
9	A	2464	G
9	A	2465	A
9	A	2466	U
9	A	2467	A
9	A	2481	C
9	A	2487	G
9	A	2493	A
9	A	2495	A
9	A	2507	G
9	A	2508	U
9	A	2509	U
9	A	2518	C
9	A	2519	G
9	A	2520	A
9	A	2521	U
9	A	2522	G
9	A	2523	U
9	A	2524	C
9	A	2526	G
9	A	2530	U
9	A	2535	C
9	A	2542	G
9	A	2546	G
9	A	2552	U
9	A	2569	U
9	A	2571	U
9	A	2576	C
9	A	2579	U
9	A	2583	A
9	A	2584	G
9	A	2589	A
9	A	2590	C
9	A	2591	G
9	A	2593	G
9	A	2594	A
9	A	2595	G
9	A	2599	G
9	A	2601	U
9	A	2602	U
9	A	2603	C
9	A	2619	A
9	A	2625	G

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Mol	Chain	Res	Type
9	A	2626	U
9	A	2627	C
9	A	2630	U
9	A	2637	U
9	A	2640	G
9	A	2646	U
9	A	2649	A
9	A	2671	A
9	A	2672	G
9	A	2680	G
9	A	2688	A
9	A	2689	A
9	A	2696	A
9	A	2702	G
9	A	2706	U
9	A	2707	A
9	A	2708	C
9	A	2719	G
9	A	2721	C
9	A	2729	A
9	A	2740	G
9	A	2744	A
9	A	2751	A
9	A	2753	C
9	A	2762	G
9	A	2766	A
9	A	2768	A
9	A	2769	G
9	A	2770	C
9	A	2774	U
9	A	2776	A
9	A	2778	U
9	A	2783	A
9	A	2784	G
9	A	2787	C
9	A	2796	A
10	B	2	A
10	B	10	G
10	B	15	A
10	B	16	G
10	B	19	G
10	B	25	G

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Mol	Chain	Res	Type
10	B	31	C
10	B	37	U
10	B	38	C
10	B	39	C
10	B	41	U
10	B	42	C
10	B	45	G
10	B	57	U
10	B	68	G
10	B	85	G
10	B	93	C
10	B	107	G
10	B	110	C
10	B	111	G
31	W	3	A
31	W	4	G
31	W	5	A
31	W	14	G
31	W	16	G
31	W	17	A
31	W	20	C
31	W	21	G
31	W	26	G
31	W	28	U
31	W	29	U
31	W	30	A
31	W	31	U
31	W	32	C
31	W	33	A
31	W	34	U
31	W	35	U
31	W	37	C
31	W	38	G
31	W	40	U
31	W	59	C
31	W	65	U
31	W	71	C
31	W	72	A
31	W	77	A
31	W	79	G
31	W	83	C
31	W	84	C

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Mol	Chain	Res	Type
31	W	90	G
31	W	95	A
31	W	96	C
31	W	97	A
31	W	99	A
31	W	103	G
35	z	3	C
35	z	16	U
35	z	19	G
35	z	20	U
35	z	21	A
35	z	25	C
35	z	31	A
35	z	32	U
35	z	33	U
35	z	34	G
35	z	36	A
35	z	37	A
35	z	40	C
35	z	41	C
35	z	42	C
35	z	52	G
35	z	59	U
35	z	70	G
35	z	71	G
35	z	73	A
35	z	75	C
35	z	76	A
37	a	2	C
37	a	3	U
37	a	5	A
37	a	6	U
37	a	7	G
37	a	8	G
37	a	10	G
37	a	14	U
37	a	20	C
37	a	23	G
37	a	31	U
37	a	32	G
37	a	33	A
37	a	39	G

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Mol	Chain	Res	Type
37	a	40	G
37	a	45	A
37	a	48	C
37	a	49	U
37	a	50	U
37	a	52	A
37	a	53	C
37	a	55	C
37	a	60	A
37	a	70	G
37	a	72	A
37	a	73	A
37	a	74	G
37	a	76	G
37	a	77	G
37	a	78	U
37	a	82	U
37	a	83	C
37	a	85	A
37	a	88	G
37	a	90	C
37	a	103	A
37	a	104	A
37	a	105	C
37	a	106	G
37	a	113	A
37	a	114	A
37	a	115	C
37	a	127	A
37	a	130	G
37	a	135	A
37	a	142	G
37	a	147	C
37	a	152	G
37	a	166	G
37	a	167	G
37	a	174	A
37	a	179	A
37	a	180	A
37	a	183	A
37	a	188	U
37	a	191	G

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Mol	Chain	Res	Type
37	a	196	A
37	a	211	C
37	a	216	U
37	a	218	G
37	a	222	G
37	a	230	G
37	a	233	A
37	a	237	G
37	a	238	C
37	a	252	G
37	a	260	G
37	a	264	G
37	a	269	A
37	a	289	G
37	a	292	A
37	a	299	C
37	a	300	A
37	a	303	G
37	a	315	A
37	a	317	G
37	a	323	C
37	a	324	A
37	a	325	G
37	a	327	A
37	a	338	U
37	a	339	U
37	a	343	C
37	a	344	A
37	a	349	G
37	a	355	G
37	a	358	U
37	a	361	C
37	a	363	G
37	a	364	A
37	a	368	A
37	a	377	G
37	a	382	C
37	a	383	A
37	a	384	G
37	a	392	A
37	a	393	C
37	a	398	C

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Mol	Chain	Res	Type
37	a	399	G
37	a	400	U
37	a	411	U
37	a	415	G
37	a	416	G
37	a	417	A
37	a	423	A
37	a	424	G
37	a	425	C
37	a	426	A
37	a	429	G
37	a	432	G
37	a	433	G
37	a	434	U
37	a	439	G
37	a	443	A
37	a	444	A
37	a	453	G
37	a	454	G
37	a	457	A
37	a	459	C
37	a	462	U
37	a	464	U
37	a	469	G
37	a	472	G
37	a	475	G
37	a	478	G
37	a	479	U
37	a	481	A
37	a	494	A
37	a	495	A
37	a	507	A
37	a	510	G
37	a	511	A
37	a	512	U
37	a	520	A
37	a	521	A
37	a	524	C
37	a	525	G
37	a	527	C
37	a	534	U
37	a	544	A

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Mol	Chain	Res	Type
37	a	545	G
37	a	555	A
37	a	579	A
37	a	597	A
37	a	598	G
37	a	600	U
37	a	613	G
37	a	623	A
37	a	634	G
37	a	635	A
37	a	637	C
37	a	658	G
37	a	659	A
37	a	660	A
37	a	670	A
37	a	671	C
37	a	672	G
37	a	690	G
37	a	696	C
37	a	697	A
37	a	703	A
37	a	708	G
37	a	725	A
37	a	735	A
37	a	741	U
37	a	742	A
37	a	757	G
37	a	762	A
37	a	763	A
37	a	765	C
37	a	767	A
37	a	768	U
37	a	775	U
37	a	776	A
37	a	780	G
37	a	784	U
37	a	791	C
37	a	792	G
37	a	793	A
37	a	794	C
37	a	796	C
37	a	797	G

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Mol	Chain	Res	Type
37	a	798	U
37	a	799	G
37	a	821	A
37	a	844	U
37	a	863	A
37	a	875	G
37	a	876	G
37	a	883	C
37	a	891	G
37	a	909	U
37	a	915	G
37	a	918	A
37	a	920	G
37	a	921	C
37	a	924	A
37	a	925	G
37	a	926	A
37	a	941	U
37	a	942	G
37	a	943	A
37	a	944	C
37	a	945	A
37	a	948	C
37	a	953	A
37	a	958	U
37	a	961	U
37	a	963	A
37	a	966	G
37	a	969	A
37	a	972	G
37	a	973	G
37	a	974	U
37	a	975	G
37	a	976	C
37	a	978	U
37	a	979	U
37	a	980	C
37	a	981	G
37	a	982	G
37	a	985	A
37	a	986	C
37	a	992	C

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Mol	Chain	Res	Type
37	a	1002	G
37	a	1003	C
37	a	1004	A
37	a	1014	U
37	a	1019	U
37	a	1033	G
37	a	1034	U
37	a	1041	A
37	a	1043	G
37	a	1044	U
37	a	1050	A
37	a	1066	G
37	a	1073	G
37	a	1075	U
37	a	1077	C
37	a	1078	C
37	a	1079	A
37	a	1080	A
37	a	1081	C
37	a	1082	G
37	a	1084	U
37	a	1085	G
37	a	1086	A
37	a	1088	U
37	a	1089	U
37	a	1091	G
37	a	1092	G
37	a	1095	C
37	a	1099	G
37	a	1100	A
37	a	1107	U
37	a	1114	G
37	a	1115	A
37	a	1116	U
37	a	1119	G
37	a	1131	U
37	a	1132	G
37	a	1134	G
37	a	1137	U
37	a	1144	A
37	a	1145	A
37	a	1149	A

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Mol	Chain	Res	Type
37	a	1150	U
37	a	1151	C
37	a	1160	U
37	a	1161	A
37	a	1162	U
37	a	1163	G
37	a	1169	G
37	a	1174	C
37	a	1175	A
37	a	1184	A
37	a	1186	A
37	a	1187	A
37	a	1188	U
37	a	1189	G
37	a	1198	A
37	a	1204	U
37	a	1205	C
37	a	1206	G
37	a	1208	G
37	a	1217	A
37	a	1223	A
37	a	1227	A
37	a	1228	A
37	a	1229	C
37	a	1233	A
37	a	1235	A
37	a	1242	U
37	a	1244	C
37	a	1245	U
37	a	1246	C
37	a	1247	A
37	a	1248	G
37	a	1249	U
37	a	1250	U
37	a	1253	G
37	a	1265	C
37	a	1266	A
37	a	1267	A
37	a	1268	C
37	a	1270	C
37	a	1271	G
37	a	1279	G

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Mol	Chain	Res	Type
37	a	1280	A
37	a	1301	G
37	a	1311	C
37	a	1312	A
37	a	1317	G
37	a	1319	G
37	a	1322	G
37	a	1328	G
37	a	1330	U
37	a	1346	C
37	a	1347	A
37	a	1363	U
37	a	1368	G
37	a	1371	G
37	a	1378	C
37	a	1390	A
37	a	1391	C
37	a	1395	A
37	a	1400	C
37	a	1401	A
37	a	1402	A
37	a	1403	G
37	a	1404	G
37	a	1405	A
37	a	1406	G
37	a	1416	G
37	a	1417	A
37	a	1418	A
37	a	1419	G
37	a	1436	G
37	a	1440	G
37	a	1441	A
37	a	1446	G
37	a	1454	G
37	a	1455	U
37	a	1456	A
37	a	1466	G
37	a	1469	G
37	a	1478	G
37	a	1479	G
37	a	1482	C

All (9) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
9	A	486	G
9	A	548	G
9	A	556	C
9	A	795	U
9	A	1520	A
9	A	2035	A
9	A	2447	A
9	A	2602	U
31	W	77	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 781 ligands modelled in this entry, 781 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
36	8	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	8	1068:UNK	C	1101:UNK	N	66.30
1	8	1143:UNK	C	1201:UNK	N	11.98

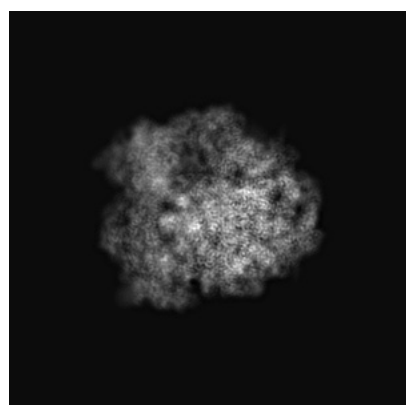
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3533. These allow visual inspection of the internal detail of the map and identification of artifacts.

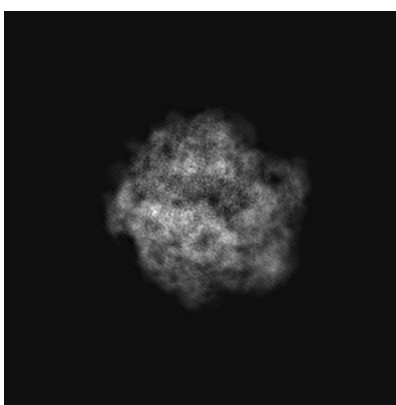
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

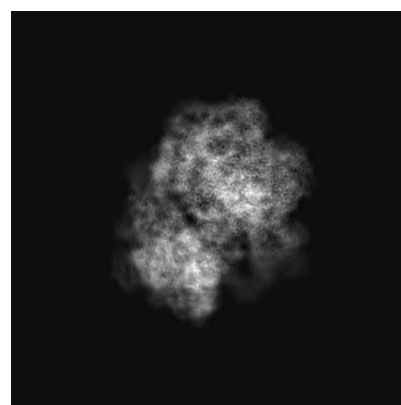
6.1.1 Primary map



X



Y

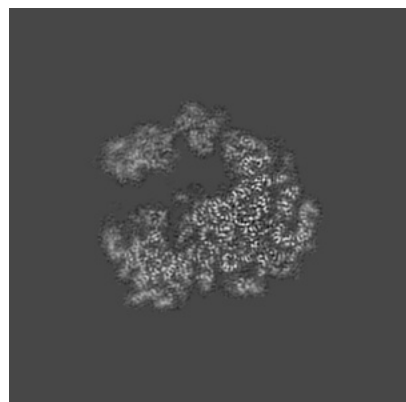


Z

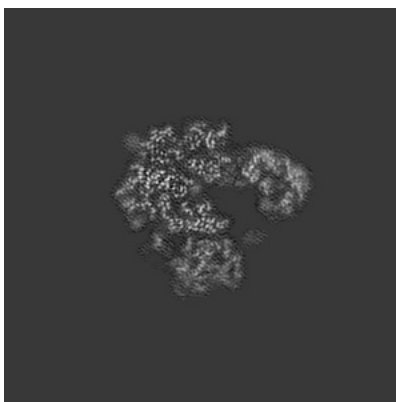
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

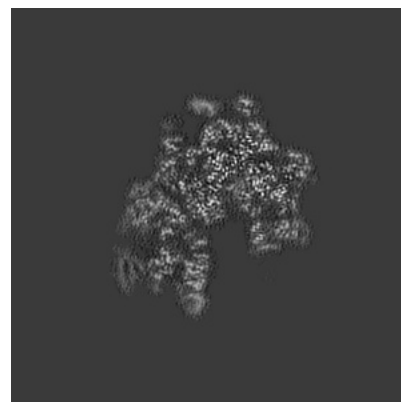
6.2.1 Primary map



X Index: 160



Y Index: 160

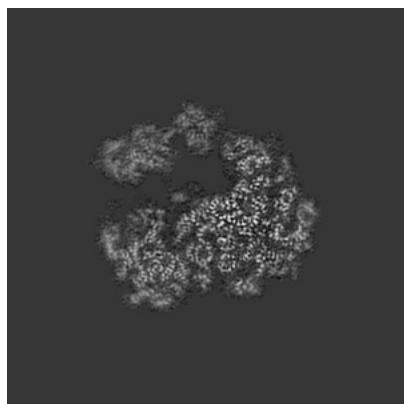


Z Index: 160

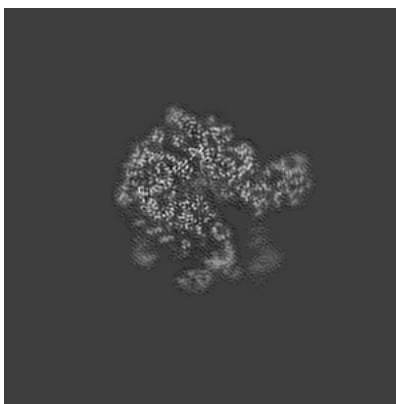
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

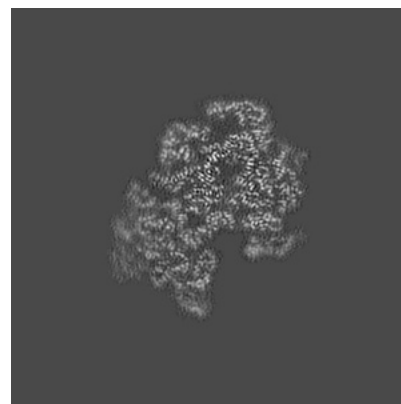
6.3.1 Primary map



X Index: 159



Y Index: 173

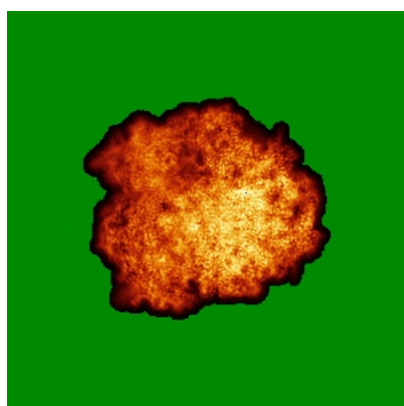


Z Index: 148

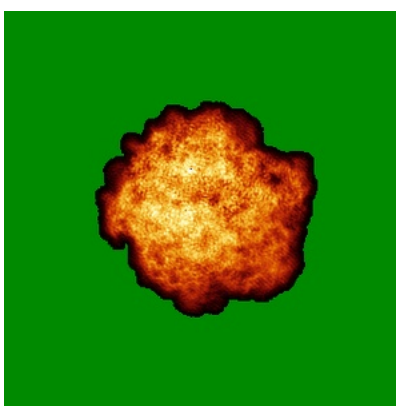
The images above show the largest variance slices of the map in three orthogonal directions.

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

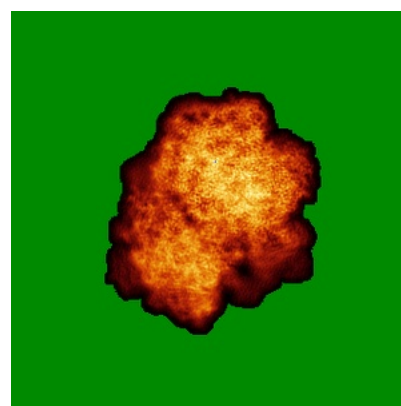
6.4.1 Primary map



X



Y

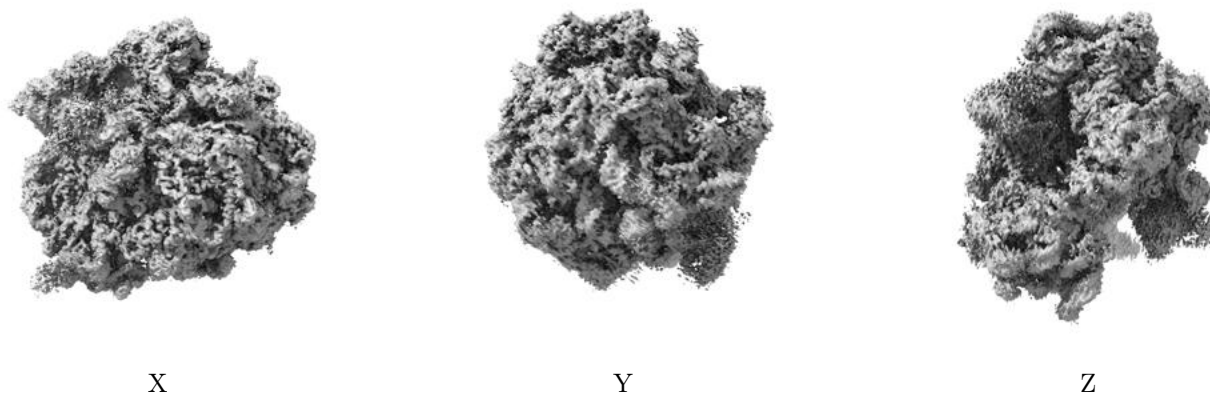


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.06. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

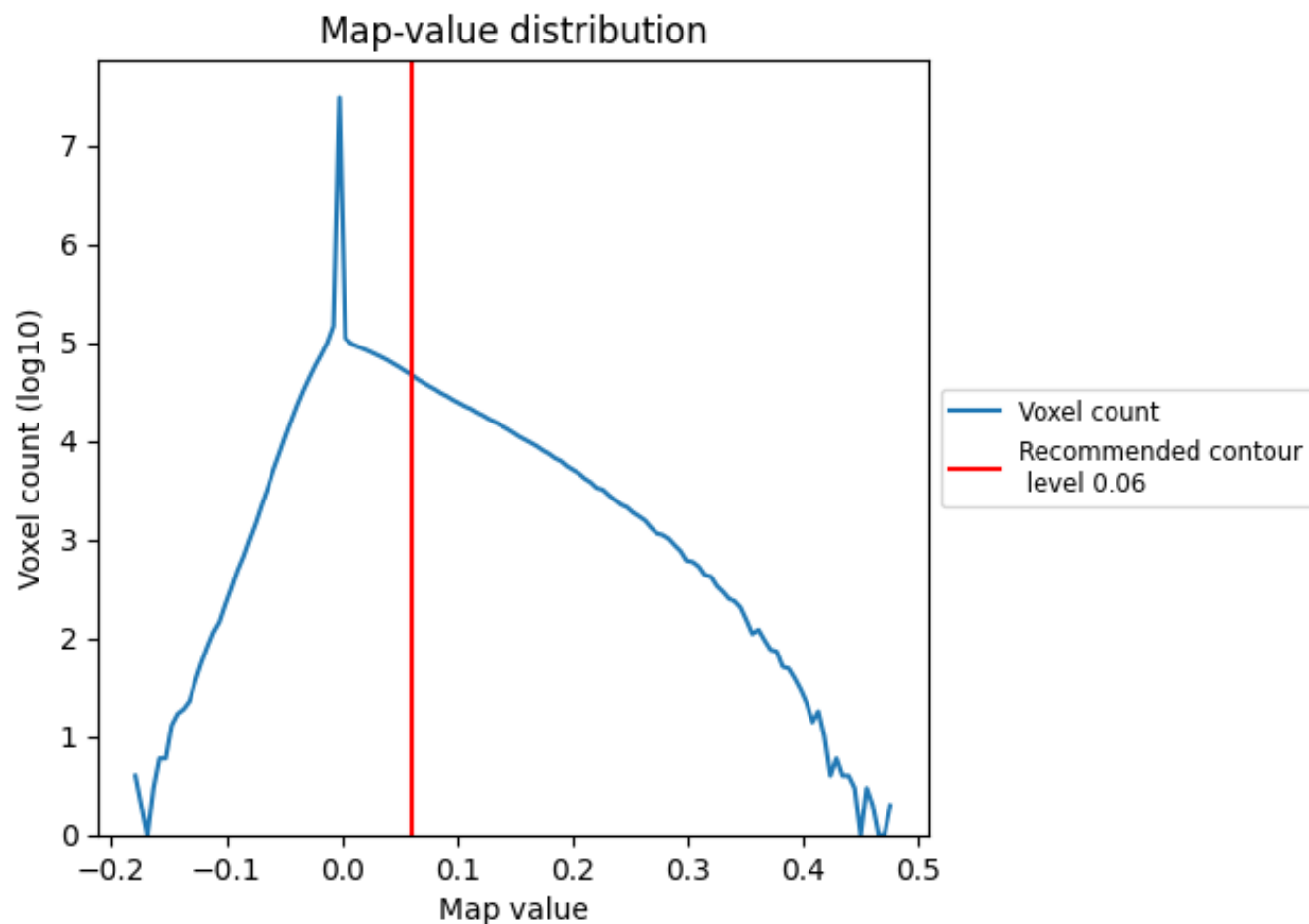
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

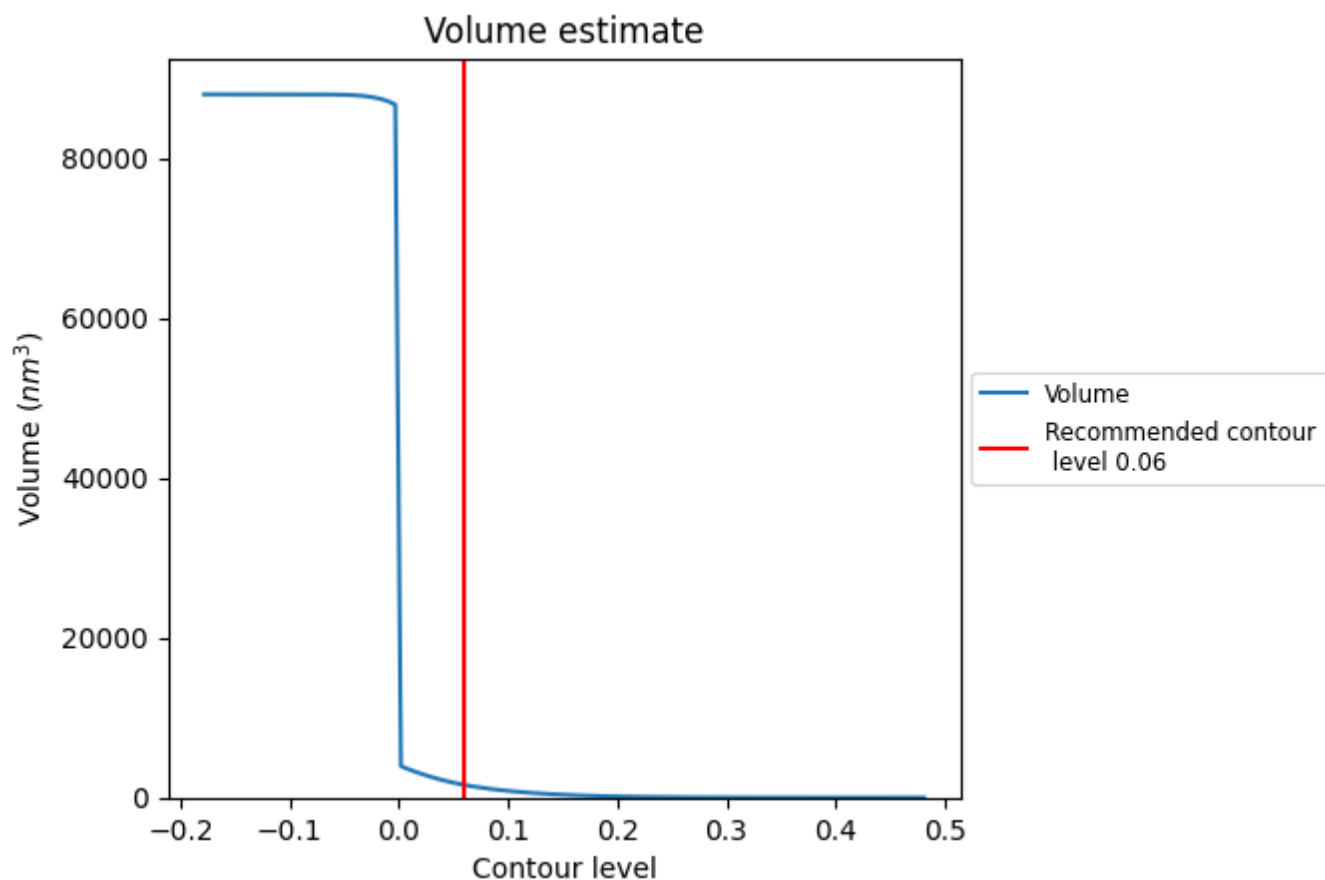
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

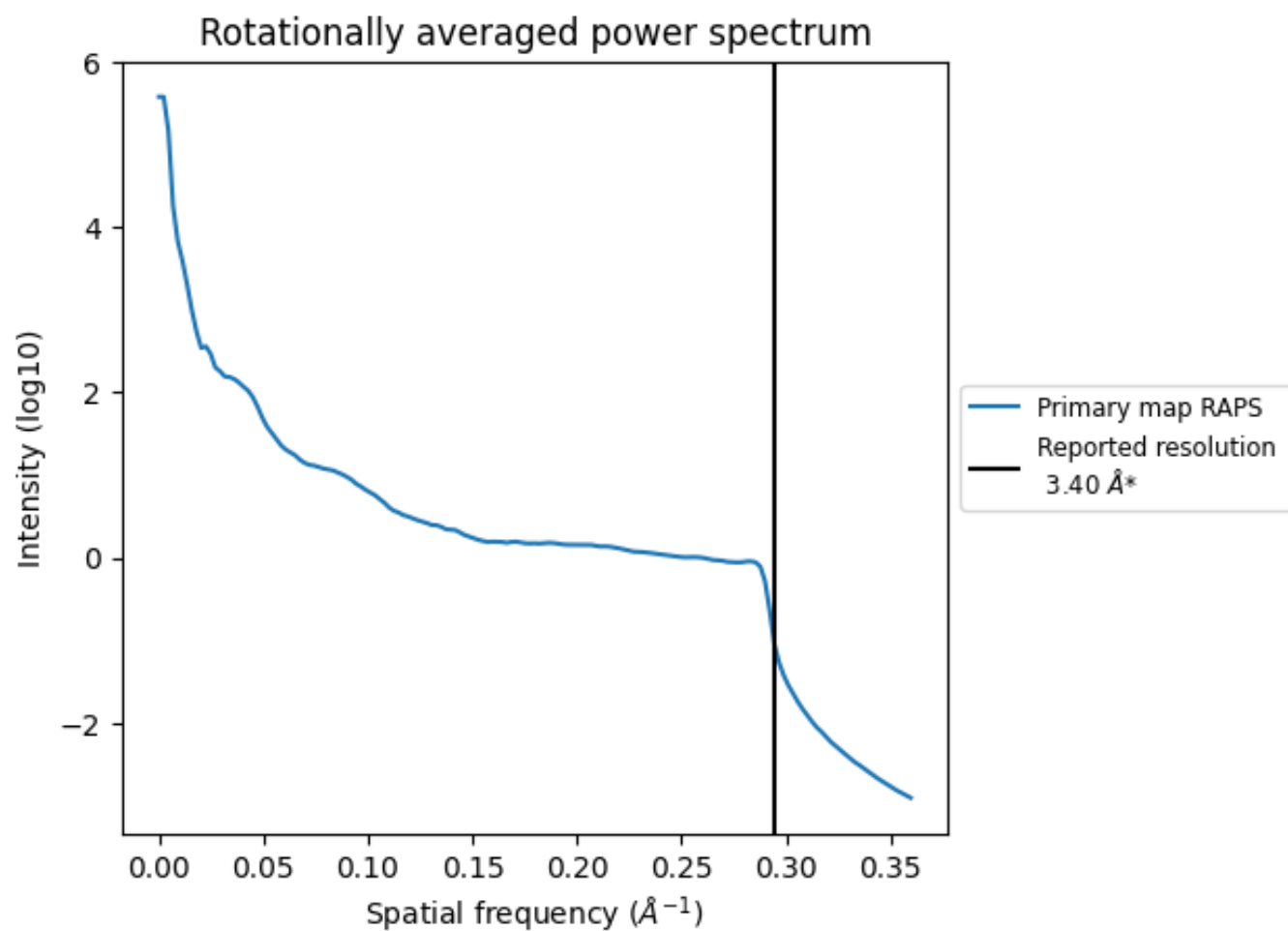
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1578 nm^3 ; this corresponds to an approximate mass of 1425 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 ⓘ

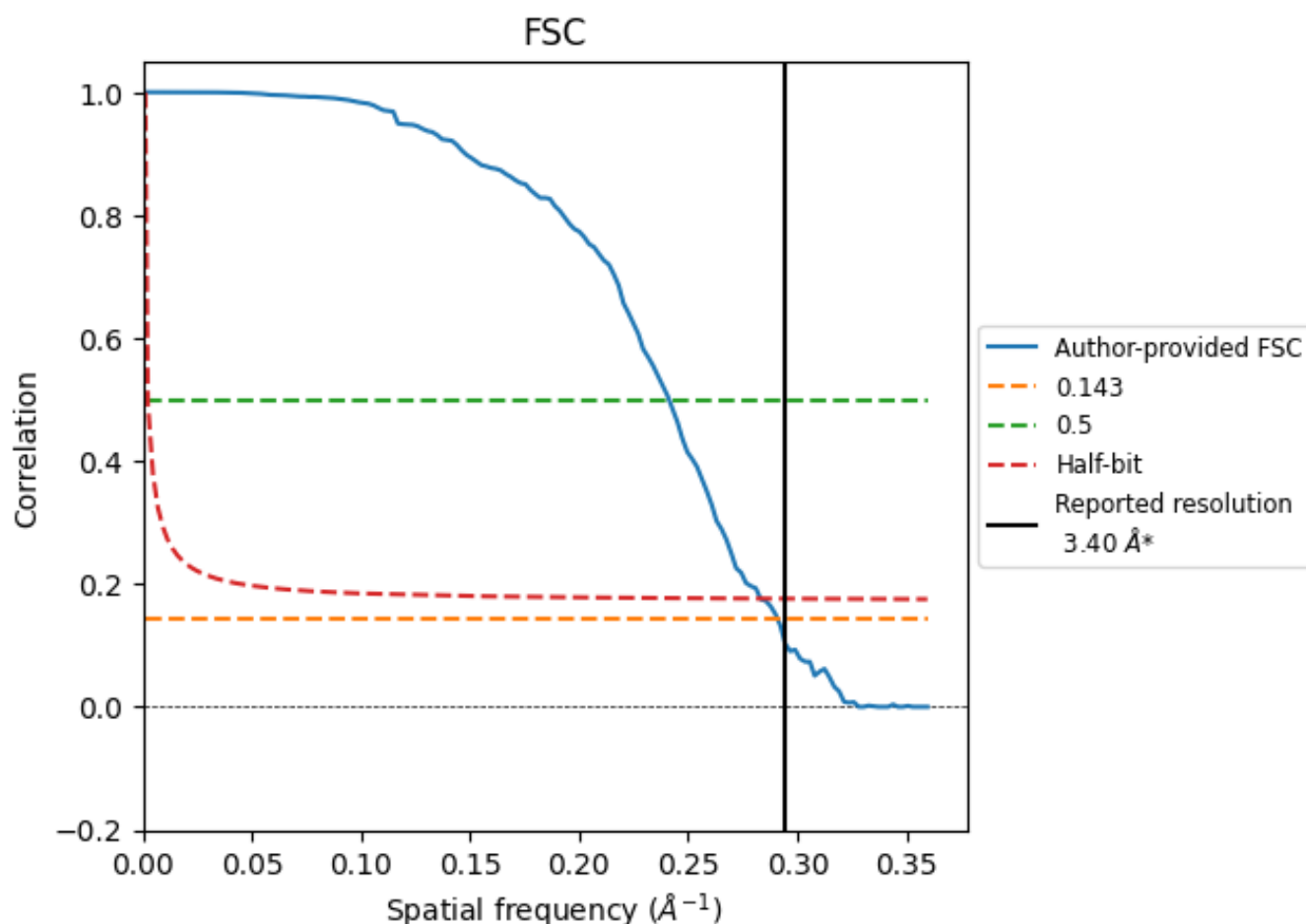


*Reported resolution corresponds to spatial frequency of 0.294 $\text{\AA}^{-1}$

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 0.294 Å⁻¹

8.2 Resolution estimates [i](#)

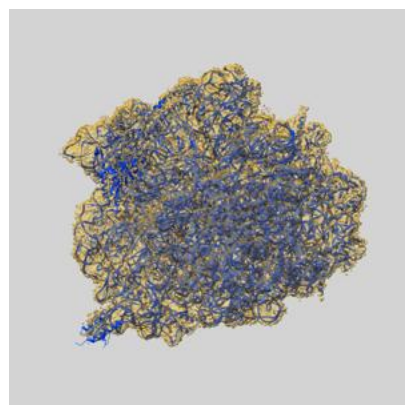
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	3.44	4.15	3.53
Unmasked-calculated*	-	-	-

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

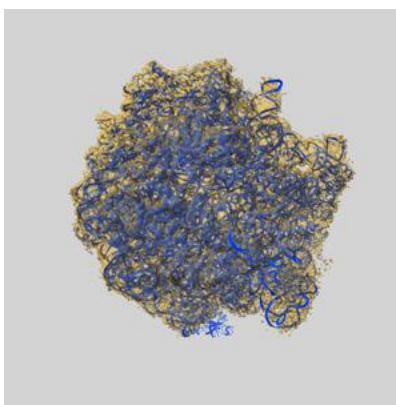
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-3533 and PDB model 5MMM. Per-residue inclusion information can be found in section 3 on page 17.

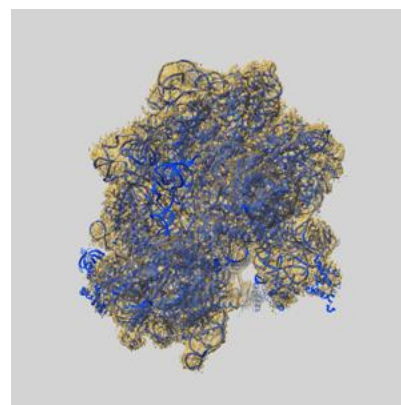
9.1 Map-model overlay [i](#)



X



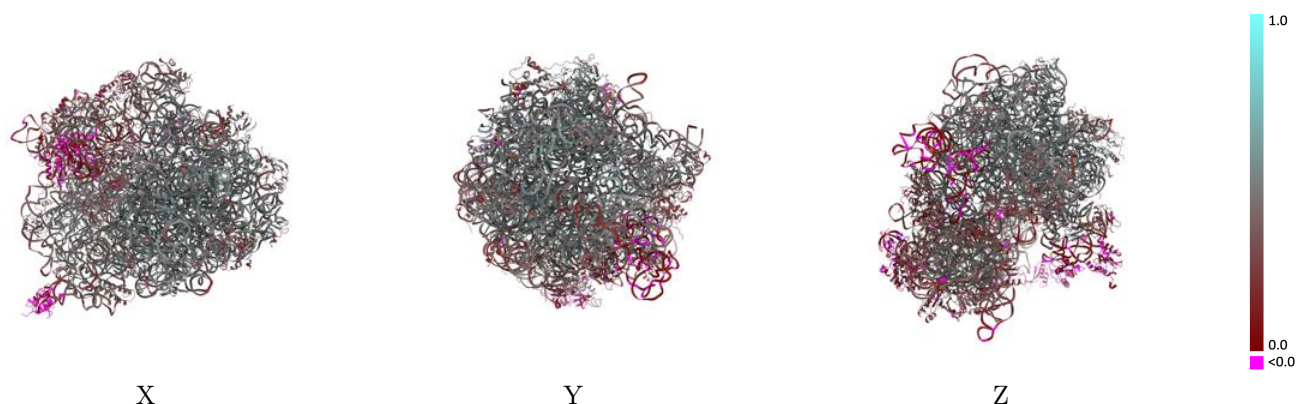
Y



Z

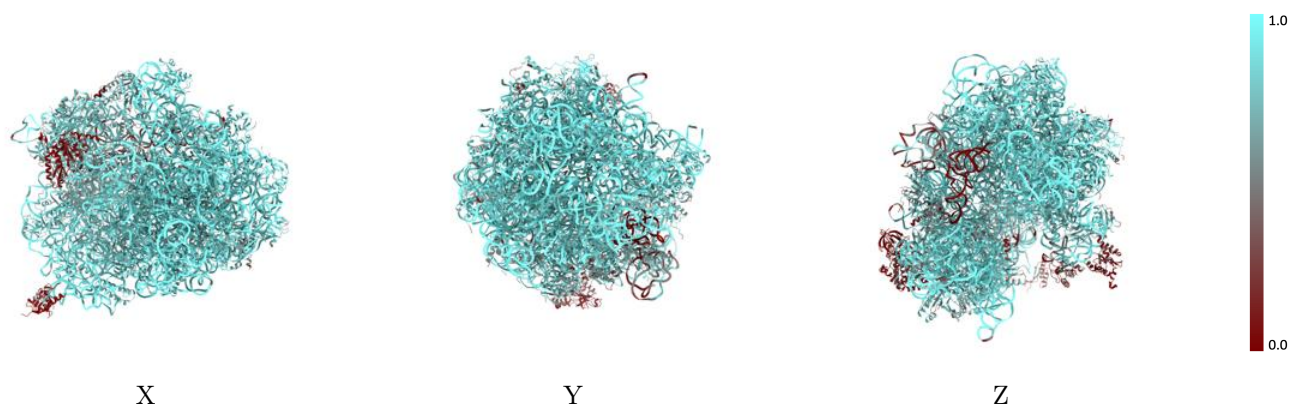
The images above show the 3D surface view of the map at the recommended contour level 0.06 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



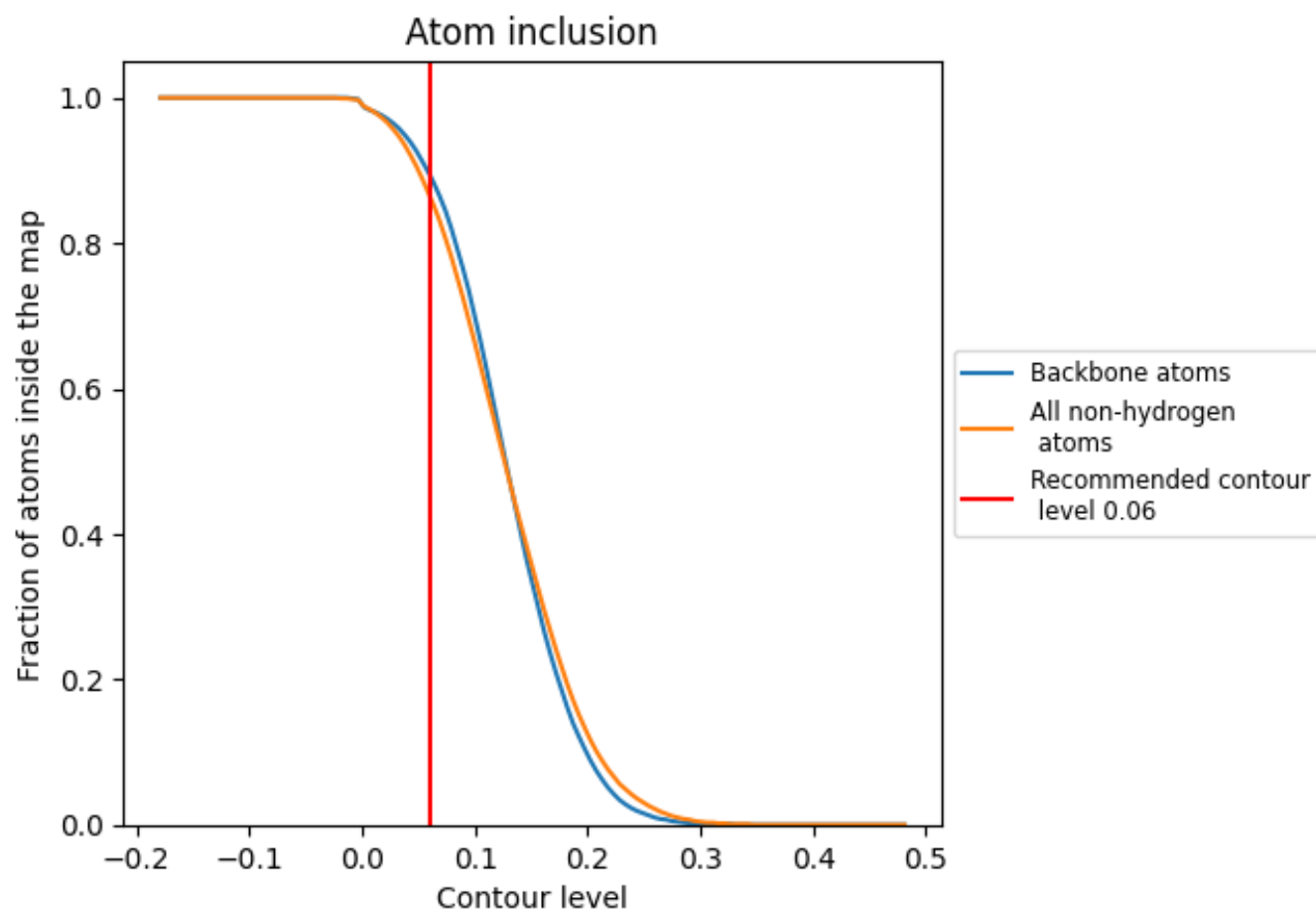
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.06).

9.4 Atom inclusion ⓘ



At the recommended contour level, 89% of all backbone atoms, 86% 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 (0.06) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8650	 0.4060
0	 0.5680	 0.1880
1	 0.8880	 0.4900
2	 0.8350	 0.4440
3	 0.8740	 0.5230
4	 0.8820	 0.5190
5	 0.8410	 0.4480
6	 0.7960	 0.4120
7	 0.8940	 0.4790
8	 0.0620	 0.0540
A	 0.9470	 0.4530
B	 0.9780	 0.4150
C	 0.8450	 0.4740
D	 0.8890	 0.4860
E	 0.8680	 0.4720
F	 0.7500	 0.3180
G	 0.7990	 0.3340
H	 0.5700	 0.3640
I	 0.1380	 0.0550
J	 0.2470	 0.0420
K	 0.8780	 0.4710
L	 0.8160	 0.4730
M	 0.8820	 0.4570
N	 0.6390	 0.3880
O	 0.9050	 0.4980
P	 0.8780	 0.4120
Q	 0.8480	 0.4600
R	 0.8990	 0.4970
S	 0.8360	 0.4410
T	 0.8380	 0.4460
U	 0.8200	 0.4390
V	 0.8270	 0.4310
W	 0.9750	 0.4680
X	 0.8790	 0.4610
Y	 0.8550	 0.4770



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Chain	Atom inclusion	Q-score
Z	 0.7990	 0.3890
a	 0.9670	 0.4080
b	 0.2830	 0.1970
c	 0.7350	 0.3250
d	 0.7810	 0.3520
e	 0.7450	 0.3810
f	 0.7000	 0.2920
g	 0.5710	 0.2520
h	 0.7480	 0.3400
i	 0.7890	 0.3030
j	 0.7800	 0.3140
k	 0.7790	 0.3370
l	 0.7980	 0.4510
m	 0.7590	 0.2780
n	 0.8300	 0.3360
o	 0.5640	 0.3050
p	 0.8550	 0.3850
q	 0.8030	 0.3690
r	 0.7610	 0.3150
s	 0.7530	 0.3000
t	 0.8080	 0.3470
u	 0.4500	 0.2220
v	 0.0030	 -0.0100
w	 0.1540	 0.0220
x	 0.8470	 0.3380
y	 0.6370	 0.3190
z	 0.0430	 0.0540