



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 08:12 AM UTC

PDB ID : 8WHX / pdb_00008whx
EMDB ID : EMD-37551
Title : Cryo- EM structure of Mycobacterium smegmatis 70S ribosome and RafH.
Authors : Kumar, N.; Sharma, S.; Kaushal, P.S.
Deposited on : 2023-09-23
Resolution : 2.80 Å(reported)
Based on initial model : 6DZI

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

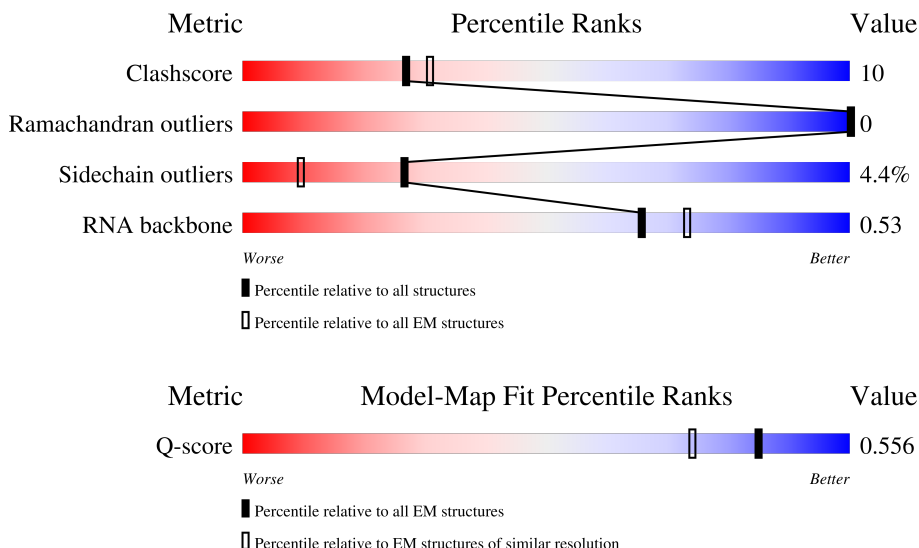
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.80 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	11806 (2.30 - 3.30)

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	E	278	 83% 14% ..
2	F	217	 82% 15% ..
3	G	215	 80% 16% .

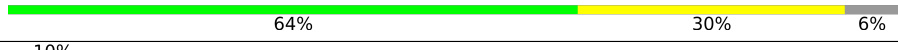
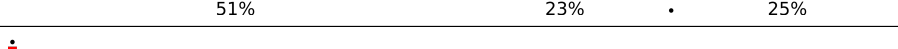
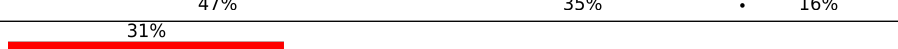
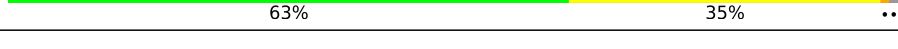
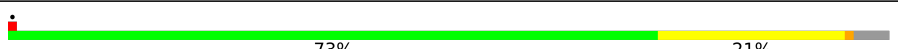
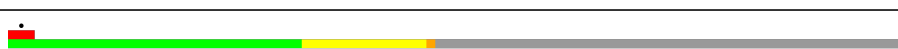
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Mol	Chain	Length	Quality of chain
4	H	187	
5	I	179	
6	J	151	
7	M	147	
8	N	122	
9	O	147	
10	Q	199	
11	R	127	
12	S	113	
13	T	129	
14	U	103	
15	V	153	
16	W	100	
17	X	105	
18	Z	88	
19	1	64	
20	2	77	
21	3	61	
22	5	57	
23	6	55	
24	7	47	
25	8	64	
26	4	75	
27	A	3119	
28	B	118	

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Mol	Chain	Length	Quality of chain
29	a	1528	
30	v	33	
31	d	275	
32	e	201	
33	f	214	
34	g	96	
35	h	156	
36	i	132	
37	j	150	
38	k	101	
39	l	138	
40	m	124	
41	n	124	
42	o	101	
43	p	89	
44	q	156	
45	r	98	
46	s	84	
47	t	93	
48	u	86	
49	c	277	
50	w	264	

2 Entry composition

There are 50 unique types of molecules in this entry. The entry contains 142363 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 L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	E	275	Total	C	N	O	S	0	0
			2110	1298	438	370	4		

- Molecule 2 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	F	214	Total	C	N	O	S	0	0
			1587	982	310	290	5		

- Molecule 3 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	G	209	Total	C	N	O	S	0	0
			1569	969	295	303	2		

- Molecule 4 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	H	181	Total	C	N	O	S	0	0
			1436	901	269	260	6		

- Molecule 5 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	I	165	Total	C	N	O	S	0	0
			1260	792	229	238	1		

- Molecule 6 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	J	41	Total	C	N	O	S	0	0
			308	195	55	57	1		

- Molecule 7 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	M	146	Total	C	N	O	S	0	0
			1130	722	207	200	1		

- Molecule 8 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	N	122	Total	C	N	O	S	0	0
			938	586	179	170	3		

- Molecule 9 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	O	145	Total	C	N	O	S	0	0
			1078	676	205	194	3		

- Molecule 10 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	Q	118	Total	C	N	O	S	0	0
			928	583	180	163	2		

- Molecule 11 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	R	124	Total	C	N	O	0	0
			941	577	195	169		

- Molecule 12 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	S	113	Total	C	N	O	S	0	0
			907	570	171	165	1		

- Molecule 13 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	T	124	Total	C	N	O	0	0
			988	613	203	172		

- Molecule 14 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	U	100	Total	C	N	O	0	0
			754	478	137	139		

- Molecule 15 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	V	113	Total	C	N	O	0	0
			864	538	170	156		

- Molecule 16 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	W	97	Total	C	N	O	0	0
			756	479	138	139		

- Molecule 17 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	X	92	Total	C	N	O	S	0	0
			703	439	132	130	2		

- Molecule 18 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	Z	77	Total	C	N	O	0	0
			574	355	121	98		

- Molecule 19 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	1	63	Total	C	N	O	S	0	0
			470	283	103	80	4		

- Molecule 20 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	2	63	Total	C	N	O	S	0	0
			527	322	102	102	1		

- Molecule 21 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	3	58	Total	C	N	O	0	0
			470	290	94	86		

- Molecule 22 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	5	54	Total	C	N	O	S	0	0
			423	260	93	69	1		

- Molecule 23 is a protein called 50S ribosomal protein L33A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	6	49	Total	C	N	O	S	0	0
			405	248	82	71	4		

- Molecule 24 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	7	45	Total	C	N	O	S	0	0
			372	222	96	53	1		

- Molecule 25 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	8	63	Total	C	N	O	0	0
			502	302	115	85		

- Molecule 26 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	4	57	Total	C	N	O	S	0	0
			445	276	81	83	5		

- Molecule 27 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	A	3020	Total	C	N	O	P	0	0
			64865	28910	11931	21004	3020		

- Molecule 28 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	B	117	Total	C	N	O	P	0	0
			2502	1117	465	803	117		

- Molecule 29 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	a	1515	Total	C	N	O	P	0	0
			32521	14485	5945	10576	1515		

- Molecule 30 is a protein called 30S ribosomal protein S22.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	v	31	Total	C	N	O	S	0	0
			271	166	69	35	1		

- Molecule 31 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	d	207	Total	C	N	O	S	0	0
			1656	1034	321	297	4		

- Molecule 32 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	e	200	Total	C	N	O	S	0	0
			1641	1028	316	295	2		

- Molecule 33 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	f	168	Total	C	N	O	S	0	0
			1223	769	230	220	4		

- Molecule 34 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	g	96	Total	C	N	O	S	0	0
			771	486	138	145	2		

- Molecule 35 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	h	153	Total	C	N	O	S	0	0
			1207	751	235	219	2		

- Molecule 36 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	i	131	Total	C	N	O	S	0	0
			1010	633	189	187	1		

- Molecule 37 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	j	126	Total	C	N	O	S	0	0
			994	630	194	170			

- Molecule 38 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	k	98	Total	C	N	O	S	0	0
			784	493	145	143	3		

- Molecule 39 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	l	115	Total	C	N	O	S	0	0
			855	528	170	156	1		

- Molecule 40 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	m	122	Total	C	N	O	S	0	0
			958	594	197	165	2		

- Molecule 41 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	n	116	Total	C	N	O	S	0	0
			935	572	191	169	3		

- Molecule 42 is a protein called 30S ribosomal protein S14A.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	o	100	Total	C	N	O	S	0	0
			819	497	183	138	1		

- Molecule 43 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	p	88	Total	C	N	O		0	0
			720	449	147	124			

- Molecule 44 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	q	113	Total	C	N	O		0	0
			891	570	162	159			

- Molecule 45 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	r	94	Total	C	N	O	S	0	0
			748	469	142	135	2		

- Molecule 46 is a protein called 30S ribosomal protein S18B.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	s	65	Total	C	N	O	S	0	0
			513	318	102	90	3		

- Molecule 47 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	t	82	Total	C	N	O	S	0	0
			662	425	124	112	1		

- Molecule 48 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	u	85	Total	C	N	O		0	0
			660	402	139	119			

- Molecule 49 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	c	217	Total	C	N	O	S	0	0
			1708	1080	305	316	7		

- Molecule 50 is a protein called Ribosome hibernation promotion factor RafH.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	w	126	Total	C	N	O	S	0	0
			1004	609	214	180	1		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
w	259	HIS	-	expression tag	UNP A0QZ86
w	260	HIS	-	expression tag	UNP A0QZ86
w	261	HIS	-	expression tag	UNP A0QZ86
w	262	HIS	-	expression tag	UNP A0QZ86
w	263	HIS	-	expression tag	UNP A0QZ86
w	264	HIS	-	expression tag	UNP A0QZ86

3 Residue-property plots [i](#)

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

- Molecule 1: 50S ribosomal protein L2

Chain E: 



- Molecule 2: 50S ribosomal protein L3

Chain F: 



- Molecule 3: 50S ribosomal protein L4

Chain G: 

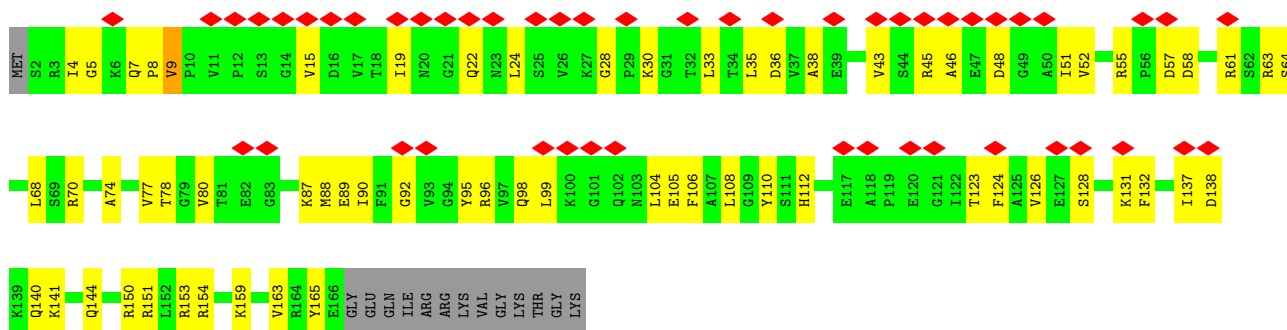


- Molecule 4: 50S ribosomal protein L5

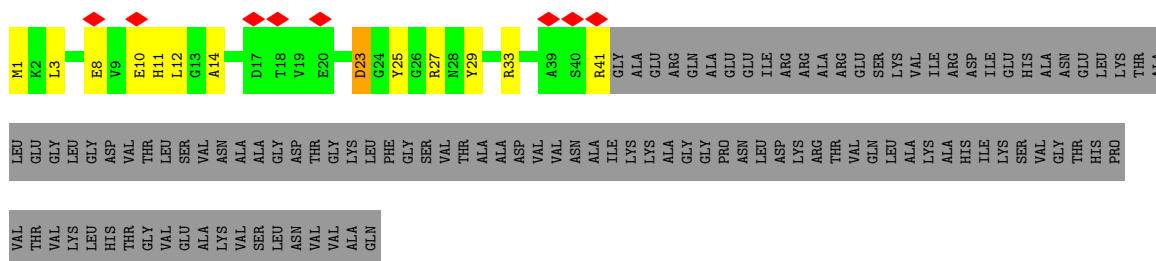
Chain H: 



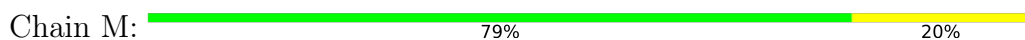
- Molecule 5: 50S ribosomal protein L6



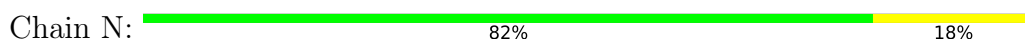
- Molecule 6: 50S ribosomal protein L9



- Molecule 7: 50S ribosomal protein L13

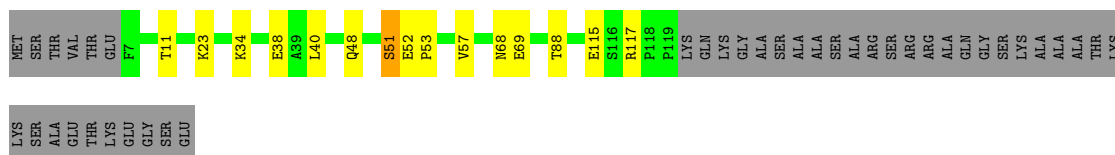


- Molecule 8: 50S ribosomal protein L14





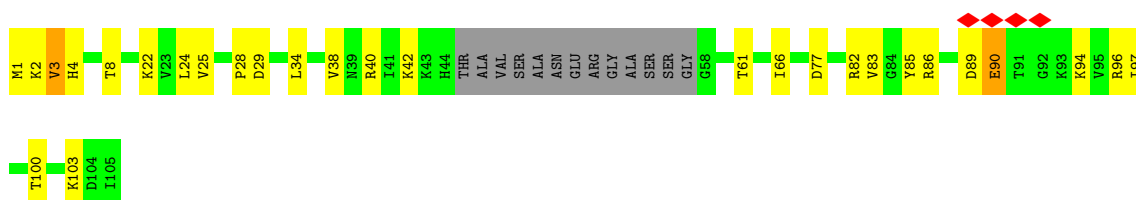
- Molecule 15: 50S ribosomal protein L22



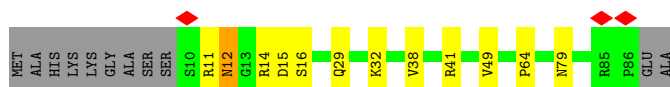
- Molecule 16: 50S ribosomal protein L23



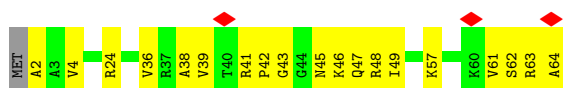
- Molecule 17: 50S ribosomal protein L24



- Molecule 18: 50S ribosomal protein L27

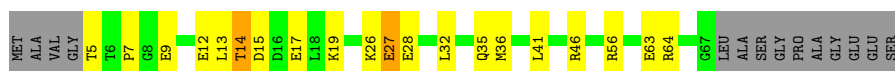


- Molecule 19: 50S ribosomal protein L28



- Molecule 20: 50S ribosomal protein L29





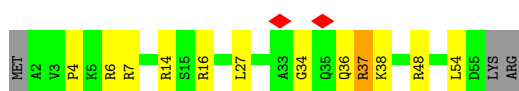
- Molecule 21: 50S ribosomal protein L30

Chain 3: 72% 23% 5%



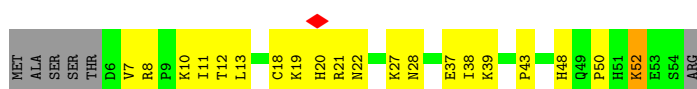
- Molecule 22: 50S ribosomal protein L32

Chain 5: 74% 19% 5%



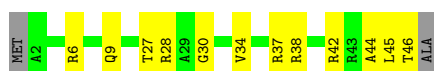
- Molecule 23: 50S ribosomal protein L33A

Chain 6: 53% 35% 11%



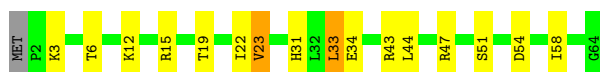
- Molecule 24: 50S ribosomal protein L34

Chain 7: 70% 26% 0%



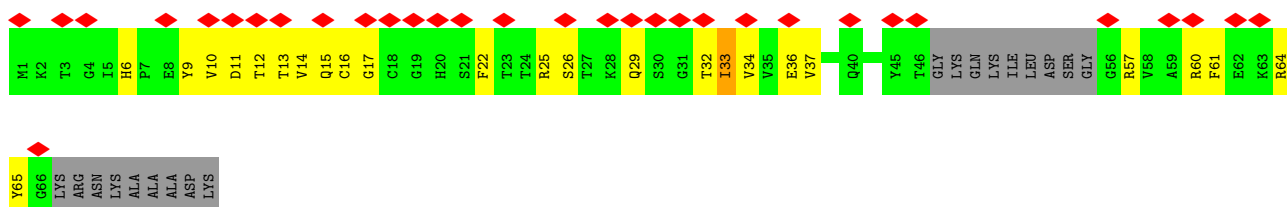
- Molecule 25: 50S ribosomal protein L35

Chain 8: 73% 22% 0%



- Molecule 26: 50S ribosomal protein L31

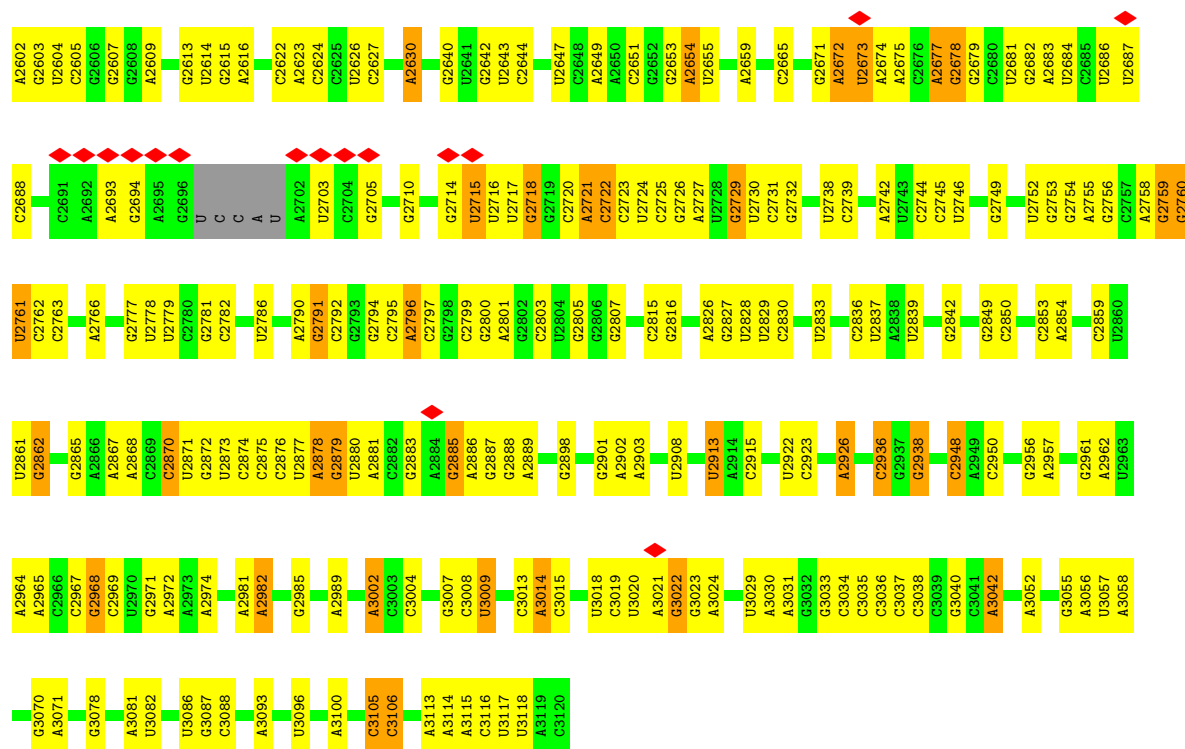
Chain 4: 43% 44% 31% 24%



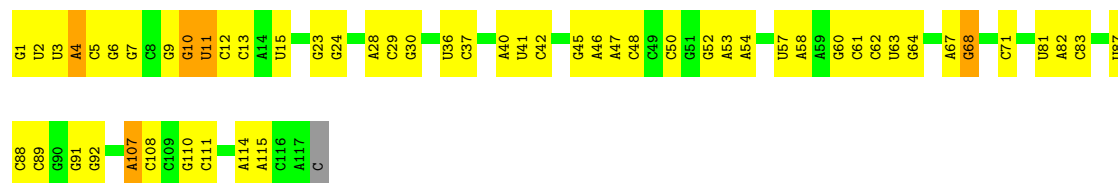
Chain A:



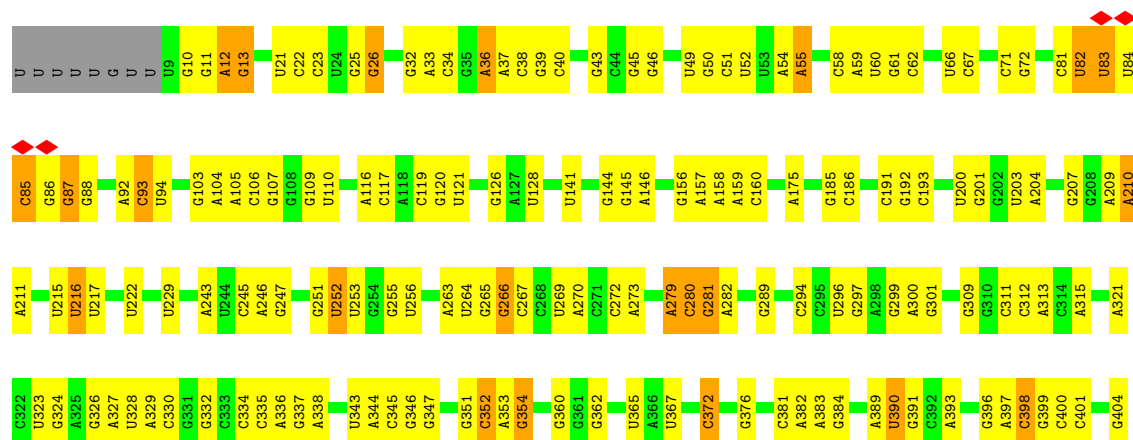
G2503	A2405	G2344	G2263	A2152	A2038	A1907	G1754	U1641	G	G1507	A1387	U1245
G2504	U2406	U2345	C2267	G2153	C2039	A1908	A1755	G1642	C	A1508	U1386	A1246
C2507	C2407	G2346		G2154	C2043	G1921	G1756		A	U1509	U1389	A1247
C2508	U2409	G2347		A2160	U2044	G1922	U1757	G1647	C	A1510	C1393	U1248
A2510	A2410	G2348		A2161	G2045	G1922	G1758	A1648	C	U1511	A1394	U1249
A2511	U2411	A2349		A2162	A2046	G1933	A1759	G1650	U	G1522	A1395	A1251
A2512	U2412	G2350		U2163		G1933	G1760	C1651	U	U1523	G1396	G1252
U2515	G2413	A2351		U2170	C2060	U1937	U1767	A1652	C	G1524	U1397	G1253
U2516	G2414	C2352		C2171	U2061	G1938	U1771	A1656	G	U1525	G1400	G1257
	G2415	G2352		U2179	G2062	U1939	G1772	G1657	G	U1529	C1258	U1259
G2527	C2416	U2353		U2179	A2064	A1940	G1772	U1658	U	G1530	U1259	U1259
G2528	C2417	G2354		U2179	A2065	A1940	G1772	A1660	U	C1531	C1260	C1260
A2529	U2418	U2355		A2190	A2070	U1946	G1786	A1660	G	U1532	A1415	A1261
	A2421	G2356		C2191	A2071	U1947	A1787		U	U1533	A1416	
G2532	U2425	A2357		A2194	G2074	A1948	G1788	A1666	G	U1534	U1427	C1272
A2535	C2426	C2358		U2196	G2075	G1949	A1789	A1666	C	C1535		A1284
U2536	G2427	C2359		G2196		G1950	A1790	G1670	C	U1536	G1434	G1285
C2537		C2360				C1953	A1791		U	U1537	C1435	
A2538	C2431	U2361		C2211	C2079	C1954	A1792	A1673	U	G1538	G1436	A1288
G2539	U2434	U2362		A2212	C2080	A1955	A1792	G1674	U	U1540	A1437	A1289
	A2435	U2363		U2215	C2081	A1955	U1798	G1675	G	G1541	C1441	G1291
U2544	A2436	U2364		G2216	C2082	G1963	G1803	G1676	U	A1542	A1442	U1292
G2545		A2365		G2217	U2089	C1964	G1804	G1677	U	U1544	G1443	U1293
A2546	U2443	C2366		G2217	U2090	C1964	G1805	G1678	U	C1545	U1444	U1294
G2547	C2444	U2367		A2221	C2088	A1955	A1808	A1679	U	A1546	C1448	U1295
U2548	G2445	U2368		A2222	C2089	A1955	U1809	U1681	U	G1547	C1449	U1296
G2549	A2449	C2368		A2226	U2090	U1981	C1817	A1690	U	G1548		G1297
U2550		C2369		U2226	U2091	U1981	G1825	A1691	U	C1549	U1455	G1302
A2551	U2457	A2370		G2234	U2092	A1990	A1826	U1697	U	G1550	G1456	U1303
A2552	G2458	G2371		G2235	C2093	U1999	G1840		U	U1551	C1465	C1314
G2553	U2462	U2372		G2236	G2094		U1852	G1703	U	A1552	C1466	C1315
U2554	U2463	C2373		G2237	G2095	A2003	A1852	U1704	U	C1553	U1467	
C2558	A2464	U2374		A2238	G2096		A1864	C1705	U	U1554	A1468	G1326
A2559	G2465	G2375		A2239	G2097	C2007	U1865	U1706	U	A1555	A1469	
A2560	G2466	G2376		C2243	U2098	A2008	G1866	G1707	U	A1556	G1476	G1335
G2569	U2467	G2377		C2244	C2106		G1867		U	C1557	C1477	
A2570	U2469	U2378		C2245	G2107	U2011	U1870	A1710	U	C1558	C1478	G1339
C2571	A2470	G2379		U2246	A2108	C2012	G1871	G1711	U	A1559	G1479	G1343
	A2471			C2247	G2109	C2013	A1872		U	U1560	A1480	A1344
	G2474	A2381		C2248	A2113	U2015	G1885	A1715	U	C1561	G1485	G1345
G2581		C2382		G2249	A2114	G2016		U1716	U	G1562	G1486	
A2582	U2482	U2383		A2250	A2114	C2017	G1888	C1718	U	A	A1352	G1353
C2583		G2384		G2251		C2018	G1888		U	A	G1365	
	U2486	G2385		U2252	G2128	A2019	G1888	G1724	U	A	U1493	
G2586	C2487	U2386		A2253	C2129	A2020	G1888		U	A	U1494	A1366
U2587	G2488	G2387		A2254	G2130	A2020	G1888		U	A	G1495	G1367
C2588	U2489	G2388		A2255	G2131	A2026	G1888	U1728	U	C	A1499	G1371
G2589	A2490	U2389		A2256	A2137	A2029	A1895	A1729	U	C	A1500	
	A2491	G2390		A2257	A2140	C2030	U1898	A1731	U	C	C1501	G1379
A2593		G2391		A2258	U2141	U2033	G1899		U	C	G1502	
A2497	A2497	G2392		U2261	U2147		G1900	A1737	U	U		
A2498	A2600	A2393		C2262	C2148		C1901		U	A		
A2601		A2394							U	A		
		U2395							U	C		
		A2396							U	C		
									U	C		
		A2399							U	C		
		C2400							U	C		
		U2401							U	C		
		C2402							U	C		
		U2403							U	C		
		G2404							U	C		

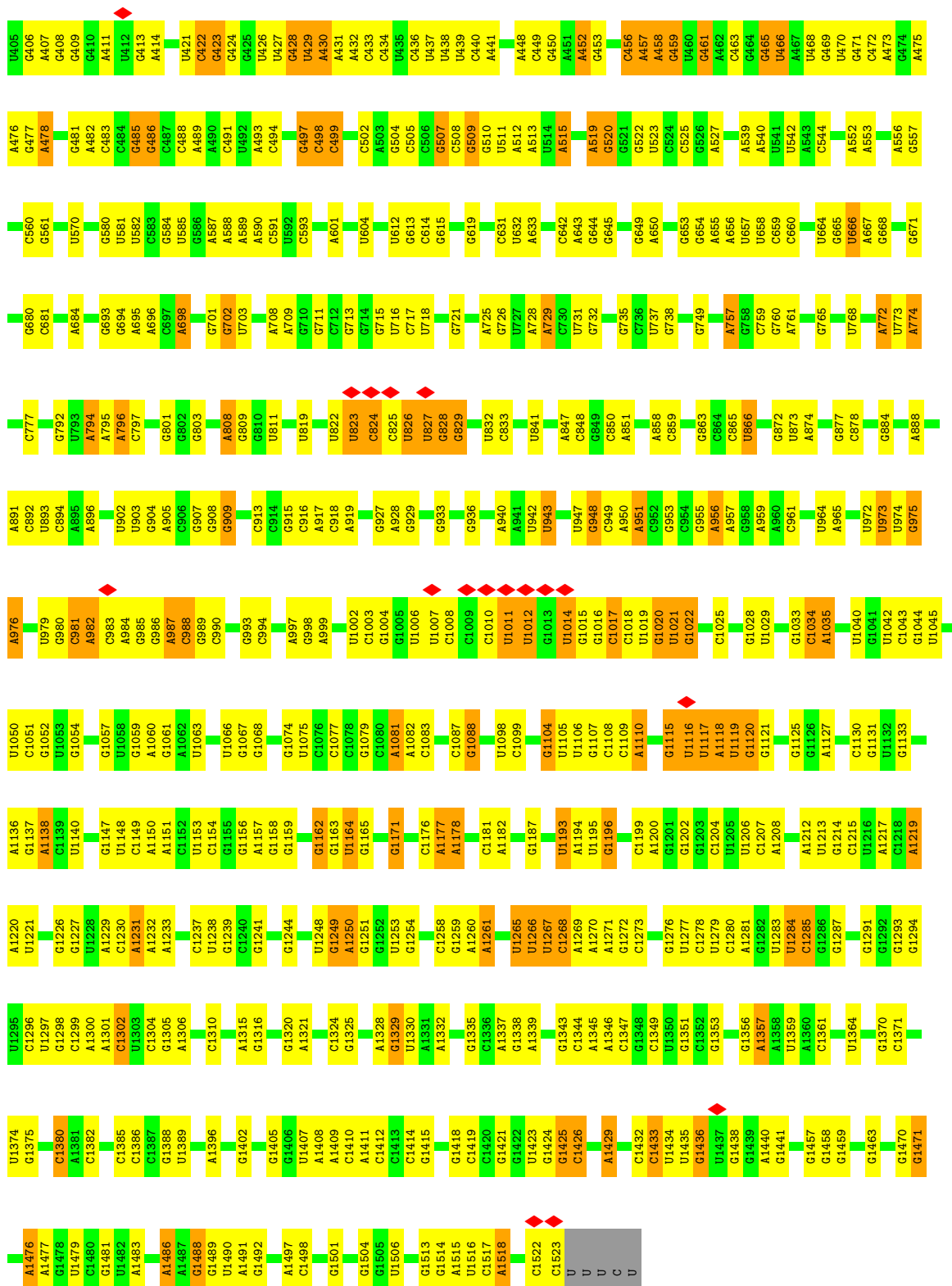


- Molecule 28: 5S rRNA



- Molecule 29: 16S rRNA

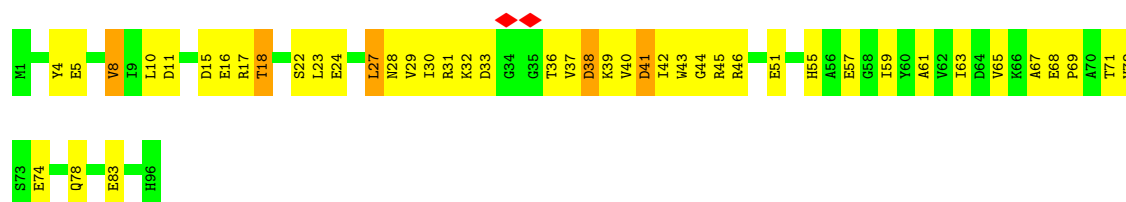




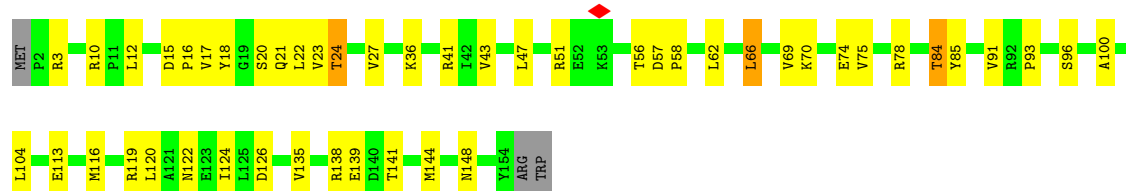
• Molecule 30: 30S ribosomal protein S22

Chain v: 64% 30% 6%

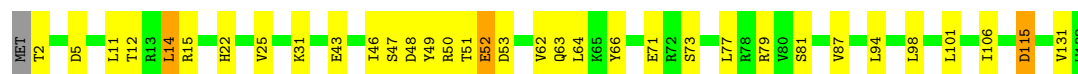




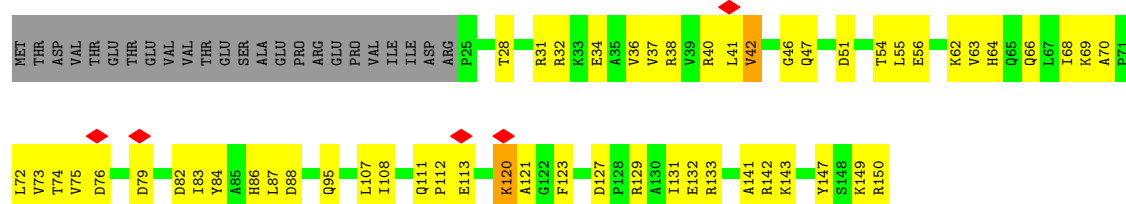
- Molecule 35: 30S ribosomal protein S7



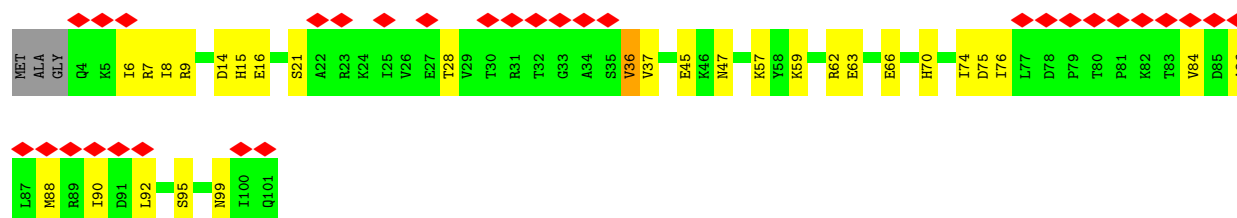
- Molecule 36: 30S ribosomal protein S8



- Molecule 37: 30S ribosomal protein S9



- Molecule 38: 30S ribosomal protein S10

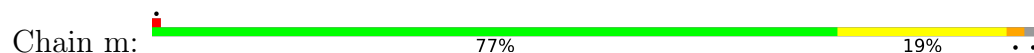


- Molecule 39: 30S ribosomal protein S11

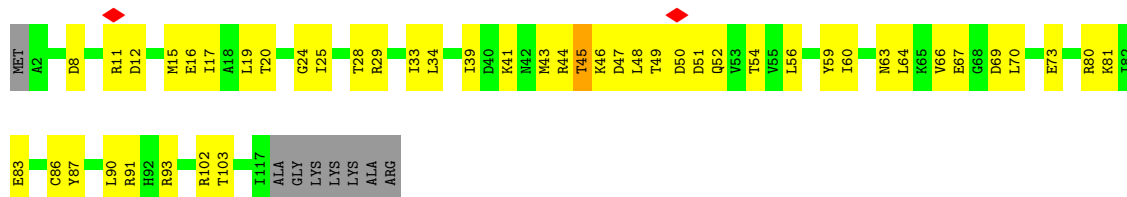




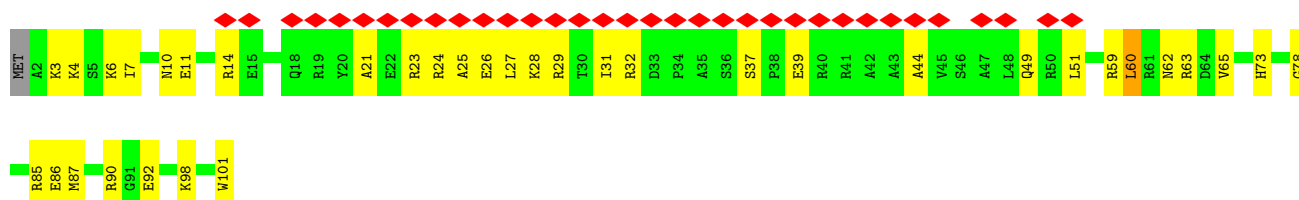
- Molecule 40: 30S ribosomal protein S12



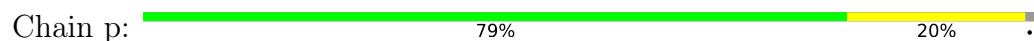
- Molecule 41: 30S ribosomal protein S13



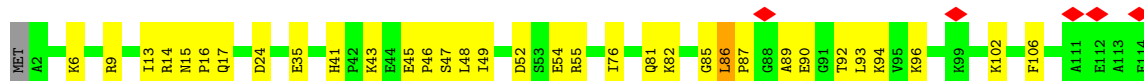
- Molecule 42: 30S ribosomal protein S14A

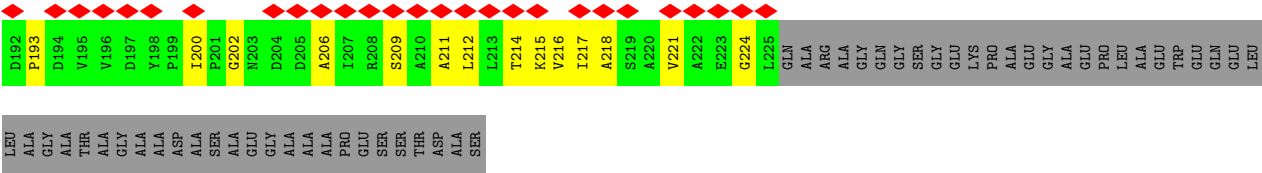


- Molecule 43: 30S ribosomal protein S15

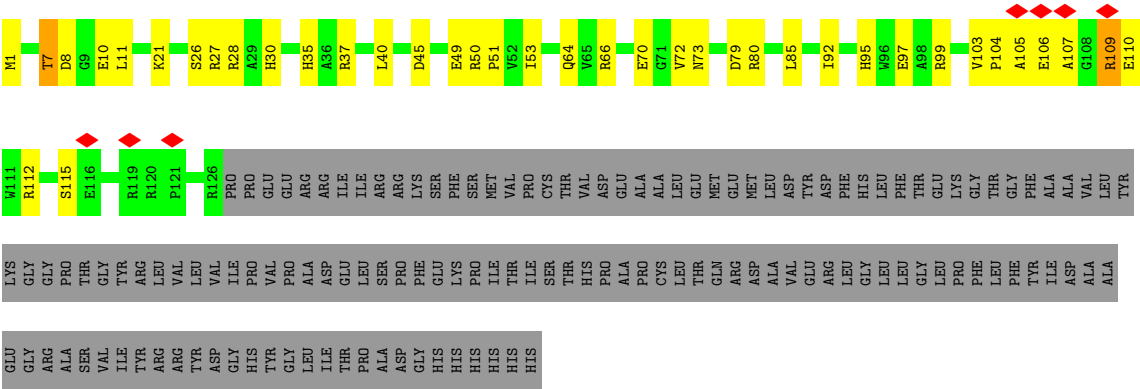
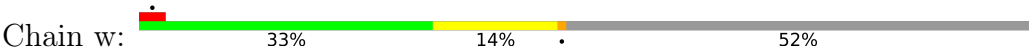


- Molecule 44: 30S ribosomal protein S16





● Molecule 50: Ribosome hibernation promotion factor RaffH



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	110934	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE; CTF correction in Relion	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.34	Depositor
Minimum defocus (nm)	1800	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.271	Depositor
Minimum map value	-0.038	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.013	Depositor
Recommended contour level	0.045	Depositor
Map size ($\text{\AA}$)	406.6, 406.6, 406.6	wwPDB
Map dimensions	380, 380, 380	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.07, 1.07, 1.07	Depositor

5 Model quality

5.1 Standard geometry

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	E	0.19	0/2153	0.27	0/2895
2	F	0.21	0/1609	0.37	0/2165
3	G	0.19	0/1592	0.34	0/2153
4	H	0.17	0/1458	0.39	0/1962
5	I	0.15	0/1281	0.39	0/1733
6	J	0.15	0/311	0.36	0/419
7	M	0.19	0/1157	0.29	0/1567
8	N	0.18	0/946	0.27	0/1268
9	O	0.17	0/1091	0.36	0/1457
10	Q	0.21	0/945	0.36	0/1267
11	R	0.18	0/950	0.42	0/1276
12	S	0.20	0/921	0.41	0/1236
13	T	0.20	0/1000	0.31	0/1341
14	U	0.19	0/764	0.31	0/1030
15	V	0.20	0/878	0.32	0/1192
16	W	0.21	0/766	0.31	0/1030
17	X	0.17	0/709	0.34	0/947
18	Z	0.17	0/583	0.33	0/782
19	1	0.16	0/478	0.35	0/641
20	2	0.19	0/530	0.46	0/708
21	3	0.18	0/473	0.33	0/635
22	5	0.15	0/427	0.25	0/572
23	6	0.25	0/413	0.68	0/553
24	7	0.19	0/375	0.31	0/493
25	8	0.17	0/507	0.30	0/672
26	4	0.14	0/454	0.35	0/610
27	A	0.20	0/72631	0.30	0/113324
28	B	0.15	0/2799	0.26	0/4362
29	a	0.25	0/36400	0.31	0/56798
30	v	0.16	0/271	0.38	0/348
31	d	0.20	0/1680	0.38	0/2256
32	e	0.21	0/1672	0.36	0/2251
33	f	0.18	0/1239	0.32	0/1673
34	g	0.30	0/782	0.54	2/1059 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	h	0.20	0/1225	0.36	0/1653
36	i	0.24	0/1025	0.33	0/1385
37	j	0.24	0/1012	0.45	0/1362
38	k	0.21	0/798	0.42	0/1081
39	l	0.26	0/873	0.45	0/1180
40	m	0.23	0/969	0.32	0/1294
41	n	0.24	0/942	0.47	0/1260
42	o	0.19	0/830	0.39	0/1106
43	p	0.25	0/729	0.38	0/977
44	q	0.25	0/908	0.40	0/1226
45	r	0.23	0/759	0.37	0/1016
46	s	0.26	0/518	0.39	0/693
47	t	0.23	0/680	0.46	0/915
48	u	0.23	0/663	0.39	0/882
49	c	0.24	1/1737 (0.1%)	0.42	0/2344
50	w	0.21	0/1023	0.37	0/1381
All	All	0.21	1/154936 (0.0%)	0.32	2/232430 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
49	c	31	ILE	CG1-CD1	-5.43	1.30	1.51

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	g	67	ALA	CA-C-N	7.14	130.63	120.49
34	g	67	ALA	C-N-CA	7.14	130.63	120.49

There are no chirality outliers.

There are no planarity outliers.

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	E	2110	0	2165	29	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	F	1587	0	1630	27	0
3	G	1569	0	1607	21	0
4	H	1436	0	1463	42	0
5	I	1260	0	1300	52	0
6	J	308	0	323	7	0
7	M	1130	0	1167	19	0
8	N	938	0	1000	15	0
9	O	1078	0	1151	15	0
10	Q	928	0	972	14	0
11	R	941	0	979	27	0
12	S	907	0	938	21	0
13	T	988	0	1038	10	0
14	U	754	0	802	15	0
15	V	864	0	903	9	0
16	W	756	0	802	9	0
17	X	703	0	753	19	0
18	Z	574	0	591	9	0
19	1	470	0	484	17	0
20	2	527	0	538	16	0
21	3	470	0	497	9	0
22	5	423	0	463	9	0
23	6	405	0	411	14	0
24	7	372	0	406	7	0
25	8	502	0	541	13	0
26	4	445	0	431	34	0
27	A	64865	0	32635	843	0
28	B	2502	0	1274	29	0
29	a	32521	0	16366	460	0
30	v	271	0	329	9	0
31	d	1656	0	1704	57	0
32	e	1641	0	1668	47	0
33	f	1223	0	1287	36	0
34	g	771	0	797	46	0
35	h	1207	0	1259	37	0
36	i	1010	0	1046	27	0
37	j	994	0	1050	49	0
38	k	784	0	816	26	0
39	l	855	0	863	21	0
40	m	958	0	1045	19	0
41	n	935	0	986	59	0
42	o	819	0	866	36	0
43	p	720	0	760	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	q	891	0	935	27	0
45	r	748	0	795	16	0
46	s	513	0	540	16	0
47	t	662	0	677	53	0
48	u	660	0	712	10	0
49	c	1708	0	1741	90	0
50	w	1004	0	991	39	0
All	All	142363	0	94497	2290	0

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

All (2290) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:s:19:LYS:HA	46:s:19:LYS:HE3	1.15	1.08
27:A:2086:U:H3	27:A:2096:G:H1	1.03	1.00
27:A:2971:G:H21	27:A:2981:A:N6	1.61	0.99
49:c:67:VAL:H	49:c:89:MET:HE3	1.26	0.99
35:h:144:MET:HE2	35:h:148:ASN:HD21	1.25	0.97
27:A:1561:C:H1'	34:g:17:ARG:HH11	1.24	0.96
38:k:6:ILE:HG22	38:k:76:ILE:HD11	1.45	0.95
27:A:2971:G:N2	27:A:2981:A:H62	1.63	0.95
34:g:45:ARG:HA	34:g:45:ARG:NH1	1.82	0.94
27:A:365:U:H3	27:A:437:G:H1	1.09	0.93
46:s:19:LYS:HA	46:s:19:LYS:CE	1.98	0.92
27:A:2971:G:H21	27:A:2981:A:H62	0.94	0.92
25:8:19:THR:HG23	27:A:745:G:H5''	1.53	0.89
29:a:82:U:H3	29:a:87:G:H1	0.95	0.89
27:A:1547:G:H1	27:A:1623:U:H3	0.87	0.86
27:A:989:G:O6	27:A:990:G:N2	2.08	0.86
49:c:27:MET:O	49:c:31:ILE:HD13	1.75	0.86
32:e:104:ARG:H	32:e:108:MET:HE3	1.42	0.85
46:s:19:LYS:HE3	46:s:19:LYS:CA	2.00	0.85
42:o:11:GLU:OE1	42:o:11:GLU:N	2.10	0.84
27:A:1542:A:H61	27:A:1628:A:H1'	1.42	0.84
49:c:27:MET:O	49:c:31:ILE:CD1	2.26	0.84
34:g:45:ARG:HA	34:g:45:ARG:HH11	1.42	0.84
36:i:48:ASP:OD1	36:i:49:TYR:N	2.11	0.83
27:A:2671:G:H1	27:A:2675:A:H62	1.20	0.83
41:n:46:LYS:H	41:n:46:LYS:HD2	1.42	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:q:45:GLU:HG3	44:q:46:PRO:HD3	1.60	0.83
42:o:6:LYS:HB3	42:o:63:ARG:HH12	1.45	0.82
27:A:1540:U:H3	27:A:1632:G:H1	1.26	0.81
32:e:104:ARG:H	32:e:108:MET:CE	1.93	0.81
41:n:12:ASP:CB	41:n:46:LYS:HZ1	1.93	0.81
27:A:1561:C:H1'	34:g:17:ARG:NH1	1.96	0.81
27:A:2671:G:H1	27:A:2675:A:N6	1.79	0.80
27:A:341:C:C4	27:A:342:C:N4	2.49	0.80
29:a:1388:G:H5'	30:v:12:MET:HE3	1.61	0.80
50:w:49:GLU:HG2	50:w:50:ARG:HG2	1.63	0.80
23:6:39:LYS:HA	23:6:50:PRO:HA	1.64	0.80
11:R:77:LYS:HB3	11:R:112:ARG:HD3	1.64	0.79
34:g:83:GLU:N	34:g:83:GLU:OE2	2.15	0.79
33:f:193:GLY:HA2	33:f:196:LYS:HE3	1.65	0.79
31:d:15:THR:HG23	31:d:207:ILE:HG12	1.65	0.78
27:A:341:C:N4	27:A:342:C:N4	2.31	0.78
35:h:27:VAL:HG12	35:h:43:VAL:HG11	1.66	0.78
18:Z:64:PRO:HB3	27:A:759:G:H1	1.49	0.78
39:l:90:LYS:NZ	39:l:117:GLY:HA3	1.97	0.78
29:a:819:U:H3	29:a:829:G:H22	1.30	0.78
12:S:33:GLU:HB2	12:S:36:LYS:HE3	1.66	0.78
35:h:22:LEU:HD11	35:h:66:LEU:HD22	1.66	0.78
27:A:1612:U:H1'	34:g:17:ARG:HH21	1.49	0.77
29:a:666:U:H1'	39:l:53:TRP:HE1	1.49	0.77
37:j:121:ALA:HB1	37:j:123:PHE:HE1	1.48	0.77
29:a:1010:C:N4	29:a:1014:U:H3	1.82	0.77
12:S:105:LYS:HG2	29:a:1415:G:OP1	1.84	0.77
27:A:217:G:H22	27:A:235:U:H4'	1.49	0.77
34:g:45:ARG:HH22	34:g:57:GLU:HG3	1.50	0.77
44:q:54:GLU:OE2	44:q:55:ARG:HD2	1.84	0.76
38:k:16:GLU:N	38:k:16:GLU:OE2	2.18	0.76
31:d:47:GLU:H	31:d:48:ARG:NH2	1.83	0.76
10:Q:10:LEU:HB2	10:Q:17:GLN:HG3	1.68	0.76
27:A:334:G:H1	27:A:347:U:H3	1.31	0.76
37:j:42:VAL:HG22	37:j:82:ASP:HB3	1.68	0.76
4:H:87:ARG:H	4:H:90:MET:HE2	1.51	0.76
27:A:1556:A:C2	27:A:1615:G:N1	2.55	0.75
32:e:197:GLU:OE1	33:f:137:ARG:NH2	2.20	0.75
38:k:63:GLU:OE1	42:o:85:ARG:NH1	2.20	0.75
29:a:461:G:O2'	29:a:463:C:N4	2.20	0.75
42:o:49:GLN:NE2	47:t:13:ASP:OD1	2.20	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:c:32:PHE:HB2	49:c:42:ASP:HB2	1.69	0.74
29:a:1349:C:O2'	38:k:62:ARG:NH2	2.20	0.74
34:g:38:ASP:N	34:g:38:ASP:OD1	2.18	0.74
13:T:25:ARG:NH1	27:A:2245:C:OP1	2.21	0.74
3:G:23:GLU:OE1	3:G:23:GLU:N	2.18	0.74
23:6:28:ASN:ND2	27:A:2509:C:OP2	2.20	0.74
27:A:1556:A:N1	27:A:1615:G:O6	2.21	0.74
47:t:17:LYS:HZ2	47:t:18:LYS:HG3	1.52	0.73
29:a:728:A:O2'	29:a:729:A:N7	2.18	0.73
44:q:90:GLU:N	44:q:90:GLU:OE2	2.20	0.73
27:A:747:A:N6	27:A:768:G:O2'	2.20	0.73
18:Z:14:ARG:NH2	27:A:2503:G:N7	2.36	0.73
29:a:489:A:H8	29:a:523:U:HO2'	1.35	0.73
49:c:50:ILE:HD11	49:c:216:VAL:HG11	1.70	0.73
43:p:10:GLU:OE2	43:p:11:ILE:HG13	1.88	0.73
27:A:326:A:N6	27:A:449:G:H1	1.87	0.72
29:a:653:G:H2'	29:a:654:G:C8	2.23	0.72
29:a:1232:A:H62	29:a:1268:C:H42	1.37	0.72
45:r:67:GLU:N	45:r:67:GLU:OE1	2.21	0.72
26:4:64:ARG:NH1	29:a:1294:G:OP2	2.22	0.72
31:d:86:ILE:HD13	31:d:100:LEU:HD13	1.70	0.72
4:H:83:GLN:OE1	4:H:83:GLN:N	2.23	0.72
14:U:66:GLU:OE1	27:A:641:U:N3	2.21	0.72
16:W:18:GLU:N	16:W:18:GLU:OE2	2.23	0.72
35:h:138:ARG:NH1	35:h:139:GLU:OE2	2.23	0.72
45:r:72:ASP:N	45:r:72:ASP:OD1	2.21	0.72
32:e:182:GLU:H	32:e:185:GLN:HE21	1.36	0.72
35:h:144:MET:HE2	35:h:148:ASN:ND2	2.04	0.72
29:a:1261:A:OP1	38:k:9:ARG:NH2	2.22	0.72
36:i:50:ARG:NE	36:i:52:GLU:OE2	2.20	0.72
36:i:12:THR:HG22	36:i:15:ARG:HH12	1.53	0.71
27:A:2356:G:H2'	27:A:2380:G:H22	1.55	0.71
4:H:68:THR:HG21	4:H:96:VAL:HG21	1.72	0.71
27:A:1543:A:N1	27:A:1628:A:O2'	2.23	0.71
28:B:67:A:H4'	28:B:68:G:H5'	1.72	0.71
2:F:43:GLU:OE2	2:F:43:GLU:N	2.21	0.71
27:A:1554:U:H2'	27:A:1555:A:C8	2.26	0.70
27:A:1561:C:H5'	34:g:16:GLU:OE1	1.90	0.70
5:I:45:ARG:HA	5:I:51:ILE:HG22	1.74	0.70
20:2:9:GLU:HA	20:2:12:GLU:HG2	1.71	0.70
27:A:2342:A:N6	27:A:2390:U:O2'	2.24	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:1:57:LYS:NZ	27:A:488:G:N7	2.38	0.70
49:c:46:THR:O	49:c:50:ILE:HG22	1.92	0.70
39:l:37:ASN:N	39:l:37:ASN:OD1	2.25	0.70
49:c:27:MET:HE2	49:c:193:PRO:HD3	1.72	0.70
26:4:65:TYR:CG	47:t:9:PRO:HD3	2.27	0.70
27:A:1532:G:O2'	27:A:1803:A:N1	2.20	0.70
29:a:644:G:H22	29:a:721:G:H1	1.40	0.70
45:r:92:GLU:N	45:r:92:GLU:OE2	2.24	0.70
1:E:71:ASP:N	1:E:71:ASP:OD1	2.23	0.70
27:A:1754:G:H1	27:A:1759:A:H61	1.40	0.70
29:a:1338:G:H2'	29:a:1339:A:C8	2.25	0.70
49:c:143:LYS:HD3	49:c:146:ARG:HH21	1.56	0.69
26:4:61:PHE:CE2	47:t:41:ILE:HD12	2.26	0.69
27:A:2552:A:H2'	27:A:2553:G:C8	2.26	0.69
41:n:90:LEU:HD23	41:n:90:LEU:H	1.56	0.69
29:a:985:G:H2'	29:a:986:G:C8	2.27	0.69
8:N:93:PRO:HG3	8:N:114:ILE:HG12	1.75	0.69
26:4:60:ARG:NH2	29:a:1293:G:OP1	2.25	0.69
29:a:915:G:N7	35:h:3:ARG:NH1	2.41	0.69
29:a:1017:C:H2'	29:a:1018:C:C6	2.27	0.69
29:a:1418:G:H2'	29:a:1419:C:C6	2.28	0.69
29:a:1517:C:H5'	29:a:1518:A:H5'	1.73	0.69
42:o:14:ARG:HD2	42:o:60:LEU:HD21	1.75	0.69
27:A:2671:G:N2	27:A:2675:A:N7	2.35	0.69
29:a:437:U:O2'	32:e:115:HIS:ND1	2.24	0.69
31:d:129:PHE:O	31:d:133:MET:HG3	1.92	0.69
39:l:99:GLY:HA2	39:l:102:ARG:HD3	1.73	0.69
42:o:87:MET:HE3	42:o:92:GLU:HB2	1.75	0.69
43:p:9:LYS:HZ3	43:p:9:LYS:HB2	1.56	0.69
49:c:117:LEU:HD21	49:c:141:LYS:HB2	1.75	0.69
27:A:2094:G:HO2'	27:A:2095:G:H8	1.41	0.69
38:k:9:ARG:HB2	38:k:99:ASN:HB3	1.75	0.69
27:A:2372:U:H2'	27:A:2373:G:C8	2.28	0.69
29:a:1159:G:N2	29:a:1162:G:OP2	2.26	0.68
11:R:40:VAL:HG12	11:R:49:VAL:HG12	1.74	0.68
12:S:52:GLY:H	12:S:56:GLU:HG2	1.57	0.68
27:A:857:U:H2'	27:A:858:A:C8	2.28	0.68
42:o:24:ARG:HD2	42:o:51:LEU:HD21	1.75	0.68
2:F:153:GLY:HA3	2:F:157:PRO:HG2	1.74	0.68
26:4:16:CYS:SG	26:4:17:GLY:N	2.65	0.68
29:a:1015:G:H2'	29:a:1016:G:H8	1.57	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:a:1066:U:H3	29:a:1079:G:H22	1.40	0.68
4:H:20:ARG:HG2	4:H:35:ILE:HG21	1.75	0.68
12:S:73:PHE:HB3	12:S:80:ILE:HD11	1.76	0.68
41:n:39:ILE:HD12	41:n:39:ILE:H	1.58	0.68
49:c:27:MET:HE1	49:c:187:LEU:HD22	1.76	0.68
5:I:151:ARG:NH2	27:A:2967:C:O2	2.23	0.68
27:A:666:A:N6	27:A:2258:U:OP1	2.26	0.68
32:e:49:GLN:HB3	32:e:198:LEU:HB2	1.76	0.68
35:h:144:MET:HE3	35:h:144:MET:HA	1.75	0.68
38:k:84:VAL:O	38:k:88:MET:HE2	1.94	0.68
1:E:26:ARG:HH22	1:E:30:GLU:HG2	1.59	0.68
2:F:96:GLU:N	2:F:96:GLU:OE2	2.27	0.68
22:5:16:ARG:NH2	27:A:1379:G:OP1	2.20	0.68
27:A:327:U:O2	27:A:449:G:N2	2.27	0.68
29:a:1338:G:H2'	29:a:1339:A:H8	1.59	0.67
4:H:37:GLY:H	4:H:166:THR:HB	1.59	0.67
5:I:150:ARG:HD2	5:I:163:VAL:HG23	1.76	0.67
5:I:98:GLN:HE22	5:I:105:GLU:HB3	1.59	0.67
15:V:69:GLU:N	15:V:69:GLU:OE2	2.28	0.67
18:Z:11:ARG:O	18:Z:14:ARG:NH1	2.27	0.67
27:A:1147:A:N6	27:A:1243:G:O2'	2.27	0.67
29:a:1014:U:H2'	29:a:1015:G:C8	2.30	0.67
29:a:1231:A:H2'	29:a:1232:A:C8	2.30	0.67
26:4:65:TYR:CD2	47:t:9:PRO:HD3	2.30	0.67
29:a:411:A:C4	29:a:413:G:H1'	2.30	0.67
17:X:40:ARG:HG2	17:X:40:ARG:HH11	1.59	0.67
32:e:104:ARG:N	32:e:108:MET:HE3	2.10	0.67
14:U:26:LYS:HA	14:U:95:THR:HG23	1.76	0.67
29:a:1232:A:H5'	37:j:34:GLU:OE1	1.95	0.67
48:u:32:ILE:HD13	48:u:79:LEU:HD11	1.77	0.67
29:a:92:A:O2'	29:a:93:C:O5'	2.13	0.67
29:a:928:A:H2'	29:a:929:G:C8	2.30	0.67
29:a:1018:C:H2'	29:a:1019:U:C6	2.29	0.67
37:j:62:LYS:HE2	37:j:62:LYS:H	1.59	0.67
39:l:46:PRO:HG2	39:l:47:GLN:OE1	1.95	0.67
27:A:2351:A:N3	27:A:2396:A:O2'	2.28	0.67
31:d:62:ARG:HH22	31:d:64:ARG:HB2	1.59	0.67
50:w:106:GLU:HB3	50:w:109:ARG:HD2	1.76	0.67
27:A:1552:A:N6	27:A:1616:A:N7	2.43	0.66
41:n:33:ILE:HB	41:n:59:TYR:HE2	1.58	0.66
3:G:160:ARG:NH2	27:A:706:G:O2'	2.28	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:a:1040:U:OP1	42:o:85:ARG:NH2	2.28	0.66
44:q:45:GLU:CG	44:q:46:PRO:HD3	2.24	0.66
49:c:73:LYS:NZ	49:c:165:ASP:OD2	2.29	0.66
49:c:206:ALA:HB3	49:c:209:SER:OG	1.95	0.66
29:a:1120:G:H4'	29:a:1121:G:H5'	1.75	0.66
27:A:279:U:H2'	27:A:280:G:H8	1.60	0.66
5:I:58:ASP:O	5:I:63:ARG:NH1	2.28	0.66
37:j:66:GLN:C	37:j:66:GLN:OE1	2.38	0.66
27:A:1541:G:H2'	27:A:1542:A:H8	1.59	0.66
39:l:37:ASN:HA	39:l:67:SER:HB3	1.77	0.66
12:S:38:ARG:NH1	29:a:346:G:OP1	2.25	0.66
19:1:39:VAL:HG22	19:1:46:LYS:HG2	1.78	0.66
27:A:3014:A:N6	27:A:3113:A:OP2	2.29	0.66
29:a:472:C:H2'	29:a:473:A:C8	2.31	0.66
42:o:21:ALA:HA	42:o:25:ALA:HB3	1.76	0.66
27:A:2357:A:O2'	27:A:2382:G:N2	2.29	0.66
27:A:2862:G:O2'	27:A:3002:A:N6	2.29	0.66
29:a:82:U:O2	29:a:87:G:N2	2.22	0.66
36:i:115:ASP:OD1	36:i:115:ASP:N	2.29	0.66
27:A:1755:A:O2'	27:A:1758:G:N2	2.29	0.66
39:l:28:GLY:HA2	39:l:46:PRO:HD3	1.76	0.66
27:A:2470:A:H2'	27:A:2471:A:H8	1.61	0.65
5:I:88:MET:HE2	5:I:88:MET:HA	1.79	0.65
29:a:372:C:H5	29:a:389:A:H62	1.43	0.65
1:E:271:ARG:NH2	27:A:2016:G:OP2	2.30	0.65
27:A:1551:U:O2'	27:A:1552:A:OP1	2.14	0.65
29:a:803:G:HO2'	36:i:2:THR:N	1.94	0.65
31:d:15:THR:HG23	31:d:207:ILE:CG1	2.25	0.65
41:n:87:TYR:HA	41:n:90:LEU:HD21	1.78	0.65
1:E:211:ARG:NH1	27:A:1786:G:OP1	2.30	0.65
27:A:664:A:H3'	27:A:665:G:H8	1.62	0.65
27:A:2386:U:OP1	27:A:2394:A:H5''	1.97	0.65
41:n:33:ILE:HB	41:n:59:TYR:CE2	2.31	0.65
49:c:151:ILE:HA	49:c:154:MET:HE1	1.77	0.65
27:A:1530:G:N2	27:A:1805:G:H1	1.95	0.65
27:A:2758:A:H2'	27:A:2759:G:O4'	1.96	0.65
29:a:936:G:H21	29:a:1208:A:H62	1.43	0.65
27:A:1530:G:H21	27:A:1805:G:H22	1.45	0.65
29:a:1359:U:O4	35:h:10:ARG:NH1	2.28	0.65
34:g:23:LEU:O	34:g:27:LEU:HD12	1.96	0.65
41:n:69:ASP:OD1	41:n:70:LEU:N	2.30	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:s:57:CYS:SG	46:s:60:HIS:ND1	2.69	0.65
49:c:24:ASN:HD22	49:c:27:MET:HG2	1.61	0.65
7:M:102:GLU:OE1	27:A:3004:C:N4	2.30	0.65
8:N:17:LYS:HE3	8:N:47:ILE:HG13	1.78	0.65
29:a:413:G:O2'	29:a:428:G:N2	2.27	0.64
29:a:485:G:H2'	29:a:486:G:C8	2.31	0.64
44:q:46:PRO:HG3	44:q:96:LYS:HD3	1.79	0.64
9:O:97:GLU:OE1	9:O:97:GLU:N	2.28	0.64
5:I:90:ILE:HD12	5:I:95:TYR:HB2	1.80	0.64
29:a:695:A:H2'	29:a:696:A:C8	2.33	0.64
29:a:858:A:H1'	36:i:12:THR:HG21	1.80	0.64
47:t:15:LEU:O	47:t:19:VAL:HG13	1.97	0.64
47:t:62:VAL:HA	47:t:66:MET:SD	2.37	0.64
4:H:76:ARG:NH1	4:H:89:GLY:O	2.30	0.64
26:4:61:PHE:HE2	47:t:41:ILE:CD1	2.10	0.64
27:A:326:A:N6	27:A:449:G:N1	2.45	0.64
27:A:341:C:N4	27:A:342:C:H41	1.96	0.64
26:4:14:VAL:HB	26:4:22:PHE:HB3	1.79	0.64
27:A:337:U:H3	27:A:344:G:H1	1.46	0.64
27:A:2353:U:N3	27:A:2354:G:O6	2.31	0.64
29:a:654:G:H2'	29:a:655:A:H8	1.62	0.64
2:F:19:GLU:N	2:F:19:GLU:OE2	2.25	0.64
24:7:42:ARG:NH2	27:A:556:G:N7	2.38	0.64
35:h:16:PRO:HB3	37:j:66:GLN:HG3	1.79	0.64
3:G:41:GLN:HG2	27:A:709:U:H1'	1.79	0.64
7:M:125:TYR:HH	7:M:132:HIS:HE2	1.42	0.64
29:a:1106:U:OP1	38:k:7:ARG:NH2	2.31	0.64
2:F:60:ARG:NH2	27:A:3052:A:OP1	2.27	0.63
29:a:82:U:H2'	29:a:83:U:C6	2.33	0.63
29:a:694:G:H2'	29:a:695:A:C8	2.33	0.63
29:a:1057:G:N2	29:a:1060:A:OP2	2.27	0.63
26:4:11:ASP:HA	26:4:25:ARG:HA	1.79	0.63
29:a:315:A:N7	29:a:328:U:H5	1.96	0.63
29:a:525:C:OP1	32:e:53:LYS:NZ	2.31	0.63
32:e:197:GLU:OE2	33:f:130:VAL:N	2.32	0.63
27:A:2759:G:H2'	27:A:2760:G:H8	1.64	0.63
38:k:63:GLU:OE2	42:o:98:LYS:NZ	2.27	0.63
19:1:38:ALA:O	19:1:47:GLN:NE2	2.32	0.63
29:a:1003:C:H2'	29:a:1004:G:C8	2.34	0.63
37:j:111:GLN:HE22	37:j:113:GLU:HB2	1.62	0.63
39:l:90:LYS:HZ3	39:l:117:GLY:HA3	1.62	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:17:SER:O	1:E:211:ARG:NH2	2.29	0.63
1:E:72:LYS:NZ	1:E:101:GLU:OE1	2.31	0.63
5:I:46:ALA:H	5:I:51:ILE:HA	1.63	0.63
26:4:13:THR:HB	26:4:32:THR:HG23	1.81	0.63
27:A:1547:G:N2	27:A:1623:U:O2	2.25	0.63
27:A:1825:C:N4	27:A:1840:G:OP2	2.25	0.63
29:a:1077:C:H5''	49:c:139:ARG:HH21	1.63	0.63
29:a:1273:C:OP1	35:h:41:ARG:NH1	2.30	0.63
29:a:928:A:H2'	29:a:929:G:H8	1.64	0.63
5:I:153:ARG:HE	5:I:154:ARG:H	1.46	0.63
29:a:438:U:O2'	29:a:439:U:O2	2.12	0.63
29:a:1305:G:H2'	29:a:1306:A:C8	2.34	0.63
27:A:993:G:N1	27:A:1015:A:OP2	2.26	0.62
29:a:408:G:O3'	32:e:104:ARG:NH1	2.31	0.62
42:o:4:LYS:HB2	42:o:4:LYS:NZ	2.13	0.62
27:A:639:C:HO2'	27:A:640:G:H8	1.47	0.62
27:A:987:A:C2	27:A:1021:G:N1	2.62	0.62
2:F:154:CYS:O	27:A:2277:G:H5'	1.99	0.62
27:A:256:A:H2'	27:A:257:A:H8	1.64	0.62
34:g:44:GLY:HA3	34:g:59:ILE:HG23	1.80	0.62
35:h:120:LEU:O	35:h:124:ILE:HG22	1.98	0.62
3:G:199:GLU:OE2	3:G:199:GLU:N	2.30	0.62
29:a:975:G:O2'	29:a:976:A:N7	2.32	0.62
17:X:24:LEU:HD12	17:X:25:VAL:HG23	1.81	0.62
34:g:40:VAL:HG22	34:g:63:ILE:HG13	1.81	0.62
17:X:82:ARG:NH2	27:A:382:A:OP2	2.33	0.62
4:H:126:PRO:O	4:H:174:ARG:NH1	2.31	0.62
27:A:654:U:H1'	27:A:664:A:H1'	1.82	0.62
27:A:1009:U:H2'	27:A:1010:U:C6	2.35	0.62
27:A:1229:A:H8	27:A:1230:G:H1'	1.64	0.62
29:a:1300:A:OP1	47:t:3:ARG:NH2	2.32	0.62
29:a:983:C:H2'	29:a:984:A:C8	2.35	0.62
29:a:1265:U:OP2	29:a:1266:U:O2'	2.18	0.62
5:I:15:VAL:HG12	5:I:28:GLY:HA2	1.80	0.62
12:S:105:LYS:CG	29:a:1415:G:OP1	2.48	0.62
29:a:1457:G:H2'	29:a:1458:G:C8	2.34	0.62
33:f:97:PHE:CZ	33:f:170:LYS:HG3	2.35	0.62
27:A:681:C:H2'	27:A:682:A:H8	1.63	0.61
27:A:2334:U:H4'	27:A:2341:U:H1'	1.81	0.61
27:A:2677:A:O2'	27:A:2796:A:N3	2.33	0.61
29:a:1506:U:OP1	39:l:137:ARG:NH1	2.32	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:I:140:GLN:NE2	27:A:2969:C:O2	2.32	0.61
27:A:2339:G:H1	27:A:2387:U:H3	1.48	0.61
27:A:2407:C:N4	27:A:2408:G:O6	2.32	0.61
27:A:2756:G:O2'	27:A:2881:A:N1	2.30	0.61
29:a:693:G:H2'	29:a:694:G:C8	2.35	0.61
29:a:452:A:H62	44:q:94:LYS:H	1.47	0.61
31:d:141:MET:HE2	31:d:149:ILE:HG22	1.81	0.61
39:l:90:LYS:HZ1	39:l:117:GLY:HA3	1.66	0.61
4:H:43:VAL:HG22	4:H:161:ILE:HG13	1.81	0.61
5:I:150:ARG:NE	5:I:163:VAL:O	2.32	0.61
10:Q:82:GLU:N	10:Q:82:GLU:OE2	2.33	0.61
27:A:247:G:OP2	27:A:249:C:N4	2.30	0.61
27:A:1608:U:H3'	27:A:1609:G:H8	1.65	0.61
29:a:644:G:OP1	46:s:62:ARG:NH1	2.34	0.61
27:A:1166:A:O2'	27:A:1230:G:N2	2.33	0.61
27:A:2470:A:H2'	27:A:2471:A:C8	2.35	0.61
27:A:1554:U:H2'	27:A:1555:A:H8	1.64	0.61
29:a:175:A:OP1	48:u:56:ARG:NH2	2.31	0.61
29:a:489:A:H8	29:a:523:U:O2'	1.84	0.61
13:T:36:LYS:NZ	27:A:1367:G:N7	2.48	0.61
27:A:2088:C:H2'	27:A:2089:C:C6	2.36	0.61
29:a:826:U:H2'	29:a:828:G:H5'	1.80	0.61
29:a:940:A:OP1	47:t:55:ARG:NH1	2.34	0.61
41:n:12:ASP:CG	41:n:46:LYS:HZ1	2.08	0.61
12:S:48:ARG:NH1	12:S:97:TYR:OH	2.30	0.61
17:X:4:HIS:NE2	27:A:81:A:OP1	2.34	0.61
26:4:57:ARG:HG2	47:t:67:VAL:O	2.01	0.61
33:f:101:LEU:HD21	33:f:145:VAL:HG22	1.82	0.61
32:e:90:GLU:O	32:e:95:ASN:ND2	2.33	0.61
49:c:113:ARG:O	49:c:113:ARG:HD3	2.01	0.61
15:V:53:PRO:O	15:V:57:VAL:HG23	2.00	0.60
27:A:1690:A:H2'	27:A:1691:A:C8	2.35	0.60
27:A:2761:U:H2'	27:A:2762:C:C6	2.36	0.60
47:t:25:LYS:HG2	47:t:27:THR:HG22	1.83	0.60
19:1:24:ARG:NH1	27:A:469:G:OP1	2.33	0.60
27:A:2:A:H2'	27:A:3:A:C8	2.36	0.60
27:A:1754:G:H1	27:A:1759:A:N6	1.98	0.60
27:A:2385:G:OP2	27:A:2387:U:N3	2.31	0.60
27:A:2716:U:H2'	27:A:2717:U:C6	2.36	0.60
36:i:71:GLU:OE2	36:i:71:GLU:N	2.33	0.60
37:j:31:ARG:HG2	37:j:36:VAL:HG22	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:m:73:ASN:HD21	40:m:105:GLN:HB2	1.66	0.60
27:A:2344:G:H2'	27:A:2345:U:C6	2.36	0.60
29:a:21:U:H2'	29:a:22:C:C6	2.36	0.60
49:c:26:LYS:HE3	49:c:193:PRO:HD2	1.83	0.60
17:X:2:LYS:O	17:X:96:ARG:NH1	2.34	0.60
20:2:7:PRO:HD3	20:2:56:ARG:HD3	1.83	0.60
27:A:1020:A:H2'	27:A:1021:G:C8	2.36	0.60
41:n:12:ASP:HA	41:n:46:LYS:NZ	2.17	0.60
29:a:1479:U:OP1	50:w:21:LYS:NZ	2.34	0.60
41:n:49:THR:HG23	41:n:52:GLN:H	1.66	0.60
27:A:1146:A:N3	27:A:2710:G:O2'	2.32	0.60
34:g:46:ARG:HB2	34:g:46:ARG:HH11	1.67	0.60
27:A:2902:A:H2'	27:A:2903:A:C8	2.37	0.59
2:F:83:GLU:OE1	27:A:2859:C:O2'	2.20	0.59
20:2:36:MET:HE2	20:2:41:LEU:HD21	1.84	0.59
27:A:217:G:N2	27:A:235:U:H4'	2.17	0.59
27:A:2364:C:H2'	27:A:2365:A:C8	2.37	0.59
29:a:144:G:H2'	29:a:145:G:C8	2.37	0.59
37:j:64:HIS:O	37:j:68:ILE:HG12	2.01	0.59
42:o:73:HIS:HE1	42:o:78:GLY:HA2	1.66	0.59
5:I:74:ALA:O	5:I:78:THR:HG22	2.01	0.59
27:A:971:G:H2'	27:A:972:A:C8	2.37	0.59
31:d:90:LEU:HB3	31:d:98:VAL:HG11	1.85	0.59
29:a:989:G:N2	29:a:1006:U:O2	2.35	0.59
47:t:22:GLN:NE2	47:t:29:GLN:OE1	2.36	0.59
49:c:50:ILE:HD11	49:c:216:VAL:CG1	2.32	0.59
17:X:29:ASP:OD1	17:X:29:ASP:N	2.34	0.59
20:2:17:GLU:OE1	20:2:17:GLU:N	2.25	0.59
27:A:2755:A:H61	27:A:2886:A:H61	1.50	0.59
28:B:37:C:N3	28:B:50:C:O2'	2.35	0.59
29:a:456:C:H1'	29:a:457:A:C5	2.37	0.59
4:H:15:TYR:HA	4:H:19:ILE:HB	1.83	0.59
27:A:502:C:H2'	27:A:503:A:C8	2.38	0.59
27:A:994:A:N7	27:A:1014:G:O2'	2.31	0.59
27:A:1754:G:N2	27:A:1759:A:N1	2.48	0.59
29:a:337:G:H2'	29:a:338:A:C8	2.38	0.59
1:E:257:THR:OG1	27:A:2014:G:O2'	2.21	0.59
29:a:654:G:H2'	29:a:655:A:C8	2.37	0.59
41:n:67:GLU:HA	41:n:67:GLU:OE2	2.01	0.59
7:M:56:VAL:HB	7:M:124:VAL:HG12	1.84	0.59
27:A:285:U:H3'	27:A:286:G:H4'	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:789:G:H2'	27:A:919:A:H61	1.68	0.59
27:A:2070:A:H2'	27:A:2071:A:C8	2.37	0.59
29:a:716:U:H2'	29:a:717:C:C6	2.37	0.59
37:j:70:ALA:O	37:j:74:THR:HG22	2.03	0.59
46:s:44:GLU:OE1	46:s:44:GLU:N	2.35	0.59
29:a:481:G:H2'	29:a:482:A:C8	2.37	0.59
31:d:87:ARG:O	31:d:91:GLU:HG2	2.03	0.59
32:e:7:PRO:HB2	32:e:10:ARG:HG3	1.85	0.59
37:j:121:ALA:HB1	37:j:123:PHE:CE1	2.36	0.59
49:c:27:MET:C	49:c:31:ILE:HD13	2.28	0.59
49:c:162:TRP:CH2	49:c:186:ILE:HG23	2.38	0.59
5:I:96:ARG:HH12	5:I:98:GLN:HG3	1.68	0.58
9:O:65:LYS:HB2	27:A:2640:G:H5''	1.84	0.58
27:A:137:G:H21	27:A:1524:G:H1'	1.68	0.58
27:A:1533:U:OP2	27:A:1535:C:N4	2.36	0.58
27:A:2325:U:H2'	27:A:2326:A:H8	1.67	0.58
29:a:92:A:H1'	29:a:93:C:H5	1.68	0.58
27:A:284:G:H1'	27:A:303:G:C2	2.39	0.58
27:A:911:U:H2'	27:A:912:C:C6	2.39	0.58
29:a:10:G:OP2	29:a:10:G:N2	2.36	0.58
29:a:1291:G:OP1	41:n:81:LYS:NZ	2.35	0.58
31:d:147:LYS:NZ	31:d:147:LYS:HB2	2.17	0.58
35:h:51:ARG:HB2	35:h:58:PRO:HG3	1.85	0.58
49:c:133:GLU:O	49:c:137:LEU:HD12	2.02	0.58
26:4:15:GLN:HB3	26:4:34:VAL:HA	1.85	0.58
49:c:32:PHE:CD2	49:c:33:THR:HG22	2.38	0.58
49:c:96:TRP:HA	49:c:100:MET:HE1	1.86	0.58
49:c:58:LYS:NZ	49:c:224:GLY:HA2	2.18	0.58
1:E:60:ARG:HA	27:A:1788:G:H5'	1.86	0.58
27:A:635:G:O2'	27:A:636:U:O4'	2.21	0.58
27:A:994:A:OP2	27:A:1014:G:N2	2.36	0.58
27:A:2367:G:N2	27:A:2369:C:O2	2.36	0.58
29:a:82:U:O4	29:a:87:G:O6	2.22	0.58
29:a:1486:A:H2	29:a:1489:G:H1	1.49	0.58
41:n:12:ASP:HA	41:n:46:LYS:HZ1	1.68	0.58
27:A:279:U:H2'	27:A:280:G:C8	2.39	0.58
27:A:672:C:H2'	27:A:673:C:C6	2.39	0.58
27:A:1551:U:H2'	27:A:1552:A:O4'	2.04	0.58
41:n:59:TYR:HE1	41:n:63:ASN:HD21	1.52	0.58
4:H:52:ARG:HH21	4:H:56:LEU:HD11	1.69	0.58
20:2:9:GLU:N	20:2:9:GLU:OE2	2.37	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:1620:U:H2'	27:A:1621:C:C6	2.39	0.58
27:A:2729:G:H2'	27:A:2800:G:H1	1.69	0.58
27:A:2761:U:H2'	27:A:2762:C:H6	1.67	0.58
27:A:2323:G:N2	27:A:2412:U:O2	2.29	0.58
29:a:1221:U:C5	35:h:116:MET:HG2	2.37	0.58
29:a:1298:G:N1	29:a:1301:A:OP2	2.37	0.58
29:a:1471:G:OP1	30:v:23:ARG:NH2	2.36	0.58
32:e:154:ARG:O	32:e:154:ARG:HG2	2.04	0.58
37:j:54:THR:HG23	37:j:56:GLU:H	1.67	0.58
49:c:80:ILE:HG12	49:c:214:THR:HG21	1.86	0.58
27:A:2339:G:N1	27:A:2385:G:OP2	2.33	0.58
29:a:1138:A:H62	29:a:1159:G:H21	1.51	0.58
41:n:45:THR:O	41:n:48:LEU:HD22	2.04	0.58
42:o:28:LYS:HD2	42:o:44:ALA:HB1	1.85	0.58
49:c:89:MET:SD	49:c:90:PRO:HD2	2.44	0.58
49:c:142:ASN:HA	49:c:145:GLU:HG3	1.85	0.58
49:c:186:ILE:HG22	49:c:200:ILE:HB	1.86	0.58
4:H:23:LEU:HD11	4:H:176:LEU:HD23	1.85	0.58
27:A:1791:A:H2'	27:A:1792:A:C8	2.38	0.58
29:a:1418:G:H2'	29:a:1419:C:H6	1.69	0.58
46:s:52:ARG:HB2	46:s:52:ARG:NH1	2.18	0.58
47:t:19:VAL:HG21	47:t:44:PHE:HE1	1.69	0.58
20:2:13:LEU:HB3	20:2:17:GLU:HG2	1.86	0.57
27:A:256:A:H2'	27:A:257:A:C8	2.39	0.57
27:A:987:A:H2	27:A:1021:G:H1	1.48	0.57
29:a:448:A:OP2	29:a:465:G:N2	2.30	0.57
30:v:25:ARG:HH11	30:v:25:ARG:HG3	1.69	0.57
41:n:15:MET:HE2	41:n:15:MET:HA	1.85	0.57
14:U:60:VAL:HG22	14:U:102:ILE:HG12	1.85	0.57
22:5:14:ARG:HB3	27:A:13:G:H5''	1.86	0.57
26:4:15:GLN:N	26:4:33:ILE:O	2.38	0.57
29:a:819:U:H3	29:a:829:G:N2	1.99	0.57
9:O:133:ALA:O	9:O:137:ILE:HG13	2.05	0.57
12:S:84:ASP:OD1	12:S:84:ASP:N	2.37	0.57
15:V:48:GLN:O	15:V:51:SER:OG	2.21	0.57
27:A:928:U:H2'	27:A:929:C:C6	2.39	0.57
27:A:1024:A:H2'	27:A:1027:C:H5	1.70	0.57
27:A:2883:G:N2	27:A:2886:A:OP2	2.25	0.57
29:a:1220:A:H62	29:a:1281:A:N6	2.01	0.57
37:j:88:ASP:OD1	37:j:88:ASP:N	2.37	0.57
49:c:212:LEU:HA	49:c:215:LYS:HG2	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:2:A:H2'	27:A:3:A:H8	1.69	0.57
35:h:23:VAL:O	35:h:27:VAL:HG13	2.03	0.57
11:R:71:ARG:NH2	28:B:28:A:OP1	2.24	0.57
27:A:701:A:H2'	27:A:702:A:C8	2.40	0.57
42:o:87:MET:CE	42:o:92:GLU:HB2	2.33	0.57
4:H:40:LYS:HA	4:H:103:MET:HE2	1.86	0.57
27:A:1606:G:H3'	27:A:1607:C:H5''	1.86	0.57
27:A:2249:G:H2'	27:A:2250:A:C8	2.40	0.57
29:a:1010:C:N4	29:a:1014:U:N3	2.43	0.57
16:W:10:ILE:HD12	16:W:37:SER:HB3	1.86	0.57
27:A:543:U:H3'	27:A:544:U:H5''	1.86	0.57
27:A:1118:A:H2'	27:A:1119:A:C8	2.38	0.57
27:A:1556:A:N1	27:A:1615:G:C6	2.72	0.57
27:A:1561:C:C5'	34:g:16:GLU:OE1	2.52	0.57
35:h:144:MET:O	35:h:148:ASN:ND2	2.35	0.57
27:A:2106:A:H3'	27:A:2107:G:H5''	1.85	0.57
29:a:382:A:H2'	29:a:383:A:C8	2.40	0.57
44:q:15:ASN:OD1	44:q:43:LYS:NZ	2.38	0.57
49:c:188:ASP:OD1	49:c:202:GLY:O	2.23	0.57
33:f:83:ALA:O	33:f:87:LYS:HG3	2.04	0.57
27:A:857:U:H2'	27:A:858:A:H8	1.70	0.57
27:A:1476:G:H2'	27:A:1477:C:C6	2.40	0.57
27:A:3022:G:H2'	27:A:3023:G:O4'	2.04	0.57
29:a:60:U:H2'	29:a:61:G:C8	2.40	0.57
41:n:48:LEU:HD23	41:n:48:LEU:H	1.69	0.57
49:c:51:ASP:OD1	49:c:52:LYS:N	2.37	0.57
27:A:1127:A:N3	27:A:1272:C:O2'	2.38	0.56
27:A:2019:A:H2'	27:A:2020:A:C8	2.40	0.56
37:j:72:LEU:O	37:j:76:ASP:N	2.37	0.56
4:H:32:VAL:HG13	4:H:33:MET:HG3	1.87	0.56
27:A:1025:A:N3	27:A:2488:C:O2'	2.32	0.56
29:a:13:G:H5'	33:f:133:GLY:HA3	1.87	0.56
29:a:481:G:H2'	29:a:482:A:H8	1.70	0.56
15:V:23:LYS:NZ	27:A:2236:G:N7	2.53	0.56
23:6:19:LYS:HD2	23:6:19:LYS:O	2.05	0.56
27:A:429:A:H2'	27:A:430:A:C8	2.40	0.56
27:A:737:A:N1	27:A:2593:A:O2'	2.39	0.56
27:A:1468:A:H2'	27:A:1469:A:C8	2.40	0.56
27:A:1756:G:H1'	27:A:1758:G:C6	2.40	0.56
27:A:2515:U:H2'	27:A:2516:U:C6	2.40	0.56
29:a:11:G:H22	33:f:122:ARG:NH1	2.02	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:a:1199:C:H2'	29:a:1200:A:C8	2.39	0.56
35:h:56:THR:OG1	35:h:57:ASP:N	2.39	0.56
47:t:17:LYS:HD2	47:t:18:LYS:N	2.21	0.56
11:R:41:ASN:ND2	28:B:7:G:O3'	2.37	0.56
27:A:239:U:HO2'	27:A:716:G:HO2'	1.51	0.56
27:A:1640:A:H2'	27:A:1642:G:N7	2.20	0.56
27:A:2729:G:H2'	27:A:2800:G:N1	2.21	0.56
34:g:57:GLU:HA	34:g:57:GLU:OE2	2.06	0.56
37:j:40:ARG:N	37:j:84:TYR:O	2.38	0.56
37:j:108:ILE:HD12	37:j:112:PRO:HA	1.88	0.56
38:k:36:VAL:HG12	38:k:76:ILE:HG22	1.87	0.56
41:n:73:GLU:C	41:n:73:GLU:OE2	2.49	0.56
47:t:22:GLN:OE1	47:t:29:GLN:OE1	2.23	0.56
49:c:108:HIS:O	49:c:112:GLN:HG2	2.04	0.56
3:G:154:VAL:HG23	3:G:193:ASP:HB2	1.88	0.56
4:H:128:GLN:O	27:A:2527:G:O2'	2.23	0.56
14:U:77:LYS:NZ	27:A:1110:C:OP1	2.36	0.56
27:A:621:U:H2'	27:A:622:C:C6	2.41	0.56
29:a:1296:C:H2'	29:a:1297:U:C6	2.41	0.56
31:d:123:LEU:HD11	31:d:129:PHE:HB3	1.88	0.56
33:f:68:LYS:O	33:f:98:ARG:NH2	2.38	0.56
27:A:567:A:H4'	27:A:568:A:H5'	1.87	0.56
29:a:961:C:O2	42:o:59:ARG:NH1	2.39	0.56
27:A:90:C:H2'	27:A:91:C:O4'	2.06	0.56
27:A:1288:A:H2'	27:A:1289:A:C8	2.40	0.56
27:A:1441:C:HO2'	27:A:2234:G:HO2'	1.44	0.56
29:a:1177:A:O2'	29:a:1178:A:OP1	2.20	0.56
27:A:265:A:N1	27:A:515:U:O2'	2.36	0.56
27:A:2682:G:O2'	27:A:2684:U:O4	2.22	0.56
29:a:49:U:H2'	29:a:50:G:C8	2.41	0.56
35:h:17:VAL:HG23	35:h:18:TYR:CD1	2.40	0.56
37:j:132:GLU:HG2	37:j:141:ALA:HB1	1.88	0.56
8:N:30:ARG:HG3	27:A:2898:G:H4'	1.86	0.56
14:U:25:GLU:OE1	27:A:1111:G:N2	2.39	0.56
29:a:1109:C:O2'	29:a:1110:A:N7	2.34	0.56
29:a:1237:C:H5'	29:a:1239:G:H1'	1.88	0.56
41:n:12:ASP:CA	41:n:46:LYS:HZ1	2.19	0.56
21:3:11:SER:HA	21:3:31:ILE:HD11	1.88	0.56
29:a:145:G:O2'	29:a:1429:A:N3	2.32	0.56
29:a:481:G:OP1	40:m:114:ARG:NH2	2.35	0.56
29:a:1266:U:O2'	29:a:1267:U:OP1	2.24	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:p:26:GLU:N	43:p:26:GLU:OE2	2.36	0.56
45:r:83:SER:O	45:r:87:ARG:NH1	2.39	0.56
17:X:86:ARG:HB3	17:X:97:ILE:HD13	1.89	0.55
27:A:72:G:H22	27:A:108:A:H2	1.53	0.55
29:a:1476:A:O2'	50:w:80:ARG:NH2	2.39	0.55
46:s:37:LEU:HD12	46:s:37:LEU:O	2.06	0.55
4:H:71:LYS:H	26:4:6:HIS:CE1	2.25	0.55
29:a:581:U:H2'	29:a:582:U:C6	2.41	0.55
35:h:17:VAL:HG23	35:h:18:TYR:HD1	1.72	0.55
47:t:22:GLN:CD	47:t:29:GLN:OE1	2.50	0.55
10:Q:42:ARG:NH2	27:A:3038:C:OP1	2.40	0.55
19:1:41:ARG:HD2	19:1:43:GLY:H	1.71	0.55
27:A:1018:U:H1'	27:A:1019:C:H5	1.71	0.55
27:A:1612:U:C1'	34:g:17:ARG:HH21	2.19	0.55
30:v:22:ARG:NH1	30:v:25:ARG:HH12	2.05	0.55
34:g:37:VAL:HG22	34:g:39:LYS:HE3	1.89	0.55
12:S:36:LYS:HD2	12:S:36:LYS:C	2.31	0.55
18:Z:15:ASP:OD1	18:Z:16:SER:N	2.40	0.55
27:A:1559:A:H2'	27:A:1560:U:C6	2.41	0.55
27:A:681:C:H2'	27:A:682:A:C8	2.40	0.55
27:A:2465:A:H2'	27:A:2466:G:C8	2.42	0.55
28:B:41:U:N3	28:B:45:G:OP2	2.37	0.55
29:a:504:G:H2'	29:a:505:C:C6	2.42	0.55
29:a:1497:A:H2'	29:a:1498:C:C6	2.41	0.55
37:j:150:ARG:NH2	50:w:35:HIS:HB2	2.22	0.55
2:F:44:ARG:NH1	27:A:3009:U:OP1	2.40	0.55
22:5:34:GLY:O	22:5:36:GLN:NE2	2.39	0.55
26:4:61:PHE:CE2	47:t:41:ILE:CD1	2.88	0.55
27:A:293:G:H2'	27:A:294:G:H8	1.72	0.55
27:A:1529:U:H3'	27:A:1530:G:C8	2.41	0.55
27:A:1224:G:H2'	27:A:1225:G:H8	1.70	0.55
27:A:2601:A:H2'	27:A:2602:A:C8	2.41	0.55
29:a:1330:U:H4'	37:j:142:ARG:HG3	1.89	0.55
45:r:21:LYS:HB2	45:r:78:GLU:HG3	1.89	0.55
1:E:123:ALA:HB3	1:E:131:LEU:HD22	1.88	0.55
6:J:29:TYR:O	6:J:33:ARG:HG3	2.07	0.55
27:A:293:G:H2'	27:A:294:G:C8	2.41	0.55
27:A:1233:A:H2'	27:A:1234:U:O4'	2.07	0.55
27:A:1509:U:H2'	27:A:1510:A:O4'	2.06	0.55
27:A:1790:A:H2'	27:A:1791:A:C8	2.41	0.55
27:A:2922:U:H2'	27:A:2923:C:C6	2.40	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:3018:U:H2'	27:A:3019:C:C6	2.42	0.55
34:g:5:GLU:C	34:g:5:GLU:OE1	2.50	0.55
38:k:45:GLU:OE1	38:k:45:GLU:HA	2.06	0.55
5:I:144:GLN:HE22	27:A:2968:G:H21	1.54	0.55
27:A:1547:G:O6	27:A:1623:U:O4	2.24	0.55
27:A:2375:G:H2'	27:A:2376:G:C8	2.42	0.55
32:e:18:ASP:C	32:e:18:ASP:OD1	2.49	0.55
49:c:45:GLN:HA	49:c:48:THR:HG22	1.88	0.55
14:U:12:LYS:NZ	27:A:1112:C:O2	2.38	0.55
27:A:357:U:H4'	27:A:358:G:O5'	2.08	0.55
27:A:1016:C:H2'	27:A:1017:G:O4'	2.07	0.55
27:A:2089:C:H2'	27:A:2090:U:C6	2.42	0.55
37:j:66:GLN:OE1	37:j:66:GLN:O	2.25	0.55
48:u:49:GLU:N	48:u:49:GLU:OE2	2.39	0.55
27:A:1236:G:H2'	27:A:1237:U:O4'	2.06	0.54
29:a:81:C:H3'	29:a:82:U:H5''	1.89	0.54
29:a:1207:C:OP1	41:n:91:ARG:NH2	2.37	0.54
39:l:47:GLN:CD	39:l:47:GLN:N	2.64	0.54
41:n:87:TYR:O	41:n:90:LEU:HD23	2.06	0.54
1:E:31:LYS:NZ	27:A:1647:G:N7	2.49	0.54
14:U:27:LEU:H	14:U:95:THR:HG21	1.72	0.54
27:A:988:U:O2'	27:A:990:G:O4'	2.25	0.54
29:a:399:G:H2'	29:a:400:C:C6	2.42	0.54
31:d:21:ARG:HH21	31:d:55:GLU:HG2	1.72	0.54
32:e:55:LYS:O	32:e:59:SER:OG	2.23	0.54
27:A:673:C:H2'	27:A:674:U:C6	2.42	0.54
27:A:966:U:H2'	27:A:967:G:H8	1.72	0.54
27:A:1284:A:H2'	27:A:1285:G:C8	2.43	0.54
27:A:2344:G:H4'	27:A:2391:G:H22	1.71	0.54
38:k:21:SER:HB3	38:k:92:LEU:HD22	1.90	0.54
41:n:83:GLU:OE2	41:n:83:GLU:C	2.51	0.54
5:I:96:ARG:NH1	5:I:98:GLN:HG3	2.22	0.54
29:a:1232:A:H2'	29:a:1233:A:C8	2.42	0.54
29:a:1425:G:H5''	29:a:1426:C:H5	1.72	0.54
27:A:1548:C:H2'	27:A:1549:G:C8	2.42	0.54
29:a:309:G:O2'	29:a:587:A:N1	2.40	0.54
29:a:485:G:H2'	29:a:486:G:H8	1.72	0.54
29:a:657:U:H3	29:a:693:G:H22	1.54	0.54
43:p:41:GLU:C	43:p:41:GLU:OE1	2.51	0.54
10:Q:70:ILE:HG22	10:Q:72:ASP:H	1.72	0.54
23:6:21:ARG:HH11	23:6:21:ARG:HG3	1.71	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:2482:U:O2'	27:A:2651:C:OP2	2.25	0.54
29:a:1125:G:N2	29:a:1127:A:H62	2.06	0.54
7:M:88:THR:OG1	7:M:91:GLU:OE1	2.24	0.54
27:A:301:U:C2	27:A:338:C:H5'	2.42	0.54
27:A:1710:A:H61	27:A:1716:A:H5''	1.73	0.54
27:A:2238:A:H2'	27:A:2239:A:C8	2.42	0.54
27:A:3078:G:N2	27:A:3081:A:OP2	2.33	0.54
29:a:299:G:H2'	29:a:300:A:C8	2.43	0.54
29:a:337:G:H2'	29:a:338:A:H8	1.72	0.54
29:a:1248:U:O2'	29:a:1249:G:O5'	2.25	0.54
37:j:127:ASP:OD2	37:j:129:ARG:NH1	2.40	0.54
49:c:15:HIS:HB3	49:c:43:LEU:HD21	1.90	0.54
33:f:196:LYS:HD2	33:f:197:ALA:N	2.23	0.54
49:c:87:VAL:HG11	49:c:221:VAL:HG13	1.89	0.54
27:A:747:A:H2	27:A:768:G:H21	1.56	0.54
27:A:1690:A:H2'	27:A:1691:A:H8	1.73	0.54
27:A:2256:G:O6	27:A:2279:C:N4	2.40	0.54
28:B:10:G:O2'	28:B:11:U:OP1	2.22	0.54
29:a:1156:G:H2'	29:a:1157:A:H8	1.72	0.54
36:i:11:LEU:HD22	36:i:77:LEU:HD22	1.89	0.54
37:j:72:LEU:HD23	37:j:107:LEU:HD11	1.90	0.54
47:t:27:THR:HG23	47:t:29:GLN:HE22	1.73	0.54
25:8:15:ARG:NH2	27:A:725:A:OP2	2.34	0.53
27:A:1529:U:H3'	27:A:1530:G:H8	1.73	0.53
29:a:269:U:H2'	29:a:270:A:C8	2.43	0.53
29:a:407:A:O2'	32:e:108:MET:HB2	2.08	0.53
29:a:1516:U:O2	50:w:110:GLU:HA	2.08	0.53
41:n:44:ARG:HB3	41:n:46:LYS:NZ	2.23	0.53
23:6:21:ARG:HG2	23:6:43:PRO:HD2	1.90	0.53
27:A:1705:C:H2'	27:A:1706:A:H8	1.72	0.53
27:A:2323:G:H1	27:A:2412:U:H3	1.54	0.53
29:a:404:G:O2'	29:a:478:A:N1	2.38	0.53
27:A:138:A:H2'	27:A:139:U:O2	2.09	0.53
29:a:1375:G:N2	29:a:1486:A:H8	2.06	0.53
34:g:8:VAL:HG22	34:g:61:ALA:HB3	1.90	0.53
49:c:57:VAL:O	49:c:61:VAL:HG12	2.06	0.53
50:w:105:ALA:O	50:w:106:GLU:C	2.51	0.53
11:R:12:GLU:OE2	28:B:60:G:H4'	2.09	0.53
26:4:61:PHE:CZ	47:t:41:ILE:HD12	2.44	0.53
27:A:273:A:H62	27:A:313:G:H21	1.56	0.53
27:A:502:C:H2'	27:A:503:A:H8	1.72	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:a:252:U:H2'	29:a:253:U:C6	2.43	0.53
29:a:488:C:H1'	29:a:489:A:H2	1.74	0.53
29:a:1104:G:N2	29:a:1105:U:O4	2.41	0.53
41:n:24:GLY:HA3	41:n:66:VAL:HG12	1.91	0.53
41:n:90:LEU:H	41:n:90:LEU:CD2	2.21	0.53
26:4:57:ARG:HA	26:4:60:ARG:HG3	1.90	0.53
27:A:726:A:H2'	27:A:727:A:C8	2.43	0.53
27:A:2297:U:H2'	27:A:2298:U:C6	2.44	0.53
29:a:498:C:H4'	29:a:499:C:O5'	2.08	0.53
33:f:188:ASP:OD1	33:f:188:ASP:C	2.52	0.53
1:E:66:ASP:OD2	1:E:103:ARG:NH1	2.42	0.53
5:I:9:VAL:HG23	5:I:51:ILE:HD11	1.90	0.53
25:8:12:LYS:NZ	27:A:249:C:O2	2.39	0.53
27:A:1403:C:H5	27:A:1441:C:N3	2.06	0.53
27:A:2294:A:H2'	27:A:2295:C:C6	2.44	0.53
29:a:203:U:H2'	29:a:204:A:H8	1.74	0.53
29:a:708:A:H2'	29:a:709:A:C8	2.44	0.53
29:a:1296:C:H2'	29:a:1297:U:H6	1.74	0.53
33:f:191:PRO:HD2	33:f:194:MET:HE3	1.91	0.53
42:o:87:MET:HE3	42:o:92:GLU:OE2	2.07	0.53
26:4:61:PHE:CZ	47:t:9:PRO:HG3	2.43	0.53
26:4:65:TYR:CE1	47:t:8:GLY:HA2	2.43	0.53
27:A:328:C:H2'	27:A:329:U:C6	2.44	0.53
27:A:1284:A:H2'	27:A:1285:G:H8	1.73	0.53
29:a:191:C:H2'	29:a:192:G:O4'	2.09	0.53
29:a:642:C:H2'	29:a:643:A:C8	2.44	0.53
29:a:1130:C:H2'	29:a:1131:G:C8	2.44	0.53
29:a:1171:G:H5''	31:d:176:HIS:CE1	2.44	0.53
41:n:12:ASP:HB2	41:n:46:LYS:HZ1	1.74	0.53
47:t:32:LYS:NZ	47:t:57:HIS:CE1	2.76	0.53
50:w:109:ARG:HD3	50:w:110:GLU:HG3	1.89	0.53
3:G:163:GLU:N	3:G:163:GLU:OE2	2.42	0.53
27:A:339:U:H2'	27:A:340:A:C8	2.44	0.53
27:A:2163:U:OP1	27:A:2828:U:O2'	2.27	0.53
27:A:2371:G:H2'	27:A:2372:U:C6	2.43	0.53
29:a:1329:G:O6	37:j:32:ARG:NH2	2.42	0.53
29:a:1414:C:H2'	29:a:1415:G:O4'	2.09	0.53
35:h:74:GLU:HG2	35:h:91:VAL:HG22	1.91	0.53
49:c:23:TRP:CH2	49:c:25:PRO:HA	2.44	0.53
1:E:37:LEU:HD13	1:E:62:TYR:HB2	1.91	0.53
27:A:277:U:H2'	27:A:278:A:C8	2.44	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:1052:U:H2'	27:A:1053:G:H8	1.74	0.53
27:A:2497:A:H2'	27:A:2498:A:C8	2.44	0.53
34:g:16:GLU:OE2	34:g:16:GLU:C	2.52	0.53
42:o:4:LYS:HB2	42:o:4:LYS:HZ3	1.74	0.53
44:q:86:LEU:HB2	44:q:87:PRO:HD3	1.91	0.53
27:A:2255:A:N6	27:A:2722:C:H1'	2.23	0.53
27:A:2682:G:H21	27:A:2683:A:H61	1.55	0.53
29:a:119:C:OP1	29:a:311:C:O2'	2.27	0.53
29:a:819:U:H3	29:a:829:G:H1	1.56	0.53
35:h:113:GLU:HB2	35:h:119:ARG:HG2	1.90	0.53
25:8:47:ARG:NH2	27:A:724:G:OP1	2.41	0.52
26:4:65:TYR:CD1	47:t:9:PRO:HD3	2.44	0.52
27:A:2003:A:H1'	27:A:2162:A:N6	2.24	0.52
29:a:297:G:N2	29:a:300:A:OP2	2.36	0.52
29:a:570:U:OP1	36:i:31:LYS:HG3	2.09	0.52
29:a:1337:A:H2'	29:a:1338:G:H8	1.74	0.52
1:E:108:PRO:HD2	1:E:111:LEU:HD22	1.90	0.52
3:G:158:ILE:HG22	3:G:197:SER:HB2	1.91	0.52
27:A:639:C:O2'	27:A:640:G:H8	1.92	0.52
27:A:2255:A:H3'	27:A:2256:G:H2'	1.91	0.52
29:a:376:G:H5''	44:q:6:LYS:HB3	1.90	0.52
29:a:1098:U:H2'	29:a:1099:C:H6	1.74	0.52
31:d:133:MET:HE2	31:d:153:CYS:SG	2.49	0.52
49:c:26:LYS:HD2	49:c:193:PRO:HG2	1.90	0.52
3:G:31:ILE:HD11	9:O:4:ILE:HD12	1.92	0.52
11:R:81:SER:HB2	11:R:116:LEU:HB3	1.92	0.52
27:A:2256:G:N2	27:A:2678:G:O2'	2.42	0.52
27:A:2872:G:H2'	27:A:2873:U:C6	2.45	0.52
27:A:3030:A:H2'	27:A:3031:A:C8	2.44	0.52
29:a:498:C:H5''	29:a:499:C:C6	2.44	0.52
29:a:993:G:H1	29:a:1002:U:H3	1.56	0.52
29:a:1098:U:H2'	29:a:1099:C:C6	2.44	0.52
31:d:15:THR:HG23	31:d:207:ILE:CD1	2.39	0.52
41:n:29:ARG:O	41:n:33:ILE:HG23	2.10	0.52
42:o:86:GLU:HG3	42:o:90:ARG:NH2	2.25	0.52
11:R:73:ILE:HD11	11:R:80:HIS:HA	1.91	0.52
27:A:1610:C:H2'	27:A:1611:A:C8	2.45	0.52
27:A:2510:A:H4'	27:A:2511:A:O4'	2.09	0.52
46:s:18:ARG:C	46:s:19:LYS:HD2	2.35	0.52
12:S:13:ARG:NH1	12:S:80:ILE:O	2.42	0.52
12:S:19:PHE:O	12:S:49:ARG:NH1	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:T:6:ARG:NH1	27:A:677:G:N7	2.50	0.52
27:A:1019:C:H2'	27:A:1020:A:O4'	2.09	0.52
27:A:2754:G:OP2	27:A:2759:G:N2	2.43	0.52
29:a:1349:C:HO2'	38:k:62:ARG:HH22	1.54	0.52
1:E:200:GLU:OE1	1:E:200:GLU:N	2.38	0.52
7:M:98:THR:HB	7:M:124:VAL:HG23	1.92	0.52
11:R:62:ALA:O	11:R:91:ARG:NH1	2.42	0.52
27:A:992:C:H2'	27:A:993:G:O4'	2.10	0.52
27:A:2467:U:H2'	27:A:2468:U:C6	2.45	0.52
29:a:973:U:O4	29:a:1193:U:O2'	2.22	0.52
29:a:1380:C:OP2	33:f:54:ARG:NH2	2.43	0.52
50:w:103:VAL:O	50:w:104:PRO:C	2.53	0.52
24:7:37:ARG:NH1	24:7:44:ALA:O	2.43	0.52
27:A:2805:G:OP2	27:A:2805:G:N2	2.42	0.52
27:A:2961:G:H2'	27:A:2962:A:C8	2.45	0.52
29:a:522:G:OP1	32:e:10:ARG:NH2	2.31	0.52
29:a:1014:U:H2'	29:a:1015:G:H8	1.72	0.52
29:a:1067:G:H2'	29:a:1068:G:C8	2.45	0.52
34:g:11:ASP:C	34:g:11:ASP:OD1	2.53	0.52
47:t:22:GLN:HA	47:t:25:LYS:NZ	2.24	0.52
2:F:27:THR:OG1	2:F:196:GLY:O	2.27	0.52
24:7:27:THR:HG23	24:7:30:GLY:H	1.75	0.52
27:A:2113:A:H2'	27:A:2114:A:C8	2.44	0.52
32:e:189:PRO:O	32:e:190:LEU:HG	2.09	0.52
21:3:9:VAL:HG11	21:3:55:GLU:HG3	1.92	0.52
27:A:2703:U:H5''	27:A:2761:U:H4'	1.92	0.52
29:a:1067:G:H2'	29:a:1068:G:H8	1.75	0.52
41:n:34:LEU:HD13	41:n:41:LYS:HA	1.92	0.52
47:t:32:LYS:HA	47:t:50:ALA:HB3	1.91	0.52
49:c:77:GLN:HG2	49:c:93:ASN:HB2	1.92	0.52
5:I:7:GLN:NE2	5:I:8:PRO:O	2.43	0.52
9:O:98:LEU:HD22	9:O:103:LEU:HD12	1.91	0.52
27:A:429:A:H2'	27:A:430:A:H8	1.74	0.52
27:A:678:A:N1	27:A:924:G:O2'	2.40	0.52
27:A:1080:U:H2'	27:A:1081:C:H6	1.74	0.52
27:A:2363:A:H2'	27:A:2364:C:C6	2.45	0.52
33:f:87:LYS:O	33:f:90:GLU:HG3	2.10	0.52
37:j:87:LEU:HD12	37:j:95:GLN:HG2	1.90	0.52
26:4:64:ARG:HG2	47:t:5:LEU:HD11	1.92	0.51
27:A:974:G:H4'	27:A:975:U:O5'	2.10	0.51
27:A:1530:G:H21	27:A:1805:G:N2	2.08	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:1534:C:H3'	27:A:1535:C:O2	2.10	0.51
27:A:1612:U:H2'	27:A:1613:G:C8	2.44	0.51
3:G:199:GLU:H	3:G:199:GLU:CD	2.16	0.51
21:3:39:ASP:OD1	21:3:44:ARG:HD3	2.11	0.51
22:5:7:ARG:NH1	27:A:671:G:O2'	2.44	0.51
27:A:2340:A:H61	27:A:2394:A:H61	1.57	0.51
29:a:407:A:H2'	29:a:408:G:H8	1.75	0.51
29:a:604:U:O2'	44:q:17:GLN:OE1	2.28	0.51
5:I:9:VAL:HG11	5:I:74:ALA:HB2	1.91	0.51
25:8:31:HIS:NE2	27:A:2616:A:OP2	2.27	0.51
27:A:32:G:H1'	27:A:542:A:C4	2.44	0.51
27:A:543:U:H3'	27:A:544:U:C5'	2.40	0.51
27:A:947:U:H2'	27:A:948:G:C8	2.45	0.51
29:a:794:A:H2'	29:a:796:A:H5''	1.92	0.51
32:e:151:GLN:HA	32:e:154:ARG:NH1	2.26	0.51
37:j:72:LEU:HA	37:j:75:VAL:HG12	1.92	0.51
42:o:73:HIS:CE1	42:o:78:GLY:HA2	2.45	0.51
11:R:34:GLU:HG2	11:R:35:VAL:HG23	1.92	0.51
16:W:10:ILE:HG22	16:W:11:ILE:HD12	1.92	0.51
27:A:483:G:H2'	27:A:484:C:C6	2.45	0.51
27:A:818:U:H2'	27:A:819:G:O4'	2.11	0.51
27:A:1296:G:H2'	27:A:1297:G:C8	2.46	0.51
27:A:1500:A:H1'	27:A:1501:C:C6	2.45	0.51
27:A:1633:U:H2'	27:A:1634:C:C6	2.46	0.51
29:a:60:U:H2'	29:a:61:G:H8	1.75	0.51
29:a:84:U:H5''	29:a:85:C:C5	2.45	0.51
29:a:229:U:O2'	44:q:24:ASP:OD2	2.27	0.51
29:a:294:C:OP1	29:a:590:A:O2'	2.23	0.51
29:a:1042:U:H2'	29:a:1043:C:C6	2.45	0.51
29:a:1440:A:H3'	29:a:1441:G:H8	1.75	0.51
41:n:52:GLN:O	41:n:56:LEU:HG	2.11	0.51
50:w:104:PRO:O	50:w:105:ALA:C	2.52	0.51
27:A:1551:U:HO2'	27:A:1552:A:P	2.34	0.51
29:a:772:A:O2'	29:a:774:A:N7	2.43	0.51
29:a:823:U:O4	29:a:826:U:N3	2.41	0.51
29:a:1302:C:O2	47:t:72:GLY:HA3	2.11	0.51
2:F:129:ARG:HA	2:F:170:MET:SD	2.51	0.51
21:3:31:ILE:HG22	21:3:32:ARG:HG3	1.93	0.51
27:A:363:A:H2'	27:A:364:A:O4'	2.11	0.51
27:A:479:A:H1'	27:A:499:G:O4'	2.11	0.51
27:A:764:U:H2'	27:A:765:G:H8	1.76	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:2873:U:H2'	27:A:2874:C:C6	2.46	0.51
29:a:436:C:H2'	29:a:437:U:C6	2.44	0.51
29:a:998:G:H2'	29:a:999:A:C8	2.46	0.51
29:a:1207:C:OP2	41:n:103:THR:OG1	2.22	0.51
43:p:83:GLU:C	43:p:83:GLU:OE2	2.53	0.51
46:s:37:LEU:O	46:s:40:THR:HG22	2.10	0.51
7:M:71:LYS:NZ	27:A:1140:G:OP1	2.43	0.51
27:A:998:G:H1	27:A:1010:U:H3	1.59	0.51
29:a:1278:C:H4'	29:a:1284:U:O4	2.10	0.51
4:H:95:ARG:NH1	27:A:2538:A:OP1	2.43	0.51
5:I:138:ASP:OD2	5:I:141:LYS:HG2	2.10	0.51
20:2:14:THR:OG1	20:2:15:ASP:N	2.40	0.51
20:2:56:ARG:NH1	27:A:74:C:OP1	2.44	0.51
27:A:1556:A:H2	27:A:1615:G:N1	2.01	0.51
27:A:2011:U:H2'	27:A:2012:C:C6	2.45	0.51
27:A:2011:U:H2'	27:A:2012:C:H6	1.75	0.51
27:A:2261:U:H2'	27:A:2262:C:C6	2.46	0.51
27:A:2674:A:H2'	27:A:2674:A:N3	2.26	0.51
28:B:10:G:O2'	28:B:11:U:H5'	2.10	0.51
11:R:93:LYS:HZ1	11:R:124:GLY:HA3	1.76	0.51
14:U:61:THR:OG1	14:U:100:THR:OG1	2.29	0.51
17:X:77:ASP:OD1	17:X:77:ASP:N	2.42	0.51
26:4:61:PHE:HE2	47:t:41:ILE:HD12	1.69	0.51
27:A:139:U:H2'	27:A:140:G:O4'	2.10	0.51
27:A:666:A:H1'	27:A:2256:G:H8	1.74	0.51
27:A:995:U:H2'	27:A:996:G:C8	2.46	0.51
27:A:2343:G:H2'	27:A:2344:G:C8	2.46	0.51
27:A:2686:U:H2'	27:A:2687:U:C6	2.46	0.51
29:a:850:C:H2'	29:a:851:A:O4'	2.11	0.51
37:j:41:LEU:HD12	37:j:83:ILE:HD11	1.91	0.51
50:w:106:GLU:HB3	50:w:109:ARG:HB3	1.92	0.51
24:7:38:ARG:HG3	24:7:45:LEU:HD21	1.92	0.51
26:4:13:THR:O	26:4:33:ILE:N	2.40	0.51
27:A:353:G:O6	27:A:442:U:O2	2.28	0.51
27:A:2800:G:O2'	27:A:2803:C:OP2	2.24	0.51
27:A:2815:C:H2'	27:A:2816:G:C8	2.46	0.51
29:a:11:G:H22	33:f:122:ARG:HH11	1.59	0.51
29:a:987:A:H2'	29:a:988:C:C6	2.45	0.51
34:g:32:LYS:HD2	34:g:32:LYS:C	2.36	0.51
36:i:5:ASP:OD2	36:i:79:ARG:NE	2.35	0.51
38:k:14:ASP:OD1	38:k:16:GLU:N	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:q:81:GLN:O	44:q:85:GLY:N	2.32	0.51
45:r:26:TYR:CZ	45:r:73:ARG:HG3	2.45	0.51
50:w:106:GLU:HG3	50:w:110:GLU:HB2	1.92	0.51
19:1:41:ARG:HG2	19:1:42:PRO:HD2	1.92	0.50
27:A:1165:G:H4'	27:A:1166:A:H5'	1.94	0.50
29:a:324:G:N1	29:a:327:A:OP2	2.42	0.50
29:a:737:U:H2'	29:a:738:G:O4'	2.11	0.50
3:G:139:LYS:NZ	27:A:401:C:OP2	2.30	0.50
7:M:112:ASN:HB2	27:A:650:G:OP1	2.11	0.50
27:A:1640:A:O2'	27:A:1641:U:OP1	2.28	0.50
29:a:933:G:OP2	41:n:102:ARG:NH2	2.44	0.50
49:c:84:ALA:O	49:c:88:GLY:N	2.43	0.50
3:G:30:ASN:O	3:G:34:MET:HG3	2.11	0.50
6:J:10:GLU:HG3	6:J:11:HIS:ND1	2.26	0.50
19:1:2:ALA:HB2	27:A:1479:G:OP1	2.10	0.50
26:4:64:ARG:HG2	47:t:5:LEU:CD1	2.41	0.50
27:A:1076:A:H1'	27:A:2682:G:H5'	1.93	0.50
27:A:1229:A:C8	27:A:1230:G:H1'	2.46	0.50
27:A:2170:U:H2'	27:A:2171:C:C6	2.46	0.50
29:a:993:G:H2'	29:a:994:C:C6	2.45	0.50
31:d:77:GLY:N	31:d:82:GLU:HB2	2.26	0.50
34:g:41:ASP:C	34:g:41:ASP:OD1	2.55	0.50
49:c:27:MET:CE	49:c:193:PRO:HD3	2.41	0.50
28:B:5:C:OP1	28:B:62:C:O2'	2.30	0.50
38:k:14:ASP:OD1	38:k:14:ASP:C	2.54	0.50
40:m:74:LEU:HD21	40:m:104:THR:HB	1.94	0.50
41:n:48:LEU:H	41:n:48:LEU:CD2	2.24	0.50
47:t:17:LYS:HA	47:t:20:ASP:OD2	2.11	0.50
27:A:764:U:H2'	27:A:765:G:C8	2.47	0.50
29:a:1284:U:C6	41:n:17:ILE:HD13	2.46	0.50
4:H:61:ILE:HD12	4:H:72:PRO:HG2	1.93	0.50
18:Z:32:LYS:HB3	27:A:759:G:C6	2.47	0.50
27:A:222:A:O2'	27:A:508:G:N3	2.42	0.50
27:A:306:U:H2'	27:A:307:G:H8	1.76	0.50
27:A:1150:A:H2	27:A:1240:G:H1	1.60	0.50
27:A:1536:A:H2'	27:A:1537:U:C6	2.47	0.50
27:A:2074:G:H21	27:A:2109:A:H62	1.58	0.50
29:a:335:C:H2'	29:a:336:A:H8	1.76	0.50
29:a:452:A:H2	44:q:47:SER:HB3	1.74	0.50
29:a:560:C:H2'	29:a:561:G:O4'	2.10	0.50
31:d:188:GLU:HB3	31:d:195:ARG:HD2	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:g:24:GLU:HA	34:g:24:GLU:OE2	2.11	0.50
42:o:65:VAL:HG12	42:o:78:GLY:O	2.12	0.50
49:c:151:ILE:HA	49:c:154:MET:CE	2.42	0.50
8:N:108:GLU:OE1	8:N:108:GLU:N	2.28	0.50
27:A:663:A:C5	27:A:2254:A:C6	3.00	0.50
27:A:1091:A:H5'	27:A:1303:U:H1'	1.94	0.50
27:A:1541:G:H1	27:A:1631:A:H62	1.59	0.50
27:A:1559:A:H2'	27:A:1560:U:H6	1.77	0.50
27:A:1678:U:H5'	27:A:1679:A:OP2	2.11	0.50
27:A:2340:A:N6	27:A:2394:A:H61	2.10	0.50
31:d:30:ASP:OD1	31:d:30:ASP:N	2.39	0.50
34:g:4:TYR:CD2	34:g:72:VAL:HG21	2.46	0.50
7:M:72:LYS:NZ	27:A:1257:G:H5''	2.27	0.50
22:5:27:LEU:HB3	22:5:38:LYS:HB3	1.92	0.50
23:6:12:THR:HG23	23:6:22:ASN:OD1	2.11	0.50
27:A:160:A:OP2	27:A:161:U:O2'	2.24	0.50
27:A:2457:U:H2'	27:A:2458:G:C8	2.46	0.50
29:a:824:C:O2'	29:a:826:U:O4	2.29	0.50
32:e:105:THR:HG23	32:e:108:MET:H	1.77	0.50
38:k:88:MET:N	38:k:88:MET:SD	2.85	0.50
2:F:154:CYS:HB2	27:A:2799:C:H5'	1.93	0.50
5:I:64:SER:O	27:A:2972:A:O2'	2.29	0.50
23:6:39:LYS:HE2	23:6:48:HIS:HB3	1.94	0.50
27:A:326:A:N1	27:A:449:G:N2	2.60	0.50
27:A:1717:U:H5''	27:A:1718:C:H5	1.76	0.50
27:A:2096:G:H2'	27:A:2097:G:H8	1.77	0.50
27:A:2279:C:N4	27:A:2724:U:H1'	2.27	0.50
27:A:2682:G:H21	27:A:2683:A:N6	2.10	0.50
29:a:1059:G:H2'	29:a:1060:A:C8	2.47	0.50
7:M:49:ASP:HB3	7:M:114:LEU:HD11	1.94	0.49
14:U:47:ASN:OD1	14:U:47:ASN:N	2.41	0.49
27:A:150:C:H2'	27:A:151:A:H8	1.77	0.49
27:A:356:G:H5''	27:A:357:U:OP1	2.11	0.49
27:A:499:G:OP2	27:A:2630:A:O2'	2.28	0.49
27:A:1704:U:H2'	27:A:1705:C:C6	2.47	0.49
27:A:1804:G:H2'	27:A:1805:G:C8	2.46	0.49
27:A:1937:U:H2'	27:A:1938:G:O4'	2.12	0.49
27:A:2538:A:H2'	27:A:2539:G:H8	1.77	0.49
27:A:2791:G:H2'	27:A:2792:C:C6	2.47	0.49
29:a:203:U:H2'	29:a:204:A:C8	2.47	0.49
34:g:46:ARG:HB2	34:g:46:ARG:NH1	2.26	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:W:68:ARG:NH2	27:A:1449:C:OP1	2.45	0.49
27:A:2098:U:H2'	27:A:2099:G:O4'	2.12	0.49
27:A:2732:G:O2'	27:A:2778:U:O2'	2.27	0.49
29:a:409:G:P	32:e:104:ARG:HH12	2.35	0.49
29:a:980:G:H2'	29:a:981:C:C6	2.47	0.49
29:a:1486:A:H2	29:a:1489:G:N1	2.09	0.49
49:c:131:LYS:HD3	49:c:134:ILE:HD11	1.93	0.49
18:Z:11:ARG:NH2	18:Z:12:ASN:OD1	2.45	0.49
27:A:1400:G:N2	27:A:1443:G:H5''	2.28	0.49
27:A:2883:G:N2	27:A:2885:G:H3'	2.28	0.49
29:a:826:U:H5'	29:a:827:U:OP1	2.11	0.49
49:c:24:ASN:O	49:c:27:MET:HB2	2.13	0.49
4:H:12:LYS:HE3	4:H:104:TRP:NE1	2.28	0.49
13:T:33:ARG:NH2	27:A:672:C:OP1	2.44	0.49
26:4:65:TYR:HE1	47:t:5:LEU:HA	1.78	0.49
27:A:49:A:H2'	27:A:50:A:C8	2.46	0.49
27:A:1018:U:H1'	27:A:1019:C:C5	2.47	0.49
27:A:2330:U:H3'	27:A:2331:U:C6	2.48	0.49
27:A:2553:G:H2'	27:A:2554:U:C6	2.47	0.49
29:a:1162:G:O2'	29:a:1163:G:N7	2.40	0.49
31:d:15:THR:CG2	31:d:207:ILE:HG12	2.38	0.49
31:d:72:PRO:O	31:d:76:ILE:HG13	2.13	0.49
45:r:77:MET:SD	45:r:89:ARG:NH2	2.85	0.49
3:G:71:THR:HB	3:G:73:ARG:HG3	1.93	0.49
6:J:25:TYR:HE1	6:J:29:TYR:HD2	1.60	0.49
27:A:277:U:H2'	27:A:278:A:H8	1.76	0.49
27:A:738:A:O2'	27:A:740:A:OP1	2.30	0.49
27:A:1537:U:H2'	27:A:1538:G:C8	2.47	0.49
27:A:2394:A:H5'	27:A:2396:A:N7	2.28	0.49
29:a:1229:A:H2'	29:a:1230:C:C6	2.47	0.49
29:a:1279:U:H1'	29:a:1280:C:H5	1.78	0.49
29:a:1375:G:H21	29:a:1486:A:H8	1.60	0.49
32:e:165:TRP:CD1	32:e:181:PRO:HB3	2.48	0.49
37:j:149:LYS:HD2	50:w:64:GLN:HG2	1.94	0.49
40:m:31:ARG:HH21	40:m:58:THR:HG21	1.76	0.49
42:o:3:LYS:O	42:o:7:ILE:HG13	2.12	0.49
2:F:153:GLY:O	27:A:2276:G:H4'	2.13	0.49
5:I:68:LEU:HD21	27:A:2982:A:C4	2.47	0.49
11:R:121:ARG:NH2	27:A:2600:A:N3	2.56	0.49
11:R:121:ARG:HG3	11:R:127:PHE:CE2	2.48	0.49
27:A:680:U:H2'	27:A:681:C:C6	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:747:A:H2'	27:A:748:U:O4'	2.12	0.49
27:A:2366:C:H3'	27:A:2367:G:H8	1.78	0.49
27:A:2715:U:H5''	27:A:2794:G:H5''	1.95	0.49
27:A:2902:A:H2'	27:A:2903:A:H8	1.77	0.49
27:A:3117:U:H2'	27:A:3118:U:C6	2.47	0.49
29:a:422:C:H4'	29:a:423:G:O5'	2.13	0.49
29:a:581:U:H2'	29:a:582:U:H6	1.76	0.49
29:a:1020:G:H2'	29:a:1021:U:C6	2.47	0.49
29:a:1281:A:H2'	29:a:1281:A:N3	2.28	0.49
34:g:68:GLU:OE2	34:g:69:PRO:HD2	2.12	0.49
35:h:70:LYS:HG3	35:h:96:SER:HB2	1.94	0.49
44:q:52:ASP:OD1	44:q:52:ASP:C	2.56	0.49
27:A:736:G:N2	27:A:738:A:H3'	2.27	0.49
27:A:994:A:H3'	27:A:995:U:C6	2.47	0.49
29:a:858:A:H2'	29:a:859:C:C6	2.47	0.49
35:h:12:LEU:HD12	35:h:21:GLN:HE22	1.76	0.49
41:n:8:ASP:C	41:n:8:ASP:OD1	2.54	0.49
27:A:9:U:O2	27:A:2850:C:H4'	2.13	0.49
27:A:646:U:H2'	27:A:647:G:O4'	2.12	0.49
27:A:1533:U:H5''	27:A:1535:C:H42	1.77	0.49
27:A:1552:A:O2'	27:A:1553:C:H5''	2.12	0.49
29:a:614:C:H2'	29:a:615:G:H8	1.78	0.49
29:a:927:G:C2	29:a:928:A:C8	3.01	0.49
38:k:66:GLU:OE1	38:k:66:GLU:N	2.46	0.49
41:n:90:LEU:HD23	41:n:90:LEU:N	2.25	0.49
43:p:34:LYS:NZ	43:p:38:ASP:OD1	2.46	0.49
44:q:52:ASP:OD2	44:q:55:ARG:HG2	2.13	0.49
2:F:104:GLU:OE2	2:F:104:GLU:N	2.43	0.49
5:I:99:LEU:HA	5:I:104:LEU:HD12	1.95	0.49
27:A:190:A:H2'	27:A:191:G:N3	2.28	0.49
27:A:1791:A:H2'	27:A:1792:A:H8	1.78	0.49
28:B:23:G:H2'	28:B:24:G:C8	2.48	0.49
31:d:46:LEU:HD22	31:d:75:VAL:HG13	1.95	0.49
33:f:192:ALA:HA	33:f:195:LEU:HD12	1.94	0.49
47:t:19:VAL:HG21	47:t:44:PHE:CE1	2.46	0.49
49:c:113:ARG:HA	49:c:116:GLU:HG2	1.95	0.49
49:c:151:ILE:HA	49:c:154:MET:SD	2.53	0.49
49:c:211:ALA:O	49:c:214:THR:OG1	2.27	0.49
5:I:33:LEU:HD11	5:I:137:ILE:HG13	1.93	0.49
27:A:66:C:H4'	27:A:72:G:N7	2.27	0.49
27:A:672:C:H2'	27:A:673:C:H6	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:1296:G:H2'	27:A:1297:G:H8	1.76	0.49
29:a:507:G:O2'	29:a:515:A:N1	2.39	0.49
29:a:964:U:H5''	42:o:6:LYS:HE2	1.94	0.49
29:a:1157:A:H2'	29:a:1158:G:C8	2.47	0.49
33:f:97:PHE:CE2	33:f:170:LYS:HG3	2.48	0.49
39:l:45:ASP:C	39:l:45:ASP:OD1	2.55	0.49
9:O:90:GLY:HA2	9:O:122:VAL:HG22	1.95	0.48
27:A:665:G:O2'	27:A:666:A:O5'	2.29	0.48
27:A:933:G:N1	27:A:1303:U:OP2	2.37	0.48
32:e:121:ASN:OD1	44:q:102:LYS:NZ	2.46	0.48
36:i:22:HIS:O	36:i:66:TYR:OH	2.29	0.48
36:i:81:SER:HB2	36:i:87:VAL:H	1.78	0.48
41:n:11:ARG:CZ	41:n:11:ARG:HA	2.42	0.48
9:O:32:THR:HG22	9:O:35:ARG:H	1.77	0.48
16:W:69:THR:OG1	16:W:72:GLY:O	2.29	0.48
20:2:13:LEU:O	20:2:64:ARG:NH2	2.46	0.48
26:4:9:TYR:CG	26:4:25:ARG:HD3	2.47	0.48
27:A:89:A:O2'	27:A:90:C:OP1	2.29	0.48
27:A:655:G:H22	27:A:670:A:H2	1.61	0.48
27:A:1535:C:H2'	27:A:1536:A:O4'	2.13	0.48
29:a:12:A:C6	32:e:201:LYS:HG3	2.47	0.48
29:a:279:A:OP1	29:a:280:C:O2'	2.29	0.48
29:a:452:A:O2'	44:q:76:ILE:HD11	2.12	0.48
29:a:1310:C:H5''	41:n:28:THR:HG21	1.94	0.48
31:d:53:ASP:OD1	31:d:54:VAL:N	2.47	0.48
5:I:22:GLN:NE2	5:I:38:ALA:O	2.46	0.48
5:I:89:GLU:OE1	5:I:89:GLU:N	2.47	0.48
27:A:310:C:H2'	27:A:311:G:H8	1.78	0.48
27:A:445:U:H4'	27:A:446:G:O5'	2.13	0.48
27:A:2094:G:O2'	27:A:2095:G:H8	1.94	0.48
27:A:2363:A:N6	27:A:2375:G:O6	2.46	0.48
27:A:3057:U:H2'	27:A:3058:A:C8	2.48	0.48
29:a:427:U:OP1	32:e:13:ARG:NH2	2.46	0.48
29:a:1301:A:C8	29:a:1305:G:C6	3.01	0.48
38:k:86:ALA:O	38:k:90:ILE:HG13	2.13	0.48
44:q:54:GLU:OE2	44:q:54:GLU:C	2.55	0.48
46:s:46:GLY:O	46:s:72:ARG:NH2	2.45	0.48
25:8:23:VAL:HG13	25:8:47:ARG:HB3	1.94	0.48
27:A:284:G:H1'	27:A:303:G:N1	2.28	0.48
27:A:384:G:H2'	27:A:385:G:H8	1.77	0.48
27:A:2781:G:H2'	27:A:2782:C:C6	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:1076:A:HO2'	27:A:2681:U:HO2'	1.62	0.48
27:A:1435:C:C5	27:A:1444:U:H5''	2.49	0.48
27:A:1501:C:H2'	27:A:1502:G:C8	2.48	0.48
29:a:731:U:H2'	29:a:732:G:O4'	2.13	0.48
29:a:1177:A:C5	31:d:162:MET:HE1	2.49	0.48
41:n:16:GLU:O	41:n:20:THR:HG23	2.13	0.48
46:s:44:GLU:HG2	46:s:45:ARG:HH12	1.78	0.48
47:t:17:LYS:HD2	47:t:17:LYS:C	2.38	0.48
48:u:43:ASP:OD2	48:u:46:LYS:HB3	2.13	0.48
27:A:324:C:O2	27:A:452:G:N2	2.46	0.48
27:A:447:A:H2'	27:A:448:U:C6	2.49	0.48
27:A:451:U:H2'	27:A:452:G:C8	2.48	0.48
27:A:487:U:H2'	27:A:488:G:O4'	2.13	0.48
27:A:619:C:H4'	27:A:620:G:C8	2.48	0.48
27:A:664:A:H3'	27:A:665:G:C8	2.45	0.48
27:A:736:G:H1'	27:A:740:A:N6	2.28	0.48
27:A:1001:C:C5	27:A:1002:C:H1'	2.49	0.48
27:A:1244:A:H4'	27:A:1245:U:O4'	2.13	0.48
27:A:1560:U:O2	34:g:17:ARG:HD2	2.13	0.48
27:A:2548:U:H5''	27:A:2549:G:H5''	1.95	0.48
27:A:3034:C:H2'	27:A:3035:C:H6	1.78	0.48
2:F:104:GLU:N	2:F:104:GLU:CD	2.71	0.48
8:N:90:ASP:OD1	8:N:90:ASP:N	2.34	0.48
21:3:40:ASN:O	21:3:44:ARG:HG2	2.13	0.48
27:A:356:G:H4'	27:A:358:G:C5	2.49	0.48
29:a:1105:U:C2	29:a:1107:G:C8	3.01	0.48
30:v:8:ARG:HA	30:v:11:ARG:HG2	1.94	0.48
33:f:126:PRO:HA	33:f:147:ASP:OD2	2.14	0.48
33:f:194:MET:HE1	36:i:101:LEU:HG	1.95	0.48
49:c:114:LEU:O	49:c:118:GLU:HG3	2.13	0.48
3:G:137:SER:O	3:G:168:SER:OG	2.32	0.48
5:I:35:LEU:HD22	5:I:36:ASP:H	1.78	0.48
20:2:14:THR:N	20:2:17:GLU:OE2	2.46	0.48
27:A:273:A:H62	27:A:313:G:N2	2.10	0.48
27:A:722:G:H2'	27:A:723:C:C6	2.49	0.48
27:A:1621:C:H2'	27:A:1622:G:C8	2.48	0.48
27:A:1715:A:N3	27:A:1798:U:O2'	2.37	0.48
27:A:2936:C:OP1	27:A:2938:G:H4'	2.13	0.48
29:a:87:G:H2'	29:a:88:G:H8	1.79	0.48
29:a:449:C:H2'	29:a:450:G:O4'	2.14	0.48
29:a:825:C:OP1	46:s:25:LYS:NZ	2.36	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:m:35:THR:N	40:m:54:ARG:O	2.45	0.48
27:A:298:G:O2'	27:A:299:G:O4'	2.23	0.48
27:A:728:G:H2'	27:A:729:C:C6	2.48	0.48
27:A:2538:A:H2'	27:A:2539:G:C8	2.49	0.48
29:a:323:U:H2'	29:a:324:G:O4'	2.14	0.48
29:a:1138:A:C8	29:a:1162:G:C2	3.02	0.48
33:f:132:ALA:O	33:f:137:ARG:NH1	2.47	0.48
40:m:50:ARG:NH1	40:m:89:ASP:OD2	2.39	0.48
43:p:10:GLU:CD	43:p:11:ILE:HG13	2.39	0.48
49:c:43:LEU:HD13	49:c:46:THR:HG21	1.95	0.48
4:H:143:SER:HA	4:H:148:ILE:HD11	1.94	0.48
5:I:88:MET:HB3	5:I:132:PHE:CE1	2.49	0.48
12:S:2:ASN:O	12:S:5:ASP:N	2.47	0.48
27:A:750:C:H2'	27:A:751:A:C8	2.49	0.48
27:A:977:G:H2'	27:A:978:A:O4'	2.13	0.48
27:A:1076:A:O2'	27:A:2681:U:O2'	2.30	0.48
27:A:2474:G:O2'	27:A:2720:C:OP1	2.24	0.48
29:a:1034:C:O2'	50:w:45:ASP:OD2	2.32	0.48
29:a:1206:U:O2	29:a:1206:U:H2'	2.12	0.48
29:a:1432:C:H2'	29:a:1433:C:C6	2.49	0.48
29:a:1488:G:OP1	29:a:1491:A:H4'	2.13	0.48
38:k:28:THR:HG21	38:k:90:ILE:HD11	1.95	0.48
20:2:28:GLU:OE2	20:2:32:LEU:HG	2.14	0.47
27:A:1259:U:O2	27:A:1261:A:N6	2.46	0.47
28:B:4:A:H4'	28:B:63:U:H4'	1.96	0.47
28:B:46:A:C4	28:B:47:A:C8	3.02	0.47
29:a:21:U:H2'	29:a:22:C:H6	1.79	0.47
29:a:680:G:H2'	29:a:681:C:C6	2.48	0.47
29:a:948:G:C5	50:w:66:ARG:HD2	2.49	0.47
14:U:16:VAL:HB	14:U:99:VAL:HG21	1.96	0.47
14:U:51:LYS:HB2	14:U:54:ASP:OD1	2.14	0.47
27:A:761:G:H2'	27:A:762:U:C6	2.49	0.47
27:A:2672:A:H5'	27:A:2673:U:H2'	1.96	0.47
27:A:2738:U:H2'	27:A:2739:C:C6	2.49	0.47
29:a:580:G:H2'	29:a:581:U:C6	2.49	0.47
29:a:667:A:C2	29:a:684:A:C5	3.02	0.47
34:g:51:GLU:OE1	34:g:55:HIS:N	2.47	0.47
40:m:5:GLN:OE1	45:r:51:LYS:NZ	2.32	0.47
50:w:95:HIS:HD2	50:w:97:GLU:H	1.62	0.47
1:E:270:ARG:HD3	1:E:273:ARG:NH2	2.29	0.47
12:S:48:ARG:HB2	12:S:95:LYS:HG2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:Z:64:PRO:HB3	27:A:759:G:N1	2.25	0.47
27:A:586:U:H2'	27:A:587:G:O4'	2.13	0.47
27:A:666:A:N6	27:A:2257:A:H4'	2.29	0.47
27:A:979:G:H2'	27:A:980:C:C6	2.50	0.47
27:A:2391:G:H3'	27:A:2392:A:H8	1.79	0.47
27:A:2569:G:N3	27:A:2605:C:H2'	2.29	0.47
27:A:2671:G:H1'	27:A:2674:A:OP2	2.14	0.47
27:A:2874:C:H2'	27:A:2875:C:H6	1.78	0.47
27:A:3014:A:O2'	27:A:3015:C:H5''	2.15	0.47
29:a:1171:G:H5''	31:d:176:HIS:NE2	2.29	0.47
43:p:10:GLU:C	43:p:10:GLU:OE1	2.57	0.47
47:t:40:ILE:HD13	47:t:40:ILE:N	2.29	0.47
4:H:81:ILE:O	4:H:86:LEU:N	2.46	0.47
9:O:121:LYS:HZ1	9:O:123:ASP:CG	2.23	0.47
10:Q:8:PRO:HG2	27:A:1870:U:C4	2.48	0.47
10:Q:106:ASP:OD2	27:A:1867:G:O2'	2.22	0.47
27:A:440:U:H2'	27:A:441:G:C8	2.50	0.47
27:A:587:G:N1	27:A:590:A:OP2	2.40	0.47
27:A:2088:C:H2'	27:A:2089:C:C5	2.50	0.47
27:A:2331:U:H1'	27:A:2405:A:N1	2.29	0.47
27:A:2877:U:H3'	27:A:2878:A:H8	1.79	0.47
27:A:2879:G:O2'	27:A:2888:G:O6	2.31	0.47
29:a:343:U:O2'	29:a:346:G:O6	2.30	0.47
29:a:1202:G:O3'	47:t:77:THR:HG21	2.13	0.47
29:a:1329:G:C8	37:j:129:ARG:HB3	2.48	0.47
36:i:48:ASP:OD1	36:i:48:ASP:C	2.57	0.47
49:c:94:GLN:NE2	49:c:146:ARG:O	2.47	0.47
27:A:287:A:C6	27:A:299:G:H1'	2.50	0.47
27:A:2074:G:O6	27:A:2075:G:N1	2.47	0.47
27:A:2170:U:H2'	27:A:2171:C:H6	1.79	0.47
27:A:2381:A:H4'	27:A:2382:G:O5'	2.14	0.47
27:A:2384:C:H5''	27:A:2387:U:O4	2.14	0.47
27:A:2777:G:C2	27:A:2807:G:H1'	2.49	0.47
29:a:1249:G:H2'	29:a:1250:A:C8	2.50	0.47
29:a:1409:A:H2'	29:a:1410:C:H6	1.80	0.47
33:f:64:VAL:HG11	33:f:93:ARG:HG3	1.95	0.47
48:u:5:LYS:HB3	48:u:5:LYS:HE2	1.66	0.47
4:H:87:ARG:N	4:H:90:MET:HE2	2.24	0.47
7:M:25:LEU:HA	7:M:62:ILE:HD11	1.96	0.47
21:3:15:ALA:O	21:3:20:ARG:NH1	2.48	0.47
24:7:6:ARG:O	24:7:9:GLN:NE2	2.42	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:997:G:H2'	27:A:998:G:C8	2.49	0.47
27:A:1415:A:H4'	27:A:1416:A:H5'	1.96	0.47
27:A:2147:U:H2'	27:A:2148:C:C6	2.50	0.47
28:B:81:U:H2'	28:B:82:A:C8	2.49	0.47
29:a:698:A:H5'	39:l:128:ASN:CG	2.40	0.47
29:a:749:G:H4'	29:a:1497:A:H4'	1.95	0.47
31:d:48:ARG:HG3	31:d:48:ARG:HH11	1.80	0.47
45:r:73:ARG:HH11	45:r:95:GLU:HG2	1.79	0.47
47:t:31:ILE:HG23	47:t:49:PHE:HA	1.96	0.47
4:H:99:ARG:HA	4:H:103:MET:HE3	1.96	0.47
5:I:153:ARG:HE	5:I:154:ARG:N	2.10	0.47
11:R:34:GLU:H	11:R:34:GLU:CD	2.19	0.47
14:U:67:HIS:ND1	14:U:95:THR:HG22	2.30	0.47
25:s:43:ARG:HH22	27:A:2586:G:H3'	1.79	0.47
27:A:356:G:H4'	27:A:358:G:C6	2.50	0.47
27:A:1087:G:H2'	27:A:1088:U:C6	2.48	0.47
27:A:2288:C:H2'	27:A:2289:C:H6	1.79	0.47
27:A:2622:C:H2'	27:A:2623:A:H8	1.80	0.47
27:A:2778:U:H2'	27:A:2779:U:C6	2.50	0.47
32:e:23:ASP:OD1	32:e:25:SER:N	2.48	0.47
32:e:94:ASP:OD1	32:e:95:ASN:N	2.47	0.47
34:g:15:ASP:HB3	34:g:18:THR:HG23	1.95	0.47
37:j:37:VAL:HG22	37:j:87:LEU:HD13	1.96	0.47
37:j:38:ARG:HB2	37:j:86:HIS:HB2	1.97	0.47
37:j:120:LYS:HD3	37:j:120:LYS:HA	1.54	0.47
41:n:33:ILE:CB	41:n:59:TYR:HE2	2.24	0.47
42:o:24:ARG:HG2	42:o:51:LEU:HD11	1.95	0.47
45:r:73:ARG:HB2	45:r:95:GLU:HG3	1.96	0.47
1:E:270:ARG:HD3	1:E:273:ARG:HH22	1.80	0.47
11:R:39:VAL:HA	11:R:103:ASP:HB3	1.96	0.47
19:1:39:VAL:N	19:1:62:SER:O	2.44	0.47
23:6:8:ARG:HA	23:6:27:LYS:O	2.15	0.47
27:A:137:G:H2'	27:A:138:A:C8	2.50	0.47
27:A:312:G:H3'	27:A:313:G:H8	1.79	0.47
27:A:1074:A:H2	27:A:2682:G:H4'	1.79	0.47
29:a:493:A:H2'	29:a:494:C:C6	2.50	0.47
2:F:59:PRO:O	2:F:62:VAL:HG22	2.15	0.47
27:A:722:G:H2'	27:A:723:C:H6	1.80	0.47
27:A:2079:C:H2'	27:A:2080:G:H8	1.80	0.47
27:A:2366:C:H3'	27:A:2367:G:C8	2.50	0.47
27:A:2815:C:H2'	27:A:2816:G:H8	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:2878:A:C2	27:A:2889:A:H5''	2.50	0.47
29:a:468:U:H2'	29:a:469:G:H8	1.80	0.47
47:t:16:LEU:HD23	47:t:17:LYS:N	2.30	0.47
27:A:247:G:H4'	27:A:474:G:C5	2.50	0.47
27:A:453:U:H2'	27:A:454:U:C6	2.50	0.47
27:A:668:U:H2'	27:A:669:G:C8	2.50	0.47
27:A:987:A:H2	27:A:1021:G:N1	2.10	0.47
27:A:2675:A:OP1	27:A:2721:A:N6	2.47	0.47
29:a:362:G:N2	29:a:365:U:OP2	2.47	0.47
29:a:488:C:H1'	29:a:489:A:C2	2.50	0.47
29:a:904:G:H2'	29:a:905:A:C8	2.50	0.47
31:d:5:ILE:HD11	31:d:10:PHE:CD1	2.51	0.47
34:g:30:ILE:O	34:g:36:THR:OG1	2.27	0.47
36:i:14:LEU:HD22	36:i:64:LEU:HD21	1.97	0.47
36:i:94:LEU:HD22	36:i:106:ILE:HD13	1.96	0.47
42:o:31:ILE:O	42:o:37:SER:OG	2.33	0.47
4:H:45:MET:HE2	4:H:64:LEU:HG	1.98	0.46
12:S:90:ASP:HA	12:S:112:LYS:NZ	2.30	0.46
22:5:48:ARG:HD3	27:A:3106:C:N4	2.30	0.46
27:A:721:A:O2'	27:A:730:G:N2	2.48	0.46
27:A:1675:U:O2'	27:A:1676:G:N7	2.45	0.46
29:a:352:C:O2'	29:a:354:G:OP1	2.29	0.46
29:a:905:A:O2'	29:a:1382:C:OP2	2.26	0.46
34:g:15:ASP:OD1	34:g:17:ARG:HG3	2.14	0.46
35:h:126:ASP:N	35:h:126:ASP:OD1	2.48	0.46
37:j:133:ARG:HG3	42:o:101:TRP:HE1	1.80	0.46
41:n:29:ARG:HD3	41:n:29:ARG:HA	1.63	0.46
50:w:95:HIS:HD2	50:w:97:GLU:N	2.13	0.46
27:A:298:G:H2'	27:A:299:G:C4	2.50	0.46
27:A:611:U:H2'	27:A:612:U:C6	2.50	0.46
27:A:625:A:N6	27:A:647:G:O2'	2.46	0.46
27:A:993:G:H21	27:A:1016:C:H5	1.62	0.46
27:A:1224:G:H2'	27:A:1225:G:C8	2.49	0.46
27:A:1288:A:H2'	27:A:1289:A:H8	1.79	0.46
27:A:1546:A:H2'	27:A:1547:G:H8	1.79	0.46
27:A:1651:C:H2'	27:A:1652:A:C8	2.50	0.46
29:a:519:A:H2'	29:a:520:G:C8	2.50	0.46
29:a:1332:A:OP1	37:j:143:LYS:HE3	2.14	0.46
29:a:1337:A:H2'	29:a:1338:G:C8	2.50	0.46
29:a:1458:G:H2'	29:a:1459:G:O4'	2.15	0.46
37:j:47:GLN:NE2	37:j:47:GLN:O	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:I:30:LYS:HE2	5:I:30:LYS:HA	1.97	0.46
5:I:98:GLN:NE2	5:I:105:GLU:HB3	2.29	0.46
8:N:68:GLU:OE2	27:A:2908:U:O2'	2.32	0.46
14:U:61:THR:O	14:U:100:THR:OG1	2.32	0.46
17:X:1:MET:SD	17:X:28:PRO:HA	2.55	0.46
27:A:1393:C:H2'	27:A:1394:A:H8	1.80	0.46
27:A:1758:G:H2'	27:A:1759:A:C8	2.50	0.46
27:A:2371:G:H2'	27:A:2372:U:C5	2.50	0.46
29:a:658:U:H2'	29:a:659:C:C6	2.51	0.46
29:a:997:A:C2	29:a:1200:A:H1'	2.50	0.46
29:a:1421:G:OP1	48:u:29:ARG:HD3	2.15	0.46
32:e:132:VAL:HG11	32:e:177:VAL:HG21	1.96	0.46
47:t:18:LYS:HB3	47:t:31:ILE:HD12	1.96	0.46
5:I:128:SER:HB2	5:I:131:LYS:HG2	1.98	0.46
23:6:52:LYS:HE2	23:6:52:LYS:HB2	1.66	0.46
27:A:389:G:N1	27:A:392:A:OP2	2.47	0.46
27:A:1294:U:H2'	27:A:1295:U:C6	2.50	0.46
27:A:1314:C:H2'	27:A:1315:C:C6	2.51	0.46
27:A:1679:A:OP1	27:A:1679:A:H4'	2.15	0.46
27:A:2309:U:H2'	27:A:2310:G:C8	2.49	0.46
27:A:2551:A:H2'	27:A:2552:A:C8	2.51	0.46
29:a:497:G:C8	29:a:510:G:H5''	2.51	0.46
31:d:46:LEU:HA	31:d:48:ARG:HH21	1.80	0.46
34:g:28:ASN:OD1	34:g:31:ARG:NH1	2.49	0.46
40:m:122:GLU:C	40:m:122:GLU:OE1	2.59	0.46
49:c:83:GLU:CG	49:c:218:ALA:HB2	2.45	0.46
4:H:92:ILE:HD11	27:A:2535:A:N3	2.30	0.46
22:5:6:ARG:HD2	27:A:2243:C:C5	2.51	0.46
24:7:28:ARG:NH2	27:A:210:G:OP1	2.37	0.46
26:4:65:TYR:CE2	47:t:9:PRO:HD3	2.51	0.46
27:A:1560:U:H2'	27:A:1561:C:C6	2.50	0.46
29:a:588:A:H2'	29:a:589:A:O4'	2.15	0.46
34:g:15:ASP:OD2	34:g:17:ARG:CZ	2.64	0.46
34:g:30:ILE:HG22	34:g:71:THR:HG22	1.98	0.46
42:o:62:ASN:N	42:o:62:ASN:OD1	2.49	0.46
44:q:9:ARG:CZ	44:q:16:PRO:HB3	2.46	0.46
49:c:67:VAL:H	49:c:89:MET:CE	2.11	0.46
50:w:73:ASN:N	50:w:73:ASN:OD1	2.48	0.46
50:w:99:ARG:O	50:w:103:VAL:HG23	2.14	0.46
1:E:256:ARG:HG2	27:A:2061:U:H5''	1.96	0.46
9:O:15:GLU:OE1	27:A:691:U:O2'	2.33	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:T:73:ASP:O	13:T:114:ARG:NH1	2.49	0.46
19:1:49:ILE:HD11	19:1:61:VAL:HG23	1.97	0.46
27:A:380:A:N1	27:A:404:A:O2'	2.40	0.46
27:A:639:C:O2'	27:A:640:G:O5'	2.33	0.46
27:A:1008:G:C2	27:A:1009:U:N3	2.84	0.46
27:A:1396:G:H2'	27:A:1397:U:C6	2.51	0.46
27:A:1476:G:H2'	27:A:1477:C:H6	1.80	0.46
27:A:1665:U:H2'	27:A:1666:A:H8	1.81	0.46
27:A:2328:G:C6	27:A:2408:G:N1	2.84	0.46
27:A:2386:U:OP1	27:A:2393:A:O2'	2.31	0.46
29:a:389:A:H3'	29:a:390:U:C6	2.51	0.46
29:a:456:C:H1'	29:a:457:A:C4	2.51	0.46
29:a:1411:A:H2'	29:a:1412:C:C6	2.50	0.46
32:e:90:GLU:HG3	32:e:95:ASN:HD21	1.79	0.46
34:g:74:GLU:OE2	34:g:78:GLN:NE2	2.49	0.46
43:p:10:GLU:OE1	43:p:11:ILE:N	2.49	0.46
49:c:113:ARG:HD3	49:c:113:ARG:C	2.40	0.46
1:E:141:VAL:HG13	1:E:162:SER:HB2	1.98	0.46
4:H:57:ILE:O	4:H:61:ILE:HG12	2.15	0.46
4:H:149:ASP:HB2	4:H:152:SER:HB3	1.98	0.46
27:A:191:G:O2'	27:A:917:A:N3	2.48	0.46
27:A:1900:C:H2'	27:A:1901:C:C6	2.51	0.46
29:a:1106:U:H6	29:a:1261:A:H2'	1.81	0.46
29:a:1329:G:O2'	29:a:1356:G:O6	2.34	0.46
49:c:27:MET:HB3	49:c:31:ILE:HD11	1.98	0.46
49:c:58:LYS:HZ3	49:c:224:GLY:HA2	1.79	0.46
2:F:18:ASP:HB2	2:F:19:GLU:OE2	2.16	0.46
4:H:44:ASN:ND2	27:A:2537:C:O4'	2.49	0.46
27:A:191:G:OP2	27:A:191:G:N2	2.39	0.46
27:A:287:A:C2	27:A:289:A:H8	2.34	0.46
27:A:1650:G:H2'	27:A:1651:C:C6	2.50	0.46
27:A:1710:A:N6	27:A:1716:A:OP2	2.49	0.46
27:A:2287:C:H42	27:A:2725:C:H1'	1.79	0.46
27:A:2364:C:H2'	27:A:2365:A:H8	1.79	0.46
29:a:215:U:H4'	29:a:216:U:H5'	1.98	0.46
29:a:1003:C:H2'	29:a:1004:G:H8	1.77	0.46
29:a:1276:G:H2'	29:a:1277:U:C6	2.51	0.46
33:f:191:PRO:HD2	33:f:194:MET:CE	2.46	0.46
49:c:143:LYS:O	49:c:146:ARG:HG3	2.15	0.46
7:M:45:THR:HG22	7:M:47:ASN:H	1.81	0.46
8:N:24:VAL:HG12	8:N:30:ARG:HD3	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:O:80:VAL:HG22	9:O:114:GLY:HA2	1.98	0.46
12:S:1:MET:HB3	27:A:3096:U:O2'	2.16	0.46
16:W:4:ILE:O	20:2:26:LYS:NZ	2.49	0.46
25:8:51:SER:OG	25:8:54:ASP:OD2	2.33	0.46
27:A:701:A:H2'	27:A:702:A:H8	1.81	0.46
27:A:736:G:H1'	27:A:740:A:H61	1.81	0.46
27:A:2088:C:N3	27:A:2095:G:N1	2.63	0.46
27:A:2096:G:H2'	27:A:2097:G:C8	2.49	0.46
27:A:2443:U:H2'	27:A:2444:C:C6	2.51	0.46
27:A:2683:A:N1	27:A:2718:G:H1'	2.31	0.46
27:A:2887:G:H2'	27:A:2888:G:O4'	2.16	0.46
29:a:715:G:H1'	46:s:73:GLU:OE2	2.15	0.46
29:a:873:U:H2'	29:a:874:A:H8	1.80	0.46
29:a:902:U:H2'	29:a:903:U:C6	2.51	0.46
41:n:19:LEU:HD23	41:n:33:ILE:HD11	1.97	0.46
43:p:19:ASP:C	43:p:19:ASP:OD1	2.58	0.46
3:G:129:GLU:HG3	3:G:131:VAL:O	2.15	0.46
8:N:16:ALA:HB2	8:N:52:VAL:HG21	1.98	0.46
27:A:2358:A:O2'	27:A:2382:G:O2'	2.29	0.46
29:a:716:U:H2'	29:a:717:C:H6	1.77	0.46
29:a:725:A:H2'	29:a:726:G:C8	2.51	0.46
29:a:1011:U:O2'	29:a:1012:U:O5'	2.33	0.46
29:a:1329:G:H5''	37:j:129:ARG:HG2	1.97	0.46
36:i:53:ASP:OD1	36:i:53:ASP:C	2.59	0.46
40:m:4:ILE:O	40:m:8:VAL:HG13	2.16	0.46
41:n:51:ASP:HA	41:n:54:THR:HG22	1.98	0.46
50:w:10:GLU:H	50:w:10:GLU:CD	2.23	0.46
6:J:8:GLU:OE1	6:J:14:ALA:HA	2.16	0.45
23:6:37:GLU:HG2	23:6:52:LYS:HD3	1.98	0.45
27:A:310:C:H2'	27:A:311:G:C8	2.51	0.45
27:A:412:A:O2'	27:A:413:G:N2	2.46	0.45
27:A:795:G:H2'	27:A:796:A:C8	2.50	0.45
27:A:1000:C:H3'	27:A:1001:C:H5''	1.98	0.45
27:A:1614:G:H2'	27:A:1615:G:H8	1.81	0.45
27:A:1630:U:H2'	27:A:1631:A:H8	1.80	0.45
29:a:45:G:H2'	29:a:46:G:H8	1.81	0.45
29:a:1374:U:H2'	29:a:1375:G:C8	2.51	0.45
30:v:25:ARG:HG3	30:v:25:ARG:NH1	2.30	0.45
31:d:92:LYS:HE2	31:d:92:LYS:HB3	1.62	0.45
39:l:77:GLU:OE2	39:l:78:ASN:N	2.49	0.45
27:A:2376:G:H2'	27:A:2377:G:H8	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:B:61:C:H2'	28:B:62:C:C6	2.50	0.45
29:a:993:G:H2'	29:a:994:C:H6	1.81	0.45
29:a:1115:G:H1'	29:a:1121:G:N2	2.32	0.45
29:a:1304:C:P	47:t:78:ARG:HH22	2.39	0.45
29:a:1382:C:C2	29:a:1486:A:N6	2.85	0.45
32:e:151:GLN:HA	32:e:154:ARG:HH12	1.82	0.45
35:h:69:VAL:HG23	35:h:100:ALA:HB1	1.97	0.45
35:h:122:ASN:O	35:h:126:ASP:OD1	2.34	0.45
38:k:8:ILE:HB	38:k:74:ILE:HB	1.97	0.45
40:m:99:ARG:NH1	40:m:105:GLN:O	2.46	0.45
46:s:28:GLN:H	46:s:28:GLN:CD	2.20	0.45
49:c:97:LEU:HB2	49:c:100:MET:SD	2.56	0.45
19:1:36:VAL:HG22	19:1:63:ARG:HH21	1.81	0.45
27:A:782:U:H2'	27:A:783:G:O4'	2.16	0.45
27:A:1002:C:H2'	27:A:1003:A:H3'	1.98	0.45
27:A:1963:G:H2'	27:A:1964:U:C6	2.52	0.45
27:A:2901:G:H2'	27:A:2902:A:C8	2.52	0.45
29:a:103:G:H2'	29:a:104:A:O4'	2.16	0.45
29:a:1061:G:N7	33:f:77:LYS:NZ	2.64	0.45
32:e:104:ARG:N	32:e:108:MET:CE	2.69	0.45
33:f:132:ALA:HB2	33:f:150:ALA:HB3	1.98	0.45
21:3:16:ARG:NH2	28:B:83:C:OP1	2.46	0.45
27:A:1009:U:H2'	27:A:1010:U:N1	2.32	0.45
27:A:1250:U:H3'	27:A:1251:A:H5''	1.97	0.45
28:B:29:C:O2'	28:B:60:G:N2	2.50	0.45
29:a:36:A:H2'	29:a:37:A:C8	2.52	0.45
29:a:49:U:H2'	29:a:50:G:H8	1.79	0.45
29:a:1050:U:H2'	29:a:1051:C:C6	2.52	0.45
31:d:83:ALA:O	31:d:86:ILE:HG13	2.16	0.45
31:d:117:GLN:HG3	31:d:187:TYR:CD2	2.52	0.45
32:e:18:ASP:OD1	32:e:21:GLY:N	2.43	0.45
44:q:35:GLU:OE2	44:q:55:ARG:NH2	2.41	0.45
1:E:258:ARG:NH1	27:A:2016:G:OP1	2.42	0.45
6:J:27:ARG:NH1	27:A:2315:U:OP2	2.47	0.45
6:J:41:ARG:NH1	27:A:305:G:H4'	2.31	0.45
10:Q:33:ARG:HB3	10:Q:114:GLU:HB3	1.99	0.45
11:R:42:ARG:HG3	11:R:47:ILE:HD12	1.97	0.45
13:T:7:ALA:O	13:T:11:GLN:HG2	2.17	0.45
27:A:620:G:H2'	27:A:621:U:C6	2.51	0.45
27:A:736:G:N2	27:A:739:U:OP2	2.29	0.45
27:A:1080:U:H2'	27:A:1081:C:C6	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:1343:G:H2'	27:A:1345:G:C8	2.52	0.45
27:A:1939:U:H2'	27:A:1940:A:H8	1.82	0.45
27:A:2913:U:H5'	27:A:2913:U:O2	2.17	0.45
28:B:63:U:H2'	28:B:64:G:C8	2.52	0.45
29:a:185:G:H2'	29:a:186:C:C6	2.51	0.45
29:a:252:U:C2	29:a:253:U:C5	3.05	0.45
29:a:863:G:P	40:m:9:ARG:HH22	2.40	0.45
29:a:1110:A:H61	29:a:1125:G:H1'	1.82	0.45
29:a:1270:A:H2'	29:a:1271:A:C8	2.51	0.45
49:c:96:TRP:CD1	49:c:96:TRP:C	2.94	0.45
16:W:19:LYS:NZ	27:A:1455:U:OP1	2.41	0.45
27:A:151:A:H2'	27:A:152:G:C8	2.51	0.45
27:A:688:A:H2'	27:A:689:U:C6	2.52	0.45
27:A:2248:C:H2'	27:A:2249:G:C8	2.52	0.45
27:A:2248:C:H2'	27:A:2249:G:H8	1.80	0.45
29:a:66:U:H2'	29:a:67:C:C6	2.52	0.45
29:a:252:U:H2'	29:a:253:U:H6	1.81	0.45
29:a:1299:C:O2	47:t:37:ARG:NH2	2.45	0.45
31:d:129:PHE:HD2	31:d:133:MET:HE3	1.81	0.45
10:Q:37:THR:HA	10:Q:110:MET:HE2	1.99	0.45
27:A:1326:G:H1'	27:A:1352:A:N6	2.32	0.45
27:A:1523:U:H2'	27:A:1524:G:C8	2.52	0.45
27:A:2061:U:H2'	27:A:2062:G:H8	1.81	0.45
27:A:2070:A:H2'	27:A:2071:A:H8	1.81	0.45
28:B:63:U:H2'	28:B:64:G:H8	1.82	0.45
29:a:185:G:H2'	29:a:186:C:H6	1.81	0.45
29:a:979:U:H2'	29:a:980:G:H8	1.82	0.45
29:a:1232:A:H62	29:a:1268:C:N4	2.09	0.45
29:a:1305:G:H2'	29:a:1306:A:H8	1.80	0.45
31:d:15:THR:HG23	31:d:207:ILE:HD11	1.99	0.45
31:d:178:LEU:HD23	31:d:178:LEU:HA	1.80	0.45
35:h:24:THR:O	35:h:27:VAL:HG22	2.17	0.45
36:i:31:LYS:HB2	36:i:31:LYS:HE3	1.65	0.45
41:n:46:LYS:HD2	41:n:46:LYS:N	2.19	0.45
44:q:54:GLU:OE2	44:q:55:ARG:N	2.49	0.45
49:c:27:MET:O	49:c:31:ILE:HD12	2.14	0.45
4:H:149:ASP:O	4:H:153:ILE:HG23	2.16	0.45
8:N:108:GLU:H	8:N:108:GLU:CD	2.20	0.45
19:1:41:ARG:HE	19:1:43:GLY:HA3	1.82	0.45
23:6:10:LYS:HE2	27:A:2644:C:H5''	1.98	0.45
27:A:1921:G:H2'	27:A:1922:G:H8	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:2425:U:O2'	27:A:2427:G:OP1	2.34	0.45
29:a:92:A:O2'	29:a:93:C:P	2.74	0.45
29:a:255:G:H2'	29:a:256:U:C6	2.50	0.45
29:a:1116:U:O2'	29:a:1117:U:H5''	2.16	0.45
44:q:45:GLU:CD	44:q:46:PRO:HD3	2.42	0.45
4:H:129:PHE:CE2	4:H:135:TYR:HB2	2.52	0.45
17:X:40:ARG:HG2	17:X:40:ARG:NH1	2.30	0.45
27:A:282:A:C6	27:A:305:G:C6	3.05	0.45
27:A:316:U:O2'	27:A:317:G:OP1	2.28	0.45
27:A:965:U:H2'	27:A:966:U:C6	2.52	0.45
27:A:1611:A:H2'	27:A:1612:U:C6	2.52	0.45
28:B:52:G:H2'	28:B:53:A:C8	2.51	0.45
29:a:470:U:C2	29:a:471:G:C8	3.05	0.45
29:a:489:A:C8	29:a:523:U:O2'	2.63	0.45
29:a:811:U:H5''	49:c:21:ARG:CZ	2.46	0.45
31:d:145:ASN:HD21	31:d:204:LYS:HE3	1.81	0.45
33:f:135:ALA:HB1	33:f:162:VAL:HG23	1.99	0.45
50:w:51:PRO:HD2	50:w:72:VAL:HA	1.99	0.45
1:E:111:LEU:HD11	1:E:117:ILE:HD11	1.98	0.45
5:I:98:GLN:HA	5:I:126:VAL:HG11	1.98	0.45
27:A:216:A:H2'	27:A:217:G:C8	2.52	0.45
27:A:278:A:H2'	27:A:279:U:C6	2.52	0.45
27:A:2350:G:O2'	27:A:2351:A:OP1	2.30	0.45
27:A:2403:U:O4	27:A:2404:G:N2	2.50	0.45
27:A:2752:U:H3'	27:A:2754:G:C8	2.51	0.45
27:A:2752:U:O2'	27:A:2754:G:OP1	2.26	0.45
29:a:207:G:O2'	48:u:59:ASP:OD2	2.30	0.45
29:a:1035:A:H8	29:a:1035:A:O5'	1.99	0.45
31:d:34:GLU:OE2	31:d:58:ARG:NE	2.49	0.45
31:d:69:THR:HG23	31:d:71:ARG:N	2.32	0.45
41:n:12:ASP:CG	41:n:46:LYS:NZ	2.74	0.45
41:n:34:LEU:HD23	41:n:34:LEU:HA	1.86	0.45
2:F:139:HIS:NE2	27:A:1888:C:O2	2.49	0.44
5:I:61:ARG:CZ	5:I:61:ARG:HA	2.47	0.44
5:I:159:LYS:HE2	5:I:159:LYS:N	2.32	0.44
8:N:76:TYR:HB2	12:S:72:THR:HB	1.99	0.44
13:T:77:ASN:OD1	13:T:78:ARG:N	2.50	0.44
15:V:52:GLU:HB2	15:V:53:PRO:HD3	1.99	0.44
27:A:856:U:H2'	27:A:857:U:C6	2.52	0.44
31:d:68:HIS:CE1	31:d:103:LEU:HD12	2.52	0.44
42:o:4:LYS:NZ	42:o:4:LYS:CB	2.80	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:I:144:GLN:NE2	27:A:2968:G:H21	2.14	0.44
7:M:92:LEU:HD11	7:M:99:ARG:HD2	2.00	0.44
27:A:691:U:H2'	27:A:692:C:C6	2.52	0.44
27:A:864:A:H4'	27:A:1386:G:N3	2.32	0.44
27:A:1052:U:H2'	27:A:1053:G:C8	2.52	0.44
27:A:1393:C:H2'	27:A:1394:A:C8	2.53	0.44
27:A:1537:U:H2'	27:A:1538:G:H8	1.82	0.44
27:A:1648:A:H4'	27:A:1649:C:O5'	2.16	0.44
27:A:1677:G:H2'	27:A:1678:U:O4'	2.18	0.44
27:A:1703:G:H2'	27:A:1704:U:C6	2.52	0.44
27:A:2029:A:H2'	27:A:2030:C:C6	2.52	0.44
27:A:2038:A:H2'	27:A:2039:C:C6	2.52	0.44
29:a:947:U:O2'	50:w:37:ARG:NH2	2.48	0.44
29:a:1028:G:H5'	29:a:1029:U:OP1	2.17	0.44
29:a:1212:A:H2'	29:a:1213:U:C6	2.52	0.44
29:a:1265:U:H5''	29:a:1266:U:H4'	1.98	0.44
38:k:57:LYS:H	38:k:57:LYS:HG2	1.56	0.44
41:n:33:ILE:CG2	41:n:59:TYR:HE2	2.30	0.44
3:G:131:VAL:HG12	3:G:140:SER:HB2	2.00	0.44
5:I:4:ILE:HB	5:I:70:ARG:HD2	1.99	0.44
5:I:77:VAL:HA	5:I:80:VAL:HG22	2.00	0.44
19:1:39:VAL:HB	19:1:64:ALA:HB3	1.99	0.44
27:A:351:G:O6	27:A:444:U:C2	2.70	0.44
27:A:1154:G:C6	27:A:1238:G:C6	3.05	0.44
27:A:2325:U:H3	27:A:2410:A:H61	1.65	0.44
29:a:55:A:N7	29:a:110:U:O2'	2.51	0.44
29:a:335:C:H2'	29:a:336:A:C8	2.51	0.44
41:n:90:LEU:HA	41:n:93:ARG:HB2	1.99	0.44
49:c:162:TRP:CH2	49:c:186:ILE:CG2	3.00	0.44
5:I:19:ILE:HG12	5:I:24:LEU:HG	1.99	0.44
10:Q:70:ILE:HD13	10:Q:70:ILE:HA	1.82	0.44
13:T:18:LEU:HD23	13:T:18:LEU:HA	1.82	0.44
27:A:388:U:H2'	27:A:389:G:O4'	2.18	0.44
27:A:667:A:H4'	27:A:2724:U:H5'	1.99	0.44
27:A:750:C:H2'	27:A:751:A:H8	1.83	0.44
27:A:844:G:H4'	27:A:878:G:H5'	2.00	0.44
27:A:990:G:N1	27:A:1018:U:C4	2.86	0.44
27:A:1003:A:OP1	27:A:1003:A:H2'	2.18	0.44
27:A:1885:G:O2'	27:A:2215:U:O4	2.25	0.44
27:A:3086:U:OP2	27:A:3087:G:O2'	2.26	0.44
29:a:45:G:H2'	29:a:46:G:C8	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:a:266:G:H2'	29:a:266:G:N3	2.33	0.44
29:a:1051:C:H2'	29:a:1052:G:H8	1.82	0.44
29:a:1117:U:H4'	29:a:1118:A:OP1	2.18	0.44
29:a:1410:C:H2'	29:a:1411:A:C8	2.53	0.44
31:d:23:TYR:HB2	38:k:95:SER:O	2.17	0.44
34:g:15:ASP:CG	34:g:17:ARG:HG3	2.42	0.44
37:j:47:GLN:HE21	37:j:82:ASP:CG	2.25	0.44
39:l:85:GLU:N	39:l:85:GLU:OE2	2.50	0.44
44:q:49:ILE:HB	44:q:93:LEU:HD11	2.00	0.44
50:w:11:LEU:HD13	50:w:40:LEU:HB3	1.99	0.44
4:H:130:ASP:HB3	27:A:2527:G:O4'	2.18	0.44
7:M:93:LEU:HD23	7:M:93:LEU:HA	1.86	0.44
27:A:666:A:H62	27:A:2257:A:H4'	1.82	0.44
27:A:1064:A:H2'	27:A:1065:C:C6	2.52	0.44
27:A:1158:U:H2'	27:A:1159:C:C6	2.53	0.44
27:A:3052:A:O2'	27:A:3105:C:OP1	2.32	0.44
29:a:390:U:H2'	29:a:391:G:C8	2.53	0.44
29:a:485:G:O2'	29:a:486:G:OP1	2.32	0.44
29:a:1258:C:O2'	29:a:1260:A:H8	2.01	0.44
31:d:29:LYS:HB3	31:d:29:LYS:HE3	1.81	0.44
32:e:134:GLN:HG2	32:e:179:GLN:HA	1.99	0.44
35:h:20:SER:OG	35:h:23:VAL:HG22	2.17	0.44
38:k:7:ARG:O	38:k:8:ILE:HD13	2.16	0.44
18:Z:41:ARG:NE	18:Z:41:ARG:HA	2.33	0.44
27:A:298:G:H22	27:A:338:C:N4	2.15	0.44
27:A:443:C:H2'	27:A:444:U:O4'	2.18	0.44
27:A:844:G:O2'	27:A:878:G:H4'	2.17	0.44
27:A:3057:U:H2'	27:A:3058:A:H8	1.82	0.44
29:a:440:C:C2	29:a:441:A:C8	3.05	0.44
29:a:539:A:H4'	29:a:540:A:H3'	1.99	0.44
29:a:590:A:C5	29:a:591:C:C5	3.06	0.44
29:a:1115:G:N2	29:a:1119:U:H3	2.15	0.44
29:a:1491:A:H2'	29:a:1492:G:C8	2.53	0.44
37:j:69:LYS:O	37:j:73:VAL:HG13	2.18	0.44
42:o:87:MET:HE2	42:o:87:MET:HB3	1.76	0.44
45:r:14:GLU:OE2	45:r:15:LYS:N	2.50	0.44
1:E:181:GLU:HG3	1:E:271:ARG:HA	1.99	0.44
1:E:247:VAL:HG12	1:E:253:PRO:HA	1.99	0.44
10:Q:95:THR:HG22	10:Q:115:LEU:HD23	1.99	0.44
11:R:37:ARG:HA	11:R:101:VAL:HG23	2.00	0.44
27:A:844:G:H5'	27:A:845:C:H5''	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:994:A:H3'	27:A:995:U:C5	2.53	0.44
27:A:997:G:H2'	27:A:998:G:H8	1.81	0.44
27:A:1290:C:H2'	27:A:1291:G:O4'	2.18	0.44
27:A:1314:C:H2'	27:A:1315:C:H6	1.82	0.44
27:A:1437:A:N1	27:A:1448:C:O2'	2.48	0.44
27:A:1656:A:H2'	27:A:1657:G:C8	2.52	0.44
27:A:1715:A:H2'	27:A:1716:A:C8	2.53	0.44
27:A:1808:A:H2'	27:A:1809:U:C6	2.52	0.44
29:a:38:C:H2'	29:a:39:G:H8	1.83	0.44
29:a:580:G:H2'	29:a:581:U:H6	1.83	0.44
29:a:725:A:H2'	29:a:726:G:H8	1.83	0.44
29:a:1410:C:H2'	29:a:1411:A:H8	1.82	0.44
29:a:1477:A:O2'	50:w:79:ASP:OD2	2.32	0.44
34:g:41:ASP:OD1	34:g:42:ILE:N	2.51	0.44
48:u:71:GLN:O	48:u:75:LYS:HG2	2.18	0.44
50:w:30:HIS:CE1	50:w:95:HIS:HE1	2.36	0.44
12:S:112:LYS:HE2	12:S:112:LYS:HB2	1.62	0.44
27:A:306:U:H2'	27:A:307:G:C8	2.52	0.44
27:A:824:G:H2'	27:A:825:C:C6	2.53	0.44
27:A:1651:C:H2'	27:A:1652:A:H8	1.83	0.44
28:B:15:U:OP2	28:B:71:C:O2'	2.34	0.44
29:a:431:A:C4	29:a:432:A:C8	3.06	0.44
29:a:1244:G:H1	29:a:1253:U:H3	1.65	0.44
40:m:49:LEU:HD23	40:m:49:LEU:HA	1.79	0.44
41:n:43:MET:HE2	41:n:43:MET:HB2	1.78	0.44
47:t:49:PHE:O	47:t:60:VAL:N	2.44	0.44
11:R:18:ARG:HE	11:R:19:LEU:HD22	1.83	0.44
26:4:10:VAL:O	26:4:26:SER:N	2.39	0.44
27:A:349:G:H2'	27:A:350:A:H8	1.83	0.44
27:A:1620:U:H2'	27:A:1621:C:H6	1.81	0.44
29:a:263:A:H2'	29:a:264:U:C6	2.52	0.44
29:a:401:C:O2'	29:a:601:A:N3	2.48	0.44
29:a:664:U:H2'	29:a:665:G:O4'	2.17	0.44
32:e:41:ILE:HD12	32:e:41:ILE:O	2.18	0.44
36:i:98:LEU:HD23	36:i:98:LEU:HA	1.88	0.44
39:l:65:ARG:HD3	39:l:65:ARG:HA	1.86	0.44
45:r:75:SER:HB2	45:r:94:LEU:HD21	2.00	0.44
50:w:106:GLU:O	50:w:107:ALA:C	2.61	0.44
2:F:96:GLU:OE2	2:F:99:GLN:NE2	2.50	0.43
9:O:81:GLY:HA3	9:O:116:GLY:HA3	2.00	0.43
17:X:8:THR:OG1	17:X:22:LYS:NZ	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:264:G:H4'	27:A:516:G:H22	1.82	0.43
27:A:1146:A:H2'	27:A:1147:A:C8	2.53	0.43
27:A:1485:C:H2'	27:A:1486:G:O4'	2.18	0.43
27:A:2271:C:H2'	27:A:2272:G:H8	1.83	0.43
27:A:2581:G:H2'	27:A:2583:C:OP2	2.18	0.43
27:A:2875:C:C2	27:A:2876:C:C5	3.06	0.43
27:A:2964:A:H2'	27:A:2965:A:C8	2.53	0.43
29:a:717:C:H2'	29:a:718:U:C6	2.53	0.43
29:a:759:C:H2'	29:a:760:G:O4'	2.18	0.43
29:a:1411:A:H2'	29:a:1412:C:H6	1.83	0.43
33:f:108:HIS:HD2	36:i:101:LEU:HD12	1.83	0.43
35:h:62:LEU:HA	35:h:124:ILE:HD11	2.00	0.43
44:q:17:GLN:HE21	44:q:41:HIS:CD2	2.36	0.43
45:r:63:ASP:OD1	45:r:63:ASP:N	2.50	0.43
49:c:132:LYS:H	49:c:132:LYS:HD2	1.83	0.43
10:Q:7:GLY:O	10:Q:9:ARG:NH1	2.51	0.43
27:A:734:C:H2'	27:A:735:U:C6	2.53	0.43
27:A:831:A:OP1	43:p:88:ARG:HD3	2.18	0.43
27:A:954:U:H2'	27:A:955:C:C6	2.52	0.43
27:A:1673:A:O2'	27:A:2926:A:OP2	2.35	0.43
28:B:91:G:H2'	28:B:92:G:H8	1.83	0.43
29:a:33:A:O2'	29:a:34:C:H5'	2.18	0.43
29:a:407:A:H2'	29:a:408:G:C8	2.54	0.43
29:a:458:A:OP1	29:a:459:G:H1'	2.17	0.43
29:a:1035:A:C6	29:a:1187:G:C5	3.06	0.43
32:e:188:VAL:HG22	32:e:189:PRO:HD2	1.99	0.43
34:g:45:ARG:HH22	34:g:57:GLU:CG	2.23	0.43
37:j:121:ALA:CB	37:j:123:PHE:CE1	3.01	0.43
42:o:87:MET:HE3	42:o:92:GLU:CB	2.46	0.43
4:H:64:LEU:O	4:H:68:THR:HG23	2.18	0.43
20:2:35:GLN:HB3	20:2:41:LEU:HD22	2.00	0.43
27:A:756:A:H3'	27:A:757:G:N2	2.33	0.43
27:A:772:U:H2'	27:A:773:G:C8	2.53	0.43
27:A:2756:G:H4'	27:A:2881:A:H2	1.83	0.43
27:A:2829:U:H2'	27:A:2830:C:C6	2.53	0.43
27:A:3019:C:H3'	27:A:3020:U:C2	2.53	0.43
28:B:107:A:H2'	28:B:108:C:C6	2.54	0.43
29:a:982:A:N6	29:a:1022:G:C6	2.86	0.43
29:a:1054:G:O2'	29:a:1081:A:N1	2.45	0.43
30:v:28:ARG:HA	30:v:31:LEU:HG	2.00	0.43
35:h:15:ASP:HB2	35:h:24:THR:HG22	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:h:138:ARG:O	35:h:141:THR:HG22	2.18	0.43
42:o:31:ILE:HB	42:o:32:ARG:NH1	2.34	0.43
47:t:32:LYS:HZ1	47:t:57:HIS:CE1	2.36	0.43
49:c:89:MET:SD	49:c:90:PRO:CD	3.06	0.43
49:c:143:LYS:O	49:c:147:SER:OG	2.30	0.43
11:R:12:GLU:OE2	28:B:60:G:O2'	2.25	0.43
16:W:39:LYS:HD2	27:A:1817:C:OP2	2.18	0.43
17:X:90:GLU:H	17:X:90:GLU:HG3	1.60	0.43
27:A:875:G:H2'	27:A:876:A:O4'	2.19	0.43
27:A:908:A:OP2	27:A:2294:A:O2'	2.31	0.43
27:A:928:U:H2'	27:A:929:C:H6	1.83	0.43
27:A:979:G:H2'	27:A:980:C:H6	1.83	0.43
27:A:1639:G:H5'	27:A:1640:A:OP1	2.18	0.43
27:A:1953:C:H2'	27:A:1954:C:O4'	2.18	0.43
27:A:2190:A:N3	27:A:2816:G:O2'	2.51	0.43
29:a:1324:C:H2'	29:a:1325:G:C8	2.54	0.43
31:d:37:ALA:O	31:d:40:LYS:HG2	2.19	0.43
33:f:50:VAL:HG13	33:f:52:GLY:H	1.84	0.43
41:n:47:ASP:OD1	41:n:47:ASP:N	2.50	0.43
42:o:32:ARG:HH21	42:o:39:GLU:HA	1.83	0.43
49:c:94:GLN:HE22	49:c:146:ARG:HD2	1.83	0.43
49:c:166:THR:OG1	49:c:173:VAL:HG21	2.18	0.43
49:c:217:ILE:O	49:c:221:VAL:HG12	2.18	0.43
1:E:118:GLU:HG3	1:E:123:ALA:HB1	2.01	0.43
4:H:52:ARG:CZ	4:H:52:ARG:HB2	2.47	0.43
4:H:80:SER:N	4:H:88:GLU:OE2	2.52	0.43
18:Z:29:GLN:OE1	27:A:1037:C:O2'	2.34	0.43
26:4:12:THR:OG1	26:4:26:SER:HB3	2.17	0.43
27:A:473:C:O2'	27:A:476:G:N2	2.52	0.43
27:A:929:C:H1'	27:A:1339:G:H21	1.83	0.43
27:A:947:U:H2'	27:A:948:G:H8	1.81	0.43
27:A:1665:U:H2'	27:A:1666:A:C8	2.53	0.43
27:A:1706:A:H2'	27:A:1707:G:H8	1.82	0.43
27:A:2086:U:H2'	27:A:2087:C:H6	1.84	0.43
29:a:32:G:O2'	29:a:296:U:OP1	2.34	0.43
29:a:106:C:H2'	29:a:107:G:O4'	2.19	0.43
31:d:87:ARG:HH21	31:d:100:LEU:H	1.67	0.43
47:t:19:VAL:HA	47:t:22:GLN:HB2	2.00	0.43
11:R:93:LYS:NZ	11:R:124:GLY:HA3	2.34	0.43
12:S:51:GLY:HA2	12:S:56:GLU:CD	2.43	0.43
27:A:1016:C:H3'	27:A:1017:G:H8	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:1545:C:H2'	27:A:1546:A:O4'	2.17	0.43
27:A:1705:C:H2'	27:A:1706:A:C8	2.52	0.43
27:A:2086:U:H2'	27:A:2087:C:C6	2.53	0.43
27:A:2342:A:C2	27:A:2392:A:H2'	2.53	0.43
27:A:2344:G:H4'	27:A:2391:G:N2	2.33	0.43
27:A:2378:U:H2'	27:A:2379:G:H8	1.84	0.43
27:A:2883:G:H2'	27:A:2885:G:OP2	2.19	0.43
29:a:71:C:H2'	29:a:72:G:C8	2.54	0.43
29:a:631:C:H2'	29:a:632:U:C6	2.54	0.43
29:a:808:A:H2'	29:a:809:G:O4'	2.18	0.43
31:d:107:ASN:OD1	31:d:107:ASN:C	2.62	0.43
37:j:70:ALA:O	37:j:73:VAL:HG22	2.18	0.43
39:l:62:LYS:HE3	39:l:62:LYS:HB3	1.78	0.43
41:n:45:THR:O	41:n:48:LEU:CD2	2.66	0.43
2:F:53:ALA:HB1	2:F:78:ARG:HB2	1.99	0.43
16:W:8:ARG:NE	20:2:27:GLU:HG3	2.33	0.43
25:8:22:ILE:HG21	25:8:58:ILE:HG21	2.01	0.43
27:A:751:A:H2'	27:A:752:C:C6	2.53	0.43
27:A:1545:C:O2	27:A:1626:G:N2	2.52	0.43
27:A:1716:A:H2'	27:A:1718:C:C5	2.53	0.43
27:A:1771:U:H2'	27:A:1772:G:O4'	2.19	0.43
27:A:2417:C:H2'	27:A:2418:U:O4'	2.19	0.43
27:A:2622:C:H2'	27:A:2623:A:C8	2.54	0.43
28:B:61:C:H2'	28:B:62:C:O4'	2.19	0.43
29:a:281:G:H8	29:a:281:G:OP2	2.02	0.43
29:a:396:G:O2'	29:a:398:C:OP1	2.25	0.43
29:a:408:G:OP1	32:e:105:THR:HG21	2.19	0.43
29:a:1117:U:O2	29:a:1118:A:O2'	2.29	0.43
32:e:86:LEU:HD23	32:e:86:LEU:HA	1.84	0.43
35:h:104:LEU:HD23	35:h:104:LEU:HA	1.79	0.43
47:t:13:ASP:OD1	47:t:13:ASP:N	2.52	0.43
4:H:12:LYS:HE3	4:H:104:TRP:HE1	1.82	0.43
7:M:29:ALA:HB3	7:M:108:MET:HE3	2.00	0.43
11:R:83:ARG:HA	11:R:86:GLN:HG3	1.99	0.43
27:A:356:G:N2	27:A:357:U:O4	2.51	0.43
27:A:2372:U:H2'	27:A:2373:G:H8	1.77	0.43
27:A:2801:A:O4'	27:A:2836:C:N4	2.52	0.43
29:a:891:A:H2'	29:a:892:C:O4'	2.19	0.43
29:a:1315:A:H2'	29:a:1316:G:O4'	2.19	0.43
39:l:29:ALA:O	39:l:44:THR:N	2.35	0.43
41:n:12:ASP:C	41:n:12:ASP:OD1	2.61	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:n:80:ARG:HA	41:n:83:GLU:HG3	2.01	0.43
43:p:18:HIS:NE2	43:p:21:ASP:HB3	2.34	0.43
1:E:120:GLY:O	1:E:131:LEU:HB3	2.19	0.43
3:G:192:ASP:OD1	9:O:5:LYS:NZ	2.45	0.43
5:I:48:ASP:OD1	5:I:48:ASP:N	2.47	0.43
12:S:33:GLU:OE1	12:S:38:ARG:NE	2.50	0.43
27:A:289:A:N7	27:A:299:G:N1	2.66	0.43
27:A:563:U:H4'	27:A:597:C:H5'	1.99	0.43
27:A:666:A:H1'	27:A:2256:G:C8	2.53	0.43
27:A:943:U:H4'	27:A:946:G:N1	2.33	0.43
27:A:1501:C:H2'	27:A:1502:G:H8	1.83	0.43
27:A:1557:C:H2'	27:A:1558:C:C6	2.54	0.43
27:A:2288:C:H2'	27:A:2289:C:C6	2.53	0.43
27:A:2681:U:H2'	27:A:2682:G:C8	2.54	0.43
27:A:2745:C:H2'	27:A:2746:U:C6	2.54	0.43
29:a:1297:U:H2'	29:a:1298:G:O4'	2.19	0.43
34:g:68:GLU:OE2	34:g:68:GLU:HA	2.19	0.43
40:m:18:LYS:HD3	40:m:18:LYS:HA	1.66	0.43
41:n:44:ARG:HB3	41:n:46:LYS:HZ2	1.83	0.43
49:c:50:ILE:CD1	49:c:216:VAL:HG11	2.45	0.43
49:c:211:ALA:O	49:c:215:LYS:HG2	2.19	0.43
10:Q:65:GLU:O	10:Q:68:LYS:HG2	2.19	0.43
11:R:36:PRO:HG2	11:R:51:LEU:HD12	2.01	0.43
17:X:42:LYS:HD2	27:A:586:U:H5''	2.00	0.43
23:6:18:CYS:C	23:6:20:HIS:H	2.27	0.43
27:A:81:A:C2	27:A:100:A:C5	3.07	0.43
27:A:2275:A:H8	27:A:2275:A:OP2	2.01	0.43
27:A:2301:C:H2'	27:A:2302:U:C6	2.54	0.43
27:A:2359:G:N1	27:A:2379:G:H1'	2.34	0.43
29:a:580:G:C6	29:a:619:G:C6	3.07	0.43
29:a:858:A:H2'	29:a:859:C:H6	1.84	0.43
29:a:1436:G:H3'	29:a:1436:G:OP2	2.18	0.43
32:e:176:LEU:HB3	44:q:106:PHE:CE1	2.54	0.43
33:f:117:GLY:HA2	33:f:155:SER:HB3	2.00	0.43
34:g:45:ARG:HD2	34:g:59:ILE:HG12	2.01	0.43
49:c:27:MET:HE2	49:c:193:PRO:CD	2.47	0.43
5:I:89:GLU:HA	5:I:131:LYS:HA	2.01	0.42
11:R:98:GLU:OE2	11:R:126:LYS:HG2	2.19	0.42
13:T:58:ARG:HA	13:T:61:TRP:CE3	2.54	0.42
27:A:2007:C:H2'	27:A:2008:A:C5	2.53	0.42
27:A:2327:C:H2'	27:A:2328:G:C8	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:3055:G:H2'	27:A:3100:A:H61	1.84	0.42
29:a:246:A:C2	29:a:282:A:C5	3.07	0.42
29:a:502:C:OP2	40:m:66:TYR:OH	2.34	0.42
29:a:1028:G:H1'	29:a:1196:G:H5'	1.99	0.42
29:a:1171:G:OP1	31:d:5:ILE:HG23	2.19	0.42
29:a:1407:U:H2'	29:a:1408:A:C8	2.54	0.42
39:l:102:ARG:NH2	39:l:121:ASP:OD2	2.37	0.42
41:n:86:CYS:O	41:n:90:LEU:CD2	2.67	0.42
42:o:10:ASN:O	42:o:14:ARG:HG2	2.19	0.42
2:F:160:VAL:HG21	27:A:2842:G:H21	1.84	0.42
4:H:8:LEU:HD11	4:H:12:LYS:HD3	2.01	0.42
10:Q:46:PRO:O	10:Q:50:LYS:HG3	2.19	0.42
27:A:149:C:H2'	27:A:150:C:C6	2.53	0.42
27:A:524:C:H2'	27:A:525:C:H6	1.85	0.42
27:A:635:G:O2'	27:A:636:U:O5'	2.37	0.42
27:A:2603:G:H2'	27:A:2604:U:C6	2.53	0.42
27:A:2870:C:OP2	27:A:2956:G:O2'	2.37	0.42
28:B:5:C:O2'	28:B:6:G:H5'	2.19	0.42
29:a:105:A:C6	29:a:326:G:C6	3.08	0.42
29:a:955:G:H2'	29:a:956:A:C2	2.54	0.42
29:a:1320:G:H2'	29:a:1321:A:C8	2.54	0.42
31:d:64:ARG:HG3	31:d:99:GLN:NE2	2.33	0.42
31:d:106:LYS:HA	31:d:106:LYS:HD3	1.81	0.42
32:e:87:ARG:O	32:e:91:SER:OG	2.33	0.42
35:h:93:PRO:O	35:h:96:SER:OG	2.29	0.42
50:w:49:GLU:H	50:w:49:GLU:CD	2.26	0.42
27:A:293:G:C6	27:A:294:G:O6	2.72	0.42
27:A:296:A:N1	27:A:340:A:N6	2.67	0.42
27:A:2674:A:OP1	27:A:2721:A:O2'	2.30	0.42
29:a:702:G:H1	29:a:713:G:H1	1.67	0.42
29:a:863:G:OP2	40:m:9:ARG:NH2	2.53	0.42
29:a:918:C:C2	29:a:919:A:C8	3.07	0.42
29:a:1269:A:H2'	29:a:1270:A:C8	2.53	0.42
31:d:117:GLN:HG3	31:d:187:TYR:CE2	2.53	0.42
37:j:47:GLN:C	37:j:47:GLN:CD	2.87	0.42
38:k:47:ASN:O	38:k:66:GLU:HA	2.19	0.42
41:n:25:ILE:HD11	41:n:60:ILE:HD13	2.01	0.42
4:H:110:LEU:HD12	4:H:114:ALA:HB3	2.01	0.42
5:I:104:LEU:HG	5:I:106:PHE:HE1	1.83	0.42
7:M:72:LYS:HG2	7:M:89:ILE:HD11	2.00	0.42
14:U:43:VAL:HG22	14:U:48:VAL:HG22	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:5:37:ARG:HD3	22:5:54:LEU:HD13	2.00	0.42
27:A:663:A:N3	27:A:663:A:H2'	2.34	0.42
27:A:1548:C:H2'	27:A:1549:G:H8	1.82	0.42
27:A:2901:G:H2'	27:A:2902:A:H8	1.85	0.42
29:a:209:A:H2'	29:a:210:A:C8	2.53	0.42
29:a:893:U:H2'	29:a:894:C:C6	2.55	0.42
29:a:1083:C:H4'	49:c:97:LEU:HD13	2.00	0.42
29:a:1133:G:OP1	38:k:70:HIS:ND1	2.45	0.42
29:a:1237:C:H2'	29:a:1259:G:N7	2.35	0.42
29:a:1396:A:H2	29:a:1471:G:H22	1.68	0.42
32:e:146:ASN:C	32:e:146:ASN:OD1	2.61	0.42
32:e:187:ASP:OD1	32:e:187:ASP:O	2.38	0.42
36:i:43:GLU:OE2	36:i:43:GLU:HA	2.19	0.42
8:N:44:LYS:HD3	8:N:44:LYS:HA	1.86	0.42
25:8:34:GLU:HB2	27:A:2644:C:OP1	2.19	0.42
27:A:72:G:H2'	27:A:72:G:N3	2.34	0.42
27:A:290:C:N4	27:A:300:G:H21	2.17	0.42
27:A:2366:C:H2'	27:A:2367:G:O4'	2.19	0.42
27:A:2395:U:OP2	27:A:2396:A:H5''	2.19	0.42
27:A:2515:U:H2'	27:A:2516:U:H6	1.81	0.42
27:A:2738:U:H2'	27:A:2739:C:H6	1.83	0.42
27:A:2867:A:H2'	27:A:2868:A:H8	1.83	0.42
29:a:109:G:H1'	29:a:354:G:H5'	2.00	0.42
29:a:429:U:O4'	29:a:430:A:H8	2.03	0.42
29:a:656:A:H2'	29:a:657:U:H6	1.84	0.42
29:a:1226:G:H2'	29:a:1227:G:H8	1.85	0.42
31:d:130:ARG:H	31:d:130:ARG:HG2	1.50	0.42
36:i:46:ILE:HD12	36:i:62:VAL:HG13	2.01	0.42
50:w:112:ARG:H	50:w:115:SER:HB2	1.84	0.42
4:H:63:ASP:OD2	4:H:157:ARG:NE	2.52	0.42
6:J:1:MET:SD	6:J:23:ASP:HA	2.59	0.42
7:M:84:LEU:HD22	27:A:1249:G:H4'	1.99	0.42
13:T:47:TYR:OH	27:A:1110:C:OP1	2.29	0.42
27:A:62:G:H2'	27:A:63:C:H6	1.84	0.42
27:A:332:C:H2'	27:A:333:C:H6	1.83	0.42
27:A:738:A:H2'	27:A:740:A:C8	2.55	0.42
27:A:868:C:H2'	27:A:869:U:H6	1.84	0.42
27:A:1898:U:H2'	27:A:1899:G:O4'	2.20	0.42
27:A:2552:A:H2'	27:A:2553:G:H8	1.78	0.42
29:a:272:C:H2'	29:a:273:A:H8	1.85	0.42
29:a:381:C:H2'	29:a:382:A:O4'	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:a:593:C:OP1	32:e:76:ARG:NH1	2.41	0.42
29:a:872:G:O2'	29:a:888:A:N6	2.53	0.42
31:d:58:ARG:HG3	31:d:63:VAL:HG22	2.01	0.42
32:e:53:LYS:HD2	32:e:199:TYR:OH	2.20	0.42
33:f:48:LYS:HB2	33:f:48:LYS:HE2	1.77	0.42
43:p:39:LEU:HD12	43:p:39:LEU:HA	1.83	0.42
47:t:29:GLN:N	47:t:29:GLN:CD	2.77	0.42
49:c:131:LYS:HB2	49:c:131:LYS:HE2	1.85	0.42
2:F:13:MET:HG3	2:F:26:VAL:O	2.20	0.42
27:A:329:U:H1'	27:A:447:A:C2	2.54	0.42
27:A:2107:G:H4'	27:A:2107:G:OP1	2.18	0.42
27:A:2351:A:H2'	27:A:2352:C:C6	2.55	0.42
27:A:2642:G:H2'	27:A:2643:U:O4'	2.19	0.42
27:A:3040:G:H2'	27:A:3042:A:N7	2.35	0.42
29:a:847:A:H2'	29:a:848:C:C6	2.54	0.42
29:a:1138:A:H1'	29:a:1162:G:N2	2.35	0.42
29:a:1253:U:H2'	29:a:1254:G:O4'	2.20	0.42
29:a:1298:G:N7	47:t:7:LYS:NZ	2.68	0.42
30:v:5:ILE:O	30:v:9:ARG:HG3	2.20	0.42
34:g:74:GLU:OE2	34:g:78:GLN:HG3	2.19	0.42
37:j:75:VAL:HG11	37:j:107:LEU:HD13	2.02	0.42
49:c:25:PRO:C	49:c:27:MET:H	2.27	0.42
50:w:104:PRO:O	50:w:106:GLU:HG2	2.19	0.42
5:I:5:GLY:HA2	5:I:70:ARG:HB2	2.02	0.42
17:X:103:LYS:HB3	17:X:103:LYS:HE3	1.79	0.42
21:3:37:ARG:HH22	27:A:1043:G:H4'	1.84	0.42
27:A:303:G:H2'	27:A:304:U:O4'	2.20	0.42
27:A:740:A:O2'	27:A:741:G:OP2	2.24	0.42
27:A:1137:U:H2'	27:A:1138:A:C8	2.55	0.42
27:A:1530:G:N2	27:A:1805:G:N1	2.66	0.42
27:A:2038:A:H2'	27:A:2039:C:H6	1.85	0.42
27:A:2211:C:H2'	27:A:2212:A:H8	1.84	0.42
27:A:2457:U:H2'	27:A:2458:G:H8	1.84	0.42
27:A:2678:G:H2'	27:A:2678:G:N3	2.35	0.42
27:A:3023:G:H2'	27:A:3024:A:O4'	2.20	0.42
29:a:209:A:N3	29:a:222:U:O2'	2.42	0.42
29:a:671:G:O2'	29:a:777:C:H4'	2.20	0.42
29:a:1388:G:H5'	30:v:12:MET:CE	2.43	0.42
40:m:74:LEU:HD11	40:m:80:VAL:HG11	2.01	0.42
4:H:64:LEU:HD23	4:H:64:LEU:HA	1.86	0.42
17:X:40:ARG:NH2	17:X:61:THR:HG22	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:8:3:LYS:HG3	27:A:242:G:C8	2.55	0.42
27:A:1002:C:H2'	27:A:1003:A:H5''	2.01	0.42
27:A:1013:U:N3	27:A:1014:G:H1'	2.34	0.42
27:A:1140:G:N2	27:A:1141:U:O4	2.37	0.42
27:A:1160:G:H2'	27:A:1161:C:C6	2.55	0.42
27:A:1947:U:H1'	27:A:1948:A:C2	2.55	0.42
27:A:2867:A:H2'	27:A:2868:A:C8	2.55	0.42
29:a:109:G:H2'	29:a:110:U:C6	2.55	0.42
29:a:584:G:H2'	29:a:585:U:O4'	2.20	0.42
29:a:964:U:H4'	29:a:965:A:O4'	2.20	0.42
31:d:145:ASN:ND2	31:d:204:LYS:HE3	2.34	0.42
33:f:175:PRO:HB2	33:f:186:ILE:HD11	2.00	0.42
8:N:24:VAL:HG13	8:N:33:ALA:HB2	2.02	0.42
17:X:34:LEU:HD12	17:X:34:LEU:HA	1.93	0.42
23:6:11:ILE:HD12	23:6:11:ILE:O	2.20	0.42
26:4:36:GLU:HG2	26:4:37:VAL:N	2.35	0.42
27:A:1018:U:O2'	27:A:1020:A:N7	2.53	0.42
27:A:1259:U:H1'	27:A:1261:A:C6	2.54	0.42
27:A:1673:A:H5''	27:A:1674:G:H5''	2.01	0.42
27:A:2873:U:H2'	27:A:2874:C:H6	1.84	0.42
28:B:40:A:H2'	28:B:41:U:C6	2.55	0.42
29:a:156:G:N2	29:a:159:A:OP2	2.51	0.42
29:a:497:G:H8	29:a:510:G:H5''	1.85	0.42
29:a:657:U:O2	29:a:757:A:O2'	2.38	0.42
29:a:658:U:H2'	29:a:659:C:H6	1.84	0.42
29:a:1271:A:H2'	29:a:1272:G:H5'	2.02	0.42
35:h:135:VAL:O	35:h:139:GLU:HG2	2.20	0.42
37:j:113:GLU:H	37:j:113:GLU:CD	2.28	0.42
42:o:90:ARG:HE	42:o:90:ARG:HB2	1.68	0.42
45:r:20:ARG:HB2	45:r:77:MET:HE2	2.02	0.42
49:c:144:LEU:HD12	49:c:144:LEU:HA	1.79	0.42
50:w:85:LEU:HD23	50:w:85:LEU:HA	1.91	0.42
11:R:125:LEU:C	11:R:126:LYS:HE2	2.45	0.41
26:4:65:TYR:CE1	47:t:5:LEU:HA	2.55	0.41
27:A:935:A:H4'	27:A:951:G:N2	2.35	0.41
27:A:2486:U:H2'	27:A:2487:C:H6	1.85	0.41
29:a:264:U:H2'	29:a:265:G:O4'	2.20	0.41
29:a:457:A:C6	29:a:458:A:N6	2.88	0.41
29:a:1470:G:H2'	29:a:1471:G:O4'	2.19	0.41
45:r:39:GLU:OE1	45:r:56:THR:HB	2.20	0.41
48:u:42:GLY:HA2	48:u:86:LEU:HD11	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:208:LYS:HB2	27:A:844:G:C5	2.55	0.41
4:H:81:ILE:HG21	4:H:84:PHE:CD2	2.55	0.41
5:I:55:ARG:HH11	5:I:63:ARG:HA	1.86	0.41
5:I:87:LYS:NZ	5:I:89:GLU:HB3	2.35	0.41
5:I:104:LEU:HD22	5:I:124:PHE:CD2	2.55	0.41
15:V:34:LYS:HD3	15:V:38:GLU:CD	2.45	0.41
27:A:673:C:H2'	27:A:674:U:H6	1.83	0.41
27:A:986:G:C2	27:A:987:A:H1'	2.55	0.41
27:A:1533:U:O2	27:A:1803:A:O2'	2.29	0.41
27:A:1546:A:H2'	27:A:1547:G:C8	2.53	0.41
27:A:2287:C:H2'	27:A:2288:C:C6	2.55	0.41
27:A:2373:G:H2'	27:A:2374:U:C6	2.55	0.41
27:A:2723:C:H2'	27:A:2724:U:C2	2.54	0.41
29:a:61:G:H2'	29:a:62:C:C6	2.55	0.41
29:a:120:G:H2'	29:a:121:U:C6	2.54	0.41
29:a:465:G:HO2'	29:a:466:U:H6	1.66	0.41
29:a:508:C:H3'	29:a:509:G:H5''	2.02	0.41
29:a:717:C:H2'	29:a:718:U:H6	1.84	0.41
29:a:943:U:OP2	29:a:1204:C:O2'	2.27	0.41
29:a:980:G:H2'	29:a:981:C:H6	1.84	0.41
32:e:41:ILE:HD12	32:e:41:ILE:C	2.45	0.41
37:j:113:GLU:OE2	37:j:113:GLU:N	2.47	0.41
42:o:27:LEU:O	42:o:31:ILE:HG12	2.21	0.41
45:r:73:ARG:HD3	45:r:95:GLU:OE1	2.21	0.41
49:c:47:LEU:HA	49:c:50:ILE:HG22	2.02	0.41
2:F:156:THR:HB	27:A:2795:C:O2'	2.20	0.41
3:G:206:SER:O	3:G:210:LYS:HB3	2.21	0.41
5:I:43:VAL:HA	5:I:52:VAL:O	2.19	0.41
17:X:1:MET:C	17:X:3:VAL:H	2.28	0.41
27:A:248:G:H5'	27:A:250:G:N7	2.36	0.41
27:A:270:U:C2'	27:A:271:A:H5'	2.50	0.41
27:A:1010:U:C5	27:A:1012:C:H5	2.38	0.41
27:A:1065:C:H2'	27:A:1066:G:H8	1.85	0.41
27:A:1146:A:OP2	27:A:1244:A:N6	2.28	0.41
27:A:1487:U:O2'	27:A:2436:A:N3	2.45	0.41
27:A:1714:A:H2'	27:A:1715:A:C8	2.56	0.41
27:A:2085:C:O2'	27:A:2086:U:O4'	2.35	0.41
27:A:2222:A:H4'	27:A:2948:C:O2'	2.20	0.41
27:A:2262:C:H2'	27:A:2263:G:O4'	2.20	0.41
27:A:2415:G:H2'	27:A:2416:C:C6	2.55	0.41
27:A:2849:G:H2'	27:A:2850:C:C6	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:2870:C:H2'	27:A:2871:U:O4'	2.20	0.41
29:a:144:G:H2'	29:a:145:G:H8	1.85	0.41
29:a:1136:A:H2'	29:a:1137:G:O4'	2.20	0.41
31:d:94:THR:C	31:d:96:LYS:H	2.28	0.41
32:e:138:ILE:N	32:e:138:ILE:HD12	2.35	0.41
33:f:63:ILE:HD12	33:f:139:VAL:HG22	2.02	0.41
4:H:132:THR:HG22	11:R:6:VAL:HG11	2.01	0.41
7:M:60:ASP:OD1	7:M:60:ASP:N	2.52	0.41
7:M:69:LEU:HD12	7:M:69:LEU:HA	1.86	0.41
9:O:24:ARG:HA	27:A:926:U:H2'	2.02	0.41
25:8:44:LEU:HD21	27:A:2586:G:OP2	2.20	0.41
27:A:987:A:C2'	27:A:988:U:H5'	2.51	0.41
27:A:1062:A:C4	27:A:2672:A:C2	3.08	0.41
27:A:1434:G:H2'	27:A:1435:C:C6	2.55	0.41
27:A:1524:G:H2'	27:A:1525:U:C6	2.55	0.41
27:A:1607:C:OP1	27:A:1607:C:H4'	2.20	0.41
36:i:25:VAL:HG13	36:i:62:VAL:HB	2.02	0.41
37:j:42:VAL:O	37:j:82:ASP:N	2.49	0.41
47:t:21:VAL:O	47:t:24:GLU:HG3	2.21	0.41
1:E:210:GLY:HA2	27:A:879:A:H5''	2.03	0.41
11:R:118:ASP:O	11:R:122:GLU:OE1	2.38	0.41
25:8:33:LEU:HD22	27:A:2643:U:OP2	2.21	0.41
27:A:296:A:C6	27:A:340:A:N6	2.89	0.41
27:A:601:A:H2'	27:A:602:A:H8	1.86	0.41
27:A:988:U:C4	27:A:990:G:C6	3.09	0.41
27:A:1612:U:H1'	34:g:17:ARG:NH2	2.24	0.41
27:A:3036:C:C4	27:A:3037:C:C5	3.09	0.41
28:B:1:G:H2'	28:B:2:U:C6	2.55	0.41
29:a:659:C:H2'	29:a:660:C:H6	1.86	0.41
29:a:940:A:C5	47:t:55:ARG:HG3	2.55	0.41
29:a:1063:U:O2'	29:a:1082:A:OP2	2.38	0.41
29:a:1125:G:H21	29:a:1127:A:H62	1.66	0.41
35:h:66:LEU:O	35:h:70:LYS:N	2.53	0.41
36:i:14:LEU:HA	36:i:14:LEU:HD23	1.76	0.41
41:n:49:THR:OG1	41:n:50:ASP:N	2.54	0.41
43:p:10:GLU:CD	43:p:11:ILE:N	2.78	0.41
49:c:120:MET:SD	49:c:120:MET:C	3.03	0.41
3:G:108:ALA:HB1	3:G:112:ARG:NH1	2.36	0.41
12:S:113:ARG:HH12	29:a:1425:G:H2'	1.85	0.41
14:U:84:TYR:CE1	27:A:1302:G:H5''	2.56	0.41
15:V:68:ASN:HB2	15:V:69:GLU:OE2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:402:G:H4'	27:A:404:A:C8	2.56	0.41
27:A:1001:C:N4	27:A:1007:G:O6	2.53	0.41
27:A:1013:U:C4	27:A:1014:G:H1'	2.56	0.41
27:A:3070:G:H4'	27:A:3071:A:H5'	2.02	0.41
29:a:1050:U:H2'	29:a:1051:C:H6	1.86	0.41
29:a:1214:G:H2'	29:a:1215:C:C6	2.56	0.41
29:a:1370:G:H2'	29:a:1371:C:C6	2.55	0.41
29:a:1385:C:H2'	29:a:1386:C:O4'	2.20	0.41
29:a:1497:A:H2'	29:a:1498:C:H6	1.83	0.41
31:d:46:LEU:HA	31:d:48:ARG:NH2	2.36	0.41
31:d:153:CYS:SG	31:d:157:LEU:HD21	2.61	0.41
37:j:46:GLY:HA3	37:j:79:ASP:HA	2.02	0.41
37:j:55:LEU:O	37:j:55:LEU:HD13	2.21	0.41
40:m:31:ARG:HE	40:m:31:ARG:HB3	1.47	0.41
47:t:22:GLN:HA	47:t:25:LYS:HZ2	1.84	0.41
48:u:50:LEU:O	48:u:54:THR:OG1	2.28	0.41
2:F:151:ILE:HD12	2:F:151:ILE:HA	1.87	0.41
5:I:61:ARG:HA	5:I:61:ARG:NH1	2.35	0.41
5:I:88:MET:HE1	5:I:165:TYR:HA	2.03	0.41
17:X:85:TYR:CD1	17:X:94:LYS:HE2	2.55	0.41
17:X:86:ARG:HG2	17:X:97:ILE:HG21	2.03	0.41
19:1:48:ARG:HB2	19:1:48:ARG:HH11	1.85	0.41
27:A:165:U:H2'	27:A:166:A:C8	2.55	0.41
27:A:270:U:H2'	27:A:271:A:H5'	2.03	0.41
27:A:422:A:H2'	27:A:423:C:O4'	2.21	0.41
27:A:601:A:H2'	27:A:602:A:C8	2.56	0.41
27:A:733:U:H2'	27:A:734:C:C6	2.55	0.41
27:A:1122:C:H2'	27:A:1129:G:H2'	2.01	0.41
27:A:1659:U:H2'	27:A:1660:A:H8	1.85	0.41
27:A:2545:G:H5'	27:A:2546:A:OP2	2.21	0.41
27:A:2876:C:C4	27:A:2877:U:C4	3.08	0.41
27:A:3033:G:H2'	27:A:3034:C:H6	1.85	0.41
27:A:3116:C:H2'	27:A:3117:U:C6	2.56	0.41
29:a:393:A:OP1	44:q:14:ARG:NH2	2.53	0.41
29:a:865:C:O2'	29:a:866:U:H5'	2.20	0.41
29:a:949:C:OP1	29:a:951:A:H5'	2.21	0.41
29:a:1153:U:H2'	29:a:1154:C:C6	2.55	0.41
29:a:1232:A:N6	29:a:1268:C:H42	2.11	0.41
29:a:1409:A:H2'	29:a:1410:C:C6	2.54	0.41
36:i:47:SER:HB3	36:i:63:GLN:HB2	2.03	0.41
39:l:103:GLU:H	39:l:103:GLU:CD	2.23	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:I:108:LEU:HD22	5:I:110:TYR:CE1	2.56	0.41
19:1:41:ARG:CD	19:1:43:GLY:H	2.34	0.41
27:A:166:A:H2'	27:A:167:G:O4'	2.20	0.41
27:A:285:U:C3'	27:A:286:G:H4'	2.50	0.41
27:A:309:G:H2'	27:A:310:C:C6	2.56	0.41
27:A:392:A:C4	27:A:394:G:C8	3.09	0.41
27:A:973:G:H3'	27:A:974:G:C8	2.56	0.41
27:A:2060:C:H2'	27:A:2061:U:C6	2.56	0.41
27:A:2128:G:O2'	27:A:2152:A:N1	2.49	0.41
27:A:2613:G:H5''	27:A:2614:U:O4'	2.21	0.41
27:A:2829:U:H2'	27:A:2830:C:H6	1.86	0.41
29:a:399:G:H2'	29:a:400:C:H6	1.84	0.41
29:a:649:G:H2'	29:a:650:A:C8	2.56	0.41
31:d:93:LEU:HD23	31:d:93:LEU:HA	1.85	0.41
33:f:70:MET:HE2	33:f:98:ARG:HH11	1.85	0.41
49:c:91:TYR:HE2	49:c:93:ASN:ND2	2.17	0.41
1:E:72:LYS:HD3	1:E:72:LYS:HA	1.78	0.41
2:F:89:GLU:HA	2:F:92:VAL:HG12	2.03	0.41
8:N:17:LYS:HD2	8:N:45:ASP:OD2	2.21	0.41
8:N:63:VAL:HG23	8:N:64:ARG:HG3	2.02	0.41
11:R:14:ARG:NH1	28:B:48:C:OP2	2.53	0.41
19:1:36:VAL:HG13	19:1:63:ARG:HE	1.85	0.41
19:1:41:ARG:HD2	19:1:43:GLY:N	2.36	0.41
20:2:15:ASP:O	20:2:19:LYS:HG2	2.21	0.41
27:A:196:A:H62	27:A:2654:A:H2'	1.85	0.41
27:A:337:U:C2	27:A:345:G:C2	3.08	0.41
27:A:784:G:N3	27:A:784:G:H2'	2.35	0.41
27:A:1139:A:H3'	27:A:1139:A:N3	2.36	0.41
27:A:1468:A:H2'	27:A:1469:A:H8	1.84	0.41
27:A:1493:A:O2'	27:A:1495:G:N7	2.46	0.41
27:A:2074:G:N2	27:A:2109:A:H62	2.19	0.41
27:A:2084:A:H2'	27:A:2085:C:O4'	2.21	0.41
27:A:2326:A:C6	27:A:2410:A:C5	3.09	0.41
27:A:2331:U:H2'	27:A:2332:U:C2	2.56	0.41
27:A:2490:A:H4'	27:A:2491:A:N3	2.36	0.41
27:A:2588:C:H2'	27:A:2589:G:O4'	2.20	0.41
27:A:2671:G:N1	27:A:2675:A:N6	2.53	0.41
27:A:2880:U:N3	27:A:2889:A:C8	2.88	0.41
27:A:3034:C:H2'	27:A:3035:C:C6	2.56	0.41
29:a:54:A:O2'	29:a:360:G:N2	2.54	0.41
29:a:482:A:H2'	29:a:483:C:O4'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:a:715:G:C1'	46:s:73:GLU:OE2	2.69	0.41
29:a:768:U:O2'	50:w:97:GLU:HG2	2.21	0.41
29:a:1277:U:H2'	29:a:1278:C:C6	2.55	0.41
31:d:78:ARG:CZ	31:d:78:ARG:H	2.34	0.41
32:e:179:GLN:NE2	32:e:185:GLN:HE22	2.18	0.41
34:g:29:VAL:HG21	34:g:74:GLU:HG3	2.02	0.41
34:g:30:ILE:HD12	34:g:36:THR:OG1	2.20	0.41
35:h:78:ARG:O	35:h:84:THR:HA	2.20	0.41
42:o:26:GLU:HA	42:o:29:ARG:HG3	2.02	0.41
42:o:31:ILE:HB	42:o:32:ARG:HH12	1.86	0.41
44:q:82:LYS:HB2	44:q:89:ALA:HB2	2.02	0.41
49:c:67:VAL:N	49:c:89:MET:HE3	2.11	0.41
49:c:120:MET:HA	49:c:123:THR:HG22	2.03	0.41
50:w:1:MET:HB2	50:w:26:SER:HB2	2.02	0.41
50:w:7:THR:OG1	50:w:8:ASP:N	2.50	0.41
50:w:27:ARG:HH22	50:w:28:ARG:HH21	1.69	0.41
1:E:156:ALA:HB2	1:E:163:ILE:HG13	2.03	0.41
2:F:56:GLU:OE2	2:F:56:GLU:HA	2.21	0.41
5:I:104:LEU:HD12	5:I:104:LEU:HA	1.77	0.41
9:O:115:ASP:OD1	27:A:731:A:H2'	2.21	0.41
27:A:27:G:H2'	27:A:28:C:C6	2.56	0.41
27:A:351:G:O6	27:A:444:U:O2	2.39	0.41
27:A:743:G:H2'	27:A:744:C:C6	2.55	0.41
27:A:1500:A:O2'	27:A:1511:U:O2	2.38	0.41
27:A:1706:A:H2'	27:A:1707:G:C8	2.56	0.41
27:A:1754:G:C2	27:A:1760:G:C2	3.08	0.41
27:A:2043:C:H2'	27:A:2044:U:C6	2.56	0.41
27:A:2378:U:H2'	27:A:2379:G:C8	2.56	0.41
29:a:23:C:H5''	33:f:116:ALA:HB3	2.03	0.41
29:a:39:G:H2'	29:a:40:C:C6	2.56	0.41
29:a:334:C:H2'	29:a:335:C:H6	1.86	0.41
29:a:1043:C:OP2	29:a:1044:G:O2'	2.38	0.41
29:a:1087:C:C4	29:a:1088:G:C8	3.09	0.41
29:a:1357:A:OP1	35:h:36:LYS:NZ	2.44	0.41
31:d:87:ARG:NH2	31:d:100:LEU:H	2.18	0.41
32:e:183:ARG:HA	32:e:183:ARG:HD2	1.82	0.41
36:i:101:LEU:HD23	36:i:101:LEU:HA	1.79	0.41
49:c:162:TRP:HH2	49:c:186:ILE:CG2	2.34	0.41
2:F:85:ARG:NH2	27:A:2862:G:OP1	2.33	0.40
4:H:126:PRO:HB2	4:H:174:ARG:NH1	2.37	0.40
9:O:5:LYS:HA	9:O:5:LYS:HD2	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:3:16:ARG:O	21:3:20:ARG:HG3	2.21	0.40
23:6:21:ARG:HD2	23:6:22:ASN:H	1.87	0.40
26:4:60:ARG:HE	26:4:60:ARG:HB3	1.78	0.40
27:A:159:A:N3	27:A:2431:C:O2'	2.49	0.40
27:A:929:C:H1'	27:A:1339:G:N2	2.36	0.40
27:A:1907:A:H2'	27:A:1908:A:C8	2.56	0.40
27:A:2253:A:C6	27:A:2255:A:H5'	2.55	0.40
27:A:2674:A:N6	27:A:2725:C:O2	2.54	0.40
27:A:3014:A:H62	27:A:3113:A:H2	1.67	0.40
31:d:53:ASP:OD1	31:d:53:ASP:C	2.65	0.40
33:f:50:VAL:HG22	33:f:51:LYS:H	1.86	0.40
43:p:7:GLN:HA	43:p:10:GLU:HG3	2.03	0.40
49:c:66:THR:HA	49:c:89:MET:HE1	2.02	0.40
49:c:97:LEU:H	49:c:100:MET:HE1	1.85	0.40
3:G:152:LYS:HE3	3:G:152:LYS:HB2	1.96	0.40
10:Q:63:ARG:HA	10:Q:80:PHE:CZ	2.57	0.40
11:R:76:ASP:OD1	11:R:77:LYS:N	2.46	0.40
20:2:28:GLU:OE1	20:2:46:ARG:NH2	2.54	0.40
24:7:34:VAL:HG13	24:7:45:LEU:HD23	2.03	0.40
26:4:60:ARG:CZ	29:a:1293:G:OP1	2.69	0.40
27:A:2443:U:H2'	27:A:2444:C:H6	1.86	0.40
29:a:702:G:N3	29:a:702:G:H2'	2.37	0.40
29:a:877:G:H2'	29:a:878:C:C6	2.56	0.40
29:a:1163:G:H4'	29:a:1164:U:H5'	2.02	0.40
29:a:1199:C:H2'	29:a:1200:A:H8	1.83	0.40
33:f:199:ARG:O	33:f:202:GLU:HG2	2.21	0.40
34:g:27:LEU:O	34:g:30:ILE:HG13	2.21	0.40
37:j:149:LYS:HD2	50:w:64:GLN:CG	2.51	0.40
41:n:87:TYR:HA	41:n:90:LEU:CD2	2.49	0.40
49:c:52:LYS:O	49:c:55:GLU:HG3	2.20	0.40
2:F:9:THR:OG1	2:F:54:TYR:OH	2.28	0.40
8:N:80:ASP:OD2	12:S:61:ARG:NH2	2.44	0.40
15:V:40:LEU:HD23	15:V:40:LEU:HA	1.91	0.40
19:1:63:ARG:NH1	27:A:2315:U:OP2	2.53	0.40
27:A:218:A:N3	27:A:234:U:O2'	2.44	0.40
27:A:1900:C:H2'	27:A:1901:C:H6	1.86	0.40
27:A:2249:G:H2'	27:A:2250:A:H8	1.84	0.40
28:B:110:G:H2'	28:B:111:C:C6	2.56	0.40
29:a:25:G:H2'	29:a:26:G:C8	2.56	0.40
29:a:157:A:H2'	29:a:158:A:O4'	2.21	0.40
29:a:312:C:H2'	29:a:313:A:C8	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:a:1515:A:C2	50:w:110:GLU:HG2	2.57	0.40
37:j:51:ASP:OD1	37:j:86:HIS:HA	2.21	0.40
37:j:123:PHE:CD1	37:j:123:PHE:N	2.89	0.40
40:m:34:CYS:SG	40:m:74:LEU:HD12	2.62	0.40
49:c:35:ARG:O	49:c:38:ILE:HG13	2.22	0.40
49:c:152:ARG:HG3	49:c:153:ASP:OD1	2.20	0.40
49:c:186:ILE:O	49:c:186:ILE:HG13	2.22	0.40
1:E:233:HIS:NE2	1:E:246:PRO:HA	2.37	0.40
22:5:4:PRO:HA	27:A:2839:U:C2	2.56	0.40
26:4:61:PHE:C	26:4:61:PHE:CD1	2.99	0.40
27:A:430:A:H2'	27:A:431:C:C6	2.56	0.40
27:A:636:U:H5''	27:A:637:G:O4'	2.21	0.40
27:A:744:C:C2	27:A:745:G:C8	3.09	0.40
27:A:1153:U:H2'	27:A:1154:G:H8	1.87	0.40
27:A:1295:U:H2'	27:A:1296:G:H8	1.87	0.40
27:A:2043:C:H2'	27:A:2044:U:H6	1.85	0.40
27:A:2623:A:H2'	27:A:2624:C:C6	2.56	0.40
29:a:832:U:H2'	29:a:833:C:C6	2.56	0.40
29:a:907:G:O2'	29:a:909:G:OP1	2.38	0.40
29:a:909:G:P	50:w:112:ARG:HH12	2.45	0.40
29:a:1219:A:N7	29:a:1285:C:H1'	2.36	0.40
29:a:1269:A:H2	29:a:1335:G:H1'	1.86	0.40
36:i:106:ILE:HD12	36:i:115:ASP:HA	2.02	0.40
39:l:53:TRP:HZ3	39:l:55:SER:HB2	1.86	0.40
41:n:64:LEU:HD23	41:n:64:LEU:HA	1.86	0.40
49:c:71:GLY:HA3	49:c:80:ILE:HD12	2.02	0.40
49:c:71:GLY:O	49:c:93:ASN:HA	2.21	0.40
49:c:79:SER:O	49:c:82:GLU:HG3	2.21	0.40
50:w:53:ILE:HG22	50:w:70:GLU:HG3	2.03	0.40
50:w:95:HIS:CD2	50:w:97:GLU:HB2	2.56	0.40
3:G:171:ASN:HB2	27:A:404:A:OP2	2.21	0.40
3:G:201:LEU:O	3:G:205:ILE:HG12	2.21	0.40
4:H:114:ALA:HB1	4:H:144:MET:HG3	2.04	0.40
5:I:92:GLY:HA3	5:I:95:TYR:HE1	1.86	0.40
7:M:35:LEU:HD23	7:M:35:LEU:HA	1.85	0.40
15:V:115:GLU:OE2	15:V:117:ARG:NE	2.50	0.40
27:A:206:A:H2'	27:A:207:C:O4'	2.22	0.40
27:A:307:G:H2'	27:A:308:U:C6	2.57	0.40
27:A:2342:A:H61	27:A:2390:U:H1'	1.86	0.40
27:A:2861:U:H2'	27:A:2862:G:O4'	2.21	0.40
27:A:3007:G:H2'	27:A:3008:C:C6	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:a:507:G:O6	40:m:46:ASN:ND2	2.52	0.40
29:a:715:G:H2'	29:a:716:U:C6	2.57	0.40
29:a:972:U:H2'	29:a:973:U:C6	2.56	0.40
31:d:71:ARG:HB3	31:d:74:ILE:HG13	2.03	0.40
33:f:198:ARG:HB3	33:f:199:ARG:NH1	2.36	0.40
35:h:47:LEU:HD22	35:h:58:PRO:HB2	2.03	0.40
38:k:37:VAL:HG22	38:k:75:ASP:O	2.22	0.40
47:t:81:LYS:HE2	47:t:81:LYS:HB3	1.97	0.40
49:c:97:LEU:N	49:c:100:MET:HE1	2.37	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	273/278 (98%)	260 (95%)	13 (5%)	0	100	100
2	F	212/217 (98%)	203 (96%)	9 (4%)	0	100	100
3	G	207/215 (96%)	202 (98%)	5 (2%)	0	100	100
4	H	179/187 (96%)	169 (94%)	10 (6%)	0	100	100
5	I	163/179 (91%)	162 (99%)	1 (1%)	0	100	100
6	J	39/151 (26%)	39 (100%)	0	0	100	100
7	M	144/147 (98%)	139 (96%)	5 (4%)	0	100	100
8	N	120/122 (98%)	117 (98%)	3 (2%)	0	100	100
9	O	143/147 (97%)	132 (92%)	11 (8%)	0	100	100
10	Q	116/199 (58%)	112 (97%)	4 (3%)	0	100	100
11	R	122/127 (96%)	121 (99%)	1 (1%)	0	100	100
12	S	111/113 (98%)	104 (94%)	7 (6%)	0	100	100
13	T	122/129 (95%)	119 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	U	98/103 (95%)	94 (96%)	4 (4%)	0	100	100
15	V	111/153 (72%)	108 (97%)	3 (3%)	0	100	100
16	W	95/100 (95%)	93 (98%)	2 (2%)	0	100	100
17	X	88/105 (84%)	84 (96%)	4 (4%)	0	100	100
18	Z	75/88 (85%)	69 (92%)	6 (8%)	0	100	100
19	1	61/64 (95%)	60 (98%)	1 (2%)	0	100	100
20	2	61/77 (79%)	60 (98%)	1 (2%)	0	100	100
21	3	56/61 (92%)	55 (98%)	1 (2%)	0	100	100
22	5	52/57 (91%)	52 (100%)	0	0	100	100
23	6	47/55 (86%)	44 (94%)	3 (6%)	0	100	100
24	7	43/47 (92%)	42 (98%)	1 (2%)	0	100	100
25	8	61/64 (95%)	59 (97%)	2 (3%)	0	100	100
26	4	53/75 (71%)	52 (98%)	1 (2%)	0	100	100
30	v	29/33 (88%)	29 (100%)	0	0	100	100
31	d	205/275 (74%)	196 (96%)	9 (4%)	0	100	100
32	e	198/201 (98%)	185 (93%)	13 (7%)	0	100	100
33	f	166/214 (78%)	159 (96%)	7 (4%)	0	100	100
34	g	94/96 (98%)	91 (97%)	3 (3%)	0	100	100
35	h	151/156 (97%)	147 (97%)	4 (3%)	0	100	100
36	i	129/132 (98%)	125 (97%)	4 (3%)	0	100	100
37	j	124/150 (83%)	117 (94%)	7 (6%)	0	100	100
38	k	96/101 (95%)	90 (94%)	6 (6%)	0	100	100
39	l	113/138 (82%)	107 (95%)	6 (5%)	0	100	100
40	m	120/124 (97%)	111 (92%)	9 (8%)	0	100	100
41	n	114/124 (92%)	110 (96%)	4 (4%)	0	100	100
42	o	98/101 (97%)	95 (97%)	3 (3%)	0	100	100
43	p	86/89 (97%)	84 (98%)	2 (2%)	0	100	100
44	q	111/156 (71%)	106 (96%)	5 (4%)	0	100	100
45	r	92/98 (94%)	89 (97%)	3 (3%)	0	100	100
46	s	63/84 (75%)	60 (95%)	3 (5%)	0	100	100
47	t	80/93 (86%)	77 (96%)	3 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
48	u	83/86 (96%)	83 (100%)	0	0	100	100
49	c	215/277 (78%)	199 (93%)	16 (7%)	0	100	100
50	w	124/264 (47%)	116 (94%)	8 (6%)	0	100	100
All	All	5343/6252 (86%)	5127 (96%)	216 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	E	215/218 (99%)	207 (96%)	8 (4%)	30	65
2	F	160/163 (98%)	151 (94%)	9 (6%)	19	50
3	G	169/173 (98%)	161 (95%)	8 (5%)	23	57
4	H	150/156 (96%)	142 (95%)	8 (5%)	20	52
5	I	139/150 (93%)	135 (97%)	4 (3%)	37	73
6	J	31/116 (27%)	28 (90%)	3 (10%)	8	25
7	M	119/120 (99%)	116 (98%)	3 (2%)	42	76
8	N	100/100 (100%)	96 (96%)	4 (4%)	28	63
9	O	112/114 (98%)	108 (96%)	4 (4%)	31	66
10	Q	97/158 (61%)	94 (97%)	3 (3%)	35	70
11	R	92/94 (98%)	89 (97%)	3 (3%)	33	69
12	S	100/100 (100%)	95 (95%)	5 (5%)	22	54
13	T	97/99 (98%)	95 (98%)	2 (2%)	47	79
14	U	81/83 (98%)	74 (91%)	7 (9%)	10	31
15	V	89/117 (76%)	86 (97%)	3 (3%)	32	68
16	W	83/85 (98%)	81 (98%)	2 (2%)	43	77
17	X	78/86 (91%)	71 (91%)	7 (9%)	9	28
18	Z	56/63 (89%)	52 (93%)	4 (7%)	13	39

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
19	1	50/51 (98%)	48 (96%)	2 (4%)	28	63
20	2	58/66 (88%)	54 (93%)	4 (7%)	14	41
21	3	52/54 (96%)	50 (96%)	2 (4%)	29	64
22	5	43/46 (94%)	42 (98%)	1 (2%)	44	78
23	6	47/52 (90%)	43 (92%)	4 (8%)	10	31
24	7	35/36 (97%)	34 (97%)	1 (3%)	37	73
25	8	53/54 (98%)	50 (94%)	3 (6%)	18	49
26	4	50/63 (79%)	48 (96%)	2 (4%)	28	63
30	v	29/31 (94%)	29 (100%)	0	100	100
31	d	170/212 (80%)	165 (97%)	5 (3%)	37	73
32	e	175/176 (99%)	170 (97%)	5 (3%)	37	73
33	f	123/147 (84%)	118 (96%)	5 (4%)	27	62
34	g	85/85 (100%)	75 (88%)	10 (12%)	5	17
35	h	129/132 (98%)	124 (96%)	5 (4%)	28	64
36	i	107/108 (99%)	101 (94%)	6 (6%)	19	50
37	j	102/125 (82%)	96 (94%)	6 (6%)	18	48
38	k	89/90 (99%)	86 (97%)	3 (3%)	32	68
39	l	89/105 (85%)	81 (91%)	8 (9%)	9	28
40	m	103/105 (98%)	97 (94%)	6 (6%)	18	49
41	n	99/104 (95%)	98 (99%)	1 (1%)	68	88
42	o	85/86 (99%)	83 (98%)	2 (2%)	43	77
43	p	76/77 (99%)	72 (95%)	4 (5%)	20	52
44	q	92/118 (78%)	88 (96%)	4 (4%)	26	60
45	r	80/83 (96%)	78 (98%)	2 (2%)	42	76
46	s	55/72 (76%)	55 (100%)	0	100	100
47	t	73/84 (87%)	68 (93%)	5 (7%)	14	42
48	u	69/70 (99%)	67 (97%)	2 (3%)	37	73
49	c	182/218 (84%)	175 (96%)	7 (4%)	29	64
50	w	98/215 (46%)	95 (97%)	3 (3%)	35	70
All	All	4466/5060 (88%)	4271 (96%)	195 (4%)	27	59

All (195) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	71	ASP
1	E	89	THR
1	E	119	SER
1	E	131	LEU
1	E	158	SER
1	E	161	VAL
1	E	224	VAL
1	E	257	THR
2	F	41	THR
2	F	84	LEU
2	F	92	VAL
2	F	99	GLN
2	F	151	ILE
2	F	167	SER
2	F	170	MET
2	F	191	VAL
2	F	192	LEU
3	G	3	LEU
3	G	27	VAL
3	G	39	THR
3	G	63	LYS
3	G	85	THR
3	G	140	SER
3	G	143	THR
3	G	181	ASP
4	H	41	VAL
4	H	74	VAL
4	H	96	VAL
4	H	113	ILE
4	H	118	ILE
4	H	125	SER
4	H	151	ASP
4	H	164	VAL
5	I	9	VAL
5	I	57	ASP
5	I	112	HIS
5	I	123	THR
6	J	3	LEU
6	J	12	LEU
6	J	23	ASP
7	M	14	SER
7	M	17	VAL
7	M	21	SER

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Mol	Chain	Res	Type
8	N	2	ILE
8	N	61	VAL
8	N	81	GLU
8	N	94	ARG
9	O	73	THR
9	O	109	LEU
9	O	132	SER
9	O	135	GLU
10	Q	15	SER
10	Q	101	GLU
10	Q	116	VAL
11	R	32	THR
11	R	47	ILE
11	R	116	LEU
12	S	18	THR
12	S	64	SER
12	S	69	VAL
12	S	87	THR
12	S	113	ARG
13	T	16	THR
13	T	88	VAL
14	U	3	THR
14	U	7	VAL
14	U	24	VAL
14	U	36	SER
14	U	39	VAL
14	U	47	ASN
14	U	61	THR
15	V	11	THR
15	V	51	SER
15	V	88	THR
16	W	40	THR
16	W	69	THR
17	X	3	VAL
17	X	38	VAL
17	X	66	ILE
17	X	83	VAL
17	X	89	ASP
17	X	90	GLU
17	X	100	THR
18	Z	12	ASN
18	Z	38	VAL

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Mol	Chain	Res	Type
18	Z	49	VAL
18	Z	79	ASN
19	1	4	VAL
19	1	45	ASN
20	2	5	THR
20	2	14	THR
20	2	27	GLU
20	2	63	GLU
21	3	7	THR
21	3	28	LEU
22	5	37	ARG
23	6	7	VAL
23	6	13	LEU
23	6	38	ILE
23	6	52	LYS
24	7	46	THR
25	8	6	THR
25	8	23	VAL
25	8	33	LEU
26	4	29	GLN
26	4	33	ILE
31	d	75	VAL
31	d	98	VAL
31	d	106	LYS
31	d	163	SER
31	d	191	THR
32	e	5	THR
32	e	59	SER
32	e	139	ASP
32	e	164	SER
32	e	198	LEU
33	f	41	VAL
33	f	62	VAL
33	f	71	VAL
33	f	152	SER
33	f	188	ASP
34	g	8	VAL
34	g	10	LEU
34	g	18	THR
34	g	22	SER
34	g	27	LEU
34	g	33	ASP

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Mol	Chain	Res	Type
34	g	38	ASP
34	g	41	ASP
34	g	43	TRP
34	g	65	VAL
35	h	24	THR
35	h	66	LEU
35	h	75	VAL
35	h	84	THR
35	h	85	TYR
36	i	14	LEU
36	i	51	THR
36	i	52	GLU
36	i	73	SER
36	i	115	ASP
36	i	131	VAL
37	j	28	THR
37	j	42	VAL
37	j	63	VAL
37	j	120	LYS
37	j	131	ILE
37	j	147	TYR
38	k	15	HIS
38	k	36	VAL
38	k	59	LYS
39	l	35	THR
39	l	37	ASN
39	l	91	VAL
39	l	100	SER
39	l	114	LEU
39	l	115	GLU
39	l	128	ASN
39	l	131	ARG
40	m	8	VAL
40	m	35	THR
40	m	63	VAL
40	m	64	THR
40	m	79	MET
40	m	104	THR
41	n	45	THR
42	o	23	ARG
42	o	60	LEU
43	p	4	THR

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Mol	Chain	Res	Type
43	p	40	THR
43	p	73	VAL
43	p	82	ILE
44	q	13	ILE
44	q	48	LEU
44	q	86	LEU
44	q	92	THR
45	r	70	ILE
45	r	72	ASP
47	t	14	HIS
47	t	34	TRP
47	t	35	SER
47	t	48	THR
47	t	79	THR
48	u	30	THR
48	u	32	ILE
49	c	19	GLN
49	c	24	ASN
49	c	26	LYS
49	c	100	MET
49	c	105	SER
49	c	163	VAL
49	c	169	GLU
50	w	7	THR
50	w	92	ILE
50	w	109	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (35) such sidechains are listed below:

Mol	Chain	Res	Type
1	E	109	GLN
1	E	203	ASN
2	F	142	GLN
3	G	91	HIS
4	H	25	GLN
5	I	98	GLN
7	M	96	HIS
11	R	86	GLN
13	T	39	GLN
16	W	58	ASN
17	X	31	ASN
19	1	47	GLN

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Mol	Chain	Res	Type
23	6	20	HIS
25	8	63	ASN
26	4	6	HIS
31	d	113	GLN
31	d	117	GLN
31	d	138	GLN
32	e	95	ASN
32	e	173	GLN
32	e	185	GLN
33	f	163	HIS
34	g	82	ASN
35	h	148	ASN
38	k	99	ASN
38	k	101	GLN
39	l	27	HIS
39	l	31	HIS
39	l	86	HIS
44	q	50	GLN
44	q	107	ASN
49	c	94	GLN
49	c	155	GLN
49	c	167	ASN
50	w	95	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
27	A	3016/3119 (96%)	547 (18%)	17 (0%)
28	B	116/118 (98%)	19 (16%)	1 (0%)
29	a	1514/1528 (99%)	272 (17%)	0
All	All	4646/4765 (97%)	838 (18%)	18 (0%)

All (838) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
27	A	7	U
27	A	9	U
27	A	12	G
27	A	20	G
27	A	33	G
27	A	55	G

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Mol	Chain	Res	Type
27	A	60	A
27	A	68	A
27	A	71	A
27	A	72	G
27	A	82	G
27	A	89	A
27	A	90	C
27	A	94	G
27	A	98	U
27	A	99	G
27	A	115	A
27	A	116	A
27	A	117	U
27	A	125	C
27	A	148	A
27	A	164	A
27	A	180	A
27	A	195	A
27	A	198	A
27	A	212	A
27	A	214	G
27	A	215	A
27	A	221	A
27	A	227	A
27	A	229	U
27	A	230	G
27	A	248	G
27	A	250	G
27	A	265	A
27	A	267	G
27	A	270	U
27	A	271	A
27	A	272	A
27	A	275	C
27	A	283	U
27	A	285	U
27	A	286	G
27	A	290	C
27	A	297	G
27	A	298	G
27	A	300	G
27	A	301	U

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Mol	Chain	Res	Type
27	A	302	U
27	A	303	G
27	A	305	G
27	A	313	G
27	A	314	G
27	A	315	U
27	A	317	G
27	A	318	U
27	A	319	G
27	A	324	C
27	A	329	U
27	A	330	U
27	A	331	U
27	A	332	C
27	A	336	C
27	A	337	U
27	A	338	C
27	A	344	G
27	A	346	C
27	A	350	A
27	A	351	G
27	A	353	G
27	A	357	U
27	A	358	G
27	A	361	A
27	A	364	A
27	A	370	U
27	A	371	G
27	A	384	G
27	A	393	U
27	A	399	G
27	A	412	A
27	A	413	G
27	A	424	G
27	A	425	U
27	A	434	G
27	A	437	G
27	A	444	U
27	A	445	U
27	A	446	G
27	A	450	G
27	A	452	G

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Mol	Chain	Res	Type
27	A	454	U
27	A	460	G
27	A	474	G
27	A	489	A
27	A	493	U
27	A	494	G
27	A	509	U
27	A	512	G
27	A	514	C
27	A	543	U
27	A	544	U
27	A	566	A
27	A	569	G
27	A	589	A
27	A	591	G
27	A	592	A
27	A	594	U
27	A	595	A
27	A	596	C
27	A	605	G
27	A	617	U
27	A	618	C
27	A	619	C
27	A	620	G
27	A	635	G
27	A	636	U
27	A	637	G
27	A	638	U
27	A	639	C
27	A	640	G
27	A	642	G
27	A	644	G
27	A	655	G
27	A	664	A
27	A	665	G
27	A	667	A
27	A	679	G
27	A	684	G
27	A	696	A
27	A	706	G
27	A	707	G
27	A	708	G

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Mol	Chain	Res	Type
27	A	709	U
27	A	721	A
27	A	728	G
27	A	731	A
27	A	738	A
27	A	740	A
27	A	742	G
27	A	747	A
27	A	754	C
27	A	756	A
27	A	758	A
27	A	760	U
27	A	764	U
27	A	766	G
27	A	768	G
27	A	784	G
27	A	785	A
27	A	794	G
27	A	801	U
27	A	832	G
27	A	838	G
27	A	839	U
27	A	845	C
27	A	862	U
27	A	863	G
27	A	868	C
27	A	871	A
27	A	872	G
27	A	878	G
27	A	879	A
27	A	880	G
27	A	890	G
27	A	891	G
27	A	897	A
27	A	899	G
27	A	907	A
27	A	920	G
27	A	927	C
27	A	942	U
27	A	960	G
27	A	961	U
27	A	972	A

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Mol	Chain	Res	Type
27	A	975	U
27	A	981	U
27	A	982	A
27	A	987	A
27	A	988	U
27	A	989	G
27	A	990	G
27	A	991	C
27	A	994	A
27	A	995	U
27	A	1001	C
27	A	1002	C
27	A	1003	A
27	A	1004	C
27	A	1005	A
27	A	1007	G
27	A	1008	G
27	A	1009	U
27	A	1010	U
27	A	1012	C
27	A	1013	U
27	A	1014	G
27	A	1018	U
27	A	1019	C
27	A	1022	C
27	A	1025	A
27	A	1030	C
27	A	1047	A
27	A	1048	A
27	A	1049	G
27	A	1058	A
27	A	1063	G
27	A	1076	A
27	A	1078	G
27	A	1085	G
27	A	1092	G
27	A	1101	A
27	A	1114	G
27	A	1130	C
27	A	1131	G
27	A	1144	A
27	A	1151	U

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Mol	Chain	Res	Type
27	A	1158	U
27	A	1164	A
27	A	1165	G
27	A	1230	G
27	A	1232	G
27	A	1235	U
27	A	1238	G
27	A	1240	G
27	A	1242	C
27	A	1245	U
27	A	1247	A
27	A	1248	U
27	A	1250	U
27	A	1251	A
27	A	1252	G
27	A	1253	C
27	A	1260	C
27	A	1261	A
27	A	1292	U
27	A	1293	G
27	A	1326	G
27	A	1335	G
27	A	1344	A
27	A	1353	G
27	A	1365	G
27	A	1371	G
27	A	1386	G
27	A	1387	A
27	A	1389	U
27	A	1415	A
27	A	1416	A
27	A	1427	U
27	A	1444	U
27	A	1456	G
27	A	1465	C
27	A	1467	U
27	A	1480	A
27	A	1494	U
27	A	1499	A
27	A	1507	G
27	A	1508	A
27	A	1510	A

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Mol	Chain	Res	Type
27	A	1511	U
27	A	1522	G
27	A	1531	C
27	A	1533	U
27	A	1534	C
27	A	1539	A
27	A	1540	U
27	A	1543	A
27	A	1548	C
27	A	1550	G
27	A	1551	U
27	A	1552	A
27	A	1553	C
27	A	1554	U
27	A	1607	C
27	A	1608	U
27	A	1609	G
27	A	1610	C
27	A	1625	G
27	A	1627	U
27	A	1628	A
27	A	1629	G
27	A	1630	U
27	A	1633	U
27	A	1639	G
27	A	1640	A
27	A	1641	U
27	A	1648	A
27	A	1649	C
27	A	1670	G
27	A	1676	G
27	A	1679	A
27	A	1680	A
27	A	1681	U
27	A	1697	U
27	A	1703	G
27	A	1710	A
27	A	1711	G
27	A	1714	A
27	A	1716	A
27	A	1717	U
27	A	1724	G

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Mol	Chain	Res	Type
27	A	1728	U
27	A	1731	A
27	A	1737	A
27	A	1754	G
27	A	1755	A
27	A	1756	G
27	A	1757	U
27	A	1767	U
27	A	1786	G
27	A	1789	A
27	A	1798	U
27	A	1825	C
27	A	1826	A
27	A	1852	A
27	A	1864	U
27	A	1866	C
27	A	1867	G
27	A	1871	G
27	A	1872	A
27	A	1892	G
27	A	1895	A
27	A	1933	G
27	A	1946	U
27	A	1947	U
27	A	1949	C
27	A	1950	G
27	A	1955	A
27	A	1973	C
27	A	1975	A
27	A	1981	U
27	A	1990	A
27	A	1999	U
27	A	2003	A
27	A	2008	A
27	A	2017	C
27	A	2018	G
27	A	2026	A
27	A	2033	U
27	A	2046	A
27	A	2064	A
27	A	2065	A
27	A	2074	G

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Mol	Chain	Res	Type
27	A	2075	G
27	A	2085	C
27	A	2086	U
27	A	2088	C
27	A	2089	C
27	A	2091	U
27	A	2092	U
27	A	2093	G
27	A	2094	G
27	A	2095	G
27	A	2096	G
27	A	2106	A
27	A	2107	G
27	A	2130	G
27	A	2137	A
27	A	2140	A
27	A	2141	U
27	A	2153	G
27	A	2154	G
27	A	2160	A
27	A	2161	A
27	A	2162	A
27	A	2163	U
27	A	2179	U
27	A	2191	C
27	A	2194	A
27	A	2195	U
27	A	2196	G
27	A	2215	U
27	A	2217	U
27	A	2221	A
27	A	2226	U
27	A	2244	A
27	A	2247	A
27	A	2251	G
27	A	2254	A
27	A	2255	A
27	A	2256	G
27	A	2263	G
27	A	2267	C
27	A	2279	C
27	A	2280	G

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Mol	Chain	Res	Type
27	A	2284	A
27	A	2285	G
27	A	2287	C
27	A	2316	G
27	A	2320	C
27	A	2322	C
27	A	2324	A
27	A	2325	U
27	A	2328	G
27	A	2329	G
27	A	2330	U
27	A	2331	U
27	A	2332	U
27	A	2334	U
27	A	2335	G
27	A	2338	G
27	A	2339	G
27	A	2340	A
27	A	2341	U
27	A	2342	A
27	A	2343	G
27	A	2345	U
27	A	2346	G
27	A	2351	A
27	A	2353	U
27	A	2354	G
27	A	2356	G
27	A	2357	A
27	A	2368	C
27	A	2370	A
27	A	2371	G
27	A	2372	U
27	A	2380	G
27	A	2382	G
27	A	2384	C
27	A	2386	U
27	A	2387	U
27	A	2388	G
27	A	2390	U
27	A	2393	A
27	A	2394	A
27	A	2395	U

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Mol	Chain	Res	Type
27	A	2396	A
27	A	2399	A
27	A	2401	U
27	A	2402	C
27	A	2403	U
27	A	2404	G
27	A	2407	C
27	A	2408	G
27	A	2410	A
27	A	2413	G
27	A	2421	A
27	A	2427	G
27	A	2434	A
27	A	2436	A
27	A	2449	A
27	A	2462	G
27	A	2463	G
27	A	2467	U
27	A	2503	G
27	A	2504	G
27	A	2507	C
27	A	2511	A
27	A	2512	A
27	A	2529	A
27	A	2532	G
27	A	2544	U
27	A	2545	G
27	A	2548	U
27	A	2549	G
27	A	2558	C
27	A	2559	A
27	A	2560	A
27	A	2571	C
27	A	2574	C
27	A	2607	G
27	A	2609	A
27	A	2615	G
27	A	2626	U
27	A	2627	C
27	A	2630	A
27	A	2647	U
27	A	2649	A

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Mol	Chain	Res	Type
27	A	2653	G
27	A	2654	A
27	A	2655	U
27	A	2659	A
27	A	2665	C
27	A	2672	A
27	A	2673	U
27	A	2677	A
27	A	2678	G
27	A	2679	G
27	A	2688	C
27	A	2693	A
27	A	2694	G
27	A	2705	G
27	A	2714	G
27	A	2715	U
27	A	2718	G
27	A	2721	A
27	A	2722	C
27	A	2726	G
27	A	2727	A
27	A	2729	G
27	A	2730	U
27	A	2731	C
27	A	2742	A
27	A	2744	C
27	A	2749	G
27	A	2753	G
27	A	2759	G
27	A	2760	G
27	A	2761	U
27	A	2763	C
27	A	2766	A
27	A	2786	U
27	A	2790	A
27	A	2791	G
27	A	2796	A
27	A	2797	C
27	A	2826	A
27	A	2827	G
27	A	2833	U
27	A	2837	U

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Mol	Chain	Res	Type
27	A	2853	C
27	A	2854	A
27	A	2862	G
27	A	2865	G
27	A	2870	C
27	A	2878	A
27	A	2879	G
27	A	2885	G
27	A	2913	U
27	A	2915	C
27	A	2926	A
27	A	2936	C
27	A	2938	G
27	A	2948	C
27	A	2950	C
27	A	2957	A
27	A	2968	G
27	A	2974	A
27	A	2982	A
27	A	2985	G
27	A	2989	A
27	A	3002	A
27	A	3009	U
27	A	3013	C
27	A	3014	A
27	A	3021	A
27	A	3022	G
27	A	3029	U
27	A	3042	A
27	A	3056	A
27	A	3082	U
27	A	3088	C
27	A	3093	A
27	A	3105	C
27	A	3106	C
27	A	3114	A
27	A	3115	A
28	B	3	U
28	B	4	A
28	B	9	G
28	B	11	U
28	B	12	C

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Mol	Chain	Res	Type
28	B	13	C
28	B	30	G
28	B	36	U
28	B	42	C
28	B	54	A
28	B	57	U
28	B	58	A
28	B	68	G
28	B	87	U
28	B	88	C
28	B	89	C
28	B	107	A
28	B	114	A
28	B	115	A
29	a	12	A
29	a	13	G
29	a	26	G
29	a	36	A
29	a	43	G
29	a	51	C
29	a	52	U
29	a	55	A
29	a	58	C
29	a	59	A
29	a	82	U
29	a	83	U
29	a	85	C
29	a	86	G
29	a	87	G
29	a	93	C
29	a	94	U
29	a	116	A
29	a	117	C
29	a	126	G
29	a	128	U
29	a	141	U
29	a	146	A
29	a	160	C
29	a	193	C
29	a	200	U
29	a	201	G
29	a	210	A

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Mol	Chain	Res	Type
29	a	211	A
29	a	216	U
29	a	217	U
29	a	243	A
29	a	245	C
29	a	247	G
29	a	251	G
29	a	252	U
29	a	266	G
29	a	267	C
29	a	279	A
29	a	280	C
29	a	281	G
29	a	289	G
29	a	301	G
29	a	321	A
29	a	329	A
29	a	330	C
29	a	332	G
29	a	344	A
29	a	345	C
29	a	347	G
29	a	351	G
29	a	352	C
29	a	353	A
29	a	354	G
29	a	367	U
29	a	372	C
29	a	384	G
29	a	390	U
29	a	397	A
29	a	398	C
29	a	406	G
29	a	414	A
29	a	421	U
29	a	422	C
29	a	423	G
29	a	424	G
29	a	426	U
29	a	428	G
29	a	429	U
29	a	430	A

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Mol	Chain	Res	Type
29	a	433	C
29	a	434	C
29	a	452	A
29	a	453	G
29	a	456	C
29	a	457	A
29	a	458	A
29	a	459	G
29	a	461	G
29	a	465	G
29	a	466	U
29	a	475	A
29	a	476	A
29	a	477	G
29	a	478	A
29	a	485	G
29	a	486	G
29	a	491	C
29	a	497	G
29	a	498	C
29	a	499	C
29	a	507	G
29	a	509	G
29	a	511	U
29	a	512	A
29	a	513	A
29	a	515	A
29	a	519	A
29	a	520	G
29	a	527	A
29	a	542	U
29	a	544	C
29	a	552	A
29	a	553	A
29	a	556	A
29	a	557	G
29	a	612	U
29	a	613	G
29	a	633	A
29	a	645	G
29	a	666	U
29	a	668	G

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Mol	Chain	Res	Type
29	a	698	A
29	a	701	G
29	a	702	G
29	a	703	U
29	a	711	G
29	a	729	A
29	a	735	G
29	a	757	A
29	a	761	A
29	a	765	G
29	a	772	A
29	a	773	U
29	a	774	A
29	a	792	G
29	a	794	A
29	a	795	A
29	a	796	A
29	a	797	C
29	a	801	G
29	a	808	A
29	a	822	U
29	a	823	U
29	a	824	C
29	a	826	U
29	a	827	U
29	a	828	G
29	a	829	G
29	a	841	U
29	a	866	U
29	a	884	G
29	a	896	A
29	a	908	G
29	a	909	G
29	a	913	C
29	a	916	C
29	a	917	A
29	a	942	U
29	a	943	U
29	a	948	G
29	a	950	A
29	a	951	A
29	a	953	G

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Mol	Chain	Res	Type
29	a	956	A
29	a	957	A
29	a	959	A
29	a	973	U
29	a	974	U
29	a	975	G
29	a	976	A
29	a	981	C
29	a	982	A
29	a	987	A
29	a	988	C
29	a	990	C
29	a	1007	U
29	a	1008	C
29	a	1011	U
29	a	1012	U
29	a	1014	U
29	a	1017	C
29	a	1020	G
29	a	1021	U
29	a	1022	G
29	a	1025	C
29	a	1033	G
29	a	1034	C
29	a	1035	A
29	a	1045	U
29	a	1074	G
29	a	1075	U
29	a	1081	A
29	a	1088	G
29	a	1104	G
29	a	1108	C
29	a	1110	A
29	a	1115	G
29	a	1116	U
29	a	1117	U
29	a	1118	A
29	a	1119	U
29	a	1120	G
29	a	1138	A
29	a	1140	U
29	a	1147	G

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Mol	Chain	Res	Type
29	a	1148	U
29	a	1149	C
29	a	1150	A
29	a	1151	A
29	a	1162	G
29	a	1164	U
29	a	1165	G
29	a	1171	G
29	a	1176	C
29	a	1177	A
29	a	1178	A
29	a	1181	C
29	a	1182	A
29	a	1193	U
29	a	1194	A
29	a	1195	U
29	a	1196	G
29	a	1217	A
29	a	1219	A
29	a	1231	A
29	a	1238	U
29	a	1241	G
29	a	1249	G
29	a	1250	A
29	a	1251	G
29	a	1261	A
29	a	1265	U
29	a	1266	U
29	a	1267	U
29	a	1268	C
29	a	1283	U
29	a	1284	U
29	a	1285	C
29	a	1287	G
29	a	1302	C
29	a	1328	A
29	a	1329	G
29	a	1343	G
29	a	1344	C
29	a	1345	A
29	a	1346	A
29	a	1347	C

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Mol	Chain	Res	Type
29	a	1351	G
29	a	1353	G
29	a	1357	A
29	a	1361	C
29	a	1364	U
29	a	1380	C
29	a	1389	U
29	a	1402	G
29	a	1405	G
29	a	1423	U
29	a	1424	G
29	a	1425	G
29	a	1426	C
29	a	1429	A
29	a	1433	C
29	a	1434	U
29	a	1435	U
29	a	1436	G
29	a	1438	G
29	a	1463	G
29	a	1471	G
29	a	1476	A
29	a	1481	G
29	a	1483	A
29	a	1486	A
29	a	1488	G
29	a	1490	U
29	a	1501	G
29	a	1504	G
29	a	1513	G
29	a	1514	G
29	a	1518	A
29	a	1522	C
29	a	1523	C

All (18) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
27	A	89	A
27	A	97	U
27	A	316	U
27	A	357	U

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Mol	Chain	Res	Type
27	A	445	U
27	A	643	G
27	A	974	G
27	A	986	G
27	A	1002	C
27	A	1004	C
27	A	1084	U
27	A	1551	U
27	A	2094	G
27	A	2343	G
27	A	2350	G
27	A	2381	A
27	A	2729	G
28	B	10	G

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

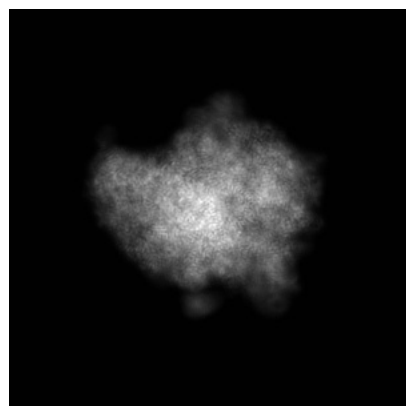
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-37551. These allow visual inspection of the internal detail of the map and identification of artifacts.

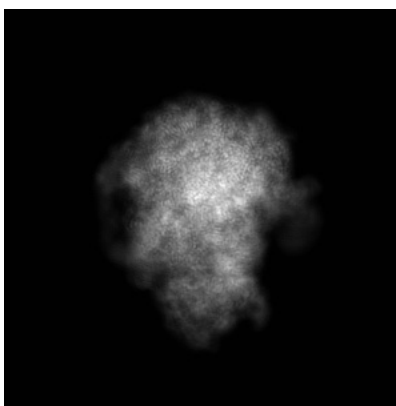
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

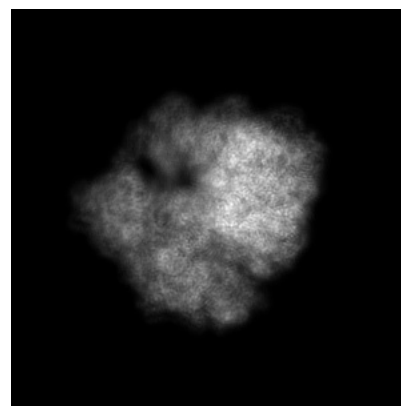
6.1.1 Primary map



X

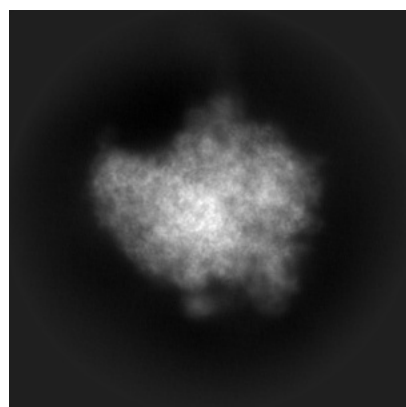


Y

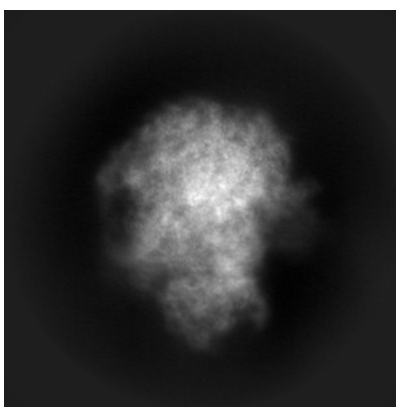


Z

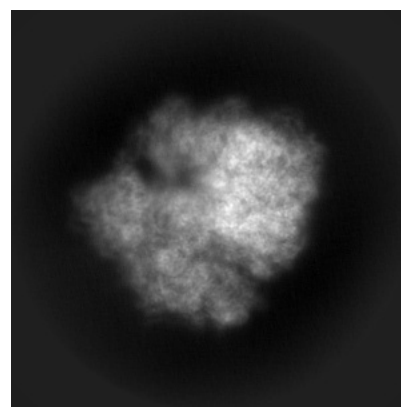
6.1.2 Raw map



X



Y

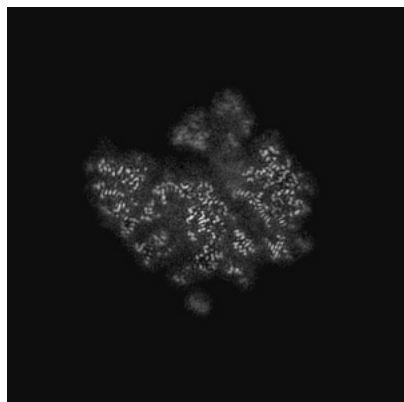


Z

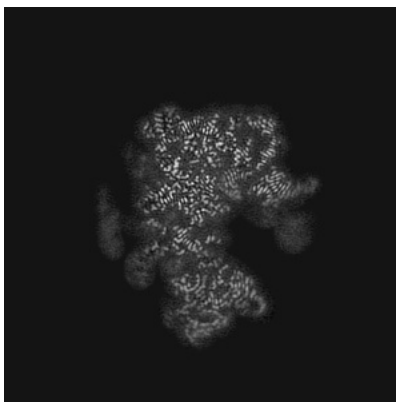
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

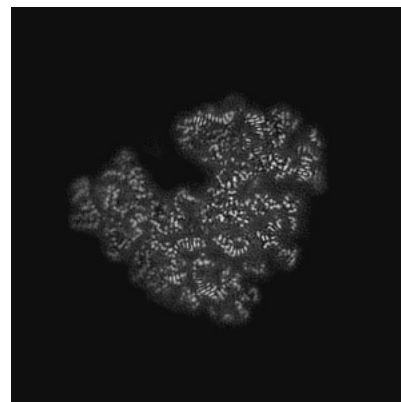
6.2.1 Primary map



X Index: 190

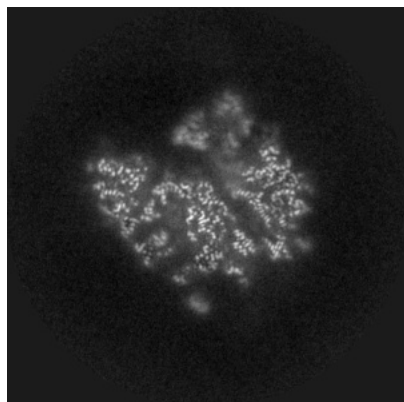


Y Index: 190

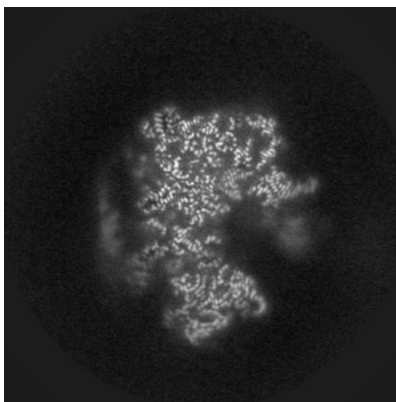


Z Index: 190

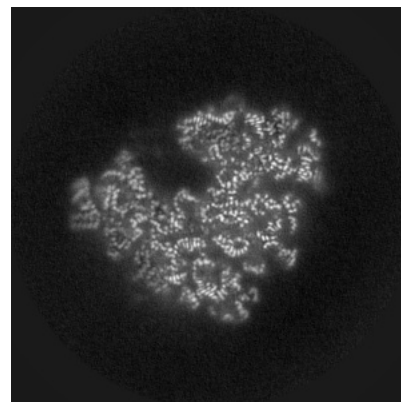
6.2.2 Raw map



X Index: 190



Y Index: 190

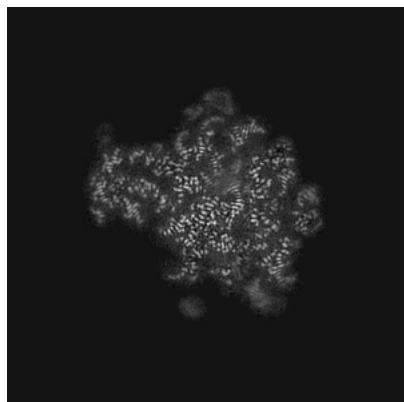


Z Index: 190

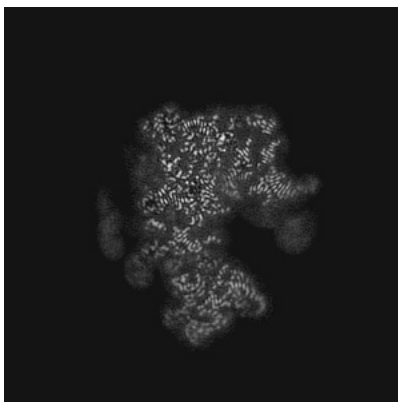
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

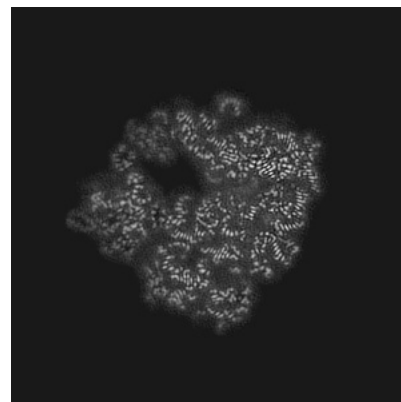
6.3.1 Primary map



X Index: 213

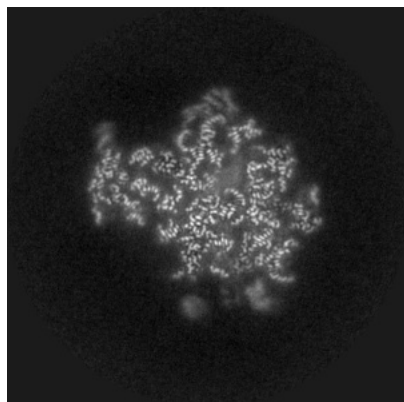


Y Index: 191

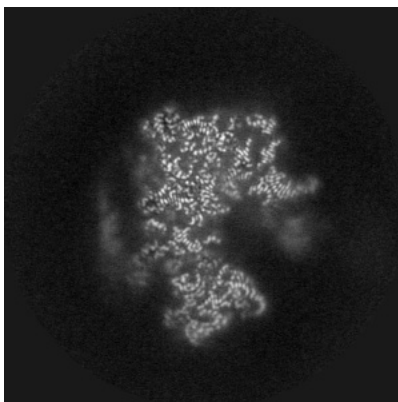


Z Index: 200

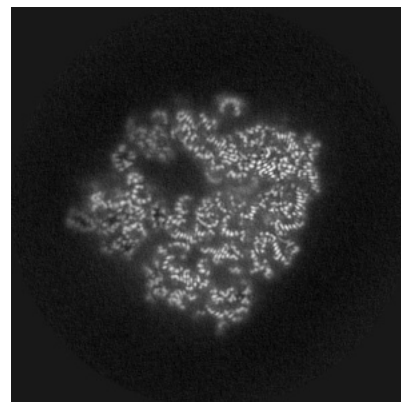
6.3.2 Raw map



X Index: 210



Y Index: 191

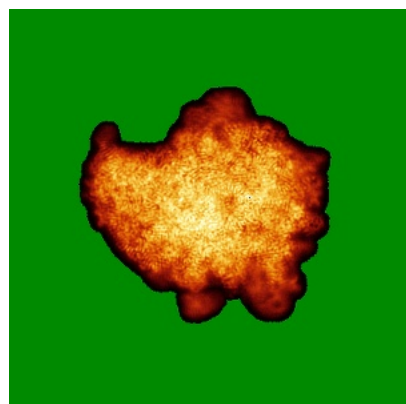


Z Index: 200

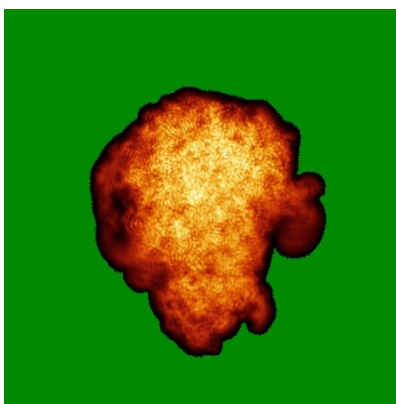
The images above show the largest variance slices of the map in three orthogonal directions.

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

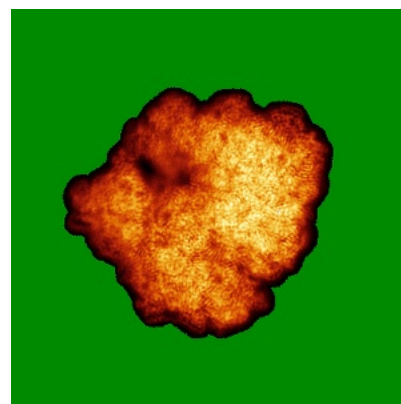
6.4.1 Primary map



X

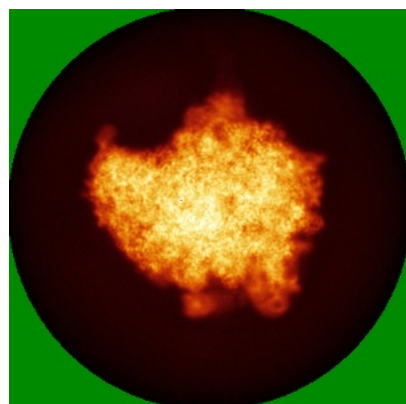


Y

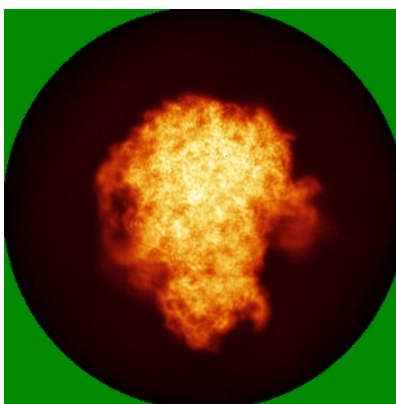


Z

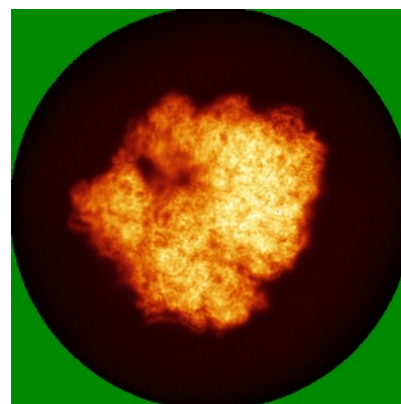
6.4.2 Raw map



X



Y

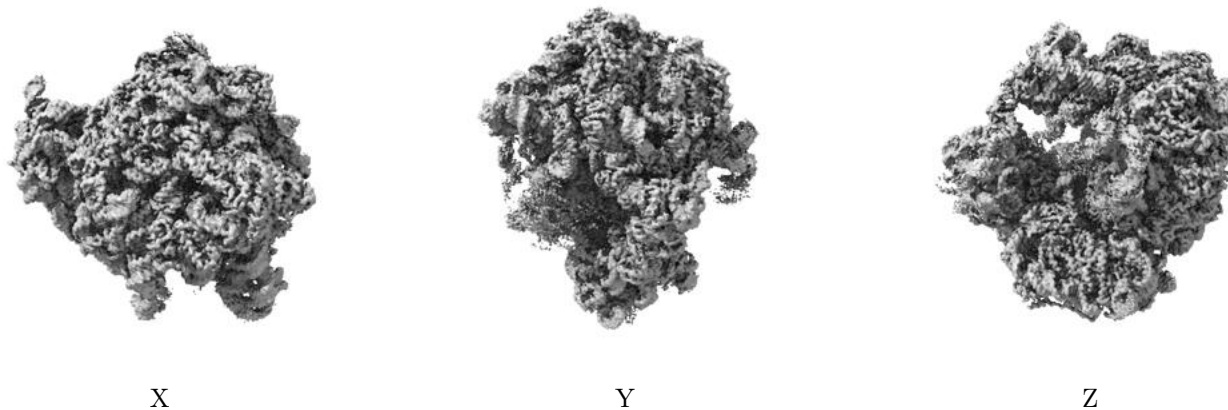


Z

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

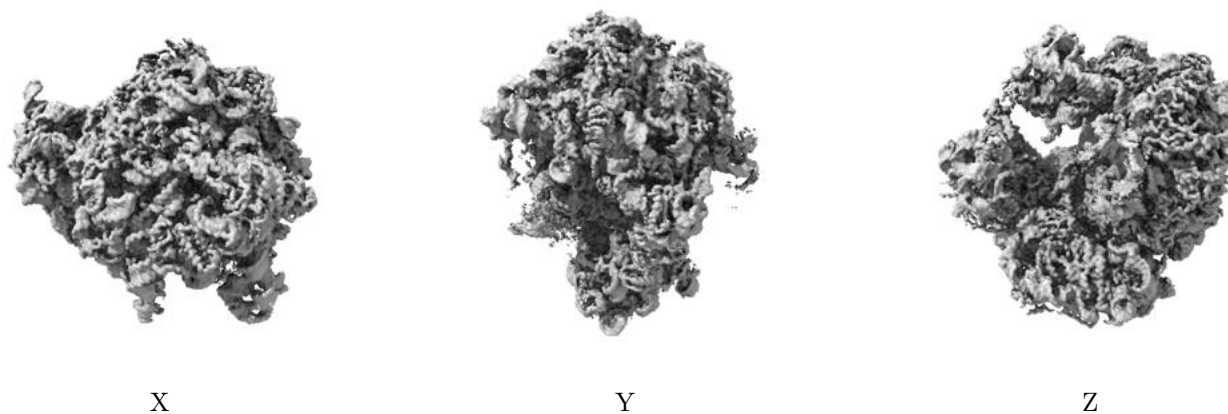
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.045. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

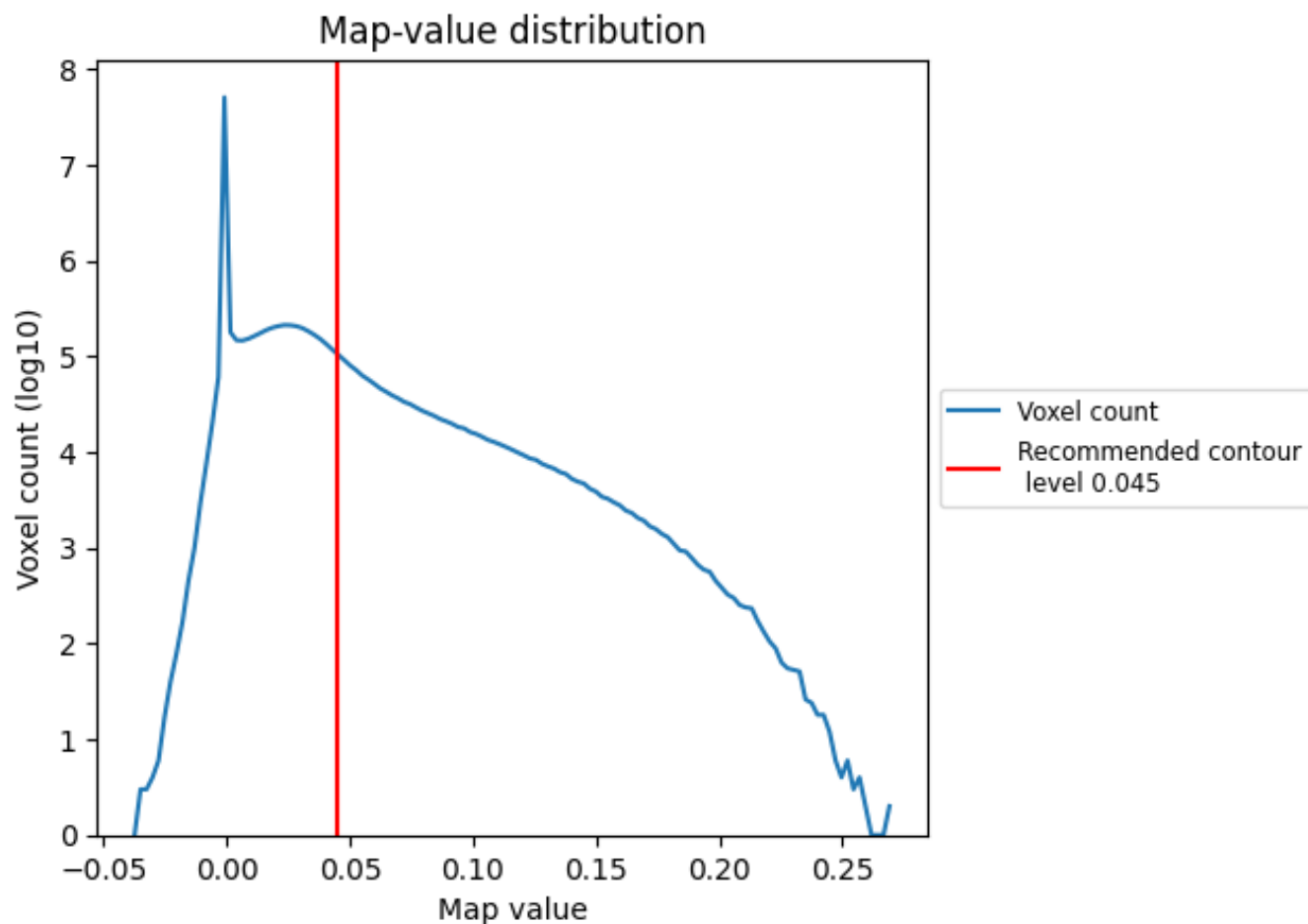
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

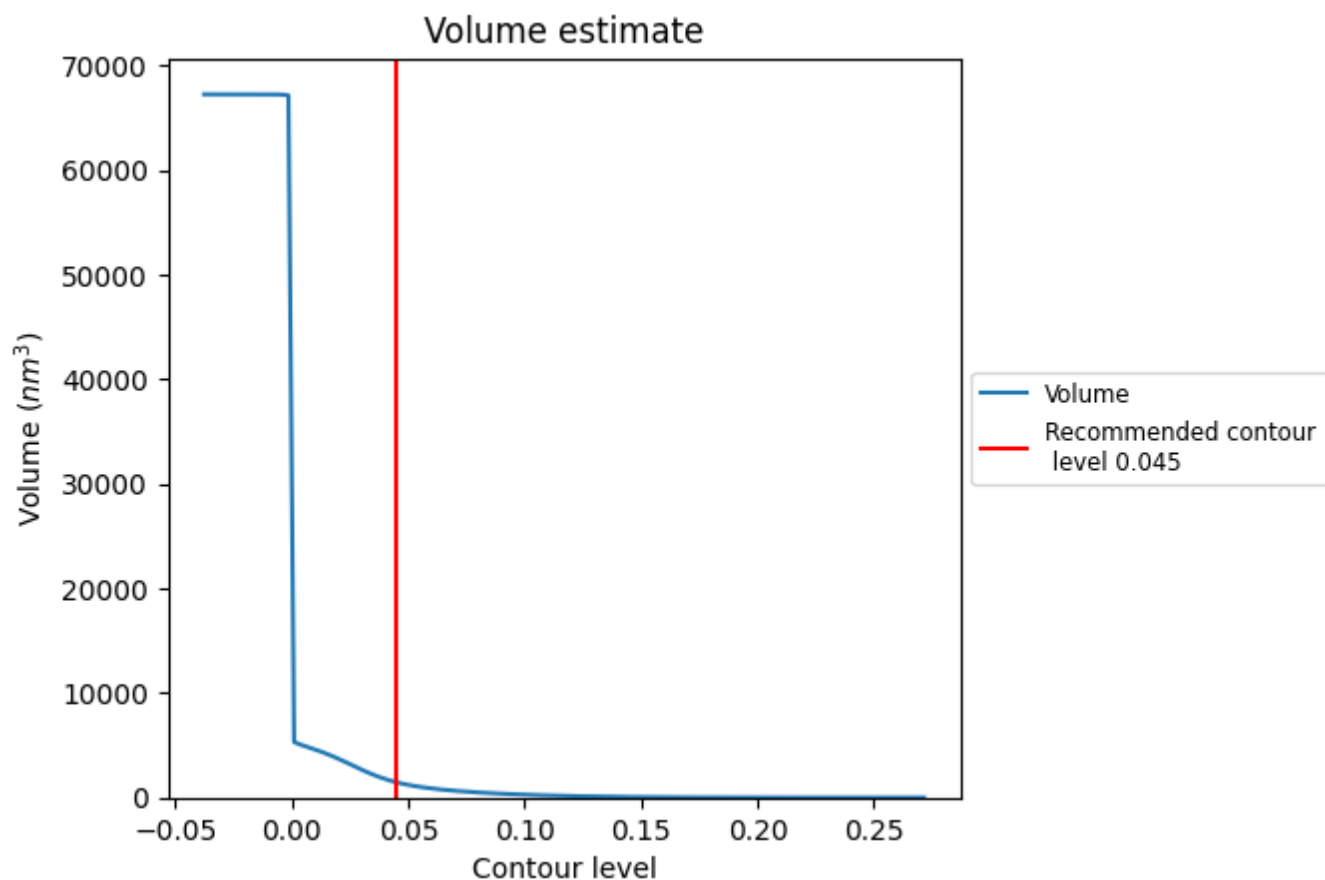
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

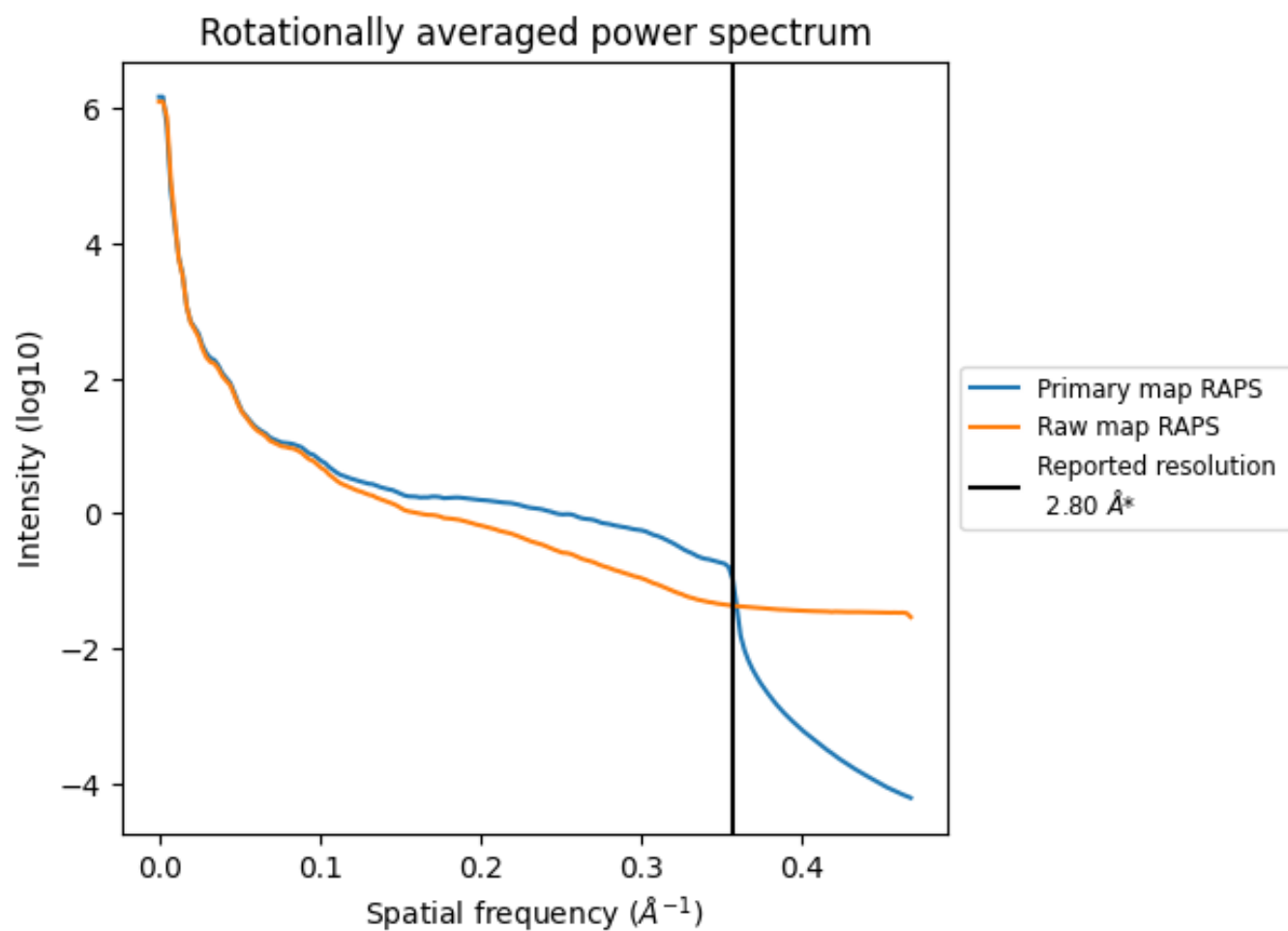
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1462 nm³; this corresponds to an approximate mass of 1321 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 ⓘ

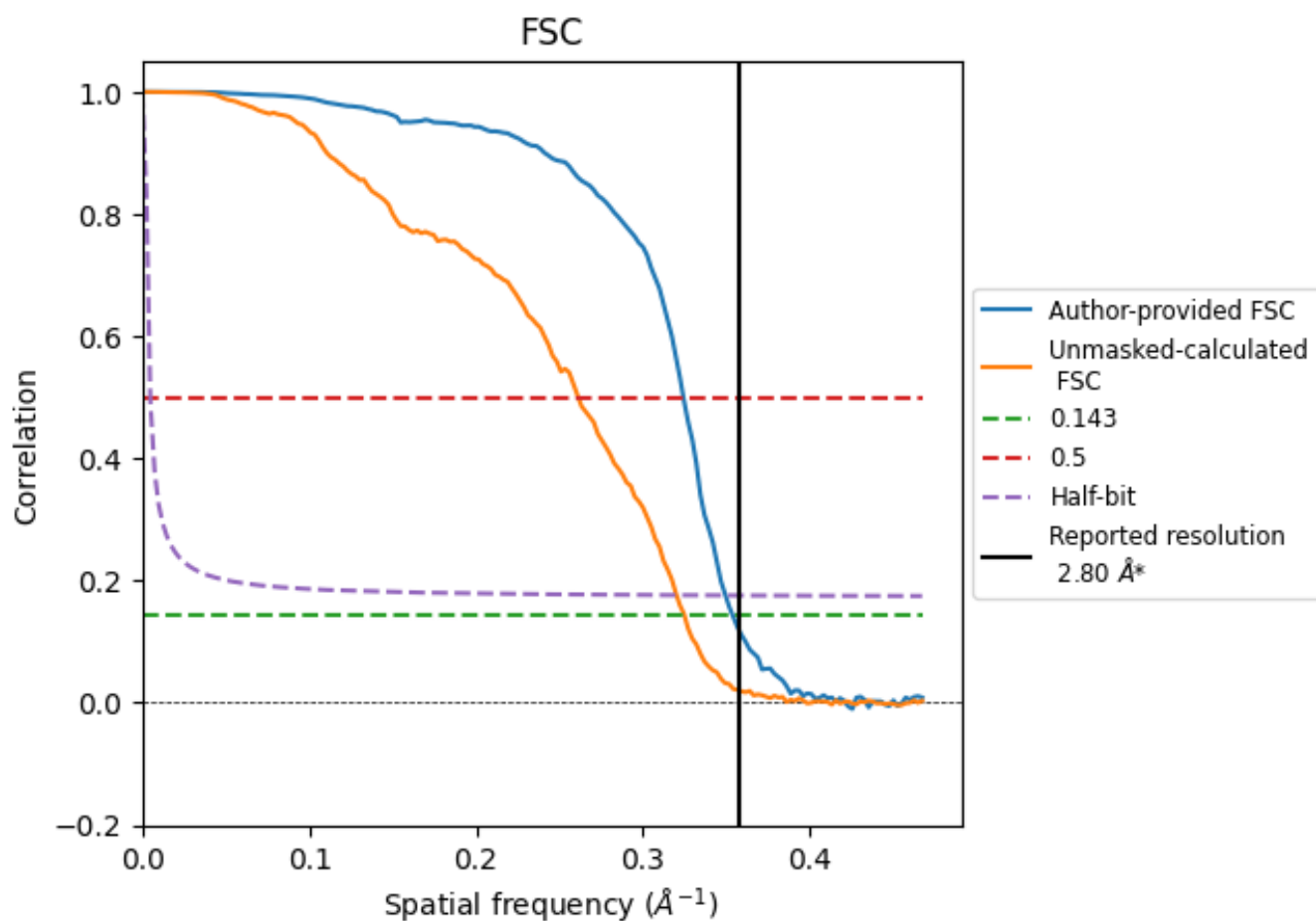


*Reported resolution corresponds to spatial frequency of 0.357 $\text{\AA}^{-1}$

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 0.357 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.80	-	-
Author-provided FSC curve	2.83	3.08	2.86
Unmasked-calculated*	3.08	3.83	3.12

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.08 differs from the reported value 2.8 by more than 10 %

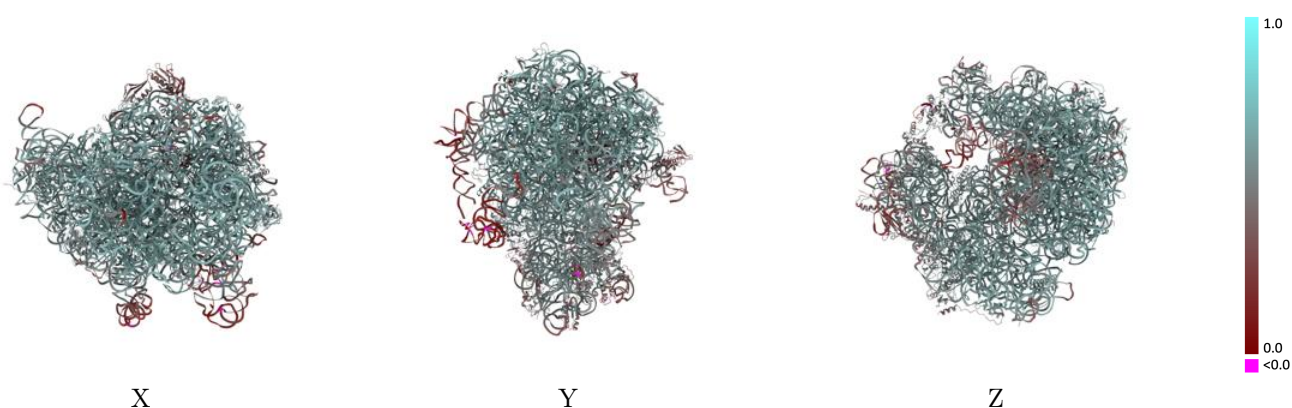
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-37551 and PDB model 8WHX. Per-residue inclusion information can be found in section 3 on page 13.

9.1 Map-model overlay [i](#)

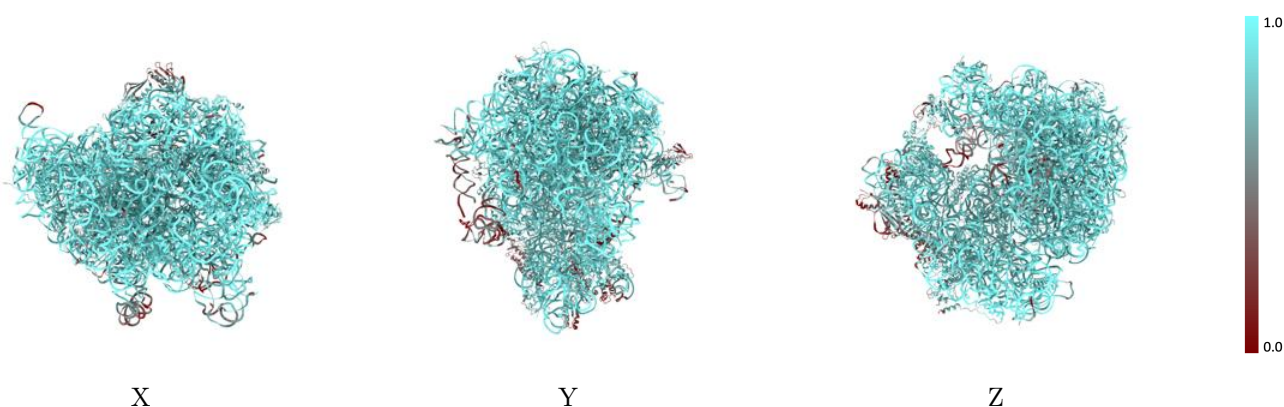
This section was not generated.

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



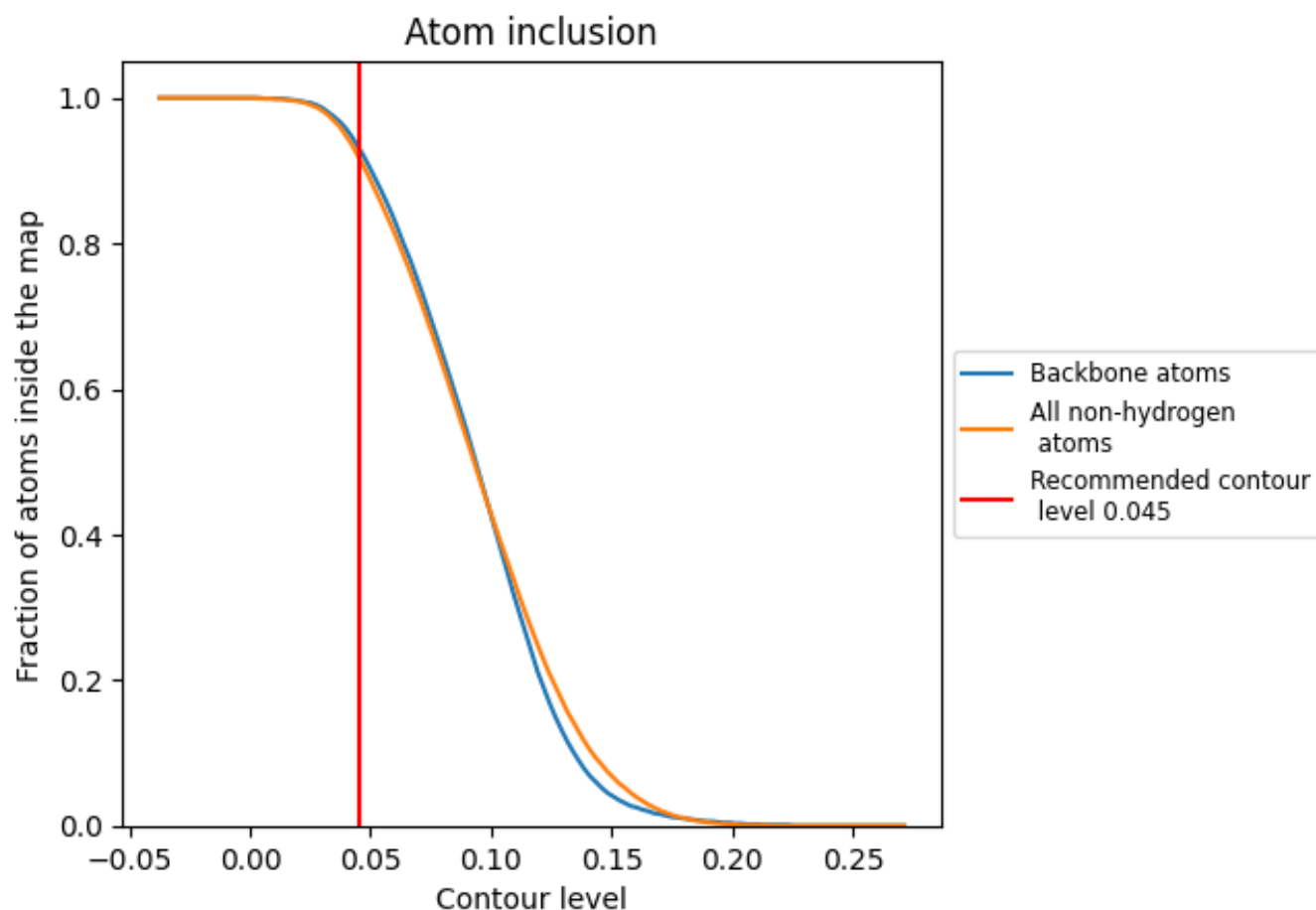
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.045).

9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 92% 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 (0.045) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9190	 0.5560
1	 0.9090	 0.5710
2	 0.8950	 0.5660
3	 0.9450	 0.6050
4	 0.3640	 0.2580
5	 0.9050	 0.6150
6	 0.7920	 0.5320
7	 0.9970	 0.6380
8	 0.9560	 0.6130
A	 0.9350	 0.5590
B	 0.9650	 0.5210
E	 0.9830	 0.6300
F	 0.9520	 0.6060
G	 0.9190	 0.5830
H	 0.8020	 0.4880
I	 0.5730	 0.3560
J	 0.6470	 0.4860
M	 0.9650	 0.6090
N	 0.9560	 0.6120
O	 0.9340	 0.6010
Q	 0.9750	 0.6240
R	 0.8690	 0.5240
S	 0.9400	 0.5910
T	 0.9700	 0.6140
U	 0.9290	 0.6130
V	 0.9830	 0.6220
W	 0.9350	 0.5970
X	 0.8650	 0.5640
Z	 0.9620	 0.5970
a	 0.9720	 0.5670
c	 0.2550	 0.3730
d	 0.7100	 0.4790
e	 0.8610	 0.5290
f	 0.8090	 0.5500
g	 0.8610	 0.5480



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Chain	Atom inclusion	Q-score
h	 0.8660	 0.5090
i	 0.9560	 0.5810
j	 0.8330	 0.4820
k	 0.6060	 0.4630
l	 0.9280	 0.5600
m	 0.9410	 0.5890
n	 0.8710	 0.5060
o	 0.6000	 0.4130
p	 0.9390	 0.5710
q	 0.8940	 0.5510
r	 0.9240	 0.5770
s	 0.9090	 0.5470
t	 0.8460	 0.5110
u	 0.9480	 0.5730
v	 0.9760	 0.5880
w	 0.8970	 0.5370